

Combined analysis of transcriptomics and metabolomics reveals the regulatory mechanism of branch bending on leaf bud development in *Carya illinoensis* (Wangenh.) K. Koch

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Electronic Supplementary Material (ESM)

The authors are fully responsible for both the content and the formal aspects of the electronic supplementary material. No editorial adjustments were made.

Table S1. Statistics of sequencing data quality and alignment results

Sample	Raw reads	Clean reads	Clean base (G)	Error rate	Q20	Q30	Reads mapped	Unique mapped
					(%)			
CK1	6.5E+07	60 717 632	9.11	0.01	98.8	96.26	58 349 235 (96.10%)	56 765 546 (93.49%)
CK2	6.6E+07	61 671 950	9.25	0.01	98.84	96.39	59 211 319 (96.01%)	57 627 719 (93.44%)
CK3	6.3E+07	59 427 528	8.91	0.01	98.72	96.04	57 080 160 (96.05%)	55 579 510 (93.52%)
T1	4.3E+07	40 364 236	6.05	0.01	98.79	96.23	38 705 946 (95.89%)	37 684 343 (93.36%)
T2	6E+07	55 142 410	8.27	0.01	98.8	96.25	52 903 445 (95.94%)	51 473 755 (93.35%)
T3	6.6E+07	60 764 184	9.11	0.01	98.86	96.44	58 187 181 (95.76%)	56 631 961 (93.20%)

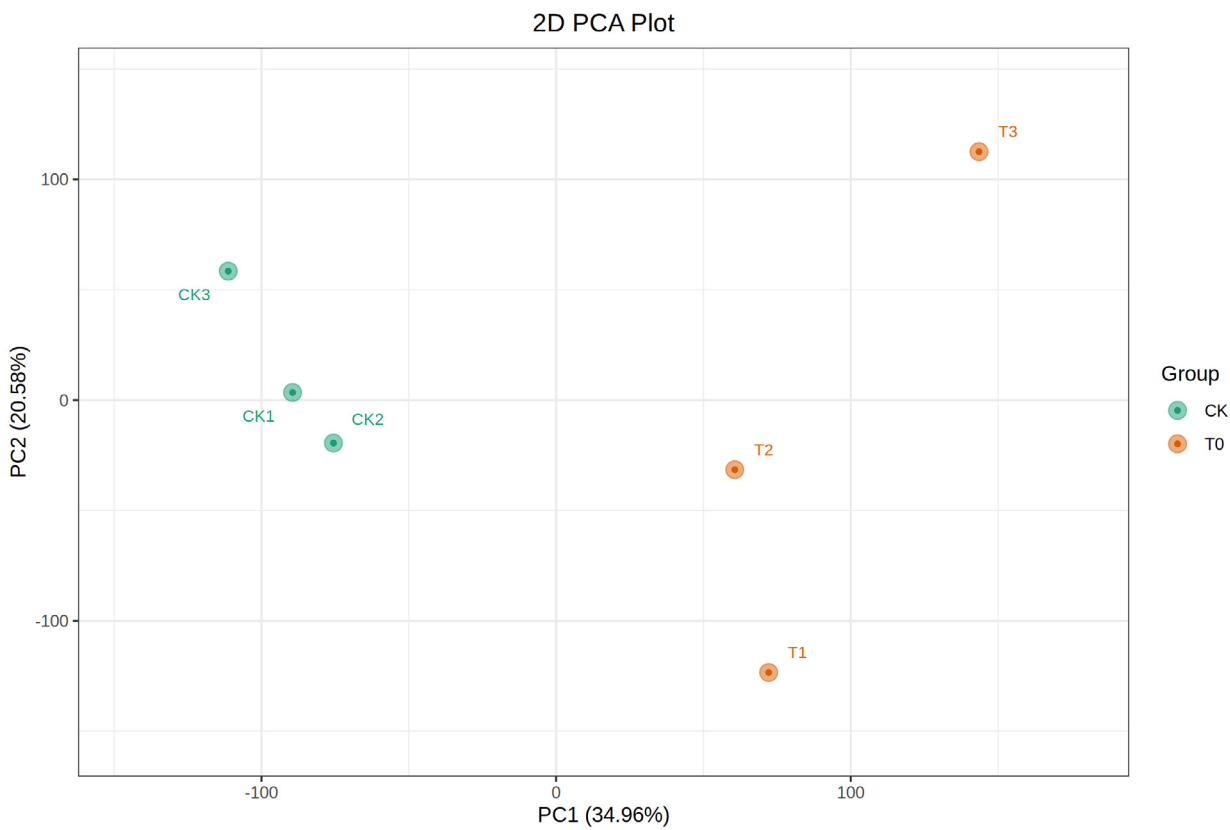


Figure S1. Principal component analysis based on all expressed genes; the control group (CK) are represented by green, and the branch bending group (T0) are represented by orange; 1, 2, and 3 represent rep1, rep2, and rep3, respectively