




Table C-1 Oxygen-responsive transcripts

| VFID | Gene name | Cht | Gly |
|---------------|---|---------------------|---------------------|
| | | + O ₂ | + O ₂ |
| VF0032 | Thiamine biosynthesis protein ThiC | 6.9 | 5.5 |
| VF0033 | Thiamin-phosphate pyrophosphorylase (EC 2.5.1.3) | 79.3 | 41.9 |
| VF0034 | Molybdopterin biosynthesis protein MoeB | 63.1 | 23.2 |
| VF0035 | Thiazole biosynthesis protein ThiG | 83.6 | 53.3 |
| VF0036 | ThiH protein | 49.0 | 37.1 |
| VF0267 | Thiamine-binding protein | 23.9 | 16.2 |
| VF0281 | Conserved hypothetical protein | 31.1 | 11.7 |
| VF0317 | Acetyltransferase (EC 2.3.1.-) | -3.8 | -3.4 |
| VF0339 | Serine--pyruvate aminotransferase (EC 2.6.1.51) | 3.7 | 6.2 |
| VF0451 | Hypothetical protein | -3.0 | -3.9 |
| VF0492 | Putative protease yhbV precursor (EC 3.4.-.-) | -4.4 | -5.6 |
| VF0495 | Sterol binding protein | 4.3 | 3.6 |
| VF0616 | Rrf2 family protein | -3.4 | -18.6 |
| VF0617 | Selenocysteine lyase (EC 4.4.1.16) | -9.5 | -3.5 |
| VF0619 | HesB protein family | -3.4 | -5.1 |
| VF0621 | Chaperone protein HscA | 4.8 | 3.8 |
| VF0776 | Nitrite reductase [NAD(P)H] large subunit (EC 1.7.1.4) | 4.2 | 5.5 |
| VF0780 | CopG protein | 4.2 | 5.9 |
| VF0878 | Multidrug resistance protein A | -19.4 | -7.2 |
| VF0920 | SSU ribosomal protein S4P | -3.6 | -4.4 |
| VF0927 | Hypothetical protein | 3.5 | 10.5 |
| VF0942 | Molybdopterin converting factor, small subunit | -3.4 | -3.4 |
| VF1052 | Transporter, Divalent Anion:Sodium Symporter family | 37.5 | 13.2 |
| VF1053 | Sensory transduction protein kinase (EC 2.7.3.-) | 3.1 | 6.0 |
| VF1060 | Peptidase T (EC 3.4.11.-) | -5.1 | -12.3 |
| VF1061 | Anaerobic C4-dicarboxylate transporter | -13.9 | -22.7 |
| VF1089 | Immunogenic protein | -4.8 | -4.9 |
| VF1090 | Transporter | -42.8 | -91.2 |
| VF1151 | Hypothetical protein | -11.4 | -13.4 |
| VF1155 | Proton glutamate symport protein | 8.9 | 4.1 |
| VF1188 | Alcohol dehydrogenase II (EC 1.1.1.1) | 5.5 | 5.2 |
| VF1190 | Hypothetical protein | 103.3 | 33.8 |
| VF1191 | Hypothetical protein | 3.7 | 3.2 |
| VF1192 | Hypothetical protein | -34.2 | -20.1 |
| VF1193 | Hypothetical protein | 254.0 | 53.3 |
| VF1220 | Hemin transport system ATP-binding protein HmuV | 31.5 | 22.5 |
| VF1221 | Hemin transport system permease protein HmuU | 18.4 | 12.2 |
| VF1222 | Hemin-binding periplasmic protein HmuT precursor HmuT | 31.8 | 17.1 |
| VF1223 | TolR protein | 25.3 | 26.7 |
| VF1224 | TolQ protein | 73.8 | 89.1 |

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| VF1225 | TonB protein | 62.3 | 51.6 |
| VF1226 | Coproporphyrinogen oxidase, anaerobic (EC 1.-.-.-) | 143.6 | 63.3 |
| | | Chit | Gly |
| | | +- | +- |
| VFID | Gene name | O2 | O2 |
| VF1227 | Hypothetical protein | 113.8 | 65.1 |
| VF1228 | Hypothetical protein | 180.0 | 154.4 |
| VF1234 | Hemin receptor | 114.4 | 67.8 |
| VF1262 | Glutaredoxin | 150.0 | 66.2 |
| VF1375 | Kinase autophosphorylation inhibitor KipI | 30.7 | 16.9 |
| VF1376 | Lactam utilization protein LAMB | 74.3 | 30.3 |
| VF1377 | Hypothetical cytosolic protein | 3.2 | 3.5 |
| VF1451 | NUCLEASE | -25.6 | -7.5 |
| VF1472 | Zinc finger protein | -33.8 | -10.2 |
| VF1494 | Transporter | -3.7 | -24.5 |
| VF1510 | Transcriptional regulator | 3.4 | 3.0 |
| VF1529 | Hypothetical protein | 7.9 | 4.1 |
| VF1551 | NrfD protein | -5.1 | -7.7 |
| VF1552 | Thiosulfate reductase electron transport subunit (EC 1.8.99.-) | -3.3 | -6.3 |
| VF1553 | Cytochrome c-type protein NrfB | -10.1 | -22.1 |
| VF1554 | Cytochrome c552 (EC 1.7.2.2) | -3.8 | -22.1 |
| VF1615 | Hypothetical protein | -4.6 | -23.2 |
| VF1630 | Na(+) H(+) antiporter | -4.0 | -24.2 |
| VF1724 | Anaerobic C4-dicarboxylate transporter | -8.9 | -40.9 |
| VF1730 | Sodium proline symporter | 3.4 | 6.4 |
| VF1798 | Chloride channel protein | -6.3 | -5.1 |
| VF1863 | Flagellin, FlaD | 5.8 | 4.3 |
| VF1866 | Flagellin, FlaA | -19.1 | -11.6 |
| VF1889 | Outer membrane porin protein precursor | -3.6 | -6.2 |
| VF1972 | Isocitrate lyase (EC 4.1.3.1) | -20.9 | -3.9 |
| VF2055 | Cytochrome c peroxidase (EC 1.11.1.5) | 4.8 | 3.9 |
| VF206 | Anaerobic C4-dicarboxylate transporter | 13.1 | 5.5 |
| VF2115 | Formate acetyltransferase (EC 2.3.1.54) | -4.2 | -5.4 |
| VF2123 | Fe-S OXIDOREDUCTASE (1.8.-.-) | -6.7 | -3.8 |
| VF2141 | Chitooligosaccharide transport system permease protein | -4.6 | -5.5 |
| VF2150 | Iron(III)-transport system permease protein SfuB | -4.3 | -3.4 |
| VF2151 | Iron(III)-binding protein | -9.5 | -7.6 |
| VF2335 | Fumarate reductase iron-sulfur protein (EC 1.3.99.1) | -6.9 | -26.5 |
| VF2336 | Fumarate reductase (EC 1.3.99.1) | -5.9 | -7.5 |
| VF2337 | Fumarate reductase, 13 kDa hydrophobic protein | -5.5 | -8.4 |
| VF2376 | Hypothetical protein | -3.5 | -5.0 |
| VF2377 | Hypothetical protein | -4.5 | -5.3 |
| VF2378 | Sodium:solute symporter family protein | -4.1 | -5.1 |
| VF2381 | Cyclic nucleotide binding protein 2 CBS domains | 55.5 | 17.8 |
| VF2382 | DNA polymerase III, epsilon chain | 8.6 | 3.6 |

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| VF2383 | Acetyl-coenzyme A synthetase (EC 6.2.1.1) | 23.2 | 10.5 |
| VF2384 | Acetyl-coenzyme A synthetase | 69.5 | 11.3 |
| VF2441 | Hypothetical protein | 23.2 | 5.6 |
| VFA0004 | Peptidase T (EC 3.4.11.-) | 20.0 | 11.6 |
| | | Chit | Gly |
| | | +- | +- |
| VFID | Gene name | O2 | O2 |
| VFA0013 | Chitin-binding protein | 21.6 | 8.8 |
| VFA0073 | Di- tripeptide transporter | -3.5 | -4.8 |
| VFA0080 | Anaerobic DMSO reductase chain C (EC 1.8.99.-) | 3.5 | 4.6 |
| VFA0081 | Anaerobic DMSO reductase chain B (EC 1.8.99.-) | -16.0 | -20.1 |
| VFA0082 | Anaerobic DMSO reductase chain A (EC 1.8.99.-) | -8.5 | -6.8 |
| VFA0083 | Anaerobic DMSO reductase chain ynfI (EC 1.8.99.-) | -57.2 | -18.7 |
| VFA0084 | Ferredoxin-type protein NapF | -53.5 | -13.2 |
| VFA0122 | Hypothetical protein | -89.7 | -42.9 |
| VFA0123 | Di- tripeptide transporter | -29.8 | -75.6 |
| VFA0124 | Di- tripeptide transporter | -9.3 | -13.0 |
| VFA0131 | CAAX amino terminal protease family | -10.5 | -19.0 |
| VFA0156 | Hypothetical conserved protein | -19.0 | -13.6 |
| VFA0157 | Permease | -12.6 | -8.8 |
| VFA0158 | Ferrichrome transport ATP-binding protein FhuC | 8.3 | 5.9 |
| VFA0159 | Ferrichrome-binding protein | 5.6 | 4.6 |
| VFA0160 | Ferrichrome transport system permease protein FhuB | 26.8 | 16.8 |
| VFA0161 | Aerobactin siderophore biosynthesis protein IucA (EC 6.-.-.-) | 32.8 | 29.5 |
| VFA0162 | N(6)-hydroxylysine O-acetyltransferase (EC 2.3.1.102) | 14.4 | 15.7 |
| VFA0163 | Siderophore biosynthesis IucC protein (EC 6.-.-.-) | 13.4 | 10.4 |
| VFA0164 | L-lysine 6-monooxygenase (EC 1.14.13.59) | 276.6 | 703.0 |
| VFA0165 | Ferric aerobactin receptor precursor | 95.7 | 179.3 |
| VFA0188 | Trimethylamine-N-oxide reductase (EC 1.7.2.3) | 93.4 | 179.0 |
| VFA0189 | Cytochrome c-type protein TorC | 165.9 | 339.5 |
| VFA0190 | Hypothetical protein | 119.6 | 136.9 |
| VFA0191 | FhuE receptor precursor | -18.2 | -7.4 |
| VFA0192 | Hypothetical protein | -16.9 | -8.1 |
| VFA0193 | TolQ protein TolR protein | 13.4 | 26.6 |
| VFA0194 | TolQ protein | 17.7 | 25.4 |
| VFA0195 | TolR protein | 15.0 | 17.6 |
| VFA0196 | TonB protein | 10.7 | 13.7 |
| VFA0197 | TPR domain protein | 10.3 | 12.2 |
| VFA0198 | Transcriptional repressor | 4.9 | 6.9 |
| VFA0199 | Oligosaccharide transport ATP-binding protein | 5.2 | 7.1 |
| VFA0200 | Oligosaccharide transport ATP-binding protein | 4.7 | 6.0 |
| VFA0201 | Hypothetical protein | 6.8 | 4.8 |
| VFA0205 | Hypothetical membrane spanning protein | 48.3 | 45.2 |
| VFA0251 | NADP-dependent formate dehydrogenase (EC 1.2.1.43) | 121.5 | 189.0 |
| VFA0259 | Hypothetical transcriptional regulatory protein | -17.9 | -20.4 |

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| VFA0274 | Acyl-CoA desaturase (EC 1.14.19.1) | -4.0 | -3.7 |
| VFA0281 | Anaerobic ribonucleoside-triphosphate reductase (EC 1.17.4.2) | -6.6 | -3.1 |
| VFA0287 | Hypothetical protein | -3.1 | -6.7 |
| VFA0316 | Hydroxymethylpyrimidine kinase (EC 2.7.1.49) | 4.6 | 7.0 |
| VFA0317 | Hydroxymethylpyrimidine transport ATP-binding protein | -3.4 | -6.8 |
| VFA0318 | Hydroxymethylpyrimidine transport system permease protein | -7.4 | -3.1 |
| | | Chit | Gly |
| | | +- | +- |
| VFID | Gene name | O2 | O2 |
| VFA0319 | Hydroxymethylpyrimidine-binding protein | 26.9 | 14.8 |
| VFA0320 | Transcriptional activator TenA | 10.2 | 9.2 |
| VFA0321 | Hydroxyethylthiazole kinase (EC 2.7.1.50) | 10.5 | 8.7 |
| VFA0322 | Thiamin-phosphate pyrophosphorylase (EC 2.5.1.3) | 6.9 | 9.5 |
| VFA0333 | Protease II (EC 3.4.21.83) | 8.8 | 10.2 |
| VFA0363 | Sodium proton-dependent alanine carrier protein | 5.1 | 6.6 |
| VFA0364 | Transporter | 3.5 | 5.6 |
| VFA0371 | Hypothetical protein  | 3.6 | 3.9 |
| VFA0386 | Formate transporter | 4.8 | 4.2 |
| VFA0502 | Outer membrane protein | 7.0 | 8.3 |
| VFA0553 | ATP-dependent RNA helicase | -4.7 | -6.0 |
| VFA0616 | Hypothetical protein | -203 | -178 |
| VFA0642 | Hypothetical protein | -9.2 | -3.2 |
| VFA0669 | Hypothetical protein | -3.4 | -4.9 |
| VFA0756 | Putative Lipoprotein | -15.3 | -3.0 |
| VFA0758 | Hypothetical membrane protein  | 7.7 | 11.0 |
| VFA0784 | Ferrichrome-iron receptor | -9.9 | -4.5 |
| VFA0794 | Acetate kinase (EC 2.7.2.1) | 14.1 | 14.7 |
| VFA0823 | Vulnibactin utilization protein VIUB | 6.3 | 5.0 |
| VFA0824 | Ferric anguibactin transport ATP-binding protein | 5.1 | 4.1 |
| VFA0827 | Ferric anguibactin-binding protein | -23.7 | -5.2 |
| VFA0829 | Sodium proline symporter | 3.0 | 3.3 |
| VFA0848 | Hypothetical protein | 13.8 | 7.6 |
| VFA0876 | Hypothetical protein | -7.6 | -4.5 |
| VFA0928 | Hypothetical protein | 14.2 | 31.0 |
| VFA0929 | Hypothetical protein | -3.4 | -6.1 |
| VFA0930 | Carboxypeptidase G precursor (EC 3.4.17.11)  | -23.5 | -20.0 |
| VFA0961 | Hypothetical protein | -11.0 | -14.6 |
| VFA0962 | Pyruvate formate-lyase activating enzyme (EC 1.97.1.4) | -5.3 | -7.3 |
| VFA0979 | Conserved hypothetical protein | -4.0 | -5.1 |
| VFA0982 | Hypothetical protein | -3.2 | -7.1 |
| VFA0983 | Hypothetical protein | -3.4 | -7.4 |
| VFA1094 | Cold shock protein | -28.0 | -30.3 |
| VFA1106 | Hypothetical protein | 5.8 | 4.1 |
| VFA1108 | Hypothetical protein | 24.1 | 4.8 |