

### **SGP-C Infection dynamics**

MV50 is the MOI at which 50% of the bacterial population is cleared by phage.

**Local Virulence (Vi):** Local virulence can be calculated by using the following formula:

$$V_i = 1 - (A_i/A_o)$$

$V_i$  can be measured at the scale of 0 to 1, where 0 indicates the complete absence and 1 represents the maximum theoretical virulence.

Here  $A_i$  is the area under curve at specific MOI of SGP-C, while  $A_o$  is the area under the curve for phage free bacterial control SG-C.

At MOI 0.01 the local virulence can be calculated as follows:

$$V_{0.01} = 1 - (1.081/2.162) \\ = 0.50$$

Then using the values of local virulence at different MOI virulence curve were generated between MOI (x-axis) and respective local virulence (y-axis).

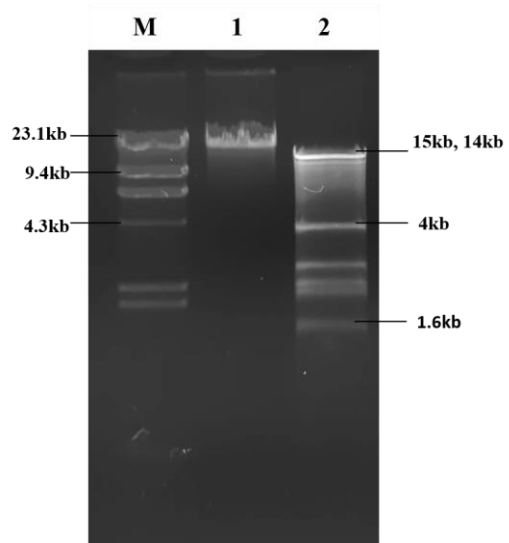
Virulence curve used for calculating virulence index by using following formula:

$$V_p = A_p/A_{max}$$

For calculating  $V_p$ , MOI were converted to  $\log_{10}$  (MOI) and were plotted against the local virulence (Fig 8). From curve ( $A_p$ ) was calculated by using trapezoid method.  $A_p$  is the area covered by SGP-C phage in experiment while  $A_{max}$  is the area for maximum theoretical virulence.

$$V_{iB-SGP-C} = A_{SGP-C} / A_{max} \\ = 3.053/6$$

=0.508



*Figure S1:* SGP-C phage genome restriction digestion with HindIII enzyme. Lane M contains Phage Lambda DNA ladder, Lane 1 with uncut SGP-C DNA and Lane 2 restricted with Hind3 enzyme.

Table S1: Primer pair for Tail Length Tape Measure Protein (2310bp) of SGP-C phage.

<b>Primer</b>	<b>Sequence</b>	<b>Tm</b>	<b>Primer Binding site</b>	<b>Product size</b>
FP-TLTP	CGTTGGCGTCAATATGCTGG	60.0	709bp	852bp
RP-TLTP	TCTGAGCGACATACGCATCC	60.0	1560bp	

Table S2: SGP-C phage Efficiency of Plating (EOP)

<b>Bacterial Host</b>	<b>SGP-C titer with SG strains</b>	<b>EOP</b>
SG-C (original host)	1.1x 10 <sup>10</sup>	1.00
Sg-4	3.3x 10 <sup>9</sup>	0.3
Sg-A	4.5x 10 <sup>9</sup>	0.41
Sg-B	4.5x 10 <sup>9</sup>	0.41
Sg-D	5.0x 10 <sup>9</sup>	0.45
Sg-E	4.0x 10 <sup>9</sup>	0.36
Sg-F	6.0x 10 <sup>9</sup>	0.55
Sg-G	5.0x 10 <sup>9</sup>	0.45
Sg-18	6.0x 10 <sup>9</sup>	0.55
Sg-12	5.0x 10 <sup>9</sup>	0.45
Sg-36	6.7x 10 <sup>9</sup>	0.61
Sg-47	6.0x 10 <sup>9</sup>	0.55
Sg-67	5.0x 10 <sup>9</sup>	0.45
Sg-60	6.0x 10 <sup>9</sup>	0.55
Sg-29	4.5x 10 <sup>9</sup>	0.45

Table S3: The comprehensive characterization of SGP-C genome and characteristics of the annotated proteins. Putative proteins with known function are highlighted

Gene #	Location on genome		Total bp	CDS	Total GC content	Function	Protein family	Total aa	Similar protein	Similarity index	Accession no.	Mol. Wt (kDa)	TMH	Isoelectric point (pH)
	Start	stop												
1.	607	2	606	-	51	Putative tail fiber protein	Bacteriophage lambda tail assembly protein I	202	Salmonella phage SETP3	99.50%	YP_001110802.1	22.0	0	5.02
2.	861	598	264	-	52	Hypothetical protein	DUF1460 ; Protein of unknown function (DUF1460)	87	Salmonella phage SETP13	100%	YP_008767029.1	9.8	0	6.34
3.	1475	960	516	-	50	Tail protein	Phage_tail_L ; Phage minor tail protein L	171	Salmonella phage SE2	98.83%	YP_005098154.1	19.2	0	4.20
4.	1972	1472	501	-	51	Tail protein	Phage_min_tail ; Phage minor tail protein	166	Salmonella phage SS3e	99.40%	YP_308655.1	18.7	0	4.67
5.	4283	1974	2310	-	52	Tail length tape measure-related protein	TMP_2 ; Prophage tail length tape measure protein	769	Salmonella phage pink	98.57	OIN98000.1	81.6	0	4.97
6.	4611	4276	336	-	46	Hypothetical protein	DUF1799 ; Phage related hypothetical protein (DUF1799)	111	Salmonella phage SETP3	95.50%	YP_001110852.1	12.6	0	5.24
7.	5003	4638	366	-	51	Tail assembly chaperone	Phage_TAC_4 ; Phage tail assembly chaperone	121	Salmonella phage SETP3	97.52%	YP_001110851.1	13.7	0	4.76
8.	5232	5561	330	+	44	Hypothetical protein		109	Salmonella phage STP03	89.91%	APM00265.1	11.6	0	4.97
9.	5624	6760	1137	+	50	Hypothetical protein		378	Salmonella phage SETP13	92.33%	YP_008767022.1	42.6	0	9.29

10.	6757	6987	231	+	43	Hypothetical protein	DUF3310 ; Protein of unknwon function (DUF3310)	76	Salmonella phage STP03	97.37	<a href="#">APM00267.1</a>	8.9	0	5.08
11.	8185	7016	1170	-	51	Putative tail protein	Phage_tube_2 ; Phage tail tube protein	389	Salmonella phage pink	97.43%	<a href="#">QIN97994.1</a>	41.1	0	4.29
12.	8604	8185	420	-	47	Hypothetical protein	DUF4128 ; Bacteriophage related domain of unknown function	139	Salmonella phage Jersey	94.96%	<a href="#">YP_008239729.1</a>	15.1	0	4.23
13.	8999	8604	396	-	46	Putative tail protein	HK97-gp10_like ; Bacteriophage HK97-gp10, putative tail-component	131	Salmonella phage SETP13	100%	<a href="#">YP_008767017.1</a>	14.5	0	10.48
14.	9355	8996	360	-	49	Hypothetical protein	Phage_attach ; Phage Head-Tail Attachment	119	Salmonella phage SETP13	98.32%	<a href="#">YP_008767016.1</a>	13.1	0	10.13
15.	9960	9355	606	-	53	Putative neck protein		201	Salmonella phage SETP7	95.52%	<a href="#">YP_008767187.1</a>	20.6	0	9.58
16.	10472	9963	510	-	51	Hypothetical protein	DUF3199 ; Protein of unknown function (DUF3199)	169	Salmonella phage vB_SpuS_Sp4	97.63%	<a href="#">AWY03048.1</a>	17.8	0	4.45
17.	10664	10476	189	-	50	Hypothetical protein		62	Salmonella phage FSL SP-101	98.39%	<a href="#">YP_009617930.1</a>	7.1	0	4.61
18.	11051	10701	351	-	48	Neck whiskers protein		116	Salmonella phage S101	98.28%	<a href="#">AXC39560.1</a>	12.2	0	4.46
19.	11347	11063	285	-	55	Head protein	Phage_head_fibr ; Head fiber protein	94	Salmonella phage vB_SenS_PVP-SE2	97.87%	<a href="#">AST15498.1</a>	9.3	0	10.48

20.			1050		54		Gp13-like ; Major capsid protein 13-like	349	Salmonella phage FSL SP- 101	99.14%	<a href="#">YP_009617927.1</a>	37.8	0	4.37
	12457	11408		-		Coat protein								
21.			702		50		Putative Scaffold protein	233	Salmonella phage SETP3	99.14%	<a href="#">YP_001110836.1</a>	25.7	0	6.18
	13162	12461		-										
22.			378		53		Putative spanin protein	128	Salmonella phage SETP7	96.03%	<a href="#">YP_008767179.1</a>	14.2	0	8.43
	13742	13356		-										
23.	13851	14009	159	+	47		hypothetical protein	52				6.0	0	9.94
24.			459		49		Tail protein	152	Salmonella phage wks13	97.37%	<a href="#">YP_009608684.1</a>	16.4	0	4.41
	14519	14061		-										
25.			1860		52		Head morphogenesis protein	619	Salmonella phage demigod	97.09%	<a href="#">OIN98040.1</a>	67.4	0	4.99
	16381	14522		-			Phage_min_cap2 ; Phage minor capsid protein 2							
26.	16484	16852	369	+	45		Hypothetical protein	122	Salmonella phage SETP13	100%	<a href="#">YP_008767003.1</a>	14.2	0	4.34
27.			1470		54		Phage_prot_Gp6 ; Phage portal protein, SPP1 Gp6-like	489	Salmonella phage pink	98.57%	<a href="#">OIN97976.1</a>	53.9	0	4.48
	18357	16888		-		Portal protein								
28.			1272		51		Terminase_1 ; Phage Terminase	423	Salmonella phage STP03	99.53%	<a href="#">APM00285.1</a>	47.6	0	6.30
	19641	18370		-		Terminase, large subunit								
29.			507		54		Phage_term_sma ; Putative bacteriophage terminase small subunit	168	Salmonella phage vB_SenS- EnJE1	100%	<a href="#">OGJ84413.1</a>	18.9	0	6.29
	20137	19631		-		Putative terminase small subunit								
30.	20501	20271	231	-	44		Hypothetical protein	76	Salmonella phage Ent1	97.37%	<a href="#">YP_007010511.1</a>	8.2	0	6.23
31.	20812	20513	300	-	45		Hypothetical protein	99	Salmonella phage Ent1	98.99%	<a href="#">YP_007010510.1</a>	11.7	1	10.25
32.	21165	20809	357	-	49		DUF2774 ; Protein of unknown function (DUF2774)	118	Salmonella phage SETP13	99.15%	<a href="#">YP_008767066.1</a>	13.6	0	8.24
						Hypothetical protein								
33.	21317	21162	156	-	50		DUF2737 ; Protein of unknown	51	Salmonella phage LSPA1	92.16%	<a href="#">YP_009113202.1</a>	6.0	0	11.43
						Hypothetical protein								

							function (DUF2737)							
34.	21511	21314	198	-	42	Hypothetical protein	DUF6501 ; Family of unknown function (DUF6501)	65	Escherichia phage vB_EcoS_XY1	84.62%	<a href="#">QIG59228.1</a>	7.2	0	4.05
35.	21693	21508	186	-	47	Hypothetical protein		61	Salmonella phage SETP7	95.08%	<a href="#">APM00294.1</a>	6.8	0	8.47
36.	21893	21699	195	-	45	Hypothetical protein		64	Salmonella phage SETP13	96.88%	<a href="#">YP_008767062.1</a>	7.0	0	4.52
37.	<a href="#">22567</a>	<a href="#">22079</a>	<a href="#">489</a>	-	<a href="#">55</a>	<a href="#">Endolysin</a>	<a href="#">Phage_lysozyme ; Phage lysozyme</a>	<a href="#">162</a>	<a href="#">Salmonella phage vB_SenS_phi135</a>	<a href="#">97.53%</a>	<a href="#">AYP69682.1</a>	<a href="#">17.3</a>	<a href="#">0</a>	<a href="#">10.35</a>
38.	22989	22837	153	-	45	Hypothetical protein	DUF6107 ; Family of unknown function (DUF6107)	50	Salmonella phage SF4	100%	<a href="#">QDH44753.1</a>	5.7	0	4.59
39.	23632	23198	435	-	48	Hypothetical protein		144	Salmonella phage SE2	97.92%	<a href="#">YP_005098116.1</a>	15.5	0	4.36
40.	24003	23638	366	-	52	Hypothetical protein		121	Salmonella phage vB_SpuS_Sp4	99.17%	<a href="#">AWY03010.1</a>	13.8	0	11.18
41.	24209	24006	204	-	53	Hypothetical protein		67	Salmonella phage Shelanagig	100%	<a href="#">QEG07391.1</a>	7.5	0	7.42
42.	24445	24206	240	-	54	Hypothetical protein		79	Salmonella phage vB_SenS_phi135	65.56%	<a href="#">AYP69680.1</a>	8.9	0	5.72
43.	24664	24458	207	-	47	Hypothetical protein		68	Salmonella phage SETP13	95.16%	<a href="#">YP_008767053.1</a>	8.1	1	10.44
44.	24846	24661	186	-	48	Hypothetical protein	DUF2680 ; Protein of unknown function (DUF2680)	61	Salmonella phage skrot	96.72%	<a href="#">QIO03728.1</a>	7.0	0	4.46



45.			204		46	Hypothetical protein		67	Salmonella phage vB_SenS_phi135	96.97%	<a href="#">AYP69705.1</a>	7.4	0	9.53
46.	25310	25107	171	-	52	Helix-turn-helix domain-containing protein	Phage_Cox ; Regulatory phage protein cox ; HTH_17	56	Salmonella phage Shelanagig	100%	<a href="#">QEG07385.1</a>	6.6	0	9.65
	25948	26118		+										
47.			234		43	Hypothetical protein	DUF4423 ; Domain of unknown function (DUF4423)	77	Salmonella phage SETP7	100%	<a href="#">YP_008767217.1</a>	8.6	0	9.55
	26115	26348		+										
48.			2187		54	DNA primase/helicase	Rad51 ; Rad51	728	Salmonella phage vB_StyS-sam	99.45%	<a href="#">BBO66012.1</a>	80.5	0	4.82
	26405	28591		+										
49.			219		53	Phage repressor Helix-turn-helix domain	P22 -Cro;DNA-binding transcriptional regulator ; Cro	72	Salmonella phage SETP13	97.18%	<a href="#">YP_008767044.1</a>	78.9	0	9.51
	28824	28606		+										
50.			537		45	13.88 kDa late protein	DUF4363 ; Domain of unknown function (DUF4363)	178	Salmonella phage NBSal007	89.56%	<a href="#">QMP81625.1</a>	20.1	0	4.27
	28959	29495		+										
51.			1431		50	Hypothetical protein	DUF2800 ; Protein of unknown function (DUF2800), Rad52-like	476	Salmonella phage BPS11Q3	95.80%	<a href="#">YP_009322843.1</a>	53.2	0	6.53
	29537	30967		+										
52.			624		48	Hypothetical protein	DUF2815 ; Protein of unknown function (DUF2815)	207	Salmonella phage SETP7	100%	<a href="#">YP_008767210.1</a>	23.4	0	4.68
	31049	31672		+										
53.			2304		51	DNA polymerase I	DNA_pol_A ; DNA polymerase family A	767	Salmonella phage STP03	87.96%	<a href="#">APM00319.1</a>	86.8	0	7.87
	31829	34132		+										

54.	34122	34253	132	+	47	Hypothetical protein		43	Salmonella phage BPS11Q3	86.05%	<a href="#">YP_009322846.1</a>	4.8	0	7.35
55.	34336	34530	195	+	48	Hypothetical protein		64	Salmonella phage FSL SP-101	96.88%	<a href="#">YP_009617954.1</a>	7.3	0	4.11
56.	<a href="#">34527</a>	<a href="#">34811</a>	<a href="#">285</a>	<a href="#">+</a>	<a href="#">50</a>	<a href="#">Restriction endonucleases</a>	<a href="#">VRR_NUC ; VRR-NUC domain</a>	<a href="#">94</a>	<a href="#">Salmonella phage BPS11Q3</a>	<a href="#">97.85%</a>	<a href="#">YP_009322848.1</a>	<a href="#">10.9</a>	<a href="#">0</a>	<a href="#">9.96</a>
57.	34843	35034	192	+	48	Hypothetical protein		63	Salmonella phage SETP7	100%	<a href="#">YP_008767205.1</a>	7.0	0	9.73
58.	35031	35528	498	+	48	Hypothetical protein	HNH_3 ; HNH endonuclease	165	Salmonella phage vB_StyS-sam	96.97%	<a href="#">BBO65957.1</a>	18.8	0	10.31
59.	<a href="#">35525</a>	<a href="#">37990</a>	<a href="#">2466</a>	<a href="#">+</a>	<a href="#">51</a>	<a href="#">Putative helicase</a>	<a href="#">Hom_end_hint ; Hom_end-associated Hint</a>	<a href="#">821</a>	<a href="#">Salmonella phage vB_SenS_PVP-SE2</a>	<a href="#">97.56%</a>	<a href="#">AST15461.1</a>	<a href="#">92.5</a>	<a href="#">0</a>	<a href="#">8.80</a>
60.	37987	38208	222	+	45	Hypothetical protein	DUF4140 ; N-terminal domain of unknown function (DUF4140)	73	Salmonella phage vB_SenS-Ent2	100%	<a href="#">YP_009009957.1</a>	8.7	0	4.56
61.	38205	38297	93	+	43	Hypothetical protein	DUF6479 ; Family of unknown function (DUF6479)	30	Salmonella phage SG2	96.67%	<a href="#">ASZ76550.1</a>	3.1	1	9.27
62.	<a href="#">40381</a>	<a href="#">38327</a>	<a href="#">2055</a>	<a href="#">-</a>	<a href="#">50</a>	<a href="#">Tailspike protein</a>	<a href="#">PhageP22-tail ; Salmonella phage P22 tail-spike</a>	<a href="#">684</a>	<a href="#">Salmonella phage wast</a>	<a href="#">98.93%</a>	<a href="#">QIN99606.1</a>	<a href="#">72.9</a>	<a href="#">0</a>	<a href="#">4.93</a>
63.	<a href="#">42361</a>	<a href="#">40394</a>	<a href="#">1968</a>	<a href="#">-</a>	<a href="#">49</a>	<a href="#">Tail fiber protein</a>	<a href="#">Phage-tail_3 ; Putative phage tail protein</a>	<a href="#">655</a>	<a href="#">Salmonella phage vB_SenS_PVP-SE2</a>	<a href="#">99.54%</a>	<a href="#">AST15460.1</a>	<a href="#">72.4</a>	<a href="#">0</a>	<a href="#">5.21</a>

Table S4: SGPC Promoter sequences and position on genome

Sr.no	Strand	Positions	Promoter Sequence	Type	Scores
1.	+	(11341..11366)	TTGACATTATATAGCCTCCGTATAAA	host	0.983
2.	+	(13994..14023)	TTTACATTGGCAATGAATAATTGGAATAAT	host	0.937
3.	+	(14907..14929)	AAATCAGCTTCACTAAAGACCAA	phage	0.804
4.	+	(16416..16445)	TAAAATATTTGTTGCTTAACCAAATATAAT	host	0.830
5.	+	(16427..16458)	TTGCTTAACCAAATATAATAGGGTACTATTAT	host	0.828
6.	-	(21440..21471)	TTGACTATGTGACAGATGGTAAAGTGTATGAT	host	0.925
7.	+	(21925..21932)	ACTAAATA	host	0.921
8.	-	(21932..21957)	TTGACTAGTAACATTAACCCTATTAT	host	0.989
9.	-	(22052..22077)	TTGACACATAGGAGTATTCCTAAGAT	host	0.977
10.	-	(25353..25381)	TAAAATGCACTTGTGTAACCCAATATAAT	host	0.914
11.	-	(25844..25872)	TTGACATTTTCATTTTTTTTCGTGTAAGTT	host	0.836
12.	+	(25888..25916)	TTGATTTCCATTATGCCGTGTGTATACT	host	0.922
13.	+	(26188..26219)	TTGACTTGCGCCGGACTTATTTTCAGTACTAT	host	0.906
14.	-	(26385..26411)	TTGACATGTGCTTTTCCTTTGTAGTGT	host	0.829
15.	+	(28901..28908)	CATAAATA	host	0.804
16.	+	(30964..30989)	TTGACAAGTTAATAGTACTCTATTAT	host	0.997
17.	+	(34780..34805)	TTGATAAATTAATAGAACACTATTAT	host	0.984
18.	-	(34805..34812)	ACTAAATA	host	0.961
19.	+	(35794..35822)	GTATACAGTAAACGAAAGCCATATATTAT	host	0.853
20.	-	(37962..37997)	TCATTATTCATCTCTTACCTCGTCTCTTCATATAAT	host	0.802
21.	+	(38264..38295)	TTTACTTACCGCTGCTGTGGTTCTGTTATCAT	host	0.826
22.	-	(38892..38919)	TTGCCACGAAACAGTATTCCTAATAT	host	0.818

Table S5: Total Rho-independent terminators In SGPC predicted by Arnold

5' end position	Predicting program	Strand	Sequence	Free energy of stem loop region (Kcal/mol)
212	<u>Rnamotif</u>	+	<u>GATGTCGTAAC TGCCTCCGTACGGGCGCGccTTGTTGTTACGG</u>	10.60
1045	<u>Rnamotif</u>	+	<u>CCGTTTCTGCGGTGAATACGCCTTTTCTTGCGT</u>	4.10
3086	<u>Rnamotif</u>	+	<u>CGGTGTCACGGGCGGCATTATATGCCGCTATCTGTTCCCT</u>	10.80
4099	<u>Rnamotif</u>	+	<u>AATTTTGACAAGCCGTGCGCCAGCGGCTTTTGACGTCGC</u>	7.10
4107	Both	+	<u>CAAGCCGTCGCCAGCGGCTTTTGACGTCGCTGagTTAGTTTTATCC</u>	10.90
4475	Both	-	<u>AAAAC TGCTAAGGCGGAAGACAAGCATCCGCCTTTTATTTTCCA</u>	9.70
4498	<u>Rnamotif</u>	+	<u>GTCTCCGCCTTAGCAGTTTTAGTGGCTGCTATTTTCCCATCG</u>	9.50
4539	<u>Rnamotif</u>	+	<u>TCGCGATAAAGGCGCCTCATGCCGCGGCTATGTTGTCGAA</u>	12.70
4552	<u>Rnamotif</u>	+	<u>CGCCTCATGCCCGCGGCTAGTTGTCGaaTTTTTGTTTAGC</u>	6.90
5091	<u>Rnamotif</u>	+	<u>AGTTGCGTCAGGCGGGAACCACCGCTTTTCCGGTGCG</u>	8.80
6982	<u>Rnamotif</u>	-	<u>CCTAAGAAAAAGGCCCTTTCCGGGCTTAGTTCATTCC</u>	13.40
6983	Both	+	<u>AATGAACTAAGGCCCGAAAGGGCCTTTTCTTAGGC</u>	14.30
8135	<u>Rnamotif</u>	-	<u>ACCATATAAGGGCGCGATGACCGCGCagTTTTACGTTCTT</u>	8.80
11361	<u>Rnamotif</u>	-	<u>GGTATACTCTTGAGGACTTCGTTCCCTCTTTTCAATTTATA</u>	13.20
12431	Both	+	<u>GATATCGCCAATAGTGGTAATTGCCATTATTTATTTCTCA</u>	6.00
14027	Both	-	<u>AAGTAACGAAAGGCCCTTCAAGGGCCTTAATTTTGCCC</u>	13.80
14028	Both	+	<u>GGCAAAATTAAGGCCCTTGAAGGGCCTTTCGTTACTTA</u>	13.80
16851	Both	-	<u>GTAAACATAAAGGCCCCATAACGGGGCCcTTATGTTCTCGTT</u>	13.40
16853	Both	+	<u>CGAGACATAAAGGCCCGTTATGGGCCTTTATGTTTACT</u>	13.10
17617	<u>Rnamotif</u>	-	<u>GGGAATCATTACGGGGGTAATCCCGTTTACTTTTATC</u>	6.90
20227	Both	-	<u>CCTACCACCAAGCCCGCTTCTGIGGGCTTTTCTGTACAC</u>	11.40
21974	Both	-	<u>TAGTCCCTTATCCCGGTAAC T GACCTACCGGGATTTTTTTTATCTG</u>	13.30
23116	Both	-	<u>AAATGTTAATCTCCGAAGGGTAAACCAACTTTCCGGAgaTTTTTATIGTG</u>	10.70
23117	Both	+	<u>ACAATAAAAAATCTCCGAAAGTTGGTTACCCTTCCGAGATTAACATTTATGC</u>	9.70
24275	<u>Rnamotif</u>	+	<u>CCCTTTCGGCAGCGGGCCCGCGcTTTTTCGATGCG</u>	7.10
25571	Both	-	<u>TACGATTAGTGGGCAGGTTTTAGACCTGCCCTTAGTTACCAG</u>	15.40
26343	Both	-	<u>TAGTGTTAAGGCCCTGACGTTCCGCGGTTGGGGCTTTTCTTTTATTC</u>	12.30
28587	Both	-	<u>TIGGGATACAGGGCCTGATGGCCCTTTCTTTTACT</u>	14.10
31683	<u>Rnamotif</u>	+	<u>AATTTAACTAAGGCCCTTCATTGGGCCTTTTACTAAGG</u>	11.00
35199	<u>Rnamotif</u>	-	<u>CGTAGACGAAAGCCCATGCCAGATGGTGGGCTTTTATTCTTAC</u>	10.10
35299	<u>Rnamotif</u>	-	<u>CTGAATCTGCTGGCTCCTTGTTGCGGGCCTTATATTATTTA</u>	7.10
35936	Both	+	<u>TATCTTAAGGGTTGGCGGTACCTGTCGATTTTCCAAGGAA</u>	6.20
38291	Both	-	<u>TAAATAGTAAAGGCCCGTAAGGGCCTTAATTTATGAT</u>	14.30
38292	Both	+	<u>TCATAAATTAAGGCCCTTACGGGGCCTTACTATTTAT</u>	13.40
39521	<u>Rnamotif</u>	+	<u>CCGAATTTCCAGGGTAGAAGATATGCTTTGCCCTTTAGCTTCCGG</u>	8.00
40164	<u>Rnamotif</u>	-	<u>CAGTCTACGTGATGCTGGTTTTCTCCCGGCATTTTTAACTTTAC</u>	12.00

Protein Superfamily	Index in Query Genome	Sequence Header
MCP	44	ORF 20
Portal	37	ORF27
TermL	36	ORF 28
MTP	53	ORF11
Sheath	NOT FOUND	
Ad1	48	ORF 16
Hc1	50	ORF 14
Ne1	51	ORF 13
Tc1	52	ORF P12

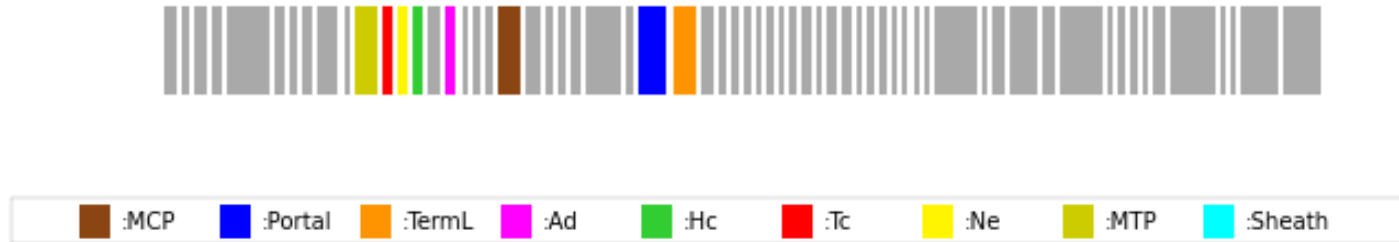


Figure S2: Neck Module and part of the Head and Tail Proteins arrangement suggesting SGPC belongs to Siphoviridae of Type1 (Cluster 5) , here MCP shows major capsid protein, Portal proteins, TermL refers to Terminal proteins, Ad for adapters, Hc for head closure, Tc for Tail completion ,Ne for neck protein and MTP refers to major tail protein