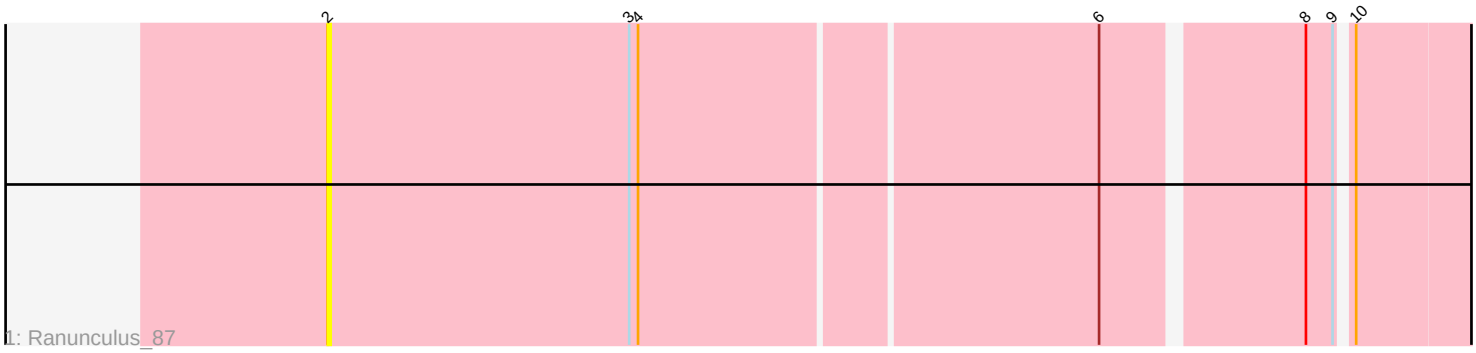
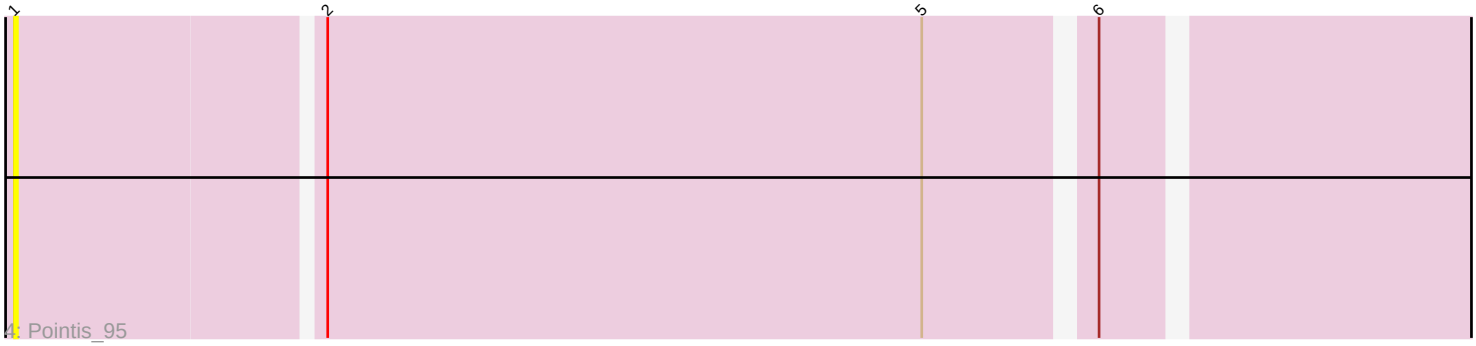
Pham 9084


2
3
4
6
8
9
10
1: Ranunculus_87


1
2
5
6
7
3: Pureglobe5_98


1
2
5
6
11
3: MellowYellow_96 + 2


1
2
5
6
4: Pointis_95

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 9084 Report

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

Pham number 9084 has 6 members, 3 are drafts.

Phages represented in each track:
• Track 1 : Ranunculus_87
• Track 2 : Pureglobe5_98
• Track 3 : MellowYellow_96, Odyssey395_98, Beagle_100
• Track 4 : Pointis_95

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

The start number called the most often in the published annotations is 1, it was called in 3 of the 3 non-draft genes in the pham.

Genes that call this "Most Annotated" start:
• Beagle_100, MellowYellow_96, Odyssey395_98, Pointis_95, Pureglobe5_98,

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

Genes that do not have the "Most Annotated" start:
• Ranunculus_87,

Summary by start number:

Start 1:
• Found in 5 of 6 (83.3%) of genes in pham
• Manual Annotations of this start: 3 of 3
• Called 100.0% of time when present
• Phage (with cluster) where this start called: Beagle_100 (AP2), MellowYellow_96 (AP2), Odyssey395_98 (AP2), Pointis_95 (AP2), Pureglobe5_98 (AP2),

Start 2:
• Found in 6 of 6 (100.0%) of genes in pham
• No Manual Annotations of this start.
• Called 16.7% of time when present
• Phage (with cluster) where this start called: Ranunculus_87 (AP),

Summary by clusters:

There are 2 clusters represented in this pham: AP2, AP,

Info for manual annotations of cluster AP2:
•Start number 1 was manually annotated 3 times for cluster AP2.

Gene Information:

Gene: Beagle_100 Start: 58664, Stop: 58173, Start Num: 1
Candidate Starts for Beagle_100:
(Start: 1 @58664 has 3 MA's), (2, 58565), (5, 58364), (6, 58313), (11, 58226),

Gene: MellowYellow_96 Start: 58279, Stop: 57788, Start Num: 1
Candidate Starts for MellowYellow_96:
(Start: 1 @58279 has 3 MA's), (2, 58180), (5, 57979), (6, 57928), (11, 57841),

Gene: Odyssey395_98 Start: 58059, Stop: 57568, Start Num: 1
Candidate Starts for Odyssey395_98:
(Start: 1 @58059 has 3 MA's), (2, 57960), (5, 57759), (6, 57708), (11, 57621),

Gene: Pointis_95 Start: 57955, Stop: 57464, Start Num: 1
Candidate Starts for Pointis_95:
(Start: 1 @57955 has 3 MA's), (2, 57856), (5, 57655), (6, 57604),

Gene: Pureglobe5_98 Start: 58620, Stop: 58126, Start Num: 1
Candidate Starts for Pureglobe5_98:
(Start: 1 @58620 has 3 MA's), (2, 58521), (5, 58320), (6, 58275), (7, 58254),

Gene: Ranunculus_87 Start: 58807, Stop: 58421, Start Num: 2
Candidate Starts for Ranunculus_87:
(2, 58807), (3, 58705), (4, 58702), (6, 58552), (8, 58489), (9, 58480), (10, 58477),