

File name: **Additional file 1**

Title: **Supplementary Methods**

RNA preparation and quantitative PCR

The following primer sequences (5' to 3') were used:	
Gene	Sequence
h <i>TGFBR3</i> forward	TGGGGTCTCCAGACTGTTTTT
h <i>TGFBR3</i> reverse	CTGCTCCATACTCTTTTCGGG
h <i>PAI-1</i> forward	GACATCCTGGAAGTCCCTA
h <i>PAI-1</i> reverse	GGTCATGTTGCCTTTCCAAGT
h <i>SMAD7</i> forward	CCAACTGCAGACTGTCCAGA
h <i>SMAD7</i> reverse	CAGGCTCCAGAAGAAGTTGG
h <i>ITGA2</i> forward	CCTACAATGTTGGTCTCCCAGA
h <i>ITGA2</i> reverse	AGTAACCAGTTGCCTTTTGATT

Immunoblotting

ANTIBODY (in alphabetical order)	COMPANY	CATALOG #	SPECIES	Concentrations
cleaved Caspase-3	Cell Signaling	9661	rabbit	1:1000
ERK	Cell Signaling	9107	mouse	1:2000
ERK, phospho	Cell Signaling	4370	rabbit	1:2000
PARP	Cell Signaling	9542	rabbit	1:1000
Smad2	Cell Signaling	5339	rabbit	1:1000
Smad2, phospho	Cell Signaling	3101	rabbit	1:1000
TβRII	Santa Cruz	SC400	rabbit	1:4000
TβRIII	SDIX	2703.00.02	rabbit	1:10000

Microarray Gene Expression GEO registration numbers

Breast Cancer GE data sets used to derive TNBC training and validation sets:

GSE-3494 , GSE-7904 , GSE-2109 , GSE-7390 , E-TABM-158 , GSE-2034 , GSE-2990 , GSE-1456 , GSE-22513 , GSE-28821, GSE-28796 , GSE-11121 , GSE-2603 , MDA133 , GSE-5364 , GSE-1561 ,GSE-5327 , GSE-5847 , GSE-12276 , GSE-16446 , GSE-18864 , GSE-19615 , GSE-20194. (*Lehmann BD, Bauer JA, Chen X, Sanders ME, Chakravarthy AB, Shyr Y, PiTENpol JA: Identification of human triple-negative breast cancer subtypes and preclinical models for selection of targeted therapies. The Journal of clinical investigation 2011, 121(7):2750-2767.*)