CDS 84 - 548

 /gene="1"

 /product="gp1"

 /function="terminase, small subunit"

 /locus tag="JuneStar\_1"

 /note=Original Glimmer call @bp 84 has strength 16.71; Genemark calls start at 84

 /note=SSC: 84-548 CP: yes SCS: both ST: SS BLAST-Start: [terminase small subunit [Arthrobacter phage Yang] ],,NCBI, q1:s1 100.0% 2.13682E-104 GAP: 0 bp gap LO: no RBS: Kibler 6, Karlin Medium, 3.207, -1.953940808934884, yes F: terminase, small subunit SIF-BLAST: ,,[terminase small subunit [Arthrobacter phage Yang] ],,YP\_009815619,99.3506,2.13682E-104 SIF-HHPRED: SIF-Syn: Similar phage Yang and Cassia have a terminase, small subunit at this location.

CDS 545 - 2242

 /gene="2"

 /product="gp2"

 /function="terminase, large subunit"

 /locus tag="JuneStar\_2"

 /note=Original Glimmer call @bp 545 has strength 19.2; Genemark calls start at 545

 /note=SSC: 545-2242 CP: yes SCS: both ST: SS BLAST-Start: [terminase large subunit [Arthrobacter phage Yang] ],,NCBI, q1:s1 100.0% 0.0 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.086, -4.394706008439538, no F: terminase, large subunit SIF-BLAST: ,,[terminase large subunit [Arthrobacter phage Yang] ],,YP\_009815620,99.115,0.0 SIF-HHPRED: SIF-Syn: Similar phage Yang and Cassia have a terminase, large subunit at this location.

CDS 2262 - 3800

 /gene="3"

 /product="gp3"

 /function="portal protein"

 /locus tag="JuneStar\_3"

 /note=Original Glimmer call @bp 2262 has strength 15.6; Genemark calls start at 2262

 /note=SSC: 2262-3800 CP: yes SCS: both ST: SS BLAST-Start: [portal protein [Arthrobacter phage Cassia]],,NCBI, q1:s1 100.0% 0.0 GAP: 19 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.207, -1.953940808934884, yes F: portal protein SIF-BLAST: ,,[portal protein [Arthrobacter phage Cassia]],,WGH21076,98.0431,0.0 SIF-HHPRED: Pam1 portal proteins; Portal and adaptor proteins, VIRUS; 3.75A {unidentified},,,7EEP\_L,95.3125,99.6 SIF-Syn: Similar phages Cassia, Yang and ObiToo have a Forward (portal protein) at this location.

CDS 3816 - 5828

 /gene="4"

 /product="gp4"

 /function="Capsid maturation protease and VIP2-like ADP-ribosyltransferase toxin"

 /locus tag="JuneStar\_4"

 /note=Original Glimmer call @bp 3816 has strength 14.47; Genemark calls start at 3852

 /note=SSC: 3816-5828 CP: yes SCS: both-gl ST: SS BLAST-Start: [head maturation protease [Arthrobacter phage Yang] ],,NCBI, q1:s1 100.0% 0.0 GAP: 15 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.054, -2.338663114094478, yes F: Capsid maturation protease and VIP2-like ADP-ribosyltransferase toxin SIF-BLAST: ,,[head maturation protease [Arthrobacter phage Yang] ],,YP\_009815622,97.7612,0.0 SIF-HHPRED: SIF-Syn: Similar phages Yang and Cassia have a capsid maturation protease and VIP2-like ADP-ribosyltransferase toxin at this location.

CDS 5877 - 6236

 /gene="5"

 /product="gp5"

 /function="Hypothetical Protein"

 /locus tag="JuneStar\_5"

 /note=Original Glimmer call @bp 5877 has strength 14.83; Genemark calls start at 5877

 /note=SSC: 5877-6236 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein HOU52\_gp05 [Arthrobacter phage Yang] ],,NCBI, q1:s1 100.0% 8.40165E-73 GAP: 48 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.207, -2.0162541296952132, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein HOU52\_gp05 [Arthrobacter phage Yang] ],,YP\_009815623,95.7983,8.40165E-73 SIF-HHPRED: SIF-Syn: This gene is similar to a hypothetical protein found in Yang and Cassia.

CDS 6355 - 6909

 /gene="6"

 /product="gp6"

 /function="scaffolding protein"

 /locus tag="JuneStar\_6"

 /note=Original Glimmer call @bp 6355 has strength 16.12; Genemark calls start at 6355

 /note=SSC: 6355-6909 CP: no SCS: both ST: SS BLAST-Start: [head scaffolding protein [Arthrobacter phage Yang] ],,NCBI, q1:s1 100.0% 5.73675E-118 GAP: 118 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.974, -3.3503726477288405, yes F: scaffolding protein SIF-BLAST: ,,[head scaffolding protein [Arthrobacter phage Yang] ],,YP\_009815624,97.8378,5.73675E-118 SIF-HHPRED: SIF-Syn: Similar phage Yang has a forward scaffolding protein at this location.

CDS 6936 - 7883

 /gene="7"

 /product="gp7"

 /function="major capsid protein"

 /locus tag="JuneStar\_7"

 /note=Original Glimmer call @bp 6936 has strength 16.23; Genemark calls start at 6936

 /note=SSC: 6936-7883 CP: yes SCS: both ST: SS BLAST-Start: [major head protein [Arthrobacter phage Yang] ],,NCBI, q1:s1 100.0% 0.0 GAP: 26 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.11, -2.8084998623841946, yes F: major capsid protein SIF-BLAST: ,,[major head protein [Arthrobacter phage Yang] ],,YP\_009815625,97.1429,0.0 SIF-HHPRED: Major capsid protein; P22 Bacteriophage, VIRUS; 3.3A {Salmonella phage P22},,,5UU5\_B,92.6984,100.0 SIF-Syn: Similar phages Yang, Crewmate and VResidence have a Forward (major capsid protein) at this location.

CDS 7957 - 8352

 /gene="8"

 /product="gp8"

 /function="head-to-tail adaptor"

 /locus tag="JuneStar\_8"

 /note=Original Glimmer call @bp 7957 has strength 13.54; Genemark calls start at 7957

 /note=SSC: 7957-8352 CP: yes SCS: both ST: SS BLAST-Start: [head-to-tail adaptor [Arthrobacter phage Cassia]],,NCBI, q1:s1 100.0% 1.48571E-77 GAP: 73 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.207, -2.0162541296952132, yes F: head-to-tail adaptor SIF-BLAST: ,,[head-to-tail adaptor [Arthrobacter phage Cassia]],,WGH21081,94.6565,1.48571E-77 SIF-HHPRED: SIF-Syn: This protein function matched up with Cassia and similarly related phage protein functions.

CDS 8364 - 8477

 /gene="9"

 /product="gp9"

 /function="Hypothetical Protein"

 /locus tag="JuneStar\_9"

 /note=Original Glimmer call @bp 8364 has strength 19.01; Genemark calls start at 8364

 /note=SSC: 8364-8477 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein HOU52\_gp09 [Arthrobacter phage Yang] ],,NCBI, q1:s1 100.0% 2.21807E-13 GAP: 11 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.054, -2.2763497933341483, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein HOU52\_gp09 [Arthrobacter phage Yang] ],,YP\_009815627,94.5946,2.21807E-13 SIF-HHPRED: SIF-Syn: This gene is similar to a hypothetical protein found in Yang.

CDS 8474 - 8821

 /gene="10"

 /product="gp10"

 /function="head-to-tail stopper"

 /locus tag="JuneStar\_10"

 /note=Original Glimmer call @bp 8474 has strength 19.8; Genemark calls start at 8474

 /note=SSC: 8474-8821 CP: yes SCS: both ST: SS BLAST-Start: [head closure Hc1 [Arthrobacter phage Yang] ],,NCBI, q1:s1 100.0% 3.46807E-67 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.523, -3.534757715066017, yes F: head-to-tail stopper SIF-BLAST: ,,[head closure Hc1 [Arthrobacter phage Yang] ],,YP\_009815628,93.0435,3.46807E-67 SIF-HHPRED: Stopper protein Rcc01689; "neck", "portal", "capsid", "tail tube", VIRUS; 3.58A {Rhodobacter capsulatus},,,6TE9\_E,96.5217,99.7 SIF-Syn: Similar phage Yang has a Forward (head-to-tail stopper) at this location.

CDS 8833 - 9135

 /gene="11"

 /product="gp11"

 /function="Hypothetical Protein"

 /locus tag="JuneStar\_11"

 /note=Original Glimmer call @bp 8833 has strength 11.21; Genemark calls start at 8833

 /note=SSC: 8833-9135 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein HOU52\_gp11 [Arthrobacter phage Yang] ],,NCBI, q1:s1 100.0% 7.26681E-61 GAP: 11 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.207, -2.033982896655645, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein HOU52\_gp11 [Arthrobacter phage Yang] ],,YP\_009815629,99.0,7.26681E-61 SIF-HHPRED: SIF-Syn: The hypothetical protein function is not closely related to any similar phages.

CDS 9135 - 9548

 /gene="12"

 /product="gp12"

 /function="tail terminator"

 /locus tag="JuneStar\_12"

 /note=Original Glimmer call @bp 9135 has strength 13.21; Genemark calls start at 9135

 /note=SSC: 9135-9548 CP: yes SCS: both ST: SS BLAST-Start: [tail terminator [Arthrobacter phage Yang] ],,NCBI, q1:s1 100.0% 1.80519E-88 GAP: -1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.506, -3.430952136556091, yes F: tail terminator SIF-BLAST: ,,[tail terminator [Arthrobacter phage Yang] ],,YP\_009815630,97.0803,1.80519E-88 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,93.4307,99.4 SIF-Syn: Similar phages Yang, Nitro, Ascela and Phives have a Forward (tail terminator) at this location.

CDS 9561 - 10112

 /gene="13"

 /product="gp13"

 /function="major tail protein"

 /locus tag="JuneStar\_13"

 /note=Original Glimmer call @bp 9561 has strength 18.76; Genemark calls start at 9561

 /note=SSC: 9561-10112 CP: yes SCS: both ST: SS BLAST-Start: [major tail protein [Arthrobacter phage Yang] ],,NCBI, q1:s1 100.0% 4.97036E-125 GAP: 12 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.217, -2.0720764396375664, yes F: major tail protein SIF-BLAST: ,,[major tail protein [Arthrobacter phage Yang] ],,YP\_009815631,97.2678,4.97036E-125 SIF-HHPRED: YSD1\_22 major tail protein; Bacteriophage tail, helical assembly, VIRAL PROTEIN; 3.5A {Bacteriophage sp.},,,6XGR\_M,93.4426,98.6 SIF-Syn: Similar phages Yang, Cassia and Adumb2043 have a Forward (major tail protein) at this location.

CDS 10206 - 10472

 /gene="14"

 /product="gp14"

 /function="tail assembly chaperone"

 /locus tag="JuneStar\_14"

 /note=Original Glimmer call @bp 10206 has strength 19.54; Genemark calls start at 10206

 /note=SSC: 10206-10472 CP: yes SCS: both ST: SS BLAST-Start: [tail assembly chaperone [Arthrobacter phage Cassia]],,NCBI, q1:s1 100.0% 5.75269E-54 GAP: 93 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.217, -2.2821867859826788, yes F: tail assembly chaperone SIF-BLAST: ,,[tail assembly chaperone [Arthrobacter phage Cassia]],,WGH21087,98.8636,5.75269E-54 SIF-HHPRED: Phage\_TAC\_8 ; Phage tail assembly chaperone protein Gp14 ()A118,,,PF10666.13,94.3182,94.5 SIF-Syn: Similar phage to Cassia and Phage\_TAC\_8. Indicates it is a tail assembly chaperone gene.

CDS 10511 - 10807

 /gene="15"

 /product="gp15"

 /function="tail assembly chaperone"

 /locus tag="JuneStar\_15"

 /note=Original Glimmer call @bp 10511 has strength 10.49; Genemark calls start at 10511

 /note=SSC: 10511-10807 CP: yes SCS: both ST: SS BLAST-Start: [tail assembly chaperone [Arthrobacter phage Yang] ],,NCBI, q1:s104 100.0% 9.79901E-61 GAP: 38 bp gap LO: no RBS: Kibler 6, Karlin Medium, 0.681, -7.627551051726395, yes F: tail assembly chaperone SIF-BLAST: ,,[tail assembly chaperone [Arthrobacter phage Yang] ],,YP\_009815632,47.7612,9.79901E-61 SIF-HHPRED: SIF-Syn: Phage similar to Yang and Cassia. Indicates it is a tail assembly chaperone gene. However, this gene does not reach the desired threshold for either HHPRED or NCBI BLAST.

CDS 10824 - 13148

 /gene="16"

 /product="gp16"

 /function="tape measure protein"

 /locus tag="JuneStar\_16"

 /note=Original Glimmer call @bp 10824 has strength 20.32; Genemark calls start at 10824

 /note=SSC: 10824-13148 CP: yes SCS: both ST: SS BLAST-Start: [tail length tape measure protein [Arthrobacter phage Yang] ],,NCBI, q1:s1 100.0% 0.0 GAP: 16 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.207, -2.86135216970947, yes F: tape measure protein SIF-BLAST: ,,[tail length tape measure protein [Arthrobacter phage Yang] ],,YP\_009815634,98.3204,0.0 SIF-HHPRED: SIF-Syn: Phage similar to Yang. Indicates is a tape measure protein gene.

CDS 13141 - 14016

 /gene="17"

 /product="gp17"

 /function="minor tail protein"

 /locus tag="JuneStar\_17"

 /note=Original Glimmer call @bp 13141 has strength 16.65; Genemark calls start at 13141

 /note=SSC: 13141-14016 CP: yes SCS: both ST: SS BLAST-Start: [minor tail protein [Arthrobacter phage Yang] ],,NCBI, q1:s1 100.0% 0.0 GAP: -8 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.821, -2.7653702713535186, yes F: minor tail protein SIF-BLAST: ,,[minor tail protein [Arthrobacter phage Yang] ],,YP\_009815635,98.6254,0.0 SIF-HHPRED: HYPOTHETICAL PROTEIN 19.1; VIRAL PROTEIN, DISTAL TAIL PROTEIN; 2.95A {BACILLUS PHAGE SPP1},,,2X8K\_C,98.9691,100.0 SIF-Syn: Phage similar to Yang. Indicates this likely a minor tail protein gene.

CDS 14029 - 15024

 /gene="18"

 /product="gp18"

 /function="minor tail protein"

 /locus tag="JuneStar\_18"

 /note=Original Glimmer call @bp 14029 has strength 15.53; Genemark calls start at 14029

 /note=SSC: 14029-15024 CP: yes SCS: both ST: SS BLAST-Start: [minor tail protein [Arthrobacter phage Cassia]],,NCBI, q1:s1 100.0% 0.0 GAP: 12 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.217, -2.0720764396375664, yes F: minor tail protein SIF-BLAST: ,,[minor tail protein [Arthrobacter phage Cassia]],,WGH21091,99.3958,0.0 SIF-HHPRED: SIF-Syn: Phage similar to Cassia. Indicates it is minor tail protein gene.

CDS 15024 - 16145

 /gene="19"

 /product="gp19"

 /function="minor tail protein"

 /locus tag="JuneStar\_19"

 /note=Original Glimmer call @bp 15024 has strength 19.47; Genemark calls start at 15024

 /note=SSC: 15024-16145 CP: yes SCS: both ST: SS BLAST-Start: [minor tail protein [Arthrobacter phage Yang] ],,NCBI, q1:s1 100.0% 0.0 GAP: -1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.316, -3.9718914447963414, yes F: minor tail protein SIF-BLAST: ,,[minor tail protein [Arthrobacter phage Yang] ],,YP\_009815637,98.3914,0.0 SIF-HHPRED: SIF-Syn: Similar phage to Cassia and Yang. Indicates it is a minor tail protein gene.

CDS 16151 - 19756

 /gene="20"

 /product="gp20"

 /function="Hypothetical Protein"

 /locus tag="JuneStar\_20"

 /note=Original Glimmer call @bp 16151 has strength 11.03; Genemark calls start at 16151

 /note=SSC: 16151-19756 CP: yes SCS: both ST: SS BLAST-Start: [tail protein [Arthrobacter phage Yang] ],,NCBI, q454:s219 62.2814% 0.0 GAP: 5 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.67, -3.7378191248686026, yes F: Hypothetical Protein SIF-BLAST: ,,[tail protein [Arthrobacter phage Yang] ],,YP\_009815638,70.6308,0.0 SIF-HHPRED: SIF-Syn: This gene is not similar to known genes.

CDS 19765 - 20106

 /gene="21"

 /product="gp21"

 /function="Hypothetical Protein"

 /locus tag="JuneStar\_21"

 /note=Original Glimmer call @bp 19765 has strength 13.42; Genemark calls start at 19765

 /note=SSC: 19765-20106 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PQE14\_gp21 [Arthrobacter phage Kaylissa] ],,NCBI, q1:s1 100.0% 1.18552E-58 GAP: 8 bp gap LO: no RBS: Kibler 6, Karlin Medium, 3.217, -2.45827804503836, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein PQE14\_gp21 [Arthrobacter phage Kaylissa] ],,YP\_010678067,90.2655,1.18552E-58 SIF-HHPRED: SIF-Syn: This gene is not similar to known genes.

CDS 20113 - 20385

 /gene="22"

 /product="gp22"

 /function="Hypothetical Protein"

 /locus tag="JuneStar\_22"

 /note=Original Glimmer call @bp 20113 has strength 10.24; Genemark calls start at 20113

 /note=SSC: 20113-20385 CP: yes SCS: both ST: SS BLAST-Start: [membrane protein [Arthrobacter phage Cassia]],,NCBI, q1:s1 100.0% 2.44906E-57 GAP: 6 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.594, -4.345350014007458, yes F: Hypothetical Protein SIF-BLAST: ,,[membrane protein [Arthrobacter phage Cassia]],,WGH21095,100.0,2.44906E-57 SIF-HHPRED: SIF-Syn: Phage similar to Yang and Cassia. Indicates it is a hypothetical/membrane protein.

CDS 20394 - 20642

 /gene="23"

 /product="gp23"

 /function="Hypothetical Protein"

 /locus tag="JuneStar\_23"

 /note=Original Glimmer call @bp 20394 has strength 14.67; Genemark calls start at 20394

 /note=SSC: 20394-20642 CP: yes SCS: both ST: SS BLAST-Start: [membrane protein [Arthrobacter phage Crewmate] ],,NCBI, q1:s1 100.0% 2.60826E-40 GAP: 8 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.313, -3.9166971242758706, yes F: Hypothetical Protein SIF-BLAST: ,,[membrane protein [Arthrobacter phage Crewmate] ],,YP\_010678275,92.6829,2.60826E-40 SIF-HHPRED: SIF-Syn: This gene is not similar to known genes.

CDS 20659 - 22146

 /gene="24"

 /product="gp24"

 /function="endolysin"

 /locus tag="JuneStar\_24"

 /note=Original Glimmer call @bp 20659 has strength 12.97; Genemark calls start at 20659

 /note=SSC: 20659-22146 CP: yes SCS: both ST: SS BLAST-Start: [tail length tape measure protein [Arthrobacter phage Elezi] ],,NCBI, q1:s1 99.1919% 0.0 GAP: 16 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.207, -2.4811409279978642, yes F: endolysin SIF-BLAST: ,,[tail length tape measure protein [Arthrobacter phage Elezi] ],,YP\_010678003,82.3293,0.0 SIF-HHPRED: SIF-Syn: Phage similar to Elezi. Indicates it is an endolysin gene. However, it does not meet the threshold in HHPRED and NCBI BLAST.

 /note=Cluster AZ tips identifies that these phages have one of 3 patterns for the endolysin. JuneStar seems to follow the pattern found in Phage Elezi, and have the endolysin in the middle (around gene 24)

CDS 22282 - 22896

 /gene="25"

 /product="gp25"

 /function="deoxynucleoside monophosphate kinase"

 /locus tag="JuneStar\_25"

 /note=Original Glimmer call @bp 22282 has strength 18.64; Genemark calls start at 22282

 /note=SSC: 22282-22896 CP: yes SCS: both ST: SS BLAST-Start: [adenylate kinase [Arthrobacter phage Yang] ],,NCBI, q1:s1 100.0% 5.03061E-130 GAP: 135 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.821, -2.827683592113848, yes F: deoxynucleoside monophosphate kinase SIF-BLAST: ,,[adenylate kinase [Arthrobacter phage Yang] ],,YP\_009815642,94.1176,5.03061E-130 SIF-HHPRED: DEOXYNUCLEOSIDE MONOPHOSPHATE KINASE; TRANSFERASE, PHOSPHOTRANSFERASE; HET: DGP, OCS; 2.0A {Enterobacteria phage T4} SCOP: c.37.1.1,,,1DEK\_A,93.1373,99.8 SIF-Syn: Phage similar to Yang. Indicates it is a DEOXYNUCLEOSIDE MONOPHOSPHATE KINASE gene.

CDS 22999 - 23568

 /gene="26"

 /product="gp26"

 /function="Hypothetical Protein"

 /locus tag="JuneStar\_26"

 /note=Original Glimmer call @bp 22999 has strength 12.1; Genemark calls start at 22999

 /note=SSC: 22999-23568 CP: yes SCS: both ST: SS BLAST-Start: GAP: 102 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.076, -5.38624690435742, yes F: Hypothetical Protein SIF-BLAST: SIF-HHPRED: SIF-Syn: This gene is not similar to any known function in related phages.

CDS 23759 - 24592

 /gene="27"

 /product="gp27"

 /function="exonuclease"

 /locus tag="JuneStar\_27"

 /note=Original Glimmer call @bp 23759 has strength 16.16; Genemark calls start at 23774

 /note=SSC: 23759-24592 CP: yes SCS: both-gl ST: SS BLAST-Start: [exonuclease [Arthrobacter phage Yang] ],,NCBI, q1:s1 99.639% 0.0 GAP: 190 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.974, -2.442961286954254, yes F: exonuclease SIF-BLAST: ,,[exonuclease [Arthrobacter phage Yang] ],,YP\_009815644,98.9209,0.0 SIF-HHPRED: SIF-Syn: Similar phages Yang, Lizalica, and Crewmate found this gene to be an exonuclease.

CDS 24589 - 24957

 /gene="28"

 /product="gp28"

 /function="nucleoside deoxyribosyltransferase"

 /locus tag="JuneStar\_28"

 /note=Original Glimmer call @bp 24589 has strength 7.57; Genemark calls start at 24613

 /note=SSC: 24589-24957 CP: yes SCS: both-gl ST: SS BLAST-Start: [nucleoside 2-deoxyribosyltransferase [Arthrobacter phage Yang] ],,NCBI, q1:s1 100.0% 9.54083E-76 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.255, -4.309531045980963, yes F: nucleoside deoxyribosyltransferase SIF-BLAST: ,,[nucleoside 2-deoxyribosyltransferase [Arthrobacter phage Yang] ],,YP\_009815646,97.541,9.54083E-76 SIF-HHPRED: SIF-Syn: Similar phages, Yang and ObiToo, found this gene to be a nucleoside deoxyribosyltransferase.

CDS 24954 - 25358

 /gene="29"

 /product="gp29"

 /function="HNH endonuclease"

 /locus tag="JuneStar\_29"

 /note=Original Glimmer call @bp 24954 has strength 14.87; Genemark calls start at 24954

 /note=SSC: 24954-25358 CP: yes SCS: both ST: SS BLAST-Start: [HNH endonuclease [Arthrobacter phage Crewmate] ],,NCBI, q1:s1 100.0% 1.5293E-91 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.496, -3.513874779476501, yes F: HNH endonuclease SIF-BLAST: ,,[HNH endonuclease [Arthrobacter phage Crewmate] ],,YP\_010678283,100.0,1.5293E-91 SIF-HHPRED: SIF-Syn: Similar phages such as ObiToo, Adumb2043, and Asa16, all found this gene to be HNH endonuclease.

CDS 25484 - 26197

 /gene="30"

 /product="gp30"

 /function="recombination directionality factor"

 /locus tag="JuneStar\_30"

 /note=Original Glimmer call @bp 25484 has strength 17.67; Genemark calls start at 25484

 /note=SSC: 25484-26197 CP: yes SCS: both ST: SS BLAST-Start: [unknown function [Arthrobacter phage Kaylissa] ],,NCBI, q1:s1 100.0% 9.24014E-168 GAP: 125 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.201, -4.423424636048095, no F: recombination directionality factor SIF-BLAST: ,,[unknown function [Arthrobacter phage Kaylissa] ],,YP\_010678075,99.5781,9.24014E-168 SIF-HHPRED: SIF-Syn: Similar phages, Lego, JohnDoe, Yang, and Kaylissa, all found this gene to be recombination directionality factor.

CDS 26197 - 26334

 /gene="31"

 /product="gp31"

 /function="Hypothetical Protein"

 /locus tag="JuneStar\_31"

 /note=Original Glimmer call @bp 26197 has strength 22.31; Genemark calls start at 26197

 /note=SSC: 26197-26334 CP: yes SCS: both ST: SS BLAST-Start: [membrane protein [Arthrobacter phage Warda] ],,NCBI, q1:s1 100.0% 1.47321E-20 GAP: -1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.086, -4.455662434380964, yes F: Hypothetical Protein SIF-BLAST: ,,[membrane protein [Arthrobacter phage Warda] ],,YP\_010677870,100.0,1.47321E-20 SIF-HHPRED: SIF-Syn: This gene has a 100% match to the hypothetical protein in the phage Warda.

CDS 26409 - 26759

 /gene="32"

 /product="gp32"

 /function="Hypothetical Protein"

 /locus tag="JuneStar\_32"

 /note=Original Glimmer call @bp 26409 has strength 12.27; Genemark calls start at 26409

 /note=SSC: 26409-26759 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PQE14\_gp32 [Arthrobacter phage Kaylissa] ],,NCBI, q1:s1 100.0% 1.67029E-77 GAP: 74 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.974, -2.442961286954254, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein PQE14\_gp32 [Arthrobacter phage Kaylissa] ],,YP\_010678078,98.2759,1.67029E-77 SIF-HHPRED: SIF-Syn: This gene is similar to a hypothetical protein in Kaylissa, YesChef, and JohnDoe.

CDS 26763 - 27023

 /gene="33"

 /product="gp33"

 /function="NrdH-like glutaredoxin"

 /locus tag="JuneStar\_33"

 /note=Original Glimmer call @bp 26763 has strength 16.06; Genemark calls start at 26763

 /note=SSC: 26763-27023 CP: yes SCS: both ST: SS BLAST-Start: [thioredoxin domain [Arthrobacter phage Kaylissa] ],,NCBI, q1:s1 93.0233% 8.87713E-51 GAP: 3 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.821, -3.6727816321281046, yes F: NrdH-like glutaredoxin SIF-BLAST: ,,[thioredoxin domain [Arthrobacter phage Kaylissa] ],,YP\_010678079,97.5,8.87713E-51 SIF-HHPRED: SIF-Syn: Similar phages, YesChef and Kaylissa, found this gene to be NrdH-like glutaredoxin.

CDS 27010 - 27216

 /gene="34"

 /product="gp34"

 /function="Hypothetical Protein"

 /locus tag="JuneStar\_34"

 /note=Original Glimmer call @bp 27010 has strength 14.58; Genemark calls start at 27010

 /note=SSC: 27010-27216 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_NITRO\_34 [Arthrobacter phage Nitro]],,NCBI, q3:s4 97.0588% 1.00973E-29 GAP: -14 bp gap LO: no RBS: Kibler 6, Karlin Medium, 3.054, -2.338663114094478, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_NITRO\_34 [Arthrobacter phage Nitro]],,WNN93990,86.9565,1.00973E-29 SIF-HHPRED: SIF-Syn: This gene is not similar to any known genes in related phages.

CDS 27209 - 27409

 /gene="35"

 /product="gp35"

 /function="Hypothetical Protein"

 /locus tag="JuneStar\_35"

 /note=Original Glimmer call @bp 27209 has strength 19.32; Genemark calls start at 27209

 /note=SSC: 27209-27409 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_CASSIA\_35 [Arthrobacter phage Cassia]],,NCBI, q1:s1 96.9697% 2.10233E-31 GAP: -8 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.974, -2.5052746077145835, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_CASSIA\_35 [Arthrobacter phage Cassia]],,WGH21108,89.5522,2.10233E-31 SIF-HHPRED: SIF-Syn: This gene is not similar to any known genes in related phages.

CDS 27406 - 27636

 /gene="36"

 /product="gp36"

 /function="Hypothetical Protein"

 /locus tag="JuneStar\_36"

 /note=Original Glimmer call @bp 27406 has strength 14.53; Genemark calls start at 27406

 /note=SSC: 27406-27636 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein HOU52\_gp35 [Arthrobacter phage Yang] ],,NCBI, q1:s1 100.0% 4.90034E-46 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.594, -3.2441186272167593, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein HOU52\_gp35 [Arthrobacter phage Yang] ],,YP\_009815653,100.0,4.90034E-46 SIF-HHPRED: SIF-Syn: This gene has a 100% match to a hypothetical protein in Yang.

CDS 27633 - 27992

 /gene="37"

 /product="gp37"

 /function="Holliday junction resolvase"

 /locus tag="JuneStar\_37"

 /note=Original Glimmer call @bp 27633 has strength 15.21; Genemark calls start at 27633

 /note=SSC: 27633-27992 CP: no SCS: both ST: SS BLAST-Start: [RusA-like Holliday junction resolvase [Arthrobacter phage Crewmate] ],,NCBI, q1:s1 100.0% 4.85878E-77 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.873, -4.763756451838196, yes F: Holliday junction resolvase SIF-BLAST: ,,[RusA-like Holliday junction resolvase [Arthrobacter phage Crewmate] ],,YP\_010678292,97.5,4.85878E-77 SIF-HHPRED: SIF-Syn: Similar phages, ObiToo, Yang, Cassia, and Crewmate, all called this gene Holliday junction resolvase.

CDS complement (27959 - 28123)

 /gene="38"

 /product="gp38"

 /function="Hypothetical Protein"

 /locus tag="JuneStar\_38"

 /note=Genemark calls start at 28123

 /note=SSC: 28123-27959 CP: yes SCS: genemark ST: SS BLAST-Start: [hypothetical protein PQE17\_gp42 [Arthrobacter phage Crewmate] ],,NCBI, q1:s1 98.1481% 1.93669E-23 GAP: 199 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.957, -3.5288488554554966, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein PQE17\_gp42 [Arthrobacter phage Crewmate] ],,YP\_010678293,87.2727,1.93669E-23 SIF-HHPRED: SIF-Syn: This gene is not similar to any known genes in related phages.

 /note=No evidence for function, not similar to other proteins.

CDS 28323 - 30806

 /gene="39"

 /product="gp39"

 /function="DNA primase/helicase"

 /locus tag="JuneStar\_39"

 /note=Original Glimmer call @bp 28323 has strength 15.38; Genemark calls start at 28323

 /note=SSC: 28323-30806 CP: yes SCS: both ST: SS BLAST-Start: [DNA primase [Arthrobacter phage Yang] ],,NCBI, q1:s1 100.0% 0.0 GAP: 199 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.974, -2.442961286954254, yes F: DNA primase/helicase SIF-BLAST: ,,[DNA primase [Arthrobacter phage Yang] ],,YP\_009815656,97.2222,0.0 SIF-HHPRED: SIF-Syn: Similar phage, Yang, called this function as DNA primase/helicase.

CDS 30816 - 30926

 /gene="40"

 /product="gp40"

 /function="Hypothetical Protein"

 /locus tag="JuneStar\_40"

 /note=Genemark calls start at 30816

 /note=SSC: 30816-30926 CP: yes SCS: genemark ST: SS BLAST-Start: [hypothetical protein PQE18\_gp37 [Arthrobacter phage DrSierra] ],,NCBI, q1:s2 100.0% 1.81893E-13 GAP: 9 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.081, -4.325675514574479, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein PQE18\_gp37 [Arthrobacter phage DrSierra] ],,YP\_010678362,91.8919,1.81893E-13 SIF-HHPRED: SIF-Syn: Protein is not above the 90 percent match with any similar phage protein functions.

CDS 30926 - 31048

 /gene="41"

 /product="gp41"

 /function="Hypothetical Protein"

 /locus tag="JuneStar\_41"

 /note=Original Glimmer call @bp 30926 has strength 8.09

 /note=SSC: 30926-31048 CP: yes SCS: glimmer ST: SS BLAST-Start: [hypothetical protein HOU52\_gp40 [Arthrobacter phage Yang] ],,NCBI, q1:s1 100.0% 4.08624E-18 GAP: -1 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.695, -5.966914258667748, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein HOU52\_gp40 [Arthrobacter phage Yang] ],,YP\_009815658,100.0,4.08624E-18 SIF-HHPRED: SIF-Syn: Protein is not above the 90 percent match with any similar phage protein functions such as Yang.

CDS 31105 - 33111

 /gene="42"

 /product="gp42"

 /function="DNA polymerase I"

 /locus tag="JuneStar\_42"

 /note=Original Glimmer call @bp 31105 has strength 20.81; Genemark calls start at 31105

 /note=SSC: 31105-33111 CP: yes SCS: both ST: SS BLAST-Start: [DNA polymerase I [Arthrobacter phage Yang] ],,NCBI, q44:s20 93.5629% 0.0 GAP: 56 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.011, -5.000302397801194, no F: DNA polymerase I SIF-BLAST: ,,[DNA polymerase I [Arthrobacter phage Yang] ],,YP\_009815659,94.0994,0.0 SIF-HHPRED: SIF-Syn: Similar phage Yang has similar protein function of DNA polymerase I.

CDS 33108 - 33290

 /gene="43"

 /product="gp43"

 /function="Hypothetical Protein"

 /locus tag="JuneStar\_43"

 /note=Original Glimmer call @bp 33138 has strength 14.84; Genemark calls start at 33138

 /note=SSC: 33108-33290 CP: yes SCS: both-cs ST: NA BLAST-Start: [hypothetical protein PQE12\_gp39 [Arthrobacter phage Adumb2043] ],,NCBI, q1:s1 96.6667% 3.40328E-28 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.591, -5.4987073736983305, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein PQE12\_gp39 [Arthrobacter phage Adumb2043] ],,YP\_010677949,88.3333,3.40328E-28 SIF-HHPRED: SIF-Syn: This gene is not closely similar to any gene in related phages.

 /note=Coding potential begins before suggested start site. This start has a -4 bp overlap.

CDS 33287 - 33589

 /gene="44"

 /product="gp44"

 /function="DNA ligase"

 /locus tag="JuneStar\_44"

 /note=Original Glimmer call @bp 33287 has strength 13.9; Genemark calls start at 33287

 /note=SSC: 33287-33589 CP: yes SCS: both ST: SS BLAST-Start: [DNA ligase [Arthrobacter phage Yang] ],,NCBI, q1:s1 100.0% 1.45413E-63 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.498, -3.7976476850020884, yes F: DNA ligase SIF-BLAST: ,,[DNA ligase [Arthrobacter phage Yang] ],,YP\_009815660,98.0,1.45413E-63 SIF-HHPRED: SIF-Syn: Similar phage Yang and Cassia share a similar protein function of DNA ligase in a close area match.

CDS 33586 - 33891

 /gene="45"

 /product="gp45"

 /function="Hypothetical Protein"

 /locus tag="JuneStar\_45"

 /note=Original Glimmer call @bp 33586 has strength 15.76; Genemark calls start at 33586

 /note=SSC: 33586-33891 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein HOU52\_gp43 [Arthrobacter phage Yang] ],,NCBI, q1:s1 100.0% 4.84848E-59 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.723, -5.080915947802713, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein HOU52\_gp43 [Arthrobacter phage Yang] ],,YP\_009815661,95.0495,4.84848E-59 SIF-HHPRED: SIF-Syn: Protein is not above the 90 percent match with any similar phage protein functions.

CDS 34096 - 34911

 /gene="46"

 /product="gp46"

 /function="DNA binding protein"

 /locus tag="JuneStar\_46"

 /note=Original Glimmer call @bp 34096 has strength 16.18; Genemark calls start at 34096

 /note=SSC: 34096-34911 CP: yes SCS: both ST: SS BLAST-Start: [RNA polymerase [Arthrobacter phage Yang] ],,NCBI, q1:s1 100.0% 0.0 GAP: 204 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.878, -2.7863799983944713, yes F: DNA binding protein SIF-BLAST: ,,[RNA polymerase [Arthrobacter phage Yang] ],,YP\_009815662,100.0,0.0 SIF-HHPRED: RNA polymerase sigma factor RpoS; Transcription-activator, DNA/RNA, SigmaS, beta`, TRANSCRIPTION, Transferase-DNA complex; 3.26A {Escherichia coli},,,6OMF\_F,97.048,100.0 SIF-Syn: Shares a similar protein function of DNA binging protein with phage Yang.

 /note=According to Offical Functions list: A misinterpretation of crystal structure chains lead to the mis-assignment of Zetzy1847 gene 42 as DNA directed RNA polymerase.

CDS 34996 - 35661

 /gene="47"

 /product="gp47"

 /function="Hypothetical Protein"

 /locus tag="JuneStar\_47"

 /note=Original Glimmer call @bp 34996 has strength 12.73; Genemark calls start at 34996

 /note=SSC: 34996-35661 CP: yes SCS: both ST: SS BLAST-Start: [endonuclease [Arthrobacter phage Phives] ],,NCBI, q1:s1 100.0% 2.97464E-106 GAP: 84 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.723, -5.160958035523474, no F: Hypothetical Protein SIF-BLAST: ,,[endonuclease [Arthrobacter phage Phives] ],,YP\_010677682,81.0811,2.97464E-106 SIF-HHPRED: SIF-Syn: This gene is not closely similar to any gene in related phages.

CDS 35661 - 36011

 /gene="48"

 /product="gp48"

 /function="DNA binding protein"

 /locus tag="JuneStar\_48"

 /note=Original Glimmer call @bp 35661 has strength 17.2; Genemark calls start at 35661

 /note=SSC: 35661-36011 CP: yes SCS: both ST: SS BLAST-Start: [DNA binding protein [Arthrobacter phage Yang] ],,NCBI, q1:s1 100.0% 1.57875E-69 GAP: -1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.929, -4.787182377296497, no F: DNA binding protein SIF-BLAST: ,,[DNA binding protein [Arthrobacter phage Yang] ],,YP\_009815664,92.2414,1.57875E-69 SIF-HHPRED: HTH-type transcriptional regulator gadX; PSI2, MCSG, structural genomics, Protein Structure Initiative, Midwest Center for Structural Genomics, DNA-binding protein, transcriptional dual; HET: MSE; 2.15A {Escherichia coli},,,3MKL\_B,90.5172,97.6 SIF-Syn: Shares a similar protein function of DNA binging protein with phage Yang.

CDS 36072 - 37253

 /gene="49"

 /product="gp49"

 /function="Hypothetical Protein"

 /locus tag="JuneStar\_49"

 /note=Original Glimmer call @bp 36072 has strength 15.3; Genemark calls start at 36072

 /note=SSC: 36072-37253 CP: yes SCS: both ST: SS BLAST-Start: [DNA methyltransferase [Arthrobacter phage MaGuCo]],,NCBI, q1:s4 100.0% 0.0 GAP: 60 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.496, -3.4515614587161716, no F: Hypothetical Protein SIF-BLAST: ,,[DNA methyltransferase [Arthrobacter phage MaGuCo]],,WGH20337,87.6263,0.0 SIF-HHPRED: DNA (cytosine-5)-methyltransferase 1; DNMT1, DNA methytransferase1, DNA methylation, TRANSFERASE; HET: ZN, SAH; 2.622A {Homo sapiens},,,4WXX\_A,99.4911,100.0 SIF-Syn: The protein function is not above the 90 percent match with any similar phage protein functions in closely matched phage MaGuCo.

CDS 37385 - 37981

 /gene="50"

 /product="gp50"

 /function="SprT-like protease"

 /locus tag="JuneStar\_50"

 /note=Original Glimmer call @bp 37385 has strength 15.57; Genemark calls start at 37385

 /note=SSC: 37385-37981 CP: yes SCS: both ST: SS BLAST-Start: [SprT-like domain-containing protein [Arthrobacter phage Yang] ],,NCBI, q1:s1 100.0% 8.70864E-140 GAP: 131 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.878, -2.707694805492614, yes F: SprT-like protease SIF-BLAST: ,,[SprT-like domain-containing protein [Arthrobacter phage Yang] ],,YP\_009815666,98.4848,8.70864E-140 SIF-HHPRED: SIF-Syn: Shares a similar protein function SprT-like protease with phages Yang and Cassia protein functions.

CDS 38077 - 39495

 /gene="51"

 /product="gp51"

 /function="serine integrase"

 /locus tag="JuneStar\_51"

 /note=Original Glimmer call @bp 38077 has strength 17.41; Genemark calls start at 38074

 /note=SSC: 38077-39495 CP: yes SCS: both-gl ST: SS BLAST-Start: [integrase [Arthrobacter phage Yang] ],,NCBI, q1:s1 100.0% 0.0 GAP: 95 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.797, -2.8970853586582503, yes F: serine integrase SIF-BLAST: ,,[integrase [Arthrobacter phage Yang] ],,YP\_009815667,98.9407,0.0 SIF-HHPRED: SIF-Syn: Shares a similar protein function with appropriate coverage with phages Yang and Cassia.

CDS 39731 - 40000

 /gene="52"

 /product="gp52"

 /function="Hypothetical Protein"

 /locus tag="JuneStar\_52"

 /note=Original Glimmer call @bp 39731 has strength 12.35; Genemark calls start at 39731

 /note=SSC: 39731-40000 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_CASSIA\_49 [Arthrobacter phage Cassia]],,NCBI, q1:s1 97.7528% 1.2822E-35 GAP: 235 bp gap LO: no RBS: Kibler 6, Karlin Medium, 3.207, -2.0162541296952132, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_CASSIA\_49 [Arthrobacter phage Cassia]],,WGH21122,81.4433,1.2822E-35 SIF-HHPRED: SIF-Syn: This gene is not closely similar to any gene in related phages.

CDS 40003 - 40233

 /gene="53"

 /product="gp53"

 /function="RNA binding protein"

 /locus tag="JuneStar\_53"

 /note=Original Glimmer call @bp 40003 has strength 16.62; Genemark calls start at 40003

 /note=SSC: 40003-40233 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PQE17\_gp57 [Arthrobacter phage Crewmate] ],,NCBI, q1:s1 100.0% 2.27266E-43 GAP: 2 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.207, -2.86135216970947, yes F: RNA binding protein SIF-BLAST: ,,[hypothetical protein PQE17\_gp57 [Arthrobacter phage Crewmate] ],,YP\_010678308,96.0526,2.27266E-43 SIF-HHPRED: Asl2047 protein; HFQ, SM, RNA-BINDING PROTEIN, SRNA, TRANSLATIONAL REGULATION, RNA BINDING PROTEIN; 2.31A {Nostoc sp.},,,3HFN\_A,96.0526,96.7 SIF-Syn: Similar phage ObiToo found gene to be RNA binding protein

CDS 40230 - 40421

 /gene="54"

 /product="gp54"

 /function="Hypothetical Protein"

 /locus tag="JuneStar\_54"

 /note=Original Glimmer call @bp 40230 has strength 7.87; Genemark calls start at 40230

 /note=SSC: 40230-40421 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PQE13\_gp51 [Arthrobacter phage Elezi] ],,NCBI, q1:s1 100.0% 1.61229E-28 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.392, -3.8116689268127657, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein PQE13\_gp51 [Arthrobacter phage Elezi] ],,YP\_010678029,90.4762,1.61229E-28 SIF-HHPRED: SIF-Syn: Similar phage Elezi has this gene listed as hypothetical.

CDS 40418 - 40774

 /gene="55"

 /product="gp55"

 /function="Hypothetical Protein"

 /locus tag="JuneStar\_55"

 /note=Original Glimmer call @bp 40418 has strength 16.73; Genemark calls start at 40418

 /note=SSC: 40418-40774 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_LEGO\_52 [Arthrobacter phage Lego]],,NCBI, q1:s1 100.0% 1.01441E-27 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.392, -3.8116689268127657, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_LEGO\_52 [Arthrobacter phage Lego]],,QIN94452,68.4615,1.01441E-27 SIF-HHPRED: SIF-Syn: This gene is not similar to known phage.

CDS 40771 - 40977

 /gene="56"

 /product="gp56"

 /function="Hypothetical Protein"

 /locus tag="JuneStar\_56"

 /note=Original Glimmer call @bp 40771 has strength 8.45; Genemark calls start at 40771

 /note=SSC: 40771-40977 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_ITER\_56 [Arthrobacter phage Iter] ],,NCBI, q1:s1 100.0% 3.58456E-9 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 0.778, -7.152009625892923, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_ITER\_56 [Arthrobacter phage Iter] ],,URQ05044,70.3125,3.58456E-9 SIF-HHPRED: SIF-Syn: This gene is not similar to any known phage gene.

CDS 40970 - 41407

 /gene="57"

 /product="gp57"

 /function="Hypothetical Protein"

 /locus tag="JuneStar\_57"

 /note=Original Glimmer call @bp 40970 has strength 18.37; Genemark calls start at 40970

 /note=SSC: 40970-41407 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_CASSIA\_54 [Arthrobacter phage Cassia]],,NCBI, q1:s1 100.0% 3.24883E-76 GAP: -8 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.878, -2.7863799983944713, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_CASSIA\_54 [Arthrobacter phage Cassia]],,WGH21127,93.1034,3.24883E-76 SIF-HHPRED: SIF-Syn: Similar phage Cassia has this gene also as a hypothetical protein.

CDS 41416 - 41610

 /gene="58"

 /product="gp58"

 /function="Hypothetical Protein"

 /locus tag="JuneStar\_58"

 /note=Original Glimmer call @bp 41416 has strength 13.39; Genemark calls start at 41416

 /note=SSC: 41416-41610 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein HOU52\_gp57 [Arthrobacter phage Yang] ],,NCBI, q1:s1 100.0% 1.50343E-35 GAP: 8 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.081, -4.4057176022952405, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein HOU52\_gp57 [Arthrobacter phage Yang] ],,YP\_009815675,100.0,1.50343E-35 SIF-HHPRED: SIF-Syn: Similar phage Yang also has this gene as a hypothetical protein.

CDS 41613 - 41819

 /gene="59"

 /product="gp59"

 /function="Hypothetical Protein"

 /locus tag="JuneStar\_59"

 /note=Original Glimmer call @bp 41613 has strength 17.66; Genemark calls start at 41613

 /note=SSC: 41613-41819 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_OBITOO\_63 [Arthrobacter phage ObiToo]],,NCBI, q5:s6 91.1765% 1.84013E-10 GAP: 2 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.201, -4.213314289702982, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_OBITOO\_63 [Arthrobacter phage ObiToo]],,WGH21239,56.9444,1.84013E-10 SIF-HHPRED: SIF-Syn: This gene is not similar to any known function in similar phages.

CDS 41943 - 42101

 /gene="60"

 /product="gp60"

 /function="Hypothetical Protein"

 /locus tag="JuneStar\_60"

 /note=Original Glimmer call @bp 41943 has strength 21.49; Genemark calls start at 41943

 /note=SSC: 41943-42101 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PQE12\_gp59 [Arthrobacter phage Adumb2043] ],,NCBI, q1:s1 94.2308% 1.17903E-12 GAP: 123 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.974, -2.5052746077145835, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein PQE12\_gp59 [Arthrobacter phage Adumb2043] ],,YP\_010677969,68.254,1.17903E-12 SIF-HHPRED: SIF-Syn: This gene is not similar to any known function in similar phages.

CDS 42226 - 42558

 /gene="61"

 /product="gp61"

 /function="Hypothetical Protein"

 /locus tag="JuneStar\_61"

 /note=Original Glimmer call @bp 42226 has strength 19.75; Genemark calls start at 42226

 /note=SSC: 42226-42558 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PQD80\_gp60 [Arthrobacter phage Lizalica] ],,NCBI, q1:s1 95.4545% 9.63809E-50 GAP: 124 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.878, -2.6453814847322845, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein PQD80\_gp60 [Arthrobacter phage Lizalica] ],,YP\_010677625,80.9091,9.63809E-50 SIF-HHPRED: SIF-Syn: This gene is not similar to any gene in related phages.

CDS 42627 - 42941

 /gene="62"

 /product="gp62"

 /function="Hypothetical Protein"

 /locus tag="JuneStar\_62"

 /note=Original Glimmer call @bp 42627 has strength 16.59; Genemark calls start at 42627

 /note=SSC: 42627-42941 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein HOU52\_gp62 [Arthrobacter phage Yang] ],,NCBI, q1:s1 100.0% 9.2605E-63 GAP: 68 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.974, -2.5052746077145835, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein HOU52\_gp62 [Arthrobacter phage Yang] ],,YP\_009815680,93.2692,9.2605E-63 SIF-HHPRED: SIF-Syn: This gene is similar to a hypothetical gene in phage Yang

CDS 42934 - 43110

 /gene="63"

 /product="gp63"

 /function="Hypothetical Protein"

 /locus tag="JuneStar\_63"

 /note=Original Glimmer call @bp 42934 has strength 17.36; Genemark calls start at 42934

 /note=SSC: 42934-43110 CP: yes SCS: both ST: SS BLAST-Start: [membrane protein [Arthrobacter phage Amyev] ],,NCBI, q1:s1 98.2759% 2.66138E-18 GAP: -8 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.974, -3.095100142625534, yes F: Hypothetical Protein SIF-BLAST: ,,[membrane protein [Arthrobacter phage Amyev] ],,YP\_010677766,93.1034,2.66138E-18 SIF-HHPRED: SIF-Syn: This gene is similar to a membrane protein in phage Amyev.

CDS 43103 - 43264

 /gene="64"

 /product="gp64"

 /function="Hypothetical Protein"

 /locus tag="JuneStar\_64"

 /note=Original Glimmer call @bp 43103 has strength 18.86; Genemark calls start at 43103

 /note=SSC: 43103-43264 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein HOU52\_gp64 [Arthrobacter phage Yang] ],,NCBI, q1:s1 100.0% 7.4962E-27 GAP: -8 bp gap LO: no RBS: Kibler 6, Karlin Medium, 3.217, -1.993391246735709, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein HOU52\_gp64 [Arthrobacter phage Yang] ],,YP\_009815682,94.4444,7.4962E-27 SIF-HHPRED: SIF-Syn: This gene is not similar to any known gene in similar phages.

CDS 43264 - 43410

 /gene="65"

 /product="gp65"

 /function="Hypothetical Protein"

 /locus tag="JuneStar\_65"

 /note=Original Glimmer call @bp 43264 has strength 24.64; Genemark calls start at 43264

 /note=SSC: 43264-43410 CP: yes SCS: both ST: SS BLAST-Start: [membrane protein [Arthrobacter phage Cassia]],,NCBI, q13:s3 75.0% 6.09319E-9 GAP: -1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.974, -2.583959800616441, yes F: Hypothetical Protein SIF-BLAST: ,,[membrane protein [Arthrobacter phage Cassia]],,WGH21138,81.5789,6.09319E-9 SIF-HHPRED: SIF-Syn: This gene is not similar to known genes in related phages.

CDS 43395 - 43697

 /gene="66"

 /product="gp66"

 /function="Hypothetical Protein"

 /locus tag="JuneStar\_66"

 /note=Genemark calls start at 43395

 /note=SSC: 43395-43697 CP: yes SCS: genemark ST: SS BLAST-Start: [endonuclease VII [Arthrobacter phage Yang] ],,NCBI, q1:s1 100.0% 6.12693E-63 GAP: -16 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.413, -3.9764835383098616, yes F: Hypothetical Protein SIF-BLAST: ,,[endonuclease VII [Arthrobacter phage Yang] ],,YP\_009815684,99.0,6.12693E-63 SIF-HHPRED: SIF-Syn: This gene is similar to a hypothetical protein in phage Yang

CDS 43955 - 44149

 /gene="67"

 /product="gp67"

 /function="Hypothetical Protein"

 /locus tag="JuneStar\_67"

 /note=Original Glimmer call @bp 43961 has strength 11.26; Genemark calls start at 43961

 /note=SSC: 43955-44149 CP: yes SCS: both-cs ST: NA BLAST-Start: [hypothetical protein SEA\_CASSIA\_67 [Arthrobacter phage Cassia]],,NCBI, q3:s1 96.875% 4.08257E-29 GAP: 257 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.207, -2.033982896655645, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_CASSIA\_67 [Arthrobacter phage Cassia]],,WGH21140,91.9355,4.08257E-29 SIF-HHPRED: SIF-Syn: This gene is not similar to known proteins in related phages.

 /note=Moved to the first start site to capture more coding potential. Z score is the same, final score is similar. This start is the LORF, and has a smaller gap.

CDS 44149 - 44457

 /gene="68"

 /product="gp68"

 /function="HNH endonuclease"

 /locus tag="JuneStar\_68"

 /note=Genemark calls start at 44149

 /note=SSC: 44149-44457 CP: yes SCS: genemark ST: SS BLAST-Start: [HNH endonuclease [Arthrobacter phage DrSierra] ],,NCBI, q1:s1 98.0392% 4.64076E-48 GAP: -1 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.427, -4.6476424945195145, no F: HNH endonuclease SIF-BLAST: ,,[HNH endonuclease [Arthrobacter phage DrSierra] ],,YP\_010678391,93.0,4.64076E-48 SIF-HHPRED: SIF-Syn: This gene is similar to known HNH endonucleases in phage Yang and other related phages.