

**Table S1. Association of identified proteins with risk of overall breast cancer and intrinsic-like subtypes.**

Encoding genes	Cytobands	No. of variants <sup>a</sup>	R <sup>2</sup> <sup>b</sup>	Overall breast cancer		Subtypes <sup>c</sup>					Index variants <sup>d</sup>
				Z	P	Luminal A	Luminal B	Luminal B /Her2-negative	HER2-enriched	TNBC	
At least 500kb away from known loci											
PARK7	1p36.23	29	0.21	-4.70	2.60×10 <sup>-6</sup>	2.73E-04	0.90	0.80	0.81	4.35E-03	-
MST1	3p21.31	73	0.52	3.45	5.52×10 <sup>-4</sup>	0.02	0.27	0.13	0.02	0.07	-
TNXB	6p21.33-p21.32	100	0.25	3.67	2.41×10 <sup>-4</sup>	0.02	7.51E-03	0.36	0.49	0.03	-
RSPO3	6q22.33	49	0.13	-4.21	2.56×10 <sup>-5</sup>	9.69E-04	0.08	0.22	0.02	0.07	-
SWAP70	11p15.4	58	0.2	3.72	1.99×10 <sup>-4</sup>	3.24E-03	0.09	0.77	0.01	0.31	-
CTSF	11q13.2	55	0.03	3.70	2.18×10 <sup>-4</sup>	9.68E-04	0.83	0.02	0.42	0.11	-
SERPINA1	14q32.13	93	0.27	3.68	2.34×10 <sup>-4</sup>	0.02	0.34	0.00	0.32	0.03	-
MIF	22q11.23	39	0.04	-3.32	8.99×10 <sup>-4</sup>	0.01	0.78	0.30	0.01	0.98	-
A4GALT	22q13.2	48	0.07	-5.06	4.26×10 <sup>-7</sup>	3.37E-03	0.10	0.01	0.38	0.16	-
At known risk loci											
PGD	1p36.22	18	0.03	-3.21	1.32×10 <sup>-3</sup>	0.04	0.02	0.64	0.01	0.12	rs616488
AKR1A1	1p34.1	51	0.27	-2.76	5.82×10 <sup>-3</sup>	2.42E-03	0.37	0.51	0.88	0.81	rs3790585
GSTM4	1p13.3	186	0.24	-6.91	4.84×10 <sup>-12</sup>	2.26E-05	0.02	0.15	0.07	1.70E-05	rs5776993
GSTM1	1p13.3	182	0.30	-6.43	1.32×10 <sup>-10</sup>	7.62E-05	0.05	0.27	0.28	6.43E-06	rs5776993
GSTM3	1p13.3	113	0.23	-6.41	1.50×10 <sup>-10</sup>	1.26E-04	4.18E-03	0.36	0.15	7.86E-07	rs5776993
SEMA4A	1q22	40	0.04	3.88	1.05×10 <sup>-4</sup>	5.24E-04	0.87	0.56	0.10	0.30	rs2758598
FH	1q43	8	0.01	-2.75	5.89×10 <sup>-3</sup>	3.07E-03	0.25	0.24	0.50	0.97	rs72755295
ANXA4	2p13.3	34	0.09	4.20	2.68×10 <sup>-5</sup>	0.01	0.02	0.03	0.88	0.13	rs4602255
TLR1	4p14	22	0.04	5.74	9.50×10 <sup>-9</sup>	1.93E-03	0.53	0.01	0.83	0.44	rs6815814
PDCD6	5p15.33	39	0.01	2.88	3.95×10 <sup>-3</sup>	9.86E-03	0.04	0.76	0.87	0.92	rs116095464
BTN3A3	6p22.2	116	0.47	3.22	1.30×10 <sup>-3</sup>	3.62E-04	0.53	0.05	0.12	0.19	rs71557345
GDI2	10p15.1	79	0.13	-3.89	9.93×10 <sup>-5</sup>	3.75E-05	7.61E-04	2.27E-03	0.55	0.86	rs2380205
KDELC2	11q22.3	76	0.15	-1.34	0.182	0.01	0.06	0.55	0.79	7.51E-11	rs11374964, rs74911261
LAYN	11q23.1	13	0.03	4.72	2.36×10 <sup>-6</sup>	6.10E-06	0.28	0.48	0.58	0.36	rs11354045
NTN4	12q22	59	0.06	4.07	4.73×10 <sup>-5</sup>	4.21E-06	1.00	0.95	0.79	0.99	rs17356907
CSK	15q24.1	24	0.08	-3.97	7.24×10 <sup>-5</sup>	4.50E-05	0.01	0.74	0.60	0.45	rs1869959
SNUPN	15q24.2	87	0.06	-4.94	7.91×10 <sup>-7</sup>	2.20E-09	0.46	0.05	0.27	0.02	rs8027365
NAGLU	17q21.2	116	0.12	2.65	8.08×10 <sup>-3</sup>	4.63E-04	0.92	0.88	0.59	0.07	rs72826962
ASIP	20q11.22	26	0.13	3.73	1.93×10 <sup>-4</sup>	0.77	8.84E-03	0.17	0.45	2.28E-03	rs2284378
CPNE1	20q11.22	51	0.43	-3.44	5.89×10 <sup>-4</sup>	0.02	0.19	0.02	0.30	0.11	rs112208395
CCDC134	22q13.2	40	0.08	-3.18	1.46×10 <sup>-3</sup>	2.13E-04	0.01	0.75	0.93	0.17	rs73161324

Abbreviation: TNBC, triple-negative breast cancer

a. Number of variants used in the prediction model for protein level; b. Performance of prediction model, correlation between predicted and measured protein levels; c. P-values for association analyses for intrinsic-like subtypes; d. GWAS-identified risk variants within 500kb from the gene boundary