Supplementary

Table S1: SNPs associated with triple negative breast cancer risk, prognosis, and survival including subpopulation frequencies

SNPs	Locus	Genes	Functional consequence	Subpopulation frequency			Effects	Reference(s)
rs3817198 (T>C)	11p15	*LSP1*	Intron variant	African	T=0.863	C=0.137*; C=0.159**	Correlated with overall survival and progression-free survival and has a prognostic effect particularly in the subgroup of patients with triple-negative BC.	[1,2]
				American	T=0.82	C=0.18*; C=0.21**		
				Ashkenazi Jewish	T=0.54**	C=0.46**		
				East Asian	T=0.897*; T=0.907**	C=0.103*; C=0.093**		
				Europe	T=0.686*; T=0.7052**	C=0.314*; C=0.2948**		
				South Asian	T=0.64*	C=0.36*		
rs13387042 (A>G)	2q35	*TNP1/IGFBP5/IGFBP2/TNS1*	Non-coding transcript variant; Intron variant	African	A=0.778*; A=0.738**	G=0.222*; G=0.262**	Associated with prognostic in TNBC	[2]; [3–5]
				American	A=0.36*; A=0.38**	G=0.64*; G=0.62**		
				Ashkenazi Jewish	A=0.54**	G=0.46**		
				East Asian	A=0.097*; A=0.087**	G=0.903*; G=0.913**		
				Europe	A=0.520*; A=0.5233**	G=0.480*; G=0.4767**		
				South Asian	A=0.48*	G=0.52*		
rs1436904 (T>G)	18q11.2	*CHST9*	Intron variant	African	T=0.747*; T=0.760**	G=0.253*; G=0.240**	Novel susceptibility SNPs in TNBC. Increased risk of disease progression. Independent prognostic genetic variant in Chinese TNBC patients. Potential prognostic biomarker for early-stage of TNBC.	[6]
				American	T=0.55*; T=0.55**	G=0.45*; G=0.45**		
				Ashkenazi Jewish	T=0.66**	G=0.34**		
				East Asian	T=0.511*; T=0.503**	G=0.489*; G=0.497**		
				Europe	T=0.588*; T=0.6179**	G=0.412*; G=0.3821**		
				South Asian	T=0.76*	G=0.24*		
rs1219648	10q26	*FGFR2*	Intron variant	African	A=0.562*;	G=0.438*;	Associated with TNBC, strong	[7-9]

(A>G)					A=0.579**	G=0.421**	predictor.	
				American	A=0.59*; A=0.61**	G=0.41*; G=0.39**		
				Ashkenazi Jewish	A=0.61**	G=0.39**		
				East Asian	A=0.618*; A=0.616**	G=0.382*; G=0.384**		
				Europe	A=0.569*; A=0.6083**	G=0.431*; G=0.3917**		
				South Asian	A=0.62*	G=0.38*		
rs4415084 (C>T)	5p12	N/A	N/A	African	C=0.350*; C=0.360**	T=0.650*; T=0.640**	Associated with a worse outcome in triple negative EBC patients	[10]
				American	C=0.44*; C=0.49**	T=0.56*; T=0.51**		
				Ashkenazi Jewish	C=0.53**	T=0.47**		
				East Asian	C=0.453*; C=0.432**	T=0.547*; T=0.568**		
				Europe	C=0.591*; C=0.5904**	T=0.409*; T=0.4096**		
				South Asian	C=0.52*	T=0.48*		
rs799917 (G>A)	17q21.31	*BRCA1*	Missense variant	African	G=0.115*; G=0.1807***	A=0.885*; A=0.8193***	Might be a potential prognostic biomarker for TNBC, especially after radiotherapy.	[11,12]
				American	G=0.57*; G=0.6565***	A=0.43*; A=0.3435***		
				Asian	G=0.5232***	A=0.4768***		
				East Asian	G=0.629*	A=0.371*		
				Europe	G=0.637*; G=0.6604***	A=0.363*; A=0.3396***		
				South Asian	G=0.47*	A=0.53*		
rs889312 (C>A)	5q11	*MAP3K1/MGC 33648/MIER3*	N/A	African	C=0.337	A=0.663	Breast cancer development, slight predisposition of ER- breast cancer development. Increased susceptibility especially when associated with BRACA	[5,13–15]
				American	C=0.41	A=0.59		
				East Asian	C=0.535	A=0.465		
				Europe	C=0.283	A=0.717		
				South Asian	C=0.39	A=0.61		
rs17468277 (C>T)	2q33.1	*ALS2CR12/CA S8*	Synonymous variant	African	C=0.957	T=0.043	Slight increase in breast cancer risk. Low penetrance genetic	[5,14,16]
				American	C=0.93	T=0.07		

				Europe	C=0.880	T=0.120	variant	
				East Asian	C=0.999	T=0.001		
				South Asian	C=0.98	T=0.02		
rs999737 (C>T)	14q24.1	*RAD51L1*	Intron variant	African	C=0.992	T=0.008	Increased breast cancer risk	[17–20]
				American	C=0.83	T=0.17		
				East Asian	C=0.997	T=0.003		
				Europe	C=0.790	T=0.210		
				South Asian	C=0.91	T=0.09		
rs10069690 (C>T)	5p15	*TERT, CLPTM1L*	Intron variant	African	C=0.338	T=0.662	Increased breast cancer risk, especially in African American women	[16]; [21–24]
				American	C=0.78	T=0.22		
				East Asian	C=0.831	T=0.169		
				Europe	C=0.724	T=0.276		
				South Asian	C=0.73	T=0.27		
rs12662670 (T>G)	6q25.1	*ESR1*	Intron variant	African	T=0.961	G=0.039	Increased risk of breast cancer	[16,17,19]
				American	T=0.94	G=0.06		
				East Asian	T=0.694	G=0.306		
				Europe	T=0.919	G=0.081		
				South Asian	T=0.95	G=0.05		
rs10483813 (T>A / T>C)	14q24.1	*RAD51L1*	Intron variant	African	T=0.962	A=0.038	Increased risk of breast cancer	[16] [18]
				American	T=0.83	A=0.17		
				East Asian	T=0.976	A=0.024		
				Europe	T=0.789	A=0.211		
				South Asian	T=0.88	A=0.12		
rs8100241 (G>A)	19p13.1	*ANKLE1*	Missense variant	African	G=0.613	A=0.387	Increased risk of triple negative breast cancer development	[19]; [17,25]; [16,26,27]
				American	G=0.62	A=0.38		
				Europe	G=0.428	A=0.572		
				East Asian	G=0.688	A=0.312		
				South Asian	G=0.51	A=0.49		
rs2284378 (T>C)	20q11	*RALY/EIF2S2*	Intron variant	African	T=0.133	C=0.867	Increased susceptibility of breast cancer	[16]; [28]
				American	T=0.35	C=0.65		
				East Asian	T=0.167	C=0.833		
				Europe	T=0.292	C=0.708		
				South Asian	T=0.14	C=0.86		
rs4245739 (C>A)	1q32.1	*MDM4*	Non-coding transcript	African	C=0.231	A=0.769	Association with ER- breast cancer, increased cancer	[16,29,30]
				American	C=0.29	A=0.71		

			variant	Europe	C=0.260	A=0.740	aggressiveness when is simultaneous with P53 (Arg72Pro variant)	
				East Asian	C=0.050	A=0.950		
				South Asian	C=0.26	A=0.74		
rs11075995 (A>T)	16q12.2	*FTO*	Intron variant	African	A=0.158	T=0.842	Increased basal-like breast cancer development in Chinese women	[4,16,31]
				American	A=0.31	T=0.69		
				East Asian	A=0.322	T=0.678		
				Europe	A=0.217	T=0.783		
				South Asian	A=0.20	T=0.80		
rs1800470 (G>A / G>C)	19q13.2	*TGFB1*	Missense variant	African	G=0.414	A=0.586	Low penetrance genetic variant, commonly attributed with familial breast cancer	[16,19] [5,32]
				American	G=0.51	A=0.49		
				East Asian	G=0.555	A=0.445		
				Europe	G=0.382	A=0.618		
				South Asian	G=0.45	A=0.55		
rs4973768 (C>T)	3p24.2	*SLC4A7, NEK10*	Non-coding transcript variant	African	C=0.683	T=0.317	Low penetrance genetic variant, commonly attributed with ER+ breast cancer, especially in East Asian population	[5,19,33,34]
				American	C=0.47	T=0.53		
				East Asian	C=0.815	T=0.185		
				Europe	C=0.519	T=0.481		
				South Asian	C=0.56	T=0.44		
rs61494113 (G>A)	19p13.11	between *ANKLE1* and *ABHD8*	N/A	African	G=0.571	A=0.429	Associated with ER- breast cancer	[35]
				American	G=0.82	A=0.18		
				East Asian	G=0.998	A=0.002		
				Europe	G=0.738	A=0.262		
				South Asian	G=0.89	A=0.11		
rs67397200 (C>G)	19p13.11	N/A	N/A	African	C=0.725	G=0.275	Associated with ER- breast cancer especially in European population	[24,35,36]
				American	C=0.84	G=0.16		
				East Asian	C=0.998	G=0.002		
				Europe	C=0.738	G=0.262		
				South Asian	C=0.89	G=0.11		
rs201360779 (C>T)	5q11.2–12.1	*PDE4D*	Missense variant	African	C=1.000	T=0.000	Increased risk of TNBC development	[26]
				American	C=1.00	T=0.00		
				Europe	C=0.998	T=0.002		
				East Asian	C=1.00	T=0.00		
				Ashkenazi Jewish	C=1.00	T=0.00		
				Asian	C=1.00	T=0.00		
				South Asian	C=1.00	T=0.00		
rs200725508	5q11.2–12.1	*PDE4D*	Missense	European	C=0.9997	T=0.0003	Increased risk of TNBC	[26]

(C>T)			variant	African	C=1.000	T=0.000	development	
				East Asian	C=1.000	T=0.000		
				American	C=1.00	T=0.00		
rs201654150 (T>C)	15q22.31	*FBXL22*	Missense variant	European	T=0.99993	C=0.00007	Increased risk of TNBC development	[26]
				American	T=1.000	C=0.000		
				African	T=1.000	C=0.000		
rs149590841 (T>G)	15q22.31	*FBXL22*	Missense variant; USP3-AS1: Intron variant	African	T=1.00	G=0.00	Increased risk of TNBC development	[26]
				American	T=1.00	G=0.00		
				East Asian	T=1.00	G=0.00		
				Europe	T=1.00	G=0.00		
rs1219648 (A>G)	10q26.13	*FGFR2*	Intron variant	African	A=0.562	G=0.438	High risk allele G associated with FGFR2 mutation induced BC in post-menopausal women	[7]
				American	A=0.59	G=0.41		
				East Asian	A=0.618	G=0.382		
				Europe	A=0.569	G=0.431		
				South Asian	A=0.62	G=0.38		
rs3757322 (T>G)	6q25.1	*CCDC170*	3′ UTR variant	African	T=0.499	G=0.501	Increased risk of ER- BC	[24]
				American	T=0.75	G=0.25		
				East Asian	T=0.664	G=0.336		
				Europe	T=0.702	G=0.298		
				South Asian	T=0.70	G=0.30		
rs2046210 (G>A)	6q25	*ESR1*	N/A	African	G=0.337	A=0.663	High risk T allele of BC development in Chinese, Japanese and Americans of European origin. The African American population shows no association	[4,17,19]; [16,34,37]
				American	G=0.73	A=0.27		
				East Asian	G=0.638	A=0.362		
				Europe	G=0.679	A=0.321		
				South Asian	G=0.68	A=0.32		
rs6678914 (G>A)	1q32.1	*LGR6*	Intron variant	African	G=0.686	A=0.314	Increased risk of BC development	[4]
				American	G=0.71	A=0.29		
				East Asian	G=0.731	A=0.269		
				Europe	G=0.569	A=0.431		
				South Asian	G=0.71	A=0.29		
rs3757318 (G>A)	6q25.1	*CCDC170*	Intron variant	African	G=0.977	A=0.023	Increased risk of BC development	[4]
				American	G=0.95	A=0.05		
				East Asian	G=0.742	A=0.258		
				Europe	G=0.920	A=0.080		
				South Asian	G=0.96	A=0.04		

rs3803662 (C>T) (A>G)	16q12.1	*TNRC9*	Non-coding transcript variant	African	A=0.567	G=0.433	Homozygotes of TT allele have a significant increased risk of BC development and a slight tendency towards ER- BC	[4,5,17,19]
				American	A=0.39	G=0.61		
				East Asian	A=0.619	G=0.381		
				Europe	A=0.291	G=0.709		
				South Asian	A=0.27	G=0.73		
rs11374964 (insertion)	11q22.3	*KDELC2*	3′ UTR variant	N/A				[24]
rs8170 (G>A)	19p13	*BABAM1*	Synonymous variant	African	G=0.814	A=0.186	Increased risk of TNBC development	[16,19,23,25, 27] [4,17]
				American	G=0.90	A=0.10		
				East Asian	G=0.999	A=0.001		
				Europe	G=0.837	A=0.163		
				South Asian	G=0.91	A=0.09		
rs6678914 (G>A)	1q32.1	*LGR6*	Intron variant	African	G=0.686	A=0.314	Increased risk of BC development	[4,16]
				American	G=0.71	A=0.29		
				East Asian	G=0.731	A=0.269		
				Europe	G=0.569	A=0.431		
				South Asian	G=0.71	A=0.29		
rs4245739 (C>A)	1q32.1	*MDM4*	Non-coding transcript variant	African	C=0.231	A=0.769	Increased risk of BC development	[4,24]
				American	C=0.29	A=0.71		
				East Asian	C=0.050	A=0.950		
				Europe	C=0.260	A=0.740		
				South Asian	C=0.26	A=0.74		
rs12710696 (T>C)	2p24.1	MIR4757	Non-coding transcript variant	African	T=0.576	C=0.424	Increased risk of BC development	[4,16]
				American	T=0.35	C=0.65		
				East Asian	T=0.308	C=0.692		
				Europe	T=0.342	C=0.658		
				South Asian	T=0.59	C=0.41		
rs2736108 (C>T)	5p15.33	N/A	N/A	African	C=0.923	T=0.077	Influences telomere length and increases the risk of BC development	[4]
				American	C=0.77	T=0.23		
				East Asian	C=0.694	T=0.306		
				Europe	C=0.720	T=0.280		
				South Asian	C=0.45	T=0.55		
rs3757318	6q25.1	*ESR1*	Intron variant	African	G=0.977	A=0.023	Significantly associated with	[4,38]

(G>A)				American	G=0.95	A=0.05	BC risk in Chinese population. No significant association in German Population	
				East Asian	G=0.742	A=0.258		
				Europe	G=0.920	A=0.080		
				South Asian	G=0.96	A=0.04		
rs2363956 (T>G)	19p13.1	*ANKLE1*	Missense variant	African	T=0.495	G=0.505	Increased risk of BC development	[4,25,27]
				American	T=0.61	G=0.39		
				East Asian	T=0.688	G=0.312		
				Europe	T=0.427	G=0.573		
				South Asian	T=0.51	G=0.49		
rs616488 (A>G)	1p36.22	*PEX14*	Intron variant	African	A=0.914	G=0.086	Associated with the risk of BC development	[4]
				American	A=0.50	G=0.50		
				East Asian	A=0.683	G=0.317		
				Europe	A=0.674	G=0.326		
				South Asian	A=0.76	G=0.24		
rs4849887 (T>C)	2q14.2	*SCTR*	N/A	African	T=0.301	C=0.699	Associated with the risk of BC development	[4]
				American	T=0.13	C=0.87		
				East Asian	T=0.209	C=0.791		
				Europe	T=0.102	C=0.898		
				South Asian	T=0.25	C=0.75		
rs2016394 (G>A)	2q31.1	*DLX2-AS1*	Intron variant	African	G=0.768	A=0.232	G allele is associated with risk of BC development	[4]
				American	G=0.57	A=0.43		
				East Asian	G=0.813	A=0.187		
				Europe	G=0.542	A=0.458		
				South Asian	G=0.66	A=0.34		
rs6828523 (C>A)	4q34.1	*ADAM29*	Intron variant	African	C=0.583	A=0.417	Increased risk of BC development, especially in relation to environmental factors response	[4]
				American	C=0.82	A=0.18		
				East Asian	C=0.762	A=0.238		
				Europe	C=0.892	A=0.108		
				South Asian	C=0.78	A=0.22		
rs1432679 (C>T)	5q33.3	*EBF1*	Intron variant	African	C=0.853	T=0.147	Associated with the risk of BC development	[4]
				American	C=0.61	T=0.39		
				East Asian	C=0.611	T=0.389		
				Europe	C=0.447	T=0.553		
				South Asian	C=0.34	T=0.66		
rs7904519 (A>G)	10q25.2	*TCF7L2*	Intron variant	African	A=0.140	G=0.860	Associated with the risk of BC development	[4]
				American	A=0.65	G=0.35		

				East Asian	A=0.965	G=0.035		
				Europe	A=0.505	G=0.495		
				South Asian	A=0.62	G=0.38		
rs3903072 (G>T)	11q13.1	*OVOL1*	N/A	African	G=0.887	T=0.113	It modulates tumor microenvironment. Associated with the risk of BC development	[4,39]
				American	G=0.70	T=0.30		
				East Asian	G=0.772	T=0.228		
				Europe	G=0.540	T=0.460		
				South Asian	G=0.45	T=0.55		
rs11820646 (T>C)	11q24.3	N/A	N/A	African	T=0.228	C=0.772	Associated with the risk of TNBC development	[4]
				American	T=0.46	C=0.54		
				East Asian	T=0.478	C=0.522		
				Europe	T=0.440	C=0.560		
				South Asian	T=0.28	C=0.72		
rs12422552 (G>C)	12p13.1	N/A	N/A	African	G=0.558	C=0.442	Associated with the risk of TNBC development	[4]
				American	G=0.80	C=0.20		
				East Asian	G=0.730	C=0.270		
				Europe	G=0.710	C=0.290		
				South Asian	G=0.60	C=0.40		
rs10771399 (A>G)	12p11.22	*PTHLH*	N/A	African	A=0.966	G=0.034	Associated with the risk of TNBC development	[4]
				American	A=0.93	G=0.07		
				East Asian	A=0.823	G=0.177		
				Europe	A=0.894	G=0.106		
				South Asian	A=0.86	G=0.14		
rs17356907 (A>G)	12q22	*NTN4*	N/A	African	A=0.825	G=0.175	Increased risk of ER- BC development	[4]
				American	A=0.65	G=0.35		
				East Asian	A=0.736	G=0.264		
				Europe	A=0.707	G=0.293		
				South Asian	A=0.70	G=0.30		
rs1292011 (A>G)	12q24	*MED13L*	Intron variant	African	A=0.554	G=0.446	Increased risk of BC development, especially when associated with BRCA1/2 mutations	[4]
				American	A=0.63	G=0.37		
				East Asian	A=0.766	G=0.234		
				Europe	A=0.586	G=0.414		
				South Asian	A=0.38	G=0.62		
rs11571833 (A>T)	13q13.1	*BRCA2*	Stop gained	African	A=0.999	T=0.001	Minor single risk factor of BC	[4]
				American	A=1.00	T=0.00		
				East Asian	A=1.000	T=0.000		

				Europe	A=0.989	T=0.011		
				South Asian	A=0.99	T=0.01		
rs2588809 (T>C)	14q24.1	*RAD51L1*	Intron variant	African	T=0.309	C=0.691	Increased risk of BC development	[4]
				American	T=0.17	C=0.83		
				East Asian	T=0.028	C=0.972		
				Europe	T=0.188	C=0.812		
				South Asian	T=0.17	C=0.83		
rs6001930a (T>C)	22q13	*MLK1*	Intron variant	African	T=0.851	C=0.149	Associated with the risk of TNBC development	[4]
				American	T=0.92	C=0.08		
				East Asian	T=0.760	C=0.240		
				Europe	T=0.898	C=0.102		
				South Asian	T=0.88	C=0.12		
rs80357794 (delC)	17q21.31	*BRCA1*	Frameshift	N/A				[11]
rs169547 (T>C)	13q13.1	*BRCA2*	Missense variant	African	T=0.089	C=0.911	Associated with the risk of TNBC development, especially hereditary BC	[11,40]
				American	T=0.00	C=1.00		
				East Asian	T=0.000	C=1.000		
				Europe	T=0.001	C=0.999		
				South Asian	T=0.00	C=1.00		
rs3750050 (A>G)	7q11.23	*PTPN12*	Missense variant	African	A=0.783	G=0.217	Associated with the risk of BC development	[11]
				American	A=0.56	G=0.44		
				East Asian	A=0.310	G=0.690		
				Europe	A=0.840	G=0.160		
				South Asian	A=0.61	G=0.39		
rs1924587 (G>C)	20p11.23	*FGF4*	Intron variant	African	G=0.371	C=0.629	Associated with the risk of TNBC development	[19]
				American	G=0.55	C=0.45		
				East Asian	G=0.624	C=0.376		
				Europe	G=0.583	C=0.417		
				South Asian	G=0.70	C=0.30		
rs6504950 (G>A)	17q23.2	*STXBP4*	Intron variant	African	G=0.641	A=0.359	Associated with the risk of TNBC development	[19]
				American	G=0.82	A=0.18		
				East Asian	G=0.899	A=0.101		
				Europe	G=0.731	A=0.269		
				South Asian	G=0.81	A=0.19		
rs1926657 (T>C)	13q32.1	*ABCC4*	Intron variant	African	T=0.324	C=0.676	Associated with the risk of TNBC development	[19]
				American	T=0.22	C=0.78		

				East Asian	T=0.307	C=0.693		
				Europe	T=0.185	C=0.815		
				South Asian	T=0.31	C=0.69		
rs981782 (A>C)	5p12	*HCN1*	Intron variant	African	A=0.974	C=0.026	Associated with the risk of TNBC development	[19]
				American	A=0.57	C=0.43		
				East Asian	A=0.654	C=0.346		
				Europe	A=0.534	C=0.466		
				South Asian	A=0.80	C=0.20		
rs10995190 (G>A)	10q21.2	*ZNF365*	Intron variant	African	G=0.826	A=0.174	Associated with the risk of TNBC development	[19]
				American	G=0.89	A=0.11		
				East Asian	G=0.978	A=0.022		
				Europe	G=0.849	A=0.151		
				South Asian	G=0.92	A=0.08		
rs1124933 (G>A)	20p11.23	*NOTCH2*	None	African	G=0.640	A=0.360	Associated with the risk of TNBC development	[19]
				American	G=0.46	A=0.54		
				East Asian	G=0.091	A=0.909		
				Europe	G=0.591	A=0.409		
				South Asian	G=0.36	A=0.64		
rs3817198 (T>C)	11p15.5	*LSP1/H19*	Intron variant	African	T=0.863	C=0.137	Risk factor for BC development in European population, but it has a protective role in African population	[19] [5]
				American	T=0.82	C=0.18		
				East Asian	T=0.897	C=0.103		
				Europe	T=0.686	C=0.314		
				South Asian	T=0.64	C=0.36		
rs2981582 (A>G) (C>T)	10q26.13	*FGFR2*	Intron variant	African	A=0.495	G=0.505	Development of ER+ BC tumors if the T allele is present Associated with the risk of TNBC development	[19]
				American	A=0.42	G=0.58		
				East Asian	A=0.316	G=0.684		
				Europe	A=0.420	G=0.580		
				South Asian	A=0.34	G=0.66		
rs9325024 (A>G)	5q32	*PPP2R2B*	Intron variant	African	A=0.896	G=0.104	Associated with the risk of TNBC development	[19]
				American	A=0.77	G=0.23		
				East Asian	A=0.563	G=0.437		
				Europe	A=0.897	G=0.103		
				South Asian	A=0.70	G=0.30		
rs458685 (A>G)	21q21.3	*GRIK1*	Intron variant	African	A=0.921	G=0.079	Associated with the risk of TNBC development	[19]
				American	A=0.86	G=0.14		
				East Asian	A=0.855	G=0.145		

				Europe	A=0.828	G=0.172		
				South Asian	A=0.89	G=0.11		
rs614367 (C>V)	11q13.3	*FGF3 MYEOV:CCND1*	N/A	African	C=0.873	T=0.127	Increased risk of BC development, especially associated with BRCA1/2 mutations	[19]
				American	C=0.92	T=0.08		
				East Asian	C=0.994	T=0.006		
				European	C=0.8379	T=0.1621		
rs2075555 (T>A / T>G)	17q21.33	*COL1A1*	Intron variant	African	T=0.273	G=0.727	Associated with the risk of TNBC development	[19]
				American	T=0.31	G=0.69		
				East Asian	T=0.324	G=0.676		
				Europe	T=0.136	G=0.864		
				South Asian	T=0.24	G=0.76		
rs7716600 (A>C)	5p12	*MRPS30*	N/A	African	A=0.170	C=0.830	Increased risk of TNBC development	[19]
				American	A=0.30	C=0.70		
				East Asian	A=0.482	C=0.518		
				Europe	A=0.204	C=0.796		
				South Asian	A=0.26	C=0.74		
rs9956546 (G>A)	18q12.2	*FHOD3*	Intron variant	African	G=0.630	A=0.370	Increased risk of TNBC development	[19]
				American	G=0.74	A=0.26		
				East Asian	G=0.520	A=0.480		
				Europe	G=0.886	A=0.114		
				South Asian	G=0.80	A=0.20		
rs7711990 (A>G)	5q35.3	*BTNL8*	Intron variant	African	A=0.336	G=0.664	Increased risk of TNBC development	[19]
				American	A=0.55	G=0.45		
				East Asian	A=0.654	G=0.346		
				Europe	A=0.596	G=0.404		
				South Asian	A=0.73	G=0.27		
rs2180341 (G>A)	6q22.33	*RNF146*	Intron variant	African	G=0.305	A=0.695	Increased risk of TNBC development	[19]
				American	G=0.23	A=0.77		
				East Asian	G=0.197	A=0.803		
				Europe	G=0.280	A=0.720		
				South Asian	G=0.41	A=0.59		
rs1294255 (G>C)	1q42.2	*K1AA1804 MAP3K21*	Intron variant	African	G=0.860	C=0.140	Decreased risk of lymph node metastasis	[19,41]
				American	G=0.77	C=0.23		
				East Asian	G=0.614	C=0.386		
				Europe	G=0.615	C=0.385		
				South Asian	G=0.66	C=0.34		

rs2380205 (C>T)	10p15.1	*ANKRD16: FBXO18*	N/A	African	C=0.356	T=0.644	When associated with BRCA1/2 mutation, it induces great risk of BC development	[19]
				American	C=0.70	T=0.30		
				East Asian	C=0.870	T=0.130		
				Europe	C=0.557	T=0.443		
				South Asian	C=0.75	T=0.25		
rs704010 (T>C)	10q22.3	*TERT/ZMIZ1*	Intron variant	African	T=0.030	C=0.970	When associated with BRCA1/2 mutation, it induces great risk of BC development	[19,23]
				American	T=0.39	C=0.61		
				East Asian	T=0.309	C=0.691		
				Europe	T=0.413	C=0.587		
				South Asian	T=0.31	C=0.69		
rs6569480 (A>G)	6q22.33	*ECHDC1*	Intron variant	African	A=0.306	G=0.694	Increased risk of BC development	[19]
				American	A=0.23	G=0.77		
				East Asian	A=0.197	G=0.803		
				Europe	A=0.280	G=0.720		
				South Asian	A=0.41	G=0.59		
rs1045485 (G>C)	2q33.1	*CASP8*	Missense variant	African	G=0.950	C=0.050	C allele offers protection against BC development	[19,42]
				American	G=0.92	C=0.08		
				East Asian	G=0.999	C=0.001		
				Europe	G=0.880	C=0.120		
				South Asian	G=0.98	C=0.02		
rs3020314 (C>T)	6q25.1	*ESR1*	Intron variant	African	C=0.752	T=0.248	C alleles causes a predisposition for ER+ BC tumors development	[19,43]
				American	C=0.56	T=0.44		
				East Asian	C=0.806	T=0.194		
				Europe	C=0.298	T=0.702		
				South Asian	C=0.61	T=0.39		
rs1876206 (T>C)	15q21.1	*FBN1*	Intron variant	African	T=0.939	C=0.061	Increased risk of BC development	[19]
				American	T=0.88	C=0.12		
				East Asian	T=0.872	C=0.128		
				Europe	T=0.851	C=0.149		
				South Asian	T=0.86	C=0.14		
rs8051542 (T>C)	16q12.1	*TOX3*	Intron variant	African	T=0.292	C=0.708	Increased risk of BC development	[19]
				American	T=0.43	C=0.57		
				East Asian	T=0.178	C=0.822		
				Europe	T=0.432	C=0.568		
				South Asian	T=0.28	C=0.72		
rs2107425	11p15.5	*H19*	Intron variant;	African	T=0.292	C=0.708	Increased risk of BC	[19]

(T>C)			MRPL23; : Intron variant	American	T=0.43	C=0.57	development	
				East Asian	T=0.178	C=0.822		
				Europe	T=0.432	C=0.568		
				South Asian	T=0.28	C=0.72		
rs61764370 (A>C)	12p12.1	*KRAS*	3′ UTR variant	African	A=0.994	C=0.006	Increased risk of BC development	[44]
				American	A=0.93	C=0.07		
				East Asian	A=1.000	C=0.000		
				Europe	A=0.904	C=0.096		
				South Asian	A=0.98	C=0.02		
rs4808611 (C>T)	19p13.11	*NR2F6*	Intron variant	African	C=0.844	T=0.156	Increased risk of BC development	[27]
				American	C=0.91	T=0.09		
				East Asian	C=0.999	T=0.001		
				Europe	C=0.841	T=0.159		
				South Asian	C=0.91	T=0.09		
rs3745185 (G>A)	19p13.11	*BABAM1*	Intron variant	African	G=0.794	A=0.206	Increased risk of BC development	[27]
				American	G=0.68	A=0.32		
				East Asian	G=0.851	A=0.149		
				Europe	G=0.521	A=0.479		
				South Asian	G=0.56	A=0.44		

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