

Table S1. General features of the coding regions of vB_StuS_MMDA13 phage. The closest homologues in INSDC databases, as resulted from a BLASTP search using “Viruses (taxid:10239)” as the organism filter, the possible conserved domains and the HHpred predicted motives are also shown. BLASTP hits of eukaryotic viruses were not taken into consideration.

<i>gp</i>	Start (nt)	Stop (nt)	Predicted putative function	Closest protein homolog	Query coverage (%)	ID (%)	Phage	Conserved domains (from-to; accession; short name)	HHpred motif of closest homologue	Motif definition	Probability (%)
1	85	516	Terminase small subunit	ARB11146.1	95	43.97	<i>Pseudomonas</i> phage JG054	-----	3ZQP_H	Terminase small subunit	99.81
2	513	1847	Terminase large subunit	ALH23824.1	100	77.25	<i>Pseudomonas</i> phage PaMx25	40-237; cl29365; Terminase_6 super family	5OE8_C	Large subunit terminase	100
3	1908	3587	Portal protein	ARB11148.1	91	57.45	<i>Pseudomonas</i> phage JG054	312-448; cl16196; DUF4055 super family	2JES_G	Unidentified fragment of portal protein	99.9
4	3625	4443	Head protein	ARB11073.1	100	50.55	<i>Pseudomonas</i> phage JG012	-----	6B0X_c	Major head protein, Scaffold protein	94.97
5	4566	5630	Major phage capsid protein	ALH23820.1	100	71.75	<i>Pseudomonas</i> phage PaMx25	172-263; cl27082; Phage_capsid super family	6R3A_C	Major capsid protein	100
6	5690	6208	Hypothetical protein	ALH23819.1	100	53.18	<i>Pseudomonas</i> phage PaMx25	-----	5FVD_B	Nucleocapsid Phosphoprotein	20.43
7	6220	7002	Peptidoglycan endopeptidase domain protein	ARB11153.1	96	34.77	<i>Pseudomonas</i> phage JG054	-----	4Q4G_X	Peptidoglycan endopeptidase RipA	93.73
8	7007	7168	Hypothetical protein	QDP58552.1	45	58.33	Prokaryotic dsDNA virus sp.	-----	1K1F_E	Breakpoint cluster region protein	70.16
9	7172	7672	Head-tail adaptor	ALH23816.1	100	45.98	<i>Pseudomonas</i> phage PaMx25	-----	1XN8_A	Hypothetical protein yqbG	97.54
10	7672	8076	Head completion protein	QDB70185.1	34	39.13	<i>Salmonella</i> virus KFS-SE2	-----	1K0H_A	gpFII	96.49
11	8073	8540	Tail completion protein	ALH23585.1	94	34.25	<i>Pseudomonas</i> phage PaMx42	-----	2L25_A	Uncharacterized protein	99.91
12	8546	10387	Major tail protein	AXC34265.1	85	48.22	<i>Escherichia</i> phage Halfdan	-----	5NGJ_B	Tail tube protein	99.47
13	10463	10906	Tail fiber protein	QDP56586.1	100	48.30	Prokaryotic dsDNA virus sp.	-----	2OB9_A	Tail assembly chaperone	94.94
14	10918	11283	Tail chaperonin	AXC34263.1	90	44.07	<i>Escherichia</i> phage Halfdan	-----	5Z2H_A	<i>Dictyostelium discoideum</i> mitochondrial calcium uniporter	50.19
15	11252	11695	Head to tail connection protein (Neck)	CUS06475.1	95	42.55	<i>Acinetobacter</i> phage vB_AbaS_Loki	7-56; pfam04883; HK97-gp10_like	4N3Y_A	Rab5 GDP/GTP exchange factor, Rab	34.75
16	11699	14569	Phage tail tape measure protein	AEX56104.1	63	29.13	<i>Burkholderia</i> phage KL1	214-320; cl06039; TMP_2 super family	5IJO_T	Nuclear pore complex protein Nup155	94.67

17	14574	15512	Hypothetical protein	AEX56075.1	99	31.23	<i>Burkholderia</i> phage KL1	-----	1J3M_B	The conserved hypothetical protein TT1751	48.86
18	15512	16504	Structural phage protein	CAO77826.1	97	26.91	<i>Pseudomonas</i> virus Yua	-----	1J3M_B	The conserved hypothetical protein TT1751	57.29
19	16504	18198	Distal tail protein	AEX56105.1	94	31.29	<i>Burkholderia</i> phage KL1	-----	6F2M_C	Distal tail protein	96.5
20	18195	19004	Hypothetical protein	AEX56106.1	100	41.39	<i>Burkholderia</i> phage KL1	178-262; cl10710; Phage_BR0599 super family) 31-268; cl37077; phg_TIGR02218 super family	6J0M_C	Pvc8	51.19
21	19004	21859	Tail protein	AEX56107.1	82	39.20	<i>Burkholderia</i> phage KL1	-----	3CDD_E	Prophage MuSo2, 43 kDa tail	96.28
22	21856	22746	Hypothetical protein	AGH31476.1	37	30.00	<i>Loktanella</i> phage pCB2051-A	-----	4OUS_A	Caprin-2	67.21
23	22746	23798	Tail assembly protein	ATS92205.1	99	31.84	<i>Stenotrophomonas</i> phage DLP4	-----	2HB0_A	CFA/I fimbrial subunit E	20.75
24	23795	25357	Hypothetical protein	AEY69562.1	15	38.55	<i>Burkholderia</i> phage vB_BceS_AH2	-----	4UWA_D	Ryanodine receptor 1	99.85
25	25357	25521	Tail assembly protein	AHB12066.1	94	37.25	<i>Xylella</i> phage Sano	-----	2QZB_B	Uncharacterized protein yfeY	25.4
26	27851	25626	DNA polymerase	ARB11098.1	98	61.41	<i>Pseudomonas</i> phage JG012	-----	5MDN_B	DNA polymerase (E,C,2,7,7, 7)	100
27	28034	27903	DNA-directed RNA polymerase	AUR82457.1	60	46.15	<i>Vibrio</i> phage 1.024.O_10N.261.45.F8	-----	4QIW_W	DNA-directed RNA polymerase (E,C,2,7,7,6)	98.49
28	29026	28034	DNA polymerase III beta subunit	ARB11176.1	96	58.81	<i>Pseudomonas</i> phage JG054	-----	3T0P_B	DNA polymerase III, beta subunit	100
29	29226	29020	Hypothetical protein	No match				-----	2CYU_A	2-oxoglutarate dehydrogenase multienzyme complex (E,C,2,3,1,61)	59.88
30	30200	29223	Queuosine tRNA ribosyltransferase (DpdA)	AND74884.1	99	70.06	<i>Pseudomonas</i> phage NP1	-----	2ASH_D	Queuine tRNA-ribosyltransferase (E,C,2,4,2,29)	100
31	31106	30219	GTP cyclohydrolase I (FolE)	AND74886.1	89	60.37	<i>Pseudomonas</i> phage NP1	-----	4UQF_C	GTP cyclohydrolase 1 (E,C,3,5,4,16)	100
32	31573	31106	6-carboxytetrahydropterin synthase (QueD-like)	AGC35897.1	96	52.35	<i>Rhizobium</i> phage RHEph06	-----	2G64_A	Putative 6-pyruvoyl tetrahydrobiopterin synthase (E.C.4.2.3.12)	100
33	31872	31576	Archeosine synthase QueF-Like	QDP52302.1	92	43.96	Prokaryotic dsDNA virus sp.	-----	5K0P_G	Archeosine synthase QueF-Like	91.16
34	32261	31848	Hypothetical protein	QDP52303.1	91	46.92	Prokaryotic dsDNA virus sp.	-----	6OHT_A	3-beta-hydroxysteroid-Delta(8), Delta(7)-isomerase (E,C,5,3,3,5)	11.85

35	33046	32261	7-cyano-7-deazaguanine synthase (QueC-like)	AGC35898.1	96	56.42	<i>Rhizobium</i> phage RHEph06	-----	3BL5_F	Queuosine biosynthesis protein queC (E,C,3,5,-,-)	99.93
36	33759	33046	7-carboxy-7-deazaguanine synthase (QueE-like)	ALH23789.1	99	53.36	<i>Pseudomonas</i> phage PaMx25	-----	4NJH_B	7-carboxy-7-deazaguanine synthase (E,C,4,3,99,3)	99.92
37	34428	33868	Hypothetical protein	ALH23788.1	52	73.20	<i>Pseudomonas</i> phage PaMx25	-----	3JCJ_f	Protein/RNA Complex	93.94
38	35227	34505	Hypothetical protein	ARB11183.1	100	42.69	<i>Pseudomonas</i> phage JG054	-----	2NP3_B	Putative TetR-family regulator	81.33
39	35579	35229	Hypothetical protein	QDP53518.1	50	41.67	Prokaryotic dsDNA virus sp.	-----	5W1S_N	DNA-directed RNA polymerase subunit alpha	81.09
40	35697	35569	Hypothetical protein	No match				-----	4D7S_B	STHK_CNBD_CGMP	68.16
41	37681	35756	Superfamily II DNA helicase	ARB11186.1	96	58.27	<i>Pseudomonas</i> phage JG054	-----	6JDE_A	Putative DNA repair helicase RadD	100
42	38649	37678	Exonuclease RecB	ARB11187.1	97	58.82	<i>Pseudomonas</i> phage JG054	-----	3SYY_A	Exonuclease	99.3
43	39739	38774	Hypothetical protein	AND74897.1	52	65.70	<i>Pseudomonas</i> phage NP1	-----	1NY4_A	30S ribosomal protein S28E	51.51
44	40497	39772	RecA ATPase	AND74898.1	100	75.10	<i>Pseudomonas</i> phage NP1	-----	1N0W_A	DNA repair protein RAD51 homolog	99.41
45	41435	40497	ATP-dependent DNA ligase	QDB70915.1	97	45.63	<i>Pseudomonas</i> virus PBPA162	-----	1FVI_A	PBCV-1 DNA ligase (E,C,6,5,1,-)	100
46	41809	41432	Hypothetical protein	No match				-----			
47	42509	41784	Primosomal protein	QFR59661.1	75	39.89	<i>Pseudomonas</i> phage Quinobequin-P09	-----	2D7E_B	Primosomal protein N'(E,C,3,6,1,-)	92.76
48	42865	42506	Ribonuclease H like protein	ARB11119.1	98	45.30	<i>Pseudomonas</i> phage JG012	-----	4IBN_A	Ribonuclease H (E,C,3,1,26,4)	98.89
49	43431	42973	Host-nuclease inhibitor	ALH23774.1	92	43.97	<i>Pseudomonas</i> phage PaMx25	-----	2P2U_A	Host-nuclease inhibitor protein Gam, putative	95.55
50	44179	43499	Nucleotide pyrophosphohydrolase	ARK07441.1	82	39.04	<i>Sphingobium</i> phage Lacusarx	-----	4QGP_B	Pyrophosphatase	98.92
51	46673	44244	Primase	ARB11197.1	99	56.01	<i>Pseudomonas</i> phage JG054	-----	6A9W_A	Primase	100
52	46869	46735	Hypothetical protein	No match				-----	6Q6G_O	Cell division cycle protein 20	50.9
53	47759	47061	Hypothetical protein	No match				-----	1P2X_A	Ras GTPase-activating-like protein	62.77
54	48946	49089	Hypothetical protein	No match				-----	6OD1_A	Regulator of RpoS, Anti-adaptor protein	52.13
55	49140	49322	Hypothetical protein	No match				-----	2N7R_A	Nicastrin	66.19
56	49324	49458	Hypothetical protein	No match				-----	6HIZ_DE	Uncharacterized protein, uS3m, UNK/RNA Complex	84
57	49463	49711	Transcriptional regulator	No match				-----	4ZA6_A	QsdR	95.48

58	49708	49920	Hypothetical protein	No match				-----	4AYB_A	DNA-directed RNA polymerase (E,C,2,7,7,6)	43.24
59	50046	50546	Hypothetical protein	ARB11185.1	97	45.78	<i>Pseudomonas</i> phage JG054	-----	2OUT_A	Mu-like prophage FluMu protein gp35	93.19
60	50923	51063	Hypothetical protein	No match				-----	2XJY_B	Rhombotin-2, LIM domain-binding protein 1	55.47
61	51090	51563	Hypothetical protein	No match				-----	4UC0_A	Purine nucleoside phosphorylase	53.72
62	51563	52039	Hypothetical protein	AEX55965.1	32	43.64	<i>Pseudomonas</i> virus PMG1	-----	6GAW_B5	Mitochondrial ribosomal protein L12, Mitochondrial	78.86
63	52039	52251	Hypothetical protein	QDP53750.1	68	50.00	Prokaryotic dsDNA virus sp.	-----	1QHK_A	Ribonuclease HI (E,C,3,1,26,4)	74.4
64	52447	52668	Hypothetical protein	No match				-----	6K15_E	RSC7, Chromatin structure-remodeling complex protein	51.94
65	52665	52892	Hypothetical protein	No match				-----	3JXO_A	TrkA-N domain protein	75.14
66	52879	53490	Hypothetical protein	QAX97590.1	95	33.58	<i>Enterococcus</i> phage EfsSzw-1	-----	6SGA_Fd	Mitochondrial ribosome, assembly intermediate, translation	54.23
67	53493	53759	Hypothetical protein	No match				-----	6MCJ_A	Putative orange carotenoid-binding protein	49.93
68	53832	54968	Hypothetical protein	ASE99804.1	42	31.52	Uncultured virus	-----	6DM9_B	DHD127_A, DHD127_B	50.34
69	54965	55180	Hypothetical protein	ARM66686.1	67	39.58	<i>Lactococcus</i> phage AM4	-----	3M9D_I	Coil coil domain, inter domain	49.13
70	55167	55505	Hypothetical protein	QBQ72133.1	57	35.38	<i>Brevundimonas</i> phage vB_BsubS-Delta	-----	1Y7T_A	Malate dehydrogenase (E,C,1,1,1,37)	41.86
71	55483	55962	Hypothetical protein	No match				-----	4OTN_A	Eukaryotic translation initiation factor 2-alpha	65.08
72	56139	56351	Antitermination protein	VCU43734.1	72	29.09	<i>Escherichia</i> virus vB_Eco_mar003J3	-----	4MO1_A	Antitermination protein Q	96.92
73	56360	56806	Nucleotide pyrophosphohydrolase	BBA65581.1	83	51.13	<i>Xanthomonas</i> phage XacN1	-----	4QGP_B	Pyrophosphatase	99.15
74	56803	56982	Hypothetical protein	No match				-----	6G2J_S	NADH-ubiquinone oxidoreductase chain 3 (E,C,1,6,5,3)	48.47
75	56975	57358	Hypothetical protein	QDP54416.1	51	47.69	Prokaryotic dsDNA virus sp.	-----	2O35_B	Hypothetical protein DUF1244	47.95

76	57358	57936	Hypothetical protein	No match				-----	6QZL_D	FAM83B	74.8
77	57933	58133	Hypothetical protein	ADU79191.1	39	38.46	<i>Enterobacter</i> phage EcP1	-----	3M05_A	Uncharacterized protein PEPE_1480	87.21
78	58133	58606	Endonuclease	QDB70880.1	98	43.75	<i>Pseudomonas</i> virus PBPA162	-----	1OB8_B	Holliday-junction resolvase	99.3
79	58606	59034	Thiol dioxygenase	AID18361.1	66	53.19	<i>Rhizobium</i> phage vB_RleM_PPF1	-----	4WVZ_B	Thiol dioxygenase	97.33
80	59036	59239	Hypothetical protein	No match				-----	1IIO_A	Conserved hypothetical protein MTH865	56.23
81	59229	59615	Hypothetical protein	No match				-----	3NH6_A	ATP-binding cassette sub- family B member	98.43
82	59612	59875	Hypothetical protein	ALY08076.1	37	39.39	<i>Bacillus</i> phage vB_BhaS-171	-----	5IJO_T	Nuclear pore complex protein Nup155	51.14
83	59945	61462	UvrD superfamily I DNA helicase	ARB11211.1	100	62.57	<i>Pseudomonas</i> phage JG054	-----	4C2T_D	DNA helicase II (E,C,3,6,4,12)	100
84	61473	61691	Hypothetical protein	No match				-----	3MSH_A	Hepatitis B virus X- interacting protein	55.43
85	61849	62481	Endolysin	AJG41882.1	71	39.74	<i>Acinetobacter</i> phage RL-2015	-----	3NE0_A	Resuscitation promoting factor Interacting Protein	98.85
86	62478	62732	Holin	APZ81838.1	86	87.67	<i>Erythrobacter</i> phage vB_EliS_R6L	-----	2O6K_B	UPF0346 protein MW1311	63.93
87	62725	63105	Rz protein	No match				-----	5LQZ_V	ATP synthase subunit f, ATP	93.62
88	62993	63283	Rz1 protein	No match				-----	4IMM_B	Outer membrane assembly lipoprotein YfgL	91.68
89	63213	63743	Peptidoglycan endopeptidase	No match				-----	4Q4G_X	Peptidoglycan endopeptidase RipA	90.83