TABLE S3. Genes that are differentially transcribed in C- $\Delta vieA$ relative to C-wt. Differentially expressed genes were determined using SAM software with ≥ 2.0 fold change in gene expression and False Discovery Rate (FDR) ≤ 0.01 as criteria. List of VpsR and σ^E regulated genes were obtained from previously published transcriptome data (12, 56). σ^E regulated genes were selected using ≥ 1.5 fold change in gene expression and P-value ≤ 0.1 as criteria from published supplementary data (12) and VpsR regulated genes were selected using ≥ 1.5 fold change in gene expression and FDR ≤ 0.01 as criteria from published supplementary data (56). Positively and negatively regulated genes by VpsR and σ^E are shown as plus (+) and minus (-), respectively.

| ChangeAmino Acid BiosynthesisVC0030acetolactate synthase II_ small subunit $ilvM$ 2.67VC1590acetolactate synthase $ilvK$ 2.10Biosynthesis of Cofactors, Prosthetic Groups, and CarriersVC0064Thiamine thiS protein $thiS$ 0.43VC0194gamma-glutamyltranspeptidase ggt 2.21VpsR(+)VC0472S-adenosylmethionine synthase $metK$ 0.48VC22541-deoxy-D-xylulose 5-phosphate reductoisomerase dxr 2.57VCA07233-hydroxy-3-methylglutaryl CoA reductase $hmgA$ 2.62Cell EnvelopeVC0240ADP-L-glycero-D-mannoheptose-6-epimerase $rfaD$ 0.50VC0533lipoprotein NlpD $nlpD$ 0.26VC0602penicillin-binding protein 1B $mrcB$ 3.21VC0700soluble lytic murein transglycosylase slt 4.66VpsR(+)VC1195lipoprotein_ putative2.32VC1622outer membrane protein_ putative3.35VC1956lytic murein transglycosylase_ putative2.59 $\sigma^E(-)$, VpsR(+)VC1962lipoprotein5.76 $\sigma^E(-)$, VpsR(+)VC2213outer membrane protein OmpA $ompA$ 2.57 $\sigma^E(-)$ |
|---|
| VC1590acetolactate synthase $ilvK$ 2.10Biosynthesis of Cofactors, Prosthetic Groups, and CarriersVC0064Thiamine thiS protein $thiS$ 0.43VC0194gamma-glutamyltranspeptidase ggt 2.21VpsR(+)VC0472S-adenosylmethionine synthase $metK$ 0.48VC22541-deoxy-D-xylulose 5-phosphate reductoisomerase dxr 2.57VCA07233-hydroxy-3-methylglutaryl CoA reductase $hmgA$ 2.62Cell EnvelopeVC0240ADP-L-glycero-D-mannoheptose-6-epimerase $rfaD$ 0.50VC0533lipoprotein NlpD $nlpD$ 0.26VC0602penicillin-binding protein 1B $mrcB$ 3.21VC0700soluble lytic murein transglycosylase slt 4.66VpsR(+)VC1195lipoprotein_ putative2.32VC1622outer membrane protein_ putative3.35VC1956lytic murein transglycosylase_ putative2.59 $\sigma^{E}(+)$, VpsR(+)VC1962lipoprotein5.76 $\sigma^{E}(-)$, VpsR(+) |
| Biosynthesis of Cofactors, Prosthetic Groups, and CarriersVC0064Thiamine thiS protein $thiS$ 0.43VC0194gamma-glutamyltranspeptidase ggt 2.21VpsR(+)VC0472S-adenosylmethionine synthase $metK$ 0.48VC22541-deoxy-D-xylulose 5-phosphate reductoisomerase dxr 2.57VCA07233-hydroxy-3-methylglutaryl CoA reductase $hmgA$ 2.62Cell Envelope2.62VC0240ADP-L-glycero-D-mannoheptose-6-epimerase $rfaD$ 0.50VC0533lipoprotein NlpD $nlpD$ 0.26VC0602penicillin-binding protein 1B $mrcB$ 3.21VC0700soluble lytic murein transglycosylase slt 4.66VpsR(+)VC1195lipoprotein_ putative2.32VC1622outer membrane protein_ putative3.35VC1956lytic murein transglycosylase_ putative2.59 $\sigma^E(+)$ VC1962lipoprotein5.76 $\sigma^E(-)$, VpsR(+) |
| VC0064Thiamine thiS protein $thiS$ 0.43VC0194gamma-glutamyltranspeptidase ggt 2.21VpsR(+)VC0472S-adenosylmethionine synthase $metK$ 0.48VC22541-deoxy-D-xylulose 5-phosphate reductoisomerase dxr 2.57VCA07233-hydroxy-3-methylglutaryl CoA reductase $hmgA$ 2.62Cell EnvelopeVC0240ADP-L-glycero-D-mannoheptose-6-epimerase $rfaD$ 0.50VC0533lipoprotein NlpD $nlpD$ 0.26VC0602penicillin-binding protein 1B $mrcB$ 3.21VC0700soluble lytic murein transglycosylase slt 4.66VpsR(+)VC1195lipoprotein_ putative2.32VC1622outer membrane protein_ putative3.35VC1956lytic murein transglycosylase_ putative2.59 $\sigma^E(+)$ VC1962lipoprotein5.76 $\sigma^E(-)$, VpsR(+) |
| VC0064Thiamine thiS protein $thiS$ 0.43VC0194gamma-glutamyltranspeptidase ggt 2.21VpsR(+)VC0472S-adenosylmethionine synthase $metK$ 0.48VC22541-deoxy-D-xylulose 5-phosphate reductoisomerase dxr 2.57VCA07233-hydroxy-3-methylglutaryl CoA reductase $hmgA$ 2.62Cell EnvelopeVC0240ADP-L-glycero-D-mannoheptose-6-epimerase $rfaD$ 0.50VC0533lipoprotein NlpD $nlpD$ 0.26VC0602penicillin-binding protein 1B $mrcB$ 3.21VC0700soluble lytic murein transglycosylase slt 4.66VpsR(+)VC1195lipoprotein_ putative2.32VC1622outer membrane protein_ putative3.35VC1956lytic murein transglycosylase_ putative2.59 $\sigma^E(+)$ VC1962lipoprotein5.76 $\sigma^E(-)$, VpsR(+) |
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| VC0472S-adenosylmethionine synthase $metK$ 0.48VC22541-deoxy-D-xylulose 5-phosphate reductoisomerase dxr 2.57VCA07233-hydroxy-3-methylglutaryl CoA reductase $hmgA$ 2.62Cell EnvelopeVC0240ADP-L-glycero-D-mannoheptose-6-epimerase $rfaD$ 0.50VC0533lipoprotein NlpD $nlpD$ 0.26VC0602penicillin-binding protein 1B $mrcB$ 3.21VC0700soluble lytic murein transglycosylase slt 4.66VpsR(+)VC1195lipoprotein_ putative2.32VC1622outer membrane protein_ putative3.35VC1956lytic murein transglycosylase_ putative2.59 $\sigma^E(+)$ VC1962lipoprotein5.76 $\sigma^E(-)$, VpsR(+) |
| VC22541-deoxy-D-xylulose 5-phosphate reductoisomerase dxr 2.57VCA07233-hydroxy-3-methylglutaryl CoA reductase $hmgA$ 2.62Cell EnvelopeVC0240ADP-L-glycero-D-mannoheptose-6-epimerase $rfaD$ 0.50VC0533lipoprotein NlpD $nlpD$ 0.26VC0602penicillin-binding protein 1B $mrcB$ 3.21VC0700soluble lytic murein transglycosylase slt 4.66VpsR(+)VC1195lipoprotein_ putative2.32VC1622outer membrane protein_ putative3.35VC1956lytic murein transglycosylase_ putative2.59 $\sigma^{E}(+)$ VC1962lipoprotein5.76 $\sigma^{E}(-)$, VpsR(+) |
| Cell EnvelopeVC0240ADP-L-glycero-D-mannoheptose-6-epimerase $rfaD$ 0.50VC0533lipoprotein NlpD $nlpD$ 0.26VC0602penicillin-binding protein 1B $mrcB$ 3.21VC0700soluble lytic murein transglycosylase slt 4.66VpsR(+)VC1195lipoprotein_ putative2.32VC1622outer membrane protein_ putative3.35VC1956lytic murein transglycosylase_ putative2.59 $\sigma^E(+)$ VC1962lipoprotein5.76 $\sigma^E(-)$, VpsR(+) |
| Cell EnvelopeVC0240ADP-L-glycero-D-mannoheptose-6-epimerase $rfaD$ 0.50VC0533lipoprotein NlpD $nlpD$ 0.26VC0602penicillin-binding protein 1B $mrcB$ 3.21VC0700soluble lytic murein transglycosylase slt 4.66VpsR(+)VC1195lipoprotein_ putative2.32VC1622outer membrane protein_ putative3.35VC1956lytic murein transglycosylase_ putative2.59 $\sigma^E(+)$ VC1962lipoprotein5.76 $\sigma^E(-)$, VpsR(+) |
| VC0240ADP-L-glycero-D-mannoheptose-6-epimerase $rfaD$ 0.50VC0533lipoprotein NlpD $nlpD$ 0.26VC0602penicillin-binding protein 1B $mrcB$ 3.21VC0700soluble lytic murein transglycosylase slt 4.66VpsR(+)VC1195lipoprotein_ putative2.32VC1622outer membrane protein_ putative3.35VC1956lytic murein transglycosylase_ putative2.59 $\sigma^{E}(+)$ VC1962lipoprotein5.76 $\sigma^{E}(-)$, VpsR(+) |
| VC0533lipoprotein NlpD $nlpD$ 0.26VC0602penicillin-binding protein 1B $mrcB$ 3.21VC0700soluble lytic murein transglycosylase slt 4.66VpsR(+)VC1195lipoprotein_ putative2.32VC1622outer membrane protein_ putative3.35VC1956lytic murein transglycosylase_ putative2.59 σ^E (+)VC1962lipoprotein5.76 σ^E (-),VpsR(+) |
| VC0602penicillin-binding protein 1B $mrcB$ 3.21VC0700soluble lytic murein transglycosylase slt 4.66 $VpsR(+)$ VC1195lipoprotein_ putative2.32VC1622outer membrane protein_ putative3.35VC1956lytic murein transglycosylase_ putative2.59 $\sigma^E(+)$ VC1962lipoprotein5.76 $\sigma^E(-)$, $VpsR(+)$ |
| VC0700soluble lytic murein transglycosylase slt 4.66VpsR(+)VC1195lipoprotein_ putative2.32VC1622outer membrane protein_ putative3.35VC1956lytic murein transglycosylase_ putative2.59 $\sigma^{E}(+)$ VC1962lipoprotein5.76 $\sigma^{E}(-)$, VpsR(+) |
| VC1195lipoprotein_putative2.32VC1622outer membrane protein_putative3.35VC1956lytic murein transglycosylase_putative2.59 $\sigma^{E}(+)$ VC1962lipoprotein5.76 $\sigma^{E}(-)$,VpsR(+ |
| VC1622outer membrane protein_ putative3.35VC1956lytic murein transglycosylase_ putative2.59 σ^E (+)VC1962lipoprotein5.76 σ^E (-), VpsR(+) |
| VC1956 lytic murein transglycosylase_putative 2.59 $\sigma^{E}(+)$ VC1962 lipoprotein 5.76 $\sigma^{E}(-)$, VpsR(+ |
| |
| |
| |
| VC2247 lipid-A-disaccharide synthase <i>lpxB</i> 2.36 |
| VC2251 outer membrane protein OmpH <i>ompH</i> 2.56 |
| VC2400 UDP-N-acetylmuramatealanine ligase <i>murC</i> 2.14 |
| VC2401 UDP-N-acetylglucosamineN-acetylmuramyl-(pentapeptide) |
| pyrophosphoryl-undecaprenol N-acetylglucosamine transferase <i>murG</i> 2.16 UDP N acetylmuramoylalanyl D glutamate 2.6 diaminonimelate |
| VC2406 ligase murE 2.18 |
| VC2514 UDP-N-acetylglucosamine 1-carboxyvinyltransferase <i>murA</i> 2.16 |
| VCA0867 outer membrane protein OmpW <i>ompW</i> 0.47 $\sigma^{E}(-)$ |
| Cellular Processes: Chemotaxis and Motility |
| VC0216 methyl-accepting chemotaxis protein 0.40 |
| VC1008 sodium-type flagellar protein MotY <i>motY</i> 0.41 |
| VC1248 methyl-accepting chemotaxis protein 0.42 |
| VC1289 methyl-accepting chemotaxis protein 0.33 |
| VC1298 methyl-accepting chemotaxis protein 0.42 |
| VC1413 methyl-accepting chemotaxis protein 0.33 VpsR(-) |
| VC1602 chemotaxis protein CheV <i>cheV-1</i> 0.47 |
| VC1898 methyl-accepting chemotaxis protein 0.30 |
| VC2059 purine-binding chemotaxis protein CheW <i>cheW-1</i> 0.50 |
| VC2064 chemotaxis protein CheZ <i>cheZ</i> 0.44 |

| VC2065 | chemotaxis protein CheY <i>cheY-3</i> | 0.48 | |
|------------------|---|-------|---------|
| VC2068 | flagellar biosynthetic protein FlhF_ putative | 0.43 | |
| VC2069 | flagellar biosynthetic protein FlhA flhA | 0.36 | |
| VC2128 | flagellar hook-length control protein FliK_ putative | 0.29 | |
| VC2130 | flagellum-specific ATP synthase FliI fliI | 0.48 | |
| VC2131 | flagellar assembly protein FliH_ putative | 0.50 | |
| VC2134 | flagellar hook-basal body complex protein FliE fliE | 0.47 | |
| VC2138 | flagellar protein FliS fliS | 0.36 | |
| VC2141 | flagellin FlaG flaG | 0.25 | |
| VC2142 | flagellin FlaB flaB | 0.16 | |
| VC2143 | flagellin FlaD flaD | 0.11 | |
| VC2144 | flagellin FlaE flaE | 0.27 | |
| VC2161 | methyl-accepting chemotaxis protein | 0.22 | |
| VC2187 | flagellin FlaC flaC | 0.13 | |
| VC2188 | flagellin core protein A flaA | 0.12 | |
| VC2190 | flagellar hook-associated protein FlgL flgL | 0.44 | |
| VC2191 | flagellar hook-associated protein FlgM flgM | 0.18 | |
| VC2192 | flagellar protein FlgJ $flgJ$ | 0.41 | |
| VC2194 | flagellar L-ring protein FlgH flgH | 0.38 | |
| VC2195 | flagellar basal-body rod protein FlgG flgG | 0.24 | |
| VC2197 | flagellar hook protein FlgE flgE | 0.32 | |
| VC2198 | basal-body rod modification protein FlgD flgD | 0.46 | |
| VC2200 | flagellar basal-body rod protein FlgB flgB | 0.13 | |
| VC2204 | negative regulator of flagellin synthesis FlgM_ putative | 0.46 | |
| VC2601 | sodium-type flagellar protein MotX <i>motX</i> | 0.34 | |
| VCA0864 | methyl-accepting chemotaxis protein | 4.32 | VpsR(+) |
| VCA0954 | chemotaxis protein CheV_putative | 0.37 | · F*() |
| | rocesses: Pathogenesis | | |
| VC0824 | tagD protein tagD | 0.31 | |
| VC0825 | toxin co-regulated pilus biosynthesis protein I <i>tcpI</i> | 0.24 | |
| VC0827 | toxin co-regulated pilus biosynthesis protein H <i>tcpH</i> | 0.49 | |
| VC0827 | toxin co-regulated pilus biosynthesis protein Q tcpQ | 0.20 | |
| VC0831 | toxin co-regulated pilus biosynthesis outer membrane protein $C tcpC$ | 0.32 | |
| VC0831 VC0832 | toxin co-regulated pilus biosynthesis protein R <i>tcpR</i> | 0.26 | |
| VC0832 VC0833 | toxin co-regulated pilus biosynthesis protein D <i>tcpD</i> | 0.17 | |
| VC0833 | toxin co-regulated pilus biosynthesis protein S <i>tcpS</i> | 0.17 | |
| VC0835 | toxin co-regulated pilus biosynthesis protein T tcpT | 0.25 | |
| VC0835 VC0836 | toxin co-regulated pilus biosynthesis protein E <i>tcpE</i> | 0.23 | |
| VC0830 VC0837 | toxin co-regulated pilus biosynthesis protein F <i>tcpF</i> | 0.23 | |
| VC0837 VC0838 | TCP pilus virulence regulatory protein tcpN/toxT | 0.23 | |
| VC0838 VC0839 | leader peptidase TcpJ tcpJ | 0.34 | |
| | • • • | 0.39 | |
| VC0840 | accessory colonization factor AcfB acfB | | |
| VC0841 | accessory colonization factor AcfC acfC | 0.39 | |
| VC0843 | tagE protein tagE-1 | 0.49 | |
| VC0844 | accessory colonization factor AcfA acfA | 0.21 | |
| VC1451 | RTX toxin RtxA rtxA | 2.01 | |
| VC2724 | cholera toxin secretion protein EpsM <i>epsM</i> | 3.03 | |
| VCA0594 | hemolysin hlx | 2.30 | |
| - | rocesses: Other | • • • | T/ D/:> |
| VC1583 | superoxide dismutase_ Cu-Zn sodC | 2.03 | VpsR(+) |
| | | | |

| VC1676 | phage shock protein C pspC | 2.89 | σ ^E (-) |
|-----------|---|------|--------------------------|
| VC1678 | phage shock protein A pspA | 3.01 | $\sigma^{E}(-)$ |
| VC2402 | cell division protein FtsW ftsW | 2.12 | () |
| VC2451 | GTP pyrophosphokinase <i>relA</i> | 3.97 | |
| | termediary Metabolism | | |
| VC0606 | nitrogen regulatory protein P-II glnB-1 | 0.45 | |
| VC1945 | FAD monooxygenase PheA/TfdB family | 8.80 | |
| VC2231 | oxidoreductase_ acyl-CoA dehydrogenase family | 2.22 | |
| VC2239 | nitrogen regulatory protein P-II <i>glnB-2</i> | 2.30 | $\sigma^{\rm E}(+)$ |
| VC2240 | decarboxylase | 2.99 | $\sigma^{E}(+), VpsR(+)$ |
| VC2559 | sulfate adenylate transferase subunit 1 <i>cysN</i> | 2.02 | VpsR(-) |
| VCA0316 | acetyltransferase putative | 2.03 | 1 (/ |
| VCA0824 | diaminobutyratepyruvate aminotransferase <i>ectB</i> | 2.12 | |
| VCA0947 | spermidine n1-acetyltransferase <i>speG</i> | 2.43 | VpsR(+) |
| DNA Meta | · · · · · · · · · · · · · · · · · · · | | 1 () |
| VC1672 | DNA-3-methyladenine glycosidase I <i>tag</i> | 3.67 | |
| VC1814 | deoxyribodipyrimidine photolyase phrB-1 | 2.67 | |
| VC1919 | DNA-binding protein HU-beta <i>hupB</i> | 0.48 | |
| VC2417 | single-stranded-DNA-specific exonuclease RecJ <i>recJ</i> | 2.19 | $\sigma^{\rm E}(+)$ |
| VCA1017 | methylated-DNAprotein-cysteine S-methyltransferase <i>ogt</i> | 2.19 | - () |
| Energy Mo | • | | |
| VC0168 | cytochrome c5 cycB | 0.40 | |
| VC0298 | acetyl-CoA synthase acs-1 | 2.44 | |
| VC0432 | malate dehydrogenase <i>mdh</i> | 0.49 | |
| VC0574 | ubiquinolcytochrome c reductase cytochrome B <i>petB</i> | 0.37 | |
| VC0575 | ubiquinolcytochrome c reductase_ cytochrome c1 <i>petC</i> | 0.42 | |
| VC0769 | chitinase_putative | 4.37 | |
| VC0819 | aldehyde dehydrogenase <i>aldA-1</i> | 0.34 | |
| VC1242 | succinylglutamate desuccinylase <i>astE</i> | 0.48 | |
| VC1300 | L-serine dehydratase 1 <i>sdaA-1</i> | 0.49 | |
| VC1337 | methylcitrate synthase <i>prpC</i> | 2.06 | |
| VC1338 | aconitate hydratase 1 acnA | 2.41 | |
| VC1439 | cytochrome c oxidase_ subunit CcoP <i>ccoP</i> | 0.39 | |
| VC1440 | cytochrome c oxidase subunit CcoQ ccoQ | 0.47 | |
| VC1441 | cytochrome c oxidase subunit CcoO ccoO | 0.36 | |
| VC1442 | cytochrome c oxidase subunit CcoN ccoN | 0.32 | |
| VC1515 | chaperone formate dehydrogenase-specific putative | 2.71 | |
| VC1573 | fumarate hydratase class II aerobic fumC | 4.38 | |
| VC1693 | cytochrome c-type protein TorC <i>torC</i> | 0.47 | |
| VC2291 | NADH:ubiquinone oxidoreductase_ Na translocating_ hydrophobic membrane protein NqrE <i>nqrE</i> | 0.45 | |
| VC2698 | aspartate ammonia-lyase aspA | 0.35 | VpsR(-) |
| VCA0136 | glycerophosphoryl diester phosphodiesterase <i>glpQ</i> | 0.37 | VpsR(-) |
| VCA0140 | spindolin-related protein | 2.66 | 1 (/ |
| VCA0538 | cytochrome b561 putative | 3.03 | |
| VCA0700 | chitodextrinase | 2.29 | |
| VCA0811 | chitinase_putative | 6.68 | VpsR(+) |
| VCA0828 | phenylalanine-4-hydroxylase <i>phhA</i> | 0.34 | 1 () |
| | and Phospholipid Metabolism | 0.51 | |
| VC1063 | acyl-CoA thioesterase II <i>tesB</i> | 0.45 | |

| VCA0035 | phosphatidylglycerophosphatase B_ putative | 3.76 | $\sigma^{E}(-)$ |
|---|--|--|---|
| VCA0690 | acetyl-CoA acetyltransferase | 2.02 | , |
| | d Extrachromosomal Element Functions | | |
| VC0516 | phage integrase | 2.04 | |
| VC0818 | transposase_ putative authentic point mutation | 2.14 | |
| VC0846 | integrase_degenerate | 0.40 | |
| VC1455 | transcriptional repressor RstR <i>rstR-1</i> | 2.04 | |
| Protein Fa | | | |
| VC0034 | thiol:disulfide interchange protein <i>tpcG</i> | 2.03 | $\sigma^{E}(+)$ |
| VC0157 | alkaline serine protease | 28.05 | VpsR(+) |
| VC0354 | peptidyl-prolyl cis-trans isomerase FKBP-type fkpA | 2.47 | |
| VC0554 | protease insulinase family/protease insulinase family | 2.60 | |
| VC0566 | protease DO htrA | 4.47 | $\sigma^{\mathrm{E}}(+)$ |
| VC1107 | outer membrane lipoproteins carrier protein <i>lolA</i> | 2.21 | $\sigma^{E}(-)$ |
| VC1674 | periplasmic linker protein putative | 3.34 | $\sigma^{E}(-)$ |
| VC1709 | zinc protease insulinase family | 0.42 | VpsR(-) |
| VC2723 | general secretion pathway protein N <i>epsN</i> | 2.49 | |
| VC2725 | general secretion pathway protein L <i>epsL</i> | 2.55 | |
| VC2726 | general secretion pathway protein K <i>epsK</i> | 2.23 | VpsR(+) |
| VC2727 | general secretion pathway protein J epsJ | 2.91 | VpsR(+) |
| VC2730 | general secretion pathway protein G epsG | 2.02 | |
| VC2731 | general secretion pathway protein F <i>epsF</i> | 2.15 | VpsR(+) |
| VC2732 | general secretion pathway protein E <i>epsE</i> | 2.01 | VpsR(+) |
| VC2733 | general secretion pathway protein D_ authentic frameshift gspD | 2.63 | VpsR(+) |
| VCA0223 | protease <i>prtV</i> | 2.06 | |
| VCA0692 | protein-export membrane protein SecF_ authentic frameshift secF-2 | 2.12 | |
| Protein Sy | nthesis | | |
| VC0007 | ribosomal protein L34 <i>rpmH</i> | 0.46 | |
| VC2452 | TrmA family RNA methyltransferase_ putative | 3.51 | |
| VC2679 | ribosomal protein L31 <i>rpmE</i> | 0.40 | VpsR(+) |
| Purine, Py | rimidines, Nucleosides, Nucleotides | | |
| VC1034 | uridine phosphorylase <i>udp-1</i> | 0.38 | VpsR(-) |
| VC2277 | xanthine-guanine phosphoribosyltransferase <i>gpt</i> | 0.46 | |
| Regulator | y Functions | | |
| VC0192 | transcriptional regulator AraC/XylS family | 2.71 | |
| VC0665 | sigma-54 dependent transcriptional regulator <i>vpsR</i> | 7.08 | |
| VC1082 | response regulator | 0.35 | |
| VC1142 | cold shock-like protein CspD cspD | 2.17 | |
| VC1638 | | | E |
| | DNA-binding response regulator | 6.77 | $\sigma^{\rm E}(\text{-})$ |
| VC1639 | DNA-binding response regulator sensor histidine kinase | 6.77 7.75 | $\sigma^{E}(-)$ |
| | | | |
| VC1651 | sensor histidine kinase | 7.75 | |
| VC1651 VC1653 | sensor histidine kinase response regulator VieB <i>vieB</i> | 7.75 0.20 | $\sigma^{E}(-)$ |
| VC1651 VC1653 VC1825 | sensor histidine kinase response regulator VieB <i>vieB</i> sensory box sensor histidine kinase/response regulator VieS <i>vieS</i> | 7.75 0.20 0.28 | σ^{E} (-) σ^{E} (-) |
| VC1651 VC1653 VC1825 VC1947 | sensor histidine kinase response regulator VieB <i>vieB</i> sensory box sensor histidine kinase/response regulator VieS <i>vieS</i> transcriptional regulator | 7.75 0.20 0.28 2.10 | $\sigma^{E}(-)$ $\sigma^{E}(-)$ $\sigma^{E}(+)$ |
| VC1651 VC1653 VC1825 VC1947 VC2464 | sensor histidine kinase response regulator VieB <i>vieB</i> sensory box sensor histidine kinase/response regulator VieS <i>vieS</i> transcriptional regulator transcriptional regulator_ LysR family | 7.75 0.20 0.28 2.10 5.38 | $\sigma^{E}(-)$ $\sigma^{E}(+)$ $\sigma^{E}(+)$ |
| VC1651 VC1653 VC1825 VC1947 VC2464 VC2465 | sensor histidine kinase response regulator VieB <i>vieB</i> sensory box sensor histidine kinase/response regulator VieS <i>vieS</i> transcriptional regulator transcriptional regulator_ LysR family sigma-E factor regulatory protein RseC <i>rseC</i> | 7.75 0.20 0.28 2.10 5.38 2.04 | $\sigma^{E}(-)$ $\sigma^{E}(-)$ $\sigma^{E}(+)$ $\sigma^{E}(+)$ $\sigma^{E}(+)$ |
| VC1651 VC1653 VC1825 VC1947 VC2464 VC2465 VC2466 | sensor histidine kinase response regulator VieB <i>vieB</i> sensory box sensor histidine kinase/response regulator VieS <i>vieS</i> transcriptional regulator transcriptional regulator_ LysR family sigma-E factor regulatory protein RseC <i>rseC</i> sigma-E factor regulatory protein RseB <i>rseB</i> | 7.75 0.20 0.28 2.10 5.38 2.04 3.09 | σ^{E} (-) σ^{E} (+) σ^{E} (+) |
| VC1639 VC1651 VC1653 VC1825 VC1947 VC2464 VC2465 VC2466 VC2516 VCA0239 | sensor histidine kinase response regulator VieB <i>vieB</i> sensory box sensor histidine kinase/response regulator VieS <i>vieS</i> transcriptional regulator transcriptional regulator_ LysR family sigma-E factor regulatory protein RseC <i>rseC</i> sigma-E factor regulatory protein RseB <i>rseB</i> sigma-E factor negative regulatory protein RseA <i>rseA</i> | 7.75 0.20 0.28 2.10 5.38 2.04 3.09 4.07 | $\sigma^{E}(-)$ $\sigma^{E}(+)$ $\sigma^{E}(+)$ |

| VCA0565 | sensor histidine kinase | 2.05 | |
|------------------|---|------|---------------------|
| VCA0566 | transcriptional regulator | 2.44 | |
| VCA0888 | transcriptional regulator_LuxR family | 2.28 | VpsR(+) |
| VCA0917 | transcriptional regulator_ TetR family | 3.88 | VpsR(+) |
| VCA0952 | transcriptional regulator_LuxR family vpsT | 6.83 | VpsR(+) |
| Transcript | ion | | |
| VC0150 | RNA polymerase sigma-32 factor <i>rpoH</i> | 2.06 | |
| VC0159 | RNA-binding protein | 0.37 | |
| VC2467 | RNA polymerase sigma-E factor <i>rpoE</i> | 3.11 | |
| Transport | and Binding Proteins | | |
| VC0172 | peptide ABC transporter_ permease protein | 0.43 | |
| VC0284 | TonB system receptor_ authentic point mutation | 2.02 | |
| VC0704 | spermidine/putrescine ABC transporter_ periplasmic spermidine/putrescine-binding protein putative | 2.59 | VpsR(-) |
| VC0724 | phosphate ABC transporter_permease protein <i>pstC-1</i> | 2.20 | |
| VC0995 | PTS system_ N-acetylglucosamine-specific IIABC component <i>nagE</i> | 2.39 | |
| VC1042 | long-chain fatty acid transport protein fadL-1 | 2.45 | |
| VC1301 | serine transporter <i>sdaC-1</i> | 0.34 | VpsR(-) |
| VC1328 | galactoside ABC transporter_ permease protein <i>mglC</i> | 2.17 | • |
| VC1486 | ABC transporter ATP-binding protein | 3.30 | $\sigma^{\rm E}(+)$ |
| VC1549 | glycerol-3-phosphate ABC transporter_periplasmic glycerol-3- | | . , |
| VC1349 | phosphate-binding protein <i>ugpB</i> | 0.34 | |
| VC1673 | transporter_ AcrB/D/F family | 3.38 | |
| VC1675 | multidrug resistance protein_ putative | 3.75 | |
| VC1854 | ompT protein ompT | 0.30 | $\sigma^{E}(-)$ |
| VC1927 | C4-dicarboxylate transport protein <i>dctM</i> | 2.20 | |
| VC1928 | C4-dicarboxylate transport protein DctQ_ putative | 3.04 | |
| VC1929 | C4-dicarboxylate-binding periplasmic protein <i>dctP-2</i> | 2.51 | |
| VC1944 | PvcB protein pvcB | 7.01 | |
| VC2013 | PTS system_ glucose-specific IIBC component ptsG | 0.37 | - |
| VC2037 | Na+/H+ antiporter yqkI | 0.48 | $\sigma^{\rm E}(+)$ |
| VC2608 | ABC transporter_ ATP-binding protein | 2.39 | |
| VCA0025 | transporter_NadC family | 0.48 | |
| VCA0036 | sodium/dicarboxylate symporter | 0.43 | |
| VCA0137 | glycerol-3-phosphate transporter <i>glpT</i> | 0.48 | VpsR(-) |
| VCA0576 | heme transport protein HutA <i>hutA</i> | 2.70 | _ |
| VCA0591 | peptide ABC transporter_periplasmic peptide-binding protein_putative | 2.55 | $\sigma^{E}(+)$ |
| VCA0745 | glycerol uptake facilitator protein_authentic frameshift glpF | 0.46 | |
| VCA0911 | TonB system transport protein ExbB1 exbB1 | 4.02 | |
| VCA0912 | TonB system transport protein ExbD1 exbD1 | 2.37 | VpsR(-) |
| VCA0914 | hemin ABC transporter_permease protein_putative | 2.09 | |
| Unkown F | unction | | |
| VC0036 | FixG-related protein | 0.42 | |
| VC0130 | GGDEF family protein | 0.49 | |
| VC0595 | glutamyl-tRNA synthetase-related protein | 2.27 | |
| VC0851 | small protein A smpA | 2.07 | $\sigma^{E}(+)$ |
| VC1029 | GGDEF family protein | 2.96 | VpsR(+) |
| | CCDEE Consider works in | 2.01 | |
| VC1353 | GGDEF family protein | 2.01 | |
| VC1353 VC1532 | ROK family protein | 0.49 | |

| VC2067 | MinD-related protein | 0.49 | |
|--|---|--|--------------------|
| VC2361 | formate acetyl transferase-related protein | 0.46 | |
| VC2450 | mazG protein mazG | 2.56 | |
| VCA0038 | Sco1-related protein | 2.08 | |
| VCA0148 | TagA-related protein | 0.36 | |
| VCA0165 | GGDEF family protein | 2.00 | |
| VCA0175 | MoxR-related protein | 3.59 | $\sigma^{E}(+)$ |
| VCA0659 | protein F-related protein | 0.47 | VpsR(+) |
| VCA0785 | GGDEF family protein | 6.41 | VpsR(+) |
| VCA0969 | pirin-related protein | 2.01 | 1 () |
| VPS Biosy | | | |
| VC0916 | phosphotyrosine protein phosphatase | 5.15 | VpsR(+) |
| VC0917 | UDP-N-acetylglucosamine 2-epimerase <i>wecB</i> | 6.52 | VpsR(+) |
| VC0918 | UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase <i>epsD</i> | 10.28 | VpsR(+) |
| VC0919 | serine acetyltransferase-related protein | 13.31 | VpsR(+) |
| VC0920 | exopolysaccharide biosynthesis protein EpsF_ putative | 2.70 | VpsR(+) |
| VC0922 | hypothetical protein | 2.97 | VpsR(+) |
| VC0923 | serine acetyltransferase-related protein | 2.17 | VpsR(+) |
| VC0924 | capK protein putative | 2.57 | VpsR(+) |
| VC0925 | polysaccharide biosynthesis protein putative | 2.84 | VpsR(+) |
| VC0926 | hypothetical protein | 4.60 | VpsR(+) |
| VC0927 | UDP-N-acetyl-D-mannosamine transferase <i>cpsF</i> | 2.07 | VpsR(+) |
| VC0928 | hypothetical protein | 14.26 | VpsR(+) |
| VC0929 | hypothetical protein | 20.81 | VpsR(+) |
| VC0930 | hemolysin-related protein | 17.79 | VpsR(+) |
| VC0932 | hypothetical protein | 8.95 | VpsR(+) |
| VC0933 | hypothetical protein | 36.40 | VpsR(+) |
| VC0935 | hypothetical protein | 9.24 | VpsR(+) |
| VC0936 | polysaccharide export-related protein | 6.92 | VpsR(+) |
| VC0937 | exopolysaccharide biosynthesis protein putative | 3.38 | VpsR(+) |
| VC0938 | hypothetical protein | 2.90 | VpsR(+) |
| | cal Proteins | | 1 () |
| VC0131 | conserved hypothetical protein | 2.36 | |
| | 71 1 | | |
| | conserved hypothetical protein | 3.02 | |
| VC0187 | conserved hypothetical protein conserved hypothetical protein | 3.02 2.90 | |
| VC0187 VC0370 | conserved hypothetical protein | 2.90 | |
| VC0187 | ** | | |
| VC0187 VC0370 VC0420 | conserved hypothetical protein conserved hypothetical protein | 2.90 2.24 | VpsR(+) |
| VC0187 VC0370 VC0420 VC0421 | conserved hypothetical protein conserved hypothetical protein conserved hypothetical protein | 2.90 2.24 2.26 | VpsR(+) |
| VC0187 VC0370 VC0420 VC0421 VC0483 VC0490 | conserved hypothetical protein | 2.90 2.24 2.26 2.97 | VpsR(+) |
| VC0187 VC0370 VC0420 VC0421 VC0483 VC0490 VC0603 | conserved hypothetical protein | 2.90 2.24 2.26 2.97 2.21 | VpsR(+) |
| VC0187 VC0370 VC0420 VC0421 VC0483 VC0490 | conserved hypothetical protein | 2.90 2.24 2.26 2.97 2.21 2.44 | VpsR(+) |
| VC0187 VC0370 VC0420 VC0421 VC0483 VC0490 VC0603 VC0694 | conserved hypothetical protein | 2.90 2.24 2.26 2.97 2.21 2.44 0.49 | VpsR(+) |
| VC0187 VC0370 VC0420 VC0421 VC0483 VC0490 VC0603 VC0694 VC0702 | conserved hypothetical protein | 2.90 2.24 2.26 2.97 2.21 2.44 0.49 2.09 | VpsR(+) |
| VC0187 VC0370 VC0420 VC0421 VC0483 VC0490 VC0603 VC0694 VC0702 VC0761 VC0872 | conserved hypothetical protein | 2.90 2.24 2.26 2.97 2.21 2.44 0.49 2.09 2.04 2.01 | |
| VC0187 VC0370 VC0420 VC0421 VC0483 VC0490 VC0603 VC0694 VC0702 VC0761 VC0872 VC0873 | conserved hypothetical protein | 2.90 2.24 2.26 2.97 2.21 2.44 0.49 2.09 2.04 2.01 4.82 | σ ^E (-) |
| VC0187 VC0370 VC0420 VC0421 VC0483 VC0490 VC0603 VC0694 VC0702 VC0761 VC0872 VC0873 VC1131 | conserved hypothetical protein | 2.90 2.24 2.26 2.97 2.21 2.44 0.49 2.09 2.04 2.01 4.82 0.34 | σ ^E (-) |
| VC0187 VC0370 VC0420 VC0421 VC0483 VC0490 VC0603 VC0694 VC0702 VC0761 VC0872 VC0873 VC1131 VC1306 | conserved hypothetical protein | 2.90 2.24 2.26 2.97 2.21 2.44 0.49 2.09 2.04 2.01 4.82 0.34 2.18 | |
| VC0187 VC0370 VC0420 VC0421 VC0483 VC0490 VC0603 VC0694 VC0702 VC0761 VC0872 VC0873 VC1131 | conserved hypothetical protein | 2.90 2.24 2.26 2.97 2.21 2.44 0.49 2.09 2.04 2.01 4.82 0.34 | σ ^E (-) |

| VC1567 | conserved hypothetical protein | 4.16 | |
|---------|--------------------------------|-------|---------------------|
| VC1576 | conserved hypothetical protein | 2.68 | |
| VC1701 | conserved hypothetical protein | 7.04 | VpsR(+) |
| VC1841 | conserved hypothetical protein | 0.46 | |
| VC1842 | conserved hypothetical protein | 0.48 | |
| VC1851 | conserved hypothetical protein | 0.44 | |
| VC1884 | conserved hypothetical protein | 2.09 | |
| VC1937 | conserved hypothetical protein | 2.00 | VpsR(+) |
| VC1957 | conserved hypothetical protein | 2.79 | $\sigma^{\rm E}(+)$ |
| VC1978 | conserved hypothetical protein | 2.02 | |
| VC1986 | conserved hypothetical protein | 2.46 | |
| VC2146 | conserved hypothetical protein | 2.22 | |
| VC2164 | conserved hypothetical protein | 2.83 | |
| VC2206 | conserved hypothetical protein | 0.46 | |
| VC2253 | conserved hypothetical protein | 2.12 | |
| VC2441 | conserved hypothetical protein | 0.43 | |
| VC2471 | conserved hypothetical protein | 0.47 | |
| VC2473 | conserved hypothetical protein | 4.35 | |
| VC2517 | conserved hypothetical protein | 2.70 | $\sigma^{E}(-)$ |
| VC2518 | conserved hypothetical protein | 2.78 | $\sigma^{E}(-)$ |
| VC2548 | conserved hypothetical protein | 2.25 | $\sigma^{E}(-)$ |
| VC2716 | conserved hypothetical protein | 2.24 | |
| VCA0094 | conserved hypothetical protein | 2.61 | |
| VCA0167 | conserved hypothetical protein | 2.06 | VpsR(+) |
| VCA0171 | conserved hypothetical protein | 2.77 | |
| VCA0172 | conserved hypothetical protein | 3.31 | |
| VCA0174 | conserved hypothetical protein | 2.48 | $\sigma^{E}(+)$ |
| VCA0323 | conserved hypothetical protein | 3.31 | |
| VCA0536 | conserved hypothetical protein | 0.30 | VpsR(-) |
| VCA0539 | conserved hypothetical protein | 2.06 | |
| VCA0546 | conserved hypothetical protein | 0.45 | |
| VCA0582 | conserved hypothetical protein | 0.42 | _ |
| VCA0732 | conserved hypothetical protein | 20.14 | $\sigma^{E}(-)$ |
| VCA0931 | conserved hypothetical protein | 0.35 | |
| VCA0948 | conserved hypothetical protein | 2.22 | |
| VCA1004 | conserved hypothetical protein | 0.49 | |
| VCA1065 | conserved hypothetical protein | 0.45 | |
| VCA1085 | conserved hypothetical protein | 0.31 | VpsR(-) |
| VCA0887 | conserved hypothetical protein | 2.97 | VpsR(+) |
| VC1307 | conserved hypothetical protein | 2.73 | |
| VC0104 | hypothetical protein | 2.00 | |
| VC0132 | hypothetical protein | 3.56 | |
| VC0189 | hypothetical protein | 2.32 | |
| VC0301 | hypothetical protein | 2.17 | |
| VC0314 | hypothetical protein | 2.03 | |
| VC0713 | hypothetical protein | 2.67 | |
| VC0860 | hypothetical protein | 2.41 | |
| VC0862 | hypothetical protein | 0.43 | |
| VC0955 | hypothetical protein | 0.50 | |
| VC1007 | hypothetical protein | 0.27 | |
| | | | |

| VC1080 | hypothetical protein | 0.12 | VpsR(+) |
|---------|----------------------|-------|--------------------------|
| VC1116 | hypothetical protein | 3.81 | • • • • |
| VC1158 | hypothetical protein | 2.16 | |
| VC1160 | hypothetical protein | 2.62 | |
| VC1162 | hypothetical protein | 3.58 | |
| VC1192 | hypothetical protein | 0.46 | |
| VC1224 | hypothetical protein | 2.64 | |
| VC1262 | hypothetical protein | 0.07 | |
| VC1384 | hypothetical protein | 0.39 | |
| VC1418 | hypothetical protein | 4.21 | |
| VC1419 | hypothetical protein | 2.69 | |
| VC1420 | hypothetical protein | 2.19 | |
| VC1423 | hypothetical protein | 2.33 | |
| VC1438 | hypothetical protein | 0.46 | |
| VC1505 | hypothetical protein | 2.17 | |
| VC1564 | hypothetical protein | 3.82 | $\sigma^{\rm E}(+)$ |
| VC1572 | hypothetical protein | 2.71 | |
| VC1613 | hypothetical protein | 0.41 | |
| VC1637 | hypothetical protein | 7.21 | $\sigma^{E}(-)$ |
| VC1699 | hypothetical protein | 0.31 | |
| VC1729 | hypothetical protein | 0.50 | |
| VC1742 | hypothetical protein | 4.84 | $\sigma^{\mathrm{E}}(+)$ |
| VC1743 | hypothetical protein | 7.40 | $\sigma^{\mathrm{E}}(+)$ |
| VC1943 | hypothetical protein | 0.49 | |
| VC1946 | hypothetical protein | 6.46 | |
| VC2005 | hypothetical protein | 0.11 | |
| VC2046 | hypothetical protein | 0.32 | $\sigma^{\mathrm{E}}(+)$ |
| VC2058 | hypothetical protein | 0.48 | |
| VC2189 | hypothetical protein | 0.15 | |
| VC2205 | hypothetical protein | 0.48 | |
| VC2207 | hypothetical protein | 0.18 | |
| VC2208 | hypothetical protein | 0.44 | - |
| VC2212 | hypothetical protein | 2.04 | $\sigma^{E}(-)$ |
| VC2221 | hypothetical protein | 0.32 | |
| VC2611 | hypothetical protein | 0.46 | |
| VC2667 | hypothetical protein | 3.25 | VpsR(+) |
| VC2717 | hypothetical protein | 0.21 | |
| VCA0003 | hypothetical protein | 2.10 | |
| VCA0081 | hypothetical protein | 2.60 | |
| VCA0095 | hypothetical protein | 8.10 | |
| VCA0096 | hypothetical protein | 6.58 | |
| VCA0122 | hypothetical protein | 2.12 | |
| VCA0125 | hypothetical protein | 3.45 | _ |
| VCA0139 | hypothetical protein | 36.96 | $\sigma^{E}(-),VpsR(+)$ |
| VCA0162 | hypothetical protein | 0.38 | |
| VCA0168 | hypothetical protein | 3.52 | |
| VCA0169 | hypothetical protein | 2.04 | |
| VCA0170 | hypothetical protein | 2.44 | |
| VCA0195 | hypothetical protein | 0.43 | VpsR(+) |
| VCA0224 | hypothetical protein | 3.29 | |
| | | | |

| VCA0236 | hypothetical protein | 0.50 | VpsR(-) |
|---------|--|-------|--------------------------|
| VCA0258 | hypothetical protein | 3.95 | VpsR(+) |
| VCA0403 | hypothetical protein | 2.02 | |
| VCA0434 | hypothetical protein | 0.41 | $\sigma^{\mathrm{E}}(+)$ |
| VCA0551 | hypothetical protein | 3.43 | $\sigma^{\mathrm{E}}(+)$ |
| VCA0567 | hypothetical protein | 2.20 | |
| VCA0701 | hypothetical protein | 4.18 | |
| VCA0721 | hypothetical protein | 3.19 | $\sigma^{E}(-), VpsR(+)$ |
| VCA0722 | hypothetical protein | 2.37 | $\sigma^{E}(-)$ |
| VCA0733 | hypothetical protein | 2.19 | $\sigma^{E}(-)$ |
| VCA0787 | hypothetical protein | 0.29 | |
| VCA0845 | hypothetical protein | 4.96 | $\sigma^{E}(-), VpsR(+)$ |
| VCA0849 | hypothetical protein | 9.91 | VpsR(+) |
| VCA0868 | hypothetical protein | 0.22 | |
| VCA0882 | hypothetical protein | 2.55 | |
| VCA0899 | hypothetical protein | 0.39 | |
| VCA0916 | hypothetical protein | 2.69 | |
| VCA0918 | hypothetical protein | 4.22 | |
| VCA0962 | hypothetical protein | 10.70 | $\sigma^{E}(-)$ |
| VCA0966 | hypothetical protein | 3.29 | $\sigma^{E}(+), VpsR(+)$ |
| VCA0967 | hypothetical protein | 3.19 | $\sigma^{\mathrm{E}}(+)$ |
| VCA0971 | hypothetical protein | 0.32 | |
| VCA0976 | hypothetical protein | 2.79 | VpsR(-) |
| VCA0997 | hypothetical protein | 0.35 | |
| VCA1032 | hypothetical protein | 2.54 | |
| VCA1075 | hypothetical protein | 0.36 | VpsR(-) |
| VCA1076 | hypothetical protein | 0.23 | |
| VCA1103 | hypothetical protein | 0.37 | |
| VCA0494 | hypothetical protein | 0.22 | |
| Others | | | |
| VC0737 | acetoin utilization protein AcuB_ putative | 0.47 | _ |
| VC1161 | gonadoliberin III-related protein | 2.32 | $\sigma^{E}(-)$ |
| VC1696 | DNA-binding protein inhibitor Id-2-related protein | 0.34 | |
| VC1888 | hemolysin-related protein | 45.28 | VpsR(+) |
| VC1935 | CDP-diacylglycerolglycerol-3-phosphate 3-phosphatidyltransferase-related protein | 2.33 | |
| VCA0907 | heme-binding protein HutZ hutZ | 3.49 | |
| VCA0908 | hutX protein <i>hutX</i> | 2.92 | VpsR(-) |