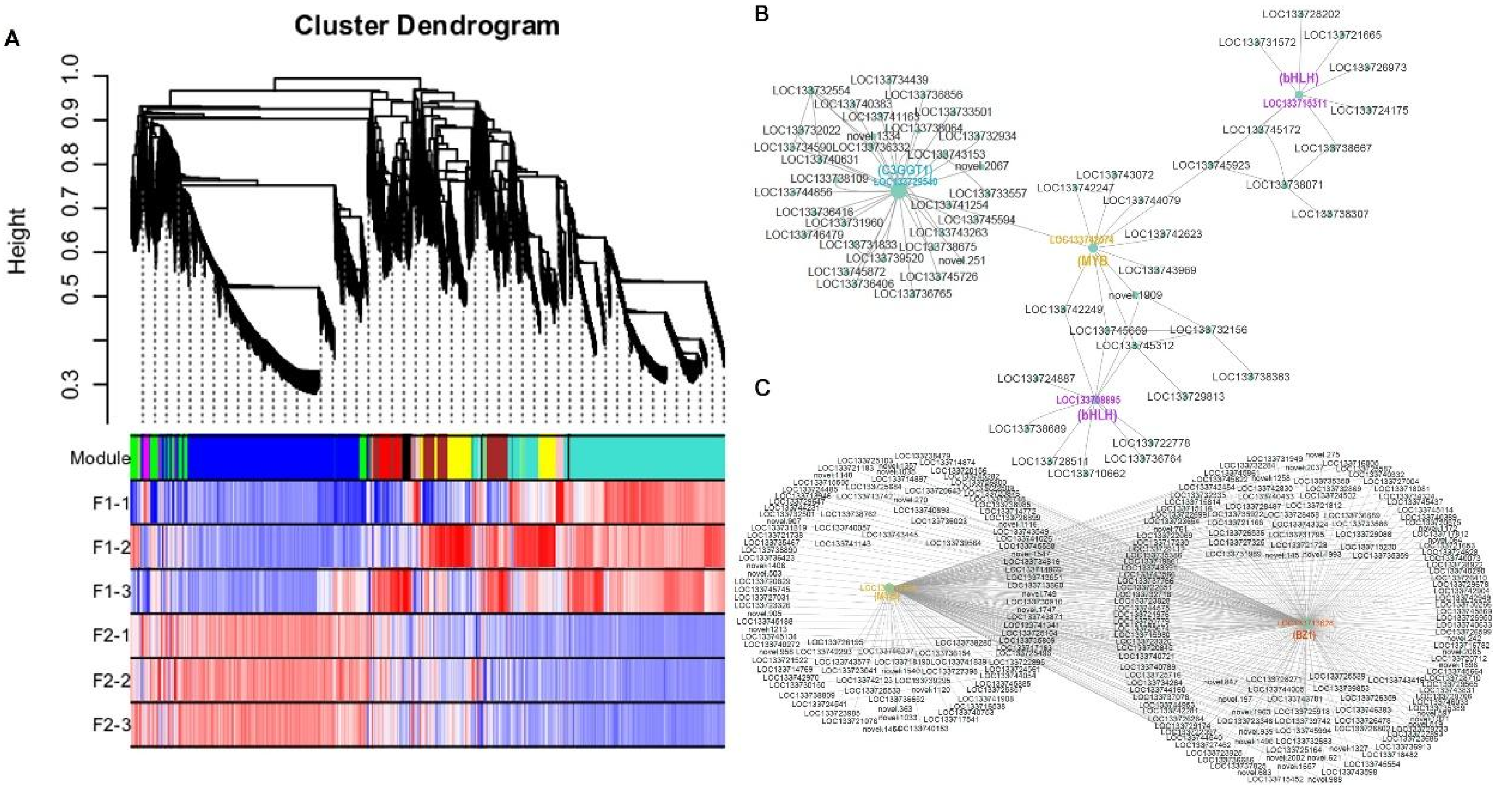

Figure S1. Establishment of a co-expression network. (A) Gene dendrogram and corresponding module colours. The clustering was based on the expression levels of genes. (B) Network component analysis of proteins associated with MYB and bHLH transcription factors as well as flavonoid biosynthesis within the turquoise module. (C) Network component analysis of proteins associated with MYB and bHLH transcription factors as well as anthocyanin biosynthesis within the blue module. Hub genes are labeled with different colors.