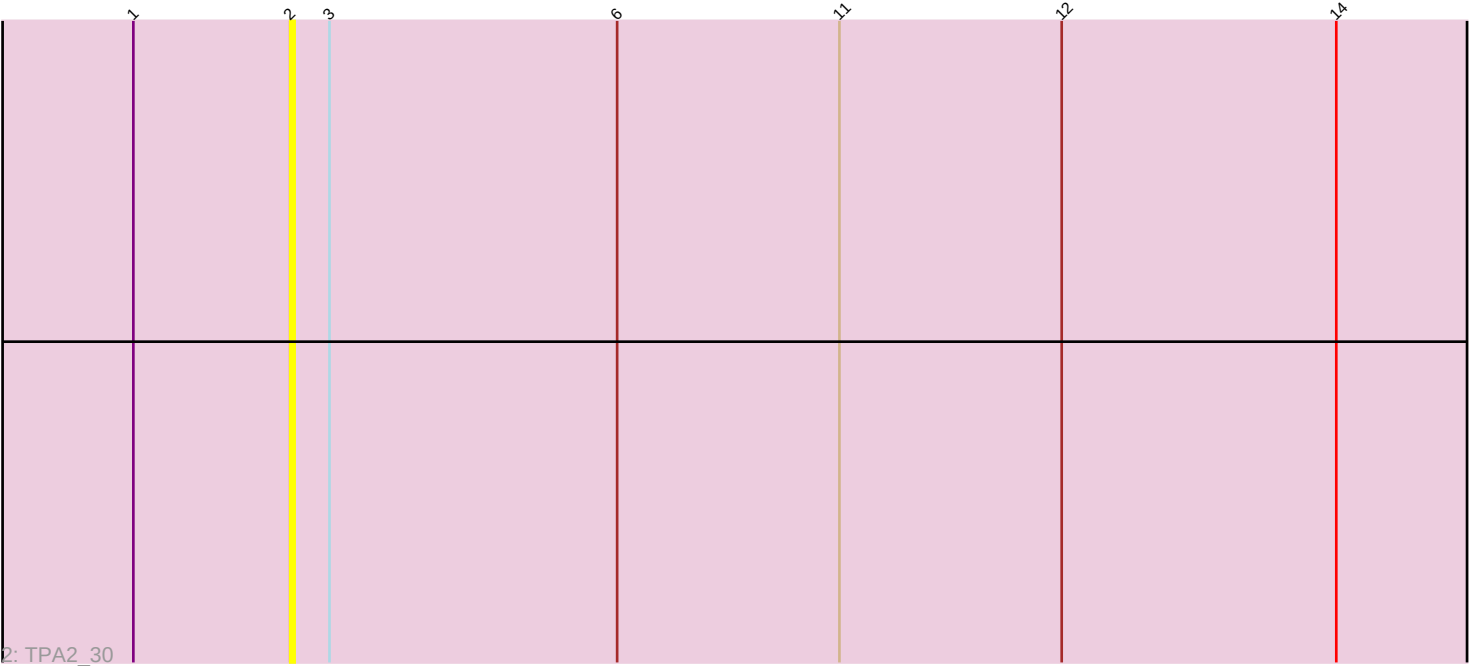
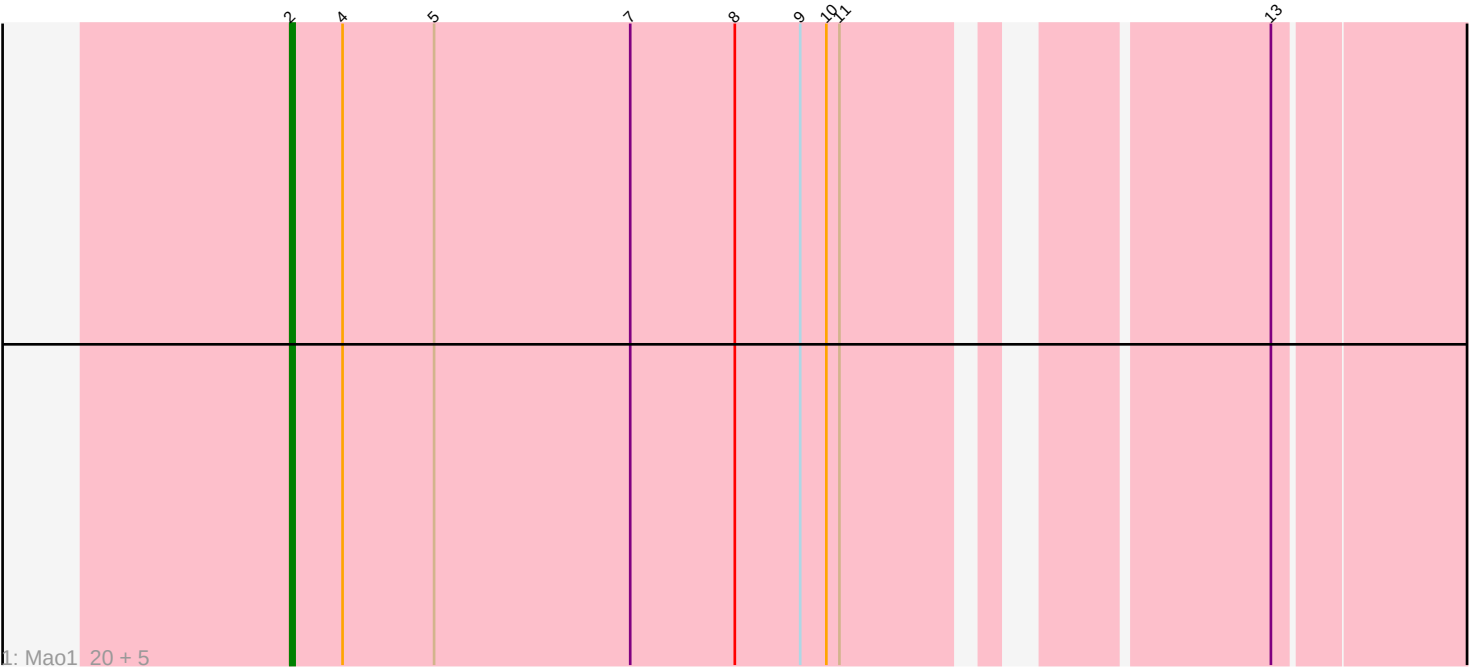




Note: Tracks are now grouped by subcluster and scaled. Switching in subcluster is indicated by changes in track color. Track scale is now set by default to display the region 30 bp upstream of start 1 to 30 bp downstream of the last possible start. If this default region is judged to be packed too tightly 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 325914 Report

This analysis was run 09/05/26 on database version 662.

Pham number 325914 has 7 members, 3 are drafts.

Phages represented in each track:

- Track 1 : Mao1_20, Mask_21, Sejanus_21, JohnLord_21, Dori_21, Caterpie_20
- Track 2 : TPA2_30

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

The start number called the most often in the published annotations is 2, it was called in 4 of the 4 non-draft genes in the pham.

Genes that call this "Most Annotated" start:

- Caterpie_20, Dori_21, JohnLord_21, Mao1_20, Mask_21, Sejanus_21, TPA2_30,

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 2:

- Found in 7 of 7 (100.0%) of genes in pham
- Manual Annotations of this start: 4 of 4
- Called 100.0% of time when present
- Phage (with cluster) where this start called: Caterpie_20 (AD), Dori_21 (AD), JohnLord_21 (AD), Mao1_20 (AD), Mask_21 (AD), Sejanus_21 (AD), TPA2_30 (singleton),

Summary by clusters:

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

Info for manual annotations of cluster AD:

- Start number 2 was manually annotated 4 times for cluster AD.

Gene Information:

Gene: Caterpie_20 Start: 16176, Stop: 16430, Start Num: 2

Candidate Starts for Caterpie_20:

(Start: 2 @16176 has 4 MA's), (4, 16188), (5, 16209), (7, 16254), (8, 16278), (9, 16293), (10, 16299), (11, 16302), (13, 16389),

Gene: Dori_21 Start: 15990, Stop: 16238, Start Num: 2

Candidate Starts for Dori_21:

(Start: 2 @15990 has 4 MA's), (4, 16002), (5, 16023), (7, 16068), (8, 16092), (9, 16107), (10, 16113), (11, 16116), (13, 16197),

Gene: JohnLord_21 Start: 15695, Stop: 15937, Start Num: 2

Candidate Starts for JohnLord_21:

(Start: 2 @15695 has 4 MA's), (4, 15707), (5, 15728), (7, 15773), (8, 15797), (9, 15812), (10, 15818), (11, 15821), (13, 15896),

Gene: Mao1_20 Start: 16386, Stop: 16634, Start Num: 2

Candidate Starts for Mao1_20:

(Start: 2 @16386 has 4 MA's), (4, 16398), (5, 16419), (7, 16464), (8, 16488), (9, 16503), (10, 16509), (11, 16512), (13, 16593),

Gene: Mask_21 Start: 16387, Stop: 16635, Start Num: 2

Candidate Starts for Mask_21:

(Start: 2 @16387 has 4 MA's), (4, 16399), (5, 16420), (7, 16465), (8, 16489), (9, 16504), (10, 16510), (11, 16513), (13, 16594),

Gene: Sejanus_21 Start: 17320, Stop: 17568, Start Num: 2

Candidate Starts for Sejanus_21:

(Start: 2 @17320 has 4 MA's), (4, 17332), (5, 17353), (7, 17398), (8, 17422), (9, 17437), (10, 17443), (11, 17446), (13, 17527),

Gene: TPA2_30 Start: 19273, Stop: 19563, Start Num: 2

Candidate Starts for TPA2_30:

(1, 19237), (Start: 2 @19273 has 4 MA's), (3, 19282), (6, 19348), (11, 19399), (12, 19450), (14, 19513),