Pham 167175

	Ŷ		10	
1: Shawty_35				
	r	<u>ر</u> ې	<i>1</i> 0 <i>1</i>	2
2: Euratis_38	0.		6	8
	<u>ې</u>		<i>1</i> 0	~∞
B: TG1_33				
	Ŷ	<u>ر</u> ې	<u>,</u> 6	P
4: Vash_36				
	<del>ې</del>	<i>\$</i> 9	40 V	<i>ب</i> ه
5: Samola_38	0.	<u>к</u>	6 1	
5: Samota_38	Ŷ	,¢	,⊚ ,1	
~~	रू •		<b>,⊚ ,1</b>	
	х 	× 	~~ ~1	
6: phiBT1_13				
6: phiBT1_13	2 	×	<b>.</b> 0	
B: phiBT1_13   Image: Control of the second seco				,°
6: phiBT1_13	2 	×	<b>.</b> 0	
6: phiBT1_13	2 	×	<b>.</b> 0	
5: phiBT1_13		,3 	<b>.</b> 0	,°
6: phiBT1_13		,3 	<b>.</b> 0	,°
6: phiBT1_13     7: Lilbooboo_36     8: Heather_40		,3 	<b>.</b> 0	,°
S: phiBT1_13   7: Lilbooboo_36   8: Heather_40   9: RemusLoopin_39		,3 		

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 167175 Report

This analysis was run 07/09/24 on database version 566.

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 167175 has 10 members, 2 are drafts.

Phages represented in each track:

- Track 1 : Shawty\_35
- Track 2 : Euratis\_38
- Track 3 : TG1\_33
- Track 4 : Vash\_36
- Track 5 : Samora\_38
- Track 6 : phiBT1\_13
- Track 7 : Lilbooboo\_36
- Track 8 : Heather\_40
- Track 9 : RemusLoopin\_39
- Track 10 : Sebastisaurus\_38

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

The start number called the most often in the published annotations is 12, it was called in 8 of the 8 non-draft genes in the pham.

Genes that call this "Most Annotated" start:

• Euratis\_38, Heather\_40, Lilbooboo\_36, RemusLoopin\_39, Samora\_38, Sebastisaurus\_38, Shawty\_35, TG1\_33, Vash\_36, phiBT1\_13,

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 12:

• Found in 10 of 10 (100.0%) of genes in pham

- Manual Annotations of this start: 8 of 8
- Called 100.0% of time when present

• Phage (with cluster) where this start called: Euratis\_38 (BB1), Heather\_40 (BB2), Lilbooboo\_36 (BB1), RemusLoopin\_39 (BB2), Samora\_38 (BB1), Sebastisaurus\_38 (BB2), Shawty\_35 (BB1), TG1\_33 (BB1), Vash\_36 (BB1), phiBT1\_13 (BB1),

### Summary by clusters:

There are 2 clusters represented in this pham: BB2, BB1,

Info for manual annotations of cluster BB1: •Start number 12 was manually annotated 5 times for cluster BB1.

Info for manual annotations of cluster BB2: •Start number 12 was manually annotated 3 times for cluster BB2.

### Gene Information:

Gene: Euratis\_38 Start: 30425, Stop: 30595, Start Num: 12 Candidate Starts for Euratis\_38: (Start: 12 @30425 has 8 MA's), (13, 30473), (16, 30521), (17, 30533), (20, 30575),

Gene: Heather\_40 Start: 31685, Stop: 31888, Start Num: 12 Candidate Starts for Heather\_40: (3, 31520), (5, 31529), (Start: 12 @31685 has 8 MA's), (14, 31748), (17, 31799), (19, 31829),

Gene: Lilbooboo\_36 Start: 30535, Stop: 30708, Start Num: 12 Candidate Starts for Lilbooboo\_36: (2, 30349), (4, 30382), (6, 30394), (Start: 12 @30535 has 8 MA's), (13, 30583), (16, 30634), (18, 30670),

Gene: RemusLoopin\_39 Start: 31906, Stop: 32109, Start Num: 12 Candidate Starts for RemusLoopin\_39: (Start: 12 @31906 has 8 MA's), (14, 31969), (19, 32050),

Gene: Samora\_38 Start: 31106, Stop: 31279, Start Num: 12 Candidate Starts for Samora\_38: (1, 30887), (Start: 12 @31106 has 8 MA's), (13, 31154), (16, 31205), (17, 31217), (18, 31241),

Gene: Sebastisaurus\_38 Start: 31594, Stop: 31797, Start Num: 12 Candidate Starts for Sebastisaurus\_38: (7, 31486), (8, 31492), (9, 31513), (11, 31534), (Start: 12 @31594 has 8 MA's), (16, 31696), (17, 31708), (19, 31738),

Gene: Shawty\_35 Start: 30307, Stop: 30474, Start Num: 12 Candidate Starts for Shawty\_35: (Start: 12 @30307 has 8 MA's), (16, 30400),

Gene: TG1\_33 Start: 29448, Stop: 29615, Start Num: 12 Candidate Starts for TG1\_33: (Start: 12 @29448 has 8 MA's), (16, 29541), (18, 29577), Gene: Vash\_36 Start: 30357, Stop: 30527, Start Num: 12 Candidate Starts for Vash\_36: (Start: 12 @30357 has 8 MA's), (13, 30405), (16, 30453), (20, 30507),

Gene: phiBT1\_13 Start: 31817, Stop: 31984, Start Num: 12 Candidate Starts for phiBT1\_13: (10, 31751), (Start: 12 @31817 has 8 MA's), (15, 31886), (16, 31910), (17, 31922),