

Supplementary Table S8. Genes with differential expression ($P < 1 \times 10^{-7}$) in at least one of the six conditions described in Fig. 7A – Node 1. 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 0 h and were repressed by 24 h in the aquatic environment.

Biological function	Number of genes	Percent of genes with annotation	Genes of interest
Protein synthesis	60	42	
Energy Metabolism	17	12	
Cellular process	12	8	flagellar genes, <i>fts</i> , <i>ssp</i> , <i>cheZ</i>
Cell Envelope	10	7	<i>ompU</i> , <i>envA</i> , <i>ompW</i> , <i>ompA</i> , <i>ompH</i>
Regulation	8	6	
Transcription	7	5	<i>rpoA</i> , <i>rpoH</i> , <i>rpoH</i>
Fatty acid metabolism	5	3	
Protein fate	5	3	sec and tat secretion systems
Transport and binding proteins	3	2	<i>ompT</i>
Biosynthesis of cofactors	2	1	
Central metabolism	2	1	
DNA metabolism	2	1	
Nucleic acid synthesis	2	1	
Hypothetical (annotated)	8	6	
Total annotated genes	143		
Hypothetical (no annotation)	9		

Protein synthesis			
Locus	Gene	Function	P Value
VC0218	ribosomal protein L28	<i>rpmB</i>	6.1E-10
VC0219	ribosomal protein L33	<i>rpmG</i>	1.7E-09
VC0321	elongation factor Tu	<i>tufB</i>	2.7E-12
VC0324	ribosomal protein L11	<i>rplK</i>	8.9E-10
VC0325	ribosomal protein L1	<i>rplA</i>	3.9E-13
VC0326	ribosomal protein L10	<i>rplJ</i>	5.4E-19
VC0327	ribosomal protein L7-L12	<i>rplL</i>	1.6E-13
VC0359	ribosomal protein S12	<i>rpsL</i>	4.4E-11
VC0360	ribosomal protein S7	<i>rpsG</i>	6.8E-10
VC0361	elongation factor G	<i>fusA-1</i>	2.0E-09
VC0366	ribosomal protein S6	<i>rpsF</i>	2.3E-17
VC0368	ribosomal protein S18	<i>rpsR</i>	2.5E-15
VC0369	ribosomal protein L9	<i>rplI</i>	1.5E-12
VC0436	ribosomal protein L27	<i>rpmA</i>	3.4E-11
VC0520	ribosomal protein S21	<i>rpsU</i>	1.5E-08
VC0561	ribosomal protein S16	<i>rpsP</i>	7.1E-09
VC0563	tRNA (guanine-N1)-methyltransferase	<i>trmD</i>	1.5E-11
VC0564	ribosomal protein L19	<i>rplS</i>	6.1E-13
VC0570	ribosomal protein L13	<i>rplM</i>	5.2E-12
VC0571	ribosomal protein S9	<i>rpsI</i>	8.5E-15
VC0643	initiation factor IF-2	<i>infB</i>	3.1E-09
VC0645	tRNA pseudouridine 55 synthase	<i>truB</i>	1.0E-08

VC0646	ribosomal protein S15	<i>rpsO</i>	1.3E-10
VC0682	isoleucyl-tRNA synthetase	<i>ileS</i>	4.5E-08
VC1179	pseudouridine synthase family 1 protein		1.8E-08
VC1640	ribosomal protein L25	<i>rplY</i>	3.5E-13
VC1915	ribosomal protein S1	<i>rpsA</i>	4.4E-12
VC2025	ribosomal protein L32	<i>rpmF</i>	1.8E-10
VC2257	ribosome recycling factor	<i>frr</i>	2.2E-09
VC2260	ribosomal protein S2	<i>rpsB</i>	1.3E-13
VC2570	ribosomal protein L17	<i>rplQ</i>	2.3E-09
VC2572	ribosomal protein S4	<i>rpsD</i>	7.0E-11
VC2573	ribosomal protein S11	<i>rpsK</i>	2.4E-16
VC2574	ribosomal protein S13	<i>rpsM</i>	5.7E-16
VC2575	ribosomal protein L36	<i>rpmJ</i>	3.6E-16
VC2577	ribosomal protein L15	<i>rplO</i>	1.7E-19
VC2578	ribosomal protein L30	<i>rpmD</i>	8.6E-17
VC2579	ribosomal protein S5	<i>rpsE</i>	2.0E-09
VC2580	ribosomal protein L18	<i>rplR</i>	1.3E-19
VC2581	ribosomal protein L6	<i>rplF</i>	4.5E-14
VC2582	ribosomal protein S8	<i>rpsH</i>	3.1E-11
VC2583	ribosomal protein S14	<i>rpsN</i>	4.1E-20
VC2584	ribosomal protein L5	<i>rplE</i>	4.1E-14
VC2585	ribosomal protein L24	<i>rplX</i>	1.3E-18
VC2586	ribosomal protein L14	<i>rplN</i>	1.8E-13
VC2587	ribosomal protein S17	<i>rpsQ</i>	1.4E-17
VC2588	ribosomal protein L29	<i>rpmC</i>	4.9E-20
VC2589	ribosomal protein L16	<i>rplP</i>	1.1E-17
VC2590	ribosomal protein S3	<i>rpsC</i>	3.2E-14
VC2591	ribosomal protein L22	<i>rplV</i>	1.1E-23
VC2592	ribosomal protein S19	<i>rpsS</i>	4.1E-13
VC2593	ribosomal protein L2	<i>rplB</i>	1.5E-17
VC2594	ribosomal protein L23	<i>rplW</i>	3.9E-16
VC2595	ribosomal protein L4	<i>rplD</i>	1.9E-13
VC2596	ribosomal protein L3	<i>rplC</i>	3.5E-15
VC2597	ribosomal protein S10	<i>rpsJ</i>	3.4E-11
VC2660	elongation factor P	<i>efp</i>	1.5E-12
VC2679	ribosomal protein L31	<i>rpmE</i>	5.3E-12
VCA0289	ribosomal protein L35	<i>rpmI</i>	6.6E-09
VCA0290	ribosomal protein L20	<i>rplT</i>	1.1E-14
Energy Metabolism			
Locus	Gene	Function	P Value
VC0112	cytochrome c4	<i>cycA</i>	1.0E-09
VC0575	ubiquinol--cytochrome c reductase, cytochrome c1	<i>petC</i>	4.8E-12
VC1146	glutaredoxin 1	<i>grxA</i>	2.7E-11
VC1441	cytochrome c oxidase, subunit CcoO	<i>ccoO</i>	6.2E-11
VC2092	citrate synthase	<i>gltA</i>	7.7E-13
VC2290	NADH:ubiquinone oxidoreductase, Na translocating, beta subunit	<i>nqrF</i>	5.1E-15
VC2291	NADH:ubiquinone oxidoreductase, Na translocating, hydrophobic membrane protein NqrE	<i>nqrE</i>	1.5E-08
VC2295	NADH:ubiquinone oxidoreductase, Na translocating, alpha subunit	<i>nqrA</i>	3.8E-08
VC2480	ribose-5-phosphate isomerase	<i>rpiA</i>	6.1E-08

VC2659	fumarate reductase, 13 kDa hydrophobic protein	<i>frdD</i>	7.7E-08
VC2738	phosphoenolpyruvate carboxykinase	<i>pckA</i>	9.5E-09
VC2764	ATP synthase F1, beta subunit	<i>atpD</i>	5.4E-12
VC2765	ATP synthase F1, gamma subunit	<i>atpG</i>	2.7E-11
VC2768	ATP synthase F0, B subunit	<i>atpF</i>	3.4E-09
VC2769	ATP synthase F0, C subunit	<i>atpE</i>	7.3E-08
VC2770	ATP synthase F0, A subunit	<i>atpB</i>	4.7E-09
VCA0843	glyceraldehyde 3-phosphate dehydrogenase	<i>gapA-2</i>	8.9E-08
Cellular processes			
Locus	Gene	Function	P Value
VC0139	DPS family protein		7.0E-08
VC0576	stringent starvation protein A	<i>sspA</i>	2.3E-10
VC0577	stringent starvation protein B	<i>sspB</i>	5.6E-11
VC1289	methyl-accepting chemotaxis protein		3.0E-08
VC2064	chemotaxis protein CheZ	<i>cheZ</i>	6.5E-11
VC2143	flagellin FlaD	<i>flaD</i>	1.3E-09
VC2187	flagellin FlaC	<i>flaC</i>	3.4E-09
VC2193	flagellar P-ring protein FlgI	<i>flgI</i>	8.2E-09
VC2198	basal-body rod modification protein FlgD	<i>flgD</i>	8.7E-09
VC2199	flagellar basal-body rod protein FlgC	<i>flgC</i>	1.5E-08
VC2397	cell division protein FtsZ	<i>ftsZ</i>	8.5E-08
VC2398	cell division protein FtsA	<i>ftsA</i>	7.1E-12
Cell Envelope			
Locus	Gene	Function	P Value
VC0243	GDP-mannose 4,6-dehydratase	<i>rfbD</i>	3.1E-08
VC0633	outer membrane protein OmpU	<i>ompU</i>	9.5E-13
VC1835	peptidoglycan-associated lipoprotein	<i>pal</i>	1.8E-08
VC2156	lipoprotein-34 NlpB	<i>nlpB</i>	7.2E-08
VC2175	2-dehydro-3-deoxyphosphooctonate aldolase	<i>kdsA</i>	4.2E-11
VC2213	outer membrane protein OmpA	<i>ompA</i>	2.2E-08
VC2250	UDP-3-O-3-hydroxymyristoyl glucosamine N-acyltransferase	<i>lpxD</i>	4.2E-12
VC2251	outer membrane protein OmpH	<i>ompH</i>	2.1E-08
VC2396	UDP-3-O-3-hydroxymyristoyl N-acetylglucosamine deacetylase	<i>envA</i>	2.6E-09
VCA0867	outer membrane protein OmpW	<i>ompW</i>	2.2E-12
Regulation			
Locus	Gene	Function	P Value
VC0290	factor-for-inversion stimulation protein	<i>fis</i>	1.2E-11
VC0378	zinc uptake regulation protein, putative		4.4E-09
VC0583	hemagglutinin-protease regulatory protein, authentic frameshift		6.2E-10
VC2106	ferric uptake regulation protein	<i>fur</i>	1.5E-10
VC2368	aerobic respiration control protein FexA	<i>fexA</i>	1.9E-08
VCA0166	cold shock transcriptional regulator CspA	<i>cspA</i>	5.5E-09
VCA0184	cold shock DNA-binding domain protein		3.5E-10

VCA0933	cold shock domain family protein		5.2E-11
Transcription			
Locus	Gene	Function	P Value
VC0150	RNA polymerase sigma-32 factor	<i>rpoH</i>	3.6E-09
VC0307	transcription termination factor Rho	<i>rho</i>	1.5E-12
VC0323	transcription antitermination protein NusG	<i>nusG</i>	3.2E-09
VC0328	DNA-directed RNA polymerase, beta subunit	<i>rpoB</i>	9.0E-08
VC0562	16S rRNA processing protein RimM	<i>rimM</i>	1.3E-13
VC2571	DNA-directed RNA polymerase, alpha subunit	<i>rpoA</i>	1.0E-17
VCA0804	ATP-dependent RNA helicase DeaD	<i>deaD</i>	4.7E-12
Fatty acid metabolism			
Locus	Gene	Function	P Value
VC0251	acyl protein synthase-acyl-CoA reductase RfbN		8.1E-08
VC0745	inositol monophosphate family protein		3.0E-09
VC2021	3-oxoacyl-(acyl-carrier-protein) reductase	<i>fabG</i>	2.3E-10
VC2022	malonyl CoA-acyl carrier protein transacylase	<i>fabD</i>	1.8E-08
VC2249	(3R)-hydroxymyristoyl-(acyl-carrier-protein) dehydratase	<i>fabZ</i>	2.0E-09
Protein fate			
Locus	Gene	Function	P Value
VC0086	tatA protein	<i>tatA-1</i>	5.8E-10
VC0322	preprotein translocase, SecE subunit	<i>secE</i>	1.3E-09
VC0640	preprotein translocase, SecG subunit	<i>secG</i>	4.3E-09
VC0744	protein-export membrane protein SecF	<i>secF-1</i>	8.8E-08
VC2576	preprotein translocase, SecY subunit	<i>secY</i>	1.6E-17
Transport and binding proteins			
Locus	Gene	Function	P Value
VC1042	long-chain fatty acid transport protein	<i>fadL-1</i>	5.2E-09
VC1091	oligopeptide ABC transporter, periplasmic oligopeptide-binding protein	<i>oppA</i>	3.9E-10
VC1854	ompT protein	<i>ompT</i>	4.7E-08
Biosynthesis of cofactors			
Locus	Gene	Function	P Value
VC0440	dihydrofolate reductase	<i>folA</i>	3.5E-08
VC2268	6,7-dimethyl-8-ribityllumazine synthase	<i>ribE</i>	2.5E-08
Central metabolism			
Locus	Gene	Function	P Value
VC2545	inorganic pyrophosphatase	<i>ppa</i>	3.2E-08
VCA0341	biphenyl-2,3-diol 1,2-dioxygenase III-related protein		1.7E-08
DNA metabolism			
Locus	Gene	Function	P Value

VC2545	inorganic pyrophosphatase	<i>ppa</i>	3.2E-08
VCA0341	biphenyl-2,3-diol 1,2-dioxygenase III-related protein		1.7E-08
Nucleic acid synthesis			
Locus	Gene	Function	<i>P</i> Value
VC0052	phosphoribosylaminoimidazole carboxylase, catalytic subunit	<i>purE</i>	6.6E-09
VC0395	UTP--glucose-1-phosphate uridylyltransferase	<i>galU</i>	7.0E-08
Hypothetical (annotated)			
Locus	Gene	Function	<i>P</i> Value
VC0253	IS1004 transposase-related protein		3.6E-08
VC2067	MinD-related protein		3.1E-08
VC2688	glpX protein	<i>glpX</i>	3.1E-09
VC0641	conserved hypothetical protein		1.2E-11
VC2026	conserved hypothetical protein		7.1E-13
VC2326	conserved hypothetical protein		4.9E-10
VC2443	conserved hypothetical protein		2.0E-09
VCA0037	conserved hypothetical protein		4.9E-09
Hypothetical (no annotation)			
Locus	Gene	Function	<i>P</i> Value
VC0059	hypothetical protein		1.0E-10
VC0895	hypothetical protein		1.5E-08
VC1517	hypothetical protein		4.3E-08
VC1752	hypothetical protein		5.7E-09
VC2208	hypothetical protein		3.0E-08
VC2496	hypothetical protein		9.8E-10
VCA0306	hypothetical protein		4.5E-08
VCA0464	hypothetical protein		7.3E-10
VCA0502	hypothetical protein		3.1E-09