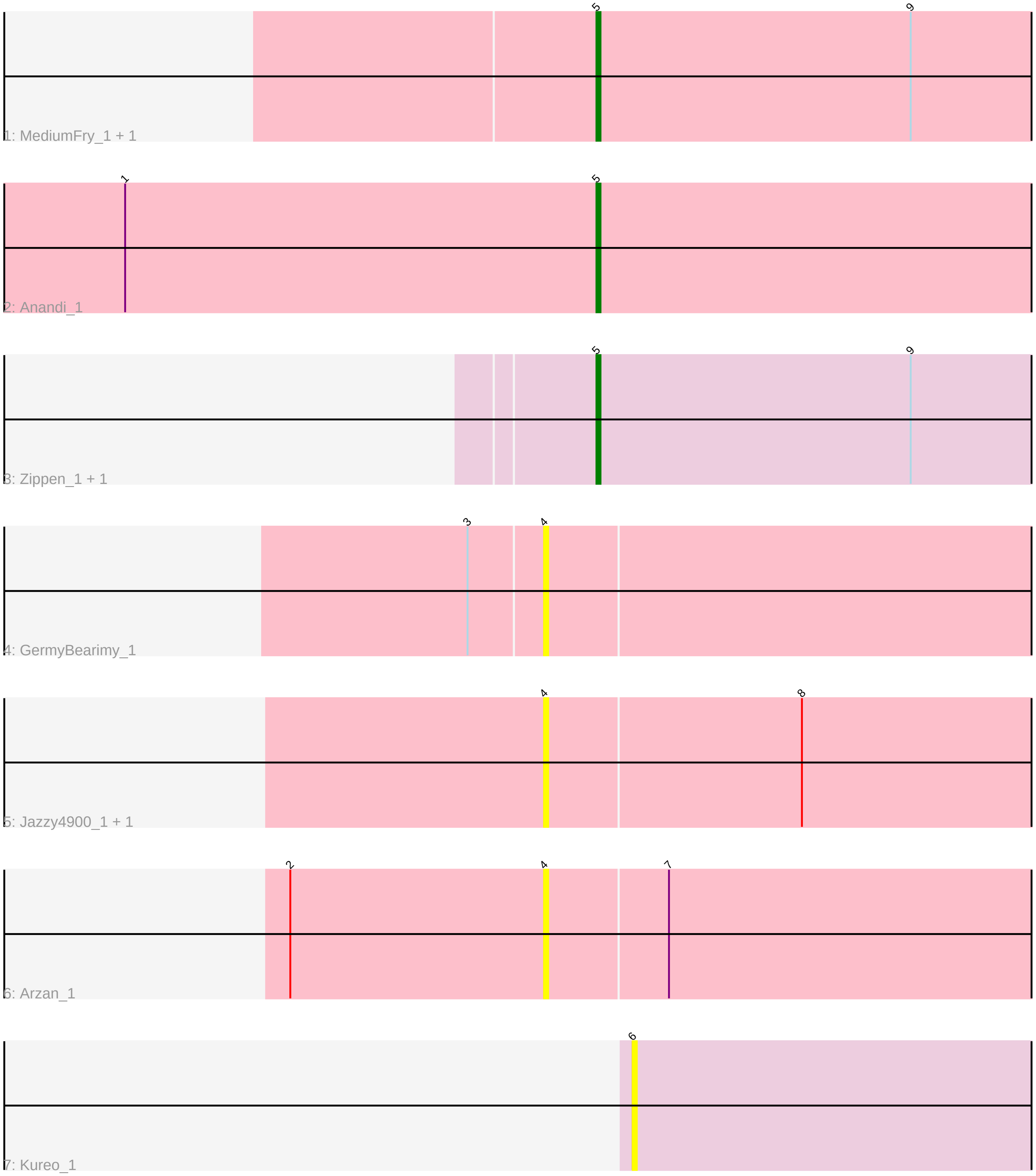
Pham 305487


5
9
1: MediumFry_1 + 1
1
5
2: Anandi_1
5
9
3: Zippen_1 + 1
3
4
4: GermyBearimy_1
4
8
5: Jazzy4900_1 + 1
2
4
7
6: Arzan_1
6
7: Kureo_1

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 305487 Report

This analysis was run 06/08/26 on database version 649.

Pham number 305487 has 10 members, 5 are drafts.

Phages represented in each track:
- Track 1 : MediumFry_1, Caterpillar_1
- Track 2 : Anandi_1
- Track 3 : Zippen_1, Inked_1
- Track 4 : GermyBearimy_1
- Track 5 : Jazzy4900_1, Sunny4976_1
- Track 6 : Arzan_1
- Track 7 : Kureo_1

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

The start number called the most often in the published annotations is 5, it was called in 5 of the 5 non-draft genes in the pham.

Genes that call this "Most Annotated" start:
- Anandi_1, Caterpillar_1, Inked_1, MediumFry_1, Zippen_1,

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

Genes that do not have the "Most Annotated" start:
- Arzan_1, GermyBearimy_1, Jazzy4900_1, Kureo_1, Sunny4976_1,

Summary by start number:

Start 4:
- Found in 4 of 10 (40.0%) of genes in pham
- No Manual Annotations of this start.
- Called 100.0% of time when present
- Phage (with cluster) where this start called: Arzan_1 (FI), GermyBearimy_1 (FI), Jazzy4900_1 (FI), Sunny4976_1 (FI),

Start 5:
- Found in 5 of 10 (50.0%) of genes in pham
- Manual Annotations of this start: 5 of 5

- Called 100.0% of time when present
- Phage (with cluster) where this start called: Anandi_1 (AU4), Caterpillar_1 (AU4), Inked_1 (AU7), MediumFry_1 (AU4), Zippen_1 (AU7),

Start 6:
- Found in 1 of 10 (10.0%) of genes in pham
- No Manual Annotations of this start.
- Called 100.0% of time when present
- Phage (with cluster) where this start called: Kureo_1 (FK),

Summary by clusters:

There are 4 clusters represented in this pham: FI, FK, AU4, AU7,

Info for manual annotations of cluster AU4:
- Start number 5 was manually annotated 3 times for cluster AU4.

Info for manual annotations of cluster AU7:
- Start number 5 was manually annotated 2 times for cluster AU7.

Gene Information:

Gene: Anandi_1 Start: 187, Stop: 372, Start Num: 5
Candidate Starts for Anandi_1:
(1, 70), (Start: 5 @187 has 5 MA's),

Gene: Arzan_1 Start: 72, Stop: 275, Start Num: 4
Candidate Starts for Arzan_1:
(2, 9), (4, 72), (7, 102),

Gene: Caterpillar_1 Start: 176, Stop: 352, Start Num: 5
Candidate Starts for Caterpillar_1:
(Start: 5 @176 has 5 MA's), (9, 254),

Gene: GermyBearimy_1 Start: 71, Stop: 274, Start Num: 4
Candidate Starts for GermyBearimy_1:
(3, 53), (4, 71),

Gene: Inked_1 Start: 176, Stop: 352, Start Num: 5
Candidate Starts for Inked_1:
(Start: 5 @176 has 5 MA's), (9, 254),

Gene: Jazzy4900_1 Start: 72, Stop: 275, Start Num: 4
Candidate Starts for Jazzy4900_1:
(4, 72), (8, 135),

Gene: Kureo_1 Start: 221, Stop: 403, Start Num: 6
Candidate Starts for Kureo_1:
(6, 221),

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Gene: MediumFry_1 Start: 176, Stop: 352, Start Num: 5
Candidate Starts for MediumFry_1:
(Start: 5 @176 has 5 MA's), (9, 254),

Gene: Sunny4976_1 Start: 72, Stop: 275, Start Num: 4
Candidate Starts for Sunny4976_1:
(4, 72), (8, 135),

Gene: Zippen_1 Start: 176, Stop: 352, Start Num: 5
Candidate Starts for Zippen_1:
(Start: 5 @176 has 5 MA's), (9, 254),
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