Figure S1: **Statistics for pan-cancer dataset derived from TCGA collected by Tokheim et al.** (A) Mutation burden various in different tumor types. (B) 24 tumor types with over 100 samples are collected for experiments.
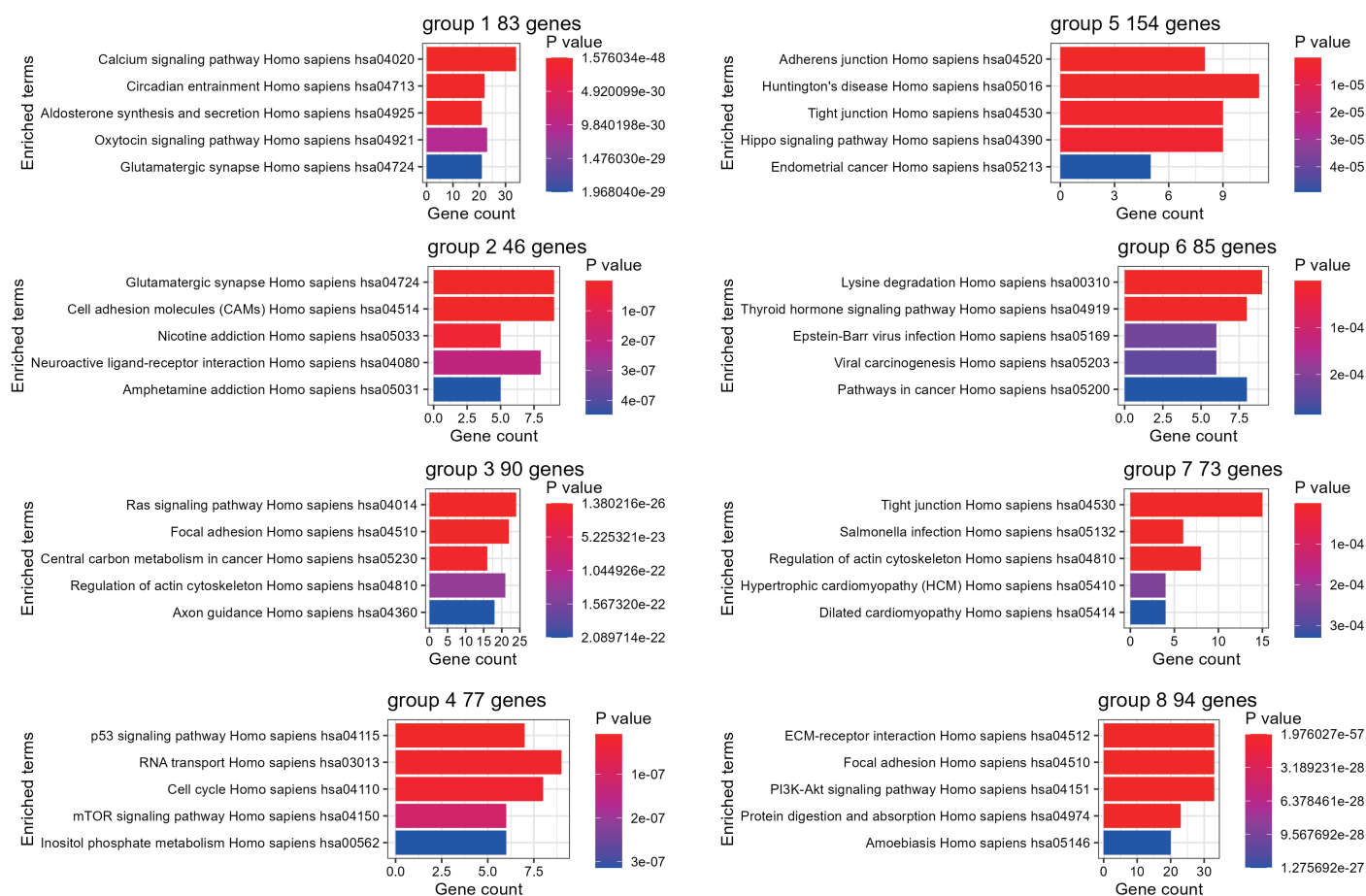
Figure S2: **MutNet predicts functional cancer genes accurately.** (A) f1 score of ranked cancer genes by different methods with four independent benchmark datasets. MutNet predicts functional cancer genes accurately. (B) Comparison of precision, recall, f1-score, and num of predicted cancer genes from different methods comparing with cancer gene from MutPanning, Cancer Gene Cosmic, and OncoKB. (C) Across methods comparation shows that MutNet reaches the highest mean correlation with all other methods. (D) Genes ranked and selected by S_{raw} reaches better AUROC and F1-value against those by mutation rate only. (E) MutNet obtains the highest performance by combining different networks and genomic features.

Figure S3: **KEGG pathway gene set enrichment of eight cancer gene modules.** The modules correspond to critical cancer hallmarks such as ECM-receptor interaction, axon guidance, cell adhesion molecules, and the Ras signaling pathway.