

Sample Name	%MD	Age	Menopausal Status	Parity	Passage
LDAF1	25%<MD<50%	47	post	Un	5
LDAF2	25%<MD<50%	19	pre	1	6
LDAF3	25%<MD<50%	66	post	5	3
LDAF4	25%<MD<50%	56	pre	1	4
LDAF5	25%<MD<50%	52	post	1	4
LDAF6	25%<MD<50%	41	pre	1	4
LDAF8	25%<MD<50%	41	pre	0	6
HDAF1	MD>75%	52	post	1	5
HDAF2	MD>75%	37	pre	2	5
HDAF3	MD>75%	42	pre	3	4
HDAF4	MD>75%	36	pre	0	4
HDAF5	MD>75%	45	pre	3	5
HDAF6	MD>75%	19	pre	0	6
HDAF7	MD>75%	50	peri	0	3

Supplementary Table S1

Sample Name	Tissue Type	Diagnosis	Age	Passage
RMF1	Reduction Mammoplasty	Normal	35	4
RMF2	Reduction Mammoplasty	Normal	66	7
RMF3	Reduction Mammoplasty	Normal	44	5
RMF4	Reduction Mammoplasty	Normal	47	4
RMF5	Reduction Mammoplasty	Normal	29	4
RMF6	Reduction Mammoplasty	Normal	17	4
RMF7	Reduction Mammoplasty	Normal	46	5
RMF8	Reduction Mammoplasty	Normal	46	4
CAF1	Invasive Cancer	IDC	73	4
CAF2	Invasive Cancer	Un	Un	15
CAF3	Invasive Cancer	Un	Un	8
CAF4	Invasive Cancer	Un	Un	8
CAF5	Invasive Cancer	Un	Un	7
CAF6	Invasive Cancer	IDC	60	4
CAF7	Invasive Cancer	IDC	63	4
CAF8	Invasive Cancer	IDC	61	4

Supplementary Table S2

Probeset #	Gene Symbol	Gene Name	Fold Change	p value	Gene Activity/Pathway
202145_at	LY6E	lymphocyte antigen 6 complex	1.6	0.0007	thought to be a membrane signal transduction protein
202275_at	G6PD	glucose-6-phosphate dehydrogenase	1.6	0.0008	enzyme in the pentose phosphate pathway, which produces NADPH
206488_s_at	CD36	CD36 molecule	-3.7	0.0012	receptor for long chain fatty acids, oxyLDL, collagen & thrombospondin; involved in fatty acid & glucose metabolism & angiogenesis
227404_s_at	EGR1	early growth response	-1.4	0.0016	EGR family member; transcription factor of genes involved in differentiation & mitogenesis; tumor suppressor
227370_at	KIAA1946/ FAM171B	family with sequence similarity 171, member B	-1.8	0.0023	
213281_at	JUN	Jun oncogene	-1.9	0.0028	together with c-Fos, forms the AP-1 transcription factor
217494_s_at	PTENP1	phosphatase and tensin homolog pseudogene 1	-1.7	0.0028	pseudogene of tumor suppressor gene PTEN; found to be hypermethylated in tumors
229067_at	SRGAP2P1	SLIT-ROBO Rho GTP-ase activating protein 2 pseudogene 1	-1.7	0.0029	
200908_s_at	RPLP2	ribosomal protein, large, P2	-2.2	0.0033	component of 60s subunit of the ribosome
209555_s_at	CD36		-4.3	0.0034	
214182_at	ARF6	ADP-ribosylation factor 6	-1.5	0.0037	part of the ras superfamily; involved in vesicular trafficking & remodeling of membrane lipids & actin cytoskeleton

Probeset #	Gene Symbol	Gene Name	Fold Change	p value	Gene Activity/Pathway
228766_at	CD36		-4.2	0.0038	
225745_at	LRP6	low density lipoprotein receptor-related protein 6	-1.4	0.0038	lipoprotein receptor; co-receptor with Frizzled for Wnt, activating the canonical Wnt signalling pathway
226880_at	NUCKS	nuclear casein kinase and cyclin-dependant kinase substrate 1	-1.5	0.0038	phosphorylated by cdk1 & casein kinase; phosphorylated after DNA damage by ATM or ATR
1565823_at	SEPT7	septin 7	-2.4	0.0039	filament forming cyoskeletal GTPase; involved in organizing actin cytoskeleton; required for mitosis
220342_x_at	EDEM3	ER degradation enhancer, mannosidase alpha-like 3	-1.3	0.0044	accelerates degradation of misfolded glycoproteins in the ER
210117_at	SPAG1	sperm associated antigen 1	-1.3	0.0044	binds to GTP & has GTPase activity
212044_s_at	RPL27A	ribosomal protein L27A	-1.8	0.0045	component of 60s subunit of the ribosome; variable expression in colorectal tumors compared to normal adjacent
220926_s_at	EDEM3		-1.4	0.0046	
228530_at	RP11-11C5.2/C13orf37	chromosome 13 open reading frame 37	-1.7	0.0046	

Supplementary Table S3

Reference	Sample Size	CD36 Fold Change/p value (IDC vs Normal)
Perou et al. <i>Nature</i> , 2000. (1)	65	-7.034/0.006
Sorlie et al. <i>PNAS</i> , 2003. (2)	167	-9.128/0.006
Zhao et al. <i>Mol Biol Cell</i> , 2004. (3)	64	-4.589/0.017
Radvanyi et al. <i>PNAS</i> , 2005. (4)	63	-3.640/0.002
Richardson et al. <i>Cancer Cell</i> , 2006. (5)	47	-12.286/2.22e-5
Turashvili et al. <i>BMC Cancer</i> , 2007. (6)	30	-3.599/0.053

1_Perou CM, Sorlie T, Eisen MB, van de Rijn M, Jeffrey SS, Rees CA, et al. Molecular portraits of human breast tumours. *Nature* 2000; 406:747-752.

2_Sorlie T, Perou CM, Tibshirani R, Aas T, Geisler S, Johnsen H, et al. Gene expression patterns of breast carcinomas distinguish tumor subclasses with clinical implications. *Proc Natl Acad Sci U S A* 2001; 98:10869-10874.

3_Zhao H, Langerod A, Ji Y, Nowels KW, Nesland JM, Tibshirani R, et al. Different gene expression patterns in invasive lobular and ductal carcinomas of the breast. *Mol Biol Cell* 2004; 15:2523-2536.

4_Radvanyi L, Singh-Sandhu D, Gallichan S, Lovitt C, Pedyczak A, Mallo G, et al. The gene associated with trichorhinophalangeal syndrome in humans is overexpressed in breast cancer. *Proc Natl Acad Sci U S A* 2005; 102:11005-11010.

5_Richardson AL, Wang ZC, De Nicolo A, Lu X, Brown M, Miron A, et al. X chromosomal abnormalities in basal-like human breast cancer. *Cancer Cell* 2006; 9:121-132.

6_Turashvili G, Bouchal J, Baumforth K, Wei W, Dziechciarkova M, Ehrmann J, et al. Novel markers for differentiation of lobular and ductal invasive breast carcinomas by laser microdissection and microarray analysis. *BMC Cancer* 2007; 7:55.

Supplementary Table S4

Patient ID	% MD	Age	Menopausal Status	Parity	Biopsy Type	Benign Diagnosis
LD1	29.9	52	Un	Nulliparous	excisional	SCA NSPA (AM, CY, FBA, PASH & UDH)
LD2	30.2	46	Pre	Parous	excisional	NSPA (AM, C, CY, P, SCA & UDH) NSPA (CY) NSPA (FBA) NSPA (SCA) NSPA (PASH) F & UDH NSPA (UDH) FBA CY (UDH) FBA NSPA
LD3	31.2	50	Un	Parous	excisional	
LD4	31.9	42	Un	Parous	excisional	
LD5	33.2	41	Un	Parous	excisional	
LD6	35.5	61	Post	Parous	excisional	
LD7	36.1	46	Pre	Parous	excisional	
LD8	37.0	54	Un	Parous	excisional	
LD9	37.9	34	Pre	Parous	excisional	
LD10	39.7	45	Un	Nulliparous	excisional	
LD11	41.6	47	Pre	Nulliparous	excisional	
LD12	46.3	45	Pre	Nulliparous	excisional	
LD13	46.3	46	Un	Nulliparous	excisional	
HD1	70.5	41	Pre	Parous	core	
HD2	70.7	61	Post	Nulliparous	core	AM, C & CY
HD3	73.8	52	Post	Parous	excisional	NSPA
HD4	74.8	39	Pre	Parous	core	NSPA
HD5	75.1	31	Pre	Nulliparous	core	NSPA (FBA)
HD6	79.0	40	Post	Nulliparous	core	FBA
HD7	80.1	33	Pre	Nulliparous	core	NSPA
HD8	80.4	53	Un	Nulliparous	excisional	F, FBA & SCA (C)
HD9	81.7	50	Un	Nulliparous	core	P
HD10	82.4	40	Pre	Nulliparous	core	C & UDH (NSPA)
HD11	83.2	37	Pre	Parous	core	NSPA
HD12	84.4	50	Pre	Nulliparous	core	P, SCA & UDH
HD13	84.9	34	Pre	Nulliparous	core	NSPA
HD14	85.0	36	Pre	Nulliparous	excisional	FBA

Abbreviations:

A = Atrophy
ADH = Atypical Ductal Hyperplasia
ALH = Atypical Lobular Hyperplasia
AM = Apocrine Metaplasia
C = Calcification
CY = Cysts
F = Fibrosis
FBA = Fibroadenoma
FEA = Flat Epithelial Atypia
G = Granulation
MDE = Mammary Duct Ectasia
N = Necrosis
NSPA = No Specific Pathology
P = Papilloma
PASH = Pseudo-angiomatosis Stromal Hyperplasia
RS = Radial Scar
SCA = Sclerosing Adenosis
UDH = Unusual Ductal Hyperplasia

Supplementary Table S5

Patient ID	Diagnosis	ER	PR	HER2	Age	Grade	BIRADS
ER+ CA1	IDC	+	+	-	36	1	2
ER+ CA2	IDC	+	+	-	43	1	3
ER+ CA3	IDC	+	+	-	44	1	4
ER+ CA4	IDC	+	+	-	59	1	Un
ER+ CA5	IDC	+	+	-	48	2	4
ER+ CA6	IDC	+	+	-	56	2	3
ER+ CA7	IDC	+	+	-	61	2	2
ER+ CA8	IDC	+	+	-	52	3	2
HER2+ CA1	IDC	-	-	+	33	3	4
HER2+ CA2	IDC	-	-	+	55	3	Un
HER2+ CA3	IDC	+	-	+	64	3	2
HER2+ CA4	IDC	-	-	+	67	3	2
HER2+ CA5	IDC	+	+	+	70	3	Un
HER2+ CA6	IDC	+	-	+	78	3	2
TN CA1	IDC	-	-	-	37	2	3
TN CA2	IDC	-	-	-	58	2	3
TN CA3	IDC	-	-	-	41	3	2
TN CA4	IDC	-	-	-	47	3	3
TN CA5	IDC	-	-	-	55	3	2
TN CA6	IDC	-	-	-	66	3	3

Supplementary Table S6

Patient ID	Age	Menopausal Status	Ethnicity	Diagnosis	ER	PR	HER2	Stage	# of CA/NA blocks analyzed	# of ND blocks analyzed	# of slices between CA tissue and ND blocks
BM1	38	pre	Caucasian	IDC/ILC	+	+	-	II	5	5	2
BM2	32	pre	Caucasian	IDC	+	-	-	I	2	4	4
BM3	31	pre	African American	IDC	+	+	-	Ib	3	3	3

Supplementary Table S7

Patient ID	Diagnosis	Age	Grade	BIRADS	MD Type
CA LD 1	ER + IDC	37	2	1	LD
CA LD 2	ER + IDC	38	3	1	LD
CA LD 3	ER + IDC	41	1	1	LD
CA LD 4	ER + IDC	43	3	1	LD
CA LD 5	ER + IDC	49	2	1	LD
CA LD 6	ER + IDC	52	1	1	LD
CA LD 7	ER + IDC	54	1	1	LD
CA LD 8	ER + IDC	54	2	1	LD
CA LD 9	ER + IDC	56	2	1	LD
CA LD 10	ER + IDC	57	2	1	LD
CA LD 11	ER + IDC	60	2	1	LD
CA LD 12	ER + IDC	60	2	1	LD
CA LD 13	ER + IDC	61	2	1	LD
CA LD 14	ER + IDC	63	3	1	LD
CA LD 15	ER + IDC	64	3	1	LD
CA LD 16	ER + IDC	64	2	1	LD
CA LD 17	ER + IDC	65	2	1	LD
CA LD 18	ER + IDC	66	2	1	LD
CA LD 19	ER + IDC	67	3	1	LD
CA LD 20	ER + IDC	75	2	1	LD
CA LD 21	ER + IDC	79	3	1	LD
CA HD 1	ER + IDC	30	2	4	HD
CA HD 2	ER + IDC	32	2	4	HD
CA HD 3	ER + IDC	33	2	4	HD
CA HD 4	ER + IDC	42	2	4	HD
CA HD 5	ER + IDC	42	2	4	HD
CA HD 6	ER + IDC	45	1	4	HD
CA HD 7	ER + IDC	47	1	4	HD
CA HD 8	ER + IDC	47	2	4	HD
CA HD 9	ER + IDC	51	2	4	HD
CA HD 10	ER + IDC	51	1	4	HD
CA HD 11	ER + IDC	58	2	4	HD
CA HD 12	ER + IDC	63	3	4	HD
CA HD 13	ER + IDC	68	2	4	HD
CA HD 14	ER + IDC	Un	2	4	HD

Supplementary Table S8

Univariate Models

Predictor Variables	Coefficient	95% CI	P value
Tumor Grade:			
Well differentiated	-Reference-	-Reference-	-Reference-
Moderately differentiated	-0.19	-0.426 – 0.047	0.116
Poorly differentiated	-0.488	-0.546	<0.001
Tumor Size (cm)	-0.114	-0.159	0.005
Patient's Age	-0.002	-0.009 – 0.006	0.66

Multivariate Model

Predictor Variables	Coefficient	95% CI	P value
Tumor Grade:			
Well differentiated	-Reference-	-Reference-	-Reference-
Moderately differentiated	-0.14	-0.377 – 0.096	0.244
Poorly differentiated	-0.382	-0.558	0.007
Tumor Size (cm)	-0.147	-0.195	0.003

Supplementary Table S9