

Supplementary Appendix

This appendix has been provided by the authors to give readers additional information about their work.

Supplement to: Fan C, Oh DS, Wessels L, et al. Concordance among gene-expression-based predictors for breast cancer. *N Engl J Med* 2006;355:560-9.

Supplemental Statistical Methods. For the 70-gene and Wound-Response predictions, we used the individual sample assignments provided by Chang *et al.*¹. Briefly, the assignments made by the 70-gene and Wound-Response predictors were as follows: for the 70-gene predictor, a sample was classified according to the correlation of its expression levels of the 70 genes to a previously determined average centroid/profile of these genes in tumors from patients with the “Good” prognosis profile. Patients with a correlation coefficient of >0.4 were classified as Good, and ≤ 0.4 as Poor^{2, 3}. For the Wound-Response predictor, a sample was classified according to the Pearson correlation of its expression levels of the “core serum response (CSR)” genes to the serum-activated fibroblast centroid. Patients with >-0.15 correlation were classified as Wound-Response Activated, and ≤ -0.15 as Wound-Response Quiescent¹.

We used a nearest centroid predictor to classify tumors according to Intrinsic Subtype⁸. Briefly, a new “intrinsic” gene set was developed as described in Sorlie *et al.* 2003⁴, using 24 new paired tumor samples assayed on Agilent Oligo microarrays, and 105 tumors in total. Next, this gene list was used in a hierarchical clustering analysis on a 311 tumor sample test set created by combining together the two-color DNA microarray data sets of Sorlie *et al.* 2001 and 2003^{4, 5}, van’t Veer *et al.*³ and Sotiriou *et al.*⁶. This cluster was then used as the starting point to create five Subtype Mean expression profiles/Centroids (Luminal A, Luminal B, HER2+/ER-, Basal-like and Normal-like) by averaging the gene expression profiles for the samples within each dendrogram branch/subtype⁸. Finally, new samples like those in the Chang *et al.* dataset, are then individually compared to each centroid using the 306 intrinsic genes, and are assigned to

the nearest centroid as determined by Spearman correlation. For more details on this nearest centroid predictor (also referred to as a Single Sample Predictor), the data and how to implement it, see <https://genome.unc.edu/pubsup/breastTumor/>.

To classify tumors using the Recurrence Score predictor, we used the microarray data for all 21 RS-genes and applied the algorithm and scaling methods described in Paik *et al.* (2004). Briefly, the expression of the 16 target genes was normalized relative to the 5 reference genes; next, the target genes were scaled as described for the qRT-PCR data, weighted averaging was performed and we then used these values and the RS algorithm to generate a Recurrence Score for each patient, which ranged from 0 to 100; scaling was done separately for the 295 patient group and for the 225 ER+ patient group. Using the cutoffs described in Paik *et al.* (0-18, 19-30, 31-100), we assigned each patient into the Low, Intermediate or High risk groups. Finally, we used the log-base-2 ratio of HOXB13:IL17BR as a means of patient stratification, using a cutoff of -0.15 as described in Ma *et al.*⁷ to classify patients as having either a High or Low 2-gene ratio.

It should be noted that for the 70-gene, Wound-Response and Intrinsic Subtype profiles, a subset of the samples in this 295-sample dataset were used to train these predictors (75 of the 295 samples were previously published³ and used to train the 70-gene profile, these same 75 samples were also part of the 311 tumor dataset used to derive the Intrinsic Subtype Centroid profiles⁸, and 148 of the 295 samples were randomly selected to train the Wound-Response profile¹). Therefore, their performance in the Kaplan-Meier and multivariate analyses described below is positively biased. However, as this paper is

focused on comparing the actual predictions themselves and is not focused on identifying the “best” predictor, we believed it best to include as many samples as possible in the analysis as opposed to removing subsets of samples due to training and test set issues (if we removed training set samples, the resulting test dataset would be greatly reduced — to fewer than 147 samples and possibly as few as 72 samples). We acknowledge that the RS and 2-gene predictors are thus at a prognostic disadvantage relative to the other three because the 295 samples represent a true test set for these two predictors; this point should be taken into consideration when interpreting the results of the survival analyses and hazard ratios from multivariate analyses.

References for Supplemental Methods

1. Chang HY, Nuyten DS, Sneddon JB, et al. Robustness, scalability, and integration of a wound-response gene expression signature in predicting breast cancer survival. *Proc Natl Acad Sci U S A* 2005;102(10):3738-43.
2. van de Vijver MJ, He YD, van't Veer LJ, et al. A gene-expression signature as a predictor of survival in breast cancer. *N Engl J Med* 2002;347(25):1999-2009.
3. van 't Veer LJ, Dai H, van de Vijver MJ, et al. Gene expression profiling predicts clinical outcome of breast cancer. *Nature* 2002;415(6871):530-6.
4. Sorlie T, Tibshirani R, Parker J, et al. Repeated observation of breast tumor subtypes in independent gene expression data sets. *Proc Natl Acad Sci U S A* 2003;100(14):8418-23.
5. Sorlie T, Perou CM, Tibshirani R, et al. Gene expression patterns of breast carcinomas distinguish tumor subclasses with clinical implications. *Proc Natl Acad Sci U S A* 2001;98(19):10869-74.
6. Sotiriou C, Neo SY, McShane LM, et al. Breast cancer classification and prognosis based on gene expression profiles from a population-based study. *Proc Natl Acad Sci U S A* 2003;100(18):10393-8.
7. Ma XJ, Wang Z, Ryan PD, et al. A two-gene expression ratio predicts clinical outcome in breast cancer patients treated with tamoxifen. *Cancer Cell* 2004;5(6):607-16.
8. Hu Z, Fan C, Oh DS, et al. The molecular portraits of breast tumors are conserved across microarray platforms. *BMC Genomics* 2006;7(1):96.

Supplemental Table 1. Individual sample classifications made by the five different gene expression-based profiles (Next Page).

SAMPLE LIST

Sample ID	Age	ER (1=positive, 0=negative)	tumor size (1= <2cm, 2=2-5)	Grade (1=well-differentiated, 2=moderately, 3=poorly)	node status (1=0 nodes, 2=1-3 nodes, 3=4+ nodes)	# of nodes positive for tumor	TREATMENT simplified (loc=local, tam=tamoxifen, chemo=chemotherapy, and=and, tam=tamoxifen)	RF5 months	RF8 months	OS event (0=alive, 1=OOD c)	O 8 months	Intrinsic Subtype (as assign)	70+ Gene Profile (from Chang)	Recurrence Profile (1=0, 2=1-3, 3=4-6, 4=7-9, 5=10-15, 6=16-20, 7=21-25, 8=26-30, 9=31-35, 10=36-40, 11=41-45, 12=46-50, 13=51-55, 14=56-60, 15=61-65, 16=66-70, 17=71-75, 18=76-80, 19=81-85, 20=86-90, 21=91-95, 22=96-100, 23=101-105, 24=106-110, 25=111-115, 26=116-120, 27=121-125, 28=126-130, 29=131-135, 30=136-140, 31=141-145, 32=146-150, 33=151-155, 34=156-160, 35=161-165, 36=166-170, 37=171-175, 38=176-180, 39=181-185, 40=186-190, 41=191-195, 42=196-200, 43=201-205, 44=206-210, 45=211-215, 46=216-220, 47=221-225, 48=226-230, 49=231-235, 50=236-240, 51=241-245, 52=246-250, 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803=4001-4005, 804=4006-4010, 805=4011-4015, 806=4016-4020, 807=4021-4025, 808=4026-4030, 809=4031-4035, 810=4036-4040, 811=4041-4045, 812=4046-4050, 813=4051-4055, 814=4056-4060, 815=4061-4065, 816=4066-4070, 817=4071-4075, 818=4076-4080, 819=4081-4085, 820=4086-4090, 821=4091-4095, 822=4096-4100, 823=4101-4105, 824=4106-4110, 825=4111-4115, 826=4116-4120, 827=4121-4125, 828=4126-4130, 829=4131-4135, 830=4136-4140, 831=4141-4145, 832=4146-4150, 833=4151-4155, 834=4156-4160, 835=4161-4165, 836=4166-4170, 837=4171-4175, 838=4176-4180, 839=4181-4185, 840=4186-4190, 841=4191-4195, 842=4196-4200, 843=4
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PNAS 312	PNAS 312	47	1	2	2	0	0	local only	0	109.2402	0	109.2402	Luminal B	Good	Activated	high	high	high
PNAS 313	PNAS 313	43	1	1	2	0	0	local only	1	72.67351	0	72.67351	Normal Breast-lik	Good	Activated	low	high	low
PNAS 314	PNAS 314	39	1	1	2	1	2	local only	1	38.63655	1	60.71458	Luminal B	Poor	Activated	high	high	high
PNAS 315	PNAS 315	40	1	1	1	1	1	chemo only	0	98.89117	0	98.89117	Luminal A	Good	Quiescent	high	high	low
PNAS 318	PNAS 318	37	1	1	1	1	2	local only	1	28.02484	0	29.20739	Luminal A	Poor	Quiescent	low	intermediate	high
PNAS 319	PNAS 319	49	1	2	0	0	0	local only	1	76.45175	1	76.45175	HER2+ER-	Poor	Activated	high	high	high
PNAS 320	PNAS 320	44	1	1	3	1	1	chemo only	0	118.7351	0	118.7351	Basal-like	Poor	Activated	high	high	low
PNAS 321	PNAS 321	39	1	2	2	2	9	local only	1	18.00411	0	21.42098	Normal Breast-lik	Poor	Activated	high	high	low
PNAS 322	PNAS 322	45	1	2	1	0	0	chemo only	0	80.9096	0	80.9096	Luminal B	Good	Activated	low	high	high
PNAS 323	PNAS 323	41	1	2	1	0	0	local only	0	105.6263	0	105.6263	Luminal A	Good	Quiescent	low	low	low
PNAS 324	PNAS 324	46	0	2	3	1	2	chemo only	0	106.3162	0	106.3162	Basal-like	Poor	Activated	low	high	low
PNAS 325	PNAS 325	42	1	2	3	2	8	chemo only	0	105.2505	0	105.2505	Basal-like	Good	Activated	low	high	low
PNAS 326	PNAS 326	39	0	2	3	2	0	local only	0	99.58111	0	99.58111	Basal-like	Poor	Activated	high	high	low
PNAS 327	PNAS 327	49	1	1	2	1	2	chemo only	1	55.45791	0	73.13347	Luminal B	Poor	Activated	low	high	high
PNAS 328	PNAS 328	41	1	1	1	1	1	chemo only	0	66.92402	0	66.92402	Luminal A	Good	Activated	low	low	low
PNAS 329	PNAS 329	49	1	2	1	0	0	local only	1	25.95057	0	25.95057	Luminal B	Good	Activated	low	high	high
PNAS 330	PNAS 330	26	0	1	3	2	13	chemo only	0	62.39014	0	62.39014	Basal-like	Poor	Activated	low	high	high
PNAS 331	PNAS 331	48	1	1	1	0	0	local only	1	25.8912	1	30.09446	Luminal B	Poor	Activated	low	high	high
PNAS 332	PNAS 332	49	0	2	3	1	1	chemo only	0	95.90144	0	95.90144	Basal-like	Poor	Activated	low	high	high
PNAS 333	PNAS 333	44	0	2	3	0	0	local only	0	101.9466	0	101.9466	HER2+ER-	Poor	Activated	low	high	high
PNAS 334	PNAS 334	36	1	2	2	1	1	chemo only	0	92.32033	0	92.32033	Luminal A	Good	Activated	low	intermediate	intermediate
PNAS 335	PNAS 335	48	0	3	1	1	1	chemo only	0	89.72485	0	89.72485	Basal-like	Poor	Activated	low	high	high
PNAS 336	PNAS 336	47	1	1	1	0	0	local only	0	88.90349	0	88.90349	Luminal A	Good	Activated	low	intermediate	low
PNAS 337	PNAS 337	29	1	1	1	1	2	chemo only	1	25.03491	0	81.83984	Luminal A	Poor	Activated	low	high	high
PNAS 338	PNAS 338	49	0	1	3	0	0	chemo only	0	76.1232	0	76.1232	Basal-like	Poor	Activated	high	high	high
PNAS 339	PNAS 339	45	1	2	0	0	0	chemo only	0	199.0965	0	199.0965	Luminal B	Poor	Activated	low	high	high
PNAS 340	PNAS 340	43	1	2	2	1	1	chemo only	1	37.4538	1	70.30801	Luminal B	Poor	Activated	low	high	high
PNAS 341	PNAS 341	46	0	2	2	2	4	chemo only	1	20.79671	1	28.35318	HER2+ER-	Poor	Activated	high	high	low
PNAS 342	PNAS 342	43	1	1	1	0	1	local only	0	73.006	0	73.006	Luminal A	Good	Quiescent	low	high	low
PNAS 343	PNAS 343	44	0	1	1	0	0	chemo only	0	82.49692	0	82.49692	Basal-like	Poor	Activated	high	high	low
PNAS 344	PNAS 344	44	0	1	1	0	0	local only	0	83.94251	0	83.94251	Luminal A	Good	Activated	low	low	low
PNAS 345	PNAS 345	47	1	2	2	2	4	chemo only	0	83.94251	0	83.94251	Luminal A	Good	Activated	low	low	low
PNAS 346	PNAS 346	45	1	2	1	1	1	chemo only	0	85.64066	0	85.64066	Luminal A	Good	Activated	low	low	low
PNAS 347	PNAS 347	41	1	1	1	2	11	tam only	0	56.64066	0	56.64066	Normal Breast-lik	Good	Activated	high	high	high
PNAS 348	PNAS 348	50	1	2	0	0	0	local only	0	74.05339	0	74.05339	Luminal A	Good	Activated	low	high	high
PNAS 349	PNAS 349	45	1	2	2	0	0	chemo and tam	0	77.58979	0	77.58979	Luminal A	Good	Quiescent	low	high	high
PNAS 350	PNAS 350	41	1	1	3	1	2	high on tam	0	39.42053	0	39.42053	Basal-like	Poor	Activated	high	high	high
PNAS 351	PNAS 351	41	1	1	3	1	2	chemo only	0	78.32444	0	78.32444	HER2+ER-	Poor	Activated	high	high	high
PNAS 352	PNAS 352	43	1	2	2	0	0	local only	0	69.71663	0	69.71663	Luminal A	Good	Activated	low	high	high
PNAS 353	PNAS 353	48	0	1	3	1	3	chemo only	1	73.92197	0	73.92197	Luminal B	Poor	Activated	low	high	high
PNAS 354	PNAS 354	47	1	2	3	0	0	local only	0	73.92197	0	73.92197	Luminal A	Poor	Quiescent	high	intermediate	high
PNAS 355	PNAS 355	50	1	2	0	0	0	chemo only	0	72.54209	0	72.54209	Normal Breast-lik	Good	Activated	high	high	high
PNAS 356	PNAS 356	40	0	1	2	0	0	local only	0	74.57906	0	74.57906	Luminal A	Good	Activated	low	low	low
PNAS 357	PNAS 357	38	1	1	1	2	2	chemo and tam	0	69.8959	0	69.8959	Luminal A	Good	Activated	low	low	low
PNAS 358	PNAS 358	45	1	1	1	0	0	local only	0	74.87474	0	74.87474	Luminal A	Good	Activated	high	high	high
PNAS 359	PNAS 359	49	1	2	1	1	1	tam only	0	72.21355	0	72.21355	Normal Breast-lik	Poor	Activated	high	intermediate	intermediate
PNAS 360	PNAS 360	42	1	1	1	1	1	chemo and tam	0	66.56429	0	66.56429	Luminal B	Good	Quiescent	low	intermediate	intermediate
PNAS 361	PNAS 361	42	1	1	1	1	1	chemo and tam	0	64.16427	0	64.16427	Luminal A	Good	Quiescent	low	low	low
PNAS 362	PNAS 362	46	1	2	3	2	5	chemo and tam	0	63.11294	0	63.11294	Luminal B	Poor	Activated	high	high	high
PNAS 363	PNAS 363	42	1	1	1	1	5	chemo and tam	1	59.1493	0	59.1493	Luminal B	Poor	Activated	low	high	high
PNAS 364	PNAS 364	49	0	1	2	0	0	local only	0	216.9692	0	216.9692	Normal Breast-lik	Poor	Quiescent	high	high	high
PNAS 365	PNAS 365	51	1	2	0	0	0	local only	0	209.8398	0	209.8398	Luminal A	Good	Activated	low	low	low
PNAS 366	PNAS 366	50	1	2	0	0	0	local only	0	205.6316	0	205.6316	Luminal A	Poor	Quiescent	high	high	high
PNAS 367	PNAS 367	49	1	2	2	0	0	local only	0	6.86653	1	11.6881	Basal-like	Poor	Activated	high	high	high
PNAS 368	PNAS 368	33	1	2	2	0	0	local only	0	114.8255	0	202.4478	Normal Breast-lik	Poor	Activated	low	high	high
PNAS 369	PNAS 369	39	0	1	2	0	0	local only	1	39.09651	1	78.8601	HER2+ER-	Poor	Activated	high	high	low
PNAS 370	PNAS 370	51	1	2	1	2	1	local only	0	112.9636	0	112.9636	Normal Breast-lik	Good	Activated	high	low	low
PNAS 371	PNAS 371	51	1	2	2	1	1	chemo only	0	93.2731	0	93.2731	Luminal B	Poor	Activated	high	intermediate	low
PNAS 372	PNAS 372	52	1	1	1	1	1	chemo only	1	32.16427	1	69.09955	Luminal B	Poor	Activated	high	high	high
PNAS 373	PNAS 373	52	0	1	3	2	6	chemo only	0	209.8113	0	209.8113	HER2+ER-	Poor	Activated	high	high	low
PNAS 374	PNAS 374	52	0	1	3	2	6	chemo only	1	102.3409	1	114.3655	Basal-like	Poor	Activated	high	high	high
PNAS 375	PNAS 375	52	1	2	3	1	1	tam only	0	167.0308	0	167.0308	Luminal B	Poor	Activated	high	high	high
PNAS 376	PNAS 376	52	1	1	1	1	1	local only	1	93.2731	1	102.3409	Luminal B	Poor	Activated	high	high	high
PNAS 377	PNAS 377	52	1	2	1	1	1	chemo only	0	132.9938	0	132.9938	Luminal A	Good	Activated	low	high	high
PNAS 378	PNAS 378	52	1	2	3	1	1	tam only	0	21.35934	1	34.66119	Luminal B	Poor	Activated	high	high	high
PNAS 379	PNAS 379	52	1	2	1	1	1	tam only	0	98.56263	0	98.56263	Luminal A	Poor	Activated	low	high	high
PNAS 380	PNAS 380	51	1	2	3	2	4	high on tam	0	86.70226	0	86.70226	Luminal A	Poor	Activated	high	high	high
PNAS 381	PNAS 381	51	1	2	3	2	4	tam only	0	41.03491	1	59.36756	Luminal B	Poor	Activated	high	high	high
PNAS 382	PNAS 382	51	1	1	1	1	1	tam only	0	81.64271	0	81.64271	Luminal A	Good	Activated	low	low	low
PNAS 383	PNAS 383	51	1	1	1	1	1	chemo only	0	81.64271	0	81.64271	Luminal A	Good	Activated	low	intermediate	low
PNAS 384	PNAS 384	51	1	1	1	1	2	tam only	0	74.05339	0	74.05339	HER2+ER-	Poor	Activated	high	high	high
PNAS 385	PNAS 385	51	1	2	1	1	1	chemo only	0	66.89117	0	66.89117	Luminal B	Poor	Activated	low	high	high
PNAS 386	PNAS 386	51	1	2	1	1	2	local only	0	68.59103	0	68.59103	Luminal B	Good	Quiescent	high	intermediate	intermediate
PNAS 387	PNAS 387	51	1	2	2	2	11	local only	0	134.539	0	180.9281	Luminal A	Good	Activated	high	intermediate	low
PNAS 388	PNAS 388	51	0	2	3	1	2	tam only	0	122.7762	0	122.7762	HER2+ER-	Poor	Activated	high	high	high
PNAS 389	PNAS 389	47	0	1	1	0	0	local only	0	88.54209	0	88.54209	Basal-like	Poor	Activated	high	high	intermediate
PNAS 390	PNAS 390	40	1	1	1	1	3	chemo only	0	81.132	0	81.132	Luminal A	Good	Activated	high	low	intermediate
PNAS 391	PNAS 391	39	1	1	1	1	3	local only	0	90.84189	0	90.84189	Luminal A	Good	Activated	high	low	intermediate
PNAS 392	PNAS 392	43	1	2	2	0	0	local only	0	177.807	0	177.807	Luminal A	Good	Activated	high	low	low
PNAS 393	PNAS 393	42	0	2	3	0	0	local only	0	79.2717	0	79.2717	Luminal A	Good	Activated	low	high	intermediate
PNAS 394	PNAS 394	42	0	2	3	0	0	local only	0	59.43326	1	59.43326	Basal-like	Poor	Activated	high	high	high
PNAS 395	PNAS 395	43	1	2	2	0	0	local only	1	57.19918	1	105.2648	Luminal A	Poor	Activated	high	intermediate	intermediate
PNAS 396	PNAS 396	41	0	1	3	0	0	tam only	0	15.49281	0	41.4028	Luminal B	Poor	Activated	high	high	high
PNAS 397	PNAS 397	41	0	1	3	0	0	local only										

Supplemental Table 2. Multivariate Cox proportional hazards analysis of (A) standard clinical prognostic factors alone, or with (B) the 70-gene predictor, (C) Wound-response predictor, (D) Ma *et al.* 2-gene ratio predictor, (E) Recurrence Score, or (F) Intrinsic Subtypes in relation to Relapse-Free Survival and Overall Survival for the 295-sample Chang *et al.* 2005 dataset. Size was a binary variable (0= diameter of 2cm or less, 1= greater than 2cm); age was a continuous variable formatted as decade-years; hazard ratios for Intrinsic Subtypes were calculated relative to the Luminal A subtype. Variables found to be significant (p<0.05) in the Cox proportional hazards model are shown in bold.

A.				
Variable	Relapse-Free survival		Overall survival	
	Hazard Ratio (95% CI)	p-value	Hazard Ratio (95% CI)	p-value
Age, per decade	0.59 (0.43-0.82)	0.001	0.67 (0.45-0.98)	0.042
ER status	0.65 (0.42-0.99)	0.045	0.44 (0.27-0.71)	0.001
Tumor grade 2 vs. 1	2.45 (1.33-4.50)	0.004	4.31 (1.49-12.47)	0.007
Tumor grade 3 vs. 1	2.53 (1.35-4.74)	0.004	5.96 (2.06-17.21)	0.001
Size	1.40 (0.96-2.05)	0.083	1.52 (0.94-2.43)	0.086
1-3 vs. 0 positive nodes	1.32 (0.72-2.41)	0.37	1.06 (0.48-2.36)	0.88
>3 vs. 0 positive nodes	2.24 (1.12-4.49)	0.023	1.85 (0.78-4.38)	0.16
Hormonal or chemotherapy vs. no adjuvant therapy	0.56 (0.31-1.01)	0.055	0.81 (0.38-1.74)	0.59
B.				
Variable	Relapse-Free survival		Overall survival	
	Hazard Ratio (95% CI)	p-value	Hazard Ratio (95% CI)	p-value
Age, per decade	0.64 (0.46-0.88)	0.006	0.71 (0.48-1.05)	0.085
ER status	0.86 (0.56-1.31)	0.47	0.59 (0.36-0.95)	0.031
Tumor grade 2 vs. 1	1.57 (0.82-2.97)	0.17	2.55 (0.86-7.63)	0.093
Tumor grade 3 vs. 1	1.32 (0.68-2.59)	0.41	2.84 (0.94-8.54)	0.064
Size	1.44 (0.99-2.11)	0.059	1.58 (0.98-2.53)	0.058
1-3 vs. 0 positive nodes	1.20 (0.66-2.18)	0.55	1.01 (0.46-2.21)	0.97
>3 vs. 0 positive nodes	2.19 (1.07-4.47)	0.032	1.97 (0.81-4.79)	0.14
Hormonal or chemotherapy vs. no adjuvant therapy	0.54 (0.30-0.99)	0.048	0.75 (0.34-1.62)	0.46
70-gene predictor (poor vs. good)	3.44 (1.98-5.99)	<0.001	4.71 (2.02-11.00)	<0.001

C.

Variable	Relapse-Free survival		Overall survival	
	Hazard Ratio (95% CI)	p-value	Hazard Ratio (95% CI)	p-value
Age, per decade	0.56 (0.40-0.77)	<0.001	0.62 (0.41-0.92)	0.019
ER status	0.69 (0.45-1.06)	0.089	0.46 (0.28-0.76)	0.002
Tumor grade 2 vs. 1	1.89 (1.02-3.52)	0.045	3.32 (1.13-9.71)	0.028
Tumor grade 3 vs. 1	1.92 (1.02-3.62)	0.045	4.46 (1.53-13.00)	0.006
Size	1.39 (0.95-2.03)	0.090	1.52 (0.95-2.44)	0.083
1-3 vs. 0 positive nodes	1.19 (0.65-2.17)	0.58	0.96 (0.43-2.12)	0.92
>3 vs. 0 positive nodes	1.74 (0.85-3.57)	0.13	1.48 (0.61-3.59)	0.38
Hormonal or chemotherapy vs. no adjuvant therapy	0.58 (0.32-1.07)	0.080	0.84 (0.39-1.81)	0.65
Wound-response signature (activated vs. quiescent)	2.88 (1.50-5.52)	0.002	3.25 (1.27-8.27)	0.014

D.

Variable	Relapse-Free survival		Overall survival	
	Hazard Ratio (95% CI)	p-value	Hazard Ratio (95% CI)	p-value
Age, per decade	0.60 (0.43-0.82)	0.001	0.67 (0.45-0.98)	0.042
ER status	0.63 (0.41-0.98)	0.040	0.44 (0.26-0.72)	0.001
Tumor grade 2 vs. 1	2.43 (1.32-4.47)	0.004	4.31 (1.49-12.48)	0.007
Tumor grade 3 vs. 1	2.57 (1.37-4.82)	0.003	5.96 (2.06-17.23)	0.001
Size	1.40 (0.96-2.05)	0.082	1.52 (0.94-2.43)	0.086
1-3 vs. 0 positive nodes	1.32 (0.72-2.42)	0.36	1.06 (0.48-2.36)	0.88
>3 vs. 0 positive nodes	2.26 (1.13-4.54)	0.022	1.85 (0.78-4.38)	0.16
Hormonal or chemotherapy vs. no adjuvant therapy	0.55 (0.30-1.00)	0.051	0.81 (0.38-1.74)	0.59
Ma <i>et al.</i> 2-gene ratio (high vs. low)	0.91 (0.61-1.34)	0.62	1.00 (0.61-1.63)	0.99

E. Variable	Relapse-Free survival		Overall survival	
	Hazard Ratio (95% CI)	p-value	Hazard Ratio (95% CI)	p-value
Age, per decade	0.57 (0.42-0.79)	<0.001	0.63 (0.42-0.94)	0.023
Tumor grade 2 vs. 1	1.61 (0.85-3.04)	0.14	2.95 (0.99-8.73)	0.051
Tumor grade 3 vs. 1	1.50 (0.79-2.86)	0.21	3.81 (1.30-11.1)	0.014
Size	1.51 (1.03-2.20)	0.035	1.66 (1.03-2.67)	0.036
1-3 vs. 0 positive nodes	1.24 (0.68-2.26)	0.48	0.95 (0.43-2.09)	0.90
>3 vs. 0 positive nodes	2.10 (1.04-4.25)	0.039	1.59 (0.66-3.82)	0.30
Hormonal or chemotherapy vs. no adjuvant therapy	0.54 (0.30-0.98)	0.044	0.80 (0.37-1.73)	0.57
Intermediate vs. Low recurrence score	1.81 (0.70-4.68)	0.22	1.81 (0.39-8.27)	0.45
High vs. Low recurrence score	4.27 (2.05-8.92)	<0.001	6.14 (1.84-20.4)	0.003

F. Variable	Relapse-Free survival		Overall survival	
	Hazard Ratio (95% CI)	p-value	Hazard Ratio (95% CI)	p-value
Age, per decade	0.59 (0.42-0.82)	0.002	0.67 (0.45-1.00)	0.051
Tumor grade 2 vs. 1	1.80 (0.96-3.39)	0.068	3.51 (1.19-10.36)	0.023
Tumor grade 3 vs. 1	1.80 (0.92-3.50)	0.087	4.47 (1.48-13.49)	0.008
Size	1.55 (1.05-2.29)	0.027	1.55 (0.96-2.51)	0.076
1-3 vs. 0 positive nodes	1.20 (0.65-2.21)	0.55	1.01 (0.45-2.28)	0.98
>3 vs. 0 positive nodes	2.01 (0.96-4.21)	0.064	1.81 (0.73-4.50)	0.20
Hormonal or chemotherapy vs. no adjuvant therapy	0.49 (0.26-0.92)	0.025	0.69 (0.31-1.54)	0.37
Luminal B	3.79 (2.17-6.61)	<0.001	2.55 (1.25-5.22)	0.010
Normal-like	2.86 (1.49-5.50)	0.002	2.00 (0.76-5.31)	0.16
Her2+/ER-	3.16 (1.61-6.18)	<0.001	3.54 (1.59-7.85)	0.002
Basal-like	2.45 (1.33-4.51)	0.004	3.05 (1.49-6.27)	0.002

Supplemental Table 3. Two-way contingency table analysis measuring the association between the 70-gene, Wound-response, and Recurrence Score predictors in the **295-sample** dataset.

A.

Two-way contingency table	Wound-Response	
	Quiescent	Activated
70-gene predictor	(# of patients)	
Good	48	67
Poor	19	161
Statistics for two-way contingency table analysis		
p-value†	<0.001	
Cramer's V††	0.36	

B.

Two-way contingency table	Recurrence Score	
	Low or Int.	High
70-gene predictor	(# of patients)	
Good	81	34
Poor	22	158
Statistics for two-way contingency table analysis		
p-value†	<0.001	
Cramer's V††	0.60	

C.

Two-way contingency table	Recurrence Score	
	Low or Int. (# of patients)	High
Wound Response		
Quiescent	48	19
Activated	55	173
Statistics for two-way contingency table analysis		
p-value†	<0.001	
Cramer's V††	0.42	

† p-value calculated from Chi-square test on contingency table. †† Cramer's V statistic (value can range from 0 to 1) measures the strength of association between the two variables analyzed in the contingency table, with 1 indicating perfect association and 0 indicating no association.

Supplemental Table 4. Multivariate Cox proportional hazards analysis of (A) standard clinical prognostic factors alone or with (B) the 70-gene predictor, (C) Wound-response predictor, (D) Ma et al.'s 2-gene predictor, (E) Recurrence Score predictor, or (F) intrinsic subtypes in relation to Relapse-Free Survival and Overall Survival for the 225 ER+ samples in the Chang et al. (2005) dataset. Size was a binary variable (0= diameter of 2cm or less, 1= greater than 2cm); age was a continuous variable formatted as decade-years; hazard ratios for intrinsic subtypes were calculated relative to the Luminal A subtype. Variables found to be significant (p<0.05) in the Cox proportional hazards model are shown in bold.

Variable	Relapse-Free survival		Overall survival	
	Hazard Ratio (95% CI)	p-value	Hazard Ratio (95% CI)	p-value
Age, per decade	0.54 (0.35-0.82)	0.005	0.56 (0.31, 0.99)	0.047
Tumor grade 2 vs. 1	2.11 (1.12-3.98)	0.021	3.28 (1.08, 9.94)	0.035
Tumor grade 3 vs. 1	2.83 (1.49-5.38)	0.002	7.36 (2.51, 21.5)	<0.001
Size	1.41 (0.88-2.26)	0.15	1.33 (0.71, 2.49)	0.36
1-3 vs. 0 positive nodes	2.11 (1.06-4.21)	0.034	2.11 (0.81, 5.53)	0.13
>3 vs. 0 positive nodes	2.92 (1.26-6.73)	0.012	2.16 (0.69, 6.72)	0.18
Hormonal or chemotherapy vs. no adjuvant therapy	0.37 (0.18-0.73)	0.004	0.52 (0.20, 1.32)	0.17

Variable	Relapse-Free survival		Overall survival	
	Hazard Ratio (95% CI)	p-value	Hazard Ratio (95% CI)	p-value
Age, per decade	0.65 (0.42-0.99)	0.047	0.68 (0.38, 1.22)	0.20
Tumor grade 2 vs. 1	1.24 (0.63-2.44)	0.53	1.75 (0.55, 5.55)	0.34
Tumor grade 3 vs. 1	1.20 (0.59-2.48)	0.61	2.72 (0.85, 8.66)	0.091
Size	1.45 (0.91-2.31)	0.12	1.41 (0.76, 2.61)	0.28
1-3 vs. 0 positive nodes	1.73 (0.88-3.40)	0.11	1.81 (0.71, 4.60)	0.21
>3 vs. 0 positive nodes	2.70 (1.12-6.49)	0.027	2.32 (0.69, 7.80)	0.17
Hormonal or chemotherapy vs. no adjuvant therapy	0.37 (0.18-0.74)	0.005	0.47 (0.18, 1.22)	0.12
70-gene predictor (poor vs. good)	3.88 (2.15-7.02)	<0.001	5.47 (2.13, 14.1)	<0.001

Variable	Relapse-Free survival		Overall survival	
	Hazard Ratio (95% CI)	p-value	Hazard Ratio (95% CI)	p-value
Age, per decade	0.50 (0.32-0.78)	0.002	0.49 (0.27, 0.90)	0.022
Tumor grade 2 vs. 1	1.60 (0.83-3.05)	0.16	2.41 (0.78, 7.39)	0.12
Tumor grade 3 vs. 1	2.10 (1.09-4.05)	0.026	5.24 (1.76, 15.6)	0.003
Size	1.39 (0.87-2.21)	0.17	1.32 (0.71, 2.46)	0.38
1-3 vs. 0 positive nodes	1.87 (0.94-3.73)	0.076	1.85 (0.71, 4.82)	0.21
>3 vs. 0 positive nodes	2.19 (0.92-5.20)	0.075	1.61 (0.50, 5.17)	0.42
Hormonal or chemotherapy vs. no adjuvant therapy	0.39 (0.20-0.78)	0.008	0.56 (0.22, 1.45)	0.23
Wound-response (activated vs. quiescent)	2.95 (1.42-6.14)	0.004	4.03 (1.20, 13.5)	0.024

D. Variable	Relapse-Free survival		Overall survival	
	Hazard Ratio (95% CI)	p-value	Hazard Ratio (95% CI)	p-value
Age, per decade	0.54 (0.35-0.84)	0.006	0.56 (0.31, 0.99)	0.048
Tumor grade 2 vs. 1	2.08 (1.10-3.93)	0.023	3.28 (1.08, 9.92)	0.036
Tumor grade 3 vs. 1	2.99 (1.55-5.74)	0.001	7.42 (2.51, 21.9)	<0.001
Size	1.42 (0.89-2.26)	0.14	1.34 (0.72, 2.49)	0.36
1-3 vs. 0 positive nodes	2.15 (1.08-4.29)	0.030	2.12 (0.80, 5.55)	0.13
>3 vs. 0 positive nodes	2.99 (1.29-6.92)	0.010	2.16 (0.69, 6.70)	0.18
Hormonal or chemotherapy vs. no adjuvant therapy	0.36 (0.18-0.72)	0.004	0.52 (0.20, 1.32)	0.17
Ma <i>et al.</i> 2-gene ratio (high vs. low)	0.81 (0.51-1.29)	0.38	0.97 (0.52, 1.79)	0.91

E. Variable	Relapse-Free survival		Overall survival	
	Hazard Ratio (95% CI)	p-value	Hazard Ratio (95% CI)	p-value
Age, per decade	0.49 (0.32-0.75)	0.001	0.50 (0.28, 0.90)	0.021
Tumor grade 2 vs. 1	1.42 (0.72, 2.79)	0.32	1.83 (0.58, 5.77)	0.30
Tumor grade 3 vs. 1	1.69 (0.83, 3.41)	0.15	3.26 (1.04, 10.2)	0.042
Size	1.52 (0.96, 2.42)	0.073	1.54 (0.83, 2.86)	0.17
1-3 vs. 0 positive nodes	1.97 (1.00, 3.87)	0.049	1.75 (0.68, 4.47)	0.24
>3 vs. 0 positive nodes	3.10 (1.32, 7.26)	0.009	2.06 (0.66, 6.39)	0.21
Hormonal or chemotherapy vs. no adjuvant therapy	0.40 (0.20, 0.80)	0.009	0.62 (0.24, 1.58)	0.32
Intermediate vs. Low recurrence score	0.82 (0.27, 2.46)	0.72	1.42 (0.27, 7.50)	0.68
High vs. Low recurrence score	2.59 (1.44, 4.65)	0.001	4.95 (1.82, 13.4)	0.002

Variable	Relapse-Free survival		Overall survival	
	Hazard Ratio (95% CI)	p-value	Hazard Ratio (95% CI)	p-value
Age, per decade	0.52 (0.33, 0.81)	0.004	0.57 (0.31, 1.04)	0.065
Tumor grade 2 vs. 1	1.40 (0.72, 2.71)	0.32	2.48 (0.80, 7.70)	0.12
Tumor grade 3 vs. 1	1.62 (0.82, 3.18)	0.16	4.92 (1.62, 14.9)	0.005
Size	1.66 (1.03, 2.65)	0.036	1.51 (0.80, 2.82)	0.20
1-3 vs. 0 positive nodes	1.82 (0.92, 3.59)	0.085	1.89 (0.73, 4.89)	0.19
>3 vs. 0 positive nodes	2.34 (0.96, 5.68)	0.061	1.98 (0.60, 6.54)	0.26
Hormonal or chemotherapy vs. no adjuvant therapy	0.34 (0.16, 0.68)	0.003	0.49 (0.18, 1.29)	0.15
Luminal B	4.40 (2.47, 7.84)	<0.001	2.81 (1.33, 5.91)	0.006
Normal-like, HER2+/ER-, or Basal-like	2.51 (1.38, 4.58)	0.003	1.92 (0.84, 4.37)	0.12

Supplemental Table 5. Two-way contingency table analysis measuring the association between the 70-gene, Wound-response, and Recurrence Score predictors in the ER+ 225-sample dataset.

A.

Two-way contingency table	Wound-Response	
	Quiescent	Activated
70-gene predictor	(# of patients)	
Good	47	66
Poor	13	99
Statistics for two-way contingency table analysis		
p-value†	<0.001	
Cramer's V††	0.34	

B.

Two-way contingency table	Recurrence Score	
	Low or Int. (# of patients)	High
70-gene predictor		
Good	83	30
Poor	22	90
Statistics for two-way contingency table analysis		
p-value†	<0.001	
Cramer's V††	0.54	

C.

Two-way contingency table	Recurrence Score	
	Low or Int. (# of patients)	High
Wound Response		
Quiescent	47	13
Activated	58	107
Statistics for two-way contingency table analysis		
p-value†	<0.001	
Cramer's V††	0.38	

† p-value calculated from Chi-square test on contingency table. †† Cramer's V statistic (value can range from 0 to 1) measures the strength of association between the two variables analyzed in the contingency table, with 1 indicating perfect association and 0 indicating no association.