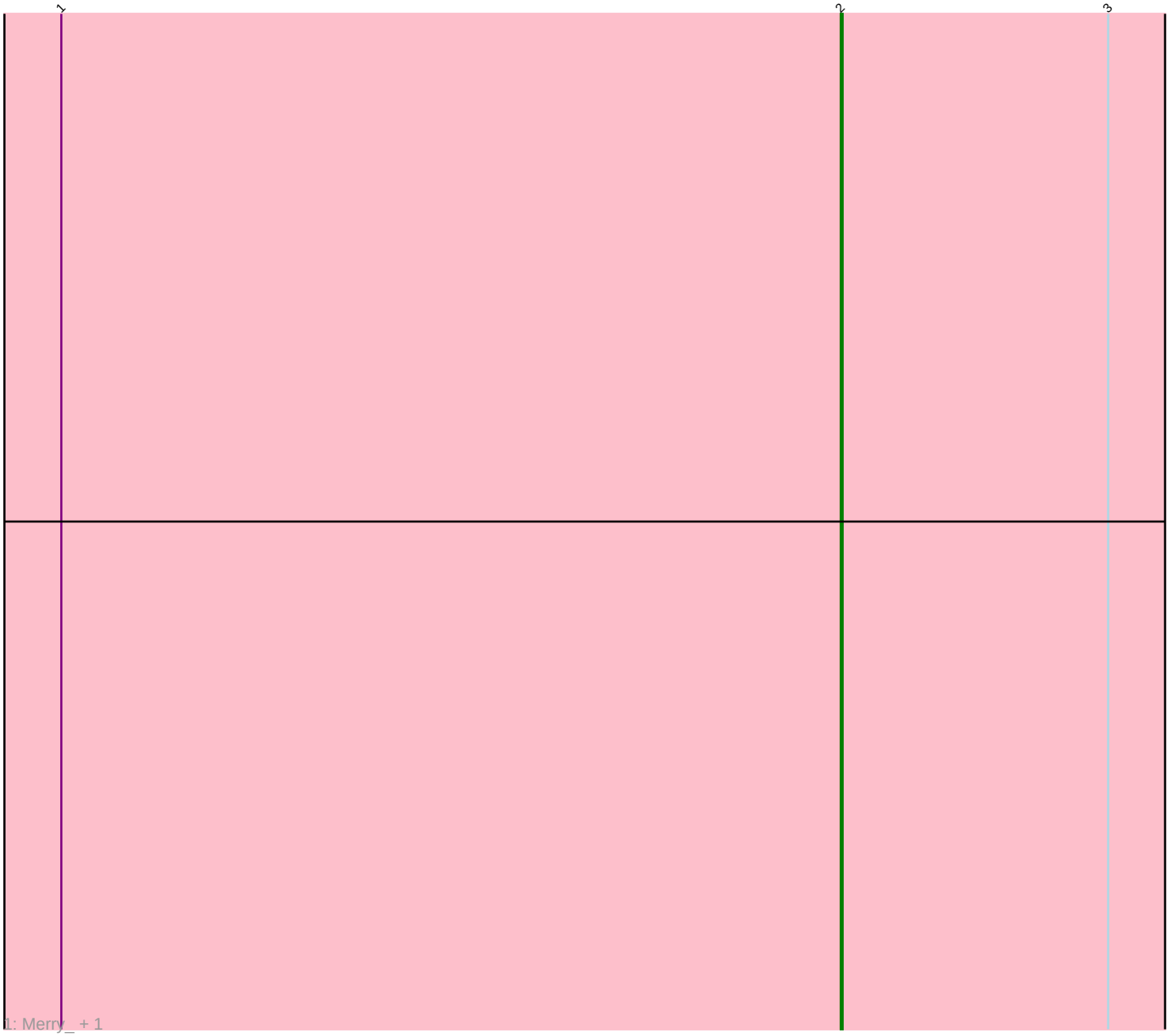
Pham 348645



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 348645 Report

This analysis was run 11/14/26 on database version 672.

Pham number 348645 has 2 members, 0 are drafts.

Phages represented in each track:
• Track 1 : Merry_, Sunny_

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 2 of the 2 non-draft genes in the pham.

Genes that call this "Most Annotated" start:
• Merry_, Sunny_,

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 2 of 2 (100.0%) of genes in pham
• Manual Annotations of this start: 2 of 2
• Called 100.0% of time when present
• Phage (with cluster) where this start called: Merry_ (EC), Sunny_ (EC),

Summary by clusters:

There is one cluster represented in this pham: EC

Info for manual annotations of cluster EC:
•Start number 2 was manually annotated 2 times for cluster EC.

Gene Information:

Gene: Merry_ Start: 33793, Stop: 33966, Start Num: 2
Candidate Starts for Merry_:
(1, 33382), (Start: 2 @33793 has 2 MA's), (3, 33934),

Gene: Sunny_ Start: 33795, Stop: 33968, Start Num: 2
Candidate Starts for Sunny_:
(1, 33384), (Start: 2 @33795 has 2 MA's), (3, 33936),