

Figure S1. Time-dependent receiver operating characteristic analysis of 13 diagnostic long non-coding RNAs. (A) AC008268.1, (B) CTA-384D8.35, (C) CTC-537E7.2, (D) HOTAIR, (E) LA16c-380H5.4, (F) LINC00993, (G) RP11-95M15.1, (H) RP11-287D1.4, (I) RP11-510J16.5, (J) RP11-612B6.2, (K) RP11-783K16.5, (L) ST8SIA6-AS1, (M) TMEM92-AS1. AUC, area under the curve.

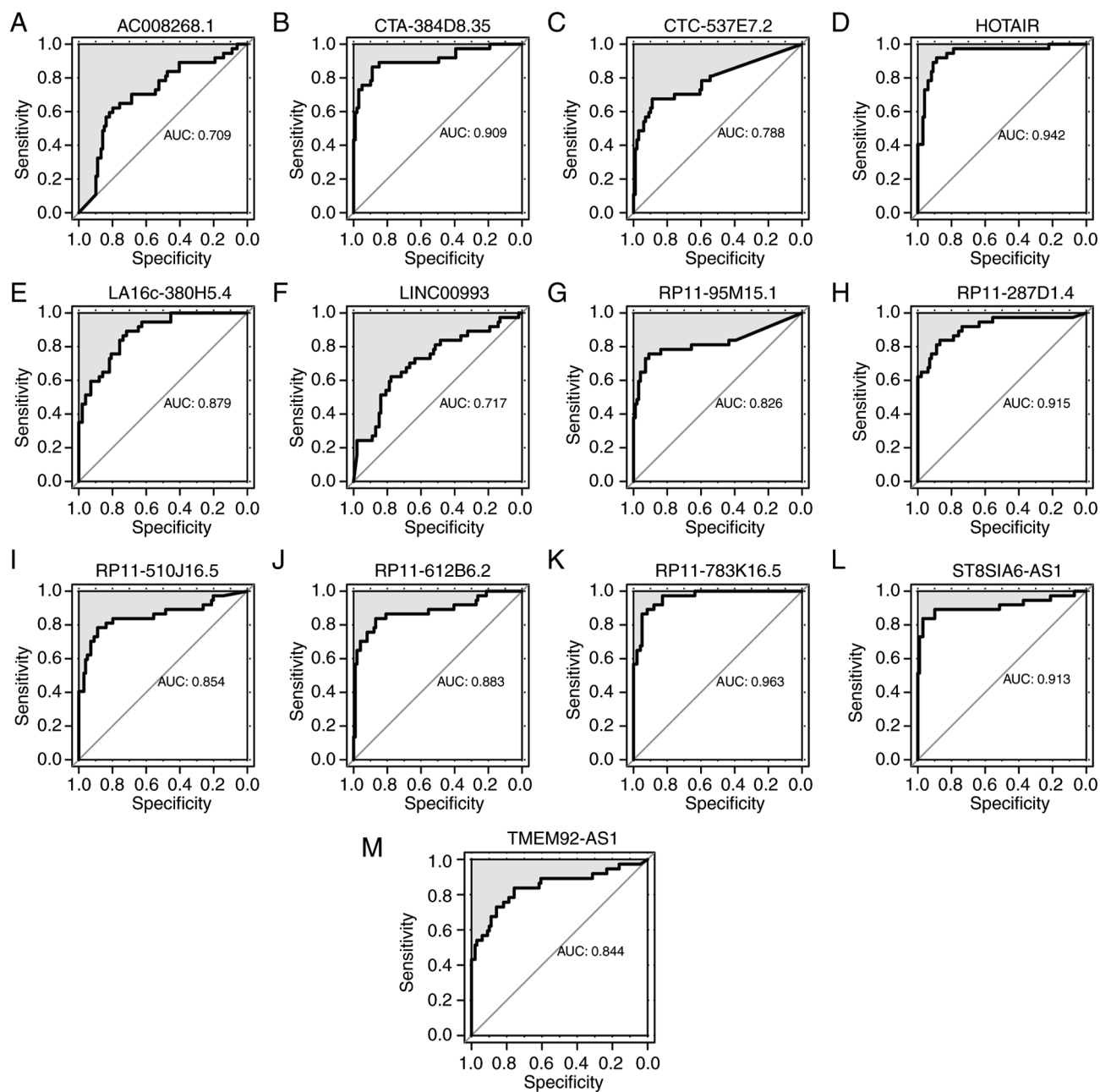


Figure S2. Results of Gene Ontology enrichment and KEGG pathway analysis of mRNAs in long non-coding RNA-mRNA co-expression networks. (A) Biological processes, (B) cellular components and (C) molecular functions. (D) KEGG pathway analysis. KEGG, Kyoto Encyclopedia of Genes and Genomes; Jak-STAT, Janus kinase-signal transducer and activator of transcription.

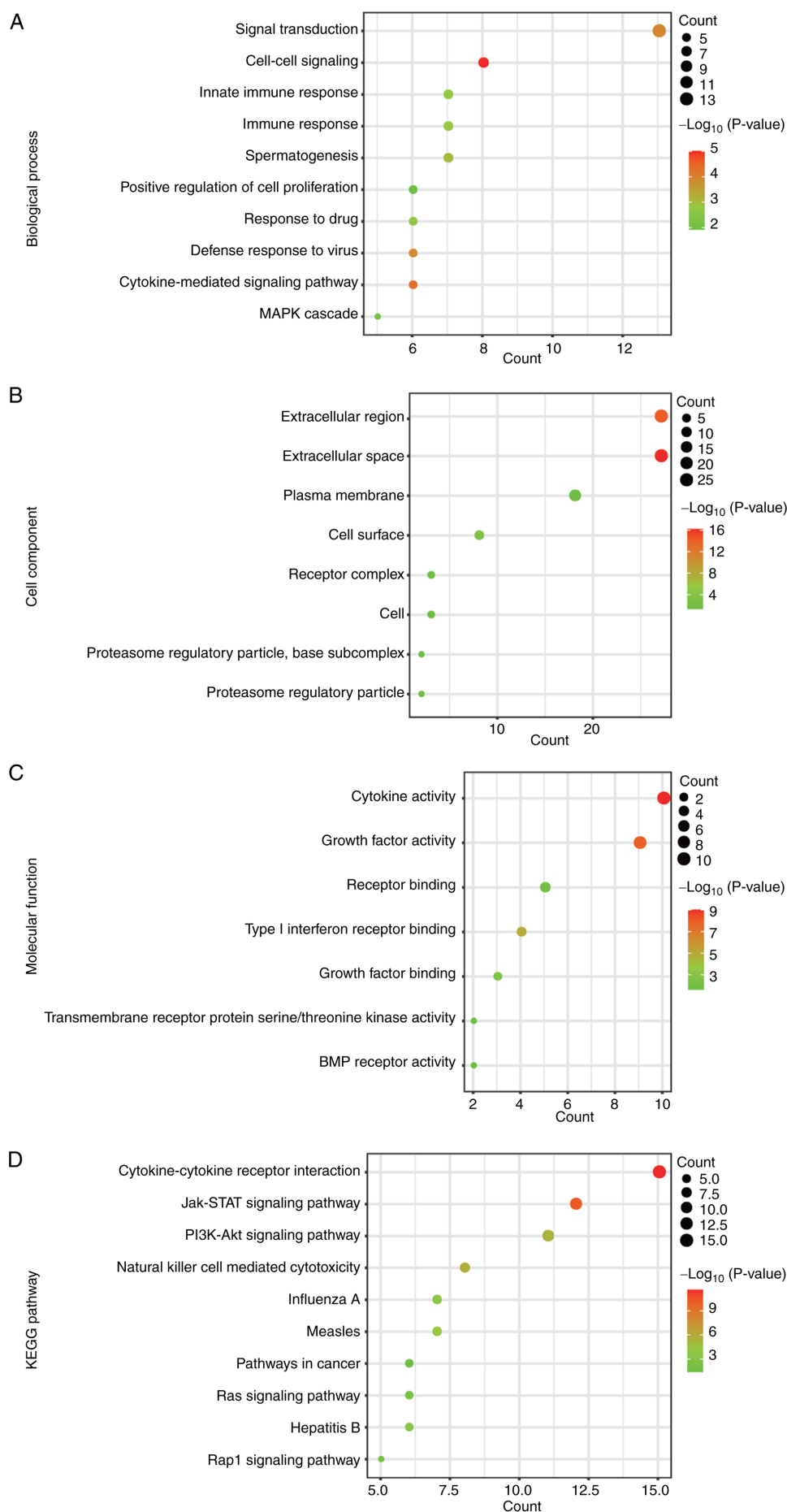


Figure S3. Results of Gene Ontology enrichment and KEGG pathway analysis of mRNAs in competing endogenous RNA networks. (A) Biological processes, (B) cellular components and (C) molecular functions. (D) KEGG pathway analysis. KEGG, Kyoto Encyclopedia of Genes and Genomes; Jak-STAT, Janus kinase-signal transducer and activator of transcription.

