Supplementary Table S6. Genes with differential expression ($P < 1 \times 10^{-7}$) in at least one of the six conditions described in Fig. 6A – Node 3. Depicted is a rank of genes by major biological function followed by each individual gene grouped by function. In general, these genes were strongly induced by patient derive *V. cholerae* at 0 h and were repressed by both patient as well as *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
Protein synthesis	60	34	
Energy Metabolism	24	14	
Cell Envelope	12	7	*ompA, ompH, ompW*
Cellular processes	11	6	*mshA, ssp, uspA*
Transcription	9	5	*rpoA, rpoB, rpoC*
Transport and binding proteins	8	5	
Protein fate	8	5	
Regulation	6	3	
Biosynthesis of cofactors	5	3	
Fatty acid metabolism	5	3	
DNA metabolism	4	2	
Amino Acid Biosynthesis	3	2	
Central metabolism	1	1	
Nucleic acid synthesis	1	1	
Mobile and extrachromosomal role	0	0	
Hypothetical (annotated)	17	10	
Total annotated genes	174	100	
Hypothetical (no annotation)	18		

Protein synthesis			
Locus	Function	Gene	*P* Value
VC0007	ribosomal protein L34	*rpmH*	7.9E-12
VC0218	ribosomal protein L28	*rpmB*	4.0E-15
VC0219	ribosomal protein L33	*rpmG*	3.0E-09
VC0321	elongation factor Tu	*tufB*	7.3E-10
VC0324	ribosomal protein L11	*rplK*	4.7E-09
VC0325	ribosomal protein L1	*rplA*	1.1E-19
VC0326	ribosomal protein L10	*rplJ*	3.2E-22
VC0327	ribosomal protein L7-L12	*rplL*	1.4E-20
VC0359	ribosomal protein S12	*rpsL*	1.8E-11
VC0360	ribosomal protein S7	*rpsG*	1.6E-10
VC0361	elongation factor G	*fusA-1*	1.3E-10
VC0366	ribosomal protein S6	*rpsF*	1.4E-16
VC0368	ribosomal protein S18	*rpsR*	5.9E-18
VC0369	ribosomal protein L9	*rplI*	6.8E-16
VC0436	ribosomal protein L27	*rpmA*	1.9E-12
VC0520	ribosomal protein S21	*rpsU*	2.8E-12
VC0561	ribosomal protein S16	*rpsP*	2.0E-13
VC0563	tRNA (guanine-N1)-methyltransferase	*trmD*	1.9E-14
VC0564	ribosomal protein L19	*rplS*	3.0E-12

VC0570	ribosomal protein L13	*rplM*	2.0E-15
VC0571	ribosomal protein S9	*rpsI*	4.0E-20
VC0643	initiation factor IF-2	*infB*	2.0E-14
VC0646	ribosomal protein S15	*rpsO*	9.0E-17
VC0682	isoleucyl-tRNA synthetase	*ileS*	1.2E-08
VC1640	ribosomal protein L25	*rplY*	5.1E-18
VC1737	initiation factor IF-1	*infA*	3.2E-08
VC1915	ribosomal protein S1	*rpsA*	2.9E-15
VC2025	ribosomal protein L32	*rpmF*	6.2E-11
VC2257	ribosome recycling factor	*frr*	1.4E-09
VC2260	ribosomal protein S2	*rpsB*	4.7E-19
VC2342	elongation factor G	*fusA-2*	8.6E-11
VC2572	ribosomal protein S4	*rpsD*	6.5E-16
VC2573	ribosomal protein S11	*rpsK*	1.4E-14
VC2574	ribosomal protein S13	*rpsM*	4.0E-20
VC2575	ribosomal protein L36	*rpmJ*	4.9E-18
VC2577	ribosomal protein L15	*rplO*	1.8E-19
VC2578	ribosomal protein L30	*rpmD*	4.3E-19
VC2579	ribosomal protein S5	*rpsE*	3.0E-13
VC2580	ribosomal protein L18	*rplR*	7.7E-20
VC2581	ribosomal protein L6	*rplF*	7.0E-14
VC2582	ribosomal protein S8	*rpsH*	2.4E-14
VC2583	ribosomal protein S14	*rpsN*	4.5E-20
VC2584	ribosomal protein L5	*rplE*	4.5E-18
VC2585	ribosomal protein L24	*rplX*	4.0E-20
VC2586	ribosomal protein L14	*rplN*	1.4E-19
VC2587	ribosomal protein S17	*rpsQ*	4.8E-18
VC2588	ribosomal protein L29	*rpmC*	6.7E-18
VC2589	ribosomal protein L16	*rplP*	4.4E-17
VC2590	ribosomal protein S3	*rpsC*	7.8E-21
VC2591	ribosomal protein L22	*rplV*	1.2E-18
VC2592	ribosomal protein S19	*rpsS*	1.8E-14
VC2593	ribosomal protein L2	*rplB*	2.1E-19
VC2594	ribosomal protein L23	*rplW*	1.7E-20
VC2595	ribosomal protein L4	*rplD*	9.0E-16
VC2596	ribosomal protein L3	*rplC*	5.6E-20
VC2660	elongation factor P	*efp*	7.4E-10
VC2679	ribosomal protein L31	*rpmE*	4.6E-12
VCA0288	initiation factor IF3	*infC*	7.4E-11
VCA0289	ribosomal protein L35	*rpmI*	1.6E-08
VCA0290	ribosomal protein L20	*rplT*	2.3E-14
Energy Metabolism			
Locus	Function	Gene	*P* Value
VC0477	phosphoglycerate kinase	*pgk*	3.7E-08
VC0573	ubiquinol--cytochrome c reductase, iron-sulfur subunit	*petA*	1.3E-10
VC0575	ubiquinol--cytochrome c reductase, cytochrome c1	*petC*	3.7E-13
VC1146	glutaredoxin 1	*grxA*	9.1E-08
VC1441	cytochrome c oxidase, subunit CcoO	*ccoO*	6.4E-08
VC1515	chaperone, formate dehydrogenase-specific, putative		4.4E-08
VC1516	iron-sulfur cluster-binding protein		2.4E-10
VC2092	citrate synthase	*gltA*	6.4E-10

VC2290	NADH:ubiquinone oxidoreductase, Na translocating, beta subunit	*nqrF*	4.2E-15
VC2291	NADH:ubiquinone oxidoreductase, Na translocating, hydrophobic membrane protein NqrE	*nqrE*	2.4E-10
VC2294	NADH:ubiquinone oxidoreductase, Na translocating, hydrophobic membrane protein NqrB	*nqrB*	2.7E-08
VC2295	NADH:ubiquinone oxidoreductase, Na translocating, alpha subunit	*nqrA*	1.5E-12
VC2412	pyruvate dehydrogenase, E3 component, lipoamide dehydrogenase	*lpdA*	6.3E-11
VC2413	pyruvate dehydrogenase, E2 component, dihydrolipoamide acetyltransferase	*aceF*	8.8E-11
VC2624	phosphoglycolate phosphatase	*gph*	1.7E-09
VC2764	ATP synthase F1, beta subunit	*atpD*	1.6E-17
VC2765	ATP synthase F1, gamma subunit	*atpG*	5.8E-12
VC2766	ATP synthase F1, alpha subunit	*atpA*	1.4E-09
VC2767	ATP synthase F1, delta subunit	*atpH*	7.3E-12
VC2768	ATP synthase F0, B subunit	*atpF*	7.2E-12
VC2769	ATP synthase F0, C subunit	*atpE*	9.3E-12
VC2770	ATP synthase F0, A subunit	*atpB*	1.3E-11
VCA0249	cytochrome b561, putative		3.4E-09
VCA0843	glyceraldehyde 3-phosphate dehydrogenase	*gapA-2*	3.9E-11
Cell Envelope			
Locus	Function	Gene	*P* Value
VC0243	GDP-mannose 4,6-dehydratase	*rfbD*	2.3E-11
VC0263	galactosyl-transferase, putative		3.9E-08
VC1835	peptidoglycan-associated lipoprotein	*pal*	6.4E-15
VC1877	tetraacyldisaccharide 4 -kinase	*lpxK*	8.6E-08
VC1962	lipoprotein		1.9E-09
VC2156	lipoprotein-34 NlpB	*nlpB*	4.1E-09
VC2213	outer membrane protein OmpA	*ompA*	2.2E-15
VC2250	UDP-3-O-3-hydroxymyristoyl glucosamine N-acyltransferase	*lpxD*	2.5E-13
VC2251	outer membrane protein OmpH	*ompH*	4.2E-10
VC2404	phospho-N-acetylmuramoyl-pentapeptide-transferase	*mraY*	3.2E-09
VCA0059	major outer membrane lipoprotein	*lpp*	3.2E-09
VCA0867	outer membrane protein OmpW	*ompW*	2.4E-14
Cellular processes			
Locus	Function	Gene	*P* Value
VC0076	universal stress protein A	*uspA*	4.6E-10
VC0304	guanosine-5-triphosphate,3-diphosphate pyrophosphatase	*gppA*	4.1E-08
VC0409	MSHA pilin protein MshA	*mshA*	8.1E-12
VC0526	undecaprenol kinase, putative		4.0E-09
VC0576	stringent starvation protein A	*sspA*	3.8E-12
VC0577	stringent starvation protein B	*sspB*	5.6E-09
VC0637	cell division protein FtsH	*ftsH*	1.1E-08
VC1289	methyl-accepting chemotaxis protein		7.5E-10
VC1663	heat shock protein HslJ	*hslJ*	7.1E-12
VC2064	chemotaxis protein CheZ	*cheZ*	2.3E-11

VC2402	cell division protein FtsW	*ftsW*	8.8E-08
Transcription			
Locus	Function	Gene	*P* Value
VC0305	ATP-dependent RNA helicase RhlB	*rhlB*	8.7E-12
VC0307	transcription termination factor Rho	*rho*	5.9E-14
VC0323	transcription antitermination protein NusG	*nusG*	2.2E-09
VC0328	DNA-directed RNA polymerase, beta subunit	*rpoB*	1.0E-08
VC0329	DNA-directed RNA polymerase, beta subunit	*rpoC*	4.6E-09
VC0562	16S rRNA processing protein RimM	*rimM*	3.6E-16
VC0647	polyribonucleotide nucleotidyltransferase	*pnp*	1.5E-08
VC2571	DNA-directed RNA polymerase, alpha subunit	*rpoA*	2.5E-17
VCA0804	ATP-dependent RNA helicase DeaD	*deaD*	2.0E-17
Transport and binding proteins			
Locus	Function	Gene	*P* Value
VC0171	peptide ABC transporter, periplasmic peptide-binding protein		7.2E-09
VC1042	long-chain fatty acid transport protein	*fadL-1*	2.1E-14
VC1091	oligopeptide ABC transporter, periplasmic oligopeptide-binding protein	*oppA*	5.7E-10
VC1426	spermidine-putrescine ABC transporter, permease protein	*potC*	3.3E-09
VC1836	tolB protein	*tolB*	1.4E-12
VC2305	outer membrane protein OmpK	*ompK*	5.1E-09
VC2352	NupC family protein		1.6E-10
VCA0183	ferrisiderophore reductase	*hmpA*	7.7E-16
Protein fate			
Locus	Function	Gene	*P* Value
VC0086	tatA protein	*tatA-1*	2.7E-10
VC0322	preprotein translocase, SecE subunit	*secE*	5.9E-11
VC0349	hflK protein	*hflK*	1.3E-08
VC0640	preprotein translocase, SecG subunit	*secG*	7.1E-13
VC0744	protein-export membrane protein SecF	*secF-1*	1.0E-11
VC1923	trigger factor	*tig*	9.1E-09
VC2576	preprotein translocase, SecY subunit	*secY*	7.8E-23
VC2723	general secretion pathway protein N	*epsN*	2.5E-08
Regulation			
Locus	Function	Gene	*P* Value
VC0290	factor-for-inversion stimulation protein	*fis*	1.0E-14
VC1276	sensor histidine kinase		8.9E-08
VC2106	ferric uptake regulation protein	*fur*	6.5E-14
VCA0166	cold shock transcriptional regulator CspA	*cspA*	2.5E-13
VCA0184	cold shock DNA-binding domain protein		6.8E-11
VCA0933	cold shock domain family protein		2.6E-13
Biosyn of cofactors			

Locus	Function	Gene	*P* Value
VC0440	dihydrofolate reductase	*folA*	8.7E-11
VC2180	glutamyl-tRNA reductase	*hemA*	8.4E-08
VC2256	undecaprenyl diphosphate synthase	*uppS*	1.9E-10
VC2268	6,7-dimethyl-8-ribityllumazine synthase	*ribE*	1.4E-10
VCA1060	3,4-dihydroxy-2-butanone 4-phosphate synthase	*ribB*	1.2E-12
Fatty acid metabolism			
Locus	Function	Gene	*P* Value
VC0251	acyl protein synthase-acyl-CoA reductase RfbN		2.1E-08
VC0745	inositol monophosphate family protein		4.3E-16
VC2020	acyl carrier protein	*acp*	2.7E-09
VC2022	malonyl CoA-acyl carrier protein transacylase	*fabD*	2.0E-11
VC2023	3-oxoacyl-(acyl-carrier-protein) synthase III	*fabH-1*	1.3E-11
DNA metabolism			
Locus	Function	Gene	*P* Value
VC0367	primosomal replication protein N	*priB*	7.1E-16
VC0397	single-strand binding protein	*ssb*	2.3E-10
VC1919	DNA-binding protein HU-beta	*hupB*	2.6E-12
VC2626	DNA adenine methylase	*dam*	4.6E-09
Amino Acid Biosynthesis			
Locus	Function	Gene	*P* Value
VC1137	phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase	*hisA*	1.6E-08
VC2364	aspartokinase I-homoserine dehydrogenase, threonine-sensitive	*thrA*	6.8E-13
VC2746	glutamate--ammonia ligase	*glnA*	4.7E-09
Amino Acid Biosynthesis			
Locus	Function	Gene	*P* Value
VCA0341	biphenyl-2,3-diol 1,2-dioxygenase III-related protein		2.1E-09
Nucleic acid synthesis			
Locus	Function	Gene	*P* Value
VC2226	phosphoribosylformylglycinamidine cyclo-ligase	*purM*	4.1E-08
Hypothetical (annotated)			
Locus	Function	Gene	*P* Value
VC0249	rfbL protein	*rfbL*	2.8E-08
VC0253	IS1004 transposase-related protein		5.5E-13
VC2688	glpX protein	*glpX*	1.2E-11
VCA0038	Sco1-related protein		1.7E-10
VCA0549	phnA protein	*phnA*	6.8E-08
VC0458	conserved hypothetical protein		3.8E-08
VC0641	conserved hypothetical protein		9.6E-13
VC1490	conserved hypothetical protein		1.5E-08
VC1876	conserved hypothetical protein		4.2E-09

VC2026	conserved hypothetical protein		1.3E-17
VC2326	conserved hypothetical protein		5.6E-10
VC2443	conserved hypothetical protein		3.1E-09
VC2706	conserved hypothetical protein		4.2E-09
VCA0006	conserved hypothetical protein		2.2E-09
VCA0037	conserved hypothetical protein		1.4E-13
VCA0689	conserved hypothetical protein		4.5E-11
VCA0769	conserved hypothetical protein		2.9E-09
Hypothetical (no annotation)			
Locus	Function	Gene	*P* Value
VC0059	hypothetical protein		3.9E-16
VC0895	hypothetical protein		1.1E-10
VC1078	hypothetical protein		5.1E-08
VC1221	hypothetical protein		5.5E-11
VC1752	hypothetical protein		2.1E-09
VC2496	hypothetical protein		2.6E-13
VCA0306	hypothetical protein		7.4E-09
VCA0375	hypothetical protein		8.9E-12
VCA0384	hypothetical protein		3.2E-08
VCA0397	hypothetical protein		7.4E-13
VCA0398	hypothetical protein		1.0E-09
VCA0407	hypothetical protein		1.4E-09
VCA0438	hypothetical protein		8.1E-08
VCA0464	hypothetical protein		1.7E-16
VCA0480	hypothetical protein		2.2E-11
VCA0502	hypothetical protein		7.6E-15
VCA0514	hypothetical protein		3.1E-12
VCA0770	hypothetical protein		2.5E-09