**Table S2.** Glycerol-induced down regulation of genes in *Escherichia coli*

|  |  |  |  |
| --- | --- | --- | --- |
| **Probe set ID** | **Fold change\*** | **Gene** | **Gene function** |
| 1763981\_s\_at | 1.8 | *aceA* | isocitrate lyase |
| 1761179\_at | 4.8 | *aceB* | malate synthase |
| 1762343\_s\_at | 2.9 | *aceB* | malate synthase |
| 1765758\_s\_at | 3.0 | *aceK* | bifunctional isocitrate dehydrogenase kinase/phosphatase protein |
| 1764023\_s\_at | 1.8 | *aldA* | aldehyde dehydrogenase A |
| 1759685\_s\_at | 1.6 | *araF* | L-arabinose-binding periplasmic protein precursor |
| 1764514\_s\_at | 1.6 | *aroE* | quinate/shikimate dehydrogenase |
| 1768176\_at | 1.6 | *arrQ* | qin prophage |
| 1759494\_s\_at | 1.7 | *ycfR* | biofilm, cell surface and signaling protein |
| 1767634\_s\_at | 1.6 | *dhaR* | DNA-binding transcriptional regulator DhaR |
| 1761434\_s\_at | 1.5 | *ydeT* | outer membrane usher protein fimD precursor |
| 1760530\_s\_at | 1.6 | *cedA* | cell division modulator |
| 1761593\_s\_at | 1.5 | *celC* | PTS system N,N'-diacetylchitobiose-specific transporter subunit IIA |
| 1766291\_s\_at | 1.5 | *clcB* | chloride channel, voltage-gated |
| 1760176\_s\_at | 1.6 | *yecO* | tRNA cmo(5)U34 methyltransferase, SAM-dependent |
| 1766086\_s\_at | 2.8 | *cobT* | nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase |
| 1766210\_at | 1.6 | *csgA* | cryptic curlin major subunit |
| 1762325\_s\_at | 2.0 | *csgB* | curlin minor subunit |
| 1762932\_s\_at | 1.9 | *cspB* | cold shock-like protein cspB |
| 1760599\_s\_at | 1.9 | *cspI* | cold shock-like protein cspI |
| 1761088\_s\_at | 1.5 | *cybB* | cytochrome b561 |
| 1759374\_s\_at | 1.5 | *cyoB* | cytochrome o ubiquinol oxidase subunit I |
| 1765526\_s\_at | 2.0 | *cysJ* | sulfite reductase subunit alpha |
| 1763056\_s\_at | 1.6 | *ddpA* | D-ala-D-a la transporter subunit |
| 1767620\_s\_at | 1.5 | *ddpC* | D-ala-D-ala transporter subunit |
| 1763357\_s\_at | 5.3 | *dnaK* | molecular chaperone DnaK |
| 1764562\_s\_at | 1.5 | *mhpT* | putative 3-hydroxyphenylpropionic transporter MhpT |
| 1762794\_s\_at | 1.6 | *ylaC* | inner membrane protein, DUF1449 family |
| 1761819\_s\_at | 1.5 | *htpG* | molecular chaperone HSP90 family |
| 1760290\_s\_at | 1.8 | *sucB* | dihydrolipoamide succinyltransferase |
| 1768954\_s\_at | 1.6 | *ycbL* | predicted metal-binding enzyme |
| 1763745\_s\_at | 1.6 | *ycbV* | putative fimbrial-like protein |
| 1765036\_s\_at | 1.6 | *hspQ* | heat shock protein HspQ |
| 1765839\_s\_at | 1.5 | *plsX* | putative glycerol-3-phosphate acyltransferase PlsX |
| 1767455\_s\_at | 1.6 | *purB* | adenylosuccinate lyase |
| **Probe set ID** | **Fold change\*** | **Gene** | **Gene function** |
| 1761216\_s\_at | 3.0 | *nohB* | terminase small subunit |
| 1760637\_s\_at | 1.5 | *fadR* | fatty acid metabolism regulator |
| 1764969\_s\_at | 3.0 | *oppA* | oligopeptide transport periplasmic binding protein |
| 1763143\_s\_at | 1.7 | *topA* | DNA topoisomerase I |
| 1761544\_s\_at | 1.6 | *rnb* | exoribonuclease II |
| 1760255\_s\_at | 1.6 | *yciW* | putative oxidoreductase |
| 1769101\_s\_at | 3.6 | *pspA* | phage shock protein PspA |
| 1762530\_s\_at | 2.5 | *pspC* | DNA-binding transcriptional activator PspC |
| 1765796\_s\_at | 1.6 | *pspD* | peripheral inner membrane phage-shock protein |
| 1762511\_s\_at | 1.6 | *ynbB* | putative phosphatidate cytidiltransferase |
| 1762566\_s\_at | 1.5 | *ydcP* | putative collagenase |
| 1764131\_s\_at | 1.6 | *ydcS* | putative transport protein |
| 1768514\_s\_at | 1.6 | *nhoA* | N-hydroxyarylamine O-acetyltransferase |
| 1765054\_s\_at | 1.7 | *yddL* | putaive outer membrane porin protein |
| 1760891\_s\_at | 1.6 | *fdnI* | formate dehydrogenase-N subunit gamma |
| 1764150\_s\_at | 1.7 | *pqqL* | putative peptidase |
| 1768362\_s\_at | 1.5 | *ydeO* | transcriptional regulator YdeO |
| 1765383\_s\_at | 1.6 | *ydeP* | putative oxidoreductase |
| 1768967\_s\_at | 1.5 | *ydeR* | putative fimbrial-like protein |
| 1768257\_s\_at | 1.6 | *ydeV* | autoinducer-2 (AI-2) kinase |
| 1761744\_s\_at | 1.5 | *ydeY* | putative transport system permease protein |
| 1761065\_s\_at | 1.5 | *ydeZ* | putative transport system permease protein |
| 1767864\_s\_at | 1.5 | *yneB* | aldolase |
| 1763406\_s\_at | 1.6 | *yneH* | glutaminase |
| 1761440\_s\_at | 1.6 | *ynfL* | putative transcriptional regulator LYSR-type |
| 1763040\_s\_at | 1.6 | *mdtI* | multidrug efflux system protein MdtI |
| 1759134\_s\_at | 1.5 | *mdtJ* | multidrug efflux system protein MdtJ |
| 1768956\_s\_at | 1.5 | *rstA* | DNA-binding transcriptional regulator RstA |
| 1759546\_s\_at | 1.5 | *tus* | DNA replication terminus site-binding protein |
| 1767184\_s\_at | 2.0 | *fumA* | fumarase A |
| 1760033\_s\_at | 1.5 | *yniC* | 2-deoxyglucose-6-phosphatase deoxyglucose-6-phosphatase |
| 1761943\_s\_at | 1.6 | *ynjD* | putative ATP-binding component of a transport system |
| 1761643\_s\_at | 1.6 | *topB* | DNA topoisomerase III |
| 1764315\_s\_at | 1.6 | *ydjF* | putative DEOR-type transcriptional regulator |
| **Probe set ID** | **Fold change\*** | **Gene** | **Gene function** |
| 1760010\_s\_at | 1.6 | *ydjK* | putative transport protein |
| 1763267\_s\_at | 1.6 | *yeaM* | putative ARAC-type regulatory protein |
| 1762151\_s\_at | 1.5 | *fliT* | flagellar biosynthesis protein FliT |
| 1768717\_s\_at | 1.5 | *yeeF* | predicted amino-acid transporter |
| 1762857\_s\_at | 1.5 | *lysP* | lysine transporter |
| 1764573\_s\_at | 1.5 | *yeiE* | putative DNA-binding transcriptional regulator |
| 1768233\_s\_at | 1.6 | *gyrA* | DNA gyrase subunit A |
| 1767449\_s\_at | 1.6 | *yqfA* | putative oxidoreductase |
| 1767563\_s\_at | 2.6 | *rpoA* | DNA-directed RNA polymerase subunit alpha |
| 1762768\_s\_at | 2.7 | *rpsK* | 30S ribosomal protein S11 |
| 1763295\_s\_at | 2.9 | *hokB* | small toxic polypeptide |
| 1763985\_s\_at | 1.6 | *ffs* | ncRNA |
| 1768518\_s\_at | 2.0 | *groEL* | chaperonin GroEL |
| 1763841\_at | 2.0 | *hrpA* | predicted ATP-dependent helicase |
| 1765954\_s\_at | 1.9 | *insH* | IS5 transposase and trans- |
| 1766197\_s\_at | 2.0 | *mltD* | membrane-bound lytic murein transglycosylase D |
| 1762726\_s\_at | 1.6 | *mnmA* | tRNA-specific 2-thiouridylase MnmA |
| 1762123\_s\_at | 1.7 | *narU* | nitrite extrusion protein 2 |
| 1761726\_s\_at | 2.6 | *oppB* | oligopeptide transporter permease |
| 1765783\_s\_at | 2.0 | *oppD* | oligopeptide transporter ATP-binding component |
| 1767860\_at | 1.6 | *paaA* | ring 1,2-phenylacetyl-CoA epoxidase subunit |
| 1764442\_at | 1.6 | *paaE* | ring 1,2-phenylacetyl-CoA epoxidase, NAD(P)H oxidoreductase component |
| 1765606\_at | 1.6 | *paaI* | thioesterase, most active with ring-hydroxylated phenylacetyl-coenzyme A thioesters |
| 1763270\_at | 1.6 | *paaK* | phenylacetyl-CoA ligase |
| 1759599\_s\_at | 1.6 | *potA* | putrescine/spermidine ABC transporter ATPase protein |
| 1760103\_s\_at | 1.6 | *pphA* | serine/threonine protein phosphatase 1 |
| 1767618\_s\_at | 1.7 | *prfA* | peptide chain release factor 1 |
| 1768435\_s\_at | 1.7 | *pspB* | phage shock protein B |
| 1766134\_at | 1.6 | *relA* | (p)ppGpp synthetase I/GTP pyrophosphokinase |
| 1760110\_at | 1.8 | *relB* | bifunctional antitoxin of the RelE-RelB toxin-antitoxin system |
| 1761308\_at | 1.6 | *rem* | qin prophage |
| 1767883\_s\_at | 2.7 | *rimM* | 16S rRNA-processing protein RimM |
| 1766400\_s\_at | 2.1 | *rplF* | 50S ribosomal protein L6 |
| 1760773\_s\_at | 2.5 | *rplN* | 50S ribosomal protein L14 |
| 1764794\_s\_at | 1.9 | *rplO* | 50S ribosomal protein L15 |
| **Probe set ID** | **Fold change\*** | **Gene** | **Gene function** |
| 1765175\_s\_at | 1.5 | *rpsP* | 30S ribosomal protein S16 |
| 1768787\_s\_at | 1.6 | *rspB* | putative dehydrogenase |
| 1765303\_at | 1.6 | *rzpQ* | Rz-like equivalent, Qin prophage |
| 1769260\_s\_at | 1.7 | *sdhB* | succinate dehydrogenase iron-sulfur subunit |
| 1767040\_s\_at | 1.8 | *sdhD* | succinate dehydrogenase cytochrome b556 small membrane subunit |
| 1759132\_at | 1.7 | *sokB* | ncRNA |
| 1760295\_s\_at | 1.5 | *sppA* | protease 4 |
| 1766868\_s\_at | 1.5 | *sucA* | 2-oxoglutarate dehydrogenase E1 component |
| 1769042\_s\_at | 2.0 | *sucC* | succinyl-CoA synthetase subunit beta |
| 1760848\_s\_at | 1.6 | *tmk* | thymidylate kinase |
| 1764937\_s\_at | 1.6 | *torD* | chaperone protein TorD |
| 1764493\_s\_at | 2.0 | *trmD* | tRNA (guanine-N(1)-)-methyltransferase |
| 1760194\_s\_at | 2.5 | *wzxC* | colanic acid exporter |
| 1764008\_s\_at | 1.6 | *ybeQ* | hypothetical protein |
| 1765399\_at | 1.7 | *ycaI* | inner membrane protein, ComEC family of competence proteins |
| 1762340\_at | 1.5 | *ydbA* | pseudo |
| 1767247\_at | 1.6 | *ydfE* | pseudo |
| 1763158\_at | 1.5 | *ydfU* | qin prophage |
| 1767166\_at | 1.5 | *ydfX* | pseudo |
| 1769219\_at | 1.6 | *yedS* | pseudo |
| 1764941\_at | 1.7 | *yehH* | pseudo |
| 1765532\_at | 1.5 | *yfcS* | predicted periplasmic pilus chaperone |
| 1767447\_s\_at | 2.0 | *yhcE* | pseudo |
| 1765949\_s\_at | 1.7 | *znuA* | high-affinity zinc transporter periplasmic component |
| 1760502\_s\_at | 1.6 | *znuB* | high-affinity zinc transporter membrane component |
| 1759812\_s\_at | 1.5 | *znuC* | high-affinity zinc transporter ATPase |
| 1760598\_s\_at | 1.9 | *Z2403* | hypothetical protein |
| 1761606\_s\_at | 1.5 | *yedI* | hypothetical protein |
| 1768215\_s\_at | 1.6 | *c1929* | hypothetical protein |
| 1762061\_s\_at | 1.7 | *ybiJ* | hypothetical protein |
| 1764771\_s\_at | 1.6 | *ycbK* | hypothetical protein |
| 1759715\_s\_at | 1.5 | *yccA* | hypothetical protein |
| 1764800\_s\_at | 1.5 | *ycdO* | hypothetical protein |
| 1765329\_s\_at | 2.3 | *ydfD* | hypothetical protein |
| 1768270\_s\_at | 1.6 | *ycjX* | hypothetical protein |
| 1760169\_s\_at | 1.5 | *ydaQ* | hypothetical protein |
| 1767994\_s\_at | 1.7 | *ynbD* | hypothetical protein |
| 1762519\_s\_at | 1.7 | *ECs2030* | hypothetical protein |
| 1760300\_s\_at | 1.5 | *yncH* | hypothetical protein |
| **Probe set ID** | **Fold change\*** | **Gene** | **Gene function** |
| 1760165\_s\_at | 1.5 | *yneF* | hypothetical protein |
| 1762245\_s\_at | 1.7 | *ydeH* | hypothetical protein |
| 1769059\_s\_at | 1.5 | *ynfC* | hypothetical protein |
| 1765419\_s\_at | 1.9 | *ECs2526* | hypothetical protein |
| 1768183\_s\_at | 1.5 | *yebO* | hypothetical protein |
| 1767917\_s\_at | 1.6 | *yebE* | hypothetical protein |
| 1759130\_s\_at | 1.7 | *ydhL* | hypothetical protein |
| 1761110\_s\_at | 1.8 | *ydhZ* | hypothetical protein |
| 1760257\_s\_at | 1.5 | *ppsR* | hypothetical protein |
| 1764585\_at | 1.5 | *-* | unknown |
| 1764779\_at | 1.6 | *-* | unknown |
| 1766272\_s\_at | 1.6 | IG | intergenic region |
| 1759377\_s\_at | 1.7 | IG | intergenic region |
| 1769180\_s\_at | 1.6 | IG | intergenic region |
| 1763183\_s\_at | 1.7 | IG | intergenic region |
| 1766595\_s\_at | 1.5 | IG | intergenic region |
| 1767517\_s\_at | 1.7 | IG | intergenic region |
| 1765268\_s\_at | 1.7 | IG | intergenic region |
| 1762784\_s\_at | 1.7 | IG | intergenic region |
| 1762102\_s\_at | 1.6 | IG | intergenic region |
| 1761933\_s\_at | 2.0 | IG | intergenic region |
| 1760857\_s\_at | 1.6 | IG | intergenic region |
| 1759623\_s\_at | 1.5 | IG | intergenic region |
| 1762043\_s\_at | 1.6 | IG | intergenic region |
| 1764389\_s\_at | 1.5 | IG | intergenic region |
| 1759370\_s\_at | 1.5 | IG | intergenic region |
| 1764282\_s\_at | 1.5 | IG | intergenic region |
| 1767526\_s\_at | 1.5 | IG | intergenic region |
| 1763779\_s\_at | 1.5 | IG | intergenic region |
| 1760035\_s\_at | 1.6 | IG | intergenic region |
| 1765865\_s\_at | 1.5 | IG | intergenic region |
| 1769161\_s\_at | 1.6 | IG | intergenic region |
| 1763393\_s\_at | 1.6 | IG | intergenic region |
| 1763179\_s\_at | 1.6 | IG | intergenic region |
| 1759577\_s\_at | 1.5 | IG | intergenic region |
| 1768016\_s\_at | 1.7 | IG | intergenic region |
| 1767198\_s\_at | 1.6 | IG | intergenic region |
| 1763395\_s\_at | 1.9 | IG | intergenic region |
| 1769034\_s\_at | 2.3 | IG | intergenic region |
| 1768367\_s\_at | 1.6 | IG | intergenic region |
| 1767722\_s\_at | 1.6 | IG | intergenic region |
| 1766159\_s\_at | 1.7 | IG | intergenic region |
| 1760296\_s\_at | 1.6 | IG | intergenic region |
| 1763854\_s\_at | 1.6 | IG | intergenic region |
| **Probe set ID** | **Fold change\*** | **Gene** | **Gene function** |
| 1762302\_s\_at | 1.5 | IG | intergenic region |
| 1760520\_s\_at | 1.5 | IG | intergenic region |
| 1759210\_s\_at | 1.6 | IG | intergenic region |
| 1763955\_s\_at | 1.5 | IG | intergenic region |
| 1768588\_s\_at | 1.5 | IG | intergenic region |
| 1764685\_s\_at | 1.7 | IG | intergenic region |
| 1761883\_s\_at | 1.6 | IG | intergenic region |
| 1764821\_s\_at | 1.9 | IG | intergenic region |
| 1768692\_s\_at | 1.5 | IG | intergenic region |
| 1759679\_s\_at | 2.0 | IG | intergenic region |
| 1759846\_s\_at | 1.5 | IG | intergenic region |
| 1766143\_s\_at | 1.5 | IG | intergenic region |
| 1761336\_s\_at | 1.5 | IG | intergenic region |
| 1762591\_s\_at | 1.6 | IG | intergenic region |
| 1760503\_s\_at | 1.5 | IG | intergenic region |
| 1769272\_s\_at | 1.9 | IG | intergenic region |
| 1760059\_s\_at | 1.7 | IG | intergenic region |
| 1761124\_s\_at | 1.6 | IG | intergenic region |
| 1761725\_s\_at | 1.5 | IG | intergenic region |
| 1761720\_s\_at | 1.5 | IG | intergenic region |
| 1762804\_s\_at | 1.6 | IG | intergenic region |
| 1768829\_s\_at | 1.5 | IG | intergenic region |

\*Genes that showed fold change greater than 1.5 (P < 0.05)