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Table S1 Selected the KIAA genes from the Gencode databases

Chr	Gene	Position (hg19)
1	<i>KIAA1324</i>	109656480-109745853
1	<i>KIAA2013</i>	11979648-11986485
1	<i>KIAA0907</i>	155882834-155904191
1	<i>KIAA0040</i>	175126123-175162135
1	<i>KIAA1614</i>	180882290-180920750
1	<i>KIAA1522</i>	33207486-33240571
1	<i>KIAA0319L</i>	35899091-36023014
1	<i>KIAA0754</i>	39876151-39882154
1	<i>KIAA1107</i>	92632542-92650280
2	<i>KIAA1715</i>	176788620-176867567
2	<i>KIAA1841</i>	61293006-61390108
2	<i>KIAA1841</i>	61293006-61390108
2	<i>KIAA1211L</i>	99410309-99552722
3	<i>KIAA1524</i>	108268716-108308491
3	<i>KIAA2018</i>	113367232-113415493
3	<i>KIAA1407</i>	113682984-113775460
3	<i>KIAA1257</i>	128628709-128721533
3	<i>KIAA0226</i>	197398264-197476598
3	<i>KIAA1143</i>	44779153-44803154
4	<i>KIAA1109</i>	123073488-123283913
4	<i>KIAA0922</i>	154387498-154557863
4	<i>KIAA1430</i>	186080819-186130658
4	<i>KIAA1239</i>	37245842-37451087
4	<i>KIAA1211</i>	57036361-57194791
4	<i>KIAA0232</i>	6783102-6885897
5	<i>KIAA1024L</i>	129083772-129102425
5	<i>KIAA0141</i>	141303373-141321612
5	<i>KIAA1191</i>	175773064-175788971
5	<i>KIAA0947</i>	5420777-5490347
5	<i>KIAA0825</i>	93488671-93918288
6	<i>KIAA1919</i>	111580551-111592370
6	<i>KIAA0408</i>	127772427-127780536
6	<i>KIAA1244</i>	138483058-138665800
6	<i>KIAA0319</i>	24544332-24646383
6	<i>KIAA1586</i>	56911347-56920023

Table S1 (continued)

Table S1 (continued)

Chr	Gene	Position (hg19)
6	<i>KIAA1009</i>	84833960-84937353
6	<i>KIAA1009</i>	84833960-84937353
7	<i>KIAA1549</i>	138516126-138666064
7	<i>KIAA1147</i>	141356611-141401953
7	<i>KIAA0087</i>	26572740-26578407
7	<i>KIAA0895</i>	36363830-36429734
7	<i>KIAA1324L</i>	86506222-86689015
8	<i>KIAA0196</i>	126036502-126103920
8	<i>KIAA0196-AS1</i>	126052926-126057231
8	<i>KIAA1456</i>	12803151-12889012
8	<i>KIAA1875</i>	145162629-145173218
8	<i>KIAA1429</i>	95499921-95565757
9	<i>KIAA0368</i>	114122972-114247025
9	<i>KIAA1958</i>	115249127-115431677
9	<i>KIAA1984</i>	139690802-139702193
9	<i>KIAA1984-AS1</i>	139698379-139703300
9	<i>KIAA0020</i>	2720469-2844241
9	<i>KIAA1161</i>	34366668-34376851
9	<i>KIAA1045</i>	34957484-34982541
9	<i>KIAA1432</i>	5629025-5776557
9	<i>KIAA2026</i>	5881596-6007825
10	<i>KIAA1598</i>	118643742-118886097
10	<i>KIAA1217</i>	23983675-24836772
10	<i>KIAA1217</i>	23983675-24836772
10	<i>KIAA1462</i>	30301729-30404423
10	<i>KIAA1279</i>	70748487-70776738
11	<i>KIAA1377</i>	101785746-101871789
11	<i>KIAA1549L</i>	33563618-33695648
11	<i>KIAA1731</i>	93394805-93463113
12	<i>KIAA1033</i>	105501102-105562912
12	<i>KIAA1467</i>	13197218-13295455
12	<i>KIAA1551</i>	32112304-32146039
13	<i>KIAA0226L</i>	46916139-46964177
14	<i>KIAA0125</i>	106383838-106391825

Table S1 (continued)

Table S1 (continued)

Chr	Gene	Position (hg19)
14	<i>KIAA0391</i>	35591052-35743271
14	<i>KIAA0586</i>	58894103-59015216
14	<i>KIAA0247</i>	70078313-70181859
14	<i>KIAA1737</i>	77564440-77583630
15	<i>KIAA0125P2</i>	21224717-21226180
15	<i>KIAA0101</i>	64657193-64679886
15	<i>KIAA1024</i>	79724858-79764632
15	<i>KIAA1199</i>	81071684-81244117
16	<i>KIAA0430</i>	15688243-15737023
16	<i>KIAA0556</i>	27561473-27791690
16	<i>KIAA0895L</i>	67209644-67217943
16	<i>KIAA0513</i>	85061375-85127836
17	<i>KIAA0100</i>	26941458-26972472
17	<i>KIAA0753</i>	6481468-6544077
17	<i>KIAA0753</i>	6481468-6544077
17	<i>KIAA0195</i>	73437240-73496163
18	<i>KIAA1328</i>	34409159-34812135
18	<i>KIAA1468</i>	59854491-59974355
19	<i>KIAA1683</i>	18367908-18385319
19	<i>KIAA0355</i>	34745442-34846491
20	<i>KIAA1755</i>	36838890-36889174
22	<i>KIAA1671</i>	25348697-25593415
22	<i>KIAA1658</i>	30814212-30814469
22	<i>KIAA1644</i>	44639547-44708731
22	<i>KIAA0930</i>	45586219-45636650
X	<i>KIAA1210</i>	118212598-118284542
X	<i>KIAA2022</i>	73952684-74145282

Chr: chromosome.

Table S2 Expression of candidate KIAA genes obtained from breast cancer TCGA database

Gene	Tumor	Normal	Log ₂ FC	P value	Call rate in tumor	Call rate in normal
KIAA0101	5.37	0.59	2.98	4.36E-44	1.00	1.00
KIAA1456	0.41	1.62	-1.76	3.05E-30	1.00	1.00
KIAA1614	0.34	0.75	-0.95	2.32E-29	1.00	1.00
KIAA1524	2.95	0.78	1.80	1.58E-25	1.00	1.00
KIAA1199	3.52	0.36	2.98	2.52E-23	1.00	1.00
KIAA1211	1.30	0.19	2.26	8.85E-23	1.00	1.00
KIAA1683	0.73	2.11	-1.42	2.88E-21	1.00	1.00
KIAA0355	5.72	8.44	-0.55	4.73E-21	1.00	1.00
KIAA1598	12.48	6.04	1.04	1.45E-18	1.00	1.00
KIAA0408	0.01	0.18	-1.29	3.09E-17	1.00	1.00
KIAA1841	2.05	1.27	0.65	7.55E-15	1.00	1.00
KIAA1107	1.46	2.23	-0.58	2.86E-13	1.00	1.00
KIAA1109	5.69	8.59	-0.58	3.97E-13	1.00	1.00
KIAA0141	9.36	12.23	-0.38	1.54E-12	1.00	1.00
KIAA0196	26.53	15.78	0.75	4.85E-12	1.00	1.00
KIAA1257	0.39	0.11	1.24	2.03E-11	1.00	1.00
KIAA1024	0.54	0.23	0.95	1.51E-10	1.00	1.00
KIAA1377	2.41	3.14	-0.37	2.42E-10	1.00	1.00
KIAA0226	4.93	3.81	0.36	8.04E-10	1.00	1.00
KIAA1671	7.17	11.14	-0.63	1.77E-09	1.00	1.00
KIAA0895	2.35	1.44	0.67	2.60E-09	1.00	1.00
KIAA0226L	0.91	1.43	-0.60	3.25E-09	1.00	1.00
KIAA1644	0.57	0.23	1.02	3.46E-09	1.00	1.00
KIAA1429	14.23	9.11	0.64	4.86E-09	1.00	1.00
KIAA0430	10.96	13.80	-0.33	6.84E-09	1.00	1.00
KIAA1244	11.88	6.31	0.90	8.36E-09	1.00	1.00
KIAA1239	0.06	0.37	-1.54	2.02E-08	1.00	1.00
KIAA1467	18.66	5.65	1.71	2.80E-08	1.00	1.00
KIAA1009	2.12	2.78	-0.38	3.44E-08	1.00	1.00
KIAA1279	15.71	12.31	0.35	5.40E-08	1.00	1.00
KIAA1522	40.19	28.43	0.50	6.70E-08	1.00	1.00
KIAA1045	0.21	0.31	-0.41	3.95E-07	1.00	1.00
KIAA0319	0.31	0.05	1.47	4.81E-07	1.00	1.00
KIAA0556	4.64	3.08	0.58	8.55E-07	1.00	1.00
KIAA1549L	1.57	0.85	0.81	2.84E-06	1.00	1.00

Table S2 (continued)

Table S2 (continued)

Gene	Tumor	Normal	Log ₂ FC	P value	Call rate in tumor	Call rate in normal
KIAA1328	0.88	1.10	-0.29	3.31E-06	1.00	1.00
KIAA0922	5.54	6.41	-0.21	4.77E-06	1.00	1.00
KIAA0513	2.76	1.94	0.49	7.40E-06	1.00	1.00
KIAA0907	9.26	6.81	0.44	7.69E-06	1.00	1.00
KIAA1143	7.65	8.95	-0.22	1.10E-05	1.00	1.00
KIAA1462	6.19	8.49	-0.45	2.90E-05	1.00	1.00
KIAA2013	19.72	16.36	0.27	5.48E-05	1.00	1.00
KIAA0319L	14.99	11.40	0.39	7.59E-05	1.00	1.00
KIAA1217	16.70	21.42	-0.36	9.23E-05	1.00	1.00
KIAA1161	7.94	5.09	0.63	1.15E-04	1.00	1.00
KIAA0040	32.41	19.93	0.70	2.18E-04	1.00	1.00
KIAA1211L	4.43	3.17	0.47	2.96E-04	1.00	1.00
KIAA0232	10.23	11.45	-0.16	4.56E-04	1.00	1.00
KIAA2022	0.45	0.28	0.54	5.83E-04	1.00	1.00
KIAA2018	3.44	3.90	-0.17	6.84E-04	1.00	1.00
KIAA1586	2.57	2.86	-0.15	8.22E-04	1.00	1.00
KIAA1024L	0.01	0.00	0.11	1.67E-03	1.00	1.00
KIAA1549	2.09	1.51	0.45	1.81E-03	1.00	1.00
KIAA1755	1.32	1.52	-0.19	3.16E-03	1.00	1.00
KIAA1958	1.40	1.11	0.31	4.61E-03	1.00	1.00
KIAA0368	21.25	22.68	-0.09	4.87E-03	1.00	1.00
KIAA1432	4.83	5.26	-0.12	7.61E-03	1.00	1.00
KIAA1324L	3.47	3.54	-0.03	8.55E-03	1.00	1.00
KIAA0930	10.33	9.37	0.14	1.65E-02	1.00	1.00
KIAA0247	21.92	19.20	0.19	2.01E-02	1.00	1.00
KIAA0391	0.93	0.82	0.16	2.83E-02	1.00	1.00
KIAA2026	5.78	6.37	-0.14	3.23E-02	1.00	1.00
KIAA1731	2.25	1.86	0.26	4.09E-02	1.00	1.00
KIAA0825	0.56	0.41	0.38	4.17E-02	1.00	1.00
KIAA1324	50.32	42.35	0.25	4.52E-02	1.00	1.00

FC, fold change.

Table S3 Demographic and selected variables in breast cancer cases and cancer-free controls

Variables	Cases ^a (N=1,032)	Controls ^b (N=1,063)	P ^c
Age, years (mean ± SD)	50.87±11.43	51.74±11.23	0.078
Age at menarche, years (mean ± SD)	15.22±1.91	16.17±1.96	<0.0001
Age at first live birth, years (mean ± SD)	25.6±3.25	24.69±3.35	<0.0001
Age at natural menopause, years (mean ± SD)	49.72±3.5	49.59±3.91	0.617
Menopausal status			<0.0001
Premenopausal	499(49.45)	470(52.63)	
Natural menopausal	438(43.41)	411(46.02)	
Unnatural menopausal	72(7.14)	12(1.34)	
Estrogen receptor (ER) ^d			
Positive	460(55.22)		
Negative	373(44.78)		
Progesterone receptor (PR) ^d			
Positive	469(56.57)		
Negative	360(43.43)		

^aCases were consecutively recruited from the First Affiliated Hospital of Nanjing Medical University, the Cancer Hospital of Jiangsu Province and the Gulou Hospital, Nanjing, China, from Jan 2004 to April 2010; ^bControls were randomly selected from a cohort of more than 30,000 participants in a community-based screening program for non-infectious diseases conducted in Jiangsu Province; ^cT-tests and χ^2 tests were used for continuous or categorical variables, respectively; ^dER and PR status information was available in 833/829 breast cancer cases.

Table S4 In silico analysis for SNPs function annotation

SNP	Chr: Position ^a	Gene	Allele ^b	MAF ^c	Regulome DB Score	I-Mutant/Mupro	HaploReg
rs2306369	4: 123268859	KIAA1109 (missense)	A/G	0.15	5	Decreased	DNase, Motifs changed, Enhancer histone marks
rs1205434	20: 36869516	KIAA1755 (missense)	C/A	0.27	5	Decreased	Motifs changed, Enhancer histone marks, Selected eQTL hits

^aBased on NCBI build 37 of the human genome. ^bReference allele/effect allele. ^cminor allele frequency in 1000 Genomes Project East Asian data. SNP: single nucleotide polymorphism, Chr: chromosome, MAF: minor allele frequency, eQTL: expression Quantitative Trait Loci.