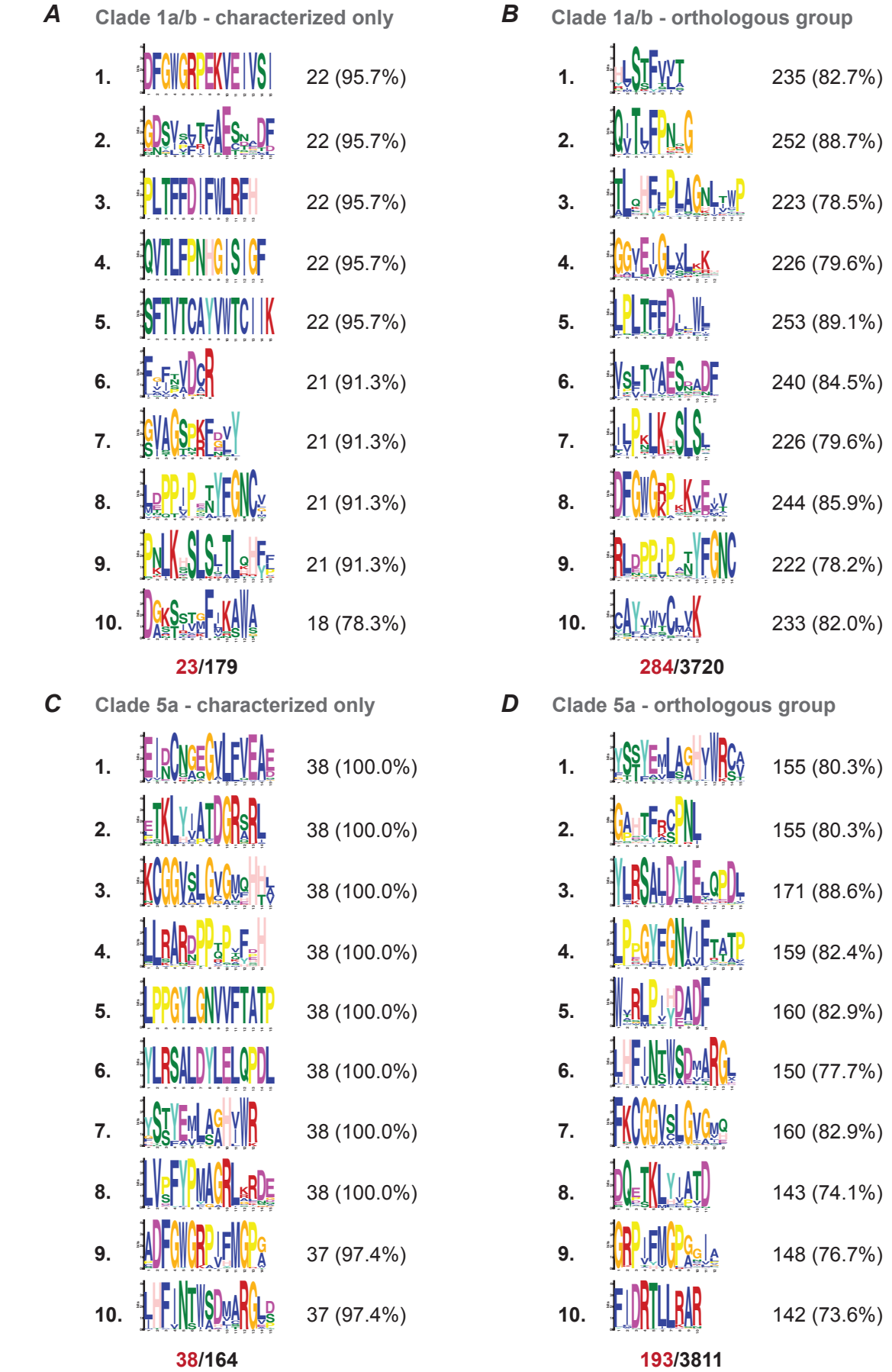
Supplementary Figure 3



Supplementary Figure 3. Motifs found to be enriched using STREME in subclades 1ab and 5a. (A) Enriched motifs detected in biochemically characterized members of clade 1a/b in comparison to all other biochemically characterized BAHD acyltransferases used in this study. **(B)** Enriched motifs detected when using orthologous sequences of clade 1a/b identified accross 52 plant genomes, in comparison to all other known BAHD orthologous groups. **(C)** Motifs enriched in biochemically characterized members of clade 5a. **(D)** Motifs enriched in orthologous sequences corresponding to clade 5a. Numbers below each panel give the number of sequences analyzed (red) vs the control sequences (black). Numbers behind each motif give the number and percentage of sequences with the respective motif.