

# Induced genes in $\Delta lrp$

| ID      | log2 | xfold | stdv | p-value  | gene         | protein name                                          |
|---------|------|-------|------|----------|--------------|-------------------------------------------------------|
| OE1014R | 0.9  | 1.9   | 0.1  | 9.61E-14 | <i>graD5</i> | glucose-1-phosphate thymidyltransferase (EC 2.7.7.24) |
| OE1059R | 1.3  | 2.5   | 0.2  | 3.42E-14 | -            | conserved hypothetical protein (nonfunctional)        |
| OE1060F | 0.4  | 1.3   | 0.3  | 1.76E-05 | -            | hypothetical protein                                  |
| OE1116F | 0.5  | 1.4   | 0.2  | 1.32E-08 | -            | conserved hypothetical protein                        |
| OE1151R | 0.5  | 1.4   | 0.2  | 1.30E-08 | -            | aminopeptidase homolog                                |
| OE1164R | 1.0  | 2.0   | 0.3  | 1.71E-09 | -            | phosphatase homolog                                   |
| OE1165R | 1.0  | 2.0   | 0.2  | 1.06E-10 | <i>serA3</i> | phosphoglycerate dehydrogenase (EC 1.1.1.95)          |
| OE1188F | 0.8  | 1.7   | 0.1  | 9.46E-13 | -            | conserved hypothetical protein                        |
| OE1205R | 0.6  | 1.5   | 0.1  | 5.59E-12 | -            | conserved hypothetical protein                        |
| OE1211F | 0.6  | 1.5   | 0.3  | 2.72E-06 | <i>hsp4</i>  | heat shock protein homolog                            |
| OE1254R | 0.9  | 1.9   | 0.1  | 1.65E-13 | -            | conserved hypothetical protein                        |
| OE1259R | 0.8  | 1.7   | 0.1  | 8.24E-14 | -            | conserved hypothetical protein                        |
| OE1260R | 0.9  | 1.8   | 0.1  | 2.46E-12 | <i>merA</i>  | mercury(II) reductase homolog                         |
| OE1299R | 0.5  | 1.4   | 0.1  | 1.28E-10 | <i>hop</i>   | halorhodopsin                                         |
| OE1362R | 0.7  | 1.6   | 0.3  | 1.68E-07 | -            | conserved hypothetical protein                        |
| OE1368R | 0.7  | 1.7   | 0.1  | 1.57E-11 | -            | conserved hypothetical protein                        |
| OE1371R | 0.7  | 1.6   | 0.1  | 7.58E-13 | <i>pfdB</i>  | prefoldin beta subunit                                |
| OE1405R | 1.0  | 2.0   | 0.3  | 4.66E-10 | -            | conserved hypothetical protein                        |
| OE1410F | 0.9  | 1.8   | 0.3  | 2.01E-08 | -            | conserved hypothetical protein                        |
| OE1414R | 1.0  | 2.0   | 0.2  | 4.60E-12 | <i>ftsZ4</i> | cell division protein ftsZ4                           |
| OE1425F | 0.7  | 1.6   | 0.1  | 1.77E-12 | -            | conserved hypothetical protein                        |
| OE1435R | 0.7  | 1.7   | 0.3  | 2.38E-08 | -            | conserved hypothetical protein                        |
| OE1461R | 0.6  | 1.5   | 0.2  | 6.39E-09 | -            | conserved hypothetical protein                        |
| OE1480F | 0.7  | 1.6   | 0.2  | 2.29E-08 | -            | ABC-type transport system substrate-binding protein   |
| OE1490R | 0.6  | 1.5   | 0.2  | 5.21E-08 | -            | conserved hypothetical protein                        |
| OE1510F | 0.6  | 1.5   | 0.4  | 1.93E-05 | -            | conserved hypothetical protein                        |
| OE1520R | 0.7  | 1.7   | 0.4  | 3.08E-06 | -            | hypothetical protein                                  |
| OE1536R | 0.8  | 1.7   | 0.4  | 1.20E-06 | <i>htr14</i> | transducer protein htr14                              |
| OE1539F | 1.3  | 2.5   | 0.1  | 2.22E-16 | -            | conserved hypothetical protein                        |
| OE1540R | 0.9  | 1.8   | 0.3  | 1.33E-08 | -            | conserved hypothetical protein                        |
| OE1541F | 0.6  | 1.5   | 0.2  | 3.71E-10 | -            | rhomboid family protein                               |
| OE1547R | 0.4  | 1.4   | 0.2  | 6.34E-08 | <i>arsA1</i> | probable anion-transporting ATPase (EC 3.6.1.-)       |
| OE1550F | 0.5  | 1.4   | 0.2  | 1.00E-07 | -            | conserved hypothetical protein                        |
| OE1566F | 1.1  | 2.1   | 0.3  | 2.40E-09 | -            | hypothetical protein                                  |
| OE1613R | 0.5  | 1.5   | 0.2  | 4.07E-09 | -            | probable acylaminoacyl-peptidase (EC 3.4.19.1)        |
| OE1632R | 0.7  | 1.7   | 0.2  | 9.31E-10 | <i>cyc</i>   | unspecific monooxygenase (EC 1.14.14.1)               |
| OE1641R | 0.8  | 1.8   | 0.1  | 6.28E-14 | <i>fad2</i>  | 3-hydroxybutyryl-CoA dehydratase (EC 4.2.1.55)        |
| OE1668R | 0.4  | 1.4   | 0.1  | 2.53E-10 | -            | conserved hypothetical protein                        |
| OE1669F | 0.4  | 1.4   | 0.2  | 2.87E-08 | -            | glucose 1-dehydrogenase homolog                       |
| OE1698R | 1.4  | 2.7   | 0.3  | 1.25E-11 | <i>oxr4</i>  | probable oxidoreductase (EC 1.1.1.-)                  |
| OE1722R | 1.0  | 2.0   | 0.2  | 1.00E-10 | -            | homolog to N-acetyltransferase                        |
| OE1726F | 0.6  | 1.5   | 0.2  | 5.15E-09 | <i>acs1</i>  | acetate--CoA ligase (EC 6.2.1.1)                      |
| OE1748R | 0.5  | 1.4   | 0.2  | 1.11E-08 | <i>cna</i>   | rRNA methylase homolog                                |
| OE1752F | 0.5  | 1.4   | 0.2  | 2.73E-09 | <i>ppd</i>   | 3-isopropylmalate dehydratase homolog                 |
| OE1761R | 0.9  | 1.8   | 0.3  | 1.15E-07 | -            | conserved hypothetical protein                        |
| OE1763F | 1.1  | 2.1   | 0.2  | 7.58E-13 | -            | conserved hypothetical protein                        |
| OE1765R | 1.0  | 2.0   | 0.2  | 1.79E-11 | <i>pan2</i>  | probable proteasome regulatory subunit                |
| OE1778R | 0.9  | 1.8   | 0.2  | 1.46E-09 | <i>oxr6</i>  | probable oxidoreductase (EC 1.1.1.-)                  |
| OE1792F | 0.9  | 1.9   | 0.4  | 6.62E-07 | -            | conserved hypothetical protein                        |
| OE1793F | 0.6  | 1.5   | 0.2  | 1.08E-09 | -            | conserved hypothetical protein                        |
| OE1806R | 1.1  | 2.1   | 0.2  | 5.17E-11 | -            | probable periplasmic protein                          |
| OE1823F | 0.7  | 1.6   | 0.2  | 1.15E-08 | -            | hypothetical protein                                  |
| OE1858F | 0.6  | 1.5   | 0.1  | 4.35E-11 | -            | conserved hypothetical protein                        |

|           |     |     |     |          |              |                                                           |
|-----------|-----|-----|-----|----------|--------------|-----------------------------------------------------------|
| OE1888R   | 0.4 | 1.4 | 0.2 | 4.17E-08 | -            | conserved hypothetical protein                            |
| OE1898A1F | 0.6 | 1.5 | 0.1 | 1.06E-10 | -            | hypothetical protein                                      |
| OE1899R   | 1.3 | 2.4 | 0.6 | 4.38E-07 | -            | conserved hypothetical protein                            |
| OE1900F   | 0.7 | 1.7 | 0.1 | 7.77E-13 | -            | conserved hypothetical protein                            |
| OE1903F   | 0.8 | 1.7 | 0.2 | 3.02E-10 | -            | glycine-rich protein                                      |
| OE1934R   | 1.0 | 1.9 | 0.2 | 1.31E-11 | <i>edp</i>   | proteinase IV (EC 3.4.-.-)                                |
| OE1936R   | 1.1 | 2.1 | 0.2 | 7.31E-13 | -            | conserved hypothetical protein                            |
| OE1944R   | 0.5 | 1.4 | 0.1 | 5.71E-10 | <i>aspB2</i> | probable aspartate aminotransferase (EC 2.6.1.1)          |
| OE1947F   | 1.1 | 2.1 | 0.3 | 2.54E-09 | -            | conserved hypothetical protein                            |
| OE1969F   | 1.2 | 2.3 | 0.2 | 3.40E-12 | -            | CBS domain protein                                        |
| OE1978R   | 0.6 | 1.5 | 0.1 | 6.88E-15 | -            | hypothetical protein                                      |
| OE2006F   | 0.4 | 1.4 | 0.3 | 1.80E-05 | -            | probable ABC-type transport system ATP-binding protein    |
| OE2007F   | 0.7 | 1.6 | 0.2 | 2.83E-10 | -            | probable hydrolase                                        |
| OE2010R   | 0.5 | 1.4 | 0.1 | 3.84E-14 | -            | conserved hypothetical protein                            |
| OE2024F   | 0.6 | 1.5 | 0.3 | 1.55E-06 | -            | conserved hypothetical protein                            |
| OE2041R   | 0.6 | 1.5 | 0.1 | 1.38E-11 | -            | conserved hypothetical protein                            |
| OE2047R   | 0.6 | 1.5 | 0.2 | 1.00E-09 | -            | conserved hypothetical protein                            |
| OE2054F   | 0.7 | 1.6 | 0.2 | 5.63E-09 | -            | conserved hypothetical protein                            |
| OE2055F   | 0.6 | 1.5 | 0.1 | 5.33E-12 | -            | conserved hypothetical protein                            |
| OE2058R   | 0.8 | 1.8 | 0.1 | 7.64E-14 | <i>afsQ2</i> | probable signal-transducing histidine kinase              |
| OE2097F   | 0.5 | 1.4 | 0.2 | 6.34E-07 | -            | upsA domain protein                                       |
| OE2118F   | 0.4 | 1.3 | 0.1 | 1.73E-09 | <i>tfeA</i>  | transcription initiation factor IIE alpha subunit homolog |
| OE2128F   | 0.9 | 1.9 | 0.2 | 1.82E-12 | -            | phoU protein homolog                                      |
| OE2133R   | 0.5 | 1.4 | 0.2 | 3.19E-06 | <i>aldH2</i> | aldehyde dehydrogenase (EC 1.2.1.-)                       |
| OE2170R   | 0.6 | 1.5 | 0.1 | 1.68E-10 | <i>tmpC</i>  | probable periplasmic substrate-binding protein            |
| OE2186R   | 0.8 | 1.7 | 0.4 | 1.11E-06 | <i>tatA</i>  | sec-independent protein translocase component tatA        |
| OE2187F   | 0.5 | 1.4 | 0.1 | 3.63E-11 | -            | conserved hypothetical protein                            |
| OE2199F   | 0.8 | 1.8 | 0.1 | 8.88E-16 | <i>adh5</i>  | probable alcohol dehydrogenase (EC 1.1.1.1)               |
| OE2217R   | 0.6 | 1.6 | 0.4 | 3.55E-05 | <i>mobA</i>  | molybdopterin-guanine dinucleotide biosynthesis protein A |
| OE2225F   | 0.7 | 1.6 | 0.2 | 5.37E-09 | <i>dmsB</i>  | dimethylsulfoxide reductase (EC 1.8.-.-) subunit B        |
| OE2243R   | 0.5 | 1.4 | 0.3 | 7.60E-06 | <i>cynT</i>  | probable carbonate dehydratase (EC 4.2.1.1)               |
| OE2249R   | 0.6 | 1.5 | 0.2 | 3.59E-07 | -            | transducer protein weak homolog                           |
| OE2254R   | 0.6 | 1.5 | 0.3 | 4.37E-06 | -            | conserved hypothetical protein                            |
| OE2259F   | 0.5 | 1.4 | 0.3 | 6.30E-06 | -            | conserved hypothetical protein                            |
| OE2306F   | 0.5 | 1.4 | 0.3 | 2.93E-06 | -            | conserved hypothetical protein                            |
| OE2311R   | 0.5 | 1.4 | 0.2 | 2.26E-08 | <i>udp2</i>  | uridine phosphorylase (EC 2.4.2.3)                        |
| OE2319R   | 0.7 | 1.6 | 0.2 | 5.39E-10 | -            | conserved hypothetical protein                            |
| OE2332F   | 0.9 | 1.9 | 0.4 | 4.94E-07 | <i>hakA</i>  | probable kynureninase (EC 3.7.1.3)                        |
| OE2343R   | 0.4 | 1.4 | 0.1 | 1.41E-08 | -            | probable ABC-type transport system ATP-binding protein    |
| OE2358F   | 0.5 | 1.4 | 0.1 | 3.61E-11 | <i>acaB2</i> | probable nonspecific lipid-transfer protein               |
| OE2367F   | 1.7 | 3.2 | 0.2 | 2.58E-14 | <i>aldH3</i> | aldehyde dehydrogenase                                    |
| OE2378R   | 0.4 | 1.3 | 0.1 | 1.53E-08 | <i>parA1</i> | parA domain protein                                       |
| OE2427F   | 0.6 | 1.5 | 0.1 | 1.39E-10 | -            | conserved hypothetical protein                            |
| OE2450F   | 1.3 | 2.5 | 0.3 | 9.25E-12 | <i>acs2</i>  | acetate-CoA ligase (EC 6.2.1.1)                           |
| OE2451R   | 0.9 | 1.8 | 0.2 | 5.90E-12 | -            | probable oxidoreductase                                   |
| OE2453R   | 0.5 | 1.4 | 0.1 | 3.38E-11 | -            | conserved hypothetical protein                            |
| OE2455F   | 0.8 | 1.7 | 0.4 | 3.16E-06 | -            | conserved hypothetical protein                            |
| OE2513F   | 0.9 | 1.9 | 0.5 | 3.28E-06 | -            | conserved hypothetical protein                            |
| OE2514F   | 0.4 | 1.3 | 0.1 | 4.03E-11 | -            | hypothetical protein                                      |
| OE2515F   | 1.0 | 2.0 | 0.4 | 3.54E-08 | -            | conserved hypothetical protein                            |
| OE2521R   | 0.5 | 1.4 | 0.2 | 2.83E-06 | -            | conserved hypothetical protein                            |
| OE2524R   | 0.9 | 1.9 | 0.2 | 4.37E-10 | <i>udg1</i>  | UDPglucose 6-dehydrogenase (EC 1.1.1.22)                  |
| OE2527F   | 1.0 | 2.0 | 0.3 | 7.79E-10 | -            | conserved hypothetical protein                            |
| OE2538R   | 0.4 | 1.3 | 0.2 | 1.55E-06 | -            | conserved hypothetical protein                            |
| OE2573F   | 0.4 | 1.3 | 0.3 | 3.87E-05 | -            | conserved hypothetical protein                            |
| OE2585R   | 0.8 | 1.8 | 0.4 | 1.39E-06 | -            | conserved hypothetical protein                            |

|         |     |      |     |          |               |                                                                   |
|---------|-----|------|-----|----------|---------------|-------------------------------------------------------------------|
| OE2612F | 0.5 | 1.4  | 0.1 | 6.35E-09 | -             | conserved hypothetical protein                                    |
| OE2618R | 0.8 | 1.7  | 0.1 | 8.32E-12 | -             | conserved hypothetical protein                                    |
| OE2622R | 0.5 | 1.4  | 0.2 | 8.62E-08 | <i>porB</i>   | pyruvate-ferredoxin oxidoreductase (EC 1.2.7.1) $\beta$ -subunit  |
| OE2623R | 0.5 | 1.4  | 0.1 | 1.02E-09 | <i>porA</i>   | pyruvate-ferredoxin oxidoreductase (EC 1.2.7.1) $\alpha$ -subunit |
| OE2642R | 0.4 | 1.4  | 0.1 | 4.11E-12 | -             | hypothetical protein                                              |
| OE2648F | 0.9 | 1.9  | 0.1 | 6.99E-14 | -             | conserved hypothetical protein                                    |
| OE2674R | 0.5 | 1.4  | 0.1 | 1.53E-09 | <i>ksgA</i>   | rRNA (adenine-N6                                                  |
| OE2676R | 1.1 | 2.2  | 0.3 | 9.76E-11 | -             | conserved hypothetical protein                                    |
| OE2695F | 0.8 | 1.7  | 0.2 | 2.02E-10 | <i>flgXXX</i> | flagellin flgXXX precursor                                        |
| OE2696F | 1.2 | 2.3  | 0.3 | 3.70E-11 | -             | conserved hypothetical protein                                    |
| OE2697R | 1.5 | 2.8  | 0.2 | 3.77E-15 | <i>pqqE2</i>  | probable coenzyme PQQ synthesis protein E                         |
| OE2698R | 1.6 | 3.1  | 0.1 | 2.22E-16 | -             | hypothetical protein                                              |
| OE2700F | 1.8 | 3.6  | 0.1 | 0        | <i>pqqE1</i>  | probable coenzyme PQQ synthesis protein E                         |
| OE2703F | 2.8 | 6.9  | 0.6 | 4.16E-11 | -             | probable copper-containing oxidoreductase                         |
| OE2708R | 1.1 | 2.1  | 0.4 | 3.41E-08 | <i>sod1</i>   | superoxide dismutase (EC 1.15.1.1) 1 (Mn containing)              |
| OE2710F | 0.7 | 1.6  | 0.2 | 6.42E-09 | <i>acd3</i>   | probable acyl/butyryl-CoA dehydrogenase (EC 1.3.99.-)             |
| OE2712R | 0.4 | 1.3  | 0.2 | 1.90E-06 | -             | probable signal-transducing histidine kinase                      |
| OE2734F | 0.6 | 1.5  | 0.1 | 7.34E-12 | <i>hutU</i>   | urocanate hydratase (EC 4.2.1.49)                                 |
| OE2762R | 0.7 | 1.6  | 0.2 | 9.36E-10 | <i>aroA</i>   | 3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19)        |
| OE2808F | 1.3 | 2.5  | 0.5 | 1.09E-07 | -             | conserved hypothetical protein                                    |
| OE2809R | 0.7 | 1.7  | 0.3 | 1.93E-08 | -             | translation initiation factor aIF-2 beta subunit                  |
| OE2813R | 0.4 | 1.3  | 0.2 | 4.94E-06 | -             | conserved hypothetical protein                                    |
| OE2821F | 1.3 | 2.4  | 0.2 | 9.60E-12 | -             | conserved hypothetical protein                                    |
| OE2825F | 0.4 | 1.4  | 0.1 | 1.93E-09 | <i>moaC</i>   | molybdenum cofactor biosynthesis protein C                        |
| OE2827R | 1.1 | 2.2  | 0.2 | 3.34E-12 | <i>hflX2</i>  | probable GTP-binding protein                                      |
| OE2828R | 1.2 | 2.2  | 0.3 | 1.87E-09 | -             | conserved hypothetical protein                                    |
| OE2856F | 0.4 | 1.4  | 0.1 | 9.05E-09 | -             | conserved hypothetical protein                                    |
| OE2863R | 0.6 | 1.5  | 0.1 | 4.43E-11 | -             | conserved hypothetical protein                                    |
| OE2872F | 1.4 | 2.7  | 0.4 | 3.93E-09 | -             | conserved hypothetical protein                                    |
| OE2874F | 0.7 | 1.6  | 0.1 | 1.34E-11 | -             | conserved hypothetical protein                                    |
| OE2900F | 0.8 | 1.7  | 0.4 | 2.88E-06 | -             | conserved hypothetical protein                                    |
| OE2906R | 1.4 | 2.7  | 0.4 | 2.11E-09 | <i>sod2</i>   | superoxide dismutase (EC 1.15.1.1) 2                              |
| OE2909F | 0.7 | 1.7  | 0.2 | 8.80E-10 | -             | conserved hypothetical protein                                    |
| OE2922F | 0.8 | 1.7  | 0.2 | 3.59E-09 | -             | conserved hypothetical protein                                    |
| OE2961F | 0.6 | 1.5  | 0.1 | 3.05E-11 | <i>kinA1</i>  | probable signal-transducing histidine kinase                      |
| OE2973F | 1.8 | 3.5  | 0.3 | 6.11E-13 | -             | conserved hypothetical protein                                    |
| OE2988R | 0.6 | 1.5  | 0.1 | 1.01E-11 | -             | conserved hypothetical protein                                    |
| OE2989R | 1.1 | 2.1  | 0.2 | 3.04E-11 | -             | conserved hypothetical protein                                    |
| OE2991F | 1.2 | 2.3  | 0.2 | 2.60E-13 | -             | transcription factor TFB homolog                                  |
| OE3008F | 1.0 | 1.9  | 0.3 | 7.74E-09 | -             | conserved hypothetical protein                                    |
| OE3030R | 0.7 | 1.6  | 0.2 | 3.04E-10 | -             | conserved hypothetical protein                                    |
| OE3065R | 0.6 | 1.5  | 0.1 | 1.12E-10 | <i>serA2</i>  | phosphoglycerate dehydrogenase (EC 1.1.1.95)                      |
| OE3073R | 1.8 | 3.4  | 0.4 | 3.52E-11 | -             | dodecin                                                           |
| OE3093R | 1.0 | 2.0  | 0.3 | 6.22E-10 | <i>crtB1</i>  | phytoene synthase (EC 2.5.1.32)                                   |
| OE3095R | 1.5 | 2.9  | 0.3 | 1.68E-11 | -             | conserved hypothetical protein                                    |
| OE3101R | 1.0 | 2.0  | 0.4 | 3.43E-07 | <i>bat</i>    | bacterioopsin activator                                           |
| OE3102R | 0.8 | 1.8  | 0.3 | 7.86E-09 | <i>brp</i>    | bop gene expression regulator brp                                 |
| OE3106F | 1.6 | 2.9  | 0.2 | 8.88E-16 | <i>bop</i>    | bacteriorhodopsin precursor                                       |
| OE3107F | 0.5 | 1.4  | 0.1 | 2.21E-10 | -             | conserved hypothetical protein                                    |
| OE3136F | 3.8 | 13.9 | 0.6 | 6.17E-13 | -             | conserved hypothetical protein                                    |
| OE3152R | 0.5 | 1.4  | 0.1 | 1.96E-10 | <i>pelA</i>   | probable peptide chain release factor aRF1                        |
| OE3153R | 0.5 | 1.4  | 0.1 | 2.59E-10 | -             | conserved hypothetical protein                                    |
| OE3187R | 0.9 | 1.9  | 0.3 | 7.53E-08 | -             | upsA domain protein                                               |
| OE3203R | 1.3 | 2.4  | 0.3 | 1.50E-10 | -             | conserved hypothetical protein                                    |
| OE3204R | 1.6 | 3.0  | 0.3 | 3.88E-12 | -             | conserved hypothetical protein                                    |
| OE3207F | 0.5 | 1.4  | 0.1 | 8.29E-12 | <i>cbiT</i>   | probable precorrin-8W decarboxylase (EC 1.-.-.-)                  |

|           |     |     |     |          |              |                                                          |
|-----------|-----|-----|-----|----------|--------------|----------------------------------------------------------|
| OE3229R   | 0.5 | 1.4 | 0.1 | 5.37E-12 | <i>hmcA</i>  | probable chelatase (EC 4.99.1.-) (cobalamin cluster)     |
| OE3278R   | 0.5 | 1.4 | 0.1 | 1.48E-13 | <i>gcvT</i>  | glycine cleavage system protein T (EC 2.1.2.10)          |
| OE3284R   | 0.9 | 1.9 | 0.1 | 8.54E-13 | -            | conserved hypothetical protein                           |
| OE3304R   | 0.6 | 1.5 | 0.2 | 3.10E-08 | -            | conserved hypothetical protein                           |
| OE3305F   | 0.6 | 1.5 | 0.1 | 1.51E-12 | <i>rfcB</i>  | replication factor C large subunit                       |
| OE3334R   | 0.9 | 1.9 | 0.1 | 0        | <i>trpD1</i> | anthranilate phosphoribosyltransferase (EC 2.4.2.18)     |
| OE3347F   | 0.8 | 1.8 | 0.2 | 1.11E-09 | <i>htrI</i>  | transducer protein htrI                                  |
| OE3349F   | 1.2 | 2.3 | 0.2 | 1.67E-12 | -            | coenzyme F420-quinone oxidoreductase 42K s.u. homolog    |
| OE3381R   | 0.4 | 1.4 | 0.2 | 8.13E-08 | <i>crtII</i> | phytoene dehydrogenase (EC 1.14.99.-)                    |
| OE3424R   | 0.9 | 1.9 | 0.3 | 8.00E-09 | -            | conserved hypothetical protein                           |
| OE3447F   | 0.6 | 1.6 | 0.1 | 2.06E-12 | -            | conserved hypothetical protein                           |
| OE3451A1F | 0.7 | 1.6 | 0.1 | 1.16E-12 | -            | conserved hypothetical protein                           |
| OE3458R   | 0.5 | 1.4 | 0.1 | 2.77E-10 | -            | probable oxidoreductase (versicolorin reductase homolog) |
| OE3462R   | 0.7 | 1.6 | 0.2 | 3.12E-09 | -            | hypothetical protein                                     |
| OE3491R   | 0.7 | 1.6 | 0.1 | 1.32E-11 | -            | heat shock protein homolog                               |
| OE3500R   | 0.4 | 1.3 | 0.1 | 1.24E-08 | <i>nirH</i>  | probable heme biosynthesis protein nirH/G                |
| OE3513R   | 0.7 | 1.7 | 0.3 | 9.88E-08 | -            | hypothetical protein                                     |
| OE3541R   | 1.7 | 3.3 | 0.3 | 1.86E-12 | <i>hsp1</i>  | probable heat shock protein                              |
| OE3542R   | 1.9 | 3.8 | 0.6 | 1.94E-09 | -            | glutamine-rich alkaline protein                          |
| OE3562R   | 0.5 | 1.4 | 0.1 | 1.49E-09 | -            | conserved hypothetical protein                           |
| OE3565F   | 0.8 | 1.8 | 0.2 | 2.91E-11 | <i>moaB</i>  | molybdenum cofactor biosynthesis protein B               |
| OE3566F   | 0.4 | 1.3 | 0.1 | 1.67E-11 | -            | conserved hypothetical protein                           |
| OE3595R   | 0.6 | 1.5 | 0.2 | 3.57E-10 | <i>moaD</i>  | molybdopterin (MPT) converting factor                    |
| OE3612R   | 0.8 | 1.8 | 0.1 | 3.39E-13 | <i>basB</i>  | chemotactic signal transduction protein basB             |
| OE3659F   | 0.4 | 1.4 | 0.1 | 7.95E-11 | -            | conserved hypothetical protein                           |
| OE3661F   | 0.4 | 1.3 | 0.1 | 2.28E-10 | <i>trp2</i>  | ABC-type transport system ATP-binding protein            |
| OE3668F   | 1.5 | 2.8 | 0.2 | 1.32E-12 | -            | upsA domain protein                                      |
| OE3681R   | 0.6 | 1.5 | 0.3 | 4.40E-07 | -            | conserved hypothetical protein                           |
| OE3691F   | 0.9 | 1.8 | 0.4 | 5.07E-07 | <i>trpD2</i> | anthranilate phosphoribosyltransferase (EC 2.4.2.18)     |
| OE3714F   | 1.4 | 2.6 | 0.1 | 2.22E-16 | -            | conserved hypothetical protein                           |
| OE3717F   | 0.9 | 1.8 | 0.1 | 2.44E-15 | <i>nolA</i>  | NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 32K subunit |
| OE3718F   | 0.7 | 1.6 | 0.1 | 5.11E-15 | <i>ftsZ3</i> | cell division protein                                    |
| OE3728R   | 0.8 | 1.7 | 0.2 | 1.44E-09 | -            | conserved hypothetical protein                           |
| OE3752R   | 0.7 | 1.6 | 0.2 | 1.94E-10 | -            | mutT domain protein                                      |
| OE3766R   | 0.8 | 1.7 | 0.2 | 2.57E-09 | -            | hypothetical protein                                     |
| OE3798R   | 0.6 | 1.5 | 0.3 | 3.08E-06 | -            | conserved hypothetical protein                           |
| OE3807R   | 0.4 | 1.3 | 0.2 | 4.96E-07 | <i>yjbG</i>  | oligoendopeptidase                                       |
| OE3814R   | 0.6 | 1.5 | 0.4 | 2.31E-05 | -            | conserved hypothetical protein                           |
| OE3815R   | 1.8 | 3.4 | 0.2 | 2.66E-15 | -            | conserved hypothetical protein                           |
| OE3836F   | 0.8 | 1.7 | 0.2 | 5.66E-10 | <i>yyaI</i>  | probable acetyltransferase                               |
| OE3843F   | 0.8 | 1.7 | 0.2 | 1.28E-09 | <i>nadE</i>  | NAD <sup>+</sup> synthase (EC 6.3.1.5)                   |
| OE3846R   | 0.5 | 1.4 | 0.1 | 1.87E-11 | <i>fadI</i>  | enoyl/3-hydroxybutyryl-CoA dehydratase (EC 4.2.1.-)      |
| OE3864R   | 1.0 | 2.0 | 0.3 | 3.71E-10 | -            | conserved hypothetical protein                           |
| OE3892R   | 0.4 | 1.4 | 0.1 | 2.02E-09 | -            | beta-lactamase homolog                                   |
| OE3903F   | 0.8 | 1.8 | 0.5 | 2.00E-05 | -            | conserved hypothetical protein                           |
| OE3925R   | 0.4 | 1.4 | 0.3 | 2.35E-05 | <i>cctB</i>  | thermosome beta subunit                                  |
| OE3942R   | 2.2 | 4.5 | 0.3 | 3.89E-14 | -            | hypothetical protein                                     |
| OE3946F   | 1.0 | 1.9 | 0.2 | 1.66E-10 | -            | conserved hypothetical protein                           |
| OE3947R   | 0.5 | 1.4 | 0.1 | 3.98E-11 | -            | conserved hypothetical protein                           |
| OE3998R   | 0.5 | 1.4 | 0.1 | 4.66E-10 | -            | conserved hypothetical protein                           |
| OE4011R   | 0.5 | 1.4 | 0.2 | 1.61E-07 | -            | conserved hypothetical protein                           |
| OE4018F   | 0.5 | 1.4 | 0.2 | 5.28E-07 | -            | conserved hypothetical protein                           |
| OE4032R   | 0.6 | 1.5 | 0.2 | 4.94E-09 | -            | conserved hypothetical protein                           |
| OE4033R   | 0.7 | 1.6 | 0.1 | 1.01E-13 | <i>dbp</i>   | probable DNA helicase (enhancer-binding protein homolog) |
| OE4039F   | 0.6 | 1.5 | 0.1 | 1.13E-14 | -            | conserved hypothetical protein                           |
| OE4052F   | 0.5 | 1.4 | 0.1 | 4.66E-10 | <i>mcm</i>   | DNA helicase (EC 3.6.1.-) mcm (intein-containing)        |

|         |     |     |     |          |               |                                                          |
|---------|-----|-----|-----|----------|---------------|----------------------------------------------------------|
| OE4056R | 0.4 | 1.3 | 0.1 | 1.77E-10 | <i>tfbA</i>   | transcription initiation factor TFB                      |
| OE4065R | 0.8 | 1.7 | 0.3 | 1.86E-07 | <i>hit1</i>   | histidine triad family protein                           |
| OE4073R | 0.9 | 1.8 | 0.3 | 8.41E-08 | <i>hcpB</i>   | halocyanin hcpB                                          |
| OE4077F | 1.9 | 3.9 | 0.2 | 5.77E-15 | -             | hypothetical protein                                     |
| OE4080F | 0.5 | 1.4 | 0.3 | 1.69E-05 | -             | conserved hypothetical protein                           |
| OE4099R | 0.5 | 1.4 | 0.2 | 4.60E-08 | -             | conserved hypothetical protein                           |
| OE4113F | 0.5 | 1.4 | 0.2 | 2.72E-08 | <i>oxdhA1</i> | 2-oxoacid dehydrogenase (EC 1.2.4.-)                     |
| OE4122R | 0.9 | 1.9 | 0.3 | 4.21E-09 | <i>cctA</i>   | thermosome alpha subunit                                 |
| OE4127R | 0.5 | 1.4 | 0.1 | 4.44E-12 | -             | conserved hypothetical protein                           |
| OE4146F | 1.2 | 2.3 | 0.2 | 1.26E-11 | <i>tbpE</i>   | TATA-binding transcription initiation factor             |
| OE4152R | 0.4 | 1.3 | 0.1 | 4.54E-10 | <i>hisG</i>   | ATP phosphoribosyltransferase (EC 2.4.2.17)              |
| OE4159F | 1.3 | 2.5 | 0.1 | 0        | <i>achY</i>   | adenosylhomocysteinase (EC 3.3.1.1)                      |
| OE4184F | 0.8 | 1.8 | 0.1 | 6.45E-13 | <i>orc6</i>   | cell division control protein cdc6 homolog               |
| OE4190F | 0.9 | 1.8 | 0.2 | 3.65E-12 | <i>pmm</i>    | probable phosphohexomutase (EC 5.4.2.-)                  |
| OE4196R | 1.0 | 1.9 | 0.3 | 1.21E-09 | -             | conserved hypothetical protein                           |
| OE4218F | 1.2 | 2.2 | 0.2 | 3.10E-13 | <i>hisA</i>   | PRFPR-imidazolecarboxamide isomerase (EC 5.3.1.16)       |
| OE4240F | 0.6 | 1.5 | 0.1 | 1.55E-10 | -             | conserved hypothetical protein                           |
| OE4244F | 0.4 | 1.3 | 0.1 | 5.95E-11 | -             | conserved hypothetical protein                           |
| OE4276F | 0.4 | 1.4 | 0.1 | 1.65E-12 | <i>hemC</i>   | hydroxymethylbilane synthase (EC 4.3.1.8)                |
| OE4283R | 0.8 | 1.7 | 0.2 | 4.72E-10 | -             | signal-transducing histidine kinase / response regulator |
| OE4296F | 0.6 | 1.5 | 0.3 | 4.37E-06 | -             | hypothetical protein                                     |
| OE4320R | 1.0 | 2.0 | 0.4 | 2.93E-08 | -             | conserved hypothetical protein                           |
| OE4325F | 0.7 | 1.6 | 0.2 | 7.87E-10 | <i>rad24b</i> | probable DNA helicase                                    |
| OE4331R | 0.5 | 1.4 | 0.1 | 2.89E-09 | <i>tnaA</i>   | tryptophanase (EC 4.1.99.1)                              |
| OE4365F | 0.7 | 1.6 | 0.2 | 2.45E-08 | -             | conserved hypothetical protein                           |
| OE4384R | 1.6 | 3.0 | 0.4 | 6.59E-11 | -             | conserved hypothetical protein                           |
| OE4399F | 0.5 | 1.5 | 0.1 | 9.10E-15 | <i>oxr8</i>   | probable oxidoreductase (EC 1.1.1.-)                     |
| OE4414R | 0.7 | 1.6 | 0.3 | 3.04E-07 | -             | salinity-regulated protein homolog                       |
| OE4418R | 0.4 | 1.3 | 0.1 | 1.46E-10 | -             | hypothetical protein                                     |
| OE4419R | 0.4 | 1.4 | 0.1 | 1.73E-08 | <i>argH</i>   | argininosuccinate lyase (EC 4.3.2.1)                     |
| OE4420R | 1.2 | 2.3 | 0.2 | 2.05E-11 | <i>argG</i>   | argininosuccinate synthase (EC 6.3.4.5)                  |
| OE4436R | 0.4 | 1.3 | 0.1 | 1.39E-10 | <i>lta</i>    | L-allo-threonine aldolase (EC 4.2.1.-)                   |
| OE4449R | 0.5 | 1.4 | 0.1 | 3.51E-12 | -             | hypothetical protein                                     |
| OE4456R | 0.5 | 1.4 | 0.2 | 8.73E-08 | <i>gimC</i>   | prefoldin alpha subunit                                  |
| OE4459R | 0.6 | 1.5 | 0.1 | 1.80E-10 | <i>rpl31R</i> | ribosomal protein L31.eR                                 |
| OE4461F | 0.5 | 1.4 | 0.2 | 7.48E-09 | -             | conserved hypothetical protein                           |
| OE4492F | 0.4 | 1.4 | 0.1 | 2.45E-12 | -             | conserved hypothetical protein                           |
| OE4496R | 0.6 | 1.5 | 0.2 | 8.52E-08 | <i>fer4</i>   | ferredoxin (3Fe-4S)(4Fe-4S)                              |
| OE4500R | 0.6 | 1.6 | 0.2 | 1.79E-09 | <i>acd6</i>   | probable acyl/butyryl-CoA dehydrogenase (EC 1.3.99.-)    |
| OE4509F | 1.6 | 3.0 | 0.5 | 2.06E-08 | -             | nonhistone chromosomal protein                           |
| OE4529F | 0.4 | 1.3 | 0.2 | 3.29E-06 | <i>aldH1</i>  | aldehyde dehydrogenase (EC 1.2.1.-)                      |
| OE4543R | 0.5 | 1.5 | 0.2 | 1.06E-07 | <i>rimI1</i>  | probable N-terminal acetyltransferase                    |
| OE4544R | 0.8 | 1.7 | 0.1 | 3.79E-13 | -             | upsA domain protein                                      |
| OE4562R | 0.7 | 1.6 | 0.1 | 4.54E-13 | <i>entB</i>   | N-carbamoylsarcosine amidase homolog                     |
| OE4563F | 0.5 | 1.4 | 0.3 | 2.82E-05 | -             | conserved hypothetical protein                           |
| OE4565F | 0.6 | 1.5 | 0.3 | 1.55E-07 | -             | conserved hypothetical protein                           |
| OE4612F | 1.2 | 2.2 | 0.2 | 3.63E-13 | <i>hly</i>    | halolysin R4 (EC 3.4.21.-)                               |
| OE4621F | 0.6 | 1.5 | 0.3 | 2.65E-07 | -             | ADP-ribose pyrophosphatase homolog                       |
| OE4633F | 0.6 | 1.5 | 0.1 | 1.15E-10 | -             | conserved hypothetical protein                           |
| OE4637R | 0.6 | 1.5 | 0.3 | 8.04E-06 | <i>gbp4</i>   | probable GTP-binding protein                             |
| OE4638F | 0.6 | 1.5 | 0.2 | 3.04E-07 | -             | hypothetical protein                                     |
| OE4648F | 0.6 | 1.5 | 0.2 | 6.62E-10 | <i>trxA2</i>  | thioredoxin                                              |
| OE4650R | 0.8 | 1.7 | 0.3 | 2.45E-08 | -             | hypothetical protein                                     |
| OE4651F | 0.4 | 1.3 | 0.2 | 2.26E-07 | -             | probable ribose-1                                        |
| OE4654F | 0.4 | 1.3 | 0.1 | 6.71E-10 | <i>thiD</i>   | phosphomethylpyrimidine kinase (EC 2.7.4.7)              |
| OE4665R | 0.4 | 1.4 | 0.1 | 2.40E-14 | <i>hflXI</i>  | GTP-binding protein                                      |

|           |     |     |     |          |              |                                                              |
|-----------|-----|-----|-----|----------|--------------|--------------------------------------------------------------|
| OE4671R   | 0.4 | 1.4 | 0.2 | 6.00E-08 | -            | conserved hypothetical protein                               |
| OE4707R   | 1.4 | 2.7 | 0.2 | 5.68E-13 | -            | conserved hypothetical protein                               |
| OE4759F   | 0.5 | 1.5 | 0.4 | 4.49E-05 | <i>csg</i>   | cell surface glycoprotein precursor                          |
| OE5106F   | 0.5 | 1.4 | 0.3 | 7.82E-06 | <i>trkA7</i> | trkA domain protein                                          |
| OE5136R   | 0.9 | 1.9 | 0.2 | 1.58E-11 | -            | conserved hypothetical protein                               |
| OE5142F   | 0.4 | 1.3 | 0.1 | 1.48E-10 | <i>ftsZ5</i> | cell division protein ftsZ5                                  |
| OE5160F   | 1.3 | 2.5 | 0.1 | 0        | <i>gldA1</i> | glycerol dehydrogenase (EC 1.1.1.6)                          |
| OE5162D1F | 2.5 | 5.7 | 0.6 | 2.72E-10 | -            | conserved hypothetical protein                               |
| OE5178F   | 0.5 | 1.4 | 0.1 | 9.27E-09 | -            | conserved hypothetical protein                               |
| OE5186R   | 0.4 | 1.4 | 0.1 | 3.13E-13 | <i>perA</i>  | catalase (EC 1.11.1.6) (including: peroxidase (EC 1.11.1.7)) |
| OE5187R   | 0.7 | 1.6 | 0.1 | 3.44E-11 | -            | probable hydrolase                                           |
| OE5204R   | 1.0 | 2.0 | 0.2 | 1.09E-12 | <i>arcD</i>  | arginine/ornithine antiporter                                |
| OE5205R   | 1.2 | 2.3 | 0.2 | 1.86E-12 | <i>arcB</i>  | ornithine carbamoyltransferase (EC 2.1.3.3)                  |
| OE5243F   | 0.8 | 1.7 | 0.2 | 6.58E-10 | <i>car</i>   | transducer protein car                                       |
| OE5276F   | 0.4 | 1.3 | 0.2 | 2.53E-07 | -            | conserved hypothetical protein                               |
| OE5322R   | 0.5 | 1.4 | 0.2 | 1.19E-06 | -            | conserved hypothetical protein                               |
| OE5378R   | 0.5 | 1.4 | 0.2 | 7.15E-07 | -            | hypothetical protein                                         |
| OE6308F   | 1.6 | 3.0 | 0.2 | 2.02E-14 | -            | hypothetical protein                                         |
| OE6345R   | 0.6 | 1.5 | 0.3 | 6.66E-06 | -            | hypothetical protein                                         |
| OE6352F   | 1.8 | 3.5 | 0.5 | 7.66E-10 | -            | IS1341-type transposase (TCE32)                              |
| OE7065F   | 0.7 | 1.7 | 0.2 | 1.18E-10 | <i>cydA1</i> | cytochrome d ubiquinol oxidase (EC 1.10.3.-) subunit I       |
| OE7129F   | 0.5 | 1.4 | 0.3 | 2.13E-05 | -            | conserved hypothetical protein                               |
| OE7187F   | 0.9 | 1.9 | 0.4 | 2.03E-07 | -            | conserved hypothetical protein                               |

#### Repressed genes in $\Delta lrp$

| ID      | log2 | fold | stdv | p-value  | gene          | protein name                                                  |
|---------|------|------|------|----------|---------------|---------------------------------------------------------------|
| OE1004F | -0.4 | -1.4 | 0.1  | 1.36E-10 | -             | probable ABC-type transport system ATP-binding protein        |
| OE1018F | -0.7 | -1.6 | 0.1  | 2.15E-11 | -             | sugar transferase                                             |
| OE1031F | -1.4 | -2.6 | 0.4  | 5.31E-10 | -             | probable transposase (ISH10)                                  |
| OE1047R | -0.7 | -1.7 | 0.2  | 7.61E-09 | -             | hypothetical protein                                          |
| OE1054F | -0.7 | -1.6 | 0.3  | 3.00E-07 | -             | hypothetical protein                                          |
| OE1055R | -0.5 | -1.4 | 0.1  | 5.66E-12 | -             | conserved hypothetical protein                                |
| OE1076F | -1.0 | -2.0 | 0.2  | 3.30E-11 | -             | cell division control protein cdc6 homolog                    |
| OE1078F | -0.5 | -1.4 | 0.2  | 1.03E-07 | <i>graD6</i>  | glucose-1-phosphate thymidyltransferase (EC 2.7.7.24)         |
| OE1080F | -0.6 | -1.5 | 0.3  | 4.08E-06 | -             | probable polysaccharide export protein                        |
| OE1094R | -1.9 | -3.7 | 0.2  | 7.11E-15 | -             | probable transposase (ISH10)                                  |
| OE1100F | -0.7 | -1.7 | 0.2  | 3.74E-09 | -             | hypothetical protein                                          |
| OE1101R | -0.4 | -1.4 | 0.2  | 2.20E-07 | -             | hypothetical protein                                          |
| OE1107R | -0.4 | -1.4 | 0.2  | 1.69E-07 | -             | conserved hypothetical protein                                |
| OE1112R | -0.6 | -1.5 | 0.2  | 2.57E-08 | <i>lpb</i>    | probable glycosyltransferase (EC 2.-.-.-)                     |
| OE1121F | -1.3 | -2.5 | 0.4  | 6.66E-09 | -             | conserved hypothetical protein                                |
| OE1134F | -0.5 | -1.4 | 0.2  | 1.51E-08 | -             | conserved hypothetical protein                                |
| OE1162R | -0.7 | -1.6 | 0.3  | 1.88E-06 | <i>cspD1</i>  | probable cold shock protein                                   |
| OE1171F | -0.6 | -1.5 | 0.1  | 6.25E-12 | <i>rmeMa</i>  | type I restriction-modification system DNA-methyltransferase  |
| OE1183F | -0.5 | -1.4 | 0.1  | 1.82E-12 | -             | hypothetical protein                                          |
| OE1197R | -0.6 | -1.5 | 0.2  | 5.66E-08 | -             | hypothetical protein                                          |
| OE1226F | -0.5 | -1.4 | 0.2  | 6.14E-07 | -             | conserved hypothetical protein                                |
| OE1239F | -1.2 | -2.3 | 0.1  | 4.44E-16 | -             | hypothetical protein                                          |
| OE1294R | -0.7 | -1.6 | 0.2  | 3.37E-10 | <i>rpl15R</i> | ribosomal protein L15.eR                                      |
| OE1372R | -0.6 | -1.5 | 0.2  | 1.24E-09 | <i>rpoP</i>   | DNA-directed RNA polymerase (EC 2.7.7.6) subunit P            |
| OE1439F | -0.7 | -1.7 | 0.3  | 1.25E-07 | -             | probable IS200-type transposase (TCE31)                       |
| OE1462R | -0.5 | -1.4 | 0.2  | 1.44E-07 | -             | nicotinamide-nucleotide adenyltransferase (EC 2.7.7.1)        |
| OE1478R | -0.6 | -1.6 | 0.2  | 1.95E-09 | <i>tbfF</i>   | transcription initiation factor TFB                           |
| OE1505F | -0.8 | -1.8 | 0.1  | 2.26E-12 | -             | probable 5'-methylthioadenosine phosphorylase (nonfunctional) |
| OE1506R | -0.5 | -1.4 | 0.2  | 2.11E-07 | -             | probable transposase (ISH8/ISH26)                             |

|           |      |      |     |          |              |                                                                       |
|-----------|------|------|-----|----------|--------------|-----------------------------------------------------------------------|
| OE1553F   | -0.6 | -1.5 | 0.2 | 1.95E-07 | -            | conserved hypothetical protein                                        |
| OE1560R   | -0.4 | -1.4 | 0.1 | 6.84E-09 | -            | conserved hypothetical protein                                        |
| OE1584R   | -1.3 | -2.5 | 0.2 | 3.45E-13 | -            | conserved hypothetical protein                                        |
| OE1620R   | -0.9 | -1.8 | 0.1 | 5.94E-13 | <i>purH</i>  | p-ribosylglycinamide formyltransferase (EC 2.1.2.2)                   |
| OE1623F   | -1.0 | -2.0 | 0.2 | 4.26E-11 | <i>purB</i>  | adenylosuccinate lyase (EC 4.3.2.2)                                   |
| OE1675R   | -0.5 | -1.4 | 0.2 | 1.59E-08 | <i>pstB2</i> | ABC-type phosphate transport system ATP-binding protein               |
| OE1678R   | -0.9 | -1.8 | 0.2 | 2.02E-09 | <i>pstC2</i> | probable ABC-type phosphate transport system permease protein         |
| OE1684F   | -0.9 | -1.9 | 0.2 | 2.00E-12 | <i>nodP</i>  | probable sulfate adenylyltransferase (EC 2.7.7.4) small subunit       |
| OE1687F   | -0.8 | -1.8 | 0.1 | 1.55E-13 | <i>aspS</i>  | aspartate-tRNA ligase (EC 6.1.1.12)                                   |
| OE1707R   | -0.5 | -1.5 | 0.1 | 3.51E-10 | -            | transcription regulator homolog                                       |
| OE1710R   | -0.9 | -1.9 | 0.2 | 1.58E-11 | <i>korB</i>  | oxoglutarate-ferredoxin oxidoreductase (EC 1.2.7.3) $\beta$ -subunit  |
| OE1711R   | -1.5 | -2.9 | 0.4 | 5.56E-10 | <i>korA</i>  | oxoglutarate-ferredoxin oxidoreductase (EC 1.2.7.3) $\alpha$ -subunit |
| OE1797R   | -0.8 | -1.8 | 0.2 | 8.68E-10 | <i>sirR</i>  | transcription regulator sirR                                          |
| OE1817R   | -0.6 | -1.5 | 0.2 | 8.60E-09 | -            | conserved hypothetical protein                                        |
| OE1840R   | -0.4 | -1.3 | 0.2 | 2.81E-08 | <i>apt</i>   | purine phosphoribosyltransferase (EC 2.4.2.7)                         |
| OE1867R   | -0.6 | -1.5 | 0.3 | 3.01E-06 | -            | conserved hypothetical protein                                        |
| OE1872R   | -0.5 | -1.4 | 0.1 | 9.13E-11 | <i>petD</i>  | probable menaquinol-cytochrome-c reductase (EC 1.10.2.-)              |
| OE1919R   | -0.6 | -1.5 | 0.1 | 1.97E-13 | -            | conserved hypothetical protein                                        |
| OE1951F   | -0.8 | -1.7 | 0.2 | 1.75E-10 | <i>purK</i>  | phosphoribosylaminoimidazole carboxylase (EC 4.1.1.21)                |
| OE1956F   | -0.4 | -1.4 | 0.2 | 3.39E-07 | <i>nuoCD</i> | NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) subunit CD               |
| OE1959F   | -0.7 | -1.7 | 0.4 | 5.02E-06 | <i>nuoJ1</i> | NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) subunit J1               |
| OE1964F   | -0.6 | -1.5 | 0.4 | 1.71E-05 | <i>nuoL</i>  | NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) subunit L                |
| OE1981R   | -0.6 | -1.5 | 0.1 | 5.68E-11 | -            | hypothetical protein                                                  |
| OE2020F   | -0.5 | -1.5 | 0.1 | 1.28E-11 | <i>fbp</i>   | fructose-bisphosphatase (EC 3.1.3.11)                                 |
| OE2044F   | -0.6 | -1.5 | 0.2 | 4.60E-09 | -            | probable heavy metal binding protein                                  |
| OE2046F   | -0.8 | -1.8 | 0.2 | 2.15E-10 | -            | conserved hypothetical protein                                        |
| OE2130F   | -0.6 | -1.5 | 0.1 | 6.49E-11 | -            | conserved hypothetical protein                                        |
| OE2142R   | -0.6 | -1.5 | 0.2 | 3.57E-08 | -            | phospholipase D                                                       |
| OE2165R   | -0.7 | -1.7 | 0.1 | 1.17E-12 | <i>rps15</i> | ribosomal protein S15                                                 |
| OE2230F   | -0.8 | -1.7 | 0.1 | 3.50E-13 | -            | conserved hypothetical protein                                        |
| OE2267F   | -0.4 | -1.3 | 0.2 | 2.61E-08 | <i>rpoL</i>  | DNA-directed RNA polymerase (EC 2.7.7.6) subunit L                    |
| OE2268R   | -0.4 | -1.3 | 0.2 | 7.43E-07 | <i>hisF</i>  | imidazoleglycerol-phosphate synthase (EC 2.4.2.-) subunit hisF        |
| OE2269F   | -0.6 | -1.5 | 0.1 | 6.06E-14 | -            | hypothetical protein                                                  |
| OE2274R   | -1.0 | -2.0 | 0.1 | 2.48E-13 | <i>purL</i>  | phosphoribosylformylglycinamide synthase (EC 6.3.5.3)                 |
| OE2307F   | -0.7 | -1.6 | 0.2 | 2.25E-08 | -            | NADH dehydrogenase homolog                                            |
| OE2309F   | -0.5 | -1.5 | 0.2 | 3.76E-08 | -            | hypothetical protein                                                  |
| OE2310F   | -0.5 | -1.4 | 0.1 | 2.81E-10 | -            | conserved hypothetical protein                                        |
| OE2348R   | -0.8 | -1.7 | 0.1 | 6.09E-13 | -            | probable ABC-type transport system substrate-binding protein          |
| OE2374R   | -0.5 | -1.4 | 0.1 | 3.81E-10 | <i>cheW2</i> | purine-binding chemotaxis protein cheW2                               |
| OE2406R   | -1.0 | -2.0 | 0.1 | 0        | <i>cheR</i>  | protein-glutamate O-methyltransferase (EC 2.1.1.80) cheR              |
| OE2432C1F | -0.8 | -1.7 | 0.3 | 1.12E-07 | -            | hypothetical protein                                                  |
| OE2458R   | -0.5 | -1.4 | 0.2 | 9.16E-09 | <i>guaB</i>  | IMP dehydrogenase (EC 1.1.1.205)                                      |
| OE2460F   | -0.5 | -1.4 | 0.1 | 4.04E-13 | -            | conserved hypothetical protein                                        |
| OE2465R   | -0.5 | -1.4 | 0.1 | 2.09E-12 | -            | hypothetical protein                                                  |
| OE2473F   | -0.5 | -1.4 | 0.3 | 1.08E-05 | -            | glutaredoxin homolog                                                  |
| OE2530F   | -0.5 | -1.5 | 0.1 | 1.74E-11 | <i>graD4</i> | glucose-1-phosphate thymidyltransferase (EC 2.7.7.24)                 |
| OE2531F   | -0.8 | -1.7 | 0.1 | 1.59E-13 | -            | conserved hypothetical protein                                        |
| OE2533F   | -1.7 | -3.3 | 0.1 | 0        | -            | hypothetical protein                                                  |
| OE2536F   | -0.4 | -1.3 | 0.2 | 2.31E-07 | -            | hypothetical protein                                                  |
| OE2537F   | -0.5 | -1.4 | 0.1 | 5.66E-09 | <i>rfbQ</i>  | sugar transferase homolog                                             |
| OE2540R   | -0.5 | -1.5 | 0.2 | 4.38E-08 | -            | probable transposase (ISH6/ISHS1)                                     |
| OE2547R   | -0.6 | -1.5 | 0.2 | 2.50E-09 | <i>exoM</i>  | probable glycosyltransferase (EC 2.-.-.-)                             |
| OE2569R   | -0.4 | -1.3 | 0.2 | 7.60E-08 | -            | sulfite oxidase homolog                                               |
| OE2572F   | -0.7 | -1.6 | 0.2 | 1.90E-09 | -            | conserved hypothetical protein                                        |
| OE2579F   | -0.5 | -1.5 | 0.1 | 1.16E-09 | <i>purA</i>  | adenylosuccinate synthase (EC 6.3.4.4)                                |
| OE2603R   | -0.7 | -1.6 | 0.2 | 1.33E-08 | <i>rpl11</i> | ribosomal protein L11                                                 |

|         |      |      |     |          |               |                                                                  |
|---------|------|------|-----|----------|---------------|------------------------------------------------------------------|
| OE2605R | -0.6 | -1.5 | 0.1 | 2.28E-10 | -             | conserved hypothetical protein                                   |
| OE2627F | -0.7 | -1.6 | 0.2 | 5.19E-09 | <i>rps13</i>  | ribosomal protein S13                                            |
| OE2629F | -0.9 | -1.8 | 0.5 | 3.54E-06 | <i>rps11</i>  | ribosomal protein S11                                            |
| OE2631F | -1.2 | -2.3 | 0.1 | 4.44E-16 | <i>rpoD</i>   | DNA-directed RNA polymerase (EC 2.7.7.6) subunit D               |
| OE2632F | -1.3 | -2.5 | 0.1 | 2.22E-16 | <i>rpl18R</i> | ribosomal protein L18.eR                                         |
| OE2633F | -1.2 | -2.4 | 0.3 | 3.75E-11 | <i>rpl13</i>  | ribosomal protein L13                                            |
| OE2635F | -0.8 | -1.8 | 0.4 | 2.98E-06 | <i>rps9</i>   | ribosomal protein S9                                             |
| OE2637F | -1.7 | -3.2 | 0.2 | 4.44E-16 | <i>rpoN</i>   | DNA-directed RNA polymerase (EC 2.7.7.6) subunit N               |
| OE2640F | -0.7 | -1.7 | 0.3 | 4.10E-08 | <i>eno</i>    | enolase (EC 4.2.1.11)                                            |
| OE2641F | -1.4 | -2.6 | 0.2 | 1.09E-14 | <i>rps2</i>   | ribosomal protein S2                                             |
| OE2683R | -0.7 | -1.6 | 0.2 | 2.54E-08 | <i>aef1b</i>  | translation elongation factor aEF-1 beta subunit                 |
| OE2715R | -0.5 | -1.4 | 0.1 | 3.19E-10 | -             | hypothetical protein                                             |
| OE2716R | -0.4 | -1.3 | 0.3 | 2.33E-05 | -             | hypothetical protein                                             |
| OE2727R | -0.5 | -1.4 | 0.2 | 9.45E-07 | -             | conserved hypothetical protein                                   |
| OE2740F | -1.0 | -2.0 | 0.3 | 1.59E-09 | -             | conserved hypothetical protein                                   |
| OE2744R | -0.4 | -1.3 | 0.2 | 1.23E-06 | -             | conserved hypothetical protein                                   |
| OE2745R | -0.5 | -1.4 | 0.3 | 5.24E-06 | <i>pgk</i>    | phosphoglycerate kinase (EC 2.7.2.3)                             |
| OE2750R | -0.6 | -1.5 | 0.2 | 4.18E-10 | -             | conserved hypothetical protein                                   |
| OE2753F | -0.8 | -1.8 | 0.1 | 2.37E-12 | <i>orc8</i>   | cell division control protein cdc6 homolog                       |
| OE2779F | -0.6 | -1.6 | 0.3 | 2.02E-06 | <i>pheP</i>   | amino acid transport protein (probable phenylalanine)            |
| OE2780F | -0.8 | -1.8 | 0.2 | 2.81E-09 | -             | hypothetical protein                                             |
| OE2782F | -1.1 | -2.1 | 0.3 | 7.28E-09 | <i>surE</i>   | probable stationary-phase survival protein                       |
| OE2847R | -0.8 | -1.7 | 0.2 | 8.91E-10 | -             | conserved hypothetical protein                                   |
| OE2853R | -0.6 | -1.5 | 0.3 | 6.04E-06 | <i>slyD</i>   | probable peptidylprolyl isomerase (EC 5.2.1.8)                   |
| OE2865R | -0.6 | -1.5 | 0.3 | 1.59E-06 | <i>sdhA</i>   | succinate dehydrogenase (EC 1.3.99.1) subunit A (flavoprotein)   |
| OE2903R | -0.5 | -1.4 | 0.2 | 9.18E-09 | -             | conserved hypothetical protein                                   |
| OE2946R | -0.6 | -1.5 | 0.3 | 6.03E-07 | -             | conserved hypothetical protein                                   |
| OE3017R | -1.1 | -2.2 | 0.1 | 5.33E-15 | <i>ush</i>    | UDP-sugar hydrolase (EC 3.6.1.45) / 5'-nucleotidase (EC 3.1.3.5) |
| OE3062F | -0.5 | -1.4 | 0.3 | 8.96E-06 | <i>rps17R</i> | ribosomal protein S17.eR                                         |
| OE3063F | -0.5 | -1.4 | 0.1 | 8.32E-11 | <i>asd</i>    | aspartate-semialdehyde dehydrogenase (EC 1.2.1.11)               |
| OE3069R | -0.7 | -1.6 | 0.2 | 1.53E-09 | -             | conserved hypothetical protein                                   |
| OE3116F | -0.9 | -1.8 | 0.3 | 2.76E-09 | -             | conserved hypothetical protein                                   |
| OE3118F | -0.6 | -1.5 | 0.3 | 7.97E-07 | -             | conserved hypothetical protein                                   |
| OE3132F | -0.6 | -1.5 | 0.2 | 8.05E-08 | -             | conserved hypothetical protein                                   |
| OE3139R | -1.6 | -2.9 | 0.3 | 7.69E-12 | <i>purF</i>   | amidophosphoribosyltransferase (EC 2.4.2.14)                     |
| OE3141R | -1.1 | -2.2 | 0.1 | 1.13E-14 | <i>rpl37R</i> | ribosomal protein L37.eR                                         |
| OE3142R | -0.9 | -1.9 | 0.2 | 1.53E-11 | <i>snp</i>    | SM protein                                                       |
| OE3155R | -0.8 | -1.8 | 0.2 | 6.81E-10 | -             | conserved hypothetical protein                                   |
| OE3262R | -0.9 | -1.9 | 0.1 | 7.25E-13 | -             | conserved hypothetical protein                                   |
| OE3317R | -0.6 | -1.5 | 0.1 | 7.15E-10 | <i>cbiQ</i>   | probable cobalt transport protein CbiQ                           |
| OE3319R | -0.5 | -1.4 | 0.1 | 1.53E-10 | <i>cbiM</i>   | CbiM protein (unassigned function)                               |
| OE3337F | -0.8 | -1.8 | 0.2 | 1.37E-11 | -             | insertion element protein (ISH2)                                 |
| OE3384R | -0.6 | -1.5 | 0.2 | 4.13E-08 | -             | conserved hypothetical protein                                   |
| OE3390F | -0.8 | -1.7 | 0.2 | 3.01E-11 | <i>rpl23</i>  | ribosomal protein L23                                            |
| OE3394F | -0.8 | -1.8 | 0.2 | 4.22E-11 | <i>rpl22</i>  | ribosomal protein L22                                            |
| OE3395F | -0.5 | -1.4 | 0.1 | 3.37E-10 | <i>rps3</i>   | ribosomal protein S3                                             |
| OE3396F | -0.5 | -1.4 | 0.2 | 8.14E-08 | <i>rpl29</i>  | ribosomal protein L29                                            |
| OE3404F | -0.5 | -1.4 | 0.2 | 3.44E-07 | <i>rpl24</i>  | ribosomal protein L24                                            |
| OE3405F | -0.6 | -1.5 | 0.3 | 2.18E-06 | <i>rps4R</i>  | ribosomal protein S4.eR                                          |
| OE3407F | -0.5 | -1.4 | 0.2 | 7.10E-07 | <i>rpl5</i>   | ribosomal protein L5                                             |
| OE3429F | -0.6 | -1.5 | 0.3 | 9.32E-07 | <i>cmk</i>    | cytidylate kinase (EC 2.7.4.14)                                  |
| OE3481R | -0.6 | -1.5 | 0.2 | 5.07E-08 | <i>htrII</i>  | transducer protein htrII                                         |
| OE3486R | -0.5 | -1.4 | 0.2 | 6.35E-08 | <i>speB</i>   | agmatinase (EC 3.5.3.11)                                         |
| OE3487R | -0.6 | -1.5 | 0.3 | 1.31E-06 | <i>eif5a</i>  | translation initiation factor aIF-5A                             |
| OE3547F | -0.6 | -1.5 | 0.3 | 3.47E-06 | -             | conserved hypothetical protein                                   |
| OE3554F | -0.9 | -1.9 | 0.5 | 1.92E-06 | <i>carB</i>   | carbamoyl-phosphate synthase (EC 6.3.-.-) large subunit          |



|         |      |      |     |          |               |                                                                                                         |
|---------|------|------|-----|----------|---------------|---------------------------------------------------------------------------------------------------------|
| OE3556R | -1.5 | -2.8 | 0.1 | 1.11E-15 | <i>carA</i>   | carbamoyl-phosphate synthase (EC 6.3.-.-) small subunit                                                 |
| OE3558F | -0.7 | -1.6 | 0.1 | 1.64E-12 | <i>trh3</i>   | probable transcription regulator                                                                        |
| OE3560F | -0.5 | -1.4 | 0.2 | 3.99E-08 | <i>idi3</i>   | probable isopentenyl-diphosphate delta-isomerase (EC 5.3.3.2) 3                                         |
| OE3571R | -0.5 | -1.4 | 0.2 | 2.76E-08 | <i>guaAb</i>  | GMP synthase (glutamine-hydrolyzing) (EC 6.3.5.2)                                                       |
| OE3572R | -1.4 | -2.6 | 0.3 | 4.69E-11 | <i>pyrG</i>   | CTP synthase (EC 6.3.4.2)                                                                               |
| OE3582F | -0.7 | -1.7 | 0.3 | 5.43E-07 | <i>cspD2</i>  | probable cold shock protein                                                                             |
| OE3639F | -0.4 | -1.4 | 0.3 | 1.12E-05 | -             | conserved hypothetical protein                                                                          |
| OE3652F | -0.5 | -1.4 | 0.1 | 5.99E-13 | -             | small multidrug export protein                                                                          |
| OE3654R | -0.8 | -1.8 | 0.1 | 6.37E-14 | -             | hypothetical protein                                                                                    |
| OE3655R | -0.4 | -1.3 | 0.1 | 3.01E-08 | -             | hypothetical protein                                                                                    |
| OE3688F | -0.4 | -1.3 | 0.1 | 9.02E-10 | -             | conserved hypothetical protein                                                                          |
| OE3712R | -0.6 | -1.5 | 0.2 | 1.98E-09 | <i>oxdhA2</i> | 2-oxoacid dehydrogenase (EC 1.2.4.-)<br>p-ribosylaminoimidazolesuccinocarboxamide synthase (EC 6.3.2.6) |
| OE3724F | -0.8 | -1.7 | 0.4 | 4.16E-06 | <i>purC</i>   | phosphoribosylformylglycinamide synthase (EC 6.3.5.3)                                                   |
| OE3731R | -1.6 | -2.9 | 0.3 | 3.02E-11 | <i>purQ</i>   | conserved hypothetical protein                                                                          |
| OE3732R | -1.3 | -2.4 | 0.3 | 1.04E-09 | -             | conserved hypothetical protein                                                                          |
| OE3749R | -0.5 | -1.4 | 0.3 | 3.30E-05 | <i>tgtAI</i>  | queuine tRNA-ribosyltransferase (EC 2.4.2.29)                                                           |
| OE3784R | -0.5 | -1.5 | 0.2 | 2.20E-09 | <i>secD</i>   | preprotein-export translocase subunit secD                                                              |
| OE3787R | -0.5 | -1.4 | 0.3 | 1.94E-05 | <i>secF</i>   | preprotein-export translocase subunit secF                                                              |
| OE3822R | -0.7 | -1.7 | 0.3 | 1.71E-07 | -             | conserved hypothetical protein                                                                          |
| OE3829R | -0.4 | -1.4 | 0.1 | 3.92E-12 | -             | conserved hypothetical protein                                                                          |
| OE3866R | -0.4 | -1.4 | 0.1 | 1.78E-14 | <i>gcp</i>    | probable O-sialoglycoprotein endopeptidase (EC 3.4.24.57)                                               |
| OE3907R | -0.8 | -1.7 | 0.1 | 1.83E-12 | <i>phnE</i>   | ABC-type transport system permease protein                                                              |
| OE3908R | -0.8 | -1.8 | 0.2 | 1.44E-10 | <i>phnC</i>   | ABC-type transport system ATP-binding protein                                                           |
| OE3922R | -0.6 | -1.5 | 0.3 | 1.85E-05 | <i>glnA</i>   | glutamate--ammonia ligase (EC 6.3.1.2)                                                                  |
| OE3923F | -3.1 | -8.8 | 1.1 | 3.99E-08 | <i>lrp</i>    | global transcription regulator                                                                          |
| OE3950R | -1.9 | -3.8 | 0.4 | 4.62E-11 | -             | conserved hypothetical protein                                                                          |
| OE3963R | -2.6 | -6.1 | 0.4 | 7.05E-13 | <i>ribB</i>   | 3,4-dihydroxy-2-butanone 4-phosphate synthase (EC 5.4.99.-)                                             |
| OE3964R | -2.9 | -7.5 | 0.2 | 0        | -             | conserved hypothetical protein                                                                          |
| OE3984R | -0.5 | -1.4 | 0.1 | 1.11E-10 | <i>atpB</i>   | H <sup>+</sup> -transporting two-sector ATPase (EC 3.6.3.14) subunit B.a                                |
| OE3985R | -0.6 | -1.6 | 0.2 | 1.62E-09 | <i>atpA</i>   | H <sup>+</sup> -transporting two-sector ATPase (EC 3.6.3.14) subunit A.a                                |
| OE3986R | -0.9 | -1.9 | 0.1 | 5.57E-13 | <i>atpF</i>   | H <sup>+</sup> -transporting two-sector ATPase (EC 3.6.3.14) subunit F.a                                |
| OE3987R | -0.4 | -1.4 | 0.2 | 2.31E-06 | <i>atpC</i>   | H <sup>+</sup> -transporting two-sector ATPase (EC 3.6.3.14) subunit C.a                                |
| OE4012F | -0.4 | -1.3 | 0.1 | 1.14E-08 | -             | conserved hypothetical protein                                                                          |
| OE4047R | -0.6 | -1.5 | 0.1 | 4.72E-12 | -             | phage PhiH1 repressor protein homolog                                                                   |
| OE4049R | -0.5 | -1.5 | 0.2 | 2.45E-09 | -             | hypothetical protein                                                                                    |
| OE4187R | -0.7 | -1.6 | 0.4 | 9.90E-06 | -             | probable DNA-binding protein                                                                            |
| OE4201R | -0.5 | -1.4 | 0.2 | 1.48E-06 | <i>flaK</i>   | probable preflagellin peptidase                                                                         |
| OE4223R | -0.6 | -1.5 | 0.2 | 1.18E-08 | -             | conserved hypothetical protein                                                                          |
| OE4300R | -0.9 | -1.8 | 0.1 | 3.75E-14 | -             | conserved hypothetical protein                                                                          |
| OE4301R | -1.1 | -2.2 | 0.1 | 2.22E-16 | <i>ykfD</i>   | ABC-type transport system ATP-binding protein                                                           |
| OE4302R | -1.3 | -2.4 | 0.1 | 8.88E-16 | <i>oppD2</i>  | ABC-type oligopeptide transport system ATP-binding protein                                              |
| OE4303R | -0.9 | -1.9 | 0.2 | 5.07E-12 | <i>dppC2</i>  | ABC-type transport system permease protein                                                              |
| OE4304R | -0.9 | -1.9 | 0.3 | 1.43E-08 | <i>dppB1</i>  | ABC-type transport system permease protein                                                              |
| OE4367R | -0.4 | -1.3 | 0.1 | 2.28E-08 | -             | conserved hypothetical protein                                                                          |
| OE4380F | -0.6 | -1.5 | 0.2 | 1.09E-08 | <i>orc7</i>   | cell division control protein cdc6 homolog                                                              |
| OE4385F | -0.5 | -1.4 | 0.1 | 5.98E-11 | -             | conserved hypothetical protein                                                                          |
| OE4387F | -0.5 | -1.4 | 0.3 | 1.00E-05 | -             | hypothetical protein                                                                                    |
| OE4435F | -0.9 | -1.9 | 0.2 | 2.23E-10 | -             | hypothetical protein                                                                                    |
| OE4523F | -0.4 | -1.3 | 0.3 | 4.95E-05 | -             | hypothetical protein                                                                                    |
| OE4524F | -0.5 | -1.4 | 0.1 | 3.81E-09 | -             | hypothetical protein                                                                                    |
| OE4552F | -1.2 | -2.3 | 0.4 | 1.97E-08 | <i>dppB2</i>  | ABC-type transport system permease protein                                                              |
| OE4572R | -0.9 | -1.9 | 0.1 | 2.51E-13 | <i>valS</i>   | valine-tRNA ligase (EC 6.1.1.9)                                                                         |
| OE4585R | -0.4 | -1.3 | 0.2 | 3.80E-07 | -             | hypothetical protein                                                                                    |
| OE4610R | -0.7 | -1.6 | 0.1 | 9.10E-15 | -             | dCTP deaminase homolog                                                                                  |
| OE4628R | -0.7 | -1.6 | 0.2 | 2.79E-10 | -             | conserved hypothetical protein                                                                          |

|           |      |      |     |          |              |                                                                |
|-----------|------|------|-----|----------|--------------|----------------------------------------------------------------|
| OE4683F   | -2.9 | -7.6 | 0.1 | 0        | <i>ribC</i>  | riboflavin synthase (EC 2.5.1.9) alpha subunit                 |
| OE4720R   | -1.0 | -2.0 | 0.2 | 1.63E-10 | <i>rps10</i> | ribosomal protein S10                                          |
| OE4721R   | -0.8 | -1.7 | 0.2 | 1.50E-10 | <i>aef1a</i> | translation elongation factor aEF-1 alpha subunit              |
| OE4735R   | -0.6 | -1.5 | 0.2 | 1.82E-09 | <i>rps7</i>  | ribosomal protein S7                                           |
| OE4740R   | -0.5 | -1.4 | 0.1 | 1.48E-12 | <i>rpoA1</i> | DNA-directed RNA polymerase (EC 2.7.7.6) subunit A' (chain A)  |
| OE4741R   | -0.5 | -1.4 | 0.3 | 3.70E-06 | <i>rpoB1</i> | DNA-directed RNA polymerase (EC 2.7.7.6) subunit B'            |
| OE5015F   | -0.7 | -1.6 | 0.3 | 3.92E-08 | -            | probable transposase (ISH8/ISH26)                              |
| OE5022F   | -0.8 | -1.7 | 0.3 | 2.90E-08 | -            | conserved hypothetical protein                                 |
| OE5031R   | -0.8 | -1.8 | 0.1 | 1.57E-12 | -            | conserved hypothetical protein                                 |
| OE5062R   | -0.6 | -1.5 | 0.2 | 1.05E-08 | -            | IS1341-type transposase (TCE31)                                |
| OE5065R   | -0.6 | -1.5 | 0.1 | 3.80E-11 | -            | conserved hypothetical protein                                 |
| OE5143F   | -0.5 | -1.4 | 0.3 | 9.41E-06 | -            | probable transport protein                                     |
| OE5162R   | -0.7 | -1.6 | 0.1 | 1.91E-14 | <i>orc5</i>  | cell division control protein cdc6 homolog                     |
| OE5201F   | -0.9 | -1.9 | 0.2 | 1.35E-10 | <i>pyrB</i>  | aspartate carbamoyltransferase (EC 2.1.3.2) catalytic subunit  |
| OE5202F   | -1.0 | -2.0 | 0.3 | 1.50E-08 | <i>pyrI</i>  | aspartate carbamoyltransferase (EC 2.1.3.2) regulatory subunit |
| OE5211F   | -0.7 | -1.6 | 0.1 | 7.23E-13 | -            | conserved hypothetical protein                                 |
| OE5234R   | -0.6 | -1.5 | 0.2 | 3.13E-07 | -            | conserved hypothetical protein (nonfunctional                  |
| OE5260F   | -1.2 | -2.3 | 0.2 | 2.49E-14 | -            | probable transposase (ISH10)                                   |
| OE5268R   | -0.5 | -1.4 | 0.1 | 7.43E-11 | -            | ABC-type transport system ATP-binding protein                  |
| OE5279R   | -1.1 | -2.2 | 0.3 | 1.14E-09 | -            | conserved hypothetical protein                                 |
| OE5307F   | -0.4 | -1.3 | 0.1 | 1.58E-11 | -            | ABC-type transport system ATP-binding protein                  |
| OE5325F   | -0.4 | -1.4 | 0.2 | 3.13E-07 | -            | conserved hypothetical protein                                 |
| OE5338R   | -1.5 | -2.8 | 0.1 | 1.11E-15 | -            | transposase homolog (ISH8/ISH26) (nonfunctional                |
| OE5340R   | -0.6 | -1.5 | 0.3 | 9.37E-07 | -            | transposase homolog (ISH8/ISH26) (nonfunctional                |
| OE5363R   | -0.9 | -1.9 | 0.2 | 5.96E-11 | -            | insertion element protein (ISH2)                               |
| OE5370R   | -1.1 | -2.2 | 0.3 | 7.41E-10 | -            | hypothetical protein                                           |
| OE5393F   | -1.1 | -2.2 | 0.2 | 3.70E-11 | -            | insertion element protein (ISH2)                               |
| OE5400F   | -0.6 | -1.5 | 0.2 | 1.12E-08 | -            | conserved hypothetical protein                                 |
| OE5407F   | -0.6 | -1.5 | 0.1 | 4.77E-11 | -            | probable transposase (ISH8/ISH26)                              |
| OE5448F   | -1.0 | -1.9 | 0.2 | 2.48E-10 | -            | IS1341-type transposase (TCE32)                                |
| OE6005R   | -0.5 | -1.4 | 0.2 | 7.45E-08 | -            | conserved hypothetical protein                                 |
| OE6006R   | -0.7 | -1.7 | 0.1 | 3.64E-14 | -            | conserved hypothetical protein                                 |
| OE6012F   | -1.1 | -2.2 | 0.3 | 9.99E-11 | -            | probable transposase (ISH6/ISHS1)                              |
| OE6027R   | -0.5 | -1.4 | 0.1 | 3.08E-13 | -            | hypothetical protein                                           |
| OE6032F   | -0.4 | -1.3 | 0.1 | 1.52E-09 | -            | conserved hypothetical protein                                 |
| OE6034F   | -0.8 | -1.7 | 0.2 | 2.76E-10 | -            | IS1341-type transposase (TCE32)                                |
| OE6046F   | -0.9 | -1.9 | 0.2 | 2.02E-11 | -            | conserved hypothetical protein                                 |
| OE6052R   | -0.5 | -1.4 | 0.3 | 8.81E-06 | -            | hypothetical protein                                           |
| OE6074R   | -1.5 | -2.9 | 0.1 | 0        | -            | hypothetical protein                                           |
| OE6075R   | -0.6 | -1.5 | 0.3 | 4.95E-06 | -            | probable transposase (ISH8/ISH26)                              |
| OE6079F   | -0.5 | -1.4 | 0.1 | 3.60E-09 | -            | conserved hypothetical protein                                 |
| OE6096A1R | -0.8 | -1.7 | 0.4 | 8.06E-07 | -            | conserved hypothetical protein                                 |
| OE6099F   | -0.7 | -1.6 | 0.1 | 1.71E-12 | -            | hypothetical protein                                           |
| OE6111A1F | -0.6 | -1.5 | 0.0 | 0        | -            | conserved hypothetical protein                                 |
| OE6113F   | -0.9 | -1.8 | 0.3 | 5.91E-09 | -            | conserved hypothetical protein                                 |
| OE6128R   | -0.4 | -1.3 | 0.1 | 2.00E-09 | -            | conserved hypothetical protein                                 |
| OE6130F   | -1.8 | -3.5 | 0.2 | 2.55E-14 | -            | conserved hypothetical protein                                 |
| OE6133R   | -1.2 | -2.3 | 0.4 | 5.03E-09 | -            | probable transposase (ISH10)                                   |
| OE6138F   | -0.4 | -1.4 | 0.1 | 6.50E-09 | -            | conserved hypothetical protein                                 |
| OE6145R   | -1.0 | -2.0 | 0.2 | 1.49E-12 | -            | probable signal-transducing histidine kinase                   |
| OE6154F   | -0.7 | -1.6 | 0.1 | 7.11E-12 | -            | hypothetical protein                                           |
| OE6156F   | -1.1 | -2.1 | 0.3 | 1.25E-09 | -            | conserved hypothetical protein                                 |
| OE6161R   | -0.7 | -1.6 | 0.3 | 9.38E-08 | -            | conserved hypothetical protein (nonfunctional                  |
| OE6166R   | -0.8 | -1.7 | 0.2 | 4.22E-10 | -            | conserved hypothetical protein (nonfunctional                  |
| OE6276R   | -0.8 | -1.8 | 0.2 | 2.89E-09 | -            | transposase homolog (TCE33) (nonfunctional)                    |
| OE6283R   | -0.8 | -1.7 | 0.2 | 8.56E-09 | -            | IS200-type transposase homolog (TCE31) (nonfunctional          |

|           |      |       |     |          |               |                                                                   |
|-----------|------|-------|-----|----------|---------------|-------------------------------------------------------------------|
| OE6285F   | -0.6 | -1.5  | 0.2 | 1.08E-09 | -             | IS1341-type transposase (TCE31)                                   |
| OE6292R   | -0.8 | -1.7  | 0.3 | 9.45E-08 | -             | probable transposase (ISH6/ISHS1)                                 |
| OE6296R   | -0.6 | -1.5  | 0.2 | 1.37E-07 | -             | probable transposase (ISH8/ISH26)                                 |
| OE6298A1R | -1.5 | -2.7  | 0.2 | 6.41E-13 | -             | insertion element protein (ISH2)                                  |
| OE7001R   | -0.4 | -1.4  | 0.2 | 7.24E-07 | -             | conserved hypothetical protein                                    |
| OE7008F   | -0.7 | -1.6  | 0.2 | 2.22E-10 | -             | hypothetical protein (encoded by ISH7/ISH24 subtype 1)            |
| OE7011R   | -0.4 | -1.3  | 0.1 | 2.10E-08 | -             | hypothetical protein                                              |
| OE7015F   | -0.5 | -1.4  | 0.3 | 4.51E-05 | -             | conserved hypothetical protein (nonfunctional                     |
| OE7023R   | -0.7 | -1.6  | 0.3 | 4.84E-07 | <i>gvpL1</i>  | gas-vesicle operon protein gvpL1                                  |
| OE7024R   | -0.7 | -1.7  | 0.2 | 3.02E-11 | <i>gvpK1</i>  | gas-vesicle operon protein gvpK1                                  |
| OE7026R   | -0.6 | -1.6  | 0.2 | 4.97E-09 | <i>gvpJ1</i>  | gas-vesicle operon protein gvpJ1                                  |
| OE7027R   | -0.5 | -1.4  | 0.3 | 3.79E-05 | <i>gvpI1</i>  | gas-vesicle operon protein gvpI1                                  |
| OE7034F   | -2.0 | -4.0  | 0.7 | 4.02E-08 | <i>gvpA1</i>  | gas-vesicle protein gvpA1                                         |
| OE7034F   | -1.0 | -2.0  | 0.3 | 6.10E-09 | <i>gvpA1</i>  | gas-vesicle protein gvpA1                                         |
| OE7036F   | -1.5 | -2.8  | 0.5 | 5.29E-09 | <i>gvpC1</i>  | gas-vesicle protein gvpC1                                         |
| OE7037F   | -1.5 | -2.8  | 0.2 | 6.44E-15 | <i>gvpN1</i>  | gas-vesicle operon protein gvpN                                   |
| OE7038F   | -1.6 | -3.0  | 0.5 | 1.70E-08 | <i>gvpO1</i>  | gas-vesicle operon protein gvpO1                                  |
| OE7039F   | -3.5 | -11.6 | 0.3 | 0        | <i>parA7</i>  | parA domain protein                                               |
| OE7042R   | -3.2 | -9.1  | 0.8 | 6.08E-10 | -             | probable signal-transducing histidine kinase / response regulator |
| OE7043A1F | -3.1 | -8.3  | 0.4 | 2.11E-14 | -             | conserved hypothetical protein                                    |
| OE7045F   | -0.5 | -1.5  | 0.1 | 5.85E-10 | <i>tbpA</i>   | TATA-binding transcription initiation factor homolog              |
| OE7049R   | -0.6 | -1.5  | 0.4 | 1.60E-05 | -             | conserved hypothetical protein (nonfunctional                     |
| OE7052F   | -0.5 | -1.4  | 0.2 | 5.87E-07 | -             | probable transposase (ISH5)                                       |
| OE7054R   | -0.4 | -1.4  | 0.3 | 1.36E-05 | -             | conserved hypothetical protein                                    |
| OE7056A1R | -0.8 | -1.8  | 0.3 | 2.38E-08 | -             | conserved hypothetical protein                                    |
| OE7057F   | -0.8 | -1.7  | 0.2 | 1.32E-10 | -             | conserved hypothetical protein                                    |
| OE7064R   | -0.5 | -1.4  | 0.2 | 5.62E-07 | -             | hypothetical protein                                              |
| OE7089R   | -0.7 | -1.7  | 0.1 | 1.69E-14 | -             | conserved hypothetical protein                                    |
| OE7092F   | -0.6 | -1.6  | 0.2 | 1.96E-09 | -             | hypothetical protein                                              |
| OE7095F   | -0.4 | -1.3  | 0.1 | 9.70E-14 | -             | conserved hypothetical protein                                    |
| OE7097F   | -1.8 | -3.5  | 0.1 | 0        | -             | probable transposase (ISH10)                                      |
| OE7100R   | -0.7 | -1.7  | 0.2 | 1.68E-10 | <i>parA6a</i> | parA domain protein                                               |
| OE7101R   | -1.3 | -2.5  | 0.6 | 5.01E-07 | -             | conserved hypothetical protein                                    |
| OE7102R   | -0.8 | -1.8  | 0.1 | 9.33E-15 | -             | conserved hypothetical protein                                    |
| OE7104R   | -0.5 | -1.4  | 0.3 | 1.56E-05 | -             | conserved hypothetical protein                                    |
| OE7106F   | -0.4 | -1.4  | 0.1 | 6.41E-09 | -             | hypothetical protein                                              |
| OE7116B1R | -0.4 | -1.3  | 0.1 | 1.82E-08 | -             | conserved hypothetical protein                                    |
| OE7141R   | -1.0 | -2.0  | 0.2 | 2.86E-12 | -             | multidrug resistance transport protein homolog                    |
| OE7144R   | -0.5 | -1.5  | 0.2 | 5.06E-08 | -             | conserved hypothetical protein                                    |
| OE7149F   | -0.6 | -1.5  | 0.2 | 6.30E-09 | -             | hypothetical protein                                              |
| OE7174R   | -0.7 | -1.6  | 0.2 | 2.80E-08 | -             | conserved hypothetical protein                                    |
| OE7180F   | -0.8 | -1.7  | 0.2 | 5.51E-09 | -             | hypothetical protein                                              |
| OE7182F   | -1.1 | -2.2  | 0.2 | 2.73E-11 | -             | probable restriction/modification enzyme                          |
| OE7186F   | -1.1 | -2.1  | 0.2 | 9.25E-13 | <i>tbpC1</i>  | probable TATA-binding transcription initiation factor             |
| OE7189F   | -0.4 | -1.3  | 0.2 | 4.20E-06 | -             | conserved hypothetical protein                                    |
| OE7190R   | -0.9 | -1.9  | 0.3 | 7.62E-09 | -             | hypothetical protein                                              |
| OE7192F   | -0.5 | -1.4  | 0.1 | 1.24E-09 | -             | conserved hypothetical protein                                    |
| OE7196F   | -0.5 | -1.4  | 0.2 | 4.58E-07 | -             | phage integrase homolog                                           |
| OE7198F   | -0.9 | -1.8  | 0.3 | 4.41E-08 | -             | probable transposase (ISH8/ISH26)                                 |
| OE7201R   | -0.5 | -1.4  | 0.1 | 5.85E-10 | -             | probable transposase (ISH4/ISH23/ISH50)                           |
| OE7210R   | -0.5 | -1.4  | 0.3 | 1.33E-06 | -             | conserved hypothetical protein                                    |
| OE7212B1F | -1.0 | -2.0  | 0.1 | 1.40E-14 | -             | conserved hypothetical protein                                    |
| OE7215F   | -1.2 | -2.4  | 0.2 | 9.65E-12 | -             | conserved hypothetical protein                                    |
| OE8005F   | -0.4 | -1.3  | 0.2 | 1.07E-07 | -             | conserved hypothetical protein                                    |
| OE8009R   | -0.6 | -1.5  | 0.3 | 8.12E-07 | -             | conserved hypothetical protein                                    |
| OE8047F   | -1.3 | -2.5  | 0.3 | 8.84E-11 | -             | conserved hypothetical protein                                    |

|         |      |      |     |          |   |                                |
|---------|------|------|-----|----------|---|--------------------------------|
| OE8050F | -0.6 | -1.5 | 0.2 | 4.18E-08 | - | conserved hypothetical protein |
|---------|------|------|-----|----------|---|--------------------------------|