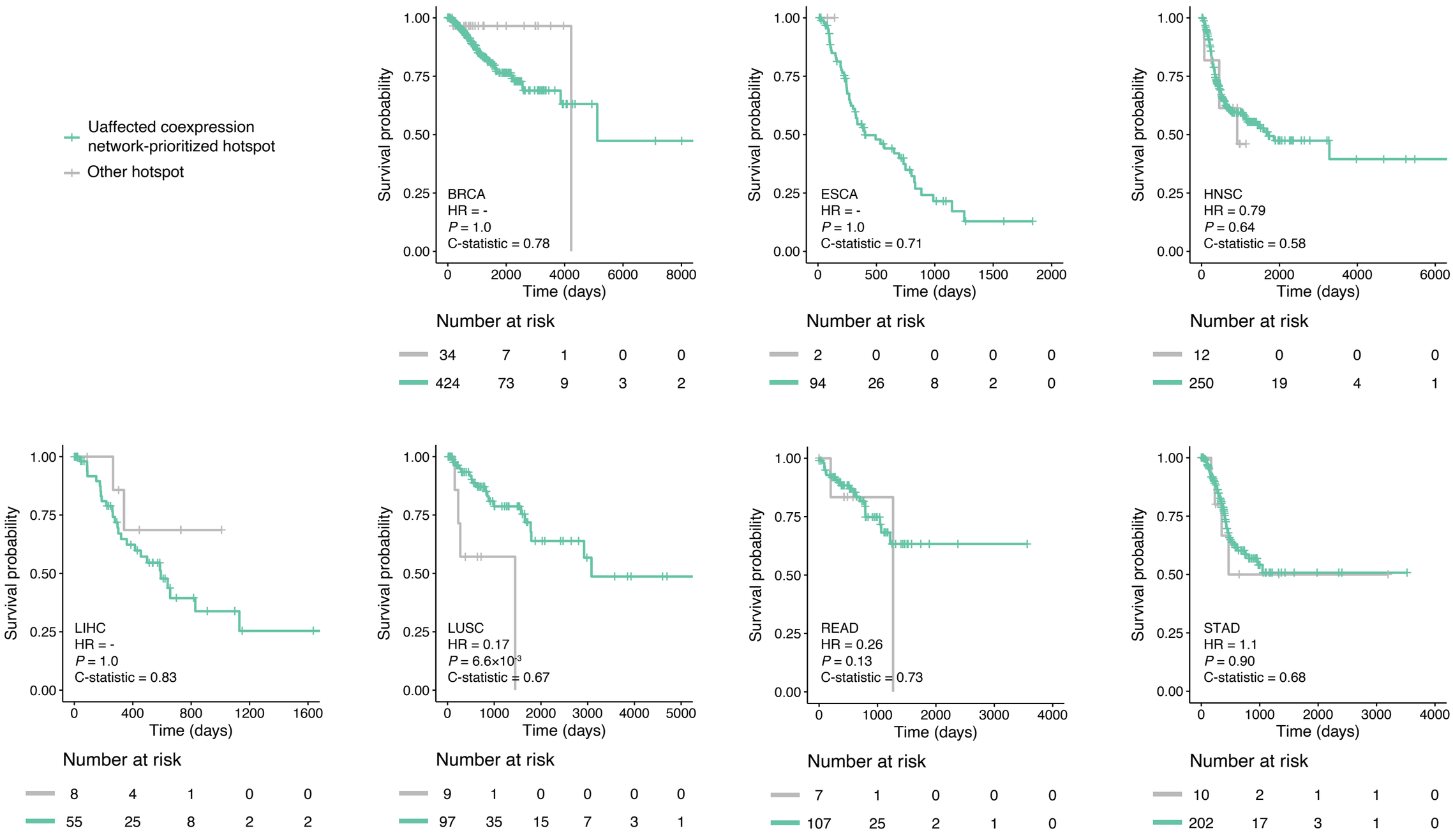

Supplementary Fig. 5: Association of hotspots prioritized by unaffected coexpression networks with patients' survival. Survival probabilities and curves were obtained using Kaplan-Meier estimates (green denotes patients harboring hotspots in the unaffected coexpression networks; grey denotes patients harboring other hotspots). 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. HR with [0, inf) 95% confidence intervals are denoted as "-". 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_(unaff-network) and N_other, respectively): BRCA=69, 15; ESCA=44, 2; HNSC=55, 7; LIHC=15, 4; LUSC=58, 10; READ=55, 8; STAD=69, 10.