

Supplementary Materials: **Additional data 1:** Multiple sequences of LRR-RLK from *A. thaliana* and *S. spontaneum* were aligned by MUSCLE software with default parameters, **Additional data 2:** Phylogenetic tree constructed. **Table S1:** The primers used in the qRT-PCR analyses, **Table S2:** Detailed information of all identified *SsLRR-RLK* genes. **Table S3:** Signal peptide analysis, **Table S4:** Subcellular localization prediction of all LRR-RLKs proteins in sugarcane, **Table S5:** Statistics of *A. thaliana* and *S. spontaneum* *LRR-RLKs* distribution among different groups and subgroups, **Table S6:** Sequence logos of the conserved motifs of all *SsLRR-RLKs* among each group and subgroup predicted by MEME, **Table S7:** *Cis*-acting regulatory element analysis of the *SsLRR-RLK* genes, **Table S8:** FPKM values of 437 *SsLRR-RLK* genes based on five different stress RNA-seq data, **Figure S1:** Exon-intron structure of all identified *LRR-RLK* members in sugarcane, **Figure S2:** Detailed schematic illustrations of the conserved motifs identified in *SsLRR-RLK* proteins. 15 conserved motifs were distinguished by different colors, **Figure S3:** Detailed schematic illustrations of the TF binding sites predicted. Only shows the top 12 transcription factor families, **Supplementary Material 3:** The upstream 2,000 bp sequence of 437 *SsLRR-RLK* genes.