

Integrating omics data and protein interaction networks to prioritize driver genes in cancer

SUPPLEMENTARY MATERIALS

Supplementary Table 1: Ranked list of candidate driver genes for HNSC, KIRC, and THCA dataset, respectively.

Rank: rank of the gene according to our method, gene: gene symbol, driver gene score: the score of driver gene calculated by our method.

See Supplementary File 1

Supplementary Table 2: KEGG pathway enrichment analysis for all driver genes identified from THCA, KIRC and HNSC respectively.

See Supplementary File 2