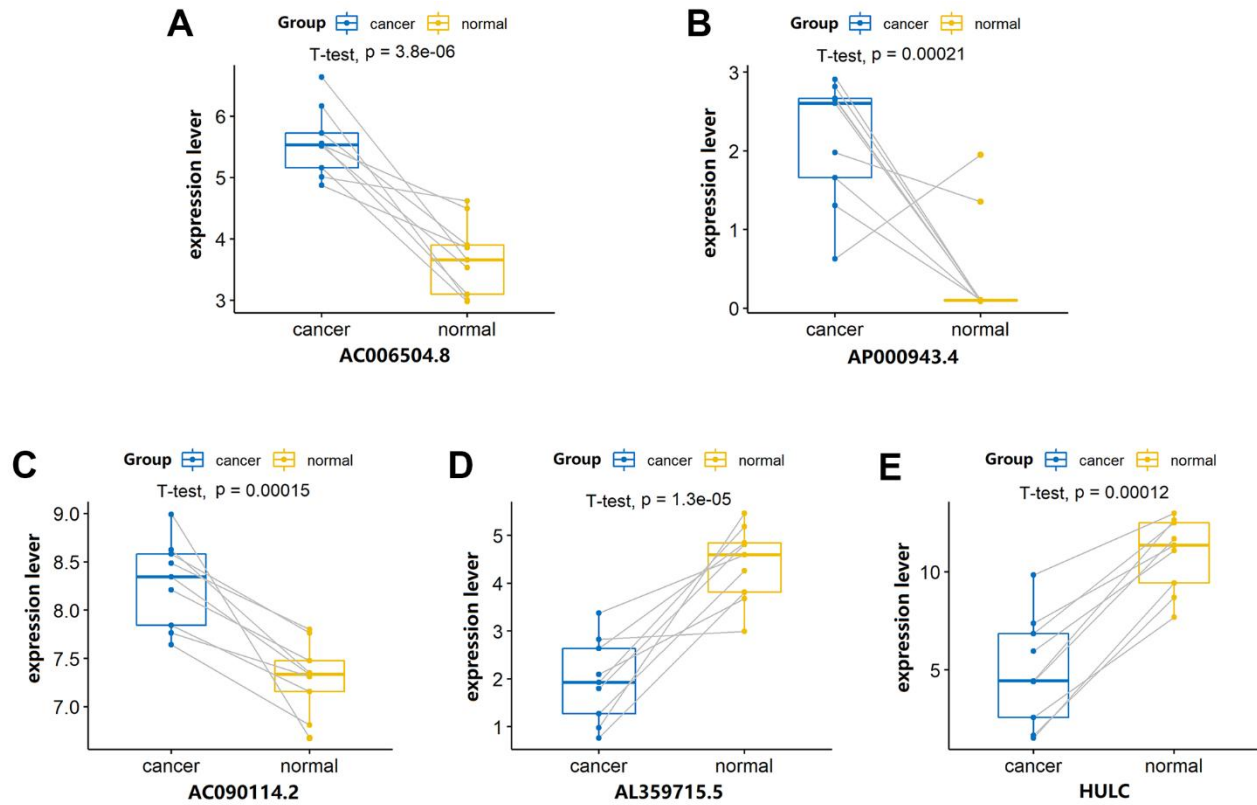
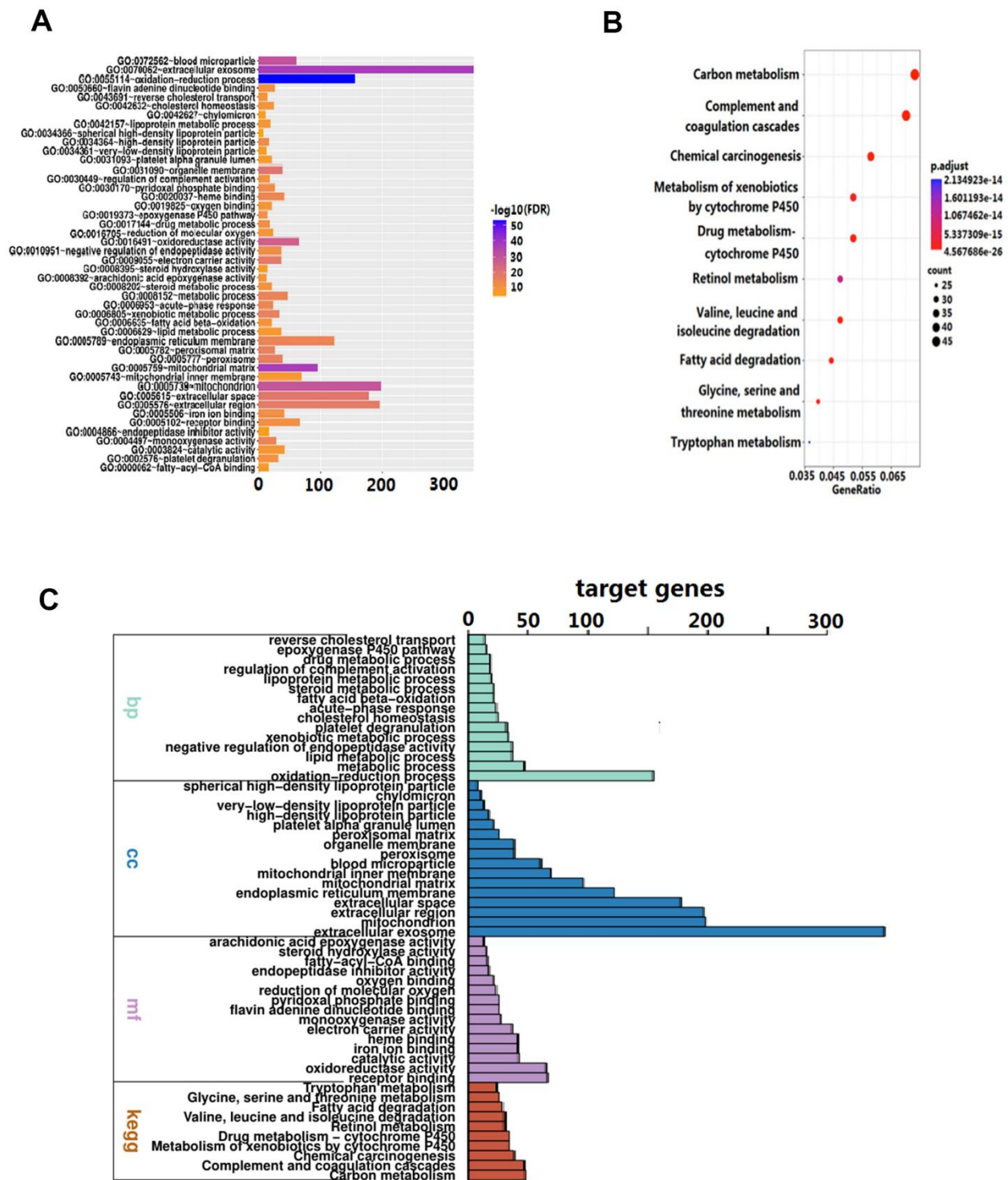


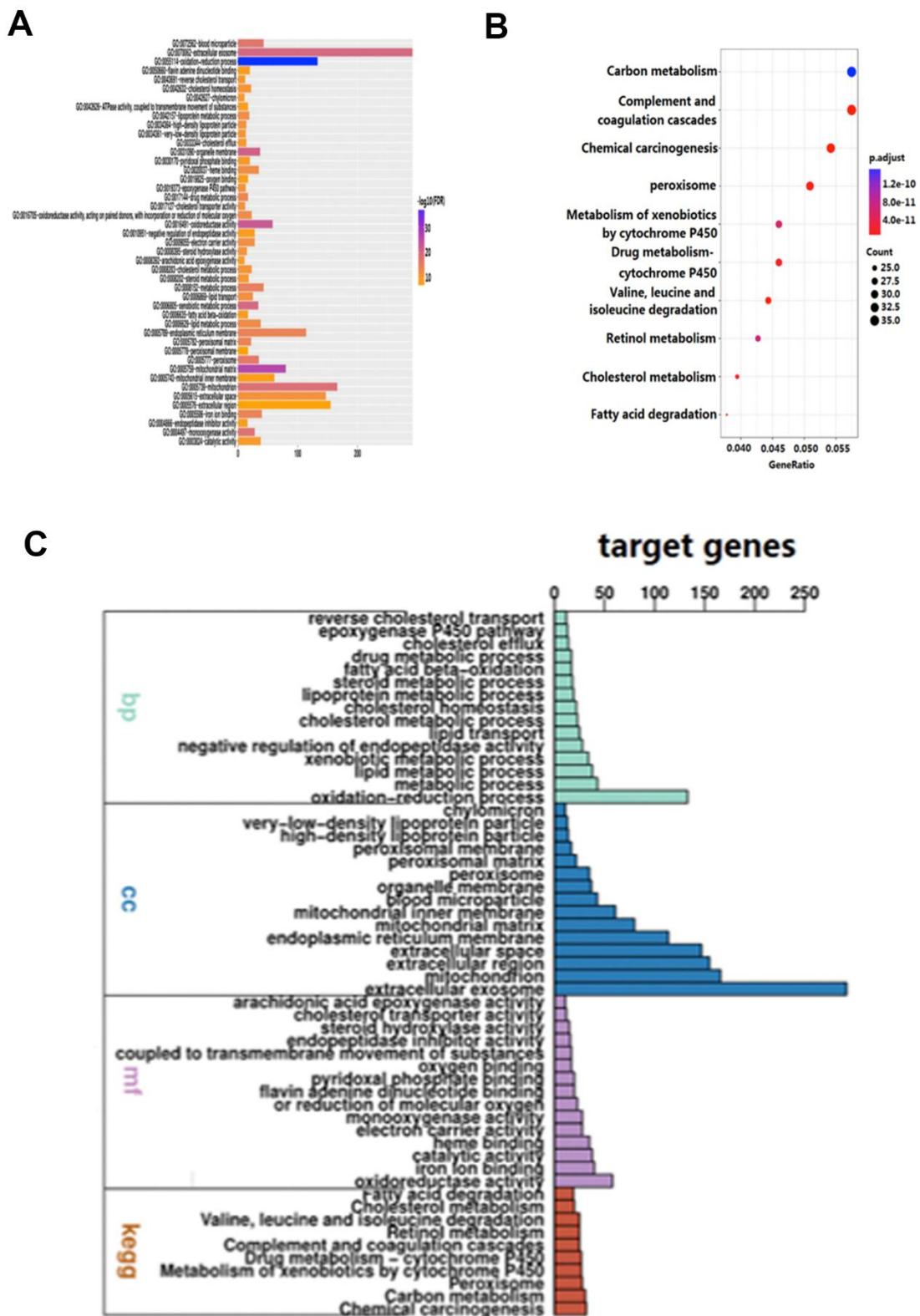
SUPPLEMENTARY FIGURES



Supplementary Figure 1. The differentially expressed level of five-lncRNA in paired carcinoma and paracancerous tissues. (A–C) AC006504.8, AP000943.4 and AC090114.2 expressed higher in cancer tissues. (D, E) AL359715.5 and HULC expressed lower in paracancerous tissues.

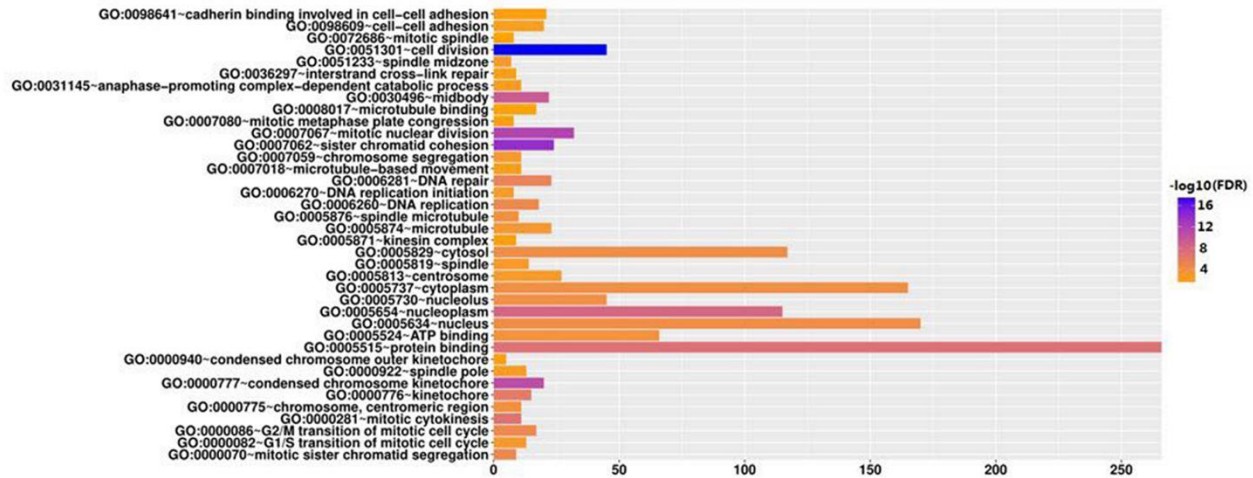


Supplementary Figure 2. Protein-coding genes co-expressed with HULC lncRNA enriched by significant KEGG pathways and GO-based functional enrichment analysis. (A) The top 15 biological processes (BP), top 15 cellular components (CC) and top 15 molecular functions (MF) enriched among 1429 DPCG targets of HULC lncRNA. (B) Top 10 KEGG pathways for HULC lncRNA-related DPCGs. (C) Number of target genes enriched (the horizontal axis represented the corresponding $-\log_{10}$ (FDR) of different paths and the vertical axis denoted the path name; bp: Biology Process; cc: Cellular Components; mf: Molecular Function).

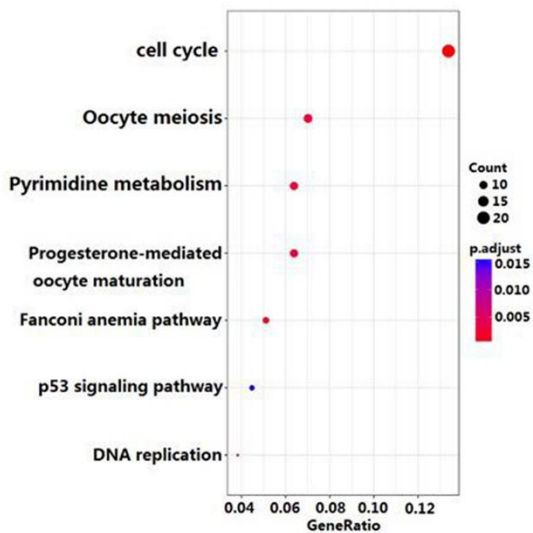


Supplementary Figure 3. Protein-coding genes co-expressed with AL359715.5 lncRNA enriched by significant KEGG pathways and GO-based functional enrichment analysis. (A) The top 15 biological processes (BP), top 15 cellular components (CC) and top 15 molecular functions (MF) enriched among 1440 DPCG targets of AL359715.5 lncRNA. **(B)** Top 10 KEGG pathways for AL359715.5 lncRNA-related DPCGs. **(C)** Number of target genes enriched (the horizontal axis represented the corresponding $-\log_{10}$ (FDR) of different paths and the vertical axis denoted the path name; bp: Biology Process; cc: Cellular Components; mf: Molecular Function).

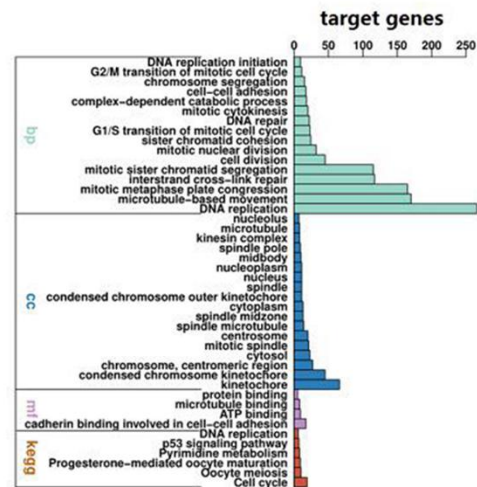
A



B

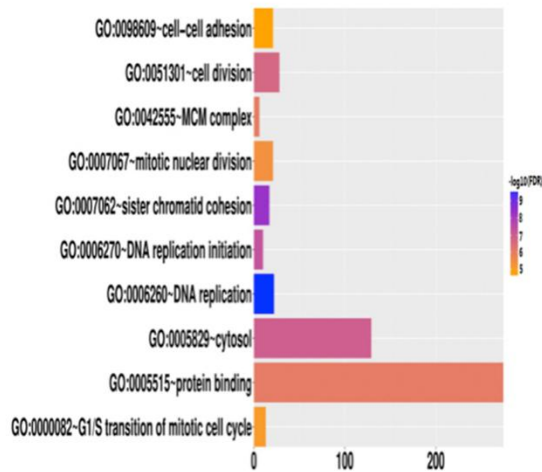


C

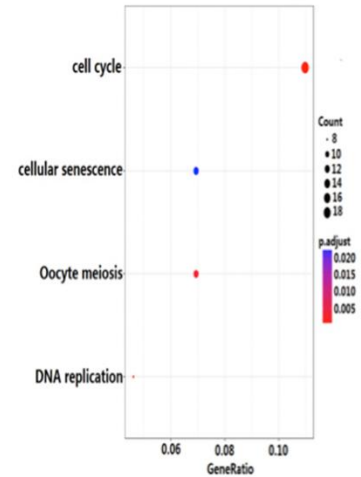


Supplementary Figure 4. Protein-coding genes co-expressed with AC006504.8 lncRNA enriched by significant KEGG pathways and GO-based functional enrichment analysis. (A) The 38 GO processes enriched among 495 DPCG targets of AC006504.8 lncRNA. **(B)** The 6 KEGG pathways for AC006504.8 lncRNA-related DPCGs. **(C)** Number of target genes enriched (the horizontal axis represented the respective $-\log_{10}(\text{FDR})$ of different paths and the vertical axis denoted the path name; bp: Biology Process, cc: Cellular Components; mf: Molecular Function).

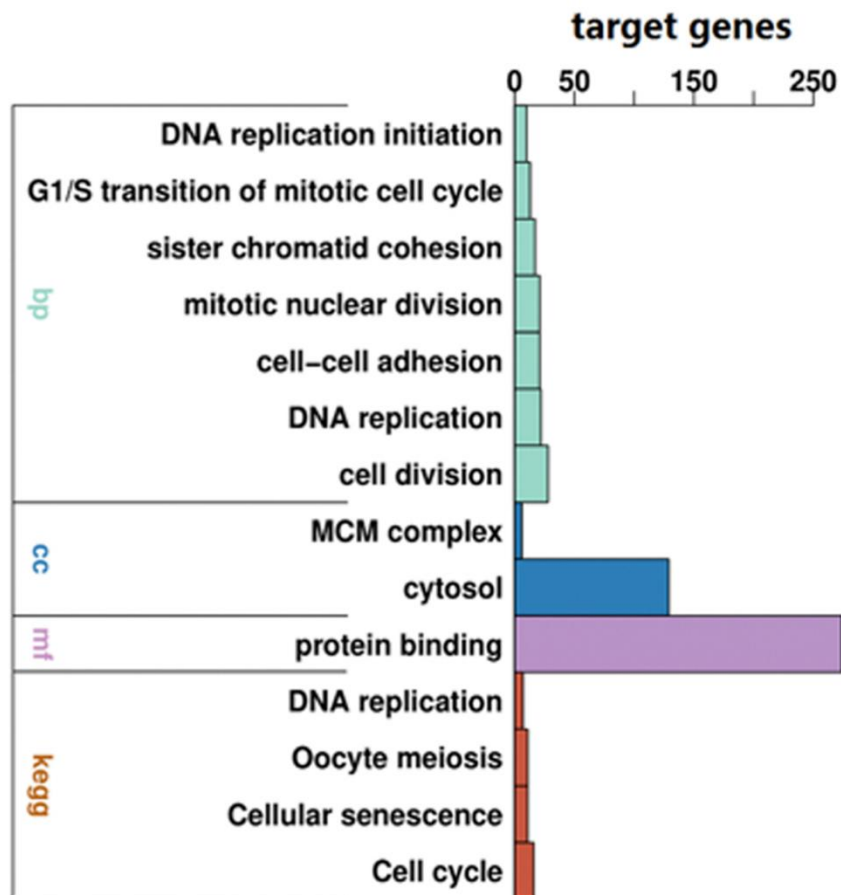
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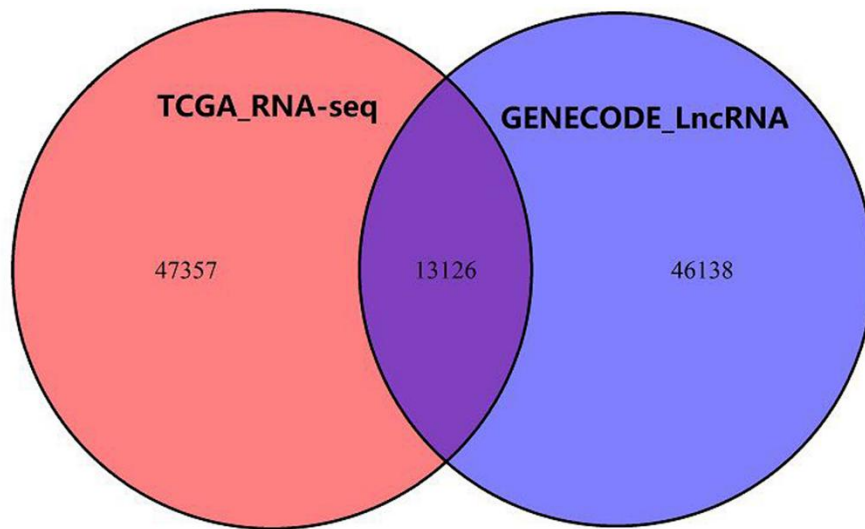
B



C



Supplementary Figure 5. Protein-coding genes co-expressed with AC090114.2 lncRNA enriched by significant KEGG pathways and GO-based functional enrichment analysis. (A) The 10 GO processes enriched among 552 DPCG targets of AC090114.2 lncRNA. (B) The 4 KEGG pathways for AC090114.2 lncRNA-related DPCGs. (C) Number of target genes enriched (the horizontal axis represented the respective $-\log_{10}$ (FDR) of different paths and the vertical axis denoted the path name; bp: Biology Process, cc: Cellular Components, mf: Molecular Function).



Supplementary Figure 6. After 60483 RNA-ENSG_ID and 59264 lncRNA-ENSG_ID were intersected to obtain 13126 lncRNA-Gene_name for this study.