RNAseq experiment was done at (??) and 150 bp pair data was produced. The data quality was assessed with FastQC (version 0.11.5), low-quality reads were removed, and remaining adapter sequences were hard clipped with cutadapt (version 1.12) whenever applicable. The quality filtered reads were aligned with STAR (version 2.6.90c) to human reference genome (hg38) with its respective RefSeq annotation, at last, the expression levels of genes were obtained with FeatureCounts (version 1.5.1). To get the differentially expression genes (DEGs), we use DESeq2 (version 1.34.1). Data matrix were normalized and the DEGs were reported according the fold change cut off and corrected modeling p-values.