Pham 6588

1: Rope_2 + 8

2: Papyrus_2
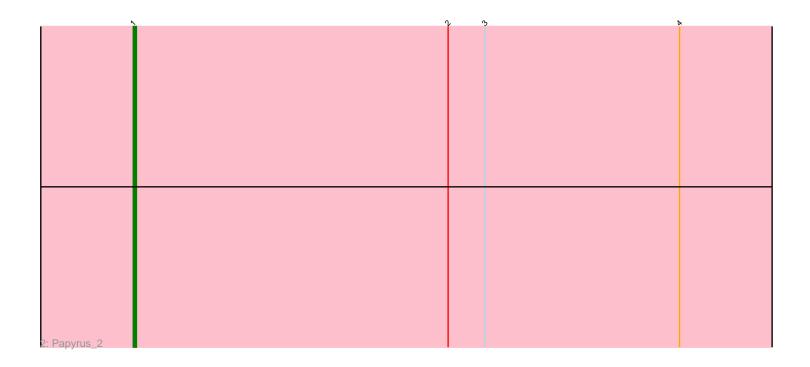
Note: Tracks are now grouped by subcluster and scaled. Switching in subcluster is indicated by changes in track color. Track scale is now set by default to display the region 30 bp upstream of start 1 to 30 bp downstream of the last possible start. If this default region is judged to be packed too tightly 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 6588 Report

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

Pham number 6588 has 10 members, 2 are drafts.

Phages represented in each track:
• Track 1 : Rope_2, Candle_2, Yelo_2, Zenon_2, Riparian_2, Send513_2, MontyDev_2, Nilo_2, Weiss13_2
• Track 2 : Papyrus_2

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

The start number called the most often in the published annotations is 1, it was called in 8 of the 8 non-draft genes in the pham.

Genes that call this "Most Annotated" start:
• Candle_2, MontyDev_2, Nilo_2, Papyrus_2, Riparian_2, Rope_2, Send513_2, Weiss13_2, Yelo_2, Zenon_2,

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 1:
• Found in 10 of 10 (100.0%) of genes in pham
• Manual Annotations of this start: 8 of 8
• Called 100.0% of time when present
• Phage (with cluster) where this start called: Candle_2 (R), MontyDev_2 (R), Nilo_2 (R), Papyrus_2 (R), Riparian_2 (R), Rope_2 (R), Send513_2 (R), Weiss13_2 (R), Yelo_2 (R), Zenon_2 (R),

Summary by clusters:

There is one cluster represented in this pham: R

Info for manual annotations of cluster R:

•Start number 1 was manually annotated 8 times for cluster R.

Gene Information:
Gene: Candle_2 Start: 1018, Stop: 1236, Start Num: 1
Candidate Starts for Candle_2:
(Start: 1 @1018 has 8 MA's), (3, 1132), (4, 1195),

Gene: MontyDev_2 Start: 1017, Stop: 1235, Start Num: 1
Candidate Starts for MontyDev_2:
(Start: 1 @1017 has 8 MA's), (3, 1131), (4, 1194),

Gene: Nilo_2 Start: 1018, Stop: 1236, Start Num: 1
Candidate Starts for Nilo_2:
(Start: 1 @1018 has 8 MA's), (3, 1132), (4, 1195),

Gene: Papyrus_2 Start: 1017, Stop: 1235, Start Num: 1
Candidate Starts for Papyrus_2:
(Start: 1 @1017 has 8 MA's), (2, 1119), (3, 1131), (4, 1194),

Gene: Riparian_2 Start: 1018, Stop: 1236, Start Num: 1
Candidate Starts for Riparian_2:
(Start: 1 @1018 has 8 MA's), (3, 1132), (4, 1195),

Gene: Rope_2 Start: 1017, Stop: 1235, Start Num: 1
Candidate Starts for Rope_2:
(Start: 1 @1017 has 8 MA's), (3, 1131), (4, 1194),

Gene: Send513_2 Start: 1018, Stop: 1236, Start Num: 1
Candidate Starts for Send513_2:
(Start: 1 @1018 has 8 MA's), (3, 1132), (4, 1195),

Gene: Weiss13_2 Start: 1018, Stop: 1236, Start Num: 1
Candidate Starts for Weiss13_2:
(Start: 1 @1018 has 8 MA's), (3, 1132), (4, 1195),

Gene: Yelo_2 Start: 1018, Stop: 1236, Start Num: 1
Candidate Starts for Yelo_2:
(Start: 1 @1018 has 8 MA's), (3, 1132), (4, 1195),

Gene: Zenon_2 Start: 1018, Stop: 1236, Start Num: 1
Candidate Starts for Zenon_2:
(Start: 1 @1018 has 8 MA's), (3, 1132), (4, 1195),