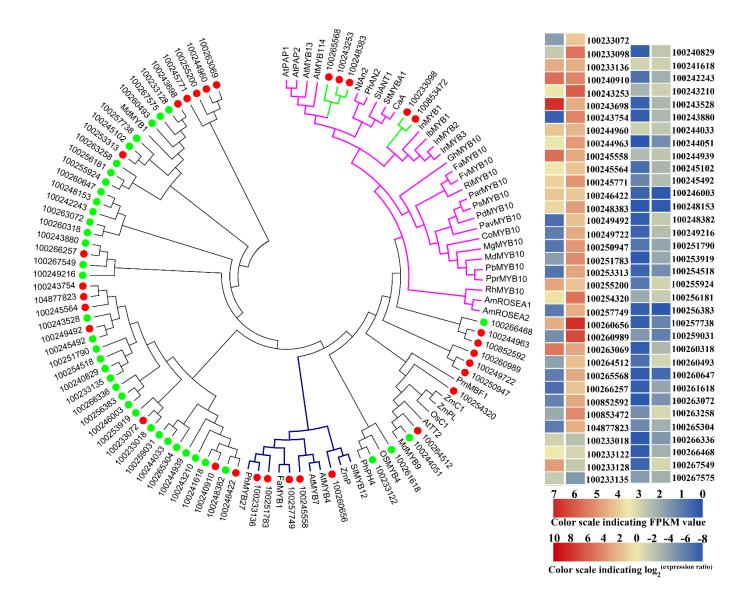
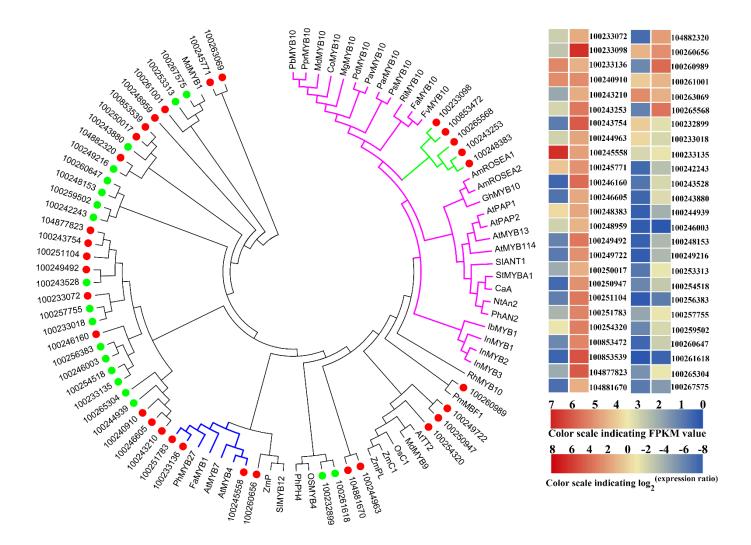


Supplementary Figure S1. Phylogenetic relationships among R2R3-MYB family members detected in Yan73 and its male parent leaves (based on RNA-seq data) and the R2R3-MYBs from other species. The gene IDs are listed in Supplementary Tables S2 and Tables S5. The up- and down-regulated transcription factors in Yan73 red leaf are indicated with red and green dots, respectively, and the corresponding transcript patterns are presented on the following two grids: the left presents the FPKM values of Yan73 red leaf, whereas the right presents the log2^(Yan73 red leaf/ its male parent leaf) values. The grid in the above with seven colors indicates the absolute expression levels in Yan73 leaf, with the FPKM values 0–2¹, 2¹–2², 2²–2³, 2³–2⁴, 2⁴–2⁵, 2⁵–2⁶ and 2⁶–2⁷ represented by 0–1, 1–2, 2–3, 3–4, 4–5, 5–6 and 6–7 respectively. Each functional clade is highlighted.



Supplementary Figure S2. Phylogenetic relationships among R2R3-MYB family members detected in Yan73 and its male parent stems (based on RNA-seq data) and the R2R3-MYBs from other species. The gene IDs are listed in Supplementary Tables S3 and Tables S5. The up- and down-regulated transcription factors in Yan73 red stem are indicated with red and green dots, respectively, and the corresponding transcript patterns are presented on the following two grids: the left presents the FPKM values of Yan73 red stem, whereas the right presents the $\log_2^{(\text{Yan73 red stem/ its male parent stem)}}$ values. The grid in the above with seven colors indicates the absolute expression levels in Yan73 stem, with the FPKM values $0-2^1$, 2^1-2^2 , 2^2-2^3 , 2^3-2^4 , 2^4-2^5 , 2^5-2^6 and 2^6-2^7 represented by 0-1, 1-2, 2-3, 3-4, 4-5, 5-6 and 6-7 respectively. Each functional clade is highlighted.



Supplementary Figure S3. Phylogenetic relationships among R2R3-MYB family members detected in Yan73 and its male parent tendrils (based on RNA-seq data) and the R2R3-MYBs from other species. The gene IDs are listed in Supplementary Tables S4 and Tables S5. The up- and down-regulated transcription factors in Yan73 red tendril are indicated with red and green dots, respectively, and the corresponding transcript patterns are presented on the following two grids: the left presents the FPKM values of Yan73 red tendril, whereas the right presents the $\log_2({\text{Yan73 red tendril/its male parent tendril})}$ values. The grid in the above with seven colors indicates the absolute expression levels in Yan73 tendril, with the FPKM values $0-2^1$, 2^1-2^2 , 2^2-2^3 , 2^3-2^4 , 2^4-2^5 , 2^5-2^6 and 2^6-2^7 represented by 0-1, 1-2, 2-3, 3-4, 4-5, 5-6 and 6-7 respectively. Each functional clade is highlighted.