

Table S2. Genes repressed 4-fold and higher in *E. coli* L-form colonies versus classical colonies

| Fold change | Gene | Product-function |
|--|-------------|--|
| 1. CELLULAR PROCESSES | | |
| Adaptation, defense and survival | | |
| 0.17 | <i>speB</i> | agmatinase |
| Post-translation modification, protein turnover, chaperones | | |
| 0.24 | <i>citX</i> | 2'-(5"-triphosphoribosyl)-3'-dephospho-CoA:apo-citrate lyase |
| Transport | | |
| 0.15 | <i>nupC</i> | nucleoside (except guanosine) transporter |
| Motility and chemotaxis | | |
| 0.21 | <i>cheR</i> | chemotaxis regulator, protein-glutamate methyltransferase |
| 0.17 | <i>fliM</i> | flagellar motor switch protein FliM |
| 2. METABOLISM | | |
| Amino acid transport and metabolism | | |
| 0.15 | <i>astB</i> | succinylarginine dihydrolase |
| Carbohydrate transport and metabolism | | |
| 0.22 | <i>araA</i> | L-arabinose isomerase |
| 0.19 | <i>treC</i> | trehalose-6-phosphate hydrolase |
| Nucleotide transport, conversions and metabolism | | |
| 0.18 | <i>xdhA</i> | xanthine dehydrogenase subunit XdhA |
| 3. EXTRACHROMOSOMAL | | |
| Phage, phage-like element, transposon | | |
| 0.17 | <i>yeeL</i> | pseudogene |
| 0.16 | <i>yeeV</i> | CP4-44 prophage |
| 0.08 | <i>phnE</i> | pseudogene |
| 4. UNKNOWN AND POORLY CHARACTERIZED | | |
| Predicted function | | |
| 0.14 | <i>ydcS</i> | putative ABC transporter periplasmic binding protein |
| 0.13 | <i>phnJ</i> | component of a carbon-phosphorous lyase enzyme |
| 0.11 | <i>rdIA</i> | misc_RNA |
| 0.09 | <i>phnI</i> | carbon-phosphorus lyase complex subunit |
| 0.08 | <i>sokB</i> | misc_RNA |
| 0.07 | <i>rydB</i> | misc_RNA |
| 0.07 | <i>rdIB</i> | misc_RNA |
| 0.06 | <i>rdIC</i> | misc_RNA |
| Predicted protein | | |
| 0.15 | <i>ytfR</i> | putative ATP-binding component of a transport system |
| 0.13 | <i>ygfQ</i> | predicted protein |
| 0.09 | <i>ychS</i> | predicted protein |