**S1 Table.** *E. coli* genes whose expression levels were with significant up- or down-regulation in Δ*rpoS* and Δ*cya* strains (difference in average signal intensity compared to wild-type *E. coli* K12 ≥ 3 or ≤ -3, p-value ≤ 0.2) in glucose-limited continuous culture cultivated at D = 0.3 h-1.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Gene** | | **b no.** | | **Gene product** | | | **Ratio cAMP** | | | | **Ratio RpoS** | | | |
| **Regulation** | | | |  | | |  | | | |  | | | |
| *sfsA*f,g | | b0146 | | | probable regulator for maltose metabolism | | | 5.7 | | | |  | | | |
| *bolA*e,h | | b0435 | | | possible regulator of murein genes | | | 7.5 | | | | 6.7 | | | |
| *hupB*f,g | | b0440 | | | DNA-binding protein HU-beta, NS1 (HU-1) | | | 7.3\* | | | |  | | | |
| *ompT* | | b0565 | | | outer membrane protein 3b (a), protease VII | | | 6.5 | | | |  | | | |
| *dps*d,e,h | | b0812 | | | global regulator, starvation conditions | | | 6.5 | | | | 19.9 | | | |
| *ybiJ* | | b0845 | | | putative DEOR-type transcriptional regulator | | | -5.9\*\* | | | | -4.9\*\* | | | |
| *clpA* | | b0882 | | | ATP-binding component of serine protease | | |  | | | | -3.0\*\* | | | |
| *wrbA* | | b1004 | | | trp repressor binding protein | | | 3.6 | | | |  | | | |
| *phoQ* | | b1129 | | | sensor protein PhoQ | | |  | | | | -3.3\*\* | | | |
| *minD* | | b1175 | | | cell division inhibitor, a membrane ATPase, activates minC | | | 4.1 | | | |  | | | |
| *Hns* | | b1237 | | | DNA-binding protein HLP-II (HU, BH2, HD, NS), pleiotropic regulator | | | 4.1 | | | |  | | | |
| *mokB* | | b1420 | | | regulatory protein, enables hokB expression | | | 4.4 | | | |  | | | |
| *ydcI* | | b1422 | | | putative transcriptional regulator LYSR-type | | | 5.6 | | | |  | | | |
| *ydeW* | | b1512 | | | putative transcriptional regulator, sorC family | | | 4.1 | | | |  | | | |
| *yneA* | | b1516 | | | putative LACI-type transcriptional regulator | | | 5.6 | | | |  | | | |
| *gatR\_2*c,i | | b2090 | | | split galactitol utilization operon repressor, fragment 2 | | | 13.0 | | | |  | | | |
| *yehH* | | b2116 | | | molybdate metabolism regulator, second fragment 2 | | | 7.9 | | | |  | | | |
| *rseA* | | b2572 | | | sigma-E factor, negative regulatory protein | | | 7.9 | | | |  | | | |
| *rpoE*i | | b2573 | | | RNA polymerase, sigma-E factor heat shock and oxidative stress | | | 5.0 | | | |  | | | |
| *yfjN* | | b2630 | | | putative cell division protein | | | 3.8 | | | |  | | | |
| *csrA*b | | b2696 | | | carbon storage regulator | | | 8.3 | | | | 7.8 | | | |
| *glcC*b | | b2980 | | | transcriptional activator for glc operon | | |  | | | | -3.1 | | | |
| *damX* | | b3388 | | | putative membrane protein; interferes with cell division | | |  | | | | -3.5\*\* | | | |
| *yhiE*e | | b3512 | | | putative regulator | | | 16.6 | | | |  | | | |
| *yiaG*d,e,h | | b3555 | | | putative transcriptional regulator | | | 5.0 | | | | 34.7\* | | | |
| *soxS* | | b4062 | | | regulation of superoxide response regulon | | | -3.9\*\* | | | | -6.2\*\* | | | |
| *adiY* | | b4116 | | | putative ARAC-type regulatory protein | | | -5.1\*\* | | | | -3.3 | | | |
| *yjjM*i | | b4357 | | | putative transcriptional regulator | | | 6.8 | | | |  | | | |
| *bglJ* | | b4366 | | | 2-component transcriptional regulator | | |  | | | | -3.3\* | | | |
| *rsmC* | | b4371 | | | 16S RNA m2G1207 methylase | | |  | | | | -3.8\*\* | | | |
|  | | | | | | |  | | | |  | | | |
| **Cell structure** | | | | | | |  | | | |  | | | |
| *ybjP* | | b0865 | | | putative lipoprotein | | | 4.3 | | | |  | | | |
| *lolA* | | b0891 | | | periplasmic protein effects translocation of lipoproteins | | |  | | | | -3.6\*\* | | | |
| *ycbQ* | | b0938 | | | putative fimbrial-like protein | | | -6.4\*\* | | | | -3.7 | | | |
| *sfa*i | | b0991 | | | suppresses fabA and ts growth mutation | | | -3.9\* | | | |  | | | |
| *ycdS* | | b1024 | | | putative outer membrane protein | | |  | | | | -3.0\*\* | | | |
| *flgD* | | b1075 | | | flagellar biosynthesis, initiation of hook assembly | | | 4.5 | | | |  | | | |
| *ycgB*e,g,h | | b1188 | | | putative sporulation protein | | | 6.9 | | | | 11.9 | | | |
| *kdsA* | | b1215 | | | 2-dehydro-3-deoxyphosphooctulonate aldolase | | |  | | | | -3.3\*\* | | | |
| *ddpX* | | b1488 | | | D-Ala-D-Ala dipeptidase | | | 4.4 | | | |  | | | |
| *ydeS* | | b1504 | | | putative fimbrial-like protein | | | 5.5 | | | |  | | | |
| *lpp* | | b1677 | | | murein lipoprotein | | | 5.8 | | | |  | | | |
| *wbbL* | | b2031 | | | putaive lipopolysaccharide biosynthesis glycosyl transferase | | | 3.7 | | | |  | | | |
| **Continuation S1 Table** | | | | | | | | | | | | | | |
| **Gene** | **b no.** | | **Gene product** | | | | | | **Ratio cAMP** | | | | **Ratio RpoS** | | | |
| *yfcX* | b2341 | | bifunctional fatty acid oxidation complex protein | | | 5.3 | | | |  | | | |
| *pssA* | b2585 | | phosphatidylserine synthase, phospholipid synthesis | | | 5.1 | | | |  | | | |
| *rfe* | b3784 | | UDP-GlcNAc:undecaprenylphosphate GlcNAc-1-phosphate transferase | | |  | | | | -3.6\*\* | | | |
| *nlpD* | b2742 | | lipoprotein | | | 4.0 | | | |  | | | |
| *blc*h | b4149 | | outer membrane lipoprotein (lipocalin) | | | 4.2 | | | | 5.5 | | | |
| *fimI* | b4315 | | fimbrial protein | | | -3.5\*\* | | | |  | | | |
| *fimD* | b4317 | | outer membrane protein export and assembly of type 1 fimbriae | | | -3.0\*\* | | | |  | | | |
| *fimG*b | b4319 | | fimbrial morphology | | | -3.2\*\* | | | | -4.5\*\* | | | |
|  | | | | | | |  | | | |  | | | |
| **Stress response** | | | | | | |  | | | |  | | | |
| *fsr* | b0479 | | fosmidomycin resistance protein | | |  | | | | -3.6\*\* | | | |
| *cspD*g | b0880 | | cold shock protein | | | 13.0 | | | |  | | | |
| *mdoG* | b1048 | | periplasmic glucans biosynthesis protein | | |  | | | | -3.2\*\* | | | |
| *umuC*i | b1184 | | SOS mutagenesis and repair | | | -4.2\*\* | | | |  | | | |
| *pspE*i | b1308 | | phage shock protein | | | 4.0 | | | |  | | | |
| *gadB*b,e,f,h | b1493 | | glutamate decarboxylase isozyme | | |  | | | | 15.4 | | | |
| *marC* | b1529 | | multiple antibiotic resistance protein | | |  | | | | 10.0 | | | |
| *cspF* | b1558 | | cold shock protein | | | -5.7\* | | | |  | | | |
| *osmE*d,h | b1739 | | activator of ntrL gene | | | 10.4 | | | | 10.2 | | | |
| *yeaA*g | b1778 | | methionine sulfoxide reductase | | | 5.9 | | | |  | | | |
| *cspC* | b1823 | | cold shock protein | | | 4.2 | | | |  | | | |
| *cutC* | b1874 | | copper homeostasis protein | | | 4.5 | | | |  | | | |
| *bfr*b,d,e,h | b3336 | | bacterioferrin, an iron storage homoprotein | | | 5.1 | | | | 14.3 | | | |
| *dcrB* | b3472 | | Resistant to lytic phage C1 | | |  | | | | -3.2\*\* | | | |
| *uspB* | b3494 | | universal stress protein B | | | 3.7 | | | |  | | | |
| *uspA* | b3495 | | universal stress protein A | | | 4.0 | | | |  | | | |
| *hdeB*b,e | b3509 | | periplasmic protein | | |  | | | | 32.9\* | | | |
| *hdeA*e | b3510 | | periplasmic chaperon of acid-denaturared proteins | | |  | | | | 23.0 | | | |
| *creD* | b4400 | | tolerance to colicin E2 | | | -3.6\*\* | | | |  | | | |
|  | | | | | | |  | | | |  | | | |
| **Protein processing** | | | | | | |  | | | |  | | | |
| *rpsV*b,d,e,h | b1480 | | 30S ribosomal subunit protein S22 | | | 9.8 | | | | 17.0 | | | |
| *pheT* | b1713 | | phenylalanine tRNA synthetase, beta-subunit | | | 6.1 | | | |  | | | |
| *yfiA*g | b2597 | | Stationary phase translation inhibitor | | | 6.7 | | | |  | | | |
| *rpmJ* | b3299 | | 50S ribosomal subunit protein L36 | | | 3.8 | | | |  | | | |
|  | | | | | | |  | | | |  | | | |
| **Amino acids biosynthesis** | | | | | | |  | | | |  | | | |
| *hisG* | b2019 | | ATP phosphoribosyltransferase | | | 4.2 | | | |  | | | |
| *hisC* | b2021 | | histidinol-phosphate aminotransferase | | | 4.6 | | | |  | | | |
| *aroC* | b2329 | | chorismate synthase | | | 7.9 | | | |  | | | |
| *ivbL*f,g | b3672 | | ilvB operon leader peptide | | | 5.2 | | | |  | | | |
|  | | | | | | |  | | | |  | | | |
| **Nucleotide biosynthesis** | | | | | | |  | | | |  | | | |
| *apbA* | b0425 | | involved in thiamin biosynthesis, pyrimidine biosynthesis | | | -8.5\*\* | | | | -6.6\*\* | | | |
| *purM* | b2499 | | phosphoribosylaminoimidazole synthetase = AIR synthetase | | | -4.1\*\* | | | |  | | | |
| *purN* | b2500 | | phosphoribosylglycinamide formyltransferase 1 | | | -3.0\*\* | | | |  | | | |
| *deoC*e,f,g | b4381 | | 2-deoxyribose-5-phosphate aldolase | | | -3.9 | | | |  | | | |
|  | | | | | | |  | | | |  | | | |
| **Miscellaneous functions** | | | | | | |  | | | |  | | | |
| *trs5\_1* | b0259 | | IS5 transposase | | | 5.2 | | | |  | | | |
| *ycjK* | b1297 | | putative glutamine synthetase (EC 6.3.1.2) | | |  | | | | -3.4\* | | | |
| *ycjL* | b1298 | | probable amidotransferase subunit | | |  | | | | -4.0\* | | | |
| *rzpR* | b1362 | | putative Rac prophage endopeptidase | | | -4.5\*\* | | | | -4.5\*\* | | | |
| **Continuation S1 Table** | | | | | | | | | | | | | | |
| **Gene** | **b no.** | | **Gene product** | | | | | | **Ratio cAMP** | | | | **Ratio RpoS** | | | |
| *ynaK* | b1365 | | Rac prophage | | | -3.5\*\* | | | | -3.1\*\* | | | |
| *rsmC* | b4371 | | 16S RNA m2G1207 methylase | | | -4.1\*\* | | | | -3.8\*\* | | | |
|  | | | | | | |  | | | |  | | | |
| **Unknown or hypothetical functions** | | | | | | |  | | | |  | | | |
| *yaaA* | b0006 | | orf, hypothetical protein | | | | | |  | | | | 5.0 | | | |
| *yahO*d,e | b0329 | | orf, hypothetical protein | | | | | | 14.7 | | | | 7.8 | | | |
| *ybaB* | b0471 | | orf, hypothetical protein | | | | | |  | | | | -5.3\*\* | | | |
| *ybaK* | b0481 | | orf, hypothetical protein | | | | | | -7.5\*\* | | | | -6.4\*\* | | | |
| *ybaS* | b0485 | | putative glutaminase | | | | | |  | | | | -3.7\* | | | |
| *ybeD* | b0631 | | orf, hypothetical protein | | | | | |  | | | | -3.0 | | | |
| *ybeL* | b0643 | | putative alpha helical protein | | | | | | 8.1 | | | |  | | | |
| *ybfB* | b0702 | | orf, hypothetical protein | | | | | | -22.3\*\* | | | | -24.5\*\* | | | |
| *ybgA*d,h | b0707 | | orf, hypothetical protein | | | | | |  | | | | 8.0 | | | |
| *yccV* | b0966 | | orf, hypothetical protein | | | | | | 5.3 | | | | 4.8 | | | |
| *yccW* | b0967 | | putative methyltransferase | | | | | |  | | | | -3.1\*\* | | | |
| *yccM*i | b0992 | | putative ferredoxin-type protein | | | | | | -3.2\*\* | | | |  | | | |
| *ycdP* | b1021 | | putative membrane protein | | | | | | -3.0\*\* | | | | 5.3 | | | |
| *ymdB* | b1045 | | putative polyprotein | | | | | | 5.2 | | | |  | | | |
| *grxB* | b1064 | | glutaredoxin 2 | | | | | | 5.4 | | | |  | | | |
| *ycfH*e | b1100 | | putative hydrolase | | | | | | 6.0 | | | | 8.8 | | | |
| *ychH*f,i | b1205 | | orf, hypothetical protein | | | | | | 6.8 | | | |  | | | |
| *ymjA* | b1295 | | orf, hypothetical protein | | | | | |  | | | | -4.1\* | | | |
| *ydbD* | b1407 | | orf, hypothetical protein | | | | | | -4.9\*\* | | | | -3.8\*\* | | | |
| *ydcX* | b1445 | | orf, hypothetical protein | | | | | |  | | | | 5.4 | | | |
| *yncH* | b1455 | | orf, hypothetical protein | | | | | | -3.3\*\* | | | | -3.3\* | | | |
| *yneC* | b1518 | | orf, hypothetical protein | | | | | | 4.1 | | | |  | | | |
| *ynfA*d | b1582 | | putative transmembrane protein | | | | | | 8.7 | | | | 11.3 | | | |
| *ydgA*h | b1614 | | orf, hypothetical protein | | | | | |  | | | | 7.0 | | | |
| *ydiZ*d,e | b1724 | | orf, hypothetical protein | | | | | | 5.4 | | | | 8.9 | | | |
| *yeaC*g | b1777 | | orf, hypothetical protein | | | | | | 3.8 | | | |  | | | |
| *yeaG*e,h | b1783 | | orf, hypothetical protein | | | | | | 13.1 | | | | 22.2 | | | |
| *yobF* | b1824 | | orf, hypothetical protein | | | | | | 5.2 | | | |  | | | |
| *yebV* | b1836 | | orf, hypothetical protein | | | | | |  | | | | 23.9 | | | |
| *yebW* | b1837 | | orf, hypothetical protein | | | | | |  | | | | 5.1 | | | |
| *yodD*e | b1953 | | orf, hypothetical protein | | | | | | 4.0 | | | | 7.5 | | | |
| *yeeI*i | b1976 | | orf, hypothetical protein | | | | | | 23.3\* | | | |  | | | |
| *wbbK* | b2032 | | putative glucose transferase | | | | | | 4.1 | | | |  | | | |
| *elaB*e,h | b2266 | | orf, hypothetical protein | | | | | |  | | | | 7.7 | | | |
| *yfbN* | b2273 | | orf, hypothetical protein | | | | | |  | | | | -3.0\*\* | | | |
| *yfdY* | b2377 | | orf, hypothetical protein | | | | | | 5.0 | | | |  | | | |
| *ucpA*i | b2426 | | putative oxidoreductase | | | | | | 3.6 | | | |  | | | |
| *yfiL*h | b2602 | | orf, hypothetical protein | | | | | |  | | | | 6.0 | | | |
| *yfjO* | b2631 | | orf, hypothetical protein | | | | | | 4.1 | | | | 8.0 | | | |
| *ygaF*d,g,h | b2660 | | orf, hypothetical protein | | | | | | 6.1 | | | | 5.0 | | | |
| *ygaM*h | b2672 | | orf, hypothetical protein | | | | | | 4.3 | | | | 8.6 | | | |
| *ygaD* | b2700 | | orf, hypothetical protein | | | | | | 4.8 | | | |  | | | |
| *ygdH* | b2795 | | orf, hypothetical protein | | | | | | 4.1 | | | |  | | | |
| *ygfJ* | b2877 | | orf, hypothetical protein | | | | | | 32.6\* | | | | 10.0 | | | |
| *glcG* | b2977 | | orf, hypothetical protein | | | | | |  | | | | -5.1 | | | |
| *yqiB* | b3033 | | putative enzyme | | | | | | 5.3 | | | |  | | | |
| *yqjC*d,e | b3097 | | orf, hypothetical protein | | | | | | 3.8 | | | | 6.9 | | | |
| *yhcO*e | b3239 | | orf, hypothetical protein | | | | | |  | | | | 6.1 | | | |
| *smg* | b3284 | | orf, hypothetical protein | | | | | | 5.7 | | | |  | | | |
| **Continuation S1 Table** | | | | | | | | | | | | | | |
| **Gene** | **b no.** | | **Gene product** | | | | | | **Ratio cAMP** | | | | **Ratio RpoS** | | | |
| *yjbB* | b4020 | | putative alpha helix protein | | | | | | -3.6\*\* | | | |  | | | |
| *yjbA*g,i | b4030 | | putative membrane protein | | | | | | -6.2\*\* | | | |  | | | |
| *yjcB*i | b4060 | | orf, hypothetical protein | | | | | | -3.4\*\* | | | |  | | | |
| *yjcH*f,i | b4068 | | orf, hypothetical protein | | | | | | 9.1 | | | |  | | | |
| *phnB*h | b4107 | | orf, hypothetical protein | | | | | |  | | | | 6.8 | | | |
| *yjdK* | b4128 | | orf, hypothetical protein | | | | | | -3.2\*\* | | | |  | | | |
| *yjfN* | b4188 | | orf, hypothetical protein | | | | | | 10.7 | | | |  | | | |
| *yjfO* | b4189 | | orf, hypothetical protein | | | | | | 63.3\* | | | | -3.4 | | | |
| *ytfI* | b4215 | | orf, hypothetical protein | | | | | | -5.1\*\* | | | |  | | | |
| *ytfJ* | b4216 | | orf, hypothetical protein | | | | | | 9.0 | | | |  | | | |
| *yjgW* | b4274 | | orf, hypothetical protein | | | | | | -3.5\*\* | | | | -5.9\* | | | |

\* p-value < 0.1, \*\* p-value < 0.05

References: a[1]; b[2]; c[3]; d[4]; e[5]; f[6]; g[7]; h[8]; i[9]

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