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Annotation of Bacteriophage BigPaolini

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Annotation of Bacteriophage BigPaolini

Bo Rost, Morgan Paolini, Hannah Sparks and Marisa L. Pedulla (Montana Tech)

What Makes a phage Great

- BigPaolini was discovered by Morgan Paolini in 2017 in Butte MT.
- The sample came from enriched soil and was named after its discoverer and its large plaque morphology.
- BigPaolini was recently sequenced and was shown to contain a DNA genome with a length of 49601 bp.
- Eighty-seven putative protein coding genes were found in BigPaolini, and functions were assigned to 32.

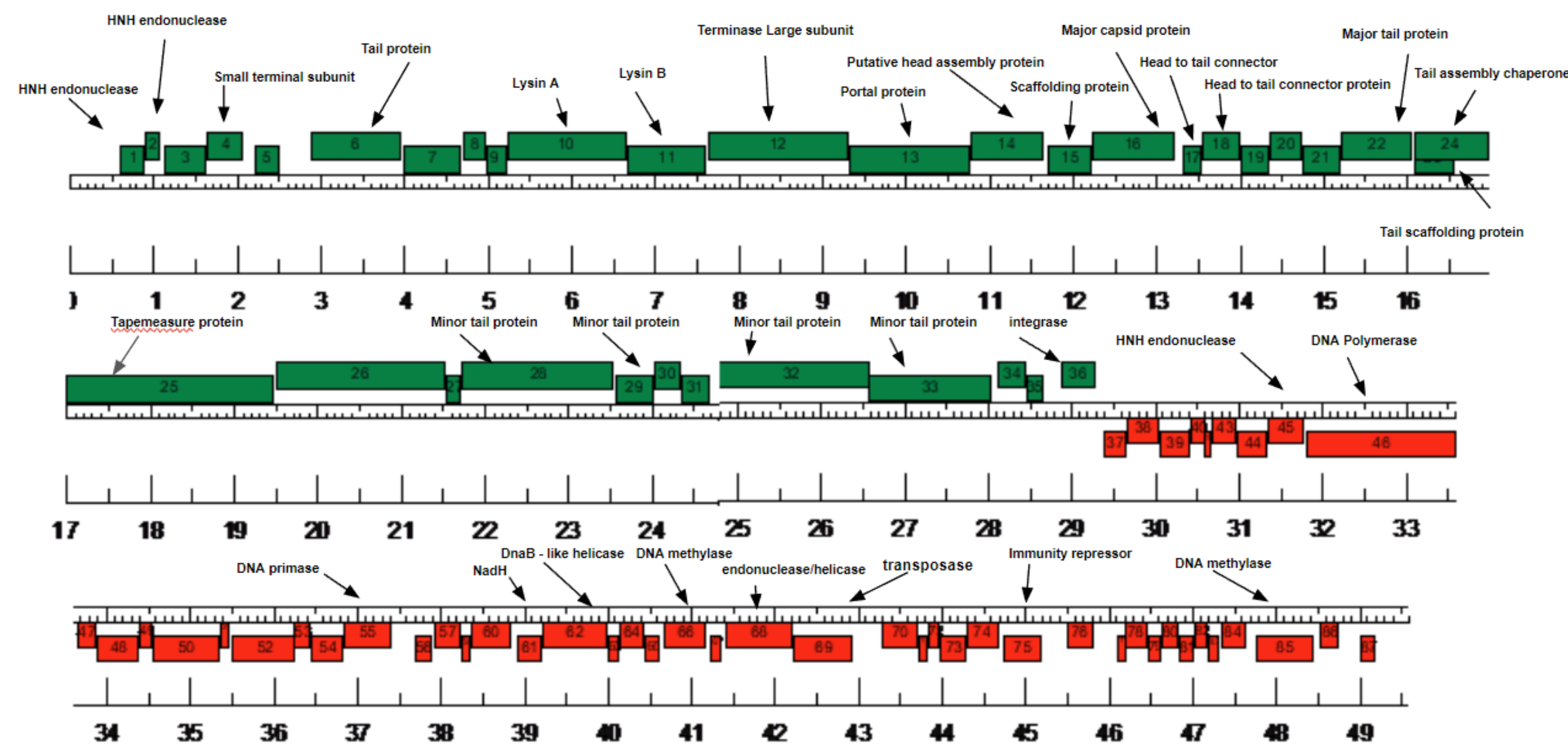
Background and Significance

- Bacteriophages were discovered nearly 100 years ago. With new interest in phages many phages are being analyzed and annotated to understand the diversity within the phage world.

Methods

- The start codon for each gene was assessed and called within DNA Master
- by comparing the overall length of the gene and the computed Shine-Dalgarno score.
- The coding potential of each gene was examined using the Genemark program.
- The completed annotated map with putative gene functions were submitted to phagesdb.org.

RESULTS



• Figure 1: Genome map for BigPaolini

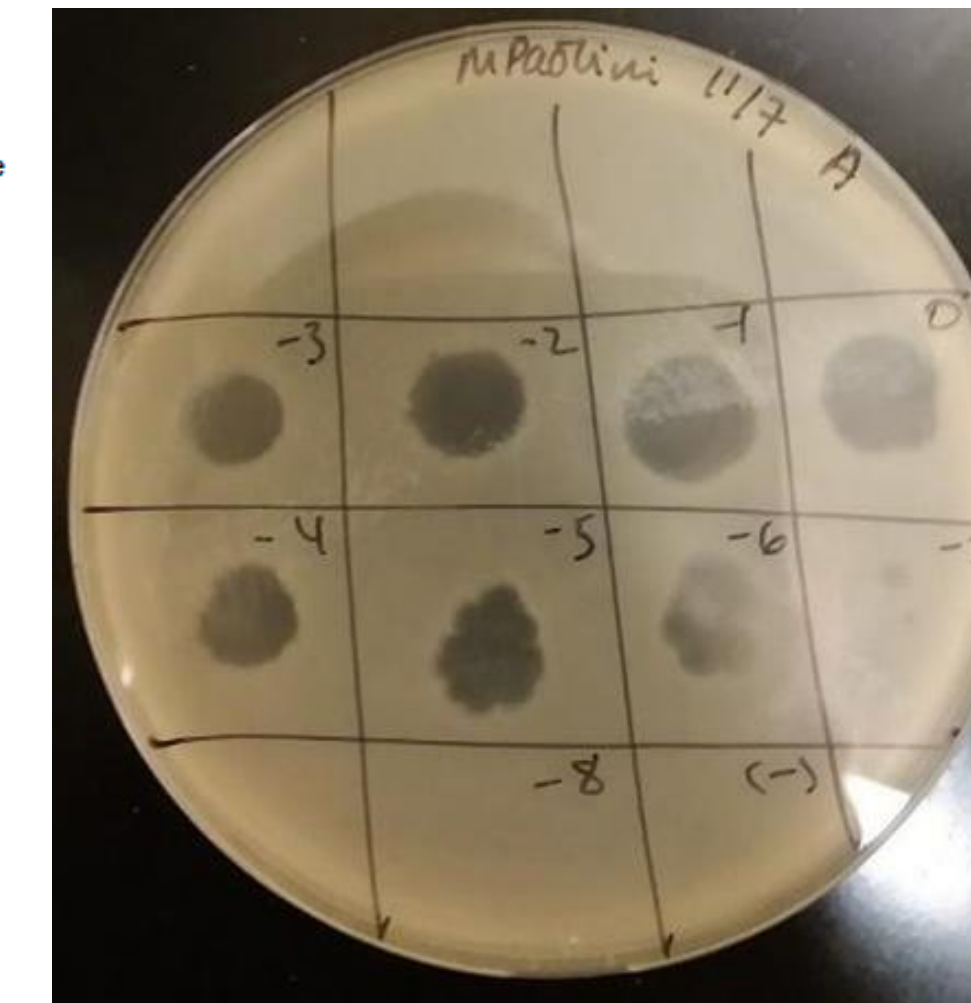


Figure 4: spot plate of BigPaolini photos by Morgan Paolini

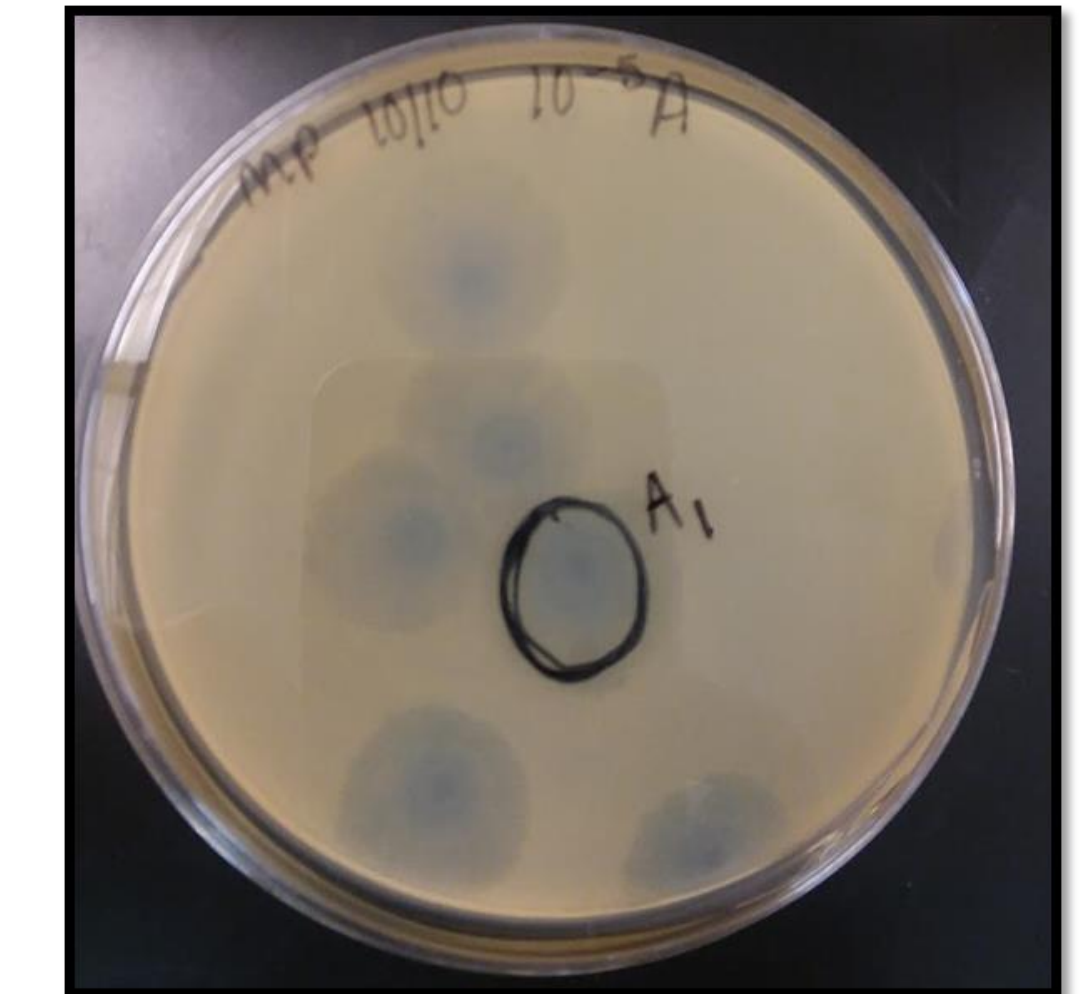


Figure 5: plate showing morphology of BigPaolini

Conclusions

- BigPaolini was successfully annotated and submitted to phagesdb.org
- many putative protein coding genes were identified in BigPaolini
- Future work
 - Annotating more phages in other phage clusters to examine a broader range of genomes.
 - Allowing for more comparisons and better understanding of phage diversity.

Acknowledgments

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Figure 2: Sequencing information for BigPaolini

Sequencing Information	
Sequencing Complete?	Yes
Date Sequencing Completed	Mar 23, 2018
Sequencing Facility	Pittsburgh Bacteriophage Institute
Shotgun Sequencing Method	Illumina Sequencing
Approximate Shotgun Coverage	716
Genome length (bp)	49601
Character of genome ends	3' Sticky Overhang
Overhang Length	10 bases
Overhang Sequence	CGGATGGTAA
GC Content	63.5%
Fasta file available?	Available upon entering GPS coordinates

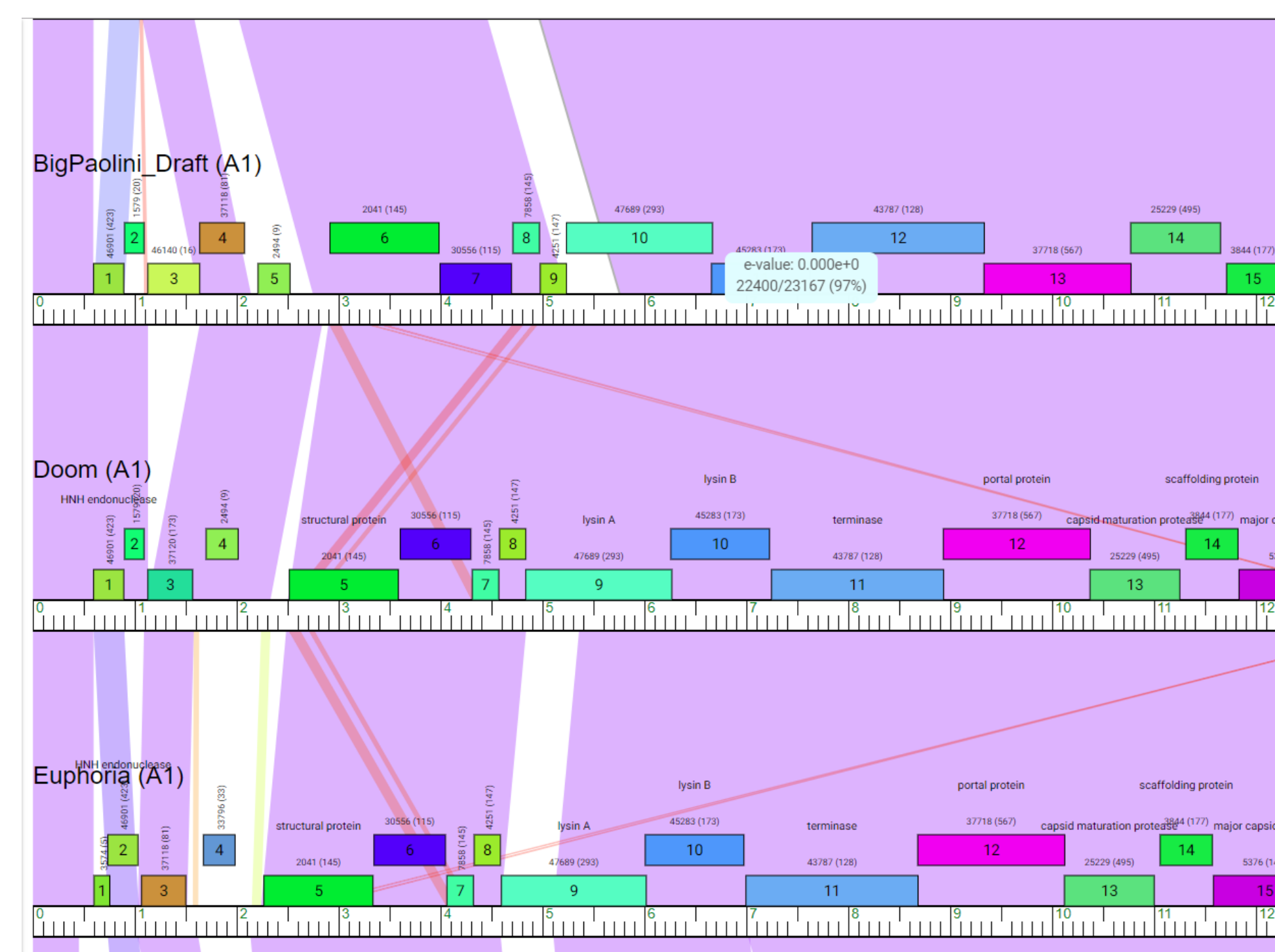


Figure 3 The phamerator comparisons of gene products and their likeness to other genes.