



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 301812 Report

This analysis was run 06/08/26 on database version 649.

Pham number 301812 has 18 members, 3 are drafts.

Phages represented in each track:

- Track 1 : Pons_53, Yucky_54, MAnor_53, SheckWes_55, Mayweather_56, Vine_54
- Track 2 : Elinal_55, KayGee_53
- Track 3 : Tarnish_52, BigChungus_51, CherryonLim_53, Feastonyeet_51, Lauer_48
- Track 4 : CocoaPuff_52, PotPie_51
- Track 5 : ElJefes_53
- Track 6 : SummitAcademy_51
- Track 7 : Bavidard_51

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 10 of the 15 non-draft genes in the pham.

Genes that call this "Most Annotated" start:

- Bavidard_51, CocoaPuff_52, ElJefes_53, Elinal_55, KayGee_53, MAnor_53, Mayweather_56, Pons_53, PotPie_51, SheckWes_55, SummitAcademy_51, Vine_54, Yucky_54,

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

- BigChungus_51, CherryonLim_53, Feastonyeet_51, Lauer_48, Tarnish_52,

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

-

Summary by start number:

Start 1:

- Found in 14 of 18 (77.8%) of genes in pham
- Manual Annotations of this start: 5 of 15
- Called 35.7% of time when present
- Phage (with cluster) where this start called: BigChungus_51 (CT), CherryonLim_53 (CT), Feastonyeet_51 (CT), Lauer_48 (CT), Tarnish_52 (CT),

Start 2:

- Found in 18 of 18 (100.0%) of genes in pham
- Manual Annotations of this start: 10 of 15
- Called 72.2% of time when present
- Phage (with cluster) where this start called: Bavidard_51 (CT), CocoaPuff_52 (CT), ElJefes_53 (CT), Elinal_55 (CT), KayGee_53 (CT), MAnor_53 (CT), Mayweather_56 (CT), Pons_53 (CT), PotPie_51 (CT), SheckWes_55 (CT), SummitAcademy_51 (CT), Vine_54 (CT), Yucky_54 (CT),

Summary by clusters:

There is one cluster represented in this pham: CT

Info for manual annotations of cluster CT:

- Start number 1 was manually annotated 5 times for cluster CT.
- Start number 2 was manually annotated 10 times for cluster CT.

Gene Information:

Gene: Bavidard_51 Start: 37206, Stop: 37057, Start Num: 2

Candidate Starts for Bavidard_51:

(Start: 2 @37206 has 10 MA's), (3, 37134), (4, 37131), (5, 37122), (6, 37119), (7, 37065),

Gene: BigChungus_51 Start: 37336, Stop: 37175, Start Num: 1

Candidate Starts for BigChungus_51:

(Start: 1 @37336 has 5 MA's), (Start: 2 @37330 has 10 MA's), (3, 37258), (4, 37255), (5, 37246), (6, 37243),

Gene: CherryonLim_53 Start: 39056, Stop: 38895, Start Num: 1

Candidate Starts for CherryonLim_53:

(Start: 1 @39056 has 5 MA's), (Start: 2 @39050 has 10 MA's), (3, 38978), (4, 38975), (5, 38966), (6, 38963),

Gene: CocoaPuff_52 Start: 37335, Stop: 37180, Start Num: 2

Candidate Starts for CocoaPuff_52:

(Start: 1 @37341 has 5 MA's), (Start: 2 @37335 has 10 MA's), (6, 37248),

Gene: ElJefes_53 Start: 37874, Stop: 37719, Start Num: 2

Candidate Starts for ElJefes_53:

(Start: 1 @37880 has 5 MA's), (Start: 2 @37874 has 10 MA's), (3, 37802), (4, 37799), (5, 37790),

Gene: Elinal_55 Start: 37842, Stop: 37687, Start Num: 2

Candidate Starts for Elinal_55:

(Start: 2 @37842 has 10 MA's), (4, 37767), (5, 37758), (6, 37755),

Gene: Feastonyeet_51 Start: 37336, Stop: 37175, Start Num: 1

Candidate Starts for Feastonyeet_51:

(Start: 1 @37336 has 5 MA's), (Start: 2 @37330 has 10 MA's), (3, 37258), (4, 37255), (5, 37246), (6, 37243),

Gene: KayGee_53 Start: 37842, Stop: 37687, Start Num: 2

Candidate Starts for KayGee_53:

(Start: 2 @37842 has 10 MA's), (4, 37767), (5, 37758), (6, 37755),

Gene: Lauer_48 Start: 38990, Stop: 38829, Start Num: 1

Candidate Starts for Lauer_48:

(Start: 1 @38990 has 5 MA's), (Start: 2 @38984 has 10 MA's), (3, 38912), (4, 38909), (5, 38900), (6, 38897),

Gene: MAnor_53 Start: 38196, Stop: 38041, Start Num: 2

Candidate Starts for MAnor_53:

(Start: 1 @38202 has 5 MA's), (Start: 2 @38196 has 10 MA's), (3, 38124), (4, 38121), (5, 38112), (6, 38109),

Gene: Mayweather_56 Start: 38941, Stop: 38786, Start Num: 2

Candidate Starts for Mayweather_56:

(Start: 1 @38947 has 5 MA's), (Start: 2 @38941 has 10 MA's), (3, 38869), (4, 38866), (5, 38857), (6, 38854),

Gene: Pons_53 Start: 37826, Stop: 37671, Start Num: 2

Candidate Starts for Pons_53:

(Start: 1 @37832 has 5 MA's), (Start: 2 @37826 has 10 MA's), (3, 37754), (4, 37751), (5, 37742), (6, 37739),

Gene: PotPie_51 Start: 38365, Stop: 38210, Start Num: 2

Candidate Starts for PotPie_51:

(Start: 1 @38371 has 5 MA's), (Start: 2 @38365 has 10 MA's), (6, 38278),

Gene: SheckWes_55 Start: 37413, Stop: 37258, Start Num: 2

Candidate Starts for SheckWes_55:

(Start: 1 @37419 has 5 MA's), (Start: 2 @37413 has 10 MA's), (3, 37341), (4, 37338), (5, 37329), (6, 37326),

Gene: SummitAcademy_51 Start: 37511, Stop: 37356, Start Num: 2

Candidate Starts for SummitAcademy_51:

(Start: 2 @37511 has 10 MA's), (6, 37424),

Gene: Tarnish_52 Start: 38101, Stop: 37940, Start Num: 1

Candidate Starts for Tarnish_52:

(Start: 1 @38101 has 5 MA's), (Start: 2 @38095 has 10 MA's), (3, 38023), (4, 38020), (5, 38011), (6, 38008),

Gene: Vine_54 Start: 38131, Stop: 37976, Start Num: 2

Candidate Starts for Vine_54:

(Start: 1 @38137 has 5 MA's), (Start: 2 @38131 has 10 MA's), (3, 38059), (4, 38056), (5, 38047), (6, 38044),

Gene: Yucky_54 Start: 37923, Stop: 37768, Start Num: 2

Candidate Starts for Yucky_54:

(Start: 1 @37929 has 5 MA's), (Start: 2 @37923 has 10 MA's), (3, 37851), (4, 37848), (5, 37839), (6, 37836),