

Table S2. List of genes that were up-regulated in the *virX* mutant TS186

CPE#	Gene	Product	Fold change (log2)	t-test p-value
CPE0033		hypothetical protein	2.62	3.17E-05
CPE0052		hypothetical protein	1.64	1.38E-03
CPE0068	<i>glgC</i>	glucose-1-phosphate adenylyltransferase	3.66	2.59E-04
CPE0069	<i>glgD</i>	glycogen biosynthesis protein glgD	3.19	2.85E-04
CPE0070		conserved hypothetical protein	2.99	8.25E-05
CPE0113		hypothetical protein	1.86	9.30E-03
CPE0114		hypothetical protein	2.40	1.31E-02
CPE0125		hypothetical protein	1.81	8.82E-03
CPE0126		hypothetical protein	2.05	1.85E-02
CPE0127		hypothetical protein	1.56	6.52E-03
CPE0130		hypothetical protein	2.80	2.92E-04
CPE0134		hypothetical protein	2.76	1.24E-04
CPE0138		phage-related hypothetical protein	1.77	6.12E-04
CPE0191	<i>nagH</i>	hyaluronidase (Mu-toxin)	3.40	4.09E-04
CPE0203		hypothetical protein	1.57	8.14E-03
CPE0206		hypothetical protein	3.30	7.58E-04
CPE0209		hypothetical protein	1.58	7.27E-04
CPE0222		sortase	1.72	2.69E-03
CPE0230		hypothetical protein	1.96	3.20E-03
CPE0237	<i>napA</i>	probable Na ⁺ /H ⁺ antiporter	2.92	4.89E-04
CPE0258		probable transcriptional regulator	2.40	2.77E-04
CPE0357		hypothetical protein	1.92	5.58E-05
CPE0383		conserved hypothetical protein	1.58	4.62E-03
CPE0428		hypothetical protein	3.06	1.77E-05
CPE0466		hypothetical protein	1.55	2.11E-02
CPE0522		conserved hypothetical protein	2.15	1.41E-03
CPE0553	<i>nanJ</i>	exo-alpha-sialidase	4.10	3.98E-04
CPE0554		hypothetical protein	4.33	3.23E-04

CPE0576		ABC transporter SBP	3.19	2.08E-04
CPE0577		ABC transporter MSD	2.54	6.95E-05
CPE0578		ABC transporter MSD	2.12	3.46E-04
CPE0645	<i>gltX</i>	glutamine--tRNA ligase	5.17	1.87E-04
CPE0802		hypothetical protein	3.45	8.14E-05
CPE0818		endo-beta-N-acetylglucosaminidase	4.60	1.79E-04
CPE0867		hypothetical protein	2.11	1.07E-03
CPE0925		hypothetical protein	1.77	9.67E-04
CPE0938		hypothetical protein	1.92	4.12E-05
CPE0952		hypothetical protein	1.51	7.21E-04
CPE1023		hypothetical protein	1.53	2.43E-04
CPE1024		hypothetical protein	1.76	8.47E-04
CPE1066		deoxycytidylate deaminase	2.75	4.23E-04
CPE1072	<i>accB</i>	acetyl-CoA carboxylase	2.66	5.83E-05
CPE1077		hypothetical protein	1.67	1.65E-04
CPE1081		conserved hypothetical protein	2.15	6.32E-05
CPE1109		hypothetical protein	2.57	1.67E-04
CPE1111		hypothetical protein	1.61	2.14E-04
CPE1113		hypothetical protein	2.34	2.58E-05
CPE1125		hypothetical protein, phage-related	1.60	3.14E-03
CPE1135		hypothetical protein	2.09	4.43E-04
CPE1136		hypothetical protein	2.72	6.61E-04
CPE1143		hypothetical protein	2.40	1.55E-03
CPE1145	<i>citG</i>	CitG protein	1.54	7.65E-02
CPE1164		hypothetical protein	3.33	1.14E-05
CPE1212	<i>uraA</i>	probable uracil permease	2.02	1.45E-03
CPE1213		hypothetical protein	1.62	1.70E-04
CPE1214		conserved hypothetical protein	2.01	6.94E-04
CPE1234	<i>nagJ</i>	hyaluronidase (Mu-toxin)	3.79	4.82E-04
CPE1235		hypothetical protein	1.82	4.68E-03
CPE1266		beta-galactosidase	3.14	3.41E-04
CPE1280		hypothetical protein	3.04	2.27E-05

CPE1341		ABC transporter SBP (galactoside importer)	6.89	2.23E-04
CPE1342		ABC transporter NBD (galactoside importer)	6.47	7.20E-05
CPE1343		ABC transporter MSD (galactoside importer)	6.33	4.99E-05
CPE1353		hypothetical protein	2.74	6.88E-04
CPE1364		conserved hypothetical protein	1.77	1.49E-03
CPE1371		sodium-/chloride-dependent transporter	1.57	2.52E-03
CPE1376		hypothetical protein	1.67	1.87E-04
CPE1499	<i>comEC</i>	probable late competence protein	2.01	3.26E-05
CPE1511		hypothetical protein	1.52	1.18E-04
CPE1515		hypothetical protein	2.08	8.35E-03
CPE1523	<i>nagL</i>	hyaluronidase (Mu-toxin)	4.58	2.10E-03
CPE1564		conserved hypothetical protein	1.61	1.18E-03
CPE1584		hypothetical protein	1.66	3.46E-04
CPE1586		hypothetical protein	2.86	6.67E-05
CPE1591		conserved hypothetical protein	1.62	2.63E-03
CPE1595		probable thioredoxin	1.77	7.84E-05
CPE1663		conserved hypothetical protein	4.35	6.22E-04
CPE1734	<i>rpmB</i>	probable 50S ribosomal protein L28	1.50	1.27E-03
CPE1749		conserved hypothetical protein	1.58	1.35E-05
CPE1753	<i>spoIVA</i>	stage IV sporulation protein A	3.02	8.74E-04
CPE1761	<i>sigG</i>	RNA polymerase sigma-G factor	2.00	1.06E-04
CPE1762	<i>sigE</i>	RNA polymerase sigma-E factor	3.28	2.64E-04
		<i>spoIIG</i>		
CPE1763	<i>A</i>	sporulation protein spoIIGA	2.98	1.16E-03
CPE1782		hypothetical protein	1.72	3.67E-04
CPE1812	<i>spo0A</i>	transcription factor Spo0A	2.23	1.12E-03
CPE1875		conserved hypothetical protein	2.14	1.49E-03
CPE1876		conserved hypothetical protein	2.63	3.34E-03
CPE1949		hypothetical protein	1.63	2.72E-02
CPE2005		conserved hypothetical protein	1.56	5.03E-03
CPE2048	<i>sigF</i>	RNA polymerase sigma-F factor	4.53	6.72E-04
CPE2049	<i>spoIIA</i>	anti-sigma F factor antagonist	4.61	1.29E-04

<i>B</i>				
<i>spoIIA</i>				
CPE2050	<i>A</i>	anti-sigma F factor antagonist	4.41	5.62E-05
CPE2146		hypothetical protein	4.53	4.48E-04
CPE2182		conserved hypothetical protein	2.23	1.73E-02
CPE2215		hypothetical protein	2.44	2.34E-03
CPE2261		hypothetical protein	2.82	1.38E-03
CPE2262		hypothetical protein	3.07	9.36E-04
CPE2263		hypothetical protein (sortase substrate)	3.70	8.51E-04
CPE2288		prepilin peptidase dependent protein A	1.56	2.08E-02
CPE2295	<i>lepW</i>	signal peptidase type I	2.92	1.69E-04
CPE2364		TCS27, two-component response regulator	1.52	5.56E-03
CPE2470	<i>ftsH2</i>	probable cell-division protein ftsH	1.75	5.15E-04
		hypoxanthine-guanine		
CPE2471	<i>hprT2</i>	phosphoribosyltransferase	1.84	1.20E-03
CPE2472		probable cell-cycle protein	2.79	1.48E-03
CPE2473	<i>spoIIE</i>	stage II sprulation protein E	5.40	2.06E-04
CPE2511	<i>fer2</i>	ferredoxin [3Fe-4S]-like protein	1.71	8.97E-04
CPE2625		tagatose-6-phosphate aldose/ketose isomerase	1.54	3.33E-02
		PTS system,, mannose-specific, component		
CPE2632		IIAB	1.76	4.51E-04

The Microarra experiment was carried out according to the method employed previously (Ohtani et al, Anaerobe, 2010). The microarray experiments were performed four times at 3 h from the start of culture, The 4 data sets were statistically analyzed by GeneSpring GX software. To find the gene whose mean log₂ expression ratio is significantly different from the all genes, we performed the Welch t-test intending for use with two samples having possibly unequal variances. T-values are calculated for each gene, and p-values are directly calculated from the theoretical t-distribution based on the gene's calculated t-value. Significantly differentially expressed genes were selected by using a p-value threshold of 0.05. Finally, the log₂ expression ratio was standardized to normal distribution, and the genes showing significant differences in expression (>1.5 σ) were picked up.

