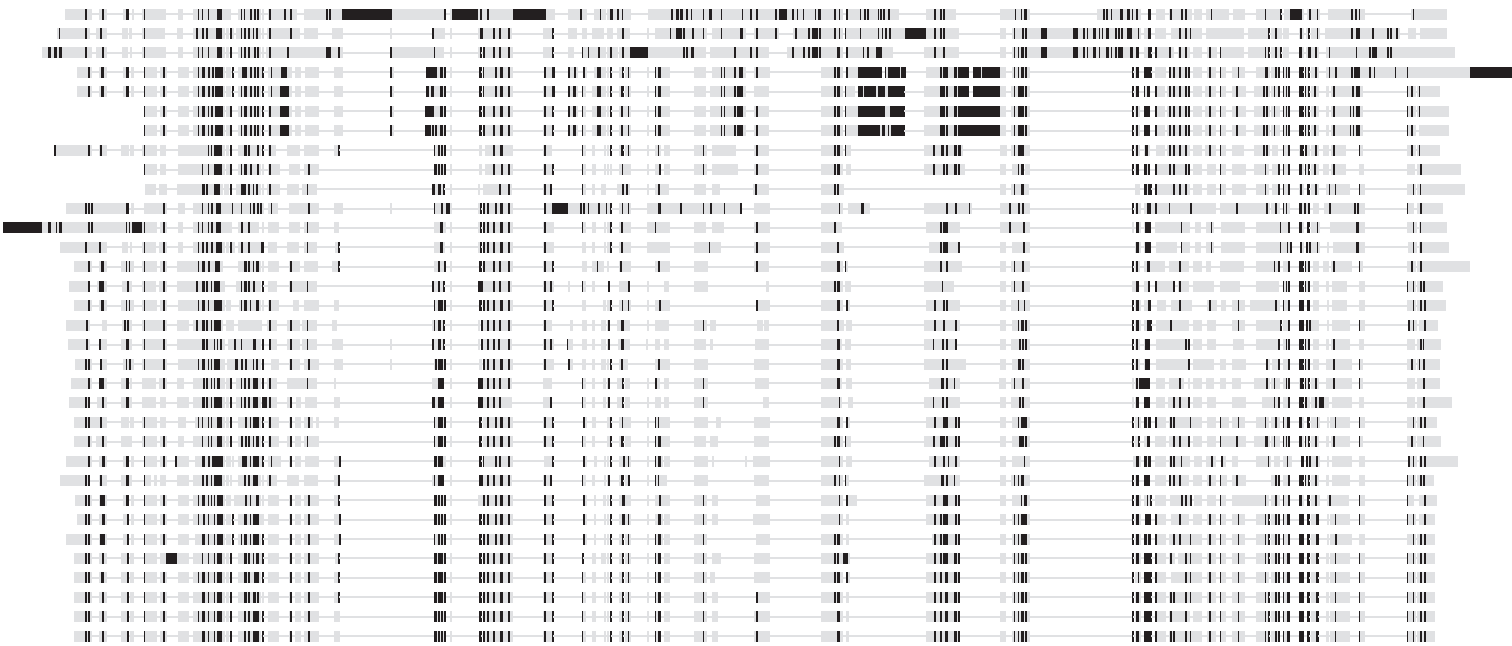


Supplementary Figure 1



Supplementary Figure 1. Alignment of selected algal BAHD sequences and 20 randomly selected plant BAHDs. The alignment was performed using MUSCLE v3.8.425 and default parameters in Geneious v2022.1.1. Highlighted in black are agreements to the consensus sequence in at least 50% of the sequences. The percentage is relative to the number of sequences having a residue at a given alignment position.