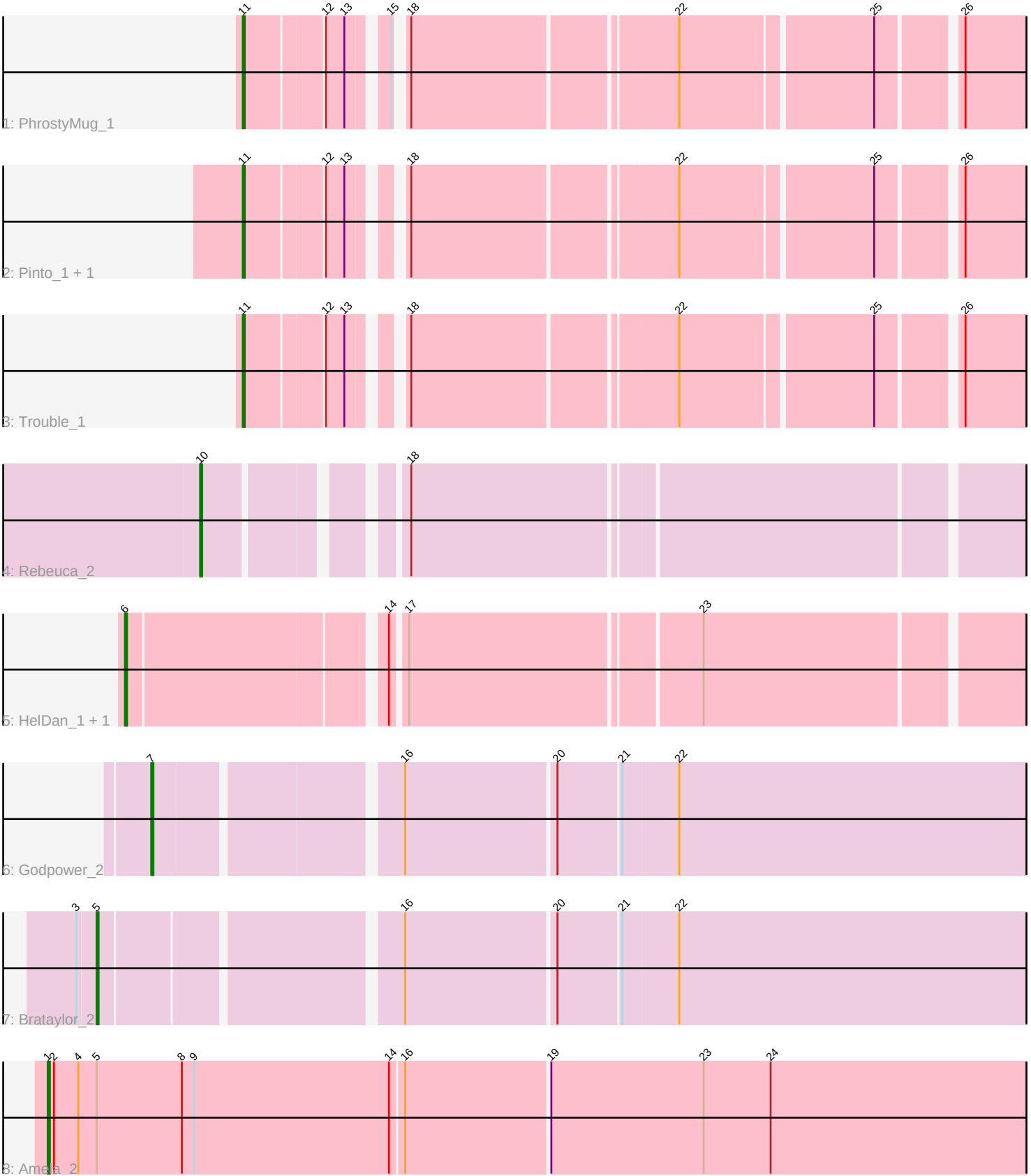


Pham 331478



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 331478 Report

This analysis was run 09/05/26 on database version 662.

Pham number 331478 has 10 members, 0 are drafts.

Phages represented in each track:

- Track 1 : PhrostyMug_1
- Track 2 : Pinto_1, Magnito_1
- Track 3 : Trouble_1
- Track 4 : Rebeuca_2
- Track 5 : HelDan_1, Heathen_1
- Track 6 : Godpower_2
- Track 7 : Brataylor_2
- Track 8 : Amela_2

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

The start number called the most often in the published annotations is 11, it was called in 4 of the 10 non-draft genes in the pham.

Genes that call this "Most Annotated" start:

- Magnito_1, PhrostyMug_1, Pinto_1, Trouble_1,

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

•

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

- Amela_2, Brataylor_2, Godpower_2, Heathen_1, HelDan_1, Rebeuca_2,

Summary by start number:

Start 1:

- Found in 1 of 10 (10.0%) of genes in pham
- Manual Annotations of this start: 1 of 10
- Called 100.0% of time when present
- Phage (with cluster) where this start called: Amela_2 (BD3),

Start 5:

- Found in 2 of 10 (20.0%) of genes in pham
- Manual Annotations of this start: 1 of 10

- Called 50.0% of time when present
- Phage (with cluster) where this start called: Brataylor_2 (BD1),

Start 6:

- Found in 2 of 10 (20.0%) of genes in pham
- Manual Annotations of this start: 2 of 10
- Called 100.0% of time when present
- Phage (with cluster) where this start called: Heathen_1 (A3), HelDan_1 (A3),

Start 7:

- Found in 1 of 10 (10.0%) of genes in pham
- Manual Annotations of this start: 1 of 10
- Called 100.0% of time when present
- Phage (with cluster) where this start called: Godpower_2 (BD1),

Start 10:

- Found in 1 of 10 (10.0%) of genes in pham
- Manual Annotations of this start: 1 of 10
- Called 100.0% of time when present
- Phage (with cluster) where this start called: Rebeuca_2 (A10),

Start 11:

- Found in 4 of 10 (40.0%) of genes in pham
- Manual Annotations of this start: 4 of 10
- Called 100.0% of time when present
- Phage (with cluster) where this start called: Magnito_1 (A1), PhrostyMug_1 (A1), Pinto_1 (A1), Trouble_1 (A1),

Summary by clusters:

There are 5 clusters represented in this pham: A1, A3, BD1, A10, BD3,

Info for manual annotations of cluster A1:

- Start number 11 was manually annotated 4 times for cluster A1.

Info for manual annotations of cluster A10:

- Start number 10 was manually annotated 1 time for cluster A10.

Info for manual annotations of cluster A3:

- Start number 6 was manually annotated 2 times for cluster A3.

Info for manual annotations of cluster BD1:

- Start number 5 was manually annotated 1 time for cluster BD1.
- Start number 7 was manually annotated 1 time for cluster BD1.

Info for manual annotations of cluster BD3:

- Start number 1 was manually annotated 1 time for cluster BD3.

Gene Information:

Gene: Amela_2 Start: 787, Stop: 1275, Start Num: 1

Candidate Starts for Amela_2:

(Start: 1 @787 has 1 MA's), (2, 790), (4, 802), (Start: 5 @811 has 1 MA's), (8, 853), (9, 859), (14, 955), (16, 961), (19, 1030), (23, 1105), (24, 1138),

Gene: Brataylor_2 Start: 590, Stop: 1036, Start Num: 5

Candidate Starts for Brataylor_2:

(3, 581), (Start: 5 @590 has 1 MA's), (16, 725), (20, 797), (21, 827), (22, 854),

Gene: Godpower_2 Start: 615, Stop: 1037, Start Num: 7

Candidate Starts for Godpower_2:

(Start: 7 @615 has 1 MA's), (16, 726), (20, 798), (21, 828), (22, 855),

Gene: Heathen_1 Start: 293, Stop: 712, Start Num: 6

Candidate Starts for Heathen_1:

(Start: 6 @293 has 2 MA's), (14, 410), (17, 416), (23, 551),

Gene: HelDan_1 Start: 293, Stop: 712, Start Num: 6

Candidate Starts for HelDan_1:

(Start: 6 @293 has 2 MA's), (14, 410), (17, 416), (23, 551),

Gene: Magnito_1 Start: 535, Stop: 894, Start Num: 11

Candidate Starts for Magnito_1:

(Start: 11 @535 has 4 MA's), (12, 571), (13, 580), (18, 598), (22, 721), (25, 811), (26, 847),

Gene: PhrostyMug_1 Start: 532, Stop: 891, Start Num: 11

Candidate Starts for PhrostyMug_1:

(Start: 11 @532 has 4 MA's), (12, 568), (13, 577), (15, 592), (18, 595), (22, 718), (25, 808), (26, 844),

Gene: Pinto_1 Start: 535, Stop: 894, Start Num: 11

Candidate Starts for Pinto_1:

(Start: 11 @535 has 4 MA's), (12, 571), (13, 580), (18, 598), (22, 721), (25, 811), (26, 847),

Gene: Rebeuca_2 Start: 549, Stop: 926, Start Num: 10

Candidate Starts for Rebeuca_2:

(Start: 10 @549 has 1 MA's), (18, 630),

Gene: Trouble_1 Start: 534, Stop: 893, Start Num: 11

Candidate Starts for Trouble_1:

(Start: 11 @534 has 4 MA's), (12, 570), (13, 579), (18, 597), (22, 720), (25, 810), (26, 846),