



S6 Fig. INCM-predicted genetic interactions correlate with patient survivals in breast invasive carcinoma (BRCA). **(A)** The putative genetic interaction network in BRCA identified by individualized network-based co-mutation (INCM) measure. **(B-D)** The identified significantly putative genetic interactions correlate with patient survival rate. BCL2L1-HRAS **(B)** and XRCC1-HRAS **(D)** are significantly co-mutated BRCA patients. Patients have mutations (Mutant [Mut] group) on both genes of BCL2L1-HRAS **(C)** or XRCC1-HRAS **(E)** are significantly correlate with poor survival rates comparing to wild-type [WT] group on both genes. P-value in **B** and **D** was computed by permutation set. P-value in **C** and **E** was computed by logrank test.