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**Figure S2. The expressional profiles of genes in RNA-seq analysis.**

(A) Hierarchical clustering analysis of differentially expressed genes in RNA-seq analysis.

(B-D) GSEA and KEGG pathway analysis showing that the top 10 overexpressed lncRNA and mRNAs were enriched in metabolic pathways, especially in glycolysis pathway.

(E-J) The expression level of 6 random selected upregulated lncRNAs in 16 paired NSCLC and adjacent normal tissues by qRT-PCR. Data shown are mean±SD (n = 3). (\*P < 0.05, \*\*P < 0.01, \*\*\*P < 0.001)