



Figure 7. Whole-genome sequencing (WGS) and RNA-sequencing (RNA-seq) analyses of the *sit1* mutant. (a) Number of sequence variants in the *sit1* mutant compared with wild-type (WT) plant. The SNPs and Indels between the *sit1* mutant and WT were determined via WGS according to their chromosome locations. (b) Characterization of SNP and Indel variants in the *sit1* mutant. Colors in the pie chart represent the different features of variant annotation based on genomic loci. Numbers indicate the number of SNPs and Indels in the *sit1* mutant. (c-d) Transcript abundance (\log_2 fold-change) and $-\log_{10}$ qvalue analyses of the genes containing SNP (c) and Indel (d) variants in the *sit1* mutant via RNA-seq. Green and pale green round symbols represent the relative gene expression level and statistical significance, respectively. Gray dot lines indicate the cut-off value of q value (0.05, $-\log_{10}$ value of 1.3). Red arrows indicate that genes containing SNPs (c) and Indels (d) in the *sit1* mutant have significantly higher or lower mRNA abundance.