CDS 601 - 837

 /gene="1"

 /product="gp1"

 /function="helicase"

 /locus tag="Psullivan\_1"

 /note=Original Glimmer call @bp 601 has strength 10.23; Genemark calls start at 601

 /note=SSC: 601-837 CP: no SCS: both ST: SS BLAST-Start: [helicase [Mycobacterium phage Gompeii16] ],,NCBI, q1:s1 100.0% 7.76775E-50 GAP: 0 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.422, -3.8079208184165134, yes F: helicase SIF-BLAST: ,,[helicase [Mycobacterium phage Gompeii16] ],,YP\_009291240,100.0,7.76775E-50 SIF-HHPRED: SIF-Syn: This gene shows synteny with Altman, Bircsak, ConceptII, Francis47, JuliaChild etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 86516

CDS 1138 - 1329

 /gene="2"

 /product="gp2"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_2"

 /note=Original Glimmer call @bp 1138 has strength 5.7; Genemark calls start at 1138

 /note=SSC: 1138-1329 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_PATTYP\_3 [Mycobacterium phage PattyP] ],,NCBI, q1:s1 100.0% 3.42249E-38 GAP: 300 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.111, -4.85287563363746, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein PBI\_PATTYP\_3 [Mycobacterium phage PattyP] ],,YP\_008050768,100.0,3.42249E-38 SIF-HHPRED: SIF-Syn: Shows synteny with Hope4Ever, JuliaChild, Molly, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 2729

CDS 1366 - 1806

 /gene="3"

 /product="gp3"

 /function="terminase, small subunit"

 /locus tag="Psullivan\_3"

 /note=Original Glimmer call @bp 1366 has strength 5.86; Genemark calls start at 1366

 /note=SSC: 1366-1806 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_PINTO\_3 [Mycobacterium phage Pinto] ],,NCBI, q1:s1 100.0% 1.83181E-101 GAP: 36 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.926, -2.6814417326944517, yes F: terminase, small subunit SIF-BLAST: ,,[hypothetical protein PBI\_PINTO\_3 [Mycobacterium phage Pinto] ],,YP\_009043787,100.0,1.83181E-101 SIF-HHPRED: SIF-Syn: Shows synteny with Big3, Ciao, DreamCatcher, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 152748

CDS 1919 - 2338

 /gene="4"

 /product="gp4"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_4"

 /note=Original Glimmer call @bp 1919 has strength 6.68; Genemark calls start at 1919

 /note=SSC: 1919-2338 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein AVV04\_gp04 [Mycobacterium phage Tasp14] ],,NCBI, q1:s1 100.0% 1.02685E-95 GAP: 112 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.137, -2.2364030944336752, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein AVV04\_gp04 [Mycobacterium phage Tasp14] ],,YP\_009197583,100.0,1.02685E-95 SIF-HHPRED: SIF-Syn: Shows synteny with JuliaChild, Pari, Pita2, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 142570

tRNA 2641 - 2716

 /gene="5"

 /product="tRNA-Trp(cca)"

 /locus tag="PSULLIVAN\_5"

 /note=tRNA-Trp(cca)

CDS 2748 - 3818

 /gene="6"

 /product="gp6"

 /function="minor tail protein"

 /locus tag="Psullivan\_6"

 /note=Original Glimmer call @bp 2748 has strength 17.6; Genemark calls start at 2748

 /note=SSC: 2748-3818 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_PITA2\_7 [Mycobacterium phage Pita2] ],,NCBI, q1:s1 100.0% 0.0 GAP: 409 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.309, -6.101211774336551, no F: minor tail protein SIF-BLAST: ,,[hypothetical protein SEA\_PITA2\_7 [Mycobacterium phage Pita2] ],,AXH65953,100.0,0.0 SIF-HHPRED: SIF-Syn: Shows synteny with JuliaChild, Pita2, Tote, etc.

 /note=Large gap may be due to presence of predicted tRNA gene upstream.`

 /note=

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 154375

CDS 3828 - 4529

 /gene="7"

 /product="gp7"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_7"

 /note=Original Glimmer call @bp 3828 has strength 12.38; Genemark calls start at 3837

 /note=SSC: 3828-4529 CP: yes SCS: both-gl ST: SS BLAST-Start: [hypothetical protein SEA\_PITA2\_8 [Mycobacterium phage Pita2]],,NCBI, q1:s1 100.0% 4.47546E-163 GAP: 9 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.342, -3.8366550365551095, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_PITA2\_8 [Mycobacterium phage Pita2]],,AXH65954,100.0,4.47546E-163 SIF-HHPRED: SIF-Syn: Shows synteny with Pita2, Tote, JuliaChild, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 154459

CDS 4543 - 4803

 /gene="8"

 /product="gp8"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_8"

 /note=Original Glimmer call @bp 4543 has strength 8.73; Genemark calls start at 4543

 /note=SSC: 4543-4803 CP: yes SCS: both ST: SS BLAST-Start: [tail protein [Mycobacterium phage Bxb1] ],,NCBI, q1:s1 100.0% 6.72832E-54 GAP: 13 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.347, -4.352843561762388, no F: Hypothetical Protein SIF-BLAST: ,,[tail protein [Mycobacterium phage Bxb1] ],,NP\_075273,100.0,6.72832E-54 SIF-HHPRED: SIF-Syn: Has synteny with A6, Abbyshoes, Acme, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 349

CDS 4811 - 5068

 /gene="9"

 /product="gp9"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_9"

 /note=Original Glimmer call @bp 4811 has strength 15.11; Genemark calls start at 4811

 /note=SSC: 4811-5068 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_U2\_7 [Mycobacterium phage U2] ],,NCBI, q1:s1 100.0% 9.78319E-52 GAP: 7 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.766, -3.7679082124642584, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein PBI\_U2\_7 [Mycobacterium phage U2] ],,YP\_001491577,100.0,9.78319E-52 SIF-HHPRED: SIF-Syn: Shows synteny with Doom, Dreamboat, Dreamcatcher, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 338

CDS 5068 - 6501

 /gene="10"

 /product="gp10"

 /function="lysin A"

 /locus tag="Psullivan\_10"

 /note=Original Glimmer call @bp 5068 has strength 12.12; Genemark calls start at 5068

 /note=SSC: 5068-6501 CP: yes SCS: both ST: SS BLAST-Start: [lysin A [Mycobacterium phage Pita2] ],,NCBI, q1:s1 100.0% 0.0 GAP: -1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.035, -7.428818319087355, no F: lysin A SIF-BLAST: ,,[lysin A [Mycobacterium phage Pita2] ],,AXH65957,100.0,0.0 SIF-HHPRED: SIF-Syn: Shows synteny with JuliaChild, Pita2, Tote, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 84643

CDS 6491 - 7459

 /gene="11"

 /product="gp11"

 /function="lysin B"

 /locus tag="Psullivan\_11"

 /note=Original Glimmer call @bp 6545 has strength 11.22; Genemark calls start at 6491

 /note=SSC: 6491-7459 CP: yes SCS: both-gm ST: SS BLAST-Start: [lysin B [Mycobacterium phage Pita2] ],,NCBI, q1:s1 100.0% 0.0 GAP: -11 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.717, -5.220380545373514, no F: lysin B SIF-BLAST: ,,[lysin B [Mycobacterium phage Pita2] ],,AXH65958,100.0,0.0 SIF-HHPRED: SIF-Syn: Shows synteny with JuliaChild, Pita2, Tote, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 152741

CDS 7479 - 9167

 /gene="12"

 /product="gp12"

 /function="terminase, large subunit"

 /locus tag="Psullivan\_12"

 /note=Original Glimmer call @bp 7479 has strength 12.47; Genemark calls start at 7479

 /note=SSC: 7479-9167 CP: yes SCS: both ST: SS BLAST-Start: [terminase [Mycobacterium phage Pita2] ],,NCBI, q1:s1 100.0% 0.0 GAP: 19 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.849, -2.8454123590742793, yes F: terminase, large subunit SIF-BLAST: ,,[terminase [Mycobacterium phage Pita2] ],,AXH65959,100.0,0.0 SIF-HHPRED: Terminase large subunit; genome packaging, bacteriophage, ATPase, nuclease, VIRAL PROTEIN; HET: BR; 2.2A {Enterobacteria phage HK97},,,6Z6D\_A,91.8149,100.0 SIF-Syn: Shows synteny with JuliaChild, Tote, Abbyshoes, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 154356

CDS 9164 - 10606

 /gene="13"

 /product="gp13"

 /function="portal protein"

 /locus tag="Psullivan\_13"

 /note=Original Glimmer call @bp 9164 has strength 12.69; Genemark calls start at 9164

 /note=SSC: 9164-10606 CP: yes SCS: both ST: SS BLAST-Start: [portal protein [Mycobacterium phage Pita2] ],,NCBI, q1:s1 100.0% 0.0 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.824, -4.423424636048095, no F: portal protein SIF-BLAST: ,,[portal protein [Mycobacterium phage Pita2] ],,AXH65960,100.0,0.0 SIF-HHPRED: Phage\_prot\_Gp6 ; Phage portal protein, SPP1 Gp6-like,,,PF05133.18,89.1667,100.0 SIF-Syn: Shows synteny with JuliaChild, Pita2, Tote, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 149907

CDS 10603 - 11484

 /gene="14"

 /product="gp14"

 /function="capsid maturation protease"

 /locus tag="Psullivan\_14"

 /note=Original Glimmer call @bp 10603 has strength 7.46; Genemark calls start at 10603

 /note=SSC: 10603-11484 CP: yes SCS: both ST: SS BLAST-Start: [head maturation protease [Mycobacterium phage Museum] ],,NCBI, q1:s1 100.0% 0.0 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.135, -4.62669054194548, no F: capsid maturation protease SIF-BLAST: ,,[head maturation protease [Mycobacterium phage Museum] ],,YP\_009637263,100.0,0.0 SIF-HHPRED: SIF-Syn: Shows synteny with BigMau, Jerm2, JuliaChild, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 154366

CDS 11543 - 12055

 /gene="15"

 /product="gp15"

 /function="scaffolding protein"

 /locus tag="Psullivan\_15"

 /note=Original Glimmer call @bp 11543 has strength 9.62; Genemark calls start at 11543

 /note=SSC: 11543-12055 CP: yes SCS: both ST: SS BLAST-Start: [scaffolding protein [Mycobacterium phage Pepe] ],,NCBI, q1:s1 100.0% 1.87004E-115 GAP: 58 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.926, -2.6013996449736907, yes F: scaffolding protein SIF-BLAST: ,,[scaffolding protein [Mycobacterium phage Pepe] ],,YP\_009189886,100.0,1.87004E-115 SIF-HHPRED: SIF-Syn: Shows synteny with Pepe, Pita2, Dexes,etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 149922

CDS 12065 - 13072

 /gene="16"

 /product="gp16"

 /function="major capsid protein"

 /locus tag="Psullivan\_16"

 /note=Original Glimmer call @bp 12065 has strength 16.68; Genemark calls start at 12065

 /note=SSC: 12065-13072 CP: yes SCS: both ST: SS BLAST-Start: [major capsid protein [Mycobacterium phage Pita2]],,NCBI, q1:s1 100.0% 0.0 GAP: 9 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.243, -2.0111200136961407, yes F: major capsid protein SIF-BLAST: ,,[major capsid protein [Mycobacterium phage Pita2]],,AXH65963,100.0,0.0 SIF-HHPRED: Major capsid protein; HK97-fold, T=7, tailed bacteriophage, VIRUS; 2.6A {Gordonia phage Cozz},,,8ECK\_E,99.1045,100.0 SIF-Syn: Shows synteny with Pita2, Arlo, JuliaChild, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 152742

CDS 13145 - 13381

 /gene="17"

 /product="gp17"

 /function="head-to-tail adaptor"

 /locus tag="Psullivan\_17"

 /note=Original Glimmer call @bp 13145 has strength 11.9; Genemark calls start at 13145

 /note=SSC: 13145-13381 CP: yes SCS: both ST: SS BLAST-Start: [head-tail connector protein [Mycobacterium phage Bethlehem] ],,NCBI, q1:s1 100.0% 1.41662E-47 GAP: 72 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.508, -3.486006226271621, yes F: head-to-tail adaptor SIF-BLAST: ,,[head-tail connector protein [Mycobacterium phage Bethlehem] ],,YP\_001491667,100.0,1.41662E-47 SIF-HHPRED: SIF-Syn: Shows synteny with ILeeKay, Niza, Dynamix, etc.

 /note=Called "head-to-tail adaptor" rather than "head-to-tail connector" in compliance with SEA PHAGES naming conventions.

 /note=

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 745

CDS 13381 - 13830

 /gene="18"

 /product="gp18"

 /function="head-to-tail adaptor"

 /locus tag="Psullivan\_18"

 /note=Original Glimmer call @bp 13381 has strength 14.76; Genemark calls start at 13381

 /note=SSC: 13381-13830 CP: yes SCS: both ST: SS BLAST-Start: [head-tail adaptor Ad1 [Mycobacterium phage U2] ],,NCBI, q1:s1 100.0% 1.36521E-103 GAP: -1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.964, -4.778071418780228, yes F: head-to-tail adaptor SIF-BLAST: ,,[head-tail adaptor Ad1 [Mycobacterium phage U2] ],,YP\_001491587,100.0,1.36521E-103 SIF-HHPRED: gp6\_gp15\_like; Head-Tail Connector Proteins gp6 and gp15, and similar proteins. Members of this family include the proteins gp6 and gp15 from bacteriophage HK97 and SPP1, respectively.,,,cd08051,68.4564,96.4 SIF-Syn: Shows synteny with Froghopper, Fushigi, Gandalf20, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 154364

CDS 13830 - 14192

 /gene="19"

 /product="gp19"

 /function="head-to-tail stopper"

 /locus tag="Psullivan\_19"

 /note=Original Glimmer call @bp 13875 has strength 7.56; Genemark calls start at 13830

 /note=SSC: 13830-14192 CP: yes SCS: both-gm ST: SS BLAST-Start: [head-to-tail stopper [Mycobacterium phage Pita2] ],,NCBI, q1:s1 100.0% 5.34369E-81 GAP: -1 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.331, -3.8600882102548564, yes F: head-to-tail stopper SIF-BLAST: ,,[head-to-tail stopper [Mycobacterium phage Pita2] ],,AXH65966,100.0,5.34369E-81 SIF-HHPRED: SIF-Syn: Shows synteny with JuliaChild, Pita2, Tote, etc.

 /note=This ORF was chosen because it was the longest ORF with a short gap, although it disagrees with GeneMark and Glimmer. HHPRED hit on protein SPP1 as mentioned in SEA-PHAGES functional naming conventions.

 /note=

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 38358

CDS 14192 - 14587

 /gene="20"

 /product="gp20"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_20"

 /note=Original Glimmer call @bp 14192 has strength 10.62; Genemark calls start at 14192

 /note=SSC: 14192-14587 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_CARLYLE\_21 [Mycobacterium phage Carlyle]],,NCBI, q1:s1 100.0% 1.07794E-90 GAP: -1 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.545, -3.4080892535965868, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_CARLYLE\_21 [Mycobacterium phage Carlyle]],,QDM57755,100.0,1.07794E-90 SIF-HHPRED: SIF-Syn: Shows synteny with GrecoEtero, Greg, HarryOW, etc.

 /note=Although there are significant hits in HHPRED, it is uncertain if this is a informative match due to the lack of function.

 /note=

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 154361

CDS 14591 - 15037

 /gene="21"

 /product="gp21"

 /function="tail terminator"

 /locus tag="Psullivan\_21"

 /note=Original Glimmer call @bp 14591 has strength 7.36; Genemark calls start at 14591

 /note=SSC: 14591-15037 CP: yes SCS: both ST: SS BLAST-Start: [tail terminator [Mycobacterium phage Pita2] ],,NCBI, q1:s1 100.0% 9.45601E-102 GAP: 3 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.672, -3.2017655760970833, yes F: tail terminator SIF-BLAST: ,,[tail terminator [Mycobacterium phage Pita2] ],,AXH65968,100.0,9.45601E-102 SIF-HHPRED: Tail terminator protein Rcc01690; "neck", "portal", "capsid", "tail tube", VIRUS; 3.58A {Rhodobacter capsulatus},,,6TE9\_F,97.2973,99.1 SIF-Syn: Shows synteny with JuliaChild, Ohno789, Pita2, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 23

CDS 15046 - 15897

 /gene="22"

 /product="gp22"

 /function="major tail protein"

 /locus tag="Psullivan\_22"

 /note=Original Glimmer call @bp 15046 has strength 18.44; Genemark calls start at 15046

 /note=SSC: 15046-15897 CP: yes SCS: both ST: SS BLAST-Start: [major tail protein [Mycobacterium phage Pita2]],,NCBI, q1:s1 100.0% 0.0 GAP: 8 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.147, -2.66069824281639, yes F: major tail protein SIF-BLAST: ,,[major tail protein [Mycobacterium phage Pita2]],,AXH65969,100.0,0.0 SIF-HHPRED: SIF-Syn: Shows synteny with JuliaChild, Pita2, Tote, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 154477

CDS 16021 - 16398

 /gene="23"

 /product="gp23"

 /function="tail assembly chaperone"

 /locus tag="Psullivan\_23"

 /note=Original Glimmer call @bp 16021 has strength 12.08; Genemark calls start at 16021

 /note=SSC: 16021-16398 CP: yes SCS: both ST: SS BLAST-Start: [tail assembly chaperone [Mycobacterium phage Manatee]],,NCBI, q1:s1 100.0% 7.69301E-82 GAP: 123 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.754, -5.432024807810012, no F: tail assembly chaperone SIF-BLAST: ,,[tail assembly chaperone [Mycobacterium phage Manatee]],,QJD53501,100.0,7.69301E-82 SIF-HHPRED: GP24\_25 ; Mycobacteriophage tail assembly protein,,,PF17388.6,95.2,100.0 SIF-Syn: Shows synteny with Manatee, JuliaChild, Anglerfish, etc.

 /note=Not the longest open reading frame with a small gap, however the longest open reading frame with a small gap shows no gene synteny, while the selected site start shows expected synteny with close members of the Pfam.

 /note=

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 152749

CDS 16419 - 16820

 /gene="24"

 /product="gp24"

 /function="tail assembly chaperone"

 /locus tag="Psullivan\_24"

 /note=Original Glimmer call @bp 16419 has strength 12.17; Genemark calls start at 16419

 /note=SSC: 16419-16820 CP: yes SCS: both ST: SS BLAST-Start: [tail assembly chaperone [Mycobacterium phage Bethlehem] ],,NCBI, q1:s1 100.0% 1.02816E-91 GAP: 20 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.696, -5.284097324023995, no F: tail assembly chaperone SIF-BLAST: ,,[tail assembly chaperone [Mycobacterium phage Bethlehem] ],,YP\_001491674,99.2481,1.02816E-91 SIF-HHPRED: SIF-Syn: Shows synteny with Petruchio, Pita2, Rufus, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 137975

CDS 16832 - 19303

 /gene="25"

 /product="gp25"

 /function="tape measure protein"

 /locus tag="Psullivan\_25"

 /note=Original Glimmer call @bp 16832 has strength 11.39; Genemark calls start at 16832

 /note=SSC: 16832-19303 CP: yes SCS: both ST: SS BLAST-Start: [tape measure protein [Mycobacterium phage Rufus] ],,NCBI, q1:s1 100.0% 0.0 GAP: 11 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.567, -3.888407369012715, no F: tape measure protein SIF-BLAST: ,,[tape measure protein [Mycobacterium phage Rufus] ],,YP\_009199539,100.0,0.0 SIF-HHPRED: SIF-Syn: Shows synteny with Pita2, JuliaChild, Rufus, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 152755

CDS 19327 - 21384

 /gene="26"

 /product="gp26"

 /function="minor tail protein"

 /locus tag="Psullivan\_26"

 /note=Original Glimmer call @bp 19327 has strength 17.86; Genemark calls start at 19327

 /note=SSC: 19327-21384 CP: yes SCS: both ST: SS BLAST-Start: [minor tail protein [Mycobacterium phage Pita2]],,NCBI, q1:s1 100.0% 0.0 GAP: 23 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.849, -3.2925703904164987, yes F: minor tail protein SIF-BLAST: ,,[minor tail protein [Mycobacterium phage Pita2]],,AXH65973,100.0,0.0 SIF-HHPRED: SIF-Syn: Shows synteny with Pita2, JuliaChild, Tote, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 151724

CDS 21403 - 21585

 /gene="27"

 /product="gp27"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_27"

 /note=Original Glimmer call @bp 21403 has strength 15.06; Genemark calls start at 21403

 /note=SSC: 21403-21585 CP: yes SCS: both ST: SS BLAST-Start: [minor tail protein [Mycobacterium phage Trouble] ],,NCBI, q1:s1 100.0% 3.80484E-32 GAP: 18 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.754, -5.143229268563043, no F: Hypothetical Protein SIF-BLAST: ,,[minor tail protein [Mycobacterium phage Trouble] ],,YP\_008409759,100.0,3.80484E-32 SIF-HHPRED: SIF-Syn: Shows synteny with Abrogate, AFIS, BeesKnees, etc.

 /note=Numerous hypothetical proteins with high identity in NCBI BLAST are identified as a minor tail protein.

 /note=

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 84864

CDS 21585 - 23387

 /gene="28"

 /product="gp28"

 /function="minor tail protein"

 /locus tag="Psullivan\_28"

 /note=Original Glimmer call @bp 21585 has strength 18.91; Genemark calls start at 21585

 /note=SSC: 21585-23387 CP: yes SCS: both ST: SS BLAST-Start: [minor tail protein [Mycobacterium phage Treddle]],,NCBI, q1:s1 100.0% 0.0 GAP: -1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.451, -5.72088676244897, no F: minor tail protein SIF-BLAST: ,,[minor tail protein [Mycobacterium phage Treddle]],,AJA43510,100.0,0.0 SIF-HHPRED: Protein gp18; NP\_465809.1, prophage tail protein gp18, Structural Genomics, Joint Center for Structural Genomics, JCSG, Protein Structure Initiative; HET: MLY, MSE; 1.7A {Listeria monocytogenes EGD-e},,,3GS9\_A,89.8333,99.0 SIF-Syn: Shows synteny with A6, Abrogate, Abbyshoes, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 151611

CDS 23482 - 23928

 /gene="29"

 /product="gp29"

 /function="minor tail protein"

 /locus tag="Psullivan\_29"

 /note=Original Glimmer call @bp 23482 has strength 6.83; Genemark calls start at 23482

 /note=SSC: 23482-23928 CP: yes SCS: both ST: SS BLAST-Start: [minor tail protein [Mycobacterium phage Bxb1] ],,NCBI, q1:s1 100.0% 2.4397E-104 GAP: 94 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.949, -5.3211856022650945, no F: minor tail protein SIF-BLAST: ,,[minor tail protein [Mycobacterium phage Bxb1] ],,NP\_075293,100.0,2.4397E-104 SIF-HHPRED: DUF2744 ; Protein of unknown function (DUF2744),,,PF10910.12,89.1892,100.0 SIF-Syn: Shows synteny with Magnar, Manatee, Marcell, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 152750

CDS 23940 - 24272

 /gene="30"

 /product="gp30"

 /function="minor tail protein"

 /locus tag="Psullivan\_30"

 /note=Original Glimmer call @bp 23940 has strength 13.98; Genemark calls start at 23925

 /note=SSC: 23940-24272 CP: yes SCS: both-gl ST: SS BLAST-Start: [minor tail protein [Mycobacterium phage SwissCheese]],,NCBI, q1:s6 100.0% 5.17694E-72 GAP: 11 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.601, -5.4833670199227385, no F: minor tail protein SIF-BLAST: ,,[minor tail protein [Mycobacterium phage SwissCheese]],,AXH45198,95.6522,5.17694E-72 SIF-HHPRED: SIF-Syn: Shows synteny with BaconJack, Blue, Dexes, etc.

 /note=The selected start site is not the longest with a small gap, however, this site has greater synteny with other genes in the Pfam.

 /note=

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 84700

CDS 24269 - 24616

 /gene="31"

 /product="gp31"

 /function="minor tail protein"

 /locus tag="Psullivan\_31"

 /note=Original Glimmer call @bp 24269 has strength 13.5; Genemark calls start at 24269

 /note=SSC: 24269-24616 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein N854\_gp31 [Mycobacterium phage Trouble] ],,NCBI, q1:s1 100.0% 1.24402E-75 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.47, -6.730876284578336, no F: minor tail protein SIF-BLAST: ,,[hypothetical protein N854\_gp31 [Mycobacterium phage Trouble] ],,YP\_008409763,100.0,1.24402E-75 SIF-HHPRED: Cell division protein FtsB; bacterial cell division, peptidoglycan synthesis, membrane protein complex, MEMBRANE PROTEIN;{Pseudomonas aeruginosa PAO1},,,8BH1\_E,94.7826,97.1 SIF-Syn: Shows synteny with Aeneas, Alsfro, Blue, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 131795

CDS 24641 - 26494

 /gene="32"

 /product="gp32"

 /function="minor tail protein"

 /locus tag="Psullivan\_32"

 /note=Original Glimmer call @bp 24641 has strength 13.86; Genemark calls start at 24641

 /note=SSC: 24641-26494 CP: yes SCS: both ST: SS BLAST-Start: [minor tail protein [Mycobacterium phage Aeneas] ],,NCBI, q1:s1 100.0% 0.0 GAP: 24 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.686, -3.1085431521568267, yes F: minor tail protein SIF-BLAST: ,,[minor tail protein [Mycobacterium phage Aeneas] ],,YP\_009016298,100.0,0.0 SIF-HHPRED: SIF-Syn: Shows synteny with Aeneas, JackSparrow, Greg, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 152880

CDS 26487 - 27731

 /gene="33"

 /product="gp33"

 /function="minor tail protein"

 /locus tag="Psullivan\_33"

 /note=Original Glimmer call @bp 26487 has strength 12.14; Genemark calls start at 26487

 /note=SSC: 26487-27731 CP: yes SCS: both ST: SS BLAST-Start: [minor tail protein [Mycobacterium phage MPlant7149]],,NCBI, q1:s1 96.6184% 0.0 GAP: -8 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.156, -4.580504230403352, no F: minor tail protein SIF-BLAST: ,,[minor tail protein [Mycobacterium phage MPlant7149]],,AVJ50412,80.4878,0.0 SIF-HHPRED: Alpha/beta hydrolase; NRPS, cyclase, PBP-binding protein, HYDROLASE; HET: SO4; 2.2A {Streptomyces albidoflavus},,,6KSU\_A,82.3671,100.0 SIF-Syn: Shows synteny with Atkinbua, JuliaChild, MPlant7149, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 84666

CDS 27860 - 28012

 /gene="34"

 /product="gp34"

 /locus tag="Psullivan\_34"

 /note=Genemark calls start at 27860

 /note=SSC: 27860-28012 CP: no SCS: genemark ST: NI BLAST-Start: GAP: 128 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.644, -4.502587993016531, yes F: SIF-BLAST: SIF-HHPRED: SIF-Syn:

CDS 28147 - 28443

 /gene="35"

 /product="gp35"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_35"

 /note=Original Glimmer call @bp 28147 has strength 10.36; Genemark calls start at 28147

 /note=SSC: 28147-28443 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein GRADUATION\_38 [Mycobacterium phage Graduation] ],,NCBI, q1:s1 100.0% 4.01446E-65 GAP: 134 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.905, -2.996490344739583, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein GRADUATION\_38 [Mycobacterium phage Graduation] ],,YP\_008858576,100.0,4.01446E-65 SIF-HHPRED: SIF-Syn: Shows synteny with Abbyshoes, Dussy, Bones, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 84614

CDS 28610 - 30097

 /gene="36"

 /product="gp36"

 /function="serine integrase"

 /locus tag="Psullivan\_36"

 /note=Original Glimmer call @bp 28610 has strength 8.88; Genemark calls start at 28520

 /note=SSC: 28610-30097 CP: yes SCS: both-gl ST: SS BLAST-Start: [serine integrase [Mycobacterium phage Jasper] ],,NCBI, q1:s6 100.0% 0.0 GAP: 166 bp gap LO: no RBS: Kibler 6, Karlin Medium, 0.529, -7.734802161381105, no F: serine integrase SIF-BLAST: ,,[serine integrase [Mycobacterium phage Jasper] ],,YP\_001994585,98.4,0.0 SIF-HHPRED: INTEGRASE; HYDROLASE, SERINE RECOMBINASE, UNIDIRECTIONAL, SITE-SPECIFIC RECOMBINATION; 2.15A {STREPTOMYCES PHAGE PHIC31},,,4BQQ\_B,61.2121,100.0 SIF-Syn: Shows synteny with Jasper, JuliaChild, Rufus, etc.

 /note=The selected start site was chosen due to its high synteny with related viruses.

 /note=

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 154378

CDS complement (30220 - 30492)

 /gene="37"

 /product="gp37"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_37"

 /note=Original Glimmer call @bp 30492 has strength 10.45; Genemark calls start at 30492

 /note=SSC: 30492-30220 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_PINTO\_40 [Mycobacterium phage Pinto] ],,NCBI, q1:s1 100.0% 1.14828E-55 GAP: 96 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.849, -2.8454123590742793, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein PBI\_PINTO\_40 [Mycobacterium phage Pinto] ],,YP\_009043824,100.0,1.14828E-55 SIF-HHPRED: SIF-Syn: Shows synteny with Arcanine, BaconJack, Bexan, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 154490

CDS complement (30589 - 30720)

 /gene="38"

 /product="gp38"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_38"

 /note=Original Glimmer call @bp 30720 has strength 1.62; Genemark calls start at 30846

 /note=SSC: 30720-30589 CP: yes SCS: both-gl ST: SS BLAST-Start: [hypothetical protein SEA\_PITA2\_41 [Mycobacterium phage Pita2]],,NCBI, q1:s1 100.0% 1.21766E-22 GAP: 1 bp gap LO: no RBS: Kibler 6, Karlin Medium, 0.822, -7.1313160653937935, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_PITA2\_41 [Mycobacterium phage Pita2]],,AXH65987,100.0,1.21766E-22 SIF-HHPRED: SIF-Syn: Shows synteny with Pita2, BaconJack, Rohr, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 13140

CDS complement (30722 - 31246)

 /gene="39"

 /product="gp39"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_39"

 /note=Original Glimmer call @bp 31246 has strength 1.79

 /note=SSC: 31246-30722 CP: yes SCS: glimmer ST: SS BLAST-Start: [hypothetical protein SEA\_PITA2\_42 [Mycobacterium phage Pita2]],,NCBI, q1:s1 100.0% 2.27626E-125 GAP: -1 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.753, -2.967790469131549, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_PITA2\_42 [Mycobacterium phage Pita2]],,AXH65988,100.0,2.27626E-125 SIF-HHPRED: Agmatine N-acetyltransferase; GCN5-related N-acetyltransferase(GNAT), Arylalkylamine N-acetyltransferase(AANAT), TRANSFERASE; HET: G0R, COA; 1.6A {Drosophila melanogaster},,,7CIW\_A,87.3563,97.7 SIF-Syn: Shows synteny with Pita2, HermioneGrange, Rohr, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 90377

CDS complement (31246 - 31416)

 /gene="40"

 /product="gp40"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_40"

 /note=Original Glimmer call @bp 31416 has strength 10.93; Genemark calls start at 31416

 /note=SSC: 31416-31246 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_ROHR\_41 [Mycobacterium phage Rohr] ],,NCBI, q1:s1 100.0% 4.45033E-34 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.137, -4.622300575606491, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_ROHR\_41 [Mycobacterium phage Rohr] ],,AXH44988,100.0,4.45033E-34 SIF-HHPRED: SIF-Syn: Shows synteny with HermioneGrange, Jerm2, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 150112

CDS complement (31413 - 31508)

 /gene="41"

 /product="gp41"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_41"

 /note=Genemark calls start at 31508

 /note=SSC: 31508-31413 CP: yes SCS: genemark ST: SS BLAST-Start: [hypothetical protein SEA\_PITA2\_44 [Mycobacterium phage Pita2]],,NCBI, q1:s1 100.0% 3.34616E-11 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.691, -3.098116455756734, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_PITA2\_44 [Mycobacterium phage Pita2]],,AXH65990,100.0,3.34616E-11 SIF-HHPRED: SIF-Syn: Shows synteny with Norz, Pita2, A6, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 85975

CDS complement (31505 - 31747)

 /gene="42"

 /product="gp42"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_42"

 /note=Original Glimmer call @bp 31747 has strength 6.74; Genemark calls start at 31747

 /note=SSC: 31747-31505 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_PITA2\_45 [Mycobacterium phage Pita2]],,NCBI, q1:s1 100.0% 2.38037E-52 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.441, -3.708514821076885, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_PITA2\_45 [Mycobacterium phage Pita2]],,AXH65991,100.0,2.38037E-52 SIF-HHPRED: SIF-Syn: Shows synteny with Pita2, Parliament, Sibs6, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 154495

CDS complement (31744 - 32100)

 /gene="43"

 /product="gp43"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_43"

 /note=Original Glimmer call @bp 32100 has strength 14.86; Genemark calls start at 32100

 /note=SSC: 32100-31744 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_PITA2\_46 [Mycobacterium phage Pita2]],,NCBI, q1:s1 100.0% 1.77758E-78 GAP: 20 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.905, -3.1725816037952645, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_PITA2\_46 [Mycobacterium phage Pita2]],,AXH65992,100.0,1.77758E-78 SIF-HHPRED: SIF-Syn: Shows synteny with Pita2, Arcanine, Killigrew, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 104644

CDS complement (32121 - 33947)

 /gene="44"

 /product="gp44"

 /function="DNA polymerase I"

 /locus tag="Psullivan\_44"

 /note=Original Glimmer call @bp 33947 has strength 16.33; Genemark calls start at 33947

 /note=SSC: 33947-32121 CP: yes SCS: both ST: SS BLAST-Start: [DNA polymerase I [Mycobacterium phage Pita2]],,NCBI, q1:s1 100.0% 0.0 GAP: 40 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.497, -3.5707972674952195, no F: DNA polymerase I SIF-BLAST: ,,[DNA polymerase I [Mycobacterium phage Pita2]],,AXH65993,100.0,0.0 SIF-HHPRED: DNA polymerase I; mycobacteria, DNA polymerase, Flap endonuclease, TRANSFERASE; 2.713A {Mycolicibacterium smegmatis},,,6VDE\_A,95.7237,100.0 SIF-Syn: Shows synteny with Pita2, Atkinbua, Pari, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 149908

CDS complement (33988 - 34113)

 /gene="45"

 /product="gp45"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_45"

 /note=Original Glimmer call @bp 34113 has strength 5.54; Genemark calls start at 34113

 /note=SSC: 34113-33988 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_PATTYP\_46 [Mycobacterium phage PattyP] ],,NCBI, q1:s1 100.0% 4.85438E-19 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.146, -4.393256767017744, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein PBI\_PATTYP\_46 [Mycobacterium phage PattyP] ],,YP\_008050811,100.0,4.85438E-19 SIF-HHPRED: SIF-Syn: Shows synteny with Blue, PattyP, Molly, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 154379

CDS complement (34110 - 34340)

 /gene="46"

 /product="gp46"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_46"

 /note=Original Glimmer call @bp 34340 has strength 15.13; Genemark calls start at 34340

 /note=SSC: 34340-34110 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein Jasper\_48 [Mycobacterium phage Jasper] ],,NCBI, q1:s1 100.0% 2.11916E-48 GAP: 30 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.111, -4.387988835334809, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein Jasper\_48 [Mycobacterium phage Jasper] ],,YP\_001994595,100.0,2.11916E-48 SIF-HHPRED: SIF-Syn: Shows synteny with Barriga, Bigfoot, BigMau, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 341

CDS complement (34371 - 34862)

 /gene="47"

 /product="gp47"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_47"

 /note=Original Glimmer call @bp 34862 has strength 12.55; Genemark calls start at 34862

 /note=SSC: 34862-34371 CP: yes SCS: both ST: SS BLAST-Start: [ribonucleoside reductase class II [Mycobacterium phage RidgeCB] ],,NCBI, q1:s1 100.0% 1.91017E-113 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.905, -2.7254235724530456, yes F: Hypothetical Protein SIF-BLAST: ,,[ribonucleoside reductase class II [Mycobacterium phage RidgeCB] ],,YP\_009014215,100.0,1.91017E-113 SIF-HHPRED: SIF-Syn: Shows synteny with JuliaChild, Pita2, BigMau, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 152852

CDS complement (34859 - 35041)

 /gene="48"

 /product="gp48"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_48"

 /note=Original Glimmer call @bp 35041 has strength 9.8; Genemark calls start at 35041

 /note=SSC: 35041-34859 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_U2\_48 [Mycobacterium phage U2] ],,NCBI, q1:s1 100.0% 4.94735E-37 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.76, -3.0149320667577513, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein PBI\_U2\_48 [Mycobacterium phage U2] ],,YP\_001491618,100.0,4.94735E-37 SIF-HHPRED: SIF-Syn: Shows synteny with Abbyshoes, Acme Alsfro, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 151628

CDS complement (35038 - 35823)

 /gene="49"

 /product="gp49"

 /function="helix-turn-helix DNA binding domain"

 /locus tag="Psullivan\_49"

 /note=Original Glimmer call @bp 35823 has strength 12.04; Genemark calls start at 35823

 /note=SSC: 35823-35038 CP: yes SCS: both ST: SS BLAST-Start: [helix-turn-helix DNA binding domain protein [Mycobacterium phage Pita2] ],,NCBI, q1:s1 100.0% 0.0 GAP: -8 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.75, -3.036436186053076, yes F: helix-turn-helix DNA binding domain SIF-BLAST: ,,[helix-turn-helix DNA binding domain protein [Mycobacterium phage Pita2] ],,AXH65998,100.0,0.0 SIF-HHPRED: SIF-Syn: Shows synteny with JuliaChild, Pita2, Tote, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 154388

CDS complement (35816 - 35956)

 /gene="50"

 /product="gp50"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_50"

 /note=Original Glimmer call @bp 35956 has strength 10.5; Genemark calls start at 35956

 /note=SSC: 35956-35816 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_GYZLAR\_46 [Mycobacterium phage Gyzlar] ],,NCBI, q1:s1 100.0% 2.20976E-23 GAP: 4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.246, -4.947056885847969, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_GYZLAR\_46 [Mycobacterium phage Gyzlar] ],,QWS69625,100.0,2.20976E-23 SIF-HHPRED: SIF-Syn: Shows synteny with Graduation, Greg, HarryOW, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 84872

CDS complement (35961 - 36728)

 /gene="51"

 /product="gp51"

 /function="metallophosphatase"

 /locus tag="Psullivan\_51"

 /note=Original Glimmer call @bp 36728 has strength 14.72; Genemark calls start at 36728

 /note=SSC: 36728-35961 CP: yes SCS: both ST: SS BLAST-Start: [metallo-phosphoesterase [Mycobacterium phage Seabiscuit] ],,NCBI, q1:s1 100.0% 0.0 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.497, -3.588526034455651, yes F: metallophosphatase SIF-BLAST: ,,[metallo-phosphoesterase [Mycobacterium phage Seabiscuit] ],,YP\_009031240,100.0,0.0 SIF-HHPRED: Vacuolar protein sorting-associated protein 29; Entamoeba histolytica, Vacuolar protein sorting 29, Metallophosphatase fold, Calcineurin-like phosphoesterase superfamily domain, PROTEIN TRANSPORT; 1.859A {Entamoeba histolytica} SCOP: d.159.1.0,,,5XCJ\_B,98.4314,99.8 SIF-Syn: Shows synteny with Dulcie, Molly, Atkinuba, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 84608

CDS complement (36725 - 36904)

 /gene="52"

 /product="gp52"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_52"

 /note=Original Glimmer call @bp 36904 has strength 11.17; Genemark calls start at 36904

 /note=SSC: 36904-36725 CP: yes SCS: both ST: SS BLAST-Start: [gp52 [Mycobacterium phage Bethlehem] ],,NCBI, q1:s1 100.0% 6.16499E-34 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.944, -4.759312672633257, yes F: Hypothetical Protein SIF-BLAST: ,,[gp52 [Mycobacterium phage Bethlehem] ],,YP\_001491704,100.0,6.16499E-34 SIF-HHPRED: SIF-Syn: Shows synteny with AFIS, Ajay, Anglerfish, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 84856

CDS complement (36901 - 37380)

 /gene="53"

 /product="gp53"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_53"

 /note=Original Glimmer call @bp 37380 has strength 14.64; Genemark calls start at 37392

 /note=SSC: 37380-36901 CP: yes SCS: both-gl ST: SS BLAST-Start: [hypothetical protein SEA\_PITA2\_56 [Mycobacterium phage Pita2]],,NCBI, q1:s1 100.0% 7.26618E-111 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.662, -3.160956374632079, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_PITA2\_56 [Mycobacterium phage Pita2]],,AXH66002,100.0,7.26618E-111 SIF-HHPRED: SIF-Syn: Shows synteny with Pita2, Scowl, BigMau, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 154654

CDS complement (37377 - 37598)

 /gene="54"

 /product="gp54"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_54"

 /note=Original Glimmer call @bp 37598 has strength 9.23; Genemark calls start at 37598

 /note=SSC: 37598-37377 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein CM08\_gp53 [Mycobacterium phage Bruns] ],,NCBI, q1:s1 100.0% 1.1263E-43 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.477, -3.630723714250106, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein CM08\_gp53 [Mycobacterium phage Bruns] ],,YP\_009011386,100.0,1.1263E-43 SIF-HHPRED: SIF-Syn: Shows synteny with Bob3, Bruns, Lopton, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 2571

CDS complement (37595 - 38239)

 /gene="55"

 /product="gp55"

 /function="DNA primase"

 /locus tag="Psullivan\_55"

 /note=Original Glimmer call @bp 38239 has strength 8.24; Genemark calls start at 38239

 /note=SSC: 38239-37595 CP: yes SCS: both ST: SS BLAST-Start: [DNA primase [Mycobacterium phage KBG] ],,NCBI, q1:s1 100.0% 2.11559E-155 GAP: 216 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 0.367, -8.077495802303662, no F: DNA primase SIF-BLAST: ,,[DNA primase [Mycobacterium phage KBG] ],,YP\_001994513,100.0,2.11559E-155 SIF-HHPRED: DNA primase; structural genomics, DNA-binding, primase, truncation, Seattle Structural Genomics Center for Infectious Disease, SSGCID, TRANSFERASE; HET: SO4; 2.4A {Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1)} SCOP: e.13.1.0,,,5VAZ\_A,98.1308,99.8 SIF-Syn: Shows synteny with Anglerfish, Euphoria, KBG, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 154359

CDS complement (38456 - 38617)

 /gene="56"

 /product="gp56"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_56"

 /note=Original Glimmer call @bp 38617 has strength 21.91; Genemark calls start at 38605

 /note=SSC: 38617-38456 CP: yes SCS: both-gl ST: SS BLAST-Start: [hypothetical protein SEA\_PITA2\_60 [Mycobacterium phage Pita2]],,NCBI, q1:s1 100.0% 3.98072E-31 GAP: 67 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.453, -4.703743182133757, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_PITA2\_60 [Mycobacterium phage Pita2]],,AXH66005,100.0,3.98072E-31 SIF-HHPRED: SIF-Syn: Shows synteny with Pita2, U2, PattyP, etc.

 /note=Start site chosen due to synteny with closely related phages.

 /note=

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 340

CDS complement (38685 - 38828)

 /gene="57"

 /product="gp57"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_57"

 /note=Original Glimmer call @bp 38828 has strength 9.71; Genemark calls start at 38828

 /note=SSC: 38828-38685 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_PITA2\_61 [Mycobacterium phage Pita2]],,NCBI, q1:s1 100.0% 3.5449E-25 GAP: 18 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.905, -3.1725816037952645, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_PITA2\_61 [Mycobacterium phage Pita2]],,AXH66006,100.0,3.5449E-25 SIF-HHPRED: SIF-Syn: Shows synteny with Pita2, Crovo, Dynamix, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 154445

CDS complement (38847 - 39335)

 /gene="58"

 /product="gp58"

 /function="endonuclease VII"

 /locus tag="Psullivan\_58"

 /note=Original Glimmer call @bp 39335 has strength 4.17; Genemark calls start at 39335

 /note=SSC: 39335-38847 CP: yes SCS: both ST: SS BLAST-Start: [endonuclease VII [Mycobacterium phage Pita2]],,NCBI, q1:s1 100.0% 8.22972E-113 GAP: 69 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.728, -5.214737599913874, no F: endonuclease VII SIF-BLAST: ,,[endonuclease VII [Mycobacterium phage Pita2]],,AXH66007,100.0,8.22972E-113 SIF-HHPRED: SIF-Syn: Shows synteny with Pita2, Beatrix, Bexan, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 154360

CDS complement (39405 - 39680)

 /gene="59"

 /product="gp59"

 /function="NrdH-like glutaredoxin"

 /locus tag="Psullivan\_59"

 /note=Original Glimmer call @bp 39680 has strength 12.59; Genemark calls start at 39680

 /note=SSC: 39680-39405 CP: yes SCS: both ST: SS BLAST-Start: [NrdH-like glutaredoxin [Mycobacterium phage Rajelicia] ],,NCBI, q1:s1 100.0% 3.71946E-60 GAP: -1 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.946, -2.6395089437464523, yes F: NrdH-like glutaredoxin SIF-BLAST: ,,[NrdH-like glutaredoxin [Mycobacterium phage Rajelicia] ],,QAY08635,100.0,3.71946E-60 SIF-HHPRED: Putative glutaredoxin Rv3198.1/MT3292; Trx fold, OXIDOREDUCTASE; NMR {Mycobacterium tuberculosis} SCOP: c.47.1.0, l.1.1.1,,,2LQO\_A,91.2088,98.4 SIF-Syn: Shows synteny with JuliaChild, Pita2, Tote, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 154348

CDS complement (39680 - 40501)

 /gene="60"

 /product="gp60"

 /function="DnaB-like dsDNA helicase"

 /locus tag="Psullivan\_60"

 /note=Original Glimmer call @bp 40501 has strength 15.79; Genemark calls start at 40501

 /note=SSC: 40501-39680 CP: yes SCS: both ST: SS BLAST-Start: [DnaB-like replicative helicase [Mycobacterium phage Nerujay] ],,NCBI, q1:s1 100.0% 0.0 GAP: -1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.664, -3.1550389437754522, no F: DnaB-like dsDNA helicase SIF-BLAST: ,,[DnaB-like replicative helicase [Mycobacterium phage Nerujay] ],,YP\_009210416,100.0,0.0 SIF-HHPRED: DNAB-LIKE REPLICATIVE HELICASE; Helicase, ATPase, REPLICATION; 2.35A {Bacillus phage SPP1},,,3BH0\_A,98.1685,100.0 SIF-Syn: Shows synteny with JuliaChild, Pita2, Tote, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 9

CDS complement (40501 - 40674)

 /gene="61"

 /product="gp61"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_61"

 /note=Original Glimmer call @bp 40674 has strength 7.76; Genemark calls start at 40674

 /note=SSC: 40674-40501 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_HANSHOTFIRST\_65 [Mycobacterium phage HanShotFirst] ],,NCBI, q1:s1 100.0% 2.02211E-34 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.455, -3.6776057178969577, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein PBI\_HANSHOTFIRST\_65 [Mycobacterium phage HanShotFirst] ],,YP\_008858254,100.0,2.02211E-34 SIF-HHPRED: SIF-Syn: Shows synteny with BigMau, Burton, Briton15, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 154586

CDS complement (40671 - 40790)

 /gene="62"

 /product="gp62"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_62"

 /note=Original Glimmer call @bp 40790 has strength 7.32; Genemark calls start at 40790

 /note=SSC: 40790-40671 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_HANSHOTFIRST\_66 [Mycobacterium phage HanShotFirst] ],,NCBI, q1:s1 100.0% 2.62294E-16 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.441, -3.628472733356124, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein PBI\_HANSHOTFIRST\_66 [Mycobacterium phage HanShotFirst] ],,YP\_008858255,100.0,2.62294E-16 SIF-HHPRED: SIF-Syn: Shows synteny with Bob3, HanShotFirst, Briton15, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 127485

CDS complement (40787 - 41080)

 /gene="63"

 /product="gp63"

 /function="helix-turn-helix DNA binding domain"

 /locus tag="Psullivan\_63"

 /note=Original Glimmer call @bp 41080 has strength 8.57; Genemark calls start at 41080

 /note=SSC: 41080-40787 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SOLON\_64 [Mycobacterium phage Solon] ],,NCBI, q1:s1 100.0% 1.48671E-61 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.421, -3.8116689268127657, yes F: helix-turn-helix DNA binding domain SIF-BLAST: ,,[hypothetical protein SOLON\_64 [Mycobacterium phage Solon] ],,YP\_002224005,100.0,1.48671E-61 SIF-HHPRED: SIF-Syn: Shows synteny with Acme, BaconJack, BeesKnees, etc.

 /note=Start site chosen due to synteny.

 /note=

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 154382

CDS complement (41077 - 41322)

 /gene="64"

 /product="gp64"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_64"

 /note=Original Glimmer call @bp 41322 has strength 6.8; Genemark calls start at 41322

 /note=SSC: 41322-41077 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_U2\_63 [Mycobacterium phage U2] ],,NCBI, q1:s1 100.0% 1.0357E-50 GAP: 78 bp gap LO: no RBS: Kibler 6, Karlin Medium, 0.382, -7.982630530089239, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein PBI\_U2\_63 [Mycobacterium phage U2] ],,YP\_001491633,100.0,1.0357E-50 SIF-HHPRED: SIF-Syn: Shows synteny with Arlo, NEHalo, DreamCatcher, etc.

 /note=Start site chosen due to synteny.

 /note=

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 152986

CDS complement (41401 - 41583)

 /gene="65"

 /product="gp65"

 /function="helix-turn-helix DNA binding domain"

 /locus tag="Psullivan\_65"

 /note=Original Glimmer call @bp 41583 has strength 6.41; Genemark calls start at 41583

 /note=SSC: 41583-41401 CP: yes SCS: both ST: SS BLAST-Start: [HTH DNA binding protein [Mycobacterium phage PattyP] ],,NCBI, q1:s1 100.0% 2.0639E-36 GAP: 2 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.556, -4.2123002476362, yes F: helix-turn-helix DNA binding domain SIF-BLAST: ,,[HTH DNA binding protein [Mycobacterium phage PattyP] ],,YP\_008050835,100.0,2.0639E-36 SIF-HHPRED: Recombination Directionality Factor RdfS; Excisionase, Recombination Directionality Factor, winged helix-turn-helix, superhelix, DNA BINDING PROTEIN; HET: GOL; 2.45A {Mesorhizobium japonicum R7A},,,8DGL\_A,98.3333,98.6 SIF-Syn: Shows synteny with Arlo, BigMau, Briton15, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 84877

CDS complement (41586 - 42452)

 /gene="66"

 /product="gp66"

 /function="DNA methyltransferase"

 /locus tag="Psullivan\_66"

 /note=Original Glimmer call @bp 42452 has strength 6.47; Genemark calls start at 42452

 /note=SSC: 42452-41586 CP: no SCS: both ST: NI BLAST-Start: [DNA methyltransferase [Mycobacterium phage Lamina13] ],,NCBI, q1:s1 100.0% 0.0 GAP: 30 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.296, -3.934452679007171, no F: DNA methyltransferase SIF-BLAST: ,,[DNA methyltransferase [Mycobacterium phage Lamina13] ],,YP\_009032117,100.0,0.0 SIF-HHPRED: SIF-Syn: Shows synteny with JuliaChild, Lamina13, Pita2, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 154431

CDS complement (42483 - 43301)

 /gene="67"

 /product="gp67"

 /function="Cas4 exonuclease"

 /locus tag="Psullivan\_67"

 /note=Original Glimmer call @bp 43301 has strength 14.41; Genemark calls start at 43301

 /note=SSC: 43301-42483 CP: yes SCS: both ST: SS BLAST-Start: [Cas4 exonuclease [Mycobacterium phage Tote] ],,NCBI, q1:s1 100.0% 0.0 GAP: 166 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.944, -4.820269098574683, no F: Cas4 exonuclease SIF-BLAST: ,,[Cas4 exonuclease [Mycobacterium phage Tote] ],,WAB08933,100.0,0.0 SIF-HHPRED: Cas4\_I-A; CRISPR/Cas system-associated protein Cas4. CRISPR (Clustered Regularly Interspaced Short Palindromic Repeats) and associated Cas proteins comprise a system for heritable host defense by prokaryotic cells against phage and other foreign DNA.,,,cd09659,93.75,99.9 SIF-Syn: Shows synteny with JuliaChild, Tote, Pita2, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 152751

CDS complement (43468 - 43785)

 /gene="68"

 /product="gp68"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_68"

 /note=Original Glimmer call @bp 43785 has strength 10.84; Genemark calls start at 43785

 /note=SSC: 43785-43468 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein CM08\_gp76 [Mycobacterium phage Bruns] ],,NCBI, q1:s1 100.0% 1.06551E-67 GAP: 20 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.232, -2.033982896655645, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein CM08\_gp76 [Mycobacterium phage Bruns] ],,YP\_009011409,100.0,1.06551E-67 SIF-HHPRED: SIF-Syn: Shows synteny with Alvin, NEHalo, Museum, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 263

CDS complement (43806 - 44096)

 /gene="69"

 /product="gp69"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_69"

 /note=Original Glimmer call @bp 44096 has strength 5.87; Genemark calls start at 44096

 /note=SSC: 44096-43806 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_PITA2\_74 [Mycobacterium phage Pita2] ],,NCBI, q1:s1 100.0% 7.70302E-66 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.08, -2.417348306996335, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_PITA2\_74 [Mycobacterium phage Pita2] ],,AXH66019,100.0,7.70302E-66 SIF-HHPRED: SIF-Syn: Shows synteny with Duke13, Pita2, JuliaChild, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 85299

CDS complement (44093 - 44488)

 /gene="70"

 /product="gp70"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_70"

 /note=Original Glimmer call @bp 44488 has strength 1.83; Genemark calls start at 44488

 /note=SSC: 44488-44093 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_PITA2\_75 [Mycobacterium phage Pita2] ],,NCBI, q1:s1 100.0% 2.61574E-91 GAP: 18 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.089, -4.513234975742373, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_PITA2\_75 [Mycobacterium phage Pita2] ],,AXH66020,100.0,2.61574E-91 SIF-HHPRED: SIF-Syn: Shows synteny with JuliaChild, Pita2, Tote, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 346

CDS complement (44507 - 45043)

 /gene="71"

 /product="gp71"

 /function="immunity repressor"

 /locus tag="Psullivan\_71"

 /note=Original Glimmer call @bp 45043 has strength 3.63

 /note=SSC: 45043-44507 CP: yes SCS: glimmer ST: SS BLAST-Start: [transcriptional repressor [Mycobacterium phage KBG] ],,NCBI, q1:s1 100.0% 1.40181E-119 GAP: 261 bp gap LO: no RBS: Kibler 6, Karlin Medium, 3.001, -2.523003374675015, yes F: immunity repressor SIF-BLAST: ,,[transcriptional repressor [Mycobacterium phage KBG] ],,YP\_001994531,96.0674,1.40181E-119 SIF-HHPRED: Immunity repressor; Immunity repressor, helix-turn-helix motif, DNA binding protein, GENE REGULATION, GENE REGULATION-DNA complex; HET: MSE; 2.79A {Mycobacterium phage TipsytheTRex},,,7TZ1\_A,84.2697,99.8 SIF-Syn: Shows synteny with Bigfoot, KBG, Burton, etc.

 /note=Start site was chosen due to synteny with similar phages.

 /note=

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 152754

CDS complement (45305 - 45604)

 /gene="72"

 /product="gp72"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_72"

 /note=Original Glimmer call @bp 45604 has strength 3.67; Genemark calls start at 45604

 /note=SSC: 45604-45305 CP: yes SCS: both ST: SS BLAST-Start: [site-specific recombination directionality factor RDF [Mycobacterium phage Kugel] ],,NCBI, q1:s1 100.0% 1.33408E-65 GAP: -8 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.235, -4.142550495753648, no F: Hypothetical Protein SIF-BLAST: ,,[site-specific recombination directionality factor RDF [Mycobacterium phage Kugel] ],,YP\_009013533,100.0,1.33408E-65 SIF-HHPRED: SIF-Syn: Shows synteny with Anglerfish, Eyeball, JuliaChild, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 154376

CDS complement (45597 - 45776)

 /gene="73"

 /product="gp73"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_73"

 /note=Original Glimmer call @bp 45749 has strength 13.1; Genemark calls start at 45776

 /note=SSC: 45776-45597 CP: yes SCS: both-gm ST: SS BLAST-Start: [hypothetical protein SEA\_CORVO\_79 [Mycobacterium phage Corvo] ],,NCBI, q1:s1 100.0% 1.03432E-31 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.993, -5.402512189985548, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_CORVO\_79 [Mycobacterium phage Corvo] ],,AVJ49544,98.3051,1.03432E-31 SIF-HHPRED: SIF-Syn: Shows synteny with Aeneas, AFIS, Burton, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 154673

CDS complement (45773 - 46042)

 /gene="74"

 /product="gp74"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_74"

 /note=Original Glimmer call @bp 45940 has strength 5.31; Genemark calls start at 46042

 /note=SSC: 46042-45773 CP: yes SCS: both-gm ST: SS BLAST-Start: [hypothetical protein AVT14\_gp75 [Mycobacterium phage Abrogate] ],,NCBI, q1:s1 100.0% 3.57356E-59 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.573, -5.605045683926418, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein AVT14\_gp75 [Mycobacterium phage Abrogate] ],,YP\_009209464,100.0,3.57356E-59 SIF-HHPRED: SIF-Syn: Shows synteny with Abrogate, Crispicous1, Forsytheast, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 86652

CDS complement (46039 - 46221)

 /gene="75"

 /product="gp75"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_75"

 /note=Genemark calls start at 46221

 /note=SSC: 46221-46039 CP: yes SCS: genemark ST: SS BLAST-Start: [hypothetical protein VIOLET\_73 [Mycobacterium phage Violet] ],,NCBI, q1:s1 100.0% 1.64344E-33 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.603, -3.364992052816827, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein VIOLET\_73 [Mycobacterium phage Violet] ],,YP\_009012761,100.0,1.64344E-33 SIF-HHPRED: SIF-Syn: Shows synteny with Anglerfish, Bigfoot, Burton, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 2049

CDS complement (46218 - 46418)

 /gene="76"

 /product="gp76"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_76"

 /note=Original Glimmer call @bp 46418 has strength 18.99; Genemark calls start at 46418

 /note=SSC: 46418-46218 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_U2\_73 [Mycobacterium phage U2] ],,NCBI, q1:s1 100.0% 1.29863E-41 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.106, -4.416294366073912, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein PBI\_U2\_73 [Mycobacterium phage U2] ],,YP\_001491643,100.0,1.29863E-41 SIF-HHPRED: SIF-Syn: Shows synteny with Arlo, Altman, Anglerfish, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 151730

CDS complement (46415 - 46603)

 /gene="77"

 /product="gp77"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_77"

 /note=Original Glimmer call @bp 46603 has strength 11.91; Genemark calls start at 46603

 /note=SSC: 46603-46415 CP: yes SCS: both ST: SS BLAST-Start: [gp74 [Mycobacterium phage Bxb1] ],,NCBI, q1:s1 100.0% 1.14513E-34 GAP: -1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.234, -4.1462986041499, yes F: Hypothetical Protein SIF-BLAST: ,,[gp74 [Mycobacterium phage Bxb1] ],,NP\_075341,100.0,1.14513E-34 SIF-HHPRED: SIF-Syn: Shows synteny with Abbyshoes, AFIS, Alsfro, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 84882

CDS complement (46603 - 46770)

 /gene="78"

 /product="gp78"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_78"

 /note=Original Glimmer call @bp 46770 has strength 6.44; Genemark calls start at 46770

 /note=SSC: 46770-46603 CP: yes SCS: both ST: SS BLAST-Start: [site-specific recombination directionality factor RDF [Mycobacterium phage PattyP] ],,NCBI, q1:s1 100.0% 8.85266E-30 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.849, -2.827683592113848, yes F: Hypothetical Protein SIF-BLAST: ,,[site-specific recombination directionality factor RDF [Mycobacterium phage PattyP] ],,YP\_008050846,100.0,8.85266E-30 SIF-HHPRED: SIF-Syn: Shows synteny with BaconJack, Bob3, BigMau, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 84692

CDS complement (46767 - 46919)

 /gene="79"

 /product="gp79"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_79"

 /note=Original Glimmer call @bp 46895 has strength 8.19; Genemark calls start at 46895

 /note=SSC: 46919-46767 CP: yes SCS: both-cs ST: NI BLAST-Start: [hypothetical protein PBI\_PATTYP\_82 [Mycobacterium phage PattyP] ],,NCBI, q1:s1 100.0% 1.19816E-25 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 0.952, -6.777087871505611, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein PBI\_PATTYP\_82 [Mycobacterium phage PattyP] ],,YP\_008050847,100.0,1.19816E-25 SIF-HHPRED: SIF-Syn: Shows synteny with Burton, HermioneGrange, MPlant719, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 84968

CDS complement (46916 - 47065)

 /gene="80"

 /product="gp80"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_80"

 /note=Original Glimmer call @bp 47065 has strength 6.26

 /note=SSC: 47065-46916 CP: yes SCS: glimmer ST: SS BLAST-Start: [hypothetical protein SOLON\_78 [Mycobacterium phage Solon] ],,NCBI, q1:s1 100.0% 9.42656E-25 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.728, -5.485804372200412, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SOLON\_78 [Mycobacterium phage Solon] ],,YP\_002224019,100.0,9.42656E-25 SIF-HHPRED: SIF-Syn: Shows synteny with A6, Abrogate, Ajay, etc.

 /note=Start site selected due to synteny with similar phages.

 /note=

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 84687

CDS complement (47062 - 47379)

 /gene="81"

 /product="gp81"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_81"

 /note=Original Glimmer call @bp 47379 has strength 9.34; Genemark calls start at 47379

 /note=SSC: 47379-47062 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein CM08\_gp89 [Mycobacterium phage Bruns] ],,NCBI, q1:s1 100.0% 5.52328E-71 GAP: 386 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.353, -3.8137921535956054, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein CM08\_gp89 [Mycobacterium phage Bruns] ],,YP\_009011422,100.0,5.52328E-71 SIF-HHPRED: SIF-Syn: Shows synteny with BaconJack, BigMau, Bruns, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 85432

CDS complement (47766 - 48122)

 /gene="82"

 /product="gp82"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_82"

 /note=Original Glimmer call @bp 48122 has strength 7.58; Genemark calls start at 48122

 /note=SSC: 48122-47766 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_PITA2\_88 [Mycobacterium phage Pita2]],,NCBI, q1:s1 100.0% 6.27938E-82 GAP: 100 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.278, -4.033958934919761, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_PITA2\_88 [Mycobacterium phage Pita2]],,AXH66031,100.0,6.27938E-82 SIF-HHPRED: SIF-Syn: Shows synteny with Pita2

 /note=Start site chosen due to synteny with Pita2.

 /note=

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 14847

CDS complement (48223 - 48462)

 /gene="83"

 /product="gp83"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_83"

 /note=Original Glimmer call @bp 48462 has strength 4.53; Genemark calls start at 48462

 /note=SSC: 48462-48223 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_PITA2\_89 [Mycobacterium phage Pita2]],,NCBI, q1:s1 100.0% 1.34216E-51 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 3.001, -2.583959800616441, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_PITA2\_89 [Mycobacterium phage Pita2]],,AXH66032,100.0,1.34216E-51 SIF-HHPRED: SIF-Syn: Shows synteny with JuliaChild, Pita2, Tote, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 4336

CDS complement (48459 - 48995)

 /gene="84"

 /product="gp84"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_84"

 /note=Original Glimmer call @bp 48995 has strength 7.98; Genemark calls start at 48995

 /note=SSC: 48995-48459 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein KBG\_86 [Mycobacterium phage KBG] ],,NCBI, q1:s1 100.0% 8.29419E-125 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.372, -3.8540125308361968, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein KBG\_86 [Mycobacterium phage KBG] ],,YP\_001994544,100.0,8.29419E-125 SIF-HHPRED: SIF-Syn: Shows synteny with Doom, Molly, KBG, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 87498

CDS complement (48992 - 49195)

 /gene="85"

 /product="gp85"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_85"

 /note=Original Glimmer call @bp 49195 has strength 14.94; Genemark calls start at 49195

 /note=SSC: 49195-48992 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_PITA2\_91 [Mycobacterium phage Pita2] ],,NCBI, q1:s1 100.0% 3.80126E-40 GAP: 73 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.755, -3.0248543014571307, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_PITA2\_91 [Mycobacterium phage Pita2] ],,AXH66034,100.0,3.80126E-40 SIF-HHPRED: SIF-Syn: Shows synteny with Gyzlar JuliaChild, Pita2, etc.

 /note=Start site chosen due to synteny.

 /note=

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 154494

CDS complement (49269 - 49457)

 /gene="86"

 /product="gp86"

 /function="Hypothetical Protein"

 /locus tag="Psullivan\_86"

 /note=Original Glimmer call @bp 49457 has strength 11.39; Genemark calls start at 49457

 /note=SSC: 49457-49269 CP: no SCS: both ST: NI BLAST-Start: [hypothetical protein SEA\_PITA2\_92 [Mycobacterium phage Pita2] ],,NCBI, q1:s1 100.0% 3.16497E-36 GAP: 86 bp gap LO: no RBS: Kibler 6, Karlin Medium, 3.232, -2.0162541296952132, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_PITA2\_92 [Mycobacterium phage Pita2] ],,AXH66035,100.0,3.16497E-36 SIF-HHPRED: SIF-Syn: Shows synteny with DLane, Petruchio, KBG, etc.

 /note=Primary Annotator: John Motter

 /note=Secondary Annotator: Hsin-Ho Wei

 /note=Starterator: 4192

BASE COUNT 9163 a 16224 c 15483 g 9120 t

ORIGIN