

Table S5: Differentially-expressed 453 genes in the *ompU* mutant whose expression is rescued by OueS, compared to WT C6706, when grown under virulence inducing AKI conditions

Name	Function	$\Delta ompU/WT$		$\Delta ompU$ -pOueS/WT	
		FC	FDR p-value	FC	FDR p-value
5Sc	5S ribosomal RNA	-2.0	2.5E-08	-34.2	3.3E-38
5Sd	5S ribosomal RNA	-2.0	2.6E-08	-35.6	1.4E-39
5Sg	5S ribosomal RNA	-142.2	4.0E-107	-46.2	8.9E-22
VC0001	hypothetical protein	-2.3	1.8E-03	-3.0	3.2E-03
VC0018	16 kDa heat shock protein A	-2.0	3.8E-05	-2.4	9.1E-04
VC0032	ComM-related protein	-2.3	5.5E-04	-2.4	2.2E-03
VC0069	multidrug resistance protein, putative	-2.9	6.1E-13	-2.7	2.8E-05
VC0079	conserved hypothetical protein	-6.2	4.4E-50	-3.5	4.5E-11
VC0089	cytochrome c551 peroxidase	-20.6	7.9E-69	-5.2	1.7E-06
VC0090	DNA-damage-inducible protein F	-4.4	3.2E-25	-3.1	3.5E-10
VC0098	methyl-accepting chemotaxis protein	-3.4	4.1E-25	-2.3	1.5E-04
VC0139	DPS family protein	-4.2	1.1E-20	-2.7	2.0E-06
VC0142	hypothetical protein	-2.4	1.5E-08	-2.2	6.4E-05
VC0169	hypothetical protein	-6.7	1.2E-23	-4.1	2.8E-06
VC0172	peptide ABC transporter, permease protein	-2.1	1.2E-06	-2.2	1.6E-03
VC0185	transposase, putative	-3.2	5.3E-15	-3.4	2.6E-12
VC0300	conserved hypothetical protein	-7.6	4.2E-34	-3.3	2.1E-03
VC0308	hypothetical protein	-3.5	6.6E-19	-2.7	1.1E-05
VC0365	bacterioferritin	-3.5	7.0E-21	-3.2	5.2E-08
VC0383	hypothetical protein	-4.1	2.3E-08	-3.2	2.3E-04
VC0403	MSHA biogenesis protein MshM	-3.1	3.5E-13	-2.5	4.6E-05
VC0404	MSHA biogenesis protein MshN	-2.3	2.3E-12	-2.1	1.4E-04
VC0407	MSHA biogenesis protein MshF	-2.1	8.6E-08	-2.4	1.2E-06
VC0412	hypothetical protein	-2.2	6.8E-13	-2.6	1.9E-07
VC0413	MshP	-2.8	5.9E-20	-3.3	4.6E-10
VC0414	MshQ	-2.3	1.6E-10	-2.2	5.6E-03
VC0501	pseudogene within VSP-II; potential transposase	-3.3	1.0E-14	-2.2	4.0E-03
VC0633	outer membrane protein OmpU	-3191116.3	3.4E-13	-21.8	3.7E-07
VC0658	c-di-GMP phosphodiesterase A-related protein	-5.0	1.2E-31	-3.0	8.7E-05
VC0697	hypothetical protein	-4.0	6.2E-28	-2.7	7.7E-06
VC0728	conserved hypothetical protein	-4.8	1.3E-26	-2.4	4.2E-06
VC0734	malate synthase A	-4.9	2.6E-21	-4.2	1.0E-11
VC0736	isocitrate lyase	-6.5	8.4E-43	-2.2	6.5E-04
VC0817	transposase, putative	-2.0	2.0E-06	-2.1	1.5E-04
VC0893	chemotaxis protein PomB	-3.2	4.0E-23	-2.3	9.8E-04
VC0935	hypothetical protein	-2.9	2.2E-08	-2.3	6.5E-03
VC0936	polysaccharide export-related protein	-5.5	1.7E-18	-5.3	1.2E-08
VC0937	exopolysaccharide biosynthesis protein, putative	-2.6	1.3E-10	-2.4	2.6E-03
VC0938	hypothetical protein	-4.2	3.2E-12	-3.6	1.2E-06
VC1008	sodium-type flagellar protein MotY	-3.7	6.7E-24	-2.2	1.0E-03
VC1009	conserved hypothetical protein	-4.2	4.6E-28	-2.6	1.3E-06
VC1029	GGDEF family protein	-3.6	6.1E-15	-2.5	3.1E-03
VC1031	inosine monophosphate dehydrogenase-related protein	-10.2	1.3E-74	-5.8	9.2E-18
VC1043	long-chain fatty acid transport protein	-2.4	1.5E-10	-2.7	1.0E-03
VC1050	response regulator	-5.1	3.4E-34	-3.1	1.5E-06
VC1066	hypothetical protein	-4.0	4.8E-22	-2.7	6.3E-08
VC1080	hypothetical protein	-3.8	6.6E-24	-2.7	2.1E-06
VC1082	response regulator	-11.2	8.6E-55	-3.0	7.9E-09
VC1083	hypothetical protein	-10.3	9.0E-65	-3.1	4.1E-11
VC1084	sensory box sensor histidine kinase	-12.6	1.2E-44	-4.3	5.5E-07
VC1085	sensor histidine kinase	-8.0	5.7E-43	-4.0	1.5E-13
VC1086	response regulator	-5.2	1.7E-44	-2.9	2.9E-07
VC1087	response regulator	-4.4	4.5E-30	-2.4	4.7E-03
VC1088	sensor histidine kinase	-5.9	1.8E-33	-4.1	4.3E-10
VC1089	periplasmic binding protein-related protein	-4.7	2.5E-31	-2.6	1.6E-03
VC1124	conserved hypothetical protein	-4.7	2.2E-24	-2.4	4.3E-06
VC1125	hypothetical protein	-4.9	6.0E-26	-3.2	3.7E-05
VC1131	conserved hypothetical protein	-2.3	7.0E-08	-2.1	1.5E-04
VC1187	hypothetical protein	-2.0	1.2E-04	-3.0	2.9E-05
VC1189	hypothetical protein	-4.5	2.5E-19	-2.5	2.5E-03
VC1207	hypothetical protein	-4.7	1.3E-21	-2.4	2.0E-03
VC1211	conserved hypothetical protein	-2.1	1.8E-06	-2.4	1.6E-03
VC1222	integration host factor, alpha subunit	-3.7	2.2E-12	-2.2	8.0E-03
VC1223	hypothetical protein	-3.9	1.5E-17	-2.6	6.2E-04
VC1247	hypothetical protein	-2.6	1.7E-10	-2.5	8.8E-04
VC1248	methyl-accepting chemotaxis protein	-10.0	1.1E-55	-6.1	1.4E-08
VC1262	hypothetical protein	-2.1	1.4E-05	-2.5	2.4E-03
VC1295	conserved hypothetical protein	-2.9	4.3E-13	-3.4	1.2E-05

VC1298	methyl-accepting chemotaxis protein	-2.1	4.4E-05	-2.4	1.6E-03
VC1312	alanine racemase, putative	-3.5	9.8E-15	-2.7	5.7E-06
VC1313	methyl-accepting chemotaxis protein	-4.2	4.7E-20	-3.0	4.9E-05
VC1316	chemotaxis protein CheY, putative	-4.3	5.9E-32	-2.1	2.2E-04
VC1322	conserved hypothetical protein	-5.8	3.5E-28	-3.8	6.7E-06
VC1323	hypothetical protein	-3.8	2.3E-20	-2.3	8.1E-04
VC1328	galactoside ABC transporter, permease protein	-3.1	7.2E-18	-2.2	4.6E-04
VC1348	response regulator	-5.1	1.0E-25	-4.4	1.8E-12
VC1349	sensory box sensor histidine kinase/responseregulator	-4.4	2.9E-25	-3.3	4.6E-08
VC1353	GGDEF family protein	-2.1	1.0E-05	-2.1	1.8E-03
VC1355	acylphosphatase	-2.9	3.0E-13	-2.2	1.9E-04
VC1359	amino acid ABC transporter, ATP-binding protein	-3.0	1.4E-13	-2.1	1.6E-03
VC1360	amino acid ABC transporter, permease protein	-4.1	1.9E-17	-2.9	3.9E-04
VC1361	amino acid ABC transporter, permease protein	-4.0	2.8E-19	-2.9	9.3E-06
VC1362	amino acid ABC transporter, periplasmic aminoacid-binding protein	-9.0	1.9E-52	-4.8	2.5E-05
VC1368	hypothetical protein	-3.4	3.1E-17	-2.2	1.6E-03
VC1369	conserved hypothetical protein	-6.1	6.2E-31	-4.4	2.5E-08
VC1370	GGDEF family protein	-7.2	9.6E-44	-5.6	1.1E-13
VC1371	hypothetical protein	-2.8	3.1E-13	-2.6	9.6E-08
VC1376	GGDEF family protein	-2.8	1.6E-16	-2.6	5.5E-05
VC1394	methyl-accepting chemotaxis protein	-6.1	1.1E-45	-5.4	3.1E-10
VC1395	response regulator cheY1	-7.3	3.3E-55	-5.9	5.0E-12
VC1396	hypothetical protein	-6.6	1.1E-33	-4.0	2.8E-07
VC1397	chemotaxis protein CheA	-9.0	5.9E-55	-5.3	9.1E-12
VC1398	chemotaxis protein CheY	-9.3	4.9E-43	-5.4	1.5E-11
VC1399	chemotaxis protein methyltransferase CheR	-8.3	3.4E-50	-6.4	9.9E-12
VC1400	hypothetical protein	-7.3	8.3E-36	-3.9	4.6E-06
VC1401	protein-glutamate methylesterase CheB	-5.3	9.9E-30	-2.9	1.4E-05
VC1403	methyl-accepting chemotaxis protein	-4.7	1.9E-23	-2.6	1.0E-03
VC1405	methyl-accepting chemotaxis protein	-3.1	1.4E-15	-3.5	7.9E-08
VC1406	methyl-accepting chemotaxis protein	-3.4	8.9E-17	-2.7	7.3E-05
VC1495	hypothetical protein	-2.8	1.9E-05	-5.7	7.4E-09
VC1509	nicotinatemononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase	-3.8	5.1E-17	-2.1	4.6E-03
VC1528	hypothetical protein	-3.0	4.7E-13	-2.6	1.5E-03
VC1538	hypothetical protein	-2.9	1.9E-14	-2.4	6.8E-05
VC1560	catalase/peroxidase	-5.0	7.2E-28	-2.9	5.9E-03
VC1593	GGDEF family protein	-2.9	3.2E-16	-2.2	5.2E-04
VC1594	aldose 1-epimerase	-3.7	3.1E-25	-2.6	1.3E-03
VC1601	hypothetical protein	-3.2	1.5E-14	-2.5	9.2E-07
VC1602	chemotaxis protein CheV	-3.1	3.8E-09	-2.7	1.5E-03
VC1603	hypothetical protein	-3.3	2.6E-18	-3.3	1.4E-06
VC1605a	hypothetical protein	-2.8	3.6E-17	-2.1	7.3E-03
VC1641	conserved hypothetical protein	-3.1	1.5E-22	-3.0	1.7E-08
VC1643	methyl-accepting chemotaxis protein	-5.5	2.9E-20	-2.7	2.5E-04
VC1661	hypothetical protein	-2.8	1.7E-11	-2.2	1.4E-03
VC1662	conserved hypothetical protein	-3.3	1.1E-15	-2.6	8.7E-04
VC1672	DNA-3-methyladenine glycosidase I	-2.9	4.0E-10	-2.5	1.2E-03
VC1674	periplasmic linker protein, putative	-3.2	6.8E-16	-2.4	1.6E-03
VC1675	multidrug resistance protein, putative	-2.8	8.8E-16	-2.1	2.4E-04
VC1707	hypothetical protein	-5.8	1.6E-28	-3.1	5.3E-06
VC1736	arginyl-tRNA-protein transferase-relatedprotein	-3.3	5.1E-19	-2.5	1.5E-04
VC1831	sensor histidine kinase	-3.4	1.7E-21	-4.0	1.7E-12
VC1851	conserved hypothetical protein	-4.8	2.0E-31	-3.6	1.1E-07
VC1868	methyl-accepting chemotaxis protein	-6.8	2.2E-42	-4.3	2.0E-08
VC1873	conserved hypothetical protein	-13.6	4.8E-49	-4.6	5.8E-08
VC1874	conserved hypothetical protein	-12.5	2.4E-82	-5.9	5.3E-09
VC1914	integration host factor, beta subunit	-2.9	2.4E-16	-2.1	7.5E-04
VC1932	hypothetical protein	-2.6	1.4E-06	-2.3	5.3E-03
VC1933	hypothetical protein	-3.8	2.0E-21	-3.8	3.2E-07
VC1934	GGDEF family protein	-3.8	6.6E-21	-4.0	1.8E-06
VC1967	methyl-accepting chemotaxis protein	-3.4	5.0E-15	-3.5	4.3E-08
VC1997	hypothetical protein	-2.5	2.3E-13	-2.1	5.2E-04
VC2038	hypothetical protein	-2.4	8.5E-07	-2.4	6.8E-04
VC2046	hypothetical protein	-3.4	9.4E-18	-2.8	5.5E-09
VC2047	oxidoreductase, short-chaindehydrogenase/reduc tase family	-3.4	1.8E-25	-2.4	4.3E-03
VC2058	hypothetical protein	-3.0	1.8E-22	-2.5	2.1E-05
VC2060	conserved hypothetical protein	-2.9	1.1E-08	-2.8	5.2E-04
VC2061	ParA family protein	-2.4	5.4E-13	-2.1	3.7E-04
VC2120	flagellar biosynthetic protein FlhB	-2.4	6.4E-12	-2.1	4.0E-03
VC2121	flagellar biosynthetic protein FliR	-2.2	1.6E-08	-2.2	2.8E-03
VC2122	flagellar biosynthetic protein FliQ	-2.8	7.4E-15	-2.8	1.5E-04
VC2123	flagellar biosynthetic protein FliP	-3.0	2.4E-12	-2.9	8.5E-06

VC2124	flagellar protein FliO	-2.8	2.6E-14	-2.1	2.6E-04
VC2128	flagellar hook-length control protein FliK,putative	-4.4	1.2E-16	-2.4	1.6E-03
VC2138	flagellar protein FliS	-3.2	4.6E-20	-2.5	8.4E-06
VC2139	flagellar rod protein Flal, putative	-2.9	1.0E-23	-2.4	2.8E-05
VC2140	flagellar hook-associated protein FliD	-4.1	7.3E-30	-2.9	7.7E-04
VC2141	flagellin FlaG	-4.1	2.3E-25	-2.8	1.0E-03
VC2144	flagellin FlaE	-4.4	3.2E-32	-3.3	1.5E-08
VC2161	methyl-accepting chemotaxis protein	-4.1	4.3E-25	-2.9	5.7E-04
VC2190	flagellar hook-associated protein FlgL	-3.9	4.2E-13	-2.8	3.2E-04
VC2192	flagellar protein FlgJ	-4.3	2.3E-28	-2.2	2.1E-04
VC2201	chemotaxis protein methyltransferase CheR	-3.4	5.2E-20	-2.7	4.1E-03
VC2204	negative regulator of flagellin synthesis FlgM,putative	-3.3	4.3E-11	-2.7	2.9E-04
VC2205	hypothetical protein	-3.6	5.2E-21	-3.1	2.0E-08
VC2206	conserved hypothetical protein	-4.0	3.8E-29	-2.6	5.9E-06
VC2207	hypothetical protein	-3.2	3.8E-11	-2.2	3.1E-03
VC2240	decarboxylase	-3.4	8.7E-16	-2.6	1.2E-06
VC2264	conserved hypothetical protein	-4.3	6.0E-30	-2.9	2.1E-04
VC2285	GGDEF family protein	-2.2	4.8E-07	-2.5	4.3E-05
VC2314	hypothetical protein	-4.5	4.5E-14	-3.9	3.5E-06
VC2316	N-acetylglutamate synthase	-3.5	9.1E-15	-2.9	2.7E-04
VC2340	conserved hypothetical protein	-7.2	2.8E-27	-4.8	4.8E-07
VC2357	hypothetical protein	-2.1	4.0E-08	-2.1	6.1E-04
VC2358	hypothetical protein	-3.9	1.8E-24	-2.6	1.3E-03
VC2370	sensory box/GGDEF family protein	-2.8	7.1E-12	-2.7	5.1E-07
VC2384	conserved hypothetical protein	-4.0	2.4E-17	-3.9	1.1E-05
VC2454	GGDEF family protein	-3.7	7.2E-23	-3.0	4.2E-06
VC2455	hypothetical protein	-5.0	6.7E-24	-3.0	2.2E-05
VC2456	hypothetical protein	-4.6	1.2E-31	-2.8	2.6E-05
VC2464	sigma-E factor regulatory protein RseC	-4.0	5.6E-32	-3.2	1.1E-04
VC2465	sigma-E factor regulatory protein RseB	-3.6	1.1E-24	-2.9	3.2E-08
VC2466	sigma-E factor negative regulatory protein RseA	-4.1	3.8E-30	-2.3	2.7E-04
VC2467	RNA polymerase sigma-E factor	-3.7	2.0E-13	-3.0	5.7E-04
VC2507	conserved hypothetical protein	-10.1	5.3E-74	-3.0	7.1E-06
VC2565	elaA protein	-6.7	6.2E-39	-4.6	6.0E-16
VC2566	conserved hypothetical protein	-3.8	4.7E-36	-3.6	5.9E-11
VC2601	sodium-type flagellar protein MotX	-4.4	4.1E-24	-2.4	3.6E-06
VC2622	hypothetical protein	-5.4	2.6E-28	-4.2	4.1E-10
VC2647	conserved hypothetical protein	-2.1	2.3E-07	-2.8	2.0E-08
VC2702	transcriptional regulator, LuxR family	-2.8	1.4E-18	-2.2	4.8E-05
VC2704	hypothetical protein	-12.6	1.6E-44	-7.7	3.3E-08
VC2705	sodium/solute symporter, putative	-13.9	6.8E-69	-11.7	1.0E-10
VC2717	hypothetical protein	-2.6	2.2E-14	-2.9	3.8E-09
VC2726	general secretion pathway protein K	-2.1	1.4E-07	-2.1	1.9E-03
VC2727	general secretion pathway protein J	-2.2	9.9E-08	-2.7	7.8E-04
VC2750	GGDEF family protein	-3.0	1.3E-15	-2.9	1.1E-04
VCA0008	methyl-accepting chemotaxis protein	-13.7	2.7E-55	-7.3	8.6E-14
VCA0009	hypothetical protein	-12.8	2.8E-23	-7.6	2.4E-12
VCA0030	hypothetical protein	-2.2	3.6E-08	-2.3	9.8E-03
VCA0031	methyl-accepting chemotaxis protein	-3.9	6.5E-22	-2.5	1.1E-03
VCA0032	hypothetical protein	-3.6	2.0E-22	-2.4	1.0E-04
VCA0074	GGDEF family protein	-3.3	9.1E-17	-4.2	4.5E-10
VCA0075	hypothetical protein	-2.5	9.2E-06	-2.6	1.4E-03
VCA0078	hypothetical protein	-2.4	2.6E-11	-2.1	4.6E-03
VCA0080	GGDEF family protein	-4.4	2.6E-29	-3.0	3.6E-06
VCA0152	conserved hypothetical protein	-10.6	6.6E-50	-4.5	4.6E-07
VCA0153	conserved hypothetical protein	-9.5	1.2E-29	-3.5	7.5E-04
VCA0154	conserved hypothetical protein	-8.0	4.0E-33	-4.2	2.0E-07
VCA0155	NADH dehydrogenase, putative	-6.5	5.1E-44	-3.8	6.3E-07
VCA0156	conserved hypothetical protein	-6.9	3.1E-29	-3.3	8.3E-07
VCA0157	NADH dehydrogenase, putative	-5.3	4.9E-37	-3.4	1.1E-05
VCA0188	hypothetical protein	-4.5	1.2E-16	-3.9	7.7E-06
VCA0191	conserved hypothetical protein	-4.1	3.9E-26	-2.5	4.0E-04
VCA0195	hypothetical protein	-3.8	1.3E-20	-2.4	9.6E-05
VCA0210	response regulator, putative	-7.3	5.9E-55	-4.2	7.9E-09
VCA0211	sensory box sensor histidine kinase	-6.6	1.7E-50	-4.7	3.3E-11
VCA0212	hypothetical protein	-4.4	7.2E-25	-3.5	6.5E-10
VCA0217	GGDEF family protein	-2.1	2.5E-06	-2.7	9.6E-05
VCA0220	hemolysin secretion protein HylB	-2.5	9.5E-14	-2.1	1.5E-03
VCA0268	methyl-accepting chemotaxis protein	-5.9	1.4E-26	-4.9	3.4E-10
VCA0269	decarboxylase, group II	-4.1	2.1E-18	-3.4	8.3E-06
VCA0319	conserved hypothetical protein	-2.3	7.5E-05	-4.8	1.0E-08
VCA0534	pseudogene; contains authentic frameshift mutation	-2.5	8.7E-08	-2.9	9.0E-05

VCA0551	hypothetical protein	-3.7	4.6E-40	-2.9	1.8E-08
VCA0557	GGDEF family protein	-2.7	4.1E-16	-3.0	1.1E-07
VCA0570	Sui1 family protein	-2.5	5.1E-11	-2.2	6.5E-04
VCA0583	hypothetical protein	-9.2	9.8E-40	-4.7	3.7E-10
VCA0593	hypothetical protein	-4.9	7.9E-32	-3.4	1.8E-08
VCA0619	hypothetical protein	-4.6	6.1E-38	-2.3	5.0E-06
VCA0646	conserved hypothetical protein/hemolysin,putative	-5.0	1.4E-25	-3.4	1.5E-06
VCA0647	hypothetical protein	-3.6	1.8E-09	-2.9	1.1E-04
VCA0648	hypothetical protein	-5.1	4.6E-11	-3.2	1.5E-04
VCA0649	hypothetical protein	-3.5	7.2E-08	-2.6	6.5E-03
VCA0650	hypothetical protein	-4.7	1.1E-11	-3.6	1.5E-04
VCA0651	conserved hypothetical protein	-4.8	6.6E-05	-2.8	8.2E-03
VCA0659	protein F-related protein	-3.9	4.2E-37	-3.6	5.2E-10
VCA0678	periplasmic nitrate reductase	-2.4	1.3E-07	2.9	1.7E-03
VCA0679	periplasmic nitrate reductase, cytochrome c-typeprotein	-2.7	9.5E-07	2.7	9.3E-04
VCA0681	conserved hypothetical protein	-6.6	2.1E-50	-4.1	6.9E-09
VCA0683	sensor protein UhpB	-2.6	1.2E-11	-2.3	1.6E-03
VCA0695	hypothetical protein	-6.0	7.1E-24	-3.6	7.8E-06
VCA0698	hypothetical protein	-7.4	6.4E-48	-4.3	6.8E-10
VCA0719	sensor histide kinase	-6.3	4.6E-30	-3.7	4.7E-05
VCA0720	guanylate cyclase-related protein	-5.2	4.8E-30	-3.5	1.3E-10
VCA0731	hypothetical protein	-6.5	1.0E-16	-6.4	4.8E-11
VCA0736	sensor histidine kinase LuxQ	-2.3	1.8E-08	-2.4	7.5E-04
VCA0757	arginine ABC transporter, permease protein	-2.6	7.8E-13	-2.1	8.3E-03
VCA0760	arginine ABC transporter, ATP-binding protein	-3.5	4.7E-18	-2.9	2.0E-08
VCA0788	DnaJ-related protein	-2.4	5.1E-11	-2.3	4.5E-04
VCA0803	serine protease, putative	-13.5	1.6E-57	-6.2	1.7E-20
VCA0834	hypothetical protein	-3.4	2.5E-20	-2.2	2.0E-04
VCA0848	GGDEF family protein	-4.3	8.2E-54	-2.9	3.8E-05
VCA0864	methyl-accepting chemotaxis protein	-2.6	7.4E-11	-2.6	2.1E-04
VCA0865	hemagglutinin/protea se	-9.4	2.1E-33	-8.9	8.6E-15
VCA0868	hypothetical protein	-4.9	1.6E-34	-2.2	9.4E-03
VCA0880	makD	-6.0	4.1E-52	-5.8	1.6E-18
VCA0881	makC	-4.8	1.3E-40	-3.8	8.0E-07
VCA0882	makB	-4.9	4.8E-34	-4.2	7.6E-07
VCA0884	hypothetical protein	-6.0	3.8E-42	-4.2	1.5E-06
VCA0892	hypothetical protein	-3.0	2.4E-13	-3.1	7.4E-09
VCA0895	chemotactic transducer-related protein	-4.1	6.0E-26	-3.4	3.0E-07
VCA0900	hypothetical protein	-3.1	1.0E-15	-2.2	4.6E-04
VCA0902	hypothetical protein	-2.1	2.9E-06	-2.4	4.4E-04
VCA0906	methyl-accepting chemotaxis protein	-8.0	1.6E-62	-4.8	1.4E-11
VCA0920	hypothetical protein	-4.5	1.1E-26	-3.3	9.6E-11
VCA0923	methyl-accepting chemotaxis protein	-6.5	1.8E-40	-4.3	2.0E-14
VCA0931	conserved hypothetical protein	-3.2	1.0E-16	-2.5	1.1E-04
VCA0935	hypothetical protein	-6.6	2.0E-35	-7.0	2.1E-07
VCA0965	GGDEF family protein	-5.7	4.5E-31	-4.7	9.1E-09
VCA0978	amino acid ABC transporter, periplasmic aminoacid-binding protein, putative	-5.6	2.8E-31	-2.9	1.3E-08
VCA0979	methyl-accepting chemotaxis protein	-4.7	1.2E-30	-2.8	3.3E-06
VCA0981	hypothetical protein	-4.7	3.8E-31	-3.3	2.2E-05
VCA0988	methyl-accepting chemotaxis protein	-2.8	2.1E-12	-3.0	9.7E-08
VCA1015	Na+/H+ antiporter	-5.9	3.1E-51	-2.5	4.9E-05
VCA1016	hypothetical protein	-7.8	2.9E-75	-3.7	1.1E-08
VCA1017	methylated-DNA--prot ein-cysteineS-methyltransferas e	-6.0	5.4E-46	-4.3	1.1E-10
VCA1024	hypothetical protein	-13.6	3.0E-82	-4.9	3.3E-12
VCA1033	extracellular solute-binding protein, putative	-6.1	1.6E-27	-3.2	8.6E-07
VCA1034	methyl-accepting chemotaxis protein	-6.8	1.4E-45	-3.7	8.6E-11
VCA1054	conserved hypothetical protein	-5.1	1.5E-28	-2.8	1.2E-06
VCA1056	methyl-accepting chemotaxis protein	-6.4	2.7E-30	-5.1	8.2E-13
VCA1086	response regulator	-5.8	5.0E-40	-3.8	1.9E-07
VCA1087	anti-sigma F factor antagonist, putative	-4.6	1.2E-24	-3.8	6.3E-05
VCA1088	methyl-accepting chemotaxis protein	-5.2	3.6E-40	-4.4	4.6E-09
VCA1089	cheB3 methylesterase	-8.1	1.2E-73	-4.6	1.1E-07
VCA1090	chemotaxis protein CheD, putative	-10.1	1.5E-61	-5.4	2.4E-09
VCA1091	chemotaxis protein methyltransferase CheR	-7.9	4.7E-36	-4.5	1.5E-06
VCA1092	methyl-accepting chemotaxis protein	-8.0	3.9E-50	-3.4	1.0E-06
VCA1093	purine-binding chemotaxis protein CheW	-7.9	5.9E-39	-2.8	1.4E-04
VCA1094	purine-binding chemotaxis protein CheW	-8.2	1.9E-42	-3.9	1.1E-05
VCA1095	chemotaxis protein CheA	-8.0	3.7E-28	-4.2	9.4E-07
VCA1096	chemotaxis protein CheY	-8.0	8.4E-45	-3.8	2.3E-05
VCA1097	conserved hypothetical protein	-7.3	1.1E-50	-3.9	7.4E-09
VCA1108	oxidoreductase, short-chaindehydrogenase/reduc tase family	-3.4	2.6E-08	-2.4	2.0E-03

VC0134	conserved hypothetical protein	2.0	2.1E-14	2.4	9.5E-04
VC0156	vitamin B12 receptor	6.3	2.4E-25	3.3	6.9E-09
VC0164	multidrug resistance protein, putative	2.7	3.3E-14	3.1	1.2E-04
VC0165	conserved hypothetical protein	3.1	6.0E-10	2.6	8.5E-06
VC0194	gamma-glutamyltranspeptidase	4.3	1.1E-24	3.2	1.2E-05
VC0219	ribosomal protein L33	3.8	4.1E-33	2.0	1.3E-03
VC0295	acetyl-CoA carboxylase, biotin carboxylase	3.4	2.6E-19	2.0	1.6E-03
VC0296	acetyl-CoA carboxylase, biotin carboxyl carrier protein	3.2	1.4E-23	2.5	1.1E-04
VC0324	ribosomal protein L11, RplK	3.3	2.3E-18	2.8	4.0E-03
VC0327	ribosomal protein L7/L12	3.2	1.7E-22	2.6	3.2E-03
VC0360	ribosomal protein S7	3.2	5.1E-26	2.3	1.1E-03
VC0368	ribosomal protein S18	3.0	1.2E-18	2.3	2.1E-03
VC0374	glucose-6-phosphate isomerase	2.8	2.3E-15	3.1	9.7E-05
VC0395	UTP--glucose-1-phosphate uridylyltransferase	2.3	3.1E-11	2.6	3.6E-05
VC0478	fructose-bisphosphate aldolase, class II	2.5	8.0E-25	2.4	7.1E-03
VC0483	conserved hypothetical protein	2.7	1.4E-17	2.2	9.7E-05
VC0485	pyruvate kinase I	2.1	9.2E-05	2.2	5.0E-03
VC0529	conserved hypothetical protein	2.5	1.4E-09	2.2	4.8E-05
VC0530	conserved hypothetical protein	2.1	2.0E-07	2.1	2.5E-03
VC0564	ribosomal protein L19	5.3	1.2E-44	2.1	4.9E-04
VC0591	pantoate--beta-alanine ligase	2.1	2.5E-10	2.4	3.8E-05
VC0592	3-methyl-2-oxobutanoate hydroxymethyltransferase	2.2	5.0E-07	2.5	9.6E-05
VC0596	dnaK suppressor protein	3.2	9.7E-11	2.1	3.4E-04
VC0608	iron(III) ABC transporter, periplasmic iron-compound-binding protein	9.3	9.4E-78	3.5	1.5E-04
VC0642	N utilization substance protein A	2.8	2.8E-17	2.8	1.3E-03
VC0664	lysyl-tRNA synthetase, heat inducible	2.6	3.1E-14	3.2	2.1E-09
VC0695	phospho-2-dehydro-3-deoxyheptonate aldolase, tyr-sensitive	3.7	4.5E-19	3.6	2.6E-14
VC0718	conserved hypothetical protein	2.2	2.2E-07	2.5	9.1E-05
VC0739	S-adenosylmethionine :tRNA ribosyltransferase-isomerase	2.3	2.4E-09	2.3	2.6E-04
VC0749	NifU-related protein	2.2	2.7E-07	2.3	2.2E-03
VC0754	conserved hypothetical protein	2.1	3.8E-05	2.3	2.8E-03
VC0771	vibriobactin-specific isochorismatase	3.9	8.6E-13	2.9	8.9E-04
VC0847	integrase, phage family	2.2	1.4E-08	2.4	1.6E-03
VC0871	hypothetical protein	2.3	4.2E-06	3.2	2.6E-07
VC0872	conserved hypothetical protein	2.3	6.0E-06	3.2	6.7E-06
VC0905	lipoprotein YaeC	3.5	2.0E-26	2.6	9.3E-05
VC0928	hypothetical protein	3.1	2.2E-14	2.7	1.4E-04
VC0930	hemolysin-related protein	2.7	1.1E-14	2.4	3.4E-07
VC0941	serine hydroxymethyltransferase	2.6	1.1E-07	2.4	2.4E-03
VC0945	conserved hypothetical protein	2.3	2.1E-07	2.3	2.4E-03
VC0962	conserved hypothetical protein	2.5	4.3E-10	2.1	1.6E-04
VC0985	heat shock protein HtpG	3.9	6.3E-17	3.5	3.6E-06
VC0991	asparagine synthetase B, glutamine-hydrolyzing	3.8	1.0E-24	3.6	2.9E-09
VC1039	asmA protein	3.1	2.1E-20	3.3	5.4E-10
VC1040	cob(I)alamin adenosyltransferase	2.9	2.0E-17	2.5	2.7E-04
VC1092	oligopeptide ABC transporter, permease protein	2.8	3.0E-12	2.6	2.8E-05
VC1093	oligopeptide ABC transporter, permease protein	3.0	2.7E-13	2.7	6.7E-06
VC1094	oligopeptide ABC transporter, ATP-binding protein	2.7	2.0E-16	2.4	4.9E-05
VC1095	oligopeptide ABC transporter, ATP-binding protein	2.1	6.5E-08	2.2	1.6E-04
VC1159	phosphoserine aminotransferase	2.5	1.4E-13	2.5	4.4E-05
VC1193	hypothetical protein	4.9	1.8E-25	2.4	3.2E-03
VC1195	lipoprotein, putative	4.1	9.5E-25	2.2	8.8E-03
VC1209	elongation factor P family protein	3.1	2.3E-22	2.2	3.6E-04
VC1221	hypothetical protein	3.2	6.8E-24	2.5	3.9E-05
VC1259	conserved hypothetical protein	2.7	6.3E-08	2.5	1.9E-03
VC1280	hypothetical protein	2.1	2.0E-07	2.7	6.0E-05
VC1317	conserved hypothetical protein	2.9	7.7E-18	2.8	2.9E-08
VC1318	outer membrane protein OmpV	4.6	2.9E-17	5.0	8.8E-03
VC1374	DnaK-related protein	3.1	6.9E-14	2.1	7.5E-04
VC1375	hypothetical protein	2.9	4.1E-12	2.5	2.2E-04
VC1410	multidrug resistance protein VceA	2.4	2.8E-09	2.8	7.9E-08
VC1414	thermostable carboxypeptidase 1	2.4	1.0E-06	2.6	4.4E-04
VC1415	hcp protein	9.5	9.4E-47	7.4	6.4E-17
VC1416	vgrG protein	4.9	5.4E-45	3.7	2.9E-08
VC1417	hypothetical protein	3.2	1.2E-15	2.6	3.2E-04
VC1418	hypothetical protein	2.9	3.0E-15	2.4	3.1E-04
VC1419	hypothetical protein	2.5	1.1E-10	2.2	1.8E-03
VC1563	conserved hypothetical protein	2.1	5.2E-06	2.2	3.5E-03
VC1565	outer membrane protein TolC, putative	2.5	1.0E-09	2.4	2.3E-03
VC1578	hypothetical protein	2.7	1.2E-09	2.2	4.6E-03
VC1623	carboxynorspermidine decarboxylase	3.3	1.2E-22	2.8	1.9E-07
VC1624	conserved hypothetical protein	2.0	2.3E-06	2.1	9.7E-05

VC1625	Pseudogene; involved in spermidine biosynthesis	3.6	1.3E-23	2.7	1.8E-07
VC1655	magnesium transporter	3.1	5.3E-17	2.3	3.7E-05
VC1738	hypothetical protein	2.5	7.1E-07	2.5	5.0E-03
VC1750	hypothetical protein	2.1	4.4E-08	2.7	2.9E-03
VC1820	PTS system, fructose-specific IIA component	54.5	5.6E-21	112.3	7.7E-16
VC1821	PTS system, fructose-specific IIBC component	2.5	2.9E-09	13.6	1.5E-10
VC1822	PTS system, fructose-specific IIABC component	4.4	6.7E-24	4.3	2.0E-10
VC1823	PTS system, fructose-specific IIB component	4.9	1.6E-25	6.5	5.8E-21
VC1825	transcriptional regulator	3.5	7.1E-13	4.7	4.0E-13
VC1826	PTS system, fructose-specific IIABC component	3.0	1.4E-09	41.9	5.3E-14
VC1849	peptidyl-prolyl cis-trans isomerase B	2.7	2.1E-15	2.4	1.8E-05
VC1853	conserved hypothetical protein	2.8	2.1E-18	2.3	3.4E-04
VC1883	ABC transporter, ATP-binding protein	2.0	1.6E-07	2.2	1.1E-04
VC1888	hemolysin-related protein	2.9	6.1E-24	2.2	1.1E-04
VC1962	lipoprotein	5.6	8.6E-55	3.6	1.3E-10
VC2022	malonyl Coa-acyl carrier protein transacylase	3.2	1.9E-14	3.4	1.7E-06
VC2053	cytochrome c-type biogenesis protein CcmE	2.2	5.6E-08	2.3	8.8E-04
VC2213	outer membrane protein OmpA	7.0	4.5E-33	5.5	6.5E-03
VC2223	pseudouridine synthase family 1 protein	2.2	6.1E-17	2.1	2.5E-03
VC2259	elongation factor Ts	4.6	1.5E-46	3.9	1.2E-04
VC2329	2,3,4,5-tetrahydropyridine-2-carboxylateN-succinyl transferase	2.3	1.2E-07	2.1	6.5E-04
VC2386	conserved hypothetical protein	2.8	7.8E-16	2.2	7.0E-05
VC2389	carbamoyl-phosphate synthase, large subunit	2.2	1.8E-11	3.2	6.8E-10
VC2400	UDP-N-acetylmuramate --alanine ligase	2.3	1.1E-12	2.0	3.6E-04
VC2414	pyruvate dehydrogenase, E1 component	2.5	1.6E-13	2.6	3.7E-04
VC2485	transcriptional regulator, LysR family	2.2	5.9E-15	2.9	7.4E-09
VC2503	valyl-tRNA synthetase	2.4	9.2E-07	2.2	9.4E-03
VC2512	conserved hypothetical protein	4.1	4.0E-28	2.1	6.1E-04
VC2568	peptidyl-prolyl cis-trans isomerase, FKBP-type	3.5	2.7E-22	3.1	4.2E-06
VC2578	ribosomal protein L30	2.4	1.4E-06	2.1	1.6E-03
VC2582	ribosomal protein S8	2.8	1.4E-14	2.6	1.7E-03
VC2583	ribosomal protein S14	2.6	4.0E-13	2.3	8.2E-03
VC2587	ribosomal protein S17	2.6	4.6E-13	2.5	6.5E-06
VC2588	ribosomal protein L29	2.5	4.2E-07	2.3	5.5E-03
VC2591	ribosomal protein L22	2.7	1.9E-13	2.7	8.2E-04
VC2592	ribosomal protein S19	2.6	9.3E-14	2.5	1.3E-03
VC2594	ribosomal protein L23	4.0	1.3E-14	3.2	2.1E-07
VC2595	ribosomal protein L4	3.4	2.0E-22	2.4	4.4E-03
VC2646	phosphoenolpyruvate carboxylase	2.1	5.2E-07	2.4	1.0E-05
VC2662	conserved hypothetical protein	5.2	1.1E-37	6.0	3.2E-09
VC2664	chaperonin, 60 Kd subunit, groES_1	3.4	1.2E-11	3.0	1.7E-04
VC2670	triosephosphate isomerase	3.5	3.8E-23	3.5	8.7E-05
VC2679	ribosomal protein L31	5.9	1.6E-47	2.2	1.3E-03
VC2691	periplasmic protein cpxP, putative	2.8	1.1E-09	4.5	1.5E-04
VC2706	conserved hypothetical protein	4.0	7.1E-18	2.1	8.1E-04
VC2715	transcription elongation factor GreB	2.3	5.7E-06	3.0	3.3E-05
VC2716	conserved hypothetical protein	3.0	5.4E-33	2.6	3.6E-07
VC2761	multidrug resistance protein	2.4	3.7E-11	3.8	1.7E-06
VC2762	UDP-N-acetylglucosamine pyrophosphorylase	3.2	5.3E-20	2.3	4.3E-04
VC2774	glucose inhibited division protein B	2.4	1.4E-11	2.0	4.5E-05
VCA0017	hcp-2 protein	12.0	4.0E-55	8.6	3.9E-18
VCA0018	vgrG protein	3.2	1.6E-14	2.8	3.4E-04
VCA0019	hypothetical protein	3.5	9.1E-13	3.8	4.0E-06
VCA0020	hypothetical protein	3.0	1.1E-32	3.0	1.4E-07
VCA0026	conserved hypothetical protein	3.5	1.2E-21	2.4	2.2E-06
VCA0035	phosphatidylglycerophosphatase B, putative	3.2	6.4E-18	5.0	5.6E-09
VCA0087	hypothetical protein	2.7	3.2E-05	2.6	3.4E-04
VCA0088	proton/glutamate symporter	6.2	2.8E-81	3.5	3.1E-14
VCA0107	conserved hypothetical protein	6.1	3.8E-31	4.3	1.1E-08
VCA0108	conserved hypothetical protein	5.8	7.3E-44	4.5	5.8E-17
VCA0109	hypothetical protein	2.6	2.0E-09	2.3	2.0E-03
VCA0112	hypothetical protein	2.1	3.5E-08	3.0	2.1E-05
VCA0136	glycerophosphoryl diester phosphodiesterase	11.6	7.0E-41	18.5	2.2E-29
VCA0137	glycerol-3-phosphate transporter	10.5	4.1E-71	14.5	2.0E-20
VCA0139	hypothetical protein	6.2	6.9E-37	4.3	6.8E-05
VCA0192	D-lactate dehydrogenase	3.6	2.0E-24	3.3	9.2E-10
VCA0223	protease	3.1	3.1E-07	2.8	1.5E-04
VCA0227	iron(III) ABC transporter, periplasmic iron-compound-binding protein	19.3	1.3E-85	5.6	4.8E-04
VCA0277	glycine cleavage system H protein	2.2	6.6E-09	2.0	1.2E-03
VCA0517	1-phosphofructokinase	2.5	1.3E-07	3.8	1.6E-06
VCA0518	PTS system, fructose-specific IIA/FPR component	6.5	2.8E-27	10.2	2.4E-22
VCA0519	fructose repressor	2.7	1.6E-09	3.8	1.0E-09

VCA0540	formate transporter 1, putative	2.4	9.4E-06	13.3	3.7E-14
VCA0563	NAD(P) transhydrogenase, alpha subunit	3.4	7.8E-12	3.5	1.8E-05
VCA0564	NAD(P) transhydrogenase, beta subunit	3.7	2.7E-26	3.6	7.6E-10
VCA0652	hypothetical protein	3.7	4.3E-18	2.7	5.5E-07
VCA0657	aerobic glycerol-3-phosphate dehydrogenase	55.0	1.4E-155	70.9	5.3E-46
VCA0692	pseudogene with authentic frameshift mutation	2.4	7.7E-07	2.5	1.8E-03
VCA0721	hypothetical protein	4.3	1.5E-19	3.3	3.3E-03
VCA0744	glycerol kinase	12.1	6.8E-67	15.6	4.7E-19
VCA0745	pseudogene with authentic frameshift mutation	12.7	1.5E-79	14.6	7.6E-33
VCA0747	anaerobic glycerol-3-phosphate dehydrogenase,subunit A	22.0	5.1E-116	43.5	1.6E-34
VCA0748	anaerobic glycerol-3-phosphate dehydrogenase,subunit B	11.9	4.3E-69	28.0	4.2E-34
VCA0749	anaerobic glycerol-3-phosphate dehydrogenase,subunit C	11.9	6.9E-59	33.0	4.0E-45
VCA0789	conserved hypothetical protein	3.4	2.6E-18	3.4	5.3E-07
VCA0811	chitinase, putative	3.0	4.8E-15	3.2	2.8E-08
VCA0819	chaperonin, 10 Kd subunit	3.4	2.3E-14	2.7	1.2E-05
VCA0820	chaperonin, 60 Kd subunit	2.4	2.0E-10	2.2	1.9E-03
VCA0862	long-chain fatty acid transport protein	3.3	2.4E-14	3.6	2.8E-04
VCA0863	lipase, putative	4.6	5.9E-32	3.4	1.7E-07
VCA0897	devB protein	2.7	1.2E-12	2.2	2.6E-03
VCA0898	6-phosphogluconate dehydrogenase,decarboxylating	3.2	2.3E-15	3.2	6.9E-09
VCA0983	L-lactate permease, putative	6.9	2.1E-56	3.1	6.9E-08
VCA0984	L-lactate dehydrogenase	11.2	1.7E-94	9.2	4.6E-25
VCA0985	oxidoreductase/iron- sulfur cluster-bindingprotein	4.5	5.8E-24	4.0	2.8E-10
VCA0987	phosphoenolpyruvate synthase	2.4	3.4E-14	2.9	3.4E-07
VCA1035	hypothetical protein	3.9	1.3E-16	2.5	3.0E-04
VCA1073	bifunctional proline dehydrogenase/pyrroline-5-carboxylate dehydrogenase	4.5	1.5E-29	4.1	2.3E-06