

Supplementary Table S4. Genes with differential expression ( $P < 1 \times 10^{-7}$ ) in at least one of the six conditions described in Fig. 6A – Node 2A. Depicted is a rank of genes by major biological function followed by each individual gene grouped by function. In general, these genes were induced at all time points by *in vitro* derived *V. cholerae* in the aquatic environment. Table S10 provides gene specific fold-changes.

Biological function	Number of genes	Percent of genes with annotation	Genes of interest
Cellular processes	29	48	Motility , <i>rpoS</i> , <i>tcpP</i>
Regulation	9	15	<i>csrA</i> , <i>rseA</i>
Cell Envelope	4	7	<i>envA</i>
Amino Acid Biosynthesis	1	2	
Central metabolism	1	2	
Energy Metabolism	1	2	
Mobile and extrachromosomal role	1	2	<i>rstR-2</i>
Transport and binding proteins	1	2	
Protein fate	1	2	
Transcription	1	2	<i>rpoH</i>
Biosyn of cofactors	0	0	
DNA metabolism	0	0	
Fatty acid metabolism	0	0	
Protein synthesis	0	0	
Nucleic acid synthesis	0	0	
Hypothetical (annotated)	11	18	
Total annotated genes	60	100	
Hypotheticals (no annotation)	28		

Cellular processes			
Locus	Function	Gene	P Value
VC0534	RNA polymerase sigma factor RpoS	<i>rpoS</i>	2.5E-12
VC0826	toxin co-regulated pilus biosynthesis protein P	<i>tcpP</i>	2.2E-15
VC0892	chemotaxis protein PomA	<i>pomA</i>	2.9E-09
VC1130	DNA-binding protein VicH	<i>vicH</i>	1.7E-16
VC1456	cholera enterotoxin, B subunit	<i>ctxB</i>	1.9E-08
VC2065	chemotaxis protein CheY	<i>cheY-3</i>	1.7E-15
VC2069	flagellar biosynthetic protein FlhA	<i>flhA</i>	2.0E-08
VC2128	flagellar hook-length control protein FliK, putative		1.6E-08
VC2134	flagellar hook-basal body complex protein FliE	<i>fliE</i>	2.5E-15
VC2138	flagellar protein FliS	<i>fliS</i>	6.8E-16
VC2139	flagellar rod protein FlaI, putative		2.9E-09
VC2142	flagellin FlaB	<i>flaB</i>	1.1E-08

VC2143	flagellin FlaD	<i>flaD</i>	8.3E-14
VC2144	flagellin FlaE	<i>flaE</i>	8.5E-12
VC2187	flagellin FlaC	<i>flaC</i>	6.3E-12
VC2188	flagellin core protein A	<i>flaA</i>	3.4E-10
VC2191	flagellar hook-associated protein FlgM	<i>flgM</i>	3.9E-10
VC2193	flagellar P-ring protein FlgI	<i>flgI</i>	2.5E-14
VC2195	flagellar basal-body rod protein FlgG	<i>flgG</i>	4.2E-08
VC2196	flagellar basal-body rod protein FlgF	<i>flgF</i>	1.2E-11
VC2197	flagellar hook protein FlgE	<i>flgE</i>	5.4E-12
VC2198	basal-body rod modification protein FlgD	<i>flgD</i>	8.1E-17
VC2199	flagellar basal-body rod protein FlgC	<i>flgC</i>	1.3E-13
VC2200	flagellar basal-body rod protein FlgB	<i>flgB</i>	1.1E-12
VC2202	chemotaxis protein CheV	<i>cheV-3</i>	3.9E-08
VC2204	negative regulator of flagellin synthesis FlgM, putative		1.1E-13
VC2397	cell division protein FtsZ	<i>ftsZ</i>	1.5E-11
VC2398	cell division protein FtsA	<i>ftsA</i>	1.3E-10
VC2601	sodium-type flagellar protein MotX	<i>motX</i>	1.0E-12
Cellular processes			
Locus	Function	Gene	<i>P</i> Value
VC0347	host factor-I, putative		6.7E-12
VC0378	zinc uptake regulation protein, putative		1.8E-10
VC0431	arginine repressor	<i>argR</i>	9.4E-08
VC0548	carbon storage regulator	<i>csrA</i>	3.2E-11
VC0583	hemagglutinin-protease regulatory protein, authentic frameshift		3.8E-14
VC1434	fumarate and nitrate reduction regulatory protein	<i>fnr</i>	8.0E-08
VC1914	integration host factor, beta subunit	<i>hipB</i>	7.5E-11
VC2368	aerobic respiration control protein FexA	<i>fexA</i>	1.9E-09
VC2466	sigma-E factor negative regulatory protein RseA	<i>rseA</i>	3.0E-14
Cellular processes			
Locus	Function	Gene	<i>P</i> Value
VC0845	lipoprotein, putative		7.9E-08
VC1064	lipoprotein-related protein		4.0E-08
VC1269	lipoprotein, putative		1.2E-13
VC2396	UDP-3-O-3-hydroxymyristoyl N-acetylglucosamine deacetylase	<i>envA</i>	2.4E-11
Amino Acid Biosynthesis			
Locus	Function	Gene	<i>P</i> Value
VC2644	N-acetyl-gamma-glutamyl-phosphate reductase	<i>argC</i>	1.9E-08

Central metabolism			
Locus	Function	Gene	P Value
VC0252	acetyltransferase RfbO, CysE-LacA-LpxA-NodL family		6.2E-08
Energy Metabolism			
Locus	Function	Gene	P Value
VC0112	cytochrome c4	<i>cycA</i>	4.3E-11
Mobile and extrachrom. Element fns			
Locus	Function	Gene	P Value
VC1464	transcriptional repressor RstR	<i>rstR-2</i>	3.4E-15
Transport and binding proteins			
Locus	Function	Gene	P Value
VC0964	PTS system, glucose-specific IIA component	<i>crr</i>	5.3E-09
Protein fate			
Locus	Function	Gene	P Value
VC0018	16 kDa heat shock protein A	<i>ibpA</i>	3.6E-13
Transcription			
Locus	Function	Gene	P Value
VC0150	RNA polymerase sigma-32 factor	<i>rpoH</i>	3.7E-12
Hypothetical (annotated)			
Locus	Function	Gene	P Value
VC0049	smg protein	<i>smg</i>	3.3E-11
VC2067	MinD-related protein		3.4E-09
VCA0659	protein F-related protein		3.0E-08
VC0079	conserved hypothetical protein		2.8E-12
VC1124	conserved hypothetical protein		2.1E-15
VC2040	conserved hypothetical protein		2.7E-13
VC2478	conserved hypothetical protein		8.1E-12
VCA0332	conserved hypothetical protein		7.6E-09
VCA0741	conserved hypothetical protein		2.3E-09
VCA0919	conserved hypothetical protein		1.3E-09
VCA1042	Ccm2-related protein		1.2E-11
Hypothetical (no annotation)			
Locus	Function	Gene	P Value
VC0038	hypothetical protein		7.2E-13
VC0174	hypothetical protein		5.5E-10
VC0588	hypothetical protein		1.2E-08

VC1125	hypothetical protein		4.1E-09
VC1154	hypothetical protein		1.6E-08
VC1384	hypothetical protein		1.8E-10
VC1538	hypothetical protein		9.6E-12
VC1613	hypothetical protein		3.2E-10
VC1699	hypothetical protein		4.0E-10
VC2005	hypothetical protein		4.5E-16
VC2010	hypothetical protein		5.5E-16
VC2189	hypothetical protein		7.1E-18
VC2205	hypothetical protein		6.7E-14
VC2207	hypothetical protein		7.4E-13
VC2208	hypothetical protein		2.2E-08
VC2263	hypothetical protein		2.5E-10
VC2357	hypothetical protein		1.2E-08
VC2365	hypothetical protein		3.4E-11
VC2717	hypothetical protein		2.1E-12
VCA0078	hypothetical protein		7.4E-11
VCA0377	hypothetical protein		5.7E-08
VCA0386	hypothetical protein		4.0E-08
VCA0568	hypothetical protein		1.4E-10
VCA0868	hypothetical protein		2.2E-17
VCA0881	hypothetical protein		8.3E-08
VCA0920	hypothetical protein		4.0E-08
VCA1016	hypothetical protein		4.4E-17
VCA1024	hypothetical protein		7.7E-14