Phage Summarizer

This work uses different softwares to find phage-like sequences from bacterial genome, and then summarize and combine their results. Please upload FASTA files as inputs (multiple files are accepted). Currently supported programs: PHASTER, Phigaro, and VIBRANT.

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Method: ☑ PHASTER ☑ Phigaro ☑ VIBRANT

Upload

Result:

Refresh

## C213_spades (Combined)

Details   Download Fasta   BLAST result

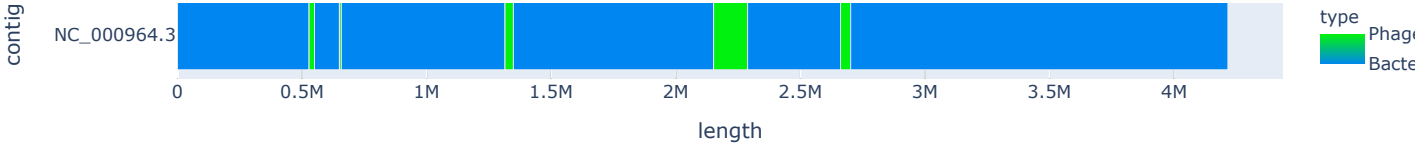| Contig	Start	End	Length	Info	BLAST hit
NODE_2_length_652681_cov_91.473123	299387	343631	44245		Salmonella virus BTP1 genome assembly
NODE_10_length_194746_cov_80.702644	131464	153220	21757		Escherichia phage RCS47
NODE_12_length_170519_cov_89.873599	140164	152902	12739		Klebsiella phage ST437-OXA245phi4.1
NODE_13_length_108864_cov_68.300532	1	108788	108788		Salmonella phage SSU5
NODE_14_length_101582_cov_90.380178	190	19770	19581		No alignment
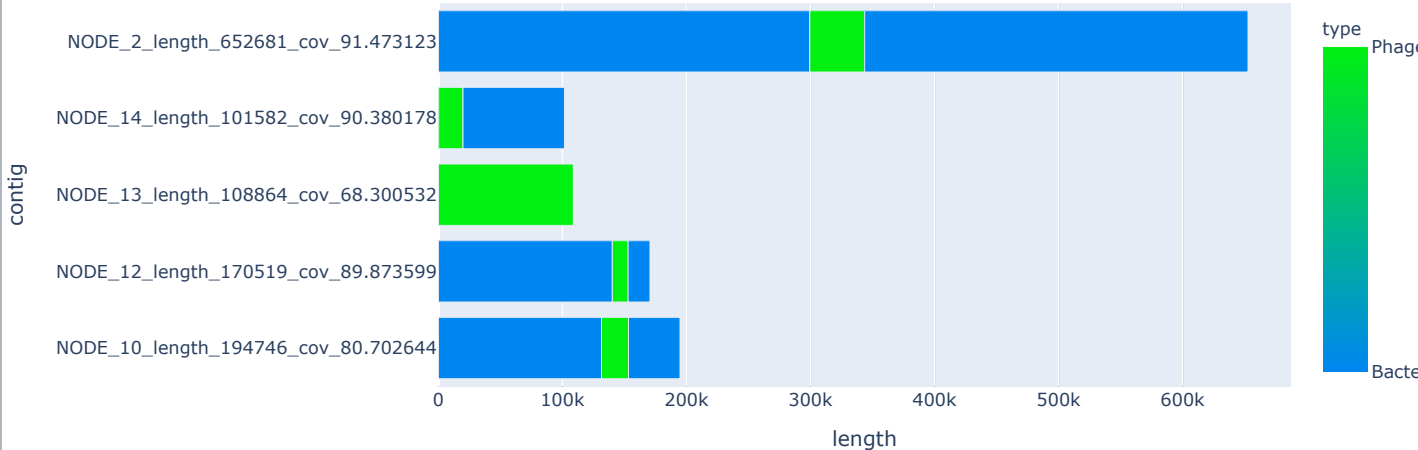
Bacillus_subtilis_subsp._subtilis_str._168 (Combined)

Details   Download Fasta   BLAST result

Contig	Start	End	Length	Info	BLAST hit
NC_000964.3	528129	549873	21745		Bacillus phage Mater
	649903	657697	7795		No alignment
	1314453	1348182	33730		No alignment
	2151626	2288090	136465		Bacillus phage SPBc2
	2661102	2701754	40653		Bacillus phage SPBc2
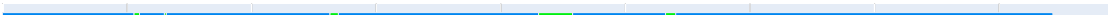
Streptococcus_pyogenes_M1_GAS (Combined)

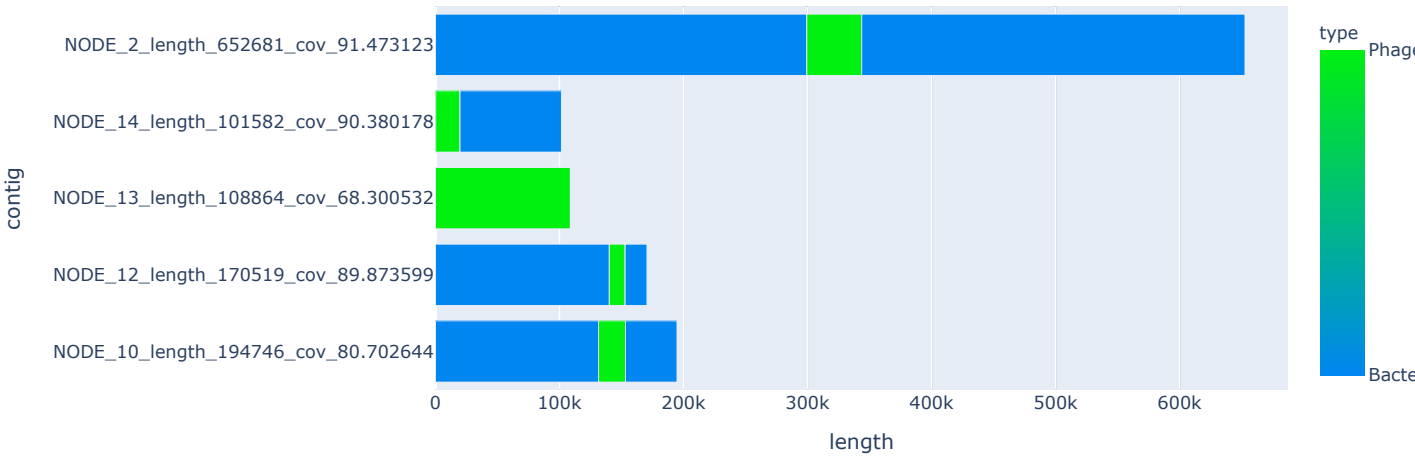Details   Download Fasta   BLAST result

Contig	Start	End	Length	Info	BLAST hit
NC_002737.2	526678	570489	43812		Streptococcus prophage 315.4
	775795	821673	45879		Streptococcus prophage 315.1
	1182563	1225245	42683		Streptococcus pyogenes phage 315.3
	1773449	1785649	12201		Streptococcus phage T12
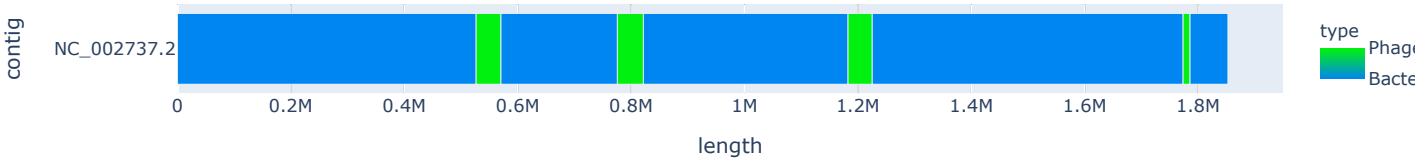
C213_spades (PHASTER)

Details   Download Fasta   BLAST result

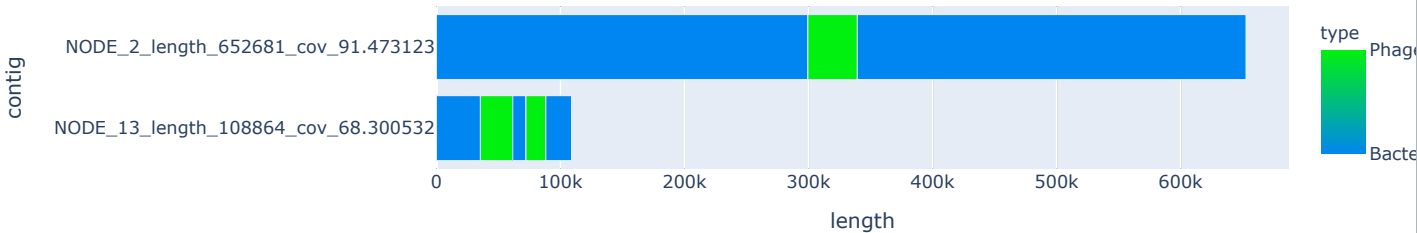| Contig	Start	End	Length	Info	BLAST hit
NODE_2_length_652681_cov_91.473123	299387	343631	44245	score=intact(140)	Salmonella virus BTP1 genome assembly
NODE_10_length_194746_cov_80.702644	131464	153220	21757	score=intact(120)	Escherichia phage RCS47
NODE_12_length_170519_cov_89.873599	140164	152902	12739	score=questionable(70)	Klebsiella phage ST437−OXA245phi4.1
NODE_13_length_108864_cov_68.300532	1	108788	108788	score=intact(150)	Salmonella phage SSU5
NODE_14_length_101582_cov_90.380178	190	19770	19581	score=incomplete(30)	No alignment

C213_spades (Phigaro)

Details   Download Fasta   BLAST result

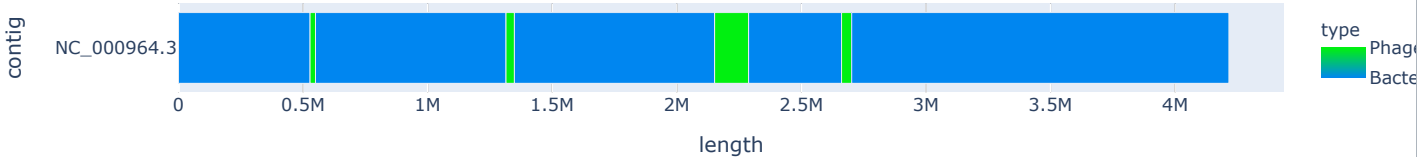| Contig	Start	End	Length	Info	BLAST hit

NODE_2_length_652681_cov_91.473123	299447	339321	39875	taxonomy=Myoviridae	Salmonella virus BTP1 genome assembly
NODE_13_length_108864_cov_68.300532	35411	61528	26118	taxonomy=Siphoviridae	Salmonella phage SSU5
	72104	88183	16080	taxonomy=Myoviridae	Salmonella phage SSU5

Bacillus_subtilis_subsp._subtilis_str._168 (PHASTER)

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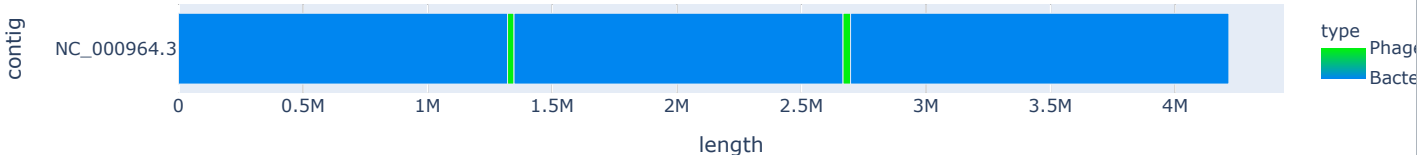
Contig	Start	End	Length	Info	BLAST hit
NC_000964.3	528129	549873	21745	score=incomplete(30)	Bacillus phage Mater
	1314453	1348182	33730	score=intact(120)	No alignment
	2151626	2288090	136465	score=intact(139)	Bacillus phage SPBc2
	2661102	2701754	40653	score=incomplete(40)	Bacillus phage SPBc2

Bacillus_subtilis_subsp._subtilis_str._168 (Phigaro)

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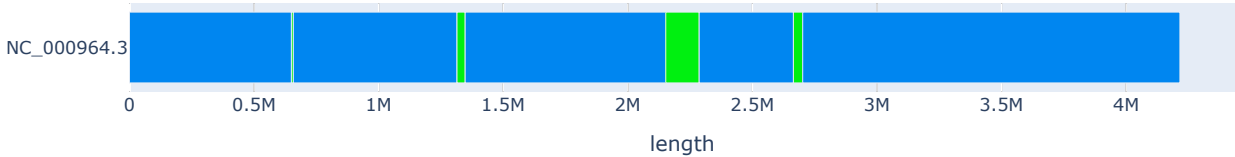| Contig	Start	End	Length	Info	BLAST hit
NC_000964.3	1320570	1346678	26109	taxonomy=Myoviridae	Waiting...
	2667045	2697289	30245	taxonomy=Myoviridae	Waiting...

Bacillus_subtilis_subsp._subtilis_str._168 (VIBRANT)

Details   Download Fasta   BLAST result

Contig	Start	End	Length	Info	BLAST hit
NC_000964.3	649903	657697	7795		No alignment
	1314453	1347276	32824		No alignment
	2152265	2286408	134144		Bacillus phage SPBc2
	2664573	2701754	37182		No alignment

Figure: Bacteria/Phage type plot for contig NC_000964.3 (length in M). Legend: type — Phage (green), Bacteria (blue).

Streptococcus_pyogenes_M1_GAS (PHASTER)

Details   Download Fasta   BLAST result

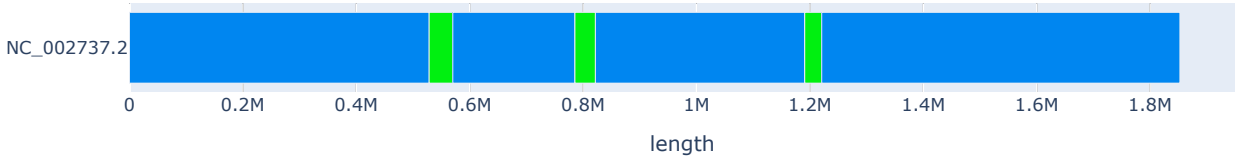| Contig	Start	End	Length	Info	BLAST hit
NC_002737.2	526678	570489	43812	score=intact(140)	Streptococcus prophage 315.4
	775795	820954	45160	score=intact(150)	Streptococcus prophage 315.1
	1182563	1225245	42683	score=intact(121)	Streptococcus pyogenes phage 315.3

Figure: type plot for contig NC_002737.2 (length in M). Legend: type — Phage (green), Bacteria (blue).
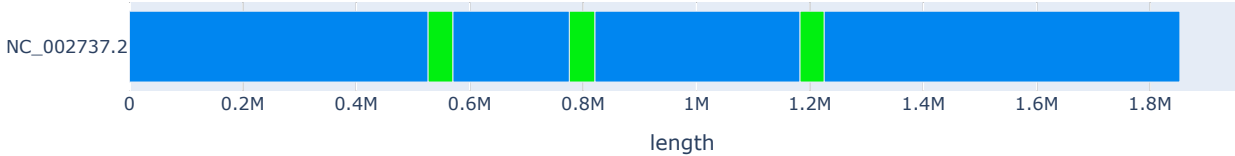
Streptococcus_pyogenes_M1_GAS (Phigaro)

Details   Download Fasta   BLAST result

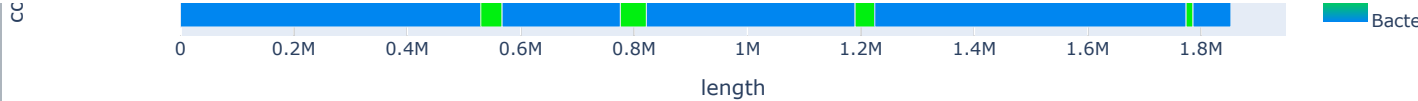| Contig	Start	End	Length	Info	BLAST hit
NC_002737.2	528539	570152	41614	taxonomy=Siphoviridae	Streptococcus prophage 315.4
	785536	821673	36138	taxonomy=Siphoviridae	Streptococcus prophage 315.1
	1190800	1220748	29949	taxonomy=Siphoviridae	Streptococcus pyogenes phage 315.3

Figure: type plot for contig NC_002737.2 (length in M). Legend: type — Phage (green), Bacteria (blue).

Streptococcus_pyogenes_M1_GAS (VIBRANT)

Details   Download Fasta   BLAST result

Contig	Start	End	Length	Info	BLAST hit
NC_002737.2	529627	567190	37564		Streptococcus prophage 315.4
	775795	821673	45879		Streptococcus prophage 315.1
	1189729	1224431	34703		Streptococcus pyogenes phage 315.3
	1773449	1785649	12201		Streptococcus phage T12

Figure: type plot for contig NC_002737.2. Legend: type — Phage.

CO

length

Bacte

C213_spades (VIBRANT)

Waiting