

Additional File 3. Metaviromes reads associated with human and bacterial genomes.

Percentage of reads are based on 5,000,000 sequences per phage metavirome.

Extraction	Phage metaviromes' sequences classified as			
	Human genome	Bacterial genomes	18S rRNA	16S rRNA
LIT_1	0.10%	44.57%	0.002%	0.005%
LIT_2	0.03%	51.34%	0.002%	0.004%
PEG_1	0.01%	22.04%	0.000%	0.001%
PEG_2	0.01%	20.20%	0.000%	0.001%
TFF_1	0.01%	15.02%	0.000%	0.001%
TFF_2	0.01%	18.65%	0.001%	0.001%