

Note: Tracks are now grouped by subcluster and scaled. Switching in subcluster is indicated by changes in track color. Track scale is now set by default to display the region 30 bp upstream of start 1 to 30 bp downstream of the last possible start. If this default region is judged to be packed too tightly with annotated starts, the track will be further scaled to only show that region of the ORF with annotated starts. This action will be indicated by adding "Zoomed" to the title. For starts, yellow indicates the location of called starts comprised solely of Glimmer/GeneMark auto-annotations, green indicates the location of called starts with at least 1 manual gene annotation.

Pham 7967 Report

This analysis was run 04/05/24 on database version 557.

Pham number 7967 has 7 members, 1 are drafts.

Phages represented in each track:

Track 1 : Euratis_11

Track 2 : TG1_11Track 3 : Shawty_11

• Track 4 : Samora 11

Track 5 : RemusLoopin_11

Track 6 : Sebastisaurus_11

Track 7 : Heather_11

Summary of Final Annotations (See graph section above for start numbers):

The start number called the most often in the published annotations is 3, it was called in 2 of the 6 non-draft genes in the pham.

Genes that call this "Most Annotated" start:

RemusLoopin_11, Sebastisaurus_11,

Genes that have the "Most Annotated" start but do not call it:

Shawty_11,

Genes that do not have the "Most Annotated" start:

Euratis_11, Heather_11, Samora_11, TG1_11,

Summary by start number:

Start 1:

- Found in 3 of 7 (42.9%) of genes in pham
- Manual Annotations of this start: 2 of 6
- Called 66.7% of time when present
- Phage (with cluster) where this start called: Euratis_11 (BB1), Shawty_11 (BB1),

Start 3:

- Found in 3 of 7 (42.9%) of genes in pham
- Manual Annotations of this start: 2 of 6
- Called 66.7% of time when present

 Phage (with cluster) where this start called: RemusLoopin_11 (BB2), Sebastisaurus_11 (BB2),

Start 6:

- Found in 7 of 7 (100.0%) of genes in pham
- Manual Annotations of this start: 2 of 6
- Called 42.9% of time when present
- Phage (with cluster) where this start called: Heather_11 (BB2), Samora_11 (BB1),
 TG1_11 (BB1),

Summary by clusters:

There are 2 clusters represented in this pham: BB2, BB1,

Info for manual annotations of cluster BB1:

- Start number 1 was manually annotated 2 times for cluster BB1.
- •Start number 6 was manually annotated 1 time for cluster BB1.

Info for manual annotations of cluster BB2:

- •Start number 3 was manually annotated 2 times for cluster BB2.
- •Start number 6 was manually annotated 1 time for cluster BB2.

Gene Information:

Gene: Euratis_11 Start: 7968, Stop: 8174, Start Num: 1

Candidate Starts for Euratis_11:

(Start: 1 @7968 has 2 MA's), (Start: 6 @8022 has 2 MA's), (7, 8031), (9, 8055), (10, 8067), (11, 8166),

Gene: Heather_11 Start: 8049, Stop: 8204, Start Num: 6

Candidate Starts for Heather 11:

(Start: 6 @8049 has 2 MA's), (9, 8082), (10, 8094), (11, 8196),

Gene: RemusLoopin 11 Start: 7979, Stop: 8182, Start Num: 3

Candidate Starts for RemusLoopin_11:

(Start: 3 @7979 has 2 MA's), (Start: 6 @8027 has 2 MA's), (8, 8042), (9, 8060), (10, 8072), (11, 8174),

Gene: Samora 11 Start: 8064, Stop: 8216, Start Num: 6

Candidate Starts for Samora 11:

(Start: 1 @8010 has 2 MA's), (5, 8049), (Start: 6 @8064 has 2 MA's), (7, 8073), (9, 8097), (10, 8109), (11, 8208),

Gene: Sebastisaurus_11 Start: 8005, Stop: 8208, Start Num: 3

Candidate Starts for Sebastisaurus_11:

(2, 8002), (Start: 3 @8005 has 2 MA's), (4, 8020), (Start: 6 @8053 has 2 MA's), (9, 8086), (10, 8098), (11, 8200),

Gene: Shawty 11 Start: 8009, Stop: 8212, Start Num: 1

Candidate Starts for Shawty 11:

(Start: 1 @8009 has 2 MA's), (Start: 3 @8015 has 2 MA's), (5, 8048), (Start: 6 @8063 has 2 MA's), (7, 8072), (9, 8096), (10, 8108), (11, 8204),

Gene: TG1_11 Start: 8027, Stop: 8179, Start Num: 6

Candidate Starts for TG1_11: (Start: 6 @8027 has 2 MA's), (7, 8036), (10, 8072), (11, 8171),