



S4 Fig. The chromatin regulation factors (CRFs)-coding gene enrichment analysis for genes in the Individualized Network-based Co-Mutation (INCM) measure-identified putative genetic interactions across 14 cancer types. Red lines represent the number (n) of the overlapped genes between CRFs coding genes (**S5 Table**) and genes in the INCM-identified putative genetic interaction network. Bar graphs represent 10,000 times random sampling, and the number of genes in each sampling test is equal to the gene set of the INCM-identified putative genetic interaction network. P-value was calculated by permutation test.