**Evaa Annotation notes from PECAAN**

CDS 1 - 699

 /gene="1"

 /product="gp1"

 /function="ParB-like nuclease domain"

 /locus tag="Evaa\_1"

 /note=Original Glimmer call @bp 1 has strength 16.79; Genemark calls start at 1

 /note=SSC: 1-699 CP: no SCS: both ST: SS BLAST-Start: [ParB-like nuclease domain protein [Gordonia phage Ligma]],,NCBI, q1:s1 64.6552% 7.02402E-64 GAP: 0 bp gap LO: no RBS: Kibler 6, Karlin Medium, 0.695, -7.392277536015967, no F: ParB-like nuclease domain SIF-BLAST: ,,[ParB-like nuclease domain protein [Gordonia phage Ligma]],,UJE15656,57.7114,7.02402E-64 SIF-HHPRED: Stage 0 sporulation protein J; ParB, Chromosome segregation, Chromosome organization, DNA BINDING PROTEIN; HET: CDP, MSE; 1.81A {Bacillus subtilis (strain 168)} SCOP: a.4.14.0, d.268.1.0,,,6SDK\_A,59.0517,99.6 SIF-Syn:

CDS 702 - 2237

 /gene="2"

 /product="gp2"

 /function="ParB-like nuclease domain"

 /locus tag="Evaa\_2"

 /note=Original Glimmer call @bp 702 has strength 14.15; Genemark calls start at 702

 /note=SSC: 702-2237 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein DCF22\_18190 [Leptolyngbya sp.]],,NCBI, q8:s1 98.2387% 1.79727E-179 GAP: 2 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.929, -5.2088931604536635, no F: ParB-like nuclease domain SIF-BLAST: ,,[hypothetical protein DCF22\_18190 [Leptolyngbya sp.]],,PZV09621,68.9861,1.79727E-179 SIF-HHPRED: ParB domain protein nuclease; ParB-N, pnob8, partition, HYDROLASE; HET: MSE, CIT; 2.45A {Sulfolobus solfataricus},,,5K5D\_B,21.7221,99.6 SIF-Syn:

 /note=ParB N-terminal domain-containing protein

CDS complement (2239 - 2619)

 /gene="3"

 /product="gp3"

 /function="hypothetical protein"

 /locus tag="Evaa\_3"

 /note=Original Glimmer call @bp 2619 has strength 20.04; Genemark calls start at 2619

 /note=SSC: 2619-2239 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein X577\_gp164 [Staphylococcus phage S25-4] ],,NCBI, q4:s1 95.2381% 2.44304E-4 GAP: 13 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.197, -2.604595770381943, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein X577\_gp164 [Staphylococcus phage S25-4] ],,YP\_008853970,54.386,2.44304E-4 SIF-HHPRED: SIF-Syn:

CDS complement (2633 - 3190)

 /gene="4"

 /product="gp4"

 /function="phosphatase"

 /locus tag="Evaa\_4"

 /note=Original Glimmer call @bp 3115 has strength 14.28; Genemark calls start at 3115

 /note=SSC: 3190-2633 CP: yes SCS: both-cs ST: NI BLAST-Start: [hypothetical protein [Ruficoccus amylovorans] ],,NCBI, q31:s2 72.973% 6.60944E-24 GAP: 45 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.116, -5.523181143081532, no F: phosphatase SIF-BLAST: ,,[hypothetical protein [Ruficoccus amylovorans] ],,WP\_185674767,59.8592,6.60944E-24 SIF-HHPRED: c.108.1.9 (A:153-301) Polynucleotide kinase, phosphatase domain {Bacteriophage T4 [TaxId: 10665]},,,d1ltqa1,74.0541,99.6 SIF-Syn:

CDS 3236 - 3952

 /gene="5"

 /product="gp5"

 /function="methyltransferase"

 /locus tag="Evaa\_5"

 /note=Original Glimmer call @bp 3236 has strength 14.09; Genemark calls start at 3236

 /note=SSC: 3236-3952 CP: no SCS: both ST: SS BLAST-Start: [methyltransferase domain-containing protein [Streptomyces sp. LBUM 1479] ],,NCBI, q3:s70 98.7395% 9.92965E-79 GAP: 45 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 0.991, -7.834082185671665, no F: methyltransferase SIF-BLAST: ,,[methyltransferase domain-containing protein [Streptomyces sp. LBUM 1479] ],,WP\_210647141,50.6452,9.92965E-79 SIF-HHPRED: CmoA; carboxy-S-adenosyl-L-methionine synthase. Carboxy-S-adenosyl-L-methionine synthase (Cx-SAM synthase) catalyzes the conversion of S-adenosyl-L-methionine (SAM) to carboxy-S-adenosyl-L-methionine (Cx-SAM) and plays a role in the role in tRNA modification, together with CmoB.,,,cd02495,87.8151,99.9 SIF-Syn:

CDS 3949 - 5649

 /gene="6"

 /product="gp6"

 /function="terminase"

 /locus tag="Evaa\_6"

 /note=Original Glimmer call @bp 3949 has strength 14.33; Genemark calls start at 3949

 /note=SSC: 3949-5649 CP: no SCS: both ST: SS BLAST-Start: [terminase [Mycobacterium phage Gadjet] ],,NCBI, q8:s31 98.5866% 0.0 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.097, -5.420490675428641, no F: terminase SIF-BLAST: ,,[terminase [Mycobacterium phage Gadjet] ],,YP\_009011237,75.4653,0.0 SIF-HHPRED: DNA packaging protein Gp17; large terminase, Alternative initiation, ATP-binding, DNA-binding, Hydrolase, Nuclease, Nucleotide-binding; HET: PO4; 2.8A {Bacteriophage T4},,,3CPE\_A,86.0424,100.0 SIF-Syn:

CDS complement (5651 - 6193)

 /gene="7"

 /product="gp7"

 /function="RuvC-like resolvase"

 /locus tag="Evaa\_7"

 /note=Original Glimmer call @bp 6193 has strength 17.26; Genemark calls start at 6193

 /note=SSC: 6193-5651 CP: no SCS: both ST: SS BLAST-Start: [RuvC-like resolvase [Mycobacterium phage Gervas]],,NCBI, q1:s1 98.3333% 4.4097E-50 GAP: 54 bp gap LO: no RBS: Kibler 6, Karlin Medium, 0.85, -7.134752732491032, no F: RuvC-like resolvase SIF-BLAST: ,,[RuvC-like resolvase [Mycobacterium phage Gervas]],,QOI67309,64.6409,4.4097E-50 SIF-HHPRED: c.55.3.6 (A:) RuvC resolvase {Thermus thermophilus [TaxId: 300852]},,,d4ep4a\_,88.8889,100.0 SIF-Syn:

CDS 6248 - 6592

 /gene="8"

 /product="gp8"

 /function="membrane protein"

 /locus tag="Evaa\_8"

 /note=Original Glimmer call @bp 6248 has strength 17.05; Genemark calls start at 6248

 /note=SSC: 6248-6592 CP: yes SCS: both ST: SS BLAST-Start: [membrane protein [Gordonia phage NHagos]],,NCBI, q1:s1 99.1228% 5.81864E-46 GAP: 54 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.493, -6.661315563983987, no F: membrane protein SIF-BLAST: ,,[membrane protein [Gordonia phage NHagos]],,QGH80018,82.3009,5.81864E-46 SIF-HHPRED: DUF2085 ; Predicted membrane protein (DUF2085),,,PF09858.12,42.9825,70.7 SIF-Syn:

CDS 6619 - 8448

 /gene="9"

 /product="gp9"

 /function="portal protein"

 /locus tag="Evaa\_9"

 /note=Original Glimmer call @bp 6664 has strength 17.12; Genemark calls start at 6664

 /note=SSC: 6619-8448 CP: yes SCS: both-cs ST: NI BLAST-Start: [portal protein [Gordonia phage AnarQue]],,NCBI, q1:s1 99.6716% 0.0 GAP: 26 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.748, -5.309117108752867, no F: portal protein SIF-BLAST: ,,[portal protein [Gordonia phage AnarQue]],,UBF41613,81.1382,0.0 SIF-HHPRED: SIF-Syn:

CDS 8448 - 10856

 /gene="10"

 /product="gp10"

 /function="capsid maturation protease"

 /locus tag="Evaa\_10"

 /note=Original Glimmer call @bp 8448 has strength 13.42; Genemark calls start at 8448

 /note=SSC: 8448-10856 CP: no SCS: both ST: SS BLAST-Start: [capsid morphogenesis protein [Mycobacterium phage CRB2] ],,NCBI, q1:s1 94.5137% 0.0 GAP: -1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.825, -3.925090669525967, no F: capsid maturation protease SIF-BLAST: ,,[capsid morphogenesis protein [Mycobacterium phage CRB2] ],,YP\_009949866,68.2095,0.0 SIF-HHPRED: Phage\_min\_cap2 ; Phage minor capsid protein 2,,,PF06152.14,11.3466,99.0 SIF-Syn:

 /note=capsid morphogeneis protein

CDS 10856 - 11044

 /gene="11"

 /product="gp11"

 /function="hypothetical protein"

 /locus tag="Evaa\_11"

 /note=Original Glimmer call @bp 10856 has strength 11.67; Genemark calls start at 10856

 /note=SSC: 10856-11044 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_NHAGOS\_10 [Gordonia phage NHagos]],,NCBI, q1:s1 100.0% 6.63481E-26 GAP: -1 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.664, -3.4892599424135016, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein SEA\_NHAGOS\_10 [Gordonia phage NHagos]],,QGH80021,80.597,6.63481E-26 SIF-HHPRED: SIF-Syn:

CDS 11135 - 12874

 /gene="12"

 /product="gp12"

 /function="major capsid protein"

 /locus tag="Evaa\_12"

 /note=Original Glimmer call @bp 11135 has strength 16.29; Genemark calls start at 11135

 /note=SSC: 11135-12874 CP: yes SCS: both ST: SS BLAST-Start: [major capsid hexamer protein [Gordonia phage Ligma]],,NCBI, q2:s4 99.8273% 0.0 GAP: 90 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.105, -2.442961286954254, yes F: major capsid protein SIF-BLAST: ,,[major capsid hexamer protein [Gordonia phage Ligma]],,UJE15666,81.1287,0.0 SIF-HHPRED: Major capsid protein; Virus Procapsid particles, VIRUS; 5.2A {Enterobacteria phage HK97},,,3QPR\_D,10.0173,33.1 SIF-Syn:

CDS 12976 - 13755

 /gene="13"

 /product="gp13"

 /function="major capsid protein"

 /locus tag="Evaa\_13"

 /note=Original Glimmer call @bp 12976 has strength 11.56; Genemark calls start at 12976

 /note=SSC: 12976-13755 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein [Gordonia otitidis] ],,NCBI, q5:s2 96.9112% 1.32372E-106 GAP: 101 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.674, -3.4076099559729456, yes F: major capsid protein SIF-BLAST: ,,[hypothetical protein [Gordonia otitidis] ],,WP\_227919753,75.2941,1.32372E-106 SIF-HHPRED: SIF-Syn:

 /note=major capsid pentamer protein

CDS 13757 - 14248

 /gene="14"

 /product="gp14"

 /function="hypothetical protein"

 /locus tag="Evaa\_14"

 /note=Original Glimmer call @bp 13757 has strength 16.43; Genemark calls start at 13757

 /note=SSC: 13757-14248 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_LIGMA\_13 [Gordonia phage Ligma]],,NCBI, q1:s1 100.0% 1.24098E-46 GAP: 1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.426, -3.8366550365551095, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein SEA\_LIGMA\_13 [Gordonia phage Ligma]],,UJE15668,64.5349,1.24098E-46 SIF-HHPRED: SIF-Syn:

CDS 14245 - 14619

 /gene="15"

 /product="gp15"

 /function="holin"

 /locus tag="Evaa\_15"

 /note=Original Glimmer call @bp 14245 has strength 11.69; Genemark calls start at 14245

 /note=SSC: 14245-14619 CP: no SCS: both ST: SS BLAST-Start: [membrane protein [Gordonia phage NHagos]],,NCBI, q2:s3 99.1936% 1.05454E-53 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.105, -2.5052746077145835, yes F: holin SIF-BLAST: ,,[membrane protein [Gordonia phage NHagos]],,QGH80025,81.6,1.05454E-53 SIF-HHPRED: Phage\_holin\_7\_1 ; Mycobacterial 2 TMS Phage Holin (M2 Hol) Family,,,PF16081.8,41.9355,94.6 SIF-Syn:

 /note=membrane protein

CDS 14619 - 15095

 /gene="16"

 /product="gp16"

 /function="membrane protein"

 /locus tag="Evaa\_16"

 /note=Original Glimmer call @bp 14619 has strength 11.99; Genemark calls start at 14619

 /note=SSC: 14619-15095 CP: no SCS: both ST: SS BLAST-Start: [membrane protein [Gordonia phage Sour] ],,NCBI, q1:s2 100.0% 3.71521E-84 GAP: -1 bp gap LO: no RBS: Kibler 6, Karlin Medium, 0.094, -8.705509164408271, no F: membrane protein SIF-BLAST: ,,[membrane protein [Gordonia phage Sour] ],,YP\_009625589,86.7924,3.71521E-84 SIF-HHPRED: SIF-Syn:

CDS 15092 - 15559

 /gene="17"

 /product="gp17"

 /function="membrane protein"

 /locus tag="Evaa\_17"

 /note=Original Glimmer call @bp 15092 has strength 10.26; Genemark calls start at 15092

 /note=SSC: 15092-15559 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_YAGO84\_16 [Gordonia phage Yago84] ],,NCBI, q1:s1 100.0% 3.53912E-75 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.664, -3.4283035164720754, yes F: membrane protein SIF-BLAST: ,,[hypothetical protein SEA\_YAGO84\_16 [Gordonia phage Yago84] ],,QDF17548,83.9744,3.53912E-75 SIF-HHPRED: SIF-Syn:

CDS 15556 - 15870

 /gene="18"

 /product="gp18"

 /function="membrane protein"

 /locus tag="Evaa\_18"

 /note=Original Glimmer call @bp 15556 has strength 17.39; Genemark calls start at 15556

 /note=SSC: 15556-15870 CP: no SCS: both ST: SS BLAST-Start: [membrane protein [Gordonia phage CloverMinnie]],,NCBI, q4:s3 97.1154% 1.93963E-50 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.006, -2.7863799983944713, yes F: membrane protein SIF-BLAST: ,,[membrane protein [Gordonia phage CloverMinnie]],,QFG11166,85.4369,1.93963E-50 SIF-HHPRED: SIF-Syn:

CDS 15945 - 16754

 /gene="19"

 /product="gp19"

 /function="major tail protein"

 /locus tag="Evaa\_19"

 /note=Original Glimmer call @bp 15945 has strength 13.65; Genemark calls start at 15945

 /note=SSC: 15945-16754 CP: no SCS: both ST: SS BLAST-Start: [major tail protein [Gordonia phage Mariokart]],,NCBI, q1:s1 100.0% 9.36698E-174 GAP: 74 bp gap LO: no RBS: Kibler 6, Karlin Medium, 3.028, -2.7423981586358774, no F: major tail protein SIF-BLAST: ,,[major tail protein [Gordonia phage Mariokart]],,QNL30145,91.1111,9.36698E-174 SIF-HHPRED: L\_lac\_phage\_MSP ; Phage tail tube protein,,,PF06488.14,67.2862,90.7 SIF-Syn:

CDS 16832 - 17593

 /gene="20"

 /product="gp20"

 /function="head-to-tail adaptor"

 /locus tag="Evaa\_20"

 /note=Original Glimmer call @bp 16832 has strength 8.89; Genemark calls start at 16832

 /note=SSC: 16832-17593 CP: no SCS: both ST: SS BLAST-Start: [head-to-tail adaptor [Gordonia phage AnClar]],,NCBI, q1:s1 100.0% 2.05163E-90 GAP: 77 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.003, -5.612695330525874, no F: head-to-tail adaptor SIF-BLAST: ,,[head-to-tail adaptor [Gordonia phage AnClar]],,QIG58947,70.5645,2.05163E-90 SIF-HHPRED: Adaptor protein Rcc01688; "neck", "portal", "capsid", "tail tube", VIRUS; 3.58A {Rhodobacter capsulatus},,,6TE9\_D,84.9802,99.6 SIF-Syn:

CDS 17590 - 18126

 /gene="21"

 /product="gp21"

 /function="hypothetical protein"

 /locus tag="Evaa\_21"

 /note=Original Glimmer call @bp 17590 has strength 11.82; Genemark calls start at 17590

 /note=SSC: 17590-18126 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_CLOVERMINNIE\_22 [Gordonia phage CloverMinnie] ],,NCBI, q1:s1 100.0% 2.08591E-79 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.614, -4.103700314387452, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_CLOVERMINNIE\_22 [Gordonia phage CloverMinnie] ],,QFG11169,77.095,2.08591E-79 SIF-HHPRED: SIF-Syn:

CDS 18139 - 18468

 /gene="22"

 /product="gp22"

 /function="tail assembly chaperone"

 /locus tag="Evaa\_22"

 /note=Original Glimmer call @bp 18139 has strength 10.63; Genemark calls start at 18139

 /note=SSC: 18139-18468 CP: yes SCS: both ST: SS BLAST-Start: [tail assembly chaperone [Gordonia phage Mariokart]],,NCBI, q2:s3 98.1651% 2.6659E-27 GAP: 12 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.186, -2.338663114094478, yes F: tail assembly chaperone SIF-BLAST: ,,[tail assembly chaperone [Gordonia phage Mariokart]],,QNL30148,64.2202,2.6659E-27 SIF-HHPRED: SIF-Syn:

CDS 18465 - 18881

 /gene="23"

 /product="gp23"

 /function="tail assembly chaperone"

 /locus tag="Evaa\_23"

 /note=Original Glimmer call @bp 18465 has strength 6.97; Genemark calls start at 18465

 /note=SSC: 18465-18881 CP: yes SCS: both ST: SS BLAST-Start: [tail assembly chaperone [Gordonia phage CloverMinnie] ],,NCBI, q3:s2 96.3768% 1.19495E-53 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.898, -5.829606170632219, no F: tail assembly chaperone SIF-BLAST: ,,[tail assembly chaperone [Gordonia phage CloverMinnie] ],,QFG11171,75.7353,1.19495E-53 SIF-HHPRED: Minor\_capsid\_2 ; Minor capsid protein,,,PF11114.11,89.1304,99.5 SIF-Syn:

CDS 18931 - 19455

 /gene="24"

 /product="gp24"

 /function="tail assembly chaperone"

 /locus tag="Evaa\_24"

 /note=Original Glimmer call @bp 18940 has strength 16.59; Genemark calls start at 18931

 /note=SSC: 18931-19455 CP: no SCS: both-gm ST: NI BLAST-Start: [hypothetical protein FDJ57\_gp27 [Gordonia phage Sour] ],,NCBI, q16:s21 79.8851% 1.2165E-49 GAP: 49 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.193, -4.9668027763900575, yes F: tail assembly chaperone SIF-BLAST: ,,[hypothetical protein FDJ57\_gp27 [Gordonia phage Sour] ],,YP\_009625598,60.355,1.2165E-49 SIF-HHPRED: SIF-Syn:

CDS 19484 - 24991

 /gene="25"

 /product="gp25"

 /function="tape measure protein"

 /locus tag="Evaa\_25"

 /note=Original Glimmer call @bp 19484 has strength 13.76; Genemark calls start at 19484

 /note=SSC: 19484-24991 CP: yes SCS: both ST: SS BLAST-Start: [tape measure protein [Gordonia phage AnClar]],,NCBI, q2:s3 99.9455% 0.0 GAP: 28 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.871, -5.884908979099125, no F: tape measure protein SIF-BLAST: ,,[tape measure protein [Gordonia phage AnClar]],,QIG58952,80.6346,0.0 SIF-HHPRED: Tape Measure Protein, gp57; phage tail, tail tip, tape measure protein, VIRAL PROTEIN; 3.7A {Staphylococcus virus 80alpha},,,6V8I\_AF,2.99728,99.8 SIF-Syn:

CDS 25002 - 26525

 /gene="26"

 /product="gp26"

 /function="minor tail protein"

 /locus tag="Evaa\_26"

 /note=Original Glimmer call @bp 25002 has strength 15.75; Genemark calls start at 25002

 /note=SSC: 25002-26525 CP: yes SCS: both ST: SS BLAST-Start: [minor tail protein [Gordonia phage CloverMinnie] ],,NCBI, q1:s1 100.0% 0.0 GAP: 10 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.197, -2.253486910374644, yes F: minor tail protein SIF-BLAST: ,,[minor tail protein [Gordonia phage CloverMinnie] ],,QFG11174,77.9528,0.0 SIF-HHPRED: ORF46; Distal tail protein, Receptor-binding protein, Phage baseplate, host adsorption apparatus, genome injection device, VIRAL PROTEIN; 3.8A {Lactococcus phage TP901-1},,,4V96\_AX,29.1913,94.5 SIF-Syn:

CDS 26530 - 27573

 /gene="27"

 /product="gp27"

 /function="minor tail protein"

 /locus tag="Evaa\_27"

 /note=Original Glimmer call @bp 26530 has strength 14.21; Genemark calls start at 26530

 /note=SSC: 26530-27573 CP: yes SCS: both ST: SS BLAST-Start: [minor tail protein [Gordonia phage NHagos]],,NCBI, q1:s1 100.0% 9.7811E-156 GAP: 4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.185, -5.239915530731485, no F: minor tail protein SIF-BLAST: ,,[minor tail protein [Gordonia phage NHagos]],,QGH80037,77.2334,9.7811E-156 SIF-HHPRED: SIF-Syn:

CDS 27570 - 28292

 /gene="28"

 /product="gp28"

 /function="minor tail protein"

 /locus tag="Evaa\_28"

 /note=Original Glimmer call @bp 27570 has strength 11.77; Genemark calls start at 27570

 /note=SSC: 27570-28292 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein [Salmonella enterica]],,NCBI, q85:s339 65.0% 1.65166E-20 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.155, -5.300501888807407, no F: minor tail protein SIF-BLAST: ,,[hypothetical protein [Salmonella enterica]],,EAS0269351,17.9959,1.65166E-20 SIF-HHPRED: SIF-Syn:

CDS 28292 - 28906

 /gene="29"

 /product="gp29"

 /function="hypothetical protein"

 /locus tag="Evaa\_29"

 /note=Original Glimmer call @bp 28292 has strength 11.52; Genemark calls start at 28292

 /note=SSC: 28292-28906 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_NHAGOS\_29 [Gordonia phage NHagos]],,NCBI, q1:s1 100.0% 7.56423E-112 GAP: -1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.664, -3.4283035164720754, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein SEA\_NHAGOS\_29 [Gordonia phage NHagos]],,QGH80040,86.2745,7.56423E-112 SIF-HHPRED: SIF-Syn:

CDS 28903 - 29499

 /gene="30"

 /product="gp30"

 /function="hypothetical protein"

 /locus tag="Evaa\_30"

 /note=Original Glimmer call @bp 28903 has strength 13.35; Genemark calls start at 28903

 /note=SSC: 28903-29499 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_CLOVERMINNIE\_32 [Gordonia phage CloverMinnie]],,NCBI, q4:s3 96.9697% 1.77614E-107 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.076, -4.6353190821692705, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein PBI\_CLOVERMINNIE\_32 [Gordonia phage CloverMinnie]],,QFG11179,84.8485,1.77614E-107 SIF-HHPRED: SIF-Syn:

CDS 29501 - 30109

 /gene="31"

 /product="gp31"

 /function="hypothetical protein"

 /locus tag="Evaa\_31"

 /note=Original Glimmer call @bp 29501 has strength 16.4; Genemark calls start at 29501

 /note=SSC: 29501-30109 CP: yes SCS: both ST: SS BLAST-Start: [minor tail protein [Gordonia phage Sour] ],,NCBI, q2:s21 99.505% 3.08814E-79 GAP: 1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.792, -3.147993589957652, yes F: hypothetical protein SIF-BLAST: ,,[minor tail protein [Gordonia phage Sour] ],,YP\_009625607,68.6636,3.08814E-79 SIF-HHPRED: SIF-Syn:

 /note=one hit to minor protein

CDS 30134 - 30493

 /gene="32"

 /product="gp32"

 /function="tail assembly chaperone"

 /locus tag="Evaa\_32"

 /note=Original Glimmer call @bp 30134 has strength 12.88; Genemark calls start at 30134

 /note=SSC: 30134-30493 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein PBI\_CLOVERMINNIE\_34 [Gordonia phage CloverMinnie]],,NCBI, q1:s3 94.958% 1.7881E-43 GAP: 24 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.235, -4.309437458116814, no F: tail assembly chaperone SIF-BLAST: ,,[hypothetical protein PBI\_CLOVERMINNIE\_34 [Gordonia phage CloverMinnie]],,QFG11181,75.6522,1.7881E-43 SIF-HHPRED: Phage\_TAC\_10 ; Phage tail assembly chaperone,,,PF10963.11,63.8655,94.5 SIF-Syn:

CDS 30616 - 30780

 /gene="33"

 /product="gp33"

 /function="hypothetical protein"

 /locus tag="Evaa\_33"

 /note=Original Glimmer call @bp 30514 has strength 9.54; Genemark calls start at 30514

 /note=SSC: 30616-30780 CP: no SCS: both-cs ST: NI BLAST-Start: [hypothetical protein FDJ57\_gp38 [Gordonia phage Sour] ],,NCBI, q4:s55 94.4444% 5.30011E-12 GAP: 122 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.597, -4.314236340998582, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein FDJ57\_gp38 [Gordonia phage Sour] ],,YP\_009625609,40.7767,5.30011E-12 SIF-HHPRED: SIF-Syn:

 /note=Z score above 2 , Final score less negative

CDS 30799 - 31209

 /gene="34"

 /product="gp34"

 /function="hypothetical protein"

 /locus tag="Evaa\_34"

 /note=Original Glimmer call @bp 30790 has strength 16.13; Genemark calls start at 30799

 /note=SSC: 30799-31209 CP: no SCS: both-gm ST: NI BLAST-Start: [hypothetical protein SEA\_LIGMA\_34 [Gordonia phage Ligma]],,NCBI, q1:s1 100.0% 2.60013E-49 GAP: 18 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.317, -6.113681602330036, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein SEA\_LIGMA\_34 [Gordonia phage Ligma]],,UJE15689,74.6377,2.60013E-49 SIF-HHPRED: SIF-Syn:

CDS 31206 - 31898

 /gene="35"

 /product="gp35"

 /function="minor tail protein"

 /locus tag="Evaa\_35"

 /note=Original Glimmer call @bp 31206 has strength 11.86; Genemark calls start at 31206

 /note=SSC: 31206-31898 CP: yes SCS: both ST: SS BLAST-Start: [minor tail protein [Gordonia phage Mariokart]],,NCBI, q1:s1 100.0% 7.59825E-86 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.102, -5.410275132747843, no F: minor tail protein SIF-BLAST: ,,[minor tail protein [Gordonia phage Mariokart]],,QNL30162,74.6725,7.59825E-86 SIF-HHPRED: SIF-Syn:

CDS 31898 - 33037

 /gene="36"

 /product="gp36"

 /function="minor tail protein"

 /locus tag="Evaa\_36"

 /note=Original Glimmer call @bp 31898 has strength 19.91; Genemark calls start at 31898

 /note=SSC: 31898-33037 CP: yes SCS: both ST: SS BLAST-Start: [minor tail protein [Gordonia phage AnClar]],,NCBI, q148:s36 60.4222% 1.69065E-62 GAP: -1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.517, -3.790975366313636, no F: minor tail protein SIF-BLAST: ,,[minor tail protein [Gordonia phage AnClar]],,QIG58964,61.6236,1.69065E-62 SIF-HHPRED: SIF-Syn:

CDS 33037 - 33708

 /gene="37"

 /product="gp37"

 /function="hypothetical protein"

 /locus tag="Evaa\_37"

 /note=Original Glimmer call @bp 33037 has strength 4.44; Genemark calls start at 33037

 /note=SSC: 33037-33708 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_BOOHOO\_8 [Gordonia Phage Boohoo]],,NCBI, q15:s14 93.2735% 2.67061E-34 GAP: -1 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.224, -4.252718798978677, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein SEA\_BOOHOO\_8 [Gordonia Phage Boohoo]],,UAJ15503,72.0721,2.67061E-34 SIF-HHPRED: SIF-Syn: phages db- minor tail protein

CDS complement (33678 - 33917)

 /gene="38"

 /product="gp38"

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

 /locus tag="Evaa\_38"

 /note=Original Glimmer call @bp 33917 has strength 10.41; Genemark calls start at 33917

 /note=SSC: 33917-33678 CP: no SCS: both ST: SS BLAST-Start: [LamD-like [Gordonia phage CloverMinnie] ],,NCBI, q1:s7 98.7342% 2.43905E-21 GAP: -20 bp gap LO: no RBS: Kibler 6, Karlin Medium, 3.105, -2.442961286954254, yes F: helix-turn-helix DNA binding domain SIF-BLAST: ,,[LamD-like [Gordonia phage CloverMinnie] ],,QFG11187,63.0952,2.43905E-21 SIF-HHPRED: SIF-Syn:

 /note=lamd-like

CDS complement (33898 - 34284)

 /gene="39"

 /product="gp39"

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

 /locus tag="Evaa\_39"

 /note=Original Glimmer call @bp 34284 has strength 12.5; Genemark calls start at 34284

 /note=SSC: 34284-33898 CP: no SCS: both ST: SS BLAST-Start: [helix-turn-helix domain-containing protein [Mycobacteroides abscessus] ],,NCBI, q1:s1 92.9688% 1.12022E-31 GAP: 643 bp gap LO: no RBS: Kibler 6, Karlin Medium, 3.099, -2.9831072272156547, yes F: helix-turn-helix DNA binding domain SIF-BLAST: ,,[helix-turn-helix domain-containing protein [Mycobacteroides abscessus] ],,WP\_074248253,61.2403,1.12022E-31 SIF-HHPRED: SIF-Syn:

CDS 34928 - 36121

 /gene="40"

 /product="gp40"

 /function="lysin A"

 /locus tag="Evaa\_40"

 /note=Original Glimmer call @bp 35093 has strength 13.72; Genemark calls start at 35093

 /note=SSC: 34928-36121 CP: no SCS: both-cs ST: NI BLAST-Start: [lysin A [Gordonia phage DumpsterDude] ],,NCBI, q56:s1 84.6348% 0.0 GAP: 643 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.177, -4.349108688274226, no F: lysin A SIF-BLAST: ,,[lysin A [Gordonia phage DumpsterDude] ],,YP\_010001091,80.8696,0.0 SIF-HHPRED: SIF-Syn:

CDS complement (34357 - 34989)

 /gene="41"

 /product="gp41"

 /function="hypothetical protein"

 /locus tag="Evaa\_41"

 /note=Original Glimmer call @bp 34989 has strength 16.97; Genemark calls start at 34989

 /note=SSC: 34989-34357 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein TPA2\_gp53 [Tsukamurella phage TPA2] ],,NCBI, q15:s25 93.3333% 1.42995E-42 GAP: 1128 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.849, -3.0301037898918786, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein TPA2\_gp53 [Tsukamurella phage TPA2] ],,YP\_004286294,51.4403,1.42995E-42 SIF-HHPRED: SIF-Syn:

CDS 36118 - 36834

 /gene="42"

 /product="gp42"

 /function="lysin B"

 /locus tag="Evaa\_42"

 /note=Original Glimmer call @bp 36118 has strength 10.71; Genemark calls start at 36118

 /note=SSC: 36118-36834 CP: no SCS: both ST: SS BLAST-Start: [lysin B [Gordonia phage PhorbesPhlower]],,NCBI, q1:s1 97.8992% 3.21902E-61 GAP: 1128 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.781, -4.41389452160345, yes F: lysin B SIF-BLAST: ,,[lysin B [Gordonia phage PhorbesPhlower]],,QDP43653,64.1026,3.21902E-61 SIF-HHPRED: SIF-Syn:

CDS complement (36944 - 37468)

 /gene="43"

 /product="gp43"

 /function="hypothetical protein"

 /locus tag="Evaa\_43"

 /note=Original Glimmer call @bp 37468 has strength 20.31; Genemark calls start at 37468

 /note=SSC: 37468-36944 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein FDJ57\_gp48 [Gordonia phage Sour] ],,NCBI, q38:s34 77.5862% 2.87905E-57 GAP: 27 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.266, -2.4634880269616195, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein FDJ57\_gp48 [Gordonia phage Sour] ],,YP\_009625619,64.9123,2.87905E-57 SIF-HHPRED: SIF-Syn:

CDS complement (37496 - 38752)

 /gene="44"

 /product="gp44"

 /function="exonuclease"

 /locus tag="Evaa\_44"

 /note=Original Glimmer call @bp 38752 has strength 12.85; Genemark calls start at 38626

 /note=SSC: 38752-37496 CP: yes SCS: both-gl ST: SS BLAST-Start: [exonuclease [Gordonia phage Yago84] ],,NCBI, q1:s1 97.3684% 0.0 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.674, -3.4685663819143713, no F: exonuclease SIF-BLAST: ,,[exonuclease [Gordonia phage Yago84] ],,QDF17576,76.7221,0.0 SIF-HHPRED: c.52.1.24 (B:899-1174) Exodeoxyribonuclease V beta chain (RecB), C-terminal domain {Escherichia coli [TaxId: 562]},,,d1w36b3,33.9713,98.6 SIF-Syn:

CDS complement (38749 - 40446)

 /gene="45"

 /product="gp45"

 /function="DNA helicase"

 /locus tag="Evaa\_45"

 /note=Original Glimmer call @bp 40446 has strength 15.23; Genemark calls start at 40446

 /note=SSC: 40446-38749 CP: yes SCS: both ST: SS BLAST-Start: [DNA helicase [Gordonia phage Sour] ],,NCBI, q7:s8 98.2301% 0.0 GAP: 111 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.841, -5.389187297999249, no F: DNA helicase SIF-BLAST: ,,[DNA helicase [Gordonia phage Sour] ],,YP\_009625621,77.6173,0.0 SIF-HHPRED: ATP-dependent DNA helicase uvsW; ATP-dependant helicase, T4-bacteriophage, Recombination, HYDROLASE; 2.7A {Enterobacteria phage T4},,,2OCA\_A,61.9469,100.0 SIF-Syn:

CDS complement (40558 - 41052)

 /gene="46"

 /product="gp46"

 /function="Hypothetical protein"

 /locus tag="Evaa\_46"

 /note=Original Glimmer call @bp 41052 has strength 14.97; Genemark calls start at 41052

 /note=SSC: 41052-40558 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein [Mycobacteroides abscessus] ],,NCBI, q4:s2 95.7317% 4.85731E-18 GAP: -1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.597, -4.3934175870462076, yes F: Hypothetical protein SIF-BLAST: ,,[hypothetical protein [Mycobacteroides abscessus] ],,WP\_074321720,48.4472,4.85731E-18 SIF-HHPRED: SIF-Syn:

CDS complement (41052 - 41342)

 /gene="47"

 /product="gp47"

 /function="Hypothetical protein"

 /locus tag="Evaa\_47"

 /note=Original Glimmer call @bp 41342 has strength 19.16; Genemark calls start at 41342

 /note=SSC: 41342-41052 CP: yes SCS: both ST: SS BLAST-Start: GAP: 18 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.088, -2.5588120788329394, yes F: Hypothetical protein SIF-BLAST: SIF-HHPRED: SIF-Syn:

CDS complement (41361 - 41735)

 /gene="48"

 /product="gp48"

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

 /locus tag="Evaa\_48"

 /note=Original Glimmer call @bp 41735 has strength 7.24; Genemark calls start at 41741

 /note=SSC: 41735-41361 CP: no SCS: both-gl ST: NI BLAST-Start: [helix-turn-helix DNA binding domain protein [Gordonia phage Ligma]],,NCBI, q1:s1 97.5806% 1.60805E-27 GAP: -14 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.864, -4.9912573797770525, no F: helix-turn-helix DNA binding domain SIF-BLAST: ,,[helix-turn-helix DNA binding domain protein [Gordonia phage Ligma]],,UJE15703,68.1034,1.60805E-27 SIF-HHPRED: Putative uncharacterized protein; DNA BINDING PROTEIN; NMR {Hyperthermus butylicus},,,2LVS\_A,72.5806,99.2 SIF-Syn:

CDS complement (41722 - 44214)

 /gene="49"

 /product="gp49"

 /function="RepA-like helicase"

 /locus tag="Evaa\_49"

 /note=Original Glimmer call @bp 44214 has strength 15.5; Genemark calls start at 44214

 /note=SSC: 44214-41722 CP: yes SCS: both ST: NI BLAST-Start: [DNA primase/helicase [Gordonia phage NHagos]],,NCBI, q4:s1 99.5181% 0.0 GAP: 52 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.764, -5.1965167960113865, no F: RepA-like helicase SIF-BLAST: ,,[DNA primase/helicase [Gordonia phage NHagos]],,QGH80061,75.6821,0.0 SIF-HHPRED: c.37.1.11 (A:) Hexameric replicative helicase repA {Escherichia coli [TaxId: 562]},,,d1nlfa\_,27.7108,99.8 SIF-Syn:

CDS complement (44267 - 46072)

 /gene="50"

 /product="gp50"

 /function="DNA polymerase I"

 /locus tag="Evaa\_50"

 /note=Original Glimmer call @bp 46072 has strength 15.3; Genemark calls start at 46072

 /note=SSC: 46072-44267 CP: yes SCS: both ST: NI BLAST-Start: [DNA polymerase I [Mycobacterium phage Zemanar] ],,NCBI, q1:s6 100.0% 0.0 GAP: -17 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.948, -2.7653702713535186, no F: DNA polymerase I SIF-BLAST: ,,[DNA polymerase I [Mycobacterium phage Zemanar] ],,YP\_009614477,78.7129,0.0 SIF-HHPRED: DNA polymerase I; mycobacteria, DNA polymerase, Flap endonuclease, TRANSFERASE; 2.713A {Mycolicibacterium smegmatis},,,6VDE\_B,97.8369,100.0 SIF-Syn:

CDS complement (46056 - 46670)

 /gene="51"

 /product="gp51"

 /function="hypothetical protein"

 /locus tag="Evaa\_51"

 /note=Original Glimmer call @bp 46670 has strength 12.52; Genemark calls start at 46670

 /note=SSC: 46670-46056 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_LIGMA\_53 [Gordonia phage Ligma]],,NCBI, q28:s10 84.3137% 2.49198E-17 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 3.277, -2.1518296047551457, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein SEA\_LIGMA\_53 [Gordonia phage Ligma]],,UJE15708,55.0336,2.49198E-17 SIF-HHPRED: SIF-Syn:

CDS complement (46667 - 46978)

 /gene="52"

 /product="gp52"

 /function="hypothetical protein"

 /locus tag="Evaa\_52"

 /note=Original Glimmer call @bp 46978 has strength 13.57; Genemark calls start at 46978

 /note=SSC: 46978-46667 CP: no SCS: both ST: SS BLAST-Start: GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.156, -4.4713484557894425, yes F: hypothetical protein SIF-BLAST: SIF-HHPRED: SIF-Syn:

CDS complement (46975 - 47418)

 /gene="53"

 /product="gp53"

 /function="hypothetical protein"

 /locus tag="Evaa\_53"

 /note=Original Glimmer call @bp 47418 has strength 19.46; Genemark calls start at 47418

 /note=SSC: 47418-46975 CP: yes SCS: both ST: SS BLAST-Start: GAP: 89 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.354, -2.0720764396375664, yes F: hypothetical protein SIF-BLAST: SIF-HHPRED: SIF-Syn:

CDS complement (47508 - 47906)

 /gene="54"

 /product="gp54"

 /function="hypothetical protein"

 /locus tag="Evaa\_54"

 /note=Original Glimmer call @bp 47906 has strength 9.99; Genemark calls start at 47906

 /note=SSC: 47906-47508 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein KCH40\_gp124 [Mycobacterium phage Typha] ],,NCBI, q1:s1 88.6364% 3.51023E-20 GAP: 56 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.685, -3.83326386801984, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein KCH40\_gp124 [Mycobacterium phage Typha] ],,YP\_010049712,29.5652,3.51023E-20 SIF-HHPRED: SIF-Syn:

CDS complement (47963 - 48256)

 /gene="55"

 /product="gp55"

 /function="Hypothetical Protein"

 /locus tag="Evaa\_55"

 /note=Original Glimmer call @bp 48256 has strength 8.08; Genemark calls start at 48256

 /note=SSC: 48256-47963 CP: no SCS: both ST: SS BLAST-Start: GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.846, -3.1151213789549335, yes F: Hypothetical Protein SIF-BLAST: SIF-HHPRED: SIF-Syn:

CDS complement (48253 - 48564)

 /gene="56"

 /product="gp56"

 /function="hypothetical protein"

 /locus tag="Evaa\_56"

 /note=Original Glimmer call @bp 48564 has strength 17.21; Genemark calls start at 48564

 /note=SSC: 48564-48253 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_LIGMA\_56 [Gordonia phage Ligma]],,NCBI, q1:s1 98.0583% 3.24517E-10 GAP: -1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.354, -6.100660902441702, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein SEA\_LIGMA\_56 [Gordonia phage Ligma]],,UJE15711,55.7692,3.24517E-10 SIF-HHPRED: SIF-Syn:

CDS complement (48564 - 48803)

 /gene="57"

 /product="gp57"

 /function="Hypothetical Protein"

 /locus tag="Evaa\_57"

 /note=Original Glimmer call @bp 48803 has strength 7.5; Genemark calls start at 48782

 /note=SSC: 48803-48564 CP: yes SCS: both-gl ST: NI BLAST-Start: GAP: 36 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.106, -5.402017758808125, yes F: Hypothetical Protein SIF-BLAST: SIF-HHPRED: SIF-Syn:

CDS complement (48840 - 48956)

 /gene="58"

 /product="gp58"

 /function="hypothetical protein"

 /locus tag="Evaa\_58"

 /note=Original Glimmer call @bp 48956 has strength 1.28

 /note=SSC: 48956-48840 CP: yes SCS: glimmer ST: NA BLAST-Start: GAP: 289 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.432, -6.405903298594267, yes F: hypothetical protein SIF-BLAST: SIF-HHPRED: SIF-Syn:

CDS 49246 - 49743

 /gene="59"

 /product="gp59"

 /function="hypothetical protein"

 /locus tag="Evaa\_59"

 /note=Original Glimmer call @bp 49246 has strength 12.11; Genemark calls start at 49246

 /note=SSC: 49246-49743 CP: no SCS: both ST: NI BLAST-Start: GAP: 289 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.237, -4.305994647947269, no F: hypothetical protein SIF-BLAST: SIF-HHPRED: SIF-Syn:

CDS 49769 - 50017

 /gene="60"

 /product="gp60"

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

 /locus tag="Evaa\_60"

 /note=Original Glimmer call @bp 49883 has strength 10.24; Genemark calls start at 49769

 /note=SSC: 49769-50017 CP: yes SCS: both-gm ST: NI BLAST-Start: [ribbon-helix-helix DNA binding domain protein [Mycobacterium phage Kloppinator]],,NCBI, q23:s43 62.1951% 1.38163E-8 GAP: 25 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.264, -4.310555060056183, no F: ribbon-helix-helix DNA binding domain SIF-BLAST: ,,[ribbon-helix-helix DNA binding domain protein [Mycobacterium phage Kloppinator]],,QGJ87727,36.0,1.38163E-8 SIF-HHPRED: omega transcriptional repressor; transcriptional repressor, ribbon-helix-helix, GENE REGULATION; 1.5A {Streptococcus pyogenes} SCOP: a.43.1.4,,,1IRQ\_B,50.0,98.7 SIF-Syn:

CDS 50014 - 50184

 /gene="61"

 /product="gp61"

 /function="hypothetical protein"

 /locus tag="Evaa\_61"

 /note=Original Glimmer call @bp 50014 has strength 4.33

 /note=SSC: 50014-50184 CP: yes SCS: glimmer ST: SS BLAST-Start: GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.367, -4.309531045980963, yes F: hypothetical protein SIF-BLAST: SIF-HHPRED: SIF-Syn:

CDS 50181 - 50537

 /gene="62"

 /product="gp62"

 /function="Hypothetical Protein"

 /locus tag="Evaa\_62"

 /note=Original Glimmer call @bp 50181 has strength 13.4; Genemark calls start at 50193

 /note=SSC: 50181-50537 CP: no SCS: both-gl ST: SS BLAST-Start: GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.475, -4.644343442981724, yes F: Hypothetical Protein SIF-BLAST: SIF-HHPRED: SIF-Syn:

CDS 50521 - 51108

 /gene="63"

 /product="gp63"

 /function="DNA binding protein"

 /locus tag="Evaa\_63"

 /note=Original Glimmer call @bp 50521 has strength 12.18; Genemark calls start at 50521

 /note=SSC: 50521-51108 CP: yes SCS: both ST: SS BLAST-Start: [DNA binding protein [Mycobacterium phage Phaedrus] ],,NCBI, q10:s11 95.3846% 7.03676E-47 GAP: -17 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.028, -2.66371296573402, yes F: DNA binding protein SIF-BLAST: ,,[DNA binding protein [Mycobacterium phage Phaedrus] ],,YP\_002014677,61.809,7.03676E-47 SIF-HHPRED: Small Terminase subunit; viral genome packaging motor, small terminase, Pseudomonas phage PaP3, DNA BINDING PROTEIN, VIRAL PROTEIN; 3.95A {Pseudomonas phage NV1},,,7JOQ\_G,69.2308,97.7 SIF-Syn:

CDS 51032 - 51514

 /gene="64"

 /product="gp64"

 /function="hypothetical protein"

 /locus tag="Evaa\_64"

 /note=Original Glimmer call @bp 51173 has strength 13.81; Genemark calls start at 51047

 /note=SSC: 51032-51514 CP: no SCS: both-cs ST: NI BLAST-Start: [hypothetical protein SEA\_MARIOKART\_62 [Gordonia phage Mariokart]],,NCBI, q27:s13 64.375% 9.25668E-7 GAP: -77 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.948, -3.2925703904164987, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein SEA\_MARIOKART\_62 [Gordonia phage Mariokart]],,QNL30189,32.4022,9.25668E-7 SIF-HHPRED: SIF-Syn:

CDS 51511 - 51681

 /gene="65"

 /product="gp65"

 /function="hypothetical protein"

 /locus tag="Evaa\_65"

 /note=Original Glimmer call @bp 51511 has strength 2.91

 /note=SSC: 51511-51681 CP: no SCS: glimmer ST: SS BLAST-Start: GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.021, -4.749088834314575, no F: hypothetical protein SIF-BLAST: SIF-HHPRED: SIF-Syn:

CDS 51678 - 52112

 /gene="66"

 /product="gp66"

 /function="hypothetical protein"

 /locus tag="Evaa\_66"

 /note=Original Glimmer call @bp 51678 has strength 11.76; Genemark calls start at 51678

 /note=SSC: 51678-52112 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_CAFASSO\_74 [Gordonia phage Cafasso]],,NCBI, q8:s68 23.6111% 1.78593E-6 GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.745, -3.2616920228519697, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein SEA\_CAFASSO\_74 [Gordonia phage Cafasso]],,QXN74289,21.5517,1.78593E-6 SIF-HHPRED: SIF-Syn:

CDS 52109 - 52291

 /gene="67"

 /product="gp67"

 /function="hypothetical protein"

 /locus tag="Evaa\_67"

 /note=Original Glimmer call @bp 52109 has strength 9.88; Genemark calls start at 52109

 /note=SSC: 52109-52291 CP: yes SCS: both ST: NI BLAST-Start: [hypothetical protein KNU68\_gp78 [Gordonia phage Nubi] ],,NCBI, q4:s12 91.6667% 2.361E-22 GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.517, -3.790975366313636, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein KNU68\_gp78 [Gordonia phage Nubi] ],,YP\_010103682,66.6667,2.361E-22 SIF-HHPRED: SIF-Syn:

CDS 52291 - 52461

 /gene="68"

 /product="gp68"

 /function="Hypothetical protein"

 /locus tag="Evaa\_68"

 /note=Original Glimmer call @bp 52291 has strength 8.8; Genemark calls start at 52291

 /note=SSC: 52291-52461 CP: yes SCS: both ST: NI BLAST-Start: [hypothetical protein FDI74\_gp76 [Gordonia phage Lennon] ],,NCBI, q1:s4 96.4286% 0.00246353 GAP: -1 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.916, -4.963787326180191, no F: Hypothetical protein SIF-BLAST: ,,[hypothetical protein FDI74\_gp76 [Gordonia phage Lennon] ],,YP\_009615826,30.5263,0.00246353 SIF-HHPRED: SIF-Syn:

CDS 52560 - 52709

 /gene="69"

 /product="gp69"

 /function="Hypothetical protein"

 /locus tag="Evaa\_69"

 /note=Original Glimmer call @bp 52488 has strength 11.78; Genemark calls start at 52488

 /note=SSC: 52560-52709 CP: no SCS: both-cs ST: NI BLAST-Start: [hypothetical protein HOT73\_gp08 [Gordonia phage Ruthy] ],,NCBI, q1:s25 83.6735% 7.09599E-11 GAP: 98 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.466, -4.857233374986333, yes F: Hypothetical protein SIF-BLAST: ,,[hypothetical protein HOT73\_gp08 [Gordonia phage Ruthy] ],,YP\_009806957,51.4286,7.09599E-11 SIF-HHPRED: SIF-Syn:

CDS 52715 - 53242

 /gene="70"

 /product="gp70"

 /function="HNH endonuclease"

 /locus tag="Evaa\_70"

 /note=Original Glimmer call @bp 52715 has strength 13.94; Genemark calls start at 52715

 /note=SSC: 52715-53242 CP: yes SCS: both ST: SS BLAST-Start: [HNH endonuclease [Gordonia phage NHagos]],,NCBI, q5:s3 96.5714% 3.83661E-53 GAP: 5 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.105, -4.847583656344026, no F: HNH endonuclease SIF-BLAST: ,,[HNH endonuclease [Gordonia phage NHagos]],,QGH80081,50.2128,3.83661E-53 SIF-HHPRED: HNH\_3 ; HNH endonuclease,,,PF13392.9,23.4286,98.2 SIF-Syn:

CDS complement (53249 - 54058)

 /gene="71"

 /product="gp71"

 /function="Hypothetical protein"

 /locus tag="Evaa\_71"

 /note=Original Glimmer call @bp 54058 has strength 16.43; Genemark calls start at 54058

 /note=SSC: 54058-53249 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein FDJ57\_gp72 [Gordonia phage Sour] ],,NCBI, q53:s57 73.9777% 1.9997E-24 GAP: 136 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.852, -2.9625409806968013, yes F: Hypothetical protein SIF-BLAST: ,,[hypothetical protein FDJ57\_gp72 [Gordonia phage Sour] ],,YP\_009625643,38.1757,1.9997E-24 SIF-HHPRED: SIF-Syn:

CDS complement (54195 - 54428)

 /gene="72"

 /product="gp72"

 /function="Hypothetical Protein"

 /locus tag="Evaa\_72"

 /note=Original Glimmer call @bp 54428 has strength 21.39; Genemark calls start at 54428

 /note=SSC: 54428-54195 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein FDJ57\_gp75 [Gordonia phage Sour] ],,NCBI, q1:s1 98.7013% 3.93618E-10 GAP: 89 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.695, -4.113180079823027, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein FDJ57\_gp75 [Gordonia phage Sour] ],,YP\_009625646,59.5238,3.93618E-10 SIF-HHPRED: SIF-Syn:

CDS complement (54518 - 55309)

 /gene="73"

 /product="gp73"

 /function="SprT-like protease"

 /locus tag="Evaa\_73"

 /note=Original Glimmer call @bp 55309 has strength 13.04; Genemark calls start at 55309

 /note=SSC: 55309-54518 CP: yes SCS: both ST: SS BLAST-Start: [SprT-like protein [Mycobacterium virus Rebeuca] ],,NCBI, q113:s6 57.4144% 6.45207E-47 GAP: 172 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.948, -2.9063687850157054, yes F: SprT-like protease SIF-BLAST: ,,[SprT-like protein [Mycobacterium virus Rebeuca] ],,YP\_009638909,63.6364,6.45207E-47 SIF-HHPRED: SprT-like domain-containing protein Spartan; DPC repair protease, DNA BINDING PROTEIN; HET: ADP, MLZ, FLC; 1.5A {Homo sapiens},,,6MDW\_A,53.6122,99.7 SIF-Syn:

CDS complement (55482 - 55805)

 /gene="74"

 /product="gp74"

 /function="Hypothetical Protein"

 /locus tag="Evaa\_74"

 /note=Original Glimmer call @bp 55805 has strength 10.31; Genemark calls start at 55805

 /note=SSC: 55805-55482 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_ANCLAR\_66 [Gordonia phage AnClar]],,NCBI, q1:s1 100.0% 2.38085E-39 GAP: -8 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.846, -3.6262617209640267, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_ANCLAR\_66 [Gordonia phage AnClar]],,QIG58993,78.3019,2.38085E-39 SIF-HHPRED: SIF-Syn:

CDS complement (55798 - 55890)

 /gene="75"

 /product="gp75"

 /function="Hypothetical Protein"

 /locus tag="Evaa\_75"

 /note=Genemark calls start at 55890

 /note=SSC: 55890-55798 CP: no SCS: genemark ST: SS BLAST-Start: GAP: -4 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.477, -5.786456154663496, no F: Hypothetical Protein SIF-BLAST: SIF-HHPRED: SIF-Syn:

CDS complement (55887 - 56357)

 /gene="76"

 /product="gp76"

 /function="Hypothetical Protein"

 /locus tag="Evaa\_76"

 /note=Original Glimmer call @bp 56357 has strength 18.81; Genemark calls start at 56357

 /note=SSC: 56357-55887 CP: yes SCS: both ST: SS BLAST-Start: GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.948, -2.9063687850157054, yes F: Hypothetical Protein SIF-BLAST: SIF-HHPRED: SIF-Syn:

CDS complement (56354 - 57028)

 /gene="77"

 /product="gp77"

 /function="hypothetical protein"

 /locus tag="Evaa\_77"

 /note=Original Glimmer call @bp 57028 has strength 16.83; Genemark calls start at 57028

 /note=SSC: 57028-56354 CP: no SCS: both ST: SS BLAST-Start: [hypothetical protein KHO65\_gp013 [Mycobacterium phage Sauce] ],,NCBI, q1:s1 95.9821% 1.08956E-24 GAP: 100 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.849, -3.3188993291388478, no F: hypothetical protein SIF-BLAST: ,,[hypothetical protein KHO65\_gp013 [Mycobacterium phage Sauce] ],,YP\_010058572,48.4581,1.08956E-24 SIF-HHPRED: SIF-Syn:

CDS complement (57129 - 57578)

 /gene="78"

 /product="gp78"

 /function="hypothetical protein"

 /locus tag="Evaa\_78"

 /note=Original Glimmer call @bp 57578 has strength 10.09; Genemark calls start at 57578

 /note=SSC: 57578-57129 CP: no SCS: both ST: NI BLAST-Start: [hypothetical protein SEA\_VIOLETZ\_92 [Mycobacterium phage VioletZ]],,NCBI, q11:s39 67.7852% 3.01678E-15 GAP: 1 bp gap LO: no RBS: Kibler 6, Karlin Medium, 2.29, -4.117143323918745, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein SEA\_VIOLETZ\_92 [Mycobacterium phage VioletZ]],,QNO13114,29.4643,3.01678E-15 SIF-HHPRED: SIF-Syn:

CDS complement (57580 - 58056)

 /gene="79"

 /product="gp79"

 /function="HNH endonuclease"

 /locus tag="Evaa\_79"

 /note=Original Glimmer call @bp 58056 has strength 12.26; Genemark calls start at 58056

 /note=SSC: 58056-57580 CP: yes SCS: both ST: SS BLAST-Start: [putative HNH endonuclease [Tsukamurella phage TPA2] ],,NCBI, q3:s6 97.4684% 1.74046E-16 GAP: 60 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.695, -3.812150084159046, yes F: HNH endonuclease SIF-BLAST: ,,[putative HNH endonuclease [Tsukamurella phage TPA2] ],,YP\_004286242,55.1724,1.74046E-16 SIF-HHPRED: SIF-Syn:

CDS complement (58117 - 59121)

 /gene="80"

 /product="gp80"

 /function="Hypothetical protein"

 /locus tag="Evaa\_80"

 /note=Original Glimmer call @bp 59121 has strength 19.65; Genemark calls start at 59121

 /note=SSC: 59121-58117 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein FDJ57\_gp74 [Gordonia phage Sour] ],,NCBI, q1:s1 98.503% 1.70549E-145 GAP: 119 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.105, -2.5052746077145835, yes F: Hypothetical protein SIF-BLAST: ,,[hypothetical protein FDJ57\_gp74 [Gordonia phage Sour] ],,YP\_009625645,73.8095,1.70549E-145 SIF-HHPRED: SIF-Syn:

 /note=possible plasmid-like protein

CDS complement (59241 - 59675)

 /gene="81"

 /product="gp81"

 /function="hypothetical protein"

 /locus tag="Evaa\_81"

 /note=Original Glimmer call @bp 59675 has strength 23.44; Genemark calls start at 59675

 /note=SSC: 59675-59241 CP: yes SCS: both ST: NA BLAST-Start: [hypothetical protein [Mycobacterium sp. OAE906]],,NCBI, q1:s1 65.2778% 4.60177E-4 GAP: 193 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.695, -4.113180079823027, yes F: hypothetical protein SIF-BLAST: ,,[hypothetical protein [Mycobacterium sp. OAE906]],,MBE1417383,44.898,4.60177E-4 SIF-HHPRED: SIF-Syn:

CDS complement (59869 - 60219)

 /gene="82"

 /product="gp82"

 /function="Hypothetical Protein"

 /locus tag="Evaa\_82"

 /note=Original Glimmer call @bp 60219 has strength 12.72; Genemark calls start at 60219

 /note=SSC: 60219-59869 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein KNT82\_gp80 [Gordonia phage Flapper] ],,NCBI, q7:s2 88.7931% 1.08966E-28 GAP: 217 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 3.105, -2.5052746077145835, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein KNT82\_gp80 [Gordonia phage Flapper] ],,YP\_010093887,68.5185,1.08966E-28 SIF-HHPRED: SIF-Syn:

 /note=possible membrane protein

CDS 60437 - 60556

 /gene="83"

 /product="gp83"

 /function="Hypothetical Protein"

 /locus tag="Evaa\_83"

 /note=Original Glimmer call @bp 60437 has strength 0.53

 /note=SSC: 60437-60556 CP: no SCS: glimmer ST: NI BLAST-Start: GAP: 217 bp gap LO: no RBS: Kibler 6, Karlin Medium, 1.877, -5.87205256917805, yes F: Hypothetical Protein SIF-BLAST: SIF-HHPRED: SIF-Syn:

tRNA complement (60389 - 60459)

 /gene="84"

 /product="tRNA-Arg(tct)"

 /locus tag="EVAA\_84"

 /note=tRNA-Arg(tct)

CDS complement (60672 - 60833)

 /gene="85"

 /product="gp85"

 /function="membrane protein"

 /locus tag="Evaa\_85"

 /note=Original Glimmer call @bp 60833 has strength 19.82; Genemark calls start at 60833

 /note=SSC: 60833-60672 CP: yes SCS: both ST: SS BLAST-Start: GAP: -4 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 2.664, -3.4892599424135016, yes F: membrane protein SIF-BLAST: SIF-HHPRED: SIF-Syn:

CDS complement (60830 - 61084)

 /gene="86"

 /product="gp86"

 /function="Hypothetical Protein"

 /locus tag="Evaa\_86"

 /note=Original Glimmer call @bp 61084 has strength 17.81; Genemark calls start at 61084

 /note=SSC: 61084-60830 CP: yes SCS: both ST: SS BLAST-Start: [hypothetical protein SEA\_REDWATTLEHOG\_203 [Gordonia phage RedWattleHog]],,NCBI, q3:s9 75.0% 4.18768E-8 GAP: 0 bp gap LO: yes RBS: Kibler 6, Karlin Medium, 1.986, -4.8822772450371135, yes F: Hypothetical Protein SIF-BLAST: ,,[hypothetical protein SEA\_REDWATTLEHOG\_203 [Gordonia phage RedWattleHog]],,QLF83706,51.7241,4.18768E-8 SIF-HHPRED: SIF-Syn: