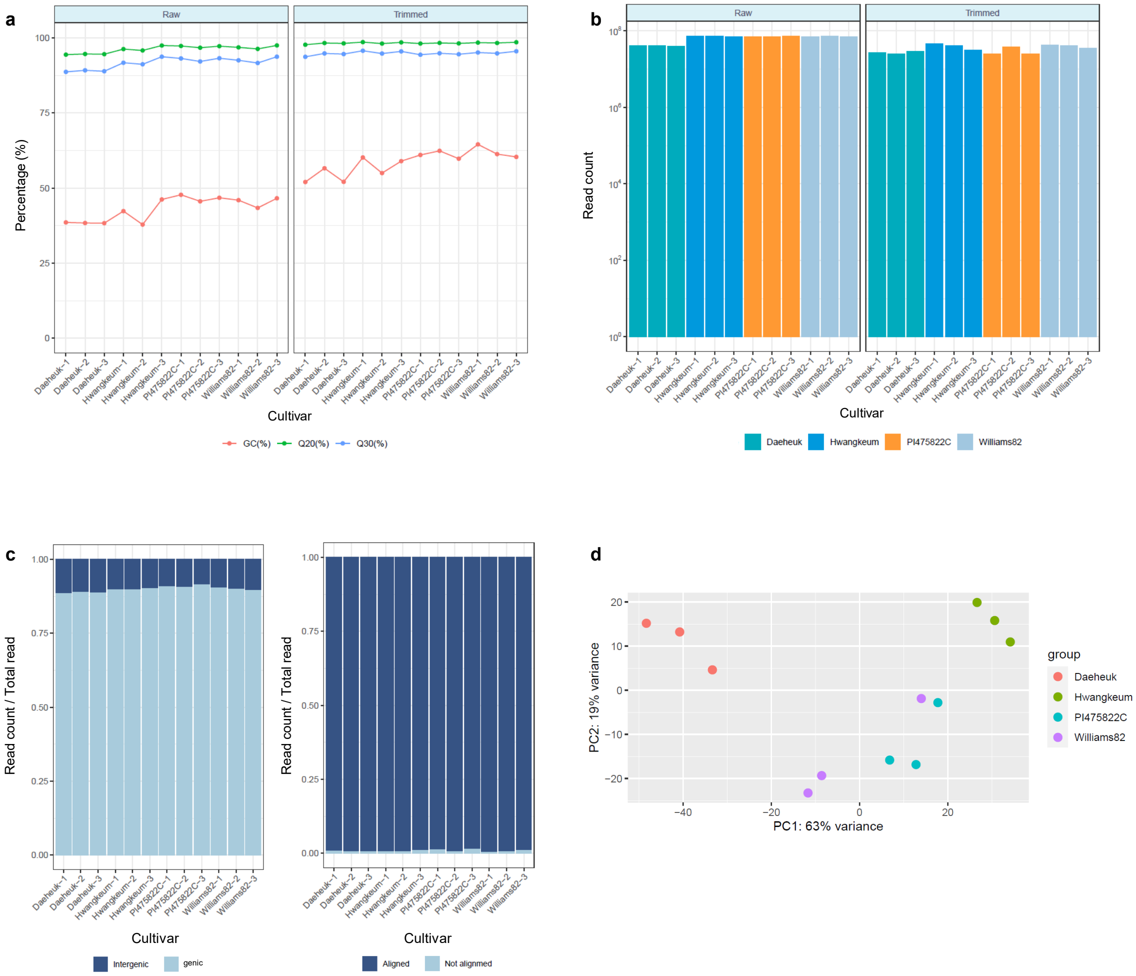

Supplementary Figure 2 | Quality control of small RNA sequencing data. (a) Line plot illustrating the GC contents, Q20, and Q30 scores of each sample. (b) Bar plot showing the quantity of small RNA sequencing reads. The left side indicates the number of raw reads, while the right side represents the number of trimmed reads. (c) Bar plot depicting the status of mapped reads. The left side displays the mapping rate according to intergenic and genic regions, while the right side shows the overall mapping rate for each sample. (d)Dot plot representing the principal component analysis (PCA) of small RNA sequencing data from soybean seed coats. Cultivars include Daeheuk (BL12), Hwangkeum (YL12), PI475822C (BR01), and Williams82 (YL07), corresponding to the *i*, *I*, i^k, and i^i alleles, respectively. Each cultivar includes three biological replicates.