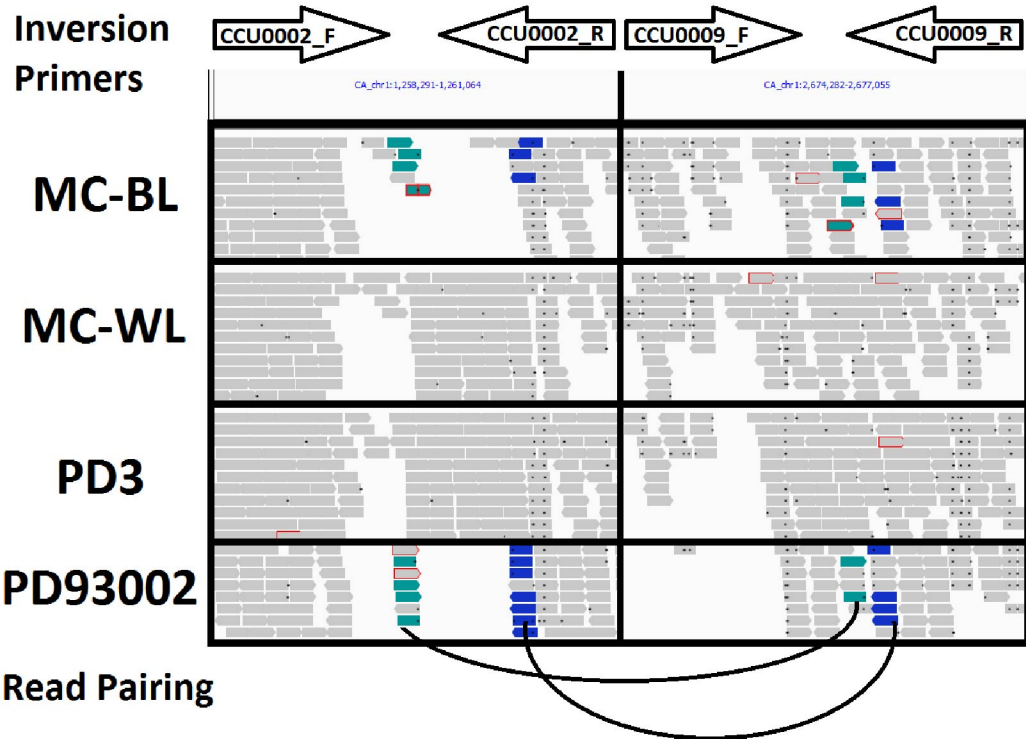
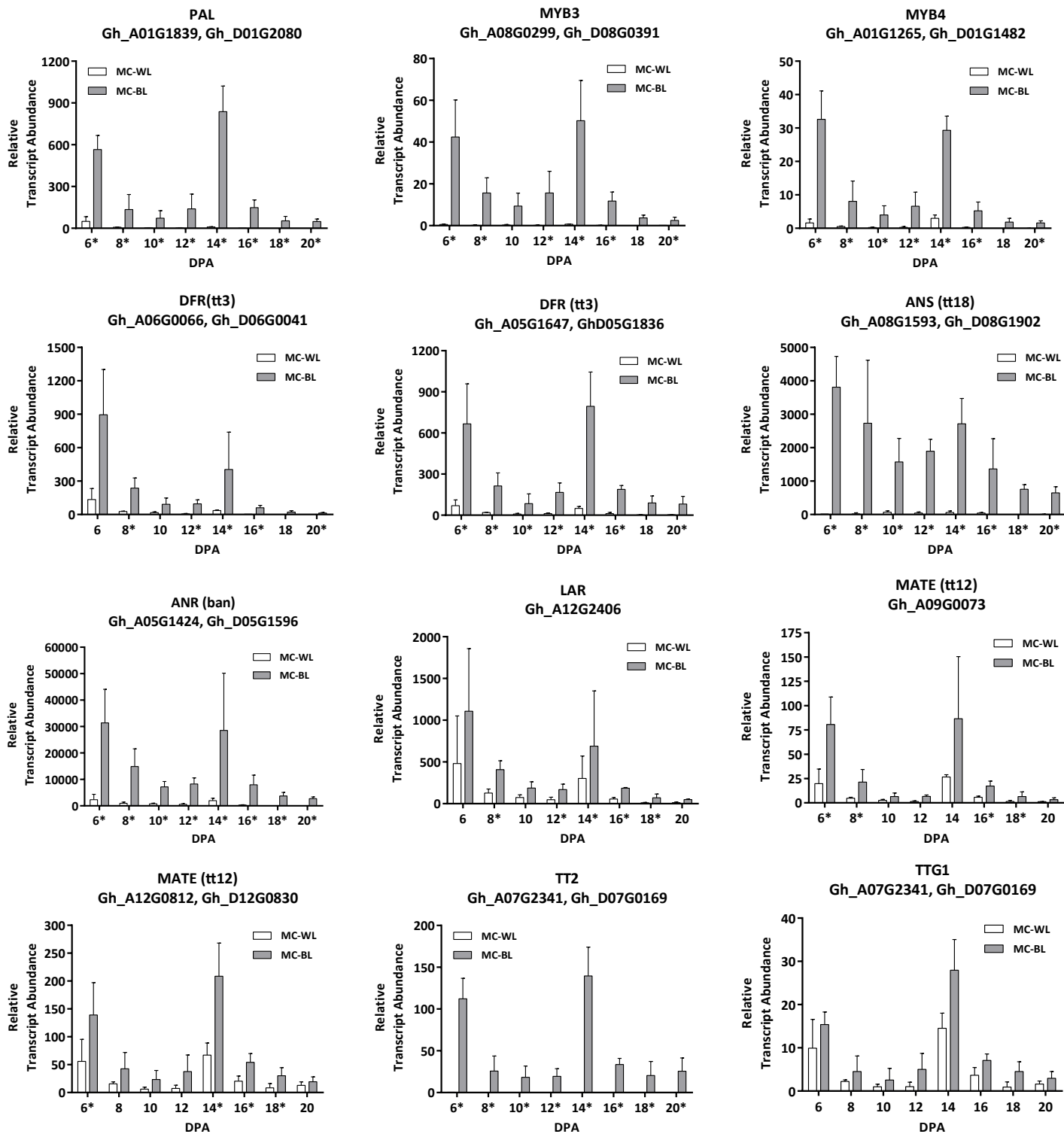


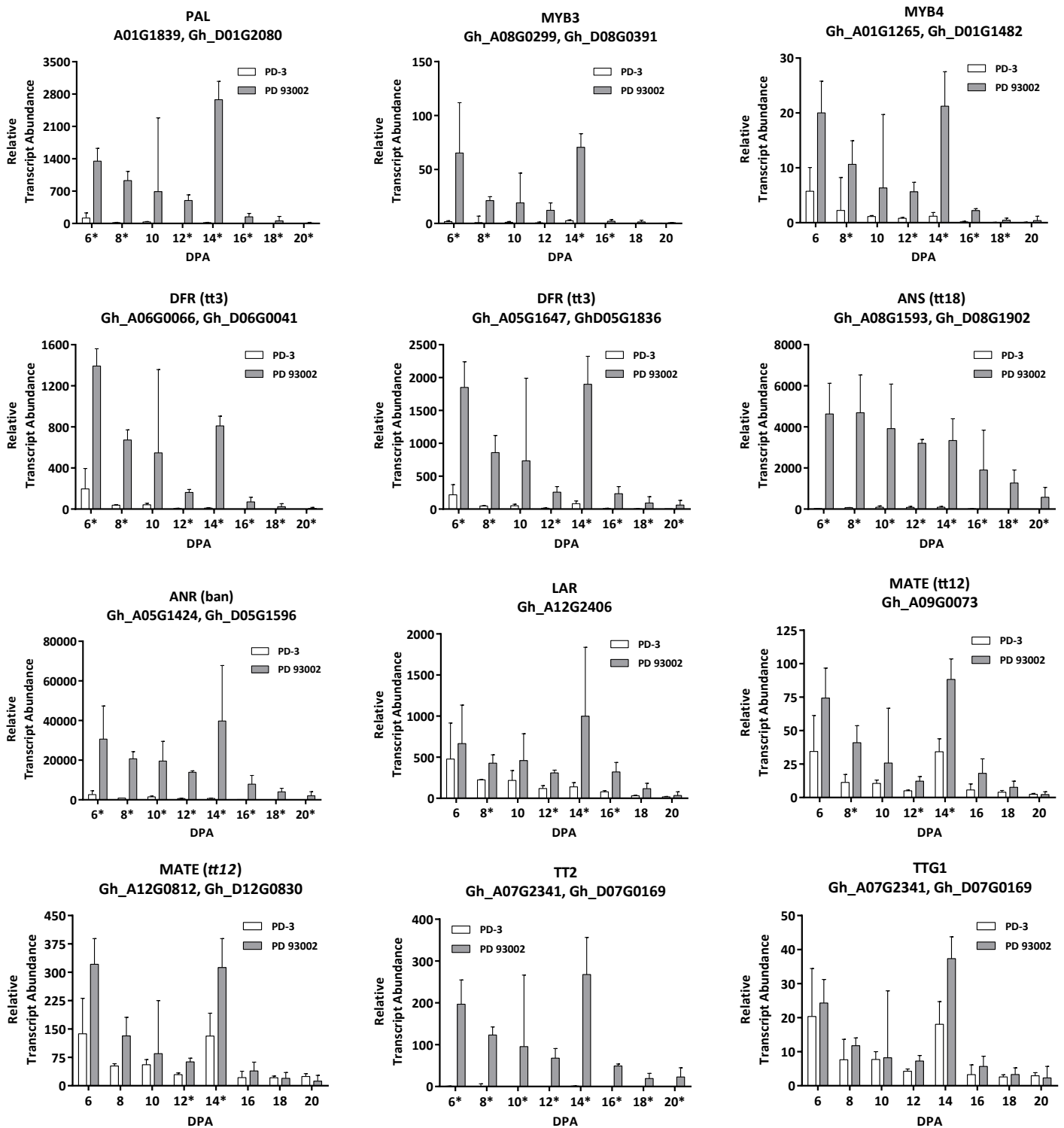
**Fig. S1.** Enhanced flame retardancy develops prior to brown colour in *Lc1* fibres. Accumulation of flavonoid PA precursor molecules demonstrated by DMACA staining is correlated with enhanced flame retardancy (lower heat release capacity) and elevated levels of inorganic material after pyrolysis (% char yield). **(A)** Bolls from the cotton lines PD 93002 and PD-3 with the carpels removed and fibres stained with DMACA and mature fibres. **(B)** Comparative analysis of fibre flammability (heat release capacity) and inorganic material remaining after pyrolysis (% char yield) from developing and mature fibre of the cotton lines PD 93002 and PD-3. Error bars represent standard deviation of three biological replicates.



**Fig. S2.** Alignment of DNA reads to pseudo-tetraploid reference genome reveals the 1.4 Mb genomic inversion upstream of *GhTT2\_A07* in *Lc1* cotton lines.



**Fig. S3.** A RT-qPCR comparative analysis of the transcript abundances of selected genes in the phenylpropanoid and flavonoid pathways from developing fibres of the cotton lines MC-BL and MC-WL. The relative transcript abundances of all genes, timepoints and cotton lines were normalized to TTG1 from 12 DPA MC-WL fibres. \* indicates greater than 2-fold difference in transcript abundance that is statistically significant at the 0.05 probability level as determined by paired t-test. The gene abbreviations can be found in Table S5.



**Fig. S4.** A RT-qPCR comparative analysis of the transcript abundances of selected genes in the phenylpropanoid and flavonoid pathways from developing fibres of the cotton lines PD 93002 and PD-3. The relative transcript abundances of all genes, timepoints and cotton lines were normalized to TTG1 from 12 DPA MC-WL fibres. \* indicates greater than 2-fold difference in transcript abundance that is statistically significant at the 0.05 probability level as determined by paired t-test. The gene abbreviations can be found in Table S5.