



Figure S1. Weighted gene co-expression network analysis (WGCNA) during fruit coloring stages in three blueberry varieties. (a) Hierarchical clustering tree of unigenes based on their expression level in 27 transcriptomes. Each branch represents an unigene, and each color below represents a module. The dynamic tree cut shows that the unigenes fall into different modules. The merged dynamic indicates that the modules are divided by clustering modules with similar expression patterns; (b) the heatmap analysis displays the module expression pattern in the 27 samples. ‘Black Pearl’, ‘Chandler’, and ‘Pink Popcorn’ are abbreviated as H, Q, and F, respectively. Each stage of sampling H, Q, and F had three biological replicates.

