

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 88553 Report

This analysis was run 04/28/24 on database version 559.

WARNING: Pham size does not match number of genes in report. Either unphamerated genes have been added (by you) or starterator has removed genes due to invalid start codon.

Pham number 88553 has 5 members, 1 are drafts.

Phages represented in each track:

Track 1 : Lilbooboo\_39
Track 2 : Samora\_40
Track 3 : TG1\_35
Track 4 : Vash\_38
Track 5 : Euratis 40

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

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

Genes that call this "Most Annotated" start:

Euratis\_40, Samora\_40, Vash\_38,

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

• Lilbooboo 39.

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

• TG1\_35,

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

#### Start 4:

- Found in 4 of 5 (80.0%) of genes in pham
- Manual Annotations of this start: 2 of 4
- Called 75.0% of time when present
- Phage (with cluster) where this start called: Euratis\_40 (BB1), Samora\_40 (BB1), Vash\_38 (BB1),

#### Start 5:

- Found in 2 of 5 (40.0%) of genes in pham
- Manual Annotations of this start: 2 of 4
- Called 100.0% of time when present
- Phage (with cluster) where this start called: Lilbooboo\_39 (BB1), TG1\_35 (BB1),

## **Summary by clusters:**

There is one cluster represented in this pham: BB1

Info for manual annotations of cluster BB1:

- •Start number 4 was manually annotated 2 times for cluster BB1.
- •Start number 5 was manually annotated 2 times for cluster BB1.

#### Gene Information:

Gene: Euratis\_40 Start: 31187, Stop: 31504, Start Num: 4

Candidate Starts for Euratis 40:

(1, 31121), (2, 31142), (Start: 4 @31187 has 2 MA's), (9, 31253), (10, 31307), (11, 31310),

Gene: Lilbooboo 39 Start: 31323, Stop: 31640, Start Num: 5

Candidate Starts for Lilbooboo 39:

(1, 31236), (3, 31305), (Start: 4 @31320 has 2 MA's), (Start: 5 @31323 has 2 MA's), (8, 31374), (10, 31440), (11, 31443), (14, 31599), (15, 31623),

Gene: Samora\_40 Start: 31892, Stop: 32212, Start Num: 4

Candidate Starts for Samora\_40:

(1, 31811), (Start: 4 @31892 has 2 MA's), (6, 31901), (8, 31946), (9, 31958), (10, 32012), (11, 32015), (13, 32081), (14, 32171), (15, 32195),

Gene: TG1 35 Start: 30127, Stop: 30423, Start Num: 5

Candidate Starts for TG1 35:

(Start: 5 @30127 has 2 MA's), (7, 30154), (8, 30178), (9, 30190), (10, 30244), (11, 30247), (12, 30271),

Gene: Vash\_38 Start: 31133, Stop: 31453, Start Num: 4

Candidate Starts for Vash\_38:

(1, 31055), (Start: 4 @ 31133 has 2 MA's), (9, 31199), (10, 31253), (11, 31256), (14, 31412),