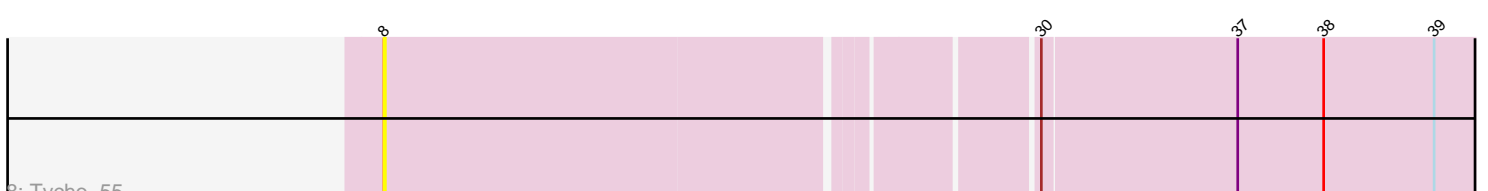
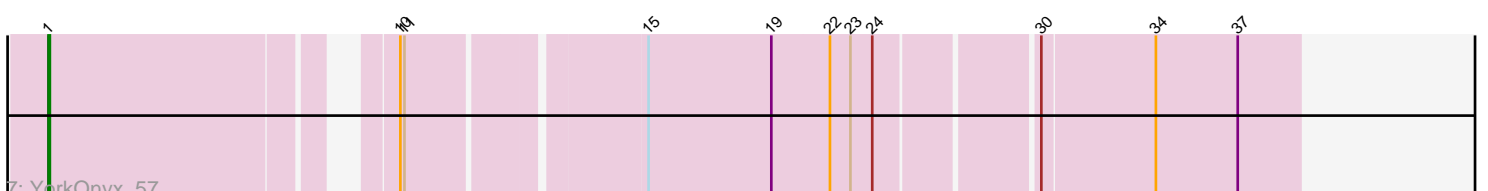
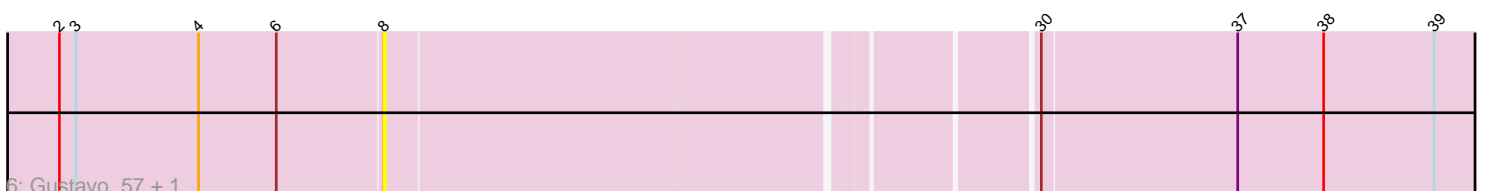
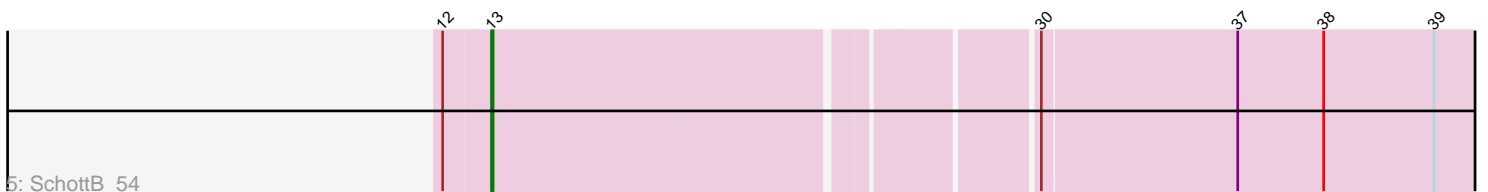
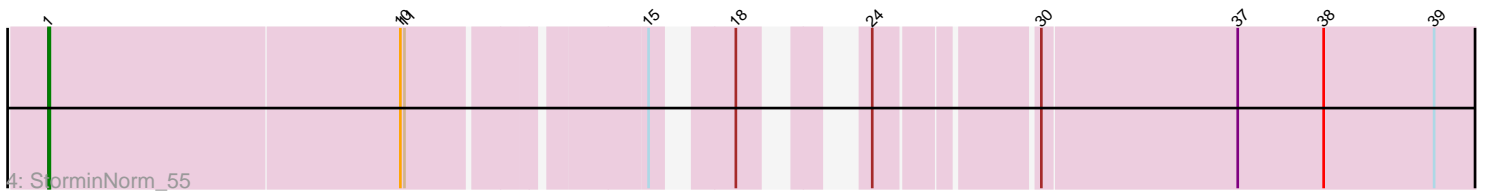
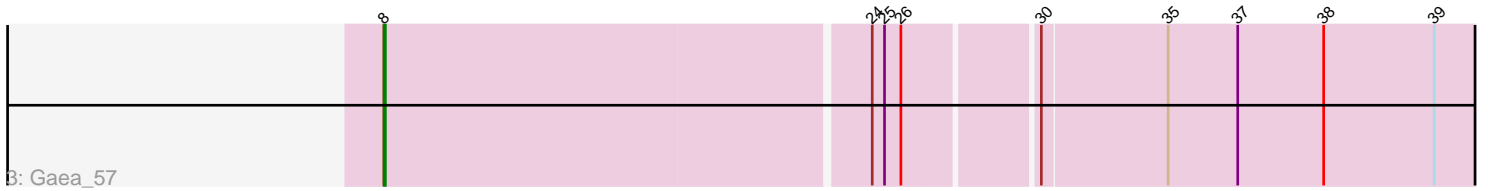
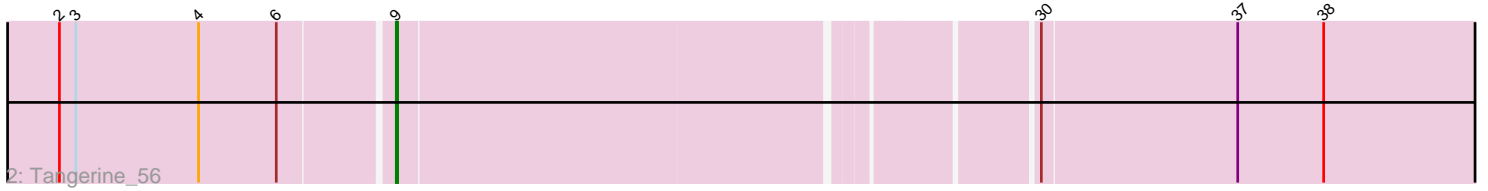
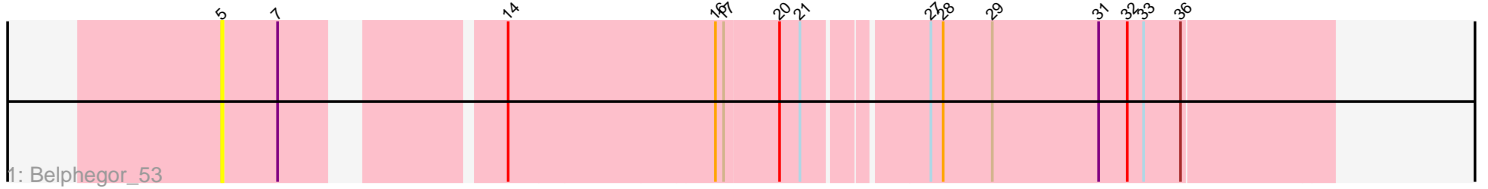


# Pham 194571



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 194571 Report

This analysis was run 11/02/24 on database version 579.

Pham number 194571 has 9 members, 4 are drafts.

Phages represented in each track:

- Track 1 : Belphegor\_53
- Track 2 : Tangerine\_56
- Track 3 : Gaea\_57
- Track 4 : StorminNorm\_55
- Track 5 : SchottB\_54
- Track 6 : Gustavo\_57, Saronaya\_57
- Track 7 : YorkOnyx\_57
- Track 8 : Tycho\_55

### ***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 2 of the 5 non-draft genes in the pham.

Genes that call this "Most Annotated" start:

- StorminNorm\_55, YorkOnyx\_57,

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

- 

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

- Belphegor\_53, Gaea\_57, Gustavo\_57, Saronaya\_57, SchottB\_54, Tangerine\_56, Tycho\_55,

### **Summary by start number:**

Start 1:

- Found in 2 of 9 ( 22.2% ) of genes in pham
- Manual Annotations of this start: 2 of 5
- Called 100.0% of time when present
- Phage (with cluster) where this start called: StorminNorm\_55 (DE1), YorkOnyx\_57 (DE1),

Start 5:

- Found in 1 of 9 ( 11.1% ) of genes in pham
- No Manual Annotations of this start.
- Called 100.0% of time when present
- Phage (with cluster) where this start called: Belphegor\_53 (DE),

Start 8:

- Found in 4 of 9 ( 44.4% ) of genes in pham
- Manual Annotations of this start: 1 of 5
- Called 100.0% of time when present
- Phage (with cluster) where this start called: Gaea\_57 (DE1), Gustavo\_57 (DE1), Saronaya\_57 (DE1), Tycho\_55 (DE1),

Start 9:

- Found in 1 of 9 ( 11.1% ) of genes in pham
- Manual Annotations of this start: 1 of 5
- Called 100.0% of time when present
- Phage (with cluster) where this start called: Tangerine\_56 (DE1),

Start 13:

- Found in 1 of 9 ( 11.1% ) of genes in pham
- Manual Annotations of this start: 1 of 5
- Called 100.0% of time when present
- Phage (with cluster) where this start called: SchottB\_54 (DE1),

### **Summary by clusters:**

There are 2 clusters represented in this pham: DE1, DE,

Info for manual annotations of cluster DE1:

- Start number 1 was manually annotated 2 times for cluster DE1.
- Start number 8 was manually annotated 1 time for cluster DE1.
- Start number 9 was manually annotated 1 time for cluster DE1.
- Start number 13 was manually annotated 1 time for cluster DE1.

### **Gene Information:**

Gene: Belphegor\_53 Start: 46167, Stop: 46916, Start Num: 5

Candidate Starts for Belphegor\_53:

(5, 46167), (7, 46206), (14, 46338), (16, 46485), (17, 46491), (20, 46530), (21, 46545), (27, 46626), (28, 46635), (29, 46671), (31, 46749), (32, 46770), (33, 46782), (36, 46809),

Gene: Gaea\_57 Start: 45626, Stop: 46414, Start Num: 8

Candidate Starts for Gaea\_57:

(Start: 8 @45626 has 1 MA's), (24, 45974), (25, 45983), (26, 45995), (30, 46085), (35, 46175), (37, 46226), (38, 46289), (39, 46370),

Gene: Gustavo\_57 Start: 46149, Stop: 46925, Start Num: 8

Candidate Starts for Gustavo\_57:

(2, 45915), (3, 45927), (4, 46017), (6, 46074), (Start: 8 @46149 has 1 MA's), (30, 46596), (37, 46737), (38, 46800), (39, 46881),

Gene: Saronaya\_57 Start: 46149, Stop: 46925, Start Num: 8

Candidate Starts for Saronaya\_57:

(2, 45915), (3, 45927), (4, 46017), (6, 46074), (Start: 8 @46149 has 1 MA's), (30, 46596), (37, 46737), (38, 46800), (39, 46881),

Gene: SchottB\_54 Start: 46419, Stop: 47117, Start Num: 13

Candidate Starts for SchottB\_54:

(12, 46386), (Start: 13 @46419 has 1 MA's), (30, 46788), (37, 46929), (38, 46992), (39, 47073),

Gene: StorminNorm\_55 Start: 45626, Stop: 46564, Start Num: 1

Candidate Starts for StorminNorm\_55:

(Start: 1 @45626 has 2 MA's), (10, 45881), (11, 45884), (15, 46040), (18, 46082), (24, 46130), (30, 46235), (37, 46376), (38, 46439), (39, 46520),

Gene: Tangerine\_56 Start: 45560, Stop: 46327, Start Num: 9

Candidate Starts for Tangerine\_56:

(2, 45326), (3, 45338), (4, 45428), (6, 45485), (Start: 9 @45560 has 1 MA's), (30, 45998), (37, 46139), (38, 46202),

Gene: Tycho\_55 Start: 45494, Stop: 46273, Start Num: 8

Candidate Starts for Tycho\_55:

(Start: 8 @45494 has 1 MA's), (30, 45944), (37, 46085), (38, 46148), (39, 46229),

Gene: YorkOnyx\_57 Start: 46072, Stop: 46905, Start Num: 1

Candidate Starts for YorkOnyx\_57:

(Start: 1 @46072 has 2 MA's), (10, 46291), (11, 46294), (15, 46450), (19, 46540), (22, 46582), (23, 46597), (24, 46612), (30, 46720), (34, 46801), (37, 46861),