Pham 305469


1
3
4
5
1: SummitAcademy_50 + 3
3
4
5
2: BigChungus_50 + 4
2
3
4
5
3: ElJefes_52 + 1

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 305469 Report

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

Pham number 305469 has 11 members, 4 are drafts.

Phages represented in each track:
- Track 1 : SummitAcademy_50, CocoaPuff_51, PotPie_50, Balloona_50
- Track 2 : BigChungus_50, Yucky_53, Feastonyeet_50, Vine_53, SheckWes_54
- Track 3 : ElJefes_52, McDazzle_53

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 7 of the 7 non-draft genes in the pham.

Genes that call this "Most Annotated" start:
- Balloona_50, BigChungus_50, CocoaPuff_51, ElJefes_52, Feastonyeet_50, McDazzle_53, PotPie_50, SheckWes_54, SummitAcademy_50, Vine_53, Yucky_53,

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

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

Summary by start number:

Start 3:
- Found in 11 of 11 (100.0%) of genes in pham
- Manual Annotations of this start: 7 of 7
- Called 100.0% of time when present
- Phage (with cluster) where this start called: Balloona_50 (CT), BigChungus_50 (CT), CocoaPuff_51 (CT), ElJefes_52 (CT), Feastonyeet_50 (CT), McDazzle_53 (CT), PotPie_50 (CT), SheckWes_54 (CT), SummitAcademy_50 (CT), Vine_53 (CT), Yucky_53 (CT),

Summary by clusters:

There is one cluster represented in this pham: CT

Info for manual annotations of cluster CT:
•Start number 3 was manually annotated 7 times for cluster CT.

Gene Information:

Gene: Balloona_50 Start: 37250, Stop: 37002, Start Num: 3
Candidate Starts for Balloona_50:
(1, 37364), (Start: 3 @37250 has 7 MA's), (4, 37205), (5, 37124),

Gene: BigChungus_50 Start: 37182, Stop: 36934, Start Num: 3
Candidate Starts for BigChungus_50:
(Start: 3 @37182 has 7 MA's), (4, 37137), (5, 37056),

Gene: CocoaPuff_51 Start: 37187, Stop: 36939, Start Num: 3
Candidate Starts for CocoaPuff_51:
(1, 37301), (Start: 3 @37187 has 7 MA's), (4, 37142), (5, 37061),

Gene: ElJefes_52 Start: 37726, Stop: 37478, Start Num: 3
Candidate Starts for ElJefes_52:
(2, 37774), (Start: 3 @37726 has 7 MA's), (4, 37681), (5, 37600),

Gene: Feastonyeet_50 Start: 37182, Stop: 36934, Start Num: 3
Candidate Starts for Feastonyeet_50:
(Start: 3 @37182 has 7 MA's), (4, 37137), (5, 37056),

Gene: McDazzle_53 Start: 37720, Stop: 37472, Start Num: 3
Candidate Starts for McDazzle_53:
(2, 37768), (Start: 3 @37720 has 7 MA's), (4, 37675), (5, 37594),

Gene: PotPie_50 Start: 38217, Stop: 37969, Start Num: 3
Candidate Starts for PotPie_50:
(1, 38331), (Start: 3 @38217 has 7 MA's), (4, 38172), (5, 38091),

Gene: SheckWes_54 Start: 37265, Stop: 37017, Start Num: 3
Candidate Starts for SheckWes_54:
(Start: 3 @37265 has 7 MA's), (4, 37220), (5, 37139),

Gene: SummitAcademy_50 Start: 37363, Stop: 37115, Start Num: 3
Candidate Starts for SummitAcademy_50:
(1, 37477), (Start: 3 @37363 has 7 MA's), (4, 37318), (5, 37237),

Gene: Vine_53 Start: 37983, Stop: 37735, Start Num: 3
Candidate Starts for Vine_53:
(Start: 3 @37983 has 7 MA's), (4, 37938), (5, 37857),

Gene: Yucky_53 Start: 37775, Stop: 37527, Start Num: 3
Candidate Starts for Yucky_53:
(Start: 3 @37775 has 7 MA's), (4, 37730), (5, 37649),