

Supplementary Materials

Figure S1. Genomic structure of T6SS related genes in *V. cholerae*. The major T6SS cluster starts from VCA0107 and encode for structural components of T6SS including sheath (VipAB), ATPase (ClpV), IcmF homologue (VasK), DotU, and secreted VgrG3. The two separate *hcp* operons encode secreted Hcp and VgrG proteins that resembles T4 phage tail tube and spike proteins.

Figure S2. Confirmation of ChIP-Seq by qPCR. The ribosomal RNA *rrsA* was used as an internal control. Experiments were performed in biological triplicate.

Table S1. Primers used in this study.

Table S2. ChIP-Seq identified binding peaks.

Table S3. RpoN positively-regulated operons by RNA-Seq analysis.

Table S4. Genes expressed higher in the *rpoN* mutant.

Figure S1.

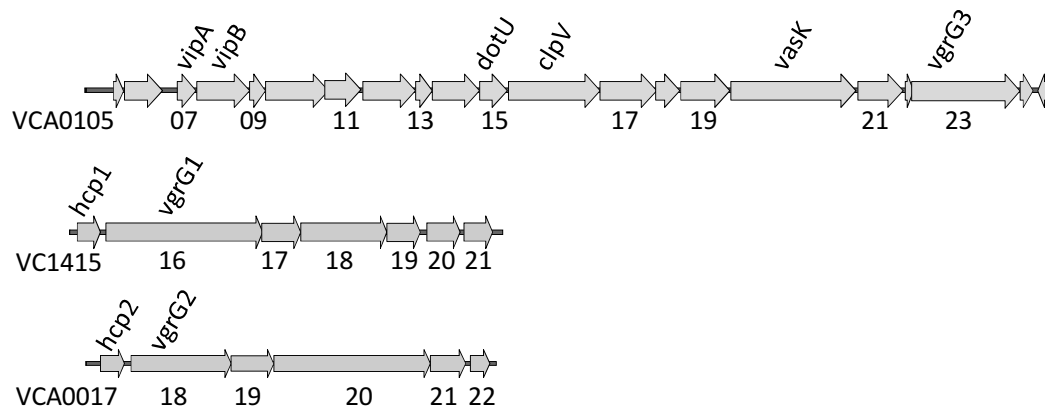


Figure S2.

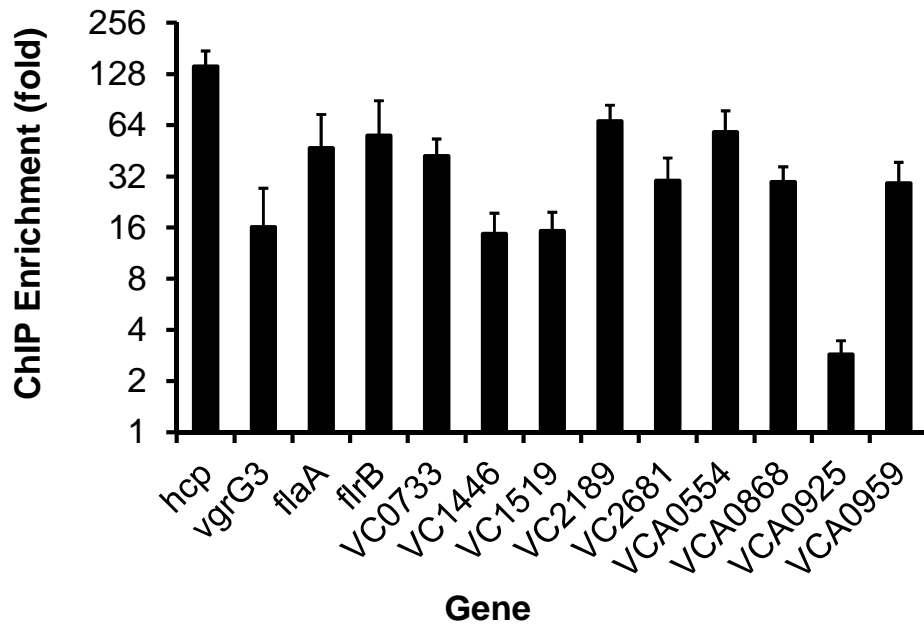


Table S1

| Primer | Sequence | Note |
|---------------|--|-----------------|
| rpoN1 | AAAAAAGGGCCCAGTCAGGACAGATTGTGG | rpoN-KO |
| rpoN4 | AAAAAACTCGAGTTATCGTTGAGGCGTTCT | rpoN-KO |
| rpoN2 | TTTCCTTCTCTAGTTTAGGCGCAGTAATGGATGCCTTGTT | rpoN-KO |
| rpoN3 | AACAAGGCATCCATTACTGCGCCTAACTAGAGAAGGAAA | rpoN-KO |
| rpoNcf | TGGCAAAGGGCGCGTCTCTA | rpoN-KO |
| rpoNcr | TAAAGGCTGTCAGCAGGCTGACGG | rpoN-KO |
| VbrpoN5' | ATAGGTACCAGGAGGAAACGATGAAACCGTCATTACAGCTCAAG | rpoN-pBAD |
| VbrpoN3' | ATAGTCGACTAGCAGGCGTTTGCCTGACT | rpoN-pBAD |
| vc1418f | ATAGGTACCAGGAGGAAACGATGGATTCAATTAATTATTGCGTG | VC1418-pBAD |
| vc1418r3v5 | ATAGTCGACTCTTATTTGCACCTTGATTTTCATCT | VC1418-pBAD |
| flaX-ko1 | AAAAAAGGGCCCAGTTCTAGCTCGGGTGAAGC | flaX-KO |
| flaX-ko2 | GCAGTTTGAAGTGAAGAGCTACATACCCACGTCTGAGCTC | flaX-KO |
| flaX-ko3 | GAGCTCAGACGTGGGTATGTAGCTCTCTCACTCAAAGTGC | flaX-KO |
| flaX-ko4 | AAAAAACTCGAGATTAAGCTCATCATTCAACG | flaX-KO |
| flaX-ko5 | ATCTCAGATTCTGCAACAGGCGG | flaX-KO |
| flaX-ko6 | GCCCTAAACCCCTCTGAAATCTATGC | flaX-KO |
| flaX-cpfd | ataTGCCAcacagggcgggactcaattc | flaX-complement |
| flaX-cprv | atagaattcGAGAACCGTTCTTCAGCGG | flaX-complement |
| flaXr | TGGTAGCCATCGCCAATGTGG | qPCR |
| flaXr2 | GAAATGAACACATTTTCGGCTAACC | qPCR |
| flaXf1 | CGAGCTCTCTCACTCAAAGTGC | qPCR |
| flaXf2 | CCAAATCTCAGATTCTGCAACAGG | qPCR |
| rrsArt1 | ACCTTACCTACTCTTGACATCCA | qPCR |
| rrsArt2 | CCCAACATTTCAACACGAG | qPCR |
| hcp1rt1 | TACCGACTGACCCACAATCT | qPCR |
| hcp1rt2 | AACCGACTTCAGCTTCTCAC | qPCR |
| vgrG2rt1 | ATCTTGACCCTGCGATGAAC | qPCR |
| vgrG2rt2 | ATGCCCTGGAATTAAGCTGA | qPCR |
| VCA0107F | TTTCAAATCCTTAGCCGACTTC | qPCR |
| VCA0107R | TAATGACTGTAACGCTCACGA | qPCR |
| VCA0108F | CCCAAATACCAAAGAAGGCAA | qPCR |
| VCA0108R | TCTTTCCAAGCACCGATCTG | qPCR |
| hcpf | AGCTTTTTGCTTTGTTGATGGGACT | ChIP-qPCR |
| hcpr | GAGTTGGCATGGCTATTTCTTTTCA | ChIP-qPCR |
| flrBf | GCAACGCTAGGGAAACCATAGTCA | ChIP-qPCR |
| flrBr | GCACTGCGCTGCTCATCATTC | ChIP-qPCR |
| flaAf | AAGCCATATGAGCGAAGTGAGTTGA | ChIP-qPCR |
| flaAr | CCCTGTACAACTTTTACCAAGGCT | ChIP-qPCR |
| vca0107f | ACTGTTTCATTGACAACGTTTGGCA | ChIP-qPCR |
| vca0107r | CCCGTCGCCGGAATATACTTGATAT | ChIP-qPCR |
| vgrG3f | GTTGAAAATATTGCGTGGCAGTCAA | ChIP-qPCR |
| vgrG3r | CAGAGTTAACCCTGGTGCGAAACA | ChIP-qPCR |
| vca0868fp | CCTTAACATTCTTCTAGTGCGA | ChIP-qPCR |
| vca0868rp | TGTGTCCATATCGTCATCCT | ChIP-qPCR |
| vc2189f | TTGCCGCTTTGGTTACCC | ChIP-qPCR |
| vc2189r | CATATGAGCGAAGTGAGTTGAG | ChIP-qPCR |
| vc1446f | TAGTACCACACTCATATTGCGG | ChIP-qPCR |
| vc1446r | TGCTGGTGGATGGAATGG | ChIP-qPCR |
| vca0925f | GTCACGCTCACCAAGCAA | ChIP-qPCR |
| vca0925r | TACTTCACTGTCCACTCGAT | ChIP-qPCR |
| vc0733f | CGTGGGATAAAGGTGTTGGA | ChIP-qPCR |
| vc0733r | AACGCTTGCCATTGTCTG | ChIP-qPCR |
| vc2681f | CGTGGGATAAAGGTGTTGGA | ChIP-qPCR |
| vc2681r | AACGCTTGCCATTGTCTG | ChIP-qPCR |
| vca0959f | AACGTCAGTTGGCTAGGT | ChIP-qPCR |
| vca0959r | AAAGTTGGCACGTAATCTGC | ChIP-qPCR |
| vca0554f | CTGCACTCCAGCCAAAGTC | ChIP-qPCR |
| vca0554r | GCGGGTTTCTGTATCAACCT | ChIP-qPCR |
| vc1519f | ACCAGTACCTTGCTTTAAGTAGAG | ChIP-qPCR |
| vc1519r | GTGCAAATCTTGCGGTAGAG | ChIP-qPCR |

Table S2

| Gene | Name | Function | Binding motif | Intergenic region (IG) | Distance from nearest 5' end (bp) |
|----------|---------------|--|------------------|------------------------|-----------------------------------|
| VC0174 | | hypothetical protein | CGGCTCTTTTTTTC | IG | 118 |
| VC0487 | <i>glmS</i> | glucosamine--fructose-6-phosphate aminotransferase (isomerizing) | TGGCATCGATCTTGA | | 309 |
| VC0606 | <i>glnB-1</i> | nitrogen regulatory protein P-II | TGGCACGCCCTTGG | IG | 35 |
| VC0665 | | sigma-54 dependent transcriptional regulator | TGGGCATTTGTTGGC | IG | 135 |
| VC0733 | | hypothetical protein | TGGTATAGCTTATGC | | 705 |
| VC1008 | <i>motY</i> | sodium-type flagellar protein MotY | TGGCTAGATTTTTGC | | 73 |
| VC1020 | | hypothetical protein | TGGCACGATATGTGC | IG | 132 |
| VC1064 | | lipoprotein, putative | TGGCATATAAATTC | IG | 44 |
| VC1144 | <i>clpA</i> | ATP-dependent Clp protease, ATP-binding subunit ClpA | TGGCACGTTTACTGC | | 127 |
| VC1154 | | hypothetical protein | TGGCACTCTAATTC | IG | 186 |
| VC1171 | | indole-3-glycerol phosphate synthase | TGGCGCGAATCTTGC | | 582 |
| VC1229 | | membrane protein, putative | TAGCACGTTTTATGC | IG | 85 |
| VC1252 | | CinA family protein | CGGTATAATAAATTC | | 313 |
| VC1269 | | lipoprotein, putative | TAGCACGTTTTATGC | IG | 71 |
| VC1384 | | hypothetical protein | AGGTACGAAATTC | | 92 |
| VC1415 | <i>hcp-1</i> | hcp protein | TGGCATCCCCTTGC | IG | 94 |
| VC1446* | | toxin secretion transporter | TGGAATGGATCTTGC | | 1633 |
| VC1516 | | iron-sulfur cluster-binding protein | TGGAACGCTAATTC | IG | 72 |
| VC1518 | | hypothetical protein | TGGCGCAATTTATGC | IG | 54 |
| VC1519* | <i>fdhD</i> | formate dehydrogenase accessory protein | CGGCACCCTTTTGC | | 87 |
| VC1523 | | conserved hypothetical protein | TGGCATCCCCTTGC | IG | 117 |
| VC1678 | <i>pspA</i> | phage shock protein A | TGGATTTATCTTTC | IG | 88 |
| VC1699 | | hypothetical protein | TGGCATCGGTTTTGC | IG | 130 |
| VC1988 | | conserved hypothetical protein | TGGCATTGGAATTC | | 549 |
| VC2005 | | hypothetical protein | AGGCACAGCATTTGC | IG | 109 |
| VC2068 | | flagellar biosynthetic protein FlhF, putative | TGGAACAAATTTGC | | 306 |
| VC2069 | <i>flhA</i> | flagellar biosynthetic protein FlhA | TGGACTGAAAATTC | IG | 211 |
| VC2128 | | flagellar hook-length control protein FliK, putative | TGGCTTACTTCTTGC | IG | 100 |
| VC2134 | <i>fliE</i> | flagellar hook-basal body complex protein FliE | TGGCATACAAATTC | IG | 54 |
| VC2136 | <i>fliB</i> | flagellar regulatory protein B | TGGCATGACTCTTGC | IG | 51 |
| VC2140 | <i>fliD</i> | flagellar rod protein | TGGCACTAAAATTC | | 434 |
| VC2177 | | conserved hypothetical protein | CGGTACGAAATTC | | 330 |
| VC2188 | <i>fliA</i> | flagellin core protein A | TGGCACACTAATTC | IG | 160 |
| VC2189 | | hypothetical protein | TGGCACGGAATTC | IG | 25 |
| VC2191 | <i>fliK</i> | flagellar hook-associated protein FlgK | TGGCATACATATTC | IG | 77 |
| VC2193 | <i>fliG</i> | flagellar P-ring protein FlgI | TGGCACGATTTTTTA | | 119 |
| VC2196 | <i>fliF</i> | flagellar basal-body rod protein FlgF | TGGCATGTGCTTGC | IG | 52 |
| VC2200 | <i>fliB</i> | flagellar basal-body rod protein FlgB | TGGTACGCTAATTC | IG | 63 |
| VC2207 | <i>fliQ</i> | flagellar membrane protein flgO | GGGTATAAATTTGC | IG | 115 |
| VC2208 | <i>fliT</i> | flagellar protein flgT | TGGAACGCTCCTTGC | IG | 106 |
| VC2287 | | DNA-damage-inducible protein P | CGGATCGCATAATTC | IG | 120 |
| VC2396 | <i>envA</i> | UDP-3-O-3-hydroxymyristoyl N-acetylglucosamine deacetylase | CGGCACAGCCTTGC | | 252 |
| VC2453 | | sensor histidine kinase/response regulator | CGGTTGAAAGAAACG | | 192 |
| VC2499 | | conserved hypothetical protein | TGGCACGCTGATATGC | | 400 |
| VC2623 | <i>trpS</i> | tryptophanyl-tRNA synthetase | TGGCACGCTGCTTGA | | 85 |
| VC2681* | | malate dehydrogenase, putative | TGGTATGCTTAATGC | | 545 |
| VC2746 | <i>glnA</i> | glutamate--ammonia ligase | TGGCACGCTTTTCGC | | 127 |
| VC2748 | <i>ntrB</i> | nitrogen regulation protein | CGGCAAGATTTATGC | | 199 |
| VCA0017 | <i>hcp-2</i> | hcp protein | TGGCATCCCCTTGC | IG | 76 |
| VCA0041 | <i>glts</i> | sodium/glutamate symporter | TGGCACGCTTCTGTC | IG | 331 |
| VCA0051 | | hypothetical protein | TGGCACAAATTTATGC | | 221 |
| VCA0101 | | conserved hypothetical protein | CGGCATTGAAAATTC | | 305 |
| VCA0105 | | conserved hypothetical protein | TGGAACATTAATTC | IG | 52 |
| VCA0123 | <i>vgrG-3</i> | vgrG protein | TGGCATTGAGTTTGC | | 129 |
| VCA0144 | | immunogenic protein | TGGCATCTTCTTTC | | 48 |
| VCA0195 | | hypothetical protein | CGGCGCATTTATTC | | 217 |
| VCA0284 | | hypothetical protein | TGTACAGAAATGAGC | | 43 |
| VCA0525 | | hypothetical protein | AGGCACAAATTTGC | | 364 |
| VCA0546 | | conserved hypothetical protein | TGGCATATAGCTTGC | | 475 |
| VCA0554* | | oxalate/formate antiporter | TGGCATCTTTATGC | | 77 |
| VCA0734 | | hypothetical protein | TGGCTGTAAATTC | IG | 53 |
| VCA0826 | | hypothetical protein | TGGCACAGATAGTGC | IG | 249 |
| VCA0868* | <i>pbpG</i> | D-alanyl-D-alanine endopeptidase | TGGCATCAAATATGC | | 16 |
| VCA0925* | | conserved hypothetical protein | CGGCATGCTTCTGTC | | 990 |
| VCA0959* | | hypothetical protein | TGGCACGTAATCTGC | | 146 |
| VCA0973 | | hypothetical protein | TGGCACTTTATTC | | 197 |
| VCA1016 | | lipoprotein, putative | TGGCACGCACTATGC | | 244 |
| VCA1075 | | hypothetical protein | CGGAATAAATTC | IG | 71 |

Note: * indicates a binding site inside the gene and the distance from its 5' end is shown. Genes underlined are known RpoN-controlled genes. The distance from the binding sites to the nearest 5' end for a gene in the same direction is indicated. IG: intergenic regions.

Table S3

| Operon | Gene | Function | Fold change (pRpoN/pBAD) | P value | ChIP-peak |
|--------------------------------|-----------------------|--|------------------------------------|---------|-----------|
| T6SS | | | | | |
| VC1415-20 | <i>hcp1/vgrG1</i> | T6SS secretion | 511.1/61.9/14.8/6.4/7.0/4.7 | 0.001 | ChIP |
| VCA0017-23 | <i>hcp2/vgrG2</i> | T6SS secretion | 532.5/94.1/19.0/14.5/12.7/2.8/3.8 | 0.001 | ChIP |
| VCA0123 | <i>vgrG3</i> | T6SS secretion | 2.4 | 0.001 | ChIP |
| Motility and Chemotaxis | | | | | |
| VC1008 | <i>motY</i> | sodium-type flagellar protein | 16.9 | 0.001 | ChIP |
| VC1384 | | putative outer membrane protein | 7.6 | 0.000 | ChIP |
| VC2065-59 | <i>cheYZAB-W</i> | chemotaxis | 2.5/2.6/2.5/2.6/2.3/2.3/1.8 | 0.030 | |
| VC2068-66 | <i>flhFG-flhA</i> | flagellar biosynthesis /sigma factor FliA | 16.2/6.8/3.3 | | ChIP |
| VC2069 | <i>flhA</i> | flagellar biosynthesis | 7.4 | 0.001 | ChIP |
| VC2123-20 | <i>fliPQR-flhB</i> | flagellar biosynthesis | 2.6/2.8/3.1/3.1 | 0.001 | |
| VC2125-24 | <i>fliNO</i> | flagellar motor switch | 3.3/2.9 | 0.001 | |
| VC2126 | <i>fliM</i> | flagellar motor switch | 2.0 | 0.001 | |
| VC2128 | <i>fliK</i> | flagellar hook-length control | 36.2 | 0.001 | ChIP |
| VC2134-29 | <i>fliEFGHIJ</i> | flagellar assembly | 5.6/5.5/5.3/4.7/6.0/6.6 | 0.001 | ChIP |
| VC2136-35 | <i>fliRBC</i> | flagellar regulator | 3.2/2.3 | 0.001 | ChIP |
| VC2140-38 | <i>fliD/flaI/fliS</i> | flagellar rod/hook-associated protein | 2.1/3.4/5.2/5.4 | 0.001 | ChIP |
| VC2143 | <i>flaD</i> | flagellin | 87.9 | 0.000 | |
| VC2144 | <i>flaE</i> | flagellin | 15.6 | 0.001 | |
| VC2187 | <i>flaC</i> | flagellin | 54.6 | 0.001 | |
| VC2188 | <i>flaA</i> | flagellin core protein | 251.0 | 0.001 | ChIP |
| VC2189 | | hypothetical protein | 176.4 | 0.001 | ChIP |
| VC2191-90 | <i>flgKL</i> | flagellar hook-associated protein | 79.0/46.2 | 0.001 | ChIP |
| VC2193-92 | <i>flgIJ</i> | flagellar P-ring /flagellar protien | 67.6/47.6 | 0.001 | ChIP |
| VC2196-94 | <i>flgFGH</i> | flagellar basal rod / L-ring | 183.9/84.0/93.1 | 0.001 | ChIP |
| VC2200-2197 | <i>flgBCDE</i> | flagellar basal-body rod protein/hook protein E | 155.2/36.9/51.0/47.3 | 0.001 | ChIP |
| VC2204 | <i>flgM</i> | negative regulator of flagelin synthesis | 2.8 | 0.030 | |
| VC2207-06 | <i>flgOP</i> | outer membrane proteins important for motility | 79.5/23.5 | 0.001 | ChIP |
| VC2208 | <i>flgT</i> | flagellar assembly protein | 2.4 | 0.001 | ChIP |
| VC2601 | <i>motX</i> | sodium-type flagellar protein | 7.8 | 0.001 | |
| VCA0176 | | methyl-accepting chemotaxis protein | 5.5 | 0.001 | |
| Regulator | | | | | |
| VC0291 | | NifR3/Smm1 family protein | 2.6 | | |
| VC0606-07 | <i>glnB-1</i> | nitrogen regulatory protein P-II | 32.7/14.8 | 0.005 | ChIP |
| VC2748 | <i>ntrB</i> | nitrogen regulation protein | 2.8 | 0.001 | ChIP |
| Enzyme and biosynthesis | | | | | |
| VC0211 | <i>pyrE</i> | orotate phosphoribosyltransferase | 2.3 | 0.003 | |
| VC0894 | <i>thil</i> | thiamin biosynthesis protein | 2.1 | 0.006 | |
| VC0916 | | phosphotyrosine protein phosphatase | 2.0 | 0.001 | |
| VC0934 | | putative glycosyltransferase | 2.1 | 0.030 | |
| VC0991 | <i>asnB</i> | asparagine synthetase B, glutamine-hydrolyzing | 3.6 | 0.002 | |
| VC0999 | <i>truA</i> | tRNA pseudouridine synthase A | 2.6 | 0.020 | |
| VC1463 | <i>rstA2</i> | DNA topoisomerase | 2.4 | 0.001 | |
| VC1516-10 | | formate dehydrogenase | 63.9/44.6/40.7/69.4/48.1/51.6/22.3 | 0.001 | ChIP |
| VC1519 | <i>fdhD</i> | formate dehydrogenase accessory protein | 3.0 | 0.001 | ChIP |
| VC1523-27 | | ABC transporter and molybdopterin synthesis | 5.4/5.7/3.9/2.3/2.1 | 0.001 | ChIP |
| VC1819 | <i>aldA-2</i> | aldehyde dehydrogenase | 2.2 | 0.004 | |
| VC1929-28 | <i>dctP2/dctQ</i> | C4-dicarboxylate-binding periplasmic protein/transport | 5.4/2.9 | 0.001 | |
| VC2502 | <i>holC</i> | DNA polymerase III, chi subunit | 2.1 | 0.002 | |
| VC2510-11 | <i>pyrBI</i> | aspartate carbamoyltransferase | 3.2/3.2 | 0.041 | |
| VC2708 | <i>gmK</i> | guanylate kinase | 2.5 | 0.004 | |
| VC2746 | <i>glnA</i> | glutamate--ammonia ligase | 3.4 | 0.004 | ChIP |
| VCA0183 | | ferrisiderophore reductase | 2.0 | 0.001 | |
| VCA0804 | <i>deaD</i> | ATP-dependent RNA helicase | 2.2 | 0.001 | |
| Unknown function | | | | | |
| VC0599 | | hypothetical protein | 8.2 | 0.020 | |
| VC0912 | | hypothetical protein | 2.8 | 0.001 | |
| VC1009 | | hypothetical protein | 2.1 | 0.016 | |
| VC1058 | | hypothetical protein | 3.8 | 0.002 | |
| VC1105 | | hypothetical protein | 2.2 | 0.014 | |
| VC1124-25 | | hypothetical protein/lipo protein | 2.1/2.3 | 0.001 | |
| VC1154 | | hypothetical protein | 3.8 | 0.001 | ChIP |
| VC1252 | | CinA family protein | 2.3 | 0.004 | |
| VC1386 | | putative chaperone | 2.8 | 0.001 | |
| VC1518-17 | | hypothetical protein | 7.5/10.9 | 0.001 | ChIP |

| | | | | | |
|------------|---------------|---|-----------------|-------|------|
| VC1587 | | hypothetical protein | 2.9 | 0.049 | |
| VC1678-76 | <i>pspABC</i> | phage shock proteins | 5.9/2.5/3.2 | 0.001 | ChIP |
| VC1699 | | hypothetical protein | 3.8 | 0.012 | ChIP |
| VC1734 | | hypothetical protein | 3.2 | 0.013 | |
| VC1891 | | hypothetical protein | 3.4 | 0.048 | |
| VC1988 | | hypothetical protein | 2.3 | 0.023 | |
| VC2005 | | hypothetical protein | 28.5 | 0.002 | ChIP |
| VC2046 | | hypothetical protein | 7.8 | 0.001 | |
| VC2058 | | hypothetical protein | 2.4 | 0.004 | |
| VC2507 | | hypothetical protein | 2.6 | 0.001 | |
| VC2706 | | hypothetical protein | 2.5 | 0.048 | |
| VC2717 | | hypothetical protein | 4.8 | 0.002 | |
| VCA0051-48 | | hypothetical protein/GGDEF family protein | 2.0/2.0/2.6/2.3 | 0.001 | ChIP |
| VCA0105-06 | | hypothetical protein | 17.5/14.4 | 0.001 | ChIP |
| VCA0144 | | immunogenic protein | 4.9 | 0.012 | ChIP |
| VCA0146 | | hypothetical protein | 2.4 | 0.030 | |
| VCA0187 | | hypothetical protein | 3.4 | 0.046 | |
| VCA0195 | | hypothetical protein | 4.6 | 0.002 | ChIP |
| VCA0284-86 | | hypothetical protein | 47.3/34.9/19.4 | 0.001 | ChIP |
| VCA0659 | | OmpA family protein | 3.7 | 0.002 | |
| VCA0734 | | hypothetical protein | 3.1 | 0.003 | ChIP |
| VCA1016 | | putative lipoprotein | 4.3 | 0.010 | ChIP |

Table S4

| Gene | Synonym | Function | Ratio (pRpoN/pBAD) | P-value |
|-------------|----------------|--|-------------------------------|----------------|
| VC0023 | | hypothetical protein | 0.51 | 0.044 |
| VC0030 | <i>ilvM</i> | acetolactate synthase II, small subunit | 0.50 | 0.013 |
| VC0076 | <i>uspA</i> | universal stress protein A | 0.43 | 0.002 |
| VC0101 | | hypothetical protein | 0.18 | 0.009 |
| VC0162 | <i>ilvC</i> | ketol-acid reductoisomerase | 0.34 | 0.007 |
| VC0171 | | peptide ABC transporter, periplasmic peptide-binding protein | 0.42 | 0.006 |
| VC0193 | | hypothetical protein | 0.27 | 0.010 |
| VC0287 | <i>gntV</i> | thermoresistant gluconokinase | 0.39 | 0.020 |
| VC0479 | | hypothetical protein | 0.50 | 0.014 |
| VC0488 | | extracellular solute-binding protein, putative | 0.46 | 0.000 |
| VC0583 | | hemagglutinin/protease regulatory protein, authentic frameshift | 0.24 | 0.000 |
| VC0654 | | conserved hypothetical protein | 0.34 | 0.021 |
| VC0765 | | conserved hypothetical protein | 0.44 | 0.006 |
| VC0800 | <i>citX</i> | apo-citrate lyase phosphoribosyl-dephospho-CoA transferase | 0.42 | 0.003 |
| VC0801 | <i>citG</i> | triphosphoribosyl-dephospho-CoA synthase CitG | 0.47 | 0.021 |
| VC0802 | | hypothetical protein | 0.48 | 0.039 |
| VC0872 | | conserved hypothetical protein | 0.47 | 0.022 |
| VC0957 | | conserved hypothetical protein | 0.44 | 0.014 |
| VC0975 | | conserved hypothetical protein | 0.41 | 0.000 |
| VC0976 | | conserved hypothetical protein | 0.39 | 0.000 |
| VC0988 | | proton/peptide symporter family protein | 0.45 | 0.001 |
| VC1080 | | hypothetical protein | 0.39 | 0.025 |
| VC1083 | | hypothetical protein | 0.49 | 0.007 |
| VC1103 | | ABC transporter, ATP-binding protein | 0.49 | 0.021 |
| VC1114 | <i>bioC</i> | biotin synthesis protein BioC | 0.31 | 0.022 |
| VC1133 | <i>hisD</i> | histidinol dehydrogenase | 0.46 | 0.002 |
| VC1135 | <i>hisB</i> | imidazoleglycerol-phosphate dehydratase/histidinol-phosphatase | 0.51 | 0.012 |
| VC1138 | <i>hisF</i> | hisF protein (cyclase) | 0.50 | 0.009 |
| VC1157 | | response regulator | 0.47 | 0.032 |
| VC1280 | | hypothetical protein | 0.44 | 0.003 |
| VC1283 | <i>celC</i> | PTS system, cellobiose-specific IIA component | 0.37 | 0.030 |
| VC1294 | | hypothetical protein | 0.36 | 0.004 |
| VC1360 | | amino acid ABC transporter, permease protein | 0.41 | 0.012 |
| VC1368 | | hypothetical protein | 0.48 | 0.004 |
| VC1433 | | conserved hypothetical protein | 0.49 | 0.006 |
| VC1484 | <i>rmf</i> | ribosome modulation factor | 0.40 | 0.001 |
| VC1528 | | hypothetical protein | 0.51 | 0.008 |
| VC1529 | | hypothetical protein | 0.33 | 0.005 |
| VC1589 | <i>aldC</i> | alpha-acetolactate decarboxylase | 0.24 | 0.006 |
| VC1590 | <i>alsS</i> | acetolactate synthase, catabolic | 0.21 | 0.003 |
| VC1591 | | oxidoreductase, short-chain dehydrogenase/reductase family | 0.24 | 0.012 |
| VC1696 | | hypothetical protein | 0.42 | 0.002 |
| VC1809 | | transcriptional regulator, putative | 0.39 | 0.004 |
| VC1825 | | transcriptional regulator | 0.44 | 0.013 |
| VC1853 | | conserved hypothetical protein | 0.49 | 0.005 |
| VC1863 | | amino acid ABC transporter, periplasmic amino acid-binding protein | 0.51 | 0.028 |
| VC1873 | | conserved hypothetical protein | 0.51 | 0.002 |
| VC1991 | | hypothetical protein | 0.39 | 0.000 |
| VC1992 | <i>purU</i> | formyltetrahydrofolate deformylase | 0.51 | 0.013 |
| VC2010 | | hypothetical protein | 0.50 | 0.002 |
| VC2070 | <i>sixA</i> | phosphohistidine phosphatase | 0.47 | 0.008 |
| VC2078 | <i>feoA</i> | ferrous iron transport protein A | 0.48 | 0.032 |

| | | | | |
|---------|---------------|--|------|-------|
| VC2145 | | tyrA protein | 0.51 | 0.000 |
| VC2216 | | conserved hypothetical protein | 0.51 | 0.006 |
| VC2220 | | conserved hypothetical protein | 0.51 | 0.002 |
| VC2221 | | hypothetical protein | 0.36 | 0.045 |
| VC2351 | | hypothetical protein | 0.46 | 0.000 |
| VC2362 | <i>thrC</i> | threonine synthase | 0.44 | 0.007 |
| VC2364 | <i>thrA</i> | aspartokinase I/homoserine dehydrogenase, threonine-sensitive | 0.40 | 0.001 |
| VC2448 | <i>pyrG</i> | CTP synthase | 0.47 | 0.001 |
| VC2490 | <i>leuA</i> | 2-isopropylmalate synthase | 0.46 | 0.006 |
| VC2491 | <i>leuB</i> | 3-isopropylmalate dehydrogenase | 0.46 | 0.013 |
| VC2492 | <i>leuC</i> | 3-isopropylmalate dehydratase, large subunit | 0.49 | 0.005 |
| VC2493 | <i>leuD</i> | 3-isopropylmalate dehydratase, small subunit | 0.47 | 0.019 |
| VC2754 | | hypothetical protein | 0.51 | 0.003 |
| VCA0013 | <i>malP</i> | maltodextrin phosphorylase | 0.49 | 0.001 |
| VCA0014 | <i>malQ</i> | 4-alpha-glucanotransferase | 0.50 | 0.000 |
| VCA0034 | | conserved hypothetical protein | 0.50 | 0.049 |
| VCA0043 | | conserved hypothetical protein | 0.51 | 0.001 |
| VCA0053 | <i>deoD-2</i> | purine nucleoside phosphorylase | 0.41 | 0.046 |
| VCA0072 | <i>pstA-2</i> | phosphate ABC transporter, permease protein | 0.47 | 0.012 |
| VCA0078 | | hypothetical protein | 0.45 | 0.000 |
| VCA0130 | <i>rbsB</i> | ribose ABC transporter, periplasmic D-ribose-binding protein | 0.50 | 0.003 |
| VCA0231 | | transcriptional regulator, AraC/XylS family | 0.50 | 0.032 |
| VCA0270 | <i>dacA-2</i> | D-alanyl-D-alanine carboxypeptidase | 0.51 | 0.003 |
| VCA0274 | <i>cah</i> | carbonic anhydrase | 0.40 | 0.000 |
| VCA0279 | | transcriptional regulator, HTH_3 family | 0.48 | 0.015 |
| VCA0306 | | hypothetical protein | 0.40 | 0.035 |
| VCA0316 | | acetyltransferase, putative | 0.49 | 0.019 |
| VCA0328 | | glyoxalase family protein | 0.43 | 0.037 |
| VCA0336 | | hypothetical protein | 0.46 | 0.011 |
| VCA0421 | | hypothetical protein | 0.51 | 0.050 |
| VCA0465 | | hypothetical protein | 0.35 | 0.012 |
| VCA0523 | | aminotransferase, class II | 0.51 | 0.023 |
| VCA0536 | | conserved hypothetical protein | 0.34 | 0.006 |
| VCA0540 | | formate transporter 1, putative | 0.46 | 0.031 |
| VCA0562 | | hypothetical protein | 0.49 | 0.030 |
| VCA0610 | <i>elbB</i> | enhancing lycopene biosynthesis protein 2 | 0.42 | 0.035 |
| VCA0623 | <i>talB</i> | transaldolase B | 0.51 | 0.007 |
| VCA0647 | | hypothetical protein | 0.30 | 0.006 |
| VCA0702 | | iron-containing alcohol dehydrogenase | 0.46 | 0.006 |
| VCA0716 | | conserved hypothetical protein | 0.43 | 0.000 |
| VCA0743 | | conserved hypothetical protein | 0.33 | 0.007 |
| VCA0759 | <i>artI</i> | arginine ABC transporter, periplasmic arginine-binding protein | 0.42 | 0.004 |
| VCA0784 | | hypothetical protein | 0.47 | 0.049 |
| VCA0823 | <i>ectC</i> | ectoine synthase | 0.47 | 0.000 |
| VCA0886 | <i>kbl</i> | 2-amino-3-ketobutyrate coenzyme A ligase | 0.41 | 0.009 |
| VCA0902 | | hypothetical protein | 0.49 | 0.004 |
| VCA1001 | | transcriptional regulator, AraC/XylS family | 0.48 | 0.016 |
| VCA1100 | | ABC transporter, permease protein | 0.49 | 0.026 |
| VCA1107 | | hypothetical protein | 0.51 | 0.016 |