



Supplementary Figure 1. Phygenic tree of Tcf/Lef proteins.

The phylogenetic tree reconstruction was calculated with the FIGENIX automated phylogenomic annotation pipeline. Bootstrap values obtained by neighbor-joining, maximum parsimony, and maximum likelihood methods are provided for each node, or replaced by an asterisk in absence of the node for a given phylogenetic method. For each sequence, corresponding name, species and accession number are indicated.