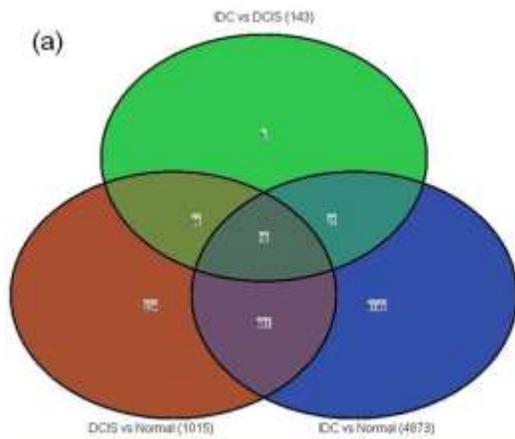


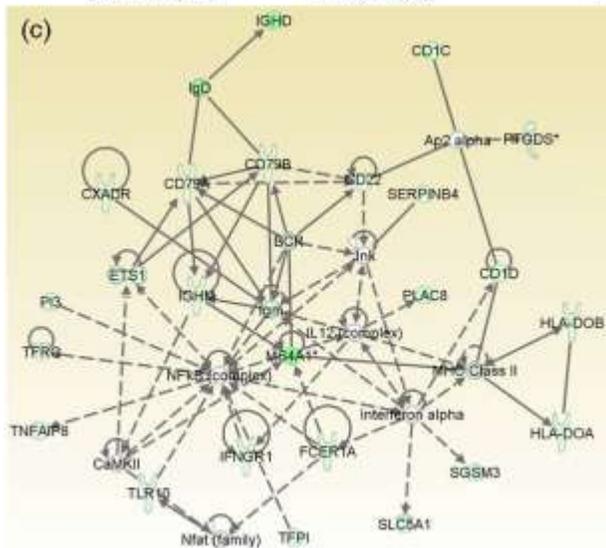
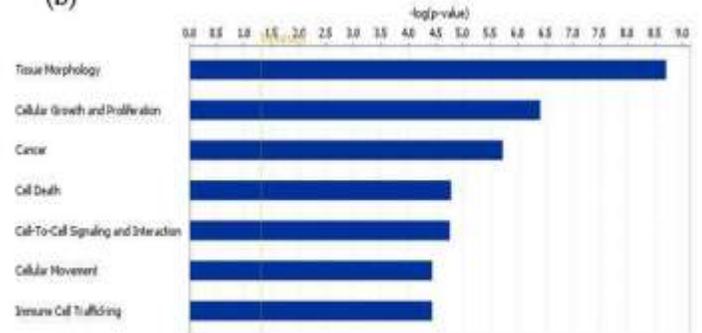
Figure S3. I. Comparison of the expression profile characteristics of IDC and DCIS. (a) 143 genes have significantly different levels of expression between DCIS compared to IDC. (b) Functional enrichment analysis of genes whose expression altered between DCIS and IDC. (c-d) The network analysis of 143 genes. Green/red indicates decreased/increased mRNA expression in IDC compared to normal controls.

II. Network analyses of genes specific to DCIS or IDC in young women (A) Venn diagram illustrating 27 genes and 94 probes (corresponding to 72 genes) that are specific to IDC and DCIS, respectively. (B) Network analyses of genes specific to IDC. Green/red indicates decreased/increased mRNA expression in IDC compared to normal controls. (C) Network analyses of genes specific to DCIS (top two significant networks shown). Green/red indicates decreased/increased mRNA expression in DCIS compared to normal controls. The color intensity is correlated with fold change. Straight lines are for direct gene to gene interactions, dashed lines are for indirect ones. DCIS: ductal carcinoma in situ; IDC: invasive ductal carcinoma.

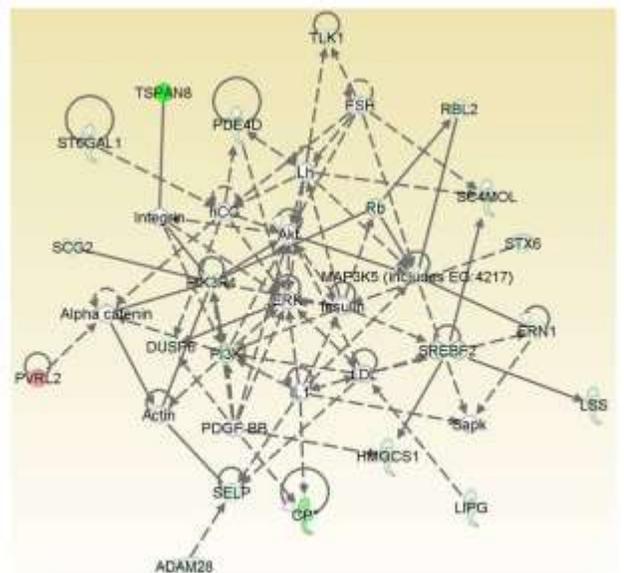
(I)



(b)



(d)



(II)

