**Supplemental Table 2. Samples genotyped† for SNPs in 5p12 by participating studies**

| Study Acronym | rs10941679 | | | | | rs981782 | | | |
|---|---|---|---|---|---|---|---|---|---|
| | Cases | DCIS | Controls | MAF | *P*-HWE | Cases | Controls | MAF | *P*-HWE |
| **Studies of white European women** | | | | | | | | | |
| ABCFS†* | 1,179 | | 415 | 0.25 | 0.5 | | | | |
| ABCS | 1,430 | 35 | 548 | 0.27 | 0.6 | | | | |
| BBCC | 962 | 52 | 811 | 0.24 | 0.5 | | | | |
| BBCS | 1,144 | | 828 | 0.25 | 0.1 | | | | |
| BIGGS | 945 | 52 | 896 | 0.27 | 0.6 | | | | |
| BSUCH | 606 | | 837 | 0.23 | 0.6 | 606 | 836 | 0.49 | 0.7 |
| CGPS* | 2,218 | | 6,636 | 0.26 | 0.3 | | | | |
| CNIO-BCS* | 702 | 33 | 808 | 0.20 | 1.0 | | | | |
| ESTHER | 484 | | 500 | 0.24 | 0.3 | 482 | 495 | 0.47 | 0.1 |
| FBCS | 1,516 | | 858 | 0.25 | 0.02 | | | | |
| GC-HBOC | 853 | | 1,211 | 0.27 | 0.2 | | | | |
| GENICA†* | 1,010 | | 1,012 | 0.25 | 0.2 | | | | |
| GESBC | 513 | 36 | 551 | 0.27 | 0.6 | | | | |
| HABCS* | 1,033 | | 998 | 0.26 | 0.005 | | | | |
| HMBCS | 1,763 | | 1,015 | 0.27 | 0.2 | | | | |
| HUBCS | 727 | | 986 | 0.28 | 0.8 | | | | |
| KBCP* | 460 | | 424 | 0.26 | 0.4 | | | | |
| kConFab/AOCS†* | 489 | 63 | 804 | 0.26 | 0.9 | 237 | 190 | 0.43 | 1.0 |
| LMBC | 1,125 | 66 | 759 | 0.27 | 0.5 | 1,132 | 759 | 0.45 | 0.7 |
| MARIE | 2,576 | 177 | 5,299 | 0.25 | 0.3 | 2,574 | 5,298 | 0.46 | 0.6 |
| MBCSG | 713 | | 1,221 | 0.22 | 0.8 | | | | |
| MCBCS* | 1,491 | 292 | 1,547 | 0.26 | 0.9 | | | | |
| MCCS* | 669 | | 747 | 0.27 | 0.7 | | | | |
| NBCS | 1,465 | | 1,737 | 0.29 | 0.4 | | | | |
| NC-BCFR | 266 | 121 | 154 | 0.22 | 0.5 | | | | |
| NHS* | 944 | 184 | 1,561 | 0.25 | 0.8 | | | | |
| OBCS | 535 | | 507 | 0.24 | 1.0 | | | | |
| OFBCR | 1,142 | | 327 | 0.24 | 0.6 | | | | |
| PBCS* | 1,836 | 125 | 2,227 | 0.26 | 0.9 | | | | |
| RBCS* | 710 | 39 | 795 | 0.25 | 0.1 | | | | |
| SBCS* | 1,124 | 86 | 1,186 | 0.27 | 0.2 | | | | |
| SEARCH* | 6,535 | | 6,777 | 0.26 | 0.7 | 2,268 | 2,267 | 0.53 | 0.4 |
| SZBCS | 895 | 37 | 859 | 0.25 | 0.9 | | | | |
| UCIBCS | 912 | | 493 | 0.24 | 0.3 | 914 | 495 | 0.44 | 0.5 |
| **Total** | **40,972** | **1,398** | **46,334** | | | **8,213** | **10,340** | | |
| **Studies of Asian women** | | | | | | | | | |
| SEBCS | 1,674 | | 1,128 | 0.48 | 0.7 | | | | |
| TBCS | 436 | | 283 | 0.48 | 0.5 | | | | |
| TWBCS | 897 | | 926 | 0.51 | 1.0 | | | | |
| **Total** | **3,007** | | **2,337** | | | | | | |

Cases, number of cases of invasive breast cancer successfully genotyped; DCIS, number of cases of ductal carcinoma in situ successfully genotyped; Controls, number of controls successfully genotyped; MAF, minor (G) allele frequency in controls; *P*-HWE, p-value for departure from Hardy Weinberg equilibrium in controls.

† Studies that used matrix-assisted laser desorption/ionization time of flight mass spectrometry (MALDI-TOF MS) for the determination of allele-specific primer extension products using Sequenom's MassARRAY system and iPLEX technology (Sequenom, San Diego, CA, USA), with oligonucleotides design carried out according to the guidelines of Sequenom and performed using MassARRAY Assay Design software (version 3.1). All other studies used Taqman nuclease assay (Taqman®), with reagents designed by Applied Biosystems (http://www.appliedbiosystems.com/) as Assays-by-Design℠

and genotyping performed using the ABI PRISM 7900HT, 7700 or 7500 Sequence Detection Systems according to manufacturer's instructions

* Studies the had already genotyped 5p12-981782 in white Europeans as part of the previously published study (Easton et al., 2008); kConFab/AOCS and SEARCH genotyped additional samples for the present study.