**JARCOB NOTES FROM PECAAN**

CDS 109 - 564

 /gene="1"

 /product="gp1"

 /function="terminase, small subunit"

 /locus tag="jarcob\_1"

 /note=Original Glimmer call @bp 208 has strength 7.63; Genemark calls start at 109

 /note=SSC: 109-564 CP: yes SCS: both-gm ST: SS BLAST-Start: [gp1 [Mycobacterium phage Pacc40] ],,NCBI, q1:s1 100.0% 1.9279E-104 GAP: 0 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.822, -3.7960205838585104, yes F: terminase, small subunit SIF-BLAST: ,,[gp1 [Mycobacterium phage Pacc40] ],,YP\_002241585,100.0,1.9279E-104 SIF-HHPRED: Terminase\_4 ; Phage terminase, small subunit,,,PF05119.15,45.0331,97.5 SIF-Syn: Saal bp 109-564;terminase small subunit

Byoungenkin bp 193-564; terminase small subunit

Inventum bp 108-563;terminase small subunut.

 /note=moved start to 109 (GM and SS, LORF, improves RBS). Function terminase small subunit supported by all SIF sources.

CDS 572 - 2209

 /gene="2"

 /product="gp2"

 /function="terminase, large subunit"

 /locus tag="jarcob\_2"

 /note=Original Glimmer call @bp 572 has strength 6.16; Genemark calls start at 572

 /note=SSC: 572-2209 CP: yes SCS: both ST: SS BLAST-Start: [terminase large subunit [Mycobacterium phage ShiLan] ],,NCBI, q1:s1 100.0% 0.0 GAP: 7 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.034, -6.668278635197846, no F: terminase, large subunit SIF-BLAST: ,,[terminase large subunit [Mycobacterium phage ShiLan] ],,YP\_009608077,100.0,0.0 SIF-HHPRED: Terminase large subunit; genome packaging, bacteriophage, ATPase, nuclease, VIRAL PROTEIN; HET: BR; 2.2A {Enterobacteria phage HK97},,,6Z6D\_A,95.0459,100.0 SIF-Syn: ShiLan\_2, bp572-2209, terminase large subunit

Burwell21, bp 271-2208, terminase large subunit

Lizziana, bp 573-2210, terminase large subunit

Nivrat, bp 572-2209, terminase large subunit

Swagpigglett, bp 573-2210, terminase

terinase, large subunit; count: 87

frequency: 94%

 /note=Start 572 (GM, Glimmer, ST). Function large subunit terminase supported by all SIF sources.

CDS 2240 - 3610

 /gene="3"

 /product="gp3"

 /function="portal protein"

 /locus tag="jarcob\_3"

 /note=Original Glimmer call @bp 2276 has strength 11.04; Genemark calls start at 2276

 /note=SSC: 2240-3610 CP: yes SCS: both-cs ST: NI BLAST-Start: [gp3 [Mycobacterium phage Pacc40] ],,NCBI, q1:s1 100.0% 0.0 GAP: 30 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.739, -3.2804507689989406, no F: portal protein SIF-BLAST: ,,[gp3 [Mycobacterium phage Pacc40] ],,YP\_002241587,100.0,0.0 SIF-HHPRED: PORTAL PROTEIN; BACTERIOPHAGE SPP1, DNA TRANSLOCATION, MOLECULAR MOTOR, VIRAL PORTAL PROTEIN, VIRAL PROTEIN; HET: CA, HG; 3.4A {BACTERIOPHAGE SPP1},,,2JES\_Q,94.0789,100.0 SIF-Syn: BodEinwohner17 portal protein

Blexus portal protein

Burwell21 portal protein

 /note=Move start to 2240 (better RBS, fits with ST cluster better, LORF, better gap). CP is low for the first 200bp but this start fits better with phagesDB and SS clusters. Function portal protein supported by all SIF sources.

CDS 3597 - 4352

 /gene="4"

 /product="gp4"

 /function="capsid maturation protease"

 /locus tag="jarcob\_4"

 /note=Original Glimmer call @bp 3597 has strength 8.8; Genemark calls start at 3597

 /note=SSC: 3597-4352 CP: yes SCS: both ST: SS BLAST-Start: [capsid maturation protease [Mycobacterium virus GUmbie] ],,NCBI, q1:s1 100.0% 0.0 GAP: -14 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.901, -4.109171212198345, yes F: capsid maturation protease SIF-BLAST: ,,[capsid maturation protease [Mycobacterium virus GUmbie] ],,YP\_009018880,100.0,0.0 SIF-HHPRED: Phage\_Mu\_F ; Phage Mu protein F like protein,,,PF04233.17,27.8884,98.9 SIF-Syn: Blexus capsid maturation protease

Burwell21 capsid maturation protease

ByChance NKF

 /note=Start 3597 agreed on by GM, glimmer, ST. CP low for first 200bp but this reduces gap and is supported by phagesDB/ST. Function capsid maturation protease supported by all SIF sources.

CDS 4436 - 5029

 /gene="5"

 /product="gp5"

 /function="scaffolding protein"

 /locus tag="jarcob\_5"

 /note=Original Glimmer call @bp 4436 has strength 14.17; Genemark calls start at 4436

 /note=SSC: 4436-5029 CP: yes SCS: both ST: SS BLAST-Start: [scaffolding protein [Mycobacterium phage Saal] ],,NCBI, q1:s1 100.0% 1.77359E-137 GAP: 83 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.214, -2.8084998623841946, yes F: scaffolding protein SIF-BLAST: ,,[scaffolding protein [Mycobacterium phage Saal] ],,YP\_009007472,100.0,1.77359E-137 SIF-HHPRED: DUF4355 ; Domain of unknown function (DUF4355),,,PF14265.9,51.269,97.7 SIF-Syn: Blexus scaffolding protein

Brocalys scaffolding protein

Burwell21 scaffolding protein

 /note=Start 4436 supported by ST, glimmer, GM. CP low first 150bp, but this reduces gap and fits with ST/phagesDB. Function scaffolding protein supported by all SIF sources.

CDS 5048 - 5869

 /gene="6"

 /product="gp6"

 /function="major capsid protein"

 /locus tag="jarcob\_6"

 /note=Original Glimmer call @bp 5048 has strength 14.28; Genemark calls start at 5048

 /note=SSC: 5048-5869 CP: yes SCS: both ST: SS BLAST-Start: [major capsid protein [Mycobacterium phage Saal] ],,NCBI, q1:s1 100.0% 0.0 GAP: 18 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.561, -3.5707972674952195, yes F: major capsid protein SIF-BLAST: ,,[major capsid protein [Mycobacterium phage Saal] ],,YP\_009007473,100.0,0.0 SIF-HHPRED: MAJOR CAPSID PROTEIN; VIRUS, MARINE VIRUS, OUTER CAPSID PROTEIN, MATURATION; 4.7A {SYNECHOCOCCUS PHAGE SYN5},,,4BML\_C,97.0696,99.9 SIF-Syn: ShiLan: Major capsid protein

Burwell21: Major capsid protein

Lizziana: Major capsid protein

Nivrat: Major capsid protein

SwagPigglett: Major capsid protein

 /note=Start 5048 supported by GM, glimmer, ST. Function major capsid protein supported by all SIF sources.

CDS 5878 - 6447

 /gene="7"

 /product="gp7"

 /function="head-to-tail adaptor"

 /locus tag="jarcob\_7"

 /note=Original Glimmer call @bp 5878 has strength 7.01; Genemark calls start at 5878

 /note=SSC: 5878-6447 CP: yes SCS: both ST: SS BLAST-Start: [gp7 [Mycobacterium phage Che8] ],,NCBI, q1:s1 100.0% 4.05366E-130 GAP: 8 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.308, -6.452925797815746, no F: head-to-tail adaptor SIF-BLAST: ,,[gp7 [Mycobacterium phage Che8] ],,NP\_817345,100.0,4.05366E-130 SIF-HHPRED: Adaptor protein Rcc01688; "neck", "portal", "capsid", "tail tube", VIRUS; 3.58A {Rhodobacter capsulatus},,,6TE9\_D,95.7672,99.9 SIF-Syn: ShiLan: Head-to-tail adaptor

Burwell21: Head-to-tail adaptor

Lizziana: Head-to-tail adaptor

Nivrat: Head-to-tail adaptor

SwagPigglett: Head-to-tail adaptor

 /note=Start 5878 supported by GM, ST, glimmer. Function head-to-tail adaptor supported by all SIF sources.

CDS 6444 - 6773

 /gene="8"

 /product="gp8"

 /function="head-to-tail stopper"

 /locus tag="jarcob\_8"

 /note=Original Glimmer call @bp 6444 has strength 8.25; Genemark calls start at 6444

 /note=SSC: 6444-6773 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein FDI15\_gp008 [Mycobacterium phage ShiLan] ],,NCBI, q1:s1 100.0% 8.82659E-72 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.787, -5.461711027312092, no F: head-to-tail stopper SIF-BLAST: ,,[hypothetical protein FDI15\_gp008 [Mycobacterium phage ShiLan] ],,YP\_009608083,100.0,8.82659E-72 SIF-HHPRED: DUF3599 ; Domain of unknown function (DUF3599),,,PF12206.11,96.3303,99.6 SIF-Syn: ShiLan: Heat-to-tail stopper

Burwell21: Heat-to-tail stopper

Lizziana: Heat-to-tail stopper

Nivrat: Heat-to-tail stopper

SwagPigglett: Heat-to-tail stopper

 /note=Start 6444 supported by GM, glimmer, ST. Function head-to-tail stopper supported by synteny.

CDS 6780 - 7106

 /gene="9"

 /product="gp9"

 /function="Hypothetical Protein"

 /locus tag="jarcob\_9"

 /note=Original Glimmer call @bp 6810 has strength 9.93; Genemark calls start at 6810

 /note=SSC: 6780-7106 CP: no SCS: both-cs ST: NI BLAST-Start: [HK97 gp10 family protein [Mycobacterium phage Velveteen] ],,NCBI, q1:s1 100.0% 9.58447E-74 GAP: 6 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.638, -3.6993702887586135, no F: Hypothetical Protein SIF-BLAST: ,,[HK97 gp10 family protein [Mycobacterium phage Velveteen] ],,YP\_008409547,100.0,9.58447E-74 SIF-HHPRED: Minor\_capsid\_2 ; Minor capsid protein,,,PF11114.11,81.4815,99.3 SIF-Syn: ShiLan: NKF

Burwell21:NKF

Lizziana: NKF

Nivrat: NKF

SwagPigglett: NKF

 /note=Move start to 6780 (supported by ST, phagesDB cluster F synteny, improves spacer and gap). Function unknown.

CDS 7096 - 7500

 /gene="10"

 /product="gp10"

 /function="tail terminator"

 /locus tag="jarcob\_10"

 /note=Original Glimmer call @bp 7096 has strength 6.99; Genemark calls start at 7096

 /note=SSC: 7096-7500 CP: yes SCS: both ST: SS BLAST-Start: [tail terminator [Mycobacterium phage Boomer] ],,NCBI, q1:s1 100.0% 1.39994E-89 GAP: -11 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.241, -6.240767779459404, no F: tail terminator SIF-BLAST: ,,[tail terminator [Mycobacterium phage Boomer] ],,YP\_002014227,100.0,1.39994E-89 SIF-HHPRED: TAIL-TO-HEAD JOINING PROTEIN GP17; VIRAL PROTEIN, VIRAL INFECTION, TAILED BACTERIOPHAGE, SIPHOVIRIDAE, SPP1, VIRAL ASSEMBLY, HEAD-TO-TAIL INTERFACE, DNA GATEKEEPER, ALLOSTERIC MECHANISM; 7.2A {BACILLUS PHAGE SPP1},,,5A21\_G,94.7761,99.4 SIF-Syn: ShiLan: Tail terminator

Burwell21: Tail terminator

Lizziana: Tail terminator

Nivrat: Tail terminator

SwagPigglett: Tail terminator

 /note=Start 7096 supported by Glimmer, GM, ST, synteny. CP low first 150bp but fits synteny, ST. Function tail terminator supported by all SIF sources.

CDS 7609 - 8418

 /gene="11"

 /product="gp11"

 /function="major tail protein"

 /locus tag="jarcob\_11"

 /note=Original Glimmer call @bp 7609 has strength 15.36; Genemark calls start at 7609

 /note=SSC: 7609-8418 CP: yes SCS: both ST: SS BLAST-Start: [gp12 [Mycobacterium phage Ramsey] ],,NCBI, q1:s1 100.0% 0.0 GAP: 108 bp gap LO: no RBS: Kibler 6, Karlin Medium, 3.156, -2.338663114094478, yes F: major tail protein SIF-BLAST: ,,[gp12 [Mycobacterium phage Ramsey] ],,YP\_002241799,100.0,0.0 SIF-HHPRED: YSD1\_22 major tail protein; Bacteriophage tail, helical assembly, VIRAL PROTEIN; 3.5A {Bacteriophage sp.},,,6XGR\_M,56.1338,96.7 SIF-Syn: ShiLan: bp 7537-8418; Major tail subunit

Burwell21: bp 7608-8417; Major tail protein

Lizziana: bp 7610-8419; Major tail protein

Nivrat: (SS) bp 7609-8418; Major tail protein

SwagPigglett: bp 7610-8419; Major tail protein

 /note=Start 7609 supported by Glimmer, GM, ST. Function major tail protein supported by all SIF sources.

CDS 8537 - 9088

 /gene="12"

 /product="gp12"

 /function="tail assembly chaperone"

 /locus tag="jarcob\_12"

 /note=Original Glimmer call @bp 8537 has strength 9.96; Genemark calls start at 8537

 /note=SSC: 8537-9088 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein M184\_gp72 [Mycobacterium phage WIVsmall] ],,NCBI, q1:s1 100.0% 6.16653E-130 GAP: 118 bp gap LO: no RBS: Kibler 6, Karlin Medium, 3.225, -2.1958114445137396, yes F: tail assembly chaperone SIF-BLAST: ,,[hypothetical protein M184\_gp72 [Mycobacterium phage WIVsmall] ],,YP\_008059973,100.0,6.16653E-130 SIF-HHPRED: GP24\_25 ; Mycobacteriophage tail assembly protein,,,PF17388.5,34.4262,96.1 SIF-Syn: Pham ~ ShiLan: 8444-9088 (645); Tail assembly chaperone

Pham ~ Burwell21: 8536-9087 (552); Tail assembly chaperone

Pham ~ Lizziana: 8538-9089 (552); Tail assembly chaperone

Pham ~ Nivrat: 8537-9088 (552); Tail assembly chaperone

Pham ~ SwagPigglett: 8538-9089 (552); Tail assembly chaperone;

count 85, frequency 96%

 /note=Start 8537 supported by Glimmer, GM, ST. Function tail assembly chaperone supported by all SIF sources.

CDS 9108 - 9473

 /gene="13"

 /product="gp13"

 /function="tail assembly chaperone"

 /locus tag="jarcob\_13"

 /note=Original Glimmer call @bp 9039 has strength 7.68; Genemark calls start at 9108

 /note=SSC: 9108-9473 CP: yes SCS: both-gm ST: NA BLAST-Start: [tail assembly chaperone [Mycobacterium phage BobaPhett] ],,NCBI, q1:s191 100.0% 1.07761E-77 GAP: 19 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.586, -6.178603076373779, no F: tail assembly chaperone SIF-BLAST: ,,[tail assembly chaperone [Mycobacterium phage BobaPhett] ],,YP\_009954800,38.9068,1.07761E-77 SIF-HHPRED: DUF5361 ; Family of unknown function (DUF5361),,,PF17318.5,33.8843,98.1 SIF-Syn:

 /note=Start moved to 9108 to reduce -50 overlap. Supported by GM and maintains good spacer/zscore. Function tail assembly chaperone supported by BLAST and synteny. Did not make gp13 overlap with gp12 since the exact start sites would not align and CP was poor for overlap region.

CDS 9491 - 13018

 /gene="14"

 /product="gp14"

 /function="tape measure protein"

 /locus tag="jarcob\_14"

 /note=Original Glimmer call @bp 9491 has strength 7.77; Genemark calls start at 9491

 /note=SSC: 9491-13018 CP: yes SCS: both ST: SS BLAST-Start: [tapemeasure protein [Mycobacterium phage ShiLan] ],,NCBI, q1:s1 100.0% 0.0 GAP: 17 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.482, -3.8116689268127657, no F: tape measure protein SIF-BLAST: ,,[tapemeasure protein [Mycobacterium phage ShiLan] ],,YP\_009608089,100.0,0.0 SIF-HHPRED: Tape Measure Protein, gp57; phage tail, tail tip, tape measure protein, VIRAL PROTEIN; 3.7A {Staphylococcus virus 80alpha},,,6V8I\_AF,38.2979,93.2 SIF-Syn: ShiLan: (SS) 9491-13018 (3528); Tape measure protein

 Burwell21: 9490-13017 (3528); Tape measure protein

Lizziana: 9492-13019 (3528); Tape measure protein

Nivrat: (SS) 9491-13018 (3528); Tape measure protein

SwagPigglett: 9492-13019 (3528); Tape measure protein; count 90, frequency 100%

 /note=Start 9491 supported by Glimmer, GM, ST. Function tape measure protein supported by all SIF sources.

CDS 13019 - 14728

 /gene="15"

 /product="gp15"

 /function="minor tail protein"

 /locus tag="jarcob\_15"

 /note=Original Glimmer call @bp 13019 has strength 12.45; Genemark calls start at 13019

 /note=SSC: 13019-14728 CP: yes SCS: both ST: SS BLAST-Start: [minor tail subunit [Mycobacterium phage ShiLan] ],,NCBI, q1:s1 100.0% 0.0 GAP: 0 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.965, -4.821320819095688, no F: minor tail protein SIF-BLAST: ,,[minor tail subunit [Mycobacterium phage ShiLan] ],,YP\_009608090,100.0,0.0 SIF-HHPRED: SIF-Syn: ShiLan: (SS) 13019-14728 (1710); Minor tail subunit

Burwell21: 13018-14727 (1710); Minor tail protein

Lizziana: 13020-14729 (1710); Minor tail protein

Nivrat: (SS) 13019-14728 (1710); Minor tail protein

SwagPigglett: 13020-14729 (1710); Minor tail protein;

count 85, frequency 99%

 /note=Start 13019 supported by Glimmer, GM. Function minor tail protein supported by synteny.

CDS 14812 - 16521

 /gene="16"

 /product="gp16"

 /function="minor tail protein"

 /locus tag="jarcob\_16"

 /note=Original Glimmer call @bp 14812 has strength 13.72; Genemark calls start at 14812

 /note=SSC: 14812-16521 CP: yes SCS: both ST: SS BLAST-Start: [minor tail subunit [Mycobacterium phage ShiLan] ],,NCBI, q1:s1 100.0% 0.0 GAP: 83 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.312, -2.606079664606164, yes F: minor tail protein SIF-BLAST: ,,[minor tail subunit [Mycobacterium phage ShiLan] ],,YP\_009608091,100.0,0.0 SIF-HHPRED: Sipho\_Gp37 ; Siphovirus ReqiPepy6 Gp37-like protein,,,PF14594.9,85.413,99.9 SIF-Syn: ShiLan: (SS) 14812-16521 (1710); Minor tail subunit

Burwell21: 14811-16520 (1710); Minor tail protein

Lizziana: 14813-16522 (1710); Minor tail protein

Nivrat: (SS) 14812-16521 (1710); Minor tail protein

SwagPigglett: 14813-16522 (1710); Minor tail protein;

count 87, frequency 99%

 /note=Start 14812 supported by Glimmer, GM, ST. Function minor tail protein supported by synteny

CDS 16578 - 17408

 /gene="17"

 /product="gp17"

 /function="minor tail protein"

 /locus tag="jarcob\_17"

 /note=Original Glimmer call @bp 16578 has strength 10.46; Genemark calls start at 16578

 /note=SSC: 16578-17408 CP: yes SCS: both ST: SS BLAST-Start: [minor tail subunit [Mycobacterium phage ShiLan] ],,NCBI, q1:s6 100.0% 0.0 GAP: 56 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.884, -3.1896562502401133, yes F: minor tail protein SIF-BLAST: ,,[minor tail subunit [Mycobacterium phage ShiLan] ],,YP\_009608092,98.2206,0.0 SIF-HHPRED: SIF-Syn: ShiLan: bp 16563-17408 (846); Minor tail subunit

Burwell21: bp 16577-17407 (831); Minor tail protein

Lizziana: bp 16579-17409 (831); Minor tail protein

Nivrat: bp 16578-17408 (831); Minor tail protein

SwagPigglett: bp 16579-17409 (831); Minor tail protein

 /note=Start 16578 supported by Glimmer, GM, ST. Function minor tail subunit supported by synteny.

CDS 17405 - 19957

 /gene="18"

 /product="gp18"

 /function="minor tail protein"

 /locus tag="jarcob\_18"

 /note=Original Glimmer call @bp 17405 has strength 7.87; Genemark calls start at 17405

 /note=SSC: 17405-19957 CP: yes SCS: both ST: SS BLAST-Start: [minor tail protein [Mycobacterium phage Cabrinians] ],,NCBI, q1:s1 100.0% 0.0 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.426, -4.694587342996602, no F: minor tail protein SIF-BLAST: ,,[minor tail protein [Mycobacterium phage Cabrinians] ],,YP\_009189740,100.0,0.0 SIF-HHPRED: SIF-Syn: ShiLan: (SS) 17405-19957 (2553); Minor tail subunit

Burwell21: 17404-19956 (2553); Minor tail protein

Lizziana: 17406-19931 (2526); Minor tail protein

Nivrat: 17405-19930 (2526); Minor tail protein

SwagPigglett: 17406-19943 (2538); Minor tail protein

 /note=Start 17405 supported by Glimmer, GM, ST. Function minor tail protein supported by synteny.

CDS 19954 - 21843

 /gene="19"

 /product="gp19"

 /function="minor tail protein"

 /locus tag="jarcob\_19"

 /note=Original Glimmer call @bp 19954 has strength 7.69; Genemark calls start at 19954

 /note=SSC: 19954-21843 CP: yes SCS: both ST: SS BLAST-Start: [D-Ala-D-Ala carboxypeptidase [Mycobacterium phage ShiLan] ],,NCBI, q1:s1 100.0% 0.0 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.03, -5.6562426662814325, no F: minor tail protein SIF-BLAST: ,,[D-Ala-D-Ala carboxypeptidase [Mycobacterium phage ShiLan] ],,YP\_009608094,100.0,0.0 SIF-HHPRED: SIF-Syn: ShiLan: (SS) 19954-21843 (1890);D-Ala-D-Ala carboxypeptidase

Pham ~ Burwell21: 19953-21842 (1890);Minor tail protein

Pham ~ Lizziana: 19928-21817 (1890);Minor tail protein

Pham ~ Nivrat: 19927-21816 (1890);Minor tail protein

Pham ~ SwagPigglett: 19940-21826 (1887); Minor tail protein

count 65, frequency 76%

 /note=Start 19954 supported by Glimmer, GM, ST. Function minor tail protein supported by synteny.

CDS 21843 - 23045

 /gene="20"

 /product="gp20"

 /function="minor tail protein"

 /locus tag="jarcob\_20"

 /note=Original Glimmer call @bp 21843 has strength 4.2; Genemark calls start at 21843

 /note=SSC: 21843-23045 CP: yes SCS: both ST: SS BLAST-Start: [minor tail protein [Mycobacterium phage Cabrinians] ],,NCBI, q1:s1 100.0% 0.0 GAP: -1 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.427, -5.916673162539987, no F: minor tail protein SIF-BLAST: ,,[minor tail protein [Mycobacterium phage Cabrinians] ],,YP\_009189742,100.0,0.0 SIF-HHPRED: SIF-Syn: ShiLan: (SS) 21843-23045 (1203); NFK

Pham ~ Burwell21: 21842-23044 (1203);Minor tail protein

Pham ~ Lizziana: 21817-23019 (1203);Minor tail protein

Pham ~ Nivrat: 21816-23018 (1203); Minor tail protein

Pham ~ SwagPigglett: 21823-22986 (1164); Minor tail protein

count 61; frequency 95%

 /note=Start 2183 supported by Glimmer, GM, ST. Function minor tail protein supported by synteny

CDS 23069 - 23410

 /gene="21"

 /product="gp21"

 /function="minor tail protein"

 /locus tag="jarcob\_21"

 /note=Original Glimmer call @bp 23069 has strength 6.3; Genemark calls start at 23069

 /note=SSC: 23069-23410 CP: yes SCS: both ST: SS BLAST-Start: [minor tail protein [Mycobacterium phage Cabrinians] ],,NCBI, q1:s1 100.0% 8.38782E-70 GAP: 23 bp gap LO: no RBS: Kibler 6, Karlin Medium, 3.214, -2.297359520375101, yes F: minor tail protein SIF-BLAST: ,,[minor tail protein [Mycobacterium phage Cabrinians] ],,YP\_009189743,100.0,8.38782E-70 SIF-HHPRED: SIF-Syn: ShiLan: bp 23069- 23410, (342); NKF

Burwell21: bp 23069- 23409, (341); minor tail protein

Lizziana: bp 23043- 23384, (342); minor tail protein

Nivrat: bp 23042- 23383, (342); minor tail protein

SwagPigglett: bp 23000- 23341, (342); NKF

count 26, frequency 93%

 /note=Start 23069 supported by Glimmer, GM, ST. Function minor tail protein supported by synteny.

CDS 23553 - 23807

 /gene="22"

 /product="gp22"

 /function="hypothetical protein"

 /locus tag="jarcob\_22"

 /note=Original Glimmer call @bp 23553 has strength 11.08; Genemark calls start at 23553

 /note=SSC: 23553-23807 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_CABRINIANS\_22 [Mycobacterium phage Cabrinians] ],,NCBI, q1:s1 100.0% 6.92718E-55 GAP: 142 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.503, -3.6907860541164537, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein SEA\_CABRINIANS\_22 [Mycobacterium phage Cabrinians] ],,YP\_009189744,100.0,6.92718E-55 SIF-HHPRED: Uncharacterized protein; ribosome, protein-protein interaction, Structural Genomics, Structural Genomics Consortium, SGC, UNKNOWN FUNCTION; NMR {Rhodopseudomonas palustris (strain ATCC BAA-98 / CGA009)},,,5JN6\_A,76.1905,94.2 SIF-Syn: BobaPhett, Burwell21

 /note=Start 23553 supported by glimmer, GM, and ST. Large gap is present in similar genomes. Function NKF.

CDS 23820 - 24458

 /gene="23"

 /product="gp23"

 /function="minor tail protein"

 /locus tag="jarcob\_23"

 /note=Original Glimmer call @bp 23820 has strength 8.8; Genemark calls start at 23820

 /note=SSC: 23820-24458 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein I5H16\_gp023 [Mycobacterium phage BobaPhett] ],,NCBI, q1:s1 100.0% 2.52911E-147 GAP: 12 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.658, -3.3060637489568596, no F: minor tail protein SIF-BLAST: ,,[hypothetical protein I5H16\_gp023 [Mycobacterium phage BobaPhett] ],,YP\_009954811,100.0,2.52911E-147 SIF-HHPRED: SIF-Syn: ShiLan: bp 23820- 24458, SS (639); NKF

Burwell21: bp 23819 - 24457 (639); minor tail protein

Lizziana: bp 23794- 24432, (639); minor tail protein

Nivrat: bp 23793- 24431(639); minor tail protein

SwagPigglett: bp 23632- 24720(639) NKF

count 34; frequency 92%

 /note=Start 23820 supported by Glimmer, GM, ST. Function minor tail protein supported by synteny.

CDS 24455 - 25279

 /gene="24"

 /product="gp24"

 /function="Hypothetical Protein"

 /locus tag="jarcob\_24"

 /note=Original Glimmer call @bp 24455 has strength 1.48; Genemark calls start at 24455

 /note=SSC: 24455-25279 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein I5H16\_gp024 [Mycobacterium phage BobaPhett] ],,NCBI, q1:s1 100.0% 1.75236E-178 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.302, -4.123435721190396, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein I5H16\_gp024 [Mycobacterium phage BobaPhett] ],,YP\_009954812,100.0,1.75236E-178 SIF-HHPRED: SIF-Syn: ShiLan: SS (825); NKF

Pham ~ Burwell21: SS (825); NFK

Pham ~ Lizziana: 24429- 25253 (825); minor tail protein

Pham ~ Nivrat: 24428- 25252 (825); minor tail protein

Pham ~ SwagPigglett: 24267- 25091 (825); NKF

 /note=Start 24455 supported by Glimmer, GM, ST. Function hypothetical protein supported by top two BLAST hits, 3/5 match for synteny. Other annotations suggest minor tail protein.

CDS complement (25285 - 25482)

 /gene="25"

 /product="gp25"

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

 /locus tag="jarcob\_25"

 /note=Original Glimmer call @bp 25482 has strength 9.95; Genemark calls start at 25482

 /note=SSC: 25482-25285 CP: yes SCS: both ST: SS BLAST-Start: [gp25 [Mycobacterium phage Pacc40] ],,NCBI, q1:s1 100.0% 7.91999E-39 GAP: 148 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.476, -6.661315563983987, no F: helix-turn-helix DNA binding domain SIF-BLAST: ,,[gp25 [Mycobacterium phage Pacc40] ],,YP\_002241609,100.0,7.91999E-39 SIF-HHPRED: SIF-Syn: ShiLan: bp 25482- 25285, SS (198); NKF

Burwell21: SS (198); helix- turn- helix DNA binding domain protein

Lizziana: bp 25456- 25259 (198); helix- turn- helix DNA binding domain protein

Nivrat: bp 25545- 25258 (288); NKF

SwagPigglett: bp 25294- 25097 (198); helix- turn- helix DNA binding domain protein

 /note=Start 25482 supported by Glimmer, GM, ST. Function helix- turn helix DNA binding protein supported 3/5 match for synteny. BLAST results suggest hypothetical protein for gene 25.

CDS 25631 - 25927

 /gene="26"

 /product="gp26"

 /function="Hypothetical Protein"

 /locus tag="jarcob\_26"

 /note=Original Glimmer call @bp 25631 has strength 10.74; Genemark calls start at 25631

 /note=SSC: 25631-25927 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_SAAL\_26 [Mycobacterium phage Saal] ],,NCBI, q1:s1 100.0% 1.25924E-64 GAP: 148 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.235, -2.253377680616507, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein PBI\_SAAL\_26 [Mycobacterium phage Saal] ],,YP\_009007493,100.0,1.25924E-64 SIF-HHPRED: SIF-Syn: ShiLan: SS (297); NKF

Burwell21: SS (297); NKF

Lizziana: 25605- 25889 (285); NKF

Nivrat: 25604- 25888 (285);NKF

Swagg- Pigglett: 25443- 25727 (285); NKF

 /note=Start 25631 supported by Glimmer, GM, ST. Function hypothetical protein supported by synteny.

CDS 25934 - 26083

 /gene="27"

 /product="gp27"

 /function="Hypothetical Protein"

 /locus tag="jarcob\_27"

 /note=Original Glimmer call @bp 25934 has strength 9.67; Genemark calls start at 25934

 /note=SSC: 25934-26083 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_SAAL\_27 [Mycobacterium phage Saal] ],,NCBI, q1:s1 100.0% 8.94272E-27 GAP: 6 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.134, -4.4536196888290105, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein PBI\_SAAL\_27 [Mycobacterium phage Saal] ],,YP\_009007494,100.0,8.94272E-27 SIF-HHPRED: SIF-Syn: Burwell21: NKF

Lizziana: NKF

Nivrat: NKF

SwagPigglett: NKF

 /note=Start 25934 supported by Glimmer, GM, ST. Function hypothetical protein supported by all SIF sources.

CDS 26080 - 26214

 /gene="28"

 /product="gp28"

 /function="Hypothetical Protein"

 /locus tag="jarcob\_28"

 /note=Original Glimmer call @bp 26080 has strength 13.6; Genemark calls start at 26080

 /note=SSC: 26080-26214 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_SAAL\_28 [Mycobacterium phage Saal] ],,NCBI, q1:s1 100.0% 2.87006E-22 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.246, -2.0895162839948163, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein PBI\_SAAL\_28 [Mycobacterium phage Saal] ],,YP\_009007495,100.0,2.87006E-22 SIF-HHPRED: SIF-Syn: ShiLan: NKF

Burwell21: NKF

Lizziana: NKF

Nivrat: NKF

SwagPigglett: NKF

 /note=Start 26080 supported by Glimmer, GM, ST. Function hypothetical protein supported by synteny.

CDS 26281 - 26556

 /gene="29"

 /product="gp29"

 /function="Hypothetical Protein"

 /locus tag="jarcob\_29"

 /note=Original Glimmer call @bp 26281 has strength 15.76; Genemark calls start at 26281

 /note=SSC: 26281-26556 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein FDI15\_gp029 [Mycobacterium phage ShiLan] ],,NCBI, q1:s1 100.0% 3.81164E-53 GAP: 66 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.824, -3.0248543014571307, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein FDI15\_gp029 [Mycobacterium phage ShiLan] ],,YP\_009608104,100.0,3.81164E-53 SIF-HHPRED: SIF-Syn: ShiLan: NKF

Burwell21: NKF

Lizziana: NKF

Nivrat: NKF

SwagPigglett: NKF

 /note=Start 26281 supported by Glimmer, GM, ST. Function hypothetical protein supported by synteny.

CDS 26553 - 27749

 /gene="30"

 /product="gp30"

 /function="lysin A"

 /locus tag="jarcob\_30"

 /note=Original Glimmer call @bp 26553 has strength 11.27; Genemark calls start at 26553

 /note=SSC: 26553-27749 CP: yes SCS: both ST: NI BLAST-Start: [lysin A [Mycobacterium phage ShiLan] ],,NCBI, q1:s1 100.0% 0.0 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.212, -4.229395370396053, no F: lysin A SIF-BLAST: ,,[lysin A [Mycobacterium phage ShiLan] ],,YP\_009608105,100.0,0.0 SIF-HHPRED: N-acetylmuramoyl-L-alanine amidase amiD; ZINC AMIDASE, PGRP, Peptidoglycan Recognizing Protein, AmpD, N-ACETYLMURAMYL-L-ALANINE AMIDASE, Cell wall biogenesis/degradation, Hydrolase, Lipoprotein, Membrane, Metal-binding; HET: GOL, AH0; 1.75A {Escherichia coli},,,3D2Y\_A,58.794,99.7 SIF-Syn: ShiLan: bp 26544- 27740 (1197); Lysin A

Burwell21: bp 26501- 27697 (1197); Lysin A

Lizziana: bp 26476- 27672 (1197); Lysin A

Nivrat: bp 26475- 27671 (1197); Lysin A

SwagPigglett: bp 26314- 27510 (1197); Lysin A

 /note=Start 26553 supported by Glimmer, GM. Function Lysin A supported by all SIF sources.

CDS 27749 - 28750

 /gene="31"

 /product="gp31"

 /function="lysin B"

 /locus tag="jarcob\_31"

 /note=Original Glimmer call @bp 27749 has strength 12.02; Genemark calls start at 27749

 /note=SSC: 27749-28750 CP: yes SCS: both ST: SS BLAST-Start: [lysin B [Mycobacterium phage ShiLan] ],,NCBI, q1:s1 100.0% 0.0 GAP: -1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.171, -4.455662434380964, no F: lysin B SIF-BLAST: ,,[lysin B [Mycobacterium phage ShiLan] ],,YP\_009608106,100.0,0.0 SIF-HHPRED: SIF-Syn: ShiLan: bp 27740- 28741 (1002);Lysin B

Pham ~ Burwell21: bp 27697- 28698 (1002);Lysin B

Pham ~ Lizziana: bp 27672- 28673 (1002);Lysin B

Pham ~ Nivrat: bp 27671- 28672 (1002);Lysin B

Pham ~ SwagPigglett: bp 27510- 28511 (1002);Lysin B

 /note=Start 27749 supported by Glimmer, GM, ST. Function Lysin B supported by synteny and NCBI BLAST results

CDS 28759 - 28992

 /gene="32"

 /product="gp32"

 /function="holin"

 /locus tag="jarcob\_32"

 /note=Original Glimmer call @bp 28759 has strength 8.77; Genemark calls start at 28759

 /note=SSC: 28759-28992 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_TWEETY\_32 [Mycobacterium phage Tweety] ],,NCBI, q1:s1 100.0% 3.59001E-44 GAP: 8 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.402, -3.9166971242758706, no F: holin SIF-BLAST: ,,[hypothetical protein PBI\_TWEETY\_32 [Mycobacterium phage Tweety] ],,YP\_001469265,100.0,3.59001E-44 SIF-HHPRED: Phage\_r1t\_holin ; Putative lactococcus lactis phage r1t holin,,,PF16945.8,89.6104,99.9 SIF-Syn: ShiLan: bp 28750- 28983 (234); holin

Burwell21: bp28707- 28940 (234); holin

Lizziana: bp 28682- 28915 (234); holin

Nivrat: bp 28681- 28914 (234); holin

SwagPigglett: bp 28520- 28753 (234); NKF

 /note=Start 28759 supported by Glimmer, GM, ST. Function holin supported by all SIF sources.

CDS 28989 - 29363

 /gene="33"

 /product="gp33"

 /function="Hypothetical Protein"

 /locus tag="jarcob\_33"

 /note=Original Glimmer call @bp 28989 has strength 8.63; Genemark calls start at 28989

 /note=SSC: 28989-29363 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_CABRINIANS\_33 [Mycobacterium phage Cabrinians] ],,NCBI, q1:s1 100.0% 2.58863E-80 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.674, -5.4858509637772555, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_CABRINIANS\_33 [Mycobacterium phage Cabrinians] ],,YP\_009189755,100.0,2.58863E-80 SIF-HHPRED: DUF2746 ; Protein of unknown function (DUF2746),,,PF10874.11,90.3226,99.9 SIF-Syn: ShiLan: SS (405);NKF

Burwell21: bp 28737- 29311 (575);NKF

Lizziana: bp 28912- 29286 (375);NKF

Nivrat: bp 28911- 29285 (375);NKF

SwagPigglett: bp 28750- 29124 (375);NKF

 /note=Start 28989 supported by Glimmer, GM, ST. Function hypothetical protein supported by all SIF sources.

CDS 29387 - 29620

 /gene="34"

 /product="gp34"

 /function="hypothetical protein"

 /locus tag="jarcob\_34"

 /note=Original Glimmer call @bp 29387 has strength 6.94; Genemark calls start at 29387

 /note=SSC: 29387-29620 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_LEPERCHAUN\_34 [Mycobacterium phage Leperchaun]],,NCBI, q1:s10 100.0% 1.60191E-49 GAP: 23 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.797, -3.081776789475849, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein SEA\_LEPERCHAUN\_34 [Mycobacterium phage Leperchaun]],,QYC53856,89.5349,1.60191E-49 SIF-HHPRED: DUF5338 ; Family of unknown function (DUF5338),,,PF17273.5,57.1429,96.4 SIF-Syn:

 /note=Start 29387 supported by glimmer, GM, and ST. Function NKF.

CDS 29607 - 30428

 /gene="35"

 /product="gp35"

 /function="DnaQ-like (DNA polymerase III subunit)"

 /locus tag="jarcob\_35"

 /note=Original Glimmer call @bp 29607 has strength 11.46; Genemark calls start at 29634

 /note=SSC: 29607-30428 CP: yes SCS: both-gl ST: SS BLAST-Start: [gp37 [Mycobacterium phage Che8] ],,NCBI, q1:s1 100.0% 0.0 GAP: -14 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.822, -3.0478325568523097, no F: DnaQ-like (DNA polymerase III subunit) SIF-BLAST: ,,[gp37 [Mycobacterium phage Che8] ],,NP\_817375,100.0,0.0 SIF-HHPRED: SIF-Syn: ShiLan: bp 29598- 30419 (822); DNAQ- like protein

Burwell21: bp 29555- 30376 (822);DNAQ-like endonuclease

Lizziana: bp 29530- 30351 (822);DNAQ-like endonuclease

Nivrat: bp 29529- 30350 (822); DNA Polymerase III subunit

SwagPigglett: bp 29368- 30189 (822);DNAQ-like endonuclease

 /note=Start 29607 supported by Glimmer, ST. DNAQ-like endonuclease supported by synteny

CDS 30512 - 30733

 /gene="36"

 /product="gp36"

 /function="hypothetical protein"

 /locus tag="jarcob\_36"

 /note=Original Glimmer call @bp 30515 has strength 7.06; Genemark calls start at 30515

 /note=SSC: 30512-30733 CP: yes SCS: both-cs ST: SS BLAST-Start: [hypothetical protein SEA\_CABRINIANS\_36 [Mycobacterium phage Cabrinians] ],,NCBI, q1:s1 100.0% 3.28805E-44 GAP: 83 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.052, -5.213475109731446, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein SEA\_CABRINIANS\_36 [Mycobacterium phage Cabrinians] ],,YP\_009189758,100.0,3.28805E-44 SIF-HHPRED: Uncharacterized protein; JCSG, Structural Genomics, PSI-Biology, Protein Structure Initiative, Joint Center for Structural Genomics, Unknown function; NMR {Bordetella bronchiseptica},,,2L25\_A,21.9178,53.3 SIF-Syn:

 /note=Start moved to 30512, supported by ST, improves gap slightly (1 codon difference). Function NKF.

CDS 30726 - 30818

 /gene="37"

 /product="gp37"

 /function="Hypothetical Protein"

 /locus tag="jarcob\_37"

 /note=Genemark calls start at 30726

 /note=SSC: 30726-30818 CP: yes SCS: genemark ST: SS BLAST-Start: [gp36 [Mycobacterium phage Fruitloop] ],,NCBI, q1:s1 100.0% 2.31031E-10 GAP: -8 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.764, -5.220380545373514, no F: Hypothetical Protein SIF-BLAST: ,,[gp36 [Mycobacterium phage Fruitloop] ],,YP\_002241721,100.0,2.31031E-10 SIF-HHPRED: SIF-Syn: ShiLan: bp 30717-30809 (93); other phages in pham had same gene length present in different locations

 /note=Start 30726 supported by GM, ST. Function NKF supported by synteny

 /note=Generally a section of genes with unknown functions. This is also typically the shortest, consistently sized gene in the area. Top 10 hits in PhagesDB are 8/10 in the same cluster, with unknown function, and 5/10 have this gene at approximately the same location and as gene 37.

CDS complement (30888 - 31034)

 /gene="38"

 /product="gp38"

 /function="Hypothetical Protein"

 /locus tag="jarcob\_38"

 /note=Original Glimmer call @bp 31034 has strength 6.12; Genemark calls start at 31034

 /note=SSC: 31034-30888 CP: yes SCS: both ST: NI BLAST-Start: [hypothetical protein PBI\_CHE9D\_42 [Mycobacterium phage Che9d] ],,NCBI, q1:s1 100.0% 7.96407E-26 GAP: -8 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.133, -4.534089041695007, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein PBI\_CHE9D\_42 [Mycobacterium phage Che9d] ],,NP\_818015,100.0,7.96407E-26 SIF-HHPRED: SIF-Syn: ShiLan: bp 31024-30878 (147); NKF

Nivrat: bp 30955-30809 (147); NKF

Burwell21: bp 30981-30835 (147); NKF

SwagPigglett: bp 30794-30648 (147); NKF

Lizziana: bp 30956-30810 (147); NKF

CDS complement (31027 - 31233)

 /gene="39"

 /product="gp39"

 /function="Hypothetical Protein"

 /locus tag="jarcob\_39"

 /note=Original Glimmer call @bp 31233 has strength 10.51; Genemark calls start at 31233

 /note=SSC: 31233-31027 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein N850\_gp046 [Mycobacterium phage Jabbawokkie] ],,NCBI, q1:s1 100.0% 1.02969E-41 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.92, -4.897971560974249, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein N850\_gp046 [Mycobacterium phage Jabbawokkie] ],,YP\_008410718,100.0,1.02969E-41 SIF-HHPRED: SIF-Syn: ShiLan: bp 31223-31017 (207); NKF

Nivrat: bp 31154-30948(207); NKF

Burwell21: bp 31180-30974 (207); NKF

SwagPigglett: bp 30794-30648 (147); NKF

Lizziana: bp 31155-30949 (207), NKF

 /note=Start 31, 233 supported by Glimmer, GM, ST. Function hypothetical protein supported by synteny

CDS complement (31230 - 31352)

 /gene="40"

 /product="gp40"

 /function="hypothetical protein"

 /locus tag="jarcob\_40"

 /note=Original Glimmer call @bp 31352 has strength 2.49; Genemark calls start at 31370

 /note=SSC: 31352-31230 CP: yes SCS: both-gl ST: SS BLAST-Start: [hypothetical protein I5H16\_gp040 [Mycobacterium phage BobaPhett] ],,NCBI, q1:s4 100.0% 2.01054E-21 GAP: -1 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.563, -5.574346888390875, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein I5H16\_gp040 [Mycobacterium phage BobaPhett] ],,YP\_009954828,93.0233,2.01054E-21 SIF-HHPRED: g.39.1.3 (A:33-67) Actin-binding LIM protein 2, abLIM2 {Human (Homo sapiens) [TaxId: 9606]},,,d1wiga2,65.0,98.1 SIF-Syn:

 /note=Start 31352 supported by glimmer and ST. Function NKF.

CDS complement (31352 - 31474)

 /gene="41"

 /product="gp41"

 /function="Hypothetical Protein"

 /locus tag="jarcob\_41"

 /note=Original Glimmer call @bp 31474 has strength 3.33

 /note=SSC: 31474-31352 CP: no SCS: glimmer ST: NA BLAST-Start: [hypothetical protein PBI\_JOB42\_42 [Mycobacterium phage Job42] ],,NCBI, q1:s10 100.0% 1.90958E-20 GAP: 7 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.764, -5.220380545373514, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein PBI\_JOB42\_42 [Mycobacterium phage Job42] ],,YP\_008126632,81.6327,1.90958E-20 SIF-HHPRED: Uncharacterized HTH-type transcriptional regulator ygiT; HTH-XRE DNA binding motif, Transcriptional Regulator, bacterial antitoxin, ZN binding protein, TRANSCRIPTION REGULATOR-DNA complex; HET: GOL; 2.0999A {Escherichia coli},,,3O9X\_B,97.5,87.6 SIF-Syn: ShiLan: bp 31464-31342 (123); NKF

Nivrat: bp 31473-31273 (201); NKF

Burwell21: bp 31421-31299 (123); NKF

SwagPigglett: bp 31234-31112 (123); NKF

Lizziana: bp 31396-31274 (123); NKF

 /note=Start 31, 474 supported by Glimmer. Function NKF supported by synteny. Low coding potential.

CDS complement (31482 - 32702)

 /gene="42"

 /product="gp42"

 /function="transposase"

 /locus tag="jarcob\_42"

 /note=Original Glimmer call @bp 32702 has strength 9.17; Genemark calls start at 32702

 /note=SSC: 32702-31482 CP: yes SCS: both ST: SS BLAST-Start: [transposase [Mycobacterium phage Pippy] ],,NCBI, q1:s1 100.0% 0.0 GAP: 10 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.913, -5.50074291708362, no F: transposase SIF-BLAST: ,,[transposase [Mycobacterium phage Pippy] ],,YP\_009961231,100.0,0.0 SIF-HHPRED: CRISPR-associated protein Cas14a.1; Cas12f, Cas14, sgRNA, target DNA, CRISPR, RNA BINDING PROTEIN-RNA-DNA complex; 3.0A {uncultured archaeon},,,7C7L\_B,89.6552,100.0 SIF-Syn: ShiLan: bp 32809-31472 (1338); NKF

Nivrat: N/A

Burwell21: bp 32766-31429 (1338); transposase

SwagPigglett: bp 32462-31242 (1221); NKF

Lizziana: bp 32741-31404 (1338); transposase

 /note=Start 32,702 supported by Glimmer, GM, ST. Function transposase supported by PhagesDB and BLAST results.

CDS complement (32713 - 32877)

 /gene="43"

 /product="gp43"

 /function="Hypothetical Protein"

 /locus tag="jarcob\_43"

 /note=Original Glimmer call @bp 32877 has strength 3.36

 /note=SSC: 32877-32713 CP: no SCS: glimmer ST: SS BLAST-Start: [hypothetical protein SEA\_CABRINIANS\_43 [Mycobacterium phage Cabrinians] ],,NCBI, q1:s1 100.0% 7.19161E-32 GAP: 396 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.641, -3.8690725721777643, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_CABRINIANS\_43 [Mycobacterium phage Cabrinians] ],,YP\_009189765,100.0,7.19161E-32 SIF-HHPRED: SIF-Syn: ShiLan: Not on pham line

Nivrat: N/A

Burwell21: N/A

SwagPigglett: bp 32637-32473 (165); NKF

Lizziana: bp 32799-32635 (165); NKF

 /note=Start 32877 supported by Glimmer, ST. Function hypothetical protein supported by synteny and BLAST results. Low coding potential.

tRNA complement (33097 - 33167)

 /gene="44"

 /product="tRNA-Lys(ctt)"

 /locus tag="JARCOB\_44"

 /note=tRNA-Lys(ctt)

CDS 33274 - 34563

 /gene="45"

 /product="gp45"

 /function="hypothetical protein"

 /locus tag="jarcob\_45"

 /note=Original Glimmer call @bp 33274 has strength 12.01; Genemark calls start at 33274

 /note=SSC: 33274-34563 CP: yes SCS: both ST: SS BLAST-Start: [tyrosine-type recombinase/integrase [Mycobacterium phage Phatniss] ],,NCBI, q1:s1 100.0% 0.0 GAP: 396 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.405, -3.9109350188549152, no F: hypothetical protein SIF-BLAST: ,,[tyrosine-type recombinase/integrase [Mycobacterium phage Phatniss] ],,YP\_009202558,100.0,0.0 SIF-HHPRED: Integrase; PROTEIN-DNA COMPLEX, DNA BINDING PROTEIN-DNA COMPLEX; HET: PTR; 3.8A {Enterobacteria phage lambda} SCOP: d.10.1.4, d.163.1.1,,,1Z1B\_B,93.007,100.0 SIF-Syn: ShiLan: bp 33263-34552 (1290)

Nivrat: bp 31868-33169 (1302)

Burwell21: bp 33220-34521 (1302)

SwagPiglett:N/A

Lizziana: bp 34269-35570 (1302)

 /note=Start 33274 supported by glimmer, GM, and ST. Gap due to tRNA. Function NKF.

CDS complement (34644 - 35090)

 /gene="46"

 /product="gp46"

 /function="Hypothetical Protein"

 /locus tag="jarcob\_46"

 /note=Original Glimmer call @bp 35090 has strength 8.07; Genemark calls start at 35090

 /note=SSC: 35090-34644 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein FDI15\_gp045 [Mycobacterium phage ShiLan] ],,NCBI, q1:s1 100.0% 5.48043E-101 GAP: 1002 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.981, -6.01284768743864, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein FDI15\_gp045 [Mycobacterium phage ShiLan] ],,YP\_009608120,100.0,5.48043E-101 SIF-HHPRED: SIF-Syn: ShiLan: bp 35079-34633 (447)

Nivrat: bp 33703-33248(276)

Burwell21: bp 35044-34598 (447)

SwagPiglett: bp 35271-34819 (453)

Lizziana: bp 36093-35647 (447)

Consistent with other phages, small hypothetical protein following a transposase

 /note=Start 35090 supported by Glimmer, GM, ST. Function hypothetical protein supported by synteny and BLAST results.

CDS 36093 - 36326

 /gene="47"

 /product="gp47"

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

 /locus tag="jarcob\_47"

 /note=Original Glimmer call @bp 36093 has strength 4.84; Genemark calls start at 36093

 /note=SSC: 36093-36326 CP: yes SCS: both ST: SS BLAST-Start: [Cro protein [Mycobacterium phage LilMoolah] ],,NCBI, q1:s43 100.0% 1.61939E-47 GAP: 1002 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.642, -5.490418349731808, no F: helix-turn-helix DNA binding domain SIF-BLAST: ,,[Cro protein [Mycobacterium phage LilMoolah] ],,YP\_010105233,64.7059,1.61939E-47 SIF-HHPRED: Transcriptional regulator ComR; RNPP family TPR domain HTH domain bacterial signaling peptide binding, TRANSCRIPTION; 1.894A {Streptococcus vestibularis F0396},,,6HU8\_A,88.3117,98.9 SIF-Syn: ShiLan: gp 36082-36315 (234); transcriptional regulator

Nivrat: n/a

Burwell21: gp 36047-36280 (234);NKF

SwagPiglett: n/a

Lizziana: gp 37033-37329 (297); Helix-turn-helix DNA domain binding protein

 /note=start 36093 supported by Glimmer, GM, ST. Function related to DNA binding, HHPRED and BLAST support HTH DBD.

CDS complement (35354 - 36094)

 /gene="48"

 /product="gp48"

 /function="immunity repressor"

 /locus tag="jarcob\_48"

 /note=Original Glimmer call @bp 36094 has strength 4.87; Genemark calls start at 35974

 /note=SSC: 36094-35354 CP: yes SCS: both-gl ST: SS BLAST-Start: [XRE family transcriptional regulator [Mycobacterium phage Cabrinians] ],,NCBI, q1:s1 100.0% 4.55586E-178 GAP: 292 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.679, -5.6853845463436965, no F: immunity repressor SIF-BLAST: ,,[XRE family transcriptional regulator [Mycobacterium phage Cabrinians] ],,YP\_009189769,99.5935,4.55586E-178 SIF-HHPRED: a.35.1.3 (A:) Antitoxin HigA {Escherichia coli [TaxId: 562]},,,d2icta\_,32.1138,98.4 SIF-Syn:

 /note=Start 36094 supported by glimmer and ST. CP low but present. Function immunity repressor supported by HHPRED and BLAST.

CDS 36387 - 36677

 /gene="49"

 /product="gp49"

 /function="Hypothetical Protein"

 /locus tag="jarcob\_49"

 /note=Original Glimmer call @bp 36387 has strength 5.95; Genemark calls start at 36387

 /note=SSC: 36387-36677 CP: yes SCS: both ST: NA BLAST-Start: [hypothetical protein SEA\_CABRINIANS\_49 [Mycobacterium phage Cabrinians] ],,NCBI, q1:s1 100.0% 3.2262E-64 GAP: 292 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.058, -2.5410833118725082, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_CABRINIANS\_49 [Mycobacterium phage Cabrinians] ],,YP\_009189771,100.0,3.2262E-64 SIF-HHPRED: SIF-Syn: ShiLan: gp 36376-36666 (291); NKF

Nivrat: gp 35996-36211 (216); NKF

Burwell21: gp 36341-36631 (291); NFK

SwagPiglett: gp 37364-37600 (237); NKF

Lizziana: gp 37390-37680 (291); NKF

 /note=start 36387 supported by Glimmer, GM. Function hypothetical protein supported by synteny. Low CP for first 100-200 bps.

CDS 36674 - 36766

 /gene="50"

 /product="gp50"

 /function="Hypothetical Protein"

 /locus tag="jarcob\_50"

 /note=Genemark calls start at 36674

 /note=SSC: 36674-36766 CP: no SCS: genemark ST: SS BLAST-Start: [hypothetical protein PBI\_BUZZLYSEYEAR\_54 [Mycobacterium phage BuzzLyseyear] ],,NCBI, q1:s1 100.0% 6.1801E-11 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.652, -3.31900957015528, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein PBI\_BUZZLYSEYEAR\_54 [Mycobacterium phage BuzzLyseyear] ],,YP\_009125047,100.0,6.1801E-11 SIF-HHPRED: SIF-Syn: ShiLan: n/a

 Nivrat: n/a

 Burwell21: n/a

 SwagPiglett: n/a

 Lizziana: gp 37677-37769 (93)

 /note=Start 36674 supported by GM, ST. Function hypothetical protein supported by synteny and BLAST results.

CDS 36763 - 36960

 /gene="51"

 /product="gp51"

 /function="Hypothetical Protein"

 /locus tag="jarcob\_51"

 /note=Original Glimmer call @bp 36763 has strength 4.92; Genemark calls start at 36763

 /note=SSC: 36763-36960 CP: no SCS: both ST: SS BLAST-Start: [gp52 [Mycobacterium phage Che8] ],,NCBI, q1:s1 100.0% 2.11933E-39 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.772, -3.1513923047253267, yes F: Hypothetical Protein SIF-BLAST: ,,[gp52 [Mycobacterium phage Che8] ],,NP\_817390,100.0,2.11933E-39 SIF-HHPRED: Putative DNA-binding protein; BldC, S. coelicolor, developmental switch, MerR-like, DNA BINDING PROTEIN-DNA complex; 3.09A {Streptomyces venezuelae},,,6AMA\_A,90.7692,99.2 SIF-Syn: ShiLan: bp 36752-36949 (198); NKF

Nivrat: bp 36297-36494 (198); NKF

Burwell21: bp 36717-36914 (198); NKF

SwagPiglett: n/a

Lizziana: bp 37766-37963 (198); NKF

 /note=Start 36763 supported by Glimmer, GM, ST. Function hypothetical protein supported by synteny and BLAST results.

CDS 37001 - 37195

 /gene="52"

 /product="gp52"

 /function="Hypothetical Protein"

 /locus tag="jarcob\_52"

 /note=Original Glimmer call @bp 37001 has strength 6.65; Genemark calls start at 37001

 /note=SSC: 37001-37195 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_CABRINIANS\_52 [Mycobacterium phage Cabrinians] ],,NCBI, q1:s1 100.0% 1.72911E-37 GAP: 40 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.499, -5.84799742031764, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_CABRINIANS\_52 [Mycobacterium phage Cabrinians] ],,YP\_009189774,100.0,1.72911E-37 SIF-HHPRED: SIF-Syn: ShiLan: bp 36990-37184 (195); NKF

Burwell21: bp 36955-37149 (195); NKF

Lizziana: bp 38004-38198 (195); NKF

Nivrat: N/A

SwagPigglett: N/A

CDS 37192 - 37476

 /gene="53"

 /product="gp53"

 /function="Hypothetical Protein"

 /locus tag="jarcob\_53"

 /note=Original Glimmer call @bp 37192 has strength 4.93; Genemark calls start at 37192

 /note=SSC: 37192-37476 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein GUMBIE\_49 [Mycobacterium virus GUmbie] ],,NCBI, q1:s1 100.0% 4.68691E-63 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.5, -4.73460372112482, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein GUMBIE\_49 [Mycobacterium virus GUmbie] ],,YP\_009018925,100.0,4.68691E-63 SIF-HHPRED: SIF-Syn: ShiLan: bp 37181-37465 (285); NKF

Burwell21: bp 37146-37430 (285); NKF

Lizziana: bp 38195-38479 (285); NKF

Nivrat: N/A

SwagPigglett: N/A

 /note=Start 37192 supported by Glimmer, GM, ST. Function hypothetical protein supported by synteny and BLAST results.

CDS 37473 - 37661

 /gene="54"

 /product="gp54"

 /function="Hypothetical Protein"

 /locus tag="jarcob\_54"

 /note=Original Glimmer call @bp 37473 has strength 2.33; Genemark calls start at 37551

 /note=SSC: 37473-37661 CP: yes SCS: both-gl ST: SS BLAST-Start: [hypothetical protein SEA\_CABRINIANS\_54 [Mycobacterium phage Cabrinians] ],,NCBI, q1:s1 100.0% 1.15422E-35 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.015, -4.717114992838803, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_CABRINIANS\_54 [Mycobacterium phage Cabrinians] ],,YP\_009189776,100.0,1.15422E-35 SIF-HHPRED: SIF-Syn: ShiLan: bp 37462-37650 (189); NKF

Burwell21: bp 37427-37615 (189); NKF

Lizziana: bp 38476-38664 (189); NKF

Nivrat: bp 36491-36682 (192); NKF

SwagPigglett: bp 39437-39628 (192); NKF

 /note=Start 37473 supported by Glimmer, ST. Function hypothetical protein supported by synteny and BLAST results. Low CP for approximately first hundred bps.

CDS 37658 - 38305

 /gene="55"

 /product="gp55"

 /function="Hypothetical Protein"

 /locus tag="jarcob\_55"

 /note=Original Glimmer call @bp 37658 has strength 4.99; Genemark calls start at 37658

 /note=SSC: 37658-38305 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_CABRINIANS\_55 [Mycobacterium phage Cabrinians] ],,NCBI, q1:s1 100.0% 2.52904E-154 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.122, -4.496270967456145, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_CABRINIANS\_55 [Mycobacterium phage Cabrinians] ],,YP\_009189777,100.0,2.52904E-154 SIF-HHPRED: SIF-Syn: ShiLan: bp 37647-38294 (648); NKF

Burwell21: bp 37612-38259 (648); NKF

Lizziana: bp 38661-39308 (648); NKF

Nivrat: bp 37041-37625 (585); NKF

SwagPigglett: bp 39987-40571 (585); NKF

 /note=Start 37658 supported by Glimmer, GM, ST. Function hypothetical protein supported by synteny and BLAST results.

CDS 38385 - 38663

 /gene="56"

 /product="gp56"

 /function="Hypothetical Protein"

 /locus tag="jarcob\_56"

 /note=Original Glimmer call @bp 38385 has strength 6.48; Genemark calls start at 38385

 /note=SSC: 38385-38663 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_SAAL\_57 [Mycobacterium phage Saal] ],,NCBI, q1:s1 100.0% 4.7743E-60 GAP: 79 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.19, -4.274735973818826, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein PBI\_SAAL\_57 [Mycobacterium phage Saal] ],,YP\_009007524,100.0,4.7743E-60 SIF-HHPRED: SIF-Syn: ShiLan: bp 38374-38652 (279); NKF

Burwell21: bp 38339-38617 (279); NKF

Lizziana: bp 39388-39666 (279); NKF

Nivrat: bp 37700-37981 (282); NKF

SwagPigglett: bp 40646-40927 (282); NKF

 /note=Start 38385 supported by Glimmer, GM, ST. Function hypothetical protein supported by synteny and BLAST results. Low CP for first hundred bps.

CDS 38660 - 39007

 /gene="57"

 /product="gp57"

 /function="Hypothetical Protein"

 /locus tag="jarcob\_57"

 /note=Original Glimmer call @bp 38660 has strength 10.24; Genemark calls start at 38660

 /note=SSC: 38660-39007 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_SAAL\_58 [Mycobacterium phage Saal] ],,NCBI, q1:s1 100.0% 7.87199E-79 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 3.235, -2.17469248771465, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein PBI\_SAAL\_58 [Mycobacterium phage Saal] ],,YP\_009007525,100.0,7.87199E-79 SIF-HHPRED: SIF-Syn: ShiLan: gp 38649-38996 (348); NKF

Burwell21: gp 38614-38961 (348); NKF

Lizziana: gp 39663-40010 (348); NKF

Nivrat: gp 37978-38325 (348); NKF

SwagPigglett: gp 40924-41271 (348); NKF

 /note=Start 38660 supported by Glimmer, GM, ST. Function hypothetical protein supported by synteny and BLAST results.

CDS 39007 - 39501

 /gene="58"

 /product="gp58"

 /function="WhiB family transcription factor"

 /locus tag="jarcob\_58"

 /note=Original Glimmer call @bp 39007 has strength 5.41; Genemark calls start at 39007

 /note=SSC: 39007-39501 CP: yes SCS: both ST: SS BLAST-Start: [WhiB [Mycobacterium phage SiSi] ],,NCBI, q1:s1 100.0% 5.30182E-118 GAP: -1 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.087, -4.550790461065498, no F: WhiB family transcription factor SIF-BLAST: ,,[WhiB [Mycobacterium phage SiSi] ],,YP\_008051181,100.0,5.30182E-118 SIF-HHPRED: SIF-Syn: ShiLan: bp 38996-39490 (495); WhiB

Burwell21: bp 38961-39455 (495); WhiB family transcription factor

Lizziana: bp 40010-40504 (495); WhiB family transcription factor

Nivrat: bp 38325-38819 (495); WhiB family transcription factor

SwagPigglett: bp 41271-41765 (495); WhiB family transcription factor;

count 82; frequency 98%

 /note=Start 39007 supported by Glimmer, GM, ST. Function WhiB family transcription supported by synteny and BLAST results.

CDS 39498 - 39983

 /gene="59"

 /product="gp59"

 /function="Hypothetical Protein"

 /locus tag="jarcob\_59"

 /note=Original Glimmer call @bp 39498 has strength 3.24; Genemark calls start at 39471

 /note=SSC: 39498-39983 CP: yes SCS: both-gl ST: SS BLAST-Start: [hypothetical protein PACC\_52 [Mycobacterium phage Pacc40] ],,NCBI, q1:s1 100.0% 5.38614E-112 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.719, -3.1816499351312086, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein PACC\_52 [Mycobacterium phage Pacc40] ],,YP\_002241636,100.0,5.38614E-112 SIF-HHPRED: SIF-Syn: ShiLan: gp 39487-39972 (486); NKF

Burwell21: gp 39452-39937 (486); NKF

Lizziana: gp 40501-40986 (486); NKF

Nivrat: gp 38816-39301 (486); NKF

SwagPigglett: gp 41762-42247 (486); NKF

 /note=Start 39498 supported by Glimmer, ST. Function hypothetical protein supported by synteny and BLAST results.

CDS 39980 - 40264

 /gene="60"

 /product="gp60"

 /function="WhiB family transcription factor"

 /locus tag="jarcob\_60"

 /note=Original Glimmer call @bp 39980 has strength 8.01; Genemark calls start at 39980

 /note=SSC: 39980-40264 CP: yes SCS: both ST: SS BLAST-Start: [WhiB [Mycobacterium phage ShiLan] ],,NCBI, q1:s1 100.0% 2.09399E-61 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.808, -3.1379842619144376, no F: WhiB family transcription factor SIF-BLAST: ,,[WhiB [Mycobacterium phage ShiLan] ],,YP\_009608133,100.0,2.09399E-61 SIF-HHPRED: Transcription regulator WhiB1; Iron-sulfur cluster, transcription regulation, redox-sensing, TRANSCRIPTION; HET: MSE, SF4, PEG; 1.85A {Mycobacterium tuberculosis H37Rv},,,6ONO\_A,71.2766,99.8 SIF-Syn: ShiLan, Burwell21

 /note=Start 39980 supported by glimmer, GM, ST. Function WhiB fam TF supported by all SIF sources.

CDS 40261 - 40626

 /gene="61"

 /product="gp61"

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

 /locus tag="jarcob\_61"

 /note=Original Glimmer call @bp 40261 has strength 4.65; Genemark calls start at 40261

 /note=SSC: 40261-40626 CP: yes SCS: both ST: SS BLAST-Start: [helix-turn-helix DNA binding protein [Mycobacterium phage Cabrinians] ],,NCBI, q1:s1 100.0% 2.57904E-84 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.863, -3.0228743540871426, yes F: helix-turn-helix DNA binding domain SIF-BLAST: ,,[helix-turn-helix DNA binding protein [Mycobacterium phage Cabrinians] ],,YP\_009189783,100.0,2.57904E-84 SIF-HHPRED: PAX Paired Box domain,,,cd00131,77.686,99.3 SIF-Syn: Burwell21, Koella

 /note=Start 40261 supported by glimmer, GM, ST. Function HTH DBD supported by all SIF sources.

CDS 40626 - 40781

 /gene="62"

 /product="gp62"

 /function="hypothetical protein"

 /locus tag="jarcob\_62"

 /note=Original Glimmer call @bp 40626 has strength 6.94

 /note=SSC: 40626-40781 CP: yes SCS: glimmer ST: SS BLAST-Start: [hypothetical protein PBI\_BUZZLYSEYEAR\_67 [Mycobacterium phage BuzzLyseyear] ],,NCBI, q1:s2 100.0% 3.32202E-30 GAP: -1 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.896, -4.963787326180191, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_BUZZLYSEYEAR\_67 [Mycobacterium phage BuzzLyseyear] ],,YP\_009125060,98.0769,3.32202E-30 SIF-HHPRED: Endothelin ; Endothelin family,,,PF00322.20,19.6078,81.6 SIF-Syn:

 /note=Start 40626 supported by glimmer, ST. CP is lower than typical but supported by synteny (pham 17302) and ST. Function NKF.

CDS 40781 - 41014

 /gene="63"

 /product="gp63"

 /function="hypothetical protein"

 /locus tag="jarcob\_63"

 /note=Original Glimmer call @bp 40781 has strength 7.86; Genemark calls start at 40781

 /note=SSC: 40781-41014 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_DAENERYS\_56 [Mycobacterium phage Daenerys] ],,NCBI, q1:s1 100.0% 3.06698E-45 GAP: -1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.588, -3.5925599723783583, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_DAENERYS\_56 [Mycobacterium phage Daenerys] ],,YP\_008410625,100.0,3.06698E-45 SIF-HHPRED: DUF2959 ; Protein of unknown function (DUF2959),,,PF11172.11,88.3117,71.4 SIF-Syn:

 /note=Start 40781 supported by glimmer, GM, ST. Function NKF.

CDS 41011 - 41475

 /gene="64"

 /product="gp64"

 /function="hypothetical protein"

 /locus tag="jarcob\_64"

 /note=Original Glimmer call @bp 41011 has strength 11.09; Genemark calls start at 41011

 /note=SSC: 41011-41475 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_JOB42\_66 [Mycobacterium phage Job42] ],,NCBI, q1:s1 100.0% 2.53288E-104 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.798, -3.36878816875868, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_JOB42\_66 [Mycobacterium phage Job42] ],,YP\_008126656,100.0,2.53288E-104 SIF-HHPRED: Phage\_Mu\_Gam ; Bacteriophage Mu Gam like protein,,,PF07352.15,53.8961,98.6 SIF-Syn:

 /note=Start 41011 supported by Glimmer, GM, ST. Function NKF.

CDS 41472 - 42449

 /gene="65"

 /product="gp65"

 /function="RecA-like DNA recombinase"

 /locus tag="jarcob\_65"

 /note=Original Glimmer call @bp 41472 has strength 13.22; Genemark calls start at 41472

 /note=SSC: 41472-42449 CP: yes SCS: both ST: SS BLAST-Start: [AAA family ATPase [Mycobacterium phage Inventum] ],,NCBI, q1:s1 100.0% 0.0 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.075, -2.583959800616441, no F: RecA-like DNA recombinase SIF-BLAST: ,,[AAA family ATPase [Mycobacterium phage Inventum] ],,YP\_009125340,100.0,0.0 SIF-HHPRED: Protein recA; Alpha and beta proteins (a/b, a+b), ATP-binding, Cytoplasm, DNA damage, DNA recombination, DNA repair, DNA-binding, Nucleotide-binding; 1.95A {Thermotoga maritima},,,3HR8\_A,65.5385,99.4 SIF-Syn:

 /note=Start 41472 supported by Glimmer, GM, ST. Function RecA supported by synteny, some HHPRED, some BLAST (some entries AAA ATPase).

CDS 42805 - 44094

 /gene="66"

 /product="gp66"

 /function="DNA helicase"

 /locus tag="jarcob\_66"

 /note=Original Glimmer call @bp 42805 has strength 10.24; Genemark calls start at 42805

 /note=SSC: 42805-44094 CP: yes SCS: both ST: NA BLAST-Start: [DNA helicase [Mycobacterium phage Emma] ],,NCBI, q1:s1 100.0% 0.0 GAP: 355 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.74, -3.2790920053347614, yes F: DNA helicase SIF-BLAST: ,,[DNA helicase [Mycobacterium phage Emma] ],,YP\_009956627,99.7669,0.0 SIF-HHPRED: DNA excision repair protein ERCC-6; transcription, DNA repair;{Sus scrofa},,,7OO3\_b,91.3753,100.0 SIF-Syn: SwagPigglett: DNA Helicase

Burwell21: DNA Helicase

 /note=Start 42805 supported by glimmer, GM, and ST (though not the most annotated start). Function DNA helicase supported by all SIF sources. Note that though the gap is 355 and there is a start/stop site with a ~400bp ORF, this region lacks CP.

CDS 44101 - 45051

 /gene="67"

 /product="gp67"

 /function="DNA methyltransferase"

 /locus tag="jarcob\_67"

 /note=Original Glimmer call @bp 44101 has strength 10.01; Genemark calls start at 44101

 /note=SSC: 44101-45051 CP: yes SCS: both ST: SS BLAST-Start: [site-specific DNA-methyltransferase [Mycobacterium phage Emma] ],,NCBI, q1:s1 100.0% 0.0 GAP: 6 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.621, -3.4463834536695686, no F: DNA methyltransferase SIF-BLAST: ,,[site-specific DNA-methyltransferase [Mycobacterium phage Emma] ],,YP\_009956628,100.0,0.0 SIF-HHPRED: Adenine specific DNA methyltransferase (DpnA); M1.HpyAVI, DNA BINDING PROTEIN; 3.0A {Helicobacter pylori (strain ATCC 700392 / 26695)} SCOP: c.66.1.0,,,5HEK\_C,91.1392,100.0 SIF-Syn: BobaPhett, Burwell21, SwagPigglett

 /note=Start 44101 supported by glimmer, GM, ST. Function DNA methylase (methyltransferase - adenosine) supported by all SIF sources.

CDS 45048 - 45269

 /gene="68"

 /product="gp68"

 /function="hypothetical protein"

 /locus tag="jarcob\_68"

 /note=Original Glimmer call @bp 45048 has strength 5.54; Genemark calls start at 45048

 /note=SSC: 45048-45269 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein I5H18\_gp064 [Mycobacterium phage Bubbles123] ],,NCBI, q1:s1 100.0% 6.07216E-45 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.682, -5.467786178606034, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein I5H18\_gp064 [Mycobacterium phage Bubbles123] ],,YP\_009955076,98.6301,6.07216E-45 SIF-HHPRED: Splicing factor 1; UHM, pre-mRNA splicing factor, protein binding, phosphorylation; HET: MSE, SEP, SO4; 2.29A {Homo sapiens},,,4FXW\_B,54.7945,78.9 SIF-Syn:

 /note=Start 45048 supported by glimmer, GM, ST. Function NKF. HHPRED suggests could be related to mRNA processing.

CDS 45266 - 45415

 /gene="69"

 /product="gp69"

 /function="hypothetical protein"

 /locus tag="jarcob\_69"

 /note=Original Glimmer call @bp 45266 has strength 10.11; Genemark calls start at 45269

 /note=SSC: 45266-45415 CP: yes SCS: both-gl ST: SS BLAST-Start: [hypothetical protein PBI\_CHE9D\_79 [Mycobacterium phage Che9d] ],,NCBI, q1:s1 100.0% 1.24779E-27 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.658, -3.4470622626190464, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_CHE9D\_79 [Mycobacterium phage Che9d] ],,NP\_818052,100.0,1.24779E-27 SIF-HHPRED: b.43.4.2 (A:2-110) Methane monooxygenase component C, MmoC {Methylococcus capsulatus [TaxId: 414]},,,d1tvca1,81.6327,73.3 SIF-Syn:

 /note=Start 45266 supported by glimmer and ST (GM similar, off by 1 codon). Function NKF.

CDS 45412 - 45819

 /gene="70"

 /product="gp70"

 /function="DNA methyltransferase"

 /locus tag="jarcob\_70"

 /note=Original Glimmer call @bp 45454 has strength 2.89; Genemark calls start at 45412

 /note=SSC: 45412-45819 CP: yes SCS: both-gm ST: SS BLAST-Start: [DNA methylase [Mycobacterium phage ShiLan] ],,NCBI, q1:s1 100.0% 3.64476E-94 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.687, -5.317780913136193, no F: DNA methyltransferase SIF-BLAST: ,,[DNA methylase [Mycobacterium phage ShiLan] ],,YP\_009608145,34.7044,3.64476E-94 SIF-HHPRED: c.66.1.26 (A:1137-1600) Methyltransferase domain from DNA methyltransferase 1 (DNMT1) {Mouse (Mus musculus) [TaxId: 10090]},,,4H0N\_A,99.2593,99.9 SIF-Syn: ShiLan, Fancypants

 /note=Start moved to 45412, supported by GM and ST, improves gap and maintains forward orientation of genes in this region. Function DNA methylase (methyltransferase - cytosine) supported by all SIF sources.

CDS 45803 - 46582

 /gene="71"

 /product="gp71"

 /function="DNA methyltransferase"

 /locus tag="jarcob\_71"

 /note=Original Glimmer call @bp 45866 has strength 3.79; Genemark calls start at 45803

 /note=SSC: 45803-46582 CP: yes SCS: both-gm ST: NI BLAST-Start: [DNA methylase [Mycobacterium phage ShiLan] ],,NCBI, q7:s137 97.6834% 3.85926E-178 GAP: -17 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.061, -7.26512022081073, no F: DNA methyltransferase SIF-BLAST: ,,[DNA methylase [Mycobacterium phage ShiLan] ],,YP\_009608145,65.0386,3.85926E-178 SIF-HHPRED: DNA CYTOSINE METHYLTRANSFERASE DNMT2; Human DNA Methyltransferase homologue, TRANSFERASE; HET: CSO, SAH; 1.8A {Homo sapiens} SCOP: c.66.1.26,,,1G55\_A,19.6911,95.6 SIF-Syn: ShiLan, Akhila

 /note=Start moved to 45803 supported by GM and reduces gap, increasing ORF, improves Z score. Function DNA methyltransferase (methylase - cytosine) supported by all SIF sources.

CDS 46579 - 46731

 /gene="72"

 /product="gp72"

 /function="hypothetical protein"

 /locus tag="jarcob\_72"

 /note=Original Glimmer call @bp 46579 has strength 8.72; Genemark calls start at 46579

 /note=SSC: 46579-46731 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_SAAL\_71 [Mycobacterium phage Saal] ],,NCBI, q1:s1 100.0% 6.64978E-27 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.74, -3.2790920053347614, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_SAAL\_71 [Mycobacterium phage Saal] ],,YP\_009007538,100.0,6.64978E-27 SIF-HHPRED: g.41.6.1 (A:) Hypothetical protein MTH1184 {Methanobacterium thermoautotrophicum [TaxId: 145262]},,,d1dw7a\_,66.0,86.6 SIF-Syn:

 /note=Start 46579 supported by glimmer, GM, ST. Function NKF

CDS 46877 - 47431

 /gene="73"

 /product="gp73"

 /function="G-I-Y Y-I-G endonuclease"

 /locus tag="jarcob\_73"

 /note=Original Glimmer call @bp 46877 has strength 3.82; Genemark calls start at 46889

 /note=SSC: 46877-47431 CP: yes SCS: both-gl ST: SS BLAST-Start: [GIY-YIG homing endonuclease [Mycobacterium phage Saal] ],,NCBI, q1:s1 100.0% 1.25897E-134 GAP: 145 bp gap LO: no RBS: Kibler 6, Karlin Medium, 3.156, -2.356391881054909, yes F: G-I-Y Y-I-G endonuclease SIF-BLAST: ,,[GIY-YIG homing endonuclease [Mycobacterium phage Saal] ],,YP\_009007540,100.0,1.25897E-134 SIF-HHPRED: UvrC; DNA BINDING PROTEIN; HET: SO4; 2.0A {Bacillus caldotenax},,,1YD6\_B,41.8478,99.4 SIF-Syn:

 /note=Start 46877 supported by glimmer and ST. Function G-I-Y Y-I-G endonuclease supported by all SIF sources.

CDS 47431 - 48390

 /gene="74"

 /product="gp74"

 /function="hypothetical protein"

 /locus tag="jarcob\_74"

 /note=Original Glimmer call @bp 47431 has strength 6.79; Genemark calls start at 47431

 /note=SSC: 47431-48390 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_SAAL\_74 [Mycobacterium phage Saal] ],,NCBI, q1:s1 100.0% 0.0 GAP: -1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.482, -3.7329837339109084, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_SAAL\_74 [Mycobacterium phage Saal] ],,YP\_009007541,100.0,0.0 SIF-HHPRED: Phage\_rep\_org\_N ; N-terminal phage replisome organiser (Phage\_rep\_org\_N),,,PF09681.13,28.5266,98.1 SIF-Syn:

 /note=Start 47431 supported by glimmer, GM, ST. Function NKF (possibly some HTH DB protein, but SIF inconclusive).

CDS 48390 - 48659

 /gene="75"

 /product="gp75"

 /function="hypothetical protein"

 /locus tag="jarcob\_75"

 /note=Original Glimmer call @bp 48390 has strength 5.67; Genemark calls start at 48390

 /note=SSC: 48390-48659 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_SAAL\_75 [Mycobacterium phage Saal] ],,NCBI, q1:s1 100.0% 1.577E-57 GAP: -1 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.772, -3.2123487306667524, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_SAAL\_75 [Mycobacterium phage Saal] ],,YP\_009007542,100.0,1.577E-57 SIF-HHPRED: Lar\_restr\_allev ; Restriction alleviation protein Lar,,,PF14354.9,8.98876,62.0 SIF-Syn:

 /note=Start 48390 supported by Glimmer, GM, ST. Function NKF.

CDS 48652 - 48939

 /gene="76"

 /product="gp76"

 /function="hypothetical protein"

 /locus tag="jarcob\_76"

 /note=Original Glimmer call @bp 48652 has strength 5.35; Genemark calls start at 48652

 /note=SSC: 48652-48939 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein BOOMER\_79 [Mycobacterium phage Boomer] ],,NCBI, q1:s1 100.0% 2.27883E-64 GAP: -8 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.999, -2.9525085049809894, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein BOOMER\_79 [Mycobacterium phage Boomer] ],,YP\_002014295,100.0,2.27883E-64 SIF-HHPRED: Putative cytoplasmic protein; N1pC/P60 papain like cysteine peptidase Tae4, peptidoglycan hydrolase, immunity protein Tai4, Tae4: cytoplasmatic, Tai4: periplasmatic, TOXIN-INHIBITOR; HET: FLC, ETX; 1.8A {Salmonella enterica subsp. enterica serovar Typhimurium},,,4J32\_A,85.2632,70.6 SIF-Syn:

 /note=Start 48652 supported by glimmer, GM, ST. Function NKF

CDS 48936 - 49130

 /gene="77"

 /product="gp77"

 /function="hypothetical protein"

 /locus tag="jarcob\_77"

 /note=Genemark calls start at 48936

 /note=SSC: 48936-49130 CP: no SCS: genemark ST: SS BLAST-Start: [hypothetical protein PBI\_SAAL\_77 [Mycobacterium phage Saal] ],,NCBI, q1:s1 100.0% 3.1016E-39 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.304, -4.947056885847969, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_SAAL\_77 [Mycobacterium phage Saal] ],,YP\_009007544,100.0,3.1016E-39 SIF-HHPRED: e.59.1.1 (A:19-308) FdhE homolog PA4809 {Pseudomonas aeruginosa [TaxId: 287]},,,d2fiya1,53.125,71.3 SIF-Syn:

 /note=Start 48936 supported by GM and ST. Lacks CP, however the gap and zscore are excellent (also LORF), so including for now. Function NKF.

CDS 49127 - 49480

 /gene="78"

 /product="gp78"

 /function="hypothetical protein"

 /locus tag="jarcob\_78"

 /note=Original Glimmer call @bp 49127 has strength 8.97; Genemark calls start at 49127

 /note=SSC: 49127-49480 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_BIPOLAR\_81 [Mycobacterium phage Bipolar] ],,NCBI, q1:s1 100.0% 1.35209E-79 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.288, -4.599515895103776, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_BIPOLAR\_81 [Mycobacterium phage Bipolar] ],,YP\_009200708,100.0,1.35209E-79 SIF-HHPRED: YorP ; YorP protein,,,PF09629.13,41.0256,92.0 SIF-Syn:

 /note=Start 49127 supported by glimmer, GM, and ST. Function NKF

CDS 49477 - 49857

 /gene="79"

 /product="gp79"

 /function="hypothetical protein"

 /locus tag="jarcob\_79"

 /note=Original Glimmer call @bp 49477 has strength 8.08; Genemark calls start at 49477

 /note=SSC: 49477-49857 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein I5H19\_gp074 [Mycobacterium phage Burwell21] ],,NCBI, q1:s65 100.0% 2.25105E-85 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.571, -4.3934175870462076, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein I5H19\_gp074 [Mycobacterium phage Burwell21] ],,YP\_009955186,66.3158,2.25105E-85 SIF-HHPRED: DUF6324 ; Family of unknown function (DUF6324),,,PF19849.2,30.9524,94.0 SIF-Syn:

 /note=Start 49477 supported by glimmer, GM, and ST. Function NKF.

CDS 49854 - 50066

 /gene="80"

 /product="gp80"

 /function="hypothetical protein"

 /locus tag="jarcob\_80"

 /note=Original Glimmer call @bp 49854 has strength 2.78; Genemark calls start at 49854

 /note=SSC: 49854-50066 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SG4\_80 [Mycobacterium virus SG4] ],,NCBI, q1:s11 100.0% 9.3721E-46 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.818, -3.0377949497172554, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein SG4\_80 [Mycobacterium virus SG4] ],,YP\_009013282,87.5,9.3721E-46 SIF-HHPRED: TRANSCRIPTIONAL ELONGATION FACTOR SII; TRANSCRIPTION REGULATION; HET: ZN; NMR {Homo sapiens} SCOP: g.41.3.1,,,1TFI\_A,48.5714,93.3 SIF-Syn:

 /note=Start 49854 supported by glimmer, GM, and ST. Function NKF

CDS 50063 - 50347

 /gene="81"

 /product="gp81"

 /function="hypothetical protein"

 /locus tag="jarcob\_81"

 /note=Original Glimmer call @bp 50063 has strength 2.56; Genemark calls start at 50063

 /note=SSC: 50063-50347 CP: yes SCS: both ST: SS BLAST-Start: [gp67 [Mycobacterium phage Ardmore] ],,NCBI, q1:s1 100.0% 2.71608E-62 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.822, -4.0178693334748665, yes F: hypothetical protein SIF-BLAST: ,,[gp67 [Mycobacterium phage Ardmore] ],,YP\_003495208,100.0,2.71608E-62 SIF-HHPRED: Nuc\_rec\_co-act ; Nuclear receptor coactivator,,,PF08815.13,7.44681,74.0 SIF-Syn:

 /note=Start 50063 support by glimmer, GM, and ST. Function NKF

CDS 50340 - 50528

 /gene="82"

 /product="gp82"

 /function="hypothetical protein"

 /locus tag="jarcob\_82"

 /note=Original Glimmer call @bp 50340 has strength 4.2; Genemark calls start at 50340

 /note=SSC: 50340-50528 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_TWEETY\_83 [Mycobacterium phage Tweety] ],,NCBI, q1:s1 100.0% 6.50556E-34 GAP: -8 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.648, -3.389881189012514, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_TWEETY\_83 [Mycobacterium phage Tweety] ],,YP\_001469316,100.0,6.50556E-34 SIF-HHPRED: SENSORY BOX PROTEIN; SIGNALING PROTEIN, VOLTAGE (LOV) DOMAIN; HET: ACE; NMR {N/A},,,2YON\_A,29.0323,79.8 SIF-Syn:

 /note=Start 50340 supported by glimmer, GM, and ST. Function NKF.

CDS 50638 - 50970

 /gene="83"

 /product="gp83"

 /function="mycobacteriophage mobile element 1 (MPME 1)"

 /locus tag="jarcob\_83"

 /note=Original Glimmer call @bp 50638 has strength 2.61; Genemark calls start at 50629

 /note=SSC: 50638-50970 CP: yes SCS: both-gl ST: SS BLAST-Start: [hypothetical protein KNV67\_gp084 [Mycobacterium phage Plumbus] ],,NCBI, q1:s4 100.0% 1.04345E-76 GAP: 109 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.289, -4.422065872383915, no F: mycobacteriophage mobile element 1 (MPME 1) SIF-BLAST: ,,[hypothetical protein KNV67\_gp084 [Mycobacterium phage Plumbus] ],,YP\_010113867,97.3451,1.04345E-76 SIF-HHPRED: CT398; hypothetical protein, DNA/RNA binding, coiled-coil, Zn ribbon domain, structural proteomics, UNKNOWN FUNCTION; 2.12A {Chlamydia trachomatis},,,4ILO\_B,39.0909,65.1 SIF-Syn:

 /note=Start 50638 supported by glimmer, GM, and ST. Function MPME1 supported by synteny and BLAST.

CDS 50957 - 51130

 /gene="84"

 /product="gp84"

 /function="hypothetical protein"

 /locus tag="jarcob\_84"

 /note=Genemark calls start at 50957

 /note=SSC: 50957-51130 CP: yes SCS: genemark ST: SS BLAST-Start: [hypothetical protein PBI\_TWEETY\_85 [Mycobacterium phage Tweety] ],,NCBI, q1:s1 100.0% 1.20084E-33 GAP: -14 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.295, -4.711479922277682, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_TWEETY\_85 [Mycobacterium phage Tweety] ],,YP\_001469318,100.0,1.20084E-33 SIF-HHPRED: Density-regulated protein; translation initiation, Ribosome, TRANSLATION; HET: GOL; 2.14A {Homo sapiens},,,5ONS\_B,17.5439,36.2 SIF-Syn:

 /note=Start 50957 supported by GM and ST. Function NKF.

CDS 51167 - 51499

 /gene="85"

 /product="gp85"

 /function="hypothetical protein"

 /locus tag="jarcob\_85"

 /note=Original Glimmer call @bp 51167 has strength 0.52; Genemark calls start at 51167

 /note=SSC: 51167-51499 CP: yes SCS: both ST: NI BLAST-Start: [hypothetical protein FDI15\_gp085 [Mycobacterium phage ShiLan] ],,NCBI, q11:s24 90.9091% 3.38321E-65 GAP: 36 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.482, -4.197870532213559, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein FDI15\_gp085 [Mycobacterium phage ShiLan] ],,YP\_009608160,81.3008,3.38321E-65 SIF-HHPRED: Nuc\_rec\_co-act ; Nuclear receptor coactivator,,,PF08815.13,6.36364,54.0 SIF-Syn:

 /note=Start 51167 supported by glimmer and GM. Function NKF.

CDS 51496 - 51711

 /gene="86"

 /product="gp86"

 /function="hypothetical protein"

 /locus tag="jarcob\_86"

 /note=Original Glimmer call @bp 51496 has strength 8.7; Genemark calls start at 51496

 /note=SSC: 51496-51711 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein FDI15\_gp086 [Mycobacterium phage ShiLan] ],,NCBI, q1:s1 100.0% 1.75291E-43 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.648, -3.3275678682521845, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein FDI15\_gp086 [Mycobacterium phage ShiLan] ],,YP\_009608161,100.0,1.75291E-43 SIF-HHPRED: MazE\_antitoxin ; Antidote-toxin recognition MazE, bacterial antitoxin,,,PF04014.21,47.8873,69.2 SIF-Syn:

 /note=Start 51496 supported by GM, glimmer, and ST. Function NKF.

CDS 51704 - 51892

 /gene="87"

 /product="gp87"

 /function="hypothetical protein"

 /locus tag="jarcob\_87"

 /note=Original Glimmer call @bp 51704 has strength 10.71; Genemark calls start at 51749

 /note=SSC: 51704-51892 CP: no SCS: both-gl ST: SS BLAST-Start: [hypothetical protein PBI\_INVENTUM\_81 [Mycobacterium phage Inventum] ],,NCBI, q1:s1 100.0% 5.56441E-37 GAP: -8 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.482, -4.197870532213559, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_INVENTUM\_81 [Mycobacterium phage Inventum] ],,YP\_009125362,100.0,5.56441E-37 SIF-HHPRED: yfhH hypothetical protein; Structural Genomics, unknown function, PSI, Protein Structure Initiative, Midwest Center for Structural Genomics, MCSG; 1.71A {Bacillus subtilis} SCOP: b.34.15.1, l.1.1.1,,,1SF9\_A,88.7097,88.5 SIF-Syn:

 /note=Start 51704 supported by glimmer and ST. Function NKF.

CDS 51889 - 52080

 /gene="88"

 /product="gp88"

 /function="hypothetical protein"

 /locus tag="jarcob\_88"

 /note=Original Glimmer call @bp 51889 has strength 4.31; Genemark calls start at 51889

 /note=SSC: 51889-52080 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein FDI15\_gp088 [Mycobacterium phage ShiLan] ],,NCBI, q1:s1 100.0% 1.37701E-38 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.652, -3.6701184301625793, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein FDI15\_gp088 [Mycobacterium phage ShiLan] ],,YP\_009608163,100.0,1.37701E-38 SIF-HHPRED: DNA-DIRECTED RNA POLYMERASE; TRANSFERASE, MULTI-SUBUNIT, TRANSCRIPTION; HET: ZN; 3.202A {SULFOLOBUS SHIBATAE},,,4AYB\_P,31.746,93.5 SIF-Syn:

 /note=Start 51889 supported by glimmer, GM, and ST. Function NKF (HHPRED indicates protein may have DNA binding abilities).

CDS 52077 - 52256

 /gene="89"

 /product="gp89"

 /function="hypothetical protein"

 /locus tag="jarcob\_89"

 /note=Original Glimmer call @bp 52077 has strength 12.0; Genemark calls start at 52077

 /note=SSC: 52077-52256 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein I5H61\_gp086 [Mycobacterium phage Mattes] ],,NCBI, q1:s8 100.0% 1.63141E-34 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 3.214, -2.6835611257758942, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein I5H61\_gp086 [Mycobacterium phage Mattes] ],,YP\_009959552,89.3939,1.63141E-34 SIF-HHPRED: DUF6700 ; Domain of unknown function (DUF6700),,,PF20416.1,98.3051,76.3 SIF-Syn:

 /note=Start 52077 supported by glimmer, GM, and ST. Function NKF.

CDS 52261 - 52398

 /gene="90"

 /product="gp90"

 /function="hypothetical protein"

 /locus tag="jarcob\_90"

 /note=Original Glimmer call @bp 52261 has strength 1.66

 /note=SSC: 52261-52398 CP: yes SCS: glimmer ST: SS BLAST-Start: [hypothetical protein GUMBIE\_87 [Mycobacterium virus GUmbie] ],,NCBI, q1:s1 100.0% 9.04199E-23 GAP: 4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 0.608, -7.613029214795732, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein GUMBIE\_87 [Mycobacterium virus GUmbie] ],,YP\_009018963,100.0,9.04199E-23 SIF-HHPRED: SMBP ; Small metal-binding protein,,,PF16785.8,62.2222,86.0 SIF-Syn:

 /note=Start 52261 supported by glimmer and ST. Function NKF.

CDS 52395 - 52523

 /gene="91"

 /product="gp91"

 /function="hypothetical protein"

 /locus tag="jarcob\_91"

 /note=Original Glimmer call @bp 52395 has strength 11.29; Genemark calls start at 52395

 /note=SSC: 52395-52523 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein GUMBIE\_88 [Mycobacterium virus GUmbie] ],,NCBI, q1:s1 100.0% 4.37075E-20 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.824, -3.0425830684175623, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein GUMBIE\_88 [Mycobacterium virus GUmbie] ],,YP\_009018964,100.0,4.37075E-20 SIF-HHPRED: RCR ; Chitin synthesis regulation, resistance to Congo red,,,PF12273.11,50.0,71.1 SIF-Syn:

 /note=Start 52395 supported by glimmer, GM, and ST. Function NKF.

CDS 52520 - 52639

 /gene="92"

 /product="gp92"

 /function="hypothetical protein"

 /locus tag="jarcob\_92"

 /note=Original Glimmer call @bp 52520 has strength 0.89

 /note=SSC: 52520-52639 CP: yes SCS: glimmer ST: SS BLAST-Start: [hypothetical protein PBI\_LLAMA\_97 [Mycobacterium phage Llama] ],,NCBI, q1:s106 100.0% 4.28589E-20 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.925, -4.905314844093283, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_LLAMA\_97 [Mycobacterium phage Llama] ],,YP\_009209646,27.0833,4.28589E-20 SIF-HHPRED: Rad50\_zn\_hook ; Rad50 zinc hook motif,,,PF04423.17,56.4103,91.4 SIF-Syn:

 /note=Start 52520 supported by glimmer and ST. Function NKF (possible DNA binding abilities).

CDS 52636 - 52872

 /gene="93"

 /product="gp93"

 /function="hypothetical protein"

 /locus tag="jarcob\_93"

 /note=Original Glimmer call @bp 52636 has strength 3.4; Genemark calls start at 52636

 /note=SSC: 52636-52872 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein FDI15\_gp092 [Mycobacterium phage ShiLan] ],,NCBI, q1:s21 100.0% 7.21449E-49 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.824, -3.0248543014571307, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein FDI15\_gp092 [Mycobacterium phage ShiLan] ],,YP\_009608167,79.5918,7.21449E-49 SIF-HHPRED: DUF1816 ; Domain of unknown function (DUF1816),,,PF08846.13,12.8205,82.9 SIF-Syn:

 /note=Start 52636 supported by glimmer, GM, and ST. Function NKF.

CDS 52969 - 53508

 /gene="94"

 /product="gp94"

 /function="G-I-Y Y-I-G endonuclease"

 /locus tag="jarcob\_94"

 /note=Original Glimmer call @bp 52981 has strength 5.14; Genemark calls start at 52981

 /note=SSC: 52969-53508 CP: yes SCS: both-cs ST: SS BLAST-Start: [GIY-YIG DNA binding domain from nucleotide excision repair endonuclease [Mycobacterium phage SiSi] ],,NCBI, q1:s1 100.0% 1.64699E-131 GAP: 96 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.54, -4.458092987303931, yes F: G-I-Y Y-I-G endonuclease SIF-BLAST: ,,[GIY-YIG DNA binding domain from nucleotide excision repair endonuclease [Mycobacterium phage SiSi] ],,YP\_008051215,100.0,1.64699E-131 SIF-HHPRED: UvrABC system protein C; DNA BINDING PROTEIN; 1.5A {Thermotoga maritima},,,1YD0\_A,45.2514,99.5 SIF-Syn:

 /note=Start 52969 supported by ST only, but reduces gap and is LORF while maintaining good spacer, zscore, and final score. Function G-I-Y Y-I-G endonuclease supported by all SIF sources.

CDS 53505 - 54176

 /gene="95"

 /product="gp95"

 /function="hypothetical protein"

 /locus tag="jarcob\_95"

 /note=Original Glimmer call @bp 53505 has strength 5.38; Genemark calls start at 53505

 /note=SSC: 53505-54176 CP: yes SCS: both ST: SS BLAST-Start: [gp90 [Mycobacterium phage Pacc40] ],,NCBI, q1:s1 100.0% 1.8389E-162 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 3.148, -2.3719785694936077, yes F: hypothetical protein SIF-BLAST: ,,[gp90 [Mycobacterium phage Pacc40] ],,YP\_002241674,100.0,1.8389E-162 SIF-HHPRED: YjdM\_Zn\_Ribbon ; PhnA Zinc-Ribbon,,,PF08274.15,18.3857,97.0 SIF-Syn:

 /note=Start 53505 supported by glimmer, GM, and ST. Function NKF

CDS 54319 - 54465

 /gene="96"

 /product="gp96"

 /function="hypothetical protein"

 /locus tag="jarcob\_96"

 /note=Original Glimmer call @bp 54319 has strength 6.99

 /note=SSC: 54319-54465 CP: yes SCS: glimmer ST: SS BLAST-Start: [hypothetical protein PBI\_SAAL\_91 [Mycobacterium phage Saal] ],,NCBI, q1:s1 100.0% 1.39489E-25 GAP: 142 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.886, -4.967562678515084, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_SAAL\_91 [Mycobacterium phage Saal] ],,YP\_009007558,100.0,1.39489E-25 SIF-HHPRED: FYVE-finger-containing Rab5 effector protein rabenosyn-5; Rab GTPases, Rab4, Rabenosyn, effector complex, vesicular trafficking, protein transport; HET: GTP, MES; 1.92A {Homo sapiens} SCOP: a.2.19.1,,,1Z0K\_D,70.8333,94.7 SIF-Syn: BobaPhett, OlympiaSaint

 /note=Start 54319 supported by glimmer and ST. Large gap, however this is consistent with other phage genomes. Function NKF.

CDS 54462 - 54764

 /gene="97"

 /product="gp97"

 /function="hypothetical protein"

 /locus tag="jarcob\_97"

 /note=Original Glimmer call @bp 54462 has strength 7.8; Genemark calls start at 54462

 /note=SSC: 54462-54764 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_SAAL\_92 [Mycobacterium phage Saal] ],,NCBI, q1:s1 100.0% 8.92181E-64 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.999, -2.9525085049809894, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_SAAL\_92 [Mycobacterium phage Saal] ],,YP\_009007559,100.0,8.92181E-64 SIF-HHPRED: DUF2244 ; Integral membrane protein (DUF2244),,,PF10003.12,35.0,78.3 SIF-Syn:

 /note=Start 54462 supported by glimmer, GM, and ST. Function NKF

CDS 54761 - 54883

 /gene="98"

 /product="gp98"

 /function="hypothetical protein"

 /locus tag="jarcob\_98"

 /note=Original Glimmer call @bp 54761 has strength 7.79; Genemark calls start at 54761

 /note=SSC: 54761-54883 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_SAAL\_93 [Mycobacterium phage Saal] ],,NCBI, q1:s1 100.0% 1.69703E-19 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.134, -4.3913063680686815, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_SAAL\_93 [Mycobacterium phage Saal] ],,YP\_009007560,100.0,1.69703E-19 SIF-HHPRED: T\_cell\_tran\_alt ; T-cell leukemia translocation-altered,,,PF15128.9,77.5,81.5 SIF-Syn:

 /note=Start 54761 supported by GM, glimmer, and ST. Function NKF.

CDS 54892 - 55173

 /gene="99"

 /product="gp99"

 /function="hypothetical protein"

 /locus tag="jarcob\_99"

 /note=Original Glimmer call @bp 54892 has strength 10.57; Genemark calls start at 54892

 /note=SSC: 54892-55173 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_SAAL\_94 [Mycobacterium phage Saal] ],,NCBI, q1:s1 100.0% 1.52365E-62 GAP: 8 bp gap LO: no RBS: Kibler 6, Karlin Medium, 3.075, -3.3503726477288405, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_SAAL\_94 [Mycobacterium phage Saal] ],,YP\_009007561,100.0,1.52365E-62 SIF-HHPRED: PGDYG ; PGDYG protein,,,PF14083.9,93.5484,99.5 SIF-Syn:

 /note=Start 54892 supported by glimmer, GM, and ST. Function NKF.

CDS 55173 - 55373

 /gene="100"

 /product="gp100"

 /function="hypothetical protein"

 /locus tag="jarcob\_100"

 /note=Original Glimmer call @bp 55173 has strength 4.39; Genemark calls start at 55173

 /note=SSC: 55173-55373 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_SAAL\_95 [Mycobacterium phage Saal] ],,NCBI, q1:s1 100.0% 6.68324E-41 GAP: -1 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.896, -5.024743752121617, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_SAAL\_95 [Mycobacterium phage Saal] ],,YP\_009007562,100.0,6.68324E-41 SIF-HHPRED: Dynactin\_p62 ; Dynactin p62 family,,,PF05502.16,28.7879,47.1 SIF-Syn:

 /note=Start 55173 supported by glimmer, GM, and ST. Function NFK.

CDS 55370 - 55783

 /gene="101"

 /product="gp101"

 /function="hypothetical protein"

 /locus tag="jarcob\_101"

 /note=Original Glimmer call @bp 55370 has strength 7.01; Genemark calls start at 55370

 /note=SSC: 55370-55783 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein I5H61\_gp099 [Mycobacterium phage Mattes] ],,NCBI, q1:s1 100.0% 2.16768E-92 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.976, -5.371913467750883, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein I5H61\_gp099 [Mycobacterium phage Mattes] ],,YP\_009959565,100.0,2.16768E-92 SIF-HHPRED: hypothetical protein Pf0610; winged-helix like protein with metal binding site, Structural Genomics, PSI, Protein Structure Initiative, Northeast Structural Genomics; NMR {Pyrococcus furiosus} SCOP: a.4.5.82, l.1.1.1,,,2GMG\_A,45.9854,75.6 SIF-Syn:

 /note=Start 55370 supported by glimmer, GM, and ST. Function NKF.

CDS 55780 - 56022

 /gene="102"

 /product="gp102"

 /function="hypothetical protein"

 /locus tag="jarcob\_102"

 /note=Original Glimmer call @bp 55780 has strength 6.23; Genemark calls start at 55780

 /note=SSC: 55780-56022 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein BOOMER\_101 [Mycobacterium phage Boomer] ],,NCBI, q1:s1 100.0% 3.59251E-51 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.435, -5.900442475007797, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein BOOMER\_101 [Mycobacterium phage Boomer] ],,YP\_002014317,100.0,3.59251E-51 SIF-HHPRED: DUF6319 ; Family of unknown function (DUF6319),,,PF19844.2,28.75,53.7 SIF-Syn:

 /note=Start 55780 supported by glimmer, GM, and ST. Function NKF.

CDS 56015 - 56176

 /gene="103"

 /product="gp103"

 /function="hypothetical protein"

 /locus tag="jarcob\_103"

 /note=Original Glimmer call @bp 56015 has strength 6.42; Genemark calls start at 56015

 /note=SSC: 56015-56176 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_DAENERYS\_98 [Mycobacterium phage Daenerys] ],,NCBI, q1:s1 100.0% 2.04961E-30 GAP: -8 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.241, -4.231869867154326, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_DAENERYS\_98 [Mycobacterium phage Daenerys] ],,YP\_008410667,100.0,2.04961E-30 SIF-HHPRED: g.50.1.2 (A:8-70) Death associated transcription factor 1, Datf1 (DIO-1) {Mouse (Mus musculus) [TaxId: 10090]},,,d1wema1,43.3962,94.5 SIF-Syn:

 /note=Start 56015 supported by glimmer, GM, and ST. Function NKF

CDS 56203 - 57639

 /gene="104"

 /product="gp104"

 /function="glycosyltransferase"

 /locus tag="jarcob\_104"

 /note=Original Glimmer call @bp 56203 has strength 13.45; Genemark calls start at 56203

 /note=SSC: 56203-57639 CP: yes SCS: both ST: NI BLAST-Start: [polypeptide N-acetylgalactosaminyltransferase [Mycobacterium phage ShiLan] ],,NCBI, q1:s1 100.0% 0.0 GAP: 26 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.42, -4.4521226836255074, no F: glycosyltransferase SIF-BLAST: ,,[polypeptide N-acetylgalactosaminyltransferase [Mycobacterium phage ShiLan] ],,YP\_009608179,100.0,0.0 SIF-HHPRED: pp-GalNAc-T; pp-GalNAc-T initiates the formation of mucin-type O-linked glycans. UDP-GalNAc: polypeptide alpha-N-acetylgalactosaminyltransferases (pp-GalNAc-T) initiate the formation of mucin-type, O-linked glycans by catalyzing the transfer of alpha-N-acetylgalactosamine (GalNAc) from UDP-GalNAc to hydroxyl groups of Ser or Thr residues of core proteins to form the Tn antigen (GalNAc-a-1-O-Ser/Thr).,,,cd02510,45.8159,99.8 SIF-Syn: ShiLan\_104: bp 1437, polypeptide N-acetylgalactosaminyltransferase

Burwell21\_96: bp 1437, glycosyltransferase

Lizziana\_102: bp 1437, glycosyltransferase

 /note=Start 56203 supported by glimmer, GM, and ST. Function glycosyltransferase supported by all SIF sources.

CDS 57642 - 57848

 /gene="105"

 /product="gp105"

 /function="hypothetical protein"

 /locus tag="jarcob\_105"

 /note=Original Glimmer call @bp 57642 has strength 10.66; Genemark calls start at 57642

 /note=SSC: 57642-57848 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_DAENERYS\_100 [Mycobacterium phage Daenerys] ],,NCBI, q1:s1 100.0% 1.40988E-42 GAP: 2 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.492, -4.751208239442148, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_DAENERYS\_100 [Mycobacterium phage Daenerys] ],,YP\_008410669,100.0,1.40988E-42 SIF-HHPRED: ProQ\_C ; ProQ C-terminal domain,,,PF17516.5,50.0,97.7 SIF-Syn:

 /note=Start 57642 supported by glimmer, GM, and ST. Function NKF (HHPRED suggests methylase activity).

CDS 57845 - 58468

 /gene="106"

 /product="gp106"

 /function="glycosyltransferase"

 /locus tag="jarcob\_106"

 /note=Original Glimmer call @bp 57845 has strength 5.31; Genemark calls start at 57845

 /note=SSC: 57845-58468 CP: yes SCS: both ST: SS BLAST-Start: [N-acetylglucosaminyltransferase [Mycobacterium phage ShiLan] ],,NCBI, q1:s1 100.0% 5.01311E-151 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.812, -5.88628317957017, no F: glycosyltransferase SIF-BLAST: ,,[N-acetylglucosaminyltransferase [Mycobacterium phage ShiLan] ],,YP\_009608181,100.0,5.01311E-151 SIF-HHPRED: Glyco\_transf\_25 ; Glycosyltransferase family 25 (LPS biosynthesis protein),,,PF01755.20,70.0483,99.8 SIF-Syn:

 /note=Start 57845 supported by glimmer, GM, and ST. Function glycosyltransferase supported by all SIF sources.

CDS 58468 - 58794

 /gene="107"

 /product="gp107"

 /function="HNH endonuclease"

 /locus tag="jarcob\_107"

 /note=Original Glimmer call @bp 58468 has strength 1.94

 /note=SSC: 58468-58794 CP: yes SCS: glimmer ST: SS BLAST-Start: [HNH endonuclease domain protein [Mycobacterium phage ShiLan] ],,NCBI, q1:s1 100.0% 1.68704E-72 GAP: -1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 0.666, -7.957975510314596, yes F: HNH endonuclease SIF-BLAST: ,,[HNH endonuclease domain protein [Mycobacterium phage ShiLan] ],,YP\_009608182,100.0,1.68704E-72 SIF-HHPRED: HNH endonuclease; Thermophilic bacteriophage, HNH Endonuclease, DNA nicking, HYDROLASE; 1.52A {Geobacillus virus E2},,,5H0M\_A,94.4444,98.8 SIF-Syn: ShiLan\_107: bp 327, HNH endonuclease domain protein

Burwell21\_99: bp 345, HNH endonuclease domain protein

Lizziana\_105: bp 327, HNH endonuclease domain protein

 /note=Start 58468 supported by ST and glimmer. Poor CP and zscore, however, similar phage consistently called this gene so we included it. Function HNH endonuclease supported by all SIF sources.