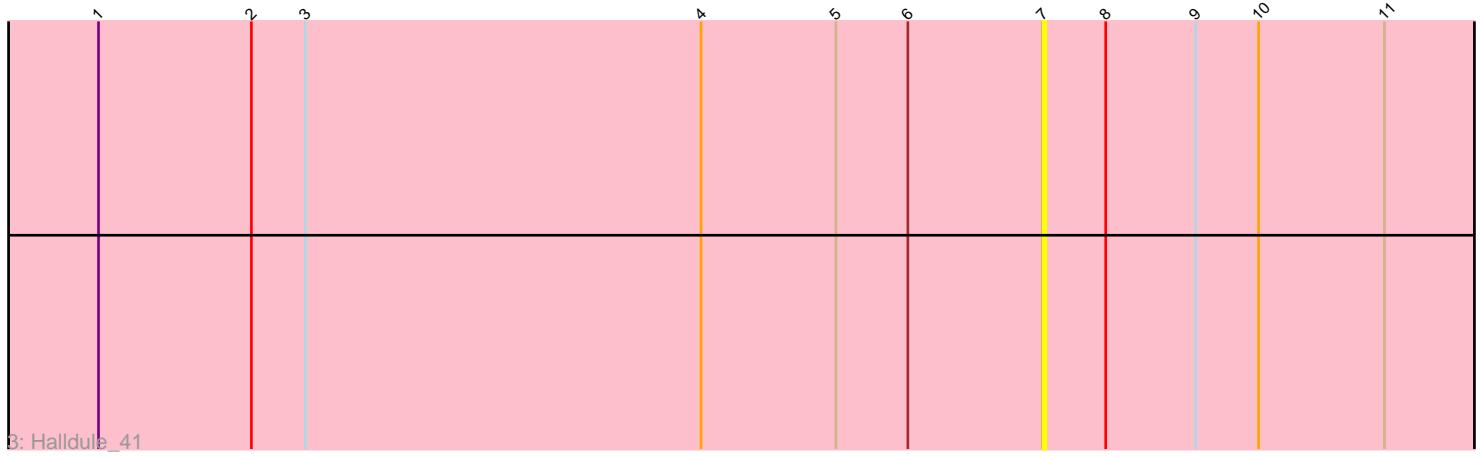
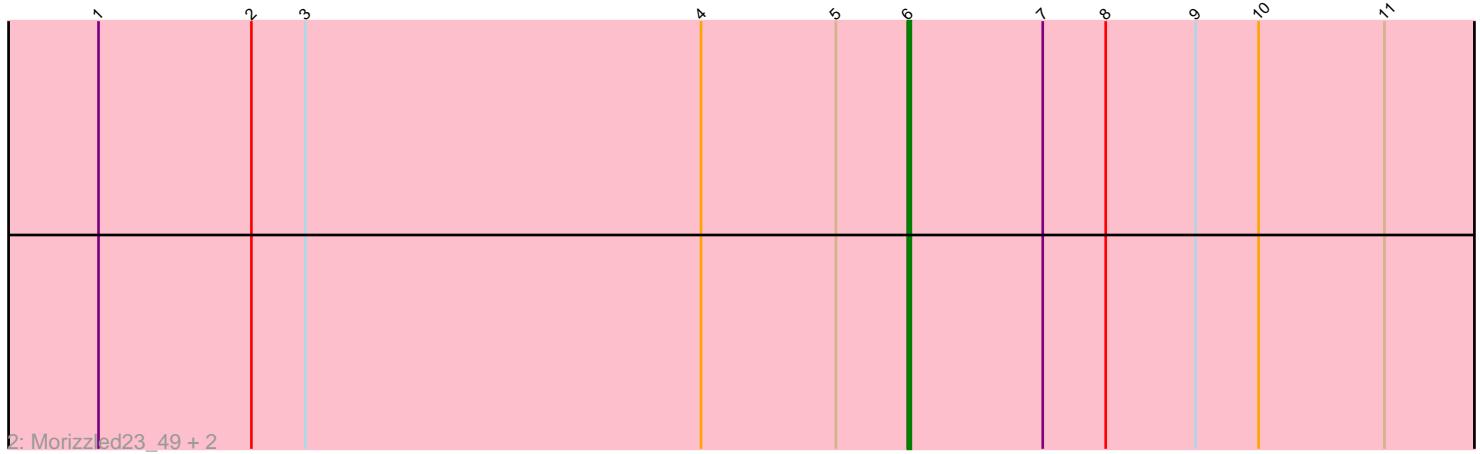
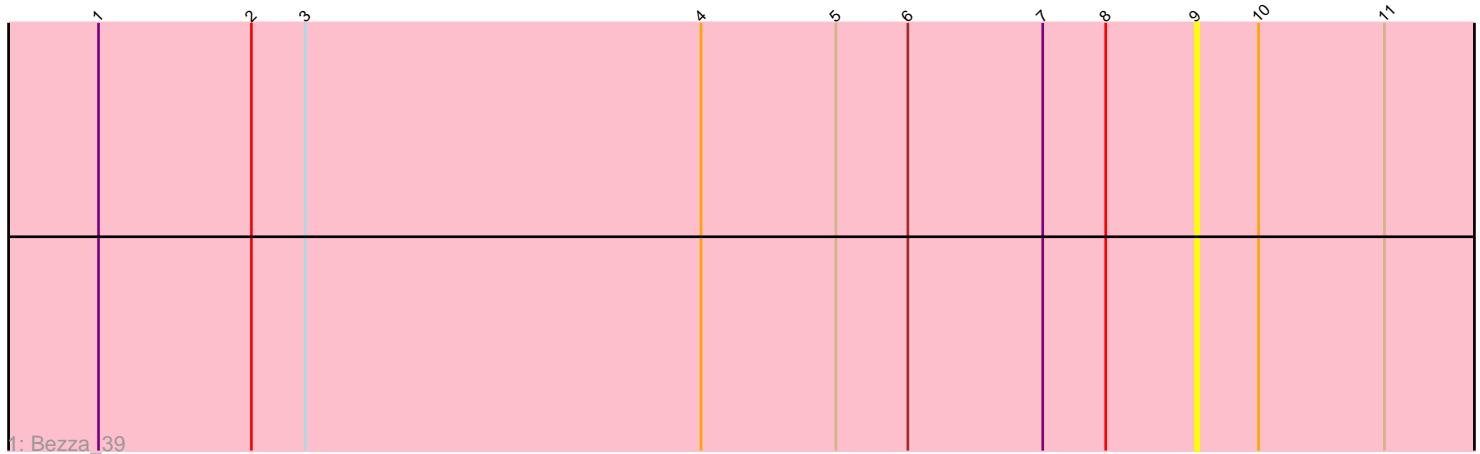


Pham 256662



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 256662 Report

This analysis was run 02/07/26 on database version 634.

Pham number 256662 has 5 members, 3 are drafts.

Phages represented in each track:

- Track 1 : Bezza_39
- Track 2 : Morizzled23_49, Pupusa_52, BadAgartude_48
- Track 3 : Halldule_41

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

The start number called the most often in the published annotations is 6, it was called in 2 of the 2 non-draft genes in the pham.

Genes that call this "Most Annotated" start:

- BadAgartude_48, Morizzled23_49, Pupusa_52,

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

- Bezza_39, Halldule_41,

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

-

Summary by start number:

Start 6:

- Found in 5 of 5 (100.0%) of genes in pham
- Manual Annotations of this start: 2 of 2
- Called 60.0% of time when present
- Phage (with cluster) where this start called: BadAgartude_48 (C1), Morizzled23_49 (C1), Pupusa_52 (C1),

Start 7:

- Found in 5 of 5 (100.0%) of genes in pham
- No Manual Annotations of this start.
- Called 20.0% of time when present
- Phage (with cluster) where this start called: Halldule_41 (C1),

Start 9:

- Found in 5 of 5 (100.0%) of genes in pham
- No Manual Annotations of this start.
- Called 20.0% of time when present
- Phage (with cluster) where this start called: Bezza_39 (C1),

Summary by clusters:

There is one cluster represented in this pham: C1

Info for manual annotations of cluster C1:

- Start number 6 was manually annotated 2 times for cluster C1.

Gene Information:

Gene: BadAgartude_48 Start: 15902, Stop: 16129, Start Num: 6

Candidate Starts for BadAgartude_48:

(1, 15632), (2, 15683), (3, 15701), (4, 15833), (5, 15878), (Start: 6 @15902 has 2 MA's), (7, 15947), (8, 15968), (9, 15998), (10, 16019), (11, 16061),

Gene: Bezza_39 Start: 14428, Stop: 14559, Start Num: 9

Candidate Starts for Bezza_39:

(1, 14062), (2, 14113), (3, 14131), (4, 14263), (5, 14308), (Start: 6 @14332 has 2 MA's), (7, 14377), (8, 14398), (9, 14428), (10, 14449), (11, 14491),

Gene: Halldule_41 Start: 13130, Stop: 13312, Start Num: 7

Candidate Starts for Halldule_41:

(1, 12815), (2, 12866), (3, 12884), (4, 13016), (5, 13061), (Start: 6 @13085 has 2 MA's), (7, 13130), (8, 13151), (9, 13181), (10, 13202), (11, 13244),

Gene: Morizzled23_49 Start: 14908, Stop: 15135, Start Num: 6

Candidate Starts for Morizzled23_49:

(1, 14638), (2, 14689), (3, 14707), (4, 14839), (5, 14884), (Start: 6 @14908 has 2 MA's), (7, 14953), (8, 14974), (9, 15004), (10, 15025), (11, 15067),

Gene: Pupusa_52 Start: 17040, Stop: 17267, Start Num: 6

Candidate Starts for Pupusa_52:

(1, 16770), (2, 16821), (3, 16839), (4, 16971), (5, 17016), (Start: 6 @17040 has 2 MA's), (7, 17085), (8, 17106), (9, 17136), (10, 17157), (11, 17199),