

Characterization of Intergenic Recurring Elements in Actinobacteriophage Cluster B11

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Introduction

Bacteriophages are interesting organisms to study because they are small and relatively simple and have led to important discoveries such as DNA as the hereditary material of cells and CRISPR/Cas systems. Actinobacteriophages are grouped into clusters and subclusters, with subcluster B11 being the major focus of this research. Bacteriophages typically have small genomes and with few intergenic regions. The B11 phages have recurring sequences in the intergenic space on the right half of the genome. This half of the genome usually contains the functional genes, as opposed to structural genes, of the bacteriophage. This has led to the hypothesis that these intergenic sequences have a role in DNA binding.

Methods

- Each phage genome was searched for potential motifs using MEME suite.
- The motifs were searched for within the genome using DNA Master,
- The motifs were located and mapped on the genome to determine if they were in the interesting region on the Phamerator map.
- A BLAST search in PhagesDb was performed to check for the motifs in other phages.
- An NCBI BLAST was performed to look for potential functions.
- Potential promoters were searched for in the genomes using DNA Master.

Observations

- Potential motifs were found in each of the five phages searched.
- These motifs were found to be recurring and intergenic on the half of the genome containing functional genes.
- The motifs were found within the region of interest (based on the Phamerator map below).
- The PhagesDb BLAST search showed that these motifs are found in many other phages belonging to other clusters.
- The BLAST shows no significant hits for any known functions.
- A preliminary search for promoters show potential promoters within these intergenic regions.

There are intergenic recurring sequences within the genomes of B11 phages that we hypothesize have a role in DNA binding.



Results

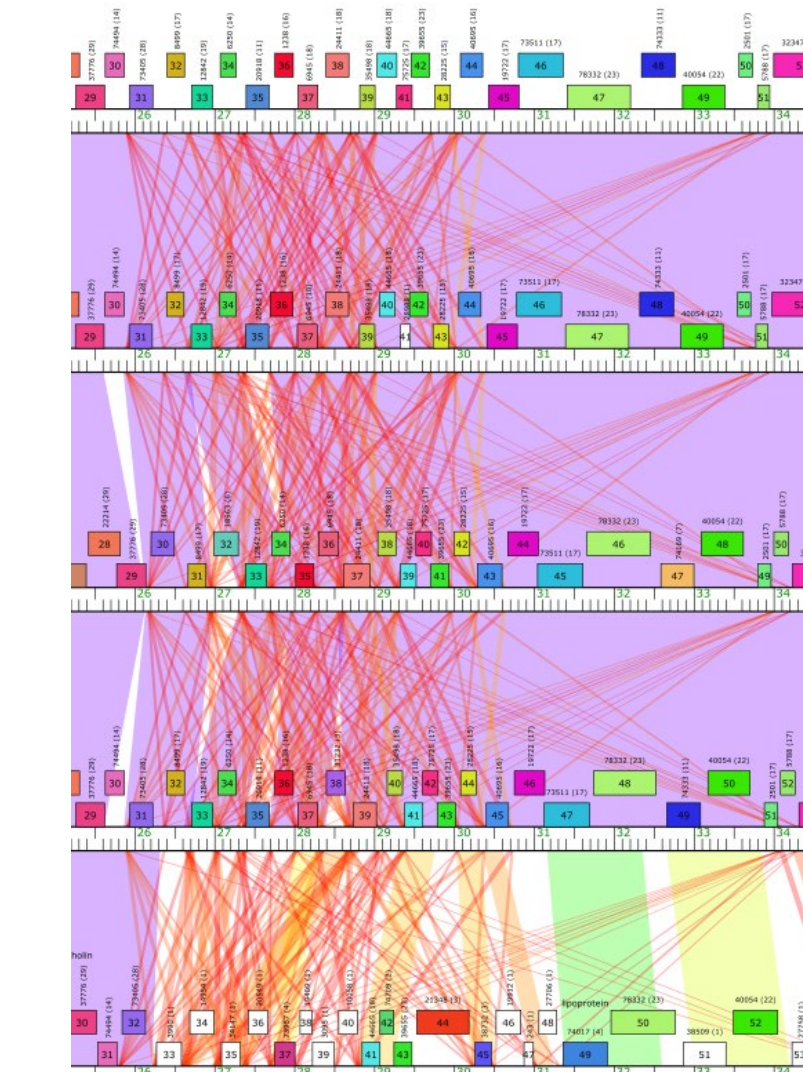


Figure 1: A zoomed in area of a Phamerator map showing the area of interest

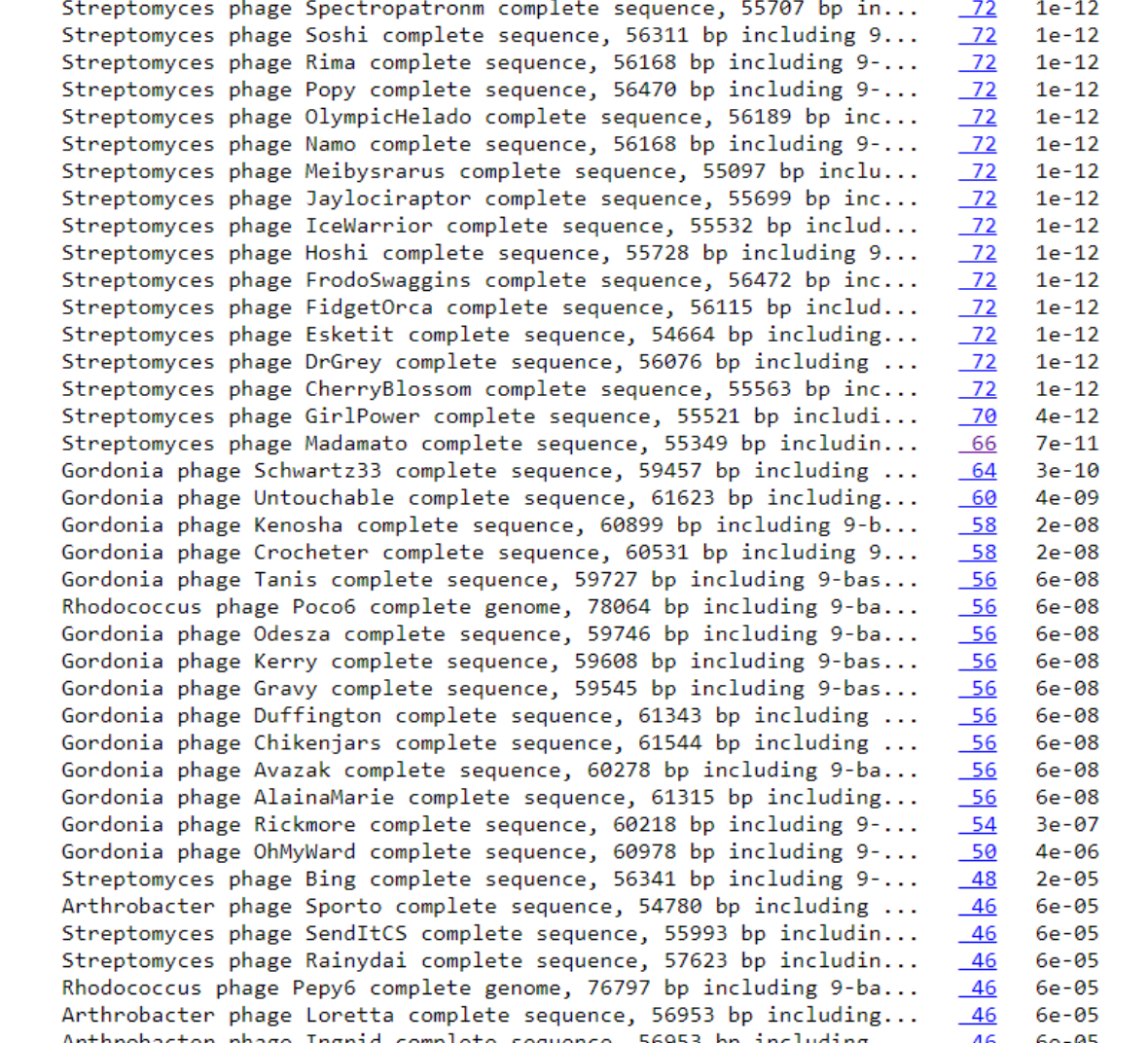


Figure 2: A screenshot of the PhagesDb BLAST search of one of the motifs found in the OlympicHelado genome

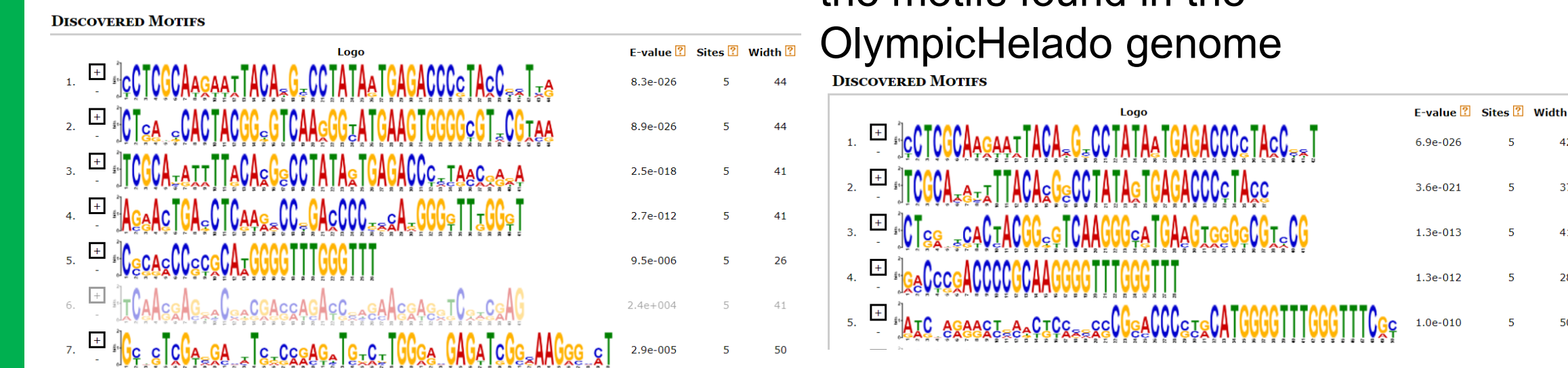


Figure 3: MEME output of motif search for DrGrey

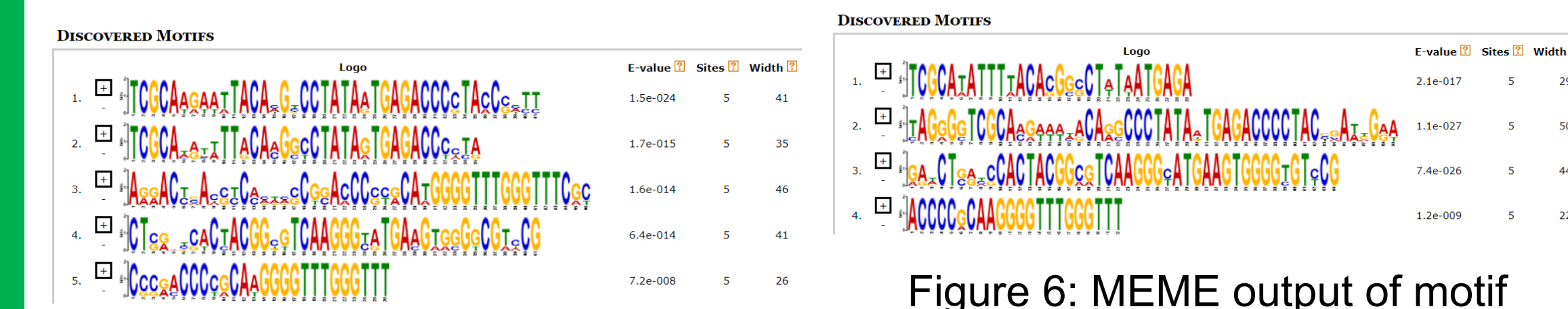


Figure 4: MEME output of motif search for Rima

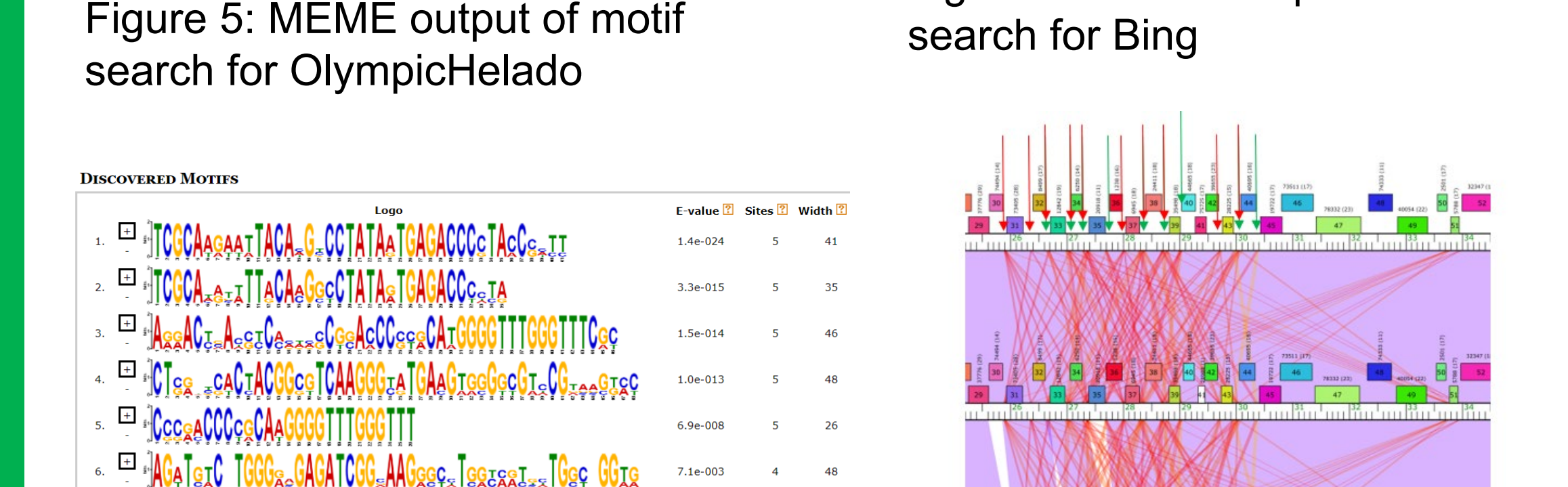


Figure 5: MEME output of motif search for OlympicHelado

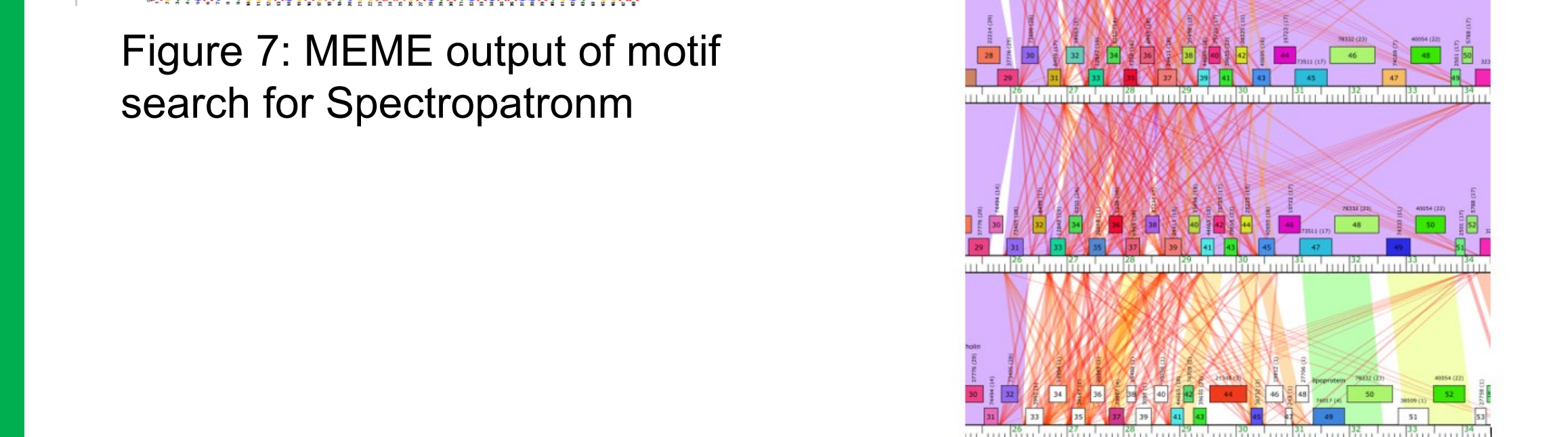


Figure 6: MEME output of motif search for Bing

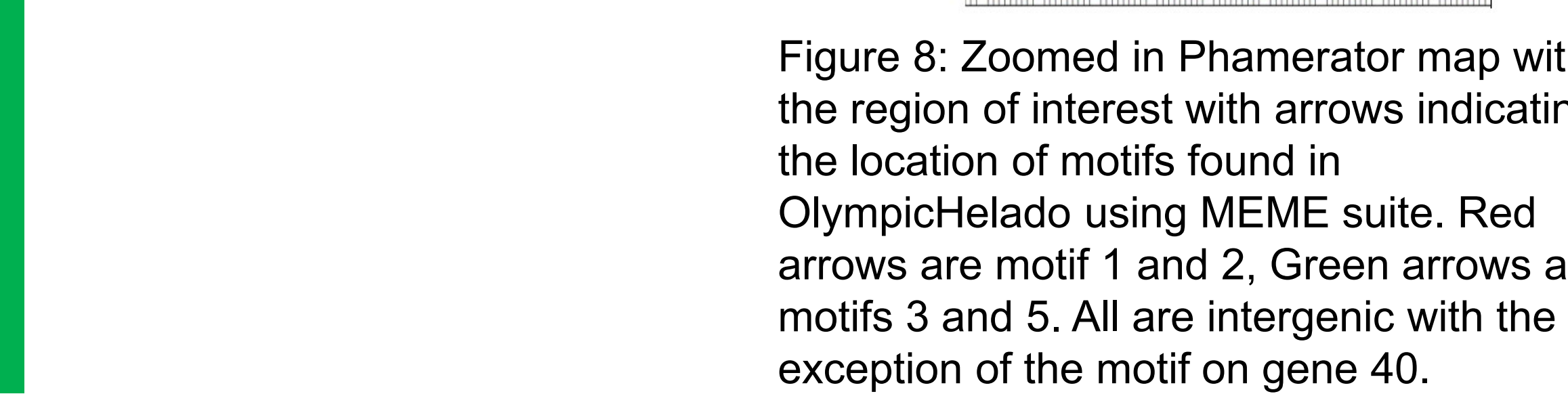


Figure 7: MEME output of motif search for Spectropatronm

Figure 8: Zoomed in Phamerator map with the region of interest with arrows indicating the location of motifs found in OlympicHelado using MEME suite. Red arrows are motif 1 and 2, Green arrows are motifs 3 and 5. All are intergenic with the exception of the motif on gene 40.

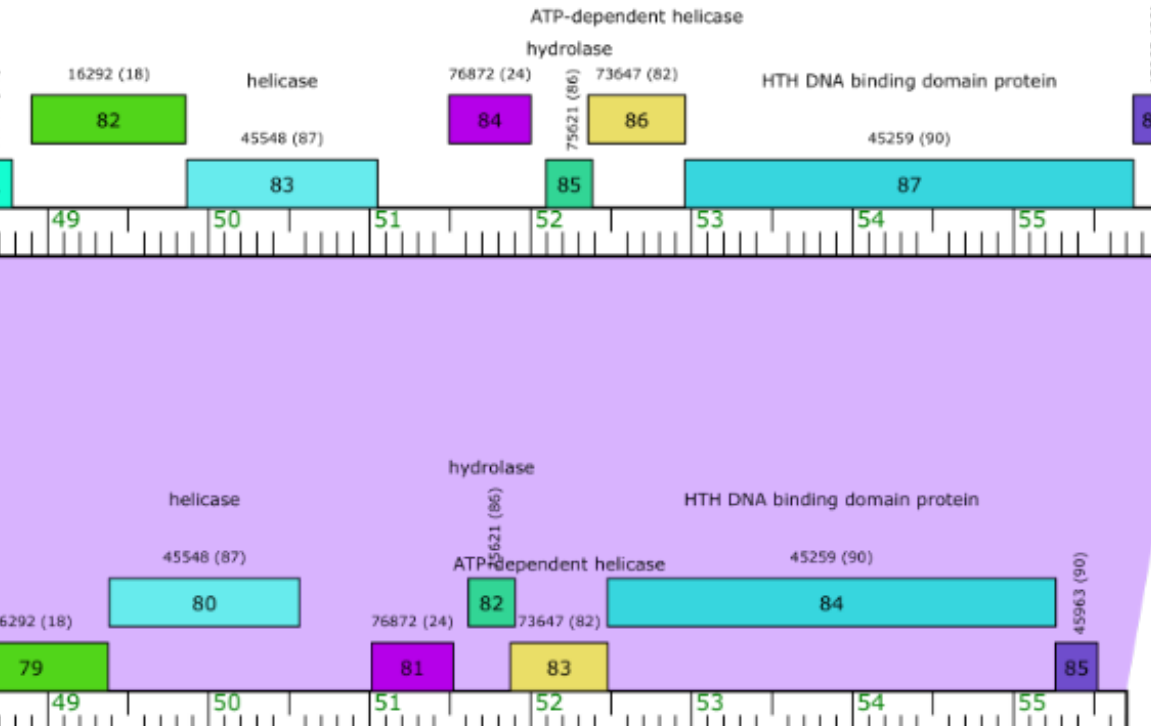


Figure 9: Phamerator map showing a comparison of the genomes of OlympicHelado and Spectropatronm