

Figure S1. Phylogenetic relationship between avocado MYB transcription factor (TF) protein sequences and experimentally validated *Arabidopsis* MYB protein sequences. Phylogenetic analysis was performed using the maximum-likelihood method with a 1000 bootstrap replications. Green AtMYB sequences marked with a 'G' represent MYB TFs which play a role in cell growth, development and metabolism, while yellow AtMYB sequences marked with a 'D' represent TFs which play a role during defence responses.

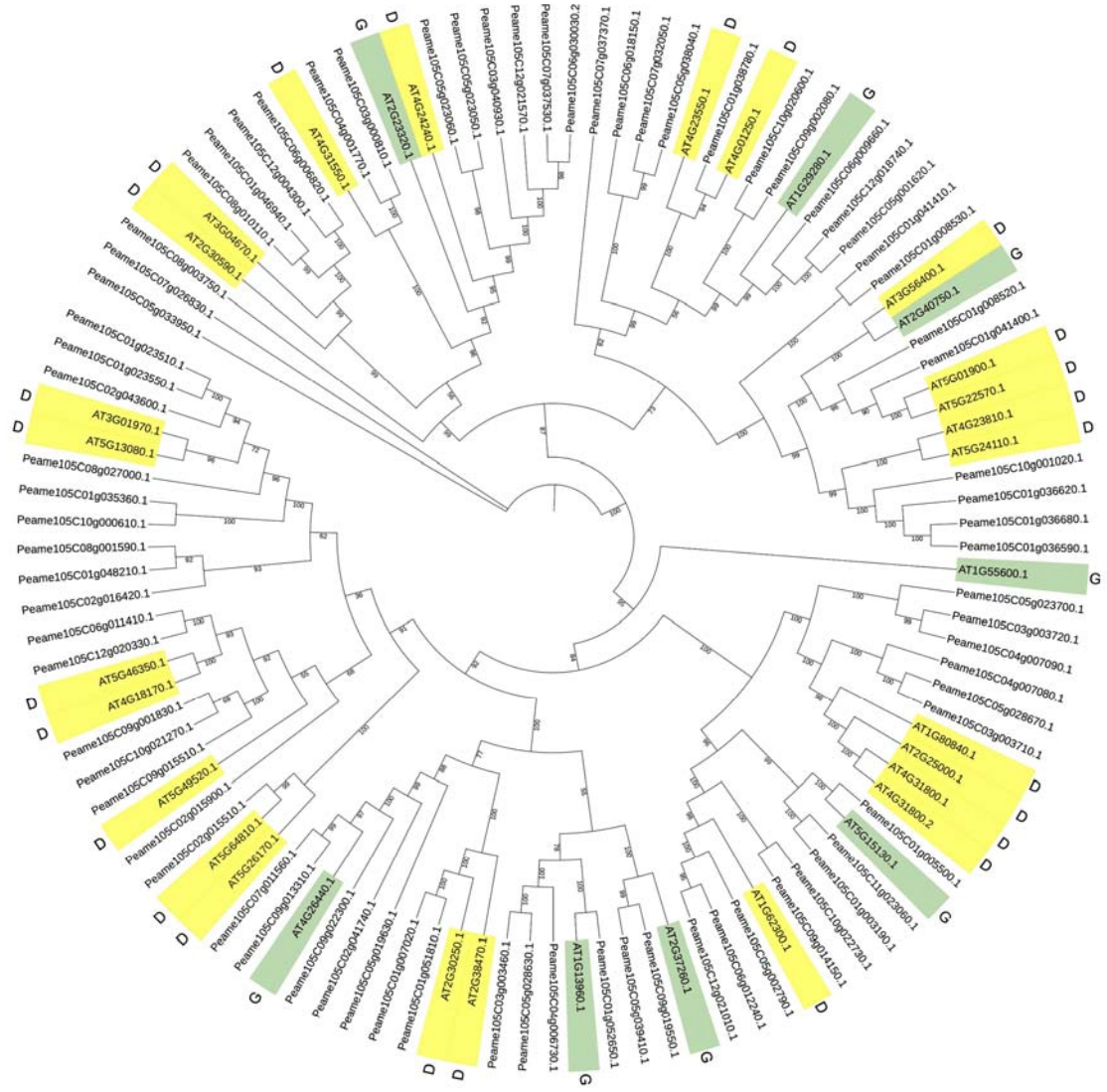


Figure S2. Phylogenetic relationship between experimentally validated *Arabidopsis* WRKY sequences and WRKY sequences identified from avocado. The maximum-likelihood method with a 1000 bootstrap replications was used to perform phylogenetic analysis. Genes marked with a 'D' and yellow labels indicate AtWRKYs shown to regulate immune responses, and genes marked with 'G' and green labels indicate AtWRKYs shown to regulate plant cell growth and development.pers

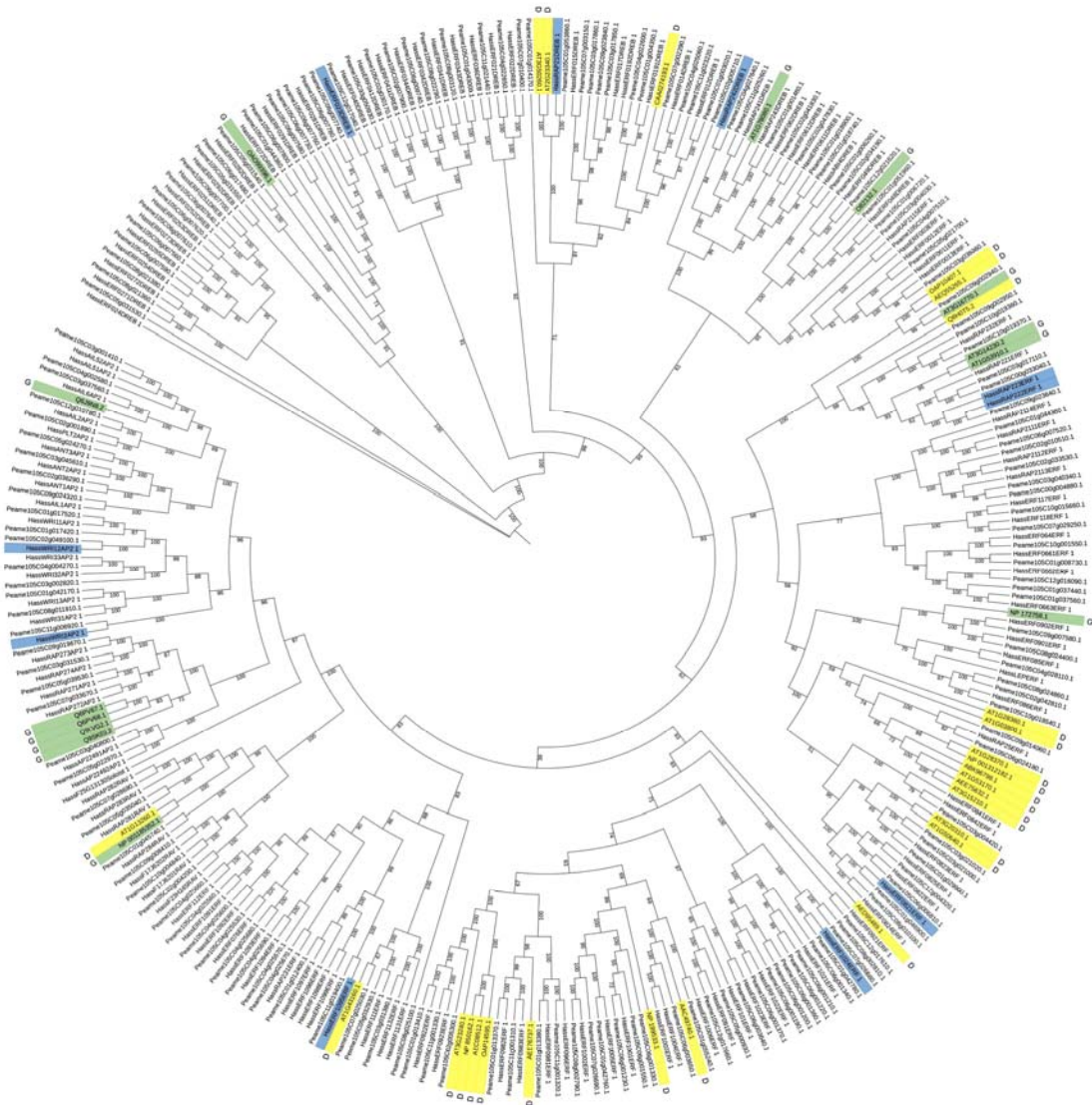


Figure S3. Phylogenetic tree of avocado AP2/ERF protein sequences and *Arabidopsis* AP2/ERF sequences. AP2/ERF sequences identified within the West Indian pure accession avocado genome are labelled as “Peame105”, while AP2/ERF sequences identified using the Hass avocado cultivar genome are labelled as “Hass”. HassAP2/ERFs shown to have regulatory roles during fatty acid accumulation are coloured with blue labels. *Arabidopsis* sequences used for the construction of the tree have been experimentally validated to either play a role in cell growth (marked ‘G’ and green labels) or defence responses (marked ‘D’ and yellow labels). Phylogenetic analysis, using the maximum-likelihood method, was performed using a 1000 bootstrap replications.