Supplementary Table 1. Intersection of Activated HIF1a Fibroblast Proteomics with the Transcriptome of Human Breast Cancer Tumor Stroma.

Gene Symbol	Tumor Stroma	Recurrence-Prone Stroma	Metastasis-Prone Stroma
TERT	1.34E-11	1.23E-02	2.17E-02
ALDOA			1.69E-03
CALD1	4.97E-16		
COL6A2			
DHX15			
EEF2			4.41E-02
ENO1			
ERO1L	1.54E-03		
FN1	8.19E-13	6.23E-04	
GAPDH			
HNRNPK			
HNRNPL			
HNRNPR			
LDHA			
LDHAL6B	3.67E-10		
LEPREL2			
MAPRE1	4.85E-27		
P4HA1			
PGAM1			
PGK1		3.21E-02	
PGM1			
PKM2			3.73E-02
PLOD2	2.04E-09		
S100A13	1.32E-13		1.90E-02
TPI1			
UQCRFS1			

Proteins that were transcriptionally upregulated in laser-capture micro-dissected human breast cancer tumor stroma are shown in **BOLD**.
LDHA was not found to be transcriptionally upregulated; however, its close relative **LDHAL6B** was transcriptionally increased in tumor stroma.
Although TERT was not detected by proteomics, it was included in this list to support the use of hTERT-transfected fibroblasts as a model system for mimicking the cancer-associated fibroblast phenotype. **P-values are as shown.**

Supplmentary Table 2. Intersection of IKBKE Fibroblast Proteomics with the Transcriptome of Human Breast Cancer Tumor Stroma.

Gene Symbol	Tumor Stroma	Recurrence-Prone Stroma	Metastasis-Prone Stroma
TERT	1.34E-11	1.23E-02	2.17E-02
ACLY	1.55E-02	2.50E-02	
ARPC2			
CCT3			
CCT4			
CCT5			
CCT6A			
CCT7			
CNBP			
EEF2			4.41E-02
ENO1			
FUBP1			
GAPDH			
HNRNPK			
HSPD1			
ISCU2			
ITGB1BP1			
KHSRP	9.43E-18	4.44E-02	1.16E-02
LDHB			
MVP			2.38E-02
NCL			
PKM2			3.73E-02
PRDX4			
PYGB	4.34E-18	9.48E-03	
SND1	3.55E-10		
TCP1			
VCP	3.91E-05		1.43E-02
VIM			
XAB2	5.39E-04		2.78E-02

Proteins that were transcriptionally upregulated in laser-capture micro-dissected human breast cancer tumor stroma are shown in **BOLD**. Although TERT was not detected by proteomics, it was included in this list to support the use of hTERT-transfected fibroblasts as a model system for mimicking the cancer-associated fibroblast phenotype. **P-values are as shown.**

Intersection of Fibroblast Proteomics with the Transcriptome of Human Breast Cancer Tumor Stroma:

We speculated that the proteomic profiles obtained from HIF1a- and IKBKE-transfected fibroblasts might overlap with the transcriptional stromal profiles obtained from human breast caners. To test this hypothesis, we obtained the transcriptional profiles of a large data set of human breast cancer patients [1] whose tumors were subjected to laser-capture micro-dissection, to selectively isolate the tumor stroma. Based on this data set [1], we then generated three human breast cancer stromal genes lists [2]:

1) **Tumor Stroma vs. Normal Stroma List-** Compares the transcriptional profiles of tumor stroma obtained 53 patients to normal stroma obtained from 38 patients. Genes transcripts that were consistently upregulated in tumor stroma were selected and assigned a p-value, with a cut-off of $p < 0.05$ (contains 6,777 genes) (See reference #2).

2) **Recurrence Stroma List-** Compares the transcriptional profiles of tumor stroma obtained from 11 patients with tumor recurrence to the tumor stroma of 42 patients without tumor recurrence. Genes transcripts that were consistently upregulated in the tumor stroma of patients with recurrence were selected and assigned a p-value, with a cut-off of $p < 0.05$ (contains 3,354 genes). (See reference #2).

3) **Lymph-node (LN) Metastasis Stroma List-** Compares the transcriptional profiles of tumor stroma obtained from 25 patients with LN metastasis to the tumor stroma of 25 patients without LN metastasis. Genes transcripts that were consistently upregulated in the tumor stroma of patients with LN metastasis were selected and assigned a p-value, with a cut-off of $p < 0.05$ (contains 1,182 genes). (See reference #2).

These three gene lists were then individually intersected with the proteomic profiles of HIF1a- and IKBKE-transfected fibroblasts. The results of these intersections are presented in **Supplementary Tables 1 and 2.**

References:

1. Finak G, Bertos N, Pepin F, Sadekova S, Souleimanova M, Zhao H, Chen H, Omeroglu G, Meterissian S, Omeroglu A, Hallett M, Park M. Stromal gene expression predicts clinical outcome in breast cancer. Nat Med 2008; 14:518-27.

2. Pavlides S, Tsirigos A, Vera I, Flomenberg N, Frank PG, Casimiro MC, Wang C, Pestell RG, Martinez-Outschoorn UE, Howell A, Sotgia F, Lisanti MP. Transcriptional evidence for the "Reverse Warburg Effect" in human breast cancer tumor stroma and metastasis: similarities with oxidative stress, inflammation, Alzheimer's disease, and "Neuron-Glia Metabolic Coupling". Aging (Albany NY) 2010; 2:185-99.