

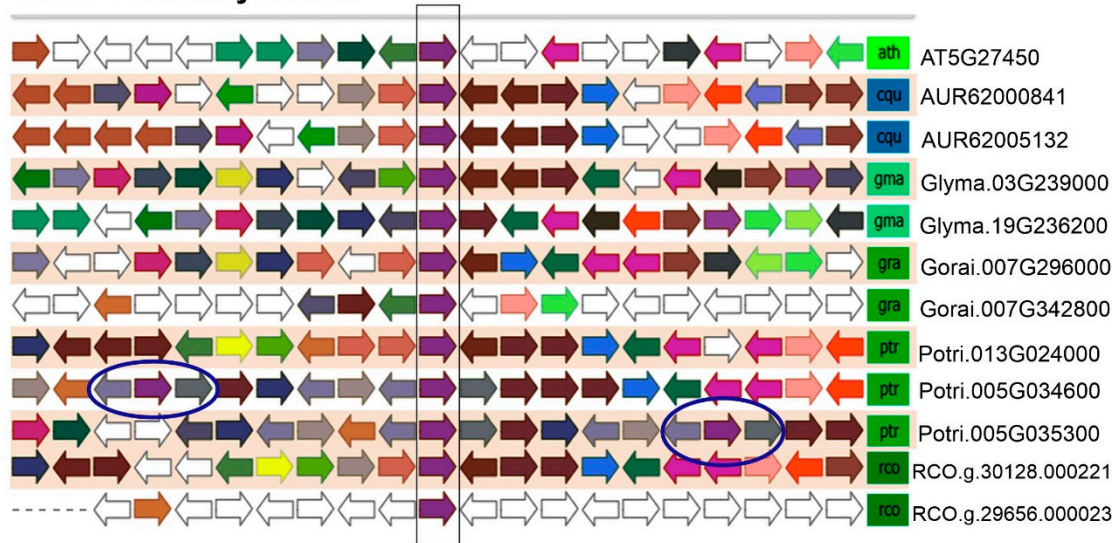
Supplementary Materials

Supplementary Table 1. Primer sequences used for RT-qPCR analyses

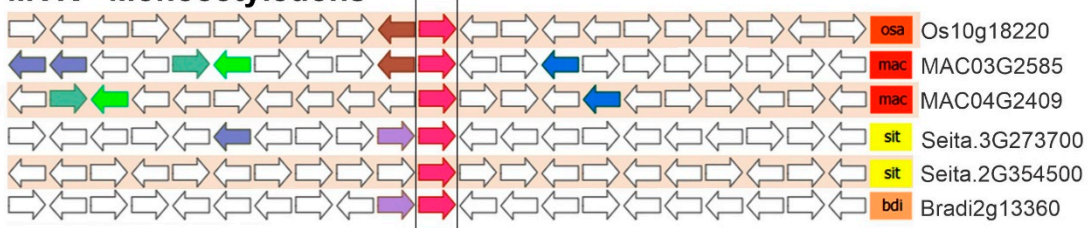
Gene ID	Primer sequence	Size (bases)	Tm (°C)	Amplicon (bp)	Efficiency
CaMVK	F: ATGTTCCCTCCGCTTCC	18	59,3	95	97%
	R: TCCAACCGGCAAGAAAAT	19	59,1		
CaDXR	F: CCTGTTCTCCCCTACGACT	19	59,3	127	92%
	R: GCCTCCATTGTCCTTCCT	18	59,1		
CaGAPDH	F: AGGCTGTTGGGAAAGTTCTTC	21	59,5	70	98%
	R: ACTGTTGGAACTCGGAATGC	20	58.4		

Supplementary Figures

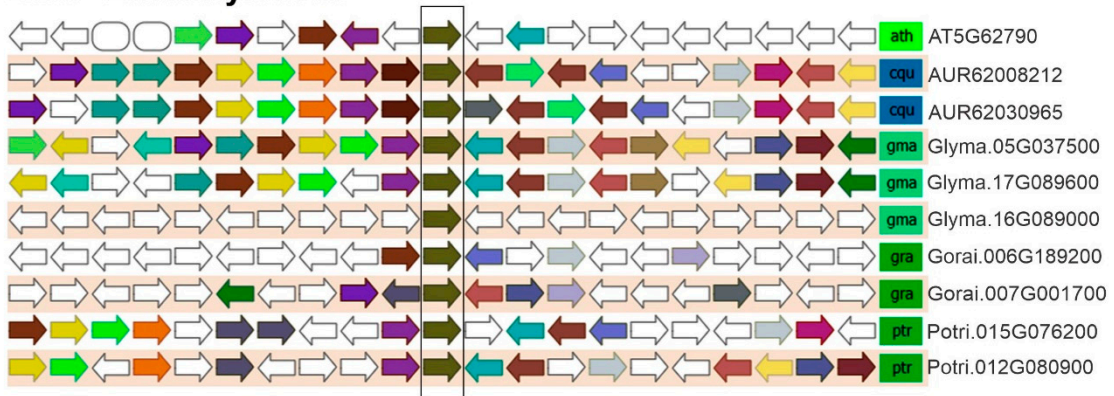
MVK - Eudicotyledons



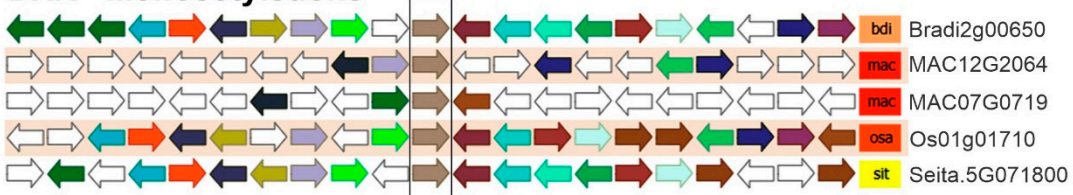
MVK - Monocotyledons



DXR - Eudicotyledons

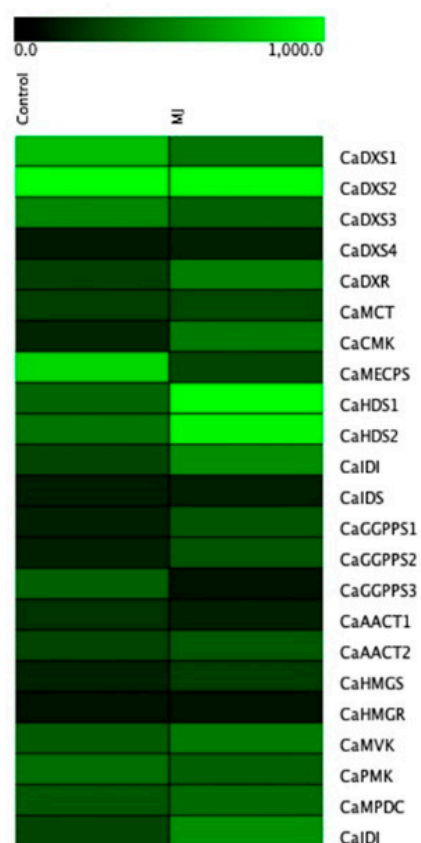


DXR - Monocotyledons

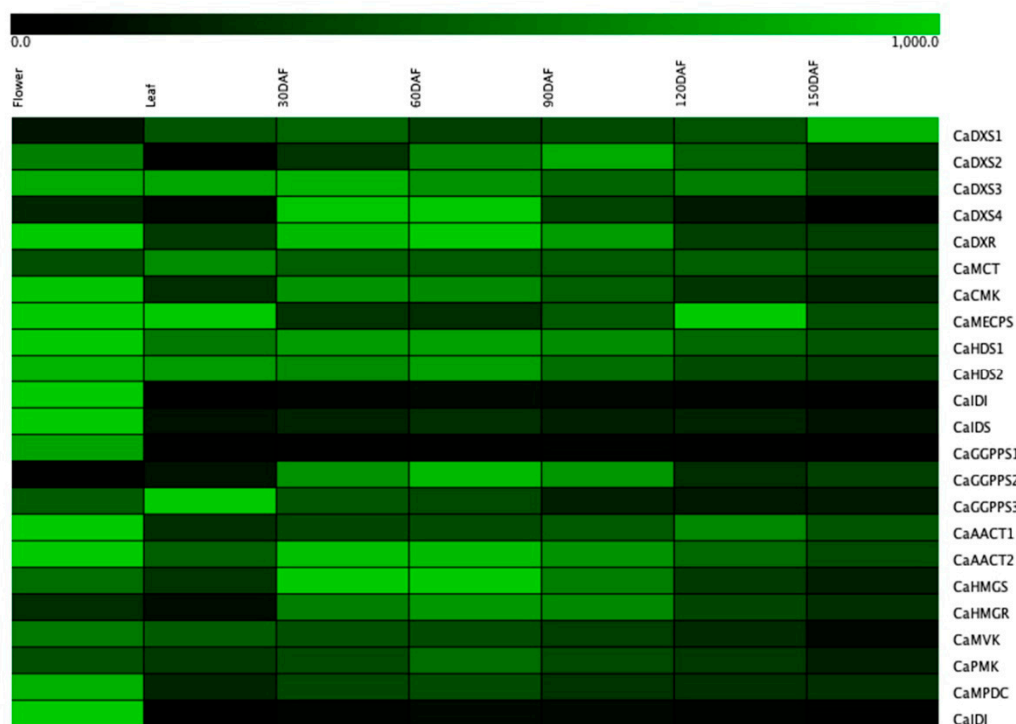


Supplementary Figure 1. Schematic representation of genomic regions containing *MVK* or *DXR* genes. We highlighted in a rectangle *DXR* and *MVK*. The figure was based on the “Synteny plot” tool of Plaza 4.0. Genes with the same color have similar function. Eudicot *MVK* genes share

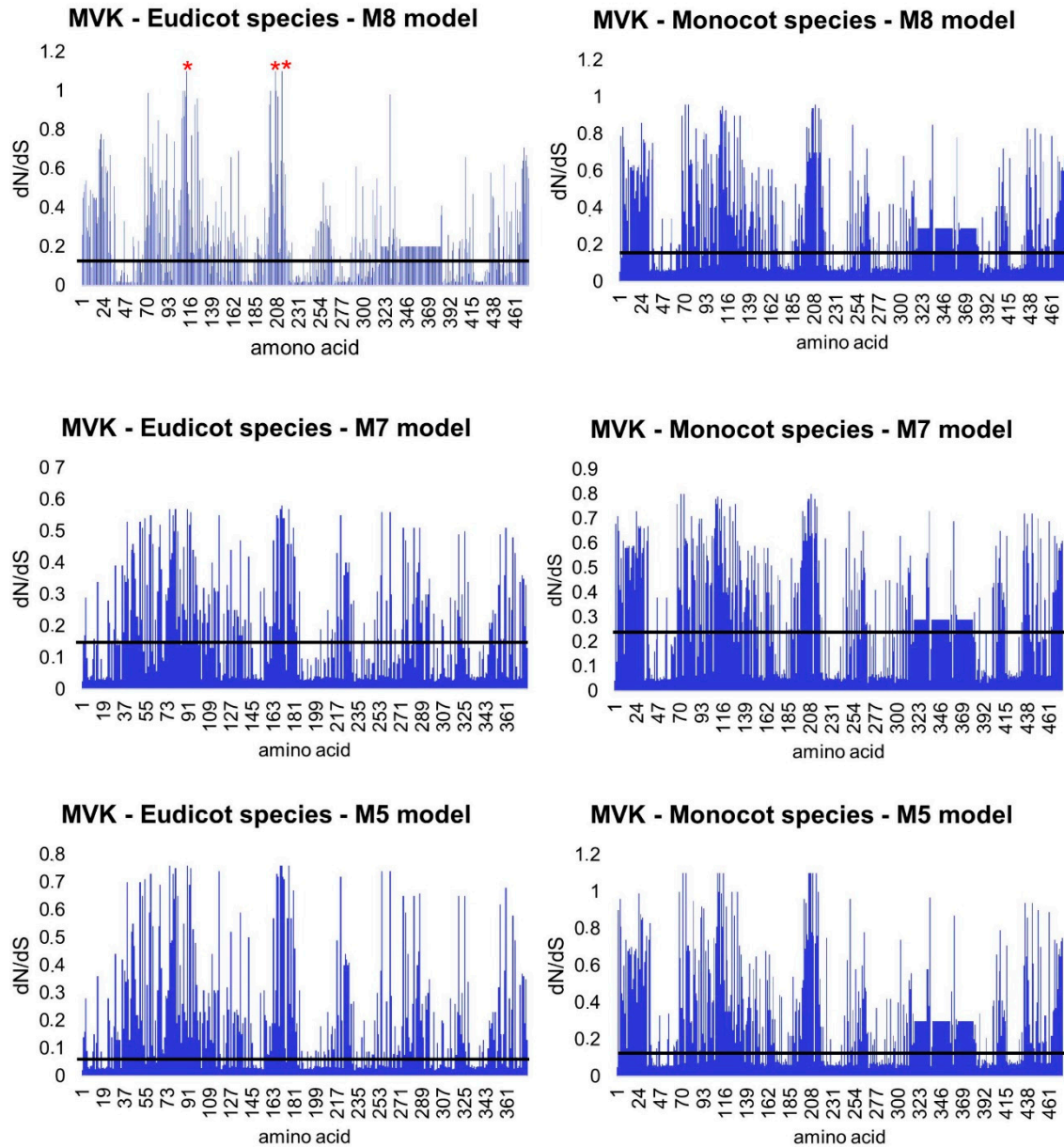
similar genomic neighborhood. We circled the *MVK* tandem duplication in *P. trichocarpa*. In monocots, genomic neighborhood among *MVK* genes has less collinear genes. In *DXR*, we also observe high similar genomic neighborhood, suggesting WGD events in soybean (*Glyma*) and *P. trichocarpa* (*Potri*). Only one gene in soybean (*Glyma.16G089000*) and one in cotton (*Gorai.006G189200*) do not share a significative genomic neighborhood, suggesting that these genes arose from segmental duplication.



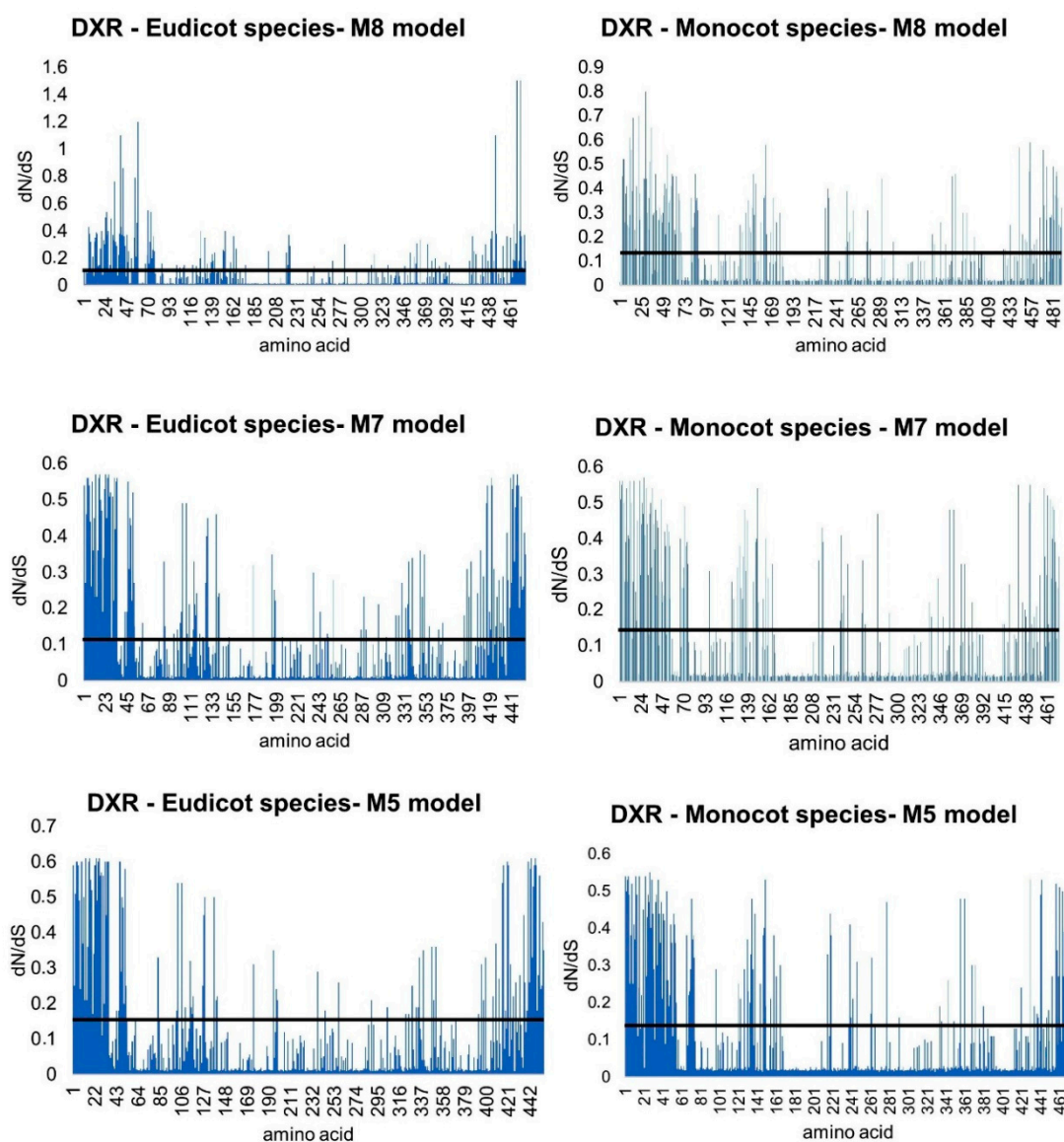
Supplementary Figure 2. RPKM values of *C. arabica* terpenoid pathway genes under methyl jasmonate application. Legend: C – control; MJ – methyl jasmonate application.



Supplementary Figure 3. RPKM values of *C. arabica* terpenoid pathway genes in flowers, leaves and along fruit development. Legend: DAF – perisperm in days after flowering.



Supplementary Figure 4. Distribution of dN/dS over individual sites in MVK, based on Selecton statistics. The horizontal line represents the average dN/dS. Asterisks (*) represent statistical significance in Bayesian analysis ($p < 0.05$).



Supplementary Figure 5. Distribution of dN/dS over individual sites in *DXR*, based on Selecton statistics. The horizontal line represents the average dN/dS.