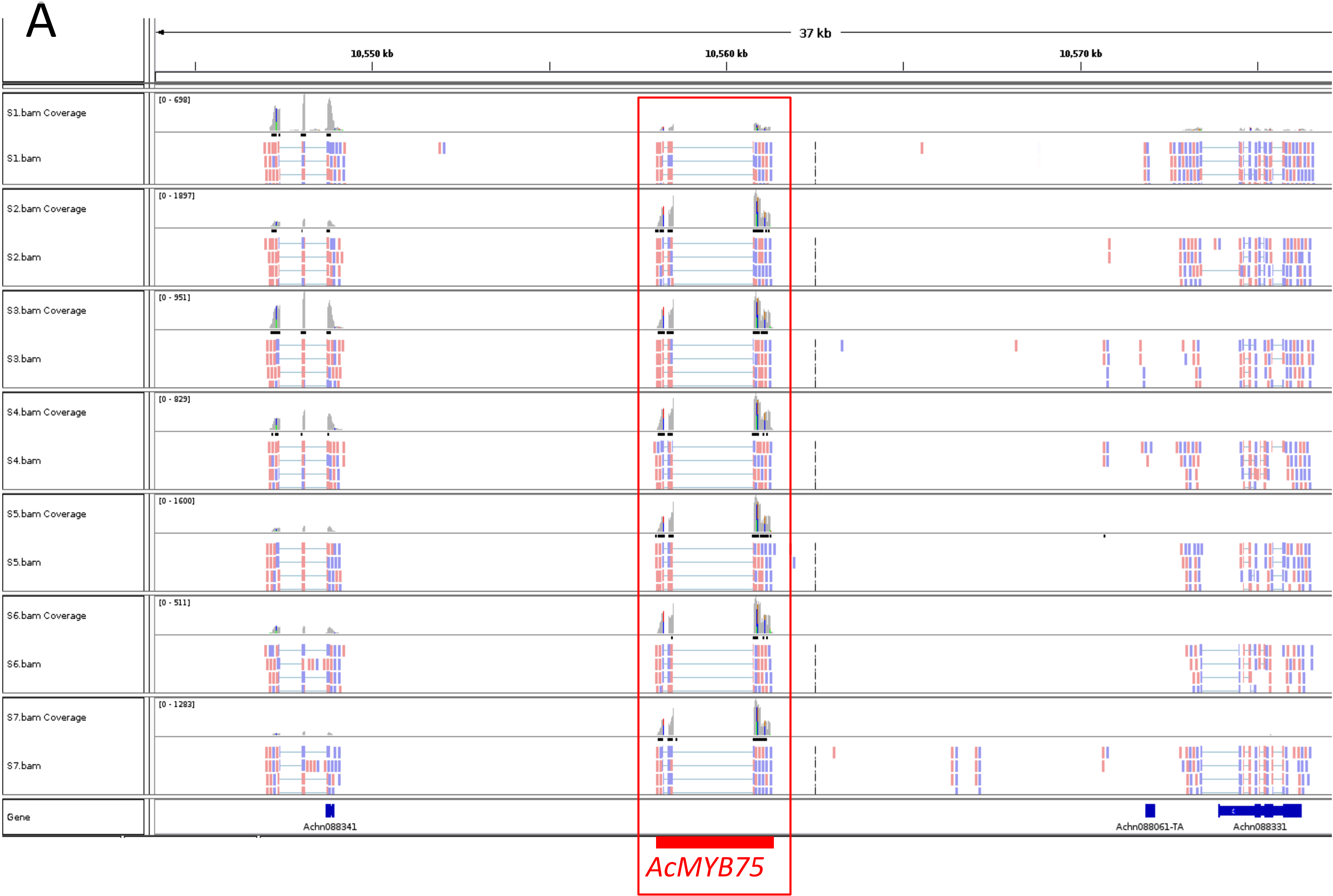


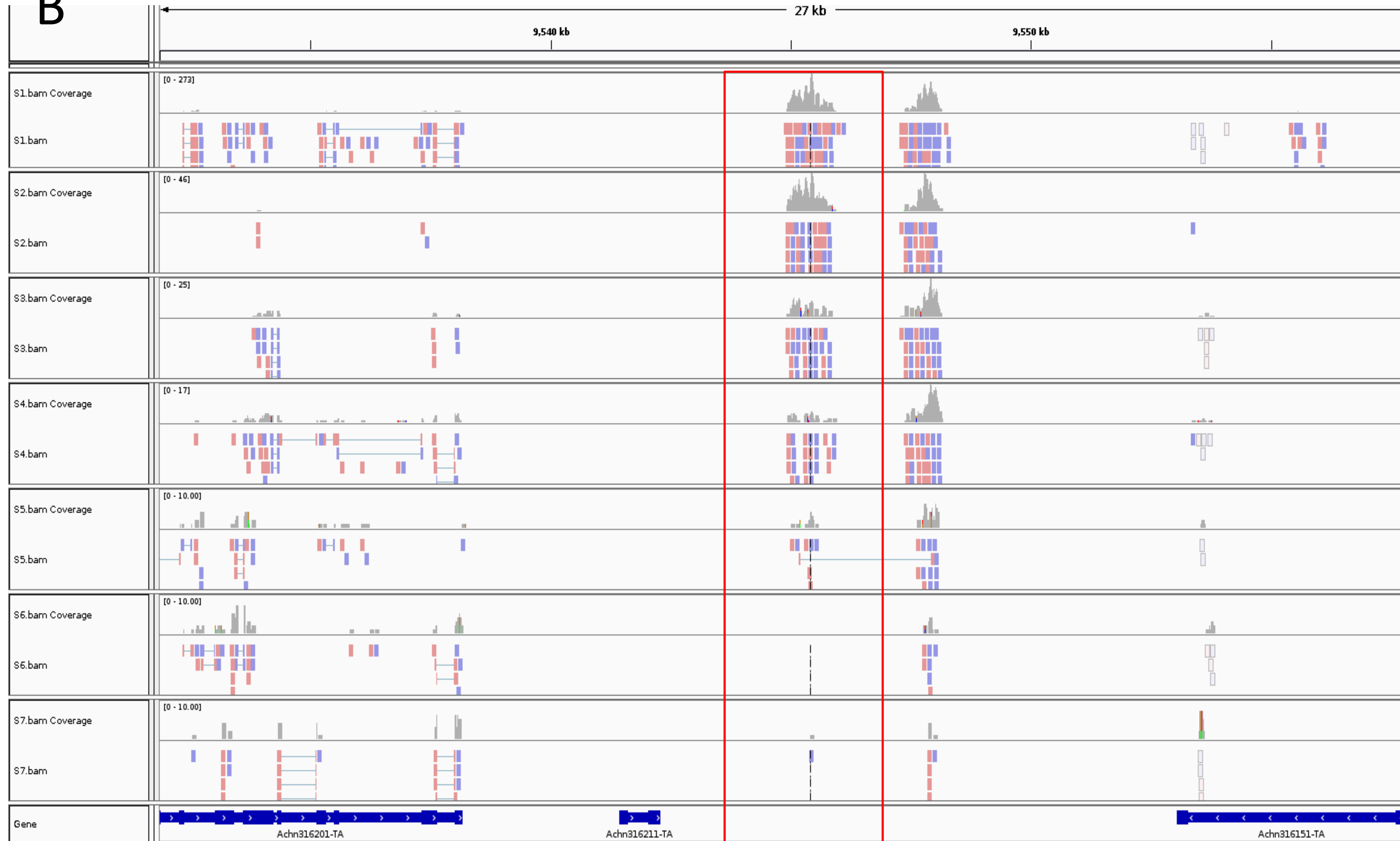
**Kiwifruit R2R3-MYB transcription factors and contribution of the novel
AcMYB75 to red kiwifruit anthocyanin biosynthesis**

Wenbin Li^{1 †}, Zehong Ding^{1 †}, Mengbin Ruan¹, Xiaolin Yu¹, Ming Peng^{1*}, Yifei Liu^{2*}

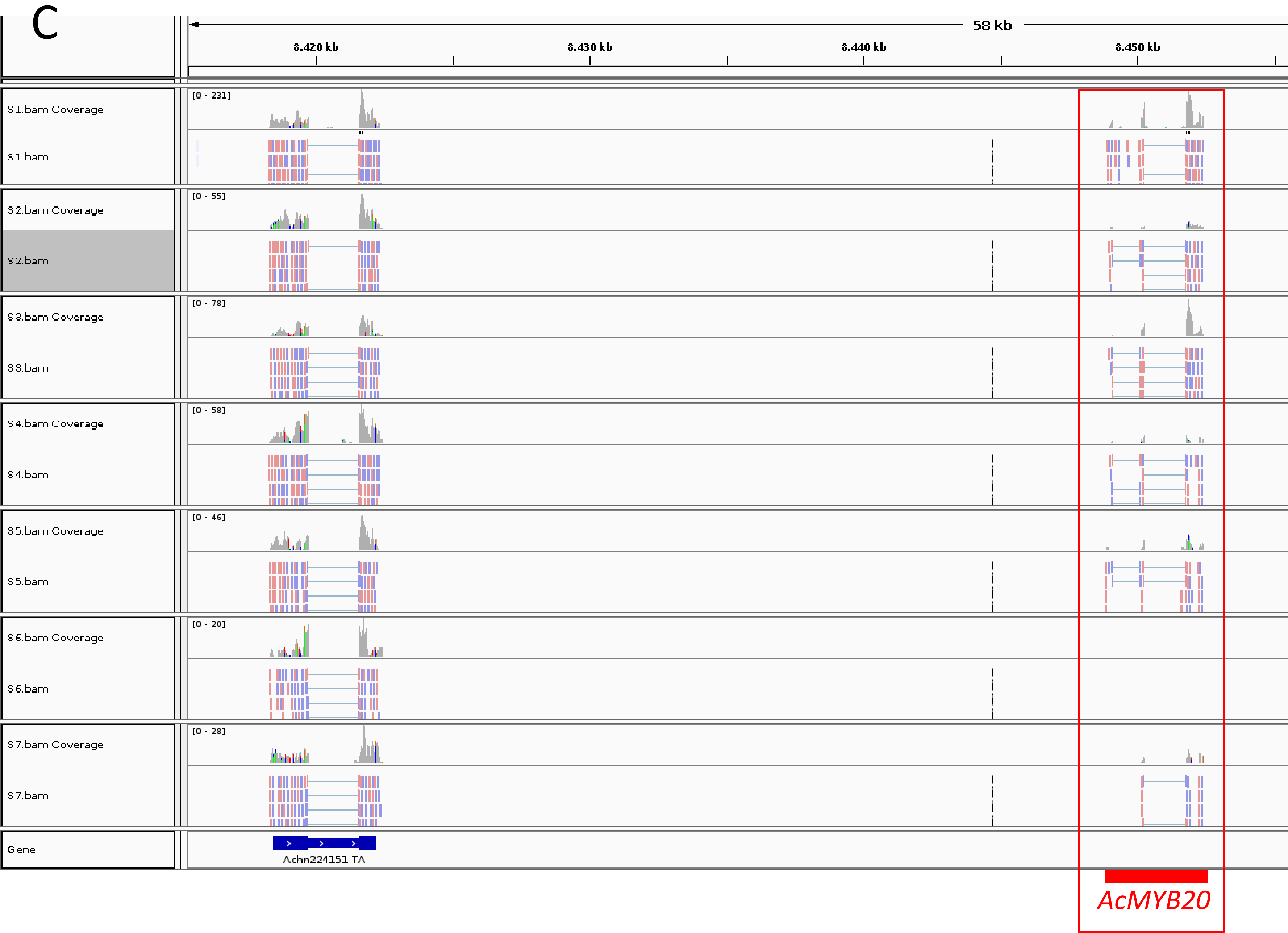
Supplementary Fig. S1
This analysis was performed in Integrative Genomics Viewer (IGV). For each of the five AcMYBs (AcMYB20, AcMYB70, AcMYB73, AcMYB77, and AcMYB75), lots of pair-end reads were mapped on a genome region without gene annotation, strongly supporting that they are novel AcMYBs and not previously identified.



B



AcMYB70



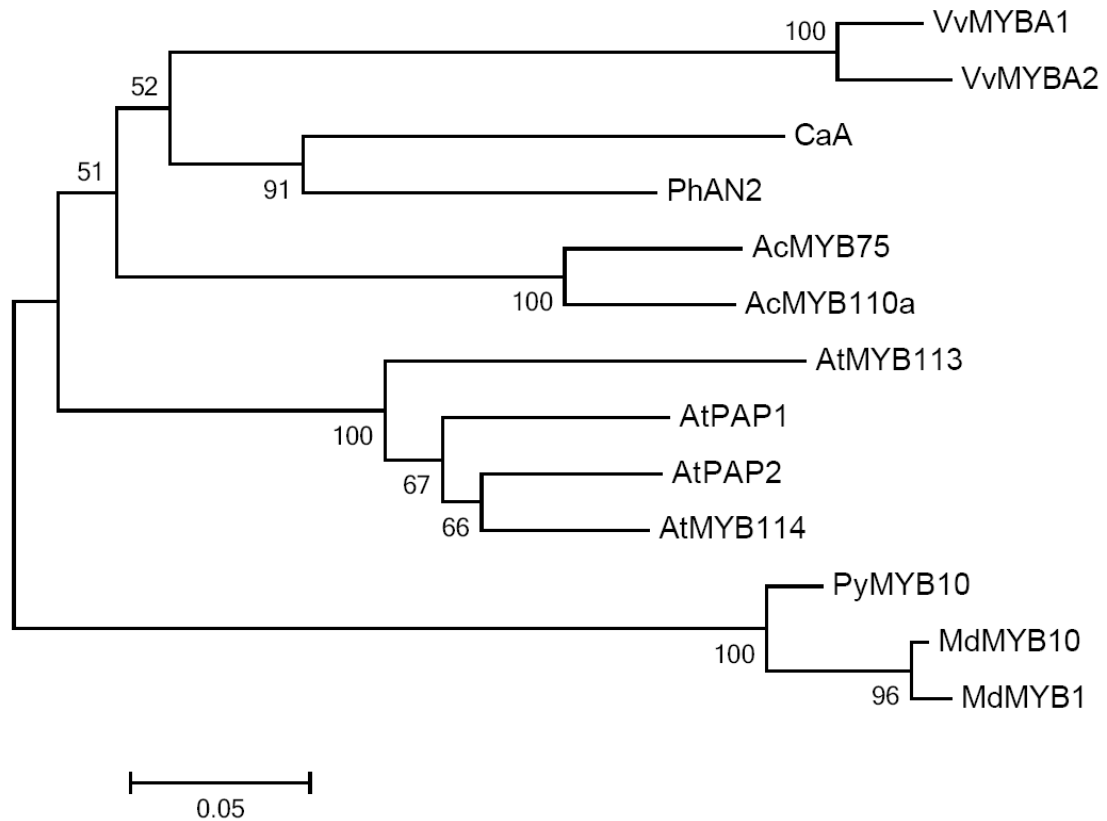
D



AcMYB73

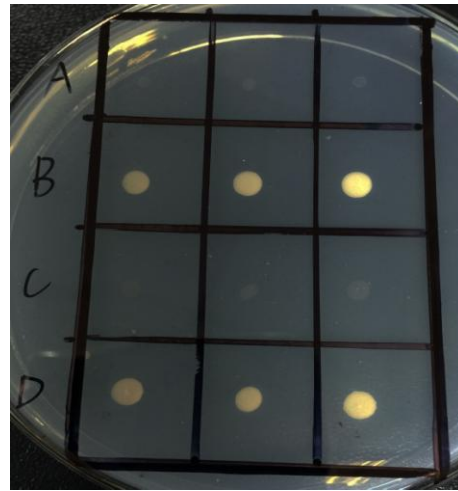
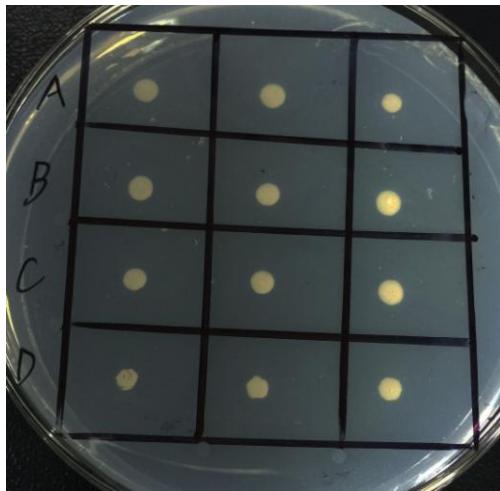


Supplementary Fig. S2



The alignment of amino acids from Fig. 4 was conducted with Clusta W. A linearized neighbor-joining tree was produced with MEGA software version 5.05. Bootstrap values for nodes are shown as numbers on branches. Evolutionary distances (Poisson-correction method) are shown as number of substitutions per amino acid site.

Supplementary Fig. S3



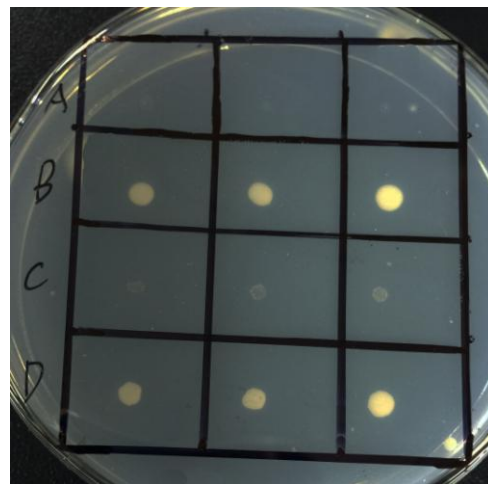
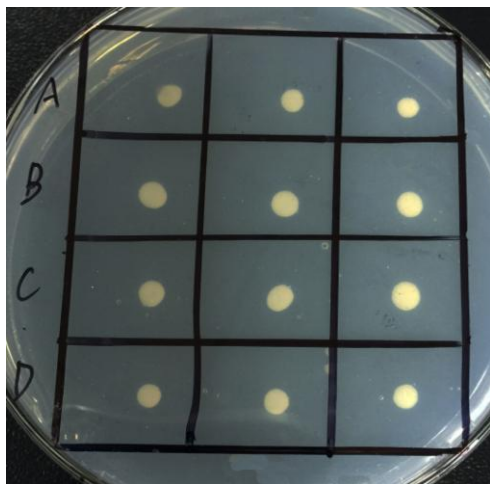
The yeast two hybrid screening between AcMYB75 and AtTT8 (At4g09820)
Left: SD/-Leu/-Trp; Right: SD/-Leu/-Trp/-His/-Ade. Three replicates

(A): BD-lam/AD-T;

(B): BD53/AD-T;

(C): AtTT8-1-BD/AcMYB75-AD (AtTT8-1 is from 58-603 bp of AtTT8 for bHLH-MYC_N superfamily);

(D): AtTT8-N-BD/AcMYB75-AD (AtTT8-N is from 1-603 bp of AtTT8)



The yeast two hybrid screening between AcMYB75 and AtGL3 (At5g41315)
Left: SD/-Leu/-Trp; Right: SD/-Leu/-Trp/-His/-Ade. Three replicates

(A): BD-lam/AD-T;

(B): BD53/AD-T;

(C): AtGL3-1-BD/AcMYB75-AD (AtGL3-1 is from 55-633 bp of AtGL3 for bHLH-MYC_N superfamily);

(D): AtGL3-N-BD/AcMYB75-AD (AtGL3-N from 1-633 bp of AtGL3).