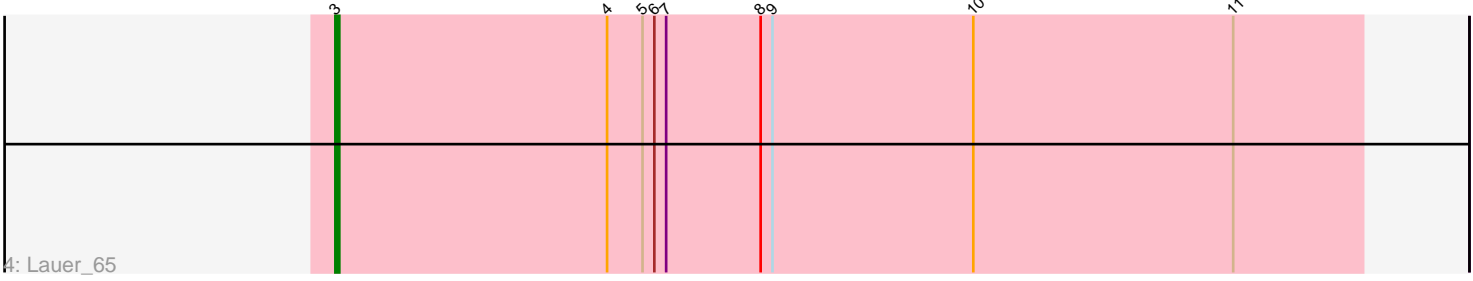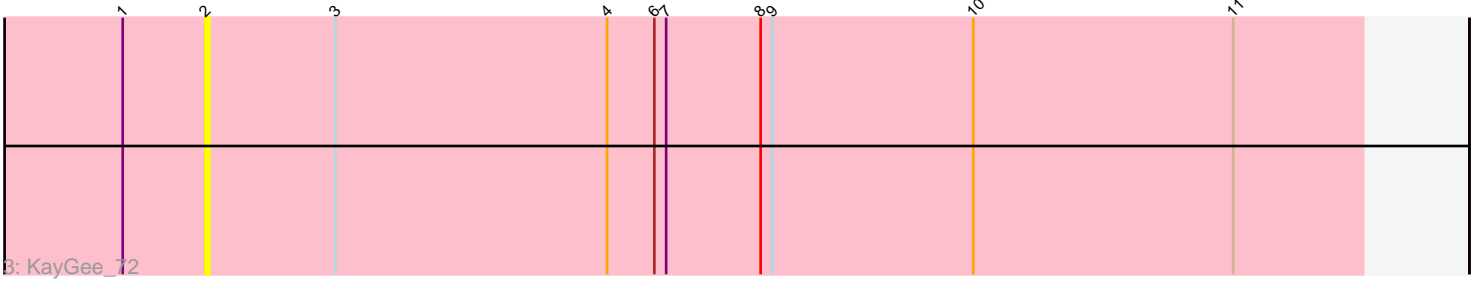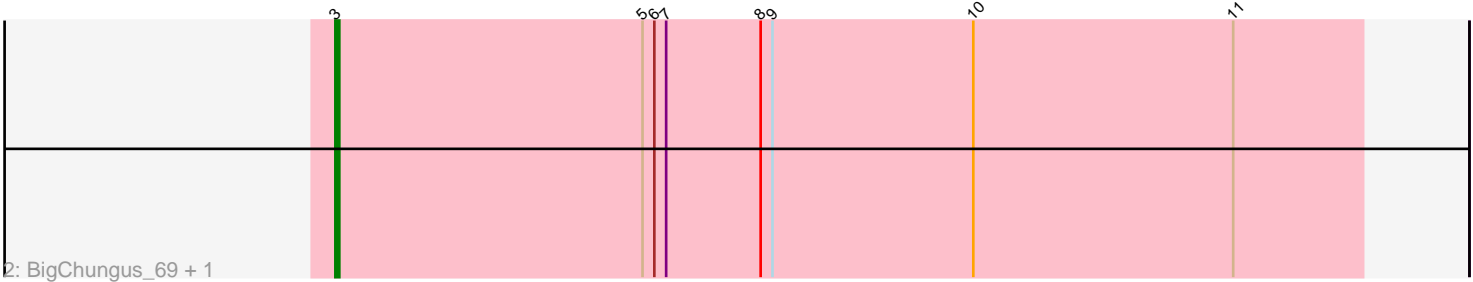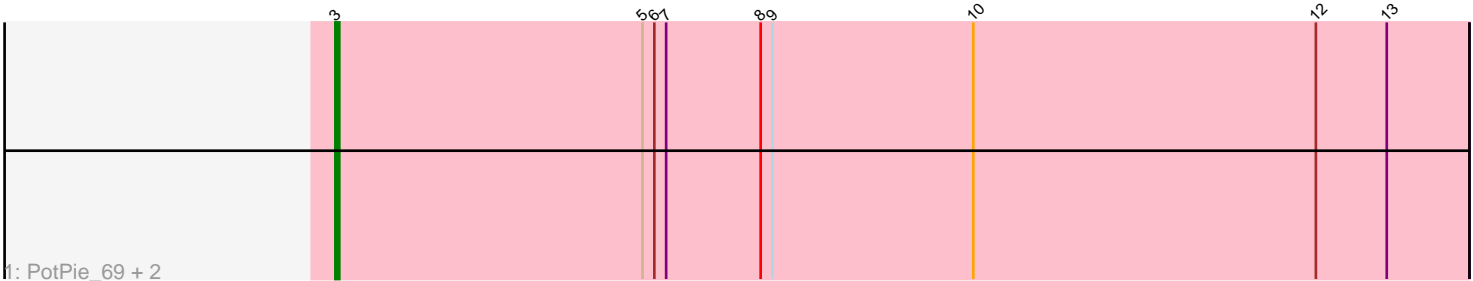# Pham 7104

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 7104 Report

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

Pham number 7104 has 8 members, 2 are drafts.

Phages represented in each track:
• Track 1 : PotPie_69, Vine_73, SummitAcademy_70
• Track 2 : BigChungus_69, Feastonyeet_69
• Track 3 : KayGee_72
• Track 4 : Lauer_65
• Track 5 : Elinal_75

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

The start number called the most often in the published annotations is 3, it was called in 6 of the 6 non-draft genes in the pham.

Genes that call this "Most Annotated" start:
• BigChungus_69, Elinal_75, Feastonyeet_69, Lauer_65, PotPie_69, SummitAcademy_70, Vine_73,

Genes that have the "Most Annotated" start but do not call it:
• KayGee_72,

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

Summary by start number:

Start 2:
• Found in 2 of 8 (25.0%) of genes in pham
• No Manual Annotations of this start.
• Called 50.0% of time when present
• Phage (with cluster) where this start called: KayGee_72 (CT),

Start 3:
• Found in 8 of 8 (100.0%) of genes in pham
• Manual Annotations of this start: 6 of 6
• Called 87.5% of time when present

• Phage (with cluster) where this start called: BigChungus_69 (CT), Elinal_75 (CT), Feastonyeet_69 (CT), Lauer_65 (CT), PotPie_69 (CT), SummitAcademy_70 (CT), Vine_73 (CT),

Summary by clusters:

There is one cluster represented in this pham: CT

Info for manual annotations of cluster CT:
•Start number 3 was manually annotated 6 times for cluster CT.

Gene Information:

Gene: BigChungus_69 Start: 46258, Stop: 46518, Start Num: 3
Candidate Starts for BigChungus_69:
(Start: 3 @46258 has 6 MA's), (5, 46336), (6, 46339), (7, 46342), (8, 46366), (9, 46369), (10, 46420), (11, 46486),

Gene: Elinal_75 Start: 47372, Stop: 47632, Start Num: 3
Candidate Starts for Elinal_75:
(1, 47318), (2, 47339), (Start: 3 @47372 has 6 MA's), (4, 47441), (6, 47453), (7, 47456), (8, 47480), (9, 47483), (10, 47534), (11, 47600),

Gene: Feastonyeet_69 Start: 46258, Stop: 46518, Start Num: 3
Candidate Starts for Feastonyeet_69:
(Start: 3 @46258 has 6 MA's), (5, 46336), (6, 46339), (7, 46342), (8, 46366), (9, 46369), (10, 46420), (11, 46486),

Gene: KayGee_72 Start: 47326, Stop: 47619, Start Num: 2
Candidate Starts for KayGee_72:
(1, 47305), (2, 47326), (Start: 3 @47359 has 6 MA's), (4, 47428), (6, 47440), (7, 47443), (8, 47467), (9, 47470), (10, 47521), (11, 47587),

Gene: Lauer_65 Start: 47203, Stop: 47463, Start Num: 3
Candidate Starts for Lauer_65:
(Start: 3 @47203 has 6 MA's), (4, 47272), (5, 47281), (6, 47284), (7, 47287), (8, 47311), (9, 47314), (10, 47365), (11, 47431),

Gene: PotPie_69 Start: 47272, Stop: 47559, Start Num: 3
Candidate Starts for PotPie_69:
(Start: 3 @47272 has 6 MA's), (5, 47350), (6, 47353), (7, 47356), (8, 47380), (9, 47383), (10, 47434), (12, 47521), (13, 47539),

Gene: SummitAcademy_70 Start: 46415, Stop: 46702, Start Num: 3
Candidate Starts for SummitAcademy_70:
(Start: 3 @46415 has 6 MA's), (5, 46493), (6, 46496), (7, 46499), (8, 46523), (9, 46526), (10, 46577), (12, 46664), (13, 46682),

Gene: Vine_73 Start: 47104, Stop: 47391, Start Num: 3
Candidate Starts for Vine_73:

(Start: 3 @47104 has 6 MA's), (5, 47182), (6, 47185), (7, 47188), (8, 47212), (9, 47215), (10, 47266), (12, 47353), (13, 47371),