

| Gene               | Hours post induction ( log <sub>2</sub> (induced / un-induced) ) |       |       |       |       |       |       | Gene Function   |
|--------------------|--|-------|-------|-------|-------|-------|-------|---|
|                    | 0.5  | 1     | 1.5   | 2     | 3     | 3.5   | 4     |   |
| <i>ACA-0244248</i> | -0.09  | -0.33 | -0.27 | -0.15 | 0.03  | 0.40  | 0.34  | transposase Tra5 []   |
| <i>allB</i>        | -0.35  | -0.45 | 0.12  | 0.24  | 0.81  | 1.68  | 1.51  | putative hydrolase [b0512]  |
| <i>alpA</i>        | -0.09  | -0.04 | 0.37  | 0.10  | 0.45  | 1.10  | 1.11  | Prophage CP4-57 Regulatory protein alpA [c_1169]                              |
| <i>amiC</i>        | -0.23  | -0.09 | 0.68  | 0.68  | 1.28  | 1.62  | 1.52  | putative amidase [b2817]  |
| <i>b2649</i>       | 0.29   | 0.29  | 0.60  | 0.75  | 0.27  | 1.34  | 1.69  | "orf, hypothetical protein [b2649]"   |
| <i>b2656</i>       | -0.10  | 0.02  | 0.20  | -0.14 | 0.43  | 0.84  | 0.82  | "orf, hypothetical protein [b2656]"   |
| <i>bioC</i>        | -0.06  | -0.17 | 0.06  | -0.11 | 0.01  | 0.53  | 0.40  | biotin biosynthesis; reaction prior to pimeloyl CoA [b0777]                   |
| <i>c_0273</i>      | -0.15  | -0.05 | -0.20 | -0.22 | 0.00  | 0.81  | 0.39  | Putative radC-like protein yeeS [c_0273]                                      |
| <i>c_0429</i>      | -0.17  | -0.24 | -0.01 | 0.42  | -0.21 | 0.35  | -0.01 | Conserved hypothetical protein [c_0429]                                       |
| <i>c_0438</i>      | -0.05  | -0.01 | -0.81 | -0.42 | -0.08 | -0.25 | -0.18 | Hypothetical protein [c_0438]   |
| <i>c_0471</i>      | 0.00   | 0.00  | -0.02 | -0.21 | 0.05  | 0.92  | 0.73  | Hypothetical protein [c_0471]   |
| <i>c_1145</i>      | 0.01   | -0.19 | 0.03  | -0.13 | 0.31  | 0.23  | 0.56  | Putative NADH dehydrogenase/NAD [c_1145]                                      |
| <i>c_1883</i>      | 0.05   | -0.46 | -0.26 | 0.22  | -0.03 | 0.17  | -0.03 | Conserved hypothetical protein [c_1883]                                       |
| <i>c_1891</i>      | 0.02   | -0.10 | 0.10  | 0.17  | -0.07 | 0.34  | 0.05  | Hypothetical protein [c_1891]   |
| <i>c_2118</i>      | 0.00   | -0.19 | 0.05  | 0.01  | 0.07  | 0.90  | 1.06  | Putative conserved protein [c_2118]   |
| <i>c_2180</i>      | -0.10  | 0.03  | -0.17 | -0.14 | -0.02 | 0.38  | 0.29  | Hypothetical protein [c_2180]   |
| <i>c_2442</i>      | -0.02  | -0.38 | -0.16 | -0.09 | 0.04  | 0.27  | 0.37  | Hypothetical protein [c_2442]   |
| <i>c_2456</i>      | 0.18   | -0.31 | -0.03 | 0.06  | -0.08 | 0.22  | 0.00  | Hypothetical protein [c_2456]   |
| <i>c_2489</i>      | 0.01   | -0.01 | -0.03 | -0.05 | 0.13  | 0.45  | 0.37  | Putative transferase [c_2489]   |
| <i>c_2525</i>      | -0.07  | -0.31 | -0.22 | -0.07 | -0.10 | 0.22  | -0.14 | Hypothetical protein [c_2525]   |
| <i>c_2924</i>      | -0.10  | -0.05 | -0.03 | -0.26 | 0.03  | 0.78  | 0.48  | Putative peptidase ypdF [c_2924]  |
| <i>c_3166</i>      | -0.02  | -0.28 | -0.12 | 0.06  | -0.12 | 0.26  | 0.03  | Putative head-tail joining protein of prophage [c_3166]                       |
| <i>c_3559</i>      | -0.09  | 0.09  | 0.28  | 0.17  | 0.01  | 0.38  | 0.23  | Hypothetical protein [c_3559]   |
| <i>c_3631</i>      | 0.05   | -0.59 | 0.48  | 0.72  | 0.08  | 0.11  | -0.03 | Hypothetical protein [c_3631]   |
| <i>c_4435</i>      | -0.54  | -0.47 | -0.26 | -0.25 | 0.00  | 0.41  | 0.57  | Hypothetical protein [c_4435]   |
| <i>c_4576</i>      | -0.04  | -0.14 | 0.05  | -0.04 | 0.11  | 0.61  | 0.44  | Hypothetical protein yeeV [c_4576]  |
| <i>c_4808</i>      | -0.17  | -0.77 | 0.45  | 0.29  | 1.15  | 2.06  | 2.21  | Hypothetical protein [c_4808]   |
| <i>c_5447</i>      | 0.08   | -0.17 | 1.77  | 1.60  | 2.21  | 2.86  | 3.60  | Hypothetical protein [c_5447]   |
| <i>c_5448</i>      | 0.16   | -0.01 | 1.53  | 1.73  | 2.71  | 3.45  | 3.60  | Hypothetical protein [c_5448]   |
| <i>caiD</i>        | -0.01  | -0.38 | -0.13 | -0.16 | 0.66  | 1.27  | 1.49  | carnitine racemase [b0036]  |
| <i>cheB</i>        | -0.06  | -0.24 | -0.01 | -0.14 | 0.22  | 0.25  | 0.36  | response regulator for chemotaxis [b1883]                                     |
| <i>cheZ</i>        | -0.30  | -0.02 | -0.08 | -0.23 | 0.72  | 0.66  | 0.55  | Chemotaxis protein cheZ [c_2296]  |
| <i>chpR</i>        | -0.04  | 0.15  | 0.95  | 0.68  | 0.86  | 1.61  | 1.77  | "suppressor of inhibitory function of ChpA, PemI-like, autoregulated [b2783]" |
| <i>citG</i>        | 0.01   | 0.03  | 0.03  | 0.12  | -0.08 | 0.68  | 0.93  | "orf, hypothetical protein [b0613]"   |
| <i>cpsG</i>        | -0.06  | 0.02  | 0.14  | -0.16 | 0.21  | 0.54  | 0.35  | phosphomannomutase [b2048]  |

|                 |       |       |       |       |       |       |       |  |
|-----------------|-------|-------|-------|-------|-------|-------|-------|--|
| <i>csgC</i>     | -0.08 | -0.25 | -0.03 | 0.05  | 0.23  | 0.43  | 0.76  | putative curli production protein [b1043]  |
| <i>cspF</i>     | -0.37 | -0.64 | 1.97  | 1.79  | 2.74  | 3.92  | 4.04  | cold shock protein [b1558]   |
| <i>cspH</i>     | 0.12  | -0.33 | 2.00  | 1.93  | 2.51  | 3.54  | 3.58  | cold shock-like protein [b0989]  |
| <i>cysH</i>     | 0.01  | -0.21 | -0.16 | -0.04 | 0.04  | 0.19  | 0.15  | 3-phosphoadenosine 5-phosphosulfate reductase [b2762]                            |
| <i>cysJ</i>     | 0.16  | -0.22 | -0.17 | -0.05 | 0.39  | -0.33 | 0.14  | Sulfite reductase [c_3323]   |
| <i>cysN</i>     | -0.04 | -0.24 | -0.18 | -0.08 | -0.06 | 0.14  | 0.15  | ATP-sulfurylase [b2751]  |
| <i>DCP_22_7</i> | -0.09 | -0.47 | -0.14 | 0.12  | -0.06 | 0.15  | -0.04 |  |
| <i>dpiB</i>     | 0.11  | -0.27 | 0.03  | -0.10 | -0.02 | 0.49  | 0.71  | putative sensor-type protein [b0619]   |
| <i>ECs0325</i>  | 0.18  | -0.18 | 0.73  | 0.57  | 1.23  | 1.95  | 1.86  | hypothetical protein [ECs0325]   |
| <i>ECs0331</i>  | 0.11  | 0.01  | 0.25  | 0.01  | -0.13 | 1.25  | 1.92  | putative NADH-dependent flavin oxidoreductase [ECs0331]                          |
| <i>ECs0337</i>  | -0.10 | -0.23 | 0.04  | -0.29 | -0.18 | 0.70  | 0.44  | putative transcription regulator [ECs0337]                                       |
| <i>ECs0573</i>  | 0.03  | -0.15 | 0.15  | 0.22  | 1.21  | 1.36  | 1.70  | allantoinase [ECs0573]   |
| <i>ECs0854</i>  | 0.06  | -0.09 | 0.09  | 0.11  | 0.37  | 0.42  | 0.42  | 8-amino-7-oxononanoate synthase [ECs0854]  |
| <i>ECs1613</i>  | 0.04  | 0.19  | 1.11  | 1.46  | 1.60  | 2.92  | 2.73  | Ren protein [ECs1613]  |
| <i>ECs1628</i>  | -0.68 | -0.20 | 0.32  | 0.13  | 0.81  | 0.90  | 1.34  | hypothetical protein [ECs1628]   |
| <i>ECs1721</i>  | 0.20  | 0.39  | 1.13  | 2.22  | 2.54  | 2.42  | 2.76  | sodium-calcium/proton antiporter [ECs1721]                                       |
| <i>ECs1946</i>  | -0.16 | 0.06  | 0.17  | 0.13  | 0.23  | 0.84  | 0.51  | hypothetical protein [ECs1946]   |
| <i>ECs2038</i>  | 0.01  | -0.75 | -0.68 | -0.52 | 0.24  | 0.16  | 1.20  | hypothetical protein [ECs2038]   |
| <i>ECs2427</i>  | -0.12 | 0.01  | -0.12 | 0.03  | -0.08 | 0.52  | 0.50  | hypothetical protein [ECs2427]   |
| <i>ECs2928</i>  | -0.16 | -0.39 | -0.10 | -0.24 | 0.21  | 0.54  | 0.61  | hypothetical protein [ECs2928]   |
| <i>ECs2985</i>  | 0.41  | 0.30  | 1.25  | 1.57  | 2.37  | 2.80  | 2.99  | Ren protein [ECs2985]  |
| <i>ECs3484</i>  | 0.01  | -0.11 | 0.69  | 0.43  | 1.83  | 2.29  | 2.71  | hypothetical protein [ECs3484]   |
| <i>ECs3559</i>  | -0.35 | -0.70 | 0.91  | 2.63  | 4.01  | 4.80  | 5.31  | interrupted glucitol/sorbitol-specific PTS system enzyme IIC component [ECs3559] |
| <i>ECs3592</i>  | 0.16  | -0.37 | -0.11 | 0.20  | 0.16  | 0.06  | 0.06  | putative 4-hydroxybenzoate decarboxylase [ECs3592]                               |
| <i>ECs3631</i>  | -0.12 | -0.19 | -0.53 | -0.23 | 0.18  | 0.61  | 0.48  | putative transport protein [ECs3631]   |
| <i>ECs4471</i>  | 0.23  | 0.04  | 0.84  | 0.65  | 1.79  | 2.60  | 3.24  | hypothetical protein [ECs4471]   |
| <i>ECs4472</i>  | -0.04 | 0.40  | 0.47  | 0.35  | 0.89  | 1.71  | 1.92  | hypothetical protein [ECs4472]   |
| <i>ECs4500</i>  | 0.01  | -0.35 | -0.19 | 0.46  | -0.10 | 0.16  | 0.03  | lipid A-core:surface polymer ligase [ECs4500]                                    |
| <i>ECs4630</i>  | 0.01  | -0.09 | 0.07  | -0.10 | 0.07  | 0.61  | 0.61  | hypothetical protein [ECs4630]   |
| <i>ECs5021</i>  | -0.18 | -0.57 | -0.19 | -0.14 | 0.18  | 0.68  | 0.74  | hypothetical protein [ECs5021]   |
| <i>ECs5058</i>  | 0.06  | -0.28 | 0.16  | -0.01 | 0.16  | 0.48  | 0.65  | part of formate-dependent nitrite reductase complex NrfG [ECs5058]               |
| <i>ECs5233</i>  | -0.23 | -0.20 | -0.12 | -0.14 | -0.23 | 0.56  | 0.12  | hypothetical protein [ECs5233]   |
| <i>eutE</i>     | -0.07 | -0.11 | 0.08  | -0.23 | 0.23  | 0.44  | 0.55  | ethanolamine utilization; similar to acetaldehyde dehydrogenase [b2455]          |
| <i>flgD</i>     | -0.07 | -0.01 | 0.03  | -0.55 | 0.10  | 0.48  | 0.23  | "flagellar biosynthesis, initiation of hook assembly [b1075]"                    |
| <i>flgE</i>     | -0.11 | -0.16 | -0.14 | -0.33 | 0.13  | 0.23  | 0.28  | "flagellar biosynthesis, hook protein [b1076]"                                   |
| <i>flgJ</i>     | 0.00  | 0.06  | 0.03  | -0.27 | -0.05 | 0.49  | 0.25  | flagellar biosynthesis [b1081]   |
| <i>flhE</i>     | -0.03 | -0.05 | 0.25  | 0.02  | 0.37  | 0.69  | 0.77  | flagellar protein [b1878]  |

|              |       |       |       |       |       |      |       |   |
|--------------|-------|-------|-------|-------|-------|------|-------|---|
| <i>fliP</i>  | -0.01 | -0.13 | 0.03  | -0.19 | 0.28  | 0.56 | 0.51  | Flagellar biosynthetic protein fliP precursor [c_2365]                                |
| <i>frwB</i>  | -0.27 | -0.88 | -0.24 | -0.07 | 0.31  | 0.63 | 0.67  | PTS system fructose-like IIB component 1 [b3950]                                      |
| <i>ggt</i>   | 0.02  | -0.25 | -0.42 | -0.40 | -0.26 | 0.00 | -0.14 | gamma-glutamyltranspeptidase [Z4813]  |
| <i>gnd</i>   | -0.99 | -0.69 | -0.80 | -0.68 | -0.02 | 0.78 | 0.98  | "gluconate-6-phosphate dehydrogenase, decarboxylating [b2029]"                        |
| <i>hha</i>   | -0.10 | -0.45 | 1.02  | 1.15  | 2.61  | 3.28 | 3.53  | haemolysin expression modulating protein [b0460]                                      |
| <i>hofP</i>  | -0.03 | -0.15 | -0.09 | -0.08 | 0.10  | 0.43 | 0.65  | "orf, hypothetical protein [b3392]"   |
| <i>hyfA</i>  | 0.00  | 0.06  | -0.09 | -0.26 | 0.01  | 0.46 | 0.48  | hydrogenase 4 Fe-S subunit [b2481]  |
| <i>iscS</i>  | 0.23  | 0.33  | 0.47  | 0.97  | 1.93  | 2.45 | 2.63  | putative aminotransferase [b2530]   |
| <i>iscU</i>  | -0.31 | 0.29  | 0.65  | 0.92  | 1.07  | 2.26 | 2.21  | "orf, hypothetical protein [b2529]"   |
| <i>ispU</i>  | -0.20 | -0.35 | 0.31  | 0.79  | 0.63  | 1.47 | 1.45  | "orf, hypothetical protein [b0174]"   |
| <i>kdpC</i>  | -0.03 | -0.13 | 0.10  | -0.02 | 0.38  | 0.85 | 1.01  | high-affinity potassium transport system [b0696]                                      |
| <i>kil</i>   | 0.02  | -0.05 | 0.23  | 0.11  | 0.19  | 0.91 | 1.45  | hypothetical protein [ECs1936]  |
| <i>kilR</i>  | -0.02 | -0.22 | 0.22  | 0.17  | 0.50  | 1.07 | 1.23  | "orf, hypothetical protein [b1352]"   |
| <i>L7026</i> | 0.06  | -0.32 | 0.16  | 0.37  | 0.00  | 0.12 | 0.00  | polysaccharide deacetylase [L7026]  |
| <i>lar</i>   | 0.10  | 0.20  | 1.21  | 0.73  | 2.58  | 3.30 | 3.70  | restriction alleviation and modification enhancement protein [ECs1932]                |
| <i>livM</i>  | -0.05 | -0.45 | -0.03 | -0.05 | 0.04  | 0.80 | 0.91  | high-affinity branched-chain amino acid transport [b3456]                             |
| <i>lsrC</i>  | 0.01  | -0.30 | -0.16 | -0.18 | -0.01 | 0.35 | 0.74  | putative transport system permease protein [b1514]                                    |
| <i>maa</i>   | 0.37  | 0.19  | 1.84  | 1.97  | 3.26  | 3.79 | 3.99  | putative transferase [b0459]  |
| <i>maoC</i>  | 0.06  | -0.28 | 0.02  | 0.01  | 0.26  | 0.68 | 0.66  | putative aldehyde dehydrogenase [b1387]   |
| <i>mdtI</i>  | 0.39  | 0.07  | 0.76  | 1.36  | 1.94  | 2.87 | 2.89  | possible chaperone [b1599]  |
| <i>mhpT</i>  | -0.10 | -0.06 | 0.08  | -0.16 | 0.04  | 0.84 | 0.70  | putative transport protein [b0353]  |
| <i>mmuP</i>  | -0.23 | -0.48 | -0.09 | -0.13 | 0.23  | 1.04 | 1.00  | putative amino acid/amine transport protein [b0260]                                   |
| <i>nrfG</i>  | 0.06  | -0.36 | 0.30  | 0.03  | 0.25  | 0.56 | 0.58  | part of formate-dependent nitrite reductase complex [b4076]                           |
| <i>nsrR</i>  | -0.09 | -0.11 | 0.36  | 0.67  | 1.19  | 1.75 | 1.79  | "orf, hypothetical protein [b4178]"   |
| <i>ompF</i>  | -0.73 | -1.02 | -0.04 | 0.35  | 0.87  | 1.01 | 1.79  | outer membrane protein 1a [b0929]   |
| <i>ompG</i>  | 0.04  | -0.09 | 0.33  | 0.15  | 0.53  | 0.93 | 1.00  | outer membrane protein [Z2462]  |
| <i>pgaC</i>  | 0.06  | -0.06 | 0.87  | 0.60  | 1.48  | 1.56 | 1.98  | "orf, hypothetical protein [b1022]"   |
| <i>pphA</i>  | -0.33 | -0.33 | -0.13 | -0.12 | 0.74  | 1.18 | 1.75  | "protein phosphatase 1 modulates phosphoproteins, signals protein misfolding [b1838]" |
| <i>puuC</i>  | 0.05  | -0.11 | 0.09  | -0.30 | 0.30  | 0.42 | 0.75  | "aldehyde dehydrogenase, prefers NADP over NAD [b1300]"                               |
| <i>puuE</i>  | -0.03 | -0.02 | 0.13  | -0.28 | 0.13  | 0.59 | 0.73  | 4-aminobutyrate aminotransferase [b1302]  |
| <i>rarD</i>  | -0.19 | -0.20 | 0.33  | 0.12  | -0.12 | 0.76 | 0.78  | "orf, hypothetical protein [b3819]"   |
| <i>rdoA</i>  | -0.23 | -0.36 | -0.11 | 0.15  | 0.44  | 1.51 | 1.92  | "orf, hypothetical protein [b3859]"   |
| <i>recE</i>  | 0.06  | 0.03  | 0.22  | 0.28  | 0.64  | 0.83 | 0.94  | Exodeoxyribonuclease VIII [c_1402]  |
| <i>rect</i>  | -0.07 | -0.07 | 1.34  | 0.79  | 2.07  | 2.93 | 3.25  | "recombinase, DNA renaturation [b1349]"   |
| <i>rpmE2</i> | -0.12 | 0.72  | 1.62  | 1.55  | 2.08  | 2.76 | 3.30  | ribosomal protein L31-like protein [ECs1330]  |
| <i>rsxA</i>  | 0.01  | 0.17  | 0.44  | 0.81  | 0.99  | 2.29 | 2.13  | "orf, hypothetical protein [b1627]"   |
| <i>sgbH</i>  | -0.03 | -0.25 | -0.09 | -0.29 | 0.05  | 0.52 | 0.35  | probable 3-hexulose 6-phosphate synthase [b3581]                                      |

|               |       |       |       |       |       |      |      |  |
|---------------|-------|-------|-------|-------|-------|------|------|--|
| <i>sgbU</i>   | -0.01 | -0.18 | -0.04 | -0.31 | 0.35  | 0.52 | 0.54 | Putative hexulose-6-phosphate isomerase [c_4405]                       |
| <i>srlA_I</i> | -0.76 | -0.58 | 0.72  | 3.55  | 3.85  | 4.81 | 5.42 | "PTS system, glucitol/sorbitol-specific IIC component, one of [Z4005]" |
| <i>tauD</i>   | -0.03 | -0.20 | 0.08  | 0.01  | 0.04  | 0.42 | 0.38 | "taurine dioxygenase, 2-oxoglutarate-dependent [Z0467]"                |
| <i>tdcR</i>   | -0.15 | -0.35 | -0.01 | -0.18 | 0.91  | 0.80 | 1.56 | threonine dehydratase operon activator protein [Z4471]                 |
| <i>tfaR</i>   | 0.06  | -0.13 | 0.27  | 0.29  | 0.86  | 1.04 | 1.37 | "orf, hypothetical protein [b1373]"                                    |
| <i>tfaX</i>   | -0.30 | 0.06  | 1.31  | 0.91  | 2.45  | 2.83 | 3.74 | "orf, hypothetical protein [b0563]"                                    |
| <i>thiG</i>   | 0.00  | -0.30 | -0.25 | -0.36 | -0.20 | 0.26 | 0.17 | "thiamin biosynthesis, thiazole moiety [b3991]"                        |
| <i>torA</i>   | -0.01 | -0.32 | -0.02 | -0.29 | -0.03 | 0.34 | 0.03 | Trimethylamine-N-oxide reductase 1 precursor [c_1133]                  |
| <i>torI</i>   | -0.85 | -0.93 | -0.93 | -0.54 | 0.56  | 1.29 | 1.10 | response regulator inhibitor for tor operon [b4501]                    |
| <i>ubiB</i>   | -0.78 | -0.62 | -0.32 | -0.08 | -0.28 | 0.21 | 0.34 | "orf, hypothetical protein [b3835]"                                    |
| <i>ugd</i>    | 0.27  | 0.21  | 0.49  | 0.57  | 0.98  | 1.17 | 1.07 | UDP-glucose 6-dehydrogenase [b2028]                                    |
| <i>ulaA</i>   | -0.02 | -0.05 | -0.04 | -0.09 | 0.00  | 0.26 | 0.23 | orf Unknown function [Z1087]   |
| <i>wcaA</i>   | -0.07 | -0.16 | 0.00  | -0.24 | 0.25  | 0.36 | 0.37 | putative regulator [b2059]   |
| <i>wcaB</i>   | 0.01  | -0.32 | -0.05 | -0.23 | 0.08  | 0.55 | 0.45 | putative transferase [Z3222]   |
| <i>wcaD</i>   | 0.03  | -0.16 | 0.48  | 0.49  | 0.27  | 1.53 | 1.63 | putative colanic acid polymerase [b2056]                               |
| <i>wcaM</i>   | 0.02  | 0.17  | 0.85  | 0.66  | 1.08  | 1.46 | 1.37 | "orf, hypothetical protein [b2043]"                                    |
| <i>xapR</i>   | 0.21  | -0.14 | 0.32  | 0.44  | 0.33  | 0.47 | 0.37 | Xanthosine operon Regulatory protein [c_2937]                          |
| <i>yagK</i>   | -0.06 | -0.45 | 0.86  | 0.74  | 2.40  | 2.60 | 2.88 | "orf, hypothetical protein [b0277]"                                    |
| <i>ybaJ</i>   | -0.27 | -0.83 | 0.63  | 0.98  | 2.34  | 3.26 | 3.50 | "orf, hypothetical protein [b0461]"                                    |
| <i>ybcV</i>   | -0.43 | -0.61 | 0.34  | 0.11  | 1.05  | 1.63 | 1.91 | putative an envelop protein [b0558]                                    |
| <i>ybcY</i>   | -0.29 | -0.48 | 0.64  | 0.66  | 0.87  | 1.80 | 1.56 | "orf, hypothetical protein [b0562]"                                    |
| <i>ybdB</i>   | -0.17 | 0.15  | 0.50  | 0.41  | 0.64  | 1.09 | 1.28 | "orf, hypothetical protein [Z0739]"                                    |
| <i>ybeA</i>   | -0.19 | -0.41 | 0.63  | 0.53  | 0.83  | 1.14 | 1.53 | "orf, hypothetical protein [b0636]"                                    |
| <i>ycaK</i>   | -0.70 | -0.36 | 0.35  | 0.56  | 0.52  | 1.29 | 1.65 | "orf, hypothetical protein [b0901]"                                    |
| <i>ycbX</i>   | -0.16 | -0.06 | 0.05  | 0.26  | -0.05 | 0.72 | 0.22 | "orf, hypothetical protein [b0947]"                                    |
| <i>ycdO</i>   | 0.07  | 0.32  | 0.25  | 0.40  | 0.11  | 1.07 | 1.12 | Protein ycdO [c_1156]  |
| <i>ycdU</i>   | 0.28  | -0.66 | 1.54  | 1.70  | 2.55  | 3.51 | 4.19 | "orf, hypothetical protein [b1029]"                                    |
| <i>ycjO</i>   | -0.10 | -0.13 | -0.28 | -0.28 | 0.34  | 0.20 | 0.54 | putative binding-protein dependent transport protein [b1311]           |
| <i>ycjP</i>   | -0.02 | -0.14 | -0.17 | -0.15 | 0.42  | 0.79 | 0.97 | putative transport system permease protein [Z2471]                     |
| <i>ycjP</i>   | -0.02 | -0.14 | -0.17 | -0.15 | 0.42  | 0.79 | 0.97 | putative transport system permease protein [Z2471]                     |
| <i>ydaC</i>   | -0.02 | 0.09  | 1.16  | 0.77  | 2.37  | 3.04 | 3.42 | unknown protein encoded within prophage CP-933R [Z2413]                |
| <i>ydaJ</i>   | 0.03  | -0.19 | -0.17 | -0.11 | 0.09  | 0.40 | 0.27 | putative aminohydrolase [Z2425]  |
| <i>ydbD</i>   | 0.02  | -0.23 | 0.18  | 0.26  | 0.05  | 1.20 | 1.23 | "orf, hypothetical protein [b1407]"                                    |
| <i>ydeK</i>   | -0.10 | -0.55 | -0.47 | -0.28 | -0.28 | 0.02 | 0.16 | "orf, hypothetical protein [b1510]"                                    |
| <i>ydeO</i>   | 0.06  | 0.25  | 0.57  | 0.33  | 1.03  | 2.24 | 2.99 | putative ARAC-type regulatory protein [b1499]                          |
| <i>ydeP</i>   | -0.12 | -0.19 | 0.08  | 0.21  | 0.50  | 1.11 | 1.25 | "putative oxidoreductase, major subunit [b1501]"                       |
| <i>ydgK</i>   | -0.93 | -0.55 | 0.19  | 0.36  | 0.81  | 2.05 | 2.71 | "orf, hypothetical protein [b1626]"                                    |

|             |       |       |       |       |       |       |       |   |
|-------------|-------|-------|-------|-------|-------|-------|-------|---|
| <i>ydiM</i> | 0.07  | -0.29 | -0.08 | -0.06 | 0.69  | 0.60  | 0.95  | putative transport system permease protein [b1690]                      |
| <i>ydiY</i> | -0.31 | -0.23 | 0.23  | 0.19  | 0.12  | 0.80  | 0.56  | "orf, hypothetical protein [b1722]"                                     |
| <i>yeaE</i> | 0.05  | -0.04 | -0.82 | -0.45 | -0.15 | -0.08 | -0.50 | Hypothetical protein yeaE [c_2186]                                      |
| <i>yebB</i> | 0.23  | 0.02  | -0.03 | 0.33  | -0.01 | 0.04  | 0.42  | Hypothetical protein yebB [c_2276]                                      |
| <i>yehA</i> | 0.05  | 0.15  | 0.28  | 0.16  | 1.00  | 1.70  | 2.01  | Hypothetical protein yehA precursor [c_2635]                            |
| <i>yeiM</i> | -0.07 | -0.44 | 0.23  | 0.31  | 0.32  | 0.69  | 0.88  | putative transport system permease protein [b2164]                      |
| <i>yeiN</i> | -0.05 | -0.10 | 0.06  | 0.22  | 0.19  | 0.35  | 0.69  | "orf, hypothetical protein [b2165]"                                     |
| <i>yfaV</i> | 0.11  | -0.41 | -0.09 | -0.08 | 0.01  | 0.51  | 1.25  | putative transport protein [b2246]                                      |
| <i>yfBL</i> | -0.02 | 0.19  | 0.28  | 0.17  | 0.09  | 0.65  | 0.59  | putative aminopeptidase [b2271]   |
| <i>yfcS</i> | 0.03  | -0.07 | 0.00  | -0.02 | 0.13  | -0.12 | 0.16  | Hypothetical fimbrial chaperone yfcS precursor [c_2882]                 |
| <i>yfdM</i> | 0.07  | -0.14 | 0.16  | 0.03  | -0.10 | 0.81  | 0.64  | "orf, hypothetical protein [b2356]"                                     |
| <i>yfJ</i>  | 0.04  | -0.13 | 0.29  | 0.42  | 0.66  | 1.36  | 2.10  | "orf, hypothetical protein [b2626]"                                     |
| <i>yfJK</i> | -0.50 | -0.22 | 0.25  | 0.14  | 0.33  | 1.30  | 1.08  | "orf, hypothetical protein [b2627]"                                     |
| <i>ygcG</i> | -0.01 | -0.29 | 0.20  | 0.05  | -0.13 | 0.28  | 0.11  | "orf, hypothetical protein [b2778]"                                     |
| <i>ygcY</i> | -0.10 | -0.12 | -0.63 | -0.45 | -0.09 | 0.27  | 0.25  | Glucarate dehydratase related protein [c_3352]                          |
| <i>ygdQ</i> | -0.06 | -0.16 | 0.59  | 0.85  | 0.82  | 1.16  | 1.55  | putative transport protein [b2832]                                      |
| <i>ygjQ</i> | 0.01  | 0.13  | 0.03  | -0.07 | 0.04  | 0.42  | -0.06 | "orf, hypothetical protein [b3086]"                                     |
| <i>yhjR</i> | 0.02  | -0.31 | 0.46  | 0.90  | 2.16  | 2.24  | 2.27  | "orf, hypothetical protein [b3535]"                                     |
| <i>yiaO</i> | -0.13 | -0.04 | 0.01  | -0.38 | 0.28  | 0.47  | 0.71  | putative solute-binding transport protein [b3579]                       |
| <i>yibG</i> | 0.39  | -0.14 | 1.03  | 0.55  | 1.40  | 2.51  | 3.22  | "orf, hypothetical protein [b3596]"                                     |
| <i>yibJ</i> | -0.39 | -0.61 | 0.25  | 0.36  | 0.93  | 1.56  | 1.88  | "orf, hypothetical protein [b3595]"                                     |
| <i>yidD</i> | -0.24 | 0.08  | 0.16  | 0.25  | 0.72  | 0.83  | 1.50  | predicted protein [b4557]   |
| <i>yieG</i> | 0.24  | 0.06  | 0.72  | 1.04  | 0.78  | 1.86  | 1.83  | Hypothetical protein yieG [c_4637]                                      |
| <i>yjcf</i> | -0.02 | -0.49 | 0.16  | 0.13  | 0.25  | 0.94  | 0.53  | "orf, hypothetical protein [b4066]"                                     |
| <i>yjgZ</i> | -0.12 | -0.16 | -0.19 | -0.20 | 0.01  | 0.51  | 0.37  | "orf, hypothetical protein [b4277]"                                     |
| <i>yjhC</i> | -0.34 | -0.80 | -0.39 | -0.01 | 2.09  | 2.84  | 2.73  | putative dehydrogenase [b4280]  |
| <i>yjhe</i> | 0.27  | 0.23  | 1.21  | 1.37  | 1.43  | 2.05  | 2.11  | "orf, hypothetical protein [b4282]"                                     |
| <i>ykgM</i> | -0.02 | 1.20  | 3.32  | 2.97  | 4.21  | 5.27  | 5.90  | putative ribosomal protein [b0296]                                      |
| <i>ynbD</i> | -0.10 | -0.25 | -0.14 | -0.02 | -0.06 | 0.40  | 0.14  | putative enzymes [Z2316]  |
| <i>ynfA</i> | 0.34  | -0.07 | 0.70  | 0.99  | 1.10  | 0.96  | 1.40  | "orf, hypothetical protein [b1582]"                                     |
| <i>yoeB</i> | -0.06 | 0.05  | 0.35  | 0.41  | 0.56  | 1.26  | 1.26  | toxin of the YoeB-YefM toxin-antitoxin system [b4539]                   |
| <i>yohF</i> | 0.00  | 0.09  | 0.03  | 0.45  | 0.39  | 0.61  | 0.53  | putative oxidoreductase [b2137]   |
| <i>ypdE</i> | -0.12 | -0.21 | 0.00  | -0.31 | 0.23  | 0.57  | 0.58  | "orf, hypothetical protein [b2384]"                                     |
| <i>yphC</i> | 0.01  | -0.36 | -0.40 | -0.27 | -0.35 | -0.12 | -0.22 | Hypothetical zinc-type alcohol dehydrogenase-like protein yphC [c_3067] |
| <i>yqcE</i> | 0.10  | -0.23 | -0.44 | -0.18 | 0.25  | 0.47  | 0.55  | putative transport protein [Z4086]                                      |
| <i>yrbF</i> | -0.22 | -0.43 | 0.26  | 0.43  | 0.59  | 0.97  | 1.26  | putative ATP-binding component of a transport system [b3195]            |
| <i>ytfI</i> | -0.03 | -0.66 | -0.13 | -0.22 | 1.10  | 1.81  | 2.59  | "orf, hypothetical protein [b4215]"                                     |

|            |       |       |       |       |       |       |       |   |
|------------|-------|-------|-------|-------|-------|-------|-------|---|
| Z0390      | 0.06  | -0.25 | 0.16  | 0.23  | 0.04  | -0.05 | -0.01 | orf Unknown function [Z0390]                                |
| Z0414      | 0.11  | -0.26 | 0.04  | 0.55  | 1.14  | 0.26  | 0.08  | orf Unknown function [Z0414]                                |
| Z1218      | -0.10 | -0.20 | -0.04 | -0.11 | 0.25  | 0.38  | 0.42  | "orf, hypothetical protein [Z1218]"                         |
| Z1362      | 0.23  | -0.13 | -0.01 | 0.28  | -0.04 | 0.37  | 0.06  | unknown protein encoded by cryptic prophage CP-933M [Z1362] |
| Z1507      | -0.10 | -0.08 | -0.05 | -0.24 | 0.01  | 0.63  | 0.55  | putative enzyme [Z1507]                                     |
| Z2286      | -0.08 | -0.68 | -0.73 | -0.50 | 0.46  | 0.46  | 1.12  | putative membrane transport protein [Z2286]                 |
| Z3306      | 0.00  | -0.26 | -0.08 | -0.10 | -0.14 | 0.22  | 0.09  | unknown protein encoded within prophage CP-933V [Z3306]     |
| Z4045      | -0.09 | -0.17 | -0.08 | 0.01  | -0.12 | 0.19  | -0.08 | orf hypothetical protein [Z4045]                            |
| Z4046      | -0.03 | -0.28 | -0.04 | 0.17  | -0.06 | 0.19  | -0.02 | orf hypothetical protein [Z4046]                            |
| Z4105      | -0.12 | -0.19 | -0.88 | -0.87 | -0.37 | 0.33  | 0.36  | putative transport protein [Z4105]                          |
| Z5154      | 0.06  | -0.07 | 0.08  | -0.03 | 0.21  | 0.47  | 0.66  | orf Unknown function [Z5154]                                |
| Z5868      | -0.03 | -0.25 | -0.06 | -0.09 | 0.01  | 0.27  | 0.22  | orf Unknown function [Z5868]                                |
| <i>zwf</i> | -0.18 | 0.13  | 0.13  | 0.19  | 0.53  | 0.62  | 0.77  | glucose-6-phosphate dehydrogenase [b1852]                   |