



Fig. S1. The distribution of mutational signal ($M=M1 \times M2$, see the section of Methods and Materials) values of the protein-protein interaction (PPI) pairs in the protein interaction network in comparison to the unfiltered interactions relative to the same number of random pairs across 9 cancer types. We found that PIN is significantly more enriched for high mutation rates than random pairs across 9 cancer types ($q < 2.2 \times 10^{-16}$, Wilcoxon sum-rank test adjusted by R-package multiple test. BRCA: breast invasive carcinoma, COAD: colon adenocarcinoma, GBM: glioblastoma multiforme, HNSC: head and neck squamous cell carcinoma, KIRC: kidney renal clear cell carcinoma, LUAD: lung adenocarcinoma, LUSC: lung squamous cell carcinoma, OV: ovarian serous cystadenocarcinoma, and UCEC: uterine corpus endometrial carcinoma.