

**Table S7.** Expression of 581 ToxR regulon genes in the WT C6706 relative to the *toxR* mutant under virulence-inducing AKI conditions.

<b>Genes activated by ToxR</b>			
<b>Locus tag</b>	<b>Function</b>	<b>FC WT/ <i>toxR</i></b>	<b>p-value</b>
VC0032	ComM-related protein	2.8	1.01E-06
VC0069	multidrug resistance protein, putative	2.5	3.34E-12
VC0078	ferritin	2.4	3.28E-04
VC0079	conserved hypothetical protein	3.0	4.18E-20
VC0089	cytochrome c551 peroxidase	9.4	6.86E-48
VC0090	DNA-damage-inducible protein F	3.0	7.64E-17
VC0096	hypothetical protein	2.4	3.15E-06
VC0098	methyl-accepting chemotaxis protein	2.8	2.47E-20
VC0121	hypothetical protein	2.7	4.50E-07
VC0139	DPS family protein	2.6	7.28E-16
VC0142	hypothetical protein	2.1	1.06E-16
VC0169	hypothetical protein	3.7	4.57E-12
VC0170	peptide ABC transporter, ATP-binding protein	2.7	2.51E-14
VC0171	peptide ABC transporter, periplasmicpeptide-binding protein	2.8	1.26E-13
VC0172	peptide ABC transporter, permease protein	2.4	4.99E-11
VC0298	acetyl-CoA synthase	11.9	5.93E-28
VC0299	DNA polymerase III, epsilon subunit, putative	4.8	8.30E-24
VC0300	conserved hypothetical protein	7.2	3.47E-27
VC0365	bacterioferritin	2.6	5.10E-13
VC0383	hypothetical protein	2.3	6.21E-04
VC0392	aminotransferase, class V	2.1	2.89E-16
VC0403	MSHA biogenesis protein MshM	2.0	1.66E-08
VC0413	MshP	2.3	1.17E-12
VC0463	twitching motility protein PilT	2.5	3.02E-10
VC0533	lipoprotein NlpD	2.0	2.74E-03
VC0534	RNA polymerase sigma-38 factor	2.3	3.55E-04
VC0552	quinone oxidoreductase	2.0	3.71E-12
VC0613	beta-N-acetylhexosam inidase	2.1	3.84E-07
VC0614	conserved hypothetical protein	2.6	2.68E-06
VC0615	endoglucanase-related protein	2.3	6.33E-09
VC0616	peptide ABC transporter, ATP-binding protein	2.0	1.01E-03
VC0617	peptide ABC transporter, ATP-binding protein	2.0	1.30E-04
VC0618	peptide ABC transporter, permease protein	2.9	1.38E-06
VC0620	peptide ABC transporter, periplasmicpeptide-binding protein	3.1	1.32E-17
VC0633	outer membrane protein OmpU	2.4	1.11E-06
VC0658	c-di-GMP phosphodiesterase A-related protein	2.7	3.73E-14
VC0665	sigma-54 dependent transcriptional regulator	2.0	9.40E-08
VC0697	hypothetical protein	2.7	2.25E-18
VC0728	conserved hypothetical protein	3.0	5.86E-18
VC0734	malate synthase A	5.7	5.92E-34
VC0736	isocitrate lyase	2.9	3.97E-14
VC0737	acetoin utilization protein AcuB, putative	2.5	1.84E-12
VC0828	toxin co-regulated pilin	24.9	1.09E-37
VC0829	toxin co-regulated pilus biosynthesis protein B	2.0	4.00E-04
VC0831	toxin co-regulated pilus biosynthesis outermembrane protein C	2.5	1.11E-08
VC0833	toxin co-regulated pilus biosynthesis protein D	2.5	4.26E-04
VC0834	toxin co-regulated pilus biosynthesis protein S	2.3	4.78E-05
VC0835	toxin co-regulated pilus biosynthesis protein T	2.3	4.87E-05
VC0836	toxin co-regulated pilus biosynthesis protein E	2.1	1.12E-03
VC0837	toxin co-regulated pilus biosynthesis protein F	2.1	4.22E-05
VC0844	accessory colonization factor AcfA	3.1	5.23E-08
VC0858	type IV pilin, putative	2.2	1.66E-03
VC0893	chemotaxis protein PomB	2.1	1.23E-11
VC0935	hypothetical protein	2.2	3.89E-06
VC0936	polysaccharide export-related protein	3.8	8.39E-16

VC0937	exopolysaccharide biosynthesis protein,putative	2.4	5.30E-10
VC0938	hypothetical protein	3.5	1.74E-11
VC0957	conserved hypothetical protein	2.3	3.45E-04
VC1008	sodium-type flagellar protein MotY	2.2	3.76E-09
VC1009	conserved hypothetical protein	2.6	1.43E-11
VC1029	GGDEF family protein	2.1	2.59E-06
VC1031	inosine monophosphate dehydrogenase-relatedprotein	6.4	1.89E-59
VC1032	zinc/cadmium/mercury/lead-transporting ATPase	3.3	2.45E-04
VC1043	long-chain fatty acid transport protein	2.4	1.94E-04
VC1050	response regulator	3.6	3.12E-24
VC1064	lipoprotein-related protein	2.1	9.83E-09
VC1080	hypothetical protein	2.3	2.80E-11
VC1082	response regulator	2.6	1.21E-19
VC1083	hypothetical protein	2.9	1.10E-13
VC1084	sensory box sensor histidine kinase	4.0	9.19E-23
VC1085	sensor histidine kinase	4.1	3.69E-31
VC1086	response regulator	3.0	5.37E-21
VC1087	response regulator	2.8	2.96E-14
VC1088	sensor histidine kinase	3.5	1.69E-19
VC1089	periplasmic binding protein-related protein	2.6	3.07E-12
VC1101	conserved hypothetical protein	2.5	7.55E-12
VC1103	ABC transporter, ATP-binding protein	2.1	7.33E-10
VC1112	biotin synthase	2.3	7.57E-05
VC1116	hypothetical protein	4.9	1.15E-13
VC1124	conserved hypothetical protein	2.7	1.09E-23
VC1125	hypothetical protein	2.7	5.39E-13
VC1142	cold shock-like protein CspD	2.5	3.53E-09
VC1153	conserved hypothetical protein	2.2	3.39E-12
VC1187	hypothetical protein	3.2	2.42E-11
VC1188	malate oxidoreductase	3.8	6.65E-09
VC1207	hypothetical protein	2.6	2.97E-12
VC1222	integration host factor, alpha subunit	2.5	1.37E-11
VC1223	hypothetical protein	3.3	5.33E-24
VC1224	hypothetical protein	2.3	1.80E-08
VC1236	PilB-related protein	2.3	5.07E-10
VC1247	hypothetical protein	2.2	2.81E-07
VC1248	methyl-accepting chemotaxis protein	7.0	1.62E-14
VC1249	conserved hypothetical protein	2.2	1.27E-03
VC1262	hypothetical protein	2.9	9.67E-10
VC1269	conserved hypothetical protein	2.4	1.79E-23
VC1295	conserved hypothetical protein	2.2	6.43E-09
VC1298	methyl-accepting chemotaxis protein	3.0	1.75E-17
VC1312	alanine racemase, putative	2.7	1.64E-10
VC1313	methyl-accepting chemotaxis protein	2.8	1.67E-13
VC1316	chemotaxis protein CheY, putative	2.6	4.94E-14
VC1322	conserved hypothetical protein	3.9	3.19E-21
VC1323	hypothetical protein	2.8	1.66E-16
VC1325	galactoside ABC transporter, periplasmicD-galactose/D-gluco se-binding protein	4.6	1.32E-20
VC1327	galactoside ABC transporter, ATP-bindingprotein	3.5	2.54E-17
VC1328	galactoside ABC transporter, permease protein	4.0	5.67E-25
VC1334	conserved hypothetical protein	3.1	4.33E-17
VC1339	conserved hypothetical protein	2.1	1.46E-06
VC1340	prpE protein	2.1	2.31E-08
VC1348	response regulator	3.3	7.56E-21
VC1349	sensory box sensor histidine kinase/responseregulator	3.1	6.93E-16
VC1355	acylphosphatase	2.2	3.67E-08
VC1359	amino acid ABC transporter, ATP-binding protein	2.5	1.24E-12
VC1360	amino acid ABC transporter, permease protein	2.9	2.28E-14
VC1361	amino acid ABC transporter, permease protein	3.0	4.30E-16
VC1362	amino acid ABC transporter, periplasmic aminoacid-binding protein	5.6	2.98E-12

VC1368	hypothetical protein	2.2	1.28E-08
VC1369	conserved hypothetical protein	3.7	1.49E-22
VC1370	GGDEF family protein	4.9	9.95E-25
VC1376	GGDEF family protein	2.2	1.43E-09
VC1394	methyl-accepting chemotaxis protein	4.1	1.36E-29
VC1395	response regulator cheY1	4.6	3.55E-40
VC1396	hypothetical protein	5.2	3.64E-43
VC1397	chemotaxis protein CheA	4.9	1.22E-34
VC1398	chemotaxis protein CheY	5.8	1.64E-27
VC1399	chemotaxis protein methyltransferase CheR	5.6	8.47E-35
VC1400	hypothetical protein	4.2	4.51E-24
VC1401	protein-glutamate methylesterase CheB	3.3	5.82E-17
VC1402	purine-binding chemotaxis protein Chew,putative	2.9	3.66E-12
VC1403	methyl-accepting chemotaxis protein	3.5	3.64E-19
VC1405	methyl-accepting chemotaxis protein	2.6	2.69E-13
VC1406	methyl-accepting chemotaxis protein	2.7	3.06E-18
VC1456	cholera enterotoxin, B subunit	18.4	3.71E-46
VC1457	cholera enterotoxin, A subunit	20.2	1.83E-59
VC1484	ribosome modulation factor	4.9	1.00E-27
VC1506	hypothetical protein	3.2	1.35E-14
VC1509	nicotinamonomonucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase	3.1	6.41E-14
VC1528	hypothetical protein	2.3	4.16E-11
VC1538	hypothetical protein	2.3	7.41E-10
VC1560	catalase/peroxidase	4.3	6.51E-09
VC1594	aldose 1-epimerase	2.6	1.05E-13
VC1595	galactokinase	2.7	1.91E-13
VC1601	hypothetical protein	2.1	2.85E-07
VC1602	chemotaxis protein CheV	2.7	3.95E-12
VC1603	hypothetical protein	2.7	2.61E-16
VC1612	fimbrial biogenesis and twitching motilityprotein, putative	2.1	3.39E-08
VC1618	multidrug resistance protein, putative	3.3	1.21E-32
VC1641	conserved hypothetical protein	2.2	6.55E-09
VC1643	methyl-accepting chemotaxis protein	3.6	1.77E-20
VC1662	conserved hypothetical protein	2.8	8.03E-13
VC1672	DNA-3-methyladenine glycosidase I	2.2	3.99E-07
VC1673	transporter, AcrB/D/F family	2.5	3.84E-12
VC1674	periplasmic linker protein, putative	3.5	1.62E-17
VC1675	multidrug resistance protein, putative	2.7	5.16E-19
VC1677	phage shock protein B	2.0	1.09E-04
VC1699	hypothetical protein	2.3	1.59E-19
VC1706	transcriptional activator MetR	2.1	7.45E-07
VC1707	hypothetical protein	3.8	1.08E-24
VC1736	arginyl-tRNA-protein transferase-relatedprotein	3.1	1.37E-20
VC1741	transcriptional regulator, TetR family	2.2	7.63E-08
VC1778	conserved hypothetical protein	2.2	3.15E-12
VC1819	aldehyde dehydrogenase	2.1	2.71E-06
VC1831	sensor histidine kinase	3.1	4.82E-27
VC1842	conserved hypothetical protein	2.1	5.72E-04
VC1851	conserved hypothetical protein	2.8	8.48E-16
VC1868	methyl-accepting chemotaxis protein	4.5	5.84E-28
VC1872	conserved hypothetical protein	5.1	5.83E-25
VC1873	conserved hypothetical protein	6.1	1.14E-42
VC1874	conserved hypothetical protein	6.9	1.33E-15
VC1914	integration host factor, beta subunit	2.7	6.48E-19
VC1932	hypothetical protein	2.6	7.44E-07
VC1933	hypothetical protein	3.7	4.51E-25
VC1934	GGDEF family protein	2.9	5.86E-12
VC1950	biotin sulfoxide reductase	2.2	5.12E-08
VC1952	chitinase	2.0	5.17E-08
VC1967	methyl-accepting chemotaxis protein	2.5	1.08E-12

VC1993	2,4-dienoyl-CoA reductase	2.1	1.48E-08
VC2008	pyruvate kinase II	2.2	2.65E-10
VC2047	oxidoreductase, short-chain dehydrogenase/reductase family	2.5	1.94E-17
VC2059	purine-binding chemotaxis protein CheW	2.4	1.41E-04
VC2060	conserved hypothetical protein	2.3	2.15E-09
VC2063	chemotaxis protein CheA	2.1	3.32E-07
VC2103	transcriptional regulator, LysR family	2.1	5.22E-14
VC2120	flagellar biosynthetic protein FlhB	2.1	1.31E-08
VC2121	flagellar biosynthetic protein FlhR	2.0	6.15E-07
VC2122	flagellar biosynthetic protein FlhQ	2.9	5.20E-16
VC2123	flagellar biosynthetic protein FlhP	2.2	2.39E-10
VC2124	flagellar protein FlhO	2.2	6.57E-13
VC2125	flagellar motor switch protein FlhN	2.0	1.03E-09
VC2126	flagellar motor switch protein FlhM	2.2	4.77E-09
VC2127	flagellar protein FlhL, putative	2.4	1.46E-10
VC2128	flagellar hook-length control protein FlhK, putative	2.7	2.75E-14
VC2129	flagellar protein FlhJ, putative	2.0	1.81E-12
VC2132	flagellar motor switch protein FlhG	2.0	2.00E-09
VC2138	flagellar protein FlhS	2.1	1.64E-09
VC2139	flagellar rod protein FlhI, putative	2.5	2.94E-15
VC2140	flagellar hook-associated protein FlhD	2.9	8.95E-06
VC2141	flagellin FlaG	3.3	1.09E-06
VC2142	flagellin FlaB	3.5	8.48E-16
VC2143	flagellin FlaD	2.4	8.21E-08
VC2144	flagellin FlaE	2.7	9.51E-15
VC2161	methyl-accepting chemotaxis protein	3.5	2.37E-07
VC2187	flagellin FlaC	3.4	3.17E-14
VC2190	flagellar hook-associated protein FlgL	2.5	4.88E-10
VC2192	flagellar protein FlgJ	2.4	4.22E-11
VC2194	flagellar L-ring protein FlgH	2.6	1.28E-14
VC2195	flagellar basal-body rod protein FlgG	2.3	1.99E-14
VC2198	basal-body rod modification protein FlgD	2.1	1.98E-08
VC2201	chemotaxis protein methyltransferase CheR	2.7	2.26E-05
VC2202	chemotaxis protein CheV	2.3	5.91E-04
VC2204	negative regulator of flagellin synthesis FlgM, putative	2.2	4.33E-10
VC2205	hypothetical protein	2.4	4.06E-11
VC2206	conserved hypothetical protein	2.4	3.83E-10
VC2207	hypothetical protein	2.2	2.19E-10
VC2221	hypothetical protein	3.5	2.35E-14
VC2231	oxidoreductase, acyl-CoA dehydrogenase family	2.4	2.10E-11
VC2240	decarboxylase	2.1	2.59E-10
VC2241	cytochrome c554	2.7	3.75E-16
VC2264	conserved hypothetical protein	2.8	9.69E-16
VC2314	hypothetical protein	3.5	2.91E-13
VC2316	N-acetylglutamate synthase	2.7	3.54E-12
VC2338	$\beta$ -galactosidase, LacZ	2.8	2.20E-05
VC2340	conserved hypothetical protein	3.5	7.33E-22
VC2357	hypothetical protein	2.5	9.02E-10
VC2358	hypothetical protein	3.0	8.14E-16
VC2370	sensory box/GGDEF family protein	2.1	1.34E-08
VC2383	transcriptional regulator, LysR family	2.0	9.54E-06
VC2384	conserved hypothetical protein	3.7	7.79E-18
VC2454	GGDEF family protein	2.7	7.59E-14
VC2455	hypothetical protein	2.9	3.28E-13
VC2456	hypothetical protein	2.8	1.09E-18
VC2464	sigma-E factor regulatory protein RseC	2.3	9.37E-10
VC2465	sigma-E factor regulatory protein RseB	2.3	1.01E-11
VC2466	sigma-E factor negative regulatory protein RseA	2.2	4.21E-09
VC2467	RNA polymerase sigma-E factor	2.3	3.21E-10
VC2507	conserved hypothetical protein	3.9	6.58E-22

VC2508	ornithine carbamoyltransferase	2.2	1.25E-10
VC2529	RNA polymerase sigma-54 factor	2.1	8.76E-08
VC2530	sigma-54 modulation protein, putative	2.7	4.54E-14
VC2565	elaA protein	2.5	1.88E-25
VC2601	sodium-type flagellar protein MotX	2.7	3.78E-17
VC2622	hypothetical protein	2.8	8.22E-17
VC2697	GGDEF family protein	2.7	4.61E-11
VC2702	transcriptional regulator, LuxR family	2.1	4.58E-09
VC2704	hypothetical protein	23.5	9.84E-52
VC2705	sodium/solute symporter, putative	29.0	1.28E-135
VC2717	hypothetical protein	3.4	5.59E-20
VC2726	general secretion pathway protein K	2.0	1.24E-07
VC2727	general secretion pathway protein J	2.2	2.97E-08
VC2750	GGDEF family protein	2.7	1.64E-14
VCA0008	methyl-accepting chemotaxis protein	8.4	1.03E-56
VCA0009	hypothetical protein	7.6	1.46E-20
VCA0013	maltodextrin phosphorylase	3.2	2.46E-14
VCA0014	4-alpha-glucanotransferase	3.0	1.42E-23
VCA0031	methyl-accepting chemotaxis protein	2.3	2.82E-09
VCA0032	hypothetical protein	2.6	2.01E-12
VCA0034	conserved hypothetical protein	2.8	2.03E-14
VCA0047	conserved hypothetical protein	2.0	2.39E-11
VCA0049	GGDEF family protein	2.1	3.14E-09
VCA0074	GGDEF family protein	2.9	4.08E-17
VCA0075	hypothetical protein	2.6	2.83E-06
VCA0078	hypothetical protein	2.4	1.39E-14
VCA0080	GGDEF family protein	2.7	2.72E-15
VCA0129	ribose ABC transporter, permease protein	2.1	2.98E-04
VCA0130	ribose ABC transporter, periplasmicD-ribose-binding protein	2.7	1.22E-12
VCA0131	ribokinase	2.2	9.74E-05
VCA0144	immunogenic protein	2.1	1.81E-06
VCA0146	conserved hypothetical protein	2.6	2.40E-06
VCA0147	transcriptional regulator, putative	2.5	5.74E-07
VCA0152	conserved hypothetical protein	5.6	1.09E-25
VCA0153	conserved hypothetical protein	5.5	2.54E-23
VCA0154	conserved hypothetical protein	5.5	2.46E-31
VCA0155	NADH dehydrogenase, putative	3.8	5.45E-24
VCA0156	conserved hypothetical protein	4.0	5.45E-22
VCA0157	NADH dehydrogenase, putative	3.6	3.49E-24
VCA0161	tryptophanase	2.7	1.48E-11
VCA0176	methyl-accepting chemotaxis protein	2.3	4.75E-10
VCA0186	hypothetical protein	2.1	1.13E-06
VCA0188	hypothetical protein	3.1	1.73E-12
VCA0189	response regulator	2.1	1.13E-16
VCA0191	conserved hypothetical protein	2.1	1.41E-09
VCA0210	response regulator, putative	4.0	1.63E-29
VCA0211	sensory box sensor histidine kinase	4.0	6.20E-48
VCA0212	hypothetical protein	3.2	8.82E-19
VCA0220	hemolysin secretion protein HylB	2.3	1.44E-20
VCA0221	lactonizing lipase	3.8	1.72E-11
VCA0222	lipase activator protein, putative	2.2	4.05E-04
VCA0268	methyl-accepting chemotaxis protein	3.5	1.84E-18
VCA0269	decarboxylase, group II	2.9	3.41E-12
VCA0282	IS5 transposase	2.0	1.05E-05
VCA0534	pseudogene; contains authentic frameshift mutation	2.4	7.95E-10
VCA0551	hypothetical protein	2.5	4.01E-17
VCA0557	GGDEF family protein	2.2	2.81E-09
VCA0558	gamma-glutamyltranspeptidase, putative	2.5	1.68E-12
VCA0574	conserved hypothetical protein	2.3	2.42E-09
VCA0583	hypothetical protein	4.2	2.32E-27

VCA0588	peptide ABC transporter, ATP-binding protein,putative	2.3	1.80E-09
VCA0593	hypothetical protein	3.1	8.74E-19
VCA0619	hypothetical protein	2.5	2.40E-15
VCA0638	transporter, AcrB/D/F family	2.0	1.35E-11
VCA0639	AcrA/AcrE family protein	2.2	4.50E-17
VCA0645	hypothetical protein	2.1	6.69E-05
VCA0646	conserved hypothetical protein/hemolysin,putative	3.9	9.23E-16
VCA0647	hypothetical protein	4.1	7.58E-12
VCA0648	hypothetical protein	2.5	1.99E-05
VCA0649	hypothetical protein	2.5	1.19E-05
VCA0650	hypothetical protein	4.4	9.33E-11
VCA0659	protein F-related protein	3.0	7.33E-20
VCA0666	L-serine dehydratase 1	2.4	1.37E-12
VCA0681	conserved hypothetical protein	3.8	1.04E-27
VCA0683	sensor protein UhpB	2.3	4.26E-09
VCA0684	regulatory protein UhpC	2.2	1.09E-12
VCA0695	hypothetical protein	5.0	2.22E-24
VCA0698	hypothetical protein	4.4	1.89E-28
VCA0707	regulatory protein UhpC, putative	2.1	1.03E-03
VCA0719	sensor histide kinase	3.5	2.97E-18
VCA0720	guanylate cyclase-related protein	3.5	5.42E-25
VCA0722	hypothetical protein	2.3	9.02E-08
VCA0731	hypothetical protein	3.1	6.01E-08
VCA0738	hypothetical protein	3.0	6.63E-15
VCA0757	arginine ABC transporter, permease protein	2.4	1.16E-07
VCA0758	arginine ABC transporter, permease protein	2.3	3.84E-07
VCA0760	arginine ABC transporter, ATP-binding protein	2.7	2.20E-21
VCA0788	DnaJ-related protein	2.3	6.99E-14
VCA0798	CbbY family protein	2.1	1.91E-07
VCA0803	serine protease, putative	4.5	7.01E-29
VCA0813	aminopeptidase	2.2	5.72E-11
VCA0831	hypothetical protein	3.7	1.05E-03
VCA0848	GGDEF family protein	2.6	9.34E-26
VCA0860	alpha-amylase	3.5	7.67E-16
VCA0864	methyl-accepting chemotaxis protein	2.1	1.21E-07
VCA0865	hemagglutinin/protea se	9.9	1.12E-44
VCA0867	outer membrane protein OmpW	2.6	5.94E-07
VCA0868	hypothetical protein	2.3	6.45E-09
VCA0880	makD	3.9	6.10E-23
VCA0881	makC	4.2	1.06E-26
VCA0882	makB	4.2	3.21E-22
VCA0883	makA	2.9	1.67E-13
VCA0884	hypothetical protein	3.8	3.67E-21
VCA0892	hypothetical protein	3.4	3.49E-23
VCA0895	chemotactic transducer-related protein	3.0	2.49E-20
VCA0900	hypothetical protein	2.6	9.54E-16
VCA0901	hypothetical protein	2.6	1.81E-14
VCA0906	methyl-accepting chemotaxis protein	5.3	5.66E-45
VCA0920	hypothetical protein	2.4	2.18E-14
VCA0923	methyl-accepting chemotaxis protein	4.0	2.82E-29
VCA0931	conserved hypothetical protein	2.2	1.29E-11
VCA0935	hypothetical protein	5.9	2.86E-12
VCA0944	maltose ABC transporter, permease protein	3.4	2.28E-13
VCA0945	maltose ABC transporter, periplasmicmaltose-binding protein	3.3	1.34E-13
VCA0946	maltose/maltodextrin ABC transporter,ATP-binding protein	2.5	8.38E-08
VCA0957	malate synthase-related protein	2.7	2.19E-16
VCA0965	GGDEF family protein	4.1	7.72E-28
VCA0978	amino acid ABC transporter, periplasmic aminoacid-binding protein, putative	4.1	1.78E-32
VCA0979	methyl-accepting chemotaxis protein	2.7	9.39E-13
VCA0981	hypothetical protein	3.6	1.09E-20

VCA0982	transcriptional regulator, LysR family	2.1	1.23E-08
VCA0988	methyl-accepting chemotaxis protein	3.2	3.93E-23
VCA1015	Na <sup>+</sup> /H <sup>+</sup> antiporter	2.9	8.35E-21
VCA1016	hypothetical protein	3.9	2.23E-23
VCA1017	methylated-DNA--prot ein-cysteineS-methyltransferas e	3.9	8.30E-22
VCA1024	hypothetical protein	6.0	6.23E-41
VCA1028	maltoporin	3.5	6.21E-14
VCA1033	extracellular solute-binding protein, putative	4.4	8.12E-23
VCA1034	methyl-accepting chemotaxis protein	5.5	2.28E-40
VCA1042	Ccm2-related protein	2.1	1.84E-11
VCA1054	conserved hypothetical protein	3.7	1.81E-29
VCA1056	methyl-accepting chemotaxis protein	4.3	3.41E-27
VCA1086	response regulator	3.4	6.64E-19
VCA1087	anti-sigma F factor antagonist, putative	3.3	5.19E-17
VCA1088	methyl-accepting chemotaxis protein	4.0	1.67E-33
VCA1089	cheB3 methylesterase	5.4	1.96E-33
VCA1090	chemotaxis protein CheD, putative	6.3	4.13E-46
VCA1091	chemotaxis protein methyltransferase CheR	4.8	2.16E-29
VCA1092	methyl-accepting chemotaxis protein	4.3	9.46E-25
VCA1093	purine-binding chemotaxis protein CheW	4.0	6.14E-22
VCA1094	purine-binding chemotaxis protein CheW	4.2	6.33E-24
VCA1095	chemotaxis protein CheA	4.2	6.28E-23
VCA1096	chemotaxis protein CheY	3.7	9.73E-32
VCA1097	conserved hypothetical protein	3.6	1.32E-30
VCA1108	oxidoreductase, short-chaindehydrogenase/reduc tase family	2.5	4.90E-05
VCr025	5S ribosomal RNA	36.4	8.81E-61
16Sa	16S ribosomal RNA	3.1	7.93E-12
16Sb	16S ribosomal RNA	2.7	2.27E-08
16Sc	16S ribosomal RNA	3.4	7.84E-12
16Se	16S ribosomal RNA	2.5	4.14E-08
16Sg	16S ribosomal RNA	2.2	9.44E-07
23Sa	23S ribosomal RNA	3.1	2.03E-09
23Sc	23S ribosomal RNA	5.6	3.27E-08
23Sd	23S ribosomal RNA	2.3	2.07E-06
23Se	23S ribosomal RNA	3.4	8.63E-13
23Sf	23S ribosomal RNA	2.6	3.24E-07
23Sg	23S ribosomal RNA	3.1	2.61E-17
5Sa	5S ribosomal RNA	3.9	1.46E-08
5Sb	5S ribosomal RNA	5.1	1.72E-06
5Sc	5S ribosomal RNA	25.8	1.04E-07
5Sd	5S ribosomal RNA	24.7	7.30E-08
5Se	5S ribosomal RNA	3.6	2.42E-05
5Sf	5S ribosomal RNA	9.2	3.89E-53
5Sg	5S ribosomal RNA	19124.1	1.84E-06
5Sh	5S ribosomal RNA	5.5	1.18E-12
<b>Genes repressed by ToxR</b>			
VC0134	conserved hypothetical protein	-2.6	6.63E-12
VC0156	vitamin B12 receptor	-3.5	1.40E-20
VC0164	multidrug resistance protein, putative	-2.2	1.03E-03
VC0218	ribosomal protein L28	-2.1	1.83E-08
VC0324	ribosomal protein L11, RplK	-3.2	1.35E-14
VC0325	ribosomal protein L1	-2.8	3.17E-12
VC0326	ribosomal protein L10	-3.0	3.02E-12
VC0327	ribosomal protein L7/L12	-2.7	1.08E-12
VC0359	ribosomal protein S12	-2.5	8.89E-10
VC0360	ribosomal protein S7	-2.5	1.81E-11
VC0362	elongation factor TU	-2.1	2.70E-06
VC0367	primosomal replication protein N	-2.1	1.13E-03
VC0368	ribosomal protein S18	-2.2	6.50E-09
VC0369	ribosomal protein L9	-2.2	9.63E-09

VC0477	phosphoglycerate kinase	-2.3	2.68E-04
VC0485	pyruvate kinase I	-2.5	2.75E-12
VC0561	ribosomal protein S16	-2.4	2.32E-10
VC0562	16S rRNA processing protein RimM	-2.1	1.00E-03
VC0563	tRNA (guanine-N1)-methyltransferase	-2.2	8.78E-04
VC0564	ribosomal protein L19	-2.8	1.24E-14
VC0596	dnaK suppressor protein	-2.0	3.95E-07
VC0606	nitrogen regulatory protein P-II	-4.4	2.95E-05
VC0607	Pseudogene	-2.8	2.46E-03
VC0608	iron(III) ABC transporter, periplasmic iron-compound-binding protein	-2.3	1.13E-10
VC0642	N utilization substance protein A	-2.6	3.92E-14
VC0643	initiation factor IF-2	-2.3	1.76E-09
VC0646	ribosomal protein S15	-2.5	9.00E-05
VC0664	lysyl-tRNA synthetase, heat inducible	-2.4	2.38E-16
VC0687	carbon starvation protein A, putative	-8.7	2.48E-45
VC0695	phospho-2-dehydro-3-deoxyheptonate aldolase, tyr-sensitive	-2.7	9.50E-26
VC0739	S-adenosylmethionine :tRNA ribosyltransferase-isomerase	-2.2	1.46E-13
VC0770	conserved hypothetical protein	-3.7	3.30E-08
VC0771	vibriobactin-specific isochorismatase	-2.1	8.52E-04
VC0810	hypothetical protein	-2.0	5.59E-04
VC0847	integrase, phage family	-2.1	9.15E-09
VC0871	hypothetical protein	-2.6	3.45E-12
VC0872	conserved hypothetical protein	-2.9	1.23E-11
VC0905	lipoprotein YaeC	-2.0	9.51E-09
VC0916	phosphotyrosine protein phosphatase	-4.3	3.63E-04
VC0928	hypothetical protein	-2.2	3.59E-07
VC0945	conserved hypothetical protein	-2.1	1.64E-06
VC0985	heat shock protein HtpG	-2.5	3.22E-11
VC0991	asparagine synthetase B, glutamine-hydrolyzing	-2.5	2.35E-17
VC1040	cob(I)alamin adenosyltransferase	-2.1	1.41E-08
VC1193	hypothetical protein	-2.1	8.15E-07
VC1317	conserved hypothetical protein	-2.5	9.72E-15
VC1318	outer membrane protein OmpV	-4.1	6.21E-15
VC1375	hypothetical protein	-2.1	8.24E-06
VC1391	multidrug transporter, putative	-2.7	3.66E-13
VC1409	multidrug resistance protein, putative	-2.2	2.40E-10
VC1410	multidrug resistance protein VceA	-2.6	9.25E-13
VC1415	hcp protein	-6.5	7.40E-36
VC1416	vgrG protein	-3.2	1.48E-21
VC1417	hypothetical protein	-3.1	3.58E-28
VC1418	hypothetical protein	-2.3	6.96E-16
VC1419	hypothetical protein	-2.2	8.38E-15
VC1420	hypothetical protein	-2.4	1.66E-09
VC1487	conserved hypothetical protein	-2.3	1.32E-04
VC1589	alpha-acetolactate decarboxylase	-2.5	3.02E-06
VC1590	acetolactate synthase	-3.3	1.04E-16
VC1591	oxidoreductase, short-chain dehydrogenase/reductase family	-3.7	8.01E-22
VC1623	carboxynorspermidine decarboxylase	-3.0	3.83E-33
VC1624	conserved hypothetical protein	-2.2	3.54E-18
VC1625	Pseudogene; involved in spermidine biosynthesis	-2.3	1.05E-12
VC1628	conserved hypothetical protein	-2.5	1.04E-19
VC1629	conserved hypothetical protein	-2.1	3.44E-08
VC1701	conserved hypothetical protein	-2.0	4.99E-04
VC1721	transcriptional regulator, LacI family	-2.0	1.31E-11
VC1748	hypothetical protein	-2.5	7.44E-08
VC1749	hypothetical protein	-2.1	5.51E-07
VC1750	hypothetical protein	-2.3	5.86E-10
VC1790	transposase OrfAB, subunit A	-2.5	1.59E-04
VC1823	PTS system, fructose-specific IIB component	-2.2	3.29E-07
VC1835	peptidoglycan-associated lipoprotein	-2.1	1.44E-03



VC1865	hypothetical protein	-2.9	1.68E-18
VC2022	malonyl Coa-acyl carrier protein transacylase	-2.2	7.09E-19
VC2033	alcohol dehydrogenase/acetaldehydedehy drogenase	-3.1	1.75E-13
VC2045	superoxide dismutase, Fe	-2.2	8.82E-09
VC2078	ferrous iron transport protein A	-2.2	1.36E-05
VC2213	outer membrane protein OmpA	-4.1	3.04E-17
VC2259	elongation factor Ts	-3.4	1.00E-18
VC2260	ribosomal protein S2	-3.0	2.34E-13
VC2371	conserved hypothetical protein	-2.5	9.91E-07
VC2385	RNA-directed DNA polymerase	-2.1	2.70E-16
VC2386	conserved hypothetical protein	-2.7	5.02E-15
VC2387	conserved hypothetical protein	-2.4	1.59E-09
VC2389	carbamoyl-phosphate synthase, large subunit	-2.2	1.31E-13
VC2413	pyruvate dehydrogenase, E2 component,dihydrolipoamide acetyltransferase	-2.2	2.36E-03
VC2414	pyruvate dehydrogenase, E1 component	-2.1	1.52E-03
VC2480	ribose-5-phosphate isomerase	-2.0	4.00E-14
VC2568	peptidyl-prolyl cis-trans isomerase, FKBP-type	-2.7	2.20E-21
VC2569	hypothetical protein	-2.2	6.50E-10
VC2579	ribosomal protein S5	-2.1	1.33E-08
VC2580	ribosomal protein L18	-2.3	4.53E-04
VC2581	ribosomal protein L6	-2.1	2.37E-07
VC2582	ribosomal protein S8	-2.3	5.82E-04
VC2583	ribosomal protein S14	-2.1	6.38E-08
VC2585	ribosomal protein L24	-2.1	3.15E-07
VC2587	ribosomal protein S17	-2.2	4.92E-12
VC2588	ribosomal protein L29	-2.2	6.64E-10
VC2589	ribosomal protein L16	-2.2	1.07E-09
VC2590	ribosomal protein S3	-2.1	9.09E-07
VC2591	ribosomal protein L22	-2.6	6.69E-05
VC2592	ribosomal protein S19	-2.3	2.77E-04
VC2593	ribosomal protein L2	-2.3	1.53E-08
VC2594	ribosomal protein L23	-2.5	1.43E-12
VC2595	ribosomal protein L4	-2.0	2.77E-03
VC2662	conserved hypothetical protein	-3.4	4.58E-19
VC2663	molecular chaperone groEL_1	-2.2	1.19E-07
VC2664	chaperonin, 60 Kd subunit, groES_1	-2.2	1.49E-08
VC2670	triosephosphate isomerase	-2.6	9.46E-14
VC2679	ribosomal protein L31	-2.6	3.02E-17
VC2687	hypothetical protein	-2.1	1.39E-03
VC2691	periplasmic protein cpxP, putative	-3.8	5.72E-15
VC2715	transcription elongation factor GreB	-2.0	1.58E-04
VC2746	glutamate--ammonia ligase	-2.2	5.23E-06
VC2753	hypothetical protein	-2.0	1.49E-04
VC2761	multidrug resistance protein	-3.6	1.89E-19
VCA0017	hcp-2 protein	-7.4	2.06E-41
VCA0018	vgrG protein	-2.1	3.35E-06
VCA0019	hypothetical protein	-3.3	7.85E-14
VCA0020	hypothetical protein	-2.7	1.40E-27
VCA0021	hypothetical protein	-2.0	8.31E-07
VCA0023	hypothetical protein	-2.1	1.28E-04
VCA0035	phosphatidylglycerop hosphatase B, putative	-3.0	8.88E-17
VCA0087	hypothetical protein	-3.0	2.25E-07
VCA0088	proton/glutamate symporter	-2.1	1.25E-10
VCA0107	conserved hypothetical protein	-2.7	1.39E-16
VCA0108	conserved hypothetical protein	-2.9	1.58E-15
VCA0112	hypothetical protein	-2.2	4.79E-11
VCA0136	glycerophosphoryl diester phosphodiesterase	-8.9	1.84E-52
VCA0137	glycerol-3-phosphate transporter	-8.8	1.31E-19
VCA0139	hypothetical protein	-3.0	1.10E-12
VCA0227	iron(III) ABC transporter, periplasmiciron-compound-binding protein	-3.3	1.42E-06

VCA0230	iron(III) ABC transporter, ATP-binding protein	-2.9	5.74E-09
VCA0363	hypothetical protein	-2.3	1.07E-04
VCA0370	hypothetical protein	-4.4	2.67E-03
VCA0407	hypothetical protein	-2.6	4.02E-04
VCA0517	1-phosphofructokinase	-2.9	2.75E-11
VCA0518	PTS system, fructose-specific IIA/FPR component	-5.7	3.31E-31
VCA0519	fructose repressor	-2.8	2.04E-15
VCA0540	formate transporter 1, putative	-9.0	2.76E-85
VCA0542	transcriptional regulator, LysR family	-2.5	7.06E-16
VCA0563	NAD(P) transhydrogenase, alpha subunit	-2.4	1.10E-11
VCA0564	NAD(P) transhydrogenase, beta subunit	-2.5	9.03E-14
VCA0576	heme transport protein HutA	-2.5	3.15E-11
VCA0657	aerobic glycerol-3-phosphate dehydrogenase	-39.8	1.99E-121
VCA0732	conserved hypothetical protein	-2.6	6.47E-10
VCA0742	hypothetical protein	-2.1	2.26E-04
VCA0744	glycerol kinase	-6.5	1.89E-39
VCA0745	pseudogene with authentic frameshift mutation	-6.1	9.74E-37
VCA0747	anaerobic glycerol-3-phosphate dehydrogenase, subunit A	-28.6	6.35E-125
VCA0748	anaerobic glycerol-3-phosphate dehydrogenase, subunit B	-17.1	3.70E-94
VCA0749	anaerobic glycerol-3-phosphate dehydrogenase, subunit C	-19.1	8.32E-91
VCA0789	conserved hypothetical protein	-2.9	2.96E-14
VCA0819	chaperonin, 10 Kd subunit	-2.1	4.20E-06
VCA0862	long-chain fatty acid transport protein	-2.5	2.92E-11
VCA0863	lipase, putative	-2.6	4.75E-17
VCA0874	hypothetical protein	-2.4	1.00E-05
VCA0898	6-phosphogluconate dehydrogenase, decarboxylating	-2.9	2.97E-22
VCA0933	cold shock domain family protein	-2.4	1.49E-10
VCA0984	L-lactate dehydrogenase	-5.7	1.09E-33
VCA0985	oxidoreductase/iron-sulfur cluster-binding protein	-3.0	3.71E-16
VCA1013	conserved hypothetical protein	-2.1	2.59E-07
VCA1035	hypothetical protein	-2.5	9.63E-10
VCA1060	3,4-dihydroxy-2-butanone 4-phosphate synthase	-2.2	5.69E-11
VCA1063	ornithine decarboxylase, inducible	-3.0	4.17E-12
tRNA-Ala-2	tRNA biosynthesis	-3.1	1.70E-05
tRNA-Gln-1	tRNA biosynthesis	-2.4	9.80E-05
tRNA-Gly-3	tRNA biosynthesis	-2.1	4.67E-08
tRNA-Gly-7	tRNA biosynthesis	-2.5	3.48E-04
tRNA-Leu-2	tRNA biosynthesis	-2.6	1.11E-04
tRNA-Leu-9	tRNA biosynthesis	-2.9	7.67E-04
tRNA-Met-4	tRNA biosynthesis	-2.2	1.53E-04
tRNA-Met-5	tRNA biosynthesis	-4.4	8.60E-09
tRNA-Met-6	tRNA biosynthesis	-2.7	1.33E-03
tRNA-Phe-1	tRNA biosynthesis	-2.2	2.73E-07
tRNA-Thr-6	tRNA biosynthesis	-2.4	6.99E-05
tRNA-Tyr-3	tRNA biosynthesis	-3.4	8.81E-07
tRNA-Tyr-4	tRNA biosynthesis	-2.2	6.29E-06
tRNA-Val-3	tRNA biosynthesis	-2.3	2.39E-05