

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 216774 Report

This analysis was run 02/22/25 on database version 588.

Pham number 216774 has 11 members, 2 are drafts.

Phages represented in each track:

- Track 1 : GoblinVoyage_1, SheRa_1, HotFries_1
- Track 2 : Moozy_1, Annihilus_1
- Track 3 : ClubPenguin_1
- Track 4: Hortihabitatio 10
- Track 5 : Capybara 7
- Track 6 : Hydrus_10
- Track 7 : Rickmore 10
- Track 8 : Sweetclover 6

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

The start number called the most often in the published annotations is 5, it was called in 3 of the 9 non-draft genes in the pham.

Genes that call this "Most Annotated" start:

GoblinVoyage_1, HotFries_1, SheRa_1,

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

Annihilus_1, ClubPenguin_1, Moozy_1,

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

Capybara_7, Hortihabitatio_10, Hydrus_10, Rickmore_10, Sweetclover_6,

Summary by start number:

Start 1:

- Found in 8 of 11 (72.7%) of genes in pham
- Manual Annotations of this start: 3 of 9
- Called 37.5% of time when present
- Phage (with cluster) where this start called: Annihilus_1 (BI2), ClubPenguin_1 (BI7), Moozy_1 (BI2),

Start 2:

• Found in 3 of 11 (27.3%) of genes in pham

- Manual Annotations of this start: 2 of 9
- Called 100.0% of time when present
- Phage (with cluster) where this start called: Hydrus_10 (DJ), Rickmore_10 (DJ), Sweetclover_6 (JA),

Start 5:

- Found in 6 of 11 (54.5%) of genes in pham
- Manual Annotations of this start: 3 of 9
- Called 50.0% of time when present
- Phage (with cluster) where this start called: GoblinVoyage_1 (BI2), HotFries_1 (BI2), SheRa_1 (BI2),

Start 7:

- Found in 1 of 11 (9.1%) of genes in pham
- No Manual Annotations of this start.
- Called 100.0% of time when present
- Phage (with cluster) where this start called: Hortihabitatio_10 (DJ),

Start 11:

- Found in 1 of 11 (9.1%) of genes in pham
- Manual Annotations of this start: 1 of 9
- Called 100.0% of time when present
- Phage (with cluster) where this start called: Capybara_7 (DJ),

Summary by clusters:

There are 4 clusters represented in this pham: BI2, DJ, JA, BI7,

Info for manual annotations of cluster BI2:

- •Start number 1 was manually annotated 2 times for cluster BI2.
- •Start number 5 was manually annotated 3 times for cluster BI2.

Info for manual annotations of cluster BI7:

•Start number 1 was manually annotated 1 time for cluster BI7.

Info for manual annotations of cluster DJ:

- •Start number 2 was manually annotated 2 times for cluster DJ.
- •Start number 11 was manually annotated 1 time for cluster DJ.

Gene Information:

Gene: Annihilus_1 Start: 137, Stop: 490, Start Num: 1

Candidate Starts for Annihilus_1:

(Start: 1 @137 has 3 MA's), (Start: 5 @221 has 3 MA's), (13, 368), (14, 383), (17, 425),

Gene: Capybara 7 Start: 2909, Stop: 3103, Start Num: 11

Candidate Starts for Capybara 7:

(Start: 1 @2747 has 3 MA's), (8, 2852), (10, 2894), (Start: 11 @2909 has 1 MA's), (14, 2993), (18, 2014), (20, 2077)

3044), (20, 3077),

Gene: ClubPenguin_1 Start: 106, Stop: 462, Start Num: 1

Candidate Starts for ClubPenguin_1:

(Start: 1 @ 106 has 3 MA's), (Start: 5 @ 190 has 3 MA's), (6, 199), (9, 214), (15, 370), (18, 403),

Gene: GoblinVoyage_1 Start: 221, Stop: 490, Start Num: 5

Candidate Starts for GoblinVoyage_1:

(Start: 1 @137 has 3 MA's), (Start: 5 @221 has 3 MA's), (13, 368), (14, 383), (17, 425),

Gene: Hortihabitatio_10 Start: 5062, Stop: 5319, Start Num: 7

Candidate Starts for Hortihabitatio_10:

(Start: 1 @ 4963 has 3 MA's), (7, 5062), (8, 5068), (14, 5209), (18, 5260), (19, 5287),

Gene: HotFries_1 Start: 221, Stop: 490, Start Num: 5

Candidate Starts for HotFries_1:

(Start: 1 @137 has 3 MA's), (Start: 5 @221 has 3 MA's), (13, 368), (14, 383), (17, 425),

Gene: Hydrus_10 Start: 4860, Stop: 5213, Start Num: 2

Candidate Starts for Hydrus_10:

(Start: 2 @4860 has 2 MA's), (8, 4962), (12, 5079), (14, 5103), (16, 5139), (18, 5154), (20, 5187),

Gene: Moozy_1 Start: 137, Stop: 490, Start Num: 1

Candidate Starts for Moozy_1:

(Start: 1 @137 has 3 MA's), (Start: 5 @221 has 3 MA's), (13, 368), (14, 383), (17, 425),

Gene: Rickmore_10 Start: 4442, Stop: 4798, Start Num: 2

Candidate Starts for Rickmore_10:

(Start: 2 @4442 has 2 MA's), (8, 4547), (14, 4688), (16, 4724), (18, 4739),

Gene: SheRa_1 Start: 221, Stop: 490, Start Num: 5

Candidate Starts for SheRa_1:

(Start: 1 @137 has 3 MA's), (Start: 5 @221 has 3 MA's), (13, 368), (14, 383), (17, 425),

Gene: Sweetclover_6 Start: 2582, Stop: 2926, Start Num: 2

Candidate Starts for Sweetclover 6:

(Start: 2 @ 2582 has 2 MA's), (3, 2624), (4, 2657), (10, 2726), (17, 2867),