

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 107366 Report

This analysis was run 04/28/24 on database version 559.

Pham number 107366 has 7 members, 2 are drafts.

Phages represented in each track:

Track 1 : Peregrin_78Track 2 : Weasels2_80Track 3 : Grayson_80

Track 4 : NiceHouse_62

Track 5 : Trina_73Track 6 : Dorin_46Track 7 : Francesca 46

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

The start number called the most often in the published annotations is 2, it was called in 3 of the 5 non-draft genes in the pham.

Genes that call this "Most Annotated" start:

Grayson_80, Peregrin_78, Weasels2_80,

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

Dorin_46, Francesca_46,

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

NiceHouse_62, Trina_73,

Summary by start number:

Start 1:

- Found in 2 of 7 (28.6%) of genes in pham
- No Manual Annotations of this start.
- Called 50.0% of time when present
- Phage (with cluster) where this start called: Dorin_46 (CG),

Start 2:

- Found in 5 of 7 (71.4%) of genes in pham
- Manual Annotations of this start: 3 of 5
- Called 60.0% of time when present

• Phage (with cluster) where this start called: Grayson_80 (CB), Peregrin_78 (CB), Weasels2 80 (CB),

Start 3:

- Found in 6 of 7 (85.7%) of genes in pham
- Manual Annotations of this start: 2 of 5
- Called 50.0% of time when present
- Phage (with cluster) where this start called: Francesca_46 (CG), NiceHouse_62 (CE), Trina_73 (CE),

Summary by clusters:

There are 3 clusters represented in this pham: CB, CG, CE,

Info for manual annotations of cluster CB:

•Start number 2 was manually annotated 3 times for cluster CB.

Info for manual annotations of cluster CE:

•Start number 3 was manually annotated 2 times for cluster CE.

Gene Information:

Gene: Dorin_46 Start: 28904, Stop: 29332, Start Num: 1

Candidate Starts for Dorin 46:

(1, 28904), (Start: 2 @28916 has 3 MA's), (Start: 3 @28925 has 2 MA's), (4, 28943), (7, 29033), (16, 29171), (18, 29177), (21, 29243), (23, 29273), (24, 29279),

Gene: Francesca_46 Start: 29057, Stop: 29464, Start Num: 3

Candidate Starts for Francesca 46:

(1, 29036), (Start: 2 @29048 has 3 MA's), (Start: 3 @29057 has 2 MA's), (4, 29075), (7, 29165), (16, 29303), (18, 29309), (21, 29375), (23, 29405), (24, 29411),

Gene: Grayson_80 Start: 41412, Stop: 41795, Start Num: 2

Candidate Starts for Grayson_80:

(Start: 2 @41412 has 3 MA's), (Start: 3 @41421 has 2 MA's), (5, 41463), (7, 41517), (11, 41580), (12, 41610), (13, 41622), (18, 41637), (19, 41691), (22, 41706), (23, 41733),

Gene: NiceHouse 62 Start: 35274, Stop: 35672, Start Num: 3

Candidate Starts for NiceHouse 62:

(Start: 3 @35274 has 2 MA's), (8, 35379), (9, 35382), (18, 35514), (22, 35583),

Gene: Peregrin_78 Start: 40192, Stop: 40575, Start Num: 2

Candidate Starts for Peregrin_78:

(Start: 2 @40192 has 3 MA's), (Start: 3 @40201 has 2 MA's), (5, 40243), (7, 40297), (11, 40360), (13, 40402), (18, 40417), (22, 40486), (23, 40513),

Gene: Trina 73 Start: 38778, Stop: 39182, Start Num: 3

Candidate Starts for Trina 73:

(Start: 3 @38778 has 2 MA's), (5, 38820), (7, 38886), (8, 38889), (10, 38937), (14, 39012), (15, 39015), (17, 39021), (18, 39024), (20, 39087), (22, 39093),

Gene: Weasels2_80 Start: 41044, Stop: 41427, Start Num: 2

Candidate Starts for Weasels2_80:

(Start: 2 @41044 has 3 MA's), (6, 41119), (14, 41257), (15, 41260), (18, 41269), (22, 41338),