**SEA\_CHEETO1 - 1**

Original Glimmer call @bp 169 has strength 11.42; GeneMark calls start at 1

SSC: 1-546 CP: Yes SCS: Both-GM ST: NI BLAST-Start: Chickenking, 1, NCBI, Q1:S1, 100%, 0 Gap: NA LO: NA RBS: K6/KM, Z=0.745, FS=-7.280, no F: NKF SIF-BLAST: NFK, NCBI, Chickenking, 1, QFG04671, 100%, 0 SIF-HHPred: NFK, no matches with a probability above 90% SIF-Syn: NKF

**SEA\_CHEETO1 - 2**

Original Glimmer call @bp 546 has strength 11.57; GeneMark calls start at 543

SSC: 543-1955 CP: Yes SCS: Both-GM ST: NI BLAST-Start: ChickenKing, 2, NCBI, Q1:S1, 100%, 0 Gap: 4 bp overlap LO: NA RBS: K6/KM, Z=2.171, FS=-5.075, no F: Terminase SIF-BLAST: Terminase, NCBI, ChickenKing, 2, QFG04672, 100%, 0 SIF-HHPred: DNA MATURASE B; HYDROLASE, ATPASE, DNA TRANSLOCATION, SINGLE-PARTICLE RECONSTRUCTION; 16.0A {ENTEROBACTERIA PHAGE T7}, PDB, NA, NA, 4BIJ\_C, 89%, 100% SIF-Syn: Terminase, upstream gene is NKF, downstream gene is portal protein, just like in phages ChickenKing and GaeCeo

**SEA\_CHEETO1 - 3**

Original Glimmer call @bp 1960 has strength 15.94

SSC: 1960-3282 CP: yes SCS: Both ST: SS BLAST-Start: GaeCeo, 3, NCBI, Q1:S1, 100.0%, 0 Gap: 4 bp LO: NA RBS: K6/KM, Z=2.065, FS=-5.045, no F: Portal Protein SIF-BLAST: Portal Protein, NCBI, GaeCeo, 3, QNL30957, 100%, 0 SIF-HHPred: PORTAL PROTEIN; BACTERIOPHAGE SPP1, DNA TRANSLOCATION, MOLECULAR MOTOR, VIRAL PORTAL PROTEIN, VIRAL PROTEIN; HET: CA, HG, PDB, NA, NA, 2JES\_S, 89.3%, 99.9% SIF-Syn: Portal protein, upstream gene is terminase, downstream gene is NKF, just like in phage GaeCeo

**SEA\_CHEETO1 - 4**

Original Glimmer call @bp 3285 has strength 14.22

SSC: 3285-3455 CP: yes SCS: Both ST: SS BLAST-Start: GaeCeo, 4, NCBI, Q1:S1, 100%, e=8.3E-30 Gap: 3 bp gap LO: NA RBS: K6/KM, Z=2.098, FS=-4.465, yes F: NKF SIF-BLAST: NKF, NCBI, GaeCeo, 4, QNL30958, 100%, 8.3E-30 SIF-HHPred: NKF, no matches with a probability above 90% SIF-Syn: NKF

**SEA\_CHEETO1 - 5**

Original Glimmer call @bp 3455 has strength 8.30

SSC: 3455-4141 CP: yes SCS: Both ST: SS BLAST-Start: GaeCeo 5, NCBI, Q1:S1, 100%, 0 Gap: 1 bp overlap LO: NA RBS: K6/KM, z=2.423, FS=-3.691, yes F: Capsid Maturation Protease SIF-BLAST: Capsid Maturation Protease, NCBI, GaeCeo, 5, QNL30959, 100%, 0 SIF-HHPred: Phage\_Mu\_F ; Phage Mu protein F like protein, EMBL-EBI, NA, NA, PF04233.17, 43.2%, 99.7%, SIF-Syn: Capsid Maturation Protease, upstream gene NKF, downstream gene is scaffolding protein, just like in phage GaeCeo

**SEA\_CHEETO1 - 6**

Original Glimmer call @bp 4225 has strength 11.87

SSC: 4225-4779 CP: Yes SCS: Both ST: SS BLAST-Start: CaeCeo, 6, NCBI, Q1;S1, 100%, 0 Gap:41 bp LO: Yes RBS: K6/KM, 2.734, -2.963, Yes F: Scaffolding protein SIF-BLAST: Scafolding Proting, NCBI, GaeCeo, 6, QNL30960, 100%, 0 SIF-HHPred: DUF2730 ; Protein of unknown function (DUF2730), EMBL-EBI, NA, NA, PF10805.11, 25.9%, 94.13 SIF Syn: Scaffolding protein, upstream gene is Capsid maturation protease, downstream gene is major capsid protein, just like in phages GaeCeo, ChickenKing

**SEA\_CHEETO1 - 7**

Original Glimmer call @bp 4820 has strength 15.51

SSC: 4820-5764 CP: Yes SCS: Both ST: SS BLAST-Start: ChickenKing, 6, NCBI, Q1;S1, 99%,0 Gap:41 bp LO: Yes RBS: K6/KM, 2.976, -2.584, yes F: Major capsid protein SIF-BLAST: Major Capsid Protein, NCBI, ChickenKing, 6, QFG04676, 99%, 0 SIF-HHPred: major capsid protein; acne, bacteriophage, HK97-like, VIRUS; 3.7A {Propionibacterium phage PA6}, PDB, 3JB5\_C, NA, NA, 99%, 100% SIF-Syn: major capsid protein, upstream gene is scaffolding protein, downstream gene is NKF, just like in phages GaeCeo, ChickenKing

**SEA\_CHEETO1 - 8**

Original Glimmer call @bp 5764 has strength 14.01

SSC: 5764-6009 CP: Yes SCS:Both ST:SS BLAST-Start: ChickenKing, 7, NCBI Q2;S1, 100%, 6.9 E-16 Gap: 1bp overlap LO:NA RBS:K6/KM, 2.075, -4.513, yes F:NKF SIF-BLAST: NKF, NCBI, Chickenking,7, QFG04677, 100%, 0 SIF-HHPred: NKF, no matches with a probability above 90% SIF-Syn: NKF

**SEA\_CHEETO1 - 9**

Original Glimmer call @bp 6093 has strength 16.63

SSC: 6093-6257 CP: Yes SCS: Both ST: SS BLAST-Start: Chickenking, 8, NCBI, Q1;S1, 58.2% , 4.4 E-11 Gap: 84 bp LO: Yes RBS: K6/KM, 2.976, -2.443, yes F: NKF SIF-BLAST: NKF, NCBI,Chickenking, 8, QFG04678, 58.2%, 4.4E-11 SIF-HHPred: NKF, no matches with a probability above 90% SIF-Syn: NFK

**SEA\_CHEETO1 - 10**

Original Glimmer call @bp 6282 has strength 9.31

SSC: 6282-6695 CP: Yes SCS: Both ST: SS BLAST-Start: GaeCeo, 10, NCBI, Q1;S1, 100%, 0 Gap: 25bp LO: Yes RBS: K6/KM, 2.976, -2.794, yes F: NKF SIF-BLAST: NKF, NCBI, GaeCeo, 10, QNL30964, 100% 0 SIF-HHPred: NKF, no matches with a probability above 90% SIF-Syn: NKF

**SEA\_CHEETO1 - 11**

Original Glimmer call @bp 6667 has strength 15.35

SSC: 6667-7077 CP: Yes SCS: Both ST: SS BLAST-Start: ChickenKing, 10, NBCI, Q1:S1, 100%, 0 Gap: 28bp overlap LO: NA RBS: K6/KM, 2.976, -2.505, yes F: NKF SIF-BLAST: NKF, NCBI, ChickenKing, 10, QFG04680, 100%, 0 SIF-HHPred: DUF6093 ; Family of unknown function (DUF6093), EMBL-EBI, NA, NA, PF19586.2, 45%, 95.17% SIF-Syn: NKF

**SEA\_CHEETO1 - 12**

Original Glimmer call @bp 7074 has strength 11.39

SSC: 7074-7415 CP: Yes SCS: Both ST: SS BLAST-Start: GaeCeo, 12, NCBI, Q1:S1, 100%, 0 Gap: 3bp overlap LO: NA RBS: K6/KM, 2.802, -2.958, yes F: NKF SIF-BLAST: NKF, NCBI, GaeCeo, 12, QNL30966, 100%, 0 SIF-HHPred: Minor\_capsid\_2 ; Minor capsid protein, EMBL-EBI, NA, NA, PF11114.11, 82%, 99.34% SIF-Syn: NKF

**SEA\_CHEETO1 - 13**

Original Glimmer call @bp 7415 has strength 5.50

SSC: 7415-7774 CP: Yes SCS: Both ST: SS BLAST-Start: GaeCeo, 13, NCBI, Q1:S1, 100%, 0 Gap: 1bp overlap LO: NA RBS: K6/KM, 1.854, -4.926, no F: Tail terminator SIF-BLAST: TaiTail terminator, GaeCeo, 13, QNL30967, 100%, 0 SIF-HHPred: Tail terminator protein Rcc01690; "neck", "portal", "capsid", "tail tube", VIRUS; 3.58A {Rhodobacter capsulatus}, PDB, NA, NA, 6TE9\_F, 60%, 98.92% SIF-Syn: NA

**SEA\_CHEETO1 - 14**

Original Glimmer call @bp 7774 has strength 17.71

SSC: 7774-8001 CP: Yes SCS: Both ST: SS BLAST-Start: ChickenKing, 13, NCBI, Q1:S1, 100%, 3.9E-44 Gap: 1bp overlap LO: NA RBS: K6/KM, 2.644, -3.296, yes F: NKF SIF-BLAST: NKF, NCBI, ChickenKing, 13, QFG04683, 100%, 3.9E-44 SIF-HHPred: NKF, no matches with a probability above 90% SIF-Syn: NKF

**SEA\_CHEETO1 - 15**

Original Glimmer call @bp 8067 has strength 14.89

SSC: 8067-8417 CP: Yes SCS: Both ST: SS BLAST-Start: ChickenKing, 14, NCBI, Q1:S50, 70.3%, 0 Gap: 66bp gap LO: Yes RBS: K6/KM, 1.078, -6.569, no F: Major tail protein SIF-BLAST: Major tail protein, NBCI, ChickenKing, 14, QFG04684, 70.3%, 0 SIF-HHPred: NKF, no matches with a probability above 90% SIF-Syn: Major tail protein, upstream gene is NKF, downstream gene is tail assembly chaperone, just like in phage GaeCeo

**SEA\_CHEETO1 - 16**

Original Glimmer call @bp 8447 has strength 14.66

SSC: 8447-8989 CP: yes SCS: both ST: SS BLAST-Start: ChickenKing, 16, NCBI, Q1:S1, 100%, 0.0 Gap: 30bp LO: yes RBS: K6/KM, 2.826, -2.828, yes F: tail assembly chaperone SIF-BLAST: tail assembly chaperone, NCBI, ChickenKing, 16, QFG04685, 100%, 0.0 SIF-HHPred: NKF, no matches with a probability above 90% SIF-Syn: tail assembly chaperone, upstream gene is major tail protein, downstream gene is tail assembly chaperone, just like in phage ChickenKing

**SEA\_CHEETO1 - 17**

Original Glimmer call @bp 8998 has strength 3.61

SSC: 8998-9375 CP: yes SCS: both ST: SS BLAST-Start: ChickenKing, 17, NCBI, Q1:S1, 100%, 0.0 Gap: 9bp LO: NA RBS: K6/KM, 1.690, -5.338, no F: tail assembly chaperone SIF-BLAST: tail assembly chaperone, NCBI, ChickenKing, 17, QFG04686, 100%, 0.0 SIF-HHPred: NKF, no matches with a probability above 90% SIF-Syn: tail assembly chaperone, upstream gene is tail assembly chaperone, downstream gene is tape measure protein, just like in phage ChickenKing

**SEA\_CHEETO1 - 18**

Original Glimmer call @bp 9400 has strength 13.93

SSC: 9400-11808 CP: yes SCS: Both ST: SS BLAST-Start: ChickenKing, 17, NCBI, Q1:S1, 100%, 0.0 Gap: 25bp LO: yes RBS: K6/KM, 2.976, -2.443, yes F: Tape measure protein SIF-BLAST: Tape measure protein, NCBI, ChickenKing, 17, QFG04687, 100%, 0.0 SIF-HHPred: Tape Measure Protein, gp57; phage tail, tail tip, tape measure protein, VIRAL PROTEIN; 3.7A {Staphylococcus virus 80alph, PBD, NA, NA, 6V8I\_CF, 20% 99.97 SIF-Syn: Tape measure protein, upstream gene is tail assembly chaperone, downstream gene is minor tail protein, just like in phage ChickenKing and GaeCeo

**SEA\_CHEETO1 - 19**

Original Glimmer call @bp 11805 has strength 15.96

SSC: 11805-12578 CP: yes SCS: Both ST: SS BLAST-Start: GaeCeo, 19, NCBI, Q1:S1, 100%, 0 Gap: 3bp overlap LO: NA RBS: K6/KM, 2.633, -3.319, yes F: Minor tail protein SIF-BLAST: Minor tail protein, NCBI, GaeCeo, 19, QNL30973, 100%, 0 SIF-HHPred: ORF46; Distal tail protein, Receptor-binding protein, Phage baseplate, host adsorption apparatus, genome injection device, PDB, NA, NA, 4V96\_AX, 98.8%, 99.94 SIF-Syn: Minor tail protein, upstream gene is tape measure protein, downstream gene is minor tail protein, just like in phages GaeCeo and ChickenKing

**SEA\_CHEETO1 - 20**

Original Glimmer call @bp 12578 has strength 16.25

SSC: 12578-15004 CP: yes SCS: Both ST: SS BLAST-Start: GaeCeo, 20, NCBI, Q1:S1, 100%, 0 Gap: 1bp overlap LO: NA RBS: K6/KM, 2.826, -2.765, yes F: Minor tail protein SIF-BLAST: Minor tail protein, NCBI, GaeCeo, 20, QNL30974, 100%, 0 SIF-HHPred: Tail-Associated Lysin, gp59; phage tail, tail tip, tape measure protein, VIRAL PROTEIN; 3.7A {Staphylococcus virus 80alp, PBD, 6V8I\_AE, 27.3% 99.94% SIF-Syn: Minor tail protein, upstream gene is minor tail protein, downstream gene is NKF, just like in phages GaeCeo and ChickenKing

**SEA\_CHEETO1 - 21**

Original Glimmer call @bp 15012 has strength 10.64; GeneMark calls start at 15006

SSC: 15012-15194 CP: yes SCS: Both-GM ST: NI BLAST-Start: GaeCeo, 21, NCBI, Q1:S1, 100%, 4.4E-35 Gap: 2 bp LO: NA RBS: K6/KM, z=2.489, fs=-3.548, yes F: NKF SIF-BLAST: NKF, NCBI, GaeCeo, 21, QNL30975, 100%, 4.4E-35 SIF-HHPred: NKF, No matches with a probability above 90% SIF-Syn: NKF

**SEA\_CHEETO1 - 22**

Original Glimmer call @bp 15194 has strength 13.47

SSC: 15194-15793 CP: yes SCS: Both ST: SS BLAST-Start: GaeCeo, 22, NCBI, Q1:S1, 100%, 0 Gap: 1 bp overlap LO: NA RBS: K6/KM, z=2.489, FS=-4.138, no F: NKF SIF-BLAST: NKF, NCBI, GaeCeo, 22, QNL30976, 100%, 0 SIF-HHPred: NKF, no matches above 90% SIF-Syn: NKF

**SEA\_CHEETO1 - 23**

Original Glimmer call @bp 15793 has strength 10.41

SSC: 15793-16284 CP: yes SCS: Both ST: SS BLAST-Start: GaeCeo, 23, NCBI, Q1:S1, 100%, 0 Gap: 1bp overlap LO: NA RBS: K6/KM, z=2.826, FS=-2.906, yes F: NKF SIF-BLAST: NKF, NCBI, GaeCeo, 23, QNL30977, 100%, 0 SIF-HHPred: Gp15 protein; Listeria, homotrimeric, receptor binding protein, Bacteriophage, VIRAL PROTEIN; HET: 1PE, ACT; 1.7A {Listeria phage PSA}, PDB, NA, NA, 6R5W\_C, 72.6%, 98.67% SIF-Syn: NKF

**SEA\_CHEETO1 - 24**

Original Glimmer call @bp 16284 has strength 10.50

SSC: 16284-18413 CP: yes SCS: Both ST: SS BLAST-Start: GaeCeo, 24, NCBI, Q1:S1, 100%, 0 Gap: 1 bp overlap LO: NA RBS: K6/KM, z=2.395, FS=-4.040, no F: Minor tail protein SIF-BLAST: Minor tail protein, NCBI, GaeCeo, 24, QNL30978, 100%, 0 SIF-HHPred: Immunomodulatory active chitinase; TsES1, immunomodulatory potential, chitinase, Eukaryotic protein expression, LEXSY, secretion, dimer, intramolecular disulphide bridge, Trichuris suis, HYDROLASE; HET: EDO; 1.74A {Trichuris suis}, PDB, NA, NA, 6G9C\_A, 49.2%, 100% SIF-Syn: Minor tail protein, upstream gene is NKF, downstream gene is endolysin, just like in phage GaeCeo

**SEA\_CHEETO1 - 25**

Original Glimmer call @bp 18442 has strength 12.33

SSC: 16284-18413 CP: yes SCS: Both ST: SS BLAST-Start: GaeCeo, 25, NCBI, Q1:S1, 100%, 0 Gap: 29 bp LO: No RBS: K6/KM, z=2.976, FS=-2.505, yes F: Endolysin SIF-BLAST: Endolysin, NCBI, GaeCeo, 25, QFG04694, 100%, 0 SIF-HHPred: Peptidoglycan recognition protein I-alpha {Human (Homo sapiens) [TaxId: 9606]}, SCOPe, NA, NA, d1sk4a\_, 44.3%, 99.82% SIF-Syn: NA

**SEA\_CHEETO1 - 26**

Original Glimmer call @bp 19465 has strength 13.55

SSC: 19465-19857 CP:Yes SCS: Both ST: SS BLAST-Start: GaeCeo, 26, Phagesdb, Q1;S1, 92%, 4e-62 0 Gap: 22bp LO: Yes RBS:K6/KM, 2.976, -2.584, Yes F: NKF SIF-BLAST: NKF, phagesdb, GaeCeo, 26, 92%, 0 SIF-HHPred: PspB ; Phage shock protein B, EMBL-EBI, NA, NA, PF06667.15 67.9%, 95.16 SIF-Syn: NKF

\*\*\*NCBI blast data indicate membrane protein, but according to TmHmm only 1 Transmembrane domain found so does not fit criteria for this function. Used Phagesb blast data to support this.

**SEA\_CHEETO1 - 27**

Original Glimmer call @bp 19860 has strength 13.68

SSC: 19860- 20216 CP: Yes SCS: Both ST: SS BLAST-Start: ChickenKing, 26, NCBI, Q1;S1, 100%, 5.9 E-44 Gap: 3bp LO: NA RBS: K6/KM, 2.960, -2.830, yes F: Holin SIF-BLAST: Holin, NCBI, ChickenKing, 26, QFG04696, 100%, 5.9 E-44 SIF-HHPred: Phage\_holin\_5\_1; Bacteriophage A118-like holin, Hol118, EMBL-EBI, NA, NA, PF06946.14, 73.1%, 99.71 SIF-Syn: Holin, upstream gene is NKF, downstream gene is NKF, just like in phages ChickenKing, GaeCeo

**SEA\_CHEETO1 - 28**

Original Glimmer call @bp 20319 has strength 11.80

SSC: 20319-20714 CP: Yes SCS: Both ST: SS BLAST-Start: ChickenKing, 27, NCBI, Q1;S1, 100%, 0 Gap: 103 bp LO: yes RBS: K6/KM, 2.330, -3.906, yes F: NKF SIF-BLAST: NKF, NCBI, ChickenKing, 27, QFG04697, 100%, 0 SIF-HHPred: NKF, no matches with a probability above 90% SIF-Syn: NKF

**SEA\_CHEETO1 - 29**

Original Glimmer call @bp 21021 has strength 19.91

SSC: 20779-21021 (rev) CP: Yes SCS: Both ST: SS BLAST-Start:ChickenKing, 28, NCBI, Q3;S4, 96.3%, 1.3E-43 Gap: 68bp LO: Yes RBS: K6/KM, 2.097, -4.326, yes F: NKF SIF-BLAST: NKF, NCBI, ChickenKing, 28, QFG04698, 96.3%,1.3E-43 SIF-HHPred: NKF, no matches with a probability above 90% SIF-Syn: NKF

**SEA\_CHEETO1 - 30**

Original Glimmer call @bp 21244 has strength 16.87

SSC: 21089-21244 (rev) CP: Yes SCS:Both ST:SS BLAST-Start: ChickenKing, 29, NCBI, Q1;S1, 100%, 6.2E-29 Gap: 21bp LO: No RBS:K6/Km, 1.852, -5.501, No F: NKF SIF-BLAST:NKF, NCBI, ChickenKing, 29, QFG04699, 100%, 6.2E-29 SIF-HHPred: d.58.4.0 (A:) automated matches {Burkholderia cepacia [TaxId: 292]}, SCOPe, NA, NA, d4lbha\_, 63%, 94.61 SIF-Syn: NKF

**SEA\_CHEETO1 - 31**

Original Glimmer call @bp 21417 has strength 10.51

SSC: 21265-21417 (rev) CP: Yes SCS: Both ST: SS BLAST-Start: GaeCeo, 31, NCBI, Q1:S1, 100%, 3.6E-23 Gap: 3bp overlap LO: NA RBS: K6/KM, 1.987, -4.072, yes F: NKF SIF-BLAST: NKF, NCBI, GaeCeo, 31, QNL30985, 100%, 3.6E-23 SIF-HHPred: NKF, no matches with a probability above 90% SIF-Syn: NKF

**SEA\_CHEETO1 - 32**

Original Glimmer call @bp 22256 has strength 18.20

SSC: 21414-22256 (rev) CP: Yes SCS: Both ST: SS BLAST-Start: GaeCeo, 32, NCBI, Q1:S1, 100%, 0 Gap: 50bp LO: No RBS: K6/KM, 1.439, -6.385, no F: NKF SIF-BLAST: NKF, NCBI, GaeCeo, 32, QNL30986, 100, 0 SIF-HHPred: DUF5351 ; Family of unknown function (DUF5351), Pfam, PF17302.5, 8.9%, 94.63 SIF-Syn: NKF

**SEA\_CHEETO1 - 33**

Original Glimmer call @bp 22587 has strength 15.40

SSC: 22306-22587 (rev) CP: Yes SCS: Both ST: SS BLAST-Start: GaeCeo, 33, NCBI, Q1:S1, 96.8%, 2.6E-25 Gap: 3bp LO: NA RBS: K6/KM, 2.902, -2.681, yes F: NKF SIF-BLAST: NKF, Phagesdb, GaeCeo, 33, QNL30987, 83%, 3E-39 SIF-HHPred: NKF, no matches with a probability above 90% SIF-Syn: NA

\*\*\*NCBI blast data indicates membrane protein, but according to TmHmm only 1 Transmembrane domain found so does not fit criteria for this function. Phagesdb indicates NKF.

**SEA\_CHEETO1 - 34**

Original Glimmer call @bp 24251 has strength 11.28

SSC: 22590-24251 (rev) CP: Yes SCS: Both ST: SS BLAST-Start: ChickenKing, 33, NCBI, Q1:S1, 100%, 0 Gap: 24bp overlap LO: NA RBS: K6/KM, 3.047, -2.433, yes F: RecA-like DNA recombinase SIF-BLAST: RecA-like DNA recombinase, NCBI, ChickenKing, 33, QFG04703, 100%, 0 SIF-HHPred: c.37.1.11 (A:) Hexameric replicative helicase repA {Escherichia coli [TaxId: 562]}, SCOPe, d1nlfa\_, 41.97%, 99.83% SIF-Syn: NA

**SEA\_CHEETO1 - 35**

Original Glimmer call @bp 24520 has strength 4.91

SSC: 24227-24520 (rev) CP: Yes SCS: Both ST: SS BLAST-Start: ChickenKing, 34, NCBI, Q1:S1, 100%, 0 Gap: 4bp LO: NA RBS: K6/KM, 1.162, -6.678, no F: Nuclease SIF-BLAST: Nuclease, NCBI, ChickenKing, 34, QFG04704, 100%, 0 SIF-HHPred: B Nuclease; Nuclease, HYDROLASE; HET: SO4; 1.85A {Salmonella phage SETP3} SCOP: c.52.1.35, PDB, NA, NA, 4QBN\_B, 96.94%, 99.84% SIF-Syn: NA

**SEA\_CHEETO1 - 36**

Original Glimmer call @bp 25345 has strength 19.74

SSC: 24524-25345 (rev) CP: yes SCS: Both ST: SS BLAST-Start: ChickenKing, 35, NCBI, Q1:S1, 74.5%, 0.0 Gap: 33bp LO: yes RBS: K6/KM, 2.087, -4.409, no F: NKF SIF-BLAST: NKF, NCBI, ChickenKing, 35, QFG04705, 74.5%, 0.0 SIF-HHPred: DUF669 ; Protein of unknown function (DUF669), Pfam, NA, NA, PF05037.16, 46% , 99.79 SIF-Syn: NKF

**SEA\_CHEETO1 - 37**

Original Glimmer call @bp 26043 has strength 16.66

SSC: 25378-26043 (rev) CP: Yes SCS: Both ST: SS BLAST-Start: GaeCeo, 37, NCBI, Q1:S1, 100%, 0.0 Gap: 3bp overlap LO: NA RBS: K6/KM, 2.102, -4.456, no F: AAA-ATPase SIF-BLAST: AAA-ATPase, NCBI, GaeCeo, 37, QNL30991, 100%, 0.0 SIF-HHPred: AAA\_24 ; AAA domain, Pfam, NA, NA, PF13479.9, 86.5%, 99.71 SIF-Syn: NA

**SEA\_CHEETO1 - 38**

Original Glimmer call @bp 27209 has strength 11.71

SSC: 26040-27209 (rev) CP: Yes SCS: Both ST: NA BLAST-Start: GaeCeo, 38, NCBI, Q1:S1, 98.2%, 0.0 Gap: 13bp overlap LO: NA RBS: K6/KM, 2.065, -4.744, no F: Cas4 family exonuclease SIF-BLAST: Cas4 family exonuclease, NCBI, GaeCeo, 38, QNL30992, 98.2%, 0.0 SIF-HHPred: PDDEXK\_1 ; PD-(D/E)XK nuclease superfamily, pfam, NA, NA, PF12705.10, 69.7%, 99.75% SIF-Syn: NA

\*\*\*Cas4 family exonuclease because shows alignment to the crystal structure 3H4R\_A and to the PD-(D/E)XK nuclease superfamily

**SEA\_CHEETO1 - 39**

Original Glimmer call @bp 29061 has strength 8.66

SSC: 27196-29061 (rev) CP: Yes SCS: Both ST: SS BLAST-Start: ChickenKing, 38, NCBI, Q1:S1, 100%, 0.0 Gap: 182bp LO: Yes RBS: K6/KM, 2.325, -3.978, no F: DNA polymerase I SIF-BLAST: DNA polymerase I, NCBI, ChickenKing, 39, QFG04708, 100%, 0.0 SIF-HHPred: DNA polymerase I; mycobacteria, DNA polymerase, Flap endonuclease, TRANSFERASE; 2.713A {Mycolicibacterium smegmatis}, PDB, NA, NA, 6VDE\_A , 98.2%, 100 SIF-Syn: NA

**SEA\_CHEETO1 - 40**

tRNA\*\*\*\*2903-29186\*\*\*\* tRNA-Pro(ggg) Identified by Aragorn v1.2.24 and tRNA ScanSE on 5/5/2022. tRNA ScanSE Infernal score = 62.8

**SEA\_CHEETO1 - 41**

Original Glimmer call @bp 29659 has strength 16.89

SSC: 29243-29659 (rev) CP: Yes SCS: Both ST: NA BLAST-Start: GaeCeo, 41, NCBI, Q23:S24, 83.5%, 1.9E-39 Gap: 129bp LO: no RBS: K6/KM, 2.976, -2.443, yes F: NKF SIF-BLAST: NKF, NCBI, GaeCeo, 38, QNL30994, 83.5%, 1.9E-39 SIF-HHPred: NKF, no matches with a probability above 90% SIF-Syn: NKF

**SEA\_CHEETO1 - 42**

Original Glimmer call @bp 31179 has strength 10.46

SSC: 29788-31179 (rev) CP: Yes SCS: Both ST: SS BLAST-Start: GaeCeo, 41, NCBI, Q1:S1, 100%, 0 Gap: 3 bp overlap LO: NA RBS: K6/KM, Z=1.771, FS=-5.164, no F: DNA helicase SIF-BLAST: DNA helicase, NCBI, GaeCeo, 41, QNL30995, 100%, 0 SIF-HHPred: Helicase SWR1; Chromatin, Remodeller, ATPase, Histone, NUCLEAR PROTEIN; HET: ADP;{Saccharomyces cerevisiae (strain ATCC 204508 / S288c)}, PDB, NA, NA, 6GEN\_M, 97%, 100% SIF-Syn: NA

**SEA\_CHEETO1 - 43**

Original Glimmer call @bp 31463 has strength 11.67

SSC: 31176-31463 [rev] CP: yes SCS: Both ST: SS BLAST-Start: GaeCeo, 43, NCBI, Q1:S1, 100%, 4.7E-33 Gap: 1bp overlap LO: NA RBS: K6/KM, Z=2.976, FS=-2.584, yes F: NKF SIF-BLAST: NKF, NCBI, GaeCeo, 43, QNL30996, 100%, 4.7e-33 SIF-HHPred: NKF, no matches with a probability above 90% SIF-Syn: NKF

**SEA\_CHEETO1 - 44**

Original Glimmer call @bp 31744 has strength 11.81

SSC: 31463-31744 [rev] CP: Yes SCS: Both ST: SS BLAST-Start: Schubert, 41, NCBI, Q1:S1, 100%, 0 Gap: 2 bp LO: NA RBS: K6/KM, Z=1.991, FS= -4.614, no F: NKF SIF-BLAST: NKF, NCBI, Schubert, 41, YP\_009818872, 100%, 0 SIF-HHPred: NKF, no matches with a probability above 90% SIF-Syn: NA

**SEA\_CHEETO1 - 45**

Original Glimmer call @bp 32549 has strength 15.74

SSC: 31746-32549 [rev] CP: yes SCS: Both ST: SS BLAST-Start: GaeCeo, 45, NCBI, Q1:S1, 100%, 0 Gap: 3 bp overlap LO: NA RBS: K6/KM, Z=2.573, FS=-3.447, no F: MazG-like Nucleotide Pyrophosphohydrolase SIF-BLAST: MazG-like Nucleotide Pyrophosphohydrolase, NCBI, GaeCeo, 45, QNL30998, 100%, 0 SIF-HHPred: MAZG-LIKE NUCLEOSIDE TRIPHOSPHATE PYROPHOSPHOHYDROLASE; HYDROLASE, DIMERIC DUTPASE; HET: GOL, SO4; 1.7A {DEINOCOCCUS RADIODURANS}, PDB, NA, NA, 2YF4\_C, 55.6%, 99.93% SIF-Syn: NA

**SEA\_CHEETO1 - 46**

Original Glimmer call @bp 33211 has strength 11.38

SSC: 32546-33211 [rev] CP: Yes SCS: Both ST: SS BLAST-Start: GaeCeo, 46, NCBI, Q1:S1, 100%, 0 Gap: 38 bp gap LO: No RBS: K6/KM, Z=1.139, FS=-7.477, no F: NKF SIF-BLAST: NKF, NCBI, GaeCeo, 46, QNL30999, 100%, 0 SIF-HHPred: NKF, no matches with a probability above 90% SIF-Syn: NKF

**SEA\_CHEETO1 - 47**

Original Glimmer call @bp 33827 has strength 15.34

SSC: 33249-33827 (rev) CP: Yes SCS: Both ST: SS BLAST-Start: ChickenKing, 45, NCBI, Q1:S1, 100%, 0 Gap: 25bp LO: Yes RBS: K6/KM, 2.976, -3.095, no F: Thymidylate Kinase SIF-BLAST: Thymidylate Kinase, NCBI, CHickenKing, 45, NCBI, QFG04715, 100%, 0 SIF-HHPred:TThymidylate kinase; TMK, kinase, thymidylate kinase, MRSA, pipiridine, transferase-transferase inhibitor complex; HET: T, PDB,4HLC\_B, 49.7%, 99.44 SIF-Syn: NA

**SEA\_CHEETO1 - 48**

Original Glimmer call @bp 34781 has strength 10.69; GeneMark calls start at 34793

SSC: 33852-34781 (rev) CP: Yes SCS: Both-GL ST: SS BLAST-Start: ChickenKing, 46, NCBI, Q1:S1,100%, 0 Gap:3 bp overlap LO: NA RBS:K6/KM, 1.866, -4.819, No F:glycosyltransferase SIF-BLAST: glycosyltransferase, NCBI, ChickenKing, 46, QFG04716, 100, 0 SIF-HHPred:Putative glycosyltransferase protein; Glycosyltransferase, Protein Structure Initiative II, PSI-II, 12059a, NYSGXRC, Structural Genomics, New York SGX Research Center for; HET: MSE; 2.35A {Bacteroides fragilis}, PDB, NA, NA, 3BCV\_A, 71.2%, 99.72 SIF-Syn: NA

**SEA\_CHEETO1 - 49**

Original Glimmer call @bp 35008 has strength 3.86

SSC:34778-35008 (rev) CP:Yes SCS: Both ST:SS BLAST-Start: ChickenKing, 48, NCBI, Q1:S1, 100, 1.0E-42 Gap: 2bp LO: NA RBS: K6/KM, 2.497, -3.549, Yes F: NKF SIF-BLAST: NKF, NCBI, ChickenKing, 48, QFG04717, 100%, 1.0E-42 SIF-HHPred: NKF, no matches with a probability above 90% SIF-Syn:NKF

**SEA\_CHEETO1 - 50**

Original Glimmer call @bp 35303 has strength 14.56

SSC: 35010-35303 (rev) CP: Yes SCS: Both ST:SS BLAST-Start:ChickenKing, 47, NCBI, Q1:S1, 100%, 2.0E-40 Gap: 3 bp overlap LO: NA RBS: K6/KM, 2.355, -3.854, No F: NKF SIF-BLAST: NKF, NCBI, ChickenKing, 47, QFG04718, 100, 2.0E-40 SIF-HHPred: NKF, no matches with a probability above 90% SIF-Syn: NKF

**SEA\_CHEETO1 - 51**

Original Glimmer call @bp 36121 has strength 16.83

SSC: 35300-36121 (rev) CP:Yes SCS:Both ST:SS BLAST-Start: GaeCeo, 51, NCBI, Q1:S1, 100%, 0 Gap:122 bp LO:Yes RBS:K6/KM, 2.976, -2.794, no F: Thymidylate Synthase SIF-BLAST: Thymidylate Synthase, NCBI, GaeCeo, 51, QNL31004, 100%, 0 SIF-HHPred: CMP 5-hydroxymethylase; CMP hydroxymethylase, TRANSFERASE; HET: C5P; 1.65A {Streptomyces rimofaciens}, PDB,5B6D\_B,92.3%, 100 SIF-Syn: NKF

**SEA\_CHEETO1 - 52**

Original Glimmer call @bp 36491 has strength 19.84

SSC: 36243-36491 (rev.) CP: Yes SCS: Both ST: SS BLAST-Start: GaeCeo, 52, NCBI, Q1:S1, 100%, 0 Gap: 118bp LO: Yes RBS: K6/KM, 2.976, -2.443, yes F: NKF SIF-BLAST: NKF, NCBI, GaeCeo, 52, QNL31005, 100%, 0 SIF-HHPred: NKF, no matches with a probability above 90% SIF-Syn: NKF

**SEA\_CHEETO1 - 53**

Original Glimmer call @bp 36803 has strength 20.09

SSC: 36609-36803 (rev.) CP: Yes SCS: Both ST: SS BLAST-Start: GaeCeo, 54, NCBI, Q1:S1, 100%, 1.1E-32 Gap: 38bp LO: Yes RBS: K6/KM, 2.009, -5.818, no F: NKF SIF-BLAST: NKF, NCBI, GaeCeo, 54, QNL31007, 100%, 1.1E-32 SIF-HHPred: Polycystin-2; PC2, PKD2, Calcium binding domain, EF hand, Cytosolic, Calcium, Coiled coil, Disease mutation, Glycoprotein, Ion transport; NMR {Homo sapiens}, PDB, NA, NA, 2KLD\_A, 95.4%, 90.21% SIF-Syn: NKF

**SEA\_CHEETO1 - 54**

Original Glimmer call @bp 37020 has strength 12.43

SSC: 36841-37020 (rev.) CP: Yes SCS: Both ST: SS BLAST-Start: Kauala, 49, NCBI, Q1:S1, 96.5%, 4.4E-12 Gap: 3bp overlap LO: NA RBS: K6/KM, 2.034, -4.812, yes F: NKF SIF-BLAST: NKF, NCBI, Kauala, 49, QNL31061, 96.5%, 4.4E-12 SIF-HHPred: NKF, no matches with a probability above 90% SIF-Syn: NKF

**SEA\_CHEETO1 - 55**

Original Glimmer call @bp 37787 has strength 17.24

SSC: 37017-37787 (rev.) CP: Yes SCS: Both ST: SS BLAST-Start: ChickenKing, 54, NCBI, Q14:S1, 99.2%, 0 Gap: 54 bp LO: Yes RBS: K6/KM, 1.429, -6.105, no F: NKF SIF-BLAST: NKF, NCBI, ChickenKing, 54, QFG04723, 99.2%, 0 SIF-HHPred: DUF2786 ; Protein of unknown function (DUF2786), EMBL-EBI, PF10979.11, 14.7%, 99.23% SIF-Syn: NKF

**SEA\_CHEETO1 - 56**

Original Glimmer call @bp 38182 has strength 14.75

SSC: 37841-38182 (rev.) CP: Yes SCS: Both ST: SS BLAST-Start: GaeCeo, 56, NCBI, Q1:S6, 95.8%, 0 Gap: 69bp LO: No RBS: K6/KM, 1.016, -6.990, no F: NKF SIF-BLAST: NKF, NCBI, GaeCeo, 56, QNL31009, 95.8%, 0 SIF-HHPred: NKF, no matches with a probability above 90% SIF-Syn: NKF

**SEA\_CHEETO1 - 57**

Original Glimmer call @bp 38499 has strength 14.81

SSC: 38251-38499 (rev) CP: Yes SCS: Both ST: SS BLAST-Start: GaeCeo, 57, NCBI, Q1:S1, 100%, 0.0 Gap: 5 bp LO: NA RBS: K6/KM, 2.537, -3.464, yes F: NKF SIF-BLAST: NKF, NCBI, GaeCeo, 57, QNL31010, 100%, 0.0 SIF-HHPred: NKF, no matches with a probability over 90% SIF-Syn: NKF

**SEA\_CHEETO1 - 58**

Original Glimmer call @bp 39028 has strength 11.06

SSC: 38504-39028 (rev) CP: Yes SCS: Both ST: SS BLAST-Start: MCubed, 61, NCBI, Q1:S1, 100%, 1.4E-23 Gap: 286 bp LO: Yes RBS: K6/KM, 3.216, -2.072, yes F: NKF SIF-BLAST: NKF, NCBI, MCubed, 61, QDK03720, 100%, 1.4E-23 SIF-HHPred: NKF, no matches with a probability above 90% SIF-Syn: NKF

🡪ORF located here was deleted from auto-annotation – no coding potential or blast hits

**SEA\_CHEETO1 - 59**

Original GeneMark call @bp 39365

SSC: 39365-39727 CP: yes SCS: GeneMark ST: SS BLAST-Start: ChickenKing, 58, NCBI, Q1:S1, 100%, 0.0 Gap: 337 bp LO: yes RBS: K6/KM, 1.786, -5.132, no F: NKF SIF-BLAST: NKF, NCBI, ChickenKing, 58, QFG04727, 100%, 0.0 SIF-HHPred: NKF, no matches with probability above 90% SIF-Syn: NKF

**SEA\_CHEETO1 - 60**

Original Glimmer call @bp 39750 has strength 4.97 \*\* not called by GeneMark

SSC: 39628-39750 (rev) CP: Yes SCS: Glimmer ST: NI BLAST-Start: no BLAST alignments Gap: NA LO: yes RBS: K6/KM, 1.168, -6.454, no F: NKF SIF-BLAST: NKF, no BLAST alignments SIF-HHPred: NKF, no matches with a probability above 90% SIF-Syn: NKF

\*\*Kept this gene because coding potential evident on GenemarkS, even though not significant hits via blast. My other hesitation is that it is only 123 bp.