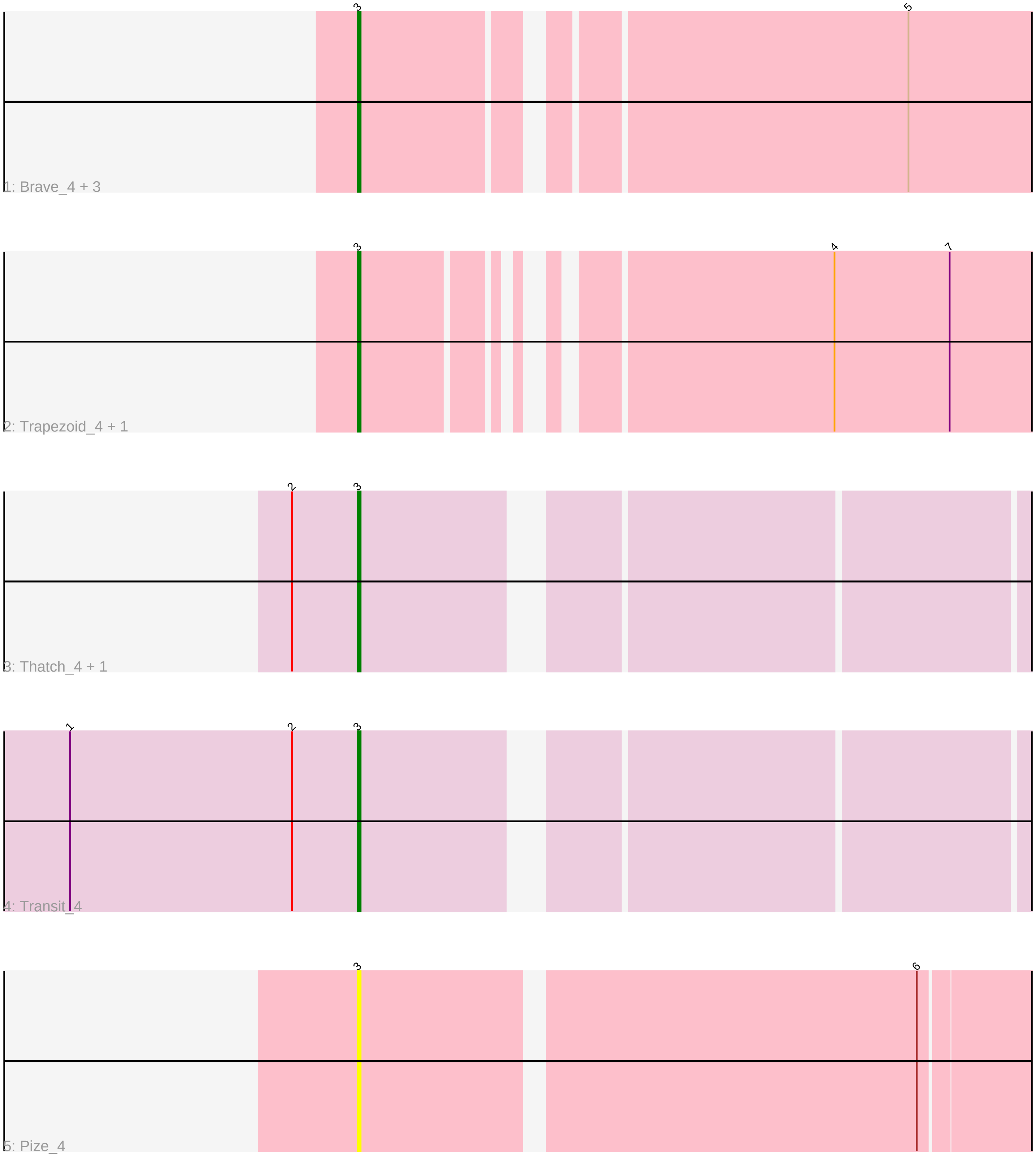
Pham 301987


3
5
1: Brave_4 + 3
3
4
7
2: Trapezoid_4 + 1
2
3
3: Thatch_4 + 1
1
2
3
4: Transit_4
3
6
5: Pize_4

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 301987 Report

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

Pham number 301987 has 10 members, 2 are drafts.

Phages represented in each track:
- Track 1 : Brave_4, Penne_4, Squall_4, Fairywren_4
- Track 2 : Trapezoid_4, Reje_4
- Track 3 : Thatch_4, Mantle_4
- Track 4 : Transit_4
- Track 5 : Pize_4

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 8 of the 8 non-draft genes in the pham.

Genes that call this "Most Annotated" start:
- Brave_4, Fairywren_4, Mantle_4, Penne_4, Pize_4, Reje_4, Squall_4, Thatch_4, Transit_4, Trapezoid_4,

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 10 of 10 (100.0%) of genes in pham
- Manual Annotations of this start: 8 of 8
- Called 100.0% of time when present
- Phage (with cluster) where this start called: Brave_4 (JB1), Fairywren_4 (JB1), Mantle_4 (JB2), Penne_4 (JB1), Pize_4 (UNK), Reje_4 (UNK), Squall_4 (JB1), Thatch_4 (JB2), Transit_4 (JB2), Trapezoid_4 (JB1),

Summary by clusters:

There are 3 clusters represented in this pham: UNK, JB2, JB1,

Info for manual annotations of cluster JB1:
•Start number 3 was manually annotated 5 times for cluster JB1.

Info for manual annotations of cluster JB2:
•Start number 3 was manually annotated 3 times for cluster JB2.

Gene Information:

Gene: Brave_4 Start: 3867, Stop: 4109, Start Num: 3
Candidate Starts for Brave_4:
(Start: 3 @3867 has 8 MA's), (5, 4050),

Gene: Fairywren_4 Start: 3836, Stop: 4078, Start Num: 3
Candidate Starts for Fairywren_4:
(Start: 3 @3836 has 8 MA's), (5, 4019),

Gene: Mantle_4 Start: 4363, Stop: 4614, Start Num: 3
Candidate Starts for Mantle_4:
(2, 4339), (Start: 3 @4363 has 8 MA's),

Gene: Penne_4 Start: 3870, Stop: 4112, Start Num: 3
Candidate Starts for Penne_4:
(Start: 3 @3870 has 8 MA's), (5, 4053),

Gene: Pize_4 Start: 3685, Stop: 3936, Start Num: 3
Candidate Starts for Pize_4:
(Start: 3 @3685 has 8 MA's), (6, 3880),

Gene: Reje_4 Start: 3729, Stop: 3959, Start Num: 3
Candidate Starts for Reje_4:
(Start: 3 @3729 has 8 MA's), (4, 3873), (7, 3915),

Gene: Squall_4 Start: 3837, Stop: 4079, Start Num: 3
Candidate Starts for Squall_4:
(Start: 3 @3837 has 8 MA's), (5, 4020),

Gene: Thatch_4 Start: 4160, Stop: 4396, Start Num: 3
Candidate Starts for Thatch_4:
(2, 4136), (Start: 3 @4160 has 8 MA's),

Gene: Transit_4 Start: 4101, Stop: 4337, Start Num: 3
Candidate Starts for Transit_4:
(1, 3996), (2, 4077), (Start: 3 @4101 has 8 MA's),

Gene: Trapezoid_4 Start: 3762, Stop: 3992, Start Num: 3
Candidate Starts for Trapezoid_4:
(Start: 3 @3762 has 8 MA's), (4, 3906), (7, 3948),