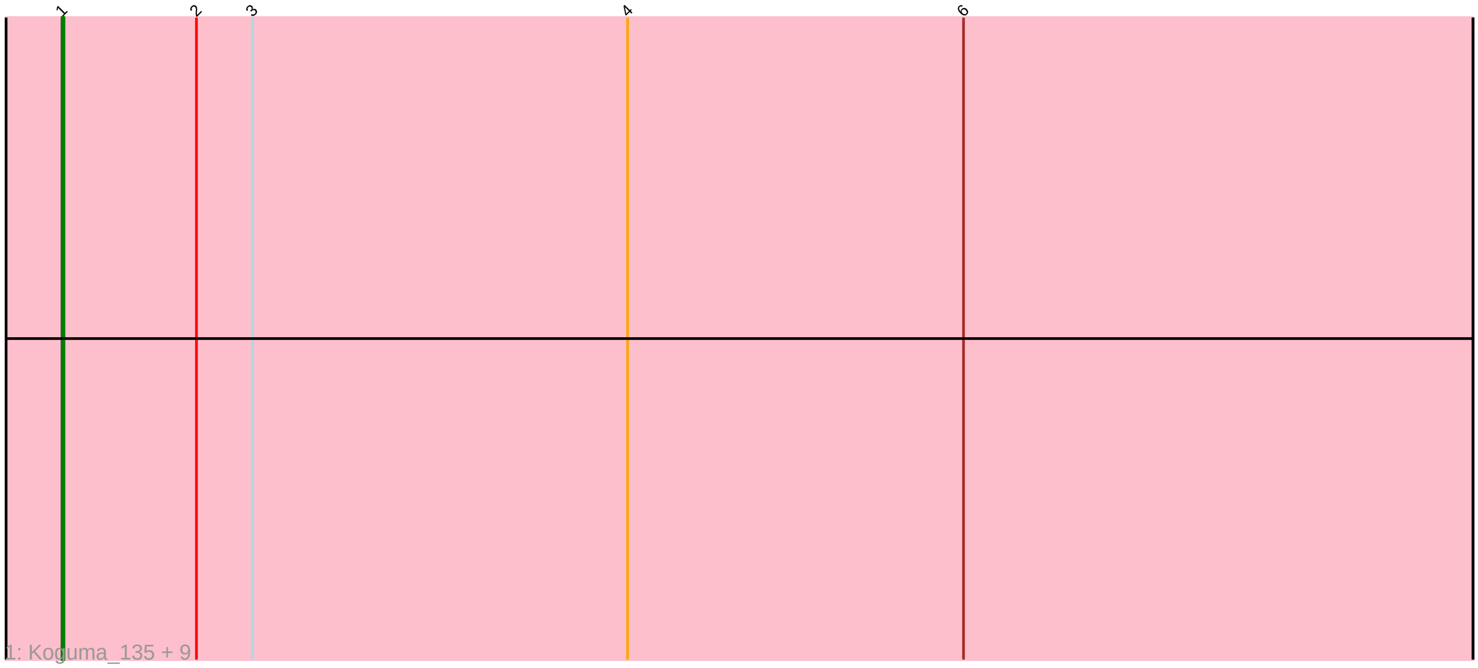
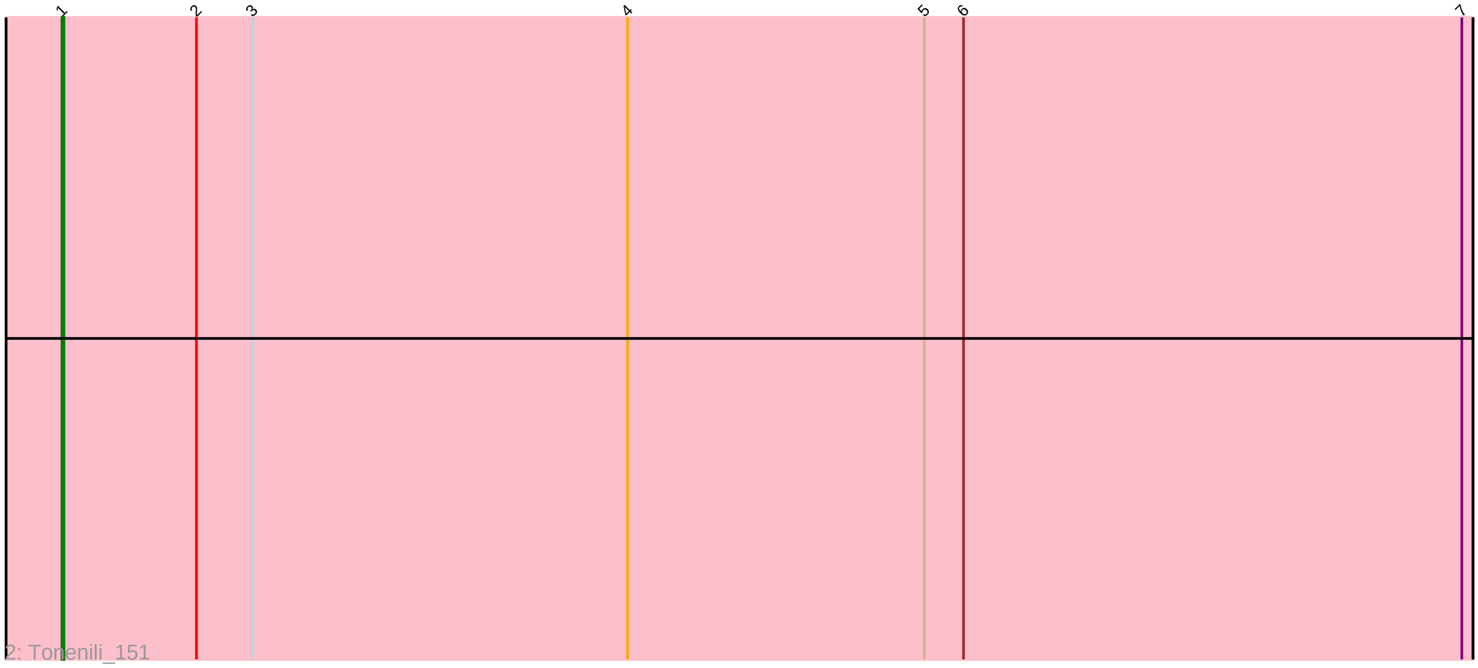
Pham 158349





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 158349 Report

This analysis was run 04/13/24 on database version 558.

Pham number 158349 has 11 members, 0 are drafts.

Phages represented in each track:
- Track 1 : Koguma_135, Pinkcreek_129, LRRHood_131, Sauce_138, Shifa_127, Grungle_125, HyRo_129, LinStu_136, Sebata_138, Lukilu_128
- Track 2 : Tonenili_151

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 11 of the 11 non-draft genes in the pham.

Genes that call this "Most Annotated" start:
- Grungle_125, HyRo_129, Koguma_135, LRRHood_131, LinStu_136, Lukilu_128, Pinkcreek_129, Sauce_138, Sebata_138, Shifa_127, Tonenili_151,

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 11 of 11 (100.0%) of genes in pham
- Manual Annotations of this start: 11 of 11
- Called 100.0% of time when present
- Phage (with cluster) where this start called: Grungle_125 (C1), HyRo_129 (C1), Koguma_135 (C1), LRRHood_131 (C1), LinStu_136 (C1), Lukilu_128 (C1), Pinkcreek_129 (C1), Sauce_138 (C1), Sebata_138 (C1), Shifa_127 (C1), Tonenili_151 (C1),

Summary by clusters:

There is one cluster represented in this pham: C1

Info for manual annotations of cluster C1:
- Start number 1 was manually annotated 11 times for cluster C1.

Gene Information:

Gene: Grungle_125 Start: 76603, Stop: 77358, Start Num: 1
Candidate Starts for Grungle_125:
(Start: 1 @76603 has 11 MA's), (2, 76675), (3, 76705), (4, 76906), (6, 77086),

Gene: HyRo_129 Start: 79281, Stop: 80036, Start Num: 1
Candidate Starts for HyRo_129:
(Start: 1 @79281 has 11 MA's), (2, 79353), (3, 79383), (4, 79584), (6, 79764),

Gene: Koguma_135 Start: 77765, Stop: 78520, Start Num: 1
Candidate Starts for Koguma_135:
(Start: 1 @77765 has 11 MA's), (2, 77837), (3, 77867), (4, 78068), (6, 78248),

Gene: LRRHood_131 Start: 79573, Stop: 80328, Start Num: 1
Candidate Starts for LRRHood_131:
(Start: 1 @79573 has 11 MA's), (2, 79645), (3, 79675), (4, 79876), (6, 80056),

Gene: LinStu_136 Start: 80182, Stop: 80937, Start Num: 1
Candidate Starts for LinStu_136:
(Start: 1 @80182 has 11 MA's), (2, 80254), (3, 80284), (4, 80485), (6, 80665),

Gene: Lukilu_128 Start: 80583, Stop: 81338, Start Num: 1
Candidate Starts for Lukilu_128:
(Start: 1 @80583 has 11 MA's), (2, 80655), (3, 80685), (4, 80886), (6, 81066),

Gene: Pinkcreek_129 Start: 77948, Stop: 78703, Start Num: 1
Candidate Starts for Pinkcreek_129:
(Start: 1 @77948 has 11 MA's), (2, 78020), (3, 78050), (4, 78251), (6, 78431),

Gene: Sauce_138 Start: 79271, Stop: 80026, Start Num: 1
Candidate Starts for Sauce_138:
(Start: 1 @79271 has 11 MA's), (2, 79343), (3, 79373), (4, 79574), (6, 79754),

Gene: Sebata_138 Start: 80740, Stop: 81495, Start Num: 1
Candidate Starts for Sebata_138:
(Start: 1 @80740 has 11 MA's), (2, 80812), (3, 80842), (4, 81043), (6, 81223),

Gene: Shifa_127 Start: 78547, Stop: 79302, Start Num: 1
Candidate Starts for Shifa_127:
(Start: 1 @78547 has 11 MA's), (2, 78619), (3, 78649), (4, 78850), (6, 79030),

Gene: Tonenili_151 Start: 82838, Stop: 83593, Start Num: 1
Candidate Starts for Tonenili_151:
(Start: 1 @82838 has 11 MA's), (2, 82910), (3, 82940), (4, 83141), (5, 83300), (6, 83321), (7, 83588),