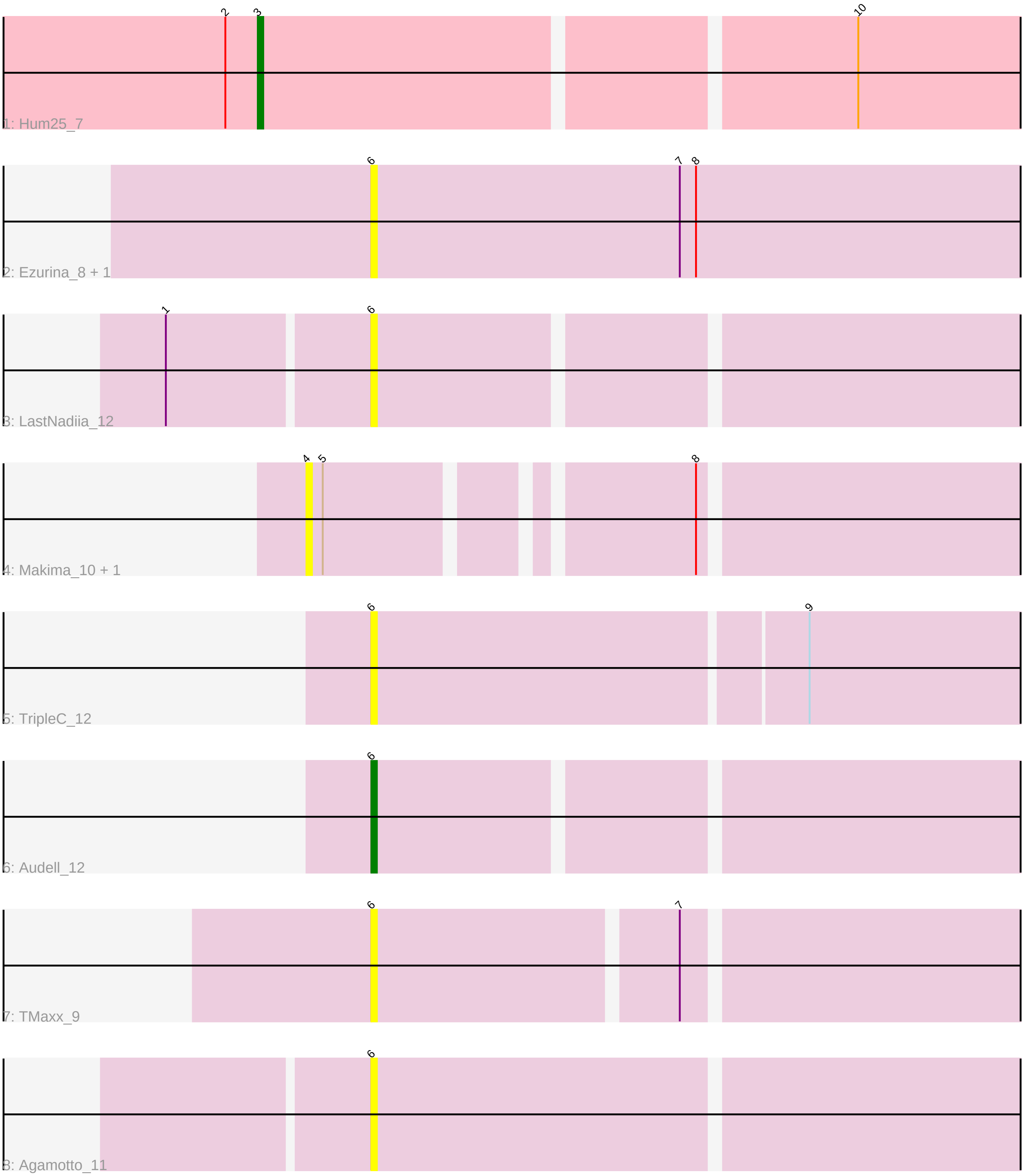
Pham 284409


2
3
10
1: Hum25_7
6
7
8
2: Ezurina_8 + 1
1
6
3: LastNadiia_12
4
5
8
4: Makima_10 + 1
6
9
5: TripleC_12
6
6: Audell_12
6
7
7: TMaxx_9
6
8: Agamotto_11

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 284409 Report

This analysis was run 02/23/26 on database version 636.

Pham number 284409 has 10 members, 8 are drafts.

Phages represented in each track:
- Track 1 : Hum25_7
- Track 2 : Ezurina_8, Studio_9
- Track 3 : LastNadiia_12
- Track 4 : Makima_10, Mireles_9
- Track 5 : TripleC_12
- Track 6 : Audell_12
- Track 7 : TMaxx_9
- Track 8 : Agamotto_11

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 1 of the 2 non-draft genes in the pham.

Genes that call this "Most Annotated" start:
- Hum25_7,

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

Genes that do not have the "Most Annotated" start:
- Agamotto_11, Audell_12, Ezurina_8, LastNadiia_12, Makima_10, Mireles_9, Studio_9, TMaxx_9, TripleC_12,

Summary by start number:

Start 3:
- Found in 1 of 10 (10.0%) of genes in pham
- Manual Annotations of this start: 1 of 2
- Called 100.0% of time when present
- Phage (with cluster) where this start called: Hum25_7 (FQ),

Start 4:
- Found in 2 of 10 (20.0%) of genes in pham

- No Manual Annotations of this start.
- Called 100.0% of time when present
- Phage (with cluster) where this start called: Makima_10 (FR), Mireles_9 (FR),

Start 6:
- Found in 7 of 10 (70.0%) of genes in pham
- Manual Annotations of this start: 1 of 2
- Called 100.0% of time when present
- Phage (with cluster) where this start called: Agamotto_11 (FR), Audell_12 (FR), Ezurina_8 (FR), LastNadiia_12 (FR), Studio_9 (FR), TMaxx_9 (FR), TripleC_12 (FR),

Summary by clusters:

There are 2 clusters represented in this pham: FQ, FR,

Info for manual annotations of cluster FQ:
•Start number 3 was manually annotated 1 time for cluster FQ.

Info for manual annotations of cluster FR:
•Start number 6 was manually annotated 1 time for cluster FR.

Gene Information:

Gene: Agamotto_11 Start: 9608, Stop: 9748, Start Num: 6
Candidate Starts for Agamotto_11:
(Start: 6 @9608 has 1 MA's),

Gene: Audell_12 Start: 9884, Stop: 10021, Start Num: 6
Candidate Starts for Audell_12:
(Start: 6 @9884 has 1 MA's),

Gene: Ezurina_8 Start: 6088, Stop: 6231, Start Num: 6
Candidate Starts for Ezurina_8:
(Start: 6 @6088 has 1 MA's), (7, 6145), (8, 6148),

Gene: Hum25_7 Start: 5931, Stop: 6089, Start Num: 3
Candidate Starts for Hum25_7:
(2, 5925), (Start: 3 @5931 has 1 MA's), (10, 6036),

Gene: LastNadiia_12 Start: 8833, Stop: 8970, Start Num: 6
Candidate Starts for LastNadiia_12:
(1, 8797), (Start: 6 @8833 has 1 MA's),

Gene: Makima_10 Start: 7916, Stop: 8059, Start Num: 4
Candidate Starts for Makima_10:
(4, 7916), (5, 7919), (8, 7979),

Gene: Mireles_9 Start: 6316, Stop: 6459, Start Num: 4
Candidate Starts for Mireles_9:
(4, 6316), (5, 6319), (8, 6379),

Gene: Studio_9 Start: 6279, Stop: 6422, Start Num: 6
Candidate Starts for Studio_9:
(Start: 6 @6279 has 1 MA's), (7, 6336), (8, 6339),

Gene: TMaxx_9 Start: 6419, Stop: 6556, Start Num: 6
Candidate Starts for TMaxx_9:
(Start: 6 @6419 has 1 MA's), (7, 6473),

Gene: TripleC_12 Start: 9899, Stop: 10039, Start Num: 6
Candidate Starts for TripleC_12:
(Start: 6 @9899 has 1 MA's), (9, 9977),