**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR0001 | DNA POLYMERASE III, beta subunit, DnaN | 0.978 | 0.323 | no | 2.707 | 0.452 | yes | 2.047 | 0.442 | yes | 1.542 | 0.349 | no | 1.110 | 0.285 | no | 0.885 | 0.428 | no | 0.811 | 0.260 | no | 0.769 | 0.219 | no | 0.974 | 0.293 | no |
| DR0002 | DnaA, AAA superfamily ATPase | 0.772 | 0.368 | no | 1.170 | 0.729 | no | 1.205 | 0.475 | no | 0.949 | 0.401 | no | 1.267 | 0.391 | no | 1.892 | 1.136 | yes | 1.502 | 0.676 | no | 1.328 | 0.285 | no | 1.324 | 0.477 | no |
| DR0003 | Predicted protein | 2.097 | 0.612 | yes | 10.192 | 4.542 | yes | 14.034 | 5.528 | yes | 8.012 | 2.856 | yes | 7.228 | 1.762 | yes | 5.504 | 3.816 | yes | 3.614 | 1.968 | yes | 1.534 | 0.674 | no | 0.679 | 0.241 | yes |
| DR0004 | MutT family hydrolase, 2 domains | 0.830 | 0.333 | no | 1.594 | 0.464 | yes | 1.437 | 0.487 | no | 0.793 | 0.303 | no | 0.847 | 0.365 | no | 1.090 | 0.430 | no | 0.834 | 0.436 | no | 0.752 | 0.107 | no | 0.598 | 0.134 | yes |
| DR0005 | HTH domain containing transcription regulator | 0.848 | 0.270 | no | 1.125 | 0.527 | no | 1.180 | 0.561 | no | 0.889 | 0.320 | no | 1.044 | 0.642 | no | 0.894 | 0.218 | no | 0.818 | 0.388 | no | 0.968 | 0.273 | no | 1.074 | 0.138 | no |
| DR0006 | Metallobetalactamase fold hydrolase | 0.900 | 0.265 | no | 0.977 | 0.462 | no | 0.953 | 0.429 | no | 0.978 | 0.406 | no | 1.555 | 0.603 | no | 1.138 | 0.339 | no | 1.469 | 0.599 | no | 1.426 | 0.140 | no | 2.657 | 0.331 | yes |
| DR0007 | Uncharacterized conserved protein | 1.023 | 0.500 | no | 3.927 | 2.693 | yes | 2.990 | 1.354 | yes | 1.386 | 0.484 | no | 1.730 | 0.868 | yes | 1.525 | 0.488 | no | 1.884 | 1.142 | yes | 1.166 | 0.334 | no | 1.781 | 1.100 | yes |
| DR0008 | Uncharacterized membrane protein | 1.007 | 0.279 | no | 3.930 | 1.828 | yes | 2.593 | 0.815 | yes | 1.517 | 0.641 | no | 1.642 | 0.760 | yes | 1.487 | 0.299 | no | 1.384 | 0.493 | no | 0.918 | 0.301 | no | 1.272 | 0.496 | no |
| DR0009 | Uncharacterized conserved protein, similar to fragment of VANW, ENTFA | 0.931 | 0.096 | no | 3.326 | 0.705 | yes | 2.894 | 0.812 | yes | 2.395 | 0.914 | yes | 2.425 | 1.480 | yes | 1.929 | 0.441 | yes | 1.736 | 0.402 | yes | 1.676 | 0.182 | yes | 1.391 | 0.234 | no |
| DR0011 | Oxidoreductase | 0.926 | 0.156 | no | 0.989 | 0.343 | no | 1.022 | 0.300 | no | 1.294 | 0.127 | no | 1.586 | 0.272 | yes | 1.597 | 0.056 | yes | 1.691 | 0.554 | yes | 1.567 | 0.320 | yes | 2.216 | 0.321 | yes |
| DR0012 | ParB/SP0J-like protein | 1.060 | 0.371 | no | 1.084 | 0.391 | no | 1.431 | 0.358 | no | 1.127 | 0.474 | no | 1.481 | 0.942 | no | 1.886 | 0.634 | yes | 1.195 | 0.614 | no | 1.021 | 0.306 | no | 1.117 | 0.592 | no |
| DR0013 | ParA/S0J-like protein, MIND family ATPase | 0.953 | 0.250 | no | 0.860 | 0.227 | no | 0.900 | 0.113 | no | 0.762 | 0.156 | no | 1.027 | 0.286 | no | 1.368 | 0.510 | no | 1.156 | 0.467 | no | 1.069 | 0.357 | no | 1.176 | 0.316 | no |
| DR0014 | Glucose-inhibited division protein, GIDB | 1.544 | 0.385 | yes | 1.914 | 0.503 | yes | 3.476 | 1.018 | yes | 3.309 | 0.469 | yes | 3.269 | 1.260 | yes | 2.567 | 0.468 | yes | 2.159 | 0.759 | yes | 1.532 | 0.447 | yes | 1.329 | 0.287 | no |
| DR0015 | Predicted protein | 1.278 | 0.291 | no | 1.771 | 0.478 | yes | 3.449 | 0.524 | yes | 3.068 | 0.265 | yes | 3.291 | 1.146 | yes | 3.172 | 0.872 | yes | 2.134 | 0.761 | yes | 1.647 | 0.449 | yes | 1.004 | 0.358 | no |
| DR0016 | NaMN\|DMB phosforibosyltransferase | 1.102 | 0.346 | no | 1.555 | 0.302 | yes | 2.102 | 0.327 | yes | 2.223 | 0.443 | yes | 1.977 | 0.529 | yes | 2.242 | 0.348 | yes | 1.836 | 0.471 | yes | 1.576 | 0.148 | yes | 1.202 | 0.149 | no |
| DR0017 | CobB/Sir2 transcriptional regulator, Uncharacterized conserved protein | 1.370 | 0.656 | no | 2.431 | 1.545 | yes | 4.059 | 1.525 | yes | 2.727 | 0.924 | yes | 3.713 | 1.143 | yes | 3.099 | 1.422 | yes | 2.769 | 0.621 | yes | 1.684 | 0.428 | yes | 0.847 | 0.289 | no |
| DR0018 | Predicted protein | 1.664 | 0.538 | yes | 2.454 | 1.209 | yes | 4.563 | 2.455 | yes | 3.458 | 1.430 | yes | 3.844 | 2.808 | yes | 4.031 | 1.872 | yes | 3.209 | 2.218 | yes | 2.061 | 0.880 | yes | 1.925 | 0.638 | yes |
| DR0019 | FTSZ fragment | 1.287 | 0.448 | no | 2.795 | 1.177 | yes | 4.818 | 2.015 | yes | 4.280 | 0.756 | yes | 4.310 | 1.486 | yes | 4.318 | 1.259 | yes | 3.500 | 0.957 | yes | 1.747 | 0.351 | yes | 1.284 | 0.364 | no |
| DR0020 | VacB type Ribonuclease | 1.063 | 0.433 | no | 0.935 | 0.368 | no | 1.276 | 0.230 | no | 1.258 | 0.475 | no | 1.596 | 1.178 | no | 1.494 | 0.573 | no | 1.419 | 0.614 | no | 1.150 | 0.080 | no | 0.921 | 0.125 | no |
| DR0021 | Predicted protein | 0.403 | 0.076 | yes | 0.404 | 0.136 | yes | 0.582 | 0.294 | yes | 0.585 | 0.187 | yes | 0.719 | 0.250 | no | 0.803 | 0.324 | no | 0.981 | 0.521 | no | 1.143 | 0.594 | no | 0.929 | 0.273 | no |
| DR0022 | Predicted uracil DNA glycosilase | 1.169 | 0.536 | no | 2.371 | 0.809 | yes | 3.329 | 0.872 | yes | 2.934 | 1.024 | yes | 2.634 | 1.288 | yes | 2.837 | 0.673 | yes | 2.685 | 0.848 | yes | 2.066 | 0.349 | yes | 1.413 | 0.189 | no |
| DR0023 | Phosphoribosylaminoimidazole carboxylase, PURE | 0.848 | 0.459 | no | 0.623 | 0.201 | yes | 0.891 | 0.377 | no | 0.501 | 0.053 | yes | 0.747 | 0.269 | no | 0.850 | 0.227 | no | 0.802 | 0.367 | no | 0.899 | 0.220 | no | 0.721 | 0.067 | no |
| DR0024 | Phosphoribosylaminoimidazole carboxylase, PURK | 0.881 | 0.082 | no | 1.181 | 0.287 | no | 2.153 | 0.993 | yes | 1.543 | 0.561 | no | 1.291 | 0.240 | no | 1.385 | 0.579 | no | 1.205 | 0.209 | no | 1.391 | 0.304 | no | 0.833 | 0.200 | no |
| DR0025 | Uncharacterized conserved protein, similar to fragment of VANW, ENTFA | 0.744 | 0.086 | no | 0.889 | 0.199 | no | 0.833 | 0.255 | no | 0.902 | 0.267 | no | 1.037 | 0.368 | no | 1.023 | 0.216 | no | 1.541 | 0.404 | yes | 1.573 | 0.394 | yes | 0.948 | 0.278 | no |
| DR0026 | SAM-methyltransferase, ubiE/GerC2/bioC-like | 1.223 | 0.334 | no | 2.971 | 1.627 | yes | 2.618 | 0.821 | yes | 2.927 | 0.428 | yes | 1.970 | 0.888 | yes | 1.651 | 0.512 | yes | 1.970 | 0.664 | yes | 1.980 | 0.363 | yes | 1.321 | 0.377 | no |
| DR0027 | Oxidoreductase, GIDA | 0.901 | 0.417 | no | 0.609 | 0.182 | yes | 0.474 | 0.098 | yes | 0.489 | 0.116 | yes | 0.676 | 0.209 | yes | 0.730 | 0.202 | no | 0.817 | 0.207 | no | 1.029 | 0.136 | no | 1.196 | 0.393 | no |
| DR0028 | NifS aminotransferase | 1.303 | 0.325 | no | 1.924 | 0.872 | yes | 1.920 | 0.432 | yes | 2.531 | 0.163 | yes | 1.715 | 0.446 | yes | 1.536 | 0.526 | no | 1.621 | 0.942 | no | 1.523 | 0.258 | yes | 1.481 | 0.454 | yes |
| DR0029 | 2-oxoisovalerate dehydrogenase, ODBA | 1.277 | 0.437 | no | 1.092 | 0.456 | no | 0.976 | 0.389 | no | 1.041 | 0.355 | no | 1.039 | 0.275 | no | 0.912 | 0.181 | no | 0.983 | 0.427 | no | 1.416 | 0.630 | no | 0.715 | 0.154 | no |
| DR0030 | 2-oxoisovalerate dehydrogenase, ODBB | 1.615 | 0.402 | yes | 1.625 | 0.792 | yes | 1.477 | 0.591 | no | 3.560 | 2.070 | yes | 1.339 | 0.715 | no | 1.802 | 0.769 | yes | 1.208 | 0.311 | no | 1.838 | 0.497 | yes | 0.713 | 0.347 | yes |
| DR0031 | Predicted protein | 0.984 | 0.353 | no | 1.158 | 0.722 | no | 1.732 | 0.882 | yes | 2.055 | 0.421 | yes | 0.958 | 0.306 | no | 1.104 | 0.219 | no | 1.122 | 0.453 | no | 2.845 | 1.300 | yes | 0.663 | 0.239 | yes |
| DR0032 | Dihydrolipoamide acetyltransferase E2, ODP2 | 1.223 | 0.658 | no | 0.806 | 0.266 | no | 1.716 | 0.849 | yes | 2.671 | 1.414 | yes | 2.172 | 1.208 | yes | 1.863 | 0.935 | yes | 1.519 | 0.504 | no | 2.537 | 0.359 | yes | 3.255 | 0.658 | yes |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR0033 | Cell-free protein synthesis inhibitor of YER057c/yjgF-family | 1.226 | 0.396 | no | 1.254 | 0.503 | no | 1.320 | 0.742 | no | 1.166 | 0.102 | no | 0.770 | 0.235 | no | 0.949 | 0.373 | no | 1.151 | 0.581 | no | 0.872 | 0.123 | no | 0.491 | 0.041 | yes |
| DR0034 | Predicted protein | 1.233 | 0.335 | no | 0.930 | 0.248 | no | 1.338 | 0.494 | no | 1.218 | 0.216 | no | 1.281 | 0.292 | no | 1.666 | 0.723 | yes | 1.968 | 1.240 | yes | 1.512 | 0.313 | yes | 1.151 | 0.544 | no |
| DR0035 | Adenylosuccinate synthase, PURA | 1.148 | 0.434 | no | 1.540 | 0.571 | yes | 1.080 | 0.479 | no | 0.783 | 0.255 | no | 0.871 | 0.337 | no | 1.537 | 0.796 | no | 1.242 | 0.496 | no | 1.319 | 0.148 | no | 0.489 | 0.073 | yes |
| DR0036 | Cyclohydrolase I, GCH1 | 0.875 | 0.142 | no | 1.600 | 0.518 | yes | 1.398 | 0.351 | no | 1.231 | 0.101 | no | 1.160 | 0.227 | no | 1.281 | 0.275 | no | 1.094 | 0.332 | no | 1.103 | 0.197 | no | 0.673 | 0.223 | no |
| DR0037 | Predicted protein | 1.041 | 0.487 | no | 1.594 | 0.409 | yes | 1.025 | 0.296 | no | 1.035 | 0.022 | no | 1.258 | 0.571 | no | 1.051 | 0.294 | no | 1.032 | 0.341 | no | 1.019 | 0.177 | no | 0.769 | 0.205 | no |
| DR0038 | Serine hydroxymethyltransferase, GLYA | 0.800 | 0.185 | no | 0.933 | 0.202 | no | 1.345 | 0.442 | no | 1.629 | 0.859 | no | 1.336 | 0.719 | no | 0.999 | 0.513 | no | 1.001 | 0.440 | no | 1.051 | 0.171 | no | 1.449 | 0.473 | no |
| DR0039 | Domain fusion: N-terminal GAF domain and C-terminal HD superfamily hydrolase | 1.058 | 0.606 | no | 0.734 | 0.334 | no | 0.507 | 0.128 | yes | 0.509 | 0.189 | yes | 0.632 | 0.211 | yes | 0.813 | 0.352 | no | 0.837 | 0.319 | no | 0.880 | 0.306 | no | 0.789 | 0.199 | no |
| DR0040 | Predicted protein | 0.891 | 0.179 | no | 0.727 | 0.232 | no | 0.553 | 0.211 | yes | 0.530 | 0.101 | yes | 0.603 | 0.294 | yes | 0.592 | 0.097 | yes | 0.526 | 0.123 | yes | 0.743 | 0.102 | no | 0.866 | 0.288 | no |
| DR0041 | Predicted protein | 0.954 | 0.500 | no | 0.512 | 0.257 | yes | 0.628 | 0.330 | yes | 0.883 | 0.371 | no | 1.024 | 0.370 | no | 0.978 | 0.200 | no | 1.006 | 0.361 | no | 1.033 | 0.246 | no | 1.551 | 0.926 | no |
| DR0042 | Predicted protein | 1.044 | 0.148 | no | 0.798 | 0.204 | no | 0.722 | 0.079 | no | 0.806 | 0.142 | no | 0.894 | 0.298 | no | 1.041 | 0.149 | no | 1.108 | 0.254 | no | 1.306 | 0.303 | no | 1.534 | 0.583 | yes |
| DR0043 | NH2- Acetyltransferase | 0.739 | 0.268 | no | 1.118 | 0.690 | no | 1.434 | 0.497 | no | 1.863 | 1.153 | no | 2.114 | 1.256 | yes | 1.161 | 0.608 | no | 1.538 | 0.336 | no | n/a | n/a | n/a | n/a | n/a | n/a |
| DR0044 | Muconate cycloisomerase II | 1.146 | 0.429 | no | 0.776 | 0.273 | no | 0.764 | 0.159 | no | 0.775 | 0.127 | no | 0.645 | 0.174 | yes | 0.800 | 0.244 | no | 0.839 | 0.233 | no | 0.777 | 0.044 | no | 0.727 | 0.085 | no |
| DR0045 | Uncharacterized conserved protein | 0.810 | 0.286 | no | 0.794 | 0.304 | no | 0.942 | 0.305 | no | 0.681 | 0.069 | no | 0.839 | 0.211 | no | 0.992 | 0.277 | no | 0.828 | 0.375 | no | 0.739 | 0.089 | no | 0.677 | 0.109 | no |
| DR0046 | L-rich repeats containing protein | 1.201 | 0.398 | no | 1.717 | 1.147 | yes | 1.631 | 0.622 | yes | 2.143 | 0.347 | yes | 1.413 | 0.500 | no | 1.683 | 0.995 | no | 1.559 | 0.408 | yes | 1.247 | 0.395 | no | 1.090 | 0.277 | no |
| DR0047 | Predicted protein | 1.349 | 0.688 | no | 1.944 | 0.740 | yes | 2.378 | 0.859 | yes | 2.478 | 1.398 | yes | 1.793 | 0.710 | yes | 1.970 | 0.391 | yes | 1.820 | 0.772 | yes | 1.143 | 0.244 | no | 0.612 | 0.178 | yes |
| DR0048 | Uncharacterized YCAP ortholog, membrane protein | 1.437 | 0.389 | no | 2.729 | 0.816 | yes | 3.848 | 1.149 | yes | 3.896 | 0.546 | yes | 2.934 | 1.041 | yes | 1.994 | 1.022 | yes | 1.555 | 0.545 | yes | 1.141 | 0.120 | no | 0.808 | 0.342 | no |
| DR0049 | SAM-dependent methyltransferase | 0.952 | 0.231 | no | 1.277 | 0.271 | no | 2.180 | 0.612 | yes | 1.638 | 0.300 | yes | 1.700 | 0.348 | yes | 1.640 | 0.745 | yes | 1.422 | 0.730 | no | 1.231 | 0.361 | no | 1.021 | 0.139 | no |
| DR0050 | DinB/YfiT family of proteins | 0.878 | 0.442 | no | 1.130 | 0.511 | no | 2.506 | 0.395 | yes | 3.837 | 0.930 | yes | 2.236 | 1.483 | yes | 1.590 | 0.368 | no | 0.804 | 0.125 | no | 1.248 | 0.692 | no | 1.063 | 0.394 | no |
| DR0051 | HesB family of small cysteine rich proteins | 1.365 | 0.585 | no | 2.203 | 0.772 | yes | 4.399 | 1.352 | yes | 5.929 | 3.319 | yes | 3.038 | 1.095 | yes | 2.003 | 0.722 | yes | 1.546 | 0.518 | yes | 1.274 | 0.217 | no | 1.697 | 0.700 | yes |
| DR0052 | Uncharacterized conserved protein, possible metal-binding enzyme | 1.091 | 0.341 | no | 2.813 | 0.711 | yes | 6.500 | 2.154 | yes | 5.828 | 1.070 | yes | 4.608 | 1.586 | yes | 2.774 | 0.752 | yes | 1.842 | 0.619 | yes | 1.326 | 0.177 | no | 0.959 | 0.204 | no |
| DR0053 | DinB/YfiT family of proteins | 1.667 | 0.631 | yes | 4.486 | 0.795 | yes | 10.162 | 4.536 | yes | 10.252 | 2.358 | yes | 6.102 | 2.297 | yes | 3.668 | 0.996 | yes | 2.296 | 0.811 | yes | 1.348 | 0.254 | no | 1.301 | 0.461 | no |
| DR0054 | Family of small proteins with a conserved cysteine | 1.249 | 0.569 | no | 0.770 | 0.230 | no | 1.018 | 0.282 | no | 1.074 | 0.058 | no | 1.639 | 1.212 | no | 1.397 | 0.262 | no | 1.359 | 0.368 | no | 1.765 | 0.748 | yes | 0.794 | 0.063 | no |
| DR0055 | HTH containing transcription factor | 1.089 | 0.237 | no | 1.017 | 0.195 | no | 0.826 | 0.261 | no | 0.805 | 0.240 | no | 1.074 | 0.447 | no | 1.071 | 0.223 | no | 0.942 | 0.262 | no | 0.885 | 0.240 | no | 0.889 | 0.046 | no |
| DR0056 | Benzoate permease | 2.318 | 1.281 | yes | 3.758 | 2.021 | yes | 1.962 | 0.892 | yes | 1.304 | 0.010 | no | 1.529 | 1.042 | no | 3.010 | 1.438 | yes | 0.978 | 0.492 | no | 1.261 | 0.561 | no | n/a | n/a | n/a |
| DR0057 | Glutaredoxin | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR0058 | PKN2 family serine/threonine kinase | 1.241 | 0.179 | no | 1.343 | 0.189 | no | 1.526 | 0.273 | yes | 1.632 | 0.174 | yes | 1.414 | 0.352 | no | 1.546 | 0.688 | no | 1.345 | 0.376 | no | 1.443 | 0.216 | no | 1.310 | 0.250 | no |
| DR0059 | Predicted protein | 0.780 | 0.232 | no | 0.964 | 0.263 | no | 1.071 | 0.419 | no | 0.844 | 0.062 | no | 1.106 | 0.428 | no | 0.941 | 0.242 | no | 0.815 | 0.213 | no | 0.892 | 0.176 | no | 0.592 | 0.126 | yes |
| DR0060 | Predicted protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR0061 | Predicted protein | 1.210 | 0.123 | no | 2.026 | 0.374 | yes | 1.736 | 0.315 | yes | 1.367 | 0.135 | no | 1.374 | 0.554 | no | 1.566 | 0.446 | yes | 1.639 | 0.408 | yes | 1.230 | 0.170 | no | 0.919 | 0.232 | no |
| DR0062 | ABC transporter ATPase | 1.051 | 0.572 | no | 0.795 | 0.261 | no | 0.755 | 0.282 | no | 0.545 | 0.141 | yes | 0.583 | 0.132 | yes | 0.893 | 0.409 | no | 0.873 | 0.289 | no | 0.884 | 0.104 | no | 0.940 | 0.202 | no |
| DR0063 | DegV like protein | 0.935 | 0.290 | no | 0.770 | 0.308 | no | 0.472 | 0.136 | yes | 0.362 | 0.186 | yes | 0.428 | 0.137 | yes | 0.537 | 0.239 | yes | 0.592 | 0.285 | yes | 0.653 | 0.078 | yes | 0.593 | 0.122 | yes |
| DR0064 | Biotin synthetase family of metal cluster enzymes | 0.688 | 0.298 | no | 0.175 | 0.092 | yes | 0.092 | 0.050 | yes | 0.107 | 0.034 | yes | 0.099 | 0.042 | yes | 0.173 | 0.067 | yes | 0.144 | 0.071 | yes | 0.216 | 0.097 | yes | 0.429 | 0.185 | yes |
| DR0065 | Superfamily II helicase with a C terminal metal rich cluster, probably Arch/eukaryotic origin | 1.053 | 0.108 | no | 1.016 | 0.251 | no | 0.808 | 0.229 | no | 0.891 | 0.157 | no | 0.807 | 0.149 | no | 0.890 | 0.281 | no | 0.881 | 0.287 | no | 0.861 | 0.143 | no | 0.860 | 0.153 | no |
| DR0066 | Antibiotic kinaseII | 1.099 | 0.481 | no | 1.011 | 0.440 | no | 0.965 | 0.549 | no | 0.583 | 0.011 | yes | 0.629 | 0.200 | yes | 0.765 | 0.210 | no | 0.558 | 0.122 | yes | 0.904 | 0.277 | no | 0.792 | 0.282 | no |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR0067 | Predicted protein | 0.849 | 0.145 | no | 0.619 | 0.227 | yes | 0.439 | 0.155 | yes | 0.302 | 0.065 | yes | 0.389 | 0.075 | yes | 0.427 | 0.135 | yes | 0.560 | 0.196 | yes | 0.621 | 0.126 | yes | 0.689 | 0.117 | no |
| DR0068 | Predicted protein | 0.627 | 0.347 | yes | 0.715 | 0.313 | yes | 0.926 | 0.232 | no | 0.429 | 0.196 | yes | 0.638 | 0.158 | yes | 0.599 | 0.201 | yes | 0.697 | 0.242 | yes | 0.708 | 0.153 | yes | 0.622 | 0.163 | yes |
| DR0069 | Predicted protein | 1.104 | 0.150 | no | 1.312 | 0.296 | no | 1.373 | 0.235 | no | 1.173 | 0.491 | no | 1.029 | 0.324 | no | 1.204 | 0.584 | no | 0.992 | 0.532 | no | 0.992 | 0.291 | no | 0.879 | 0.348 | no |
| DR0070 | Possible alkaline protease (expressed only under alkaline conditions) | 1.139 | 0.657 | no | 1.491 | 0.376 | no | 3.346 | 1.024 | yes | 2.967 | 1.038 | yes | 2.833 | 1.988 | yes | 3.889 | 1.718 | yes | 3.560 | 1.254 | yes | 0.881 | 0.180 | no | 0.160 | 0.015 | yes |
| DR0071 | Parvulin family peptidyl-prolyl isomerase, PRTM | 0.798 | 0.192 | no | 3.253 | 2.105 | yes | 2.667 | 0.514 | yes | 3.397 | 1.400 | yes | 2.543 | 1.617 | yes | 2.266 | 0.768 | yes | 2.172 | 1.021 | yes | 1.885 | 0.445 | yes | 1.339 | 0.619 | no |
| DR0072 | Predicted protein | 0.804 | 0.361 | no | 0.875 | 0.378 | no | 1.209 | 0.799 | no | 0.666 | 0.237 | no | 0.853 | 0.355 | no | 0.892 | 0.255 | no | 0.861 | 0.494 | no | 0.872 | 0.100 | no | 0.591 | 0.159 | yes |
| DR0073 | Phosphate acetyltransferase | 1.175 | 0.640 | no | 1.036 | 0.298 | no | 1.263 | 0.704 | no | 1.219 | 0.582 | no | 0.928 | 0.523 | no | 0.889 | 0.266 | no | 0.826 | 0.448 | no | 0.804 | 0.282 | no | 0.699 | 0.333 | yes |
| DR0074 | HTH transcriptional regulator, TTK-like | 0.885 | 0.316 | no | 1.095 | 0.244 | no | 0.954 | 0.269 | no | 0.695 | 0.138 | no | 0.690 | 0.173 | no | 0.812 | 0.199 | no | 1.117 | 0.279 | no | 1.078 | 0.124 | no | 0.952 | 0.325 | no |
| DR0075 | Conserved membrane protein with low complexity regions | 0.997 | 0.209 | no | 0.769 | 0.212 | no | 0.548 | 0.126 | yes | 0.569 | 0.019 | yes | 0.616 | 0.178 | yes | 0.909 | 0.237 | no | 0.920 | 0.263 | no | 0.978 | 0.276 | no | 1.720 | 0.488 | yes |
| DR0076 | MoeA ortholog, Molybdopterin biosynthesis | 1.669 | 0.930 | no | 1.391 | 0.418 | no | 2.679 | 0.882 | yes | 0.848 | 0.301 | no | 3.536 | 2.514 | yes | 0.940 | 0.159 | no | 1.649 | 0.765 | yes | 1.429 | 0.652 | no | 0.430 | 0.294 | yes |
| DR0077 | Shikimate dehydrogenase related protein | 1.100 | 0.350 | no | 1.172 | 0.463 | no | 1.092 | 0.329 | no | 0.944 | 0.290 | no | 0.874 | 0.394 | no | 1.063 | 0.433 | no | 1.144 | 0.416 | no | 1.100 | 0.211 | no | 0.903 | 0.262 | no |
| DR0078 | N-acetylglutamate semialdehyde reductase, ArgC | 0.845 | 0.235 | no | 0.779 | 0.239 | no | 0.768 | 0.179 | no | 0.802 | 0.349 | no | 0.999 | 0.220 | no | 1.143 | 0.261 | no | 1.279 | 0.428 | no | 1.333 | 0.177 | no | 1.146 | 0.130 | no |
| DR0079 | MutT family pyrophosphohydrolase | 1.024 | 0.265 | no | 0.980 | 0.166 | no | 0.754 | 0.159 | no | 0.754 | 0.198 | no | 0.741 | 0.107 | no | 0.766 | 0.147 | no | 0.773 | 0.204 | no | 0.863 | 0.192 | no | 0.975 | 0.137 | no |
| DR0080 | Ornithine carbamoyltransferase | 0.996 | 0.243 | no | 0.644 | 0.103 | yes | 0.632 | 0.145 | yes | 0.549 | 0.115 | yes | 0.619 | 0.163 | yes | 0.819 | 0.210 | no | 0.902 | 0.244 | no | 1.043 | 0.252 | no | 1.018 | 0.145 | no |
| DR0081 | Conserved protein of PIG-L family | 0.940 | 0.128 | no | 0.844 | 0.202 | no | 0.734 | 0.221 | no | 0.712 | 0.077 | no | 0.747 | 0.116 | no | 0.775 | 0.186 | no | 0.873 | 0.190 | no | 0.977 | 0.165 | no | 1.045 | 0.233 | no |
| DR0082 | Predicted protein | 0.699 | 0.118 | no | 0.675 | 0.289 | yes | 0.639 | 0.262 | yes | 0.603 | 0.325 | yes | 0.486 | 0.173 | yes | 0.606 | 0.157 | yes | 0.832 | 0.296 | no | 0.857 | 0.201 | no | 0.748 | 0.091 | no |
| DR0083 | Dihydrolipoamide succinyltransferase | 1.283 | 0.871 | no | 0.465 | 0.114 | yes | 0.440 | 0.129 | yes | 0.481 | 0.129 | yes | 0.556 | 0.281 | yes | 0.822 | 0.129 | no | 0.885 | 0.211 | no | 1.388 | 0.220 | no | 1.933 | 0.311 | yes |
| DR0084 | OBG family GTPase | 0.848 | 0.148 | no | 1.442 | 0.525 | no | 1.712 | 0.612 | yes | 1.672 | 0.389 | yes | 1.980 | 0.973 | yes | 1.528 | 0.567 | no | 1.356 | 0.446 | no | 1.371 | 0.142 | no | 1.030 | 0.342 | no |
| DR0085 | Ribosomal protein L27 | 1.007 | 0.197 | no | 0.963 | 0.098 | no | 1.160 | 0.248 | no | 1.385 | 0.345 | no | 1.594 | 0.678 | yes | 1.135 | 0.461 | no | 0.972 | 0.189 | no | 0.999 | 0.219 | no | 0.997 | 0.203 | no |
| DR0086 | Ribosomal protein L21, RL21 | 0.832 | 0.264 | no | 0.718 | 0.262 | no | 0.956 | 0.404 | no | 0.755 | 0.149 | no | 0.906 | 0.243 | no | 1.270 | 0.874 | no | 1.171 | 0.603 | no | 1.076 | 0.192 | no | 0.984 | 0.290 | no |
| DR0087 | Conserved proteins with C2C2 fingers, YBAD -like | 0.914 | 0.235 | no | 0.958 | 0.151 | no | 1.026 | 0.347 | no | 1.061 | 0.524 | no | 1.063 | 0.341 | no | 1.359 | 0.638 | no | 1.156 | 0.405 | no | 1.340 | 0.334 | no | 1.202 | 0.227 | no |
| DR0088 | Oxido-reductase | 0.870 | 0.366 | no | 0.717 | 0.229 | no | 0.754 | 0.204 | no | 0.627 | 0.068 | yes | 0.836 | 0.517 | no | 0.919 | 0.203 | no | 0.912 | 0.286 | no | 1.214 | 0.150 | no | 1.154 | 0.166 | no |
| DR0089 | Glycosyltransferase | 1.249 | 0.258 | no | 1.531 | 0.458 | yes | 1.722 | 0.549 | yes | 1.490 | 0.076 | no | 1.275 | 0.230 | no | 1.716 | 1.121 | yes | 1.440 | 0.609 | no | 1.553 | 0.592 | yes | 1.293 | 0.237 | no |
| DR0090 | 0-acyltransferase PLSC/PLSB family | 1.068 | 0.387 | no | 1.022 | 0.273 | no | 0.870 | 0.217 | no | 0.697 | 0.193 | no | 0.861 | 0.295 | no | 1.087 | 0.301 | no | 1.145 | 0.370 | no | 1.383 | 0.401 | no | 1.127 | 0.204 | no |
| DR0091 | Conserved membrane protein | 1.258 | 0.274 | no | 1.416 | 0.320 | yes | 1.212 | 0.340 | no | 1.284 | 0.441 | no | 1.246 | 0.477 | no | 1.079 | 0.290 | no | 1.184 | 0.283 | no | 1.142 | 0.300 | no | 1.163 | 0.323 | no |
| DR0092 | MutT hydrolase domain | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR0093 | Rossmann fold oxidoreductase | 1.134 | 0.338 | no | 1.040 | 0.185 | no | 1.294 | 0.587 | no | 1.309 | 0.445 | no | 1.635 | 0.155 | yes | 1.330 | 0.256 | no | 1.227 | 0.194 | no | 0.981 | 0.342 | no | 0.649 | 0.238 | yes |
| DR0094 | Predicted protein | 1.114 | 0.252 | no | 0.996 | 0.235 | no | 0.808 | 0.197 | no | 0.872 | 0.156 | no | 0.760 | 0.218 | no | 0.942 | 0.312 | no | 1.260 | 0.308 | no | 1.281 | 0.283 | no | 1.840 | 0.668 | yes |
| DR0095 | ABC Transporter with ATPase domain | 1.125 | 0.410 | no | 1.513 | 0.384 | yes | 1.701 | 0.606 | yes | 2.000 | 0.826 | yes | 1.457 | 0.410 | no | 1.924 | 0.687 | yes | 1.603 | 0.862 | no | 1.989 | 0.477 | yes | 1.420 | 0.186 | no |
| DR0096 | ABC Transporter with ATPase domain | 1.178 | 0.420 | no | 1.717 | 0.847 | yes | 2.065 | 0.672 | yes | 3.492 | 1.930 | yes | 2.050 | 1.389 | yes | 1.770 | 0.686 | yes | 1.734 | 0.739 | yes | 1.300 | 0.267 | no | 1.254 | 0.222 | no |
| DR0097 | Uncharacterized homolog of Rv2825c/Rv2828c | 0.794 | 0.190 | no | 1.476 | 0.209 | yes | 1.553 | 0.917 | no | 1.548 | 0.363 | no | 0.812 | 0.481 | no | 1.826 | 0.539 | yes | 1.526 | 0.459 | yes | 1.527 | 0.532 | yes | 1.157 | 0.170 | no |
| DR0098 | Ribosomal protein S6 | 0.794 | 0.174 | no | 1.513 | 0.371 | yes | 2.115 | 0.778 | yes | 1.512 | 0.642 | no | 1.976 | 1.273 | yes | 2.087 | 0.732 | yes | 2.493 | 1.376 | yes | 2.724 | 1.182 | yes | 1.474 | 0.586 | no |
| DR0099 | SsDNA binding protein (ssb) | 0.907 | 0.320 | no | 3.010 | 1.198 | yes | 2.905 | 1.150 | yes | 1.578 | 0.302 | no | 2.488 | 1.317 | yes | 2.332 | 1.358 | yes | 2.906 | 1.214 | yes | 2.627 | 0.458 | yes | 1.360 | 0.511 | no |
| DR0101 | Ribosomal protein S18 | 0.743 | 0.288 | no | 4.145 | 1.934 | yes | 3.804 | 2.070 | yes | 3.280 | 0.992 | yes | 3.294 | 2.342 | yes | 2.305 | 1.555 | yes | 2.296 | 0.999 | yes | 2.147 | 0.757 | yes | 1.625 | 1.031 | yes |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR0102 | Ribosomal protein L9 | 0.878 | 0.210 | no | 3.777 | 1.704 | yes | 3.408 | 1.370 | yes | 1.989 | 0.557 | yes | 3.024 | 1.279 | yes | 2.554 | 1.495 | yes | 2.363 | 1.195 | yes | 2.284 | 0.920 | yes | 1.229 | 0.386 | no |
| DR0103 | Metal binding protein, HIS diad | 0.995 | 0.349 | no | 6.331 | 2.766 | yes | 6.460 | 4.019 | yes | 3.363 | 0.336 | yes | 2.589 | 0.443 | yes | 1.824 | 0.208 | yes | 1.473 | 0.541 | no | 1.317 | 0.431 | no | 0.802 | 0.229 | no |
| DR0104 | HTH transcriptonal regulator | 0.951 | 0.281 | no | 2.477 | 0.410 | yes | 2.354 | 0.974 | yes | 2.152 | 1.276 | yes | 1.957 | 1.141 | yes | 1.457 | 0.243 | no | 1.080 | 0.293 | no | 1.122 | 0.147 | no | 0.905 | 0.263 | no |
| DR0105 | LEA76 family desiccation resistance protein | 1.109 | 0.283 | no | 3.111 | 0.933 | yes | 2.514 | 0.824 | yes | 2.248 | 0.824 | yes | 2.084 | 0.390 | yes | 3.716 | 1.448 | yes | 5.750 | 2.257 | yes | 5.272 | 1.004 | yes | 2.403 | 0.755 | yes |
| DR0106 | Conserved membrane protein | 0.987 | 0.223 | no | 2.055 | 0.619 | yes | 1.789 | 0.569 | yes | 1.472 | 0.112 | no | 1.467 | 0.404 | no | 1.377 | 0.471 | no | 1.598 | 0.369 | yes | 1.690 | 0.438 | yes | 1.364 | 0.351 | no |
| DR0107 | Conserved membrane protein, YDHE-like | 1.026 | 0.332 | no | 1.352 | 0.320 | no | 1.212 | 0.567 | no | 0.851 | 0.137 | no | 0.994 | 0.223 | no | 1.166 | 0.232 | no | 1.299 | 0.318 | no | 1.267 | 0.122 | no | 1.031 | 0.214 | no |
| DR0108 | Conserved membrane protein, transporter | 1.047 | 0.150 | no | 1.625 | 0.443 | yes | 1.748 | 0.401 | yes | 1.729 | 0.254 | yes | 1.641 | 0.614 | yes | 1.587 | 0.359 | yes | 1.322 | 0.502 | no | 1.273 | 0.169 | no | 1.180 | 0.322 | no |
| DR0109 | Glyoxalase/Dioxygenase family protein | 1.295 | 0.469 | no | 1.249 | 0.512 | no | 1.208 | 0.716 | no | 0.762 | 0.410 | no | 1.235 | 0.534 | no | 1.195 | 0.180 | no | 1.605 | 0.609 | yes | 1.206 | 0.324 | no | 0.884 | 0.195 | no |
| DR0110 | Conserved protein of YBGI family | 0.843 | 0.132 | no | 0.522 | 0.115 | yes | 0.491 | 0.170 | yes | 0.491 | 0.098 | yes | 0.526 | 0.044 | yes | 0.568 | 0.168 | yes | 0.565 | 0.104 | yes | 0.850 | 0.109 | no | 1.034 | 0.171 | no |
| DR0111 | Thymidylate kinase, KTHY | 0.877 | 0.341 | no | 0.850 | 0.208 | no | 1.087 | 0.633 | no | 0.784 | 0.350 | no | 0.828 | 0.213 | no | 0.867 | 0.253 | no | 0.809 | 0.202 | no | 0.821 | 0.202 | no | 0.647 | 0.318 | yes |
| DR0112 | Ortholog of plant protein, claimed to be glutamine cyclotransferase | 1.043 | 0.282 | no | 0.920 | 0.223 | no | 0.964 | 0.224 | no | 0.850 | 0.201 | no | 1.047 | 0.151 | no | 1.320 | 0.583 | no | 1.446 | 0.542 | no | 1.523 | 0.187 | yes | 1.336 | 0.206 | no |
| DR0113 | Oxidoreductase | 0.948 | 0.425 | no | 0.744 | 0.209 | no | 0.764 | 0.249 | no | 0.689 | 0.330 | yes | 0.817 | 0.353 | no | 0.839 | 0.187 | no | 0.810 | 0.248 | no | 1.347 | 0.397 | no | 0.963 | 0.192 | no |
| DR0114 | Enoyl-CoA hydratase | 0.933 | 0.324 | no | 0.653 | 0.308 | yes | 0.470 | 0.189 | yes | 0.385 | 0.162 | yes | 0.401 | 0.070 | yes | 0.522 | 0.251 | yes | 0.654 | 0.411 | yes | 0.919 | 0.471 | no | 1.399 | 0.379 | no |
| DR0115 | S-layer protein | 0.936 | 0.504 | no | 0.418 | 0.195 | yes | 0.263 | 0.065 | yes | 0.370 | 0.183 | yes | 0.418 | 0.178 | yes | 0.653 | 0.139 | yes | 1.136 | 0.442 | no | 1.464 | 0.105 | yes | 2.622 | 0.887 | yes |
| DR0116 | Predicted protein | 0.926 | 0.308 | no | 0.592 | 0.234 | yes | 0.545 | 0.234 | yes | 0.830 | 0.003 | no | 0.734 | 0.406 | yes | 0.874 | 0.380 | no | 1.383 | 0.510 | no | 1.806 | 0.436 | yes | 2.810 | 0.710 | yes |
| DR0117 | Biotin carboxylase | 0.924 | 0.314 | no | 0.741 | 0.321 | no | 0.920 | 0.327 | no | 0.995 | 0.192 | no | 1.060 | 0.500 | no | 0.849 | 0.454 | no | 0.923 | 0.420 | no | 1.472 | 0.211 | yes | 1.142 | 0.465 | no |
| DR0118 | Biotin carboxyl carrier protein | 0.974 | 0.281 | no | 0.775 | 0.274 | no | 0.712 | 0.132 | no | 0.796 | 0.049 | no | 0.736 | 0.183 | no | 0.778 | 0.171 | no | 0.854 | 0.217 | no | 1.304 | 0.065 | no | 1.095 | 0.180 | no |
| DR0119 | Elongation factor P | 0.938 | 0.403 | no | 0.658 | 0.234 | yes | 0.797 | 0.321 | no | 0.708 | 0.316 | no | 0.895 | 0.630 | no | 0.936 | 0.419 | no | 1.159 | 0.434 | no | 1.566 | 0.292 | yes | 1.729 | 0.364 | yes |
| DR0120 | SMF protein, DNA processing chain A dprA | 1.676 | 0.923 | no | 1.388 | 0.573 | no | 1.099 | 0.544 | no | 1.666 | 1.115 | no | 1.351 | 0.603 | no | 0.825 | 0.223 | no | 1.199 | 0.641 | no | 1.066 | 0.130 | no | 1.182 | 0.478 | no |
| DR0121 | Contains TPR-like repeats | 1.515 | 0.504 | no | 0.809 | 0.365 | no | 0.746 | 0.359 | yes | 1.198 | 0.146 | no | 0.795 | 0.321 | no | 0.796 | 0.374 | no | 1.240 | 0.685 | no | 1.624 | 0.344 | yes | 0.872 | 0.402 | no |
| DR0122 | PMGI fragment? | 1.219 | 0.615 | no | 1.358 | 0.352 | no | 1.670 | 0.676 | yes | 1.666 | 0.573 | yes | 1.618 | 1.134 | no | 1.216 | 0.219 | no | 1.332 | 0.536 | no | 1.293 | 0.170 | no | 0.844 | 0.163 | no |
| DR0123 | Phosphoribosylanthranilate isomerase | 1.156 | 0.324 | no | 0.794 | 0.251 | no | 0.563 | 0.172 | yes | 0.501 | 0.113 | yes | 0.579 | 0.173 | yes | 0.892 | 0.514 | no | 0.869 | 0.375 | no | 0.701 | 0.200 | yes | 0.875 | 0.249 | no |
| DR0124 | Predicted protein | 1.342 | 0.660 | no | 1.497 | 0.991 | no | 1.041 | 0.469 | no | 1.638 | 1.122 | no | 0.914 | 0.323 | no | 0.724 | 0.114 | no | 0.939 | 0.419 | no | 0.939 | 0.175 | no | 0.967 | 0.247 | no |
| DR0125 | NH2 acetyltransferase | 1.173 | 0.190 | no | 1.125 | 0.410 | no | 0.821 | 0.176 | no | 0.699 | 0.251 | no | 0.736 | 0.243 | no | 0.786 | 0.255 | no | 0.923 | 0.324 | no | 0.871 | 0.223 | no | 1.001 | 0.366 | no |
| DR0127 | Ankyrin repeats related protein | 0.868 | 0.265 | no | 0.856 | 0.180 | no | 0.563 | 0.224 | yes | 0.246 | 0.079 | yes | 0.335 | 0.129 | yes | 0.481 | 0.183 | yes | 0.575 | 0.183 | yes | 0.611 | 0.233 | yes | 0.944 | 0.295 | no |
| DR0128 | Chaperonin GrpE, HSP20 | 1.253 | 0.830 | no | 1.113 | 0.682 | no | 0.578 | 0.369 | yes | 0.518 | 0.154 | yes | 0.375 | 0.175 | yes | 0.465 | 0.143 | yes | 0.671 | 0.283 | yes | 0.527 | 0.155 | yes | 0.880 | 0.296 | no |
| DR0129 | DNAK/Hsp70 | 1.387 | 0.568 | no | 1.232 | 0.353 | no | 0.705 | 0.235 | yes | 0.577 | 0.226 | yes | 0.686 | 0.402 | yes | 0.704 | 0.282 | no | 1.121 | 0.442 | no | 0.869 | 0.285 | no | 1.496 | 0.411 | yes |
| DR0130 | Coproporphyrinogen III oxidase HemN, metal dependent enzyme | 1.353 | 0.609 | no | 1.051 | 0.314 | no | 0.878 | 0.234 | no | 0.867 | 0.277 | no | 0.637 | 0.291 | yes | 0.611 | 0.139 | yes | 0.866 | 0.263 | no | 0.847 | 0.206 | no | 0.795 | 0.168 | no |
| DR0131 | Predicted protein (low complexity) | 0.964 | 0.374 | no | 0.657 | 0.144 | yes | 0.415 | 0.144 | yes | 0.518 | 0.190 | yes | 0.579 | 0.184 | yes | 0.700 | 0.248 | no | 0.923 | 0.348 | no | 1.257 | 0.552 | no | 0.762 | 0.176 | no |
| DR0132 | Uncracterized conserved protein, pvdS ortholog | 1.304 | 0.258 | no | 0.873 | 0.252 | no | 0.551 | 0.104 | yes | 0.757 | 0.062 | no | 0.928 | 0.236 | no | 1.589 | 0.660 | yes | 2.379 | 0.641 | yes | 3.033 | 0.720 | yes | 1.699 | 0.382 | yes |
| DR0133 | Lipase, a/b superfamily hydrolase | 1.336 | 0.102 | no | 1.083 | 0.191 | no | 0.870 | 0.435 | no | 0.946 | 0.297 | no | 0.742 | 0.240 | no | 0.826 | 0.281 | no | 0.845 | 0.293 | no | 0.951 | 0.240 | no | 0.804 | 0.097 | no |
| DR0134 | YIIM family of bacterial proteins | 1.643 | 0.551 | yes | 1.377 | 0.472 | no | 1.293 | 0.574 | no | 1.031 | 0.202 | no | 0.690 | 0.122 | no | 0.940 | 0.498 | no | 1.008 | 0.449 | no | 0.966 | 0.299 | no | 0.965 | 0.503 | no |
| DR0135 | Conserved membrane protein | 1.103 | 0.177 | no | 1.223 | 0.179 | no | 0.843 | 0.243 | no | 0.857 | 0.083 | no | 0.863 | 0.229 | no | 1.048 | 0.153 | no | 0.868 | 0.082 | no | 1.057 | 0.189 | no | 0.849 | 0.191 | no |

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| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR0136 | Glutaredoxin family redox enzyme, ArsC arsenate reductase ortholog | 1.091 | 0.432 | no | 1.121 | 0.365 | no | 0.906 | 0.203 | no | 0.943 | 0.301 | no | 0.976 | 0.451 | no | 0.951 | 0.128 | no | 0.879 | 0.245 | no | 0.940 | 0.050 | no | 0.841 | 0.108 | no |
| DR0137 | Uncharacterized conserved protein | 1.167 | 0.325 | no | 1.395 | 0.482 | no | 1.283 | 0.532 | no | 0.960 | 0.357 | no | 0.956 | 0.424 | no | 0.991 | 0.214 | no | 1.013 | 0.279 | no | 1.122 | 0.254 | no | 0.961 | 0.242 | no |
| DR0138 | Membrane protein, similar to slr0686 of Synechocystis | 0.973 | 0.375 | no | 1.796 | 0.784 | yes | 1.224 | 0.333 | no | 1.328 | 0.535 | no | 1.094 | 0.355 | no | 0.722 | 0.201 | no | 0.790 | 0.079 | no | 0.719 | 0.051 | no | 0.558 | 0.131 | yes |
| DR0139 | OBG family GTPase | 1.071 | 0.198 | no | 0.573 | 0.103 | yes | 0.404 | 0.077 | yes | 0.442 | 0.081 | yes | 0.522 | 0.168 | yes | 0.786 | 0.224 | no | 0.913 | 0.195 | no | 0.796 | 0.197 | no | 1.046 | 0.234 | no |
| DR0140 | Predicted protein | 1.404 | 0.751 | no | 4.745 | 3.091 | yes | 6.443 | 2.873 | yes | 5.793 | 3.171 | yes | 4.080 | 1.163 | yes | 1.676 | 0.858 | no | 2.248 | 1.504 | yes | 1.609 | 0.583 | yes | 0.796 | 0.249 | no |
| DR0143 | Predicted protein | 1.447 | 0.521 | no | 2.721 | 0.692 | yes | 2.414 | 0.452 | yes | 3.188 | 0.541 | yes | 2.339 | 0.634 | yes | 1.713 | 0.614 | yes | 1.523 | 0.533 | no | 1.266 | 0.644 | no | 1.210 | 0.496 | no |
| DR0144 | Transposase | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR0145 | Uncharacterized protein | 1.471 | 0.552 | no | 1.197 | 0.462 | no | 1.598 | 0.690 | yes | 1.274 | 0.380 | no | 1.431 | 0.624 | no | 1.347 | 0.614 | no | 0.773 | 0.349 | no | 0.871 | 0.124 | no | 1.519 | 0.522 | yes |
| DR0146 | Family of metal binding hydrolases of the TIM barrel fold | 1.606 | 0.344 | yes | 1.802 | 0.802 | yes | 1.807 | 0.938 | yes | 1.234 | 0.394 | no | 0.985 | 0.305 | no | 1.238 | 0.728 | no | 1.332 | 0.359 | no | 1.206 | 0.308 | no | 1.170 | 0.535 | no |
| DR0147 | Predicted protein | 1.582 | 0.868 | no | 1.246 | 0.592 | no | 1.537 | 1.007 | no | 1.826 | 0.662 | yes | 1.667 | 0.929 | no | 1.320 | 0.569 | no | 1.096 | 0.456 | no | 1.179 | 0.535 | no | 1.117 | 0.485 | no |
| DR0148 | Valyl tRNA synthetase, class I | 0.953 | 0.184 | no | 0.790 | 0.121 | no | 1.098 | 0.245 | no | 1.048 | 0.124 | no | 1.055 | 0.249 | no | 1.288 | 0.348 | no | 1.314 | 0.549 | no | 1.301 | 0.224 | no | 1.517 | 0.231 | yes |
| DR0149 | MutT family hydrolase | 1.288 | 0.674 | no | 0.855 | 0.110 | no | 1.150 | 0.339 | no | 1.348 | 0.710 | no | 0.984 | 0.285 | no | 1.117 | 0.229 | no | 1.183 | 0.614 | no | 1.172 | 0.228 | no | 1.288 | 0.285 | no |
| DR0150 | Oligopeptidase B, PTRB | 1.016 | 0.331 | no | 0.611 | 0.239 | yes | 0.316 | 0.062 | yes | 0.370 | 0.150 | yes | 0.339 | 0.077 | yes | 0.506 | 0.135 | yes | 0.496 | 0.198 | yes | 0.573 | 0.184 | yes | 0.595 | 0.139 | yes |
| DR0151 | NifS-like protein | 1.303 | 0.554 | no | 0.820 | 0.324 | no | 0.305 | 0.122 | yes | 0.454 | 0.288 | yes | 0.311 | 0.060 | yes | 0.388 | 0.135 | yes | 0.411 | 0.121 | yes | 0.517 | 0.150 | yes | 0.421 | 0.127 | yes |
| DR0152 | Predicted decarboxylase from acetoacetate decarboxylase family | 1.140 | 0.260 | no | 0.398 | 0.115 | yes | 0.174 | 0.066 | yes | 0.161 | 0.046 | yes | 0.185 | 0.085 | yes | 0.207 | 0.055 | yes | 0.303 | 0.154 | yes | 0.409 | 0.100 | yes | 0.624 | 0.202 | yes |
| DR0153 | Riboflavin Deaminase, RibD | 0.937 | 0.312 | no | 1.001 | 0.327 | no | 0.699 | 0.304 | yes | 1.473 | 0.957 | no | 1.352 | 0.966 | no | 0.822 | 0.245 | no | 0.834 | 0.460 | no | 0.741 | 0.187 | no | 0.986 | 0.290 | no |
| DR0154 | Riboflavin synthase alpha chain, RisA | 1.072 | 0.206 | no | 1.162 | 0.277 | no | 1.362 | 0.336 | no | 1.420 | 0.345 | no | 1.452 | 0.779 | no | 1.249 | 0.230 | no | 1.173 | 0.450 | no | 0.845 | 0.120 | no | 0.898 | 0.201 | no |
| DR0155 | GTP cyclohydrolase II, GCH2 | 1.171 | 0.644 | no | 1.419 | 0.471 | no | 1.255 | 0.601 | no | 1.412 | 0.603 | no | 1.154 | 0.417 | no | 1.079 | 0.198 | no | 1.054 | 0.453 | no | 0.834 | 0.168 | no | 1.252 | 0.222 | no |
| DR0156 | Riboflavin synthase beta subunit, RisB | 1.035 | 0.372 | no | 1.328 | 0.150 | no | 1.269 | 0.185 | no | 1.007 | 0.040 | no | 1.134 | 0.253 | no | 1.189 | 0.144 | no | 1.037 | 0.151 | no | 0.968 | 0.240 | no | 1.388 | 0.377 | no |
| DR0157 | Predicted protein | 1.321 | 0.637 | no | 2.075 | 1.195 | yes | 1.746 | 0.497 | yes | 1.504 | 0.581 | no | 2.392 | 1.895 | yes | 2.080 | 0.667 | yes | 1.520 | 0.592 | no | 1.308 | 0.303 | no | 1.163 | 0.315 | no |
| DR0158 | Leucine dehydrogenase | 1.352 | 0.277 | no | 0.941 | 0.222 | no | 0.677 | 0.085 | yes | 0.556 | 0.176 | yes | 0.624 | 0.232 | yes | 0.763 | 0.261 | no | 0.741 | 0.299 | no | 0.775 | 0.204 | no | 1.119 | 0.069 | no |
| DR0159 | Uridine kinase, URK | 1.214 | 0.442 | no | 0.963 | 0.217 | no | 0.982 | 0.270 | no | 0.857 | 0.363 | no | 0.726 | 0.254 | no | 0.900 | 0.171 | no | 0.849 | 0.258 | no | 0.895 | 0.088 | no | 1.058 | 0.148 | no |
| DR0160 | Conserved membrane protein | 0.778 | 0.244 | no | 3.080 | 0.619 | yes | 3.899 | 0.861 | yes | 2.755 | 0.731 | yes | 2.362 | 0.761 | yes | 1.956 | 0.526 | yes | 1.380 | 0.621 | no | 1.049 | 0.119 | no | 0.733 | 0.241 | no |
| DR0161 | AMSJ/WCAK related protein, possibly involved in biosyntesis of exopolysaccharide | 1.032 | 0.475 | no | 5.974 | 1.973 | yes | 8.116 | 4.070 | yes | 4.422 | 1.803 | yes | 3.097 | 1.287 | yes | 2.927 | 0.842 | yes | 2.049 | 0.729 | yes | 1.777 | 0.472 | yes | 1.157 | 0.375 | no |
| DR0162 | Predicted protein | 0.852 | 0.282 | no | 1.644 | 0.510 | yes | 1.771 | 0.613 | yes | 1.166 | 0.424 | no | 1.251 | 0.600 | no | 1.275 | 0.412 | no | 0.995 | 0.226 | no | 1.030 | 0.199 | no | 0.877 | 0.124 | no |
| DR0163 | ABC transporter with ATPase domain | 1.193 | 0.537 | no | 2.724 | 0.983 | yes | 2.768 | 0.515 | yes | 2.365 | 0.580 | yes | 1.705 | 0.573 | yes | 1.699 | 0.292 | yes | 1.316 | 0.338 | no | 0.986 | 0.086 | no | 0.698 | 0.097 | no |
| DR0164 | Similar to pseudomonas protein claimed to be endo alpha-1,4 polygalactosaminidase | 1.347 | 0.230 | no | 1.748 | 0.642 | yes | 2.333 | 0.784 | yes | 1.656 | 0.403 | yes | 1.554 | 0.845 | no | 1.228 | 0.542 | no | 1.040 | 0.451 | no | 1.078 | 0.196 | no | 1.019 | 0.330 | no |
| DR0165 | Peptidase of the a/b hydrolase fold + regulatory beta propeller domain | 1.314 | 0.370 | no | 1.153 | 0.424 | no | 1.518 | 0.913 | no | 1.215 | 0.324 | no | 0.911 | 0.398 | no | 1.192 | 0.358 | no | 1.197 | 0.507 | no | 1.231 | 0.111 | no | 0.875 | 0.150 | no |
| DR0166 | Acyl-CoA-binding protein | 1.325 | 0.477 | no | 1.223 | 0.474 | no | 1.064 | 0.490 | no | 1.116 | 0.354 | no | 1.360 | 0.498 | no | 1.702 | 0.520 | yes | 2.258 | 1.531 | yes | 1.938 | 0.175 | yes | 2.208 | 0.961 | yes |
| DR0167 | HxxxH (metal binding) motif containing protein | 1.079 | 0.527 | no | 1.487 | 0.550 | yes | 1.455 | 0.560 | no | 1.141 | 0.440 | no | 0.972 | 0.390 | no | 0.988 | 0.355 | no | 0.877 | 0.256 | no | 1.028 | 0.179 | no | 0.939 | 0.243 | no |
| DR0168 | Dihydropteroate synthase, DHPS | 1.089 | 0.198 | no | 0.696 | 0.208 | no | 0.604 | 0.168 | yes | 0.781 | 0.155 | no | 0.724 | 0.231 | no | 0.989 | 0.247 | no | 0.984 | 0.297 | no | 0.985 | 0.323 | no | 0.965 | 0.276 | no |
| DR0169 | Dihydroneopterin aldolase, DHNA, FolB | 1.141 | 0.284 | no | 1.756 | 0.293 | yes | 1.516 | 0.307 | yes | 1.994 | 0.295 | yes | 1.184 | 0.313 | no | 1.239 | 0.304 | no | 1.267 | 0.426 | no | 1.070 | 0.291 | no | 0.962 | 0.294 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR0170 | 6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase, HPPK | 1.497 | 0.657 | no | 1.400 | 0.604 | no | 1.374 | 0.532 | no | 1.175 | 0.502 | no | 1.209 | 0.495 | no | 1.256 | 0.577 | no | 1.238 | 0.404 | no | 1.112 | 0.249 | no | 1.219 | 0.438 | no |
| DR0171 | HTH transcriptional regulator | 1.528 | 0.643 | no | 3.254 | 1.837 | yes | 3.353 | 1.211 | yes | 2.928 | 0.317 | yes | 2.116 | 1.071 | yes | 1.545 | 0.161 | yes | 1.331 | 0.457 | no | 1.021 | 0.092 | no | 0.667 | 0.097 | no |
| DR0172 | Metalo beta lactamase fold hydrolase | 1.164 | 0.459 | no | 1.744 | 0.498 | yes | 1.928 | 0.762 | yes | 1.113 | 0.334 | no | 1.265 | 0.366 | no | 1.249 | 0.376 | no | 0.836 | 0.363 | no | 0.890 | 0.140 | no | 0.843 | 0.152 | no |
| DR0174 | Ribosomal protein L13 | 0.512 | 0.109 | yes | 0.987 | 0.247 | no | 1.442 | 0.171 | yes | 1.073 | 0.302 | no | 1.401 | 0.406 | no | 1.582 | 0.625 | no | 1.780 | 0.803 | yes | 1.835 | 0.689 | yes | 0.917 | 0.463 | no |
| DR0175 | Ribosomal protein S9 | 0.675 | 0.351 | yes | 1.143 | 0.571 | no | 1.829 | 0.651 | yes | 1.676 | 0.902 | no | 1.508 | 0.361 | yes | 1.456 | 0.446 | no | 1.590 | 0.669 | yes | 1.463 | 0.643 | no | 0.851 | 0.396 | no |
| DR0176 | Penicillin-binding protein, D-alanyl-D-alanine carboxypeptidase | 0.927 | 0.175 | no | 0.934 | 0.223 | no | 0.883 | 0.156 | no | 0.715 | 0.073 | no | 0.806 | 0.204 | no | 0.817 | 0.162 | no | 0.711 | 0.282 | yes | 0.687 | 0.210 | yes | 1.008 | 0.310 | no |
| DR0177 | Transposon DORF | 2.553 | 0.470 | yes | 1.487 | 0.752 | no | 2.115 | 0.958 | yes | 1.962 | 0.372 | yes | 0.949 | 0.258 | no | 1.913 | 1.204 | yes | 2.288 | 1.559 | yes | 1.098 | 0.306 | no | 2.617 | 0.932 | yes |
| DR0178 | Transposon DORF | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR0179 | HAM1-like, NTP pyrophosphatase | 1.161 | 0.319 | no | 0.964 | 0.168 | no | 0.844 | 0.230 | no | 0.888 | 0.139 | no | 1.097 | 0.398 | no | 1.227 | 0.461 | no | 1.246 | 0.497 | no | 1.091 | 0.122 | no | 1.026 | 0.194 | no |
| DR0180 | Sigma factor Sigma E | 1.185 | 0.557 | no | 1.380 | 0.735 | no | 1.761 | 1.018 | yes | 1.835 | 0.931 | yes | 2.040 | 0.920 | yes | 1.485 | 0.624 | no | 1.022 | 0.156 | no | 1.292 | 0.128 | no | 0.956 | 0.187 | no |
| DR0181 | Predicted protein | 1.382 | 0.620 | no | 1.845 | 0.823 | yes | 2.053 | 0.889 | yes | 1.640 | 0.107 | yes | 1.778 | 0.624 | yes | 1.446 | 0.589 | no | 1.279 | 0.777 | no | 0.956 | 0.175 | no | 0.770 | 0.102 | no |
| DR0182 | Glutamate synthase small subunit | 1.345 | 0.223 | no | 2.671 | 1.290 | yes | 4.127 | 1.924 | yes | 5.859 | 3.856 | yes | 3.853 | 2.565 | yes | 2.127 | 0.786 | yes | 1.462 | 0.930 | no | 1.480 | 0.775 | no | 2.221 | 0.912 | yes |
| DR0183 | Glutamate synthase large subunit | 1.297 | 0.455 | no | 1.563 | 0.584 | yes | 1.555 | 0.537 | yes | 2.226 | 1.241 | yes | 1.873 | 0.988 | yes | 1.607 | 0.444 | yes | 1.441 | 0.283 | no | 1.572 | 0.706 | yes | 2.959 | 1.736 | yes |
| DR0184 | Enoyl-CoA hydratase | 1.479 | 0.396 | no | 1.593 | 0.433 | yes | 1.502 | 0.627 | no | 1.631 | 0.655 | no | 1.175 | 0.485 | no | 1.333 | 0.372 | no | 1.031 | 0.593 | no | 1.034 | 0.140 | no | 0.994 | 0.133 | no |
| DR0185 | Conserved membrane protein, MJ1523-like | 1.227 | 0.463 | no | 1.540 | 0.907 | no | 1.070 | 0.395 | no | 1.012 | 0.232 | no | 0.758 | 0.393 | no | 0.932 | 0.438 | no | 1.249 | 0.872 | no | 0.757 | 0.167 | no | 0.642 | 0.210 | yes |
| DR0186 | Exonuclease VII, large subunit, xseA | 1.221 | 0.601 | no | 1.922 | 0.510 | yes | 2.191 | 0.830 | yes | 1.838 | 0.666 | yes | 1.383 | 0.633 | no | 1.206 | 0.121 | no | 1.135 | 0.269 | no | 1.040 | 0.254 | no | 0.979 | 0.239 | no |
| DR0187 | SanA family of bacterial proteins | 1.230 | 0.497 | no | 0.975 | 0.310 | no | 0.760 | 0.152 | no | 0.540 | 0.170 | yes | 0.573 | 0.329 | yes | 0.962 | 0.472 | no | 0.625 | 0.320 | yes | 0.718 | 0.161 | yes | 0.574 | 0.173 | yes |
| DR0188 | NH2-acetyltransferase | 1.233 | 0.364 | no | 0.998 | 0.412 | no | 0.663 | 0.210 | yes | 0.744 | 0.430 | no | 0.817 | 0.610 | no | 0.601 | 0.189 | yes | 0.724 | 0.193 | no | 0.649 | 0.090 | yes | 0.794 | 0.252 | no |
| DR0189 | DSBA like thioredoxin fold protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR0190 | HTPX superfamily Metalloprotease | 0.909 | 0.127 | no | 0.535 | 0.057 | yes | 0.418 | 0.040 | yes | 0.315 | 0.026 | yes | 0.444 | 0.171 | yes | 0.682 | 0.301 | yes | 0.701 | 0.284 | yes | 0.776 | 0.151 | no | 0.834 | 0.211 | no |
| DR0191 | Glycogen debranching enzyme | 1.359 | 0.732 | no | 1.210 | 0.587 | no | 1.100 | 0.220 | no | 1.231 | 0.464 | no | 1.229 | 0.281 | no | 1.318 | 0.644 | no | 1.188 | 0.347 | no | 0.867 | 0.314 | no | 0.702 | 0.284 | no |
| DR0192 | MutT family hydrolase | 0.791 | 0.260 | no | 0.316 | 0.105 | yes | 0.132 | 0.056 | yes | 0.065 | 0.013 | yes | 0.134 | 0.086 | yes | 0.261 | 0.127 | yes | 0.355 | 0.114 | yes | 0.297 | 0.119 | yes | 0.445 | 0.079 | yes |
| DR0193 | Small membrane protein from predominantly archaeal/eukaryotic family | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR0194 | Predicted HTPX superfamily Metalloprotease, Bacillus yugP ortholog | 1.565 | 0.929 | no | 1.172 | 0.320 | no | 1.120 | 0.487 | no | 0.756 | 0.179 | no | 0.716 | 0.239 | no | 0.784 | 0.449 | no | 1.192 | 0.374 | no | 0.857 | 0.194 | no | 1.149 | 0.293 | no |
| DR0195 | Aminotransferase, possible ADC LYASE | 1.256 | 0.177 | no | 1.171 | 0.278 | no | 1.272 | 0.333 | no | 1.057 | 0.309 | no | 1.071 | 0.433 | no | 1.157 | 0.480 | no | 0.896 | 0.225 | no | 0.933 | 0.050 | no | 0.888 | 0.314 | no |
| DR0196 | Anthranilate synthase fusion of components I and II | 1.245 | 0.273 | no | 1.627 | 0.721 | yes | 1.362 | 0.429 | no | 1.836 | 0.902 | yes | 1.664 | 1.283 | no | 1.189 | 0.442 | no | 1.313 | 0.638 | no | 1.008 | 0.191 | no | 0.772 | 0.217 | no |
| DR0197 | NH2 acetyltransferase | 1.193 | 0.270 | no | 1.034 | 0.234 | no | 1.100 | 0.233 | no | 1.073 | 0.300 | no | 0.932 | 0.285 | no | 1.395 | 0.520 | no | 1.256 | 0.483 | no | 1.247 | 0.213 | no | 1.562 | 0.506 | yes |
| DR0198 | RecR ptotein (HhH +C4 + degenerate Toprim protein) | 1.024 | 0.306 | no | 0.805 | 0.118 | no | 0.943 | 0.154 | no | 1.063 | 0.099 | no | 0.922 | 0.269 | no | 0.777 | 0.151 | no | 0.875 | 0.093 | no | 1.025 | 0.294 | no | 1.024 | 0.203 | no |
| DR0199 | Uncharacterized small conserved protein, YBAB_ECOLI family | 0.940 | 0.229 | no | 0.742 | 0.244 | no | 0.638 | 0.230 | yes | 0.821 | 0.120 | no | 0.836 | 0.237 | no | 0.800 | 0.247 | no | 0.772 | 0.255 | no | 0.901 | 0.110 | no | 1.048 | 0.355 | no |
| DR0200 | HTH transcription factor, LRP family of proteins | 1.519 | 0.795 | no | 1.771 | 0.829 | yes | 1.486 | 0.503 | no | 1.986 | 1.071 | yes | 1.517 | 0.716 | no | 1.285 | 0.566 | no | 1.037 | 0.349 | no | 1.134 | 0.095 | no | 0.756 | 0.105 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR0201 | Uncharacterized conserved protein | 1.102 | 0.220 | no | 0.839 | 0.252 | no | 0.855 | 0.226 | no | 1.163 | 0.246 | no | 1.212 | 0.393 | no | 1.844 | 0.770 | yes | 1.999 | 0.428 | yes | 1.886 | 0.150 | yes | 0.921 | 0.161 | no |
| DR0202 | P-loop ATPase | 1.239 | 0.701 | no | 1.376 | 0.435 | no | 1.795 | 0.900 | yes | 1.967 | 0.595 | yes | 1.456 | 0.581 | no | 1.439 | 0.353 | no | 1.521 | 0.558 | no | 1.326 | 0.075 | no | 0.880 | 0.287 | no |
| DR0203 | Membrane protein, similar to gi\|1653436 of Synechocystis | 1.492 | 0.479 | no | 1.514 | 0.680 | no | 3.819 | 0.856 | yes | 3.760 | 1.151 | yes | 2.740 | 0.992 | yes | 1.890 | 0.415 | yes | 1.706 | 0.701 | yes | 1.361 | 0.455 | no | 0.770 | 0.063 | no |
| DR0204 | Membrane protein, similar to gi\|1653967 of Synechocystis | 1.542 | 0.822 | no | 4.114 | 2.730 | yes | 4.833 | 1.051 | yes | 6.010 | 1.353 | yes | 4.754 | 2.526 | yes | 2.452 | 0.656 | yes | 2.092 | 1.059 | yes | 1.502 | 0.376 | yes | 0.921 | 0.079 | no |
| DR0205 | ABC transporter ATPase | 1.281 | 0.313 | no | 1.990 | 0.648 | yes | 3.705 | 1.906 | yes | 4.104 | 2.452 | yes | 2.987 | 1.217 | yes | 2.375 | 0.975 | yes | 2.321 | 0.710 | yes | 1.172 | 0.269 | no | 0.849 | 0.104 | no |
| DR0206 | Predicted protein | 1.503 | 0.547 | no | 3.212 | 1.735 | yes | 4.248 | 1.758 | yes | 5.452 | 2.648 | yes | 3.165 | 1.231 | yes | 1.721 | 0.625 | yes | 1.627 | 0.798 | yes | 1.217 | 0.166 | no | 0.870 | 0.115 | no |
| DR0207 | ComEA related protein, secreted | 2.138 | 0.948 | yes | 2.829 | 1.149 | yes | 10.889 | 6.028 | yes | 15.471 | 10.313 | yes | 12.405 | 8.329 | yes | 3.856 | 2.064 | yes | 3.866 | 2.099 | yes | 1.866 | 0.504 | yes | 1.350 | 0.269 | no |
| DR0208 | Predicted protein | 1.255 | 0.471 | no | 1.053 | 0.556 | no | 1.144 | 0.395 | no | 1.298 | 0.587 | no | 1.115 | 0.671 | no | 1.273 | 0.580 | no | 1.184 | 0.754 | no | 0.895 | 0.137 | no | 0.876 | 0.257 | no |
| DR0209 | GidA Rossman fold oxidoreductase | 1.052 | 0.411 | no | 0.609 | 0.163 | yes | 0.746 | 0.132 | no | 0.891 | 0.103 | no | 0.855 | 0.254 | no | 1.077 | 0.180 | no | 0.791 | 0.160 | no | 1.012 | 0.057 | no | 0.919 | 0.108 | no |
| DR0210 | Conserved membrane protein, releated to SANA protein family | 1.243 | 0.410 | no | 1.210 | 0.558 | no | 1.776 | 0.472 | yes | 2.109 | 0.428 | yes | 1.718 | 1.103 | no | 1.513 | 0.850 | no | 0.948 | 0.321 | no | 1.102 | 0.125 | no | 0.964 | 0.283 | no |
| DR0211 | Conserved membrane protein | 1.301 | 0.646 | no | 1.054 | 0.358 | no | 1.244 | 0.659 | no | 1.271 | 0.489 | no | 1.463 | 0.612 | no | 1.320 | 0.469 | no | 1.004 | 0.163 | no | 0.814 | 0.086 | no | 0.655 | 0.041 | no |
| DR0212 | Predicted protein | 1.096 | 0.292 | no | 0.603 | 0.225 | yes | 0.508 | 0.258 | yes | 0.686 | 0.157 | no | 0.526 | 0.088 | yes | 0.529 | 0.184 | yes | 0.552 | 0.163 | yes | 0.667 | 0.168 | yes | 0.624 | 0.189 | yes |
| DR0213 | NH2 acetyltransferase | 0.846 | 0.271 | no | 0.364 | 0.110 | yes | 0.478 | 0.351 | yes | 1.424 | 0.409 | no | 0.863 | 0.692 | yes | 0.632 | 0.294 | yes | 1.266 | 0.548 | no | 0.974 | 0.422 | no | 0.645 | 0.219 | yes |
| DR0214 | Predicted protein | 0.977 | 0.419 | no | 0.578 | 0.163 | yes | 0.424 | 0.143 | yes | 0.307 | 0.112 | yes | 0.462 | 0.153 | yes | 0.419 | 0.075 | yes | 0.553 | 0.132 | yes | 0.416 | 0.089 | yes | 0.523 | 0.152 | yes |
| DR0215 | NIfS family of Aminotransferase | 0.938 | 0.154 | no | 0.988 | 0.191 | no | 0.710 | 0.102 | no | 0.812 | 0.233 | no | 0.912 | 0.196 | no | 1.090 | 0.201 | no | 0.899 | 0.210 | no | 0.896 | 0.130 | no | 1.149 | 0.421 | no |
| DR0216 | Uncharacterized YNHA ortholog; small bacterial proteins | 0.962 | 0.188 | no | 0.550 | 0.307 | yes | 0.506 | 0.174 | yes | 0.895 | 0.125 | no | 0.957 | 0.315 | no | 0.884 | 0.241 | no | 0.973 | 0.394 | no | 0.919 | 0.211 | no | 1.519 | 0.208 | yes |
| DR0217 | Thiosulfate sulfurtransferase Rhodanese superfamily enzyme | 0.750 | 0.222 | no | 0.736 | 0.225 | no | 1.296 | 0.491 | no | 1.123 | 0.138 | no | 1.722 | 0.488 | yes | 1.953 | 0.768 | yes | 1.511 | 0.418 | no | 2.173 | 0.618 | yes | 4.795 | 0.782 | yes |
| DR0218 | Predicted protein | 1.145 | 0.517 | no | 0.608 | 0.102 | yes | 0.541 | 0.070 | yes | 0.704 | 0.234 | no | 0.776 | 0.190 | no | 0.546 | 0.074 | yes | 0.663 | 0.157 | yes | 0.606 | 0.149 | yes | 0.895 | 0.163 | no |
| DR0219 | Predicted protein | 1.176 | 0.837 | no | 2.689 | 1.683 | yes | 2.113 | 0.901 | yes | 8.479 | 1.675 | yes | 7.752 | 5.456 | yes | 2.009 | 1.087 | yes | 2.266 | 1.767 | yes | 3.099 | 1.291 | yes | 2.652 | 1.203 | yes |
| DR0220 | Amidophosphoribosyltransferase | 1.043 | 0.170 | no | 1.390 | 0.270 | no | 1.510 | 0.474 | yes | 1.619 | 0.496 | no | 1.563 | 0.555 | yes | 1.423 | 0.252 | no | 1.345 | 0.168 | no | 1.296 | 0.175 | no | 1.304 | 0.156 | no |
| DR0221 | Homolog of HPAII repair protein uncharacterized YCJD ortholog; small conserved bacterial proteins | 1.261 | 0.377 | no | 1.519 | 0.237 | yes | 1.939 | 0.493 | yes | 1.942 | 0.810 | yes | 1.942 | 0.968 | yes | 1.548 | 0.470 | no | 1.699 | 0.340 | yes | 1.561 | 0.402 | yes | 1.685 | 0.296 | yes |
| DR0222 | Phosphoribosylformylglycinamidine synthase large subunit | 0.861 | 0.128 | no | 0.997 | 0.179 | no | 0.977 | 0.156 | no | 0.817 | 0.193 | no | 0.857 | 0.215 | no | 0.758 | 0.088 | no | 0.646 | 0.128 | yes | 0.722 | 0.155 | yes | 0.624 | 0.112 | yes |
| DR0223 | Phosphoribosylformylglycinamidine synthase small subunit | 1.152 | 0.250 | no | 1.105 | 0.386 | no | 1.486 | 0.336 | yes | 1.684 | 0.334 | yes | 1.396 | 0.353 | no | 1.243 | 0.215 | no | 1.102 | 0.358 | no | 1.182 | 0.237 | no | 1.171 | 0.217 | no |
| DR0224 | Uncharacterized conserved protein | 1.012 | 0.185 | no | 1.185 | 0.275 | no | 1.571 | 0.633 | yes | 2.244 | 0.905 | yes | 1.840 | 0.343 | yes | 1.686 | 0.640 | yes | 1.364 | 0.505 | no | 1.549 | 0.687 | yes | 1.454 | 0.229 | yes |
| DR0225 | Predicted protein | 1.122 | 0.351 | no | 1.661 | 0.707 | yes | 2.434 | 0.844 | yes | 3.106 | 0.400 | yes | 3.018 | 1.358 | yes | 1.991 | 1.220 | yes | 2.459 | 1.329 | yes | 1.519 | 0.682 | no | 2.223 | 0.745 | yes |
| DR0226 | Phosphoribosylaminoimidazolesuccinocarboxamide synthase | 0.680 | 0.038 | no | 1.044 | 0.262 | no | 1.326 | 0.319 | no | 1.204 | 0.133 | no | 1.387 | 0.468 | no | 1.074 | 0.175 | no | 0.964 | 0.297 | no | 1.001 | 0.133 | no | 1.513 | 0.175 | yes |
| DR0227 | Predicted protein | 0.924 | 0.229 | no | 1.104 | 0.294 | no | 0.674 | 0.203 | yes | 0.639 | 0.157 | yes | 0.911 | 0.368 | no | 0.951 | 0.309 | no | 1.280 | 0.269 | no | 0.966 | 0.212 | no | 0.812 | 0.225 | no |
| DR0228 | Uncharacterized APAG ortholog | 0.984 | 0.328 | no | 0.755 | 0.136 | no | 0.627 | 0.168 | yes | 0.521 | 0.243 | yes | 0.688 | 0.127 | no | 0.847 | 0.090 | no | 0.947 | 0.278 | no | 1.068 | 0.148 | no | 1.281 | 0.256 | no |
| DR0229 | Endo-1,4-beta-glucanase | 0.793 | 0.188 | no | 0.461 | 0.097 | yes | 0.452 | 0.146 | yes | 0.394 | 0.118 | yes | 0.594 | 0.191 | yes | 0.880 | 0.313 | no | 0.914 | 0.318 | no | 1.135 | 0.189 | no | 1.449 | 0.359 | no |
| DR0230 | Therpenoid biosynthesis enzyme, YgbB ortholog | 0.846 | 0.453 | no | 0.668 | 0.187 | yes | 0.483 | 0.239 | yes | 0.523 | 0.209 | yes | 0.613 | 0.302 | yes | 0.778 | 0.192 | no | 0.780 | 0.287 | no | 0.994 | 0.443 | no | 0.962 | 0.291 | no |
| DR0231 | SPOU family rRNA methylase | 0.963 | 0.435 | no | 0.601 | 0.322 | yes | 0.557 | 0.248 | yes | 0.513 | 0.212 | yes | 0.500 | 0.177 | yes | 0.655 | 0.164 | yes | 0.693 | 0.287 | yes | 0.837 | 0.151 | no | 0.965 | 0.048 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR0232 | Predicted protein | 0.730 | 0.138 | no | 0.761 | 0.205 | no | 0.961 | 0.299 | no | 1.005 | 0.152 | no | 1.198 | 0.437 | no | 1.360 | 0.563 | no | 1.249 | 0.416 | no | 1.266 | 0.277 | no | 0.880 | 0.231 | no |
| DR0233 | HTH transcriptional regulator of ArsR family | 1.234 | 0.456 | no | 1.138 | 0.399 | no | 1.764 | 0.631 | yes | 2.488 | 1.226 | yes | 1.836 | 0.384 | yes | 1.527 | 0.750 | no | 1.148 | 0.405 | no | 1.101 | 0.324 | no | 0.850 | 0.360 | no |
| DR0234 | Conserved domain (in some organism fused to transcription regulator of ArsR family) | 0.880 | 0.267 | no | 1.016 | 0.412 | no | 1.239 | 0.426 | no | 1.355 | 0.509 | no | 1.789 | 0.756 | yes | 1.328 | 0.369 | no | 1.229 | 0.437 | no | 1.199 | 0.288 | no | 0.998 | 0.332 | no |
| DR0235 | Amidase | 1.306 | 0.359 | no | 1.185 | 0.353 | no | 1.161 | 0.470 | no | 1.114 | 0.152 | no | 1.029 | 0.294 | no | 1.193 | 0.205 | no | 1.464 | 0.396 | no | 1.138 | 0.174 | no | 1.272 | 0.158 | no |
| DR0236 | Aminopeptidase T | 0.667 | 0.286 | yes | 0.729 | 0.108 | no | 1.188 | 0.730 | no | 0.829 | 0.109 | no | 0.885 | 0.327 | no | 1.019 | 0.355 | no | 1.099 | 0.357 | no | 1.998 | 0.673 | yes | n/a | n/a | n/a |
| DR0237 | Cyclophilin, peptidyl-prolyl isomerase | 1.143 | 0.581 | no | 0.570 | 0.236 | yes | 0.897 | 0.343 | no | 1.357 | 0.483 | no | 1.880 | 0.825 | yes | 2.655 | 0.562 | yes | 3.269 | 0.804 | yes | 4.434 | 1.042 | yes | 4.234 | 0.472 | yes |
| DR0239 | Predicted protein | 0.724 | 0.181 | no | 1.016 | 0.391 | no | 1.205 | 0.289 | no | 1.464 | 0.319 | no | 1.543 | 0.530 | yes | 1.487 | 0.177 | no | 1.476 | 0.339 | no | 1.777 | 0.256 | yes | 2.157 | 0.752 | yes |
| DR0240 | HAD superfamily hydrolase | 0.966 | 0.361 | no | 1.231 | 0.524 | no | 1.235 | 0.564 | no | 0.950 | 0.109 | no | 1.234 | 0.181 | no | 1.420 | 0.780 | no | 1.531 | 0.687 | no | 1.472 | 0.722 | no | 0.780 | 0.301 | no |
| DR0241 | Predicted protein | 1.414 | 0.930 | no | 1.969 | 0.712 | yes | 1.712 | 0.627 | yes | 2.089 | 1.129 | yes | 1.755 | 0.669 | yes | 1.286 | 0.611 | no | 1.743 | 0.564 | yes | 1.595 | 0.304 | yes | 1.307 | 0.352 | no |
| DR0242 | Uncharacterized conserved, possible enzyme | 1.067 | 0.319 | no | 1.313 | 0.339 | no | 1.296 | 0.295 | no | 1.644 | 0.781 | no | 1.734 | 0.696 | yes | 1.188 | 0.198 | no | 1.581 | 0.452 | yes | 1.298 | 0.362 | no | 0.760 | 0.111 | no |
| DR0243 | Arginine decarboxylase | 1.051 | 0.281 | no | 0.937 | 0.156 | no | 0.849 | 0.183 | no | 0.830 | 0.095 | no | 0.869 | 0.313 | no | 0.785 | 0.130 | no | 0.990 | 0.213 | no | 1.261 | 0.209 | no | 1.049 | 0.255 | no |
| DR0244 | NH2-Acetyltransferase | 0.911 | 0.364 | no | 1.390 | 0.491 | no | 1.541 | 0.444 | yes | 1.169 | 0.020 | no | 1.080 | 0.277 | no | 1.332 | 0.508 | no | 1.343 | 0.605 | no | 1.225 | 0.426 | no | 0.789 | 0.253 | no |
| DR0245 | Protoporphyrinogen oxidase, HemK | 0.985 | 0.187 | no | 1.063 | 0.186 | no | 1.057 | 0.148 | no | 1.062 | 0.121 | no | 1.141 | 0.199 | no | 1.062 | 0.174 | no | 0.895 | 0.280 | no | 1.006 | 0.170 | no | 0.880 | 0.157 | no |
| DR0246 | Jag protein, SpoIIIJ-associated | 0.617 | 0.199 | yes | 0.721 | 0.327 | yes | 0.504 | 0.149 | yes | 0.491 | 0.029 | yes | 0.579 | 0.108 | yes | 0.804 | 0.422 | no | 0.890 | 0.417 | no | 0.918 | 0.108 | no | 0.933 | 0.114 | no |
| DR0247 | Acyl-carrier Protein Synthase | 1.233 | 0.591 | no | 2.323 | 1.131 | yes | 2.075 | 0.506 | yes | 2.037 | 0.279 | yes | 1.926 | 0.901 | yes | 1.780 | 1.209 | no | 1.784 | 0.709 | yes | 2.295 | 0.977 | yes | 1.124 | 0.215 | no |
| DR0248 | Fusion small nucleotidyltransferase-like gene with uncharacterized protein, usually next to it in other species | 0.662 | 0.257 | yes | 0.885 | 0.607 | no | 0.659 | 0.348 | yes | 0.498 | 0.319 | yes | 0.501 | 0.212 | yes | 0.841 | 0.366 | no | 0.810 | 0.273 | no | 0.871 | 0.173 | no | n/a | n/a | n/a |
| DR0249 | Oxidoreductase | 1.125 | 0.358 | no | 1.051 | 0.412 | no | 0.926 | 0.381 | no | 0.827 | 0.243 | no | 0.852 | 0.247 | no | 0.838 | 0.270 | no | 1.024 | 0.442 | no | 0.899 | 0.073 | no | 1.074 | 0.152 | no |
| DR0250 | Probable ribose/galactose ABC transporter, permease protein | 0.927 | 0.164 | no | 0.756 | 0.099 | no | 0.788 | 0.113 | no | 0.645 | 0.043 | no | 0.745 | 0.229 | no | 1.196 | 0.513 | no | 1.196 | 0.350 | no | 1.316 | 0.231 | no | 1.533 | 0.222 | yes |
| DR0252 | Probable permease | 0.825 | 0.263 | no | 0.760 | 0.247 | no | 0.874 | 0.271 | no | 0.637 | 0.122 | yes | 0.928 | 0.294 | no | 1.248 | 0.281 | no | 1.590 | 0.499 | yes | 1.576 | 0.419 | yes | 1.873 | 0.273 | yes |
| DR0253 | Predicted protein | 1.298 | 0.575 | no | 1.295 | 0.392 | no | 1.347 | 0.330 | no | 1.443 | 0.312 | no | 1.343 | 0.605 | no | 1.135 | 0.396 | no | 1.454 | 0.300 | no | 1.135 | 0.227 | no | 1.190 | 0.170 | no |
| DR0254 | Predicted protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR0256 | Transposase, putative, authentic frameshift | 0.825 | 0.218 | no | 1.836 | 0.472 | yes | 2.362 | 0.728 | yes | 1.996 | 0.356 | yes | 2.155 | 0.796 | yes | 2.182 | 0.712 | yes | 2.394 | 0.523 | yes | 1.788 | 0.639 | yes | 1.978 | 0.782 | yes |
| DR0257 | Pyruvate dehydrogenase, ODP1 | 0.800 | 0.308 | no | 1.021 | 0.551 | no | 1.060 | 0.501 | no | 1.292 | 0.472 | no | 1.169 | 0.539 | no | 1.133 | 0.552 | no | 1.238 | 0.440 | no | 0.861 | 0.041 | no | 0.787 | 0.237 | no |
| DR0258 | Membrane transporter, MDR-type | 0.984 | 0.384 | no | 2.022 | 0.376 | yes | 1.948 | 0.304 | yes | 1.766 | 0.158 | yes | 1.535 | 0.456 | yes | 1.779 | 0.542 | yes | 1.586 | 0.533 | yes | 1.105 | 0.208 | no | 1.008 | 0.103 | no |
| DR0259 | HTH transcription factor, similar to MDR operon repressor | 0.803 | 0.208 | no | 1.101 | 0.303 | no | 1.071 | 0.283 | no | 0.951 | 0.166 | no | 1.084 | 0.189 | no | 1.078 | 0.211 | no | 1.143 | 0.302 | no | 0.990 | 0.282 | no | 0.873 | 0.220 | no |
| DR0260 | Permease, probably cyanate transport | 1.187 | 0.292 | no | 2.284 | 0.499 | yes | 2.325 | 1.213 | yes | 2.435 | 0.689 | yes | 2.675 | 1.207 | yes | 3.128 | 1.733 | yes | 2.359 | 1.632 | yes | 1.288 | 0.148 | no | 0.974 | 0.243 | no |
| DR0261 | MutT family hydrolase, probably real MUTT | 1.123 | 0.497 | no | 3.362 | 1.565 | yes | 3.087 | 1.497 | yes | 2.445 | 0.439 | yes | 2.503 | 1.588 | yes | 2.978 | 2.124 | yes | 3.847 | 1.676 | yes | 1.380 | 0.414 | no | 0.855 | 0.086 | no |
| DR0262 | Periplasmic binding protein | 1.221 | 0.243 | no | 1.673 | 0.495 | yes | 1.789 | 0.601 | yes | 1.897 | 0.409 | yes | 1.860 | 0.829 | yes | 2.365 | 0.829 | yes | 2.395 | 0.816 | yes | 1.540 | 0.333 | yes | 1.252 | 0.352 | no |
| DR0263 | Predicted protein | 0.564 | 0.123 | yes | 0.379 | 0.190 | yes | 0.827 | 0.169 | no | 0.774 | 0.351 | no | 1.210 | 0.398 | no | 1.376 | 0.335 | no | 1.095 | 0.344 | no | 1.348 | 0.400 | no | n/a | n/a | n/a |
| DR0264 | 1,4-alpha-glucan branching enzyme, GlgX | 1.070 | 0.189 | no | 1.207 | 0.142 | no | 1.455 | 0.168 | yes | 1.873 | 0.490 | yes | 1.705 | 0.398 | yes | 2.208 | 0.494 | yes | 2.293 | 0.613 | yes | 1.960 | 0.357 | yes | 1.424 | 0.323 | no |
| DR0265 | HTH transcription factor, GntR family | 0.945 | 0.382 | no | 0.752 | 0.412 | no | 1.016 | 0.564 | no | 0.854 | 0.130 | no | 1.048 | 0.315 | no | 1.682 | 0.797 | yes | 1.940 | 1.176 | yes | 1.384 | 0.707 | no | 3.438 | 1.539 | yes |
| DR0267 | Solo GGDEF domain of sensor regulator | 1.144 | 0.224 | no | 0.971 | 0.247 | no | 0.818 | 0.141 | no | 0.857 | 0.270 | no | 0.967 | 0.238 | no | 1.148 | 0.316 | no | 0.995 | 0.178 | no | 0.970 | 0.166 | no | 1.017 | 0.379 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR0268 | Membrane protein, periplasmic binding protein | 0.845 | 0.129 | no | 0.510 | 0.176 | yes | 0.318 | 0.113 | yes | 0.289 | 0.058 | yes | 0.453 | 0.255 | yes | 0.574 | 0.202 | yes | 0.488 | 0.163 | yes | 0.768 | 0.112 | no | 1.301 | 0.321 | no |
| DR0269 | Predicted protein (low complexity) | 0.757 | 0.284 | no | 0.769 | 0.416 | yes | 1.274 | 0.342 | no | 0.907 | 0.340 | no | 1.324 | 0.617 | no | 1.406 | 0.464 | no | 1.741 | 0.830 | yes | 0.991 | 0.117 | no | 1.696 | 0.388 | yes |
| DR0270 | Metallobetalactamase fold hydrolase | 1.114 | 0.292 | no | 0.868 | 0.153 | no | 1.044 | 0.292 | no | 1.084 | 0.059 | no | 1.143 | 0.286 | no | 0.982 | 0.236 | no | 0.959 | 0.168 | no | 1.095 | 0.109 | no | 1.049 | 0.079 | no |
| DR0271 | Predicted protein | 1.124 | 0.439 | no | 0.863 | 0.308 | no | 1.080 | 0.444 | no | 1.042 | 0.329 | no | 0.991 | 0.346 | no | 1.215 | 0.621 | no | 1.158 | 0.794 | no | 1.226 | 0.636 | no | 1.023 | 0.415 | no |
| DR0272 | SnoB family of small proteins, monooxygenase | 1.180 | 0.244 | no | 1.127 | 0.397 | no | 0.917 | 0.181 | no | 1.672 | 0.626 | no | 1.109 | 0.241 | no | 1.375 | 0.497 | no | 1.334 | 0.547 | no | 1.148 | 0.371 | no | 1.421 | 0.644 | no |
| DR0273 | Uncharacterized YIIM family, conserved C | 1.221 | 0.614 | no | 0.743 | 0.331 | no | 0.950 | 0.233 | no | 0.786 | 0.322 | no | 0.756 | 0.242 | no | 0.981 | 0.343 | no | 1.085 | 0.421 | no | 0.952 | 0.110 | no | 0.786 | 0.100 | no |
| DR0274 | MutT family hydrolase | 1.585 | 0.533 | no | 1.827 | 1.208 | yes | 1.619 | 0.802 | yes | 2.415 | 1.272 | yes | 1.092 | 0.375 | no | 1.669 | 1.187 | no | 1.987 | 1.059 | yes | 1.868 | 1.085 | yes | 1.581 | 0.604 | yes |
| DR0275 | Uncharacterized membrane or secreted protein, similar to gi\|2982987 of Aquifex aeolicus | 1.116 | 0.382 | no | 1.009 | 0.613 | no | 0.982 | 0.660 | no | 0.770 | 0.170 | no | 0.811 | 0.297 | no | 1.050 | 0.192 | no | 1.343 | 0.759 | no | 1.229 | 0.335 | no | 0.851 | 0.217 | no |
| DR0276 | SAM-dependent methyltransferase | 1.225 | 0.256 | no | 1.394 | 0.445 | no | 1.153 | 0.273 | no | 1.137 | 0.386 | no | 0.908 | 0.328 | no | 0.912 | 0.270 | no | 1.046 | 0.322 | no | 0.974 | 0.147 | no | 1.102 | 0.410 | no |
| DR0277 | Ortholog of gluconolactonase of Zymomonas, paraoxonase/serine esterase | 0.677 | 0.123 | no | 0.760 | 0.112 | no | 0.856 | 0.057 | no | 0.848 | 0.037 | no | 1.097 | 0.125 | no | 1.243 | 0.135 | no | 1.313 | 0.233 | no | 1.501 | 0.268 | yes | 1.154 | 0.108 | no |
| DR0278 | Phosphoglycerate mutase | 1.367 | 0.450 | no | 1.328 | 0.736 | no | 1.562 | 0.480 | yes | 1.408 | 0.722 | no | 1.205 | 0.538 | no | 1.349 | 0.543 | no | 1.342 | 0.600 | no | 1.059 | 0.205 | no | 0.734 | 0.196 | no |
| DR0279 | Thioester hydrolase, YCIA | 1.059 | 0.226 | no | 1.138 | 0.531 | no | 1.005 | 0.210 | no | 0.923 | 0.122 | no | 0.846 | 0.264 | no | 1.187 | 0.325 | no | 1.601 | 0.741 | yes | 1.407 | 0.471 | no | 1.108 | 0.337 | no |
| DR0280 | Periplasmic binding protein of BRA transporter | 1.712 | 1.173 | no | 0.998 | 0.538 | no | 0.664 | 0.361 | yes | 1.251 | 0.733 | no | 0.908 | 0.485 | no | 0.665 | 0.276 | yes | 1.061 | 0.733 | no | 1.036 | 0.430 | no | 1.070 | 0.483 | no |
| DR0281 | Permease of BRA transporter | 1.192 | 0.437 | no | 0.938 | 0.382 | no | 0.784 | 0.349 | no | 1.153 | 0.563 | no | 1.095 | 0.797 | no | 0.871 | 0.286 | no | 1.063 | 0.430 | no | 0.801 | 0.097 | no | 0.698 | 0.130 | no |
| DR0282 | Permease of BRA transporter | 1.622 | 0.593 | yes | 1.444 | 0.652 | no | 1.216 | 0.405 | no | 1.079 | 0.334 | no | 0.901 | 0.440 | no | 0.942 | 0.468 | no | 1.065 | 0.176 | no | 0.992 | 0.088 | no | 0.823 | 0.238 | no |
| DR0283 | ABC ATPase of BRA transporter | 0.926 | 0.214 | no | 0.966 | 0.247 | no | 1.007 | 0.309 | no | 0.819 | 0.135 | no | 0.886 | 0.246 | no | 1.025 | 0.195 | no | 1.068 | 0.209 | no | 1.068 | 0.096 | no | 0.947 | 0.134 | no |
| DR0284 | ABC ATPase of BRA transporter | 1.533 | 0.627 | no | 2.329 | 1.116 | yes | 1.672 | 0.921 | yes | 2.081 | 0.167 | yes | 1.453 | 0.580 | no | 0.905 | 0.173 | no | 1.202 | 0.552 | no | 1.097 | 0.298 | no | 1.056 | 0.352 | no |
| DR0285 | Possible secreted protein, uncharacterized | 0.829 | 0.360 | no | 0.598 | 0.132 | yes | 0.875 | 0.168 | no | 0.831 | 0.068 | no | 1.141 | 0.306 | no | 1.672 | 0.849 | no | 2.403 | 1.564 | yes | n/a | n/a | n/a | n/a | n/a | n/a |
| DR0286 | Possible secreted protein, uncharacterized | 0.943 | 0.219 | no | 0.759 | 0.235 | no | 0.988 | 0.226 | no | 1.393 | 0.368 | no | 1.080 | 0.371 | no | 1.046 | 0.355 | no | 1.331 | 0.400 | no | 2.161 | 0.971 | yes | 1.272 | 0.113 | no |
| DR0287 | 2-oxoglutarate dehydrogenase, ODO1 | 0.856 | 0.281 | no | 0.481 | 0.175 | yes | 0.304 | 0.104 | yes | 0.243 | 0.013 | yes | 0.462 | 0.280 | yes | 0.529 | 0.265 | yes | 0.621 | 0.347 | yes | 1.449 | 0.178 | no | n/a | n/a | n/a |
| DR0288 | Predicted protein | 1.036 | 0.298 | no | 0.739 | 0.221 | no | 0.592 | 0.229 | yes | 0.777 | 0.323 | no | 0.769 | 0.208 | no | 0.737 | 0.292 | no | 0.940 | 0.268 | no | 0.815 | 0.261 | no | 1.009 | 0.133 | no |
| DR0289 | UV endonuclease III, pyrimidine dimer glycosylase | 0.936 | 0.352 | no | 0.980 | 0.306 | no | 1.017 | 0.270 | no | 1.195 | 0.271 | no | 1.049 | 0.326 | no | 1.203 | 0.383 | no | 1.136 | 0.397 | no | 1.552 | 0.767 | no | 0.878 | 0.293 | no |
| DR0290 | Permease MDR-type | 1.489 | 0.615 | no | 1.481 | 0.423 | yes | 1.231 | 0.347 | no | 1.189 | 0.228 | no | 1.050 | 0.265 | no | 0.934 | 0.140 | no | 1.304 | 0.293 | no | 1.267 | 0.201 | no | 1.150 | 0.366 | no |
| DR0291 | Uncharcterized protein with Zn finger | 0.553 | 0.208 | yes | 0.308 | 0.117 | yes | 0.261 | 0.103 | yes | 0.263 | 0.033 | yes | 0.285 | 0.090 | yes | 0.432 | 0.124 | yes | 0.526 | 0.205 | yes | 0.629 | 0.135 | yes | 1.073 | 0.137 | no |
| DR0292 | Conserved secreted small protein related to TatA/TatB of e.coli. | 1.111 | 0.308 | no | 0.685 | 0.189 | yes | 0.449 | 0.091 | yes | 0.400 | 0.089 | yes | 0.415 | 0.069 | yes | 0.390 | 0.106 | yes | 0.449 | 0.202 | yes | 0.438 | 0.167 | yes | 0.649 | 0.137 | yes |
| DR0293 | Phosphatase, HAD superfamily hydrolase | 1.127 | 0.417 | no | 1.098 | 0.513 | no | 1.185 | 0.565 | no | 1.038 | 0.195 | no | 0.977 | 0.289 | no | 1.330 | 0.811 | no | 1.326 | 0.679 | no | 1.498 | 0.625 | no | 1.127 | 0.422 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR0294 | Nicotinate phosphoribosyltransferase, PCNB family protein | 1.308 | 0.343 | no | 1.043 | 0.205 | no | 1.061 | 0.448 | no | 1.522 | 0.130 | no | 1.076 | 0.550 | no | 1.207 | 0.465 | no | 0.995 | 0.353 | no | 1.075 | 0.230 | no | 1.249 | 0.143 | no |
| DR0295 | Protein phosphatase, Calcineurin like phosphoesterase superfamily | 0.944 | 0.378 | no | 0.995 | 0.425 | no | 0.975 | 0.477 | no | 0.745 | 0.193 | no | 1.088 | 0.244 | no | 1.502 | 0.837 | no | 1.457 | 0.697 | no | 1.049 | 0.153 | no | 1.909 | 0.917 | yes |
| DR0296 | Predicted protein | 1.089 | 0.312 | no | 0.951 | 0.314 | no | 0.951 | 0.194 | no | 1.118 | 0.159 | no | 1.126 | 0.329 | no | 1.066 | 0.303 | no | 0.777 | 0.343 | no | 1.196 | 0.511 | no | 1.021 | 0.191 | no |
| DR0297 | UDP-N-acetylmuramyl tripeptide synthetase | 0.769 | 0.297 | no | 0.979 | 0.350 | no | 0.939 | 0.319 | no | 0.736 | 0.188 | no | 0.873 | 0.288 | no | 1.289 | 0.612 | no | 1.247 | 0.783 | no | 1.203 | 0.394 | no | 1.017 | 0.480 | no |
| DR0298 | Nucleotide kinase (deoxyguanosine) P- loop | 1.230 | 0.313 | no | 1.551 | 0.499 | yes | 1.152 | 0.195 | no | 1.139 | 0.129 | no | 1.058 | 0.402 | no | 0.992 | 0.270 | no | 0.890 | 0.374 | no | 0.873 | 0.143 | no | 0.920 | 0.380 | no |
| DR0299 | Nucleotide kinase (deoxyguanosine) P- loop | 0.911 | 0.453 | no | 1.234 | 0.653 | no | 0.874 | 0.276 | no | 0.895 | 0.090 | no | 1.036 | 0.253 | no | 1.245 | 0.612 | no | 0.890 | 0.425 | no | 1.078 | 0.506 | no | 0.999 | 0.297 | no |
| DR0301 | Possible transcriptional regulator | 0.680 | 0.305 | yes | 0.852 | 0.120 | no | 0.794 | 0.322 | no | 0.744 | 0.290 | no | 1.066 | 0.507 | no | 0.829 | 0.169 | no | 0.900 | 0.158 | no | 1.216 | 0.359 | no | 1.606 | 0.345 | yes |
| DR0302 | Glutamine--fructose-6-phosphate aminotransferase | 0.627 | 0.370 | yes | 0.486 | 0.085 | yes | 0.942 | 0.454 | no | 0.709 | 0.114 | no | 1.203 | 0.567 | no | 1.868 | 0.942 | yes | 1.063 | 0.672 | no | 1.097 | 0.359 | no | 2.109 | 1.216 | yes |
| DR0304 | Predicted protein | 0.834 | 0.193 | no | 1.101 | 0.243 | no | 1.561 | 0.363 | yes | 2.007 | 0.309 | yes | 1.962 | 0.408 | yes | 1.982 | 0.570 | yes | 1.746 | 0.557 | yes | 1.593 | 0.373 | yes | 0.986 | 0.252 | no |
| DR0305 | Ribosomal protein S12 | 0.603 | 0.215 | yes | 0.955 | 0.236 | no | 1.525 | 0.357 | yes | 1.304 | 0.627 | no | 1.768 | 0.786 | yes | 1.695 | 0.701 | yes | 2.073 | 0.884 | yes | 1.938 | 0.378 | yes | 0.796 | 0.224 | no |
| DR0306 | Ribosomal Protein S7 | 0.750 | 0.328 | no | 1.460 | 0.773 | no | 2.002 | 0.887 | yes | 1.750 | 1.085 | no | 1.758 | 0.487 | yes | 1.777 | 0.757 | yes | 1.756 | 0.721 | yes | 1.534 | 0.431 | yes | 0.521 | 0.186 | yes |
| DR0307 | Elongation factor EF-G | 0.891 | 0.367 | no | 1.404 | 0.406 | no | 1.313 | 0.369 | no | 1.047 | 0.465 | no | 1.884 | 1.340 | yes | 1.830 | 1.142 | yes | 1.789 | 0.811 | yes | 1.247 | 0.376 | no | 1.082 | 0.242 | no |
| DR0308 | Predicted protein | 0.827 | 0.226 | no | 1.692 | 0.440 | yes | 2.244 | 0.617 | yes | 1.968 | 0.339 | yes | 1.713 | 0.242 | yes | 1.325 | 0.343 | no | 1.258 | 0.319 | no | 1.217 | 0.174 | no | 1.313 | 0.293 | no |
| DR0309 | Elongation factor, EF-TU | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR0310 | Ribosomal protein S10 | 1.052 | 0.567 | no | 1.909 | 1.167 | yes | 2.084 | 1.672 | yes | 1.187 | 0.346 | no | 0.931 | 0.349 | no | 1.674 | 1.165 | no | 1.345 | 0.562 | no | 3.201 | 0.542 | yes | n/a | n/a | n/a |
| DR0311 | Ribosomal protein L3 | 0.924 | 0.527 | no | 1.946 | 0.831 | yes | 1.787 | 0.471 | yes | 0.875 | 0.652 | no | 1.248 | 0.687 | no | 1.470 | 0.599 | no | 1.176 | 0.285 | no | 1.083 | 0.334 | no | 0.521 | 0.234 | yes |
| DR0312 | Ribosomal protein L04 | 0.692 | 0.371 | yes | 1.757 | 0.641 | yes | 1.456 | 0.437 | yes | 1.070 | 0.357 | no | 2.145 | 0.990 | yes | 1.536 | 0.858 | no | 1.729 | 0.743 | yes | 1.644 | 0.622 | yes | 0.863 | 0.304 | no |
| DR0313 | Ribosomal protein L23 | 0.735 | 0.148 | no | 3.057 | 0.548 | yes | 2.213 | 0.849 | yes | 2.326 | 0.506 | yes | 2.181 | 0.849 | yes | 2.062 | 1.201 | yes | 1.674 | 0.664 | yes | 1.843 | 0.532 | yes | 0.823 | 0.430 | no |
| DR0314 | Ribosomal protein L2 | 0.727 | 0.300 | no | 1.690 | 0.826 | yes | 1.422 | 0.617 | no | 0.670 | 0.207 | no | 1.911 | 1.398 | no | 1.701 | 0.775 | yes | 1.910 | 0.958 | yes | 0.804 | 0.069 | no | 1.139 | 0.380 | no |
| DR0315 | Ribosomal protein S19 | 0.762 | 0.298 | no | 3.781 | 1.446 | yes | 3.871 | 1.491 | yes | 3.802 | 2.472 | yes | 3.728 | 1.750 | yes | 3.148 | 1.302 | yes | 2.993 | 0.838 | yes | 2.628 | 0.769 | yes | 1.091 | 0.477 | no |
| DR0316 | Ribosomal protein L22 | 0.685 | 0.208 | yes | 2.673 | 1.268 | yes | 2.264 | 0.736 | yes | 1.888 | 0.840 | yes | 2.575 | 0.978 | yes | 1.937 | 0.948 | yes | 3.006 | 2.110 | yes | 2.547 | 0.443 | yes | 1.149 | 0.574 | no |
| DR0317 | Ribosomal protein S3 | 0.743 | 0.161 | no | 2.845 | 1.019 | yes | 2.658 | 0.711 | yes | 2.021 | 0.621 | yes | 2.357 | 1.134 | yes | 2.530 | 1.220 | yes | 2.588 | 1.069 | yes | 2.581 | 0.515 | yes | 1.330 | 0.503 | no |
| DR0318 | Ribosomal protein L16 | 0.659 | 0.292 | yes | 2.609 | 1.108 | yes | 2.268 | 1.264 | yes | 1.269 | 0.368 | no | 3.132 | 2.220 | yes | 1.568 | 0.473 | no | 3.014 | 1.828 | yes | 2.421 | 0.904 | yes | 2.083 | 0.651 | yes |
| DR0319 | Ribosomal protein L29 | 0.728 | 0.134 | no | 3.648 | 0.929 | yes | 3.441 | 1.101 | yes | 3.183 | 1.373 | yes | 2.827 | 1.278 | yes | 2.824 | 1.494 | yes | 1.913 | 0.714 | yes | 1.940 | 0.544 | yes | 1.167 | 0.257 | no |
| DR0320 | Ribosomal protein S17 | 0.641 | 0.106 | yes | 3.087 | 1.219 | yes | 3.021 | 1.157 | yes | 3.039 | 0.876 | yes | 3.322 | 1.124 | yes | 3.077 | 1.528 | yes | 3.841 | 2.283 | yes | 3.340 | 0.784 | yes | 1.264 | 0.481 | no |
| DR0321 | Ribosomal protein L14 | 0.689 | 0.104 | no | 4.547 | 1.231 | yes | 5.136 | 2.583 | yes | 3.326 | 0.689 | yes | 3.352 | 0.500 | yes | 4.339 | 2.856 | yes | 5.033 | 2.938 | yes | 4.008 | 1.043 | yes | 1.863 | 0.616 | yes |
| DR0322 | Ribosomal protein L24 | 0.636 | 0.140 | yes | 2.030 | 0.802 | yes | 2.313 | 0.807 | yes | 1.719 | 0.319 | yes | 2.272 | 0.872 | yes | 2.252 | 0.585 | yes | 3.066 | 1.778 | yes | 3.188 | 1.476 | yes | 1.319 | 0.620 | no |
| DR0323 | Ribosomal protein L5 | 0.860 | 0.207 | no | 5.934 | 2.047 | yes | 5.146 | 1.461 | yes | 4.772 | 2.527 | yes | 4.363 | 1.510 | yes | 3.846 | 1.529 | yes | 5.338 | 3.249 | yes | 4.269 | 0.534 | yes | 2.308 | 0.345 | yes |
| DR0324 | Probable glutamate formiminotransferase | 0.874 | 0.493 | no | 3.301 | 1.469 | yes | 1.929 | 0.917 | yes | 1.996 | 1.145 | yes | 2.478 | 1.033 | yes | 1.955 | 1.006 | yes | 1.830 | 0.539 | yes | 1.817 | 0.163 | yes | 1.242 | 0.137 | no |
| DR0325 | Malate dehydrogenase | 1.431 | 0.704 | no | 2.599 | 1.202 | yes | 3.463 | 1.812 | yes | 4.044 | 0.823 | yes | 2.952 | 1.170 | yes | 2.805 | 1.360 | yes | 2.304 | 0.981 | yes | 2.297 | 0.478 | yes | 2.817 | 0.636 | yes |
| DR0326 | Predicted protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR0327 | HTRA like serine protease with PDZ domain | 0.822 | 0.193 | no | 0.725 | 0.170 | no | 0.588 | 0.225 | yes | 0.703 | 0.153 | no | 0.895 | 0.330 | no | 0.720 | 0.364 | yes | 0.589 | 0.200 | yes | 0.620 | 0.259 | yes | 0.650 | 0.254 | yes |
| DR0328 | VYG containing motif, small sporadic proteins | 1.289 | 0.465 | no | 1.545 | 0.542 | yes | 1.280 | 0.479 | no | 1.158 | 0.101 | no | 1.341 | 0.487 | no | 1.053 | 0.289 | no | 1.034 | 0.432 | no | 0.938 | 0.027 | no | 0.713 | 0.153 | no |
| DR0329 | MutT superfamily Hydrolase, 2 domains | 0.961 | 0.268 | no | 1.186 | 0.399 | no | 1.434 | 0.602 | no | 1.149 | 0.310 | no | 1.098 | 0.353 | no | 1.055 | 0.293 | no | 1.077 | 0.399 | no | 1.103 | 0.120 | no | 0.980 | 0.305 | no |
| DR0330 | Shares domain with Y4BJ RHISN | 1.024 | 0.278 | no | 0.610 | 0.210 | yes | 0.379 | 0.114 | yes | 0.422 | 0.010 | yes | 0.470 | 0.103 | yes | 0.531 | 0.189 | yes | 0.578 | 0.204 | yes | 0.683 | 0.164 | yes | 1.150 | 0.190 | no |
| DR0331 | Predicted protein | 1.481 | 0.564 | no | 0.649 | 0.342 | yes | 0.650 | 0.341 | yes | 1.887 | 0.307 | yes | 1.416 | 1.000 | no | 0.619 | 0.237 | yes | 1.399 | 0.855 | no | 1.144 | 0.214 | no | 1.249 | 0.271 | no |
| DR0332 | Uncharacterized conserved protein family, YIGC E.coli ortholog | 1.084 | 0.642 | no | 0.787 | 0.481 | no | 0.617 | 0.397 | yes | 0.774 | 0.399 | no | 0.825 | 0.648 | no | 0.625 | 0.248 | yes | 0.647 | 0.361 | yes | 0.590 | 0.121 | yes | 0.759 | 0.174 | no |
| DR0333 | Predicted protein | 0.997 | 0.212 | no | 0.783 | 0.147 | no | 0.574 | 0.247 | yes | 0.614 | 0.184 | yes | 0.826 | 0.291 | no | 0.687 | 0.260 | yes | 0.736 | 0.280 | no | 0.643 | 0.221 | yes | 0.687 | 0.052 | no |
| DR0334 | Lipase, a/b hydrolase fold | 1.401 | 0.492 | no | 1.246 | 0.578 | no | 0.975 | 0.366 | no | 1.235 | 0.582 | no | 1.260 | 0.892 | no | 0.874 | 0.209 | no | 0.776 | 0.387 | no | 0.618 | 0.183 | yes | 0.558 | 0.068 | yes |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR0335 | Superfamily II helicase, ATP-dependent RNA helicase | 0.737 | 0.189 | no | 0.869 | 0.190 | no | 0.968 | 0.116 | no | 0.996 | 0.108 | no | 1.279 | 0.142 | no | 1.120 | 0.299 | no | 0.995 | 0.215 | no | 0.671 | 0.253 | yes | 0.464 | 0.088 | yes |
| DR0336 | Acyl-CoA ligase, AMP-binding | 1.137 | 0.452 | no | 0.642 | 0.277 | yes | 0.559 | 0.390 | yes | 1.252 | 0.505 | no | 0.646 | 0.265 | yes | 0.568 | 0.361 | yes | 0.706 | 0.337 | yes | 0.661 | 0.228 | yes | 0.660 | 0.238 | yes |
| DR0337 | Predicted protein | 0.921 | 0.290 | no | 2.085 | 0.620 | yes | 1.780 | 0.557 | yes | 2.113 | 1.093 | yes | 2.146 | 0.874 | yes | 1.611 | 0.541 | yes | 1.645 | 0.993 | no | 1.049 | 0.107 | no | 0.623 | 0.195 | yes |
| DR0338 | Predicted protein | 1.092 | 0.505 | no | 1.477 | 0.766 | no | 0.992 | 0.304 | no | 1.371 | 0.113 | no | 1.290 | 0.448 | no | 1.436 | 0.375 | no | 1.924 | 0.270 | yes | 1.896 | 0.222 | yes | 1.463 | 0.443 | no |
| DR0339 | Amidohydrolase, aminoacylase/desuccinylase/peptidase family | 0.840 | 0.273 | no | 0.731 | 0.268 | no | 0.595 | 0.234 | yes | 0.516 | 0.212 | yes | 0.643 | 0.250 | yes | 0.684 | 0.243 | yes | 0.620 | 0.322 | yes | 0.783 | 0.342 | no | 0.918 | 0.353 | no |
| DR0340 | Folylpolyglutamate synthetase | 0.752 | 0.154 | no | 2.610 | 1.345 | yes | 2.319 | 0.830 | yes | 3.487 | 1.686 | yes | 1.521 | 0.513 | no | 1.781 | 0.935 | yes | 1.989 | 0.697 | yes | 1.927 | 0.357 | yes | 1.103 | 0.445 | no |
| DR0341 | Ribosomal protein S15 | 0.930 | 0.378 | no | 0.762 | 0.213 | no | 1.120 | 0.449 | no | 1.255 | 0.351 | no | 1.882 | 0.969 | yes | 1.357 | 0.414 | no | 1.431 | 0.380 | no | 1.290 | 0.273 | no | 0.630 | 0.172 | yes |
| DR0342 | Iron sulfur protein, Rieske type | 1.047 | 0.237 | no | 3.096 | 1.054 | yes | 2.362 | 0.526 | yes | 1.640 | 0.360 | yes | 1.211 | 0.473 | no | 0.866 | 0.158 | no | 0.959 | 0.182 | no | 0.873 | 0.127 | no | 0.973 | 0.175 | no |
| DR0343 | Cytochrome oxidase family protein | 0.968 | 0.388 | no | 1.920 | 0.931 | yes | 1.546 | 0.767 | yes | 0.592 | 0.034 | no | 0.729 | 0.192 | no | 0.674 | 0.239 | yes | 0.566 | 0.200 | yes | 0.638 | 0.219 | yes | 0.610 | 0.170 | yes |
| DR0344 | Cytochrome C-Type biogenesis protein CCL2 | 0.906 | 0.178 | no | 1.987 | 1.024 | yes | 1.129 | 0.407 | no | 1.094 | 0.169 | no | 1.193 | 0.717 | no | 0.708 | 0.170 | no | 0.579 | 0.154 | yes | 0.671 | 0.085 | yes | 0.727 | 0.139 | no |
| DR0345 | Thioredoxin fold protein | 0.821 | 0.344 | no | 2.265 | 1.349 | yes | 1.172 | 0.339 | no | 0.670 | 0.297 | yes | 0.690 | 0.436 | yes | 0.764 | 0.334 | no | 0.428 | 0.093 | yes | 0.658 | 0.088 | yes | 0.722 | 0.172 | no |
| DR0346 | Cytochrome C-Type biogenesis protein CYCK | 0.836 | 0.454 | no | 1.922 | 0.834 | yes | 0.834 | 0.369 | no | 0.613 | 0.223 | yes | 0.294 | 0.166 | yes | 0.429 | 0.169 | yes | 0.344 | 0.142 | yes | 0.377 | 0.180 | yes | 0.446 | 0.196 | yes |
| DR0347 | Cytochrome C-Type biogenesis protein CYCJ | 0.760 | 0.253 | no | 1.343 | 0.382 | no | 0.691 | 0.133 | yes | 0.344 | 0.147 | yes | 0.282 | 0.099 | yes | 0.270 | 0.135 | yes | 0.225 | 0.116 | yes | 0.228 | 0.097 | yes | 0.456 | 0.190 | yes |
| DR0348 | Heme exporter protein C, CYCZ | 1.149 | 0.443 | no | 1.016 | 0.627 | no | 0.622 | 0.332 | yes | 0.274 | 0.120 | yes | 0.302 | 0.122 | yes | 0.261 | 0.097 | yes | 0.267 | 0.086 | yes | 0.347 | 0.112 | yes | 0.718 | 0.292 | no |
| DR0349 | LON protease, AAA superfamily ATPase + protease domain | 1.455 | 0.801 | no | 1.390 | 0.443 | no | 0.930 | 0.549 | no | 0.442 | 0.176 | yes | 0.910 | 0.581 | no | 0.884 | 0.438 | no | 0.913 | 0.430 | no | 0.675 | 0.224 | yes | 1.286 | 0.270 | no |
| DR0350 | Pkn2 related beta propeller domain | 0.885 | 0.324 | no | 1.161 | 0.303 | no | 1.231 | 0.422 | no | 1.298 | 0.367 | no | 1.269 | 0.694 | no | 0.846 | 0.181 | no | 0.969 | 0.314 | no | 0.885 | 0.145 | no | 1.081 | 0.171 | no |
| DR0351 | Conserved membrane protein | 0.958 | 0.234 | no | 1.668 | 0.444 | yes | 1.290 | 0.207 | no | 1.091 | 0.039 | no | 1.062 | 0.151 | no | 0.832 | 0.166 | no | 0.713 | 0.203 | no | 0.828 | 0.186 | no | 1.016 | 0.166 | no |
| DR0352 | Predicted protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR0353 | VacB, S1 domain nuclease | 1.524 | 0.825 | no | 1.554 | 0.807 | no | 1.002 | 0.442 | no | 2.570 | 2.051 | yes | 2.133 | 1.557 | yes | 1.327 | 0.417 | no | 0.866 | 0.334 | no | 1.290 | 0.222 | no | 1.177 | 0.128 | no |
| DR0354 | Protein of apurinic/apyrimidinic endonuclease/exodeoribonuclease family | 0.984 | 0.296 | no | 1.143 | 0.142 | no | 1.128 | 0.213 | no | 0.818 | 0.068 | no | 0.960 | 0.132 | no | 0.705 | 0.110 | no | 0.791 | 0.180 | no | 0.877 | 0.170 | no | 1.018 | 0.275 | no |
| DR0355 | Predicted protein | 1.168 | 0.417 | no | 0.606 | 0.163 | yes | 0.454 | 0.132 | yes | 0.493 | 0.102 | yes | 0.628 | 0.216 | yes | 0.517 | 0.181 | yes | 0.700 | 0.200 | no | 0.786 | 0.303 | no | 1.067 | 0.149 | no |
| DR0356 | SAM dependent methylase | 1.010 | 0.246 | no | 0.637 | 0.219 | yes | 0.352 | 0.150 | yes | 0.276 | 0.119 | yes | 0.329 | 0.089 | yes | 0.395 | 0.225 | yes | 0.409 | 0.146 | yes | 0.381 | 0.094 | yes | 0.501 | 0.084 | yes |
| DR0357 | Uncharacterized protein, YQGE E.coli ortholog | 0.937 | 0.132 | no | 0.666 | 0.184 | yes | 0.389 | 0.129 | yes | 0.362 | 0.024 | yes | 0.455 | 0.207 | yes | 0.433 | 0.168 | yes | 0.583 | 0.184 | yes | 0.457 | 0.122 | yes | 0.518 | 0.151 | yes |
| DR0358 | Related to aminomethyl transferase, UP14 of E.coli | 1.129 | 0.458 | no | 0.872 | 0.364 | no | 0.713 | 0.252 | yes | 0.599 | 0.322 | yes | 0.620 | 0.212 | yes | 0.518 | 0.137 | yes | 0.639 | 0.238 | yes | 0.570 | 0.149 | yes | 0.821 | 0.086 | no |
| DR0359 | Predicted protein | 1.152 | 0.505 | no | 1.335 | 0.570 | no | 1.036 | 0.386 | no | 1.062 | 0.459 | no | 0.858 | 0.208 | no | 0.651 | 0.246 | yes | 0.606 | 0.171 | yes | 0.732 | 0.221 | yes | 0.627 | 0.183 | yes |
| DR0360 | Predicted protein | 1.214 | 0.688 | no | 1.023 | 0.617 | no | 1.048 | 0.631 | no | 1.119 | 0.512 | no | 1.044 | 0.527 | no | 0.719 | 0.499 | yes | 0.608 | 0.287 | yes | 0.626 | 0.141 | yes | 0.579 | 0.128 | yes |
| DR0361 | Metalo betalactamase fold hydrolase, ComE like | 1.280 | 0.329 | no | 2.573 | 0.784 | yes | 2.925 | 1.727 | yes | 2.605 | 1.015 | yes | 3.081 | 1.133 | yes | 1.109 | 0.639 | no | 0.978 | 0.315 | no | 0.724 | 0.279 | yes | 0.748 | 0.306 | no |
| DR0362 | D-alanine--D-alanine ligase, ATP grasp superfamily | 1.009 | 0.407 | no | 2.190 | 0.821 | yes | 3.061 | 1.173 | yes | 2.630 | 0.515 | yes | 1.919 | 0.681 | yes | 1.379 | 0.119 | no | 1.036 | 0.348 | no | 1.512 | 0.397 | yes | 1.459 | 0.202 | yes |
| DR0363 | Periplasmic DP binding protein, DppA | 0.918 | 0.269 | no | 2.115 | 0.571 | yes | 2.903 | 0.960 | yes | 2.925 | 1.374 | yes | 2.649 | 1.100 | yes | 1.797 | 1.149 | yes | 1.293 | 0.279 | no | 2.377 | 1.118 | yes | 4.091 | 1.748 | yes |
| DR0364 | Permease of DP transporter, DppB | 0.881 | 0.249 | no | 0.730 | 0.162 | no | 1.122 | 0.493 | no | 1.072 | 0.337 | no | 0.946 | 0.244 | no | 0.705 | 0.260 | no | 0.661 | 0.266 | yes | 0.934 | 0.340 | no | 1.223 | 0.467 | no |
| DR0365 | Permease of DP transporter,DppC | 0.972 | 0.035 | no | 0.778 | 0.189 | no | 1.161 | 0.441 | no | 1.149 | 0.135 | no | 1.484 | 0.844 | no | 0.870 | 0.314 | no | 0.811 | 0.111 | no | 1.000 | 0.150 | no | 1.000 | 0.296 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR0366 | Biotin synthetase family of Metal cluster enzymes | 0.762 | 0.143 | no | 0.314 | 0.126 | yes | 0.249 | 0.078 | yes | 0.210 | 0.055 | yes | 0.422 | 0.142 | yes | 0.356 | 0.164 | yes | 0.412 | 0.223 | yes | 0.509 | 0.125 | yes | 0.803 | 0.110 | no |
| DR0367 | Probable NH2-acetyltransferase | 1.007 | 0.312 | no | 0.821 | 0.321 | no | 0.948 | 0.111 | no | 0.875 | 0.420 | no | 0.840 | 0.485 | no | 0.744 | 0.281 | no | 0.732 | 0.304 | no | 0.710 | 0.176 | yes | 0.660 | 0.234 | yes |
| DR0368 | Uncharacterized conserved protein | 1.150 | 0.787 | no | 0.682 | 0.278 | yes | 0.788 | 0.354 | no | 0.626 | 0.087 | no | 1.147 | 0.512 | no | 1.772 | 0.994 | yes | 1.415 | 0.412 | no | 1.053 | 0.235 | no | 0.692 | 0.140 | no |
| DR0369 | Predicted protein | 1.323 | 0.413 | no | 1.213 | 0.502 | no | 1.386 | 0.614 | no | 2.507 | 1.488 | yes | 2.365 | 1.119 | yes | 2.198 | 1.199 | yes | 2.351 | 0.660 | yes | 1.612 | 0.258 | yes | 0.927 | 0.178 | no |
| DR0370 | Uncharacterized conserved protein | 0.897 | 0.284 | no | 0.730 | 0.216 | no | 0.714 | 0.206 | no | 1.028 | 0.376 | no | 1.566 | 0.328 | yes | 1.601 | 0.472 | yes | 2.359 | 0.631 | yes | 2.510 | 0.505 | yes | 0.843 | 0.284 | no |
| DR0371 | Predicted protein | 1.270 | 0.596 | no | 0.565 | 0.154 | yes | 0.699 | 0.313 | yes | 4.712 | 1.821 | yes | 2.982 | 1.832 | yes | 2.508 | 0.413 | yes | 6.269 | 3.390 | yes | 5.341 | 0.430 | yes | 3.383 | 0.966 | yes |
| DR0372 | Lysyl-tRNA synthetase | 0.659 | 0.208 | yes | 0.566 | 0.186 | yes | 0.413 | 0.117 | yes | 0.335 | 0.047 | yes | 0.600 | 0.317 | yes | 0.559 | 0.246 | yes | 0.436 | 0.301 | yes | 0.455 | 0.188 | yes | 0.851 | 0.414 | no |
| DR0373 | H+/Ca2+ exchanger, CHAA | 1.316 | 0.544 | no | 1.238 | 0.648 | no | 1.134 | 0.613 | no | 0.741 | 0.182 | no | 0.961 | 0.427 | no | 0.984 | 0.399 | no | 0.843 | 0.259 | no | 1.003 | 0.346 | no | 1.076 | 0.373 | no |
| DR0374 | HTH transcription factor | 1.120 | 0.547 | no | 1.171 | 0.332 | no | 0.789 | 0.351 | no | 1.257 | 0.020 | no | 0.830 | 0.368 | no | 0.707 | 0.382 | yes | 1.071 | 0.477 | no | 0.705 | 0.218 | yes | 0.875 | 0.461 | no |
| DR0375 | Predicted protein | 1.414 | 0.604 | no | 1.717 | 0.652 | yes | 1.356 | 0.406 | no | 1.712 | 0.224 | yes | 1.421 | 0.357 | no | 1.119 | 0.296 | no | 1.309 | 0.658 | no | 0.880 | 0.076 | no | 0.751 | 0.250 | no |
| DR0377 | L-serine dehydratase, SDHM | 1.284 | 0.324 | no | 1.258 | 0.360 | no | 1.000 | 0.277 | no | 1.084 | 0.214 | no | 1.019 | 0.222 | no | 1.102 | 0.295 | no | 1.158 | 0.418 | no | 1.037 | 0.154 | no | 1.105 | 0.417 | no |
| DR0378 | HTH transcription factor, TetR/AcrR family | 0.821 | 0.248 | no | 1.338 | 0.282 | no | 1.092 | 0.243 | no | 0.989 | 0.162 | no | 1.236 | 0.268 | no | 1.283 | 0.376 | no | 1.166 | 0.385 | no | 0.904 | 0.148 | no | 1.049 | 0.071 | no |
| DR0379 | Conserved membrane protein | 0.808 | 0.208 | no | 1.046 | 0.292 | no | 1.328 | 0.228 | no | 1.756 | 0.426 | yes | 1.826 | 0.763 | yes | 1.921 | 0.665 | yes | 1.748 | 0.420 | yes | 2.177 | 0.355 | yes | 3.490 | 1.273 | yes |
| DR0380 | Conserved membrane protein | 0.852 | 0.190 | no | 4.012 | 0.783 | yes | 2.527 | 1.003 | yes | 1.945 | 0.608 | yes | 2.198 | 1.251 | yes | 1.929 | 0.584 | yes | 2.264 | 1.258 | yes | 1.580 | 0.431 | yes | 1.767 | 0.423 | yes |
| DR0381 | Predicted protein | 0.977 | 0.319 | no | 3.610 | 0.878 | yes | 2.662 | 0.871 | yes | 3.530 | 1.256 | yes | 2.777 | 1.632 | yes | 2.076 | 0.249 | yes | 2.038 | 0.937 | yes | 1.588 | 0.245 | yes | 1.986 | 0.664 | yes |
| DR0383 | S-layer protein | 0.839 | 0.386 | no | 1.395 | 0.177 | yes | 1.046 | 0.407 | no | 0.760 | 0.371 | no | 1.438 | 0.538 | no | 1.397 | 0.542 | no | 1.725 | 0.968 | yes | 1.578 | 0.601 | yes | 2.443 | 1.058 | yes |
| DR0384 | Predicted protein | 0.893 | 0.145 | no | 0.805 | 0.257 | no | 0.662 | 0.200 | yes | 0.742 | 0.123 | no | 0.853 | 0.126 | no | 0.948 | 0.361 | no | 0.873 | 0.294 | no | 1.120 | 0.061 | no | 0.899 | 0.280 | no |
| DR0385 | Predicted protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR0386 | GCPE ortholog, involved in peptidoglycan acetylation | 1.045 | 0.190 | no | 0.679 | 0.117 | no | 0.669 | 0.294 | yes | 0.869 | 0.240 | no | 0.651 | 0.216 | yes | 0.548 | 0.095 | yes | 0.588 | 0.145 | yes | 0.669 | 0.107 | yes | 1.074 | 0.315 | no |
| DR0387 | Predicted protein | 1.032 | 0.287 | no | 0.876 | 0.237 | no | 0.724 | 0.210 | no | 0.631 | 0.096 | yes | 0.681 | 0.176 | no | 0.757 | 0.194 | no | 0.796 | 0.128 | no | 0.884 | 0.221 | no | 1.196 | 0.413 | no |
| DR0388 | Predicted protein | 0.988 | 0.264 | no | 1.364 | 0.391 | no | 1.755 | 0.545 | yes | 2.337 | 0.307 | yes | 1.508 | 0.528 | no | 0.872 | 0.205 | no | 0.980 | 0.364 | no | 1.546 | 0.408 | yes | 1.970 | 0.445 | yes |
| DR0389 | Alkaline-shock-like protein | 0.867 | 0.177 | no | 0.872 | 0.405 | no | 0.757 | 0.245 | no | 0.886 | 0.285 | no | 0.722 | 0.114 | no | 0.983 | 0.326 | no | 1.101 | 0.634 | no | 0.979 | 0.038 | no | 1.061 | 0.212 | no |
| DR0390 | YloV ortholog, related to a domain of dihydroxy acetone kinase | 0.859 | 0.278 | no | 0.610 | 0.241 | yes | 0.415 | 0.148 | yes | 0.474 | 0.147 | yes | 0.529 | 0.138 | yes | 0.667 | 0.189 | yes | 0.667 | 0.179 | yes | 0.796 | 0.228 | no | 0.912 | 0.127 | no |
| DR0391 | Predicted protein | 0.983 | 0.295 | no | 0.651 | 0.458 | yes | 0.370 | 0.173 | yes | 0.464 | 0.073 | yes | 0.497 | 0.316 | yes | 0.551 | 0.271 | yes | 0.493 | 0.246 | yes | 0.614 | 0.204 | yes | n/a | n/a | n/a |
| DR0392 | Probably fragment of similarity to OSMY of E.coli | 0.904 | 0.314 | no | 0.404 | 0.152 | yes | 0.292 | 0.074 | yes | 0.287 | 0.068 | yes | 0.316 | 0.135 | yes | 0.463 | 0.162 | yes | 0.509 | 0.206 | yes | 0.676 | 0.229 | yes | 0.360 | 0.088 | yes |
| DR0393 | Elongation factor EF-G | 1.365 | 0.831 | no | 2.238 | 0.666 | yes | 2.339 | 0.943 | yes | 2.482 | 0.325 | yes | 1.586 | 0.768 | no | 1.267 | 0.160 | no | 1.221 | 0.190 | no | 0.913 | 0.120 | no | 0.485 | 0.199 | yes |
| DR0394 | Antibiotic/homoserin kinase related protein | 1.346 | 0.387 | no | 4.701 | 1.304 | yes | 7.509 | 2.755 | yes | 7.041 | 1.994 | yes | 4.846 | 3.127 | yes | 2.259 | 0.364 | yes | 1.876 | 0.490 | yes | 1.074 | 0.287 | no | 0.850 | 0.189 | no |
| DR0395 | Permease MDR-type | 0.952 | 0.347 | no | 3.939 | 2.462 | yes | 4.397 | 2.117 | yes | 3.543 | 1.585 | yes | 3.447 | 2.488 | yes | 1.887 | 0.436 | yes | 1.648 | 0.474 | yes | 1.132 | 0.258 | no | 0.902 | 0.108 | no |
| DR0396 | Predicted protein | 0.658 | 0.317 | yes | 3.774 | 1.681 | yes | 5.575 | 2.385 | yes | 3.836 | 2.040 | yes | 3.725 | 1.185 | yes | 2.692 | 0.562 | yes | 1.961 | 0.745 | yes | 1.078 | 0.398 | no | 0.768 | 0.265 | no |
| DR0397 | Metal cluster oxidoreductase, probably formate dehydrogenase | 1.117 | 0.240 | no | 0.661 | 0.273 | yes | 0.569 | 0.202 | yes | 0.523 | 0.122 | yes | 0.716 | 0.208 | no | 0.641 | 0.152 | yes | 0.753 | 0.068 | no | 0.752 | 0.158 | no | 0.845 | 0.135 | no |
| DR0398 | Predicted protein | 1.037 | 0.329 | no | 0.925 | 0.255 | no | 1.067 | 0.421 | no | 0.838 | 0.182 | no | 1.228 | 0.579 | no | 1.090 | 0.152 | no | 0.939 | 0.270 | no | 1.083 | 0.339 | no | 0.817 | 0.208 | no |
| DR0399 | Triple fascilin-like repeat, possible cell surface protein, homologs in predominantly mycobacteriacaea/cyanobacteria/eukaryotes | 1.369 | 0.808 | no | 1.016 | 0.391 | no | 1.054 | 0.525 | no | 1.980 | 0.264 | yes | 1.990 | 1.207 | yes | 2.844 | 1.411 | yes | 3.414 | 1.189 | yes | 3.553 | 0.149 | yes | 1.962 | 0.124 | yes |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR0400 | FTSK, cell division ATPase | 1.031 | 0.179 | no | 1.586 | 0.473 | yes | 1.732 | 0.407 | yes | 1.759 | 0.141 | yes | 1.993 | 1.251 | yes | 1.382 | 0.329 | no | 1.323 | 0.520 | no | 1.190 | 0.215 | no | 1.115 | 0.087 | no |
| DR0401 | Membrane protein | 1.083 | 0.469 | no | 1.315 | 0.265 | no | 1.073 | 0.185 | no | 0.859 | 0.184 | no | 1.170 | 0.505 | no | 1.217 | 0.357 | no | 1.183 | 0.420 | no | 1.043 | 0.239 | no | 0.842 | 0.160 | no |
| DR0402 | PAD1/JAB1-related domain superfamily related protein | 1.401 | 0.228 | no | 1.327 | 0.666 | no | 1.250 | 0.818 | no | 1.667 | 1.267 | no | 0.888 | 0.408 | no | 1.066 | 0.600 | no | 0.999 | 0.314 | no | 0.983 | 0.237 | no | 0.971 | 0.311 | no |
| DR0403 | Inosine-uridine nucleoside hydrolase | 1.025 | 0.305 | no | 1.037 | 0.085 | no | 0.657 | 0.197 | yes | 0.692 | 0.053 | no | 0.791 | 0.241 | no | 1.047 | 0.272 | no | 0.927 | 0.289 | no | 0.956 | 0.152 | no | 1.191 | 0.227 | no |
| DR0404 | Predicted protein | 1.201 | 0.409 | no | 0.673 | 0.185 | yes | 0.751 | 0.230 | no | 1.252 | 0.290 | no | 1.311 | 0.358 | no | 1.365 | 0.566 | no | 1.706 | 0.488 | yes | 1.863 | 0.204 | yes | 2.650 | 0.405 | yes |
| DR0405 | Pullulanase, starch debranching enzyme | 1.139 | 0.346 | no | 1.111 | 0.195 | no | 1.011 | 0.339 | no | 1.336 | 0.405 | no | 1.155 | 0.612 | no | 1.071 | 0.424 | no | 1.194 | 0.550 | no | 1.028 | 0.100 | no | 0.771 | 0.150 | no |
| DR0406 | ABC ATPase | 0.887 | 0.130 | no | 0.736 | 0.097 | no | 0.950 | 0.183 | no | 1.090 | 0.081 | no | 1.235 | 0.198 | no | 1.186 | 0.221 | no | 1.310 | 0.145 | no | 1.135 | 0.053 | no | 0.623 | 0.092 | yes |
| DR0407 | Membrane protein related to cytochrome c maturation protein B | 1.232 | 0.246 | no | 0.871 | 0.254 | no | 0.648 | 0.214 | yes | 0.860 | 0.387 | no | 0.857 | 0.141 | no | 0.994 | 0.309 | no | 1.047 | 0.243 | no | 0.867 | 0.239 | no | 0.800 | 0.089 | no |
| DR0408 | Receiver domain, CHEY family | 0.985 | 0.244 | no | 0.798 | 0.226 | no | 0.583 | 0.149 | yes | 1.076 | 0.384 | no | 1.171 | 0.325 | no | 1.210 | 0.461 | no | 2.023 | 0.665 | yes | 1.900 | 0.144 | yes | 1.372 | 0.449 | no |
| DR0409 | YfiT-like metal-binding protein | 0.939 | 0.180 | no | 1.482 | 0.381 | yes | 1.461 | 0.486 | no | 1.226 | 0.188 | no | 1.277 | 0.329 | no | 1.197 | 0.059 | no | 0.978 | 0.326 | no | 1.046 | 0.385 | no | 0.601 | 0.100 | yes |
| DR0410 | Protein with the DXD active site, related to inorganic pyrophosphatase | 1.066 | 0.374 | no | 1.335 | 0.589 | no | 1.349 | 0.441 | no | 1.433 | 0.264 | no | 1.316 | 0.703 | no | 0.880 | 0.237 | no | 0.813 | 0.416 | no | 0.828 | 0.101 | no | 0.654 | 0.082 | no |
| DR0411 | Rossman fold Oxidoreductase | 0.736 | 0.090 | no | 1.500 | 0.577 | yes | 1.174 | 0.275 | no | 1.016 | 0.094 | no | 1.161 | 0.613 | no | 1.108 | 0.249 | no | 1.025 | 0.378 | no | 0.834 | 0.209 | no | 0.721 | 0.262 | no |
| DR0412 | Thioredoxin fold reductase, AHPF | 0.754 | 0.281 | no | 2.587 | 0.904 | yes | 2.481 | 1.232 | yes | 2.798 | 1.535 | yes | 3.759 | 3.166 | yes | 1.823 | 0.974 | yes | 1.277 | 0.441 | no | 1.285 | 0.216 | no | 1.025 | 0.518 | no |
| DR0413 | Predicted protein | 0.745 | 0.086 | no | 2.658 | 0.657 | yes | 2.714 | 0.607 | yes | 1.995 | 0.658 | yes | 2.820 | 0.961 | yes | 2.243 | 0.760 | yes | 2.188 | 1.240 | yes | 2.140 | 0.252 | yes | 0.615 | 0.365 | yes |
| DR0414 | HAD superfamily Hydrolase | 1.131 | 0.363 | no | 1.535 | 0.454 | yes | 1.525 | 0.455 | yes | 1.425 | 0.242 | no | 1.473 | 0.846 | no | 1.088 | 0.217 | no | 1.122 | 0.345 | no | 1.086 | 0.110 | no | 0.778 | 0.180 | no |
| DR0415 | Esterase of the acetylcholinesterase family | 1.096 | 0.430 | no | 2.498 | 0.579 | yes | 1.379 | 0.977 | no | 2.686 | 0.500 | yes | 2.038 | 0.578 | yes | 2.553 | 0.535 | yes | 1.505 | 0.533 | no | 1.576 | 0.616 | no | 0.612 | 0.002 | no |
| DR0416 | Regulatory protein mazE/PEMI family | 1.018 | 0.182 | no | 1.396 | 0.427 | no | 1.391 | 0.290 | no | 1.379 | 0.275 | no | 1.419 | 0.610 | no | 1.318 | 0.506 | no | 1.152 | 0.326 | no | 1.173 | 0.388 | no | 0.623 | 0.269 | yes |
| DR0417 | PEMK ortholog, DNA binding protein, regulator of replication of plasmids, CHPA oe MazF | 0.802 | 0.243 | no | 1.518 | 0.285 | yes | 1.969 | 0.624 | yes | 1.235 | 0.402 | no | 1.757 | 0.684 | yes | 1.323 | 0.461 | no | 1.335 | 0.597 | no | 1.448 | 0.648 | no | 0.785 | 0.386 | no |
| DR0418 | Predicted protein | 0.926 | 0.344 | no | 0.905 | 0.345 | no | 0.965 | 0.523 | no | 1.083 | 0.315 | no | 1.502 | 1.181 | no | 0.691 | 0.149 | no | 0.676 | 0.234 | yes | 0.766 | 0.308 | no | 0.456 | 0.122 | yes |
| DR0419 | PIN domain containing protein, VapC family | 0.777 | 0.187 | no | 1.037 | 0.271 | no | 1.114 | 0.184 | no | 0.927 | 0.389 | no | 0.885 | 0.246 | no | 0.948 | 0.368 | no | 0.726 | 0.127 | no | 0.784 | 0.100 | no | 0.440 | 0.147 | yes |
| DR0420 | Superfamily II helicase, HrpB ortholog | 1.028 | 0.265 | no | 1.705 | 0.519 | yes | 2.037 | 1.216 | yes | 1.373 | 0.394 | no | 1.565 | 0.768 | no | 1.606 | 0.487 | yes | 1.234 | 0.465 | no | 0.901 | 0.234 | no | 0.595 | 0.132 | yes |
| DR0421 | Predicted protein | 0.931 | 0.292 | no | 4.086 | 1.421 | yes | 4.939 | 2.302 | yes | 3.807 | 1.748 | yes | 3.071 | 1.332 | yes | 2.030 | 1.088 | yes | 2.064 | 0.886 | yes | 1.426 | 0.315 | no | 1.473 | 0.325 | yes |
| DR0422 | SAM dependent methyltransferase | 1.277 | 0.268 | no | 13.988 | 5.291 | yes | 18.845 | 7.461 | yes | 10.954 | 5.139 | yes | 8.176 | 1.434 | yes | 4.392 | 1.837 | yes | 2.693 | 0.969 | yes | 1.787 | 0.591 | yes | 1.138 | 0.528 | no |
| DR0423 | Phage related protein | 1.462 | 0.896 | no | 4.512 | 2.862 | yes | 2.780 | 1.121 | yes | 2.806 | 0.787 | yes | 2.979 | 1.449 | yes | 1.886 | 1.218 | yes | 1.946 | 1.073 | yes | 1.655 | 0.206 | yes | 0.606 | 0.259 | yes |
| DR0424 | Imidazoleglycerol-phosphate dehydratase, HIS7 | 1.211 | 0.357 | no | 1.668 | 0.724 | yes | 1.125 | 0.467 | no | 1.000 | 0.193 | no | 0.941 | 0.120 | no | 0.849 | 0.242 | no | 0.894 | 0.246 | no | 0.865 | 0.224 | no | 0.934 | 0.192 | no |
| DR0425 | Predicted protein | 1.087 | 0.363 | no | 1.268 | 0.651 | no | 0.888 | 0.353 | no | 0.745 | 0.271 | no | 0.802 | 0.401 | no | 0.600 | 0.179 | yes | 0.773 | 0.216 | no | 0.860 | 0.095 | no | 0.929 | 0.330 | no |
| DR0426 | Imidazoleglycerol-phosphate synthase, HIS5 | 1.757 | 1.270 | no | 1.427 | 0.947 | no | 0.823 | 0.516 | no | 1.101 | 0.780 | no | 0.892 | 0.418 | no | 0.689 | 0.150 | no | 1.075 | 0.513 | no | 1.014 | 0.263 | no | 1.211 | 0.405 | no |
| DR0427 | General stress protein Ctc | 0.822 | 0.444 | no | 0.969 | 0.506 | no | 0.833 | 0.233 | no | 0.441 | 0.164 | yes | 0.767 | 0.353 | no | 0.911 | 0.475 | no | 0.983 | 0.308 | no | 0.881 | 0.307 | no | 1.105 | 0.277 | no |
| DR0428 | Methylguanine-DNA methyltransferase | 0.812 | 0.294 | no | 1.923 | 0.597 | yes | 1.743 | 0.602 | yes | 1.172 | 0.326 | no | 1.203 | 0.244 | no | 0.977 | 0.235 | no | 0.742 | 0.134 | no | 0.819 | 0.240 | no | 0.803 | 0.209 | no |
| DR0429 | Cytochrome C related protein | 0.858 | 0.343 | no | 0.620 | 0.268 | yes | 0.370 | 0.147 | yes | 0.241 | 0.068 | yes | 0.360 | 0.145 | yes | 0.398 | 0.130 | yes | 0.486 | 0.152 | yes | 0.603 | 0.234 | yes | 1.027 | 0.392 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR0430 | E.coli RTCB family protein | 0.996 | 0.442 | no | 1.128 | 0.337 | no | 3.064 | 1.032 | yes | 3.487 | 1.344 | yes | 2.887 | 1.007 | yes | 2.557 | 0.227 | yes | 2.725 | 0.535 | yes | 2.201 | 0.361 | yes | 1.367 | 0.183 | no |
| DR0431 | SAM-dependent methyltransferase | 0.913 | 0.293 | no | 0.842 | 0.382 | no | 1.349 | 0.605 | no | 1.508 | 0.218 | no | 1.168 | 0.257 | no | 1.169 | 0.580 | no | 1.284 | 0.571 | no | 1.029 | 0.161 | no | 0.864 | 0.222 | no |
| DR0432 | Response regulator: receiver domain, CHEY family + HTH transcriptional regulator | 0.751 | 0.309 | no | 0.422 | 0.092 | yes | 0.607 | 0.111 | yes | 0.621 | 0.088 | yes | 0.630 | 0.227 | yes | 0.491 | 0.180 | yes | 0.670 | 0.203 | yes | 0.582 | 0.216 | yes | 1.012 | 0.304 | no |
| DR0433 | Beta lactamase | 0.895 | 0.495 | no | 0.608 | 0.355 | yes | 0.687 | 0.342 | yes | 0.475 | 0.061 | yes | 0.650 | 0.149 | yes | 0.678 | 0.354 | yes | 0.700 | 0.293 | yes | 0.637 | 0.155 | yes | 0.766 | 0.069 | no |
| DR0434 | Metal binding cluster, cytochrome C6 like | 0.915 | 0.231 | no | 0.586 | 0.139 | yes | 0.460 | 0.064 | yes | 0.374 | 0.099 | yes | 0.380 | 0.111 | yes | 0.443 | 0.221 | yes | 0.438 | 0.176 | yes | 0.472 | 0.133 | yes | 1.322 | 0.682 | no |
| DR0435 | Rieske like Fe-S protein | 0.774 | 0.358 | no | 0.665 | 0.233 | yes | 0.559 | 0.226 | yes | 0.465 | 0.179 | yes | 0.480 | 0.179 | yes | 0.488 | 0.264 | yes | 0.477 | 0.212 | yes | 0.528 | 0.121 | yes | 1.776 | 0.719 | yes |
| DR0436 | Cytochrome B6 | 1.243 | 0.878 | no | 0.757 | 0.317 | no | 0.863 | 0.502 | no | 0.709 | 0.418 | yes | 0.627 | 0.283 | yes | 0.679 | 0.353 | yes | 0.691 | 0.248 | yes | 0.693 | 0.167 | yes | 2.408 | 0.907 | yes |
| DR0437 | Predicted protein | 0.947 | 0.277 | no | 0.799 | 0.249 | no | 0.748 | 0.170 | no | 0.695 | 0.096 | no | 0.706 | 0.220 | no | 0.549 | 0.146 | yes | 0.680 | 0.164 | yes | 0.639 | 0.192 | yes | 0.779 | 0.219 | no |
| DR0438 | Predicted protein | 1.005 | 0.250 | no | 0.552 | 0.115 | yes | 0.515 | 0.066 | yes | 0.496 | 0.122 | yes | 0.465 | 0.139 | yes | 0.377 | 0.191 | yes | 0.425 | 0.157 | yes | 0.296 | 0.075 | yes | 0.439 | 0.047 | yes |
| DR0439 | Hes2 family of small cysteine rich proteins | 0.864 | 0.310 | no | 0.434 | 0.161 | yes | 0.293 | 0.120 | yes | 0.310 | 0.049 | yes | 0.472 | 0.235 | yes | 0.397 | 0.061 | yes | 0.405 | 0.162 | yes | 0.411 | 0.103 | yes | 0.828 | 0.356 | no |
| DR0440 | RuvC, crossover junction endodeoxyribonuclease, HhH domain | 0.933 | 0.451 | no | 0.855 | 0.396 | no | 0.616 | 0.334 | yes | 0.586 | 0.412 | yes | 0.473 | 0.209 | yes | 0.457 | 0.262 | yes | 0.350 | 0.151 | yes | 0.231 | 0.088 | yes | 0.195 | 0.089 | yes |
| DR0441 | Conserved membrane protein | 1.370 | 0.837 | no | 0.797 | 0.484 | no | 0.826 | 0.622 | no | 0.524 | 0.392 | yes | 0.579 | 0.259 | yes | 0.584 | 0.292 | yes | 0.388 | 0.142 | yes | 0.375 | 0.137 | yes | 0.441 | 0.172 | yes |
| DR0442 | PilT protein, ATPase | 1.182 | 0.560 | no | 1.424 | 0.479 | no | 1.091 | 0.392 | no | 0.869 | 0.184 | no | 0.962 | 0.266 | no | 0.780 | 0.267 | no | 0.732 | 0.210 | no | 0.864 | 0.317 | no | 1.009 | 0.499 | no |
| DR0443 | Pyrimidine nucleoside phosphorylase, DeoA ortholog | 1.125 | 0.352 | no | 1.171 | 0.361 | no | 0.817 | 0.280 | no | 0.608 | 0.307 | yes | 0.703 | 0.499 | yes | 0.720 | 0.114 | no | 0.667 | 0.357 | yes | 0.764 | 0.033 | no | 0.759 | 0.139 | no |
| DR0444 | LPS glycosyltransferase | 0.920 | 0.549 | no | 1.540 | 0.467 | yes | 1.255 | 0.407 | no | 2.485 | 0.249 | yes | 2.330 | 1.422 | yes | 1.663 | 0.533 | yes | 1.157 | 0.436 | no | 1.345 | 0.560 | no | 0.693 | 0.424 | yes |
| DR0445 | Related to 2 bacillus proteins yjfC, yjaZ; histidine dyad similar to some proteases | 0.977 | 0.403 | no | 1.050 | 0.457 | no | 0.724 | 0.261 | no | 3.174 | 1.848 | yes | 0.603 | 0.291 | yes | 0.184 | 0.021 | yes | 0.745 | 0.328 | no | 1.038 | 0.190 | no | n/a | n/a | n/a |
| DR0446 | Monooxygenase snoB | 0.981 | 0.394 | no | 0.578 | 0.200 | yes | 0.427 | 0.145 | yes | 0.363 | 0.106 | yes | 0.451 | 0.158 | yes | 0.447 | 0.128 | yes | 0.429 | 0.110 | yes | 0.651 | 0.081 | yes | 0.939 | 0.103 | no |
| DR0447 | Orotate/uridine Phosphoribosyltransferase, PyrE | 1.051 | 0.493 | no | 0.843 | 0.390 | no | 0.728 | 0.519 | yes | 0.520 | 0.166 | yes | 0.602 | 0.193 | yes | 0.639 | 0.246 | yes | 0.891 | 0.211 | no | 0.825 | 0.107 | no | 1.572 | 0.419 | yes |
| DR0448 | Probable cro-like HTH | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR0449 | Predicted protein | 1.106 | 0.231 | no | 1.268 | 0.223 | no | 1.176 | 0.327 | no | 1.056 | 0.198 | no | 1.222 | 0.522 | no | 0.940 | 0.147 | no | 0.930 | 0.237 | no | 0.936 | 0.185 | no | 0.960 | 0.164 | no |
| DR0450 | Conserved family related to PIG-L (a possible N-acetylglucosaminyl-phosphatidylinositoldeacetylase) | 0.876 | 0.320 | no | 1.172 | 0.625 | no | 1.475 | 0.883 | no | 1.000 | 0.109 | no | 1.085 | 0.314 | no | 1.270 | 0.384 | no | 1.409 | 0.520 | no | 1.551 | 0.545 | yes | 1.417 | 0.776 | no |
| DR0451 | Glutamine synthetase, GLNA | 1.283 | 0.352 | no | 1.370 | 0.303 | no | 1.410 | 0.440 | no | 1.203 | 0.295 | no | 1.303 | 0.395 | no | 1.046 | 0.255 | no | 1.258 | 0.362 | no | 1.250 | 0.169 | no | 1.444 | 0.570 | no |
| DR0452 | Barstar-like nuclease inhibitor | 0.742 | 0.247 | no | 0.829 | 0.290 | no | 0.749 | 0.248 | no | 0.634 | 0.213 | yes | 0.830 | 0.120 | no | 0.922 | 0.111 | no | 1.072 | 0.198 | no | 1.133 | 0.242 | no | 1.467 | 0.479 | no |
| DR0453 | Guanyl-specific ribonuclease SA3 | 0.945 | 0.325 | no | 1.141 | 0.338 | no | 1.171 | 0.415 | no | 1.106 | 0.530 | no | 1.193 | 0.408 | no | 1.106 | 0.370 | no | 1.353 | 0.224 | no | 1.609 | 0.349 | yes | 1.972 | 0.357 | yes |
| DR0454 | BacA bacitracin resistance protein, claimed to be an undecaprenol kinase | 0.924 | 0.392 | no | 0.969 | 0.409 | no | 1.029 | 0.365 | no | 0.606 | 0.110 | yes | 0.781 | 0.283 | no | 1.224 | 0.639 | no | 0.851 | 0.221 | no | 1.117 | 0.323 | no | 1.902 | 0.707 | yes |
| DR0455 | STR streptomycin resistance protein, streptomycin phosphotransferase | 1.386 | 0.337 | no | 1.129 | 0.284 | no | 1.131 | 0.215 | no | 1.137 | 0.284 | no | 0.987 | 0.402 | no | 0.956 | 0.290 | no | 0.871 | 0.429 | no | 0.874 | 0.053 | no | 0.931 | 0.144 | no |
| DR0456 | Conserved membrane protein, ExbB/TolQ ortholog, biopolymer transport | 0.661 | 0.194 | yes | 1.202 | 0.423 | no | 1.393 | 0.489 | no | 1.132 | 0.146 | no | 1.223 | 0.379 | no | 1.423 | 0.717 | no | 1.749 | 0.561 | yes | 1.546 | 0.197 | yes | 2.141 | 0.305 | yes |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR0457 | ExbD/TolR biopolymer transport membrane protein | 0.746 | 0.436 | yes | 2.188 | 0.968 | yes | 2.456 | 0.493 | yes | 2.610 | 0.731 | yes | 1.641 | 0.480 | yes | 1.276 | 0.262 | no | 0.862 | 0.296 | no | 0.777 | 0.049 | no | 1.970 | 0.427 | yes |
| DR0458 | Predicted protein (low complexity) | 0.952 | 0.452 | no | 1.651 | 0.639 | yes | 2.473 | 0.932 | yes | 1.945 | 0.440 | yes | 2.539 | 1.842 | yes | 1.728 | 0.329 | yes | 1.211 | 0.189 | no | 1.233 | 0.211 | no | 1.804 | 0.322 | yes |
| DR0459 | Secreted protein, uncharacterized | 0.689 | 0.259 | yes | 1.530 | 0.475 | yes | 2.326 | 1.081 | yes | 1.154 | 0.076 | no | 2.525 | 1.212 | yes | 2.361 | 1.012 | yes | 1.899 | 0.855 | yes | 2.086 | 0.965 | yes | 3.309 | 1.358 | yes |
| DR0460 | Acetyl-CoA synthetase | 0.935 | 0.251 | no | 0.306 | 0.085 | yes | 0.852 | 0.453 | no | 1.361 | 0.074 | no | 0.763 | 0.427 | no | 0.564 | 0.355 | yes | 1.383 | 0.576 | no | 0.571 | 0.152 | yes | 1.706 | 0.718 | yes |
| DR0461 | Hsp-70-sugar kinase superfamily protein, Bacillus yacB ortholog | 1.217 | 0.700 | no | 1.347 | 0.662 | no | 1.886 | 1.165 | yes | 1.576 | 0.728 | no | 1.092 | 0.357 | no | 1.242 | 0.768 | no | 1.121 | 0.471 | no | 1.732 | 0.837 | yes | 2.584 | 0.807 | yes |
| DR0462 | Periplasmic binding protein, similar to iron-binding protein | 1.434 | 0.747 | no | 0.929 | 0.101 | no | 0.938 | 0.281 | no | 0.845 | 0.208 | no | 1.038 | 0.647 | no | 0.954 | 0.313 | no | 1.017 | 0.302 | no | 0.974 | 0.120 | no | 1.015 | 0.422 | no |
| DR0463 | Maltooligosyl trehalose synthase | 0.965 | 0.154 | no | 0.882 | 0.269 | no | 0.833 | 0.209 | no | 0.828 | 0.046 | no | 1.152 | 0.789 | no | 0.886 | 0.167 | no | 0.754 | 0.158 | no | 0.709 | 0.111 | no | 0.843 | 0.145 | no |
| DR0464 | Trehalose trehalohydrolase, glucan branching enzyme | 0.827 | 0.201 | no | 0.717 | 0.140 | no | 0.899 | 0.398 | no | 0.682 | 0.045 | no | 1.029 | 0.463 | no | 1.031 | 0.257 | no | 0.781 | 0.086 | no | 0.728 | 0.209 | yes | 0.691 | 0.145 | no |
| DR0465 | PR1 domain protein, plant pathogenesis-related protein | 1.310 | 0.418 | no | 1.206 | 0.758 | no | 1.235 | 0.838 | no | 0.718 | 0.266 | no | 0.754 | 0.295 | no | 0.792 | 0.216 | no | 0.790 | 0.171 | no | 0.790 | 0.104 | no | 1.114 | 0.414 | no |
| DR0466 | 2 PAS domains + Truncated PAS (PAC) + GGDEF + YJCC domain signalling protein | 0.882 | 0.185 | no | 1.424 | 0.885 | no | 0.802 | 0.389 | no | 0.673 | 0.197 | no | 1.237 | 0.906 | no | 0.588 | 0.101 | yes | 0.563 | 0.198 | yes | 0.597 | 0.172 | yes | n/a | n/a | n/a |
| DR0467 | DNA polymerase of the X family with C terminal PHP domain | 1.159 | 0.219 | no | 1.205 | 0.425 | no | 0.829 | 0.269 | no | 0.790 | 0.062 | no | 0.923 | 0.340 | no | 0.883 | 0.340 | no | 0.671 | 0.111 | yes | 0.836 | 0.106 | no | 0.903 | 0.243 | no |
| DR0468 | Possible SAM dependent methyltransferase | 1.207 | 0.815 | no | 1.181 | 0.491 | no | 0.541 | 0.119 | yes | 0.727 | 0.362 | no | 1.000 | 0.514 | no | 0.993 | 0.483 | no | 0.728 | 0.224 | no | 0.867 | 0.072 | no | 0.685 | 0.407 | yes |
| DR0469 | Uncharacterized, member of large family of Synechocystis | 1.143 | 0.370 | no | 0.788 | 0.206 | no | 0.482 | 0.216 | yes | 0.562 | 0.060 | yes | 0.588 | 0.171 | yes | 0.844 | 0.458 | no | 0.947 | 0.464 | no | 0.908 | 0.276 | no | 1.690 | 0.709 | yes |
| DR0470 | PHP superfamily histidinol phosphatase, HIS9 | 1.163 | 0.371 | no | 0.754 | 0.064 | no | 0.485 | 0.135 | yes | 0.581 | 0.319 | yes | 0.526 | 0.244 | yes | 0.817 | 0.361 | no | 0.661 | 0.400 | yes | 0.819 | 0.398 | no | 1.172 | 0.576 | no |
| DR0471 | SMF family of proteins | 1.326 | 0.554 | no | 0.978 | 0.489 | no | 0.873 | 0.438 | no | 0.516 | 0.135 | yes | 0.591 | 0.366 | yes | 0.824 | 0.493 | no | 0.808 | 0.373 | no | 0.856 | 0.213 | no | 1.154 | 0.561 | no |
| DR0472 | TCR tetracyclin resistance protein | 1.042 | 0.343 | no | 0.822 | 0.141 | no | 0.846 | 0.335 | no | 0.605 | 0.094 | yes | 0.668 | 0.267 | yes | 0.931 | 0.302 | no | 0.713 | 0.236 | no | 0.897 | 0.259 | no | 0.773 | 0.184 | no |
| DR0473 | ABC transporter, ATPase | 1.035 | 0.336 | no | 1.324 | 0.376 | no | 1.296 | 0.461 | no | 1.211 | 0.313 | no | 0.967 | 0.165 | no | 1.171 | 0.176 | no | 1.025 | 0.353 | no | 1.006 | 0.155 | no | 0.943 | 0.090 | no |
| DR0474 | ABC transporter, permease | 0.884 | 0.235 | no | 1.074 | 0.282 | no | 1.033 | 0.331 | no | 0.879 | 0.073 | no | 1.002 | 0.217 | no | 1.137 | 0.318 | no | 0.956 | 0.445 | no | 1.139 | 0.417 | no | 0.919 | 0.512 | no |
| DR0475 | Double ABC transporter ATPase | 1.299 | 0.417 | no | 2.393 | 1.258 | yes | 1.998 | 0.607 | yes | 2.128 | 0.913 | yes | 1.836 | 0.827 | yes | 1.462 | 0.657 | no | 1.427 | 0.791 | no | 0.982 | 0.126 | no | 0.864 | 0.150 | no |
| DR0476 | Small membrane protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR0477 | Membrane permease, DhlC homolog | 1.226 | 0.312 | no | 4.278 | 2.075 | yes | 4.629 | 1.705 | yes | 3.738 | 0.961 | yes | 2.553 | 0.658 | yes | 1.960 | 0.488 | yes | 1.625 | 0.755 | yes | 1.407 | 0.646 | no | 1.055 | 0.456 | no |
| DR0478 | Aminopeptidase P | 1.020 | 0.179 | no | 2.863 | 0.554 | yes | 2.860 | 1.347 | yes | 2.778 | 0.446 | yes | 2.186 | 0.852 | yes | 1.754 | 0.448 | yes | 1.509 | 0.366 | yes | 1.384 | 0.212 | no | 1.363 | 0.243 | no |
| DR0479 | PBP1 penicillin-binding protein 1 | 0.630 | 0.251 | yes | 5.678 | 1.738 | yes | 7.072 | 2.419 | yes | 4.170 | 0.586 | yes | 4.172 | 1.130 | yes | 2.899 | 0.959 | yes | 1.839 | 0.955 | yes | 1.138 | 0.306 | no | 0.924 | 0.160 | no |
| DR0480 | PP- loop superfamily ATPase | 1.041 | 0.423 | no | 2.371 | 1.145 | yes | 1.556 | 0.534 | yes | 0.899 | 0.051 | no | 1.285 | 0.545 | no | 1.400 | 0.687 | no | 1.087 | 0.456 | no | 0.931 | 0.134 | no | 1.049 | 0.111 | no |
| DR0481 | Predicted protein | 0.799 | 0.217 | no | 1.230 | 0.389 | no | 0.655 | 0.277 | yes | 0.583 | 0.280 | yes | 0.691 | 0.227 | yes | 0.510 | 0.167 | yes | 0.551 | 0.139 | yes | 0.544 | 0.119 | yes | 0.604 | 0.128 | yes |
| DR0482 | Prohibitin like protein | 0.911 | 0.297 | no | 2.441 | 0.924 | yes | 0.928 | 0.320 | no | 1.143 | 0.241 | no | 0.893 | 0.194 | no | 0.813 | 0.170 | no | 1.077 | 0.234 | no | 0.868 | 0.201 | no | 0.711 | 0.200 | no |
| DR0483 | Cysteine rich protein, SECA-type C-motif | 1.181 | 0.228 | no | 1.360 | 0.271 | no | 1.283 | 0.526 | no | 0.909 | 0.100 | no | 1.058 | 0.302 | no | 0.991 | 0.329 | no | 0.977 | 0.347 | no | 1.188 | 0.324 | no | 0.954 | 0.247 | no |
| DR0484 | TPR-repeat protein | 1.030 | 0.510 | no | 1.859 | 0.439 | yes | 1.387 | 0.317 | no | 1.237 | 0.279 | no | 1.353 | 0.490 | no | 1.130 | 0.239 | no | 1.340 | 0.316 | no | 1.110 | 0.356 | no | 1.397 | 0.181 | no |
| DR0485 | Glutamyl tRNA synthetase | 1.076 | 0.398 | no | 0.794 | 0.359 | no | 0.526 | 0.211 | yes | 0.361 | 0.172 | yes | 0.508 | 0.237 | yes | 0.761 | 0.374 | no | 1.005 | 0.514 | no | 1.409 | 0.628 | no | 1.744 | 0.570 | yes |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR0486 | Possible secreted protein, uncharacterized | 0.849 | 0.111 | no | 0.622 | 0.157 | yes | 0.507 | 0.130 | yes | 0.499 | 0.032 | yes | 0.553 | 0.040 | yes | 0.608 | 0.153 | yes | 0.546 | 0.165 | yes | 0.830 | 0.177 | no | 1.022 | 0.419 | no |
| DR0487 | Membrane protein | 1.077 | 0.550 | no | 0.766 | 0.259 | no | 0.818 | 0.410 | no | 0.580 | 0.274 | yes | 0.447 | 0.226 | yes | 0.532 | 0.294 | yes | 0.653 | 0.449 | yes | 0.651 | 0.119 | yes | 0.411 | 0.189 | yes |
| DR0488 | Related to murein-degrading hydrolase, MLTA | 0.850 | 0.360 | no | 0.861 | 0.297 | no | 0.599 | 0.308 | yes | 0.514 | 0.244 | yes | 0.709 | 0.252 | no | 0.501 | 0.119 | yes | 0.543 | 0.187 | yes | 0.607 | 0.137 | yes | 1.092 | 0.523 | no |
| DR0489 | Predicted protein | 1.100 | 0.273 | no | 0.857 | 0.383 | no | 0.853 | 0.248 | no | 1.261 | 0.158 | no | 1.372 | 0.284 | no | 1.597 | 0.419 | yes | 2.112 | 0.775 | yes | 1.873 | 0.228 | yes | 1.677 | 0.389 | yes |
| DR0490 | Pyrrolidone Carboxyl Peptidase, PDXH | 1.083 | 0.416 | no | 0.925 | 0.234 | no | 0.734 | 0.204 | no | 1.186 | 0.809 | no | 0.698 | 0.156 | no | 0.795 | 0.186 | no | 0.865 | 0.311 | no | 0.815 | 0.230 | no | 0.781 | 0.255 | no |
| DR0491 | ThiJ superfamily of proteins, possible intracellular protease | 1.158 | 0.408 | no | 0.867 | 0.307 | no | 0.831 | 0.311 | no | 1.049 | 0.327 | no | 1.701 | 0.502 | yes | 2.354 | 1.271 | yes | 2.526 | 1.176 | yes | 2.005 | 0.601 | yes | 1.703 | 0.623 | yes |
| DR0492 | Uncharacterized small protein | 0.679 | 0.312 | no | 0.372 | 0.161 | yes | 0.621 | 0.192 | yes | 0.691 | 0.398 | no | 1.698 | 0.531 | yes | 1.858 | 0.563 | yes | 1.161 | 0.437 | no | 0.717 | 0.248 | no | n/a | n/a | n/a |
| DR0493 | Formamidopyrimidine-DNA glycosidase, MutM | 1.087 | 0.214 | no | 0.628 | 0.089 | yes | 0.459 | 0.086 | yes | 0.563 | 0.127 | yes | 0.645 | 0.118 | yes | 0.828 | 0.270 | no | 0.871 | 0.238 | no | 1.129 | 0.292 | no | 1.311 | 0.417 | no |
| DR0494 | P-loop kinase, Flar protein ortholog | 0.930 | 0.344 | no | 1.288 | 0.767 | no | 1.061 | 0.217 | no | 1.011 | 0.109 | no | 1.052 | 0.513 | no | 1.116 | 0.614 | no | 0.985 | 0.605 | no | 0.675 | 0.214 | yes | 0.520 | 0.234 | yes |
| DR0495 | Pyridoxamine 5'-phosphate oxidase | 1.088 | 0.359 | no | 0.970 | 0.451 | no | 0.839 | 0.563 | no | 0.616 | 0.062 | yes | 0.675 | 0.144 | no | 1.056 | 0.600 | no | 0.947 | 0.621 | no | 1.049 | 0.428 | no | 1.253 | 0.564 | no |
| DR0496 | Rossman fold oxidoreductase | 1.025 | 0.339 | no | 0.683 | 0.174 | yes | 0.617 | 0.163 | yes | 0.537 | 0.037 | yes | 0.679 | 0.211 | yes | 0.989 | 0.367 | no | 0.940 | 0.305 | no | 1.143 | 0.236 | no | 1.321 | 0.275 | no |
| DR0497 | Similar to phosphoglycerate dehydrogenase, shares domain with beta-subunit of L-serine dehydratase | 0.930 | 0.169 | no | 0.805 | 0.220 | no | 0.739 | 0.070 | no | 0.779 | 0.230 | no | 0.916 | 0.138 | no | 1.053 | 0.339 | no | 0.981 | 0.220 | no | 1.246 | 0.241 | no | 1.225 | 0.252 | no |
| DR0498 | MVIN-like membrane protein | 0.656 | 0.237 | yes | 0.521 | 0.238 | yes | 0.334 | 0.090 | yes | 0.245 | 0.055 | yes | 0.334 | 0.136 | yes | 0.384 | 0.129 | yes | 0.527 | 0.217 | yes | 0.642 | 0.089 | yes | 0.915 | 0.145 | no |
| DR0499 | 3-hydroxyisobutyrate dehydrogenase | 1.020 | 0.234 | no | 0.943 | 0.232 | no | 0.790 | 0.172 | no | 0.776 | 0.130 | no | 0.739 | 0.111 | no | 0.991 | 0.233 | no | 1.043 | 0.214 | no | 1.114 | 0.228 | no | 1.167 | 0.106 | no |
| DR0500 | DegV-like protein N-terminus | 0.785 | 0.185 | no | 0.713 | 0.177 | no | 0.638 | 0.055 | yes | 0.565 | 0.115 | yes | 0.691 | 0.132 | no | 1.028 | 0.204 | no | 1.085 | 0.243 | no | 1.408 | 0.315 | no | 1.381 | 0.359 | no |
| DR0501 | Dihydroorotate dehydrogenase, pyrD | 1.141 | 0.320 | no | 1.026 | 0.273 | no | 1.033 | 0.273 | no | 1.221 | 0.275 | no | 1.252 | 0.455 | no | 1.143 | 0.380 | no | 1.135 | 0.291 | no | 1.234 | 0.220 | no | 1.086 | 0.228 | no |
| DR0502 | Alanyl tRNA synthetase, short form | 1.043 | 0.193 | no | 0.891 | 0.185 | no | 1.229 | 0.452 | no | 1.065 | 0.049 | no | 1.192 | 0.256 | no | 0.957 | 0.210 | no | 0.964 | 0.258 | no | 0.954 | 0.228 | no | 0.986 | 0.346 | no |
| DR0503 | Protein with beta propeller domain | 1.049 | 0.344 | no | 1.122 | 0.515 | no | 1.217 | 0.337 | no | 1.560 | 0.355 | no | 1.600 | 0.314 | yes | 0.995 | 0.293 | no | 1.040 | 0.542 | no | 1.010 | 0.231 | no | 1.016 | 0.564 | no |
| DR0504 | SAM dependent methyltransferase | 0.801 | 0.316 | no | 1.063 | 0.298 | no | 1.355 | 0.704 | no | 1.078 | 0.016 | no | 1.065 | 0.250 | no | 1.084 | 0.211 | no | 1.004 | 0.506 | no | 1.204 | 0.602 | no | 0.647 | 0.152 | yes |
| DR0505 | 2',3'-cyclic-nucleotidase, calcineurin like phosphoesterases | 1.151 | 0.752 | no | 1.370 | 0.634 | no | 1.735 | 0.676 | yes | 2.116 | 0.556 | yes | 1.721 | 0.746 | yes | 1.220 | 0.335 | no | 1.313 | 0.562 | no | 1.397 | 0.123 | no | 2.584 | 0.559 | yes |
| DR0506 | Predicted protein | 0.792 | 0.137 | no | 1.340 | 0.354 | no | 1.838 | 0.618 | yes | 1.731 | 0.098 | yes | 2.057 | 1.145 | yes | 1.281 | 0.474 | no | 1.171 | 0.440 | no | 0.891 | 0.032 | no | 0.959 | 0.254 | no |
| DR0507 | DNA polymerase III alpha chain, Active PHP, long insert between PHP and rest of the protein | 0.846 | 0.109 | no | 0.826 | 0.145 | no | 0.796 | 0.179 | no | 1.199 | 0.284 | no | 0.902 | 0.202 | no | 0.634 | 0.404 | yes | 0.427 | 0.151 | yes | 0.580 | 0.217 | yes | 0.785 | 0.338 | no |
| DR0508 | Restriction system protein MRR | 1.031 | 0.325 | no | 0.864 | 0.249 | no | 0.796 | 0.184 | no | 0.603 | 0.083 | yes | 0.729 | 0.213 | no | 0.915 | 0.431 | no | 0.801 | 0.445 | no | 0.785 | 0.081 | no | 1.002 | 0.543 | no |
| DR0509 | Predicted protein | 1.192 | 0.274 | no | 1.577 | 0.611 | yes | 1.198 | 0.393 | no | 1.151 | 0.120 | no | 1.037 | 0.336 | no | 0.954 | 0.316 | no | 0.942 | 0.280 | no | 0.946 | 0.027 | no | 0.823 | 0.185 | no |
| DR0510 | Fragm. of sensor histidine kinase | 1.134 | 0.441 | no | 0.772 | 0.188 | no | 0.408 | 0.131 | yes | 0.452 | 0.168 | yes | 0.425 | 0.142 | yes | 0.549 | 0.119 | yes | 0.619 | 0.185 | yes | 0.916 | 0.306 | no | 1.006 | 0.373 | no |
| DR0511 | Nitrate transport ATPase, NRTC | 1.049 | 0.143 | no | 1.531 | 0.191 | yes | 1.492 | 0.369 | yes | 1.156 | 0.043 | no | 1.396 | 0.569 | no | 1.230 | 0.216 | no | 1.074 | 0.201 | no | 0.847 | 0.268 | no | 0.842 | 0.099 | no |
| DR0512 | Conserved membrane protein | 1.171 | 0.335 | no | 1.483 | 0.739 | no | 0.992 | 0.517 | no | 0.781 | 0.294 | no | 1.015 | 0.291 | no | 1.005 | 0.280 | no | 1.118 | 0.347 | no | 1.167 | 0.223 | no | 1.093 | 0.183 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR0513 | Integrase TRANSPOSON OR PHAGE | 1.221 | 0.432 | no | 1.126 | 0.534 | no | 0.961 | 0.467 | no | 0.733 | 0.275 | no | 0.860 | 0.267 | no | 0.989 | 0.458 | no | 1.154 | 0.361 | no | 1.240 | 0.339 | no | 1.321 | 0.316 | no |
| DR0514 | Predicted protein | 1.738 | 0.645 | yes | 2.085 | 1.275 | yes | 0.808 | 0.297 | no | 1.303 | 0.157 | no | 0.871 | 0.139 | no | 1.628 | 0.916 | no | 0.906 | 0.651 | no | 1.156 | 0.465 | no | 0.665 | 0.229 | no |
| DR0515 | Predicted protein | 0.876 | 0.172 | no | 1.975 | 0.498 | yes | 2.275 | 0.565 | yes | 1.945 | 0.130 | yes | 2.055 | 0.268 | yes | 1.930 | 0.529 | yes | 2.101 | 0.452 | yes | 2.065 | 0.348 | yes | 1.320 | 0.310 | no |
| DR0516 | Predicted protein | 1.496 | 0.923 | no | 1.408 | 0.342 | no | 1.682 | 0.843 | yes | 1.914 | 1.176 | yes | 1.398 | 0.543 | no | 1.031 | 0.342 | no | 2.049 | 1.360 | yes | 1.152 | 0.584 | no | 1.026 | 0.113 | no |
| DR0517 | Predicted protein | 1.397 | 0.404 | no | 1.253 | 0.465 | no | 1.489 | 0.208 | yes | 1.655 | 0.765 | no | 1.779 | 1.047 | yes | 1.098 | 0.131 | no | 0.909 | 0.223 | no | 1.059 | 0.136 | no | 1.056 | 0.477 | no |
| DR0518 | Predicted protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR0519 | Predicted protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR0520 | Predicted protein | 2.454 | 1.195 | yes | 2.098 | 0.916 | yes | 2.076 | 0.968 | yes | 1.369 | 0.741 | no | 1.859 | 0.771 | yes | 0.912 | 0.316 | no | 0.906 | 0.531 | no | 0.815 | 0.394 | no | 0.552 | 0.223 | yes |
| DR0521 | Predicted protein | 1.494 | 0.488 | no | 1.441 | 0.326 | yes | 1.684 | 0.307 | yes | 1.529 | 0.329 | no | 1.464 | 0.352 | no | 1.414 | 0.623 | no | 1.005 | 0.344 | no | 1.021 | 0.039 | no | 0.916 | 0.196 | no |
| DR0522 | Predicted protein | 0.902 | 0.307 | no | 1.912 | 1.011 | yes | 3.196 | 1.446 | yes | 2.245 | 0.410 | yes | 1.602 | 0.454 | yes | 1.367 | 0.712 | no | 2.301 | 1.372 | yes | 1.138 | 0.420 | no | 0.481 | 0.257 | yes |
| DR0523 | Predicted protein | 1.663 | 0.406 | yes | 2.420 | 0.943 | yes | 2.962 | 1.333 | yes | 2.514 | 1.072 | yes | 2.453 | 1.156 | yes | 1.337 | 0.779 | no | 2.113 | 1.017 | yes | 1.407 | 0.343 | no | 1.085 | 0.399 | no |
| DR0524 | DNAJ-type Zn-finger protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR0525 | Predicted protein | 1.361 | 0.360 | no | 1.786 | 0.872 | yes | 1.471 | 0.693 | no | 1.132 | 0.424 | no | 1.013 | 0.584 | no | 0.800 | 0.163 | no | 0.917 | 0.572 | no | 0.617 | 0.048 | yes | 0.668 | 0.405 | yes |
| DR0526 | Predicted protein | 2.208 | 0.928 | yes | 1.567 | 0.672 | yes | 1.736 | 0.885 | yes | 1.635 | 1.211 | no | 0.934 | 0.376 | no | 0.821 | 0.310 | no | 0.963 | 0.551 | no | 1.035 | 0.521 | no | 1.013 | 0.298 | no |
| DR0527 | Predicted protein | 1.984 | 0.940 | yes | 1.081 | 0.438 | no | 0.826 | 0.142 | no | 1.076 | 0.008 | no | 0.737 | 0.282 | no | 0.999 | 0.081 | no | 0.862 | 0.437 | no | 0.795 | 0.273 | no | 0.722 | 0.339 | no |
| DR0528 | Predicted protein | 2.023 | 0.666 | yes | 1.302 | 0.259 | no | 2.093 | 1.387 | yes | 1.928 | 1.238 | yes | 1.154 | 0.649 | no | 1.057 | 0.444 | no | 0.804 | 0.419 | no | 0.863 | 0.056 | no | 0.866 | 0.363 | no |
| DR0529 | Predicted protein | 0.882 | 0.235 | no | 1.042 | 0.258 | no | 1.057 | 0.215 | no | 0.867 | 0.215 | no | 0.863 | 0.125 | no | 0.827 | 0.289 | no | 0.883 | 0.316 | no | 0.811 | 0.252 | no | 0.587 | 0.248 | yes |
| DR0530 | Predicted membrane or surface protein, similar to Brucella GI:17983721 | 1.347 | 0.813 | no | 2.213 | 0.883 | yes | 2.381 | 1.181 | yes | 2.456 | 1.324 | yes | 1.306 | 0.367 | no | 1.074 | 0.287 | no | 0.680 | 0.103 | no | 0.635 | 0.254 | yes | 0.534 | 0.219 | yes |
| DR0531 | Predicted protein | 1.047 | 0.184 | no | 1.297 | 0.229 | no | 1.554 | 0.556 | yes | 1.265 | 0.151 | no | 1.309 | 0.306 | no | 1.017 | 0.226 | no | 0.879 | 0.377 | no | 1.011 | 0.462 | no | 0.894 | 0.205 | no |
| DR0532 | Predicted protein | 1.101 | 0.267 | no | 0.556 | 0.197 | yes | 0.685 | 0.243 | yes | 0.622 | 0.175 | yes | 0.672 | 0.159 | yes | 0.511 | 0.103 | yes | 0.617 | 0.123 | yes | 0.512 | 0.138 | yes | 0.613 | 0.127 | yes |
| DR0533 | Predicted protein | 0.854 | 0.322 | no | 0.741 | 0.483 | yes | 0.519 | 0.116 | yes | 0.485 | 0.075 | yes | 0.593 | 0.152 | yes | 0.516 | 0.197 | yes | 0.822 | 0.580 | no | 1.103 | 0.476 | no | 0.594 | 0.176 | yes |
| DR0534 | Serine/Threonin protein kinase, disrupted HRDL | 1.509 | 0.409 | no | 0.971 | 0.349 | no | 0.878 | 0.280 | no | 0.993 | 0.134 | no | 1.098 | 0.798 | no | 0.675 | 0.282 | yes | 0.669 | 0.289 | yes | 0.963 | 0.131 | no | 0.861 | 0.286 | no |
| DR0535 | L-rich repeats protein | 1.137 | 0.247 | no | 0.814 | 0.304 | no | 0.741 | 0.251 | no | 0.717 | 0.096 | no | 0.682 | 0.231 | yes | 0.767 | 0.358 | no | 0.711 | 0.245 | no | 0.687 | 0.123 | yes | 0.745 | 0.131 | no |
| DR0536 | MotB/OMPA family | 1.355 | 0.564 | no | 0.971 | 0.423 | no | 0.456 | 0.220 | yes | 0.570 | 0.170 | yes | 0.471 | 0.214 | yes | 0.470 | 0.110 | yes | 0.601 | 0.224 | yes | 0.558 | 0.096 | yes | 0.780 | 0.171 | no |
| DR0537 | Possible phage related protein | 1.462 | 0.181 | no | 1.168 | 0.837 | no | 0.884 | 0.631 | no | 0.633 | 0.089 | no | 0.737 | 0.199 | no | 0.909 | 0.418 | no | 0.730 | 0.179 | no | 0.697 | 0.194 | yes | 0.720 | 0.203 | no |
| DR0538 | Predicted possible surface protein, similarity to Nostoc GI:17131134 | 1.424 | 0.618 | no | 1.178 | 0.382 | no | 0.976 | 0.410 | no | 1.289 | 0.496 | no | 1.033 | 0.567 | no | 0.877 | 0.346 | no | 0.778 | 0.457 | no | 0.896 | 0.118 | no | 0.957 | 0.233 | no |
| DR0539 | Predicted protein | 1.651 | 0.949 | no | 1.811 | 0.463 | yes | 0.613 | 0.295 | yes | 0.955 | 0.267 | no | 0.867 | 0.293 | no | 0.592 | 0.131 | yes | 0.744 | 0.167 | no | 0.761 | 0.195 | no | 0.875 | 0.053 | no |
| DR0540 | Predicted protein | 1.595 | 0.248 | yes | 1.079 | 0.390 | no | 0.824 | 0.356 | no | 0.752 | 0.105 | no | 0.706 | 0.329 | yes | 0.577 | 0.242 | yes | 0.692 | 0.184 | no | 0.788 | 0.143 | no | 1.022 | 0.335 | no |
| DR0541 | Uncharacterized, Bacillus yunF-like protein | 1.226 | 0.518 | no | 1.091 | 0.371 | no | 0.935 | 0.497 | no | 0.688 | 0.080 | no | 0.956 | 0.314 | no | 0.881 | 0.212 | no | 1.115 | 0.353 | no | 0.903 | 0.135 | no | 1.131 | 0.212 | no |
| DR0542 | Similar to glycerophosphodiester phosphodiesterase | 1.336 | 0.627 | no | 1.137 | 0.337 | no | 0.785 | 0.132 | no | 0.708 | 0.186 | no | 0.667 | 0.259 | yes | 0.591 | 0.168 | yes | 0.616 | 0.171 | yes | 0.625 | 0.112 | yes | 0.601 | 0.232 | yes |
| DR0543 | Oxidoreductase | 0.928 | 0.135 | no | 0.473 | 0.100 | yes | 0.413 | 0.077 | yes | 0.435 | 0.040 | yes | 0.546 | 0.163 | yes | 0.638 | 0.165 | yes | 0.608 | 0.106 | yes | 0.713 | 0.201 | yes | 1.093 | 0.319 | no |
| DR0544 | Highly conserved memrane transport protein | 1.107 | 0.318 | no | 0.684 | 0.220 | yes | 0.635 | 0.106 | yes | 0.709 | 0.136 | no | 0.827 | 0.258 | no | 0.970 | 0.188 | no | 0.873 | 0.364 | no | 0.862 | 0.321 | no | 1.026 | 0.188 | no |
| DR0545 | Small conserved membrane protein, possibly MDR resistance | 0.950 | 0.491 | no | 0.695 | 0.253 | yes | 0.922 | 0.363 | no | 0.747 | 0.311 | no | 1.042 | 0.583 | no | 0.812 | 0.182 | no | 1.053 | 0.296 | no | 0.938 | 0.156 | no | 0.902 | 0.132 | no |
| DR0546 | Leader peptidase IV, TAPA-like | 1.365 | 0.551 | no | 1.330 | 0.487 | no | 1.845 | 0.931 | yes | 1.919 | 0.913 | yes | 1.754 | 0.646 | yes | 1.337 | 0.468 | no | 1.646 | 0.560 | yes | 1.334 | 0.294 | no | 1.441 | 0.746 | no |
| DR0547 | Predicted membrane protein | 1.276 | 0.263 | no | 1.325 | 0.232 | no | 1.352 | 0.396 | no | 1.414 | 0.146 | no | 1.547 | 0.416 | yes | 1.173 | 0.482 | no | 1.051 | 0.402 | no | 1.069 | 0.270 | no | 1.242 | 0.165 | no |
| DR0548 | Pilin IV like secreted protein, most similar to leader peptidase IV, TAPA | 1.170 | 0.456 | no | 0.531 | 0.232 | yes | 0.603 | 0.228 | yes | 1.135 | 0.448 | no | 2.015 | 0.859 | yes | 1.860 | 0.593 | yes | 2.646 | 0.828 | yes | 3.588 | 1.092 | yes | 5.408 | 1.749 | yes |
| DR0549 | DNAB, ATPase/helicase | 0.818 | 0.219 | no | 0.648 | 0.166 | yes | 0.789 | 0.238 | no | 0.944 | 0.229 | no | 1.199 | 0.435 | no | 1.606 | 0.420 | yes | 1.270 | 0.163 | no | 1.185 | 0.154 | no | 1.366 | 0.390 | no |
| DR0550 | MutT family hydrolase | 0.991 | 0.403 | no | 0.904 | 0.356 | no | 0.887 | 0.332 | no | 1.069 | 0.179 | no | 1.237 | 0.492 | no | 1.367 | 0.275 | no | 1.078 | 0.307 | no | 1.048 | 0.114 | no | 1.007 | 0.021 | no |
| DR0551 | Glutaryl-CoA dehydrogenase | 1.158 | 0.245 | no | 0.575 | 0.158 | yes | 0.416 | 0.100 | yes | 0.461 | 0.095 | yes | 0.520 | 0.196 | yes | 0.632 | 0.131 | yes | 0.685 | 0.156 | no | 0.795 | 0.139 | no | 0.899 | 0.126 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR0552 | Thiamin pyrophosphokinase related protein | 1.085 | 0.316 | no | 0.944 | 0.114 | no | 0.798 | 0.212 | no | 0.869 | 0.197 | no | 0.911 | 0.286 | no | 0.788 | 0.117 | no | 0.770 | 0.258 | no | 0.790 | 0.146 | no | 0.801 | 0.119 | no |
| DR0553 | A/b hydrolase | 1.231 | 0.288 | no | 1.078 | 0.288 | no | 0.962 | 0.323 | no | 0.951 | 0.139 | no | 0.929 | 0.273 | no | 1.034 | 0.176 | no | 1.143 | 0.137 | no | 1.126 | 0.194 | no | 0.959 | 0.191 | no |
| DR0554 | Predicted protein | 1.563 | 0.893 | no | 1.554 | 0.944 | yes | 1.487 | 0.583 | no | 0.978 | 0.077 | no | 1.544 | 1.070 | no | 1.066 | 0.179 | no | 1.408 | 0.703 | no | 1.072 | 0.145 | no | 1.019 | 0.240 | no |
| DR0555 | Glutamate-1-semialdehyde aminotransferase, GSA | 0.836 | 0.362 | no | 0.539 | 0.259 | yes | 0.532 | 0.212 | yes | 0.799 | 0.544 | no | 0.938 | 0.564 | no | 0.822 | 0.235 | no | 0.982 | 0.664 | no | 0.828 | 0.161 | no | 0.848 | 0.167 | no |
| DR0556 | ATP grasp superfamily protein | 0.991 | 0.184 | no | 0.504 | 0.117 | yes | 0.511 | 0.146 | yes | 0.877 | 0.058 | no | 1.274 | 0.603 | no | 1.778 | 0.723 | yes | 2.726 | 1.526 | yes | 1.689 | 0.311 | yes | 1.967 | 0.249 | yes |
| DR0557 | Uncharcterized homolog of YPUG BACSU | 1.206 | 0.305 | no | 1.046 | 0.312 | no | 1.346 | 0.454 | no | 2.001 | 0.380 | yes | 1.438 | 0.608 | no | 1.031 | 0.229 | no | 0.992 | 0.384 | no | 0.918 | 0.098 | no | 0.791 | 0.131 | no |
| DR0558 | Tryptophanyl-tRNA synthetase, SYW | 0.954 | 0.256 | no | 0.578 | 0.106 | yes | 0.637 | 0.134 | yes | 0.646 | 0.122 | no | 0.822 | 0.159 | no | 0.860 | 0.162 | no | 1.112 | 0.232 | no | 1.285 | 0.188 | no | 1.452 | 0.201 | yes |
| DR0559 | Membrane protein, related to fibronectin/fibrinogen-binding protein | 1.217 | 0.593 | no | 0.719 | 0.264 | no | 0.977 | 0.383 | no | 0.871 | 0.264 | no | 0.907 | 0.213 | no | 0.754 | 0.287 | no | 0.879 | 0.277 | no | 0.997 | 0.202 | no | 0.947 | 0.340 | no |
| DR0560 | Membrane associated thioredoxin fold protein, probable disulfide bond chaperone | 1.284 | 0.520 | no | 1.035 | 0.484 | no | 0.812 | 0.156 | no | 1.079 | 0.487 | no | 0.851 | 0.158 | no | 0.992 | 0.262 | no | 1.106 | 0.193 | no | 1.176 | 0.181 | no | 1.369 | 0.292 | no |
| DR0561 | Maltodextrin-Binding periplasmic Protein, MALE | 1.618 | 1.008 | no | 0.885 | 0.588 | no | 1.173 | 0.861 | no | 1.542 | 1.148 | no | 1.304 | 0.817 | no | 1.541 | 1.113 | no | 1.858 | 1.054 | yes | 1.491 | 0.469 | no | 1.315 | 0.665 | no |
| DR0562 | Maltose transport system permease, MALF | 1.094 | 0.481 | no | 0.863 | 0.416 | no | 1.110 | 0.539 | no | 1.988 | 0.041 | yes | 1.315 | 0.767 | no | 1.321 | 0.694 | no | 2.217 | 0.812 | yes | 1.967 | 0.329 | yes | 1.066 | 0.220 | no |
| DR0563 | Maltose transport system permease, MalG | 1.209 | 0.516 | no | 1.086 | 0.579 | no | 1.308 | 0.443 | no | 1.812 | 0.639 | yes | 1.497 | 0.659 | no | 1.403 | 0.757 | no | 1.613 | 0.769 | no | 1.519 | 0.661 | no | 1.105 | 0.342 | no |
| DR0564 | Periplasmic amino acid binding protein, FLIY | 1.076 | 0.374 | no | 1.287 | 0.696 | no | 1.395 | 0.638 | no | 1.633 | 0.996 | no | 2.172 | 0.688 | yes | 2.281 | 0.906 | yes | 2.883 | 0.896 | yes | 2.931 | 0.739 | yes | 1.519 | 0.166 | yes |
| DR0565 | Related to amino acid permease | 1.290 | 0.341 | no | 1.481 | 0.380 | yes | 1.450 | 0.436 | no | 1.943 | 0.152 | yes | 1.554 | 0.461 | yes | 1.101 | 0.273 | no | 1.127 | 0.434 | no | 1.322 | 0.252 | no | 1.410 | 0.124 | no |
| DR0566 | Hypothetical Thy28kD ortholog | 1.142 | 0.425 | no | 0.966 | 0.131 | no | 0.993 | 0.408 | no | 1.134 | 0.294 | no | 1.215 | 0.459 | no | 0.972 | 0.303 | no | 0.793 | 0.293 | no | 0.918 | 0.364 | no | 1.006 | 0.307 | no |
| DR0567 | Threonine dehydratase, THD1 | 1.664 | 0.510 | yes | 1.020 | 0.285 | no | 1.583 | 0.831 | no | 1.070 | 0.461 | no | 3.853 | 1.117 | yes | 1.493 | 0.675 | no | 0.962 | 0.427 | no | 0.751 | 0.413 | yes | 0.648 | 0.056 | no |
| DR0568 | Adenine phosphoribosyl transferase, APT | 0.981 | 0.207 | no | 0.897 | 0.260 | no | 0.671 | 0.112 | yes | 0.643 | 0.073 | no | 0.818 | 0.258 | no | 0.990 | 0.148 | no | 0.904 | 0.260 | no | 1.059 | 0.149 | no | 1.162 | 0.227 | no |
| DR0569 | Predicted protein | 1.151 | 0.385 | no | 1.003 | 0.304 | no | 1.004 | 0.304 | no | 1.090 | 0.300 | no | 1.156 | 0.353 | no | 1.163 | 0.269 | no | 1.299 | 0.213 | no | 1.105 | 0.089 | no | 0.871 | 0.179 | no |
| DR0570 | Predicted protein | 0.962 | 0.308 | no | 0.830 | 0.324 | no | 0.826 | 0.247 | no | 0.813 | 0.178 | no | 0.810 | 0.280 | no | 0.874 | 0.198 | no | 0.754 | 0.144 | no | 0.829 | 0.106 | no | 0.769 | 0.189 | no |
| DR0571 | Very divergent Rossman fold oxidoreductase | 1.607 | 0.676 | no | 1.156 | 0.438 | no | 0.962 | 0.348 | no | 1.104 | 0.614 | no | 1.099 | 0.606 | no | 0.887 | 0.324 | no | 1.037 | 0.429 | no | 1.031 | 0.161 | no | 1.225 | 0.314 | no |
| DR0572 | Stage II sporulation protein D, SP2D related | 1.180 | 0.283 | no | 1.352 | 0.205 | no | 1.120 | 0.381 | no | 1.036 | 0.199 | no | 1.244 | 0.338 | no | 1.093 | 0.256 | no | 1.109 | 0.436 | no | 1.336 | 0.304 | no | 1.435 | 0.411 | no |
| DR0573 | Secreted surface protein, uncharacterized | 1.058 | 0.246 | no | 3.002 | 0.446 | yes | 2.102 | 0.303 | yes | 2.052 | 0.621 | yes | 1.397 | 0.533 | no | 1.490 | 0.254 | no | 1.228 | 0.289 | no | 1.165 | 0.053 | no | 1.131 | 0.183 | no |
| DR0574 | Predicted membrane protein, uncharacterized | 1.093 | 0.299 | no | 1.904 | 0.504 | yes | 1.631 | 0.748 | yes | 1.255 | 0.162 | no | 1.163 | 0.467 | no | 1.472 | 0.613 | no | 1.223 | 0.458 | no | 1.395 | 0.264 | no | 1.368 | 0.238 | no |
| DR0575 | SecA translocase | 2.090 | 1.350 | yes | 0.710 | 0.310 | no | 0.598 | 0.315 | yes | 0.588 | 0.308 | yes | 1.434 | 0.765 | no | 1.870 | 0.533 | yes | 1.025 | 0.370 | no | 0.631 | 0.290 | yes | 0.522 | 0.176 | yes |
| DR0576 | SpoU family methyltransferase | 1.346 | 0.618 | no | 1.345 | 0.406 | no | 1.218 | 0.807 | no | 0.841 | 0.157 | no | 0.911 | 0.396 | no | 0.965 | 0.323 | no | 0.838 | 0.072 | no | 0.926 | 0.158 | no | 0.848 | 0.153 | no |
| DR0577 | Membrane accosiated histidine kinase + GAF domain, related to DEGS protein | 1.323 | 0.579 | no | 1.105 | 0.644 | no | 1.050 | 0.555 | no | 1.615 | 0.957 | no | 1.042 | 0.791 | no | 0.851 | 0.393 | no | 0.701 | 0.234 | no | 0.736 | 0.116 | no | 0.715 | 0.218 | no |
| DR0578 | Secreted protein, uncharacterized | 0.955 | 0.343 | no | 0.859 | 0.184 | no | 0.888 | 0.383 | no | 1.236 | 0.283 | no | 1.134 | 0.276 | no | 1.266 | 0.408 | no | 1.118 | 0.252 | no | 0.958 | 0.126 | no | 1.479 | 0.425 | yes |

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PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR0579 | DFP protein, DNA/pantothenate metabolism flavoprotein | 1.156 | 0.468 | no | 1.155 | 0.512 | no | 1.500 | 0.750 | no | 2.082 | 0.872 | yes | 1.871 | 0.693 | yes | 2.081 | 0.718 | yes | 1.347 | 0.358 | no | 1.463 | 0.204 | yes | 2.091 | 0.984 | yes |
| DR0580 | O-Acetyltransferase, chloramphenicol AT like | 0.885 | 0.169 | no | 0.827 | 0.239 | no | 0.632 | 0.132 | yes | 0.746 | 0.063 | no | 0.858 | 0.187 | no | 0.731 | 0.115 | no | 0.792 | 0.192 | no | 0.783 | 0.182 | no | 1.276 | 0.091 | no |
| DR0581 | Secreted protein, uncharacterized | 1.007 | 0.315 | no | 0.828 | 0.218 | no | 0.785 | 0.266 | no | 1.232 | 0.111 | no | 1.105 | 0.356 | no | 0.986 | 0.436 | no | 0.970 | 0.283 | no | 0.980 | 0.209 | no | 1.319 | 0.453 | no |
| DR0582 | Predicted protein | 1.171 | 0.397 | no | 0.618 | 0.247 | yes | 0.309 | 0.039 | yes | 0.312 | 0.026 | yes | 0.387 | 0.119 | yes | 0.540 | 0.160 | yes | 0.596 | 0.199 | yes | 0.805 | 0.174 | no | 1.027 | 0.086 | no |
| DR0583 | FTSH, AAA superfamily ATPase + metalloprotease | 1.060 | 0.503 | no | 0.488 | 0.214 | yes | 0.429 | 0.195 | yes | 0.544 | 0.285 | yes | 0.469 | 0.151 | yes | 0.342 | 0.121 | yes | 0.391 | 0.170 | yes | 0.357 | 0.123 | yes | 0.588 | 0.157 | yes |
| DR0584 | Phosphoribosylglycinamide formyltransferase PurU | 0.945 | 0.260 | no | 0.804 | 0.232 | no | 0.624 | 0.317 | yes | 0.570 | 0.123 | yes | 0.758 | 0.209 | no | 1.200 | 0.824 | no | 0.765 | 0.133 | no | 0.780 | 0.091 | no | 0.927 | 0.262 | no |
| DR0585 | Aminopeptidase T | 1.125 | 0.725 | no | 1.059 | 0.640 | no | 0.627 | 0.353 | yes | 0.527 | 0.079 | yes | 1.383 | 0.858 | no | 1.271 | 0.942 | no | 0.838 | 0.377 | no | 0.290 | 0.061 | yes | 2.390 | 0.363 | yes |
| DR0586 | Uncharacterized small conserved protein, YlJA ortholog | 0.936 | 0.522 | no | 0.481 | 0.199 | yes | 0.439 | 0.166 | yes | 0.549 | 0.140 | yes | 0.948 | 0.382 | no | 0.784 | 0.293 | no | 0.567 | 0.227 | yes | 1.029 | 0.194 | no | 0.681 | 0.281 | yes |
| DR0587 | Mrr restriction system protein | 1.071 | 0.590 | no | 0.915 | 0.519 | no | 0.970 | 0.517 | no | 1.078 | 0.801 | no | 0.978 | 0.454 | no | 0.815 | 0.215 | no | 0.912 | 0.501 | no | 0.797 | 0.118 | no | 0.989 | 0.112 | no |
| DR0588 | ClpA AAA superfamily ATPase | 0.925 | 0.221 | no | 0.905 | 0.339 | no | 0.660 | 0.088 | yes | 0.581 | 0.032 | yes | 0.733 | 0.089 | no | 0.881 | 0.290 | no | 0.741 | 0.164 | no | 0.716 | 0.200 | yes | 0.826 | 0.203 | no |
| DR0589 | Predicted protein | 1.103 | 0.257 | no | 1.718 | 0.503 | yes | 1.642 | 0.752 | yes | 1.679 | 0.540 | yes | 1.490 | 0.446 | no | 1.128 | 0.168 | no | 1.115 | 0.423 | no | 1.118 | 0.232 | no | 1.005 | 0.281 | no |
| DR0590 | Predicted protein | 0.978 | 0.333 | no | 1.365 | 0.383 | no | 1.260 | 0.307 | no | 0.899 | 0.034 | no | 1.028 | 0.228 | no | 1.354 | 0.370 | no | 0.892 | 0.374 | no | 1.121 | 0.302 | no | 0.993 | 0.288 | no |
| DR0591 | Predicted protein | 1.012 | 0.226 | no | 1.063 | 0.447 | no | 0.847 | 0.217 | no | 0.745 | 0.217 | no | 0.895 | 0.385 | no | 0.804 | 0.190 | no | 0.925 | 0.121 | no | 1.003 | 0.112 | no | 1.166 | 0.384 | no |
| DR0592 | Predicted protein | 1.043 | 0.277 | no | 0.947 | 0.303 | no | 0.822 | 0.264 | no | 0.857 | 0.051 | no | 0.525 | 0.096 | yes | 0.598 | 0.147 | yes | 0.646 | 0.168 | yes | 0.632 | 0.140 | yes | 0.861 | 0.085 | no |
| DR0593 | Alpha/beta hydrolase superfamily protein | 0.993 | 0.177 | no | 1.158 | 0.173 | no | 0.996 | 0.275 | no | 0.728 | 0.056 | no | 0.839 | 0.357 | no | 1.064 | 0.201 | no | 0.882 | 0.180 | no | 0.946 | 0.128 | no | 1.004 | 0.116 | no |
| DR0594 | Glycogen synthase, GlgA | 0.867 | 0.160 | no | 1.296 | 0.194 | no | 1.304 | 0.299 | no | 0.698 | 0.104 | no | 0.817 | 0.233 | no | 0.795 | 0.216 | no | 0.690 | 0.164 | no | 0.738 | 0.052 | no | 0.926 | 0.081 | no |
| DR0595 | Predicted protein | 0.682 | 0.187 | no | 3.253 | 1.612 | yes | 3.115 | 1.776 | yes | 2.269 | 1.145 | yes | 1.954 | 1.110 | yes | 1.327 | 0.934 | no | 1.506 | 0.592 | no | 1.166 | 0.152 | no | 0.719 | 0.219 | no |
| DR0596 | RuvB, AAA superfamily ATPase | 1.016 | 0.476 | no | 3.220 | 1.315 | yes | 2.847 | 0.549 | yes | 3.027 | 1.768 | yes | 3.030 | 2.175 | yes | 1.234 | 0.712 | no | 0.697 | 0.099 | no | 0.575 | 0.142 | yes | 0.393 | 0.112 | yes |
| DR0597 | Thioredoxin fold protein, probably secreted of yeast Sco1/sco2 family | 0.869 | 0.288 | no | 1.655 | 0.460 | yes | 1.541 | 0.549 | yes | 0.934 | 0.188 | no | 1.006 | 0.392 | no | 0.830 | 0.283 | no | 0.589 | 0.228 | yes | 0.502 | 0.198 | yes | 0.549 | 0.284 | yes |
| DR0598 | Kinase, related to adenylate kinase family, ortholog of Pseudomonas NlnD | 1.016 | 0.567 | no | 6.395 | 3.714 | yes | 5.489 | 2.355 | yes | 2.642 | 0.130 | yes | 4.332 | 2.849 | yes | 3.180 | 1.168 | yes | 2.251 | 0.907 | yes | 1.157 | 0.362 | no | 0.675 | 0.214 | no |
| DR0599 | Aminoglycoside N3'-acetyltransferase family | 0.665 | 0.290 | yes | 3.509 | 0.970 | yes | 4.244 | 1.414 | yes | 2.599 | 1.522 | yes | 2.872 | 1.189 | yes | 2.248 | 0.709 | yes | 1.537 | 0.451 | yes | 1.065 | 0.328 | no | 0.636 | 0.153 | yes |
| DR0600 | Predicted protein | 0.644 | 0.282 | yes | 4.178 | 0.868 | yes | 5.476 | 2.762 | yes | 4.594 | 0.801 | yes | 6.019 | 3.991 | yes | 3.236 | 0.649 | yes | 2.933 | 0.873 | yes | 1.347 | 0.264 | no | 0.885 | 0.133 | no |
| DR0601 | DNA Primase | 0.806 | 0.088 | no | 0.711 | 0.195 | no | 0.653 | 0.205 | yes | 0.592 | 0.044 | yes | 0.747 | 0.104 | no | 0.623 | 0.131 | yes | 0.618 | 0.139 | yes | 0.661 | 0.118 | yes | 0.648 | 0.114 | no |
| DR0602 | Phosphoglycerate mutase family protein | 1.248 | 0.662 | no | 1.054 | 0.096 | no | 1.318 | 0.457 | no | 1.034 | 0.016 | no | 1.222 | 0.708 | no | 0.921 | 0.319 | no | 0.789 | 0.249 | no | 0.713 | 0.126 | yes | 0.656 | 0.162 | no |
| DR0603 | N-terminal cytidine deaminase domain + MutT hydrolase + C-terminal methyltransferase | 1.412 | 0.460 | no | 1.554 | 0.901 | yes | 1.335 | 0.663 | no | 1.535 | 0.716 | no | 1.455 | 0.647 | no | 0.884 | 0.116 | no | 0.899 | 0.239 | no | 0.830 | 0.221 | no | 0.935 | 0.210 | no |
| DR0604 | NH2-acetyl transferase | 1.324 | 0.455 | no | 1.493 | 0.738 | no | 1.723 | 0.709 | yes | 2.414 | 0.196 | yes | 1.636 | 0.480 | yes | 1.009 | 0.302 | no | 1.032 | 0.410 | no | 0.888 | 0.336 | no | 1.094 | 0.246 | no |
| DR0605 | GGDEF domain signalling protein fused to HTH domain | 1.113 | 0.378 | no | 1.225 | 0.448 | no | 1.091 | 0.341 | no | 1.484 | 0.072 | no | 1.307 | 0.469 | no | 0.953 | 0.326 | no | 0.988 | 0.435 | no | 0.872 | 0.311 | no | 0.991 | 0.267 | no |
| DR0606 | GroES/Hsp10 protein, chaperonin | 0.992 | 0.242 | no | 0.462 | 0.200 | yes | 0.515 | 0.181 | yes | 0.722 | 0.222 | no | 0.648 | 0.290 | yes | 0.601 | 0.226 | yes | 0.695 | 0.151 | no | 0.797 | 0.228 | no | 1.602 | 0.414 | yes |
| DR0607 | GroEL/Hsp60 protein, chaperonin | 0.865 | 0.293 | no | 0.465 | 0.151 | yes | 0.460 | 0.114 | yes | 0.436 | 0.097 | yes | 0.580 | 0.252 | yes | 0.458 | 0.293 | yes | 0.598 | 0.270 | yes | 0.691 | 0.138 | no | 1.592 | 0.221 | yes |
| DR0608 | NH2 -acetyltransferase | 1.033 | 0.670 | no | 1.032 | 0.651 | no | 1.282 | 0.652 | no | 0.895 | 0.042 | no | 1.677 | 1.228 | no | 0.831 | 0.315 | no | 0.828 | 0.369 | no | 0.750 | 0.157 | no | 1.023 | 0.068 | no |
| DR0609 | Kinase, related to adenylate kinase | 1.414 | 0.645 | no | 2.401 | 1.060 | yes | 1.943 | 0.861 | yes | 2.433 | 1.142 | yes | 2.032 | 0.746 | yes | 1.505 | 0.791 | no | 1.100 | 0.165 | no | 0.841 | 0.220 | no | 0.528 | 0.193 | yes |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR0610 | Predicted protein | 1.327 | 0.428 | no | 2.598 | 1.696 | yes | 3.568 | 1.512 | yes | 6.098 | 4.508 | yes | 3.120 | 1.921 | yes | 1.346 | 0.508 | no | 1.217 | 0.605 | no | 1.012 | 0.470 | no | 0.686 | 0.131 | no |
| DR0611 | FMN dependent monooxygenase | 0.863 | 0.161 | no | 1.084 | 0.469 | no | 1.031 | 0.179 | no | 0.940 | 0.113 | no | 1.000 | 0.190 | no | 1.082 | 0.375 | no | 1.034 | 0.557 | no | 0.828 | 0.258 | no | 0.626 | 0.220 | yes |
| DR0612 | Succinyl-diaminopimelate desuccinylase DapE, Bacillus RocB ortholog | 1.325 | 0.773 | no | 1.848 | 0.714 | yes | 1.893 | 0.809 | yes | 2.135 | 1.299 | yes | 1.535 | 0.722 | no | 1.203 | 0.205 | no | 1.240 | 0.696 | no | 1.134 | 0.064 | no | 1.141 | 0.200 | no |
| DR0613 | Uncharacterized protein, similar to ycgI bacillus and yao3 S.pombe | 1.077 | 0.328 | no | 0.840 | 0.411 | no | 0.771 | 0.450 | yes | 1.627 | 0.535 | no | 1.451 | 0.647 | no | 1.611 | 0.502 | yes | 1.893 | 0.624 | yes | 1.634 | 0.309 | yes | 1.033 | 0.243 | no |
| DR0614 | Uncharacterized protein, similar to vcgG | 0.997 | 0.231 | no | 0.789 | 0.066 | no | 0.734 | 0.114 | no | 0.937 | 0.016 | no | 0.976 | 0.169 | no | 1.036 | 0.361 | no | 1.080 | 0.215 | no | 0.795 | 0.211 | no | 0.716 | 0.142 | no |
| DR0615 | HTH transcriptional regulator, LysR family | 1.058 | 0.092 | no | 0.842 | 0.129 | no | 0.770 | 0.255 | no | 0.719 | 0.159 | no | 0.646 | 0.155 | yes | 0.751 | 0.180 | no | 0.771 | 0.248 | no | 0.850 | 0.140 | no | 0.849 | 0.082 | no |
| DR0616 | Small uncharacterized conserved protein | 2.029 | 1.029 | yes | 1.285 | 0.616 | no | 0.978 | 0.412 | no | 0.281 | 0.015 | yes | 0.799 | 0.229 | no | 0.581 | 0.344 | yes | 1.226 | 0.867 | no | 0.843 | 0.285 | no | 0.968 | 0.343 | no |
| DR0617 | Zinc Metalloprotease, insulinase family | 0.884 | 0.322 | no | 0.337 | 0.102 | yes | 0.250 | 0.100 | yes | 0.281 | 0.135 | yes | 0.295 | 0.122 | yes | 0.317 | 0.089 | yes | 0.398 | 0.142 | yes | 0.527 | 0.177 | yes | 0.746 | 0.200 | no |
| DR0618 | Predicted protein | 1.179 | 0.514 | no | 0.899 | 0.378 | no | 0.777 | 0.288 | no | 0.921 | 0.588 | no | 0.744 | 0.274 | no | 0.707 | 0.300 | yes | 0.849 | 0.240 | no | 0.863 | 0.140 | no | 0.914 | 0.361 | no |
| DR0619 | Uncharacterized conserved protein, YBEA ortholog | 1.070 | 0.495 | no | 0.979 | 0.348 | no | 0.894 | 0.280 | no | 0.565 | 0.197 | yes | 0.586 | 0.232 | yes | 0.907 | 0.437 | no | 0.592 | 0.418 | yes | 0.793 | 0.115 | no | 0.623 | 0.110 | yes |
| DR0620 | Predicted protease of transglutaminase family (membrane bounded, has additional common to PepX domain | 1.137 | 0.261 | no | 1.157 | 0.296 | no | 1.103 | 0.336 | no | 1.078 | 0.232 | no | 1.138 | 0.790 | no | 0.759 | 0.129 | no | 0.756 | 0.124 | no | 0.847 | 0.095 | no | 0.842 | 0.121 | no |
| DR0621 | MoxR family of AAA superclass ATPases | 1.173 | 0.283 | no | 1.167 | 0.176 | no | 0.959 | 0.252 | no | 0.860 | 0.180 | no | 0.820 | 0.233 | no | 0.965 | 0.454 | no | 0.969 | 0.386 | no | 1.109 | 0.384 | no | 1.380 | 0.401 | no |
| DR0622 | Predicted protein | 1.004 | 0.290 | no | 1.529 | 0.843 | no | 1.305 | 0.567 | no | 1.400 | 0.266 | no | 1.065 | 0.332 | no | 1.172 | 0.463 | no | 1.299 | 0.193 | no | 1.206 | 0.288 | no | 1.030 | 0.213 | no |
| DR0623 | Aspartate aminotransferase | 0.924 | 0.239 | no | 1.334 | 0.173 | no | 1.272 | 0.243 | no | 1.059 | 0.194 | no | 1.317 | 0.265 | no | 1.208 | 0.422 | no | 1.293 | 0.362 | no | 0.957 | 0.101 | no | 0.880 | 0.163 | no |
| DR0624 | Flavoprotein, similar to YIEF_ECOLI | 1.213 | 0.511 | no | 0.973 | 0.368 | no | 0.827 | 0.398 | no | 0.909 | 0.624 | no | 0.754 | 0.315 | no | 0.745 | 0.313 | no | 0.904 | 0.277 | no | 0.794 | 0.075 | no | 0.683 | 0.147 | no |
| DR0625 | Uncharacterized protein, similar to gi\|2621836 of Methanobacterium thermoautotrophicum | 1.048 | 0.397 | no | 1.075 | 0.255 | no | 0.927 | 0.320 | no | 0.662 | 0.169 | no | 0.861 | 0.364 | no | 0.961 | 0.362 | no | 0.994 | 0.376 | no | 0.915 | 0.199 | no | 0.848 | 0.167 | no |
| DR0626 | N-acetylmuramyl-pentapeptide pyrophosphoryl-undecaprenol N-acetylglucosamine, MurG | 0.833 | 0.404 | no | 0.951 | 0.574 | no | 0.846 | 0.599 | yes | 0.585 | 0.401 | yes | 0.684 | 0.364 | yes | 0.867 | 0.456 | no | 0.789 | 0.550 | no | 0.708 | 0.235 | yes | 0.831 | 0.218 | no |
| DR0627 | UDP-N-acetyl muramate-alanine ligase, MurC | 0.621 | 0.138 | yes | 0.982 | 0.343 | no | 0.971 | 0.357 | no | 0.768 | 0.175 | no | 1.199 | 0.456 | no | 1.088 | 0.299 | no | 1.300 | 0.474 | no | 0.939 | 0.169 | no | 0.862 | 0.274 | no |
| DR0628 | UDP-N-acetylmuramate dehydrogenase, MurB | 0.964 | 0.559 | no | 0.779 | 0.254 | no | 0.856 | 0.473 | no | 0.713 | 0.416 | no | 0.961 | 0.354 | no | 1.285 | 0.477 | no | 1.085 | 0.449 | no | 1.016 | 0.235 | no | 1.292 | 0.064 | no |
| DR0629 | DIVB/FtsQ, cell division protein | 0.691 | 0.228 | no | 1.189 | 0.329 | no | 1.127 | 0.413 | no | 1.033 | 0.310 | no | 1.395 | 0.376 | no | 1.165 | 0.180 | no | 1.380 | 0.425 | no | 0.988 | 0.323 | no | 0.886 | 0.237 | no |
| DR0630 | FtsA, actin superfamily ATPase | 0.839 | 0.203 | no | 0.794 | 0.332 | no | 0.873 | 0.178 | no | 0.844 | 0.096 | no | 0.790 | 0.189 | no | 0.964 | 0.371 | no | 1.004 | 0.342 | no | 1.059 | 0.345 | no | 1.420 | 0.423 | no |
| DR0631 | FtsZ, Tubulin superfamily GTPase | 0.686 | 0.231 | no | 0.683 | 0.414 | yes | 1.067 | 0.366 | no | 0.836 | 0.233 | no | 1.050 | 0.415 | no | 1.112 | 0.345 | no | 1.181 | 0.579 | no | 1.176 | 0.210 | no | 1.492 | 0.485 | yes |
| DR0632 | Related to YAFD_ECOLI | 1.151 | 0.686 | no | 3.255 | 1.044 | yes | 3.834 | 2.411 | yes | 1.983 | 0.190 | yes | 2.527 | 1.760 | yes | 2.432 | 0.812 | yes | 1.743 | 0.934 | yes | 1.005 | 0.246 | no | 0.729 | 0.167 | no |
| DR0633 | Conserved membrane protein, AZLC-like-BCAA transport | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR0634 | Fragment of membrane protein | 1.091 | 0.278 | no | 2.058 | 1.042 | yes | 1.681 | 0.497 | yes | 2.284 | 0.546 | yes | 2.018 | 0.671 | yes | 1.225 | 0.297 | no | 1.463 | 0.612 | no | 0.977 | 0.382 | no | 0.757 | 0.272 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR0635 | 6-phosphofructokinase, K6P1 | 1.024 | 0.404 | no | 1.895 | 0.666 | yes | 2.077 | 0.771 | yes | 2.001 | 0.840 | yes | 1.618 | 0.503 | yes | 1.352 | 0.377 | no | 1.070 | 0.436 | no | 1.096 | 0.110 | no | 1.208 | 0.419 | no |
| DR0636 | SAM-dependent methyltransferase | 0.771 | 0.255 | no | 1.116 | 0.478 | no | 0.944 | 0.161 | no | 0.712 | 0.156 | no | 0.898 | 0.437 | no | 0.825 | 0.234 | no | 0.734 | 0.270 | no | 0.821 | 0.091 | no | 0.815 | 0.128 | no |
| DR0637 | Predicted protein | 0.656 | 0.398 | yes | 0.590 | 0.277 | yes | 0.780 | 0.524 | yes | 0.433 | 0.096 | yes | 0.564 | 0.325 | yes | 0.645 | 0.449 | yes | 0.560 | 0.388 | yes | 0.512 | 0.179 | yes | 0.680 | 0.358 | yes |
| DR0638 | Uncharacterized conserved protein | 0.689 | 0.463 | yes | 0.765 | 0.424 | no | 0.668 | 0.328 | yes | 0.336 | 0.107 | yes | 0.530 | 0.302 | yes | 0.652 | 0.238 | yes | 0.571 | 0.314 | yes | 0.535 | 0.150 | yes | 0.592 | 0.147 | yes |
| DR0639 | Predicted protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR0640 | Methionine adenosyltransferase, SAM synthase, METK | 1.066 | 0.272 | no | 0.635 | 0.106 | yes | 0.327 | 0.114 | yes | 0.239 | 0.078 | yes | 0.235 | 0.101 | yes | 0.245 | 0.062 | yes | 0.287 | 0.091 | yes | 0.315 | 0.068 | yes | 0.669 | 0.137 | no |
| DR0641 | Possibly secreted protein, uncharacterized | 0.848 | 0.274 | no | 0.704 | 0.085 | no | 0.593 | 0.041 | yes | 0.646 | 0.254 | yes | 0.736 | 0.098 | no | 0.670 | 0.154 | yes | 0.672 | 0.078 | yes | 0.883 | 0.311 | no | 0.656 | 0.046 | no |
| DR0642 | Lipopolysaccharide core biosynthesis protein, belongs to KdtB/TagD | 0.979 | 0.168 | no | 1.005 | 0.267 | no | 0.751 | 0.193 | no | 0.769 | 0.300 | no | 0.799 | 0.175 | no | 0.827 | 0.185 | no | 1.027 | 0.174 | no | 1.263 | 0.325 | no | 1.404 | 0.389 | no |
| DR0643 | SAM-dependent methyltransferase | 0.778 | 0.385 | no | 0.615 | 0.410 | yes | 0.442 | 0.166 | yes | 0.393 | 0.046 | yes | 0.444 | 0.101 | yes | 0.734 | 0.361 | no | 0.694 | 0.345 | yes | 1.032 | 0.425 | no | 1.015 | 0.289 | no |
| DR0644 | Predicted protein | 1.655 | 0.693 | no | 0.747 | 0.492 | yes | 0.922 | 0.545 | no | 2.678 | 0.499 | yes | 3.428 | 0.861 | yes | 2.012 | 0.788 | yes | 4.441 | 2.513 | yes | 3.969 | 1.012 | yes | 3.687 | 1.468 | yes |
| DR0645 | Molybdopterin-guanine dinucleotide biosynthesis protein A, MobA | 2.803 | 0.515 | yes | 0.979 | 0.623 | no | 4.367 | 0.104 | yes | n/a | n/a | n/a | 1.009 | 0.680 | no | 1.267 | 0.732 | no | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR0646 | ERA ortholog GTPase | 0.837 | 0.302 | no | 0.919 | 0.205 | no | 1.405 | 0.371 | no | 1.723 | 0.526 | yes | 1.766 | 0.634 | yes | 1.771 | 0.485 | yes | 1.832 | 0.372 | yes | 1.917 | 0.494 | yes | 1.532 | 0.351 | yes |
| DR0647 | AAA superfamily ATPase | 1.058 | 0.444 | no | 0.839 | 0.272 | no | 0.645 | 0.261 | yes | 0.662 | 0.097 | no | 0.815 | 0.258 | no | 0.989 | 0.279 | no | 0.879 | 0.191 | no | 1.064 | 0.165 | no | 0.978 | 0.194 | no |
| DR0648 | Predicted protein | 1.066 | 0.153 | no | 0.873 | 0.244 | no | 0.631 | 0.155 | yes | 0.724 | 0.157 | no | 0.727 | 0.277 | no | 1.003 | 0.325 | no | 0.912 | 0.278 | no | 0.876 | 0.205 | no | 1.075 | 0.128 | no |
| DR0649 | Predicted protein | 0.852 | 0.258 | no | 0.585 | 0.297 | yes | 0.506 | 0.139 | yes | 0.597 | 0.057 | yes | 0.807 | 0.163 | no | 0.847 | 0.189 | no | 0.969 | 0.543 | no | 1.136 | 0.403 | no | 0.776 | 0.252 | no |
| DR0650 | Predicted protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR0651 | Arginase | 0.806 | 0.136 | no | 0.432 | 0.122 | yes | 0.300 | 0.081 | yes | 0.307 | 0.018 | yes | 0.451 | 0.153 | yes | 0.476 | 0.101 | yes | 0.562 | 0.182 | yes | 0.762 | 0.081 | no | 0.829 | 0.134 | no |
| DR0652 | Na+/H+ exchanger | 0.756 | 0.380 | no | 0.964 | 0.402 | no | 1.933 | 0.883 | yes | 3.015 | 1.718 | yes | 4.038 | 1.643 | yes | 3.387 | 0.771 | yes | 5.092 | 0.876 | yes | 4.114 | 2.362 | yes | 5.099 | 2.272 | yes |
| DR0653 | NH2 acetyltransferase | 0.960 | 0.391 | no | 2.094 | 1.061 | yes | 1.478 | 0.932 | no | 1.178 | 0.572 | no | 1.323 | 0.740 | no | 1.336 | 0.586 | no | 1.405 | 0.782 | no | 0.951 | 0.317 | no | 0.958 | 0.314 | no |
| DR0654 | A/b fold hydrolase, related to proline iminopeptidase | 0.852 | 0.179 | no | 0.691 | 0.129 | no | 0.769 | 0.402 | no | 0.477 | 0.047 | yes | 0.677 | 0.205 | yes | 0.903 | 0.113 | no | 0.810 | 0.127 | no | 0.870 | 0.073 | no | 0.895 | 0.171 | no |
| DR0655 | Predicted protein | 1.795 | 1.215 | no | 1.436 | 0.596 | no | 1.472 | 0.509 | no | 1.755 | 0.715 | yes | 1.495 | 0.531 | no | 1.276 | 0.239 | no | 1.119 | 0.304 | no | 1.046 | 0.184 | no | 1.061 | 0.234 | no |
| DR0656 | Na+-dependent glutamate transporter | 1.429 | 0.479 | no | 1.351 | 0.615 | no | 1.024 | 0.346 | no | 1.150 | 0.104 | no | 1.249 | 0.279 | no | 1.421 | 0.394 | no | 1.338 | 0.411 | no | 1.104 | 0.137 | no | 1.142 | 0.250 | no |
| DR0657 | A/b fold hydrolase | 1.138 | 0.300 | no | 0.695 | 0.135 | no | 0.571 | 0.161 | yes | 0.697 | 0.200 | no | 1.099 | 0.297 | no | 1.003 | 0.315 | no | 1.373 | 0.393 | no | 1.238 | 0.291 | no | 1.014 | 0.346 | no |
| DR0658 | Beta-lactamase superfamily of Zn-dependent hydrolases | 0.952 | 0.247 | no | 0.466 | 0.118 | yes | 0.270 | 0.079 | yes | 0.430 | 0.129 | yes | 0.551 | 0.226 | yes | 0.625 | 0.203 | yes | 1.016 | 0.294 | no | 1.001 | 0.197 | no | 0.939 | 0.298 | no |
| DR0659 | Uncharacterized conserved protein, probably metal-binding | 1.405 | 0.359 | no | 1.317 | 0.464 | no | 1.106 | 0.530 | no | 0.864 | 0.253 | no | 1.057 | 0.244 | no | 1.005 | 0.358 | no | 1.182 | 0.344 | no | 1.340 | 0.702 | no | 0.804 | 0.208 | no |
| DR0660 | PilT-N-terminal-domain-like/vapc family protein | 1.464 | 0.506 | no | 1.932 | 0.660 | yes | 1.595 | 0.565 | yes | 2.198 | 0.796 | yes | 1.394 | 0.287 | no | 0.796 | 0.311 | no | 0.901 | 0.396 | no | 0.722 | 0.259 | no | 0.900 | 0.115 | no |
| DR0661 | Probably YhhG family protein | 0.876 | 0.304 | no | 1.813 | 0.643 | yes | 2.188 | 0.533 | yes | 3.063 | 1.436 | yes | 3.459 | 1.117 | yes | 2.141 | 1.160 | yes | 2.865 | 1.115 | yes | 1.372 | 0.484 | no | 1.282 | 0.543 | no |
| DR0662 | PemK family of DNA binding proteins | 0.906 | 0.237 | no | 1.816 | 0.589 | yes | 2.425 | 0.603 | yes | 3.085 | 0.338 | yes | 3.083 | 0.761 | yes | 2.257 | 0.807 | yes | 2.038 | 0.731 | yes | 1.230 | 0.198 | no | 1.155 | 0.157 | no |
| DR0663 | Predicted protein | 0.962 | 0.318 | no | 2.091 | 0.783 | yes | 2.355 | 1.217 | yes | 3.385 | 1.436 | yes | 3.150 | 1.873 | yes | 1.732 | 0.975 | yes | 2.305 | 1.048 | yes | 1.550 | 0.711 | no | 1.093 | 0.569 | no |
| DR0664 | Predicted protein | 1.077 | 0.465 | no | 2.275 | 1.490 | yes | 3.508 | 2.124 | yes | 3.487 | 1.906 | yes | 2.901 | 1.341 | yes | 2.457 | 1.352 | yes | 2.185 | 0.907 | yes | 2.144 | 0.419 | yes | 2.093 | 0.123 | yes |
| DR0665 | Predicted protein | 1.133 | 0.431 | no | 2.242 | 1.022 | yes | 9.104 | 5.586 | yes | 11.660 | 5.742 | yes | 4.941 | 3.316 | yes | 2.037 | 1.267 | yes | 3.700 | 2.746 | yes | 1.945 | 0.256 | yes | 1.909 | 0.446 | yes |
| DR0666 | Transposase | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR0667 | Transposon DORF | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR0668 | Carbamoyl phosphate synthetase | 0.695 | 0.257 | no | 0.738 | 0.289 | no | 0.963 | 0.532 | no | 0.847 | 0.211 | no | 0.859 | 0.228 | no | 0.910 | 0.267 | no | 0.948 | 0.470 | no | 0.779 | 0.144 | no | 0.834 | 0.173 | no |
| DR0669 | Antibiotic Kinase family protein | 1.924 | 0.337 | yes | 2.107 | 1.023 | yes | 1.305 | 0.462 | no | 1.364 | 0.203 | no | 1.483 | 0.514 | no | 1.244 | 0.403 | no | 1.186 | 0.539 | no | 0.971 | 0.245 | no | 0.972 | 0.285 | no |
| DR0670 | NH2- acetyltransferase | 1.219 | 0.508 | no | 1.245 | 0.515 | no | 0.946 | 0.514 | no | 0.905 | 0.422 | no | 1.067 | 0.379 | no | 1.093 | 0.297 | no | 1.075 | 0.500 | no | 0.872 | 0.180 | no | 0.896 | 0.434 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR0671 | Aspartate aminotransferase | 1.079 | 0.287 | no | 0.718 | 0.239 | no | 0.579 | 0.209 | yes | 0.407 | 0.060 | yes | 0.459 | 0.096 | yes | 0.421 | 0.127 | yes | 0.423 | 0.175 | yes | 0.568 | 0.080 | yes | 0.620 | 0.149 | yes |
| DR0672 | Predicted protein | 1.138 | 0.395 | no | 1.137 | 0.557 | no | 0.790 | 0.274 | no | 1.113 | 0.595 | no | 0.682 | 0.151 | no | 1.091 | 0.425 | no | 1.386 | 0.588 | no | 1.488 | 0.644 | no | 1.073 | 0.365 | no |
| DR0673 | Predicted protein | 0.977 | 0.149 | no | 0.387 | 0.137 | yes | 0.227 | 0.083 | yes | 0.287 | 0.096 | yes | 0.421 | 0.198 | yes | 0.459 | 0.068 | yes | 0.737 | 0.261 | no | 1.095 | 0.315 | no | 1.842 | 0.588 | yes |
| DR0674 | Argininosuccinate synthase, ASSY | 0.939 | 0.307 | no | 0.502 | 0.198 | yes | 0.356 | 0.125 | yes | 0.350 | 0.153 | yes | 0.469 | 0.163 | yes | 0.661 | 0.238 | yes | 0.727 | 0.224 | no | 1.069 | 0.219 | no | 1.178 | 0.261 | no |
| DR0675 | NH2- acetyltransferase | 1.243 | 0.444 | no | 0.807 | 0.366 | no | 0.788 | 0.547 | yes | 1.276 | 0.438 | no | 1.032 | 0.693 | no | 1.206 | 0.714 | no | 1.474 | 0.728 | no | 1.693 | 0.568 | yes | 1.288 | 0.490 | no |
| DR0676 | NH2- acetyltransferase | 0.985 | 0.356 | no | 0.566 | 0.153 | yes | 0.514 | 0.073 | yes | 0.502 | 0.181 | yes | 0.648 | 0.252 | yes | 0.762 | 0.361 | no | 0.777 | 0.164 | no | 0.695 | 0.167 | yes | 0.620 | 0.115 | no |
| DR0677 | NH2- Acetyltransferase | 1.210 | 0.461 | no | 1.069 | 0.282 | no | 1.114 | 0.472 | no | 0.976 | 0.464 | no | 1.292 | 0.782 | no | 1.196 | 0.386 | no | 1.229 | 0.563 | no | 1.033 | 0.260 | no | n/a | n/a | n/a |
| DR0678 | Argininosuccinate lyase | 1.127 | 0.579 | no | 0.919 | 0.344 | no | 0.735 | 0.366 | yes | 1.026 | 0.389 | no | 0.915 | 0.259 | no | 0.811 | 0.174 | no | 0.992 | 0.129 | no | 1.215 | 0.636 | no | 1.077 | 0.289 | no |
| DR0679 | Small nucleotidyltransferase-like protein | 1.390 | 0.165 | no | 1.704 | 1.019 | yes | 1.084 | 0.295 | no | 1.486 | 0.239 | no | 1.008 | 0.428 | no | 1.051 | 0.403 | no | 0.960 | 0.446 | no | 0.871 | 0.150 | no | 0.775 | 0.104 | no |
| DR0680 | Uncharacterized protein next to small nucleotidyltransferases | 2.052 | 1.034 | yes | 1.581 | 0.418 | yes | 1.558 | 0.515 | yes | 2.238 | 0.582 | yes | 1.423 | 0.534 | no | 1.269 | 0.420 | no | 1.258 | 0.492 | no | 1.091 | 0.428 | no | 1.062 | 0.364 | no |
| DR0681 | NH2- Acetyltransferase | 1.099 | 0.532 | no | 0.870 | 0.308 | no | 0.979 | 0.355 | no | 1.067 | 0.406 | no | 0.984 | 0.178 | no | 1.309 | 0.310 | no | 1.296 | 0.463 | no | 1.193 | 0.353 | no | 1.130 | 0.262 | no |
| DR0682 | NH2- acetyltransferase | 0.946 | 0.437 | no | 0.915 | 0.541 | no | 0.383 | 0.279 | yes | 1.435 | 0.233 | no | 1.068 | 0.627 | no | 0.479 | 0.158 | yes | 0.892 | 0.505 | no | 0.812 | 0.291 | no | 1.357 | 0.181 | no |
| DR0683 | NH2- acetyltransferase | 1.108 | 0.540 | no | 0.978 | 0.329 | no | 0.967 | 0.469 | no | 1.425 | 0.271 | no | 0.966 | 0.483 | no | 0.921 | 0.270 | no | 1.317 | 0.488 | no | 1.175 | 0.397 | no | 1.201 | 0.494 | no |
| DR0684 | Carbamoyl-phosphate synthase, carA | 0.952 | 0.337 | no | 0.829 | 0.426 | no | 0.945 | 0.338 | no | 0.937 | 0.188 | no | 0.836 | 0.242 | no | 0.786 | 0.305 | no | 0.789 | 0.154 | no | 0.898 | 0.194 | no | 0.949 | 0.138 | no |
| DR0685 | Uncharacterized secreted protein, DR-1 | 0.967 | 0.399 | no | 0.680 | 0.385 | yes | 0.905 | 0.450 | no | 0.798 | 0.440 | no | 1.195 | 0.805 | no | 1.273 | 0.790 | no | 1.670 | 0.993 | yes | 1.117 | 0.208 | no | 2.414 | 0.592 | yes |
| DR0686 | Uncharacterized secreted protein, DR-1 | 1.025 | 0.394 | no | 0.919 | 0.331 | no | 1.343 | 0.458 | no | 2.110 | 0.554 | yes | 1.631 | 0.613 | yes | 1.960 | 0.733 | yes | 1.689 | 0.566 | yes | 1.326 | 0.166 | no | 1.664 | 0.604 | yes |
| DR0687 | Uncharacterized protein, DR-1 | 0.719 | 0.237 | no | 0.665 | 0.369 | yes | 0.751 | 0.185 | no | 0.606 | 0.062 | yes | 0.836 | 0.291 | no | 1.099 | 0.294 | no | 1.190 | 0.531 | no | 0.934 | 0.242 | no | 1.250 | 0.328 | no |
| DR0688 | Large membrane protein, uncharacterized, DR-1 | 0.940 | 0.380 | no | 0.647 | 0.219 | yes | 0.932 | 0.165 | no | 1.383 | 0.273 | no | 1.524 | 0.539 | no | 2.205 | 0.753 | yes | 1.949 | 0.643 | yes | 1.574 | 0.245 | yes | 2.160 | 0.469 | yes |
| DR0689 | Uracil-DNA gylcosylase, UNG | 1.133 | 0.625 | no | 0.906 | 0.548 | no | 0.704 | 0.294 | yes | 1.383 | 0.183 | no | 1.466 | 1.022 | no | 1.528 | 1.086 | no | 2.032 | 1.410 | yes | 1.704 | 0.381 | yes | 1.564 | 0.573 | yes |
| DR0690 | Topoisomerase IB | 1.463 | 0.511 | no | 0.959 | 0.328 | no | 0.821 | 0.226 | no | 1.076 | 0.246 | no | 1.113 | 0.309 | no | 1.534 | 0.921 | no | 1.862 | 1.068 | yes | 1.207 | 0.402 | no | 1.307 | 0.451 | no |
| DR0691 | Secreted protein, uncharacterized | 0.889 | 0.321 | no | 0.560 | 0.172 | yes | 0.324 | 0.051 | yes | 0.268 | 0.044 | yes | 0.361 | 0.150 | yes | 0.484 | 0.069 | yes | 0.650 | 0.160 | yes | 0.743 | 0.127 | no | 0.804 | 0.122 | no |
| DR0692 | GlnB regulatory protein | 1.227 | 0.318 | no | 4.031 | 1.988 | yes | 4.025 | 2.643 | yes | 3.030 | 1.001 | yes | 2.378 | 0.791 | yes | 1.876 | 0.628 | yes | 1.756 | 0.721 | yes | 1.497 | 0.584 | no | 3.134 | 1.318 | yes |
| DR0693 | AMT ammonium transporter protein | 1.181 | 0.397 | no | 2.115 | 0.688 | yes | 2.206 | 0.738 | yes | 1.758 | 0.285 | yes | 2.217 | 1.382 | yes | 1.404 | 0.211 | no | 1.232 | 0.226 | no | 1.211 | 0.171 | no | 2.735 | 0.395 | yes |
| DR0694 | Phage related protein | 0.984 | 0.339 | no | 5.229 | 1.638 | yes | 5.567 | 2.020 | yes | 5.078 | 2.046 | yes | 4.647 | 2.234 | yes | 4.081 | 2.255 | yes | 3.098 | 1.193 | yes | 3.751 | 0.529 | yes | 2.335 | 1.048 | yes |
| DR0695 | V-type ATPase subunit I | 0.641 | 0.182 | yes | 2.446 | 1.250 | yes | 1.943 | 0.620 | yes | 1.652 | 0.213 | yes | 2.003 | 0.477 | yes | 1.585 | 0.571 | yes | 1.697 | 0.529 | yes | 1.481 | 0.440 | yes | 1.272 | 0.360 | no |
| DR0696 | V-type ATPase subunit K | 0.895 | 0.347 | no | 6.641 | 1.644 | yes | 7.186 | 2.159 | yes | 5.257 | 2.156 | yes | 4.658 | 1.766 | yes | 2.856 | 1.069 | yes | 2.217 | 0.811 | yes | 2.119 | 0.509 | yes | 1.780 | 0.402 | yes |
| DR0697 | V-type ATPase subunit E | 0.710 | 0.283 | no | 8.100 | 5.293 | yes | 7.528 | 5.074 | yes | 5.076 | 2.849 | yes | 4.442 | 2.073 | yes | 2.882 | 1.283 | yes | 3.656 | 1.697 | yes | 4.574 | 1.289 | yes | 2.899 | 1.451 | yes |
| DR0698 | V-type ATPase subunit C | 0.942 | 0.202 | no | 6.145 | 1.466 | yes | 6.154 | 2.630 | yes | 4.522 | 0.019 | yes | 3.942 | 0.861 | yes | 3.328 | 1.124 | yes | 2.935 | 0.671 | yes | 3.841 | 0.751 | yes | 3.893 | 1.732 | yes |
| DR0699 | V-type ATPase subunit G | 1.096 | 0.592 | no | 2.189 | 1.596 | yes | 0.880 | 0.482 | no | 0.947 | 0.602 | no | 1.413 | 0.939 | no | 3.119 | 1.411 | yes | 0.625 | 0.251 | yes | 0.795 | 0.344 | no | 1.713 | 1.049 | no |
| DR0700 | V-type ATPase subunit A | 0.925 | 0.302 | no | 2.065 | 0.862 | yes | 2.195 | 1.293 | yes | 2.394 | 0.867 | yes | 1.775 | 0.873 | yes | 1.743 | 1.084 | no | 1.677 | 0.718 | yes | 2.809 | 0.330 | yes | 2.367 | 1.231 | yes |
| DR0701 | V-type ATPase subunit B | 1.126 | 0.656 | no | 2.003 | 0.806 | yes | 1.979 | 1.056 | yes | 1.479 | 0.492 | no | 2.326 | 1.260 | yes | 1.611 | 1.145 | no | 1.971 | 0.591 | yes | 1.707 | 0.560 | yes | 2.514 | 0.281 | yes |
| DR0702 | V-type ATPase subunit D | 0.883 | 0.313 | no | 0.964 | 0.478 | no | 0.644 | 0.150 | yes | 0.487 | 0.134 | yes | 0.431 | 0.184 | yes | 0.453 | 0.179 | yes | 0.330 | 0.059 | yes | 0.417 | 0.171 | yes | 1.507 | 0.471 | yes |
| DR0703 | Double stranded Beta helix superfamily protein with HxH motif | 0.879 | 0.144 | no | 1.220 | 0.590 | no | 1.127 | 0.565 | no | 0.910 | 0.094 | no | 0.774 | 0.215 | no | 0.682 | 0.278 | yes | 0.636 | 0.204 | yes | 0.787 | 0.149 | no | 0.752 | 0.204 | no |
| DR0704 | HD superfamily Hydrolase | 1.022 | 0.211 | no | 1.168 | 0.132 | no | 1.159 | 0.191 | no | 1.270 | 0.054 | no | 1.074 | 0.193 | no | 0.813 | 0.219 | no | 0.715 | 0.239 | no | 0.812 | 0.144 | no | 0.863 | 0.169 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR0705 | Glucanotransferase, similar to endo alpha-1,4 polygalactosaminidase | 1.018 | 0.357 | no | 1.218 | 0.344 | no | 1.609 | 0.652 | yes | 1.848 | 0.609 | yes | 1.410 | 0.463 | no | 0.991 | 0.257 | no | 1.111 | 0.727 | no | 1.206 | 0.670 | no | 0.929 | 0.115 | no |
| DR0706 | Glucanotransferase, similar to endo alpha-1,4 polygalactosaminidase | 1.100 | 0.325 | no | 1.648 | 0.822 | yes | 1.253 | 0.252 | no | 1.694 | 0.252 | yes | 1.423 | 0.349 | no | 1.082 | 0.283 | no | 1.210 | 0.383 | no | 0.908 | 0.220 | no | 0.880 | 0.249 | no |
| DR0707 | Predicted protein, with high similarity to DR0708 | 0.719 | 0.277 | no | 0.913 | 0.291 | no | 0.986 | 0.653 | no | 1.035 | 0.494 | no | 0.911 | 0.210 | no | 0.761 | 0.229 | no | 0.958 | 0.422 | no | 0.930 | 0.182 | no | 0.928 | 0.204 | no |
| DR0708 | Predicted protein, with high similarity to DR0707 | 1.502 | 0.744 | no | 1.300 | 0.772 | no | 1.406 | 0.685 | no | 2.545 | 1.090 | yes | 1.750 | 0.744 | yes | 1.330 | 0.819 | no | 1.421 | 0.425 | no | 1.425 | 0.277 | no | 1.002 | 0.387 | no |
| DR0709 | UDP-glucose 4-epimerase | 0.930 | 0.636 | no | 0.889 | 0.355 | no | 1.067 | 0.642 | no | 2.129 | 0.224 | yes | 1.945 | 0.715 | yes | 1.389 | 0.884 | no | 2.193 | 0.959 | yes | 1.525 | 0.726 | no | 1.840 | 0.733 | yes |
| DR0710 | Mannose-1-phosphate guanyltransferase | 1.001 | 0.247 | no | 3.137 | 1.281 | yes | 4.717 | 1.227 | yes | 4.689 | 0.499 | yes | 3.460 | 1.322 | yes | 2.248 | 0.559 | yes | 2.059 | 1.147 | yes | 1.455 | 0.536 | no | 1.063 | 0.398 | no |
| DR0711 | UDP-glucose-4-epimerase | 0.948 | 0.388 | no | 1.989 | 0.640 | yes | 2.265 | 0.481 | yes | 1.948 | 0.062 | yes | 1.981 | 0.436 | yes | 1.844 | 0.633 | yes | 1.629 | 0.419 | yes | 1.378 | 0.258 | no | 0.939 | 0.222 | no |
| DR0712 | Predicted protein | 0.934 | 0.272 | no | 0.662 | 0.144 | yes | 0.719 | 0.357 | yes | 0.809 | 0.369 | no | 0.740 | 0.275 | no | 0.831 | 0.246 | no | 0.623 | 0.227 | yes | 1.016 | 0.296 | no | 1.608 | 0.918 | no |
| DR0714 | Predicted protein | 1.077 | 0.553 | no | 2.038 | 1.162 | yes | 1.389 | 0.788 | no | 1.697 | 0.779 | yes | 1.474 | 0.967 | no | 1.223 | 0.407 | no | 1.356 | 0.726 | no | 0.988 | 0.310 | no | 0.689 | 0.295 | yes |
| DR0715 | G/T mismatch-specific thymine DNA glycosylase | 0.863 | 0.354 | no | 0.438 | 0.231 | yes | 0.240 | 0.115 | yes | 0.172 | 0.013 | yes | 0.385 | 0.155 | yes | 0.632 | 0.171 | yes | 0.539 | 0.186 | yes | 0.711 | 0.238 | yes | 0.554 | 0.284 | yes |
| DR0716 | Molybdopterin-binding domain, similar to the same domain of Nitrate reductase | 0.792 | 0.322 | no | 0.384 | 0.163 | yes | 0.299 | 0.140 | yes | 0.298 | 0.103 | yes | 0.479 | 0.161 | yes | 0.723 | 0.231 | no | 0.890 | 0.278 | no | 1.110 | 0.387 | no | 0.900 | 0.150 | no |
| DR0717 | Leucine/ prolyl aminopeptidase | 0.840 | 0.271 | no | 0.698 | 0.154 | no | 0.639 | 0.098 | yes | 0.542 | 0.069 | yes | 0.696 | 0.302 | yes | 0.863 | 0.230 | no | 0.864 | 0.260 | no | 1.195 | 0.467 | no | 1.099 | 0.218 | no |
| DR0718 | Aspartate-1-decarboxylase, PAND | 0.752 | 0.328 | no | 0.729 | 0.526 | yes | 0.754 | 0.398 | yes | 0.413 | 0.024 | yes | 1.250 | 0.680 | no | 1.276 | 0.767 | no | 1.080 | 0.246 | no | 1.077 | 0.227 | no | 1.004 | 0.119 | no |
| DR0719 | GAF domain + HD superfamily hydrolase | 0.721 | 0.236 | no | 0.904 | 0.281 | no | 0.919 | 0.214 | no | 0.836 | 0.098 | no | 0.825 | 0.202 | no | 0.839 | 0.258 | no | 0.879 | 0.297 | no | 0.904 | 0.065 | no | 0.905 | 0.147 | no |
| DR0720 | HTH transcription factor, TetR/AcrR family | 1.355 | 0.358 | no | 1.499 | 0.454 | yes | 1.383 | 0.493 | no | 1.336 | 0.520 | no | 1.269 | 0.380 | no | 0.965 | 0.334 | no | 1.315 | 0.491 | no | 1.426 | 0.377 | no | 1.522 | 0.613 | no |
| DR0721 | Uncharacterized small conserved protein, probable polyketide cyclase or dehydratase | 1.122 | 0.553 | no | 1.424 | 0.444 | no | 1.388 | 0.459 | no | 1.648 | 0.847 | no | 1.403 | 0.652 | no | 1.126 | 0.228 | no | 1.074 | 0.321 | no | 1.017 | 0.355 | no | 0.997 | 0.644 | no |
| DR0722 | Predicted protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR0723 | Alpha-glucosidase | 1.139 | 0.406 | no | 2.643 | 1.688 | yes | 2.401 | 1.358 | yes | 3.251 | 2.101 | yes | 2.287 | 0.981 | yes | 1.823 | 0.943 | yes | 2.165 | 1.472 | yes | 1.392 | 0.483 | no | 3.593 | 1.524 | yes |
| DR0724 | Uncharacterized conserved protein, possible regulatory protein | 0.960 | 0.415 | no | 1.282 | 0.546 | no | 1.347 | 0.327 | no | 1.149 | 0.517 | no | 0.865 | 0.236 | no | 1.187 | 0.647 | no | 1.066 | 0.544 | no | 1.025 | 0.271 | no | 0.807 | 0.133 | no |
| DR0725 | Predicted protein | 1.455 | 0.689 | no | 1.064 | 0.626 | no | 0.960 | 0.306 | no | 1.285 | 0.492 | no | 1.106 | 0.343 | no | 0.915 | 0.301 | no | 0.846 | 0.208 | no | 0.925 | 0.287 | no | 0.966 | 0.045 | no |
| DR0726 | Membrane protein, uncharcterized | 1.054 | 0.353 | no | 0.816 | 0.451 | no | 0.803 | 0.431 | no | 0.830 | 0.374 | no | 0.825 | 0.319 | no | 0.647 | 0.257 | yes | 0.779 | 0.297 | no | 0.951 | 0.323 | no | 0.929 | 0.245 | no |
| DR0727 | Predicted protein | 0.899 | 0.388 | no | 0.930 | 0.512 | no | 0.872 | 0.545 | no | 0.903 | 0.431 | no | 0.967 | 0.570 | no | 0.797 | 0.217 | no | 1.058 | 0.334 | no | 1.622 | 0.637 | yes | 1.005 | 0.403 | no |
| DR0728 | Fructokinase, SCRK | 0.947 | 0.282 | no | 0.792 | 0.115 | no | 0.522 | 0.160 | yes | 0.367 | 0.127 | yes | 0.399 | 0.202 | yes | 0.424 | 0.296 | yes | 0.384 | 0.152 | yes | 0.518 | 0.139 | yes | 0.676 | 0.071 | no |
| DR0729 | Dehalogenase fold hydrolase, probably phosphoglycolate phosphatase | 1.079 | 0.313 | no | 0.995 | 0.172 | no | 0.797 | 0.126 | no | 0.817 | 0.142 | no | 0.875 | 0.123 | no | 1.188 | 0.417 | no | 1.332 | 0.471 | no | 1.590 | 0.498 | yes | 1.103 | 0.220 | no |
| DR0730 | Rossman fold oxidoreductase | 1.241 | 0.360 | no | 1.183 | 0.420 | no | 0.915 | 0.185 | no | 1.033 | 0.099 | no | 1.115 | 0.246 | no | 0.858 | 0.300 | no | 0.738 | 0.140 | no | 1.040 | 0.576 | no | 0.719 | 0.092 | no |
| DR0731 | Receiver domain, CHEY family | 1.101 | 0.526 | no | 1.267 | 0.608 | no | 1.036 | 0.608 | no | 0.927 | 0.307 | no | 1.088 | 0.730 | no | 0.586 | 0.191 | yes | 1.022 | 0.381 | no | 0.802 | 0.078 | no | 0.550 | 0.153 | yes |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR0732 | Imidazoleglycerol-phosphate synthase, hisF or His4 | 0.929 | 0.277 | no | 0.773 | 0.138 | no | 0.740 | 0.253 | no | 0.690 | 0.254 | no | 0.719 | 0.315 | yes | 0.899 | 0.270 | no | 0.921 | 0.179 | no | 0.950 | 0.101 | no | 0.811 | 0.152 | no |
| DR0733 | Phosphoribosyl-AMP cyclohydrolase, His2 | 1.038 | 0.414 | no | 0.824 | 0.262 | no | 0.998 | 0.373 | no | 0.834 | 0.166 | no | 0.960 | 0.410 | no | 0.888 | 0.121 | no | 1.194 | 0.512 | no | 1.106 | 0.289 | no | 0.669 | 0.219 | no |
| DR0734 | Predicted protein | 1.103 | 0.163 | no | 1.927 | 0.895 | yes | 1.316 | 0.576 | no | 1.539 | 0.562 | no | 1.285 | 0.924 | no | 1.000 | 0.213 | no | 0.973 | 0.437 | no | 0.762 | 0.116 | no | 0.738 | 0.261 | no |
| DR0735 | HTH transcripition factor, TetR/AcrR family | 0.960 | 0.280 | no | 0.744 | 0.333 | no | 0.584 | 0.221 | yes | 0.606 | 0.214 | yes | 0.666 | 0.306 | yes | 0.573 | 0.202 | yes | 0.621 | 0.209 | yes | 0.696 | 0.226 | yes | 0.774 | 0.274 | no |
| DR0736 | Predicted protein | 1.027 | 0.319 | no | 1.108 | 0.318 | no | 0.955 | 0.448 | no | 0.876 | 0.446 | no | 0.801 | 0.274 | no | 0.648 | 0.194 | yes | 0.833 | 0.256 | no | 0.711 | 0.133 | yes | 0.682 | 0.281 | no |
| DR0737 | Predicted protein | 0.979 | 0.295 | no | 0.733 | 0.261 | no | 0.652 | 0.234 | yes | 0.624 | 0.260 | yes | 0.659 | 0.243 | yes | 0.622 | 0.281 | yes | 0.640 | 0.263 | yes | 0.807 | 0.136 | no | 0.845 | 0.327 | no |
| DR0738 | CyaE/NodT-like, probable hemolysin transport protein | 1.125 | 0.353 | no | 0.801 | 0.214 | no | 0.844 | 0.284 | no | 1.246 | 0.481 | no | 0.925 | 0.274 | no | 0.706 | 0.340 | yes | 0.697 | 0.269 | yes | 0.883 | 0.125 | no | 0.807 | 0.264 | no |
| DR0739 | Membrane protein, probably cation efflux | 0.996 | 0.318 | no | 1.003 | 0.284 | no | 0.929 | 0.365 | no | 0.796 | 0.182 | no | 0.852 | 0.180 | no | 0.863 | 0.290 | no | 0.789 | 0.230 | no | 1.091 | 0.431 | no | 0.874 | 0.273 | no |
| DR0740 | Membrane transporter, probably cation efflux | 1.261 | 0.752 | no | 1.407 | 0.364 | no | 1.301 | 0.344 | no | 1.566 | 0.339 | no | 1.304 | 1.012 | no | 0.927 | 0.237 | no | 0.982 | 0.256 | no | 0.836 | 0.144 | no | 0.816 | 0.243 | no |
| DR0741 | Predicted protein | 0.823 | 0.333 | no | 0.332 | 0.128 | yes | 0.273 | 0.098 | yes | 0.266 | 0.019 | yes | 0.408 | 0.189 | yes | 0.597 | 0.257 | yes | 0.596 | 0.080 | yes | 0.814 | 0.046 | no | 0.864 | 0.127 | no |
| DR0742 | ArgR regulator of arginine metabolism | 1.438 | 0.897 | no | 1.024 | 0.559 | no | 0.701 | 0.336 | yes | 0.725 | 0.346 | no | 0.746 | 0.283 | no | 0.842 | 0.388 | no | 1.277 | 0.536 | no | 1.053 | 0.183 | no | 1.024 | 0.471 | no |
| DR0743 | Receiver domain, CHEY family | 0.745 | 0.184 | no | 0.609 | 0.217 | yes | 0.679 | 0.433 | yes | 0.828 | 0.596 | no | 0.840 | 0.374 | no | 2.249 | 1.509 | yes | 2.875 | 0.955 | yes | 2.873 | 1.449 | yes | 4.041 | 1.493 | yes |
| DR0744 | Histidine kinase | 1.039 | 0.397 | no | 1.045 | 0.336 | no | 0.798 | 0.168 | no | 0.728 | 0.194 | no | 0.757 | 0.216 | no | 1.022 | 0.238 | no | 1.029 | 0.509 | no | 0.996 | 0.209 | no | 1.196 | 0.222 | no |
| DR0745 | Serine protease HhoA/DegP | 0.797 | 0.155 | no | 0.740 | 0.128 | no | 0.674 | 0.109 | yes | 0.476 | 0.103 | yes | 0.510 | 0.177 | yes | 0.593 | 0.111 | yes | 0.549 | 0.145 | yes | 0.608 | 0.146 | yes | 0.662 | 0.100 | no |
| DR0746 | Predicted protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR0747 | Sugar epimerase, GalM-like family | 1.041 | 0.250 | no | 1.289 | 0.747 | no | 0.965 | 0.195 | no | 0.861 | 0.210 | no | 0.725 | 0.368 | yes | 0.787 | 0.220 | no | 0.707 | 0.115 | no | 0.717 | 0.157 | yes | 0.955 | 0.274 | no |
| DR0748 | rRNA methylase | 1.147 | 0.324 | no | 2.374 | 0.643 | yes | 1.959 | 0.592 | yes | 1.092 | 0.416 | no | 1.591 | 0.990 | no | 1.201 | 0.361 | no | 1.246 | 0.398 | no | 1.032 | 0.227 | no | 0.861 | 0.361 | no |
| DR0749 | Predicted protein | 1.353 | 0.430 | no | 2.424 | 1.004 | yes | 1.607 | 0.698 | yes | 1.521 | 0.186 | no | 1.422 | 0.695 | no | 1.267 | 0.515 | no | 1.138 | 0.320 | no | 0.986 | 0.317 | no | 1.139 | 0.444 | no |
| DR0750 | Signal membrane protein, similar to c-di-GMP phosphodiesterase A, three domains: 2 PAS + GGDEF + YJCC | 0.889 | 0.147 | no | 0.780 | 0.315 | no | 0.585 | 0.280 | yes | 0.398 | 0.028 | yes | 0.770 | 0.404 | no | 0.694 | 0.119 | no | 0.783 | 0.223 | no | 0.813 | 0.260 | no | 0.900 | 0.274 | no |
| DR0751 | Cell division topological specificity factor, MinE | 1.026 | 0.214 | no | 0.838 | 0.225 | no | 0.951 | 0.335 | no | 1.262 | 0.325 | no | 1.471 | 0.542 | no | 1.700 | 0.502 | yes | 1.903 | 0.568 | yes | 1.985 | 1.001 | yes | 1.602 | 0.898 | yes |
| DR0752 | Division inhibitor MinD, ATPase | 0.592 | 0.179 | yes | 0.638 | 0.261 | yes | 0.619 | 0.112 | yes | 0.531 | 0.173 | yes | 1.006 | 0.354 | no | 1.189 | 0.335 | no | 1.021 | 0.248 | no | 1.578 | 0.342 | yes | 1.465 | 0.321 | yes |
| DR0753 | Thioredoxin family protein | 0.722 | 0.178 | no | 0.630 | 0.219 | yes | 0.767 | 0.212 | no | 0.728 | 0.140 | no | 1.393 | 0.610 | no | 0.929 | 0.136 | no | 0.991 | 0.106 | no | 1.216 | 0.163 | no | 1.470 | 0.278 | yes |
| DR0754 | Thioredoxin family protein | 0.866 | 0.130 | no | 0.971 | 0.251 | no | 1.239 | 0.280 | no | 1.108 | 0.101 | no | 1.171 | 0.253 | no | 0.959 | 0.199 | no | 0.818 | 0.174 | no | 0.863 | 0.151 | no | 0.923 | 0.240 | no |
| DR0755 | Ribosomal protein L19 | 0.782 | 0.158 | no | 0.867 | 0.228 | no | 1.918 | 0.630 | yes | 1.713 | 0.765 | no | 1.717 | 0.256 | yes | 2.192 | 1.029 | yes | 2.143 | 0.794 | yes | 2.027 | 0.851 | yes | 2.253 | 0.811 | yes |
| DR0756 | O-sialoglycoprotein endopeptidase family protein, inactivated? | 0.854 | 0.242 | no | 0.599 | 0.119 | yes | 0.734 | 0.202 | no | 0.595 | 0.073 | no | 0.913 | 0.284 | no | 1.151 | 0.415 | no | 1.069 | 0.543 | no | 0.828 | 0.288 | no | 1.410 | 0.492 | no |
| DR0757 | Citrate synthase II | 0.972 | 0.474 | no | 0.354 | 0.140 | yes | 0.556 | 0.119 | yes | 0.766 | 0.419 | no | 0.739 | 0.310 | no | 0.873 | 0.294 | no | 0.872 | 0.185 | no | 1.119 | 0.579 | no | 1.839 | 0.281 | yes |
| DR0758 | Uncharacterized conserved protein, YunF/Yece like protein | 1.073 | 0.370 | no | 0.856 | 0.311 | no | 0.864 | 0.261 | no | 0.808 | 0.228 | no | 1.004 | 0.230 | no | 0.972 | 0.392 | no | 0.926 | 0.134 | no | 1.144 | 0.221 | no | 1.190 | 0.329 | no |
| DR0759 | AAA supefamily ATPase, similar to DNAA | 1.085 | 0.404 | no | 0.670 | 0.210 | yes | 0.865 | 0.218 | no | 1.143 | 0.465 | no | 1.007 | 0.136 | no | 0.911 | 0.240 | no | 0.993 | 0.267 | no | 1.079 | 0.145 | no | 1.642 | 0.262 | yes |
| DR0760 | Beta-lactamase class C family protein, PBP-like | 1.270 | 0.413 | no | 0.809 | 0.184 | no | 0.720 | 0.117 | no | 0.803 | 0.199 | no | 0.831 | 0.299 | no | 0.778 | 0.222 | no | 0.794 | 0.187 | no | 0.851 | 0.209 | no | 0.897 | 0.279 | no |
| DR0761 | Calcineurin family phosphoesterase | 1.429 | 0.528 | no | 0.846 | 0.363 | no | 0.838 | 0.401 | no | 1.274 | 0.586 | no | 0.746 | 0.343 | no | 0.719 | 0.134 | no | 0.945 | 0.397 | no | 0.847 | 0.170 | no | 1.162 | 0.365 | no |
| DR0762 | Possibly secreted protein, uncharacterized | 0.783 | 0.205 | no | 0.269 | 0.132 | yes | 0.355 | 0.168 | yes | 0.434 | 0.139 | yes | 1.068 | 0.818 | no | 1.345 | 0.049 | no | 2.070 | 1.482 | yes | 1.858 | 0.636 | yes | 3.327 | 0.592 | yes |
| DR0763 | Probable N-acetyltransferase | 1.046 | 0.488 | no | 0.585 | 0.274 | yes | 0.539 | 0.215 | yes | 0.628 | 0.292 | yes | 0.709 | 0.310 | yes | 0.623 | 0.172 | yes | 0.671 | 0.332 | yes | 0.623 | 0.107 | yes | 0.882 | 0.244 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR0764 | Lipoate-protein ligase, LIPB | 0.674 | 0.138 | no | 0.348 | 0.097 | yes | 0.263 | 0.086 | yes | 0.291 | 0.091 | yes | 0.356 | 0.102 | yes | 0.397 | 0.098 | yes | 0.426 | 0.173 | yes | 0.534 | 0.089 | yes | 0.753 | 0.139 | no |
| DR0765 | Lipoic acid synthetase (metal cluster protein), LIPA | 0.998 | 0.468 | no | 0.466 | 0.157 | yes | 0.465 | 0.114 | yes | 0.554 | 0.243 | yes | 0.576 | 0.377 | yes | 0.525 | 0.284 | yes | 0.484 | 0.130 | yes | 0.416 | 0.091 | yes | 0.883 | 0.160 | no |
| DR0766 | Beta propeller protein, related to serine/threonine kinase | 0.928 | 0.425 | no | 1.157 | 0.334 | no | 1.503 | 0.532 | yes | 0.818 | 0.110 | no | 1.060 | 0.378 | no | 0.792 | 0.240 | no | 0.706 | 0.238 | no | 0.734 | 0.206 | yes | 0.568 | 0.127 | yes |
| DR0767 | Secreted protein, uncharacterized | 1.675 | 0.818 | yes | 1.373 | 0.201 | no | 1.994 | 1.044 | yes | 1.203 | 0.043 | no | 1.240 | 0.739 | no | 0.878 | 0.165 | no | 1.195 | 0.601 | no | 0.944 | 0.235 | no | 1.122 | 0.514 | no |
| DR0768 | Muramoyl-DAP Ligase, MurF | 0.851 | 0.171 | no | 1.259 | 0.353 | no | 1.544 | 0.348 | yes | 1.300 | 0.348 | no | 1.189 | 0.358 | no | 1.084 | 0.265 | no | 1.000 | 0.155 | no | 1.182 | 0.317 | no | 1.343 | 0.251 | no |
| DR0769 | Secreted low complexity protein, uncharacterized | 1.436 | 0.642 | no | 1.782 | 0.752 | yes | 1.976 | 0.663 | yes | 2.153 | 1.078 | yes | 1.615 | 1.096 | no | 1.190 | 0.344 | no | 1.366 | 0.643 | no | 1.104 | 0.256 | no | 0.966 | 0.391 | no |
| DR0770 | FTSA like Actin-Hsp70 superfamily protein | 0.786 | 0.396 | no | 1.338 | 0.590 | no | 2.006 | 0.651 | yes | 1.515 | 0.262 | no | 1.698 | 0.818 | yes | 1.115 | 0.209 | no | 1.012 | 0.193 | no | 0.978 | 0.200 | no | 1.645 | 0.458 | yes |
| DR0771 | Secreted protein, uncharacterized | 1.057 | 0.165 | no | 1.251 | 0.102 | no | 1.752 | 0.380 | yes | 1.989 | 0.349 | yes | 1.651 | 0.351 | yes | 1.169 | 0.170 | no | 1.029 | 0.184 | no | 1.008 | 0.268 | no | 1.817 | 0.903 | yes |
| DR0772 | Secreted protein, uncharacterized | 0.908 | 0.242 | no | 1.218 | 0.292 | no | 1.838 | 0.541 | yes | 1.974 | 0.496 | yes | 1.538 | 0.485 | no | 1.426 | 0.476 | no | 1.038 | 0.231 | no | 0.892 | 0.322 | no | 1.441 | 0.367 | no |
| DR0773 | Predicted protein (low complexity) | 0.964 | 0.210 | no | 1.142 | 0.146 | no | 1.538 | 0.307 | yes | 1.403 | 0.309 | no | 1.458 | 0.302 | no | 1.204 | 0.125 | no | 0.949 | 0.131 | no | 0.920 | 0.240 | no | 1.534 | 0.267 | yes |
| DR0774 | GspD general secretion pathway protein | 0.598 | 0.250 | yes | 1.087 | 0.515 | no | 1.085 | 0.663 | no | 0.821 | 0.335 | no | 0.663 | 0.381 | yes | 0.768 | 0.470 | yes | 0.383 | 0.188 | yes | 0.864 | 0.284 | no | 0.519 | 0.376 | yes |
| DR0775 | Chorismate synthase, AroC | 1.002 | 0.270 | no | 0.423 | 0.117 | yes | 0.397 | 0.131 | yes | 0.616 | 0.146 | yes | 0.597 | 0.122 | yes | 0.516 | 0.169 | yes | 0.619 | 0.279 | yes | 0.667 | 0.121 | yes | 1.337 | 0.208 | no |
| DR0776 | Shikimate kinase, AroK | 0.757 | 0.068 | no | 0.431 | 0.183 | yes | 0.394 | 0.082 | yes | 0.460 | 0.111 | yes | 0.763 | 0.160 | no | 0.915 | 0.247 | no | 0.572 | 0.175 | yes | 0.650 | 0.209 | yes | 0.919 | 0.077 | no |
| DR0777 | 3-dehydroquinate synthase, AroB | 0.916 | 0.305 | no | 0.869 | 0.418 | no | 0.747 | 0.232 | no | 0.758 | 0.237 | no | 0.931 | 0.307 | no | 0.976 | 0.196 | no | 0.849 | 0.209 | no | 0.784 | 0.106 | no | 0.966 | 0.349 | no |
| DR0778 | 3-dehydroquinate dehydratase, AroD | 0.902 | 0.278 | no | 1.185 | 0.363 | no | 1.615 | 0.734 | yes | 1.028 | 0.167 | no | 1.222 | 0.203 | no | 0.913 | 0.123 | no | 1.142 | 0.475 | no | 0.718 | 0.303 | yes | 1.014 | 0.050 | no |
| DR0779 | A/b hydrolase, homolog of ybbA, serine esterase family | 0.940 | 0.246 | no | 1.011 | 0.265 | no | 1.647 | 0.485 | yes | 1.735 | 0.265 | yes | 2.177 | 1.120 | yes | 1.592 | 0.312 | yes | 1.397 | 0.291 | no | 1.395 | 0.191 | no | 1.158 | 0.236 | no |
| DR0780 | Predicted protein | 0.910 | 0.179 | no | 0.565 | 0.273 | yes | 0.497 | 0.144 | yes | 0.753 | 0.135 | no | 1.010 | 0.268 | no | 1.249 | 0.225 | no | 1.687 | 0.316 | yes | 1.832 | 0.079 | yes | 1.794 | 0.699 | yes |
| DR0781 | Receiver domain, CHEY family + HTH domain | 0.899 | 0.170 | no | 0.431 | 0.168 | yes | 0.406 | 0.136 | yes | 0.709 | 0.081 | no | 0.946 | 0.297 | no | 1.370 | 0.227 | no | 1.172 | 0.298 | no | 1.571 | 0.415 | yes | 1.957 | 0.631 | yes |
| DR0782 | Ortholog endo-type 6-aminohexanoate oligomer hydrolase, related to D-aminopeptidase | 1.107 | 0.254 | no | 0.794 | 0.252 | no | 0.926 | 0.420 | no | 0.594 | 0.169 | yes | 0.909 | 0.254 | no | 1.020 | 0.241 | no | 1.073 | 0.273 | no | 0.957 | 0.199 | no | 1.063 | 0.259 | no |
| DR0783 | MutT like hydrolase | 1.161 | 0.442 | no | 0.997 | 0.396 | no | 1.018 | 0.351 | no | 1.182 | 0.461 | no | 0.846 | 0.288 | no | 0.976 | 0.225 | no | 1.030 | 0.394 | no | 0.844 | 0.134 | no | 0.868 | 0.069 | no |
| DR0784 | MutT like hydrolase | 0.982 | 0.423 | no | 0.856 | 0.362 | no | 1.008 | 0.224 | no | 1.173 | 0.500 | no | 1.297 | 0.467 | no | 1.187 | 0.439 | no | 1.206 | 0.497 | no | 0.919 | 0.204 | no | 1.447 | 0.519 | no |
| DR0785 | Predicted protein | 1.387 | 0.631 | no | 1.692 | 1.160 | yes | 1.331 | 0.365 | no | 1.879 | 1.199 | yes | 1.376 | 0.575 | no | 1.084 | 0.403 | no | 1.299 | 0.717 | no | 0.951 | 0.157 | no | 1.035 | 0.247 | no |
| DR0786 | UroporphyrinogenIII cosynthase, HEM4 | 0.992 | 0.187 | no | 1.111 | 0.219 | no | 1.151 | 0.376 | no | 1.116 | 0.289 | no | 1.174 | 0.218 | no | 1.033 | 0.255 | no | 1.098 | 0.190 | no | 0.989 | 0.103 | no | 1.003 | 0.067 | no |
| DR0787 | S4 domain containing protein | 1.246 | 0.541 | no | 0.978 | 0.509 | no | 0.738 | 0.286 | no | 0.981 | 0.350 | no | 1.069 | 0.454 | no | 0.920 | 0.238 | no | 1.042 | 0.378 | no | 1.139 | 0.147 | no | 1.137 | 0.333 | no |
| DR0788 | Branched-chain amino acid periplasmic binding protein | 1.118 | 0.197 | no | 0.808 | 0.334 | no | 0.526 | 0.279 | yes | 0.730 | 0.238 | no | 0.668 | 0.311 | yes | 0.761 | 0.348 | no | 0.811 | 0.292 | no | 1.003 | 0.148 | no | 1.145 | 0.421 | no |
| DR0789 | Cysteine synthase, CYSK | 1.273 | 0.618 | no | 0.576 | 0.212 | yes | 0.443 | 0.158 | yes | 0.589 | 0.297 | yes | 0.517 | 0.093 | yes | 0.534 | 0.089 | yes | 0.616 | 0.211 | yes | 0.625 | 0.136 | yes | 1.014 | 0.369 | no |
| DR0790 | Fusion uncharacterized conserved membrane bounded domain, similar to YGIH_ECOLI domain with glutamyl tRNA reductase + Fe-S Oxidoreductase | 0.789 | 0.228 | no | 0.517 | 0.095 | yes | 0.402 | 0.151 | yes | 0.556 | 0.044 | yes | 0.609 | 0.197 | yes | 0.641 | 0.175 | yes | 0.566 | 0.098 | yes | 0.687 | 0.058 | yes | 0.765 | 0.151 | no |
| DR0791 | A/b fold hydrolase | 1.745 | 0.426 | yes | 1.028 | 0.439 | no | 1.289 | 0.313 | no | 3.929 | 2.080 | yes | 4.636 | 2.354 | yes | 4.057 | 2.625 | yes | 4.656 | 3.424 | yes | 3.481 | 1.773 | yes | 1.312 | 0.393 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR0792 | DinF-like protein | 1.272 | 0.275 | no | 1.097 | 0.170 | no | 0.963 | 0.321 | no | 1.140 | 0.249 | no | 1.122 | 0.300 | no | 1.029 | 0.270 | no | 1.077 | 0.303 | no | 1.119 | 0.138 | no | 1.134 | 0.211 | no |
| DR0793 | Dihydrofolate reductase, DYR | 1.459 | 0.443 | no | 1.350 | 0.918 | no | 1.108 | 0.254 | no | 1.490 | 0.506 | no | 1.372 | 0.606 | no | 0.924 | 0.178 | no | 0.936 | 0.423 | no | 0.959 | 0.133 | no | 0.869 | 0.211 | no |
| DR0794 | Ornithine Aminotransferase, ARGD | 0.890 | 0.113 | no | 0.580 | 0.143 | yes | 0.626 | 0.083 | yes | 0.797 | 0.157 | no | 0.767 | 0.225 | no | 0.683 | 0.182 | yes | 0.744 | 0.169 | no | 0.932 | 0.172 | no | 1.357 | 0.155 | no |
| DR0795 | Predicted protein | 1.115 | 0.295 | no | 0.968 | 0.291 | no | 0.986 | 0.256 | no | 1.313 | 0.099 | no | 0.982 | 0.168 | no | 0.811 | 0.147 | no | 0.835 | 0.174 | no | 0.905 | 0.153 | no | 0.973 | 0.142 | no |
| DR0796 | NH2 acetyltransferase | 0.860 | 0.239 | no | 0.709 | 0.265 | yes | 0.622 | 0.164 | yes | 0.728 | 0.128 | no | 0.705 | 0.106 | no | 0.763 | 0.427 | no | 0.709 | 0.205 | no | 0.833 | 0.252 | no | 0.991 | 0.345 | no |
| DR0797 | NH2 acetyltransferase | 1.295 | 0.395 | no | 0.751 | 0.165 | no | 0.647 | 0.196 | yes | 0.919 | 0.327 | no | 0.866 | 0.382 | no | 0.579 | 0.106 | yes | 0.752 | 0.187 | no | 0.808 | 0.124 | no | 1.172 | 0.180 | no |
| DR0798 | NH2 acetyltransferase | 1.469 | 0.442 | no | 0.878 | 0.251 | no | 1.085 | 0.528 | no | 1.528 | 0.379 | no | 1.309 | 0.485 | no | 0.963 | 0.288 | no | 1.228 | 0.830 | no | 1.235 | 0.673 | no | 1.358 | 0.784 | no |
| DR0799 | GFOR family oxidoreductase, Gal80 like | 1.076 | 0.125 | no | 0.468 | 0.091 | yes | 0.404 | 0.103 | yes | 0.590 | 0.219 | yes | 0.972 | 0.240 | no | 1.520 | 0.592 | no | 1.512 | 0.400 | yes | 1.919 | 0.365 | yes | 1.604 | 0.361 | yes |
| DR0800 | Predicted protein | 1.082 | 0.384 | no | 0.311 | 0.114 | yes | 0.565 | 0.221 | yes | 1.046 | 0.541 | no | 1.313 | 0.736 | no | 1.233 | 0.826 | no | 1.438 | 0.794 | no | 1.226 | 0.368 | no | 1.729 | 0.692 | yes |
| DR0801 | Lycopene cyclase | 0.956 | 0.300 | no | 0.811 | 0.372 | no | 0.558 | 0.172 | yes | 0.483 | 0.183 | yes | 0.638 | 0.356 | yes | 0.638 | 0.088 | yes | 0.628 | 0.189 | yes | 0.745 | 0.075 | no | 1.007 | 0.067 | no |
| DR0802 | Predicted protein | 1.087 | 0.235 | no | 1.018 | 0.182 | no | 1.094 | 0.403 | no | 1.111 | 0.299 | no | 0.983 | 0.255 | no | 0.864 | 0.084 | no | 0.562 | 0.087 | yes | 0.625 | 0.146 | yes | 0.607 | 0.154 | yes |
| DR0803 | Predicted protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR0804 | Probable sigma factor, sigK-like protein | 0.825 | 0.096 | no | 0.659 | 0.236 | yes | 0.744 | 0.285 | no | 0.919 | 0.079 | no | 1.054 | 0.421 | no | 0.738 | 0.055 | no | 0.775 | 0.076 | no | 0.897 | 0.166 | no | 0.846 | 0.185 | no |
| DR0805 | Small conserved membrane or secreted protein | 0.880 | 0.079 | no | 0.308 | 0.095 | yes | 0.219 | 0.092 | yes | 0.161 | 0.077 | yes | 0.424 | 0.163 | yes | 0.277 | 0.127 | yes | 0.419 | 0.235 | yes | 0.459 | 0.158 | yes | 0.958 | 0.102 | no |
| DR0806 | Conserved membrane protein | 0.980 | 0.393 | no | 0.340 | 0.115 | yes | 0.174 | 0.053 | yes | 0.096 | 0.041 | yes | 0.193 | 0.066 | yes | 0.187 | 0.030 | yes | 0.312 | 0.172 | yes | 0.345 | 0.125 | yes | 0.780 | 0.421 | no |
| DR0807 | Prolipoprotein diacylglycerol transferase, Lgt | 0.828 | 0.158 | no | 0.607 | 0.193 | yes | 0.889 | 0.446 | no | 0.751 | 0.184 | no | 0.841 | 0.294 | no | 0.864 | 0.192 | no | 0.675 | 0.228 | yes | 0.716 | 0.090 | yes | 0.593 | 0.126 | yes |
| DR0808 | GlmU, UDP-N-acetylglucosamine pyrophosphorylase | 1.498 | 0.502 | no | 0.944 | 0.253 | no | 0.817 | 0.282 | no | 1.214 | 0.319 | no | 1.002 | 0.253 | no | 0.817 | 0.149 | no | 0.953 | 0.330 | no | 0.881 | 0.131 | no | 0.717 | 0.325 | no |
| DR0809 | Bacteriochlorophyll synthase like protein | 1.021 | 0.215 | no | 1.017 | 0.216 | no | 1.147 | 0.529 | no | 0.736 | 0.168 | no | 0.891 | 0.211 | no | 0.849 | 0.152 | no | 0.780 | 0.083 | no | 0.968 | 0.246 | no | 0.973 | 0.102 | no |
| DR0810 | Phytoene dehydrogenase | 1.104 | 0.318 | no | 1.064 | 0.254 | no | 1.590 | 0.898 | no | 1.839 | 0.725 | yes | 1.194 | 0.752 | no | 0.844 | 0.181 | no | 0.941 | 0.508 | no | 0.786 | 0.121 | no | 0.692 | 0.217 | no |
| DR0811 | Conserved membrane protein | 1.121 | 0.206 | no | 1.248 | 0.360 | no | 1.184 | 0.243 | no | 1.309 | 0.246 | no | 1.188 | 0.298 | no | 1.173 | 0.115 | no | 1.160 | 0.164 | no | 0.876 | 0.166 | no | 0.738 | 0.199 | no |
| DR0812 | Extracellular alkaline serine protease | 1.333 | 0.504 | no | 1.383 | 0.554 | no | 1.852 | 0.597 | yes | 3.315 | 1.244 | yes | 2.335 | 1.182 | yes | 1.252 | 0.210 | no | 1.054 | 0.402 | no | 1.307 | 0.516 | no | 1.136 | 0.280 | no |
| DR0813 | Pyrroline-5 carboxylate dehydrogenase, ROCA | 0.765 | 0.157 | no | 0.903 | 0.232 | no | 1.350 | 0.353 | no | 1.542 | 0.269 | no | 1.652 | 0.426 | yes | 1.062 | 0.455 | no | 0.854 | 0.374 | no | 1.022 | 0.166 | no | 1.087 | 0.374 | no |
| DR0814 | Proline dehydrogenase | 0.795 | 0.220 | no | 1.005 | 0.367 | no | 1.389 | 0.343 | no | 1.821 | 0.074 | yes | 1.477 | 0.698 | no | 1.058 | 0.602 | no | 0.805 | 0.197 | no | 0.923 | 0.258 | no | 1.044 | 0.471 | no |
| DR0815 | YjcC domain signalling protein, transcriptional regulator GntR family, | 0.784 | 0.351 | no | 0.757 | 0.198 | no | 0.859 | 0.319 | no | 0.970 | 0.318 | no | 0.765 | 0.315 | no | 0.674 | 0.219 | yes | 0.620 | 0.272 | yes | 0.653 | 0.199 | yes | 0.802 | 0.202 | no |
| DR0816 | MgtC, Mg2+ transport protein C | 1.220 | 0.689 | no | 2.675 | 1.137 | yes | 2.545 | 0.953 | yes | 2.665 | 1.831 | yes | 1.769 | 0.490 | yes | 1.453 | 0.410 | no | 1.090 | 0.349 | no | 0.823 | 0.187 | no | 0.619 | 0.117 | yes |
| DR0817 | Predicted protein | 0.919 | 0.356 | no | 1.900 | 0.765 | yes | 1.791 | 0.573 | yes | 1.254 | 0.416 | no | 1.264 | 0.460 | no | 1.077 | 0.215 | no | 0.692 | 0.179 | no | 0.720 | 0.111 | yes | 0.643 | 0.096 | yes |
| DR0818 | Predicted protein | 0.728 | 0.372 | no | 1.905 | 1.189 | yes | 1.790 | 0.700 | yes | 1.840 | 0.597 | yes | 1.408 | 0.523 | no | 0.908 | 0.322 | no | 0.662 | 0.233 | yes | 0.487 | 0.161 | yes | 0.662 | 0.138 | no |
| DR0819 | C2C2 fingers seen in Mycobacterium, N-term. domain related to RecO | 0.706 | 0.266 | no | 1.381 | 0.444 | no | 1.389 | 0.283 | no | 0.867 | 0.108 | no | 0.988 | 0.274 | no | 0.871 | 0.194 | no | 0.999 | 0.355 | no | 0.659 | 0.237 | yes | 0.590 | 0.139 | yes |
| DR0820 | Predicted protein | 1.125 | 0.276 | no | 1.467 | 0.583 | no | 1.505 | 0.582 | yes | 0.969 | 0.089 | no | 1.346 | 0.671 | no | 0.938 | 0.129 | no | 0.844 | 0.153 | no | 0.764 | 0.125 | no | 0.666 | 0.328 | yes |
| DR0821 | Acetylcholinesterase family protein | 1.273 | 0.799 | no | 0.555 | 0.145 | yes | 0.788 | 0.109 | no | 0.833 | 0.099 | no | 0.896 | 0.494 | no | 1.022 | 0.712 | no | 0.584 | 0.213 | yes | 0.704 | 0.244 | yes | n/a | n/a | n/a |
| DR0822 | Oxidoreductase FABG | 1.381 | 0.621 | no | 0.595 | 0.171 | yes | 0.736 | 0.337 | yes | 0.722 | 0.148 | no | 1.057 | 0.555 | no | 0.592 | 0.249 | yes | 0.779 | 0.102 | no | 0.850 | 0.122 | no | 0.726 | 0.338 | no |
| DR0823 | Glucokinase, GLK | 1.372 | 0.492 | no | 1.147 | 0.444 | no | 1.029 | 0.349 | no | 0.725 | 0.288 | no | 0.929 | 0.572 | no | 1.003 | 0.446 | no | 0.716 | 0.239 | no | 0.915 | 0.187 | no | 0.999 | 0.355 | no |
| DR0824 | TIM barrel family of metalloenzymes, similar N-ethylammeline chlorohydrolase | 0.986 | 0.095 | no | 0.682 | 0.189 | yes | 0.699 | 0.164 | no | 0.711 | 0.068 | no | 0.942 | 0.124 | no | 0.914 | 0.164 | no | 0.862 | 0.123 | no | 1.074 | 0.100 | no | 1.000 | 0.065 | no |
| DR0825 | Ribosomal protein L31 | 1.080 | 0.288 | no | 2.826 | 1.104 | yes | 2.401 | 0.994 | yes | 1.940 | 0.370 | yes | 1.499 | 0.536 | no | 0.973 | 0.464 | no | 1.069 | 0.551 | no | 0.824 | 0.243 | no | 0.855 | 0.258 | no |
| DR0826 | DHH superfamily hydrolase | 0.897 | 0.294 | no | 1.506 | 0.365 | yes | 1.435 | 0.399 | no | 1.198 | 0.290 | no | 1.223 | 0.386 | no | 1.075 | 0.241 | no | 0.943 | 0.107 | no | 0.915 | 0.156 | no | 0.900 | 0.110 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR0827 | HAD superfamily hydrolase | 1.242 | 0.536 | no | 1.683 | 0.619 | yes | 1.956 | 0.697 | yes | 1.747 | 0.394 | yes | 1.320 | 0.344 | no | 0.836 | 0.320 | no | 1.238 | 0.475 | no | 1.000 | 0.087 | no | 1.143 | 0.333 | no |
| DR0828 | Isocitrate lyase, ACEA | 1.340 | 0.429 | no | 2.177 | 0.702 | yes | 2.513 | 0.792 | yes | 1.825 | 0.191 | yes | 1.775 | 0.710 | yes | 0.954 | 0.213 | no | 1.096 | 0.332 | no | 1.123 | 0.361 | no | 0.970 | 0.253 | no |
| DR0829 | WD-repeat protein | 1.150 | 0.356 | no | 1.136 | 0.416 | no | 1.240 | 0.250 | no | 0.976 | 0.174 | no | 1.357 | 0.806 | no | 1.076 | 0.418 | no | 1.050 | 0.444 | no | 0.977 | 0.164 | no | 0.909 | 0.469 | no |
| DR0830 | Similar to C-term. half of potassium channel protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR0831 | Predicted protein | 0.857 | 0.137 | no | 0.439 | 0.213 | yes | 0.352 | 0.207 | yes | 0.277 | 0.033 | yes | 0.547 | 0.390 | yes | 0.569 | 0.203 | yes | 0.485 | 0.182 | yes | 0.610 | 0.173 | yes | 1.101 | 0.148 | no |
| DR0832 | Oxidoreductase | 1.217 | 0.608 | no | 0.601 | 0.177 | yes | 1.140 | 0.789 | no | 1.130 | 0.734 | no | 1.589 | 0.602 | no | 2.871 | 1.766 | yes | 0.929 | 0.604 | no | 0.794 | 0.399 | no | n/a | n/a | n/a |
| DR0833 | Deacetylase, similar to histone deacetylase domain of eukaryotes | 1.276 | 0.498 | no | 1.135 | 0.694 | no | 1.308 | 0.917 | no | 1.099 | 0.723 | no | 0.878 | 0.368 | no | 0.735 | 0.261 | no | 0.894 | 0.559 | no | 0.818 | 0.116 | no | 0.860 | 0.191 | no |
| DR0834 | HTH transcription factor, NTCA - like, CAP family | 1.352 | 0.676 | no | 1.186 | 0.289 | no | 0.954 | 0.361 | no | 1.357 | 0.015 | no | 1.147 | 0.573 | no | 1.342 | 0.513 | no | 1.913 | 0.773 | yes | 1.337 | 0.592 | no | 1.159 | 0.192 | no |
| DR0835 | Predicted protein | 2.244 | 1.157 | yes | 1.298 | 0.482 | no | 1.558 | 0.426 | yes | 1.832 | 0.282 | yes | 1.332 | 0.388 | no | 1.221 | 0.177 | no | 1.086 | 0.288 | no | 0.896 | 0.338 | no | 1.265 | 0.767 | no |
| DR0836 | Shares a domain with unchacterized protein | 1.134 | 0.232 | no | 1.277 | 0.443 | no | 1.451 | 0.248 | yes | 1.851 | 0.702 | yes | 1.256 | 0.350 | no | 1.273 | 0.615 | no | 1.052 | 0.667 | no | 0.951 | 0.194 | no | 0.855 | 0.107 | no |
| DR0837 | Predicted P-loop ATPase, (inactivated) | 1.009 | 0.448 | no | 0.981 | 0.298 | no | 0.811 | 0.322 | no | 1.184 | 0.221 | no | 1.164 | 0.411 | no | 1.065 | 0.383 | no | 0.904 | 0.379 | no | 0.935 | 0.409 | no | 0.625 | 0.148 | yes |
| DR0838 | Memrane protein | 1.118 | 0.258 | no | 1.892 | 0.527 | yes | 1.854 | 0.282 | yes | 2.026 | 0.319 | yes | 1.879 | 0.797 | yes | 1.308 | 0.398 | no | 1.271 | 0.310 | no | 1.087 | 0.171 | no | 0.919 | 0.230 | no |
| DR0839 | Secreted protein, uncharacterized | 0.978 | 0.245 | no | 1.745 | 0.849 | yes | 1.724 | 0.344 | yes | 2.163 | 0.558 | yes | 1.939 | 0.517 | yes | 1.438 | 0.054 | no | 1.536 | 0.322 | yes | 1.338 | 0.449 | no | 1.114 | 0.633 | no |
| DR0840 | MocR protein transcriptional regulator GntR family/aminotransferase, MocR-like | 1.195 | 0.336 | no | 1.578 | 0.778 | yes | 1.473 | 0.522 | no | 1.992 | 0.943 | yes | 1.402 | 0.517 | no | 1.222 | 0.365 | no | 1.239 | 0.385 | no | 1.391 | 0.554 | no | 1.374 | 0.561 | no |
| DR0841 | Bacillus YfiT/DinB like protein | 1.123 | 0.212 | no | 3.407 | 0.680 | yes | 5.927 | 1.472 | yes | 5.487 | 0.742 | yes | 4.950 | 1.339 | yes | 2.608 | 0.540 | yes | 2.243 | 0.822 | yes | 1.219 | 0.421 | no | 0.773 | 0.303 | no |
| DR0842 | NimC like (5-Nitroimidazole antibiotics resistance) protein | 1.230 | 0.655 | no | 0.881 | 0.263 | no | 1.115 | 0.254 | no | 1.597 | 0.391 | no | 1.320 | 0.401 | no | 1.049 | 0.319 | no | 1.255 | 0.573 | no | 1.308 | 0.220 | no | 1.890 | 0.693 | yes |
| DR0843 | Predicted protease of transglutaminase family | 0.830 | 0.261 | no | 0.626 | 0.227 | yes | 0.576 | 0.238 | yes | 0.751 | 0.304 | no | 0.837 | 0.305 | no | 0.728 | 0.213 | no | 0.777 | 0.182 | no | 0.874 | 0.089 | no | 1.392 | 0.201 | no |
| DR0844 | Large proteins with thioredoxin like domains | 1.185 | 0.333 | no | 1.190 | 0.330 | no | 1.271 | 0.700 | no | 1.657 | 0.158 | yes | 1.464 | 0.257 | no | 1.452 | 0.216 | no | 1.410 | 0.549 | no | 0.989 | 0.224 | no | 1.008 | 0.179 | no |
| DR0845 | Ribose 5-phosphate isomerase, RPIA | 0.870 | 0.478 | no | 0.829 | 0.312 | no | 0.748 | 0.336 | yes | 0.628 | 0.133 | yes | 0.867 | 0.336 | no | 1.206 | 0.407 | no | 1.080 | 0.493 | no | 1.205 | 0.315 | no | 1.475 | 0.366 | yes |
| DR0846 | Antioxidant type thioredoxin fold protein, BCP_ECOLI ortholog | 0.881 | 0.126 | no | 0.948 | 0.121 | no | 1.032 | 0.199 | no | 0.985 | 0.053 | no | 1.212 | 0.436 | no | 1.363 | 0.368 | no | 1.106 | 0.294 | no | 1.184 | 0.118 | no | 2.310 | 0.760 | yes |
| DR0847 | ComA like protein, thioesterase superfamily | 0.668 | 0.234 | yes | 1.099 | 0.287 | no | 1.051 | 0.389 | no | 0.937 | 0.419 | no | 1.195 | 0.551 | no | 1.398 | 0.415 | no | 0.957 | 0.380 | no | 0.799 | 0.058 | no | 0.961 | 0.206 | no |
| DR0848 | Ortholog of lipoprotein NlpD, cell-wall associated protease | 0.793 | 0.263 | no | 1.111 | 0.471 | no | 0.808 | 0.154 | no | 0.818 | 0.285 | no | 0.881 | 0.477 | no | 1.080 | 0.475 | no | 0.813 | 0.259 | no | 0.724 | 0.239 | yes | 0.953 | 0.280 | no |
| DR0849 | Predicted protein | 0.848 | 0.319 | no | 1.038 | 0.188 | no | 0.857 | 0.240 | no | 0.579 | 0.081 | yes | 0.744 | 0.254 | no | 0.958 | 0.498 | no | 0.832 | 0.542 | no | 0.727 | 0.251 | yes | 0.654 | 0.206 | yes |
| DR0850 | Predicted protein | 0.920 | 0.207 | no | 1.031 | 0.373 | no | 0.706 | 0.192 | no | 0.687 | 0.069 | no | 0.744 | 0.207 | no | 0.897 | 0.464 | no | 1.031 | 0.068 | no | 1.146 | 0.216 | no | 0.736 | 0.187 | no |
| DR0851 | 4-hydroxybenzoate octaprenyltransferase, ubiA | 0.996 | 0.499 | no | 0.730 | 0.368 | no | 0.576 | 0.138 | yes | 0.459 | 0.184 | yes | 0.717 | 0.375 | yes | 0.539 | 0.126 | yes | 0.707 | 0.310 | yes | 0.586 | 0.128 | yes | 0.504 | 0.136 | yes |
| DR0852 | Predicted protein | 1.267 | 0.566 | no | 1.128 | 0.383 | no | 1.023 | 0.386 | no | 0.792 | 0.124 | no | 0.819 | 0.194 | no | 0.912 | 0.322 | no | 1.153 | 0.154 | no | 0.816 | 0.228 | no | 1.691 | 1.064 | yes |
| DR0853 | Rab/Ras family small GTPase | 1.087 | 0.294 | no | 2.083 | 0.546 | yes | 2.006 | 0.398 | yes | 1.687 | 0.249 | yes | 1.730 | 0.700 | yes | 1.587 | 0.304 | yes | 1.267 | 0.157 | no | 1.361 | 0.218 | no | 1.435 | 0.428 | no |
| DR0854 | Small family of predominantly archaeal proteins, associated with a GTPase even in Myxococcus and the actinomycetes | 1.183 | 0.565 | no | 1.694 | 0.883 | yes | 1.074 | 0.424 | no | 0.587 | 0.115 | yes | 0.972 | 0.489 | no | 1.094 | 0.439 | no | 0.953 | 0.202 | no | 0.814 | 0.182 | no | 1.273 | 0.291 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR0855 | Secreted uncharacterized conserved protein | 1.030 | 0.315 | no | 1.032 | 0.249 | no | 1.154 | 0.378 | no | 0.973 | 0.120 | no | 1.036 | 0.353 | no | 1.868 | 0.788 | yes | 2.145 | 0.784 | yes | 1.061 | 0.309 | no | 1.109 | 0.301 | no |
| DR0856 | Nuclease subunit/ DNA pol III epsilon subunit, DP3E | 1.201 | 0.537 | no | 1.971 | 1.037 | yes | 1.618 | 0.471 | yes | 1.494 | 0.106 | no | 1.273 | 0.238 | no | 1.332 | 0.350 | no | 1.821 | 0.779 | yes | 1.501 | 0.470 | yes | 1.082 | 0.292 | no |
| DR0857 | Conserved membrane protein, possible homolog of CAAX-like membrane endopeptidase | 1.086 | 0.701 | no | 0.837 | 0.608 | no | 0.717 | 0.290 | yes | 0.669 | 0.391 | yes | 0.915 | 0.628 | no | 0.587 | 0.156 | yes | 0.706 | 0.290 | no | 0.472 | 0.144 | yes | 1.404 | 0.860 | no |
| DR0858 | Membrane protein. | 1.201 | 0.309 | no | 1.144 | 0.267 | no | 1.630 | 0.814 | yes | 0.801 | 0.345 | no | 0.914 | 0.274 | no | 1.077 | 0.372 | no | 1.074 | 0.435 | no | 1.073 | 0.173 | no | 0.780 | 0.052 | no |
| DR0859 | SAM dependent methyltransferase, MENG ortholog | 0.978 | 0.301 | no | 0.704 | 0.165 | no | 0.718 | 0.181 | no | 0.760 | 0.382 | no | 0.636 | 0.131 | yes | 0.886 | 0.286 | no | 0.885 | 0.389 | no | 0.833 | 0.076 | no | 0.991 | 0.178 | no |
| DR0860 | Sensor histidine kinase + diverged CheY domain | 0.820 | 0.203 | no | 0.662 | 0.165 | yes | 0.492 | 0.141 | yes | 0.395 | 0.065 | yes | 0.563 | 0.096 | yes | 0.756 | 0.231 | no | 0.847 | 0.251 | no | 0.813 | 0.126 | no | 1.021 | 0.235 | no |
| DR0861 | Phytoene dehydrogenase, CRTI | 1.703 | 0.726 | yes | 1.203 | 0.547 | no | 1.067 | 0.497 | no | 1.327 | 0.524 | no | 0.897 | 0.204 | no | 1.071 | 0.319 | no | 1.210 | 0.517 | no | 1.177 | 0.109 | no | 1.050 | 0.415 | no |
| DR0862 | Phytoene synthase, CRTB | 1.013 | 0.253 | no | 0.698 | 0.217 | no | 0.568 | 0.078 | yes | 0.616 | 0.225 | yes | 0.775 | 0.235 | no | 0.967 | 0.335 | no | 1.179 | 0.433 | no | 1.179 | 0.272 | no | 1.250 | 0.369 | no |
| DR0863 | Membrane protein. | 1.076 | 0.377 | no | 0.548 | 0.169 | yes | 0.443 | 0.154 | yes | 1.058 | 0.091 | no | 1.075 | 0.443 | no | 1.172 | 0.536 | no | 1.816 | 0.422 | yes | 1.748 | 0.378 | yes | 2.219 | 0.656 | yes |
| DR0864 | Predicted protein | 0.902 | 0.411 | no | 0.370 | 0.176 | yes | 0.250 | 0.105 | yes | 0.461 | 0.244 | yes | 0.640 | 0.331 | yes | 0.951 | 0.521 | no | 1.578 | 0.504 | yes | 1.582 | 0.317 | yes | 1.719 | 0.497 | yes |
| DR0865 | HTH transcription factor, FUR1 iron regulator | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR0866 | LPS glycosyltransferase | 1.098 | 0.287 | no | 0.692 | 0.230 | yes | 0.691 | 0.192 | yes | 0.849 | 0.215 | no | 0.772 | 0.068 | no | 0.866 | 0.244 | no | 0.900 | 0.320 | no | 0.875 | 0.247 | no | 0.851 | 0.124 | no |
| DR0867 | Methylenetetrahydrofolate dehydrogenase, FOLD | 1.244 | 0.500 | no | 0.839 | 0.172 | no | 0.754 | 0.314 | no | 0.720 | 0.116 | no | 0.842 | 0.161 | no | 1.091 | 0.439 | no | 1.147 | 0.344 | no | 1.018 | 0.140 | no | 0.841 | 0.118 | no |
| DR0868 | Inosine monophosphate cyclohydrolase, purH/PUR9 | 0.741 | 0.349 | no | 0.607 | 0.232 | yes | 1.309 | 0.706 | no | 4.486 | 0.582 | yes | 2.291 | 1.751 | yes | 0.962 | 0.441 | no | 1.589 | 0.958 | no | 1.832 | 0.360 | yes | 2.101 | 0.559 | yes |
| DR0869 | Transposon DORF | 1.914 | 0.501 | yes | 2.199 | 0.855 | yes | 3.527 | 1.333 | yes | 2.155 | 0.410 | yes | 2.259 | 0.444 | yes | 2.335 | 0.831 | yes | 2.484 | 0.913 | yes | 1.541 | 0.602 | yes | 1.270 | 0.345 | no |
| DR0870 | Transposon IS2621 | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR0871 | Predicted protein | 1.519 | 0.555 | no | 1.596 | 0.687 | yes | 1.207 | 0.421 | no | 1.360 | 0.347 | no | 1.227 | 0.469 | no | 1.262 | 0.435 | no | 1.219 | 0.537 | no | 1.037 | 0.191 | no | 0.868 | 0.152 | no |
| DR0872 | Homoserine O-trans-acetylase, a/b hydrolase fold | 1.002 | 0.557 | no | 1.051 | 0.230 | no | 1.062 | 0.378 | no | 0.718 | 0.069 | no | 0.979 | 0.438 | no | 1.034 | 0.419 | no | 1.025 | 0.469 | no | 0.833 | 0.128 | no | 0.731 | 0.258 | no |
| DR0873 | O-acetyl-L-homoserine sulfhydrylase | 0.892 | 0.148 | no | 0.650 | 0.211 | yes | 0.714 | 0.220 | no | 0.900 | 0.190 | no | 1.055 | 0.578 | no | 0.790 | 0.126 | no | 0.689 | 0.093 | no | 0.807 | 0.061 | no | 1.321 | 0.533 | no |
| DR0874 | Contains INTEGRIN(alpha)-like repeat motif | 1.059 | 0.239 | no | 1.701 | 0.570 | yes | 2.121 | 0.842 | yes | 1.624 | 0.282 | yes | 1.614 | 0.417 | yes | 1.774 | 0.602 | yes | 1.571 | 0.521 | yes | 1.170 | 0.415 | no | 0.872 | 0.135 | no |
| DR0875 | AMPN family zinc metalloprotease | 1.036 | 0.195 | no | 0.871 | 0.170 | no | 0.865 | 0.173 | no | 0.889 | 0.228 | no | 0.921 | 0.438 | no | 1.200 | 0.267 | no | 0.990 | 0.359 | no | 1.030 | 0.183 | no | 1.033 | 0.153 | no |
| DR0876 | MutT superfamily hydrolase | 0.691 | 0.156 | no | 0.775 | 0.193 | no | 1.065 | 0.174 | no | 0.793 | 0.163 | no | 1.169 | 0.235 | no | 1.634 | 0.283 | yes | 1.604 | 0.512 | yes | 1.238 | 0.165 | no | 1.180 | 0.277 | no |
| DR0877 | Predicted protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR0878 | Adenine phosphoribosyltransferase | 0.931 | 0.105 | no | 0.618 | 0.124 | yes | 0.552 | 0.164 | yes | 0.648 | 0.073 | no | 0.888 | 0.125 | no | 1.033 | 0.170 | no | 1.113 | 0.170 | no | 1.263 | 0.151 | no | 1.602 | 0.247 | yes |
| DR0879 | Predicted protein | 0.955 | 0.341 | no | 0.937 | 0.339 | no | 1.190 | 0.319 | no | 1.198 | 0.418 | no | 1.340 | 0.355 | no | 1.257 | 0.377 | no | 1.530 | 0.739 | no | 0.983 | 0.074 | no | 0.697 | 0.319 | yes |
| DR0880 | Subunit of probable cation transport system, orthologous to Bacilus operon or pha operon from Sinorhizobium meliloti | 1.036 | 0.159 | no | 1.238 | 0.349 | no | 1.282 | 0.326 | no | 0.833 | 0.087 | no | 0.879 | 0.131 | no | 1.138 | 0.701 | no | 1.020 | 0.642 | no | 1.019 | 0.422 | no | 1.059 | 0.426 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR0881 | Subunit of probable cation transport system, orthologous to Bacilus operon | 1.777 | 0.809 | yes | 1.352 | 0.237 | no | 1.261 | 0.356 | no | 1.218 | 0.309 | no | 1.175 | 0.211 | no | 1.384 | 0.483 | no | 1.437 | 0.636 | no | 1.207 | 0.288 | no | 1.369 | 0.250 | no |
| DR0882 | Subunit of probable cation transport system, orthologous to Bacilus operon | 1.290 | 0.554 | no | 1.277 | 0.193 | no | 1.168 | 0.347 | no | 1.147 | 0.064 | no | 1.261 | 0.412 | no | 1.536 | 0.445 | no | 1.794 | 0.532 | yes | 1.040 | 0.168 | no | 1.130 | 0.107 | no |
| DR0884 | Subunit of K+ efflux system, ortholog phaE | 1.060 | 0.241 | no | 0.214 | 0.097 | yes | 0.723 | 0.295 | no | 1.420 | 0.373 | no | 0.797 | 0.360 | no | 1.800 | 1.189 | no | 1.897 | 1.448 | yes | 1.972 | 0.916 | yes | 1.374 | 0.873 | no |
| DR0885 | Subunit of K+ efflux system, ortholog phaF | 1.771 | 0.299 | yes | 1.794 | 1.153 | yes | 1.117 | 0.568 | no | 1.641 | 0.300 | yes | 2.456 | 0.660 | yes | 1.501 | 0.840 | no | 2.119 | 0.945 | yes | 0.867 | 0.023 | no | 1.498 | 1.007 | no |
| DR0886 | Subunit of K+ efflux system | 1.298 | 0.292 | no | 1.749 | 0.575 | yes | 1.396 | 0.371 | no | 1.550 | 0.548 | no | 1.446 | 0.405 | no | 1.855 | 0.816 | yes | 1.512 | 0.602 | no | 1.055 | 0.212 | no | 0.995 | 0.239 | no |
| DR0887 | Predicted protein | 0.979 | 0.303 | no | 0.934 | 0.331 | no | 0.918 | 0.303 | no | 0.781 | 0.279 | no | 1.113 | 0.319 | no | 1.297 | 0.386 | no | 1.443 | 0.893 | no | 1.129 | 0.159 | no | 1.146 | 0.144 | no |
| DR0888 | Some domain + invasin domain protein | 0.851 | 0.285 | no | 1.961 | 0.762 | yes | 3.377 | 1.005 | yes | 5.168 | 2.701 | yes | 5.312 | 1.981 | yes | 7.907 | 4.066 | yes | 8.466 | 4.134 | yes | 7.191 | 1.338 | yes | 3.870 | 1.789 | yes |
| DR0889 | Predicted protein | 0.997 | 0.471 | no | 0.852 | 0.248 | no | 1.020 | 0.558 | no | 1.770 | 0.326 | no | 1.445 | 0.351 | no | 1.614 | 0.340 | yes | 2.534 | 0.526 | yes | 2.128 | 0.868 | yes | 1.261 | 0.449 | no |
| DR0890 | Highly conserved uncharacterized protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR0891 | Receiver domain, CHEY family + HTH domain | 1.268 | 0.437 | no | 2.875 | 1.727 | yes | 1.686 | 0.711 | yes | 1.251 | 0.191 | no | 1.479 | 0.502 | no | 1.417 | 0.541 | no | 1.448 | 0.346 | no | 1.339 | 0.213 | no | 1.351 | 0.299 | no |
| DR0892 | Sensory transduction histidine protein kinase, similar to CutC | 0.962 | 0.380 | no | 2.246 | 0.841 | yes | 1.479 | 0.849 | no | 0.644 | 0.074 | no | 0.758 | 0.237 | no | 1.010 | 0.604 | no | 1.043 | 0.617 | no | 0.966 | 0.368 | no | 0.866 | 0.176 | no |
| DR0893 | Conserved membrane protein, possible permease | 0.954 | 0.185 | no | 3.138 | 0.857 | yes | 1.341 | 0.210 | no | 1.091 | 0.098 | no | 1.001 | 0.411 | no | 0.932 | 0.335 | no | 0.945 | 0.303 | no | 0.931 | 0.279 | no | 0.873 | 0.194 | no |
| DR0894 | Uncharacterized conserved protein | 1.080 | 0.429 | no | 0.817 | 0.304 | no | 0.548 | 0.203 | yes | 0.592 | 0.092 | yes | 0.660 | 0.209 | yes | 0.887 | 0.214 | no | 0.953 | 0.221 | no | 0.894 | 0.130 | no | 0.731 | 0.064 | no |
| DR0895 | Predicted membrane protein, uncharacterized | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR0896 | Predicted pseudouridine synthase | 1.100 | 0.247 | no | 1.055 | 0.314 | no | 0.560 | 0.175 | yes | 0.494 | 0.090 | yes | 0.618 | 0.117 | yes | 0.672 | 0.214 | yes | 1.023 | 0.424 | no | 1.012 | 0.237 | no | 0.864 | 0.316 | no |
| DR0897 | Membrane protein | 1.299 | 0.362 | no | 1.327 | 0.374 | no | 1.143 | 0.346 | no | 0.914 | 0.149 | no | 0.882 | 0.163 | no | 1.013 | 0.164 | no | 1.051 | 0.407 | no | 1.138 | 0.165 | no | 0.984 | 0.107 | no |
| DR0898 | Conserved membrane protein | 1.237 | 0.445 | no | 1.270 | 0.665 | no | 1.057 | 0.409 | no | 1.152 | 0.369 | no | 0.806 | 0.317 | no | 0.790 | 0.245 | no | 0.896 | 0.300 | no | 0.805 | 0.193 | no | 0.784 | 0.261 | no |
| DR0899 | Ribonuclease H | 0.758 | 0.369 | no | 0.807 | 0.286 | no | 0.729 | 0.154 | no | 0.606 | 0.150 | yes | 0.713 | 0.105 | no | 0.805 | 0.214 | no | 0.806 | 0.299 | no | 0.883 | 0.255 | no | 0.816 | 0.250 | no |
| DR0900 | Predicted protein | 0.959 | 0.162 | no | 0.880 | 0.366 | no | 0.805 | 0.256 | no | 0.720 | 0.070 | no | 0.960 | 0.690 | no | 0.737 | 0.110 | no | 0.640 | 0.136 | yes | 0.886 | 0.086 | no | 0.856 | 0.128 | no |
| DR0901 | Ribosome-binding factor A, RBFA | 0.735 | 0.262 | no | 0.742 | 0.188 | no | 0.669 | 0.091 | yes | 0.631 | 0.116 | yes | 0.659 | 0.108 | yes | 0.718 | 0.006 | no | 0.575 | 0.108 | yes | 0.731 | 0.210 | yes | 0.726 | 0.053 | no |
| DR0902 | Thioesterase family protein, a/b hydrolase, ortholog of YBGC | 0.959 | 0.339 | no | 0.980 | 0.506 | no | 0.996 | 0.274 | no | 1.017 | 0.381 | no | 1.015 | 0.212 | no | 0.852 | 0.190 | no | 0.905 | 0.331 | no | 1.169 | 0.265 | no | 1.394 | 0.460 | no |
| DR0903 | Predicted protein | 0.744 | 0.364 | no | 1.333 | 0.233 | no | 1.202 | 0.545 | no | 1.220 | 0.632 | no | 1.324 | 0.540 | no | 0.982 | 0.300 | no | 1.243 | 0.464 | no | 1.153 | 0.215 | no | 0.966 | 0.188 | no |
| DR0904 | VWFA Mg-binding domain protein | 1.001 | 0.220 | no | 1.121 | 0.470 | no | 1.087 | 0.223 | no | 0.997 | 0.163 | no | 1.091 | 0.189 | no | 1.039 | 0.149 | no | 1.039 | 0.182 | no | 1.110 | 0.110 | no | 1.178 | 0.163 | no |
| DR0905 | Uncharacterized protein similar to YGY4 HALSO | 1.619 | 0.696 | no | 3.075 | 0.983 | yes | 3.131 | 1.370 | yes | 3.096 | 0.834 | yes | 1.778 | 0.776 | yes | 1.125 | 0.582 | no | 0.807 | 0.290 | no | 0.661 | 0.116 | yes | 0.830 | 0.105 | no |
| DR0906 | DNA gyrase B subunit, GYRB | 0.878 | 0.568 | no | 4.414 | 2.977 | yes | 3.739 | 2.173 | yes | 2.470 | 1.579 | yes | 2.310 | 1.556 | yes | 0.352 | 0.068 | yes | 1.115 | 0.110 | no | 0.516 | 0.133 | yes | 0.724 | 0.331 | no |
| DR0907 | Cold-shock protein CSPA, OB fold nucleic acid binding protein | 0.812 | 0.201 | no | 0.960 | 0.421 | no | 1.807 | 0.851 | yes | 1.554 | 0.620 | no | 2.560 | 0.811 | yes | 2.059 | 0.952 | yes | 3.011 | 1.371 | yes | 2.700 | 1.134 | yes | 1.871 | 0.453 | yes |
| DR0908 | Predicted protein | 0.932 | 0.178 | no | 1.307 | 0.562 | no | 1.395 | 0.239 | no | 1.523 | 0.265 | no | 1.651 | 0.759 | yes | 0.967 | 0.272 | no | 0.946 | 0.168 | no | 0.906 | 0.171 | no | 0.958 | 0.121 | no |
| DR0909 | Predicted protein | 0.931 | 0.327 | no | 0.980 | 0.356 | no | 1.151 | 0.638 | no | 0.886 | 0.080 | no | 1.345 | 0.981 | no | 0.807 | 0.439 | no | 0.692 | 0.212 | yes | 0.559 | 0.202 | yes | 0.600 | 0.232 | yes |
| DR0910 | Invasin repeat domane fused to uncharacterized domain | 0.912 | 0.126 | no | 0.715 | 0.195 | no | 0.790 | 0.165 | no | 0.954 | 0.171 | no | 0.920 | 0.103 | no | 0.765 | 0.147 | no | 0.750 | 0.210 | no | 0.937 | 0.262 | no | 1.356 | 0.241 | no |
| DR0911 | DNA-directed rna polymerase BETA' subunit | 0.713 | 0.480 | yes | 1.987 | 1.365 | yes | 1.628 | 0.821 | yes | 0.845 | 0.425 | no | 0.831 | 0.364 | no | 0.736 | 0.223 | no | 0.956 | 0.567 | no | 0.949 | 0.254 | no | 0.881 | 0.419 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR0912 | DNA-directed rna polymerase BETA subunit | 0.848 | 0.426 | no | 3.194 | 0.795 | yes | 2.426 | 0.795 | yes | 2.286 | 0.868 | yes | 1.412 | 0.509 | no | 1.139 | 0.805 | no | 0.884 | 0.352 | no | 0.893 | 0.084 | no | 0.585 | 0.380 | yes |
| DR0913 | Predicted protein | 0.850 | 0.188 | no | 2.595 | 0.884 | yes | 2.764 | 0.954 | yes | 2.312 | 1.121 | yes | 1.864 | 0.968 | yes | 0.980 | 0.378 | no | 0.953 | 0.261 | no | 0.844 | 0.245 | no | 0.552 | 0.288 | yes |
| DR0914 | SAM dependent methyltransferase | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR0915 | Predicted protein | 0.947 | 0.190 | no | 2.065 | 0.634 | yes | 1.407 | 0.442 | no | 1.181 | 0.250 | no | 1.340 | 0.674 | no | 1.249 | 0.812 | no | 1.199 | 0.284 | no | 1.100 | 0.197 | no | 1.603 | 0.645 | yes |
| DR0917 | Membrane protein | 1.191 | 0.264 | no | 3.348 | 1.241 | yes | 3.149 | 1.039 | yes | 2.663 | 0.110 | yes | 2.613 | 0.567 | yes | 1.859 | 0.540 | yes | 2.344 | 0.860 | yes | 1.527 | 0.437 | yes | 0.885 | 0.162 | no |
| DR0918 | Methanol dehydrogenase regulatory protein, moxR ortholog, ATPase AAA family | 1.070 | 0.270 | no | 3.806 | 2.344 | yes | 3.257 | 1.368 | yes | 2.419 | 0.586 | yes | 2.184 | 0.332 | yes | 1.543 | 0.421 | yes | 1.576 | 0.479 | yes | 1.140 | 0.214 | no | 0.825 | 0.091 | no |
| DR0919 | PepX type II pullulanase homolog | 1.410 | 0.883 | no | 1.426 | 0.419 | no | 1.877 | 1.395 | yes | 1.605 | 0.579 | no | 1.369 | 0.587 | no | 1.022 | 0.225 | no | 1.447 | 0.955 | no | 1.038 | 0.297 | no | 0.945 | 0.406 | no |
| DR0920 | Predicted protein | 1.286 | 0.430 | no | 0.862 | 0.491 | no | 1.470 | 0.381 | yes | 3.355 | 1.113 | yes | 2.499 | 1.394 | yes | 3.094 | 2.022 | yes | 2.957 | 1.427 | yes | 3.047 | 1.007 | yes | 3.551 | 1.767 | yes |
| DR0921 | Methionine gamma-lyase | 1.055 | 0.399 | no | 1.389 | 0.254 | no | 2.393 | 0.909 | yes | 1.916 | 0.227 | yes | 2.610 | 1.173 | yes | 2.067 | 0.813 | yes | 1.984 | 0.409 | yes | 1.698 | 0.286 | yes | 1.281 | 0.221 | no |
| DR0922 | Acyl-COA dehydrogenase | 1.055 | 0.318 | no | 0.652 | 0.299 | yes | 0.574 | 0.328 | yes | 0.904 | 0.295 | no | 0.701 | 0.215 | no | 0.639 | 0.207 | yes | 0.722 | 0.276 | yes | 0.907 | 0.155 | no | 0.721 | 0.369 | no |
| DR0923 | Uncharacterized ortholog of Mycobacterial and Cyanobacterial proteins | 1.057 | 0.385 | no | 0.592 | 0.218 | yes | 0.678 | 0.303 | yes | 0.708 | 0.429 | yes | 0.806 | 0.186 | no | 0.693 | 0.149 | no | 0.744 | 0.224 | no | 0.848 | 0.203 | no | 1.595 | 1.048 | no |
| DR0924 | Phosphate transport protein pit | 1.178 | 0.497 | no | 0.824 | 0.391 | no | 0.919 | 0.350 | no | 1.349 | 0.371 | no | 1.597 | 0.485 | yes | 1.294 | 0.422 | no | 1.602 | 1.038 | no | 1.238 | 0.405 | no | 2.229 | 1.361 | yes |
| DR0925 | Phosphate transport protein permease | 0.889 | 0.537 | no | 0.740 | 0.298 | no | 0.858 | 0.368 | no | 0.869 | 0.159 | no | 1.029 | 0.396 | no | 1.185 | 0.329 | no | 1.347 | 0.416 | no | 1.202 | 0.192 | no | 1.401 | 0.132 | no |
| DR0926 | Na+ Membrane transporter | 1.080 | 0.165 | no | 1.263 | 0.343 | no | 1.580 | 0.405 | yes | 1.443 | 0.211 | no | 1.610 | 0.717 | yes | 1.301 | 0.183 | no | 0.970 | 0.164 | no | 0.996 | 0.106 | no | 0.832 | 0.130 | no |
| DR0927 | ABC transporter ATPase, Na+ transporter | 1.120 | 0.502 | no | 1.031 | 0.212 | no | 1.103 | 0.362 | no | 1.060 | 0.294 | no | 1.427 | 0.517 | no | 1.117 | 0.230 | no | 1.005 | 0.195 | no | 0.912 | 0.062 | no | 0.704 | 0.100 | no |
| DR0928 | Endonuclease III, END3, alpha helical glycosidase fold | 1.015 | 0.215 | no | 0.921 | 0.303 | no | 0.850 | 0.191 | no | 0.842 | 0.186 | no | 0.917 | 0.215 | no | 0.913 | 0.244 | no | 0.797 | 0.315 | no | 0.803 | 0.307 | no | 0.901 | 0.292 | no |
| DR0929 | Acylphosphatase, acyP | 0.532 | 0.190 | yes | 0.910 | 0.540 | no | 0.919 | 0.514 | no | 1.214 | 0.734 | no | 0.814 | 0.477 | no | 0.617 | 0.216 | yes | 0.719 | 0.124 | no | 0.694 | 0.211 | yes | 0.522 | 0.203 | yes |
| DR0930 | TIM barrel Metalohydrolase | 0.994 | 0.118 | no | 0.658 | 0.199 | yes | 0.681 | 0.155 | yes | 0.655 | 0.123 | no | 0.787 | 0.168 | no | 0.781 | 0.170 | no | 0.790 | 0.208 | no | 1.017 | 0.407 | no | 0.771 | 0.115 | no |
| DR0931 | Predicted protein | 0.769 | 0.299 | no | 0.323 | 0.188 | yes | 0.153 | 0.095 | yes | 0.089 | 0.011 | yes | 0.137 | 0.060 | yes | 0.142 | 0.043 | yes | 0.197 | 0.074 | yes | 0.357 | 0.180 | yes | 1.198 | 0.406 | no |
| DR0932 | Octaprenyl-diphosphate synthase, ISPB | 0.941 | 0.221 | no | 0.462 | 0.261 | yes | 0.281 | 0.156 | yes | 0.200 | 0.056 | yes | 0.267 | 0.079 | yes | 0.311 | 0.128 | yes | 0.324 | 0.132 | yes | 0.380 | 0.132 | yes | 0.679 | 0.177 | no |
| DR0933 | Trehalose synthase | 0.829 | 0.395 | no | 0.909 | 0.281 | no | 1.121 | 0.715 | no | 3.258 | 0.601 | yes | 2.433 | 1.350 | yes | 1.762 | 0.766 | yes | 3.130 | 1.858 | yes | 2.985 | 1.294 | yes | 1.136 | 0.482 | no |
| DR0934 | HTH transcriiption factor, duplicated domains, MerR family | 0.946 | 0.263 | no | 0.828 | 0.133 | no | 0.841 | 0.171 | no | 0.757 | 0.294 | no | 0.759 | 0.197 | no | 0.534 | 0.110 | yes | 0.766 | 0.255 | no | 0.699 | 0.146 | yes | 0.979 | 0.088 | no |
| DR0935 | Serine/threonine phosphatase | 0.892 | 0.360 | no | 1.193 | 0.370 | no | 1.519 | 0.854 | no | 0.733 | 0.008 | no | 0.775 | 0.156 | no | 0.944 | 0.336 | no | 1.086 | 0.196 | no | 0.858 | 0.048 | no | 0.724 | 0.150 | no |
| DR0936 | NifB like metal cluster enzyme | 0.884 | 0.314 | no | 1.229 | 0.535 | no | 1.198 | 0.379 | no | 0.764 | 0.151 | no | 0.853 | 0.212 | no | 0.728 | 0.261 | no | 0.642 | 0.202 | yes | 0.592 | 0.159 | yes | 0.775 | 0.218 | no |
| DR0937 | TPR repeats containing protein | 0.887 | 0.301 | no | 1.305 | 0.667 | no | 1.079 | 0.632 | no | 0.637 | 0.273 | yes | 1.468 | 1.200 | no | 0.905 | 0.424 | no | 0.829 | 0.347 | no | 0.777 | 0.370 | no | 0.451 | 0.209 | yes |
| DR0938 | Predicted protein (low complexity) | 1.008 | 0.496 | no | 1.331 | 0.185 | no | 2.058 | 0.919 | yes | 1.768 | 0.341 | yes | 1.718 | 0.608 | yes | 1.010 | 0.201 | no | 1.165 | 0.299 | no | 1.025 | 0.132 | no | 1.798 | 0.467 | yes |
| DR0939 | AT-rich DNA-binding protein | 0.910 | 0.138 | no | 1.704 | 0.719 | yes | 1.291 | 0.769 | no | 1.633 | 0.450 | yes | 1.427 | 0.364 | no | 1.294 | 0.421 | no | 0.961 | 0.287 | no | 1.214 | 0.547 | no | 1.088 | 0.491 | no |
| DR0940 | Secreted protein, uncharacterized | 0.945 | 0.550 | no | 1.215 | 0.419 | no | 1.959 | 1.107 | yes | 1.966 | 1.038 | yes | 1.168 | 0.419 | no | 0.990 | 0.558 | no | 0.761 | 0.343 | no | 0.609 | 0.184 | yes | 0.821 | 0.140 | no |
| DR0941 | Tryptophan synthase beta subunit, TRPB | 0.738 | 0.277 | no | 0.817 | 0.474 | no | 0.654 | 0.429 | yes | 0.481 | 0.124 | yes | 0.442 | 0.092 | yes | 0.569 | 0.263 | yes | 0.551 | 0.157 | yes | 0.493 | 0.175 | yes | 0.528 | 0.243 | yes |
| DR0942 | Tryptophan synthase alpha subunit, TRPA | 1.164 | 0.437 | no | 0.745 | 0.185 | no | 0.599 | 0.205 | yes | 0.593 | 0.086 | yes | 0.601 | 0.182 | yes | 0.495 | 0.222 | yes | 0.451 | 0.186 | yes | 0.440 | 0.164 | yes | 0.512 | 0.209 | yes |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR0943 | Uncharacterized possible metal-dependent enzyme with HXXXE mconserved motif | 1.425 | 0.634 | no | 1.294 | 0.871 | no | 0.822 | 0.262 | no | 1.220 | 0.253 | no | 0.967 | 0.143 | no | 0.926 | 0.253 | no | 1.054 | 0.533 | no | 0.863 | 0.066 | no | 0.677 | 0.300 | yes |
| DR0944 | Thioredoxin TRX-1 | 1.138 | 0.412 | no | 0.768 | 0.241 | no | 0.837 | 0.130 | no | 0.851 | 0.302 | no | 0.942 | 0.281 | no | 0.796 | 0.238 | no | 1.120 | 0.404 | no | 1.082 | 0.365 | no | 1.829 | 0.566 | yes |
| DR0945 | Distantly related to lecithin:cholesterol O-acyltransferase and lipases | 1.017 | 0.430 | no | 0.880 | 0.302 | no | 0.975 | 0.386 | no | 1.135 | 0.120 | no | 1.271 | 0.494 | no | 1.520 | 1.095 | no | 1.166 | 0.733 | no | 1.185 | 0.417 | no | 1.162 | 0.378 | no |
| DR0946 | Endoglucanase homolog | 1.017 | 0.320 | no | 1.018 | 0.369 | no | 1.138 | 0.506 | no | 1.551 | 0.715 | no | 1.568 | 0.756 | no | 1.068 | 0.342 | no | 1.124 | 0.428 | no | 0.819 | 0.159 | no | 0.998 | 0.351 | no |
| DR0947 | Phe ammonia lyase, isochorismatase, PAL | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR0948 | Thioredoxin fold protein | 0.978 | 0.510 | no | 0.704 | 0.214 | no | 0.822 | 0.179 | no | 0.769 | 0.080 | no | 0.904 | 0.268 | no | 1.108 | 0.322 | no | 0.864 | 0.186 | no | 1.117 | 0.117 | no | 0.935 | 0.328 | no |
| DR0949 | Secreted protein, uncharacterized | 1.179 | 0.422 | no | 1.884 | 1.227 | yes | 1.597 | 0.594 | yes | 2.905 | 1.779 | yes | 1.963 | 1.029 | yes | 1.161 | 0.196 | no | 1.043 | 0.488 | no | 0.874 | 0.162 | no | 0.712 | 0.192 | no |
| DR0950 | NADH dehydrogenase-like protein | 1.128 | 0.478 | no | 0.723 | 0.231 | no | 0.683 | 0.182 | yes | 0.785 | 0.279 | no | 0.609 | 0.252 | yes | 0.530 | 0.222 | yes | 0.847 | 0.363 | no | 0.978 | 0.211 | no | 0.931 | 0.232 | no |
| DR0951 | Fumarate/succinate dehydrogenase type iron sulfur protein, sdhB | 0.703 | 0.320 | yes | 0.498 | 0.232 | yes | 0.759 | 0.221 | no | 1.019 | 0.223 | no | 0.954 | 0.618 | no | 0.978 | 0.467 | no | 0.906 | 0.491 | no | 0.997 | 0.289 | no | 2.377 | 0.550 | yes |
| DR0952 | Succinate dehydrogenase Rossman fold oxidoreductase, sdhA | 0.938 | 0.069 | no | 1.354 | 0.282 | no | 1.235 | 0.290 | no | 1.263 | 0.087 | no | 1.086 | 0.283 | no | 1.109 | 0.251 | no | 0.998 | 0.177 | no | 0.960 | 0.085 | no | 0.934 | 0.202 | no |
| DR0953 | Small succinate dehydrogenase associated protein, sdhD | 0.803 | 0.194 | no | 0.571 | 0.130 | yes | 0.725 | 0.123 | no | 0.753 | 0.154 | no | 1.013 | 0.269 | no | 0.882 | 0.341 | no | 0.835 | 0.296 | no | 1.101 | 0.215 | no | 2.368 | 1.015 | yes |
| DR0954 | Small succinate dehydrogenase associated protein, sdhC | 0.835 | 0.072 | no | 0.673 | 0.127 | yes | 0.706 | 0.083 | no | 0.675 | 0.036 | no | 0.757 | 0.140 | no | 0.894 | 0.149 | no | 0.852 | 0.256 | no | 0.897 | 0.107 | no | 1.426 | 0.351 | no |
| DR0955 | Predicted protein | 1.348 | 0.324 | no | 0.932 | 0.218 | no | 0.882 | 0.584 | no | 1.441 | 0.169 | no | 1.044 | 0.348 | no | 1.207 | 0.627 | no | 1.097 | 0.516 | no | 1.071 | 0.224 | no | 1.166 | 0.162 | no |
| DR0956 | Membrane hydrolase related to phosphatidylglycerophosphate phosphatase B, PGPB_ECOLI | 1.047 | 0.244 | no | 0.953 | 0.179 | no | 0.837 | 0.203 | no | 0.611 | 0.163 | yes | 0.761 | 0.285 | no | 1.080 | 0.544 | no | 0.967 | 0.271 | no | 0.960 | 0.049 | no | 1.087 | 0.086 | no |
| DR0957 | ABC transporter ABC ATPase (transporter) | 0.954 | 0.316 | no | 0.797 | 0.253 | no | 0.527 | 0.160 | yes | 0.591 | 0.062 | yes | 0.748 | 0.181 | no | 0.667 | 0.159 | yes | 0.787 | 0.177 | no | 0.848 | 0.092 | no | 1.429 | 0.107 | yes |
| DR0958 | ABC transporter permease dipeptide transporter? | 1.095 | 0.463 | no | 1.004 | 0.508 | no | 1.043 | 0.579 | no | 1.153 | 0.674 | no | 1.060 | 0.585 | no | 0.915 | 0.249 | no | 0.937 | 0.578 | no | 1.212 | 0.224 | no | 0.913 | 0.218 | no |
| DR0959 | ABC transporter permease dipeptide transporter? | 1.073 | 0.431 | no | 0.841 | 0.239 | no | 0.846 | 0.316 | no | 1.135 | 0.541 | no | 1.166 | 0.824 | no | 0.954 | 0.349 | no | 0.933 | 0.313 | no | 0.998 | 0.183 | no | 1.024 | 0.296 | no |
| DR0960 | WD40 repeats | 0.820 | 0.222 | no | 2.158 | 0.580 | yes | 2.108 | 0.814 | yes | 1.235 | 0.255 | no | 1.435 | 0.515 | no | 1.433 | 0.481 | no | 1.204 | 0.281 | no | 1.355 | 0.499 | no | 0.946 | 0.090 | no |
| DR0961 | Pseudouridine synthase | 1.127 | 0.247 | no | 0.844 | 0.229 | no | 0.682 | 0.143 | no | 0.822 | 0.210 | no | 0.780 | 0.237 | no | 0.976 | 0.197 | no | 1.158 | 0.302 | no | 1.269 | 0.286 | no | 1.348 | 0.304 | no |
| DR0962 | Iron-sulfur flavoprotein | 1.023 | 0.230 | no | 0.886 | 0.183 | no | 0.785 | 0.285 | no | 0.739 | 0.110 | no | 0.854 | 0.357 | no | 0.848 | 0.247 | no | 0.766 | 0.363 | no | 1.108 | 0.368 | no | 1.202 | 0.594 | no |
| DR0963 | N-acetyl-gamma-glutamyl-phosphatase | 1.129 | 0.458 | no | 1.337 | 0.447 | no | 1.460 | 0.718 | no | 1.523 | 0.394 | no | 1.133 | 0.497 | no | 0.950 | 0.129 | no | 0.990 | 0.191 | no | 0.848 | 0.158 | no | 1.045 | 0.355 | no |
| DR0964 | Serine carboxypeptidase | 1.101 | 0.192 | no | 0.700 | 0.258 | yes | 0.732 | 0.282 | no | 0.754 | 0.246 | no | 0.754 | 0.185 | no | 0.674 | 0.118 | no | 0.689 | 0.133 | no | 0.793 | 0.070 | no | 0.663 | 0.037 | no |
| DR0965 | Alcohol or sugar? dehydrogenase | 2.180 | 1.310 | yes | 1.595 | 0.757 | yes | 1.453 | 0.622 | no | 1.811 | 0.402 | yes | 1.281 | 0.753 | no | 0.937 | 0.642 | no | 1.017 | 0.576 | no | 0.864 | 0.400 | no | 0.859 | 0.418 | no |
| DR0966 | Methionine synthase | 1.627 | 1.082 | no | 0.831 | 0.578 | no | 0.645 | 0.170 | no | 1.273 | 0.477 | no | 1.457 | 0.942 | no | 0.840 | 0.231 | no | 0.585 | 0.090 | yes | 0.911 | 0.122 | no | 0.840 | 0.166 | no |
| DR0967 | Contains INTEGRIN(alpha)-like repeat motif | 1.107 | 0.374 | no | 0.737 | 0.224 | no | 0.610 | 0.215 | yes | 0.536 | 0.154 | yes | 0.543 | 0.256 | yes | 0.598 | 0.149 | yes | 0.824 | 0.297 | no | 0.823 | 0.170 | no | 0.969 | 0.146 | no |
| DR0968 | 5,10-methylenetetrahydrofolate reductase, MetF | 1.358 | 0.737 | no | 0.759 | 0.224 | no | 0.935 | 0.642 | no | 0.578 | 0.158 | yes | 0.541 | 0.164 | yes | 0.914 | 0.660 | no | 0.604 | 0.182 | yes | 0.648 | 0.194 | yes | 0.784 | 0.264 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR0969 | Conserved secreted protein (probably cellulase) | 1.163 | 0.530 | no | 0.703 | 0.146 | no | 0.631 | 0.191 | yes | 0.792 | 0.043 | no | 0.704 | 0.144 | no | 0.721 | 0.199 | no | 1.146 | 0.372 | no | 1.227 | 0.192 | no | 1.680 | 0.552 | yes |
| DR0970 | FixB like oxidoreductase | 0.925 | 0.205 | no | 1.127 | 0.287 | no | 0.858 | 0.420 | no | 0.628 | 0.139 | yes | 0.523 | 0.187 | yes | 0.753 | 0.346 | no | 0.573 | 0.231 | yes | 0.752 | 0.097 | no | 0.868 | 0.480 | no |
| DR0971 | FixA electron transfer flavoprotein subunit | 1.077 | 0.372 | no | 1.015 | 0.546 | no | 0.722 | 0.284 | yes | 0.697 | 0.259 | no | 0.628 | 0.307 | yes | 0.518 | 0.310 | yes | 0.473 | 0.159 | yes | 0.441 | 0.157 | yes | 0.948 | 0.420 | no |
| DR0972 | Uncharacterized secreted protein, possible outer membrane protein | 0.919 | 0.284 | no | 0.437 | 0.107 | yes | 0.244 | 0.087 | yes | 0.276 | 0.120 | yes | 0.458 | 0.127 | yes | 0.938 | 0.327 | no | 1.637 | 0.542 | yes | 1.990 | 0.363 | yes | 2.499 | 1.209 | yes |
| DR0973 | 3-oxoadipate enol-lactone hydrolase/4-carboxymuconolactone decarboxylase | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR0974 | P-loop ATPase, destroyed P-loop | 1.118 | 0.610 | no | 1.937 | 1.096 | yes | 1.703 | 0.558 | yes | 1.493 | 0.681 | no | 1.521 | 0.821 | no | 0.974 | 0.204 | no | 0.992 | 0.526 | no | 0.997 | 0.099 | no | 0.998 | 0.206 | no |
| DR0975 | MutT family hydrolase | 0.960 | 0.312 | no | 0.800 | 0.232 | no | 0.849 | 0.364 | no | 0.600 | 0.106 | yes | 0.559 | 0.188 | yes | 0.798 | 0.277 | no | 0.908 | 0.416 | no | 0.881 | 0.121 | no | 1.151 | 0.113 | no |
| DR0976 | Peptide chain release factor RF-1 | 1.129 | 0.417 | no | 0.944 | 0.333 | no | 0.533 | 0.224 | yes | 0.550 | 0.068 | yes | 0.556 | 0.137 | yes | 0.507 | 0.047 | yes | 0.542 | 0.182 | yes | 0.820 | 0.089 | no | 0.994 | 0.343 | no |
| DR0977 | Phosphoenolpyruvate carboxykinase, PPCK | 0.759 | 0.156 | no | 0.718 | 0.210 | no | 0.483 | 0.223 | yes | 0.553 | 0.183 | yes | 0.701 | 0.236 | no | 0.604 | 0.257 | yes | 0.525 | 0.201 | yes | 0.833 | 0.254 | no | 1.145 | 0.384 | no |
| DR0978 | Transposase | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR0979 | Transposon DORF | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR0980 | Glutamate dehydrogenase | 0.902 | 0.379 | no | 0.914 | 0.516 | no | 1.008 | 0.259 | no | 1.852 | 0.944 | yes | 1.498 | 0.879 | no | 0.920 | 0.352 | no | 0.952 | 0.326 | no | 1.218 | 0.085 | no | 2.342 | 1.256 | yes |
| DR0981 | GGEEF domain + N-terminal transmembrane region | 0.979 | 0.242 | no | 1.509 | 0.369 | yes | 1.252 | 0.352 | no | 0.817 | 0.204 | no | 1.030 | 0.415 | no | 1.221 | 0.532 | no | 0.827 | 0.337 | no | 0.869 | 0.152 | no | 0.604 | 0.245 | yes |
| DR0982 | Predicted metal-dependent periplasmic protease with PDZ domain | 1.259 | 0.526 | no | 1.041 | 0.278 | no | 1.348 | 0.373 | no | 1.526 | 0.860 | no | 1.207 | 0.877 | no | 1.538 | 0.526 | no | 1.067 | 0.450 | no | 0.935 | 0.182 | no | 0.769 | 0.142 | no |
| DR0983 | TRNA nucleotidyltransferase, CCA | 0.964 | 0.215 | no | 0.942 | 0.280 | no | 0.768 | 0.306 | no | 0.454 | 0.252 | yes | 0.580 | 0.219 | yes | 0.720 | 0.287 | no | 0.620 | 0.222 | yes | 0.730 | 0.130 | no | 0.691 | 0.254 | no |
| DR0985 | Uncharacterized protein, bacillus YACC ortholog | 0.953 | 0.331 | no | 0.870 | 0.448 | no | 0.696 | 0.451 | yes | 0.288 | 0.098 | yes | 0.408 | 0.174 | yes | 0.493 | 0.357 | yes | 0.352 | 0.157 | yes | 0.590 | 0.173 | yes | 0.696 | 0.224 | no |
| DR0986 | Periplasmic binding protein | 1.152 | 0.430 | no | 2.883 | 1.718 | yes | 1.378 | 0.598 | no | 1.084 | 0.558 | no | 1.283 | 0.693 | no | 2.735 | 1.472 | yes | 1.074 | 0.431 | no | 0.533 | 0.114 | yes | 0.729 | 0.041 | no |
| DR0987 | Receiver domain, CHEY family + HTH domain | 0.850 | 0.075 | no | 2.250 | 0.342 | yes | 1.617 | 0.242 | yes | 1.378 | 0.160 | no | 1.294 | 0.272 | no | 1.144 | 0.094 | no | 0.939 | 0.275 | no | 1.351 | 0.385 | no | 1.021 | 0.192 | no |
| DR0988 | HLPA/OMPH family protein | 0.680 | 0.245 | yes | 1.250 | 0.338 | no | 1.674 | 1.032 | yes | 1.242 | 0.676 | no | 1.473 | 0.791 | no | 1.813 | 0.764 | yes | 1.616 | 0.431 | yes | 1.709 | 0.624 | yes | 1.342 | 0.463 | no |
| DR0989 | Membrane protein | 0.593 | 0.289 | yes | 0.774 | 0.398 | no | 0.907 | 0.453 | no | 0.794 | 0.051 | no | 1.432 | 0.610 | no | 1.680 | 0.352 | yes | 2.303 | 0.939 | yes | 2.562 | 0.490 | yes | 3.762 | 1.336 | yes |
| DR0990 | CBS domain protein | 1.173 | 0.727 | no | 0.862 | 0.231 | no | 0.820 | 0.311 | no | 0.912 | 0.394 | no | 0.906 | 0.159 | no | 0.960 | 0.371 | no | 1.101 | 0.620 | no | 1.088 | 0.188 | no | 1.682 | 0.435 | yes |
| DR0991 | Aminotransferase | 1.232 | 0.367 | no | 1.510 | 0.460 | yes | 1.472 | 0.265 | yes | 1.687 | 0.055 | yes | 1.695 | 0.375 | yes | 1.272 | 0.312 | no | 1.282 | 0.555 | no | 1.153 | 0.123 | no | 1.331 | 0.278 | no |
| DR0992 | Rossmann fold Oxidoreductase, probably NADH oxidase, NAOX | 0.918 | 0.354 | no | 1.967 | 0.998 | yes | 1.418 | 0.668 | no | 1.210 | 0.118 | no | 1.123 | 0.316 | no | 1.087 | 0.499 | no | 1.075 | 0.303 | no | 0.896 | 0.113 | no | 0.670 | 0.168 | no |
| DR0993 | Protein of uncharacterized conserved family | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR0994 | Uncharacterized small conserved protein, many archaeal homologs | 1.022 | 0.219 | no | 0.914 | 0.431 | no | 0.710 | 0.462 | yes | 0.433 | 0.192 | yes | 0.803 | 0.173 | no | 0.770 | 0.198 | no | 0.783 | 0.509 | no | 0.874 | 0.144 | no | 0.823 | 0.117 | no |
| DR0995 | Protein of uncharacterized conserved family | 0.995 | 0.547 | no | 0.945 | 0.354 | no | 0.848 | 0.305 | no | 1.175 | 0.424 | no | 0.929 | 0.414 | no | 0.994 | 0.385 | no | 0.811 | 0.333 | no | 0.862 | 0.281 | no | 0.826 | 0.278 | no |
| DR0996 | Predicted protein | 1.432 | 0.809 | no | 1.064 | 0.245 | no | 1.206 | 0.360 | no | 1.055 | 0.439 | no | 1.854 | 1.233 | yes | 1.262 | 0.381 | no | 1.727 | 1.229 | yes | 0.697 | 0.297 | yes | 1.109 | 0.187 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR0997 | HTH transcription factor, CAP family | 1.124 | 0.398 | no | 1.044 | 0.171 | no | 1.633 | 0.488 | yes | 1.903 | 0.480 | yes | 2.390 | 0.628 | yes | 2.040 | 0.907 | yes | 2.271 | 0.732 | yes | 1.362 | 0.294 | no | 1.048 | 0.123 | no |
| DR0998 | MinD family ATpase, MRP | 0.761 | 0.189 | no | 0.423 | 0.214 | yes | 0.257 | 0.172 | yes | 0.352 | 0.246 | yes | 0.418 | 0.220 | yes | 0.413 | 0.122 | yes | 0.448 | 0.253 | yes | 0.425 | 0.165 | yes | 0.493 | 0.239 | yes |
| DR0999 | HTH transcription factor | 0.863 | 0.396 | no | 0.568 | 0.312 | yes | 0.541 | 0.254 | yes | 0.592 | 0.256 | yes | 0.599 | 0.260 | yes | 0.461 | 0.189 | yes | 0.459 | 0.239 | yes | 0.457 | 0.132 | yes | 0.618 | 0.169 | yes |
| DR1000 | 2'-5' phosphodiesterase of the 2H superfamily | 0.741 | 0.308 | no | 0.556 | 0.317 | yes | 0.655 | 0.385 | yes | 0.401 | 0.121 | yes | 0.823 | 0.360 | no | 0.740 | 0.244 | no | 0.912 | 0.444 | no | 1.076 | 0.309 | no | 1.073 | 0.447 | no |
| DR1001 | Chorismate mutase/2-dehydro-3-deoxyphosphoheptonate aldolase, AROG | 1.054 | 0.416 | no | 0.479 | 0.127 | yes | 0.319 | 0.152 | yes | 0.580 | 0.108 | yes | 0.543 | 0.184 | yes | 0.440 | 0.212 | yes | 0.539 | 0.180 | yes | 0.583 | 0.222 | yes | 1.604 | 0.969 | no |
| DR1002 | Globin-like protein | 1.023 | 0.356 | no | 0.578 | 0.173 | yes | 0.512 | 0.149 | yes | 0.490 | 0.112 | yes | 0.514 | 0.212 | yes | 0.613 | 0.177 | yes | 0.807 | 0.326 | no | 0.937 | 0.241 | no | 1.045 | 0.215 | no |
| DR1003 | HTH transcription factor | 1.229 | 0.275 | no | 1.094 | 0.214 | no | 0.804 | 0.199 | no | 1.105 | 0.047 | no | 1.094 | 0.672 | no | 0.919 | 0.198 | no | 1.012 | 0.135 | no | 1.011 | 0.158 | no | 0.913 | 0.098 | no |
| DR1004 | SugE family protein, membrane charerone | 1.150 | 0.167 | no | 0.770 | 0.084 | no | 0.692 | 0.269 | yes | 0.718 | 0.091 | no | 0.881 | 0.369 | no | 0.842 | 0.276 | no | 0.780 | 0.107 | no | 0.854 | 0.082 | no | 1.080 | 0.212 | no |
| DR1005 | SugE protein, membrane charerone | 1.182 | 0.388 | no | 0.930 | 0.223 | no | 0.659 | 0.182 | yes | 1.119 | 0.458 | no | 1.026 | 0.479 | no | 0.792 | 0.151 | no | 0.897 | 0.225 | no | 1.053 | 0.397 | no | 0.918 | 0.313 | no |
| DR1006 | DGTP triphosphohydrolase, DGTP, HD hydrlase superfamily | 1.072 | 0.490 | no | 0.877 | 0.220 | no | 0.690 | 0.238 | yes | 1.069 | 0.189 | no | 1.078 | 0.297 | no | 0.997 | 0.620 | no | 0.658 | 0.137 | yes | 0.721 | 0.236 | yes | 0.692 | 0.121 | no |
| DR1007 | MutT family Hydrolase | 1.118 | 0.271 | no | 0.871 | 0.311 | no | 0.563 | 0.116 | yes | 0.890 | 0.149 | no | 0.692 | 0.253 | yes | 0.835 | 0.221 | no | 0.944 | 0.360 | no | 0.989 | 0.306 | no | 0.890 | 0.217 | no |
| DR1008 | Riboflavin kinase, RibF | 1.031 | 0.320 | no | 1.244 | 0.213 | no | 0.912 | 0.170 | no | 0.924 | 0.308 | no | 0.882 | 0.234 | no | 0.882 | 0.157 | no | 0.695 | 0.189 | no | 0.895 | 0.145 | no | 1.003 | 0.175 | no |
| DR1009 | PR1 domain protein, plant pathogenesis related protein | 1.375 | 0.651 | no | 1.356 | 0.518 | no | 1.057 | 0.365 | no | 1.805 | 0.803 | yes | 1.191 | 0.736 | no | 1.060 | 0.149 | no | 0.898 | 0.111 | no | 0.919 | 0.102 | no | 1.070 | 0.191 | no |
| DR1010 | Predicted protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR1011 | Uncharacterized conserved protein | 0.906 | 0.264 | no | 0.889 | 0.208 | no | 1.579 | 0.360 | yes | 1.527 | 0.504 | no | 1.285 | 0.336 | no | 1.477 | 0.576 | no | 1.533 | 0.321 | yes | 1.347 | 0.439 | no | 1.032 | 0.210 | no |
| DR1012 | ABC transporter ATPase | 1.033 | 0.431 | no | 0.951 | 0.491 | no | 0.664 | 0.335 | yes | 0.877 | 0.297 | no | 0.967 | 0.780 | no | 0.531 | 0.272 | yes | 0.571 | 0.124 | yes | 0.628 | 0.149 | yes | 0.572 | 0.183 | yes |
| DR1013 | NosY homolog, membrane protein | 0.960 | 0.213 | no | 1.355 | 0.493 | no | 1.231 | 0.315 | no | 1.079 | 0.440 | no | 1.002 | 0.464 | no | 1.005 | 0.307 | no | 0.863 | 0.238 | no | 0.956 | 0.342 | no | 0.877 | 0.322 | no |
| DR1014 | FRAGMENT OR REAL phosphatase domain | 0.941 | 0.305 | no | 1.498 | 0.838 | no | 1.097 | 0.310 | no | 1.027 | 0.561 | no | 1.006 | 0.341 | no | 1.150 | 0.507 | no | 1.059 | 0.388 | no | 0.935 | 0.241 | no | 0.677 | 0.255 | yes |
| DR1015 | Predicted protein | 0.772 | 0.312 | no | 1.081 | 0.512 | no | 0.900 | 0.550 | no | 0.526 | 0.006 | yes | 0.675 | 0.163 | yes | 1.065 | 0.748 | no | 1.016 | 0.666 | no | 0.819 | 0.126 | no | 1.544 | 0.511 | no |
| DR1016 | Thiophene/Furan Oxidation Protein, THDF, GTPase | 1.128 | 0.551 | no | 1.032 | 0.594 | no | 0.644 | 0.306 | yes | 0.538 | 0.268 | yes | 0.554 | 0.205 | yes | 0.369 | 0.152 | yes | 0.371 | 0.129 | yes | 0.279 | 0.122 | yes | 0.161 | 0.063 | yes |
| DR1017 | RNA Methylase | 1.114 | 0.337 | no | 0.914 | 0.313 | no | 0.792 | 0.268 | no | 0.721 | 0.336 | no | 0.849 | 0.209 | no | 0.678 | 0.099 | no | 0.702 | 0.177 | no | 0.799 | 0.130 | no | 1.039 | 0.130 | no |
| DR1018 | Predicted protein | 0.871 | 0.309 | no | 0.612 | 0.186 | yes | 0.473 | 0.197 | yes | 0.597 | 0.233 | yes | 0.655 | 0.254 | yes | 0.701 | 0.116 | no | 0.894 | 0.227 | no | 0.837 | 0.229 | no | 0.913 | 0.300 | no |
| DR1019 | Glycerol-3-phosphate dehydrogenase, GLPA | 0.975 | 0.229 | no | 1.269 | 0.852 | no | 0.710 | 0.211 | yes | 0.703 | 0.057 | no | 0.868 | 0.296 | no | 1.132 | 0.473 | no | 1.549 | 0.665 | no | 0.886 | 0.147 | no | 0.681 | 0.289 | yes |
| DR1020 | FtsH, AAA superfamily ATPase with metalloprotease domain | 1.026 | 0.503 | no | 0.533 | 0.299 | yes | 0.437 | 0.236 | yes | 0.644 | 0.211 | yes | 0.439 | 0.196 | yes | 0.455 | 0.179 | yes | 0.434 | 0.155 | yes | 0.593 | 0.171 | yes | 0.873 | 0.223 | no |
| DR1021 | Secreted protein, uncharacterized | 0.568 | 0.257 | yes | 0.369 | 0.096 | yes | 0.476 | 0.140 | yes | 0.677 | 0.309 | yes | 1.327 | 0.552 | no | 1.386 | 0.366 | no | 1.999 | 0.764 | yes | 2.452 | 0.594 | yes | 2.406 | 0.639 | yes |
| DR1022 | MazG family of proteins, related to phosphoribosyl-ATP pyrophosphatase | 1.020 | 0.318 | no | 0.551 | 0.190 | yes | 0.441 | 0.142 | yes | 0.678 | 0.081 | no | 0.667 | 0.301 | yes | 0.621 | 0.106 | yes | 0.940 | 0.291 | no | 0.952 | 0.132 | no | 0.800 | 0.190 | no |
| DR1023 | Predicted protein | 1.139 | 0.435 | no | 0.433 | 0.156 | yes | 0.285 | 0.153 | yes | 0.653 | 0.077 | no | 0.482 | 0.271 | yes | 0.619 | 0.198 | yes | 0.600 | 0.098 | yes | 0.762 | 0.193 | no | 0.636 | 0.261 | yes |
| DR1024 | Possible metal-binding protein | 1.009 | 0.575 | no | 0.621 | 0.399 | yes | 0.541 | 0.287 | yes | 0.668 | 0.196 | no | 0.634 | 0.447 | yes | 0.565 | 0.204 | yes | 0.651 | 0.420 | yes | 0.565 | 0.142 | yes | 0.571 | 0.170 | yes |
| DR1025 | MutT family hydrolase | 1.024 | 0.270 | no | 0.737 | 0.283 | no | 0.575 | 0.176 | yes | 0.707 | 0.320 | no | 0.871 | 0.327 | no | 1.218 | 0.842 | no | 0.722 | 0.222 | no | 0.635 | 0.169 | yes | 0.662 | 0.226 | yes |
| DR1026 | Dimunito like oxidoreductases | 1.542 | 0.652 | no | 1.227 | 0.821 | no | 0.918 | 0.279 | no | 1.231 | 0.269 | no | 0.721 | 0.280 | no | 0.717 | 0.208 | no | 0.779 | 0.296 | no | 0.794 | 0.069 | no | 0.939 | 0.206 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR1028 | Amino acid ABC transporter, periplasmic amino acid-binding protein, authentic frameshift | 1.994 | 0.624 | yes | 1.860 | 0.347 | yes | 1.419 | 0.670 | no | 1.600 | 0.705 | no | 1.191 | 0.364 | no | 1.172 | 0.403 | no | 1.077 | 0.221 | no | 1.129 | 0.198 | no | 1.246 | 0.258 | no |
| DR1029 | ABC-type transporter permease | 1.555 | 0.231 | yes | 1.582 | 0.547 | yes | 1.285 | 0.444 | no | 1.160 | 0.146 | no | 1.116 | 0.619 | no | 1.181 | 0.175 | no | 0.737 | 0.273 | no | 0.834 | 0.093 | no | 0.892 | 0.115 | no |
| DR1030 | Aminotransferase | 1.818 | 0.572 | yes | 1.651 | 0.633 | yes | 1.205 | 0.664 | no | 1.082 | 0.115 | no | 0.951 | 0.583 | no | 0.865 | 0.308 | no | 0.775 | 0.302 | no | 0.893 | 0.266 | no | 0.841 | 0.215 | no |
| DR1031 | Glycolate oxidase | 1.295 | 0.346 | no | 1.045 | 0.287 | no | 0.886 | 0.129 | no | 0.878 | 0.178 | no | 0.746 | 0.245 | no | 0.747 | 0.138 | no | 0.714 | 0.265 | no | 0.830 | 0.143 | no | 0.941 | 0.309 | no |
| DR1032 | GUFA-like membrane protein | 1.531 | 0.444 | no | 1.323 | 0.670 | no | 1.297 | 0.773 | no | 1.114 | 0.367 | no | 0.948 | 0.160 | no | 0.763 | 0.081 | no | 1.128 | 0.542 | no | 1.156 | 0.329 | no | 1.219 | 0.464 | no |
| DR1033 | Secreted (or probably membrane) protein, uncharacterized | 0.849 | 0.234 | no | 0.674 | 0.240 | yes | 0.651 | 0.244 | yes | 0.504 | 0.270 | yes | 0.663 | 0.321 | yes | 0.567 | 0.121 | yes | 0.522 | 0.189 | yes | 0.659 | 0.108 | yes | 0.878 | 0.375 | no |
| DR1034 | ABC ATPase, BRA amino acid transport | 1.118 | 0.371 | no | 0.940 | 0.249 | no | 1.415 | 0.411 | no | 1.162 | 0.470 | no | 1.283 | 0.365 | no | 1.238 | 0.439 | no | 0.941 | 0.198 | no | 1.004 | 0.184 | no | 1.911 | 1.008 | yes |
| DR1035 | ABC ATPase, BRA amino acid transport | 1.318 | 0.362 | no | 0.963 | 0.362 | no | 0.782 | 0.199 | no | 0.821 | 0.056 | no | 1.035 | 0.739 | no | 0.681 | 0.109 | no | 0.761 | 0.344 | no | 0.767 | 0.182 | no | 1.328 | 0.331 | no |
| DR1036 | BRA amino acid transporter membrane permease | 1.339 | 0.376 | no | 1.074 | 0.409 | no | 1.677 | 0.560 | yes | 2.130 | 0.578 | yes | 1.337 | 0.233 | no | 1.090 | 0.366 | no | 0.842 | 0.250 | no | 0.891 | 0.168 | no | 1.609 | 0.324 | yes |
| DR1037 | BRA amino acid transporter membrane permease | 0.804 | 0.196 | no | 0.700 | 0.185 | no | 0.809 | 0.180 | no | 0.816 | 0.047 | no | 0.928 | 0.229 | no | 1.124 | 0.320 | no | 0.964 | 0.294 | no | 1.144 | 0.252 | no | 2.059 | 0.638 | yes |
| DR1038 | BRA amino acid transporter periplasmic binding protein | 0.833 | 0.184 | no | 0.917 | 0.144 | no | 1.677 | 0.601 | yes | 3.206 | 0.479 | yes | 2.261 | 0.716 | yes | 1.522 | 0.935 | no | 1.061 | 0.109 | no | 1.041 | 0.184 | no | 3.830 | 0.252 | yes |
| DR1040 | Predicted protein | 1.245 | 0.431 | no | 1.073 | 0.263 | no | 1.367 | 0.239 | no | 1.487 | 0.253 | no | 1.317 | 0.673 | no | 0.800 | 0.192 | no | 0.720 | 0.298 | no | 0.750 | 0.078 | no | 0.717 | 0.035 | no |
| DR1041 | Protein homologous to phytoalexin detoxication enzyme (755011, Fusarium solani) | 0.925 | 0.291 | no | 1.071 | 0.341 | no | 1.648 | 1.083 | yes | 1.756 | 0.819 | yes | 1.847 | 1.222 | yes | 0.927 | 0.387 | no | 0.867 | 0.310 | no | 0.723 | 0.227 | yes | 0.831 | 0.394 | no |
| DR1042 | HTH Transcription factor | 0.726 | 0.112 | no | 0.465 | 0.233 | yes | 0.686 | 0.121 | yes | 0.851 | 0.183 | no | 0.694 | 0.169 | no | 0.526 | 0.151 | yes | 0.553 | 0.186 | yes | 0.616 | 0.162 | yes | 0.634 | 0.232 | yes |
| DR1043 | Predicted protein | 0.712 | 0.444 | yes | 0.551 | 0.310 | yes | 0.523 | 0.214 | yes | 0.741 | 0.352 | no | 0.544 | 0.146 | yes | 0.553 | 0.131 | yes | 0.566 | 0.200 | yes | 0.506 | 0.235 | yes | 0.558 | 0.228 | yes |
| DR1044 | Predicted protein | 0.962 | 0.345 | no | 0.634 | 0.177 | yes | 0.685 | 0.134 | yes | 0.808 | 0.106 | no | 0.702 | 0.224 | no | 0.569 | 0.294 | yes | 0.547 | 0.230 | yes | 0.462 | 0.202 | yes | 0.550 | 0.249 | yes |
| DR1045 | Predicted protein | 1.002 | 0.325 | no | 0.625 | 0.250 | yes | 0.530 | 0.171 | yes | 0.503 | 0.250 | yes | 0.505 | 0.208 | yes | 0.572 | 0.201 | yes | 0.692 | 0.358 | yes | 0.841 | 0.250 | no | 0.594 | 0.213 | yes |
| DR1046 | ClpB, AAA superfamily ATPase | 1.183 | 0.337 | no | 0.946 | 0.258 | no | 0.405 | 0.112 | yes | 0.475 | 0.035 | yes | 0.454 | 0.305 | yes | 0.346 | 0.198 | yes | 0.613 | 0.267 | yes | 0.454 | 0.163 | yes | 0.821 | 0.337 | no |
| DR1047 | Thioredoxin fold protein | 1.085 | 0.134 | no | 0.911 | 0.224 | no | 0.810 | 0.442 | no | 0.609 | 0.211 | yes | 0.666 | 0.154 | yes | 0.655 | 0.193 | yes | 0.710 | 0.238 | no | 0.730 | 0.221 | yes | 0.863 | 0.164 | no |
| DR1048 | Predicted membrane protein, uncharacterized | 1.689 | 0.575 | yes | 1.454 | 0.555 | no | 0.941 | 0.361 | no | 1.022 | 0.230 | no | 1.149 | 0.409 | no | 0.753 | 0.201 | no | 0.869 | 0.391 | no | 0.838 | 0.132 | no | 0.885 | 0.304 | no |
| DR1049 | Predicted protein | 0.947 | 0.223 | no | 1.020 | 0.327 | no | 0.951 | 0.373 | no | 1.059 | 0.183 | no | 1.046 | 0.291 | no | 0.836 | 0.256 | no | 0.969 | 0.316 | no | 0.924 | 0.139 | no | 0.603 | 0.118 | yes |
| DR1050 | Predicted protein | 0.914 | 0.362 | no | 0.672 | 0.121 | yes | 0.412 | 0.159 | yes | 0.471 | 0.134 | yes | 0.492 | 0.111 | yes | 0.538 | 0.130 | yes | 0.563 | 0.166 | yes | 0.774 | 0.045 | no | 0.847 | 0.317 | no |
| DR1051 | YiiM family of proteins | 0.953 | 0.215 | no | 0.927 | 0.458 | no | 0.790 | 0.290 | no | 0.726 | 0.335 | no | 0.660 | 0.214 | yes | 0.588 | 0.129 | yes | 0.686 | 0.170 | no | 0.818 | 0.099 | no | 0.894 | 0.063 | no |
| DR1052 | SAM dependent methylase | 1.218 | 0.462 | no | 0.598 | 0.284 | yes | 0.642 | 0.217 | yes | 0.965 | 0.427 | no | 0.783 | 0.230 | no | 0.986 | 0.230 | no | 1.103 | 0.362 | no | 1.334 | 0.499 | no | 1.644 | 0.429 | yes |
| DR1053 | A/b hydrolase | 1.137 | 0.407 | no | 1.134 | 0.206 | no | 0.655 | 0.052 | yes | 1.011 | 0.413 | no | 0.902 | 0.262 | no | 0.790 | 0.291 | no | 0.809 | 0.245 | no | 0.886 | 0.306 | no | 0.806 | 0.501 | no |
| DR1054 | Predicted protein | 1.073 | 0.256 | no | 0.567 | 0.118 | yes | 0.549 | 0.187 | yes | 0.805 | 0.222 | no | 0.790 | 0.227 | no | 0.899 | 0.227 | no | 0.985 | 0.467 | no | 1.088 | 0.337 | no | 1.463 | 0.548 | no |
| DR1055 | Aspartyl tRNA synthetase, archaeal type | 0.946 | 0.393 | no | 0.405 | 0.157 | yes | 0.418 | 0.142 | yes | 0.666 | 0.290 | yes | 0.683 | 0.321 | yes | 0.562 | 0.325 | yes | 0.410 | 0.133 | yes | 0.587 | 0.124 | yes | 1.232 | 0.383 | no |
| DR1056 | Membrane protein, transporter | 1.105 | 0.303 | no | 1.030 | 0.297 | no | 1.031 | 0.251 | no | 1.151 | 0.394 | no | 1.019 | 0.309 | no | 1.007 | 0.190 | no | 0.970 | 0.206 | no | 1.032 | 0.360 | no | 1.052 | 0.198 | no |
| DR1057 | NH2- Acetyltransferase | 0.997 | 0.438 | no | 0.668 | 0.367 | yes | 0.992 | 0.253 | no | 1.543 | 0.373 | no | 0.975 | 0.264 | no | 0.883 | 0.152 | no | 1.326 | 0.471 | no | 1.500 | 0.802 | no | 1.481 | 0.444 | yes |
| DR1058 | NH2- Acetyltransferase | 1.272 | 0.371 | no | 1.045 | 0.280 | no | 1.116 | 0.266 | no | 1.534 | 0.384 | no | 1.092 | 0.205 | no | 1.239 | 0.316 | no | 1.242 | 0.443 | no | 1.268 | 0.517 | no | 2.206 | 0.628 | yes |
| DR1059 | HD superfamily hydrolase | 1.125 | 0.436 | no | 0.964 | 0.244 | no | 0.826 | 0.350 | no | 0.998 | 0.288 | no | 0.802 | 0.424 | no | 1.176 | 0.433 | no | 1.101 | 0.380 | no | 1.034 | 0.262 | no | 1.175 | 0.200 | no |
| DR1060 | ArgK-related kinase | 0.992 | 0.327 | no | 0.733 | 0.255 | no | 0.621 | 0.160 | yes | 0.682 | 0.310 | no | 0.576 | 0.257 | yes | 0.818 | 0.306 | no | 0.666 | 0.188 | yes | 0.887 | 0.186 | no | 0.909 | 0.395 | no |
| DR1061 | Rossman fold oxidoreductase | 1.095 | 0.382 | no | 0.801 | 0.411 | no | 0.567 | 0.127 | yes | 0.589 | 0.251 | yes | 0.695 | 0.235 | no | 0.798 | 0.176 | no | 0.855 | 0.209 | no | 1.128 | 0.233 | no | 0.936 | 0.110 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR1062 | FemA-like protein | 0.804 | 0.415 | no | 0.589 | 0.236 | yes | 0.604 | 0.175 | yes | 0.453 | 0.157 | yes | 0.593 | 0.286 | yes | 0.655 | 0.187 | yes | 0.647 | 0.192 | yes | 0.839 | 0.285 | no | 1.096 | 0.276 | no |
| DR1063 | Parvulin family peptidyl prolyl isomerase | 0.704 | 0.238 | no | 0.383 | 0.251 | yes | 0.363 | 0.190 | yes | 1.963 | 0.501 | yes | 0.416 | 0.220 | yes | 0.673 | 0.285 | yes | 1.366 | 0.336 | no | 1.458 | 0.073 | no | n/a | n/a | n/a |
| DR1064 | Deverged a/b hydrolase superfamily protein | 1.049 | 0.603 | no | 0.625 | 0.389 | yes | 0.400 | 0.239 | yes | 0.546 | 0.383 | yes | 0.510 | 0.215 | yes | 0.737 | 0.446 | yes | 0.815 | 0.339 | no | 0.805 | 0.188 | no | 0.771 | 0.107 | no |
| DR1065 | Belongs to Yfit/DinB family | 0.880 | 0.228 | no | 0.342 | 0.106 | yes | 0.296 | 0.073 | yes | 0.318 | 0.064 | yes | 0.517 | 0.176 | yes | 0.797 | 0.079 | no | 0.794 | 0.118 | no | 1.077 | 0.175 | no | 1.159 | 0.283 | no |
| DR1066 | Predicted protein | 1.217 | 0.508 | no | 0.368 | 0.128 | yes | 0.410 | 0.143 | yes | 0.847 | 0.065 | no | 0.936 | 0.297 | no | 1.443 | 0.977 | no | 2.010 | 0.687 | yes | 1.937 | 0.454 | yes | 1.873 | 0.266 | yes |
| DR1067 | Predicted protein | 0.924 | 0.456 | no | 0.404 | 0.243 | yes | 0.474 | 0.329 | yes | 0.623 | 0.343 | yes | 1.189 | 0.921 | no | 2.084 | 0.554 | yes | 4.207 | 1.871 | yes | 5.682 | 1.671 | yes | 5.585 | 2.383 | yes |
| DR1068 | 3-hydroxyacyl-CoA dehydrogenase | 1.028 | 0.221 | no | 0.657 | 0.101 | yes | 0.605 | 0.121 | yes | 0.761 | 0.133 | no | 0.813 | 0.355 | no | 0.889 | 0.263 | no | 1.127 | 0.283 | no | 1.440 | 0.610 | no | 2.562 | 0.513 | yes |
| DR1069 | Predicted protein | 0.956 | 0.285 | no | 0.720 | 0.249 | no | 0.479 | 0.107 | yes | 0.436 | 0.102 | yes | 0.594 | 0.186 | yes | 0.858 | 0.136 | no | 1.079 | 0.385 | no | 1.093 | 0.195 | no | 1.171 | 0.167 | no |
| DR1070 | Aspartyl dipeptidase, PEPE | 1.037 | 0.196 | no | 0.510 | 0.125 | yes | 0.401 | 0.107 | yes | 0.447 | 0.064 | yes | 0.424 | 0.095 | yes | 0.524 | 0.166 | yes | 0.501 | 0.145 | yes | 0.919 | 0.179 | no | 1.173 | 0.160 | no |
| DR1071 | Protein related to YCII-like bacterial family | 0.831 | 0.129 | no | 0.370 | 0.149 | yes | 0.246 | 0.064 | yes | 0.362 | 0.055 | yes | 0.317 | 0.046 | yes | 0.493 | 0.206 | yes | 0.590 | 0.279 | yes | 1.011 | 0.099 | no | 1.223 | 0.341 | no |
| DR1072 | Acetyl coA acetyltransferase | 1.157 | 0.343 | no | 0.592 | 0.238 | yes | 0.430 | 0.182 | yes | 0.444 | 0.024 | yes | 0.403 | 0.153 | yes | 0.415 | 0.111 | yes | 0.624 | 0.306 | yes | 0.984 | 0.326 | no | 1.364 | 0.396 | no |
| DR1073 | Predicted protein | 1.022 | 0.197 | no | 0.627 | 0.156 | yes | 0.422 | 0.159 | yes | 0.395 | 0.072 | yes | 0.535 | 0.172 | yes | 0.841 | 0.127 | no | 0.979 | 0.304 | no | 1.299 | 0.338 | no | 0.982 | 0.232 | no |
| DR1074 | Acyl Carrier Dehydratase, FabZ | 1.034 | 0.194 | no | 0.997 | 0.312 | no | 1.007 | 0.407 | no | 0.685 | 0.067 | no | 0.694 | 0.269 | yes | 0.797 | 0.134 | no | 1.014 | 0.189 | no | 1.116 | 0.150 | no | 1.317 | 0.151 | no |
| DR1075 | Conserved membrane protein | 0.818 | 0.267 | no | 0.684 | 0.211 | yes | 0.560 | 0.082 | yes | 0.526 | 0.065 | yes | 0.669 | 0.168 | yes | 0.853 | 0.190 | no | 1.017 | 0.459 | no | 1.083 | 0.260 | no | 1.215 | 0.177 | no |
| DR1076 | Monogalactosyldiacylglycerol synthase | 1.216 | 0.383 | no | 0.780 | 0.228 | no | 0.765 | 0.171 | no | 1.149 | 0.515 | no | 1.071 | 0.354 | no | 1.157 | 0.206 | no | 0.894 | 0.252 | no | 1.090 | 0.096 | no | 1.044 | 0.127 | no |
| DR1077 | Chitooligosaccharide deacetylase | 0.977 | 0.302 | no | 0.844 | 0.270 | no | 0.884 | 0.272 | no | 0.842 | 0.197 | no | 0.950 | 0.217 | no | 1.010 | 0.313 | no | 1.066 | 0.241 | no | 1.232 | 0.276 | no | 1.080 | 0.183 | no |
| DR1078 | SAM dependent methyltransferase | 1.075 | 0.153 | no | 0.772 | 0.094 | no | 0.647 | 0.235 | yes | 0.870 | 0.269 | no | 0.851 | 0.234 | no | 1.002 | 0.275 | no | 1.164 | 0.235 | no | 1.101 | 0.139 | no | 1.249 | 0.196 | no |
| DR1079 | Predicted protein | 1.029 | 0.598 | no | 0.557 | 0.254 | yes | 0.455 | 0.270 | yes | 0.689 | 0.396 | yes | 0.913 | 0.538 | no | 1.021 | 0.130 | no | 1.782 | 0.513 | yes | 2.427 | 1.235 | yes | 2.193 | 1.010 | yes |
| DR1080 | Dolichol-P-glucose synthetase | 0.981 | 0.299 | no | 0.727 | 0.274 | no | 0.735 | 0.184 | no | 0.724 | 0.191 | no | 0.754 | 0.236 | no | 0.706 | 0.180 | no | 0.821 | 0.220 | no | 0.826 | 0.149 | no | 0.896 | 0.109 | no |
| DR1081 | HTH transcription factor | 0.617 | 0.243 | yes | 0.433 | 0.197 | yes | 0.410 | 0.198 | yes | 0.398 | 0.092 | yes | 0.527 | 0.232 | yes | 0.532 | 0.157 | yes | 0.556 | 0.185 | yes | 0.780 | 0.269 | no | 0.859 | 0.216 | no |
| DR1082 | RP5M-like or sigma modulatory protein homolog | 1.008 | 0.345 | no | 0.852 | 0.553 | no | 0.929 | 0.401 | no | 0.608 | 0.221 | no | 0.925 | 0.572 | no | 0.842 | 0.421 | no | 0.488 | 0.114 | yes | 0.953 | 0.254 | no | 1.350 | 0.215 | no |
| DR1083 | Predicted protein | 0.740 | 0.217 | no | 0.606 | 0.397 | yes | 0.322 | 0.128 | yes | 0.229 | 0.065 | yes | 0.326 | 0.100 | yes | 0.366 | 0.086 | yes | 0.302 | 0.105 | yes | 0.428 | 0.031 | yes | 0.977 | 0.300 | no |
| DR1084 | Methylmalonyl-CoA mutase, MUTA | 1.053 | 0.405 | no | 1.031 | 0.420 | no | 1.040 | 0.455 | no | 1.248 | 0.405 | no | 1.001 | 0.319 | no | 0.962 | 0.443 | no | 0.876 | 0.320 | no | 0.850 | 0.212 | no | 0.960 | 0.276 | no |
| DR1085 | SAM dependent methylase | 0.961 | 0.253 | no | 0.971 | 0.437 | no | 0.713 | 0.331 | yes | 1.256 | 0.110 | no | 0.953 | 0.310 | no | 0.784 | 0.211 | no | 0.938 | 0.283 | no | 0.904 | 0.364 | no | 0.968 | 0.487 | no |
| DR1086 | Alanine racemase, ALR | 0.819 | 0.143 | no | 0.681 | 0.121 | no | 0.712 | 0.199 | no | 0.636 | 0.156 | yes | 0.550 | 0.162 | yes | 0.738 | 0.115 | no | 0.714 | 0.166 | no | 0.893 | 0.108 | no | 0.963 | 0.238 | no |
| DR1087 | Oxidoreductase | 0.783 | 0.265 | no | 1.485 | 0.867 | no | 0.859 | 0.431 | no | 0.810 | 0.493 | no | 0.703 | 0.181 | no | 0.786 | 0.274 | no | 1.367 | 0.670 | no | 1.154 | 0.257 | no | n/a | n/a | n/a |
| DR1088 | Zn-finger containing protein | 1.197 | 0.282 | no | 0.826 | 0.376 | no | 0.736 | 0.340 | yes | 0.869 | 0.378 | no | 0.924 | 0.577 | no | 0.985 | 0.556 | no | 0.841 | 0.416 | no | 1.122 | 0.045 | no | 1.372 | 0.584 | no |
| DR1089 | RecF protein | 0.997 | 0.441 | no | 0.806 | 0.256 | no | 0.588 | 0.322 | yes | 0.976 | 0.610 | no | 0.958 | 0.376 | no | 0.944 | 0.245 | no | 0.956 | 0.302 | no | 0.801 | 0.346 | no | 0.602 | 0.272 | yes |
| DR1090 | Membrane bounded protein with GGDEF domain signalling protein | 1.384 | 0.407 | no | 0.962 | 0.285 | no | 0.766 | 0.198 | no | 0.876 | 0.361 | no | 0.891 | 0.327 | no | 0.735 | 0.173 | no | 0.710 | 0.116 | no | 0.719 | 0.079 | yes | 0.841 | 0.230 | no |
| DR1091 | Uncharacterized conserved protein | 1.041 | 0.353 | no | 0.693 | 0.216 | yes | 0.675 | 0.346 | yes | 0.724 | 0.266 | no | 0.812 | 0.317 | no | 0.737 | 0.295 | no | 1.071 | 0.374 | no | 0.958 | 0.257 | no | 1.181 | 0.343 | no |
| DR1092 | Secreted protein with metal-binding site, possibly hydrolase | 1.476 | 0.427 | no | 1.716 | 0.908 | yes | 1.284 | 0.404 | no | 1.483 | 0.748 | no | 1.031 | 0.246 | no | 1.001 | 0.334 | no | 1.277 | 0.466 | no | 1.222 | 0.250 | no | 1.273 | 0.312 | no |
| DR1093 | Tryptophanyl-tRNA synthetase | 0.969 | 0.309 | no | 0.916 | 0.171 | no | 1.947 | 1.285 | yes | 2.222 | 1.394 | yes | 2.043 | 0.985 | yes | 1.270 | 0.401 | no | 1.392 | 0.571 | no | 1.434 | 0.261 | no | 1.585 | 0.700 | yes |
| DR1094 | Uncharcterized small protein similar to SCI30A.21C os S.coelicolor | 1.358 | 0.357 | no | 1.232 | 0.515 | no | 2.677 | 0.799 | yes | 5.391 | 0.916 | yes | 2.783 | 0.941 | yes | 1.716 | 0.495 | yes | 1.550 | 0.545 | yes | 1.188 | 0.296 | no | 0.941 | 0.054 | no |
| DR1095 | Predicted protein | 1.408 | 0.370 | no | 1.055 | 0.233 | no | 3.026 | 1.070 | yes | 5.178 | 2.042 | yes | 3.696 | 1.846 | yes | 1.703 | 0.288 | yes | 1.268 | 0.334 | no | 1.079 | 0.299 | no | 1.060 | 0.415 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR1096 | 3-phosphoshikimate 1-carboxyvinyltransferase | 1.314 | 0.175 | no | 1.130 | 0.177 | no | 1.157 | 0.223 | no | 1.471 | 0.180 | no | 1.186 | 0.281 | no | 0.966 | 0.165 | no | 1.021 | 0.242 | no | 1.008 | 0.069 | no | 0.998 | 0.217 | no |
| DR1097 | Phosphoglycerate mutase, PMG | 0.882 | 0.277 | no | 1.103 | 0.403 | no | 1.153 | 0.310 | no | 0.758 | 0.136 | no | 1.090 | 0.528 | no | 0.945 | 0.283 | no | 0.908 | 0.310 | no | 0.940 | 0.196 | no | 0.840 | 0.133 | no |
| DR1098 | Membrane protein | 1.115 | 0.362 | no | 1.774 | 0.535 | yes | 1.338 | 0.355 | no | 1.128 | 0.249 | no | 1.179 | 0.428 | no | 0.944 | 0.259 | no | 0.924 | 0.358 | no | 0.820 | 0.104 | no | 0.827 | 0.121 | no |
| DR1099 | Uncharacterized conserved protein containing duplicated domain with conserved HH motif | 1.097 | 0.397 | no | 0.874 | 0.362 | no | 0.702 | 0.235 | no | 0.983 | 0.625 | no | 0.901 | 0.202 | no | 0.846 | 0.294 | no | 1.263 | 0.807 | no | 1.215 | 0.594 | no | 1.080 | 0.364 | no |
| DR1100 | Rhodenese superfamily protein | 1.050 | 0.387 | no | 0.770 | 0.287 | no | 0.360 | 0.097 | yes | 0.313 | 0.188 | yes | 0.310 | 0.111 | yes | 0.217 | 0.090 | yes | 0.190 | 0.052 | yes | 0.276 | 0.092 | yes | 0.367 | 0.105 | yes |
| DR1101 | SAM dependent methyltransferase | 1.071 | 0.429 | no | 1.117 | 0.265 | no | 0.856 | 0.307 | no | 1.032 | 0.033 | no | 1.304 | 1.013 | no | 0.823 | 0.221 | no | 0.834 | 0.212 | no | 0.983 | 0.063 | no | 0.692 | 0.093 | no |
| DR1102 | Cation transport protein (CDF) family | 1.257 | 0.154 | no | 0.951 | 0.368 | no | 0.632 | 0.147 | yes | 0.730 | 0.160 | no | 0.839 | 0.438 | no | 0.654 | 0.178 | yes | 0.576 | 0.108 | yes | 0.737 | 0.064 | no | 0.791 | 0.179 | no |
| DR1103 | ABC transporter ATPase, 2 domains | 1.020 | 0.378 | no | 1.095 | 0.394 | no | 1.119 | 0.365 | no | 1.438 | 0.395 | no | 1.159 | 0.381 | no | 0.993 | 0.144 | no | 0.980 | 0.281 | no | 0.856 | 0.134 | no | 0.725 | 0.068 | no |
| DR1104 | Predicted protein | 1.022 | 0.420 | no | 0.712 | 0.163 | no | 0.508 | 0.179 | yes | 0.788 | 0.144 | no | 0.830 | 0.269 | no | 0.647 | 0.134 | yes | 0.738 | 0.145 | no | 0.740 | 0.297 | yes | 1.184 | 0.526 | no |
| DR1105 | RADA/SMS RecA superfamily | 0.925 | 0.420 | no | 1.013 | 0.329 | no | 0.999 | 0.374 | no | 1.192 | 0.135 | no | 1.106 | 0.363 | no | 1.079 | 0.306 | no | 1.064 | 0.499 | no | 1.150 | 0.153 | no | 0.823 | 0.175 | no |
| DR1106 | Dihydro-orotase | 1.486 | 0.390 | no | 1.472 | 0.691 | no | 1.314 | 0.355 | no | 1.566 | 0.727 | no | 1.631 | 0.923 | no | 1.306 | 0.329 | no | 1.129 | 0.265 | no | 1.007 | 0.171 | no | 1.188 | 0.131 | no |
| DR1107 | Predicted protein | 1.046 | 0.295 | no | 1.259 | 0.339 | no | 2.463 | 0.722 | yes | 2.653 | 0.827 | yes | 2.852 | 1.421 | yes | 2.091 | 0.606 | yes | 2.343 | 0.668 | yes | 1.829 | 0.458 | yes | 1.214 | 0.245 | no |
| DR1108 | Predicted protein | 1.236 | 0.330 | no | 1.330 | 0.412 | no | 1.710 | 0.798 | yes | 1.908 | 0.631 | yes | 1.978 | 0.783 | yes | 1.145 | 0.408 | no | 0.984 | 0.349 | no | 0.907 | 0.040 | no | 0.885 | 0.049 | no |
| DR1109 | Aspartate transcarbamoylase, PYRB | 1.085 | 0.432 | no | 1.368 | 0.705 | no | 1.343 | 0.606 | no | 1.503 | 0.475 | no | 1.312 | 0.371 | no | 0.936 | 0.237 | no | 0.988 | 0.347 | no | 0.863 | 0.186 | no | 0.770 | 0.193 | no |
| DR1110 | Uracil phosphoribosyltransferase, PYRR | 0.924 | 0.307 | no | 0.936 | 0.190 | no | 1.018 | 0.234 | no | 0.980 | 0.112 | no | 1.095 | 0.312 | no | 1.040 | 0.192 | no | 0.902 | 0.153 | no | 1.134 | 0.263 | no | 0.988 | 0.177 | no |
| DR1111 | HTH transcriptional regulator MerR family | 0.646 | 0.317 | yes | 0.520 | 0.335 | yes | 0.894 | 0.629 | no | 0.665 | 0.331 | yes | 0.861 | 0.336 | no | 0.943 | 0.635 | no | 1.028 | 0.080 | no | n/a | n/a | n/a | n/a | n/a | n/a |
| DR1112 | Membrane protein, related to YDCZ_ECOLI | 0.926 | 0.284 | no | 0.882 | 0.612 | no | 1.950 | 1.047 | yes | 0.521 | 0.305 | yes | 0.861 | 0.694 | no | 1.138 | 0.460 | no | 0.801 | 0.445 | no | 0.710 | 0.095 | no | 0.557 | 0.048 | no |
| DR1113 | Membrane protein, similar to YDCZ E.coli | 0.955 | 0.166 | no | 0.769 | 0.162 | no | 0.696 | 0.074 | no | 0.779 | 0.091 | no | 0.771 | 0.229 | no | 0.695 | 0.154 | no | 0.614 | 0.163 | yes | 0.753 | 0.152 | no | 0.660 | 0.101 | no |
| DR1114 | Hsp20 small heatshock family protein | 1.249 | 0.606 | no | 0.543 | 0.119 | yes | 0.147 | 0.030 | yes | 0.091 | 0.015 | yes | 0.118 | 0.047 | yes | 0.118 | 0.019 | yes | 0.115 | 0.025 | yes | 0.137 | 0.050 | yes | 0.436 | 0.235 | yes |
| DR1115 | S-layer protein | 0.681 | 0.274 | yes | 0.626 | 0.229 | yes | 0.417 | 0.251 | yes | 0.246 | 0.045 | yes | 0.617 | 0.315 | yes | 1.142 | 0.447 | no | 1.621 | 0.753 | yes | 1.649 | 0.456 | yes | 1.025 | 0.339 | no |
| DR1116 | Predicted protein | 0.831 | 0.167 | no | 1.078 | 0.306 | no | 1.599 | 0.187 | yes | 2.167 | 0.272 | yes | 2.338 | 0.552 | yes | 1.741 | 0.576 | yes | 2.096 | 0.640 | yes | 1.285 | 0.491 | no | 1.627 | 0.183 | yes |
| DR1117 | ClpC AAA ATPase | 0.695 | 0.288 | yes | 0.461 | 0.155 | yes | 0.564 | 0.178 | yes | 0.607 | 0.017 | yes | 0.747 | 0.400 | no | 0.851 | 0.598 | no | 0.828 | 0.332 | no | 0.814 | 0.248 | no | 1.354 | 0.528 | no |
| DR1118 | PilT N-terminal domain like protein, merged with transmembrane segments | 0.930 | 0.135 | no | 0.965 | 0.187 | no | 1.343 | 0.187 | no | 1.689 | 0.238 | yes | 1.629 | 0.425 | yes | 1.575 | 0.470 | yes | 1.421 | 0.212 | no | 1.100 | 0.126 | no | 1.148 | 0.224 | no |
| DR1119 | Calcineurin like phosphoesterase | 0.608 | 0.264 | yes | 0.703 | 0.187 | no | 1.165 | 0.333 | no | 0.781 | 0.042 | no | 1.515 | 0.328 | yes | 1.464 | 0.525 | no | 1.380 | 0.450 | no | 1.316 | 0.363 | no | 0.845 | 0.093 | no |
| DR1120 | Butyrate kinase | 0.862 | 0.228 | no | 0.800 | 0.240 | no | 0.753 | 0.250 | no | 0.699 | 0.160 | no | 0.896 | 0.178 | no | 0.852 | 0.137 | no | 0.786 | 0.198 | no | 0.937 | 0.235 | no | 1.061 | 0.324 | no |
| DR1121 | Predicted protein | 0.857 | 0.311 | no | 0.635 | 0.234 | yes | 0.538 | 0.226 | yes | 0.494 | 0.161 | yes | 0.754 | 0.246 | no | 0.711 | 0.180 | no | 0.637 | 0.218 | yes | 0.761 | 0.095 | no | 0.816 | 0.094 | no |
| DR1122 | Prephenate dehydrogenase, TYRA | 0.765 | 0.167 | no | 0.724 | 0.159 | no | 0.850 | 0.279 | no | 0.857 | 0.071 | no | 1.029 | 0.290 | no | 0.879 | 0.209 | no | 0.819 | 0.169 | no | 0.792 | 0.173 | no | 0.910 | 0.203 | no |
| DR1123 | UDP-N-acetylglucosamine 1-carboxyvinyltransferase, MURA | 0.773 | 0.302 | no | 0.419 | 0.210 | yes | 0.425 | 0.246 | yes | 0.475 | 0.159 | yes | 0.612 | 0.218 | yes | 0.562 | 0.317 | yes | 0.701 | 0.355 | yes | 0.862 | 0.212 | no | 1.236 | 0.510 | no |
| DR1124 | S-layer protein | 0.864 | 0.431 | no | 0.793 | 0.343 | no | 0.829 | 0.356 | no | 0.482 | 0.127 | yes | 1.036 | 0.675 | no | 1.270 | 0.654 | no | 1.123 | 0.280 | no | 1.158 | 0.551 | no | 2.513 | 0.905 | yes |
| DR1125 | Predicted protein | 0.925 | 0.229 | no | 1.189 | 0.494 | no | 1.092 | 0.555 | no | 1.171 | 0.433 | no | 1.068 | 0.456 | no | 0.944 | 0.493 | no | 0.721 | 0.396 | yes | 0.886 | 0.240 | no | 0.832 | 0.321 | no |
| DR1126 | RecJ like DHH superfamily Phosphohydrolase | 0.859 | 0.229 | no | 0.693 | 0.204 | no | 0.529 | 0.067 | yes | 0.577 | 0.087 | yes | 0.557 | 0.199 | yes | 0.435 | 0.147 | yes | 0.330 | 0.123 | yes | 0.442 | 0.123 | yes | 0.614 | 0.138 | yes |
| DR1127 | Similar to toxic anion resistance protein, Tellurite resistance | 0.550 | 0.210 | yes | 1.242 | 0.381 | no | 1.116 | 0.253 | no | 0.998 | 0.200 | no | 1.058 | 0.338 | no | 0.747 | 0.218 | no | 0.704 | 0.314 | yes | 0.695 | 0.125 | yes | 0.635 | 0.257 | yes |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR1128 | Predicted protein | 1.064 | 0.232 | no | 1.010 | 0.217 | no | 1.086 | 0.256 | no | 1.000 | 0.197 | no | 0.856 | 0.261 | no | 0.755 | 0.234 | no | 0.780 | 0.125 | no | 0.750 | 0.114 | no | 1.047 | 0.267 | no |
| DR1129 | Predicted protein | 0.874 | 0.451 | no | 0.973 | 0.343 | no | 1.163 | 0.503 | no | 0.781 | 0.293 | no | 0.616 | 0.150 | yes | 0.596 | 0.225 | yes | 0.603 | 0.307 | yes | 0.606 | 0.132 | yes | 0.737 | 0.224 | no |
| DR1130 | Rossman fold oxidoreductase HemG | 0.919 | 0.323 | no | 0.930 | 0.267 | no | 1.118 | 0.343 | no | 0.874 | 0.585 | no | 0.710 | 0.173 | no | 0.694 | 0.335 | yes | 0.495 | 0.156 | yes | 0.688 | 0.109 | yes | 1.219 | 0.627 | no |
| DR1131 | HemZ, Ferrochelatase | 0.794 | 0.204 | no | 0.685 | 0.222 | yes | 0.904 | 0.176 | no | 0.569 | 0.199 | yes | 0.514 | 0.193 | yes | 0.451 | 0.250 | yes | 0.333 | 0.176 | yes | 0.433 | 0.088 | yes | 1.099 | 0.472 | no |
| DR1132 | Dihydroxy-acid dehydratase, ILVD | 0.717 | 0.207 | no | 0.585 | 0.187 | yes | 0.618 | 0.176 | yes | 0.290 | 0.119 | yes | 0.284 | 0.069 | yes | 0.327 | 0.117 | yes | 0.281 | 0.127 | yes | 0.374 | 0.127 | yes | 0.945 | 0.311 | no |
| DR1133 | Uroporphyrinogen decarboxylase | 0.447 | 0.175 | yes | 0.344 | 0.155 | yes | 0.532 | 0.229 | yes | 0.184 | 0.047 | yes | 0.250 | 0.132 | yes | 0.266 | 0.092 | yes | 0.320 | 0.119 | yes | 0.358 | 0.085 | yes | 1.016 | 0.315 | no |
| DR1134 | Predicted protein | 0.927 | 0.203 | no | 1.089 | 0.678 | no | 1.395 | 0.623 | no | 1.573 | 0.846 | no | 0.918 | 0.346 | no | 0.818 | 0.124 | no | 0.695 | 0.230 | yes | 0.838 | 0.308 | no | 1.118 | 0.280 | no |
| DR1135 | Secreted protein, uncharacterized | 0.692 | 0.206 | no | 0.841 | 0.257 | no | 0.632 | 0.199 | yes | 0.716 | 0.477 | no | 1.155 | 0.494 | no | 1.618 | 0.475 | no | 1.846 | 0.677 | yes | 1.472 | 0.345 | no | n/a | n/a | n/a |
| DR1136 | Predicted protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR1137 | NH2 acetyltransferase | 1.239 | 0.700 | no | 2.051 | 1.124 | yes | 2.441 | 1.116 | yes | 4.131 | 2.325 | yes | 2.516 | 1.804 | yes | 1.591 | 0.259 | yes | 1.557 | 0.873 | no | 1.304 | 0.177 | no | 1.161 | 0.021 | no |
| DR1138 | Predicted protein | 1.060 | 0.418 | no | 2.057 | 0.309 | yes | 2.161 | 0.532 | yes | 1.563 | 0.334 | no | 1.101 | 0.205 | no | 1.192 | 0.351 | no | 1.536 | 0.377 | yes | 2.038 | 0.795 | yes | 1.721 | 0.488 | yes |
| DR1139 | Protein with the disrupted DXD active site, related to inorganic pyrophosphatase | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR1140 | Predicted protein | 1.154 | 0.401 | no | 2.705 | 1.408 | yes | 2.990 | 0.927 | yes | 2.496 | 1.088 | yes | 1.535 | 0.560 | no | 1.179 | 0.381 | no | 1.128 | 0.347 | no | 1.347 | 0.631 | no | 1.085 | 0.010 | no |
| DR1141 | Pullulanase/amylase | 1.259 | 0.335 | no | 8.243 | 3.586 | yes | 9.073 | 1.551 | yes | 7.474 | 1.998 | yes | 3.778 | 1.835 | yes | 1.756 | 0.504 | yes | 1.288 | 0.369 | no | 1.225 | 0.398 | no | 0.694 | 0.180 | no |
| DR1142 | Predicted protein | 1.291 | 0.517 | no | 10.003 | 5.373 | yes | 9.661 | 2.889 | yes | 8.086 | 3.149 | yes | 3.843 | 2.346 | yes | 1.846 | 0.233 | yes | 1.535 | 0.658 | no | 1.063 | 0.094 | no | 0.791 | 0.189 | no |
| DR1143 | Predicted protein | 1.160 | 0.161 | no | 7.374 | 2.521 | yes | 8.850 | 4.259 | yes | 5.722 | 0.910 | yes | 3.174 | 1.009 | yes | 2.146 | 0.886 | yes | 1.631 | 0.822 | yes | 1.364 | 0.320 | no | 0.861 | 0.212 | no |
| DR1144 | Uncharacterized conserved protein | 1.388 | 0.747 | no | 2.138 | 0.979 | yes | 2.689 | 1.313 | yes | 2.147 | 1.374 | yes | 1.557 | 0.808 | no | 1.377 | 0.285 | no | 1.393 | 0.772 | no | 1.061 | 0.347 | no | 1.005 | 0.245 | no |
| DR1145 | LEPA, GTPase | 0.698 | 0.251 | no | 0.964 | 0.144 | no | 0.996 | 0.320 | no | 0.765 | 0.068 | no | 0.872 | 0.232 | no | 0.930 | 0.191 | no | 0.956 | 0.285 | no | 1.005 | 0.229 | no | 1.070 | 0.202 | no |
| DR1146 | GSP26 general stress like protein | 0.991 | 0.223 | no | 0.316 | 0.087 | yes | 0.251 | 0.059 | yes | 0.336 | 0.061 | yes | 0.556 | 0.250 | yes | 0.560 | 0.113 | yes | 0.698 | 0.208 | no | 1.057 | 0.212 | no | 1.441 | 0.191 | yes |
| DR1147 | Chorismate mutase/prephenate dehydratase | 0.942 | 0.160 | no | 1.514 | 0.729 | yes | 1.024 | 0.331 | no | 0.836 | 0.424 | no | 0.770 | 0.271 | no | 0.946 | 0.386 | no | 0.649 | 0.151 | yes | 0.778 | 0.159 | no | 0.865 | 0.075 | no |
| DR1148 | Potassium Channel subunit, NAD-binding domain | 0.839 | 0.470 | no | 1.453 | 0.499 | no | 0.899 | 0.279 | no | 1.889 | 0.835 | yes | 1.104 | 0.338 | no | 1.071 | 0.467 | no | 1.137 | 0.431 | no | 1.208 | 0.229 | no | 1.293 | 0.310 | no |
| DR1149 | Na(+)/H(+) antiporter like protein | 1.034 | 0.210 | no | 0.865 | 0.384 | no | 0.887 | 0.244 | no | 0.837 | 0.367 | no | 0.814 | 0.216 | no | 1.025 | 0.175 | no | 0.853 | 0.246 | no | 1.010 | 0.110 | no | 1.283 | 0.304 | no |
| DR1150 | Biotin synthase like cysteine cluster enzyme | 0.845 | 0.110 | no | 1.026 | 0.544 | no | 0.998 | 0.139 | no | 0.990 | 0.140 | no | 1.299 | 0.350 | no | 1.004 | 0.158 | no | 1.168 | 0.128 | no | 1.022 | 0.218 | no | 1.067 | 0.285 | no |
| DR1151 | Enoyl-COA hydrarase | 1.032 | 0.155 | no | 1.057 | 0.313 | no | 1.397 | 0.680 | no | 1.652 | 0.515 | yes | 2.164 | 1.054 | yes | 1.564 | 0.332 | yes | 1.281 | 0.462 | no | 1.381 | 0.434 | no | 1.747 | 0.561 | yes |
| DR1152 | Releated to double stranded Beta- helix domain of AraC, YLBA E coli ortholog | 1.552 | 0.365 | yes | 2.024 | 0.607 | yes | 3.772 | 1.181 | yes | 3.090 | 0.552 | yes | 3.042 | 0.807 | yes | 2.677 | 0.691 | yes | 1.994 | 0.615 | yes | 1.834 | 0.456 | yes | 1.950 | 0.452 | yes |
| DR1153 | Allantoinase, TIM barrel metallohydrolase | 1.231 | 0.764 | no | 1.182 | 0.271 | no | 1.660 | 0.443 | yes | 1.894 | 0.517 | yes | 2.229 | 0.497 | yes | 1.983 | 0.212 | yes | 1.699 | 0.186 | yes | 1.422 | 0.122 | no | 1.902 | 0.240 | yes |
| DR1154 | Hydantoinase HYUC, N-carbamyl-L-amino acid amidohydrolase | 1.200 | 0.244 | no | 1.263 | 0.416 | no | 1.354 | 0.111 | no | 1.278 | 0.213 | no | 1.912 | 1.283 | yes | 1.571 | 0.327 | yes | 1.174 | 0.332 | no | 1.281 | 0.345 | no | 1.392 | 0.353 | no |
| DR1155 | Malate synthase, MASY | 0.757 | 0.289 | no | 1.452 | 0.149 | yes | 2.083 | 0.793 | yes | 1.536 | 0.122 | no | 2.042 | 0.960 | yes | 1.807 | 0.390 | yes | 1.219 | 0.359 | no | 1.329 | 0.346 | no | 1.515 | 0.124 | yes |
| DR1156 | HTH transcription factor, KdgR repressor | 1.131 | 0.285 | no | 1.444 | 0.260 | yes | 1.690 | 0.303 | yes | 1.799 | 0.086 | yes | 1.687 | 0.513 | yes | 1.376 | 0.415 | no | 1.278 | 0.390 | no | 1.223 | 0.164 | no | 1.458 | 0.316 | yes |
| DR1158 | Uncharacterized protein, share a domain with | 1.002 | 0.120 | no | 1.221 | 0.344 | no | 1.097 | 0.243 | no | 1.154 | 0.300 | no | 1.307 | 0.287 | no | 1.120 | 0.261 | no | 1.241 | 0.433 | no | 1.435 | 0.701 | no | 1.394 | 0.637 | no |
| DR1159 | HTH transcription regulator, MarR family | 1.210 | 0.719 | no | 1.276 | 0.303 | no | 1.060 | 0.358 | no | 0.967 | 0.104 | no | 1.324 | 0.885 | no | 1.141 | 0.171 | no | 0.794 | 0.257 | no | 0.853 | 0.279 | no | 0.569 | 0.252 | yes |
| DR1160 | Uricase | 1.162 | 0.637 | no | 0.780 | 0.383 | no | 0.719 | 0.193 | no | 2.070 | 1.210 | yes | 1.428 | 0.824 | no | 0.708 | 0.563 | yes | 0.990 | 0.413 | no | 0.952 | 0.276 | no | 0.831 | 0.177 | no |
| DR1161 | Transthyretin | 1.247 | 0.760 | no | 0.929 | 0.544 | no | 1.058 | 0.760 | no | 1.236 | 0.420 | no | 1.717 | 1.036 | no | 1.049 | 0.749 | no | 1.234 | 0.528 | no | 1.103 | 0.272 | no | 0.689 | 0.209 | no |
| DR1162 | Transcription elongation factor GreA | 1.025 | 0.588 | no | 0.915 | 0.468 | no | 1.068 | 0.445 | no | 2.028 | 0.841 | yes | 1.659 | 1.031 | no | 1.155 | 0.407 | no | 1.158 | 0.713 | no | 0.942 | 0.339 | no | 0.667 | 0.282 | yes |
| DR1163 | PilT family ATPase | 0.975 | 0.229 | no | 0.689 | 0.221 | yes | 0.517 | 0.152 | yes | 0.521 | 0.189 | yes | 0.579 | 0.215 | yes | 0.863 | 0.340 | no | 0.916 | 0.271 | no | 0.983 | 0.185 | no | 0.890 | 0.113 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR1164 | Pantothenate synthetase, PANC | 1.350 | 0.627 | no | 0.776 | 0.337 | no | 0.381 | 0.169 | yes | 0.185 | 0.060 | yes | 0.295 | 0.122 | yes | 0.564 | 0.278 | yes | 0.742 | 0.247 | no | 0.762 | 0.152 | no | 0.926 | 0.280 | no |
| DR1165 | Conserved membrane protein (>gi\|2276323 Mycobacterium leprae | 0.939 | 0.376 | no | 0.591 | 0.266 | yes | 0.432 | 0.217 | yes | 0.484 | 0.155 | yes | 0.640 | 0.264 | yes | 0.946 | 0.321 | no | 0.994 | 0.337 | no | 1.235 | 0.155 | no | 1.399 | 0.206 | no |
| DR1166 | Shares a fragment with uricase URIC | 0.812 | 0.390 | no | 0.641 | 0.176 | yes | 0.678 | 0.263 | yes | 0.741 | 0.193 | no | 0.674 | 0.315 | yes | 0.672 | 0.238 | yes | 0.704 | 0.326 | yes | 0.765 | 0.201 | no | 1.248 | 0.104 | no |
| DR1167 | DEDA like Membrane protein | 0.798 | 0.252 | no | 0.843 | 0.298 | no | 0.758 | 0.268 | no | 0.758 | 0.131 | no | 0.709 | 0.307 | yes | 0.859 | 0.344 | no | 0.737 | 0.294 | no | 0.781 | 0.200 | no | 0.878 | 0.203 | no |
| DR1168 | C-terminal finger domain + MutT like hydrolase, ortholog of YJAD_ECOLI | 1.165 | 0.703 | no | 0.719 | 0.382 | yes | 1.088 | 0.395 | no | 0.552 | 0.113 | yes | 0.985 | 0.522 | no | 1.087 | 0.269 | no | 0.656 | 0.193 | yes | 0.861 | 0.251 | no | 0.671 | 0.211 | no |
| DR1169 | N-terminal domain probably metal dependent hydrolase | 1.024 | 0.367 | no | 0.846 | 0.224 | no | 0.741 | 0.192 | no | 0.736 | 0.229 | no | 0.787 | 0.190 | no | 1.022 | 0.326 | no | 1.012 | 0.329 | no | 1.041 | 0.307 | no | 1.055 | 0.313 | no |
| DR1170 | Predicted protein | 1.199 | 0.418 | no | 0.731 | 0.228 | no | 0.673 | 0.169 | yes | 0.763 | 0.211 | no | 0.763 | 0.232 | no | 0.865 | 0.101 | no | 0.963 | 0.300 | no | 0.957 | 0.236 | no | 0.864 | 0.159 | no |
| DR1171 | MoxR related AAA superfamily ATPase | 0.865 | 0.185 | no | 0.662 | 0.157 | yes | 0.467 | 0.147 | yes | 0.566 | 0.150 | yes | 0.659 | 0.075 | yes | 0.897 | 0.203 | no | 0.804 | 0.161 | no | 1.058 | 0.232 | no | 1.025 | 0.302 | no |
| DR1172 | Lea76/LEa29-like desiccation resistance protein | 1.173 | 0.723 | no | 0.441 | 0.187 | yes | 0.365 | 0.109 | yes | 0.558 | 0.171 | yes | 0.892 | 0.418 | no | 1.520 | 0.558 | no | 1.588 | 0.556 | yes | 1.504 | 0.690 | no | 2.657 | 0.603 | yes |
| DR1173 | Shikimate dehydrogenase, AroE | 0.825 | 0.176 | no | 0.743 | 0.269 | no | 0.520 | 0.163 | yes | 0.684 | 0.142 | no | 0.668 | 0.166 | yes | 0.705 | 0.293 | no | 0.861 | 0.288 | no | 0.830 | 0.126 | no | 0.855 | 0.224 | no |
| DR1174 | Histidine kinase with 3 PAS +3 PAC + GAF domains | 1.033 | 0.112 | no | 1.667 | 0.928 | yes | 1.284 | 0.229 | no | 0.996 | 0.443 | no | 1.009 | 0.348 | no | 0.957 | 0.188 | no | 0.872 | 0.129 | no | 0.992 | 0.261 | no | 0.794 | 0.206 | no |
| DR1175 | N-terminal receiver domain, CHEY family + C terminal Histidine kinase | 0.938 | 0.176 | no | 0.674 | 0.114 | yes | 0.605 | 0.202 | yes | 0.592 | 0.053 | yes | 0.859 | 0.233 | no | 0.993 | 0.173 | no | 0.991 | 0.300 | no | 1.356 | 0.174 | no | 1.437 | 0.292 | no |
| DR1176 | Predicted protein | 1.788 | 1.010 | yes | 0.757 | 0.389 | yes | 0.752 | 0.480 | yes | 2.191 | 0.698 | yes | 1.941 | 1.091 | yes | 2.160 | 1.530 | yes | 2.415 | 1.311 | yes | 2.963 | 1.467 | yes | 2.052 | 0.733 | yes |
| DR1177 | Conserved bacterial/archaeal proteins involved in alkylperoxide and oxidative stress response | 1.373 | 0.493 | no | 1.327 | 0.835 | no | 0.941 | 0.347 | no | 0.793 | 0.258 | no | 1.281 | 0.960 | no | 0.887 | 0.157 | no | 0.848 | 0.444 | no | 0.998 | 0.481 | no | 0.927 | 0.539 | no |
| DR1178 | Predicted epimerases, related YDDE_ECOLI and PHZF_PSEFL | 1.047 | 0.116 | no | 0.775 | 0.294 | no | 0.720 | 0.127 | no | 0.687 | 0.031 | no | 0.737 | 0.142 | no | 0.880 | 0.233 | no | 0.889 | 0.240 | no | 1.047 | 0.174 | no | 1.114 | 0.176 | no |
| DR1179 | HKD superfamily hydrolase | 1.176 | 0.297 | no | 0.872 | 0.145 | no | 0.753 | 0.294 | no | 1.044 | 0.300 | no | 1.416 | 1.022 | no | 1.253 | 0.460 | no | 0.916 | 0.313 | no | 1.173 | 0.125 | no | n/a | n/a | n/a |
| DR1180 | Secreted protein, uncharacterized | 0.815 | 0.211 | no | 0.630 | 0.135 | yes | 0.505 | 0.245 | yes | 0.657 | 0.073 | no | 0.626 | 0.189 | yes | 0.661 | 0.156 | yes | 0.750 | 0.091 | no | 0.795 | 0.037 | no | 1.175 | 0.170 | no |
| DR1181 | Similar to GSP26 | 0.888 | 0.346 | no | 0.796 | 0.192 | no | 0.745 | 0.158 | no | 0.703 | 0.115 | no | 1.006 | 0.443 | no | 1.113 | 0.196 | no | 0.963 | 0.280 | no | 1.037 | 0.455 | no | 1.046 | 0.180 | no |
| DR1182 | NH2- acetyltransferase, probably phosphinothricin N-acetyltransferase | 1.135 | 0.199 | no | 1.196 | 0.464 | no | 0.956 | 0.515 | no | 1.085 | 0.413 | no | 1.027 | 0.276 | no | 0.934 | 0.258 | no | 1.031 | 0.328 | no | 1.087 | 0.228 | no | 0.907 | 0.237 | no |
| DR1183 | MAZG family protein | 0.861 | 0.140 | no | 0.611 | 0.200 | yes | 0.575 | 0.383 | yes | 0.412 | 0.110 | yes | 0.513 | 0.184 | yes | 0.647 | 0.246 | yes | 0.518 | 0.239 | yes | 0.773 | 0.249 | no | 0.870 | 0.273 | no |
| DR1184 | MutT family hydrolase | 1.141 | 0.282 | no | 1.104 | 0.332 | no | 1.192 | 0.383 | no | 1.454 | 0.524 | no | 1.483 | 0.922 | no | 1.048 | 0.423 | no | 0.895 | 0.249 | no | 0.961 | 0.140 | no | 0.826 | 0.136 | no |
| DR1185 | Surface protein | 0.861 | 0.278 | no | 0.901 | 0.425 | no | 0.619 | 0.388 | yes | 0.505 | 0.227 | yes | 0.906 | 0.474 | no | 0.958 | 0.555 | no | 1.462 | 0.845 | no | 1.649 | 0.381 | yes | 2.990 | 1.848 | yes |
| DR1186 | Predicted protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR1187 | Conserved membrane protein YGDO | 1.233 | 0.415 | no | 1.206 | 0.293 | no | 0.878 | 0.202 | no | 1.363 | 0.291 | no | 1.429 | 0.497 | no | 1.362 | 0.544 | no | 1.606 | 0.604 | yes | 1.207 | 0.184 | no | 1.285 | 0.281 | no |
| DR1188 | Conserved membrane protein, permease PERM | 1.083 | 0.197 | no | 1.161 | 0.228 | no | 1.065 | 0.141 | no | 0.897 | 0.150 | no | 0.958 | 0.170 | no | 1.415 | 0.490 | no | 1.390 | 0.313 | no | 1.280 | 0.157 | no | 0.831 | 0.170 | no |
| DR1189 | Methylmalonyl-CoA mutase | 1.099 | 0.558 | no | 1.195 | 0.523 | no | 0.940 | 0.560 | no | 0.966 | 0.507 | no | 0.567 | 0.272 | yes | 0.413 | 0.281 | yes | 0.550 | 0.162 | yes | 0.682 | 0.236 | yes | 0.835 | 0.349 | no |
| DR1190 | Conserved membrane protein | 1.087 | 0.181 | no | 1.556 | 0.276 | yes | 1.285 | 0.205 | no | 0.814 | 0.050 | no | 0.945 | 0.395 | no | 0.958 | 0.296 | no | 1.129 | 0.380 | no | 0.914 | 0.292 | no | 0.826 | 0.184 | no |
| DR1191 | Poly A polymerase | 1.091 | 0.579 | no | 1.594 | 1.027 | yes | 1.102 | 0.643 | no | 1.188 | 0.425 | no | 0.899 | 0.410 | no | 0.842 | 0.402 | no | 0.861 | 0.600 | no | 0.703 | 0.223 | yes | 0.752 | 0.265 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR1192 | Uncharacterized protein with domain similar to 2 yeast proteins | 1.062 | 0.404 | no | 1.235 | 0.337 | no | 1.094 | 0.389 | no | 1.128 | 0.403 | no | 1.114 | 0.397 | no | 1.353 | 0.525 | no | 0.924 | 0.495 | no | 0.783 | 0.067 | no | 0.758 | 0.189 | no |
| DR1193 | Predicted protein | 1.140 | 0.590 | no | 2.665 | 1.620 | yes | 1.678 | 0.760 | yes | 2.089 | 0.824 | yes | 1.680 | 1.255 | no | 1.110 | 0.095 | no | 1.000 | 0.459 | no | 0.895 | 0.346 | no | 0.511 | 0.081 | yes |
| DR1194 | Predicted protein | 0.882 | 0.317 | no | 1.043 | 0.257 | no | 0.720 | 0.268 | yes | 0.722 | 0.307 | no | 0.796 | 0.302 | no | 0.860 | 0.291 | no | 0.657 | 0.231 | yes | 0.717 | 0.176 | yes | 0.888 | 0.255 | no |
| DR1195 | Predicted protein | 1.246 | 0.603 | no | 1.573 | 0.435 | yes | 1.322 | 0.439 | no | 1.093 | 0.434 | no | 0.959 | 0.308 | no | 0.872 | 0.118 | no | 1.036 | 0.441 | no | 0.877 | 0.156 | no | 0.773 | 0.220 | no |
| DR1196 | Transposon DORF | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR1197 | Predicted protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR1198 | TYPA like GTPase | 0.822 | 0.116 | no | 3.841 | 1.592 | yes | 3.929 | 1.188 | yes | 3.307 | 0.810 | yes | 3.442 | 1.236 | yes | 2.264 | 1.031 | yes | 2.032 | 0.564 | yes | 1.406 | 0.262 | no | 0.746 | 0.174 | no |
| DR1199 | Protease I, related to general stress protein 18, ThiJ superfamily protein | 1.263 | 0.367 | no | 0.531 | 0.112 | yes | 0.560 | 0.145 | yes | 0.916 | 0.240 | no | 1.130 | 0.768 | no | 1.598 | 0.428 | yes | 1.561 | 0.352 | yes | 2.246 | 0.364 | yes | 2.155 | 0.568 | yes |
| DR1200 | Uncharacterized conserved protein | 0.589 | 0.261 | yes | 1.311 | 0.556 | no | 1.552 | 0.508 | yes | 1.546 | 0.614 | no | 1.735 | 0.725 | yes | 1.463 | 0.548 | no | 2.270 | 0.858 | yes | 2.551 | 0.217 | yes | 1.448 | 0.618 | no |
| DR1201 | P-loop (related to LuxR family ATPase domain) containing very diverged protein with possible TPR repeats | 0.988 | 0.216 | no | 1.465 | 0.514 | yes | 1.528 | 0.442 | yes | 1.182 | 0.240 | no | 1.470 | 0.802 | no | 1.036 | 0.171 | no | 0.912 | 0.227 | no | 0.823 | 0.241 | no | 0.673 | 0.252 | yes |
| DR1202 | Predicted protein | 0.707 | 0.153 | no | 0.770 | 0.271 | no | 1.008 | 0.301 | no | 0.788 | 0.262 | no | 0.680 | 0.313 | yes | 0.603 | 0.281 | yes | 0.569 | 0.376 | yes | 0.897 | 0.163 | no | n/a | n/a | n/a |
| DR1203 | N-term. domain of ImbE family protein, chracteristic HPDD motif | 0.964 | 0.203 | no | 0.474 | 0.168 | yes | 0.344 | 0.166 | yes | 0.439 | 0.098 | yes | 0.713 | 0.427 | yes | 0.481 | 0.139 | yes | 0.559 | 0.191 | yes | 0.739 | 0.128 | no | 1.011 | 0.193 | no |
| DR1204 | 3-oxoadipate enol-lactone hydrolase/4-carboxymuconolactone decarboxylase | 1.307 | 0.282 | no | 0.981 | 0.377 | no | 0.793 | 0.500 | yes | 1.075 | 0.166 | no | 0.967 | 0.452 | no | 1.017 | 0.480 | no | 0.756 | 0.306 | no | 0.681 | 0.127 | yes | 0.546 | 0.296 | yes |
| DR1205 | Deoxyribose-phosphate aldolase, DeoC | 1.222 | 0.119 | no | 1.029 | 0.372 | no | 0.921 | 0.343 | no | 1.133 | 0.435 | no | 0.945 | 0.112 | no | 1.012 | 0.181 | no | 0.922 | 0.177 | no | 0.895 | 0.203 | no | 1.039 | 0.268 | no |
| DR1206 | MAF-like protein | 1.179 | 0.607 | no | 0.654 | 0.241 | yes | 0.553 | 0.295 | yes | 0.498 | 0.198 | yes | 0.769 | 0.260 | no | 1.138 | 0.552 | no | 0.600 | 0.204 | yes | 0.741 | 0.222 | yes | 0.906 | 0.235 | no |
| DR1207 | Fusion cell cycle protein MesJ and cytosine deaminase | 1.672 | 0.829 | no | 1.202 | 0.636 | no | 1.412 | 0.897 | no | 2.246 | 1.278 | yes | 2.111 | 1.416 | yes | 1.417 | 0.519 | no | 0.857 | 0.243 | no | 0.795 | 0.186 | no | 0.628 | 0.142 | yes |
| DR1208 | Thioredoxin fold protein, BCP-like | 1.277 | 0.415 | no | 1.152 | 0.473 | no | 2.314 | 1.501 | yes | 2.018 | 0.241 | yes | 2.007 | 0.760 | yes | 1.664 | 0.649 | yes | 1.275 | 0.217 | no | 1.338 | 0.425 | no | 0.672 | 0.297 | yes |
| DR1209 | Thioredoxin fold protein, BCP-like | 1.317 | 0.500 | no | 1.215 | 0.322 | no | 1.119 | 0.602 | no | 0.799 | 0.248 | no | 0.749 | 0.229 | no | 0.876 | 0.173 | no | 0.970 | 0.219 | no | 0.916 | 0.200 | no | 0.883 | 0.219 | no |
| DR1210 | Predicted protein | 0.918 | 0.116 | no | 0.729 | 0.127 | no | 0.560 | 0.222 | yes | 0.635 | 0.261 | yes | 0.718 | 0.383 | yes | 0.958 | 0.492 | no | 0.603 | 0.219 | yes | 0.656 | 0.127 | yes | 0.591 | 0.131 | yes |
| DR1211 | Predicted protein | 1.103 | 0.141 | no | 1.314 | 0.810 | no | 1.392 | 0.371 | no | 1.017 | 0.139 | no | 1.228 | 0.650 | no | 0.923 | 0.145 | no | 0.869 | 0.100 | no | 0.955 | 0.094 | no | 0.821 | 0.192 | no |
| DR1212 | Predicted protein | 0.806 | 0.295 | no | 0.856 | 0.417 | no | 0.500 | 0.297 | yes | 0.599 | 0.294 | yes | 0.885 | 0.438 | no | 0.924 | 0.422 | no | 1.284 | 0.536 | no | 1.901 | 0.467 | yes | 2.511 | 1.447 | yes |
| DR1213 | PKN2 type protein serine threonine kinase | 1.367 | 0.535 | no | 1.349 | 0.661 | no | 1.730 | 1.188 | yes | 1.684 | 0.888 | no | 1.078 | 0.392 | no | 0.898 | 0.356 | no | 1.033 | 0.637 | no | 0.839 | 0.174 | no | 0.806 | 0.261 | no |
| DR1214 | Acetyl-CoA carboxylase alpha subunit, ACCA | 0.830 | 0.298 | no | 0.675 | 0.253 | yes | 0.776 | 0.239 | no | 0.618 | 0.211 | yes | 0.656 | 0.221 | yes | 0.905 | 0.360 | no | 0.968 | 0.492 | no | 1.010 | 0.255 | no | 0.869 | 0.222 | no |
| DR1215 | Acetyl-CoA carboxylase beta subunit, ACCD | 1.091 | 0.524 | no | 0.750 | 0.345 | no | 0.465 | 0.099 | yes | 0.558 | 0.132 | yes | 0.636 | 0.328 | yes | 0.554 | 0.113 | yes | 0.551 | 0.217 | yes | 0.680 | 0.212 | yes | 0.811 | 0.106 | no |
| DR1216 | Predicted protein | 0.984 | 0.231 | no | 1.551 | 0.670 | yes | 1.926 | 0.748 | yes | 1.368 | 0.378 | no | 1.496 | 0.413 | no | 1.475 | 0.461 | no | 1.236 | 0.264 | no | 0.961 | 0.222 | no | 1.104 | 0.179 | no |
| DR1217 | HTH transcriptional regulator | 1.068 | 0.328 | no | 1.465 | 0.370 | yes | 1.514 | 0.392 | yes | 1.826 | 0.354 | yes | 1.451 | 0.493 | no | 0.986 | 0.199 | no | 0.922 | 0.288 | no | 0.908 | 0.107 | no | 1.301 | 0.241 | no |
| DR1218 | Predicted protein | 0.687 | 0.261 | yes | 0.763 | 0.301 | no | 0.690 | 0.240 | no | 0.545 | 0.229 | yes | 0.519 | 0.143 | yes | 0.530 | 0.216 | yes | 0.498 | 0.234 | yes | 0.587 | 0.093 | yes | 0.681 | 0.227 | no |
| DR1219 | FeoB, ferrous iron transport protein B, GTPase | 0.743 | 0.435 | yes | 0.864 | 0.568 | no | 1.027 | 0.488 | no | 0.537 | 0.395 | yes | 0.297 | 0.205 | yes | 0.350 | 0.115 | yes | 0.330 | 0.228 | yes | 0.362 | 0.048 | yes | 0.437 | 0.089 | yes |
| DR1220 | HTH repressor FeoA | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR1221 | Predicted protein | 0.774 | 0.222 | no | 1.388 | 0.658 | no | 1.350 | 0.481 | no | 0.976 | 0.445 | no | 1.253 | 0.546 | no | 1.269 | 0.479 | no | 1.003 | 0.612 | no | 0.807 | 0.248 | no | 0.604 | 0.217 | yes |
| DR1222 | Acetyl-xylan esterase, NODB-like deacetylase | 1.347 | 0.604 | no | 1.274 | 0.593 | no | 2.302 | 1.106 | yes | 2.040 | 1.371 | yes | 0.794 | 0.361 | no | 1.147 | 0.414 | no | 0.926 | 0.349 | no | 0.868 | 0.219 | no | 0.774 | 0.399 | no |
| DR1223 | Permease MDR-type | 0.909 | 0.205 | no | 1.328 | 0.536 | no | 1.685 | 0.502 | yes | 1.430 | 0.088 | no | 1.371 | 0.540 | no | 0.997 | 0.318 | no | 0.980 | 0.233 | no | 0.763 | 0.116 | no | 0.611 | 0.299 | yes |
| DR1224 | (FRAME SHIFT?) Glycosyltransferase | 1.064 | 0.520 | no | 0.631 | 0.159 | yes | 0.640 | 0.368 | yes | 0.724 | 0.202 | no | 0.703 | 0.312 | yes | 0.972 | 0.448 | no | 1.164 | 0.551 | no | 1.143 | 0.314 | no | 1.317 | 0.315 | no |
| DR1225 | Glycosyltransferase | 0.684 | 0.218 | no | 0.686 | 0.156 | no | 0.667 | 0.311 | yes | 0.644 | 0.269 | yes | 0.730 | 0.187 | no | 0.720 | 0.219 | no | 1.112 | 0.268 | no | 1.155 | 0.389 | no | 0.802 | 0.103 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR1226 | Acetyl-xylan esterase, NODB-like deacetylase | 0.962 | 0.240 | no | 0.717 | 0.389 | yes | 0.622 | 0.147 | yes | 0.750 | 0.215 | no | 0.920 | 0.495 | no | 0.894 | 0.285 | no | 0.981 | 0.317 | no | 1.121 | 0.114 | no | 1.621 | 0.459 | yes |
| DR1227 | Sensor histidine kinase + PAS domain, related to sensor DEGS of B.subtilis | 1.305 | 0.672 | no | 0.964 | 0.435 | no | 1.025 | 0.315 | no | 0.813 | 0.083 | no | 0.906 | 0.318 | no | 0.875 | 0.337 | no | 0.683 | 0.160 | yes | 0.806 | 0.158 | no | 0.776 | 0.214 | no |
| DR1228 | Predicted protein | 1.192 | 0.406 | no | 0.807 | 0.251 | no | 0.699 | 0.231 | yes | 0.662 | 0.046 | no | 0.815 | 0.204 | no | 0.819 | 0.218 | no | 0.758 | 0.237 | no | 1.054 | 0.335 | no | 1.519 | 0.671 | no |
| DR1229 | Predicted protein | 1.190 | 0.299 | no | 1.240 | 0.439 | no | 1.048 | 0.411 | no | 1.096 | 0.550 | no | 0.872 | 0.159 | no | 0.790 | 0.343 | no | 1.037 | 0.278 | no | 1.051 | 0.290 | no | 1.058 | 0.554 | no |
| DR1230 | Predicted protein | 0.934 | 0.195 | no | 0.540 | 0.199 | yes | 0.672 | 0.278 | yes | 0.817 | 0.120 | no | 0.815 | 0.230 | no | 0.607 | 0.098 | yes | 0.561 | 0.108 | yes | 0.770 | 0.050 | no | 1.131 | 0.347 | no |
| DR1231 | Predicted protein | 0.671 | 0.103 | no | 0.401 | 0.139 | yes | 0.450 | 0.079 | yes | 0.529 | 0.219 | yes | 0.781 | 0.461 | no | 0.785 | 0.552 | no | 0.559 | 0.261 | yes | 0.678 | 0.233 | yes | 1.998 | 0.670 | yes |
| DR1232 | Pilin IV like secreted protein | 1.097 | 0.330 | no | 0.861 | 0.264 | no | 1.432 | 0.338 | no | 1.500 | 0.285 | no | 2.277 | 1.124 | yes | 1.493 | 0.689 | no | 0.928 | 0.176 | no | 1.146 | 0.245 | no | 1.688 | 0.496 | yes |
| DR1233 | Pilin IV like secreted protein | 0.881 | 0.234 | no | 0.787 | 0.187 | no | 1.724 | 0.894 | yes | 1.926 | 0.425 | yes | 2.221 | 0.634 | yes | 1.324 | 0.621 | no | 0.904 | 0.232 | no | 1.031 | 0.161 | no | 1.676 | 0.781 | yes |
| DR1234 | Pilin IV like secreted protein | 1.266 | 0.230 | no | 1.079 | 0.239 | no | 1.473 | 0.333 | yes | 1.719 | 0.329 | yes | 2.336 | 1.722 | yes | 1.298 | 0.307 | no | 0.976 | 0.345 | no | 0.851 | 0.252 | no | 1.560 | 0.519 | no |
| DR1235 | GTPase with low complexity tail | 0.911 | 0.189 | no | 0.638 | 0.143 | yes | 0.600 | 0.113 | yes | 0.551 | 0.120 | yes | 0.591 | 0.171 | yes | 1.020 | 0.699 | no | 0.679 | 0.187 | yes | 0.900 | 0.228 | no | 1.004 | 0.121 | no |
| DR1236 | Membrane transporter | 0.858 | 0.119 | no | 1.389 | 0.233 | no | 2.187 | 0.371 | yes | 2.427 | 0.429 | yes | 2.193 | 0.996 | yes | 1.500 | 0.677 | no | 1.020 | 0.210 | no | 0.905 | 0.199 | no | 0.864 | 0.227 | no |
| DR1237 | Uncharacterized protein, homolog | 0.902 | 0.247 | no | 0.874 | 0.246 | no | 0.897 | 0.490 | no | 0.928 | 0.511 | no | 0.822 | 0.316 | no | 0.772 | 0.223 | no | 0.589 | 0.050 | yes | 0.706 | 0.115 | yes | 0.561 | 0.129 | yes |
| DR1238 | Homocitrate synthase, HOSM | 0.890 | 0.302 | no | 1.265 | 0.426 | no | 1.209 | 0.436 | no | 1.187 | 0.085 | no | 1.216 | 0.092 | no | 1.171 | 0.434 | no | 1.079 | 0.210 | no | 0.992 | 0.325 | no | 0.844 | 0.239 | no |
| DR1239 | MaoC Oxidase subunit | 0.908 | 0.285 | no | 0.823 | 0.276 | no | 0.638 | 0.163 | yes | 0.692 | 0.003 | no | 0.695 | 0.245 | yes | 0.624 | 0.161 | yes | 1.214 | 0.524 | no | 1.353 | 0.254 | no | 1.571 | 0.840 | yes |
| DR1240 | Citrate lyase beta subunit, CILB | 0.785 | 0.113 | no | 0.736 | 0.125 | no | 0.632 | 0.227 | yes | 0.595 | 0.083 | yes | 0.476 | 0.108 | yes | 0.513 | 0.084 | yes | 0.617 | 0.194 | yes | 0.984 | 0.109 | no | 0.942 | 0.204 | no |
| DR1241 | Predicted protein | 1.172 | 0.438 | no | 2.024 | 1.154 | yes | 2.193 | 0.302 | yes | 1.799 | 0.482 | yes | 1.662 | 0.474 | yes | 1.439 | 0.288 | no | 1.300 | 0.342 | no | 0.821 | 0.133 | no | 0.785 | 0.321 | no |
| DR1242 | Predicted protein | 1.208 | 0.247 | no | 1.540 | 0.534 | yes | 1.205 | 0.560 | no | 1.000 | 0.431 | no | 1.062 | 0.345 | no | 1.127 | 0.487 | no | 1.319 | 0.542 | no | 1.241 | 0.274 | no | 1.637 | 0.981 | yes |
| DR1243 | PKN2 type protein serine threonine kinase | 0.948 | 0.291 | no | 0.916 | 0.399 | no | 0.499 | 0.247 | yes | 0.450 | 0.134 | yes | 0.659 | 0.237 | yes | 0.699 | 0.163 | no | 0.989 | 0.282 | no | 0.995 | 0.162 | no | 0.891 | 0.253 | no |
| DR1244 | Uncharacterized protein | 0.821 | 0.179 | no | 1.968 | 0.398 | yes | 1.910 | 0.689 | yes | 1.587 | 0.217 | no | 1.247 | 0.363 | no | 0.799 | 0.180 | no | 0.928 | 0.326 | no | 0.796 | 0.169 | no | 0.542 | 0.137 | yes |
| DR1245 | Predicted protein | 0.738 | 0.324 | no | 0.784 | 0.251 | no | 0.878 | 0.349 | no | 0.593 | 0.184 | yes | 0.988 | 0.551 | no | 0.947 | 0.534 | no | 1.021 | 0.383 | no | 0.856 | 0.169 | no | 1.692 | 0.544 | yes |
| DR1246 | Aminopeptidase/prolidase family, PEPO | 0.784 | 0.181 | no | 0.924 | 0.180 | no | 1.031 | 0.372 | no | 0.785 | 0.181 | no | 0.833 | 0.141 | no | 0.797 | 0.190 | no | 0.940 | 0.308 | no | 0.902 | 0.158 | no | 1.092 | 0.443 | no |
| DR1247 | Succinyl-CoA synthetase, beta chain SUCC | 1.101 | 0.421 | no | 1.120 | 0.459 | no | 1.614 | 0.805 | yes | 2.183 | 0.482 | yes | 1.774 | 0.611 | yes | 2.227 | 0.969 | yes | 1.894 | 0.464 | yes | 1.953 | 0.698 | yes | 1.081 | 0.140 | no |
| DR1248 | Succinyl CoA synthetase, alpha chain SUCD | 1.305 | 0.413 | no | 1.126 | 0.483 | no | 1.742 | 0.791 | yes | 1.913 | 0.687 | yes | 1.756 | 0.882 | yes | 2.006 | 0.756 | yes | 1.851 | 0.575 | yes | 1.925 | 0.655 | yes | 0.811 | 0.401 | no |
| DR1249 | Predicted protein | 1.158 | 0.566 | no | 1.134 | 0.406 | no | 1.039 | 0.292 | no | 0.746 | 0.182 | no | 0.776 | 0.215 | no | 0.793 | 0.162 | no | 0.746 | 0.324 | no | 0.658 | 0.094 | yes | 0.508 | 0.075 | yes |
| DR1250 | Predicted protein | 1.138 | 0.411 | no | 0.630 | 0.153 | yes | 0.483 | 0.219 | yes | 0.710 | 0.155 | no | 0.643 | 0.229 | yes | 0.705 | 0.250 | no | 0.682 | 0.226 | yes | 0.835 | 0.050 | no | 0.845 | 0.415 | no |
| DR1251 | Predicted protein | 0.952 | 0.273 | no | 0.707 | 0.213 | no | 0.583 | 0.204 | yes | 0.483 | 0.126 | yes | 0.622 | 0.188 | yes | 0.948 | 0.544 | no | 0.890 | 0.298 | no | 1.058 | 0.211 | no | 1.416 | 0.249 | no |
| DR1252 | Rossman fold oxidoreductase | 1.069 | 0.517 | no | 0.698 | 0.398 | yes | 0.877 | 0.507 | no | 0.749 | 0.149 | no | 0.925 | 0.335 | no | 1.262 | 0.786 | no | 1.052 | 0.485 | no | 1.354 | 0.288 | no | 1.944 | 0.452 | yes |
| DR1253 | Predicted protein | 0.763 | 0.291 | no | 0.817 | 0.330 | no | 0.615 | 0.199 | yes | 0.712 | 0.522 | yes | 0.586 | 0.255 | yes | 0.809 | 0.475 | no | 0.491 | 0.200 | yes | 0.603 | 0.125 | yes | 0.775 | 0.256 | no |
| DR1254 | Predicted protein | 1.106 | 0.235 | no | 1.120 | 0.420 | no | 0.890 | 0.386 | no | 0.759 | 0.227 | no | 0.873 | 0.492 | no | 1.106 | 0.469 | no | 0.895 | 0.333 | no | 0.814 | 0.211 | no | 1.102 | 0.169 | no |
| DR1255 | Acyl-COA dehydrogenase, ACDB | 0.758 | 0.291 | no | 0.453 | 0.132 | yes | 0.432 | 0.179 | yes | 0.380 | 0.040 | yes | 0.627 | 0.235 | yes | 0.579 | 0.197 | yes | 0.614 | 0.162 | yes | 0.838 | 0.188 | no | 0.755 | 0.203 | no |
| DR1256 | Predicted protein | 1.398 | 0.521 | no | 1.120 | 0.322 | no | 1.299 | 0.373 | no | 1.664 | 0.193 | yes | 1.671 | 0.696 | yes | 1.058 | 0.274 | no | 1.031 | 0.278 | no | 0.955 | 0.195 | no | 1.174 | 0.230 | no |
| DR1257 | Dehydrogenase, beta propeller protein | 0.889 | 0.387 | no | 0.428 | 0.265 | yes | 0.283 | 0.088 | yes | 0.261 | 0.107 | yes | 0.466 | 0.089 | yes | 0.594 | 0.226 | yes | 0.729 | 0.238 | no | 0.713 | 0.139 | yes | 0.651 | 0.240 | yes |
| DR1258 | Snf2/Swi2 family Helicase | 0.864 | 0.166 | no | 0.508 | 0.134 | yes | 0.481 | 0.172 | yes | 0.715 | 0.188 | no | 0.642 | 0.381 | yes | 0.549 | 0.222 | yes | 0.455 | 0.164 | yes | 0.522 | 0.145 | yes | 0.712 | 0.246 | no |
| DR1259 | Snf2/Swi2 family Helicase | 0.965 | 0.274 | no | 0.911 | 0.317 | no | 1.394 | 0.681 | no | 1.240 | 0.539 | no | 1.282 | 0.392 | no | 0.901 | 0.313 | no | 0.775 | 0.205 | no | 0.920 | 0.098 | no | 0.843 | 0.082 | no |
| DR1260 | Calcineurin like phosphoesterase, archaeal type | 0.821 | 0.249 | no | 0.794 | 0.386 | no | 1.363 | 0.573 | no | 1.168 | 0.352 | no | 1.670 | 0.674 | yes | 1.243 | 0.354 | no | 1.082 | 0.276 | no | 1.099 | 0.060 | no | 1.343 | 0.158 | no |
| DR1261 | Conserved histidine rich protein | 0.910 | 0.323 | no | 0.443 | 0.181 | yes | 2.203 | 1.101 | yes | 3.098 | 1.009 | yes | 3.718 | 1.554 | yes | 2.579 | 0.927 | yes | 3.671 | 2.406 | yes | 4.107 | 1.789 | yes | 3.511 | 1.150 | yes |
| DR1262 | Ro-like RNA binding protein | 1.361 | 0.259 | no | 0.814 | 0.290 | no | 0.957 | 0.380 | no | 1.234 | 0.284 | no | 1.086 | 0.434 | no | 1.090 | 0.370 | no | 1.207 | 0.564 | no | 1.235 | 0.323 | no | 1.022 | 0.297 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR1263 | Protein of uncharacterized conserved family predominantly in C elegans, YBIA_ECOLI in E coli | 0.951 | 0.419 | no | 2.549 | 1.138 | yes | 7.817 | 2.968 | yes | 7.206 | 2.773 | yes | 7.010 | 3.590 | yes | 5.655 | 2.604 | yes | 14.711 | 8.520 | yes | 7.257 | 1.885 | yes | 6.844 | 3.939 | yes |
| DR1264 | Predicted protein | 1.028 | 0.195 | no | 1.181 | 0.154 | no | 4.423 | 2.538 | yes | 3.982 | 2.540 | yes | 4.560 | 1.596 | yes | 3.587 | 2.416 | yes | 9.634 | 5.733 | yes | 4.118 | 1.959 | yes | 4.988 | 3.084 | yes |
| DR1265 | NH2-acetyltransferase | 1.109 | 0.376 | no | 1.030 | 0.254 | no | 1.393 | 0.771 | no | 0.773 | 0.117 | no | 1.285 | 0.616 | no | 0.977 | 0.334 | no | 0.831 | 0.226 | no | 0.908 | 0.101 | no | 0.844 | 0.104 | no |
| DR1266 | Prolyl-tRNA synthetase Borrelia burgdorferi) | 0.902 | 0.256 | no | 0.807 | 0.219 | no | 1.448 | 0.253 | yes | 1.296 | 0.077 | no | 1.538 | 0.513 | no | 1.417 | 0.242 | no | 1.114 | 0.301 | no | 1.289 | 0.315 | no | 1.416 | 0.171 | no |
| DR1267 | Distantly related to TPR repeats proteins | 1.358 | 0.489 | no | 0.950 | 0.283 | no | 0.764 | 0.174 | no | 0.715 | 0.235 | no | 0.856 | 0.253 | no | 0.879 | 0.258 | no | 0.825 | 0.264 | no | 0.891 | 0.116 | no | 1.125 | 0.207 | no |
| DR1268 | YfiT-like metal-binding protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR1269 | Predicted protein | 0.914 | 0.139 | no | 0.683 | 0.162 | yes | 0.899 | 0.300 | no | 0.955 | 0.116 | no | 1.132 | 0.300 | no | 1.038 | 0.214 | no | 1.045 | 0.207 | no | 1.030 | 0.188 | no | 0.956 | 0.289 | no |
| DR1271 | Distantly related to NAD(P)H-flavin | 0.952 | 0.463 | no | 0.668 | 0.225 | yes | 1.091 | 0.291 | no | 0.697 | 0.115 | no | 0.909 | 0.200 | no | 0.898 | 0.124 | no | 1.019 | 0.169 | no | 0.993 | 0.099 | no | 1.223 | 0.245 | no |
| DR1272 | Membrane protein? | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR1273 | Membrane protein, homolog | 1.237 | 0.283 | no | 1.411 | 0.515 | no | 1.337 | 0.487 | no | 1.268 | 0.313 | no | 1.115 | 0.357 | no | 1.229 | 0.462 | no | 1.183 | 0.362 | no | 1.037 | 0.123 | no | 0.974 | 0.164 | no |
| DR1274 | RUVA, Holliday junction helicase | 0.949 | 0.360 | no | 0.898 | 0.191 | no | 1.396 | 0.878 | no | 0.778 | 0.078 | no | 0.835 | 0.117 | no | 0.838 | 0.076 | no | 0.965 | 0.365 | no | 0.852 | 0.107 | no | 0.941 | 0.229 | no |
| DR1275 | Glutamyl-tRNA(Gln) amidotransferase subunit C | 1.191 | 0.683 | no | 0.566 | 0.267 | yes | 0.894 | 0.402 | no | 1.385 | 0.273 | no | 1.392 | 0.483 | no | 1.006 | 0.404 | no | 1.134 | 0.370 | no | 1.461 | 0.548 | no | 1.110 | 0.397 | no |
| DR1276 | Seryl tRNA Synthetase | 0.668 | 0.276 | yes | 0.336 | 0.134 | yes | 0.244 | 0.101 | yes | 0.288 | 0.108 | yes | 0.414 | 0.152 | yes | 0.601 | 0.187 | yes | 0.576 | 0.278 | yes | 0.802 | 0.294 | no | 1.506 | 0.305 | yes |
| DR1277 | Periplasmic substrate-binding protein | 0.973 | 0.166 | no | 1.018 | 0.272 | no | 1.766 | 0.728 | yes | 2.533 | 1.228 | yes | 3.077 | 1.195 | yes | 2.654 | 1.367 | yes | 2.053 | 0.821 | yes | 1.882 | 0.434 | yes | 4.942 | 2.048 | yes |
| DR1278 | Homoserine dehydrogenase, DHOM | 0.995 | 0.400 | no | 0.695 | 0.152 | no | 0.585 | 0.259 | yes | 0.621 | 0.133 | yes | 0.790 | 0.193 | no | 0.814 | 0.186 | no | 1.006 | 0.342 | no | 1.001 | 0.209 | no | 1.185 | 0.241 | no |
| DR1279 | Superoxide dismutase (Mn), SODM | 1.241 | 0.441 | no | 0.816 | 0.325 | no | 0.887 | 0.317 | no | 1.028 | 0.511 | no | 1.240 | 0.748 | no | 1.456 | 0.537 | no | 1.621 | 0.576 | yes | 2.174 | 0.455 | yes | 3.915 | 1.431 | yes |
| DR1280 | Predicted protein | 1.276 | 0.454 | no | 1.244 | 0.340 | no | 1.062 | 0.353 | no | 1.246 | 0.453 | no | 1.274 | 0.408 | no | 1.157 | 0.313 | no | 1.012 | 0.425 | no | 1.092 | 0.281 | no | 1.019 | 0.351 | no |
| DR1281 | Calcineurin like phosphatase superfamily | 0.906 | 0.242 | no | 0.847 | 0.214 | no | 0.945 | 0.213 | no | 0.948 | 0.196 | no | 0.960 | 0.296 | no | 0.985 | 0.226 | no | 0.868 | 0.208 | no | 1.071 | 0.327 | no | 1.185 | 0.334 | no |
| DR1282 | Predicted protein | 0.874 | 0.232 | no | 0.800 | 0.295 | no | 0.859 | 0.457 | no | 0.548 | 0.183 | yes | 0.997 | 0.258 | no | 0.870 | 0.162 | no | 0.893 | 0.208 | no | 0.801 | 0.203 | no | 0.937 | 0.292 | no |
| DR1283 | Phosphoenolpyruvate carboxylase, CAPP | 1.053 | 0.306 | no | 0.986 | 0.257 | no | 1.091 | 0.392 | no | 0.986 | 0.396 | no | 1.103 | 0.297 | no | 1.035 | 0.295 | no | 0.927 | 0.365 | no | 1.072 | 0.171 | no | 1.303 | 0.251 | no |
| DR1284 | Transposon ORF | 1.479 | 0.952 | no | 1.211 | 0.402 | no | 1.076 | 0.752 | no | 0.772 | 0.210 | no | 0.816 | 0.247 | no | 0.669 | 0.145 | yes | 0.679 | 0.180 | no | 0.475 | 0.040 | yes | 0.662 | 0.258 | yes |
| DR1285 | Transposon DORF | 2.031 | 0.491 | yes | 1.656 | 0.449 | yes | 2.232 | 1.437 | yes | 1.676 | 0.242 | yes | 1.532 | 0.585 | no | 1.026 | 0.404 | no | 1.039 | 0.550 | no | 1.055 | 0.312 | no | 0.915 | 0.190 | no |
| DR1286 | Predicted protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR1287 | Uncharacterized protein, E.coli YCEI ortholog | 1.242 | 0.350 | no | 2.743 | 1.014 | yes | 3.236 | 1.045 | yes | 2.522 | 0.697 | yes | 2.070 | 0.247 | yes | 1.309 | 0.331 | no | 0.776 | 0.239 | no | 0.800 | 0.090 | no | 0.788 | 0.237 | no |
| DR1288 | Predicted protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR1289 | RecQ- SF2 helicase; C-terminal Cysteine rich domain + triplicated HRD domain | 1.067 | 0.310 | no | 1.192 | 0.770 | no | 1.155 | 0.716 | no | 1.765 | 0.866 | yes | 1.016 | 0.382 | no | 0.799 | 0.318 | no | 0.785 | 0.188 | no | 0.707 | 0.212 | yes | 0.686 | 0.246 | no |
| DR1290 | Periplasmic peptide binding protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR1291 | D-3-phosphoglycerate dehydrogenase, SERA | 0.776 | 0.179 | no | 0.585 | 0.274 | yes | 0.672 | 0.256 | yes | 0.906 | 0.225 | no | 1.059 | 0.491 | no | 0.849 | 0.400 | no | 0.772 | 0.280 | no | 0.693 | 0.154 | yes | 1.245 | 0.355 | no |
| DR1292 | Molybdenum cofactor biosynthesis protein B, MoaB protein | 1.080 | 0.260 | no | 0.981 | 0.151 | no | 1.033 | 0.194 | no | 0.900 | 0.203 | no | 0.964 | 0.217 | no | 0.938 | 0.320 | no | 0.945 | 0.396 | no | 1.061 | 0.274 | no | 1.221 | 0.139 | no |
| DR1293 | Predicted protein | 1.017 | 0.532 | no | 2.331 | 1.025 | yes | 2.812 | 1.038 | yes | 2.604 | 0.544 | yes | 2.469 | 0.513 | yes | 2.505 | 0.690 | yes | 2.426 | 0.953 | yes | 2.320 | 0.592 | yes | 1.909 | 0.792 | yes |
| DR1294 | Ribosomal protein S16 | 1.252 | 0.294 | no | 0.876 | 0.227 | no | 0.762 | 0.180 | no | 1.012 | 0.120 | no | 1.006 | 0.291 | no | 0.854 | 0.272 | no | 0.835 | 0.268 | no | 0.875 | 0.183 | no | 1.143 | 0.292 | no |
| DR1295 | Conserved membrane protein | 0.881 | 0.226 | no | 1.260 | 0.538 | no | 1.195 | 0.261 | no | 0.733 | 0.110 | no | 0.954 | 0.204 | no | 0.996 | 0.228 | no | 1.030 | 0.289 | no | 1.042 | 0.300 | no | 0.912 | 0.066 | no |
| DR1296 | Transposase | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR1297 | Conserved membrane protein | 1.260 | 0.210 | no | 1.943 | 0.761 | yes | 1.565 | 0.498 | yes | 1.175 | 0.258 | no | 1.159 | 0.369 | no | 0.883 | 0.298 | no | 0.947 | 0.204 | no | 0.845 | 0.146 | no | 0.759 | 0.157 | no |
| DR1298 | Biotin synthase/ P-methylase like metal cluster enzyme | 0.627 | 0.106 | yes | 1.009 | 0.316 | no | 0.780 | 0.258 | no | 0.595 | 0.057 | yes | 0.914 | 0.548 | no | 0.398 | 0.116 | yes | 0.536 | 0.223 | yes | 0.454 | 0.115 | yes | 0.512 | 0.158 | yes |
| DR1299 | Predicted protein | 1.076 | 0.407 | no | 0.984 | 0.184 | no | 0.700 | 0.180 | no | 0.426 | 0.137 | yes | 0.410 | 0.101 | yes | 0.369 | 0.179 | yes | 0.330 | 0.113 | yes | 0.457 | 0.186 | yes | 0.785 | 0.218 | no |
| DR1300 | Cytochrome C-type biogenesis protein CCDA | 0.837 | 0.270 | no | 0.920 | 0.250 | no | 0.744 | 0.116 | no | 0.558 | 0.222 | yes | 0.568 | 0.377 | yes | 0.461 | 0.169 | yes | 0.668 | 0.330 | yes | 0.593 | 0.079 | yes | 0.620 | 0.042 | yes |
| DR1301 | Predicted protein | 1.228 | 0.380 | no | 1.426 | 0.881 | no | 1.357 | 0.381 | no | 1.260 | 0.508 | no | 1.326 | 0.437 | no | 1.348 | 0.889 | no | 1.282 | 0.879 | no | 0.886 | 0.119 | no | 0.834 | 0.138 | no |
| DR1302 | ABC-typr polyamine transporter, ATPase | 0.919 | 0.292 | no | 1.182 | 0.115 | no | 0.991 | 0.238 | no | 0.639 | 0.073 | no | 0.759 | 0.187 | no | 0.922 | 0.229 | no | 0.725 | 0.381 | yes | 0.841 | 0.320 | no | 0.929 | 0.113 | no |
| DR1303 | Polyamine transport membrane component | 1.081 | 0.169 | no | 1.388 | 0.357 | no | 1.299 | 0.191 | no | 1.064 | 0.040 | no | 1.119 | 0.270 | no | 1.075 | 0.176 | no | 0.993 | 0.336 | no | 0.992 | 0.225 | no | 1.009 | 0.255 | no |
| DR1304 | Polyamine transport membrane component | 0.839 | 0.068 | no | 1.673 | 0.670 | yes | 1.684 | 0.297 | yes | 1.551 | 0.380 | no | 1.437 | 0.380 | no | 1.451 | 0.369 | no | 1.521 | 0.403 | yes | 1.118 | 0.069 | no | 1.083 | 0.226 | no |
| DR1305 | Polyamine binding periplasmic protein | 1.140 | 0.254 | no | 1.323 | 0.311 | no | 1.232 | 0.491 | no | 1.156 | 0.258 | no | 1.045 | 0.356 | no | 0.875 | 0.180 | no | 1.152 | 0.382 | no | 1.246 | 0.241 | no | 1.329 | 0.246 | no |
| DR1306 | Predicted protein | 0.851 | 0.315 | no | 0.484 | 0.245 | yes | 0.409 | 0.133 | yes | 0.367 | 0.035 | yes | 0.558 | 0.302 | yes | 0.744 | 0.416 | yes | 1.254 | 0.697 | no | 1.595 | 0.375 | yes | 1.409 | 0.349 | no |
| DR1307 | Membrane transporter | 1.163 | 0.302 | no | 1.928 | 0.491 | yes | 2.566 | 0.824 | yes | 2.309 | 0.447 | yes | 2.479 | 0.853 | yes | 2.025 | 0.816 | yes | 1.573 | 0.728 | yes | 1.464 | 0.485 | no | 1.426 | 0.483 | no |
| DR1308 | Tail specific protease (C-terminal fragment) | 0.576 | 0.172 | yes | 0.743 | 0.398 | no | 0.616 | 0.111 | yes | 0.676 | 0.124 | no | 0.839 | 0.534 | no | 0.907 | 0.549 | no | 0.439 | 0.263 | yes | 1.108 | 0.110 | no | n/a | n/a | n/a |
| DR1309 | Ribosomal protein S20 | 0.997 | 0.365 | no | 1.494 | 0.517 | yes | 2.906 | 0.984 | yes | 3.308 | 1.269 | yes | 3.121 | 1.435 | yes | 2.284 | 1.112 | yes | 1.609 | 0.527 | yes | 1.349 | 0.307 | no | 1.104 | 0.195 | no |
| DR1310 | RecX regulatory protein | 0.920 | 0.327 | no | 0.915 | 0.266 | no | 0.671 | 0.178 | yes | 0.598 | 0.113 | no | 1.284 | 0.728 | no | 0.904 | 0.226 | no | 0.961 | 0.236 | no | 0.722 | 0.182 | yes | 0.952 | 0.391 | no |
| DR1311 | Methionine aminopeptidase, AMP | 0.994 | 0.302 | no | 0.486 | 0.277 | yes | 0.285 | 0.098 | yes | 0.211 | 0.034 | yes | 0.358 | 0.158 | yes | 0.439 | 0.197 | yes | 0.455 | 0.162 | yes | 0.565 | 0.107 | yes | 0.788 | 0.253 | no |
| DR1312 | Nuclease McrA superfamily | 0.710 | 0.363 | no | 1.273 | 0.823 | no | 1.245 | 0.475 | no | 0.979 | 0.042 | no | 1.878 | 1.118 | yes | 2.591 | 1.597 | yes | 1.271 | 0.769 | no | 0.973 | 0.095 | no | 1.076 | 0.523 | no |
| DR1313 | L-allo-threonine aldolase, LTAA | 1.027 | 0.273 | no | 0.627 | 0.403 | yes | 0.357 | 0.132 | yes | 0.504 | 0.098 | yes | 0.620 | 0.147 | yes | 0.975 | 0.466 | no | 0.852 | 0.178 | no | 1.035 | 0.309 | no | 1.293 | 0.224 | no |
| DR1314 | Uncharacterized proteins, ysnf-like repeats | 0.889 | 0.383 | no | 0.234 | 0.078 | yes | 0.174 | 0.062 | yes | 0.388 | 0.176 | yes | 0.897 | 0.449 | no | 0.996 | 0.411 | no | 1.671 | 1.190 | no | 2.038 | 0.572 | yes | 2.417 | 1.217 | yes |
| DR1315 | Uncharacterized proteins, ysnf-like domain | 0.885 | 0.220 | no | 0.295 | 0.121 | yes | 0.357 | 0.104 | yes | 0.817 | 0.050 | no | 1.264 | 0.646 | no | 1.942 | 0.646 | yes | 2.349 | 0.802 | yes | 2.629 | 1.106 | yes | 1.362 | 0.441 | no |
| DR1316 | Propionyl-CoA carboxylase | 0.773 | 0.235 | no | 0.475 | 0.190 | yes | 0.579 | 0.228 | yes | 0.807 | 0.324 | no | 1.254 | 0.735 | no | 1.004 | 0.260 | no | 1.003 | 0.252 | no | 0.964 | 0.079 | no | 0.949 | 0.346 | no |
| DR1317 | Predicted protein | 1.385 | 0.584 | no | 0.555 | 0.219 | yes | 0.749 | 0.336 | yes | 0.922 | 0.442 | no | 1.178 | 0.427 | no | 1.616 | 0.686 | yes | 2.232 | 0.540 | yes | 3.949 | 0.575 | yes | 2.912 | 0.212 | yes |
| DR1318 | Branched-chain enoyl CoA reductase | 1.151 | 0.473 | no | 1.133 | 0.436 | no | 1.014 | 0.657 | no | 1.266 | 0.539 | no | 1.515 | 1.087 | no | 1.426 | 0.739 | no | 1.738 | 0.540 | yes | 2.376 | 0.238 | yes | 2.957 | 1.285 | yes |
| DR1319 | Predicted protein | 0.898 | 0.302 | no | 1.578 | 0.867 | yes | 2.150 | 1.341 | yes | 1.893 | 0.897 | yes | 1.926 | 0.854 | yes | 1.356 | 0.884 | no | 0.912 | 0.572 | no | 0.692 | 0.047 | yes | 0.433 | 0.154 | yes |
| DR1320 | Predicted protein | 1.151 | 0.719 | no | 1.773 | 1.037 | yes | 1.650 | 1.092 | yes | 2.426 | 0.277 | yes | 1.557 | 1.129 | no | 0.648 | 0.418 | yes | 0.915 | 0.469 | no | 0.977 | 0.220 | no | 0.812 | 0.233 | no |
| DR1321 | Signal peptidase I | 1.002 | 0.350 | no | 1.151 | 0.477 | no | 1.044 | 0.336 | no | 0.698 | 0.052 | no | 1.154 | 0.507 | no | 1.072 | 0.487 | no | 0.939 | 0.323 | no | 0.807 | 0.132 | no | 0.967 | 0.293 | no |
| DR1322 | Permease MDR-type | 1.096 | 0.367 | no | 1.103 | 0.389 | no | 1.202 | 0.643 | no | 0.808 | 0.091 | no | 0.899 | 0.188 | no | 1.125 | 0.551 | no | 1.049 | 0.542 | no | 0.998 | 0.409 | no | 0.969 | 0.308 | no |
| DR1323 | TRNA pseudouridine synthase TruB | 1.084 | 0.256 | no | 0.842 | 0.272 | no | 0.863 | 0.300 | no | 0.890 | 0.104 | no | 0.845 | 0.209 | no | 0.889 | 0.427 | no | 0.759 | 0.272 | no | 0.721 | 0.202 | yes | 0.731 | 0.143 | no |
| DR1324 | Permease MDR-type | 1.005 | 0.441 | no | 1.033 | 0.236 | no | 0.969 | 0.348 | no | 0.596 | 0.044 | yes | 0.731 | 0.249 | no | 0.680 | 0.153 | no | 0.729 | 0.434 | yes | 0.906 | 0.380 | no | 0.827 | 0.311 | no |
| DR1325 | Phosphatase-associated protein PAPQ, invasin repeat | 1.357 | 0.359 | no | 1.256 | 0.333 | no | 1.419 | 0.497 | no | 1.867 | 0.634 | yes | 1.080 | 0.382 | no | 1.097 | 0.368 | no | 1.121 | 0.517 | no | 0.881 | 0.044 | no | 0.832 | 0.057 | no |
| DR1326 | A/b hydrolase | 1.090 | 0.249 | no | 0.955 | 0.262 | no | 1.293 | 0.191 | no | 1.534 | 0.397 | no | 1.385 | 0.610 | no | 1.213 | 0.553 | no | 0.980 | 0.285 | no | 1.001 | 0.390 | no | 0.755 | 0.191 | no |
| DR1327 | Permease MDR-type | 1.081 | 0.379 | no | 0.900 | 0.354 | no | 0.788 | 0.370 | no | 1.014 | 0.322 | no | 1.057 | 0.716 | no | 0.617 | 0.296 | yes | 0.797 | 0.378 | no | 0.630 | 0.212 | yes | 0.754 | 0.201 | no |
| DR1328 | Small conserved membrane protein | 0.902 | 0.254 | no | 0.746 | 0.218 | no | 0.832 | 0.363 | no | 0.678 | 0.113 | no | 0.767 | 0.193 | no | 0.690 | 0.205 | yes | 0.726 | 0.195 | no | 0.769 | 0.217 | no | 0.687 | 0.259 | no |
| DR1329 | HAD superfamily hydrolase | 0.963 | 0.407 | no | 0.822 | 0.317 | no | 0.664 | 0.237 | yes | 0.767 | 0.225 | no | 1.004 | 0.431 | no | 1.285 | 0.261 | no | 2.052 | 0.659 | yes | 2.227 | 0.463 | yes | 2.153 | 0.242 | yes |
| DR1330 | Diaminopimelate epimerase family protein, close to PHZC of Pseudomonas | 0.884 | 0.552 | no | 0.494 | 0.219 | yes | 0.423 | 0.105 | yes | 0.348 | 0.071 | yes | 0.444 | 0.112 | yes | 0.638 | 0.148 | yes | 0.809 | 0.400 | no | 0.991 | 0.477 | no | 0.899 | 0.150 | no |
| DR1331 | Predicted protein | 1.218 | 0.535 | no | 0.733 | 0.341 | yes | 0.747 | 0.290 | no | 1.306 | 0.694 | no | 1.468 | 0.704 | no | 1.984 | 1.098 | yes | 1.807 | 0.777 | yes | 1.536 | 0.215 | yes | 1.799 | 0.263 | yes |
| DR1332 | Predicted protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |

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| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR1333 | Beta-glucosidase | 0.913 | 0.366 | no | 0.295 | 0.094 | yes | 0.210 | 0.057 | yes | 0.530 | 0.023 | yes | 0.811 | 0.553 | yes | 0.839 | 0.422 | no | 1.455 | 0.751 | no | 1.759 | 0.483 | yes | 1.240 | 0.472 | no |
| DR1334 | Transposon ORF | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR1335 | Isoleucyl-tRNA Synthetase | 0.893 | 0.207 | no | 1.176 | 0.227 | no | 2.488 | 0.533 | yes | 3.240 | 0.860 | yes | 3.083 | 1.131 | yes | 2.449 | 0.927 | yes | 2.074 | 0.724 | yes | 1.876 | 0.202 | yes | 2.627 | 0.669 | yes |
| DR1336 | Membrane protein, possible transporter | 1.042 | 0.325 | no | 0.736 | 0.248 | no | 0.801 | 0.132 | no | 0.845 | 0.205 | no | 1.005 | 0.169 | no | 0.833 | 0.267 | no | 0.805 | 0.198 | no | 0.904 | 0.133 | no | 1.367 | 0.484 | no |
| DR1337 | Transaldolase, TAL | 0.879 | 0.320 | no | 0.387 | 0.179 | yes | 0.330 | 0.148 | yes | 0.252 | 0.054 | yes | 0.344 | 0.125 | yes | 0.364 | 0.199 | yes | 0.336 | 0.139 | yes | 0.418 | 0.090 | yes | 0.645 | 0.230 | yes |
| DR1338 | Transcriptional terminator Rho, F1/F0 like ATpase | 0.729 | 0.251 | no | 0.431 | 0.172 | yes | 0.385 | 0.105 | yes | 0.424 | 0.024 | yes | 0.435 | 0.219 | yes | 0.425 | 0.214 | yes | 0.421 | 0.176 | yes | 0.459 | 0.139 | yes | 0.700 | 0.359 | yes |
| DR1339 | Triose-phosphate isomerase, TPIS | 0.937 | 0.126 | no | 0.591 | 0.164 | yes | 0.361 | 0.140 | yes | 0.454 | 0.137 | yes | 0.508 | 0.085 | yes | 0.706 | 0.172 | no | 0.807 | 0.201 | no | 0.940 | 0.115 | no | 1.237 | 0.140 | no |
| DR1340 | Uncharacterized protein | 1.114 | 0.458 | no | 0.518 | 0.158 | yes | 0.330 | 0.135 | yes | 0.915 | 0.287 | no | 1.113 | 0.304 | no | 1.805 | 0.916 | yes | 2.308 | 1.029 | yes | 2.598 | 0.961 | yes | 3.390 | 1.451 | yes |
| DR1341 | Diverged aldoketomutase of glyoxalase I family | 1.094 | 0.169 | no | 0.558 | 0.193 | yes | 0.799 | 0.228 | no | 1.006 | 0.084 | no | 1.270 | 0.114 | no | 1.575 | 0.351 | yes | 1.944 | 0.626 | yes | 1.725 | 0.328 | yes | 2.028 | 0.420 | yes |
| DR1342 | Phosphoglycerate kinase, PGK | 0.878 | 0.387 | no | 0.452 | 0.222 | yes | 0.490 | 0.160 | yes | 0.628 | 0.199 | yes | 0.796 | 0.347 | no | 1.077 | 0.316 | no | 0.983 | 0.450 | no | 1.666 | 0.381 | yes | 2.607 | 0.703 | yes |
| DR1343 | Glyceraldehyde-3-phosphate dehydrogenase, G3PB | 1.033 | 0.535 | no | 0.567 | 0.328 | yes | 0.978 | 0.439 | no | 0.715 | 0.197 | no | 1.214 | 0.686 | no | 1.555 | 1.045 | no | 1.998 | 1.335 | yes | 1.436 | 0.087 | no | 4.006 | 1.411 | yes |
| DR1344 | HAD superfamily hydrolase | 0.897 | 0.299 | no | 0.679 | 0.506 | yes | 0.461 | 0.283 | yes | 0.874 | 0.221 | no | 0.896 | 0.378 | no | 0.783 | 0.174 | no | 0.847 | 0.358 | no | 1.249 | 0.284 | no | 1.193 | 0.243 | no |
| DR1345 | Dipeptidase FRAMESHIFT | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR1346 | Dipeptidase | 1.202 | 0.578 | no | 1.042 | 0.488 | no | 0.958 | 0.369 | no | 0.902 | 0.358 | no | 0.945 | 0.465 | no | 0.812 | 0.149 | no | 0.781 | 0.558 | yes | 0.841 | 0.286 | no | 1.375 | 0.274 | no |
| DR1347 | Aspartyl-tRNA synthetase | 0.894 | 0.279 | no | 0.598 | 0.161 | yes | 0.759 | 0.416 | no | 0.587 | 0.334 | yes | 0.642 | 0.215 | yes | 0.733 | 0.224 | no | 0.700 | 0.224 | yes | 0.863 | 0.274 | no | 1.195 | 0.282 | no |
| DR1348 | Conserved histidine rich protein | 1.057 | 0.263 | no | 0.524 | 0.133 | yes | 0.501 | 0.165 | yes | 0.811 | 0.324 | no | 0.798 | 0.313 | no | 0.719 | 0.146 | no | 0.838 | 0.222 | no | 1.126 | 0.152 | no | 1.521 | 0.355 | yes |
| DR1349 | Histidyl-tRNA synthetase | 0.942 | 0.272 | no | 0.841 | 0.288 | no | 0.756 | 0.302 | no | 0.647 | 0.318 | yes | 0.668 | 0.226 | yes | 0.678 | 0.183 | yes | 0.755 | 0.257 | no | 0.817 | 0.130 | no | 1.013 | 0.187 | no |
| DR1350 | Aspartate aminotransferase | 1.077 | 0.511 | no | 0.657 | 0.313 | yes | 0.784 | 0.325 | no | 0.728 | 0.306 | no | 1.004 | 0.406 | no | 0.917 | 0.427 | no | 0.747 | 0.240 | no | 0.697 | 0.228 | yes | 0.664 | 0.123 | no |
| DR1351 | A/b hydrolase , possible 3-oxoadipate enol-lacton hydrolase/4-carboxymuconolactone decarboxylase | 1.031 | 0.580 | no | 0.815 | 0.188 | no | 1.243 | 0.368 | no | 1.048 | 0.163 | no | 1.326 | 0.433 | no | 1.080 | 0.314 | no | 1.184 | 0.158 | no | 0.944 | 0.082 | no | 1.126 | 0.187 | no |
| DR1352 | A/b hydrolase, possible dihydrolipoamide acetyltransferase | 1.069 | 0.497 | no | 0.907 | 0.430 | no | 0.988 | 0.468 | no | 1.059 | 0.580 | no | 1.033 | 0.291 | no | 0.906 | 0.361 | no | 0.931 | 0.306 | no | 0.706 | 0.164 | no | 0.726 | 0.068 | no |
| DR1353 | Apolipoprotein N-acetyltransferase, similar to acid-inducible protein and LNT_ECOLI | 0.946 | 0.358 | no | 1.480 | 0.334 | yes | 1.103 | 0.309 | no | 0.812 | 0.365 | no | 0.948 | 0.326 | no | 0.867 | 0.257 | no | 0.759 | 0.184 | no | 0.758 | 0.257 | no | 0.859 | 0.259 | no |
| DR1354 | Excinuclease ABC subunit C, UVRC | 0.955 | 0.358 | no | 1.396 | 0.714 | no | 3.199 | 1.232 | yes | 3.783 | 0.417 | yes | 2.479 | 0.697 | yes | 2.298 | 1.205 | yes | 1.959 | 0.730 | yes | 1.320 | 0.340 | no | 1.164 | 0.280 | no |
| DR1355 | Membrane hydrolase related to phosphatidylglycerophosphate phosphatase B | 0.843 | 0.218 | no | 0.795 | 0.221 | no | 0.927 | 0.261 | no | 0.722 | 0.225 | no | 0.974 | 0.268 | no | 1.063 | 0.281 | no | 0.884 | 0.183 | no | 0.859 | 0.163 | no | 0.852 | 0.187 | no |
| DR1356 | ABC transporter, ATP-binding protein | 1.114 | 0.205 | no | 2.517 | 1.307 | yes | 5.090 | 2.082 | yes | 9.849 | 5.977 | yes | 5.336 | 1.169 | yes | 6.781 | 0.396 | yes | 2.237 | 0.808 | yes | 2.314 | 0.866 | yes | 0.839 | 0.190 | no |
| DR1357 | Conserved membrane protein, related to PROW_ECOLI | 1.353 | 0.505 | no | 2.787 | 1.124 | yes | 6.790 | 2.558 | yes | 6.423 | 2.085 | yes | 4.329 | 1.496 | yes | 4.115 | 0.729 | yes | 3.214 | 2.263 | yes | 1.345 | 0.252 | no | 0.537 | 0.248 | yes |
| DR1358 | NlpA like Lipoprotein | 1.391 | 0.270 | no | 13.012 | 5.051 | yes | 22.735 | 13.730 | yes | 19.458 | 10.309 | yes | 20.413 | 12.072 | yes | 16.261 | 9.469 | yes | 3.235 | 1.654 | yes | 3.117 | 0.815 | yes | 1.961 | 0.631 | yes |
| DR1359 | NlpA like Lipoprotein | 0.934 | 0.320 | no | 8.018 | 4.768 | yes | 24.834 | 11.129 | yes | 15.981 | 9.286 | yes | 16.907 | 8.373 | yes | 6.925 | 2.958 | yes | 10.631 | 5.877 | yes | 2.824 | 0.920 | yes | 1.080 | 0.064 | no |
| DR1360 | Calcineurin like phosphoesterase, inactive? | 1.174 | 0.267 | no | 1.764 | 0.929 | yes | 2.507 | 0.439 | yes | 2.144 | 0.645 | yes | 1.844 | 0.783 | yes | 2.019 | 0.780 | yes | 1.463 | 0.462 | no | 1.150 | 0.321 | no | 1.128 | 0.472 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR1361 | Bacterial DCSG sequence containing hydrolase, probably gamma-D-glutamyl-L-diamino acid endopeptidase II | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR1362 | GFOR family oxidoreductase, Gal80-like | 0.947 | 0.334 | no | 1.274 | 0.237 | no | 1.986 | 0.265 | yes | 1.575 | 0.436 | no | 1.704 | 0.592 | yes | 1.792 | 0.705 | yes | 1.231 | 0.323 | no | 1.119 | 0.374 | no | 0.999 | 0.248 | no |
| DR1363 | Diacylglycerolkinase | 1.097 | 0.196 | no | 0.709 | 0.237 | no | 0.858 | 0.284 | no | 0.658 | 0.267 | yes | 0.722 | 0.302 | no | 0.864 | 0.348 | no | 0.740 | 0.231 | no | 1.111 | 0.218 | no | 0.829 | 0.309 | no |
| DR1364 | TIG domain containing protein (domain present in some starch degradation enzymes) | 1.068 | 0.400 | no | 0.828 | 0.164 | no | 0.881 | 0.349 | no | 0.885 | 0.451 | no | 1.038 | 0.385 | no | 0.872 | 0.317 | no | 0.880 | 0.215 | no | 1.188 | 0.456 | no | 1.739 | 0.596 | yes |
| DR1365 | Aspartate kinase | 1.201 | 0.342 | no | 0.990 | 0.655 | no | 0.752 | 0.249 | no | 0.725 | 0.122 | no | 0.930 | 0.623 | no | 0.801 | 0.363 | no | 0.908 | 0.226 | no | 1.056 | 0.136 | no | 1.278 | 0.339 | no |
| DR1366 | Glutamine amidotransferase, possibly imidazoleglycerol-phosphate synthase, subunit H | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR1367 | Snz1 His4 family enzymes | 0.889 | 0.147 | no | 0.488 | 0.167 | yes | 0.182 | 0.031 | yes | 0.144 | 0.022 | yes | 0.149 | 0.056 | yes | 0.199 | 0.096 | yes | 0.261 | 0.151 | yes | 0.348 | 0.145 | yes | 0.629 | 0.231 | yes |
| DR1368 | Conserved protein of YGGS family | 1.058 | 0.292 | no | 1.753 | 0.485 | yes | 1.610 | 0.391 | yes | 1.390 | 0.502 | no | 1.274 | 0.214 | no | 1.099 | 0.442 | no | 1.058 | 0.149 | no | 0.777 | 0.191 | no | 0.941 | 0.150 | no |
| DR1369 | Low complexity, possible homolog of DIVIVA of Bacillus | 0.915 | 0.216 | no | 1.240 | 0.586 | no | 1.145 | 0.647 | no | 0.936 | 0.430 | no | 0.943 | 0.492 | no | 0.838 | 0.246 | no | 0.866 | 0.171 | no | 0.950 | 0.211 | no | 0.990 | 0.194 | no |
| DR1370 | Membrane protein related to MJ0687 | 1.126 | 0.706 | no | 1.718 | 0.339 | yes | 1.588 | 0.146 | yes | 1.348 | 0.406 | no | 1.293 | 0.482 | no | 1.192 | 0.420 | no | 1.162 | 0.277 | no | 1.095 | 0.243 | no | 1.765 | 0.764 | yes |
| DR1371 | Predicted protein | 0.929 | 0.470 | no | 0.881 | 0.232 | no | 1.519 | 0.925 | no | 2.162 | 1.068 | yes | 1.310 | 0.683 | no | 0.997 | 0.536 | no | 1.202 | 0.578 | no | 1.085 | 0.377 | no | 1.202 | 0.802 | no |
| DR1372 | LEA14-like desiccation protectant | 0.933 | 0.492 | no | 0.691 | 0.232 | no | 0.707 | 0.394 | yes | 0.727 | 0.288 | no | 0.822 | 0.466 | no | 0.613 | 0.270 | yes | 0.647 | 0.435 | yes | 0.608 | 0.115 | yes | 0.771 | 0.231 | no |
| DR1373 | HutB like Haemin binding protein | 0.946 | 0.392 | no | 0.700 | 0.097 | no | 0.489 | 0.208 | yes | 0.352 | 0.205 | yes | 0.426 | 0.207 | yes | 0.481 | 0.126 | yes | 0.462 | 0.314 | yes | 0.565 | 0.211 | yes | 0.755 | 0.194 | no |
| DR1374 | DNA topoisomerase I | 1.109 | 0.508 | no | 0.740 | 0.275 | no | 0.604 | 0.219 | yes | 0.579 | 0.331 | yes | 0.543 | 0.208 | yes | 0.454 | 0.105 | yes | 0.621 | 0.205 | yes | 0.603 | 0.108 | yes | 0.665 | 0.090 | no |
| DR1375 | Maltase, MAL | 1.090 | 0.191 | no | 2.048 | 0.813 | yes | 2.583 | 1.243 | yes | 2.722 | 1.441 | yes | 1.772 | 0.663 | yes | 1.327 | 0.316 | no | 1.447 | 0.542 | no | 0.813 | 0.107 | no | 1.006 | 0.181 | no |
| DR1376 | Hypoxanthine phosphoribosyltransferase, HPRT | 1.100 | 0.408 | no | 1.364 | 0.395 | no | 2.270 | 1.094 | yes | 2.449 | 1.183 | yes | 1.928 | 0.729 | yes | 1.442 | 0.394 | no | 1.032 | 0.268 | no | 1.130 | 0.242 | no | 1.001 | 0.186 | no |
| DR1377 | Amidase | 1.179 | 0.522 | no | 1.089 | 0.125 | no | 1.243 | 0.458 | no | 1.071 | 0.180 | no | 1.230 | 0.471 | no | 1.128 | 0.475 | no | 1.271 | 0.784 | no | 1.140 | 0.255 | no | 1.008 | 0.112 | no |
| DR1378 | PilB domain | 1.170 | 0.386 | no | 0.566 | 0.177 | yes | 0.576 | 0.249 | yes | 0.681 | 0.250 | no | 0.743 | 0.541 | yes | 0.440 | 0.180 | yes | 0.452 | 0.278 | yes | 0.369 | 0.102 | yes | 0.675 | 0.185 | no |
| DR1379 | HTH transcription factor | 1.112 | 0.514 | no | 1.160 | 0.394 | no | 1.151 | 0.379 | no | 0.895 | 0.372 | no | 0.886 | 0.334 | no | 1.046 | 0.531 | no | 0.710 | 0.170 | no | 0.756 | 0.134 | no | 0.656 | 0.140 | no |
| DR1380 | Conserved membrane protein | 1.357 | 0.325 | no | 2.336 | 1.006 | yes | 2.577 | 1.221 | yes | 1.883 | 0.443 | yes | 1.708 | 1.054 | yes | 1.137 | 0.265 | no | 0.959 | 0.300 | no | 0.870 | 0.097 | no | 1.020 | 0.057 | no |
| DR1381 | Transposase | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR1382 | Transposon ORF | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR1383 | Predicted protein | 0.931 | 0.215 | no | 0.692 | 0.192 | yes | 0.725 | 0.223 | no | 0.795 | 0.278 | no | 0.959 | 0.398 | no | 0.942 | 0.366 | no | 1.134 | 0.482 | no | 1.896 | 0.651 | yes | 0.948 | 0.074 | no |
| DR1384 | HTH transcriptional regulator, TetR/ArcR family | 1.096 | 0.514 | no | 1.379 | 0.647 | no | 1.138 | 0.279 | no | 1.158 | 0.180 | no | 1.314 | 0.320 | no | 1.029 | 0.351 | no | 1.167 | 0.412 | no | 1.228 | 0.366 | no | 1.025 | 0.110 | no |
| DR1385 | Uncharacterized conserved protein | 1.125 | 0.373 | no | 1.152 | 0.444 | no | 0.983 | 0.147 | no | 1.109 | 0.516 | no | 2.658 | 1.757 | yes | 1.349 | 0.592 | no | 2.255 | 0.587 | yes | 3.873 | 2.131 | yes | 2.369 | 0.785 | yes |
| DR1386 | GTPase | 1.196 | 0.359 | no | 1.056 | 0.145 | no | 1.459 | 0.575 | no | 1.954 | 0.502 | yes | 1.513 | 0.438 | no | 1.758 | 0.586 | yes | 1.631 | 0.318 | yes | 1.502 | 0.238 | yes | 1.643 | 0.459 | yes |
| DR1387 | N-acetylmuramoyl-L-alanine amidase, AMIA | 0.915 | 0.374 | no | 1.761 | 0.616 | yes | 2.856 | 0.997 | yes | 1.964 | 0.442 | yes | 1.803 | 0.703 | yes | 1.768 | 0.601 | yes | 1.484 | 0.655 | no | 1.426 | 0.744 | no | 1.363 | 0.750 | no |
| DR1388 | Probable S-layer protein | 0.912 | 0.372 | no | 1.710 | 0.630 | yes | 1.925 | 0.834 | yes | 2.451 | 1.530 | yes | 1.463 | 0.630 | no | 1.684 | 0.460 | yes | 1.529 | 0.398 | yes | 1.534 | 0.225 | yes | 2.267 | 0.323 | yes |
| DR1389 | DNA transformation protein COMF | 0.966 | 0.216 | no | 1.231 | 0.345 | no | 1.266 | 0.346 | no | 1.135 | 0.418 | no | 1.181 | 0.370 | no | 1.096 | 0.378 | no | 0.943 | 0.375 | no | 0.993 | 0.368 | no | 1.035 | 0.289 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR1390 | Homolog of C-terminal domain of XF0761 and SCI11.36c | 1.061 | 0.214 | no | 0.906 | 0.376 | no | 0.758 | 0.264 | no | 0.709 | 0.328 | no | 0.585 | 0.173 | yes | 0.766 | 0.293 | no | 0.736 | 0.358 | no | 0.931 | 0.091 | no | 0.944 | 0.364 | no |
| DR1391 | Small conserved protein | 1.005 | 0.268 | no | 1.066 | 0.450 | no | 0.988 | 0.438 | no | 0.883 | 0.448 | no | 1.250 | 0.588 | no | 1.103 | 0.467 | no | 0.962 | 0.464 | no | 1.084 | 0.289 | no | 1.456 | 0.667 | no |
| DR1392 | Predicted protein | 1.222 | 0.275 | no | 0.859 | 0.303 | no | 0.813 | 0.364 | no | 0.984 | 0.685 | no | 0.728 | 0.400 | no | 0.730 | 0.310 | no | 0.563 | 0.089 | yes | 0.822 | 0.143 | no | 1.045 | 0.181 | no |
| DR1393 | Phosphoglycerate mutase family protein | 0.946 | 0.137 | no | 0.569 | 0.103 | yes | 0.329 | 0.181 | yes | 0.340 | 0.046 | yes | 0.396 | 0.245 | yes | 0.368 | 0.066 | yes | 0.387 | 0.148 | yes | 0.605 | 0.168 | yes | 0.677 | 0.101 | no |
| DR1394 | Phosphoribosylaminoimidazole synthetase | 1.098 | 0.230 | no | 1.248 | 0.479 | no | 1.116 | 0.376 | no | 0.943 | 0.169 | no | 0.996 | 0.373 | no | 0.984 | 0.370 | no | 0.916 | 0.097 | no | 1.037 | 0.135 | no | 1.104 | 0.160 | no |
| DR1395 | Geranylgeranyl pyrophosphate synthase, IDSA | 0.895 | 0.294 | no | 0.802 | 0.137 | no | 0.759 | 0.234 | no | 0.734 | 0.166 | no | 0.726 | 0.283 | no | 0.799 | 0.094 | no | 0.653 | 0.182 | yes | 0.791 | 0.156 | no | 0.899 | 0.197 | no |
| DR1396 | NH2-acetyltransferase | 0.909 | 0.256 | no | 1.403 | 0.291 | no | 1.342 | 0.275 | no | 1.076 | 0.047 | no | 1.097 | 0.249 | no | 1.065 | 0.248 | no | 1.010 | 0.160 | no | 1.032 | 0.192 | no | 1.567 | 0.307 | yes |
| DR1397 | Protein, similar to N-formylglutamate amidohydrolase | 1.153 | 0.571 | no | 0.718 | 0.171 | no | 0.827 | 0.539 | no | 1.171 | 0.593 | no | 1.094 | 0.567 | no | 0.774 | 0.141 | no | 1.024 | 0.300 | no | 0.975 | 0.313 | no | 1.030 | 0.384 | no |
| DR1398 | Predicted protein | 1.110 | 0.310 | no | 4.085 | 1.675 | yes | 4.173 | 1.036 | yes | 3.349 | 0.250 | yes | 2.555 | 1.294 | yes | 1.480 | 0.502 | no | 1.409 | 0.669 | no | 1.134 | 0.139 | no | 0.975 | 0.084 | no |
| DR1399 | Flavin dependent oxidoreductase | 0.927 | 0.473 | no | 1.308 | 0.757 | no | 1.590 | 1.123 | no | 1.490 | 0.493 | no | 0.984 | 0.555 | no | 0.997 | 0.447 | no | 0.854 | 0.312 | no | 0.752 | 0.158 | no | 0.725 | 0.287 | no |
| DR1400 | Invasin repeat membrane protein | 1.280 | 0.510 | no | 0.802 | 0.428 | no | 0.846 | 0.300 | no | 0.830 | 0.413 | no | 0.610 | 0.204 | yes | 0.706 | 0.219 | no | 0.527 | 0.198 | yes | 0.376 | 0.158 | yes | 0.565 | 0.100 | yes |
| DR1401 | Ribulose-phosphate 3-epimerase | 0.848 | 0.346 | no | 1.062 | 0.587 | no | 0.821 | 0.282 | no | 0.799 | 0.451 | no | 0.724 | 0.314 | no | 0.761 | 0.417 | no | 0.755 | 0.219 | no | 0.739 | 0.211 | yes | 0.764 | 0.269 | no |
| DR1402 | HTH transcription factor, TetR/AcrR family | 0.859 | 0.312 | no | 0.829 | 0.224 | no | 0.832 | 0.251 | no | 0.850 | 0.166 | no | 0.646 | 0.294 | yes | 0.611 | 0.239 | yes | 0.515 | 0.222 | yes | 0.827 | 0.346 | no | 0.742 | 0.263 | no |
| DR1403 | a/b hydrolase | 1.171 | 0.483 | no | 0.986 | 0.293 | no | 1.510 | 0.420 | yes | 0.948 | 0.248 | no | 0.843 | 0.298 | no | 0.985 | 0.558 | no | 0.901 | 0.297 | no | 0.831 | 0.071 | no | 0.773 | 0.148 | no |
| DR1404 | Predicted protein | 0.673 | 0.202 | yes | 0.965 | 0.265 | no | 0.876 | 0.251 | no | 0.634 | 0.132 | yes | 0.690 | 0.237 | yes | 0.656 | 0.376 | yes | 0.637 | 0.199 | yes | 0.627 | 0.269 | yes | 1.008 | 0.462 | no |
| DR1405 | Predicted protein | 0.859 | 0.298 | no | 0.856 | 0.266 | no | 0.844 | 0.201 | no | 0.842 | 0.237 | no | 0.850 | 0.272 | no | 0.680 | 0.267 | yes | 0.431 | 0.158 | yes | 0.522 | 0.156 | yes | 1.080 | 0.211 | no |
| DR1406 | Predicted protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR1407 | Predicted protein (low complexity) | 0.670 | 0.204 | yes | 0.680 | 0.270 | yes | 0.736 | 0.450 | yes | 0.449 | 0.155 | yes | 0.658 | 0.491 | yes | 0.463 | 0.202 | yes | 0.457 | 0.137 | yes | 0.482 | 0.163 | yes | 0.962 | 0.466 | no |
| DR1408 | Predicted protein | 0.996 | 0.389 | no | 1.335 | 0.380 | no | 0.999 | 0.331 | no | 0.635 | 0.105 | yes | 0.750 | 0.419 | no | 0.458 | 0.085 | yes | 0.615 | 0.179 | yes | 0.371 | 0.119 | yes | 0.324 | 0.068 | yes |
| DR1409 | Predicted protein | 1.216 | 0.484 | no | 1.000 | 0.427 | no | 1.011 | 0.350 | no | 0.908 | 0.270 | no | 0.877 | 0.345 | no | 0.760 | 0.219 | no | 0.991 | 0.179 | no | 0.925 | 0.053 | no | 1.316 | 0.358 | no |
| DR1410 | Carboxynorspermidine decarboxylase | 1.016 | 0.282 | no | 2.662 | 1.366 | yes | 1.761 | 0.753 | yes | 1.040 | 0.470 | no | 1.514 | 0.828 | no | 0.974 | 0.732 | no | 1.224 | 0.620 | no | 0.752 | 0.251 | yes | 0.383 | 0.206 | yes |
| DR1411 | Membrane transporter, homolog of sac1 | 1.110 | 0.237 | no | 1.042 | 0.240 | no | 1.259 | 0.584 | no | 1.266 | 0.818 | no | 1.001 | 0.349 | no | 1.071 | 0.591 | no | 0.959 | 0.312 | no | 1.029 | 0.491 | no | 1.043 | 0.632 | no |
| DR1412 | Predicted protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR1413 | Hydrolase of desuccinylase family, same fold as carboxypeptidase G2 1cg2 and Aminopeptidase Hydrolase | 0.837 | 0.272 | no | 1.207 | 0.443 | no | 1.598 | 0.608 | yes | 1.423 | 0.886 | no | 1.290 | 0.565 | no | 1.367 | 0.740 | no | 1.035 | 0.402 | no | 0.753 | 0.261 | no | 1.131 | 0.678 | no |
| DR1414 | Predicted protein (low complexity) | 1.238 | 0.343 | no | 1.216 | 0.306 | no | 1.382 | 0.362 | no | 1.454 | 0.506 | no | 1.156 | 0.306 | no | 1.281 | 0.575 | no | 1.312 | 0.310 | no | 1.339 | 0.280 | no | 1.389 | 0.193 | no |
| DR1415 | Orthinine aminotransferase, ARGD | 0.859 | 0.103 | no | 1.015 | 0.336 | no | 1.276 | 0.622 | no | 0.911 | 0.452 | no | 0.997 | 0.340 | no | 1.054 | 0.271 | no | 0.905 | 0.332 | no | 1.008 | 0.215 | no | 0.933 | 0.201 | no |
| DR1416 | Predicted protein | 0.981 | 0.271 | no | 0.695 | 0.210 | yes | 0.723 | 0.172 | no | 0.590 | 0.077 | yes | 0.656 | 0.165 | yes | 0.685 | 0.227 | yes | 0.680 | 0.188 | yes | 0.893 | 0.147 | no | 0.858 | 0.234 | no |
| DR1417 | Penicilin-binding protein, PBP | 1.006 | 0.194 | no | 1.252 | 0.325 | no | 1.229 | 0.458 | no | 0.948 | 0.181 | no | 0.948 | 0.361 | no | 0.843 | 0.206 | no | 0.883 | 0.201 | no | 0.870 | 0.062 | no | 0.880 | 0.259 | no |
| DR1418 | Receiver domain, CHEY family + HTH domain | 0.876 | 0.392 | no | 0.718 | 0.257 | no | 1.045 | 0.491 | no | 0.812 | 0.171 | no | 0.878 | 0.323 | no | 0.814 | 0.357 | no | 0.639 | 0.214 | yes | 0.767 | 0.168 | no | 0.917 | 0.419 | no |
| DR1419 | P-loop containing protein, tunicamycin resistance protein ortholog | 1.047 | 0.382 | no | 0.411 | 0.163 | yes | 0.281 | 0.112 | yes | 0.474 | 0.208 | yes | 0.819 | 0.248 | no | 0.803 | 0.254 | no | 1.188 | 0.398 | no | 1.550 | 0.418 | yes | 1.378 | 0.407 | no |
| DR1420 | Acetylglutamate kinase | 1.361 | 0.243 | no | 1.275 | 0.141 | no | 1.008 | 0.098 | no | 1.028 | 0.202 | no | 0.925 | 0.102 | no | 0.898 | 0.301 | no | 0.947 | 0.119 | no | 1.042 | 0.185 | no | 0.970 | 0.182 | no |
| DR1421 | Predicted protein | 0.971 | 0.196 | no | 0.816 | 0.139 | no | 0.786 | 0.287 | no | 0.848 | 0.318 | no | 0.784 | 0.248 | no | 0.661 | 0.083 | yes | 0.660 | 0.177 | yes | 0.826 | 0.169 | no | 0.776 | 0.156 | no |
| DR1422 | HTH transcriptional regulator | 1.046 | 0.227 | no | 1.770 | 0.601 | yes | 1.385 | 0.218 | no | 1.043 | 0.164 | no | 0.866 | 0.230 | no | 0.675 | 0.325 | yes | 0.698 | 0.148 | no | 0.696 | 0.098 | yes | 0.720 | 0.162 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR1423 | Related to Nitrogen regulatory protein P-II, ortholog YAAQ of Bacilus | 0.915 | 0.203 | no | 1.127 | 0.463 | no | 0.829 | 0.257 | no | 0.792 | 0.239 | no | 0.955 | 0.262 | no | 0.742 | 0.223 | no | 0.841 | 0.159 | no | 1.096 | 0.073 | no | 1.346 | 0.406 | no |
| DR1424 | DNAJ heat shock protein | 1.042 | 0.476 | no | 0.825 | 0.381 | no | 0.663 | 0.255 | yes | 0.613 | 0.283 | yes | 0.521 | 0.160 | yes | 0.456 | 0.111 | yes | 0.529 | 0.166 | yes | 0.416 | 0.107 | yes | 0.424 | 0.079 | yes |
| DR1425 | Predicted protein | 0.872 | 0.165 | no | 0.546 | 0.298 | yes | 0.480 | 0.243 | yes | 0.486 | 0.200 | yes | 0.505 | 0.157 | yes | 0.515 | 0.151 | yes | 0.547 | 0.316 | yes | 0.610 | 0.142 | yes | 0.828 | 0.120 | no |
| DR1426 | Indole-3-glycerol-phosphate synthase, TRPC | 0.883 | 0.360 | no | 0.657 | 0.287 | yes | 0.510 | 0.218 | yes | 0.456 | 0.301 | yes | 0.470 | 0.156 | yes | 0.476 | 0.189 | yes | 0.497 | 0.210 | yes | 0.564 | 0.098 | yes | 0.789 | 0.123 | no |
| DR1427 | Signal peptidase I | 0.736 | 0.262 | no | 0.803 | 0.275 | no | 0.860 | 0.337 | no | 0.710 | 0.263 | no | 0.834 | 0.256 | no | 1.209 | 0.572 | no | 0.996 | 0.691 | no | 0.799 | 0.190 | no | 0.875 | 0.363 | no |
| DR1428 | 3-ketoacyl-CoA thiolase | 1.186 | 0.211 | no | 1.152 | 0.366 | no | 1.545 | 0.401 | yes | 2.239 | 0.650 | yes | 1.785 | 0.900 | yes | 1.256 | 0.574 | no | 1.099 | 0.374 | no | 1.396 | 0.420 | no | 0.741 | 0.162 | no |
| DR1429 | Predicted protein | 0.778 | 0.233 | no | 0.910 | 0.157 | no | 1.107 | 0.224 | no | 1.501 | 0.413 | no | 1.191 | 0.235 | no | 0.976 | 0.319 | no | 0.774 | 0.157 | no | 1.041 | 0.275 | no | 0.916 | 0.236 | no |
| DR1430 | Metallo beta lacatmase fold hydrolase | 1.205 | 0.496 | no | 0.910 | 0.242 | no | 1.068 | 0.352 | no | 1.294 | 0.451 | no | 1.371 | 0.393 | no | 0.880 | 0.341 | no | 0.684 | 0.106 | no | 0.701 | 0.077 | yes | 1.242 | 0.534 | no |
| DR1431 | Phosphoribosylamine-glycine ligase | 1.267 | 0.353 | no | 0.890 | 0.363 | no | 0.953 | 0.389 | no | 1.070 | 0.085 | no | 0.975 | 0.294 | no | 0.920 | 0.365 | no | 1.012 | 0.375 | no | 0.850 | 0.075 | no | 0.905 | 0.592 | no |
| DR1432 | Predicted protein | 0.873 | 0.075 | no | 0.724 | 0.218 | no | 0.727 | 0.191 | no | 0.846 | 0.277 | no | 1.332 | 0.803 | no | 1.172 | 0.602 | no | 0.816 | 0.362 | no | 0.726 | 0.097 | no | 1.073 | 0.293 | no |
| DR1433 | Methionyl-tRNA synthetase + EMAP domain | 1.114 | 0.441 | no | 1.221 | 0.290 | no | 0.855 | 0.160 | no | 0.749 | 0.173 | no | 0.698 | 0.224 | no | 0.471 | 0.213 | yes | 0.368 | 0.098 | yes | 0.350 | 0.060 | yes | 0.282 | 0.107 | yes |
| DR1434 | YVCJ like ATPase | 0.945 | 0.223 | no | 0.694 | 0.160 | no | 0.682 | 0.271 | yes | 0.906 | 0.269 | no | 0.813 | 0.402 | no | 0.691 | 0.096 | no | 0.751 | 0.215 | no | 0.829 | 0.064 | no | 1.070 | 0.141 | no |
| DR1435 | Uncharacterized YBHK E coli ortholog, probably NTP utilizing enzyme | 1.249 | 0.458 | no | 4.125 | 3.000 | yes | 2.907 | 2.123 | yes | 3.850 | 1.108 | yes | 2.088 | 1.417 | yes | 1.018 | 0.727 | no | 1.235 | 0.559 | no | 0.694 | 0.223 | yes | 0.257 | 0.076 | yes |
| DR1436 | Sugar transporter permease | 1.165 | 0.298 | no | 1.021 | 0.255 | no | 1.035 | 0.418 | no | 1.155 | 0.469 | no | 1.162 | 0.330 | no | 0.961 | 0.418 | no | 0.974 | 0.193 | no | 1.172 | 0.254 | no | 1.379 | 0.515 | no |
| DR1437 | Sugar transporter | 1.316 | 0.658 | no | 0.970 | 0.416 | no | 1.217 | 0.397 | no | 1.271 | 0.076 | no | 1.184 | 0.587 | no | 1.062 | 0.532 | no | 1.096 | 0.322 | no | 1.167 | 0.305 | no | 0.793 | 0.389 | no |
| DR1438 | Periplasmic sugar binding protein | 0.888 | 0.162 | no | 0.652 | 0.257 | yes | 0.443 | 0.321 | yes | 0.452 | 0.185 | yes | 0.530 | 0.270 | yes | 0.524 | 0.251 | yes | 0.556 | 0.223 | yes | 1.210 | 0.262 | no | 0.539 | 0.089 | yes |
| DR1439 | Predicted protein | 1.455 | 0.676 | no | 1.205 | 0.514 | no | 0.487 | 0.221 | yes | 0.253 | 0.129 | yes | 0.290 | 0.128 | yes | 0.295 | 0.096 | yes | 0.444 | 0.138 | yes | 0.484 | 0.167 | yes | 1.389 | 0.402 | no |
| DR1441 | Conserved membrane protein | 0.975 | 0.326 | no | 0.859 | 0.256 | no | 0.709 | 0.310 | yes | 0.548 | 0.120 | yes | 0.698 | 0.253 | yes | 0.560 | 0.174 | yes | 0.688 | 0.205 | yes | 0.748 | 0.154 | no | 0.803 | 0.256 | no |
| DR1442 | PR1 family protein | 0.926 | 0.290 | no | 0.866 | 0.298 | no | 0.720 | 0.335 | yes | 0.868 | 0.475 | no | 0.497 | 0.121 | yes | 0.672 | 0.154 | yes | 0.612 | 0.186 | yes | 0.684 | 0.033 | yes | 0.704 | 0.178 | no |
| DR1443 | HD supefamily hydrolase | 0.969 | 0.249 | no | 0.748 | 0.230 | no | 0.545 | 0.188 | yes | 0.520 | 0.244 | yes | 0.586 | 0.277 | yes | 0.615 | 0.060 | yes | 0.633 | 0.171 | yes | 0.719 | 0.148 | yes | 0.910 | 0.127 | no |
| DR1444 | Histidyl-tRNA synthetase, hisS | 1.305 | 0.176 | no | 1.312 | 0.402 | no | 1.266 | 0.151 | no | 1.200 | 0.205 | no | 1.017 | 0.156 | no | 1.196 | 0.416 | no | 0.961 | 0.134 | no | 1.089 | 0.185 | no | 0.996 | 0.213 | no |
| DR1445 | ATP phosphoribosyltransferase, HIS1 | 0.816 | 0.292 | no | 0.565 | 0.256 | yes | 0.364 | 0.160 | yes | 0.289 | 0.213 | yes | 0.357 | 0.190 | yes | 0.432 | 0.196 | yes | 0.395 | 0.228 | yes | 0.483 | 0.234 | yes | 0.596 | 0.294 | yes |
| DR1446 | Predicted protein | 1.260 | 0.576 | no | 0.953 | 0.634 | no | 0.853 | 0.535 | no | 0.691 | 0.253 | no | 0.556 | 0.323 | yes | 0.535 | 0.251 | yes | 0.522 | 0.216 | yes | 0.644 | 0.113 | yes | 0.849 | 0.308 | no |
| DR1447 | Probably S-layer, DR-2 | 0.743 | 0.193 | no | 0.406 | 0.122 | yes | 0.414 | 0.126 | yes | 0.351 | 0.059 | yes | 0.417 | 0.077 | yes | 0.473 | 0.130 | yes | 0.489 | 0.130 | yes | 0.577 | 0.202 | yes | 1.102 | 0.540 | no |
| DR1448 | Predicted protein, DR-2 | 0.622 | 0.186 | yes | 0.404 | 0.150 | yes | 0.365 | 0.118 | yes | 0.298 | 0.041 | yes | 0.426 | 0.125 | yes | 0.562 | 0.178 | yes | 0.568 | 0.214 | yes | 0.759 | 0.153 | no | 1.136 | 0.348 | no |
| DR1449 | Conserved membrane protein, possible permease MDR-type | 0.886 | 0.198 | no | 0.730 | 0.123 | no | 0.562 | 0.034 | yes | 0.486 | 0.060 | yes | 0.626 | 0.121 | yes | 0.765 | 0.287 | no | 0.779 | 0.248 | no | 0.883 | 0.212 | no | 1.105 | 0.216 | no |
| DR1450 | Small conserved membrane protein | 1.063 | 0.280 | no | 0.760 | 0.155 | no | 0.705 | 0.210 | no | 0.683 | 0.106 | no | 0.621 | 0.111 | yes | 0.640 | 0.082 | yes | 0.771 | 0.151 | no | 0.810 | 0.109 | no | 0.874 | 0.194 | no |
| DR1451 | 5'-methylthioadenosine/ S-adenosylhomocysteine nucleosidase | 0.881 | 0.217 | no | 0.881 | 0.188 | no | 0.756 | 0.094 | no | 0.635 | 0.112 | yes | 0.726 | 0.167 | no | 0.737 | 0.117 | no | 0.857 | 0.340 | no | 0.975 | 0.272 | no | 0.956 | 0.143 | no |
| DR1452 | Aminotransferase | 0.942 | 0.162 | no | 0.564 | 0.136 | yes | 0.398 | 0.149 | yes | 0.325 | 0.137 | yes | 0.386 | 0.098 | yes | 0.447 | 0.186 | yes | 0.580 | 0.161 | yes | 0.654 | 0.173 | yes | 0.918 | 0.108 | no |
| DR1454 | Transposase | 0.728 | 0.219 | no | 0.545 | 0.207 | yes | 0.518 | 0.200 | yes | 0.365 | 0.131 | yes | 0.455 | 0.102 | yes | 0.489 | 0.134 | yes | 0.616 | 0.266 | yes | 0.612 | 0.137 | yes | 0.832 | 0.240 | no |
| DR1455 | Small phage protein | 1.058 | 0.441 | no | 0.619 | 0.147 | yes | 0.554 | 0.149 | yes | 0.738 | 0.309 | no | 0.664 | 0.176 | yes | 0.756 | 0.191 | no | 0.885 | 0.380 | no | 0.940 | 0.079 | no | 1.762 | 0.360 | yes |
| DR1456 | Phosphoribosylpyrophosphate synthetase | 0.886 | 0.191 | no | 0.780 | 0.153 | no | 0.836 | 0.288 | no | 0.937 | 0.102 | no | 1.317 | 0.302 | no | 1.197 | 0.346 | no | 1.335 | 0.301 | no | 1.677 | 0.343 | yes | 2.036 | 0.077 | yes |
| DR1457 | Membrane protein similar to YBAN E.coli | 1.005 | 0.417 | no | 0.516 | 0.254 | yes | 0.232 | 0.192 | yes | 0.125 | 0.026 | yes | 0.437 | 0.292 | yes | 0.591 | 0.287 | yes | 0.521 | 0.400 | yes | 0.389 | 0.178 | yes | 0.723 | 0.291 | no |
| DR1459 | Serine protease | 0.629 | 0.245 | yes | 0.460 | 0.152 | yes | 0.487 | 0.169 | yes | 0.438 | 0.225 | yes | 0.337 | 0.122 | yes | 0.634 | 0.282 | yes | 0.311 | 0.061 | yes | 0.895 | 0.153 | no | 1.233 | 0.403 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR1460 | Predicted probable surface protein | 0.985 | 0.444 | no | 0.904 | 0.358 | no | 0.486 | 0.158 | yes | 0.412 | 0.100 | yes | 0.439 | 0.149 | yes | 0.456 | 0.141 | yes | 0.607 | 0.209 | yes | 0.686 | 0.075 | yes | 0.873 | 0.101 | no |
| DR1461 | Possible surface protein, similar to _DR1462 | 0.972 | 0.178 | no | 1.884 | 1.034 | yes | 2.234 | 1.251 | yes | 1.921 | 0.799 | yes | 1.586 | 0.701 | no | 1.224 | 0.334 | no | 1.214 | 0.338 | no | 1.027 | 0.060 | no | 1.171 | 0.031 | no |
| DR1462 | Possible surface protein, similar to _DR1461 | 0.827 | 0.326 | no | 0.609 | 0.110 | yes | 0.803 | 0.414 | no | 0.561 | 0.078 | yes | 0.587 | 0.194 | yes | 0.775 | 0.214 | no | 0.545 | 0.279 | yes | 0.747 | 0.222 | yes | 1.145 | 0.380 | no |
| DR1463 | Predicted protein | 1.188 | 0.244 | no | 1.755 | 0.652 | yes | 1.450 | 0.542 | no | 1.082 | 0.284 | no | 1.142 | 0.283 | no | 1.088 | 0.289 | no | 0.833 | 0.328 | no | 1.112 | 0.400 | no | 0.946 | 0.292 | no |
| DR1464 | Predicted protein | 0.853 | 0.268 | no | 0.406 | 0.081 | yes | 0.297 | 0.072 | yes | 0.327 | 0.095 | yes | 0.324 | 0.117 | yes | 0.474 | 0.223 | yes | 0.476 | 0.294 | yes | 0.689 | 0.144 | yes | 0.498 | 0.233 | yes |
| DR1465 | Predicted protein | 1.005 | 0.290 | no | 1.155 | 0.334 | no | 1.233 | 0.525 | no | 1.198 | 0.129 | no | 1.075 | 0.395 | no | 1.027 | 0.286 | no | 1.023 | 0.200 | no | 1.102 | 0.243 | no | 1.156 | 0.406 | no |
| DR1466 | Predicted protein | 1.015 | 0.734 | no | 2.480 | 1.316 | yes | 1.920 | 1.381 | yes | 1.186 | 0.593 | no | 0.828 | 0.375 | no | 1.300 | 0.400 | no | 1.423 | 0.482 | no | n/a | n/a | n/a | n/a | n/a | n/a |
| DR1467 | Rossman fold oxidoreductase, Alcohol dehydrogenase like | 1.256 | 0.309 | no | 1.268 | 0.377 | no | 1.271 | 0.418 | no | 1.003 | 0.044 | no | 1.343 | 0.567 | no | 1.531 | 0.599 | no | 1.102 | 0.319 | no | 1.098 | 0.178 | no | 1.246 | 0.549 | no |
| DR1468 | SMALL protein B | 0.661 | 0.176 | yes | 0.423 | 0.215 | yes | 0.395 | 0.112 | yes | 0.425 | 0.081 | yes | 0.574 | 0.200 | yes | 0.607 | 0.172 | yes | 0.728 | 0.244 | no | 1.153 | 0.154 | no | 1.694 | 0.391 | yes |
| DR1469 | N-acetylmuramoyl-L-alanine amidase | 0.791 | 0.271 | no | 0.732 | 0.345 | no | 0.808 | 0.453 | no | 0.610 | 0.295 | yes | 0.853 | 0.257 | no | 0.723 | 0.300 | no | 0.744 | 0.343 | no | 0.842 | 0.240 | no | 0.913 | 0.199 | no |
| DR1470 | Predicted protein | 0.652 | 0.252 | yes | 0.455 | 0.191 | yes | 0.571 | 0.220 | yes | 0.487 | 0.033 | yes | 0.489 | 0.105 | yes | 0.666 | 0.235 | yes | 0.663 | 0.324 | yes | 0.918 | 0.226 | no | 1.170 | 0.290 | no |
| DR1472 | Alpha-amylase | 0.681 | 0.186 | no | 0.988 | 0.612 | no | 0.795 | 0.459 | no | 1.299 | 0.555 | no | 1.062 | 0.430 | no | 0.891 | 0.225 | no | 0.986 | 0.281 | no | 1.133 | 0.303 | no | 0.862 | 0.116 | no |
| DR1473 | Phage shock protein A, PSPA ortholog | 0.980 | 0.282 | no | 0.716 | 0.274 | no | 0.466 | 0.149 | yes | 0.488 | 0.182 | yes | 0.550 | 0.194 | yes | 0.655 | 0.224 | yes | 0.697 | 0.175 | no | 0.610 | 0.109 | yes | 0.690 | 0.304 | no |
| DR1474 | Membrane protein | 0.921 | 0.331 | no | 0.739 | 0.256 | no | 0.518 | 0.247 | yes | 0.538 | 0.265 | yes | 0.556 | 0.223 | yes | 0.518 | 0.144 | yes | 0.553 | 0.209 | yes | 0.602 | 0.072 | yes | 0.650 | 0.089 | no |
| DR1475 | 1-deoxyxylulose-5-phosphate synthase, DXS, Transketolase | 0.919 | 0.179 | no | 0.635 | 0.133 | yes | 0.546 | 0.124 | yes | 0.499 | 0.047 | yes | 0.492 | 0.090 | yes | 0.646 | 0.128 | yes | 0.618 | 0.169 | yes | 0.606 | 0.151 | yes | 0.650 | 0.043 | no |
| DR1476 | Predicted protein | 1.085 | 0.468 | no | 0.990 | 0.343 | no | 1.114 | 0.313 | no | 1.212 | 0.260 | no | 1.084 | 0.245 | no | 0.890 | 0.325 | no | 1.032 | 0.336 | no | 0.897 | 0.207 | no | 1.017 | 0.391 | no |
| DR1477 | DNA repair protein, recN | 0.943 | 0.209 | no | 0.884 | 0.118 | no | 0.904 | 0.195 | no | 1.151 | 0.253 | no | 0.885 | 0.165 | no | 0.834 | 0.194 | no | 0.819 | 0.149 | no | 0.803 | 0.105 | no | 0.845 | 0.080 | no |
| DR1478 | Uncharcterized protein | 0.822 | 0.283 | no | 0.546 | 0.193 | yes | 0.421 | 0.165 | yes | 0.406 | 0.145 | yes | 0.558 | 0.158 | yes | 0.472 | 0.163 | yes | 0.520 | 0.225 | yes | 0.591 | 0.083 | yes | 0.600 | 0.165 | yes |
| DR1479 | Predicted protein | 0.996 | 0.206 | no | 0.556 | 0.115 | yes | 0.361 | 0.177 | yes | 0.636 | 0.100 | yes | 0.497 | 0.127 | yes | 0.483 | 0.150 | yes | 0.508 | 0.142 | yes | 0.614 | 0.138 | yes | 0.968 | 0.108 | no |
| DR1480 | Predicted protein (low complexity) | 0.896 | 0.198 | no | 0.549 | 0.166 | yes | 0.319 | 0.116 | yes | 0.393 | 0.050 | yes | 0.574 | 0.147 | yes | 0.543 | 0.140 | yes | 0.708 | 0.176 | no | 0.958 | 0.415 | no | 1.187 | 0.165 | no |
| DR1481 | Conserved protein in the actinomycetes, DXD motif | 0.716 | 0.358 | yes | 0.395 | 0.210 | yes | 0.338 | 0.182 | yes | 0.180 | 0.081 | yes | 0.221 | 0.050 | yes | 0.200 | 0.059 | yes | 0.256 | 0.092 | yes | 0.333 | 0.116 | yes | 0.950 | 0.177 | no |
| DR1482 | 2-isopropylmalate synthase, LEU1 | 0.633 | 0.313 | yes | 0.321 | 0.114 | yes | 0.246 | 0.087 | yes | 0.237 | 0.007 | yes | 0.346 | 0.133 | yes | 0.328 | 0.158 | yes | 0.298 | 0.107 | yes | 0.295 | 0.090 | yes | 0.459 | 0.158 | yes |
| DR1483 | Membrane protein | 1.086 | 0.712 | no | 0.646 | 0.308 | yes | 0.472 | 0.303 | yes | 0.583 | 0.182 | yes | 0.519 | 0.196 | yes | 0.323 | 0.103 | yes | 0.435 | 0.151 | yes | 0.616 | 0.260 | yes | 1.076 | 0.370 | no |
| DR1484 | Predicted protein | 0.771 | 0.311 | no | 0.976 | 0.532 | no | 1.069 | 0.633 | no | 0.659 | 0.234 | yes | 1.319 | 0.757 | no | 1.300 | 0.595 | no | 1.637 | 0.529 | yes | 1.431 | 0.169 | no | 2.044 | 0.848 | yes |
| DR1485 | Lipase, a/b hydrolase | 1.109 | 0.230 | no | 1.149 | 0.339 | no | 1.030 | 0.213 | no | 1.177 | 0.315 | no | 1.325 | 0.200 | no | 1.124 | 0.275 | no | 1.451 | 0.477 | no | 1.393 | 0.190 | no | 1.766 | 0.399 | yes |
| DR1486 | Zn-finger protein | 0.627 | 0.089 | no | 1.077 | 0.807 | no | 0.799 | 0.248 | no | 3.632 | 0.269 | yes | 2.492 | 1.373 | yes | 0.978 | 0.817 | no | 1.019 | 0.575 | no | 0.831 | 0.271 | no | 0.606 | 0.317 | yes |
| DR1487 | ENOYL-COA HYDRATASE | 1.407 | 0.680 | no | 1.665 | 0.803 | yes | 1.525 | 0.628 | no | 2.100 | 1.352 | yes | 1.474 | 0.804 | no | 1.089 | 0.754 | no | 1.037 | 0.382 | no | 1.005 | 0.072 | no | 0.723 | 0.279 | no |
| DR1488 | HTH containing LYTR ortholog membrane protein | 1.244 | 0.834 | no | 2.536 | 1.420 | yes | 1.797 | 0.493 | yes | 1.735 | 0.949 | no | 1.978 | 1.528 | yes | 1.131 | 0.552 | no | 0.641 | 0.232 | no | n/a | n/a | n/a | n/a | n/a | n/a |
| DR1490 | Predicted protein | 0.661 | 0.238 | no | 1.186 | 0.339 | no | 0.882 | 0.273 | no | 1.263 | 0.527 | no | 0.842 | 0.320 | no | 1.118 | 0.289 | no | 2.223 | 1.287 | yes | 1.054 | 0.070 | no | n/a | n/a | n/a |
| DR1491 | Carboxyl-terminal protease | 0.950 | 0.361 | no | 2.342 | 0.948 | yes | 3.153 | 1.186 | yes | 2.300 | 0.634 | yes | 2.242 | 0.870 | yes | 2.036 | 1.186 | yes | 1.611 | 0.336 | yes | 1.208 | 0.323 | no | 0.968 | 0.045 | no |
| DR1492 | NADH DEHYDROGENASE subunit N (NOO14) | 1.060 | 0.446 | no | 2.626 | 0.972 | yes | 3.538 | 1.281 | yes | 4.178 | 0.227 | yes | 1.991 | 1.510 | yes | 1.141 | 0.529 | no | 1.158 | 0.583 | no | 0.965 | 0.194 | no | 0.835 | 0.288 | no |
| DR1493 | NADH DEHYDROGENASE subunit M (NOO13) | 1.337 | 0.279 | no | 2.191 | 1.126 | yes | 3.799 | 2.705 | yes | 2.887 | 1.309 | yes | 2.031 | 1.264 | yes | 1.258 | 0.343 | no | 0.972 | 0.269 | no | 0.962 | 0.314 | no | 0.828 | 0.234 | no |
| DR1494 | NADH DEHYDROGENASE subunit L (NOO12) | 1.078 | 0.403 | no | 1.282 | 0.552 | no | 1.655 | 0.607 | yes | 1.188 | 0.566 | no | 1.109 | 0.449 | no | 0.944 | 0.457 | no | 0.951 | 0.434 | no | 1.125 | 0.454 | no | 1.058 | 0.283 | no |
| DR1495 | NADH DEHYDROGENASE subunit K (NOO11) | 1.050 | 0.474 | no | 1.157 | 0.619 | no | 0.991 | 0.416 | no | 1.112 | 0.465 | no | 1.213 | 0.866 | no | 0.925 | 0.348 | no | 0.763 | 0.209 | no | 0.887 | 0.070 | no | 1.051 | 0.153 | no |
| DR1496 | NADH DEHYDROGENASE subunit J (NOO10) | 0.992 | 0.582 | no | 1.847 | 0.873 | yes | 1.403 | 0.853 | no | 1.589 | 0.807 | no | 1.378 | 0.652 | no | 0.928 | 0.370 | no | 1.341 | 0.633 | no | 1.143 | 0.165 | no | 0.936 | 0.265 | no |
| DR1497 | NADH DEHYDROGENASE subunit I (NOO9) | 0.985 | 0.245 | no | 0.864 | 0.221 | no | 0.598 | 0.188 | yes | 0.553 | 0.094 | yes | 0.639 | 0.267 | yes | 0.671 | 0.069 | no | 0.710 | 0.156 | no | 0.639 | 0.170 | yes | 0.706 | 0.175 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR1498 | NADH DEHYDROGENASE subunit H (NOO8) | 0.987 | 0.263 | no | 1.143 | 0.368 | no | 1.318 | 0.925 | no | 0.981 | 0.247 | no | 1.010 | 0.323 | no | 0.997 | 0.156 | no | 1.227 | 0.404 | no | 1.021 | 0.081 | no | 0.792 | 0.450 | no |
| DR1499 | NADH DEHYDROGENASE subunit G (NOO3) | 1.520 | 0.788 | no | 0.951 | 0.332 | no | 0.567 | 0.226 | yes | 0.749 | 0.267 | no | 0.715 | 0.194 | no | 0.639 | 0.156 | yes | 0.919 | 0.319 | no | 0.963 | 0.184 | no | 1.064 | 0.500 | no |
| DR1500 | NADH DEHYDROGENASE subunit F (NOO1) | 1.297 | 0.491 | no | 1.209 | 0.409 | no | 0.970 | 0.193 | no | 0.954 | 0.092 | no | 0.932 | 0.227 | no | 0.844 | 0.280 | no | 0.921 | 0.270 | no | 0.909 | 0.113 | no | 0.703 | 0.145 | no |
| DR1501 | NADH DEHYDROGENASE subunit E (NOO2) | 1.715 | 0.869 | yes | 1.442 | 0.770 | no | 0.821 | 0.319 | no | 0.805 | 0.113 | no | 0.988 | 0.447 | no | 0.814 | 0.212 | no | 0.963 | 0.281 | no | 0.996 | 0.133 | no | 1.014 | 0.324 | no |
| DR1502 | NADH DEHYDROGENASE subunit (Divergent) ?? | 1.160 | 0.668 | no | 0.830 | 0.311 | no | 0.546 | 0.127 | yes | 0.549 | 0.217 | yes | 0.792 | 0.313 | no | 0.778 | 0.331 | no | 0.961 | 0.394 | no | 1.033 | 0.175 | no | 1.054 | 0.389 | no |
| DR1503 | NADH DEHYDROGENASE subunit D (NOO4) | 1.550 | 0.636 | no | 1.426 | 0.797 | no | 1.057 | 0.404 | no | 0.951 | 0.274 | no | 0.964 | 0.419 | no | 0.753 | 0.402 | no | 0.855 | 0.620 | no | 1.143 | 0.280 | no | 0.822 | 0.251 | no |
| DR1504 | NADH DEHYDROGENASE subunit C (NOO5) | 0.811 | 0.247 | no | 0.543 | 0.153 | yes | 0.498 | 0.155 | yes | 0.322 | 0.027 | yes | 0.432 | 0.190 | yes | 0.372 | 0.130 | yes | 0.432 | 0.246 | yes | 0.540 | 0.195 | yes | 0.839 | 0.102 | no |
| DR1505 | NADH DEHYDROGENASE subunit B (NOO6) | 1.150 | 0.421 | no | 0.609 | 0.299 | yes | 0.433 | 0.109 | yes | 0.328 | 0.125 | yes | 0.468 | 0.173 | yes | 0.489 | 0.112 | yes | 0.553 | 0.331 | yes | 0.806 | 0.390 | no | 0.778 | 0.256 | no |
| DR1506 | NADH DEHYDROGENASE subunit A (NOO7) | 0.784 | 0.179 | no | 0.737 | 0.234 | no | 0.633 | 0.172 | yes | 0.477 | 0.196 | yes | 0.560 | 0.182 | yes | 0.430 | 0.164 | yes | 0.393 | 0.113 | yes | 0.408 | 0.104 | yes | 0.422 | 0.058 | yes |
| DR1507 | YAEL family Membrane metalloprotease with PDZ domain | 0.867 | 0.270 | no | 0.791 | 0.195 | no | 0.632 | 0.206 | yes | 0.519 | 0.058 | yes | 0.637 | 0.289 | yes | 0.559 | 0.280 | yes | 0.492 | 0.206 | yes | 0.591 | 0.212 | yes | 0.884 | 0.211 | no |
| DR1508 | YAEM ortholog, Rossman fold oxidoreductase | 0.796 | 0.287 | no | 0.810 | 0.390 | no | 1.139 | 0.210 | no | 0.936 | 0.145 | no | 0.980 | 0.450 | no | 1.118 | 0.578 | no | 1.527 | 0.742 | no | 1.243 | 0.249 | no | 1.294 | 0.377 | no |
| DR1509 | CDP-diacylglycerol synthase | 0.880 | 0.373 | no | 2.895 | 0.750 | yes | 2.346 | 0.586 | yes | 1.336 | 0.070 | no | 1.379 | 0.232 | no | 1.200 | 0.456 | no | 0.972 | 0.301 | no | 1.090 | 0.244 | no | 0.804 | 0.415 | no |
| DR1510 | Ribosome recycling factor, RRF | 0.696 | 0.165 | no | 2.651 | 0.502 | yes | 2.207 | 0.369 | yes | 1.918 | 0.483 | yes | 1.893 | 0.311 | yes | 1.136 | 0.339 | no | 0.939 | 0.185 | no | 0.941 | 0.071 | no | 0.497 | 0.120 | yes |
| DR1511 | Uridylate kinase ,PYRH | 0.923 | 0.315 | no | 2.257 | 0.604 | yes | 1.827 | 0.424 | yes | 1.206 | 0.281 | no | 1.229 | 0.428 | no | 1.018 | 0.477 | no | 0.856 | 0.279 | no | 0.902 | 0.158 | no | 0.490 | 0.116 | yes |
| DR1512 | Elongation factor EF-Ts | 0.712 | 0.217 | no | 2.563 | 1.748 | yes | 1.460 | 0.371 | yes | 0.854 | 0.195 | no | 1.294 | 0.691 | no | 1.286 | 0.554 | no | 1.000 | 0.296 | no | 0.290 | 0.050 | yes | n/a | n/a | n/a |
| DR1513 | 30S RIBOSOMAL PROTEIN S2 | 0.846 | 0.292 | no | 1.491 | 0.635 | no | 1.321 | 0.306 | no | 0.863 | 0.371 | no | 1.132 | 0.266 | no | 0.960 | 0.369 | no | 0.997 | 0.168 | no | 0.799 | 0.154 | no | 0.563 | 0.209 | yes |
| DR1514 | 2-phosphoglycerate kinase, domain duplication?, Archaeal type | 0.803 | 0.352 | no | 1.160 | 0.384 | no | 0.941 | 0.201 | no | 0.748 | 0.119 | no | 0.959 | 0.439 | no | 0.813 | 0.214 | no | 0.913 | 0.261 | no | 1.011 | 0.221 | no | 0.679 | 0.084 | no |
| DR1515 | Predicted protein | 1.304 | 0.113 | no | 1.304 | 0.279 | no | 1.272 | 0.744 | no | 1.216 | 0.148 | no | 1.182 | 0.333 | no | 1.009 | 0.181 | no | 1.020 | 0.192 | no | 1.094 | 0.164 | no | 1.234 | 0.152 | no |
| DR1516 | Acetolactate synthase; large subunit | 0.870 | 0.255 | no | 1.059 | 0.440 | no | 1.262 | 0.495 | no | 1.086 | 0.377 | no | 1.357 | 0.497 | no | 1.201 | 0.391 | no | 1.441 | 0.519 | no | 1.375 | 0.274 | no | 1.402 | 0.395 | no |
| DR1518 | Predicted protein | 1.223 | 0.345 | no | 1.050 | 0.466 | no | 1.641 | 0.601 | yes | 1.457 | 0.291 | no | 2.078 | 1.166 | yes | 1.182 | 0.498 | no | 0.940 | 0.128 | no | 1.006 | 0.139 | no | 0.922 | 0.342 | no |
| DR1519 | Ketol-acid reductoisomerase | 0.894 | 0.401 | no | 1.277 | 0.471 | no | 1.348 | 0.474 | no | 1.608 | 0.693 | no | 1.469 | 0.662 | no | 1.262 | 0.657 | no | 1.043 | 0.538 | no | 1.229 | 0.430 | no | 1.075 | 0.156 | no |
| DR1520 | Uncharacterized conserved protein, YGGJ ortholog | 1.071 | 0.360 | no | 0.928 | 0.233 | no | 0.996 | 0.330 | no | 1.004 | 0.092 | no | 1.129 | 0.491 | no | 0.718 | 0.215 | no | 0.588 | 0.143 | yes | 0.857 | 0.114 | no | 0.798 | 0.136 | no |
| DR1521 | Ribosomal protein methyltransferase, PRMA ortholog; | 0.771 | 0.447 | no | 0.784 | 0.387 | no | 0.616 | 0.126 | yes | 0.627 | 0.261 | yes | 0.698 | 0.190 | no | 0.681 | 0.239 | yes | 0.804 | 0.502 | yes | 1.105 | 0.305 | no | 1.037 | 0.133 | no |
| DR1522 | Pyrroline-5-carboxylate reductase, PROC | 0.994 | 0.191 | no | 0.716 | 0.151 | no | 0.516 | 0.201 | yes | 0.515 | 0.076 | yes | 0.623 | 0.184 | yes | 0.679 | 0.170 | yes | 0.642 | 0.190 | yes | 0.682 | 0.204 | yes | 0.801 | 0.283 | no |
| DR1524 | Gamma-glutamyltranspeptidase, cephalosporin acylase I | 0.800 | 0.259 | no | 0.936 | 0.243 | no | 0.991 | 0.337 | no | 0.903 | 0.227 | no | 1.038 | 0.237 | no | 0.809 | 0.195 | no | 0.981 | 0.168 | no | 0.889 | 0.133 | no | 0.945 | 0.227 | no |
| DR1525 | Fructokinase RBSK ortholog | 0.947 | 0.150 | no | 0.865 | 0.134 | no | 0.953 | 0.186 | no | 1.045 | 0.273 | no | 1.194 | 0.394 | no | 0.963 | 0.333 | no | 0.883 | 0.143 | no | 0.935 | 0.156 | no | 0.907 | 0.300 | no |
| DR1526 | Dimethyladenosine transferase, KsgA ortholog, rRNA methylase | 0.739 | 0.241 | no | 0.824 | 0.353 | no | 0.923 | 0.221 | no | 0.641 | 0.332 | yes | 0.794 | 0.314 | no | 0.689 | 0.199 | yes | 0.738 | 0.200 | no | 0.818 | 0.085 | no | 0.913 | 0.356 | no |
| DR1527 | Predicted protein | 0.817 | 0.131 | no | 0.689 | 0.149 | no | 0.631 | 0.181 | yes | 0.590 | 0.239 | yes | 0.547 | 0.221 | yes | 0.546 | 0.209 | yes | 0.538 | 0.124 | yes | 0.710 | 0.147 | yes | 0.801 | 0.130 | no |
| DR1528 | TPR repeat protein | 0.701 | 0.165 | no | 0.597 | 0.239 | yes | 0.428 | 0.197 | yes | 0.465 | 0.084 | yes | 0.482 | 0.045 | yes | 0.516 | 0.128 | yes | 0.669 | 0.259 | yes | 0.735 | 0.098 | no | 0.657 | 0.076 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR1529 | YJEF ortholog, sugar kinase of the RBSK family | 1.087 | 0.399 | no | 0.960 | 0.270 | no | 0.926 | 0.270 | no | 0.736 | 0.219 | no | 0.789 | 0.271 | no | 0.718 | 0.200 | no | 0.774 | 0.168 | no | 0.909 | 0.250 | no | 0.979 | 0.309 | no |
| DR1530 | PIN domain containing protein, VapC family | 0.968 | 0.362 | no | 0.681 | 0.140 | yes | 0.699 | 0.122 | no | 0.629 | 0.224 | yes | 0.735 | 0.112 | no | 0.716 | 0.114 | no | 0.714 | 0.322 | yes | 0.817 | 0.225 | no | 0.815 | 0.230 | no |
| DR1531 | Predicted protein | 0.725 | 0.158 | no | 0.585 | 0.188 | yes | 0.509 | 0.131 | yes | 0.488 | 0.233 | yes | 0.421 | 0.205 | yes | 0.448 | 0.256 | yes | 0.288 | 0.095 | yes | 0.480 | 0.165 | yes | 0.772 | 0.293 | no |
| DR1532 | Transcription-repair coupling factor; MFD superfamily II helicase | 0.875 | 0.237 | no | 0.751 | 0.197 | no | 0.709 | 0.220 | no | 0.714 | 0.279 | no | 0.657 | 0.193 | yes | 0.616 | 0.211 | yes | 0.647 | 0.185 | yes | 0.665 | 0.100 | yes | 0.771 | 0.259 | no |
| DR1533 | C-terminal McrA nuclease domain + shares a domain with eukaryotic proteins | 0.882 | 0.246 | no | 0.820 | 0.207 | no | 0.913 | 0.148 | no | 0.903 | 0.086 | no | 0.881 | 0.183 | no | 0.703 | 0.252 | no | 0.715 | 0.108 | no | 0.772 | 0.097 | no | 1.030 | 0.165 | no |
| DR1534 | Protein N-Acetyltransferase | 0.766 | 0.268 | no | 0.846 | 0.399 | no | 0.836 | 0.205 | no | 0.885 | 0.124 | no | 0.926 | 0.439 | no | 1.129 | 0.473 | no | 1.231 | 0.524 | no | 1.098 | 0.289 | no | 1.170 | 0.444 | no |
| DR1535 | Degenerate lipase, inactive enzyme? | 1.001 | 0.223 | no | 1.526 | 0.493 | yes | 1.417 | 0.743 | no | 1.072 | 0.063 | no | 0.953 | 0.182 | no | 0.890 | 0.359 | no | 0.825 | 0.257 | no | 0.976 | 0.277 | no | 0.888 | 0.289 | no |
| DR1536 | Extracellular subtitlisin-like serine protease | 0.856 | 0.380 | no | 0.411 | 0.141 | yes | 0.187 | 0.055 | yes | 0.200 | 0.037 | yes | 0.238 | 0.111 | yes | 0.304 | 0.136 | yes | 0.394 | 0.179 | yes | 0.648 | 0.246 | yes | 0.776 | 0.423 | no |
| DR1537 | Phospholipase, a/b hydrolase | 0.996 | 0.312 | no | 1.402 | 0.577 | no | 1.364 | 0.423 | no | 1.517 | 0.375 | no | 1.420 | 0.507 | no | 0.910 | 0.299 | no | 0.762 | 0.173 | no | 0.810 | 0.102 | no | 0.990 | 0.347 | no |
| DR1538 | OSMC ortholog, conserved bacterial/archaeal proteins involved in alkylperoxide and oxidative stress response, osmotically induced protein | 0.826 | 0.224 | no | 0.717 | 0.309 | no | 1.104 | 0.415 | no | 0.841 | 0.366 | no | 1.304 | 0.865 | no | 1.549 | 0.565 | no | 2.250 | 1.895 | no | n/a | n/a | n/a | n/a | n/a | n/a |
| DR1539 | Predicted protein | 1.182 | 0.458 | no | 0.807 | 0.363 | no | 0.622 | 0.324 | yes | 0.601 | 0.241 | yes | 0.788 | 0.263 | no | 0.743 | 0.135 | no | 1.021 | 0.341 | no | 1.041 | 0.425 | no | 1.933 | 0.826 | yes |
| DR1540 | Isocitrate dehydrogenase, IDH | 0.659 | 0.213 | yes | 0.269 | 0.121 | yes | 0.336 | 0.107 | yes | 0.388 | 0.021 | yes | 0.449 | 0.253 | yes | 0.568 | 0.257 | yes | 0.520 | 0.232 | yes | 0.879 | 0.138 | no | 1.510 | 0.380 | yes |
| DR1541 | Membrane protein | 0.972 | 0.364 | no | 1.032 | 0.375 | no | 1.353 | 0.673 | no | 0.891 | 0.440 | no | 1.135 | 0.599 | no | 1.006 | 0.426 | no | 0.914 | 0.306 | no | 0.920 | 0.288 | no | 0.779 | 0.183 | no |
| DR1542 | Acetyl-CoA carboxylase | 0.645 | 0.248 | yes | 0.444 | 0.208 | yes | 0.618 | 0.224 | yes | 0.490 | 0.040 | yes | 0.489 | 0.145 | yes | 0.503 | 0.280 | yes | 0.481 | 0.238 | yes | 0.842 | 0.269 | no | 0.722 | 0.223 | no |
| DR1543 | Unknown DORF? Secreted? | 0.835 | 0.341 | no | 0.896 | 0.571 | no | 1.321 | 0.379 | no | 0.961 | 0.164 | no | 0.976 | 0.350 | no | 0.669 | 0.270 | yes | 0.562 | 0.116 | yes | 0.948 | 0.100 | no | 0.845 | 0.090 | no |
| DR1544 | Acyl-CoA dehydrogenase, ACDS | 0.715 | 0.249 | no | 1.194 | 0.850 | no | 1.004 | 0.232 | no | 1.271 | 0.482 | no | 0.701 | 0.147 | no | 0.846 | 0.430 | no | 0.995 | 0.393 | no | 1.250 | 0.406 | no | n/a | n/a | n/a |
| DR1545 | Predicted protein | 1.053 | 0.201 | no | 1.016 | 0.316 | no | 1.482 | 0.612 | yes | 1.602 | 0.393 | no | 1.480 | 0.452 | no | 1.140 | 0.385 | no | 0.875 | 0.273 | no | 1.275 | 0.578 | no | 1.435 | 0.573 | no |
| DR1546 | Copper/zinc-superoxide dismutase, SODC | 0.926 | 0.461 | no | 0.500 | 0.305 | yes | 0.852 | 0.523 | no | 2.477 | 0.539 | yes | 2.629 | 1.411 | yes | 1.492 | 0.890 | no | 2.550 | 1.741 | yes | 1.214 | 0.143 | no | 1.596 | 0.372 | yes |
| DR1547 | Predicted protein | 1.659 | 0.767 | yes | 1.085 | 0.421 | no | 1.856 | 1.055 | yes | 1.681 | 0.574 | yes | 1.383 | 0.529 | no | 1.331 | 0.391 | no | 1.485 | 0.726 | no | 1.583 | 0.621 | yes | 1.354 | 0.435 | no |
| DR1548 | Bacillus ykwD ortholog, Divergent member of the secreted PRP1, plant pathogenesis related protein superfamily | 0.944 | 0.469 | no | 1.188 | 0.388 | no | 2.326 | 1.040 | yes | 5.624 | 2.348 | yes | 4.938 | 3.196 | yes | 1.559 | 0.649 | no | 1.623 | 0.787 | yes | 1.452 | 0.281 | yes | 1.359 | 0.239 | no |
| DR1549 | Lipoprotein NLPD-like family; contains metalloendopeptidase domain | 1.207 | 0.195 | no | 1.732 | 0.364 | yes | 2.189 | 0.743 | yes | 1.882 | 0.424 | yes | 1.301 | 0.263 | no | 1.142 | 0.348 | no | 1.113 | 0.199 | no | 1.166 | 0.366 | no | 1.491 | 0.592 | no |
| DR1550 | FtsE ATPase fusion with ftsX domain | 0.980 | 0.343 | no | 0.957 | 0.244 | no | 1.212 | 0.571 | no | 1.037 | 0.264 | no | 0.893 | 0.291 | no | 0.765 | 0.275 | no | 0.710 | 0.139 | no | 0.790 | 0.217 | no | 1.037 | 0.215 | no |
| DR1551 | Carboxyl-terminal protease, PDZ and IRBP domain containing | 1.216 | 0.292 | no | 1.137 | 0.147 | no | 1.382 | 0.299 | no | 1.248 | 0.230 | no | 1.095 | 0.624 | no | 1.218 | 0.569 | no | 1.129 | 0.173 | no | 1.243 | 0.339 | no | 1.895 | 0.447 | yes |
| DR1552 | Predicted protein | 1.131 | 0.444 | no | 0.599 | 0.199 | yes | 0.438 | 0.178 | yes | 0.581 | 0.209 | yes | 0.523 | 0.248 | yes | 0.533 | 0.155 | yes | 0.593 | 0.202 | yes | 0.604 | 0.119 | yes | 0.580 | 0.220 | yes |
| DR1553 | Peptide chain release factor (RF3) GTPase | 0.774 | 0.078 | no | 0.581 | 0.156 | yes | 0.477 | 0.157 | yes | 0.434 | 0.091 | yes | 0.525 | 0.094 | yes | 0.492 | 0.187 | yes | 0.459 | 0.132 | yes | 0.424 | 0.103 | yes | 0.642 | 0.120 | yes |
| DR1555 | Glycosyltransferase of the SPT4 class, Bacillus YPJH ortholog | 1.117 | 0.546 | no | 1.018 | 0.148 | no | 1.026 | 0.144 | no | 0.955 | 0.107 | no | 0.963 | 0.334 | no | 0.941 | 0.142 | no | 0.896 | 0.102 | no | 0.973 | 0.331 | no | 1.003 | 0.276 | no |

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| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR1556 | Membrane bounded sensor histidine kinase | 1.140 | 0.496 | no | 2.657 | 0.755 | yes | 3.614 | 1.707 | yes | 2.403 | 1.482 | yes | 1.934 | 0.589 | yes | 1.999 | 0.693 | yes | 1.440 | 0.682 | no | 1.090 | 0.546 | no | 0.596 | 0.139 | yes |
| DR1557 | Predicted protein | 0.993 | 0.589 | no | 3.150 | 0.577 | yes | 5.059 | 1.571 | yes | 2.799 | 0.576 | yes | 2.947 | 0.832 | yes | 2.357 | 1.160 | yes | 1.711 | 0.258 | yes | 1.133 | 0.371 | no | 1.061 | 0.349 | no |
| DR1558 | Receiver domain (flavodoxin, CHEY family) of 2 component system + C- terminal HTH | 1.272 | 0.471 | no | 3.552 | 0.569 | yes | 5.639 | 1.490 | yes | 3.859 | 0.630 | yes | 2.521 | 0.479 | yes | 2.534 | 0.651 | yes | 1.639 | 0.479 | yes | 1.240 | 0.327 | no | 1.268 | 0.395 | no |
| DR1559 | Predicted protein | 0.874 | 0.161 | no | 3.187 | 1.185 | yes | 4.393 | 1.602 | yes | 2.781 | 0.203 | yes | 2.092 | 0.619 | yes | 1.724 | 0.544 | yes | 1.411 | 0.278 | no | 0.982 | 0.304 | no | 1.023 | 0.348 | no |
| DR1560 | Diacylglycerol kinase, Bacillus BMRU homolog | 0.978 | 0.310 | no | 3.052 | 1.188 | yes | 3.914 | 1.941 | yes | 2.970 | 0.804 | yes | 1.639 | 0.315 | yes | 1.444 | 0.574 | no | 1.164 | 0.175 | no | 0.978 | 0.209 | no | 0.732 | 0.266 | no |
| DR1561 | UDP-N-acetylglucosamine 2-epimerase | 0.800 | 0.481 | no | 4.266 | 1.054 | yes | 5.999 | 1.396 | yes | 2.959 | 0.538 | yes | 3.547 | 1.775 | yes | 2.380 | 0.822 | yes | 1.345 | 0.459 | no | 1.057 | 0.380 | no | 0.965 | 0.376 | no |
| DR1562 | Undecaprenyl-phosphate N-acetylglucosaminyltransferase, RFF | 0.970 | 0.287 | no | 2.403 | 0.721 | yes | 2.443 | 0.579 | yes | 1.891 | 0.207 | yes | 2.102 | 1.103 | yes | 1.358 | 0.387 | no | 1.090 | 0.249 | no | 1.065 | 0.506 | no | 1.171 | 0.720 | no |
| DR1563 | Uracil phosphoribosyltransferase | 0.731 | 0.153 | no | 1.529 | 0.620 | yes | 1.796 | 0.508 | yes | 1.392 | 0.131 | no | 1.595 | 0.433 | yes | 1.156 | 0.269 | no | 0.849 | 0.137 | no | 0.942 | 0.156 | no | 1.010 | 0.235 | no |
| DR1564 | Possible choline kinase - like, very divergent | 0.940 | 0.443 | no | 1.376 | 0.765 | no | 2.006 | 0.748 | yes | 1.593 | 0.193 | yes | 1.873 | 1.068 | yes | 1.112 | 0.436 | no | 0.951 | 0.216 | no | 0.972 | 0.445 | no | 1.033 | 0.388 | no |
| DR1565 | HD superfamily phosphohydrolase | 1.176 | 0.258 | no | 1.532 | 0.978 | no | 1.215 | 0.153 | no | 1.204 | 0.192 | no | 1.743 | 0.792 | yes | 0.960 | 0.256 | no | 1.068 | 0.493 | no | 0.808 | 0.166 | no | 0.864 | 0.264 | no |
| DR1566 | Predicted protein | 0.957 | 0.284 | no | 1.175 | 0.204 | no | 1.508 | 0.351 | yes | 1.593 | 0.134 | yes | 1.624 | 0.543 | yes | 1.033 | 0.212 | no | 1.170 | 0.276 | no | 1.124 | 0.393 | no | 1.139 | 0.235 | no |
| DR1567 | ABC ATPase, oligopeptide transporter, OppF | 0.653 | 0.301 | yes | 0.587 | 0.136 | yes | 1.813 | 0.507 | yes | 1.324 | 0.550 | no | 2.240 | 1.038 | yes | 1.670 | 0.894 | no | 1.043 | 0.434 | no | 1.418 | 0.253 | no | 2.282 | 0.542 | yes |
| DR1568 | ABC ATPase, oligopeptide transporter, OppD | 0.823 | 0.176 | no | 0.889 | 0.367 | no | 1.577 | 0.354 | yes | 1.696 | 0.280 | yes | 1.899 | 1.207 | yes | 1.474 | 0.977 | no | 0.914 | 0.178 | no | 1.301 | 0.297 | no | 2.353 | 0.901 | yes |
| DR1569 | Permease; oligopeptide transporter, OppC | 0.975 | 0.326 | no | 1.219 | 0.629 | no | 2.465 | 1.216 | yes | 2.524 | 0.982 | yes | 2.190 | 0.840 | yes | 1.471 | 1.041 | no | 1.029 | 0.370 | no | 1.251 | 0.366 | no | 1.888 | 0.722 | yes |
| DR1570 | Permease; oligopeptide transporter, OppB | 0.895 | 0.132 | no | 0.933 | 0.153 | no | 1.886 | 0.485 | yes | 2.221 | 0.469 | yes | 1.988 | 0.837 | yes | 0.973 | 0.251 | no | 1.108 | 0.228 | no | 1.360 | 0.168 | no | 2.129 | 0.448 | yes |
| DR1571 | Oligopeptide binding protein; oligopeptide transporter OppA | 0.797 | 0.261 | no | 0.385 | 0.203 | yes | 0.754 | 0.385 | no | 0.758 | 0.379 | no | 0.745 | 0.302 | no | 0.432 | 0.166 | yes | 0.605 | 0.315 | yes | 1.050 | 0.432 | no | 4.688 | 2.421 | yes |
| DR1573 | CTP synthase, PYRG | 0.866 | 0.163 | no | 0.668 | 0.219 | yes | 0.464 | 0.132 | yes | 0.434 | 0.181 | yes | 0.354 | 0.117 | yes | 0.297 | 0.128 | yes | 0.281 | 0.117 | yes | 0.184 | 0.076 | yes | 0.274 | 0.081 | yes |
| DR1574 | Phosphatidyl serine decarboxylase, Archaeal and Mycobacterium type | 1.414 | 0.680 | no | 0.867 | 0.408 | no | 1.191 | 0.761 | no | 0.632 | 0.051 | no | 0.803 | 0.280 | no | 0.551 | 0.096 | yes | 0.994 | 0.388 | no | 0.913 | 0.412 | no | 0.641 | 0.087 | no |
| DR1575 | Predicted protein | 0.898 | 0.192 | no | 0.932 | 0.170 | no | 1.018 | 0.363 | no | 0.887 | 0.246 | no | 0.672 | 0.146 | yes | 0.733 | 0.153 | no | 0.709 | 0.147 | no | 0.734 | 0.242 | yes | 0.828 | 0.361 | no |
| DR1576 | Predicted protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR1577 | QueA ortholog, S-adenosylmethionine:tRNA ribosyltransferase-isomerase | 1.096 | 0.380 | no | 0.893 | 0.302 | no | 1.053 | 0.416 | no | 1.135 | 0.391 | no | 0.791 | 0.241 | no | 0.903 | 0.379 | no | 0.969 | 0.287 | no | 0.958 | 0.450 | no | 1.098 | 0.366 | no |
| DR1578 | Uncharacterized enzyme | 0.811 | 0.087 | no | 0.523 | 0.116 | yes | 0.524 | 0.113 | yes | 0.475 | 0.026 | yes | 0.576 | 0.123 | yes | 0.557 | 0.126 | yes | 0.655 | 0.155 | yes | 0.531 | 0.108 | yes | 0.747 | 0.097 | no |
| DR1579 | Aminotransferase | 1.112 | 0.529 | no | 0.705 | 0.300 | yes | 0.864 | 0.316 | no | 0.930 | 0.578 | no | 0.713 | 0.382 | yes | 0.715 | 0.351 | yes | 0.800 | 0.341 | no | 0.624 | 0.179 | yes | 1.097 | 0.619 | no |
| DR1580 | Predicted protein | 0.931 | 0.238 | no | 0.736 | 0.118 | no | 1.007 | 0.374 | no | 0.955 | 0.154 | no | 1.257 | 0.484 | no | 1.004 | 0.171 | no | 1.042 | 0.510 | no | 0.740 | 0.159 | no | 0.809 | 0.334 | no |
| DR1581 | ABC ATPase, MDR type | 1.254 | 0.469 | no | 1.864 | 1.194 | yes | 2.860 | 1.209 | yes | 3.179 | 0.773 | yes | 2.408 | 1.479 | yes | 2.165 | 0.811 | yes | 1.648 | 0.750 | yes | 1.158 | 0.564 | no | 0.960 | 0.593 | no |
| DR1582 | Conserved membrane protein | 0.974 | 0.229 | no | 1.529 | 0.731 | yes | 2.355 | 1.508 | yes | 2.261 | 0.515 | yes | 1.870 | 0.603 | yes | 1.641 | 0.558 | yes | 1.278 | 0.425 | no | 1.031 | 0.305 | no | 0.884 | 0.389 | no |
| DR1583 | Conserved membrane protein | 1.388 | 0.226 | no | 2.593 | 0.721 | yes | 3.852 | 0.942 | yes | 3.820 | 0.341 | yes | 2.430 | 1.000 | yes | 2.301 | 0.599 | yes | 1.764 | 0.685 | yes | 1.212 | 0.360 | no | 1.139 | 0.438 | no |
| DR1584 | Predicted protein | 0.997 | 0.145 | no | 1.424 | 0.414 | no | 2.122 | 0.519 | yes | 2.240 | 0.352 | yes | 1.927 | 0.600 | yes | 1.489 | 0.326 | no | 1.749 | 0.479 | yes | 1.369 | 0.054 | no | 1.405 | 0.509 | no |
| DR1585 | Rnase PH, TRNA nucleotidyltransferase | 1.181 | 0.138 | no | 1.778 | 0.521 | yes | 2.007 | 0.486 | yes | 2.236 | 0.365 | yes | 1.771 | 0.299 | yes | 1.588 | 0.521 | yes | 1.500 | 0.161 | yes | 1.547 | 0.140 | yes | 1.615 | 0.217 | yes |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR1586 | Glutamate racemase, MURI | 0.977 | 0.184 | no | 2.032 | 0.939 | yes | 2.526 | 1.062 | yes | 1.792 | 0.171 | yes | 1.727 | 0.466 | yes | 1.598 | 0.492 | yes | 1.217 | 0.366 | no | 1.222 | 0.258 | no | 1.251 | 0.200 | no |
| DR1587 | Predicted protein | 1.461 | 0.715 | no | 2.028 | 0.547 | yes | 2.249 | 0.633 | yes | 3.304 | 1.560 | yes | 1.668 | 0.268 | yes | 1.250 | 0.354 | no | 1.075 | 0.167 | no | 1.066 | 0.295 | no | 0.979 | 0.578 | no |
| DR1588 | Aminotransferase | 0.968 | 0.272 | no | 1.006 | 0.283 | no | 1.040 | 0.266 | no | 0.793 | 0.192 | no | 1.374 | 0.503 | no | 1.003 | 0.208 | no | 0.875 | 0.118 | no | 0.930 | 0.119 | no | 1.154 | 0.325 | no |
| DR1589 | Fructose-1,6-bisphosphate aldolase, | 1.196 | 0.413 | no | 0.881 | 0.335 | no | 1.086 | 0.567 | no | 1.392 | 0.528 | no | 1.246 | 0.533 | no | 1.195 | 0.406 | no | 1.072 | 0.125 | no | 1.503 | 0.388 | yes | 2.449 | 0.430 | yes |
| DR1590 | Predicted protein | 0.800 | 0.079 | no | 0.726 | 0.247 | no | 0.555 | 0.196 | yes | 0.703 | 0.069 | no | 1.315 | 0.584 | no | 1.034 | 0.406 | no | 1.031 | 0.731 | no | 1.086 | 0.174 | no | 1.366 | 0.241 | no |
| DR1591 | Predicted protein | 1.300 | 0.111 | no | 1.630 | 0.541 | yes | 1.788 | 0.653 | yes | 1.923 | 0.223 | yes | 1.276 | 0.265 | no | 1.122 | 0.452 | no | 1.074 | 0.375 | no | 1.020 | 0.436 | no | 0.863 | 0.405 | no |
| DR1592 | Transposon DORF | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR1593 | Transposase with conserved C- terminal C2C2 finger | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR1594 | Predicted protein | 0.803 | 0.346 | no | 1.055 | 0.437 | no | 1.915 | 1.246 | yes | 1.808 | 0.696 | yes | 1.761 | 0.469 | yes | 0.982 | 0.379 | no | 0.799 | 0.224 | no | 1.306 | 0.505 | no | 1.353 | 0.639 | no |
| DR1595 | 6-phosphogluconate dehydrogenase | 0.992 | 0.148 | no | 1.195 | 0.254 | no | 1.269 | 0.390 | no | 1.388 | 0.492 | no | 1.554 | 0.746 | no | 1.285 | 0.289 | no | 1.118 | 0.150 | no | 1.366 | 0.115 | no | 2.299 | 0.517 | yes |
| DR1596 | Glucose-6-phosphate 1-dehydrogenase | 0.984 | 0.210 | no | 1.185 | 0.287 | no | 1.405 | 0.441 | no | 1.492 | 0.261 | no | 1.498 | 0.350 | no | 1.431 | 0.456 | no | 1.225 | 0.486 | no | 1.091 | 0.441 | no | 1.223 | 0.470 | no |
| DR1597 | OPCA, OxPPCycle gene, involved in the assembly of above protein | 0.963 | 0.277 | no | 1.011 | 0.299 | no | 1.917 | 0.891 | yes | 2.328 | 1.000 | yes | 1.618 | 0.156 | yes | 1.185 | 0.302 | no | 1.049 | 0.239 | no | 1.286 | 0.133 | no | 1.808 | 0.441 | yes |
| DR1598 | Zinc metalloprotease | 0.990 | 0.541 | no | 0.536 | 0.127 | yes | 0.613 | 0.271 | yes | 0.720 | 0.363 | no | 0.883 | 0.247 | no | 0.743 | 0.278 | no | 0.601 | 0.230 | yes | 1.027 | 0.109 | no | 1.621 | 0.576 | yes |
| DR1599 | Serine protease | 1.348 | 0.447 | no | 0.877 | 0.261 | no | 0.733 | 0.438 | yes | 0.960 | 0.347 | no | 0.801 | 0.222 | no | 0.944 | 0.263 | no | 1.081 | 0.345 | no | 1.169 | 0.317 | no | 1.099 | 0.374 | no |
| DR1600 | Secreted nuclease, E.coli Endo I homolog | 0.998 | 0.166 | no | 0.689 | 0.175 | no | 0.463 | 0.131 | yes | 0.702 | 0.125 | no | 0.665 | 0.183 | yes | 0.697 | 0.206 | no | 0.848 | 0.309 | no | 0.754 | 0.229 | no | 0.560 | 0.190 | yes |
| DR1601 | Uncharacterized family of membrane proteins, moderately conserved in archaea and eukaryotes | 1.401 | 0.470 | no | 1.141 | 0.441 | no | 1.356 | 0.730 | no | 1.526 | 0.330 | no | 1.437 | 0.548 | no | 1.769 | 0.669 | yes | 1.868 | 0.472 | yes | 1.524 | 0.232 | yes | 1.790 | 0.347 | yes |
| DR1602 | Predicted membrane protein similar to CG6903 of D.melanogaster | 1.351 | 0.923 | no | 1.145 | 0.195 | no | 1.031 | 0.244 | no | 1.104 | 0.254 | no | 0.780 | 0.203 | no | 0.825 | 0.168 | no | 0.934 | 0.258 | no | 0.936 | 0.101 | no | 1.214 | 0.306 | no |
| DR1603 | Predicted protein | 1.199 | 0.303 | no | 1.350 | 0.178 | no | 1.368 | 0.149 | no | 1.458 | 0.182 | no | 0.965 | 0.285 | no | 0.998 | 0.331 | no | 1.019 | 0.118 | no | 1.031 | 0.248 | no | 1.316 | 0.194 | no |
| DR1604 | Chitin deacetylase, NODB (a conserved family including amylases) | 0.919 | 0.233 | no | 1.077 | 0.359 | no | 1.360 | 0.643 | no | 1.038 | 0.468 | no | 1.019 | 0.441 | no | 0.860 | 0.234 | no | 0.960 | 0.252 | no | 0.892 | 0.071 | no | 1.740 | 0.234 | yes |
| DR1606 | Secreted sensor histidine kinase | 1.015 | 0.219 | no | 1.368 | 0.414 | no | 1.544 | 0.427 | yes | 1.319 | 0.036 | no | 1.172 | 0.322 | no | 1.064 | 0.425 | no | 0.861 | 0.238 | no | 0.774 | 0.067 | no | 0.712 | 0.301 | no |
| DR1607 | Predicted protein | 1.309 | 0.450 | no | 1.428 | 0.598 | no | 1.727 | 1.160 | yes | 1.605 | 1.047 | no | 1.576 | 0.966 | no | 1.537 | 0.873 | no | 1.370 | 0.690 | no | 1.151 | 0.517 | no | 1.125 | 0.367 | no |
| DR1608 | Distant homolog of YuaE of Babillus subtilis | 0.947 | 0.271 | no | 1.125 | 0.607 | no | 0.573 | 0.032 | yes | 0.965 | 0.711 | no | 1.021 | 0.575 | no | 0.941 | 0.483 | no | 0.862 | 0.396 | no | 0.947 | 0.240 | no | 0.950 | 0.266 | no |
| DR1609 | 2-hydroxyhepta-2,4-diene-1,7-dioate, alkene isomerase/decarboxylase | 0.971 | 0.428 | no | 1.237 | 0.575 | no | 1.865 | 1.281 | yes | 1.421 | 0.870 | no | 1.202 | 0.515 | no | 1.409 | 0.608 | no | 1.179 | 0.526 | no | 1.054 | 0.248 | no | 1.441 | 0.205 | yes |
| DR1610 | Isopropylmalate isomerase | 0.984 | 0.348 | no | 0.942 | 0.498 | no | 0.577 | 0.241 | yes | 0.522 | 0.285 | yes | 0.702 | 0.243 | no | 0.690 | 0.436 | yes | 0.721 | 0.381 | yes | 0.745 | 0.344 | yes | 0.758 | 0.346 | no |
| DR1611 | Predicted protein | 1.172 | 0.485 | no | 1.003 | 0.479 | no | 0.683 | 0.258 | yes | 0.785 | 0.496 | no | 1.093 | 0.752 | no | 0.869 | 0.310 | no | 0.915 | 0.264 | no | 0.939 | 0.415 | no | 1.804 | 0.696 | yes |
| DR1612 | Conserved archaeal family seen in some bacteria | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR1613 | HTH transcripition factor, ArsR family | 0.922 | 0.426 | no | 1.925 | 0.926 | yes | 1.632 | 0.610 | yes | 1.314 | 0.091 | no | 1.305 | 0.478 | no | 1.113 | 0.359 | no | 0.813 | 0.333 | no | 0.840 | 0.053 | no | 1.024 | 0.433 | no |
| DR1614 | 3-isopropylmalate dehydratase | 1.042 | 0.177 | no | 1.310 | 0.441 | no | 1.381 | 0.634 | no | 1.311 | 0.215 | no | 1.470 | 0.854 | no | 1.060 | 0.385 | no | 0.920 | 0.246 | no | 1.009 | 0.178 | no | 1.314 | 0.214 | no |
| DR1615 | Predicted protein | 0.849 | 0.177 | no | 1.486 | 0.465 | yes | 1.922 | 1.373 | yes | 1.102 | 0.241 | no | 1.295 | 0.273 | no | 1.066 | 0.404 | no | 0.698 | 0.294 | yes | 0.999 | 0.253 | no | 0.701 | 0.191 | no |
| DR1616 | Uncharacterized conserved membrane | 1.054 | 0.124 | no | 1.274 | 0.307 | no | 1.377 | 0.304 | no | 1.438 | 0.240 | no | 1.466 | 0.315 | no | 1.477 | 0.457 | no | 1.341 | 0.173 | no | 1.554 | 0.315 | yes | 1.488 | 0.358 | yes |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR1617 | Xanthine phosphoribosyltransferase | 1.044 | 0.275 | no | 0.908 | 0.229 | no | 1.297 | 0.441 | no | 0.960 | 0.325 | no | 1.304 | 0.227 | no | 0.958 | 0.227 | no | 1.263 | 0.438 | no | 1.218 | 0.436 | no | 1.754 | 0.877 | yes |
| DR1618 | Transposon DORF | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR1619 | Uncharacterized, Bacillus YoaR ortholog, Entrococcus VANW ortholog | 0.957 | 0.177 | no | 1.433 | 0.389 | yes | 1.122 | 0.240 | no | 0.922 | 0.150 | no | 0.822 | 0.338 | no | 0.829 | 0.240 | no | 0.805 | 0.200 | no | 0.966 | 0.242 | no | 1.044 | 0.216 | no |
| DR1620 | 3-ketoacyl-acyl carrier protein reductase. polyketide synthesis type oxidoreductase | 1.002 | 0.376 | no | 1.290 | 0.348 | no | 1.341 | 0.571 | no | 0.901 | 0.167 | no | 1.303 | 0.280 | no | 1.349 | 0.342 | no | 1.113 | 0.313 | no | 1.326 | 0.520 | no | 1.281 | 0.284 | no |
| DR1621 | HIT family protein | 0.883 | 0.193 | no | 1.160 | 0.425 | no | 1.051 | 0.467 | no | 1.204 | 0.405 | no | 0.905 | 0.437 | no | 1.050 | 0.305 | no | 0.901 | 0.338 | no | 0.991 | 0.288 | no | 1.482 | 0.431 | yes |
| DR1622 | HAD superfamily hydrolase | 1.048 | 0.140 | no | 1.963 | 1.100 | yes | 1.941 | 0.614 | yes | 1.823 | 0.517 | yes | 1.509 | 0.305 | no | 1.411 | 0.995 | no | 1.108 | 0.208 | no | 1.269 | 0.031 | no | 0.913 | 0.229 | no |
| DR1623 | Predicted protein | 1.010 | 0.253 | no | 0.908 | 0.322 | no | 0.564 | 0.164 | yes | 0.474 | 0.154 | yes | 0.753 | 0.438 | yes | 0.622 | 0.156 | yes | 0.754 | 0.105 | no | 1.005 | 0.235 | no | 1.103 | 0.238 | no |
| DR1625 | RNA helicase, authentic frameshift | 0.972 | 0.537 | no | 0.772 | 0.320 | no | 0.832 | 0.488 | no | 0.795 | 0.407 | no | 0.773 | 0.242 | no | 0.766 | 0.220 | no | 0.915 | 0.289 | no | 1.020 | 0.307 | no | 1.548 | 0.273 | yes |
| DR1626 | Branched-chain-amino-acid transaminase (isoleucine biosynthesis) | 0.861 | 0.094 | no | 0.771 | 0.195 | no | 0.692 | 0.154 | yes | 0.545 | 0.151 | yes | 0.660 | 0.263 | yes | 0.633 | 0.148 | yes | 0.610 | 0.168 | yes | 0.727 | 0.199 | yes | 1.235 | 0.405 | no |
| DR1627 | Oligoendopeptidase F type metalloprotease | 1.195 | 0.267 | no | 0.992 | 0.300 | no | 1.116 | 0.464 | no | 0.903 | 0.204 | no | 0.773 | 0.205 | no | 0.900 | 0.517 | no | 0.979 | 0.281 | no | 1.191 | 0.394 | no | 1.117 | 0.398 | no |
| DR1629 | TPR-repeat domain, GGDEF + YJCC domain protein, unknown signal transducer | 1.152 | 0.252 | no | 1.589 | 0.491 | yes | 1.631 | 0.171 | yes | 1.703 | 0.193 | yes | 1.158 | 0.204 | no | 1.322 | 0.355 | no | 1.203 | 0.199 | no | 1.071 | 0.167 | no | 1.088 | 0.322 | no |
| DR1630 | Conserved transport protein | 0.795 | 0.197 | no | 2.108 | 0.865 | yes | 2.596 | 1.278 | yes | 2.370 | 1.197 | yes | 2.116 | 1.047 | yes | 1.806 | 0.761 | yes | 1.889 | 0.660 | yes | 1.221 | 0.272 | no | 1.025 | 0.216 | no |
| DR1631 | Conserved domain seen in the bacterial SpoT | 1.193 | 0.453 | no | 1.140 | 0.398 | no | 1.026 | 0.307 | no | 1.025 | 0.489 | no | 0.814 | 0.286 | no | 0.993 | 0.408 | no | 1.039 | 0.366 | no | 0.957 | 0.390 | no | 1.128 | 0.717 | no |
| DR1632 | N-acetylmuramoyl-L-alanine amidase, AMIA | 1.067 | 0.317 | no | 1.004 | 0.215 | no | 0.941 | 0.177 | no | 0.839 | 0.135 | no | 1.000 | 0.400 | no | 0.953 | 0.334 | no | 0.854 | 0.237 | no | 0.963 | 0.256 | no | 0.927 | 0.332 | no |
| DR1633 | GGDEF-domain sensor regulator | 1.329 | 0.272 | no | 1.418 | 0.396 | no | 1.891 | 0.737 | yes | 1.462 | 0.327 | no | 1.300 | 0.711 | no | 1.375 | 0.798 | no | 1.155 | 0.446 | no | 1.087 | 0.426 | no | 0.996 | 0.434 | no |
| DR1634 | Predicted protein | 0.926 | 0.236 | no | 1.073 | 0.540 | no | 0.888 | 0.596 | no | 0.810 | 0.456 | no | 0.819 | 0.343 | no | 0.988 | 0.685 | no | 0.817 | 0.434 | no | 0.885 | 0.333 | no | 1.119 | 0.273 | no |
| DR1635 | ABC ATPase | 1.221 | 0.291 | no | 1.285 | 0.330 | no | 1.220 | 0.550 | no | 1.165 | 0.222 | no | 1.209 | 0.549 | no | 1.165 | 0.446 | no | 1.016 | 0.213 | no | 1.016 | 0.208 | no | 1.076 | 0.182 | no |
| DR1636 | CurD (N-term.) domain family of small proteins, involved in polyketide synthesis | 1.152 | 0.437 | no | 1.209 | 0.296 | no | 1.441 | 0.393 | no | 1.099 | 0.314 | no | 0.956 | 0.454 | no | 1.150 | 0.451 | no | 0.863 | 0.268 | no | 0.847 | 0.162 | no | 0.765 | 0.251 | no |
| DR1638 | Uncharacterized ACR, yvgK ortholog | 0.905 | 0.169 | no | 1.085 | 0.136 | no | 1.312 | 0.446 | no | 0.809 | 0.013 | no | 0.953 | 0.459 | no | 0.789 | 0.291 | no | 0.850 | 0.275 | no | 0.855 | 0.163 | no | 1.010 | 0.428 | no |
| DR1639 | Predicted protein | 0.697 | 0.334 | yes | 2.955 | 1.019 | yes | 4.406 | 1.839 | yes | 3.508 | 2.147 | yes | 3.810 | 2.441 | yes | 2.438 | 1.156 | yes | 1.501 | 0.392 | yes | 1.143 | 0.310 | no | 0.694 | 0.375 | yes |
| DR1640 | Predicted protein | 0.761 | 0.278 | no | 3.869 | 1.432 | yes | 2.039 | 0.756 | yes | 1.312 | 0.511 | no | 1.736 | 0.656 | yes | 1.943 | 0.710 | yes | 1.138 | 0.760 | no | 1.214 | 0.159 | no | 0.651 | 0.165 | no |
| DR1641 | YfiT-like metal-binding protein | 1.061 | 0.197 | no | 1.141 | 0.184 | no | 1.454 | 0.402 | yes | 1.529 | 0.246 | no | 1.884 | 0.777 | yes | 1.369 | 0.476 | no | 1.203 | 0.286 | no | 1.121 | 0.283 | no | 1.355 | 0.272 | no |
| DR1642 | YfiT-like metal-binding protein | 0.763 | 0.237 | no | 2.530 | 0.772 | yes | 3.706 | 1.298 | yes | 2.236 | 0.926 | yes | 2.541 | 1.154 | yes | 2.597 | 1.354 | yes | 1.673 | 0.574 | yes | 1.049 | 0.262 | no | 0.679 | 0.296 | yes |
| DR1643 | Predicted protein | 1.027 | 0.335 | no | 3.991 | 2.212 | yes | 4.058 | 2.210 | yes | 3.180 | 1.380 | yes | 2.697 | 1.136 | yes | 2.096 | 1.172 | yes | 1.383 | 0.409 | no | 1.111 | 0.262 | no | 1.042 | 0.365 | no |
| DR1644 | Predicted protein | 0.923 | 0.395 | no | 2.159 | 0.395 | yes | 2.451 | 0.559 | yes | 1.887 | 0.565 | yes | 2.069 | 0.976 | yes | 1.649 | 0.971 | no | 1.146 | 0.301 | no | 0.761 | 0.331 | yes | 0.847 | 0.206 | no |
| DR1645 | WECG ortholog UDP-N-acetyl-D-mannosaminuronic acid transferase | 0.933 | 0.270 | no | 5.098 | 1.927 | yes | 5.883 | 2.785 | yes | 5.037 | 1.452 | yes | 4.017 | 1.148 | yes | 3.210 | 1.576 | yes | 2.465 | 0.642 | yes | 1.394 | 0.266 | no | 1.252 | 0.562 | no |
| DR1646 | Cyclic AMP receptor protein, CRP | 0.818 | 0.374 | no | 2.014 | 0.679 | yes | 2.045 | 0.360 | yes | 1.052 | 0.370 | no | 1.916 | 0.589 | yes | 2.246 | 0.971 | yes | 1.190 | 0.376 | no | 0.896 | 0.274 | no | 0.625 | 0.225 | yes |
| DR1648 | ABC ATPase of amino acid transporter | 0.664 | 0.173 | yes | 0.740 | 0.188 | no | 0.691 | 0.196 | yes | 0.700 | 0.150 | no | 0.859 | 0.350 | no | 1.027 | 0.414 | no | 0.733 | 0.146 | no | 0.801 | 0.045 | no | 1.126 | 0.207 | no |
| DR1649 | Periplasmic binding protein | 1.490 | 0.529 | no | 1.307 | 0.592 | no | 1.184 | 0.530 | no | 1.799 | 0.377 | yes | 1.344 | 0.868 | no | 1.311 | 0.672 | no | 1.329 | 0.259 | no | 1.728 | 0.686 | yes | 1.270 | 0.142 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR1650 | Conserved membrane protein | 1.177 | 0.386 | no | 1.770 | 0.734 | yes | 1.393 | 0.594 | no | 1.598 | 0.960 | no | 1.636 | 0.559 | yes | 1.039 | 0.305 | no | 1.332 | 0.890 | no | 1.473 | 0.433 | no | 1.083 | 0.280 | no |
| DR1651 | Transposase | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR1652 | Transposon DORF1 | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR1653 | Conserved membrane protein (possible transporter) | 1.119 | 0.439 | no | 0.782 | 0.246 | no | 0.868 | 0.476 | no | 0.804 | 0.022 | no | 0.979 | 0.347 | no | 1.074 | 0.422 | no | 1.114 | 0.176 | no | 1.484 | 0.327 | yes | 1.240 | 0.184 | no |
| DR1654 | Possible outer membrane protein | 0.876 | 0.418 | no | 0.341 | 0.140 | yes | 0.390 | 0.161 | yes | 0.345 | 0.132 | yes | 0.621 | 0.237 | yes | 0.732 | 0.251 | no | 1.220 | 0.297 | no | 1.521 | 0.619 | yes | 2.023 | 0.702 | yes |
| DR1655 | Periplasmic substrate binding protein, amine binding | 1.077 | 0.053 | no | 2.484 | 0.633 | yes | 2.528 | 0.948 | yes | 3.054 | 0.718 | yes | 3.224 | 1.840 | yes | 3.994 | 1.694 | yes | 3.411 | 1.231 | yes | 2.126 | 0.597 | yes | 2.448 | 0.631 | yes |
| DR1656 | ATP-dependent protease Lon type + ATPase AAA superfamily , YifB ortholog | 0.805 | 0.462 | no | 1.989 | 0.631 | yes | 2.797 | 1.375 | yes | 1.695 | 0.062 | no | 1.605 | 0.922 | no | 2.008 | 0.534 | yes | 1.259 | 0.666 | no | 0.815 | 0.281 | no | 0.922 | 0.472 | no |
| DR1657 | Predicted protein | 1.475 | 0.532 | no | 1.397 | 0.400 | no | 1.114 | 0.311 | no | 1.297 | 0.251 | no | 1.429 | 0.542 | no | 1.505 | 0.938 | no | 1.396 | 0.691 | no | 0.970 | 0.124 | no | 1.154 | 0.611 | no |
| DR1658 | Predicted protein | 1.363 | 0.601 | no | 1.740 | 0.815 | yes | 1.062 | 0.358 | no | 1.729 | 0.631 | no | 1.429 | 0.579 | no | 1.354 | 0.650 | no | 1.324 | 0.521 | no | 1.272 | 0.668 | no | 1.046 | 0.430 | no |
| DR1659 | Oligopeptidase A Metalloprotease | 1.180 | 0.580 | no | 1.462 | 0.925 | no | 1.811 | 0.966 | yes | 1.424 | 0.251 | no | 1.340 | 0.392 | no | 1.327 | 0.367 | no | 1.275 | 0.177 | no | 1.407 | 0.532 | no | 1.523 | 0.313 | yes |
| DR1660 | Predicted protein | 1.100 | 0.442 | no | 1.169 | 0.424 | no | 1.233 | 0.430 | no | 1.068 | 0.476 | no | 1.132 | 0.465 | no | 1.310 | 0.451 | no | 1.203 | 0.438 | no | 1.075 | 0.433 | no | 1.265 | 0.573 | no |
| DR1661 | SpoVS protein | 1.164 | 0.315 | no | 1.140 | 0.327 | no | 1.074 | 0.293 | no | 1.071 | 0.255 | no | 0.999 | 0.445 | no | 0.963 | 0.289 | no | 1.001 | 0.292 | no | 1.063 | 0.096 | no | 1.190 | 0.192 | no |
| DR1662 | Threonine 3-dehydrogenase | 1.151 | 0.597 | no | 0.583 | 0.214 | yes | 0.602 | 0.332 | yes | 1.384 | 0.531 | no | 0.848 | 0.490 | no | 0.676 | 0.356 | yes | 1.356 | 0.483 | no | 1.495 | 0.533 | no | 1.771 | 0.456 | yes |
| DR1663 | Distantly related to uracil-DNA glycosylase, UNG FRAGMENT? | 1.069 | 0.549 | no | 0.448 | 0.138 | yes | 0.906 | 0.281 | no | 1.386 | 0.620 | no | 1.657 | 0.997 | no | 1.537 | 0.492 | no | 1.699 | 0.702 | yes | 2.179 | 0.785 | yes | 2.525 | 0.762 | yes |
| DR1664 | 5'-methylthioadenosine / S-adenosylhomocysteine nucleosidase related protein | 1.242 | 0.227 | no | 1.164 | 0.399 | no | 1.147 | 0.373 | no | 1.188 | 0.126 | no | 1.198 | 0.225 | no | 1.092 | 0.392 | no | 1.041 | 0.489 | no | 1.151 | 0.409 | no | 0.913 | 0.405 | no |
| DR1665 | Predicted protein | 0.923 | 0.384 | no | 0.486 | 0.235 | yes | 0.535 | 0.259 | yes | 0.457 | 0.204 | yes | 0.767 | 0.292 | no | 0.977 | 0.550 | no | 0.988 | 0.623 | no | 0.868 | 0.168 | no | 1.071 | 0.246 | no |
| DR1666 | TrkA potassium uptake system protein | 1.090 | 0.277 | no | 0.683 | 0.315 | yes | 0.493 | 0.258 | yes | 0.369 | 0.223 | yes | 0.617 | 0.422 | yes | 0.701 | 0.306 | yes | 0.663 | 0.295 | yes | 0.797 | 0.177 | no | 0.811 | 0.167 | no |
| DR1667 | TrkG Na+-transporting ATP synthase | 1.305 | 0.629 | no | 0.776 | 0.337 | no | 0.723 | 0.313 | yes | 0.756 | 0.258 | no | 0.653 | 0.190 | yes | 1.028 | 0.593 | no | 0.922 | 0.612 | no | 0.692 | 0.160 | yes | 0.537 | 0.038 | yes |
| DR1668 | TrkG Na+-transporting ATP synthase | 1.330 | 0.447 | no | 0.860 | 0.546 | no | 0.760 | 0.540 | yes | 0.568 | 0.183 | yes | 0.657 | 0.284 | yes | 1.003 | 0.698 | no | 0.551 | 0.241 | yes | 0.782 | 0.138 | no | 0.926 | 0.602 | no |
| DR1669 | SAM dependent methyltransferase | 0.944 | 0.198 | no | 0.725 | 0.211 | no | 0.894 | 0.358 | no | 1.038 | 0.119 | no | 1.149 | 0.441 | no | 1.164 | 0.342 | no | 0.989 | 0.214 | no | 1.080 | 0.399 | no | 1.134 | 0.625 | no |
| DR1670 | Cys tRNA synthetase, Class I | 0.662 | 0.317 | yes | 0.261 | 0.107 | yes | 0.354 | 0.071 | yes | 0.428 | 0.030 | yes | 0.753 | 0.473 | yes | 0.425 | 0.229 | yes | 0.427 | 0.076 | yes | 0.525 | 0.076 | yes | 0.623 | 0.123 | yes |
| DR1671 | Predicted protein | 0.864 | 0.422 | no | 0.804 | 0.501 | no | 0.828 | 0.554 | no | 0.595 | 0.081 | yes | 0.642 | 0.181 | yes | 0.931 | 0.425 | no | 0.985 | 0.376 | no | 1.097 | 0.425 | no | 1.212 | 0.744 | no |
| DR1672 | SAM dependent methyltransferase | 1.042 | 0.353 | no | 1.092 | 0.287 | no | 1.097 | 0.458 | no | 1.032 | 0.302 | no | 0.883 | 0.322 | no | 1.088 | 0.475 | no | 1.240 | 0.733 | no | 1.021 | 0.295 | no | 0.932 | 0.315 | no |
| DR1673 | Fragment of dehydrogenase | 0.891 | 0.092 | no | 4.172 | 2.093 | yes | 4.533 | 1.294 | yes | 3.466 | 0.636 | yes | 3.575 | 1.921 | yes | 2.594 | 1.430 | yes | 1.801 | 0.347 | yes | 1.952 | 0.504 | yes | 1.336 | 0.474 | no |
| DR1674 | Isocitrate dehydrogenase, IDH | 0.772 | 0.261 | no | 1.029 | 0.363 | no | 1.157 | 0.240 | no | 0.851 | 0.203 | no | 1.045 | 0.264 | no | 1.307 | 0.584 | no | 0.917 | 0.349 | no | 1.095 | 0.206 | no | 2.410 | 1.002 | yes |
| DR1675 | Uncharacterized conserved protein (possibly metal-binding) | 1.241 | 0.359 | no | 0.923 | 0.136 | no | 0.904 | 0.337 | no | 0.689 | 0.072 | no | 0.792 | 0.296 | no | 0.910 | 0.367 | no | 0.767 | 0.386 | no | 0.625 | 0.122 | yes | 0.743 | 0.439 | no |
| DR1676 | SAM dependent Methyltransferase | 1.061 | 0.353 | no | 1.036 | 0.574 | no | 0.566 | 0.125 | yes | 0.467 | 0.038 | yes | 0.580 | 0.176 | yes | 0.624 | 0.204 | yes | 0.607 | 0.309 | yes | 0.536 | 0.108 | yes | 0.626 | 0.242 | yes |
| DR1677 | Predicted protein | 1.051 | 0.211 | no | 1.190 | 0.457 | no | 1.032 | 0.400 | no | 0.799 | 0.044 | no | 0.749 | 0.223 | no | 0.973 | 0.323 | no | 0.887 | 0.324 | no | 1.034 | 0.509 | no | 0.907 | 0.331 | no |
| DR1678 | NH2 acetyltransferase, cyanobacteria type | 0.952 | 0.340 | no | 0.532 | 0.349 | yes | 0.407 | 0.095 | yes | 0.389 | 0.130 | yes | 0.575 | 0.235 | yes | 0.823 | 0.287 | no | 1.135 | 0.373 | no | 1.741 | 0.556 | yes | 1.603 | 0.324 | yes |
| DR1679 | SAM dependent Methyltransferase | 1.482 | 0.483 | no | 1.714 | 0.584 | yes | 1.685 | 0.414 | yes | 2.190 | 0.398 | yes | 1.921 | 0.506 | yes | 1.929 | 0.722 | yes | 1.639 | 0.810 | yes | 1.800 | 0.990 | yes | 1.206 | 0.792 | no |
| DR1680 | SAM dependent methyltransferase | 1.100 | 0.594 | no | 1.116 | 0.395 | no | 1.354 | 0.681 | no | 0.907 | 0.466 | no | 1.058 | 0.458 | no | 1.336 | 0.899 | no | 1.248 | 0.855 | no | 1.025 | 0.126 | no | 1.225 | 0.500 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR1681 | GIDA(glucose inhibited division protein A) C-terminal domain or E.coli 21k protein ortholog, Rossman fold oxidoreductase | 1.325 | 0.207 | no | 1.137 | 0.484 | no | 1.241 | 0.407 | no | 1.255 | 0.443 | no | 1.059 | 0.273 | no | 1.445 | 0.536 | no | 1.258 | 0.677 | no | 0.878 | 0.018 | no | 1.135 | 0.562 | no |
| DR1682 | Predicted protein | 1.064 | 0.323 | no | 0.805 | 0.347 | no | 0.988 | 0.449 | no | 0.747 | 0.237 | no | 0.927 | 0.492 | no | 0.989 | 0.450 | no | 1.216 | 0.471 | no | 1.343 | 0.592 | no | 0.880 | 0.365 | no |
| DR1683 | Transcriptional regulator, Bacillus PAIB ortholog | 1.151 | 0.286 | no | 1.282 | 0.471 | no | 1.619 | 1.010 | yes | 1.458 | 0.501 | no | 0.962 | 0.386 | no | 1.115 | 0.486 | no | 1.045 | 0.400 | no | 1.524 | 0.779 | no | 1.033 | 0.426 | no |
| DR1684 | Pseudouridine synthetase SFHB/YABO/YCEC like + S4 domain | 1.061 | 0.356 | no | 0.812 | 0.241 | no | 0.585 | 0.224 | yes | 0.555 | 0.133 | yes | 0.756 | 0.348 | no | 0.890 | 0.336 | no | 0.883 | 0.413 | no | 1.089 | 0.337 | no | 1.161 | 0.435 | no |
| DR1685 | ATPase, ParA/Soj-like protein | 1.290 | 0.330 | no | 0.907 | 0.266 | no | 0.838 | 0.211 | no | 0.909 | 0.061 | no | 0.754 | 0.330 | no | 0.793 | 0.163 | no | 0.944 | 0.319 | no | 0.872 | 0.152 | no | 0.872 | 0.209 | no |
| DR1686 | Predicted protein | 0.969 | 0.255 | no | 0.411 | 0.177 | yes | 0.317 | 0.082 | yes | 0.378 | 0.103 | yes | 0.515 | 0.149 | yes | 0.759 | 0.249 | no | 1.056 | 0.331 | no | 1.360 | 0.281 | no | 1.436 | 0.442 | no |
| DR1687 | Glutamyl-tRNA synthetase | 1.146 | 0.399 | no | 0.731 | 0.306 | no | 0.898 | 0.253 | no | 1.207 | 0.386 | no | 1.291 | 0.471 | no | 1.342 | 0.375 | no | 1.328 | 0.117 | no | 1.313 | 0.109 | no | 2.027 | 0.805 | yes |
| DR1688 | PGRS-family repeats protein? | 1.205 | 0.250 | no | 1.449 | 0.673 | no | 1.296 | 0.506 | no | 1.084 | 0.189 | no | 1.037 | 0.454 | no | 1.561 | 0.847 | no | 1.352 | 0.630 | no | 1.460 | 0.785 | no | 1.235 | 0.570 | no |
| DR1689 | ADP-glucose pyrophosphorylase, GlgC | 0.974 | 0.455 | no | 0.974 | 0.613 | no | 0.514 | 0.244 | yes | 4.816 | 1.186 | yes | 1.027 | 0.633 | no | 1.314 | 0.358 | no | 2.973 | 2.230 | yes | 2.147 | 0.481 | yes | 2.070 | 1.146 | yes |
| DR1690 | TRNA delta 2-isopentenylpyrophosphate transferase | 0.853 | 0.429 | no | 0.641 | 0.378 | yes | 0.312 | 0.166 | yes | 0.342 | 0.176 | yes | 0.713 | 0.250 | no | 0.858 | 0.414 | no | 1.068 | 0.337 | no | 1.633 | 0.580 | yes | 1.518 | 0.547 | yes |
| DR1691 | Small heat-shock protein, class I | 1.085 | 0.304 | no | 0.951 | 0.464 | no | 1.076 | 0.473 | no | 1.178 | 0.716 | no | 1.040 | 0.419 | no | 1.036 | 0.533 | no | 1.041 | 0.476 | no | 1.341 | 0.554 | no | 1.200 | 0.455 | no |
| DR1692 | Long-chain-fatty-acid--CoA ligase, LCFA | 2.088 | 1.110 | yes | 1.251 | 0.408 | no | 1.370 | 0.730 | no | 1.324 | 0.009 | no | 1.234 | 0.631 | no | 1.104 | 0.536 | no | 1.252 | 0.535 | no | 1.428 | 0.712 | no | 1.383 | 0.284 | no |
| DR1693 | Predicted protein | 0.765 | 0.127 | no | 0.673 | 0.196 | yes | 0.800 | 0.186 | no | 0.804 | 0.174 | no | 1.005 | 0.306 | no | 0.905 | 0.313 | no | 1.103 | 0.250 | no | 1.268 | 0.425 | no | 1.397 | 0.128 | no |
| DR1694 | SAM dependent Methylase | 0.547 | 0.248 | yes | 0.476 | 0.131 | yes | 0.529 | 0.173 | yes | 0.497 | 0.155 | yes | 0.898 | 0.294 | no | 0.950 | 0.238 | no | 0.669 | 0.212 | yes | 0.767 | 0.217 | no | 0.825 | 0.444 | no |
| DR1695 | Lactoyl glutathione lyase, LGUL | 0.993 | 0.474 | no | 1.039 | 0.353 | no | 1.049 | 0.467 | no | 0.875 | 0.069 | no | 0.978 | 0.323 | no | 1.038 | 0.392 | no | 0.976 | 0.272 | no | 1.230 | 0.427 | no | 1.255 | 0.524 | no |
| DR1696 | Hexb/MutL | 1.833 | 1.289 | yes | 1.207 | 0.626 | no | 1.315 | 0.655 | no | 1.508 | 0.340 | no | 1.546 | 0.942 | no | 1.027 | 0.396 | no | 1.164 | 0.349 | no | 1.060 | 0.384 | no | 0.846 | 0.356 | no |
| DR1697 | Predicted protein | 1.035 | 0.229 | no | 1.133 | 0.574 | no | 1.320 | 0.712 | no | 1.475 | 0.503 | no | 1.222 | 0.321 | no | 1.151 | 0.448 | no | 1.165 | 0.420 | no | 1.462 | 0.403 | no | 1.226 | 0.256 | no |
| DR1698 | TIM barrel dinucleotide dependent enzyme, E.coli YJBN ortholog | 0.697 | 0.388 | yes | 0.692 | 0.383 | yes | 0.649 | 0.140 | yes | 0.548 | 0.094 | yes | 0.817 | 0.272 | no | 0.977 | 0.503 | no | 0.954 | 0.614 | no | 0.920 | 0.073 | no | 0.710 | 0.171 | no |
| DR1699 | Secreted protein, uncharacterized | 0.934 | 0.271 | no | 0.628 | 0.206 | yes | 0.636 | 0.211 | yes | 0.580 | 0.221 | yes | 0.655 | 0.136 | yes | 0.969 | 0.430 | no | 1.018 | 0.212 | no | 1.290 | 0.406 | no | 1.925 | 0.697 | yes |
| DR1700 | Oxidoreductase | 0.991 | 0.539 | no | 0.746 | 0.179 | no | 0.792 | 0.235 | no | 0.785 | 0.294 | no | 0.784 | 0.177 | no | 1.043 | 0.266 | no | 1.045 | 0.277 | no | 1.108 | 0.365 | no | 0.937 | 0.226 | no |
| DR1701 | Phosphoglycerate dehydrogenase, serA | 1.305 | 0.176 | no | 0.856 | 0.164 | no | 0.819 | 0.217 | no | 0.851 | 0.037 | no | 0.901 | 0.219 | no | 1.061 | 0.213 | no | 1.023 | 0.290 | no | 1.255 | 0.467 | no | 1.008 | 0.254 | no |
| DR1702 | NH2 acetyltransferase | 0.854 | 0.288 | no | 0.419 | 0.205 | yes | 0.332 | 0.087 | yes | 0.366 | 0.119 | yes | 0.456 | 0.107 | yes | 0.699 | 0.257 | yes | 1.047 | 0.535 | no | 1.583 | 0.613 | yes | 1.263 | 0.274 | no |
| DR1703 | Myo-inositol monophosphatase, IMP | 1.262 | 0.215 | no | 1.228 | 0.394 | no | 1.097 | 0.223 | no | 1.403 | 0.378 | no | 1.299 | 0.446 | no | 1.256 | 0.690 | no | 1.358 | 0.719 | no | 0.975 | 0.106 | no | 1.485 | 0.462 | yes |
| DR1704 | Ornithine N-acetyltransferase, ARGJ family | 0.809 | 0.505 | no | 0.585 | 0.269 | yes | 0.477 | 0.179 | yes | 0.447 | 0.089 | yes | 0.599 | 0.163 | yes | 0.814 | 0.546 | no | 0.971 | 0.655 | no | 0.917 | 0.114 | no | 1.204 | 0.554 | no |
| DR1705 | HAD superfamily hydrolase, epoxide hydrolases | 1.291 | 0.419 | no | 1.038 | 0.399 | no | 1.000 | 0.454 | no | 0.819 | 0.295 | no | 0.744 | 0.377 | yes | 0.758 | 0.438 | yes | 0.982 | 0.349 | no | 0.958 | 0.278 | no | 0.826 | 0.300 | no |
| DR1706 | Predicted protein | 1.086 | 0.389 | no | 0.641 | 0.164 | yes | 0.529 | 0.175 | yes | 0.560 | 0.096 | yes | 0.563 | 0.080 | yes | 0.798 | 0.325 | no | 0.796 | 0.426 | no | 1.175 | 0.474 | no | 1.041 | 0.451 | no |
| DR1707 | DNA polymerase I | 1.035 | 0.332 | no | 0.866 | 0.438 | no | 0.954 | 0.446 | no | 0.766 | 0.110 | no | 0.896 | 0.223 | no | 0.839 | 0.368 | no | 0.957 | 0.189 | no | 0.945 | 0.290 | no | 1.220 | 0.230 | no |
| DR1708 | Secreted protein | 0.889 | 0.322 | no | 0.403 | 0.166 | yes | 0.283 | 0.156 | yes | 0.701 | 0.399 | yes | 0.699 | 0.149 | no | 1.042 | 0.232 | no | 1.934 | 0.734 | yes | 1.400 | 0.676 | no | 1.461 | 0.395 | no |
| DR1709 | NRAM family membrane transporter | 0.808 | 0.287 | no | 0.694 | 0.337 | yes | 0.161 | 0.088 | yes | 0.120 | 0.078 | yes | 0.119 | 0.051 | yes | 0.192 | 0.130 | yes | 0.333 | 0.100 | yes | 0.466 | 0.128 | yes | 1.015 | 0.308 | no |
| DR1710 | Predicted protein | 0.702 | 0.257 | no | 0.581 | 0.273 | yes | 0.632 | 0.313 | yes | 0.504 | 0.145 | yes | 0.473 | 0.057 | yes | 0.492 | 0.180 | yes | 0.794 | 0.493 | no | 0.715 | 0.116 | yes | 0.796 | 0.298 | no |
| DR1711 | N-acyl-L-amino acid amidohydrolase | 0.974 | 0.165 | no | 0.653 | 0.275 | yes | 0.548 | 0.146 | yes | 0.818 | 0.123 | no | 0.809 | 0.241 | no | 1.020 | 0.398 | no | 0.907 | 0.416 | no | 0.948 | 0.086 | no | 0.930 | 0.219 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR1712 | Peptide binding periplasmic protein | 0.321 | 0.182 | yes | 0.694 | 0.401 | yes | 0.302 | 0.229 | yes | 1.479 | 0.316 | no | 1.169 | 0.727 | no | 0.737 | 0.435 | no | 0.840 | 0.269 | no | 0.770 | 0.249 | no | 0.891 | 0.415 | no |
| DR1713 | Leu/Phe-tRNA-protein transferase, LPTP (seen in very few bacteria and plasmodium) | 1.084 | 0.291 | no | 0.809 | 0.092 | no | 1.061 | 0.228 | no | 0.845 | 0.357 | no | 0.850 | 0.448 | no | 0.892 | 0.383 | no | 1.291 | 0.378 | no | 1.701 | 0.704 | yes | 0.943 | 0.539 | no |
| DR1714 | Predicted protein | 0.963 | 0.253 | no | 0.944 | 0.409 | no | 0.585 | 0.416 | yes | 0.361 | 0.106 | yes | 0.606 | 0.315 | yes | 0.988 | 0.540 | no | 0.984 | 0.537 | no | 1.378 | 0.575 | no | 1.366 | 0.370 | no |
| DR1715 | Solo ACT domain protein, AF1477 ortholog | 1.024 | 0.367 | no | 1.356 | 0.860 | no | 0.743 | 0.251 | no | 0.846 | 0.190 | no | 0.772 | 0.325 | no | 0.874 | 0.435 | no | 0.983 | 0.191 | no | 1.655 | 0.312 | yes | 1.222 | 0.328 | no |
| DR1716 | NH2 acetyltransferase | 1.225 | 0.275 | no | 0.898 | 0.475 | no | 0.851 | 0.422 | no | 0.691 | 0.242 | no | 0.741 | 0.289 | no | 0.839 | 0.241 | no | 0.949 | 0.403 | no | 1.067 | 0.213 | no | 0.989 | 0.142 | no |
| DR1717 | Racemase, L-carnitine Dehydratase family enzyme | 1.080 | 0.297 | no | 0.951 | 0.254 | no | 0.895 | 0.144 | no | 0.862 | 0.079 | no | 0.841 | 0.134 | no | 1.056 | 0.534 | no | 0.980 | 0.257 | no | 1.294 | 0.576 | no | 1.225 | 0.420 | no |
| DR1718 | Glutamate dehydrogenase, NADP dependent | 0.979 | 0.371 | no | 0.886 | 0.435 | no | 0.761 | 0.325 | no | 0.777 | 0.288 | no | 0.886 | 0.243 | no | 0.943 | 0.169 | no | 0.730 | 0.356 | yes | 0.930 | 0.212 | no | 0.799 | 0.117 | no |
| DR1719 | Predicted protein | 1.202 | 0.269 | no | 0.994 | 0.264 | no | 1.083 | 0.551 | no | 1.023 | 0.162 | no | 0.909 | 0.384 | no | 1.036 | 0.408 | no | 0.893 | 0.416 | no | 1.228 | 0.499 | no | 1.284 | 0.484 | no |
| DR1720 | Aconitase, ACON | 0.891 | 0.447 | no | 2.191 | 1.537 | yes | 1.482 | 0.713 | no | 0.858 | 0.309 | no | 1.423 | 0.825 | no | 1.104 | 0.424 | no | 1.067 | 0.500 | no | 1.167 | 0.283 | no | 1.074 | 0.051 | no |
| DR1721 | 3'->5' nuclease domain | 1.015 | 0.423 | no | 0.988 | 0.486 | no | 1.054 | 0.397 | no | 1.676 | 0.966 | no | 1.824 | 1.218 | yes | 1.248 | 0.735 | no | 1.256 | 0.632 | no | 1.233 | 0.528 | no | 0.625 | 0.267 | yes |
| DR1722 | Uncharacterized conserved protein | 0.926 | 0.209 | no | 1.109 | 0.348 | no | 1.419 | 0.375 | no | 1.509 | 0.230 | no | 1.257 | 0.101 | no | 1.132 | 0.275 | no | 1.111 | 0.440 | no | 1.238 | 0.534 | no | 1.231 | 0.362 | no |
| DR1723 | Cytochrome P450 | 0.934 | 0.404 | no | 1.750 | 0.806 | yes | 3.541 | 1.636 | yes | 3.090 | 1.019 | yes | 2.881 | 0.946 | yes | 1.940 | 0.657 | yes | 1.343 | 0.678 | no | 1.310 | 0.709 | no | 0.742 | 0.124 | no |
| DR1724 | Oxidoredcutase of the Rossman fold | 1.015 | 0.308 | no | 1.334 | 0.453 | no | 2.841 | 1.914 | yes | 1.659 | 0.595 | no | 1.513 | 0.671 | no | 1.613 | 0.581 | yes | 1.125 | 0.172 | no | 1.249 | 0.522 | no | 1.117 | 0.207 | no |
| DR1725 | WD40 repeat protein, secreted | 0.942 | 0.307 | no | 0.772 | 0.289 | no | 1.635 | 0.935 | yes | 1.118 | 0.566 | no | 1.285 | 0.688 | no | 1.490 | 0.808 | no | 1.043 | 0.282 | no | 1.206 | 0.268 | no | 0.875 | 0.451 | no |
| DR1726 | McrA superfamily nuclease. | 1.509 | 0.616 | no | 1.022 | 0.299 | no | 0.891 | 0.308 | no | 0.930 | 0.164 | no | 0.848 | 0.350 | no | 0.861 | 0.217 | no | 0.885 | 0.425 | no | 1.031 | 0.360 | no | 1.541 | 0.296 | yes |
| DR1727 | Phosphoenolpyruvate synthase | 1.321 | 0.350 | no | 0.799 | 0.352 | no | 0.462 | 0.282 | yes | 0.608 | 0.136 | no | 0.489 | 0.268 | yes | 0.622 | 0.341 | yes | 0.865 | 0.321 | no | 1.241 | 0.470 | no | 1.175 | 0.239 | no |
| DR1728 | P-loop ATPase, YQFL of Bacillus family | 1.472 | 0.697 | no | 1.093 | 0.302 | no | 0.880 | 0.393 | no | 0.998 | 0.477 | no | 1.141 | 0.436 | no | 1.349 | 0.771 | no | 1.470 | 0.493 | no | 1.472 | 0.517 | no | 1.582 | 0.555 | yes |
| DR1729 | Predicted protein | 1.039 | 0.376 | no | 0.782 | 0.342 | no | 0.572 | 0.249 | yes | 0.663 | 0.226 | yes | 0.702 | 0.286 | yes | 0.796 | 0.364 | no | 0.890 | 0.605 | no | 0.805 | 0.363 | no | 0.977 | 0.440 | no |
| DR1730 | Glycolate oxidase subunit, Fe-S subunit | 1.532 | 0.525 | no | 0.861 | 0.263 | no | 0.605 | 0.155 | yes | 0.788 | 0.444 | no | 0.624 | 0.168 | yes | 0.721 | 0.360 | no | 1.026 | 0.315 | no | 1.055 | 0.227 | no | 1.312 | 0.414 | no |
| DR1731 | Glycolate oxidase subunit, GLCD, Dimunito like FAD binding subunit | 0.956 | 0.304 | no | 0.613 | 0.292 | yes | 0.454 | 0.237 | yes | 0.361 | 0.029 | yes | 0.462 | 0.127 | yes | 0.694 | 0.435 | yes | 0.776 | 0.393 | no | 0.948 | 0.425 | no | 1.148 | 0.468 | no |
| DR1732 | Glycolate oxidase subunit, GLCE, | 1.232 | 0.499 | no | 0.895 | 0.188 | no | 0.831 | 0.312 | no | 0.956 | 0.217 | no | 0.761 | 0.239 | no | 0.825 | 0.332 | no | 0.843 | 0.188 | no | 0.932 | 0.189 | no | 1.060 | 0.262 | no |
| DR1733 | CSGG (assembly/transport component in n curli production), membrane or secreted of E.coli distant homolog(>gi\|2983611 Aquifex) | 1.259 | 0.589 | no | 0.477 | 0.331 | yes | 0.821 | 0.435 | no | 1.075 | 0.044 | no | 0.816 | 0.597 | yes | 0.907 | 0.261 | no | 0.994 | 0.341 | no | 1.124 | 0.225 | no | 2.957 | 0.537 | yes |
| DR1734 | Predicted protein | 1.165 | 0.256 | no | 0.743 | 0.198 | no | 0.389 | 0.100 | yes | 0.376 | 0.054 | yes | 0.343 | 0.157 | yes | 0.488 | 0.153 | yes | 0.375 | 0.096 | yes | 0.584 | 0.167 | yes | 0.714 | 0.094 | no |
| DR1735 | Predicted protein | 1.304 | 0.482 | no | 1.151 | 0.617 | no | 1.222 | 0.523 | no | 1.102 | 0.655 | no | 0.883 | 0.495 | no | 0.733 | 0.287 | no | 1.117 | 0.527 | no | 1.337 | 0.690 | no | 1.097 | 0.335 | no |
| DR1736 | 2',3'-cyclic-nucleotide 2'-phosphodiesterase, CN16, Calcineurin like phosphoesterase | 1.154 | 0.338 | no | 0.483 | 0.263 | yes | 0.612 | 0.108 | yes | 0.948 | 0.302 | no | 1.332 | 0.410 | no | 1.094 | 0.390 | no | 1.020 | 0.170 | no | 1.423 | 0.312 | no | 1.615 | 0.498 | yes |
| DR1737 | Signal peptidase I | 0.869 | 0.230 | no | 1.083 | 0.147 | no | 0.674 | 0.189 | yes | 0.652 | 0.027 | no | 0.824 | 0.337 | no | 0.684 | 0.185 | no | 0.748 | 0.266 | no | 1.041 | 0.244 | no | 0.752 | 0.309 | no |
| DR1738 | Predicted protein | 1.389 | 0.875 | no | 0.903 | 0.376 | no | 0.909 | 0.366 | no | 0.985 | 0.476 | no | 0.987 | 0.633 | no | 0.934 | 0.386 | no | 1.099 | 0.650 | no | 1.524 | 0.879 | no | 0.853 | 0.525 | no |
| DR1739 | Small HTH transcriptional regulator, archaeal and mycobacterium type | 1.289 | 0.535 | no | 2.594 | 1.650 | yes | 1.585 | 0.528 | yes | 0.817 | 0.159 | no | 1.247 | 0.406 | no | 1.289 | 0.691 | no | 1.219 | 0.691 | no | 1.385 | 0.427 | no | 0.923 | 0.254 | no |
| DR1740 | Predicted protein | 1.125 | 0.222 | no | 0.862 | 0.156 | no | 0.792 | 0.217 | no | 0.774 | 0.149 | no | 0.921 | 0.223 | no | 0.926 | 0.302 | no | 0.960 | 0.262 | no | 1.110 | 0.236 | no | 1.336 | 0.479 | no |
| DR1741 | Predicted protein | 0.905 | 0.406 | no | 0.629 | 0.343 | yes | 0.433 | 0.095 | yes | 0.732 | 0.279 | no | 0.801 | 0.328 | no | 0.894 | 0.525 | no | 0.816 | 0.537 | no | 0.900 | 0.179 | no | 0.707 | 0.312 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR1742 | Glucose-6-phosphate isomerase, | 1.086 | 0.449 | no | 0.781 | 0.444 | no | 0.424 | 0.123 | yes | 0.492 | 0.044 | yes | 0.560 | 0.108 | yes | 0.702 | 0.346 | yes | 0.689 | 0.241 | yes | 0.968 | 0.469 | no | 1.614 | 0.841 | yes |
| DR1743 | Permease MDR type | 1.282 | 0.304 | no | 0.984 | 0.258 | no | 0.841 | 0.312 | no | 0.897 | 0.121 | no | 0.945 | 0.277 | no | 0.853 | 0.161 | no | 0.900 | 0.347 | no | 0.883 | 0.178 | no | 0.888 | 0.299 | no |
| DR1744 | Predicted protein | 0.992 | 0.321 | no | 4.174 | 2.234 | yes | 5.023 | 1.642 | yes | 3.234 | 0.156 | yes | 3.547 | 2.296 | yes | 2.718 | 1.518 | yes | 1.893 | 0.409 | yes | 1.890 | 0.725 | yes | 1.540 | 0.737 | no |
| DR1745 | Conserved membrane protein, distantly related to CZCN protein/C-14 sterol reductase | 1.049 | 0.425 | no | 0.712 | 0.323 | yes | 0.710 | 0.284 | yes | 0.630 | 0.044 | no | 0.508 | 0.252 | yes | 0.850 | 0.436 | no | 0.715 | 0.464 | yes | 0.857 | 0.250 | no | 1.076 | 0.291 | no |
| DR1746 | Predicted protein | 0.914 | 0.171 | no | 1.078 | 0.410 | no | 1.312 | 0.483 | no | 1.131 | 0.336 | no | 1.095 | 0.447 | no | 1.002 | 0.535 | no | 0.833 | 0.451 | no | 1.017 | 0.459 | no | 1.038 | 0.535 | no |
| DR1747 | GTPase, ortholog YGFD_ECOLI, ArgK | 1.113 | 0.552 | no | 1.822 | 1.024 | yes | 2.195 | 1.044 | yes | 1.694 | 0.267 | yes | 1.244 | 0.404 | no | 1.157 | 0.749 | no | 1.277 | 0.890 | no | 1.195 | 0.607 | no | 1.037 | 0.514 | no |
| DR1748 | Predicted protein | 1.018 | 0.384 | no | 0.934 | 0.322 | no | 1.282 | 0.467 | no | 1.509 | 0.554 | no | 1.690 | 0.901 | yes | 1.424 | 0.149 | no | 1.888 | 0.764 | yes | 1.861 | 0.162 | yes | 3.961 | 1.646 | yes |
| DR1749 | DSCG containing bacterial hydrolase family, extracellular protein, Listeria P60 type | 0.414 | 0.248 | yes | 2.232 | 0.722 | yes | 3.106 | 1.774 | yes | 1.583 | 0.876 | no | 1.210 | 0.678 | no | 0.691 | 0.399 | yes | 0.672 | 0.139 | yes | 0.547 | 0.161 | yes | 0.619 | 0.160 | no |
| DR1750 | Predicted protein | 1.139 | 0.440 | no | 0.576 | 0.225 | yes | 0.676 | 0.293 | yes | 0.816 | 0.216 | no | 0.741 | 0.428 | yes | 0.589 | 0.178 | yes | 0.670 | 0.249 | yes | 0.748 | 0.161 | no | 1.396 | 0.459 | no |
| DR1751 | Domain with Uracil DNA glycosilase similarity | 0.822 | 0.187 | no | 0.675 | 0.470 | yes | 0.599 | 0.243 | yes | 0.551 | 0.051 | yes | 0.706 | 0.148 | no | 0.679 | 0.157 | no | 1.093 | 0.525 | no | 1.235 | 0.434 | no | 1.111 | 0.510 | no |
| DR1752 | Chloride channel, YADO_ECOLI | 1.171 | 0.214 | no | 1.231 | 0.260 | no | 1.375 | 0.290 | no | 1.284 | 0.242 | no | 1.203 | 0.188 | no | 1.153 | 0.431 | no | 1.454 | 0.394 | no | 1.275 | 0.546 | no | 1.362 | 0.557 | no |
| DR1753 | Septum site-determining protein MinC | 0.775 | 0.296 | no | 1.425 | 0.547 | no | 1.672 | 0.645 | yes | 1.435 | 0.266 | no | 1.401 | 0.503 | no | 1.069 | 0.351 | no | 0.755 | 0.146 | no | 0.869 | 0.315 | no | 0.679 | 0.145 | no |
| DR1754 | S1 domain RNA binding protein | 0.570 | 0.294 | yes | 0.928 | 0.391 | no | 1.572 | 0.645 | yes | 1.886 | 0.874 | yes | 1.961 | 1.279 | yes | 1.467 | 0.340 | no | 1.689 | 0.830 | yes | 1.643 | 0.410 | yes | 1.674 | 0.392 | yes |
| DR1755 | Predicted protein | 0.937 | 0.139 | no | 0.637 | 0.192 | yes | 0.444 | 0.115 | yes | 0.515 | 0.102 | yes | 0.798 | 0.227 | no | 1.150 | 0.223 | no | 1.375 | 0.434 | no | 1.661 | 0.431 | yes | 2.301 | 0.732 | yes |
| DR1756 | Do protease, Serine protease with PDZ domains | 1.332 | 0.374 | no | 0.646 | 0.290 | yes | 0.813 | 0.395 | no | 0.967 | 0.461 | no | 0.648 | 0.410 | yes | 0.668 | 0.223 | yes | 0.743 | 0.289 | no | 1.091 | 0.367 | no | 0.895 | 0.273 | no |
| DR1757 | Predicted nuclease and Zinc finger domain containing protein | 1.171 | 0.607 | no | 1.066 | 0.416 | no | 1.009 | 0.279 | no | 0.829 | 0.209 | no | 0.920 | 0.558 | no | 0.961 | 0.420 | no | 0.860 | 0.239 | no | 0.884 | 0.136 | no | 0.910 | 0.334 | no |
| DR1758 | Diaminopimelate decarboxylase | 1.395 | 0.763 | no | 0.928 | 0.450 | no | 0.815 | 0.377 | no | 1.230 | 0.782 | no | 0.956 | 0.523 | no | 0.814 | 0.327 | no | 0.878 | 0.415 | no | 0.904 | 0.263 | no | 0.808 | 0.246 | no |
| DR1759 | TRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase, TrmU, PP-loop superfamily ATPase | 0.829 | 0.403 | no | 0.666 | 0.155 | yes | 0.669 | 0.221 | yes | 0.532 | 0.057 | yes | 0.699 | 0.270 | no | 0.636 | 0.168 | yes | 0.578 | 0.044 | yes | 0.888 | 0.157 | no | 0.891 | 0.188 | no |
| DR1760 | Transposon orf | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR1763 | Transposon orf | 1.374 | 0.397 | no | 1.268 | 0.213 | no | 1.222 | 0.240 | no | 1.011 | 0.057 | no | 1.457 | 0.892 | no | 0.884 | 0.285 | no | 0.974 | 0.190 | no | 0.874 | 0.258 | no | 0.953 | 0.081 | no |
| DR1764 | Related to 2,3-dihydroxybiphenyl 1,2-dioxygenase | 0.962 | 0.370 | no | 0.843 | 0.280 | no | 0.944 | 0.349 | no | 0.600 | 0.099 | yes | 0.833 | 0.481 | no | 0.966 | 0.420 | no | 0.847 | 0.265 | no | 0.984 | 0.237 | no | 1.162 | 0.419 | no |
| DR1765 | Thioredoxin fold protein, DsbA homolog | 0.894 | 0.320 | no | 0.820 | 0.221 | no | 0.936 | 0.303 | no | 1.026 | 0.363 | no | 0.870 | 0.165 | no | 1.201 | 0.517 | no | 0.932 | 0.273 | no | 1.153 | 0.071 | no | 1.086 | 0.180 | no |
| DR1766 | Anthranilate synthase component II, TRPG | 0.853 | 0.232 | no | 0.744 | 0.215 | no | 0.728 | 0.301 | yes | 0.574 | 0.073 | yes | 0.795 | 0.428 | no | 0.626 | 0.200 | yes | 0.636 | 0.166 | yes | 0.879 | 0.145 | no | 0.892 | 0.158 | no |
| DR1767 | Anthranilate phosphoribosyltransferase | 1.085 | 0.287 | no | 0.864 | 0.327 | no | 1.004 | 0.558 | no | 0.812 | 0.084 | no | 1.083 | 0.286 | no | 0.975 | 0.253 | no | 0.861 | 0.130 | no | 0.894 | 0.179 | no | 0.962 | 0.126 | no |
| DR1768 | Predicted protein | 1.026 | 0.391 | no | 1.270 | 0.564 | no | 1.348 | 0.671 | no | 2.665 | 0.302 | yes | 1.685 | 0.997 | no | 2.543 | 1.554 | yes | 3.228 | 1.327 | yes | 3.163 | 1.068 | yes | 2.817 | 1.181 | yes |
| DR1769 | Beta propeller protein, related to serine/threonine kinase | 0.943 | 0.160 | no | 0.706 | 0.123 | no | 0.711 | 0.254 | yes | 0.794 | 0.025 | no | 1.031 | 0.308 | no | 1.234 | 0.597 | no | 1.266 | 0.209 | no | 1.354 | 0.736 | no | 2.329 | 0.247 | yes |
| DR1770 | Possible membrane protein | 0.993 | 0.194 | no | 2.157 | 0.552 | yes | 2.794 | 1.499 | yes | 2.155 | 0.555 | yes | 1.803 | 0.573 | yes | 1.630 | 0.278 | yes | 1.443 | 0.275 | no | 1.395 | 0.598 | no | 1.145 | 0.193 | no |
| DR1771 | UVRA ABC family ATPase | 1.378 | 0.515 | no | 2.991 | 1.018 | yes | 3.517 | 1.145 | yes | 2.940 | 1.252 | yes | 1.940 | 0.605 | yes | 1.724 | 0.728 | yes | 1.477 | 0.311 | no | 1.314 | 0.497 | no | 0.970 | 0.458 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR1772 | Predicted protein | 1.039 | 0.293 | no | 1.259 | 0.434 | no | 1.353 | 0.813 | no | 1.053 | 0.221 | no | 1.120 | 0.339 | no | 1.143 | 0.481 | no | 1.035 | 0.485 | no | 1.196 | 0.583 | no | 1.192 | 0.412 | no |
| DR1773 | L-rich repeates protein | 1.059 | 0.193 | no | 1.504 | 0.573 | yes | 1.643 | 0.482 | yes | 1.297 | 0.328 | no | 1.418 | 0.879 | no | 1.337 | 0.586 | no | 1.245 | 0.428 | no | 1.279 | 0.486 | no | 1.031 | 0.282 | no |
| DR1774 | Predicted protein | 1.436 | 0.282 | no | 2.275 | 0.948 | yes | 2.439 | 1.166 | yes | 2.540 | 1.362 | yes | 1.983 | 0.490 | yes | 1.728 | 0.749 | yes | 1.419 | 0.394 | no | 1.346 | 0.546 | no | 0.913 | 0.406 | no |
| DR1775 | UVRD Superfamily I helicase | 0.935 | 0.305 | no | 2.439 | 1.146 | yes | 3.302 | 1.692 | yes | 2.848 | 0.811 | yes | 2.309 | 0.988 | yes | 1.799 | 0.603 | yes | 1.330 | 0.514 | no | 1.162 | 0.503 | no | 1.199 | 0.315 | no |
| DR1776 | MutT family Hydrolase | 1.261 | 0.377 | no | 3.119 | 1.752 | yes | 4.698 | 2.827 | yes | 3.170 | 1.127 | yes | 2.856 | 1.100 | yes | 1.808 | 0.488 | yes | 1.387 | 0.544 | no | 1.125 | 0.594 | no | 0.804 | 0.140 | no |
| DR1777 | Predicted protein | 0.822 | 0.182 | no | 1.983 | 0.414 | yes | 2.012 | 0.479 | yes | 1.673 | 0.854 | no | 1.298 | 0.379 | no | 0.732 | 0.270 | no | 0.676 | 0.162 | yes | 0.480 | 0.137 | yes | 0.390 | 0.169 | yes |
| DR1778 | 3-isopropylmalate dehydratase, LEU2 leucine biosynthesis | 1.360 | 0.609 | no | 0.890 | 0.353 | no | 1.285 | 0.509 | no | 1.874 | 1.077 | yes | 1.280 | 0.387 | no | 1.231 | 0.421 | no | 0.835 | 0.195 | no | 0.938 | 0.256 | no | 1.248 | 0.246 | no |
| DR1779 | Predicted protein | 1.107 | 0.345 | no | 1.169 | 0.189 | no | 1.354 | 0.247 | no | 1.345 | 0.186 | no | 1.485 | 0.376 | no | 1.087 | 0.381 | no | 0.971 | 0.252 | no | 0.884 | 0.193 | no | 0.725 | 0.240 | no |
| DR1780 | Predicted protein | 1.140 | 0.206 | no | 1.146 | 0.196 | no | 1.385 | 0.250 | no | 1.569 | 0.338 | no | 1.441 | 0.335 | no | 1.504 | 0.419 | no | 1.239 | 0.278 | no | 1.209 | 0.374 | no | 1.323 | 0.244 | no |
| DR1781 | Predicted protein | 0.948 | 0.360 | no | 1.118 | 0.327 | no | 1.320 | 0.529 | no | 1.278 | 0.079 | no | 1.787 | 0.420 | yes | 1.339 | 0.389 | no | 0.909 | 0.246 | no | 0.922 | 0.086 | no | 1.023 | 0.267 | no |
| DR1782 | Predicted protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR1783 | Predicted protein | 0.996 | 0.385 | no | 1.144 | 0.384 | no | 1.530 | 0.548 | yes | 1.692 | 0.568 | yes | 1.370 | 0.480 | no | 1.354 | 0.272 | no | 1.421 | 0.574 | no | 1.481 | 0.473 | no | 1.143 | 0.174 | no |
| DR1784 | 3-isopropylmalate dehydratase small subunit, LEUD | 1.051 | 0.238 | no | 1.058 | 0.228 | no | 1.189 | 0.452 | no | 1.620 | 0.716 | no | 1.683 | 0.730 | yes | 1.560 | 0.561 | no | 1.558 | 0.660 | no | 1.512 | 0.310 | yes | 1.623 | 0.416 | yes |
| DR1785 | 3-isopropylmalate dehydrogenase, LEU3 | 1.052 | 0.412 | no | 1.043 | 0.326 | no | 1.402 | 0.292 | no | 1.737 | 0.351 | yes | 1.487 | 0.239 | yes | 1.662 | 0.625 | yes | 1.265 | 0.261 | no | 1.295 | 0.160 | no | 1.403 | 0.181 | no |
| DR1786 | Predicted protein | 1.122 | 0.459 | no | 1.006 | 0.402 | no | 1.009 | 0.432 | no | 0.977 | 0.200 | no | 0.938 | 0.422 | no | 1.046 | 0.444 | no | 1.081 | 0.315 | no | 1.001 | 0.280 | no | 0.758 | 0.195 | no |
| DR1787 | MocR-like protein, EXUR_ECOLI, GntR-like HTH transcriptional regulator + aminotransferase | 1.169 | 0.392 | no | 1.085 | 0.305 | no | 1.019 | 0.209 | no | 1.185 | 0.518 | no | 1.054 | 0.432 | no | 0.938 | 0.315 | no | 1.044 | 0.400 | no | 0.978 | 0.448 | no | 0.959 | 0.294 | no |
| DR1788 | Predicted protein | 1.055 | 0.557 | no | 0.784 | 0.315 | no | 0.822 | 0.330 | no | 0.656 | 0.236 | yes | 0.750 | 0.331 | no | 0.893 | 0.391 | no | 0.842 | 0.315 | no | 1.104 | 0.286 | no | 0.794 | 0.285 | no |
| DR1789 | SFHB Pseudouridine synthase, S4 domain containing | 1.430 | 0.310 | no | 1.205 | 0.356 | no | 1.086 | 0.439 | no | 1.351 | 0.303 | no | 1.064 | 0.362 | no | 1.159 | 0.490 | no | 1.227 | 0.440 | no | 1.047 | 0.335 | no | 1.034 | 0.353 | no |
| DR1790 | Homolog of Yellow/royal jelly protein of insects | 1.059 | 0.271 | no | 0.610 | 0.205 | yes | 0.453 | 0.135 | yes | 0.389 | 0.053 | yes | 0.545 | 0.123 | yes | 0.803 | 0.272 | no | 0.953 | 0.202 | no | 1.263 | 0.081 | no | 1.296 | 0.209 | no |
| DR1791 | Anthranilate synthase component I | 1.380 | 0.393 | no | 1.252 | 0.523 | no | 0.962 | 0.317 | no | 0.964 | 0.158 | no | 0.996 | 0.196 | no | 1.178 | 0.720 | no | 1.085 | 0.397 | no | 1.225 | 0.395 | no | 1.234 | 0.186 | no |
| DR1792 | Conserved membrane protein | 1.042 | 0.264 | no | 1.061 | 0.186 | no | 0.772 | 0.292 | no | 0.648 | 0.046 | no | 0.899 | 0.450 | no | 0.912 | 0.213 | no | 0.818 | 0.145 | no | 0.985 | 0.245 | no | 1.093 | 0.156 | no |
| DR1793 | Uncharacterized conserved protein | 1.197 | 0.199 | no | 1.203 | 0.572 | no | 1.015 | 0.374 | no | 1.074 | 0.306 | no | 1.046 | 0.235 | no | 1.036 | 0.181 | no | 0.766 | 0.201 | no | 1.081 | 0.172 | no | 0.944 | 0.141 | no |
| DR1794 | NosX/YOJL_ECOLI homolog | 1.047 | 0.270 | no | 1.158 | 0.375 | no | 1.046 | 0.433 | no | 0.866 | 0.362 | no | 1.100 | 0.586 | no | 1.364 | 0.531 | no | 1.641 | 0.736 | yes | 1.846 | 0.999 | yes | 1.483 | 0.766 | no |
| DR1795 | Predicted protein | 1.220 | 0.205 | no | 1.300 | 0.517 | no | 1.104 | 0.421 | no | 0.935 | 0.249 | no | 1.012 | 0.263 | no | 1.381 | 0.636 | no | 1.305 | 0.397 | no | 1.716 | 0.763 | yes | 1.747 | 0.848 | yes |
| DR1796 | Small highly conserved protein always associated with the NusA gene, YHBC | 0.960 | 0.156 | no | 4.854 | 2.302 | yes | 5.269 | 1.884 | yes | 3.293 | 0.551 | yes | 3.162 | 0.826 | yes | 2.796 | 1.417 | yes | 1.944 | 0.549 | yes | 1.419 | 0.404 | no | 1.194 | 0.188 | no |
| DR1797 | NusA ortholog | 1.110 | 0.202 | no | 3.669 | 1.221 | yes | 3.971 | 1.437 | yes | 2.839 | 0.190 | yes | 2.783 | 1.635 | yes | 2.449 | 1.130 | yes | 1.684 | 0.434 | yes | 1.465 | 0.600 | no | 1.138 | 0.321 | no |
| DR1798 | Small conserved 2 cysteine protein, often seen in the vicnity of the above 2 proteins | 0.887 | 0.178 | no | 2.923 | 1.513 | yes | 3.320 | 1.193 | yes | 2.326 | 0.618 | yes | 2.462 | 1.392 | yes | 2.360 | 1.152 | yes | 1.702 | 0.614 | yes | 1.584 | 0.248 | yes | 1.044 | 0.326 | no |
| DR1799 | Initiation factor IF-2 | 1.195 | 0.375 | no | 3.794 | 0.913 | yes | 4.565 | 1.282 | yes | 2.894 | 0.550 | yes | 2.881 | 1.306 | yes | 2.753 | 1.180 | yes | 1.852 | 0.413 | yes | 1.495 | 0.691 | no | 1.125 | 0.474 | no |
| DR1800 | NH2-acetyltransferase | 0.904 | 0.316 | no | 1.698 | 0.397 | yes | 1.739 | 0.818 | yes | 1.073 | 0.491 | no | 1.159 | 0.450 | no | 1.121 | 0.479 | no | 1.060 | 0.420 | no | 1.279 | 0.440 | no | 1.257 | 0.379 | no |
| DR1801 | Membrane protein | 1.108 | 0.183 | no | 1.585 | 0.562 | yes | 2.141 | 0.934 | yes | 1.637 | 0.708 | no | 1.554 | 0.235 | yes | 1.419 | 0.236 | no | 1.420 | 0.351 | no | 1.391 | 0.730 | no | 1.566 | 0.672 | yes |
| DR1802 | Membrane protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR1803 | Predicted protein | 1.050 | 0.340 | no | 1.721 | 0.370 | yes | 2.365 | 1.179 | yes | 1.697 | 0.779 | no | 1.463 | 0.841 | no | 1.494 | 0.298 | no | 1.271 | 0.544 | no | 1.463 | 0.331 | no | 1.212 | 0.346 | no |
| DR1804 | Solo Double stranded beta helix protein, curC | 1.309 | 0.626 | no | 1.085 | 0.308 | no | 1.523 | 0.590 | yes | 2.142 | 0.831 | yes | 1.772 | 0.474 | yes | 1.528 | 0.779 | no | 2.264 | 1.257 | yes | 2.465 | 0.969 | yes | 2.450 | 0.884 | yes |
| DR1805 | Predicted protein | 1.687 | 1.003 | no | 1.396 | 0.400 | no | 1.339 | 0.512 | no | 1.304 | 0.626 | no | 1.193 | 0.440 | no | 1.121 | 0.375 | no | 0.978 | 0.356 | no | 1.103 | 0.536 | no | 0.835 | 0.317 | no |
| DR1806 | Small nucleotidyl transferase related protein | 1.193 | 0.454 | no | 0.926 | 0.526 | no | 0.910 | 0.433 | no | 1.320 | 0.582 | no | 1.377 | 0.489 | no | 1.035 | 0.420 | no | 0.971 | 0.327 | no | 1.018 | 0.440 | no | 0.996 | 0.324 | no |
| DR1807 | Nucleotidyl transferase associated DORF | 0.758 | 0.124 | no | 0.631 | 0.210 | yes | 0.465 | 0.110 | yes | 0.490 | 0.077 | yes | 0.785 | 0.336 | no | 0.586 | 0.107 | yes | 0.677 | 0.349 | yes | 0.679 | 0.093 | yes | 0.804 | 0.096 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR1808 | DGTPase, HD superfamily hydrolase | 1.122 | 0.412 | no | 0.903 | 0.321 | no | 0.805 | 0.362 | no | 1.401 | 0.668 | no | 1.064 | 0.467 | no | 0.767 | 0.226 | no | 0.776 | 0.221 | no | 0.892 | 0.212 | no | 1.028 | 0.201 | no |
| DR1809 | Glycine dehydrogenase, glycine cleavage system P protein | 0.971 | 0.294 | no | 0.833 | 0.216 | no | 0.857 | 0.299 | no | 1.022 | 0.357 | no | 1.096 | 0.256 | no | 0.858 | 0.107 | no | 0.968 | 0.260 | no | 1.344 | 0.480 | no | 1.224 | 0.116 | no |
| DR1810 | Predicted protein | 0.758 | 0.445 | no | 0.965 | 0.379 | no | 0.795 | 0.360 | no | 1.106 | 0.436 | no | 1.192 | 0.516 | no | 0.854 | 0.183 | no | 1.056 | 0.611 | no | 0.742 | 0.190 | no | 0.983 | 0.643 | no |
| DR1811 | Glycine cleavage system H protein | 0.904 | 0.357 | no | 0.768 | 0.237 | no | 0.760 | 0.238 | no | 0.997 | 0.383 | no | 0.973 | 0.346 | no | 0.938 | 0.311 | no | 1.005 | 0.398 | no | 1.184 | 0.230 | no | 1.034 | 0.148 | no |
| DR1813 | Predicted protein | 1.140 | 0.537 | no | 1.418 | 0.255 | yes | 0.907 | 0.360 | no | 1.025 | 0.561 | no | 0.943 | 0.346 | no | 0.992 | 0.367 | no | 1.049 | 0.296 | no | 0.910 | 0.366 | no | 0.848 | 0.320 | no |
| DR1814 | 2'-5' phosphodiesterase of the 2H superfamily | 1.232 | 0.406 | no | 0.863 | 0.239 | no | 0.629 | 0.076 | yes | 0.756 | 0.240 | no | 0.658 | 0.277 | yes | 0.678 | 0.236 | yes | 0.727 | 0.169 | no | 0.965 | 0.173 | no | 0.776 | 0.305 | no |
| DR1815 | 5,10-methenyltetrahydrofolate synthetase, YGFA | 1.094 | 0.470 | no | 1.810 | 0.503 | yes | 1.385 | 0.653 | no | 1.238 | 0.161 | no | 1.289 | 0.512 | no | 0.926 | 0.204 | no | 0.925 | 0.146 | no | 0.933 | 0.206 | no | 0.627 | 0.320 | yes |
| DR1816 | Predicted protein | 0.818 | 0.330 | no | 1.026 | 0.332 | no | 0.804 | 0.302 | no | 0.718 | 0.349 | no | 0.674 | 0.204 | yes | 0.635 | 0.178 | yes | 0.677 | 0.270 | yes | 0.842 | 0.132 | no | 0.574 | 0.198 | yes |
| DR1817 | 2-dehydro-3-deoxyphosphoheptonate aldolase, AROF | 1.076 | 0.372 | no | 0.657 | 0.292 | yes | 0.406 | 0.209 | yes | 0.435 | 0.109 | yes | 0.473 | 0.175 | yes | 0.546 | 0.398 | yes | 0.431 | 0.252 | yes | 0.588 | 0.243 | yes | 0.575 | 0.253 | yes |
| DR1818 | Secreted conserved protein, YDHA-like family | 0.862 | 0.237 | no | 0.504 | 0.217 | yes | 0.398 | 0.129 | yes | 0.379 | 0.073 | yes | 0.520 | 0.153 | yes | 0.707 | 0.302 | yes | 0.968 | 0.384 | no | 1.184 | 0.267 | no | 0.950 | 0.253 | no |
| DR1819 | UV endonuclease mus18 Neurospora homolog, YwjD Bacillus, TIM barrel nuclease | 1.018 | 0.283 | no | 1.257 | 0.487 | no | 0.967 | 0.254 | no | 1.157 | 0.141 | no | 0.953 | 0.297 | no | 0.950 | 0.278 | no | 0.967 | 0.152 | no | 1.203 | 0.253 | no | 0.880 | 0.172 | no |
| DR1820 | Secreted protein, uncharacterized | 1.049 | 0.344 | no | 0.831 | 0.156 | no | 0.679 | 0.222 | yes | 0.642 | 0.065 | no | 0.858 | 0.186 | no | 1.175 | 0.580 | no | 1.280 | 0.671 | no | 1.035 | 0.049 | no | 1.346 | 0.520 | no |
| DR1821 | Predicted protein | 1.089 | 0.208 | no | 1.183 | 0.338 | no | 1.146 | 0.337 | no | 1.110 | 0.309 | no | 1.044 | 0.329 | no | 1.383 | 0.572 | no | 1.273 | 0.356 | no | 1.483 | 0.762 | no | 0.946 | 0.281 | no |
| DR1822 | Protein export membrane protein SecD | 0.939 | 0.503 | no | 1.367 | 0.535 | no | 1.747 | 0.809 | yes | 1.038 | 0.137 | no | 1.111 | 0.315 | no | 1.247 | 0.564 | no | 1.108 | 0.454 | no | 1.422 | 0.451 | no | 1.282 | 0.319 | no |
| DR1823 | Metallobetalactamase fold superfamily | 0.983 | 0.156 | no | 2.037 | 0.811 | yes | 1.827 | 0.641 | yes | 2.245 | 0.380 | yes | 1.498 | 0.617 | no | 1.312 | 0.777 | no | 1.199 | 0.354 | no | 1.277 | 0.660 | no | 1.244 | 0.091 | no |
| DR1824 | ADP-glucose pyrophosphorylase, glgC ortholog | 0.783 | 0.304 | no | 0.819 | 0.293 | no | 0.815 | 0.408 | no | 0.604 | 0.150 | yes | 0.976 | 0.305 | no | 1.153 | 0.648 | no | 1.066 | 0.369 | no | 1.266 | 0.503 | no | 1.501 | 0.389 | yes |
| DR1825 | Protein-export membrane protein SECG | 1.131 | 0.316 | no | 2.440 | 0.977 | yes | 3.210 | 1.481 | yes | 2.433 | 0.737 | yes | 1.764 | 0.620 | yes | 1.740 | 0.792 | yes | 1.460 | 0.563 | no | 1.492 | 0.433 | yes | 1.310 | 0.302 | no |
| DR1826 | Gamma-glutamyl phosphate reductase | 1.022 | 0.436 | no | 0.881 | 0.520 | no | 0.871 | 0.465 | no | 0.671 | 0.205 | no | 0.843 | 0.303 | no | 0.982 | 0.585 | no | 0.931 | 0.538 | no | 1.140 | 0.561 | no | 1.255 | 0.317 | no |
| DR1827 | Glutamate 5-kinase | 1.074 | 0.291 | no | 0.921 | 0.360 | no | 1.057 | 0.483 | no | 1.313 | 0.728 | no | 1.035 | 0.290 | no | 1.001 | 0.321 | no | 1.087 | 0.494 | no | 1.207 | 0.635 | no | 1.256 | 0.753 | no |
| DR1828 | Secreted protein, uncharacterized | 1.033 | 0.299 | no | 1.512 | 0.334 | yes | 1.430 | 0.538 | no | 1.358 | 0.875 | no | 1.168 | 0.496 | no | 0.926 | 0.435 | no | 0.846 | 0.507 | no | 1.027 | 0.414 | no | 0.603 | 0.241 | yes |
| DR1829 | Membrane protein, with domain shared by signal proteins, HAMP domain | 1.141 | 0.594 | no | 0.941 | 0.469 | no | 1.047 | 0.467 | no | 1.577 | 0.868 | no | 1.414 | 0.529 | no | 1.290 | 0.552 | no | 1.431 | 0.828 | no | 1.460 | 0.640 | no | 1.222 | 0.171 | no |
| DR1830 | Predicted protein | 0.811 | 0.343 | no | 0.859 | 0.475 | no | 0.787 | 0.445 | no | 0.557 | 0.204 | yes | 0.654 | 0.135 | yes | 0.887 | 0.214 | no | 0.802 | 0.352 | no | 0.788 | 0.234 | no | 0.829 | 0.218 | no |
| DR1831 | Predicted protein | 1.009 | 0.290 | no | 0.946 | 0.564 | no | 1.027 | 0.553 | no | 1.033 | 0.378 | no | 0.739 | 0.310 | no | 1.105 | 0.445 | no | 0.975 | 0.502 | no | 1.001 | 0.220 | no | 0.911 | 0.268 | no |
| DR1832 | Bacillus YTXJ homolog | 0.695 | 0.144 | no | 0.527 | 0.208 | yes | 0.526 | 0.110 | yes | 0.660 | 0.091 | no | 1.081 | 0.369 | no | 0.880 | 0.148 | no | 1.109 | 0.422 | no | 1.011 | 0.229 | no | 1.301 | 0.309 | no |
| DR1833 | Predicted protein | 1.013 | 0.301 | no | 0.847 | 0.288 | no | 0.892 | 0.233 | no | 1.152 | 0.384 | no | 0.935 | 0.259 | no | 0.911 | 0.150 | no | 0.829 | 0.215 | no | 1.289 | 0.449 | no | 0.968 | 0.214 | no |
| DR1834 | SAM dependent methyltransferase | 0.923 | 0.283 | no | 0.818 | 0.302 | no | 0.796 | 0.227 | no | 0.662 | 0.158 | no | 0.840 | 0.206 | no | 0.870 | 0.337 | no | 0.764 | 0.140 | no | 0.943 | 0.190 | no | 0.917 | 0.277 | no |
| DR1835 | Phospho-N-acetylmuramoyl-pentapeptide-transferase, MraY | 1.028 | 0.429 | no | 0.929 | 0.439 | no | 0.850 | 0.307 | no | 1.053 | 0.594 | no | 1.162 | 0.582 | no | 1.112 | 0.164 | no | 1.029 | 0.386 | no | 1.033 | 0.300 | no | 0.865 | 0.220 | no |
| DR1836 | SR54 signal recognition GTPase | 0.666 | 0.266 | yes | 0.617 | 0.095 | yes | 0.466 | 0.143 | yes | 0.437 | 0.072 | yes | 0.678 | 0.281 | yes | 0.682 | 0.295 | yes | 0.765 | 0.275 | no | 1.014 | 0.300 | no | 1.403 | 0.170 | no |
| DR1837 | Predicted protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR1838 | SpoT GTP pyrophosphokinase, HD superfamily hydrolase | 1.048 | 0.412 | no | 1.047 | 0.326 | no | 0.698 | 0.284 | yes | 0.628 | 0.268 | yes | 0.564 | 0.181 | yes | 0.612 | 0.249 | yes | 0.584 | 0.145 | yes | 0.588 | 0.141 | yes | 0.916 | 0.173 | no |
| DR1839 | FKBP, peptidylprolyl isomerase | 1.106 | 0.470 | no | 0.676 | 0.114 | yes | 0.641 | 0.228 | yes | 0.879 | 0.459 | no | 1.594 | 1.204 | no | 1.659 | 0.658 | yes | 2.878 | 1.317 | yes | 2.625 | 0.963 | yes | 2.211 | 1.278 | yes |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR1840 | Predicted protein | 1.233 | 0.568 | no | 0.603 | 0.313 | yes | 0.501 | 0.129 | yes | 0.987 | 0.356 | no | 1.131 | 0.462 | no | 1.307 | 0.481 | no | 1.462 | 0.185 | no | 1.514 | 0.158 | yes | 1.682 | 0.521 | yes |
| DR1841 | Membrane protein of YOJF family | 0.758 | 0.126 | no | 0.600 | 0.153 | yes | 0.490 | 0.075 | yes | 0.483 | 0.051 | yes | 0.621 | 0.196 | yes | 0.703 | 0.129 | no | 0.701 | 0.203 | no | 0.819 | 0.107 | no | 0.853 | 0.138 | no |
| DR1842 | Predicted protein | 1.019 | 0.450 | no | 0.859 | 0.208 | no | 0.707 | 0.110 | no | 0.621 | 0.189 | yes | 0.733 | 0.255 | no | 0.926 | 0.361 | no | 0.843 | 0.321 | no | 0.901 | 0.205 | no | 0.842 | 0.265 | no |
| DR1843 | DPPA, dipeptide transporter subunit | 1.020 | 0.314 | no | 0.658 | 0.155 | yes | 0.576 | 0.167 | yes | 0.438 | 0.036 | yes | 0.637 | 0.290 | yes | 0.789 | 0.162 | no | 0.921 | 0.249 | no | 0.921 | 0.178 | no | 0.957 | 0.149 | no |
| DR1844 | NH2-acetyltransferase | 1.078 | 0.321 | no | 0.414 | 0.137 | yes | 0.522 | 0.100 | yes | 0.839 | 0.093 | no | 1.355 | 0.700 | no | 1.846 | 0.328 | yes | 2.082 | 0.291 | yes | 2.269 | 0.425 | yes | 2.762 | 0.336 | yes |
| DR1845 | Predicted protein | 0.987 | 0.297 | no | 0.574 | 0.250 | yes | 0.508 | 0.338 | yes | 0.429 | 0.079 | yes | 0.527 | 0.238 | yes | 0.870 | 0.539 | no | 0.953 | 0.644 | no | 0.823 | 0.116 | no | 0.930 | 0.466 | no |
| DR1846 | HTH transcriptional regulator | 1.168 | 0.305 | no | 0.757 | 0.225 | no | 0.629 | 0.228 | yes | 0.727 | 0.062 | no | 0.857 | 0.288 | no | 1.194 | 0.485 | no | 1.083 | 0.301 | no | 1.413 | 0.633 | no | 1.247 | 0.699 | no |
| DR1847 | Predicted protein | 1.019 | 0.386 | no | 1.237 | 0.800 | no | 1.256 | 0.887 | no | 0.895 | 0.202 | no | 0.865 | 0.124 | no | 1.120 | 0.595 | no | 1.192 | 0.467 | no | 1.387 | 0.556 | no | 1.156 | 0.346 | no |
| DR1848 | 1,4-alpha-glucan branching enzyme, GLGB | 1.157 | 0.252 | no | 1.124 | 0.694 | no | 1.274 | 0.610 | no | 1.250 | 0.413 | no | 1.118 | 0.668 | no | 1.259 | 0.667 | no | 1.226 | 0.382 | no | 1.268 | 0.481 | no | 1.076 | 0.222 | no |
| DR1849 | Peptide methionine sulfoxide reductase | 0.903 | 0.343 | no | 0.674 | 0.422 | yes | 0.582 | 0.404 | yes | 0.561 | 0.271 | yes | 0.773 | 0.276 | no | 0.874 | 0.334 | no | 0.914 | 0.389 | no | 1.144 | 0.306 | no | 1.071 | 0.250 | no |
| DR1850 | Predicted protein | 1.134 | 0.213 | no | 3.046 | 0.907 | yes | 4.361 | 1.134 | yes | 3.267 | 0.397 | yes | 2.622 | 1.212 | yes | 2.011 | 0.852 | yes | 1.384 | 0.355 | no | 1.333 | 0.465 | no | 1.011 | 0.282 | no |
| DR1851 | Related to S/T Protein Kinase | 1.017 | 0.380 | no | 0.994 | 0.396 | no | 0.907 | 0.466 | no | 0.621 | 0.174 | yes | 0.839 | 0.232 | no | 1.033 | 0.602 | no | 0.983 | 0.554 | no | 1.111 | 0.459 | no | 1.013 | 0.460 | no |
| DR1852 | Predicted protein | 1.356 | 0.444 | no | 0.700 | 0.326 | yes | 0.758 | 0.257 | no | 0.882 | 0.419 | no | 0.798 | 0.440 | no | 0.676 | 0.190 | yes | 0.945 | 0.209 | no | 0.984 | 0.116 | no | 2.181 | 0.365 | yes |
| DR1853 | Predicted protein | 0.993 | 0.311 | no | 0.892 | 0.120 | no | 1.169 | 0.425 | no | 1.327 | 0.242 | no | 1.182 | 0.149 | no | 1.012 | 0.280 | no | 0.896 | 0.326 | no | 0.986 | 0.027 | no | 1.061 | 0.083 | no |
| DR1854 | ComEC/rec2 ortholog, membrane associated hydrolase of the Metallobetalactamase fold superfamily | 0.952 | 0.250 | no | 1.004 | 0.295 | no | 1.076 | 0.212 | no | 0.991 | 0.155 | no | 0.962 | 0.226 | no | 1.024 | 0.399 | no | 0.993 | 0.322 | no | 0.997 | 0.285 | no | 1.024 | 0.375 | no |
| DR1855 | ComEA, COMA operon | 1.001 | 0.146 | no | 0.924 | 0.181 | no | 1.172 | 0.503 | no | 1.054 | 0.014 | no | 0.906 | 0.083 | no | 0.997 | 0.124 | no | 1.025 | 0.153 | no | 1.097 | 0.070 | no | 1.337 | 0.356 | no |
| DR1856 | GatA amidase subunit | 0.713 | 0.285 | no | 0.541 | 0.266 | yes | 0.547 | 0.388 | yes | 0.372 | 0.091 | yes | 0.525 | 0.099 | yes | 0.707 | 0.425 | yes | 0.797 | 0.420 | no | 0.972 | 0.384 | no | 1.060 | 0.193 | no |
| DR1857 | OSMC homolog, conserved bacterial/archaeal proteins involved in alkylperoxide and oxidative stress responce | 0.880 | 0.125 | no | 0.592 | 0.175 | yes | 0.525 | 0.140 | yes | 0.447 | 0.029 | yes | 0.671 | 0.159 | yes | 0.528 | 0.143 | yes | 0.734 | 0.232 | no | 0.742 | 0.190 | no | 1.018 | 0.179 | no |
| DR1858 | Conserved membrane protein, probably transporter, ortholog YECA | 0.810 | 0.359 | no | 0.630 | 0.254 | yes | 0.566 | 0.127 | yes | 0.448 | 0.092 | yes | 0.539 | 0.221 | yes | 0.667 | 0.314 | yes | 0.755 | 0.318 | no | 0.749 | 0.139 | no | 0.676 | 0.207 | no |
| DR1859 | Predicted protein | 0.983 | 0.286 | no | 0.794 | 0.256 | no | 0.968 | 0.346 | no | 1.040 | 0.411 | no | 0.979 | 0.547 | no | 0.857 | 0.155 | no | 0.966 | 0.241 | no | 0.843 | 0.107 | no | 0.857 | 0.232 | no |
| DR1860 | Predicted protein | 0.870 | 0.241 | no | 0.941 | 0.135 | no | 0.605 | 0.162 | yes | 0.596 | 0.113 | yes | 0.844 | 0.212 | no | 1.077 | 0.261 | no | 1.149 | 0.641 | no | 1.401 | 0.504 | no | 0.919 | 0.270 | no |
| DR1861 | HTH transcriptional regulator | 1.068 | 0.217 | no | 1.150 | 0.390 | no | 1.313 | 0.492 | no | 1.362 | 0.288 | no | 1.506 | 0.288 | yes | 1.546 | 0.241 | yes | 1.742 | 0.474 | yes | 1.421 | 0.303 | no | 1.499 | 0.090 | yes |
| DR1862 | Putative translation factor, SUA5 superfamily | 0.704 | 0.164 | no | 0.837 | 0.258 | no | 0.703 | 0.238 | yes | 0.549 | 0.269 | yes | 0.685 | 0.263 | yes | 0.647 | 0.297 | yes | 0.755 | 0.364 | no | 0.690 | 0.193 | yes | 0.611 | 0.125 | yes |
| DR1863 | Leader peptidase IV, GSPF/PilC general secretion pathway protein | 0.964 | 0.546 | no | 0.542 | 0.274 | yes | 0.344 | 0.181 | yes | 0.184 | 0.134 | yes | 0.293 | 0.201 | yes | 0.348 | 0.152 | yes | 0.451 | 0.175 | yes | 0.564 | 0.065 | yes | 0.604 | 0.212 | yes |
| DR1864 | Uncharacterized conserved small membrane protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR1865 | Uncharacterized protein YABB ortholog | 0.547 | 0.168 | yes | 0.789 | 0.274 | no | 1.129 | 0.635 | no | 0.592 | 0.124 | yes | 0.850 | 0.376 | no | 1.215 | 0.512 | no | 1.415 | 0.550 | no | 1.638 | 0.242 | yes | 2.506 | 0.857 | yes |
| DR1866 | MraW/YabC like SAM dependent methylase | 0.634 | 0.292 | yes | 0.816 | 0.413 | no | 1.302 | 0.694 | no | 0.668 | 0.179 | no | 0.836 | 0.322 | no | 1.017 | 0.543 | no | 1.021 | 0.164 | no | 1.406 | 0.172 | no | 1.596 | 0.344 | yes |
| DR1867 | Predicted protein | 0.585 | 0.224 | yes | 0.721 | 0.377 | yes | 0.745 | 0.163 | no | 0.617 | 0.116 | yes | 0.601 | 0.211 | yes | 0.919 | 0.213 | no | 1.247 | 0.515 | no | 1.238 | 0.108 | no | 1.087 | 0.239 | no |
| DR1868 | Penicillin binding protein 2, PBP-2 | 0.810 | 0.288 | no | 0.969 | 0.230 | no | 1.647 | 0.854 | yes | 1.276 | 0.257 | no | 1.214 | 0.311 | no | 1.476 | 0.560 | no | 1.369 | 0.303 | no | 1.793 | 0.598 | yes | 1.702 | 0.532 | yes |
| DR1869 | Polyferredoxin | 0.795 | 0.449 | no | 0.550 | 0.212 | yes | 0.460 | 0.193 | yes | 0.454 | 0.233 | yes | 0.579 | 0.158 | yes | 0.486 | 0.119 | yes | 0.560 | 0.202 | yes | 0.758 | 0.218 | no | 0.673 | 0.210 | no |
| DR1870 | P-loop ATPase | 0.986 | 0.266 | no | 1.695 | 0.386 | yes | 2.308 | 0.529 | yes | 2.064 | 0.517 | yes | 1.666 | 0.567 | yes | 1.220 | 0.186 | no | 1.404 | 0.345 | no | 1.249 | 0.277 | no | 1.155 | 0.513 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR1871 | Chloromuconate cycloisomerase, TIM barrel enzyme with insert | 0.844 | 0.342 | no | 1.009 | 0.331 | no | 1.171 | 0.396 | no | 0.977 | 0.391 | no | 1.082 | 0.415 | no | 0.969 | 0.367 | no | 1.231 | 0.718 | no | 1.326 | 0.534 | no | 0.984 | 0.417 | no |
| DR1872 | MetJ/Arc family transcriptional regulator | 0.961 | 0.156 | no | 0.659 | 0.146 | yes | 0.607 | 0.184 | yes | 0.910 | 0.011 | no | 0.999 | 0.205 | no | 1.101 | 0.138 | no | 1.106 | 0.293 | no | 1.665 | 0.399 | yes | 1.568 | 0.220 | yes |
| DR1873 | Membrane protein | 0.953 | 0.370 | no | 0.858 | 0.435 | no | 0.767 | 0.210 | no | 0.568 | 0.115 | yes | 0.605 | 0.147 | yes | 0.706 | 0.280 | no | 0.829 | 0.424 | no | 1.003 | 0.379 | no | 0.924 | 0.255 | no |
| DR1874 | GMP synthase, PP-loop ATPase | 0.917 | 0.245 | no | 1.109 | 0.311 | no | 1.343 | 0.352 | no | 1.248 | 0.237 | no | 1.096 | 0.305 | no | 0.973 | 0.296 | no | 1.009 | 0.370 | no | 1.294 | 0.538 | no | 1.192 | 0.233 | no |
| DR1875 | Conserved membrane protein | 1.180 | 0.664 | no | 0.778 | 0.292 | no | 0.794 | 0.245 | no | 0.829 | 0.373 | no | 0.965 | 0.365 | no | 0.909 | 0.363 | no | 0.994 | 0.331 | no | 1.170 | 0.425 | no | 0.930 | 0.362 | no |
| DR1876 | Hydrolase of the Metallobetalactamase fold superfamily | 1.078 | 0.225 | no | 1.025 | 0.301 | no | 0.868 | 0.292 | no | 0.891 | 0.139 | no | 1.076 | 0.418 | no | 0.890 | 0.186 | no | 1.049 | 0.351 | no | 1.185 | 0.397 | no | 1.182 | 0.414 | no |
| DR1877 | Conserved membrane protein, with MRR-like nuclease domain | 0.873 | 0.465 | no | 0.873 | 0.149 | no | 0.790 | 0.097 | no | 0.728 | 0.095 | no | 0.753 | 0.177 | no | 0.814 | 0.248 | no | 0.882 | 0.359 | no | 0.989 | 0.503 | no | 0.870 | 0.228 | no |
| DR1878 | IMP dehydrogenase | 0.940 | 0.187 | no | 0.548 | 0.121 | yes | 0.595 | 0.241 | yes | 0.542 | 0.078 | yes | 0.504 | 0.196 | yes | 0.619 | 0.158 | yes | 0.683 | 0.092 | no | 0.826 | 0.040 | no | 1.924 | 0.476 | yes |
| DR1879 | Conserved membrane protein | 0.927 | 0.232 | no | 0.940 | 0.265 | no | 1.060 | 0.606 | no | 0.947 | 0.160 | no | 0.862 | 0.085 | no | 1.080 | 0.457 | no | 1.111 | 0.358 | no | 0.951 | 0.309 | no | 0.970 | 0.294 | no |
| DR1880 | Hemolysin III homolog, metal dependent hydrolase | 1.059 | 0.218 | no | 0.849 | 0.174 | no | 0.884 | 0.426 | no | 0.874 | 0.173 | no | 0.785 | 0.090 | no | 0.743 | 0.195 | no | 0.929 | 0.201 | no | 0.970 | 0.221 | no | 1.226 | 0.480 | no |
| DR1881 | Predicted Zinc binding protein | 0.969 | 0.158 | no | 0.588 | 0.116 | yes | 0.426 | 0.187 | yes | 0.495 | 0.033 | yes | 0.526 | 0.132 | yes | 0.531 | 0.112 | yes | 0.563 | 0.240 | yes | 0.631 | 0.179 | yes | 0.851 | 0.160 | no |
| DR1882 | Membrane protein, probable transporter | 0.763 | 0.172 | no | 0.616 | 0.192 | yes | 0.536 | 0.186 | yes | 0.430 | 0.137 | yes | 0.487 | 0.139 | yes | 0.693 | 0.322 | yes | 0.712 | 0.349 | yes | 0.665 | 0.316 | yes | 0.809 | 0.165 | no |
| DR1883 | YIIM/YflK ortholog, bacterial family note conserved HGG motif | 0.934 | 0.286 | no | 0.725 | 0.180 | no | 0.665 | 0.219 | yes | 0.484 | 0.182 | yes | 0.744 | 0.325 | no | 0.728 | 0.254 | no | 0.917 | 0.361 | no | 0.920 | 0.277 | no | 1.045 | 0.517 | no |
| DR1884 | HTH transcriptional regulator, LacI family | 0.981 | 0.171 | no | 0.621 | 0.205 | yes | 0.598 | 0.316 | yes | 0.587 | 0.270 | yes | 0.631 | 0.381 | yes | 0.527 | 0.230 | yes | 0.651 | 0.176 | yes | 0.666 | 0.169 | yes | 0.741 | 0.173 | no |
| DR1885 | Uncharacterized conserved secreted or membrane protein | 0.921 | 0.288 | no | 0.353 | 0.169 | yes | 0.098 | 0.021 | yes | 0.081 | 0.011 | yes | 0.146 | 0.100 | yes | 0.150 | 0.101 | yes | 0.275 | 0.142 | yes | 0.218 | 0.050 | yes | 0.340 | 0.082 | yes |
| DR1886 | Yeast Sco1/sco2 family Thioredoxin fold protein | 0.949 | 0.213 | no | 0.379 | 0.099 | yes | 0.208 | 0.150 | yes | 0.139 | 0.051 | yes | 0.173 | 0.110 | yes | 0.153 | 0.118 | yes | 0.170 | 0.091 | yes | 0.157 | 0.066 | yes | 0.500 | 0.228 | yes |
| DR1887 | Predicted membrane protein | 0.817 | 0.454 | no | 0.445 | 0.244 | yes | 0.210 | 0.089 | yes | 0.143 | 0.080 | yes | 0.206 | 0.085 | yes | 0.237 | 0.102 | yes | 0.276 | 0.136 | yes | 0.349 | 0.019 | yes | 0.544 | 0.153 | yes |
| DR1888 | Predicted decarboxylase from acetoacetate decarboxylase family | 0.982 | 0.304 | no | 0.552 | 0.156 | yes | 0.505 | 0.228 | yes | 0.348 | 0.024 | yes | 0.367 | 0.137 | yes | 0.450 | 0.127 | yes | 0.428 | 0.167 | yes | 0.518 | 0.157 | yes | 0.522 | 0.219 | yes |
| DR1889 | Conserved membrane protein metal-hydrolase MJ0790 family | 0.655 | 0.241 | yes | 0.701 | 0.227 | yes | 0.683 | 0.270 | yes | 0.457 | 0.041 | yes | 0.565 | 0.136 | yes | 0.770 | 0.304 | no | 0.753 | 0.401 | no | 0.976 | 0.515 | no | 1.111 | 0.381 | no |
| DR1890 | Rossman fold oxidoreductase | 0.859 | 0.335 | no | 0.576 | 0.163 | yes | 0.520 | 0.307 | yes | 0.443 | 0.074 | yes | 0.593 | 0.160 | yes | 0.741 | 0.145 | no | 0.998 | 0.278 | no | 1.448 | 0.419 | no | 1.653 | 0.276 | yes |
| DR1891 | TPR repeat protein | 0.749 | 0.213 | no | 1.502 | 0.459 | yes | 1.608 | 0.571 | yes | 1.362 | 0.635 | no | 1.527 | 0.406 | yes | 1.134 | 0.415 | no | 1.107 | 0.282 | no | 1.463 | 0.208 | yes | 1.393 | 0.523 | no |
| DR1892 | Small ABC superfamily ATPases, YACE ortholog | 0.859 | 0.152 | no | 1.336 | 0.650 | no | 1.512 | 0.874 | no | 1.645 | 0.453 | yes | 1.207 | 0.366 | no | 1.368 | 0.401 | no | 1.220 | 0.353 | no | 1.521 | 0.756 | no | 1.423 | 0.675 | no |
| DR1893 | Cyclophilin, peptidyl-prolyl isomerase | 1.108 | 0.483 | no | 0.367 | 0.126 | yes | 0.344 | 0.144 | yes | 0.486 | 0.236 | yes | 0.851 | 0.389 | no | 1.317 | 0.457 | no | 2.208 | 0.381 | yes | 1.880 | 0.504 | yes | 1.797 | 0.524 | yes |
| DR1894 | HTH, LRP family transcriptional regulators | 1.027 | 0.242 | no | 0.895 | 0.342 | no | 0.915 | 0.427 | no | 0.897 | 0.194 | no | 0.960 | 0.201 | no | 0.950 | 0.136 | no | 1.076 | 0.211 | no | 1.298 | 0.211 | no | 1.350 | 0.224 | no |
| DR1895 | Alanine dehydrogenase, Rossman fold oxidoreductases | 1.110 | 0.616 | no | 0.994 | 0.409 | no | 1.079 | 0.742 | no | 1.764 | 0.971 | no | 1.536 | 0.849 | no | 1.003 | 0.220 | no | 1.439 | 0.588 | no | 1.713 | 0.651 | yes | 1.087 | 0.118 | no |
| DR1896 | Predicted protein | 1.153 | 0.171 | no | 0.911 | 0.302 | no | 1.595 | 0.724 | yes | 2.636 | 1.121 | yes | 2.387 | 1.346 | yes | 1.374 | 0.437 | no | 1.485 | 0.815 | no | 1.392 | 0.197 | no | 1.392 | 0.545 | no |
| DR1897 | Predicted protein | 0.805 | 0.327 | no | 0.689 | 0.431 | yes | 0.689 | 0.402 | yes | 0.997 | 0.416 | no | 1.875 | 0.766 | yes | 1.996 | 0.444 | yes | 2.301 | 0.652 | yes | 2.038 | 0.189 | yes | 2.581 | 0.386 | yes |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR1898 | AAA superfamily ATPase, YCAJ ortholog | 0.970 | 0.203 | no | 1.380 | 0.389 | no | 1.593 | 0.403 | yes | 1.515 | 0.161 | no | 1.302 | 0.235 | no | 1.225 | 0.315 | no | 0.955 | 0.303 | no | 1.182 | 0.446 | no | 1.002 | 0.325 | no |
| DR1899 | Yfit/DinB family | 1.028 | 0.550 | no | 1.272 | 0.758 | no | 1.604 | 0.647 | yes | 1.258 | 0.521 | no | 0.977 | 0.334 | no | 0.970 | 0.541 | no | 1.084 | 0.372 | no | 1.098 | 0.249 | no | 0.953 | 0.223 | no |
| DR1900 | Predicted protein | 1.192 | 0.275 | no | 2.557 | 0.702 | yes | 3.138 | 1.040 | yes | 2.838 | 0.941 | yes | 2.088 | 0.429 | yes | 1.595 | 0.117 | yes | 1.487 | 0.454 | no | 1.222 | 0.248 | no | 1.114 | 0.309 | no |
| DR1901 | Predicted protein | 1.152 | 0.782 | no | 3.585 | 2.171 | yes | 10.745 | 4.853 | yes | 9.959 | 3.516 | yes | 5.884 | 3.031 | yes | 2.257 | 1.023 | yes | 2.733 | 1.658 | yes | 5.221 | 1.085 | yes | 1.029 | 0.484 | no |
| DR1902 | Exodeoxyribonuclease V, Alpha subunit, Superfamily I helicase, RecD | 1.012 | 0.369 | no | 0.753 | 0.163 | no | 0.800 | 0.181 | no | 0.998 | 0.493 | no | 0.605 | 0.253 | yes | 0.832 | 0.305 | no | 0.735 | 0.077 | no | 0.929 | 0.125 | no | 1.720 | 0.423 | yes |
| DR1903 | DegV homolog | 0.893 | 0.236 | no | 1.289 | 0.279 | no | 1.576 | 0.231 | yes | 1.278 | 0.173 | no | 1.197 | 0.291 | no | 1.172 | 0.325 | no | 1.201 | 0.337 | no | 1.106 | 0.344 | no | 1.240 | 0.473 | no |
| DR1904 | Predicted protein | 0.973 | 0.208 | no | 1.004 | 0.374 | no | 1.341 | 0.681 | no | 1.280 | 0.157 | no | 1.037 | 0.108 | no | 0.974 | 0.191 | no | 1.101 | 0.255 | no | 1.062 | 0.166 | no | 1.208 | 0.496 | no |
| DR1905 | HTH, transcriptional regulator closely related to LLDR and PHDR of E.coli | 0.730 | 0.269 | no | 0.731 | 0.224 | no | 0.834 | 0.443 | no | 0.617 | 0.256 | yes | 0.582 | 0.158 | yes | 0.765 | 0.202 | no | 0.776 | 0.349 | no | 0.759 | 0.161 | no | 0.849 | 0.109 | no |
| DR1906 | L-lactate permease | 1.176 | 0.384 | no | 1.145 | 0.475 | no | 2.133 | 1.009 | yes | 3.541 | 1.635 | yes | 3.047 | 1.728 | yes | 2.032 | 0.905 | yes | 1.985 | 1.096 | yes | 0.883 | 0.158 | no | 0.953 | 0.298 | no |
| DR1907 | Fe-S subunit of glycolate oxidase, YKGE | 1.075 | 0.520 | no | 0.795 | 0.238 | no | 1.204 | 0.821 | no | 1.232 | 0.577 | no | 1.278 | 0.625 | no | 1.119 | 0.506 | no | 1.069 | 0.342 | no | 0.787 | 0.151 | no | 1.230 | 0.276 | no |
| DR1909 | Fe-S protein YKGG, similar domain to YKGF | 0.875 | 0.212 | no | 0.606 | 0.248 | yes | 0.817 | 0.318 | no | 1.503 | 0.134 | no | 1.073 | 0.439 | no | 0.970 | 0.334 | no | 0.811 | 0.357 | no | 0.506 | 0.164 | yes | 0.963 | 0.298 | no |
| DR1910 | Gluconokinase, GNTK | 1.088 | 0.275 | no | 0.836 | 0.330 | no | 0.636 | 0.266 | yes | 0.700 | 0.405 | yes | 0.699 | 0.355 | yes | 0.659 | 0.200 | yes | 0.541 | 0.080 | yes | 0.596 | 0.143 | yes | 0.733 | 0.165 | no |
| DR1911 | Bacillus ydjJ ortholog | 0.783 | 0.213 | no | 0.943 | 0.270 | no | 0.917 | 0.306 | no | 0.759 | 0.252 | no | 0.736 | 0.193 | no | 0.779 | 0.260 | no | 0.733 | 0.229 | no | 0.966 | 0.080 | no | 1.025 | 0.168 | no |
| DR1912 | Bacterial "eukaryotic type" tyrosine/S/T phosphatase | 1.319 | 0.252 | no | 1.456 | 0.672 | no | 1.592 | 1.139 | no | 1.045 | 0.615 | no | 0.943 | 0.467 | no | 0.781 | 0.245 | no | 0.706 | 0.392 | yes | 0.598 | 0.124 | yes | 0.791 | 0.130 | no |
| DR1913 | DNA gyrase subunit A | 0.960 | 0.449 | no | 3.291 | 1.564 | yes | 3.067 | 1.481 | yes | 1.557 | 0.524 | no | 2.487 | 1.781 | yes | 0.925 | 0.719 | no | 1.053 | 0.454 | no | 0.886 | 0.139 | no | 1.371 | 0.229 | no |
| DR1914 | Predicted protein | 0.943 | 0.259 | no | 2.281 | 1.593 | yes | 1.555 | 0.899 | no | 1.005 | 0.305 | no | 1.040 | 0.551 | no | 1.004 | 0.321 | no | 0.891 | 0.095 | no | 1.275 | 0.235 | no | 1.304 | 0.439 | no |
| DR1915 | A/b hydrolase | 0.966 | 0.438 | no | 2.405 | 0.774 | yes | 2.021 | 0.512 | yes | 1.421 | 0.550 | no | 1.606 | 0.400 | yes | 1.284 | 0.509 | no | 1.302 | 0.449 | no | 1.268 | 0.161 | no | 1.266 | 0.161 | no |
| DR1916 | RecG superfamily II helicase | 1.049 | 0.159 | no | 2.662 | 0.868 | yes | 2.329 | 0.694 | yes | 1.951 | 0.410 | yes | 1.444 | 0.346 | no | 1.267 | 0.408 | no | 1.026 | 0.376 | no | 1.208 | 0.584 | no | 1.054 | 0.603 | no |
| DR1917 | NH2-acetyltransferase | 1.222 | 0.385 | no | 2.490 | 1.511 | yes | 2.362 | 0.564 | yes | 1.821 | 0.450 | yes | 1.137 | 0.611 | no | 1.063 | 0.284 | no | 1.319 | 0.637 | no | 1.620 | 0.620 | yes | 1.088 | 0.419 | no |
| DR1918 | NH2- acetyltransferase | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR1919 | P-loop ATPase similar to the C -terminus of the NodO enzymes | 0.856 | 0.339 | no | 1.738 | 0.815 | yes | 1.386 | 0.469 | no | 1.189 | 0.455 | no | 1.206 | 0.421 | no | 1.010 | 0.341 | no | 0.803 | 0.253 | no | 0.983 | 0.179 | no | 0.508 | 0.147 | yes |
| DR1920 | Predicted protein | 0.870 | 0.251 | no | 0.946 | 0.287 | no | 0.855 | 0.299 | no | 0.797 | 0.126 | no | 1.027 | 0.359 | no | 0.966 | 0.198 | no | 1.481 | 0.433 | no | 1.141 | 0.412 | no | 1.479 | 0.885 | no |
| DR1921 | SbcD nuclease, calcineurin like phosphoesterase | 0.993 | 0.219 | no | 1.513 | 0.473 | yes | 1.578 | 0.438 | yes | 1.820 | 0.274 | yes | 1.445 | 0.356 | no | 1.159 | 0.207 | no | 1.123 | 0.199 | no | 1.136 | 0.260 | no | 0.955 | 0.220 | no |
| DR1922 | SbcD nuclease FRAMESHIFT OR INSERION | 0.953 | 0.313 | no | 1.428 | 0.610 | no | 1.457 | 0.488 | no | 1.295 | 0.455 | no | 1.336 | 0.333 | no | 1.454 | 0.711 | no | 1.233 | 0.718 | no | 1.329 | 0.555 | no | 0.860 | 0.286 | no |
| DR1923 | Conserved secreted protein (probably cellulase) | 0.894 | 0.297 | no | 0.881 | 0.490 | no | 1.089 | 0.426 | no | 1.045 | 0.345 | no | 0.970 | 0.424 | no | 1.075 | 0.309 | no | 0.811 | 0.393 | no | 1.075 | 0.290 | no | 0.992 | 0.321 | no |
| DR1924 | Conserved protein (probably cellulase) | 0.678 | 0.424 | yes | 0.556 | 0.271 | yes | 0.597 | 0.166 | yes | 0.420 | 0.157 | yes | 0.642 | 0.139 | yes | 0.750 | 0.232 | no | 0.817 | 0.360 | no | 1.111 | 0.141 | no | 0.830 | 0.178 | no |
| DR1925 | Predicted protein | 0.970 | 0.196 | no | 1.028 | 0.356 | no | 1.154 | 0.405 | no | 1.032 | 0.312 | no | 0.965 | 0.292 | no | 0.993 | 0.332 | no | 0.930 | 0.230 | no | 1.187 | 0.440 | no | 1.075 | 0.204 | no |
| DR1926 | Predicted protein | 0.902 | 0.334 | no | 1.333 | 0.337 | no | 1.451 | 0.373 | yes | 1.529 | 0.261 | no | 1.282 | 0.346 | no | 0.986 | 0.340 | no | 1.449 | 0.783 | no | 0.905 | 0.087 | no | 0.878 | 0.418 | no |
| DR1927 | Transposase | 0.872 | 0.404 | no | 1.517 | 0.741 | no | 1.270 | 0.657 | no | 1.073 | 0.570 | no | 1.006 | 0.363 | no | 0.682 | 0.368 | yes | 0.648 | 0.298 | yes | 0.670 | 0.134 | yes | 0.890 | 0.225 | no |
| DR1928 | Glycerol kinase, glpK | 1.111 | 0.341 | no | 0.888 | 0.297 | no | 1.322 | 0.401 | no | 1.792 | 0.822 | yes | 1.594 | 0.668 | yes | 1.365 | 0.454 | no | 1.380 | 0.374 | no | 1.458 | 0.457 | no | 1.465 | 0.351 | yes |
| DR1929 | Glycerol uptake facilitator glpF, MIP/Aquaporin family of transporters | 0.910 | 0.290 | no | 0.949 | 0.186 | no | 0.946 | 0.211 | no | 1.149 | 0.184 | no | 1.300 | 0.388 | no | 1.171 | 0.324 | no | 1.371 | 0.346 | no | 1.367 | 0.233 | no | 1.116 | 0.178 | no |
| DR1930 | Conserved membrane protein | 1.062 | 0.298 | no | 1.080 | 0.405 | no | 1.295 | 0.496 | no | 1.872 | 0.840 | yes | 2.200 | 1.088 | yes | 1.577 | 0.658 | no | 1.559 | 0.596 | yes | 1.063 | 0.176 | no | 0.960 | 0.296 | no |
| DR1931 | a/b family hydrolase | 0.875 | 0.357 | no | 0.657 | 0.296 | yes | 0.448 | 0.192 | yes | 0.516 | 0.135 | yes | 0.579 | 0.245 | yes | 0.722 | 0.212 | no | 0.778 | 0.413 | no | 0.738 | 0.109 | no | 0.819 | 0.244 | no |
| DR1932 | Transposon DORF | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR1933 | Transposase | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR1934 | Predicted protein | 1.335 | 0.400 | no | 4.003 | 1.915 | yes | 2.441 | 1.616 | yes | 5.045 | 0.715 | yes | 2.836 | 1.934 | yes | 2.111 | 1.249 | yes | 2.666 | 1.525 | yes | 1.253 | 0.399 | no | 1.051 | 0.219 | no |
| DR1935 | Transcription factor, DeoR family | 0.754 | 0.271 | no | 1.459 | 0.464 | no | 0.970 | 0.241 | no | 0.584 | 0.127 | yes | 0.777 | 0.221 | no | 1.126 | 0.384 | no | 1.240 | 0.608 | no | 1.177 | 0.399 | no | 1.056 | 0.295 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR1936 | Predicted protein | 1.248 | 0.510 | no | 0.934 | 0.551 | no | 1.174 | 0.281 | no | 2.446 | 1.316 | yes | 2.749 | 1.775 | yes | 1.874 | 0.477 | yes | 3.053 | 1.511 | yes | 2.536 | 1.214 | yes | 1.884 | 0.620 | yes |
| DR1937 | Serine protease, subtilisin-like | 0.841 | 0.276 | no | 0.633 | 0.301 | yes | 0.359 | 0.138 | yes | 0.930 | 0.159 | no | 0.697 | 0.144 | no | 0.695 | 0.389 | yes | 0.590 | 0.233 | yes | 0.970 | 0.349 | no | 0.687 | 0.230 | no |
| DR1938 | 3-oxoacyl-[acyl-carrier-protein reductase FabG | 0.952 | 0.132 | no | 0.678 | 0.267 | yes | 0.531 | 0.204 | yes | 0.548 | 0.201 | yes | 0.560 | 0.238 | yes | 0.597 | 0.191 | yes | 0.600 | 0.209 | yes | 0.652 | 0.233 | yes | 0.731 | 0.151 | no |
| DR1940 | Uncharacterized protein with duplication of protein from Synechocystis, HSLJ related | 1.051 | 0.410 | no | 1.752 | 1.094 | yes | 2.259 | 0.981 | yes | 0.812 | 0.288 | no | 1.097 | 0.587 | no | 1.409 | 0.427 | no | 1.323 | 0.812 | no | 1.304 | 0.151 | no | 1.021 | 0.251 | no |
| DR1941 | Beta-ketoacyl-ACP synthase II, FabF | 0.963 | 0.153 | no | 0.563 | 0.202 | yes | 0.591 | 0.163 | yes | 0.767 | 0.237 | no | 1.106 | 0.122 | no | 1.262 | 0.291 | no | 1.356 | 0.473 | no | 1.680 | 0.626 | yes | 1.188 | 0.399 | no |
| DR1942 | Acyl carrier protein, ACP | 1.469 | 0.787 | no | 0.899 | 0.565 | no | 1.452 | 0.918 | no | 3.739 | 1.671 | yes | 2.483 | 0.800 | yes | 2.261 | 1.070 | yes | 3.449 | 2.366 | yes | 3.417 | 1.077 | yes | 2.639 | 0.919 | yes |
| DR1943 | 3-oxoacyl-acyl-carrier-protein reductase, FabG | 0.770 | 0.357 | no | 0.477 | 0.245 | yes | 0.453 | 0.254 | yes | 0.515 | 0.095 | yes | 1.029 | 0.433 | no | 0.976 | 0.394 | no | 1.583 | 0.819 | no | 1.381 | 0.271 | no | n/a | n/a | n/a |
| DR1944 | Predicted protein | 1.289 | 0.859 | no | 0.926 | 0.623 | no | 0.706 | 0.387 | yes | 0.827 | 0.338 | no | 1.012 | 0.616 | no | 1.173 | 0.247 | no | 1.411 | 0.742 | no | 1.841 | 0.543 | yes | 1.430 | 0.710 | no |
| DR1945 | Malonyl Acyl Carrier Transcyclase, FabD | 0.803 | 0.190 | no | 0.747 | 0.236 | no | 0.894 | 0.276 | no | 0.919 | 0.263 | no | 1.075 | 0.251 | no | 1.751 | 0.780 | yes | 1.954 | 1.144 | yes | 2.331 | 0.926 | yes | 1.589 | 0.407 | yes |
| DR1946 | 3-ketoacyl carrier protein synthase, FabH | 0.989 | 0.428 | no | 0.975 | 0.643 | no | 0.941 | 0.464 | no | 1.397 | 0.620 | no | 1.495 | 0.784 | no | 1.306 | 0.422 | no | 1.613 | 1.105 | no | 1.767 | 0.382 | yes | 1.349 | 0.462 | no |
| DR1947 | 3-ketoacyl carrier protein synthase, FabH | 1.065 | 0.546 | no | 0.985 | 0.612 | no | 1.483 | 0.585 | no | 1.335 | 0.858 | no | 1.479 | 1.139 | no | 1.203 | 0.548 | no | 0.774 | 0.178 | no | 0.954 | 0.160 | no | 0.895 | 0.271 | no |
| DR1948 | FKBP family Peptidyl prolyl isomerase, TIG | 0.836 | 0.364 | no | 0.946 | 0.520 | no | 1.309 | 0.722 | no | 1.446 | 0.531 | no | 1.278 | 0.565 | no | 1.292 | 0.524 | no | 1.324 | 0.818 | no | 1.298 | 0.458 | no | 1.733 | 0.711 | yes |
| DR1949 | Ribonuclease HII | 1.241 | 0.682 | no | 1.168 | 0.760 | no | 1.122 | 0.567 | no | 0.968 | 0.371 | no | 1.183 | 0.401 | no | 1.078 | 0.471 | no | 1.293 | 0.674 | no | 0.993 | 0.177 | no | 1.068 | 0.151 | no |
| DR1950 | Aromatic compound dioxygenase, ferredoxin | 1.472 | 0.723 | no | 1.337 | 0.514 | no | 1.417 | 0.542 | no | 1.535 | 0.424 | no | 1.408 | 0.577 | no | 1.200 | 0.379 | no | 1.374 | 0.625 | no | 1.324 | 0.403 | no | 1.288 | 0.399 | no |
| DR1951 | Predicted protein | 1.454 | 0.362 | no | 0.997 | 0.345 | no | 0.989 | 0.310 | no | 1.051 | 0.178 | no | 1.171 | 0.373 | no | 1.039 | 0.511 | no | 1.136 | 0.284 | no | 0.785 | 0.122 | no | 0.872 | 0.166 | no |
| DR1952 | Predicted protein | 1.797 | 1.033 | yes | 1.564 | 0.647 | yes | 1.295 | 0.336 | no | 1.778 | 0.791 | yes | 1.355 | 0.282 | no | 1.300 | 0.380 | no | 1.431 | 0.820 | no | 1.721 | 0.737 | yes | 1.326 | 0.243 | no |
| DR1953 | Predicted protein | 1.290 | 0.494 | no | 1.434 | 0.620 | no | 1.816 | 0.912 | yes | 1.675 | 0.465 | no | 1.413 | 0.468 | no | 1.474 | 0.520 | no | 1.400 | 0.466 | no | 1.233 | 0.545 | no | n/a | n/a | n/a |
| DR1954 | Predicted HTH transcriptional regulator | 1.277 | 0.687 | no | 0.999 | 0.322 | no | 1.148 | 0.322 | no | 2.152 | 0.477 | yes | 2.259 | 1.236 | yes | 1.693 | 0.485 | yes | 2.172 | 0.844 | yes | 2.065 | 0.460 | yes | 1.759 | 0.755 | yes |
| DR1955 | Periplasmic Heme binding protein | 1.097 | 0.441 | no | 1.643 | 0.444 | yes | 2.218 | 0.703 | yes | 1.701 | 0.541 | yes | 1.695 | 0.588 | yes | 1.608 | 0.350 | yes | 1.383 | 0.260 | no | 1.880 | 0.484 | yes | 4.804 | 1.991 | yes |
| DR1956 | Predicted protein | 1.561 | 0.314 | yes | 1.432 | 0.589 | no | 1.126 | 0.373 | no | 1.153 | 0.263 | no | 0.948 | 0.346 | no | 1.021 | 0.299 | no | 1.160 | 0.477 | no | 1.017 | 0.249 | no | 1.266 | 0.189 | no |
| DR1957 | Predicted protein | 0.914 | 0.105 | no | 0.731 | 0.265 | no | 0.479 | 0.182 | yes | 0.452 | 0.025 | yes | 0.582 | 0.275 | yes | 0.925 | 0.337 | no | 0.734 | 0.229 | no | 0.947 | 0.176 | no | 1.221 | 0.257 | no |
| DR1958 | Dinitrogenase reductase activationg ADP-ribosylglycohydrolase, DraG | 1.325 | 0.358 | no | 1.334 | 0.509 | no | 1.360 | 0.372 | no | 1.819 | 0.855 | yes | 1.274 | 0.438 | no | 0.890 | 0.193 | no | 1.038 | 0.312 | no | 1.059 | 0.326 | no | 2.583 | 0.975 | yes |
| DR1959 | Uncharacterized conserved protein | 1.085 | 0.409 | no | 0.824 | 0.242 | no | 0.716 | 0.209 | no | 0.802 | 0.440 | no | 0.918 | 0.367 | no | 1.168 | 0.599 | no | 1.013 | 0.413 | no | 0.863 | 0.061 | no | 0.881 | 0.088 | no |
| DR1960 | Acetyl-COA acetyltransferase, THIL | 1.257 | 0.259 | no | 0.924 | 0.435 | no | 0.847 | 0.266 | no | 0.938 | 0.201 | no | 1.202 | 0.821 | no | 0.807 | 0.166 | no | 0.639 | 0.141 | yes | 0.948 | 0.223 | no | 0.649 | 0.141 | yes |
| DR1961 | Probably ankyrin-like repeat protein | 1.062 | 0.054 | no | 0.969 | 0.224 | no | 0.841 | 0.157 | no | 0.746 | 0.292 | no | 0.798 | 0.245 | no | 0.926 | 0.160 | no | 0.776 | 0.186 | no | 0.902 | 0.203 | no | 0.901 | 0.148 | no |
| DR1962 | Predicted protein | 2.898 | 1.840 | yes | 1.513 | 0.632 | no | 1.938 | 1.036 | yes | 0.917 | 0.279 | no | 1.119 | 0.431 | no | 1.472 | 0.395 | no | 0.673 | 0.286 | no | 1.042 | 0.041 | no | 2.143 | 1.285 | yes |
| DR1963 | PilT-like ATPase | 0.896 | 0.275 | no | 0.480 | 0.189 | yes | 0.378 | 0.154 | yes | 0.512 | 0.058 | yes | 0.623 | 0.163 | yes | 0.569 | 0.160 | yes | 0.545 | 0.173 | yes | 0.767 | 0.181 | no | 1.070 | 0.309 | no |
| DR1964 | GSPE general secretion pathway protein E, P-loop ATPase | 0.835 | 0.221 | no | 0.520 | 0.148 | yes | 0.300 | 0.171 | yes | 0.607 | 0.219 | yes | 0.436 | 0.112 | yes | 0.754 | 0.477 | yes | 0.409 | 0.138 | yes | 0.527 | 0.162 | yes | 0.849 | 0.286 | no |
| DR1965 | HAD superfamily hydrolase | 1.003 | 0.376 | no | 0.909 | 0.432 | no | 0.943 | 0.331 | no | 0.878 | 0.167 | no | 2.159 | 1.675 | yes | 2.092 | 1.396 | yes | 2.050 | 0.622 | yes | 2.191 | 0.911 | yes | n/a | n/a | n/a |
| DR1966 | YfiH-like protein, conserved bacterial family of proteins | 1.016 | 0.436 | no | 2.027 | 0.853 | yes | 2.367 | 1.499 | yes | 2.415 | 1.294 | yes | 1.730 | 0.661 | yes | 1.528 | 0.218 | no | 2.193 | 0.475 | yes | 1.604 | 0.393 | yes | 1.828 | 0.916 | yes |
| DR1967 | Enoyl-ACP reductase, FabI | 1.038 | 0.540 | no | 0.645 | 0.202 | yes | 0.574 | 0.209 | yes | 1.077 | 0.173 | no | 0.948 | 0.451 | no | 1.043 | 0.289 | no | 1.335 | 0.691 | no | 1.411 | 0.086 | no | 1.787 | 0.229 | yes |
| DR1968 | NADH Oxidase subunit, FMN containing | 1.477 | 0.697 | no | 1.007 | 0.645 | no | 0.919 | 0.437 | no | 1.044 | 0.142 | no | 1.898 | 0.904 | yes | 1.165 | 0.218 | no | 1.678 | 0.921 | yes | 1.372 | 0.242 | no | 1.213 | 0.378 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR1969 | HTH transcription factor | 0.862 | 0.395 | no | 0.331 | 0.222 | yes | 0.158 | 0.024 | yes | 0.131 | 0.054 | yes | 0.191 | 0.059 | yes | 0.208 | 0.100 | yes | 0.165 | 0.063 | yes | 0.196 | 0.070 | yes | 0.427 | 0.076 | yes |
| DR1970 | GreA, transcription elongation factor | 0.956 | 0.629 | no | 0.438 | 0.157 | yes | 0.435 | 0.184 | yes | 0.919 | 0.480 | no | 0.839 | 0.396 | no | 0.910 | 0.406 | no | 0.852 | 0.455 | no | 1.019 | 0.168 | no | 2.086 | 0.836 | yes |
| DR1971 | Transmembrane transport protein | 1.317 | 0.452 | no | 1.123 | 0.381 | no | 1.068 | 0.377 | no | 1.167 | 0.601 | no | 0.888 | 0.299 | no | 0.769 | 0.095 | no | 1.094 | 0.249 | no | 0.906 | 0.110 | no | 0.975 | 0.214 | no |
| DR1972 | ClpP protease | 0.867 | 0.255 | no | 0.686 | 0.147 | no | 0.680 | 0.094 | yes | 0.753 | 0.302 | no | 0.804 | 0.409 | no | 0.504 | 0.213 | yes | 0.451 | 0.082 | yes | 0.458 | 0.101 | yes | 0.946 | 0.336 | no |
| DR1973 | ClpX, AAA superfamily ATPase | 0.922 | 0.517 | no | 0.576 | 0.153 | yes | 0.425 | 0.078 | yes | 0.449 | 0.146 | yes | 0.480 | 0.168 | yes | 0.381 | 0.150 | yes | 0.374 | 0.117 | yes | 0.317 | 0.072 | yes | 0.696 | 0.069 | no |
| DR1974 | Lon protease, AAA superfamily domain | 0.983 | 0.477 | no | 0.901 | 0.409 | no | 0.778 | 0.245 | no | 0.643 | 0.271 | yes | 0.809 | 0.558 | yes | 0.867 | 0.403 | no | 0.815 | 0.295 | no | 0.509 | 0.135 | yes | 0.994 | 0.317 | no |
| DR1975 | NH2-acetyltransferase | 1.044 | 0.191 | no | 1.224 | 0.271 | no | 1.814 | 0.610 | yes | 2.232 | 0.460 | yes | 1.893 | 0.824 | yes | 1.358 | 0.366 | no | 1.102 | 0.205 | no | 0.995 | 0.195 | no | 3.977 | 0.830 | yes |
| DR1976 | MutS- Mismatch repair, ABC superfamily ATPase | 0.894 | 0.434 | no | 0.815 | 0.320 | no | 1.429 | 0.455 | no | 1.636 | 0.812 | no | 1.462 | 0.463 | no | 1.191 | 0.647 | no | 0.967 | 0.336 | no | 0.906 | 0.306 | no | 0.998 | 0.296 | no |
| DR1977 | Deverged NH2-Acetyltransferase | 0.961 | 0.287 | no | 0.906 | 0.238 | no | 0.765 | 0.203 | no | 0.796 | 0.063 | no | 0.819 | 0.232 | no | 0.762 | 0.120 | no | 0.818 | 0.184 | no | 0.908 | 0.168 | no | 0.903 | 0.228 | no |
| DR1978 | NH2-acetyltransferase family | 1.538 | 0.681 | no | 1.292 | 0.540 | no | 1.312 | 0.335 | no | 1.672 | 0.743 | no | 1.417 | 0.709 | no | 1.065 | 0.180 | no | 1.406 | 0.492 | no | 1.270 | 0.033 | no | 1.351 | 0.093 | no |
| DR1979 | Uncharacterized conserved protein | 1.000 | 0.188 | no | 0.867 | 0.212 | no | 0.781 | 0.149 | no | 0.858 | 0.059 | no | 0.701 | 0.268 | yes | 0.874 | 0.161 | no | 0.797 | 0.093 | no | 0.995 | 0.053 | no | 1.569 | 0.182 | yes |
| DR1980 | NADH dehydrogenase, Rossman fold oxidoreductase | 0.984 | 0.338 | no | 0.703 | 0.167 | no | 0.774 | 0.152 | no | 0.885 | 0.054 | no | 1.022 | 0.357 | no | 1.244 | 0.195 | no | 1.304 | 0.123 | no | 1.319 | 0.239 | no | 1.222 | 0.197 | no |
| DR1981 | Diverged HD hydrolase domain (mostly similar to this domain of GLND, uridylyltransferase) | 0.771 | 0.129 | no | 0.578 | 0.054 | yes | 0.567 | 0.088 | yes | 0.419 | 0.091 | yes | 0.545 | 0.116 | yes | 0.739 | 0.115 | no | 0.725 | 0.143 | no | 0.782 | 0.292 | no | 0.856 | 0.140 | no |
| DR1982 | Thioredoxin reductase, TRXB | 1.119 | 0.639 | no | 0.806 | 0.428 | no | 0.515 | 0.222 | yes | 0.489 | 0.315 | yes | 0.555 | 0.289 | yes | 0.475 | 0.196 | yes | 0.467 | 0.144 | yes | 0.520 | 0.123 | yes | 0.911 | 0.154 | no |
| DR1983 | Ribosomal protein S1 | 0.796 | 0.140 | no | 2.308 | 0.899 | yes | 1.887 | 0.353 | yes | 1.344 | 0.749 | no | 1.601 | 0.622 | yes | 1.492 | 0.651 | no | 1.458 | 0.551 | no | 1.135 | 0.400 | no | 0.840 | 0.264 | no |
| DR1984 | Thymidine kinase, KITH | 1.107 | 0.527 | no | 2.707 | 1.180 | yes | 2.472 | 0.812 | yes | 2.047 | 1.184 | yes | 1.533 | 0.674 | no | 1.422 | 0.343 | no | 1.131 | 0.337 | no | 1.257 | 0.169 | no | 0.883 | 0.194 | no |
| DR1985 | Beta lactamase fragment, contamination?? | 0.857 | 0.273 | no | 1.038 | 0.177 | no | 1.148 | 0.321 | no | 0.855 | 0.143 | no | 0.924 | 0.242 | no | 1.034 | 0.246 | no | 0.962 | 0.459 | no | 0.942 | 0.232 | no | 0.961 | 0.097 | no |
| DR1986 | DegV homolog | 1.379 | 0.351 | no | 1.530 | 0.578 | yes | 1.748 | 0.574 | yes | 1.775 | 0.608 | yes | 1.146 | 0.605 | no | 0.998 | 0.309 | no | 1.289 | 0.927 | no | 0.939 | 0.314 | no | 1.021 | 0.266 | no |
| DR1987 | Predicted protein | 1.072 | 0.311 | no | 0.614 | 0.290 | yes | 0.533 | 0.096 | yes | 0.854 | 0.086 | no | 1.195 | 0.500 | no | 2.218 | 0.438 | yes | 3.149 | 1.212 | yes | 2.846 | 0.630 | yes | 2.820 | 0.829 | yes |
| DR1988 | PhoH ATPase | 0.785 | 0.378 | no | 0.506 | 0.204 | yes | 0.583 | 0.261 | yes | 0.810 | 0.373 | no | 1.003 | 0.284 | no | 0.855 | 0.343 | no | 0.924 | 0.409 | no | 1.010 | 0.503 | no | 1.551 | 0.503 | no |
| DR1989 | Uncharacterized homolog of gi\|2384692 from Myxococcus | 1.111 | 0.372 | no | 1.095 | 0.258 | no | 0.663 | 0.438 | yes | 0.838 | 0.174 | no | 1.211 | 0.822 | no | 1.177 | 0.693 | no | 0.952 | 0.062 | no | 0.932 | 0.050 | no | 0.934 | 0.279 | no |
| DR1990 | Predicted protein | 1.216 | 0.333 | no | 1.442 | 0.819 | no | 1.949 | 0.926 | yes | 3.381 | 1.577 | yes | 0.878 | 0.496 | no | 1.104 | 0.358 | no | 1.297 | 0.565 | no | 1.033 | 0.209 | no | 1.151 | 0.491 | no |
| DR1991 | Conserved bacterial/archaeal protein, YGBO | 0.813 | 0.461 | no | 0.696 | 0.355 | yes | 0.442 | 0.151 | yes | 0.362 | 0.144 | yes | 0.483 | 0.155 | yes | 0.538 | 0.154 | yes | 1.050 | 0.800 | no | 0.801 | 0.213 | no | 0.949 | 0.068 | no |
| DR1992 | GlpG or rhomboid-related membrane protein | 1.179 | 0.719 | no | 0.883 | 0.252 | no | 0.798 | 0.367 | no | 1.096 | 0.693 | no | 0.911 | 0.644 | no | 0.850 | 0.268 | no | 0.993 | 0.451 | no | 0.942 | 0.142 | no | 1.019 | 0.282 | no |
| DR1993 | Predicted transglutaminase related protease | 0.748 | 0.146 | no | 0.607 | 0.116 | yes | 0.510 | 0.067 | yes | 0.607 | 0.121 | yes | 1.023 | 0.337 | no | 1.048 | 0.151 | no | 1.255 | 0.294 | no | 0.978 | 0.167 | no | 1.196 | 0.130 | no |
| DR1994 | Membrane protein | 0.694 | 0.176 | no | 0.923 | 0.275 | no | 0.826 | 0.587 | no | 1.140 | 0.318 | no | 0.934 | 0.374 | no | 0.696 | 0.195 | no | 0.881 | 0.395 | no | 0.622 | 0.203 | yes | 0.553 | 0.153 | yes |
| DR1995 | Conserved membrane protein | 1.507 | 0.525 | no | 0.948 | 0.296 | no | 0.882 | 0.263 | no | 1.132 | 0.342 | no | 1.215 | 0.274 | no | 1.164 | 0.220 | no | 1.084 | 0.165 | no | 0.969 | 0.187 | no | 1.281 | 0.104 | no |
| DR1997 | Small conserved archaeael/bacterial proteins | 0.953 | 0.443 | no | 0.543 | 0.189 | yes | 0.510 | 0.151 | yes | 0.684 | 0.120 | no | 0.598 | 0.243 | yes | 0.625 | 0.151 | yes | 0.630 | 0.206 | yes | 0.648 | 0.188 | yes | 1.268 | 0.583 | no |
| DR1998 | Catalase, CATX | 0.886 | 0.418 | no | 0.508 | 0.155 | yes | 0.241 | 0.043 | yes | 0.232 | 0.071 | yes | 0.409 | 0.209 | yes | 0.420 | 0.109 | yes | 0.487 | 0.205 | yes | 0.574 | 0.096 | yes | 3.132 | 0.659 | yes |
| DR1999 | Small conserved transporters, YIGK | 0.929 | 0.149 | no | 0.537 | 0.074 | yes | 0.626 | 0.114 | yes | 0.599 | 0.061 | yes | 0.689 | 0.154 | no | 0.608 | 0.111 | yes | 0.570 | 0.169 | yes | 0.646 | 0.148 | yes | 1.549 | 0.226 | yes |
| DR2000 | YocD, Mccf family of bacterial proteins | 1.057 | 0.515 | no | 0.933 | 0.186 | no | 0.857 | 0.179 | no | 1.012 | 0.401 | no | 0.974 | 0.401 | no | 0.673 | 0.183 | yes | 0.669 | 0.135 | yes | 0.657 | 0.104 | yes | 1.151 | 0.374 | no |
| DR2001 | Predicted protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR2002 | Yfit/DinB family of the metal binding proteins | 0.962 | 0.292 | no | 0.806 | 0.122 | no | 0.788 | 0.148 | no | 0.703 | 0.078 | no | 0.736 | 0.222 | no | 0.658 | 0.201 | yes | 0.494 | 0.177 | yes | 0.558 | 0.136 | yes | 0.704 | 0.069 | no |
| DR2003 | Predicted protein | 1.160 | 0.320 | no | 0.939 | 0.240 | no | 0.782 | 0.145 | no | 0.911 | 0.068 | no | 0.601 | 0.197 | yes | 0.557 | 0.119 | yes | 0.679 | 0.208 | yes | 0.656 | 0.223 | yes | 0.710 | 0.109 | no |
| DR2004 | L20 ribosomal protein | 0.766 | 0.232 | no | 0.730 | 0.200 | no | 0.767 | 0.209 | no | 0.459 | 0.071 | yes | 0.566 | 0.184 | yes | 0.549 | 0.129 | yes | 0.653 | 0.119 | yes | 0.515 | 0.201 | yes | 0.443 | 0.151 | yes |
| DR2005 | L35 ribosomal protein | 1.096 | 0.479 | no | 0.858 | 0.200 | no | 1.040 | 0.335 | no | 0.979 | 0.688 | no | 0.760 | 0.344 | no | 0.757 | 0.145 | no | 0.671 | 0.116 | yes | 0.572 | 0.035 | yes | 0.593 | 0.217 | yes |
| DR2006 | Predicted protein | 1.114 | 0.624 | no | 0.813 | 0.433 | no | 0.568 | 0.318 | yes | 0.319 | 0.022 | yes | 0.609 | 0.303 | yes | 0.428 | 0.125 | yes | 0.487 | 0.155 | yes | 0.444 | 0.186 | yes | 0.541 | 0.109 | yes |
| DR2007 | Predicted protein | 0.795 | 0.143 | no | 0.488 | 0.135 | yes | 0.358 | 0.113 | yes | 0.354 | 0.108 | yes | 0.406 | 0.089 | yes | 0.468 | 0.126 | yes | 0.453 | 0.159 | yes | 0.522 | 0.176 | yes | 0.695 | 0.141 | no |
| DR2008 | Aspartate-semialdehyde dehydrogenase, DHAS | 0.745 | 0.266 | no | 0.418 | 0.097 | yes | 0.318 | 0.081 | yes | 0.378 | 0.185 | yes | 0.590 | 0.203 | yes | 0.522 | 0.182 | yes | 0.454 | 0.136 | yes | 0.459 | 0.076 | yes | 0.938 | 0.386 | no |
| DR2009 | KH domain containing protein possibly involved in nucleic acid binding | 0.937 | 0.546 | no | 0.974 | 0.450 | no | 0.694 | 0.237 | no | 0.692 | 0.488 | yes | 0.512 | 0.303 | yes | 0.633 | 0.207 | yes | 0.567 | 0.226 | yes | 0.613 | 0.123 | yes | 0.756 | 0.031 | no |
| DR2010 | 16S rRNA processing protein RIMM | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR2011 | TrmD, tRNA methyltransferase | 0.839 | 0.251 | no | 0.675 | 0.202 | yes | 0.754 | 0.319 | no | 0.696 | 0.269 | no | 0.646 | 0.255 | yes | 0.863 | 0.265 | no | 0.646 | 0.268 | yes | 0.638 | 0.204 | yes | 0.685 | 0.114 | no |
| DR2012 | Predicted protein | 1.092 | 0.407 | no | 1.181 | 0.570 | no | 1.206 | 0.322 | no | 1.049 | 0.179 | no | 1.126 | 0.344 | no | 0.909 | 0.107 | no | 0.905 | 0.175 | no | 0.731 | 0.114 | no | 0.595 | 0.105 | yes |
| DR2014 | Glyoxalase I/ dioxygenase superfamily protein | 1.121 | 0.687 | no | 0.755 | 0.291 | no | 0.682 | 0.301 | yes | 0.769 | 0.217 | no | 0.715 | 0.327 | yes | 1.096 | 0.644 | no | 0.973 | 0.434 | no | 0.930 | 0.364 | no | 1.165 | 0.366 | no |
| DR2015 | Dehydrogenase, putrescine oxidase? | 1.064 | 0.502 | no | 0.481 | 0.272 | yes | 0.475 | 0.271 | yes | 0.288 | 0.162 | yes | 0.685 | 0.208 | no | 1.210 | 0.881 | no | 0.700 | 0.351 | yes | 0.955 | 0.318 | no | n/a | n/a | n/a |
| DR2016 | Predicted protein | 2.345 | 1.040 | yes | 2.512 | 0.754 | yes | 1.809 | 1.191 | yes | 2.975 | 1.030 | yes | 1.809 | 0.735 | yes | 1.206 | 0.472 | no | 1.368 | 0.804 | no | 0.914 | 0.192 | no | 0.776 | 0.112 | no |
| DR2017 | Aminoacylase/desuccinylase/peptidase family protein | 1.012 | 0.245 | no | 0.701 | 0.297 | yes | 0.770 | 0.291 | no | 0.602 | 0.158 | yes | 0.933 | 0.476 | no | 0.764 | 0.523 | yes | 0.807 | 0.492 | no | 0.603 | 0.264 | yes | 0.649 | 0.235 | no |
| DR2018 | Predicted protein | 0.987 | 0.338 | no | 0.850 | 0.188 | no | 0.864 | 0.182 | no | 1.228 | 0.666 | no | 1.121 | 0.829 | no | 1.114 | 0.593 | no | 1.009 | 0.611 | no | 0.913 | 0.147 | no | 1.051 | 0.150 | no |
| DR2019 | Thioredoxin fold protein, possible disulfide bond chaperone | 0.929 | 0.145 | no | 1.200 | 0.435 | no | 0.949 | 0.352 | no | 1.493 | 0.550 | no | 1.144 | 0.524 | no | 1.288 | 0.267 | no | 1.045 | 0.400 | no | 1.103 | 0.123 | no | 1.309 | 0.244 | no |
| DR2020 | Predicted protein | 1.233 | 0.547 | no | 0.915 | 0.296 | no | 0.974 | 0.395 | no | 1.391 | 0.322 | no | 1.253 | 0.375 | no | 0.958 | 0.380 | no | 1.011 | 0.386 | no | 0.825 | 0.192 | no | 0.667 | 0.292 | yes |
| DR2021 | Conserved bacterial membrane protein, YGIH-like | 1.181 | 0.489 | no | 1.313 | 0.693 | no | 1.449 | 0.583 | no | 1.247 | 0.570 | no | 1.128 | 0.567 | no | 1.225 | 0.410 | no | 0.983 | 0.407 | no | 1.056 | 0.271 | no | 0.902 | 0.134 | no |
| DR2022 | Glyoxalase I/ dioxygenase superfamily protein, an archaeal subfamily | 1.151 | 0.714 | no | 0.444 | 0.201 | yes | 0.270 | 0.188 | yes | 0.367 | 0.184 | yes | 0.282 | 0.192 | yes | 0.405 | 0.234 | yes | 0.415 | 0.265 | yes | 0.516 | 0.190 | yes | 0.848 | 0.210 | no |
| DR2023 | Uncharacterized conserved protein | 1.037 | 0.262 | no | 0.395 | 0.087 | yes | 0.228 | 0.091 | yes | 0.212 | 0.050 | yes | 0.306 | 0.074 | yes | 0.330 | 0.105 | yes | 0.418 | 0.201 | yes | 0.420 | 0.097 | yes | 2.171 | 0.839 | yes |
| DR2024 | Uncharacterized conserved protein (membrane) | 0.851 | 0.514 | no | 0.401 | 0.106 | yes | 0.258 | 0.130 | yes | 0.254 | 0.096 | yes | 0.215 | 0.107 | yes | 0.264 | 0.089 | yes | 0.265 | 0.141 | yes | 0.405 | 0.202 | yes | 0.741 | 0.102 | no |
| DR2025 | Aminoacylase/desuccinylase/peptidase family protein | 0.840 | 0.223 | no | 0.526 | 0.226 | yes | 0.476 | 0.157 | yes | 0.427 | 0.022 | yes | 0.730 | 0.209 | no | 0.735 | 0.171 | no | 0.743 | 0.186 | no | 0.846 | 0.109 | no | 1.154 | 0.239 | no |
| DR2026 | Phosphoribosylglycinamide formyltransferase | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR2027 | Predicted protein | 1.390 | 0.873 | no | 1.384 | 0.530 | no | 1.232 | 0.369 | no | 1.372 | 0.865 | no | 1.253 | 0.673 | no | 0.929 | 0.085 | no | 0.972 | 0.330 | no | 0.956 | 0.160 | no | 1.033 | 0.289 | no |
| DR2029 | Uncharacterized conserved protein | 1.153 | 0.223 | no | 0.986 | 0.200 | no | 0.935 | 0.485 | no | 0.681 | 0.092 | no | 0.696 | 0.364 | yes | 0.793 | 0.130 | no | 0.791 | 0.120 | no | 0.753 | 0.159 | no | 1.281 | 0.138 | no |
| DR2030 | Thioesterase related to COMAB | 1.318 | 0.223 | no | 1.046 | 0.169 | no | 0.963 | 0.180 | no | 1.284 | 0.250 | no | 1.165 | 0.296 | no | 1.148 | 0.223 | no | 0.932 | 0.237 | no | 1.138 | 0.056 | no | 1.196 | 0.085 | no |
| DR2031 | Membrane transporter | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR2032 | Methylmalonyl-CoA mutase | 0.810 | 0.313 | no | 0.786 | 0.147 | no | 0.829 | 0.176 | no | 0.802 | 0.115 | no | 0.750 | 0.123 | no | 0.644 | 0.227 | yes | 0.477 | 0.168 | yes | 0.768 | 0.227 | no | 0.728 | 0.258 | no |
| DR2033 | Glutamine synthetase | 1.003 | 0.277 | no | 2.701 | 0.463 | yes | 3.542 | 0.785 | yes | 3.365 | 0.711 | yes | 2.767 | 1.158 | yes | 1.924 | 1.111 | yes | 1.058 | 0.178 | no | 1.126 | 0.109 | no | 7.172 | 1.010 | yes |
| DR2034 | Aminoglycosid N3-acetyltransferase | 0.777 | 0.322 | no | 0.422 | 0.180 | yes | 0.332 | 0.112 | yes | 0.240 | 0.111 | yes | 0.312 | 0.161 | yes | 0.442 | 0.160 | yes | 0.413 | 0.180 | yes | 0.506 | 0.169 | yes | 0.658 | 0.133 | no |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR2035 | Uncharactherized conserved protein | 1.085 | 0.589 | no | 1.313 | 0.648 | no | 1.096 | 0.557 | no | 0.724 | 0.542 | yes | 0.858 | 0.489 | no | 0.793 | 0.266 | no | 0.653 | 0.373 | yes | 0.691 | 0.314 | yes | 0.716 | 0.378 | yes |
| DR2036 | Alpha-glucosidase, trephalose synthase? | 0.996 | 0.296 | no | 0.938 | 0.215 | no | 1.037 | 0.177 | no | 1.008 | 0.186 | no | 1.002 | 0.189 | no | 1.110 | 0.249 | no | 0.959 | 0.297 | no | 1.063 | 0.277 | no | 1.588 | 0.524 | yes |
| DR2037 | Predicted protein | 1.279 | 0.525 | no | 1.554 | 0.665 | yes | 1.465 | 0.693 | no | 1.637 | 0.642 | no | 1.892 | 0.775 | yes | 1.190 | 0.307 | no | 1.049 | 0.340 | no | 0.908 | 0.141 | no | 1.514 | 0.945 | no |
| DR2038 | Uncharacterized protein, similar to DR0387 | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR2039 | Uncharacterized protein, similar to DR0387 | 0.821 | 0.287 | no | 1.503 | 0.629 | no | 2.328 | 0.733 | yes | 1.842 | 0.302 | yes | 1.331 | 0.474 | no | 1.424 | 0.379 | no | 0.868 | 0.281 | no | 0.966 | 0.382 | no | 0.647 | 0.157 | yes |
| DR2040 | ParA/SoJ protein, MinD superfamily ATPase | 0.993 | 0.172 | no | 1.209 | 0.403 | no | 1.640 | 0.290 | yes | 1.701 | 0.209 | yes | 1.530 | 0.202 | yes | 1.236 | 0.276 | no | 0.967 | 0.222 | no | 0.882 | 0.075 | no | 0.832 | 0.096 | no |
| DR2041 | Uncharacterized conserved cyano/myco-bacterial protein | 0.946 | 0.202 | no | 0.950 | 0.298 | no | 0.968 | 0.164 | no | 0.808 | 0.035 | no | 0.918 | 0.208 | no | 1.063 | 0.259 | no | 0.832 | 0.197 | no | 0.843 | 0.196 | no | 1.000 | 0.154 | no |
| DR2042 | Uncharacterized highly conserved cyano/myco-bacterial protein | 1.030 | 0.502 | no | 1.703 | 0.685 | yes | 2.001 | 0.890 | yes | 2.165 | 1.072 | yes | 2.394 | 1.476 | yes | 1.609 | 0.506 | no | 1.305 | 0.504 | no | 1.206 | 0.181 | no | 1.329 | 0.275 | no |
| DR2043 | Ribosomal protein L7/L12 | 1.015 | 0.293 | no | 2.771 | 1.187 | yes | 3.332 | 0.858 | yes | 1.902 | 0.642 | yes | 2.752 | 1.781 | yes | 3.511 | 1.341 | yes | 4.436 | 2.220 | yes | 3.606 | 0.964 | yes | 1.597 | 0.250 | yes |
| DR2044 | Ribosomal protein L10 | 0.920 | 0.294 | no | 2.769 | 1.099 | yes | 2.890 | 0.842 | yes | 2.675 | 0.933 | yes | 2.613 | 1.183 | yes | 2.921 | 1.928 | yes | 3.046 | 1.459 | yes | 2.788 | 1.227 | yes | 1.387 | 0.723 | no |
| DR2045 | Ribosomal protein L1 | 0.668 | 0.195 | yes | 1.647 | 0.640 | yes | 1.851 | 0.396 | yes | 1.137 | 0.319 | no | 1.477 | 0.566 | no | 1.425 | 0.815 | no | 1.372 | 0.748 | no | 1.164 | 0.391 | no | 0.526 | 0.247 | yes |
| DR2046 | Ribosomal protein L11 | 0.917 | 0.265 | no | 1.952 | 0.666 | yes | 2.467 | 0.709 | yes | 1.808 | 1.061 | yes | 2.315 | 1.045 | yes | 1.898 | 0.918 | yes | 1.697 | 0.695 | yes | 1.702 | 0.434 | yes | 0.719 | 0.363 | no |
| DR2047 | Transcription factor nusG | 0.612 | 0.330 | yes | 1.135 | 0.392 | no | 1.364 | 0.362 | no | 0.829 | 0.190 | no | 1.148 | 0.485 | no | 1.198 | 0.440 | no | 1.523 | 0.758 | no | 1.629 | 0.496 | yes | 0.815 | 0.389 | no |
| DR2048 | Preprotein translocase SECE | 1.677 | 0.775 | no | 1.410 | 0.667 | no | 2.017 | 1.055 | yes | 2.464 | 1.177 | yes | 2.399 | 1.382 | yes | 1.987 | 0.772 | yes | 1.945 | 1.083 | yes | 2.064 | 0.682 | yes | 0.493 | 0.218 | yes |
| DR2049 | Ribosomal protein L33 | 0.984 | 0.598 | no | 2.462 | 1.451 | yes | 2.457 | 1.158 | yes | 2.259 | 0.797 | yes | 3.276 | 1.449 | yes | 1.760 | 0.530 | yes | 2.289 | 0.745 | yes | 1.794 | 0.172 | yes | 1.126 | 0.287 | no |
| DR2050 | Elongation factor Tu | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR2051 | ABC Transporter ATPase, MDR-type | 1.147 | 0.567 | no | 3.151 | 1.639 | yes | 4.074 | 2.179 | yes | 3.762 | 1.393 | yes | 2.278 | 1.071 | yes | 2.516 | 1.689 | yes | 1.769 | 0.724 | yes | 1.600 | 0.234 | yes | 1.260 | 0.358 | no |
| DR2052 | ABC Transporter ATPase, | 0.798 | 0.243 | no | 1.194 | 0.459 | no | 1.399 | 0.371 | no | 1.361 | 0.381 | no | 1.351 | 0.529 | no | 1.095 | 0.362 | no | 1.236 | 0.474 | no | 1.159 | 0.137 | no | 0.959 | 0.149 | no |
| DR2053 | PhoU homolog, possibly regulator of phosphate regulon | 1.022 | 0.163 | no | 1.872 | 1.173 | yes | 1.842 | 1.042 | yes | 1.932 | 0.813 | yes | 1.590 | 0.485 | yes | 1.582 | 0.443 | yes | 1.455 | 0.594 | no | 1.252 | 0.346 | no | 0.936 | 0.146 | no |
| DR2054 | Predicted protein | 0.782 | 0.342 | no | 0.840 | 0.284 | no | 0.953 | 0.503 | no | 1.012 | 0.511 | no | 0.863 | 0.313 | no | 0.820 | 0.327 | no | 1.010 | 0.313 | no | 1.387 | 0.470 | no | 0.859 | 0.361 | no |
| DR2055 | Oligopeptidase F, metalloprotease | 0.652 | 0.217 | yes | 1.162 | 0.505 | no | 1.515 | 0.661 | no | 0.834 | 0.451 | no | 1.448 | 0.512 | no | 1.287 | 0.461 | no | 1.056 | 0.368 | no | 1.423 | 0.358 | no | 0.791 | 0.413 | no |
| DR2056 | Related to heat shock protein, HSLJ | 1.038 | 0.350 | no | 1.514 | 0.581 | yes | 1.448 | 0.306 | yes | 1.494 | 0.250 | no | 1.468 | 0.554 | no | 1.388 | 0.426 | no | 1.234 | 0.523 | no | 1.130 | 0.101 | no | 0.957 | 0.149 | no |
| DR2057 | Uncharacterized, shares unknown domain with GTPases from Synechocystis | 0.737 | 0.146 | no | 0.513 | 0.181 | yes | 0.821 | 0.567 | no | 0.764 | 0.374 | no | 1.074 | 0.436 | no | 1.342 | 0.215 | no | 1.576 | 0.488 | yes | 1.435 | 0.500 | no | 1.922 | 0.467 | yes |
| DR2058 | Secreted protein, uncharacterized | 0.930 | 0.212 | no | 1.655 | 0.468 | yes | 1.316 | 0.223 | no | 1.322 | 0.114 | no | 1.234 | 0.188 | no | 1.072 | 0.389 | no | 0.980 | 0.261 | no | 1.004 | 0.129 | no | 1.504 | 0.438 | yes |
| DR2059 | Glycyl tRNA synthetase | 0.906 | 0.243 | no | 2.020 | 0.594 | yes | 3.435 | 1.015 | yes | 3.174 | 0.393 | yes | 3.150 | 1.266 | yes | 2.343 | 0.661 | yes | 2.204 | 0.764 | yes | 2.003 | 0.897 | yes | 1.203 | 0.255 | no |
| DR2060 | Predicted protein | 1.043 | 0.391 | no | 3.044 | 1.634 | yes | 3.234 | 0.933 | yes | 3.197 | 1.114 | yes | 2.814 | 1.362 | yes | 2.139 | 0.462 | yes | 1.881 | 0.501 | yes | 1.450 | 0.293 | no | 0.830 | 0.136 | no |
| DR2061 | Predicted protein | 0.796 | 0.403 | no | 2.268 | 1.097 | yes | 3.495 | 1.212 | yes | 3.199 | 1.906 | yes | 2.797 | 1.620 | yes | 2.211 | 0.667 | yes | 1.730 | 0.631 | yes | 1.308 | 0.099 | no | 0.796 | 0.260 | no |
| DR2062 | WD40 repeat protein | 0.932 | 0.430 | no | 1.559 | 0.686 | yes | 2.240 | 0.769 | yes | 1.357 | 0.173 | no | 1.861 | 0.862 | yes | 1.934 | 0.830 | yes | 1.612 | 1.075 | no | 1.231 | 0.145 | no | 0.826 | 0.258 | no |
| DR2063 | Polyribonucleotide nucleotidyltransferase, contains S1 domain | 0.692 | 0.175 | no | 0.431 | 0.155 | yes | 0.516 | 0.122 | yes | 0.553 | 0.205 | yes | 0.703 | 0.318 | yes | 0.732 | 0.309 | no | 0.725 | 0.210 | no | 0.971 | 0.098 | no | 1.589 | 0.324 | yes |
| DR2064 | Predicted protein | 0.722 | 0.255 | no | 1.089 | 0.420 | no | 1.319 | 0.710 | no | 1.297 | 0.225 | no | 0.797 | 0.192 | no | 0.867 | 0.200 | no | 1.100 | 0.499 | no | 1.200 | 0.520 | no | 0.852 | 0.242 | no |
| DR2065 | Prepilin peptidase? | 1.267 | 0.554 | no | 1.795 | 0.526 | yes | 1.991 | 0.758 | yes | 1.982 | 0.403 | yes | 1.607 | 0.774 | no | 1.247 | 0.735 | no | 1.223 | 0.527 | no | 1.004 | 0.341 | no | 0.690 | 0.223 | no |
| DR2066 | Uncharacterized member of conserved protein family | 0.818 | 0.311 | no | 0.849 | 0.393 | no | 0.994 | 0.479 | no | 0.657 | 0.147 | no | 0.963 | 0.245 | no | 1.174 | 0.381 | no | 1.145 | 0.558 | no | 1.179 | 0.151 | no | 1.239 | 0.364 | no |
| DR2067 | Transcription termination factor nusB | 0.344 | 0.177 | yes | 0.638 | 0.352 | yes | 0.707 | 0.283 | no | 1.604 | 0.614 | no | 1.278 | 0.642 | no | 0.837 | 0.628 | no | 0.948 | 0.472 | no | 0.241 | 0.115 | yes | n/a | n/a | n/a |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR2068 | Ortholog of alkaline shock protein | 0.685 | 0.089 | no | 0.611 | 0.158 | yes | 0.744 | 0.099 | no | 0.915 | 0.203 | no | 1.003 | 0.221 | no | 0.908 | 0.278 | no | 0.967 | 0.396 | no | 0.951 | 0.146 | no | 1.854 | 0.385 | yes |
| DR2069 | NAD dependent ligase, DNLJ | 0.793 | 0.453 | no | 0.545 | 0.308 | yes | 0.285 | 0.077 | yes | 0.172 | 0.049 | yes | 0.762 | 0.434 | no | 0.604 | 0.249 | yes | 0.235 | 0.128 | yes | 0.354 | 0.039 | yes | 0.674 | 0.271 | yes |
| DR2070 | Conserved lipoprotein | 0.891 | 0.386 | no | 4.920 | 1.933 | yes | 2.945 | 1.409 | yes | 1.568 | 0.410 | no | 2.911 | 2.060 | yes | 2.341 | 0.961 | yes | 1.887 | 0.928 | yes | 2.376 | 1.179 | yes | 2.302 | 0.664 | yes |
| DR2071 | Phosphogluco/manno-mutase | 0.741 | 0.333 | no | 1.020 | 0.590 | no | 0.952 | 0.520 | no | 1.092 | 0.601 | no | 0.967 | 0.378 | no | 1.057 | 0.660 | no | 1.041 | 0.612 | no | 0.895 | 0.246 | no | 1.109 | 0.411 | no |
| DR2072 | Uncharacterized ortholog of vcaO | 1.123 | 0.702 | no | 2.038 | 0.880 | yes | 1.800 | 0.577 | yes | 1.504 | 0.342 | no | 1.078 | 0.371 | no | 1.554 | 0.571 | no | 1.118 | 0.252 | no | 1.168 | 0.059 | no | 0.625 | 0.273 | yes |
| DR2073 | Shikimate kinase homolog, P-loop (substitution GKT->GKR) | 1.000 | 0.308 | no | 1.605 | 0.478 | yes | 1.567 | 0.743 | yes | 1.301 | 0.248 | no | 1.235 | 0.532 | no | 1.087 | 0.395 | no | 1.099 | 0.284 | no | 1.133 | 0.243 | no | 1.027 | 0.282 | no |
| DR2074 | 3-methyl-adenine DNA glycosylase | 0.791 | 0.350 | no | 0.775 | 0.389 | no | 0.691 | 0.238 | yes | 0.548 | 0.082 | yes | 0.697 | 0.281 | yes | 0.794 | 0.115 | no | 0.882 | 0.302 | no | 0.931 | 0.228 | no | 0.827 | 0.231 | no |
| DR2075 | 2FE-2S Ferredoxin, FER | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR2076 | Metallobetalactamase fold hydrolase | 0.977 | 0.280 | no | 0.922 | 0.390 | no | 0.595 | 0.350 | yes | 0.780 | 0.233 | no | 0.690 | 0.221 | no | 1.028 | 0.466 | no | 0.925 | 0.619 | no | 0.877 | 0.054 | no | 1.135 | 0.291 | no |
| DR2077 | Predicted protein | 0.673 | 0.230 | yes | 0.583 | 0.202 | yes | 0.667 | 0.460 | yes | 0.643 | 0.182 | yes | 0.796 | 0.386 | no | 0.664 | 0.216 | yes | 0.715 | 0.150 | no | 0.744 | 0.164 | no | 0.826 | 0.192 | no |
| DR2078 | Extracellular lipase, a/b fold hydrolase | 0.856 | 0.210 | no | 0.772 | 0.363 | no | 1.080 | 0.455 | no | 1.124 | 0.501 | no | 1.523 | 0.765 | no | 1.065 | 0.269 | no | 1.283 | 0.474 | no | 1.224 | 0.395 | no | 1.612 | 0.613 | yes |
| DR2079 | Predicted HTH transcriptional regulator | 0.670 | 0.138 | no | 0.679 | 0.187 | yes | 0.837 | 0.418 | no | 0.615 | 0.333 | yes | 0.718 | 0.300 | no | 0.749 | 0.294 | no | 0.678 | 0.243 | yes | 0.757 | 0.167 | no | 0.701 | 0.258 | no |
| DR2080 | Predicted membrane protein, uncharacterized | 0.948 | 0.163 | no | 0.745 | 0.223 | no | 0.750 | 0.201 | no | 0.761 | 0.057 | no | 0.698 | 0.163 | no | 0.667 | 0.198 | yes | 0.595 | 0.237 | yes | 0.535 | 0.232 | yes | 0.548 | 0.095 | yes |
| DR2081 | Threonyl-tRNA synthetase, shares a domain with SPOT/RelA and OBG GTPases | 0.571 | 0.213 | yes | 0.939 | 0.191 | no | 1.142 | 0.444 | no | 0.826 | 0.206 | no | 1.015 | 0.239 | no | 1.109 | 0.252 | no | 0.976 | 0.358 | no | 1.017 | 0.146 | no | 1.110 | 0.256 | no |
| DR2082 | Predicted protein | 1.835 | 1.365 | no | 1.413 | 0.559 | no | 1.999 | 0.747 | yes | 2.023 | 0.407 | yes | 1.326 | 0.700 | no | 1.103 | 0.505 | no | 1.491 | 0.856 | no | 0.852 | 0.237 | no | 1.028 | 0.315 | no |
| DR2083 | Predicted protein | 1.086 | 0.558 | no | 1.873 | 0.965 | yes | 1.536 | 0.527 | yes | 1.328 | 0.390 | no | 1.274 | 0.460 | no | 1.150 | 0.285 | no | 1.119 | 0.317 | no | 0.918 | 0.184 | no | 0.755 | 0.102 | no |
| DR2084 | Glycerophosphoryl diester phosphodiesterase, glpQ | 0.621 | 0.207 | yes | 1.362 | 0.790 | no | 1.015 | 0.340 | no | 0.828 | 0.070 | no | 0.900 | 0.334 | no | 0.845 | 0.371 | no | 0.845 | 0.214 | no | 0.878 | 0.055 | no | 0.671 | 0.161 | no |
| DR2085 | Glutaredoxin-like protein NRDH | 1.299 | 0.374 | no | 1.988 | 0.656 | yes | 2.312 | 0.868 | yes | 2.002 | 0.251 | yes | 1.772 | 1.018 | yes | 1.457 | 0.474 | no | 1.560 | 0.487 | yes | 1.258 | 0.305 | no | 1.172 | 0.087 | no |
| DR2086 | Predicted protein | 0.701 | 0.184 | no | 0.820 | 0.522 | no | 0.674 | 0.128 | yes | 1.166 | 0.797 | no | 0.986 | 0.351 | no | 0.894 | 0.261 | no | 0.989 | 0.550 | no | 1.523 | 0.517 | no | 1.241 | 0.398 | no |
| DR2087 | Translation initiation factor IF-3 | 0.922 | 0.240 | no | 1.281 | 0.450 | no | 1.203 | 0.403 | no | 0.861 | 0.310 | no | 0.983 | 0.369 | no | 0.904 | 0.365 | no | 1.014 | 0.358 | no | 0.935 | 0.298 | no | 1.018 | 0.322 | no |
| DR2088 | Conserved membrane protein | 0.767 | 0.337 | no | 0.747 | 0.234 | no | 0.674 | 0.085 | yes | 0.629 | 0.033 | yes | 0.572 | 0.165 | yes | 0.800 | 0.112 | no | 0.759 | 0.273 | no | 0.792 | 0.219 | no | 0.860 | 0.261 | no |
| DR2089 | Ferripyochelin binding protein, FBP | 0.756 | 0.294 | no | 0.767 | 0.314 | no | 0.565 | 0.120 | yes | 0.698 | 0.059 | no | 0.663 | 0.226 | yes | 0.676 | 0.298 | yes | 0.740 | 0.293 | no | 0.813 | 0.194 | no | 1.096 | 0.235 | no |
| DR2090 | Predicted protein (low complexity) | 0.683 | 0.158 | no | 1.149 | 0.463 | no | 1.266 | 0.704 | no | 1.411 | 0.526 | no | 0.831 | 0.328 | no | 1.423 | 0.533 | no | 1.024 | 0.685 | no | 1.269 | 0.179 | no | 1.363 | 0.375 | no |
| DR2091 | Chalcone/stilbene synthase | 0.988 | 0.377 | no | 1.054 | 0.647 | no | 0.771 | 0.340 | no | 0.702 | 0.507 | yes | 0.737 | 0.473 | yes | 0.743 | 0.253 | no | 0.676 | 0.302 | yes | 0.532 | 0.177 | yes | 0.513 | 0.145 | yes |
| DR2092 | Predicted metalloenzyme with 3 conserved histidines | 0.851 | 0.338 | no | 0.889 | 0.315 | no | 0.687 | 0.286 | yes | 0.423 | 0.131 | yes | 0.542 | 0.181 | yes | 0.730 | 0.314 | no | 0.663 | 0.379 | yes | 0.637 | 0.076 | yes | 0.519 | 0.205 | yes |
| DR2093 | Diacylglycerol kinase, dgkA | 0.798 | 0.238 | no | 0.676 | 0.307 | yes | 0.457 | 0.189 | yes | 0.429 | 0.183 | yes | 0.495 | 0.159 | yes | 0.472 | 0.176 | yes | 0.420 | 0.201 | yes | 0.489 | 0.111 | yes | 0.473 | 0.201 | yes |
| DR2094 | Predicted HTH transcription factor, winged helix type | 0.933 | 0.439 | no | 0.777 | 0.325 | no | 0.561 | 0.225 | yes | 0.578 | 0.169 | yes | 0.477 | 0.182 | yes | 0.535 | 0.238 | yes | 0.444 | 0.186 | yes | 0.426 | 0.180 | yes | 0.652 | 0.225 | yes |
| DR2095 | Membrane protein, cytochrome C related | 0.992 | 0.512 | no | 0.644 | 0.263 | yes | 0.257 | 0.087 | yes | 0.276 | 0.120 | yes | 0.298 | 0.117 | yes | 0.248 | 0.088 | yes | 0.362 | 0.230 | yes | 0.607 | 0.277 | yes | 0.784 | 0.315 | no |
| DR2096 | Endopeptidase IV, clpP superfamily | 0.689 | 0.109 | no | 1.582 | 0.427 | yes | 1.524 | 0.899 | no | 0.842 | 0.039 | no | 1.283 | 0.569 | no | 1.055 | 0.290 | no | 1.156 | 0.326 | no | 0.897 | 0.259 | no | 0.784 | 0.292 | no |
| DR2097 | Predicted protein | 1.155 | 0.450 | no | 6.493 | 3.347 | yes | 6.955 | 2.082 | yes | 6.023 | 1.154 | yes | 3.570 | 2.090 | yes | 2.671 | 0.660 | yes | 1.779 | 0.595 | yes | 1.040 | 0.366 | no | 0.818 | 0.222 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR2098 | Transport membrane protein, MDR-type exporter | 0.929 | 0.273 | no | 3.273 | 0.531 | yes | 2.957 | 0.596 | yes | 2.313 | 0.322 | yes | 2.742 | 1.810 | yes | 1.654 | 0.570 | yes | 1.320 | 0.435 | no | 1.019 | 0.120 | no | 0.728 | 0.077 | no |
| DR2099 | Predicted protein | 0.891 | 0.509 | no | 4.926 | 2.115 | yes | 4.837 | 2.619 | yes | 2.175 | 0.166 | yes | 3.444 | 1.738 | yes | 3.122 | 1.251 | yes | 2.474 | 1.291 | yes | 1.118 | 0.461 | no | 0.933 | 0.289 | no |
| DR2100 | Uncharacterized protein, YcnE family | 0.711 | 0.256 | no | 1.019 | 0.346 | no | 1.169 | 0.515 | no | 1.046 | 0.419 | no | 1.260 | 0.504 | no | 1.041 | 0.366 | no | 1.396 | 0.728 | no | 0.981 | 0.094 | no | 0.868 | 0.317 | no |
| DR2101 | ABC transporter subunit | 0.991 | 0.289 | no | 1.762 | 0.572 | yes | 2.166 | 0.395 | yes | 1.881 | 0.350 | yes | 1.912 | 0.642 | yes | 1.394 | 0.602 | no | 1.182 | 0.330 | no | 1.023 | 0.334 | no | 1.935 | 0.842 | yes |
| DR2102 | Protein of VapC family or plasmid stability ptotein STBB | 0.880 | 0.289 | no | 1.528 | 0.563 | yes | 1.925 | 0.542 | yes | 1.690 | 0.831 | no | 1.903 | 0.889 | yes | 1.398 | 0.853 | no | 1.078 | 0.445 | no | 1.023 | 0.225 | no | 1.740 | 0.817 | yes |
| DR2103 | Predicted protein | 1.050 | 0.658 | no | 1.627 | 0.745 | yes | 1.843 | 1.124 | yes | 1.829 | 0.702 | yes | 1.761 | 1.314 | no | 1.794 | 1.191 | yes | 0.934 | 0.332 | no | 1.109 | 0.259 | no | 0.946 | 0.661 | no |
| DR2104 | Glyoxalase/dioxygenase family protein | 0.801 | 0.252 | no | 0.800 | 0.327 | no | 0.857 | 0.311 | no | 0.534 | 0.058 | yes | 0.898 | 0.499 | no | 0.773 | 0.368 | no | 0.634 | 0.358 | yes | 0.696 | 0.138 | yes | 2.164 | 0.906 | yes |
| DR2105 | Predicted protein | 0.817 | 0.282 | no | 1.511 | 0.361 | yes | 1.426 | 0.355 | no | 1.290 | 0.232 | no | 1.433 | 0.683 | no | 1.305 | 0.887 | no | 0.966 | 0.448 | no | 0.995 | 0.252 | no | 1.887 | 0.879 | yes |
| DR2106 | ABC transporter subunit | 0.794 | 0.295 | no | 1.056 | 0.321 | no | 1.123 | 0.493 | no | 1.003 | 0.455 | no | 0.969 | 0.353 | no | 0.843 | 0.417 | no | 0.931 | 0.582 | no | 0.795 | 0.258 | no | 1.483 | 0.607 | no |
| DR2107 | ABC transporter ATPase | 1.013 | 0.526 | no | 0.983 | 0.276 | no | 0.955 | 0.159 | no | 0.755 | 0.111 | no | 0.900 | 0.482 | no | 0.836 | 0.474 | no | 0.838 | 0.323 | no | 0.650 | 0.271 | yes | 1.675 | 0.462 | yes |
| DR2108 | Shares a domain with the MolR protein and PARP (ADP polymerases) + beta-propeller domain as in S/T protein kinases | 0.667 | 0.257 | no | 1.585 | 0.347 | yes | 1.995 | 0.788 | yes | 2.054 | 0.273 | yes | 2.341 | 1.122 | yes | 1.216 | 0.443 | no | 1.214 | 0.423 | no | 1.444 | 0.686 | no | 0.577 | 0.147 | yes |
| DR2109 | Ribosomal Protein S14 | 1.366 | 0.569 | no | 1.544 | 0.544 | yes | 2.191 | 1.105 | yes | 1.156 | 0.562 | no | 1.388 | 0.723 | no | 0.813 | 0.399 | no | 1.685 | 0.750 | no | 0.982 | 0.317 | no | n/a | n/a | n/a |
| DR2110 | Ribosomal Protein S8 | 0.560 | 0.235 | yes | 0.428 | 0.116 | yes | 0.659 | 0.242 | yes | 0.498 | 0.243 | yes | 0.709 | 0.225 | no | 1.076 | 0.431 | no | 0.990 | 0.458 | no | 0.795 | 0.250 | no | 0.282 | 0.070 | yes |
| DR2111 | Ribosomal protein L6 | 0.725 | 0.160 | no | 0.847 | 0.189 | no | 1.065 | 0.221 | no | 0.863 | 0.384 | no | 1.275 | 0.423 | no | 1.218 | 0.437 | no | 1.311 | 0.348 | no | 1.002 | 0.289 | no | 0.365 | 0.166 | yes |
| DR2112 | Ribosomal protein L18 | 0.340 | 0.126 | yes | 0.704 | 0.440 | yes | 0.878 | 0.535 | no | 0.563 | 0.132 | yes | 0.969 | 0.579 | no | 1.355 | 0.568 | no | 1.218 | 0.471 | no | 1.355 | 0.496 | no | 0.474 | 0.056 | yes |
| DR2113 | Ribosomal protein S5 | 0.628 | 0.193 | yes | 1.079 | 0.509 | no | 1.248 | 0.319 | no | 0.996 | 0.281 | no | 1.230 | 0.372 | no | 1.409 | 0.483 | no | 1.431 | 0.712 | no | 1.290 | 0.549 | no | 0.404 | 0.147 | yes |
| DR2114 | Ribosomal protein L30 | 0.527 | 0.172 | yes | 0.858 | 0.372 | no | 1.099 | 0.417 | no | 1.129 | 0.258 | no | 1.582 | 0.712 | no | 1.437 | 0.663 | no | 1.327 | 0.506 | no | 1.417 | 0.374 | no | 0.566 | 0.089 | yes |
| DR2115 | Ribosomal protein L15 | 0.659 | 0.338 | yes | 1.269 | 0.698 | no | 1.459 | 0.489 | no | 1.198 | 0.614 | no | 1.364 | 0.577 | no | 1.610 | 0.480 | yes | 1.698 | 0.716 | yes | 1.556 | 0.770 | no | 0.509 | 0.170 | yes |
| DR2116 | Preprotein translocase SecY | 0.628 | 0.282 | yes | 1.015 | 0.577 | no | 1.335 | 0.574 | no | 1.036 | 0.050 | no | 1.337 | 0.576 | no | 1.646 | 0.581 | yes | 1.927 | 0.787 | yes | 1.638 | 0.219 | yes | 0.629 | 0.204 | yes |
| DR2117 | Adenylate kinase | 1.064 | 0.222 | no | 0.880 | 0.253 | no | 0.968 | 0.221 | no | 1.102 | 0.156 | no | 1.054 | 0.339 | no | 1.049 | 0.346 | no | 1.056 | 0.344 | no | 1.101 | 0.222 | no | 1.742 | 0.385 | yes |
| DR2118 | ABC ATPase, transporter, LIVF | 0.901 | 0.463 | no | 1.893 | 0.778 | yes | 2.672 | 1.830 | yes | 2.253 | 0.710 | yes | 3.045 | 1.380 | yes | 1.452 | 0.564 | no | 1.238 | 0.473 | no | 0.921 | 0.323 | no | 0.641 | 0.093 | yes |
| DR2119 | ABC ATPase, transporter, LIVG | 0.921 | 0.364 | no | 1.101 | 0.340 | no | 1.182 | 0.268 | no | 1.375 | 0.269 | no | 1.258 | 0.374 | no | 1.004 | 0.633 | no | 0.819 | 0.371 | no | 0.724 | 0.274 | yes | 1.243 | 0.481 | no |
| DR2120 | Transporter Membrane spanning subunit, LIVM | 0.801 | 0.113 | no | 1.420 | 0.203 | yes | 1.844 | 0.263 | yes | 1.824 | 0.489 | yes | 1.973 | 0.646 | yes | 1.342 | 0.182 | no | 1.309 | 0.371 | no | 1.272 | 0.194 | no | 0.867 | 0.256 | no |
| DR2121 | Leucine-specific periplasmic binding protein, LIVH protein | 1.302 | 0.519 | no | 1.365 | 0.455 | no | 1.403 | 0.358 | no | 1.645 | 0.085 | yes | 1.333 | 0.215 | no | 1.050 | 0.370 | no | 0.979 | 0.280 | no | 0.880 | 0.288 | no | 1.063 | 0.160 | no |
| DR2122 | Branched aminoacid periplasmic binding protein, LIVBP | 0.740 | 0.437 | no | 2.000 | 1.313 | yes | 2.016 | 0.890 | yes | 2.465 | 0.294 | yes | 2.432 | 1.032 | yes | 1.839 | 1.022 | yes | 1.467 | 0.647 | no | 1.411 | 0.602 | no | 0.735 | 0.309 | no |
| DR2123 | Initiation factor IF-1 | 1.103 | 0.492 | no | 2.425 | 1.560 | yes | 1.969 | 0.547 | yes | 1.716 | 0.746 | yes | 1.900 | 0.519 | yes | 2.136 | 1.303 | yes | 2.059 | 0.977 | yes | 1.796 | 0.864 | yes | 1.031 | 0.285 | no |
| DR2124 | Ribosomal protein L36 | 0.825 | 0.189 | no | 3.305 | 0.867 | yes | 4.070 | 1.232 | yes | 2.524 | 0.511 | yes | 3.491 | 1.994 | yes | 2.481 | 0.983 | yes | 2.920 | 1.620 | yes | 2.225 | 0.635 | yes | 0.690 | 0.350 | yes |
| DR2125 | Ribosomal protein S13 | 0.889 | 0.242 | no | 3.025 | 1.180 | yes | 3.062 | 0.970 | yes | 2.419 | 1.582 | yes | 2.180 | 0.856 | yes | 1.959 | 1.139 | yes | 1.755 | 0.673 | yes | 1.500 | 0.424 | yes | 0.869 | 0.465 | no |
| DR2126 | Ribosomal protein S11 | 0.653 | 0.200 | yes | 2.679 | 0.841 | yes | 2.246 | 0.713 | yes | 1.997 | 0.644 | yes | 1.859 | 0.679 | yes | 1.535 | 0.509 | no | 1.815 | 1.024 | yes | 1.251 | 0.128 | no | 0.712 | 0.245 | no |
| DR2127 | Ribosomal protein S4 | 0.768 | 0.244 | no | 4.374 | 1.595 | yes | 4.353 | 1.370 | yes | 5.402 | 1.501 | yes | 3.326 | 1.490 | yes | 3.324 | 1.434 | yes | 2.482 | 1.094 | yes | 2.052 | 0.714 | yes | 1.066 | 0.470 | no |
| DR2128 | RNA polymerase alpha subunit | 0.585 | 0.239 | yes | 3.787 | 1.381 | yes | 4.030 | 2.800 | yes | 2.181 | 0.880 | yes | 3.028 | 1.778 | yes | 3.532 | 1.331 | yes | 3.139 | 1.446 | yes | 2.369 | 0.833 | yes | 1.125 | 0.549 | no |
| DR2129 | Ribosomal component L17 | 0.640 | 0.320 | yes | 5.649 | 1.233 | yes | 5.922 | 2.086 | yes | 3.758 | 1.390 | yes | 3.987 | 1.663 | yes | 3.805 | 1.085 | yes | 3.487 | 1.237 | yes | 2.990 | 0.530 | yes | 1.294 | 0.643 | no |
| DR2130 | Protease, collagenase family | 0.698 | 0.223 | no | 0.938 | 0.164 | no | 0.769 | 0.262 | no | 0.557 | 0.163 | yes | 0.552 | 0.167 | yes | 0.446 | 0.165 | yes | 0.432 | 0.108 | yes | 0.440 | 0.135 | yes | 0.466 | 0.086 | yes |
| DR2131 | Predicted protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR2132 | UspA domain containing protein, nucleotide-binding protein | 0.923 | 0.383 | no | 0.674 | 0.346 | yes | 0.355 | 0.130 | yes | 0.328 | 0.154 | yes | 0.298 | 0.122 | yes | 0.295 | 0.191 | yes | 0.260 | 0.129 | yes | 0.257 | 0.047 | yes | 0.479 | 0.067 | yes |
| DR2133 | Secreted low complexity protein related to YNT5, ANASP | 0.893 | 0.334 | no | 3.016 | 1.252 | yes | 1.540 | 0.307 | yes | 1.089 | 0.515 | no | 0.918 | 0.298 | no | 0.979 | 0.449 | no | 0.961 | 0.526 | no | 0.773 | 0.257 | no | 0.857 | 0.511 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR2134 | ABC ATPase, transporter | 0.879 | 0.313 | no | 3.146 | 1.194 | yes | 1.671 | 0.945 | yes | 1.466 | 0.292 | no | 0.922 | 0.335 | no | 1.010 | 0.422 | no | 0.779 | 0.409 | no | 0.786 | 0.322 | no | 0.811 | 0.197 | no |
| DR2135 | Phosphopentomutase, DeoB family | 0.731 | 0.220 | no | 0.426 | 0.160 | yes | 0.281 | 0.076 | yes | 0.280 | 0.055 | yes | 0.388 | 0.094 | yes | 0.560 | 0.216 | yes | 0.658 | 0.369 | yes | 0.777 | 0.141 | no | 1.116 | 0.191 | no |
| DR2136 | Predicted protein | 0.817 | 0.219 | no | 0.900 | 0.193 | no | 1.044 | 0.320 | no | 0.978 | 0.275 | no | 0.916 | 0.283 | no | 0.914 | 0.251 | no | 0.759 | 0.264 | no | 0.884 | 0.090 | no | 1.311 | 0.361 | no |
| DR2137 | Predicted protein | 0.881 | 0.444 | no | 0.605 | 0.168 | yes | 0.486 | 0.140 | yes | 0.371 | 0.051 | yes | 0.566 | 0.115 | yes | 0.666 | 0.107 | yes | 0.913 | 0.629 | no | 0.894 | 0.095 | no | 0.774 | 0.108 | no |
| DR2138 | Predicted protein | 0.782 | 0.189 | no | 1.040 | 0.362 | no | 1.030 | 0.318 | no | 0.847 | 0.188 | no | 1.042 | 0.221 | no | 1.017 | 0.189 | no | 1.045 | 0.276 | no | 1.001 | 0.246 | no | 0.656 | 0.238 | yes |
| DR2139 | P-loop ATPase, possible frameshift | 1.187 | 0.363 | no | 0.945 | 0.102 | no | 0.820 | 0.179 | no | 0.926 | 0.167 | no | 0.999 | 0.255 | no | 0.981 | 0.229 | no | 0.955 | 0.201 | no | 1.056 | 0.204 | no | 0.897 | 0.139 | no |
| DR2140 | Histidinol dehydrogenase, HisX | 0.644 | 0.289 | yes | 1.427 | 1.091 | no | 1.448 | 0.447 | no | 0.934 | 0.203 | no | 1.528 | 0.818 | no | 1.653 | 0.520 | yes | 1.680 | 0.947 | no | 1.598 | 0.382 | yes | 0.466 | 0.236 | yes |
| DR2141 | Cyanobacterial membrane protein homolog | 0.794 | 0.386 | no | 0.879 | 0.243 | no | 0.720 | 0.280 | yes | 0.716 | 0.264 | no | 0.728 | 0.312 | no | 0.705 | 0.236 | no | 0.711 | 0.335 | yes | 0.703 | 0.127 | yes | 0.570 | 0.099 | yes |
| DR2142 | Conserved membrane protein | 1.109 | 0.269 | no | 1.504 | 0.632 | yes | 1.055 | 0.264 | no | 1.086 | 0.384 | no | 1.284 | 0.451 | no | 1.122 | 0.585 | no | 0.963 | 0.304 | no | 1.038 | 0.289 | no | 0.911 | 0.185 | no |
| DR2143 | Stomatin family protein | 0.731 | 0.240 | no | 1.300 | 0.622 | no | 0.769 | 0.219 | no | 1.031 | 0.198 | no | 1.117 | 0.417 | no | 0.928 | 0.355 | no | 1.065 | 0.373 | no | 0.958 | 0.042 | no | 0.642 | 0.203 | yes |
| DR2144 | MoIR N-terminal domain + uncharacterized domain ortologous to ywqG | 1.098 | 0.527 | no | 0.939 | 0.315 | no | 0.921 | 0.153 | no | 1.244 | 0.404 | no | 0.892 | 0.204 | no | 0.968 | 0.403 | no | 0.956 | 0.287 | no | 0.762 | 0.218 | no | 1.550 | 0.762 | no |
| DR2145 | ABC transporter ATPase | 1.250 | 0.361 | no | 1.246 | 0.106 | no | 1.165 | 0.275 | no | 1.071 | 0.253 | no | 1.083 | 0.124 | no | 0.919 | 0.093 | no | 1.048 | 0.243 | no | 0.933 | 0.029 | no | n/a | n/a | n/a |
| DR2146 | Predicted protein | 0.552 | 0.134 | yes | 1.311 | 0.666 | no | 1.157 | 0.684 | no | 0.728 | 0.080 | no | 1.069 | 0.323 | no | 1.365 | 0.514 | no | 1.501 | 0.976 | no | 1.182 | 0.270 | no | 1.396 | 0.396 | no |
| DR2147 | HAD superfamily hydrolase | 0.949 | 0.281 | no | 1.735 | 0.498 | yes | 2.124 | 0.439 | yes | 1.480 | 0.405 | no | 1.551 | 0.382 | yes | 1.280 | 0.238 | no | 1.186 | 0.310 | no | 1.101 | 0.353 | no | 1.025 | 0.291 | no |
| DR2148 | HTH transcriptional regulator, TetR/AcrR family | 0.768 | 0.179 | no | 0.775 | 0.187 | no | 0.853 | 0.266 | no | 0.751 | 0.096 | no | 0.873 | 0.219 | no | 0.689 | 0.110 | no | 0.866 | 0.252 | no | 0.916 | 0.170 | no | 1.116 | 0.349 | no |
| DR2149 | Conserved membrane protein | 0.690 | 0.210 | no | 1.593 | 0.327 | yes | 2.081 | 0.611 | yes | 1.679 | 0.123 | yes | 1.679 | 0.424 | yes | 1.210 | 0.405 | no | 1.395 | 0.458 | no | 1.197 | 0.172 | no | 0.664 | 0.344 | yes |
| DR2150 | YIDD family of small conserved proteins with characteristic cysteines | 0.920 | 0.213 | no | 1.722 | 0.739 | yes | 2.364 | 1.297 | yes | 1.715 | 0.513 | yes | 1.690 | 0.417 | yes | 1.434 | 0.244 | no | 1.321 | 0.467 | no | 1.135 | 0.177 | no | 0.713 | 0.179 | no |
| DR2151 | RnpA Ribonuclease P protein component | 1.046 | 0.304 | no | 1.124 | 0.401 | no | 1.166 | 0.533 | no | 0.540 | 0.131 | yes | 0.897 | 0.348 | no | 0.880 | 0.394 | no | 0.847 | 0.276 | no | 0.877 | 0.109 | no | 0.898 | 0.209 | no |
| DR2152 | Ribosomal protein L34 | 0.925 | 0.323 | no | 3.200 | 0.612 | yes | 3.146 | 0.977 | yes | 3.494 | 1.381 | yes | 2.958 | 1.462 | yes | 1.874 | 0.449 | yes | 1.679 | 0.490 | yes | 1.552 | 0.191 | yes | 1.128 | 0.391 | no |
| DR2153 | ABC-type transporter, ATPase component | 1.024 | 0.238 | no | 0.568 | 0.221 | yes | 0.819 | 0.232 | no | 1.098 | 0.475 | no | 1.221 | 0.604 | no | 1.031 | 0.491 | no | 1.047 | 0.359 | no | 1.384 | 0.470 | no | 1.143 | 0.369 | no |
| DR2154 | Periplasmic (glutamine) binding protein | 1.168 | 0.280 | no | 0.752 | 0.143 | no | 0.954 | 0.370 | no | 2.184 | 1.616 | yes | 1.059 | 0.269 | no | 1.060 | 0.410 | no | 1.099 | 0.190 | no | 1.060 | 0.269 | no | 1.093 | 0.375 | no |
| DR2155 | Glutamine ABC transporter, permease protein | 0.977 | 0.394 | no | 0.744 | 0.214 | no | 0.933 | 0.142 | no | 0.933 | 0.123 | no | 1.158 | 0.351 | no | 1.010 | 0.241 | no | 0.947 | 0.326 | no | 1.068 | 0.348 | no | 0.904 | 0.226 | no |
| DR2156 | Predicted protein | 0.658 | 0.129 | yes | 0.497 | 0.215 | yes | 0.563 | 0.144 | yes | 0.572 | 0.129 | yes | 0.815 | 0.372 | no | 0.620 | 0.145 | yes | 0.514 | 0.165 | yes | 0.793 | 0.134 | no | 0.789 | 0.252 | no |
| DR2157 | Predicted protein | 1.218 | 0.854 | no | 0.612 | 0.209 | yes | 0.690 | 0.244 | yes | 0.656 | 0.139 | no | 0.751 | 0.413 | no | 0.981 | 0.647 | no | 0.869 | 0.064 | no | 0.799 | 0.201 | no | n/a | n/a | n/a |
| DR2158 | Predicted protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR2159 | Probable N-acetylmuramoyl-L-alanine amidase, cell wall hydrolase, contains peptidoglycan-binding domain | 0.807 | 0.154 | no | 1.004 | 0.358 | no | 1.074 | 0.346 | no | 0.903 | 0.170 | no | 1.157 | 0.634 | no | 0.715 | 0.112 | no | 0.863 | 0.213 | no | 1.282 | 0.603 | no | 0.920 | 0.060 | no |
| DR2160 | Aminolevulinate dehydratase, HEM2 | 0.728 | 0.105 | no | 0.596 | 0.180 | yes | 0.623 | 0.103 | yes | 0.576 | 0.167 | yes | 0.698 | 0.196 | no | 0.701 | 0.183 | no | 0.583 | 0.170 | yes | 0.668 | 0.087 | yes | 0.738 | 0.203 | no |
| DR2161 | Bacterial "eukaryote type" tyrosine/S/T phosphatase | 1.063 | 0.384 | no | 0.790 | 0.321 | no | 0.973 | 0.569 | no | 0.794 | 0.171 | no | 1.096 | 0.355 | no | 0.975 | 0.266 | no | 0.853 | 0.188 | no | 0.803 | 0.208 | no | 0.696 | 0.113 | no |
| DR2162 | Nuclease, related to endonuclease V | 0.998 | 0.233 | no | 1.238 | 0.210 | no | 1.612 | 0.546 | yes | 1.282 | 0.478 | no | 1.456 | 0.518 | no | 1.231 | 0.185 | no | 0.989 | 0.109 | no | 0.975 | 0.090 | no | 0.686 | 0.213 | no |
| DR2163 | Predicted protein | 1.016 | 0.326 | no | 1.873 | 0.434 | yes | 2.615 | 1.180 | yes | 2.313 | 0.555 | yes | 2.521 | 1.118 | yes | 1.681 | 0.717 | yes | 1.903 | 1.221 | yes | 1.205 | 0.085 | no | 0.877 | 0.143 | no |
| DR2164 | LytB ortholog | 0.863 | 0.198 | no | 1.386 | 0.211 | no | 1.661 | 0.333 | yes | 1.594 | 0.315 | no | 1.897 | 0.474 | yes | 1.860 | 0.378 | yes | 1.662 | 0.462 | yes | 1.303 | 0.258 | no | 1.363 | 0.100 | no |
| DR2165 | MinD N- terminal domain-like protein | 0.926 | 0.161 | no | 0.770 | 0.331 | no | 0.799 | 0.264 | no | 0.998 | 0.079 | no | 1.327 | 0.375 | no | 0.967 | 0.163 | no | 1.249 | 0.173 | no | 1.551 | 0.274 | yes | 1.421 | 0.404 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR2166 | Purine-nucleoside phosphorylase, DeoD | 0.913 | 0.193 | no | 0.767 | 0.223 | no | 0.814 | 0.224 | no | 0.846 | 0.181 | no | 1.256 | 0.352 | no | 1.186 | 0.171 | no | 1.055 | 0.134 | no | 1.631 | 0.369 | yes | 1.775 | 0.208 | yes |
| DR2167 | Predicted protein | 0.990 | 0.365 | no | 0.865 | 0.315 | no | 0.856 | 0.200 | no | 0.984 | 0.141 | no | 1.200 | 0.411 | no | 1.211 | 0.168 | no | 1.298 | 0.529 | no | 1.288 | 0.099 | no | 1.282 | 0.183 | no |
| DR2168 | Sun family protein of rRNA methyltransferases | 1.275 | 0.459 | no | 1.377 | 0.409 | no | 1.354 | 1.024 | no | 1.249 | 0.194 | no | 0.924 | 0.522 | no | 2.048 | 1.077 | yes | 2.079 | 0.954 | yes | 1.094 | 0.171 | no | 2.005 | 0.582 | yes |
| DR2169 | TetA like MFS transporter | 1.201 | 0.513 | no | 0.790 | 0.208 | no | 0.704 | 0.146 | no | 0.751 | 0.160 | no | 0.682 | 0.146 | no | 0.679 | 0.174 | yes | 0.846 | 0.248 | no | 0.742 | 0.076 | no | 0.812 | 0.084 | no |
| DR2170 | Predicted protein | 1.755 | 0.726 | yes | 3.587 | 2.598 | yes | 3.575 | 1.465 | yes | 2.531 | 0.645 | yes | 2.168 | 1.256 | yes | 1.690 | 0.654 | yes | 1.798 | 0.516 | yes | 1.791 | 0.906 | yes | 0.986 | 0.102 | no |
| DR2171 | Predicted protein | 1.910 | 1.036 | yes | 1.808 | 0.879 | yes | 2.540 | 1.038 | yes | 2.971 | 0.216 | yes | 1.959 | 1.148 | yes | 1.047 | 0.307 | no | 1.303 | 0.678 | no | 0.975 | 0.323 | no | 0.923 | 0.308 | no |
| DR2172 | Predicted protein | 1.319 | 0.553 | no | 1.787 | 0.506 | yes | 2.907 | 1.028 | yes | 2.149 | 0.149 | yes | 1.769 | 0.556 | yes | 1.460 | 0.264 | no | 1.117 | 0.425 | no | 0.913 | 0.143 | no | 0.816 | 0.194 | no |
| DR2173 | Shares N-terminal domain with the MolR protein | 1.266 | 0.388 | no | 1.494 | 0.481 | yes | 2.276 | 0.641 | yes | 2.189 | 0.273 | yes | 1.719 | 0.821 | yes | 1.146 | 0.343 | no | 1.090 | 0.554 | no | 1.093 | 0.385 | no | 0.808 | 0.211 | no |
| DR2174 | Leucyl tRNA synthetase Class I | 0.802 | 0.127 | no | 0.410 | 0.092 | yes | 0.269 | 0.062 | yes | 0.353 | 0.022 | yes | 0.375 | 0.112 | yes | 0.328 | 0.137 | yes | 0.411 | 0.211 | yes | 0.414 | 0.132 | yes | 0.631 | 0.097 | yes |
| DR2175 | Predicted protein | 1.174 | 0.389 | no | 0.541 | 0.139 | yes | 0.870 | 0.199 | no | 2.439 | 0.898 | yes | 2.439 | 0.607 | yes | 1.937 | 0.521 | yes | 2.985 | 1.174 | yes | 2.287 | 0.663 | yes | 2.445 | 0.614 | yes |
| DR2176 | Conserved CBS domain protein, so called hemolysin | 0.646 | 0.339 | yes | 1.213 | 0.564 | no | 1.666 | 0.847 | yes | 0.983 | 0.131 | no | 1.342 | 0.374 | no | 1.705 | 0.571 | yes | 1.629 | 0.878 | yes | 1.284 | 0.246 | no | 0.636 | 0.177 | yes |
| DR2177 | Cytidine deaminase | 0.920 | 0.176 | no | 0.728 | 0.148 | no | 0.704 | 0.146 | no | 0.740 | 0.096 | no | 1.049 | 0.255 | no | 1.009 | 0.255 | no | 0.969 | 0.351 | no | 0.890 | 0.167 | no | 0.944 | 0.188 | no |
| DR2178 | Adenylosuccinate lyase, PUR8 | 1.169 | 0.364 | no | 1.238 | 0.299 | no | 1.693 | 0.544 | yes | 1.889 | 0.971 | yes | 2.069 | 1.072 | yes | 1.448 | 0.341 | no | 1.431 | 0.585 | no | 1.354 | 0.205 | no | 1.460 | 0.392 | no |
| DR2179 | Predicted protein | 0.917 | 0.117 | no | 0.676 | 0.152 | yes | 0.774 | 0.156 | no | 0.842 | 0.080 | no | 1.113 | 0.425 | no | 1.297 | 0.361 | no | 1.293 | 0.302 | no | 1.267 | 0.273 | no | 1.392 | 0.105 | no |
| DR2180 | Uncharacterized small family of predominantly archaeal proteins, associated with a GTPase | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR2181 | RAB/RAS like small bacterial GTPase | 0.822 | 0.224 | no | 0.934 | 0.330 | no | 1.158 | 0.301 | no | 1.230 | 0.193 | no | 2.127 | 1.497 | yes | 1.717 | 0.370 | yes | 1.489 | 0.425 | no | 1.470 | 0.116 | yes | 1.302 | 0.320 | no |
| DR2182 | Predicted protein | 0.740 | 0.285 | no | 0.710 | 0.128 | no | 0.678 | 0.133 | yes | 0.584 | 0.053 | yes | 1.013 | 0.374 | no | 1.162 | 0.358 | no | 1.243 | 0.394 | no | 1.273 | 0.208 | no | 1.184 | 0.174 | no |
| DR2183 | Predicted protein | 0.644 | 0.166 | yes | 0.812 | 0.333 | no | 0.799 | 0.381 | no | 0.823 | 0.316 | no | 0.832 | 0.309 | no | 0.813 | 0.103 | no | 0.928 | 0.284 | no | 1.043 | 0.285 | no | 0.770 | 0.204 | no |
| DR2184 | Nitrilase, amidohydrolase family protein | 1.065 | 0.089 | no | 0.932 | 0.455 | no | 0.555 | 0.305 | yes | 0.973 | 0.703 | no | 0.836 | 0.383 | no | 0.693 | 0.200 | no | 0.743 | 0.164 | no | 0.846 | 0.306 | no | 0.869 | 0.275 | no |
| DR2185 | Predicted protein | 0.618 | 0.317 | yes | 1.201 | 0.517 | no | 1.440 | 0.400 | no | 1.279 | 0.543 | no | 1.299 | 0.510 | no | 1.425 | 0.307 | no | 1.054 | 0.364 | no | 1.079 | 0.053 | no | 0.720 | 0.175 | no |
| DR2186 | Cystathionine gamma-synthase | 1.049 | 0.217 | no | 1.597 | 0.813 | yes | 1.555 | 0.336 | yes | 0.857 | 0.036 | no | 1.283 | 0.558 | no | 1.237 | 0.434 | no | 0.938 | 0.247 | no | 0.988 | 0.151 | no | 0.867 | 0.128 | no |
| DR2187 | Cyclopropane fatty acid synthase, CFA | 1.117 | 0.292 | no | 1.690 | 0.653 | yes | 2.011 | 0.625 | yes | 2.218 | 1.199 | yes | 1.534 | 0.987 | no | 1.605 | 0.321 | yes | 1.332 | 0.360 | no | 1.137 | 0.343 | no | 0.985 | 0.288 | no |
| DR2188 | Aminopeptidase T, AMP2 | 0.771 | 0.172 | no | 0.778 | 0.162 | no | 0.807 | 0.132 | no | 0.629 | 0.222 | yes | 1.054 | 0.300 | no | 1.728 | 0.556 | yes | 1.535 | 0.275 | yes | 1.940 | 0.168 | yes | 1.900 | 0.393 | yes |
| DR2189 | Solo Lon protease domain | 0.954 | 0.420 | no | 1.705 | 0.540 | yes | 1.781 | 0.794 | yes | 2.292 | 0.833 | yes | 1.447 | 0.270 | no | 1.708 | 0.407 | yes | 1.531 | 0.814 | no | 1.257 | 0.145 | no | 0.868 | 0.277 | no |
| DR2190 | NADH-dependent flavin oxidoreductase | 1.008 | 0.168 | no | 0.680 | 0.292 | yes | 0.379 | 0.068 | yes | 0.413 | 0.095 | yes | 0.538 | 0.191 | yes | 0.998 | 0.532 | no | 0.899 | 0.238 | no | 0.992 | 0.148 | no | 0.998 | 0.252 | no |
| DR2192 | ABC transporter ATPase component | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR2193 | 2 pairs C4-fingers, uncharacterized | 0.880 | 0.166 | no | 0.899 | 0.265 | no | 1.140 | 0.241 | no | 1.160 | 0.231 | no | 1.535 | 0.556 | no | 1.783 | 0.154 | yes | 1.402 | 0.518 | no | 1.573 | 0.582 | yes | 1.314 | 0.222 | no |
| DR2194 | RimK, ATP-grasp S6 modifying protein | 0.752 | 0.111 | no | 0.746 | 0.208 | no | 1.399 | 0.824 | no | 0.939 | 0.160 | no | 0.679 | 0.405 | yes | 1.038 | 0.241 | no | 1.452 | 0.534 | no | 1.074 | 0.125 | no | 1.173 | 0.092 | no |
| DR2195 | Glycogen phosphorylase | 0.668 | 0.308 | yes | 0.560 | 0.392 | yes | 1.233 | 0.451 | no | 0.852 | 0.277 | no | 0.954 | 0.552 | no | 1.355 | 0.497 | no | 1.587 | 0.411 | yes | 1.336 | 0.235 | no | 0.924 | 0.440 | no |
| DR2196 | Uncharacterized protein, YDGA ortholog | 1.196 | 0.438 | no | 0.942 | 0.230 | no | 0.762 | 0.317 | no | 0.674 | 0.122 | no | 0.854 | 0.417 | no | 0.907 | 0.264 | no | 1.236 | 0.428 | no | 1.139 | 0.279 | no | 0.852 | 0.138 | no |
| DR2197 | ABC permease | 1.076 | 0.355 | no | 1.001 | 0.256 | no | 1.047 | 0.442 | no | 1.342 | 0.548 | no | 0.969 | 0.237 | no | 1.158 | 0.333 | no | 1.169 | 0.609 | no | 0.988 | 0.054 | no | 1.248 | 0.324 | no |
| DR2198 | ABC-type nitrate transporter, ATPase component | 0.942 | 0.403 | no | 1.088 | 0.218 | no | 1.179 | 0.612 | no | 1.774 | 0.753 | yes | 1.058 | 0.595 | no | 0.971 | 0.208 | no | 1.094 | 0.160 | no | 1.087 | 0.113 | no | n/a | n/a | n/a |
| DR2199 | HTH containing, highly similar to archaea | 1.139 | 0.331 | no | 0.824 | 0.153 | no | 0.475 | 0.129 | yes | 0.845 | 0.496 | no | 0.603 | 0.284 | yes | 1.002 | 0.498 | no | 1.356 | 0.421 | no | 1.374 | 0.416 | no | 1.090 | 0.177 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR2200 | Orotidine-5'-phosphate decarboxylase | 0.973 | 0.347 | no | 1.495 | 0.402 | yes | 1.259 | 0.417 | no | 1.522 | 0.553 | no | 1.191 | 0.441 | no | 1.244 | 0.586 | no | 1.030 | 0.240 | no | 0.940 | 0.183 | no | 0.665 | 0.153 | no |
| DR2201 | HTH, transcription factor | 1.080 | 0.528 | no | 1.153 | 0.486 | no | 0.949 | 0.256 | no | 0.805 | 0.129 | no | 0.670 | 0.357 | yes | 1.003 | 0.497 | no | 0.850 | 0.484 | no | 0.873 | 0.206 | no | 0.832 | 0.265 | no |
| DR2202 | UDP-galactose 4-epimerase | 0.766 | 0.139 | no | 0.656 | 0.188 | yes | 0.830 | 0.148 | no | 0.993 | 0.435 | no | 1.314 | 0.547 | no | 1.206 | 0.351 | no | 1.070 | 0.445 | no | 0.867 | 0.215 | no | 0.764 | 0.215 | no |
| DR2203 | Conserved protein of unknown bacterial/eukaryotic family, YIGZ_ECOLI-like | 0.934 | 0.423 | no | 1.383 | 0.593 | no | 1.628 | 0.786 | yes | 1.517 | 0.655 | no | 1.993 | 1.328 | yes | 1.644 | 0.299 | yes | 1.513 | 0.785 | no | 1.241 | 0.193 | no | 1.020 | 0.136 | no |
| DR2204 | MutT family hydrolase, YRFE_ECOLI-like | 1.017 | 0.314 | no | 1.274 | 0.414 | no | 1.296 | 0.299 | no | 1.453 | 0.614 | no | 1.539 | 0.659 | no | 1.451 | 0.423 | no | 1.193 | 0.459 | no | 0.994 | 0.169 | no | 0.854 | 0.096 | no |
| DR2205 | Membrane protein, MDR type permease | 0.953 | 0.283 | no | 2.988 | 2.306 | yes | 6.917 | 2.599 | yes | 0.961 | 0.592 | no | 1.039 | 0.855 | no | 1.374 | 0.361 | no | 1.657 | 0.987 | no | 0.508 | 0.313 | yes | n/a | n/a | n/a |
| DR2206 | Citrate lyase beta chain, CilB | 0.856 | 0.029 | no | 0.976 | 0.350 | no | 0.974 | 0.537 | no | 0.694 | 0.357 | no | 2.019 | 1.517 | yes | 1.128 | 0.614 | no | 1.236 | 0.494 | no | 1.032 | 0.387 | no | 2.045 | 0.985 | yes |
| DR2207 | Predicted protein | 1.030 | 0.285 | no | 0.731 | 0.136 | no | 0.688 | 0.230 | yes | 0.970 | 0.213 | no | 0.801 | 0.282 | no | 0.837 | 0.215 | no | 1.015 | 0.364 | no | 1.106 | 0.112 | no | 1.656 | 0.260 | yes |
| DR2208 | Glyoxalase/Dioxygenase family protein | 0.693 | 0.153 | no | 1.184 | 0.241 | no | 1.671 | 0.649 | yes | 1.518 | 0.777 | no | 1.699 | 0.796 | yes | 1.601 | 0.437 | yes | 1.521 | 0.586 | no | 1.454 | 0.047 | yes | 1.260 | 0.191 | no |
| DR2209 | Rio1 family Protein kinase | 0.731 | 0.222 | no | 0.550 | 0.260 | yes | 1.075 | 0.585 | no | 0.819 | 0.231 | no | 0.942 | 0.463 | no | 0.827 | 0.181 | no | 0.872 | 0.207 | no | 1.252 | 0.401 | no | 1.676 | 0.566 | yes |
| DR2210 | Protein with conserved cysteines similar to UmoC of Proteus mirabilis claimed to be transcriptional regulator protein | 1.070 | 0.298 | no | 1.134 | 0.220 | no | 1.284 | 0.439 | no | 1.368 | 0.491 | no | 1.413 | 0.274 | no | 1.362 | 0.376 | no | 1.272 | 0.178 | no | 1.182 | 0.310 | no | 1.174 | 0.381 | no |
| DR2211 | RRNA methylase SpoU type | 1.010 | 0.228 | no | 0.894 | 0.270 | no | 0.911 | 0.232 | no | 1.099 | 0.344 | no | 0.967 | 0.183 | no | 1.091 | 0.170 | no | 1.021 | 0.223 | no | 1.001 | 0.020 | no | 1.060 | 0.264 | no |
| DR2212 | Predicted protein | 0.863 | 0.143 | no | 0.652 | 0.161 | yes | 0.635 | 0.203 | yes | 0.710 | 0.057 | no | 1.011 | 0.366 | no | 0.911 | 0.185 | no | 0.796 | 0.143 | no | 0.949 | 0.107 | no | 0.928 | 0.298 | no |
| DR2213 | Carbamoyl phosphate synthetase homolog | 0.964 | 0.180 | no | 0.766 | 0.200 | no | 0.733 | 0.264 | no | 0.889 | 0.229 | no | 0.976 | 0.504 | no | 0.957 | 0.209 | no | 0.885 | 0.184 | no | 0.923 | 0.231 | no | 0.932 | 0.157 | no |
| DR2214 | Uncharacterized conserved protein | 1.016 | 0.472 | no | 0.945 | 0.334 | no | 1.084 | 0.684 | no | 0.560 | 0.158 | yes | 0.996 | 0.549 | no | 1.203 | 0.249 | no | 1.060 | 0.431 | no | 1.096 | 0.170 | no | 0.775 | 0.118 | no |
| DR2215 | HAD superfamily hydrolase | 1.315 | 0.324 | no | 1.467 | 0.507 | yes | 1.315 | 0.415 | no | 1.302 | 0.073 | no | 1.543 | 0.873 | no | 1.230 | 0.240 | no | 1.248 | 0.350 | no | 1.230 | 0.313 | no | 1.041 | 0.274 | no |
| DR2216 | Uncharacterized conserved protein | 1.122 | 0.317 | no | 0.901 | 0.249 | no | 0.763 | 0.124 | no | 0.779 | 0.062 | no | 1.169 | 0.508 | no | 1.015 | 0.248 | no | 0.880 | 0.317 | no | 1.145 | 0.282 | no | 0.925 | 0.359 | no |
| DR2218 | Uncharacterized conserved protein (G-rich loop) | 1.283 | 0.899 | no | 1.587 | 0.935 | no | 1.226 | 0.650 | no | 1.632 | 0.716 | no | 3.363 | 2.221 | yes | 1.642 | 0.829 | no | 3.416 | 2.629 | yes | 2.384 | 0.903 | yes | 0.684 | 0.338 | no |
| DR2219 | Divergent citrate lyase, citE | 1.393 | 0.936 | no | 1.461 | 0.855 | no | 1.595 | 0.476 | no | 1.017 | 0.645 | no | 2.322 | 1.518 | yes | 2.266 | 0.874 | yes | 1.449 | 0.476 | no | 1.530 | 0.756 | no | 1.902 | 0.824 | yes |
| DR2220 | Tellurium resistance protein TerB | 0.936 | 0.206 | no | 2.540 | 0.482 | yes | 2.421 | 0.261 | yes | 2.624 | 0.484 | yes | 3.130 | 1.490 | yes | 2.469 | 0.548 | yes | 2.206 | 0.293 | yes | 1.950 | 0.190 | yes | 2.100 | 0.205 | yes |
| DR2221 | Tellurium resistance/ dictyostelium cAMP binding family of proteins, TerF | 1.323 | 0.558 | no | 3.308 | 1.323 | yes | 4.541 | 2.165 | yes | 5.239 | 2.937 | yes | 4.056 | 2.890 | yes | 2.606 | 0.978 | yes | 2.867 | 1.840 | yes | 2.562 | 1.090 | yes | 4.143 | 0.902 | yes |
| DR2222 | Transposase | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR2223 | Tellurium resistance/ dictyostelium cAMP binding family of proteins, TerA | 1.168 | 0.289 | no | 2.205 | 1.039 | yes | 3.027 | 1.269 | yes | 3.627 | 1.358 | yes | 2.850 | 0.781 | yes | 2.067 | 0.593 | yes | 1.831 | 0.620 | yes | 1.459 | 0.304 | yes | 1.165 | 0.411 | no |
| DR2224 | Tellurium resistance/ dictyostelium cAMP binding family of proteins | 1.426 | 0.459 | no | 1.697 | 0.479 | yes | 2.262 | 0.569 | yes | 3.378 | 0.623 | yes | 1.937 | 0.579 | yes | 1.698 | 0.535 | yes | 1.620 | 0.552 | yes | 1.301 | 0.211 | no | 1.329 | 0.470 | no |
| DR2225 | Tellurium resistance/ dictyostelium cAMP binding family of proteins | 0.939 | 0.218 | no | 1.396 | 0.396 | no | 1.624 | 0.355 | yes | 2.144 | 0.414 | yes | 1.938 | 0.446 | yes | 1.676 | 0.724 | yes | 1.694 | 0.477 | yes | 1.525 | 0.208 | yes | 1.601 | 0.440 | yes |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
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| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR2226 | TerC family, Membrane protein, also seen in Mycobacterium | 1.125 | 0.401 | no | 0.782 | 0.202 | no | 0.748 | 0.075 | no | 1.161 | 0.223 | no | 1.395 | 0.944 | no | 1.086 | 0.299 | no | 1.049 | 0.344 | no | 1.110 | 0.220 | no | 1.191 | 0.141 | no |
| DR2227 | Phosphonopyruvate decarboxylase, DeoB family of enzymes | 0.711 | 0.097 | no | 0.354 | 0.103 | yes | 0.234 | 0.052 | yes | 0.226 | 0.039 | yes | 0.310 | 0.119 | yes | 0.354 | 0.103 | yes | 0.500 | 0.199 | yes | 0.544 | 0.135 | yes | 1.093 | 0.215 | no |
| DR2228 | Predicted protein | 1.121 | 0.497 | no | 1.055 | 0.444 | no | 1.039 | 0.331 | no | 1.230 | 0.604 | no | 1.145 | 0.273 | no | 0.883 | 0.147 | no | 1.039 | 0.318 | no | 1.074 | 0.102 | no | 0.975 | 0.178 | no |
| DR2229 | Predicted protein | 0.927 | 0.117 | no | 0.443 | 0.104 | yes | 0.546 | 0.170 | yes | 0.580 | 0.160 | yes | 0.848 | 0.562 | no | 0.769 | 0.218 | no | 0.871 | 0.272 | no | 1.154 | 0.363 | no | 0.950 | 0.143 | no |
| DR2230 | Predicted protein | 1.012 | 0.371 | no | 0.830 | 0.243 | no | 0.849 | 0.382 | no | 1.069 | 0.489 | no | 0.955 | 0.315 | no | 0.976 | 0.192 | no | 0.980 | 0.286 | no | 1.082 | 0.320 | no | 1.145 | 0.210 | no |
| DR2231 | Uncharacterized conserved protein | 0.946 | 0.223 | no | 0.834 | 0.218 | no | 0.859 | 0.186 | no | 0.859 | 0.242 | no | 1.196 | 0.296 | no | 1.240 | 0.242 | no | 1.359 | 0.485 | no | 1.253 | 0.131 | no | 1.107 | 0.052 | no |
| DR2232 | Conserved membrane protein | 1.129 | 0.505 | no | 1.423 | 0.718 | no | 1.454 | 0.461 | no | 1.591 | 0.704 | no | 1.587 | 0.690 | yes | 1.461 | 0.518 | no | 1.158 | 0.243 | no | 1.145 | 0.152 | no | 1.181 | 0.102 | no |
| DR2233 | Calcineurin like phosphoesterase | 0.954 | 0.170 | no | 0.998 | 0.216 | no | 1.024 | 0.251 | no | 1.128 | 0.305 | no | 1.417 | 0.337 | no | 1.579 | 0.358 | yes | 1.409 | 0.458 | no | 1.091 | 0.049 | no | 1.039 | 0.213 | no |
| DR2234 | Diacylglycerol Kinase family protein | 0.827 | 0.212 | no | 0.493 | 0.221 | yes | 0.415 | 0.136 | yes | 0.410 | 0.079 | yes | 0.725 | 0.486 | yes | 0.476 | 0.031 | yes | 0.621 | 0.135 | yes | 0.947 | 0.338 | no | 1.118 | 0.235 | no |
| DR2235 | PHP family phosphoesterase | 0.808 | 0.223 | no | 0.501 | 0.114 | yes | 0.367 | 0.084 | yes | 0.287 | 0.081 | yes | 0.449 | 0.226 | yes | 0.793 | 0.279 | no | 0.690 | 0.361 | yes | 0.895 | 0.065 | no | 1.128 | 0.412 | no |
| DR2236 | Predicted protein | 1.155 | 0.153 | no | 1.184 | 0.260 | no | 1.377 | 0.270 | no | 1.845 | 0.270 | yes | 1.845 | 0.788 | yes | 1.403 | 0.188 | no | 1.249 | 0.284 | no | 1.287 | 0.203 | no | 1.086 | 0.284 | no |
| DR2237 | Predicted protein | 1.050 | 0.214 | no | 1.022 | 0.125 | no | 1.127 | 0.289 | no | 1.430 | 0.164 | no | 1.443 | 0.389 | no | 1.279 | 0.225 | no | 1.484 | 0.375 | no | 1.409 | 0.396 | no | 1.182 | 0.153 | no |
| DR2238 | Carbonic anhydrase | 0.959 | 0.246 | no | 0.564 | 0.162 | yes | 0.650 | 0.151 | yes | 0.832 | 0.105 | no | 1.039 | 0.262 | no | 1.011 | 0.135 | no | 1.108 | 0.268 | no | 1.478 | 0.228 | yes | 1.216 | 0.097 | no |
| DR2239 | Peptidase D/acetylornithine deacetylase family protein, PEPD | 0.871 | 0.366 | no | 0.565 | 0.223 | yes | 0.453 | 0.172 | yes | 0.727 | 0.255 | no | 1.269 | 0.337 | no | 1.023 | 0.135 | no | 1.317 | 0.307 | no | 1.661 | 0.280 | yes | 1.204 | 0.203 | no |
| DR2240 | Predicted protein | 1.086 | 0.385 | no | 0.480 | 0.168 | yes | 0.501 | 0.150 | yes | 1.440 | 0.341 | no | 1.678 | 0.578 | yes | 1.490 | 0.649 | no | 1.945 | 0.566 | yes | 1.931 | 0.304 | yes | 2.175 | 0.510 | yes |
| DR2241 | Multidomain protein, has 2 domains, probably metal-binding, related to MJ0970 | 1.468 | 0.544 | no | 0.737 | 0.167 | no | 5.326 | 3.050 | yes | 0.810 | 0.496 | no | 1.042 | 0.658 | no | 2.304 | 1.664 | yes | 0.904 | 0.252 | no | 0.897 | 0.123 | no | 1.177 | 0.431 | no |
| DR2242 | Thioredoxin peroxidase | 1.021 | 0.169 | no | 0.748 | 0.204 | no | 0.801 | 0.189 | no | 1.010 | 0.181 | no | 1.303 | 0.662 | no | 1.174 | 0.203 | no | 1.255 | 0.325 | no | 1.400 | 0.210 | no | 1.278 | 0.216 | no |
| DR2243 | PhoU ortholog | 1.436 | 0.933 | no | 0.981 | 0.260 | no | 0.812 | 0.185 | no | 0.874 | 0.377 | no | 1.038 | 0.266 | no | 1.253 | 0.510 | no | 1.303 | 0.252 | no | 1.216 | 0.134 | no | 1.490 | 0.403 | yes |
| DR2244 | Histidine kinase | 1.164 | 0.306 | no | 1.475 | 0.720 | no | 2.050 | 0.687 | yes | 1.964 | 0.544 | yes | 2.472 | 1.654 | yes | 1.723 | 0.669 | yes | 1.421 | 0.643 | no | 1.261 | 0.304 | no | 0.875 | 0.230 | no |
| DR2245 | CheY-like family of responce regulator + HTH domain; PhoB ortholog | 1.053 | 0.435 | no | 1.066 | 0.337 | no | 0.776 | 0.217 | no | 0.973 | 0.302 | no | 1.126 | 0.289 | no | 1.295 | 0.221 | no | 1.023 | 0.139 | no | 0.959 | 0.345 | no | 0.673 | 0.273 | yes |
| DR2246 | Predicted protein | 1.214 | 0.546 | no | 1.389 | 0.550 | no | 1.530 | 0.318 | yes | 1.514 | 0.877 | no | 1.105 | 0.447 | no | 2.016 | 1.477 | yes | 1.209 | 0.663 | no | 1.205 | 0.420 | no | 0.878 | 0.233 | no |
| DR2247 | Uncharacterized conserved protein | 0.709 | 0.292 | no | 0.811 | 0.360 | no | 1.089 | 0.711 | no | 1.437 | 0.311 | no | 0.947 | 0.253 | no | 1.226 | 0.218 | no | 1.332 | 0.931 | no | 1.300 | 0.483 | no | 0.987 | 0.253 | no |
| DR2248 | a/b fold hydrolase | 1.363 | 0.477 | no | 1.686 | 0.468 | yes | 1.875 | 0.439 | yes | 1.931 | 0.258 | yes | 1.520 | 0.199 | yes | 1.362 | 0.260 | no | 1.319 | 0.365 | no | 1.449 | 0.587 | no | 1.110 | 0.319 | no |
| DR2249 | Protein phosphatase, calcineurin like phosphoesterase | 1.063 | 0.703 | no | 1.319 | 0.468 | no | 1.098 | 0.398 | no | 1.507 | 0.411 | no | 1.248 | 0.531 | no | 1.160 | 0.116 | no | 1.172 | 0.359 | no | 1.083 | 0.221 | no | 0.987 | 0.157 | no |
| DR2250 | Methoxyneurosporene dehydrogenase | 1.228 | 0.324 | no | 1.524 | 0.356 | yes | 1.683 | 0.560 | yes | 1.413 | 0.220 | no | 1.237 | 0.500 | no | 1.133 | 0.288 | no | 1.236 | 0.243 | no | 1.210 | 0.246 | no | 1.252 | 0.183 | no |
| DR2251 | Predicted protein | 0.729 | 0.297 | no | 0.818 | 0.079 | no | 0.720 | 0.377 | yes | 1.018 | 0.077 | no | 0.944 | 0.491 | no | 1.304 | 0.359 | no | 2.008 | 0.717 | yes | 2.783 | 0.525 | yes | 2.478 | 0.410 | yes |
| DR2252 | Predicted protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR2253 | Membrane protein, transporter, YEIB_ECOLI ortholog | 1.307 | 0.309 | no | 1.138 | 0.307 | no | 1.085 | 0.234 | no | 1.176 | 0.141 | no | 0.969 | 0.256 | no | 1.027 | 0.273 | no | 1.092 | 0.282 | no | 1.069 | 0.205 | no | 1.200 | 0.223 | no |
| DR2254 | NH2- acetyltransferase | 1.073 | 0.245 | no | 1.095 | 0.280 | no | 1.105 | 0.156 | no | 1.039 | 0.184 | no | 0.905 | 0.230 | no | 0.978 | 0.342 | no | 1.092 | 0.312 | no | 1.043 | 0.179 | no | 1.114 | 0.338 | no |
| DR2255 | NH2- acetyltransferase | 1.199 | 0.232 | no | 2.412 | 0.978 | yes | 1.873 | 0.483 | yes | 1.663 | 0.490 | yes | 1.365 | 0.325 | no | 1.111 | 0.334 | no | 1.213 | 0.331 | no | 1.249 | 0.199 | no | 1.353 | 0.325 | no |
| DR2256 | Transketolase, TKT | 0.871 | 0.257 | no | 3.856 | 1.631 | yes | 3.017 | 0.813 | yes | 1.912 | 0.621 | yes | 2.271 | 1.122 | yes | 2.107 | 0.753 | yes | 2.576 | 1.461 | yes | 1.862 | 0.113 | yes | 2.317 | 0.255 | yes |
| DR2257 | Erythromycin esterase family | 1.352 | 0.407 | no | 2.477 | 0.380 | yes | 2.035 | 0.525 | yes | 1.729 | 0.165 | yes | 1.600 | 0.374 | yes | 1.532 | 0.491 | no | 1.709 | 0.436 | yes | 1.423 | 0.176 | no | 1.274 | 0.273 | no |
| DR2258 | Predicted protein | 0.970 | 0.597 | no | 1.940 | 0.644 | yes | 3.412 | 1.637 | yes | 1.449 | 0.253 | no | 1.736 | 0.494 | yes | 1.295 | 0.170 | no | 1.685 | 0.584 | yes | 1.205 | 0.379 | no | 0.735 | 0.209 | no |
| DR2259 | HTH transcriptional regulator | 0.871 | 0.246 | no | 2.530 | 0.701 | yes | 2.286 | 0.608 | yes | 1.707 | 0.291 | yes | 1.652 | 0.793 | yes | 1.460 | 0.366 | no | 1.387 | 0.676 | no | 1.053 | 0.167 | no | 0.780 | 0.315 | no |
| DR2260 | FtsY ortholog P-loop enzyme | 0.888 | 0.559 | no | 4.984 | 1.902 | yes | 1.672 | 0.622 | yes | n/a | n/a | n/a | 0.900 | 0.505 | no | 0.270 | 0.168 | yes | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR2261 | Oxidoreductase | 1.007 | 0.223 | no | 0.952 | 0.182 | no | 0.697 | 0.156 | no | 0.654 | 0.090 | no | 0.862 | 0.271 | no | 1.147 | 0.186 | no | 1.586 | 0.283 | yes | 1.693 | 0.250 | yes | 1.390 | 0.248 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR2262 | Predicted protein | 1.116 | 0.263 | no | 1.769 | 0.146 | yes | 1.670 | 0.539 | yes | 1.446 | 0.050 | no | 1.626 | 0.353 | yes | 1.947 | 0.350 | yes | 3.595 | 1.232 | yes | 3.091 | 1.506 | yes | 1.045 | 0.277 | no |
| DR2263 | Bacterioferritin, Iron chelating protein | 1.522 | 0.788 | no | 0.564 | 0.229 | yes | 0.512 | 0.225 | yes | 1.712 | 0.181 | no | 1.836 | 1.033 | yes | 3.102 | 1.847 | yes | 4.912 | 2.412 | yes | 6.408 | 1.969 | yes | 4.844 | 1.952 | yes |
| DR2264 | Metallobetalactmase fold hydrolase | 1.588 | 0.813 | no | 1.201 | 0.622 | no | 1.452 | 0.747 | no | 1.316 | 0.152 | no | 1.585 | 0.757 | no | 1.824 | 0.920 | yes | 1.642 | 0.765 | yes | 1.033 | 0.537 | no | n/a | n/a | n/a |
| DR2265 | Large membrane protein | 1.192 | 0.326 | no | 3.430 | 0.749 | yes | 5.316 | 2.775 | yes | 5.447 | 1.462 | yes | 4.845 | 2.272 | yes | 2.490 | 0.717 | yes | 2.016 | 0.693 | yes | 1.497 | 0.040 | yes | 1.032 | 0.197 | no |
| DR2266 | Predicted protein | 1.097 | 0.456 | no | 1.441 | 0.356 | yes | 1.820 | 0.766 | yes | 1.532 | 0.469 | no | 1.479 | 0.466 | no | 1.445 | 0.597 | no | 1.622 | 0.654 | yes | 1.177 | 0.404 | no | 0.784 | 0.356 | no |
| DR2267 | Type I restriction-modification system methylase subunit | 1.107 | 0.342 | no | 1.435 | 0.341 | yes | 1.363 | 0.372 | no | 1.355 | 0.075 | no | 1.245 | 0.426 | no | 1.332 | 0.405 | no | 1.223 | 0.448 | no | 1.111 | 0.236 | no | 0.827 | 0.166 | no |
| DR2268 | Aspartate transaminase | 0.947 | 0.296 | no | 0.615 | 0.224 | yes | 0.481 | 0.191 | yes | 0.423 | 0.210 | yes | 0.481 | 0.114 | yes | 0.640 | 0.214 | yes | 0.881 | 0.360 | no | 0.940 | 0.222 | no | 0.876 | 0.114 | no |
| DR2269 | GlpE/MoeB rhodanese related protein | 1.556 | 0.565 | no | 1.078 | 0.352 | no | 1.398 | 0.221 | no | 2.108 | 1.207 | yes | 1.279 | 0.562 | no | 2.102 | 1.133 | yes | 3.710 | 2.051 | yes | 3.938 | 0.295 | yes | 3.102 | 0.229 | yes |
| DR2270 | conserved membrane protein, YGIH_ECOLI-like | 1.237 | 0.551 | no | 0.830 | 0.359 | no | 0.674 | 0.154 | no | 0.732 | 0.161 | no | 0.550 | 0.084 | yes | 0.839 | 0.278 | no | 0.802 | 0.305 | no | 0.819 | 0.156 | no | 0.767 | 0.205 | no |
| DR2271 | Predicted membrane protein | 1.050 | 0.272 | no | 0.936 | 0.275 | no | 0.802 | 0.408 | no | 0.804 | 0.076 | no | 0.780 | 0.388 | no | 0.766 | 0.254 | no | 0.760 | 0.296 | no | 0.845 | 0.129 | no | 0.868 | 0.160 | no |
| DR2272 | MutT family hydrolase | 1.045 | 0.218 | no | 2.077 | 1.356 | yes | 2.307 | 0.893 | yes | 2.163 | 0.680 | yes | 1.642 | 0.354 | yes | 1.342 | 0.392 | no | 1.479 | 0.580 | no | 1.471 | 0.650 | no | 1.254 | 0.438 | no |
| DR2273 | Probable P-loop containing kinase, FlaR-like protein | 1.771 | 0.885 | yes | 1.380 | 0.383 | no | 1.597 | 0.626 | yes | 2.542 | 0.859 | yes | 1.702 | 0.406 | yes | 1.712 | 1.123 | no | 1.971 | 0.859 | yes | 1.465 | 0.302 | yes | 1.830 | 0.810 | yes |
| DR2274 | SAM dependent Methylase | 1.310 | 0.705 | no | 1.426 | 0.339 | yes | 1.860 | 0.529 | yes | 1.935 | 0.435 | yes | 1.567 | 0.429 | yes | 1.471 | 0.240 | no | 1.714 | 0.411 | yes | 1.498 | 0.253 | yes | 1.203 | 0.204 | no |
| DR2275 | UvrB | 1.564 | 0.907 | no | 2.475 | 1.293 | yes | 3.525 | 1.512 | yes | 4.931 | 1.813 | yes | 3.588 | 1.704 | yes | 1.566 | 0.932 | no | 1.486 | 0.745 | no | 1.358 | 0.340 | no | 1.012 | 0.385 | no |
| DR2276 | Predicted protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR2277 | Glutamine transporter, permease protein, GLNP_ECOLI | 0.909 | 0.360 | no | 1.979 | 0.742 | yes | 4.473 | 2.366 | yes | 2.848 | 0.767 | yes | 2.166 | 0.794 | yes | 1.222 | 0.386 | no | 1.095 | 0.314 | no | 0.949 | 0.331 | no | 0.875 | 0.172 | no |
| DR2278 | Glutamate binding periplasmic protein, FLIY | 1.003 | 0.195 | no | 1.453 | 0.322 | yes | 1.767 | 0.745 | yes | 2.272 | 0.798 | yes | 2.048 | 0.984 | yes | 1.143 | 0.537 | no | 0.953 | 0.385 | no | 0.981 | 0.159 | no | 1.341 | 0.234 | no |
| DR2279 | Alcohol dehydrogenase | 1.207 | 0.307 | no | 2.234 | 0.982 | yes | 3.386 | 1.489 | yes | 3.492 | 0.933 | yes | 2.370 | 0.738 | yes | 2.005 | 0.578 | yes | 1.631 | 0.567 | yes | 1.176 | 0.378 | no | 0.891 | 0.390 | no |
| DR2280 | Uracil permease | 1.559 | 0.255 | yes | 1.690 | 0.519 | yes | 1.807 | 0.490 | yes | 2.006 | 0.546 | yes | 1.587 | 0.554 | yes | 1.350 | 0.441 | no | 1.337 | 0.408 | no | 1.138 | 0.122 | no | 1.081 | 0.364 | no |
| DR2281 | Shares nucleic acid binding domain with RNase III | 1.049 | 0.343 | no | 2.148 | 0.778 | yes | 2.045 | 0.964 | yes | 1.772 | 0.207 | yes | 1.529 | 0.311 | yes | 1.562 | 0.570 | no | 1.722 | 0.579 | yes | 1.368 | 0.287 | no | 1.368 | 0.461 | no |
| DR2282 | Uncharacterized conserved protein, ortholog YRAN, novel Holliday junction resolvase | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR2283 | Chelated iron transport system membrane protein, MNTB -like | 1.112 | 0.323 | no | 1.408 | 0.309 | no | 1.484 | 0.511 | yes | 1.433 | 0.368 | no | 1.293 | 0.201 | no | 1.251 | 0.170 | no | 1.251 | 0.168 | no | 1.120 | 0.187 | no | 1.117 | 0.323 | no |
| DR2284 | ABC ATPase, possible Manganese/Iron transporter | 0.851 | 0.440 | no | 1.010 | 0.419 | no | 1.309 | 0.502 | no | 1.155 | 0.398 | no | 1.100 | 0.348 | no | 1.490 | 0.740 | no | 1.544 | 0.658 | no | 1.053 | 0.273 | no | 1.015 | 0.200 | no |
| DR2285 | MutY, A/G-specific adenine glycosylase | 1.670 | 0.685 | yes | 1.801 | 0.465 | yes | 2.137 | 0.785 | yes | 2.365 | 0.398 | yes | 1.766 | 0.739 | yes | 1.401 | 0.350 | no | 1.514 | 0.389 | yes | 1.266 | 0.229 | no | 1.073 | 0.191 | no |
| DR2286 | Predicted protein | 0.809 | 0.240 | no | 1.072 | 0.381 | no | 1.282 | 0.320 | no | 1.254 | 0.230 | no | 1.249 | 0.440 | no | 1.676 | 1.113 | no | 1.337 | 0.525 | no | 1.199 | 0.139 | no | 1.320 | 0.184 | no |
| DR2287 | HTH transcription factor, LRP family | 0.896 | 0.223 | no | 1.559 | 0.566 | yes | 1.892 | 0.664 | yes | 2.013 | 0.452 | yes | 1.850 | 0.591 | yes | 1.571 | 0.448 | yes | 1.784 | 0.268 | yes | 1.715 | 0.514 | yes | 1.776 | 0.559 | yes |
| DR2288 | Macrohistone MACRO-H2A.1, virus X domain | 0.923 | 0.530 | no | 0.616 | 0.103 | yes | 0.627 | 0.262 | yes | 0.630 | 0.096 | yes | 0.673 | 0.208 | yes | 1.189 | 0.440 | no | 1.140 | 0.287 | no | 1.481 | 0.190 | yes | 1.585 | 0.313 | yes |
| DR2289 | Guanylate kinase | 1.300 | 0.807 | no | 0.693 | 0.131 | no | 0.547 | 0.154 | yes | 0.526 | 0.084 | yes | 0.563 | 0.142 | yes | 1.046 | 0.417 | no | 1.201 | 0.449 | no | 1.450 | 0.284 | no | 1.828 | 0.392 | yes |
| DR2290 | TruA family of Pseudouridine synthase, HisT | 1.001 | 0.530 | no | 0.948 | 0.567 | no | 1.000 | 0.587 | no | 0.615 | 0.201 | yes | 0.702 | 0.379 | yes | 0.752 | 0.131 | no | 0.714 | 0.181 | no | 1.385 | 0.588 | no | 1.187 | 0.192 | no |
| DR2291 | NlpD/PA elastase family of membrane proteases/murein hydrolases | 1.153 | 0.162 | no | 1.308 | 0.240 | no | 1.698 | 0.510 | yes | 1.638 | 0.492 | yes | 1.457 | 0.360 | no | 1.261 | 0.318 | no | 1.484 | 0.419 | no | 1.254 | 0.226 | no | 1.120 | 0.144 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR2292 | Predicted protein | 1.373 | 0.585 | no | 1.022 | 0.349 | no | 1.010 | 0.596 | no | 0.856 | 0.048 | no | 0.992 | 0.247 | no | 1.223 | 0.338 | no | 1.184 | 0.218 | no | 0.971 | 0.260 | no | 0.955 | 0.516 | no |
| DR2293 | Probably permease MDR-type | 0.876 | 0.259 | no | 0.966 | 0.391 | no | 0.968 | 0.285 | no | 0.839 | 0.068 | no | 1.002 | 0.276 | no | 1.203 | 0.220 | no | 1.093 | 0.235 | no | 1.056 | 0.097 | no | 1.097 | 0.048 | no |
| DR2294 | CutA ortholog, periplasmic divalent cation tolerance | 0.608 | 0.213 | yes | 0.532 | 0.233 | yes | 0.490 | 0.194 | yes | 0.431 | 0.060 | yes | 0.815 | 0.526 | no | 1.141 | 0.264 | no | 0.985 | 0.369 | no | 1.321 | 0.293 | no | 1.108 | 0.315 | no |
| DR2295 | Predicted protein | 0.889 | 0.380 | no | 0.658 | 0.212 | yes | 1.290 | 0.540 | no | 1.477 | 0.115 | no | 1.426 | 0.573 | no | 1.583 | 0.332 | yes | 2.365 | 0.956 | yes | 2.260 | 0.972 | yes | 1.510 | 0.468 | yes |
| DR2296 | Glucose kinase, GLK | 0.436 | 0.172 | yes | 0.884 | 0.389 | no | 0.756 | 0.299 | no | n/a | n/a | n/a | 2.488 | 1.349 | yes | 0.355 | 0.139 | yes | 1.247 | 0.020 | no | n/a | n/a | n/a | n/a | n/a | n/a |
| DR2297 | Predicted protein | 1.108 | 0.326 | no | 1.211 | 0.521 | no | 0.945 | 0.473 | no | 0.958 | 0.071 | no | 0.586 | 0.221 | yes | 0.850 | 0.332 | no | 0.795 | 0.247 | no | 0.690 | 0.123 | yes | 0.705 | 0.217 | no |
| DR2298 | Acyl-ACP thioesterase | 0.750 | 0.116 | no | 0.680 | 0.324 | yes | 0.436 | 0.153 | yes | 0.444 | 0.140 | yes | 0.575 | 0.099 | yes | 0.566 | 0.077 | yes | 0.740 | 0.240 | no | 0.848 | 0.142 | no | 0.964 | 0.244 | no |
| DR2299 | TPR repeats + GGDEF domain + YjcC domain signalling protein | 1.445 | 0.354 | no | 2.543 | 0.942 | yes | 2.186 | 1.254 | yes | 1.777 | 0.273 | yes | 1.169 | 0.532 | no | 1.553 | 0.708 | no | 2.115 | 0.771 | yes | 1.671 | 0.785 | yes | 2.604 | 1.456 | yes |
| DR2300 | Alanyl tRNA synthetase | 0.994 | 0.588 | no | 1.159 | 0.698 | no | 0.438 | 0.185 | yes | 0.913 | 0.136 | no | 0.933 | 0.641 | no | 0.696 | 0.386 | yes | 0.967 | 0.491 | no | 1.525 | 0.455 | no | 0.828 | 0.311 | no |
| DR2301 | Predicted protein | 1.275 | 0.331 | no | 1.272 | 0.488 | no | 1.248 | 0.406 | no | 0.974 | 0.388 | no | 0.897 | 0.261 | no | 1.015 | 0.463 | no | 1.120 | 0.294 | no | 1.275 | 0.385 | no | 1.289 | 0.675 | no |
| DR2302 | Yfit/DinB family of the metal binding proteins | 1.317 | 0.599 | no | 1.478 | 0.453 | yes | 1.476 | 0.544 | yes | 1.560 | 0.731 | no | 1.381 | 0.400 | no | 1.278 | 0.249 | no | 1.263 | 0.454 | no | 1.097 | 0.139 | no | 1.258 | 0.522 | no |
| DR2303 | Chloramphenicol acetyltransferase, CatP | 0.878 | 0.295 | no | 1.316 | 0.334 | no | 1.055 | 0.134 | no | 0.967 | 0.282 | no | 0.950 | 0.342 | no | 0.969 | 0.215 | no | 1.219 | 0.340 | no | 1.347 | 0.320 | no | 1.088 | 0.373 | no |
| DR2304 | Permease MDR-type | 1.464 | 0.474 | no | 1.661 | 0.529 | yes | 1.569 | 0.270 | yes | 1.854 | 0.678 | yes | 1.274 | 0.329 | no | 1.253 | 0.369 | no | 1.681 | 0.664 | yes | 1.346 | 0.102 | no | 1.600 | 0.592 | yes |
| DR2305 | HTH transcription factor | 0.937 | 0.368 | no | 1.523 | 0.334 | yes | 1.351 | 0.262 | no | 1.151 | 0.074 | no | 0.984 | 0.263 | no | 0.949 | 0.178 | no | 1.078 | 0.342 | no | 0.906 | 0.146 | no | 0.707 | 0.350 | no |
| DR2306 | HTH transcription factor, MerR family | 0.986 | 0.145 | no | 1.042 | 0.266 | no | 0.653 | 0.210 | yes | 0.629 | 0.102 | yes | 0.580 | 0.172 | yes | 0.460 | 0.200 | yes | 0.443 | 0.072 | yes | 0.568 | 0.091 | yes | 0.554 | 0.162 | yes |
| DR2307 | Membrane permease, MDR-type | 0.576 | 0.271 | yes | 0.494 | 0.294 | yes | 0.215 | 0.067 | yes | 0.138 | 0.022 | yes | 0.125 | 0.064 | yes | 0.205 | 0.118 | yes | 0.272 | 0.145 | yes | 0.332 | 0.037 | yes | 0.282 | 0.161 | yes |
| DR2308 | OBG family GTPase | 1.336 | 0.253 | no | 2.062 | 0.973 | yes | 1.407 | 0.699 | no | 1.557 | 0.598 | no | 2.676 | 2.140 | yes | 2.080 | 1.400 | yes | 1.308 | 0.673 | no | 1.471 | 0.188 | no | 1.968 | 0.965 | yes |
| DR2309 | Predicted protein | 0.653 | 0.225 | yes | 2.282 | 1.420 | yes | 1.623 | 0.875 | yes | 1.439 | 0.606 | no | 1.327 | 0.850 | no | 0.950 | 0.228 | no | 1.277 | 0.497 | no | 1.049 | 0.475 | no | 0.974 | 0.324 | no |
| DR2310 | Predicted protein | 0.701 | 0.338 | no | 1.028 | 0.624 | no | 0.431 | 0.232 | yes | 2.845 | 0.558 | yes | 1.242 | 0.825 | no | 0.909 | 0.630 | no | 0.923 | 0.508 | no | 1.224 | 0.396 | no | 2.587 | 1.053 | yes |
| DR2311 | Uncharacterized YeiN ortholog, seen also in C.elegans | 0.658 | 0.235 | no | 3.216 | 1.000 | yes | 0.137 | 0.076 | yes | 1.451 | 0.257 | no | 1.250 | 0.543 | no | 0.214 | 0.158 | yes | 1.274 | 0.401 | no | 0.865 | 0.325 | no | 6.753 | 1.102 | yes |
| DR2312 | RBSK family ribokinase, YeiI ortholog, fusion to HTH - domain | 0.919 | 0.392 | no | 0.745 | 0.277 | no | 1.815 | 1.027 | yes | 0.442 | 0.032 | yes | 1.005 | 0.615 | no | 0.746 | 0.145 | no | 0.703 | 0.334 | yes | 1.697 | 0.857 | yes | 0.470 | 0.145 | yes |
| DR2313 | Predicted protein | 1.220 | 0.579 | no | 1.318 | 0.247 | no | 1.261 | 0.479 | no | 1.281 | 0.420 | no | 1.016 | 0.241 | no | 0.960 | 0.296 | no | 1.046 | 0.625 | no | 1.029 | 0.260 | no | 1.100 | 0.344 | no |
| DR2314 | Predicted protein | 1.216 | 0.428 | no | 1.002 | 0.420 | no | 0.798 | 0.084 | no | 0.852 | 0.139 | no | 0.852 | 0.068 | no | 0.902 | 0.300 | no | 0.984 | 0.391 | no | 1.299 | 0.600 | no | 1.438 | 0.295 | no |
| DR2315 | NosY-like transporter, membrane protein | 1.029 | 0.506 | no | 2.034 | 0.919 | yes | 2.313 | 0.812 | yes | 2.219 | 0.548 | yes | 2.252 | 1.122 | yes | 1.479 | 0.548 | no | 1.758 | 0.652 | yes | 1.154 | 0.265 | no | 0.868 | 0.299 | no |
| DR2316 | ABC transporter ATPase, NosF-like | 1.343 | 0.494 | no | 1.651 | 0.447 | yes | 2.147 | 0.399 | yes | 2.162 | 0.487 | yes | 1.804 | 0.655 | yes | 1.749 | 0.434 | yes | 1.672 | 0.565 | yes | 1.272 | 0.330 | no | 0.996 | 0.261 | no |
| DR2317 | Oxidoreductase | 1.232 | 0.840 | no | 0.664 | 0.239 | yes | 0.719 | 0.233 | no | 0.899 | 0.430 | no | 1.073 | 0.404 | no | 1.078 | 0.278 | no | 1.477 | 0.453 | no | 2.161 | 1.127 | yes | 1.296 | 0.236 | no |
| DR2318 | Predicted protein | 1.105 | 0.398 | no | 1.973 | 0.481 | yes | 1.422 | 0.243 | yes | 1.324 | 0.216 | no | 1.795 | 0.414 | yes | 2.673 | 0.868 | yes | 2.943 | 0.542 | yes | 3.055 | 1.100 | yes | 2.844 | 0.307 | yes |
| DR2319 | Contains a domain related to OtsA N-term. domain family | 1.085 | 0.457 | no | 2.614 | 0.669 | yes | 1.937 | 0.485 | yes | 1.475 | 0.325 | no | 1.668 | 0.266 | yes | 3.077 | 1.192 | yes | 3.395 | 0.856 | yes | 2.800 | 0.571 | yes | 2.390 | 0.226 | yes |
| DR2320 | Contains a domain related to OtsA N-term. domain family | 1.183 | 0.599 | no | 3.154 | 1.617 | yes | 2.828 | 1.205 | yes | 2.083 | 1.001 | yes | 1.957 | 0.677 | yes | 3.216 | 1.948 | yes | 3.102 | 1.858 | yes | 2.685 | 1.036 | yes | 2.381 | 0.884 | yes |
| DR2321 | Fabz-like domain, probably ortholog of phenylacetic acid degradation protein PAAI | 1.094 | 0.740 | no | 1.913 | 1.266 | yes | 1.170 | 0.461 | no | 1.542 | 0.532 | no | 1.613 | 0.731 | no | 1.313 | 0.220 | no | 1.444 | 0.469 | no | 1.270 | 0.290 | no | 2.016 | 0.833 | yes |
| DR2322 | Alkaline serine exoprotease A | 1.074 | 0.251 | no | 1.232 | 0.335 | no | 1.687 | 0.555 | yes | 3.862 | 0.415 | yes | 4.374 | 1.228 | yes | 2.109 | 0.756 | yes | 1.623 | 0.747 | yes | 2.297 | 1.217 | yes | 1.570 | 0.197 | yes |
| DR2323 | Transposon DORF | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR2324 | Transposase | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR2325 | Probable disruption by transposon | 1.092 | 0.290 | no | 1.911 | 1.200 | yes | 2.286 | 0.958 | yes | 5.788 | 1.330 | yes | 5.971 | 2.009 | yes | 3.679 | 1.508 | yes | 2.566 | 1.035 | yes | 2.911 | 0.930 | yes | 5.483 | 3.501 | yes |
| DR2326 | Membrane protein? | 0.908 | 0.455 | no | 1.759 | 0.833 | yes | 1.549 | 0.829 | no | 1.326 | 0.957 | no | 1.315 | 0.413 | no | 1.326 | 0.481 | no | 1.171 | 0.443 | no | 1.075 | 0.330 | no | 0.891 | 0.080 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR2327 | Response regulator, CheY family, HTH domain + flavodoxin | 0.653 | 0.300 | yes | 1.354 | 0.562 | no | 1.569 | 0.587 | yes | 0.486 | 0.039 | yes | 1.305 | 0.745 | no | 1.427 | 0.647 | no | 0.971 | 0.441 | no | 1.221 | 0.469 | no | 0.594 | 0.198 | yes |
| DR2328 | Histidine kinase domain of sensor system, CUTS-like | 1.184 | 0.523 | no | 2.025 | 0.838 | yes | 1.991 | 1.162 | yes | 7.240 | 4.246 | yes | 2.909 | 1.370 | yes | 2.025 | 0.765 | yes | 1.507 | 0.713 | no | 1.381 | 0.177 | no | 1.005 | 0.516 | no |
| DR2329 | Unchracterized, uncertain relationships with GlmU and MobA | 0.804 | 0.303 | no | 0.748 | 0.219 | no | 0.728 | 0.278 | no | 0.689 | 0.140 | no | 0.777 | 0.098 | no | 0.782 | 0.115 | no | 0.993 | 0.530 | no | 0.896 | 0.147 | no | 1.007 | 0.173 | no |
| DR2330 | Ferredoxin | 1.476 | 0.464 | no | 1.103 | 0.709 | no | 0.641 | 0.348 | yes | 0.952 | 0.202 | no | 0.797 | 0.328 | no | 0.915 | 0.421 | no | 1.268 | 0.564 | no | 1.758 | 0.771 | yes | 3.198 | 2.079 | yes |
| DR2331 | Protein phosphatase, calcineurin like phosphoesterase | 0.893 | 0.551 | no | 0.749 | 0.204 | no | 0.858 | 0.373 | no | 0.602 | 0.162 | yes | 0.765 | 0.288 | no | 0.919 | 0.215 | no | 1.037 | 0.528 | no | 1.146 | 0.087 | no | 0.926 | 0.118 | no |
| DR2332 | DNA polymerase III gamma, tau subunit | 1.112 | 0.302 | no | 2.053 | 0.213 | yes | 1.510 | 0.387 | yes | 1.461 | 0.418 | no | 1.579 | 0.704 | no | 1.881 | 0.899 | yes | 2.730 | 1.739 | yes | 1.963 | 0.614 | yes | 1.058 | 0.534 | no |
| DR2333 | NADH oxidase, FADH | 1.006 | 0.394 | no | 1.377 | 0.319 | no | 1.338 | 0.734 | no | 0.966 | 0.440 | no | 1.347 | 0.445 | no | 1.664 | 1.094 | no | 2.218 | 1.072 | yes | 1.679 | 0.483 | yes | 1.713 | 0.846 | yes |
| DR2334 | NH2-Acetyltransferase, distantly related | 1.226 | 0.574 | no | 1.693 | 0.576 | yes | 2.027 | 0.937 | yes | 1.844 | 0.675 | yes | 1.778 | 0.729 | yes | 1.635 | 0.931 | no | 1.539 | 0.532 | yes | 1.357 | 0.191 | no | 1.303 | 0.621 | no |
| DR2335 | Protein-disulfide isomerase of DsbC/DsbG family | 0.808 | 0.324 | no | 0.897 | 0.293 | no | 1.095 | 0.603 | no | 0.782 | 0.080 | no | 0.938 | 0.279 | no | 0.943 | 0.209 | no | 1.442 | 0.609 | no | 1.385 | 0.321 | no | 1.142 | 0.404 | no |
| DR2336 | Potassium channel | 1.147 | 0.421 | no | 1.151 | 0.638 | no | 1.229 | 0.226 | no | 1.714 | 0.816 | no | 1.562 | 0.732 | no | 1.034 | 0.099 | no | 0.984 | 0.262 | no | 0.968 | 0.116 | no | 1.118 | 0.440 | no |
| DR2337 | Predicted protein | 2.105 | 0.900 | yes | 3.480 | 0.751 | yes | 7.414 | 5.712 | yes | 4.762 | 2.356 | yes | 2.549 | 0.986 | yes | 1.801 | 0.937 | yes | 2.697 | 1.181 | yes | 1.258 | 0.082 | no | 1.424 | 0.322 | no |
| DR2338 | CinA ortholog, CinA MoeB family | 0.836 | 0.308 | no | 1.073 | 0.227 | no | 1.001 | 0.393 | no | 2.751 | 1.950 | yes | 1.018 | 0.599 | no | 1.135 | 0.675 | no | 1.308 | 0.927 | no | 1.102 | 0.648 | no | 0.299 | 0.074 | yes |
| DR2339 | LigT, 2'-5' RNA LIGASE | 1.681 | 0.929 | no | 6.002 | 2.394 | yes | 14.056 | 10.544 | yes | 13.442 | 0.030 | yes | 13.849 | 7.480 | yes | 9.497 | 2.276 | yes | 5.006 | 2.880 | yes | 1.223 | 0.400 | no | n/a | n/a | n/a |
| DR2340 | RecA | 1.126 | 0.385 | no | 6.622 | 3.082 | yes | 7.975 | 3.860 | yes | 5.020 | 1.286 | yes | 5.272 | 2.015 | yes | 4.064 | 2.142 | yes | 3.702 | 1.375 | yes | 2.147 | 0.566 | yes | 1.439 | 0.218 | yes |
| DR2341 | BIRA bifuctional protein, biotin operon repressor, HTH and biotin-protein ligase | 0.697 | 0.297 | no | 1.453 | 0.874 | no | 1.477 | 0.932 | no | 2.076 | 1.270 | yes | 1.161 | 0.690 | no | 1.325 | 0.055 | no | 0.787 | 0.410 | no | 0.976 | 0.215 | no | 1.378 | 0.911 | no |
| DR2342 | Membrane protein, unchracterized | 1.027 | 0.274 | no | 1.684 | 0.657 | yes | 1.932 | 0.495 | yes | 1.206 | 0.088 | no | 1.490 | 0.801 | no | 1.144 | 0.296 | no | 0.911 | 0.288 | no | 0.966 | 0.178 | no | 0.618 | 0.138 | yes |
| DR2343 | Conserved memprane protein | 0.783 | 0.198 | no | 1.667 | 0.396 | yes | 2.001 | 0.539 | yes | 1.521 | 0.255 | no | 1.931 | 1.014 | yes | 1.919 | 0.651 | yes | 1.542 | 0.953 | no | 1.400 | 0.336 | no | 0.876 | 0.248 | no |
| DR2344 | Predicted protein | 1.221 | 0.467 | no | 0.872 | 0.314 | no | 1.305 | 0.547 | no | 2.495 | 0.541 | yes | 2.359 | 0.996 | yes | 4.076 | 2.947 | yes | 4.098 | 1.056 | yes | 4.806 | 2.326 | yes | 4.543 | 1.610 | yes |
| DR2345 | Calcineurin like phosphoesterase | 0.966 | 0.355 | no | 1.499 | 1.081 | no | 0.727 | 0.372 | no | 4.127 | 2.354 | yes | 0.402 | 0.294 | yes | 1.001 | 0.703 | no | 2.094 | 0.812 | yes | 2.093 | 0.249 | yes | n/a | n/a | n/a |
| DR2346 | 8-amino-7-oxononanoate synthase | 0.861 | 0.312 | no | 1.123 | 0.411 | no | 1.303 | 0.494 | no | 0.666 | 0.077 | no | 0.995 | 0.557 | no | 1.372 | 0.695 | no | 1.325 | 0.819 | no | 1.746 | 0.453 | yes | 1.339 | 0.631 | no |
| DR2347 | Predicted protein | 3.061 | 0.301 | yes | 2.323 | 0.536 | yes | 3.803 | 2.517 | yes | 0.635 | 0.354 | no | 0.778 | 0.408 | no | 1.945 | 0.607 | yes | 2.718 | 1.748 | yes | n/a | n/a | n/a | n/a | n/a | n/a |
| DR2348 | Predicted protein | 1.545 | 0.425 | no | 1.847 | 0.747 | yes | 1.764 | 1.038 | yes | 2.639 | 1.185 | yes | 1.853 | 1.059 | yes | 1.361 | 0.501 | no | 1.363 | 0.734 | no | 0.950 | 0.074 | no | 0.808 | 0.130 | no |
| DR2349 | Predicted protein | 1.172 | 0.404 | no | 0.803 | 0.307 | no | 0.203 | 0.127 | yes | 0.184 | 0.070 | yes | 0.184 | 0.095 | yes | 0.255 | 0.132 | yes | 0.297 | 0.177 | yes | 0.548 | 0.210 | yes | 0.394 | 0.164 | yes |
| DR2350 | Predicted protein | 1.234 | 0.590 | no | 2.128 | 0.874 | yes | 0.729 | 0.268 | no | 0.735 | 0.307 | no | 0.613 | 0.230 | yes | 0.541 | 0.164 | yes | 0.649 | 0.318 | yes | 0.713 | 0.188 | yes | 0.669 | 0.240 | yes |
| DR2351 | Small ATP-binding protein | 1.590 | 0.663 | no | 1.907 | 0.927 | yes | 1.178 | 0.168 | no | 1.035 | 0.517 | no | 1.320 | 0.758 | no | 1.101 | 0.393 | no | 1.355 | 0.686 | no | 1.163 | 0.404 | no | 1.001 | 0.518 | no |
| DR2352 | Porphobilinogen deaminase, HEM3 | 0.730 | 0.338 | no | 4.820 | 3.061 | yes | 4.116 | 1.628 | yes | 1.255 | 0.058 | no | 2.135 | 1.180 | yes | 2.491 | 1.193 | yes | 1.973 | 0.736 | yes | 1.249 | 0.371 | no | 0.946 | 0.375 | no |
| DR2353 | L-asparaginase | 1.339 | 0.472 | no | 1.237 | 0.562 | no | 0.940 | 0.340 | no | 1.532 | 0.771 | no | 1.868 | 0.804 | yes | 2.401 | 1.729 | yes | 3.173 | 1.409 | yes | 2.117 | 0.903 | yes | 1.299 | 0.233 | no |
| DR2354 | Phenylalanyl-tRNA synthetase alpha chain | 1.314 | 0.634 | no | 2.692 | 0.379 | yes | 1.877 | 0.578 | yes | 2.297 | 0.389 | yes | 2.380 | 0.704 | yes | 2.461 | 1.114 | yes | 3.560 | 1.348 | yes | 2.328 | 0.589 | yes | 1.295 | 0.052 | no |
| DR2355 | N-acetyltransferase | 1.248 | 0.389 | no | 5.185 | 3.229 | yes | 3.728 | 1.436 | yes | 1.963 | 0.235 | yes | 2.476 | 0.835 | yes | 2.606 | 0.981 | yes | 1.553 | 0.362 | yes | 1.392 | 0.262 | no | 1.042 | 0.085 | no |
| DR2356 | MutT family hydrolase | 1.349 | 0.480 | no | 2.522 | 0.559 | yes | 2.541 | 0.942 | yes | 3.352 | 0.449 | yes | 2.320 | 0.963 | yes | 1.591 | 0.583 | yes | 1.865 | 1.003 | yes | 1.343 | 0.567 | no | 0.809 | 0.177 | no |
| DR2357 | Phenylalanyl-tRNA synthetase beta chain | 1.035 | 0.529 | no | 1.191 | 0.493 | no | 1.057 | 0.539 | no | 1.044 | 0.399 | no | 1.476 | 0.751 | no | 1.075 | 0.330 | no | 1.120 | 0.457 | no | 0.930 | 0.235 | no | 0.714 | 0.208 | no |
| DR2358 | TPR repeat protein | 1.088 | 0.508 | no | 1.129 | 0.613 | no | 0.808 | 0.448 | no | 0.864 | 0.591 | no | 0.902 | 0.534 | no | 0.757 | 0.275 | no | 0.855 | 0.433 | no | 0.736 | 0.146 | no | 0.704 | 0.144 | no |
| DR2359 | Uncharacterized ortholog of Streptomyces, H.pylori and PBCV A638R protein | 0.862 | 0.177 | no | 0.727 | 0.124 | no | 0.908 | 0.243 | no | 0.739 | 0.044 | no | 0.947 | 0.360 | no | 1.166 | 0.324 | no | 1.215 | 0.363 | no | 0.973 | 0.126 | no | 1.172 | 0.124 | no |
| DR2360 | Predicted protein | 1.050 | 0.409 | no | 0.767 | 0.235 | no | 0.559 | 0.106 | yes | 0.548 | 0.091 | yes | 0.760 | 0.068 | no | 0.892 | 0.232 | no | 1.348 | 0.269 | no | 1.524 | 0.274 | yes | 1.025 | 0.196 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR2361 | Acyl-coA dehydrogenase | 1.546 | 0.459 | no | 1.975 | 0.912 | yes | 2.183 | 0.546 | yes | 2.697 | 1.434 | yes | 1.763 | 0.990 | no | 1.246 | 0.503 | no | 1.574 | 0.441 | yes | 1.247 | 0.011 | no | 0.919 | 0.163 | no |
| DR2362 | CAMP binding protein | 1.082 | 0.515 | no | 1.731 | 0.449 | yes | 1.612 | 0.422 | yes | 1.448 | 0.404 | no | 1.212 | 0.302 | no | 1.581 | 0.379 | yes | 1.263 | 0.211 | no | 1.241 | 0.195 | no | 0.826 | 0.140 | no |
| DR2363 | UspA domain containing protein | 0.962 | 0.375 | no | 1.162 | 0.344 | no | 0.865 | 0.229 | no | 0.577 | 0.039 | yes | 0.725 | 0.278 | no | 0.852 | 0.197 | no | 0.784 | 0.183 | no | 0.911 | 0.228 | no | 0.928 | 0.296 | no |
| DR2364 | L-lactate dehydrogenase | 1.090 | 0.484 | no | 1.050 | 0.265 | no | 0.783 | 0.181 | no | 0.781 | 0.137 | no | 0.778 | 0.288 | no | 0.728 | 0.162 | no | 0.992 | 0.244 | no | 1.006 | 0.113 | no | 0.959 | 0.114 | no |
| DR2366 | Ribosomal protein L32 | 0.948 | 0.223 | no | 1.051 | 0.207 | no | 1.101 | 0.449 | no | 0.819 | 0.364 | no | 0.825 | 0.382 | no | 1.252 | 0.692 | no | 1.089 | 0.592 | no | 0.933 | 0.188 | no | 1.079 | 0.206 | no |
| DR2367 | Gluthatione-regulated K+/H+ antiporter | 1.642 | 0.771 | yes | 1.841 | 0.497 | yes | 1.677 | 0.370 | yes | 1.572 | 0.506 | no | 1.549 | 0.793 | no | 1.223 | 0.341 | no | 1.634 | 0.618 | yes | 1.321 | 0.190 | no | 1.366 | 0.340 | no |
| DR2368 | Conserved membrane protein | 1.037 | 0.325 | no | 1.055 | 0.309 | no | 0.966 | 0.330 | no | 0.799 | 0.139 | no | 0.920 | 0.414 | no | 1.172 | 0.399 | no | 1.044 | 0.296 | no | 1.017 | 0.203 | no | 0.942 | 0.133 | no |
| DR2369 | Predicted protein | 1.276 | 0.439 | no | 0.862 | 0.195 | no | 0.724 | 0.263 | no | 1.143 | 0.575 | no | 0.682 | 0.239 | no | 0.761 | 0.211 | no | 0.753 | 0.244 | no | 0.880 | 0.118 | no | 0.676 | 0.060 | no |
| DR2370 | Dihydrolipoamide dehydrogenase, DLDH | 1.128 | 0.139 | no | 1.036 | 0.224 | no | 0.987 | 0.204 | no | 1.027 | 0.250 | no | 0.916 | 0.425 | no | 1.152 | 0.355 | no | 0.971 | 0.279 | no | 0.947 | 0.116 | no | 0.796 | 0.107 | no |
| DR2371 | Predicted protein | 0.865 | 0.220 | no | 2.429 | 1.107 | yes | 2.466 | 1.818 | yes | 1.570 | 0.666 | no | 1.694 | 0.403 | yes | 1.527 | 0.642 | no | 1.725 | 0.598 | yes | 1.024 | 0.330 | no | 0.890 | 0.159 | no |
| DR2372 | Peptidyl-Trna Hydrolase | 1.293 | 0.227 | no | 2.468 | 1.147 | yes | 2.080 | 1.144 | yes | 1.744 | 0.411 | yes | 1.467 | 0.531 | no | 1.358 | 0.470 | no | 1.394 | 0.596 | no | 1.055 | 0.217 | no | 1.091 | 0.596 | no |
| DR2373 | Predicted protein | 1.445 | 0.499 | no | 1.589 | 0.319 | yes | 1.509 | 0.361 | yes | 1.598 | 0.899 | no | 1.150 | 0.432 | no | 1.037 | 0.316 | no | 1.156 | 0.815 | no | 1.060 | 0.144 | no | 0.940 | 0.148 | no |
| DR2374 | Ribonucleotide reductase, archeal type | 1.155 | 0.325 | no | 2.567 | 0.995 | yes | 2.710 | 0.920 | yes | 2.720 | 0.666 | yes | 2.344 | 0.869 | yes | 1.994 | 0.548 | yes | 2.348 | 0.950 | yes | 1.150 | 0.518 | no | 0.959 | 0.349 | no |
| DR2375 | GREA, transcription elongation factor | 1.235 | 0.743 | no | 1.452 | 0.712 | no | 1.502 | 0.668 | no | 0.947 | 0.130 | no | 1.162 | 0.454 | no | 1.029 | 0.255 | no | 1.067 | 0.647 | no | 0.942 | 0.213 | no | 0.940 | 0.092 | no |
| DR2376 | HTH transcription factor, | 0.760 | 0.184 | no | 0.708 | 0.199 | no | 0.685 | 0.249 | yes | 0.680 | 0.327 | yes | 0.648 | 0.277 | yes | 0.676 | 0.293 | yes | 0.663 | 0.330 | yes | 0.762 | 0.097 | no | 0.995 | 0.047 | no |
| DR2377 | Small proteins conserved proteins, distantly related to polyketide cyclases? | 1.131 | 0.420 | no | 3.113 | 1.412 | yes | 2.126 | 1.158 | yes | 2.369 | 1.598 | yes | 1.608 | 0.309 | yes | 1.230 | 0.811 | no | 1.655 | 0.491 | yes | 1.472 | 0.217 | no | 0.890 | 0.166 | no |
| DR2378 | Predicted protein | 1.119 | 0.551 | no | 0.639 | 0.332 | yes | 0.377 | 0.187 | yes | 0.490 | 0.210 | yes | 0.533 | 0.119 | yes | 0.522 | 0.164 | yes | 0.962 | 0.256 | no | 0.775 | 0.259 | no | 2.402 | 0.740 | yes |
| DR2379 | ABC transporter, with ATPase domain | 1.312 | 0.693 | no | 3.314 | 1.965 | yes | 2.290 | 1.108 | yes | 2.470 | 1.577 | yes | 1.942 | 0.900 | yes | 1.753 | 0.284 | yes | 2.010 | 1.344 | yes | 1.641 | 0.498 | yes | 1.177 | 0.312 | no |
| DR2380 | Uncharacterized conserved protein of PHD/YEFM family | 0.904 | 0.198 | no | 1.482 | 0.626 | yes | 1.151 | 0.463 | no | 1.194 | 0.708 | no | 1.104 | 0.350 | no | 1.290 | 0.457 | no | 1.196 | 0.413 | no | 1.263 | 0.325 | no | 1.226 | 0.348 | no |
| DR2381 | MaoC like aldehyde dehydrogenase, PaaZ | 0.666 | 0.213 | no | 1.631 | 0.996 | yes | 1.501 | 0.895 | no | 1.440 | 0.657 | no | 1.160 | 0.515 | no | 1.209 | 0.359 | no | 1.653 | 0.729 | yes | 1.459 | 0.437 | no | 1.394 | 0.634 | no |
| DR2382 | Predicted protein | 1.029 | 0.202 | no | 1.113 | 0.500 | no | 1.682 | 1.007 | yes | 1.703 | 0.770 | no | 1.463 | 0.589 | no | 1.037 | 0.470 | no | 0.777 | 0.261 | no | 0.879 | 0.270 | no | 1.065 | 0.400 | no |
| DR2383 | MinD N- terminal domain, PaaD ortholog | 1.566 | 0.459 | yes | 2.001 | 0.874 | yes | 3.104 | 1.779 | yes | 2.716 | 1.825 | yes | 2.184 | 1.308 | yes | 1.583 | 0.756 | no | 1.460 | 0.496 | no | 1.214 | 0.063 | no | 1.100 | 0.237 | no |
| DR2384 | Phenylacetic acid degradation protein PaaC | 1.023 | 0.484 | no | 1.855 | 0.632 | yes | 2.575 | 1.056 | yes | 2.477 | 0.411 | yes | 1.805 | 1.005 | yes | 1.388 | 0.358 | no | 1.261 | 0.615 | no | 0.995 | 0.183 | no | 0.819 | 0.153 | no |
| DR2385 | Phenylacetic acid degradation protein PaaB | 0.920 | 0.187 | no | 0.927 | 0.295 | no | 0.757 | 0.176 | no | 0.808 | 0.077 | no | 0.776 | 0.206 | no | 0.534 | 0.226 | yes | 0.562 | 0.157 | yes | 0.527 | 0.126 | yes | 0.581 | 0.190 | yes |
| DR2386 | MaoC like aldehyde dehydrogenase PaaA | 1.316 | 0.583 | no | 0.640 | 0.222 | yes | 0.515 | 0.063 | yes | 0.761 | 0.313 | no | 0.719 | 0.183 | no | 0.842 | 0.240 | no | 1.250 | 0.306 | no | 1.375 | 0.106 | no | 1.951 | 0.576 | yes |
| DR2387 | Uncharacterized, YGAG ortholog | 1.068 | 0.355 | no | 0.911 | 0.288 | no | 0.652 | 0.302 | yes | 0.596 | 0.263 | yes | 0.683 | 0.318 | yes | 1.027 | 0.690 | no | 0.836 | 0.282 | no | 0.960 | 0.090 | no | 0.839 | 0.428 | no |
| DR2388 | Lipoprotein signal peptidase, SPASE II | 1.313 | 0.702 | no | 0.610 | 0.253 | yes | 0.362 | 0.141 | yes | 0.424 | 0.248 | yes | 0.430 | 0.168 | yes | 0.771 | 0.386 | no | 1.030 | 0.290 | no | 1.200 | 0.280 | no | 1.294 | 0.544 | no |
| DR2389 | Small conserved membrane protein | 0.878 | 0.166 | no | 0.485 | 0.167 | yes | 0.250 | 0.057 | yes | 0.249 | 0.095 | yes | 0.340 | 0.111 | yes | 0.626 | 0.127 | yes | 0.664 | 0.238 | yes | 0.769 | 0.230 | no | 0.572 | 0.084 | yes |
| DR2390 | Homoserine kinase | 1.227 | 0.543 | no | 0.840 | 0.561 | no | 0.535 | 0.229 | yes | 0.688 | 0.364 | yes | 0.754 | 0.224 | no | 0.930 | 0.195 | no | 1.089 | 0.348 | no | 1.013 | 0.125 | no | 0.727 | 0.086 | no |
| DR2391 | Von-willebrand-factor A domain containing protein, Mg-binding | 1.313 | 0.520 | no | 1.447 | 0.352 | yes | 1.368 | 0.169 | no | 1.103 | 0.145 | no | 1.218 | 0.472 | no | 1.293 | 0.621 | no | 1.137 | 0.395 | no | 0.892 | 0.071 | no | 0.872 | 0.349 | no |
| DR2392 | S-layer protein, DR-2 | 1.448 | 0.493 | no | 1.951 | 0.717 | yes | 1.436 | 0.395 | no | 1.411 | 0.579 | no | 0.920 | 0.342 | no | 0.933 | 0.231 | no | 1.041 | 0.391 | no | 0.967 | 0.072 | no | 0.814 | 0.253 | no |
| DR2393 | Conserved membrane protein | 1.445 | 0.524 | no | 1.466 | 0.206 | yes | 1.171 | 0.312 | no | 1.200 | 0.537 | no | 1.103 | 0.589 | no | 1.151 | 0.141 | no | 1.050 | 0.248 | no | 0.968 | 0.323 | no | 0.791 | 0.058 | no |
| DR2394 | N-acetylmuramoyl-L-alanine amidase | 1.258 | 0.427 | no | 1.641 | 0.596 | yes | 1.323 | 0.490 | no | 1.390 | 0.277 | no | 1.281 | 0.633 | no | 0.941 | 0.272 | no | 1.054 | 0.284 | no | 1.116 | 0.277 | no | 0.994 | 0.381 | no |
| DR2395 | Na+/H+ antiporter | 1.013 | 0.369 | no | 0.915 | 0.189 | no | 0.716 | 0.293 | yes | 0.636 | 0.124 | yes | 0.728 | 0.404 | yes | 0.874 | 0.267 | no | 0.685 | 0.192 | yes | 0.896 | 0.129 | no | 1.012 | 0.151 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR2396 | HTH transcription factor | 1.438 | 0.290 | no | 1.240 | 0.196 | no | 1.015 | 0.285 | no | 0.782 | 0.125 | no | 0.806 | 0.179 | no | 0.975 | 0.298 | no | 1.110 | 0.288 | no | 1.015 | 0.147 | no | 1.296 | 0.577 | no |
| DR2397 | SurE ortholog, acid phosphatase | 0.872 | 0.417 | no | 0.786 | 0.434 | no | 0.580 | 0.354 | yes | 1.282 | 0.110 | no | 0.943 | 0.479 | no | 0.909 | 0.480 | no | 1.169 | 0.747 | no | 1.195 | 0.335 | no | 0.888 | 0.390 | no |
| DR2398 | Uncharacterized domain homolog of MTH413 | 0.911 | 0.260 | no | 1.627 | 0.926 | yes | 1.492 | 0.683 | no | 1.611 | 0.880 | no | 1.387 | 0.928 | no | 1.041 | 0.279 | no | 1.115 | 0.667 | no | 1.073 | 0.183 | no | 0.977 | 0.271 | no |
| DR2399 | Magnesium and cobalt transport protein | 0.879 | 0.255 | no | 1.077 | 0.383 | no | 1.060 | 0.232 | no | 0.955 | 0.158 | no | 0.954 | 0.414 | no | 1.553 | 0.810 | no | 1.263 | 0.354 | no | 1.283 | 0.202 | no | 1.116 | 0.188 | no |
| DR2400 | YBDF ortholog (small bacterial proteins) | 1.427 | 0.907 | no | 1.195 | 0.694 | no | 1.354 | 0.863 | no | 1.676 | 1.038 | no | 1.249 | 0.973 | no | 0.901 | 0.167 | no | 1.045 | 0.446 | no | 0.882 | 0.147 | no | 0.820 | 0.078 | no |
| DR2401 | Predicted protein | 1.061 | 0.484 | no | 0.757 | 0.405 | no | 1.319 | 0.769 | no | 1.360 | 0.915 | no | 1.602 | 1.011 | no | 1.524 | 0.863 | no | 1.590 | 0.721 | yes | 1.449 | 0.404 | no | 4.503 | 2.270 | yes |
| DR2402 | Predicted protein | 1.041 | 0.387 | no | 1.366 | 0.233 | no | 1.059 | 0.320 | no | 1.049 | 0.096 | no | 0.745 | 0.311 | no | 0.743 | 0.090 | no | 0.872 | 0.253 | no | 0.924 | 0.178 | no | 0.899 | 0.283 | no |
| DR2403 | Predicted protein | 1.283 | 0.429 | no | 0.909 | 0.307 | no | 1.057 | 0.311 | no | 0.942 | 0.237 | no | 0.878 | 0.241 | no | 0.716 | 0.128 | no | 0.943 | 0.519 | no | 0.885 | 0.229 | no | 1.028 | 0.143 | no |
| DR2404 | ABC ATPase, large peptide transporter | 1.231 | 0.537 | no | 0.510 | 0.158 | yes | 0.399 | 0.106 | yes | 0.556 | 0.078 | yes | 0.504 | 0.221 | yes | 0.406 | 0.252 | yes | 0.425 | 0.134 | yes | 0.416 | 0.189 | yes | 0.999 | 0.274 | no |
| DR2405 | Ubiquinone methyltransferase | 0.788 | 0.395 | no | 1.453 | 0.431 | yes | 1.433 | 0.526 | no | 1.578 | 0.852 | no | 1.209 | 0.496 | no | 1.167 | 0.373 | no | 1.055 | 0.169 | no | 2.351 | 0.842 | yes | 0.896 | 0.342 | no |
| DR2406 | HGG containing thioesterase superfamily | 0.964 | 0.172 | no | 0.748 | 0.411 | yes | 1.155 | 0.476 | no | 2.283 | 0.159 | yes | 2.132 | 1.048 | yes | 3.170 | 1.697 | yes | 6.737 | 2.433 | yes | 4.032 | 1.723 | yes | 3.643 | 1.516 | yes |
| DR2407 | Conserved membrane protein, uncharacterized | 0.841 | 0.284 | no | 0.573 | 0.179 | yes | 0.583 | 0.184 | yes | 0.528 | 0.108 | yes | 0.748 | 0.148 | no | 0.713 | 0.175 | no | 1.105 | 0.173 | no | 0.859 | 0.332 | no | 0.843 | 0.164 | no |
| DR2408 | CobW family P- loop GTPase | 0.859 | 0.243 | no | 0.408 | 0.110 | yes | 0.487 | 0.182 | yes | 0.794 | 0.240 | no | 0.681 | 0.299 | yes | 0.535 | 0.267 | yes | 0.703 | 0.272 | yes | 0.687 | 0.248 | yes | 0.812 | 0.243 | no |
| DR2409 | McrA family nuclease | 0.942 | 0.345 | no | 0.574 | 0.188 | yes | 0.339 | 0.096 | yes | 0.210 | 0.048 | yes | 0.217 | 0.066 | yes | 0.177 | 0.033 | yes | 0.152 | 0.089 | yes | 0.225 | 0.099 | yes | 1.057 | 0.487 | no |
| DR2410 | DNA polymerase III gamma and tau subunit, active AAA superfamily ATPase | 1.083 | 0.172 | no | 0.637 | 0.186 | yes | 0.605 | 0.137 | yes | 0.435 | 0.069 | yes | 0.383 | 0.159 | yes | 0.291 | 0.139 | yes | 0.372 | 0.200 | yes | 0.502 | 0.116 | yes | 1.441 | 0.589 | no |
| DR2411 | Predicted protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR2412 | Possible glucosyl hydrolase | 0.928 | 0.150 | no | 0.486 | 0.169 | yes | 0.393 | 0.121 | yes | 0.295 | 0.031 | yes | 0.251 | 0.090 | yes | 0.233 | 0.144 | yes | 0.172 | 0.075 | yes | 0.261 | 0.111 | yes | 1.077 | 0.372 | no |
| DR2413 | Similar to ChrA chromate transport protein | 1.145 | 0.697 | no | 0.811 | 0.432 | no | 0.803 | 0.363 | no | 0.732 | 0.378 | no | 0.612 | 0.472 | yes | 0.448 | 0.260 | yes | 0.333 | 0.139 | yes | 0.500 | 0.190 | yes | 1.318 | 0.632 | no |
| DR2414 | Predicted protein | 0.960 | 0.076 | no | 0.915 | 0.188 | no | 1.072 | 0.354 | no | 0.946 | 0.185 | no | 0.755 | 0.138 | no | 0.833 | 0.111 | no | 0.868 | 0.447 | no | 0.859 | 0.233 | no | 1.280 | 0.148 | no |
| DR2415 | Receiver domain, CHEY family + HTH domain | 1.138 | 0.370 | no | 1.091 | 0.287 | no | 1.703 | 0.577 | yes | 1.436 | 0.512 | no | 1.722 | 1.262 | no | 1.077 | 0.300 | no | 0.961 | 0.382 | no | 0.885 | 0.320 | no | 0.985 | 0.391 | no |
| DR2416 | Sensor Histidine kinase | 1.038 | 0.133 | no | 1.582 | 0.322 | yes | 5.752 | 1.328 | yes | 4.980 | 0.017 | yes | 5.343 | 1.479 | yes | 4.798 | 0.530 | yes | 4.134 | 1.081 | yes | 3.474 | 0.824 | yes | 1.898 | 0.632 | yes |
| DR2418 | Response regulator CHEY domain + HTH domain | 0.622 | 0.253 | yes | 1.236 | 0.575 | no | 1.425 | 0.665 | no | 1.181 | 0.498 | no | 1.254 | 0.428 | no | 1.197 | 0.419 | no | 1.420 | 0.391 | no | 1.488 | 0.432 | yes | 2.019 | 0.410 | yes |
| DR2419 | Histidine kinase + 3 PAS domain + 2 PAC | 1.106 | 0.162 | no | 0.810 | 0.174 | no | 0.693 | 0.166 | yes | 0.901 | 0.272 | no | 0.793 | 0.179 | no | 0.915 | 0.078 | no | 1.029 | 0.162 | no | 0.938 | 0.165 | no | 0.881 | 0.061 | no |
| DR2420 | Receiver domain (CheY family) of 2 component system | 0.725 | 0.331 | no | 0.820 | 0.213 | no | 1.022 | 0.277 | no | 1.396 | 0.517 | no | 1.223 | 0.691 | no | 0.882 | 0.425 | no | 0.711 | 0.273 | yes | 0.727 | 0.192 | yes | 0.620 | 0.093 | yes |
| DR2421 | HD superfamily hydrolase | 1.017 | 0.129 | no | 1.169 | 0.381 | no | 1.983 | 0.508 | yes | 2.714 | 1.063 | yes | 2.179 | 0.904 | yes | 1.648 | 0.332 | yes | 1.357 | 0.434 | no | 1.266 | 0.260 | no | 1.059 | 0.355 | no |
| DR2422 | Large conductance mechanosensitive channel protein, MSCL | 2.353 | 1.645 | yes | 1.931 | 0.279 | yes | 2.087 | 1.478 | yes | 1.348 | 0.273 | no | 1.669 | 0.770 | yes | 2.253 | 1.625 | yes | 1.525 | 0.453 | yes | 1.324 | 0.614 | no | 0.978 | 0.308 | no |
| DR2423 | Metal dependent carboxypeptidase | 0.793 | 0.205 | no | 0.503 | 0.224 | yes | 0.537 | 0.171 | yes | 0.527 | 0.018 | yes | 0.860 | 0.355 | no | 0.962 | 0.158 | no | 1.148 | 0.427 | no | 1.371 | 0.046 | no | 1.402 | 0.135 | no |
| DR2425 | Transposon ORF | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR2427 | Shares a domain with YjiI | 1.024 | 0.334 | no | 0.752 | 0.203 | no | 0.852 | 0.417 | no | 1.074 | 0.316 | no | 1.185 | 0.642 | no | 1.098 | 0.441 | no | 0.908 | 0.276 | no | 1.162 | 0.407 | no | 0.831 | 0.257 | no |
| DR2428 | N-terminal TagD like nucleotidyl transferase domain with C-terminal MutT like hydrolase domain | 1.284 | 0.553 | no | 0.599 | 0.118 | yes | 0.671 | 0.118 | yes | 0.952 | 0.202 | no | 0.872 | 0.317 | no | 0.776 | 0.211 | no | 0.869 | 0.206 | no | 0.934 | 0.212 | no | 0.830 | 0.323 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR2429 | Predicted protein | 0.950 | 0.472 | no | 0.543 | 0.284 | yes | 1.032 | 0.563 | no | 2.100 | 0.745 | yes | 2.598 | 1.484 | yes | 1.436 | 0.649 | no | 1.646 | 0.968 | no | 1.469 | 0.480 | no | 2.138 | 0.631 | yes |
| DR2430 | Conserved membrane protein | 1.268 | 0.654 | no | 1.039 | 0.615 | no | 1.020 | 0.710 | no | 1.705 | 1.224 | no | 1.468 | 0.950 | no | 1.059 | 0.235 | no | 1.073 | 0.609 | no | 0.908 | 0.196 | no | 0.957 | 0.194 | no |
| DR2431 | Possible membrane protein, homolog YJGP family | 1.199 | 0.427 | no | 0.794 | 0.518 | no | 0.693 | 0.159 | yes | 0.734 | 0.029 | no | 0.829 | 0.208 | no | 0.789 | 0.149 | no | 0.671 | 0.086 | yes | 0.783 | 0.120 | no | 0.772 | 0.146 | no |
| DR2432 | NH2- acetyltransferase | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR2433 | Protein of nitrilase/amidohydrolase family | 1.200 | 0.460 | no | 1.650 | 0.659 | yes | 1.827 | 0.642 | yes | 2.270 | 1.361 | yes | 1.806 | 0.531 | yes | 1.323 | 0.551 | no | 1.637 | 0.580 | yes | 1.507 | 0.272 | yes | 1.238 | 0.147 | no |
| DR2434 | Peptide Deformylase | 0.976 | 0.246 | no | 0.639 | 0.078 | yes | 0.427 | 0.084 | yes | 0.421 | 0.114 | yes | 0.721 | 0.215 | no | 1.113 | 0.264 | no | 1.444 | 0.298 | no | 1.320 | 0.521 | no | 0.960 | 0.245 | no |
| DR2435 | Methionyl-tRNA formyltransferase | 1.111 | 0.704 | no | 0.729 | 0.438 | yes | 0.727 | 0.427 | yes | 1.206 | 0.642 | no | 1.258 | 0.413 | no | 1.400 | 0.434 | no | 2.187 | 0.858 | yes | 1.727 | 0.526 | yes | 1.413 | 0.399 | no |
| DR2436 | Predicted protein | 0.524 | 0.210 | yes | 0.374 | 0.129 | yes | 0.442 | 0.095 | yes | 0.631 | 0.199 | yes | 0.974 | 0.343 | no | 0.819 | 0.209 | no | 1.016 | 0.338 | no | 1.009 | 0.330 | no | 1.134 | 0.406 | no |
| DR2437 | Membrane protein, YDED/PecM-like | 1.245 | 0.423 | no | 0.882 | 0.333 | no | 1.010 | 0.588 | no | 1.482 | 0.558 | no | 1.859 | 0.421 | yes | 1.227 | 0.842 | no | 1.200 | 0.345 | no | 1.436 | 0.356 | no | 1.673 | 0.324 | yes |
| DR2438 | Endonuclease III, alpha helical glycosidase superfamily | 1.027 | 0.206 | no | 0.458 | 0.099 | yes | 0.517 | 0.245 | yes | 0.358 | 0.115 | yes | 0.589 | 0.309 | yes | 0.515 | 0.224 | yes | 0.469 | 0.222 | yes | 0.500 | 0.179 | yes | 0.854 | 0.265 | no |
| DR2439 | Yfit/DinB family protein | 1.077 | 0.303 | no | 1.024 | 0.612 | no | 1.009 | 0.555 | no | 0.924 | 0.415 | no | 0.966 | 0.433 | no | 1.093 | 0.782 | no | 0.788 | 0.329 | no | 0.679 | 0.091 | yes | 1.222 | 0.683 | no |
| DR2440 | YohI/YHDG family of TIM barrel dinucleotide binding enzymes | 0.932 | 0.103 | no | 0.761 | 0.244 | no | 0.883 | 0.270 | no | 1.044 | 0.079 | no | 0.937 | 0.348 | no | 0.929 | 0.231 | no | 0.642 | 0.170 | yes | 0.771 | 0.206 | no | 0.931 | 0.090 | no |
| DR2441 | NH2-acetyltransferase | 0.845 | 0.183 | no | 1.694 | 0.695 | yes | 1.942 | 0.681 | yes | 2.651 | 0.727 | yes | 2.344 | 1.206 | yes | 2.564 | 1.013 | yes | 1.872 | 0.579 | yes | 1.368 | 0.497 | no | 1.506 | 0.530 | yes |
| DR2442 | N-acetylglutamate kinase, ArgB | 0.782 | 0.313 | no | 0.622 | 0.124 | yes | 0.575 | 0.101 | yes | 0.466 | 0.047 | yes | 0.562 | 0.162 | yes | 0.583 | 0.128 | yes | 0.551 | 0.194 | yes | 0.574 | 0.115 | yes | 0.673 | 0.168 | no |
| DR2443 | NH2-acetyltransferase | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR2444 | CysA like N-term. domain? + HRD domain protein | 0.875 | 0.233 | no | 2.429 | 0.272 | yes | 1.447 | 0.316 | yes | 1.454 | 0.425 | no | 1.419 | 0.444 | no | 1.407 | 0.333 | no | 1.521 | 0.385 | yes | 1.214 | 0.415 | no | 0.958 | 0.256 | no |
| DR2445 | Predicted protein | 0.764 | 0.190 | no | 0.475 | 0.098 | yes | 0.416 | 0.117 | yes | 0.311 | 0.074 | yes | 0.410 | 0.138 | yes | 0.518 | 0.158 | yes | 0.563 | 0.153 | yes | 0.611 | 0.084 | yes | 0.591 | 0.170 | yes |
| DR2446 | Predicted protein | 1.412 | 0.412 | no | 1.417 | 0.791 | no | 1.232 | 0.638 | no | 1.100 | 0.404 | no | 0.990 | 0.394 | no | 1.219 | 0.650 | no | 1.198 | 0.326 | no | 1.281 | 0.419 | no | 1.193 | 0.312 | no |
| DR2447 | Undecaprenyl pyrophosphate synthase | 0.722 | 0.198 | no | 0.691 | 0.120 | no | 0.833 | 0.241 | no | 0.819 | 0.098 | no | 1.014 | 0.326 | no | 1.490 | 0.549 | no | 1.186 | 0.404 | no | 1.236 | 0.391 | no | 0.780 | 0.244 | no |
| DR2448 | HTH transcription factor, MerR family | 1.157 | 0.233 | no | 0.988 | 0.221 | no | 1.405 | 0.293 | no | 1.480 | 0.171 | no | 1.803 | 0.682 | yes | 1.986 | 0.304 | yes | 2.339 | 0.624 | yes | 1.992 | 0.818 | yes | 1.661 | 0.640 | yes |
| DR2449 | Small conserved bacterial proteins, YOHL_ECOLI | 0.849 | 0.200 | no | 0.911 | 0.245 | no | 1.234 | 0.191 | no | 1.340 | 0.238 | no | 1.192 | 0.091 | no | 1.374 | 0.471 | no | 1.040 | 0.186 | no | 0.906 | 0.166 | no | 0.630 | 0.070 | yes |
| DR2450 | Predicted protein | 1.476 | 0.846 | no | 1.681 | 0.556 | yes | 0.694 | 0.285 | yes | 0.503 | 0.159 | yes | 0.659 | 0.228 | yes | 0.641 | 0.314 | yes | 0.664 | 0.244 | yes | 0.763 | 0.368 | yes | 0.687 | 0.226 | no |
| DR2451 | Uncharacterized conserved protein containing duplicated domain with conserved HH motif | 1.031 | 0.482 | no | 1.024 | 0.434 | no | 1.222 | 0.533 | no | 0.852 | 0.244 | no | 1.355 | 0.577 | no | 1.754 | 0.516 | yes | 1.438 | 0.830 | no | 1.018 | 0.275 | no | 0.965 | 0.392 | no |
| DR2452 | Metal-binding subunit of ATPase metal efflux | 0.958 | 0.255 | no | 0.677 | 0.157 | yes | 0.426 | 0.079 | yes | 0.319 | 0.046 | yes | 0.357 | 0.154 | yes | 0.514 | 0.185 | yes | 0.712 | 0.297 | yes | 0.657 | 0.055 | yes | 0.927 | 0.104 | no |
| DR2453 | P-type ATPase metal efflux | 1.209 | 0.472 | no | 1.532 | 0.400 | yes | 1.269 | 0.394 | no | 1.618 | 0.460 | no | 0.985 | 0.435 | no | 0.744 | 0.300 | no | 0.827 | 0.276 | no | 0.954 | 0.181 | no | 1.345 | 0.385 | no |
| DR2454 | HTH transcriptional regulator | 1.132 | 0.591 | no | 2.111 | 0.840 | yes | 2.635 | 1.267 | yes | 1.537 | 0.526 | no | 1.614 | 0.493 | yes | 1.289 | 0.599 | no | 1.298 | 0.531 | no | 0.926 | 0.284 | no | 0.798 | 0.395 | no |
| DR2455 | Membrane protein | 1.394 | 0.300 | no | 2.542 | 0.633 | yes | 2.262 | 0.604 | yes | 2.134 | 0.257 | yes | 1.837 | 0.363 | yes | 1.859 | 1.238 | yes | 1.920 | 1.362 | yes | 0.961 | 0.290 | no | 0.784 | 0.227 | no |
| DR2456 | Predicted protein | 1.143 | 0.491 | no | 1.717 | 0.552 | yes | 2.310 | 0.460 | yes | 2.087 | 0.110 | yes | 1.579 | 0.541 | yes | 1.445 | 0.422 | no | 2.006 | 0.672 | yes | 0.972 | 0.213 | no | 1.026 | 0.660 | no |
| DR2457 | Predicted protein | 1.082 | 0.712 | no | 1.484 | 0.463 | yes | 1.864 | 0.748 | yes | 1.468 | 0.081 | no | 1.916 | 0.701 | yes | 1.640 | 0.332 | yes | 2.170 | 0.772 | yes | 1.785 | 0.560 | yes | 0.842 | 0.267 | no |
| DR2458 | Predicted protein | 0.924 | 0.190 | no | 1.867 | 0.443 | yes | 1.512 | 0.631 | yes | 1.396 | 0.054 | no | 1.232 | 0.260 | no | 1.264 | 0.324 | no | 1.577 | 0.225 | yes | 1.390 | 0.524 | no | 0.965 | 0.182 | no |
| DR2459 | NADH-dependent FMN oxidoreductase | 0.908 | 0.303 | no | 0.785 | 0.230 | no | 0.805 | 0.175 | no | 0.859 | 0.110 | no | 0.948 | 0.248 | no | 0.992 | 0.244 | no | 1.372 | 0.303 | no | 1.334 | 0.122 | no | 1.225 | 0.224 | no |
| DR2460 | Zinc finger like structure | 0.818 | 0.283 | no | 0.932 | 0.294 | no | 0.749 | 0.446 | yes | 0.661 | 0.075 | no | 0.689 | 0.172 | no | 0.863 | 0.105 | no | 1.022 | 0.349 | no | 0.885 | 0.147 | no | 0.756 | 0.244 | no |
| DR2461 | Histidinol phosphate aminotransferase | 1.054 | 0.362 | no | 0.915 | 0.360 | no | 0.975 | 0.230 | no | 1.244 | 0.447 | no | 1.152 | 0.411 | no | 1.109 | 0.328 | no | 1.278 | 0.337 | no | 1.102 | 0.325 | no | 1.611 | 0.471 | yes |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR2462 | HD superfamily hydrolase | 1.076 | 0.374 | no | 0.992 | 0.296 | no | 0.948 | 0.352 | no | 0.976 | 0.253 | no | 0.991 | 0.365 | no | 1.162 | 0.285 | no | 1.281 | 0.454 | no | 1.218 | 0.070 | no | 1.289 | 0.193 | no |
| DR2463 | Mg2+ or Co2+ transporter | 0.992 | 0.300 | no | 0.456 | 0.199 | yes | 0.440 | 0.150 | yes | 0.575 | 0.091 | yes | 0.583 | 0.151 | yes | 0.574 | 0.227 | yes | 0.594 | 0.257 | yes | 0.703 | 0.317 | yes | 1.547 | 0.429 | yes |
| DR2464 | FKBP, peptidyl prolyl isomerase, SLYD | 0.942 | 0.445 | no | 0.537 | 0.243 | yes | 0.624 | 0.277 | yes | 0.672 | 0.230 | no | 0.938 | 0.408 | no | 0.831 | 0.248 | no | 1.104 | 0.310 | no | 1.167 | 0.179 | no | 2.542 | 0.225 | yes |
| DR2465 | Aminotransferase | 0.966 | 0.285 | no | 0.879 | 0.242 | no | 1.019 | 0.293 | no | 1.224 | 0.418 | no | 1.269 | 0.505 | no | 1.365 | 0.379 | no | 1.212 | 0.395 | no | 1.358 | 0.405 | no | 1.156 | 0.082 | no |
| DR2466 | YBGI-like family protein | 1.191 | 0.661 | no | 1.568 | 0.969 | yes | 1.943 | 0.581 | yes | 1.447 | 0.389 | no | 1.524 | 0.765 | no | 1.847 | 0.715 | yes | 1.476 | 0.493 | no | 1.367 | 0.247 | no | 0.827 | 0.208 | no |
| DR2467 | P-loop ATpase of adenylate kinase family | 1.225 | 0.371 | no | 1.399 | 0.340 | no | 1.714 | 0.424 | yes | 2.118 | 1.029 | yes | 1.983 | 0.851 | yes | 2.035 | 0.677 | yes | 2.078 | 0.396 | yes | 1.870 | 0.250 | yes | 1.466 | 0.201 | yes |
| DR2468 | Conserved membrane protein | 1.086 | 0.206 | no | 1.411 | 0.406 | no | 1.520 | 0.468 | yes | 1.418 | 0.210 | no | 1.616 | 0.675 | yes | 1.342 | 0.194 | no | 1.107 | 0.127 | no | 1.321 | 0.403 | no | 0.769 | 0.156 | no |
| DR2469 | ABC ATPase, transporter of cobalt | 0.965 | 0.358 | no | 1.606 | 0.674 | yes | 2.297 | 0.682 | yes | 1.473 | 0.338 | no | 2.086 | 0.995 | yes | 1.557 | 0.584 | no | 1.379 | 0.486 | no | 1.080 | 0.243 | no | 0.760 | 0.068 | no |
| DR2470 | Conserved membrane protein, related to biothin biosysnthesis protein BioY | 1.004 | 0.295 | no | 1.233 | 0.542 | no | 1.846 | 1.075 | yes | 1.193 | 0.432 | no | 1.274 | 0.375 | no | 1.850 | 1.127 | yes | 1.545 | 0.963 | no | 1.492 | 0.541 | no | 0.992 | 0.320 | no |
| DR2471 | Acetyl-coA synthetase | 0.879 | 0.192 | no | 1.454 | 0.228 | yes | 1.881 | 0.471 | yes | 1.437 | 0.438 | no | 1.385 | 0.593 | no | 1.429 | 0.587 | no | 1.163 | 0.317 | no | 1.012 | 0.224 | no | 0.574 | 0.173 | yes |
| DR2472 | Distantly related to N-term. domain of CarD transcription factor | 0.759 | 0.273 | no | 1.226 | 0.546 | no | 1.493 | 0.427 | yes | 1.047 | 0.749 | no | 1.041 | 0.506 | no | 1.200 | 0.414 | no | 1.184 | 0.600 | no | 0.806 | 0.273 | no | 0.545 | 0.236 | yes |
| DR2473 | Cytochrome P450 domain | 1.108 | 0.286 | no | 0.910 | 0.290 | no | 0.671 | 0.214 | yes | 1.095 | 0.485 | no | 0.934 | 0.259 | no | 1.091 | 0.392 | no | 1.010 | 0.208 | no | 1.032 | 0.196 | no | 1.432 | 0.115 | yes |
| DR2474 | Degenerate a/b hydrolase | 1.034 | 0.179 | no | 0.655 | 0.124 | yes | 0.608 | 0.090 | yes | 0.596 | 0.109 | yes | 0.629 | 0.169 | yes | 0.855 | 0.087 | no | 1.136 | 0.543 | no | 1.156 | 0.241 | no | 1.535 | 0.410 | yes |
| DR2475 | Possible FS, C-terminal fragment of previous protein or similar domain | 1.117 | 0.182 | no | 0.632 | 0.152 | yes | 0.561 | 0.152 | yes | 0.649 | 0.077 | no | 0.732 | 0.284 | no | 0.833 | 0.245 | no | 0.650 | 0.186 | yes | 0.944 | 0.136 | no | 1.663 | 0.169 | yes |
| DR2476 | Membrane protein. | 1.092 | 0.302 | no | 0.636 | 0.179 | yes | 0.649 | 0.121 | yes | 0.640 | 0.133 | yes | 0.877 | 0.369 | no | 1.139 | 0.374 | no | 1.183 | 0.446 | no | 1.446 | 0.436 | no | 1.540 | 0.445 | yes |
| DR2478 | a/b hydrolase | 1.170 | 0.298 | no | 1.349 | 0.197 | no | 2.275 | 0.657 | yes | 3.206 | 0.456 | yes | 3.560 | 0.947 | yes | 3.906 | 1.085 | yes | 3.199 | 1.282 | yes | 3.225 | 0.921 | yes | 2.423 | 0.276 | yes |
| DR2479 | Predicted protein | 1.156 | 0.436 | no | 1.782 | 1.012 | yes | 2.235 | 1.134 | yes | 4.652 | 1.708 | yes | 4.293 | 1.412 | yes | 3.803 | 1.878 | yes | 2.875 | 1.423 | yes | 2.205 | 0.515 | yes | 2.229 | 0.964 | yes |
| DR2480 | Acetyl-CoA C-acetyltransferase | 1.082 | 0.399 | no | 1.213 | 0.490 | no | 2.091 | 0.642 | yes | 3.222 | 0.676 | yes | 3.176 | 0.931 | yes | 3.450 | 1.413 | yes | 2.865 | 1.989 | yes | 2.519 | 0.862 | yes | 1.843 | 0.279 | yes |
| DR2481 | Predicted protein | 1.006 | 0.199 | no | 2.576 | 0.686 | yes | 4.662 | 1.266 | yes | 4.481 | 0.744 | yes | 3.837 | 1.629 | yes | 2.249 | 0.391 | yes | 1.897 | 0.687 | yes | 1.466 | 0.250 | yes | 1.072 | 0.364 | no |
| DR2482 | contains fragment similar to HTH transcription factor Sigma factor | 1.340 | 0.449 | no | 2.822 | 1.290 | yes | 5.751 | 2.924 | yes | 4.994 | 1.456 | yes | 3.755 | 2.060 | yes | 2.644 | 0.855 | yes | 2.000 | 0.718 | yes | 1.434 | 0.354 | no | 0.726 | 0.236 | no |
| DR2483 | McrA nuclease | 0.985 | 0.242 | no | 2.871 | 1.033 | yes | 5.431 | 1.222 | yes | 4.215 | 0.741 | yes | 3.737 | 1.328 | yes | 2.426 | 0.418 | yes | 1.888 | 0.348 | yes | 1.397 | 0.393 | no | 0.985 | 0.424 | no |
| DR2484 | WD40 repeat protein | 1.107 | 0.667 | no | 2.736 | 1.565 | yes | 5.124 | 2.531 | yes | 3.227 | 0.039 | yes | 3.231 | 1.693 | yes | 2.072 | 0.801 | yes | 1.609 | 0.995 | no | 1.145 | 0.233 | no | 0.738 | 0.082 | no |
| DR2485 | Predicted protein | 3.871 | 1.328 | yes | 1.100 | 0.645 | no | 2.187 | 1.184 | yes | 1.244 | 0.309 | no | 1.064 | 0.633 | no | 2.913 | 2.167 | yes | 0.801 | 0.601 | yes | 0.286 | 0.032 | yes | 0.543 | 0.113 | yes |
| DR2486 | Membrane or secreted protein | 1.335 | 0.511 | no | 1.474 | 0.816 | no | 1.263 | 0.513 | no | 1.423 | 0.677 | no | 1.216 | 0.431 | no | 1.141 | 0.452 | no | 1.226 | 0.478 | no | 1.056 | 0.124 | no | 1.069 | 0.199 | no |
| DR2487 | Cytochrome C4, CYC4 | 1.092 | 0.652 | no | 0.555 | 0.321 | yes | 0.585 | 0.327 | yes | 0.995 | 0.149 | no | 0.686 | 0.364 | yes | 0.741 | 0.414 | yes | 0.911 | 0.414 | no | 1.254 | 0.408 | no | 0.804 | 0.340 | no |
| DR2488 | Membrane protein, transporter, YABK_ECOLI | 1.157 | 0.282 | no | 1.021 | 0.302 | no | 0.987 | 0.272 | no | 1.115 | 0.393 | no | 1.058 | 0.320 | no | 1.016 | 0.336 | no | 1.117 | 0.407 | no | 0.997 | 0.241 | no | 1.295 | 0.210 | no |
| DR2489 | Check for ankyrin repeats | 0.875 | 0.205 | no | 0.653 | 0.107 | yes | 0.510 | 0.145 | yes | 0.466 | 0.071 | yes | 0.557 | 0.115 | yes | 0.800 | 0.039 | no | 0.960 | 0.372 | no | 0.947 | 0.176 | no | 1.156 | 0.285 | no |
| DR2490 | Zn-dependent hydrolase | 1.103 | 0.381 | no | 0.912 | 0.469 | no | 0.628 | 0.202 | yes | 0.902 | 0.287 | no | 0.806 | 0.200 | no | 0.900 | 0.259 | no | 0.880 | 0.270 | no | 1.018 | 0.170 | no | 1.211 | 0.110 | no |
| DR2491 | Predicted protein | 1.095 | 0.369 | no | 1.034 | 0.105 | no | 1.013 | 0.192 | no | 1.138 | 0.135 | no | 1.291 | 0.327 | no | 1.106 | 0.152 | no | 1.489 | 0.271 | yes | 1.279 | 0.286 | no | 1.213 | 0.169 | no |
| DR2493 | Aminoacylase/desuccinylase/peptidase family protein | 0.925 | 0.334 | no | 0.624 | 0.259 | yes | 0.418 | 0.125 | yes | 0.376 | 0.128 | yes | 0.434 | 0.155 | yes | 0.673 | 0.231 | yes | 0.681 | 0.346 | yes | 0.796 | 0.130 | no | 0.848 | 0.174 | no |
| DR2494 | RpoZ-like protein, RNA polymerase omega subunit | 1.207 | 0.265 | no | 1.005 | 0.410 | no | 0.902 | 0.300 | no | 0.930 | 0.215 | no | 0.661 | 0.229 | yes | 0.515 | 0.247 | yes | 0.539 | 0.207 | yes | 0.637 | 0.194 | yes | 0.891 | 0.160 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR2495 | Phosphorybosilformimino-5-amino-phosphorybosil-4-imidazolecarboxamideisomerase | 0.647 | 0.324 | yes | 2.659 | 0.537 | yes | 4.126 | 1.918 | yes | 2.134 | 1.190 | yes | 2.372 | 1.186 | yes | 2.188 | 1.081 | yes | 1.482 | 0.758 | no | 1.230 | 0.372 | no | 0.663 | 0.241 | yes |
| DR2496 | UDP-N-acetylmuramoylalanine-D-glutamate ligase, murD | 1.046 | 0.378 | no | 1.867 | 0.562 | yes | 2.266 | 0.975 | yes | 1.020 | 0.141 | no | 1.664 | 1.030 | no | 1.547 | 0.987 | no | 0.866 | 0.391 | no | 0.920 | 0.102 | no | 0.668 | 0.168 | no |
| DR2497 | RodA, RodA/FTSW family protein | 0.946 | 0.126 | no | 1.612 | 0.224 | yes | 2.000 | 0.625 | yes | 1.437 | 0.166 | no | 1.467 | 0.403 | no | 1.336 | 0.258 | no | 1.202 | 0.375 | no | 1.222 | 0.149 | no | 0.982 | 0.173 | no |
| DR2498 | GGDEF domain signaling protein, fussion with transmembrane region | 0.921 | 0.347 | no | 0.902 | 0.469 | no | 0.937 | 0.315 | no | 0.941 | 0.519 | no | 0.760 | 0.360 | no | 0.784 | 0.516 | no | 0.654 | 0.286 | yes | 0.712 | 0.176 | yes | 0.447 | 0.151 | yes |
| DR2499 | Nucleoside Diphosphate Kinase | 0.741 | 0.093 | no | 0.521 | 0.088 | yes | 0.618 | 0.139 | yes | 0.625 | 0.320 | yes | 0.742 | 0.158 | no | 0.941 | 0.351 | no | 0.785 | 0.184 | no | 0.891 | 0.109 | no | 1.624 | 0.492 | yes |
| DR2500 | Predicted protein | 0.911 | 0.408 | no | 0.875 | 0.196 | no | 0.699 | 0.286 | yes | 0.624 | 0.122 | yes | 0.807 | 0.495 | no | 0.767 | 0.153 | no | 0.857 | 0.096 | no | 1.072 | 0.131 | no | 0.780 | 0.254 | no |
| DR2501 | HTH transcriptional repressor, LacI/RBSR family | 0.837 | 0.325 | no | 0.723 | 0.328 | yes | 0.843 | 0.364 | no | 1.074 | 0.559 | no | 0.889 | 0.254 | no | 0.909 | 0.172 | no | 1.137 | 0.398 | no | 1.387 | 0.388 | no | 1.484 | 0.254 | yes |
| DR2502 | Transmembrane transport protein | 0.988 | 0.302 | no | 1.176 | 0.392 | no | 1.205 | 0.275 | no | 1.319 | 0.275 | no | 1.102 | 0.315 | no | 1.206 | 0.383 | no | 1.484 | 0.717 | no | 1.236 | 0.297 | no | 1.034 | 0.083 | no |
| DR2503 | Prolyl endopeptidase, a/b hydrolase fusion to WD-repeats domain | 0.917 | 0.309 | no | 1.045 | 0.273 | no | 1.444 | 0.703 | no | 1.298 | 0.404 | no | 1.489 | 0.542 | no | 1.605 | 0.546 | yes | 1.648 | 0.552 | yes | 1.778 | 0.502 | yes | 1.293 | 0.205 | no |
| DR2504 | Zn-finger containing protein, uncharacterized | 1.035 | 0.274 | no | 1.160 | 0.263 | no | 1.182 | 0.292 | no | 1.456 | 0.615 | no | 1.219 | 0.147 | no | 1.121 | 0.335 | no | 1.150 | 0.334 | no | 1.108 | 0.358 | no | 1.256 | 0.350 | no |
| DR2505 | Conserved membrane protein | 0.719 | 0.164 | no | 0.606 | 0.218 | yes | 0.655 | 0.243 | yes | 0.512 | 0.116 | yes | 0.733 | 0.299 | no | 0.850 | 0.212 | no | 0.909 | 0.276 | no | 1.004 | 0.096 | no | 1.075 | 0.259 | no |
| DR2506 | a/b hydrolase | 1.063 | 0.261 | no | 0.629 | 0.184 | yes | 0.605 | 0.203 | yes | 0.597 | 0.259 | yes | 0.597 | 0.150 | yes | 0.612 | 0.190 | yes | 0.708 | 0.154 | no | 0.777 | 0.244 | no | 1.205 | 0.303 | no |
| DR2507 | Fatty-acid-CoA ligase | 0.811 | 0.311 | no | 0.714 | 0.245 | no | 1.089 | 0.367 | no | 1.353 | 0.340 | no | 1.173 | 0.479 | no | 1.079 | 0.433 | no | 1.156 | 0.407 | no | 1.413 | 0.291 | no | 1.259 | 0.542 | no |
| DR2508 | Deinococcal hexagonally packed intermediate-layer (HPI) surface protein | 1.029 | 0.475 | no | 0.496 | 0.187 | yes | 0.985 | 0.304 | no | 1.688 | 0.632 | yes | 1.323 | 0.749 | no | 1.126 | 0.824 | no | 1.245 | 0.649 | no | 1.420 | 0.786 | no | 3.486 | 2.245 | yes |
| DR2509 | Conserved bacterial protein of YqgF family, predicted holiday junction resolvase | 0.969 | 0.261 | no | 0.565 | 0.248 | yes | 0.885 | 0.273 | no | 0.924 | 0.290 | no | 1.136 | 0.393 | no | 0.886 | 0.251 | no | 1.001 | 0.306 | no | 1.388 | 0.430 | no | 1.316 | 0.417 | no |
| DR2510 | Enoyl-COA hydratase | 1.200 | 0.267 | no | 0.475 | 0.148 | yes | 0.463 | 0.148 | yes | 0.483 | 0.081 | yes | 0.601 | 0.290 | yes | 0.571 | 0.243 | yes | 0.637 | 0.144 | yes | 1.008 | 0.202 | no | 1.337 | 0.534 | no |
| DR2511 | Bacillus YaaT ortholog (conserved bacterial proteins), signal peptidase II-like protein | 0.704 | 0.157 | no | 0.489 | 0.118 | yes | 0.672 | 0.184 | yes | 0.713 | 0.166 | no | 0.925 | 0.308 | no | 0.928 | 0.361 | no | 0.879 | 0.309 | no | 0.961 | 0.225 | no | 1.000 | 0.454 | no |
| DR2512 | YabJ ortholog, family of small highly conserved proteins, claimed as translational inhibitor protein | 0.870 | 0.175 | no | 0.810 | 0.419 | no | 0.923 | 0.268 | no | 0.953 | 0.090 | no | 0.971 | 0.357 | no | 1.137 | 0.317 | no | 1.382 | 0.776 | no | 1.228 | 0.214 | no | 1.879 | 0.125 | yes |
| DR2513 | PP2C phosphatase family | 0.829 | 0.230 | no | 0.469 | 0.149 | yes | 0.374 | 0.119 | yes | 0.293 | 0.027 | yes | 0.409 | 0.167 | yes | 0.465 | 0.160 | yes | 0.507 | 0.354 | yes | 0.509 | 0.115 | yes | 0.748 | 0.180 | no |
| DR2514 | 0-acyltransferase PLSC/PLSB family | 0.970 | 0.145 | no | 0.909 | 0.139 | no | 0.865 | 0.238 | no | 1.066 | 0.078 | no | 1.133 | 0.427 | no | 1.146 | 0.280 | no | 0.893 | 0.392 | no | 1.054 | 0.253 | no | 1.131 | 0.438 | no |
| DR2515 | Zinc metallo protease | 0.931 | 0.243 | no | 0.919 | 0.352 | no | 0.746 | 0.222 | no | 0.778 | 0.362 | no | 0.806 | 0.137 | no | 0.949 | 0.189 | no | 0.955 | 0.396 | no | 0.982 | 0.103 | no | 0.828 | 0.156 | no |
| DR2516 | FRAMESHIFT zinc metallo protease | 0.854 | 0.225 | no | 1.590 | 0.846 | yes | 1.347 | 0.628 | no | 0.998 | 0.245 | no | 1.179 | 0.508 | no | 1.030 | 0.173 | no | 1.341 | 0.873 | no | 0.902 | 0.364 | no | n/a | n/a | n/a |
| DR2517 | Fibronectin III domains containing secreted protein | 3.821 | 1.411 | yes | 0.583 | 0.202 | yes | 1.310 | 0.898 | no | n/a | n/a | n/a | 1.099 | 0.651 | no | 0.735 | 0.240 | no | 0.424 | 0.244 | yes | 0.381 | 0.165 | yes | n/a | n/a | n/a |
| DR2518 | Pkn2 type serine threonine kinase | 1.361 | 0.600 | no | 1.657 | 0.296 | yes | 1.465 | 0.251 | yes | 1.341 | 0.206 | no | 1.331 | 0.389 | no | 1.250 | 0.357 | no | 1.087 | 0.226 | no | 1.027 | 0.090 | no | n/a | n/a | n/a |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR2519 | HTH transcriptional regulator, MERR family | 1.038 | 0.604 | no | 2.406 | 1.396 | yes | 2.126 | 0.952 | yes | 1.522 | 0.350 | no | 1.534 | 0.333 | yes | 1.273 | 0.322 | no | 1.445 | 0.601 | no | 1.220 | 0.390 | no | 0.622 | 0.264 | yes |
| DR2520 | Predicted protein | 1.201 | 0.187 | no | 1.501 | 0.365 | yes | 1.526 | 0.316 | yes | 1.315 | 0.040 | no | 1.194 | 0.469 | no | 1.014 | 0.092 | no | 0.821 | 0.154 | no | 0.850 | 0.169 | no | 0.753 | 0.228 | no |
| DR2521 | Fe-S oxidoreductase, related to NifB/MoaA family + PDZ domain | 1.227 | 0.581 | no | 0.749 | 0.226 | no | 0.908 | 0.353 | no | 1.282 | 0.285 | no | 1.034 | 0.201 | no | 0.849 | 0.383 | no | 1.073 | 0.363 | no | 1.226 | 0.154 | no | 0.769 | 0.343 | no |
| DR2522 | a/b hydrolase domain | 0.551 | 0.350 | yes | 0.864 | 0.501 | no | 0.991 | 0.605 | no | 4.406 | 3.109 | yes | 3.621 | 1.361 | yes | 1.537 | 0.803 | no | 0.596 | 0.437 | yes | 0.578 | 0.100 | yes | n/a | n/a | n/a |
| DR2524 | Ribosomal protein L28 | 1.111 | 0.354 | no | 2.286 | 0.708 | yes | 2.420 | 0.349 | yes | 2.242 | 0.593 | yes | 1.618 | 0.542 | yes | 1.392 | 0.554 | no | 1.238 | 0.302 | no | 1.143 | 0.286 | no | 0.933 | 0.123 | no |
| DR2525 | C4-dicarboxylate transport protein, membrane permease | 0.852 | 0.316 | no | 0.872 | 0.255 | no | 0.725 | 0.474 | yes | 0.662 | 0.295 | yes | 0.662 | 0.166 | yes | 0.801 | 0.122 | no | 1.133 | 0.350 | no | 1.121 | 0.244 | no | 0.799 | 0.113 | no |
| DR2526 | Lipoamide dehydrogenase, component E3 | 1.046 | 0.282 | no | 0.510 | 0.156 | yes | 0.294 | 0.063 | yes | 0.328 | 0.048 | yes | 0.424 | 0.172 | yes | 0.504 | 0.157 | yes | 0.819 | 0.308 | no | 0.890 | 0.301 | no | 1.194 | 0.444 | no |
| DR2527 | Predicted protein | 0.944 | 0.393 | no | 0.528 | 0.277 | yes | 0.524 | 0.262 | yes | 0.909 | 0.446 | no | 1.327 | 0.772 | no | 2.240 | 1.010 | yes | 2.849 | 1.407 | yes | 2.914 | 1.380 | yes | 2.729 | 0.745 | yes |
| DR2528 | Probable membrane protein with repeats | 1.117 | 0.399 | no | 0.695 | 0.306 | yes | 0.344 | 0.103 | yes | 0.768 | 0.091 | no | 0.724 | 0.492 | yes | 1.014 | 0.627 | no | 1.850 | 0.906 | yes | 1.602 | 0.435 | yes | 1.739 | 0.726 | yes |
| DR2529 | Predicted protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR2530 | Predicted protein | 0.988 | 0.419 | no | 0.523 | 0.201 | yes | 0.385 | 0.157 | yes | 0.418 | 0.102 | yes | 0.555 | 0.288 | yes | 1.095 | 0.472 | no | 1.835 | 0.501 | yes | 1.954 | 0.547 | yes | 1.234 | 0.304 | no |
| DR2531 | Thiosulfate sulfurtransferase Rhodanese superfamily enzyme | 1.070 | 0.267 | no | 0.913 | 0.355 | no | 0.548 | 0.233 | yes | 0.548 | 0.195 | yes | 0.576 | 0.228 | yes | 0.751 | 0.219 | no | 0.946 | 0.215 | no | 0.814 | 0.258 | no | 0.871 | 0.129 | no |
| DR2532 | Predicted protein | 0.989 | 0.365 | no | 0.706 | 0.100 | no | 0.407 | 0.104 | yes | 0.449 | 0.117 | yes | 0.530 | 0.125 | yes | 0.909 | 0.192 | no | 1.197 | 0.435 | no | 1.125 | 0.380 | no | 0.850 | 0.347 | no |
| DR2533 | Predicted protein | 1.042 | 0.262 | no | 0.913 | 0.159 | no | 0.963 | 0.422 | no | 0.926 | 0.339 | no | 1.004 | 0.369 | no | 0.980 | 0.432 | no | 1.223 | 0.309 | no | 1.320 | 0.450 | no | 1.266 | 0.107 | no |
| DR2534 | Bacillus GRPB ortholog | 1.448 | 0.513 | no | 1.310 | 0.733 | no | 1.139 | 0.294 | no | 1.287 | 0.300 | no | 1.079 | 0.458 | no | 0.922 | 0.359 | no | 1.214 | 0.596 | no | 1.163 | 0.315 | no | 1.283 | 0.572 | no |
| DR2535 | Nitrilase family enzyme | 0.831 | 0.233 | no | 0.512 | 0.120 | yes | 0.400 | 0.204 | yes | 0.390 | 0.112 | yes | 0.456 | 0.076 | yes | 0.667 | 0.226 | yes | 0.868 | 0.431 | no | 0.737 | 0.225 | yes | 0.697 | 0.312 | no |
| DR2536 | Protein similar to molybdopterin-binding domain of nitrate reductase | 0.950 | 0.305 | no | 0.856 | 0.332 | no | 1.024 | 0.366 | no | 1.152 | 0.532 | no | 0.916 | 0.232 | no | 0.970 | 0.287 | no | 0.872 | 0.272 | no | 0.827 | 0.173 | no | 0.641 | 0.073 | yes |
| DR2537 | Conserved membrane protein | 0.839 | 0.166 | no | 1.014 | 0.301 | no | 1.239 | 0.387 | no | 1.236 | 0.259 | no | 1.308 | 0.369 | no | 1.122 | 0.203 | no | 0.895 | 0.158 | no | 1.004 | 0.097 | no | 0.815 | 0.186 | no |
| DR2538 | Cytochrome p450 | 0.982 | 0.329 | no | 0.994 | 0.352 | no | 0.990 | 0.269 | no | 1.293 | 0.331 | no | 1.043 | 0.167 | no | 0.995 | 0.269 | no | 0.987 | 0.297 | no | 1.011 | 0.178 | no | 1.090 | 0.223 | no |
| DR2539 | HTH transcriptional regulator, iron repressor | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR2540 | TIM barrel metal dependent hydrolase | 0.793 | 0.277 | no | 0.884 | 0.415 | no | 0.709 | 0.288 | yes | 0.549 | 0.126 | yes | 0.820 | 0.362 | no | 0.827 | 0.164 | no | 1.007 | 0.517 | no | 0.761 | 0.124 | no | 0.891 | 0.195 | no |
| DR2541 | Predicted protein | 1.176 | 0.298 | no | 0.972 | 0.308 | no | 1.046 | 0.414 | no | 1.320 | 0.845 | no | 1.286 | 0.537 | no | 1.140 | 0.213 | no | 0.934 | 0.268 | no | 1.267 | 0.266 | no | 1.290 | 0.182 | no |
| DR2542 | Cyclophilin Peptidyl prolyl isomerase | 0.874 | 0.141 | no | 0.840 | 0.180 | no | 0.646 | 0.087 | yes | 0.868 | 0.198 | no | 0.924 | 0.262 | no | 1.425 | 0.138 | no | 1.710 | 0.292 | yes | 1.930 | 0.475 | yes | 2.035 | 0.542 | yes |
| DR2543 | Cytidylate kinase homolog | 1.162 | 0.400 | no | 0.825 | 0.114 | no | 0.828 | 0.277 | no | 0.953 | 0.160 | no | 1.090 | 0.201 | no | 1.838 | 0.952 | yes | 2.275 | 1.007 | yes | 1.539 | 0.403 | no | 1.315 | 0.463 | no |
| DR2544 | Predicted protein | 1.057 | 0.306 | no | 1.001 | 0.428 | no | 1.753 | 1.013 | yes | 0.771 | 0.272 | no | 1.775 | 0.298 | yes | 2.489 | 0.853 | yes | 2.896 | 1.030 | yes | 1.745 | 0.329 | yes | 1.539 | 0.251 | no |
| DR2545 | Nitropane dioxygenase/ IMP dehydrogenase related protein | 0.889 | 0.359 | no | 0.770 | 0.402 | no | 0.899 | 0.368 | no | 0.994 | 0.289 | no | 1.293 | 0.332 | no | 1.721 | 0.405 | yes | 1.957 | 0.887 | yes | 2.076 | 0.443 | yes | 0.981 | 0.191 | no |
| DR2546 | Related to PKN2 type of S/T kinases | 1.126 | 0.330 | no | 1.414 | 0.219 | yes | 1.275 | 0.250 | no | 1.065 | 0.346 | no | 1.066 | 0.241 | no | 1.318 | 0.460 | no | 1.044 | 0.098 | no | 1.079 | 0.239 | no | 0.856 | 0.116 | no |
| DR2547 | Glutamyl tRNA reductase | 0.539 | 0.300 | yes | 0.474 | 0.253 | yes | 0.148 | 0.051 | yes | 0.055 | 0.014 | yes | 0.063 | 0.032 | yes | 0.104 | 0.045 | yes | 0.103 | 0.061 | yes | 0.134 | 0.024 | yes | 0.722 | 0.462 | yes |
| DR2548 | Uncharacterized conserved protein family member, YEBC_ECOLI | 0.948 | 0.419 | no | 1.230 | 0.243 | no | 1.213 | 0.272 | no | 1.361 | 1.030 | no | 1.260 | 0.465 | no | 1.378 | 0.429 | no | 0.936 | 0.269 | no | 0.825 | 0.237 | no | 1.627 | 0.651 | yes |
| DR2549 | a/b hydrolase | 0.908 | 0.305 | no | 0.710 | 0.274 | yes | 0.527 | 0.227 | yes | 0.334 | 0.069 | yes | 0.447 | 0.091 | yes | 0.710 | 0.317 | no | 0.648 | 0.229 | yes | 0.745 | 0.180 | no | 0.769 | 0.302 | no |
| DR2550 | HTH tr. regulator | 0.988 | 0.161 | no | 0.684 | 0.197 | yes | 0.645 | 0.084 | yes | 0.821 | 0.136 | no | 0.848 | 0.193 | no | 1.205 | 0.499 | no | 1.342 | 0.644 | no | 1.081 | 0.265 | no | 0.955 | 0.188 | no |
| DR2551 | a/b hydrolase | 0.660 | 0.254 | yes | 0.973 | 0.585 | no | 1.044 | 0.506 | no | 0.960 | 0.129 | no | 1.843 | 1.139 | yes | 1.602 | 0.573 | yes | 1.839 | 0.694 | yes | 1.874 | 0.674 | yes | 1.735 | 0.534 | yes |
| DR2552 | YCEG ortholog (family of bacterial proteins), claimed aminodeoxychorismate lyase, pabC homolog | 1.022 | 0.297 | no | 1.340 | 0.430 | no | 1.312 | 0.371 | no | 1.420 | 0.519 | no | 1.256 | 0.350 | no | 1.267 | 0.236 | no | 1.104 | 0.200 | no | 1.127 | 0.281 | no | 1.030 | 0.112 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR2553 | Sugar kinase (Ribokinase RbsK superfamily), fructokinase | 0.854 | 0.311 | no | 0.870 | 0.471 | no | 0.841 | 0.318 | no | 0.713 | 0.055 | no | 0.844 | 0.207 | no | 1.350 | 0.944 | no | 1.311 | 0.555 | no | 1.128 | 0.128 | no | 0.735 | 0.227 | no |
| DR2554 | Predicted protein | 1.073 | 0.723 | no | 1.021 | 0.622 | no | 0.918 | 0.588 | no | 0.451 | 0.080 | yes | 0.843 | 0.592 | no | 0.902 | 0.391 | no | 0.817 | 0.566 | no | 0.781 | 0.168 | no | 0.827 | 0.140 | no |
| DR2555 | Pet112 GatB, Glu-tRNA amidotransferase, subunit B | 0.743 | 0.162 | no | 0.642 | 0.223 | yes | 0.533 | 0.141 | yes | 0.526 | 0.085 | yes | 0.658 | 0.208 | yes | 0.683 | 0.248 | yes | 0.644 | 0.145 | yes | 0.711 | 0.165 | yes | 1.161 | 0.142 | no |
| DR2556 | Receiver domain, CheY family, fusion with uncharacterized domain | 0.965 | 0.511 | no | 0.944 | 0.428 | no | 0.850 | 0.344 | no | 0.825 | 0.242 | no | 0.824 | 0.332 | no | 1.047 | 0.413 | no | 1.009 | 0.436 | no | 1.017 | 0.205 | no | 1.376 | 0.211 | no |
| DR2557 | Zn-dependent hydrolases of beta-lactamase | 0.810 | 0.223 | no | 0.817 | 0.272 | no | 0.698 | 0.183 | yes | 0.756 | 0.041 | no | 0.913 | 0.160 | no | 1.224 | 0.409 | no | 1.129 | 0.301 | no | 1.169 | 0.146 | no | 1.439 | 0.378 | no |
| DR2558 | Predicted protein | 1.102 | 0.261 | no | 0.965 | 0.240 | no | 0.796 | 0.337 | no | 0.871 | 0.225 | no | 0.848 | 0.219 | no | 1.017 | 0.319 | no | 1.106 | 0.335 | no | 1.072 | 0.097 | no | 1.234 | 0.083 | no |
| DR2559 | Predicted protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR2560 | Uncharacterized conserved protein | 1.245 | 0.417 | no | 0.611 | 0.322 | yes | 0.416 | 0.293 | yes | 0.701 | 0.313 | no | 1.057 | 0.535 | no | 1.685 | 0.725 | yes | 2.634 | 1.141 | yes | 2.453 | 0.347 | yes | 2.085 | 0.772 | yes |
| DR2561 | Uncharacterized conserved protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR2562 | 3-demethylubiquinone-9 3-methyltransferase, UBIG | 1.356 | 0.453 | no | 1.347 | 0.571 | no | 1.402 | 0.640 | no | 1.695 | 0.886 | no | 1.662 | 0.709 | yes | 1.430 | 0.240 | no | 1.621 | 0.791 | yes | 1.158 | 0.184 | no | 1.149 | 0.181 | no |
| DR2563 | Predicted protein | 1.310 | 0.550 | no | 0.873 | 0.557 | no | 1.634 | 0.877 | yes | 6.771 | 0.680 | yes | 6.906 | 4.181 | yes | 3.798 | 2.093 | yes | 5.287 | 2.451 | yes | 2.982 | 0.989 | yes | 4.068 | 1.415 | yes |
| DR2564 | Phosphoglycerate mutase related protein | 1.268 | 0.288 | no | 1.131 | 0.281 | no | 1.141 | 0.271 | no | 1.302 | 0.276 | no | 1.189 | 0.410 | no | 1.116 | 0.411 | no | 1.374 | 0.616 | no | 1.095 | 0.211 | no | 1.185 | 0.264 | no |
| DR2565 | Fe_S binding subunit of reductase | 0.954 | 0.355 | no | 0.845 | 0.240 | no | 0.950 | 0.320 | no | 1.261 | 0.382 | no | 1.121 | 0.196 | no | 1.159 | 0.256 | no | 1.032 | 0.354 | no | 1.380 | 0.595 | no | 1.704 | 0.230 | yes |
| DR2566 | Homolog of HPAII repair protein, uncharacterized YCJD ortholog; small conserved bacterial proteins | 1.376 | 0.451 | no | 4.027 | 2.246 | yes | 3.485 | 1.828 | yes | 4.104 | 1.087 | yes | 2.324 | 1.281 | yes | 1.377 | 0.530 | no | 1.689 | 0.859 | yes | 1.117 | 0.137 | no | 0.923 | 0.315 | no |
| DR2567 | N-acetylmuramoyl-L-alanine amidase | 1.178 | 0.332 | no | 0.926 | 0.177 | no | 0.955 | 0.193 | no | 0.987 | 0.317 | no | 1.066 | 0.150 | no | 1.092 | 0.277 | no | 1.130 | 0.363 | no | 1.369 | 0.202 | no | 1.144 | 0.374 | no |
| DR2568 | Arginyl-tRNA synthetase, Class I | 1.261 | 0.368 | no | 0.998 | 0.362 | no | 0.929 | 0.232 | no | 1.045 | 0.275 | no | 1.439 | 0.773 | no | 1.132 | 0.365 | no | 1.241 | 0.305 | no | 1.310 | 0.145 | no | 1.556 | 0.349 | yes |
| DR2569 | Predicted protein | 0.573 | 0.175 | yes | 0.641 | 0.395 | yes | 0.832 | 0.406 | no | 0.607 | 0.068 | yes | 0.713 | 0.398 | yes | 1.056 | 0.499 | no | 0.750 | 0.444 | no | 0.699 | 0.190 | yes | 0.976 | 0.468 | no |
| DR2570 | Cysteine rich protein | 0.859 | 0.152 | no | 1.138 | 0.451 | no | 1.299 | 0.532 | no | 1.042 | 0.269 | no | 1.314 | 0.777 | no | 0.992 | 0.368 | no | 1.151 | 0.432 | no | 1.195 | 0.184 | no | 1.242 | 0.444 | no |
| DR2571 | Molybdenum cofactor biosynthesis protein C, MOAC | 0.896 | 0.146 | no | 0.822 | 0.174 | no | 1.177 | 0.254 | no | 0.858 | 0.051 | no | 1.124 | 0.349 | no | 0.955 | 0.206 | no | 0.762 | 0.205 | no | 0.957 | 0.216 | no | 0.940 | 0.263 | no |
| DR2572 | Predicted protein | 0.859 | 0.167 | no | 1.744 | 0.649 | yes | 1.592 | 0.223 | yes | 1.475 | 0.327 | no | 1.491 | 0.404 | no | 1.279 | 0.330 | no | 1.100 | 0.257 | no | 1.001 | 0.276 | no | 0.779 | 0.244 | no |
| DR2573 | Predicted protein | 0.915 | 0.491 | no | 3.926 | 2.573 | yes | 3.541 | 1.287 | yes | 3.920 | 2.146 | yes | 3.684 | 2.199 | yes | 2.057 | 0.851 | yes | 1.378 | 0.631 | no | 1.618 | 0.116 | yes | 0.876 | 0.318 | no |
| DR2574 | HTH transcription factor, phage type | 1.436 | 0.607 | no | 3.429 | 1.770 | yes | 5.227 | 1.301 | yes | 3.617 | 0.675 | yes | 3.683 | 1.787 | yes | 3.452 | 2.193 | yes | 1.929 | 0.805 | yes | 1.193 | 0.270 | no | 0.650 | 0.070 | no |
| DR2576 | DHH family phosphohydrolase | 0.981 | 0.228 | no | 0.748 | 0.205 | no | 0.766 | 0.164 | no | 0.930 | 0.114 | no | 1.329 | 0.784 | no | 0.998 | 0.380 | no | 1.051 | 0.242 | no | 1.339 | 0.310 | no | 1.744 | 0.562 | yes |
| DR2577 | S-layer protein | 0.907 | 0.360 | no | 0.712 | 0.367 | yes | 0.879 | 0.307 | no | 0.765 | 0.284 | no | 1.050 | 0.472 | no | 1.353 | 0.831 | no | 1.307 | 0.462 | no | 1.178 | 0.286 | no | 3.744 | 1.701 | yes |
| DR2578 | Queuine tRNA-ribosyltransferase, Tgt | 1.020 | 0.191 | no | 1.675 | 0.352 | yes | 2.385 | 0.560 | yes | 2.695 | 0.183 | yes | 2.276 | 0.991 | yes | 2.043 | 0.577 | yes | 1.928 | 0.456 | yes | 1.692 | 0.295 | yes | 1.742 | 0.200 | yes |
| DR2580 | Iojap family of conserved proteins | 0.684 | 0.104 | no | 0.733 | 0.288 | no | 0.816 | 0.149 | no | 0.602 | 0.071 | yes | 0.679 | 0.247 | yes | 1.001 | 0.370 | no | 1.039 | 0.509 | no | 0.850 | 0.384 | no | 1.201 | 0.042 | no |
| DR2581 | HTH transcription factor, LYTR family | 0.849 | 0.241 | no | 1.213 | 0.400 | no | 1.244 | 0.455 | no | 0.953 | 0.208 | no | 0.781 | 0.201 | no | 0.936 | 0.145 | no | 1.110 | 0.476 | no | 0.975 | 0.084 | no | 1.089 | 0.278 | no |
| DR2582 | HD superfamily Hydrolase | 0.641 | 0.183 | yes | 0.350 | 0.130 | yes | 0.269 | 0.114 | yes | 0.208 | 0.099 | yes | 0.262 | 0.102 | yes | 0.346 | 0.129 | yes | 0.369 | 0.161 | yes | 0.441 | 0.179 | yes | 0.525 | 0.112 | yes |
| DR2583 | Malate dehydrogenase | 1.129 | 0.316 | no | 1.070 | 0.412 | no | 0.928 | 0.364 | no | 1.228 | 0.274 | no | 0.898 | 0.247 | no | 0.987 | 0.276 | no | 1.090 | 0.408 | no | 1.026 | 0.064 | no | 1.280 | 0.224 | no |
| DR2584 | 3-methyladenine DNA glycosylase | 1.158 | 0.244 | no | 0.870 | 0.134 | no | 0.855 | 0.234 | no | 0.985 | 0.385 | no | 0.941 | 0.154 | no | 1.009 | 0.434 | no | 1.034 | 0.390 | no | 1.119 | 0.226 | no | 1.244 | 0.379 | no |
| DR2585 | Monooxygenase, FMN oxidoreductase family | 1.169 | 0.359 | no | 1.105 | 0.491 | no | 0.908 | 0.188 | no | 1.194 | 0.688 | no | 0.849 | 0.229 | no | 0.894 | 0.186 | no | 1.038 | 0.257 | no | 1.044 | 0.080 | no | 1.165 | 0.194 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR2586 | Exonuclease VII small subunit XseB | 0.885 | 0.207 | no | 0.909 | 0.187 | no | 1.095 | 0.300 | no | 0.869 | 0.089 | no | 0.883 | 0.225 | no | 1.130 | 0.350 | no | 0.996 | 0.371 | no | 0.910 | 0.149 | no | 0.874 | 0.094 | no |
| DR2587 | Lysophosphatidic acid acyltransferase | 1.050 | 0.515 | no | 0.922 | 0.338 | no | 0.866 | 0.428 | no | 0.949 | 0.533 | no | 0.716 | 0.235 | no | 0.832 | 0.207 | no | 0.888 | 0.551 | no | 0.878 | 0.111 | no | 0.963 | 0.136 | no |
| DR2588 | periplasmic metal-binding protein | 0.906 | 0.287 | no | 0.577 | 0.098 | yes | 0.666 | 0.185 | yes | 0.710 | 0.217 | no | 1.058 | 0.609 | no | 1.182 | 0.400 | no | 1.347 | 0.396 | no | 1.391 | 0.434 | no | 3.094 | 0.788 | yes |
| DR2589 | Iron permease | 1.322 | 0.491 | no | 1.050 | 0.403 | no | 1.400 | 0.927 | no | 1.206 | 0.244 | no | 1.183 | 0.910 | no | 1.421 | 0.580 | no | 1.247 | 0.881 | no | 1.216 | 0.135 | no | 1.017 | 0.623 | no |
| DR2590 | ABC ATPase, iron(III) dicitrate transport system permease protein FecF | 1.017 | 0.190 | no | 0.883 | 0.123 | no | 0.839 | 0.164 | no | 0.902 | 0.399 | no | 0.904 | 0.214 | no | 1.212 | 0.310 | no | 1.108 | 0.205 | no | 1.222 | 0.314 | no | 1.460 | 0.245 | yes |
| DR2591 | Ferredoxin | 1.256 | 0.569 | no | 1.698 | 0.771 | yes | 2.013 | 0.692 | yes | 3.843 | 2.593 | yes | 2.397 | 1.142 | yes | 1.843 | 0.249 | yes | 2.163 | 0.732 | yes | 1.913 | 0.862 | yes | 1.298 | 0.271 | no |
| DR2592 | Predicted protein | 0.931 | 0.214 | no | 0.723 | 0.143 | no | 0.958 | 0.075 | no | 1.133 | 0.292 | no | 1.293 | 0.284 | no | 1.270 | 0.299 | no | 1.513 | 0.767 | no | 1.317 | 0.369 | no | 0.887 | 0.126 | no |
| DR2593 | Predicted protein | 0.915 | 0.353 | no | 1.118 | 0.349 | no | 0.986 | 0.462 | no | 1.264 | 0.473 | no | 1.400 | 0.999 | no | 1.251 | 0.383 | no | 1.355 | 0.136 | no | 1.323 | 0.271 | no | 0.873 | 0.297 | no |
| DR2594 | Mg chelatase, AAA ATPase | 0.609 | 0.136 | yes | 0.453 | 0.128 | yes | 0.484 | 0.120 | yes | 0.520 | 0.004 | yes | 0.825 | 0.403 | no | 0.838 | 0.346 | no | 0.731 | 0.262 | no | 0.787 | 0.230 | no | 0.917 | 0.393 | no |
| DR2595 | NADP-dependent Oxidoreductase | 1.072 | 0.310 | no | 1.183 | 0.451 | no | 0.972 | 0.193 | no | 0.841 | 0.208 | no | 0.856 | 0.528 | no | 0.840 | 0.198 | no | 0.944 | 0.120 | no | 0.859 | 0.151 | no | 0.825 | 0.248 | no |
| DR2596 | Possible metalloprotease | 0.813 | 0.104 | no | 0.698 | 0.166 | no | 0.337 | 0.061 | yes | 0.329 | 0.052 | yes | 0.390 | 0.137 | yes | 0.610 | 0.148 | yes | 0.861 | 0.499 | no | 1.097 | 0.167 | no | 0.714 | 0.326 | no |
| DR2597 | Nitric oxide synthase (second bacterial member, first YflM bacillus) | 0.814 | 0.273 | no | 0.840 | 0.348 | no | 0.268 | 0.080 | yes | 0.146 | 0.052 | yes | 0.137 | 0.080 | yes | 0.206 | 0.060 | yes | 0.273 | 0.114 | yes | 0.261 | 0.085 | yes | 0.493 | 0.271 | yes |
| DR2598 | Conserved protein | 1.147 | 0.416 | no | 0.912 | 0.360 | no | 0.724 | 0.426 | yes | 0.755 | 0.123 | no | 0.693 | 0.188 | no | 0.816 | 0.172 | no | 0.884 | 0.194 | no | 0.784 | 0.149 | no | 0.683 | 0.132 | no |
| DR2599 | Predicted protein | 1.296 | 0.375 | no | 1.595 | 0.321 | yes | 2.381 | 1.296 | yes | 3.661 | 0.609 | yes | 2.164 | 1.041 | yes | 1.534 | 0.705 | no | 1.405 | 0.377 | no | 1.059 | 0.191 | no | 0.725 | 0.081 | no |
| DR2600 | PR1 domain protein, plant pathogenesis related protein | 1.033 | 0.248 | no | 0.897 | 0.186 | no | 0.711 | 0.205 | no | 0.683 | 0.116 | no | 0.764 | 0.139 | no | 0.975 | 0.399 | no | 0.944 | 0.203 | no | 0.934 | 0.328 | no | 1.046 | 0.160 | no |
| DR2601 | YIGE_ECOLI related protein | 1.341 | 0.322 | no | 1.387 | 0.373 | no | 1.059 | 0.227 | no | 1.541 | 0.590 | no | 1.287 | 0.605 | no | 1.436 | 0.320 | no | 1.404 | 0.436 | no | 1.326 | 0.217 | no | 1.153 | 0.186 | no |
| DR2602 | Acetate/propionate kinase | 1.074 | 0.382 | no | 0.728 | 0.168 | no | 1.046 | 0.463 | no | 1.224 | 0.449 | no | 1.640 | 0.606 | yes | 1.149 | 0.480 | no | 1.576 | 0.283 | yes | 2.532 | 1.044 | yes | n/a | n/a | n/a |
| DR2603 | Decarboxlyase phenylacrylic acid decarboxylase, PAD1 family | 1.169 | 0.317 | no | 1.133 | 0.348 | no | 1.029 | 0.263 | no | 0.880 | 0.103 | no | 0.880 | 0.204 | no | 1.128 | 0.335 | no | 1.082 | 0.325 | no | 1.171 | 0.165 | no | 1.636 | 0.373 | yes |
| DR2604 | Sugar nucleotide phosphorilase | 1.147 | 0.346 | no | 1.070 | 0.499 | no | 0.943 | 0.333 | no | 1.201 | 0.645 | no | 0.892 | 0.269 | no | 1.202 | 0.102 | no | 1.508 | 0.487 | no | 1.070 | 0.302 | no | 1.083 | 0.139 | no |
| DR2605 | Predicted Kinase, YCHB_ECOLI | 1.359 | 0.622 | no | 1.964 | 0.945 | yes | 1.736 | 1.083 | yes | 1.645 | 0.898 | no | 1.732 | 1.071 | no | 1.690 | 0.398 | yes | 1.321 | 0.301 | no | 1.134 | 0.115 | no | 1.218 | 0.139 | no |
| DR2607 | MOAE protein, involved in molybdenum metabolism | 1.489 | 0.570 | no | 1.937 | 0.665 | yes | 1.720 | 0.750 | yes | 1.239 | 0.193 | no | 1.012 | 0.335 | no | 1.006 | 0.320 | no | 1.206 | 0.624 | no | 0.950 | 0.111 | no | 0.925 | 0.211 | no |
| DR2608 | Predicted protein | 1.192 | 0.237 | no | 1.243 | 0.373 | no | 0.986 | 0.353 | no | 0.724 | 0.108 | no | 0.856 | 0.207 | no | 0.959 | 0.355 | no | 0.877 | 0.326 | no | 1.076 | 0.525 | no | 0.935 | 0.302 | no |
| DR2609 | TRNA-processing ribonuclease BN, RBN | 0.908 | 0.239 | no | 0.768 | 0.271 | no | 0.506 | 0.177 | yes | 0.493 | 0.110 | yes | 0.724 | 0.173 | no | 1.083 | 0.343 | no | 1.251 | 0.400 | no | 1.348 | 0.453 | no | 1.307 | 0.310 | no |
| DR2610 | Periplasmic binding protein, FLIY | 1.245 | 0.193 | no | 4.130 | 1.671 | yes | 3.907 | 1.569 | yes | 3.416 | 0.851 | yes | 2.978 | 1.858 | yes | 2.656 | 0.544 | yes | 1.857 | 0.980 | yes | 1.583 | 0.454 | yes | 1.375 | 0.501 | no |
| DR2611 | Glutaminyl tRNA synthetase fused to pet112, class I | 1.174 | 0.476 | no | 1.080 | 0.414 | no | 2.451 | 1.736 | yes | 1.029 | 0.383 | no | 1.080 | 0.344 | no | 5.482 | 2.929 | yes | 0.749 | 0.162 | no | 1.484 | 0.642 | no | n/a | n/a | n/a |
| DR2612 | DEDA like Membrane protein | 0.854 | 0.314 | no | 4.200 | 1.731 | yes | 4.033 | 1.510 | yes | 1.879 | 0.331 | yes | 1.782 | 0.542 | yes | 1.960 | 0.512 | yes | 1.747 | 0.991 | yes | 0.990 | 0.215 | no | 0.761 | 0.183 | no |
| DR2613 | HAD superfamily hydrolase, probable Phosphoglycolate phosphatase | 1.000 | 0.160 | no | 1.126 | 0.401 | no | 0.720 | 0.154 | no | 0.586 | 0.057 | yes | 0.807 | 0.231 | no | 0.901 | 0.229 | no | 0.919 | 0.220 | no | 0.925 | 0.180 | no | 1.250 | 0.204 | no |
| DR2614 | Predicted protein | 1.030 | 0.374 | no | 1.448 | 0.350 | yes | 0.695 | 0.289 | yes | 0.503 | 0.102 | yes | 0.780 | 0.569 | no | 0.653 | 0.108 | yes | 0.856 | 0.279 | no | 0.914 | 0.257 | no | 0.897 | 0.187 | no |
| DR2615 | Ketopantoate hydroxymethyltransferase | 0.790 | 0.275 | no | 1.199 | 0.330 | no | 0.676 | 0.202 | yes | 0.337 | 0.157 | yes | 0.446 | 0.159 | yes | 0.552 | 0.202 | yes | 0.481 | 0.196 | yes | 0.558 | 0.167 | yes | 0.669 | 0.205 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DR2616 | Conserved membrane protein, cytochrome oxidase subunit | 0.850 | 0.338 | no | 0.803 | 0.371 | no | 0.444 | 0.161 | yes | 0.222 | 0.136 | yes | 0.198 | 0.069 | yes | 0.254 | 0.111 | yes | 0.229 | 0.088 | yes | 0.288 | 0.104 | yes | 0.594 | 0.168 | yes |
| DR2617 | Cytochrome AA3 controlling protein, ctaA | 0.825 | 0.184 | no | 0.638 | 0.359 | yes | 0.286 | 0.068 | yes | 0.178 | 0.017 | yes | 0.177 | 0.052 | yes | 0.227 | 0.077 | yes | 0.200 | 0.100 | yes | 0.295 | 0.085 | yes | 0.489 | 0.153 | yes |
| DR2618 | Cytochrome c oxidase assembly factor, ctaB | 0.911 | 0.307 | no | 0.823 | 0.411 | no | 0.497 | 0.138 | yes | 0.358 | 0.071 | yes | 0.402 | 0.295 | yes | 0.319 | 0.095 | yes | 0.373 | 0.126 | yes | 0.419 | 0.113 | yes | 0.922 | 0.400 | no |
| DR2620 | Cytochrome oxidase subunit I, COX1 | 0.832 | 0.468 | no | 0.557 | 0.183 | yes | 0.465 | 0.219 | yes | 0.631 | 0.375 | yes | 0.449 | 0.253 | yes | 0.637 | 0.263 | yes | 0.724 | 0.386 | yes | 1.112 | 0.179 | no | 2.674 | 1.609 | yes |
| DR2621 | Glycerol-3-phosphate dehydrogenase | 0.996 | 0.420 | no | 0.955 | 0.414 | no | 0.429 | 0.202 | yes | 0.438 | 0.076 | yes | 0.627 | 0.241 | yes | 0.666 | 0.147 | yes | 0.684 | 0.249 | yes | 0.725 | 0.170 | no | 0.622 | 0.388 | yes |
| DR2622 | SAM dependent methyltransferase | 1.022 | 0.255 | no | 0.656 | 0.204 | yes | 0.297 | 0.092 | yes | 0.195 | 0.050 | yes | 0.289 | 0.189 | yes | 0.342 | 0.135 | yes | 0.284 | 0.128 | yes | 0.337 | 0.104 | yes | 0.395 | 0.100 | yes |
| DR2623 | Thioredoxin reductase ortholog | 0.783 | 0.139 | no | 0.484 | 0.151 | yes | 0.416 | 0.054 | yes | 0.434 | 0.020 | yes | 0.572 | 0.218 | yes | 0.614 | 0.208 | yes | 0.504 | 0.229 | yes | 0.564 | 0.127 | yes | 0.934 | 0.106 | no |
| DR2624 | Uncharacterized conserved protein | 1.411 | 0.557 | no | 1.337 | 0.200 | no | 1.254 | 0.204 | no | 1.731 | 0.102 | yes | 1.482 | 0.616 | no | 1.229 | 0.395 | no | 1.256 | 0.338 | no | 1.308 | 0.079 | no | 1.439 | 0.056 | yes |
| DR2625 | Uncharacterized ortholog of 2 proteins from Synechocystis | 1.208 | 0.138 | no | 1.763 | 0.561 | yes | 1.437 | 0.737 | no | 0.771 | 0.123 | no | 0.781 | 0.297 | no | 0.957 | 0.292 | no | 0.893 | 0.263 | no | 0.877 | 0.164 | no | 0.906 | 0.188 | no |
| DR2626 | Acetylcholinesterase family esterase | 0.969 | 0.186 | no | 1.036 | 0.296 | no | 0.778 | 0.227 | no | 0.765 | 0.264 | no | 0.629 | 0.230 | yes | 0.748 | 0.190 | no | 0.775 | 0.247 | no | 0.907 | 0.230 | no | 0.783 | 0.160 | no |
| DR2627 | Fumarase | 0.867 | 0.175 | no | 0.658 | 0.084 | no | 0.760 | 0.117 | no | 0.753 | 0.183 | no | 0.913 | 0.378 | no | 0.899 | 0.224 | no | 0.476 | 0.343 | yes | 1.132 | 0.182 | no | 1.210 | 0.392 | no |
| DR2628 | Predicted protein | 1.503 | 0.239 | no | 1.820 | 0.761 | yes | 1.818 | 0.592 | yes | 1.627 | 0.096 | yes | 0.967 | 0.236 | no | 1.235 | 0.728 | no | 1.359 | 0.474 | no | 1.309 | 0.370 | no | 1.186 | 0.354 | no |
| DR2629 | Predicted HTH transcriptional regulator | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DR2630 | Thymidylate synthase | 0.922 | 0.298 | no | 0.727 | 0.146 | no | 0.707 | 0.206 | no | 0.577 | 0.171 | yes | 0.755 | 0.535 | yes | 0.980 | 0.554 | no | 0.701 | 0.347 | yes | 1.021 | 0.089 | no | 1.051 | 0.134 | no |
| DR2631 | dCMP deaminase | 1.001 | 0.445 | no | 1.350 | 0.408 | no | 1.087 | 0.570 | no | 1.196 | 0.490 | no | 0.957 | 0.302 | no | 1.024 | 0.320 | no | 1.036 | 0.373 | no | 1.005 | 0.274 | no | 1.010 | 0.424 | no |
| DR2632 | Dihydrofolate reductase, DYR | 0.880 | 0.232 | no | 1.324 | 0.197 | no | 1.252 | 0.337 | no | 0.896 | 0.031 | no | 0.923 | 0.166 | no | 1.114 | 0.453 | no | 1.079 | 0.303 | no | 1.334 | 0.354 | no | 0.883 | 0.173 | no |
| DR2633 | Uncharacterized protein with C-term. domain similar to domains present in HglK/OxrA genes | 1.234 | 0.400 | no | 1.736 | 0.389 | yes | 1.866 | 0.314 | yes | 1.741 | 0.123 | yes | 1.511 | 0.443 | no | 1.363 | 0.324 | no | 1.607 | 0.491 | yes | 1.599 | 0.232 | yes | 1.107 | 0.067 | no |
| DR2634 | Tyrosyl tRNA synthetase | 0.707 | 0.099 | no | 0.492 | 0.145 | yes | 0.324 | 0.061 | yes | 0.255 | 0.033 | yes | 0.340 | 0.136 | yes | 0.305 | 0.070 | yes | 0.412 | 0.228 | yes | 0.449 | 0.144 | yes | 0.453 | 0.148 | yes |
| DR2635 | Pyruvate kinase | 0.986 | 0.222 | no | 1.486 | 0.381 | yes | 1.297 | 0.313 | no | 1.262 | 0.349 | no | 1.002 | 0.363 | no | 1.178 | 0.331 | no | 1.028 | 0.284 | no | 1.180 | 0.286 | no | 1.718 | 0.540 | yes |
| DR2637 | Enolase | 0.758 | 0.081 | no | 1.010 | 0.368 | no | 0.750 | 0.202 | no | 0.665 | 0.406 | yes | 0.840 | 0.536 | no | 1.079 | 0.514 | no | 0.933 | 0.321 | no | 1.094 | 0.302 | no | 1.992 | 0.550 | yes |
| DRA0001 | SOJ/RepA protein | 0.920 | 0.282 | no | 0.584 | 0.259 | yes | 0.545 | 0.121 | yes | 0.662 | 0.374 | yes | 0.694 | 0.144 | no | 0.930 | 0.369 | no | 0.871 | 0.279 | no | 0.931 | 0.153 | no | 1.552 | 0.189 | yes |
| DRA0002 | Spo0J/RepB-like protein | 0.834 | 0.179 | no | 0.648 | 0.150 | yes | 0.774 | 0.208 | no | 0.852 | 0.167 | no | 0.833 | 0.316 | no | 1.025 | 0.190 | no | 0.940 | 0.271 | no | 1.083 | 0.136 | no | 1.806 | 0.655 | yes |
| DRA0003 | Succinate-semialdehyde dehydrogenase | 1.053 | 0.248 | no | 0.375 | 0.133 | yes | 0.252 | 0.075 | yes | 0.341 | 0.144 | yes | 0.388 | 0.159 | yes | 0.448 | 0.118 | yes | 0.610 | 0.285 | yes | 0.735 | 0.104 | no | 1.081 | 0.343 | no |
| DRA0004 | Sugar nucleotidyl transferase | 1.228 | 0.412 | no | 0.784 | 0.164 | no | 0.611 | 0.092 | yes | 0.768 | 0.171 | no | 0.675 | 0.281 | yes | 1.027 | 0.436 | no | 0.951 | 0.411 | no | 1.005 | 0.465 | no | 0.778 | 0.193 | no |
| DRA0005 | NAD alcohol dehydrogenase | 1.161 | 0.503 | no | 0.356 | 0.088 | yes | 0.273 | 0.045 | yes | 0.528 | 0.175 | yes | 0.807 | 0.367 | no | 1.263 | 0.406 | no | 1.833 | 0.817 | yes | 1.602 | 0.245 | yes | 1.392 | 0.829 | no |
| DRA0006 | Small conserved proteins, distantly related to polyketide cyclases? | 1.074 | 0.264 | no | 0.358 | 0.108 | yes | 0.459 | 0.315 | yes | 0.662 | 0.338 | yes | 0.835 | 0.316 | no | 1.096 | 0.251 | no | 1.339 | 0.341 | no | 2.126 | 0.610 | yes | 1.739 | 0.354 | yes |
| DRA0007 | NODI ABC ATPase | 1.455 | 0.440 | no | 1.815 | 0.855 | yes | 1.622 | 0.793 | yes | 2.036 | 0.465 | yes | 1.819 | 1.336 | yes | 1.705 | 0.399 | yes | 1.473 | 0.588 | no | 1.170 | 0.204 | no | 0.956 | 0.035 | no |
| DRA0008 | Conserved membrane protein (possible transporter) | 1.768 | 0.636 | yes | 3.553 | 1.727 | yes | 6.235 | 3.328 | yes | 6.597 | 1.996 | yes | 5.089 | 2.128 | yes | 3.067 | 0.779 | yes | 2.717 | 1.026 | yes | 1.389 | 0.514 | no | 1.106 | 0.284 | no |
| DRA0009 | Membrane bounded sensor histidine kinase | 1.565 | 0.377 | yes | 2.676 | 1.145 | yes | 2.605 | 0.381 | yes | 2.870 | 0.570 | yes | 3.026 | 1.250 | yes | 2.481 | 0.591 | yes | 2.842 | 1.730 | yes | 1.702 | 0.236 | yes | 1.153 | 0.282 | no |
| DRA0010 | CheY -like sensor regulator + HTH domain | 1.397 | 0.385 | no | 2.915 | 0.735 | yes | 4.034 | 1.095 | yes | 3.845 | 0.763 | yes | 4.657 | 2.117 | yes | 2.775 | 0.591 | yes | 2.780 | 1.275 | yes | 1.897 | 0.408 | yes | 1.754 | 0.453 | yes |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DRA0011 | Uroporphyrin-III c-methyltransferase, CYSG | 1.373 | 0.333 | no | 1.964 | 0.521 | yes | 2.531 | 0.958 | yes | 2.054 | 0.613 | yes | 1.499 | 0.424 | no | 2.244 | 0.898 | yes | 1.877 | 0.787 | yes | 1.608 | 0.655 | yes | 2.168 | 0.706 | yes |
| DRA0012 | Multidomain protein, has 2 domains metal-binding, related to MJ0970 | 1.176 | 0.238 | no | 2.286 | 0.875 | yes | 2.947 | 1.467 | yes | 2.287 | 0.932 | yes | 2.847 | 1.290 | yes | 2.418 | 0.632 | yes | 2.601 | 1.594 | yes | 2.475 | 1.257 | yes | 2.807 | 1.090 | yes |
| DRA0013 | Nitrite/sulfite reductase | 1.188 | 0.243 | no | 1.387 | 0.276 | no | 2.792 | 0.914 | yes | 4.503 | 2.054 | yes | 5.400 | 2.454 | yes | 4.264 | 0.823 | yes | 2.870 | 1.050 | yes | 1.741 | 0.604 | yes | 8.266 | 1.845 | yes |
| DRA0014 | PAPS synthase (APS kinase domain), CysC | 1.324 | 0.292 | no | 1.491 | 0.504 | yes | 2.085 | 0.881 | yes | 2.122 | 0.270 | yes | 3.350 | 1.965 | yes | 2.505 | 0.678 | yes | 1.614 | 0.406 | yes | 1.634 | 0.550 | yes | 4.326 | 1.659 | yes |
| DRA0015 | PAPS reductase | 1.263 | 0.717 | no | 2.153 | 0.582 | yes | 5.927 | 1.658 | yes | 7.022 | 0.621 | yes | 7.707 | 2.438 | yes | 6.942 | 2.762 | yes | 4.993 | 2.344 | yes | 3.460 | 1.581 | yes | 11.423 | 5.732 | yes |
| DRA0016 | Sulfate adenylyltransferase | 1.657 | 0.328 | yes | 3.194 | 0.367 | yes | 7.267 | 3.594 | yes | 12.120 | 2.450 | yes | 9.687 | 3.480 | yes | 7.869 | 2.226 | yes | 6.669 | 4.543 | yes | 2.181 | 0.231 | yes | 12.124 | 5.828 | yes |
| DRA0017 | Thioesterase | 1.064 | 0.207 | no | 1.288 | 0.358 | no | 2.016 | 0.151 | yes | 2.394 | 0.458 | yes | 3.158 | 0.820 | yes | 2.263 | 0.320 | yes | 2.832 | 0.840 | yes | 1.987 | 0.712 | yes | 2.373 | 0.299 | yes |
| DRA0019 | NH2-acetyltransferase | 1.086 | 0.362 | no | 0.706 | 0.146 | no | 1.216 | 0.142 | no | 1.523 | 0.636 | no | 1.834 | 0.611 | yes | 1.378 | 0.422 | no | 1.474 | 0.390 | no | 1.548 | 0.669 | yes | 1.339 | 0.192 | no |
| DRA0020 | COBU cobinamide kinase/cobinamide phosphate guanylyltransferase | 1.225 | 0.463 | no | 1.208 | 0.181 | no | 1.624 | 0.183 | yes | 2.127 | 0.511 | yes | 1.905 | 0.308 | yes | 1.685 | 0.534 | yes | 1.410 | 0.342 | no | 1.148 | 0.087 | no | 1.585 | 0.148 | yes |
| DRA0021 | Contains INTEGRIN(alpha)-like repeat motif | 1.736 | 0.803 | yes | 2.862 | 1.195 | yes | 3.393 | 2.193 | yes | 5.724 | 4.132 | yes | 4.833 | 3.612 | yes | 2.420 | 0.805 | yes | 4.085 | 2.070 | yes | 1.270 | 0.288 | no | 1.277 | 0.359 | no |
| DRA0022 | Icd? | 1.220 | 0.588 | no | 0.704 | 0.239 | no | 0.749 | 0.281 | no | 1.501 | 0.914 | no | 1.298 | 0.538 | no | 1.157 | 0.494 | no | 1.080 | 0.649 | no | 0.873 | 0.156 | no | 1.215 | 0.187 | no |
| DRA0023 | Capsular polyglutamate biosynthesis protein | 1.439 | 0.324 | no | 0.815 | 0.277 | no | 0.701 | 0.140 | no | 0.845 | 0.128 | no | 0.872 | 0.240 | no | 0.979 | 0.400 | no | 1.039 | 0.322 | no | 0.991 | 0.335 | no | 1.224 | 0.132 | no |
| DRA0024 | Predicted protein | 1.242 | 0.649 | no | 0.623 | 0.296 | yes | 0.695 | 0.174 | no | 0.737 | 0.087 | no | 0.731 | 0.311 | no | 0.746 | 0.242 | no | 0.787 | 0.266 | no | 0.686 | 0.123 | yes | 0.789 | 0.442 | no |
| DRA0026 | Predicted protein | 1.406 | 0.868 | no | 0.741 | 0.320 | no | 0.625 | 0.366 | yes | 1.043 | 0.534 | no | 0.828 | 0.322 | no | 1.387 | 0.962 | no | 3.901 | 2.131 | yes | 3.308 | 0.975 | yes | 2.331 | 0.890 | yes |
| DRA0027 | Biotin synthase/P-methylase family of metal cluster enzymes | 0.631 | 0.273 | yes | 0.187 | 0.086 | yes | 0.155 | 0.069 | yes | 2.811 | 0.722 | yes | 0.458 | 0.356 | yes | 0.350 | 0.192 | yes | 2.039 | 1.411 | yes | 1.111 | 0.267 | no | 0.544 | 0.197 | yes |
| DRA0028 | Uncharacterized conserved protein | 1.022 | 0.489 | no | 1.087 | 0.925 | no | 0.333 | 0.105 | yes | 5.781 | 1.869 | yes | 3.158 | 1.492 | yes | 0.391 | 0.133 | yes | 1.275 | 1.051 | no | 1.408 | 0.637 | no | 0.591 | 0.168 | yes |
| DRA0029 | 4-aminobutyrate aminotransferase | 0.904 | 0.176 | no | 1.628 | 0.696 | no | 0.256 | 0.042 | yes | 4.878 | 1.527 | yes | 0.376 | 0.046 | yes | 0.600 | 0.436 | yes | 2.120 | 0.831 | yes | 1.962 | 0.602 | yes | 0.776 | 0.309 | no |
| DRA0030 | Aldehyde dehydrogenase | 1.185 | 0.591 | no | 0.673 | 0.230 | no | 0.809 | 0.418 | no | 4.713 | 0.934 | yes | 2.685 | 1.722 | yes | 1.358 | 0.811 | no | 1.929 | 1.406 | yes | 2.625 | 1.366 | yes | 0.771 | 0.139 | no |
| DRA0031 | Glucose-1-phosphate thymidylyltransferase | 1.281 | 0.478 | no | 0.843 | 0.380 | no | 0.853 | 0.185 | no | 1.746 | 0.787 | yes | 1.545 | 0.679 | no | 1.866 | 1.010 | yes | 2.482 | 1.643 | yes | 1.364 | 0.212 | no | 1.562 | 0.879 | no |
| DRA0032 | GDP-mannose pyrophosphorylase | 1.390 | 0.439 | no | 1.134 | 0.407 | no | 1.491 | 0.546 | yes | 1.705 | 0.537 | yes | 1.455 | 0.223 | no | 1.794 | 0.378 | yes | 1.742 | 0.655 | yes | 1.781 | 0.414 | yes | 2.230 | 0.303 | yes |
| DRA0033 | Polysaccharide export protein EPSB, MinD family ATPase | 0.948 | 0.323 | no | 0.882 | 0.444 | no | 0.932 | 0.316 | no | 1.063 | 0.098 | no | 1.136 | 0.263 | no | 1.211 | 0.348 | no | 2.171 | 0.823 | yes | 2.040 | 0.735 | yes | 2.183 | 0.526 | yes |
| DRA0034 | RfbP glycosyl transferase | 1.824 | 0.744 | yes | 1.904 | 0.638 | yes | 3.047 | 0.829 | yes | 2.340 | 0.850 | yes | 2.584 | 0.791 | yes | 2.692 | 0.868 | yes | 3.522 | 1.593 | yes | 3.065 | 1.410 | yes | 2.924 | 0.701 | yes |
| DRA0035 | RfbX Membrane transporter | 2.738 | 1.413 | yes | 2.490 | 1.214 | yes | 2.715 | 1.227 | yes | 3.044 | 1.346 | yes | 3.895 | 2.433 | yes | 3.763 | 1.298 | yes | 4.958 | 3.026 | yes | 3.819 | 2.303 | yes | 2.636 | 1.295 | yes |
| DRA0036 | Possible membrane protein | 2.840 | 0.633 | yes | 3.287 | 1.840 | yes | 2.831 | 1.328 | yes | 4.569 | 1.321 | yes | 4.278 | 1.984 | yes | 6.272 | 1.801 | yes | 9.089 | 4.511 | yes | 2.085 | 0.519 | yes | 2.140 | 1.201 | yes |
| DRA0037 | Glycosyltransferase | 2.830 | 1.288 | yes | 3.504 | 2.089 | yes | 4.191 | 2.154 | yes | 3.213 | 0.770 | yes | 7.249 | 3.690 | yes | 9.468 | 2.219 | yes | 9.142 | 6.103 | yes | 12.103 | 4.192 | yes | 2.972 | 1.396 | yes |
| DRA0038 | RfbQ rhamnosyl transferase | 1.847 | 0.727 | yes | 1.508 | 0.671 | yes | 1.897 | 0.935 | yes | 4.360 | 2.302 | yes | 3.687 | 2.239 | yes | 11.297 | 7.707 | yes | 8.653 | 5.330 | yes | 7.627 | 2.464 | yes | 3.753 | 0.910 | yes |
| DRA0039 | RfbU transferase | 1.341 | 0.538 | no | 1.794 | 1.010 | yes | 1.413 | 0.828 | no | 1.846 | 0.977 | yes | 2.344 | 1.242 | yes | 3.024 | 1.634 | yes | 5.194 | 3.200 | yes | 4.318 | 1.609 | yes | 2.560 | 1.223 | yes |
| DRA0040 | RfbU transferase | 1.273 | 0.461 | no | 1.582 | 0.339 | yes | 1.627 | 0.578 | yes | 1.876 | 0.590 | yes | 2.138 | 0.664 | yes | 2.883 | 1.479 | yes | 3.007 | 0.999 | yes | 2.587 | 1.313 | yes | 1.658 | 0.555 | yes |
| DRA0041 | RfbB dTDP-glucose 4,6-dehydratase | 1.087 | 0.194 | no | 1.368 | 0.349 | no | 1.200 | 0.322 | no | 1.661 | 0.342 | yes | 1.844 | 0.264 | yes | 3.555 | 1.229 | yes | 4.542 | 0.871 | yes | 3.974 | 1.695 | yes | 2.706 | 0.565 | yes |
| DRA0042 | RfbA glucose-1-phosphate thymidylyltransferase | 1.314 | 0.247 | no | 1.266 | 0.179 | no | 1.830 | 1.067 | yes | 1.513 | 0.432 | no | 1.508 | 0.301 | yes | 3.289 | 1.126 | yes | 3.700 | 1.187 | yes | 1.801 | 0.538 | yes | 2.421 | 0.300 | yes |
| DRA0043 | TDP-rhamnose synthetase | 1.285 | 0.347 | no | 1.417 | 0.222 | yes | 1.511 | 0.398 | yes | 1.685 | 0.246 | yes | 2.515 | 0.748 | yes | 3.221 | 1.321 | yes | 5.083 | 2.120 | yes | 3.140 | 0.840 | yes | 2.627 | 0.479 | yes |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DRA0044 | RfbD/C? dTDP-4-dehydrorhamnose reductase | 1.394 | 0.338 | no | 1.531 | 0.336 | yes | 1.815 | 0.382 | yes | 1.955 | 0.384 | yes | 2.423 | 0.881 | yes | 4.194 | 1.797 | yes | 3.571 | 0.850 | yes | 1.705 | 0.547 | yes | 2.293 | 0.252 | yes |
| DRA0045 | Predicted protein | 1.303 | 0.312 | no | 1.269 | 0.389 | no | 1.050 | 0.487 | no | 1.011 | 0.456 | no | 0.935 | 0.454 | no | 1.451 | 0.479 | no | 2.105 | 0.993 | yes | 2.263 | 1.267 | yes | 1.503 | 0.508 | no |
| DRA0046 | Membrane protein possibly related to exopolysaccharide production | 1.040 | 0.287 | no | 0.844 | 0.253 | no | 0.719 | 0.234 | no | 0.802 | 0.200 | no | 0.931 | 0.290 | no | 1.040 | 0.297 | no | 1.124 | 0.284 | no | 1.294 | 0.393 | no | 1.191 | 0.256 | no |
| DRA0047 | Phosphoglucomutase/phosphomannomutase | 1.004 | 0.327 | no | 0.669 | 0.118 | yes | 0.655 | 0.101 | yes | 0.904 | 0.095 | no | 1.297 | 0.374 | no | 2.026 | 0.631 | yes | 2.339 | 0.429 | yes | 2.239 | 0.953 | yes | 1.411 | 0.191 | no |
| DRA0048 | PMI mannose-6-phosphate isomerase | 1.266 | 0.459 | no | 1.283 | 0.683 | no | 1.513 | 0.839 | no | 1.516 | 0.750 | no | 1.349 | 0.226 | no | 1.946 | 0.768 | yes | 1.574 | 0.513 | yes | 1.350 | 0.577 | no | 1.569 | 0.384 | yes |
| DRA0049 | Response regulator CHEY family, flavodoxin | 2.016 | 1.148 | yes | 1.395 | 0.556 | no | 2.139 | 0.688 | yes | 2.025 | 0.497 | yes | 2.727 | 1.117 | yes | 3.160 | 1.698 | yes | 2.856 | 0.779 | yes | 1.462 | 0.496 | no | 1.027 | 0.515 | no |
| DRA0050 | Phytochrome like histidine kinase + GAF domain | 1.698 | 0.562 | yes | 1.343 | 0.249 | no | 2.105 | 1.359 | yes | 2.182 | 1.212 | yes | 2.032 | 1.331 | yes | 1.821 | 0.865 | yes | 1.857 | 1.004 | yes | 1.132 | 0.226 | no | 0.876 | 0.100 | no |
| DRA0051 | Iron-starvation protein PigA/HemO | 0.841 | 0.460 | no | 1.031 | 0.503 | no | 2.353 | 1.862 | yes | 0.573 | 0.219 | yes | 0.480 | 0.168 | yes | 0.745 | 0.311 | no | 0.732 | 0.198 | no | 0.827 | 0.426 | no | 0.474 | 0.117 | yes |
| DRA0052 | Predicted protein | 1.355 | 0.867 | no | 1.594 | 0.823 | yes | 1.489 | 0.905 | no | 0.840 | 0.063 | no | 3.157 | 2.227 | yes | 1.777 | 1.148 | no | 2.339 | 1.693 | yes | 1.325 | 0.543 | no | 0.548 | 0.135 | yes |
| DRA0053 | 3-ketoacyl-CoA thiolase | 0.975 | 0.444 | no | 0.697 | 0.341 | yes | 0.829 | 0.304 | no | 0.837 | 0.627 | no | 0.740 | 0.225 | no | 0.882 | 0.370 | no | 0.966 | 0.403 | no | 0.958 | 0.429 | no | 0.621 | 0.174 | yes |
| DRA0054 | Succinyl-COA:3-ketoacid-CoA transferase | 1.088 | 0.470 | no | 0.850 | 0.185 | no | 1.239 | 0.473 | no | 1.061 | 0.042 | no | 1.240 | 0.274 | no | 1.326 | 0.516 | no | 1.046 | 0.283 | no | 1.066 | 0.340 | no | 1.136 | 0.221 | no |
| DRA0055 | RBSK-like ribokinase | 1.688 | 0.736 | yes | 1.320 | 0.449 | no | 1.440 | 0.396 | no | 1.983 | 0.958 | yes | 1.934 | 1.270 | yes | 1.373 | 0.386 | no | 1.498 | 0.751 | no | 1.483 | 0.630 | no | 0.709 | 0.198 | no |
| DRA0056 | Predicted protein | 1.730 | 0.751 | yes | 2.850 | 1.744 | yes | 3.638 | 1.322 | yes | 5.889 | 3.055 | yes | 2.697 | 0.693 | yes | 3.235 | 1.693 | yes | 3.448 | 1.464 | yes | 1.549 | 0.492 | yes | 0.783 | 0.238 | no |
| DRA0057 | Tellurium resistance protein TERE + McrA family nuclease | 1.831 | 0.755 | yes | 2.246 | 1.095 | yes | 2.336 | 1.061 | yes | 2.804 | 1.536 | yes | 2.418 | 1.102 | yes | 2.285 | 1.067 | yes | 2.282 | 1.570 | yes | 1.235 | 0.382 | no | 0.860 | 0.230 | no |
| DRA0058 | Predicted protein | 1.383 | 0.503 | no | 1.930 | 1.068 | yes | 1.394 | 0.792 | no | 2.210 | 0.604 | yes | 1.684 | 0.747 | yes | 2.117 | 0.427 | yes | 1.512 | 0.568 | no | 1.196 | 0.378 | no | 0.952 | 0.458 | no |
| DRA0059 | HTH containing transcriptional regulator | 1.288 | 0.504 | no | 1.086 | 0.373 | no | 1.234 | 0.450 | no | 0.800 | 0.266 | no | 1.504 | 0.886 | no | 1.344 | 0.507 | no | 1.329 | 0.807 | no | 1.015 | 0.388 | no | 0.827 | 0.210 | no |
| DRA0060 | a/b hydrolase | 1.305 | 0.372 | no | 0.865 | 0.371 | no | 0.809 | 0.345 | no | 1.121 | 0.243 | no | 1.497 | 0.555 | no | 1.687 | 0.349 | yes | 1.547 | 0.382 | yes | 1.274 | 0.146 | no | 0.912 | 0.361 | no |
| DRA0061 | Permease, MDR-type | 1.422 | 0.292 | no | 1.558 | 0.578 | yes | 1.560 | 0.918 | no | 1.624 | 0.206 | yes | 1.440 | 0.376 | no | 1.820 | 0.487 | yes | 1.495 | 0.626 | no | 1.122 | 0.451 | no | 1.013 | 0.409 | no |
| DRA0062 | Nourseothricin? NH2 acetyltransferase | 0.979 | 0.360 | no | 1.357 | 0.261 | no | 1.809 | 0.831 | yes | 1.153 | 0.284 | no | 1.389 | 0.468 | no | 1.385 | 0.672 | no | 1.395 | 0.636 | no | 1.416 | 0.734 | no | 1.178 | 0.193 | no |
| DRA0063 | Probably sugar deacetylase, HPDD motif containing LmbE/PIG-L like proteins | 1.068 | 0.177 | no | 0.921 | 0.113 | no | 1.158 | 0.178 | no | 1.483 | 0.056 | no | 1.313 | 0.630 | no | 1.004 | 0.270 | no | 0.802 | 0.156 | no | 0.765 | 0.195 | no | 0.972 | 0.066 | no |
| DRA0064 | Thermostable? alkaline proteinase | 1.099 | 0.437 | no | 0.630 | 0.204 | yes | 0.721 | 0.137 | no | 0.440 | 0.059 | yes | 0.559 | 0.171 | yes | 0.676 | 0.419 | yes | 0.604 | 0.155 | yes | 0.661 | 0.124 | yes | 0.754 | 0.235 | no |
| DRA0065 | Chromosomal protein HU HupA | 1.304 | 0.800 | no | 0.345 | 0.073 | yes | 0.499 | 0.076 | yes | 0.669 | 0.107 | no | 1.464 | 0.649 | no | 3.420 | 1.344 | yes | 5.004 | 2.001 | yes | 4.882 | 2.007 | yes | 7.715 | 2.066 | yes |
| DRA0066 | N-acetylglucosamine-6-phosphate deacetylase | 1.048 | 0.350 | no | 1.044 | 0.308 | no | 1.466 | 0.544 | no | 0.996 | 0.352 | no | 1.307 | 0.574 | no | 1.425 | 0.583 | no | 1.122 | 0.340 | no | 1.089 | 0.387 | no | 1.167 | 0.512 | no |
| DRA0067 | SU? succinyl-coa:3-ketoacid CoA transferase | 1.072 | 0.178 | no | 1.029 | 0.315 | no | 0.930 | 0.186 | no | 0.763 | 0.221 | no | 0.962 | 0.325 | no | 0.669 | 0.179 | yes | 0.925 | 0.408 | no | 0.983 | 0.273 | no | 0.674 | 0.189 | no |
| DRA0068 | SU? succinyl-coa:3-ketoacid CoA transferase | 0.662 | 0.081 | no | 0.687 | 0.172 | no | 0.529 | 0.098 | yes | 0.432 | 0.068 | yes | 0.491 | 0.126 | yes | 0.561 | 0.121 | yes | 0.546 | 0.235 | yes | 0.718 | 0.145 | yes | 0.580 | 0.145 | yes |
| DRA0069 | Metallobetalactmase fold hydrolase, RNA processing family | 0.995 | 0.217 | no | 0.942 | 0.251 | no | 0.780 | 0.091 | no | 0.777 | 0.147 | no | 0.800 | 0.422 | no | 0.813 | 0.153 | no | 0.793 | 0.130 | no | 0.847 | 0.206 | no | 1.027 | 0.073 | no |
| DRA0070 | HTH transcription regulator | 0.784 | 0.120 | no | 0.904 | 0.433 | no | 0.677 | 0.182 | yes | 0.688 | 0.111 | no | 0.554 | 0.155 | yes | 0.566 | 0.388 | yes | 0.493 | 0.140 | yes | 0.421 | 0.074 | yes | 0.394 | 0.078 | yes |
| DRA0071 | HTH transcription regulator, Ars family | 0.925 | 0.488 | no | 2.040 | 0.951 | yes | 1.276 | 0.234 | no | 1.191 | 0.515 | no | 0.707 | 0.320 | no | 0.802 | 0.268 | no | 0.699 | 0.189 | no | 0.729 | 0.144 | no | 0.495 | 0.174 | yes |
| DRA0072 | NRDH/GLR glutaredoxin-like protein | 0.970 | 0.274 | no | 1.202 | 0.255 | no | 1.322 | 0.396 | no | 0.900 | 0.041 | no | 0.857 | 0.228 | no | 1.022 | 0.484 | no | 0.783 | 0.490 | no | 0.924 | 0.381 | no | 0.514 | 0.034 | yes |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DRA0073 | Zinc-transporting atpase | 1.127 | 0.413 | no | 2.433 | 0.935 | yes | 2.478 | 1.370 | yes | 1.598 | 0.680 | no | 1.749 | 1.314 | yes | 1.263 | 0.726 | no | 1.227 | 0.549 | no | 1.192 | 0.573 | no | 0.780 | 0.399 | no |
| DRA0074 | Probably phage repressor, LexA-related protein | 0.763 | 0.315 | no | 0.461 | 0.233 | yes | 0.745 | 0.305 | no | 0.750 | 0.335 | no | 1.356 | 1.018 | no | 0.710 | 0.431 | yes | 0.879 | 0.453 | no | 0.514 | 0.126 | yes | 1.223 | 0.330 | no |
| DRA0075 | TRANSPOSON, retovirus-like integrase | 1.337 | 0.416 | no | 1.054 | 0.444 | no | 0.823 | 0.177 | no | 1.560 | 0.623 | no | 5.055 | 3.306 | yes | 7.575 | 3.194 | yes | 8.313 | 5.558 | yes | 1.713 | 0.260 | yes | 0.923 | 0.279 | no |
| DRA0076 | P-loop ATPase phage related | 2.570 | 1.776 | yes | 1.561 | 0.748 | yes | 1.284 | 0.849 | no | 1.052 | 0.268 | no | 3.789 | 2.607 | yes | 5.373 | 2.896 | yes | 3.090 | 0.962 | yes | 2.754 | 1.398 | yes | 1.368 | 0.524 | no |
| DRA0077 | Predicted protein | 2.374 | 0.533 | yes | 3.721 | 2.475 | yes | 1.448 | 0.677 | no | 1.783 | 0.369 | yes | 3.797 | 2.260 | yes | 5.332 | 2.853 | yes | 3.686 | 2.156 | yes | 1.415 | 0.427 | no | 0.721 | 0.278 | no |
| DRA0078 | HTH transcription regulator | 1.913 | 0.792 | yes | 1.925 | 1.169 | yes | 1.799 | 1.120 | yes | 3.947 | 1.038 | yes | 5.647 | 2.429 | yes | 6.150 | 3.335 | yes | 6.488 | 4.170 | yes | 2.132 | 0.176 | yes | 1.313 | 0.175 | no |
| DRA0079 | Predicted protein | 1.428 | 0.381 | no | 1.536 | 0.774 | yes | 0.770 | 0.147 | no | 1.826 | 0.869 | yes | 6.660 | 4.666 | yes | 6.384 | 2.938 | yes | 8.097 | 4.925 | yes | 3.133 | 1.789 | yes | 1.397 | 0.415 | no |
| DRA0080 | Predicted protein | 1.912 | 0.815 | yes | 0.939 | 0.347 | no | 0.665 | 0.151 | yes | 1.083 | 0.655 | no | 3.258 | 2.437 | yes | 6.112 | 1.758 | yes | 2.364 | 1.364 | yes | 1.997 | 1.098 | yes | 1.119 | 0.504 | no |
| DRA0081 | Predicted protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DRA0082 | Predicted protein | 0.997 | 0.246 | no | 1.314 | 0.362 | no | 1.295 | 0.396 | no | 1.125 | 0.145 | no | 1.361 | 0.350 | no | 1.190 | 0.224 | no | 1.075 | 0.297 | no | 0.917 | 0.159 | no | 0.837 | 0.094 | no |
| DRA0083 | Predicted protein | 1.440 | 0.615 | no | 1.041 | 0.306 | no | 0.849 | 0.195 | no | 1.196 | 0.588 | no | 3.395 | 1.242 | yes | 4.758 | 1.650 | yes | 4.898 | 2.204 | yes | 2.563 | 0.836 | yes | 1.111 | 0.134 | no |
| DRA0084 | Predicted protein | 1.453 | 0.483 | no | 2.634 | 1.408 | yes | 1.720 | 0.878 | yes | 1.354 | 0.295 | no | 7.486 | 3.697 | yes | 9.889 | 7.062 | yes | 9.239 | 4.295 | yes | 2.140 | 0.949 | yes | 0.990 | 0.218 | no |
| DRA0085 | Predicted protein | 1.968 | 0.452 | yes | 2.891 | 0.771 | yes | 1.685 | 1.017 | yes | 3.344 | 1.552 | yes | 4.027 | 2.363 | yes | 7.506 | 4.069 | yes | 7.239 | 3.891 | yes | 1.591 | 0.473 | yes | 0.832 | 0.129 | no |
| DRA0086 | Predicted protein | 1.873 | 0.831 | yes | 1.590 | 0.805 | yes | 1.188 | 0.637 | no | 1.399 | 0.805 | no | 3.629 | 2.403 | yes | 1.924 | 1.076 | yes | 2.298 | 0.861 | yes | 2.336 | 1.050 | yes | 1.482 | 0.541 | no |
| DRA0087 | Predicted protein | 2.866 | 1.150 | yes | 2.131 | 0.223 | yes | 2.198 | 1.672 | yes | 1.570 | 0.578 | no | 1.888 | 0.973 | yes | 2.418 | 1.010 | yes | 1.507 | 1.121 | no | 1.009 | 0.150 | no | 0.717 | 0.382 | yes |
| DRA0088 | Predicted protein | 2.471 | 1.397 | yes | 2.133 | 1.212 | yes | 1.610 | 0.685 | yes | 1.774 | 0.215 | yes | 8.202 | 3.484 | yes | 7.412 | 2.448 | yes | 11.177 | 5.479 | yes | 1.009 | 0.044 | no | 0.686 | 0.342 | no |
| DRA0089 | Predicted protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DRA0090 | Predicted protein | 2.472 | 1.280 | yes | 2.447 | 0.878 | yes | 1.377 | 0.564 | no | 1.988 | 0.841 | yes | 3.976 | 0.847 | yes | 4.138 | 1.295 | yes | 1.884 | 1.041 | yes | 1.232 | 0.257 | no | 0.933 | 0.153 | no |
| DRA0091 | Predicted protein | 1.461 | 0.437 | no | 1.520 | 0.599 | yes | 1.462 | 0.573 | no | 1.002 | 0.128 | no | 1.326 | 0.750 | no | 1.283 | 0.786 | no | 1.053 | 0.477 | no | 0.892 | 0.152 | no | 0.697 | 0.206 | no |
| DRA0092 | Predicted protein | 1.636 | 0.917 | no | 1.444 | 0.891 | no | 1.196 | 0.649 | no | 1.538 | 0.179 | no | 1.501 | 0.561 | no | 1.862 | 0.412 | yes | 2.170 | 0.973 | yes | 1.968 | 1.207 | yes | 1.284 | 0.507 | no |
| DRA0093 | Predicted protein | 2.146 | 0.742 | yes | 1.666 | 0.672 | yes | 0.941 | 0.184 | no | 1.062 | 0.577 | no | 1.758 | 1.211 | no | 2.034 | 0.969 | yes | 1.083 | 0.747 | no | 0.971 | 0.197 | no | 0.769 | 0.486 | no |
| DRA0094 | Uncharacterized protein related to phage terminase | 1.606 | 1.035 | no | 0.576 | 0.095 | yes | 0.282 | 0.128 | yes | 1.521 | 0.838 | no | 0.381 | 0.173 | yes | 0.638 | 0.261 | yes | 0.903 | 0.441 | no | 0.852 | 0.497 | no | n/a | n/a | n/a |
| DRA0095 | Phage protein, pre-neck appendage protein? | 2.113 | 0.897 | yes | 0.804 | 0.527 | no | 0.860 | 0.693 | no | 0.597 | 0.286 | yes | 0.530 | 0.293 | yes | 0.572 | 0.401 | yes | 0.761 | 0.566 | yes | 0.913 | 0.302 | no | 0.370 | 0.107 | yes |
| DRA0096 | Predicted protein | 1.638 | 0.705 | no | 1.239 | 0.457 | no | 1.372 | 0.478 | no | 1.177 | 0.295 | no | 1.106 | 0.532 | no | 1.479 | 0.568 | no | 1.577 | 1.111 | no | 1.380 | 0.587 | no | 1.224 | 0.637 | no |
| DRA0097 | Phage-related protein | 1.602 | 0.546 | yes | 1.062 | 0.374 | no | 0.595 | 0.287 | yes | 0.951 | 0.125 | no | 0.619 | 0.270 | yes | 0.998 | 0.478 | no | 0.726 | 0.375 | no | 1.034 | 0.136 | no | 0.753 | 0.238 | no |
| DRA0098 | Predicted protein | 2.510 | 1.466 | yes | 1.366 | 0.966 | no | 1.783 | 1.223 | yes | 9.333 | 0.727 | yes | 14.020 | 2.766 | yes | 4.485 | 3.361 | yes | 5.858 | 3.799 | yes | 2.889 | 1.176 | yes | 1.514 | 0.459 | no |
| DRA0099 | Predicted protein | 1.477 | 0.648 | no | 0.974 | 0.333 | no | 1.068 | 0.487 | no | 1.045 | 0.240 | no | 1.672 | 0.954 | no | 1.317 | 0.418 | no | 1.406 | 1.016 | no | 1.435 | 0.533 | no | 1.290 | 0.549 | no |
| DRA0100 | Predicted protein | 0.808 | 0.457 | no | 1.425 | 0.589 | no | 0.937 | 0.807 | no | 3.717 | 0.398 | yes | 1.208 | 0.641 | no | 1.414 | 0.475 | no | 2.373 | 1.297 | yes | 0.667 | 0.183 | yes | 0.335 | 0.093 | yes |
| DRA0101 | Predicted protein | 1.355 | 0.469 | no | 1.533 | 0.782 | no | 1.424 | 0.360 | no | 5.253 | 2.474 | yes | 1.547 | 0.579 | no | 1.625 | 0.973 | no | 1.026 | 0.235 | no | 1.044 | 0.162 | no | 0.997 | 0.522 | no |
| DRA0102 | Predicted protein | 1.667 | 0.648 | yes | 1.419 | 0.354 | no | 1.739 | 0.727 | yes | 1.593 | 0.460 | no | 1.638 | 0.851 | yes | 1.534 | 0.588 | no | 1.526 | 0.933 | no | 1.114 | 0.432 | no | 0.675 | 0.302 | yes |
| DRA0103 | Predicted protein | 0.987 | 0.499 | no | 1.081 | 0.433 | no | 1.175 | 0.427 | no | 0.921 | 0.341 | no | 0.932 | 0.280 | no | 0.783 | 0.199 | no | 0.865 | 0.234 | no | 1.160 | 0.392 | no | 1.324 | 0.580 | no |
| DRA0104 | Predicted protein | 1.108 | 0.242 | no | 1.383 | 0.299 | no | 1.669 | 0.381 | yes | 1.583 | 0.577 | no | 1.310 | 0.615 | no | 1.073 | 0.215 | no | 1.101 | 0.422 | no | 0.991 | 0.313 | no | 0.999 | 0.421 | no |
| DRA0105 | Predicted protein | 0.991 | 0.541 | no | 0.838 | 0.195 | no | 0.797 | 0.344 | no | 0.820 | 0.208 | no | 1.116 | 0.713 | no | 0.757 | 0.242 | no | 0.710 | 0.353 | yes | 0.807 | 0.265 | no | 0.690 | 0.209 | no |
| DRA0106 | Predicted protein | 1.652 | 0.748 | yes | 1.460 | 0.409 | yes | 1.651 | 0.351 | yes | 1.490 | 0.480 | no | 1.068 | 0.452 | no | 1.143 | 0.663 | no | 0.736 | 0.281 | no | 0.942 | 0.442 | no | 0.877 | 0.221 | no |
| DRA0107 | Predicted protein | 1.224 | 0.501 | no | 1.553 | 0.903 | no | 2.345 | 1.584 | yes | 0.741 | 0.187 | no | 0.830 | 0.483 | no | 0.428 | 0.221 | yes | 1.302 | 0.713 | no | 0.716 | 0.191 | no | 0.529 | 0.092 | yes |
| DRA0108 | Phage-related protein | 2.187 | 1.454 | yes | 1.093 | 0.221 | no | 1.021 | 0.401 | no | 1.427 | 0.808 | no | 1.279 | 0.601 | no | 1.557 | 0.701 | no | 1.062 | 0.619 | no | 1.747 | 0.723 | yes | n/a | n/a | n/a |
| DRA0109 | Phage-related protein | 0.815 | 0.452 | no | 1.003 | 0.323 | no | 1.115 | 0.593 | no | 1.767 | 0.863 | no | 1.124 | 0.392 | no | 0.836 | 0.322 | no | 1.264 | 0.881 | no | 0.714 | 0.197 | yes | 0.400 | 0.139 | yes |
| DRA0110 | Predicted protein | 2.354 | 0.604 | yes | 1.980 | 0.603 | yes | 1.473 | 0.406 | yes | 2.180 | 0.301 | yes | 1.302 | 0.377 | no | 1.572 | 0.634 | no | 1.161 | 0.491 | no | 0.738 | 0.151 | no | 0.836 | 0.498 | no |
| DRA0111 | Predicted protein | 2.568 | 1.333 | yes | 1.916 | 0.906 | yes | 2.027 | 1.303 | yes | 1.327 | 0.297 | no | 1.130 | 0.533 | no | 1.574 | 0.869 | no | 1.164 | 0.659 | no | 0.959 | 0.550 | no | 1.142 | 0.665 | no |
| DRA0112 | Predicted protein, most likely S-layer | 1.026 | 0.287 | no | 1.027 | 0.628 | no | 1.207 | 0.795 | no | 1.805 | 0.664 | no | 0.783 | 0.346 | no | 1.093 | 0.704 | no | 1.028 | 0.283 | no | 1.100 | 0.557 | no | 0.897 | 0.455 | no |
| DRA0113 | Predicted protein | 2.346 | 1.555 | yes | 1.170 | 0.566 | no | 1.656 | 0.362 | yes | 1.387 | 0.160 | no | 1.260 | 0.484 | no | 1.195 | 0.763 | no | 1.050 | 0.518 | no | 1.033 | 0.431 | no | 0.833 | 0.561 | no |
| DRA0114 | Predicted protein | 1.596 | 1.053 | no | 0.946 | 0.409 | no | 0.947 | 0.564 | no | 0.748 | 0.292 | no | 0.835 | 0.323 | no | 0.880 | 0.120 | no | 0.708 | 0.435 | yes | 0.840 | 0.325 | no | 0.558 | 0.378 | yes |
| DRA0115 | Predicted protein | 1.752 | 0.607 | yes | 1.347 | 0.284 | no | 1.067 | 0.462 | no | 1.136 | 0.262 | no | 0.816 | 0.266 | no | 0.852 | 0.358 | no | 0.933 | 0.358 | no | 0.930 | 0.346 | no | 0.809 | 0.304 | no |
| DRA0116 | Predicted protein | 1.288 | 0.469 | no | 0.939 | 0.408 | no | 0.680 | 0.280 | yes | 0.958 | 0.058 | no | 0.763 | 0.257 | no | 0.601 | 0.120 | yes | 0.778 | 0.275 | no | 1.054 | 0.402 | no | 0.897 | 0.426 | no |
| DRA0117 | Bacteriophage protein | 1.592 | 0.620 | no | 1.269 | 0.531 | no | 1.241 | 0.298 | no | 1.141 | 0.167 | no | 0.904 | 0.366 | no | 0.782 | 0.330 | no | 0.801 | 0.393 | no | 0.859 | 0.247 | no | 0.739 | 0.158 | no |
| DRA0118 | Predicted protein | 1.517 | 0.902 | no | 0.730 | 0.377 | yes | 1.024 | 0.777 | no | 1.369 | 0.758 | no | 1.239 | 0.745 | no | 1.989 | 0.272 | yes | 2.190 | 0.675 | yes | 1.141 | 0.555 | no | 0.606 | 0.045 | no |
| DRA0119 | Fragment of methyltransferase?? | 1.243 | 0.527 | no | 0.651 | 0.330 | yes | 0.247 | 0.179 | yes | 0.634 | 0.113 | no | 0.438 | 0.190 | yes | 0.516 | 0.221 | yes | 0.538 | 0.200 | yes | 0.817 | 0.407 | no | 0.923 | 0.492 | no |
| DRA0119 5 | | 1.244 | 0.527 | no | 1.251 | 0.437 | no | 1.031 | 0.086 | no | 1.367 | 0.825 | no | 0.672 | 0.257 | yes | 0.752 | 0.155 | no | 0.795 | 0.294 | no | 0.780 | 0.029 | no | 0.884 | 0.371 | no |
| DRA0120 | Flavin dependent monooxygenase | 1.316 | 0.334 | no | 0.576 | 0.320 | yes | 0.371 | 0.080 | yes | 0.406 | 0.116 | yes | 0.375 | 0.081 | yes | 0.498 | 0.143 | yes | 0.610 | 0.199 | yes | 0.724 | 0.186 | yes | 1.073 | 0.197 | no |
| DRA0121 | Aminotransferase | 1.129 | 0.571 | no | 1.198 | 0.775 | no | 0.949 | 0.310 | no | 0.486 | 0.131 | yes | 0.638 | 0.294 | yes | 0.697 | 0.159 | no | 0.672 | 0.140 | yes | 0.968 | 0.297 | no | 0.763 | 0.243 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DRA0122 | 2-oxo-hept-3-ene-1,7-dioate hydratase | 1.313 | 0.225 | no | 0.806 | 0.200 | no | 0.481 | 0.171 | yes | 0.489 | 0.257 | yes | 0.498 | 0.124 | yes | 0.672 | 0.024 | no | 0.727 | 0.182 | no | 1.130 | 0.175 | no | 1.704 | 0.999 | yes |
| DRA0123 | Arsenate reductase, arsC-like, Rhodanese/phosphatase superfamily protein | 1.777 | 0.731 | yes | 1.395 | 0.667 | no | 0.977 | 0.480 | no | 1.005 | 0.518 | no | 1.020 | 0.596 | no | 1.083 | 0.746 | no | 0.996 | 0.290 | no | 0.633 | 0.044 | yes | 0.488 | 0.059 | yes |
| DRA0124 | Serine/threonine protein phosphatase, calcineurin family | 1.186 | 0.349 | no | 1.292 | 0.320 | no | 0.904 | 0.395 | no | 1.581 | 0.325 | no | 0.839 | 0.371 | no | 0.827 | 0.412 | no | 0.878 | 0.365 | no | 1.019 | 0.472 | no | 0.681 | 0.240 | no |
| DRA0125 | Repair protein Zn-ribbon domain (present in some helicases) | 2.045 | 1.068 | yes | 1.361 | 0.705 | no | 2.334 | 0.746 | yes | 1.484 | 0.944 | no | 0.846 | 0.505 | no | 0.853 | 0.281 | no | 1.095 | 0.668 | no | 0.845 | 0.308 | no | 0.468 | 0.225 | yes |
| DRA0126 | Aldehyde dehydrogenase, DHAB-like | 1.479 | 0.547 | no | 1.012 | 0.324 | no | 1.264 | 0.444 | no | 2.552 | 1.747 | yes | 1.211 | 0.299 | no | 1.043 | 0.314 | no | 1.166 | 0.258 | no | 1.050 | 0.185 | no | 0.900 | 0.373 | no |
| DRA0127 | BETA-like protein, similar to choline oxidase of plants; | 1.009 | 0.494 | no | 1.305 | 0.234 | no | 1.510 | 0.634 | no | 1.843 | 1.069 | yes | 2.605 | 1.005 | yes | 1.372 | 0.487 | no | 1.321 | 0.446 | no | 1.234 | 0.218 | no | 0.893 | 0.137 | no |
| DRA0128 | Predicted transcriptional regulator, HTH containing | 1.191 | 0.283 | no | 0.808 | 0.355 | no | 1.531 | 0.538 | no | 0.853 | 0.441 | no | 1.134 | 0.260 | no | 1.349 | 0.516 | no | 1.043 | 0.297 | no | 1.299 | 0.296 | no | 1.367 | 0.553 | no |
| DRA0129 | Related to oxidoreductase. homolog of yurF of Bacillus | 0.947 | 0.436 | no | 0.728 | 0.217 | no | 0.604 | 0.192 | yes | 0.434 | 0.104 | yes | 0.488 | 0.090 | yes | 0.734 | 0.338 | no | 0.842 | 0.428 | no | 0.904 | 0.263 | no | 0.714 | 0.095 | no |
| DRA0130 | NODS, SAM dependent methyltransferase | 1.050 | 0.227 | no | 0.794 | 0.360 | no | 0.853 | 0.351 | no | 0.787 | 0.237 | no | 0.601 | 0.270 | yes | 0.880 | 0.435 | no | 0.935 | 0.446 | no | 0.882 | 0.235 | no | 0.866 | 0.166 | no |
| DRA0131 | DNA repair helicase + mcra domain | 1.080 | 0.535 | no | 1.351 | 0.607 | no | 0.574 | 0.276 | yes | 0.511 | 0.319 | yes | 1.001 | 0.432 | no | 0.848 | 0.608 | no | 0.888 | 0.359 | no | 1.031 | 0.510 | no | 0.978 | 0.114 | no |
| DRA0132 | N-acetylglucosaminyl-phosphatidylinositol deacetylase related protein | 1.232 | 0.191 | no | 1.139 | 0.393 | no | 0.997 | 0.176 | no | 1.038 | 0.188 | no | 0.966 | 0.389 | no | 0.909 | 0.500 | no | 1.004 | 0.394 | no | 0.809 | 0.139 | no | 0.678 | 0.268 | yes |
| DRA0133 | Acyl-CoA-dehydrogenase | 1.209 | 0.323 | no | 0.869 | 0.136 | no | 0.830 | 0.196 | no | 0.984 | 0.201 | no | 1.131 | 0.598 | no | 1.434 | 0.323 | no | 1.202 | 0.511 | no | 1.112 | 0.388 | no | 0.805 | 0.278 | no |
| DRA0134 | Furostanol glycoside 26-O-beta-glucosidase | 1.848 | 1.073 | yes | 1.673 | 1.231 | no | 1.265 | 0.559 | no | 0.943 | 0.273 | no | 2.270 | 1.629 | yes | 0.821 | 0.355 | no | 0.481 | 0.286 | yes | 0.997 | 0.375 | no | 0.842 | 0.481 | no |
| DRA0135 | Periplasmic binding protein | 0.902 | 0.251 | no | 0.661 | 0.311 | yes | 0.447 | 0.164 | yes | 0.536 | 0.184 | yes | 0.750 | 0.264 | no | 0.747 | 0.247 | no | 1.071 | 0.550 | no | 0.933 | 0.091 | no | 1.027 | 0.237 | no |
| DRA0136 | Membrane, possible permease | 1.409 | 0.442 | no | 1.623 | 0.209 | yes | 1.445 | 0.887 | no | 1.551 | 0.062 | no | 1.362 | 0.463 | no | 0.901 | 0.310 | no | 1.074 | 0.166 | no | 1.016 | 0.142 | no | 0.892 | 0.094 | no |
| DRA0137 | ABC ATPase | 0.869 | 0.409 | no | 1.051 | 0.234 | no | 0.748 | 0.042 | no | 0.481 | 0.115 | yes | 0.694 | 0.221 | no | 0.960 | 0.261 | no | 0.840 | 0.328 | no | 1.053 | 0.201 | no | 0.871 | 0.148 | no |
| DRA0138 | Permease | 1.224 | 0.291 | no | 1.397 | 0.327 | no | 1.059 | 0.648 | no | 0.767 | 0.170 | no | 0.725 | 0.158 | no | 0.831 | 0.289 | no | 0.810 | 0.309 | no | 1.045 | 0.300 | no | 0.810 | 0.146 | no |
| DRA0139 | CHEY-like response regulator | 0.839 | 0.434 | no | 0.540 | 0.138 | yes | 0.433 | 0.081 | yes | 0.398 | 0.159 | yes | 0.498 | 0.204 | yes | 0.581 | 0.192 | yes | 0.759 | 0.216 | no | 0.902 | 0.192 | no | 0.720 | 0.270 | no |
| DRA0140 | Predicted protein | 1.079 | 0.275 | no | 0.698 | 0.158 | no | 0.583 | 0.120 | yes | 0.618 | 0.116 | yes | 0.548 | 0.182 | yes | 0.681 | 0.184 | yes | 0.850 | 0.283 | no | 0.945 | 0.308 | no | 0.979 | 0.215 | no |
| DRA0141 | Predicted protein | 0.756 | 0.169 | no | 0.550 | 0.194 | yes | 0.515 | 0.118 | yes | 0.765 | 0.458 | no | 1.310 | 0.624 | no | 2.850 | 1.525 | yes | 4.246 | 1.984 | yes | 4.510 | 1.467 | yes | 2.697 | 1.436 | yes |
| DRA0142 | TetR tetracycline repressor, HTH regulator | 1.093 | 0.145 | no | 0.960 | 0.184 | no | 1.019 | 0.227 | no | 1.026 | 0.181 | no | 0.978 | 0.216 | no | 0.793 | 0.187 | no | 0.864 | 0.272 | no | 0.958 | 0.191 | no | 0.924 | 0.240 | no |
| DRA0143 | 3-hydroxyacyl-CoA dehydrogenase | 0.969 | 0.362 | no | 0.371 | 0.120 | yes | 0.182 | 0.122 | yes | 0.138 | 0.072 | yes | 0.360 | 0.183 | yes | 0.333 | 0.121 | yes | 0.481 | 0.168 | yes | 0.720 | 0.090 | yes | 1.228 | 0.395 | no |
| DRA0144 | Predicted protein | 1.090 | 0.217 | no | 0.396 | 0.095 | yes | 0.181 | 0.061 | yes | 0.209 | 0.029 | yes | 0.294 | 0.114 | yes | 0.324 | 0.126 | yes | 0.447 | 0.070 | yes | 0.751 | 0.110 | no | 1.153 | 0.204 | no |
| DRA0145 | Peroxidase | 0.921 | 0.449 | no | 0.388 | 0.169 | yes | 0.241 | 0.160 | yes | 0.124 | 0.045 | yes | 0.213 | 0.127 | yes | 0.320 | 0.123 | yes | 0.522 | 0.205 | yes | 0.838 | 0.061 | no | 1.184 | 0.364 | no |
| DRA0146 | Catalase | 1.081 | 0.269 | no | 0.564 | 0.199 | yes | 0.298 | 0.139 | yes | 0.231 | 0.031 | yes | 0.345 | 0.106 | yes | 0.482 | 0.188 | yes | 0.667 | 0.175 | yes | 1.076 | 0.126 | no | 2.204 | 0.498 | yes |
| DRA0147 | Histidine ammonia-lyase, histidase | 1.248 | 0.491 | no | 1.084 | 0.372 | no | 1.759 | 1.100 | yes | 2.451 | 0.480 | yes | 1.842 | 0.357 | yes | 1.331 | 0.433 | no | 1.041 | 0.132 | no | 0.940 | 0.324 | no | 1.052 | 0.356 | no |
| DRA0148 | Imidazolonepropionase, TIM barrel metallohydrolase | 0.907 | 0.191 | no | 0.926 | 0.231 | no | 0.974 | 0.269 | no | 2.130 | 0.400 | yes | 1.359 | 0.771 | no | 1.050 | 0.414 | no | 1.026 | 0.250 | no | 0.875 | 0.095 | no | 1.039 | 0.525 | no |
| DRA0149 | Agmatinase, (arginase) | 1.239 | 0.474 | no | 1.413 | 0.688 | no | 3.735 | 1.702 | yes | 2.871 | 1.366 | yes | 1.839 | 0.386 | yes | 1.909 | 0.596 | yes | 1.566 | 0.483 | yes | 1.224 | 0.419 | no | 0.924 | 0.358 | no |
| DRA0150 | A/b hydrolase | 1.326 | 0.477 | no | 1.327 | 0.280 | no | 2.879 | 1.696 | yes | 2.291 | 1.438 | yes | 1.730 | 0.267 | yes | 1.531 | 0.345 | yes | 1.208 | 0.204 | no | 1.460 | 0.470 | no | 1.000 | 0.194 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DRA0151 | Urocanase hydratase | 1.100 | 0.595 | no | 1.590 | 0.501 | yes | 2.375 | 0.750 | yes | 2.717 | 0.031 | yes | 2.629 | 1.419 | yes | 1.582 | 0.437 | yes | 1.483 | 0.655 | no | 1.625 | 0.704 | yes | 1.263 | 0.164 | no |
| DRA0152 | HTH transcription regulator | 1.268 | 0.534 | no | 0.894 | 0.367 | no | 1.015 | 0.384 | no | 1.136 | 0.304 | no | 1.153 | 0.390 | no | 1.200 | 0.566 | no | 1.147 | 0.421 | no | 1.568 | 0.593 | yes | 1.350 | 0.288 | no |
| DRA0153 | DEDA like Membrane protein | 1.276 | 0.765 | no | 0.953 | 0.092 | no | 1.064 | 0.376 | no | 0.739 | 0.414 | no | 0.862 | 0.234 | no | 1.312 | 0.593 | no | 1.129 | 0.448 | no | 1.183 | 0.303 | no | 0.919 | 0.468 | no |
| DRA0154 | Glutamine-fructose-6-phosphate transaminase, GLMS | 1.408 | 0.522 | no | 0.821 | 0.248 | no | 1.201 | 0.823 | no | 0.792 | 0.187 | no | 1.022 | 0.478 | no | 0.871 | 0.550 | no | 0.985 | 0.309 | no | 0.896 | 0.370 | no | 0.900 | 0.354 | no |
| DRA0155 | XerC recombinase | 1.023 | 0.468 | no | 0.969 | 0.175 | no | 1.036 | 0.320 | no | 0.767 | 0.079 | no | 0.912 | 0.347 | no | 1.076 | 0.449 | no | 1.140 | 0.362 | no | 1.268 | 0.351 | no | 0.767 | 0.058 | no |
| DRA0156 | Small conserved bacterial proteins, YOHL_ECOLI | 1.264 | 0.360 | no | 1.536 | 0.432 | yes | 1.415 | 0.556 | no | 1.409 | 0.168 | no | 1.231 | 0.509 | no | 1.458 | 0.945 | no | 1.039 | 0.558 | no | 0.993 | 0.408 | no | 0.963 | 0.443 | no |
| DRA0157 | Periplasmic phosphate-binding protein PSTS | 1.480 | 0.653 | no | 1.344 | 0.458 | no | 1.237 | 0.343 | no | 2.118 | 0.767 | yes | 3.024 | 1.423 | yes | 2.196 | 1.134 | yes | 1.432 | 0.638 | no | 1.114 | 0.376 | no | 0.998 | 0.646 | no |
| DRA0158 | Phosphate transport system permease PSTA | 2.163 | 0.855 | yes | 2.136 | 1.220 | yes | 1.930 | 0.372 | yes | 2.439 | 1.305 | yes | 2.361 | 1.084 | yes | 2.153 | 1.581 | yes | 1.716 | 1.148 | no | 0.840 | 0.083 | no | 0.596 | 0.201 | yes |
| DRA0159 | Phosphate transport permease PSTA | 1.370 | 0.785 | no | 1.113 | 0.420 | no | 1.678 | 0.811 | yes | 1.497 | 0.661 | no | 1.907 | 0.570 | yes | 1.560 | 0.615 | no | 1.626 | 0.885 | no | 1.130 | 0.378 | no | 0.926 | 0.351 | no |
| DRA0160 | Phosphate transport ATPase, PhoT/PSTB | 1.510 | 0.496 | no | 1.467 | 0.538 | no | 1.837 | 0.889 | yes | 2.434 | 0.579 | yes | 2.097 | 1.031 | yes | 1.344 | 0.599 | no | 1.286 | 0.614 | no | 1.177 | 0.426 | no | 0.852 | 0.212 | no |
| DRA0161 | Regulator PhoU | 1.368 | 0.399 | no | 1.439 | 0.702 | no | 0.986 | 0.422 | no | 6.172 | 2.232 | yes | 2.679 | 1.473 | yes | 1.730 | 0.667 | yes | 1.454 | 1.062 | no | 1.063 | 0.037 | no | 0.745 | 0.264 | no |
| DRA0162 | Uncharcterized, possible component of trasport system, homolog of YEEE | 1.286 | 0.597 | no | 1.052 | 0.404 | no | 0.739 | 0.350 | yes | 1.203 | 0.426 | no | 0.782 | 0.253 | no | 0.733 | 0.262 | no | 0.685 | 0.168 | no | 0.852 | 0.148 | no | 0.614 | 0.043 | yes |
| DRA0163 | Uncharcterized, possible component of trasport system, homolog of YEEE | 1.769 | 1.139 | no | 1.351 | 0.583 | no | 1.280 | 0.271 | no | 1.723 | 0.554 | yes | 1.151 | 0.687 | no | 0.993 | 0.515 | no | 1.115 | 0.541 | no | 0.970 | 0.375 | no | 1.117 | 0.474 | no |
| DRA0164 | Thioredoxin | 1.052 | 0.436 | no | 0.891 | 0.429 | no | 1.046 | 0.645 | no | 0.913 | 0.387 | no | 0.711 | 0.262 | yes | 0.991 | 0.173 | no | 1.050 | 0.562 | no | 1.052 | 0.217 | no | 1.049 | 0.389 | no |
| DRA0165 | Predicted protein | 1.489 | 0.473 | no | 1.461 | 0.722 | no | 1.420 | 0.898 | no | 1.296 | 0.534 | no | 0.861 | 0.453 | no | 0.940 | 0.590 | no | 0.718 | 0.262 | no | 0.855 | 0.299 | no | 0.937 | 0.290 | no |
| DRA0166 | Multidomain protein containing MolR-like domain fused to probable ABC transportes (including ATPase domain) | 1.194 | 0.805 | no | 0.431 | 0.250 | yes | 0.167 | 0.125 | yes | 5.678 | 2.573 | yes | 1.485 | 0.786 | no | 0.288 | 0.153 | yes | 0.793 | 0.481 | no | 1.003 | 0.336 | no | 2.430 | 0.913 | yes |
| DRA0167 | Conserved protein | 1.458 | 0.671 | no | 1.979 | 1.182 | yes | 2.216 | 1.248 | yes | 2.165 | 0.907 | yes | 1.220 | 0.360 | no | 1.178 | 0.322 | no | 1.520 | 0.845 | no | 1.512 | 0.355 | yes | 1.459 | 0.762 | no |
| DRA0168 | ModB permease | 1.694 | 0.667 | yes | 1.676 | 1.237 | no | 4.334 | 2.212 | yes | 5.113 | 0.172 | yes | 0.903 | 0.528 | no | 1.071 | 0.539 | no | 0.745 | 0.405 | no | 0.964 | 0.500 | no | 0.848 | 0.318 | no |
| DRA0169 | Molibdate-binding periplasmic protein | 1.634 | 0.582 | yes | 1.505 | 0.722 | no | 2.036 | 0.777 | yes | 1.310 | 0.515 | no | 1.509 | 0.679 | no | 1.589 | 0.702 | no | 1.170 | 0.374 | no | 0.999 | 0.227 | no | 1.027 | 0.620 | no |
| DRA0170 | Predicted protein | 2.075 | 0.994 | yes | 1.176 | 0.517 | no | 1.243 | 0.631 | no | 2.042 | 1.041 | yes | 1.194 | 0.743 | no | 0.806 | 0.274 | no | 1.017 | 0.641 | no | 1.172 | 0.586 | no | 1.093 | 0.707 | no |
| DRA0171 | Phosphomethylpyrimidine kinase, THID protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DRA0172 | ThiG protein | 2.948 | 1.953 | yes | 2.819 | 1.053 | yes | 2.312 | 1.330 | yes | 3.353 | 1.163 | yes | 2.365 | 0.651 | yes | 1.464 | 0.496 | no | 1.097 | 0.632 | no | 0.918 | 0.084 | no | 0.658 | 0.182 | no |
| DRA0173 | THIS protein | 1.346 | 0.559 | no | 1.894 | 0.670 | yes | 2.299 | 0.550 | yes | 2.149 | 0.514 | yes | 1.684 | 0.804 | yes | 1.114 | 0.201 | no | 0.942 | 0.483 | no | 0.937 | 0.296 | no | 0.774 | 0.113 | no |
| DRA0174 | TMP-PPASE, THIE protein | 1.562 | 0.520 | yes | 1.198 | 0.115 | no | 1.315 | 0.281 | no | 1.499 | 0.591 | no | 1.119 | 0.478 | no | 1.189 | 0.362 | no | 1.190 | 0.445 | no | 1.253 | 0.382 | no | 0.981 | 0.432 | no |
| DRA0175 | Thiamin biosynthesis protein THIC | 1.533 | 0.800 | no | 1.315 | 0.818 | no | 1.139 | 0.498 | no | 2.047 | 0.779 | yes | 2.042 | 0.945 | yes | 1.636 | 0.567 | yes | 1.681 | 1.026 | no | 0.722 | 0.228 | no | 0.791 | 0.298 | no |
| DRA0176 | Xantine/uracil permease | 0.979 | 0.483 | no | 1.182 | 0.309 | no | 1.403 | 0.824 | no | 1.306 | 0.394 | no | 1.136 | 0.567 | no | 0.958 | 0.220 | no | 0.806 | 0.175 | no | 1.069 | 0.380 | no | 1.055 | 0.501 | no |
| DRA0178 | Xanthine dehydrogenase | 1.067 | 0.587 | no | 1.101 | 0.332 | no | 1.387 | 0.543 | no | 1.515 | 0.328 | no | 1.864 | 1.073 | yes | 0.957 | 0.307 | no | 1.081 | 0.427 | no | 1.600 | 0.786 | yes | 1.005 | 0.183 | no |
| DRA0179 | NAD-hydrolase | 2.234 | 1.356 | yes | 1.301 | 0.474 | no | 1.650 | 0.682 | yes | 2.738 | 1.982 | yes | 1.903 | 1.089 | yes | 1.559 | 0.499 | no | 1.733 | 0.495 | yes | 2.102 | 1.127 | yes | 1.041 | 0.417 | no |
| DRA0180 | N-ethylammeline chlorohydrolase , TIM barrel metal-dependent hydrolases | 1.288 | 0.513 | no | 1.258 | 0.504 | no | 1.895 | 0.554 | yes | 3.049 | 1.433 | yes | 1.918 | 0.766 | yes | 1.844 | 0.720 | yes | 1.727 | 0.991 | yes | 1.909 | 0.727 | yes | 1.032 | 0.313 | no |
| DRA0181 | Response regulator protein, GGEEF domain | 1.361 | 0.329 | no | 0.856 | 0.155 | no | 1.104 | 0.488 | no | 0.834 | 0.155 | no | 1.028 | 0.322 | no | 0.812 | 0.294 | no | 0.994 | 0.413 | no | 0.981 | 0.334 | no | 1.001 | 0.640 | no |
| DRA0182 | Sss/XerC protein | 0.650 | 0.283 | yes | 0.375 | 0.163 | yes | 0.375 | 0.159 | yes | 0.336 | 0.137 | yes | 0.313 | 0.131 | yes | 0.282 | 0.130 | yes | 0.520 | 0.372 | yes | 0.571 | 0.135 | yes | 0.687 | 0.149 | no |
| DRA0183 | Conserved integral membrane protein | 0.974 | 0.239 | no | 0.960 | 0.505 | no | 0.844 | 0.397 | no | 4.729 | 0.285 | yes | 0.961 | 0.470 | no | 1.007 | 0.076 | no | 0.557 | 0.261 | yes | 0.555 | 0.228 | yes | n/a | n/a | n/a |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DRA0184 | Pyridoxamine kinase | 1.389 | 0.360 | no | 1.198 | 0.583 | no | 1.147 | 0.307 | no | 1.305 | 0.381 | no | 1.023 | 0.451 | no | 1.403 | 0.866 | no | 1.323 | 0.649 | no | 1.062 | 0.236 | no | 1.045 | 0.230 | no |
| DRA0185 | Exopolyphosphatase, HSP70 superfamily | 1.196 | 0.545 | no | 1.013 | 0.471 | no | 3.057 | 2.132 | yes | 4.271 | 1.928 | yes | 4.010 | 2.219 | yes | 2.837 | 1.686 | yes | 7.651 | 4.843 | yes | 5.203 | 1.731 | yes | 1.754 | 0.678 | yes |
| DRA0188 | UVRA protein | 1.037 | 0.406 | no | 1.850 | 1.077 | yes | 1.333 | 0.349 | no | 1.290 | 0.482 | no | 2.034 | 0.904 | yes | 1.451 | 0.580 | no | 1.612 | 0.941 | no | 1.313 | 0.739 | no | n/a | n/a | n/a |
| DRA0189 | Fe-S oxidoreductase, P methylase superfamily | 1.061 | 0.527 | no | 1.391 | 0.859 | no | 2.154 | 1.232 | yes | 1.881 | 0.624 | yes | 2.020 | 0.769 | yes | 1.843 | 0.589 | yes | 1.416 | 0.611 | no | 1.170 | 0.297 | no | 0.863 | 0.218 | no |
| DRA0190 | Predicted protein | 0.891 | 0.164 | no | 1.738 | 0.353 | yes | 1.687 | 0.463 | yes | 1.558 | 0.078 | no | 1.486 | 0.399 | no | 1.165 | 0.473 | no | 1.188 | 0.199 | no | 1.085 | 0.141 | no | 1.046 | 0.133 | no |
| DRA0191 | NagC/XylR family transcriptional regulator, sugar kinase superfamily | 1.148 | 0.506 | no | 1.108 | 0.676 | no | 0.705 | 0.419 | yes | 0.973 | 0.115 | no | 0.757 | 0.318 | no | 0.684 | 0.201 | yes | 0.801 | 0.234 | no | 0.959 | 0.202 | no | 1.084 | 0.431 | no |
| DRA0192 | Predicted protein | 1.617 | 0.705 | yes | 1.801 | 0.767 | yes | 1.175 | 0.753 | no | 2.051 | 0.705 | yes | 2.129 | 1.368 | yes | 2.092 | 1.325 | yes | 1.017 | 0.607 | no | 1.049 | 0.303 | no | 0.843 | 0.288 | no |
| DRA0193 | Phosphoglycomutase 2 | 1.236 | 0.329 | no | 0.985 | 0.478 | no | 1.033 | 0.497 | no | 1.220 | 0.867 | no | 1.224 | 0.550 | no | 0.857 | 0.303 | no | 0.919 | 0.216 | no | 1.024 | 0.213 | no | 0.914 | 0.461 | no |
| DRA0194 | Predicted aminoglycoside phosphotransferase | 1.516 | 0.388 | no | 1.257 | 0.628 | no | 1.297 | 0.517 | no | 0.980 | 0.464 | no | 0.815 | 0.539 | no | 0.763 | 0.350 | no | 0.737 | 0.253 | no | 0.768 | 0.203 | no | 0.852 | 0.213 | no |
| DRA0195 | Zinc-independent alcohol dehydrogenase | 1.187 | 0.392 | no | 1.611 | 0.971 | no | 2.516 | 1.174 | yes | 2.164 | 1.024 | yes | 1.804 | 0.816 | yes | 1.663 | 0.236 | yes | 1.084 | 0.547 | no | 0.833 | 0.152 | no | 1.038 | 0.646 | no |
| DRA0196 | Acyl-CoA dehydrogenase | 1.897 | 1.209 | yes | 1.611 | 0.524 | yes | 1.189 | 0.265 | no | 1.639 | 0.191 | yes | 1.143 | 0.213 | no | 1.016 | 0.313 | no | 0.834 | 0.243 | no | 1.171 | 0.308 | no | 0.586 | 0.156 | yes |
| DRA0197 | Predicted protein | 1.300 | 0.639 | no | 0.711 | 0.323 | no | 1.295 | 0.430 | no | 2.606 | 1.222 | yes | 1.340 | 1.093 | no | 0.905 | 0.124 | no | 0.667 | 0.489 | yes | 0.740 | 0.185 | no | 0.425 | 0.033 | yes |
| DRA0198 | HGG containing thioesterase superfamily | 1.044 | 0.464 | no | 1.282 | 0.437 | no | 1.200 | 0.538 | no | 2.899 | 0.909 | yes | 2.460 | 0.924 | yes | 1.006 | 0.305 | no | 1.193 | 0.861 | no | 1.062 | 0.431 | no | 0.635 | 0.313 | yes |
| DRA0199 | NODN - monoamine oxidase regulatory protein | 1.161 | 0.720 | no | 0.795 | 0.395 | no | 0.320 | 0.173 | yes | 1.435 | 0.053 | no | 0.875 | 0.621 | no | 0.897 | 0.519 | no | 1.149 | 0.455 | no | 0.808 | 0.253 | no | 0.553 | 0.188 | yes |
| DRA0200 | 3-oxoacyl-[acyl-carrier-protein] reductase, FABG | 1.261 | 0.778 | no | 0.635 | 0.432 | yes | 0.649 | 0.346 | yes | 1.005 | 0.090 | no | 0.725 | 0.455 | yes | 0.632 | 0.203 | yes | 0.568 | 0.237 | yes | 0.655 | 0.067 | yes | 0.565 | 0.211 | yes |
| DRA0201 | NH(3)-dependent NAD+ synthetase | 0.925 | 0.198 | no | 0.651 | 0.334 | yes | 0.523 | 0.288 | yes | 0.602 | 0.286 | yes | 0.468 | 0.139 | yes | 0.576 | 0.346 | yes | 0.691 | 0.256 | yes | 0.758 | 0.414 | yes | 0.833 | 0.328 | no |
| DRA0202 | Superoxide dismutase CU-ZN, fusion with uncharacterized plant protein | 1.212 | 0.456 | no | 0.838 | 0.541 | no | 0.509 | 0.305 | yes | 0.707 | 0.034 | no | 1.330 | 0.617 | no | 2.285 | 1.601 | yes | 1.222 | 0.589 | no | 1.053 | 0.299 | no | 1.068 | 0.050 | no |
| DRA0203 | Dehydrogenase | 1.137 | 0.454 | no | 0.830 | 0.254 | no | 0.752 | 0.305 | no | 0.885 | 0.261 | no | 0.913 | 0.367 | no | 1.174 | 0.331 | no | 1.235 | 0.395 | no | 1.468 | 0.370 | yes | 1.453 | 0.074 | yes |
| DRA0204 | CheY-like family protein of sensory transduction regulatory protein | 0.701 | 0.376 | yes | 0.587 | 0.350 | yes | 0.482 | 0.264 | yes | 0.616 | 0.314 | yes | 0.823 | 0.267 | no | 0.890 | 0.139 | no | 0.925 | 0.420 | no | 0.935 | 0.333 | no | 1.257 | 0.444 | no |
| DRA0205 | Sensory transduction histidine kinase | 1.320 | 0.144 | no | 0.976 | 0.209 | no | 0.760 | 0.345 | yes | 0.925 | 0.279 | no | 1.036 | 0.355 | no | 1.255 | 0.434 | no | 1.380 | 0.466 | no | 1.423 | 0.344 | no | 1.124 | 0.403 | no |
| DRA0206 | Oligoendopeptidase, FDCP-like | 0.969 | 0.414 | no | 0.729 | 0.462 | yes | 0.959 | 0.584 | no | 1.178 | 0.332 | no | 1.043 | 0.532 | no | 1.154 | 0.367 | no | 1.383 | 0.451 | no | 1.224 | 0.250 | no | 0.877 | 0.457 | no |
| DRA0207 | Glucosidase | 1.265 | 0.195 | no | 1.009 | 0.321 | no | 0.981 | 0.253 | no | 1.225 | 0.317 | no | 1.116 | 0.264 | no | 1.271 | 0.635 | no | 1.301 | 0.358 | no | 1.582 | 0.525 | yes | 1.154 | 0.434 | no |
| DRA0208 | Oligopeptide permease-like protein | 1.193 | 0.602 | no | 0.727 | 0.342 | yes | 0.732 | 0.303 | yes | 1.438 | 0.255 | no | 1.124 | 0.632 | no | 0.958 | 0.364 | no | 1.317 | 0.787 | no | 1.058 | 0.251 | no | 0.668 | 0.116 | no |
| DRA0209 | Oligopeptide transport system permease protein | 1.488 | 0.851 | no | 0.808 | 0.456 | no | 0.824 | 0.420 | no | 1.281 | 0.642 | no | 0.905 | 0.464 | no | 0.740 | 0.380 | no | 0.871 | 0.339 | no | 1.068 | 0.406 | no | 0.794 | 0.241 | no |
| DRA0211 | HTH transcriptional regulator, GntR family | 0.911 | 0.267 | no | 0.435 | 0.143 | yes | 0.412 | 0.214 | yes | 0.553 | 0.124 | yes | 0.583 | 0.239 | yes | 0.663 | 0.128 | yes | 0.998 | 0.405 | no | 0.763 | 0.171 | no | 0.726 | 0.206 | no |
| DRA0213 | GLMS/KpsF family protein, possible sugar isomerase | 1.138 | 0.321 | no | 0.827 | 0.229 | no | 0.725 | 0.162 | no | 0.731 | 0.069 | no | 0.695 | 0.200 | no | 0.771 | 0.212 | no | 0.888 | 0.081 | no | 0.967 | 0.121 | no | 1.081 | 0.362 | no |
| DRA0214 | WRBA-like flavodoxin | 1.005 | 0.141 | no | 0.807 | 0.114 | no | 0.591 | 0.159 | yes | 0.641 | 0.129 | yes | 0.739 | 0.169 | no | 1.018 | 0.174 | no | 1.207 | 0.527 | no | 1.251 | 0.227 | no | 1.398 | 0.406 | no |
| DRA0215 | Predicted protein | 1.072 | 0.115 | no | 1.216 | 0.401 | no | 1.086 | 0.261 | no | 1.121 | 0.135 | no | 0.843 | 0.318 | no | 0.849 | 0.208 | no | 0.914 | 0.192 | no | 0.882 | 0.117 | no | 0.808 | 0.316 | no |
| DRA0216 | Beta-lactamase superfamily hydrolase | 1.083 | 0.274 | no | 0.949 | 0.430 | no | 0.756 | 0.279 | no | 0.621 | 0.161 | yes | 0.734 | 0.328 | no | 0.808 | 0.336 | no | 0.868 | 0.346 | no | 0.932 | 0.345 | no | 0.988 | 0.405 | no |
| DRA0217 | Possible regulatory protein from leu-rich protein LRPR family | 1.431 | 0.252 | no | 1.050 | 0.267 | no | 1.222 | 0.555 | no | 0.896 | 0.167 | no | 0.665 | 0.231 | yes | 0.897 | 0.328 | no | 0.934 | 0.306 | no | 0.979 | 0.314 | no | 0.919 | 0.259 | no |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DRA0218 | Hydrolase beta-lactamase superfamily | 1.262 | 0.286 | no | 1.398 | 0.471 | no | 1.455 | 0.576 | no | 1.377 | 0.070 | no | 1.154 | 0.370 | no | 1.066 | 0.365 | no | 1.205 | 0.494 | no | 1.353 | 0.624 | no | 0.764 | 0.251 | no |
| DRA0219 | Predicted protein | 1.960 | 0.881 | yes | 1.625 | 0.865 | yes | 1.234 | 0.438 | no | 1.601 | 0.290 | no | 1.173 | 0.519 | no | 1.077 | 0.391 | no | 1.545 | 0.918 | no | 1.135 | 0.530 | no | 0.870 | 0.352 | no |
| DRA0220 | Aldehyde dehydrogenase | 1.038 | 0.251 | no | 1.127 | 0.480 | no | 1.325 | 0.705 | no | 1.389 | 0.482 | no | 1.391 | 0.532 | no | 1.398 | 0.761 | no | 0.888 | 0.298 | no | 0.796 | 0.193 | no | 0.890 | 0.264 | no |
| DRA0221 | Putative glucan synthase | 1.561 | 0.897 | no | 2.233 | 0.779 | yes | 2.247 | 0.577 | yes | 2.863 | 1.726 | yes | 1.670 | 0.693 | yes | 1.153 | 0.661 | no | 0.806 | 0.234 | no | 0.769 | 0.117 | no | 0.581 | 0.197 | yes |
| DRA0222 | UDP-glucose 4-epimerase | 0.832 | 0.502 | no | 0.567 | 0.196 | yes | 0.344 | 0.181 | yes | 0.244 | 0.133 | yes | 0.561 | 0.232 | yes | 0.454 | 0.137 | yes | 0.555 | 0.371 | yes | 0.445 | 0.108 | yes | 0.165 | 0.048 | yes |
| DRA0223 | 4-hydroxyphenylacetate-3-hydroxylase | 1.060 | 0.401 | no | 1.559 | 0.611 | yes | 1.827 | 0.290 | yes | 4.467 | 1.821 | yes | 2.163 | 0.552 | yes | 1.339 | 0.568 | no | 1.189 | 0.540 | no | 1.192 | 0.505 | no | 0.774 | 0.367 | no |
| DRA0224 | Catechol 2,3-dioxygenase | 1.078 | 0.179 | no | 0.972 | 0.243 | no | 1.012 | 0.568 | no | 1.002 | 0.363 | no | 1.031 | 0.468 | no | 1.146 | 0.124 | no | 0.879 | 0.224 | no | 0.965 | 0.024 | no | 0.994 | 0.202 | no |
| DRA0225 | Molybdopterin-binding domain, similar to the same domain of Sulfite oxidase | 1.498 | 0.251 | no | 1.342 | 0.541 | no | 1.063 | 0.555 | no | 0.982 | 0.119 | no | 0.890 | 0.230 | no | 1.096 | 0.626 | no | 1.115 | 0.408 | no | 0.978 | 0.108 | no | 1.085 | 0.664 | no |
| DRA0226 | 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase | 1.399 | 0.279 | no | 0.991 | 0.401 | no | 0.854 | 0.236 | no | 1.117 | 0.217 | no | 1.516 | 0.657 | no | 1.245 | 0.609 | no | 1.636 | 0.909 | no | 0.972 | 0.380 | no | 0.530 | 0.036 | yes |
| DRA0227 | 5-carboxymethyl-2-hydroxymuconate isomerase | 1.487 | 0.586 | no | 1.041 | 0.266 | no | 0.721 | 0.211 | no | 0.901 | 0.435 | no | 0.975 | 0.250 | no | 1.108 | 0.303 | no | 1.068 | 0.144 | no | 1.501 | 0.576 | no | 0.883 | 0.127 | no |
| DRA0228 | Distantly related to lactoylglutathione lyase | 1.203 | 0.680 | no | 0.562 | 0.149 | yes | 0.558 | 0.213 | yes | 0.600 | 0.226 | yes | 0.828 | 0.303 | no | 1.589 | 0.614 | no | 1.126 | 0.672 | no | 1.813 | 0.233 | yes | 1.031 | 0.464 | no |
| DRA0229 | Predicted protein | 1.314 | 0.308 | no | 0.612 | 0.217 | yes | 0.448 | 0.251 | yes | 0.739 | 0.203 | no | 0.935 | 0.169 | no | 1.332 | 0.640 | no | 1.682 | 0.383 | yes | 1.723 | 0.440 | yes | 1.353 | 0.118 | no |
| DRA0230 | Predicted protein | 0.837 | 0.199 | no | 0.651 | 0.384 | yes | 0.418 | 0.144 | yes | 0.723 | 0.257 | no | 0.974 | 0.307 | no | 2.214 | 0.704 | yes | 1.806 | 0.543 | yes | 2.055 | 0.361 | yes | 1.360 | 0.576 | no |
| DRA0231 | Oxidoreductase | 1.060 | 0.202 | no | 0.652 | 0.366 | yes | 0.311 | 0.124 | yes | 0.474 | 0.039 | yes | 0.767 | 0.242 | no | 0.999 | 0.463 | no | 1.233 | 0.288 | no | 1.414 | 0.253 | no | 1.222 | 0.559 | no |
| DRA0232 | Flavoprotein dehydrogenase; probable CO dehydrogenase subunit | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DRA0233 | Dehydrogenase, iron sulfur protein; probable CO dehydrogenase subunit | 0.995 | 0.611 | no | 0.530 | 0.109 | yes | 0.507 | 0.198 | yes | 0.590 | 0.251 | yes | 0.842 | 0.201 | no | 1.053 | 0.352 | no | 1.301 | 0.334 | no | 1.305 | 0.170 | no | 0.680 | 0.199 | no |
| DRA0234 | Predicted protein | 1.286 | 0.543 | no | 5.973 | 1.738 | yes | 12.758 | 5.267 | yes | 12.150 | 1.489 | yes | 6.003 | 4.758 | yes | 6.532 | 2.837 | yes | 2.988 | 1.855 | yes | 2.186 | 0.346 | yes | 0.891 | 0.281 | no |
| DRA0235 | Dehydrogenase, iron sulfur protein; probable CO dehydrogenase subunit | 0.772 | 0.159 | no | 0.712 | 0.174 | no | 0.917 | 0.553 | no | 0.881 | 0.241 | no | 0.745 | 0.450 | no | 0.718 | 0.223 | no | 0.839 | 0.377 | no | 1.166 | 0.424 | no | 0.967 | 0.273 | no |
| DRA0236 | Flavoprotein dehydrogenase; probable CO dehydrogenase subunit | 2.204 | 1.191 | yes | 0.403 | 0.110 | yes | 0.420 | 0.222 | yes | 0.732 | 0.158 | no | 0.642 | 0.338 | yes | 0.858 | 0.260 | no | 1.114 | 0.596 | no | 1.037 | 0.301 | no | 1.359 | 0.317 | no |
| DRA0237 | Oxidoreductase; probable CO dehydrogenase subunit | 1.010 | 0.098 | no | 0.616 | 0.245 | yes | 0.552 | 0.382 | yes | 0.335 | 0.096 | yes | 0.609 | 0.245 | yes | 0.620 | 0.181 | yes | 1.195 | 0.280 | no | 1.160 | 0.270 | no | 1.680 | 0.260 | yes |
| DRA0238 | Flavoprotein, related to 3-ketosteroid-delta1-dehydrogenase | 1.227 | 0.441 | no | 0.617 | 0.348 | yes | 0.237 | 0.122 | yes | 0.375 | 0.108 | yes | 0.419 | 0.099 | yes | 0.593 | 0.260 | yes | 0.677 | 0.179 | yes | 0.759 | 0.202 | no | 1.467 | 0.386 | yes |
| DRA0239 | Cobalamin 5'-phosphate synthase CobS | 1.147 | 0.248 | no | 0.777 | 0.296 | no | 0.613 | 0.221 | yes | 0.625 | 0.091 | yes | 0.723 | 0.231 | no | 0.760 | 0.218 | no | 0.839 | 0.229 | no | 1.204 | 0.175 | no | 0.924 | 0.328 | no |
| DRA0240 | Nicotinate-nucleotide-dimethylbenzimidazole phosphoribosyltransferase | 1.102 | 0.116 | no | 1.205 | 0.349 | no | 1.202 | 0.230 | no | 1.257 | 0.153 | no | 0.917 | 0.212 | no | 0.885 | 0.240 | no | 1.136 | 0.252 | no | 0.974 | 0.076 | no | 1.039 | 0.307 | no |
| DRA0241 | Beta-lactamase, BLA2_ECOLI | 1.061 | 0.171 | no | 1.032 | 0.290 | no | 0.817 | 0.295 | no | 0.699 | 0.233 | no | 0.758 | 0.325 | no | 0.925 | 0.293 | no | 0.993 | 0.268 | no | 0.925 | 0.241 | no | 0.988 | 0.237 | no |
| DRA0242 | HTH transcriptional regulator | 1.101 | 0.173 | no | 0.885 | 0.112 | no | 0.759 | 0.155 | no | 0.773 | 0.158 | no | 0.699 | 0.095 | no | 0.819 | 0.296 | no | 0.936 | 0.238 | no | 0.977 | 0.232 | no | 0.892 | 0.198 | no |
| DRA0243 | Flavohemoglobin | 0.960 | 0.370 | no | 2.363 | 0.760 | yes | 1.563 | 0.547 | yes | 1.502 | 0.055 | no | 1.406 | 0.586 | no | 1.139 | 0.458 | no | 0.875 | 0.271 | no | 0.824 | 0.072 | no | 0.577 | 0.238 | yes |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DRA0244 | Oxygen-independent coproporphyrinogen III oxidase, P methylase superfamily protein | 1.472 | 0.388 | no | 1.174 | 0.399 | no | 1.220 | 0.330 | no | 1.506 | 0.358 | no | 1.257 | 0.664 | no | 1.152 | 0.405 | no | 1.328 | 0.695 | no | 1.026 | 0.182 | no | 0.954 | 0.307 | no |
| DRA0245 | Predicted protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DRA0246 | Peripliplasmic binding protein | 0.984 | 0.423 | no | 1.208 | 0.295 | no | 1.252 | 0.449 | no | 1.323 | 0.285 | no | 1.052 | 0.541 | no | 1.078 | 0.248 | no | 1.168 | 0.412 | no | 0.925 | 0.313 | no | 0.938 | 0.419 | no |
| DRA0247 | Permease, MDR-type | 1.139 | 0.496 | no | 1.922 | 0.505 | yes | 1.723 | 0.588 | yes | 1.528 | 0.379 | no | 1.506 | 0.705 | no | 0.863 | 0.402 | no | 0.874 | 0.169 | no | 0.831 | 0.204 | no | 0.462 | 0.082 | yes |
| DRA0248 | Transcriptional regulator, MarR/SlyA family | 0.672 | 0.234 | yes | 0.581 | 0.150 | yes | 0.301 | 0.121 | yes | 0.230 | 0.097 | yes | 0.363 | 0.155 | yes | 0.409 | 0.185 | yes | 0.310 | 0.137 | yes | 0.312 | 0.139 | yes | 0.263 | 0.112 | yes |
| DRA0249 | Metalloproteinase, leishmanolysin-like | 0.962 | 0.587 | no | 1.204 | 0.383 | no | 3.959 | 2.554 | yes | 6.471 | 4.428 | yes | 5.147 | 3.288 | yes | 1.080 | 0.323 | no | 1.338 | 0.761 | no | 1.221 | 0.400 | no | 0.761 | 0.234 | no |
| DRA0250 | Acyl-CoA dehydrogenase | 1.264 | 0.356 | no | 0.717 | 0.248 | no | 0.682 | 0.465 | yes | 0.658 | 0.235 | yes | 0.705 | 0.253 | no | 0.819 | 0.244 | no | 0.834 | 0.224 | no | 1.184 | 0.198 | no | 1.387 | 0.256 | no |
| DRA0251 | Quinone oxidoreductase | 1.141 | 0.171 | no | 0.950 | 0.211 | no | 0.903 | 0.291 | no | 0.941 | 0.199 | no | 1.010 | 0.425 | no | 0.850 | 0.333 | no | 0.876 | 0.253 | no | 0.949 | 0.406 | no | 0.891 | 0.452 | no |
| DRA0252 | Transcriptional regulator, MerR-like | 1.038 | 0.304 | no | 1.156 | 0.711 | no | 0.930 | 0.330 | no | 1.217 | 0.306 | no | 2.437 | 1.113 | yes | 1.067 | 0.141 | no | 1.265 | 0.398 | no | 0.864 | 0.132 | no | 0.676 | 0.104 | no |
| DRA0254 | IS2621 FULL COPY | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DRA0255 | Aculeacin a acylase | 1.127 | 0.291 | no | 1.016 | 0.205 | no | 0.810 | 0.271 | no | 0.924 | 0.336 | no | 0.920 | 0.356 | no | 0.920 | 0.280 | no | 0.871 | 0.152 | no | 1.084 | 0.108 | no | 0.954 | 0.095 | no |
| DRA0256 | Phenylacetyl-CoA-Ligase | 0.951 | 0.447 | no | 0.683 | 0.229 | no | 0.514 | 0.249 | yes | 0.859 | 0.310 | no | 0.631 | 0.064 | yes | 1.037 | 0.702 | no | 0.821 | 0.251 | no | 0.861 | 0.156 | no | 0.777 | 0.346 | no |
| DRA0257 | Ankyrin repeat protein | 1.378 | 0.423 | no | 0.829 | 0.370 | no | 0.576 | 0.390 | yes | 0.823 | 0.207 | no | 0.992 | 0.372 | no | 1.210 | 0.617 | no | 1.317 | 0.338 | no | 1.319 | 0.265 | no | 1.934 | 0.592 | yes |
| DRA0258 | Predicted protein | 1.053 | 0.419 | no | 0.553 | 0.198 | yes | 0.559 | 0.296 | yes | 0.914 | 0.053 | no | 1.148 | 0.463 | no | 0.987 | 0.378 | no | 0.988 | 0.268 | no | 1.021 | 0.047 | no | 1.576 | 0.218 | yes |
| DRA0259 | Catalase with C-terminal domain similar to pfpI (intacellular protease) domain of thiJ family | 1.264 | 0.567 | no | 0.798 | 0.537 | no | 0.633 | 0.457 | yes | 1.020 | 0.414 | no | 1.798 | 1.187 | yes | 1.325 | 0.791 | no | 1.339 | 0.454 | no | 1.145 | 0.229 | no | 2.765 | 0.742 | yes |
| DRA0260 | BRA ATPase | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DRA0261 | BRA ATPase and permease | 1.037 | 0.298 | no | 1.003 | 0.417 | no | 0.819 | 0.319 | no | 0.909 | 0.232 | no | 1.040 | 0.190 | no | 0.921 | 0.196 | no | 0.990 | 0.251 | no | 0.928 | 0.153 | no | 0.979 | 0.212 | no |
| DRA0262 | BRA transport protein, permease | 1.319 | 0.224 | no | 0.812 | 0.221 | no | 0.679 | 0.278 | yes | 0.764 | 0.076 | no | 0.796 | 0.216 | no | 0.950 | 0.328 | no | 1.150 | 0.247 | no | 1.145 | 0.257 | no | 1.050 | 0.258 | no |
| DRA0263 | Branched-chain amino acid ABC transporter , periplasmic binding protein Archaeoglobus) | 1.149 | 0.509 | no | 0.841 | 0.380 | no | 0.863 | 0.599 | no | 1.152 | 0.442 | no | 0.811 | 0.335 | no | 0.740 | 0.200 | no | 0.848 | 0.296 | no | 0.882 | 0.108 | no | 0.924 | 0.403 | no |
| DRA0265 | Predicted protein | 1.142 | 0.476 | no | 1.067 | 0.263 | no | 1.676 | 0.379 | yes | 1.811 | 0.240 | yes | 1.480 | 0.424 | no | 1.586 | 0.403 | yes | 1.578 | 0.282 | yes | 1.583 | 0.304 | yes | 1.779 | 0.529 | yes |
| DRA0266 | ATPase AAA superfamily | 1.451 | 0.201 | no | 1.550 | 0.601 | yes | 1.475 | 0.279 | yes | 1.273 | 0.182 | no | 1.126 | 0.299 | no | 1.126 | 0.470 | no | 1.226 | 0.325 | no | 1.077 | 0.387 | no | 1.088 | 0.560 | no |
| DRA0267 | Related to tungsten formylmethanofuran dehydrogenase, subunit E, fwdE | 1.308 | 0.562 | no | 1.428 | 0.455 | no | 1.080 | 0.315 | no | 0.837 | 0.149 | no | 0.957 | 0.332 | no | 0.955 | 0.314 | no | 1.124 | 0.342 | no | 1.058 | 0.201 | no | 1.234 | 0.515 | no |
| DRA0268 | Adenine deaminase | 1.097 | 0.331 | no | 1.769 | 0.528 | yes | 1.538 | 0.491 | yes | 1.926 | 0.616 | yes | 1.129 | 0.242 | no | 0.983 | 0.294 | no | 1.003 | 0.258 | no | 1.095 | 0.194 | no | 1.056 | 0.379 | no |
| DRA0269 | ABC-type transporter, ATPase | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DRA0270 | Adenine deaminase adeC | 1.158 | 0.337 | no | 1.076 | 0.483 | no | 0.981 | 0.590 | no | 0.685 | 0.198 | no | 0.748 | 0.302 | no | 0.908 | 0.332 | no | 0.922 | 0.321 | no | 0.984 | 0.192 | no | 0.922 | 0.231 | no |
| DRA0271 | Glucose permease | 1.688 | 0.232 | yes | 1.589 | 0.619 | yes | 1.215 | 0.644 | no | 0.926 | 0.527 | no | 0.828 | 0.488 | no | 0.959 | 0.349 | no | 1.307 | 0.568 | no | 1.038 | 0.276 | no | 0.926 | 0.336 | no |
| DRA0272 | Nicotinate phosphoribosyltransferase conserved hypothetical protein | 1.348 | 0.515 | no | 1.165 | 0.467 | no | 1.227 | 0.741 | no | 1.032 | 0.271 | no | 0.930 | 0.237 | no | 1.168 | 0.683 | no | 1.204 | 0.455 | no | 1.165 | 0.473 | no | 1.221 | 0.439 | no |
| DRA0273 | NadR/TagD family nucleotidyltransferase | 1.330 | 0.587 | no | 1.907 | 1.177 | yes | 1.351 | 0.893 | no | 1.081 | 0.003 | no | 0.821 | 0.223 | no | 1.116 | 0.264 | no | 1.126 | 0.500 | no | 0.944 | 0.440 | no | 0.810 | 0.183 | no |
| DRA0274 | Amine oxidase, flavin-containing,Rossman fold oxidoreductase | 1.200 | 0.412 | no | 0.724 | 0.298 | no | 0.541 | 0.308 | yes | 0.701 | 0.340 | yes | 0.797 | 0.454 | no | 1.517 | 0.891 | no | 2.505 | 0.889 | yes | 2.236 | 0.619 | yes | 3.271 | 0.905 | yes |
| DRA0275 | Soluble cytochrome C | 1.117 | 0.616 | no | 0.814 | 0.362 | no | 0.477 | 0.279 | yes | 0.957 | 0.225 | no | 1.427 | 0.719 | no | 1.782 | 0.659 | yes | 4.346 | 1.931 | yes | 4.213 | 1.041 | yes | 4.799 | 1.216 | yes |
| DRA0276 | Probable malate oxidoreductase | 1.234 | 0.543 | no | 1.522 | 0.697 | no | 0.980 | 0.579 | no | 0.910 | 0.445 | no | 0.864 | 0.213 | no | 0.937 | 0.443 | no | 0.932 | 0.331 | no | 1.244 | 0.124 | no | 1.026 | 0.394 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DRA0277 | Malate synthase A, MSA | 0.551 | 0.166 | yes | 1.326 | 0.194 | no | 0.385 | 0.276 | yes | 0.934 | 0.003 | no | 0.817 | 0.611 | yes | 0.365 | 0.272 | yes | 0.624 | 0.372 | yes | 0.624 | 0.336 | yes | 0.631 | 0.282 | yes |
| DRA0278 | Predicted protein | 1.224 | 0.717 | no | 0.947 | 0.513 | no | 0.823 | 0.490 | no | 2.261 | 1.152 | yes | 1.041 | 0.642 | no | 0.778 | 0.476 | no | 0.858 | 0.316 | no | 1.120 | 0.413 | no | 0.902 | 0.150 | no |
| DRA0279 | Conserved membrane protein | 1.483 | 0.476 | no | 1.064 | 0.405 | no | 0.726 | 0.419 | yes | 0.879 | 0.195 | no | 0.840 | 0.236 | no | 0.789 | 0.177 | no | 0.812 | 0.306 | no | 0.950 | 0.152 | no | 1.160 | 0.285 | no |
| DRA0281 | Predicted protein | 0.435 | 0.227 | yes | 0.808 | 0.024 | no | 0.255 | 0.071 | yes | 2.589 | 0.228 | yes | 1.779 | 1.354 | no | 0.626 | 0.353 | yes | 1.613 | 0.836 | no | 3.354 | 0.918 | yes | 5.183 | 1.667 | yes |
| DRA0282 | Uncharacterized protein similar to DRB0068 and other some other DR proteins | 0.658 | 0.246 | no | 0.213 | 0.111 | yes | 0.427 | 0.226 | yes | 4.406 | 1.182 | yes | 2.004 | 1.411 | yes | 0.848 | 0.526 | no | 0.910 | 0.563 | no | 1.641 | 0.128 | yes | 4.617 | 2.064 | yes |
| DRA0283 | Subtilisin | 0.944 | 0.528 | no | 0.588 | 0.328 | yes | 0.714 | 0.374 | yes | 1.507 | 0.136 | no | 1.186 | 0.678 | no | 1.016 | 0.521 | no | 0.949 | 0.287 | no | 1.864 | 0.911 | yes | 2.874 | 0.180 | yes |
| DRA0284 | Lactam utylization protein | 1.230 | 0.460 | no | 1.050 | 0.409 | no | 1.079 | 0.278 | no | 1.333 | 0.300 | no | 1.039 | 0.361 | no | 0.983 | 0.295 | no | 1.035 | 0.468 | no | 1.066 | 0.236 | no | 1.132 | 0.418 | no |
| DRA0285 | YBGJ-like protein | 0.892 | 0.234 | no | 1.084 | 0.670 | no | 0.993 | 0.471 | no | 1.148 | 0.149 | no | 1.101 | 0.353 | no | 1.121 | 0.479 | no | 0.859 | 0.112 | no | 0.943 | 0.508 | no | 0.693 | 0.338 | yes |
| DRA0287 | Glycosyltransferase | 1.305 | 0.247 | no | 1.406 | 0.469 | no | 1.338 | 0.233 | no | 1.271 | 0.557 | no | 0.989 | 0.195 | no | 1.137 | 0.279 | no | 1.156 | 0.212 | no | 1.027 | 0.180 | no | 1.050 | 0.192 | no |
| DRA0288 | TPR-repeat protein | 0.763 | 0.213 | no | 0.765 | 0.097 | no | 1.091 | 0.535 | no | 0.811 | 0.161 | no | 0.891 | 0.220 | no | 0.810 | 0.090 | no | 0.883 | 0.398 | no | 0.783 | 0.225 | no | 0.912 | 0.242 | no |
| DRA0289 | Predicted protein | 1.418 | 0.348 | no | 1.532 | 0.734 | no | 1.111 | 0.502 | no | 1.316 | 0.728 | no | 0.942 | 0.353 | no | 0.829 | 0.305 | no | 0.840 | 0.377 | no | 1.087 | 0.215 | no | 0.893 | 0.113 | no |
| DRA0290 | FTSH-like protein, AAA superfamily ATPase with metalloprotease domain | 0.930 | 0.271 | no | 1.491 | 0.457 | yes | 1.338 | 0.448 | no | 1.447 | 0.905 | no | 1.289 | 0.690 | no | 1.216 | 0.614 | no | 1.216 | 0.467 | no | 0.930 | 0.182 | no | 1.360 | 0.447 | no |
| DRA0291 | 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase | 1.025 | 0.440 | no | 1.482 | 0.732 | no | 1.269 | 0.557 | no | 0.678 | 0.089 | no | 1.037 | 0.706 | no | 1.290 | 0.843 | no | 0.933 | 0.442 | no | n/a | n/a | n/a | n/a | n/a | n/a |
| DRA0292 | Predicted protein | 0.953 | 0.222 | no | 1.324 | 0.869 | no | 0.972 | 0.332 | no | 0.680 | 0.103 | no | 0.731 | 0.334 | yes | 0.757 | 0.289 | no | 0.567 | 0.156 | yes | 0.768 | 0.231 | no | 0.735 | 0.150 | no |
| DRA0293 | Bacterial macroglobulin family protein | 1.040 | 0.182 | no | 1.153 | 0.150 | no | 0.926 | 0.296 | no | 0.877 | 0.066 | no | 0.820 | 0.286 | no | 0.843 | 0.155 | no | 0.926 | 0.309 | no | 0.968 | 0.223 | no | 0.962 | 0.244 | no |
| DRA0294 | Predicted protein | 0.918 | 0.241 | no | 0.793 | 0.243 | no | 1.300 | 0.721 | no | 0.575 | 0.136 | yes | 1.002 | 0.647 | no | 1.024 | 0.237 | no | 0.884 | 0.367 | no | 0.758 | 0.068 | no | 0.880 | 0.478 | no |
| DRA0295 | Predicted protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DRA0296 | Predicted protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DRA0297 | Sensor regulator, TPR repeats domain + GGEEF domain | 1.615 | 0.511 | yes | 1.170 | 0.413 | no | 1.258 | 0.303 | no | 1.829 | 0.492 | yes | 1.136 | 0.390 | no | 0.951 | 0.332 | no | 1.048 | 0.304 | no | 1.038 | 0.428 | no | 0.866 | 0.170 | no |
| DRA0298 | Similar to copper export protein | 1.100 | 0.378 | no | 1.334 | 0.294 | no | 1.375 | 0.355 | no | 0.832 | 0.321 | no | 1.118 | 0.459 | no | 0.914 | 0.160 | no | 1.006 | 0.256 | no | 0.914 | 0.074 | no | 0.852 | 0.132 | no |
| DRA0299 | Copper-binding protein | 2.052 | 0.914 | yes | 1.575 | 0.976 | no | 2.263 | 1.031 | yes | 3.929 | 1.080 | yes | 2.604 | 0.828 | yes | 1.576 | 0.449 | yes | 1.477 | 0.798 | no | 1.172 | 0.085 | no | 1.721 | 0.271 | yes |
| DRA0300 | Predicted protein | 1.289 | 0.396 | no | 1.481 | 0.430 | yes | 2.019 | 1.137 | yes | 2.032 | 0.454 | yes | 1.665 | 0.634 | yes | 1.580 | 0.398 | yes | 1.253 | 0.300 | no | 1.253 | 0.313 | no | 1.744 | 0.301 | yes |
| DRA0301 | MAUG-like metal cluster protein, cytochrome C peroxidase | 1.738 | 0.822 | yes | 1.608 | 0.579 | yes | 2.756 | 1.310 | yes | 2.093 | 0.751 | yes | 1.742 | 0.332 | yes | 2.356 | 1.413 | yes | 2.172 | 1.163 | yes | 2.083 | 0.697 | yes | 2.670 | 1.136 | yes |
| DRA0302 | Predicted protein | 0.882 | 0.230 | no | 0.863 | 0.223 | no | 1.393 | 0.391 | no | 1.783 | 0.967 | yes | 1.388 | 0.469 | no | 1.530 | 0.301 | yes | 1.334 | 0.328 | no | 1.408 | 0.061 | no | 2.092 | 0.676 | yes |
| DRA0303 | Predicted protein | 0.697 | 0.333 | yes | 0.305 | 0.125 | yes | 0.404 | 0.285 | yes | 0.356 | 0.123 | yes | 0.267 | 0.143 | yes | 0.399 | 0.160 | yes | 0.588 | 0.355 | yes | 0.564 | 0.171 | yes | 0.983 | 0.246 | no |
| DRA0304 | Metallobetalactamase family hydrolase fused to rhodanese-like domain | 1.045 | 0.327 | no | 0.412 | 0.105 | yes | 0.263 | 0.143 | yes | 0.277 | 0.114 | yes | 0.273 | 0.119 | yes | 0.335 | 0.026 | yes | 0.483 | 0.203 | yes | 0.680 | 0.172 | yes | 0.862 | 0.094 | no |
| DRA0305 | Predicted membrane protein | 1.340 | 0.566 | no | 0.632 | 0.210 | yes | 0.505 | 0.234 | yes | 0.389 | 0.118 | yes | 0.363 | 0.072 | yes | 0.520 | 0.135 | yes | 0.538 | 0.159 | yes | 0.779 | 0.055 | no | 0.790 | 0.267 | no |
| DRA0306 | Predicted protein | 0.968 | 0.304 | no | 1.165 | 0.215 | no | 1.613 | 0.469 | yes | 1.166 | 0.365 | no | 1.332 | 0.451 | no | 1.688 | 0.501 | yes | 1.406 | 0.498 | no | 1.030 | 0.097 | no | 0.700 | 0.107 | no |
| DRA0307 | Predicted protein | 1.343 | 0.829 | no | 0.927 | 0.345 | no | 1.071 | 0.495 | no | 0.967 | 0.253 | no | 1.122 | 0.511 | no | 1.158 | 0.280 | no | 1.233 | 0.581 | no | 1.110 | 0.368 | no | 0.811 | 0.147 | no |
| DRA0308 | HTH transcriptional regulator, TetR/AcrR family | 1.115 | 0.695 | no | 0.765 | 0.292 | no | 0.805 | 0.393 | no | 0.994 | 0.659 | no | 1.221 | 0.660 | no | 1.254 | 0.350 | no | 1.523 | 0.886 | no | 1.404 | 0.368 | no | 1.275 | 0.231 | no |
| DRA0309 | Long-chain-fatty-acid--CoA ligase | 1.290 | 0.488 | no | 0.972 | 0.509 | no | 2.377 | 1.623 | yes | 2.489 | 1.545 | yes | 1.695 | 1.155 | no | 1.177 | 0.430 | no | 1.153 | 0.637 | no | 0.752 | 0.229 | no | 0.814 | 0.412 | no |
| DRA0310 | Fusion pyruvate carboxylase and acetyl_CoA decarboxylase subunit XCD | 1.808 | 1.114 | yes | 1.417 | 0.604 | no | 1.420 | 0.516 | no | 1.295 | 0.324 | no | 1.162 | 0.329 | no | 1.155 | 0.561 | no | 1.319 | 0.579 | no | 1.268 | 0.437 | no | 1.453 | 0.664 | no |
| DRA0311 | URED urease operon protein | 0.529 | 0.171 | no | 5.952 | 3.713 | yes | 0.417 | 0.205 | yes | n/a | n/a | n/a | 2.667 | 0.738 | yes | 2.171 | 0.873 | yes | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DRA0312 | Urease accessory protein UREG, HypB like ATPase | 1.433 | 0.355 | no | 1.304 | 0.384 | no | 1.088 | 0.271 | no | 1.210 | 0.347 | no | 1.191 | 0.338 | no | 1.161 | 0.345 | no | 1.168 | 0.508 | no | 1.057 | 0.160 | no | 1.154 | 0.203 | no |
| DRA0313 | Urease accessory protein UREF | 0.879 | 0.490 | no | 1.085 | 0.411 | no | 1.179 | 0.379 | no | 1.003 | 0.337 | no | 1.101 | 0.442 | no | 0.962 | 0.309 | no | 1.107 | 0.567 | no | 1.027 | 0.444 | no | 0.942 | 0.240 | no |
| DRA0314 | Urease accessory protein UREE | 1.020 | 0.668 | no | 1.083 | 0.493 | no | 0.472 | 0.213 | yes | 0.893 | 0.291 | no | 0.977 | 0.218 | no | 1.829 | 0.847 | yes | 1.202 | 0.570 | no | 3.222 | 1.186 | yes | n/a | n/a | n/a |
| DRA0315 | HypB ATPase | 2.088 | 0.425 | yes | 2.564 | 0.957 | yes | 2.309 | 1.406 | yes | 2.089 | 0.087 | yes | 1.524 | 0.652 | no | 1.819 | 0.540 | yes | 1.050 | 0.443 | no | 0.856 | 0.195 | no | 0.919 | 0.176 | no |
| DRA0316 | Hydrogenase expression/formation protein HypA | 1.281 | 0.453 | no | 0.986 | 0.238 | no | 0.907 | 0.344 | no | 0.662 | 0.244 | yes | 0.718 | 0.164 | no | 0.949 | 0.185 | no | 0.791 | 0.293 | no | 0.932 | 0.279 | no | 0.831 | 0.222 | no |
| DRA0317 | Membrane-bound hydrogenase; HUPE protein | 2.168 | 0.695 | yes | 2.344 | 0.595 | yes | 2.013 | 1.062 | yes | 1.749 | 0.189 | yes | 2.114 | 0.385 | yes | 1.431 | 0.252 | no | 1.846 | 0.821 | yes | 1.011 | 0.304 | no | 1.036 | 0.541 | no |
| DRA0318 | Urease alpha subunit, UREA amidohydrolase | 1.163 | 0.351 | no | 1.053 | 0.362 | no | 1.054 | 0.396 | no | 1.198 | 0.342 | no | 1.538 | 0.628 | no | 1.006 | 0.380 | no | 0.879 | 0.284 | no | 0.935 | 0.136 | no | 1.323 | 0.609 | no |
| DRA0319 | Urease alpha subunit, UREA amidohydrolase | 1.701 | 0.705 | yes | 1.929 | 0.839 | yes | 1.855 | 0.545 | yes | 1.801 | 0.317 | yes | 1.539 | 0.427 | yes | 1.193 | 0.501 | no | 1.367 | 0.705 | no | 0.895 | 0.169 | no | 1.006 | 0.195 | no |
| DRA0320 | Transporter subunit LIVK ECOLI-like | 1.291 | 0.617 | no | 1.151 | 0.382 | no | 1.820 | 1.152 | yes | 1.453 | 0.882 | no | 1.171 | 0.566 | no | 0.873 | 0.500 | no | 1.273 | 0.466 | no | n/a | n/a | n/a | n/a | n/a | n/a |
| DRA0321 | ABC type transporter permease | 1.302 | 0.353 | no | 1.407 | 0.487 | no | 1.258 | 0.500 | no | 1.284 | 0.091 | no | 1.055 | 0.487 | no | 0.926 | 0.453 | no | 0.835 | 0.298 | no | 0.890 | 0.193 | no | 0.855 | 0.125 | no |
| DRA0322 | ABC type transporter permease | 1.488 | 0.528 | no | 1.430 | 0.309 | yes | 1.488 | 0.531 | yes | 1.235 | 0.183 | no | 1.214 | 0.294 | no | 1.084 | 0.134 | no | 1.289 | 0.599 | no | 0.984 | 0.186 | no | 1.028 | 0.272 | no |
| DRA0323 | ABC type transporter ATPase | 1.692 | 0.473 | yes | 2.180 | 0.953 | yes | 1.319 | 0.561 | no | 1.281 | 0.372 | no | 1.417 | 0.674 | no | 1.301 | 0.567 | no | 1.156 | 0.463 | no | 0.881 | 0.131 | no | 1.151 | 0.326 | no |
| DRA0324 | ABC type transporter ATPase | 1.343 | 0.525 | no | 1.318 | 0.412 | no | 1.270 | 0.246 | no | 0.995 | 0.194 | no | 1.017 | 0.336 | no | 0.812 | 0.196 | no | 0.891 | 0.366 | no | 0.779 | 0.070 | no | 0.782 | 0.145 | no |
| DRA0325 | Pngase F, peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase | 1.828 | 1.093 | yes | 0.968 | 0.384 | no | 0.657 | 0.436 | yes | 1.134 | 0.021 | no | 0.946 | 0.535 | no | 0.860 | 0.319 | no | 0.791 | 0.419 | no | 1.231 | 0.467 | no | 0.912 | 0.245 | no |
| DRA0326 | Chalcone synthase | 1.273 | 0.607 | no | 2.586 | 1.229 | yes | 2.214 | 0.846 | yes | 1.406 | 0.631 | no | 1.254 | 0.635 | no | 1.726 | 0.964 | no | 1.471 | 1.004 | no | 1.410 | 0.691 | no | 1.030 | 0.424 | no |
| DRA0327 | SAM dependent dihydroxypolyprenylbenzoate? methyltransferase | 1.453 | 0.442 | no | 1.738 | 0.547 | yes | 1.748 | 1.082 | yes | 1.340 | 0.406 | no | 1.240 | 0.654 | no | 1.496 | 0.489 | no | 1.222 | 0.316 | no | 0.972 | 0.257 | no | 0.932 | 0.278 | no |
| DRA0328 | FAD dependent hydroxylase/monoxygenase | 1.206 | 0.546 | no | 1.332 | 0.149 | no | 0.906 | 0.285 | no | 0.915 | 0.055 | no | 0.776 | 0.229 | no | 1.049 | 0.296 | no | 0.784 | 0.220 | no | 1.049 | 0.363 | no | 0.784 | 0.184 | no |
| DRA0329 | NDP-glucuronosyltransferase | 1.099 | 0.256 | no | 1.506 | 0.600 | yes | 1.459 | 0.509 | no | 1.221 | 0.433 | no | 1.021 | 0.362 | no | 0.997 | 0.266 | no | 1.227 | 0.333 | no | 1.239 | 0.250 | no | 1.062 | 0.389 | no |
| DRA0330 | HKD superfamily hydrolase, cardiolipin synthase-like | 1.808 | 1.164 | yes | 1.192 | 0.179 | no | 1.099 | 0.350 | no | 0.740 | 0.299 | no | 0.876 | 0.300 | no | 1.151 | 0.359 | no | 1.192 | 0.447 | no | 1.280 | 0.430 | no | 1.013 | 0.133 | no |
| DRA0331 | VWFA Mg-binding domain protein | 1.092 | 0.208 | no | 1.147 | 0.171 | no | 1.237 | 0.379 | no | 1.142 | 0.079 | no | 1.229 | 0.223 | no | 1.281 | 0.192 | no | 1.299 | 0.269 | no | 1.129 | 0.205 | no | 1.278 | 0.102 | no |
| DRA0332 | PKN2 family Serine/Threonine kinase | 1.226 | 0.387 | no | 0.732 | 0.265 | no | 0.745 | 0.200 | no | 0.777 | 0.286 | no | 0.816 | 0.265 | no | 1.343 | 0.452 | no | 1.546 | 0.392 | yes | 1.512 | 0.377 | yes | 1.333 | 0.439 | no |
| DRA0333 | Zn-finger + FHA domain containing protein, ortholog of FRAH protein of Anabaena | 1.251 | 0.541 | no | 0.763 | 0.293 | no | 0.792 | 0.392 | no | 1.017 | 0.490 | no | 1.522 | 0.795 | no | 2.152 | 0.630 | yes | 2.667 | 0.942 | yes | 2.504 | 0.883 | yes | 2.400 | 0.440 | yes |
| DRA0334 | PP2C phosphoprotein phosphatase fused to PKN2 family Serine/Threonine kinase | 1.087 | 0.345 | no | 0.810 | 0.239 | no | 0.678 | 0.194 | yes | 0.585 | 0.240 | yes | 0.830 | 0.216 | no | 1.811 | 1.121 | yes | 1.915 | 1.157 | yes | 1.270 | 0.435 | no | 2.215 | 0.876 | yes |
| DRA0336 | HTH transcription factor | 1.215 | 0.707 | no | 1.240 | 0.405 | no | 1.213 | 0.520 | no | 1.387 | 0.727 | no | 1.869 | 0.853 | yes | 1.005 | 0.280 | no | 1.073 | 0.435 | no | 1.239 | 0.443 | no | 1.062 | 0.207 | no |
| DRA0337 | ACDM/ACDS acyl-CoA dehydrogenase | 1.463 | 0.514 | no | 0.997 | 0.418 | no | 0.912 | 0.442 | no | 1.192 | 0.140 | no | 1.331 | 0.555 | no | 1.375 | 0.453 | no | 1.250 | 0.505 | no | 1.376 | 0.274 | no | 0.869 | 0.266 | no |
| DRA0338 | L-kynurenine hydrolase | 1.108 | 0.379 | no | 0.858 | 0.597 | no | 1.029 | 0.388 | no | 0.859 | 0.327 | no | 0.823 | 0.324 | no | 0.889 | 0.318 | no | 0.942 | 0.413 | no | 1.016 | 0.410 | no | 0.952 | 0.407 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DRA0339 | Tryptophan-2,3-dioxygenase | 1.271 | 0.382 | no | 1.504 | 0.723 | yes | 1.721 | 0.643 | yes | 1.778 | 0.448 | yes | 1.179 | 0.542 | no | 1.035 | 0.310 | no | 1.262 | 0.753 | no | 1.234 | 0.487 | no | 0.932 | 0.047 | no |
| DRA0340 | A/b hydrolase | 1.030 | 0.387 | no | 1.014 | 0.372 | no | 0.920 | 0.316 | no | 0.852 | 0.173 | no | 0.997 | 0.220 | no | 1.048 | 0.257 | no | 0.996 | 0.224 | no | 1.188 | 0.343 | no | 0.942 | 0.191 | no |
| DRA0341 | Termostable? alkaline proteinase | 1.421 | 0.394 | no | 1.348 | 0.813 | no | 1.467 | 0.716 | no | 2.645 | 0.051 | yes | 2.204 | 0.754 | yes | 1.993 | 0.613 | yes | 1.657 | 0.852 | yes | 1.664 | 0.900 | yes | 1.791 | 0.639 | yes |
| DRA0342 | Sensor regulator, TPR-repeats + GGEEF domain + HD hydrolase | 0.703 | 0.331 | yes | 0.398 | 0.161 | yes | 0.532 | 0.177 | yes | 1.445 | 0.285 | no | 2.261 | 1.296 | yes | 0.978 | 0.670 | no | 1.543 | 0.893 | no | 1.749 | 1.030 | no | n/a | n/a | n/a |
| DRA0343 | Succinic semialdehyde dehydrogenase | 1.099 | 0.260 | no | 1.831 | 0.280 | yes | 1.688 | 0.299 | yes | 1.357 | 0.023 | no | 1.263 | 0.378 | no | 1.333 | 0.240 | no | 1.552 | 0.208 | yes | 1.789 | 0.668 | yes | 0.898 | 0.254 | no |
| DRA0344 | LEXA repressor, HTH+protease | 1.110 | 0.199 | no | 1.796 | 0.666 | yes | 1.798 | 1.077 | yes | 1.051 | 0.057 | no | 1.379 | 0.640 | no | 1.404 | 0.520 | no | 1.473 | 0.914 | no | 1.162 | 0.299 | no | 1.018 | 0.297 | no |
| DRA0345 | EREB_ECOLI ERYTHROMYCIN ESTERASE TYPE II | 1.359 | 0.224 | no | 9.299 | 3.800 | yes | 10.051 | 4.394 | yes | 8.024 | 1.365 | yes | 5.091 | 1.600 | yes | 2.767 | 0.439 | yes | 2.438 | 0.997 | yes | 1.265 | 0.254 | no | 1.144 | 0.368 | no |
| DRA0346 | PPRA protein, possibly involved in DNA damage resistance mechanisms | 1.137 | 0.506 | no | 3.515 | 1.938 | yes | 2.639 | 1.206 | yes | 2.271 | 0.725 | yes | 1.936 | 0.728 | yes | 1.374 | 0.075 | no | 1.166 | 0.353 | no | 1.015 | 0.137 | no | 1.114 | 0.185 | no |
| DRA0347 | Metallobetalactamase family hydrolase | 1.379 | 0.348 | no | 2.518 | 1.372 | yes | 2.401 | 0.812 | yes | 2.005 | 0.243 | yes | 1.763 | 0.444 | yes | 1.184 | 0.267 | no | 1.284 | 0.448 | no | 1.022 | 0.145 | no | 1.156 | 0.192 | no |
| DRA0348 | Acetaldehyde dehydrogenase II | 1.316 | 0.568 | no | 1.258 | 0.676 | no | 0.905 | 0.585 | no | 0.596 | 0.258 | yes | 0.656 | 0.223 | yes | 0.576 | 0.229 | yes | 0.784 | 0.347 | no | 0.818 | 0.130 | no | 1.041 | 0.360 | no |
| DRA0349 | ABC transporter ATPase | 1.539 | 0.236 | yes | 1.304 | 0.637 | no | 1.195 | 0.606 | no | 0.935 | 0.265 | no | 0.845 | 0.327 | no | 0.887 | 0.505 | no | 0.976 | 0.323 | no | 0.938 | 0.168 | no | 1.140 | 0.178 | no |
| DRA0350 | CheY-family sensor regulator | 1.723 | 0.183 | yes | 1.834 | 0.675 | yes | 1.673 | 0.883 | yes | 1.754 | 0.213 | yes | 1.346 | 0.747 | no | 1.476 | 0.626 | no | 1.313 | 0.536 | no | 1.018 | 0.251 | no | 1.115 | 0.494 | no |
| DRA0351 | Related to PILI protein | 1.241 | 0.380 | no | 1.057 | 0.368 | no | 1.270 | 0.390 | no | 0.991 | 0.143 | no | 1.126 | 0.604 | no | 0.961 | 0.253 | no | 0.956 | 0.312 | no | 0.983 | 0.212 | no | 0.901 | 0.383 | no |
| DRA0352 | PILJ ortholog, similar to methyl-accepting chemotaxis protein | 1.784 | 0.407 | yes | 1.979 | 0.777 | yes | 1.351 | 0.284 | no | 1.531 | 0.392 | no | 1.397 | 0.544 | no | 1.308 | 0.397 | no | 1.294 | 0.799 | no | 0.987 | 0.255 | no | 1.131 | 0.478 | no |
| DRA0353 | Similar to methyl-accepting chemotaxis protein | 1.933 | 0.485 | yes | 2.220 | 0.935 | yes | 1.876 | 0.546 | yes | 1.654 | 0.396 | yes | 1.504 | 0.923 | no | 1.803 | 0.735 | yes | 1.423 | 0.558 | no | 1.155 | 0.232 | no | 1.119 | 0.220 | no |
| DRA0354 | Similar to methyl-accepting chemotaxis protein PIL operon? | 1.197 | 0.390 | no | 1.175 | 0.140 | no | 0.953 | 0.373 | no | 0.783 | 0.115 | no | 0.773 | 0.199 | no | 0.864 | 0.375 | no | 0.908 | 0.446 | no | 0.736 | 0.179 | no | 0.876 | 0.263 | no |
| DRA0356 | Predicted protein | 1.767 | 0.910 | yes | 1.381 | 0.390 | no | 2.107 | 1.289 | yes | 3.381 | 1.238 | yes | 2.180 | 1.128 | yes | 1.857 | 0.904 | yes | 2.714 | 1.903 | yes | 1.845 | 0.775 | yes | 3.763 | 1.210 | yes |
| DRA0357 | Sensor regulator CHEY family | 1.590 | 0.545 | no | 1.423 | 0.491 | no | 1.627 | 0.630 | yes | 1.381 | 0.337 | no | 1.672 | 0.680 | yes | 1.602 | 0.961 | no | 1.576 | 0.696 | no | 1.382 | 0.351 | no | 2.487 | 0.618 | yes |
| DRA0358 | Uncharacterized protein with domain one similar to 2 yeast proteins | 1.129 | 0.297 | no | 0.704 | 0.275 | yes | 0.879 | 0.183 | no | 1.015 | 0.368 | no | 0.920 | 0.086 | no | 1.351 | 0.415 | no | 0.826 | 0.329 | no | 0.824 | 0.172 | no | 0.664 | 0.140 | no |
| DRA0359 | Possible membrane protein | 0.986 | 0.436 | no | 0.687 | 0.303 | yes | 0.599 | 0.264 | yes | 0.539 | 0.358 | yes | 0.616 | 0.319 | yes | 0.501 | 0.205 | yes | 0.552 | 0.135 | yes | 0.740 | 0.121 | no | 0.622 | 0.230 | yes |
| DRA0360 | Threonine synthase | 0.906 | 0.320 | no | 0.504 | 0.175 | yes | 0.667 | 0.229 | yes | 0.640 | 0.217 | yes | 0.748 | 0.327 | no | 0.673 | 0.276 | yes | 0.781 | 0.266 | no | 0.831 | 0.229 | no | 1.036 | 0.409 | no |
| DRA0361 | Similar to divalent cation transport | 1.116 | 0.203 | no | 0.904 | 0.319 | no | 0.752 | 0.328 | yes | 0.975 | 0.209 | no | 0.815 | 0.173 | no | 0.906 | 0.152 | no | 0.787 | 0.136 | no | 0.837 | 0.063 | no | 0.936 | 0.100 | no |
| DRA0362 | Predicted protein | 1.075 | 0.168 | no | 0.979 | 0.281 | no | 0.958 | 0.374 | no | 1.323 | 0.341 | no | 1.301 | 0.522 | no | 1.737 | 1.118 | no | 1.890 | 0.815 | yes | 1.473 | 0.526 | no | 1.209 | 0.410 | no |
| DRA0363 | Dehydrogenase | 1.202 | 0.387 | no | 1.180 | 0.510 | no | 0.914 | 0.315 | no | 0.985 | 0.444 | no | 0.870 | 0.225 | no | 1.290 | 0.589 | no | 1.259 | 0.780 | no | 1.005 | 0.181 | no | 1.083 | 0.423 | no |
| DRA0364 | ADG Oxidoreductase | 0.841 | 0.429 | no | 0.568 | 0.174 | yes | 0.496 | 0.200 | yes | 2.026 | 0.423 | yes | 2.454 | 1.768 | yes | 2.745 | 1.118 | yes | 3.770 | 2.207 | yes | 2.917 | 0.609 | yes | 2.389 | 0.869 | yes |
| DRA0365 | Predicted protein | 2.129 | 1.015 | yes | 2.172 | 0.630 | yes | 4.048 | 2.783 | yes | 7.102 | 3.392 | yes | 5.574 | 3.214 | yes | 4.821 | 2.868 | yes | 4.302 | 3.120 | yes | 1.455 | 0.251 | no | 0.888 | 0.121 | no |
| DRA0366 | Predicted protein | 1.353 | 0.339 | no | 1.298 | 0.343 | no | 1.602 | 0.740 | yes | 2.898 | 1.707 | yes | 3.464 | 2.011 | yes | 2.382 | 0.662 | yes | 3.204 | 1.443 | yes | 1.927 | 0.785 | yes | 1.053 | 0.468 | no |
| DRA0367 | UDP-galactopyranose mutase | 1.908 | 1.271 | yes | 1.550 | 0.526 | yes | 2.239 | 0.939 | yes | 4.820 | 2.128 | yes | 5.514 | 3.573 | yes | 4.503 | 2.606 | yes | 3.802 | 1.675 | yes | 2.301 | 0.358 | yes | 1.311 | 0.345 | no |
| DRA0368 | LPS glycosyltransferase | 2.018 | 1.206 | yes | 1.355 | 0.753 | no | 2.134 | 1.187 | yes | 3.758 | 1.988 | yes | 3.790 | 2.309 | yes | 3.844 | 1.223 | yes | 5.641 | 4.394 | yes | 1.790 | 0.122 | yes | 1.264 | 0.852 | no |
| DRA0369 | Predicted protein | 1.103 | 0.375 | no | 0.479 | 0.144 | yes | 0.422 | 0.150 | yes | 0.631 | 0.137 | yes | 0.945 | 0.305 | no | 0.964 | 0.240 | no | 0.924 | 0.341 | no | 1.088 | 0.304 | no | 1.854 | 0.524 | yes |
| DRB0001 | Chromosome partitioning protein RepA/MinD/SoJ ATPase SOJ_BACSU | 1.230 | 0.403 | no | 1.350 | 0.267 | no | 1.365 | 0.261 | no | 1.473 | 0.172 | no | 1.058 | 0.168 | no | 1.028 | 0.377 | no | 1.303 | 0.450 | no | 1.394 | 0.486 | no | 1.544 | 0.642 | yes |
| DRB0002 | Plasmid replication-partition related protein SP0J/RepB antagonist of Soj | 1.054 | 0.393 | no | 1.298 | 0.314 | no | 1.448 | 0.337 | yes | 0.980 | 0.242 | no | 1.301 | 0.339 | no | 1.201 | 0.467 | no | 1.430 | 0.542 | no | 0.950 | 0.070 | no | 1.459 | 0.649 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DRB0003 | Predicted protein | 0.995 | 0.090 | no | 0.777 | 0.277 | no | 0.493 | 0.171 | yes | 0.429 | 0.086 | yes | 0.546 | 0.194 | yes | 0.626 | 0.202 | yes | 0.543 | 0.118 | yes | 0.640 | 0.113 | yes | 0.869 | 0.122 | no |
| DRB0004 | TNPA (transposase) homolog | 2.153 | 0.396 | yes | 2.461 | 0.437 | yes | 2.214 | 0.378 | yes | 3.106 | 0.535 | yes | 2.420 | 1.238 | yes | 2.139 | 0.744 | yes | 2.378 | 1.385 | yes | 2.251 | 1.273 | yes | 2.677 | 1.229 | yes |
| DRB0005 | Transposase | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DRB0006 | Predicted protein | 1.474 | 0.913 | no | 1.952 | 0.924 | yes | 1.856 | 0.586 | yes | 5.550 | 0.039 | yes | 2.290 | 0.774 | yes | 1.728 | 0.729 | yes | 1.600 | 0.805 | no | 1.672 | 0.260 | yes | 1.856 | 0.316 | yes |
| DRB0007 | Iron(III) dicitrate-binding protein | 0.979 | 0.350 | no | 1.545 | 0.581 | yes | 2.373 | 0.871 | yes | 1.934 | 0.448 | yes | 2.586 | 1.205 | yes | 2.511 | 0.738 | yes | 2.606 | 0.240 | yes | 2.683 | 0.910 | yes | 3.655 | 0.560 | yes |
| DRB0008 | CobA, cob(I)alamin adenosyltransferase | 1.278 | 0.539 | no | 2.050 | 0.779 | yes | 2.270 | 0.520 | yes | 2.526 | 0.829 | yes | 2.044 | 0.735 | yes | 2.013 | 0.489 | yes | 1.701 | 0.832 | yes | 1.382 | 0.401 | no | 1.525 | 0.515 | yes |
| DRB0009 | CobB, cobyrinic acid a,c-diamide synthase | 0.990 | 0.134 | no | 1.987 | 0.535 | yes | 3.491 | 1.105 | yes | 3.091 | 0.808 | yes | 3.677 | 1.917 | yes | 3.775 | 1.712 | yes | 3.282 | 1.784 | yes | 3.675 | 1.926 | yes | 2.220 | 0.566 | yes |
| DRB0010 | Cobalamin biosynthesis protein, cbiB | 1.304 | 0.371 | no | 2.518 | 0.985 | yes | 2.621 | 0.885 | yes | 2.850 | 1.740 | yes | 1.680 | 0.606 | yes | 2.174 | 0.613 | yes | 1.943 | 1.053 | yes | 1.852 | 0.615 | yes | 1.440 | 0.579 | no |
| DRB0011 | Histidinol-phosphate transaminase, HIS8 | 1.252 | 0.252 | no | 2.470 | 0.972 | yes | 3.846 | 1.102 | yes | 4.437 | 1.749 | yes | 3.321 | 1.189 | yes | 2.357 | 1.650 | yes | 2.539 | 1.134 | yes | 2.351 | 0.593 | yes | 1.782 | 0.571 | yes |
| DRB0012 | Cobyric acid synthase | 6.515 | 3.327 | yes | 1.793 | 1.180 | yes | 1.591 | 1.451 | no | 0.646 | 0.428 | yes | 0.744 | 0.386 | no | 0.577 | 0.360 | yes | 0.815 | 0.429 | no | 0.747 | 0.133 | no | n/a | n/a | n/a |
| DRB0013 | Unknown protein similar to Sphingomonas >gi\|3378341 | 0.885 | 0.472 | no | 1.069 | 0.570 | no | 0.934 | 0.573 | no | 0.714 | 0.513 | yes | 0.845 | 0.454 | no | 0.874 | 0.548 | no | 0.656 | 0.359 | yes | 0.701 | 0.203 | yes | 0.598 | 0.201 | yes |
| DRB0014 | Predicted protein | 0.488 | 0.218 | yes | 0.466 | 0.167 | yes | 0.618 | 0.201 | yes | 0.301 | 0.119 | yes | 0.278 | 0.138 | yes | 0.261 | 0.130 | yes | 0.174 | 0.075 | yes | 0.256 | 0.093 | yes | 0.293 | 0.093 | yes |
| DRB0015 | Periplasmic binding protein HutB | 0.916 | 0.287 | no | 1.336 | 0.654 | no | 1.614 | 0.759 | yes | 0.260 | 0.060 | yes | 0.508 | 0.403 | yes | 0.609 | 0.104 | yes | 0.437 | 0.179 | yes | 0.253 | 0.108 | yes | 0.409 | 0.146 | yes |
| DRB0016 | ABC-type permease hemin HutC | 0.633 | 0.295 | yes | 1.380 | 0.352 | no | 2.390 | 0.836 | yes | 0.786 | 0.564 | no | 0.776 | 0.326 | no | 0.743 | 0.339 | yes | 0.494 | 0.197 | yes | 0.519 | 0.163 | yes | 0.564 | 0.203 | yes |
| DRB0017 | ABC ATPase HutD | 0.852 | 0.432 | no | 3.400 | 1.508 | yes | 5.723 | 2.191 | yes | 1.920 | 0.154 | yes | 1.565 | 0.559 | yes | 1.144 | 0.340 | no | 0.983 | 0.442 | no | 0.873 | 0.110 | no | 1.058 | 0.316 | no |
| DRB0020 | Transposase | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DRB0021 | Predicted protein | 2.109 | 0.911 | yes | 2.550 | 1.559 | yes | 2.700 | 1.338 | yes | 2.315 | 0.680 | yes | 1.663 | 0.894 | no | 2.602 | 1.184 | yes | 1.574 | 0.593 | yes | 1.534 | 0.646 | no | 0.913 | 0.428 | no |
| DRB0022 | HTH tr. regulator | 1.749 | 0.406 | yes | 2.010 | 0.660 | yes | 1.674 | 0.225 | yes | 1.542 | 0.231 | no | 1.428 | 0.703 | no | 1.338 | 0.521 | no | 1.104 | 0.574 | no | 1.134 | 0.309 | no | 0.913 | 0.213 | no |
| DRB0023 | a/b hydrolase + HAD hydrolase | 1.127 | 0.247 | no | 0.678 | 0.111 | no | 0.466 | 0.136 | yes | 0.376 | 0.030 | yes | 0.550 | 0.249 | yes | 0.658 | 0.227 | yes | 0.693 | 0.247 | yes | 0.849 | 0.237 | no | 1.422 | 0.336 | no |
| DRB0024 | Sigma B factor regulator, RSBR | 1.230 | 0.249 | no | 0.913 | 0.257 | no | 0.937 | 0.331 | no | 0.965 | 0.069 | no | 0.887 | 0.219 | no | 1.066 | 0.237 | no | 1.297 | 0.254 | no | 1.662 | 0.779 | yes | 1.340 | 0.477 | no |
| DRB0025 | Anti-sigma B factor antagonist, RSBS | 1.359 | 0.298 | no | 0.735 | 0.323 | no | 1.043 | 0.347 | no | 0.838 | 0.187 | no | 1.094 | 0.689 | no | 1.011 | 0.416 | no | 0.882 | 0.270 | no | 1.219 | 0.642 | no | 0.649 | 0.250 | yes |
| DRB0026 | Anti-sigma B factor RSBT, switch protein/serine kinase | 1.481 | 0.422 | no | 1.646 | 0.656 | yes | 1.979 | 0.746 | yes | 1.890 | 0.611 | yes | 1.597 | 0.309 | yes | 1.528 | 0.661 | no | 1.418 | 0.459 | no | 1.324 | 0.408 | no | 0.818 | 0.367 | no |
| DRB0027 | Fusion anti-sigma B factor RSBT/TORS + RSBX regulator | 1.837 | 1.110 | yes | 0.953 | 0.526 | no | 1.636 | 0.753 | yes | 0.943 | 0.319 | no | 1.517 | 0.819 | no | 1.832 | 1.124 | yes | 1.194 | 0.571 | no | 1.055 | 0.409 | no | 0.594 | 0.218 | yes |
| DRB0028 | Sensory transduction histidine kinase + CheY-like domain | 1.675 | 0.640 | yes | 1.275 | 0.340 | no | 1.457 | 0.525 | no | 1.806 | 0.703 | yes | 1.667 | 1.245 | no | 1.864 | 0.691 | yes | 1.673 | 0.661 | yes | 1.792 | 0.820 | yes | 0.942 | 0.501 | no |
| DRB0029 | CheY-like domain + sensory transduction histidine kinase | 1.172 | 0.198 | no | 0.714 | 0.166 | no | 0.869 | 0.335 | no | 0.901 | 0.335 | no | 0.709 | 0.271 | no | 1.014 | 0.073 | no | 0.964 | 0.116 | no | 0.852 | 0.198 | no | 0.556 | 0.187 | yes |
| DRB0030 | ParB/SpoJ plasmid replication protein | 0.804 | 0.211 | no | 0.483 | 0.140 | yes | 0.641 | 0.206 | yes | 0.525 | 0.105 | yes | 0.757 | 0.155 | no | 0.778 | 0.187 | no | 0.775 | 0.280 | no | 0.825 | 0.149 | no | 1.041 | 0.209 | no |
| DRB0031 | Soj-like protein | 0.902 | 0.147 | no | 0.819 | 0.206 | no | 0.739 | 0.226 | no | 0.707 | 0.251 | no | 0.919 | 0.324 | no | 0.825 | 0.114 | no | 0.831 | 0.187 | no | 1.127 | 0.135 | no | 1.002 | 0.143 | no |
| DRB0032 | Predicted protein | 1.872 | 0.847 | yes | 1.797 | 0.218 | yes | 1.287 | 0.402 | no | 1.597 | 0.752 | no | 1.010 | 0.724 | no | 1.118 | 0.395 | no | 1.499 | 0.779 | no | 1.117 | 0.467 | no | 1.179 | 0.465 | no |
| DRB0033 | Arylesterase lipW, a/b hydrolase + steroid monooxigenase | 1.338 | 0.352 | no | 0.977 | 0.354 | no | 0.795 | 0.414 | no | 0.748 | 0.164 | no | 0.611 | 0.225 | yes | 0.648 | 0.109 | no | 0.957 | 0.505 | no | 0.905 | 0.388 | no | 1.760 | 0.274 | yes |
| DRB0034 | GGDEF domain regulatory components of sensory transduction system small variant as in Vibrio | 2.007 | 1.234 | yes | 1.523 | 0.608 | yes | 1.108 | 0.171 | no | 1.103 | 0.083 | no | 0.985 | 0.534 | no | 0.993 | 0.447 | no | 1.231 | 0.533 | no | 1.061 | 0.172 | no | 1.248 | 0.613 | no |
| DRB0035 | Possible TRP-repeat containing protein | 1.533 | 0.465 | no | 2.283 | 1.047 | yes | 1.721 | 0.819 | yes | 1.394 | 0.845 | no | 1.571 | 0.746 | no | 1.198 | 0.619 | no | 1.056 | 0.841 | no | 0.770 | 0.178 | no | 0.888 | 0.393 | no |
| DRB0037 | Uncharacterized secreted protein, DR-1 | 1.602 | 0.520 | yes | 1.606 | 0.833 | yes | 1.332 | 0.419 | no | 1.202 | 0.372 | no | 1.315 | 0.611 | no | 1.610 | 0.376 | yes | 1.529 | 0.421 | no | 1.541 | 0.818 | no | 1.875 | 1.285 | yes |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DRB0038 | Uncharacterized secreted protein, DR-1 fragment | 2.057 | 0.842 | yes | 1.867 | 0.756 | yes | 2.203 | 0.851 | yes | 2.869 | 1.085 | yes | 1.980 | 1.467 | yes | 1.929 | 1.216 | yes | 2.377 | 1.184 | yes | 0.906 | 0.149 | no | 0.998 | 0.228 | no |
| DRB0039 | Uncharacterized protein, DR-1 | 0.962 | 0.223 | no | 1.717 | 0.643 | yes | 2.778 | 1.427 | yes | 3.131 | 1.314 | yes | 2.575 | 0.881 | yes | 2.407 | 0.644 | yes | 2.887 | 0.730 | yes | 1.946 | 0.639 | yes | 2.302 | 0.794 | yes |
| DRB0040 | Predicted protein | 1.528 | 0.577 | no | 1.041 | 0.368 | no | 0.970 | 0.269 | no | 0.620 | 0.155 | yes | 0.768 | 0.365 | no | 0.944 | 0.443 | no | 0.874 | 0.334 | no | 1.070 | 0.324 | no | 1.378 | 0.283 | no |
| DRB0041 | Predicted protein, DR-2 | 1.459 | 0.392 | no | 1.669 | 0.895 | yes | 1.310 | 0.624 | no | 1.438 | 0.733 | no | 1.086 | 0.714 | no | 1.276 | 0.642 | no | 1.434 | 0.748 | no | 1.136 | 0.151 | no | 1.234 | 0.552 | no |
| DRB0042 | Periplasmic-binding protein | 1.548 | 0.453 | no | 1.503 | 0.532 | yes | 1.207 | 0.328 | no | 1.215 | 0.325 | no | 1.373 | 0.552 | no | 1.398 | 0.797 | no | 1.500 | 0.694 | no | 1.629 | 0.626 | yes | 1.172 | 0.189 | no |
| DRB0043 | Permease | 2.871 | 1.121 | yes | 4.064 | 2.143 | yes | 2.229 | 1.003 | yes | 2.313 | 1.226 | yes | 1.933 | 1.033 | yes | 1.897 | 0.544 | yes | 1.299 | 0.787 | no | 1.149 | 0.512 | no | 1.450 | 0.848 | no |
| DRB0044 | Regulatory component of sensory transduction system, GGEEF domain + GAF domain | 1.839 | 0.840 | yes | 1.268 | 0.307 | no | 1.808 | 0.622 | yes | 2.250 | 0.592 | yes | 1.423 | 0.887 | no | 1.502 | 1.159 | no | 1.458 | 0.377 | no | 1.430 | 0.461 | no | 1.083 | 0.299 | no |
| DRB0045 | Predicted protein | 2.484 | 1.423 | yes | 1.775 | 0.795 | yes | 1.004 | 0.256 | no | 0.681 | 0.098 | no | 0.851 | 0.398 | no | 1.372 | 0.664 | no | 1.153 | 0.604 | no | 1.062 | 0.622 | no | 0.418 | 0.104 | yes |
| DRB0047 | Predicted protein | 2.430 | 1.546 | yes | 1.574 | 1.095 | no | 0.881 | 0.427 | no | 0.713 | 0.066 | no | 0.863 | 0.449 | no | 0.936 | 0.394 | no | 1.182 | 0.625 | no | 1.657 | 0.882 | no | n/a | n/a | n/a |
| DRB0048 | Predicted protein | 0.659 | 0.401 | yes | 0.706 | 0.395 | yes | 0.725 | 0.207 | no | 0.449 | 0.215 | yes | 0.348 | 0.248 | yes | 0.591 | 0.465 | yes | 0.282 | 0.169 | yes | 0.415 | 0.125 | yes | 0.381 | 0.176 | yes |
| DRB0049 | ABC transporter ATPase | 2.505 | 0.941 | yes | 1.612 | 0.825 | yes | 1.239 | 0.425 | no | 1.024 | 0.587 | no | 0.950 | 0.303 | no | 1.062 | 0.577 | no | 1.318 | 0.868 | no | 1.124 | 0.405 | no | 0.998 | 0.291 | no |
| DRB0050 | Conserved membrane protein | 1.592 | 0.683 | no | 1.371 | 0.566 | no | 1.203 | 0.316 | no | 1.233 | 0.654 | no | 0.937 | 0.514 | no | 0.988 | 0.310 | no | 1.003 | 0.651 | no | 0.881 | 0.135 | no | 0.867 | 0.247 | no |
| DRB0051 | Predicted protein | 1.867 | 0.680 | yes | 1.255 | 0.546 | no | 1.128 | 0.355 | no | 0.903 | 0.218 | no | 0.772 | 0.425 | no | 0.821 | 0.343 | no | 0.922 | 0.356 | no | 0.918 | 0.239 | no | 1.329 | 0.851 | no |
| DRB0052 | Uncharacterized protein with N_term. fragment similar to YCGC_ECOLI | 2.066 | 0.759 | yes | 1.972 | 0.873 | yes | 1.163 | 0.313 | no | 1.603 | 0.132 | yes | 1.362 | 0.586 | no | 1.183 | 0.428 | no | 1.198 | 0.472 | no | 1.245 | 0.281 | no | 0.792 | 0.038 | no |
| DRB0054 | Predicted protein | 1.546 | 0.320 | yes | 1.114 | 0.308 | no | 1.037 | 0.450 | no | 0.717 | 0.106 | no | 0.869 | 0.367 | no | 1.412 | 0.666 | no | 1.451 | 0.557 | no | 1.575 | 0.579 | yes | 1.091 | 0.205 | no |
| DRB0055 | Transposon ORF | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DRB0057 | Transposon ORF | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DRB0059 | Transposase, putative | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DRB0060 | Uncharacterized conserved protein, similar to spore coat protein II | 2.034 | 0.589 | yes | 3.449 | 0.751 | yes | 3.303 | 1.257 | yes | 3.171 | 0.703 | yes | 2.420 | 1.294 | yes | 3.691 | 2.334 | yes | 2.456 | 1.699 | yes | 1.795 | 1.153 | yes | 0.956 | 0.642 | no |
| DRB0061 | Predicted protein | 1.638 | 0.347 | yes | 1.769 | 0.434 | yes | 1.255 | 0.394 | no | 1.017 | 0.246 | no | 1.026 | 0.331 | no | 1.065 | 0.386 | no | 1.052 | 0.331 | no | 1.163 | 0.276 | no | 1.092 | 0.216 | no |
| DRB0062 | Homolog of ECPD pili assembly chaperon | 1.225 | 0.201 | no | 0.824 | 0.522 | no | 0.795 | 0.469 | no | 0.676 | 0.095 | no | 0.824 | 0.371 | no | 0.884 | 0.552 | no | 0.707 | 0.187 | no | 0.851 | 0.141 | no | 1.092 | 0.235 | no |
| DRB0063 | Outer membrane usher protein | 1.842 | 0.690 | yes | 1.530 | 0.581 | yes | 1.948 | 0.352 | yes | 1.273 | 0.798 | no | 1.342 | 0.593 | no | 2.030 | 1.052 | yes | 1.168 | 0.395 | no | 1.101 | 0.370 | no | 0.844 | 0.242 | no |
| DRB0064 | Predicted protein | 1.137 | 0.143 | no | 1.425 | 0.937 | no | 1.897 | 1.157 | yes | 2.256 | 0.511 | yes | 0.887 | 0.398 | no | 0.664 | 0.545 | yes | 0.708 | 0.450 | yes | 0.453 | 0.180 | yes | n/a | n/a | n/a |
| DRB0065 | Contains cell adhesion domains | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DRB0066 | Predicted protein | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DRB0067 | Extracellular nuclease with Fibronectin III domains | 1.511 | 0.752 | no | 1.545 | 0.589 | yes | 2.823 | 0.674 | yes | 4.371 | 1.205 | yes | 3.670 | 1.444 | yes | 3.204 | 0.661 | yes | 2.498 | 0.932 | yes | 4.137 | 2.260 | yes | 2.045 | 0.416 | yes |
| DRB0068 | Secreted protein with Fibronectin III domains | 1.761 | 0.405 | yes | 1.292 | 0.749 | no | 2.309 | 1.065 | yes | 2.502 | 1.339 | yes | 2.227 | 0.829 | yes | 2.356 | 1.063 | yes | 0.790 | 0.496 | no | 1.259 | 0.312 | no | 0.731 | 0.177 | no |
| DRB0069 | Subtilisin serine protease | 2.064 | 0.748 | yes | 2.428 | 0.875 | yes | 2.573 | 1.221 | yes | 3.179 | 1.387 | yes | 2.264 | 1.180 | yes | 2.358 | 0.254 | yes | 3.095 | 1.010 | yes | 1.575 | 0.954 | no | 2.389 | 1.193 | yes |
| DRB0070 | P-loop ATPase, probably from ABC family | 1.141 | 0.451 | no | 1.210 | 0.377 | no | 3.996 | 1.908 | yes | 3.701 | 0.191 | yes | 3.470 | 1.472 | yes | 2.399 | 1.056 | yes | 0.998 | 0.379 | no | 1.337 | 0.656 | no | 1.363 | 0.468 | no |
| DRB0071 | Predicted protein | 0.889 | 0.148 | no | 0.866 | 0.305 | no | 2.296 | 0.966 | yes | 2.595 | 0.532 | yes | 2.337 | 0.744 | yes | 2.369 | 0.727 | yes | 1.175 | 0.419 | no | 1.117 | 0.202 | no | 0.781 | 0.248 | no |
| DRB0072 | Salicylate 1-monooxygenase | 1.923 | 0.946 | yes | 2.069 | 1.083 | yes | 4.908 | 2.309 | yes | 3.819 | 0.454 | yes | 3.395 | 0.793 | yes | 2.883 | 1.059 | yes | 1.538 | 0.852 | no | 1.169 | 0.422 | no | 0.859 | 0.330 | no |
| DRB0073 | Phosphotransferase system enzyme II | 1.848 | 0.855 | yes | 3.412 | 1.860 | yes | 8.032 | 5.290 | yes | 7.113 | 0.885 | yes | 6.876 | 1.827 | yes | 5.058 | 1.379 | yes | 1.792 | 1.149 | yes | 1.090 | 0.162 | no | 1.049 | 0.279 | no |
| DRB0074 | 1-phosphofructokinase | 2.245 | 0.903 | yes | 4.074 | 1.510 | yes | 13.205 | 5.620 | yes | 13.512 | 4.957 | yes | 9.306 | 4.093 | yes | 7.042 | 1.630 | yes | 2.126 | 1.081 | yes | 1.264 | 0.407 | no | 1.008 | 0.390 | no |
| DRB0076 | Specific sugar metabolism transcriptional regulator | 2.012 | 0.802 | yes | 1.874 | 0.615 | yes | 1.851 | 0.424 | yes | 1.672 | 0.261 | yes | 1.617 | 0.449 | yes | 1.674 | 0.634 | yes | 0.982 | 0.552 | no | 1.135 | 0.338 | no | 1.034 | 0.424 | no |
| DRB0077 | NH2-acetyltransferase | 1.699 | 0.881 | yes | 1.467 | 0.338 | yes | 2.120 | 1.080 | yes | 1.144 | 0.030 | no | 1.733 | 0.729 | yes | 2.026 | 0.841 | yes | 1.334 | 0.466 | no | 1.076 | 0.393 | no | 1.040 | 0.464 | no |
| DRB0079 | N-Acylamino acid racemase | 1.411 | 0.492 | no | 1.297 | 0.596 | no | 1.348 | 0.759 | no | 1.403 | 0.472 | no | 1.366 | 0.853 | no | 1.264 | 0.298 | no | 1.177 | 0.530 | no | 0.989 | 0.226 | no | 0.927 | 0.146 | no |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DRB0080 | 3-alpha-hydroxysteroid dehydrogenase | 0.992 | 0.290 | no | 0.735 | 0.197 | no | 0.698 | 0.417 | yes | 0.714 | 0.284 | no | 0.747 | 0.376 | yes | 0.958 | 0.593 | no | 0.867 | 0.220 | no | 0.774 | 0.098 | no | 1.236 | 0.472 | no |
| DRB0081 | CheY-like regulatory component of sensory transduction system + HTH domain | 2.406 | 1.179 | yes | 1.308 | 0.694 | no | 1.359 | 0.571 | no | 1.318 | 0.343 | no | 1.041 | 0.327 | no | 1.547 | 0.475 | no | 0.935 | 0.624 | no | 1.011 | 0.253 | no | 1.076 | 0.479 | no |
| DRB0083 | Potassium-transporting atpase B chain | 2.619 | 1.538 | yes | 1.478 | 0.650 | no | 1.335 | 0.729 | no | 1.654 | 0.452 | no | 2.476 | 2.000 | yes | 1.373 | 0.497 | no | 0.937 | 0.419 | no | 0.838 | 0.360 | no | 0.679 | 0.237 | no |
| DRB0084 | Predicted protein | 2.105 | 0.858 | yes | 1.985 | 0.644 | yes | 1.246 | 0.361 | no | 1.462 | 0.489 | no | 1.137 | 0.286 | no | 2.123 | 0.786 | yes | 0.967 | 0.521 | no | 0.578 | 0.221 | yes | 0.454 | 0.038 | yes |
| DRB0085 | Predicted protein | 1.127 | 0.182 | no | 1.462 | 0.451 | no | 1.518 | 0.936 | no | 0.931 | 0.608 | no | 2.025 | 1.221 | yes | 1.407 | 0.389 | no | 1.237 | 0.784 | no | 1.038 | 0.300 | no | 1.723 | 0.876 | yes |
| DRB0086 | Potassium-transporting ATPase A chain | 2.705 | 0.721 | yes | 2.417 | 0.813 | yes | 1.631 | 0.640 | yes | 1.250 | 0.175 | no | 1.269 | 0.621 | no | 1.102 | 0.544 | no | 1.387 | 0.808 | no | 1.024 | 0.352 | no | 0.888 | 0.461 | no |
| DRB0087 | Potassium-transporting ATPase C chain | 1.506 | 0.317 | no | 1.649 | 0.776 | yes | 1.262 | 0.473 | no | 1.421 | 0.579 | no | 0.960 | 0.399 | no | 1.270 | 0.241 | no | 1.231 | 0.454 | no | 1.088 | 0.343 | no | 0.988 | 0.341 | no |
| DRB0088 | Potassium-transporting ATPase D chain | 2.283 | 1.002 | yes | 1.564 | 0.702 | no | 1.450 | 0.737 | no | 1.812 | 0.706 | yes | 1.372 | 0.843 | no | 0.978 | 0.280 | no | 1.257 | 0.817 | no | 1.101 | 0.512 | no | 0.911 | 0.167 | no |
| DRB0089 | Predicted protein | 0.877 | 0.110 | no | 0.999 | 0.306 | no | 0.623 | 0.079 | yes | 0.431 | 0.037 | yes | 0.591 | 0.389 | yes | 0.633 | 0.138 | yes | 0.869 | 0.371 | no | 0.621 | 0.197 | yes | 2.413 | 0.181 | yes |
| DRB0090 | Sensory transduction histidine kinase phoR/BaeS-like | 1.391 | 0.543 | no | 1.826 | 0.624 | yes | 1.328 | 0.721 | no | 1.333 | 0.930 | no | 1.021 | 0.548 | no | 1.028 | 0.368 | no | 0.813 | 0.283 | no | 0.942 | 0.293 | no | 0.673 | 0.171 | no |
| DRB0091 | CheY-like responce regulator + HTH domain, ortholog tcrA/phoP/phoB signalling protein | 1.286 | 0.469 | no | 1.932 | 0.944 | yes | 1.487 | 0.425 | no | 1.339 | 0.269 | no | 1.005 | 0.462 | no | 2.338 | 1.671 | yes | 2.136 | 1.428 | yes | 0.800 | 0.290 | no | 0.924 | 0.344 | no |
| DRB0092 | DNA-binding protein belonging to Dps/ ferritin family | 2.079 | 0.969 | yes | 3.134 | 1.417 | yes | 2.322 | 0.804 | yes | 2.861 | 1.262 | yes | 1.685 | 0.543 | yes | 2.213 | 0.784 | yes | 1.965 | 0.833 | yes | 2.206 | 1.159 | yes | 1.262 | 0.591 | no |
| DRB0093 | Membrane bounded GGEEF domain, component of sensory transduction system | 1.618 | 0.476 | yes | 1.527 | 0.861 | no | 1.570 | 0.541 | yes | 2.281 | 1.178 | yes | 2.789 | 1.595 | yes | 1.619 | 0.746 | no | 1.046 | 0.618 | no | 1.333 | 0.662 | no | 0.886 | 0.301 | no |
| DRB0094 | EMAP-domain + unknown domain | 2.369 | 1.174 | yes | 1.758 | 0.717 | yes | 2.607 | 1.410 | yes | 3.011 | 0.792 | yes | 2.166 | 0.521 | yes | 2.238 | 0.873 | yes | 2.000 | 0.718 | yes | 1.756 | 0.764 | yes | 1.588 | 0.685 | yes |
| DRB0095 | Conserved protein disrupted by SMR | 1.529 | 0.527 | no | 1.391 | 0.341 | no | 1.930 | 0.769 | yes | 3.248 | 1.248 | yes | 2.521 | 0.757 | yes | 1.805 | 0.468 | yes | 1.988 | 0.814 | yes | 1.304 | 0.499 | no | 1.031 | 0.618 | no |
| DRB0096 | Predicted protein | 1.258 | 0.399 | no | 1.829 | 1.041 | yes | 2.659 | 0.833 | yes | 2.388 | 0.811 | yes | 3.641 | 2.763 | yes | 2.225 | 0.525 | yes | 1.452 | 0.812 | no | 0.877 | 0.116 | no | 0.769 | 0.280 | no |
| DRB0097 | Epoxide hydrolase, a/b superfamily | 2.078 | 0.961 | yes | 1.519 | 0.413 | yes | 4.486 | 1.001 | yes | 6.783 | 2.223 | yes | 5.564 | 2.093 | yes | 4.859 | 1.328 | yes | 4.526 | 1.751 | yes | 3.568 | 1.935 | yes | 1.903 | 0.858 | yes |
| DRB0098 | Fusion a domain from tRNA nucleotidyltransferase and P-loop ATPase domain | 1.807 | 0.279 | yes | 1.861 | 0.964 | yes | 6.803 | 3.598 | yes | 5.423 | 0.729 | yes | 4.847 | 3.263 | yes | 3.316 | 1.450 | yes | 11.890 | 6.543 | yes | 1.470 | 0.104 | no | 0.999 | 0.021 | no |
| DRB0099 | Uncharacterized conserved protein | 1.239 | 0.462 | no | 1.536 | 0.606 | yes | 5.506 | 1.713 | yes | 8.454 | 3.055 | yes | 9.322 | 5.928 | yes | 5.971 | 2.582 | yes | 6.554 | 4.573 | yes | 2.110 | 0.229 | yes | 2.038 | 1.350 | yes |
| DRB0100 | Homolog of eukaryotic DNA ligase III | 1.633 | 0.798 | no | 1.468 | 0.589 | no | 9.236 | 4.017 | yes | 14.434 | 2.788 | yes | 9.418 | 4.301 | yes | 6.238 | 2.599 | yes | 4.419 | 1.849 | yes | 4.163 | 2.286 | yes | 2.284 | 0.873 | yes |
| DRB0102 | Transposon ORF | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DRB0103 | Transposase | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DRB0104 | XerC-like recombinase | 0.964 | 0.194 | no | 0.784 | 0.271 | no | 0.749 | 0.285 | no | 0.528 | 0.109 | yes | 0.926 | 0.476 | no | 1.066 | 0.327 | no | 0.899 | 0.203 | no | 0.973 | 0.122 | no | 1.340 | 0.190 | no |
| DRB0105 | Predicted protein | 1.943 | 0.536 | yes | 0.600 | 0.334 | yes | 1.113 | 0.736 | no | 5.697 | 3.608 | yes | 1.332 | 0.719 | no | 1.662 | 0.377 | yes | 1.524 | 0.971 | no | 2.025 | 0.471 | yes | 2.569 | 1.364 | yes |
| DRB0106 | Acyl-CoA Thioesterase superfamily protein | 0.429 | 0.259 | yes | 0.310 | 0.127 | yes | 0.547 | 0.195 | yes | 0.779 | 0.141 | no | 2.288 | 1.227 | yes | 2.189 | 0.708 | yes | 2.405 | 1.025 | yes | 2.069 | 0.840 | yes | 4.802 | 1.643 | yes |
| DRB0107 | NRDI ribonucleoprotein | 0.997 | 0.260 | no | 0.887 | 0.331 | no | 2.040 | 1.159 | yes | 2.605 | 0.863 | yes | 3.683 | 1.253 | yes | 4.309 | 1.256 | yes | 3.653 | 1.355 | yes | 3.445 | 1.357 | yes | 5.700 | 1.383 | yes |
| DRB0108 | Large SU ribonucleoside-diphosphate reductase | 0.857 | 0.376 | no | 0.980 | 0.326 | no | 2.101 | 0.784 | yes | 2.758 | 0.201 | yes | 4.042 | 1.601 | yes | 5.143 | 1.947 | yes | 3.832 | 0.725 | yes | 3.587 | 1.313 | yes | 6.938 | 2.833 | yes |
| DRB0109 | Small SU ribonucleoside-diphosphate reductase | 1.167 | 0.303 | no | 1.672 | 0.617 | yes | 4.191 | 1.580 | yes | 6.083 | 0.878 | yes | 5.694 | 2.367 | yes | 6.253 | 0.792 | yes | 5.149 | 1.947 | yes | 3.213 | 1.519 | yes | 6.124 | 2.559 | yes |
| DRB0110 | Thioredoxin | 2.264 | 1.071 | yes | 1.346 | 0.283 | no | 1.823 | 1.244 | yes | 1.830 | 0.823 | yes | 6.093 | 4.670 | yes | 4.111 | 0.689 | yes | 3.081 | 1.763 | yes | 2.180 | 0.011 | yes | 3.196 | 0.020 | yes |
| DRB0111 | Glycerophosphodiester phosphodiesterase | 1.169 | 0.248 | no | 1.328 | 0.533 | no | 2.056 | 0.534 | yes | 2.211 | 0.074 | yes | 3.016 | 1.103 | yes | 2.024 | 0.588 | yes | 1.544 | 0.625 | no | 1.524 | 0.662 | no | 1.399 | 0.605 | no |
| DRB0112 | Predicted protein | 0.988 | 0.312 | no | 0.763 | 0.219 | no | 1.061 | 0.332 | no | 1.431 | 0.384 | no | 1.811 | 0.605 | yes | 1.670 | 0.380 | yes | 1.244 | 0.563 | no | 1.621 | 0.642 | yes | 2.833 | 1.393 | yes |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DRB0114 | Transposase | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DRB0115 | Predicted protein | 1.604 | 0.519 | yes | 2.388 | 1.522 | yes | 2.093 | 0.398 | yes | 2.143 | 0.473 | yes | 1.756 | 0.827 | yes | 1.168 | 0.444 | no | 1.355 | 0.572 | no | 0.941 | 0.291 | no | 0.982 | 0.331 | no |
| DRB0116 | Predicted protein | 1.555 | 0.765 | no | 1.101 | 0.510 | no | 1.285 | 0.369 | no | 0.965 | 0.180 | no | 0.803 | 0.274 | no | 0.920 | 0.221 | no | 0.979 | 0.348 | no | 0.817 | 0.177 | no | 1.094 | 0.305 | no |
| DRB0117 | Transposase | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DRB0118 | Unch. protein related to desiccation-related protein Craterostigma plantagineum (gi\|118926) | 1.068 | 0.327 | no | 1.136 | 0.413 | no | 1.357 | 0.312 | no | 1.344 | 0.557 | no | 1.322 | 0.189 | no | 1.364 | 0.482 | no | 1.302 | 0.636 | no | 1.074 | 0.258 | no | 0.696 | 0.099 | no |
| DRB0119 | Na+/H+ antiporter (nhe2) | 2.184 | 0.957 | yes | 2.361 | 0.944 | yes | 2.165 | 0.683 | yes | 2.218 | 1.170 | yes | 1.520 | 0.590 | no | 1.144 | 0.411 | no | 1.340 | 0.715 | no | 1.051 | 0.387 | no | 0.902 | 0.353 | no |
| DRB0121 | Ferrichrome iron(III) transport protein, FhuC, ATPase | 1.136 | 0.575 | no | 2.371 | 1.528 | yes | 5.088 | 2.001 | yes | 3.336 | 1.999 | yes | 2.237 | 1.537 | yes | 2.219 | 1.148 | yes | 1.513 | 0.907 | no | 1.073 | 0.061 | no | 0.934 | 0.333 | no |
| DRB0122 | Ferrichrome iron(III) ABC transporter permease fecD | 1.158 | 0.542 | no | 2.060 | 1.372 | yes | 2.705 | 1.185 | yes | 1.402 | 0.396 | no | 1.440 | 0.874 | no | 1.294 | 0.337 | no | 1.276 | 0.818 | no | 0.901 | 0.103 | no | 0.650 | 0.230 | yes |
| DRB0123 | Ferrichrome iron(III) transport permease protein FHUB permease | 1.423 | 0.406 | no | 1.006 | 0.564 | no | 1.289 | 0.516 | no | 0.473 | 0.051 | yes | 1.726 | 0.829 | no | 1.388 | 0.804 | no | 0.696 | 0.406 | yes | 0.767 | 0.056 | no | 0.612 | 0.148 | yes |
| DRB0124 | VIUB-like (Fe(III) tr. system component?) | 1.230 | 0.542 | no | 0.690 | 0.395 | yes | 1.484 | 0.433 | no | 0.236 | 0.014 | yes | 0.568 | 0.417 | yes | 0.629 | 0.142 | yes | 0.273 | 0.106 | yes | 0.323 | 0.122 | yes | 0.430 | 0.151 | yes |
| DRB0125 | Iron(III) dicitrate-binding periplasmic protein | 0.681 | 0.315 | yes | 0.330 | 0.089 | yes | 0.520 | 0.202 | yes | 0.295 | 0.168 | yes | 0.369 | 0.157 | yes | 0.358 | 0.145 | yes | 0.292 | 0.093 | yes | 0.328 | 0.053 | yes | 0.552 | 0.082 | yes |
| DRB0126 | Transcription regulator | 1.058 | 0.397 | no | 1.586 | 0.655 | yes | 1.273 | 0.178 | no | 1.747 | 1.102 | no | 1.200 | 0.402 | no | 0.868 | 0.517 | no | 0.782 | 0.070 | no | 0.720 | 0.149 | yes | 0.621 | 0.320 | yes |
| DRB0127 | Predicted protein | 1.892 | 0.561 | yes | 2.565 | 1.098 | yes | 2.517 | 1.139 | yes | 2.408 | 1.386 | yes | 2.878 | 1.555 | yes | 1.696 | 0.478 | yes | 1.141 | 0.202 | no | 0.881 | 0.133 | no | 0.867 | 0.575 | no |
| DRB0128 | Hemolysin-like CBS domain containing protein | 1.358 | 0.554 | no | 1.244 | 0.427 | no | 1.593 | 0.632 | yes | 1.013 | 0.215 | no | 0.970 | 0.389 | no | 1.299 | 0.824 | no | 1.429 | 0.997 | no | 0.795 | 0.016 | no | 0.698 | 0.327 | yes |
| DRB0129 | Hemolysin-like CBS domain containing protein | 1.581 | 0.191 | yes | 1.610 | 0.333 | yes | 1.732 | 0.398 | yes | 1.701 | 0.225 | yes | 1.503 | 0.549 | no | 1.619 | 0.482 | yes | 1.583 | 0.548 | yes | 1.737 | 1.006 | yes | 1.399 | 0.655 | no |
| DRB0130 | Predicted protein | 1.628 | 0.429 | yes | 1.633 | 0.699 | yes | 1.876 | 0.482 | yes | 1.886 | 0.721 | yes | 1.549 | 0.227 | yes | 1.826 | 0.792 | yes | 1.698 | 0.788 | yes | 1.001 | 0.607 | no | 0.605 | 0.219 | yes |
| DRB0131 | Conserved hypothetical transmembrane protein YGDO_ECOLI | 1.856 | 0.638 | yes | 2.753 | 0.946 | yes | 1.557 | 0.755 | yes | 1.456 | 0.295 | no | 1.820 | 0.948 | yes | 1.359 | 0.501 | no | 1.024 | 0.490 | no | 1.176 | 0.555 | no | 0.850 | 0.521 | no |
| DRB0132 | Transposase | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DRB0133 | D-alanine permease | 2.545 | 0.926 | yes | 3.237 | 1.199 | yes | 3.508 | 1.390 | yes | 2.667 | 0.922 | yes | 1.846 | 0.582 | yes | 1.895 | 0.958 | yes | 1.668 | 0.974 | no | 1.384 | 0.593 | no | 1.363 | 0.694 | no |
| DRB0134 | Transposase | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DRB0135 | ATP-dependent RNA helicase, II superfamily, contains intein and vcr-like endonuclease domain | 2.042 | 1.091 | yes | 2.300 | 0.760 | yes | 2.374 | 1.027 | yes | 2.239 | 0.640 | yes | 2.607 | 1.242 | yes | 1.252 | 0.747 | no | 1.595 | 0.961 | no | 1.397 | 0.339 | no | 0.930 | 0.152 | no |
| DRB0136 | Putative DEAH ATP-dependent helicase, Snf2/Swi2 family, II superfamily | 2.335 | 0.941 | yes | 1.618 | 0.558 | yes | 2.735 | 0.660 | yes | 5.224 | 0.463 | yes | 4.687 | 1.812 | yes | 2.367 | 0.912 | yes | 1.786 | 0.991 | yes | 1.192 | 0.486 | no | 1.041 | 0.532 | no |
| DRB0137 | SAM-dependent methylase | 1.888 | 0.240 | yes | 1.657 | 0.324 | yes | 1.698 | 0.715 | yes | 0.238 | 0.138 | yes | 1.630 | 0.720 | no | 2.257 | 1.394 | yes | 1.772 | 0.728 | yes | 1.487 | 0.204 | no | n/a | n/a | n/a |
| DRB0138 | SAM-dependent methylase | 1.474 | 0.452 | no | 1.807 | 0.596 | yes | 2.285 | 0.431 | yes | 2.533 | 0.303 | yes | 2.257 | 0.936 | yes | 1.787 | 0.507 | yes | 1.948 | 0.631 | yes | 1.546 | 0.414 | yes | 1.565 | 0.343 | yes |
| DRB0140 | Predicted protein | 1.196 | 0.317 | no | 1.534 | 0.543 | yes | 1.785 | 1.126 | yes | 1.526 | 0.159 | no | 2.433 | 1.535 | yes | 1.878 | 0.670 | yes | 1.566 | 0.680 | no | 1.120 | 0.375 | no | 1.191 | 0.555 | no |
| DRB0141 | Uncharacterized homolog of HicB protein | 0.924 | 0.499 | no | 1.955 | 0.847 | yes | 2.349 | 1.711 | yes | 2.294 | 1.367 | yes | 1.751 | 0.880 | yes | 1.316 | 0.631 | no | 1.446 | 0.937 | no | 1.915 | 0.519 | yes | 1.481 | 0.590 | no |
| DRB0142 | Predicted protein | 0.792 | 0.297 | no | 2.194 | 0.991 | yes | 2.062 | 1.178 | yes | 1.835 | 0.897 | yes | 2.060 | 0.928 | yes | 1.866 | 0.783 | yes | 2.281 | 0.657 | yes | 1.888 | 0.936 | yes | 2.046 | 0.557 | yes |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DRB0143 | Restrictase component, ATPase AAA superfamily, related to 5-methylcytosine-specific restriction enzyme subunit McrB of E. coli | 0.920 | 0.126 | no | 2.072 | 0.758 | yes | 2.626 | 0.867 | yes | 2.348 | 0.957 | yes | 2.235 | 1.401 | yes | 1.495 | 0.681 | no | 1.402 | 0.374 | no | 1.249 | 0.358 | no | 1.324 | 0.346 | no |
| DRB0144 | Related to McrC protein of restriction/modification system McrBC | 1.144 | 0.314 | no | 2.118 | 1.054 | yes | 2.386 | 0.896 | yes | 1.801 | 0.585 | yes | 2.351 | 1.240 | yes | 1.606 | 0.297 | yes | 1.501 | 0.277 | yes | 1.573 | 0.420 | yes | 1.681 | 0.431 | yes |
| DRB0145 | Predicted protein | 2.081 | 0.672 | yes | 3.276 | 1.255 | yes | 4.772 | 1.796 | yes | 4.610 | 1.805 | yes | 2.086 | 0.694 | yes | 1.672 | 0.636 | yes | 1.831 | 1.173 | yes | 1.379 | 0.732 | no | 0.977 | 0.461 | no |
| DRC0001 | Cytochrome P450 | 1.102 | 0.563 | no | 3.784 | 1.957 | yes | 4.821 | 2.975 | yes | 1.872 | 0.786 | yes | 4.678 | 2.203 | yes | 6.663 | 3.069 | yes | 14.398 | 4.199 | yes | 6.189 | 1.370 | yes | 6.987 | 2.786 | yes |
| DRC0002 | Phosphoenolpyruvate synthase | 1.007 | 0.355 | no | 1.407 | 0.559 | no | 0.704 | 0.186 | no | 0.574 | 0.164 | yes | 0.537 | 0.217 | yes | 0.948 | 0.246 | no | 1.384 | 0.361 | no | 1.201 | 0.297 | no | 1.370 | 0.526 | no |
| DRC0003 | Phosphoenolpyruvate synthase | 0.870 | 0.234 | no | 2.429 | 0.567 | yes | 2.276 | 1.551 | yes | 1.732 | 0.439 | yes | 1.845 | 0.973 | yes | 2.955 | 0.872 | yes | 5.512 | 2.703 | yes | 5.024 | 1.373 | yes | 2.853 | 0.916 | yes |
| DRC0005 | Transposase | 0.900 | 0.448 | no | 1.978 | 1.104 | yes | 1.215 | 0.600 | no | 0.958 | 0.299 | no | 1.104 | 0.498 | no | 1.772 | 0.140 | yes | 2.861 | 1.778 | yes | 2.563 | 0.887 | yes | 1.923 | 0.765 | yes |
| DRC0006 | Zn-dependent hydrolase, urease-like (distorted TIM barrel) | 1.554 | 0.752 | no | 2.184 | 0.667 | yes | 2.306 | 0.717 | yes | 1.747 | 0.780 | yes | 2.153 | 1.114 | yes | 3.496 | 0.909 | yes | 4.503 | 2.049 | yes | 6.623 | 1.679 | yes | 3.087 | 0.920 | yes |
| DRC0007 | Diverged PP-loop ATPase related to ExsB, 4 conserved C | 1.591 | 0.589 | no | 2.034 | 0.811 | yes | 1.678 | 0.718 | yes | 1.515 | 0.084 | no | 1.644 | 0.481 | yes | 2.640 | 1.541 | yes | 2.542 | 1.141 | yes | 2.388 | 0.863 | yes | 2.068 | 0.669 | yes |
| DRC0008 | Predicted protein | 1.578 | 0.866 | no | 1.834 | 0.663 | yes | 1.182 | 0.518 | no | 1.580 | 0.698 | no | 2.217 | 0.983 | yes | 2.340 | 0.999 | yes | 4.367 | 2.599 | yes | 5.213 | 1.252 | yes | 6.056 | 1.240 | yes |
| DRC0009 | P-loop ATPase containing protein, similarity to MJ0182 | 2.092 | 0.977 | yes | 2.190 | 0.926 | yes | 2.688 | 1.621 | yes | 1.611 | 0.569 | no | 3.130 | 1.570 | yes | 3.164 | 0.558 | yes | 4.543 | 2.220 | yes | 3.771 | 1.031 | yes | 2.937 | 0.381 | yes |
| DRC0010 | Related to eco29kIR restriction endonuclease | 2.688 | 0.825 | yes | 3.084 | 1.014 | yes | 2.689 | 0.532 | yes | 2.965 | 0.157 | yes | 3.057 | 1.047 | yes | 2.649 | 0.751 | yes | 4.420 | 2.213 | yes | 3.127 | 1.209 | yes | 2.113 | 1.393 | yes |
| DRC0012 | HTH transcriptional regulator | 2.363 | 1.209 | yes | 4.175 | 2.640 | yes | 3.144 | 1.408 | yes | 3.289 | 0.929 | yes | 4.365 | 2.178 | yes | 5.693 | 3.690 | yes | 6.275 | 2.088 | yes | 6.790 | 1.128 | yes | 4.115 | 1.632 | yes |
| DRC0013 | N-acetylmuramoyl-L-alanine amidase | 2.380 | 0.878 | yes | 3.616 | 0.709 | yes | 2.405 | 0.910 | yes | 4.641 | 1.429 | yes | 11.193 | 6.025 | yes | 20.919 | 4.914 | yes | 42.908 | 26.077 | yes | 11.895 | 3.364 | yes | 11.136 | 3.706 | yes |
| DRC0014 | Predicted protein | 1.180 | 0.316 | no | 1.757 | 1.029 | yes | 1.054 | 0.556 | no | 0.972 | 0.006 | no | 1.555 | 0.724 | no | 2.818 | 1.003 | yes | 4.694 | 2.296 | yes | 5.725 | 2.023 | yes | 3.916 | 1.454 | yes |
| DRC0015 | Serine/threonine protein kinase | 1.189 | 0.314 | no | 2.274 | 1.209 | yes | 2.037 | 0.683 | yes | 1.260 | 0.416 | no | 1.746 | 0.369 | yes | 5.310 | 2.116 | yes | 7.004 | 2.191 | yes | 8.116 | 1.698 | yes | 2.972 | 0.828 | yes |
| DRC0016 | Predicted protein | 2.082 | 0.591 | yes | 2.416 | 1.080 | yes | 4.523 | 2.179 | yes | 4.199 | 1.646 | yes | 12.937 | 6.781 | yes | 16.633 | 10.122 | yes | 35.508 | 23.180 | yes | 28.787 | 15.843 | yes | 19.179 | 3.044 | yes |
| DRC0018 | XERC/XERD family protein | 1.939 | 0.683 | yes | 2.707 | 1.033 | yes | 1.905 | 0.950 | yes | 1.651 | 0.448 | yes | 2.017 | 0.918 | yes | 2.206 | 0.959 | yes | 2.724 | 0.768 | yes | 2.264 | 0.576 | yes | 1.656 | 0.604 | yes |
| DRC0019 | Transposase | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DRC0021 | Predicted protein | 1.291 | 0.330 | no | 1.846 | 1.002 | yes | 1.602 | 0.316 | yes | 1.790 | 0.550 | yes | 1.895 | 0.681 | yes | 1.823 | 0.093 | yes | 2.143 | 1.058 | yes | 1.683 | 0.900 | yes | 1.341 | 0.334 | no |
| DRC0022 | Predicted protein | 1.592 | 0.526 | yes | 2.271 | 0.952 | yes | 2.591 | 0.715 | yes | 1.534 | 0.123 | no | 2.299 | 0.487 | yes | 2.717 | 1.020 | yes | 3.605 | 1.813 | yes | 3.737 | 1.435 | yes | 1.618 | 0.788 | yes |
| DRC0023 | Predicted protein | 1.524 | 0.699 | no | 2.287 | 0.903 | yes | 2.180 | 0.372 | yes | 2.300 | 1.120 | yes | 1.983 | 0.586 | yes | 1.854 | 0.484 | yes | 2.174 | 0.613 | yes | 1.935 | 0.564 | yes | 1.458 | 0.324 | yes |
| DRC0024 | Predicted protein | 1.238 | 0.292 | no | 2.005 | 1.028 | yes | 1.216 | 0.241 | no | 1.219 | 0.217 | no | 1.001 | 0.399 | no | 1.896 | 0.884 | yes | 2.335 | 0.998 | yes | 1.757 | 0.509 | yes | 1.893 | 0.611 | yes |
| DRC0025 | Plasmid partitioning protein: ParA | 0.757 | 0.307 | no | 1.159 | 0.522 | no | 0.550 | 0.232 | yes | 0.353 | 0.052 | yes | 0.674 | 0.493 | yes | 1.162 | 0.347 | no | 1.768 | 1.083 | yes | 1.479 | 0.418 | no | 0.642 | 0.146 | yes |
| DRC0026 | Predicted protein | 0.731 | 0.442 | yes | 1.316 | 0.362 | no | 0.535 | 0.112 | yes | 0.441 | 0.212 | yes | 0.960 | 0.494 | no | 1.473 | 0.649 | no | 1.591 | 0.892 | no | 1.984 | 0.916 | yes | 0.600 | 0.288 | yes |
| DRC0027 | Predicted protein | 1.112 | 0.325 | no | 1.739 | 0.291 | yes | 0.827 | 0.158 | no | 0.902 | 0.119 | no | 1.340 | 0.244 | no | 1.877 | 0.716 | yes | 2.337 | 0.645 | yes | 2.036 | 0.539 | yes | 1.337 | 0.478 | no |
| DRC0028 | Transposon ORF | 1.160 | 0.716 | no | 3.327 | 2.049 | yes | 1.580 | 0.723 | yes | 0.925 | 0.187 | no | 1.868 | 1.036 | yes | 2.594 | 0.508 | yes | 3.085 | 0.531 | yes | 2.556 | 0.590 | yes | 1.263 | 0.370 | no |
| DRC0029 | Transposon ORF | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DRC0030 | Predicted protein | 0.956 | 0.451 | no | 3.400 | 1.385 | yes | 2.928 | 1.152 | yes | 1.597 | 0.202 | yes | 2.116 | 0.876 | yes | 1.764 | 0.885 | yes | 1.504 | 0.353 | yes | 1.793 | 0.560 | yes | 1.534 | 0.195 | yes |
| DRC0033 | Transposon ORF | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a | n/a |
| DRC0034 | Coenzyme PQQ synthesis protein | 1.598 | 0.419 | yes | 4.748 | 2.036 | yes | 7.881 | 4.530 | yes | 6.490 | 2.706 | yes | 5.372 | 1.725 | yes | 10.135 | 2.746 | yes | 11.630 | 4.342 | yes | 8.951 | 1.955 | yes | 3.074 | 0.811 | yes |
| DRC0035 | Predicted protein | 1.533 | 0.507 | no | 3.631 | 0.896 | yes | 3.651 | 0.719 | yes | 4.697 | 0.660 | yes | 4.489 | 1.779 | yes | 4.241 | 1.099 | yes | 5.520 | 3.215 | yes | 3.550 | 1.093 | yes | 2.471 | 1.242 | yes |
| DRC0036 | Mg-protoporphyrin IX monomethyl ester oxidative cyclase, Biotin synthase/P-methylase family | 1.469 | 0.446 | no | 1.485 | 0.513 | yes | 1.313 | 0.440 | no | 1.327 | 0.586 | no | 1.182 | 0.360 | no | 2.245 | 0.958 | yes | 3.062 | 0.915 | yes | 2.988 | 1.090 | yes | 3.315 | 1.153 | yes |

**Table A.** Master table for normalized whole-genome microarray data (AVG) of Deinococcus radiodurans strain R1 cells recovering from 15kGy gamma radiation with standard deviation (STD), and t-test results (Sign.)
PNAS publication: Transcriptome Dynamics of Deinococcus radiodurans Recovering from Ionizing Radiation, Liu, Y. et al., 2003.



| Gene_ID | COG-name, putative function | AVG (0h) | STD (0h) | Sign. (0h) | AVG (0.5h) | STD (0.5h) | Sign. (0.5h) | AVG (1.5h) | STD (1.5h) | Sign. (1.5h) | AVG (3h) | STD (3h) | Sign. (3h) | AVG (5h) | STD (5h) | Sign. (5h) | AVG (9h) | STD (9h) | Sign. (9h) | AVG (12h) | STD (12h) | Sign. (12h) | AVG (16h) | STD (16h) | Sign. (16h) | AVG (24h) | STD (24h) | Sign. (24h) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DRC0037 | Nodulation protein U, carbomoyltransferase of the HSP70/actin fold | 1.148 | 0.447 | no | 1.775 | 0.530 | yes | 1.757 | 0.484 | yes | 1.539 | 0.393 | no | 1.823 | 0.659 | yes | 2.627 | 0.280 | yes | 5.151 | 2.753 | yes | 3.623 | 0.694 | yes | 2.274 | 0.394 | yes |
| DRC0038 | Zn-dependent hydrolase MET MTH856 3123064 | 1.192 | 0.268 | no | 2.407 | 0.637 | yes | 2.448 | 0.624 | yes | 2.954 | 0.276 | yes | 2.945 | 0.692 | yes | 3.645 | 2.322 | yes | 5.724 | 2.140 | yes | 2.786 | 0.948 | yes | 2.765 | 0.643 | yes |
| DRC0039 | Predicted protein | 1.229 | 0.317 | no | 3.246 | 1.201 | yes | 2.320 | 0.648 | yes | 2.070 | 0.589 | yes | 2.686 | 0.749 | yes | 4.137 | 1.826 | yes | 6.990 | 4.245 | yes | 5.301 | 1.185 | yes | 3.077 | 0.810 | yes |
| DRC0040 | Predicted permease | 1.510 | 0.682 | no | 4.610 | 2.482 | yes | 4.080 | 1.659 | yes | 3.201 | 0.737 | yes | 3.308 | 2.082 | yes | 5.644 | 2.715 | yes | 7.004 | 2.646 | yes | 5.477 | 1.983 | yes | 3.229 | 1.077 | yes |
| DRC0041 | Predicted protein | 1.329 | 0.338 | no | 3.580 | 0.818 | yes | 4.306 | 1.384 | yes | 2.849 | 0.599 | yes | 3.660 | 2.236 | yes | 4.255 | 0.977 | yes | 4.232 | 1.219 | yes | 4.007 | 1.180 | yes | 2.426 | 0.736 | yes |