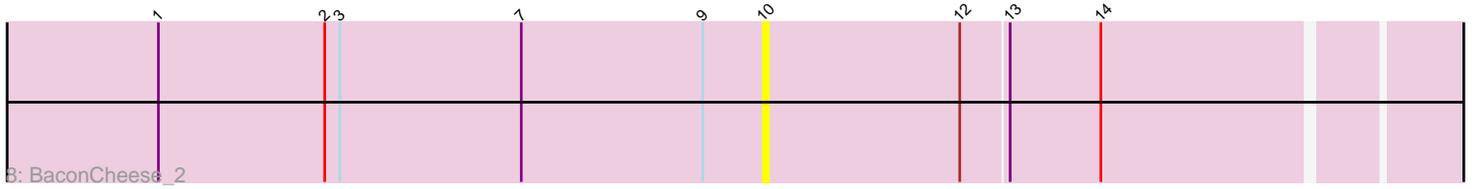
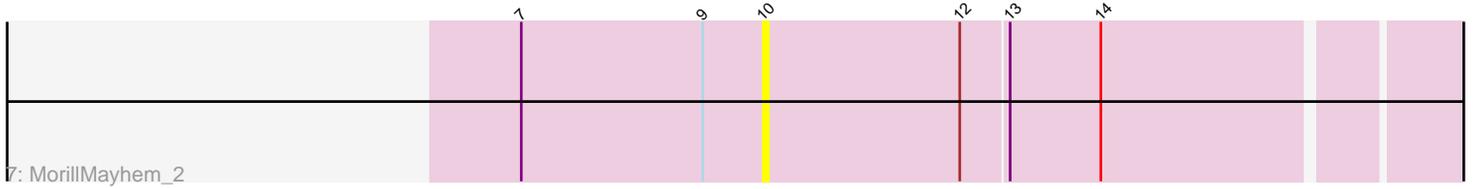
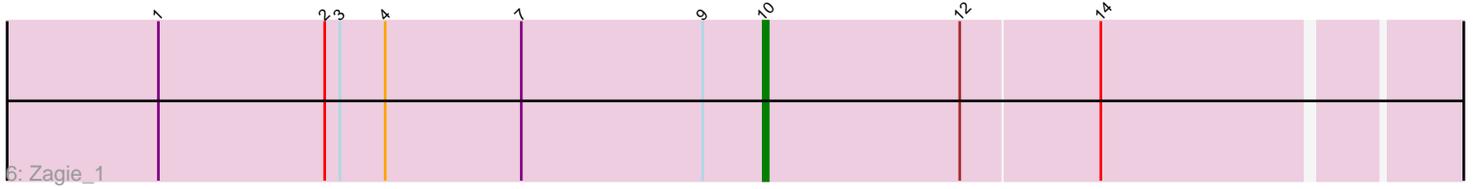
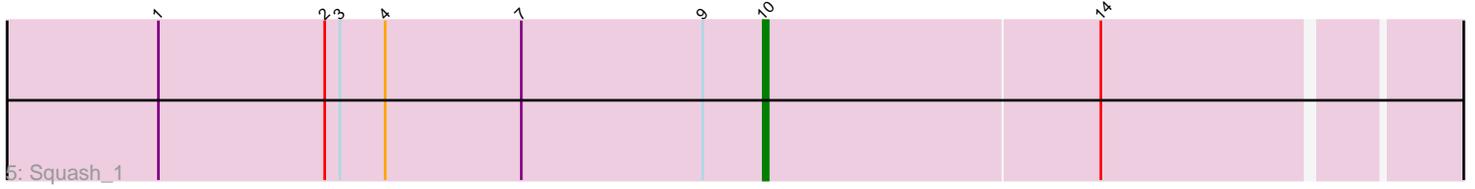
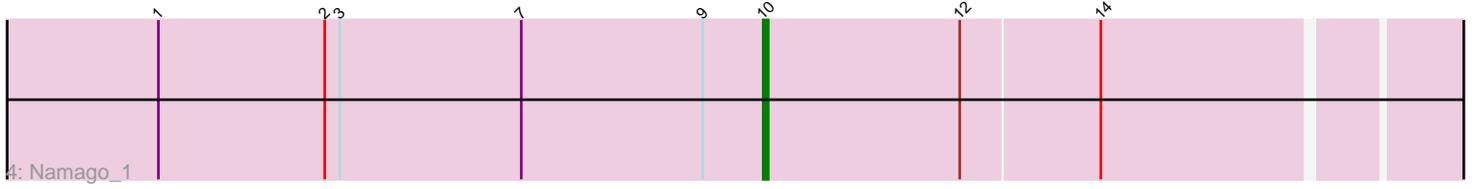
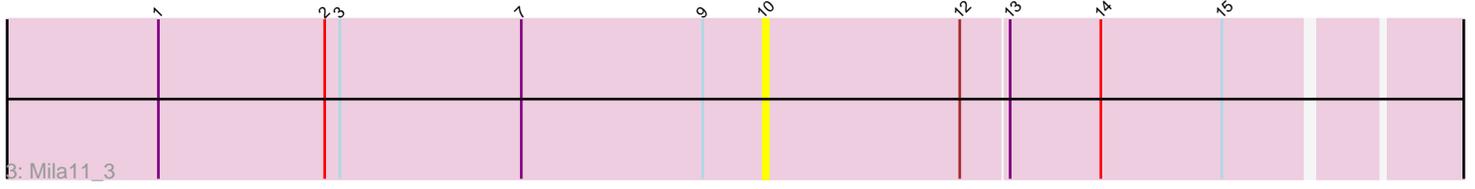
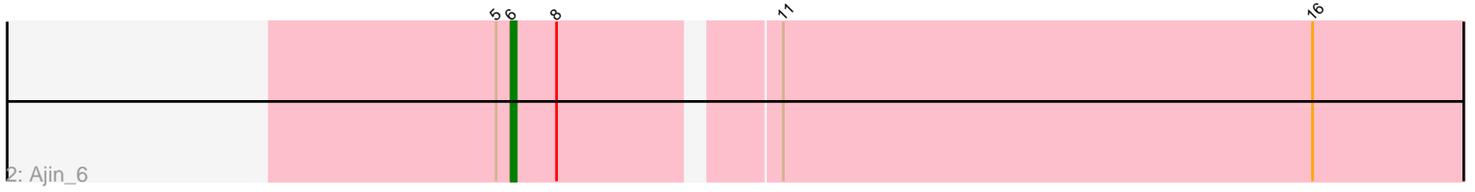
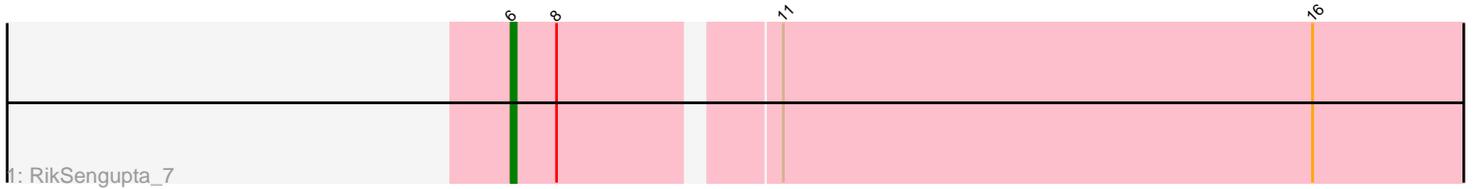


Pham 282691



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 282691 Report

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

Pham number 282691 has 8 members, 3 are drafts.

Phages represented in each track:

- Track 1 : RikSengupta\_7
- Track 2 : Ajin\_6
- Track 3 : Mila11\_3
- Track 4 : Namago\_1
- Track 5 : Squash\_1
- Track 6 : Zagie\_1
- Track 7 : MorillMayhem\_2
- Track 8 : BaconCheese\_2

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

The start number called the most often in the published annotations is 10, it was called in 3 of the 5 non-draft genes in the pham.

Genes that call this "Most Annotated" start:

- BaconCheese\_2, Mila11\_3, MorillMayhem\_2, Namago\_1, Squash\_1, Zagie\_1,

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

- 

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

- Ajin\_6, RikSengupta\_7,

### **Summary by start number:**

Start 6:

- Found in 2 of 8 ( 25.0% ) of genes in pham
- Manual Annotations of this start: 2 of 5
- Called 100.0% of time when present
- Phage (with cluster) where this start called: Ajin\_6 (EF), RikSengupta\_7 (EF),

Start 10:

- Found in 6 of 8 ( 75.0% ) of genes in pham
- Manual Annotations of this start: 3 of 5

- Called 100.0% of time when present
- Phage (with cluster) where this start called: BaconCheese\_2 (EG), Mila11\_3 (EG), MorillMayhem\_2 (EG), Namago\_1 (EG), Squash\_1 (EG), Zagie\_1 (EG),

### **Summary by clusters:**

There are 2 clusters represented in this pham: EG, EF,

Info for manual annotations of cluster EF:

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

Info for manual annotations of cluster EG:

- Start number 10 was manually annotated 3 times for cluster EG.

### **Gene Information:**

Gene: Ajin\_6 Start: 1946, Stop: 2167, Start Num: 6

Candidate Starts for Ajin\_6:

(5, 1943), (Start: 6 @1946 has 2 MA's), (8, 1955), (11, 1994), (16, 2099),

Gene: BaconCheese\_2 Start: 1237, Stop: 1073, Start Num: 10

Candidate Starts for BaconCheese\_2:

(1, 1357), (2, 1324), (3, 1321), (7, 1285), (9, 1249), (Start: 10 @1237 has 3 MA's), (12, 1198), (13, 1189), (14, 1171),

Gene: Mila11\_3 Start: 1222, Stop: 1058, Start Num: 10

Candidate Starts for Mila11\_3:

(1, 1342), (2, 1309), (3, 1306), (7, 1270), (9, 1234), (Start: 10 @1222 has 3 MA's), (12, 1183), (13, 1174), (14, 1156), (15, 1132),

Gene: MorillMayhem\_2 Start: 1239, Stop: 1075, Start Num: 10

Candidate Starts for MorillMayhem\_2:

(7, 1287), (9, 1251), (Start: 10 @1239 has 3 MA's), (12, 1200), (13, 1191), (14, 1173),

Gene: Namago\_1 Start: 833, Stop: 663, Start Num: 10

Candidate Starts for Namago\_1:

(1, 953), (2, 920), (3, 917), (7, 881), (9, 845), (Start: 10 @833 has 3 MA's), (12, 794), (14, 767),

Gene: RikSengupta\_7 Start: 2098, Stop: 2319, Start Num: 6

Candidate Starts for RikSengupta\_7:

(Start: 6 @2098 has 2 MA's), (8, 2107), (11, 2146), (16, 2251),

Gene: Squash\_1 Start: 847, Stop: 677, Start Num: 10

Candidate Starts for Squash\_1:

(1, 967), (2, 934), (3, 931), (4, 922), (7, 895), (9, 859), (Start: 10 @847 has 3 MA's), (14, 781),

Gene: Zagie\_1 Start: 838, Stop: 668, Start Num: 10

Candidate Starts for Zagie\_1:

(1, 958), (2, 925), (3, 922), (4, 913), (7, 886), (9, 850), (Start: 10 @838 has 3 MA's), (12, 799), (14, 772),