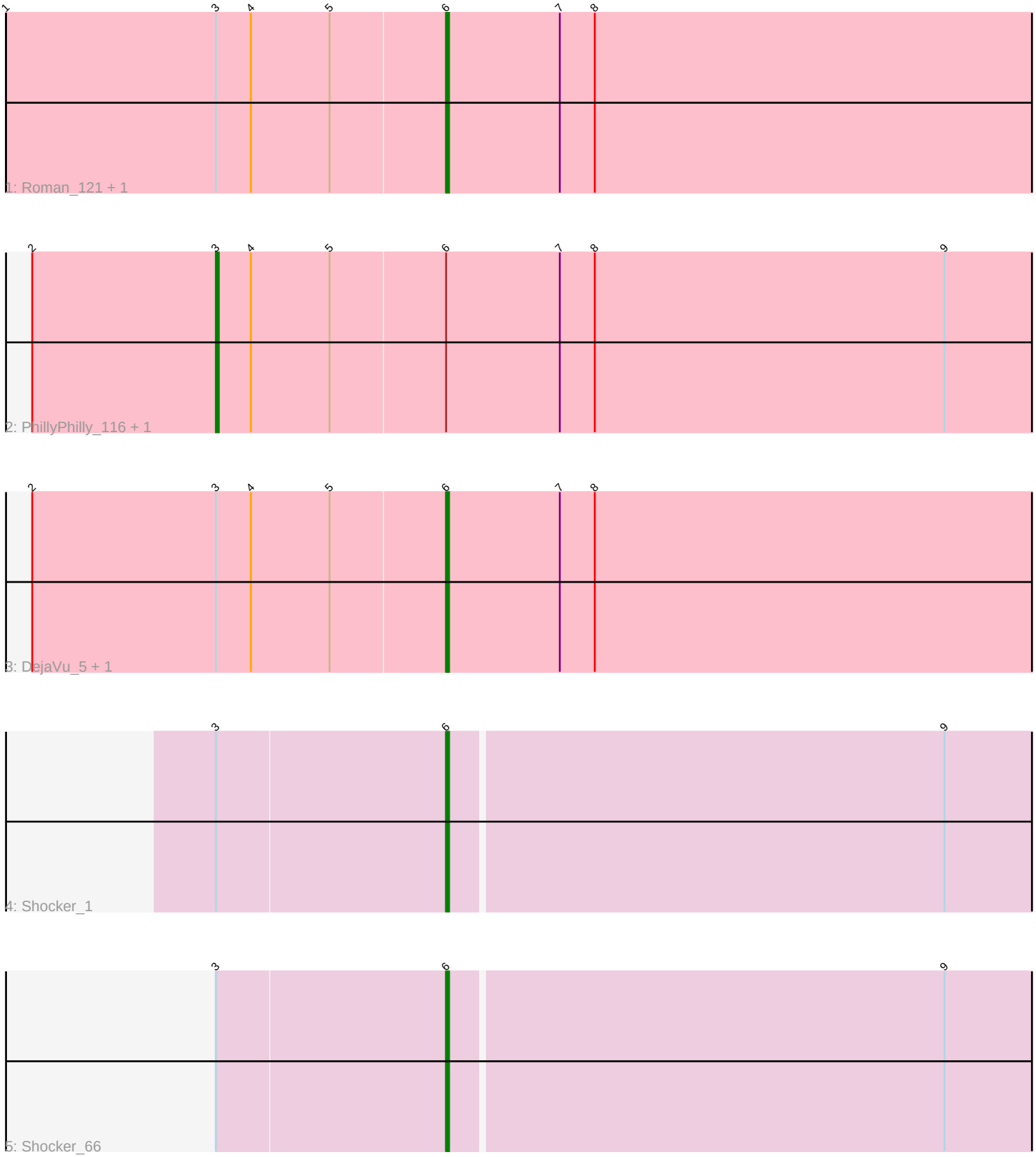
Pham 7379


1
3
4
5
6
7
8
1: Roman_121 + 1
2
3
4
5
6
7
8
9
2: PhillyPhilly_116 + 1
2
3
4
5
6
7
8
3: DejaVu_5 + 1
3
6
9
4: Shocker_1
3
6
9
5: Shocker_66

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 7379 Report

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

Pham number 7379 has 8 members, 0 are drafts.

Phages represented in each track:
• Track 1 : Roman_121, Roman_5
• Track 2 : PhillyPhilly_116, PhillyPhilly_6
• Track 3 : DejaVu_5, DejaVu_121
• Track 4 : Shocker_1
• Track 5 : Shocker_66

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

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

Genes that call this "Most Annotated" start:
• DejaVu_121, DejaVu_5, Roman_121, Roman_5, Shocker_1, Shocker_66,

Genes that have the "Most Annotated" start but do not call it:
• PhillyPhilly_116, PhillyPhilly_6,

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

Summary by start number:

Start 3:
• Found in 8 of 8 (100.0%) of genes in pham
• Manual Annotations of this start: 2 of 8
• Called 25.0% of time when present
• Phage (with cluster) where this start called: PhillyPhilly_116 (ED1), PhillyPhilly_6 (ED1),

Start 6:
• 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: DejaVu_121 (ED1), DejaVu_5 (ED1), Roman_121 (ED1), Roman_5 (ED1), Shocker_1 (singleton), Shocker_66 (singleton),

Summary by clusters:

There are 2 clusters represented in this pham: singleton, ED1,

Info for manual annotations of cluster ED1:
•Start number 3 was manually annotated 2 times for cluster ED1.
•Start number 6 was manually annotated 4 times for cluster ED1.

Gene Information:

Gene: DejaVu_5 Start: 2030, Stop: 1809, Start Num: 6
Candidate Starts for DejaVu_5:
(2, 2171), (Start: 3 @2108 has 2 MA's), (4, 2096), (5, 2069), (Start: 6 @2030 has 6 MA's), (7, 1991), (8, 1979),

Gene: DejaVu_121 Start: 62410, Stop: 62189, Start Num: 6
Candidate Starts for DejaVu_121:
(2, 62551), (Start: 3 @62488 has 2 MA's), (4, 62476), (5, 62449), (Start: 6 @62410 has 6 MA's), (7, 62371), (8, 62359),

Gene: PhillyPhilly_116 Start: 62018, Stop: 61719, Start Num: 3
Candidate Starts for PhillyPhilly_116:
(2, 62081), (Start: 3 @62018 has 2 MA's), (4, 62006), (5, 61979), (Start: 6 @61940 has 6 MA's), (7, 61901), (8, 61889), (9, 61769),

Gene: PhillyPhilly_6 Start: 2529, Stop: 2230, Start Num: 3
Candidate Starts for PhillyPhilly_6:
(2, 2592), (Start: 3 @2529 has 2 MA's), (4, 2517), (5, 2490), (Start: 6 @2451 has 6 MA's), (7, 2412), (8, 2400), (9, 2280),

Gene: Roman_121 Start: 63321, Stop: 63100, Start Num: 6
Candidate Starts for Roman_121:
(1, 63471), (Start: 3 @63399 has 2 MA's), (4, 63387), (5, 63360), (Start: 6 @63321 has 6 MA's), (7, 63282), (8, 63270),

Gene: Roman_5 Start: 2234, Stop: 2013, Start Num: 6
Candidate Starts for Roman_5:
(1, 2384), (Start: 3 @2312 has 2 MA's), (4, 2300), (5, 2273), (Start: 6 @2234 has 6 MA's), (7, 2195), (8, 2183),

Gene: Shocker_1 Start: 406, Stop: 188, Start Num: 6
Candidate Starts for Shocker_1:
(Start: 3 @484 has 2 MA's), (Start: 6 @406 has 6 MA's), (9, 238),

Gene: Shocker_66 Start: 45353, Stop: 45135, Start Num: 6
Candidate Starts for Shocker_66:
(Start: 3 @45431 has 2 MA's), (Start: 6 @45353 has 6 MA's), (9, 45185),