



Figure S4. Relationship between interface protein residues and positions of the corresponding R2R3-MYB target elements as calculated for three (A, B, C) clusters of neighbor subgroups as seen in Figure 5. Arrows connect bases to residues displaying maximum mutual information (in bits) calculated between columns of multiply aligned recognition helices and columns of aligned *cis*-elements. Dashed lines mark residues that are not directly contacting DNA but affect helix packing.