

## Supplementary Materials

Table S2 The viral contigs containing genes encoding integrase, site-specific recombinases, and transposases in viromes based on Pfam and KEGG.

Contig_ID	Contig_Taxonomy	Protein_Accession / Pfam_ID /		Description	Evalue	Sources
		Gene ID	KO			
NE_P contig_11857	Unknown	GL0005598	PF14659	Phage integrase, N-terminal SAM-like domain	2.10E-13	Pfam
NE_P contig_29415	Unknown	GL0008359	PF02945	Recombination endonuclease VII	8.20E-09	Pfam
NE_P contig_42090	Unknown	GL0010261	PF09588	YqaJ-like viral recombinase domain	4.80E-08	Pfam
NE_P contig_51394	Unknown	GL0011536	PF00589	Phage integrase family	5.80E-09	Pfam
NE_P contig_5394	Unknown	GL0004501	PF02945	Recombination endonuclease VII	3.70E-12	Pfam
NE_P contig_56145	Unknown	GL0012112	PF09588	YqaJ-like viral recombinase domain	3.60E-15	Pfam
NE_P contig_59860	Caudovirales Siphoviridae unclassified TM7 phage DoIZOral124_53_65	GL0012608	PF09588	YqaJ-like viral recombinase domain	2.10E-07	Pfam
NE_P contig_61680	Unknown	GL0012935	PF02945	Recombination endonuclease VII	5.30E-21	Pfam
NE_P contig_6400	unclassified Microviridae unclassified Microviridae sp.	GL0004723	PF00589	Phage integrase family	3.40E-07	Pfam
NE_P contig_65943	Unknown	GL0013757	PF00589	Phage integrase family	3.70E-15	Pfam
NE_P contig_8479	Unknown	GL0005055	PF02945	Recombination endonuclease VII	2.80E-09	Pfam

SW_M contig_11510	Unknown	GL0016847	PF09588	YqaJ-like viral recombinase domain	3.60E-08	Pfam
SW_M contig_1330	Unknown	GL0016222	PF09588	YqaJ-like viral recombinase domain	2.40E-11	Pfam
SW_M contig_20849	Unknown	GL0017396	PF02945	Recombination endonuclease VII	2.80E-14	Pfam
SW_M contig_34426	Unknown	GL0019308	PF00589	Phage integrase family	1.10E-06	Pfam
SW_M contig_35326	Unknown	GL0019379	PF07282	Putative transposase DNA-binding domain	2.30E-13	Pfam
SW_M contig_35442	Unknown	GL0019391	PF02945	Recombination endonuclease VII	6.70E-11	Pfam
SW_M contig_35934	unclassified Pithoviridae unclassified Pithovirus LCPAC104	GL0019428	PF09588	YqaJ-like viral recombinase domain	4.70E-10	Pfam
SW_M contig_36223	Caudovirales Herelleviridae unclassified Bacillus phage SP-10	GL0019477	PF11056	Recombination, repair and ssDNA binding protein UvsY	2.00E-06	Pfam
SW_M contig_36949	Unknown	GL0019650	PF02945	Recombination endonuclease VII	5.20E-11	Pfam
SW_M contig_6761	Caudovirales Siphoviridae unclassified Geobacillus phage GBK2	GL0016533	PF13102	Phage integrase SAM-like domain	5.70E-06	Pfam
SW_M contig_9807	Unknown	GL0016758	PF02945	Recombination endonuclease VII	1.20E-19	Pfam
SW_P contig_1513	Caudovirales Herelleviridae Sepunavirus Staphylococcus phage Terranova	GL0021789	PF00589	Phage integrase family	8.60E-11	Pfam
NE_P contig_4363	unclassified Microviridae unclassified Microviridae sp.	GL0004289	K03553	recombination protein RecA (A)	0.00033	KEGG

SW_M contig_24176	Caudovirales Myoviridae unclassified Xanthomonas phage XacN1	GL0017816	K03553	recombination protein RecA (A)	0.000000016	KEGG
SW_M contig_29539	Caudovirales Myoviridae Emdodocavirus Sinorhizobium virus M7	GL0018699	K00527	ribonucleoside-triphosphate reductase [EC:1.17.4.2] (A)	2.1E-130	KEGG
SW_M contig_35326	Unknown	GL0019379	K07496	putative transposase (A)	0.000021	KEGG
SW_M contig_36223	Caudovirales Herelleviridae unclassified Bacillus phage SP-10	GL0019479	K03553	recombination protein RecA (A)	1.6E-15	KEGG
SW_P contig_1513	Caudovirales Herelleviridae Sepunavirus Staphylococcus phage Terranova	GL0021789	K04763	integrase/recombinase XerD (A)	2.5E-12	KEGG

Table S3 Phage-bacteria linkages between viral contigs and bacterial genomes by CRISPR spacer

Bacteria		Phages	
Phyla	Species	Family	Species
Proteobacteria	<i>Aeromonas caviae</i>	<i>Myoviridae</i>	<i>Aeromonas phage</i> <i>62AhydR11PP</i>
Firmicutes	<i>Megamonas funiformis</i>	<i>Microviridae</i>	<i>Apis mellifera associated</i> <i>microvirus 3</i>
Chlorobi	<i>Prosthecochloris aestuarii</i>	<i>Microviridae</i>	<i>Apis mellifera associated</i> <i>microvirus 33</i>
Chlorobi	<i>Prosthecochloris sp._ZM_2</i>	<i>Microviridae</i>	<i>Apis mellifera associated</i> <i>microvirus 33</i>
Firmicutes	<i>Tyzzerella nexilis</i>	<i>Microviridae</i>	<i>Apis mellifera associated</i> <i>microvirus 4</i>
Proteobacteria	<i>Legionella pneumophila</i>	<i>Microviridae</i>	<i>Apis mellifera associated</i> <i>microvirus 51</i>

Firmicutes	<i>Coprobacillus_sp._AF09-1A</i>	Microviridae	<i>Apis mellifera associated microvirus 61</i>
Bacteroidetes	<i>Butyricimonas_synergistica</i>	Microviridae	<i>Blackfly microvirus SF02</i>
Chlorobi	<i>Prosthecochloris_sp._ZM</i>	Microviridae	<i>Blackfly microvirus SF02</i>
Firmicutes	<i>[Clostridium]_spiroforme</i>	Microviridae	<i>Blackfly microvirus SF02</i>
Firmicutes	<i>Clostridiales_bacterium_VE202-01</i>	Microviridae	<i>Blackfly microvirus SF02</i>
Firmicutes	<i>Megasphaera_sp._An286</i>	Microviridae	<i>Blackfly microvirus SF02</i>
Firmicutes	<i>Megasphaera_stantonii</i>	Microviridae	<i>Blackfly microvirus SF02</i>
Firmicutes	<i>Pseudoflavonifractor_capillosus</i>	Microviridae	<i>Blackfly microvirus SF02</i>
Proteobacteria	<i>Legionella_pneumophila</i>	Microviridae	<i>Blackfly microvirus SF02</i>
Proteobacteria	<i>Nitrosospira_multiformis;</i>	Microviridae	<i>Blackfly microvirus SF02</i>
Proteobacteria	<i>Nitrosospira_sp._Nsp5</i>	Microviridae	<i>Blackfly microvirus SF02</i>
Proteobacteria	<i>Nitrosospira_sp._Nsp6;</i>	Microviridae	<i>Blackfly microvirus SF02</i>
Proteobacteria	<i>Vibrio_parahaemolyticus</i>	Microviridae	<i>Blackfly microvirus SF02</i>
Proteobacteria	<i>Neisseria_lactamica;</i>	Ackermannviridae	<i>Dickeya phage phiDP10.3</i>
Proteobacteria	<i>Neisseria_meningitidis;</i>	Ackermannviridae	<i>Dickeya phage phiDP10.3</i>
Proteobacteria	<i>Pseudomonas_formosensis</i>	Ackermannviridae	<i>Dickeya phage phiDP10.3</i>
Firmicutes	<i>Mycoplasma_dispar</i>	Ackermannviridae	<i>Dickeya phage phiDP23.1</i>
			<i>Diporeia-associated</i>
Chlamydiae	<i>Chlamydia_abortus</i>	unclassified	<i>CRESS-DNA virus LH481</i>
			<i>Eel River basin pequenovirus</i>
Proteobacteria	<i>Enterobacter_roggenkampii</i>	Microviridae	<i>Gokushovirinae</i>
Proteobacteria	<i>Enterobacter_hormaechei</i>	Microviridae	<i>Bog1183_53</i>

Proteobacteria	<i>Legionella_pneumophila</i>	Microviridae	Gokushovirinae Bog1183_53
Firmicutes	<i>Phascolarctobacterium_succinatutens</i>	Microviridae	Gokushovirinae Fen672_31
Proteobacteria	<i>Candidimonas_nitroreducens</i>	Microviridae	Gokushovirinae GAIR4
Proteobacteria	<i>Orbus_hercynius</i>	Microviridae	Gokushovirinae GAIR4
Proteobacteria	<i>Acinetobacter_indicus</i> ;	Inoviridae	Inoviridae sp.
Proteobacteria	<i>Acinetobacter_parvus</i> ;	Inoviridae	Inoviridae sp.
Proteobacteria	<i>Acinetobacter_sp._479375</i> ;	Inoviridae	Inoviridae sp.
Proteobacteria	<i>Acinetobacter_sp._B51(2017)</i> ;	Inoviridae	Inoviridae sp.
Proteobacteria	<i>Acinetobacter_sp._CIP_102082</i>	Inoviridae	Inoviridae sp.
Proteobacteria	<i>Acinetobacter_sp._CIP_102529</i> ;	Inoviridae	Inoviridae sp.
Proteobacteria	<i>Acinetobacter_sp._WCHA39</i>	Inoviridae	Inoviridae sp.
Proteobacteria	<i>Acinetobacter_ursingii</i>	Inoviridae	Inoviridae sp.
Actinobacteria	<i>Pseudonocardia_sp._Ae717_Ps2</i>	Microviridae	Microviridae sp.
Chlorobi	<i>Chlorobium_ferrooxidans</i>	Microviridae	Microviridae sp.
Chlorobi	<i>Parapedobacter_composti</i>	Microviridae	Microviridae sp.
Chlorobi	<i>Prosthecochloris_sp._HL-130-GSB</i>	Microviridae	Microviridae sp.
Chlorobi	<i>Prosthecochloris_sp._ZM_2</i>	Microviridae	Microviridae sp.
Firmicutes	<i>[Clostridium]_spiroforme</i>	Microviridae	Microviridae sp.
Firmicutes	<i>Blautia_sp._KGMB01111</i>	Microviridae	Microviridae sp.
Firmicutes	<i>Clostridiales_bacterium_VE202-01</i>	Microviridae	Microviridae sp.
Planctomycetes	<i>Sedimentisphaera_salicampi</i>	Microviridae	Microviridae sp.
Proteobacteria	<i>Bathymodiolus_thermophilus_thioautotrophic_gill_symbiont</i>	Microviridae	Microviridae sp.
Proteobacteria	<i>Bordetella_pseudohinzii</i>	Microviridae	Microviridae sp.

Proteobacteria	<i>Burkholderiales_bacterium_YL45</i>	<i>Microviridae</i>	<i>Microviridae</i> sp.
Proteobacteria	<i>Candidatus_Berkiella_cookevillensis</i>	<i>Microviridae</i>	<i>Microviridae</i> sp.
Proteobacteria	<i>Enterobacter_cancerogenus</i>	<i>Microviridae</i>	<i>Microviridae</i> sp.
Proteobacteria	<i>Enterobacter_kobei</i>	<i>Microviridae</i>	<i>Microviridae</i> sp.
Proteobacteria	<i>Enterobacter_roggenkampii</i>	<i>Microviridae</i>	<i>Microviridae</i> sp.
Proteobacteria	<i>Filomicrobium_insigne</i>	<i>Microviridae</i>	<i>Microviridae</i> sp.
Proteobacteria	<i>Leclercia_adecarboxylata</i>	<i>Microviridae</i>	<i>Microviridae</i> sp.
Proteobacteria	<i>Legionella_drozanskii</i>	<i>Microviridae</i>	<i>Microviridae</i> sp.
Proteobacteria	<i>Legionella_pneumophila</i>	<i>Microviridae</i>	<i>Microviridae</i> sp.
Proteobacteria	<i>Marinomonas_arctica</i>	<i>Microviridae</i>	<i>Microviridae</i> sp.
Proteobacteria	<i>Marinomonas_sp._DSL-35</i>	<i>Microviridae</i>	<i>Microviridae</i> sp.
Proteobacteria	<i>Methylobacillus_flagellatus</i>	<i>Microviridae</i>	<i>Microviridae</i> sp.
Proteobacteria	<i>Methylobacter_tundripaludum</i>	<i>Microviridae</i>	<i>Microviridae</i> sp.
Proteobacteria	<i>Nitrosospira_multiformis</i> ;	<i>Microviridae</i>	<i>Microviridae</i> sp.
Proteobacteria	<i>Nitrosospira_sp._Nsp5</i>	<i>Microviridae</i>	<i>Microviridae</i> sp.
Proteobacteria	<i>Nitrosospira_sp._Nsp6</i> ;	<i>Microviridae</i>	<i>Microviridae</i> sp.
Proteobacteria	<i>Pigmentiphaga_sp._NML030171</i>	<i>Microviridae</i>	<i>Microviridae</i> sp.
Proteobacteria	<i>Salmonella_enterica</i>	<i>Microviridae</i>	<i>Microviridae</i> sp.
Proteobacteria	<i>Turicimonas_muris</i> ;	<i>Microviridae</i>	<i>Microviridae</i> sp.
Proteobacteria	<i>Vibrio_parahaemolyticus</i>	<i>Microviridae</i>	<i>Microviridae</i> sp.

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