MolecularMedicine

Supplemental Data

A New Gene Expression Signature for Triple-Negative Breast Cancer Using Frozen Fresh Tissue before Neoadjuvant Chemotherapy

Sandra K Santuario-Facio,[1,7] Servando Cardona-Huerta,[2*] Yadira X Perez-Paramo,[3] Victor Trevino,[4] Francisco Hernandez-Cabrera,[5] Augusto Rojas-Martinez,[1,7] Grecia Uscanga-Perales,[6] Jorge L Martinez-Rodriguez,[2,8] Lizeth Martinez-Jacobo,[6] Gerardo Padilla-Rivas,[6] Gerardo Muñoz-Maldonado,[9] Juan Francisco Gonzalez-Guerrero,[10] Javier Valero-Gomez,[2] Ana L Vazquez-Guerrero,[2] Herminia G Martinez-Rodriguez,[6] Alvaro Barboza-Quintana,[2] Oralia Barboza-Quintana,[11] Raquel Garza-Guajardo,[11] and Rocio Ortiz-Lopez[1,7]*

Online address: http://www.molmed.org

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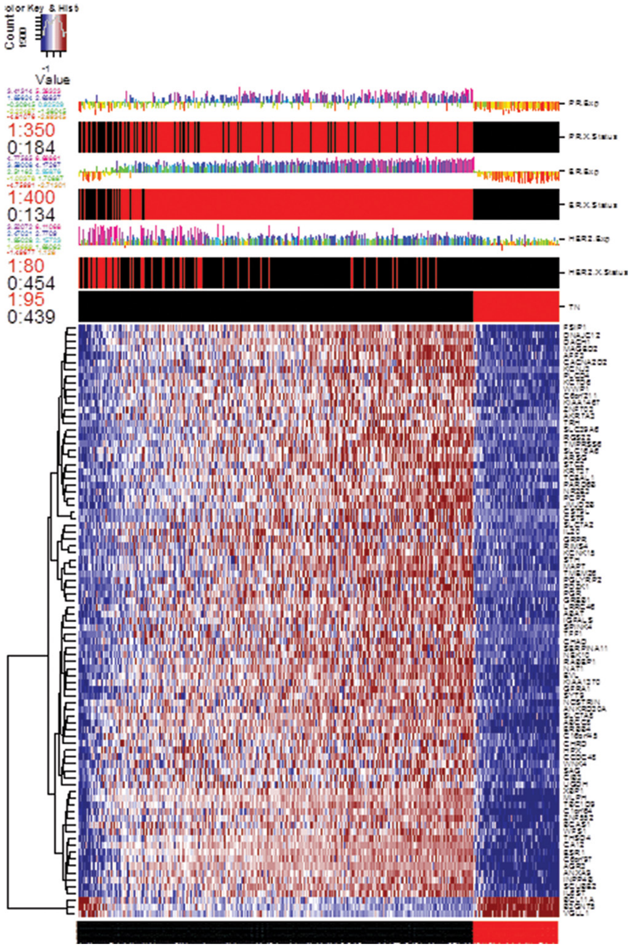
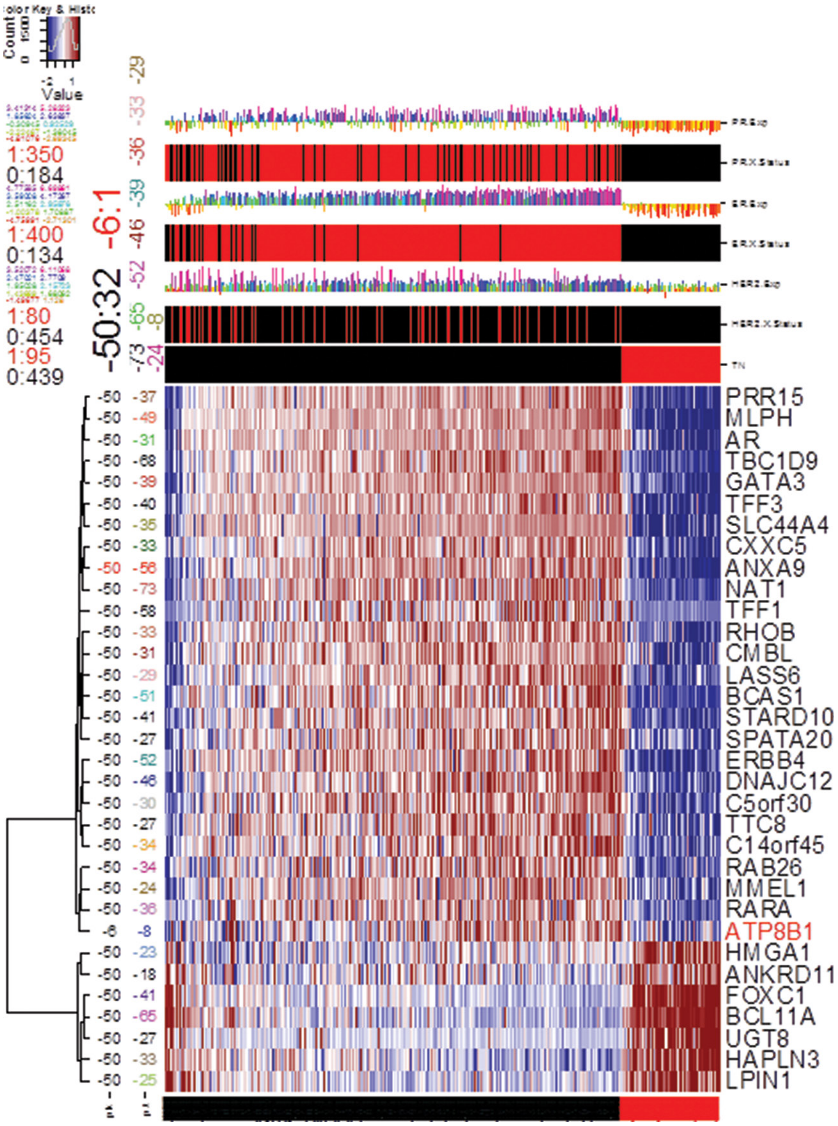


Supplementary Figure S1. TCGA Validation, first approach. Gene signature of 87 differentialy expressed genes with high significance (q < 1e-40), only nine genes overlap with our signature.



Supplementary Figure S2. TCGA Validation, second approach. Differential expression of TNBC versus nTNBC using only 33 of 40 genes of our signature.

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Supplemental Table S1. TNBC signature (40 genes and 49 probes).

Expression TNBC	Gene Symbol	ID Probe	Gene Title	*t* test *p* value	Kolmogorov test *p* value	FDR test *p* value	FDR k *p* value
Over	ANKRD11	238538_at	Ankyrin repeat domain 11	2.01e-07	9.19e-07	0.0001076	0.00048764
Over	BCL11A	1559078_at	B-cell cll/lymphoma 11a (zinc finger protein)	4.12e-08	3.49e-08	4.00e-05	0.00014361
Over	BCL11A	210347_s_at	B-cell cll/lymphoma 11a (zinc finger protein)	2.66e-10	1.15e-07	4.52e-06	0.00020489
Over	BCL11A	222891_s_at	B-cell cll/lymphoma 11a (zinc finger protein)	7.57e-09	4.04e-07	1.71e-05	0.00029192
Over	FAM171A1	212771_at	Family with sequence similarity 171, member a1	7.42e-08	6.21e-07	6.14e-05	0.00036378
Over	FOXC1	1553613_s_at	Forkhead box c1	2.71e-09	2.52e-07	1.32e-05	0.00023999
Over	HAPLN3	227262_at	Hyaluronan and proteoglycan link protein 3	2.29e-07	4.23e-08	0.0001132	0.00014361
Over	HMGA1	210457_x_at	High mobility group at-hook 1	8.39e-07	6.79e-08	0.000259	0.00016469
Over	LPIN1	212276_at	Lipin 1	9.37e-08	1.15e-07	6.69e-05	0.00020489
Over	PRKX /// PRKY	204060_s_at	Protein kinase, x-linked /// protein kinase, y-linked	4.79e-09	1.04e-08	1.58e-05	8.84E-05
Over	UGT8	208358_s_at	Udp glycosyltransferase 8	4.54e-07	1.87e-08	0.0001837	0.00010584
Over	UGT8	228956_at	Udp glycosyltransferase 8	3.17e-07	1.72e-07	0.0001418	0.00023999
Under	ANXA9	211712_s_at	Annexin a9	2.45e-08	3.79e-09	2.98e-05	6.43E-05
Under	ANXA9	210085_s_at	Annexin a9	1.35e-06	2.52e-07	0.0003491	0.00023999
Under	AR	211110_s_at	Androgen receptor	1.72e-08	2.93e-07	2.65e-05	0.00024238
Under	ATP8B1	226302_at	Atpase, aminophospholipid transporter, class I, type 8b, member 1	2.49e-07	9.19e-07	0.000121	0.00048764
Under	BCAS1	204378_at	Breast carcinoma amplified sequence 1	2.15e-06	1.15e-07	0.0004628	0.00020489
Under	C5orf30	221823_at	Chromosome 5 open reading frame 30	1.46e-06	6.21e-07	0.0003575	0.00036378
Under	CCDC96	238682_at	Coiled-coil domain containing 96	5.08e-06	2.61e-07	0.0007376	0.00023999
Under	CMBL	227522_at	Carboxymethylenebutenolidase homolog (pseudomonas)	1.40e-08	6.21e-07	2.32e-05	0.00036378
Under	CXXC5	224516_s_at	Cxxc finger protein 5	6.75e-07	2.22e-07	0.0002293	0.00023999
Under	DNAJC12	223721_s_at	Dnaj (hsp40) homolog, subfamily c, member 12	2.11e-07	4.23e-08	0.0001102	0.00014361
Under	DNAJC12	218976_at	Dnaj (hsp40) homolog, subfamily c, member 12	2.19e-08	6.79e-08	2.87e-05	0.00016469
Under	ERBB4	214053_at	V-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	5.30e-07	6.21e-07	0.0001998	0.00036378
Under	FAM174B	51158_at	Family with sequence similarity 174, member b	7.50e-09	2.22e-07	1.71e-05	0.00023999
Under	FAM174B	221880_s_at	Family with sequence similarity 174, member b	7.34e-08	2.93e-07	6.14e-05	0.00024238
Under	FLJ38379	1556474_a_at	Hypothetical flj38379	8.76e-09	2.73e-08	1.75e-05	0.00013249
Under	GATA3	209603_at	Gata binding protein 3	5.34e-09	9.19e-07	1.58e-05	0.00048764
Under	GATA3	209602_s_at	Gata binding protein 3	8.54e-10	9.19e-07	7.25e-06	0.00048764
Under	LASS6	212446_s_at	Lag1 homolog, ceramide synthase 6	5.95e-08	1.72e-07	5.32e-05	0.00023999
Under	LASS6	242019_at	Lag1 homolog, ceramide synthase 6	1.88e-05	6.21e-07	0.001669	0.00036378
Under	LOC100505614	237339_at	Hypothetical loc100505614	3.79e-08	6.21e-07	3.84e-05	0.00036378
Under	LOC692247	1569453_a_at	Hypothetical locus loc692247	9.45e-08	6.06e-10	6.69e-05	2.06E-05
Under	MLPH	218211_s_at	Melanophilin	5.19e-10	1.15e-07	5.88e-06	0.00020489
Under	MMEL1	1552930_at	Membrane metallo-endopeptidase-like 1	1.21e-06	2.19e-07	0.0003269	0.00023999
Under	NAT1	214440_at	N-acetyltransferase 1 (arylamine n-acetyltransferase)	3.04e-07	1.04e-08	0.0001397	8.84E-05
Under	TTC6	1556666_a_at	Non-protein coding rna 291	1.57e-06	6.79e-08	0.0003728	0.00016469
Under	PRR15	226961_at	Proline rich 15	2.15e-09	4.04e-07	1.24e-05	0.00029192
Under	RAB26	50965_at	Rab26, member ras oncogene family	1.19e-07	2.22e-07	7.80e-05	0.00023999
Under	RARA	203749_s_at	Retinoic acid receptor, alpha	7.68e-08	4.04e-07	6.21e-05	0.00029192
Under	RHOB	212099_at	Ras homolog gene family, member b	3.99e-07	2.93e-07	0.0001693	0.00024238
Under	SLC44A4	205597_at	Solute carrier family 44, member 4	1.65e-07	1.87e-08	9.20e-05	0.00010584
Under	SPATA20	218164_at	Spermatogenesis associated 20	1.82e-08	2.49e-07	2.68e-05	0.00023999
Under	STARD10	223103_at	Star-related lipid transfer (start) domain containing 10	2.91e-08	1.72e-07	3.40e-05	0.00023999
Under	TBC1D9	212960_at	Tbc1 domain family, member 9 (with gram domain)	1.44e-07	2.22e-07	8.44e-05	0.00023999
Under	TBC1D9	212956_at	Tbc1 domain family, member 9 (with gram domain)	4.32e-09	6.21e-07	1.58e-05	0.00036378
Under	TFF1	205009_at	Trefoil factor 1	4.91e-07	2.22e-07	0.0001877	0.00023999
Under	TFF3	204623_at	Trefoil factor 3 (intestinal)	6.32e-09	2.93e-07	1.65e-05	0.00024238
Under	TTC8	226120_at	Tetratricopeptide repeat domain 8	1.29e-06	6.21e-07	0.0003421	0.00036378