

Annotation

USE: photos 4, 7, or 8

Avg capsule head is 58.079 nm

Width of tail: 9.147 nm

Length of tail: 189.411 nm

Metadata

- G&C content:
- Genome length:
- Morphology: Siphoviridae
- Naming:
- Source of isolation:
- Host range: M Smegmatis
- Temperate/lysogenic: Lytic/temperate
- Nucleotide bias:
- Taxonomy: Caudoviricetes

Template

SSC: (Start/stop coordinates). [coordinate numbers], CP: (coding potential) [yes/no] , SCS (Start choice source) - whichever has lower e value, ST: (Starterator) [SS, NA(not applicable), NI(not informative) NA if not found, NI if not most annotated start, Blast-Start: [phage name, gene number, NCBI, Q: S, coverage, e value/no significant BLAST alignments], Gap (or overlap): [number of bp], LO (Longest ORF) [yes/no/NA], RBS: (ribosome binding site) [NA/Scoring Matrix, spacing matrix, Z score, Final score, yes/no] and (DNAMASTER), F (Function): SIF (Supporting information for function). include the results for each line of evidence of, Function as below:, SIF-BLAST [NKF / function, NCBI, phage name and gene number, NCBI gene accession number, %alignment, evalule], SIF-HHPred [NKF / function, NCBI, phage name and gene number (if applicable), Hit, %alignment*, probability], SIF-Syn: ("syn" refers to "synteny") [NKF / function, flanking genes and phage(s) used to infer] (PHAMERATOR)

Links

HHPred: <https://toolkit.tuebingen.mpg.de/jobs/5411092>

Phamerator: <https://phamerator.org/phages>

NCBI: <https://blast.ncbi.nlm.nih.gov/Blast.cgi>

ORF	Annotation
1	Original Glimmer call @bp 41 has strength 2.35 SSC: 41-373, CP: Yes, SCS: Both, ST: NI, Blast-Start: Bobi, 1, BioProject, Q1:S1, 99%, 4e-74, Gap: 0, LO: No, RBS: Kibler6, Karlin Medium, 2.297, -4.133, No, F: [HNH endonuclease], SIF-BLAST: HNH endonuclease, NCBI, Bobi, gp1, YP_008408958.1, 99%, 4e-74 , SIF-HHPred: HNH endonuclease, PDB, Geobacillus virus E2, 5H0M_A, 60.4%, 97.57%, SIF-Syn: [HNH endonuclease, flanked by downstream terminase small subunit on Coco12]
2	Original Glimmer call @bp 445 has strength 10.85 SSC: 445-699, CP: Yes, SCS: Both, ST: SS, Blast-Start: Velveten, 2, BioProject, Q1:S1, 99%, 8e-51, Gap: 71, LO: No, RBS: Kibler6, Karlin Medium, 2.861, -2.985, Yes, F: [terminase small subunit], SIF-BLAST: terminase small subunit, NCBI, Velveten, gp2, YP_008409539.1, 99%, 8e⁻⁵¹ , SIF-HHPred: NKF, no matches with a probability above 90% , SIF-Syn: [terminase small subunit, flanked by upstream endonuclease on Boomer, downstream terminase large subunit on Boomer]
3	Original Glimmer call @bp 671 has strength 5.76; GeneMark call starts at 797 SSC: 671-2158, CP: Yes, SCS: Both - GL, ST: NI, Blast-Start: Velveten, 3, BioProject, Q1: S43, 100%, 0, Gap: -29, LO: No, RBS: Kibler6, Karlin Medium, 2.303, -4.629, No, F: [Terminase large subunit], SIF-BLAST: hypothetical protein, NCBI, Velveten, 3, YP_008409540.1 Q1:S43, 100%, 0, SIF-HHPred: Terminase large subunit, PDB, Byrnievirus HK97, 6Z6D_A, 89.49%, 100%, SIF-Syn:

	[Terminase large subunit, flanked by upstream terminase small subunit on Drago, downstream portal protein on Drago]
4	Original Glimmer call @bp 2199 has strength 5.59 SSC: 2199-3620, CP: Yes, SCS: Both, ST: NI, Blast-Start: Velvetten, 4, BioProject, Q1:S1, 100%, 0.0, Gap: 40, LO: Yes, RBS: Kibler6, Karlin Medium, 2.45, -3.812, No, F: [portal protein], SIF-BLAST: hypothetical protein, NCBI, Velvetten, 4, YP_008409541.1, 100%, 0.0, SIF-HHPred: portal protein, PDB, Mycobacterium phage Bxb1, 9D94_Fd, 92.18%, 100%, SIF-Syn: [Portal protein, flanked by upstream terminase large subunit on Ramsey, downstream capsid maturation protease on Velvetten]
5	Original Glimmer call @bp 3604 has strength 5.88; GeneMark calls start at 3631 SSC: 3604-4329, CP: Yes, SCS: Both - GL, ST: SS, Blast-Start: Ramsey, 5, BioProject, Q1:S1, 100%, 4e-176 , Gap: -17, LO: Yes, RBS: Kibler6, Karlin Medium, 2.431, -3.709, Yes, F: [capsid maturation protease], SIF-BLAST: head maturation protease, NCBI, Ramsey, 5, YP_002241792.1, 100%, 4e-176, SIF-HHPred: minor capsid protein, Interpro, Parageobacillus genome, PF06152.16, 20.75%, 97.5%, SIF-Syn: [capsid maturation protease, flanked by upstream portal protein on Ramsey, downstream scaffolding protein on Ramsey]
6	Original Glimmer call @bp 4408 has strength 11.36 SSC: 4408-4944, CP: Yes, SCS: Both, ST: NI, Blast-Start: Bobi, 6, BioProject, Q1:S1, 99%, 4e-122, Gap: 78, LO: Yes, RBS: Kibler6, Karlin Medium, 2.148, -4.440, Yes, F: [scaffolding protein], SIF-BLAST: head scaffolding protein, NCBI, Bobi, 6, YP_008408963.1, 99%, 4e-122, SIF-HHPred:

	Capsid assembly scaffolding protein Gp46, InterPro, Staphylococcus phage 80alpha, PF14265.11, 57.87%, 99.2%, SIF-Syn: [scaffolding protein, flanked by upstream capsid maturation protease on Velveten, downstream major capsid protein on Velveten]
7	Original Glimmer call @bp 5007 has strength 12.92 SSC: 5007-5915, CP: Yes, SCS: Both, ST: SS, Blast-Start: Boomer, 7, BioProject, Q1:S1, 100%, 0.0, Gap: 62, LO: Yes, RBS: Kibler6, Karlin Medium, 3.177, -2.219, Yes, F: [major capsid protein], SIF-BLAST: hypothetical protein, NCBI, Boomer, 7, YP_002014223.1, 100%, 0.0, SIF-HHPred: major capsid protein, PDB, Gordonia phage Ziko, 8EB4_E, 99.34%, 100%, SIF-Syn: [major capsid protein, flanked by upstream scaffolding protein on Boomer, downstream major head-to-tail adaptor on Boomer]
8	Original Glimmer call @bp 5927 has strength 6.00 SSC: 5927-6298, CP: Yes, SCS: Both, ST: NI, Blast-Start: WIVsmall, 76, BioProject, Q1:S1, 99%, 4e-81, Gap: 11, LO: Yes, RBS: Kibler6, Karlin Medium, 2.268, -4.112, No, F: [head-to-tail adaptor], SIF-BLAST: head-to-tail adaptor, NCBI, WIVsmall, 76, YP_008059977.1, 99%, 4e-81, SIF-HHPred: head-to-tail adaptor, PDB, Mycobacterium phage Bxb1, 9D94_Ga, 95.12%, 99.8%, SIF-Syn: [head-to-tail adaptor, flanked by upstream major capsid protein on Bobi, downstream major head-to-tail stopper on Bobi]
9	Original Glimmer call @bp 6295 has strength 5.99 SSC: 6295-6624, CP: Yes, SCS: Both, ST: SS, Blast-Start: Velveten, 9, BioProject, Q1:S1, 99%, 2e-71, Gap:-4, LO: Yes, RBS: Kibler6, Karlin Medium, 2.666, -3.220, Yes, F:

	[head-to-tail adaptor], SIF-BLAST: head-to-tail adaptor, NCBI, Velvet, 9, YP_008409546.1, 99%, 2e-71, SIF-HHPred: head-to-tail adaptor, PDB, Mycobacterium phage Bxb1, 9D94_Hc, 92.66%, 99.6%, SIF-Syn: [head-to-tail stopper, flanked by upstream head-to-tail adaptor on Velvet, downstream hypothetical on Velvet]
10	Original Glimmer call @bp 6631 has strength 7.68; GeneMark calls start at 6676 SSC: 6631-6957, CP: Yes, SCS: Both - GL, ST: SS, Blast-Start: Velvet, 10, BioProject, Q1:S1, 99%, 2e-73, Gap: 6, LO: Yes, RBS: Kibler6, Karlin Medium, 2.604, -3.699, Yes, F: [hypothetical protein], SIF-BLAST: head-tail connector protein, NCBI, Velvet, 10, YP_008409547.1, 99%, 2e-73, SIF-HHPred: unknown function, Interpro, unknown, PF17395.7, 64.81%, 99.2%, SIF-Syn: [hypothetical, flanked by upstream head-to-tail stopper on Velvet, downstream tail terminator on Velvet]
11	Original Glimmer call @bp 6947 has strength 8.48; GeneMark calls start at 7028 SSC: 6947-7351, CP: Yes, SCS: Both - GL, ST: SS, Blast-Start: Velvet, 11, NCBI, Q1:S1, 99%, 4e-89, Gap: -11, LO: Yes, RBS: Kibler6, Karlin Medium, 1.214, -6.241, No, F: [tail terminator], SIF-BLAST: head-tail adaptor, NCBI, Velvet, 11, YP_008409548.1, Q1:S1, 99%, 4e-89, SIF-HHPred: tail terminator, PDB, Mycobacterium phage Bxb1, 9D94_Ic, 98.5%, 99.4%, SIF-Syn: [tail terminator, flanked by upstream hypothetical on Velvet, downstream major tail subunit on Velvet]
12	Original Glimmer call @bp 7460 has strength 13.12

	SSC: 7460-8269, CP: Yes, SCS: Both, ST: SS, Blast-Start: <i>Sneathia anguinegens</i>, NCBI, Q1:S1; 100%, 0.0, Gap: 108, LO: No, RBS: Kibler6, Karlin Medium, 3.12, -2.339, Yes, F: [major tail protein], SIF-BLAST: hypothetical protein, NCBI, <i>Sneathia sanguinegens</i>, WP_015982045.1, Q1:S1, 100%, 0.0, SIF-HHPred: major tail protein, PDB, <i>Mycobacterium</i> phage Bxb1, 9D9L_J, 80.3%, 99.8%, SIF-Syn: [major tail subunit, flanked by upstream tail terminator on Velveteen, downstream tail assembly chaperone on Velveteen]
13	Original Glimmer call @bp 8383 has strength 8.97 SSC: 8383-8934, CP: Yes, SCS: Both, ST: SS, Blast-Start: Velveteen, 13, NCBI, Q1:S1, 99%, 9e-130, Gap: 113, LO: Yes, RBS: Kibler6, Karlin Medium, 2.942, -2.708, Yes, F: [tail assembly chaperone], SIF-BLAST: tail assembly chaperone, NCBI, Velveteen, 13, YP_008409551.1, Q1:S1, 99%, 9e-130, SIF-HHPred: tail assembly protein, Interpro, <i>Mycobacterium</i> phage Kampy, 31.70%, 95.8%, SIF-Syn: [tail assembly chaperone, flanked by upstream major tail subunit on Velveteen, downstream tail assembly chaperone on Velveteen]
14	Original Glimmer call @bp 8993 has strength 8.82 SSC: 8993-9319, CP: Yes, SCS: Both, ST: SS, Blast-Start: Henu3 PeY-2017, 76, NCBI, Q1:S60, 99%, 4e-68, Gap: 58, LO: No, RBS: Kibler6, Karlin Medium, 2.226, -4.197, No, F: [hypothetical protein], SIF-BLAST: tail assembly chaperone, NCBI, Henu3 PeY-2017, 76, QBJ00840.1, Q1:S60; 99%, 4e-68, SIF-HHPred: bacteriophage Gp15 protein, InterPro, Bacteriophage A500, PF06854.16 31.48%, 94%, SIF-Syn: [hypothetical, flanked by upstream tail

	assembly chaperone on Velvet, downstream tape measure protein on Velvet]
15	Original Glimmer call @bp 9337 has strength 6.04 SSC: 9337- 12867, CP: Yes, SCS: Both, ST: SS, Blast-Start: BigPhil, 15, NCBI, Q1:S8; 100%, 0.0, Gap: 17, LO: No, RBS: Kibler6, Karlin Medium, 2.45, -3.812, No, F: [tape measure protein], SIF-BLAST: tape measure protein, NCBI, BigPhil, 15, AVR76409.1, Q1:S8, 100%, 0.0, SIF-HHPred: tape measure protein, PDB, Chivirus chi, 8VJH_Q, 39.71%, 98%, SIF-Syn: [tape measure protein, flanked by upstream tail assembly chaperone on Velvet, downstream minor tail subunit on Velvet]
16	Original Glimmer call @bp 12943 has strength 7.28; GeneMark calls start at 12868 SSC: 12943-14577, CP: Yes, SCS: Both - GL, ST: NI - MAS but do not call it, Blast-Start: Job42, 18, NCBI, Q1:S26, 100%, 0.0, Gap: 75, LO: No, RBS: Kibler6, Karlin Medium, 2.323, -4.286, Yes, F: [minor tail protein], SIF-BLAST: minor tail protein, NCBI, Job42, 18, YP_008126608.1, Q1:S26, 100%, 0.0, SIF-HHPred: minor tail protein, PDB, Mycobacterium phage Bxb1, 9D93_Mf, 28.13%, 99.6%, SIF-Syn: [minor tail subunit, flanked by upstream tape measure protein on BigPhil, downstream minor tail protein on BigPhil]
17	Original Glimmer call @bp 14663 has strength 8.23 SSC: 14663-16372 , CP: Yes, SCS: Both, ST: NI, Blast-Start: Velvet, 17, BioProject, Q1:S1, 100%, 0.0, Gap: 85, LO: Yes, RBS: Kibler6, Karlin Medium, 3.275, -2.606, Yes, F: [minor tail protein], SIF-BLAST: minor tail protein, NCBI, Velvet, 17, YP_008409554.1, Q1:S1, 100%, 0.0,

	SIF-HHPred: minor tail protein, PDB, Mycobacterium phage Bxb1, 9D93_Oa, 96.66%, 100%, SIF-Syn: [minor tail protein, flanked by upstream minor tail protein on BigPhil, downstream minor tail subunit on BigPhil]
18	Original Glimmer call @bp 16427 has strength 9.98 SSC: 16427-17257, CP: Yes, SCS: Both, ST: SS, Blast-Start: Kingsley, 18, NCBI, Q1:S1, 100%, 0.0, Gap: 54, LO: No, RBS: Kibler6, Karlin Medium, 2.849, -2980, Yes, F: [minor tail protein], SIF-BLAST: minor tail protein, NCBI, Kingsley, 18, ARM70613.1, Q1:S1, 100%, 0.0, SIF-HHPred: NKF, SIF-Syn: [minor tail protein, flanked by upstream minor tail protein on Coco12, downstream minor tail protein on Bobi]
19	Original Glimmer call @bp 17254 has strength 8.44 SSC: 17254-19731, CP: Yes, SCS: Both, ST: SS, Blast-Start: Kingsley, 19, NCBI, Q1:S1, 100%, 0.0, Gap: -4, LO: No, RBS: Kibler6, Karlin Medium, 2.394, -4.695, No, F: [minor tail protein], SIF-BLAST: minor tail protein, NCBI, Kingsley, 19, ARM70614.1, Q1:S1, 100%, 0.0, SIF-HHPred: minor tail protein, PDB, Mycobacterium phage Bxb1, 9D93_Pb, 73.45%, 100%, SIF-Syn: [minor tail subunit, flanked by upstream minor tail protein on Coco12, downstream minor tail protein on Coco12]
20	Original Glimmer call @bp 19728 has strength 7.21 SSC: 19728-22562, CP: Yes, SCS: Both, ST: SS, Blast-Start: Shauna1, 19, BioProject, Q1:S1, 100%, 0.0, Gap: -4, LO: Yes, RBS: Kibler6, Karlin Medium, 2.102, -4.744, No, F: [minor tail protein], SIF-BLAST: minor tail protein, NCBI, Shauna1, 19, YP_009608201.1, Q1:S1, 100%, 0.0, SIF-HHPred: esterase, PDB, Dehalococcoidia bacterium, 7SPN_A, 37.5%, 100%, SIF-Syn: [minor tail protein, flanked

	by upstream minor tail protein on Coco12, downstream minor tail protein on Shauna1]
21	Original Glimmer call @bp 22559 has strength 7.55; GeneMark calls start at 22562 SSC: 22559-23509, CP: Yes , SCS: Both- GL, ST: SS, Blast-Start: Shauna1, 20, BioProject, Q1:S1, 100%, 0.0, Gap: -4, LO: Yes, RBS: Kibler6, Karlin Medium, 2.2, -4.718, No, F: [hypothetical protein], SIF-BLAST: minor tail protein, NCBI, Shauna1, 20, YP_009608202.1, Q1:S1, 100%, 0.0, SIF-HHPred: NKF, SIF-Syn: [hypothetical protein, flanked by upstream minor tail protein on Shauna1, downstream hypothetical protein on Shauna1]
22	Original Glimmer call @bp 23575 has strength 11.04 SSC: 23575-24012, CP: Yes, SCS: Both, ST: SS, Blast-Start: Shauna1, 21, BioProject, Q1:S1, 99%, 5e-92, Gap: 65, LO: Yes, RBS: Kibler6, Karlin Medium, 3.177, -2.156, Yes, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Shauna1, 21, YP_009608203.1, Q1:S1, 99%, 5e-92, SIF-HHPred: minor tail protein, PDB, Mycobacterium phage Bxb1, 9D93_Rc, 77.24%, 99.6% , SIF-Syn: [hypothetical protein, flanked by upstream hypothetical protein on Shauna1, downstream hypothetical protein on Shauna1]
23	Original Glimmer call @bp 24248 has strength 6.49 SSC: 24048-24248, CP: Yes, SCS: Both, ST: SS, Blast-Start: Shauna1, 22, BioProject, Q1:S1, 99%, 6e-39, Gap: NA, LO: Yes, RBS: Kibler6, Karlin Medium, 1.737, -6.835, No, F: [HTH DNA binding protein], SIF-BLAST: HTH DNA binding protein, NCBI, Shauna1, 22, YP_009608204.1, Q1:S1, 99%, 6e-39, SIF-HHPred: RNA polymerase sigma factor, PDB, Aquifex aeolicus, 1RP3_A, 89.39%, 97.4%,

	SIF-Syn: [hypothetical protein, flanked by upstream hypothetical on Shauna1, downstream hypothetical protein on Coco12]
24	Original Glimmer call @bp 24399 has strength 8.34 SSC: 24399-24683 , CP: No, SCS: Both, ST: SS, Blast-Start: Tweety, 27, BioProject, Q1:S1, 99%, 1e-59, Gap: 150, LO: Yes, RBS: Kibler6, Karlin Medium, 3.198, -2.253, Yes, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Tweety, 27, YP_001469260.1, Q1:S1, 99%, 1e-59, SIF-HHPred: NKF, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical protein on Coco12, downstream hypothetical on Coco12]
25	Original Glimmer call @bp 24690 has strength 5.93 ** not called by GeneMark SSC: 24690-24836, CP: No, SCS: Glimmer, ST: SS, Blast-Start: Bobi, 29, BioProject, Q1:S1, 100%, 5e-25, Gap: 6, LO: Yes, RBS: Kibler6, Karlin Medium, 2.103, -4.454, Yes, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Bobi, 29, YP_002241815.1 Q1:S1, 100%, 5e-25, SIF-HHPred: NKF, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical protein on Coco12, downstream hypothetical on Coco12]
26	Original Glimmer call @bp 24863 has strength 10.02; GeneMark calls start at 24833 SSC: 24833-25000, CP: Yes, SCS: GeneMark, ST: NI, Blast-Start: hypothetical protein, NCBI, Klebsiella pneumoniae, XXX, WP_016032723.1, Q1:S1, 98%, 5e-31, Gap: -4, LO: Yes, RBS: Kibler6, Karlin Medium, 3.209, -2.090, Yes, F: [hypothetical protein], SIF-BLAST: Klebsiella pneumoniae, NCBI, Q1:S1, 98%, 5e-31, SIF-HHPred: NKF,

	SIF-Syn: [hypothetical protein, flanked by upstream hypothetical protein on Coco12, downstream hypothetical on Coco12]
27	Original Glimmer call @bp 25074 has strength 13.05 SSC: 25074- 25307, CP: Yes, SCS: Both , ST: SS, Blast-Start: DeadP, 29, BioProject, Q1:S1, 99%, 1e-42, Gap: 73, LO: No, RBS: Kibler6, Karlin Medium, 3.177, -2.297, Yes, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, DeadP, 29, YP_009016919.1 Q1:S1, 99%, 1e-42, SIF-HHPred: NKf SIF-Syn: [hypothetical protein, flanked by upstream lysin A on Shauna1, downstream hypothetical on Coco12]
28	Original Glimmer call @bp 25304 has strength 8.28 SSC: 25304-26458, CP: Yes, SCS: Both, ST: SS, Blast-Start: Shauna1, 27, BioProject, Q1:S1, 100%, 0.0, Gap: -4, LO: No, RBS: Kibler6, Karlin Medium, 2.181, -4.229, No, F: [endolysin], SIF-BLAST: endolysin, NCBI, Shauna1, 27, YP_009608209.1, Q1:S1, 100%, 0.0, SIF-HHPred: Bifunctional autolysin, PDB, Staphylococcus aureus subsp. aureus NCTC 8325, 4KNK_A, 41.41%, 99.3%, SIF-Syn: [lysine A, flanked by upstream hypothetical protein on Coco12, downstream lysine B on Coco12]
29	Original Glimmer call @bp 26458 has strength 12.28 SSC: 26458-27456, CP: Yes, SCS: Both, ST: NI, Blast-Start: Velvetin, 27, BioProject, Q1:S1, 100%, 0.0, Gap: -1, LO: Yes, RBS: Kibler6, Karlin Medium, 1.141, -6.394, No, F: [endolysin], SIF-BLAST: endolysin, NCBI, Velvetin, 27, YP_008409564.1, Q1:S1, 100%, 0.0, SIF-HHPred: Gene 12 protein, PDB, Fromavirus D29, 3HC7_A, 72.59%, 100%,

	SIF-Syn: [lysine B, flanked by upstream lysine A on Shauna1, downstream hypothetical protein]
30	Original Glimmer call @bp 27677 has strength 7.78 ** not called by GeneMark SSC: 27441-27677, CP: Yes, SCS: Glimmer, ST: NI, Blast-Start: WIVsmall, 48, BioProject, Q1:S157, 90%, 3e-29, Gap: NA, LO: Yes, RBS: Kibler6, Karlin Medium, 2.063, -4.906, Yes, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, WIVsmall, 48, YP_008059949.1, Q1:S157, 90%, 3-29, SIF-HHPred: Holin, InterPro, Lactococcus, PF16945.10, 89.61%, 99.9%, SIF-Syn: [hypothetical, flanked by upstream holin on Shauna1, downstream lysine B on Shauna1]
31	Original GeneMark call @bp 27466 SSC: 27466-27699, CP: Yes, SCS: Both, ST: NI, Blast-Start: Fruitloop, 31, BioProject, Q1:S1, 99%, 6e-44, Gap: 27, LO: No, RBS: Kibler6, Karlin Medium, 1.792, -5.389, No, F: [holin], SIF-BLAST: holin, NCBI, Fruitloop, 31, YP_002241716.1, Q1:S1, 99%, 6e-44, SIF-HHPred: NKF, SIF-Syn: [holin, flanked by upstream hypothetical, downstream hypothetical on Shauna1]
32	Original GeneMark call @bp 27696 has strength 9.67 SSC: 27696-28070, CP: Yes, SCS: Both, ST: SS, Blast-Start: Fruitloop, 32, BioProject, Q1:S1, 99%, 5e-81, Gap: 33, LO: Yes, RBS: Kibler6, Karlin Medium, 1.645, -5.486, No, F: [hypothetical protein], SIF-BLAST: minor tail protein, NCBI, Fruitloop, 32, YP_002241717.1, Q1:S1, 99%, 5e-81, SIF-HHPred: unknown function, InterPro, Mycobacterium phage D29, PF10874.13, 89.52%, 99.9%, SIF-Syn:

	[hypothetical protein, flanked by upstream holin on Shauna1, downstream hypothetical protein on Shauna1]
33	Original Glimmer call @bp 28095 has strength 4.93 SSC: 28095-28328, CP: Yes, SCS: Both , ST: SS, Blast-Start: Boomer, 36, BioProject, Q1:S1, 99%, 3e-50, Gap: 24, LO: Yes, RBS: Kibler6, Karlin Medium, 2.14, -4.315, Yes, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Boomer, 36, YP_002014252.1, Q1:S1, 99% 3e-50, SIF-HHPred: unknown function, InterPro, TraK E. coli, PF17273.7, 57.14%, 97.4%, SIF-Syn: [hypothetical protein, flanked by upstream DNAQ-like DNA Polymerase III subunit on Shauna1, downstream hypothetical on Shauna1]
34	Original Glimmer call @bp 28315 has strength 11.70; GeneMark calls start at 28360 SSC: 28315-29136, CP: Yes, SCS: Both - GL, ST: SS, Blast-Start: Shauna1, 32, BioProject, Q1:S1, 100%, 0.0, Gap: 9, LO: Yes, RBS: Kibler6, Karlin Medium, 2.787, -3.048, Yes, F: [DNAQ-like DNA Polymerase III subunit], SIF-BLAST: DNAQ-like exonuclease, NCBI, Shauna1, 32, YP_009608214.1, Q1:S1, 100%, 0.0, SIF-HHPred: Exonuclease, PDB, Bacillus subtilis, 8AN9_A, 70.70%, 99.6%, SIF-Syn: [DNAQ-like DNA Polymerase III subunit, flanked by upstream hypothetical on Shauna1, downstream hypothetical protein on Shauna1]
35	Original Glimmer call @bp 29120 has strength 1.11 ** not called by GeneMark SSC: 29120-29233, CP: No, SCS: Glimmer, ST: NI - MAS but do not call it, Blast-Start: Shauna1, 33, BioProject, Q1:S1, 97%, 3e-17, Gap: -17, LO: Yes, RBS: Kibler6, Karlin Medium, 1.814, -6.044, No, F: [hypothetical protein],

	SIF-BLAST: hypothetical protein, NCBI, Shauna1, 33, YP_009608215.1, Q1:S1, 97%, 3e-17, SIF-HHPred: NKF, SIF-Syn: [hypothetical protein, flanked by upstream DNAQ-like DNA Polymerase III subunit on Shauna1, downstream hypothetical protein on Shauna1]
36	Original Glimmer call @bp 29223 has strength 3.99 SSC: 29223-29441, CP: Yes, SCS: Both, ST: NI - MAS but do not call it, Blast-Start: Astraea, 50, BioProject, Q1:S1, 99%, 4e-43, Gap: -11, LO: No, RBS: Kibler6, Karlin Medium, 1.742, -5.282, No, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Astraea, 50, YP_008061546.1, Q1:S1, 99%, 4e-43, SIF-HHPred: NKF, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical on Shauna1, downstream hypothetical protein on Shauna1]
37	Original GeneMark call @bp 29434 SSC: 29434-29526, CP: Yes, SCS: Both, ST: SS, Blast-Start: Florinda, 38, BioProject, Q1:S2, 97%, 5e-10, Gap: -8, LO: No, RBS: Kibler6, Karlin Medium, 1.735, -5.220, No, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Florinda, 38, YP_009206756.1, Q1:S2, 97%, 5e-10, SIF-HHPred: NKF, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical on Shauna1, downstream hypothetical protein on Shauna1]
38	Original Glimmer call @bp 30105 has strength 4.37 SSC: 29569-30105, CP: Yes, SCS: Both, ST: NI, Blast-Start: Shauna1, 36, BioProject, Q1:S1, 99%, 2e-128, Gap: 44, LO: Yes, RBS: Kibler6, Karlin Medium, 3.131, -2.253, Yes, F: [immunity repressor], SIF-BLAST: transcriptional repressor, NCBI, Shauna1, 36, YP_009608218.1, Q1:S1, 99%, 2e-128,

	SIF-HHPred: immunity repressor, PDB Mycobacterium phage TopsytheTRex, 7TZ1_A, 93.26%, 100%, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical on Shauna1, downstream hypothetical protein on Shauna1]
39	Original Glimmer call @bp 30476 has strength 9.06; GeneMark calls start at 30485 SSC: 30150-30476, CP: Yes, SCS: Both - GL, ST: NI, Blast-Start: LOCARD, NCBI, Q1:S27, 99%, 6e-75, Gap: 377, LO: No, RBS: Kibler6, Karlin Medium, 1.716, -5.724, No, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, LOCARD, WDW20013.1, Q1:S27, 99%, 6e-75, SIF-HHPred: NKF, SIF-Syn: [hypothetical protein, flanked by upstream integrase on Coco12, downstream hypothetical on Coco12]
40	Original Glimmer call @bp 30854 has strength 7.13 SSC: 30854-31972, CP: Yes, SCS: Both, ST: SS, Blast-Start: Velveten, 37, BioProject, Q1:S1, 100%, 0.0, Gap: 377, LO: Yes, RBS: Kibler6, Karlin Medium, 2.418, -4.644, No, F: [integrase], SIF-BLAST: integrase, NCBI, Velveten, 37, YP_008409574.1, Q1:S24, 99%, 1e-77, SIF-HHPred: integrase protein, PDB, Enterococcus faecalis, Clostridioides difficile, 6EMY_B, 79.03%, 100%, SIF-Syn: [integrase, flanked upstream by hypothetical on Coco12, downstream hypothetical on Coco12]
41	Original Glimmer call @bp 32487 has strength 12.24 SSC: 32035-32487, CP: Yes, SCS: Both, ST: SS, Blast-Start: Cerasum, 39, BioProject, Q1:S12, 100%, 2e-103, Gap: 265, LO: No, RBS: Kibler6, Karlin Medium, 1.716, -6.298, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Cerasum, 39, YP_009125892.1, Q1:S24, 100%,

	2e-103, SIF-HHPred: NKF, SIF-Syn: [hypothetical protein, flanked upstream hypothetical protein on Coco12, downstream on integrase on Coco12]
42	Original Glimmer call @bp 33286 has strength 2.21 SSC: 32753-33286, CP: No, SCS: Both, ST: NI - MAS but do not call it, Blast-Start: Velvetten, 39, BioProject, Q1:S1, 99%, 8e-123, Gap: 85, LO: No, RBS: Kibler6, Karlin Medium, 2.353, -4.224, No, F: [hypothetical protein], SIF-BLAST: transcriptional repressor, NCBI, Velvetten, 39, YP_008409576.1, Q1:S1, 99%, 8e-123, SIF-HHPred: transcription regulator, PDB, Streptococcus suis 05ZYH33, 5FD4_B, 38.98%, 98.2%, SIF-Syn: [hypothetical protein, flanked upstream CRO protein on Coco12, downstream on hypothetical protein on Coco12]
43	Original GeneMark call @bp 33372 has strength 4.66; GeneMark calls start at 33453 SSC: 33372-33776, CP: Yes, SCS: Both - GL, ST: NI - MAS but do not call it, Blast-Start: Cornie, 38, BioProject, Q1:S1, 99%, 7e-83, Gap: 85, LO: Yes, RBS: Kibler6, Karlin Medium, 0.914, -7.967, No, F: [Helix-turn-helix DNA binding protein], SIF-BLAST: HTH DNA binding protein, NCBI, Cornie, 38, YP_009856224.1, Q1:S1, 99%, 7e-83, SIF-HHPred: transcription regulator, PDB, Streptococcus suis 05ZYH33, 5FD4_B, 88.06%, 97.6%, SIF-Syn: [CRO protein, flanked by upstream hypothetical protein on Coco12, downstream DNA damage-inducible protein D-like protein on Velvetten]
44	Original Glimmer call @bp 33833 has strength 11.78 SSC: 33833-34699, CP: Yes, SCS: Both, ST: SS, Blast-Start: Velvetten, 41, BioProject, Q1:S1, 100%, 0.0, Gap: 56, LO:

	Yes, RBS: Kibler6, Karlin Medium, 3.022, -2.541, Yes, F: [DNA damage-inducible protein D-like protein], SIF-BLAST: DNA damage-inducible protein D-like protein, NCBI, Velvet, 41, YP_008409578.1, Q1:S1, 100%, 0.0, SIF-HHPred: phage antirepressor protein, InterPro, Enterobacteria phage P1, PF03374.19, 38.89%, 97.7%, SIF-Syn: [DNA damage-inducible protein D-like protein, flanked upstream by CRO protein on Coco12, downstream hypothetical on Coco12]
45	Original Glimmer call @bp 35274 has strength 5.14 SSC: 35274-35573, CP: Yes, SCS: Both, ST: SS, Blast-Start: Velvet, 43, BioProject, Q1:S1, 99%, 2e-66, Gap: 574, LO: Yes, RBS: Kibler6, Karlin Medium, 2.527, -3.589, Yes, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Velvet, 43, YP_008409580.1, Q1:S1, 99%, 2e-66, SIF-HHPred: NKF, SIF-Syn: [hypothetical protein, flanked by hypothetical protein on Velvet, downstream DNA damage-inducible protein D-like protein on Velvet]
46	Original Glimmer call @bp 35558 has strength 6.28; GeneMark calls start at 35570 SSC: 35570-35782, CP: Yes, SCS: Both - GM, ST: NI - MAS but do not call it, Blast-Start: Velvet, 44, BioProject, Q1:S1, 99%, 2e-42, Gap: -4, LO: No, RBS: Kibler6, Karlin Medium, 1.203, -6.265, No, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Velvet, 44, YP_008409581.1, Q1:S1, 99%, 2e-42, SIF-HHPred: unknown function, InterPro, unknown, PF19887.4, 65.33%, 94.1%, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical protein on Velvet, downstream excise on Coco12]

47	Original Glimmer call @bp 35871 has strength 8.56 SSC: 35871-36131, CP: Yes, SCS: Both, ST: SS, Blast-Start: Velvet, 45, BioProject, Q1:S1, 99%, 2e-54, Gap: 88, LO: Yes, RBS: Kibler6, Karlin Medium, 2.86, -2.879, Yes, F: [excise], SIF-BLAST: excisionase, NCBI, Velvet, 45, YP_008409582.1, Q1:S1, 99%, 2e-54, SIF-HHPred: excisionase, PDB, Mesorhizobium japonicum R7A, 8DGL_C, 66.28%, 98.4%, SIF-Syn: [excise, flanked by upstream hypothetical protein on Velvet, downstream hypothetical on Coco12]
48	Original Glimmer call @bp 36158 has strength 7.22; GeneMark calls start at 36128 SSC: 36128-36319, CP: Yes, SCS: Both - GM, ST: NI - MAS but do not call it, Blast-Start: Philus, 55, NCBI, Q1:S1, 98%, 4e-28, Gap: -4, LO: Yes, RBS: Kibler6, Karlin Medium, 2.33, -4.271, No, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Philus, 55, WVX89191.1, Q1:S1, 98%, 4e-28, SIF-HHPred: cell division protein, PDB, E. coli, 2JEE_B, 66.04%, 96.9%, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical protein on Velvet, downstream hypothetical on Velvet]
49	Original Glimmer call @bp 36536 has strength 3.55 ** not called by GeneMark SSC: 36360-36536, CP: No, SCS: Glimmer, ST: SS, Blast-Start: No significant BLAST alignments, Gap: 593, LO: No, RBS: Kibler6, Karlin Medium, 2.027, -4.611, Yes, F: [hypothetical protein], SIF-BLAST: No significant BLAST alignments, SIF-HHPred: NKF, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical protein on Velvet, downstream hypothetical on Velvet]

50	Original Glimmer call @bp 36528 has strength 8.88; GeneMark calls start at 36489 SSC: 36489-37112, CP: Yes, SCS: Both- GM, ST: NI - MAS but do not call it, Blast-Start: Boomer, 58, BioProject, Q1:S1, 99%, 5e-138, Gap: 208, LO: No, RBS: Kibler6, Karlin Medium, 2.226, -4.197, No, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Boomer, 58, YP_002014274.1, Q1:S1, 99%, 5e-138, SIF-HHPred: NKF, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical protein on Velveten, downstream hypothetical on Velveten]
51	Original Glimmer call @bp 37130 has strength 3.36 SSC: 37130-37411, CP: Yes, SCS: Both, ST: SS, Blast-Start: Che9d, 61, BioProject, Q1:S1, 99%, 4e-60, Gap: 593, LO: No, RBS: Kibler6, Karlin Medium, 2.714, -4.171, Yes, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Che9d, 61, NP_818034.1, Q1:S1, 99%, 4e-60, SIF-HHPred: NKF, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical protein on Coco12, downstream hypothetical on Coco12]
52	Original Glimmer call @bp 37487 has strength 9.63 SSC: 37487-37768, CP: Yes, SCS: Both, ST: SS, Blast-Start: Velveten, 50, BioProject, Q1:S1, 99%, 5e-60, Gap: 75, LO: Yes, RBS: Kibler6, Karlin Medium, 3.286, -2.072, Yes, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Velveten, 50, YP_008409587.1, Q1:S1, 99%, 5e-60 , SIF-HHPred: NKF, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical protein on Coco12, downstream hypothetical on Coco12]
53	Original Glimmer call @bp 37765 has strength 9.04

	SSC: 37765-38112, CP: Yes, SCS: Both, ST: SS, Blast-Start: Velvet, 51, BioProject, Q1:S1, 99%, 4e-78, Gap: -4, LO: Yes, RBS: Kibler6, Karlin Medium, 2.373, -3.972, Yes, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Velvet, 50, YP_008409588.1, Q1:S1, 99%, 5e-60, SIF-HHPred: unknown function, InterPro, Mycobacterium tuberculosis, PF05305.19, 60%, 99.6%, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical protein on Coco12, downstream WhiB family transcription factor on Coco12]
54	Original Glimmer call @bp 38103 has strength 11.04; GeneMark calls start at 38112 SSC: 38103-38606, CP: Yes, SCS: Glimmer, ST: NI - MAS but do not call it, Blast-Start: Cerasum, 53, BioProject, Q3:S1, 98%, 1e-118, Gap: -10, LO: Yes, RBS: Kibler6, Karlin Medium, 2.467, -4.161, No, F: [WhiB family transcription factor], SIF-BLAST: transcriptional regulator, NCBI, Cerasum, 53, YP_009125906.1, Q3:S1, 98%, 1e-118, SIF-HHPred: transcriptional regulator WhiB3, PDB, Mycobacterium tuberculosis, 8CYF_A, 47.90%, 99.8%, SIF-Syn: [WhiB family transcription factor, flanked by upstream hypothetical protein on Coco12, downstream HTH DNA binding protein on Velvet]
55	Original Glimmer call @bp 38603 has strength 8.50 SSC: 38603-38950, CP: Yes, SCS: Both, ST: SS, Blast-Start: Che8, 63, BioProject, Q1:S1, 99%, 9e-77, Gap: -4, LO: No, RBS: Kibler6, Karlin Medium, 2.685, -3.182, No, F: [helix-turn-helix DNA binding domain protein], SIF-BLAST: helix-turn-helix DNA binding domain protein, NCBI, Che8, 63, NP_81740.1, Q1:S1, 99%, 9e-77, SIF-HHPred: Dna

	binding protein, PDB, <i>Hyperthermus butylicus</i> DSM 5456, 2LVS_A, 80%, 99.3%, SIF-Syn: [HTH DNA binding protein, flanked upstream WhiB family transcription factor on Coco12, downstream HTH DNA binding protein on Velveteen]
56	Original Glimmer call @bp 38947 has strength 6.75 SSC: 38947-39300 , CP: Yes, SCS: Both, ST: SS, Blast-Start: Che9d, 67, BioProject, Q1:S1, 99%, 4e-77, Gap: -4, LO: No, RBS: Kibler6, Karlin Medium, 2.784, -2.975, Yes, F: [DNA binding protein], SIF-BLAST: DNA binding protein, Che9d, 67, NP_818040.1, Q1:S1, 99%, 4e-77, SIF-HHPred: DNA binding protein, PDB, <i>Hyperthermus butylicus</i> DSM 5456, 2LVS_A, 78.63%, 99.3%, SIF-Syn: [HTH DNA binding protein, flanked by upstream HTH DNA binding protein on Velveteen, downstream hypothetical on Coco12]
57	Original Glimmer call @bp 39297 has strength 7.24 SSC: 39297-39944, CP: Yes, SCS: Both, ST: SS, Blast-Start: Velveteen, 55, BioProject, Q1:S1, 100%, 6e-155, Gap: -4, LO: No, RBS: Kibler6, Karlin Medium, 2.517, -4.437, No, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Velveteen, 55, YP_008409592.1, Q1:S1, 100%, 6e-155, SIF-HHPred: transcription regulator WhiB, PDB, <i>Streptomyces venezuelae</i> , 8DY7_H, 39.07%, 99.8%, SIF-Syn: [hypothetical protein, flanked by upstream HTH DNA binding protein on Velveteen, downstream hypothetical protein on Velveteen]
58	Original Glimmer call @bp 39944 has strength 2.42 ** not called by GeneMark SSC: 39944-40099, CP: No, SCS: Glimmer, ST: SS, Blast-Start: Velveteen, 56, BioProject, Q1:S1, 98%, 9e-30,

	Gap: -1, LO: No, RBS: Kibler6, Karlin Medium, 2.373, -4.182, No, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Velvet, 56, YP_008409593.1, Q1:S1, 98%, 9e-30, SIF-HHPred: NKF, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical protein on Coco12, downstream hypothetical on Coco12]
59	Original Glimmer call @bp 40099 has strength 8.04 SSC: 40099-40329 , CP: Yes, SCS: Both, ST: SS, Blast-Start: Velvet, 57, BioProject, Q1:S1, 99%, 2e-44, Gap: -1, LO: Yes, RBS: Kibler6, Karlin Medium, 2.555, -3.593, No, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Velvet, 57, YP_008409594.1, Q1:S1, 99%, 2e-44, SIF-HHPred: NKF, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical protein on Coco12, downstream hypothetical on Coco12]
60	Original Glimmer call @bp 40326 has strength 9.08 SSC: 40326-40667, CP: Yes, SCS: Both, ST: SS, Blast-Start: Velvet, 58, BioProject, Q1:S1, 99%, 7e-75, Gap: -4, LO: No, RBS: Kibler6, Karlin Medium, 2.763, -3.018, No, F: [hypothetical protein], SIF-BLAST: DNA methyltransferase, NCBI, Velvet, 58, YP_008409595.1, Q1:S1, 99%, 7e-75, SIF-HHPred: unknown function, InterPro, unknown, PF19849.4, 18.58%, 93.6%, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical protein on Coco12, downstream hypothetical on Coco12]
61	Original Glimmer call @bp 40664 has strength 13.42 SSC: 40664-41128, CP: Yes, SCS: Both, ST: SS, Blast-Start: Velvet, 59, BioProject, Q1:S1, 99%, 4e-104, Gap: -4, LO: Yes, RBS: Kibler6, Karlin Medium, 2.576, -3.549, Yes, F: [hypothetical protein], SIF-BLAST: hypothetical protein,

	NCBI, Velvet, 59, YP_008409596.1, Q1:S1, 99%, 4e-104, SIF-HHPred: Host-nuclease inhibitor protein Gam, InterPro, Bacteriophage Mu, PF07352.17, 53.90%, 99%, SIF-Syn: [hypothetical protein, flanked by upstream RecA-like DNA recombinase on Coco12, downstream hypothetical on Coco12]
62	Original Glimmer call @bp 41125 has strength 12.58 SSC: 41125-42102, CP: Yes, SCS: Both, ST: SS, Blast-Start: Velvet, 60, BioProject, Q1:S1, 100%, 0.0, Gap: -4, LO: Yes, RBS: Kibler6, Karlin Medium, 3.04, -2.584, Yes, F: [RecA-like DNA recombinase], SIF-BLAST: RecA-like DNA recombinase, NCBI, Velvet, 60, YP_008409597.1, Q1:S1, 100%, 0.0, SIF-HHPred: AAA domain, InterPro, unknown, PF13479.11, 63.38%, 99.4%, SIF-Syn: [RecA-like DNA recombinase, flanked by upstream HNH endonuclease on Coco12, downstream hypothetical on Coco12]
63	Original Glimmer call @bp 42099 has strength 3.12 SSC: 42099-42461, CP: Yes, SCS: Both, ST: SS, Blast-Start: Velvet, 61, BioProject, Q1:S1, 99%, 5e-84, Gap: -4, LO: Yes, RBS: Kibler6, Karlin Medium, 2.232, -4.202, No, F: [HNH endonuclease], SIF-BLAST: HNH endonuclease, NCBI, Velvet, 61, YP_008409598, Q1:S1, 99%, 5e-84, SIF-HHPred: HNH endonuclease, PDB, E. coli K-12, 6GHC_B, 55%, 96.4%, SIF-Syn: [HNH endonuclease, flanked by upstream RecA-like DNA recombinase on Coco12, downstream DNA methylase on Bobi]
64	Original Glimmer call @bp 42458 has strength 7.34 SSC: 42458-44977, CP: Yes, SCS: Both, ST: SS, Blast-Start: Velvet, 62, BioProject, Q1:S1, 100%, 0.0, Gap: -4, LO: Yes, RBS: Kibler6, Karlin Medium, 2.705, -3.279, Yes, F:

	[hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Velveten, 62, YP_008409599.1, Q1:S1, 100%, 0.0, SIF-HHPred: DNA binding protein, PDB, Xenopus laevis Homo sapiens, 8V6V_X, 48.51%, 100%, SIF-Syn: [DNA methylase, flanked by upstream HNH endonuclease on Coco12, downstream hypothetical on Velveten]
65	Original Glimmer call @bp 44974 has strength 5.42** not called by GeneMark SSC: 44974-45195, CP: Yes, SCS: Glimmer, ST: SS, Blast-Start: Velveten, 63, BioProject, Q1:S1, 99%, 6e-45, Gap: -4, LO: Yes, RBS: Kibler6, Karlin Medium, 2.646, -3.342, No, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Velveten, 63, YP_008409600.1, Q1:S1, 99%, 6e-45, SIF-HHPred: NKF, SIF-Syn: [hypothetical protein, flanked by upstream DNA methylase on Bobi, downstream hypothetical on Velveten]
66	Original Glimmer call @bp 45195 has strength 8.05 SSC: 45195-45341, CP: Yes, SCS: Both, ST: NI - MAS but do not call it, Blast-Start: Cerasum, 65, BioProject, Q1:S2, 98%, 2e-26, Gap: -1, LO: No, RBS: Kibler6, Karlin Medium, 2.625, -4.213, No, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Cerasum, 65, YP_009125918.1, Q1:S2, 98%, 2e-26, SIF-HHPred: NKF, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical on Velveten, downstream hypothetical on Velveten]
67	Original Glimmer call @bp 45338 has strength 7.11 **not called by GeneMark SSC: 45338-45487, CP: Yes, SCS: Glimmer, ST: SS, Blast-Start: Cerasum, 66, BioProject, Q1:S1, 98%, 4e-26,

	Gap: -4, LO: No, RBS: Kibler6, Karlin Medium, 1.658, -5318, No, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Cerasum, 66, YP_009125919.1, Q1:S1, 98%, 4e-26, SIF-HHPred: NKF, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical on Velvet, downstream hypothetical on Velvet]
68	Original Glimmer call @bp 45477 has strength 0.74 ** not called by GeneMark SSC: 45477-45656, CP: No, SCS: Glimmer, ST: SS, Blast-Start: Cerasum, 67, BioProject, Q1:S1, 98%, 8e-34, Gap: -11, LO: No, RBS: Kibler6, Karlin Medium, 3.131, -3.559, Yes, F: [hypothetical protein], SIF-BLAST: endonuclease, NCBI, Cerasum, 67, YP_009125920.1, Q1:S1, 98%, 8e-34, SIF-HHPred: NKF, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical on Velvet, downstream hypothetical on Velvet]
69	Original Glimmer call @bp 45653 has strength 1.99; GeneMark calls start at 45731 SSC: 45653-46369, CP: Yes, SCS: Both - GL, ST: NI - MAS but do not call it, Blast-Start: BigPhil, 68, NCBI, Q1:S1, 100%, 1e-177, Gap: -4, LO: Yes, RBS: Kibler6, Karlin Medium, 2.37, -4.364, No, F: [helix-turn-helix DNA binding protein], SIF-BLAST: HTH DNA binding protein, NCBI, BigPhil, 68, AVR76460.1, Q1:S1, 100%, 1e-177, SIF-HHPred: N-terminal phage organiser, InterPro, N-terminal domain of small family of phage proteins, PF09681.15, 35.71%, 98.6%, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical on Velvet, downstream hypothetical on Velvet]
70	Original Glimmer call @bp 46369 has strength 5.01

	SSC: 46369-46632, CP: Yes, SCS: Both , ST: SS, Blast-Start: Cerasum, 69, BioProject, Q1:S1, 99%, 7e-55, Gap: -1, LO: No, RBS: Kibler6, Karlin Medium, 2.738, -3.212, Yes, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Cerasum, 69, YP_009125922.1, Q1:S1, 99%, 7e-55, SIF-HHPred: NKF, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical on Velvetten, downstream hypothetical on Velvetten]
71	Original Glimmer call @bp 46629 has strength 3.52; GeneMark calls start at 46635 SSC: 46629-47009, CP: Yes, SCS: Both - GL, ST: SS, Blast-Start: Cerasum, 70, BioProject, Q1:S1, 99%, 1e-85, Gap: -4, LO: Yes, RBS: Kibler6, Karlin Medium, 2.963, -2.664, Yes, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Cerasum, 70, YP_009125923.1, Q1:S1, 99%, 1e-85, SIF-HHPred: NKF, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical on Coco12, downstream hypothetical on Coco12]
72	Original Glimmer call @bp 47385 has strength 5.58 **not called by GeneMark SSC: 46987-47385, CP: No, SCS: Glimmer, ST: NA, Blast-Start: No significant BLAST alignments, Gap: 11, LO: Yes, RBS: Kibler6, Karlin Medium, 1.444, -5.825, No, F: [hypothetical protein], SIF-BLAST: NKF, SIF-HHPred: NKF, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical on Velvetten, downstream hypothetical on Velvetten]
73	Called start by Megan Howard @bp 46997 SSC: 46997-47203, CP: Yes, SCS: Me, ST: NI - MAS but do not call it, Blast-Start: Velvetten, 73, BioProject, Q5:S1,

	93%, 1e-86, Gap: -13, LO: No, RBS: Kibler6, Karlin Medium, 0.469, -7.934, No, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Velvet, 73, YP_008409609.1, Q5:S1, 93%, 6e-39, SIF-HHPred: unknown function, InterPro, unknown, PF19849.4, 23.2%, 90%, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical on Velvet, downstream hypothetical]
74	Original GeneMark call @bp 47200 SSC: 47200-47577, CP: Yes, SCS: Both, ST: NI, Blast-Start: Velvet, 74, BioProject, Q1:S1, 99%, 1e-86, Gap: -4, LO: Yes, RBS: Kibler6, Karlin Medium, 2.257, -4.600, No, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Velvet, 74, YP_008409610.1, Q1:S1, 99%, 1e-86, SIF-HHPred: NKF, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical on Coco12, downstream hypothetical on Coco12]
75	Original Glimmer call @bp 47574 has strength 2.32 SSC: 47574-47741, CP: Yes, SCS: Both, ST: SS, Blast-Start: Velvet, 74, BioProject, Q1:S1, 98%, 8e-30, Gap: 188, LO: Yes, RBS: Kibler6, Karlin Medium, 2.625, -4.213, Yes, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Velvet, 74, YP_008409611.1, Q1:S1, 98%, 8e-30, SIF-HHPred: NKF, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical on Velvet, downstream hypothetical]
76	Original Glimmer call @bp 47692 has strength 0.86 ** not called by GeneMark SSC: 47692-47844, CP: No, SCS: Glimmer, ST: NA, Blast-Start: ValleyTerrace, Q10:S42, 80%, 1e-05, Gap: -50, LO: No, RBS: Kibler6, Karlin Medium, 2.028, -5.377, No,

	F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, ValleyTerrace, QAX94769.1, Q10:S42, 80%, 1e-05, SIF-HHPred: NKF, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical on Coco12, downstream hypothetical on Coco12]
77	Called start by Megan Howard @bp 47878 SSC: 47878-48162, CP: Yes, SCS: Me, ST: SS, Blast-Start: Avani, 90, BioProject, Q1:S1, 99%, 1e-60, Gap: 33, LO: No, RBS: Kibler6, Karlin Medium, 2.787, -4.018, Yes, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Avani, 90, YP_009013185.1, Q1:S1, 99%, 1e-60, SIF-HHPred: NKF, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical, downstream hypothetical]
78	Original Glimmer call @bp 48138 has strength 3.88** not called by GeneMark SSC: 47935-48138, CP: Yes, SCS: Glimmer, ST: SS, Blast-Start: Ksenia, 73, NCBI, Q1:S7, 99%, 2e-35, Gap: 16, LO: No, RBS: Kibler6, Karlin Medium, 2.677, -3.849, Yes, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Ksenia, 73, XLY78053.1, Q1:S7, 99%, 2e-35, SIF-HHPred: NKF, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical on Coco12, downstream hypothetical on Coco12]
79	Original Glimmer call @bp 48155 has strength 1.14 SSC: 48155-48499, CP: Yes, SCS: Both, ST: SS, Blast-Start: Velveteen, 76, BioProject, Q1:S1, 99%, 9e-75, Gap: 11, LO: Yes, RBS: Kibler6, Karlin Medium, 2.614, -3.390, Yes, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Velveteen, 76, YP_008409613.1, Q1:S1, 99%, 9e-75, SIF-HHPred: NKF, SIF-Syn: [hypothetical protein, flanked

	by upstream hypothetical on Coco12, downstream hypothetical on Coco12]
80	Original Glimmer call @bp 48496 has strength 0.97 ** not called by GeneMark SSC: 48496-48738, CP: No, SCS: Glimmer, ST: SS, Blast-Start: Velvetten, 77, BioProject, Q1:S1, 99%, 5e-52, Gap: -4, LO: Yes, RBS: Kibler6, Karlin Medium, 2.787, -4.018, No, F: [hypothetical protein], SIF-BLAST: hypothetical protein, Velvetten, 77, YP_008409614.1, Q1:S1, 99%, 5e-52, SIF-HHPred: NKF, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical on Coco12, downstream mycobacteriophage mobile element 2 protein on Coco12]
81	Original Glimmer call @bp 48741 has strength 1.40 SSC: 48741-49073, CP: Yes, SCS: Both, ST: NI - MAS but do not call it, Blast-Start: Babsiella, 69, BioProject, Q1:S23, 99%, 3e-76, Gap: 2, LO: No, RBS: Kibler6, Karlin Medium, 2.373, -3.831, Yes, F: [Mycobacteriophage mobile element 2], SIF-BLAST: mobile element MPME, Babsiella, NCBI, 69, YP_009013086.1, Q1:S23, 99%, 3e-76, SIF-HHPred: NKF, SIF-Syn: [Mycobacteriophage mobile element 2 protein, flanked by upstream hypothetical on Coco12, downstream hypothetical protein on Coco12]
82	Original Glimmer call @bp 49307 has strength 3.03 ** not called by GeneMark SSC: 49307-49435, CP: No, SCS: Glimmer, ST: SS, Blast-Start: Job42, 85, BioProject, Q1:S1, 98%, 5e-22, Gap: 233, LO: No, RBS: Kibler6, Karlin Medium, 2.2, -4.191, No, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Job42, 85, YP_008126675.1, Q1:S1, 98%, 5e-22,

	SIF-HHPred: DNA-directed RNA polymerase subunit P, PDB, Thermococcus kodakarensis KOD1, 4QIW_W, 83.33%, 97%, SIF-Syn: [hypothetical protein, flanked by upstream Mycobacteriophage mobile element 2 protein on Coco12, downstream hypothetical protein on Coco12]
83	Original Glimmer call @bp 49432 has strength 3.96; GeneMark calls start at 49360 SSC: 49360-49623, CP: Yes, SCS: Both - GM, ST: SS, Blast-Start: Bipolar, 87, BioProject, Q1:S7, 99%, 4e-55, Gap: -76, LO: No, RBS: Kibler6, Karlin Medium, 2.478, -4.263, Yes, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Bipolar, 87, YP_009200714.1, Q1:S7, 99%, 4e-55, SIF-HHPred: NKF, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical protein on BigPhil, downstream hypothetical protein on BigPhil]
84	Original Glimmer call @bp 49620 has strength 5.22 SSC: 49620-49916, CP: Yes, SCS: Both, ST: SS, Blast-Start: Velveten, 82, BioProject, Q1:S1, 99%, 3e-64, Gap: -4, LO: No, RBS: Kibler6, Karlin Medium, 3.177, -2.684, Yes, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Velveten, 82, YP_008409619.1, Q1:S1, 99%, 3e-64, SIF-HHPred: NKF, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical protein on BigPhil, downstream hypothetical protein on BigPhil]
85	Original Glimmer call @bp 49898 has strength 10.26; GeneMark calls start at 49913 SSC: 49898-50092, CP: Yes, SCS: Both - GL, ST: NI - MAS but do not call it, Blast-Start: phi1_186001, NCBI, Q1:S1, 98%, 1e-38, Gap: -19, LO: No, RBS: Kibler6, Karlin Medium, 2.46, -4.557, No, F: [hypothetical protein],

	SIF-BLAST: hypothetical protein, NCBI, phi1_186001, XAL85148.1, Q1:S1, 98%, 1e-38, SIF-HHPred: NKF, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical protein on BigPhil, downstream hypothetical protein on BigPhil]
86	Original Glimmer call @bp 50092 has strength 5.88 SSC: 50092-50229, CP: Yes, SCS: Both, ST: SS, Blast-Start: Phi1_186001, NA, NA, Q1:S1, 98%, 1e-38, Gap: -1, LO: Yes, RBS: Kibler6, Karlin Medium, 1.639, -6.459, Yes, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Phi1_186001, NA, XAL85148.1, Q1:S1, 98%, 1e-38, SIF-HHPred: NKF, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical protein on BigPhil, downstream hypothetical protein on BigPhil]
87	Original Glimmer call @bp 50268 has strength 4.71; GeneMark calls start at 50250 SSC: 50250-50399, CP: Yes, SCS: Both - GM, ST: NI - MAS but do not call it, Blast-Start: Tweety, 91, BioProject, Q1:S9, 98%, 6e-27, Gap: 20, LO: No, RBS: Kibler6, Karlin Medium, 0.003, -9.863, No, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Tweety, 91, YP_001469324.1, Q1:S9, 98%, 6e-27, SIF-HHPred: NKF, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical protein on BigPhil, downstream hypothetical protein on BigPhil]
88	Original Glimmer call @bp 50452 has strength 2.23 ** not called by GeneMark SSC: 50452-50610, CP: Yes, SCS: Glimmer, ST: SS, Blast-Start: Velveten, 86, BioProject, Q1:S1, 98%, 2e-30, Gap: 52, LO: Yes, RBS: Kibler6, Karlin Medium, 1.335,

	-6.131, No, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Velvet, 86, YP_008409623.1, Q1:S1, 98%, 2e-30, SIF-HHPred: NKF, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical protein on Coco12, downstream hypothetical protein]
89	Original Glimmer call @bp 50733 has strength 5.21; GeneMark calls start at 50622 SSC: 50622-50891, CP: Yes, SCS: Both - GM, ST: SS, Blast-Start: Velvet, 87, BioProject, Q1:S6, 99% 7e-60, Gap: 11, LO: No, RBS: Kibler6, Karlin Medium, 2.763, -4.119, No, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Velvet, 87, YP_008409624.1, Q1:S6, 99% 7e-60, SIF-HHPred: unknown function, InterPro, unknown protein, PF06348.16, 61.54%, 98.9%, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical protein on Coco12, downstream hypothetical protein on Poenanya]
90	Original Glimmer call @bp 50888 has strength 7.77 SSC: 50888-51151, CP: Yes, SCS: Both, ST: NI, Blast-Start: Poenanya, 96, BioProject, Q1:S1, 100%, 1e-55, Gap: -4, LO: Yes, RBS: Kibler6, Karlin Medium, 2.731, -3.166, No, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Poenanya, 96, YP_009961394.1, Q1:S1, 100%, 1e-55, SIF-HHPred: NKF, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical protein, downstream hypothetical protein]
91	Original Glimmer call @bp 51261 has strength 2.59 ** not called by GeneMark SSC: 51109-51261, CP: No, SCS: Glimmer, ST: NA, Blast-Start: No significant BLAST results, Gap: 522, LO:

	No, RBS: Kibler6, Karlin Medium, 2.394, -3.928, Yes, F: [hypothetical protein], SIF-BLAST: NKF, SIF-HHPred: DNA binding protein, PDB, Thermotoga maritima, 1YD0_A, 44%, 99.3%, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical protein on Poenanya, downstream G-I-Y Y-I-G endonuclease on BigPhil]
92	Original Glimmer call @bp 51260 has strength 4.02 SSC: 51260-51787 , CP: Yes, SCS: Both, ST: NI - MAS but do not call it, Blast-Start: Cabrinians, 88, BioProject, Q1:S1, 99%, 3e-128, Gap: 108, LO: No, RBS: Kibler6, Karlin Medium, 2.45, -4.499, No, F: [G-I-Y Y-I-G endonuclease], SIF-BLAST: endonuclease, NCBI, Cabrinians, 88, YP_009189810.1, Q1:S1, 99%, 3e-128, SIF-HHPred: NKF, SIF-Syn: [G-I-Y Y-I-G endonuclease, flanked by upstream hypothetical protein on Coco12, downstream hypothetical on Coco12]
93	Original Glimmer call @bp 51784 has strength 4.39 SSC: 51784-52455, CP: Yes, SCS: Both, ST: SS, Blast-Start: Whouxphf, 95, BioProject, Q1:S31, 100%, 1e-161, Gap: 522, LO: No, RBS: Kibler6, Karlin Medium, 3.112, -2.372, Yes, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Whouxphf, 95, YP_009963380.1, Q1:S31, 100%, 1e-161, SIF-HHPred: metal binding protein, PDB, Haloferax volcanii DS2, 8Q5B_A, 19.28%, 97.4%, SIF-Syn: [hypothetical protein, flanked by upstream G-I-Y Y-I-G endonuclease on Coco12, downstream hypothetical on Coco12]
94	Original Glimmer call @bp 52598 has strength 6.37 SSC: 52598-52765 , CP: Yes, SCS: Both, ST: SS, Blast-Start: Batiatus, 93, BioProject, Q1:S31, 98%, 1e-30, Gap: 142, LO:

	No, RBS: Kibler6, Karlin Medium, 1.856, -4.968, Yes, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Batiatus, 93, YP_009954675.1, Q1:S31, 98%, 1e-30, SIF-HHPred: FYVE-finger-containing Rab5 effector protein, PDB, Mus musculus Homo sapiens, 1Z0J_B, 69.09%, 94.6%, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical on Coco12, downstream hypothetical on Coco12]
95	Original Glimmer call @bp 52772 has strength 11.32 SSC: 52772-52981, CP: Yes, SCS: Both, ST: SS, Blast-Start: Velveten, 92, BioProject, Q1:S1, 99%, 2e-41, Gap: 6, LO: Yes, RBS: Kibler6, Karlin Medium, 2.963, -3.703, Yes, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Velveten, 92, YP_008409629.1, Q1:S1, 99%, 2e-41, SIF-HHPred: NKF, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical on Coco12, downstream hypothetical on Coco12]
96	Original GeneMark call @bp 52981 SSC: 52981-53166 , CP: Yes, SCS: Both, ST: SS, Blast-Start: Squirty, 96, BioProject, Q1:S1, 98%, 2e-37, Gap: -1, LO: Yes, RBS: Kibler6, Karlin Medium, 2.113, -4.513, No, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Squirty, 96, YP_009124648.1, Q1:S1, 98%, 2e-37, SIF-HHPred: NKF, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical on Coco12, downstream hypothetical on Coco12]
97	Original Glimmer call @bp 53163 has strength 10.24 SSC: 53163-53315, CP: Yes, SCS: Both, ST: SS, Blast-Start: Fruitloop, 95, BioProject, Q1:S1, 98%, 8e-27, Gap: -4, LO: No, RBS: Kibler6, Karlin Medium, 3.04, -2.584, Yes, F:

	[hypothetical protein], SIF-BLAST: membrane protein, NCBI, Fruitloop, 95, YP_002241780.1, Q1:S1, 98%, 8e-27, SIF-HHPred: NKF, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical on Coco12, downstream hypothetical on Coco12]
98	Called Start by Megan Howard @bp 53312 SSC: 53312-53404 , CP: Yes, SCS: Me, ST: SS, Blast-Start: Cerasum, 96, BioProject, Q1:S1, 97%, 9e-12, Gap: -4, LO: Yes, RBS: Kibler6, Karlin Medium, 2.461, -3.997, Yes, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Cerasum, 96, YP_009125949.1, Q1:S1, 97%, 9e-12, SIF-HHPred: Tetradcapep, InterPro, Eisenia foetida, PF08187.16, 33.33%, 91.2%, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical on Coco12, downstream hypothetical on Coco12]
99	Original Glimmer call @bp 53401 has strength 10.10 SSC: 53401-53814, CP: Yes, SCS: Both, ST: SS, Blast-Start: Velvetten, 95, BioProject, Q1:S1, 99%, 3e-92, Gap: -4, LO: Yes, RBS: Kibler6, Karlin Medium, 1.945, -5.372, Yes, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Velvetten, 95, YP_008409632.1, Q1:S1, 99%, 3e-92, SIF-HHPred: NKF, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical on Coco12, downstream hypothetical on Coco12]
100	Original Glimmer call @bp 53811 has strength 7.67 SSC: 53811-54053, CP: Yes, SCS: Both, ST: SS, Blast-Start: Tweety, 100, BioProject, Q1:S1, 99%, 1e-50, Gap: -4, LO: Yes, RBS: Kibler6, Karlin Medium, 2.478, -4.712, No, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Tweety, 100, YP_001469333.1, Q1:S1, 99%, 1e-50,

	SIF-HHPred: NKF, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical on Coco12, downstream hypothetical on Coco12]
101	Original Glimmer call @bp 54046 has strength 5.93 SSC: 54046-54207, CP: Yes, SCS: Both, ST: SS, Blast-Start: Tweety, 101, BioProject, Q1:S1, 98%, 3e-30, Gap: -8, LO: Yes, RBS: Kibler6, Karlin Medium, 2.13, -4.398, Yes, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Tweety, 101, YP_001469334.1, Q1:S1, 98%, 3e-30, SIF-HHPred: NKF, SIF-Syn: [hypothetical protein, flanked by upstream hypothetical on Coco12, downstream glycosyltransferase on Coco12]
102	Original Glimmer call @bp 54224 has strength 9.32 SSC: 54224-55660, CP: Yes, SCS: Both, ST: SS, Blast-Start: Velvetene, 98, BioProject, Q1:S1, 100%, 0.0, Gap: 16, LO: No, RBS: Kibler6, Karlin Medium, 1.605, -5.564, No, F: [glycosyltransferase], SIF-BLAST: glycosyltransferase, NCBI, Velvetene, 98, YP_008409635.1, Q1:S1, 100%, 0.0, SIF-HHPred: acetylgalactosaminyltransferase, SCOPe, SCOP_d1xhba2, 47.91%, 99.8%, SIF-Syn: [glycosyltransferase, flanked by upstream hypothetical on Coco12, downstream hypothetical on Coco12]
103	Original Glimmer call @bp 55657 has strength 7.82; GeneMark calls start at 55663 SSC: 55657-55869, CP: Yes, SCS: Both - GL, ST: NI - MAS but do not call it, Blast-Start: Velvetene, 99, BioProject, Q1:S1, 99%, 1e-43, Gap: -4, LO: No, RBS: Kibler6, Karlin Medium, 2.179, -4.584, No, F: [hypothetical protein], SIF-BLAST: hypothetical protein, NCBI, Velvetene, 99, YP_008409636.1, Q1:S1, 99%, 1e-43, SIF-HHPred:

	Tudor_SETDB1_rpt2, NCBI, 99, cd21181, 71.43%, 97.7%, SIF-Syn: [hypothetical protein, flanked by upstream glycosyltransferase on Coco12, downstream glycosyltransferase on Coco12]
104	Original Glimmer call @bp 55866 has strength 5.40 SSC: 55866-56477, CP: Yes, SCS: Both, ST: SS, Blast-Start: Velveten, 100, BioProject, Q1:S1, 100%, 6e-147, Gap: -4, LO: No, RBS: Kibler6, Karlin Medium, 1.783, -5.886, No, F: [glycosyltransferase], SIF-BLAST: glycosyltransferase, NCBI, Velveten, 100, YP_008409637.1, Q1:S1, 100%, 6e-147, SIF-HHPred: glycosyltransferase protein, NCBI, Aggregatibacter actinomycetemcomitans NUM4039, 8XKD_A, 87.19%, 99.9%, SIF-Syn: [glycosyltransferase, flanked by upstream hypothetical on Coco12]