

Table S4: Differentially expressed genes in the *ompU* and *rpoE* mutants compared to WT C6706 when grown in virulence inducing AKI conditions.

789 differentially-expressed genes in AKI-grown *ΔompU* cells, independent of *ΔrpoE*, compared to WT C6706

Locus Tag	Function	FC in <i>ΔompU</i>	p-value
VC0001	hypothetical protein	-2.30	7.11E-04
VC0002	mioC protein	2.17	2.19E-07
VC0018	16 kDa heat shock protein A	-2.02	1.17E-05
VC0032	ComM-related protein	-2.25	2.01E-04
VC0049	smg protein	-2.73	2.77E-12
VC0050	DNA topoisomerase I-related protein	-2.22	1.32E-07
VC0070	hypothetical protein	2.02	6.54E-07
VC0076	universal stress protein A	-2.52	1.86E-09
VC0078	ferritin	-2.69	6.51E-15
VC0079	conserved hypothetical protein	-6.23	5.29E-52
VC0080	conserved hypothetical protein	-2.16	1.63E-08
VC0089	cytochrome c551 peroxidase	-20.61	3.85E-71
VC0090	DNA-damage-inducible protein F	-4.44	1.57E-26
VC0098	methyl-accepting chemotaxis protein	-3.40	2.04E-26
VC0134	conserved hypothetical protein	2.04	2.40E-15
VC0139	DPS family protein	-4.21	7.81E-22
VC0142	hypothetical protein	-2.42	2.89E-09
VC0156	vitamin B12 receptor	6.26	1.15E-26
VC0164	multidrug resistance protein, putative	2.68	3.83E-15
VC0165	conserved hypothetical protein	3.06	1.01E-10
VC0166	transcriptional regulator, TetR family	2.78	9.52E-13
VC0169	hypothetical protein	-6.72	6.99E-25
VC0172	peptide ABC transporter, permease protein	-2.06	3.08E-07
VC0174	hypothetical protein	-2.03	4.01E-15
VC0185	transposase, putative	-3.19	5.71E-16
VC0191	conserved hypothetical protein	-2.00	1.04E-05
VC0194	gamma-glutamyltransp eptidase	4.29	5.66E-26
VC0228	hypothetical protein	2.38	7.43E-14
VC0242	phosphomannomutase	2.26	2.50E-10
VC0243	GDP-mannose 4,6-dehydratase	2.44	8.73E-11
VC0273	DNA-binding protein HU	2.06	2.34E-05
VC0281	lysine decarboxylase, inducible	-3.22	5.70E-08
VC0295	acetyl-CoA carboxylase, biotin carboxylase	3.38	1.97E-20
VC0296	acetyl-CoA carboxylase, biotin carboxyl carrierprotein	3.17	8.26E-25
VC0297	3-dehydroquinate dehydratase	2.20	1.01E-10
VC0298	acetyl-CoA synthase	-10.02	2.66E-43
VC0304	guanosine-5	-2.23	3.24E-16
VC0308	hypothetical protein	-3.46	5.04E-20
VC0330	regulator of sigma D	-2.30	1.95E-11
VC0354	peptidyl-prolyl cis-trans isomerase, FKBP-type	3.20	3.10E-23
VC0357	conserved hypothetical protein	-2.01	5.99E-08
VC0360	ribosomal protein S7	3.15	2.32E-27
VC0361	elongation factor G	2.01	9.91E-09
VC0365	bacterioferritin	-3.46	4.82E-22
VC0367	primosomal replication protein N	2.48	3.09E-14
VC0370	conserved hypothetical protein	2.91	9.52E-11
VC0377	conserved hypothetical protein	-2.33	9.32E-12
VC0378	zinc uptake regulation protein, putative	-2.34	4.39E-12
VC0383	hypothetical protein	-4.12	4.41E-09
VC0395	UTP--glucose-1-phosp hate uridylyltransferase	2.32	4.59E-12
VC0397	single-strand binding protein	2.22	1.13E-09
VC0403	MSHA biogenesis protein MshM	-3.10	4.37E-14
VC0404	MSHA biogenesis protein MshN	-2.32	3.13E-13
VC0405	MSHA biogenesis protein MshE	-2.01	4.65E-10
VC0407	MSHA biogenesis protein MshF	-2.12	1.82E-08
VC0412	hypothetical protein	-2.23	8.91E-14
VC0413	hypothetical protein	-2.76	4.25E-21
VC0414	hypothetical protein	-2.25	2.47E-11
VC0445	survival protein SurA	2.34	2.91E-09
VC0452	A/G-specific adenine glycosylase	2.34	3.11E-09
VC0462	twitching motility protein PilT	-2.39	3.20E-09
VC0463	twitching motility protein PilT	-2.60	1.10E-19
VC0465	tyrosyl-tRNA synthetase	-2.18	5.66E-07
VC0472	S-adenosylmethionine synthase	2.25	1.01E-12
VC0478	fructose-bisphosphat e aldolase, class II	2.46	4.06E-26
VC0483	conserved hypothetical protein	2.73	1.21E-18
VC0485	pyruvate kinase I	2.11	2.97E-05
VC0496	hypothetical protein	-2.25	8.04E-05
VC0501	pseudogene within VSP-II; potential transposase	-3.27	1.16E-15
VC0533	lipoprotein NlpD	-2.18	8.74E-09
VC0534	RNA polymerase sigma-38 factor	-4.11	1.50E-23
VC0549	hypothetical protein	-2.21	1.70E-11
VC0550	oxaloacetate decarboxylase, alpha subunit	-2.68	7.49E-09
VC0551	oxaloacetate decarboxylase, beta subunit	-2.14	2.26E-07
VC0552	quinone oxidoreductase	-2.14	1.95E-13
VC0596	dnaK suppressor protein	3.15	1.51E-11
VC0613	beta-N-acetylhexosam inidase	-2.19	1.57E-06
VC0614	conserved hypothetical protein	-2.68	3.49E-06
VC0615	endoglucanase-relate d protein	-2.38	1.26E-08
VC0618	peptide ABC transporter, permease protein	-2.62	3.33E-05
VC0619	peptide ABC transporter, permease protein	-2.03	1.39E-03
VC0620	peptide ABC transporter, periplasmicpeptide-binding protein	-2.60	2.26E-13
VC0631	tyrosyl-tRNA synthetase	2.57	2.72E-12
VC0641	conserved hypothetical protein	2.12	3.10E-12
VC0647	polyribonucleotide nucleotidyltransferase	2.28	1.39E-11
VC0649	transcriptional regulator, MarR family	-2.23	1.37E-07
VC0658	c-di-GMP phosphodiesterase A-related protein	-4.99	3.61E-33
VC0661	conserved hypothetical protein	-2.74	1.31E-10
VC0692	beta-hexosaminidase	2.31	3.47E-10
VC0695	phospho-2-dehydro-3- deoxyheptonate aldolase,tyr-sensitive	3.72	3.41E-20
VC0697	hypothetical protein	-3.96	2.47E-29

VC0703	c-di-GMP phosphodiesterase A-related protein	2.05	4.74E-07
VC0728	conserved hypothetical protein	-4.83	5.72E-28
VC0731	antioxidant, AhpC/Tsa family	2.10	3.02E-07
VC0736	isocitrate lyase	-6.45	1.48E-44
VC0737	acetoin utilization protein AcuB, putative	-5.32	7.50E-22
VC0749	NifU-related protein	2.16	6.23E-08
VC0754	conserved hypothetical protein	2.11	1.18E-05
VC0771	vibriobactin-specific isochorismatase	3.91	1.14E-13
VC0790	transcriptional regulator CitB	-2.33	5.27E-05
VC0804	ferredoxin	-2.28	2.83E-04
VC0812	helicase-related protein	2.20	1.69E-09
VC0817	transposase, putative	-2.04	5.05E-07
VC0820	ToxR-activated gene A protein	2.05	1.08E-05
VC0821	hypothetical protein	2.09	2.61E-08
VC0840	accessory colonization factor AcfB	2.28	3.37E-07
VC0841	accessory colonization factor AcfC	2.02	4.50E-04
VC0847	integrase, phage family	2.17	2.61E-09
VC0854	heat shock protein GrpE	2.39	7.57E-18
VC0856	dnaJ protein	2.04	1.56E-10
VC0871	hypothetical protein	2.27	1.12E-06
VC0872	conserved hypothetical protein	2.34	1.62E-06
VC0875	prolyl-tRNA synthetase	2.42	2.66E-12
VC0882	conserved hypothetical protein	2.12	1.38E-04
VC0884	acetyltransferase-related protein	-2.14	1.45E-07
VC0892	chemotaxis protein PomA	-3.14	1.84E-17
VC0894	thiamin biosynthesis protein ThiI	2.25	3.01E-11
VC0901	hypothetical protein	2.32	3.02E-16
VC0910	PTS system, trehalose-specific IIBC component	-2.48	4.65E-10
VC0928	hypothetical protein	3.08	2.46E-15
VC0935	hypothetical protein	-2.90	4.24E-09
VC0936	polysaccharide export-related protein	-5.54	1.29E-19
VC0937	exopolysaccharide biosynthesis protein, putative	-2.56	2.07E-11
VC0938	hypothetical protein	-4.19	4.46E-13
VC0957	conserved hypothetical protein	-4.36	1.31E-27
VC0962	conserved hypothetical protein	2.47	7.02E-11
VC0985	heat shock protein HtpG	3.94	5.75E-18
VC0995	PTS system, N-acetylglucosamine-specific IIBC component	-2.10	7.43E-11
VC1008	sodium-type flagellar protein MotY	-3.67	3.75E-25
VC1009	conserved hypothetical protein	-4.19	1.81E-29
VC1029	GGDEF family protein	-3.63	6.64E-16
VC1031	inosine monophosphate dehydrogenase-related protein	-10.24	4.21E-77
VC1039	asmA protein	3.09	1.46E-21
VC1040	cob(I)alamin adenosyltransferase	2.91	1.71E-18
VC1043	long-chain fatty acid transport protein	-2.35	2.35E-11
VC1050	response regulator	-5.11	8.29E-36
VC1057	proteinase inhibitor, putative	-2.30	4.60E-05
VC1064	lipoprotein-related protein	-2.79	7.05E-16
VC1066	hypothetical protein	-3.97	3.04E-23
VC1080	hypothetical protein	-3.79	3.64E-25
VC1081	response regulator	-4.90	1.00E-33
VC1082	response regulator	-11.21	7.83E-57
VC1083	hypothetical protein	-10.25	4.88E-67
VC1084	sensory box sensor histidine kinase	-12.57	1.86E-46
VC1085	sensor histidine kinase	-7.96	9.90E-45
VC1086	response regulator	-5.24	2.72E-46
VC1087	response regulator	-4.39	1.48E-31
VC1088	sensor histidine kinase	-5.87	4.64E-35
VC1089	periplasmic binding protein-related protein	-4.69	7.66E-33
VC1093	oligopeptide ABC transporter, permease protein	3.04	3.37E-14
VC1095	oligopeptide ABC transporter, ATP-binding protein	2.05	1.35E-08
VC1099	conserved hypothetical protein	-2.11	4.01E-07
VC1100	hypothetical protein	-2.12	1.56E-06
VC1118	transcriptional regulator, putative	-2.10	1.95E-07
VC1119	oxidoreductase, short-chain dehydrogenase/reductase family	-2.92	4.10E-10
VC1120	conserved hypothetical protein	-2.19	3.39E-09
VC1121	conserved hypothetical protein	-2.13	1.59E-07
VC1124	conserved hypothetical protein	-4.65	1.15E-25
VC1125	hypothetical protein	-4.90	2.76E-27
VC1126	adenylosuccinate lyase	2.46	7.18E-11
VC1131	conserved hypothetical protein	-2.27	1.46E-08
VC1147	iron-containing alcohol dehydrogenase	-3.03	7.10E-19
VC1153	conserved hypothetical protein	-2.45	1.59E-15
VC1155	response regulator	-3.76	2.97E-29
VC1156	sensor histidine kinase	-2.47	3.84E-13
VC1159	phosphoserine aminotransferase	2.47	1.71E-14
VC1185	GGDEF family protein	-2.41	2.46E-08
VC1189	hypothetical protein	-4.50	1.89E-20
VC1193	hypothetical protein	4.87	8.78E-27
VC1195	lipoprotein, putative	4.13	4.85E-26
VC1208	conserved hypothetical protein	2.72	1.70E-19
VC1209	elongation factor P family protein	3.07	1.44E-23
VC1211	conserved hypothetical protein	-2.11	4.68E-07
VC1216	GGDEF family protein	-2.38	1.56E-11
VC1223	hypothetical protein	-3.89	1.28E-18
VC1224	hypothetical protein	-4.29	3.65E-17
VC1235	sodium/dicarboxylate symporter	2.28	4.21E-08
VC1236	PilB-related protein	-2.80	4.77E-13
VC1240	alpha-ribazole-5'-phosphate phosphatase CobC, putative	2.05	6.59E-07
VC1246	hypothetical protein	2.61	3.39E-15
VC1247	hypothetical protein	-2.58	2.74E-11
VC1248	methyl-accepting chemotaxis protein	-10.03	7.68E-58
VC1249	conserved hypothetical protein	-5.61	6.63E-43
VC1259	conserved hypothetical protein	2.67	1.29E-08
VC1262	hypothetical protein	-2.12	4.04E-06
VC1269	conserved hypothetical protein	-2.83	5.12E-19
VC1271	hypothetical protein	-2.03	5.12E-04
VC1272	hypothetical protein	2.51	4.97E-07

VC1289	methyl-accepting chemotaxis protein	2.42	1.23E-14
VC1295	conserved hypothetical protein	-2.87	5.54E-14
VC1298	methyl-accepting chemotaxis protein	-2.11	1.36E-05
VC1313	methyl-accepting chemotaxis protein	-4.18	3.37E-21
VC1315	sensor histidine kinase	-3.50	4.44E-10
VC1316	chemotaxis protein CheY, putative	-4.26	1.70E-33
VC1317	conserved hypothetical protein	2.87	6.48E-19
VC1318	outer membrane protein OmpV	4.57	2.54E-18
VC1322	conserved hypothetical protein	-5.75	1.38E-29
VC1323	hypothetical protein	-3.76	1.63E-21
VC1340	prpE protein	-2.14	1.53E-08
VC1348	response regulator	-5.12	4.72E-27
VC1349	sensory box sensor histidine kinase/responseregulator	-4.38	1.43E-26
VC1353	GGDEF family protein	-2.07	2.85E-06
VC1359	amino acid ABC transporter, ATP-binding protein	-2.96	1.69E-14
VC1360	amino acid ABC transporter, permease protein	-4.06	1.63E-18
VC1361	amino acid ABC transporter, permease protein	-3.99	2.10E-20
VC1362	amino acid ABC transporter, periplasmic aminoacid-binding protein	-9.03	1.86E-54
VC1368	hypothetical protein	-3.42	2.74E-18
VC1369	conserved hypothetical protein	-6.14	1.98E-32
VC1371	hypothetical protein	-2.83	3.88E-14
VC1374	DnaK-related protein	3.14	8.27E-15
VC1375	hypothetical protein	2.91	5.78E-13
VC1376	GGDEF family protein	-2.76	1.52E-17
VC1391	multidrug transporter, putative	2.31	1.50E-08
VC1393	sugE protein	-2.27	2.95E-08
VC1394	methyl-accepting chemotaxis protein	-6.06	1.57E-47
VC1395	response regulator cheY1	-7.29	2.58E-57
VC1396	hypothetical protein	-6.61	2.72E-35
VC1397	chemotaxis protein CheA	-9.00	5.14E-57
VC1398	chemotaxis protein CheY	-9.32	8.38E-45
VC1399	chemotaxis protein methyltransferase CheR	-8.30	3.89E-52
VC1400	hypothetical protein	-7.28	1.95E-37
VC1403	methyl-accepting chemotaxis protein	-4.70	1.11E-24
VC1405	methyl-accepting chemotaxis protein	-3.05	1.39E-16
VC1406	methyl-accepting chemotaxis protein	-3.42	8.09E-18
VC1410	multidrug resistance protein VceA	2.43	5.08E-10
VC1414	thermostable carboxypeptidase 1	2.43	2.50E-07
VC1416	vgrG protein	4.88	7.98E-47
VC1417	hypothetical protein	3.15	1.25E-16
VC1418	hypothetical protein	2.85	3.19E-16
VC1419	hypothetical protein	2.47	1.75E-11
VC1425	spermidine/putrescin e ABC transporter,periplasmic spermidine/putrescine-binding protein	2.26	4.78E-11
VC1433	conserved hypothetical protein	-2.61	1.36E-13
VC1486	ABC transporter, ATP-binding protein	2.01	8.91E-15
VC1487	conserved hypothetical protein	2.61	2.94E-06
VC1498	conserved hypothetical protein	2.35	1.93E-09
VC1517	hypothetical protein	-2.08	3.43E-08
VC1528	hypothetical protein	-2.99	6.05E-14
VC1535	methyl-accepting chemotaxis protein	-2.53	1.77E-05
VC1538	hypothetical protein	-2.87	2.20E-15
VC1539	conserved hypothetical protein	-2.61	7.02E-12
VC1549	glycerol-3-phosphate ABC transporter,periplasmic glycerol-3-phosphate-binding protein	-2.02	5.97E-04
VC1551	glycerol-3-phosphate ABC transporter, permeaseprotein	-2.92	6.83E-05
VC1577	hypothetical protein	2.84	2.53E-15
VC1578	hypothetical protein	2.74	2.11E-10
VC1579	enterobactin synthetase component F-relatedprotein	2.63	3.77E-19
VC1581	NADH dehydrogenase, putative	-2.07	3.22E-03
VC1601	hypothetical protein	-3.21	1.63E-15
VC1602	chemotaxis protein CheV	-3.10	6.91E-10
VC1603	hypothetical protein	-3.30	2.08E-19
VC1612	fimbrial biogenesis and twitching motilityprotein, putative	-2.72	2.10E-13
VC1613	hypothetical protein	-4.25	1.52E-22
VC1614	conserved hypothetical protein	-2.34	2.20E-09
VC1623	carboxynorspermidine decarboxylase	3.25	7.45E-24
VC1624	conserved hypothetical protein	2.02	5.90E-07
VC1625	Pseudogene; involved in spermidine biosynthesis	3.58	7.16E-25
VC1641	conserved hypothetical protein	-3.13	8.84E-24
VC1643	methyl-accepting chemotaxis protein	-5.49	2.04E-21
VC1659	conserved hypothetical protein	-2.57	6.67E-12
VC1660	ABC transporter ATP-binding protein	-3.34	1.87E-18
VC1660a	ABC transporter permease	-2.90	3.10E-13
VC1662	conserved hypothetical protein	-3.34	1.07E-16
VC1663	heat shock protein HslJ	3.36	2.33E-24
VC1672	DNA-3-methyladenine glycosidase I	-2.90	6.65E-11
VC1673	transporter, AcrB/D/F family	-2.36	9.63E-09
VC1674	periplasmic linker protein, putative	-3.18	6.76E-17
VC1675	multidrug resistance protein, putative	-2.82	8.93E-17
VC1699	hypothetical protein	-2.29	2.05E-16
VC1701	conserved hypothetical protein	2.08	9.24E-04
VC1704	5-methyltetrahydropt eroyltrypt glutamate--homocystein e methyltransferase	2.14	1.17E-08
VC1710	conserved hypothetical protein	-2.12	3.53E-11
VC1723	conserved hypothetical protein	-2.43	1.26E-08
VC1736	arginyl-tRNA-protein transferase-relatedprotein	-3.30	3.87E-20
VC1738	hypothetical protein	2.46	1.70E-07
VC1748	hypothetical protein	2.03	8.37E-05
VC1750	hypothetical protein	2.10	8.91E-09
VC1758	integrase, phage family	2.01	1.45E-07
VC1778	conserved hypothetical protein	-2.76	3.18E-16
VC1812	conserved hypothetical protein	-2.14	9.34E-04
VC1820	PTS system, fructose-specific IIA component	54.45	3.79E-22
VC1821	PTS system, fructose-specific IIBC component	2.53	5.12E-10
VC1822	PTS system, fructose-specific IIBC component	4.36	3.68E-25
VC1823	PTS system, fructose-specific IIB component	4.85	7.59E-27
VC1825	transcriptional regulator	3.49	9.30E-14
VC1826	PTS system, fructose-specific IABC component	2.99	2.36E-10
VC1831	sensor histidine kinase	-3.42	1.11E-22

VC1835	peptidoglycan-associated lipoprotein	3.94	3.46E-30
VC1841	conserved hypothetical protein	-2.75	4.54E-16
VC1842	conserved hypothetical protein	-2.13	2.77E-04
VC1843	cytochrome d ubiquinol oxidase, subunit II	-2.85	6.25E-16
VC1844	cytochrome d ubiquinol oxidase, subunit I	-3.07	5.60E-17
VC1849	peptidyl-prolyl cis-trans isomerase B	2.68	2.22E-16
VC1851	conserved hypothetical protein	-4.78	5.95E-33
VC1853	conserved hypothetical protein	2.77	1.66E-19
VC1867	conserved hypothetical protein	-2.28	2.00E-08
VC1868	methyl-accepting chemotaxis protein	-6.82	4.06E-44
VC1872	conserved hypothetical protein	-10.36	1.02E-61
VC1873	conserved hypothetical protein	-13.64	6.01E-51
VC1874	conserved hypothetical protein	-12.48	3.91E-85
VC1876	conserved hypothetical protein	2.61	1.10E-11
VC1883	ABC transporter, ATP-binding protein	2.03	3.46E-08
VC1889	ribosomal-protein-se rine acetyltransferase, putative	-2.11	5.03E-06
VC1898	methyl-accepting chemotaxis protein	-2.21	3.06E-13
VC1905	alanine dehydrogenase	3.67	1.11E-28
VC1920	ATP-dependent protease LA	2.43	6.17E-14
VC1929	C4-dicarboxylate-binding periplasmic protein	3.02	5.15E-16
VC1932	hypothetical protein	-2.56	3.48E-07
VC1933	hypothetical protein	-3.78	1.32E-22
VC1934	GGDEF family protein	-3.82	4.49E-22
VC1935	CDP-diacylglycerol- glycerol-3-phosphate3-phosphatidyltransferase-related protein	2.40	5.83E-10
VC1936	phosphatidate cytidyltransferase, putative	3.18	6.28E-13
VC1937	conserved hypothetical protein	2.65	3.18E-07
VC1944	PvcB protein	-2.44	2.49E-06
VC1945	FAD monooxygenase, PheA/TfdB family	-2.11	2.38E-06
VC1947	transcriptional regulator, LysR family	2.08	3.05E-06
VC1950	biotin sulfoxide reductase	-4.11	1.52E-22
VC1953	NupC family protein	-2.35	1.96E-05
VC1962	lipoprotein	5.58	7.92E-57
VC1967	methyl-accepting chemotaxis protein	-3.39	5.40E-16
VC1987	outer membrane lipoprotein Slp, putative	-2.09	1.09E-08
VC1991	hypothetical protein	-4.50	1.12E-27
VC1994	protease IV	2.16	3.08E-11
VC1997	hypothetical protein	-2.47	2.84E-14
VC2005	hypothetical protein	-3.55	2.01E-26
VC2008	pyruvate kinase II	-3.20	5.97E-19
VC2009	conserved hypothetical protein	-2.69	1.82E-15
VC2012	sodium-dependent transporter	-2.09	1.10E-08
VC2022	malonyl Coa-acyl carrier protein transacylase	3.20	2.12E-15
VC2026	conserved hypothetical protein	2.45	2.30E-11
VC2038	hypothetical protein	-2.42	2.04E-07
VC2044	conserved hypothetical protein	3.41	7.17E-27
VC2045	superoxide dismutase, Fe	2.18	1.94E-09
VC2046	hypothetical protein	-3.44	7.98E-19
VC2047	oxidoreductase, short-chain dehydrogenase/reductase family	-3.41	8.51E-27
VC2053	cytochrome c-type biogenesis protein CcmE	2.20	1.14E-08
VC2058	hypothetical protein	-3.03	1.09E-23
VC2059	purine-binding chemotaxis protein CheW	-2.83	9.36E-18
VC2060	conserved hypothetical protein	-2.85	1.98E-09
VC2061	ParA family protein	-2.44	7.06E-14
VC2062	protein-glutamate methyltransferase CheB	-2.48	4.01E-13
VC2063	chemotaxis protein CheA	-2.74	2.86E-15
VC2064	chemotaxis protein CheZ	-2.40	2.57E-07
VC2065	chemotaxis protein CheY	-2.44	3.59E-07
VC2067	MinD-related protein	-2.05	6.33E-10
VC2070	phosphohistidine phosphatase	-2.24	1.14E-09
VC2078	ferrous iron transport protein A	3.74	4.66E-16
VC2103	transcriptional regulator, LysR family	-2.70	5.34E-12
VC2105	hypothetical protein	-2.10	3.13E-06
VC2107	aspartate-semialdehyde dehydrogenase, putative	2.24	3.48E-19
VC2109	pseudogene; 3' encodes Vcr076	2.12	7.20E-09
VC2124	flagellar protein FljO	-2.75	3.06E-15
VC2128	flagellar hook-length control protein FljK, putative	-4.36	1.08E-17
VC2139	flagellar rod protein FljI, putative	-2.86	5.76E-25
VC2141	flagellin FlaG	-4.12	1.12E-26
VC2142	flagellin FlaB	-4.56	6.73E-27
VC2143	flagellin FlaD	-3.37	2.13E-17
VC2144	flagellin FlaE	-4.36	8.81E-34
VC2161	methyl-accepting chemotaxis protein	-4.10	2.14E-26
VC2171	uracil permease	2.29	1.98E-09
VC2187	flagellin FlaC	-3.43	6.86E-17
VC2188	flagellin core protein A	-2.81	4.79E-14
VC2201	chemotaxis protein methyltransferase CheR	-3.41	3.77E-21
VC2202	chemotaxis protein CheV	-3.22	3.30E-19
VC2204	negative regulator of flagellin synthesis FigM, putative	-3.27	6.37E-12
VC2205	hypothetical protein	-3.62	3.54E-22
VC2206	conserved hypothetical protein	-3.95	1.39E-30
VC2207	hypothetical protein	-3.24	5.69E-12
VC2210	vibriobactin utilization protein ViuB	2.05	4.89E-06
VC2221	hypothetical protein	-2.38	3.12E-08
VC2241	cytochrome c554	-3.89	1.46E-15
VC2264	conserved hypothetical protein	-4.33	2.04E-31
VC2285	GGDEF family protein	-2.21	1.12E-07
VC2293	NADH:ubiquinone oxidoreductase, Natranslocating, gamma subunit	2.11	9.58E-11
VC2296	bolA protein	-2.53	1.25E-24
VC2314	hypothetical protein	-4.50	5.31E-15
VC2316	N-acetylglutamate synthase	-3.46	1.01E-15
VC2329	2,3,4,5-tetrahydroxy ridine-2-carboxylateN-succinyl transferase	2.25	2.56E-08
VC2330	conserved hypothetical protein	-2.20	1.43E-05
VC2340	conserved hypothetical protein	-7.15	1.20E-28
VC2342	elongation factor G	3.07	3.75E-14
VC2344	hypothetical protein	-2.00	3.43E-09
VC2352	NupC family protein	2.02	1.55E-07
VC2356	sodium/alanine symporter	2.23	1.85E-18

VC2357	hypothetical protein	-2.10	8.02E-09
VC2358	hypothetical protein	-3.88	9.58E-26
VC2360	endonuclease IV	2.77	5.76E-14
VC2370	sensory box/GGDEF family protein	-2.84	1.01E-12
VC2378	conserved hypothetical protein	-2.94	2.69E-32
VC2383	transcriptional regulator, LysR family	-2.15	5.43E-08
VC2384	conserved hypothetical protein	-4.04	2.11E-18
VC2386	conserved hypothetical protein	2.79	7.79E-17
VC2439	methyl-accepting chemotaxis protein	-2.03	3.63E-09
VC2454	GGDEF family protein	-3.68	4.31E-24
VC2455	hypothetical protein	-5.04	3.72E-25
VC2456	hypothetical protein	-4.55	3.61E-33
VC2462	signal peptidase I	2.22	1.08E-18
VC2472	conserved hypothetical protein	2.09	6.46E-07
VC2487	conserved hypothetical protein	-2.06	1.09E-06
VC2494	hypothetical protein	-4.95	1.30E-27
VC2507	conserved hypothetical protein	-10.11	1.88E-76
VC2508	ornithine carbamoyltransferase	-5.98	1.08E-28
VC2512	conserved hypothetical protein	4.11	1.56E-29
VC2513	1-acyl-sn-glycerol-3-phosphate acyltransferase	2.18	7.12E-07
VC2517	conserved hypothetical protein	2.20	1.97E-11
VC2518	conserved hypothetical protein	2.03	3.38E-11
VC2529	RNA polymerase sigma-54 factor	-2.52	2.87E-14
VC2530	sigma-54 modulation protein, putative	-2.91	9.61E-10
VC2533	phosphocarrier protein NPr	-2.00	6.50E-04
VC2545	inorganic pyrophosphatase	2.07	2.78E-05
VC2568	peptidyl-prolyl cis-trans isomerase, FKBP-type	3.51	1.68E-23
VC2571	DNA-directed RNA polymerase, alpha subunit	2.07	3.17E-07
VC2598	RNA methyltransferase, TrmH family	-2.64	7.60E-12
VC2599	ribonuclease R	-2.64	3.32E-13
VC2601	sodium-type flagellar protein MotX	-4.40	2.18E-25
VC2617	arginine/ornithine succinyltransferase, putative	2.28	2.68E-10
VC2622	hypothetical protein	-5.42	1.00E-29
VC2646	phosphoenolpyruvate carboxylase	2.13	1.20E-07
VC2647	conserved hypothetical protein	-2.13	5.09E-08
VC2656	fumarate reductase, flavoprotein subunit	-2.73	2.37E-12
VC2657	fumarate reductase, iron-sulfur protein	-5.09	6.43E-31
VC2658	fumarate reductase, 15 kDa hydrophobic protein	-5.05	3.13E-36
VC2659	fumarate reductase, 13 kDa hydrophobic protein	-3.92	6.47E-29
VC2660	elongation factor P	2.54	6.84E-11
VC2682	met repressor	2.06	6.34E-08
VC2699	C4-dicarboxylate transporter, anaerobic	-2.07	2.42E-08
VC2702	transcriptional regulator, LuxR family	-2.77	1.10E-19
VC2704	hypothetical protein	-12.57	2.56E-46
VC2705	sodium/solute symporter, putative	-13.90	3.15E-71
VC2706	conserved hypothetical protein	4.01	5.94E-19
VC2716	conserved hypothetical protein	3.04	1.46E-34
VC2717	hypothetical protein	-2.61	2.49E-15
VC2726	general secretion pathway protein K	-2.12	2.94E-08
VC2727	general secretion pathway protein J	-2.24	2.12E-08
VC2738	phosphoenolpyruvate carboxykinase	-2.19	2.33E-07
VC2749	nitrogen regulation protein NR(I)	-2.68	1.70E-19
VC2750	GGDEF family protein	-3.02	1.28E-16
VC2761	multidrug resistance protein	2.38	5.49E-12
VC2765	ATP synthase F1, gamma subunit	2.13	7.53E-12
VC2766	ATP synthase F1, alpha subunit	2.09	4.76E-07
VC2767	ATP synthase F1, delta subunit	2.05	8.55E-09
VC2768	ATP synthase F0, B subunit	2.01	3.88E-09
VC2775	glucose inhibited division protein A	2.00	3.11E-10
VCA0005	hypothetical protein	2.70	5.26E-13
VCA0006	conserved hypothetical protein	2.70	6.79E-19
VCA0009	hypothetical protein	-12.82	1.64E-24
VCA0018	vgrG protein	3.18	1.83E-15
VCA0019	hypothetical protein	3.45	1.22E-13
VCA0020	hypothetical protein	3.03	2.93E-34
VCA0026	conserved hypothetical protein	3.53	7.83E-23
VCA0030	hypothetical protein	-2.15	7.05E-09
VCA0031	methyl-accepting chemotaxis protein	-3.93	4.17E-23
VCA0032	hypothetical protein	-3.60	1.23E-23
VCA0034	conserved hypothetical protein	-3.90	1.12E-27
VCA0037	conserved hypothetical protein	2.08	4.08E-09
VCA0042	hypothetical protein	-2.02	3.61E-08
VCA0047	conserved hypothetical protein	-2.26	8.65E-13
VCA0049	GGDEF family protein	-2.47	9.05E-14
VCA0051	hypothetical protein	-2.30	3.86E-12
VCA0074	GGDEF family protein	-3.34	8.30E-18
VCA0075	hypothetical protein	-2.48	2.55E-06
VCA0078	hypothetical protein	-2.37	3.77E-12
VCA0088	proton/glutamate symporter	6.17	5.99E-84
VCA0107	conserved hypothetical protein	6.09	1.17E-32
VCA0108	conserved hypothetical protein	5.78	1.21E-45
VCA0109	hypothetical protein	2.62	3.51E-10
VCA0110	hypothetical protein	2.07	4.80E-07
VCA0111	hypothetical protein	2.05	6.80E-07
VCA0112	hypothetical protein	2.13	6.92E-09
VCA0130	ribose ABC transporter, periplasmicD-ribose-binding protein	-2.46	3.01E-10
VCA0139	hypothetical protein	6.20	1.58E-38
VCA0141	C4-dicarboxylate transport sensor protein, putative	-2.10	3.10E-11
VCA0144	immunogenic protein	-2.24	5.35E-09
VCA0146	conserved hypothetical protein	-2.35	2.56E-05
VCA0147	transcriptional regulator, putative	-2.88	9.33E-09
VCA0151	oxidoreductase, putative	-2.26	4.48E-06
VCA0152	conserved hypothetical protein	-10.63	8.09E-52
VCA0153	conserved hypothetical protein	-9.45	4.16E-31
VCA0154	conserved hypothetical protein	-8.01	1.05E-34
VCA0155	NADH dehydrogenase, putative	-6.46	8.26E-46
VCA0157	NADH dehydrogenase, putative	-5.28	1.10E-38

VCA0160	tryptophan-specific transport protein	-2.45	1.04E-05
VCA0184	cold shock DNA-binding domain protein	2.08	3.55E-08
VCA0186	hypothetical protein	-3.41	2.08E-28
VCA0188	hypothetical protein	-4.49	1.10E-17
VCA0189	response regulator	-2.78	1.37E-15
VCA0191	conserved hypothetical protein	-4.10	1.75E-27
VCA0192	D-lactate dehydrogenase	3.57	1.07E-25
VCA0195	hypothetical protein	-3.77	8.80E-22
VCA0205	C4-dicarboxylate transporter, anaerobic	-3.06	2.89E-21
VCA0210	response regulator, putative	-7.27	5.10E-57
VCA0211	sensory box sensor histidine kinase	-6.60	1.85E-52
VCA0217	GGDEF family protein	-2.11	6.53E-07
VCA0220	hemolysin secretion protein HylB	-2.45	1.14E-14
VCA0221	lactonizing lipase	-2.36	3.43E-06
VCA0229	iron(III) ABC transporter, permease protein	4.15	3.94E-07
VCA0230	iron(III) ABC transporter, ATP-binding protein	5.12	1.96E-27
VCA0241	hexulose-6-phosphate isomerase SgbU, putative	-3.24	1.11E-05
VCA0250	alpha-amylase	-2.37	1.16E-08
VCA0260	hypothetical protein	-2.50	8.19E-10
VCA0277	glycine cleavage system H protein	2.18	1.22E-09
VCA0293	hypothetical protein	-2.01	3.59E-07
VCA0319	conserved hypothetical protein	-2.31	2.38E-05
VCA0344	hypothetical protein	-2.34	1.94E-09
VCA0363	hypothetical protein	2.15	1.01E-04
VCA0369	hypothetical protein	6.69	3.62E-04
VCA0375	hypothetical protein	-2.01	2.45E-03
VCA0428	hypothetical protein	-2.30	2.13E-11
VCA0490	lipase, GDXG family	2.01	8.59E-11
VCA0518	PTS system, fructose-specific IIA/FPR component	6.47	1.19E-28
VCA0519	fructose repressor	2.69	2.73E-10
VCA0524	conserved hypothetical protein	-2.22	6.10E-08
VCA0534	pseudogene; contains authentic frameshift mutation	-2.53	1.84E-08
VCA0539	conserved hypothetical protein	2.02	1.76E-09
VCA0544	conserved hypothetical protein	-2.03	6.46E-11
VCA0549	phnA protein	2.43	1.68E-19
VCA0551	hypothetical protein	-3.69	9.28E-42
VCA0556	hypothetical protein	2.61	1.77E-06
VCA0557	GGDEF family protein	-2.73	4.08E-17
VCA0558	gamma-glutamyltransp eptidase, putative	-2.69	1.01E-13
VCA0570	Sui1 family protein	-2.46	7.75E-12
VCA0574	conserved hypothetical protein	-3.35	4.84E-23
VCA0583	hypothetical protein	-9.15	2.06E-41
VCA0584	glutathione S-transferase, putative	-2.01	1.03E-08
VCA0588	peptide ABC transporter, ATP-binding protein,putative	-2.47	2.37E-11
VCA0590	peptide ABC transporter, permease protein,putative	-2.61	6.00E-10
VCA0591	peptide ABC transporter, periplasmicpeptide-binding protein, putative	-2.27	1.89E-11
VCA0593	hypothetical protein	-4.90	2.30E-33
VCA0603	ABC transporter, periplasmic substrate-bindingprotein	-2.55	1.58E-09
VCA0607	regulator of nucleoside diphosphate kinase	2.03	9.21E-07
VCA0608	conserved hypothetical protein	2.31	1.51E-11
VCA0610	sigma cross-reacting protein 27A	-2.30	2.17E-11
VCA0619	hypothetical protein	-4.55	1.32E-39
VCA0620	thiosulfate sulfurtransferase SseA, putative	-2.15	2.89E-11
VCA0638	transporter, AcrB/D/F family	-2.70	1.95E-11
VCA0639	AcrA/AcrE family protein	-3.09	6.07E-21
VCA0643	conserved hypothetical protein	2.32	9.44E-06
VCA0646	conserved hypothetical protein/hemolysin,putative	-5.04	6.55E-27
VCA0652	hypothetical protein	3.72	3.45E-19
VCA0658	methyl-accepting chemotaxis protein	2.17	6.52E-11
VCA0659	protein F-related protein	-3.90	9.31E-39
VCA0666	L-serine dehydratase 1	-3.36	1.01E-20
VCA0679	periplasmic nitrate reductase, cytochrome c-typeprotein	-2.74	2.30E-07
VCA0680	periplasmic nitrate reductase, cytochrome c-typeprotein	-3.03	1.40E-08
VCA0681	conserved hypothetical protein	-6.55	2.37E-52
VCA0682	transcriptional regulator UhpA	-2.17	1.50E-07
VCA0683	sensor protein UhpB	-2.59	1.69E-12
VCA0691	acetoacetyl-CoA reductase	-2.13	2.34E-07
VCA0692	pseudogene with authentic frameshift mutation	2.40	1.83E-07
VCA0695	hypothetical protein	-6.03	3.97E-25
VCA0700	chitodextrinase	-2.19	6.84E-07
VCA0719	sensor histide kinase	-6.32	1.54E-31
VCA0720	guanylate cyclase-related protein	-5.21	1.63E-31
VCA0722	hypothetical protein	-2.17	1.49E-05
VCA0732	conserved hypothetical protein	2.61	2.77E-09
VCA0734	hypothetical protein	-2.52	6.06E-17
VCA0736	sensor histidine kinase LuxQ	-2.32	3.45E-09
VCA0738	hypothetical protein	-3.87	1.42E-23
VCA0748	anaerobic glycerol-3-phosphate dehydrogenase,subunit B	11.86	1.88E-71
VCA0752	thioredoxin 2	3.20	8.66E-18
VCA0766	cytochrome c554	-2.42	1.71E-06
VCA0787	hypothetical protein	-4.36	5.35E-04
VCA0788	DnaJ-related protein	-2.39	7.80E-12
VCA0789	conserved hypothetical protein	3.41	2.09E-19
VCA0798	CbbY family protein	-4.07	2.72E-33
VCA0803	serine protease, putative	-13.51	1.07E-59
VCA0806	hypothetical protein	-2.11	1.22E-07
VCA0811	chitinase, putative	3.04	5.12E-16
VCA0834	hypothetical protein	-3.35	1.79E-21
VCA0843	glyceraldehyde 3-phosphate dehydrogenase	2.74	5.94E-09
VCA0848	GGDEF family protein	-4.30	7.84E-56
VCA0862	long-chain fatty acid transport protein	3.33	2.79E-15
VCA0863	lipase, putative	4.64	1.68E-33
VCA0864	methyl-accepting chemotaxis protein	-2.62	1.13E-11
VCA0867	outer membrane protein OmpW	-2.23	4.34E-06
VCA0868	hypothetical protein	-4.91	3.92E-36
VCA0884	hypothetical protein	-5.96	7.08E-44
VCA0892	hypothetical protein	-2.95	2.98E-14

VCA0895	chemotactic transducer-related protein	-4.14	2.76E-27
VCA0897	devB protein	2.74	1.56E-13
VCA0898	6-phosphogluconate dehydrogenase,decarboxylating	3.18	2.40E-16
VCA0900	hypothetical protein	-3.09	1.02E-16
VCA0902	hypothetical protein	-2.08	7.54E-07
VCA0906	methyl-accepting chemotaxis protein	-8.00	8.96E-65
VCA0920	hypothetical protein	-4.50	4.76E-28
VCA0923	methyl-accepting chemotaxis protein	-6.54	3.56E-42
VCA0931	conserved hypothetical protein	-3.22	9.52E-18
VCA0939	sensory box/GGDEF family protein	-2.82	9.90E-16
VCA0940	transcriptional regulator, DeoR family	2.19	1.36E-08
VCA0960	GGDEF family protein	-2.32	1.36E-11
VCA0965	GGDEF family protein	-5.71	1.42E-32
VCA0966	hypothetical protein	-3.14	8.78E-12
VCA0978	amino acid ABC transporter, periplasmic aminoacid-binding protein, putative	-5.61	8.54E-33
VCA0979	methyl-accepting chemotaxis protein	-4.70	3.75E-32
VCA0981	hypothetical protein	-4.69	1.17E-32
VCA0983	L-lactate permease, putative	6.86	1.46E-58
VCA0985	oxidoreductase/iron- sulfur cluster-bindingprotein	4.52	3.16E-25
VCA0987	phosphoenolpyruvate synthase	2.37	4.00E-15
VCA0997	hypothetical protein	2.00	4.68E-06
VCA1001	transcriptional regulator, AraC/XylS family	-2.65	2.48E-09
VCA1003	hypothetical protein	-2.31	2.70E-05
VCA1008	outer membrane protein, putative	-2.34	3.84E-04
VCA1011	glutaredoxin-related protein	-2.19	3.64E-07
VCA1015	Na ⁺ /H ⁺ antiporter	-5.89	3.22E-53
VCA1016	hypothetical protein	-7.75	8.56E-78
VCA1017	methylated-DNA--prot ein-cysteineS-methyltransferas e	-6.04	7.41E-48
VCA1033	extracellular solute-binding protein, putative	-6.13	6.46E-29
VCA1034	methyl-accepting chemotaxis protein	-6.84	2.03E-47
VCA1035	hypothetical protein	3.88	1.18E-17
VCA1054	conserved hypothetical protein	-5.07	5.59E-30
VCA1055	transcriptional regulator, LysR family	-2.11	2.66E-12
VCA1056	methyl-accepting chemotaxis protein	-6.37	8.71E-32
VCA1066	hypothetical protein	-2.05	1.57E-03
VCA1073	bifunctional proline dehydrogenase/pyrroline-5-carboxylate dehydrogenase	4.47	5.15E-31
VCA1079	pyridoxamine 5'-phosphate oxidase	2.12	1.38E-16
VCA1087	anti-sigma F factor antagonist, putative	-4.60	6.45E-26
VCA1088	methyl-accepting chemotaxis protein	-5.16	7.21E-42
VCA1089	cheB3 methyltransferase	-8.12	4.37E-76
VCA1090	chemotaxis protein CheD, putative	-10.11	8.89E-64
VCA1094	purine-binding chemotaxis protein CheW	-8.18	3.39E-44
VCA1095	chemotaxis protein CheA	-8.00	1.43E-29
VCA1096	chemotaxis protein CheY	-8.00	1.26E-46
VCA1097	conserved hypothetical protein	-7.34	1.21E-52
VCA1104	phoP homolog	-2.28	1.13E-11
VCA1105	DNA-binding response regulator	-2.16	1.23E-07
VCA1106	hypothetical protein	-2.25	7.14E-09
16Sf	16Sf	3.47	8.14E-04
23Sh	23Sh	2.44	2.09E-11
tRNA-Asp-4	tRNA-Asp-4	2.51	3.41E-14
tRNA-Gly-3	tRNA-Gly-3	2.54	4.38E-11
tRNA-Met-5	tRNA-Met-5	3.11	1.86E-05
tRNA-Ser-1	tRNA-Ser-1	3.05	8.63E-06
tRNA-Thr-3	tRNA-Thr-3	2.16	1.88E-06
VC0007	ribosomal protein L34	2.42	3.02E-10
VC0030	acetolactate synthase II, small subunit	2.06	9.88E-05
VC0123	cyaY protein	2.16	3.24E-09
VC0218	ribosomal protein L28	3.46	5.63E-13
VC0219	ribosomal protein L33	3.78	1.08E-34
VC0321	elongation factor Tu	2.41	4.12E-09
VC0322	preprotein translocase, SecE subunit	2.18	2.83E-08
VC0323	transcription antitermination protein NusG	2.36	2.60E-13
VC0324	ribosomal protein L11, RplK	3.34	1.85E-19
VC0325	ribosomal protein L1	2.92	2.16E-16
VC0326	ribosomal protein L10	3.35	1.26E-17
VC0359	ribosomal protein S12	3.21	5.80E-17
VC0362	elongation factor TU	3.75	2.54E-17
VC0366	ribosomal protein S6	2.69	1.22E-17
VC0368	ribosomal protein S18	3.01	9.56E-20
VC0369	ribosomal protein L9	2.65	5.41E-16
VC0374	glucose-6-phosphate isomerase	2.76	2.41E-16
VC0435	ribosomal protein L21	2.64	4.50E-14
VC0436	ribosomal protein L27	2.30	2.31E-13
VC0441	bis(5'-nucleosyl)-te traphosphatase	-2.03	7.58E-09
VC0529	conserved hypothetical protein	2.48	2.48E-10
VC0530	conserved hypothetical protein	2.11	4.35E-08
VC0561	ribosomal protein S16	4.06	2.45E-16
VC0562	16S rRNA processing protein RimM	3.45	6.68E-23
VC0563	tRNA (guanine-N1)-methyltransferase	3.72	5.58E-30
VC0564	ribosomal protein L19	5.28	1.77E-46
VC0569	hypothetical protein	2.42	6.19E-14
VC0570	ribosomal protein L13	2.42	4.09E-14
VC0591	pantoate--beta-alanine liqase	2.09	4.04E-11
VC0592	3-methyl-2-oxobutano atehydroxymethyltransferase	2.16	1.15E-07
VC0634	transcription elongation factor GreA	2.09	1.00E-06
VC0639	phosphoglucomutase/p hosphomannomutase familyprotein MrsA	2.15	5.52E-11
VC0642	N utilization substance protein A	2.82	2.46E-18
VC0646	ribosomal protein S15	3.33	5.05E-19
VC0650	multidrug efflux pump VmrA	-2.42	5.01E-09
VC0664	lysyl-tRNA synthetase, heat inducible	2.62	3.62E-15
VC0679	ribosomal protein S20	2.61	6.10E-15
VC0718	conserved hypothetical protein	2.21	4.94E-08
VC0739	S-adenosylmethionine :tRNARibosyltransferase-isomer ase	2.32	4.25E-10
VC0877	hypothetical protein	2.57	1.72E-10
VC0893	chemotaxis protein PomB	-3.20	2.39E-24
VC0905	lipoprotein YaeC	3.53	8.59E-28

VC0907	ABC transporter, ATP-binding protein	2.40	2.26E-10
VC0918	UDP-N-acetyl-D-manno saminuronic acidehydrogenase	-2.80	1.14E-10
VC0941	serine hydroxymethyltransferase	2.64	2.38E-08
VC0991	asparagine synthetase B, glutamine-hydrolyzing	3.76	5.26E-26
VC1036	methionyl-tRNA synthetase	2.03	7.53E-09
VC1092	oligopeptide ABC transporter, permease protein	2.77	4.12E-13
VC1094	oligopeptide ABC transporter, ATP-bindingprotein	2.71	1.94E-17
VC1143	conserved hypothetical protein	-2.03	1.33E-08
VC1144	ATP-dependent Clp protease, ATP-binding subunitClpA	-3.05	4.43E-18
VC1146	glutaredoxin 1	4.37	8.24E-24
VC1190	phosphoribosylaminoimidazole-succinocarboxamidesyn thase, putative	-2.30	7.43E-09
VC1221	hypothetical protein	3.20	3.79E-25
VC1239	cobinamide kinase/cobinamide phosphateguanylyltransferase	2.12	3.71E-05
VC1312	alanine racemase, putative	-3.46	1.08E-15
VC1627	Na+/H+ antiporter protein	-2.66	3.14E-13
VC1836	tolB protein	2.67	5.33E-14
VC1914	integration host factor, beta subunit	-2.88	2.33E-17
VC1915	ribosomal protein S1	2.26	2.20E-07
VC1923	trigger factor	2.39	6.52E-10
VC2020	acyl carrier protein	2.83	2.28E-18
VC2021	3-oxoacyl-(acyl carrier-protein) reductase	2.30	1.29E-11
VC2025	ribosomal protein L32	2.56	2.57E-25
VC2066	RNA polymerase sigma factor for flagellar operonFlhA	-2.11	7.61E-10
VC2068	flagellar biosynthetic protein FlhF, putative	-2.08	1.16E-10
VC2069	flagellar biosynthetic protein FlhA	-2.05	7.65E-11
VC2120	flagellar biosynthetic protein FlhB	-2.42	9.06E-13
VC2121	flagellar biosynthetic protein FlhR	-2.24	3.06E-09
VC2122	flagellar biosynthetic protein FlhQ	-2.83	8.09E-16
VC2123	flagellar biosynthetic protein FlhP	-2.98	3.26E-13
VC2125	flagellar motor switch protein FlhN	-2.88	3.46E-13
VC2126	flagellar motor switch protein FlhM	-3.14	5.10E-20
VC2127	flagellar protein FlhL, putative	-3.22	7.43E-20
VC2129	flagellar protein FlhJ, putative	-2.32	7.72E-10
VC2130	flagellum-specific ATP synthase FlhI	-2.52	1.57E-14
VC2131	flagellar assembly protein FlhH, putative	-2.22	3.24E-14
VC2132	flagellar motor switch protein FlhG	-2.24	1.76E-10
VC2138	flagellar protein FlhS	-3.20	3.31E-21
VC2140	flagellar hook-associated protein FlhD	-4.12	2.50E-31
VC2190	flagellar hook-associated protein FlgL	-3.89	5.39E-14
VC2191	flagellar hook-associated protein FlgM	-2.80	1.98E-18
VC2192	flagellar protein FlgJ	-4.30	8.88E-30
VC2193	flagellar P-ring protein FlgI	-3.18	5.45E-21
VC2194	flagellar L-ring protein FlgH	-2.56	1.62E-13
VC2195	flagellar basal-body rod protein FlgG	-2.82	6.74E-17
VC2196	flagellar basal-body rod protein FlgF	-2.34	2.96E-12
VC2197	flagellar hook protein FlgE	-2.87	2.48E-19
VC2198	basal-body rod modification protein FlgD	-3.26	1.07E-21
VC2199	flagellar basal-body rod protein FlgC	-2.26	9.52E-11
VC2214	glutamyl-tRNA synthetase	2.42	2.72E-11
VC2223	pseudouridine synthase family 1 protein	2.18	5.49E-18
VC2231	oxidoreductase, acyl-CoA dehydrogenase family	-2.67	7.45E-11
VC2234	ribonuclease HI	-2.24	2.75E-08
VC2257	ribosome recycling factor	2.21	7.43E-11
VC2258	uridylate kinase	2.31	9.35E-14
VC2259	elongation factor Ts	4.64	2.08E-48
VC2260	ribosomal protein S2	3.46	1.78E-19
VC2400	UDP-N-acetylmuramate --alanine ligase	2.28	1.46E-13
VC2414	pyruvate dehydrogenase, E1 component	2.54	1.97E-14
VC2485	transcriptional regulator, LysR family	2.19	6.39E-16
VC2503	valyl-tRNA synthetase	2.42	2.23E-07
VC2570	ribosomal protein L17	2.56	3.49E-08
VC2572	ribosomal protein S4	2.25	4.04E-13
VC2578	ribosomal protein L30	2.42	3.53E-07
VC2579	ribosomal protein S5	2.30	1.14E-22
VC2580	ribosomal protein L18	2.50	6.49E-13
VC2581	ribosomal protein L6	2.50	1.73E-12
VC2582	ribosomal protein S8	2.84	1.62E-15
VC2583	ribosomal protein S14	2.56	5.09E-14
VC2584	ribosomal protein L5	2.35	6.74E-13
VC2585	ribosomal protein L24	2.55	4.40E-15
VC2586	ribosomal protein L14	2.46	5.91E-14
VC2587	ribosomal protein S17	2.58	5.97E-14
VC2588	ribosomal protein L29	2.48	9.54E-08
VC2589	ribosomal protein L16	2.23	4.40E-21
VC2590	ribosomal protein S3	2.04	2.81E-07
VC2591	ribosomal protein L22	2.73	2.30E-14
VC2592	ribosomal protein S19	2.61	1.11E-14
VC2593	ribosomal protein L2	3.30	3.93E-17
VC2594	ribosomal protein L23	4.00	1.50E-15
VC2595	ribosomal protein L4	3.39	1.20E-23
VC2596	ribosomal protein L3	3.03	1.44E-20
VC2597	ribosomal protein S10	3.01	2.44E-17
VC2618	acetylmethionine aminotransferase	2.75	5.24E-14
VC2663	molecular chaperone groEL_1	3.09	4.53E-16
VC2664	chaperonin, 60 Kd subunit, groES_1	3.41	1.78E-12
VC2670	triosephosphate isomerase	3.45	2.23E-24
VC2679	ribosomal protein L31	5.91	2.02E-49
VC2691	periplasmic protein cpxP, putative	2.80	1.89E-10
VC2715	transcription elongation factor GreB	2.28	1.54E-06
VC2748	nitrogen regulation protein	-2.39	6.91E-10
VC2762	UDP-N-acetylglucosamine pyrophosphorylase	3.19	3.81E-21
VC2774	glucose inhibited division protein B	2.43	1.98E-12
VCA0014	4-alpha-glucanotransferase	-2.80	3.79E-15
VCA0149	hypothetical protein	2.53	4.83E-09
VCA0246	SqaT protein	-2.53	1.97E-06
VCA0289	ribosomal protein L35	2.89	1.35E-16
VCA0290	ribosomal protein L20	2.91	2.33E-17

VCA0512	anaerobic ribonucleoside-triphosphate reductaseactivating protein	-2.75	4.13E-14
VCA0563	NAD(P) transhydrogenase, alpha subunit	3.43	1.11E-12
VCA0564	NAD(P) transhydrogenase, beta subunit	3.74	1.21E-27
VCA0698	hypothetical protein	-7.35	8.18E-50
VCA0747	anaerobic glycerol-3-phosphate dehydrogenase,subunit A	21.97	2.79E-119
VCA0749	anaerobic glycerol-3-phosphate dehydrogenase,subunit C	11.92	4.52E-61
VCA0757	arginine ABC transporter, permease protein	-2.57	1.04E-13
VCA0760	arginine ABC transporter, ATP-binding protein	-3.49	3.83E-19
VCA0819	chaperonin, 10 Kd subunit	3.41	2.70E-15
VCA0820	chaperonin, 60 Kd subunit	2.40	3.16E-11
VCA0870	D-alanyl-D-alanine endopeptidase	-2.04	1.54E-07
VCA0880	hypothetical protein	-5.95	4.13E-54
VCA0881	hypothetical protein	-4.84	2.55E-42
VCA0882	hypothetical protein	-4.92	1.20E-35
VCA0883	hypothetical protein	-2.02	8.81E-09
VCA0943	maltose ABC transporter, permease protein	-2.32	1.30E-11
VCA0945	maltose ABC transporter, periplasmicmaltose-binding protein	-3.16	4.64E-14
VCA0984	L-lactate dehydrogenase	11.24	1.86E-97
VCA1060	3,4-dihydroxy-2-buta none 4-phosphate synthase	3.70	1.25E-20

190 differentially-expressed genes in AKI-grown $\Delta rpoE$ cells, independent of $\Delta ompU$, compared to WT C6706			
Locus Tag	Function	FC in $\Delta rpoE$	p-value
16Sa	16Sa	-20.22	1.48E-28
16Sb	16Sb	-20.79	6.49E-32
16Sc	16Sc	-13.13	1.37E-22
16Sd	16Sd	-2.44	8.07E-04
16Se	16Se	-10.18	1.19E-16
16Sq	16Sq	-34.94	2.73E-45
16Sh	16Sh	-6.03	3.87E-08
23Sa	23Sa	-7.43	2.45E-15
23Sb	23Sb	3.68	1.05E-07
23Sc	23Sc	-4.56	5.27E-06
23Sd	23Sd	-7.85	8.81E-17
23Se	23Se	-85.13	2.53E-65
23Sf	23Sf	-4.10	2.62E-08
23Sg	23Sg	-24.58	4.35E-43
5Sa	5Sa	-79.61	6.43E-47
5Sb	5Sb	-156.53	3.58E-15
5Se	5Se	-207.22	2.11E-16
5Sf	5Sf	#####	6.29E-08
5Sh	5Sh	-159.57	2.83E-50
tRNA-Ala-3	tRNA-Ala-3	5.00	4.53E-05
tRNA-Ala-5	tRNA-Ala-5	10.78	5.22E-14
tRNA-Asn-3	tRNA-Asn-3	2.97	5.03E-05
tRNA-Gly-5	tRNA-Gly-5	-5.09	1.64E-07
tRNA-Ile-2	tRNA-Ile-2	6.55	3.83E-09
tRNA-Met-8	tRNA-Met-8	-3.60	1.31E-04
tRNA-Val-4	tRNA-Val-4	3.43	1.34E-05
VC0005	conserved hypothetical protein	-2.39	4.60E-04
VC0021	glycyl-tRNA synthetase, alpha chain; glyQ	-2.35	7.69E-07
VC0026	zinc-binding alcohol dehydrogenase	-2.21	9.13E-05
VC0027	threonine dehydratase	-2.37	4.51E-06
VC0034	thiol:disulfide interchange protein	-2.92	2.68E-11
VC0038	hypothetical protein	2.27	5.13E-04
VC0127	conserved hypothetical protein	-2.17	2.79E-04
VC0161	transcriptional activator IlvY	-2.07	2.01E-04
VC0171	peptide ABC transporter, periplasmicpeptide-binding protein	2.12	7.27E-04
VC0175	deoxycytidylate deaminase-related protein	-2.56	1.64E-08
VC0176	transcriptional regulator, putative	-2.68	2.54E-05
VC0178	patatin-related protein	-2.30	8.34E-06
VC0181	conserved hypothetical protein	-3.09	5.22E-10
VC0184	hypothetical protein	-3.24	5.26E-07
VC0202	iron(III) ABC transporter, periplasmiciron-compound-binding protein	2.79	2.55E-04
VC0204	conserved hypothetical protein	-2.44	2.38E-04
VC0217	DNA repair protein RadC	-2.12	1.13E-03
VC0274	hypothetical protein	-2.50	5.80E-06
VC0286	gluconate permease, putative	-2.95	4.46E-09
VC0353	conserved hypothetical protein	-2.39	3.69E-07
VC0411	MSHA pilin protein MshD	-2.23	2.15E-04
VC0443	dimethyladenosine transferase	-2.09	4.40E-06
VC0490	conserved hypothetical protein	-2.46	6.39E-05
VC0491	hypothetical protein	-3.01	7.96E-11
VC0492	hypothetical protein	-2.38	1.23E-04
VC0493	hypothetical protein	-2.76	2.83E-09
VC0566	protease DO	-2.85	4.15E-10
VC0583	quorum sensing regulator HapR	2.43	7.87E-04
VC0676	nptA protein	8.30	1.29E-11
VC0708	conserved hypothetical protein	-2.47	7.94E-08
VC0720	histidine protein kinase PhoR	2.51	4.55E-04
VC0743	protein-export membrane protein SecD	-2.02	3.16E-05
VC0761	conserved hypothetical protein	2.10	3.80E-04
VC0770	conserved hypothetical protein	-2.37	9.06E-04
VC0774	vibriobactin-specific 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase	6.91	1.15E-06
VC0775	vibriobactin synthesis protein, putative	6.03	5.29E-07
VC0776	ferric vibriobactin ABC transporter, periplasmicferric vibriobactin-binding protein	3.44	5.97E-06
VC0777	ferric vibriobactin ABC transporter, permeaseprotein	3.76	2.75E-05
VC0811	hypothetical protein	-2.18	4.89E-05
VC0823	hypothetical protein	-2.11	2.69E-05
VC0827	toxin co-regulated pilus biosynthesis protein H	2.99	2.34E-09
VC0829	toxin co-regulated pilus biosynthesis protein B	3.00	5.06E-06
VC0830	toxin co-regulated pilus biosynthesis protein Q	2.96	2.15E-05
VC0831	toxin co-regulated pilus biosynthesis outermembrane protein C	3.09	1.96E-06
VC0832	toxin co-regulated pilus biosynthesis protein R	2.73	3.55E-04
VC0862	hypothetical protein	-3.01	6.38E-06
VC0869	phosphoribosylformyl glycinamide synthase	2.28	1.55E-06
VC0916	phosphotyrosine protein phosphatase	6.69	4.30E-04

VC0947	D-alanyl-D-alanine carboxypeptidase	-2.16	2.84E-05
VC1051	hypothetical protein	2.18	1.59E-04
VC1059	oxidoreductase, short-chain dehydrogenase/reduc tase family	-2.03	7.75E-05
VC1184	NifS-related protein	2.10	6.98E-06
VC1186	sanA protein	-2.35	7.78E-07
VC1188	malate oxidoreductase	-7.83	1.08E-25
VC1205	imidazolonepropionas e	-2.38	6.54E-05
VC1206	histidine utilization repressor	-2.90	7.98E-07
VC1255	ribonucleoside-diphosphate reductase, betasubunit	2.44	1.61E-05
VC1267	hypothetical protein	2.49	3.26E-06
VC1307	pseudogene with authentic frameshift mutation	2.01	4.61E-04
VC1319	sensor histidine kinase	-2.33	2.41E-05
VC1329	opacity protein-related protein	-3.65	5.91E-07
VC1332	conserved hypothetical protein	2.07	5.40E-05
VC1333	hypothetical protein	3.60	2.35E-14
VC1334	conserved hypothetical protein	3.10	6.54E-13
VC1336	carboxyphosphoenol pyruvate phosphonmutase	2.55	1.77E-04
VC1337	methylcitrate synthase	2.97	2.18E-06
VC1338	aconitate hydratase 1	2.27	1.85E-05
VC1341	acetyltransferase, putative	2.04	5.13E-05
VC1344	4-hydroxyphenylpyruv ate dioxygenase	3.22	3.51E-12
VC1345	oxidoreductase, putative	3.07	9.30E-11
VC1346	conserved hypothetical protein	3.47	1.91E-11
VC1367	GGDEF family protein	-2.08	6.19E-06
VC1449	hypothetical protein	2.47	3.33E-04
VC1463	RstA2 protein	-2.33	1.79E-04
VC1470	XRE family transcriptional regulator	-3.28	2.89E-06
VC1524	ABC transporter, permease protein	-2.16	3.64E-04
VC1543	hypothetical protein	2.48	4.94E-05
VC1544	tonB2 protein	3.29	2.20E-06
VC1556	conserved hypothetical protein	2.12	3.26E-04
VC1566	conserved hypothetical protein	-2.21	7.62E-04
VC1567	conserved hypothetical protein	-2.46	1.18E-04
VC1568	ABC transporter, ATP-binding protein	-3.11	2.09E-06
VC1583	superoxide dismutase, Cu-Zn	2.15	1.13E-03
VC1587	conserved hypothetical protein	16.79	4.96E-06
VC1598	ABC transporter, periplasmic substrate-bindingprotein-relat ed protein	-2.12	2.87E-05
VC1610	hypothetical protein	2.02	1.13E-03
VC1678	phage shock protein A	11.08	1.01E-15
VC1741	transcriptional regulator, TetR family	2.48	1.79E-06
VC1764	hypothetical protein	-2.20	2.64E-06
VC1777	conserved hypothetical protein	-2.39	1.07E-07
VC1781	conserved hypothetical protein	-2.96	4.34E-06
VC1819	aldehyde dehydrogenase	-6.43	1.31E-18
VC1871	conserved hypothetical protein	-2.43	1.83E-04
VC1972	o-succinylbenzoate-C oA synthase	-2.14	3.89E-04
VC1973	naphthoate synthase	-2.37	6.26E-06
VC1974	conserved hypothetical protein	-2.77	4.67E-06
VC2019	3-oxoacyl-(acyl-carr ier-protein) synthase II	-2.10	1.81E-05
VC2032	hypothetical protein	-2.16	6.39E-04
VC2076	hypothetical protein	4.36	1.66E-12
VC2077	ferrous iron transport protein B	2.69	1.28E-07
VC2156	lipoprotein-34 NlpB	-2.02	3.93E-04
VC2209	nonribosomal peptide synthetase VibF	2.44	5.37E-04
VC2275	transcriptional regulator Crl	-2.73	9.66E-06
VC2371	conserved hypothetical protein	-2.42	2.93E-04
VC2510	aspartate carbamoyltransferase, catalyticsubunit	3.05	1.74E-10
VC2511	aspartate carbamoyltransferase, regulatorysubunit	3.16	1.60E-09
VC2636	transcriptional regulator, LysR family	-2.85	1.96E-08
VC2652	conserved hypothetical protein	-3.13	2.84E-04
VC2653	protein-transport protein SecB	-2.85	3.89E-06
VC2711	ATP-dependent DNA helicase RecG	-2.48	9.17E-09
VC2720	conserved hypothetical protein	-2.10	4.43E-05
VCA0004	hypothetical protein	2.19	2.76E-04
VCA0033	hypothetical protein	2.05	3.38E-04
VCA0059	major outer membrane lipoprotein	3.25	3.45E-06
VCA0070	phosphate ABC transporter, periplasmicphosphate-binding protein	21.64	2.45E-13
VCA0071	phosphate ABC transporter, permease protein	8.84	6.71E-08
VCA0072	phosphate ABC transporter, permease protein	12.70	1.17E-08
VCA0073	phosphate ABC transporter, ATP-binding protein	8.42	1.24E-05
VCA0106	hypothetical protein	-2.13	8.16E-04
VCA0119	hypothetical protein	-2.43	1.04E-03
VCA0140	spindolin-related protein	2.65	7.86E-04
VCA0165	GGDEF family protein	-2.49	9.55E-09
VCA0166	cold shock transcriptional regulator CspA	-2.26	1.01E-03
VCA0168	hypothetical protein	-2.87	1.47E-07
VCA0172	conserved hypothetical protein	-2.04	1.70E-04
VCA0175	MoxR-related protein	-4.72	2.14E-14
VCA0202	IS1004 transposase	-28.66	8.81E-06
VCA0215	hypothetical protein	2.91	2.68E-09
VCA0256	transcriptional regulator	2.07	8.91E-04
VCA0281	integrase, putative	-2.34	4.59E-06
VCA0283	hypothetical protein	-3.54	8.79E-12
VCA0284	hypothetical protein	-2.68	2.77E-05
VCA0306	hypothetical protein	-2.12	4.62E-04
VCA0336	hypothetical protein	-6.31	2.11E-12
VCA0337	microcin immunity protein MccF	-2.07	7.72E-05
VCA0340	hypothetical protein	-2.36	1.29E-05
VCA0354	hypothetical protein	-2.14	4.89E-05
VCA0355	conserved hypothetical protein	-2.10	5.90E-04
VCA0468	hypothetical protein	2.03	1.62E-04
VCA0486	hypothetical protein	3.49	8.38E-09
VCA0526	conserved hypothetical protein	-2.10	1.36E-04
VCA0532	DNA-binding response regulator	2.07	1.15E-03
VCA0533	tatA protein	2.51	4.92E-06
VCA0546	conserved hypothetical protein	2.31	2.72E-04
VCA0547	hypothetical protein	2.02	8.18E-05

VCA0635	transcriptional regulator, LysR family	2.19	7.00E-04
VCA0676	iron-sulfur cluster-binding protein NapF	4.73	3.15E-04
VCA0677	napD protein	4.11	2.40E-04
VCA0686	iron(III) ABC transporter, permease protein	-2.98	1.11E-05
VCA0704	phosphoglycerate transport systemtranscriptional regulatory protein PgtA	2.31	2.19E-06
VCA0707	regulatory protein UhpC, putative	17.03	1.60E-27
VCA0708	pyruvate kinase II	4.67	7.48E-08
VCA0831	hypothetical protein	5.11	3.91E-10
VCA0849	hypothetical protein	2.85	4.33E-09
VCA0874	hypothetical protein	-4.09	4.35E-06
VCA0887	pseudogene with authentic frameshift mutation	3.14	2.39E-06
VCA0888	transcriptional regulator, LuxR family	2.24	1.39E-04
VCA0933	cold shock domain family protein	-7.03	3.55E-14
VCA0951	conserved hypothetical protein	-21.68	1.60E-20
VCA0952	transcriptional regulator, LuxR family	4.02	1.03E-05
VCA0994	hypothetical protein	2.57	1.41E-08
VCA1021	conserved hypothetical protein	2.46	1.50E-07
VCA1037	amino acid ABC transporter, ATP-binding protein	-2.03	2.04E-04
VCr025	5S ribosomal RNA	-567.55	5.36E-57

158 differentially-expressed genes common to both $\Delta ompU$ and $\Delta rpoE$, compared to AKI-grown WT cells					
Name	Function	FC $\Delta rpoE$	p-value	FC $\Delta ompU$	p-value
5Sc	5Sc	-3453.75	2.04E-98	-2.04	4.94E-09
5Sd	5Sd	-4720.44	6.75E-88	-2.04	5.09E-09
5Sq	5Sq	-17365.49	5.77E-06	-142.21	3.27E-110
tRNA-Ala-2	tRNA-Ala-2	10.50	1.71E-10	3.09	2.68E-06
tRNA-Lys-2	tRNA-Lys-2	2.88	3.60E-04	2.01	9.21E-05
tRNA-Tyr-3	tRNA-Tyr-3	3.25	7.15E-05	4.39	4.74E-12
VC0015a	hypothetical protein	2.30	7.86E-07	-2.15	1.01E-09
VC0017	hypothetical protein	2.68	1.08E-04	-2.94	2.18E-05
VC0040	hemolysin, putative	-2.04	9.12E-06	-2.19	4.65E-18
VC0069	multidrug resistance protein, putative	2.45	1.16E-06	-2.85	7.90E-14
VC0075	MadN protein	-2.20	1.63E-06	-2.56	3.15E-19
VC0107	hypothetical protein	15.91	7.64E-14	2.53	2.05E-10
VC0280	cadaverine/lysine antiporter CadB, putative	-2.98	7.28E-05	-2.69	5.87E-05
VC0287	thermoresistant gluconokinase	-2.49	2.38E-04	2.21	3.49E-09
VC0299	DNA polymerase III, epsilon subunit, putative	2.47	7.66E-05	-5.44	2.00E-23
VC0300	conserved hypothetical protein	2.76	1.60E-04	-7.61	1.06E-35
VC0327	ribosomal protein L7/L12	-2.01	5.82E-05	3.24	1.00E-23
VC0364	bacterioferritin-ass ociated ferredoxin	11.80	6.48E-24	3.52	2.57E-15
VC0379a	phage shock protein G	5.22	2.49E-07	-2.10	1.38E-06
VC0553	conserved hypothetical protein	-2.00	8.07E-04	-2.11	1.63E-06
VC0608	iron(III) ABC transporter, periplasmiciron-compound-binding protein	5.27	2.72E-12	9.28	2.55E-80
VC0633	outer membrane protein OmpU	-4.62	2.06E-07	-3191116.29	4.23E-14
VC0734	malate synthase A	2.23	6.39E-04	-4.94	1.71E-22
VC0863	conserved hypothetical protein	-2.94	5.76E-06	-2.27	3.19E-08
VC0930	hemolysin-related protein	3.17	8.42E-08	2.66	1.16E-15
VC0945	conserved hypothetical protein	3.19	1.38E-05	2.26	4.57E-08
VC1032	zinc/cadmium/mercury/lead-transporting ATPase	3.67	1.28E-04	-3.26	7.57E-06
VC1061	cysteine synthase/cystathionine beta-synthasefamily protein	-2.73	1.04E-05	-4.04	2.31E-14
VC1116	hypothetical protein	3.65	9.06E-12	-5.03	5.97E-23
VC1187	hypothetical protein	-4.48	6.63E-10	-2.04	3.98E-05
VC1207	hypothetical protein	2.00	8.97E-04	-4.68	8.53E-23
VC1222	integration host factor, alpha subunit	2.93	4.67E-05	-3.69	3.05E-13
VC1264	iron-regulated protein A, putative	3.80	1.72E-14	2.58	4.53E-24
VC1265	hypothetical protein	2.70	9.29E-06	2.02	5.96E-07
VC1266	hypothetical protein	4.26	3.08E-08	2.00	1.98E-07
VC1280	hypothetical protein	-2.46	2.23E-06	2.12	4.52E-08
VC1325	galactoside ABC transporter, periplasmicD-galactose/D-glucose-binding protein	-5.61	2.10E-10	-5.16	4.85E-31
VC1327	galactoside ABC transporter, ATP-bindingprotein	-6.83	5.27E-24	-3.55	2.73E-23
VC1328	galactoside ABC transporter, permease protein	-6.33	2.28E-28	-3.14	6.08E-19
VC1339	conserved hypothetical protein	2.11	3.10E-05	-2.13	1.39E-06
VC1355	acylphosphatase	2.04	9.87E-05	-2.92	3.76E-14
VC1370	GGDEF family protein	2.06	4.56E-05	-7.21	1.61E-45
VC1401	protein-glutamate methyltransferase CheB	2.52	1.05E-05	-5.28	3.40E-31
VC1402	purine-binding chemotaxis protein Chew,putative	2.25	9.75E-04	-4.64	3.77E-19
VC1415	hcp protein	-4.56	5.20E-09	9.53	1.25E-48
VC1456	cholera enterotoxin, B subunit	4.05	3.30E-06	-3.08	3.18E-03
VC1457	cholera enterotoxin, A subunit	4.12	8.65E-06	-3.83	3.52E-04
VC1484	ribosome modulation factor	3.22	3.72E-06	-5.91	2.99E-22
VC1495	hypothetical protein	2.44	2.92E-04	-2.82	5.53E-06
VC1509	nicotinatemononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase	2.44	9.97E-04	-3.76	4.54E-18
VC1545	TonB system transport protein ExbD2	5.63	8.68E-10	2.20	3.41E-05
VC1546	TonB system transport protein ExbB2	4.13	9.34E-08	4.04	1.39E-18
VC1547	biopolymer transport protein ExbB-relatedprotein	4.16	5.15E-08	5.45	4.20E-31
VC1548	hypothetical protein	2.60	2.69E-04	3.82	1.92E-17
VC1560	catalase/peroxidase	2.78	6.31E-04	-5.03	2.90E-29
VC1563	conserved hypothetical protein	-3.77	2.54E-08	2.07	1.41E-06
VC1565	outer membrane protein TolC, putative	-4.17	1.48E-10	2.49	1.78E-10
VC1593	GGDEF family protein	-4.81	3.96E-15	-2.87	3.16E-17
VC1594	aldose 1-epimerase	-19.71	6.47E-70	-3.72	1.55E-26
VC1595	galactokinase	-26.28	1.39E-85	-3.60	6.83E-26
VC1596	galactose-1-phosphate uridylyltransferase	-33.92	6.31E-60	-2.86	2.44E-17
VC1605a	hypothetical protein	2.38	4.83E-04	-2.80	3.18E-18
VC1618	multidrug resistance protein, putative	2.45	1.22E-07	-2.80	2.24E-05
VC1640	ribosomal protein L25	-4.96	4.61E-19	3.64	6.24E-25
VC1655	magnesium transporter	9.75	1.08E-10	3.05	4.82E-18
VC1661	hypothetical protein	2.18	7.18E-06	-2.80	2.43E-12
VC1676	phage shock protein C	6.27	1.52E-11	-2.31	1.67E-08
VC1677	phage shock protein B	8.74	6.09E-17	-2.02	1.90E-06
VC1706	transcriptional activator MetR	2.11	6.34E-05	-2.15	9.18E-07
VC1707	hypothetical protein	3.53	2.32E-06	-5.78	6.11E-30
VC1743	hypothetical protein	-4.13	2.88E-09	-2.35	1.35E-07
VC1854	porin, putative	12.73	5.64E-22	2.37	3.17E-07
VC1888	hemolysin-related protein	2.91	2.75E-07	2.85	3.31E-25
VC2213	outer membrane protein OmpA	5.56	2.72E-10	6.97	1.20E-34

VC2240	decarboxylase	-3.31	4.67E-09	-3.35	8.81E-17
VC2337	transcriptional regulator, LacI family	-2.48	6.00E-07	-2.24	4.90E-10
VC2338	β -lactamase lacZ	-12.10	3.81E-28	-2.91	1.40E-17
VC2361	formate acetyl transferase-related protein	4.14	4.05E-08	-2.67	1.94E-17
VC2385	RNA-directed DNA polymerase	-2.07	8.01E-05	2.11	2.88E-07
VC2387	conserved hypothetical protein	-2.81	2.04E-04	2.50	9.87E-11
VC2389	carbamoyl-phosphate synthase, large subunit	2.19	6.87E-04	2.23	2.62E-12
VC2464	sigma-E factor regulatory protein RseC	-11.00	4.83E-43	-3.96	1.58E-33
VC2465	sigma-E factor regulatory protein RseB	-14.73	2.43E-43	-3.58	5.91E-26
VC2466	sigma-E factor negative regulatory protein RseA	-19.88	4.50E-68	-4.14	1.26E-31
VC2467	RNA polymerase sigma-E factor	-71453.09	2.13E-07	-3.70	2.47E-14
VC2565	elaA protein	-5.79	2.29E-12	-6.72	1.33E-40
VC2566	conserved hypothetical protein	-6.70	1.71E-18	-3.78	1.10E-37
VC2662	conserved hypothetical protein	3.56	1.70E-08	5.18	2.38E-39
VC2667	hypothetical protein	2.58	2.97E-04	-2.17	3.54E-05
VC2697	GGDEF family protein	2.00	4.11E-04	-2.66	5.11E-11
VC2753	hypothetical protein	5.14	6.70E-08	2.48	9.55E-10
VCA0008	methyl-accepting chemotaxis protein	2.16	6.90E-04	-13.72	2.04E-57
VCA0013	maltodextrin phosphorylase	-2.07	2.09E-04	-2.92	2.19E-11
VCA0017	hcp protein	-4.19	4.72E-09	12.02	3.29E-57
VCA0035	phosphatidylglycerol phosphatase B, putative	5.19	5.60E-24	3.19	5.28E-19
VCA0052	hypothetical protein	-2.09	4.17E-05	-2.07	3.00E-08
VCA0080	GGDEF family protein	2.76	2.10E-05	-4.35	9.21E-31
VCA0087	hypothetical protein	3.29	1.59E-05	2.70	9.55E-06
VCA0136	glycerophosphoryl diester phosphodiesterase	-2.71	1.06E-06	11.57	1.35E-42
VCA0137	glycerol-3-phosphate transporter	-7.45	3.84E-30	10.54	1.65E-73
VCA0156	conserved hypothetical protein	2.22	1.15E-05	-6.93	1.13E-30
VCA0158	hypothetical protein	4.00	4.34E-10	-2.72	4.52E-10
VCA0159	conserved hypothetical protein	4.39	3.44E-09	-2.27	2.67E-16
VCA0161	tryptophanase	4.48	8.61E-14	-2.95	3.88E-11
VCA0190	hypothetical protein	2.04	2.84E-04	-3.92	1.45E-25
VCA0212	hypothetical protein	2.06	2.86E-04	-4.39	3.64E-26
VCA0219	haemolysin	2.51	1.80E-05	-2.09	4.01E-08
VCA0223	protease	2.69	3.92E-05	3.11	7.09E-08
VCA0227	iron(III) ABC transporter, periplasmic iron-compound-binding protein	7.08	1.35E-11	19.29	1.75E-88
VCA0228	iron(III) ABC transporter, permease protein	2.45	8.32E-04	2.99	2.18E-09
VCA0268	methyl-accepting chemotaxis protein	2.19	5.80E-04	-5.91	5.83E-28
VCA0269	decarboxylase, group II	2.57	3.15E-05	-4.12	1.67E-19
VCA0282	IS5 transposase	-2.16	4.40E-04	-2.45	1.93E-08
VCA0288	initiation factor IF3	7.94	2.02E-09	2.29	1.04E-08
VCA0308	deoxyguanosinetriphosphate triphosphohydrolase-related protein	-2.15	1.34E-05	2.11	1.16E-05
VCA0441	hypothetical protein	-2.16	1.59E-05	2.83	2.26E-22
VCA0507	transposase OrfAB, subunit A	-2.50	2.67E-07	-2.54	2.06E-17
VCA0508	transposase OrfAB, subunit B	-2.90	5.62E-12	-2.61	7.82E-11
VCA0517	1-phosphofructokinase	-2.61	4.97E-05	2.47	2.70E-08
VCA0540	formate transporter 1, putative	-2.55	1.04E-05	2.37	2.63E-06
VCA0576	heme transport protein HutA	2.33	8.47E-05	5.15	1.04E-29
VCA0615	peptide methionine sulfoxide reductase	11.68	1.47E-06	-2.28	3.45E-07
VCA0647	hypothetical protein	4.07	4.68E-05	-3.61	3.13E-10
VCA0648	hypothetical protein	3.53	2.14E-04	-5.07	6.90E-12
VCA0649	hypothetical protein	4.07	1.12E-04	-3.48	1.50E-08
VCA0650	hypothetical protein	5.14	3.16E-05	-4.66	1.55E-12
VCA0651	conserved hypothetical protein	7.46	8.48E-06	-4.80	2.08E-05
VCA0657	aerobic glycerol-3-phosphate dehydrogenase	-3.08	1.75E-05	55.01	3.66E-159
VCA0678	periplasmic nitrate reductase	3.18	8.96E-04	-2.37	2.89E-08
VCA0684	regulatory protein UhpC	-3.08	1.29E-04	-2.47	8.11E-14
VCA0721	hypothetical protein	2.77	4.00E-05	4.34	1.11E-20
VCA0731	hypothetical protein	2.98	1.69E-04	-6.51	9.17E-18
VCA0744	glycerol kinase	-2.15	2.10E-05	12.12	3.52E-69
VCA0745	pseudogene with authentic frameshift mutation	-2.80	3.72E-06	12.67	3.63E-82
VCA0758	arginine ABC transporter, permease protein	2.01	4.68E-05	-2.40	1.02E-07
VCA0828	phenylalanine-4-hydroxylase	3.40	4.09E-12	2.38	7.71E-09
VCA0845	hypothetical protein	2.44	1.21E-03	2.02	1.48E-07
VCA0860	alpha-amylase	-2.11	2.95E-04	-3.42	1.45E-12
VCA0865	hemagglutinin/protease	5.87	3.93E-10	-9.40	5.40E-35
VCA0907	conserved hypothetical protein	3.12	3.05E-04	2.46	9.55E-09
VCA0908	conserved hypothetical protein	3.71	3.81E-05	2.51	6.72E-09
VCA0909	oxygen-independent coproporphyrinogen III oxidase, putative	6.26	4.41E-11	2.99	3.95E-10
VCA0910	tonB1 protein	6.77	1.91E-09	2.58	3.79E-05
VCA0911	TonB system transport protein ExbB1	6.04	1.98E-07	3.78	3.70E-08
VCA0912	TonB system transport protein ExbD1	4.53	1.35E-05	3.35	5.33E-07
VCA0913	hemin ABC transporter, periplasmic hemin-binding protein HutB	4.01	7.10E-06	2.42	4.57E-05
VCA0935	hypothetical protein	4.63	2.25E-08	-6.55	4.68E-37
VCA0944	maltose ABC transporter, permease protein	-2.36	1.24E-04	-4.30	4.21E-15
VCA0946	maltose/maltodextrin ABC transporter, ATP-binding protein	-2.38	1.43E-04	-2.46	1.93E-07
VCA0957	malate synthase-related protein	3.92	2.17E-16	-2.18	4.50E-08
VCA0988	methyl-accepting chemotaxis protein	2.28	4.11E-06	-2.77	2.89E-13
VCA1024	hypothetical protein	3.54	9.46E-06	-13.60	5.70E-85
VCA1028	maltoporin	-3.98	1.50E-07	-2.79	2.80E-06
VCA1086	response regulator	2.23	4.99E-04	-5.77	1.04E-41
VCA1091	chemotaxis protein methyltransferase CheR	2.42	8.38E-07	-7.93	1.10E-37
VCA1092	methyl-accepting chemotaxis protein	2.34	3.94E-04	-7.96	4.56E-52
VCA1093	purine-binding chemotaxis protein CheW	2.14	3.27E-06	-7.87	1.24E-40
VCA1108	oxidoreductase, short-chain dehydrogenase/reductase family	2.74	1.18E-05	-3.38	5.12E-09