**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.