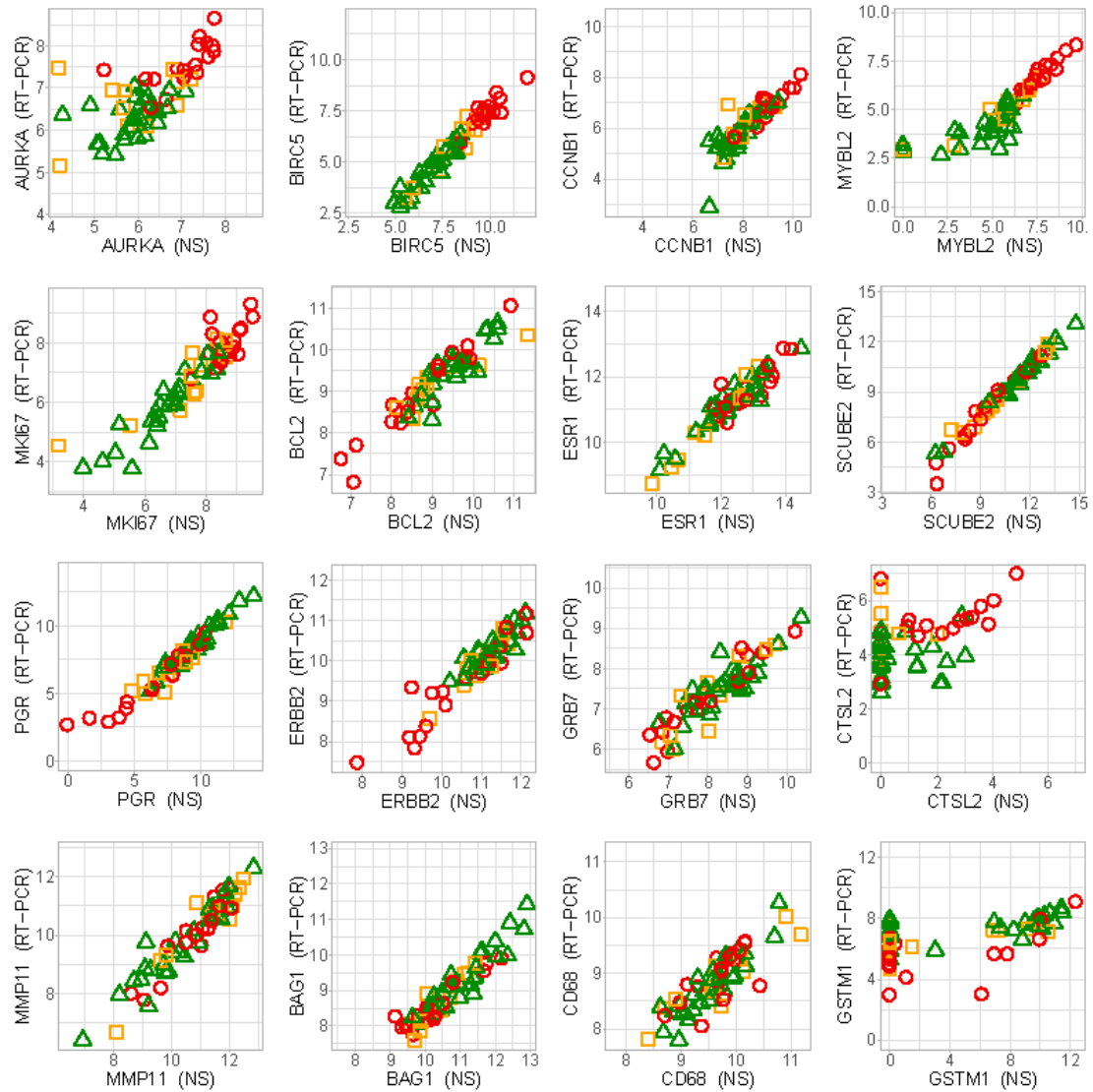
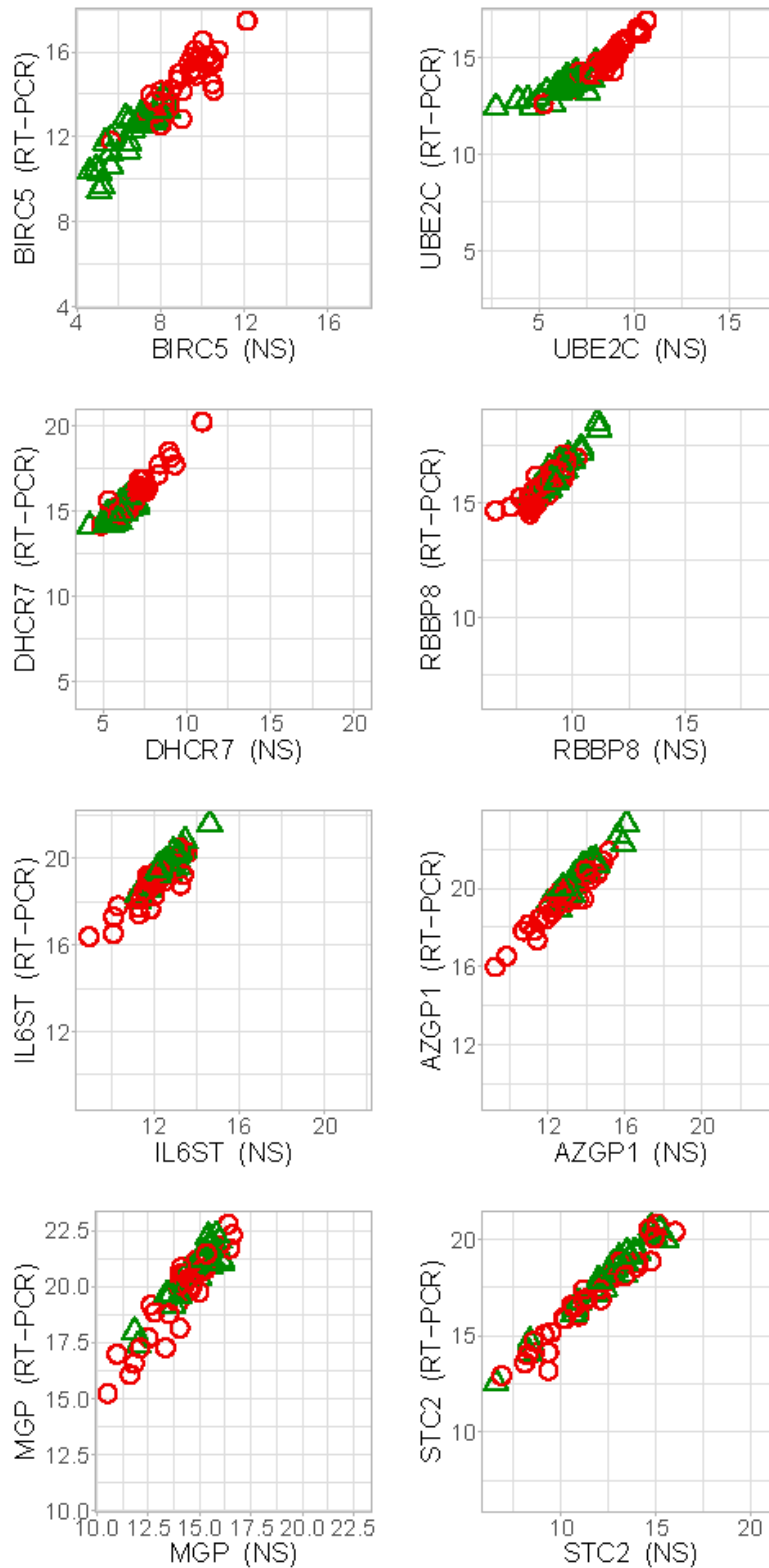


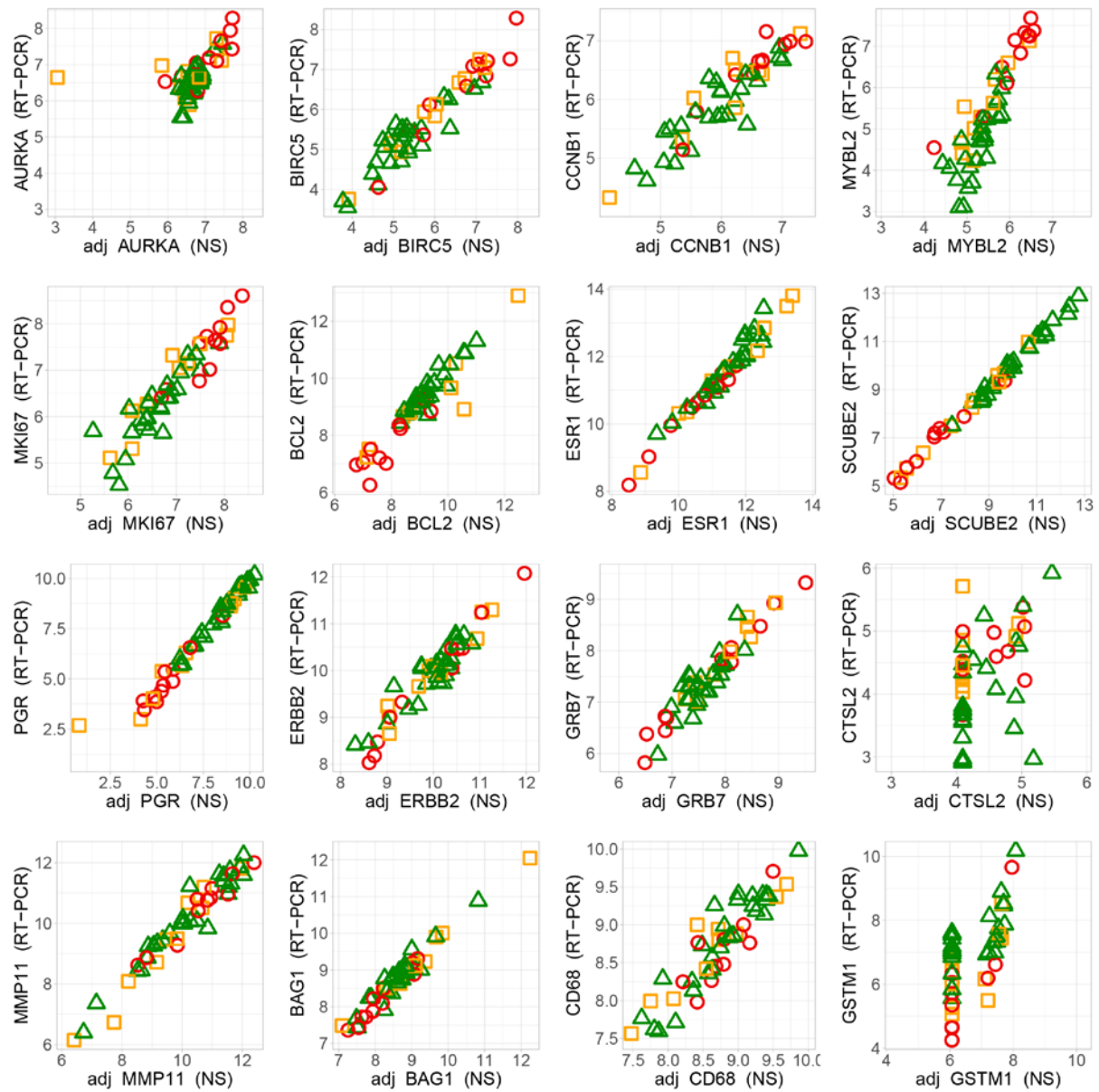
Supplemental Figure 1. Scatterplots of RS gene expression levels measured by RT-PCR and NanoString in the training set (n=59). Patients are presented according to risk groups as defined by the commercial RS assay (low risk with green, intermediate risk with orange and high risk with red). NS: NanoString



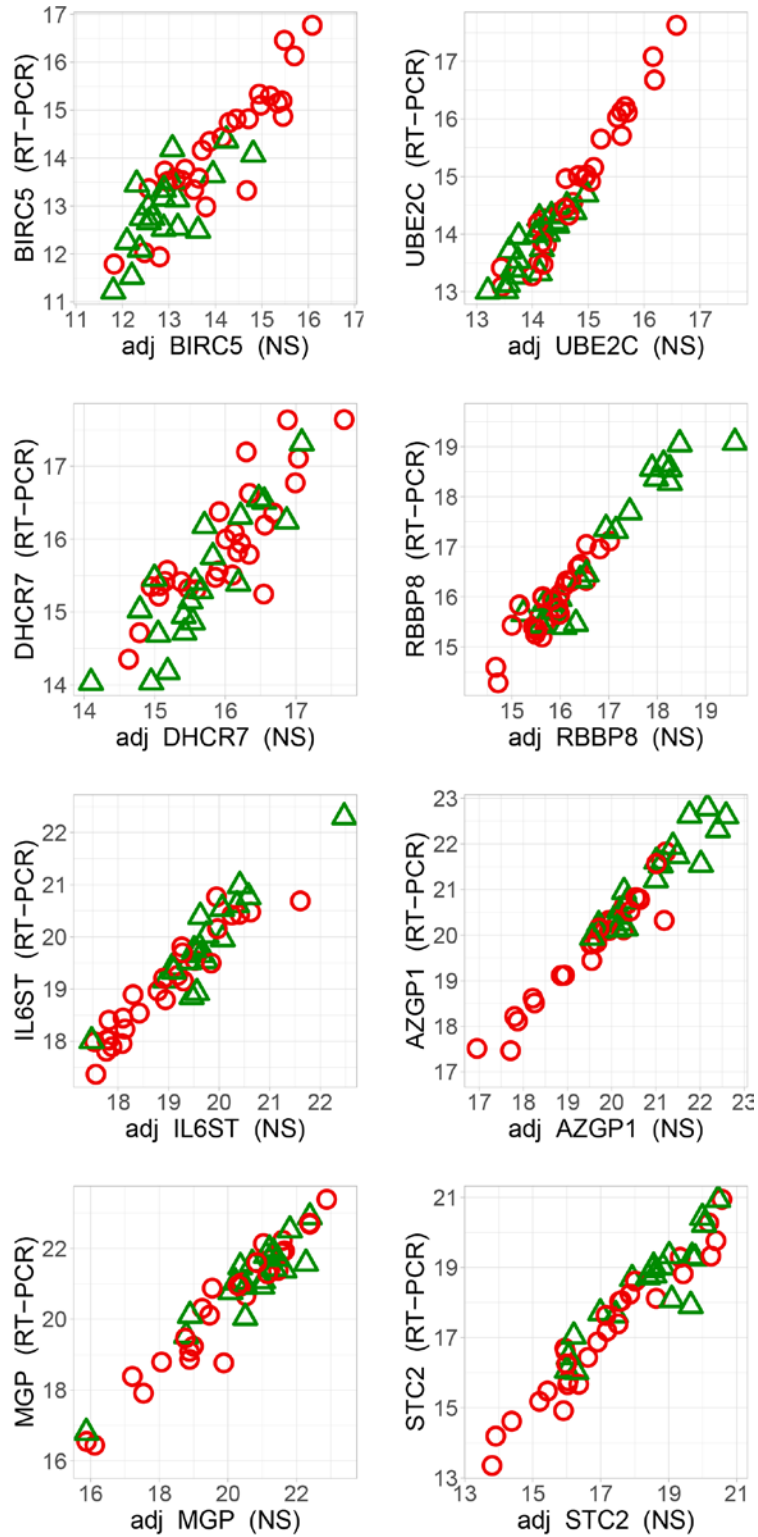
Supplemental Figure 2. Scatterplots of EP gene expression levels measured by RT-PCR and NanoString in the training set (n=59). Patients are presented according to risk groups as defined by the commercial EP assay (low risk with green, high risk with red). NS: NanoString



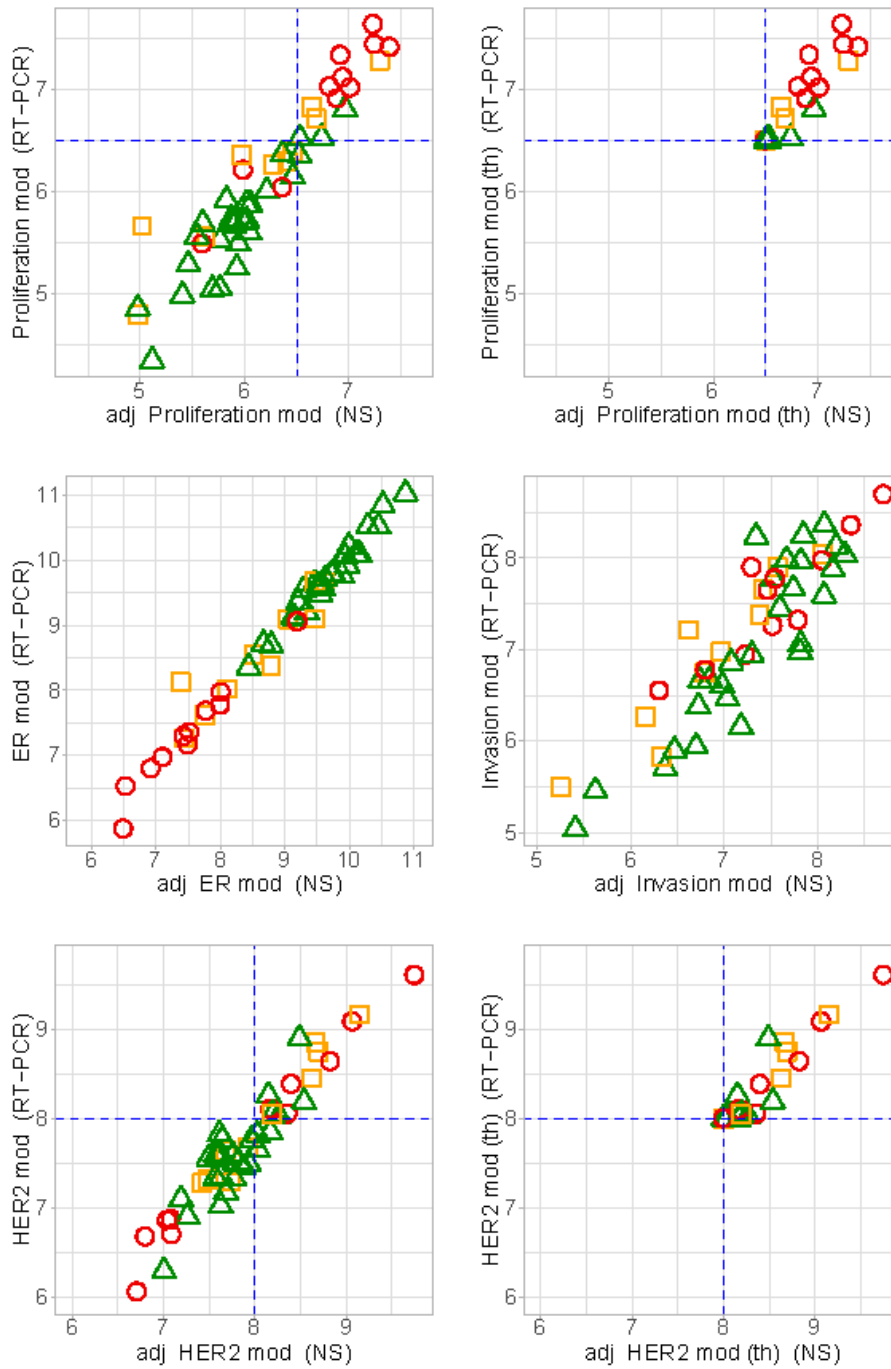
Supplemental Figure 3. Scatterplots of RS gene expression levels measured by RT-PCR and NanoString adjusted by the conversion factors in the validation set (n=48). Patients are presented according to risk groups as defined by the commercial RS assay (low risk with green, intermediate risk with orange and high risk with red). RS: Recurrence Score; adj: adjusted; NS: NanoString



Supplemental Figure 4. Scatterplots of EP gene expression levels measured by RT-PCR and NanoString adjusted by the conversion factors in the validation set (n=48). Patients are presented according to risk groups as defined by the commercial EP assay (low risk with green, high risk with red).
 adj: adjusted; NS: NanoString

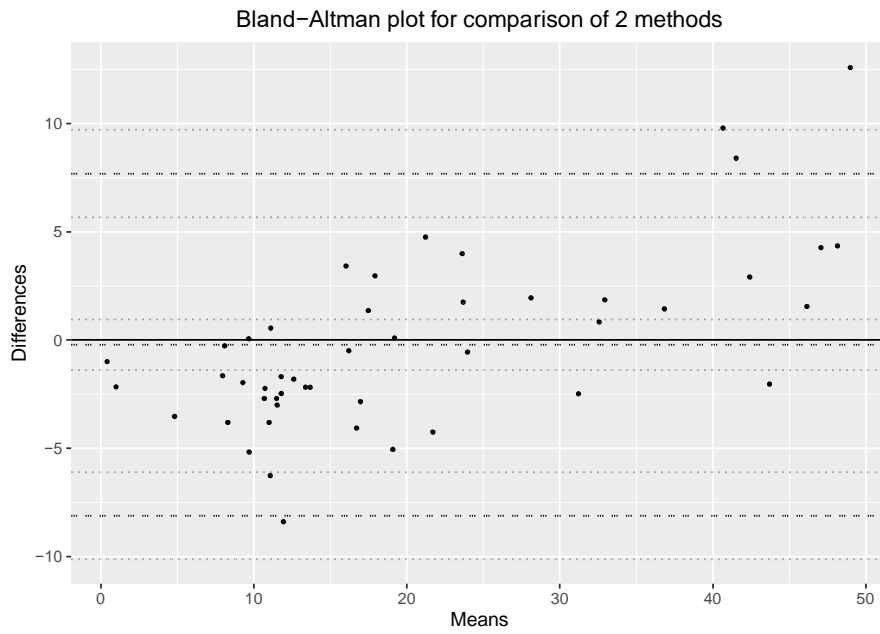


Supplemental Figure 5. Scatterplots of the commercial RS module scores versus NanoString-derived RUO RS module scores in the validation set (n=48). Patients are presented according to risk groups as defined by the commercial RS assay (low risk with green, intermediate risk with orange and high risk with red). Blue lines are the reference lines for the thresholds of the HER2 (threshold = 8) and proliferation (threshold = 6.5) modules. NS: NanoString; mod: module' th: thresholded

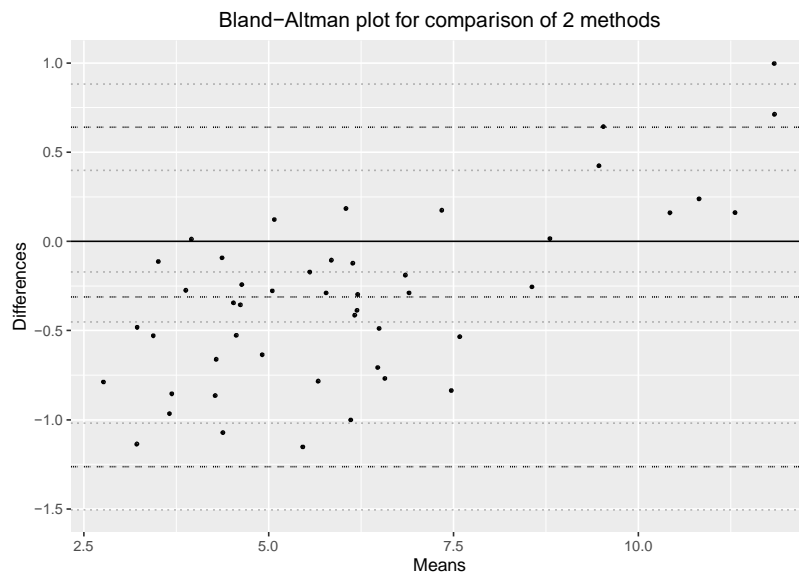


Supplemental Figure 6. Bland-Altman graphical assessment of the agreements between the commercial and RUO (a) RS, (b) EP and (c) ROR scores in the validation set (n = 48).

(a)

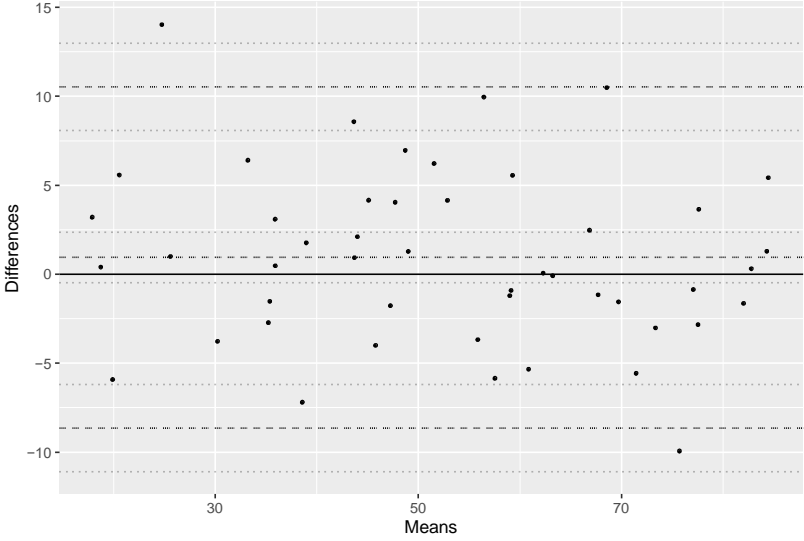


(b)

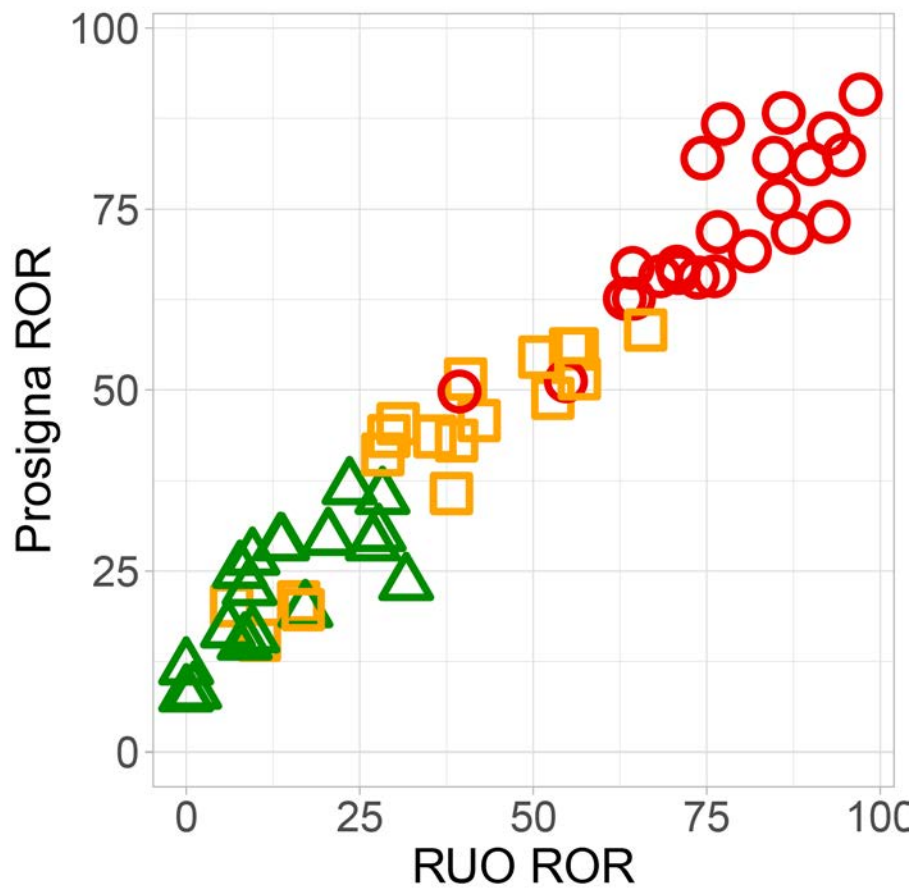


(c)

Bland-Altman plot for comparison of 2 methods

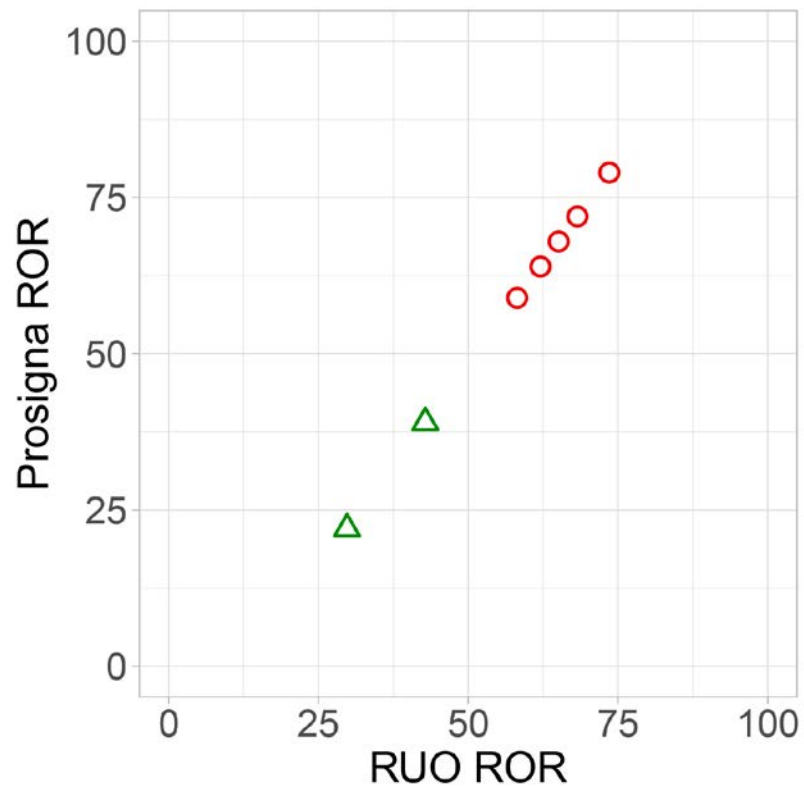


Supplemental Figure 7. Assessment of correlation between commercial and RUO ROR scores in the training set (n=59). Patients are presented in low-risk group with green, in intermediate-risk group with orange and high-risk group with red as categorised by the commercial test. RUO: research use only

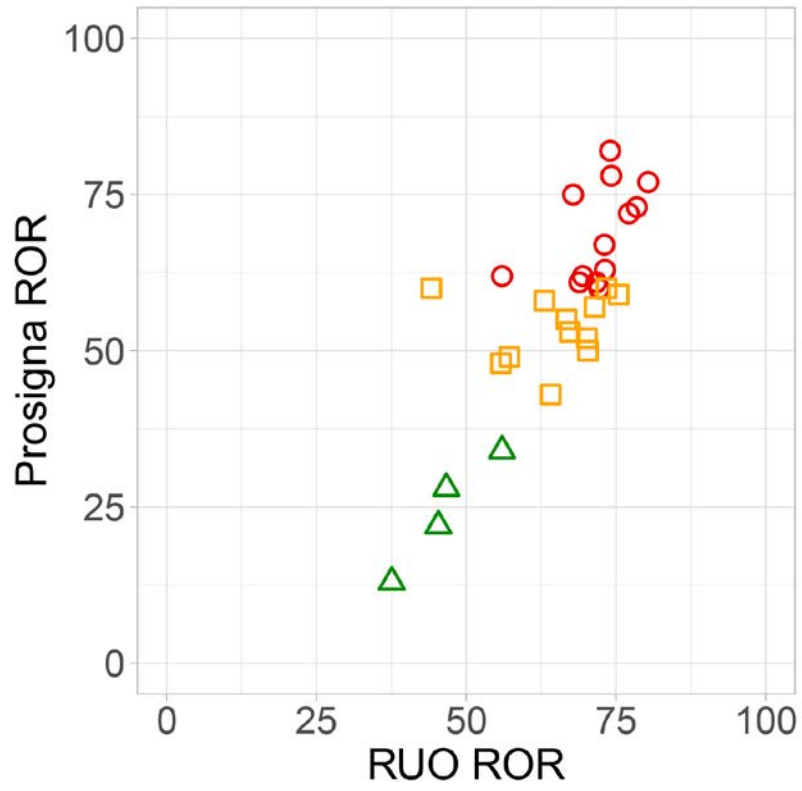


Supplemental Figure 8. Assessment of correlation between commercial and RUO ROR (a) in 7 (b) in 29 and (c) in 107 samples of the Spanish cohort. Patients are presented in low-risk group with green, in intermediate-risk group with orange and high-risk group with red as categorised by the commercial test. RUO: research use only

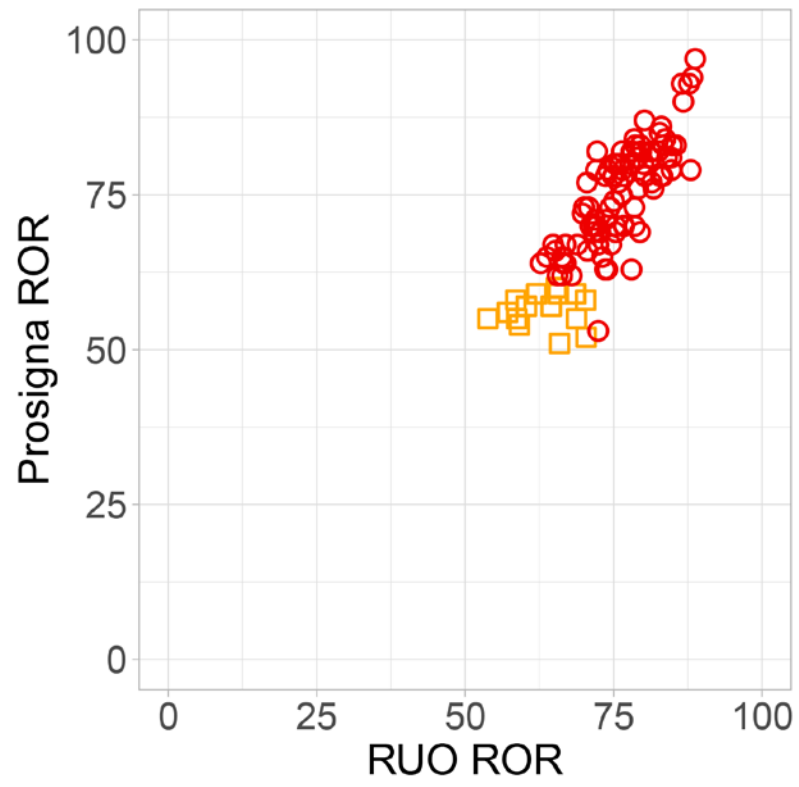
(a)



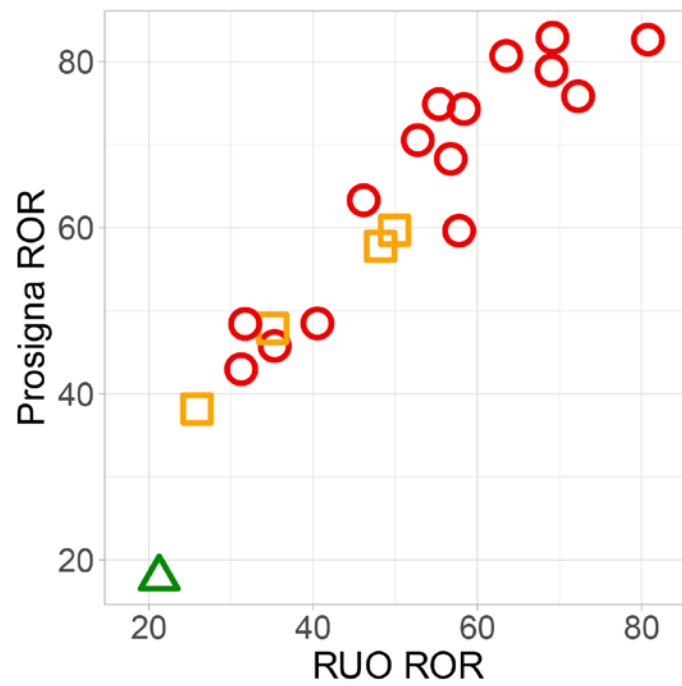
(b)



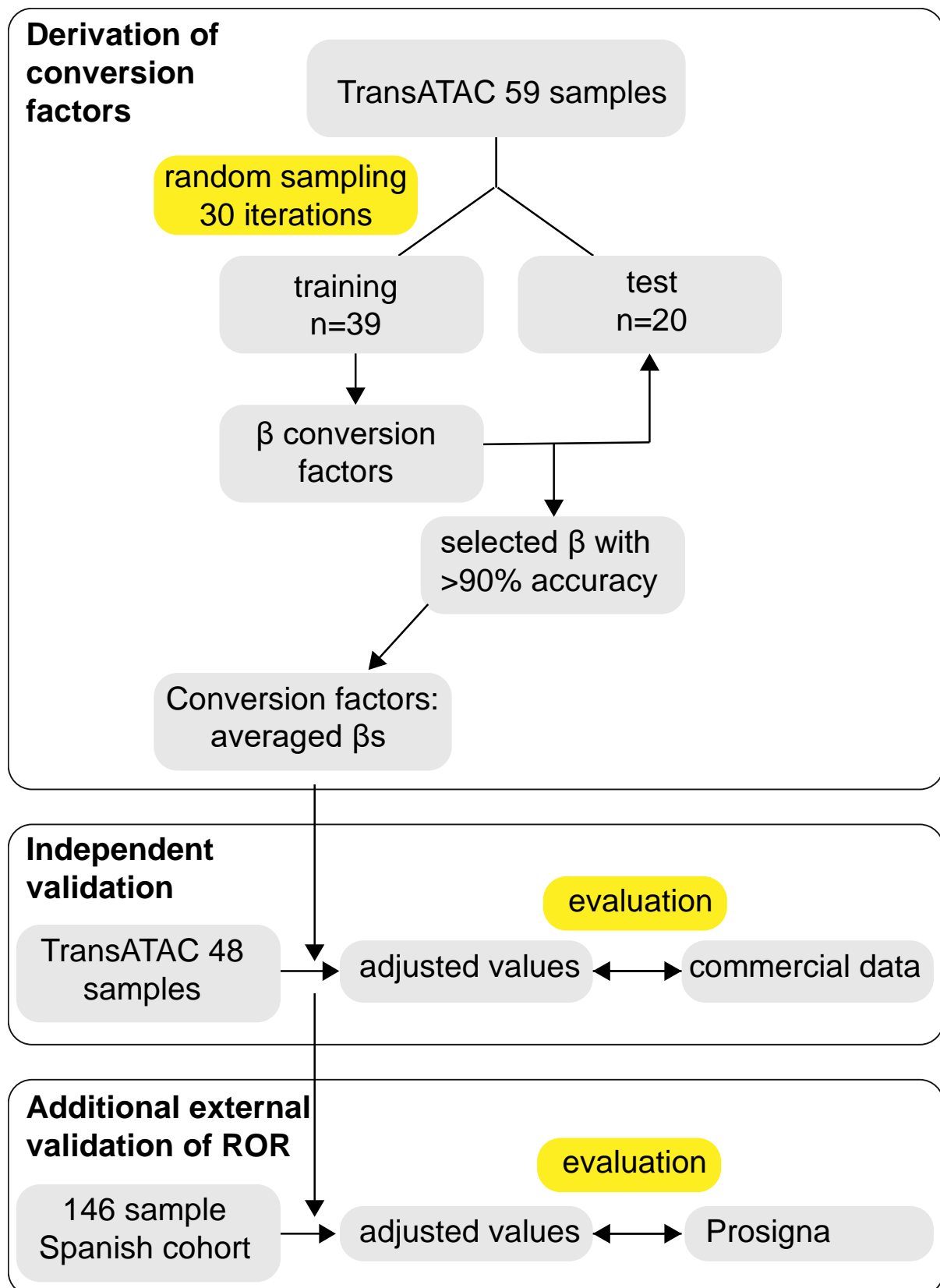
(c)



Supplemental Figure 9. Assessment of correlation between commercial and RUO ROR scores as single sample predictor (n=20). Patients are presented in low-risk group with green, in intermediate-risk group with orange and high-risk group with red as categorised by the commercial test. RUO: research use only



Supplemental Figure 10. Study workflow: computation and validation of conversion methodologies



Supplemental Table 1. Agreements between the RT-PCR and the adjusted NanoString gene expression levels for the RS in the validation set (n=48). ^a r_c : concordance correlation coefficient; ^b IQR: interquartile range; ^c LL: lower limit; ^d UL: upper limit; ^e Mean difference of the commercial RT-PCR and adjusted NanoString gene expression levels; ^f SD: standard deviation; ^g LOA: Limits of agreements

Gene	r_c^a	95% CI ^b		Mean difference ^e	SD ^f difference	95% LOA ^g	
		LL ^c	UL ^d			LL	UL
Proliferation							
<i>AURKA</i>	0.47	0.22	0.66	-0.01	0.65	-1.29	1.27
<i>BIRC5</i>	0.95	0.92	0.97	0.07	0.32	-0.56	0.69
<i>CCNB1</i>	0.92	0.86	0.95	0.02	0.29	-0.54	0.59
<i>MKI67</i>	0.86	0.78	0.91	0.28	0.37	-0.45	1.00
<i>MYBL2</i>	0.67	0.59	0.75	0.16	0.75	-1.31	1.63
Estrogen							
<i>BAG1</i>	0.96	0.94	0.98	-0.13	0.2	-0.51	0.26
<i>BCL2</i>	0.93	0.89	0.96	-0.09	0.42	-0.91	0.74
<i>PGR</i>	0.97	0.94	0.98	0.28	0.46	-0.62	1.18
<i>SCUBE2</i>	1.00	0.99	1.00	-0.08	0.17	-0.41	0.26
HER2							
<i>GRB7</i>	0.9	0.84	0.94	0.2	0.25	-0.29	0.69
<i>ERBB2</i>	0.95	0.92	0.97	0.06	0.25	-0.43	0.55
Invasion							
<i>CTSL2</i>	0.34	0.12	0.52	0.14	0.71	-1.25	1.52
<i>MMP11</i>	0.97	0.95	0.98	0.08	0.36	-0.64	0.79
Other							
<i>GSTM1</i>	0.55	0.38	0.69	-0.15	0.99	-2.09	1.79
<i>CD68</i>	0.91	0.85	0.95	0.01	0.24	-0.47	0.48
<i>BAG1</i>	0.96	0.94	0.98	-0.13	0.2	-0.51	0.26

Supplemental Table 2. Agreements between the RT-PCR and adjusted NanoString gene expression levels for the EP in the validation set (n=24). ^ar_c: concordance correlation coefficient; ^bIQR: interquartile range; ^cLL: lower limit; ^dUL: upper limit; ^eMean difference of the commercial RT-PCR and adjusted NanoString gene expression levels; ^fSD: standard deviation; ^gLOA: Limits of agreements

Gene	r _c ^a	95% CI ^b		Mean difference ^e	SD ^f difference.	95% LOA ^g	
		LL ^c	UL ^d			LL	UL
<i>AZGP1</i>	0.95	0.91	0.97	-0.25	0.31	-0.85	0.35
<i>BIRC5</i>	0.89	0.81	0.93	-0.07	0.57	-1.18	1.04
<i>DHCR7</i>	0.84	0.73	0.9	0.13	0.45	-0.75	1.02
<i>IL6ST</i>	0.94	0.89	0.96	-0.14	0.34	-0.81	0.54
<i>MGP</i>	0.92	0.87	0.95	-0.45	0.49	-1.41	0.5
<i>RBBP8</i>	0.95	0.92	0.97	-0.05	0.34	-0.71	0.61
<i>STC2</i>	0.96	0.92	0.97	-0.03	0.54	-1.1	1.03
<i>UBE2C</i>	0.91	0.88	0.94	0.06	0.4	-0.73	0.84

Supplemental Table 3. Classification of 48 validation set patients by the commercial and RUO RS scores based on two TAILORx-tested cut-points: (a) RS<16 vs RS≥16 and (b) RS<26 vs RS≥26

(a)

<u>Commercial RS</u> <u>(RT-PCR)</u>	<u>RUO RS (NanoString-derived) data</u>		<u>Total</u>
	<u><16</u>	<u>≥16</u>	
<u><16</u>	<u>21</u>	<u>3</u>	<u>24</u>
<u>≥16</u>	<u>1</u>	<u>23</u>	<u>24</u>
<u>Total</u>	<u>22</u>	<u>26</u>	<u>48</u>

(b)

<u>Commercial RS</u> <u>(RT-PCR)</u>	<u>RUO RS (NanoString-derived) data</u>		<u>Total</u>
	<u><26</u>	<u>≥26</u>	
<u><26</u>	<u>35</u>	<u>0</u>	<u>35</u>
<u>≥26</u>	<u>0</u>	<u>13</u>	<u>13</u>
<u>Total</u>	<u>35</u>	<u>13</u>	<u>48</u>

Supplemental Table 4. Breast cancer intrinsic subtype calls by commercial and RUO ROR methods for the TransATAC training and validation sets (n=107).

		RUO ROR				
		Luminal A	Luminal B	Basal-like	HER2-enriched	Total
Prosigna ROR	Luminal A	49	6	2	1	58
	Luminal B	2	29	2	10	43
	Basal-like	0	0	0	1	1
	HER2-enriched	0	0	0	5	5
Total		51	35	4	17	107

Supplemental Table 5. The custom NanoString gene expression panel used in the TransATAC training (n=59) and validation sets (n=48).

HUGO Gene	Accession	NSID	Target Sequence	R	R	E	Referenc
				S	O	P	e
					R		
					O		
					R		
ACTB	NM_001101.2	NM_001101.2:1685	CCAATTGAGATGTATGAAGGCTTTTGGTCTCCCTGGGAGTGGGTGGA GGCAGCCAGGGCTTACCTGTACACTGACTTGAGACCAGTTGAATAAAA GTGC	R	R		Referenc
ACTR3B	NM_001040135.1	NM_001040135.1:905	CCAGAAGAAGTTTGTaTATAGACGTTGGTTACGAAAGATTCTGGGACC TGAAATATTCTTTCACCCGGAGTTTGCCAACCCAGACTTTATGGAGTCC ATC		R		
ANLN	NM_018685.2	NM_018685.2:240	CGTGCCAGGCGAGAGAATCTTCAGAGAAAAATGGCTGAGAGGCCAC AGCAGCTCCAAGGTCTATGACTCATGCTAAGCGAGCTAGACAGCCACT TTCAG		R		
AURKA	NM_003600.2	NM_003600.2:405	AGTCCAGTTGGAGGTCCAAAACGTGTTCTCGTGAAGTCAAGTTCCT TGTCAGAATCCATTACCTGTAATAGTGCCAGGCTCAGCGGGTCTTG TGT	R			
AZGP1	NM_001185.2	NM_001185.2:123	GTTACTCTCTGACCTATATCTACACTGGGCTGTCCAAGCATGTTGAAGA CGTCCCCGCGTTTCAGGCCCTTGGCTCACTCAATGACCTCCAGTTCTT TAG			E	P
BAG1	NM_004323.3	NM_004323.3:540	CTTCATGTTACCTCCCAGCAGGGCAGCAGTGAACCAGTTGTCCAAGAC CTGGCCAGGTTGTTGAAGAGGTCATAGGGTTCCACAGTCTTTTCAG AAAC	R	R		
BCL2	NM_000633.2	NM_000633.2:1525	CCAAGCACCGCTTCGTGTGGCTCCACCTGGATGTTCTGTGCCTGTAAA CATAGATTCGCTTTCATGTTGTTGGCCGGATCACCATCTGAAGAGCA GACG	R	R		
BIRC5	NM_001168.2	NM_001168.2:1215	CCATTCTAAGTCATTGGGGAACGGGGTGAACCTTCAGGTGGATGAGGA GACAGAATAGAGTGATAGGAAGCGTCTGGCAGATACTCCTTTTGCAC TGCT	R	R	E	P
BLVR1A	NM_000712.3	NM_000712.3:485	TTCCTGAAAAAAGAAGTGGTGGGAAAGACCTGCTGAAAGGGTCGCTC CTCTTACAGCTGGCCCGTTGGAAGAAGAGCGGTTTGGCTTCCCTGCA TTCA		R		
CALM2	NM_001743.3	NM_001743.3:868	TGGAGTTGTAAGTCTGCGTGGACTATGGACAGTCAACAATATGTACTTA AAAGTTGCACTATTGCAAAACGGGTGTATTATCCAGGTACTCGTACACT AT			E	Referenc
CCNB1	NM_031966.2	NM_031966.2:710	GAGACAAGTGGAGGAAGAGCAAGCAGTCAGACCAAAATACCTACTGGG TCGGGAAGTCACTGGAAACATGAGAGCCATCCTAATTGACTGGCTAGT ACAG	R	R		
CCNE1	NM_001238.1	NM_001238.1:1155	GAGAAGTGTGCAAGTGGATGGTTCCATTTGCCATGGTTATAAGGGAG ACGGGGAGCTCAAACTGAAGCACTTCAGGGGCGTCGCTGATGAAGA TGAC		R		
CD68	NM_001251.2	NM_001251.2:1140	ACCGGTCCATCTTGTGCCTCTCATCATCGGCCTGATCCTTCTTGGCCT CCTCGCCCTGGTGCTTATTGCTTTCTGCATCATCCGGAGACGCCCATC CGC	R			
CDC20	NM_001255.1	NM_001255.1:915	CCCGAGTGGGCTCCCTAAGCTGGAACAGCTATATCCTGTCCAGTGGTT CACGTTCTGGCCACATCCACCACCATGATGTTCCGGGTAGCAGAACACC ATGT		R		
CDC6	NM_001254.3	NM_001254.3:1655	GGGGAAGTTATATGAAGCCTACAGTAAAGTCTGTGCAAAACAGCAGGT GGCGGCTGTGGACCAGTCAGAGTGTGTTGCTACTTTCAGGGCTTTGGA AGCC		R		
CDH3	NM_001793.3	NM_001793.3:2005	CCCTCGACCGTGAGGATGAGCAGTTTGTGAGGAACAACATCTATGAAG TCATGGTCTTGGCCATGGACAATGGAAGCCCTCCACCAGTGGCACGG GAAC		R		
CENPF	NM_016343.3	NM_016343.3:9260	AGAAAATCTTGAGAGTCCCAAACCAACAGCTGGTGGCAGCAGATC ACAAAAGGTCAAAGTTGCTCAGCGGAGCCCAGTAGATTCAGGCACCAT CCTC		R		
CEP55	NM_018131.3	NM_018131.3:570	GTAAGTACCGCATTGCTTGAACAGCTGGAAGAGACAACGAGAGAAGGAG AAAGGAGGGAGCAGGTGTTGAAAGCCTTATCTGAAGAGAAAGACGTAT TGAA		R		
CTSV	NM_001333.3	NM_001333.3:2820	GTGAAATTTAATCGAAAGGTGATCCATTGTGAATGCAATGGGAGGGAA GGGCATGTGGGACTGTGTATCCCAAAAACCCCTTTGATAGCCTATGTC CACA	R			
CXXC5	NM_016463.5	NM_016463.5:1630	AGCTGCCCTCTCCGTGCAATGTACTGCTCGTGTGGTCTCCAGCAAGG GATTCGGGCGAAGACAAACGGATGCACCCGCTTTTAGAACCAAAAATA TTCT		R		
DHCR7	NM_001360.2	NM_001360.2:780	CCCACCATCATCTTCGACAACCTGGATCCCACTGCTGTGGTGCGCCAAC ATCCTTGGCTATGCCGTCTCCACCTTCGCCATGGTCAAGGGCTACTTC TTCC			E	P

EGFR	NM_005 228.3	NM_0052 28.3:2760	GCAGCCAGGAACGTAAGTGGTGAAAACACCGCAGCATGTCAAGATCACA GATTTTGGGCTGGCCAAACTGCTGGGTGCGGAAGAGAAAAGAATACCAT GCAG					R O R		
ERB B2	NM_004 448.2	NM_0044 48.2:2405	TGAAGGTGCTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATCT GGATCCCTGATGGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGT TGAG	R S				R O R		
ESR 1	NM_000 125.2	NM_0001 25.2:1595	AGGAACCAGGGAAAATGTGTAGAGGGCATGGTGGAGATCTTCGACATG CTGCTGGCTACATCATCTCGTTCCGCATGATGAATCTGCAGGGAGAG GAGT	R S				R O R		
EXO 1	NM_006 027.3	NM_0060 27.3:820	TGGCCACAAAAGTAATTAAGCTGCCCGGTCTCAGGGGGTAGATTGCC TCGTGGCTCCCTATGAAGCTGATGCGCAGTTGGCCTATCTTAACAAAG CGGG					R O R		
FGF R4	NM_002 011.3	NM_0020 11.3:1002	CCCACATCCAGTGGCTGAAGCACATCGTCATCAACGGCAGCAGCTTCG GAGCCGACGGTTTCCCTATGTGCAAGTCTAAAGACTGCAGACATCA ATAG					R O R		
FOX A1	NM_004 496.2	NM_0044 96.2:280	TGGATGGTTGTATTGGGCAGGGTGGCTCCAGGATGTTAGGAACTGTGA AGATGGAAGGGCATGAAACCAGCGACTGGAACAGCTACTACGCAGAC ACGCA					R O R		
FOX C1	NM_001 453.1	NM_0014 53.1:1530	TTCGAGTCACAGAGGATCGGCTTGAACAACCTCCAGTGAACGGGAAT AGTAGCTGTCAAATGGCCTTCCCTTCCAGCCAGTCTCTGTACCGCAGC TCCG					R O R		
GAP DH	NM_002 046.3	NM_0020 46.3:972	CACTCCTCCACCTTTGACGCTGGGGCTGGCATTGCCCTCAACGACCAC TTTGTCAAGCTCATTTCTGGTATGACAACGAATTTGGCTACAGCAACA GGG	R S						Refere nce
GPR 160	NM_014 373.1	NM_0143 73.1:760	GGATTTCAAGTCTTGGCTTATGTTTTGGGAGACCCAGCCATCTACCAAAG CCTGAAGGCACAGAATGCTTATTCTCGTCACTGTCTTTCTATGTGACG AT					R O R		
GRB 7	NM_005 310.2	NM_0053 10.2:1010	GCCGATCTGGCTCTATTACTCCACCAAGGGCACCTCTAAGGATCCGA GGCACCTGCAGTACGTGGCAGATGTGAACGAGTCCAACGTGTACGTG GTGAC	R S				R O R		
GST M1	NM_000 561.2	NM_0005 61.2:335	GATTCGTGTGGACATTTTGGAGAACCAGACCATGGACAACCATATGCA GCTGGGCATGATCTGCTACAATCCAGAATTTGAGAACTGAAGCCAAA GTAC	R S						
GUS B	NM_000 181.1	NM_0001 81.1:1350	CGGTCGTGATGTGGTCTGTGGCCAACGAGCCTGCGTCCCACCTAGAAT CTGCTGGCTACTACTTGAAGATGGTGTGCTCACACCAAATCCTTGG ACCC	R S				R O R		Refere nce
IL6S T	NM_002 184.2	NM_0021 84.2:2505	CAAAACACTTCGAGCACTGTCCAGTATTCTACCGTGGTACACAGTGGC TACAGACACCAAGTCCGTGAGTCCAAGTCTTCAAGATCCGAGTCTA CCC						E P	
KIF2 C	NM_006 845.2	NM_0068 45.2:1020	GTTGTCTACAGTTTACAGCAAGGCCACTGGTACAGACAATCTTTGAA GGTGAAAAGCAACTGTTTTGCATATGGCCAGACAGGAAGTGGAAG ACAC					R O R		
KRT 14	NM_000 526.3	NM_0005 26.3:1365	GCAGTCATCCAGAGATGTGACCTCCTCCAGCCGCCAAATCCGCACCAA GGTCATGGATGTGCACGATGGCAAGGTGGTGTCCACCCACGAGCAGG TCCTT					R O R		
KRT 17	NM_000 422.1	NM_0004 22.1:1230	CTGACTCAGTACAAGAAAGAACCGGTGACCACCCGTGAGGTGCGTACC ATTGTGGAAGAGGTCCAGGATGGCAAGTTCATCTCTCCCGCGAGCA GGTCC					R O R		
KRT 5	NM_000 424.2	NM_0004 24.2:130	CTGGTTCTCTTGTCCACCAGGAACAAGCCACCATGTCTCGCCAGTCA AGTGTGTCTTCCGGAGCGGGGCGAGTCTGAGCTTACGACCCGCCTC TGCCA					R O R		
MAP T	NM_016 835.3	NM_0168 35.3:1425	GCCGGGTCCCTCAACTCAAAGCTCGCATGGTCAGTAAAAGCAAAGACG GGACTGGAAGCGATGACAAAAAGCCAAGACATCCACACGTTCTCTGT CTAA					R O R		
MD M2	NM_006 878.2	NM_0068 78.2:280	GGTGAGGAGCAGGCAAATGTGCAATACCAACATGTCTGTACTACTGA TGGTGTGTAACCACCTCACAGATTCCAGCTTCGGAACAAGAGACCCT GGTT					R O R		
MEL K	NM_014 791.2	NM_0147 91.2:365	AGAGACAGCCAACAAAATATTCATGGTTCTTGAAGTACTGCCCTGGAGG AGAGCTGTTGACTATATAATTTCCAGGATCGCTGTCAGAAGAGGA GACC					R O R		
MG P	NM_000 900.2	NM_0009 00.2:305	TCAATAGGGAAGCCTGTGATGACTACAGACTTTGCGAACGCTACGCCA TGGTTTATGGATACAATGCTGCCTATAATCGTACTTTCAGGAAGCGCCG AGG						E P	
MIA	NM_006 533.1	NM_0065 33.1:265	CCGGGGCCAAGTGGTGTATGTCTTCTCCAAGCTGAAGGGCCGTGGGC GGCTCTTCTGGGGAGGCAGCGTTCAGGGAGATTACTATGGAGATCTG GCTGCT					R O R		
MKI 67	NM_002 417.2	NM_0024 17.2:2005	GCTTCCAGCAGCAAATCTCAGACAGAGGTTCTAAGAGAGGAGAGAAA AGAGTGGCAACCTGCCTTCAAAGAGAGTGTCTATCAGCCGAAGTCAA CATG	R S				R O R		
MLP H	NM_024 101.4	NM_0241 01.4:1695	GAGGAAGTCAAACCTCCCGATATTTCTCCCTCGAGTGGCTGGGAAACT TGGCAAGAGACCAGAGGACCCAAATGCAGACCCTTCAAGTGAGGCCA AGGCA					R O R		

MM P11	NM_005 940.3	NM_0059 40.3:702	AGCAGCCAAGGCCCTGATGTCCGCTTCTACACCTTTGCTACCCACT GAGTCTCAGCCAGATGACTGCAGGGGCGTTCAACACCTATATGGCCA GCCC	R S	R O R		
MRP L19	NM_014 763.3	NM_0147 63.3:385	ACAGCTGACCCATATGCCAGTGGAAAAATCAGCCAGTTTCTGGGGATT TGCATTGAGAGATCAGGAAGAGGACTTGAGCTACTTTTCATCCTTAGG AATG		R O R		Referenc e
MYB L2	NM_002 466.2	NM_0024 66.2:675	GCAACCGCTGGGCCGAGATCGCCAAGATGTTGCCAGGGAGGACAGAC AATGCTGTGAAGAATCACTGGAACCTACCATCAAAGGAAGGTGGAC ACAGG	R S	R O R		
MYC	NM_002 467.3	NM_0024 67.3:1615	CACCGAGGAGAATGTCAAGAGGGCAACACACAACGTCTTGAGCGCC AGAGGAGGAACGAGCTAAAACGGAGCTTTTTTGCCTGCGTGACCAGA TCCCG		R O R		
NAT 1	NM_000 662.4	NM_0006 62.4:0	AGCACTTCCTCATAGACCTTGGATGTGGGAGGATTGCATTGAGTCTAGT TCCTGGTTGCCGGCTGAAATAACCTGAATTCAGCCAGGAAGAAGCAG CAA		R O R		
NDC 80	NM_006 101.1	NM_0061 01.1:90	AAAAGGTCATAAGCATGAAGCGCAGTTTCCAGCGGTGGTGCTG GCCGCTCTCCATGCAGGAGTTAAGATCCCAGGATGTAAATAACAAG GCCT		R O R		
NUF 2	NM_145 697.1	NM_1456 97.1:215	GCCTGGCGGTGTTTTGCTGCTCAGCGTGGGAGGAGCGGAAGA AACCCAGAGCCTGGGAGATTAACAGGAAACTTCCAAGATGGAACCTTG TCTTT		R O R		
OAZ 1	NM_004 152.2	NM_0041 52.2:313	GGTGGGCGAGGGAATAGTCAGAGGGATCACAATCTTTCAGCTAACTTA TTCTACTCCGATGATCGGCTGAATGTAACAGAGGAACTAACGTCCAAC GACA			E P	Referenc e
ORC 6	NM_014 321.2	NM_0143 21.2:580	GACTGTGTAAACAAGTAGAGAAGATTGGACAGCAGGTCGACAGAGAAC CTGGAGATGTAGCTACTCCACCACGGAAGAGAAAGAAGATAGTGGTTG AAGC		R O R		
PGR	NM_000 926.2	NM_0009 26.2:3165	GGGATGAAGCATCAGGCTGTCATTATGGTGTCTTACCTGTGGGAGCT GTAAGGTCTTTTAAAGAGGGCAATGGAAGGGCAGCACAACACTACTTAT GTGC	R S	R O R		
PHG DH	NM_006 623.2	NM_0066 23.2:505	GCGACGGCTTCGATGAAGGACGGCAAATGGGAGCGGAAGAAGTTCAT GGGAACAGAGCTGAATGGAAAGACCCTGGGAATTCTTGGCCTGGGCA GGATTG		R O R		
PSM C4	NM_006 503.2	NM_0065 03.2:300	CATCGGACAATTTCTGGAGGCTGTGGATCAGAATACAGCCATCGTGGG CTCTACCACAGGCTCAAATAATTATGTGCCATCCTGAGCACCATCGAT CGG		R O R		Referenc e
PTT G1	NM_004 219.2	NM_0042 19.2:202	CACCAGCCTTACCTAAAGCTACTAGAAAGGCTTTGGGAACTGTCAACA GAGCTACAGAAAAGTCTGTAAGACCAAGGGACCCTCAAACAAAAAC AGCC		R O R		
PUM 1	NM_001 020658. 1	NM_0010 20658.1:6 40	CTGGGGAACATCAGATCATTGATTTCCAGCCAATCATGGTGCAGAG AAGACCTGGTCAGAGTTTCCATGTGAACAGTGAGGTCAATTCTGTACTG TCC		R O R		Referenc e
RBB P8	NM_002 894.2	NM_0028 94.2:760	AATGATCAACAGCATCAAGCAGCTGAGCTTGAATGTGAGGAAGACGTT ATTCCAGATTCACCGATAACAGCCTTCTATTTTCTGGCGTTAACGGGC TAC			E P	
RPL 37A	NM_000 998.4	NM_0009 98.4:298	CTTCCGCTGTCACGGTAAAGTCCGCCATCAGAAGACTGAAGGAGTTGA AAGACCAGTAGACGCTCCTTACTCTTTGAGACATCACTGGCCTATAAT AAA			E P	Referenc e
RPL P0	NM_001 002.3	NM_0010 02.3:250	CGAAATGTTTCATTGTGGGAGCAGACAATGTGGGCTCCAAGCAGATGC AGCAGATCCGCATGTCCCTTCGCGGGAAGGCTGTGGTGCTGATGGGC AAGAA	R S	R O R		Referenc e
RR M2	NM_001 034.1	NM_0010 34.1:490	TTCTTTTGGACCGCCGAGGAGGTTGACCTCTCCAAGGACATTCAGCA CTGGGAATCCCTGAAACCCGAGGAGAGATATTTTATATCCCATGTTCTG GCT		R O R		
SCU BE2	NM_020 974.1	NM_0209 74.1:1835	CGTAAAGCCATCCGCACGCTCAGAAAGGCCGTCCACAGGGAGCAGTT TCACCTCCAGCTCTCAGGCATGAACCTCGACGTGGCTAAAAAGCCTCC CAGAA	R S			
SF3 A1	NM_005 877.4	NM_0058 77.4:1485	GATGATGAGGTGTACGCACCAGGTCTGGATATTGAGAGCAGCTTGAAG CAGTTGGCTGAGCGGCTACTGACATCTTCGGTGTAGAGGAAACAGCC ATTG		R O R		Referenc e
SFR P1	NM_003 012.3	NM_0030 12.3:1320	GTGGGTACACACACGCACTGCGCCTGTCAGTAGTGGACATTGTAATC CAGTCGGCTTGTCTTGCAGCATTCCCGCTCCCTCCCTCCATAGCCA CGCT		R O R		
SLC 39A 6	NM_012 319.2	NM_0123 19.2:1580	GATCGAACTGAAGGCTATTTACGAGCAGACTCACAAGAGCCCTCCAC TTTGATTCTCAGCAGCCTGCAGTCTTGAAGAAGAAGAGGTCATGATA GCTC		R O R		
STC 2	NM_003 714.2	NM_0037 14.2:2825	ATTTCTATGTGTAATTTCTGAGCATTGACTGTCTGGGCTGGGGGGGA CACTGTCCAAGGAGTGCCCTATGAGTTTATATTTTAAACCACTGCTT CA			E P	
TFR C	NM_003 234.1	NM_0032 34.1:1220	CAGTTTCCACCATCTCGGTCATCAGGATTGCCTAATATACCTGTCCAGA CAATCTCCAGAGCTGCTGCAGAAAAGCTGTTTGGGAATATGGAAGGAG ACT	R S	R O R		Referenc e

TME M45 B	NM_138 788.3	NM_1387 88.3:730	CTGGCTGCCCTCAGCATTGTGGCCGTCAACTATTCTTGTGTTACTGCC TTTTGACTCGGATGAAGAGACACGGAAGGGGAGAAATCATTGGAATTC AGA		R O R		
TYM S	NM_001 071.1	NM_0010 71.1:395	TGCTAAAGAGCTGTCTTCCAAGGGAGTGAAAATCTGGGATGCCAATGG ATCCCGAGACTTTTTGGACAGCCTGGGATTCTCCACCAGAGAAGAAGG GGAC		R O R		
UBE 2C	NM_007 019.2	NM_0070 19.2:445	GTCTGCCCTGTATGATGTCAGGACCATTCTGCTCTCCATCCAGAGCCTT CTAGGAGAACCCAACATTGATAGTCCCTTGAACACACATGCTGCCGAG CTC		R O R	E P	
UBE 2T	NM_014 176.1	NM_0141 76.1:50	GTGTCAGCTCAGTGCATCCCAGGCAGCTCTTAGTGTGGAGCAGTGAAC TGTGTGTGGTTCCTTCTACTTGGGGATCATGCAGAGAGCTTCACGTCT GAAG		R O R		

Supplemental Table 6. Normalised expression data of the 229 sample ERPosHER2Neg sample set for 46 ROR genes and 8 housekeeping genes.

(in separate Excel file)

Supplemental Table 7. Normalisation factors used to adjust expression values in order to calculate RUO ROR in TransATAC samples. These factors were calculated by scaling the 59 TransATAC training set samples to the 229 sample ER+/HER2- tumours (ERPosHER2Neg set) previously subjected to the Prosigna® assay.

Gene	Cohort median adjustment factors
ACTR3B	0.063
ANLN	-1.043
BAG1	0.325
BCL2	0.362
BLVRA	0.421
CCNE1	-0.78
CDC20	-0.604
CDC6	0.093
CDCA1	0.242
CDH3	-0.019
CENPF	-0.641
CEP55	-0.715
CXXC5	0.732
EGFR	0.471
ERBB2	1.034
ESR1	1.555
EXO1	-0.374

FGFR4	-0.98
FOXA1	-0.108
FOXC1	-0.027
GPR160	0.633
KIF2C	0.779
KNTC2	-0.2
KRT14	0.981
KRT17	1.715
KRT5	0.672
MAPT	0.831
MDM2	-0.167
MELK	-0.024
MIA	1.076
MKI67	0.013
MLPH	0.761
MMP11	0.404
MYC	-0.362
NAT1	1.066
ORC6L	-0.127
PGR	0.86
PHGDH	-0.099
PTTG1	-1.386
RRM2	-1.105
SFRP1	0.078
SLC39A6	0.821
TMEM45B	-0.082
TYMS	-0.619
UBE2C	-0.563
UBE2T	-0.023

Supplemental Table 8. Calibration factors to adjust for microarray derived centroids

	PAM50RUO calibration factor
ACTR3B	-3.0222214
ANLN	-3.9565307
BAG1	-1.485749
BCL2	-3.0901392
BIRC5	-2.5264471
BLVRA	-1.7121774
CCNB1	-2.6797027
CCNE1	-5.0101326
CDC20	-4.6649842
CDC6	-3.8592176
CDCA1	-6.285376
CDH3	-3.9795265
CENPF	-2.9930417
CEP55	-4.1826523
CXXC5	-1.4574313
EGFR	-5.3645631
ERBB2	-1.910135
ESR1	-1.3917915
EXO1	-4.8670732
FGFR4	-5.1261057
FOXA1	-1.0402642
FOXC1	-5.1657298
GPR160	-1.8332197
GRB7	-4.5871578
KIF2C	-6.0513213
KNTC2	-4.7378452
KRT14	-3.216056
KRT17	-4.1054272
KRT5	-4.8900259
MAPT	-3.994877

MDM2	-0.9628511
MELK	-4.6168289
MIA	-7.7403848
MKI67	-4.0156607
MLPH	-1.1954999
MMP11	-1.3008179
MYBL2	-4.7857388
MYC	-0.8680514
NAT1	-3.3472933
ORC6L	-5.2980294
PGR	-6.014928
PHGDH	-3.1518718
PTTG1	-3.2230568
RRM2	-2.4655345
SFRP1	-3.3553648
SLC39A6	-0.6547639
TMEM45B	-6.9167267
TYMS	-3.0764834
UBE2C	-2.7563288
UBE2T	-4.5865595

Supplemental Table 9. Centroids representing the Basal-like, HER2-enriched, Luminal A, Luminal B and Normal-like subtypes.

	Basal	Her2	LumA	LumB	Normal
ACTR3B	0.71833189	-0.4816657	0.00998107	-0.1905513	0.46572287
ANLN	0.5373723	0.26693161	-0.5792457	0.09880418	-0.8369396
BAG1	-0.5745069	-0.4760729	0.75822116	-0.4054586	0.31655297
BCL2	-0.1187604	-0.157914	0.28748744	-0.4413395	0.53397887
BLVRA	-0.6426775	0.33533604	0.04204202	0.69120496	-0.1634128

CCNE1	0.56027103	0.06687223	-0.4302912	-0.0166614	-0.2554761
CDC20	0.39969524	0.00835552	-0.469044	-0.0704125	-0.0455048
CDC6	0.15941828	0.58900682	-0.6128243	0.51089597	-0.5957522
CDCA1	0.47240017	-0.0238192	-0.7125208	0.58962688	-0.3705334
CDH3	0.50836201	0.21088969	-0.5136493	-1.4191344	0.75792062
CENPF	0.48297629	-0.0292662	-0.5437402	0.27822856	-0.0705831
CEP55	0.56774889	0.27638102	-0.7467217	0.46001576	-1.1623742
CXXC5	-0.9203858	-0.2415506	0.46741157	0.32133502	0.05090144
EGFR	-0.0304168	-0.0963826	0.00916296	-0.4124013	0.34163708
ERBB2	-0.808354	1.75984423	0.60819126	0.15965187	-0.8702385
ESR1	-2.7465131	-1.5131113	2.16141188	1.60589991	-0.4182823
EXO1	0.42809036	0.04929719	-0.5674745	0.14124128	-0.4507805
FGFR4	-0.271238	0.82177815	0.17081193	-0.247036	0.85747278
FOXA1	-2.6269467	0.02282715	1.01745742	0.3607578	-0.7828121
FOXC1	1.49045147	-0.9471742	-0.174958	-1.564855	1.11154786
GPR160	-1.0549747	0.58319483	0.68548997	0.7144076	-0.4235685
KIF2C	0.20357258	-0.165102	-0.5053947	-0.1828907	-0.3900145
KNTC2	0.60035617	0.04254679	-0.588221	0.38670684	-1.0696289
KRT14	0.09682672	-0.4436461	0.36837594	-0.639447	1.73568631
KRT17	0.48256553	-0.3378371	0.01420986	-1.4637429	1.75959844
KRT5	0.50664042	-0.4282618	0.21532007	-0.9116073	1.7851169
MAPT	-0.4258293	-0.3575065	0.70062272	-0.1903406	0.1178285
MDM2	-0.2513662	-0.1067287	0.14195743	-0.133779	0.27421401
MELK	0.52303387	0.19801312	-0.5820881	0.44793463	-0.7437647
MIA	1.57827637	-0.9048986	-0.1652586	-1.4229263	2.03885956
MKI67	0.47653745	0.06566236	-0.5018716	-0.1452179	-0.1660041
MLPH	-0.3399725	-0.1952287	0.33930442	-0.4561499	0.75075837
MMP11	-0.5560377	0.50675876	-0.0062551	0.33419931	-2.3269851
MYC	0.17876381	-1.0468328	-0.0908308	0.0152644	1.0291762
NAT1	-0.9368489	-0.0899885	2.92278679	0.47078804	-0.3632738
ORC6L	0.2163048	0.20440245	-0.3522207	0.11062765	-0.2558795
PGR	-0.4291334	-0.2794099	0.445785	-0.4488398	0.12601148
PHGDH	0.63451887	-0.1866259	-0.3986822	-1.0301393	0.66043775

PTTG1	0.26413189	0.0558099	-0.6344683	0.24972528	-0.5497813
RRM2	0.15620468	0.68272489	-0.9507602	0.35066384	-1.1210549
SFRP1	0.98798846	-1.0482027	0.13156636	-1.7204583	2.43628867
SLC39A6	-1.0511251	-0.6957365	2.06145908	1.65330302	0.11688969
TMEM45B	-1.1094582	1.33063617	0.44624205	0.37568823	0.03620891
TYMS	0.4498009	0.0529449	-0.6446021	0.49260652	-0.7269895
UBE2C	0.21853415	0.0610806	-0.5198184	0.29279931	-0.4088947
UBE2T	0.3899089	0.28453681	-0.5392594	0.73895213	-0.952381