Table S1. List of genes that were down-regulated in the *virX* mutant TS186

CPE#	gene	product	Fold change (log2)	t-test p-value
CPE0168	*arcA*	arginine deiminase	-3.95	3.49E-04
CPE0169	*arcB*	ornithine carbamoyl transferase	-3.74	1.04E-03
CPE0170	*arcD*	arginine ornithine antiporter	-4.30	6.92E-04
CPE0171	*arcC*	carbamate kinase	-4.02	4.57E-04
CPE0172	*argR*	arginine repressor	-2.33	3.45E-03
CPE0173	*colA*	collagenase (kappa-toxin)	-1.73	6.03E-04
CPE0299	*ftsE*	cell-division ATP-binding protein ftsE	-1.60	5.25E-04
CPE0300	*ftsX*	cell-division protein ftsX	-1.62	1.15E-03
CPE0494		probable NDP-suger dehydrogenase	-1.97	1.34E-05
CPE0659		conserved hypothetical protein	-1.79	4.01E-04
CPE0821		PTS system, mannnose-specific component IIAB	-2.27	6.52E-04
CPE0822		PTS system, mannnose-specific component IIC	-2.24	9.28E-04
CPE0823		PTS system, mannnose-specific component IID	-2.29	2.13E-03
CPE0824		PTS system, mannnose-specific component IID	-1.90	2.00E-04
CPE0892		NADPH-dependent butanol dehydrogenase	-2.09	8.41E-03
CPE0897	*eutA*	ethanolamine utilization protein	-2.06	4.48E-02
CPE0898	*eutB*	ethanolamine ammonia lyase heavy chain	-2.37	1.34E-02
CPE0899	*eutC*	ethanolamine ammonia lyase light chain	-2.52	1.61E-02
CPE0900	*eutL*	ethanolamine utilization protein	-2.43	1.17E-02
CPE0901	*pduJ*	propanediol utilization protein	-2.50	1.55E-02
CPE0902	*adhE*	probable alcohol dehydrogenase	-3.02	1.11E-02
CPE0903	*pduJ2*	propanediol utilization protein	-1.72	2.16E-02
CPE0904	*eutT*	cobalamin adenosyltransferase	-2.64	1.35E-02
CPE0905	*pduL*	propanediol utilization protein	-2.12	2.07E-02
CPE0906		hypothetical protein	-2.51	1.49E-02
CPE0908	*pduT*	propanediol utilization protein	-1.89	4.67E-02
CPE0909	*eutH*	ethanolamine utilization protein	-2.34	1.68E-02
CPE0910	*eutQ*	ethanolamine utilization protein	-1.77	1.82E-02

CPE1041		ABC transporter SBP (ferric ion importer)	-1.64	8.21E-05
CPE1092	*pac*	probable penicillin acylase	-2.41	9.11E-05
CPE1358		hypothetical protein	-1.79	4.51E-03
CPE1430	*clsD*	cardiolipin synthase	-1.92	1.13E-03
CPE1497		conserved hypothetical protein	-1.71	3.49E-03
CPE1512	*reeS*	two-component sensor kinase/regulator	-2.05	1.44E-04
CPE1518	*gdhA*	NADP-specific glutamate dehydrogenase	-1.55	7.39E-04
CPE1604		probable multidrug-efflux transporter	-1.93	7.06E-04
CPE1795		nitrate reductase NADH oxydase subunit	-1.61	4.03E-04
CPE1815	*recN*	DNA repair andrecombination protein recN	-2.20	5.18E-04
CPE1819		1-deoxyxylulose-5-phosphate synthase	-1.77	1.27E-04
CPE1907	*patA*	probable aspartate aminotransferase	-1.72	9.58E-04
CPE1926		two-component sensor histidine kinase	-2.06	1.09E-04
CPE1991		conserved hypothetical protein	-1.80	6.37E-05
CPE2276		inositol-monophosphate dehydrogenase	-1.73	1.33E-04
CPE2285		probable pilin biogenesis protein	-1.70	6.80E-05
CPE2286		probable pilin biogenesis protein	-2.01	9.54E-04
CPE2310	*aldH*	aldehyde dehydrogenase	-2.01	2.24E-04
CPE2317		probable Na+/H+ antiporter, putative	-1.77	9.21E-03
CPE2331		two-component sensor histidine kinase	-1.68	2.98E-03
CPE2424		tRNA/rRNA methyltransferase	-1.71	1.80E-03
CPE2528		conserved hypothetical protein	-1.75	1.40E-03
CPE2615		conserved hypothetical protein	-1.87	3.86E-04
CPE2623	*sdhB2*	L-serine dehydratase, beta subunit	-2.07	1.04E-05
CPE2654	*gidA*	glucose-inhibited division protein GidA	-1.51	1.32E-05

The microarrya 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 ($<-1.5\ \sigma$) were picked up.