**Supplementary information**

**Determination of the set of collective-dissemination associated genes**

Cheung *et al.* (1) observed that in a mouse model of breast cancer, locally disseminated tumor cell clusters, clusters of circulating tumor cells, and lung micrometastases were enriched for cells expressing the protein keratin-14 (K14) as compared to single disseminated cells. To compare the transcriptomes of K14+ and K14- cells, Cheung *et al.* first isolated epithelial organoids from the primary MMTV-PyMT tumor (2,3) and used differential centrifugation to deplete immune and fibroblastic cells in order to focus on differences in gene expression between the two cancer cell subpopulations. The organoids were then processed into single cells and fluorescence-activated cell sorting (FACS) was used to isolate the K14+ and K14- cells. RNA-seq reads were aligned to the mouse reference genome Genomic Reference Consortium build 38. A total of 4 such independent experiments were carried out. Number of reads mapped to each gene were determined using HTSeq v0.6.1p1 (4). Raw counts were then normalized and p-values for paired sample differential gene expression were calculated using EdgeR (4). Genes with less than 1 read per million in 4 of the 8 samples were excluded from further analysis. The procedure yielded a total of 12,190 mapped genes of which 11,968 had known annotations. DAVID Gene Set Analysis v6.7 with the functional annotation chart algorithm (5) was used for determining the Gene Ontology category enrichment, and p-values for GO category enrichment were calculated using a Fisher exact test. A total of 87 genes from GO categories functionally enriched or depleted in K14+ cell lines listed in table S1 of Cheung *et al.* (1) formed the set of collective dissemination-associated genes used in the present study.

**Determination of the set of IBC-associated genes**

Van Laere *et al.* (6) analyzed breast tumor samples from patients treated at 3 different institutions. After RNA-extraction from the 137 IBC and 252 non-IBC samples, hybridization onto Affymetrix GeneChips (HGU133-series) was carried out. Gene expression data were normalized by guanine cytosine robust multi-array analysis (7). Thereafter, in each of the 3 datasets (1 from each institution), probe sets with expression values above log2100 in at least 1% of the arrays were used for further analysis. A total of 9926 informative probes common to the 3 datasets were determined and used to merge the three datasets. Regression normalization was carried out using the Limma-package in BioConductor to remove technical, laboratory-specific variation in gene expression in the distinct datasets. To distinguish the variations in gene expression that discriminate between IBC and non-IBC type breast cancer from the variations discriminating between different breast cancer molecular subtypes such as luminal A, luminal B, basal-like, HER2-enriched, and normal-like, the dataset was divided into a training set with 250 samples (80 IBC and 166 non-IBC samples) and a validation set with 139 samples (53 IBC samples and 86 non-IBC samples). The training set was analyzed using linear regression models that incorporated the molecular subtype classification and the IBC/non-IBC classification to identify the probe sets associated with IBC-specific gene expression. Lists of probe sets were analyzed for expression differences between IBC and non-IBC samples in the validation set using a global test (8). Classifier models based on these lists of probe sets were constructed using the nearest shrunken centroid algorithm with 10-fold cross-validation to determine an appropriate -value for minimizing the cross-validated training error rate. The performance of classifier models was also tested on more homogeneous sub-groups of tumor samples such as comparing IBC and non-IBC tumor samples with the luminal molecular subtype. Finally, a 79-gene IBC / non-IBC signature was identified from this supervised analysis. This set of genes formed the set of IBC-associated genes used in the present study.

**Gene expression profiles of epithelial and mesenchymal cell lines in the study by Grosse-Wilde *et al.***

Grosse-Wilde *et al.* (9) labeled the isolated total RNA using the one color Low Input Quick Amp Labeling Kit (Agilent). The labeled probes were run on Human 4x44K Microarrays (Agilent), and spot quantification was performed using Agilent’s Feature Extractor software. Data normalization was carried out in Genedata Analyst 7.0 (Genedata, Basel, Switzerland) using central tendency followed by relative normalization.

**Gene expression profiles of cell lines in the NCI60 panel**

Biotinylated cRNA was combined with a hybridization mix, applied to HG-U133A microarray, and hybridized overnight. Arrays were then washed and stained according to the manufacturer’s instructions and scanned on an Affymetrix GS2500 scanner. The MAS5 algorithm was used to generate signal intensities, and the expression values were normalized to a mean target level of 100 (10).

**Gene expression profiles of tumor samples in the study by Iwamoto *et al.***

Gene expression profiling was carried out using Affymetrix U133A gene chips. The data were normalized using the MAS5 algorithm, mean centered to 600, and log2 transformed (11).

**Gene expression profiles of tumor samples in the study by Boersma *et al.***

Boersma *et al.* (12) hybridized the labeled cRNA onto Affymetrix HG-U133A GeneChips. The data were normalized using the robust multichip analysis procedure ([www.bioconductor.org](http://www.bioconductor.org)).

**Gene expression profiles of tumor samples in the study by Woodward *et al.***

Woodward *et al.* (13) hybridized the labeled cRNA onto Whole Human genome 4x44K microarray (Agilent Technologies). Expression data were obtained using an Agilent Microarray Scanner, analyzed with Agilent’s Feature Extraction Software version 9.5.1, and normalized using global-normalization methods.

**Gene expression profiles of tumor samples in the study by Wang *et al.***

Wang *et al.* (14) isolated the total RNA, prepared biotinylated targets, and hybridized these onto Affymetrix U133a GeneChip. Gene expression data were calculated using Affymetrix GeneChip analysis software MAS 5.0. Chips with average intensity less than 40 and those with background signal greater than 100 were filtered out. All probes were scaled to a target intensity of 600.

**Gene expression profiles of tumor samples in the study by Rousseaux *et al.***

Rousseaux *et al.* (15) hybridized biotinylated cRNA onto GeneChip Human Genome U133 plus 2.0 array, scanned the GeneChips using the Affymetrix GeneArray scanner, and normalized the expression data using the Robust Multi-Array average (RMA) algorithm (Genespring software; Agilent).

**Gene expression profiles of tumor samples in the study by Kimbung *et al.***

Kimbung *et al.* (16) hybridized the isolated total RNA onto custom-made Affymetrix HuRSTA-2a520709 gene chips. Raw gene expression levels were normalized using the robust multichip average (RMA) algorithm. The data were log2 transformed and mean-centered across the entire dataset.

**Gene expression profiles of tumor samples in the TCGA dataset**

Agilent custom 244K whole genome microarrays were hybridized and the expression data were gene-median centered (17).

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