

Novel Insights into Breast Cancer Genetic Variance through RNA Sequencing

SUPPLEMENTARY DATA

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Manuscript Information

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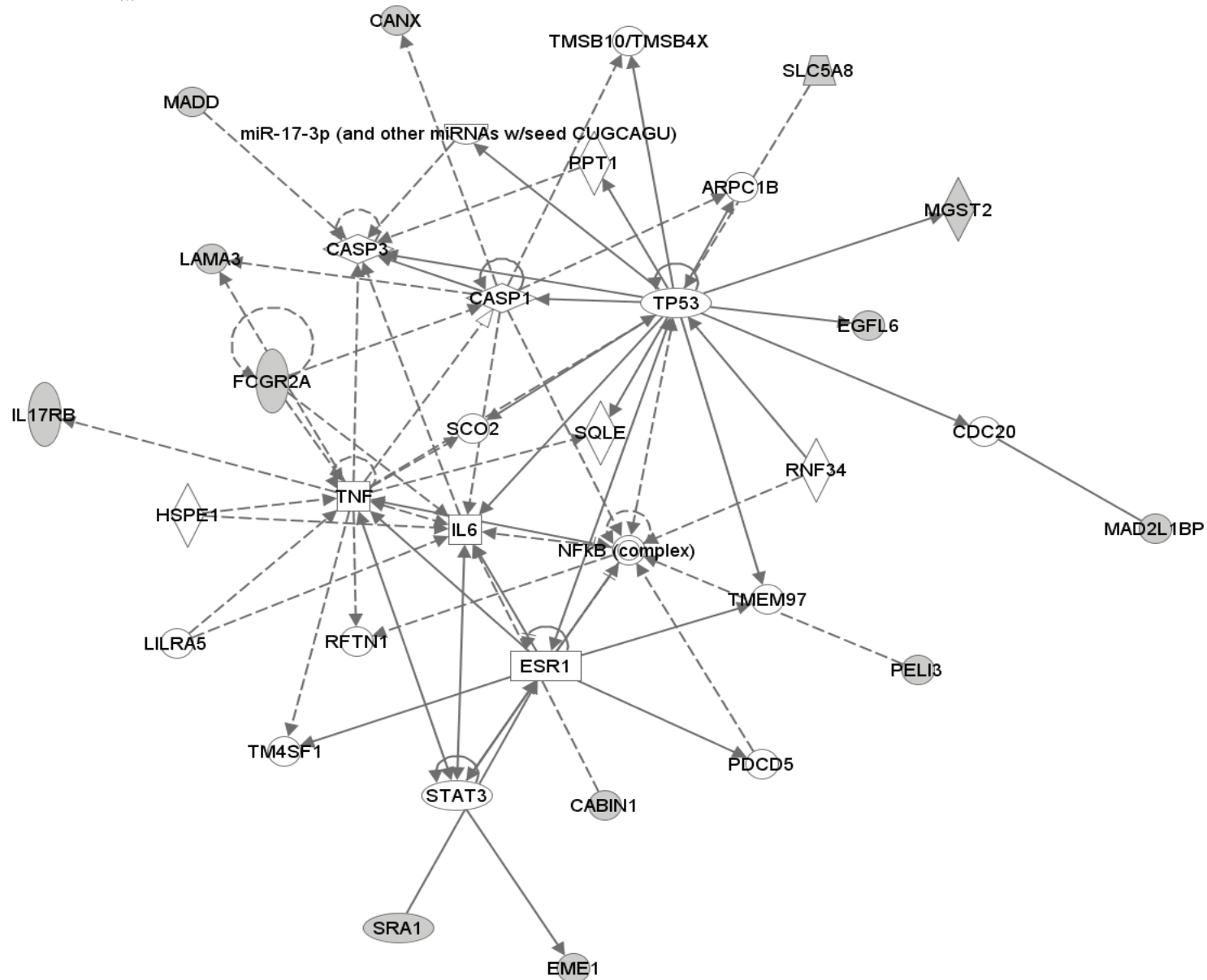
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Supplementary Figure 1. Top affected molecular networks were cell death and survival, cellular development, and cellular growth and proliferation, and the top affected canonical pathway was estrogen receptor signaling ...



Supplementary Table 1. SNPs and INDELs identified across 17 Breast Cancer Samples.

Sample Variant		TNBC						Non-TNBC						HER-2 Positive					Summary		
		IP2-50	IP2-69	IP2-76	IP2-78	IP2-83	IP2-90	IP2-42	IP2-48	IP2-49	IP2-65	IP2-66	IP2-71	26	56	83	171	IP2-53	SUM	AVE	UNIQUE
Total (prior to filtering)	SNPs	176856	37089	258465	59744	63498	84893	111183	104833	110135	123226	97225	81115	184298	117153	97275	139335	30294	1876617	110389	1109301
	Genes	13032	8244	13209	10382	10300	11074	12236	11538	11862	11581	11691	10338	10902	10102	9851	10649	7602	184593	10858	17722
	Indels	8076	2126	14003	3651	3355	4977	7391	6080	6302	6858	5320	4369	11467	7419	5840	8211	1918	107363	6315	78872
	Genes	3775	1484	5008	2300	2129	2713	3956	3223	3377	3476	2913	2532	4642	3638	3032	3804	1369	53371	3139	16757
Novel (prior to filtering)	SNP	31901	9347	40252	14064	13222	22718	26316	20209	22997	14768	18625	16658	24361	14052	13503	20732	7472	331197	19482	225537
	Genes	6647	2687	7217	3940	3643	5678	6311	5166	5750	3911	4662	4221	5280	3783	3689	5042	2008	79635	4684	14300
	Indels	1300	398	2333	701	572	1139	1487	946	1046	631	829	666	1161	654	657	947	339	15806	930	13125
	Genes	682	228	1071	391	331	666	827	562	613	357	445	397	735	391	388	606	190	8880	522	4903
Known + Novel Filtered	SNPs	145182	27808	218411	45864	50380	62382	85370	84879	87409	108694	78770	64755	161083	103408	84023	119089	22914	1550421	91201	888525
	Genes	12028	7388	12087	9378	9431	9705	11087	10558	10811	11032	10879	9481	10223	9488	9126	9875	6937	169514	9971	17221
	Indels	6863	1760	11777	2996	2834	3908	6036	5216	5317	6289	4552	3752	10451	6833	5246	7354	1618	92802	5459	69013
	Genes	3326	1299	4372	1989	1876	2218	3443	2858	2949	3272	2596	2251	4341	3445	2789	3514	1221	47759	2809	15977
Known + Novel Filtered (genic)	SNPs	83982	22367	97387	33350	35006	38463	58395	59848	59819	79699	50435	50099	133570	85843	66261	99308	18745	1072577	63093	545791
	Genes	12027	7387	12086	9377	9430	9704	11086	10557	10810	11031	10878	9480	10222	9487	9125	9874	6936	169497	9970	17220
	Indels	4578	1448	5825	2278	2126	2638	4430	3860	3843	4834	3194	2958	8771	5714	4183	6220	1338	68238	4014	50039
	Genes	3213	1273	4028	1917	1836	2150	3320	2757	2851	3184	2508	2193	4218	3365	2716	3427	1201	46157	2715	14560
Known + Novel Filtered (Exonic)	SNPs	5234	4469	4722	5650	5279	4273	6964	5697	5753	6554	5926	5749	6292	5769	5582	6117	4374	94404	5553	24960
	Genes	3334	2777	3126	3509	3300	2777	4124	3555	3628	3858	3703	3477	3676	3393	3340	3679	2803	58059	3415	9836
	Indels	1095	856	1138	1095	1007	1014	1761	1132	1263	1442	1294	1132	1211	1207	1074	1187	887	19795	1164	12825
	Genes	1002	797	1046	988	945	911	1571	1052	1170	1281	1173	1038	1102	1099	980	1066	830	18051	1062	7071

Supplementary Table 2. Overlap between the variations found by our study and the publically available genome wide association studies (GWAS)

geneList	#rsID	Sample	QUAL	INFO	accepted_hits.k	accession	functionGV	scorePhast	(consScoreG	AFR	EUR	AS	genomesESP
none	rs13281615	83	3.41	DP=2;VDB=0.0156;AF1=1;AC1=2;DP4=0,0,2,0;MQ=20;FQ=-33	1/1:32,6,0:4	none	intergenic	0	1.36	43.3	45.8	41.3	unknown
PBX1	rs1387389	IP2-48	55.5	DP=8;VDB=0.0300;AF1=1;AC1=2;DP4=0,1,5,2;MQ=20;FQ=-31;PV4=0.37,0.0014,1,1	1/1:86,4,0:7	NM_002585.3	intron	0.001	3.19	50	34.7	48.2	unknown
PBX1	rs1387389	IP2-49	6.98	DP=8;VDB=0.0453;AF1=0.4999;AC1=1;DP4=3,1,2,1;MQ=20;FQ=9.38;PV4=1,0.0005,1,1	0/1:36,0,50:37	NM_002585.3	intron	0.001	3.19	50	34.7	48.2	unknown
PBX1	rs1387389	26	19.1	DP=14;VDB=0.0453;AF1=0.5;AC1=1;DP4=4,3,4,1;MQ=20;FQ=22;PV4=0.58,0.0057,1,1	0/1:49,0,77:52	NM_002585.3	intron	0.001	3.19	50	34.7	48.2	unknown
PBX1	rs1387389	171	57.1	DP=6;VDB=0.0640;AF1=1;AC1=2;DP4=0,0,2,4;MQ=20;FQ=-45	1/1:90,18,0:33	NM_002585.3	intron	0.001	3.19	50	34.7	48.2	unknown
RNF146	rs2180341	56	83	DP=8;VDB=0.0527;AF1=1;AC1=2;DP4=0,0,2,6;MQ=20;FQ=-51	1/1:116,24,0:45	NM_030963.3	intron	0	-4.45	35.5	26.3	22.3	unknown
RNF146	rs2180341	IP2-50	9.31	DP=2;VDB=0.0673;AF1=1;AC1=2;DP4=0,0,1,1;MQ=20;FQ=-33	1/1:40,6,0:8	NM_030963.3	intron	0	-4.45	35.5	26.3	22.3	unknown
RNF146	rs2180341	26	52.3	DP=5;VDB=0.0673;AF1=1;AC1=2;DP4=0,0,3,2;MQ=20;FQ=-42	1/1:85,15,0:27	NM_030963.3	intron	0	-4.45	35.5	26.3	22.3	unknown
RNF146	rs2180341	171	6.02	DP=2;VDB=0.0640;AF1=1;AC1=2;DP4=0,0,2,0;MQ=20;FQ=-33	1/1:36,6,0:6	NM_030963.3	intron	0	-4.45	35.5	26.3	22.3	unknown
FGFR2	rs2420946	IP2-48	40.5	DP=4;VDB=0.0453;AF1=1;AC1=2;DP4=0,0,2,2;MQ=20;FQ=-39	1/1:73,12,0:21	NM_023029.2	intron	0	-7.82	40.2	46.9	35.9	unknown
FGFR2	rs2420946	26	90	DP=9;VDB=0.0591;AF1=1;AC1=2;DP4=0,0,6,3;MQ=20;FQ=-54	1/1:123,27,0:51	NM_023029.2	intron	0	-7.82	40.2	46.9	35.9	unknown
FGFR2	rs2981582	IP2-42	24	DP=4;VDB=0.0668;AF1=1;AC1=2;DP4=0,0,2,1;MQ=20;FQ=-36	1/1:56,9,0:15	NM_023029.2	intron	0.975	3.39	48.6	44.5	26.9	unknown
FGFR2	rs2981582	26	52.3	DP=5;VDB=0.0661;AF1=1;AC1=2;DP4=0,0,3,2;MQ=20;FQ=-42	1/1:85,15,0:27	NM_023029.2	intron	0.975	3.39	48.6	44.5	26.9	unknown
LSP1	rs3817198	IP2-76	9.31	DP=2;VDB=0.0527;AF1=1;AC1=2;DP4=0,0,1,1;MQ=20;FQ=-33	1/1:40,6,0:8	NM_002339.2	intron	0	-5.19	11.2	33.5	11.6	unknown
LSP1	rs3817198	171	9.31	DP=2;VDB=0.0591;AF1=1;AC1=2;DP4=0,0,1,1;MQ=20;FQ=-33	1/1:40,6,0:8	NM_002339.2	intron	0	-5.19	11.2	33.5	11.6	unknown
none	rs4415084	IP2-48	81.8	DP=12;VDB=0.0300;AF1=1;AC1=2;DP4=0,1,4,5;MQ=20;FQ=-37;PV4=1,7.7e-07,1,0.3	1/1:114,10,0:17	none	intergenic	0.004	1.95	36.2	37.9	45.9	unknown
none	rs4415084	IP2-49	65.1	DP=6;VDB=0.0232;AF1=1;AC1=2;DP4=0,0,2,4;MQ=20;FQ=-45	1/1:98,18,0:33	none	intergenic	0.004	1.95	36.2	37.9	45.9	unknown
none	rs4415084	IP2-76	6.02	DP=2;VDB=0.0167;AF1=1;AC1=2;DP4=0,0,0,2;MQ=20;FQ=-33	1/1:36,6,0:6	none	intergenic	0.004	1.95	36.2	37.9	45.9	unknown
none	rs4415084	IP2-66	15.5	DP=4;VDB=0.0029;AF1=0.543;AC1=1;DP4=1,0,1,2;MQ=20;FQ=-19;PV4=1,0.013,1,1	0/1:45,0,8:11	none	intergenic	0.004	1.95	36.2	37.9	45.9	unknown
ZMI21	rs704010	IP2-48	6.02	DP=2;VDB=0.0233;AF1=1;AC1=2;DP4=0,0,2,0;MQ=20;FQ=-33	1/1:36,6,0:6	NM_020338.3	intron	0	-2.22	1.3	42.6	22.9	unknown
ZMI21	rs704010	IP2-50	24	DP=4;VDB=0.0542;AF1=1;AC1=2;DP4=0,0,2,1;MQ=20;FQ=-36	1/1:56,9,0:15	NM_020338.3	intron	0	-2.22	1.3	42.6	22.9	unknown
BABAM1	rs8170	IP2-48	46.2	DP=34;VDB=0.0673;AF1=1;AC1=2;DP4=3,2,2,3;MQ=20;FQ=-35;PV4=0.15,0.0003,1,0.19	1/1:78,8,0:14	NM_014173.2	coding-sync	1	2.78	19.2	20.2	0.4	A=2226/G=10096
BABAM1	rs8170	IP2-50	134	DP=30;VDB=0.0673;AF1=1;AC1=2;DP4=0,0,21,7;MQ=20;FQ=-111	1/1:167,84,0:99	NM_014173.2	coding-sync	1	2.78	19.2	20.2	0.4	A=2226/G=10096
BABAM1	rs8170	IP2-49	46	DP=22;VDB=0.0376;AF1=0.5;AC1=1;DP4=10,2,8,2;MQ=20;FQ=48.5;PV4=1,0.00015,1,0.087	0/1:76,0,85:78	NM_014173.2	coding-sync	1	2.78	19.2	20.2	0.4	A=2226/G=10096
SLC4A7	rs4973768	IP2-65	95.2	DP=19;VDB=0.0591;AF1=1;AC1=2;DP4=1,1,5,12;MQ=20;FQ=-44;PV4=1,1.2e-07,1,1	1/1:128,17,0:31	NM_003615.4	utr-3	0.832	3.78	30.4	43.8	17.5	unknown
SLC4A7	rs4973768	IP2-50	65.1	DP=6;VDB=0.0527;AF1=1;AC1=2;DP4=0,0,3,3;MQ=20;FQ=-45	1/1:98,18,0:33	NM_003615.4	utr-3	0.832	3.78	30.4	43.8	17.5	unknown
SLC4A7	rs4973768	56	3.54	DP=7;VDB=0.0368;AF1=0.4998;AC1=1;DP4=2,2,2,1;MQ=20;FQ=5.45;PV4=1,0.00024,1,0.2	0/1:31,0,53:30	NM_003615.4	utr-3	0.832	3.78	30.4	43.8	17.5	unknown
SLC4A7	rs4973768	IP2-49	78.4	DP=13;VDB=0.0640;AF1=1;AC1=2;DP4=0,1,7,3;MQ=20;FQ=-40;PV4=0.36,9.7e-07,1,1	1/1:111,13,0:23	NM_003615.4	utr-3	0.832	3.78	30.4	43.8	17.5	unknown
SLC4A7	rs4973768	26	38	DP=9;VDB=0.0376;AF1=0.5003;AC1=1;DP4=2,1,4,2;MQ=20;FQ=4.77;PV4=1,0.00078,1,0.34	0/1:68,0,30:33	NM_003615.4	utr-3	0.832	3.78	30.4	43.8	17.5	unknown
SLC4A7	rs4973768	171	31.5	DP=4;VDB=0.0268;AF1=1;AC1=2;DP4=0,0,3,1;MQ=20;FQ=-39	1/1:64,12,0:21	NM_003615.4	utr-3	0.832	3.78	30.4	43.8	17.5	unknown

Supplementary Table 3. Number of novel SNPs and INDELS after filtering; the within gene located variants and protein altering variant numbers are also shown, together with the affected genes number

Samples		TNBC						Non-TNBC						HER-2 Positive					Summary		
		IP2-50	IP2-69	IP2-76	IP2-78	IP2-83	IP2-90	IP2-42	IP2-48	IP2-49	IP2-65	IP2-66	IP2-71	26	56	83	171	IP2-53	SUM	AVE	UNIQ
Novel (Total)	SNPs	214	60	193	161	100	179	477	248	285	232	172	282	1143	288	246	475	92	4847	285	4616
	Indels	72	18	88	37	34	54	109	61	38	58	52	34	142	55	54	75	28	1009	59	966
Novel (Within Genes)	SNPs	145	48	113	89	74	113	300	165	171	170	109	179	922	187	169	371	59	3384	199	3240
	Genes	130	46	107	83	70	107	271	141	155	161	99	141	654	168	118	300	54	2805	165	2102
	Indels	49	12	47	27	23	30	70	47	20	38	29	20	109	40	34	53	15	663	39	641
	Genes	49	12	47	27	23	30	70	46	20	37	28	20	107	40	34	53	15	658	38	565
Novel (Exonic)	Total*	13	15	19	25	15	20	65	21	27	18	19	15	52	12	19	22	13	390	22	380
	Nonsense	0	0	1	0	0	0	0	1	2	0	1	0	0	0	0	0	0	5	0.3	3
	Missense	3	7	7	10	8	15	23	8	7	11	3	8	28	8	13	10	6	175	10	174
	Splice Site	4	4	3	11	4	0	31	7	10	3	12	2	12	4	5	7	3	122	7.2	118
	Genes	13	15	19	25	15	20	63	21	26	18	19	12	52	12	19	22	13	384	22	368
	Indels	3	1	2	4	3	2	6	2	2	2	3	0	3	3	2	0	2	40	2.4	40
	Genes	3	1	2	4	3	2	6	2	2	2	3	0	3	3	2	0	2	40	2.4	38

*Total number SNPs includes synonymous

Supplementary Table 4. Novel variants showing allele preferential expression

Gene	Sample	Subtype	CHR	POS	REF	ALT	QUAL	Function GVS	AA	PROT	PPH	CONS Phas	Cons GER	# Ref reads	# Var reads
AGRN	IP2-78	TNBC	1	984982	G	A	131	coding-synonymous	none	1517/204	unknown	0.351	0.091	1	22
AP2A1	IP2-83	TNBC	19	5E+07	G	T,A	25.1	splice-3	none	NA	unknown	1	5.54	1	10
ARHGAP18	IP2-90	TNBC	6	1.3E+08	C	T	78.1	missense	ALA,THR	382/664	0.97	1	5.15	0	7
ATM	IP2-66	Non-TNBC	11	1.1E+08	T	G	98	splice-5	none	NA	unknown	0.992	6.06	0	9
BRK1	IP2-48	Non-TNBC	3	1E+07	A	G	27.3	splice-3	none	NA	unknown	1	5.62	0	5
BTBD18	26	HER2	11	5.8E+07	C	T	116	missense	GLU,LYS	564/713	0.734	1	5.32	2	17
CACNA1C	IP2-66	Non-TNBC	12	2224713	T	C	89.4	splice-5	none	NA	unknown	1	5.58	1	10
CASC3	56	HER2	17	3.8E+07	G	A	53.1	missense	ALA,THR	670/704	0.85	0.971	5.03	0	6
CASP3	26	HER2	4	1.9E+08	A	T	90.2	splice-5	none	NA	unknown	0.996	5.54	1	11
CD44	IP2-42	Non-TNBC	11	3.5E+07	A	C	24.2	splice-3	none	NA	unknown	0.93	5.85	1	5
CHD3	IP2-48	Non-TNBC	17	7809901	G	T	89.4	coding-synonymous	none	1463/196	unknown	0.971	-2.47	1	10
CHD4	IP2-69	TNBC	12	6692363	C	T	89.1	splice-5	none	NA	unknown	1	5.96	3	17
CHGB	IP2-66	Non-TNBC	20	5892329	G	C	28.5	splice-5	none	NA	unknown	1	4.54	0	4
COL16A1	IP2-49	Non-TNBC	1	3.2E+07	A	T,C	26.5	splice-5	none	NA	unknown	1	5.21	0	6
CP	IP2-42	Non-TNBC	3	1.5E+08	C	G	49.5	splice-5	none	NA	unknown	1	5.16	1	8
CYC1	26	HER2	8	1.5E+08	T	G	127	coding-synonymous	none	207/326	unknown	1	2.75	26	176
DBI	IP2-83	TNBC	2	1.2E+08	T	G	28.1	splice-5	none	NA	unknown	0.998	5.09	0	6
DDX52	56	HER2	17	3.6E+07	T	A	87.2	missense	ILE,PHE	463/600	1	1	5.6	1	11
DHX8	IP2-76	TNBC	17	4.2E+07	G	A	45.5	coding-synonymous	none	902/1221	unknown	1	1.43	1	7
DIP2A	IP2-78	TNBC	21	4.8E+07	T	A	40.2	missense	SER,THR	1096/157	0.98	0.992	5	1	5
DPM1	IP2-69	TNBC	20	5E+07	A	T	101	splice-5	none	NA	unknown	1	5.81	0	13
DRAP1	IP2-48	Non-TNBC	11	6.6E+07	A	C	66.1	splice-3	none	NA	unknown	0.37	2.68	0	6
DSG1	26	HER2	18	2.9E+07	G	A	53.1	missense	VAL,ILE	808/1050	0.496	0.967	3.31	0	6
EFCAB4A	IP2-49	Non-TNBC	11	830105	G	C	78.1	missense	ARG,PRO	193/295	1	0.976	4.39	0	7
EIF3H	IP2-48	Non-TNBC	8	1.2E+08	C	G	113	coding-synonymous	none	173/353	unknown	1	5.3	3	19
ENO1	IP2-42	Non-TNBC	1	8927251	G	A	124	coding-synonymous	none	123/435	unknown	0.454	-8.51	22	181
EXOC2	IP2-42	Non-TNBC	6	564121	A	G	86	coding-synonymous	none	567/925	unknown	0.983	-4.77	0	12
FASN	IP2-53	HER2	17	8E+07	G	A	93.8	coding-synonymous	none	294/2512	unknown	0.994	3.88	2	14
FBN1	IP2-65	Non-TNBC	15	4.9E+07	T	A	28.5	splice-3	none	NA	unknown	0.942	5.93	0	4
FBXO21	IP2-42	Non-TNBC	12	1.2E+08	A	C	52.1	splice-5	none	NA	unknown	1	5.93	0	6
FLNB	IP2-42	Non-TNBC	3	5.8E+07	A	C	56.1	splice-3	none	NA	unknown	1	5.51	0	7
GOLGA4	IP2-78	TNBC	3	3.7E+07	G	A	130	missense	VAL,ILE	887/2231	0.022	0.083	2.38	2	30
HCFC2	IP2-90	TNBC	12	1E+08	G	C	40.1	missense	LYS,ASN	787/793	0.004	0.998	0.022	1	6
HDAC1	IP2-42	Non-TNBC	1	3.3E+07	T	G	42.3	splice-5	none	NA	unknown	1	1.89	0	5
HDDC2	IP2-42	Non-TNBC	6	1.3E+08	G	C	112	missense	LEU,VAL	117/205	0.001	1	3.63	7	36
HDLBP	IP2-90	TNBC	2	2.4E+08	G	A	156	coding-synonymous	none	1018/126	unknown	0.018	-7.55	2	38
IBTK	IP2-49	Non-TNBC	6	8.3E+07	C	T	64	splice-5	none	NA	unknown	1	5.25	0	8
ILF3	IP2-42	Non-TNBC	19	1.1E+07	T	G	25.2	splice-5	none	NA	unknown	0.971	5.33	1	5
INPP4A	IP2-83	TNBC	2	9.9E+07	A	G	53.1	splice-3	none	NA	unknown	0.979	5.16	0	6
ITPR1	IP2-71	Non-TNBC	3	4681139	T	C	55.5	coding-synonymous	none	117/2696	unknown	1	1.37	1	7
KDM2A	IP2-78	TNBC	11	6.7E+07	T	G	132	splice-5	none	NA	unknown	1	5.24	0	14
LMF2	IP2-90	TNBC	22	5.1E+07	G	A	59.5	missense	PRO,LEU	632/708	0.514	0.06	5.36	1	7
LOC64213	IP2-71	Non-TNBC	15	2.2E+07	T	C	118	coding-synonymous	none	70/190	unknown	0	-4.36	1	34
LOC64213	IP2-71	Non-TNBC	15	2.2E+07	T	A	77	coding-synonymous	none	91/190	unknown	0	-3.47	3	29
LOC64213	IP2-71	Non-TNBC	15	2.2E+07	C	G	45.5	missense	GLN,HIS	97/190	unknown	0.015	-1.92	3	16
LRRC42	IP2-42	Non-TNBC	1	5.4E+07	G	A	25.5	splice-5	none	NA	unknown	1	5.79	0	4
LYZ	IP2-42	Non-TNBC	12	7E+07	T	G	29.1	splice-5	none	NA	unknown	1	5.72	0	6
MAGED1	IP2-90	TNBC	X	5.2E+07	G	C	105	missense	GLY,ALA	87/779	1	0.999	2.79	3	30
MARS	26	HER2	12	5.8E+07	C	T	129	missense	THR,ILE	217/901	0.201	1	2.59	2	21
MCM6	IP2-49	Non-TNBC	2	1.4E+08	A	T,C	42.1	splice-5	none	NA	unknown	0.914	5.23	0	8
MCTS1	IP2-48	Non-TNBC	X	1.2E+08	G	T	72.5	splice-3	none	NA	unknown	1	5	1	8
MLH1	IP2-76	TNBC	3	3.7E+07	A	T	60.1	splice-3	none	NA	unknown	1	5.55	0	7
MTAP	IP2-53	HER2	9	2.2E+07	A	G	47.1	missense	LYS,ARG	71/284	0.03	0.989	4.03	0	6
MTIF2	26	HER2	2	5.5E+07	G	A	113	missense	HIS,TYR	678/728	0.999	1	5.93	5	26
MYO1B	IP2-76	TNBC	2	1.9E+08	G	A	90	coding-synonymous	none	210/1079	unknown	1	3.91	0	9

Supplementary Table 4 (cont). Novel variants showing allele preferential expression

Gene	Sample	Subtype	CHR	POS	REF	ALT	QUAL	Function GVS	AA	PROT	PPH	CONS Phas	Cons GER	# Ref reads	# Var reads
MYOF	56	HER2	10	9.5E+07	A	G	109	splice-5	none	NA	unknown	1	5.21	1	13
MYT1	IP2-90	TNBC	20	6.3E+07	T	A	31.5	coding-synonymous	none	836/1122	unknown	1	5.37	0	4
NCAPD3	26	HER2	11	1.3E+08	A	C	137	missense	LEU,TRP	1087/1499	1	1	5.73	0	20
NOP58	IP2-78	TNBC	2	2E+08	G	A	38.2	splice-5	none	NA	unknown	1	5.91	1	5
NOTCH3	IP2-48	Non-TNBC	19	1.5E+07	T	C	25.5	splice-3	none	NA	unknown	0.995	5.07	0	4
NR2F6	IP2-50	TNBC	19	1.7E+07	G	A	148	coding-synonymous	none	170/405	unknown	1	2.71	1	25
NR3C1	IP2-42	Non-TNBC	5	1.4E+08	A	G	19.2	splice-5	none	NA	unknown	1	5.88	1	5
PFKL	IP2-83	TNBC	21	4.6E+07	C	T	116	coding-synonymous	none	532/781	unknown	0.949	-3.21	1	20
PKM	IP2-42	Non-TNBC	15	7.2E+07	G	C	106	missense	PRO,ALA	477/532	0.001	0.073	0.699	3	24
PKN2	IP2-50	TNBC	1	8.9E+07	A	G	31.5	splice-3	none	NA	unknown	0.953	5.84	0	4
PLOD1	IP2-78	TNBC	1	1.2E+07	G	A	25.3	splice-5	none	NA	unknown	1	4.73	0	5
PPA1	IP2-42	Non-TNBC	10	7.2E+07	C	T	67.1	splice-5	none	NA	unknown	1	5.5	0	7
PPP2CB	83	HER2	8	3.1E+07	C	T	60.1	splice-5	none	NA	unknown	0.994	3.83	1	12
PPP4C	IP2-42	Non-TNBC	16	3E+07	G	C	36.1	splice-5	none	NA	unknown	1	5.79	0	6
PRKDC	26	HER2	8	4.9E+07	C	T	36.5	splice-3	none	NA	unknown	0.25	5.33	0	4
PTPRA	56	HER2	20	3007766	G	T	78.1	splice-3	none	NA	unknown	1	5.09	0	7
PTPRS	26	HER2	19	5218429	A	G	89.4	splice-5	none	NA	unknown	0.954	4.3	1	10
RBBP4	IP2-53	HER2	1	3.3E+07	G	A	66.1	coding-synonymous	none	26/426	unknown	1	3.99	0	7
RDX	IP2-42	Non-TNBC	11	1.1E+08	A	T,G	103	splice-5	none	NA	unknown	0.956	2.8	0	13
RFC4	IP2-83	TNBC	3	1.9E+08	T	A	46.3	splice-3	none	NA	unknown	0.062	3.21	0	5
RGPD3	IP2-53	HER2	2	1.1E+08	A	G	84	missense-near-splice	MET,THR	586/1759	0	0.988	0.58	0	8
RNF40	IP2-42	Non-TNBC	16	3.1E+07	G	C	46.3	splice-5	none	NA	unknown	0.999	5.51	0	5
RNF41	26	HER2	12	5.7E+07	C	T	146	coding-synonymous-n	none	166/318	unknown	1	4.83	0	21
RRP7A	IP2-42	Non-TNBC	22	4.3E+07	A	T	34.2	splice-5	none	NA	unknown	0.707	3.99	1	5
SCNN1A	IP2-42	Non-TNBC	12	6463692	G	A	62.1	coding-synonymous	none	483/729	unknown	0.955	4.8	0	6
SERPINA3	IP2-69	TNBC	14	9.5E+07	T	A	222	missense	SER,THR	302/424	0.032	0.013	3.64	0	290
SHARPIN	IP2-42	Non-TNBC	8	1.5E+08	C	T	119	coding-synonymous-n	none	67/388	unknown	0.475	3.72	5	31
SIPA1L2	IP2-78	TNBC	1	2.3E+08	C	T	94	splice-5	none	NA	unknown	0.993	5.36	0	10
SPHK1	26	HER2	17	7.4E+07	C	T	74.1	missense	ARG,CYS	365/471	0.565	0.974	2.93	2	13
SPTBN1	IP2-53	HER2	2	5.5E+07	T	C	82.1	coding-synonymous	none	1547/2156	unknown	0.067	-12.1	2	11
ST6GALNA8	83	HER2	9	1.3E+08	G	A	40.2	missense	ARG,CYS	198/334	1	0.983	4.7	1	5
STRN3	IP2-42	Non-TNBC	14	3.1E+07	C	T	57	splice-5	none	NA	unknown	1	5.44	0	8
SUN2	26	HER2	22	3.9E+07	C	T	89.4	coding-synonymous	none	718/718	unknown	0.181	1.95	1	10
SYTL4	IP2-49	Non-TNBC	X	1E+08	A	T	106	splice-5	none	NA	unknown	0.354	3.88	0	10
TDFP2	IP2-66	Non-TNBC	3	1.4E+08	C	T	48.1	splice-5	none	NA	unknown	1	4.5	1	6
TMEM237	IP2-48	Non-TNBC	2	2E+08	A	C	73	splice-5	none	NA	unknown	1	5.1	0	12
TNS3	83	HER2	7	4.7E+07	C	T	30.2	splice-5	none	NA	unknown	0.829	4.38	1	5
TRAP1	26	HER2	16	3724401	G	A	58.5	missense	THR,ILE	328/705	0.003	0.969	2.76	1	8
TRAPPC9	26	HER2	8	1.4E+08	G	A	128	coding-synonymous	none	255/1247	unknown	0.171	-11.1	6	52
TRIM2	IP2-90	TNBC	4	1.5E+08	C	G	126	missense	SER,CYS	522/772	0.999	0.976	5.42	0	26
TRIP12	IP2-66	Non-TNBC	2	2.3E+08	T	A	30.5	splice-3	none	NA	unknown	0.997	5.78	0	4
TSPAN5	IP2-78	TNBC	4	9.9E+07	A	T	97	splice-5	none	NA	unknown	0.991	5.13	0	11
TTBK2	26	HER2	15	4.3E+07	A	T	24.8	splice-5	none	NA	unknown	1	5.42	1	5
UTP20	IP2-42	Non-TNBC	12	1E+08	A	T	21.3	splice-3	none	NA	unknown	0.999	5.62	0	5
VTI1B	IP2-42	Non-TNBC	14	6.8E+07	A	C	66.1	splice-5	none	NA	unknown	1	3.87	0	6
WARS	IP2-50	TNBC	14	1E+08	A	C	46.3	splice-5	none	NA	unknown	0.972	5.66	0	5
WDR47	IP2-49	Non-TNBC	1	1.1E+08	A	G	34.2	splice-5	none	NA	unknown	1	5.1	1	5
XYLT1	171	HER2	16	1.7E+07	G	A	66.1	missense	SER,LEU	450/960	1	1	4.9	0	6
YIF1B	IP2-69	TNBC	19	3.9E+07	G	T	66.1	missense	ASP,GLU	104/284	0.935	1	3.1	0	6
ZC3H13	171	HER2	13	4.7E+07	C	T	115	splice-5	none	NA	unknown	0.998	5.81	1	18
ZC3H15	IP2-42	Non-TNBC	2	1.9E+08	G	A	50.1	splice-5	none	NA	unknown	1	5.29	0	6
ZFYVE26	171	HER2	14	6.8E+07	A	G	53.1	splice-5	none	NA	unknown	0.999	5.31	0	6
ZRANB2	IP2-66	Non-TNBC	1	7.2E+07	C	T	122	splice-5	none	NA	unknown	1	5.82	0	15