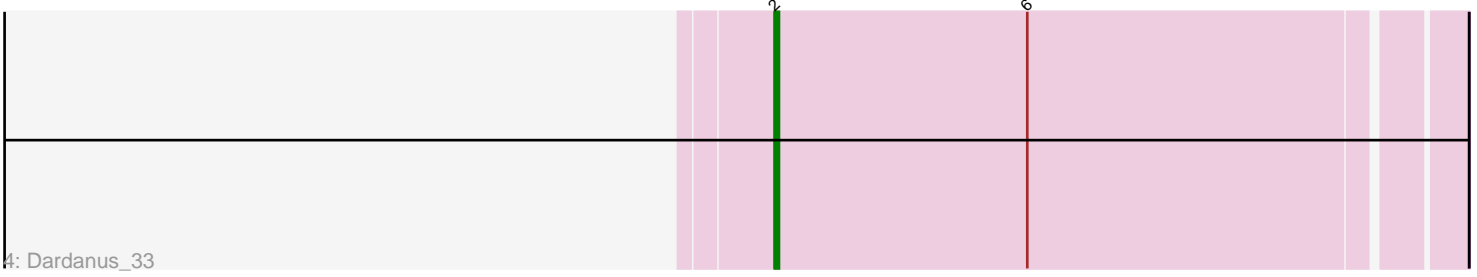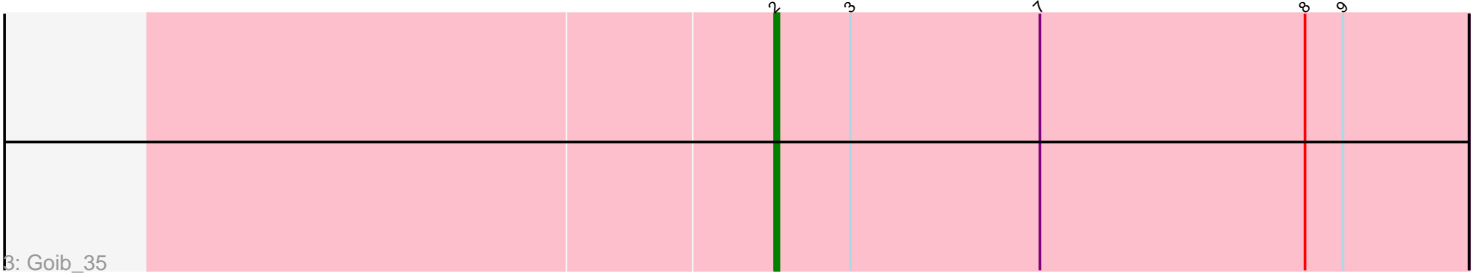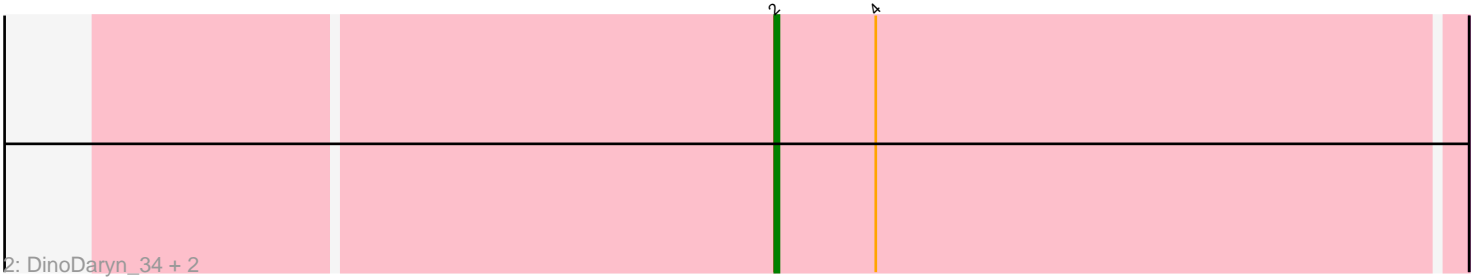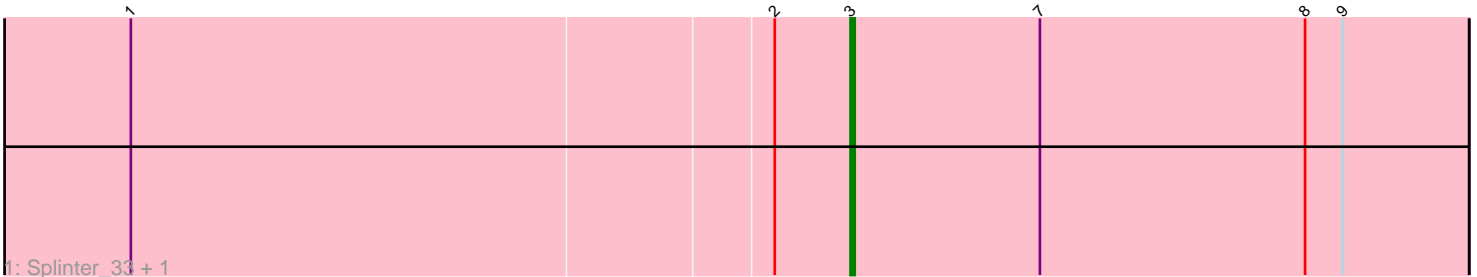# Pham 28017

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 28017 Report

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

Pham number 28017 has 8 members, 0 are drafts.

Phages represented in each track:
• Track 1 : Splinter_33, Vendetta_33
• Track 2 : DinoDaryn_34, Huffy_34, TZGordon_35
• Track 3 : Goib_35
• Track 4 : Dardanus_33
• Track 5 : Catfish_33

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

The start number called the most often in the published annotations is 2, it was called in 6 of the 8 non-draft genes in the pham.

Genes that call this "Most Annotated" start:
• Catfish_33, Dardanus_33, DinoDaryn_34, Goib_35, Huffy_34, TZGordon_35,

Genes that have the "Most Annotated" start but do not call it:
• Splinter_33, Vendetta_33,

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

Summary by start number:

Start 2:
• Found in 8 of 8 (100.0%) of genes in pham
• Manual Annotations of this start: 6 of 8
• Called 75.0% of time when present
• Phage (with cluster) where this start called: Catfish_33 (CU5), Dardanus_33 (CU3), DinoDaryn_34 (CU1), Goib_35 (CU1), Huffy_34 (CU1), TZGordon_35 (CU1),

Start 3:
• Found in 4 of 8 (50.0%) of genes in pham
• Manual Annotations of this start: 2 of 8
• Called 50.0% of time when present
• Phage (with cluster) where this start called: Splinter_33 (CU1), Vendetta_33 (CU1),

Summary by clusters:

There are 3 clusters represented in this pham: CU5, CU3, CU1,

Info for manual annotations of cluster CU1:
•Start number 2 was manually annotated 4 times for cluster CU1.
•Start number 3 was manually annotated 2 times for cluster CU1.

Info for manual annotations of cluster CU3:
•Start number 2 was manually annotated 1 time for cluster CU3.

Info for manual annotations of cluster CU5:
•Start number 2 was manually annotated 1 time for cluster CU5.

Gene Information:
Gene: Catfish_33 Start: 26393, Stop: 26232, Start Num: 2
Candidate Starts for Catfish_33:
(Start: 2 @26393 has 6 MA's), (Start: 3 @26375 has 2 MA's), (5, 26354), (6, 26333), (8, 26267), (9, 26258),

Gene: Dardanus_33 Start: 24884, Stop: 24726, Start Num: 2
Candidate Starts for Dardanus_33:
(Start: 2 @24884 has 6 MA's), (6, 24824),

Gene: DinoDaryn_34 Start: 24825, Stop: 24664, Start Num: 2
Candidate Starts for DinoDaryn_34:
(Start: 2 @24825 has 6 MA's), (4, 24801),

Gene: Goib_35 Start: 24950, Stop: 24786, Start Num: 2
Candidate Starts for Goib_35:
(Start: 2 @24950 has 6 MA's), (Start: 3 @24932 has 2 MA's), (7, 24887), (8, 24824), (9, 24815),

Gene: Huffy_34 Start: 24825, Stop: 24664, Start Num: 2
Candidate Starts for Huffy_34:
(Start: 2 @24825 has 6 MA's), (4, 24801),

Gene: Splinter_33 Start: 24925, Stop: 24779, Start Num: 3
Candidate Starts for Splinter_33:
(1, 25093), (Start: 2 @24943 has 6 MA's), (Start: 3 @24925 has 2 MA's), (7, 24880), (8, 24817), (9, 24808),

Gene: TZGordon_35 Start: 24748, Stop: 24587, Start Num: 2
Candidate Starts for TZGordon_35:
(Start: 2 @24748 has 6 MA's), (4, 24724),

Gene: Vendetta_33 Start: 24925, Stop: 24779, Start Num: 3
Candidate Starts for Vendetta_33:
(1, 25093), (Start: 2 @24943 has 6 MA's), (Start: 3 @24925 has 2 MA's), (7, 24880), (8, 24817), (9, 24808),