

Supplementary Tables

Table S1. Phasest output for PluMu 3457-1 showing CDS position, top BLASTP hit and E-value.

Region 1, total 41 CDS

#	CDS Position	BLAST Hit	E-Value
1	66..1106	PP_00001;integrase;phage;-;PHAGE_Mannhe_vB_MhS_1152AP2_NC_028956	0.0
2	1116..1274	PP_00002;hypothetical protein;phage;-;PHAGE_Mannhe_vB_MhS_1152AP2_NC_028956	8.28e-12
3	1364..1585	PP_00003;hypothetical protein;phage;-;PHAGE_Haemop_HP1_NC_001697	8.71e-18
4	1730..2230	PP_00005;methyltransferase;phage;-;PHAGE_Mannhe_vB_MhS_535AP2_NC_028853	4.61e-78
5	2241..2960	PP_00006;DNA methyltransferase;phage;-;PHAGE_Strept_9873_NC_047763	1.17e-91
6	3617..4414	PP_00008;DUF2303 protein;phage;-;PHAGE_Burkho_BcepMig1_NC_019917	2.89e-32
7	4460..4819	PP_00009;hypothetical protein;phage;-;PHAGE_Burkho_BcepMig1_NC_019917	6.59e-14
8	4882..5196	PP_00010;hypothetical protein;phage;-;PHAGE_Burkho_BcepC6B_NC_005887	6.1e-10
9	7236..7463	PP_00014;hypothetical protein;phage;-;PHAGE_Mannhe_vB_MhS_1152AP2_NC_028956	4.51e-30
10	7728..8003	PP_00015;plasmid maintenance system killer HigB;phage;-;PHAGE_Mannhe_vB_MhS_535AP2_NC_028853	7.24e-61
11	8013..8303	PP_00016;plasmid maintenance system killer HigA;phage;-;PHAGE_Mannhe_vB_MhS_535AP2_NC_028853	5.14e-55
12	8312..8479	PP_00017;gp6, putative addiction module antidote protein;phage;-;PHAGE_Burkho_phiE12_2_NC_009236	1.6e-07
13	8671..9486	PP_00018;putative DNA adenine methylase;phage;-;PHAGE_Geobac_E3_NC_029073	1.06e-20
14	11209..11883	PP_00020;CI repressor;phage;-;PHAGE_Mannhe_vB_MhS_535AP2_NC_028853	4.72e-49
15	11992..12207	PP_00021;phage protein;phage;-;PHAGE_Aggreg_S1249_NC_013597	5.76e-20
16	12266..12961	PP_00022;uncharacterized phage-encoded protein;phage;-;PHAGE_Aggreg_S1249_NC_013597	1.36e-59
17	12958..13326	PP_00023;hypothetical protein;phage;-;PHAGE_Mannhe_vB_MhS_587AP2_NC_028743	1.64e-35
18	13265..13981	PP_00024;hypothetical protein;phage;-;PHAGE_Enterо_mEp390_NC_019721	4.29e-16
19	13984..14508	PP_00025;DNA N-6-adenine-methyltransferase;phage;-;PHAGE_Mannhe_vB_MhS_587AP2_NC_028743	1.44e-36
20	14703..15725	PP_00026;hypothetical protein;phage;-;PHAGE_Shigel_SfII_NC_021857	5.4e-66
21	15797..16162	PP_00028;endodeoxyribonuclease RusA;phage;-;PHAGE_Mannhe_vB_MhS_587AP2_NC_028743	1.9e-34
22	16152..16511	PP_00029;antitermination protein Q;phage;-;PHAGE_Mannhe_vB_MhS_587AP2_NC_028743	2.73e-13
23	18069..19217	PP_00032;hypothetical protein;phage;-;PHAGE_Coryne_Juicebox_NC_048070	7.54e-34
24	19541..20215	PP_00033;antirepressor protein Ant;phage;-;PHAGE_Mannhe_vB_MhS_1152AP2_NC_028956	4.2e-23
25	21067..21426	PP_00036;holin;phage;-;PHAGE_Mannhe_vB_MhS_587AP2_NC_028743	6.26e-49
26	21416..21862	PP_00037;lysozyme;phage;-;PHAGE_Erwini_vB_EhrS_59_NC_048198	5.3e-53

#	CDS Position	BLAST Hit	E-Value
27	21855..22217	PP_00038;lytic protein Rz;phage;-;PHAGE_Mannhe_vB_MhS_535AP2_NC_028853	6.88e-55
28	22162..22395	PP_00039;lytic protein Rz1;phage;-;PHAGE_Mannhe_vB_MhS_587AP2_NC_028743	1.49e-31
29	22675..23154	PP_00040;terminase small subunit;phage;-;PHAGE_Enteroc_1_NC_019706	8.02e-60
30	23154..25271	PP_00041;bacteriophage DNA packaging protein;terminase, large subunit;phage;-;PHAGE_Phage_Gifsy_2_NC_010393	0.0
31	25492..27000	PP_00043;bacteriophage portal protein;phage;-;PHAGE_Phage_Gifsy_2_NC_010393	0.0
32	27032..28990	PP_00044;head maturation protease;phage;-;PHAGE_Enteroc_1_NC_019706	0.0
33	29064..29387	PP_00045;hypothetical protein;phage;-;PHAGE_Enteroc_mEp460_NC_019716	1.37e-21
34	29685..30212	PP_00047;bacteriophage head-tail assembly protein;Lambda gpZ homolog;phage;-;PHAGE_Phage_Gifsy_1_NC_010392	1.07e-27
35	30209..30496	PP_00048;putative minor tail protein U;phage;-;PROPHAGE_Escher_Sakai	6.69e-10
36	31415..35014	PP_00051;putative tail component protein;phage;-;PHAGE_Pseudo_MP22_NC_009818	1.22e-42
37	35014..35754	PP_00052;tail protein;phage;-;PHAGE_Enteroc_Ajan_NC_028776	2.27e-08
38	35765..36319	PP_00053;hypothetical protein;phage;-;PHAGE_Acinet_vB_AbaS_Loki_NC_042137	8.55e-26
39	36319..36726	PP_00054;hypothetical protein;phage;-;PHAGE_Yersin_PY54_NC_005069	2.53e-10
40	36728..38770	PP_00055;putative tail fibre protein;phage;-;PHAGE_Acinet_vB_AbaS_Loki_NC_042137	3.19e-77
41	38815..40785	PP_00056;tail fiber protein;phage;-;PHAGE_Klebsi_TSK1_NC_048126	2.95e-10

Table S2. Phasest output for PluMu 3457-2 showing CDS position, top BLASTP hit and E-value.

#	CDS Position	BLAST Hit	E-Value
1	1..423	PP_00001;transposase;phage;-;PHAGE_Mannhe_vB_MhM_3927AP2_NC_028766	5.81e-15
2	635..847	PP_00002;transcriptional regulatory protein;phage;-;PHAGE_Mannhe_vB_MhM_3927AP2_NC_028766	4.92e-28
3	859..2823	PP_00003;transposase;phage;-;PHAGE_Vibrio_12B12_NC_021070	0.0
4	2883..3800	PP_00004;transposase B;phage;-;PHAGE_Bacill_BalMu_1_NC_030945	3.32e-30
5	3804..4115	PP_00005;hypothetical protein;phage;-;PHAGE_Mannhe_vB_MhM_3927AP2_NC_028766	2.03e-09
6	4391..4921	PP_00007;host-nuclease inhibitor protein;phage;-;PHAGE_Haemop_SuMu_NC_019455	9.97e-64
7	5296..5484	PP_00009;hypothetical protein;phage;-;PHAGE_Mannhe_vB_MhM_3927AP2_NC_028766	1.66e-08
8	5494..5667	PP_00010;hypothetical protein;phage;-;PHAGE_Mannhe_vB_MhM_3927AP2_NC_028766	8.56e-11
9	6074..6691	PP_00011;antirepressor;phage;-;PHAGE_Mannhe_vB_MhS_587AP2_NC_028743	1.49e-27
10	7070..7615	PP_00013;hypothetical protein;phage;-;PHAGE_Vibrio_12B12_NC_021070	5.07e-20
11	7602..8156	PP_00014;hypothetical protein;phage;-;PHAGE_Mannhe_vB_MhM_3927AP2_NC_028766	8.76e-55

#	CDS Position	BLAST Hit	E-Value
12	8301..8723	PP_00015;putative transcription regulator;phage;-;PHAGE_Enterо_Mu_NC_000929	3.33e-34
13	8812..9357	PP_00016;putative N-acetylmuramoyl-L-alanine amidase;phage;-;PHAGE_Haemop_SuMu_NC_019455	6.94e-105
14	9984..10211	PP_00018;DksA-like zinc finger domain containing protein;phage;-;PHAGE_Yersin_L_413C_NC_004745	1.05e-07
15	10208..10537	PP_00019;hypothetical protein;phage;-;PHAGE_Escher_D108_NC_013594	1.66e-06
16	10543..10836	PP_00020;hypothetical protein;phage;-;PHAGE_Escher_D108_NC_013594	9.11e-36
17	10870..11442	PP_00021;hypothetical protein;phage;-;PHAGE_Vibrio_12B12_NC_021070	3.32e-56
18	11439..13019	PP_00022;portal protein;phage;-;PHAGE_Vibrio_12B12_NC_021070	1.28e-178
19	13021..14586	PP_00023;portal protein;phage;-;PHAGE_Enterо_SfMu_NC_027382	1.15e-180
20	14573..15910	PP_00024;head morphogenesis protein;phage;-;PHAGE_Enterо_SfMu_NC_027382	4.31e-113
21	16115..16549	PP_00025;putative virion morphogenesis protein;phage;-;PHAGE_Enterо_Mu_NC_000929	1.28e-15
22	16780..17853	PP_00026;putative protease protein;phage;-;PHAGE_Enterо_Mu_NC_000929	3.95e-95
23	17853..18779	PP_00027;major head protein;phage;-;PHAGE_Escher_D108_NC_013594	1.84e-113
24	19249..19656	PP_00029;hypothetical protein;phage;-;PHAGE_Enterо_SfMu_NC_027382	1.01e-25
25	19653..20078	PP_00030;hypothetical protein;phage;-;PHAGE_Enterо_SfMu_NC_027382	2.87e-31
26	20092..20835	PP_00031;hypothetical protein;phage;-;PHAGE_Ralsto_RS138_NC_029107	1.05e-47
27	21627..21974	PP_00033;hypothetical protein;phage;-;PHAGE_Stx2_c_Stx2a_WGPS9_NC_049923	6.57e-16
28	22030..22626	PP_00034;hypothetical protein;phage;-;PHAGE_Stx2_c_Stx2a_WGPS9_NC_049923	6.08e-15
29	22676..23041	PP_00035;hypothetical protein;phage;-;PHAGE_Stx2_c_Stx2a_WGPS9_NC_049923	2.08e-18

Table S3. Phasest output for PluMu 3459-1 showing CDS position, top BLASTP hit and E-value.

#	CDS Position	BLAST Hit	E-Value
1	1..423	PP_00001;transposase;phage;-;PHAGE_Mannhe_vB_MhM_3927AP2_NC_028766	5.81e-15
2	635..847	PP_00002;transcriptional regulatory protein;phage;-;PHAGE_Mannhe_vB_MhM_3927AP2_NC_028766	4.92e-28
3	859..2823	PP_00003;transposase;phage;-;PHAGE_Vibrio_12B12_NC_021070	0.0
4	2883..3800	PP_00004;transposase B;phage;-;PHAGE_Bacill_BalMu_1_NC_030945	3.32e-30
5	3804..4115	PP_00005;hypothetical protein;phage;-;PHAGE_Mannhe_vB_MhM_3927AP2_NC_028766	2.03e-09
6	4391..4921	PP_00007;host-nuclease inhibitor protein;phage;-;PHAGE_Haemop_SuMu_NC_019455	9.97e-64
7	5296..5490	PP_00009;hypothetical protein;phage;-;PHAGE_Mannhe_vB_MhM_3927AP2_NC_028766	1.65e-08

#	CDS Position	BLAST Hit	E-Value
8	5716..6390	PP_00011;hypothetical protein;phage;-;PHAGE_Aeromo_phiA8_29_NC_048660	2.71e-32
9	6883..7431	PP_00014;hypothetical protein;phage;-;PHAGE_Vibrio_12B12_NC_021070	1.62e-20
10	7418..7972	PP_00015;hypothetical protein;phage;-;PHAGE_Mannhe_vB_MhM_3927AP2_NC_028766	8.76e-55
11	8117..8539	PP_00016;putative transcription regulator;phage;-;PHAGE_Enterо_Mu_NC_000929	3.33e-34
12	8628..9173	PP_00017;putative N-acetylmuramoyl-L-alanine amidase;phage;-;PHAGE_Haemop_SuMu_NC_019455	6.94e-105
13	9180..9404	PP_00018;hypothetical protein;phage;-;PHAGE_Haemop_SuMu_NC_019455	2.73e-16
14	9800..10027	PP_00020;DksA-like zinc finger domain containing protein;phage;-;PHAGE_Yersin_L_413C_NC_004745	1.05e-07
15	10027..10353	PP_00021;hypothetical protein;phage;-;PHAGE_Escher_D108_NC_013594	1.62e-06
16	10359..10652	PP_00022;hypothetical protein;phage;-;PHAGE_Escher_D108_NC_013594	9.11e-36
17	10686..11258	PP_00023;hypothetical protein;phage;-;PHAGE_Vibrio_12B12_NC_021070	3.32e-56
18	11255..12835	PP_00024;portal protein;phage;-;PHAGE_Vibrio_12B12_NC_021070	1.28e-178
19	12837..14402	PP_00025;portal protein;phage;-;PHAGE_Enterо_SfMu_NC_027382	1.15e-180
20	14389..15726	PP_00026;head morphogenesis protein;phage;-;PHAGE_Enterо_SfMu_NC_027382	4.31e-113
21	15931..16365	PP_00027;putative virion morphogenesis protein;phage;-;PHAGE_Enterо_Mu_NC_000929	1.28e-15
22	16596..17669	PP_00028;putative protease protein;phage;-;PHAGE_Enterо_Mu_NC_000929	3.95e-95
23	17669..18595	PP_00029;major head protein;phage;-;PHAGE_Escher_D108_NC_013594	1.84e-113
24	19065..19472	PP_00031;hypothetical protein;phage;-;PHAGE_Enterо_SfMu_NC_027382	1.01e-25
25	19469..19894	PP_00032;hypothetical protein;phage;-;PHAGE_Enterо_SfMu_NC_027382	2.87e-31
26	19908..20651	PP_00033;hypothetical protein;phage;-;PHAGE_Ralsto_RS138_NC_029107	1.05e-47
27	20709..21119	PP_00034;hypothetical protein;phage;-;PHAGE_Pseudo_JBD93_NC_030918	7.75e-22
28	21565..24924	PP_00036;tail length tape measure protein;phage;-;PHAGE_Enterо_mEр390_NC_019721	3.74e-40
29	24924..25922	PP_00037;hypothetical protein;phage;-;PHAGE_Pseudo_JBD67_NC_042135	8.49e-42
30	25925..26890	PP_00038;hypothetical protein;phage;-;PHAGE_Pseudo_vB_PaeS_PM105_NC_028667	2.3e-40
31	26893..28575	PP_00039;hypothetical protein;phage;-;PHAGE_Pseudo_DMS3_NC_008717	2.52e-108
32	28612..29421	PP_00040;BR0599 family protein;phage;-;PHAGE_Salmon_KFS_SE1_NC_048683	3.29e-56
33	29439..29690	PP_00041;conserved tail assembly protein;phage;-;PHAGE_Burkho_BcepNazgul_NC_005091	1.08e-19
34	29695..29898	PP_00042;tail assembly protein;phage;-;PHAGE_Vibrio_VpKK5_NC_026610	1.73e-16
35	29898..32681	PP_00043;conserved tail assembly protein;phage;-;PHAGE_Burkho_BcepNazgul_NC_005091	6.5e-142
36	33040..33435	PP_00044;phage protein;phage;-;PHAGE_Strept_phiBHN167_NC_022791	5.03e-47
37	33413..33796	PP_00045;putative C-5 cytosine-specific DNA methylase;phage;-;PHAGE_Strept_phiNJ2_NC_019418	1.7e-38
38	33789..34625	PP_00046;hypothetical protein;phage;-;PHAGE_Haemop_SuMu_NC_019455	2.04e-137

# CDS Position	BLAST Hit	E-Value
39 35450..36028	PP_00048;DNA-directed RNA polymerase specialized sigma subunit;phage;-;PHAGE_Sinorh_phiM9_NC_028676	2.77e-08

Table S4. Phasest output for PluMu 3459-2 showing CDS position, top BLASTP hit and E-value.

# CDS Position	BLAST Hit	E-Value
1 9118..11088	PP_00011;tail fiber protein;phage;-;PHAGE_Klebsi_TSK1_NC_048126	2.95e-10
2 11133..13175	PP_00012;putative tail fibre protein;phage;-;PHAGE_Acinet_vB_AbaS_Loki_NC_042137	3.19e-77
3 13177..13584	PP_00013;hypothetical protein;phage;-;PHAGE_Yersin_PY54_NC_005069	2.53e-10
4 13584..14138	PP_00014;hypothetical protein;phage;-;PHAGE_Acinet_vB_AbaS_Loki_NC_042137	8.55e-26
5 14138..14878	PP_00015;tail protein;phage;-;PHAGE_Entero_CAjan_NC_028776	1.43e-13
6 14878..18477	PP_00016;putative tail component protein;phage;-;PHAGE_Pseudo_MP22_NC_009818	1.22e-42
7 19260..19676	PP_00019;putative minor tail protein U;phage;-;PROPHAGE_Escher_Sakai	3.79e-14
8 19673..20200	PP_00020;bacteriophage head-tail assembly protein;Lambda gpZ homolog;phage;-;PHAGE_Phage_Gifsy_1_NC_010392	1.07e-27
9 20498..20821	PP_00022;hypothetical protein;phage;-;PHAGE_Entero_mEp460_NC_019716	1.37e-21
10 20895..22853	PP_00023;head maturation protease;phage;-;PHAGE_Entero_c_1_NC_019706	0.0
11 22885..24393	PP_00024;bacteriophage portal protein;phage;-;PHAGE_Phage_Gifsy_2_NC_010393	0.0
12 24614..26731	PP_00026;bacteriophage DNA packaging protein;terminase, large subunit;phage;-;PHAGE_Phage_Gifsy_2_NC_010393	0.0
13 26731..27210	PP_00027;terminase small subunit;phage;-;PHAGE_Entero_c_1_NC_019706	8.02e-60
14 27490..27723	PP_00028;lytic protein Rz1;phage;-;PHAGE_Mannhe_vB_MhS_587AP2_NC_028743	1.49e-31
15 27668..28030	PP_00029;lytic protein Rz;phage;-;PHAGE_Mannhe_vB_MhS_535AP2_NC_028853	6.88e-55
16 28023..28469	PP_00030;lysozyme;phage;-;PHAGE_Erwini_vB_EhrS_59_NC_048198	5.3e-53
17 28459..28818	PP_00031;holin;phage;-;PHAGE_Mannhe_vB_MhS_587AP2_NC_028743	6.26e-49
18 29670..30344	PP_00034;antirepressor protein Ant;phage;-;PHAGE_Mannhe_vB_MhS_1152AP2_NC_028956	4.2e-23
19 30668..31816	PP_00035;hypothetical protein;phage;-;PHAGE_Coryne_Juicebox_NC_048070	1.02e-33
20 33374..33733	PP_00038;antitermination protein Q;phage;-;PHAGE_Mannhe_vB_MhS_587AP2_NC_028743	2.73e-13
21 33723..34088	PP_00039;endodeoxyribonuclease RusA;phage;-;PHAGE_Mannhe_vB_MhS_587AP2_NC_028743	1.9e-34
22 34160..35182	PP_00041;hypothetical protein;phage;-;PHAGE_Shigel_SfII_NC_021857	5.4e-66
23 35175..35393	PP_00042;hypothetical protein;phage;-;PHAGE_Mannhe_vB_MhS_535AP2_NC_028853	2.78e-08
24 35377..35901	PP_00043;DNA N-6-adenine-methyltransferase;phage;-;PHAGE_Mannhe_vB_MhS_587AP2_NC_028743	1.44e-36
25 35904..36620	PP_00044;hypothetical protein;phage;-;PHAGE_Entero_mEp390_NC_019721	4.29e-16
26 36559..36927	PP_00045;hypothetical protein;phage;-;PHAGE_Mannhe_vB_MhS_587AP2_NC_028743	1.64e-35

#	CDS Position	BLAST Hit	E-Value
27	36924..37619	PP_00046;uncharacterized phage-encoded protein;phage;-;PHAGE_Aggreg_S1249_NC_013597	1.36e-59
28	37678..37893	PP_00047;phage protein;phage;-;PHAGE_Aggreg_S1249_NC_013597	5.76e-20
29	38002..38676	PP_00048;CI repressor;phage;-;PHAGE_Mannhe_vB_MhS_535AP2_NC_028853	4.72e-49
30	40399..41214	PP_00050;putative DNA adenine methylase;phage;-;PHAGE_Geobac_E3_NC_029073	1.06e-20
31	41406..41573	PP_00051;gp6, putative addiction module antidote protein;phage;-;PHAGE_Burkho_phiE12_2_NC_009236	1.6e-07
32	41582..41872	PP_00052;plasmid maintenance system killer HigA;phage;-;PHAGE_Mannhe_vB_MhS_535AP2_NC_028853	5.14e-55
33	41882..42157	PP_00053;plasmid maintenance system killer HigB;phage;-;PHAGE_Mannhe_vB_MhS_535AP2_NC_028853	7.24e-61
34	42422..42649	PP_00054;hypothetical protein;phage;-;PHAGE_Mannhe_vB_MhS_1152AP2_NC_028956	4.51e-30
35	44689..45003	PP_00058;hypothetical protein;phage;-;PHAGE_Burkho_BcepC6B_NC_005887	6.1e-10
36	45066..45425	PP_00059;hypothetical protein;phage;-;PHAGE_Burkho_BcepMigl_NC_019917	6.59e-14
37	45471..46268	PP_00060;DUF2303 protein;phage;-;PHAGE_Burkho_BcepMigl_NC_019917	2.89e-32
38	46861..47664	PP_00062;hypothetical protein;phage;-;PHAGE_Strept_phiARI0468_4_NC_031915	1.96e-101
39	47675..48175	PP_00063;methyltransferase;phage;-;PHAGE_Mannhe_vB_MhS_535AP2_NC_028853	4.61e-78
40	48320..48541	PP_00065;hypothetical protein;phage;-;PHAGE_Haemop_HP1_NC_001697	8.71e-18
41	48631..48789	PP_00066;hypothetical protein;phage;-;PHAGE_Mannhe_vB_MhS_1152AP2_NC_028956	8.28e-12
42	48799..49839	PP_00067;integrase;phage;-;PHAGE_Mannhe_vB_MhS_1152AP2_NC_028956	0.0