

Attachment 4. Supplementary Figures.

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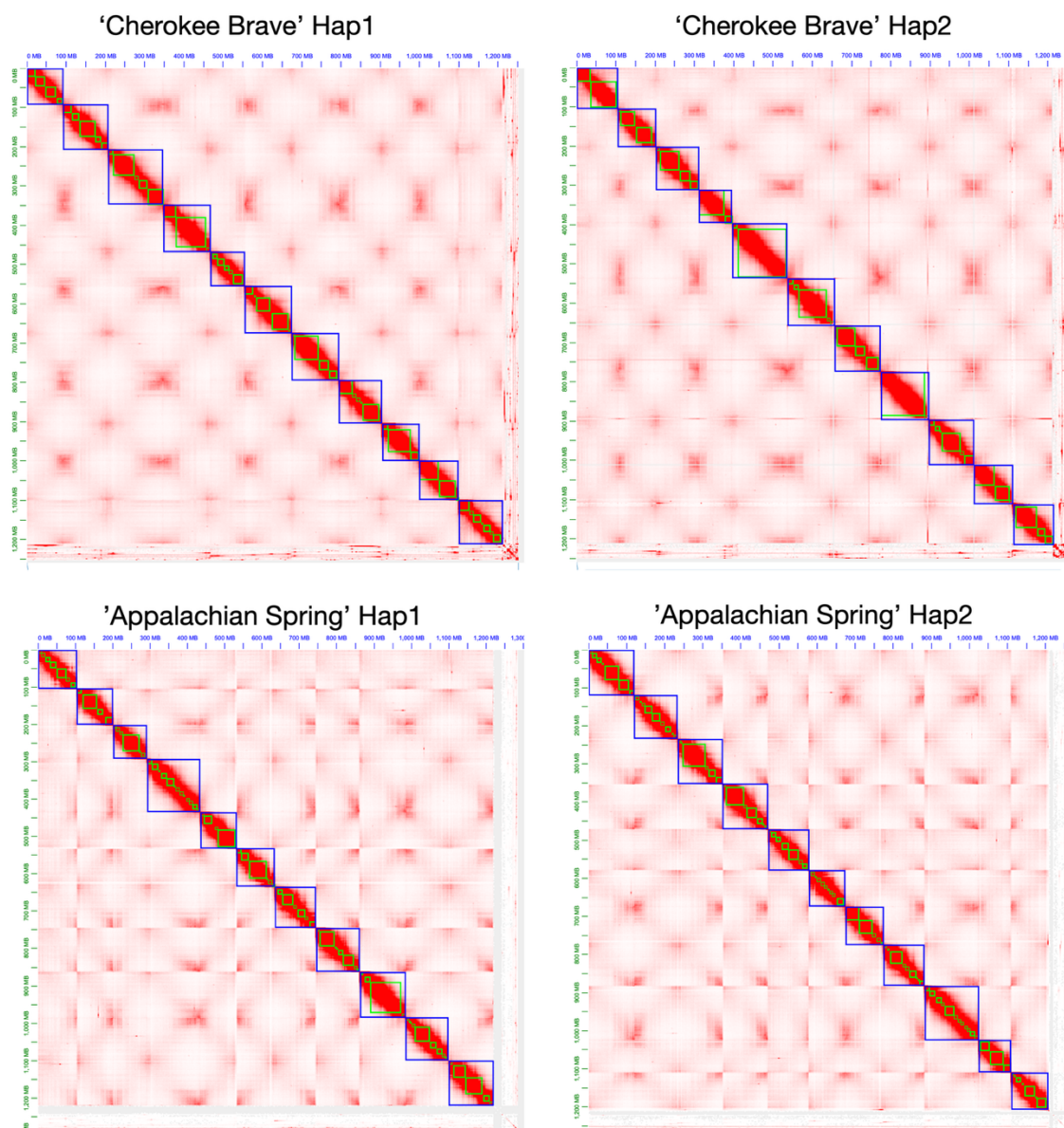


Figure S2. Hi-C contact maps for the four chromosome scale assemblies of flowering dogwood.

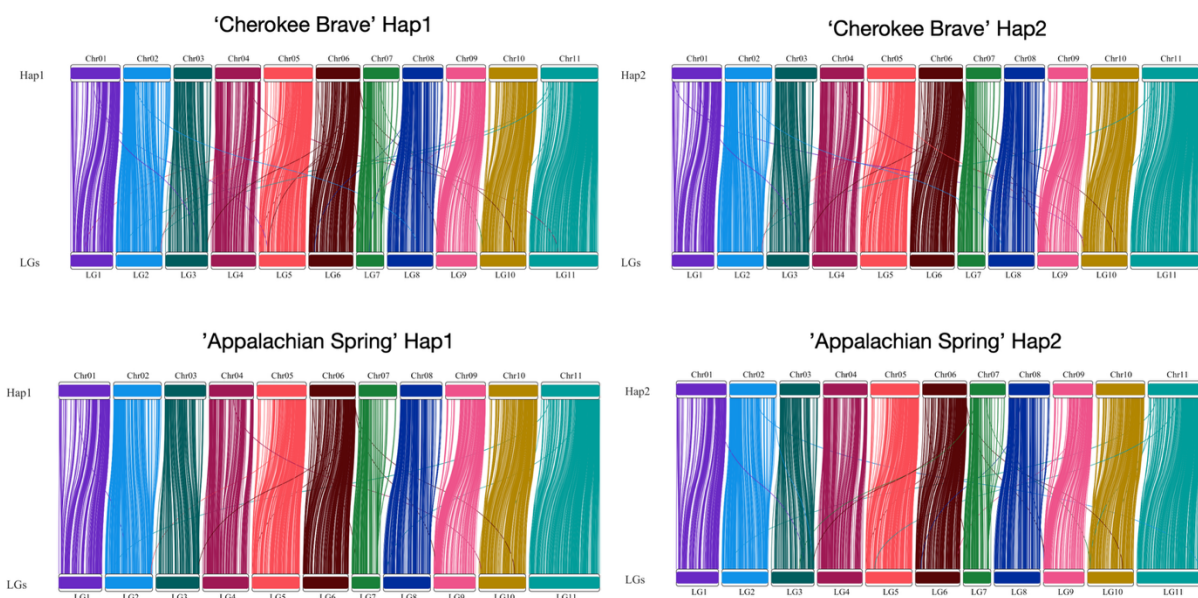


Figure S3. Visualization of the P25xP28 linkage map genetic markers from Moreau et al., 2022 mapped to the four flowering dogwood genome assemblies.

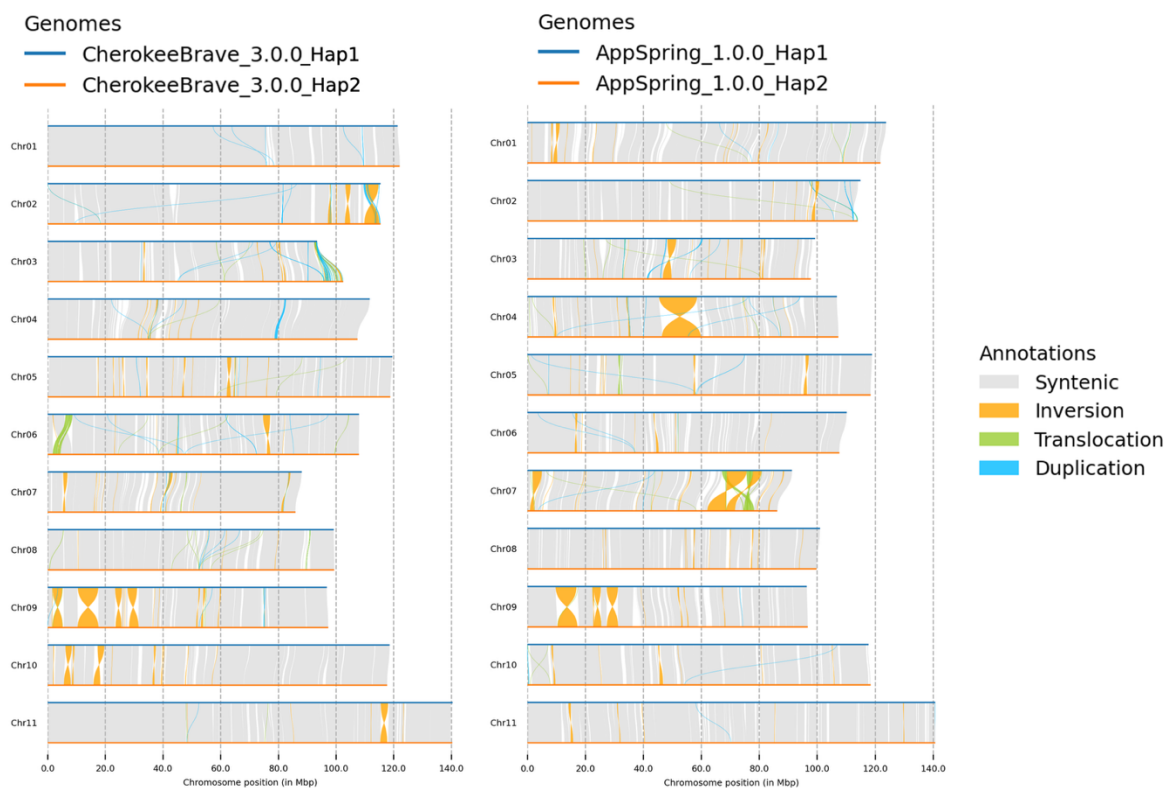


Figure S4. SyRI plot comparing haplotype 1 and 2 for *Cornus florida* 'Cherokee Brave' (left) and *C. florida* 'Appalachian Spring' (right) genomes.

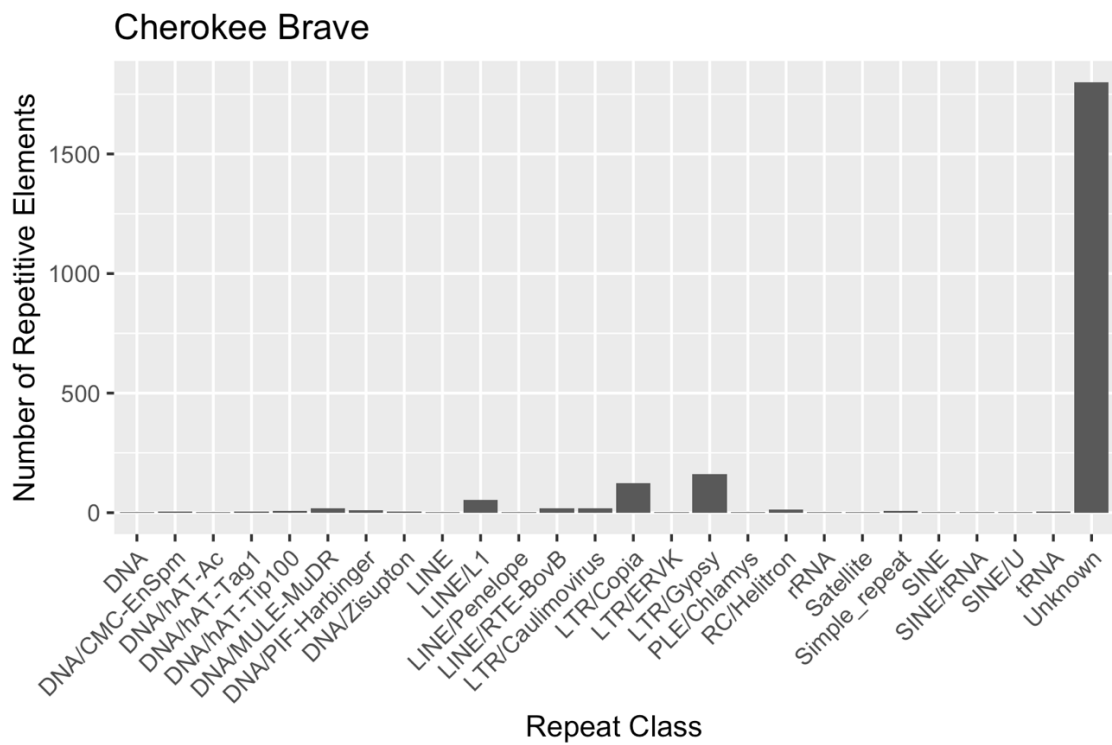
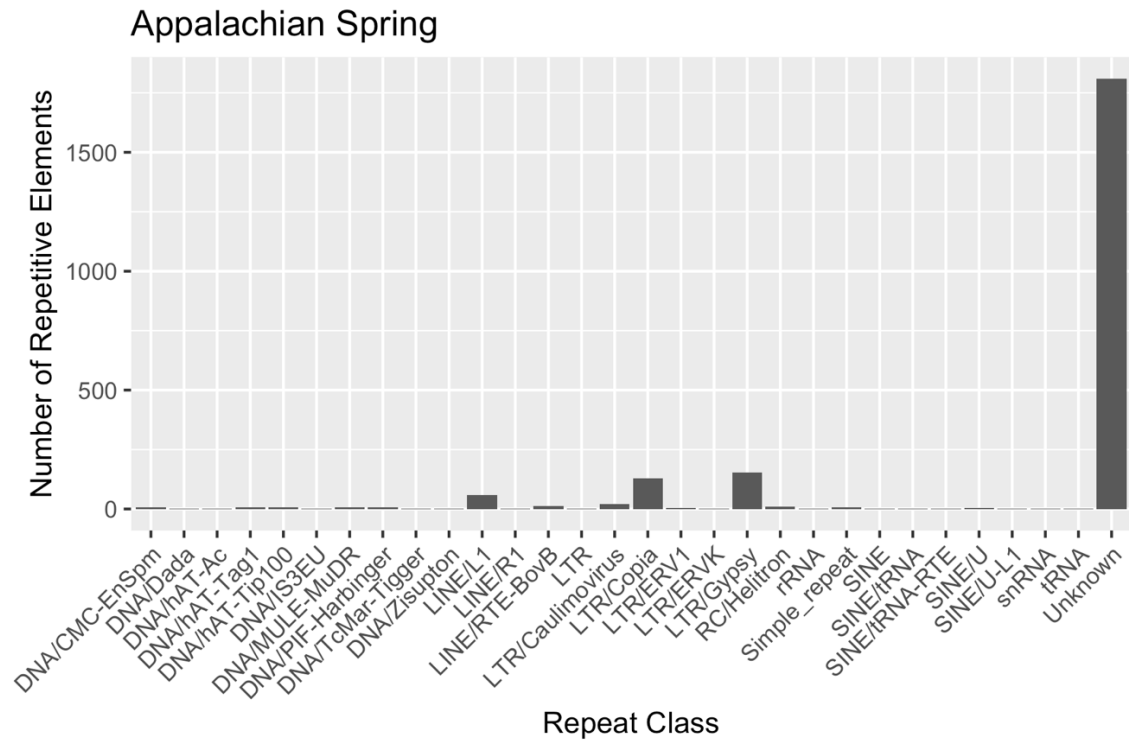


Figure S5. Repeat classes soft-masked in *Cornus florida* 'Appalachian Spring' and 'Cherokee Brave' genomes.

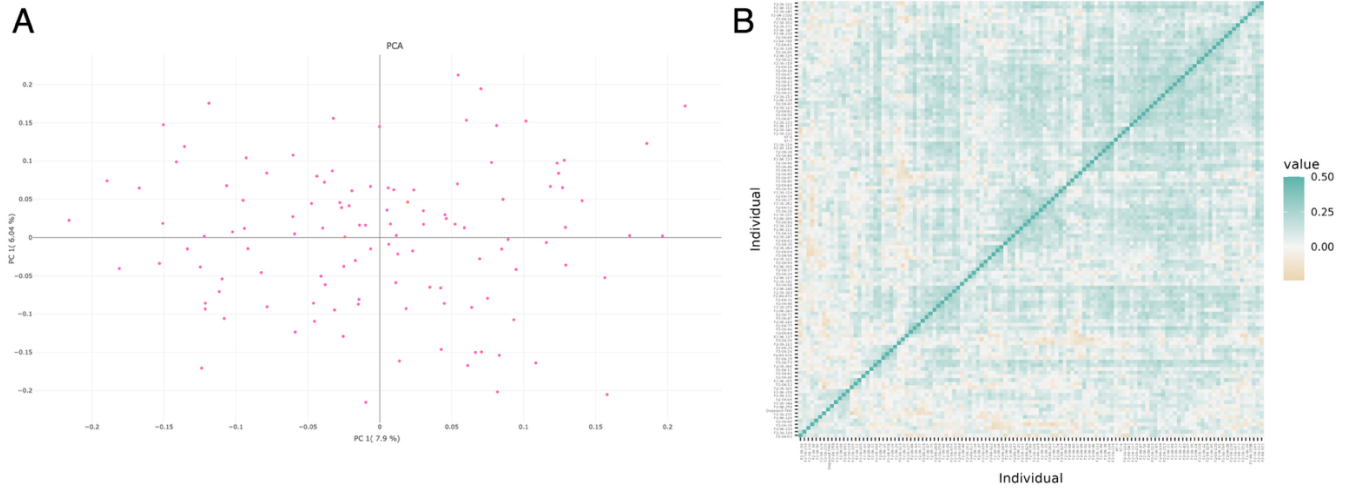


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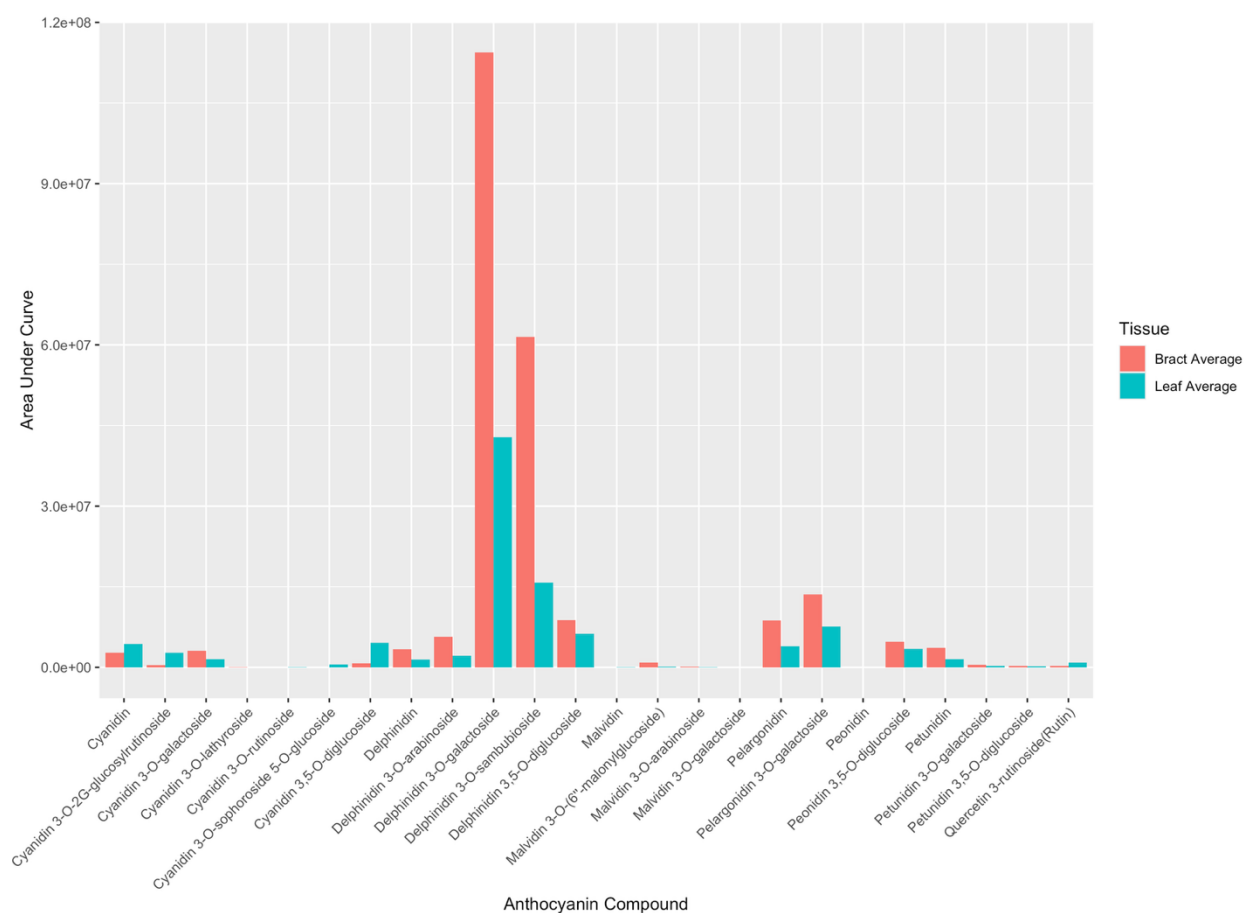


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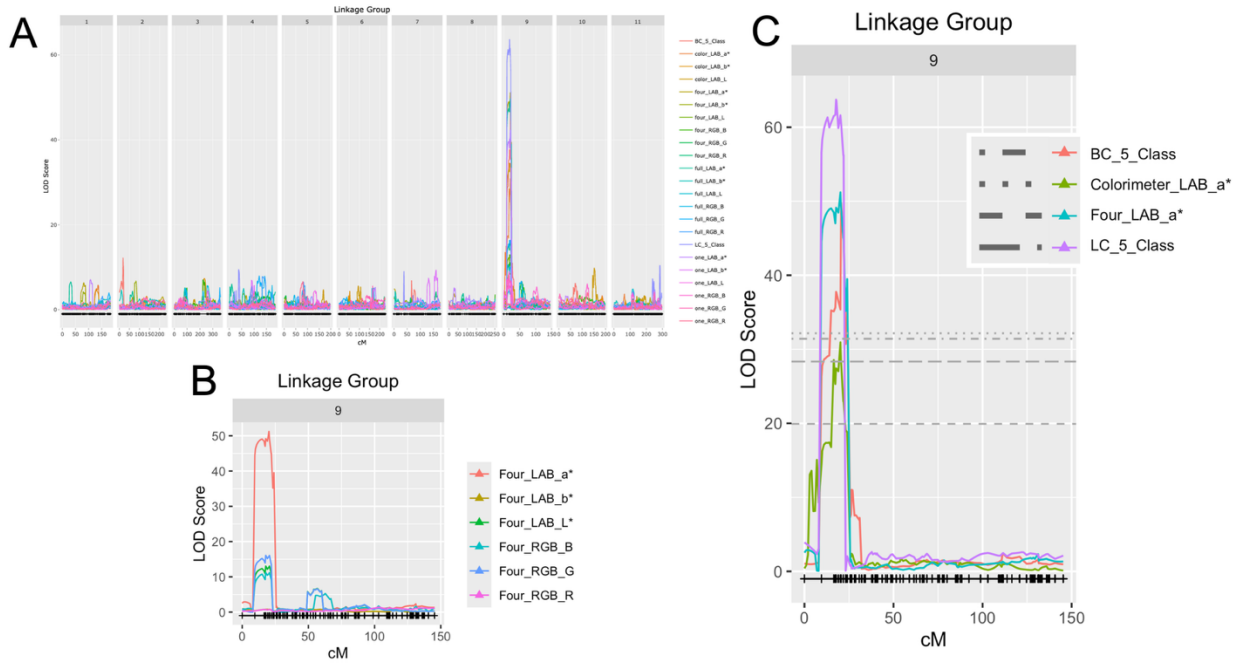


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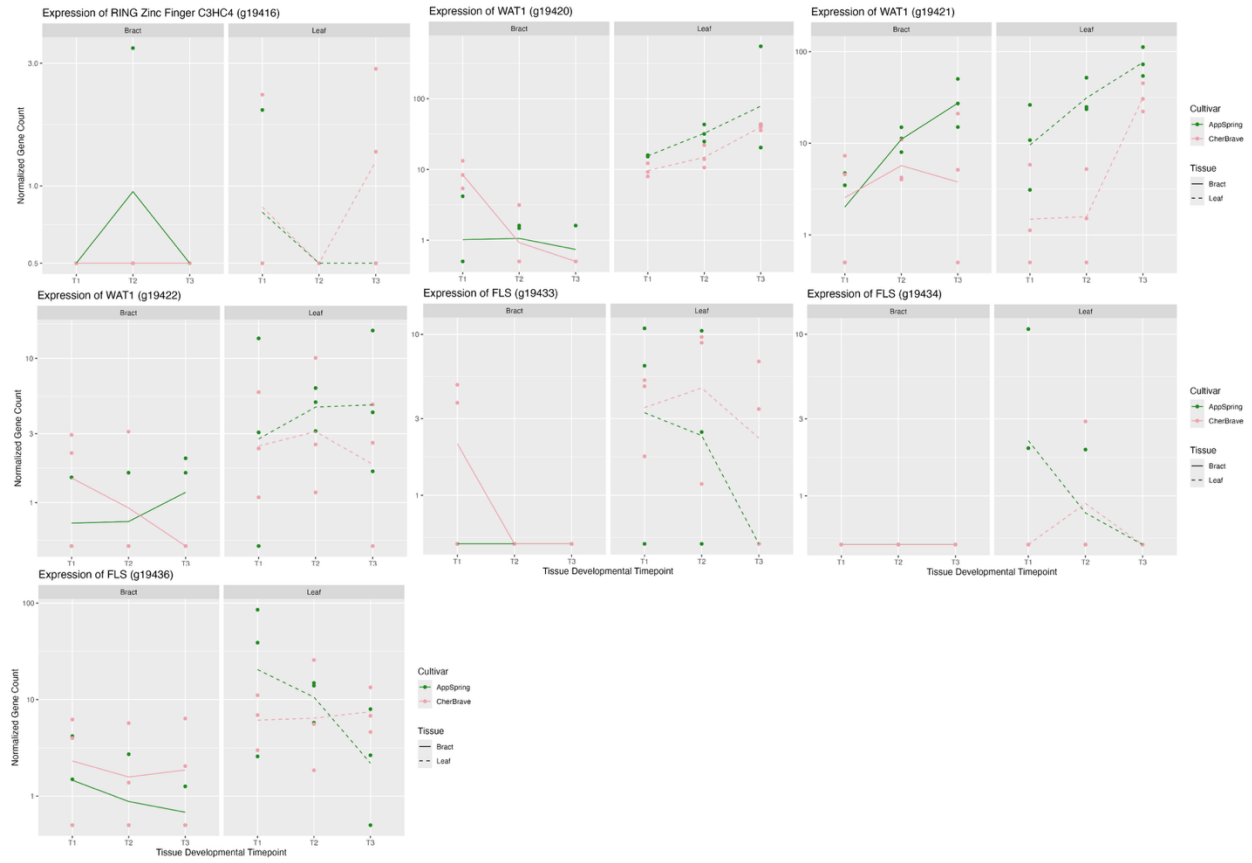


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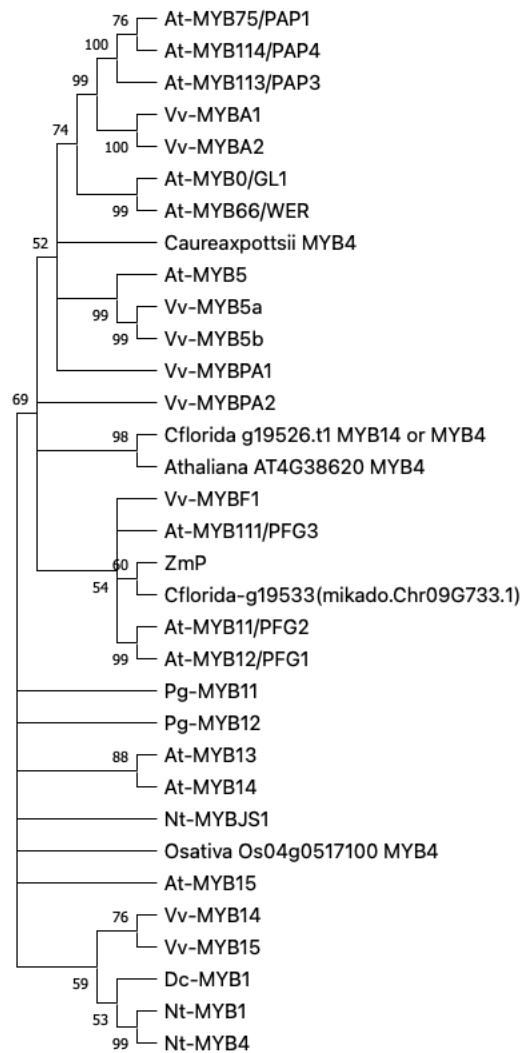


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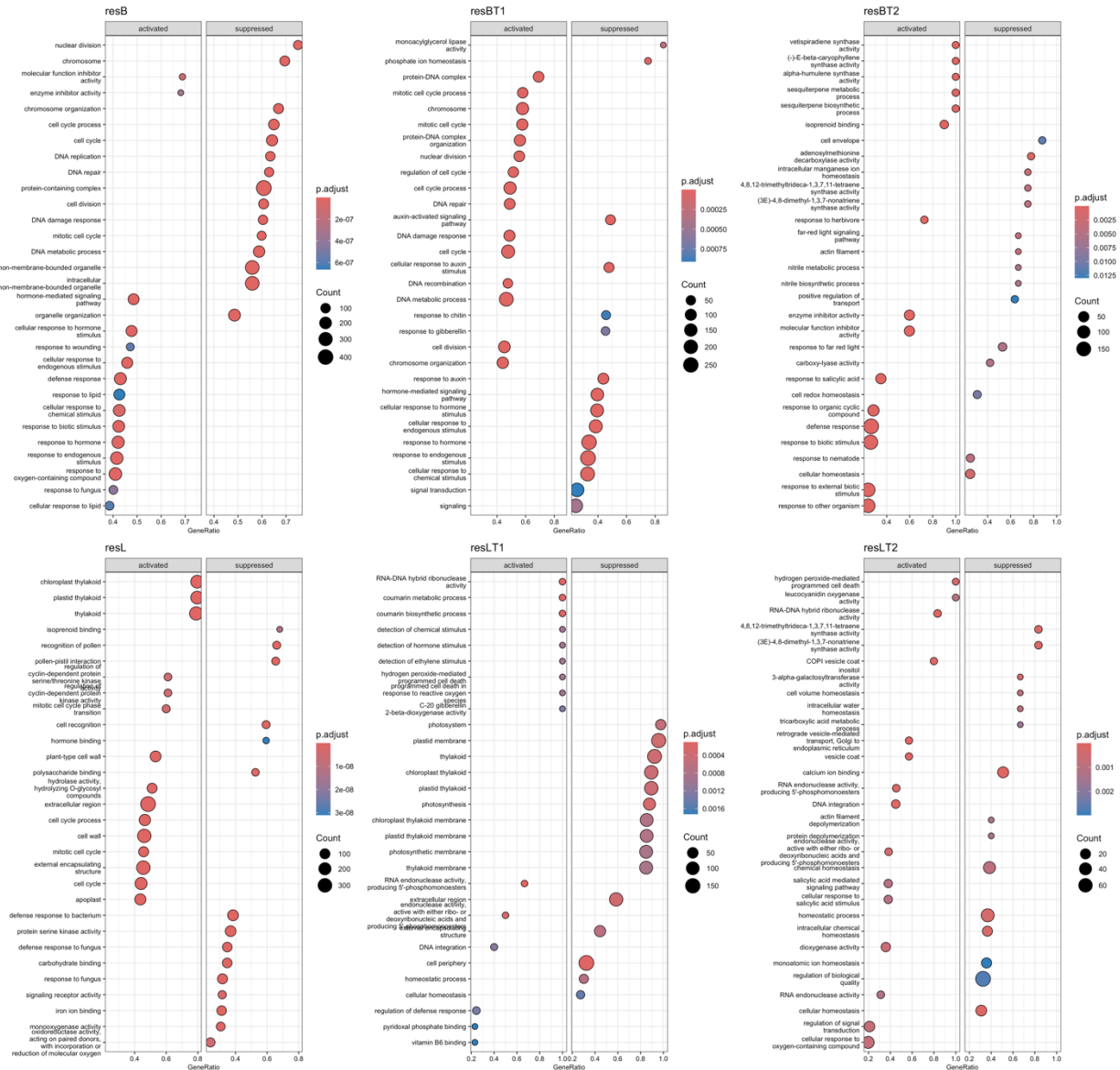


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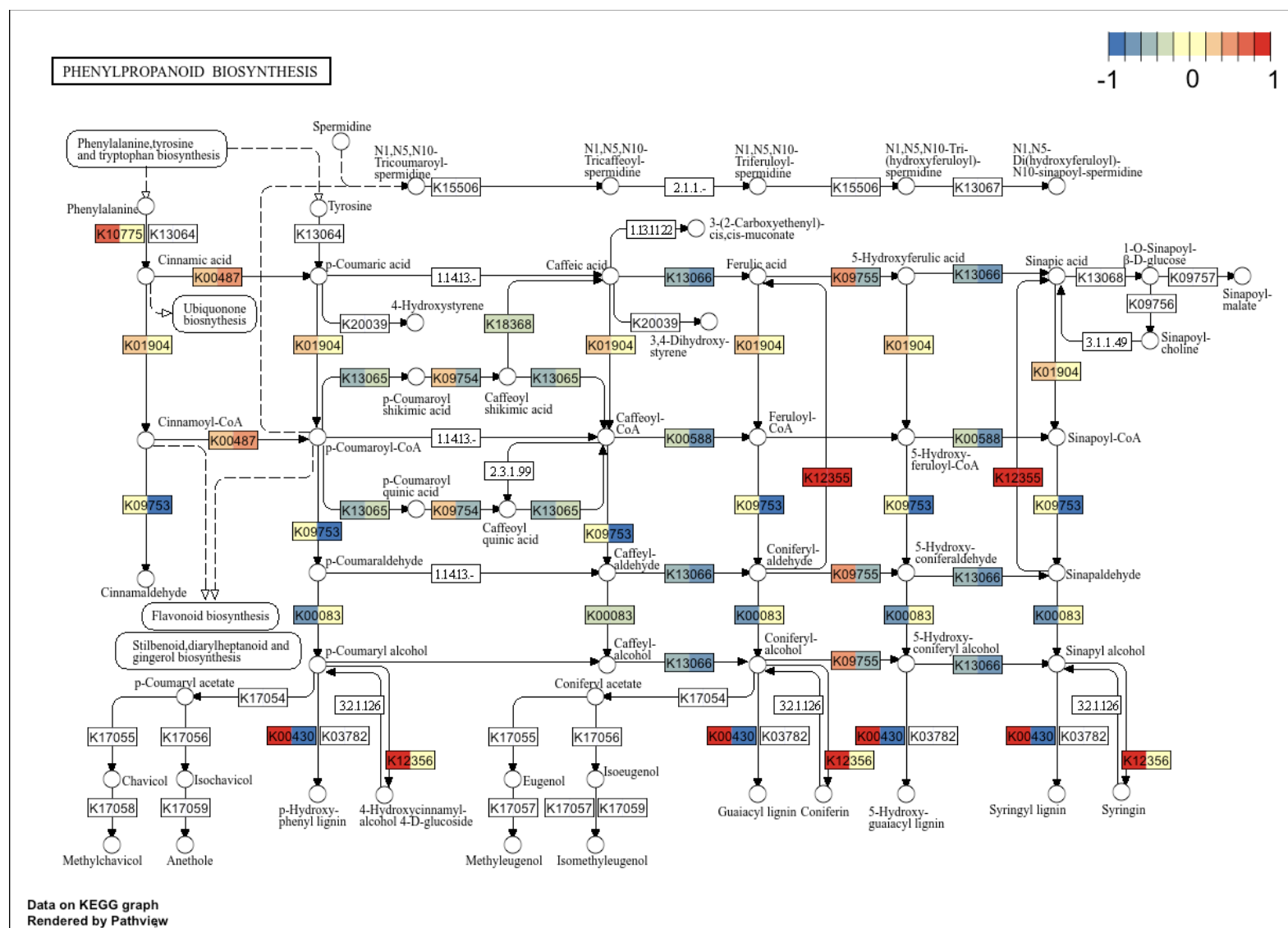


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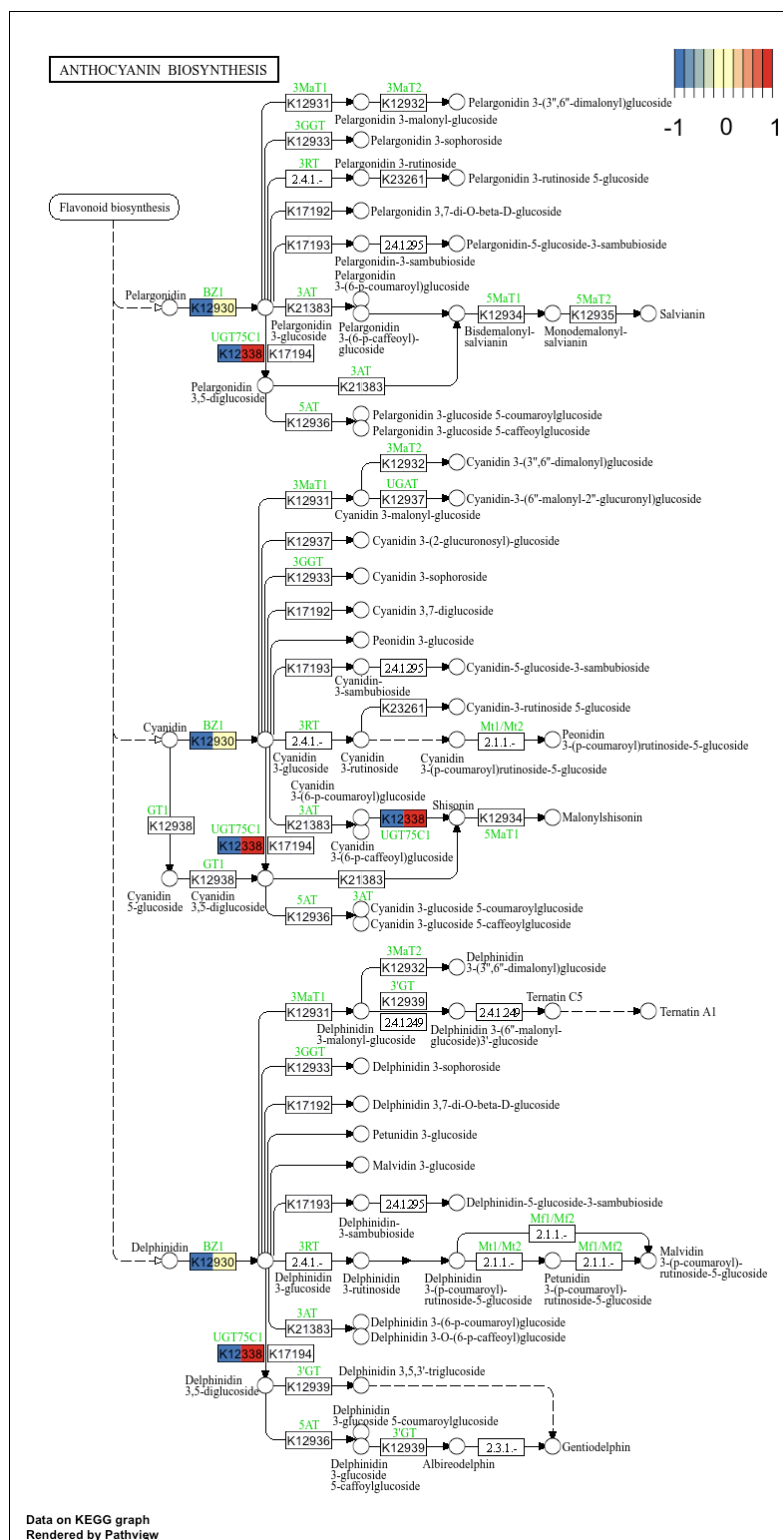


Figure S17. Maximum likelihood estimates of log2fold change of cultivar-specific gene expression within the KEGG anthocyanin biosynthetic pathway for timepoint 2 of time course experiment. Log2fold change in bracts is on the left and leaves are on the right.