

**Table S1. Primer and probe sequences for all 21 genes in the 21-gene RS assay.**

Gene Name	Primer/Probe Name	Oligo Sequence
ACTB	S0034/B-acti.f2	CAGCAGATGTGGATCAGCAAG
ACTB	S4730/B-acti.p2	AGGAGTATGACGAGTCCGGCCCC
ACTB	S0036/B-acti.r2	GCATTTGCGGTGGACGAT
BAG1	S1386/BAG1.f2	CGTTGTCAGCACTTGGAAATAACA
BAG1	S1387/BAG1.r2	GTTCAACCTCTTCTGTGGACTGT
BAG1	S4731/BAG1.p2	CCCAATTAACATGACCCGGCAACCAT
Bcl2	S0043/Bcl2.f2	CAGATGGACCTAGTACCCACTGAGA
Bcl2	S4732/Bcl2.p2	TTCCACGCCGAAGGACAGCGAT
Bcl2	S0045/Bcl2.r2	CCTATGATTTAAGGGCATTTTTCC
CCNB1	S1720/CCNB1.f2	TTCAGGTTGTTGCAGGAGAC
CCNB1	S1721/CCNB1.r2	CATCTTCTTGGGCACACAAT
CCNB1	S4733/CCNB1.p2	TGTCTCCATTATTGATCGGTTTCATGCA
CD68	S0067/CD68.f2	TGGTTCACAGCCCTGTGT
CD68	S4734/CD68.p2	CTCCAAGCCCAGATTCAGATTCGAGTCA
CD68	S0069/CD68.r2	CTCCTCCACCCTGGGTTGT
CEGP1	S1494/CEGP1.f2	TGACAATCAGCACACCTGCAT
CEGP1	S1495/CEGP1.r2	TGTGACTACAGCCGTGATCCTTA
CEGP1	S4735/CEGP1.p2	CAGGCCCTCTTCCGAGCGGT
CTSL2	S4354/CTSL2.f1	TGTCTCACTGAGCGAGCAGAA
CTSL2	S4355/CTSL2.r1	ACCATTGCAGCCCTGATTG
CTSL2	S4356/CTSL2.p1	CTTGAGGACGCGAACAGTCCACCA
ER	S0115/EstR1.f1	CGTGGTGCCCTCTATGAC
ER	S4737/EstR1.p1	CTGGAGATGCTGGACGCCC
ER	S0117/EstR1.r1	GGCTAGTGGGCGCATGTAG
GAPD	S4738/GAPDH.p1	CCGTTCTCAGCCTTGACGGTGC
GAPD	S0374/GAPDH.f1	ATCCACCCATGGCAAATTC
GAPD	S0375/GAPDH.r1	GATGGGATTTCCATTGATGACA

GRB7	S0130/GRB7.f2	CCATCTGCATCCATCTTGTT
GRB7	S4726/GRB7.p2	CTCCCCACCCTTGAGAAGTGCCT
GRB7	S0132/GRB7.r2	GGCCACCAGGGTATTATCTG
GSTM1	S2026/GSTM1.r1	GGCCCAGCTTGAATTTTTCA
GSTM1	S2027/GSTM1.f1	AAGCTATGAGGAAAAGAAGTACACGAT
GSTM1	S4739/GSTM1.p1	TCAGCCACTGGCTTCTGTCATAATCAGGAG
GUSB	S0139/GUS.f1	CCCACTCAGTAGCCAAGTCA
GUSB	S4740/GUS.p1	TCAAGTAAACGGGCTGTTTTCCAAACA
GUSB	S0141/GUS.r1	CACGCAGGTGGTATCAGTCT
HER2	S0142/HER2.f3	CGGTGTGAGAAGTGCAGCAA
HER2	S4729/HER2.p3	CCAGACCATAGCACACTCGGGCAC
HER2	S0144/HER2.r3	CCTCTCGCAAGTGCTCCAT
Ki67	S4741/Ki-67.p2	CCACTTGTCGAACCACCGCTCGT
Ki67	S0436/Ki-67.f2	CGGACTTTGGGTGCGACTT
Ki67	S0437/Ki-67.r2	TTACAACCTCTTCCACTGGGACGAT
MYBL2	S3270/MYBL2.f1	GCCGAGATCGCCAAGATG
MYBL2	S3271/MYBL2.r1	CTTTTGATGGTAGAGTTCCAGTGATTC
MYBL2	S4742/MYBL2.p1	CAGCATTGTCTGTCCTCCCTGGCA
PR	S1336/PR.f6	GCATCAGGCTGTCATTATGG
PR	S1337/PR.r6	AGTAGTTGTGCTGCCCTTCC
PR	S4743/PR.p6	TGTCCTTACCTGTGGGAGCTGTAAGGTC
RPLP0	S0256/RPLP0.f2	CCATTCTATCATCAACGGGTACAA
RPLP0	S4744/RPLP0.p2	TCTCCACAGACAAGGCCAGGACTCG
RPLP0	S0258/RPLP0.r2	TCAGCAAGTGGGAAGGTGTAATC
STK15	S0794/STK15.f2	CATCTTCCAGGAGGACCACT
STK15	S0795/STK15.r2	TCCGACCTTCAATCATTCA
STK15	S4745/STK15.p2	CTCTGTGGCACCCCTGGACTACCTG
STMY3	S2067/STMY3.f3	CCTGGAGGCTGCAACATAACC
STMY3	S2068/STMY3.r3	TACAATGGCTTTGGAGGATAGCA

STMY3	S4746/STMY3.p3	ATCCTCCTGAAGCCCTTTTCGCAGC
SURV	S0259/SURV.f2	TGTTTTGATTCCCGGGCTTA
SURV	S4747/SURV.p2	TGCCTTCTTCCTCCCTCACTTCTCACCT
SURV	S0261/SURV.r2	CAAAGCTGTCAGCTCTAGCAAAG
TFRC	S1352/TFRC.f3	GCCAACTGCTTTCATTTGTG
TFRC	S1353/TFRC.r3	ACTCAGGCCCATTTCTTTA
TFRC	S4748/TFRC.p3	AGGGATCTGAACCAATACAGAGCAGACA

Abbreviation: RS = recurrence score

**Table S2. Patient clinico-pathologic characteristics of mucinous tumors by RS groups**

	Low	Intermediate	High	P value
<b>Age (years)</b>				<b>0.012</b>
<50	2 (18.18%)	11 (52.38%)	3 (100.00%)	
≥50	9 (81.82%)	10 (47.62%)	0 (0.00%)	
<b>Operation type</b>				<b>0.081</b>
Mastectomy	8 (72.73%)	10 (47.62%)	0 (0.00%)	
BCS	3 (27.27%)	11 (52.38%)	3 (100.00%)	
<b>Tumor size stage</b>				<b>0.799</b>
T <sub>1</sub>	6 (54.55%)	10 (47.62%)	2 (66.67%)	
T <sub>2</sub>	5 (45.45%)	11 (52.38%)	1 (33.33%)	
<b>Nuclear grade</b>				<b>0.724</b>
Low	9 (18.18%)	19 (90.48%)	3 (100.00%)	
Intermediate	2 (81.82%)	2 (9.52%)	0 (0.00%)	
<b>Ki-67</b>				<b>0.287</b>
≤14	7 (63.64%)	16 (76.19%)	1 (33.33%)	
>14	4 (36.36%)	5 (23.81%)	2 (66.67%)	
<b>PR</b>				<b>0.596</b>
<20%	5 (45.45%)	7 (33.33%)	2 (66.67%)	
≥20%	6 (54.55%)	14 (66.67%)	1 (33.33%)	
<b>Molecular Subtype</b>				<b>0.044</b>
Luminal A	3 (27.27%)	12 (57.14%)	0 (0.00%)	
Luminal B	8 (72.73%)	9 (42.86%)	3 (100.00%)	
<b>Variant</b>				<b>0.678</b>
Hypocellular	5 (45.45%)	13 (61.90%)	2 (66.67%)	
Hypercellular	6 (54.55%)	8 (38.10%)	1 (33.33%)	

Abbreviation: BCS = Breast conserving surgery, PR = Progesterone receptor.

**Table S3. Difference of genes expression levels between PMBC and IDC**

Groups and Genes		PMBC	IDC	P value
		$\Delta$ CT $\pm$ SD	$\Delta$ CT $\pm$ SD	
Her2 Group	GRB7	-3.85 $\pm$ 0.82	-3.74 $\pm$ 0.96	0.575
	HER2	-2.79 $\pm$ 1.17	-2.10 $\pm$ 0.99	0.002
ER Group	ER	-0.60 $\pm$ 1.13	-0.54 $\pm$ 1.12	0.822
	PR	-2.01 $\pm$ 1.44	-2.41 $\pm$ 1.99	0.295
	Bcl2	-2.18 $\pm$ 1.12	-2.34 $\pm$ 0.71	0.382
	CEGP1	-2.57 $\pm$ 1.71	-2.96 $\pm$ 1.69	0.270
Proliferation Group	CCNB1	-3.48 $\pm$ 0.84	-3.46 $\pm$ 0.93	0.904
	Ki67	-5.19 $\pm$ 0.98	-4.87 $\pm$ 0.96	0.120
	MYBL2	-5.92 $\pm$ 0.73	-5.72 $\pm$ 0.99	0.308
	STK15	-4.14 $\pm$ 0.98	-3.62 $\pm$ 1.15	0.025
	SURV	-6.18 $\pm$ 0.94	-6.03 $\pm$ 1.00	0.476
Invasion Group	CTSL2	-5.21 $\pm$ 0.88	-5.01 $\pm$ 1.01	0.339
	STMY3	-2.08 $\pm$ 1.18	-1.23 $\pm$ 1.10	<0.001
Other Group	GSTM1	-1.67 $\pm$ 0.72	-1.48 $\pm$ 0.73	0.214
	CD68	-3.74 $\pm$ 1.10	-3.56 $\pm$ 0.96	0.414
	BAG1	-1.65 $\pm$ 1.02	-2.25 $\pm$ 0.75	0.001

Abbreviation: PMBC=Pure mucinous breast cancer, IDC= Invasive ductal carcinoma,  
CT= Threshold cycle, SD= Standard deviation