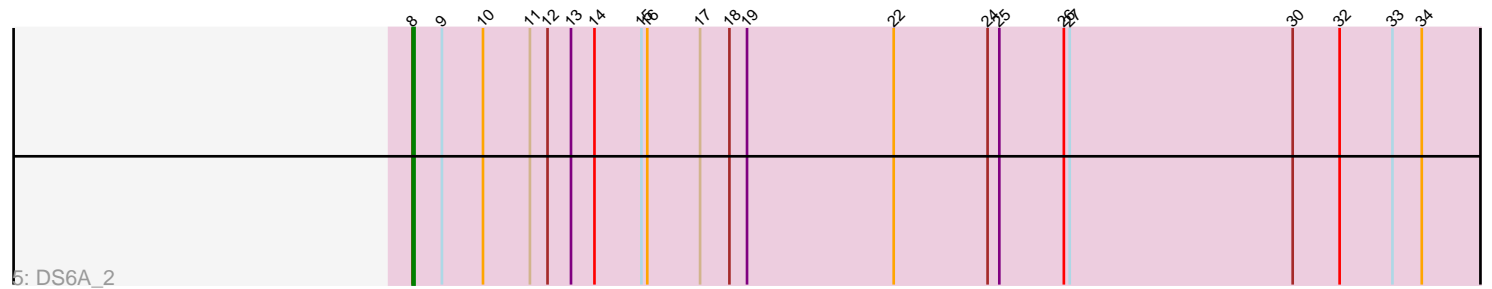
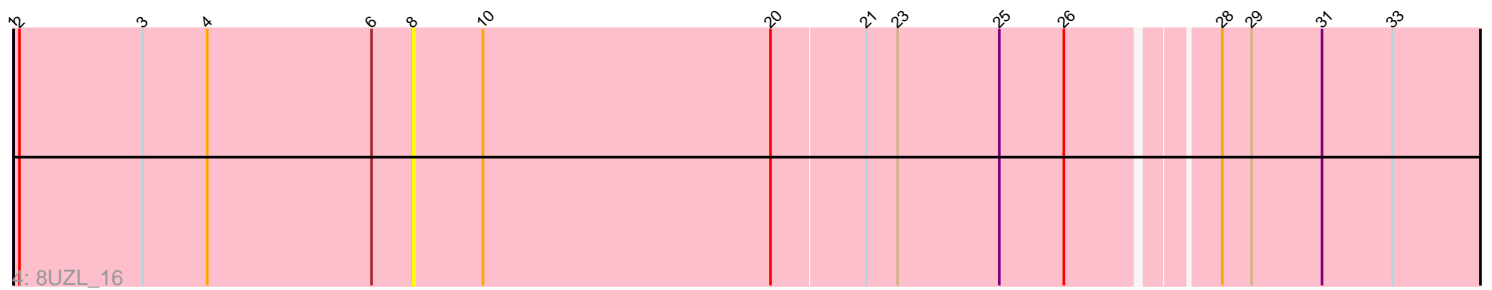
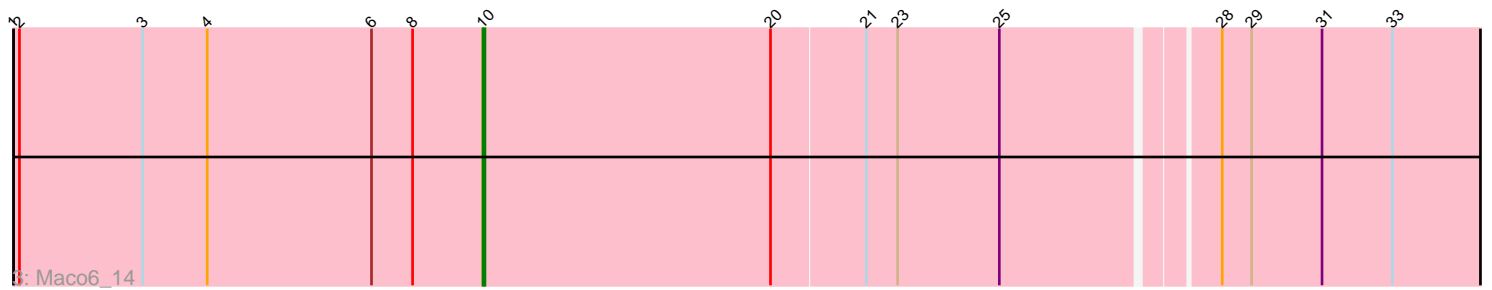
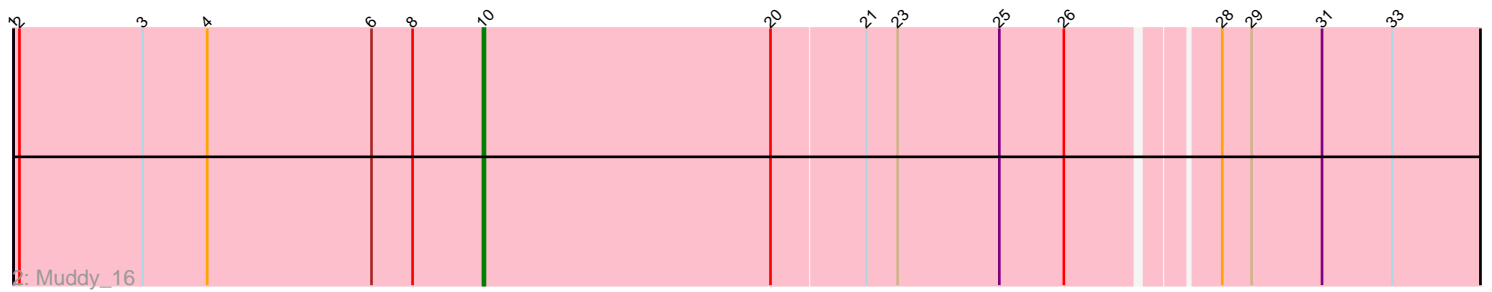
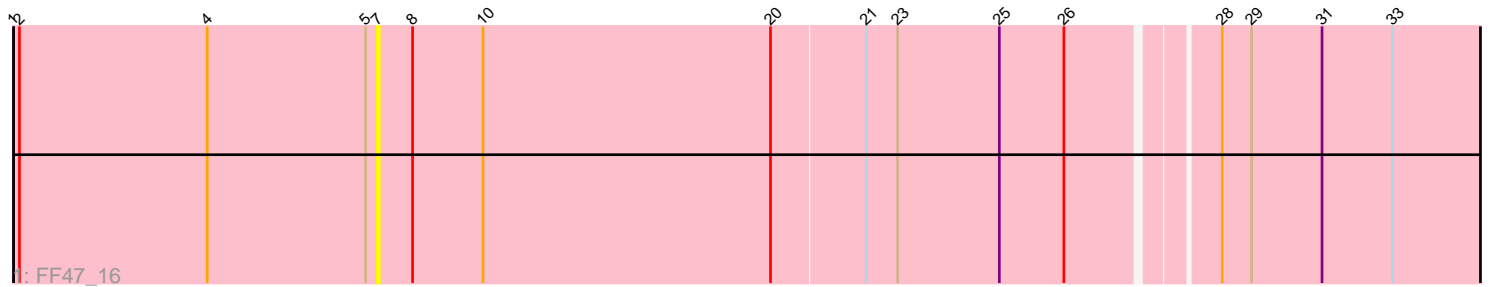


# Pham 8292



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 8292 Report

This analysis was run 04/05/24 on database version 557.

Pham number 8292 has 5 members, 2 are drafts.

Phages represented in each track:

- Track 1 : FF47\_16
- Track 2 : Muddy\_16
- Track 3 : Maco6\_14
- Track 4 : 8UZL\_16
- Track 5 : DS6A\_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 2 of the 3 non-draft genes in the pham.

Genes that call this "Most Annotated" start:

- Maco6\_14, Muddy\_16,

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

- 8UZL\_16, DS6A\_2, FF47\_16,

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

- 

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

Start 7:

- Found in 1 of 5 ( 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: FF47\_16 (AB),

Start 8:

- Found in 5 of 5 ( 100.0% ) of genes in pham
- Manual Annotations of this start: 1 of 3
- Called 40.0% of time when present
- Phage (with cluster) where this start called: 8UZL\_16 (AB), DS6A\_2 (singleton),

Start 10:

- Found in 5 of 5 ( 100.0% ) of genes in pham
- Manual Annotations of this start: 2 of 3
- Called 40.0% of time when present
- Phage (with cluster) where this start called: Maco6\_14 (AB), Muddy\_16 (AB),

### **Summary by clusters:**

There are 2 clusters represented in this pham: singleton, AB,

Info for manual annotations of cluster AB:

- Start number 10 was manually annotated 2 times for cluster AB.

### **Gene Information:**

Gene: 8UZL\_16 Start: 9972, Stop: 10559, Start Num: 8

Candidate Starts for 8UZL\_16:

(1, 9768), (2, 9771), (3, 9834), (4, 9867), (6, 9951), (Start: 8 @9972 has 1 MA's), (Start: 10 @10008 has 2 MA's), (20, 10155), (21, 10200), (23, 10215), (25, 10266), (26, 10299), (28, 10368), (29, 10383), (31, 10419), (33, 10455),

Gene: DS6A\_2 Start: 693, Stop: 1319, Start Num: 8

Candidate Starts for DS6A\_2:

(Start: 8 @693 has 1 MA's), (9, 708), (Start: 10 @729 has 2 MA's), (11, 753), (12, 762), (13, 774), (14, 786), (15, 810), (16, 813), (17, 840), (18, 855), (19, 864), (22, 939), (24, 987), (25, 993), (26, 1026), (27, 1029), (30, 1143), (32, 1167), (33, 1194), (34, 1209),

Gene: FF47\_16 Start: 9920, Stop: 10525, Start Num: 7

Candidate Starts for FF47\_16:

(1, 9734), (2, 9737), (4, 9833), (5, 9914), (7, 9920), (Start: 8 @9938 has 1 MA's), (Start: 10 @9974 has 2 MA's), (20, 10121), (21, 10166), (23, 10181), (25, 10232), (26, 10265), (28, 10334), (29, 10349), (31, 10385), (33, 10421),

Gene: Maco6\_14 Start: 9266, Stop: 9817, Start Num: 10

Candidate Starts for Maco6\_14:

(1, 9026), (2, 9029), (3, 9092), (4, 9125), (6, 9209), (Start: 8 @9230 has 1 MA's), (Start: 10 @9266 has 2 MA's), (20, 9413), (21, 9458), (23, 9473), (25, 9524), (28, 9626), (29, 9641), (31, 9677), (33, 9713),

Gene: Muddy\_16 Start: 10216, Stop: 10767, Start Num: 10

Candidate Starts for Muddy\_16:

(1, 9976), (2, 9979), (3, 10042), (4, 10075), (6, 10159), (Start: 8 @10180 has 1 MA's), (Start: 10 @10216 has 2 MA's), (20, 10363), (21, 10408), (23, 10423), (25, 10474), (26, 10507), (28, 10576), (29, 10591), (31, 10627), (33, 10663),