

Supplemental Table II. Genes induced or repressed in filamentous cells^a

| b. no. | Gene | Description ^b | Log ₂ ratio ^c | Arabinose Effect ^d |
|---|---------------|---|-------------------------------------|-------------------------------|
| Induced upon inhibition of FtsI function with aztreonam | | | | |
| b2055 | <i>wcaE</i> | colanic acid biosynthesis | 3.4 (2.0) | - |
| b4026 | <i>yjbE</i> | orf, hypothetical protein | 0.7 (0.6) | - |
| b1505 | <i>b1505</i> | putative outer membrane protein | 0.7 (0.2) | - |
| b3359 | <i>argD</i> | acetylornithine delta-aminotransferase | 0.6 (0.2) | - |
| b4043 | <i>lexA</i> | regulator for SOS(<i>lexA</i>) regulon | 0.5 (0.1) | - |
| b1374 | <i>b1374</i> | putative transposon resolvase | 0.5 (0.4) | - |
| b3670 | <i>ilvN</i> | acetolactate synthase I, small subunit | 0.5 (0.3) | - |
| b3172 | <i>argG</i> | argininosuccinate synthetase | 0.5 (0.4) | - |
| b3939 | <i>metB</i> | cystathionine gamma-synthase | 0.4 (0.3) | - |
| b3294 | <i>rplQ</i> | 50S ribosomal subunit protein L17 | 0.4 (0.1) | - |
| b3424 | <i>glpG</i> | protein of <i>glp</i> regulon | 0.4 (0.2) | - |
| b0016 | <i>yi81_1</i> | IS186 hypothetical protein | 0.4 (0.2) | - |
| b2424 | <i>cysU</i> | sulfate, thiosulfate transport | 0.4 (0.2) | - |
| b4202 | <i>rpsR</i> | 30S ribosomal subunit protein S18 | 0.3 (0.1) | - |
| b2567 | <i>rnc</i> | RNase III, ds RNA | 0.2 (0.1) | - |
| b2414 | <i>cysK</i> | cysteine synthase A | 0.1 (0.1) | - |
| Repressed upon inhibition of FtsI function with aztreonam | | | | |
| b3517 | <i>gadA</i> | glutamate decarboxylase isozyme | -2.5 (0.3) | - |
| b3512 | <i>yhiE</i> | orf, hypothetical protein | -2.1 (0.6) | - |
| b1493 | <i>gadB</i> | glutamate decarboxylase isozyme | -2.1 (0.2) | - |
| b3508 | <i>yhiD</i> | putative transport ATPase | -1.4 (0.4) | - |
| b3510 | <i>hdeA</i> | orf, hypothetical protein | -1.1 (0.5) | - |
| b1050 | <i>yceK</i> | orf, hypothetical protein | -1.0 (0.7) | - |
| b3507 | <i>yhiF</i> | orf, hypothetical protein | -1.0 (0.2) | - |
| b3515 | <i>yhiW</i> | putative ARAC-type regulatory protein | -0.9 (0.4) | - |
| b1188 | <i>ycgB</i> | putative sporulation protein | -0.8 (0.3) | - |
| b0812 | <i>dps</i> | global regulator, starvation conditions | -0.7 (0.3) | - |
| b3238 | <i>yhcN</i> | orf, hypothetical protein | -0.7 (0.3) | - |
| b0456 | <i>ybaA</i> | orf, hypothetical protein | -0.6 (0.2) | - |
| b2687 | <i>ygaG</i> | orf, hypothetical protein | -0.5 (0.4) | - |
| b1191 | <i>b1191</i> | orf, hypothetical protein | -0.4 (0.3) | - |
| b0075 | <i>leuL</i> | leu operon leader peptide | -0.4 (0.1) | - |
| b1480 | <i>rpsV</i> | 30S ribosomal subunit protein S22 | -0.4 (0.3) | - |
| b0394 | <i>yajF</i> | possible NAGC-like transcriptional regulator | -0.3 (0.3) | - |
| b1164 | <i>ycgZ</i> | orf, hypothetical protein | -0.2 (0.5) | - |
| Induced upon inhibition of FtsZ function via arabinose-induction of <i>sulA</i> | | | | |
| b2841 | <i>araE</i> | low-affinity L-arabinose transport | 5.9 (0.5) | 5.8 |
| b1901 | <i>araF</i> | L-arabinose-binding periplasmic protein | 5.6 (0.6) | 6.2 |
| b0958 | <i>sulA</i> | inhibits cell division and <i>ftsZ</i> ring formation | 4.9 (0.3) | 0.8 |

| | | | | |
|-------|---------------|---|-----------|------|
| b1898 | <i>araH_2</i> | high-affinity L-arabinose transport system | 4.8 (0.8) | 4.7 |
| b1899 | <i>araH_1</i> | high-affinity L-arabinose transport system | 4.6 (0.3) | 5.9 |
| b0573 | <i>ylcC</i> | orf, hypothetical protein | 3.7 (1.5) | 4.5 |
| b2840 | <i>ygeA</i> | putative resistance proteins | 3.2 (0.5) | 3.4 |
| b0572 | <i>ylcB</i> | putative resistance protein | 2.3 (0.9) | 3.8 |
| b4229 | <i>ytfS</i> | putative component of a transport system | 2.1 (1.0) | 1.9 |
| b2148 | <i>mglC</i> | methyl-galactoside transport and galactose taxis | 2.0 (0.3) | 2.2 |
| b2149 | <i>mglA</i> | methyl-galactoside transport and galactose taxis | 1.9 (0.4) | 2.5 |
| b3561 | <i>yiaH</i> | orf, hypothetical protein | 1.8 (0.8) | 0.7 |
| b0759 | <i>galE</i> | UDP-galactose-4-epimerase | 1.8 (0.3) | 2.1 |
| b2943 | <i>galP</i> | galactose-proton symport of transport system | 1.6 (0.2) | 1.9 |
| b0758 | <i>galT</i> | galactose-1-phosphate uridylyltransferase | 1.4 (0.5) | 2.4 |
| b3566 | <i>xylF</i> | xylose binding protein transport system | 1.2 (0.2) | 1.9 |
| b4228 | <i>ytfR</i> | putative component of a transport system | 1.1 (0.9) | 1.7 |
| b3011 | <i>yqhD</i> | putative oxidoreductase | 1.1 (0.4) | 1.9 |
| b1505 | <i>b1505</i> | putative outer membrane protein | 1.0 (0.7) | 1.0 |
| b4375 | <i>prfC</i> | peptide chain release factor RF-3 | 0.9 (0.2) | 1.1 |
| b0410 | <i>yajD</i> | orf, hypothetical protein | 0.9 (0.3) | 0.7 |
| b1573 | <i>ydfC</i> | orf, hypothetical protein | 0.9 (0.4) | 0.5 |
| b1612 | <i>fumA</i> | fumarate hydratase Class I; aerobic isozyme | 0.8 (0.3) | 0.3 |
| b2622 | <i>intA</i> | prophage CP4-57 integrase | 0.8 (0.3) | 0.9 |
| b0083 | <i>ftsL</i> | cell division protein; ingrowth of wall at septum | 0.8 (0.1) | -0.1 |
| b3002 | <i>yqhA</i> | orf, hypothetical protein | 0.7 (0.4) | 0.6 |
| b3537 | <i>yhjT</i> | orf, hypothetical protein | 0.7 (0.2) | 0.7 |
| b4151 | <i>frdD</i> | fumarate reductase | 0.6 (0.1) | 0.7 |
| b1794 | <i>yeaP</i> | orf, hypothetical protein | 0.6 (0.2) | 0.6 |
| b0382 | <i>yaiB</i> | orf, hypothetical protein | 0.6 (0.2) | -0.2 |
| b1848 | <i>yebG</i> | orf, hypothetical protein | 0.5 (0.2) | 0.5 |
| b0849 | <i>grxA</i> | glutaredoxin1 redox coenzyme | 0.5 (0.2) | 1.3 |

Repressed upon inhibition of FtsZ function via arabinose induction of *sulA*

| | | | | |
|-------|--------------|--|------------|------|
| b2678 | <i>proW</i> | transport system for glycine betaine and proline | -3.0 (0.8) | -3.1 |
| b1493 | <i>gadB</i> | glutamate decarboxylase isozyme | -2.6 (0.7) | -1.3 |
| b3512 | <i>yhiE</i> | orf, hypothetical protein | -2.3 (0.8) | -0.2 |
| b3511 | <i>hdeD</i> | orf, hypothetical protein | -2.2 (0.4) | -0.2 |
| b2677 | <i>proV</i> | transport system for glycine, betaine and proline | -2.1 (0.1) | -2.5 |
| b1492 | <i>xasA</i> | acid sensitivity protein, putative transporter | -2.0 (0.2) | -1.1 |
| b2679 | <i>proX</i> | transport system for glycine betaine and proline | -2.0 (0.4) | -2.3 |
| b0805 | <i>b0805</i> | putative receptor for iron transport | -1.9 (1.0) | -2.7 |
| b3506 | <i>slp</i> | induced after carbon starvation | -1.9 (0.5) | -0.3 |
| b2155 | <i>cirA</i> | receptor for iron-regulated colicin I receptor | -1.7 (0.5) | -2.6 |
| b2675 | <i>nrdE</i> | ribonucleoside-diphosphate reductase 2 | -1.6 (0.5) | -2.9 |
| b1481 | <i>b1481</i> | orf, hypothetical protein | -1.6 (0.3) | -0.9 |
| b0584 | <i>fepA</i> | receptor for ferric enterobactin and colicins B, D | -1.5 (0.6) | -2.6 |
| b0595 | <i>entB</i> | 2,3-dihydro-2,3-dihydroxybenzoate synthetase | -1.5 (0.7) | -2.0 |
| b3508 | <i>yhiD</i> | putative transport ATPase | -1.5 (0.7) | -0.2 |
| b1679 | <i>ynhA</i> | orf, hypothetical protein | -1.5 (0.2) | -1.1 |
| b2673 | <i>nrdH</i> | glutaredoxin-like protein; hydrogen donor | -1.4 (0.6) | -2.0 |
| b0597 | <i>ybdB</i> | orf, hypothetical protein | -1.3 (0.6) | -3.6 |

| | | | | |
|-------|--------------|---|------------|------|
| b3510 | <i>hdeA</i> | orf, hypothetical protein | -1.3 (0.4) | -1.6 |
| b3509 | <i>hdeB</i> | orf, hypothetical protein | -1.3 (0.1) | -0.9 |
| b0804 | <i>ybiX</i> | putative enzyme | -1.2 (0.4) | -1.4 |
| b3516 | <i>yhiX</i> | putative ARAC-type regulatory protein | -1.2 (0.3) | -0.0 |
| b0596 | <i>entA</i> | enterochelin biosynthesis | -1.2 (0.4) | -2.3 |
| b0583 | <i>entD</i> | enterochelin synthetase, component D | -1.2 (0.4) | -1.8 |
| b1681 | <i>ynhC</i> | orf, hypothetical protein | -1.2 (0.3) | -1.0 |
| b2674 | <i>nrdI</i> | orf, hypothetical protein | -1.2 (0.7) | -1.5 |
| b1683 | <i>ynhE</i> | orf, hypothetical protein | -1.1 (0.6) | -0.7 |
| b1836 | <i>b1836</i> | orf, hypothetical protein | -1.1 (0.2) | -0.9 |
| b4163 | <i>glyV</i> | Glycine tRNA3 | -1.1 (0.8) | -0.2 |
| b2392 | <i>b2392</i> | putative transport system permease | -1.0 (0.1) | -1.0 |
| b0593 | <i>entC</i> | enterochelin biosynthesis | -1.0 (0.3) | -2.1 |
| b4240 | <i>treB</i> | PTS system enzyme II, trehalose specific | -1.0 (0.6) | 1.4 |
| b1897 | <i>otsB</i> | trehalose-6-phosphate phosphatase, biosynthetic | -1.0 (0.1) | 1.0 |
| b0050 | <i>apaG</i> | orf, hypothetical protein | -0.9 (0.0) | -0.5 |
| b3515 | <i>yhiW</i> | putative ARAC-type regulatory protein | -0.9 (0.5) | -0.3 |
| b1684 | <i>ydiC</i> | orf, hypothetical protein | -0.8 (0.3) | -1.3 |
| b2094 | <i>gatA</i> | enzyme of phosphotransferase system | -0.7 (0.2) | -1.5 |
| b0744 | <i>valT</i> | Valine tRNA1 | -0.7 (0.1) | -1.2 |
| b0051 | <i>ksgA</i> | SAM-6-N,N -adenosyl dimethyltransferase | -0.7 (0.1) | -0.2 |
| b0746 | <i>valZ</i> | Valine tRNA1 | -0.7 (0.2) | -0.8 |
| b0707 | <i>ybgA</i> | orf, hypothetical protein | -0.6 (0.2) | -0.4 |
| b1452 | <i>b1452</i> | putative receptor | -0.6 (0.2) | -2.0 |
| b2402 | <i>valX</i> | Valine tRNA1; tandemly triplicate | -0.6 (0.2) | -1.0 |
| b2742 | <i>nlpD</i> | lipoprotein | -0.6 (0.1) | -1.7 |
| b2464 | <i>talA</i> | transaldolase A | -0.6 (0.2) | -0.1 |
| b2573 | <i>rpoE</i> | sigma-E factor; heat shock and oxidative stress | -0.6 (0.2) | -0.5 |
| b3588 | <i>aldB</i> | aldehyde dehydrogenase B | -0.5 (0.3) | -0.2 |
| b2465 | <i>tktB</i> | transketolase 2 isozyme | -0.5 (0.4) | -0.3 |
| b4015 | <i>aceA</i> | isocitrate lyase | -0.5 (0.1) | -1.0 |
| b1478 | <i>adhP</i> | alcohol dehydrogenase | -0.5 (0.2) | -0.5 |
| b4126 | <i>yjdl</i> | orf, hypothetical protein | -0.5 (0.2) | -0.2 |
| b0585 | <i>fes</i> | enterochelin esterase | -0.4 (0.4) | -1.4 |
| b2095 | <i>gatZ</i> | putative tagatose 6-phosphate kinase 1 | -0.4 (0.5) | -1.7 |
| b0775 | <i>bioB</i> | biotin synthesis, sulfur insertion? | -0.4 (0.2) | -0.5 |
| b2537 | <i>hcaR</i> | transcriptional activator of hca cluster | -0.4 (0.3) | -0.1 |
| b0565 | <i>ompT</i> | outer membrane protein 3b (a), protease VII | -0.2 (0.5) | -1.1 |

^aThis list includes all genes whose expression changes were judged statistically significant by the Affymetrix software regardless of the magnitude of the change.

^bGene descriptions are from the Affymetrix sequence information database.

^cMean (standard deviation) for three independent experiments.

^dLog₂ ratio for induction or repression in EC1097 (one experiment).