

Supplement File 2. Predicted Fur-regulated genes and operons and the annotated function of the gene products in the 5 sequenced vibrio genomes and the *V. salmonicida* draft genome.

<i>V. salmonicida</i>	Patser score Forward	Patser score Reverse	Distance from translational start to Fur-box	COG(s)
Iron Metabolism				
pVS320_0029-32-Iron ABC-transporter (Plasmid pVS320)	12.4/13.7	7.4/10.1	-46	NA
small regulatory RNA ryhB	12.8/12.9	9.1/9.3	-20	NA
(TVS1684-Heme receptor)	10.56/15.684.44	5.92/13.56/6.91	-74	COG1629
				COG0635
				COG3721
TVS1702-00-Putative coproporphyrinogen oxidase PhuW	4.54/12.92	7.16/5.0/12.37	-146	COG0748
				COG0810
				COG0811
				COG0848
				COG0614
				COG0609
(TVS1703-09- <i>tonB1</i> -system/heme transporter)	7.16/5.0/12.37	4.54/12.92	-65	COG1120
TVS1742-Putative iron-regulated protein	4.72/4.62/11.99	7.40/6.07/13.35	-82	COG3487
				COG1918
				COG0370
TVS2229-31-Ferrous iron transport protein FeoAB	4.93/12.48	6.42/11.46/7.06	-44	-
				COG1840
				COG1178
TVS2601-599-Iron(III) ABC transporter FbpABC	11.45/6.82	6.12/11.924.05	-52	COG3841

				COG0076
				COG3486
				-
				COG1629
				COG0614
				COG0609
				COG0609
TVS3255-48 Siderophore biosynthetic enzyme	9.59/14.91	4.88/15.77/4.69	-129	COG1120
				-
				-
				-
				COG0811
				COG0848
				COG0457
TVS3559-65-TonB dependent receptor/ <i>tonB2</i> -system	5.60/13.14	11.46	-74	COG0457
				COG0614
				COG0609
				COG0609
TVS3601-03-Ferrichrome transporter FhuCDB	5.25/13.26/4.90	12.14/5.84	-80	COG1120
TVS4198-Ferric aerobactin receptor precursor lutA	7.54	4.54	-63	COG1629
(TVS4204-Siderophore biosynthesis protein lucA)				NA

Energy Metabolism

TVS0566-2Fe-2S ferredoxin				COG0633
TVS0692-Flavodoxin 1	7.16	7.43	-46	COG0716
TVS1372-73-Putative ferredoxin	9.89/14.20	6.09/13.35	-281	COG1145
				COG1132
TVS1802-01-Transport ATP-binding protein CydDC	5.61	7.01	-69	COG1132

				COG2209
				COG2878
				-
				COG1805
				COG2869
TVS1837-32-Electron transport complex protein RnfA		4.93/4.55	-22	COG1347
TVS1855-Cytochrome d ubiquinol oxidase subunit I				COG1271
TVS1970-Cytochrome c-552 precursor	5.26/9.91	4.01/10.51	-226	COG3303
				-
				COG0437
				COG3301
				COG1138
				COG0526
TVS1971-76-Cytochrome c-type protein NrfB precursor	4.01/10.51	5.26/9.91	-284	COG3088
				COG1131
				COG2386
				COG0755
				COG3114
				COG2332
				COG1138
				COG0526
				-
TVS2276-68-Cytochrome biogenesis protein ABCD	7.08/7.73/8.22	5.75/4.76/4.39	-142	-
TVS3168-Putative ferredoxin	7.3	4.81	-23	COG0526
TVS4048-Putative ferredoxin	6.48	5.96	-7	COG3217
				COG1622
				COG0843
				COG1845
				COG3125
(TVS4328-33-Cytochrome o ubiquinol oxidase)	4.95	5.88/5.97	-188	COG0109

				COG1629
				COG1120
				COG0614
(TVS4426-22-Ferrioxamine B receptor)	5.46/7.18	9.14/7.78	-55	COG0609
Virulence Factors				
(TVS0720-Accessory colonization factor AcfD)	8.15/6.21	4.72/6.21	-75	NA
(TVS1367-Methyl-accepting chemotaxis protein)	7.53	4.91/7.93	-174	COG0840
(TVS1654-Putative hemolysin)				NA
(TVS1797-Hemolysin HlyA)	4.05	5.03/4.69	-108	NA
TVS1921-Methyl-accepting chemotaxis protein	4.27	5.22/4.74	-82	COG0840
TVS2034-Virulence protein VirC	4.96/4.16	4.97	-129	COG1648
TVS2182-Methyl-accepting chemotaxis protein	4.43		-99	COG0840
				COG1298
TVS2288-77-Polar flagellar assembly protein FlhA/FlhH	4.77/4.35	4.39/7.03/5.98	-43	COG1419
TVS2327-Flagellin subunit A	5.81/6.30/4.16/7.08	6.53/5.56	-82	COG1344
TVS3342-Methyl-accepting chemotaxis protein	4.01/4.61	5.47/4.71	-19	COG0840
				COG0845
				COG3672
TVS3429-25-Secretion protein, HlyD family	8.82	5.06	-44	COG2274
TVS3458-Hemolysin-type calcium-binding protein	5.03	5.57	-215	NA
TVS3730-Methyl-accepting chemotaxis protein	5.06	9.22	-304	COG0840
TVS3769-Methyl-accepting chemotaxis protein	4.74	4.67	-162	COG0840
TVS3926-Hemolysin secretion protein	6.89/5.23	5.58/4.79	-189	COG0840
(TVS4016-Methyl-accepting chemotaxis protein)				COG0840
TVS4321-Methyl-accepting chemotaxis protein	4.91		-117	COG0840
Miscellaneous				
TVS0304-Type IV pilus, mannose-sensitive hemagglutinin A	9.53	8.70/6.37	-151	NA
TVS0515-Putative membrane protein	8.35	4.92	-7	COG2165

TVS0535-Glycine cleavage system transcriptional activator	8.21/4.84	10.66	-51	COG0583
TVS0540-Conserved hypothetical protein	9.51	6.67	-14	NA
TVS0658-Copper-transporting P-type ATPase				COG2217
TVS0708-07-High-affinity zinc uptake system, atp-binding protein ZnuC	8.45	6.77	-24	COG1121 COG1108
TVS0709-High-affinity zinc uptake system protein ZnuA precursor	6.77	8.45	-83	COG0803
TVS0742-40-Putative exported protein	7.47	4.25/4.95/8.72	-19	NA
TVS0743-Putative exported protein	8.9	10.25	-49	NA
TVS0751-Conserved hypothetical protein	11.17	5.74/9.49	-88	COG1720
TVS0843-Membrane permease	6.71	6.06	-165	COG2252
TVS0934-Putative exported protein	7.24/4.69	5.32	-38	NA
TVS0990-Putative exported protein	5.27/7.73	4.29/4.40/9.10	-33	NA
TVS1048-Probable protease SohB	9.86	10.12	-83	COG0616
TVS1078-Transcriptional regulator, AraC-family	7.83	5.56/4.49	-97	COG2207
TVS1113-Putative exported protein	6.64		-1	NA
TVS1146-Membrane protein	5.64/13.24	4.33/12.69	-261	COG2020
TVS1251-Hypothetical protein	5.55		-125	NA
TVS1252-L-serine dehydratase 1	8.05	5.17/4.11	-55	COG1760
TVS1382-HTH-type transcriptional regulator, AraC family	4.27/4.97	6.46	-105	COG2207 COG1132 COG2995 COG3008
TVS1472-70-ABC transporter	4.37/11.57/5.45	4.99/11.83	-19	COG3008
TVS1637-Hypothetical protein	6.57/8.73	7.78/5.49	6	NA
TVS1829-Putative outer membrane protein	15.45	4.02/15.09	-60	NA
TVS1886-Inner membrane protein	9.57	6.88	-55	COG0697
TVS1888-Putative membrane protein	7.58	5.23	-268	NA
TVS2006-HTH-type transcriptional regulator HexR	7.3/6.14	5.94/5.96	-105	COG1737
TVS2038-FAD linked oxidase				COG0277

				COG0226
				COG0573
				COG0581
TVS2098-101-Phosphate ABC transporter	4.65/9.63	6.53/10.48/7.24	-161	COG1117
TVS2374-Hypothetical protein	5.01/9.46	4.56/10.99	-35	NA
TVS2635-HTH-type luminescence regulator LitR				COG1309
TVS2767-50S ribosomal protein L31	4.59/4.66	6.62	-83	COG0254
				COG1053
				COG0479
				COG3029
TVS2812-15-Fumarate reductase flavoprotein	9.11	10.55/7.11	-255	COG3080
TVS2877-HTH-type transcriptional regulator, MerR-family	9.48	5.77	-8	COG0789
TVS2888-Uroporphyrinogen decarboxylase				COG0407
TVS2918-Hypothetical protein	12.46/10.49	11.71/5.96	-39	COG3315
TVS3010-Hypothetical protein/				
TVS3011 Zn-dependent peptidase	10.57/6.43	9.13	-17	NA
TVS3183-Putative exported protein	8.24/4.53	6.91/7.48/5.12	14	NA
TVS3265-Protein CyaY				COG1965
TVS3375-Hypothetical protein	7.84	5.46	-128	NA
TVS3395-MFS transporter	7.14/7.77	5.61/4.73	-65	COG0477
(TVS3491-Putative membrane protein)				COG0672
TVS3517-Membrane protein	6.96/13/63/4.56	7.42/12.64/7.17	-64	NA
TVS3599-Hypothetical protein	4.90/9.96	5.25/12.32	-79	NA
TVS3618-HTH-type transcriptional regulator, AraC-family				COG2207
TVS3627-Extracellular solute-binding protein				COG1840
TVS3703-Manganese-dependent inorganic pyrophosphatase				COG1227
TVS3855-MFS transporter				COG0477
TVS3901-Hypothetical protein	7.47/4.26/5.73	6.71/4.39	-60	NA
TVS3985-Hypothetical protein	9.86	10.83	-44	NA

TVS4066-Peptidase T	6.50/5.55	9.17/7.24	-244	COG2195
TVS4118-Hypothetical protein	4.56/6.62	4.46/6.68	-202	NA
TVS4132-Membrane protein	7.69/4.94	6.9	-71	COG3217
TVS4161-60-Putative exported protein	10.01/4.97/5.0	10.00/7.33/6.46	-151	NA
TVS4187-Putative exported protein	8.35	7.81	-166	NA
TVS4235-Putative exported protein	5.19/9.85	6.53/4.01/7.16	-120	NA
TVS4310-Divalent cation transporter, putative Mg transporter	4.80/7.79	6.92	-61	COG2239
TVS4348-ATP-dependent protease LA-related protein	6.73/4.90	6.00/5.23	-179	COG1067
TVS4378-Hypothetical protein	9.07/8.60	8.51/8.70	-81	COG3016
TVS4394-Cell aggregate formation protein, BsmA	4.98/9.47	7.16/8.73	-83	NA
TVS4439-Response regulator protein	6.93	4.19/4.39	-4	NA

V. cholerae

Iron Metabolism

small regulatory RNA ryhB [#]	12.16/13.45	11.60/13.04	-29	NA
VCA0576-Heme transport protein Huta [#]	7.70/14.74/8.04	6.89/11.67/7.96	-62	COG1629
VCA0909-07-Oxygen-independent coproporphyrinogen III oxidase [#]	11.88	9.26/8.27	-106	COG0635
				COG3721
				COG0748
				COG0810
				COG0811
				COG0848
				COG0614
				COG0609
VCA0910-15- <i>tonB1</i> -system/heme transporter [#]	8.27/9.26	11.88	-177	COG1120
VC1264-Iron-regulated protein A [#]	6.85/12.61	4.70/4.73/13.28	-4	COG3487
				COG1918
				COG0370
VC2078-76-Ferrous iron transport protein AB [#]	6.57/8.86/4.51	6.18/4.57	-42	-

				COG1840
				COG1178
VC0608-10-Iron(III) ABC transporter [#]	10.09	10.94	5	COG3841
VC0123-CyaY Protein implicated in iron transport	7.85	5.21	3	COG1965
				-
				-
				-
				COG0811
				COG0848
VC0284/VC1548-43-TonB dependent receptor/ <i>tonB2</i> -system [#]	5.21/12.84/5.24 10.740	15.06/4.78 6.250	-95 -60	COG0457
				COG0457
				COG0614
				COG0609
				COG0609
VCA0227-30-Iron(III) ABC transporter [#]	11.53/6.52	11.33/6.72	29	COG1120
VCA0685-Iron(III) ABC transporter	7.33	9.20	-117	COG1840
				COG1629
				COG1120
	6.82/8.36/7.22/ 10.35	9.43/5.98/4.83/ 8.49	-26	COG0614
VC0200-03-Iron(III) compound receptor [#]				COG0609
VCA0686-Iron(III) ABC transporter				COG1178
VC0199-Ferrichrome-iron receptor A	4.83/5.98/9.43	7.22/8.36	-37	COG1132
				COG2906
VC0364-65-Bacterioferritin Bfd-Bfr [#]	10.35	5.76	-56	COG2193
VC0771-Vibriobactin-specific isochorismatase VibB [#]	12.75	13.97	-163	NA
VC0773-72-Vibriobactin-specific isochorismate synthase				COG1169
VibC-VibE [#]	6.12/12.88/5.67	9.21/12.28	-62	COG1021
VC0474-Iron-regulated virulence regulatory protein IrgB [#]	13.48	13.80	-127	COG0583
VC0475-Iron-regulated outer membrane				

virulence protein IrgA [#]	13.80	13.48	-33	COG1629
VC0774-Vibriobactin-specific dehydrogenase VibA ^{**}	9.21/12.28	6.12/12.88/5.67	-76	COG1028
VC0775-Vibriobactin synthesis protein VibH ^{**}	10.98/4.82/9.38	8.97/8.62	-192	COG1020
				COG0614
				COG0609
No/VC0776-78-Ferric vibriobactin ABC transporter ViuPDG ^{**}	8.62/8.97	9.38/4.82/10.98	-1	COG0609
VC0779-81 Ferric vibriobactin ABC transporter [#]	6.89		-34	COG1120
VC2210-Vibriobactin utilization protein ViuB ^{**}	10.56	12.64	-142	COG2375
VC2211-Vibriobactin receptor ViuA [#]	6.59/11.46/7.45/5.60	10.74/7.03/8.01	-272	COG1629
				COG1770
				COG1629
				-
				-
VCA0063-67-Protease II PrtB/Haem receptor HutR [#]	11.66	12.40	-72	-
VCA0232-Enterobactin receptor VctA [#]	10.180	11.72/6.59	-47	NA
VCA0575-Transcriptional regulator, LysR family HupR ³	7.96/11.67/6.89	8.04/14.74/7.70	-177	COG0583
Energy Metabolism				
VC0753-Ferredoxin				COG0633
VC2099- Flavodoxin				COG0716
VC1516-Iron-sulfur cluster-binding protein [#]	6.45	7.95	-109	COG1145
				COG1132
VC1181-80-Transport ATP-binding protein CydDC	8.15	7.77	-32	COG1132

				COG2209
				COG2878
				-
				COG1805
				COG2869
				COG1347
				COG0177
VC1017-10-Electron transport complex protein RnfB	5.61	5.30	-290	COG0346
VC1844-Cytochrome d ubiquinol oxidase, subunit I				COG1271
				COG1131
				COG2386
				COG0755
				COG3114
				COG2332
				COG1138
				COG0526
				-
				-
VC2057-48-Cytochrome biogenesis protein ABCD	6.62/6.67	5.71	-310	COG2853
VC2241-Cytochrome c554	4.94		20	COG2863
Virulence Factors				
VC0857-Fimbrial assembly protein Pile	4.85/6.66	5.40	-1	COG2165
VCA1069-Methyl-accepting chemotaxis protein	4.96	4.79	-1	COG0840
VC0838-TCP pilus virulence regulatory protein				COG2207
VCA0219-Hemolysin precursor HlyA	5.19		-164	NA
VCA0219-Haemolysin	5.19		-164	NA
VC1859-Methyl-accepting chemotaxis protein	4.60	4.62	-199	COG0840
				COG1298
VC2069-68-Polar flagellar assembly protein FlhA/FlhH				COG1419

VC2188-Flagellin A				COG1344
VCA0988-Methyl-accepting chemotaxis protein*	5.19	5.30	-65	COG0840
VC1618-Multidrug resistance protein				COG0477
				COG0845
				COG3672
				-
				COG2200
VCA1080-84-Type I secretion, HlyD family				COG2274
VCA0068-Methyl-accepting chemotaxis protein*	11.60/4.99	10.27	-40	COG0840
VCA0176-Methyl-accepting chemotaxis protein				COG0840
VC1403-Methyl-accepting chemotaxis protein*	5.14	5.70	-135	COG0840
VC0825-Toxin co-regulated pilus biosynthesis protein I [#]	7.91	6.33	-1	COG0840
VC1313-Methyl-accepting chemotaxis protein				COG0840
VCA0219-Hemolysin precursor HlyA	5.19		-164	NA
VC0825-Methyl-accepting chemotaxis protein* [#]	7.91	6.33	-1	COG0454
VC0826-Methyl-accepting chemotaxis protein*	5.31/4.87/6.67	4.70	-191	COG0745
VC1643-Methyl-accepting chemotaxis protein*	5.60	6.08	-1	COG0840
VCA0923-Methyl-accepting chemotaxis protein*	5.17		44	COG0840

Miscellaneous

VC0409-Type IV pilus, mannose-sensitive hemagglutinin A				NA
VC0896-Transcriptional regulator, LysR family	5.68		-49	COG0583
VC0900-Conserved hypothetical protein				NA
VC2215-Copper-transporting P-type ATPase				COG2217
VC1917-Hypothetical protein				COG1555
VC0992-Glutathione-regulated potassium-efflux system protein KefB				COG0475
				COG1121
VC2082-83-Zinc ABC transporter	4.68	5.26	-21	COG1108
VC2081-Zinc ABC transporter	5.26/5.19	4.68	-72	COG0803

VC0845-Conserved hypothetical protein [#]	6.21		-292	NA
VC0876-Hypothetical protein	5.12/7.32	9.97	21	COG1720
VC2278-Hypothetical protein				COG2252
VC1060-SohB protein, peptidase U7 family				COG0616
VCA1001-Transcriptional regulator, AraC-family				COG2207
VC1199-Hypothetical protein				COG2020
VC2212-Hypothetical protein	8.01/7.03/10.74	5.60/7.45/11.46	-149	NA
VC1300-L-serine dehydratase 1	6.11		-8	COG1760
				COG1132
				COG2995
VC1499-501-ABC transporter	5.06/7.91	7.79/9.16	-14	COG3008
VC1189-Hypothetical protein				NA
VC1009-Hypothetical protein	12.65	10.17	-52	NA
VC0075-MadN protein				COG0697
VC1148-Hypothetical protein				COG1737
VC1363-Siroheme synthase component enzyme				COG1648
VC1198-Hypothetical protein				COG0277
				COG0226
				COG0573
				COG0581
VCA0070-73-Phosphate ABC transporter [*]	10.27	11.60	-270	COG1117
VC2149-Hypothetical protein				NA
VC0878-Ribosomal protein L31	9.97	7.32/5.12	-60	COG0254
				COG1053
				COG0479
				COG3029
VC2656-59-Fumarate reductase, flavoprotein				COG3080
VC0277-Transcriptional regulator, MerR family				COG0789
VC0332-Uroporphyrinogen decarboxylase (HemE)	8.94		-165	COG0407
VC0091-O-methyltransferase-related protein [#]	9.10	10.44	14	COG3315

VC0036-FixG-related protein				COG0526
VC1688-Hypothetical protein [#]	8.97/11.74	8.66/9.11	5	NA
VCA0231-Transcriptional regulator, AraC/XylS family [#]	11.72/6.59	10.18	-1	COG2207
VC1687-Hypothetical protein	8.66	8.97	-141	COG1227
VCA0554-Oxalate/formate antiporter	6.03		-1	COG0477
VCA0924-Hypothetical protein				COG3217
VCA0180-Peptidase T				COG2195
VCA0818-Putative magnesium transporter				COG2239
VCA0975-ATP-dependent protease LA-related protein	9.47/9.70	8.15/10.02	-52	COG1067
VC2004-Conserved hypothetical protein	10.55	8.28	-21	COG3016
VC1183-Hypothetical protein				NA
VC0139-Ferritin-like DNA-binding protein	7.44	5.02	-1	COG0783
VC0617-Peptide ABC transporter, ATP-binding protein				COG0444
VC2275-Transcriptional regulator Crl				NA
VCA0070-Phosphate ABC transporter				COG0226
VCA0075-Hypothetical protein	6.95	5.07	-198	NA
VCA0676-Iron-sulfur cluster-binding protein NapF [#]				COG1145
VCA0976-77-Hypothetical protein and ABC transporter, ATP-binding protein [#]	9.47/9.70	8.15/10.02	-66	COG1123
VCA1048-Oxidoreductase	6.05	6.39	-1	COG0673
VC1048 Hypothetical protein [#]	10.31	6.55	-71	COG0778
VC1562 Beta-lactamase-related protein	7.14		-116	COG0491
VC2209-Non-ribosomal peptide synthetase VibF ^{**}	6.64/14.06/4.89	5.26/12.66	-88	COG1020
VC2694-Superoxide dismutase SodA ^{**}	7.22/15.28/6.12	15.09/8.31	-39	COG0605
VCA0216-Hypothetical protein [#]	13.19	13.44	-36	NA
VCA1041-Putative phosphomannomutase [#]	11.35	11.23	-57	COG1109
VC1572-73-Hypothetical protein and fumarate hydratase [#]	12.49	12.23	-54	COG0114

V. parahaemolyticus

Iron Metabolism

small regulatory RNA ryhB ⁴	12.16/13.70 6.34/11.02/12.04/	11.60/14.81 6.21/12.01/12.03/	-29	NA
VPA0882-Heme transport protein HutA	7.40	7.74/5.08	-80	COG1629 COG0635 COG3721
VPA0427-29-Coproporphyrinogen oxidase homolog PhuW	9.16/5.11/8.03	5.59/6.52/7.52	-108	COG0748 COG0810 COG0811 COG0848 COG0614 COG0609
VPA0426-21- <i>tonB1</i> -system/heme transporter	5.59/6.52/7.52	9.16/5.11/8.03	-75	COG1120
VP1920-Putative iron-regulated protein A	10.62	8.04/7.28	-32	COG3487 COG1918 COG0370
VP0857-59-Ferrous iron transport protein AB	11.62/9.53	7.87/12.06	-41	- COG1840 COG1178
VP2491-89-Iron(III) ABC transporter	8.34/7.34	9.50/5.96	-39	COG3841 - - -
VPA1657/VPA0150-56-TonB dependent receptor/ <i>tonB2</i> -system	9.75/6.60 6.07/10.70/7.58	11.05/6.08 8.75/5.80	-59 -97	COG0811 COG0848 COG0457 COG0457

				COG0614
				COG0609
				COG0609
VPA0657-60-Iron(III) ABC transporter	8.23	9.83	-32	COG1120
VPA0979-Ferric aerobactin receptor precursor ¹	12.34/9.20	6.50/12.75	-54	COG1629
				COG1629
				COG1120
				COG0614
VPA1435-38-Putative iron(III) compound receptor	11.60	12.84/6.59	-56	COG0609
VP2769-68-Bacterioferritin-associated ferredoxin/ Bacterioferritin	6.29	6.66/7.08	-64	COG2906
VP2603-Iron-regulated virulence regulatory protein homolog	13.04/10.46	8.02/13.85	-123	COG2193
VP2602-Iron-regulated outer membrane virulence protein homolog	8.02/13.85	13.04/10.46	-33	COG0583
				COG1629
				COG0614
				COG0609
VPA1657-1652-Ferric siderophore receptor	7.63/8.13	7.23/6.59/5.40	-65	COG0609
VPA0089-Putative siderophore utilization protein	7.43/8.59	5.67/8.44	-35	COG2375
				COG1770
				COG1629
				-
				-
VPA1467-63-Protease II/Putative TonB system receptor	8.21/11.26/6.31	12.33/7.56/5.46	-79	-
Energy Metabolism				
VP0601-Ferredoxin				COG0633
VP0835-Flavodoxin 1				COG0716
				COG1132
VP1250-49-Transport ATP-binding protein CydDC	8.17	8.46	-30	COG1132
VP1053-Cytochrome d ubiquinol oxidase, subunit I				COG1271

VP1929-Nitrite reductase periplasmic cytochrome c552	8.42	7.35/6.67	-354	COG3303
				COG0437
				COG3301
				COG1138
				COG0526
VP1928-23-Cytochrome c-type protein NrfB precursor	7.35/6.67	8.42	-139	COG3088
				COG1131
				COG2386
				COG0755
				COG3114
				COG2332
				COG1138
				COG0526
VP2223-15-Cytochrome biogenesis protein ABCD	5.09		-138	-
				-
				COG1622
				COG0843
				COG1845
				COG3125
VPA0627-31-Cytochrome o ubiquinol oxidase				COG0109
VP2300-Cytochrome c554				COG2863

Virulence Factors

VP0656-Putative fimbrial assembly protein				COG2165
VPA1651-Methyl-accepting chemotaxis protein	12.04	11.04	-308	COG0840
VP1981-Methyl-accepting chemotaxis protein	6.01	6.01	-301	COG0840
VP1088-Methyl-accepting chemotaxis protein	6.44		-125	COG0840
				COG1298
VP2235-34-Polar flagellar assembly protein FlhA/FlhH				COG1419

VP0788-Polar flagellin C				COG1344
VPA0596-Putative methyl-accepting chemotaxis protein				COG0840
VP1315-Multidrug resistance protein				COG0477
				COG0845
				COG3672
VPA1733-36-Type I secretion, HlyD family				COG2274
VP1633-Putative RTX toxin	5.6	5.75	-45	NA
	5.56/5.70/5.78/	6.36/7.21/9.34/		
VPA1462-Methyl-accepting chemotaxis protein	5.61/7.78/7.92	6.10/6.27	-39	COG0840
VP0963-Methyl-accepting chemotaxis protein				COG0840
VPA1000-Methyl-accepting chemotaxis protein				COG0840
VPA1434-Putative hemolysin secretion ATP-binding protein	12.84/6.59	11.66	-108	COG1132
	5.56/5.70/5.78/	6.36/7.21/9.34/		
VPA1462-Methyl-accepting chemotaxis protein	5.61/7.78/7.92	6.10/6.27	-40	COG0454
VPA1332-Methyl-accepting chemotaxis protein				COG0745
VPA1651-Methyl-accepting chemotaxis protein	12.04	11.04	-308	COG0840
VPA0511-Methyl-accepting chemotaxis protein				COG0840

Miscellaneous

VP2698-Type IV pilus, mannose-sensitive hemagglutinin A				NA
VP0692-Transcriptional regulator LysR family				COG0583
VP0699-Conserved hypothetical protein				NA
VP0758-Cation transport ATPase	6.05		-319	COG2217
VP0922-Hypothetical protein				COG1555
VP0827-Glutathione-regulated potassium-efflux system	8.45	8.86	-1	COG0475
				COG1121
VP0852-51-Zinc ABC transporter	7.02	8.36	-20	COG1108
VP0853-Zinc ABC transporter	8.36	7.02	-77	COG0803
VPA1376-Conserved hypothetical protein				NA
VP2332-Conserved hypothetical protein	6.65/9.48	9.7/5.97	-81	COG1720

VP0672-Hypothetical protein				COG2252
VP2126-Hypothetical protein				NA
VP2032-SohB protein, peptidase U7 family				COG0616
VPA0531-Transcriptional regulator, AraC-family	4.90/7.14	8.64/6.75	-79	COG2207
VP1271-Hypothetical protein				COG2020
VP0766-Conserved hypothetical protein	6.30	5.95	-55	NA
VP1880-L-serine dehydratase 1	7.17	5.36	-7	COG1760
VP1510-Iron-sulfur cluster-binding protein				COG1145
VP0377-Putative CFA/I fimbrial subunit D	5.02/11.82/6.15	6.75/6.30/10.09/ 5.93	-270	COG2207 COG1132 COG2995 COG3008
VP1609-11-ABC transporter	7.73	5.61/6.57	-23	COG3008
VP1261-Hypothetical protein				NA
VP2110-Hypothetical protein	10.30/6.90	7.10/10.33	-56	NA
				COG2209 COG2878 - COG1805 COG2869 COG1347 COG0177 COG0346
VP2102-09-RnfB-related protein				COG0346
VP0075-MadN protein	8.07	7.55	-20	COG0697
VP1236-Hypothetical protein				COG1737
VP1619-Uroporphyrin-III C-methyltransferase	5.33		-241	COG1648
VP1270-Hypothetical protein				COG0277

				COG0226
				COG0573
				COG0581
VPA1461-58-Phosphate ABC transporter	6.36/7.21/9.34/ 6.10/6.27	5.56/5.70/5.78/ 5.61/7.78/7.92	-312	COG1117
VP2266-Hypothetical protein				NA
VP2516-OpaR	8.93	6.75	-65	COG1309
VP2331-Ribosomal protein L31P family	9.70/5.97	6.65/9.48	-61	COG0254
VP2894-Transcriptional regulator, MerR family				COG0789
VP2916-Uroporphyrinogen decarboxylase				COG0407
VP2944-O-methyltransferase-related protein	9.82/8.88	10.57/9.49/4.90	-1	COG3315
VP3052-FixG-related protein	5.08	5.40/5.18	-42	COG0526
VP2986-CyaY protein				COG1965
	8.58/6.17/14.16/ 9.99	7.89/15.11/5.93/ 5.24/10.20	-35	NA
VP1164-Hypothetical protein	9.99	5.24/10.20	-35	NA
VPA0980-Hypothetical protein	8.83	6.34/4.83	-75	NA
VPA0663-Putative transcriptional regulator	8.77/10.22	6.72/10.07	-1	COG2207
VPA0236-ABC transporter, periplasmic substrate-binding protein				COG1840
	7.89/15.11/5.93/ 5.24/10.20	8.58/6.17/14.16/ 9.99	-179	COG1227
VP1165-Conserved hypothetical protein	5.24/10.20	9.99	-179	COG1227
VPA0701-Putative oxalate/formate antiporter	6.04	7.93	-7	COG0477
VPA1449-Hypothetical protein	6.06		-300	COG0840
VPA0411-Hypothetical protein	6.25	5.5	-293	COG3217
VPA1193-Peptidase T	6.88	7.42	-13	COG2195
VP0936-Membrane protein				COG3217
VPA1172-73-Hypothetical protein				NA
VPA1661-Putative AcsD				NA
VPA1240-Putative magnesium transporter				COG2239
VPA1493-ATP-dependent protease LA-related protein	12.93/6.09/6.37	8.65/11.94	-150	COG1067
VP2161-Conserved hypothetical protein	12.61/7.40	5.28/13.71	-79	COG3016

VP1252-Hypothetical protein				NA
VP1482-Putative response regulator				NA
VPA0563-DPS family protein	4.97		-129	COG0783
VPA0004-Peptide ABC transporter, ATP-binding protein	8.71/13.96/6.81	6.19/13.83/11.49	-1	COG0444
VP0675-Transcriptional regulator Crl	7.71/7.36/6.50	7.12/8.61/5.89	-59	NA
	6.36/7.21/9.34/	5.56/5.70/5.78/		
VPA1461-Phosphate ABC transporter	6.10/6.27	5.61/7.78/7.92	-310	COG0226
VPA0069-Hypothetical protein	10.92	9.10/7.96	-259	NA
VPA1197-Iron-sulfur cluster-binding protein NapF	4.91		-139	COG1145
VP1451-Putative ferredoxin-type protein NapF				COG1145
VPA0239-ABC transporter, permease protein				COG1178
VP1721-Diaminobutyrate--2-oxoglutarate transaminase				COG0160
VPA1494-95-Hypothetical protein and ABC transporter, ATP-binding protein	8.65/11.94	12.93/6.09/6.37	-56	COG1123
VPA1496-Prolyl endopeptidase	9.32	10.07	-56	COG1505
VPA1281-Oxidoreductase	6.45	7.73	-1	COG0673
VP2150 Putative nitroreductase				COG0778
VP2860-Superoxide dismutase, Mn	9.42/10.70	9.46/7.36	-52	COG0605
	6.21/12.01/12.03/	6.34/11.02/12.04		
VPA0883-Transcriptional regulator, LysR family	7.74/5.08	/7.40	-173	COG0583
VPA0535-Putative phosphomannomutase	7.25/9.87	10.08/7.36	-99	COG1109
VP2072-73-Hypothetical protein and fumarate hydratase				COG0114

***V. vulnificus* (CMPC6)**

Iron Metabolism

small regulatory RNA ryhB ⁴	12.16/12.50	13.99/11.60	-29	NA
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				COG0635
				COG3721
VV21615-17-Coproporphyrinogen III oxidase	9.16/6.52/8.03	5.59/6.52/7.52	-107	COG0748
				COG0810
				COG0811
				COG0848
				COG0614
VV21614-09- <i>tonB1</i> -system/ ABC-type Fe ³⁺ -siderophore transport system	5.59/6.52/7.52	9.16/6.52/8.03	-115	COG0609
VV12968-Uncharacterized iron-regulated protein	10.62	10.62/7.28	-38	COG1120
				COG3487
				COG1918
				COG0370
VV10149-47-Fe ²⁺ transport system protein AB	9.56/5.94	5.94/10.07	-41	-
VV11124-Protein implicated in iron transport	5.18	7.72	-93	COG1965
				-
				-
				-
				COG0811
				COG0848
VV21337VV20364-59-TonB dependent receptor/ <i>tonB2</i> -system	6.70/10.45/13.89/ 6.98	13.68/12.69	-57	COG0457
				COG0457
				COG0614
				COG0609
				COG0609
No/VV20110-12-ABC-type enterochelin transport system				COG1120
VV21665-ABC-type Fe ³⁺ transport system, periplasmic component				COG1840

				COG1629
				COG1120
				COG0614
No/VV21011-13-OMP/Fe ³⁺ -siderophores transport system	5.33/5.53/8.93/ 10.96	10.96/8.93/5.53	-81	COG0609
VV11340-41-Bacterioferritin-associated ferredoxin/ Bacterioferritin	10.41/13.31/6.83	6.83/13.10/10.41	-56	COG2906 COG2193
VV20839-37-Chorismate mutase/ Siderophore-interacting protein	8.95/12.86 6.77/5.58/15.00/ 10.92/4.95	9.88/12.86 4.95/9.24/13.97/ 5.58/5.04	-133	NA COG1169
VV20835-36-Isochorismate synthase			-269	COG1021
VV20837-Siderophore-interacting protein				COG2375

Energy Metabolism

VV10433-Ferredoxin				COG0633
VV10173-Flavodoxin				COG0716
VV12587-Ferredoxin				COG1145
				COG1132
VV12811-12-Transport ATP-binding protein CydDC	7.56	6.87	-29	COG1132 COG2209 COG2878
				- COG1805
				COG2869
VV13093-98-Electron transport complex protein RnfB	6.93	5.64	-344	COG1347
VV12162-Cytochrome d ubiquinol oxidase, subunit I				COG1271
VV13035-Formate-dependent nitrite reductase, periplasmic cytochrome c552 subunit				COG3303

				COG0437
				COG3301
				COG1138
				COG0526
VV13034-30-Nitrate/TMAO reductase, membrane-bound tetraheme cytochrome c subunit	7.35/9.84	10.19/8.42	-143	COG3088
				COG1131
				COG2386
				COG0755
				COG3114
				COG2332
				COG1138
				COG0526
				-
VV11961-69-Cytochrome biogenesis protein ABCD	5.21		-130	-
VV21598-Flavodoxin reductase family 1 protein	5.68	5.68	-31	COG3217
				COG1622
				COG0843
		4.84/6.71/6.52/		COG1845
VV20568-65-Cytochrome o ubiquinol oxidase	13.90/6.52/4.84	14.65	-316	COG3125
VV11878-Cytochrome c554	5.51	5.51	-42	COG2863
VV12587-Ferredoxin				COG1145

Virulence Factors

VV10353-Type IV pilus (Tfp) assembly protein	COG2165
VV13118-Methyl-accepting chemotaxis protein	NA

VV20402-Methyl-accepting chemotaxis protein	6.11	6.11	-342	COG0840
VV20404-Hemolysin/cytolysin	5.19	5.19	-1	NA
VV12107-Methyl-accepting chemotaxis protein	4.93		-234	COG0840
VV10186-Methyl-accepting chemotaxis protein				COG0840
				COG1298
VV11949-50-Polar flagellar assembly protein FlhA/FlhH				COG1419
VV10215-Polar flagellin FlaC				COG1344
VV20072-Methyl-accepting chemotaxis protein	11.01/6.23	6.23/11.01	-87	COG0840
VV12715-Autotransporter adhesin	6.07	5.30	-230	NA
VV21555-Methyl-accepting chemotaxis protein	6.00/12.77	12.77/6.29	-49	COG0840
VV21567-Methyl-accepting chemotaxis protein				COG0840
VV12066-Methyl-accepting chemotaxis protein				COG0840
VV11805-Methyl-accepting chemotaxis protein	5.04		-342	COG0840
VV12563-CheY-like receiver protein				NA
VV20477-Methyl-accepting chemotaxis protein	5.15/7.90	6.61/5.15	-113	COG0840
VV20404-Hemolysin/cytolysin	5.19	5.19	-1	NA
VV11805-Methyl-accepting chemotaxis protein	5.04		-342	COG0454
VV11774-Methyl-accepting chemotaxis protein	5.17		-87	COG0840
VV21623-Methyl-accepting chemotaxis protein				COG0840
VV20404-Cytolysin	5.19	5.19	-1	NA

Miscellaneous

VV11443-Type IV pilus, mannose-sensitive hemagglutinin A				NA
VV10306-Transcriptional regulator	6.76	7.95	-45	COG0583
VV10299-Conserved hypothetical protein				NA
VV10239-Cation transport ATPase	6.48	6.48	-321	COG2217
VV10017-DNA uptake protein				COG1555
VV10182-Kef-type K ⁺ transport system	6.47	6.47	-1	COG0475
				COG1121
VV10152-53-Zinc ABC transporter	6.62	6.62	-20	COG1108

VV10151-Zinc ABC transporter	6.51	6.51/5.68	-7	COG0803
VV10767-Conserved hypothetical protein				NA
VV11839-Hypothetical protein	6.21/5.22	5.22/8.78	-82	COG1720
VV12985-Periplasmic serine protease				COG0616
VV20572-AraC-type DNA-binding domain	5.78/5.48	4.82/5.20	-248	COG2207
VV12386-Hypothetical protein				COG2020
VV10235-ABC-type Fe ³⁺ -citrate transport system	6.35	6.35	-280	NA
VV12260-L-serine dehydratase 1	7.78	7.78/6.01	-8	COG1760
VV20934-AraC-type DNA-binding domain-containing protein				COG2207
				COG1132
				COG2995
VV12646-48-ABC-type multidrug transport system	8.87	8.23	-21	COG3008
VV12798-Hypothetical protein				NA
VV20276-Outer membrane receptor protein	14.12	7.66/14.05/5.00	-351	COG1629
VV13101-Hypothetical 16.4 kDa protein in MOTY 3'region	12.53/7.10	6.24/12.53	-54	NA
VV11114-MadN protein				COG0697
VV12825-Transcriptional regulator	6.58	5.12	-289	COG1737
VV12702-Uroporphyrin-III C-methyltransferase				COG1648
VV12385-Fe-S oxidoreductase	5.3		-224	COG0277
				COG0226
				COG0573
				COG0581
VV21556-59-Phosphate ABC transporter	12.77/6.29	6.99/12.77	-440	COG1117
				COG1840
				COG1178
VV11660-63-ABC-type Fe ³⁺ transport system	5.51/6.95/9.50/5.45	9.50/6.95/5.51	-65	COG3841
VV11634-SmcR	6.89	6.89	-141	COG1309
VV11840-Ribosomal protein L31	5.22/8.78	6.21/5.22	-57	COG0254
VV11229-Transcriptional regulator, MerR family				COG0789
VV11218-Uroporphyrinogen decarboxylase				COG0407

VV11167-O-Methyltransferase involved in polyketide biosynthesis	6.04/11.99	11.99/6.04	-54	COG3315
VV11038-FixG-related protein				COG0526
VV12778-Permease				COG0477
				COG0845
				COG3672
VV21125-28-Membrane-fusion protein				COG2274
	9.86/5.27/8.39/	6.85/13.76/8.39/		
VV12889-Conserved hypothetical protein	14.16/8.93	8.33	-35	NA
VV21010-Hypothetical protein	7.86	7.7	-74	NA
VV21119-AraC-type DNA-binding domain-containing protein	6.98	6.98	-190	COG2207
VV12888-Inorganic pyrophosphatase/ exopolyphosphatase	9.94	9.94	-8	COG1227
VV20166-Permease of the major facilitator superfamily	5.4	5.4	-118	COG0477
VV20532-Di- and tripeptidase	5.04	5.04	-140	COG2195
VV13166-Membrane protein				COG3217
VV21016-Outer membrane receptor protein ²				COG1629
VV20785-Putative magnesium transpor				COG2239
VV20792-ATP-dependent protease LA-related protein	12.16/5.64	8.36/12.16/5.85	-231	COG1067
VV12020-Conserved hypothetical protein	12.06/8.72	8.72/12.19/6.05	-113	COG3016
VV12809-Hypothetical protein				NA
VV10327-Transcriptional regulator Crl-like prot	11.1	11.2	-35	NA
VV21556-ABC-type phosphate transport system	12.77/6.29	6.00/12.77	-440	COG0226
VV21280-Uncharacterized protein conserved in bacteria	5.64	5.64	-186	NA
VV21670-ABC-type Fe ³⁺ transport system	8.38/6.05	6.05/8.38	-13	COG1178
VV13050-Glutamate decarboxylase				COG0160
VV20793-94-Hypothetical protein and ABC transporter, ATP-binding protein	8.36/12.16/5.85	12.16/5.64	-78	COG1123
VV20795-Serine protease of the peptidase family S9A	8.05	8.15	-109	COG1505
VV21089-ABC-type multidrug transport system	5.82	5.72	-211	COG1132
VV20600-Predicted dehydrogenase	5.42/6.88	6.88/5.42	-1	COG0673

VV20834-Dehydrogenase	4.95/9.24/13.97/ 5.58/5.04	6.77/5.58/15.00/ 10.92/4.95	-122	COG1028
VV20844-Non-ribosomal peptide synthetase modules	5.14/12.86	13.56/6.78/5.34	-78	COG1020
VV13131 Nitroreductase				COG0778
VV21502 Zn-dependent hydrolase	6.67		-52	COG0491
	6.36/14.71/5.67/	8.58/5.67/14.99/		
VV20831-29-Non-ribosomal peptide synthetase modules	8.58	9.41	-7	COG1020
VV20843-Outer membrane receptor protein	10.58/5.19	5.19/10.85/6.54	-298	COG1629
VV11252-Superoxide dismutase	10.83/10.35/5.58	5.58/10.35/10.83	-57	COG0605
				COG1770
				COG1629
				-
				-
VV21548-52-Protease II/Outer membrane receptor protein	10.64/9.24/5.91	9.24/10.14	-154	-
VV20277-Transcriptional regulator, LysR family	7.66/14.05/5.00	14.12	-145	COG0583
	4.84/6.71/6.52/			
VV20569-Putative phosphomannomutase	14.65	13,90/6,52/4,84	-57	COG1109

***V. vulnificus* (YJ106)**

Iron Metabolism

small regulatory RNA ryhB ⁴	10.21/9.46	10.18/10.74	-29	NA
				COG0635
				COG3721
VVA0425-27-Coproporphyrinogen III oxidase	9.16/5.11/8.03	7.52/6.52/5.59	-101	COG0748

				COG0810
				COG0811
				COG0848
				COG0614
VVA0424-19- <i>tonB1</i> -system/				COG0609
ABC-type Fe ³⁺ -siderophore transport system	7.52/6.52/5.59	9.16/5.11/8.03	-84	COG1120
VV2119-Uncharacterized iron-regulated protein	10.62	8.04/7.28	-50	COG3487
				COG1918
				COG0370
VV1040-42-Fe ²⁺ transport system protein AB	9.56/5.94	10.07	-41	-
				COG1840
				COG1178
VV2746-44-ABC-type Fe ³⁺ transport system	5.98/8.34/5.45	5.51/6.95/9.50	-41	COG3841
				-
				-
				-
				COG0811
				COG0848
				COG0457
VVA0920-15-TonB dependent receptor/ <i>tonB2</i> -system	11.03/5.28	12.33/6.85	-57	COG0457
				COG0614
				COG0609
				COG0609
No/VVA0618-20-ABC-type enterochelin transport system	7.29	7.31	-205	COG1120
VVA0477-ABC-type Fe ³⁺ transport system				COG1840
VVA1508-Ferric aerobactin receptor precursor ²	10.47/7.16/10.34	9.86/5.83/10.29	-144	COG1629
				COG1629
				COG1120
				COG0614
No/VVA1504-06-Fe ³⁺ -siderophores transport system	7.76	5.53/6.89/9.83	-80	COG0609

VVA0479-ABC-type Fe ³⁺ transport system	7.37	8.38/6.05	8	COG1178
VV3028-27-Bacterioferritin-associated ferredoxin/ Bacterioferritin	6.41/10.63/8.31	6.56/12.02/10.41	-44	COG2906 COG2193
VVA1305-02-Chorismate mutase/ Siderophore-interacting protein	12.86/6.29	10.71/4.84	-124	NA
VVA1300-01-Vulnibactin-specific isochorismate synthase/Ligase	6.77/15.00/10.92	5.58/13.97/9.24	-270	COG1169 COG1021
VVA1299-Vulnibactin-specific 2,3-dihydro-2,3-DHBA dehydrogenase	5.58/13.97/9.24	6.77/15.00/10.92	-121	COG1028
VVA1310-Vulnibactin synthetase, amide synthase subunit	14.42/7.07	15.18/7.99	-45	COG1020
VVA1303-Vulnibactin utilization protein				COG2375
VVA1309-Ferric vulnibactin outer membrane receptor	10.58/5.19	10.85/6.54	-298	COG1629 COG1770 COG1629
				-
				-
VVA0361-65-Protease II/Heme transport protein	10.64/8.30	10.14/9.24		-
Energy Metabolism				
VV0760-Ferredoxin				COG0633
VV1016-Flavodoxin				COG0716
VV1703-Ferredoxin				COG1145
				COG1132
VV1454-53--Transport ATP-binding protein CydDC	7.56	6.87	-30	COG1132 COG2209 COG2878
				-
				COG1805
				COG2869
VV1192-87-Electron transport complex protein RnfB	6.93	5.64	-285	COG1347

VV2283-Cytochrome d ubiquinol oxidase, subunit I				COG1271
VV1250-Formate-dependent nitrite reductase, periplasmic cytochrome c552 subunit				COG3303
				COG0437
				COG3301
				COG1138
				COG0526
VV1251-56-Cytochrome c-type protein NrfB precursor	9.84	10.19	-45	COG3088
				COG1131
				COG2386
				COG0755
				COG3114
				COG2332
				COG1138
				COG0526
VV2455-47-Cytochrome biogenesis protein ABCD				COG1622
				COG0843
				COG1845
VVA1116-13-Cytochrome o ubiquinol oxidase	13.90/6.52/4.84	5.19/6.52	-292	COG3125
VV2537-Cytochrome c554				COG2863
VVA1189-Ferredoxin				COG1145
VV1703-Ferredoxin2 NapF				COG1145

Virulence Factors

VV0835-Tfp pilus assembly protein				COG2165
VVA0963-Methyl-accepting chemotaxis protein	5.57/4.81/6.11		-343	COG0840
VV2333-Methyl-accepting chemotaxis protein	4.93		-233	COG0840

VV1004-Methyl-accepting chemotaxis protein	5.72	7.26	-73	COG0840
VV2467-66-Polar flagellar assembly protein FlhA/FlhH				COG1298
VV0971-Polar flagellin FlaC				COG1419
VVA0579-Methyl-accepting chemotaxis protein	11.01/6.23	10.86/5.37	-87	COG1344
VV1546-Putative RTX protein				COG0840
VVA0368-Methyl-accepting chemotaxis protein	12.77/6.00	11.29/6.29	-48	NA
VVA0380-Methyl-accepting chemotaxis protein				COG0840
VV2375-Methyl-accepting chemotaxis protein				COG0840
VVA0340-Methyl-accepting chemotaxis protein				COG0840
VVA1028-Methyl-accepting chemotaxis protein	7.9	6.61	-113	COG0840
VVA0340-Methyl-accepting chemotaxis protein				COG0454
VV2635-Methyl-accepting chemotaxis protein				COG0840
VVA0435-Methyl-accepting chemotaxis protein				COG0840
VVA0965-Cytotoxin, cytolysin VvhA		5.19	-8	NA
VVA0965-Cytotoxin, cytolysin VvhA		5.19	8	NA
VVA0965-Cytotoxin, cytolysin VvhA	5.19		8	NA
Miscellaneous				
VV2940-Type IV pilus, mannose-sensitive hemagglutinin A				NA
VV0878-Transcriptional regulator	6.76	7.95	-45	COG0583
VV0885-Conserved hypothetical protein				NA
VV0944-Cation transport ATPase	4.97	6.48	-291	COG2217
VV1109-DNA uptake protein				COG1555
VV1009-Putative glutathione-regulated potassium-efflux system protein KefB	5.43	6.47	-1	COG0475
				COG1121
VV1037-36-Zinc ABC transporter	5.68	6.62/6.51	-87	COG1108
VV1038-Zinc ABC transporter	6.62/6.51	5.68	-80	COG0803
VV2571-Hypothetical protein	6.21/5.22	8.78	-81	COG1720

VV1169-Hypothetical protein				NA
VV1298-Periplasmic serine protease				COG0616
VVA1120-AraC-type DNA-binding domain	5.78/5.48	4.82/5.20	-248	COG2207
VV1955-Hypothetical protein				COG2020
VV1562-ABC-type Fe ³⁺ -citrate transport system	7.98/7.56	5.76/6.90/7.09	-70	NA
VV2085-L-serine dehydratase 1	7.78	6.01/5.51	-7	COG1760
VV2219-AraC-type DNA-binding domain-containing protein				COG2207
				COG1132
				COG2995
VV1644-42-ABC-type multidrug transport system	8.87	8.23	-22	COG3008
VV1467-Hypothetical protein				NA
VVA0781-Outer membrane receptor protein	14.12	7.66/14.05	-75	COG1629
VV1184-Hypothetical protein	12.05/7.10	12.53/6.24	-55	NA
VV0073-Permease				COG0697
VV1441-Transcriptional regulator	6.58	5.12	-281	COG1737
VV1558-Uroporphyrin-III C-methyltransferase				COG1648
VV1956-Fe-S oxidoreductase GlcD	5.3		-226	COG0277
				COG0226
				COG0573
				COG0581
VVA0369-72-Phosphate ABC transporter	11.29/6.29	12.77/6.00	-437	COG1117
VV2770-SmcR-like protein VvpR	5.28/6.89		-78	COG1309
VV2570-Ribosomal protein L31	8.78	6.21/5.22	-57	COG0254
VV3141-Transcriptional regulator, MerR family				COG0789
VV3150-Uroporphyrinogen decarboxylase				COG0407
VV0124-O-methyltransferase-related protein	11.99	11.99	-51	COG3315
VV3234-FixG-related protein				COG0526
VV0085-CyaY protein	5.18	7.72	-93	COG1965
VV1484-Permease				COG0477

				COG0845
				COG3672
				COG2274
VVA1651-54-Membrane-fusion protein				
VV1380-Conserved hypothetical protein	11.00/7.30/14.16	11.64/8.39/13.76	-36	NA
VVA1503-Hypothetical protein	5.15/7.86	5.08/7.70	-74	NA
VVA1645-AraC-type DNA-binding domain-containing protein	5.05		-82	COG2207
VV1381-Hypothetical protein	13.76/8.39/11.64	14.16/7.84/11.00	-27	COG1227
VVA0675-Permease	5.4		-85	COG0477
VVA0408-Conserved hypothetical protein	7.32	6.41	-149	COG3217
VVA1081-Di- and tripeptidase	5.04		-24	COG2195
VV1122-Membrane protein				COG3217
VVA1252-Putative magnesium transporter				COG2239
VVA1256-ATP-dependent protease LA-related protein	12.16/5.64	12.03/8.36	-200	COG1067
VV2393-Conserved hypothetical protein	12.06/8.72	6.05/12.19/5.99	-80	COG3016
VV1457-Hypothetical protein				NA
VV1726-CheY-like receiver protein				NA
VV2050-DPS family protein				COG0783
VVA0004 Peptide ABC transporter, ATP-binding protein	16.32/5.21/7.49	16.09/7.43	-40	COG0444
VV0857-Transcriptional regulator Crl	11.1	11.2	-47	NA
VVA0369-ABC-type phosphate transport system	11.29/6.29	12.77/6.00	-437	COG0226
VVA0120-Hypothetical protein	5.64		-186	NA
VV1236-Glutamate decarboxylase				COG0160
VVA1257-58-Hypothetical protein and ABC transporter, ATP-binding protein	8.36/12.03/8.15	5.64/12.16	-56	COG1123
VVA1259-Serine protease	8.05	6.5	-109	COG1505
VVA1612-ABC-type multidrug transport system	5.17/5.85	5.72	-181	COG1132
VVA1152-Predicted dehydrogenase		5.42/6.88	-16	COG0673
VV1154 Nitroreductase		5.65	-33	COG0778
VVA0320 Zn-dependent hydrolase	5.8		-2	COG0491
VVA1297-94-Non-ribosomal peptide synthetase modules	8.58/5.67/14.71	7.06/14.99/9.41	-51	COG1020

VV3115-Superoxide dismutase	10.83/10.35	9.28/10.10	-57	COG0605
VVA0782-Transcriptional regulator, LysR family	7.66/14.05/5.00	14.12	-145	COG0583
VVA1117-Putative phosphomannomutase	6.71/14.65	6.52/13.90/6.69	-56	COG1109

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Iron Metabolism

	4.09/4.36/8.24/			
small regulatory RNA ryhB	12.78	6.41/12.91	-29	NA
VF1506-Iron-regulated protein FrpC	4.39		-164	NA
VF1234-Hemin receptor	10.56/15.68/4.03	5.92/13.56/6.60	-74	COG1629
				COG0635
				COG3721
VF1226-28-Coproporphyrinogen III oxidase	5.21/12.92/4.54/4.23	12.37/5.00	-99	COG0748
				COG0810
				COG0811
				COG0848
				COG0614
				COG0609
VF1225-20- <i>tonB1</i> -system/heme transporter	12.37/5.00	5.21/12.92/4.54/4.23	-64	COG1120
VF1531-Ferrochelataase (uroporphyrin-III C-methyltransferase)	10.35/4.10	8.54	-130	COG1648
				COG1918
				COG0370
VF0833-35-Ferrous iron transport protein AB	4.93/12.48	6.42/11.46	-34	-
				COG1840
				COG1178
VF2151-49-Iron(III)-transporter	11.16/4.26	11.77/4.22	-78	COG3841
VFA1162-Iron-regulated protein FrpC	7.65	7.15	-365	NA
VFA0995-High-affinity iron permease	6.08/11.16/12.81	8.73/12.29/5.49	-54	COG0672

				-
				-
				-
				-
				COG0811
				COG0848
				COG0457
VFA0191-97-TonB dependent receptor/ <i>tonB2</i> -system	5.76/13.65/4.55	11.46/5.41	-82	COG0457
				COG0614
				COG0609
				COG0609
VFA0827-23-Ferric anguibactin-binding protein	12.28/9.09	12.32/9.27	-64	COG1120
VFA0165-Ferric aerobactin receptor precursor	7.54	4.08	-61	COG1629
VFA0161-Aerobactin siderophore biosynthesis protein, <i>lucA</i>	4.68/13.06/5.92	15.06/10.04	-51	NA
				COG1629
				COG1120
				COG0614
VFA0784-81-Ferrichrome-iron receptor	7.18/5.46	7.78/9.14	-54	COG0609
VF1234-Hemin receptor	10.56/15.68/4.03	5.92/13.56/6.60	-74	COG1629
				COG0614
				COG0609
No/VFA0827-Ferric anguibactin-binding protein	12.28/9.09	12.32/9.27	-64	COG0609
VFA0823-Vulnibactin utilization protein <i>ViuB</i>				COG2375
				COG1770
				COG1629
				-
				-
VFA0333-29-Protease II/Hemin receptor	13.23/7.67	14.09/7.85	-78	-
				-
Energy Metabolism				
VF0622-Ferredoxin	5.15	8.34	-1	COG0633

VF0812-Flavodoxin				COG0716
VF1363-Ferredoxin	11.31/14.20	8.99/13.35	-247	COG1145
VF0901-02-Transport ATP-binding protein CydDC				COG1132
				COG1132
				COG2209
				COG2878
				-
				COG1805
				COG2869
				COG1347
				COG0177
VF0935-28-Electron transport complex protein RnfB	5.46		-22	COG0346
VF0953-Cytochrome d ubiquinol oxidase subunit I (CDD cydA)	5.81	7.66	-237	COG1271
VF1554-Cytochrome c552	6.73/10.86	7.50/12.13	-225	COG3303
				-
				COG0437
				COG3301
				COG1138
				COG0526
VF1553-48-Cytochrome c-type protein NrfB	7.50/12.13/7.28	6.73/10.86/9.63	-260	COG3088
				COG1131
				COG2386
				COG0755
				COG3114
				COG2332
				COG1138
				COG0526
				-
VF1824-16-Cytochrome biogenesis protein ABCD	4.24/5.31	8.02	-147	-

VF1943-Cytochrome c554				COG2863
VF1907-Ferredoxin-type protein NapF	5.28		-37	COG1145
VFA0084-Ferredoxin-type protein NapF	8.89/4.13	10.08/6.15	15	COG1145
VFA0116-Virulence factor MviM	8.03	7.72	-1	COG0673

Virulence Factors

VF0572-Pili subunit PilA1				COG2165
VF0696-Accessory colonization factor AcfD-like protein	5.69/4.10/4.53		-243	NA
VF1369-Methyl-accepting chemotaxis protein	5.30		-97	COG0840
VF1789-Methyl-accepting chemotaxis protein	7.58	5.02	-100	COG0840
				COG1298
VF1837-36-Polar flagellar assembly protein FlhA/FlhH				COG1419
VF1866-Flagellin, FlaA	5.61		-66	COG1344
VFA0092-Methyl-accepting chemotaxis protein	4.60	6.99	-156	COG0840
				COG0845
				COG3672
VFA1168-65-Type I secretion, HlyD family	8.44	6.95	-171	COG2274
VFA0448-Methyl-accepting chemotaxis protein	5.28		-35	COG0840
VFA0481-Methyl-accepting chemotaxis protein	6.35	4.81	-45	COG0840
VFA0677-Methyl-accepting chemotaxis protein	7.39	4.15	-83	COG0840
VFA0389-Methyl-accepting chemotaxis protein	4.58	6.85	-195	COG0840
VF1138-Methyl-accepting chemotaxis protein	4.84/4.42		-106	COG0840
VFA0169-Methyl-accepting chemotaxis protein				COG0840
VF1138-Methyl-accepting chemotaxis protein	4.84/4.42		-106	COG0454
VFA0473-Methyl-accepting chemotaxis protein	4.28/6.15	4.11/4.15	-1	COG0745
VFA0170-Methyl-accepting chemotaxis protein	6.57	5.05	-260	COG0840
VFA0389-Methyl-accepting chemotaxis protein	4.58	6.85	-195	COG0840

Miscellaneous

VF0366-Type IV pilus, mannose-sensitive hemagglutinin A				NA
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VF0591-Glycine cleavage system transcriptional activator	8.10/4.66	7.50	-51	COG0583
VF0596-Conserved hypothetical protein	9.74/5.61	8.61	-134	NA
VF0781-Copper-exporting ATPase	4.63	7.01	-38	COG2217
VF0801-COME operon protein 1	6.13	7.19	-1	COG1555
VF0805-Glutathione-regulated potassium-efflux system protein KefC				COG0475
				COG1121
VF0829-28-Zinc ABC transporter	8.05	6.77	-24	COG1108
VF0830-Zinc ABC transporter	6.77	8.05	-83	COG0803
VF0683-Putative transcriptional regulator				COG1720
VF0737-Guanine-hypoxanthine permease				COG2252
VF1647-Hypothetical protein				NA
VF0988-Hypothetical protein	4.68		-181	NA
VF1040-Possible protease SohB	9.39	9.11	-82	COG0616
VF1074-Transcriptional regulator, AraC family				COG2207
VF1103-Hypothetical protein	4.77	6.09	-62	COG2020
VF1175-Conserved hypothetical protein	4.08/5.18	4.68/4.86	-1	NA
VF1176 L-serine dehydratase	4.52	4.25	-53	COG1760
VFA0931-Transcriptional regulatory, AraC-like				COG2207
				COG1132
				COG2995
VF1277-75-Transporter	7.06/9.23	6.77/9.84	-19	COG3008
VF1494-Transporter	6.13/5.04	6.76/4.42	-60	NA
	11.31/4.40/6.28/	11.90/4.54/4.48/		
VF1190-Conserved hypothetical protein	13.79/4.58/5.69	4.53/5.69	-86	COG3487
VF0927-Hypothetical protein	10.66	9.76/4.02	-69	NA
VF0982-Transporter				COG0697
VF0891-Transcriptional regulator, RpiR				COG1737
VF1525-Aerobic glycerol-3-phosphate dehydrogenase subunit C	6.63	5.52	-160	COG0277

				COG0226
				COG0573
				COG0581
VF1610-13-Phosphate transport system	5.96		-173	COG1117
VF1911-Hypothetical protein	9.46/6.66	10.99/6.42	-35	NA
VF2177-LitR, transcriptional regulator	9.92/4.67	7.11	-64	COG1309
VF2273-50S ribosomal protein L31	4.94		-303	COG0254
				COG1053
				COG0479
				COG3029
VF2334-37-Fumarate reductase flavoprotein subunit	11.24/6.99	12.69/4.65	-299	COG3080
VF2393-Transcriptional regulator, MerR family				COG0789
VF2402-Uroporphyrinogen decarboxylase HemE	6.45	4.17	-180	COG0407
VF2441-Hypothetical protein	15.28/7.53	13.96	-46	COG3315
VF2551-Hypothetical protein	5.09		-29	COG0526
VF2486-CyaY protein				COG1965
VFA0140-Hypothetical protein				NA
VFA0977-Possible efflux permease	7.82	4.35	-65	COG0477
	5.08/6.96/13.63/	6.56/7.42/12.64/		
VFA0848-Conserved hypothetical protein	4.56	7.17	-64	NA
VFA0156-Hypothetical protein	12.52	13.37	-79	NA
VFA0833-AraC-type DNA-binding domain-containing protein	5.26/4.12		-192	COG2207
VFA0421-Manganese-dependent inorganic pyrophosphatase				COG1227
VFA0611-Oxalate/formate antiporter	4.88		-4	COG0477
VFA0264-Oxidoreductase (iron-sulfur cluster biosynthesis)				COG3217
VFA0253-Tripeptidase T				COG2195
VFA0205-Hypothetical membrane spanning protein				COG3217
VFA1019-18-Hypothetical cytosolic protein				NA
VFA0120-Hypothetical cytosolic protein				NA

VFA1047-Mg ²⁺ transporter MgtE	5.72	4.02	-255	COG2239
VFA0414-ATP-dependent protease La	4.07	4.70	-32	COG1067
	9.06/6.63/4.30/	8.49/8.62/8.53/		
VFA0756-Putative lipoprotein	9.03/11.20/4.63	12.58/5.29	-59	COG3016
VFA0769-Agglutination protein	4.49		-149	NA
VFA0795-Two component response regulator	4.83		-7	NA
VFA0200-Oligosaccharide transport ATP-binding protein	10.82/12.24	9.20/11.16	-37	COG0444
VF1610-Phosphate-binding protein				COG0226
VFA1123-Diaminobutyrate--pyruvate aminotransferase				COG0160
VF1122-Prolyl endopeptidase				COG1505
VFA0509-Multidrug resistance ABC transporter	5.56	6.92	-217	COG1132
VF0921-Superoxide dismutase				COG0605
VFA1160-Transcriptional regulator	5.45/4.92		-29	COG0583
VF1056-Phosphoglucomutase	13.15/5.33	10.70/6.31	-58	COG1109

Identified by Mey et al., 2005b

¹identified by Funahashi et al., 2003

²identified by Tanabe et al., 2005

³identified by Litwin et al., 2001

⁴Identified by Mey et al., 2005a

*Predicted by Panina et al., 2001

Grey cells indicates no predicted Fur-boxes in this study

() indicates pseudogenes/disrupted genes

in *V. salmonicida*