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**Figure S4.** Validation of RNA-seq results using qRT-PCR in sensitive popular cultivars. About fourteen different *PopdaWRKys* from Group I, II and III were analyzed. The qRT-PCR values were used to calculate log2 of fold change (white bars) in Seogwang15 (A, B and C) and Junguk6-2 (D, E and F) popular cultivars and compared with fold change from RNA-seq analysis (black bars). The *R* value represents correlation coefficient while error bars represents ± SE from at least three replicates.