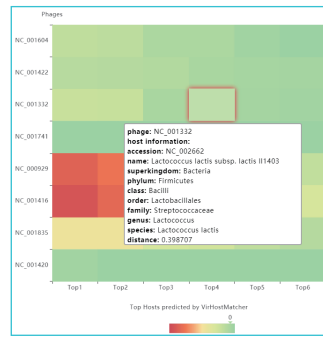


Modules

Functions & Visualizations

1. Oligonucleotide profile analysis

- VirHostMatcher
- WlsH



Best hit host for each phage

Phage_ID	Phage_Def	Host_ID(best hit)	Host_Def(best hit)	LogLikelihood
NC_000866	Enterobacteria phage T4, complete genome	NC_002662	Lactococcus lactis subsp. lactis I1403 chromosome, complete	-1.35086
NC_000871	Streptococcus phage 5619, complete genome	NC_002662	Lactococcus lactis subsp. lactis I1403 chromosome, complete	-1.3667
NC_000872	Streptococcus phage 5621, complete genome	NC_006448	Streptococcus thermophilus LMG 18311, complete genome	-1.36507
NC_000902	Enterobacteria phage VT2-Sakai, complete genome	NC_000913	Escherichia coli str. K-12 substr. MG1655, complete genome	-1.37093
NC_000924	Enterobacteria phage 933W, complete genome	NC_000913	Escherichia coli str. K-12 substr. MG1655, complete genome	-1.37133

2. CRISPR analysis

- Seq2CRISPR
- CRISPRFinder
- PILER-CR

Search:

Bacterium	Spacer_Info	HL_ID	HL_Def	Identity	E-value	Mismatch	Detail_Info
NC_017545.1 Listeria monocytogenes J0161, complete genome	2.31569024 NC_017545 36	NC_00812.1	Listeria phage B025, complete genome	97%	2e-10	1	Detail
NC_017545.1 Listeria monocytogenes J0161, complete genome	2.31569024 NC_017545 36	NC_024387.1	Listeria phage LP-101, complete genome	94%	1e-08	2	Detail
NC_017545.1 Listeria monocytogenes J0161, complete genome	2.91569414 NC_017545 36	NC_003216.1	Listeria phage A118, complete genome	100%	4e-12	0	Detail
NC_017545.1 Listeria monocytogenes J0161, complete genome	2.131569671 NC_017545 34	NC_003216.1	Listeria phage A118, complete genome	100%	5e-11	0	Detail
NC_017545.1 Listeria monocytogenes J0161, complete genome	2.14569734 NC_017545 36	NC_024384.1	Listeria phage LP-030-3, complete genome	100%	2e-10	0	Detail

Spacers Information

coverage = 0.9722222222222222

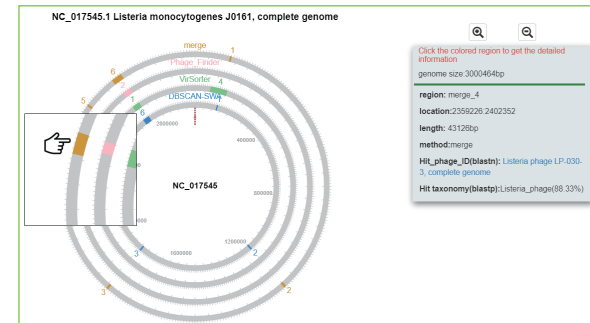
Query: 1:36
 CCTCTACGTTGATTTTTCGTACCAATTGCTAAA
 Sbjct: 27538:27583

Search:

Phage	HL_Spacer_Info	HL_ID	HL_Def	Identity	E-value	Mismatch	Detail_Info
NC_003216.1 Listeria phage A118, complete genome	4.25297423 37	NC_021823	Listeria monocytogenes strain C1-387, complete genome	100%	3e-11	0	Detail
NC_003216.1 Listeria phage A118, complete genome	2.18575714 37	NC_020833	Listeria monocytogenes strain CFSA0004305, complete genome	100%	3e-11	0	Detail
NC_003216.1 Listeria phage A118, complete genome	2.25145230 37	NC_020827	Listeria monocytogenes strain CFSA028536, complete genome	100%	3e-11	0	Detail
NC_003216.1 Listeria phage A118, complete genome	2.25154549 37	NC_017547	Listeria monocytogenes strain H98-1, complete genome	100%	3e-11	0	Detail

3. Prophage analysis

- Phage_Finder
- VirSorter
- DBSCAN-SWA

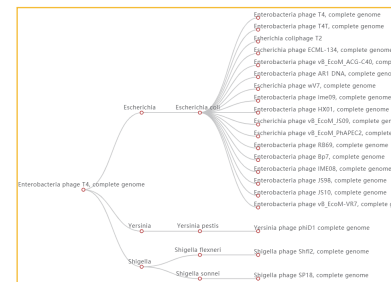


Search:

Region	Region Position	Best matching Phage(s)	Best matching Phage(s)	Prophage annotation
DBSCAN-SWA_1	126289 - 132816	Not Available	Listeria phage (33.33%)	Detail
DBSCAN-SWA_2	1146320 - 1154078	Not Available	Holovir (28.57%)	Detail
DBSCAN-SWA_3	1836780 - 1845066	Not Available	Synechococcus phage (33.33%)	Detail
DBSCAN-SWA_4	2359226 - 2402352	Listeria phage LP-030-3, complete genome	Listeria phage (88.33%)	Detail
DBSCAN-SWA_5	2558805 - 2563649	Not Available	Streptococcus phage (50.0%)	Detail
DBSCAN-SWA_6	2682415 - 2721802	Listeria phage A118, complete genome	Listeria phage (94.34%)	Detail

4. Similarity analysis

- HostPhinder
- GeneNet

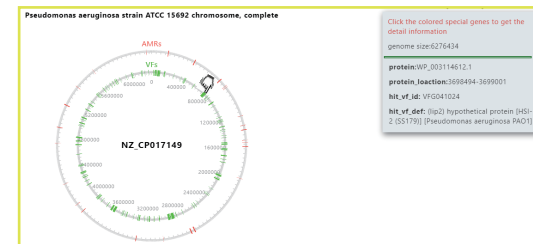


Phage_ID	Phage_Def	E-value	Host Species	Frequency(%)
NC_000866	Enterobacteria phage T4, complete genome.	0.05	Escherichia coli	85.0%
NC_000866	Enterobacteria phage T4, complete genome.	0.05	Yersinia pestis	5.0%
NC_000866	Enterobacteria phage T4, complete genome.	0.05	Shigella flexneri	5.0%
NC_000866	Enterobacteria phage T4, complete genome.	0.05	Shigella sonnei	5.0%

Phage_ID	Phage_Def	Host(genus)
NC_000866	Enterobacteria phage T4, complete genome.	Escherichia

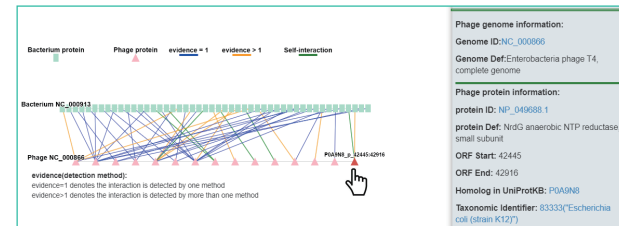
5. specialty gene check

- ShortBRED
- RGI



Protein_ID	Protein_Def	VFDB_HL_ID	VFDB_HL_Def
WP_003082146.1	flagellar basal body rod protein FlgB	VFG014148	(FlgB) flagellar basal body rod prote...
WP_003082153.1	flagellar hook assembly protein FlgD	VFG014176	(FlgD) flagellar basal-body rod mod...
WP_003082154.1	flagellar hook protein FlgE	VFG014188	(FlgE) flagellar hook protein (Flagell...
WP_003082154.1	flagellar hook protein FlgE	VFG014188	(FlgE) flagellar hook protein (Flagell...
WP_003082159.1	flagellar basal-body rod protein FlgF	VFG014199	(FlgF) flagellar basal-body rod prote...
WP_003082190.1	B-type flagellar hook-associated protein 2	VFG014319	(FlgD) flagellar capping protein FlgD...
WP_003082190.1	B-type flagellar hook-associated protein 2	VFG014319	(FlgD) flagellar capping protein FlgD...
WP_003082192.1	flagellar export chaperone FlgH	VFG014330	(FlgH) flagellar protein FlgH (Desoxyh...
WP_003082192.1	flagellar export chaperone FlgH	VFG014330	(FlgH) flagellar protein FlgH (Desoxyh...
WP_003082194.1	flagellar protein FlgT	VFG014343	(FlgT) flagellar protein FlgT (Desoxyh...

6. protein-protein interaction analysis

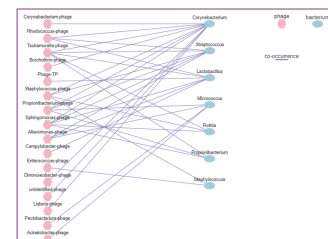


Search:

Bacterium_Protein_ID	Phage_Protein_ID	Bacterium_Protein_Def	Phage_Protein_Def	Detection_Method	Interaction_Type
NP_049588.1	NP_049588.1	interfacial (diffusion) kinase P8B	DNA helicase	ps-m (M 009) (pull down)	ps-m (M 009) (pull down)
NP_049588.1	NP_049588.1	interfacial (diffusion) kinase P8B	DNA helicase	ps-m (M 009) (pull down)	ps-m (M 009) (pull down)
NP_049588.1	NP_049588.1	putative fibroblast outer protein HSE	DNA polymerase	ps-m (M 009) (pull down)	ps-m (M 009) (pull down)
NP_049588.1	NP_049588.1	hedge factor	Thy thymidine kinase	ps-m (M 009) (pull down)	ps-m (M 009) (pull down)

7. co-occurrence analysis

- CoNet app



Search:

Host_Def	Phage_Def	Interaction_Type
Corynebacterium	Corynebacterium-phage	corel_spearman=0.1013523920004386 dist_kullbackleib=0.0
Corynebacterium	Toukamura-phage	dist_spearman=0.1460909570004046 corel_spearman=0.08838420921205 corel_spearman=0.1077133481786466 dist_kullbackleib=0.0
Corynebacterium	Brochothrix-phage	corel_spearman=0.2201850104817283 corel_spearman=0.2318018710474662 dist_kullbackleib=0.4044207007876696.4
Corynebacterium	Staphylococcus-phage	dist_spearman=0.2917870488368345 dist_kullbackleib=0.437026179773125.4 corel_spearman=0.202100007660846 corel_spearman=0.235023671469338