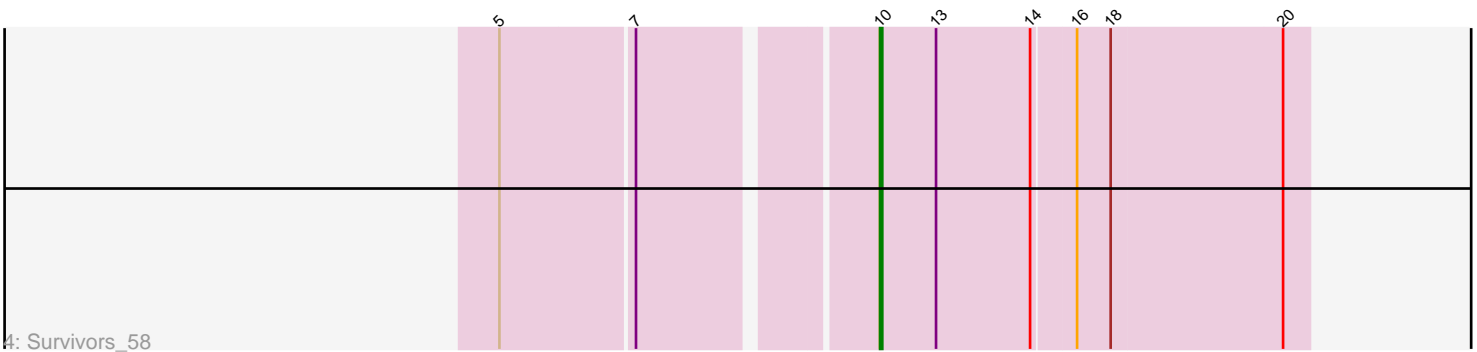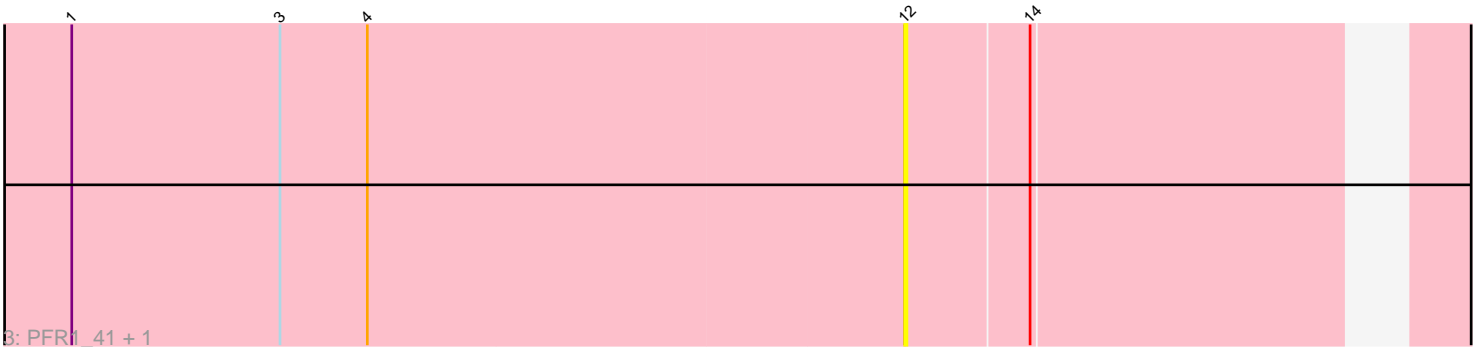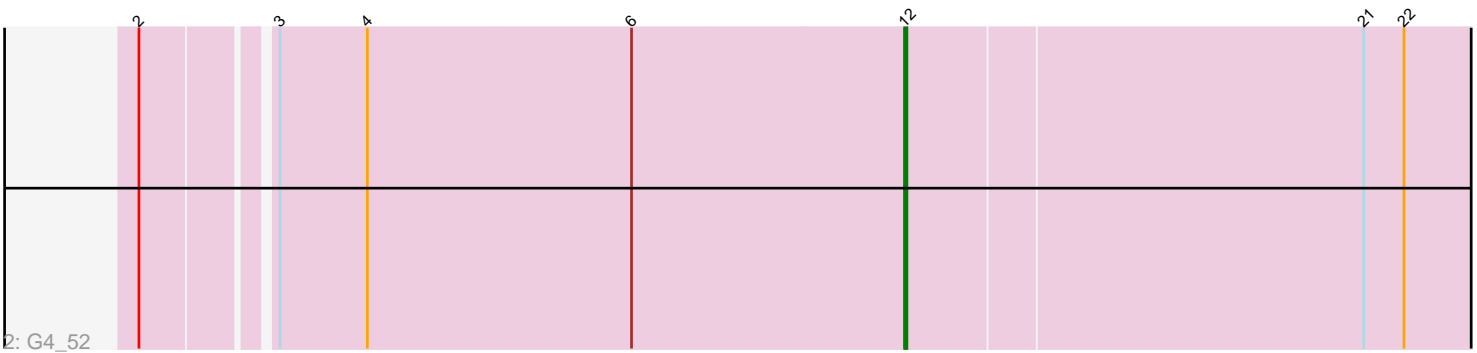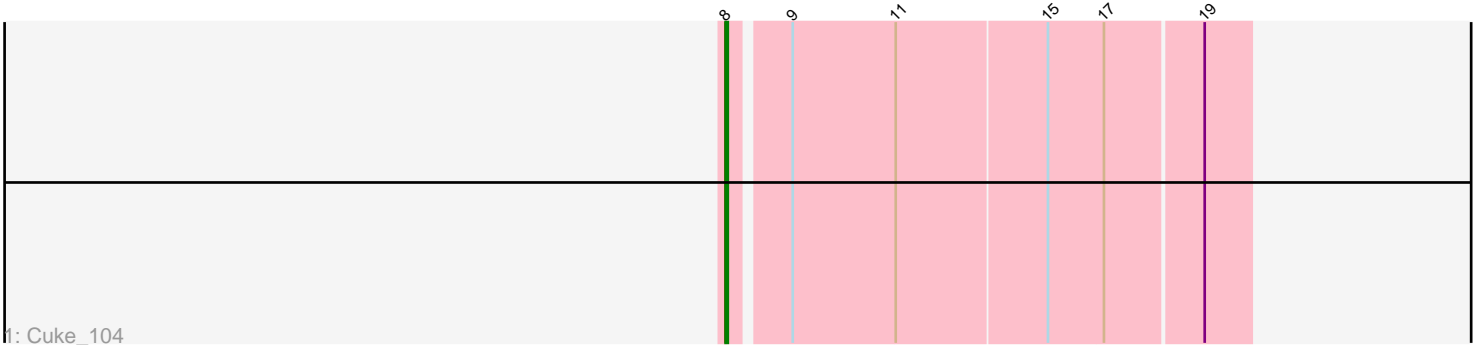# Pham 8317

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 8317 Report

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

Pham number 8317 has 5 members, 2 are drafts.

Phages represented in each track:
• Track 1 : Cuke_104
• Track 2 : G4_52
• Track 3 : PFR1_41, PFR2_43
• Track 4 : Survivors_58

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

The start number called the most often in the published annotations is 10, it was called in 1 of the 3 non-draft genes in the pham.

Genes that call this "Most Annotated" start:
• Survivors_58,

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

Genes that do not have the "Most Annotated" start:
• Cuke_104, G4_52, PFR1_41, PFR2_43,

Summary by start number:

Start 8:
• Found in 1 of 5 (20.0%) of genes in pham
• Manual Annotations of this start: 1 of 3
• Called 100.0% of time when present
• Phage (with cluster) where this start called: Cuke_104 (AC),

Start 10:
• Found in 1 of 5 (20.0%) of genes in pham
• Manual Annotations of this start: 1 of 3
• Called 100.0% of time when present
• Phage (with cluster) where this start called: Survivors_58 (CT),

Start 12:

• Found in 3 of 5 (60.0%) of genes in pham
• Manual Annotations of this start: 1 of 3
• Called 100.0% of time when present
• Phage (with cluster) where this start called: G4_52 (BW), PFR1_41 (BX), PFR2_43 (BX),

Summary by clusters:

There are 4 clusters represented in this pham: AC, BW, BX, CT,

Info for manual annotations of cluster AC:
•Start number 8 was manually annotated 1 time for cluster AC.

Info for manual annotations of cluster BW:
•Start number 12 was manually annotated 1 time for cluster BW.

Info for manual annotations of cluster CT:
•Start number 10 was manually annotated 1 time for cluster CT.

Gene Information:
Gene: Cuke_104 Start: 58088, Stop: 58309, Start Num: 8
Candidate Starts for Cuke_104:
(Start: 8 @58088 has 1 MA's), (9, 58112), (11, 58157), (15, 58223), (17, 58247), (19, 58289),

Gene: G4_52 Start: 31728, Stop: 31997, Start Num: 12
Candidate Starts for G4_52:
(2, 31401), (3, 31452), (4, 31491), (6, 31608), (Start: 12 @31728 has 1 MA's), (21, 31929), (22, 31947),

Gene: PFR1_41 Start: 30224, Stop: 30463, Start Num: 12
Candidate Starts for PFR1_41:
(1, 29855), (3, 29948), (4, 29987), (Start: 12 @30224 has 1 MA's), (14, 30278),

Gene: PFR2_43 Start: 31793, Stop: 32032, Start Num: 12
Candidate Starts for PFR2_43:
(1, 31424), (3, 31517), (4, 31556), (Start: 12 @31793 has 1 MA's), (14, 31847),

Gene: Survivors_58 Start: 42125, Stop: 42310, Start Num: 10
Candidate Starts for Survivors_58:
(5, 41972), (7, 42029), (Start: 10 @42125 has 1 MA's), (13, 42149), (14, 42191), (16, 42209), (18, 42224), (20, 42299),