

Online Only Tables and Figure Legends

Fig. S1. CONSORT diagram of the various cohorts evaluated in this study.

Fig. S2. Principal components (PC) 1 and 2 loading plots using the PAM50 genes and all the normalized datasets evaluated, including the PAM50 training dataset. Note: GEICAM/2006-03 dataset has only triple-negative breast cancers.

Fig. S3. Biological heterogeneity within TNBC tumors of the BLBC subtype.

Immunohistochemical staining (10X) of Ki-67, keratins 5/6 and EGFR antigens from three selected Core Basal tumor samples of the GEICAM/2006-03 clinical trial. **(A)** BLBC with a Ki-67 labeling index of 95%; **(B)** BLBC with a Ki-67 labeling index of 60%; **(C)** Claudin-low tumor with a Ki-67 labeling index of 35%.

Fig. S4. Adjusted survival hazard rates (HRs) of various clinical-pathological variables and gene signatures (for unit increase) in the MDACC TNBC combined dataset based on intrinsic subtype (Basal-like versus others). The PAM50-based signatures represent either a correlation coefficient to a gene expression centroid (for Basal-like, HER2-enriched, Luminal A, Luminal B and Normal), or a score (for RORS, Proliferation score and RORP), and they are evaluated as a continuous variable. The Claudin-high signature represents an Euclidean distance to the Claudin-low centroid, and it is evaluated as a continuous variable. Each signature has been standardized to have a mean of 0 and a standard deviation of 1. The size of the square is inversely proportional to the SE; horizontal bars represent the 95% CIs of HRs. Statistically significant variables are shown in blue. Each gene signature has been evaluated individually after adjustment for standard clinical-pathological variables. The variables used for adjustment were age at diagnosis, nodal status, histological grade and tumor size.

Fig. S5. Principal components (PC) 1 and 2 loading plots using 479 genes and the normalized MDACC and GEICAM/2006-03 datasets.

Table S1. List of 159 genes whose expression was found to deviate at least 2-fold within Core Basal tumors of the BLBC subtype in the GEICAM/2006-03 clinical trial.

Table S2. List of genes significantly associated with pCR versus residual disease within Core Basal tumors of the BLBC subtype in the GEICAM/2006-03 clinical trial.

Table S3. Pearson correlation coefficients among the PAM50-based signatures in the MDACC combined cohort (all TNBC).

Table S4. Pearson correlation coefficients among the PAM50-based signatures in the GEICAM/2006-03 samples (all TNBC).

Figure S1

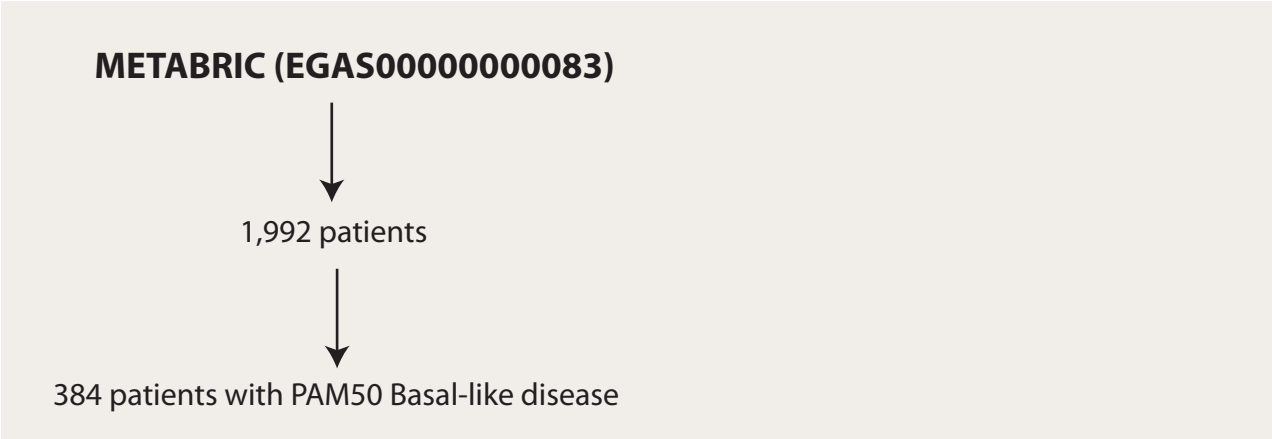
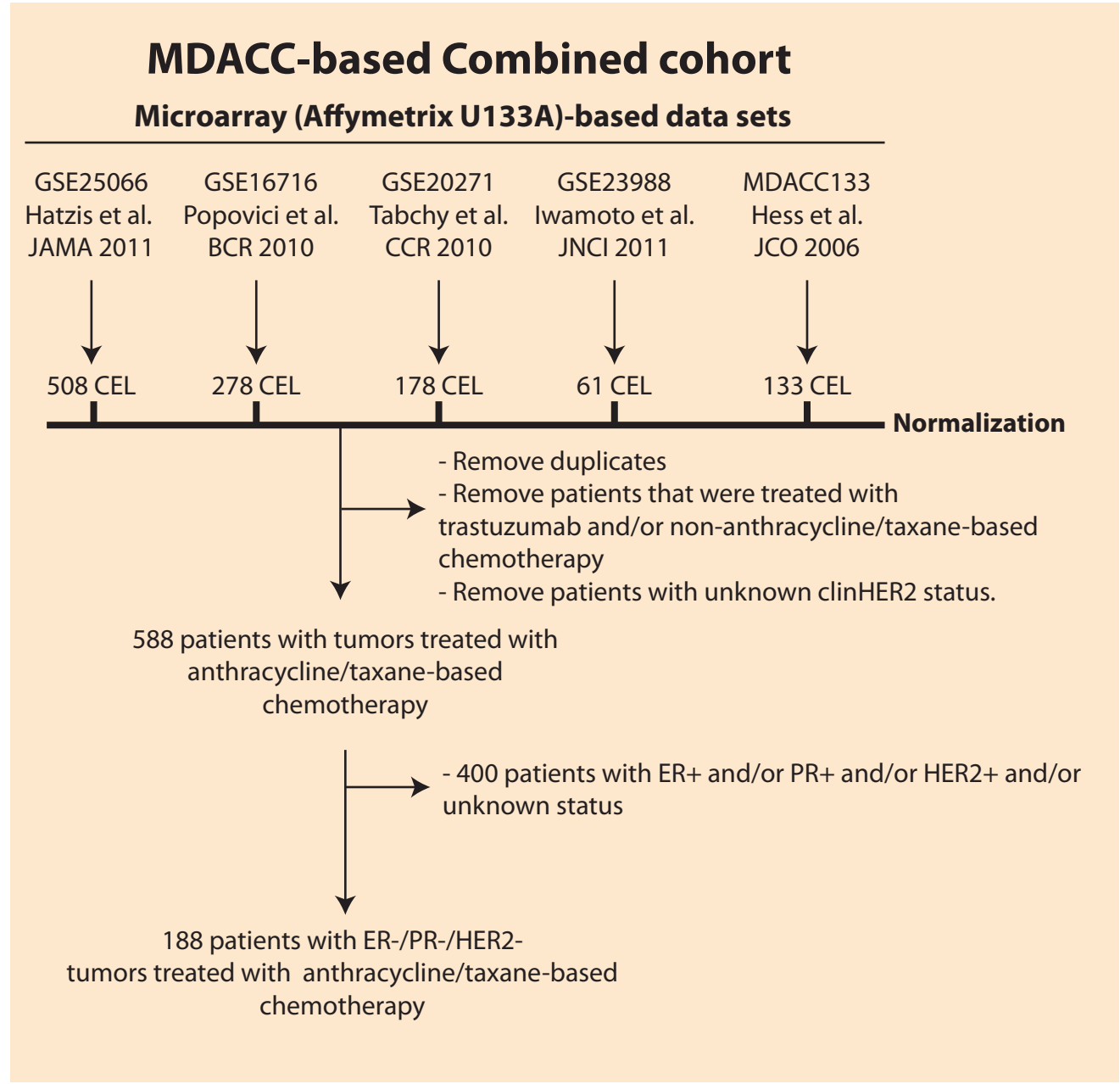
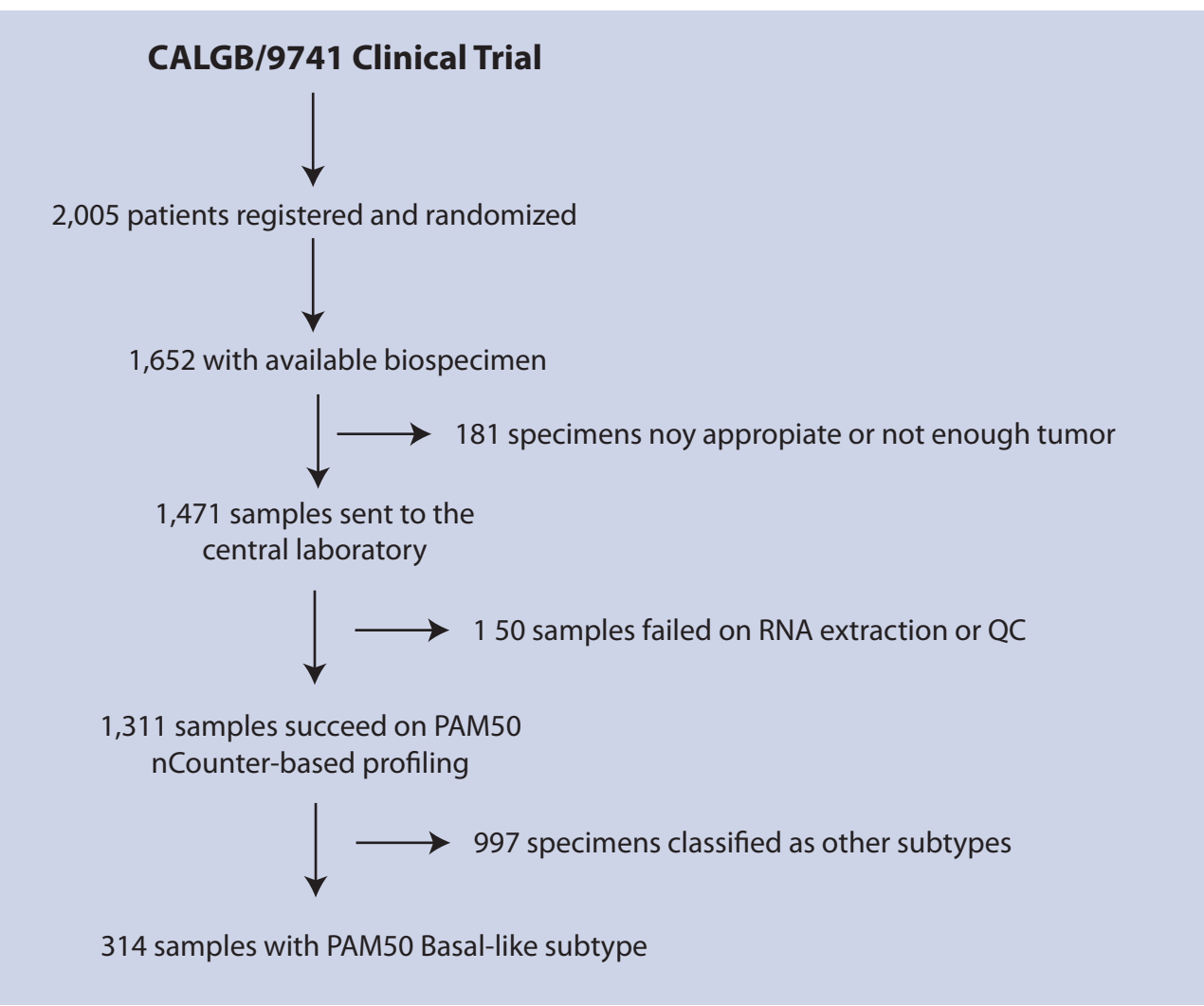
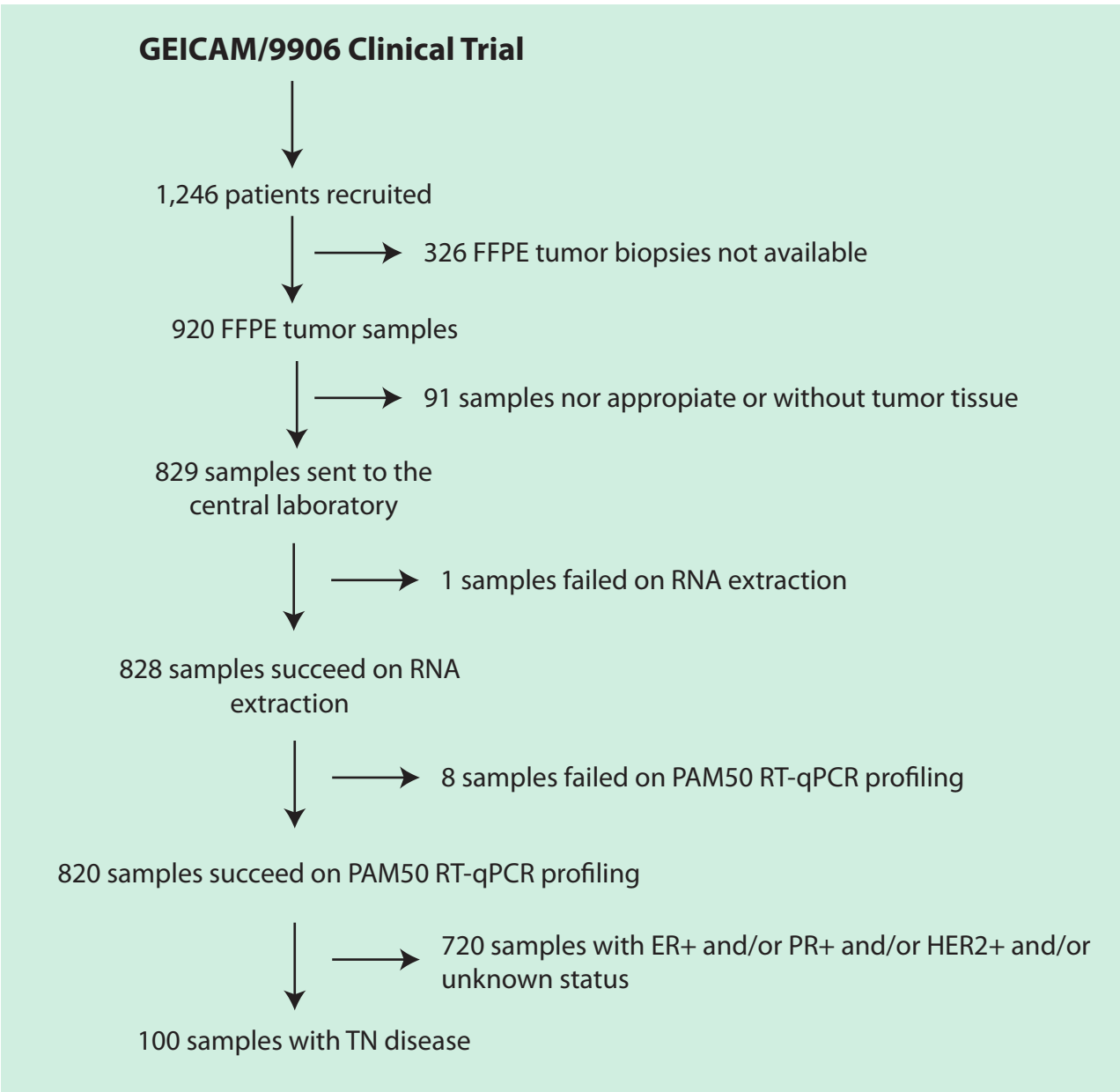
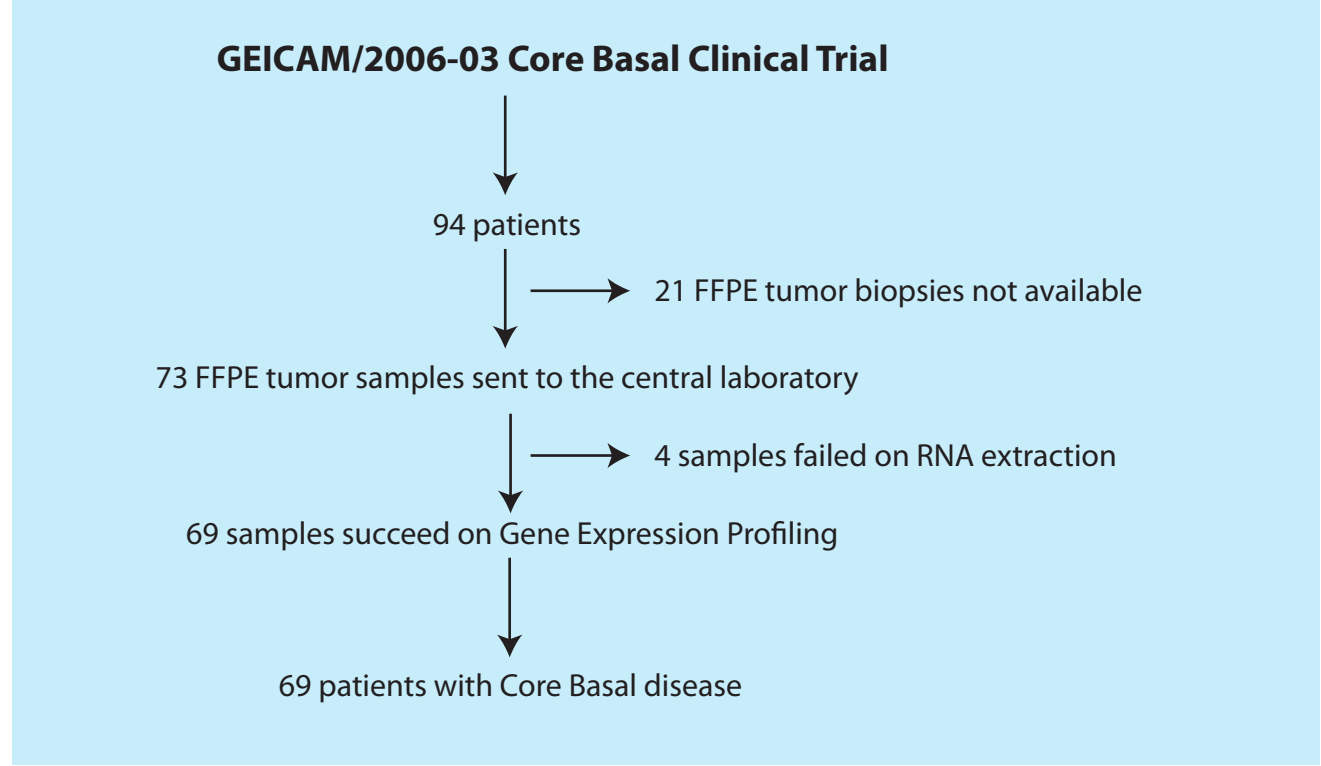


Figure S2

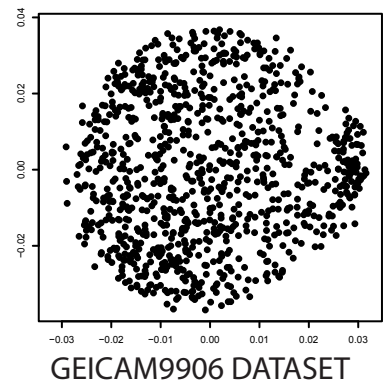
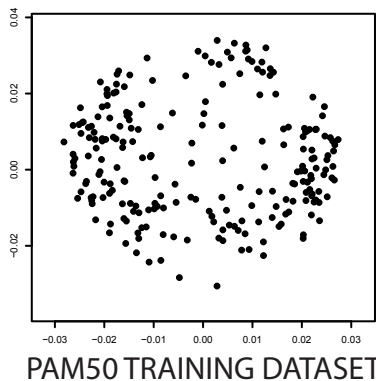
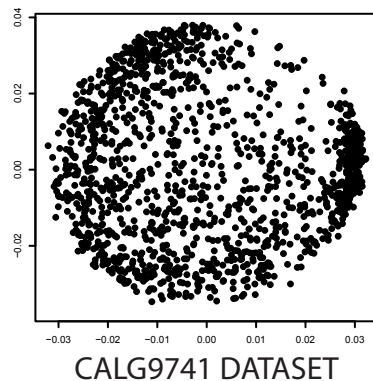
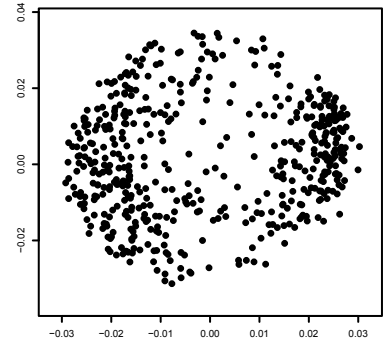
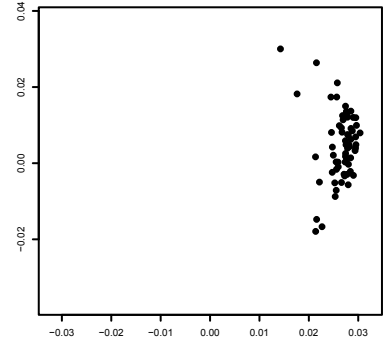
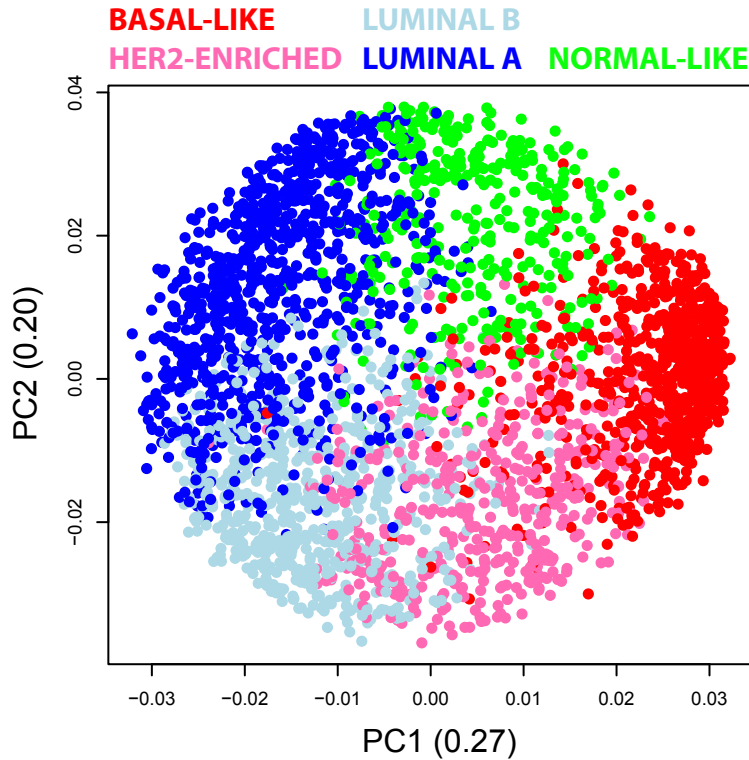


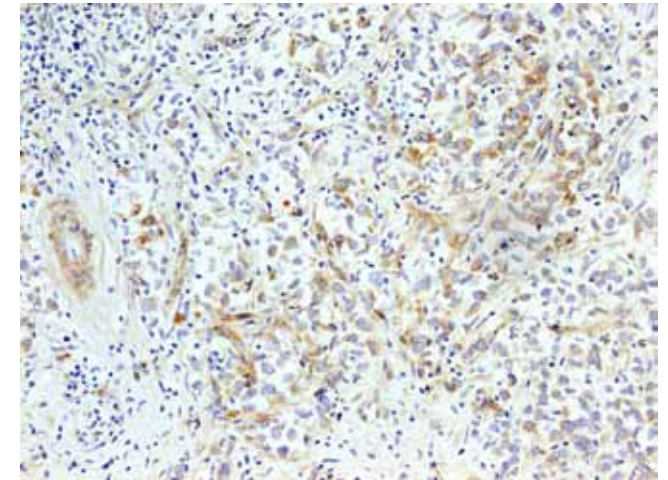
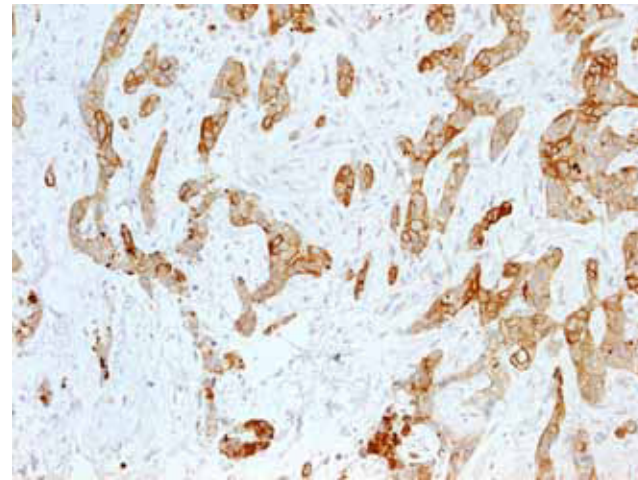
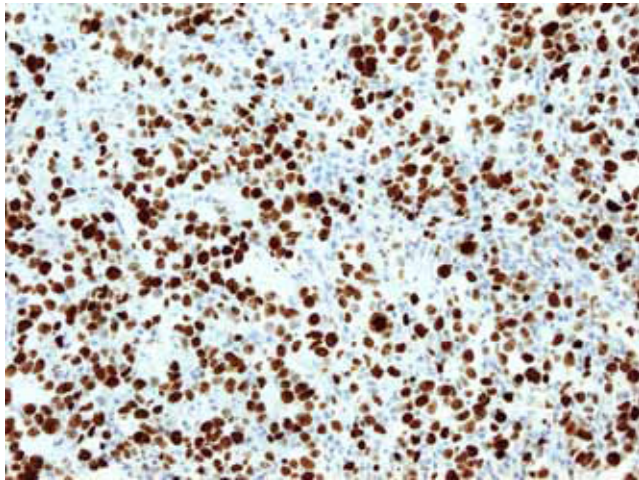
Figure S3

Ki-67

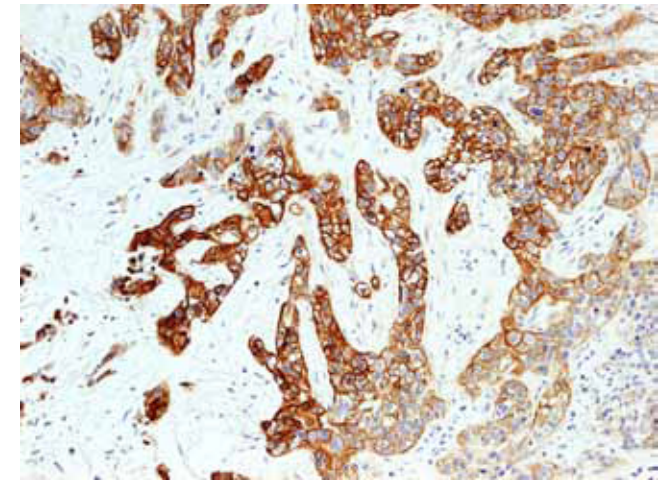
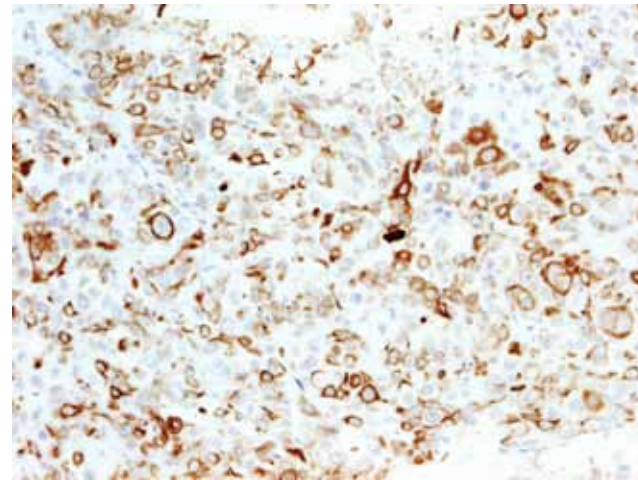
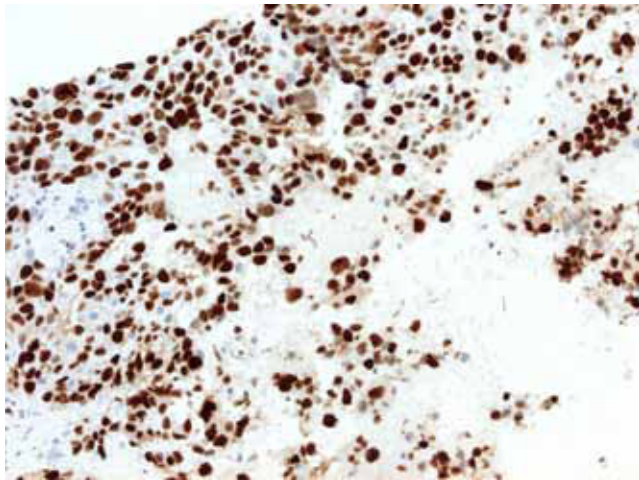
CK5/6

EGFR

A



B



C

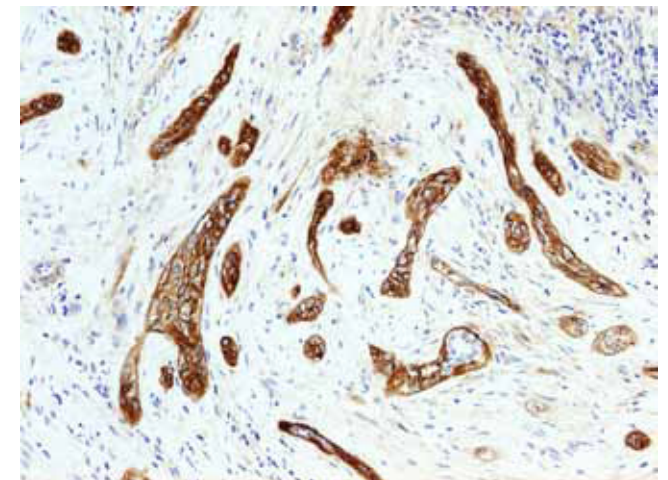
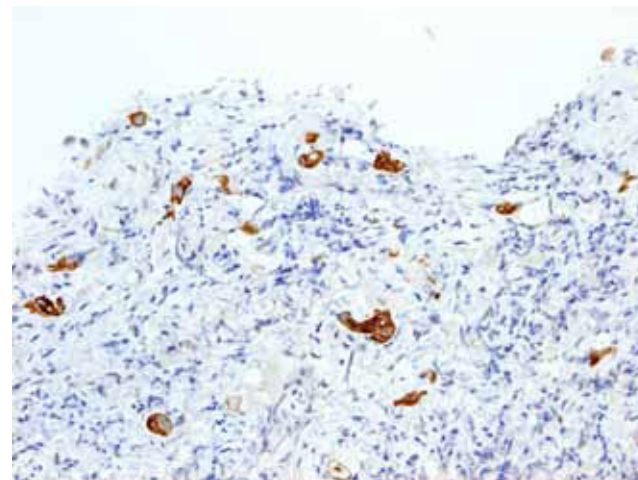
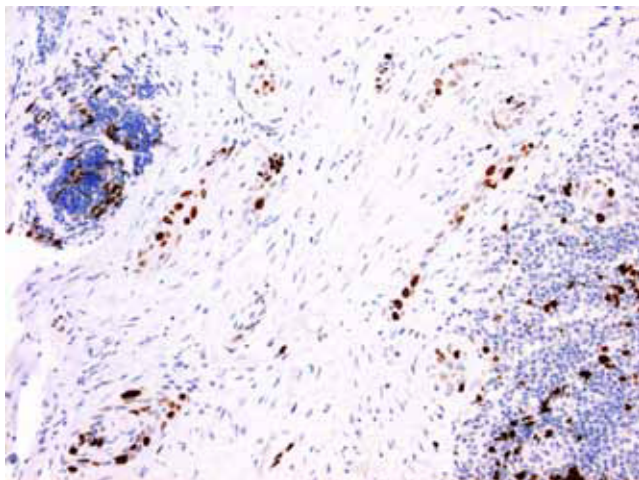


Figure S4

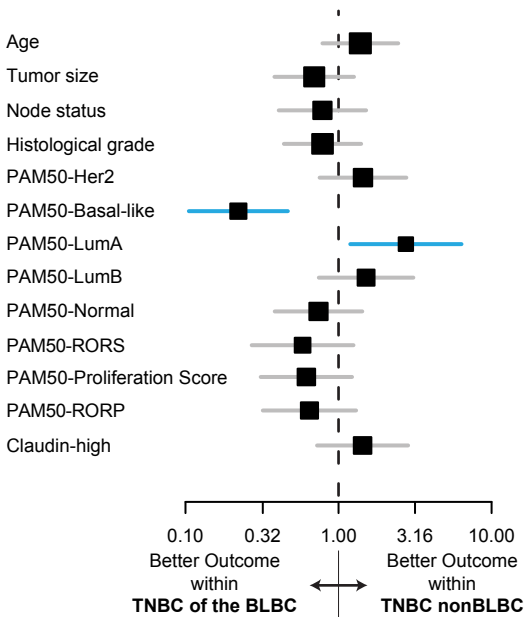


Figure S5

● GEICAM/2006-03

● MDACC

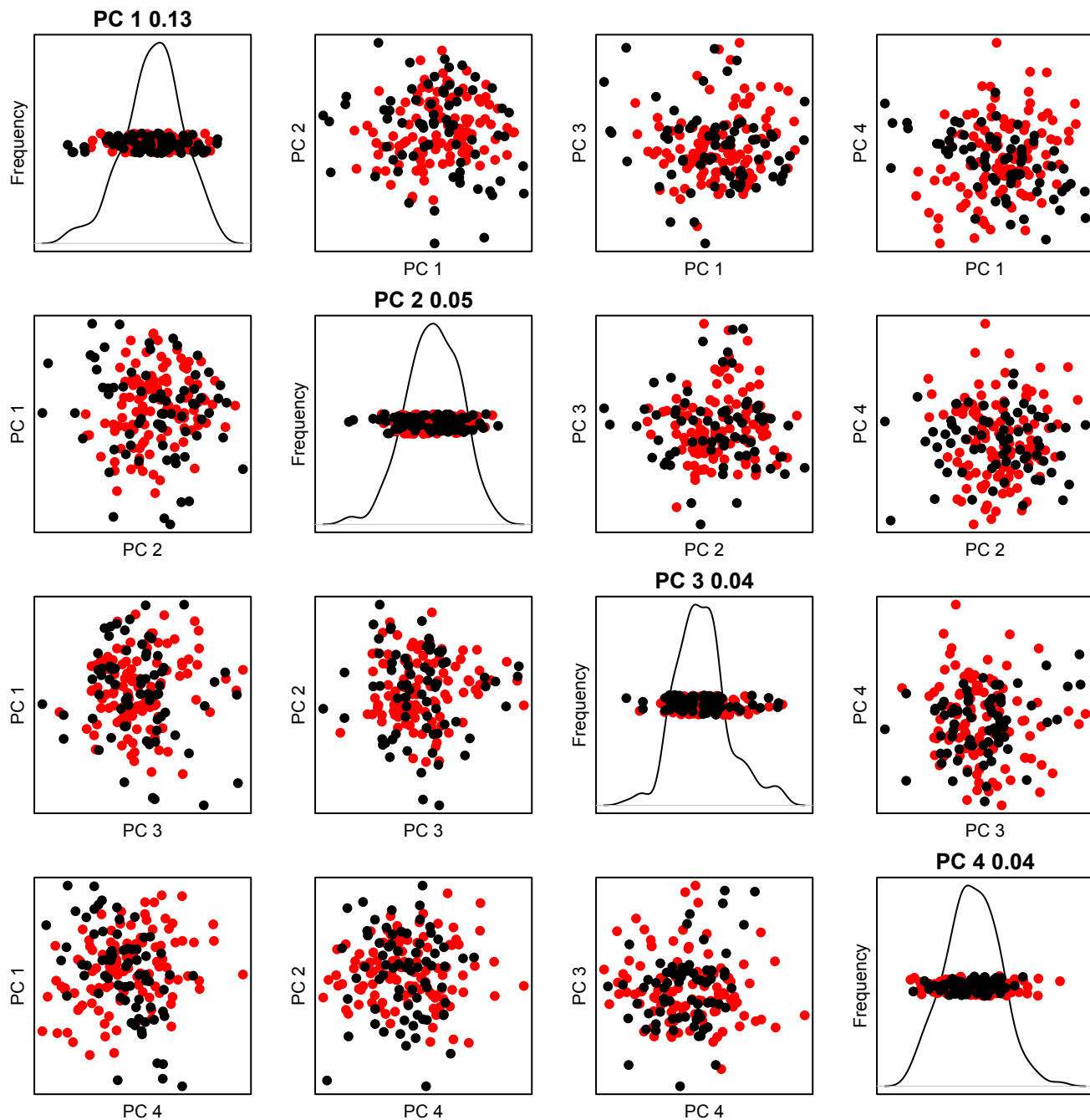


Table S1. List of 159 genes whose expression was found to deviate at least 2-fold within Core Basal tumors of the Basal-like subtype in the GEICAM/2006-03 clinical trial.

KRT14 Keratin 14 17q12-q21
AZGP1 Alpha-2-glycoprotein 1, zinc-binding 7q22.1
FABP4 Fatty acid binding protein 4, adipocyte 8q21
S100A8 S100 calcium binding protein A8 1q21
KRT6C Keratin 6C 12q13.13
KRT6B Keratin 6B 12q12-q13
S100A9 S100 calcium binding protein A9 1q21
CAPN6 Calpain 6 Xq23
FOXA1 Forkhead box A1 14q12-q13
KRT17 Keratin 17 17q21.2
PIP Prolactin-induced protein 7q34
KRT23 Keratin 23 (histone deacetylase inducible) 17q21.2
MMP11 Matrix metalloproteinase 11 (stromelysin 3) 22q11.2 22q11.23
CXCL14 Chemokine (C-X-C motif) ligand 14 5q31
IL8 Interleukin 8 4q13-q21
GSTM1 Glutathione S-transferase mu 1 1p13.3
IDO1 Indoleamine 2,3-dioxygenase 1 8p12-p11
SERPINA3 Serpin peptidase inhibitor, clade A (alpha-1 antitrypsin), member 3 14q32.1
ACTL8 Actin-like 8 1p36.2-p35
CRYAB Crystallin, alpha B 11q22.3-q23.1
KRT5 Keratin 5 12q
KRT16 Keratin 16 17q21.2
KIAA1324 KIAA1324 1p13.3
PROM1 Prominin 1 4p15.32
MUC5B Mucin 5B, oligomeric mucus/gel-forming 11p15.5
KRT6A Keratin 6A 12q12-q13
ANXA8L2 Annexin A8-like 2 10q11.22
UCHL1 Ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase) 4p14
MIA Melanoma inhibitory activity 19q13.32-q13.33
SPDEF SAM pointed domain containing ets transcription factor 6p21.3
CLDN3 Claudin 3 7q11.23
PRAME Preferentially expressed antigen in melanoma 22q11.22
FGFR2 Fibroblast growth factor receptor 2 10q26
ANGPTL4 Angiopoietin-like 4 19p13.3
CAPN13 Calpain 13 2p22-p21
AR Androgen receptor Xq12
PTGS2 Prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase) 1q25.2-q25.3
ID4 Inhibitor of DNA binding 4, dominant negative helix-loop-helix protein 6p22.3
CDKN2A Cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4) 9p21

IGFBP2 Insulin-like growth factor binding protein 2, 36kDa 2q33-q34
TFF3 Trefoil factor 3 (intestinal) 21q22.3
MUC1 Mucin 1, cell surface associated 1q21
TMEM139 Transmembrane protein 139 7q34
ALDH1A1 Aldehyde dehydrogenase 1 family, member A1 9q21.13
CXCL1 Chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha) 4q21
TP63 Tumor protein p63 3q28
SFRP1 Secreted frizzled-related protein 1 8p11.21
AREG Amphiregulin 4q13-q21
TMEM158 Transmembrane protein 158 (gene/pseudogene) 3p21.3
CEACAM6 Carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen) 19q13.2
MYB V-myb myeloblastosis viral oncogene homolog (avian) 6q22-q23
S100A14 S100 calcium binding protein A14 1q21.3
RERG RAS-like, estrogen-regulated, growth inhibitor 12p12.3
IGF1 Insulin-like growth factor 1 (somatomedin C) 12q23.2
SCGB2A2 Secretoglobin, family 2A, member 2 11q13
KRT19 Keratin 19 17q21.2
CDKN2B Cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4) 9p21
CTGF Connective tissue growth factor 6q23.1
NDRG1 N-myc downstream regulated 1 8q24.3
MET Met proto-oncogene (hepatocyte growth factor receptor) 7q31
KIT V-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog 4q11-q12
ADRA2C Adrenergic, alpha-2C-, receptor 4p16
LAMC2 Laminin, gamma 2 1q25-q31
ADM Adrenomedullin 11p15.4
CLDN7 Claudin 7 17p13
SLC40A1 Solute carrier family 40 (iron-regulated transporter), member 1 2q32
GREM1 Gremlin 1 15q13.3
FABP5 Fatty acid binding protein 5 (psoriasis-associated) 8q21.13
NFIA Nuclear factor I/A 1p31.3-p31.2
LAG3 Lymphocyte-activation gene 3 12p13.32
OGN Osteoglycin 9q22
DEGS2 Degenerative spermatocyte homolog 2, lipid desaturase (Drosophila) 14q32.2
EGFR Epidermal growth factor receptor 7p12
NTN4 Netrin 4 12q22
MLPH Melanophilin 2q37.3
CCND1 Cyclin D1 11q13
CYR61 Cysteine-rich, angiogenic inducer, 61 1p22.3
TRIM29 Tripartite motif containing 29 11q23.3
FBP1 Fructose-1,6-bisphosphatase 1 9q22.3
LAMA3 Laminin, alpha 3 18q11.2

CA12 Carbonic anhydrase XII 15q22
INHBA Inhibin, beta A 7p15-p13
PITX1 Paired-like homeodomain 1 5q31
GAL Galanin prepropeptide 11q13.3
BCL2A1 BCL2-related protein A1 15q24.3
MME Membrane metallo-endopeptidase 3q25.1-q25.2
STC2 Stanniocalcin 2 5q35.1
AGR2 Anterior gradient homolog 2 (<i>Xenopus laevis</i>) 7p21.3
GPR160 G protein-coupled receptor 160 3q26.2-q27
SCUBE2 Signal peptide, CUB domain, EGF-like 2 11p15.3
TAP1 Transporter 1, ATP-binding cassette, sub-family B (MDR/TAP) 6p21.3
REEP6 Receptor accessory protein 6 19p13.3
THBS1 Thrombospondin 1 15q15
EPCAM Epithelial cell adhesion molecule 2p21
VAV3 Vav 3 guanine nucleotide exchange factor 1p13.3
NQO1 NAD(P)H dehydrogenase, quinone 1 16q22.1
TGFB3 Transforming growth factor, beta receptor III 1p33-p32
BRCA1 Breast cancer 1, early onset 17q21
ITGA6 Integrin, alpha 6 2q31.1
PDGFRA Platelet-derived growth factor receptor, alpha polypeptide 4q12
FAM174B Family with sequence similarity 174, member B 15q26.1
PCDH8 Protocadherin 8 13q21.1
C1orf106 Chromosome 1 open reading frame 106 1q32.1
LTBP2 Latent transforming growth factor beta binding protein 2 14q24
EPSTI1 Epithelial stromal interaction 1 (breast) 13q13.3
FBN1 Fibrillin 1 15q21.1
VEGFA Vascular endothelial growth factor A 6p12
AFF3 AF4/FMR2 family, member 3 2q11.2-q12
AKT3 V-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma) 1q44
ADRA2A Adrenergic, alpha-2A-, receptor 10q24-q26
OCLN Occludin 5q13.1
ESR1 Estrogen receptor 1 6q25.1
PID1 Phosphotyrosine interaction domain containing 1 2q36.3
RHBG Rh family, B glycoprotein (gene/pseudogene) 1q21.3
SLC16A3 Solute carrier family 16, member 3 (monocarboxylic acid transporter 4) 17q25
TMCC2 Transmembrane and coiled-coil domain family 2 1q32.1
FGFR1 Fibroblast growth factor receptor 1 8p12
BTG2 BTG family, member 2 1q32
CD24 CD24 molecule 6q21
XPB1 X-box binding protein 1 22q12.1 22q12
FOXC1 Forkhead box C1 6p25

SEMA3C Sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C 7q21-q31
MYC V-myc myelocytomatosis viral oncogene homolog (avian) 8q24.21
ABCC3 ATP-binding cassette, sub-family C (CFTR/MRP), member 3 17q22
CAMK2N1 Calcium/calmodulin-dependent protein kinase II inhibitor 1 1p36.12
F3 Coagulation factor III (thromboplastin, tissue factor) 1p22-p21
CLDN4 Claudin 4 7q11.23
IL1B Interleukin 1, beta 2q14
MAGEA1 Melanoma antigen family A, 1 (directs expression of antigen MZ2-E) Xq28
STAT1 Signal transducer and activator of transcription 1, 91kDa 2q32.2
TMEM45B Transmembrane protein 45B 11q24.3
PIR Pirin (iron-binding nuclear protein) Xp22.2
CYBRD1 Cytochrome b reductase 1 2q31.1
NFIB Nuclear factor I/B 9p24.1
THY1 Thy-1 cell surface antigen 11q23.3
TMEM125 Transmembrane protein 125 1p34.2
FZD7 Frizzled homolog 7 (Drosophila) 2q33
RRAGD Ras-related GTP binding D 6q15-q16
CLMN Calmin (calponin-like, transmembrane) 14q32.13
CITED4 Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4 1p34.2 1p35-p34
GOLT1A Golgi transport 1A 1q32.1
NEO1 Neogenin 1 15q22.3-q23
TWIST2 Twist homolog 2 (Drosophila) 2q37.3
GRHL1 Grainyhead-like 1 (Drosophila) 2p25.1
PLA1A Phospholipase A1 member A 3q13.13-q13.2
CHPF Chondroitin polymerizing factor 2q35
OGFRL1 Opioid growth factor receptor-like 1 6q13
TSPAN13 Tetraspanin 13 7p21.1
IL6 Interleukin 6 (interferon, beta 2) 7p21
TP53 Tumor protein p53 17p13.1
NT5E 5'-nucleotidase, ecto (CD73) 6q14-q21
RAI2 Retinoic acid induced 2 Xp22
TWIST1 Twist homolog 1 (Drosophila) 7p21.2
SLC5A6 Solute carrier family 5 (sodium-dependent vitamin transporter), member 6 2p23
BCL2 B-cell CLL/lymphoma 2 18q21.33 18q21.3
DSP Desmoplakin 6p24
SPINT2 Serine peptidase inhibitor, Kunitz type, 2 19q13.1
DNAJC12 DnaJ (Hsp40) homolog, subfamily C, member 12 10q22.1
PIK3R1 Phosphoinositide-3-kinase, regulatory subunit 1 (alpha) 5q13.1

Table S2. List of genes significantly associated with pCR versus residual disease within Core Basal tumors of the Basal-like subtype in the GEICAM/2006-03 clinical trial.

GENE	Odds Ratio (OR)	95% CI Low	95% CI High	P-value
OGN Osteoglycin 9q22	0.737	0.623	0.871	0.001
MUC1 Mucin 1, cell surface associated 1q21	0.760	0.669	0.862	0.000
MLPH Melanophilin 2q37.3	0.787	0.683	0.907	0.002
RARA Retinoic acid receptor, alpha 17q21	0.789	0.691	0.900	0.001
SNAIL1 Snail homolog 1 (Drosophila) 20q13.2	0.791	0.707	0.885	0.000
NACC2 NACC family member 2, BEN and BTB (POZ) domain containing 9q34.3	0.793	0.701	0.897	0.001
CLDN7 Claudin 7 17p13	0.793	0.699	0.899	0.001
ERBB4 V-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian) 2q33.3-q34	0.797	0.681	0.933	0.007
NQO1 NAD(P)H dehydrogenase, quinone 1 16q22.1	0.797	0.708	0.897	0.000
ADRA2A Adrenergic, alpha-2A-, receptor 10q24-q26	0.798	0.691	0.921	0.003
REEP6 Receptor accessory protein 6 19p13.3	0.799	0.686	0.930	0.006
FOXA1 Forkhead box A1 14q12-q13	0.805	0.700	0.926	0.004
IGF1 Insulin-like growth factor 1 (somatomedin C) 12q23.2	0.806	0.698	0.932	0.005
AFF3 AF4/FMR2 family, member 3 2q11.2-q12	0.810	0.688	0.954	0.015
PGR Progesterone receptor 11q22-q23	0.817	0.705	0.946	0.010
RNF103 Ring finger protein 103 2p11.2	0.821	0.712	0.948	0.010
CXCL14 Chemokine (C-X-C motif) ligand 14 5q31	0.823	0.716	0.945	0.008
ADRA2C Adrenergic, alpha-2C-, receptor 4p16	0.823	0.725	0.934	0.004
KIF20A Kinesin family member 20A 5q31	0.826	0.721	0.947	0.008
TFF3 Trefoil factor 3 (intestinal) 21q22.3	0.827	0.689	0.993	0.047
PIP Prolactin-induced protein 7q34	0.830	0.713	0.966	0.020
SPDEF SAM pointed domain containing ets transcription factor 6p21.3	0.833	0.722	0.962	0.017
LHFP Lipoma HMGIC fusion partner 13q12	0.835	0.717	0.971	0.024
NCS1 Neuronal calcium sensor 1 9q34	0.837	0.731	0.959	0.013
TMEM25 Transmembrane protein 25 11q23.3	0.838	0.740	0.948	0.007
ZEB1 Zinc finger E-box binding homeobox 1 10p11.2	0.841	0.730	0.967	0.019
SCUBE2 Signal peptide, CUB domain, EGF-like 2 11p15.3	0.842	0.721	0.982	0.034
CAPN13 Calpain 13 2p22-p21	0.845	0.732	0.974	0.025
MYO5C Myosin VC 15q21	0.857	0.741	0.992	0.044
SERPINA3 Serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3 14q32.1	0.860	0.748	0.988	0.038
MAGEA1 Melanoma antigen family A, 1 (directs expression of antigen MZ2-E) Xq28	0.860	0.759	0.974	0.022
CXCR1 Chemokine (C-X-C motif) receptor 1 2q35	0.861	0.753	0.984	0.032

TWIST2 Twist homolog 2 (Drosophila) 2q37.3	0.862	0.751	0.988	0.039
CLDN4 Claudin 4 7q11.23	0.863	0.755	0.986	0.036
SLC9A3 Solute carrier family 9 (sodium/hydrogen exchanger), member 3 5p15.3	0.865	0.755	0.990	0.041
GOLT1A Golgi transport 1A 1q32.1	0.866	0.763	0.984	0.031
CAMK2N1 Calcium/calmodulin-dependent protein kinase II inhibitor 1 1p36.12	0.866	0.759	0.988	0.038
SQLE Squalene epoxidase 8q24.1	0.867	0.760	0.989	0.039
TWIST1 Twist homolog 1 (Drosophila) 7p21.2	0.867	0.756	0.996	0.049
CXXC5 CXXC finger protein 5 5q31.2	0.868	0.765	0.984	0.032
CABP7 Calcium binding protein 7 22q12.2	0.874	0.770	0.991	0.041
CLDN3 Claudin 3 7q11.23	0.875	0.768	0.995	0.048
GAL Galanin prepropeptide 11q13.3	1.144	1.011	1.294	0.038
YBX1 Y box binding protein 1 1p34	1.150	1.004	1.317	0.050
CTSL1 Cathepsin L1 9q21.33	1.151	1.015	1.306	0.034
PSMA7 Proteasome (prosome, macropain) subunit, alpha type, 7 20q13.33	1.154	1.012	1.314	0.037
SUV39H2 Suppressor of variegation 3-9 homolog 2 (Drosophila) 10p13	1.156	1.005	1.330	0.047
IDO1 Indoleamine 2,3-dioxygenase 1 8p12-p11	1.157	1.006	1.330	0.046
MAD2L1 MAD2 mitotic arrest deficient-like 1 (yeast) 4q27	1.159	1.019	1.319	0.029
CDK4 Cyclin-dependent kinase 4 12q14	1.160	1.027	1.310	0.021
CCNA2 Cyclin A2 4q25-q31	1.164	1.012	1.339	0.038
AREG Amphiregulin 4q13-q21	1.168	1.011	1.349	0.040
TAP1 Transporter 1, ATP-binding cassette, sub-family B (MDR/TAP) 6p21.3	1.172	1.030	1.335	0.020
MYB V-myb myeloblastosis viral oncogene homolog (avian) 6q22-q23	1.174	1.026	1.344	0.024
MPP1 Membrane protein, palmitoylated 1, 55kDa Xq28	1.175	1.024	1.348	0.026
CENPN Centromere protein N 16q23.2	1.180	1.020	1.365	0.030
CCNE1 Cyclin E1 19q12	1.181	1.019	1.367	0.031
MTHFD1L Methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like 6q25.1	1.185	1.030	1.362	0.021
BUB1 Budding uninhibited by benzimidazoles 1 homolog (yeast) 2q14	1.185	1.007	1.395	0.046
GSTP1 Glutathione S-transferase pi 1 11q13	1.190	1.047	1.352	0.010
BYSL Bystin-like 6p21.1	1.192	1.035	1.371	0.018
KIF23 Kinesin family member 23 15q23	1.196	1.024	1.398	0.029
EXO1 Exonuclease 1 1q42-q43	1.197	1.025	1.398	0.027
STAT1 Signal transducer and activator of transcription 1, 91kDa 2q32.2	1.199	1.052	1.368	0.009
ORC6 Origin recognition complex, subunit 6 16q12	1.201	1.007	1.432	0.047
RANBP1 RAN binding protein 1 22q11.21	1.201	1.042	1.383	0.015

MKI67 Antigen identified by monoclonal antibody Ki-67 10q26.2	1.204	1.007	1.438	0.047
BIRC5 Baculoviral IAP repeat containing 5 17q25	1.205	1.010	1.437	0.044
PTDSS1 Phosphatidylserine synthase 1 8q22	1.205	1.056	1.376	0.008
GINS2 GINS complex subunit 2 (Psf2 homolog) 16q24.1	1.208	1.033	1.411	0.022
KIFC1 Kinesin family member C1 6p21.3	1.211	1.030	1.423	0.025
CDK1 Cyclin-dependent kinase 1 10q21.1	1.211	1.049	1.399	0.012
MAGOHB Mago-nashi homolog B (Drosophila) 12p13.2	1.213	1.077	1.366	0.002
MCM3 Minichromosome maintenance complex component 3 6p12	1.214	1.050	1.404	0.012
KIF2C Kinesin family member 2C 1p34.1	1.214	1.031	1.430	0.024
SLC25A19 Solute carrier family 25 (mitochondrial thiamine pyrophosphate carrier), member 19 17q25.3	1.222	1.082	1.380	0.002
PTTG1 Pituitary tumor-transforming 1 5q35.1	1.225	1.055	1.423	0.011
NUF2 NUF2, NDC80 kinetochore complex component, homolog (S. cerevisiae) 1q23.3	1.239	1.061	1.447	0.009
EZH2 Enhancer of zeste homolog 2 (Drosophila) 7q35-q36	1.256	1.092	1.444	0.002
CDC45 Cell division cycle 45 homolog (S. cerevisiae) 22q11.21	1.258	1.080	1.465	0.005
TTK TTK protein kinase 6q13-q21	1.267	1.087	1.477	0.004
FANCA Fanconi anemia, complementation group A 16q24.3	1.298	1.122	1.502	0.001

Table S3. Pearson correlation coefficients among the PAM50-based signatures in the MDACC combined cohort (all TNBC).

	PAM50Basal	PAM50Her2	PAM50LumA	PAM50LumB	PAM50Normal	PAM50RORS	PAM50PROLIF	PAM50RORP
PAM50Basal Pearson correlation coeff.	1	-.184	-.705	-.351	.197	.459	.340	.324
PAM50Her2 Pearson correlation coeff.	-.184	1	-.508	.803	-.876	.731	.622	.707
PAM50LumA Pearson correlation coeff.	-.705	-.508	1	-.362	.522	-.949	-.832	-.861
PAM50LumB Pearson correlation coeff.	-.351	.803	-.362	1	-.961	.624	.653	.700
PAM50Normal Pearson correlation coeff.	.197	-.876	.522	-.961	1	-.755	-.745	-.799
PAM50RORS Pearson correlation coeff.	.459	.731	-.949	.624	-.755	1	.894	.940
PAM50PROLIF Pearson correlation coeff.	.340	.622	-.832	.653	-.745	.894	1	.990
PAM50RORP Pearson correlation coeff.	.324	.707	-.861	.700	-.799	.940	.990	1

Table S4. Pearson correlation coefficients among the PAM50-based signatures in the GEICAM/2006-03 samples (all TNBC).

		PAM50Basal	PAM50Her2	PAM50LumA	PAM50LumB	PAM50Normal	PAM50RORS	PAM50PROLIF	PAM50RORP
PAM50Basal	Pearson correlation coeff.	1	-.493	-.756	-.221	-.031	.498	.628	.560
PAM50Her2	Pearson correlation coeff.	-.493	1	-.105	.760	-.726	.426	.115	.253
PAM50LumA	Pearson correlation coeff.	-.756	-.105	1	-.422	.649	-.938	-.917	-.928
PAM50LumB	Pearson correlation coeff.	-.221	.760	-.422	1	-.925	.693	.519	.618
PAM50Normal	Pearson correlation coeff.	-.031	-.726	.649	-.925	1	-.861	-.684	-.778
PAM50RORS	Pearson correlation coeff.	.498	.426	-.938	.693	-.861	1	.889	.944
PAM50PROLIF	Pearson correlation coeff.	.628	.115	-.917	.519	-.684	.889	1	.988
PAM50RORP	Pearson correlation coeff.	.560	.253	-.928	.618	-.778	.944	.988	1