Fig. S1

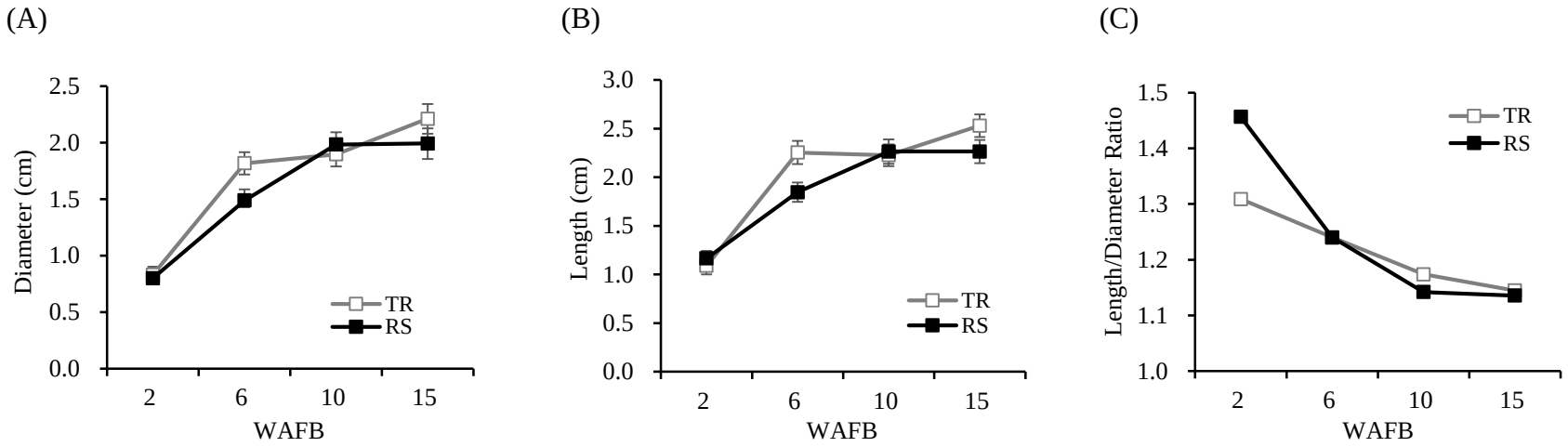

Fig. S1. Comparison of berry diameter, length, and length/diameter ratio between Tano Red (TR) and Ruby Seedless (RS) cultivars during four developmental stages (2, 6, 10, and 15 WAFB).

Fig. S2

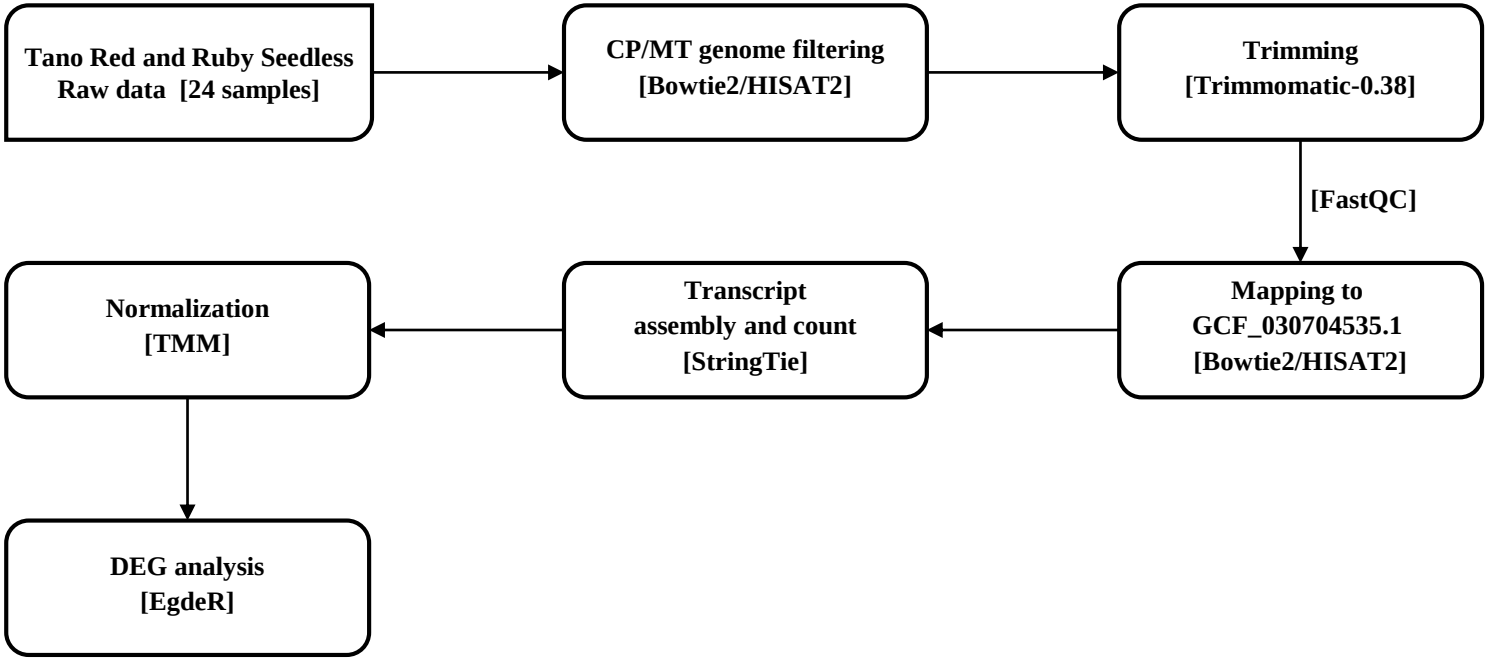

Fig. S2. Workflow for identifying differentially expressed genes (DEGs) through total RNA sequencing of Tano Red and Ruby Seedless berry skins. Total RNA was extracted from the berry skins of the two grape cultivars at four developmental stages (2, 6, 10, and 15 WAFB), using three biological replicates per stage. Illumina reads (2×101 bp) from 24 samples were processed by removing chloroplast and mitochondrial sequences, then trimming adapters and low-quality sequences, followed by mapping to the reference genome *V. vinifera* Pinot Noir 40024 (GCF_030704535.1). From 24,020 genes with mapped reads, 5,692 DEGs with a |fold change| ≥ 4 and a *p*-value < 0.001 between Tano Red and Ruby Seedless were identified using the EdgeR package.

Fig. S3

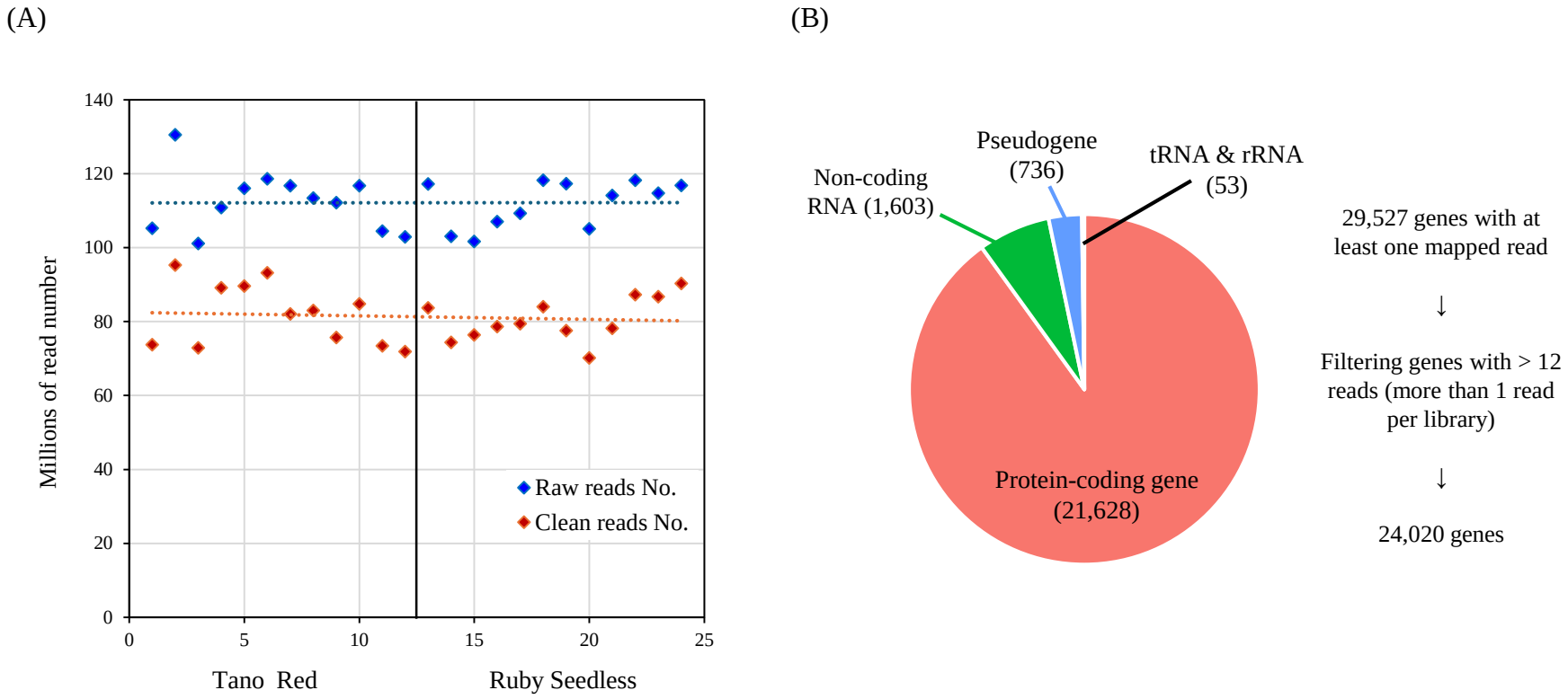

Fig. S3. RNA-seq reads per sample and their transcriptional origin. (A) Distribution of raw and clean reads per sample. (B) Classification of genes with transcriptional evidence by read mapping. Genes with more than 12 read counts per cultivar were considered.

Fig. S4

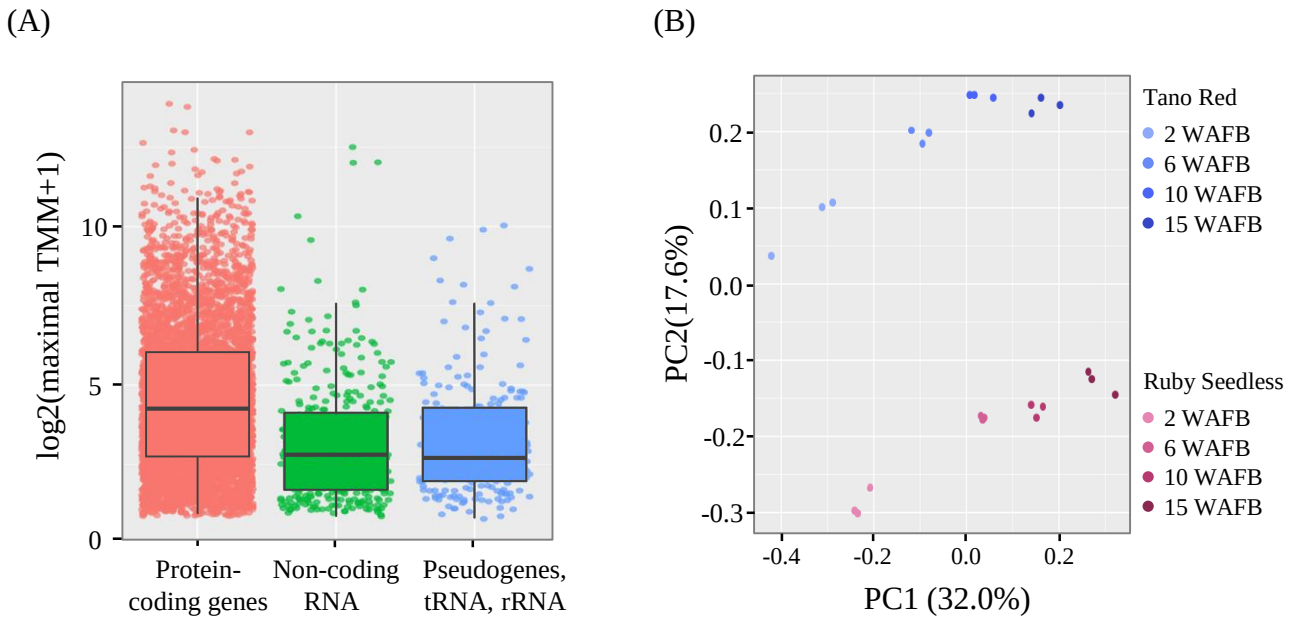

Fig. S4. Characteristic of DEGs identified from RNA sequencing analysis of Tano Red and Ruby Seedless berry skins. (A) Comparison of expression levels among three genomic fractions: protein-coding genes, non-coding RNAs, and pseudogenes or tRNA/rRNA, for the 5,692 DEGs. The maximal expression level of each transcript across samples was used, with $\log_2$-transformed TMM normalized read counts for visualization. (B) Principal component analysis of the DEGs, with sample names and developmental stages indicated by cultivar names. Color-coded circles represent the time elapsed after the full bloom stage (2, 6, 10, and 15 WAFB).

Fig. S5

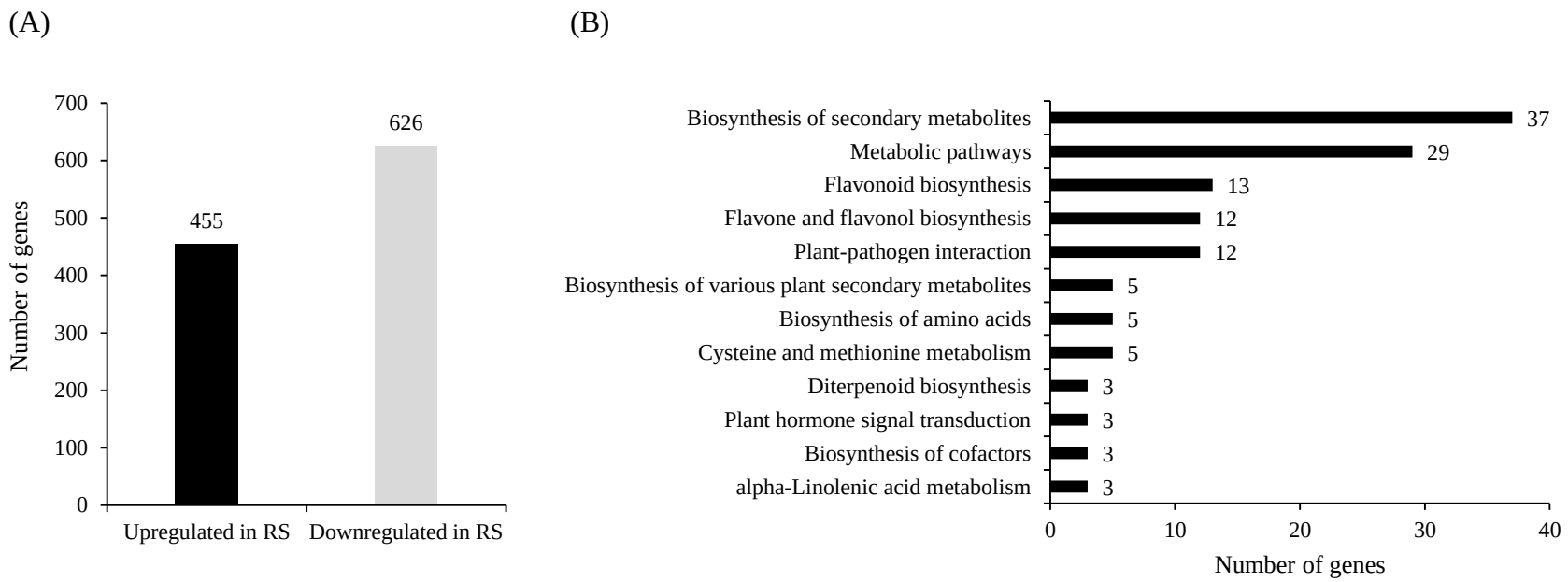

Fig. S5. DEGs between Tano Red and Ruby Seedless at 2 WAFB. (A) Number of DEGs upregulated or downregulated in Ruby Seedless (RS) at 2 WAFB. (B) KEGG pathway annotations of DEGs upregulated in Ruby Seedless at 2 WAFB.

Fig. S6

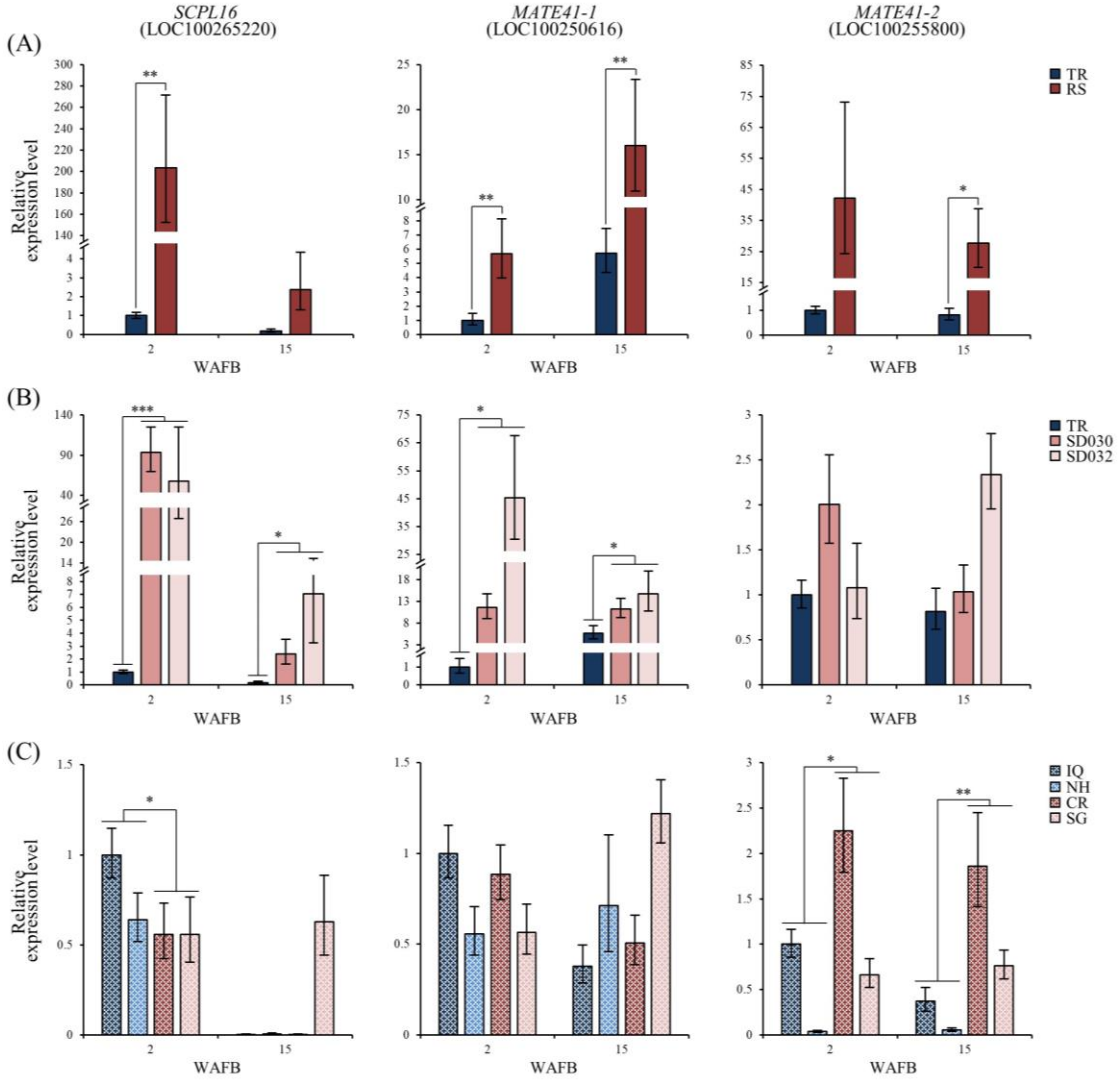

Fig. S6. Relative expression patterns of genes identified from a co-expression network analysis for tannin biosynthesis-related genes. qPCR of three genes (*SCPL16*, *MATE41-1*, *MATE41-2*) was performed to quantify expression in the berry skin at 2 WAFB and 15 WAFB. The calculation of relative expression values, reference gene, grape cultivars, and varieties are the same as in the caption of Fig. 6. (A) Comparison of relative expression levels between Tano Red and Ruby Seedless. (B) Comparison of relative expression levels between Tano Red and two hybrid progeny lines with high total PTC (SD030 and SD032). (C) Comparison of relative expression levels between grapevine cultivars with low total PTC (Izumo Queen (IQ) and Nehelescol (NH)) and those with high total PTC (Chasselas Rosé De Fall (CR) and Shigyoku (SG)).