Supplementary Table 1. Proportion of mapped genes used for the subtype classifications and the prognostic gene signatures*

Dataset	Percent of mapped genes in each model								
	SCMGENE	**SCMOD2**	**SCMOD1**	**PAM50**	**SSP2006**	**SSP2003**	***MAMMAPRINT***	***ONCOTYPE***	***GGI***
CAL	100	100	100	88	70	80	63	100	100
DFHCC	100	100	100	100	71	86	74	100	100
DFHCC2	100	100	100	100	71	86	74	100	100
DFHCC3	100	100	100	100	71	86	74	100	100
DFHCC4	100	100	100	100	71	86	74	100	100
DUKE	100	76	70	80	66	70	43	88	55
DUKE2	100	100	99	100	71	86	74	88	81
EMC2	100	100	100	100	71	86	74	100	100
EORTC10994	100	100	100	88	70	80	63	100	100
EXPO	100	100	100	100	71	86	74	100	100
FNCLCC	100	59	53	76	55	59	46	94	54
HLP	100	99	99	98	71	85	73	100	81
KOO	100	76	70	80	66	70	43	88	55
LUND	100	84	84	82	60	72	64	88	73
LUND2	100	73	62	72	58	70	46	81	56
MAINZ	100	100	100	88	70	80	63	100	100
MAQC2	100	100	100	88	70	80	63	100	100
MCCC	100	99	99	98	71	84	73	100	81
MDA4	100	100	100	88	70	80	63	100	100
MSK	100	100	100	88	70	80	63	100	100
MUG	100	96	96	96	69	83	73	94	77
NCCS	100	100	100	88	70	80	63	100	100
NCI	100	45	36	62	66	61	24	75	36
NKI	100	95	100	96	69	82	100	100	77
JBI	100	100	100	100	71	86	74	100	100
STK	100	100	100	100	71	86	73	100	100
STNO2	100	54	46	66	66	84	36	69	38
MDA5	100	100	100	88	70	80	63	100	100
VDX3	100	100	100	88	70	80	63	100	100
TAM (HGU133A)	100	100	100	88	70	80	63	100	100
TAM	100	100	100	100	71	86	74	100	100
TRANSBIG	100	100	100	88	70	80	63	100	100
UCSF	100	58	51	62	63	64	34	88	44
UNC4	100	98	99	100	71	86	74	100	80
UNT	100	100	100	100	71	86	73	100	100
UPP	100	100	100	100	71	86	73	100	100
VDX	100	100	100	88	70	80	63	100	100

* The three genes used in SCMGENE are present in all the microarray platforms. Note that ONCOTYPE models do not allow for

missing genes; therefore the ONCOTYPE risk predictions were not computed when genes were missing. SCMGENE: three-gene subtype classification model; SCMOD2: subtype classification model published by Wirapati et al. (8); SCMOD1: subtype classification model published by Desmedt et al. (1); PAM50: single sample predictor published by Parker et al. (3); SSP2006: single sample predictor published by Hu et al. (2). SSP2003: single sample predictor published Sorlie et al. (6); MAMMAPRINT: prognostic gene signature published by van't Veer et al. (14); ONCOTYPE: prognostic gene signature published by Paik et al. (15); GGI: prognostic gene signature published by Sotiriou et al. (16). Each dataset was assigned a short acronym and an instance number if several datasets were published by the same institution or consortium: EXPO: expression project for oncology, large dataset of microarray data published by the International Genomics Consortium (United States); VDX: Veridex (The Netherlands); NKI: National Kanker Instituut (The Netherlands); UCSF: University of California, San Francisco (United States); STNO: Stanford/Norway (United States and Norway); NCI: National Cancer Institute (United States); MSK Memorial Sloan-Kettering (United States); UPP: Uppsala hospital (Sweden); STK: Stockholm. Karolinska university hospital (Sweden); UNT: cohort of untreated breast cancer patients from the Oxford Radcliffe (United Kingdom) and Karolinska (Sweden) hospitals; UNC: University of North Carolina (United States); DUKE: Duke university hospital (United States); CAL: dataset of breast cancer patients from the University of California, San Francisco and the California Pacific Medical Center (United States); TRANSBIG: dataset collected by the TransBIG consortium (Europe); MAINZ: Mainz hospital (Germany); LUND: Lund University Hospital (Sweden); FNCLCC: Fédération Nationale des Centres de Lutte contre le Cancer (France); MDA: MD Anderson Cancer Centter (United States); EMC: Erasmus Medical Center (The Netherlands); MUG: Medical University of Graz (Austria); NCCS: National Cancer Centre of Singapore (Singapore); MCCC: Peter MacCallum Cancer Centre (Australia); KOO: Koo Foundation Sun Yat-Sen Cancer Centre (Taiwan); EORTC10994: Trial number 10994 from the European Organization for Research and Treatment of Cancer Breast Cancer; (Europe) HLP: University Hospital La Paz (Spain); DFHCC: Dana-Farber Harvard Cancer Center (United States); MAQC: Microarray quality control consortium (United States); JBI: Jules Bordet Institute (Belgium).

Supplementary Table 2. Robustness of the subtyping as estimated by the prediction strength for classification into three subtypes in all the test sets*

Dataset	SCMGENE	SCMOD2	SCMOD1	PAM50	SSP2006	SSP2003
CAL	0.875	1.000	0.875	0.505	0.491	0.000
DFHCC	0.875	0.795	0.732	0.584	0.528	0.522
DFHCC2	1.000	0.655	0.673	0.857	0.663	0.000
DFHCC3	0.900	0.750	0.500	1.000	0.500	0.753
DUKE	0.750	0.579	0.682	0.771	0.405	0.479
DUKE2	0.642	0.535	0.586	0.913	0.495	0.496
EMC2	0.867	0.908	0.878	0.699	0.568	0.333
EORTC10994	1.000	0.909	0.718	0.467	0.333	0.791
FNCLCC	0.768	0.830	0.905	0.687	0.425	0.200
HLP	0.931	0.833	0.591	0.600	0.487	0.558
DFHCC4	0.601	0.618	0.767	0.875	0.534	0.925
KOO	0.628	0.458	0.970	0.685	0.444	0.439
LUND	0.760	0.824	0.799	0.483	0.498	0.495
LUND2	0.662	0.644	1.000	0.803	0.379	0.455
MAINZ	0.419	0.987	0.987	0.686	0.495	0.703
MAQC2	0.970	0.384	0.867	0.581	0.596	0.478
MCCC	0.929	0.714	0.827	0.583	0.623	0.000
MDA4	1.000	0.463	0.900	0.492	0.599	0.333
MSK	1.000	0.833	0.900	0.488	0.667	0.300
MUG	0.429	0.426	0.519	0.382	0.436	0.331
NCCS	0.964	0.618	0.537	0.770	0.507	0.333
NCI	0.636	0.846	0.697	0.392	0.429	0.321
NKI	0.892	0.820	0.959	0.715	0.531	0.400
JBI	1.000	0.905	0.882	0.720	0.333	0.000
STK	0.605	0.948	0.915	0.537	0.455	0.440
STNO2	0.912	0.913	0.580	0.464	0.382	0.467
TRANSBIG	0.969	1.000	0.844	0.517	0.486	0.333
UCSF	0.823	0.905	0.926	0.448	0.471	0.477
UNC4	0.896	1.000	0.897	0.579	0.533	0.677
UNT	0.978	0.820	0.889	0.958	0.485	0.456
UPP	0.887	0.738	0.914	0.621	0.498	0.512
VDX	0.805	0.958	0.829	0.512	0.407	0.301
median	0.881	0.822	0.856	0.592	0.493	0.448
mad	0.156	0.173	0.118	0.160	0.066	0.170
mean	0.824	0.769	0.798	0.637	0.490	0.416
sd	0.167	0.182	0.148	0.167	0.084	0.223

*Prediction strength statistics for the identification of three main subtypes by each subtype classifier in each test dataset. SCMGENE: three-gene subtype classification model; SCMOD2: subtype classification model published by Wirapati et al. (8); SCMOD1: subtype classification model published by Desmedt et al. (1); PAM50: single sample predictor published by Parker et al. (3); SSP2006: single sample predictor published by Hu et al. (2). SSP2003: single sample predictor published Sorlie et al. (6). Each dataset was assigned a short acronym and an instance number if several datasets were published by the same institution or consortium: EXPO: expression project for oncology, large dataset of microarray data published by the International Genomics Consortium (United States); VDX: Veridex (The Netherlands); NKI: National Kanker Instituut (The Netherlands); UCSF: University of California, San Francisco (United States); STNO: Stanford/Norway (United States and Norway); NCI: National Cancer Institute (United States); MSK Memorial Sloan-Kettering (United States); UPP: Uppsala hospital (Sweden); STK: Stockholm. Karolinska university hospital (Sweden); UNT: cohort of untreated breast cancer patients from the Oxford Radcliffe (United Kingdom) and Karolinska (Sweden) hospitals; UNC: University of North Carolina (United States); DUKE: Duke university hospital (United States); CAL: dataset of breast cancer patients from the University of California, San Francisco and the California Pacific Medical Center (United States); TRANSBIG: dataset collected by the TransBIG consortium (Europe); MAINZ: Mainz hospital (Germany); LUND: Lund University Hospital (Sweden); FNCLCC: Fédération Nationale des Centres de Lutte contre le Cancer (France); MDA: MD Anderson Cancer Centter (United States); EMC: Erasmus Medical Center (The Netherlands); MUG: Medical University of Graz (Austria); NCCS: National Cancer Centre of Singapore (Singapore); MCCC: Peter MacCallum Cancer Centre

(Australia); KOO: Koo Foundation Sun Yat-Sen Cancer Centre (Taiwan); EORTC10994: Trial number 10994 from the European Organization for Research and Treatment of Cancer Breast Cancer; (Europe) HLP: University Hospital La Paz (Spain); DFHCC: Dana-Farber Harvard Cancer Center (United States); MAQC: Microarray quality control consortium (United States); JBI: Jules Bordet Institute (Belgium). Median and median-absolute deviation (mad), mean and standard deviation (sd) are provided as a summary for each subtype classifier.

Supplementary Table 3. Robustness of the subtyping as estimated by the prediction strength for classification into four subtypes in all the test sets.*

Dataset	SCMGENE	SCMOD2	SCMOD1	PAM50	SSP2006	SSP2003
CAL	0.875	1.000	0.843	0.000	0.489	0.467
DFHCC	0.875	0.795	0.732	0.584	0.194	0.000
DFHCC2	1.000	0.655	0.655	0.500	0.000	0.000
DFHCC3	0.900	0.750	0.444	1.000	0.000	0.575
DUKE	0.749	0.579	0.671	0.500	0.345	0.456
DUKE2	0.636	0.513	0.545	0.000	0.352	0.333
EMC2	0.865	0.908	0.876	0.000	0.251	0.300
EORTC10994	1.000	0.867	0.705	0.000	0.000	0.000
FNCLCC	0.764	0.830	0.892	0.489	0.310	0.167
HLP	0.857	0.800	0.561	0.600	0.435	0.558
DFHCC4	0.556	0.618	0.767	0.875	0.167	0.516
KOO	0.628	0.458	0.926	0.100	0.393	0.167
LUND	0.751	0.806	0.747	0.344	0.325	0.342
LUND2	0.652	0.644	1.000	0.500	0.309	0.167
MAINZ	0.252	0.974	0.976	0.462	0.293	0.218
MAQC2	0.970	0.261	0.866	0.493	0.353	0.389
MCCC	0.929	0.714	0.786	0.341	0.000	0.000
MDA4	1.000	0.259	0.870	0.365	0.509	0.461
MSK	1.000	0.833	0.900	0.143	0.257	0.400
MUG	0.321	0.200	0.504	0.244	0.281	0.271
NCCS	0.964	0.610	0.504	0.489	0.251	0.333
NCI	0.618	0.846	0.697	0.364	0.394	0.286
NKI	0.892	0.820	0.959	0.167	0.380	0.300
JBI	1.000	0.905	0.882	0.508	0.000	0.000
STK	0.605	0.908	0.875	0.267	0.437	0.250
STNO2	0.907	0.913	0.553	0.361	0.238	0.410
TRANSBIG	0.952	1.000	0.800	0.414	0.307	0.333
UCSF	0.820	0.905	0.924	0.420	0.286	0.357
UNC4	0.896	1.000	0.858	0.539	0.221	0.486
UNT	0.970	0.728	0.854	0.000	0.179	0.167
UPP	0.887	0.734	0.843	0.300	0.416	0.228
VDX	0.805	0.958	0.829	0.327	0.245	0.342
median	0.875	0.803	0.836	0.364	0.290	0.317
mad	0.152	0.160	0.131	0.201	0.118	0.176
mean	0.809	0.743	0.776	0.366	0.269	0.290
sd	0.191	0.218	0.152	0.240	0.144	0.168

*****Prediction strength statistics for the identification of four main subtypes by each subtype classifier in each test dataset. SCMGENE: three-gene subtype classification model; SCMOD2: subtype classification model published by Wirapati et al. (8); SCMOD1: subtype classification model published by Desmedt et al. (1); PAM50: single sample predictor published by Parker et al. (3); SSP2006: single sample predictor published by Hu et al. (2). SSP2003: single sample predictor published Sorlie et al. (6). Each dataset was assigned a short acronym and an instance number if several datasets were published by the same institution or consortium: EXPO: expression project for oncology, large dataset of microarray data published by the International Genomics Consortium (United States); VDX: Veridex (The Netherlands); NKI: National Kanker Instituut (The Netherlands); UCSF: University of California, San Francisco (United States); STNO: Stanford/Norway (United States and Norway); NCI: National Cancer Institute (United States); MSK Memorial Sloan-Kettering (United States); UPP: Uppsala hospital (Sweden); STK: Stockholm. Karolinska university hospital (Sweden); UNT: cohort of untreated breast cancer patients from the Oxford Radcliffe (United Kingdom) and Karolinska (Sweden) hospitals; UNC: University of North Carolina (United States); DUKE: Duke university hospital (United States); CAL: dataset of breast cancer patients from the University of California, San Francisco and the California Pacific Medical Center (United States); TRANSBIG: dataset collected by the TransBIG consortium (Europe); MAINZ: Mainz hospital (Germany); LUND: Lund University Hospital (Sweden); FNCLCC: Fédération Nationale des Centres de Lutte contre le Cancer (France); MDA: MD Anderson Cancer Centter (United States); EMC: Erasmus Medical Center (The Netherlands); MUG:

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Supplementary Table 4. Robustness of the subtyping as estimated by the prediction strength for classification into five subtypes in all the test sets*

Dataset	PAM50	SSP2006	SSP2003
CAL	0.575	0.000	0.651
DFHCC	0.493	0.267	0.000
DFHCC2	0.000	0.000	0.000
DFHCC3	0.000	0.000	0.000
DUKE	0.428	0.397	0.345
DUKE2	0.412	0.250	0.333
EMC2	0.000	0.390	0.167
EORTC10994	0.471	0.000	0.000
FNCLCC	0.282	0.228	0.167
HLP	0.321	0.382	0.558
DFHCC4	0.000	0.000	0.000
KOO	0.167	0.421	0.000
LUND	0.298	0.228	0.285
LUND2	0.278	0.167	0.300
MAINZ	0.424	0.319	0.200
MAQC2	0.167	0.325	0.296
MCCC	0.000	0.000	0.000
MDA4	0.000	0.333	0.435
MSK	0.067	0.000	0.333
MUG	0.190	0.195	0.242
NCCS	0.503	0.291	0.232
NCI	0.167	0.500	0.000
NKI	0.167	0.448	0.200
JBI	0.000	0.000	0.000
STK	0.200	0.248	0.333
STNO2	0.190	0.333	0.318
TRANSBIG	0.000	0.448	0.000
UCSF	0.249	0.250	0.258
UNC4	0.333	0.324	0.381
UNT	0.000	0.300	0.000
UPP	0.300	0.456	0.250
VDX	0.255	0.243	0.324
median	0.195	0.258	0.237
mad	0.247	0.160	0.151
mean	0.217	0.242	0.206
sd	0.178	0.162	0.180

*****Prediction strength statistics for the identification of five main subtypes by the single sample predictors in each test dataset. PAM50: single sample predictor published by Parker et al. (3); SSP2006: single sample predictor published by Hu et al. (2). SSP2003: single sample predictor published Sorlie et al. (6). Each dataset was assigned a short acronym and an instance number if several datasets were published by the same institution or consortium: EXPO: expression project for oncology, large dataset of microarray data published by the International Genomics Consortium (United States); VDX: Veridex (The Netherlands); NKI: National Kanker Instituut (The Netherlands); UCSF: University of California, San Francisco (United States); STNO: Stanford/Norway (United States and Norway); NCI: National Cancer Institute (United States); MSK Memorial Sloan-Kettering (United States); UPP: Uppsala hospital (Sweden); STK: Stockholm. Karolinska university hospital (Sweden); UNT: cohort of untreated breast cancer patients from the Oxford Radcliffe (United Kingdom) and Karolinska (Sweden) hospitals; UNC: University of North Carolina (United States); DUKE: Duke university hospital (United States); CAL: dataset of breast cancer patients from the University of California, San Francisco and the California Pacific Medical Center (United States); TRANSBIG: dataset collected by the TransBIG consortium (Europe); MAINZ: Mainz hospital (Germany); LUND: Lund University Hospital (Sweden); FNCLCC: Fédération Nationale des Centres de Lutte contre le Cancer (France); MDA: MD Anderson Cancer Centter (United States); EMC: Erasmus Medical Center (The Netherlands); MUG: Medical University of Graz (Austria); NCCS: National Cancer Centre of Singapore (Singapore); MCCC: Peter MacCallum Cancer Centre (Australia); KOO: Koo Foundation Sun Yat-Sen Cancer Centre (Taiwan); EORTC10994: Trial number 10994 from the European Organization for Research and Treatment of Cancer Breast Cancer; (Europe) HLP:

University Hospital La Paz (Spain); DFHCC: Dana-Farber Harvard Cancer Center (United States); MAQC: Microarray quality control consortium (United States); JBI: Jules Bordet Institute (Belgium). Median and median-absolute deviation (mad), mean and standard deviation (sd) are provided as a summary for each subtype classifier.

Supplementary Table 5. Comparison of the prediction strength of the six subtype classifiers for classification into three, four, and five subtypes*

Model	Median difference (95% CI), *P*				
	SCMGENE	**SCMOD2**	**SCMOD1**	**PAM50**	**SSP2006**
Classification into three subtypes					
SCMOD2	-0.052 (-0.12 to 0.015), *P*=.36				
SCMOD1	-0.03 (-0.11 to 0.039), *P*=.86	0.012 (-0.052 to 0.084]) P=.86			
PAM50	-0.2 (-0.29 to -0.11), *P*<.001	-0.13 (-0.26 to -0.032), *P*=.078	-0.2 (-0.27 to -0.088), *P*=.0046		
SSP2006	-0.35 (-0.39,-0.28), P<.001	-0.29 (-0.37 to -0.2), *P*<.001	-0.33 (-0.38 to -0.26), P<.001	-0.14 (-0.22 to -0.072), *P*<.001	
SSP2003	-0.4 (-0.52 to -0.3), *P*<.001	-0.35 (-0.46 to -0.24), *P*<.001	-0.38 (-0.5 to -0.29), *P*<.001	-0.21 (-0.3 to -0.12), *P*<.001	-0.061 (-0.15 to 0.013), *P*=.36
Classification into four subtypes					
SCMOD2	-0.056 (-0.14 to 0.007), *P*=0.50				
SCMOD1	-0.046 (-0.12 to 0.039), P=0.76	0.0043 (-0.064 to 0.099), *P*=1.0			
PAM50	-0.45 (-0.56 to -0.35), *P*<.001	-0.4 (-0.51 to -0.26), *P*<.001	-0.43 (-0.52 to -0.33), *P*<.001		
SSP2006	-0.54 (-0.64 to -0.44), *P*<.001	-0.51 (-0.59 to -0.39), *P*=<.001	-0.51 (-0.58 to -0.44), *P*<.001	-0.085 (-0.19 to 0.024), *P*=.60	
SSP2003	-0.51 (-0.61 to -0.43), *P*<.001	-0.48 (-0.58 to -0.36), *P*<.001	-0.49 (-0.59 to -0.4), *P*<.001	-0.063 (-0.18 to 0.015), *P*=.50	0.0083 (-0.049 to 0.075), *P*=1.0
Classification into five subtypes					
SSP2006				0.035 (-0.061 to 0.14), *P* = 1.0	
SSP2003				-0.0013 (-0.09 to 0.077), *P* = 1.0	-0.045 (-0.15 to 0.052), *P* = 1.0

* Two-sided *P*-values estimated by two-sample Wilcoxon signed rank test in order to compare the prediction strength (the higher the better) of the six subtype classifiers for classification into three, four, and five subtypes. The median difference is to be interpreted as the prediction strength of the classifier in row minus the prediction strength of the classifier in column. Note that P-values were corrected for multiple testing using Holm's method. SCMGENE: three-gene subtype classification model; SCMOD2: subtype classification model published by Wirapati et al. (8); SCMOD1: subtype classification model published by Desmedt et al. (1); PAM50: single sample predictor published by Parker et al. (3); SSP2006: single sample predictor published by Hu et al. (2). SSP2003: single sample predictor published Sorlie et al. (6).

Supplementary Table 6. Estimation of the prognostic value of the subtype classifiers and prognostic gene signatures through cross-validated partial (log-)likelihood.

	SCMGENE	**SCMOD2**	**SCMOD1**	**PAM50**	**SSP2006**	**SSP2003**	***MAMMAPRINT***	***ONCOTYPE***	***GGI***
CVPL	1.649	1.651	1.656	1.658	1.653	1.667	1.648	1.646	1.651

*Two-sided *P*-values estimated by two-sample Wilcoxon signed rank test comparing the cross-validated partial (log-)likelihood (CVPL, the lower the better) of the subtype classifiers and published prognostic gene signatures. The median difference is to be interpreted as the CVPL of the classifier in row minus the CVPL of the classifier in column. Note that P-values were corrected for multiple testing using Holm's method. SCMGENE: three-gene subtype classification model; SCMOD2: subtype classification model published by Wirapati et al. (8); SCMOD1: subtype classification model published by Desmedt et al. (1); PAM50: single sample predictor published by Parker et al. (3); SSP2006: single sample predictor published by Hu et al. (2). SSP2003: single sample predictor published Sorlie et al. (6); MAMMAPRINT: prognostic gene signature published by van't Veer et al. (14); ONCOTYPE: prognostic gene signature published by Paik et al. (15); GGI: prognostic gene signature published by Sotiriou et al. (16), CVPL: cross-validated partial (log-)likelihood.

Supplementary Table 7. Comparison of comparing the cross-validated partial (log-)likelihood (CVPL, the lower the better) of the subtype classifiers and published prognostic gene signatures*

Model	Median difference (95% CI), *P*					
	SCMGENE	**SCMOD2**	**SCMOD1**	**PAM50**	**SSP2006**	**SSP2003**
Subtype classifiers						
SCMOD2	-0.008 (-0.018 to 0.0022, *P* = 1.0					
SCMOD1	-0.0031 (-0.011 to 0.0078), *P*=1.0	0.0045 (-0.00024 to 0.0099), *P*=.9				
PAM50	-0.00042 (-0.0082 to 0.0073), *P*=1.0	0.0073 (-0.0002 to 0.013), *P*=.9	0.0014 (-0.0084 to 0.011), *P*=1.0	-0.0008 (-0.02 to 0.0067), *P*=1.0		
SSP2006	-0.0056 (-0.016 to 0.0072), *P*=1.0	0.006 (-0.012 to 0.013), *P*=1.0	-0.0028 (-0.016= to 0.011), *P*=1.0			
SSP2003	0.0091 (-0.0058 to 0.024), *P*=1.0	0.016 (0.0037 to 0.028), *P*=.41	0.011 (-0.00086 to 0.024), *P*=1.0	0.0085 (-0.0052 to 0.022] *P*=1.0	0.012 (-0.0021 to 0.031), *P*=1.0	
Published prognostic gene signatures						
MAMMAPRINT	-0.012 (-0.021 to 0.00034), *P*=.9	-0.0015 (-0.011 to 0.0039), *P*=1.0	-0.0076 (-0.019 to 0.00045), *P*=1.0	-0.007 (-0.022 to -0.00022), *P*=.73	-0.008 (-0.023 to 0.018), *P*=1.0	-0.022 (-0.031 to -0.0079), *P*=.33
ONCOTYPEDX	-0.012 (-0.025 to 0.0037), *P*=1.0	-0.0046 (-0.016 to 0.0038), *P*=1.0	-0.0094 (-0.022 to 0.003), *P*=.9	-0.012 (-0.026 to 0.0019), *P*=1.0	-0.0081 (-0.02 to 0.0036), *P*=1.0	-0.021 (-0.039 to -0.0053), *P*=.33
GGI	-0.0084 (-0.015 to 0.0017), *P*=1.0	-0.00055 (-0.0058 to 0.0056), *P*=1.0	-0.0051 (-0.012 to 0.0019), *P*=1.0	-0.0076 (-0.015 to 0.0021), *P*=1.0	-0.0042 (-0.015 to 0.011), *P*=1.0	-0.016 (-0.024 to -0.0081), *P*=0.035

*Two-sided *P*-values estimated by two-sample Wilcoxon signed rank test comparing the cross-validated partial (log-)likelihood (CVPL, the lower the better) of the subtype classifiers and published prognostic gene signatures. The median difference is to be interpreted as the CVPL of the classifier in row minus the CVPL of the classifier in column. Note that P-values were corrected for multiple testing using Holm's method. SCMGENE: three-gene subtype classification model; SCMOD2: subtype classification model published by Wirapati et al. (8); SCMOD1: subtype classification model published by Desmedt et al. (1); PAM50: single sample predictor published by Parker et al. (3); SSP2006: single sample predictor published by Hu et al. (2). SSP2003: single sample predictor published Sorlie et al. (6); MAMMAPRINT: prognostic gene signature published by van't Veer et al. (14); ONCOTYPE: prognostic gene signature published by Paik et al. (15); GGI: prognostic gene signature published by Sotiriou et al. (16).