CDS 86 - 550

/gene="1"

/product="gp1"

/function="terminase, small subunit"

/locus tag="Pumpkins\_1"

/note=Genemark calls start at 86

/note=SSC: 86-550 CP: yes SCS: genemark ST: SS BLAST-Start: [terminase small subunit [Arthrobacter phage Cassia]],,NCBI, q1:s1 100.0% 1.26442E-103 GAP: 0 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.215, -2.0949393225970705, yes F: terminase, small subunit SIF-BLAST: ,,[terminase small subunit [Arthrobacter phage Cassia]],,WGH21074,98.7013,1.26442E-103 SIF-HHPRED: SIF-Syn: Similar phage Yang and Cassia have a Terminase, small subunit at this location.

CDS 547 - 2244

/gene="2"

/product="gp2"

/function="terminase, large subunit"

/locus tag="Pumpkins\_2"

/note=Original Glimmer call @bp 547 has strength 10.05; Genemark calls start at 547

/note=SSC: 547-2244 CP: yes SCS: both ST: SS BLAST-Start: [terminase large subunit [Arthrobacter phage Cassia]],,NCBI, q1:s1 100.0% 0.0 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.087, -4.394706008439538, no F: terminase, large subunit SIF-BLAST: ,,[terminase large subunit [Arthrobacter phage Cassia]],,WGH21075,100.0,0.0 SIF-HHPRED: SIF-Syn: Similar phage Yang and Cassia have a terminase, large subunit at this location.

CDS 2263 - 3798

/gene="3"

/product="gp3"

/function="portal protein"

/locus tag="Pumpkins\_3"

/note=Genemark calls start at 2263

/note=SSC: 2263-3798 CP: yes SCS: genemark ST: SS BLAST-Start: [portal protein [Arthrobacter phage Cassia]],,NCBI, q1:s1 100.0% 0.0 GAP: 18 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.215, -2.033982896655645, yes F: portal protein SIF-BLAST: ,,[portal protein [Arthrobacter phage Cassia]],,WGH21076,99.0215,0.0 SIF-HHPRED: SIF-Syn: Similar phages, Yang and Cassia, have a portal protein at this location.

CDS 3814 - 5826

/gene="4"

/product="gp4"

/function="ADP-ribosyltransferase"

/locus tag="Pumpkins\_4"

/note=Genemark calls start at 3850

/note=SSC: 3814-5826 CP: yes SCS: genemark-cs 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, 3.061, -2.338663114094478, yes F: ADP-ribosyltransferase SIF-BLAST: ,,[head maturation protease [Arthrobacter phage Yang] ],,YP\_009815622,95.8209,0.0 SIF-HHPRED: SIF-Syn: Similar phages, Yang and Cassia, have a ADP-ribosyltransferase at this location.

CDS 5874 - 6233

/gene="5"

/product="gp5"

/function="Hypothetical Protein"

/locus tag="Pumpkins\_5"

/note=Genemark calls start at 5874

/note=SSC: 5874-6233 CP: yes SCS: genemark ST: SS BLAST-Start: [hypothetical protein SEA\_CASSIA\_5 [Arthrobacter phage Cassia]],,NCBI, q1:s1 100.0% 1.05039E-75 GAP: 47 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.215, -1.953940808934884, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_CASSIA\_5 [Arthrobacter phage Cassia]],,WGH21078,99.1597,1.05039E-75 SIF-HHPRED: SIF-Syn: The hypothetical protein function is not closely related to any similar phages but is in a similar place as in Cassia and Yang.

CDS 6350 - 6907

/gene="6"

/product="gp6"

/function="scaffolding protein"

/locus tag="Pumpkins\_6"

/note=Genemark calls start at 6350

/note=SSC: 6350-6907 CP: yes SCS: genemark ST: SS BLAST-Start: [scaffolding protein [Arthrobacter phage Cassia]],,NCBI, q1:s1 100.0% 6.89693E-115 GAP: 116 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.982, -3.3503726477288405, yes F: scaffolding protein SIF-BLAST: ,,[scaffolding protein [Arthrobacter phage Cassia]],,WGH21079,97.2826,6.89693E-115 SIF-HHPRED: DUF4355 ; Domain of unknown function (DUF4355),,,PF14265.10,60.5405,99.0 SIF-Syn: Similar phages, Yang and Cassia, have a Scaffolding protein at this location.

CDS 6934 - 7881

/gene="7"

/product="gp7"

/function="major capsid protein"

/locus tag="Pumpkins\_7"

/note=Genemark calls start at 6934

/note=SSC: 6934-7881 CP: yes SCS: genemark ST: SS BLAST-Start: [major capsid protein [Arthrobacter phage Cassia]],,NCBI, q1:s1 100.0% 0.0 GAP: 26 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.119, -2.8084998623841946, yes F: major capsid protein SIF-BLAST: ,,[major capsid protein [Arthrobacter phage Cassia]],,WGH21080,100.0,0.0 SIF-HHPRED: SIF-Syn: Similar phages, Yang and Cassia, have a forward major capsid protein at this location.

CDS 7958 - 8353

/gene="8"

/product="gp8"

/function="head-to-tail adaptor"

/locus tag="Pumpkins\_8"

/note=Original Glimmer call @bp 7958 has strength 7.58; Genemark calls start at 7958

/note=SSC: 7958-8353 CP: yes SCS: both ST: SS BLAST-Start: [head-to-tail adaptor [Arthrobacter phage Cassia]],,NCBI, q1:s1 100.0% 4.78232E-85 GAP: 76 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.982, -2.5052746077145835, yes F: head-to-tail adaptor SIF-BLAST: ,,[head-to-tail adaptor [Arthrobacter phage Cassia]],,WGH21081,99.2366,4.78232E-85 SIF-HHPRED: SIF-Syn: Similar phages, Yang and Cassia, have a head-to-tail adaptor protein at this location.

CDS 8365 - 8481

/gene="9"

/product="gp9"

/function="Hypothetical Protein"

/locus tag="Pumpkins\_9"

/note=Original Glimmer call @bp 8365 has strength 15.52; Genemark calls start at 8365

/note=SSC: 8365-8481 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_CASSIA\_9 [Arthrobacter phage Cassia]],,NCBI, q1:s1 100.0% 3.05618E-16 GAP: 11 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.061, -2.2763497933341483, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_CASSIA\_9 [Arthrobacter phage Cassia]],,WGH21082,100.0,3.05618E-16 SIF-HHPRED: SIF-Syn: The hypothetical protein function is not closely related to any similar phages but is in a similar place as in Cassia and Yang.

CDS 8478 - 8828

/gene="10"

/product="gp10"

/function="head-to-tail stopper"

/locus tag="Pumpkins\_10"

/note=Original Glimmer call @bp 8478 has strength 11.27; Genemark calls start at 8478

/note=SSC: 8478-8828 CP: yes SCS: both ST: SS BLAST-Start: [head-to-tail stopper [Arthrobacter phage Cassia]],,NCBI, q1:s1 100.0% 4.58786E-68 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.072, -3.16089827114923, yes F: head-to-tail stopper SIF-BLAST: ,,[head-to-tail stopper [Arthrobacter phage Cassia]],,WGH21083,95.6897,4.58786E-68 SIF-HHPRED: SIF-Syn: Similar phage Yang and Cassia has a Forward (head-to-tail stopper) at this location.

CDS 8839 - 9144

/gene="11"

/product="gp11"

/function="Hypothetical Protein"

/locus tag="Pumpkins\_11"

/note=Genemark calls start at 8839

/note=SSC: 8839-9144 CP: yes SCS: genemark ST: SS BLAST-Start: [hypothetical protein SEA\_CASSIA\_11 [Arthrobacter phage Cassia]],,NCBI, q1:s1 100.0% 1.61495E-56 GAP: 10 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.215, -2.4811409279978642, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_CASSIA\_11 [Arthrobacter phage Cassia]],,WGH21084,97.0,1.61495E-56 SIF-HHPRED: SIF-Syn: The hypothetical protein function is not closely related to any similar phages but is in a similar place as in Cassia and Yang.

CDS 9144 - 9557

/gene="12"

/product="gp12"

/function="tail terminator"

/locus tag="Pumpkins\_12"

/note=Genemark calls start at 9144

/note=SSC: 9144-9557 CP: yes SCS: genemark ST: SS BLAST-Start: [tail terminator [Arthrobacter phage Yang] ],,NCBI, q1:s1 100.0% 3.04197E-85 GAP: -1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.502, -4.547770211785489, yes F: tail terminator SIF-BLAST: ,,[tail terminator [Arthrobacter phage Yang] ],,YP\_009815630,95.6204,3.04197E-85 SIF-HHPRED: SIF-Syn: Similar phage Yang has a Forward (tail terminator) at this location.

CDS 9570 - 10121

/gene="13"

/product="gp13"

/function="major tail protein"

/locus tag="Pumpkins\_13"

/note=Genemark calls start at 9570

/note=SSC: 9570-10121 CP: yes SCS: genemark ST: SS BLAST-Start: [major tail protein [Arthrobacter phage Cassia]],,NCBI, q1:s1 98.3607% 5.608E-125 GAP: 12 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.226, -2.0720764396375664, yes F: major tail protein SIF-BLAST: ,,[major tail protein [Arthrobacter phage Cassia]],,WGH21086,97.2678,5.608E-125 SIF-HHPRED: YSD1\_22 major tail protein; Bacteriophage tail, helical assembly, VIRAL PROTEIN; 3.5A {Bacteriophage sp.},,,6XGR\_M,92.3497,98.4 SIF-Syn: Similar phage Yang has a Forward (major tail protein) at this location.

CDS 10215 - 10484

/gene="14"

/product="gp14"

/function="tail assembly chaperone"

/locus tag="Pumpkins\_14"

/note=Genemark calls start at 10215

/note=SSC: 10215-10484 CP: yes SCS: genemark ST: SS BLAST-Start: [tail assembly chaperone [Arthrobacter phage Yang] ],,NCBI, q1:s1 100.0% 3.48154E-55 GAP: 93 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.226, -2.2821867859826788, yes F: tail assembly chaperone SIF-BLAST: ,,[tail assembly chaperone [Arthrobacter phage Yang] ],,YP\_009815633,98.8764,3.48154E-55 SIF-HHPRED: SIF-Syn: Similar phage Yang has a Forward (tail assembly chaperone) at this location.

CDS 10523 - 10819

/gene="15"

/product="gp15"

/function="tail assembly chaperone"

/locus tag="Pumpkins\_15"

/note=Genemark calls start at 10523

/note=SSC: 10523-10819 CP: yes SCS: genemark ST: SS BLAST-Start: [tail assembly chaperone [Arthrobacter phage Cassia]],,NCBI, q1:s103 100.0% 2.04477E-63 GAP: 38 bp gap LO: no RBS: Kibler 6, Karlin Medium, 0.916, -7.115667690747521, yes F: tail assembly chaperone SIF-BLAST: ,,[tail assembly chaperone [Arthrobacter phage Cassia]],,WGH21088,49.0,2.04477E-63 SIF-HHPRED: SIF-Syn:

CDS 10836 - 13160

/gene="16"

/product="gp16"

/function="tape measure protein"

/locus tag="Pumpkins\_16"

/note=Original Glimmer call @bp 10836 has strength 10.45; Genemark calls start at 10836

/note=SSC: 10836-13160 CP: no SCS: both ST: SS BLAST-Start: [tape measure protein [Arthrobacter phage Cassia]],,NCBI, q1:s1 100.0% 0.0 GAP: 16 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.215, -2.86135216970947, yes F: tape measure protein SIF-BLAST: ,,[tape measure protein [Arthrobacter phage Cassia]],,WGH21089,98.8372,0.0 SIF-HHPRED: SIF-Syn: Similar phage Yang and Cassia has a Forward (tape measure protein) at this location.

CDS 13153 - 14028

/gene="17"

/product="gp17"

/function="minor tail protein"

/locus tag="Pumpkins\_17"

/note=Original Glimmer call @bp 13153 has strength 11.09; Genemark calls start at 13153

/note=SSC: 13153-14028 CP: yes SCS: both ST: SS BLAST-Start: [minor tail protein [Arthrobacter phage Cassia]],,NCBI, q1:s1 100.0% 0.0 GAP: -8 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.827, -2.7653702713535186, yes F: minor tail protein SIF-BLAST: ,,[minor tail protein [Arthrobacter phage Cassia]],,WGH21090,98.9691,0.0 SIF-HHPRED: HYPOTHETICAL PROTEIN 19.1; VIRAL PROTEIN, DISTAL TAIL PROTEIN; 2.95A {BACILLUS PHAGE SPP1},,,2X8K\_C,98.9691,100.0 SIF-Syn: Similar phages Yang and Cassia has a Forward (minor tail protein) at this location.

CDS 14041 - 15036

/gene="18"

/product="gp18"

/function="minor tail protein"

/locus tag="Pumpkins\_18"

/note=Genemark calls start at 14041

/note=SSC: 14041-15036 CP: yes SCS: genemark 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, 3.226, -2.0720764396375664, yes F: minor tail protein SIF-BLAST: ,,[minor tail protein [Arthrobacter phage Cassia]],,WGH21091,99.6979,0.0 SIF-HHPRED: SIF-Syn: Similar phages Yang and Cassia has a Forward (minor tail protein) at this location.

CDS 15036 - 16157

/gene="19"

/product="gp19"

/function="minor tail protein"

/locus tag="Pumpkins\_19"

/note=Genemark calls start at 15036

/note=SSC: 15036-16157 CP: yes SCS: genemark ST: SS BLAST-Start: [minor tail protein [Arthrobacter phage Cassia]],,NCBI, q1:s1 100.0% 0.0 GAP: -1 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.318, -3.9718914447963414, no F: minor tail protein SIF-BLAST: ,,[minor tail protein [Arthrobacter phage Cassia]],,WGH21092,98.3914,0.0 SIF-HHPRED: Sipho\_Gp37 ; Siphovirus ReqiPepy6 Gp37-like protein,,,PF14594.10,91.689,99.9 SIF-Syn: Similar phages Yang and Cassia has a Forward (minor tail protein) at this location.

CDS 16163 - 19783

/gene="20"

/product="gp20"

/function="Hypothetical Protein"

/locus tag="Pumpkins\_20"

/note=Original Glimmer call @bp 16520 has strength 6.57; Genemark calls start at 16163

/note=SSC: 16163-19783 CP: yes SCS: both-gm ST: SS BLAST-Start: [tail protein [Arthrobacter phage Yang] ],,NCBI, q458:s219 62.1061% 0.0 GAP: 5 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.674, -3.7378191248686026, yes F: Hypothetical Protein SIF-BLAST: ,,[tail protein [Arthrobacter phage Yang] ],,YP\_009815638,73.423,0.0 SIF-HHPRED: SIF-Syn: The hypothetical protein function is not closely related to any similar phages but is in a similar place as in Cassia and Yang.

/note=This gene is not similar to any other, and does reach 90% desired threshold on HHPRED or NCBI BLAST.

CDS 19793 - 20134

/gene="21"

/product="gp21"

/function="Hypothetical Protein"

/locus tag="Pumpkins\_21"

/note=Original Glimmer call @bp 19793 has strength 9.06; Genemark calls start at 19793

/note=SSC: 19793-20134 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_CASSIA\_21 [Arthrobacter phage Cassia]],,NCBI, q1:s1 100.0% 1.41725E-72 GAP: 9 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.226, -2.0111200136961407, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_CASSIA\_21 [Arthrobacter phage Cassia]],,WGH21094,100.0,1.41725E-72 SIF-HHPRED: SIF-Syn: The hypothetical protein function is not closely related to any similar phages but is in a similar place as in Cassia and Yang.

CDS 20140 - 20412

/gene="22"

/product="gp22"

/function="membrane protein"

/locus tag="Pumpkins\_22"

/note=Genemark calls start at 20140

/note=SSC: 20140-20412 CP: yes SCS: genemark ST: SS BLAST-Start: [membrane protein [Arthrobacter phage Cassia]],,NCBI, q1:s1 100.0% 2.44906E-57 GAP: 5 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.354, -4.66341334897022, no F: membrane protein SIF-BLAST: ,,[membrane protein [Arthrobacter phage Cassia]],,WGH21095,100.0,2.44906E-57 SIF-HHPRED: SIF-Syn: The hypothetical protein function is not closely related to any similar phages but is in a similar place as in Cassia and Yang.

CDS 20421 - 20672

/gene="23"

/product="gp23"

/function="membrane protein"

/locus tag="Pumpkins\_23"

/note=Genemark calls start at 20442

/note=SSC: 20421-20672 CP: yes SCS: genemark-cs ST: SS BLAST-Start: [membrane protein [Arthrobacter phage Cassia]],,NCBI, q1:s1 100.0% 2.62929E-45 GAP: 8 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.315, -3.9166971242758706, yes F: membrane protein SIF-BLAST: ,,[membrane protein [Arthrobacter phage Cassia]],,WGH21096,100.0,2.62929E-45 SIF-HHPRED: SIF-Syn:

CDS 20823 - 21440

/gene="24"

/product="gp24"

/function="deoxynucleoside monophosphate kinase"

/locus tag="Pumpkins\_24"

/note=Genemark calls start at 20823

/note=SSC: 20823-21440 CP: no SCS: genemark ST: SS BLAST-Start: [deoxynucleoside monophosphate kinase [Arthrobacter phage Cassia]],,NCBI, q1:s1 100.0% 3.5984E-143 GAP: 150 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.215, -1.953940808934884, yes F: deoxynucleoside monophosphate kinase SIF-BLAST: ,,[deoxynucleoside monophosphate kinase [Arthrobacter phage Cassia]],,WGH21097,99.0244,3.5984E-143 SIF-HHPRED: DEOXYNUCLEOSIDE MONOPHOSPHATE KINASE; TRANSFERASE, PHOSPHOTRANSFERASE; HET: DGP, OCS; 2.0A {Enterobacteria phage T4} SCOP: c.37.1.1,,,1DEK\_A,92.6829,99.8 SIF-Syn: Similar phages Yang and Cassia has a Forward (deoyynucleoside monophosphate kinase protein) at this location.

/note=Start doesn`t capture all coding potential, but this is the earliest start available.

CDS 21546 - 22124

/gene="25"

/product="gp25"

/function="Hypothetical Protein"

/locus tag="Pumpkins\_25"

/note=Original Glimmer call @bp 21546 has strength 9.54; Genemark calls start at 21546

/note=SSC: 21546-22124 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein HOU52\_gp25 [Arthrobacter phage Yang] ],,NCBI, q1:s1 100.0% 3.30599E-121 GAP: 105 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.996, -5.333306234940948, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein HOU52\_gp25 [Arthrobacter phage Yang] ],,YP\_009815643,95.8333,3.30599E-121 SIF-HHPRED: SIF-Syn: The hypothetical protein function is not closely related to any similar phages but is in a similar place as in Cassia and Yang.

CDS 22329 - 23159

/gene="26"

/product="gp26"

/function="exonuclease"

/locus tag="Pumpkins\_26"

/note=Genemark calls start at 22329

/note=SSC: 22329-23159 CP: yes SCS: genemark ST: SS BLAST-Start: [Cas4 family exonuclease [Arthrobacter phage Cassia]],,NCBI, q1:s1 100.0% 0.0 GAP: 204 bp gap LO: no RBS: Kibler 6, Karlin Medium, 3.215, -2.606079664606164, yes F: exonuclease SIF-BLAST: ,,[Cas4 family exonuclease [Arthrobacter phage Cassia]],,WGH21099,99.6377,0.0 SIF-HHPRED: SIF-Syn: Similar phages Yang and Cassia has a Forward (exonuclease protein) at this location.

/note=Could be a Cas 4 exonuclease--need to double check

CDS 23159 - 23314

/gene="27"

/product="gp27"

/function="Hypothetical Protein"

/locus tag="Pumpkins\_27"

/note=Genemark calls start at 23159

/note=SSC: 23159-23314 CP: yes SCS: genemark ST: SS BLAST-Start: [hypothetical protein SEA\_CASSIA\_27 [Arthrobacter phage Cassia]],,NCBI, q1:s1 100.0% 1.06637E-25 GAP: -1 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.809, -3.90505122954242, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_CASSIA\_27 [Arthrobacter phage Cassia]],,WGH21100,100.0,1.06637E-25 SIF-HHPRED: SIF-Syn: The hypothetical protein function is not closely related to any similar phages but is in a similar place as in Cassia and Yang.

CDS 23311 - 23679

/gene="28"

/product="gp28"

/function="nucleoside deoxyribosyltransferase"

/locus tag="Pumpkins\_28"

/note=Original Glimmer call @bp 23521 has strength 1.42; Genemark calls start at 23335

/note=SSC: 23311-23679 CP: yes SCS: both-cs ST: NA BLAST-Start: [MazG-like pyrophosphatase [Arthrobacter phage Crewmate] ],,NCBI, q1:s1 100.0% 4.35952E-76 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.097, -5.122284713285658, yes F: nucleoside deoxyribosyltransferase SIF-BLAST: ,,[MazG-like pyrophosphatase [Arthrobacter phage Crewmate] ],,YP\_010678282,99.1803,4.35952E-76 SIF-HHPRED: SIF-Syn: Similar phages Yang and Cassia has a Forward (nucleoside deoxyribosyltransferase protein) at this location.

/note=No starterator data. Not choosing either the glimmer or genemark start sites. Choosing the start with a -4 overlap. The final score is a little better in the chosen start site and the z score is better.

CDS 23676 - 24080

/gene="29"

/product="gp29"

/function="LAGLIDADG endonuclease"

/locus tag="Pumpkins\_29"

/note=Original Glimmer call @bp 23676 has strength 7.25; Genemark calls start at 23676

/note=SSC: 23676-24080 CP: yes SCS: both ST: SS BLAST-Start: [HNH endonuclease [Arthrobacter phage Adumb2043] ],,NCBI, q1:s1 100.0% 6.03087E-91 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.499, -3.513874779476501, no F: LAGLIDADG endonuclease SIF-BLAST: ,,[HNH endonuclease [Arthrobacter phage Adumb2043] ],,YP\_010677938,100.0,6.03087E-91 SIF-HHPRED: SIF-Syn: Similar phages Yang and Cassia has a Forward (LAGLIDADG endonuclease protein) at this location.

CDS 24203 - 24916

/gene="30"

/product="gp30"

/function="recombination directionality factor"

/locus tag="Pumpkins\_30"

/note=Original Glimmer call @bp 24203 has strength 15.61; Genemark calls start at 24203

/note=SSC: 24203-24916 CP: yes SCS: both ST: SS BLAST-Start: [recombination directionality factor [Arthrobacter phage Cassia]],,NCBI, q1:s1 100.0% 3.60176E-167 GAP: 122 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.203, -4.423424636048095, no F: recombination directionality factor SIF-BLAST: ,,[recombination directionality factor [Arthrobacter phage Cassia]],,WGH21103,99.1561,3.60176E-167 SIF-HHPRED: SIF-Syn: Similar phages Yang and Cassia has a Forward (recombination directionality factor protein) at this location.

CDS 24916 - 25062

/gene="31"

/product="gp31"

/function="membrane protein"

/locus tag="Pumpkins\_31"

/note=Original Glimmer call @bp 24916 has strength 13.03; Genemark calls start at 24916

/note=SSC: 24916-25062 CP: yes SCS: both ST: SS BLAST-Start: [membrane protein [Arthrobacter phage Cassia]],,NCBI, q1:s1 100.0% 8.92121E-22 GAP: -1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.087, -4.455662434380964, no F: membrane protein SIF-BLAST: ,,[membrane protein [Arthrobacter phage Cassia]],,WGH21104,95.8333,8.92121E-22 SIF-HHPRED: SIF-Syn:

CDS 25142 - 25492

/gene="32"

/product="gp32"

/function="Hypothetical Protein"

/locus tag="Pumpkins\_32"

/note=Genemark calls start at 25142

/note=SSC: 25142-25492 CP: yes SCS: genemark ST: SS BLAST-Start: [hypothetical protein SEA\_CASSIA\_33 [Arthrobacter phage Cassia]],,NCBI, q1:s1 100.0% 1.8034E-73 GAP: 79 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.885, -2.6453814847322845, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_CASSIA\_33 [Arthrobacter phage Cassia]],,WGH21106,96.5517,1.8034E-73 SIF-HHPRED: SIF-Syn: The hypothetical protein function is not closely related to any similar phages but is in a similar place as in Cassia and Yang.

/note=Similar phage Cassia and Powerpuff indicate a hypothetical protein at this location.

CDS 25496 - 25762

/gene="33"

/product="gp33"

/function="NrdH-like glutaredoxin"

/locus tag="Pumpkins\_33"

/note=Genemark calls start at 25496

/note=SSC: 25496-25762 CP: yes SCS: genemark ST: SS BLAST-Start: [NrdH-like glutaredoxin [Arthrobacter phage Cassia]],,NCBI, q1:s1 100.0% 5.08207E-58 GAP: 3 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.061, -3.1837611541087343, yes F: NrdH-like glutaredoxin SIF-BLAST: ,,[NrdH-like glutaredoxin [Arthrobacter phage Cassia]],,WGH21107,100.0,5.08207E-58 SIF-HHPRED: Circadian clock protein KaiB; Transcription Regulator, foldswitch; HET: ADP; 1.8A {Thermosynechococcus elongatus} SCOP: c.47.1.15,,,5JWO\_B,96.5909,99.2 SIF-Syn: Similar phage Cassia and Iter have a Forward NrdH-like glutaredoxin gene in this location.

CDS 25759 - 25959

/gene="34"

/product="gp34"

/function="Hypothetical Protein"

/locus tag="Pumpkins\_34"

/note=Genemark calls start at 25759

/note=SSC: 25759-25959 CP: yes SCS: genemark ST: SS BLAST-Start: [hypothetical protein SEA\_CASSIA\_35 [Arthrobacter phage Cassia]],,NCBI, q1:s1 96.9697% 3.11005E-32 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.129, -3.040909484527996, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_CASSIA\_35 [Arthrobacter phage Cassia]],,WGH21108,89.5522,3.11005E-32 SIF-HHPRED: SIF-Syn: The hypothetical protein function is not closely related to any similar phages but is in a similar place as in Cassia and Yang.

/note=This protein is not similar to any known protein. Similar phages, ObiToo and Cassia do not call a function.

CDS 25956 - 26183

/gene="35"

/product="gp35"

/function="Hypothetical Protein"

/locus tag="Pumpkins\_35"

/note=Genemark calls start at 25956

/note=SSC: 25956-26183 CP: yes SCS: genemark ST: SS BLAST-Start: [hypothetical protein PQE17\_gp39 [Arthrobacter phage Crewmate] ],,NCBI, q1:s1 96.0% 7.75578E-18 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.599, -3.2441186272167593, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein PQE17\_gp39 [Arthrobacter phage Crewmate] ],,YP\_010678290,72.3684,7.75578E-18 SIF-HHPRED: SIF-Syn: The hypothetical protein function is not closely related to any similar phages but is in a similar place as in Cassia and Yang.

/note=This gene is not similar to any other.

CDS 26180 - 26539

/gene="36"

/product="gp36"

/function="Holliday junction resolvase"

/locus tag="Pumpkins\_36"

/note=Genemark calls start at 26180

/note=SSC: 26180-26539 CP: yes SCS: genemark ST: SS BLAST-Start: [holliday junction resolvase [Arthrobacter phage Yang] ],,NCBI, q1:s1 100.0% 2.76862E-78 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.906, -2.6013996449736907, yes F: Holliday junction resolvase SIF-BLAST: ,,[holliday junction resolvase [Arthrobacter phage Yang] ],,YP\_009815654,98.3193,2.76862E-78 SIF-HHPRED: SIF-Syn: Similar phages Yang and Cassia has a Forward (Holliday junction resolvase protein) at this location.

CDS 26872 - 29361

/gene="37"

/product="gp37"

/function="DNA primase/helicase"

/locus tag="Pumpkins\_37"

/note=Original Glimmer call @bp 26872 has strength 10.38; Genemark calls start at 26872

/note=SSC: 26872-29361 CP: yes SCS: both ST: SS BLAST-Start: [DNA primase/helicase [Arthrobacter phage Cassia]],,NCBI, q1:s1 100.0% 0.0 GAP: 332 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.982, -2.442961286954254, yes F: DNA primase/helicase SIF-BLAST: ,,[DNA primase/helicase [Arthrobacter phage Cassia]],,WGH21110,95.4106,0.0 SIF-HHPRED: SIF-Syn: Similar phages Yang and Cassia has a Forward (DNA primase/helicase protein) at this location.

CDS 29378 - 29488

/gene="38"

/product="gp38"

/function="Hypothetical Protein"

/locus tag="Pumpkins\_38"

/note=Genemark calls start at 29378

/note=SSC: 29378-29488 CP: no SCS: genemark ST: NI BLAST-Start: [hypothetical protein PQE13\_gp38 [Arthrobacter phage Elezi] ],,NCBI, q1:s2 100.0% 4.47931E-13 GAP: 16 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.982, -2.583959800616441, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein PQE13\_gp38 [Arthrobacter phage Elezi] ],,YP\_010678016,89.1892,4.47931E-13 SIF-HHPRED: SIF-Syn: This gene is not similar to known genes.

CDS 29488 - 29610

/gene="39"

/product="gp39"

/function="Hypothetical Protein"

/locus tag="Pumpkins\_39"

/note=

/note=SSC: 29488-29610 CP: yes SCS: neither ST: NA BLAST-Start: [hypothetical protein SEA\_CASSIA\_39 [Arthrobacter phage Cassia]],,NCBI, q1:s1 100.0% 2.20217E-18 GAP: -1 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.693, -5.966914258667748, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_CASSIA\_39 [Arthrobacter phage Cassia]],,WGH21112,100.0,2.20217E-18 SIF-HHPRED: SIF-Syn:

/note=This gene was added to capture coding potential. Cassia has a similar gene in the annotation.

CDS 29815 - 31680

/gene="40"

/product="gp40"

/function="DNA polymerase I"

/locus tag="Pumpkins\_40"

/note=Original Glimmer call @bp 29815 has strength 11.73; Genemark calls start at 29815

/note=SSC: 29815-31680 CP: yes SCS: both ST: SS BLAST-Start: [DNA polymerase I [Arthrobacter phage Cassia]],,NCBI, q1:s1 100.0% 0.0 GAP: 204 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.982, -2.5052746077145835, yes F: DNA polymerase I SIF-BLAST: ,,[DNA polymerase I [Arthrobacter phage Cassia]],,WGH21113,99.6779,0.0 SIF-HHPRED: Apicoplast DNA polymerase; DNA polymerase, exonulease, apicoplast, Plasmodium falciparum, REPLICATION, TRANSFERASE; HET: PEG, EDO; 2.5A {Plasmodium falciparum (isolate 3D7)},,,7SXQ\_B,96.7794,100.0 SIF-Syn: This gene is similar to a known gene in Cassia and ObiToo.

CDS 31677 - 31853

/gene="41"

/product="gp41"

/function="Hypothetical Protein"

/locus tag="Pumpkins\_41"

/note=Genemark calls start at 31692

/note=SSC: 31677-31853 CP: yes SCS: genemark-cs ST: SS BLAST-Start: [hypothetical protein SEA\_OBITOO\_47 [Arthrobacter phage ObiToo]],,NCBI, q1:s1 100.0% 3.57748E-17 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.588, -5.4987073736983305, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_OBITOO\_47 [Arthrobacter phage ObiToo]],,WGH21223,94.8276,3.57748E-17 SIF-HHPRED: SIF-Syn: This gene is not similar to known genes.

CDS 31846 - 32148

/gene="42"

/product="gp42"

/function="DNA ligase"

/locus tag="Pumpkins\_42"

/note=Genemark calls start at 31846

/note=SSC: 31846-32148 CP: yes SCS: genemark ST: SS BLAST-Start: [DNA ligase [Arthrobacter phage Cassia]],,NCBI, q1:s1 100.0% 4.13904E-62 GAP: -8 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.766, -5.065537362076858, yes F: DNA ligase SIF-BLAST: ,,[DNA ligase [Arthrobacter phage Cassia]],,WGH21115,98.0,4.13904E-62 SIF-HHPRED: SIF-Syn: This gene is similar to a DNA ligase in similar phages, Yang and Cassia.

CDS 32145 - 32450

/gene="43"

/product="gp43"

/function="Hypothetical Protein"

/locus tag="Pumpkins\_43"

/note=Original Glimmer call @bp 32145 has strength 11.2; Genemark calls start at 32145

/note=SSC: 32145-32450 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_CASSIA\_43 [Arthrobacter phage Cassia]],,NCBI, q1:s1 100.0% 9.89455E-63 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.721, -5.080915947802713, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_CASSIA\_43 [Arthrobacter phage Cassia]],,WGH21116,99.0099,9.89455E-63 SIF-HHPRED: SIF-Syn: This gene is similar to a hypothetical protein in both Yang and Cassia.

CDS 32640 - 33479

/gene="44"

/product="gp44"

/function="DNA binding protein"

/locus tag="Pumpkins\_44"

/note=Original Glimmer call @bp 32640 has strength 12.26; Genemark calls start at 32640

/note=SSC: 32640-33479 CP: yes SCS: both ST: SS BLAST-Start: [DNA binding protein [Arthrobacter phage Powerpuff] ],,NCBI, q1:s1 100.0% 1.66959E-143 GAP: 189 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.885, -2.6453814847322845, yes F: DNA binding protein SIF-BLAST: ,,[DNA binding protein [Arthrobacter phage Powerpuff] ],,QGZ17345,86.3971,1.66959E-143 SIF-HHPRED: RNA polymerase sigma factor RpoS; Transcription-activator, DNA/RNA, SigmaS, beta`, TRANSCRIPTION, Transferase-DNA complex; 3.26A {Escherichia coli},,,6OMF\_F,96.0574,100.0 SIF-Syn: This gene is similar to other AZ1 phages. It is a DNA binding protein.

/note=The official functions list calls RNA polymerase sigma factor a DNA binding protein.

CDS 33749 - 33961

/gene="45"

/product="gp45"

/function="Hypothetical Protein"

/locus tag="Pumpkins\_45"

/note=Genemark calls start at 33566

/note=SSC: 33749-33961 CP: yes SCS: genemark-cs ST: SS BLAST-Start: [helix-turn-helix DNA binding domain protein [Arthrobacter phage Cassia]],,NCBI, q1:s61 85.7143% 1.32138E-28 GAP: 269 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.605, -3.2921018957843318, yes F: Hypothetical Protein SIF-BLAST: ,,[helix-turn-helix DNA binding domain protein [Arthrobacter phage Cassia]],,WGH21118,43.4109,1.32138E-28 SIF-HHPRED: SIF-Syn: This gene is not similar to known genes.

/note=This gene is not similar to any other gene.

CDS 33990 - 34940

/gene="46"

/product="gp46"

/function="DNA Methyltransferase"

/locus tag="Pumpkins\_46"

/note=Original Glimmer call @bp 33990 has strength 11.92; Genemark calls start at 33990

/note=SSC: 33990-34940 CP: no SCS: both ST: NI BLAST-Start: [DNA methyltransferase [Arthrobacter phage Yang] ],,NCBI, q1:s1 100.0% 1.51655E-174 GAP: 28 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.499, -3.513874779476501, no F: DNA Methyltransferase SIF-BLAST: ,,[DNA methyltransferase [Arthrobacter phage Yang] ],,YP\_009815665,86.875,1.51655E-174 SIF-HHPRED: Modification methylase HhaI; CG-SPECIFICITY, CPG SEQUENCE, C5-METHYLCYTOSINE, NUCLEOTIDE FLIPPING, S-ADENOSYL-L-HOMOCYSTEINE, COMPLEX (METHYLTRANSFERASE- DNA), transferase-DNA complex; HET: 3DR, SO4, SAH; 1.594A {Haemophilus parahaemolyticus},,,5CIY\_A,99.3671,100.0 SIF-Syn: This gene matches similar AZ1 phages as a DNA methyltransferase.

CDS 35058 - 35654

/gene="47"

/product="gp47"

/function="SprT-like protease"

/locus tag="Pumpkins\_47"

/note=Genemark calls start at 35058

/note=SSC: 35058-35654 CP: yes SCS: genemark ST: SS BLAST-Start: [SprT-like protease [Arthrobacter phage Cassia]],,NCBI, q1:s1 100.0% 8.39612E-142 GAP: 117 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.499, -3.513874779476501, yes F: SprT-like protease SIF-BLAST: ,,[SprT-like protease [Arthrobacter phage Cassia]],,WGH21119,98.9899,8.39612E-142 SIF-HHPRED: SIF-Syn: This gene matches similar phages such as Yang, Cassia, and ObiToo as a SprT-like protease.

CDS 35749 - 37167

/gene="48"

/product="gp48"

/function="serine integrase"

/locus tag="Pumpkins\_48"

/note=Original Glimmer call @bp 35749 has strength 9.19; Genemark calls start at 35746

/note=SSC: 35749-37167 CP: yes SCS: both-gl ST: SS BLAST-Start: [serine integrase [Arthrobacter phage Cassia]],,NCBI, q1:s1 100.0% 0.0 GAP: 94 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.803, -2.8970853586582503, yes F: serine integrase SIF-BLAST: ,,[serine integrase [Arthrobacter phage Cassia]],,WGH21121,99.1525,0.0 SIF-HHPRED: SIF-Syn: This gene matches similar phages such as Yang and Cassia, as a serine integrase.

CDS 37435 - 37743

/gene="49"

/product="gp49"

/function="Hypothetical Protein"

/locus tag="Pumpkins\_49"

/note=Genemark calls start at 37435

/note=SSC: 37435-37743 CP: yes SCS: genemark ST: SS BLAST-Start: [hypothetical protein SEA\_CASSIA\_49 [Arthrobacter phage Cassia]],,NCBI, q1:s1 100.0% 5.5417E-43 GAP: 267 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.982, -2.5052746077145835, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_CASSIA\_49 [Arthrobacter phage Cassia]],,WGH21122,90.7216,5.5417E-43 SIF-HHPRED: SIF-Syn: This gene is not similar to known genes.

CDS 37746 - 37976

/gene="50"

/product="gp50"

/function="RNA binding protein"

/locus tag="Pumpkins\_50"

/note=Genemark calls start at 37746

/note=SSC: 37746-37976 CP: yes SCS: genemark ST: SS BLAST-Start: [hypothetical protein SEA\_ITER\_53 [Arthrobacter phage Iter] ],,NCBI, q1:s1 100.0% 8.27365E-41 GAP: 2 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.982, -2.583959800616441, yes F: RNA binding protein SIF-BLAST: ,,[hypothetical protein SEA\_ITER\_53 [Arthrobacter phage Iter] ],,URQ05041,92.1053,8.27365E-41 SIF-HHPRED: Asl2047 protein; HFQ, SM, RNA-BINDING PROTEIN, SRNA, TRANSLATIONAL REGULATION, RNA BINDING PROTEIN; 2.31A {Nostoc sp.},,,3HFN\_A,96.0526,96.6 SIF-Syn: This gene is similar to an RNA binding protein in other AZ1 clusters.

CDS 37973 - 38164

/gene="51"

/product="gp51"

/function="RNA binding protein"

/locus tag="Pumpkins\_51"

/note=Genemark calls start at 37973

/note=SSC: 37973-38164 CP: yes SCS: genemark ST: SS BLAST-Start: [hypothetical protein HOU52\_gp52 [Arthrobacter phage Yang] ],,NCBI, q1:s1 100.0% 1.49509E-33 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.395, -3.8116689268127657, yes F: RNA binding protein SIF-BLAST: ,,[hypothetical protein HOU52\_gp52 [Arthrobacter phage Yang] ],,YP\_009815670,98.4127,1.49509E-33 SIF-HHPRED: Asl2047 protein; HFQ, SM, RNA-BINDING PROTEIN, SRNA, TRANSLATIONAL REGULATION, RNA BINDING PROTEIN; 2.31A {Nostoc sp.},,,3HFN\_A,93.6508,97.4 SIF-Syn: This gene is similar to an RNA binding protein in the phage Yang.

CDS 38161 - 38529

/gene="52"

/product="gp52"

/function="Hypothetical Protein"

/locus tag="Pumpkins\_52"

/note=Genemark calls start at 38161

/note=SSC: 38161-38529 CP: yes SCS: genemark ST: SS BLAST-Start: [hypothetical protein SEA\_POWERPUFF\_55 [Arthrobacter phage Powerpuff] ],,NCBI, q3:s2 98.3607% 9.76092E-33 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.395, -3.8116689268127657, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_POWERPUFF\_55 [Arthrobacter phage Powerpuff] ],,QGZ17353,63.2353,9.76092E-33 SIF-HHPRED: SIF-Syn: This gene is not similar to known genes.

CDS 38710 - 39114

/gene="53"

/product="gp53"

/function="Hypothetical Protein"

/locus tag="Pumpkins\_53"

/note=Genemark calls start at 38710

/note=SSC: 38710-39114 CP: yes SCS: genemark ST: SS BLAST-Start: [hypothetical protein HOU52\_gp56 [Arthrobacter phage Yang] ],,NCBI, q1:s1 100.0% 3.76596E-28 GAP: 180 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.885, -2.7863799983944713, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein HOU52\_gp56 [Arthrobacter phage Yang] ],,YP\_009815674,64.8276,3.76596E-28 SIF-HHPRED: SIF-Syn: This gene is not similar to known genes.

CDS 39127 - 39321

/gene="54"

/product="gp54"

/function="Hypothetical Protein"

/locus tag="Pumpkins\_54"

/note=Genemark calls start at 39127

/note=SSC: 39127-39321 CP: yes SCS: genemark ST: SS BLAST-Start: [hypothetical protein HOU52\_gp57 [Arthrobacter phage Yang] ],,NCBI, q1:s1 100.0% 2.89091E-31 GAP: 12 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.226, -2.0720764396375664, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein HOU52\_gp57 [Arthrobacter phage Yang] ],,YP\_009815675,93.75,2.89091E-31 SIF-HHPRED: SIF-Syn: This gene is not similar to known genes.

CDS 39324 - 39527

/gene="55"

/product="gp55"

/function="Hypothetical Protein"

/locus tag="Pumpkins\_55"

/note=Genemark calls start at 39324

/note=SSC: 39324-39527 CP: yes SCS: genemark ST: SS BLAST-Start: [hypothetical protein SEA\_TFORTROY\_58 [Arthrobacter phage TforTroy]],,NCBI, q1:s1 100.0% 1.81065E-34 GAP: 2 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.203, -4.213314289702982, no F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_TFORTROY\_58 [Arthrobacter phage TforTroy]],,WVX88046,92.5373,1.81065E-34 SIF-HHPRED: SIF-Syn: This gene is not similar to known genes.

CDS 39599 - 40567

/gene="56"

/product="gp56"

/function="endolysin"

/locus tag="Pumpkins\_56"

/note=Genemark calls start at 39599

/note=SSC: 39599-40567 CP: yes SCS: genemark ST: SS BLAST-Start: [peptidase [Arthrobacter phage Yang] ],,NCBI, q1:s1 100.0% 0.0 GAP: 71 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.215, -1.953940808934884, yes F: endolysin SIF-BLAST: ,,[peptidase [Arthrobacter phage Yang] ],,YP\_009815677,95.6522,0.0 SIF-HHPRED: SIF-Syn: This gene matches similar phages such as Yang and Cassia, as an endolysin.

CDS 40685 - 40864

/gene="57"

/product="gp57"

/function="Hypothetical Protein"

/locus tag="Pumpkins\_57"

/note=Genemark calls start at 40685

/note=SSC: 40685-40864 CP: no SCS: genemark ST: SS BLAST-Start: [hypothetical protein SEA\_ITER\_61 [Arthrobacter phage Iter] ],,NCBI, q1:s1 96.6102% 5.25444E-27 GAP: 117 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.982, -2.5052746077145835, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_ITER\_61 [Arthrobacter phage Iter] ],,URQ05049,91.5254,5.25444E-27 SIF-HHPRED: SIF-Syn: This gene is not similar to known genes.

/note=There is more coding potential before this start, but the final score and zScore are not good.

CDS 40921 - 41250

/gene="58"

/product="gp58"

/function="Hypothetical Protein"

/locus tag="Pumpkins\_58"

/note=Genemark calls start at 40921

/note=SSC: 40921-41250 CP: yes SCS: genemark ST: SS BLAST-Start: [hypothetical protein SEA\_ASCELA\_61 [Arthrobacter phage Ascela]],,NCBI, q1:s1 97.2477% 4.86744E-43 GAP: 56 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.915, -2.644643059745525, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_ASCELA\_61 [Arthrobacter phage Ascela]],,WGH21584,51.4451,4.86744E-43 SIF-HHPRED: SIF-Syn: This gene is not similar to known genes.

CDS 41312 - 41512

/gene="59"

/product="gp59"

/function="Hypothetical Protein"

/locus tag="Pumpkins\_59"

/note=Genemark calls start at 41312

/note=SSC: 41312-41512 CP: yes SCS: genemark ST: SS BLAST-Start: [hypothetical protein PQE12\_gp58 [Arthrobacter phage Adumb2043] ],,NCBI, q3:s2 96.9697% 2.5066E-34 GAP: 61 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.982, -2.5052746077145835, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein PQE12\_gp58 [Arthrobacter phage Adumb2043] ],,YP\_010677968,92.3077,2.5066E-34 SIF-HHPRED: SIF-Syn: This gene is not similar to known genes.

CDS 41637 - 41981

/gene="60"

/product="gp60"

/function="Hypothetical Protein"

/locus tag="Pumpkins\_60"

/note=Genemark calls start at 41637

/note=SSC: 41637-41981 CP: yes SCS: genemark ST: SS BLAST-Start: [hypothetical protein SEA\_CASSIA\_61 [Arthrobacter phage Cassia]],,NCBI, q1:s1 99.1228% 3.37775E-49 GAP: 124 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.885, -2.7863799983944713, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_CASSIA\_61 [Arthrobacter phage Cassia]],,WGH21134,86.6071,3.37775E-49 SIF-HHPRED: SIF-Syn: This gene is not similar to known genes.

CDS 42050 - 42364

/gene="61"

/product="gp61"

/function="Hypothetical Protein"

/locus tag="Pumpkins\_61"

/note=Genemark calls start at 42050

/note=SSC: 42050-42364 CP: yes SCS: genemark ST: SS BLAST-Start: [hypothetical protein SEA\_CASSIA\_62 [Arthrobacter phage Cassia]],,NCBI, q1:s1 100.0% 2.22786E-66 GAP: 68 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.982, -2.442961286954254, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_CASSIA\_62 [Arthrobacter phage Cassia]],,WGH21135,97.1154,2.22786E-66 SIF-HHPRED: SIF-Syn: This gene is not similar to known genes.

CDS 42357 - 42533

/gene="62"

/product="gp62"

/function="membrane protein"

/locus tag="Pumpkins\_62"

/note=Original Glimmer call @bp 42357 has strength 12.04; Genemark calls start at 42357

/note=SSC: 42357-42533 CP: yes SCS: both ST: SS BLAST-Start: [membrane protein [Arthrobacter phage Adumb2043] ],,NCBI, q3:s2 91.3793% 1.12249E-16 GAP: -8 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.982, -3.095100142625534, yes F: membrane protein SIF-BLAST: ,,[membrane protein [Arthrobacter phage Adumb2043] ],,YP\_010677973,75.4386,1.12249E-16 SIF-HHPRED: Heme exporter protein D; ATP-binding exporter, Heme transmembrane transporter, Cytochrome c biogenesis protein., MEMBRANE PROTEIN; HET: PO4, 3PE; 3.24A {Escherichia coli BL21(DE3)},,,7F02\_D,96.5517,96.2 SIF-Syn: This gene is similar to a membrane protein in Cassia.

CDS 42526 - 42690

/gene="63"

/product="gp63"

/function="Hypothetical Protein"

/locus tag="Pumpkins\_63"

/note=Genemark calls start at 42565

/note=SSC: 42526-42690 CP: yes SCS: genemark-cs ST: SS BLAST-Start: [hypothetical protein SEA\_TFORTROY\_65 [Arthrobacter phage TforTroy]],,NCBI, q1:s1 100.0% 1.87391E-25 GAP: -8 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.226, -1.993391246735709, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_TFORTROY\_65 [Arthrobacter phage TforTroy]],,WVX88053,88.8889,1.87391E-25 SIF-HHPRED: SIF-Syn: This gene is not similar to known genes.

CDS 42687 - 42800

/gene="64"

/product="gp64"

/function="Hypothetical Protein"

/locus tag="Pumpkins\_64"

/note=Original Glimmer call @bp 42687 has strength 14.22; Genemark calls start at 42687

/note=SSC: 42687-42800 CP: yes SCS: both ST: SS BLAST-Start: [membrane protein [Arthrobacter phage Amyev] ],,NCBI, q1:s1 100.0% 1.92234E-11 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.982, -2.583959800616441, yes F: Hypothetical Protein SIF-BLAST: ,,[membrane protein [Arthrobacter phage Amyev] ],,YP\_010677768,94.5946,1.92234E-11 SIF-HHPRED: SIF-Syn: This gene is not similar to known genes.

CDS 42797 - 43141

/gene="65"

/product="gp65"

/function="Hypothetical Protein"

/locus tag="Pumpkins\_65"

/note=Genemark calls start at 42797

/note=SSC: 42797-43141 CP: yes SCS: genemark ST: SS BLAST-Start: [hypothetical protein SEA\_ITER\_68 [Arthrobacter phage Iter]],,NCBI, q5:s4 93.8596% 3.26829E-48 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.05, -4.3913063680686815, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_ITER\_68 [Arthrobacter phage Iter]],,URQ05056,77.6786,3.26829E-48 SIF-HHPRED: SIF-Syn: This gene is not similar to known genes.

CDS 43401 - 43607

/gene="66"

/product="gp66"

/function="Hypothetical Protein"

/locus tag="Pumpkins\_66"

/note=Original Glimmer call @bp 43401 has strength 6.17; Genemark calls start at 43401

/note=SSC: 43401-43607 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_CASSIA\_67 [Arthrobacter phage Cassia]],,NCBI, q1:s1 83.8235% 8.55951E-27 GAP: 259 bp gap LO: no RBS: Kibler 6, Karlin Medium, 3.215, -2.606079664606164, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_CASSIA\_67 [Arthrobacter phage Cassia]],,WGH21140,83.871,8.55951E-27 SIF-HHPRED: SIF-Syn: This gene is not similar to known genes.

/note=Does have a large gap. Both Yang and Cassia also have the gap