

Table S11

Table S11: Putative phage contigs that has a Log2FC above 1 (Green dots) or below – 1 (Red dots) (Figure 5A). Contigs were blasted using megablast. Denoted below are the top viral hit with lowest E-value and highest query coverage.

Contig	Size (Bp)	> 1: Log2FC > 1 < -1: Log2FC < -1	Blast hit (Accession no.)	Query Coverage	Per. Identity	E-Value
tig00010143	20829	> 1	Lactobacillus phage iLp1308 (KR905070.1)	7%	77.16%	0.0
NODE_45	50899	> 1	Siphoviridae NHS-Seq1 (MH029512.1)	32%	80%	0.0
tig00000588	18290	> 1	Lactobacillus phage 3-SAC12 (MK504442.1)	3%	91.75%	2e-161
NODE_3	59207	> 1	Enterobacteria phage CAjan (KP064094.1)	100%	100%	0.0
NODE_45	10380	> 1	Lactococcus phage 56301 (NC_049405.1)	45%	85.77%	0.0
NODE_220	5166	> 1	Lactobacillus phage AQ113 (HE956704.1)	8%	84.40%	3e-119
NODE_2743	5420	> 1	Leuconostoc phage CHB (KX578043.1)	8%	67.40%	3e-29
tig00001464	9726	< -1	Lactobacillus phage Lenus (NC_047897.1)	89%	97.35%	0.0
NODE_830	5136	< -1	Paramecium bursaria Chlerella virus CVM-1 (JX997163.1)	1%	75.29%	0.003
NODE_690	6178	< -1	Lactobacillus phage 3-521 (NC_048753.1)	100%	97.28%	0.0
NODE_2693	5480	< -1	Lactobacillus phage 3-521 (NC_048753.1)	93%	97.70%	0.0
NODE_132	40054	< -1	Uncultured Caudivirales phage (LR796317.1)	1%	68.32%	1e-37
tig00000648	32820	< -1	Lactobacillus phage LR2 (MH837543.1)	5%	67.97%	3e-64
tig00000040	44196	< -1	Escherichia phage C130_2 (NC_048067.1)	2%	76.66%	4e-127
NODE_852	11518	< -1	Phage apr34_1789 (MK415401.1)	0%	80.21%	2e-11
tig00000828	11199	< -1	Proteus phage vB_PmiP_RS8pmA (MG575419.1)	88%	93.04%	0.0
NODE_830	5580	< -1	<i>Lactococcus lactis</i> . Subs. <i>Lactis</i> strain G423 (CP024958.1)	1%	80%	0.047
NODE_214	32484	< -1	Proteus phage PM75 (NC_027363.1)	61%	92.01%	0.0