Supplemental Figure legends

**Figure S1:** **Converting .bcl file to .fastq file using CASAVA software.**

**Figure S2: Mapping reads to reference genome using Tophat.**

**Figure S3: Detection of novel transcripts and expression level estimation.**

**Figure S4: Calling differential expressed gene using DESeq package.**

**Figure S5: Identification of differentially expressed transcription factors.**

**Figure S6: Converting mapping result for data visualization.**