

Additional Data File 5: Putative Hymenoptera-specific Genes

The 10,000 bp region around the ant-bee alignment of every putative Hymenoptera-specific gene is depicted relative to the annotated honey bee genome.

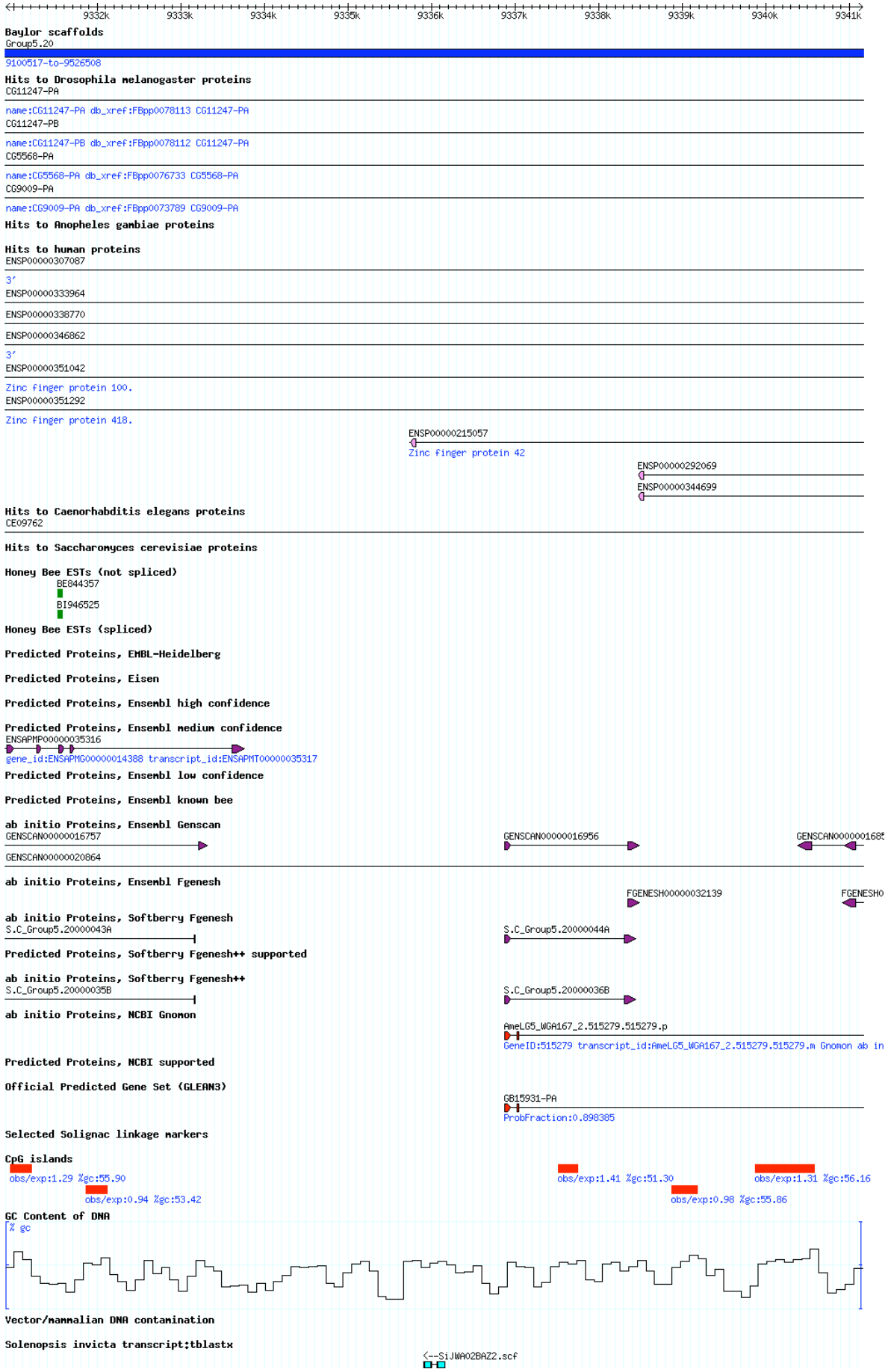
The honey bee genome assembly 2.0 chromosome coordinates are at the top of each image. Below, the alignment of proteins from *A. gambiae*, *C. elegans*, *D. melanogaster*, *H. sapiens* and *S. cerevisiae* are shown. Additionally, honey bee proteins predicted by several different groups (Eisen, EMBL, Ensembl, NCBI) as well as with multiple *ab initio* prediction methods are displayed. Finally, genes from the honey bee Official Gene Set (GLEAN3) are in red. The alignment of fire ant transcripts are in light blue; 5' to 3' direction is indicated by an arrow.

Coordinates may differ from those in Table 3 because Table 3 was generated using assembly 4 of the honey bee genome.

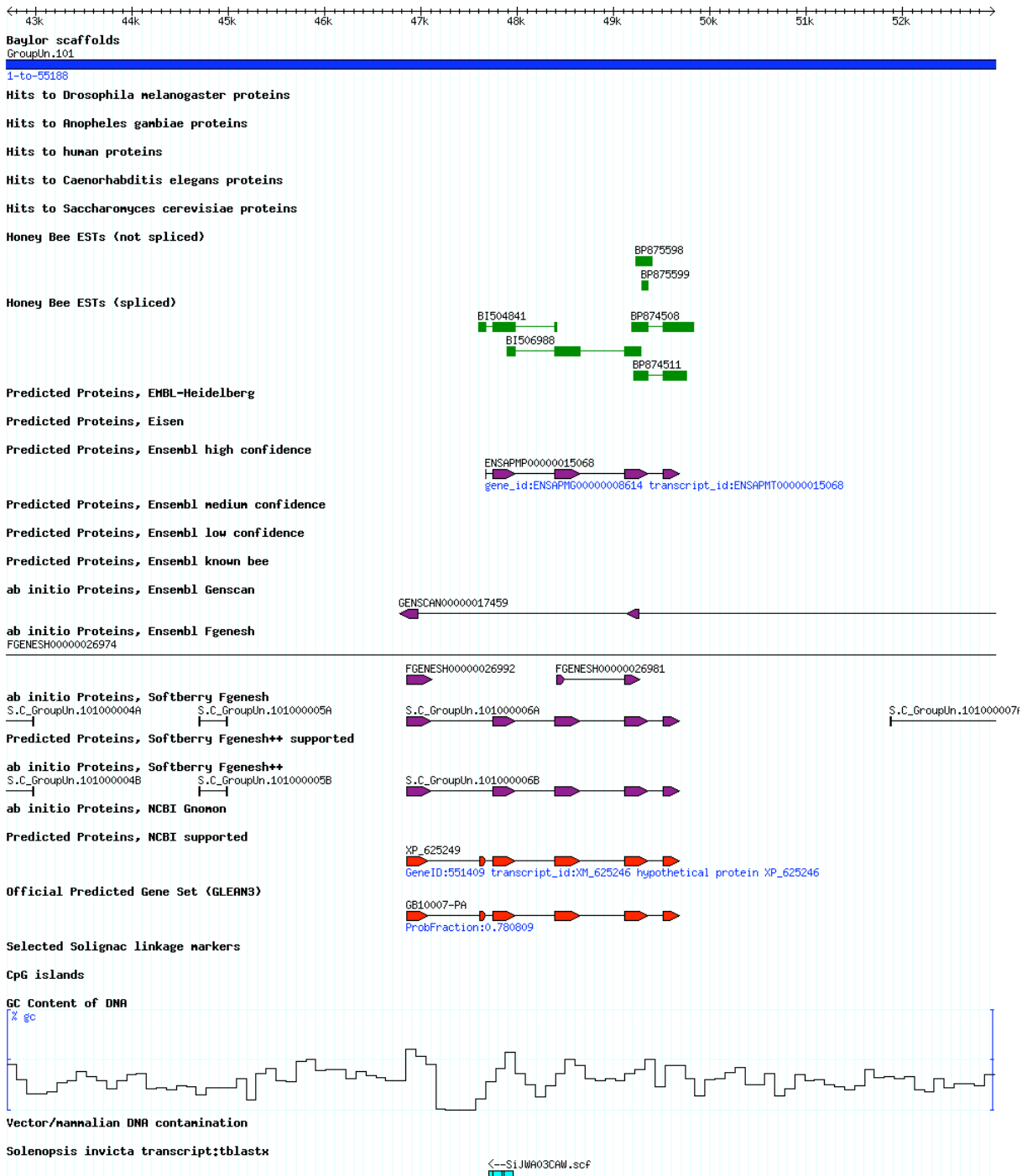
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a.SiJWA02BAZ2.scf



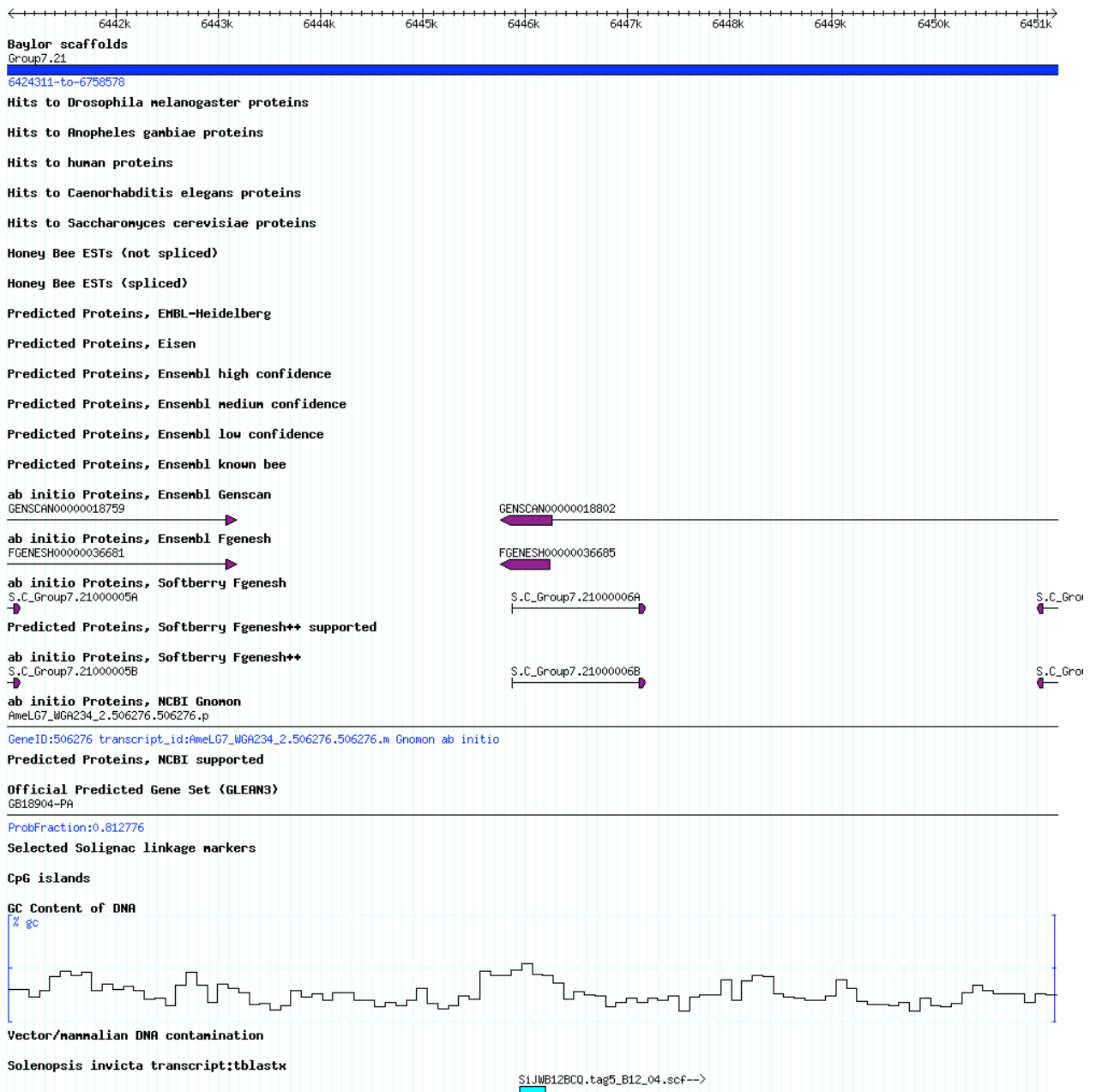
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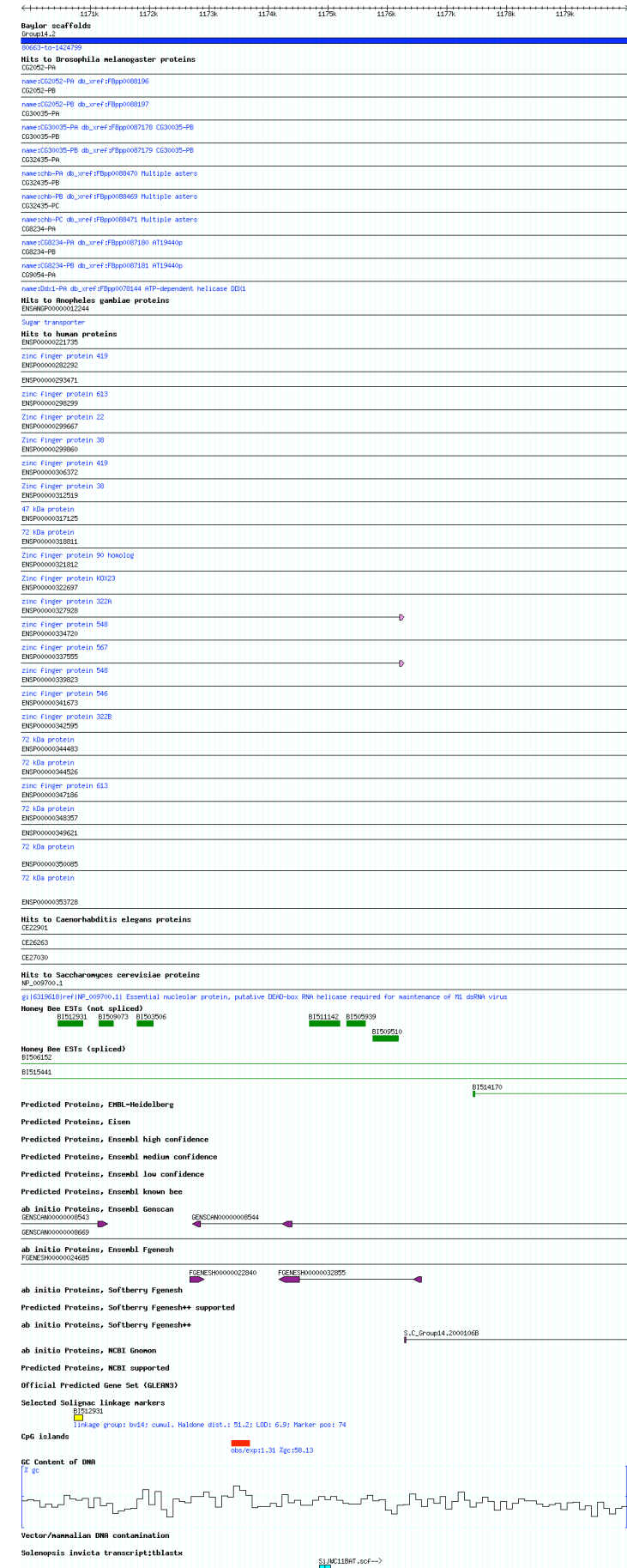
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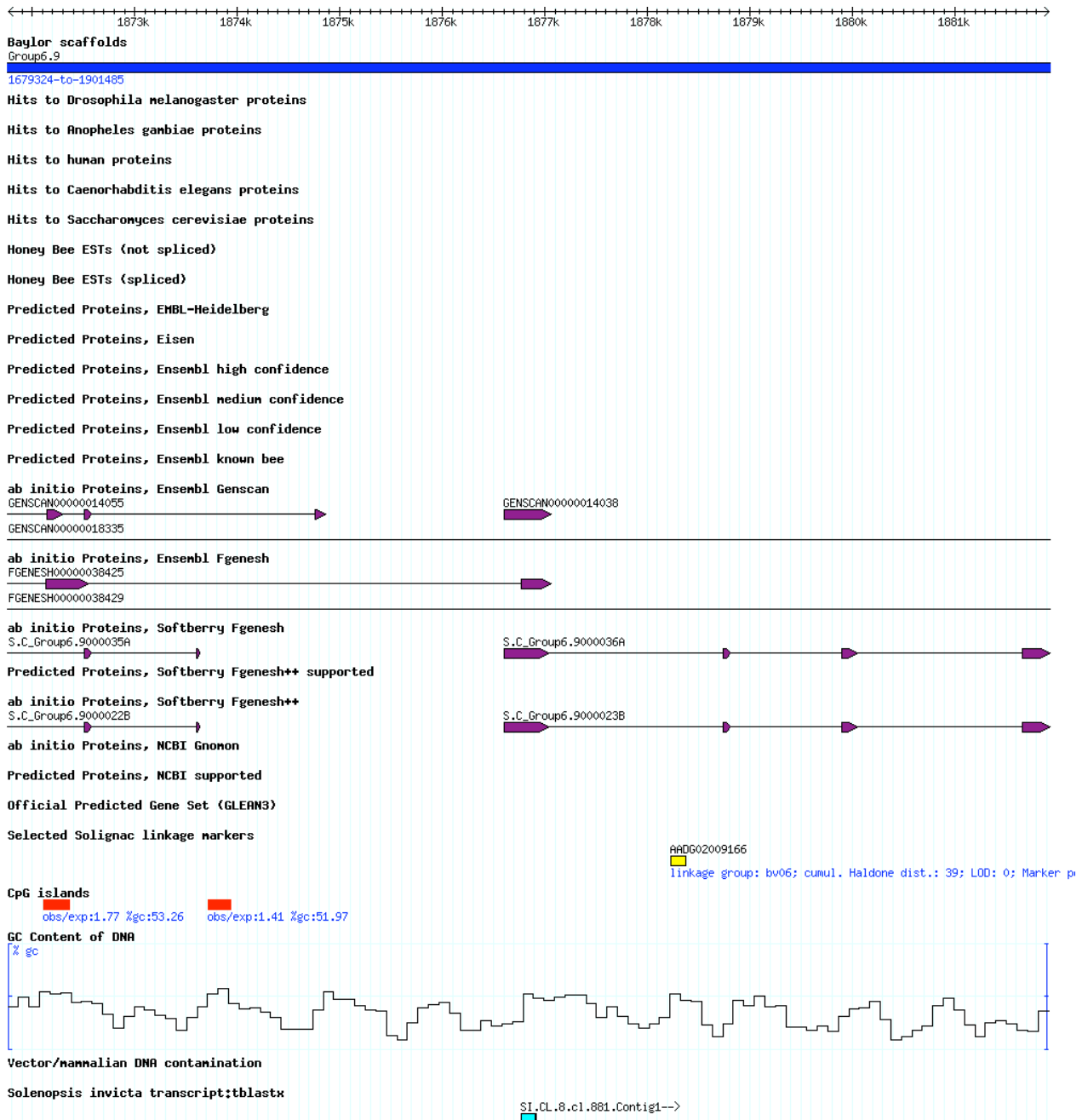
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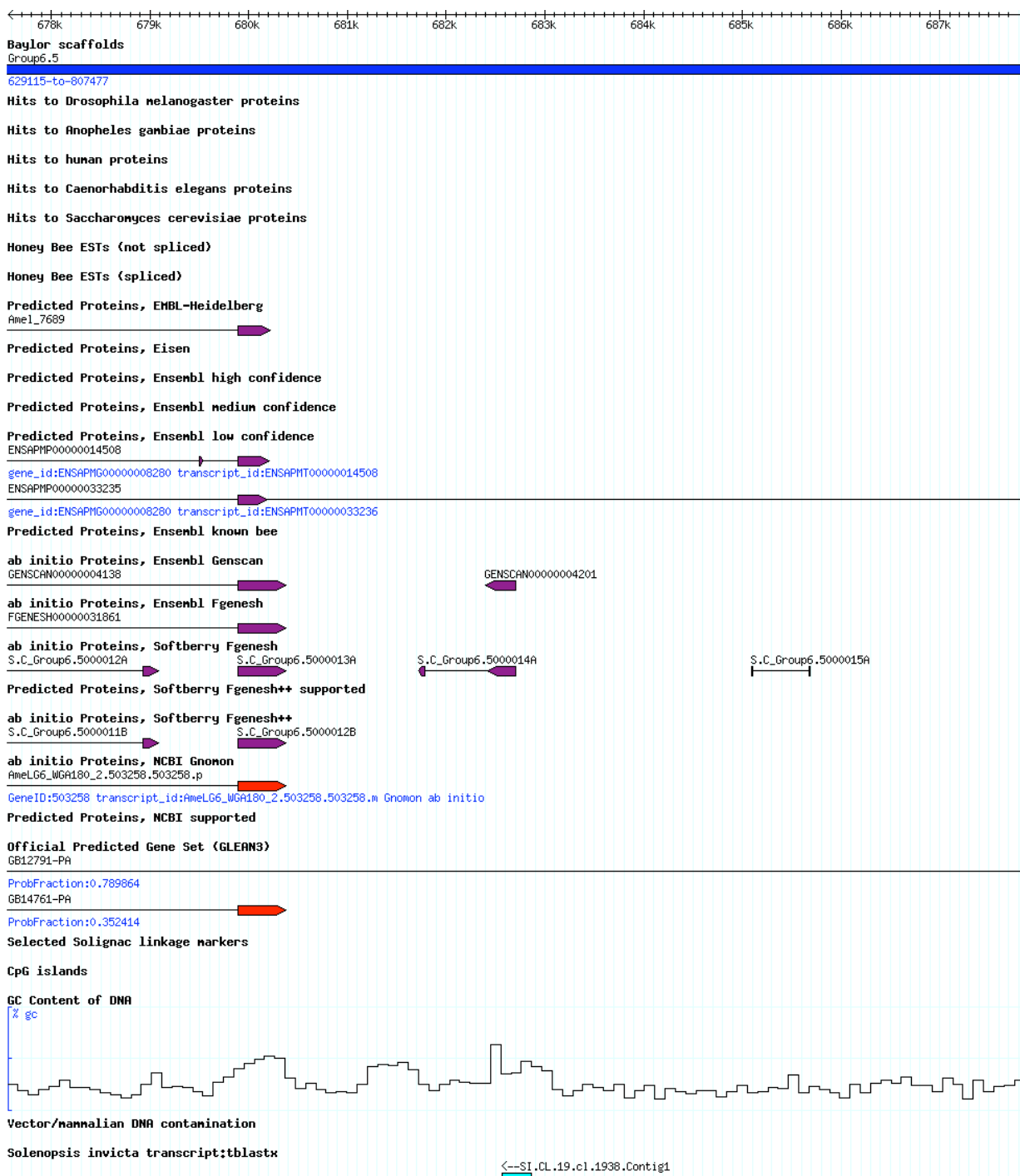
e.SiJWC11BAT.scf



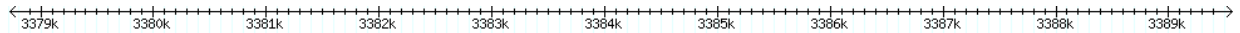
f. SI.CL.8.cl.881.Contig1



h. SI.CL.19.cl.1938.Contig1



i.SI.CL.19.cl.1953.SiJWC11BBX.scf



Baylor scaffolds

Group8.14

3242228-to-4259416

Hits to *Drosophila melanogaster* proteins

CG10068-PA
name:CG10068-PA db_xref:FBpp

Hits to *Anopheles gambiae* proteins

ENSANGP00000011527
Protein of unknown function

Hits to human proteins

ENSP00000265840
ELMO domain containing 1
ENSP00000326342
ELMO domain containing

Hits to *Caenorhabditis elegans* proteins

CE01041

Leucine-rich repeats

CE23886

Hits to *Saccharomyces cerevisiae* proteins

Honey Bee ESTs (not spliced)

B1515351

Honey Bee ESTs (spliced)

B1512402

Predicted Proteins, EMBL-Heidelberg

Ame1_8646

Ame1_8647

Ame1_8648

Predicted Proteins, Eisen

Predicted Proteins, Ensembl high confidence

ENSAPMP00000020198

gene_id:ENSAPMG00000014031 transcript_id:ENSAPMT00000020193

ENSAPMP00000025292

gene_id:ENSAPMG00000011026 tra

ENSAPMP00000020883

gene_id:ENSAPMG00000011026 t

ENSAPMP00000019730

gene_id:ENSAPMG0000001102

Predicted Proteins, Ensembl medium confidence

Predicted Proteins, Ensembl low confidence

Predicted Proteins, Ensembl known bee

ab initio Proteins, Ensembl Genscan

GENSCAN00000000647

GENSCAN00000014270

GENSCAN00000014269

ab initio Proteins, Ensembl Fgenesh

FGENESH00000027869

FGENESH00000036405

FGENESH00000040570

FGENESH00000040610

FGENESH00000040639

ab initio Proteins, Softberry Fgenesh

S.C_Group8.14000018A

S.C_Group8.14000019A

S.C_Group8.14000020A

S.C_Group8.14000021A

Predicted Proteins, Softberry Fgenesh++ supported

S.C_Group8.14000007B

S.C_Group8.14000008B

S.C_Group8.14000009B

ab initio Proteins, NCBI Gnonon

Predicted Proteins, NCBI supported

XP_394726

XP_624380

GeneID:411253 transcript_id:XM_394726 similar to ENSANGP00000015204

GeneID:551995 transcript_id:

XP_397571

GeneID:409562 transcript_id:XM_397571 similar to hypothetical protein

Official Predicted Gene Set (GLERN3)

GB19925-PA

GB14543-PA

GB14887-PA

ProbFraction:0.781819

ProbFraction:0.433441

ProbFraction:0.999993

Selected Solignac linkage markers

CpG islands

GC Content of DNA

% gc

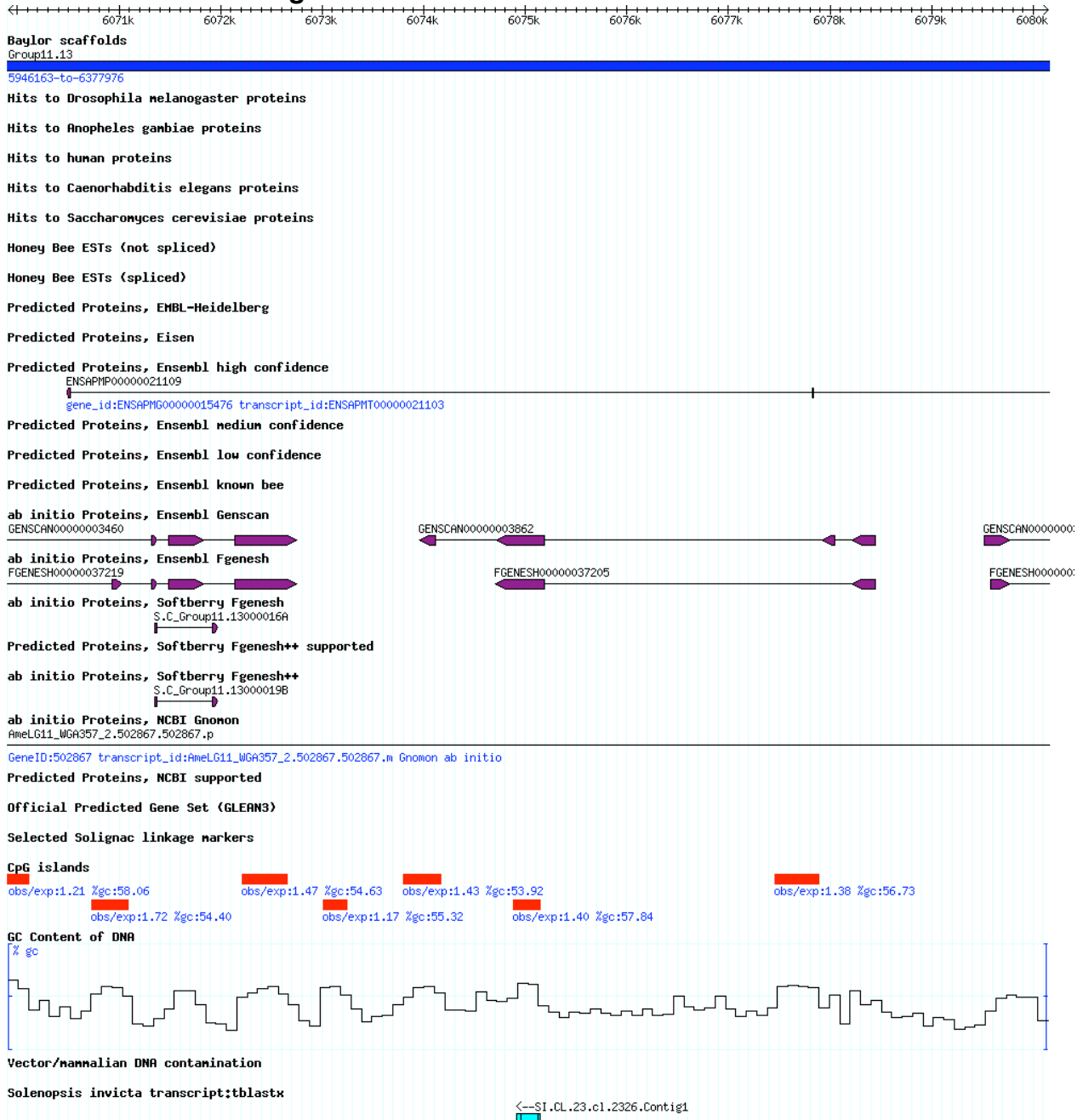


Vector/mammalian DNA contamination

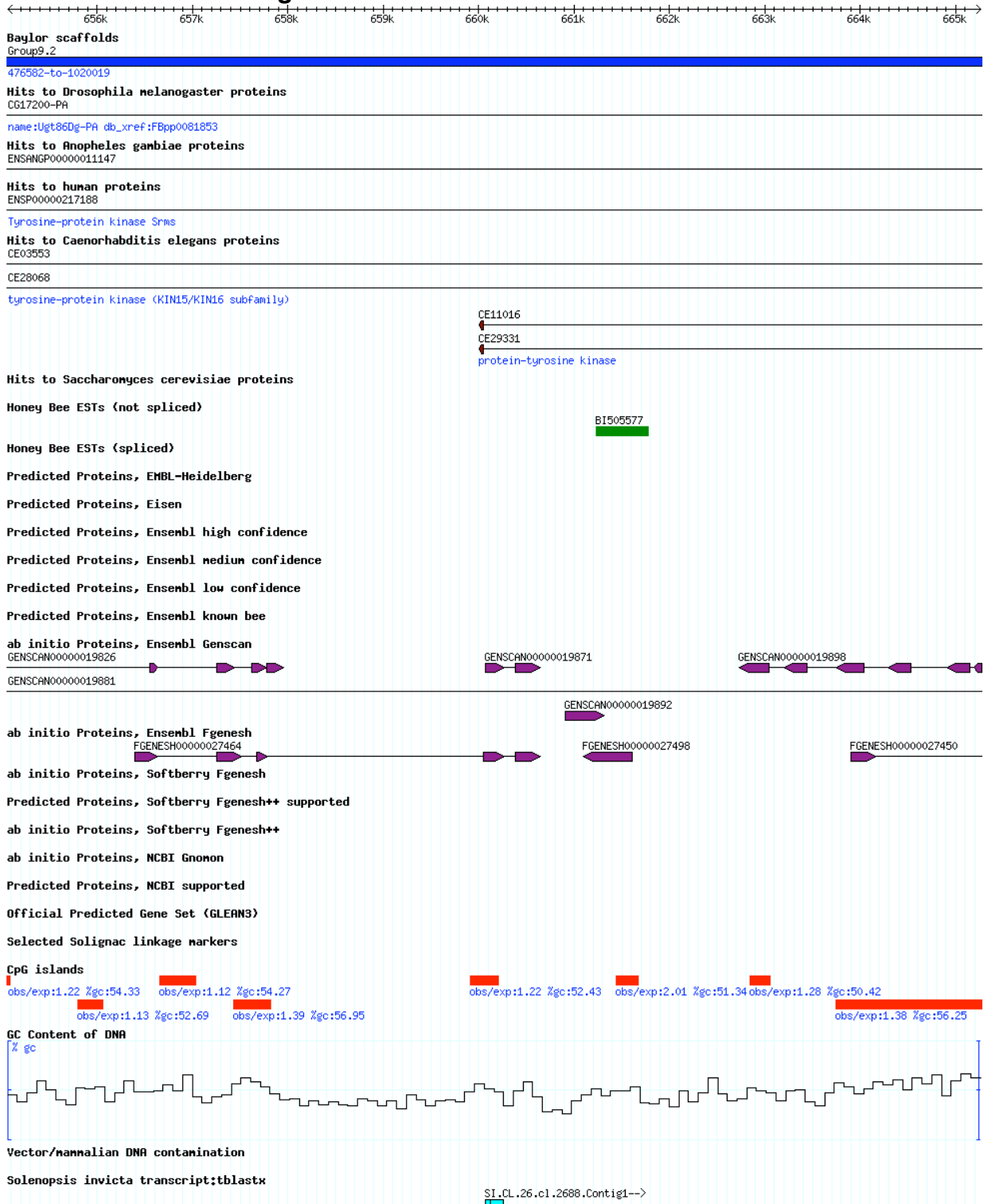
Solenopsis invicta transcript:tblastx

<--SI.CL.19.cl.1953.SiJWC11BBX.scf

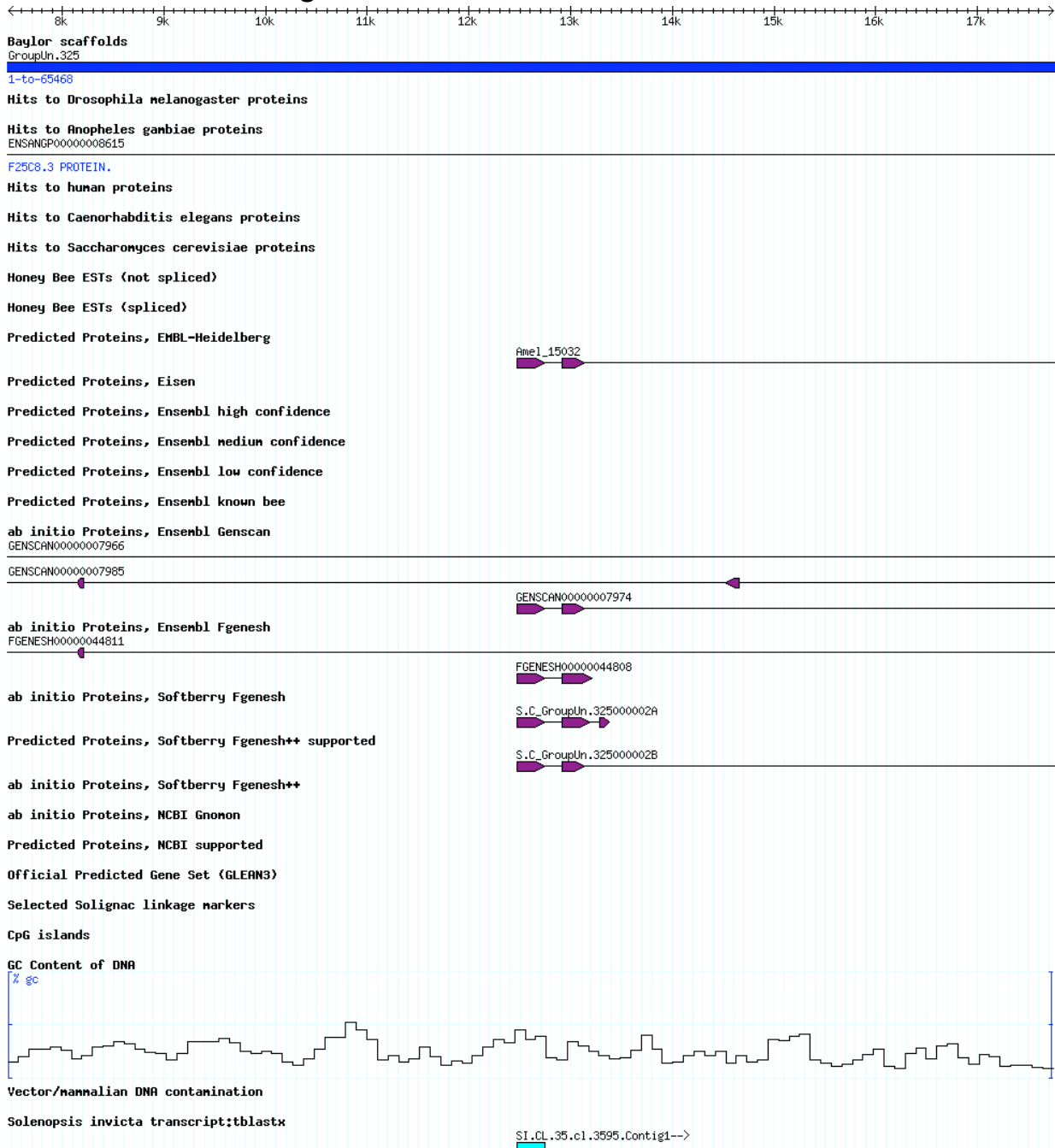
j. SI.CL.23.cl.2326.Contig1



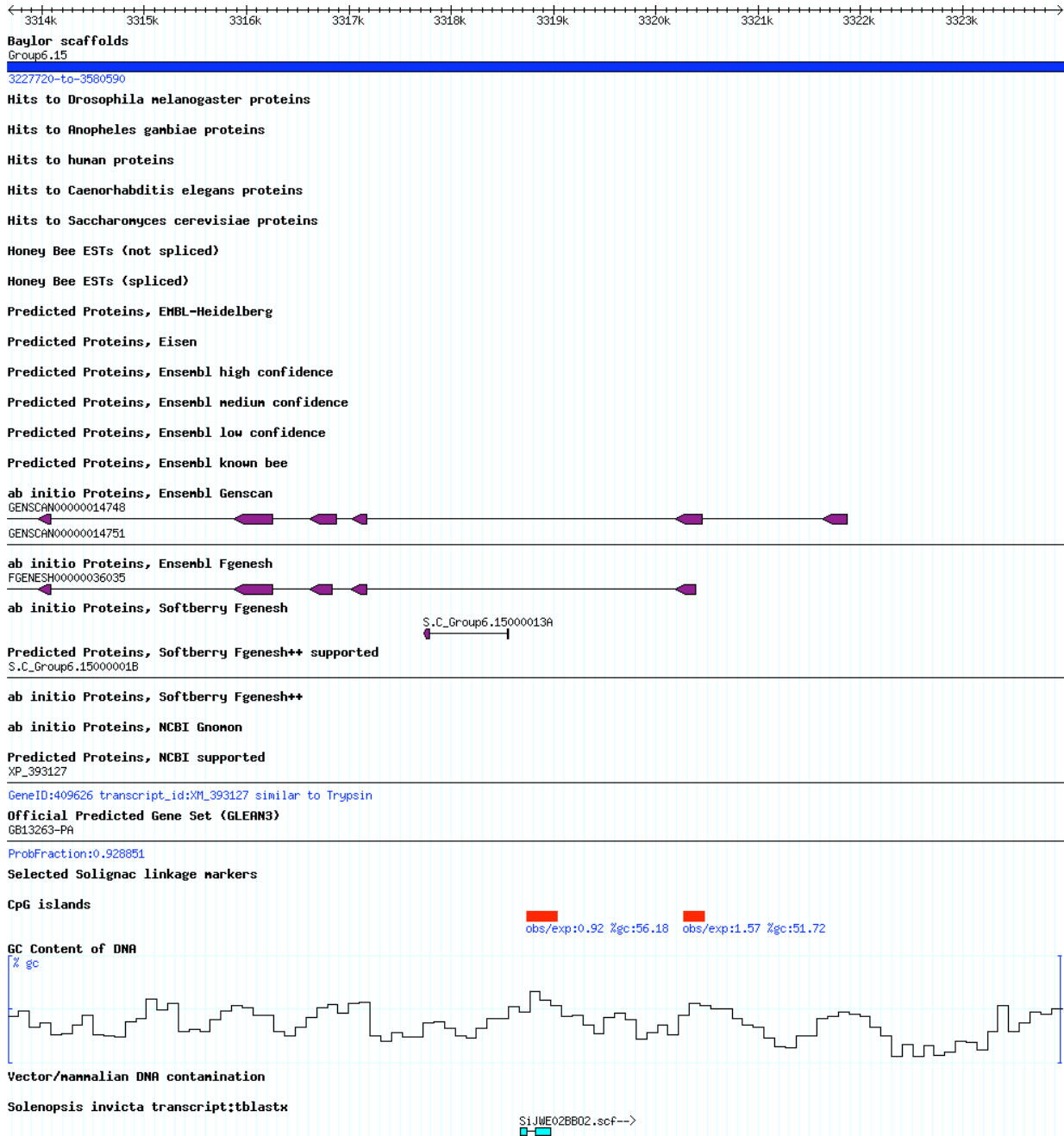
k. SI.CL.26.cl.2688.Contig1



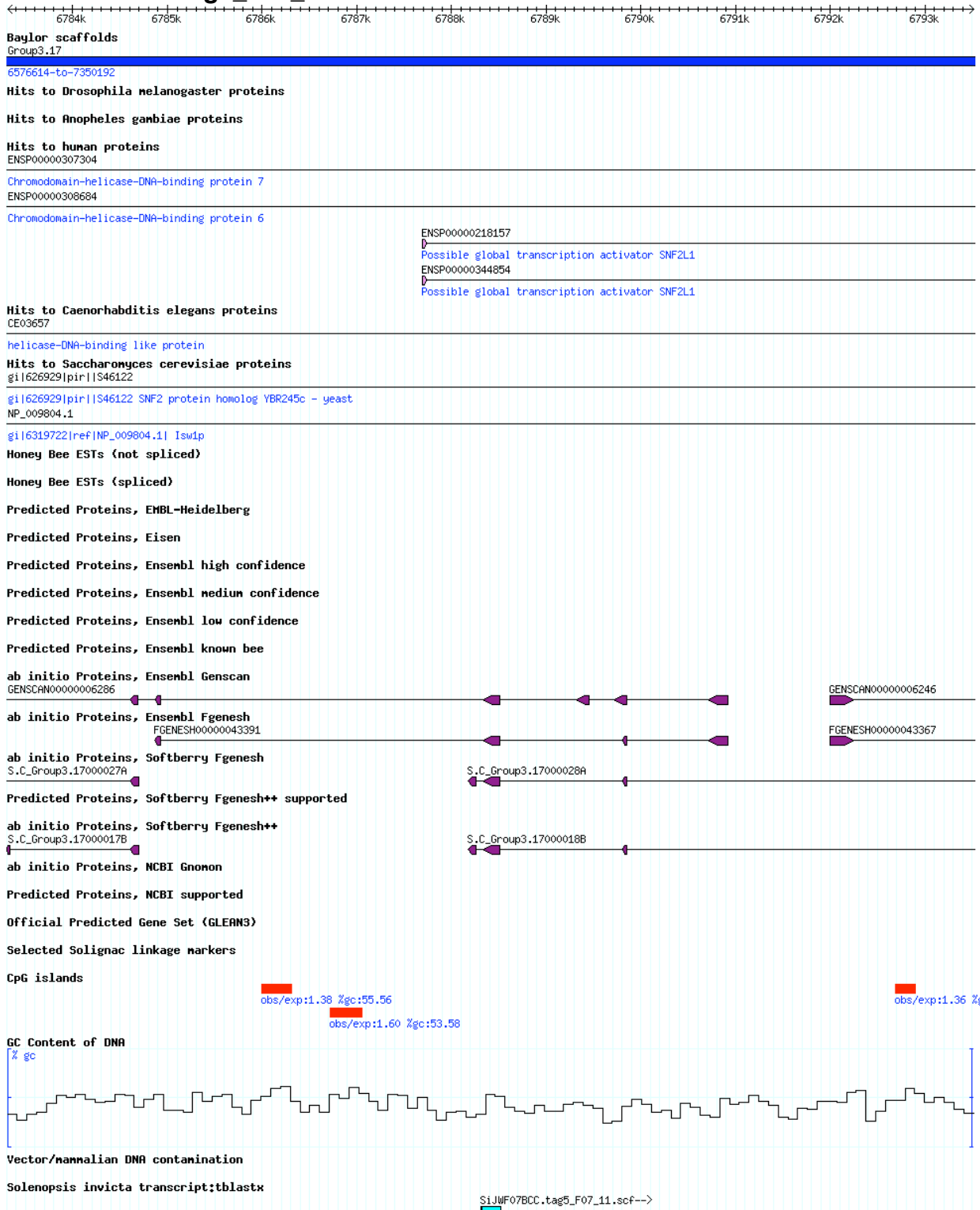
n. SI.CL.35.cl.3595.Contig1



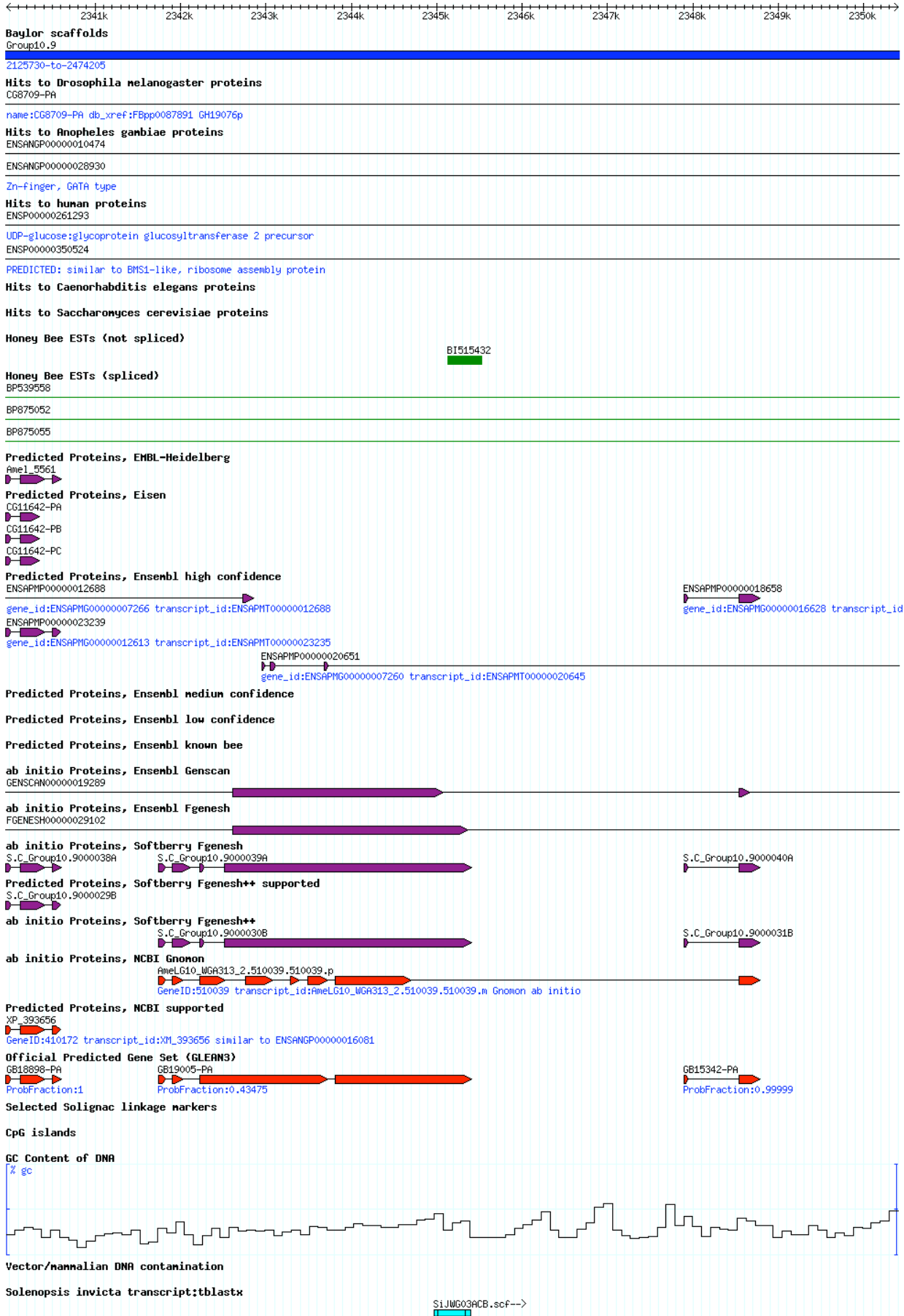
o.SiJWE02BBO2.scf



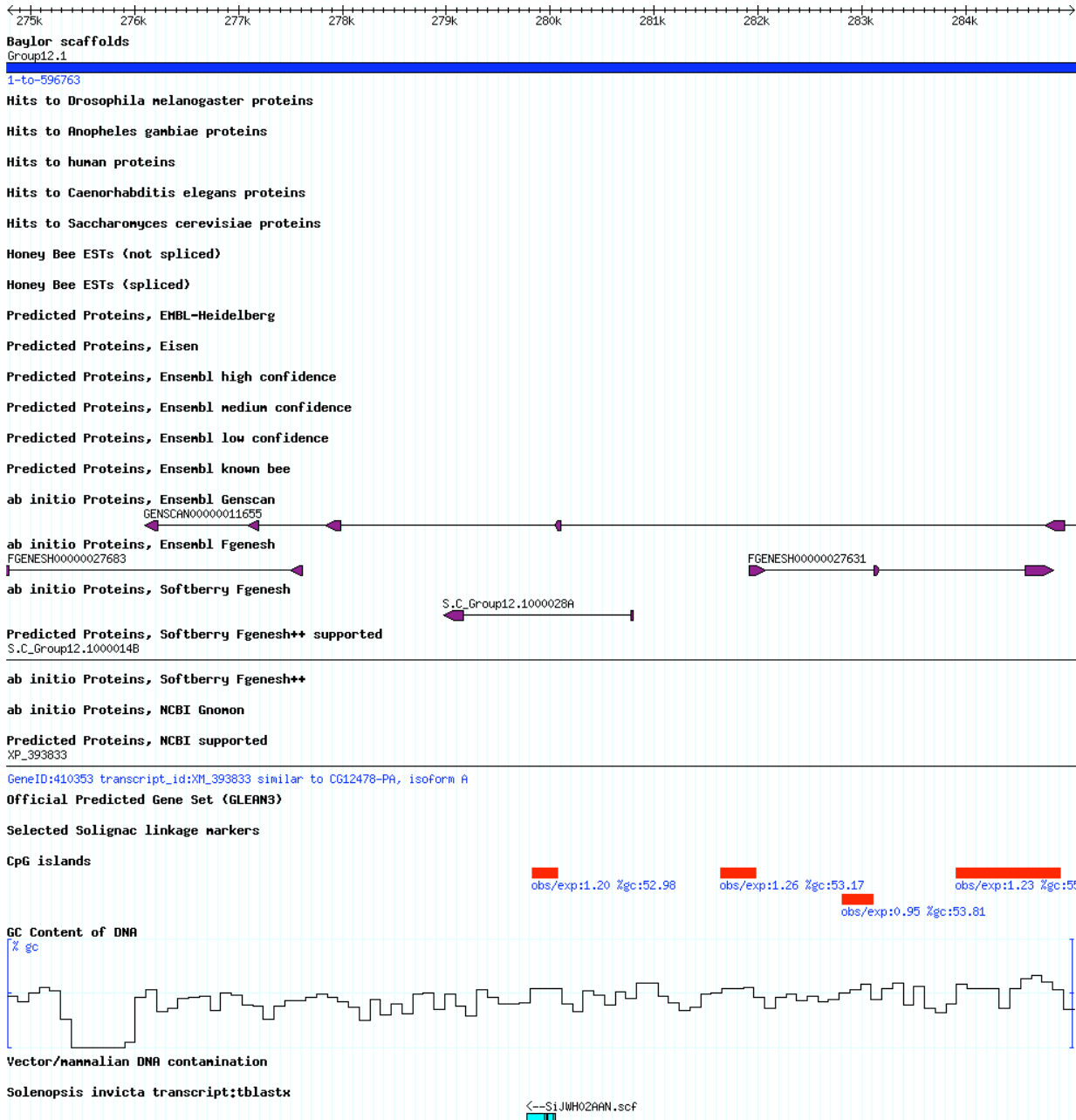
p. SiJWF07BCC.tag5_F07_11.scf



r. SiJWG03ACB.scf



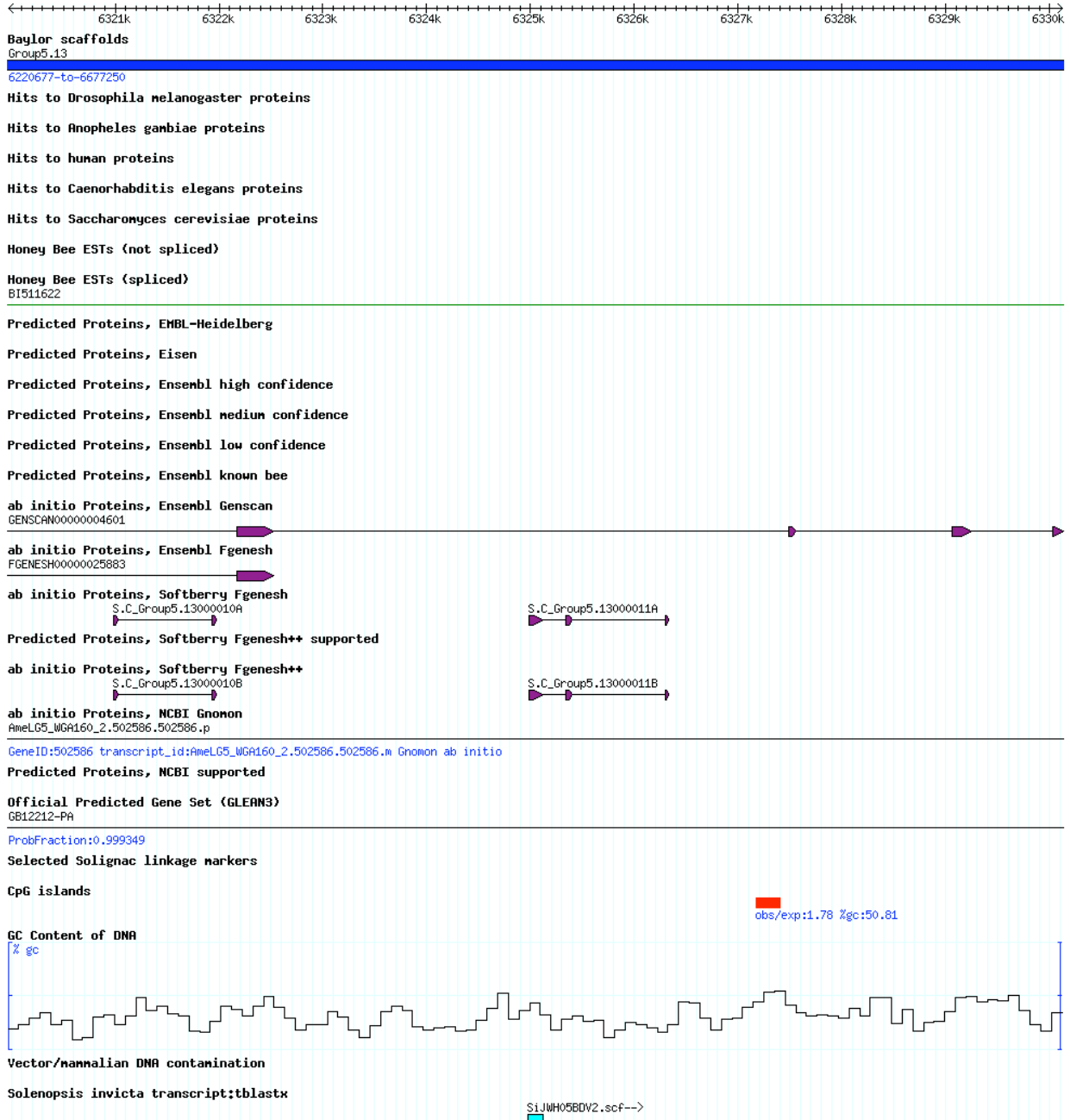
s. SiJWH02AAN.scf



t. SiJWH05BDPR5A08.scf



u. SiJWH05BDV2.scf



w.SiJWH08ADY

