

Additional file 3

Similarity matrices of the RBP and its domains after MUSCLE multiple sequence alignment.

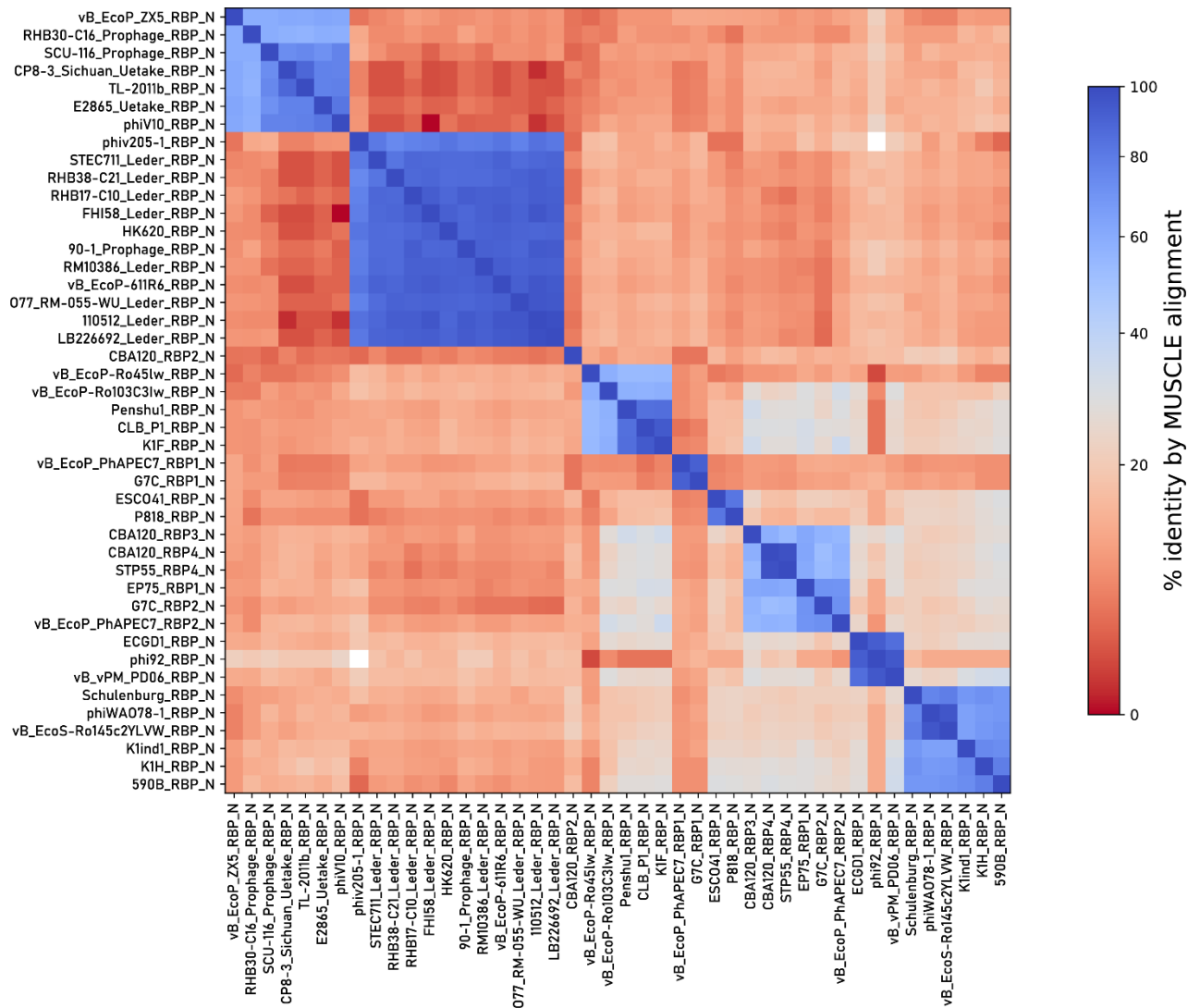


Figure S1: Similarity matrix of the RBP anchor domains after MUSCLE multiple sequence alignment.

The % aa identity between all delineated anchor amino acid sequences is visualized. Clustering corresponds to the branching of the phylogenetic tree of the RBP anchor domains (**Figure 5, b**).

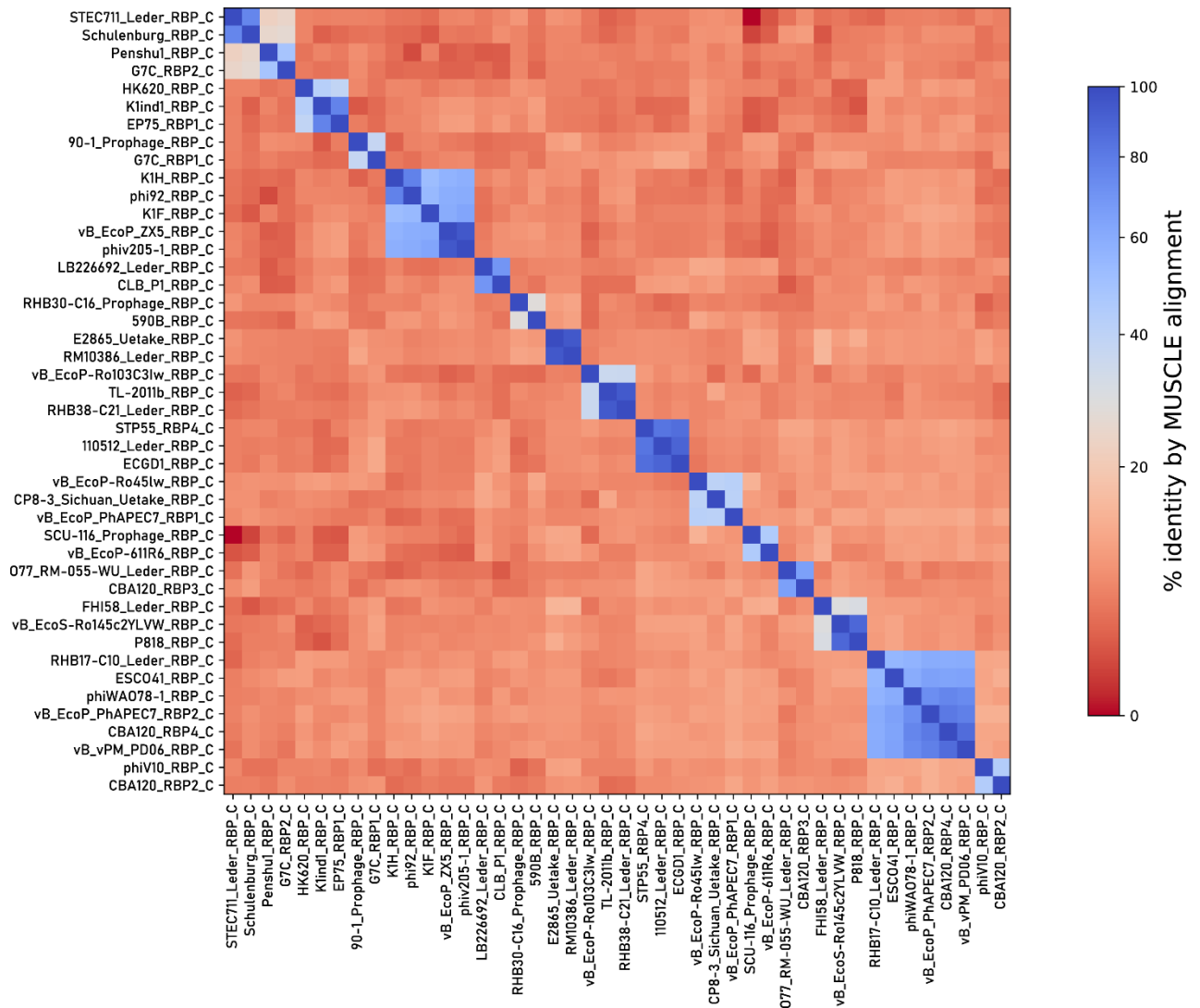


Figure S2: Similarity matrix of the RBP RBDs after MUSCLE multiple sequence alignment. The % aa identity between all delineated RBD amino acid sequences is visualized. Clustering corresponds to the branching of the phylogenetic tree of the RBDs (Figure 5, c).

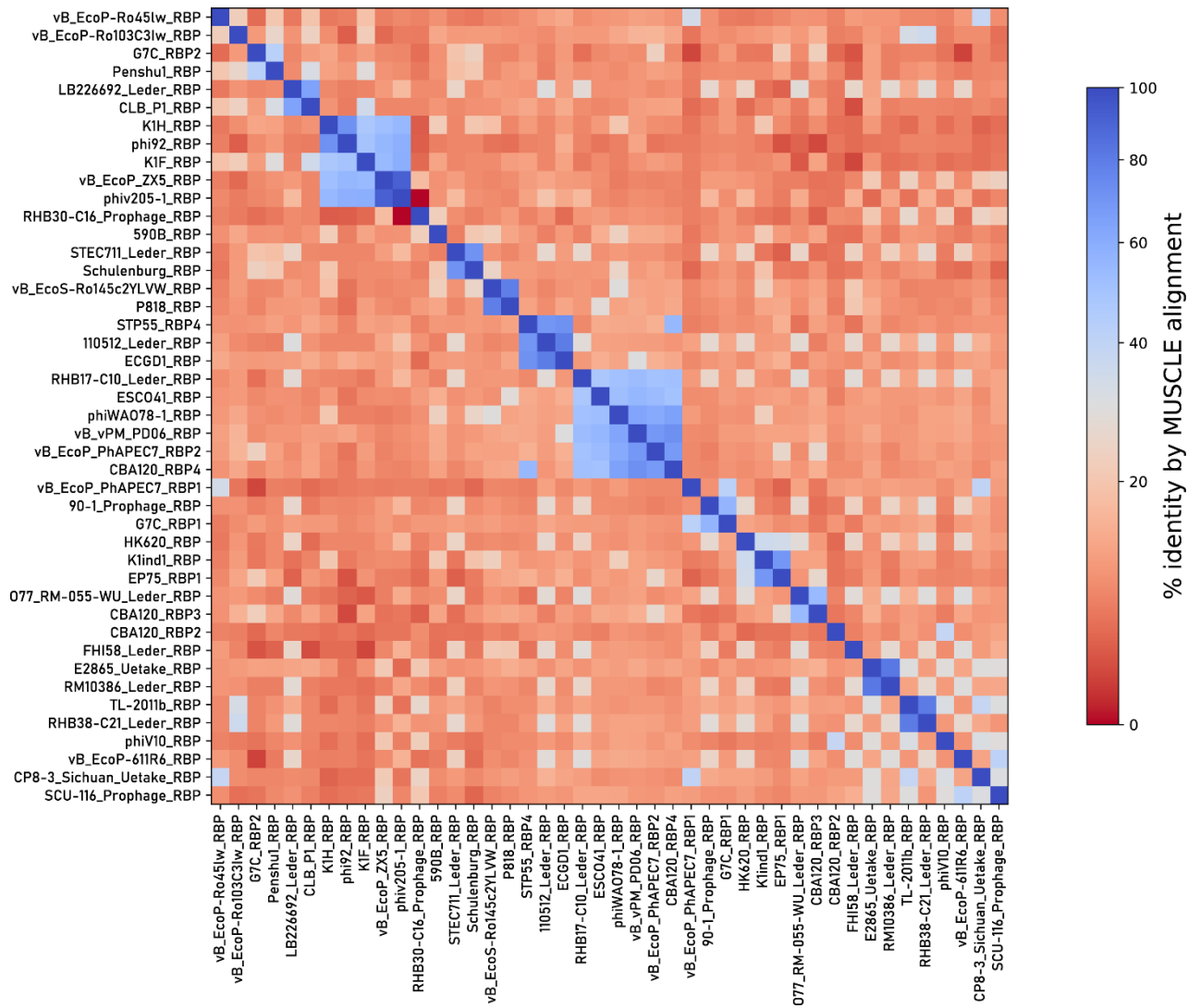


Figure S3: Similarity matrix of the complete RBPs after MUSCLE multiple sequence alignment. The % aa identity between all RBP amino acid sequences is visualized. Similarity matches correspond to the branching of the phylogenetic tree of the RBP coding sequences (**Figure 5, d**).