

**Table S2.** Differentially expressed genes in biofilms in *ompU* and *rpoE* mutants compared to WT C6706.144 differentially-expressed genes exclusively in  $\Delta ompU$  and not  $\Delta rpoE$ , compared to the WT

Name	Function	Fold change	FDR <i>p</i> -value
VC0176	transcriptional regulator, putative	-2.75	6.55E-04
VC0177	hypothetical protein	-2.63	3.84E-06
VC0178	patatin-related protein	-2.22	8.01E-06
VC0179	hypothetical protein	-2.45	2.59E-07
VC0180	conserved hypothetical protein	-2.30	2.75E-08
VC0495	conserved hypothetical protein	-2.06	9.36E-04
VC0502	type IV pilin, putative	-2.69	2.63E-08
VC0504	hypothetical protein	-2.46	3.14E-06
VC0505	hypothetical protein	-2.86	7.32E-06
VC0506	hypothetical protein	-2.63	2.69E-05
VC0507	hypothetical protein	-4.79	1.07E-05
VC0633	outer membrane protein OmpU	-15766.55	0.00E+00
VC0711	clpB protein	-2.00	2.84E-05
VC0817	transposase, putative	-2.08	1.67E-04
VC0856	dnaJ protein	-2.12	8.37E-07
VC0886	hypothetical protein	-2.27	9.61E-07
VC0985	heat shock protein HtpG	-2.09	2.60E-06
VC1217	conserved hypothetical protein	-2.15	2.56E-04
VC1316	chemotaxis protein CheY, putative	-2.28	4.53E-06
VC1562	beta-lactamase-related protein	-2.19	3.31E-04
VC1676	phage shock protein C	-2.33	1.27E-06
VC1677	phage shock protein B, pspB	-2.15	3.76E-05
VC1762	hypothetical protein	-2.09	6.59E-05
VC1763	chemotaxis protein MotB-related protein	-2.84	3.22E-07
VC1774	conserved hypothetical protein	-2.01	2.78E-04
VC1793	hypothetical protein	-2.92	4.44E-04
VC2149	hypothetical protein	-2.03	4.67E-05
VC2663	molecular chaperone groEL_1	-2.12	4.68E-05
VC2664	chaperonin, 60 Kd subunit, groES_1	-2.00	6.87E-05
VCA0275	IS1004 transposase	-5.01	8.16E-04
VCA0298	hypothetical protein	-2.22	8.51E-04
VCA0336	hypothetical protein	-3.17	2.75E-07
VCA0344	hypothetical protein	-2.06	7.21E-06
VCA0354	hypothetical protein	-2.02	1.45E-04
VCA0357	hypothetical protein	-2.97	2.16E-04
VCA0358	hypothetical protein	-2.04	3.62E-04
VCA0367	hypothetical protein	-2.05	1.39E-05
VCA0382a	membrane protein	-2.00	9.91E-04
VCA0397	hypothetical protein	-2.43	7.81E-06
VCA0398	hypothetical protein	-2.74	5.30E-06
VCA0409	hypothetical protein	-2.16	3.44E-05
VCA0410	hypothetical protein	-2.03	4.45E-04
VCA0415	conserved hypothetical protein	-3.06	9.79E-05
VCA0420	hypothetical protein	-2.45	3.34E-05
VCA0428	hypothetical protein	-2.17	5.40E-07
VCA0431	hypothetical protein	-2.95	8.75E-10
VCA0443	lipoprotein Blc	-2.42	4.27E-06
VCA0446	haemagglutinin	-3.57	9.29E-13
VCA0447	haemagglutinin associated protein	-2.40	1.17E-06
VCA0448	hypothetical protein	-3.19	6.07E-09
VCA0449	hypothetical protein	-4.72	2.87E-07
VCA0450	hypothetical protein	-2.69	7.69E-04
VCA0451	hypothetical protein	-2.65	8.98E-04
VCA0455	conserved hypothetical protein	-2.12	8.65E-06
VCA0508	transposase OrfAB, subunit B	-2.81	1.01E-08
VCA0697	sensory box/GGDEF family protein	-2.01	2.57E-05
VC0065	thiG protein	3.25	2.71E-08
VC0066	thiH protein	2.48	2.44E-05
VC0199	hemolysin secretion ATP-binding protein, putative	3.43	1.12E-06
VC0200	iron(III) compound receptor	6.52	9.92E-13
VC0202	iron(III) ABC transporter, periplasmic iron-compound-binding protein	2.47	3.19E-04
VC0284	putative outer membrane receptor	3.05	2.37E-10
VC0474	iron-regulated virulence regulatory protein IrgB	3.29	1.74E-06

VC0719	DNA-binding response regulator PhoB	2.39	1.09E-06
VC0773	vibriobactin-specific isochorismate synthase	4.96	4.85E-07
VC0775	vibriobactin synthesis protein, putative	2.70	2.65E-06
VC0777	ferric vibriobactin ABC transporter, permease protein	3.51	3.53E-07
VC0778	ferric vibriobactin ABC transporter, permease protein	3.12	3.68E-07
VC0820	ToxR-activated gene A protein	4.04	1.01E-10
VC0821	hypothetical protein	3.56	3.27E-15
VC0823	hypothetical protein	2.76	1.59E-10
VC0929	hypothetical protein	5.80	9.83E-30
VC0931	conserved hypothetical protein	3.07	1.60E-05
VC0932	hypothetical protein	4.84	9.46E-09
VC0935	hypothetical protein	3.19	7.66E-05
VC0937	exopolysaccharide biosynthesis protein, putative	2.29	3.01E-04
VC0940	conserved hypothetical protein	2.08	2.76E-04
VC1154	hypothetical protein	2.04	1.37E-05
VC1264	iron-regulated protein A, putative	2.22	7.50E-06
VC1265	hypothetical protein	2.35	1.36E-06
VC1268	conserved hypothetical protein	2.35	6.02E-05
VC1313	methyl-accepting chemotaxis protein	2.55	2.57E-07
VC1330	hypothetical protein	4.29	1.94E-14
VC1347	glutathione S-transferase, putative	4.40	2.47E-15
VC1418	hypothetical protein	2.44	3.36E-07
VC1419	hypothetical protein	2.97	5.04E-09
VC1420	hypothetical protein	2.18	1.03E-04
VC1448	RTX toxin transporter	2.34	6.17E-05
VC1543	hypothetical protein	2.61	1.53E-09
VC1544	tonB2 protein	2.82	3.21E-08
VC1545	TonB system transport protein ExbD2	2.84	4.65E-06
VC1546	TonB system transport protein ExbB2	3.67	8.91E-11
VC1547	biopolymer transport protein ExbB-related protein	3.61	2.63E-13
VC1573	fumarate hydratase, class II, fumC	4.43	5.59E-09
VC1585	catalase	5.65	3.81E-12
VC1634	multidrug resistance protein	2.18	1.66E-04
VC1688	hypothetical protein	9.33	9.07E-14
VC1776	N-acetylneuraminase, putative	2.18	3.80E-05
VC1808	hypothetical protein	3.19	6.45E-14
VC1945	FAD monooxygenase, PheA/TfdB family	2.58	5.40E-08
VC1947	transcriptional regulator, LysR family	3.24	1.25E-07
VC1948	hypothetical protein	52.72	2.54E-08
VC1949	pvcA protein	6.42	3.26E-15
VC2004	conserved hypothetical protein	3.36	2.22E-12
VC2069	flagellar biosynthetic protein FlhA	2.19	3.16E-06
VC2209	nonribosomal peptide synthetase VibF	4.50	1.20E-15
VC2210	vibriobactin utilization protein ViuB	7.05	1.28E-31
VC2211	ferric vibriobactin receptor	5.50	6.13E-13
VC2212	hypothetical protein	3.05	9.59E-11
VC2385	RNA-directed DNA polymerase	2.44	1.82E-08
VC2386	conserved hypothetical protein	2.08	2.69E-05
VC2387	conserved hypothetical protein	2.96	2.44E-07
VC2416	2',3'-cyclic-nucleotide 2'-phosphodiesterase, putative	2.35	3.80E-07
VC2667	hypothetical protein	6.70	3.09E-14
VC2694	superoxide dismutase, Mn	3.54	6.01E-16
VC2704	hypothetical protein	2.10	1.18E-06
VC2705	sodium/solute symporter, putative	2.02	6.89E-06
VCA0073	phosphate ABC transporter, ATP-binding protein	2.71	2.44E-07
VCA0084	soxR protein	2.17	3.34E-04
VCA0095	hypothetical protein	5.84	2.18E-06
VCA0140	spindolin-related protein	4.73	7.10E-17
VCA0144	immunogenic protein	2.98	2.24E-04
VCA0147	transcriptional regulator, putative	3.56	6.02E-06
VCA0160	tryptophan-specific transport protein	5.17	7.59E-15
VCA0218	thermolabile hemolysin	3.35	2.36E-09
VCA0222	lipase activator protein, putative	3.41	2.80E-06
VCA0228	iron(III) ABC transporter, permease protein	2.85	5.14E-07
VCA0229	iron(III) ABC transporter, permease protein	2.24	2.48E-04
VCA0230	iron(III) ABC transporter, ATP-binding protein	2.91	1.52E-07
VCA0232	enterobactin receptor, VctA	6.91	2.52E-15
VCA0233	hypothetical protein	4.59	1.82E-09
VCA0277	glycine cleavage system H protein	2.15	2.12E-06
VCA0312	hypothetical protein	18.88	3.27E-22

VCA0454	sulfate-binding protein	2.20	5.46E-04
VCA0682	transcriptional regulator UhpA	2.37	1.21E-05
VCA0865	hemagglutinin/protea se	2.37	6.83E-04
VCA0866	hypothetical protein	2.37	5.08E-04
VCA0908	conserved hypothetical protein	7.45	3.55E-31
VCA0912	TonB system transport protein ExbD1	7.31	2.80E-13
VCA0913	hemin ABC transporter, periplasmic hemin-bindingprotein HutB	6.55	1.27E-11
VCA0914	hemin ABC transporter, permease protein,putative	5.58	8.99E-13
VCA0928	hypothetical protein	2.37	7.18E-05
VCA0946	maltose/maltodextrin ABC transporter,ATP-binding protein	2.32	1.33E-06
VCA0962	hypothetical protein	2.29	3.20E-07

1288 differentially-expressed genes exclusively in  $\Delta rpoE$  and not  $\Delta ompU$ , compared to the WT

Locus Tag	Function	Fold change	FDR p-value
16Sa	16S ribosomal RNA	-36.78	1.29531E-47
16Sb	16S ribosomal RNA	-28.41	1.16083E-37
16Sc	16S ribosomal RNA	-26.06	7.26317E-41
16Sd	16S ribosomal RNA	-4.18	7.97962E-10
16Se	16S ribosomal RNA	-17.77	3.85367E-32
16Sg	16S ribosomal RNA	-37.00	8.65305E-43
23Sa	23S ribosomal RNA	-10.75	1.09283E-22
23Sc	23S ribosomal RNA	-9.75	1.49741E-08
23Sd	23S ribosomal RNA	-9.86	6.53025E-24
23Se	23S ribosomal RNA	-166.20	1.0355E-104
23Sf	23S ribosomal RNA	-5.76	9.09732E-15
23Sg	23S ribosomal RNA	-28.39	1.48846E-41
23Sh	23S ribosomal RNA	-2.74	1.45461E-05
5Sa	5S ribosomal RNA	-87.55	1.01597E-32
5Se	5S ribosomal RNA	-48.28	3.09435E-38
5Sg	5S ribosomal RNA	-19110.69	5.183E-06
VC0008	amino acid ABC transporter, ATP-binding protein	-2.31	6.66E-09
VC0026	zinc-binding alcohol dehydrogenase	-2.22	1.01E-12
VC0027	threonine dehydratase	-5.38	6.61E-78
VC0028	dihydroxy-acid dehydratase	-3.87	6.59E-35
VC0030	acetolactate synthase II, small subunit	-2.67	4.91E-07
VC0032	ComM-related protein	-2.05	3.72E-05
VC0036	FixG-related protein	-2.82	4.20E-24
VC0048	smf protein	-2.43	6.46E-11
VC0049	smg protein	-3.10	3.89E-29
VC0050	DNA topoisomerase I-related protein	-3.73	1.53E-22
VC0075	MadN protein	-5.69	6.52E-47
VC0076	universal stress protein A	-7.29	5.00E-20
VC0079	conserved hypothetical protein	-3.77	8.23E-31
VC0089	cytochrome c551 peroxidase	-11.01	2.78E-62
VC0098	methyl-accepting chemotaxis protein	-3.64	1.68E-25
VC0131	conserved hypothetical protein	-2.59	9.19E-12
VC0139	DPS family protein	-2.12	2.39E-09
VC0159	RNA-binding protein	-2.02	1.19E-09
VC0164	multidrug resistance protein, putative	-2.57	6.38E-13
VC0174	hypothetical protein	-4.59	8.79E-41
VC0185	transposase, putative	-2.32	2.50E-10
VC0204	conserved hypothetical protein	-5.16	4.30E-22
VC0216	methyl-accepting chemotaxis protein	-3.90	2.32E-32
VC0217	DNA repair protein RadC	-4.77	1.00E-19
VC0229	hypothetical protein	-2.53	9.68E-22
VC0235	lipopolysaccharide biosynthesis protein,putative	-2.39	7.92E-18
VC0245	rfbG protein	-2.27	1.18E-07
VC0246	lipopolysaccharide/O -antigen transport protein	-2.16	7.35E-13
VC0247	lipopolysaccharide/O -antigen transport protein	-2.71	3.25E-26
VC0248	acyl carrier protein, putative	-2.57	1.79E-26
VC0249	rfbL protein	-2.92	9.84E-14
VC0250	iron-containing alcohol dehydrogenase familyprotein RfbM	-3.35	2.61E-20
VC0251	acyl protein synthase/acyl-CoA reductase RfbN	-2.96	2.28E-08
VC0252	acetyltransferase RfbO, CysE/LacA/LpxA/NodLfamily	-2.11	3.22E-10
VC0254	conserved hypothetical protein	-2.50	2.00E-12
VC0266	conserved hypothetical protein	-2.05	5.44E-05
VC0274	hypothetical protein	-2.03	1.42E-11
VC0280	cadaverine/lysine antiporter CadB, putative	-2.88	1.05E-06
VC0281	lysine decarboxylase, inducible	-2.02	2.89E-04

VC0282	methyl-accepting chemotaxis protein	-3.39	6.66E-28
VC0285	4-hydroxy-2-oxoglutarate aldolase/2-dehydro-3-deoxyphosphoglucose	-2.25	1.92E-09
VC0286	gluconate permease, putative	-3.94	2.35E-22
VC0287	thermo-resistant gluconokinase	-2.76	7.42E-10
VC0288	phosphoglucuronate dehydratase	-3.41	6.32E-11
VC0295	acetyl-CoA carboxylase, biotin carboxylase	-2.91	3.64E-21
VC0296	acetyl-CoA carboxylase, biotin carboxyl carrier protein	-2.10	1.13E-11
VC0298	acetyl-CoA synthase	-2.59	8.76E-12
VC0329	DNA-directed RNA polymerase, beta	-2.29	3.47E-05
VC0330	regulator of sigma D	-2.91	1.58E-16
VC0338	transporter, putative	-4.26	3.61E-33
VC0353	conserved hypothetical protein	-2.73	6.55E-18
VC0357	conserved hypothetical protein	-2.56	1.03E-12
VC0377	conserved hypothetical protein	-2.36	9.24E-13
VC0389	Na <sup>+</sup> /H <sup>+</sup> antiporter, putative	-2.81	5.15E-19
VC0400	MSHA biogenesis protein MshJ	-2.43	2.46E-12
VC0401	MSHA biogenesis protein MshK	-2.97	2.02E-12
VC0402	MSHA biogenesis protein MshL	-4.06	1.81E-25
VC0403	MSHA biogenesis protein MshM	-5.95	7.61E-51
VC0404	MSHA biogenesis protein MshN	-6.21	9.01E-61
VC0405	MSHA biogenesis protein MshE	-5.30	5.04E-55
VC0406	MSHA biogenesis protein MshG	-4.31	1.89E-53
VC0410	MSHA pilin protein MshC	-2.40	5.41E-23
VC0411	MSHA pilin protein MshD	-2.65	4.40E-16
VC0412	hypothetical protein	-3.50	3.33E-40
VC0413	hypothetical protein	-3.32	1.19E-24
VC0414	hypothetical protein	-4.50	1.51E-49
VC0419	cytoplasmic axial filament protein	-2.06	2.55E-11
VC0420	conserved hypothetical protein	-2.25	2.54E-16
VC0423	arginine deiminase	-4.29	1.69E-34
VC0441	bis(5'-nucleosyl)-triphosphate	-2.81	3.17E-28
VC0442	ApaG protein	-2.38	1.41E-19
VC0443	16S rRNA (adenine(1518)-N(6)/adenine(1519)-N(6))-dimethyltransferase	-2.63	8.59E-27
VC0445	survival protein SurA	-2.04	1.76E-14
VC0462	twitching motility protein PilT	-3.94	1.72E-27
VC0463	twitching motility protein PilT	-5.05	5.50E-36
VC0488	extracellular solute-binding protein, putative	-2.58	3.01E-22
VC0490	conserved hypothetical protein	-2.72	6.90E-13
VC0491	hypothetical protein	-3.58	5.04E-46
VC0492	hypothetical protein	-2.67	1.37E-11
VC0534	RNA polymerase sigma-38 factor	-3.13	7.30E-15
VC0550	oxaloacetate decarboxylase, alpha subunit	-3.11	2.68E-22
VC0551	oxaloacetate decarboxylase, beta subunit	-2.86	3.11E-19
VC0552	quinone oxidoreductase	-4.52	2.50E-36
VC0553	conserved hypothetical protein	-4.48	2.79E-24
VC0554	protease, insulinase family/protease, insulinase family	-4.19	1.75E-38
VC0653	c-di-GMP phosphodiesterase A-related protein	-2.27	1.39E-10
VC0658	c-di-GMP phosphodiesterase A-related protein	-3.92	4.46E-21
VC0661	conserved hypothetical protein	-3.65	4.98E-17
VC0665	sigma-54 dependent transcriptional regulator	-3.19	5.27E-22
VC0691	anhydro-N-acetylmuramic acid kinase	-2.14	4.55E-16
VC0708	conserved hypothetical protein	-2.20	1.15E-12
VC0730	copper homeostasis protein	-3.78	2.09E-16
VC0737	acetoin utilization protein AcuB, putative	-2.70	7.81E-24
VC0762	conserved hypothetical protein	-2.83	3.60E-20
VC0770	conserved hypothetical protein	-2.01	5.69E-04
VC0788	DOPA-dioxygenase-related protein	-2.07	7.53E-07
VC0802	hypothetical protein	-3.60	2.79E-14
VC0824	2-Cys peroxiredoxin	-3.34	1.82E-12
VC0828	toxin co-regulated pilin	-41.51	1.65E-47
VC0829	toxin co-regulated pilus biosynthesis protein B	-2.92	1.21E-07
VC0830	toxin co-regulated pilus biosynthesis protein Q	-2.55	2.00E-04
VC0831	toxin co-regulated pilus biosynthesis outer membrane protein C	-4.38	1.60E-17
VC0832	toxin co-regulated pilus biosynthesis protein R	-7.24	8.28E-12
VC0833	toxin co-regulated pilus biosynthesis protein D	-7.42	1.40E-11
VC0836	toxin co-regulated pilus biosynthesis protein E	-4.02	1.38E-08
VC0837	toxin co-regulated pilus biosynthesis protein F	-5.34	4.26E-18
VC0839	leader peptidase TcpJ	-5.10	1.37E-06
VC0841	accessory colonization factor AcfC	-2.12	1.25E-04
VC0844	accessory colonization factor AcfA	-5.63	1.56E-16

VC0845	conserved hypothetical protein	-2.42	3.22E-08
VC0863	conserved hypothetical protein	-2.18	1.15E-18
VC0893	chemotaxis protein PomB	-2.25	4.51E-20
VC0896	transcriptional regulator, LysR family	-2.17	6.01E-07
VC0899	conserved hypothetical protein	-8.39	6.82E-56
VC0910	PTS system, trehalose-specific IIBC component	-3.47	5.66E-19
VC0911	trehalose-6-phosphate hydrolase	-2.95	2.52E-11
VC0925	polysaccharide biosynthesis protein, putative	-2.06	7.89E-06
VC0926	hypothetical protein	-2.09	2.08E-08
VC0927	UDP-N-acetyl-D-manno samine transferase	-2.46	3.60E-10
VC0957	conserved hypothetical protein	-2.13	1.19E-08
VC0958	apolipoprotein N-acyltransferase	-2.13	5.61E-16
VC0975	conserved hypothetical protein	-2.00	3.89E-13
VC0976	conserved hypothetical protein	-2.39	2.10E-13
VC0979	oxidoreductase, short-chain dehydrogenase/reductase family	-2.95	7.86E-09
VC0980	epimerase	-3.22	5.97E-17
VC0995	PTS system, N-acetylglucosamine-specific IIBC component	-2.73	1.51E-14
VC0998	hypothetical protein	-2.58	4.78E-13
VC1008	sodium-type flagellar protein MotY	-2.06	3.75E-14
VC1022	phosphorelay protein	-2.22	7.16E-09
VC1026	molybdenum cofactor biosynthesis protein MoaC	-2.48	3.07E-05
VC1028	molybdenum cofactor biosynthesis protein E	-2.40	2.22E-06
VC1031	inosine monophosphate dehydrogenase-related protein	-6.90	1.52E-94
VC1032	zinc/cadmium/mercury/lead-transporting ATPase	-2.21	5.37E-03
VC1049	transcriptional regulator, LysR family	-3.09	1.51E-20
VC1050	response regulator	-4.16	6.22E-25
VC1062	transcriptional regulator, AsnC family	-2.29	1.20E-05
VC1063	acyl-CoA thioesterase II	-2.20	2.98E-16
VC1074	hypothetical protein	-3.29	5.09E-14
VC1080	hypothetical protein	-4.52	6.31E-40
VC1081	response regulator	-7.60	1.41E-53
VC1082	response regulator	-15.06	1.19E-78
VC1083	hypothetical protein	-12.71	5.94E-81
VC1084	sensory box sensor histidine kinase	-14.82	3.96E-103
VC1085	sensor histidine kinase	-10.04	3.20E-78
VC1086	response regulator	-8.65	1.41E-68
VC1087	response regulator	-6.46	3.88E-43
VC1088	sensor histidine kinase	-5.72	4.06E-37
VC1089	periplasmic binding protein-related protein	-10.26	2.76E-57
VC1103	ABC transporter, ATP-binding protein	-2.01	1.08E-07
VC1130	DNA-binding protein H-NS	-2.61	2.76E-19
VC1137	phosphoribosylformimino-5-aminoimidazolecarboxamide ribotide is	-2.07	7.55E-07
VC1138	imidazoleglycerol-phosphate synthase, cyclase subunit	-2.84	3.23E-13
VC1143	conserved hypothetical protein	-2.06	2.63E-07
VC1144	ATP-dependent Clp protease, ATP-binding subunit ClpA	-3.07	1.31E-14
VC1147	iron-containing alcohol dehydrogenase	-6.99	6.32E-71
VC1150	hypothetical protein	-2.02	2.00E-07
VC1153	conserved hypothetical protein	-2.18	2.42E-11
VC1155	response regulator	-4.40	1.54E-32
VC1156	sensor histidine kinase	-4.38	2.11E-29
VC1158	hypothetical protein	-2.41	1.23E-11
VC1187	hypothetical protein	-5.18	9.45E-17
VC1188	malate oxidoreductase	-11.77	2.17E-72
VC1201	hypothetical protein	-4.17	5.76E-33
VC1202	histidine ammonia-lyase	-5.35	1.80E-46
VC1203	urocanate hydratase	-6.96	6.50E-47
VC1205	imidazolepropionate	-4.04	1.00E-18
VC1206	histidine utilization repressor	-4.14	2.00E-20
VC1207	hypothetical protein	-2.59	1.83E-11
VC1222	integration host factor, alpha subunit	-3.47	2.08E-21
VC1223	hypothetical protein	-2.40	2.08E-09
VC1235	sodium/dicarboxylate symporter	-2.43	4.62E-08
VC1236	PilB-related protein	-2.28	1.16E-11
VC1248	methyl-accepting chemotaxis protein	-10.14	1.43E-50
VC1267	hypothetical protein	-2.41	1.56E-08
VC1283	PTS system, cellobiose-specific IIA component	-2.01	6.77E-04
VC1284	6-phospho-beta-glucosidase	-2.33	3.41E-11
VC1287	periplasmic glucans biosynthesis protein MdoH	-2.18	2.97E-12
VC1295	conserved hypothetical protein	-2.74	1.41E-09
VC1298	methyl-accepting chemotaxis protein	-2.04	3.01E-10

VC1312	alanine racemase, putative	-3.17	9.70E-14
VC1317	conserved hypothetical protein	-3.47	3.15E-26
VC1319	sensor histidine kinase	-4.70	1.81E-25
VC1320	DNA-binding response regulator	-5.04	1.55E-33
VC1322	conserved hypothetical protein	-6.92	2.62E-42
VC1323	hypothetical protein	-5.95	4.85E-40
VC1325	galactoside ABC transporter, periplasmicD-galactose/D-gluco se-bir	-89.16	9.08E-109
VC1327	galactoside ABC transporter, ATP-bindingprotein	-67.63	1.89E-182
VC1328	galactoside ABC transporter, permease protein	-46.24	1.92E-169
VC1332	conserved hypothetical protein	-2.06	1.69E-09
VC1339	conserved hypothetical protein	-2.09	8.47E-06
VC1340	prpE protein	-2.35	1.36E-11
VC1348	response regulator	-3.37	1.99E-26
VC1349	sensory box sensor histidine kinase/responseregulator	-2.63	7.80E-12
VC1353	GGDEF family protein	-2.41	9.11E-10
VC1359	amino acid ABC transporter, ATP-binding protein	-4.62	3.86E-45
VC1360	amino acid ABC transporter, permease protein	-5.94	7.82E-36
VC1361	amino acid ABC transporter, permease protein	-6.67	2.32E-35
VC1362	amino acid ABC transporter, periplasmic aminoacid-binding protein	-8.05	5.24E-40
VC1367	GGDEF family protein	-3.74	7.48E-32
VC1376	GGDEF family protein	-2.87	3.97E-17
VC1394	methyl-accepting chemotaxis protein	-6.14	2.73E-48
VC1395	response regulator CheY1	-9.46	1.30E-78
VC1396	hypothetical protein	-12.14	5.03E-61
VC1397	chemotaxis protein CheA	-17.12	2.74E-103
VC1398	chemotaxis protein CheY	-19.30	6.90E-66
VC1399	chemotaxis protein methyltransferase CheR	-19.21	3.61E-85
VC1400	hypothetical protein	-10.21	1.92E-52
VC1401	protein-glutamate methylesterase CheB	-9.36	8.25E-49
VC1402	purine-binding chemotaxis protein Chew,putative	-9.80	2.22E-48
VC1403	methyl-accepting chemotaxis protein	-12.04	1.81E-69
VC1406	methyl-accepting chemotaxis protein	-4.82	4.38E-40
VC1409	multidrug resistance protein, putative	-4.64	1.55E-19
VC1415	hcp protein	-2.16	1.14E-05
VC1433	conserved hypothetical protein	-3.23	2.02E-15
VC1437	cation transport ATPase, E1-E2 family	-2.33	5.57E-22
VC1444	hypothetical protein	-2.25	7.37E-13
VC1445	sensor histidine kinase/response regulator	-3.50	6.41E-24
VC1468	conserved hypothetical protein	-2.34	1.06E-05
VC1470	XRE family transcriptional regulator	-2.38	3.22E-03
VC1474	conserved hypothetical protein	-2.60	1.23E-05
VC1524	ABC transporter, permease protein	-3.05	3.34E-12
VC1539	conserved hypothetical protein	-2.21	2.01E-16
VC1560	catalase/peroxidase	-4.78	1.21E-26
VC1563	conserved hypothetical protein	-4.71	1.41E-16
VC1565	outer membrane protein TolC, putative	-7.31	1.13E-21
VC1566	conserved hypothetical protein	-3.19	2.20E-10
VC1567	hypothetical protein	-2.09	5.06E-08
VC1568	ABC transporter, ATP-binding protein	-3.37	7.73E-11
VC1583	superoxide dismutase, Cu-Zn	-2.12	2.47E-05
VC1590	acetolactate synthase	-6.14	2.76E-27
VC1591	oxidoreductase, short-chaindehydrogenase/reduc tase family	-6.96	5.22E-22
VC1593	GGDEF family protein	-4.35	1.66E-28
VC1594	aldose 1-epimerase	-41.74	1.37E-180
VC1595	galactokinase	-101.86	0.00E+00
VC1596	galactose-1-phosphat e uridylyltransferase	-80.75	0.00E+00
VC1598	ABC transporter, periplasmic substrate-bindingprotein-relat ed prote	-3.43	2.47E-20
VC1602	chemotaxis protein CheV	-2.51	3.46E-12
VC1603	hypothetical protein	-2.37	3.05E-15
VC1606	conserved hypothetical protein	-2.04	1.21E-09
VC1608	conserved hypothetical protein	-2.13	1.33E-07
VC1618	multidrug resistance protein, putative	-2.25	9.81E-11
VC1620	c-di-GMP-regulated adhesin	-2.34	9.24E-06
VC1623	carboxynorspermidine decarboxylase	-3.20	3.55E-18
VC1624	conserved hypothetical protein	-2.61	3.57E-25
VC1627	Na+/H+ antiporter protein	-2.26	9.17E-19
VC1641	conserved hypothetical protein	-2.84	3.41E-19
VC1643	methyl-accepting chemotaxis protein	-11.04	2.84E-80
VC1651	response regulator VieB	-4.73	1.17E-26
VC1652	response regulator VieA	-3.53	2.34E-20

VC1653	sensory box sensor histidine kinase/responseregulator VieS	-2.67	2.85E-19
VC1659	conserved hypothetical protein	-2.03	1.97E-13
VC1660a	ABC transporter permease	-3.09	9.50E-17
VC1662	conserved hypothetical protein	-2.19	6.15E-10
VC1672	DNA-3-methyladenine glycosidase I	-2.36	2.18E-05
VC1673	transporter, AcrB/D/F family	-4.64	9.34E-32
VC1674	periplasmic linker protein, putative	-5.73	2.69E-35
VC1679	psp operon transcriptional activator	-2.11	4.09E-06
VC1689	hypothetical protein	-2.19	1.84E-12
VC1695	formate transporter 1, putative	-2.28	8.13E-08
VC1710	conserved hypothetical protein	-2.47	2.80E-12
VC1726	glycogen synthase	-3.19	1.89E-34
VC1727	glucose-1-phosphate adenylyltransferase	-3.02	1.67E-16
VC1736	arginyl-tRNA-protein transferase-relatedprotein	-4.31	5.05E-26
VC1746	transcriptional regulator, TetR family	-2.40	1.36E-09
VC1750	hypothetical protein	-2.08	9.96E-06
VC1756	periplasmic linker protein, putative	-3.89	2.48E-31
VC1757	transporter, AcrB/D/F family	-3.76	2.21E-33
VC1777	conserved hypothetical protein	-2.21	3.51E-09
VC1821	PTS system, fructose-specific IIBC component	-2.08	4.90E-07
VC1831	sensor histidine kinase	-2.20	2.73E-10
VC1841	conserved hypothetical protein	-2.07	4.83E-10
VC1842	conserved hypothetical protein	-2.74	1.29E-05
VC1843	cytochrome d ubiquinol oxidase, subunit II	-3.72	1.92E-22
VC1844	cytochrome d ubiquinol oxidase, subunit I	-3.92	3.11E-20
VC1851	conserved hypothetical protein	-4.04	4.77E-25
VC1867	conserved hypothetical protein	-2.03	1.62E-11
VC1868	methyl-accepting chemotaxis protein	-6.30	3.06E-40
VC1872	conserved hypothetical protein	-8.71	8.50E-25
VC1873	conserved hypothetical protein	-12.76	3.48E-99
VC1874	conserved hypothetical protein	-6.23	1.64E-31
VC1933	hypothetical protein	-5.21	3.17E-59
VC1934	GGDEF family protein	-4.81	2.03E-27
VC1950	biotin sulfoxide reductase	-3.16	2.93E-18
VC1952	chitinase	-2.52	1.66E-12
VC1979	deoxyguanosinetriphosphate triphosphohydrolase	-2.89	6.91E-28
VC1987	outer membrane lipoprotein Slp, putative	-2.02	3.06E-14
VC1991	hypothetical protein	-3.48	1.87E-28
VC2000	glyceraldehyde 3-phosphate dehydrogenase	-2.29	2.71E-05
VC2001	conserved hypothetical protein	-3.87	6.61E-21
VC2007	transcriptional regulator, ROK family	-3.04	1.18E-29
VC2008	pyruvate kinase II	-2.85	5.99E-32
VC2009	conserved hypothetical protein	-2.21	4.49E-08
VC2013	PTS system, glucose-specific IIBC component	-6.28	2.99E-36
VC2032	hypothetical protein	-2.26	8.72E-09
VC2058	hypothetical protein	-2.79	6.19E-22
VC2059	purine-binding chemotaxis protein CheW	-2.16	6.27E-09
VC2060	conserved hypothetical protein	-4.48	3.75E-36
VC2061	ParA family protein	-2.58	2.17E-16
VC2062	protein-glutamate methyltransferase CheB	-2.56	4.66E-16
VC2063	chemotaxis protein CheA	-2.90	6.15E-11
VC2064	chemotaxis protein CheZ	-2.52	4.12E-13
VC2085	succinyl-CoA synthetase subunit beta	-2.20	9.44E-07
VC2120	flagellar biosynthetic protein FlhB	-2.24	2.84E-10
VC2121	flagellar biosynthetic protein FliR	-2.70	3.40E-13
VC2123	flagellar biosynthetic protein FliP	-3.61	5.50E-21
VC2124	flagellar protein FliO	-4.26	2.17E-32
VC2125	flagellar motor switch protein FliN	-3.22	1.64E-25
VC2126	flagellar motor switch protein FliM	-3.29	3.23E-20
VC2127	flagellar protein FliL, putative	-2.68	2.87E-16
VC2128	flagellar hook-length control protein FliK, putative	-3.29	9.33E-20
VC2130	flagellum-specific ATP synthase FliI	-2.31	2.70E-11
VC2142	flagellin FlaB	-2.42	4.07E-05
VC2143	flagellin FlaD	-2.34	1.17E-04
VC2161	methyl-accepting chemotaxis protein	-4.03	5.86E-24
VC2166	Trp repressor-binding protein	-2.12	9.64E-09
VC2167	hypothetical protein	-2.14	2.11E-05
VC2188	flagellin core protein A	-2.07	2.84E-04
VC2190	flagellar hook-associated protein FlgL	-2.49	2.23E-13

VC2191	flagellar hook-associated protein FlgM	-2.33	5.65E-11
VC2192	flagellar protein FlgJ	-2.20	1.18E-09
VC2193	flagellar P-ring protein FlgI	-3.30	1.92E-25
VC2195	flagellar basal-body rod protein FlgG	-2.12	4.19E-09
VC2196	flagellar basal-body rod protein FlgF	-2.25	1.86E-10
VC2197	flagellar hook protein FlgE	-2.02	9.99E-06
VC2198	basal-body rod modification protein FlgD	-2.10	1.88E-07
VC2201	chemotaxis protein methyltransferase CheR	-4.29	8.95E-23
VC2202	chemotaxis protein CheV	-3.54	3.24E-20
VC2206	conserved hypothetical protein	-2.86	2.57E-16
VC2207	hypothetical protein	-2.95	2.24E-18
VC2208	hypothetical protein	-2.30	1.03E-13
VC2240	decarboxylase	-8.45	7.67E-45
VC2241	cytochrome c554	-2.61	1.89E-15
VC2246	ribonuclease HII	-2.52	8.60E-09
VC2247	lipid-A-disaccharide synthase	-2.24	1.03E-08
VC2248	acyl-(acyl-carrier-p rotein)--UDP-N-acetylglucosamine O-acy	-2.90	1.24E-20
VC2249	(3R)-hydroxymyristoyl-ACP dehydratase	-3.43	1.24E-27
VC2250	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferas	-2.99	1.60E-20
VC2264	conserved hypothetical protein	-2.75	5.62E-20
VC2275	transcriptional regulator Crl	-4.45	4.01E-31
VC2285	GGDEF family protein	-2.48	1.06E-13
VC2314	hypothetical protein	-3.17	1.47E-07
VC2320	exodeoxyribonuclease V, 135 kDa subunit	-2.73	8.75E-29
VC2333	ribosomal protein S6 modificationprotein-related protein	-2.01	1.15E-13
VC2336	methionyl-tRNA synthetase-related protein	-2.51	2.23E-08
VC2337	transcriptional regulator, LacI family	-2.63	9.04E-28
VC2338	$\beta$ -lactamase lacZ	-24.31	2.47E-129
VC2340	conserved hypothetical protein	-4.09	7.89E-32
VC2344	hypothetical protein	-2.33	1.02E-11
VC2348	phosphopentomutase	-3.10	1.12E-24
VC2362	threonine synthase	-4.03	4.91E-30
VC2363	homoserine kinase	-4.30	7.69E-53
VC2364	bifunctional aspartokinase I/homoserine dehydrogenase I	-2.89	3.87E-28
VC2366	s-adenosylmethionine :2-demethylmenaquinonemethyltr ansferase	-4.50	1.33E-43
VC2367	hypothetical protein	-2.27	1.09E-11
VC2370	sensory box/GGDEF family protein	-3.78	8.35E-19
VC2371	conserved hypothetical protein	-2.85	2.05E-07
VC2374	glutamate synthase subunit beta	-4.66	5.34E-26
VC2378	conserved hypothetical protein	-4.06	7.71E-32
VC2384	conserved hypothetical protein	-2.72	3.42E-12
VC2413	dihydrolipoamide acetyltransferase	-2.38	6.22E-17
VC2429	conserved hypothetical protein	-2.87	2.69E-06
VC2436	outer membrane channel protein	-2.08	2.20E-08
VC2438	glutamate-ammonia-li gase adenyllyltransferase	-2.25	1.62E-18
VC2454	GGDEF family protein	-3.04	5.23E-22
VC2455	hypothetical protein	-5.83	2.97E-29
VC2456	hypothetical protein	-5.41	7.94E-59
VC2464	sigma-E factor regulatory protein RseC	-11.06	1.60E-118
VC2465	sigma-E factor regulatory protein RseB	-10.98	1.52E-116
VC2466	sigma-E factor negative regulatory protein RseA	-17.25	1.45E-202
VC2467	RNA polymerase sigma-E factor	-78682.69	1.92E-07
VC2469	L-aspartate oxidase	-2.71	1.76E-19
VC2487	conserved hypothetical protein	-2.89	3.81E-13
VC2491	3-isopropylmalate dehydrogenase	-2.46	1.03E-16
VC2492	3-isopropylmalate dehydratase, large subunit	-3.47	1.14E-27
VC2493	3-isopropylmalate dehydratase small subunit	-3.96	1.31E-46
VC2494	hypothetical protein	-3.74	8.42E-23
VC2497	conserved hypothetical protein	-2.09	6.80E-17
VC2507	conserved hypothetical protein	-2.77	2.15E-19
VC2529	RNA polymerase sigma-54 factor	-3.13	3.95E-13
VC2530	sigma-54 modulation protein, putative	-3.36	1.37E-44
VC2550	conserved hypothetical protein	-2.41	3.33E-14
VC2565	elaA protein	-10.52	4.34E-96
VC2566	conserved hypothetical protein	-6.24	8.02E-48
VC2605	hypothetical protein	-2.15	8.09E-09
VC2613	phosphoribulokinase	-4.69	8.49E-59



VC2615	conserved hypothetical protein	-2.60	6.67E-10
VC2622	hypothetical protein	-3.64	4.30E-20
VC2630	fimbrial assembly protein	-2.34	6.34E-15
VC2632	fimbrial assembly protein PilO, putative	-2.21	5.71E-03
VC2677	transcriptional repressor, LacI family	-4.94	1.08E-47
VC2697	GGDEF family protein	-2.64	4.07E-12
VC2702	transcriptional regulator, LuxR family	-4.99	8.51E-39
VC2703	conserved hypothetical protein	-2.44	5.54E-22
VC2711	ATP-dependent DNA helicase RecG	-2.21	1.54E-09
VC2722	cysQ protein	-2.48	2.17E-11
VC2725	general secretion pathway protein L	-2.02	2.69E-08
VC2726	general secretion pathway protein K	-3.05	5.86E-20
VC2727	general secretion pathway protein J	-3.02	5.77E-08
VC2728	general secretion pathway protein I	-3.89	7.83E-15
VC2729	general secretion pathway protein H	-2.82	9.78E-29
VC2730	general secretion pathway protein G	-2.64	2.61E-26
VC2738	phosphoenolpyruvate carboxykinase	-2.98	2.20E-07
VC2746	glutamine synthetase	-2.10	4.18E-08
VC2750	GGDEF family protein	-2.17	3.98E-08
VC2751	adenosine deaminase	-3.22	6.13E-36
VCA0008	methyl-accepting chemotaxis protein	-7.91	2.92E-42
VCA0009	hypothetical protein	-5.82	2.46E-19
VCA0015	hypothetical protein	-2.33	1.52E-17
VCA0018	vgrG protein	-2.14	5.78E-06
VCA0025	transporter, NadC family	-2.19	1.52E-15
VCA0030	hypothetical protein	-2.11	6.80E-09
VCA0031	methyl-accepting chemotaxis protein	-10.20	2.69E-64
VCA0032	hypothetical protein	-8.72	1.62E-66
VCA0033	hypothetical protein	-2.30	1.21E-10
VCA0034	conserved hypothetical protein	-15.84	2.27E-93
VCA0047	conserved hypothetical protein	-3.11	1.63E-21
VCA0048	conserved hypothetical protein	-2.90	1.76E-15
VCA0049	GGDEF family protein	-2.21	2.38E-10
VCA0051	hypothetical protein	-2.30	1.07E-15
VCA0052	hypothetical protein	-2.81	2.26E-16
VCA0074	GGDEF family protein	-2.35	3.95E-11
VCA0080	GGDEF family protein	-2.39	5.04E-13
VCA0101	conserved hypothetical protein	-2.09	1.10E-08
VCA0105	conserved hypothetical protein	-2.83	3.11E-08
VCA0106	hypothetical protein	-2.50	4.49E-09
VCA0109	hypothetical protein	-2.15	1.21E-07
VCA0111	hypothetical protein	-2.35	8.06E-08
VCA0112	hypothetical protein	-3.34	1.81E-20
VCA0113	hypothetical protein	-5.15	3.10E-27
VCA0114	hypothetical protein	-4.44	7.33E-21
VCA0115	hypothetical protein	-4.99	4.84E-20
VCA0116	clpB protein	-3.98	2.19E-34
VCA0117	sigma-54 dependent transcriptional regulator	-3.66	2.65E-23
VCA0118	hypothetical protein	-4.74	1.52E-14
VCA0119	hypothetical protein	-4.41	1.38E-19
VCA0120	IcmF-related protein	-2.84	8.76E-22
VCA0121	hypothetical protein	-3.64	7.67E-23
VCA0122	hypothetical protein	-2.89	8.93E-06
VCA0129	ribose ABC transporter permease	-2.16	7.31E-07
VCA0130	ribose ABC transporter, periplasmicD-ribose-binding protein	-3.58	1.13E-21
VCA0131	ribokinase	-2.21	1.75E-07
VCA0136	glycerophosphoryl diester phosphodiesterase	-2.45	7.26E-13
VCA0137	glycerol-3-phosphate transporter	-3.30	2.15E-18
VCA0153	conserved hypothetical protein	-4.32	7.50E-20
VCA0154	conserved hypothetical protein	-3.22	4.65E-15
VCA0155	NADH dehydrogenase, putative	-4.23	3.06E-27
VCA0156	conserved hypothetical protein	-3.55	1.60E-19
VCA0157	NADH dehydrogenase, putative	-3.21	1.65E-20
VCA0165	GGDEF family protein	-4.21	1.03E-29
VCA0168	hypothetical protein	-4.44	2.02E-54
VCA0171	conserved hypothetical protein	-2.15	3.34E-09
VCA0172	conserved hypothetical protein	-3.48	1.71E-12
VCA0173	hypothetical protein	-3.80	2.12E-20
VCA0174	conserved hypothetical protein	-2.14	7.05E-05

VCA0175	MoxR-related protein	-4.72	3.14E-20
VCA0189	response regulator	-2.16	1.04E-11
VCA0190	hypothetical protein	-2.22	5.55E-09
VCA0191	conserved hypothetical protein	-3.11	2.93E-18
VCA0200	hypothetical protein	-2.17	1.25E-11
VCA0201	hypothetical protein	-2.59	6.99E-15
VCA0205	C4-dicarboxylate transporter, anaerobic	-5.23	3.86E-29
VCA0210	response regulator, putative	-5.39	2.21E-38
VCA0211	sensory box sensor histidine kinase	-5.30	3.47E-40
VCA0219	haemolysin	-4.94	1.28E-36
VCA0220	hemolysin secretion protein HylB	-2.58	6.81E-19
VCA0223	protease	-2.85	1.16E-16
VCA0224	hypothetical protein	-2.19	1.40E-05
VCA0265	hypothetical protein	-4.36	3.14E-26
VCA0268	methyl-accepting chemotaxis protein	-3.76	2.36E-15
VCA0274a	hypothetical protein	-2.42	1.38E-10
VCA0281	integrase, putative	-2.72	6.35E-17
VCA0282	IS5 transposase	-3.61	7.72E-22
VCA0283	hypothetical protein	-2.42	1.09E-10
VCA0301	oxidoreductase, short-chain dehydrogenase/reductase family	-2.07	1.34E-11
VCA0302	hypothetical protein	-2.95	5.39E-13
VCA0303	hypothetical protein	-4.41	5.55E-54
VCA0304	hypothetical protein	-2.86	4.07E-10
VCA0306	hypothetical protein	-2.58	3.79E-10
VCA0307	hypothetical protein	-2.82	7.53E-18
VCA0309	conserved hypothetical protein	-3.19	6.68E-19
VCA0315	hypothetical protein	-2.44	8.31E-08
VCA0317	lipoprotein Blc	-2.58	1.85E-13
VCA0328	biphenyl-2,3-diol 1,2-dioxygenase III-related protein	-3.97	5.12E-36
VCA0329	hypothetical protein	-2.02	3.93E-06
VCA0329b	hypothetical protein	-2.07	1.94E-04
VCA0331	hypothetical protein	-2.35	1.55E-11
VCA0337	microcin immunity protein MccF	-3.31	2.33E-23
VCA0338	conserved hypothetical protein	-3.28	2.16E-18
VCA0340	hypothetical protein	-3.09	2.79E-17
VCA0341	biphenyl-2,3-diol 1,2-dioxygenase III-related protein	-2.31	9.27E-10
VCA0353	hypothetical protein	-2.71	5.75E-03
VCA0365	hypothetical protein	-10.53	2.60E-04
VCA0366	hypothetical protein	-2.53	5.14E-13
VCA0381	hypothetical protein	-2.47	9.42E-07
VCA0416	hypothetical protein	-2.01	1.18E-04
VCA0417	acetyltransferase, putative	-2.93	9.66E-16
VCA0439	microcin immunity protein MccF	-2.83	2.20E-20
VCA0440	hypothetical protein	-2.29	2.78E-06
VCA0442	acetyltransferase, putative	-2.89	9.49E-12
VCA0511	anaerobic ribonucleoside-triphosphate reductase	-2.89	2.14E-21
VCA0512	anaerobic ribonucleoside-triphosphate reductase activating protein	-2.34	1.18E-07
VCA0516	PTS system, fructose-specific IIBC component	-2.13	3.65E-15
VCA0526	conserved hypothetical protein	-3.16	1.03E-11
VCA0536	conserved hypothetical protein	-2.06	3.19E-16
VCA0544	conserved hypothetical protein	-5.68	1.69E-56
VCA0563	NAD(P) transhydrogenase, alpha subunit	-2.05	3.93E-16
VCA0570	Sui1 family protein	-4.11	5.21E-30
VCA0571	hypothetical protein	-2.97	7.34E-18
VCA0573	DamX-related protein	-2.28	8.59E-21
VCA0574	conserved hypothetical protein	-3.05	5.92E-38
VCA0583	hypothetical protein	-4.76	3.87E-27
VCA0584	glutathione S-transferase, putative	-3.07	1.59E-30
VCA0588	peptide ABC transporter, ATP-binding protein, putative	-2.41	7.71E-11
VCA0589	peptide ABC transporter, permease protein, putative	-3.66	2.79E-11
VCA0590	peptide ABC transporter, permease protein, putative	-4.33	3.60E-16
VCA0591	peptide ABC transporter, periplasmic peptide-binding protein, putative	-3.95	1.42E-43
VCA0592	MutT/nudix family protein	-2.44	5.79E-22
VCA0593	hypothetical protein	-4.26	6.16E-26
VCA0607	regulator of nucleoside diphosphate kinase	-2.11	8.41E-16
VCA0620	thiosulfate sulfurtransferase SseA, putative	-2.23	1.14E-17
VCA0624	transketolase 1	-2.31	3.04E-12
VCA0637	oxygen-insensitive NAD(P)H nitroreductase	-2.50	3.00E-07
VCA0638	transporter, AcrB/D/F family	-6.26	1.23E-52
VCA0639	AcrA/AcrE family protein	-5.56	8.46E-64

VCA0644	NADH oxidase, putative	-2.02	1.11E-07
VCA0646	conserved hypothetical protein/hemolysin,putative	-5.01	4.16E-26
VCA0647	hypothetical protein	-6.07	1.36E-19
VCA0648	hypothetical protein	-3.54	9.82E-08
VCA0649	hypothetical protein	-2.79	1.30E-05
VCA0650	hypothetical protein	-5.35	2.05E-13
VCA0651	conserved hypothetical protein	-4.73	1.72E-05
VCA0653	PTS system, sucrose-specific IIBC component	-2.85	1.04E-08
VCA0666	L-serine dehydratase 1	-3.95	4.19E-30
VCA0669	sugar transporter family protein	-2.41	1.68E-07
VCA0676	iron-sulfur cluster-binding protein NapF	-3.11	7.72E-13
VCA0677	napD protein	-2.30	7.17E-05
VCA0678	periplasmic nitrate reductase	-2.96	2.02E-13
VCA0679	periplasmic nitrate reductase, cytochrome c-typeprotein	-2.70	9.13E-06
VCA0680	periplasmic nitrate reductase, cytochrome c-typeprotein	-2.22	1.89E-05
VCA0681	conserved hypothetical protein	-4.36	3.46E-36
VCA0684	regulatory protein UhpC	-2.30	8.38E-14
VCA0686	iron(III) ABC transporter, permease protein	-2.24	2.79E-18
VCA0687	ferric transporter ATP-binding subunit	-2.28	7.45E-14
VCA0688	polyhydroxyalkanoic acid synthase	-4.59	6.57E-23
VCA0689	conserved hypothetical protein	-2.22	2.42E-04
VCA0698	hypothetical protein	-5.51	1.08E-38
VCA0704	phosphoglycerate transport systemtranscriptional regulatory protein	-2.40	3.12E-10
VCA0719	sensor histide kinase	-7.03	2.41E-47
VCA0720	guanylate cyclase-related protein	-6.48	9.43E-79
VCA0728	hypothetical protein	-3.01	4.84E-17
VCA0729	hypothetical protein	-3.35	4.29E-29
VCA0731	hypothetical protein	-2.90	1.78E-09
VCA0736	sensor histidine kinase LuxQ	-3.78	1.20E-27
VCA0737	luxP protein	-2.77	1.08E-28
VCA0738	hypothetical protein	-7.06	7.02E-45
VCA0743	conserved hypothetical protein	-3.89	9.25E-26
VCA0744	glycerol kinase	-4.50	5.04E-27
VCA0762	hypothetical	-2.86	1.21E-14
VCA0763	conserved hypothetical protein	-2.45	2.15E-21
VCA0764	MutT/nudix family protein	-2.61	8.80E-12
VCA0798	CbbY family protein	-2.17	6.82E-17
VCA0802	conserved hypothetical protein	-3.43	3.57E-43
VCA0803	serine protease, putative	-5.29	5.57E-39
VCA0822	aspartokinase, putative	-2.04	2.57E-09
VCA0829	acetyl-CoA synthase	-3.20	1.48E-21
VCA0851	conserved hypothetical protein	-2.61	1.06E-08
VCA0870	D-alanyl-D-alanine endopeptidase	-2.60	8.34E-17
VCA0877	hydrolase, putative	-5.18	8.45E-44
VCA0878	integrase-related protein	-8.11	4.38E-71
VCA0880	hypothetical protein	-7.70	6.63E-53
VCA0881	hypothetical protein	-5.39	7.30E-31
VCA0882	hypothetical protein	-6.43	4.05E-30
VCA0883	hypothetical protein	-3.40	2.07E-12
VCA0884	hypothetical protein	-6.27	3.10E-40
VCA0895	chemotactic transducer-related protein	-6.15	1.19E-55
VCA0900	hypothetical protein	-3.98	1.43E-29
VCA0901	hypothetical protein	-2.16	2.96E-09
VCA0906	methyl-accepting chemotaxis protein	-8.73	1.12E-75
VCA0915	hemin importer ATP-binding protein	-3.67	1.88E-24
VCA0917	transcriptional regulator, TetR family	-2.66	2.94E-14
VCA0920	hypothetical protein	-2.06	1.09E-09
VCA0923	methyl-accepting chemotaxis protein	-4.94	7.94E-61
VCA0931	conserved hypothetical protein	-2.53	1.76E-14
VCA0936	hypothetical protein	-2.83	2.77E-10
VCA0951	conserved hypothetical protein	-9.24	1.06E-28
VCA0965	GGDEF family protein	-7.93	8.88E-45
VCA0966	hypothetical protein	-5.70	8.07E-29
VCA0975	ATP-dependent protease LA-related protein	-7.10	7.15E-64
VCA0978	amino acid ABC transporter, periplasmic aminoacid-binding protein,	-14.38	5.27E-96
VCA0979	methyl-accepting chemotaxis protein	-7.77	2.89E-58
VCA0981	hypothetical protein	-11.43	2.01E-79
VCA0984	L-lactate dehydrogenase	-4.59	1.39E-16
VCA0985	oxidoreductase/iron- sulfur cluster-bindingprotein	-6.31	2.65E-39
VCA0986	conserved hypothetical protein	-2.65	9.09E-14

VCA0987	phosphoenolpyruvate synthase	-2.91	3.49E-19
VCA0988	methyl-accepting chemotaxis protein	-5.67	9.43E-33
VCA0993	N-ethylmaleimide reductase	-2.56	5.78E-12
VCA0994	hypothetical protein	-2.25	2.51E-13
VCA0998	NADH-dependent flavin oxidoreductase, Oye family	-3.20	1.16E-10
VCA1011	glutaredoxin-related protein	-2.04	8.45E-07
VCA1015	Na <sup>+</sup> /H <sup>+</sup> antiporter	-6.55	1.09E-94
VCA1016	hypothetical protein	-3.81	9.08E-29
VCA1017	methylated-DNA--prot ein-cysteineS-methyltransferas e	-5.12	2.93E-36
VCA1023	hypothetical protein	-2.23	7.65E-11
VCA1024	hypothetical protein	-3.59	3.42E-22
VCA1025	glucosamine-6-phosphate deaminase	-2.38	3.24E-11
VCA1029	glycogen operon protein GlgX	-3.55	1.90E-28
VCA1030	hypothetical protein	-3.08	6.32E-27
VCA1033	extracellular solute-binding protein, putative	-6.68	2.09E-42
VCA1034	methyl-accepting chemotaxis protein	-9.98	6.86E-75
VCA1036	pseudogene	-2.10	1.46E-13
VCA1038	amino acid ABC transporter, permease protein	-2.87	1.27E-16
VCA1039	amino acid ABC transporter, periplasmic aminoacid-binding protein	-2.65	3.50E-27
VCA1040	amino acid ABC transporter, permease protein	-2.93	1.74E-23
VCA1042	Ccm2-related protein	-2.43	7.19E-13
VCA1045	PTS system, mannitol-specific IIABC component	-2.02	1.37E-09
VCA1054	conserved hypothetical protein	-4.20	1.84E-51
VCA1056	methyl-accepting chemotaxis protein	-5.07	9.89E-37
VCA1067	aldehyde dehydrogenase	-3.43	1.11E-20
VCA1069	methyl-accepting chemotaxis protein	-2.36	8.73E-15
VCA1071	sodium/proline symporter	-2.82	1.11E-16
VCA1080	secretion protein, HlyD family	-2.20	1.39E-13
VCA1082	hypothetical protein	-2.91	6.26E-24
VCA1084	toxin secretion ATP-binding protein	-2.35	1.52E-17
VCA1086	response regulator	-3.88	1.74E-20
VCA1087	anti-sigma F factor antagonist, putative	-2.72	2.10E-14
VCA1088	methyl-accepting chemotaxis protein	-3.15	6.83E-21
VCA1089	cheB3 methyltransferase	-8.91	7.17E-63
VCA1090	chemotaxis protein CheD, putative	-7.52	1.14E-46
VCA1091	chemotaxis protein methyltransferase CheR	-5.22	2.24E-32
VCA1092	methyl-accepting chemotaxis protein	-5.87	9.07E-37
VCA1093	purine-binding chemotaxis protein CheW	-6.63	1.83E-37
VCA1094	purine-binding chemotaxis protein CheW	-5.99	9.54E-33
VCA1095	chemotaxis protein CheA	-5.70	2.79E-44
VCA1096	chemotaxis protein CheY	-6.75	8.92E-48
VCA1097	conserved hypothetical protein	-6.41	1.30E-72
VCA1104	phoP homolog	-2.96	9.29E-18
VCA1105	DNA-binding response regulator	-3.54	2.32E-22
VCA1106	hypothetical protein	-2.60	3.77E-15
VCA1113	spermidine/putrescin e ABC transporter,periplasmic spermidine/putr	-2.60	4.85E-10
23Sb	23Sb	2.65	9.10419E-06
tRNA-Ala-2	tRNA-Ala-2	2.37	1.25E-03
tRNA-Ala-3	tRNA-Ala-3	2.57	4.27E-03
tRNA-Ala-5	tRNA-Ala-5	4.69	6.08E-11
tRNA-Arg-4	tRNA-Arg-4	4.85	4.28E-24
tRNA-Arg-5	tRNA-Arg-5	5.59	5.30E-28
tRNA-Arg-6	tRNA-Arg-6	7.33	1.65E-08
tRNA-Arg-7	tRNA-Arg-7	5.10	8.07E-04
tRNA-Arg-8	tRNA-Arg-8	8.08	1.11E-07
tRNA-Asn-1	tRNA-Asn-1	6.11	2.00E-06
tRNA-Asn-2	tRNA-Asn-2	3.23	4.48E-05
tRNA-Asn-3	tRNA-Asn-3	3.67	7.49E-10
tRNA-Asn-4	tRNA-Asn-4	5.08	5.57E-04
tRNA-Asp-4	tRNA-Asp-4	2.98	9.36E-15
tRNA-Asp-5	tRNA-Asp-5	9.07	2.02E-12
tRNA-Cys-1	tRNA-Cys-1	5.10	4.09E-20
tRNA-Gln-1	tRNA-Gln-1	2.27	6.96E-04
tRNA-Gln-3	tRNA-Gln-3	2.46	1.82E-04
tRNA-Gln-5	tRNA-Gln-5	2.64	3.08E-04
tRNA-Glu-2	tRNA-Glu-2	4.41	3.99E-43
tRNA-Glu-3	tRNA-Glu-3	5.52	1.58E-27
tRNA-Gly-1	tRNA-Gly-1	8.36	5.15E-17
tRNA-Gly-3	tRNA-Gly-3	2.80	1.82E-17
tRNA-Gly-4	tRNA-Gly-4	2.92	1.51E-13

tRNA-Gly-1	tRNA-Gly-5	3.11	6.67E-11
tRNA-Gly-2	tRNA-Gly-6	5.16	1.63E-06
tRNA-Gly-3	tRNA-Gly-7	3.33	6.33E-06
tRNA-His-1	tRNA-His-1	3.67	8.56E-27
tRNA-His-2	tRNA-His-2	2.21	2.61E-05
tRNA-Ile-1	tRNA-Ile-1	7.64	2.50E-19
tRNA-Ile-2	tRNA-Ile-2	6.67	5.21E-17
tRNA-Leu-1	tRNA-Leu-1	5.09	5.71E-13
tRNA-Leu-2	tRNA-Leu-12	5.85	1.30E-07
tRNA-Leu-3	tRNA-Leu-2	2.56	5.61E-06
tRNA-Leu-4	tRNA-Leu-3	2.09	2.40E-04
tRNA-Leu-5	tRNA-Leu-4	4.94	3.32E-10
tRNA-Leu-6	tRNA-Leu-5	2.18	1.53E-10
tRNA-Leu-7	tRNA-Leu-6	2.19	3.39E-07
tRNA-Leu-8	tRNA-Leu-7	3.35	1.25E-09
tRNA-Leu-9	tRNA-Leu-8	5.53	4.61E-24
tRNA-Leu-10	tRNA-Leu-9	2.85	8.54E-04
tRNA-Lys-1	tRNA-Lys-1	3.64	7.05E-21
tRNA-Lys-2	tRNA-Lys-2	4.39	5.68E-19
tRNA-Met-1	tRNA-Met-2	3.56	2.05E-21
tRNA-Met-2	tRNA-Met-3	4.29	1.42E-23
tRNA-Met-3	tRNA-Met-4	4.91	2.19E-17
tRNA-Met-4	tRNA-Met-5	8.41	6.48E-21
tRNA-Met-5	tRNA-Met-6	6.98	2.81E-15
tRNA-Met-6	tRNA-Met-7	3.02	3.87E-04
tRNA-Met-7	tRNA-Met-9	2.17	2.12E-07
tRNA-Phe-1	tRNA-Phe-1	5.09	2.06E-38
tRNA-Phe-2	tRNA-Phe-2	5.79	3.29E-16
tRNA-Phe-3	tRNA-Phe-3	2.39	9.10E-19
tRNA-Pro-1	tRNA-Pro-2	4.08	5.37E-14
tRNA-Ser-1	tRNA-Ser-4	8.45	3.19E-43
tRNA-Ser-2	tRNA-Ser-5	7.49	6.15E-67
tRNA-Thr-1	tRNA-Thr-2	2.21	4.40E-13
tRNA-Thr-2	tRNA-Thr-3	2.22	1.07E-07
tRNA-Thr-3	tRNA-Thr-4	4.46	9.80E-14
tRNA-Thr-4	tRNA-Thr-5	7.09	6.36E-31
tRNA-Thr-5	tRNA-Thr-6	4.93	1.70E-17
tRNA-Trp-1	tRNA-Trp-1	3.26	1.23E-04
tRNA-Tyr-1	tRNA-Tyr-1	2.27	1.95E-14
tRNA-Tyr-2	tRNA-Tyr-2	2.90	2.79E-04
tRNA-Tyr-3	tRNA-Tyr-3	5.41	2.49E-14
tRNA-Tyr-4	tRNA-Tyr-4	4.66	9.34E-25
tRNA-Tyr-5	tRNA-Tyr-5	5.92	6.72E-25
tRNA-Val-1	tRNA-Val-2	2.81	1.71E-04
tRNA-Val-2	tRNA-Val-3	3.79	9.26E-20
tRNA-Val-3	tRNA-Val-4	3.36	3.40E-19
VC0006	ribonuclease P	2.07	1.03E-10
VC0007	ribosomal protein L34	2.25	3.27E-09
VC0011	chromosome replication initiator DnaA	2.30	2.46E-16
VC0015a	hypothetical protein	52.55	3.29E-87
VC0018	16 kDa heat shock protein A	3.30	4.73E-17
VC0022	conserved hypothetical protein	2.65	3.35E-20
VC0025	hypothetical protein	8.66	5.50E-51
VC0038	hypothetical protein	2.10	1.06E-06
VC0040	hemolysin, putative	3.14	6.65E-25
VC0051	phosphoribosylaminoimidazole carboxylase, ATPase subunit	2.02	4.16E-14
VC0052	phosphoribosylaminoimidazole carboxylase, catalytic subunit	2.93	9.32E-29
VC0059	hypothetical protein	5.79	8.37E-34
VC0061	thiamin biosynthesis protein ThiC	3.71	3.40E-38
VC0064	thiS protein	3.44	2.16E-03
VC0069	multidrug resistance protein, putative	2.99	4.61E-18
VC0070	hypothetical protein	3.37	6.71E-30
VC0074	hypothetical protein	2.38	5.09E-10
VC0083	ubiquinone/menaquinone biosynthesis methyltransferase	2.06	3.13E-11
VC0093	glycerol-3-phosphate acyltransferase	3.10	2.50E-26
VC0109	ribosome biogenesis GTP-binding protein YsxC	2.12	1.82E-14
VC0113	methyltransferase-related protein	2.47	3.65E-14
VC0114	conserved hypothetical protein	2.83	3.30E-28
VC0115	conserved hypothetical protein	4.93	4.84E-46
VC0120	porphobilinogen deaminase	2.16	7.11E-11

VC0123	cyaY protein	3.10	2.39E-21
VC0140	conserved hypothetical protein	2.55	3.71E-13
VC0142a	hypothetical protein	5.05	9.07E-22
VC0143	hypothetical protein	17.24	1.92E-73
VC0144	conserved hypothetical protein	2.15	2.18E-09
VC0154	tRNA (uracil-5-)-methyltransferase	2.54	4.40E-16
VC0156	vitamin B12 receptor	2.45	1.88E-14
VC0194	gamma-glutamyltranspeptidase	2.16	1.41E-10
VC0195	rarD protein	2.12	1.34E-06
VC0196	ATP-dependent DNA helicase RecQ	3.14	3.20E-23
VC0197	gene 3 protein-related protein	2.02	2.69E-05
VC0201	iron(III) ABC transporter, ATP-binding protein	2.09	1.29E-03
VC0210	ribonuclease PH	2.30	9.38E-12
VC0218	ribosomal protein L28	6.89	4.95E-37
VC0219	ribosomal protein L33	7.07	3.44E-55
VC0223	ADP-heptose--LPS heptosyltransferase II, putative	2.14	4.15E-16
VC0271	conserved hypothetical protein	2.62	2.06E-14
VC0275	phosphoribosylamine- glycine ligase	4.69	1.25E-31
VC0276	bifunctional phosphoribosylaminoimidazolecarboxamide formyltrans	4.31	9.46E-36
VC0290	Fis family transcriptional regulator	7.14	8.48E-66
VC0291	NifR3/Smm1 family protein	5.49	8.62E-64
VC0292	ribosomal protein L11 methyltransferase	3.02	2.00E-22
VC0302	conserved hypothetical protein	2.17	2.55E-11
VC0308	hypothetical protein	2.12	1.20E-11
VC0339	phosphatidylserine decarboxylase	2.08	2.23E-08
VC0341	oligoribonuclease	2.39	3.19E-20
VC0342	iron-sulfur cluster-binding protein	2.05	2.11E-14
VC0359	ribosomal protein S12	5.48	5.49E-17
VC0360	ribosomal protein S7	4.94	2.98E-13
VC0366	ribosomal protein S6	3.07	4.55E-11
VC0367	primosomal replication protein N	2.99	5.03E-14
VC0368	ribosomal protein S18	2.44	1.07E-11
VC0369	ribosomal protein L9	2.16	1.41E-08
VC0370	conserved hypothetical protein	2.03	6.35E-04
VC0390	B12-dependent methionine synthase	3.23	4.67E-20
VC0397	single-strand binding protein	3.52	1.17E-24
VC0424	conserved hypothetical protein	6.30	9.06E-44
VC0425	hypothetical protein	2.25	6.07E-10
VC0426	hypothetical protein	2.59	1.24E-06
VC0428	conserved hypothetical protein	2.06	4.04E-09
VC0431	arginine repressor	2.47	6.51E-13
VC0435	ribosomal protein L21	5.29	4.92E-15
VC0436	ribosomal protein L27	5.45	5.54E-40
VC0437	GTPase ObgE	3.31	4.40E-20
VC0438	conserved hypothetical protein	2.39	2.62E-13
VC0451	conserved hypothetical protein	2.05	4.45E-06
VC0453	tRNA (guanine-N(7)-)-methyltransferase	2.09	3.40E-15
VC0469	conserved hypothetical protein	5.72	5.79E-48
VC0476	D-erythrose 4-phosphate dehydrogenase	3.05	1.73E-29
VC0483	conserved hypothetical protein	3.87	9.40E-26
VC0509	hypothetical protein	2.77	1.08E-03
VC0516	phage integrase	2.85	3.26E-21
VC0518	DNA primase	2.09	2.10E-10
VC0520	30S ribosomal protein S21	2.25	6.57E-21
VC0527	cell division protein FtsB	3.23	4.81E-20
VC0542	CinA-related protein	3.03	4.54E-31
VC0543	recombinase A	2.19	1.20E-08
VC0544	recombination regulator RecX	2.19	1.19E-06
VC0561	ribosomal protein S16	3.65	2.66E-22
VC0562	16S rRNA processing protein RimM	3.22	5.83E-14
VC0564	ribosomal protein L19	2.28	2.31E-21
VC0576	stringent starvation protein A	2.37	3.02E-15
VC0582	conserved hypothetical protein	2.38	1.08E-15
VC0585	hypoxanthine phosphoribosyltransferase	2.92	9.63E-17
VC0587	sulfate permease family protein	2.74	4.26E-17
VC0596	dnaK suppressor protein	5.20	1.12E-31
VC0605	conserved hypothetical protein	2.04	9.96E-06
VC0635	conserved hypothetical protein	4.10	8.80E-27
VC0636	23S rRNA methyltransferase	2.13	6.95E-09
VC0640	preprotein translocase subunit SecG	2.98	2.92E-14

VC0641	conserved hypothetical protein	3.27	7.38E-40
VC0642	N utilization substance protein A	2.67	1.88E-18
VC0646	ribosomal protein S15	2.92	2.46E-13
VC0647	polyribonucleotide nucleotidyltransferase	2.39	6.55E-07
VC0649	transcriptional regulator, MarR family	4.40	4.71E-32
VC0650	multidrug efflux pump VmrA	3.17	3.97E-28
VC0654	conserved hypothetical protein	3.58	7.11E-30
VC0660	ATP-dependent RNA helicase SrmB	2.45	5.62E-15
VC0668	DNA mismatch repair protein MthH	2.67	2.81E-12
VC0679	ribosomal protein S20	5.40	5.62E-23
VC0681	riboflavin kinase/FMN adenylyltransferase	2.12	3.40E-13
VC0693	response regulator	2.65	4.13E-13
VC0694	conserved hypothetical protein	2.92	2.56E-16
VC0695	phospho-2-dehydro-3- deoxyheptonate aldolase,tyr-sensitive	7.53	2.67E-70
VC0709	23S rRNA pseudouridine synthase D	2.97	7.11E-18
VC0710	conserved hypothetical protein	2.57	4.19E-26
VC0717	protease, putative	2.33	4.79E-14
VC0718	conserved hypothetical protein	3.20	1.54E-22
VC0734	malate synthase A	5.80	9.78E-45
VC0736	isocitrate lyase	2.72	1.63E-16
VC0738	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	4.38	7.99E-38
VC0739	S-adenosylmethionine :tRNAribosyltransferase-isomerase	2.27	2.30E-20
VC0745	inositol monophosphate family protein	4.04	1.79E-57
VC0746	RNA methyltransferase, TrmH family	3.01	5.83E-19
VC0750	hesB family protein	2.80	1.88E-16
VC0757	conserved hypothetical protein	3.34	2.60E-27
VC0767	inosine-5'-monophosphate dehydrogenase	2.55	3.46E-15
VC0791	sensor kinase citA	3.04	1.24E-15
VC0804	ferredoxin	2.31	1.32E-06
VC0806	conserved hypothetical protein	2.99	8.96E-18
VC0807	hypothetical protein	9.61	2.26E-69
VC0847	integrase, phage family	4.06	8.23E-48
VC0854	heat shock protein GrpE	2.27	2.22E-10
VC0864	yfhC protein	2.05	5.45E-07
VC0869	phosphoribosylformyl glycinamide synthase	2.81	1.86E-15
VC0870	IS1004 transposase	6.73	8.00E-33
VC0871	hypothetical protein	2.65	3.19E-11
VC0872	conserved hypothetical protein	2.76	2.40E-13
VC0873	conserved hypothetical protein	2.91	1.41E-13
VC0875	prolyl-tRNA synthetase	2.59	1.88E-17
VC0877	hypothetical protein	13.82	9.58E-92
VC0879	50S ribosomal protein L36	6.56	1.14E-23
VC0880	conserved hypothetical protein	2.30	1.97E-14
VC0888	pseudouridine synthase Rlu family protein	2.29	1.45E-05
VC0891	exodeoxyribonuclease , small subunit	2.17	6.48E-09
VC0894	thiamin biosynthesis protein Thil	4.60	2.05E-28
VC0906	ABC transporter, permease protein	2.07	1.60E-13
VC0907	ABC transporter, ATP-binding protein	3.44	1.19E-23
VC0908	histidinol phosphatase-related protein	2.40	4.65E-21
VC0916	phosphotyrosine protein phosphatase	57.66	3.04E-41
VC0917	UDP-N-acetylglucosamine 2-epimerase	2.92	2.20E-08
VC0934	capsular polysaccharide biosynthesisglycosyltransferase, putative	4.86	2.30E-10
VC0945	conserved hypothetical protein	7.43	3.64E-74
VC0952	conserved hypothetical protein	2.02	8.23E-13
VC0962	conserved hypothetical protein	3.67	7.80E-23
VC0963	VisC-related protein	2.52	2.58E-17
VC0986	adenylate kinase	3.02	1.10E-14
VC0987	ferrochelatase	2.21	5.56E-18
VC1002	dedD protein	2.13	6.38E-09
VC1003	bacteriocin production protein	2.97	2.01E-22
VC1006	ribonuclease T	3.70	1.85E-29
VC1017	RnfA-related protein	2.04	1.32E-07
VC1040	cob(I)alamin adenosyltransferase	2.85	1.01E-14
VC1046	3-ketoacyl-CoA thiolase	6.40	7.46E-46
VC1047	multifunctional fatty acid oxidation complex subunit alpha	5.85	1.06E-41
VC1058	conserved hypothetical protein	2.20	3.88E-09
VC1068	transcriptional regulator, ArsR family	2.13	3.80E-05
VC1078	hypothetical protein	2.20	1.19E-06
VC1079	conserved hypothetical protein	4.11	1.07E-29
VC1105	conserved hypothetical protein	2.62	4.01E-13

VC1107	outer-membrane lipoprotein carrier protein	2.10	1.32E-15
VC1111	adenosylmethionine-8-amino-7-oxononanoateaminotransferase	3.07	9.17E-13
VC1112	biotin synthase	4.26	9.86E-24
VC1113	8-amino-7-oxononanoate synthase	2.65	6.74E-12
VC1114	biotin synthesis protein BioC	3.49	1.16E-17
VC1115	dithiobiotin synthetase	2.05	6.07E-16
VC1116	hypothetical protein	7.00	2.03E-48
VC1117	heat shock protein HtpX	2.45	5.48E-14
VC1118	transcriptional regulator, putative	10.59	4.65E-81
VC1119	oxidoreductase, short-chain dehydrogenase/reductase family	5.00	2.05E-37
VC1120	conserved hypothetical protein	4.65	1.30E-41
VC1121	conserved hypothetical protein	3.36	2.36E-29
VC1122	cyclopropane-fatty-acyl-phospholipid synthase	5.41	2.08E-42
VC1123	hypothetical protein	4.88	3.80E-40
VC1126	adenylosuccinate lyase	2.03	1.32E-06
VC1128	tRNA-specific 2-thiouridylase MnmA	2.08	1.70E-16
VC1132	ATP phosphoribosyltransferase	2.64	2.46E-15
VC1146	glutaredoxin 1	3.71	2.25E-31
VC1152	hypothetical protein	2.50	1.82E-25
VC1191	hypothetical protein	3.29	1.20E-24
VC1193	hypothetical protein	6.29	3.47E-47
VC1196	hypothetical protein	2.03	4.06E-08
VC1208	conserved hypothetical protein	2.01	6.68E-09
VC1209	elongation factor P family protein	2.12	1.66E-10
VC1221	hypothetical protein	2.22	1.21E-08
VC1228	phosphoribosylglycinamide formyltransferase 2	2.34	2.32E-11
VC1237	nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase	3.84	1.24E-28
VC1238	adenosylcobinamide-GDP ribazoletransferase	3.49	5.41E-19
VC1239	cobinamide kinase/cobinamide phosphoguananylyltransferase	3.84	5.99E-19
VC1240	alpha-ribazole-5'-phosphate phosphatase CobC, putative	2.27	2.27E-05
VC1246	hypothetical protein	2.28	7.73E-18
VC1253	hypothetical protein	4.41	4.56E-34
VC1257	3-demethylubiquinone-9-3-methyltransferase	2.06	7.25E-15
VC1258	DNA gyrase, subunit A	2.47	2.47E-07
VC1259	conserved hypothetical protein	4.67	1.38E-19
VC1262	hypothetical protein	3.09	5.84E-12
VC1263	GTP cyclohydrolase II	6.90	3.29E-68
VC1271	hypothetical protein	3.23	8.49E-17
VC1278	transcriptional regulator, MarR family	3.97	1.96E-45
VC1279	transporter, BCCT family	3.07	3.79E-18
VC1296	phosphomethylpyrimidine kinase	2.40	1.22E-11
VC1299	6-pyruvoyl tetrahydrobiopterin synthase, putative	2.72	3.51E-07
VC1300	L-serine dehydratase 1	2.01	5.37E-08
VC1306	conserved hypothetical protein	2.72	3.33E-13
VC1341	acetyltransferase, putative	3.78	2.66E-27
VC1342	MutT/nudix family protein	2.15	6.83E-11
VC1350	antioxidant, putative	5.52	1.64E-53
VC1354	conserved hypothetical protein	4.32	2.28E-53
VC1358	conserved hypothetical protein	3.95	8.44E-13
VC1363	siroheme synthase component enzyme	2.06	2.43E-11
VC1365	conserved hypothetical protein	2.94	4.69E-16
VC1366	exsB protein	3.44	5.24E-31
VC1368	hypothetical protein	2.68	1.36E-10
VC1374	DnaK-related protein	2.01	5.06E-08
VC1375	hypothetical protein	3.55	4.97E-14
VC1382	ATP-dependent helicase HrpA	2.23	7.59E-17
VC1386	heat shock protein 70 family protein	2.91	6.16E-14
VC1387	lipoate-protein ligase A	2.27	1.93E-10
VC1389	hypothetical protein	19.85	2.78E-09
VC1390	transcriptional regulator, LysR family	3.44	9.15E-15
VC1392	deoxyribodipyrimidine photolyase, putative	6.04	3.70E-74
VC1422a	membrane protein	2.85	1.21E-16
VC1423	hypothetical protein	2.83	1.09E-26
VC1424	spermidine/putrescine ABC transporter, periplasmic spermidine/putrescine ABC transporter	2.26	1.86E-12
VC1428	putrescine/spermidine ABC transporter ATPase protein	2.42	9.81E-17
VC1432	conserved hypothetical protein	2.21	1.46E-12
VC1434	fumarate and nitrate reduction regulatory protein	2.47	3.63E-13
VC1449	hypothetical protein	3.15	9.85E-14
VC1452	RstC protein	2.26	4.38E-05
VC1454	RstA1 protein	770.61	4.06E-04



VC1455	transcriptional repressor RstR	3.73	1.68E-28
VC1464	transcriptional repressor RstR	3.85	9.51E-27
VC1465	hypothetical protein	2.01	5.75E-13
VC1467	hypothetical protein	3.02	2.82E-30
VC1473	hypothetical protein	3.01	3.64E-30
VC1486	ABC transporter, ATP-binding protein	2.11	1.06E-09
VC1487	conserved hypothetical protein	3.80	4.92E-16
VC1488	23S rRNA m(2)G2445 methyltransferase	2.33	1.30E-13
VC1491	dihydroorotate dehydrogenase	2.50	2.87E-15
VC1502	16S rRNA (cytosine(1407)-C(5))-methyltransferase RsmF	2.82	1.62E-25
VC1503	conserved hypothetical protein	4.10	2.40E-30
VC1505	hypothetical protein	3.65	4.53E-32
VC1506	hypothetical protein	4.84	3.48E-41
VC1520	ABC transporter, ATP-binding protein	2.47	7.60E-13
VC1530	hypothetical protein	6.45	5.02E-22
VC1531	hypothetical protein	2.34	7.92E-20
VC1541	hypothetical protein	3.20	3.12E-12
VC1552	glycerol-3-phosphate transporter ATP-binding subunit, ugpC	2.19	3.87E-04
VC1605	sensor kinase citA, putative	2.26	2.04E-18
VC1605a	hypothetical protein	3.22	5.20E-15
VC1610	hypothetical protein	3.61	1.17E-19
VC1616	glutaredoxin, putative	2.73	1.13E-12
VC1630	ABC transporter, ATP-binding protein	2.14	4.35E-16
VC1635	ribosomal small subunit pseudouridine synthaseA	4.13	1.30E-31
VC1637	hypothetical protein	8.21	1.62E-55
VC1638	DNA-binding response regulator	4.48	2.29E-26
VC1639	sensor histidine kinase	2.77	1.48E-16
VC1645	conserved hypothetical protein	3.72	4.45E-29
VC1668	pseudouridine synthase Rlu family protein	2.34	5.31E-12
VC1686	hypothetical protein	3.02	1.44E-31
VC1687	conserved hypothetical protein	2.30	6.95E-09
VC1701	conserved hypothetical protein	2.81	1.19E-09
VC1704	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	13.44	8.15E-159
VC1708	conserved hypothetical protein	2.64	1.11E-13
VC1711	conserved hypothetical protein	3.84	6.67E-25
VC1719	DNA-binding response regulator TorR	8.60	1.60E-74
VC1720	chaperone protein TorD	2.03	2.15E-05
VC1722	conserved hypothetical protein	3.26	9.28E-28
VC1725	beta-ketoadipate enol-lactone hydrolase, putative	2.53	1.72E-24
VC1731	conserved hypothetical protein	4.03	8.27E-26
VC1737	translation initiation factor IF-1	4.10	1.61E-27
VC1740	oxidoreductase, acyl-CoA dehydrogenase family	7.88	3.05E-50
VC1741	transcriptional regulator, TetR family	8.10	1.40E-109
VC1785	transcriptional regulator	4.03	2.02E-04
VC1801	hypothetical protein	4.00	1.14E-08
VC1803	hypothetical protein	2.64	9.26E-15
VC1804	hypothetical protein	2.02	3.77E-05
VC1810	hypothetical protein	2.83	1.03E-19
VC1811	conserved hypothetical protein	3.13	3.02E-23
VC1812	conserved hypothetical protein	4.41	1.00E-12
VC1814	deoxyribodipyrimidine photolyase	15.11	4.31E-62
VC1815	C-factor, putative	10.31	1.64E-47
VC1816	hypothetical protein	3.70	2.43E-12
VC1823	PTS system, fructose-specific IIB component	3.03	1.67E-11
VC1832	hypothetical protein	2.13	1.30E-17
VC1833	quinolinate synthetase A	2.23	2.59E-19
VC1835	peptidoglycan-associated lipoprotein	2.27	1.53E-07
VC1837	tolA protein	2.19	6.11E-13
VC1838	tolR membrane protein	2.29	5.77E-13
VC1839	tolQ protein	3.17	5.40E-22
VC1840	conserved hypothetical protein	8.64	1.10E-115
VC1845	Holliday junction DNA helicase RuvB	2.42	2.31E-18
VC1846	Holliday junction DNA helicase RuvA	2.67	1.19E-16
VC1849	peptidyl-prolyl cis-trans isomerase B	3.30	4.03E-22
VC1860	exodeoxyribonuclease III	2.71	4.14E-15
VC1863	amino acid ABC transporter, periplasmic amino acid-binding protein	2.02	3.93E-09
VC1864	amino acid ABC transporter, ATP-binding protein	2.40	3.55E-12
VC1876	conserved hypothetical protein	2.39	1.99E-09
VC1883	ABC transporter, ATP-binding protein	2.20	4.56E-10

VC1890	NADH dehydrogenase	2.77	8.51E-17
VC1906	hypothetical protein	2.08	5.15E-08
VC1913	conserved hypothetical protein	3.54	6.93E-26
VC1915	ribosomal protein S1	2.11	1.36E-03
VC1916	cytidylate kinase	2.43	9.70E-12
VC1924	hypothetical protein	2.29	2.70E-09
VC1927	C4-dicarboxylate transport protein	5.19	1.09E-34
VC1929	C4-dicarboxylate-binding periplasmic protein	7.73	2.56E-19
VC1931	conserved hypothetical protein	2.76	3.76E-24
VC1938	conserved hypothetical protein	2.38	4.70E-20
VC1942	methylenetetrahydrofolate dehydrogenase/methylenetetrahydrofolate	2.03	3.22E-12
VC1961	cell division topological specificity factor MinE	2.67	2.27E-14
VC1963	conserved hypothetical protein	2.25	7.15E-11
VC1964	hypothetical protein	4.83	3.03E-20
VC1980	conserved hypothetical protein	2.36	2.41E-09
VC1983	peptidase, putative	2.74	7.03E-20
VC1993	2,4-dienoyl-CoA reductase	2.89	1.01E-16
VC2020	acyl carrier protein	2.42	4.75E-12
VC2025	ribosomal protein L32	2.54	3.07E-12
VC2026	conserved hypothetical protein	2.66	6.28E-06
VC2027	Maf-like protein	2.79	7.64E-27
VC2028	ribosomal large subunit pseudouridine synthase C	2.38	1.44E-20
VC2031	sulfate permease family protein	2.31	1.03E-11
VC2035	conserved hypothetical protein	2.25	1.01E-16
VC2042	histone deacetylase/AcuC/AphA family protein	3.14	1.02E-16
VC2044	conserved hypothetical protein	7.01	1.75E-51
VC2057	heme exporter protein A	2.40	1.89E-15
VC2073	conserved hypothetical protein	2.34	9.71E-08
VC2078	ferrous iron transport protein A	4.21	2.12E-13
VC2081	zinc ABC transporter, periplasmic zinc-binding protein	2.33	8.94E-14
VC2082	zinc ABC transporter, ATP-binding protein	4.70	3.79E-32
VC2098	hypothetical protein	2.02	4.47E-14
VC2115	conserved hypothetical protein	2.05	3.24E-09
VC2134	flagellar hook-basal body protein FlIE	2.38	3.44E-11
VC2146	conserved hypothetical protein	2.55	7.11E-23
VC2160	thioredoxin-dependent thiol peroxidase	2.55	4.78E-18
VC2163	conserved hypothetical protein	2.64	1.53E-14
VC2180	glutamyl-tRNA reductase	2.76	3.43E-21
VC2184	peptidyl-tRNA hydrolase	2.92	1.22E-24
VC2185	GTP-binding protein	2.17	1.14E-10
VC2213	outer membrane protein OmpA	2.45	1.08E-04
VC2214	glutamyl-tRNA synthetase	2.39	3.40E-13
VC2215	cation transport ATPase, E1-E2 family	2.01	3.72E-12
VC2223	pseudouridine synthase family 1 protein	2.47	9.03E-14
VC2226	phosphoribosylformyl glycinamide cyclo-ligase	2.79	4.66E-15
VC2227	phosphoribosylglycinamide formyltransferase	2.90	6.91E-22
VC2239	nitrogen regulatory protein P-II	2.85	4.65E-15
VC2259	elongation factor Ts	2.89	1.26E-08
VC2268	6,7-dimethyl-8-ribityllumazine synthase	2.20	1.69E-10
VC2272	transcriptional regulator NrdR	2.73	1.99E-17
VC2296	bolA protein	5.38	1.11E-81
VC2301	transcriptional activator, putative	52.55	3.29E-87
VC2302	RNA polymerase sigma-70 factor, ECF subfamily	5.01	1.58E-46
VC2303	conserved hypothetical protein	17.42	2.97E-107
VC2305	outer membrane protein OmpK	4.26	3.18E-40
VC2311	HesA/MoeB/ThiF family protein	2.30	6.30E-11
VC2318	hypothetical protein	16.03	6.47E-111
VC2326	conserved hypothetical protein	5.14	5.82E-35
VC2342	elongation factor G	2.14	2.38E-04
VC2346	smp protein, putative	2.39	8.75E-20
VC2361	formate acetyl transferase-related protein	2.30	1.43E-04
VC2388	hypothetical protein	2.46	4.29E-08
VC2389	carbamoyl-phosphate synthase, large subunit	9.74	4.42E-65
VC2390	carbamoyl-phosphate synthase, small subunit	6.18	2.83E-47
VC2444	general secretion pathway protein B, putative	2.02	4.41E-07
VC2478	conserved hypothetical protein	2.89	7.72E-14
VC2479	conserved hypothetical protein	2.08	1.56E-08
VC2480	ribose-5-phosphate isomerase	2.63	1.18E-16
VC2484	long-chain-fatty-acyl-CoA ligase, putative	5.57	6.68E-61
VC2485	transcriptional regulator, LysR family	3.45	1.60E-26

VC2500	conserved hypothetical protein	3.23	4.03E-39
VC2509	aspartate carbamoyltransferase	3.68	1.29E-30
VC2511	aspartate carbamoyltransferase, regulatory subunit	5.44	1.57E-44
VC2512	conserved hypothetical protein	2.51	3.74E-14
VC2540	hypothetical protein	4.03	5.34E-20
VC2541	3-octaprenyl-4-hydroxybenzoate carboxy-lyase	3.21	1.25E-30
VC2542	UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate transferase	3.43	1.44E-33
VC2551	conserved hypothetical protein	2.16	2.41E-10
VC2554	conserved hypothetical protein	2.06	2.45E-08
VC2555	hypothetical protein	3.08	9.43E-17
VC2562	bifunctional 2',3'-cyclic nucleotide 2'-phosphodiesterase/3'-nucleotidyl transferase	2.04	7.76E-08
VC2563	hypothetical protein	2.50	1.66E-13
VC2564	ATP-dependent RNA helicase DbpA	2.41	3.00E-10
VC2568	peptidyl-prolyl cis-trans isomerase, FKBP-type	2.88	1.24E-14
VC2569	hypothetical protein	3.51	1.76E-21
VC2582	ribosomal protein S8	2.10	3.85E-07
VC2583	ribosomal protein S14	2.44	1.40E-11
VC2584	ribosomal protein L5	2.89	1.76E-07
VC2585	ribosomal protein L24	5.26	8.46E-15
VC2586	ribosomal protein L14	4.43	5.38E-13
VC2594	ribosomal protein L23	2.31	1.68E-10
VC2597	ribosomal protein S10	2.29	6.74E-10
VC2600	conserved hypothetical protein	3.51	1.28E-30
VC2617	arginine/ornithine succinyltransferase, putative	2.05	5.66E-09
VC2618	acetylornithine aminotransferase	2.37	1.57E-10
VC2624	phosphoglycolate phosphatase	2.04	1.42E-08
VC2625	ribulose-phosphate 3-epimerase	2.04	7.58E-15
VC2629	shikimate kinase I	2.61	1.69E-22
VC2642	argininosuccinate synthase	4.59	1.94E-38
VC2643	acetylglutamate kinase	7.65	2.81E-58
VC2644	N-acetyl-gamma-glutamyl-phosphate reductase	13.23	4.12E-97
VC2647	conserved hypothetical protein	3.07	1.84E-22
VC2660	elongation factor P	3.23	2.14E-24
VC2662	conserved hypothetical protein	4.61	3.54E-28
VC2670	triosephosphate isomerase	2.90	1.21E-13
VC2675	protease HsIV, subunit HsIV	2.92	2.92E-24
VC2679	ribosomal protein L31	4.32	7.95E-28
VC2682	met repressor	3.73	8.95E-39
VC2685	5,10-methylenetetrahydrofolate reductase	3.74	1.79E-28
VC2687	glutamyl-tRNA synthetase	2.70	9.20E-16
VC2712	xanthine/uracil permease family protein	2.30	4.22E-10
VC2715	transcription elongation factor GreB	2.05	6.74E-06
VC2717	hypothetical protein	2.24	3.87E-09
VC2718	bioH protein	2.83	4.23E-13
VC2735	conserved hypothetical protein	2.09	1.67E-08
VC2744	GTP-binding protein TypA	2.07	4.77E-11
VC2753	hypothetical protein	6.07	3.08E-30
VC2757	conserved hypothetical protein	3.81	4.37E-34
VC2758	multifunctional fatty acid oxidation complex subunit alpha	6.02	1.48E-29
VC2759	3-ketoacyl-CoA thiolase	5.41	8.40E-31
VC2774	glucose inhibited division protein B	2.85	1.12E-20
VC2775	glucose inhibited division protein A	3.11	5.61E-39
VCA0005	hypothetical protein	2.58	2.86E-22
VCA0010	conserved hypothetical protein	13.25	5.69E-90
VCA0035	phosphatidylglycerol phosphatase B, putative	2.92	2.74E-18
VCA0040	conserved hypothetical protein	2.46	5.18E-22
VCA0076	conserved hypothetical protein	7.58	2.41E-80
VCA0086	hypothetical protein	7.44	6.08E-80
VCA0087	hypothetical protein	8.94	5.82E-33
VCA0098	nicotinate phosphoribosyltransferase	3.66	1.42E-40
VCA0125	hypothetical protein	6.81	1.70E-94
VCA0133	pseudogene	2.48	1.32E-11
VCA0139	hypothetical protein	6.82	2.28E-47
VCA0143	hypothetical protein	3.04	2.40E-04
VCA0149	hypothetical protein	4.18	1.98E-21
VCA0158	hypothetical protein	3.96	9.80E-27
VCA0159	conserved hypothetical protein	4.38	5.48E-64
VCA0166	cold shock transcriptional regulator CspA	3.76	1.48E-10
VCA0177	hypothetical protein	2.74	4.45E-16
VCA0179	NupC family protein	2.36	5.07E-06

VCA0184	cold shock DNA-binding domain protein	2.67	2.31E-11
VCA0185	conserved hypothetical protein	3.55	9.71E-14
VCA0197	GMP reductase	2.66	9.55E-13
VCA0198	site-specific DNA-methyltransferase, putative	2.93	3.70E-26
VCA0204	ATP-dependent RNA helicase RhlE	2.89	1.99E-19
VCA0215	multidrug resistance protein D	8.05	2.03E-109
VCA0240	hypothetical protein	2.02	1.58E-05
VCA0246	PTS system ascorbate-specific transporter subunits IICB	2.08	7.69E-08
VCA0269	decarboxylase, group II	4.59	5.30E-39
VCA0279	transcriptional regulator, HTH_3 family	8.66	5.50E-51
VCA0287	threonyl-tRNA synthetase	2.37	4.60E-07
VCA0288	initiation factor IF3	3.43	1.36E-08
VCA0289	ribosomal protein L35	4.09	1.52E-16
VCA0290	ribosomal protein L20	3.74	7.27E-15
VCA0332	conserved hypothetical protein	2.99	4.68E-18
VCA0333	hypothetical protein	2.83	3.28E-28
VCA0349	relB protein	2.03	2.57E-07
VCA0369	hypothetical protein	5.85	4.21E-04
VCA0385	conserved hypothetical protein	2.21	2.75E-09
VCA0391	killer protein, putative	3.03	8.92E-26
VCA0392	antidote protein, putative	2.44	2.64E-14
VCA0422	conserved hypothetical protein	3.30	4.39E-33
VCA0423	conserved hypothetical protein	3.65	4.39E-40
VCA0426	conserved hypothetical protein	2.40	2.65E-10
VCA0444	relE protein	3.04	1.94E-19
VCA0445	conserved hypothetical protein	3.19	1.13E-16
VCA0468	hypothetical protein	3.09	3.72E-24
VCA0481	conserved hypothetical protein	2.10	1.69E-09
VCA0486	hypothetical protein	3.75	1.76E-32
VCA0487	conserved hypothetical protein	2.39	1.40E-22
VCA0488	conserved hypothetical protein	2.68	5.78E-18
VCA0490	lipase, GDYG family	3.59	1.96E-22
VCA0491	hypothetical protein	3.63	4.06E-25
VCA0492	pseudogene	3.06	2.63E-29
VCA0493	IS1004 transposase	3.09	4.51E-14
VCA0494	hypothetical protein, interruption	3.96	5.99E-11
VCA0497	hypothetical protein	2.35	2.47E-15
VCA0503	conserved hypothetical protein	2.35	4.24E-11
VCA0504	relB protein	2.30	3.12E-09
VCA0505	acetyltransferase, putative	2.22	1.71E-10
VCA0506	conserved hypothetical protein	2.14	1.26E-08
VCA0518	PTS system, fructose-specific IIA/FPR component	4.65	1.78E-31
VCA0520	exonuclease SbcD, putative	3.19	3.63E-31
VCA0531	sensor histidine kinase	2.89	1.99E-24
VCA0532	DNA-binding response regulator	2.24	7.24E-09
VCA0535	hypothetical protein	5.38	5.93E-71
VCA0546	conserved hypothetical protein	3.56	4.82E-30
VCA0547	hypothetical protein	3.17	8.12E-17
VCA0549	phnA protein	3.04	2.09E-35
VCA0575	transcriptional regulator, LysR family	2.05	2.72E-14
VCA0580	conserved hypothetical protein	2.15	3.21E-16
VCA0582	conserved hypothetical protein	3.21	7.18E-20
VCA0586	conserved hypothetical protein	3.56	1.83E-10
VCA0587	conserved hypothetical protein	2.76	1.89E-09
VCA0596	pseudogene	2.73	1.30E-12
VCA0608	conserved hypothetical protein	2.78	1.62E-27
VCA0614	formate--tetrahydrofolate ligase	3.72	8.45E-43
VCA0616	GTP cyclohydrolase I	2.07	4.16E-08
VCA0627	rRNA methylase, putative	2.42	1.26E-07
VCA0634	conserved hypothetical protein	2.54	2.24E-11
VCA0635	transcriptional regulator, LysR family	2.20	3.41E-06
VCA0652	hypothetical protein	3.81	7.06E-22
VCA0693	preprotein translocase subunit SecD	3.80	1.48E-21
VCA0694	hypothetical protein	3.48	3.09E-29
VCA0707	regulatory protein UhpC, putative	3.74	6.71E-19
VCA0732	conserved hypothetical protein	10.18	3.60E-41
VCA0733	hypothetical protein	16.28	2.11E-48
VCA0741	conserved hypothetical protein	2.60	7.59E-14
VCA0742	hypothetical protein	2.27	6.48E-07
VCA0753	conserved hypothetical protein	2.70	6.19E-10

VCA0754	lipase-related protein	2.28	1.33E-06
VCA0758	arginine ABC transporter, permease protein	2.51	8.07E-11
VCA0759	arginine ABC transporter, periplasmic arginine-binding protein	4.78	8.04E-32
VCA0760	arginine ABC transporter, ATP-binding protein	3.07	1.93E-21
VCA0768	ATP-dependent RNA helicase, DEAD box family	3.13	3.00E-34
VCA0770	hypothetical protein	2.94	4.75E-13
VCA0779	hypothetical protein	2.49	9.52E-15
VCA0793	hypothetical protein	2.96	1.83E-11
VCA0794	hypothetical protein	4.05	1.62E-11
VCA0795	resolvase, putative	2.54	1.09E-17
VCA0804	ATP-dependent RNA helicase Dead	3.84	2.19E-22
VCA0805	exoribonuclease II	2.00	4.63E-15
VCA0809	conserved hypothetical protein	2.88	4.30E-19
VCA0821	hypothetical protein	2.29	4.27E-09
VCA0831	hypothetical protein	2.31	4.65E-04
VCA0834	hypothetical protein	2.01	9.21E-10
VCA0837	hemolysin, putative	2.13	4.68E-10
VCA0838	conserved hypothetical protein	6.12	9.28E-63
VCA0843	glyceraldehyde 3-phosphate dehydrogenase	2.19	6.33E-14
VCA0845	hypothetical protein	6.81	8.45E-49
VCA0846	conserved hypothetical protein	4.22	7.56E-30
VCA0847	conserved hypothetical protein	6.06	3.93E-34
VCA0862	long-chain fatty acid transport protein	2.37	1.29E-10
VCA0863	lipase, putative	2.78	2.61E-15
VCA0890	glyoxylase I family protein	2.26	2.83E-07
VCA0893	hypothetical protein	4.21	1.68E-34
VCA0898	6-phosphogluconate dehydrogenase, decarboxylating	2.19	2.41E-10
VCA0899	hypothetical protein	9.48	5.23E-23
VCA0902	hypothetical protein	3.27	5.86E-25
VCA0925	dihydroorotase	3.17	5.99E-24
VCA0926	transcriptional regulator, AraC/XylS family	2.68	2.14E-15
VCA0927	conserved hypothetical protein	2.42	4.55E-08
VCA0933	cold shock domain family protein	7.50	5.01E-44
VCA0938	pseudogene	3.50	4.82E-24
VCA0953	peptidyl-prolyl cis-trans isomerase C	2.19	1.59E-09
VCA0989	conserved hypothetical protein	2.89	5.46E-28
VCA1004	conserved hypothetical protein	2.58	7.62E-13
VCA1005	transcriptional regulator, MarR family	2.45	9.77E-08
VCA1012	conserved hypothetical protein	2.06	6.67E-05
VCA1013	conserved hypothetical protein	2.20	4.29E-09
VCA1035	hypothetical protein	2.01	1.85E-07
VCA1044	hypothetical protein	3.68	2.52E-32
VCA1051	conserved hypothetical protein	2.00	5.15E-07
VCA1058	transcriptional regulator, LysR family	2.26	7.28E-07
VCA1073	bifunctional proline dehydrogenase/pyrroline-5-carboxylate dehydro	2.30	1.88E-09
VCA1078	transcriptional regulator, LuxR family	2.02	1.08E-13
VCA1111	thermostable hemolysin	2.96	2.81E-06

126 differentially-expressed genes common to both $\Delta ompU$ and $\Delta rpoE$ compared to the WT					
Name	Function	FC	FDR p-value	FC $\Delta rpoE$	FDR p-value
16Sh	16Sh	-2.33	7.18E-07	-14.86	4.22E-24
5Sb	5Sb	4.89	4.55E-07	-134.06	1.60E-42
5Sc	5Sc	15.97	9.85E-05	-6749.82	5.39E-96
5Sd	5Sd	8.98	3.91E-04	-18963.94	9.00E-47
5Sf	5Sf	7.07	6.64E-05	-1328.85	2.23E-165
5Sh	5Sh	3.07	8.58E-04	-104.01	5.06E-35
tRNA-Arg-	tRNA-Arg-1	-2.37	5.68E-04	3.43	2.00E-15
tRNA-Gly-	tRNA-Gly-8	-2.14	1.70E-04	5.58	3.56E-21
tRNA-Met-	tRNA-Met-8	-2.88	8.91E-06	2.34	1.75E-07
VC0017	hypothetical protein	2.66	3.25E-07	55.57	1.21E-126
VC0062	thiamin-phosphate pyrophosphorylase	2.85	3.43E-04	3.28	1.12E-12
VC0063	thiF protein	3.13	4.31E-06	2.17	5.22E-07
VC0091	O-methyltransferase- related protein	3.70	8.88E-09	2.50	7.91E-13
VC0107	hypothetical protein	8.41	8.16E-19	19.52	3.08E-55
VC0157	alkaline serine protease	4.50	2.07E-14	-3.76	1.14E-49
VC0181	conserved hypothetical protein	-2.19	3.52E-04	-2.94	4.51E-25
VC0364	bacterioferritin-associated ferredoxin	3.25	2.53E-07	4.95	4.53E-45
VC0379a	phage shock protein G	-2.16	1.54E-06	3.31	1.34E-34
VC0475	iron-regulated outer membrane virulence protein, TonB receptor fam	8.15	2.02E-40	6.82	1.95E-52
VC0494	conserved hypothetical protein	-2.94	8.03E-06	3.86	6.19E-11

VC0503	conserved hypothetical protein	-3.27	9.60E-14	2.05	4.62E-09
VC0566	protease DO	-2.31	2.88E-07	-9.28	3.02E-78
VC0608	iron(III) ABC transporter, periplasmic iron-compound-binding protein	4.76	1.21E-14	6.66	5.37E-54
VC0676	nptA protein	4.54	1.54E-17	6.60	1.36E-36
VC0747	conserved hypothetical protein	2.24	1.34E-05	2.70	7.67E-29
VC0748	aminotransferase NifS, class V	2.13	4.83E-04	2.64	5.88E-18
VC0749	NifU-related protein	2.28	3.31E-05	2.50	1.73E-21
VC0754	conserved hypothetical protein	2.20	4.81E-05	2.24	4.17E-06
VC0771	vibriobactin-specific isochorismatase	8.03	3.45E-15	2.80	5.69E-07
VC0774	vibriobactin-specific 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase	5.82	1.08E-16	2.45	2.07E-03
VC0776	ferric vibriobactin ABC transporter, periplasmic ferric vibriobactin-binding protein	4.16	3.49E-13	2.90	2.62E-08
VC0818	pseudogene; within VPI-I; unknown function	-2.18	4.36E-04	2.17	1.20E-06
VC0825	toxin co-regulated pilus biosynthesis protein I	-2.13	3.69E-04	2.48	1.93E-09
VC0827	toxin co-regulated pilus biosynthesis protein H	2.53	9.33E-08	6.22	2.09E-86
VC0828	toxin co-regulated pilin	2.54	2.88E-06	4.21	4.00E-34
VC0834	toxin co-regulated pilus biosynthesis protein S	2.92	4.33E-05	-4.78	2.26E-12
VC0835	toxin co-regulated pilus biosynthesis protein T	2.78	3.37E-08	-4.75	4.99E-11
VC0838	TCP pilus virulence regulatory protein	4.64	8.40E-07	-4.74	3.04E-08
VC0885	hypothetical protein	3.04	2.60E-13	-6.13	1.36E-44
VC0928	hypothetical protein	2.20	1.60E-04	7.33	7.48E-43
VC0930	hemolysin-related protein	2.66	6.13E-04	2.38	5.54E-12
VC0936	polysaccharide export-related protein	2.37	9.24E-04	-3.16	1.76E-13
VC0938	hypothetical protein	2.52	2.37E-05	-2.12	1.49E-06
VC0972	porin, putative	2.25	1.65E-05	-2.36	1.43E-10
VC1029	GGDEF family protein	2.34	4.79E-04	-2.19	5.33E-08
VC1051	hypothetical protein	2.08	9.34E-04	2.18	1.92E-06
VC1061	cysteine synthase/cystathionine beta-synthase family protein	3.39	1.33E-10	-4.75	1.78E-26
VC1204	formiminoglutamase	2.82	3.80E-06	-5.80	3.41E-24
VC1318	outer membrane protein OmpV	7.89	6.00E-24	-43.63	1.39E-99
VC1329	opacity protein-related protein	13.58	1.78E-40	-2.62	1.55E-07
VC1344	4-hydroxyphenylpyruvate dioxygenase	3.94	2.76E-14	3.54	5.79E-40
VC1345	oxidoreductase, putative	5.22	1.54E-23	2.83	1.78E-19
VC1346	conserved hypothetical protein	4.94	8.80E-24	2.21	1.57E-13
VC1422	sodium/alanine symporter	-2.20	8.66E-07	3.80	1.79E-38
VC1456	cholera enterotoxin, B subunit	6.16	1.83E-11	-68.23	3.51E-85
VC1457	cholera enterotoxin, A subunit	3.61	4.52E-09	-79.05	1.69E-110
VC1472	hypothetical protein	-4.32	6.83E-06	2.29	9.71E-04
VC1548	hypothetical protein	3.62	1.11E-07	2.32	4.93E-08
VC1570	quinol oxidase, subunit II	3.93	3.72E-09	6.38	1.77E-24
VC1571	quinol oxidase, subunit I	3.34	1.53E-09	8.16	3.85E-42
VC1572	hypothetical protein	2.74	5.92E-06	2.60	6.65E-05
VC1577	hypothetical protein	4.99	1.11E-09	-8.10	9.05E-43
VC1578	hypothetical protein	5.82	7.21E-12	-4.58	3.17E-16
VC1579	enterobactin synthetase component F-related protein	5.77	4.43E-17	-8.22	7.70E-98
VC1633	hypothetical protein	2.63	7.14E-07	2.36	5.54E-20
VC1644	hypothetical protein	2.27	8.49E-07	3.41	2.66E-42
VC1675	multidrug resistance protein, putative	-2.04	6.66E-05	-2.35	7.60E-20
VC1678	phage shock protein A	-2.58	1.16E-07	3.67	1.55E-27
VC1786	DNA repair protein RadC, putative	-3.45	7.95E-05	2.19	4.11E-03
VC1802	hypothetical protein	-3.45	2.37E-04	19.79	6.26E-18
VC1807	pseudogene	3.04	1.31E-04	5.57	3.57E-05
VC1819	aldehyde dehydrogenase	5.72	1.75E-24	6.09	5.03E-37
VC1888	hemolysin-related protein	4.06	4.04E-14	8.63	4.61E-61
VC1928	C4-dicarboxylate transport protein DctQ, putative	2.21	3.24E-07	2.92	1.56E-16
VC1962	lipoprotein	2.10	1.40E-06	3.27	2.23E-20
VC2359	uracil-DNA glycosylase	2.70	9.86E-07	3.19	2.03E-16
VC2691	periplasmic protein cpxP, putative	2.28	5.08E-05	9.30	2.28E-53
VCA0063	protease II	2.76	1.03E-06	2.29	5.66E-10
VCA0070	phosphate ABC transporter, periplasmic phosphate-binding protein	3.04	1.24E-08	4.86	5.38E-31
VCA0071	phosphate ABC transporter, permease protein	2.79	1.04E-07	3.11	1.43E-07
VCA0072	phosphate ABC transporter, permease protein	2.45	1.19E-04	2.66	1.69E-07
VCA0083	multidrug resistance protein D	4.84	4.39E-07	5.85	5.39E-35
VCA0094	conserved hypothetical protein	14.05	4.79E-26	2.45	1.98E-03
VCA0146	conserved hypothetical protein	2.91	1.07E-04	-2.61	1.59E-07
VCA0152	conserved hypothetical protein	2.04	2.58E-04	-5.85	4.33E-33
VCA0161	tryptophanase	5.99	1.14E-24	2.06	5.45E-09
VCA0163	conserved hypothetical protein	2.72	2.20E-06	2.72	3.05E-10
VCA0221	lactonizing lipase	5.71	1.80E-17	-2.02	2.90E-06
VCA0227	iron(III) ABC transporter, periplasmic iron-compound-binding protein	4.29	7.98E-16	10.77	9.88E-55
VCA0231	transcriptional regulator, AraC/XylS family	7.89	4.42E-22	2.13	3.30E-06

VCA0271	hypothetical protein	2.18	6.77E-07	2.42	1.83E-14
VCA0276	Glycine cleavage system P protein GcvP, authentic frameshift	2.77	9.97E-11	-4.31	5.27E-29
VCA0278	serine hydroxymethyltransferase	2.39	6.88E-08	-3.79	2.00E-24
VCA0280	glycine cleavage system protein GcvT; contains authentic frameshift	2.09	3.53E-06	-6.09	3.49E-49
VCA0308	deoxyguanosinetriphosphate triphosphohydrolyase-related protein	-2.05	3.77E-06	-3.77	1.09E-31
VCA0310	hypothetical protein	-2.14	6.61E-05	-2.71	1.56E-21
VCA0316	acetyltransferase, putative	-2.51	2.09E-05	-2.69	8.89E-16
VCA0339	hypothetical protein	-3.10	3.06E-04	-5.50	1.62E-17
VCA0346	H-REV 107-related protein	-3.12	3.56E-12	2.58	6.75E-21
VCA0355	conserved hypothetical protein	-2.48	2.11E-07	-3.14	4.55E-16
VCA0356	hypothetical protein	-2.11	1.80E-05	-2.15	1.04E-16
VCA0356a	hypothetical protein	-2.25	5.64E-04	-2.53	1.77E-10
VCA0386	hypothetical protein	-2.68	3.71E-08	3.15	5.73E-15
VCA0419	hypothetical protein	-2.60	6.58E-07	-2.57	7.76E-14
VCA0465	hypothetical protein	-2.10	4.67E-04	-2.03	8.28E-08
VCA0480	hypothetical protein	-2.16	1.78E-04	2.04	1.46E-06
VCA0519	fructose repressor	-2.04	5.56E-05	7.90	2.08E-64
VCA0576	heme transport protein HutA	6.55	2.04E-16	7.27	2.22E-63
VCA0683	sensor protein UhpB	2.12	2.73E-04	-2.75	1.66E-17
VCA0690	acetyl-CoA acetyltransferase	-2.05	6.52E-06	-6.07	9.62E-25
VCA0691	acetoacetyl-CoA reductase	-2.18	1.61E-07	-5.35	2.47E-36
VCA0849	hypothetical protein	2.33	2.45E-05	2.08	3.12E-12
VCA0864	methyl-accepting chemotaxis protein	3.00	2.23E-07	-2.23	2.27E-13
VCA0874	hypothetical protein	2.31	2.24E-04	3.29	7.44E-09
VCA0886	2-amino-3-ketobutyrate coenzyme A ligase	3.12	3.86E-10	-5.41	2.20E-48
VCA0907	conserved hypothetical protein	5.91	5.51E-24	2.25	1.96E-11
VCA0909	oxygen-independent coproporphyrinogen III oxidase, putative	9.80	7.27E-18	3.74	7.85E-18
VCA0910	tonB1 protein	9.83	2.96E-22	2.83	1.19E-05
VCA0911	TonB system transport protein ExbB1	10.30	7.54E-20	2.43	2.77E-03
VCA0952	transcriptional regulator, LuxR family	3.48	3.76E-05	11.33	3.96E-58
VCA0976	hypothetical protein	7.46	1.72E-15	3.12	1.02E-08
VCA0977	ABC transporter, ATP-binding protein	5.44	3.75E-24	2.94	9.34E-16
VCA1031	putative methyl-accepting chemotaxis protein; authentic frameshift	2.26	8.10E-06	7.13	3.58E-51
VCA1041	phosphomannomutase, putative	2.18	1.07E-05	-3.62	1.21E-30
VCA1115	ParA family protein	-2.02	1.21E-05	5.66	2.23E-47
VCr025	5S ribosomal RNA	4.65	1.50E-05	-239.23	3.68E-98