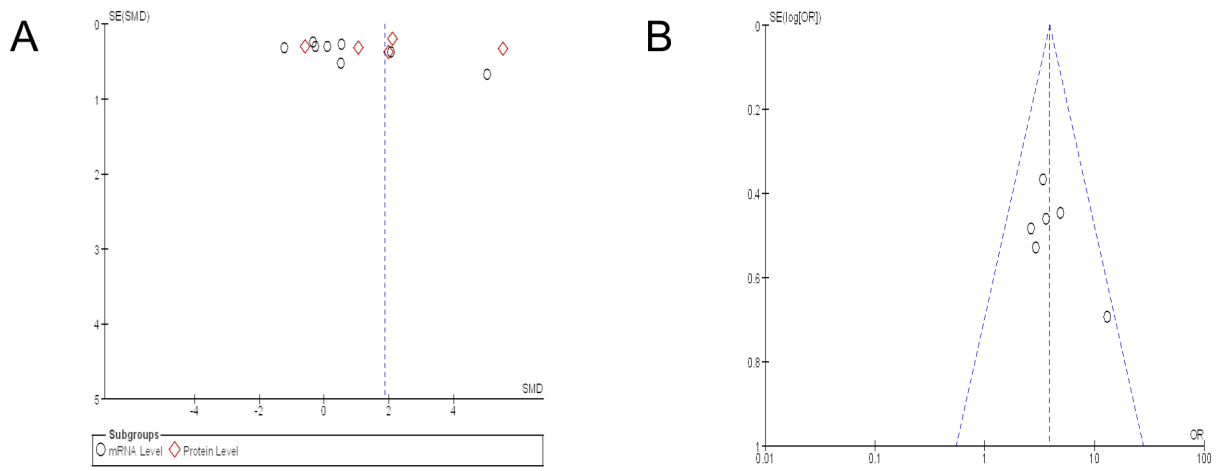
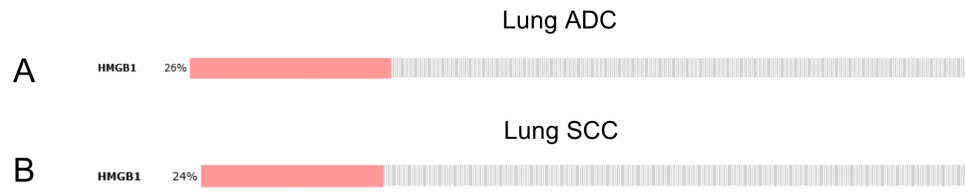


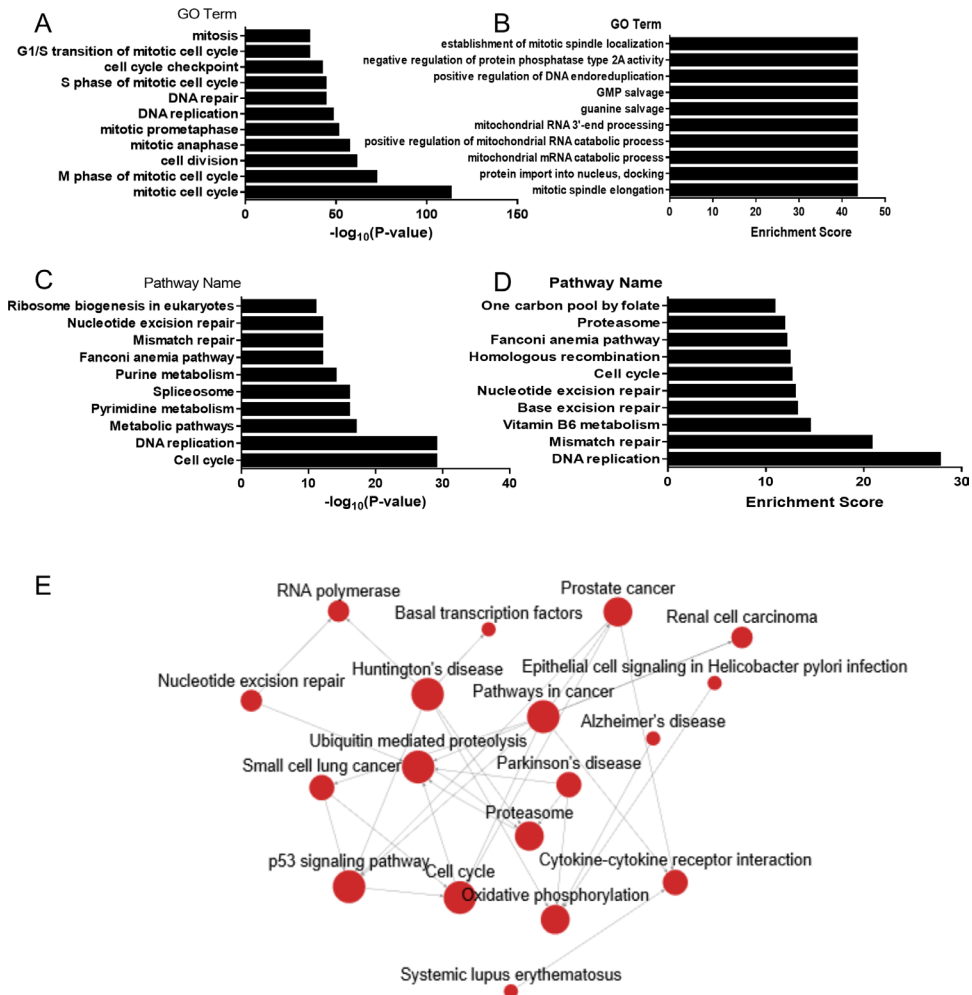
SUPPLEMENTARY FIGURES AND TABLE



Supplementary Figure S1: Funnel plot for meta-analysis. **A.** Funnel plot for HMGB1 in NSCLC and normal tissues. **B.** Funnel plot for HMGB1 in tumor and para-tumor tissues.



Supplementary Figure S2: The results of analysis for TCGA datasets. **A.** HMGB1 was altered in 148 (28%) of 576 cases in lung adenocarcinoma (TCGA, Provisional). **B.** HMGB1 was altered in 119 (24%) of 504 cases in lung squamous cell carcinoma (TCGA, Provisional).



Supplementary Figure S3: The bioinformatics analysis of molecular mechanisms of HMGB1 in SCC. A-B. Significantly over-represented biological processes in DEGs. C-D. Significantly over-represented pathways in DEGs. E. Pathway network.

Supplementary Table S1

See Supplementary File 1