

**Table S12**

**Table S12:** Putative phage contigs that has a Log2FC between -1 and 1 without a significant abundance (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)	0-1: Log2FC -1-0: Log2FC	Blast hit (accession no.)	Query coverage	Per. identity	E-value
NODE_364	6226	0-1	Proteus phage vB_PmiP_RS51pmB (MG575421.1)	6%	79.59%	5e-44
NODE_209	8610	0-1	Bacteriophage sp. Isolate 179 (MN855830.1)	54%	84.73%	0.0
NODE_445	5408	0-1	Lactobacillus phage ATCCB (MK504445.1)	21%	76.79%	1e-174
tig00001258	5764	0-1	Lactobacillus phage AQ113 (HE956704.1)	16%	72.53%	1e-154
NODE_2231	6180	0-1	Myoviridae sp. ctThM1 (MN582070.1)	9%	72.78%	9e-50
NODE_507	5015	0-1	Bacteriophage sp. Isolate 103 (MN855801.1)	3%	73.96%	1e-15
NODE_165	6157	0-1	Bacteriophage sp. Isolate 32 (MN855637.1)	0%	88.89%	4e-05
NODE_281	9947	-1-0	Xylella phage Usme (LR743523.1)	1%	75.94%	1e-46
NODE_244	10727	-1-0	Salmonella phage assan (MT074440.1)	20%	69.49%	3e-97
tig00000616	17334	-1-0	Lactobacillus phage CL2 (KR905067.1)	5%	83.54%	0.0
tig00010057	16105	-1-0	Lactobacillus phage LBR48 (GU967410.1)	8%	92.67%	0.0
NODE_966	5065	-1-0	Bacteriophage sp. isolate 230 (MN855846.1)	41%	83.45%	0.0
NODE_1644	7563	-1-0	Lactobacillus phage ATCC 8014-B2 (NC_047739.1)	22%	80.31%	0.0
NODE_2505	5716	-1-0	Lactobacillus phage ATCC 8014-B2 (NC_047739.1)	84%	85.48%	0.0