



Supplementary Fig. 9: Association of our network-prioritized hotspots with patients' survival, with known therapeutic biomarkers excluded. Survival probabilities and curves were obtained using Kaplan-Meier estimates (red denotes patients harboring network-prioritized hotspot mutations; grey denotes patients harboring other hotspot mutations). Number at risk tables are shown under corresponding Kaplan-Meier plots, indicating the number of subjects at risk immediately before the time point. Hazard ratio (HR), P value, and C-statistic were calculated using a Cox regression model. BRCA: breast invasive carcinoma, ESCA: esophageal carcinoma, HNSC: head and neck squamous cell carcinoma, LIHC: liver hepatocellular carcinoma, LUSC: lung squamous cell carcinoma, READ: rectum adenocarcinoma, STAD: stomach adenocarcinoma. Number of hotspots included in each Kaplan-Meier analysis (N_prioritized and N_other, respectively): BRCA=15, 58; ESCA=8, 31; HNSC=10, 47; LIHC=8, 9; LUSC=12, 49; READ=14, 35; STAD=13, 54.