Supplemental Table 2: Genes previously associated with breast cancer risk in GWAS

Associated SNP*	Study	Associated Gene	location	Smallest p-value in CGEMS[§]	minP in CGEMS[†]
rs1045485	BCAC[(1)]	CASP8	2q33-34	0.0843	0.4801
rs4973768	CGEMS-III[(2)]	SLC4A7	3p24	0.0060	0.0549
rs7716600 **rs4415084**	deCODE[(3)] CGEMS-II[(4)]	MRPS30	5p12	0.0090	**0.0187**
rs889312 **rs16886165**	Cambridge[(5)] CGEMS-II[(4)]	MAP3K1	5q11.2	0.0209	0.1546
rs1219648 **rs2981582** **rs2981579**	CGEMS-I[(6)] Cambridge[(5)] CGEMS-II[(4)]	FGFR2	10q25.3-26	1.62×10^{-6}	**0.0002**
rs3817198 **rs3817198**	Cambridge[(5)] CGEMS-II[(4)]	LSP1	11p15.5	0.0343	0.3847
rs999737	CGEMS-II[(4)]	RAD51L1	14q23-24	0.0066	0.3615
rs12443621 **rs3803662** **rs3803662**	Cambridge[(5)] deCODE[(3)] CGEMS-II[(4)]	TOX3 (TNRC9)	16q12.1	0.0222	0.2615
rs6504950	CGEMS-III[(2)]	COX11	17q23.2	0.0663	0.2734
rs6504950	CGEMS-III[(2)]	STXBP4	17q23.2	0.0677	0.7514
rs1982073	BCAC[(1)]	TGFB1	19q13.1	0.0079	**0.0355**

* The SNP that was associated with breast cancer risk in the original study.

[§] The smallest p-value of a SNP trend test among all SNPs that are within the boundaries of 20kb 5' and 10kb 3' of the gene's coding region

[†] Adjusted minimal p-value calculated as the fraction of times the observed minimal p-value within a gene is smaller than the minimal p-value in 10,000 permutations.

Studies:

1. Cox A, Dunning AM, Garcia-Closas M, et al. A common coding variant in CASP8 is associated with breast cancer risk. Nature genetics 2007; 39: 352-8.

2. Ahmed S, Thomas G, Ghoussaini M, et al. Newly discovered breast cancer susceptibility loci on 3p24 and 17q23.2. Nature genetics 2009; 41: 585-90.

3. Stacey SN, Manolescu A, Sulem P, et al. Common variants on chromosomes 2q35 and 16q12 confer susceptibility to estrogen receptor-positive breast cancer. Nature genetics 2007; 39: 865-9.

4. Thomas G, Jacobs KB, Kraft P, et al. A multistage genome-wide association study in breast cancer identifies two new risk alleles at 1p11.2 and 14q24.1 (RAD51L1). Nature genetics 2009; 41: 579-84.

5. Easton DF, Pooley KA, Dunning AM, et al. Genome-wide association study identifies novel breast cancer susceptibility loci. Nature 2007; 447: 1087-93.

6. Hunter DJ, Kraft P, Jacobs KB, et al. A genome-wide association study identifies alleles in FGFR2 associated with risk of sporadic postmenopausal breast cancer. Nature genetics 2007; 39: 870-4.