

A table with a pink background, a yellow vertical line, and a red vertical line. The table is divided into two rows and three columns. The first column is the narrowest, the second is the widest, and the third is the narrowest. The yellow vertical line is positioned at the start of the second column, and the red vertical line is at the end of the second column.

1: JoyLin_39

A table with a pink background, a yellow vertical line, and a grey vertical bar. The table is divided into two rows and three columns. The first column is the narrowest, the second is the widest, and the third is the narrowest. The yellow vertical line is positioned at the start of the second column, and the grey vertical bar is at the end of the second column.

2: Eevee_39

A table with a pink background, a yellow vertical line, a red vertical line, and a grey vertical bar. The table is divided into two rows and four columns. The first column is the narrowest, the second is the widest, the third is the narrowest, and the fourth is the narrowest. The yellow vertical line is positioned at the start of the second column, the red vertical line is at the end of the second column, and the grey vertical bar is at the end of the third column.

3: Yotsuba_39

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 194855 Report

This analysis was run 11/02/24 on database version 579.

Pham number 194855 has 3 members, 3 are drafts.

Phages represented in each track:

- Track 1 : JoyLin_39
- Track 2 : Eevee_39
- Track 3 : Yotsuba_39

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

This pham is comprised of all draft annotations. There are no annotations to summarize.

Summary by start number:

Start 1:

- Found in 3 of 3 (100.0%) of genes in pham
- No Manual Annotations of this start.
- Called 100.0% of time when present
- Phage (with cluster) where this start called: Eevee_39 (JA), JoyLin_39 (JA), Yotsuba_39 (JA),

Summary by clusters:

There is one cluster represented in this pham: JA

Gene Information:

Gene: Eevee_39 Start: 31180, Stop: 31341, Start Num: 1

Candidate Starts for Eevee_39:

(1, 31180),

Gene: JoyLin_39 Start: 31279, Stop: 31461, Start Num: 1

Candidate Starts for JoyLin_39:

(1, 31279), (2, 31432),

Gene: Yotsuba_39 Start: 31297, Stop: 31479, Start Num: 1

Candidate Starts for Yotsuba_39:
(1, 31297), (2, 31450),