Figure S6.2. The survival analyses on probes in *STAT3* driven subnetworks in coupling with its major transcription factor partner-*MYC* for proliferation, sustained angiogenesis, ES like, Warburg effect, FOXC1 and ERBB2 signaling in ER(+) IDCs. We compared the probe in both 90A and 72A to find out the influence of cohort patients in interpreting the predicted role for that probe of interest in its clinical outcome that was evaluated by overall disease free survival. We only picked the significant one ( $p \le 0.05$  in 90A and/or 72A).

a. STAT3 subnetwork components for proliferation



## b. STAT3 subnetwork components for sustained angiogenesis



## c. *STAT3* subnetwork components for Warburg effect





d. *STAT3* subnetwork components for ES like phenotype



## e. STAT3 subnetwork components in FOXC1 driven subnetwork



f. STAT3 subnetwork components for ERBB2 signal transduction pathway



**Figure S6.3.** The survival analysis on a probe - FOXC1(12715) not in the *STAT3* subnetwork. We compared this probe in cohorts 90A and 72A for predicting clinical outcome that was evaluated by overall disease free survival.



## Supplementary file 7

Figure S7.1. Mean plot analyses of mRNA levels for *MELK* in eight clinical categories and in two cohorts of infiltrating ductal carcinoma (IDCs), respectively. Lymphovascular invasion (LVI), nodal category (lymph node metastasis (LYM), number of nodal metastasis(LNM)), histological grade(Grade) category (nuclear pleomorphism (NP), mitotic count (MC) and tubule formation (TF)) and stage were analyzed. Cohort 1 (90IDCs) has Groups IE and IIE. Cohort 2 (72A) has Luminal A and Luminal B (see main text for definitions).

A. Cohort 1.



B. Cohort 2.



- Figure S7.2. Mean plot analyses of mRNA levels for *METAP2* in eight clinical categories and in two cohorts of infiltrating ductal carcinoma (IDCs), respectively. Lymphovascular invasion (LVI), nodal category (lymph node metastasis (LYM), number of nodal metastasis(LNM)), histological grade (Grade) category (nuclear pleomorphism (NP), mitotic count (MC) and tubule formation (TF)) and stage were analyzed. Cohort 1 (90IDCs) has Groups IE and IIE. Cohort 2 (72A) has Luminal A and Luminal B (see main text for definitions).
  - A. Cohort 1.



B. Cohort 2.



- Figure S7.3. Mean plot analyses of mRNA levels for SRC(6926) in eight clinical categories and in two cohorts of infiltrating ductal carcinoma (IDCs), respectively. Lymphovascular invasion (LVI), nodal category (lymph node metastasis (LYM), number of nodal metastasis(LNM)), histological grade (Grade) category (nuclear pleomorphism (NP), mitotic count (MC) and tubule formation (TF)) and stage were analyzed. Cohort 1 (90IDCs) has Groups IE and IIE. Cohort 2 (72A) has Luminal A and Luminal B (see main text for definitions).
  - A. Cohort 1.



B. Cohort 2.



- Figure S7.4. Mean plot analyses of mRNA levels for SRC(17104) in eight clinical categories and in two cohorts of infiltrating ductal carcinoma (IDCs), respectively. Lymphovascular invasion (LVI), nodal category (lymph node metastasis (LYM), number of nodal metastasis(LNM)), histological grade(Grade) category (nuclear pleomorphism (NP), mitotic count (MC) and tubule formation (TF)) and stage were analyzed. Cohort 1 (90IDCs) has Groups IE and IIE. Cohort 2 (72A) has Luminal A and Luminal B (see main text for definitions).
  - A. Cohort 1.



B. Cohort 2.



- Figure S7.5. Mean plot analyses of mRNA levels for *OIP5* in eight clinical categories and in two cohorts of infiltrating ductal carcinoma (IDCs), respectively. Lymphovascular invasion (LVI), nodal category (lymph node metastasis (LYM), number of nodal metastasis(LNM)), histological grade (Grade) category (nuclear pleomorphism (NP), mitotic count (MC) and tubule formation (TF)) and stage were analyzed. Cohort 1 (90IDCs) has Groups IE and IIE. Cohort 2 (72A) has Luminal A and Luminal B (see main text for definitions).
  - A. Cohort 1.



B. Cohort 2.

