Supplementary Table 1: Patient characteristics

Patient and Tumor characteristics			
	Analysis population		**Total target population (N=931)**
	No (N=550)	**Yes (N=381)**	
	N (%)	**N (%)**	**N (%)**
Age at diagnosis (years)			
<= 40	8 (1.5)	5 (1.3)	13 (1.4)
41 - 50	35 (6.4)	31 (8.1)	66 (7.1)
51 - 65	179 (32.5)	116 (30.4)	295 (31.7)
66 - 75	159 (28.9)	127 (33.3)	286 (30.7)
> 75	169 (30.7)	102 (26.8)	271 (29.1)
Age at diagnosis (years)			
Median	68.6	68.1	68.3
Range	25.1 - 98.7	31.6 - 95.8	25.1 - 98.7
N obs	550	381	931
M status*			
M0	550 (100.0)	381 (100.0)	931 (100.0)
LN status (path., clin. if path. is missing)			
N0	331 (60.2)	200 (52.5)	531 (57.0)
N1	141 (25.6)	132 (34.6)	273 (29.3)
N2	22 (4.0)	26 (6.8)	48 (5.2)
N3	12 (2.2)	12 (3.1)	24 (2.6)
Nx	44 (8.0)	11 (2.9)	55 (5.9)
T status			
T1	276 (50.2)	180 (47.2)	456 (49.0)
T2	189 (34.4)	160 (42.0)	349 (37.5)
T3	8 (1.5)	10 (2.6)	18 (1.9)
T4	74 (13.5)	31 (8.1)	105 (11.3)
Tx	3 (0.5)	0 (0.0)	3 (0.3)

Supplementary Table 2: Distribution of risk scores by each test.

(n = 381)*	Oncotype Dx-trained	Prosigna-trained**	IHC4-RNA	MammaPrint-trained	GGI-like risk	Risk-95 gene
Low	129 (33.9)	39 (9.4)	109 (28.6)	204 (53.5)	139 (36.5)	180 (47.2)
Intermediate	146 (38.3)	152 (39.9)	212 (55.6)	-	-	-
High	106 (27.8)	174 (45.7)	60 (15.7)	177 (46.5)	242 (63.5)	201 (52.8)

*19 missing values for Prosigna-trained, **Prosigna-trained uses the trained ROR-PT score, including tumour size.

Supplementary Table 3: Cross Tabs :Oncotype Dx-trained and Prosigna-trained

Oncotype Dx-trained vs Prosigna-trained					
	Prosigna_PT-trained				Final sample
N (% of 381)	High	Int.	Low	Missing	
Oncotype Dx-trained					
High	81 (21.3)	23 (6.0)	2 (0.5)	-	106
Intermediate	68 (17.8)	58 (15.2)	11 (2.9)	9 (2.4)	146
Low	25 (6.6)	71 (18.6)	23 (6.0)	10 (2.6)	129
Final sample	174	152	36	19	381

Supplementary Table 4: Oncotype Dx-trained and IHC4-RNA

Oncotype Dx-trained vs IHC4-RNA				
	IHC4-RNA			Total (N=381)
N (% of 381)	High	Int.	Low	
Oncotype Dx-trained				
High	52 (13.6)	54 (14.2)	-	106
Intermediate	8 (2.1)	116 (30.4)	22 (5.8)	146
Low	-	42 (11.0)	87 (22.8)	129
Final sample	60	212	109	381

Supplementary Table 5: Prosigna-trained and IHC4-RNA

N (% of 381)	IHC4-RNA			Final sample
	High	**Int.**	**Low**	
Prosigna_PT-trained				
High	47 (12.3)	105 (27.6)	22 (5.8)	174
Intermediate	11 (2.9)	79 (20.7)	62 (16.3)	152
Low	2 (0.5)	14 (3.7)	20 (5.8)	36
Missing	-	14 (3.7)	5 (1.3)	19
Final sample	60	212	109	381

Supplementary Table 6: Oncotype Dx-trained and MammaPrint-trained

N (% of 381)	MammaPrint-trained		Final sample
	High	**Low**	
Oncotype Dx-trained			
High	90 (23.6)	16 (4.2)	106
Intermediate	75 (19.7)	71 (18.6)	146
Low	12 (3.1)	117 (30.7)	129
Final sample	177	204	381

Supplementary Table 7: Prosigna-trained and MammaPrint-trained

N (% of 381)	MammaPrint-trained		Final sample
	High	**Low**	
Prosigna_PT-trained			
High	130 (34.1)	44 (11.5)	174
Intermediate	39 (10.2)	113 (29.7)	152
Low	4 (1.0)	32 (8.4)	36
Missing	4 (1.0)	15 (3.9)	19
Final sample	177	204	381

Supplementary Table 8: IHC4-RNA and MammaPrint-like

N (% of 381)	MammaPrint-trained		Final sample
	High	**Low**	
IHC4-RNA			
High	52 (13.6)	8 (2.1)	60
Intermediate	109 (28.6)	103 (27.0)	212
Low	16 (4.2)	93 (24.4)	109
Final sample	177	204	381

IHC4-RNA vs MammaPrint-trained

Supplementary Table 9: MammaPrint-trained and GG-like risk

N (% of 381)	GGI risk		Final sample
	High	**Low**	
MammaPrint-trained			
High	162 (42.5)	15 (3.9)	177
Low	80 (21.0)	124 (32.5)	204
Final sample	242	139	381

MammaPrint-trained vs GGI-like risk

Supplementary Table 10 MammaPrint-trained and Risk-95 gene

N (% of 381)	Risk-95 gene		Final sample
	High	**Low**	
MammaPrint-trained			
High	142 (37.3)	35 (9.2)	177
Low	59 (15.5)	145 (38.1)	204
Final sample	201	180	381

MammaPrint-trained vs Risk-95 gene

Supplementary Table 11 Oncotype Dx-trained and GGI-like risk

Oncotype Dx-trained vs GGI-like risk			
N (% of 381)	**GGI risk**		**Final sample**
	High	**Low**	
Oncotype Dx			
High	102 (26.8)	4 (1.0)	106
Intermediate	109 (28.6)	37 (9.7)	146
Low	31 (8.1)	98 (25.7)	129
Final sample	242	139	381

Supplementary Table 12: Prosigna-like and GGI risk

Prosigna-trained vs GGI risk			
	GGI risk		**Final sample**
N (% of 381)	**High**	**Low**	
Prosigna_PT			
High	163 (42.8)	11 (2.9)	174
Intermediate	64 (16.8)	88 (23.1)	152
Low	4 (1.0)	32 (8.4)	36
Missing	11 (2.9)	8 (2.1)	19
Final sample	242	139	381

Supplementary Table 13 IHC4-RNA and GGI risk

IHC4-RNA vs GGI risk			
	GGI risk		**Final sample**
N (% of 381)	**High**	**Low**	
IHC4-RNA			
High	57 (15.0)	3 (0.8)	60
Intermediate	148 (38.8)	64 (16.8)	212
Low	37 (9.7)	72 (18.9)	109
Final sample	242	139	381

Supplementary Table 14: Oncotype Dx and Risk-95 gene

N (% of 381)	Risk-95 gene		Final sample
	High	Low	
Oncotype Dx			
High	91 (23.9)	15 (3.9)	106
Intermediate	81 (21.3)	65 (17.1)	146
Low	29 (7.6)	100 (26.2)	129
Final sample	201	180	381

Oncotype Dx vs Risk-95 gene

Supplementary Table 15: Prosigna-trained and Risk-95 gene

N (% of 381)	Risk-95 gene		Final sample
	High	Low	
Prosigna_PT			
High	139 (36.5)	35 (9.2)	174
Intermediate	50 (13.1)	102 (26.8)	152
Low	8 (2.1)	28 (7.3)	36
Missing	4 (1.0)	15 (3.9)	19
Final sample	201	180	381

Prosigna-trained vs Risk-95 gene

Supplementary Table 16: IHC4-RNA and Risk-95 gene

N (% of 381)	Risk-95 gene		Final sample
	High	Low	
IHC4-RNA			
High	52 (13.6)	8 (2.1)	60
Intermediate	120 (31.5)	92 (24.1)	212
Low	29 (7.6)	80 (21.0)	109
Final sample	201	180	381

IHC4-RNA vs Risk-95 gene

Supplementary Figure 1:

Male breast cancer cohort
N= 1822

N=317 samples with no tissue
N=22 samples ineligible

Main analysis population
N= 1483

N=554 samples ineligible (ie. ER-ve/M1 etc)

Clinical eligibility criteria
(M0, ER+, HER2-)
N= 931

N=232 samples with missing data

Clinical outcome of RFS available
N= 699

Patients with sufficient sample material available
N= 389

Patients with samples passing quality control
N= 381

NanoString analysis population
N= 381

Supplementary Figure 2: IHC4-RNA:


TIME TO RELAPSE
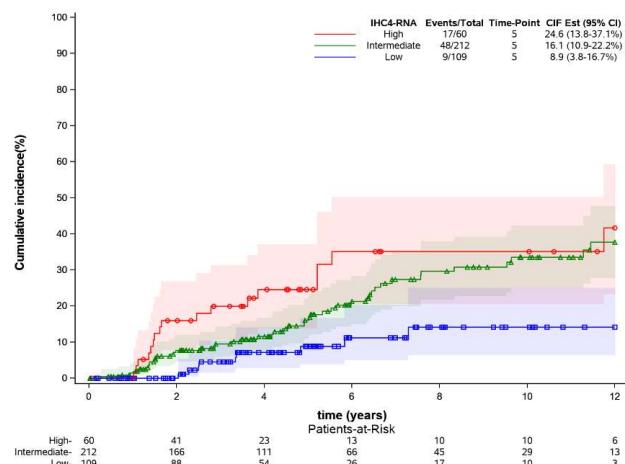
TIME TO DISTANT RELAPSE
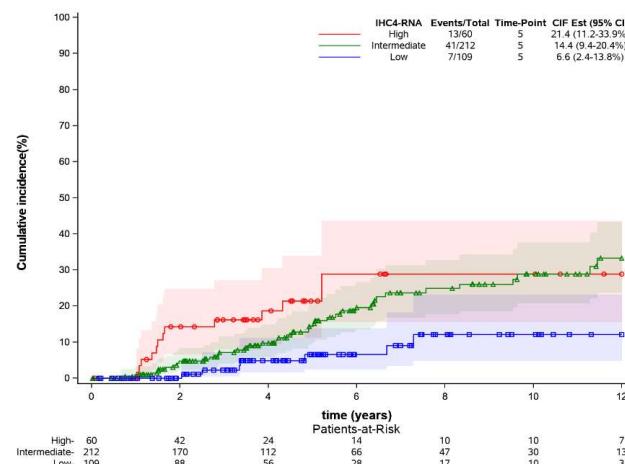
BREAST CANCER SPECIFIC SURVIVAL
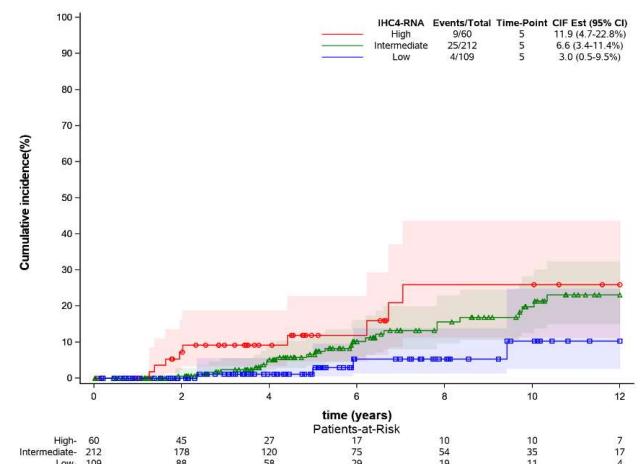
Supplementary Figure 3: MammaPrint-Trained:

TIME TO RELAPSE

Mammaprint-like	Events/Total	Time-Point	CIF Est (95% CI)
High	43/177	5	21.9 (15.3-29.4%)
Low	31/204	5	10.0 (5.9-15.4%)

TIME TO DISTANT RELAPSE

Mammaprint-like	Events/Total	Time-Point	CIF Est (95% CI)
High	37/177	5	20.7 (14.1-28.3%)
Low	24/204	5	7.2 (3.8-12.2%)

BREAST CANCER SPECIFIC SURVIVAL

Mammaprint-like	Events/Total	Time-Point	CIF Est (95% CI)
High	25/177	5	12.1 (6.9-18.7%)
Low	13/204	5	2.1 (0.6-5.6%)
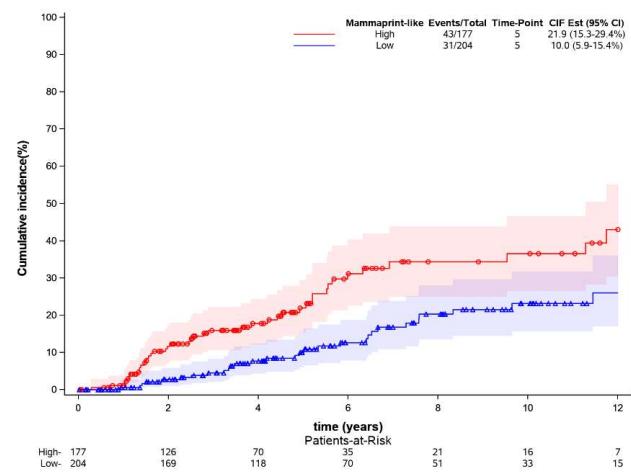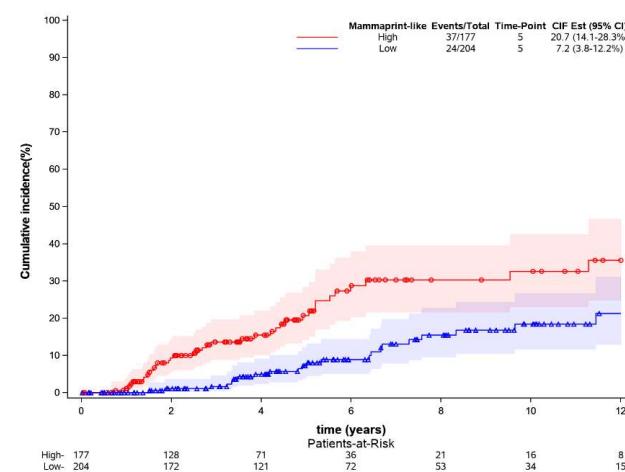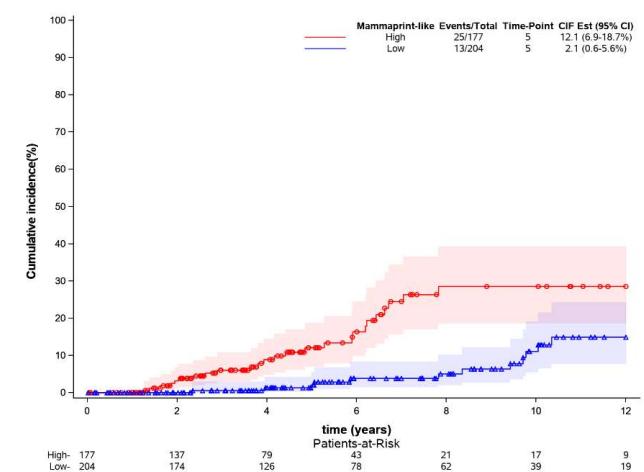
# Supplementary Figure 4: 95 Gene-Trained:


TIME TO RELAPSE   TIME TO DISTANT RELAPSE   BREAST CANCER SPECIFIC SURVIVAL
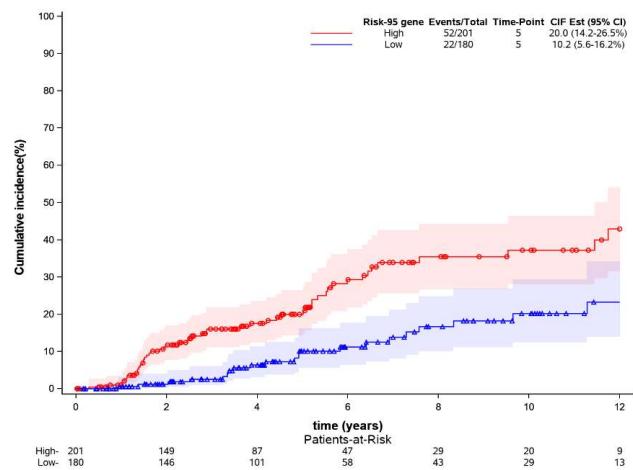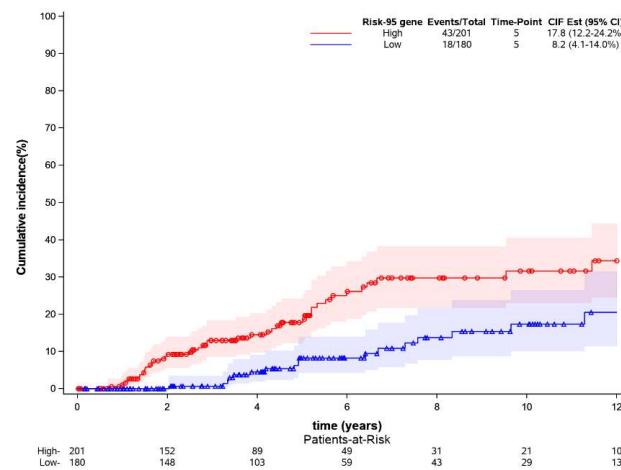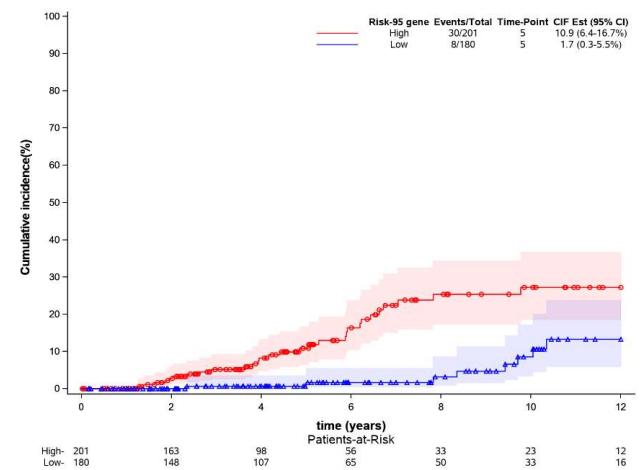
Supplementary Figure 5: GGI-like:

TIME TO RELAPSE

GGI risk	Events/Total	Time-Point	CIF Est (95% CI)
High	59/242	5	20.5 (15.0-26.6%)
Low	15/139	5	6.7 (2.9-12.6%)

TIME TO DISTANT RELAPSE

GGI risk	Events/Total	Time-Point	CIF Est (95% CI)
High	50/242	5	18.7 (13.3-24.8%)
Low	11/139	5	4.1 (1.3-9.4%)

BREAST CANCER SPECIFIC SURVIVAL

| GGI risk	Events/Total	Time-Point	CIF Est (95% CI)
High	34/242	5	9.8 (5.8-14.9%)
Low	4/139	5	0.9 (0.1-4.5%)
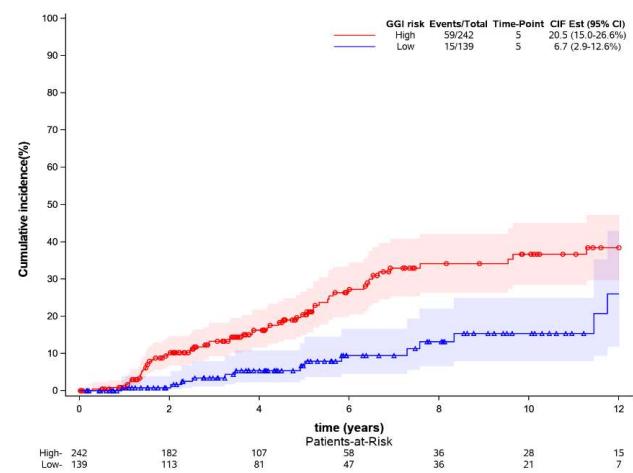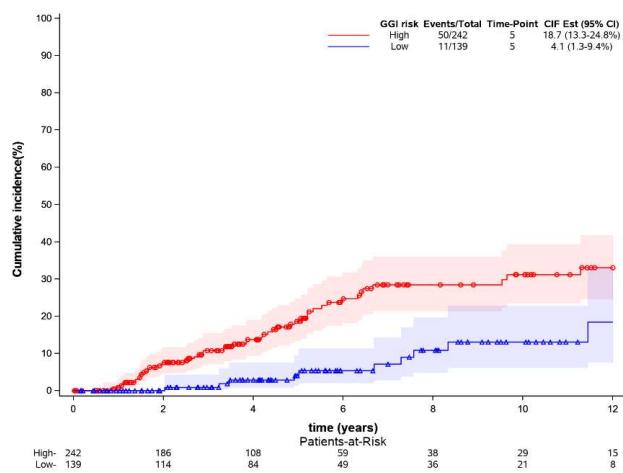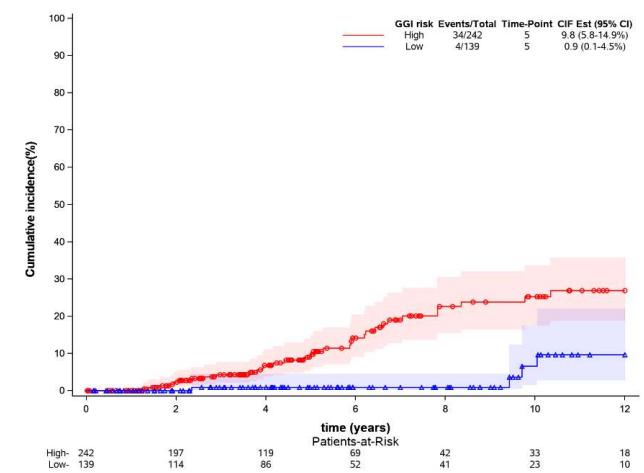
Supplementary Figure 6: Time-dependent ROC curve for time to relapse at 5 years
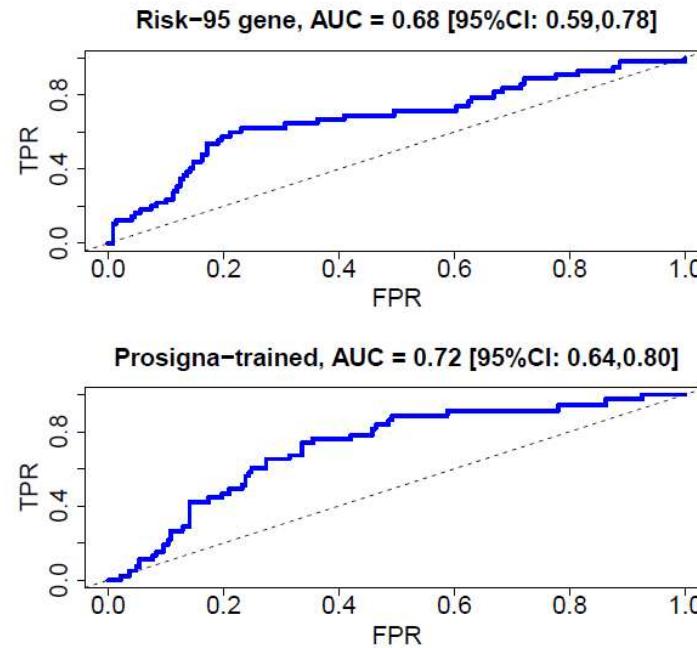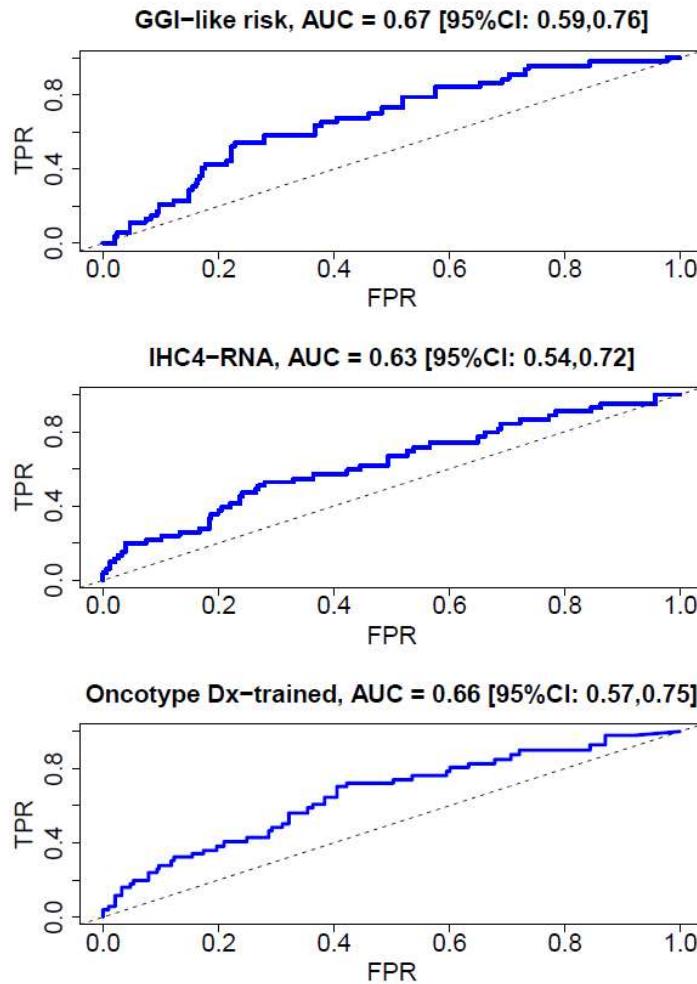
Supplementary Figure 7: Time-dependent ROC curve for time to distant relapse at 5 years
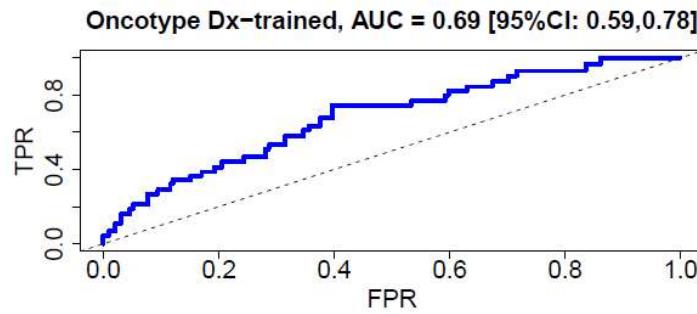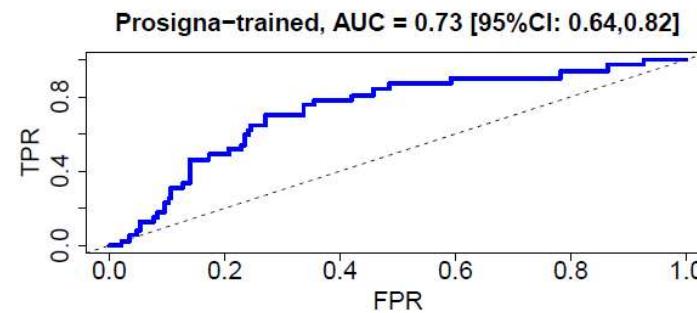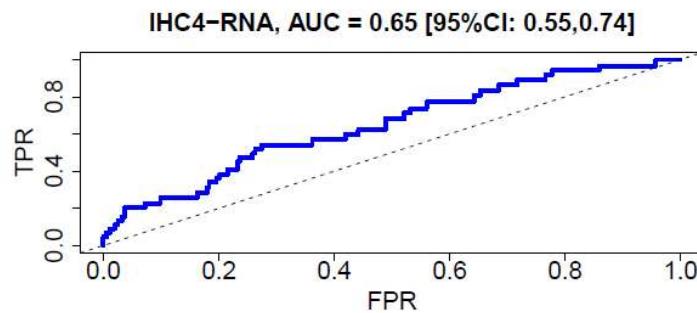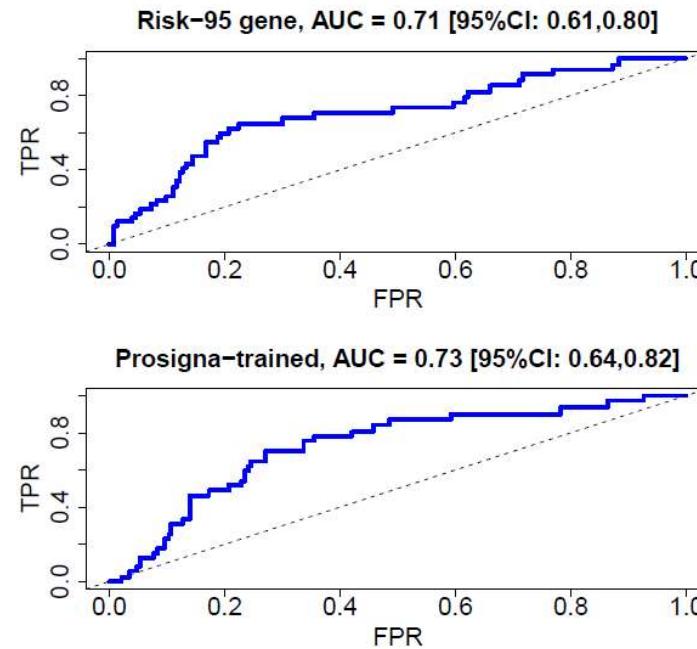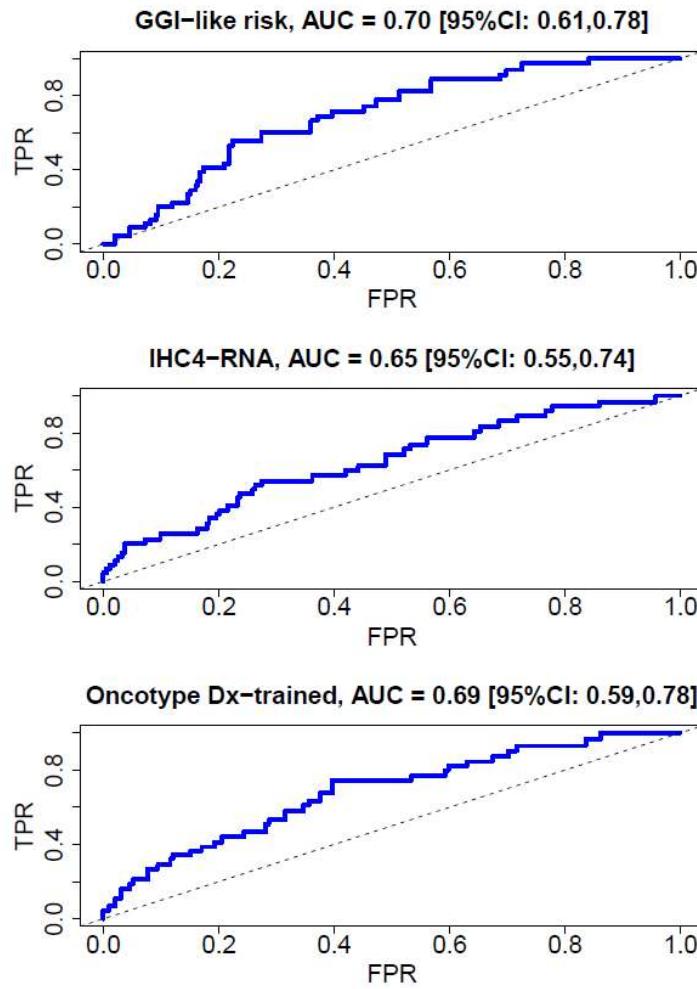
Supplementary Figure 8: Time-dependent ROC curve for breast cancer specific-survival at 5 years