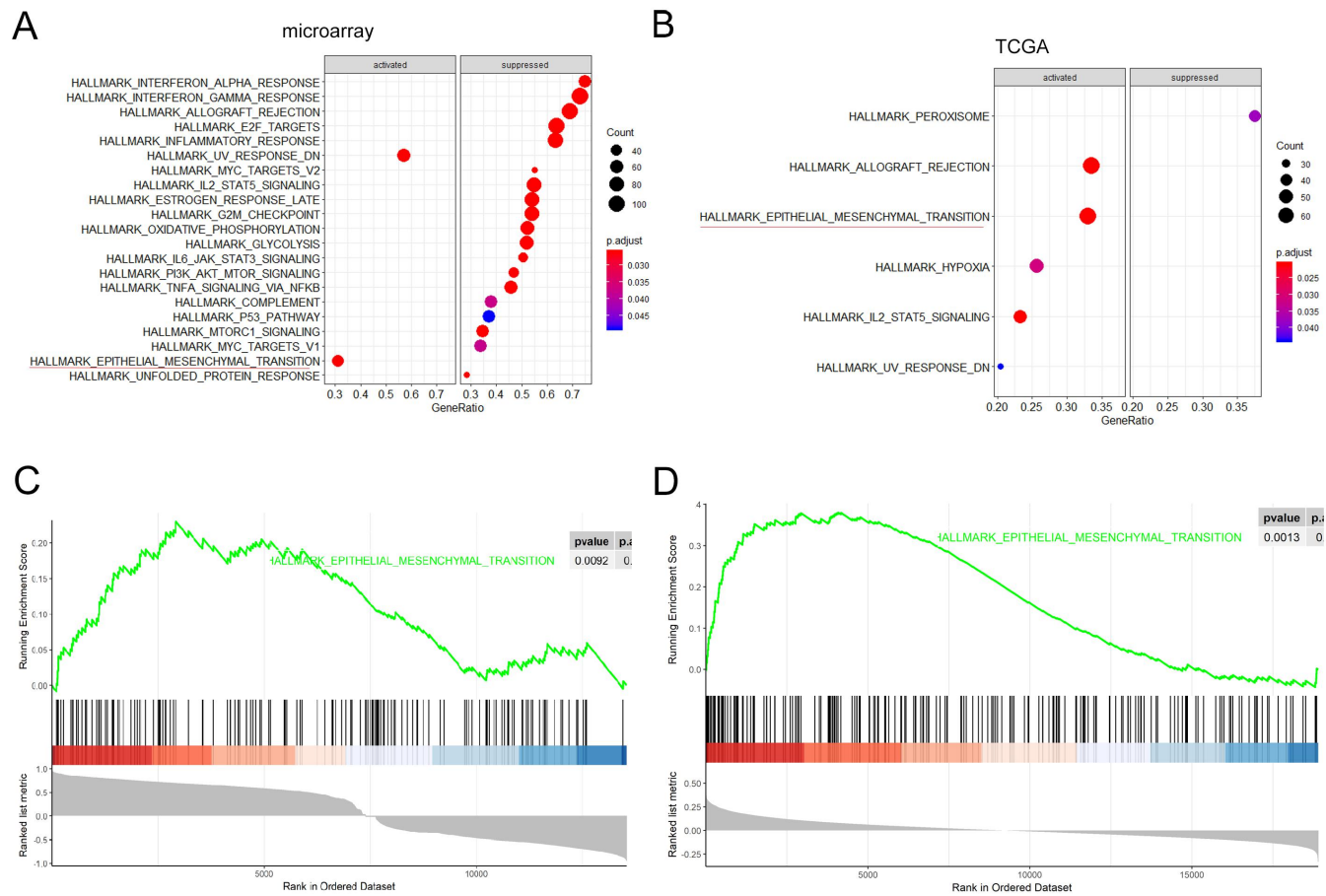
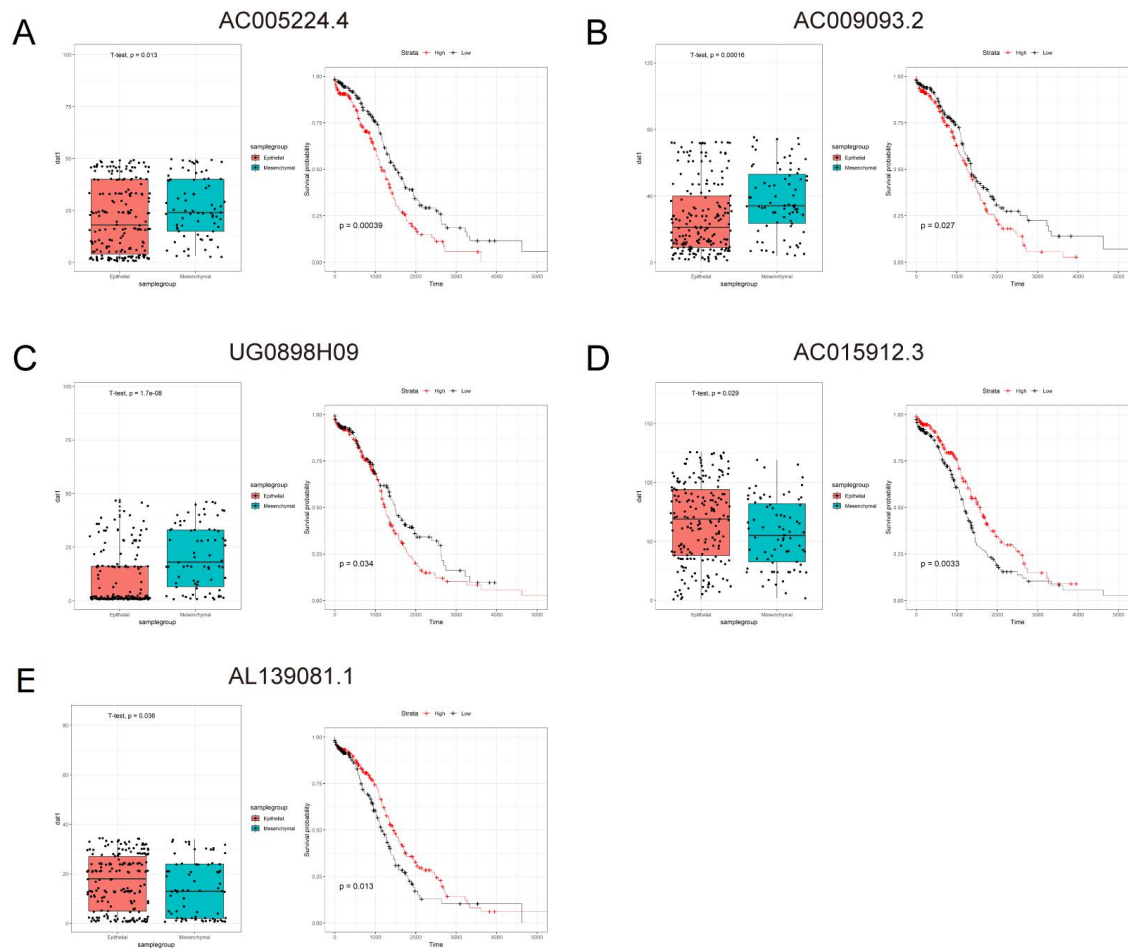


Supplementary



Supplementary Figure 1: GO term enrichment analysis of DEGs of our microarray and TCGA-ovarian cancer database. (A) The DEGs in ovarian cancer in our microarray were classified into multiple subcategories according to Biological Process. **(B)** EMT was markedly activated in our microarray. **(C)** The DEGs in ovarian cancer in TCGA-ovarian cancer database were classified into multiple subcategories. **(D)** EMT was markedly activated in the TCGA-ovarian cancer database. DEGs: Differential expression genes; EMT: Epithelial-mesenchymal transition; GO: Gene Ontology; TCGA: The Cancer Genome Atlas.



Supplementary Figure 2: The relationship between five lncRNAs and the overall survival of TCGA-ovarian cancer patients. Bioinformatics analysis was applied to determine the relationship between the five lncRNAs (AC005224.4, AC009093.2, UG0898H09, AC015912.3, and AL139081.1) and the overall survival of TCGA-ovarian cancer patients, and the expression level of these five lncRNAs in TCGA interstitial ovarian cancer cells and epithelial cells was detected. (A) AC005224.4. (B) AC009093.2. (C) UG0898H09. (D) AC015912.3. (E) AL139081.1. lncRNA: Long non-coding RNA; TCGA: The Cancer Genome Atlas.