Pham 7210

1: Ranunculus_77

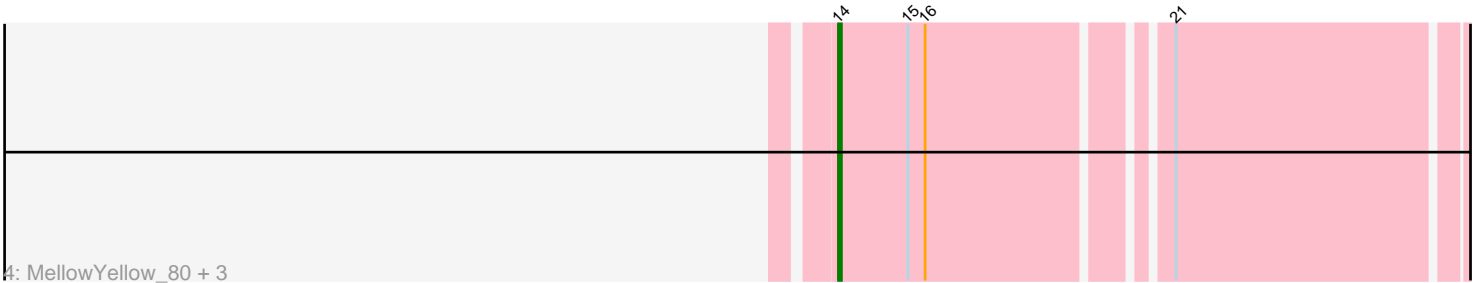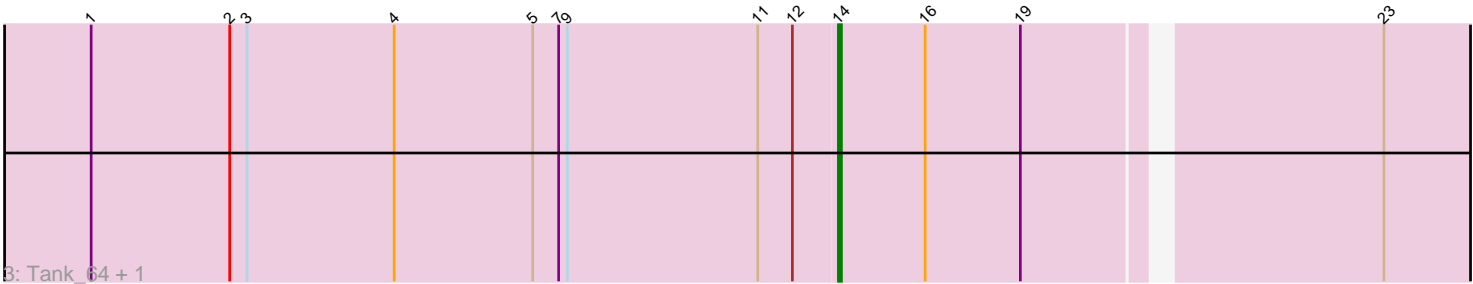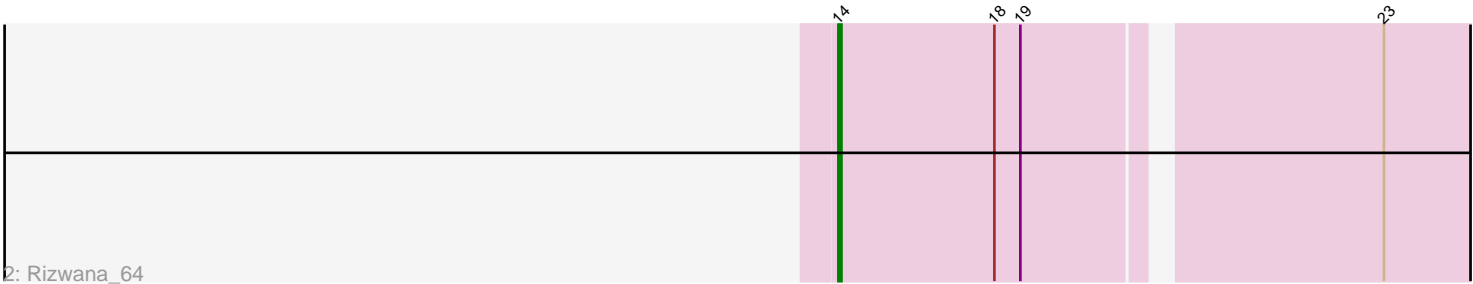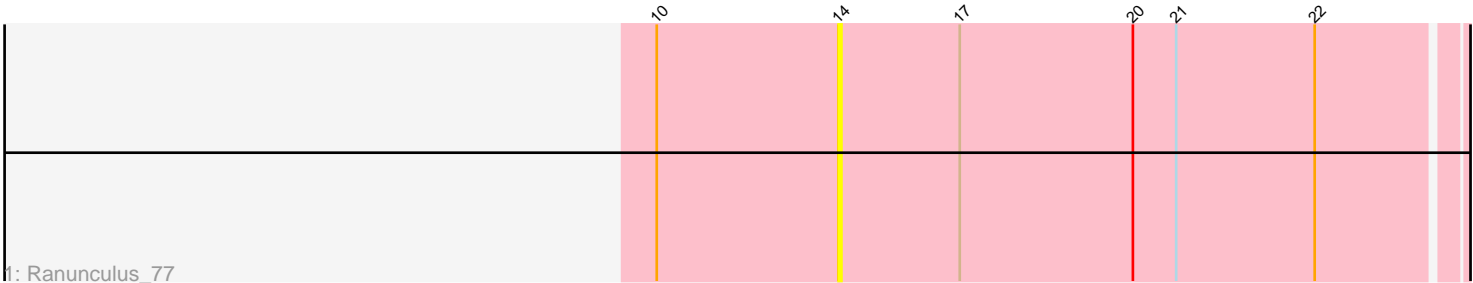2: Rizwana_64

3: Tank_64 + 1

4: MellowYellow_80 + 3

5: Beagle_84

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 7210 Report

This analysis was run 04/05/24 on database version 557.

Pham number 7210 has 9 members, 3 are drafts.

Phages represented in each track:
• Track 1 : Ranunculus_77
• Track 2 : Rizwana_64
• Track 3 : Tank_64, Wilde_66
• Track 4 : MellowYellow_80, Odyssey395_84, Pointis_79, Pureglobe5_82
• Track 5 : Beagle_84

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

The start number called the most often in the published annotations is 14, it was called in 6 of the 6 non-draft genes in the pham.

Genes that call this "Most Annotated" start:
• Beagle_84, MellowYellow_80, Odyssey395_84, Pointis_79, Pureglobe5_82, Ranunculus_77, Rizwana_64, Tank_64, Wilde_66,

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 14:
• Found in 9 of 9 (100.0%) of genes in pham
• Manual Annotations of this start: 6 of 6
• Called 100.0% of time when present
• Phage (with cluster) where this start called: Beagle_84 (AP2), MellowYellow_80 (AP2), Odyssey395_84 (AP2), Pointis_79 (AP2), Pureglobe5_82 (AP2), Ranunculus_77 (AP), Rizwana_64 (AP1), Tank_64 (AP1), Wilde_66 (AP1),

Summary by clusters:

There are 3 clusters represented in this pham: AP2, AP, AP1,

Info for manual annotations of cluster AP1:
•Start number 14 was manually annotated 3 times for cluster AP1.

Info for manual annotations of cluster AP2:
•Start number 14 was manually annotated 3 times for cluster AP2.

Gene Information:

Gene: Beagle_84 Start: 49755, Stop: 49549, Start Num: 14
Candidate Starts for Beagle_84:
(6, 49848), (8, 49845), (13, 49758), (Start: 14 @49755 has 6 MA's), (15, 49731), (16, 49725), (21, 49650),

Gene: MellowYellow_80 Start: 49883, Stop: 49677, Start Num: 14
Candidate Starts for MellowYellow_80:
(Start: 14 @49883 has 6 MA's), (15, 49859), (16, 49853), (21, 49778),

Gene: Odyssey395_84 Start: 49992, Stop: 49786, Start Num: 14
Candidate Starts for Odyssey395_84:
(Start: 14 @49992 has 6 MA's), (15, 49968), (16, 49962), (21, 49887),

Gene: Pointis_79 Start: 49568, Stop: 49362, Start Num: 14
Candidate Starts for Pointis_79:
(Start: 14 @49568 has 6 MA's), (15, 49544), (16, 49538), (21, 49463),

Gene: Pureglobe5_82 Start: 50015, Stop: 49809, Start Num: 14
Candidate Starts for Pureglobe5_82:
(Start: 14 @50015 has 6 MA's), (15, 49991), (16, 49985), (21, 49910),

Gene: Ranunculus_77 Start: 52321, Stop: 52103, Start Num: 14
Candidate Starts for Ranunculus_77:
(10, 52384), (Start: 14 @52321 has 6 MA's), (17, 52279), (20, 52219), (21, 52204), (22, 52156),

Gene: Rizwana_64 Start: 46358, Stop: 46125, Start Num: 14
Candidate Starts for Rizwana_64:
(Start: 14 @46358 has 6 MA's), (18, 46304), (19, 46295), (23, 46181),

Gene: Tank_64 Start: 46354, Stop: 46121, Start Num: 14
Candidate Starts for Tank_64:
(1, 46612), (2, 46564), (3, 46558), (4, 46507), (5, 46459), (7, 46450), (9, 46447), (11, 46381), (12, 46369), (Start: 14 @46354 has 6 MA's), (16, 46324), (19, 46291), (23, 46177),

Gene: Wilde_66 Start: 46653, Stop: 46420, Start Num: 14
Candidate Starts for Wilde_66:
(1, 46911), (2, 46863), (3, 46857), (4, 46806), (5, 46758), (7, 46749), (9, 46746), (11, 46680), (12, 46668), (Start: 14 @46653 has 6 MA's), (16, 46623), (19, 46590), (23, 46476),