

Table S1 Phage vB_SenS_TUMS_E19 gene Blastp annotations.

CDS	start	stop	strand	RAST assigned function	Other possible function
1	1	546	+	Phage protein	terminase small subunit protein
2	536	1807	+	Phage terminase, large subunit	Phage terminase, large subunit
3	1820	3292	+	62kDa structural protein	putative portal protein
4	3976	3323	-	Phage protein	Amidase
5	4198	4347	+	hypothetical protein	
6	5014	4361	-	Phage protein	kilA-N domain-containing protein
7	5285	6328	+	NAD ⁺ --asparagine ADP-ribosyltransferase	head morphogenesis protein
8	6331	6789	+	Phage fibrin (wac) protein	neck whiskers protein
9	6943	7062	+	hypothetical protein	
10	7107	7493	+	Phage protein	putative spanin
11	7477	7602	+	hypothetical protein	putative spanin
12	7687	8388	+	Phage protein	Scaffold protein
13	8392	9441	+	Phage major capsid protein of Caudovirales	major capsid
14	9502	9789	+	Phage capsid and scaffold	head fiber
15	9801	10151	+	Phage protein	immunoglobulin domain contain protein
16	10188	10376	+	Phage protein	head-tail joining protein
17	10380	10889	+	Phage protein	head-tail joining protein
18	10892	11497	+	Phage protein	putative neck protein
19	11497	11856	+	Phage protein	putative neck protein
20	11853	12248	+	Phage protein	HK97 gp10 family protein
21	12248	12667	+	Phage protein	tail protein
22	12667	13836	+	Phage protein	putative tail protein
23	14542	13871	-	Putative DNA-binding protein Roi of bacteriophage BP-933W	putative DNA-binding protein
24	14884	14654	-	JK_43P	
25	15394	14894	-	Phage HNH homing endonuclease (ACLAME 27)	HNH endonuclease
26	16564	15410	-	Phage protein	helix-turn-helix domain
27	16806	16627	-	Phage protein	superinfection immunity protein
28	16977	17393	+	Phage protein	tail assembly chaperon
29	17399	17758	+	Phage protein	tail assembly chaperon
30	17751	20084	+	Phage tail tape measure	Phage tail tape measure
31	20086	20586	+	Phage protein	
32	20583	21098	+	Phage protein	
33	21095	21460	+	Phage protein	Peptidase
34	21451	24009	+	Phage protein	tail fiber protein
35	24022	26076	+	Phage tailspike	Phage tailspike
36	26198	26106	-	hypothetical protein	
37	26365	26195	-	Phage protein	exonuclease subunit

38	28827	26362	-	Phage DNA helicase	Phage DNA helicase
39	29321	28824	-	Phage-associated homing endonuclease	putative restriction endonuclease
40	29509	29318	-	Phage protein	
41	29825	29541	-	Phage-related protein	putative restriction endonuclease
42	30016	29822	-	hypothetical protein	DNA polymerase I
43	30230	30099	-	hypothetical protein	DUF2815 family protein
44	32421	30220	-	DNA polymerase I (EC 2.7.7.7), phage-associated	DNA polymerase I
45	33105	32479	-	Phage protein	
46	33363	33187	-	hypothetical protein	
47	34787	33363	-	Phage protein	
48	35366	34830	-	13.88 kDa late protein	13.88 kDa late protein
49	35500	35718	+	Phage repressor	helix-turn-helix domain
50	37919	35733	-	Phage replicative DNA helicase	Phage replicative DNA helicase
51	38208	37975	-	Phage protein	
52	38375	38205	-	Phage protein	helix-turn-helix domain
53	39345	39548	+	Phage protein	
54	39551	39922	+	Phage protein	
55	39928	40362	+	Phage protein	
56	40442	40723	+	Phage protein	holin
57	40725	41012	+	Phage protein	holin-like class
58	40993	41481	+	Phage lysin (EC 3.2.1.17)	lysin
59	41667	41852	+	Phage protein	
60	41849	42004	+	Phage protein	
61	42001	42357	+	Phage protein	
62	42474	42653	+	Phage protein	

Table S2 Predicted conserved promoter sequences of the E19 genome using PhagePromoter (CPT Galaxy).

Strand	Position	Promoter Sequence	Type	Scores
+	(5054..5061)	TATAAATA	host	0.856
+	(15921..15949)	TTGATAACCTTAATGGCGGTACGTATCAT	host	0.953
+	(23340..23360)	TCAGGTTTTTGACAGCCTTAA	phage	0.581
+	(29540..29547)	ACTAAATA	host	0.812
+	(33234..33261)	TTGAGTCTAGCATCCTGTCCGCTAAAAT	host	0.569
+	(38886..38908)	AATAAAGGCACTCTAATGGGGCA	phage	0.769
+	(41483..41508)	TTGACACATAGGAGGATTCTAAGAT	host	0.908
+	(41605..41630)	TTGACTAGTAACATTAACCCTATTAT	host	0.914

Table S3 Rho-factor-independent terminators of E19 genome using Arnold.

Position	Strand	Sequence	ΔG (kcal/mol)
3288	-	GTAAAACTAAGGCCCGTAATGGGGCCTTTTCTTACT	-13.10
3289	+	GTAAAGAAAAAGGCCCATACGGGGCTTAGTTTAAACA	-13.40
4079	+	TAATTATGGTCGCCTATAGCCTTGGAATGGGCTTTCCTTAGTA	-6.40
4323	-	TGTTAAAAATAAGGCCCGTTATGGGGTCTTTGTCTACTGCTC	-11.70
6783	-	GACAAAATTAAGGCCCTTGAAGGGGCCTTTCGTTACTCA	-13.80
6784	+	GAGTAACGAAAGGCCCTTCAAGGGGCCCTAATTTTGTC	-13.80
7729	-	TGTGTACATTTTGGTGCGTACCCGACAGCTTTATCTTCTGC	-11.60
9448	+	GGTATACTCTTGAAGGACTTCGTCCCTCTTTTCATTATA	-13.20
10145	-	TAATCCTTAAAGCGGCCGGAGGCCGCTGTATTAACTT	-12.60
10282	-	TAATGCGGTTCTTCGGCCACTGGCTGAGTTTCGATTAATG	-8.10
10963	-	GAATCCGCGATTTCGCTGGTAACCTCGCGCACTTTCCGGTGTA	-9.70
12678	+	ACCATATAAAGGCGGATGACCGCGCTTTTACGTACTT	-8.80
13835	-	ATTTAAACTAAGGCCCGAAAGGGGCCTTTTTTTTTTCTT	NA
13836	+	AGAAAAAAAAAAGGCCCTTTCGGGGCCTTaGTTTAAATCAAG	-15.90
13837	-	TTTAAACTAAGGCCCGAAAGGGGCCTTTTTTTTTTCT	-14.30
13838	+	AAAAAAAAAAGGCCCTTTCGGGGCCTTAGTTTAAAT	-13.40
14618	-	GAGTGAGAAAAAGGCCCTTTCGGGGCCTTTTTTATCGTCA	NA
14619	+	GACGATAAAAAAAGGCCCGAAAGGGGCCTTTTCTCACTCATC	-16.50
14620	-	AGTGAGAAAAAGGCCCTTTCGGGGCCTTTTTTTATCGT	-13.40
14621	+	CGATAAAAAAAGGCCCGAAAGGGGCCTTTTCTCACTC	-14.30
16903	-	AGTTGCGTCAGGCGGAACACCCGCTTTCTGGCGCG	-8.80
24838	-	CCTAATTTCCAAGGTAGAAGATATGCTTTGCCCTTAGCTTCCGG	-8.00
25448	+	CCGTAGAAGATTGCGCTGGCAGTGGCGCATATCTGTTGACG	-8.90
26073	-	CCATAAATTAAGGCCCTTTCGGGGCCTTTACTATTTAT	-13.40
26074	+	TAAATAGTAAAGGCCCGAAAGGGGCCTTAATTTATGGT	-14.30
27857	-	TTACTTCCGTGTGTCGGTATCCGGCTaTTTTCTGAGGT	-6.00
28376	-	TATCTTAAGGGTTGGCGGTACCTGTCTGATTTTCCAAGGAA	-6.20
29013	+	CTGAATCTGCTGGCTCCTTGTGCGGGCCTATATTATTTA	-7.10
29111	+	CGTAGACGAAAAGCCCATGCCAGATGTGGGCCTTTTATTCTTAC	-10.10
32431	-	ATTTCAATTAAGGCGGCTTCGTGCGCCTTTCTATAAGG	-10.40
35699	+	TTGGTGATACTGGGGCTGATGGGCCCTTCTTTTTACT	-14.30
37934	+	TTGTGTTAAGGCCCTGACGTTTCGCGGTTGGGGCTTCTTTTATTC	-12.30
38708	+	TAACGATTAGTGGGCAGGTTTAGACCTGCCCTTAGTTACCAG	-15.40
40391	-	ACAATAAAAAATCTCCGAAGTGTGTTACCTTCGGAGATTAACATTTATAC	-9.70
40395	+	AAATGTTAATCTCCGAAGGGTAAACCAACTTTCGGAgaTTTTTATTGTG	-10.70
41539	+	TAGCTCCTTTATCCCGGTAACTGACCTTACCGGATTTTTTTTATC	-12.40
42709	-	ATGTACAGAAAAAGCCCGCAGGAGCGGGCTTGATGGTGGCTaTTTTACAGATGAT	NA
42725	+	CCCACCATCAAGCCCGCTCCTGCGGGCTTTTCTGTACAT	-13.30

Table S4 ANI values of E19 and other phages of the genus Jersey virus using JSpeciesWS.

	E19	E15	E4	Ent1	Ent2	Ent3	5sent1	VSe101
E19	*	98.97	07.85	92.78	92.89	92.76	93.89	91.60
E4	98.89	*	98.19	92.65	92.55	92.66	93.59	91.56
E15	97.73	98.19	*	92.67	92.74	92.74	93.92	91.00
Ent1	93.41	93.42	*	97.77	98.98	94.82	91.89	91.89
Ent2	93.02	93.10	93.30	97.68	*	98.34	94.27	91.87
Ent3	93.13	93.23	93.31	98.88	98.23	*	94.35	92.10
5sent1	93.67	94.04	94.16	93.83	94.07	*	92.16	92.16
VSe101	91.45	91.38	91.75	91.82	91.89	92.16	*	*