

Supplementary Table S9. Genes with differential expression ($P < 1 \times 10^{-7}$) in at least one of the six conditions described in Fig. 7A – Node 2. Depicted is a rank of genes by major biological function followed by each individual gene grouped by function. In general, these genes were repressed at 0 h and were induced by 24 h in the aquatic environment.

Biological function	Number of genes	Percent of genes with annotation	Genes of interest
Transport and binding proteins	5	23	
Cellular processes	4	18	<i>cheY-4</i>
Cell Envelope	2	9	fimbrial proteins
Biosynthesis of cofactors	1	5	
Central metabolism	1	5	
DNA metabolism	1	5	
Energy Metabolism	1	5	
Fatty acid metabolism	0	0	
Protein fate	0	0	
Protein synthesis	0	0	
Nucleic acid synthesis	0	0	
Regulation	0	0	
Transcription	0	0	
Hypothetical (annotated)	7	32	
Total annotated genes	22		
Hypotheticals (no annotation)	8		

Transport and binding proteins			
Locus	Function	Gene	P Value
VC1547	biopolymer transport protein ExbB-related protein		4.8E-08
VC1665	ABC transporter, permease protein, putative		2.5E-08
VCA0070	phosphate ABC transporter, periplasmic phosphate-binding protein	<i>pstS</i>	9.7E-12
VCA0267	multidrug resistance protein D	<i>emrD-3</i>	1.0E-09
VCA0772	tyrosine-specific transport protein	<i>tyrP</i>	2.7E-12
Cellular process			
Locus	Function	Gene	P Value
VC0304	guanosine-5-triphosphate,3-diphosphate pyrophosphatase	<i>gppA</i>	1.7E-09
VC1898	methyl-accepting chemotaxis protein		7.5E-13
VCA0068	methyl-accepting chemotaxis protein		3.8E-09
VCA1096	chemotaxis protein CheY	<i>cheY-4</i>	1.8E-10
Cell Envelope			
Locus	Function	Gene	P Value
VC2631	fimbrial assembly protein PilP, putative		6.2E-11
VC2632	fimbrial assembly protein PilO, putative		1.9E-08
Biosynthesis of cofactors			
Locus	Function	Gene	P Value
VC0222	lipopolysaccharide core biosynthesis	<i>kdtB</i>	9.5E-08

	protein KdtB		
Central, DNA, and Energy metabolism			
Locus	Function	Gene	<i>P</i> Value
VC1591	oxidoreductase, short-chain dehydrogenase-reductase family		1.1E-08
VC0345	DNA mismatch repair protein MutL	<i>mutL</i>	6.4E-11
VCA0155	NADH dehydrogenase, putative		3.7E-08
Hypothetical (annotated)			
Locus	Function	Gene	<i>P</i> Value
VC1782	ROK family protein		5.0E-08
VC2750	GGDEF family protein		4.3E-09
VC1322	conserved hypothetical protein		7.0E-11
VCA0489	conserved hypothetical protein		2.4E-08
VCA0716	conserved hypothetical protein		9.1E-15
VCA0948	conserved hypothetical protein		6.5E-12
VCA1021	conserved hypothetical protein		1.7E-10
Hypothetical (no annotation)			
Locus	Function	Gene	<i>P</i> Value
VC0101	hypothetical protein		7.6E-08
VC0932	hypothetical protein		3.2E-09
VCA0118	hypothetical protein		6.8E-08
VCA0631	hypothetical protein		8.6E-08
VCA0715	hypothetical protein		5.5E-11
VCA0868	hypothetical protein		2.7E-09
VCA1016	hypothetical protein		2.3E-08
VCA1107	hypothetical protein		2.1E-08