Polymorphisms in a putative enhancer at the 10q21.2 breast cancer risk locus regulate *NRBF2* expression

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ABSTRACT

Genome-wide association studies have identified SNPs near *ZNF365* at 10q21.2 associated with both breast cancer risk and mammographic density. To identify the most likely causal SNPs, we fine-mapped the association signal by genotyping 428 SNPs across the region in 89,050 European and 12,893 Asian cases and controls from the Breast Cancer Association Consortium. We identified four independent sets of correlated, highly trait-associated variants (iCHAVs), three of which were located within *ZNF365*. The most strongly risk-associated SNP, rs10995201 in iCHAV1, showed clear evidence of association with both estrogen receptor (ER)-positive [OR = 0.85 (0.82-0.88)] and ER-negative [OR = 0.87 (0.82-0.91)] disease, and was also the SNP most strongly associated with percent mammographic density. iCHAV2 (lead SNP - chr10:64258684:D) and iCHAV3 (lead SNP - rs7922449) were also associated with ER-positive [OR = 0.93 (0.91,0.95) and OR = 1.06 (1.03.1.09)] and ER-negative [OR = 0.95 (0.91,0.98) and OR = 1.08 (1.04.1.13)] disease. There was weaker evidence for iCHAV4, located 5′ of *ADO*, associated only with ER-positive breast cancer [OR = 0.93 (0.90 – 0.96)]. We found 12, 17, 18 and two candidate causal SNPs for breast cancer in iCHAVs1-4 respectively. Chromosome conformation capture analysis showed that iCHAV2 interacts with the *ZNF365* and *NRBF2* (more than 600kb away) promoters in normal and cancerous breast epithelial cells. Luciferase assays did not identify SNPs that affect transactivation of *ZNF365,* but identified a protective haplotype in iCHAV2, associated with silencing of the *NRBF2* promoter, implicating this gene in the etiology of breast cancer for the first time.

INTRODUCTION

Breast cancer is one of the most commonly occurring epithelial malignancies in women, with an estimated 1.7 million new cases and over 520,000 deaths annually worldwide [1; 2]. Familial aggregation and twin studies have shown a substantial contribution of inherited susceptibility to breast cancer [3]. Genome-wide association studies (GWAS) provide a powerful approach to identify common disease alleles. In a two-stage genome-wide association study conducted in European descendants, Turnbull et al. [4] identified five new susceptibility loci. One of the identified single nucleotide polymorphisms (SNPs), rs10995190 (combined *P* = 5.1×10^{-15}), lies within intron 4 of *ZNF365* (MIM 607818) at 10q21.2. Analysis by the Breast Cancer Association Consortium (BCAC) confirmed this association (*P* =1.3×10^{-36}) [5], with a non-significant association among Asians where this variant is rare [6]. Instead, about 26.7 kb away Cai et al. [7] identified a common SNP, rs10822013, about 26.7 kb away, associated with breast cancer risk among East Asians. Further analysis by the Consortium of Investigators of Modifiers of *BRAC1* and *BRACA2* (CIMBA) showed that rs10995190 is associated with breast cancer risk among *BRCA2* carriers [8], particularly for estrogen receptor positive breast cancer. This 10q21.2 locus was the first to be associated with percent mammographic density (PD) (combined *P* = 9.6×10^{-10}) [9] and also shows a possible association with breast size [10]. Varghese et al. [11] showed that rs10995190 and rs10509168 (r^2=0.13) are both associated with mammographic density, and through analysis of polygenic risk scores found that PD and breast cancer have a shared genetic basis. These data indicate that 10q21.2 is an important susceptibility region for both breast cancer and mammographic density, and must harbour one or more SNPs causally related to these phenotypes. In an attempt to identify the most likely causal SNPs underlying these associations, we assessed 428 SNPs across the 10q21.2 region, applying multiple analyses aimed at exploring the target genes and functional basis of the associations with breast cancer risk and mammographic density.

MATERIAL and METHODS

Genetic Mapping

Tagging strategy for the fine-scale mapping

We identified the fine-mapping region by taking the furthest SNPs upstream and downstream with minor allele frequency (MAF) > 2% and detectable correlation (r^2>0.1) with rs10995190, based on the 1000 genomes project European population (March 2010 Pilot version 60 CEU project data). We also selected SNPs that tagged all remaining SNPs in the 560kb interval with $r^2 > 0.9$. Using this strategy, we selected for inclusion on the iCOGS array (see below) a total of 440 SNPs, between positions 64205327 to 64765654 (NCBI build 37 assembly), that had an Illumina designability score (DS) above 0.9. Of these, 428 were successfully genotyped on the iCOGS array and passed QC filters.

iCOGS genotyping and imputation

Case and control samples were drawn from 50 studies participating in the BCAC, of which 41 were from populations of predominantly European ancestry and nine from populations of Asian ancestry, as described previously [5]. We performed iCOGS genotyping in four centers, as part of the Collaborative Oncological Gene-Environment Study (COGS). All BCAC studies were approved by the relevant local ethics committees, as described previously [5]. We used the genotype data from the 428 SNPs that passed quality control to impute genotypes at all additional known SNPs in the interval, using IMPUTE version 2.0 (IMPUTE2) and the 1000 genome project data (March 2012 version) as a reference panel [14]. Rather than preselecting a reference population, we followed the approach of Howie et al. [15] and used a multi-population reference panel. IMPUTE2 was applied with default parameters and effective population size (N_e) of 20,000.

Mammographic density

Mammographic density measurements were available for 6,886 women from nine BCAC studies that were also part of the Marker Of DEnsity (MODE) consortium [6] and DENSNP consortium [16] (**Table S1**). Covariate data were obtained through self-administered postal questioners, in-person interviews or telephone interviews; and anthropometric variables were self-reported or measured by trained staff (Supplementary Table 2 of Vachon et al. [16]). Seven studies estimated density (absolute and percent dense area) using the CUMULUS program [17], while two of the studies, the BBCC and NBCS studies, used the Madena software [18].

Statistical Analysis

For each SNP, we estimated a per-allele log-odds ratio (OR) and standard error using logistic regression, including principal components and per-study fixed-effects to adjust for study specific differences in allele frequency, as described previously [5]. Analyses were carried out separately for Europeans and Asians. We estimated genetic main effects for ER-positive and ER-negative breast cancer using logistic regression and restricting the cases to a specific subtype. We evaluated heterogeneity of association by tumour subtype in a case-only analysis, treating subtype status as the dependent variable. We derived the *P*-values for association by means of a likelihood-ratio test (one degree of freedom); all tests were two-sided. To identify the most parsimonious model, we identified all SNPs with $P < 10^{-4}$ and MAF ≥ 2% in the single SNP analysis, and included these in forward selection regression analyses, utilizing the step function in R with penalty term set to 10 [19]. To account for uncertainty in the data resulting from the imputation process, we conducted analysis by regressing on the allele dosage for each genotype. We estimated haplotype-specific ORs using an EM algorithm implemented in the haplo.stats package in R. For this analysis we used the most probable genotypes, and included study and principal components as covariates. We grouped haplotypes with a frequency < 0.01 together into one subgroup of rare haplotypes.

We assessed individual SNP associations with percentage density (PD), dense area (DA) and non-dense area (nDA) using linear regression. Because the distributions of estimated PD, DA and nDA were positively skewed (skewness = 1.31, 2.32 and 1.02, respectively), each phenotype was square-root transformed. This transformation reduces skewness and has previously been shown to generate variables that are approximately normally distributed [18]. In addition to study and principal components, we included age, body mass index (BMI), postmenopausal hormone replacement therapy (HRT), mammographic view, menopausal status, and case-control status as covariates in each model. Age and BMI were treated as continuous variables, while use of postmenopausal hormones (0 = Never, 1 = stopped prior to mammogram date, 2 = current use at date of mammogram, 9 = unknown), menopausal status at mammogram (0=postmenopausal;

1=premenopausal; 2=perimenopausal, 9=unknown) and case-control status were treated as categorical variables in the regression model. We also included mammographic view (1 = medio-lateral oblique (MLO) view, 2 = craniocaudal (CC) view) and treated it as categorical variable as it has been shown that the percent density measurements from the MLO view are systematically lower than those from the CC view [9]. The mean percentage density across all studies was 17 from the MLO view as compared to 25 from the CC view.

Expression quantitative trait locus analysis

We examined the associations of germline genotyped and imputed SNPs within 1Mb of the risk region with the expression levels of all genes within 1Mb, up and downstream, of the SNP in question (including *ADO* (MIM 611392)*, ARID5B* (MIM 608538)*, c10orf107, EGR2* (MIM 129010)*, JMJD1C* (MIM 604503)*, JMJD1C-AS1, REEP3* (MIM 609348)*, RTKN2* (MIM 113705) and *ZNF365*) in normal breast, adjacent normal and breast cancerous tissue from the following four cohorts: **Normal Breast (NB) I** (n=116) is a comprised women of European descent ascertained through multiple Norwegian hospitals. Gene expression data for the majority of women was derived from normal breast tissue in women who had not been affected with breast cancer; data for 10 women was derived from normal tissue adjacent to a tumor. Genotyping was performed using the iCOGS SNP array, and gene expression levels were measured with the Agilent 44K array [20; 21]. **NB II** (n=93) is the European subset of the TCGA study, for whom expression data were available from normal tissue adjacent to a tumor. Germline genotype data from Affymetrix SNP 6 array, processed through Birdseed, were obtained from TCGA dbGAP data portal [22]. Gene expression levels were assayed by RNA sequencing, RSEM (RNAseq by Expectation-Maximization [23]) normalized per gene, as obtained from the TCGA consortium [22]. The data were $\log_2$ transformed, and unexpressed genes were excluded prior to eQTL analysis. **Breast carcinomas (BC) I** (n=241) is a series of women of European ancestry diagnosed with breast cancer, and recruited through multiple Norwegian hospitals. Genotypes were obtained with the iCOGS SNP array, and mRNA expression data was from the Agilent 44K array [24]. **BC II** (n=765) is the TCGA breast cancer cohort; all non-European samples (as determined by clustering and PCA) were excluded from this analysis [22]. The genotyping platform was Affymetrix SNP 6, and gene expression data, for the breast tumors, was derived from RNA sequencing analysis, in a similar manner to NBII. There is no overlap between women recruited to each of these studies.

In addition, we examined all the genotyped or imputed SNPs used in the risk analysis for association with expression of nine genes (*ADO, ARID5B, c10orf107, EGR2, JMJD1C, NRBF2, REEP3, RTNK2* and *ZNF365* - represented by 14 expression probes) in the 1 Mb region on either side of the fine-mapping interval, using data from normal tissue in patients from METABRIC. **METABRIC** (n=135) comprises normal tissues adjacent to the tumours from breast cancer patients of genetically-confirmed European ancestry from the Molecular Taxonomy of Breast Cancer International Consortium (METABRIC) study [25]. The samples were assayed using the Illumina HT-12 v3 microarray. Matched germline SNP genotypes were available from the Affymetrix SNP 6·0 platform.

For all cohorts, the genotyping data was processed as follows: SNPs with call rates <0.95 or minor allele frequencies < 0.05 were excluded, as were SNPs out of Hardy Weinberg equilibrium with $P<10^{-6}$. All samples with a call rate below 80% were excluded. Identity by state was computed using the R GenABEL package [26], and closely related samples with IBS>0.95 were removed. The SNP and sample filtration criteria were applied iteratively until all samples and SNPs met the stated thresholds. In total, 489 samples and 662,521 SNPs passed were kept in the analysis. Imputation was run on both the iCOGS and Affymetrix6 germline genotype data using the 1000 genomes project March 2012 v3 release as the reference dataset [27]. A two-stage imputation procedure, using SHAPEIT to derive phased genotypes and IMPUTEv2 to perform the imputation on the phased data, which has been found to significantly reduce the computational burden [28]. The influence of germline genetic variations on gene expression was assessed using a linear regression model, as implemented in the R library eMAP (http://www.bios.unc.edu/~weisun/software.htm). An additive effect was assumed by modeling copy number of the rare allele, i.e. 0, 1 or 2 for a given genotype. Only relationships in *cis*, i.e. where the SNP resided less than 1 MB up or down from the center of the transcript, were investigated. Correction for multiple testing was performed using the false discovery rate (FDR) as implemented in the p.adjust function in R. Only FDR-adjusted, significant *P*-values, are reported in the Results section of the paper. Genotyping quality control and imputation for the METABRIC data are described in Guo et al. (Identification of novel genetic markers of breast cancer survival, JNCI, in press). For the METABRIC data, association between genotype and expression was tested by linear regression with FDR control as implemented in the MatrixEQTL package in R. We also conducted eQTL haplotype analysis in NBI and BCII which had been genotyped on iCOGS. The correlations with expression for the haplotypes residing in the four iCHAVs were estimated using the haplo.score function implemented in the R library haplo.stats, assuming a Gaussian distribution for the expression data.

Cell lines

Normal breast epithelial cell lines, MCF10A and Bre80 were grown in DMEM/F12 media supplemented with 5% horse serum, 10μg/ml insulin, 0.5μg/ml hydrocortisone, 20ng/ml EGF, 100ng/ml cholera toxin and antibiotics. The MCF7 breast cancer cell line was grown in DMEM media supplemented with 10% fetal bovine serum, 10μg/ml insulin, sodium pyruvate and antibiotics. All cell lines were routinely tested for *Mycoplasma* and profiled with short tandem repeats to confirm their identity.

Chromatin conformation capture (3C)

Cross-linked DNA from the above cell lines, was digested with EcoRI to generate 3C libraries as previously described [19]. 3C interactions were quantitated by real time PCR, on at least two independent 3C libraries, using primers designed against the EcoRI restriction fragments across the 10q21.2 locus. Interactions were quantified in triplicate.

The primers are listed in **Table S2**. Primer efficiencies were calculated using an artificial library of ligation products generated from two BAC clones (RP11-629KB and RP11-1021P21) that spanned the 10q21 locus and *NRBF2.* 3C interaction products were visualised by gel electrophoresis, gel purified and sequenced to verify the 3C product.

***In silico* analysis**

Genomic regions encompassing independent sets of correlated, highly trait-associated variants (iCHAVs) were examined for potential regulatory signals by overlaying epigenetic marks derived from ENCODE data using the UCSC Genome Browser. Tracks representing potential regulatory signals marked by DNaseI hypersensitivity, H3K4me1, H3K4me3 and H3K27ac histone modification, and transcription factor binding sites were obtained for the normal mammary cell types, human mammary epithelial cells (HMECs) and human mammary fibroblasts (HMFs), and two breast cancer cell lines, MCF7 and T47D. SNPs in each iCHAV were examined for potential functional consequences using HaploReg v2 [29] and RegulomeDB [30].

Plasmid generation

A 1287 bp fragment containing the *ZNF365* promoter and a 1163 bp fragment containing the *NRBF2* promoter were cloned into the pGL3 basic luciferase reporter. Using a sample heterozygous for rs2393886 as template, we then generated 1875 bp PCR fragments containing part of iCHAV2 using PCR primers modified with BamH1 and Sal1 and cloned each haplotype into both the *ZNF365* and *NRBF2* promoter constructs. PCR primers are listed in **Table S2**.

Reporter assays

Bre80, MCF10A and MCF7 cells were transiently transfected with equimolar amounts of luciferase reporter constructs using *Renilla* luciferase as an internal control reporter. Luciferase activity was measured 24hrs after transfection using Dual-Glo Luciferase (Promega). To correct for any differences in transfection efficiency or cell lysate preparation, *Firefly* luciferase activity was normalized to *Renilla* luciferase, and the activity of each construct was measured relative to the promoter alone construct, which had a defined activity of 1. Association was assessed by log transforming the data and performing two-way ANOVA, followed by Dunnett's multiple comparisons test; for ease of interpretation, values were back transformed to the original scale for the graphs.

RESULTS

We successfully genotyped 428 SNPs across the 560kb fine-mapping region in 46,450 cases and 42,600 controls from 41 case-control studies in populations of European ancestry, and in 6,269 cases and 6,624 controls from nine case-control studies of Asian ancestry [5]. We imputed genotypes for 3,409 SNPs in the interval in the European studies, at imputation-$r^2>0.3$ and MAF ≥ 1%, using known genotypes in combination with data from the 1000 Genomes Project reference panel. Based on data from the European studies, 87 genotyped or imputed SNPs were convincingly associated with overall risk of breast cancer (P-values 10^{-7} to 10^{-29}; **Figure 1**). The results for all SNPs in the interval with an association P-value < $1\text{x}10^{-3}$ for overall breast cancer risk (382 SNPs) are presented in **Table S3**.

Among the genotyped SNPs, the strongest evidence of association with overall breast cancer risk among Europeans was for rs10995194 (OR (95% CI) = 0.86 (0.84 - 0.88), $P = 3.77 \times 10^{-29}$). This SNP lies within intron 4 of *ZNF365* and is strongly correlated with the original GWAS hit rs10995190 ($r^2 = 0.99$). Analysis of the imputed SNPs identified two markers with slightly stronger associations: the most significantly associated marker was rs10995201 (OR = 0.85 (0.83 – 0.88), $P = 1.05 \times 10^{-29}$) which is also strongly correlated with rs10995194 ($r^2 = 0.94$).

Multiple independent signals at 10q21.2

To determine whether there were additional independent signals of association at the locus, we included in a forward stepwise regression model 230 SNPs with MAF ≥ 2% that displayed evidence of association with overall breast cancer risk at $P < 10^{-4}$. The most parsimonious model included four independent SNPs that mark four iCHAVs (**Figure 1; Table 1**). These were: **iCHAV1 -** rs10995201 (OR = 0.85 (0.83-0.88), $P = 1.05 \times 10^{-29}$; conditional $P = 4.92 \times 10^{-16}$); **iCHAV2 -** chr10:64258684:D (OR = 0.93 (0.91-0.95), $P = 4.24 \times 10^{-14}$; conditional $P = 3.24 \times 10^{-05}$); **iCHAV3** - rs7922449 (OR = 1.06 (1.04-1.08), $P = 1.68 \times 10^{-07}$; conditional $P = 5.78 \times 10^{-05}$); **iCHAV4** - rs9971363 (OR = 0.94 (0.92-0.97), $P = 6.54 \times 10^{-5}$; conditional $P = 3.95 \times 10^{-04}$) (**Figure 1B**). These four SNPs were all imputed, with IMPUTE2 info-score above 0.85. The strongest pairwise LD r^2 value amongst the four markers was 0.12 (between rs10995201 and chr10:64258684:D). Amongst the genotyped SNPs, the top SNP correlated with the lead iCHAV1 SNP was rs10995194 (OR = 0.86 (0.84-0.88), P = 3.77 x 10-29, r^2 = 0.94), with the lead iCHAV2 SNP was rs2393886 (OR = 0.93 (0.91-0.95), P = 4.50 x 10-14, r^2 = 0.99), with the lead iCHAV3 SNP was rs4746428 (OR = 1.06 (1.04-1.08), P = 3.24 x 10-08, r^2 = 0.68), and with the lead iCHAV4 SNP was rs10995312 (OR = 0.95 (0.92-0.97), P = 1.38 x 10-04, r^2 =0.97).

In order to identify the candidate causal SNPs in each iCHAV for subsequent functional analysis, we calculated the likelihood ratio of each SNP relative to the best independent signal with which it was correlated (r^2 >0.6), after adjusting for the lead SNP of preceding iCHAV(s). SNPs with a relative likelihood ratio of <1:100 compared with the most significant SNP for each iCHAV were excluded from consideration as being potentially causative [18; 31]. Eleven SNPs had a relative likelihood ratio of >1:100 compared with the most significant SNP (rs10995201) and hence could not be excluded as causative for the lead signal – these SNPs were all strongly correlated with rs10995201 and span an interval of 31.2kb (iCHAV1, **Figure 1, Table S4**). A twelfth SNP, a single base insertion chr10:64291099, was excluded at this threshold, but not strongly so (likelihood ratio~1:600); all other SNPs could be clearly excluded (likelihood ratios <1:10^{12}). After adjustment for lead SNP of iCHAV1, we identified 16 strongly correlated SNPs and with a likelihood ratio >1:100 relative to the lead SNP in iCHAV2 (chr10:64258684:D); these SNPs span an interval of 25kb (iCHAV2, **Figure 1, Table S5**). SNP rs16917302 (OR = 0.96 (0.93 - 0.99), P = 1.03 x 10^{-02}), reported by Couch et al. [13], lies within the region that iCHAV2 spans. However, rs16917302 is only weakly correlated with the lead SNP (r^2 = 0.12) in iCHAV2. After adjusting for the effects of lead SNPs of iCHAV1 and iCHAV2 17 highly correlated SNPs had a relative likelihood >1:100 compared to rs7922449 (iCHAV3, **Figure 1, Table S6**) and span an interval of 29.1kb. Finally, only one other SNP, rs7090365, had a relative likelihood of >1:100 with respect to rs9971363 the lead SNP of iCHAV4, after adjusting for the lead SNPs in iCHAVs1-3 (**Figure 1, Table S7**). iCHAVs1, 2 and 3 all lie within *ZNF365*. The SNPs in iCHAV1 and iCHAV3 span regions that physically overlap, while the SNPs in iCHAV2 lie telomeric to iCHAV1 and iCHAV3. iCHAV4 lies 5′ of the *ADO* gene, which encodes 2-aminoethanethiol dioxygenase (**Figure 1**).

Association with breast cancer subtypes

Based on data from European studies, 31 genotyped SNPs and 14 imputed SNPs were associated with risk of ER-positive breast cancer (P-values 10^{-7} to 10^{-23}). The most strongly associated SNP for overall breast cancer (rs10995201) was also the most strongly associated SNP for ER-positive disease (OR = 0.85 (0.82-0.88), P = 2.51 x 10^{-23}) and had a similar association for ER-negative disease (OR = 0.87 (0.82-0.91), P = 9.60 x 10^{-08}, $P_{heterogenetiy}$ = 0.34) (**Table 1, Figures S1 and S2**). The most strongly associated, well imputed, SNP (IMPUTE2 info-score > 0.9) for ER-negative disease was rs10995182 (OR = 0.85 (0.8-0.9), P = 6.68 x 10^{-08}), another SNP within iCHAV1 strongly correlated with rs10995201. Thus, the results indicate that susceptibility SNPs in iCHAV1 confer similar relative risks for ER-positive and ER-negative disease. Similarly, the lead SNPs in iCHAV2 and 3 showed similar associations for ER-positive and ER-negative disease (OR_{ER+}= 0.96 (0.94 - 0.98) P_{ER+}= 8.77 x 10^{-04}, OR_{ER-}= 0.98 (0.94 – 1.02) P_{ER-}=

0.309, $P_{heterogeneity}$ = 0.44 for chr10:64258684:D adjusted for iCHAV1, OR_{ER+}= 1.04 (1.02 – 1.07) P_{ER+}= 1.54 x 10^{-03} , OR_{ER-}=1.07 (1.02 – 1.11) P_{ER-}= 4.36 x 10^{-03}, $P_{heterogeneity}$ = 0.44 for rs7922449 adjusted for iCHAV1 and 2). However, the lead SNP in iCHAV4 showed no association with ER-negative disease (OR_{ER+}= 0.93 (0.90 – 0.97) P_{ER+}= 7.72 x 10^{-05}, OR_{ER-}= 1.00 (0.94 – 1.05) P_{ER-}= 0.862, $P_{heterogeneity}$ = 0.016 for rs9971363 adjusted for iCHAVs1, 2 and 3).

To determine whether there were additional subtype-specific signals of association, we included all SNPs displaying evidence for association with ER-positive disease (222 SNPs, $P < 10^{-4}$ and MAF ≥ 2%) and ER-negative disease (19 SNPs, $P < 10^{-4}$ and MAF ≥ 2%) in separate forward stepwise regression models. For ER-positive disease, two iCHAVs were identified: **iCHAV1-ER+** rs10995201 (OR = 0.85 (0.83-0.88), P = 2.51 x 10^{-23}; conditional P = 1.65 x 10^{-18}) in iCHAV1; **iCHAV2-ER+** chr10:64258684:D (OR = 0.93 (0.91-0.95), P = 8.01 x 10^{-11}; conditional P = 2.59 x 10^{-05}) in iCHAV2.

Breast cancer risk associations in Asian studies

The top associated marker among Asians was the genotyped SNP rs7914770 (OR =0.93 (0.89, 0.98), P = 0.006). This SNP, which lies between iCHAV1 and iCHAV4, as defined in analysis of the European population, was not associated with overall breast cancer risk among Europeans (OR =1.01 (0.98, 1.03), P = 0.534; **Table S8**). The most strongly associated genotyped SNP in Europeans, rs10995194 in iCHAV1, showed a borderline association with breast cancer risk in Asians, but in the opposite direction (Asians: OR =1.18 (1.00-1.39), P = 0.04; Europeans: OR = 0.86 (0.84-0.88), P= 3.77 x 10^{-29}). The minor (C) allele of rs10995194 (MAF = 0.15), and the other iCHAV1 SNPs, were much rarer in Asians (MAF = 0.02), but the ORs estimates nevertheless differed significantly (P = 10^{-4}). In iCHAV2, the most strongly associated genotyped SNP in Europeans, rs2393886 (OR = 0.93, MAF = 0.47 for the A allele), was also associated with risk in Asians; however, in contrast to iCHAV1, the effects were in the same direction and of comparable magnitude (OR = 0.95 (0.90-1.00), P = 0.04, allele frequency 0.51 for the A allele in Asians). In this iCHAV the most strongly associated SNP in Asians was rs4746409 (OR =1.06 (1.00-1.11), *P* = 0.03), but this is strongly correlated with the lead SNP rs2393886 (r^2 = 0.88). SNP rs10822013 within iCHAV2, recently identified by Cai et al. in an Asian GWAS [7], was more weakly associated with risk in Asians in our data (OR = 0.96 (0.90-1.10), *P* = 0.07). None of the genotyped markers in iCHAV3 or iCHAV4 that were significant in Europeans showed association with overall breast cancer risk in the Asian population.

Haplotype analysis

We conducted haplotype analysis using the most probable genotype for the imputed lead SNPs in each of the iCHAVs. We grouped haplotypes with a frequency < 0.01 into one (rare) group. The haplo.score procedure estimated eleven haplotypes with non-zero frequencies for all three phenotypes (Overall, ER+ and ER- risk) (**Table S9**). The most significant association was observed for haplotype H6, carrying the rare allele of the lead SNPs of iCHAV1 and iCHAV2: OR=0.86 (0.82-0.90), P = 8.52 x 10^{-10}. Consistent with the regression analyses, the three haplotypes (H6, H14, H5) carrying the rare allele of the iCHAV1 SNP rs10995201 were all associated with a similar, reduced breast cancer risk. Three other haplotypes, all carrying the rare allele of the iCHAV2 SNP, chr10:64258684:D, were also associated with a reduced risk, relative to the baseline haplotype, consistent with an independent effect of iCHAV2.

Association with mammographic density phenotypes

Multiple linear regression was used to investigate the association between mammographic density phenotypes (PD – percent density, DA – dense area, nDA – non-dense area) and genotypes after adjustment for other covariates. Amongst the three density phenotypes, the strongest associations were observed with DA. The strongest association with DA and PD was seen with the lead SNP of iCHAV-1, rs10995201 (β=-0.25 (0.05), *P* = 1.45 x 10^{-07} for DA, β (se) =-0.15 (0.04), *P* = 1.32 x 10^{-05} for PD;

Tables S10-S11; Figures S3-S4). After adjusting for the lead SNP in iCHAV1, no SNPs in iCHAV2 were associated with any of the density phenotypes at $P < 0.01$ (**Table S12**); similarly, none of the iCHAV3 or iCHAV4 SNPs were associated with density phenotypes (**Tables S13-S14)**. The strongest association with nDA was seen with imputed marker rs224303 about 33kb away from iCHAV4 (**Figure S5**), which was not associated with overall risk of breast cancer ($P = 0.745$).

To assess the extent to which the observed association with breast cancer risk might be mediated through a mammographic density phenotype, we estimated the association with breast cancer risk before and after adjustment for PD, DA or nDA in a pooled analysis of the 2,379 breast cancer cases and 4,507 controls on whom density measurements were available. The association between lead iCHAV1 SNP rs10995201 (i.e. the only iCHAV for which an association with mammographic density had been identified) and breast cancer in this subset (OR= 0.87 (0.77-0.98), $P = 0.02$) was similar to that in the complete BCAC set, and was only slightly attenuated after adjustment for PD (OR=0.88 (0.78-1.00) P=0.05) or DA (OR=0.89 (0.79-1.01) P=0.06) (**Table S15**).

eQTL analysis

We analyzed 2238, 5122, 2250, 5211 and 3814 SNPs in NBI, NBII, BCI, BCII and METABRIC respectively for association with the expression levels of all genes within 1Mb, up and downstream, of the SNP in question. Significant eQTL associations were observed for both normal breast and tumors. Multiple SNPs within the fine mapping region associated with expression of *c10orf107* in the NB II cohort (strongest association chr10:63427159:D, which is not a candidate causal risk SNP – FDR-adjusted $P = 6.1\text{x}10^{-5}$ and $r^2=0.325$). For the breast carcinoma BC I cohort, multiple eQTLs were found for both *c10orf107* and *RTKN2* (strongest associations chr10:63427159:D - FDR-adjusted $P = 4.3\text{x}10^{-6}$ and $r^2=0.15$, and rs870988 - FDR-adjusted $P = 1.4\text{x}10^{-5}$ and $r^2=0.13$, respectively). In BC II we observed multiple eQTLs for three different genes, *c10orf107*, *EGR2* and *ADO* (rs12781009 - FDR-adjusted $P=5.6\text{x}10^{-9}$ and $r^2=0.066$, rs34632941 -

FDR-adjusted *P*=0.02 and r^2=0.02 and rs224045 **-** FDR-adjusted *P*=0.02 and r^2=0.02, respectively). No significant associations with expression were found for NBI or METABRIC, and there were no significant associations between the putative causal SNPs in iCHAV1-4 and expression of any of the genes analyzed in the region in any study (**Tables S16-S17**). Significant associations (without correction for multiple testing) were found between haplotypes of iCHAV1 and *NRBF2* in NBI and BCI (*P* = 0.005 and *P* = 0.042 respectively), and between haplotypes of iCHAV2 and *NRBF2* in NBI (*P*= 0.011). In addition, we found associations between haplotypes of iCHAV1 and *REEP3, EGR2* and *RTKN2* (*P* = 0.011-0.049), haplotypes of iCHAV2 and *RTKN2* (*P* = 0.012), haplotypes of iCHAV3 and *REEP3, JMJD1C, ARID5B, ADO*, *RTKN2* and *TMEM26* (*P* = 0.001-0.036), and haplotypes of iCHAV4 and *ARID5B* (*P* = 0.012) in either NBI or BCI, but not both.

Chromosome conformation capture analyses identify *ZNF365* and *NRBF2* as target genes

We performed 3C experiments to determine whether there were any chromatin interactions between the *ZNF365* and *NRBF2* promoters and iCHAVs1, 2 and 3. We identified significant interactions between iCHAV2 at the 10q21.2 locus and both promoter regions in the breast cancer cell line, MCF7, and in two normal breast cell lines, MCF10A and Bre80 (**Figure 2, Figure S6**). No reproducible interactions were detected between iCHAVs 1 or 3 and *ZNF365* and *NRBF2* in the cell lines analyzed. Although we did observe some possible interactions in MCF7 and MCF10A between different parts of iCHAV1/3 and the promoters of both *ZNF365* and *NRBF2* they were not reproducible (**Figure 2, Figure S6**).

Identification of a putative regulatory region within iCHAV2 regulating both *ZNF365* and *NRBF2*

We used available ENCODE ChIP-seq data to identify putative regulatory elements (PREs) within iCHAV2 (**Figure 3A**). We identified two PREs called PRE1 and PRE2, as defined by DNaseI hypersensitivity sites (indicative of regions of open chromatin) in several normal and cancer breast cell lines, and H3K4me1 and H3K4me2 histone modifications in HMEC cells (**Figure 3B**). PRE1 lies in a complex repetitive region and we were unable to clone and analyse this region. However, six (chr10:64258684:D, rs2393886, rs10995176, c10_pos64258017, rs10509168 and chr10:64258692:D) of the 17 candidate causal SNPs lie within PRE2 (**Figure 3B**). We examined the regulatory capability of PRE2, combined with the effect of the protective haplotype, using luciferase constructs containing the *ZNF365* or *NRBF2* promoters. Inclusion of the reference haplotype of iCHAV2 did not significantly alter the effect of the *NRBF2* promoter in Bre80 cells. However, the construct containing the protective haplotype acted as a silencer relative to the iCHAV2 reference allele (P=0.003; **Figure 4A; Figure S7**). A similar trend was seen in MCF7 cells (P=0.029; **Figure 4C**). Although constructs containing the *ZNF365* promoter showed a trend reducing its activity with the reference haplotype of iCHAV2, this was only significant in MCF7 cells (**Figures 4B and D**). Similarly, inclusion of the protective haplotype reduced the *ZNF365* promoter activity, but had no effect relative to the iCHAV2 reference haplotype in either Bre80 or MCF7 cells (**Figures 4B and D**).

DISCUSSION

Our large combined dataset provides clear confirmation of a susceptibility locus for breast cancer at 10q21.2 for breast cancer as originally reported by Turnbull et al [4], and for mammographic density as reported by Lindström et al [9]. Multiple regression and haplotype analyses showed clear evidence of at least two, and potentially four, independent susceptibility loci in this region in Europeans. The most strongly associated SNP, rs10995201 in iCHAV1, showed clear evidence of association with both ER-positive and ER-negative disease, with the ORs being similar, and was also the SNP most strongly associated with mammographic density (DA, and hence PD). iCHAV2 (lead SNP - chr10:64258684) and iCHAV3 (lead SNP - rs7922449) also appeared to be associated with both ER-positive and ER-negative disease. Evidence of a fourth iCHAV, associated only with ER-positive breast cancer, was weaker. In contrast to the results in Europeans, there was less evidence of association between SNPs at this locus and breast cancer risk in Asian women. The top associated genotyped SNP among Asians was rs7914770, which was not associated with overall breast cancer risk among Europeans. Furthermore, the lead genotyped SNP in Europeans, rs10995194, showed borderline evidence of association with breast cancer in Asians in the opposite direction, such that the effect sizes were clearly different. There are several possible explanations for the difference in the effect of iCHAV1 by ethnicity. The difference might reflect the differential effect of another SNP, or SNPs, in the 10q21.2 region. Alternatively it might reflect trans-interactions with SNPs elsewhere in the genome. Larger studies in Asian populations, both for breast cancer risk and mammographic density, might help to resolve this paradox. The SNPs in iCHAV2, however, showed effects that were consistent between the two populations.

The *A* allele of rs10995190 in iCHAV1 is associated with decreased ER-positive and ER-negative breast cancer risk, as well as with lower percent mammographic density and reduced dense area. These results are consistent with the hypothesis that the same causal SNP confers susceptibility to both mammographic density and breast cancer risk. However, adjustment for percent density or dense area caused only a minor attenuation of the association between breast cancer risk and the lead iCHAV1 SNP. The implications of this finding are not clear, but it is likely that percent and absolute mammographic density as captured by a two-dimensional mammogram, despite being strong predictors of breast cancer risk, are imperfect measures of the underlying mechanism that drives breast cancer risk. Alternatively, it may be that different SNPs in this iCHAV are acting independently on mammographic density and breast cancer risk, and through different mechanisms. We did not observe associations with mammographic density for breast cancer-associated SNPs in the other iCHAVs, but the smaller sample size, and hence lower statistical power, for the mammographic density analysis mean that more subtle effects in other iCHAVs would not have been detectable.

As we have reported for the breast cancer loci at 11q13 [19] and 2q35 [32], we did not find any evidence for single SNP eQTLs for any of the putatively causal SNPs in iCHAVs1-4 in normal or cancerous breast samples. This may be because the power of the eQTL studies (n=93-765) is limited, or because eQTLs are context dependent and may only be expressed in certain cell types or in response to certain stimuli. We have, however, identified a putative regulatory element in iCHAV2 at the 10q21.2 locus that interacts with both the *NRBF2* and *ZNF365* promoters in both normal breast and breast epithelial tumor cells. It is interesting that we detected haplotype associations with iCHAV1 and iCHAV2 and *NRBF2* expression, but the significance of these is difficult to interpret given their modest P values, and the fact that these iCHAVs are far too big to be cloned in their entirety for luciferase assays.

We prioritized the 3C analysis to look for interactions between iCHAVs 1, 2 and 3 and the promoters of *ZNF365* and *NRBF2* because of their function. *NRBF2* encodes nuclear receptor binding protein 2, an interaction partner of the peroxisome proliferator-activated receptor alpha (PPARα) and exhibits a gene activation function in mammalian cells [33]. Furthermore, NRFB2 is thought to have a role in cell survival in neural progenitor cells [34] and to suppress autophagy [35], a process which needs to be tightly controlled in breast cells during normal development, tissue differentiation, and response to stress [36]. To our knowledge, NRBF2 has not previously been implicated in breast cancer tumorigenesis. Our results suggest that the haplotype in iCHAV2 associated with reduced risk of breast cancer is associated with silencing of the *NRBF2* promoter. *ZNF365* encodes the zinc finger protein 365, which plays a critical role in stabilizing fragile sites within the genome and telomeres [37] and maintaining genome stability [38], and is therefore a good candidate for a breast cancer susceptibility gene. Although we did not observe a differential effect of the protective haplotype on the *ZNF365* promoter in luciferase assays, the protective SNPs might act through differential looping as we have previously observed at the 2q35 breast cancer risk locus [32]. Alternatively, other candidate causal SNPs in PRE1 or elsewhere in iCHAV2 may have a differential effect on transactivation of the *ZNF365* promoter. We did not find any convincing evidence for interactions between iCHAV1/3 and the promoters of *ZNF365* or *NRBF2* in MCF7, MCF10A or Bre80 cells. It is possible that other genes, such as *ADO*, which encodes 2-aminoethanethiol dioxygenase, or *EGR2* encoding early growth response-2, are the targets of these iCHAVs, or that their interactions with *ZNF365* or *NRBF2* are manifest in different cell types, such as of the immune system, or only in response to specific stimuli.

In conclusion, we have found evidence for four sets of correlated genetic variants (iCHAVs)at 10q21.2 independently associated with breast cancer risk, one of which is also associated with mammographic density. In one of these iCHAVs, we have identified candidate causal SNPs that affect expression of the *NRBF2* gene which lies more than 600kb away, suggesting that expression of NRFB2 may play a role in transformation or progression of transformed breast cells.

SUPPLEMENTAL DATA

Supplemental data include seven figures and seventeen tables.

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Acknowledgements are included in Supplemental data.

WEB RESOURCES

The URLs for data presented are as follows:

BLAST,http://blast.ncbi.nlm.nih.gov/Blast.cgi
NCBI,http:www.ncbi.nlm.nih.gov/
Online Mendelian Inheritance in Man (OMIM), http://www.omim.org/
UCSC Genome Browser, http://genome.ucsc.edu
HaploRegv2, www.broadinstitute.org/mammals/haploreg/
RegulomeDB, regulomedb.org/

1000 Genomes, www.1000genomes.org/

R library eMAP, http://www.bios.unc.edu/~weisun/software.htm

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Legends

Figure 1. Association results for overall breast cancer risk. Directly genotyped SNPs are shown as filled black circles, and imputed SNPs ($r^2 > 0.3$, MAF > 0.02) are shown as open red circles, plotted as the negative log of the P value against relative position across the locus. A) A schematic of the gene structures is shown. iCHAVs, encompassing all SNPs with a likelihood ratio of <1:100 compared with the most significant SNP, are labelled and are shown as grey regions. The pattern of LD for all SNPs from the 1000 Genomes Project CEU population is shown as a plot of pairwise r^2 values using a greyscale, where white and black signify $r^2 = 0$ and 1, respectively. The dashed purple line represents genome-wide significance ($P < 5 \times 10^{-8}$). B) iCHAV4 is shown in more detail.

Figure 2. Chromatin interactions with the *ZNF365* and *NRBF2* promoters at the 10q21.2 locus. A) 10q21.2 locus showing the distances from iCHAVs1-4 and the nearest genes. Chromatin interaction frequencies were plotted at the corresponding chromosomal position for MCF7 (B and E), MCF10A (C and F) and Bre80 (D and G) for the *ZNF365* and *NRBF2* promoters, respectively. iCHAV2 is marked in green, iCHAV1 (which physically overlaps iCHAV3) in blue and iCHAV3 in red. Representative graphs are shown (N=3) and error bars denote SD.

Figure 3. Chromatin marks in breast cells in iCHAVs at 10q21.2. The region encompassing 1 Mb at 10q21.2 is shown in (A). Candidate causal SNPs lying within iCHAVs 1-4 are shown as tick marks in matching colours to iCHAVs. DNaseI hypersensitive sites found in mammary cell types from ENCODE are depicted under the gene schematics. iCHAV2 is shown in panel (B). ENCODE tracks are shown for mammary DNaseI HS, histone modification ChIP-seq, and transcription factor ChIP-seq. The cloned PRE2 region for the iCHAV2 reporter construct is marked.

Figure 4. Protective haplotype of iCHAV2 silences *NRBF2* promoter activity. Both haplotypes of the iCHAV2 PRE2 were cloned upstream of *NRBF2*- and *ZNF365*- promoter-driven luciferase reporters. Cells were transiently transfected with the common ('PRE2'), and the protective ('Prot Hap') haplotype constructs and assayed for luciferase activity 24 hours later. Panels A and B show results for the *NRBF2* and *ZNF365* promoters in Bre80 cells and panels C and D show results for *NRBF2* and *ZNF365* promoters in MCF7 cells. Error bars denote 95% confidence intervals from three independent experiments performed in triplicate. P-values were determined by two-way ANOVA followed by Dunnett's multiple comparisons test (**P<0.01, *P<0.05) on log transformed data; for ease of interpretation back transformed data has been graphed.

Table 1: Four iCHAVs at 10q21.2 associated with breast cancer risk or mammographic density phenotype in Europeans

	iCHAV1		iCHAV2		iCHAV3		iCHAV4	
	rs10995201*		chr10:64258684:D*		rs7922449*		rs9971363*	
	P-value [a]	OR (95%CI) [a]	P-value [a]	OR (95%CI) [a]	P-value [a]	OR (95%CI) [a]	P-value [a]	OR (95%CI) [a]
Overall	1.05E-29	0.85 (0.83,0.88)	4.24E-14	0.93 (0.91,0.95)	1.68E-07	1.06 (1.04,1.08)	6.54E-05	0.94 (0.92,0.97)
ER+	2.51E-23	0.85 (0.82,0.88)	8.01E-11	0.93 (0.91,0.95)	6.70E-06	1.06 (1.03,1.09)	1.26E-05	0.93 (0.90,0.96)
ER-	9.60E-08	0.87 (0.82,0.91)	0.0055	0.95 (0.91,0.98)	0.000268	1.08 (1.04,1.13)	0.776	0.99 (0.94,1.05)
	P-value [b]	β (se) [b]	P-value [b]	β (se) [b]	P-value [b]	β (se) [b]	P-value [b]	β (se) [b]
Density area	1.45E-07	-0.25 (0.05)	0.00555	-0.09 (0.03)	0.308	0.04 (0.04)	0.634	-0.02 (0.05)
Percent density	1.32E-05	-0.15 (0.04)	0.00155	-0.08 (0.02)	0.634	0.01 (0.03)	0.629	-0.02 (0.04)

SNP [c]	P-value [c]	Info [d]	SNP [c]	P-value [c]	Info [d]	SNP [c]	P-value [c]	Info [d]	SNP [c]	P-value [c]	Info [d]
rs10995181§	5.07E-28	1	rs4489633§	1.45E-09	0.96	rs1878253§	6.54E-08	1	rs9971363§§*	6.54E-05	0.97
rs10995182§§	3.42E-28	0.92	rs4282885§	8.51E-10	0.99	rs1914200§	1.03E-07	1	rs7090365§§	6.59E-05	0.97
rs10995187§	6.66E-29	1	rs10995173§	3.89E-10	1	rs10740081§§	9.17E-08	0.99			
rs4746419§	4.43E-29	1	rs10822012§§	3.93E-10	0.99	rs10761639§§	1.01E-07	0.98			
rs34511355§	6.22E-29	1	rs10761637§§	3.92E-10	0.99	rs7901318§§	7.26E-08	0.98			
rs10995189§	6.04E-29	1	rs12098307§§	4.16E-10	0.99	rs2393894§§	5.95E-08	0.97			
rs10995190§	5.61E-29	1	rs10822013§	8.81E-11	1	rs7922449§§*	1.68E-07	0.86			
rs10995191§	6.04E-29	1	rs10509168§	2.22E-13	1	rs10995196§§	2.70E-08	0.98			
rs11524313§§	4.16E-29	0.97	rs10995176§§	7.17E-14	0.99	rs4746428§	3.24E-08	1			
rs10995193§§	3.67E-29	0.99	c10_pos64258017§	1.03E-13	1	chr10:64293571:D§§	1.94E-08	0.88			
rs10995194§	3.77E-29	1	rs2393886§	4.50E-14	1	rs9633558§§	2.62E-08	0.99			
rs10995201§§*	1.05E-29	0.95	chr10:64258684:D§§*	4.24E-14	0.98	rs7915519§§	2.63E-08	0.99			
			chr10:64258692:D§§	8.51E-13	0.86	rs6479823§§	2.66E-08	0.99			
			rs12243471§	4.00E-10	0.99	rs1914182§§	2.62E-08	0.99			
			rs12245332§	3.95E-10	1	rs10822017§§	2.07E-08	0.99			
			rs2393887§	6.94E-10	1	rs7901573§§	2.93E-08	0.99			
			rs4746409§	3.06E-12	1	rs12258134§§	2.94E-08	0.99			
						rs1949356§	3.61E-08	1			

a: P-value, Odds ratio (OR) and 95% Confidence Interval (CI) for association with overall breast cancer risk,Estrogen Positive (ER+) and Estrogen Negative (ER-) disease.

b: P-value, Beta and standard error (SE) for association with percentage density, dense area.

c: SNPs correlated ($r^2 > 0.6$) with a likelihood ratio of >1:100 with respect to overall risk association relative to lead SNP of each iCHAV and corresponding P-value for association with overall breast cancer risk.

d: IMPUTE2 info score.

§: Genotyped marker.

§§: Imputed marker.

SUPPLEMENTAL DATA

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For members of AOCS see http://www.aocstudy.org/org_coll.asp; for kConFab, see http://www.kconfab.org/Organisation/Members.aspx.

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SUPPLEMENTAL FIGURES

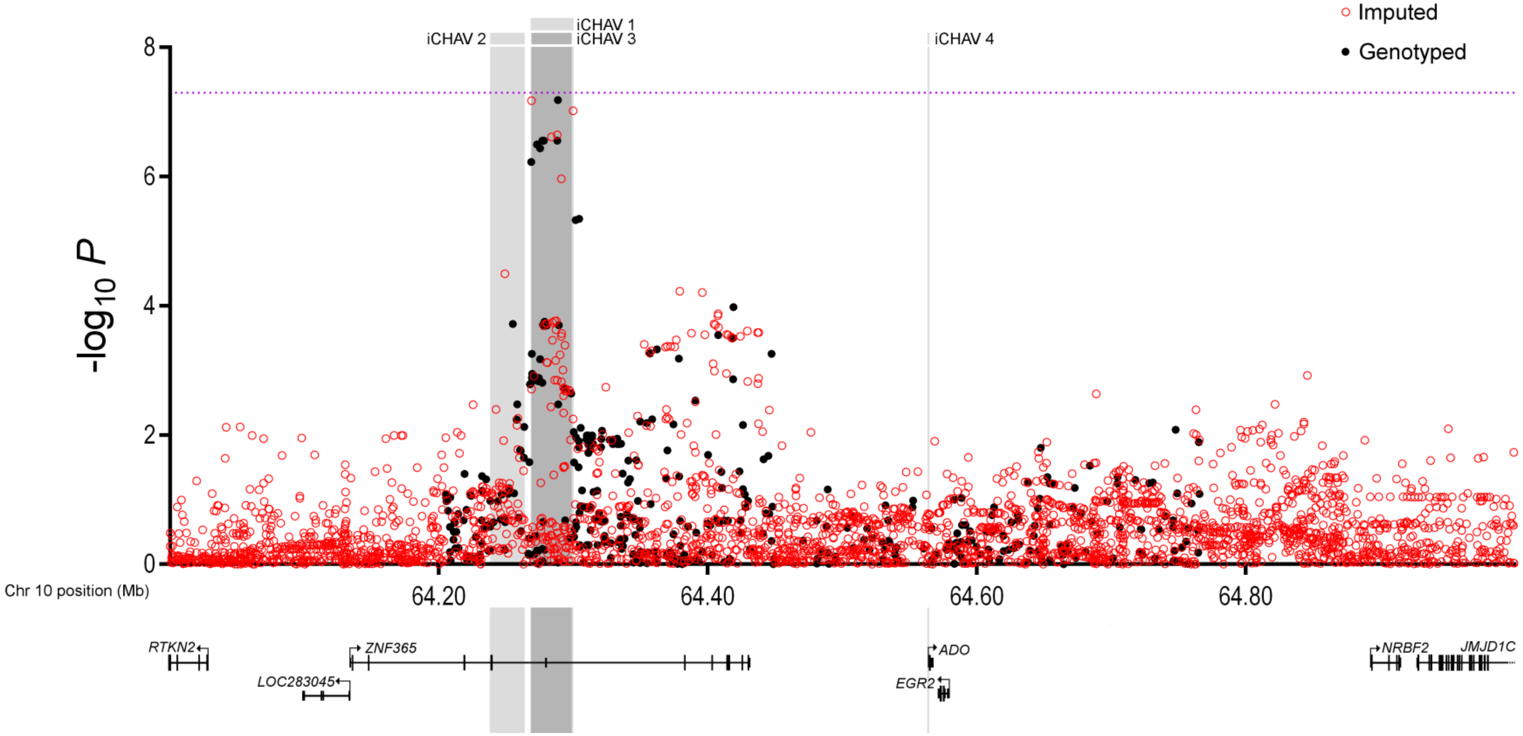

Figure S1. Association results for ER-negative breast cancer risk. Directly genotyped SNPs are shown as filled black circles and imputed SNPs (r^2 >0.3, MAF >0.02) are shown as open red circles, plotted as the negative log of the P value against relative position across the locus. A schematic of the gene structures is shown. Association peaks, shown as grey bars, are labelled.

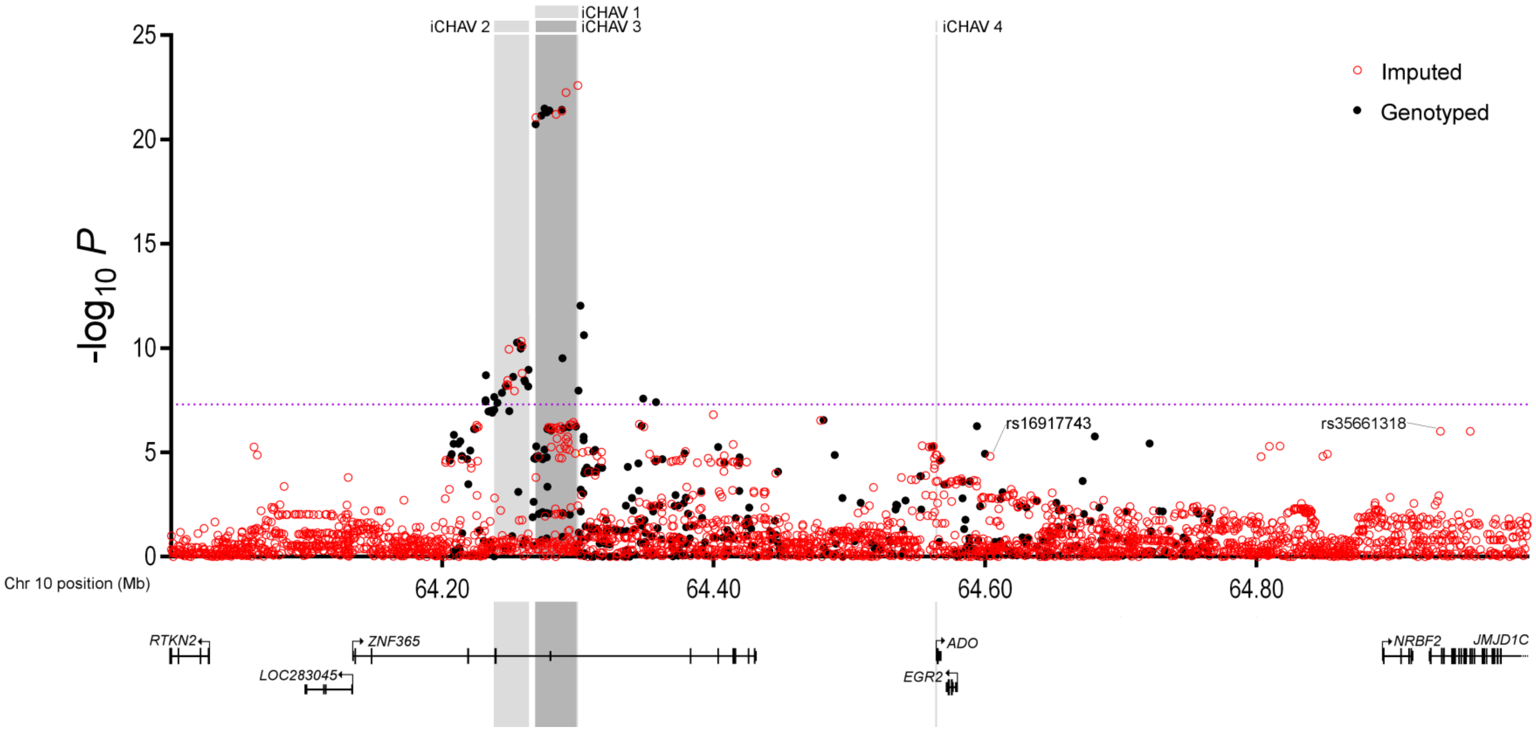

Figure S2. Association results for ER-positive breast cancer risk. Directly genotyped SNPs are shown as filled black circles and imputed SNPs (r^2 >0.3, MAF >0.02) are shown as open red circles, plotted as the negative log of the P value against relative position across the locus. A schematic of the gene structures is shown. Association peaks, shown as grey bars, are labelled..

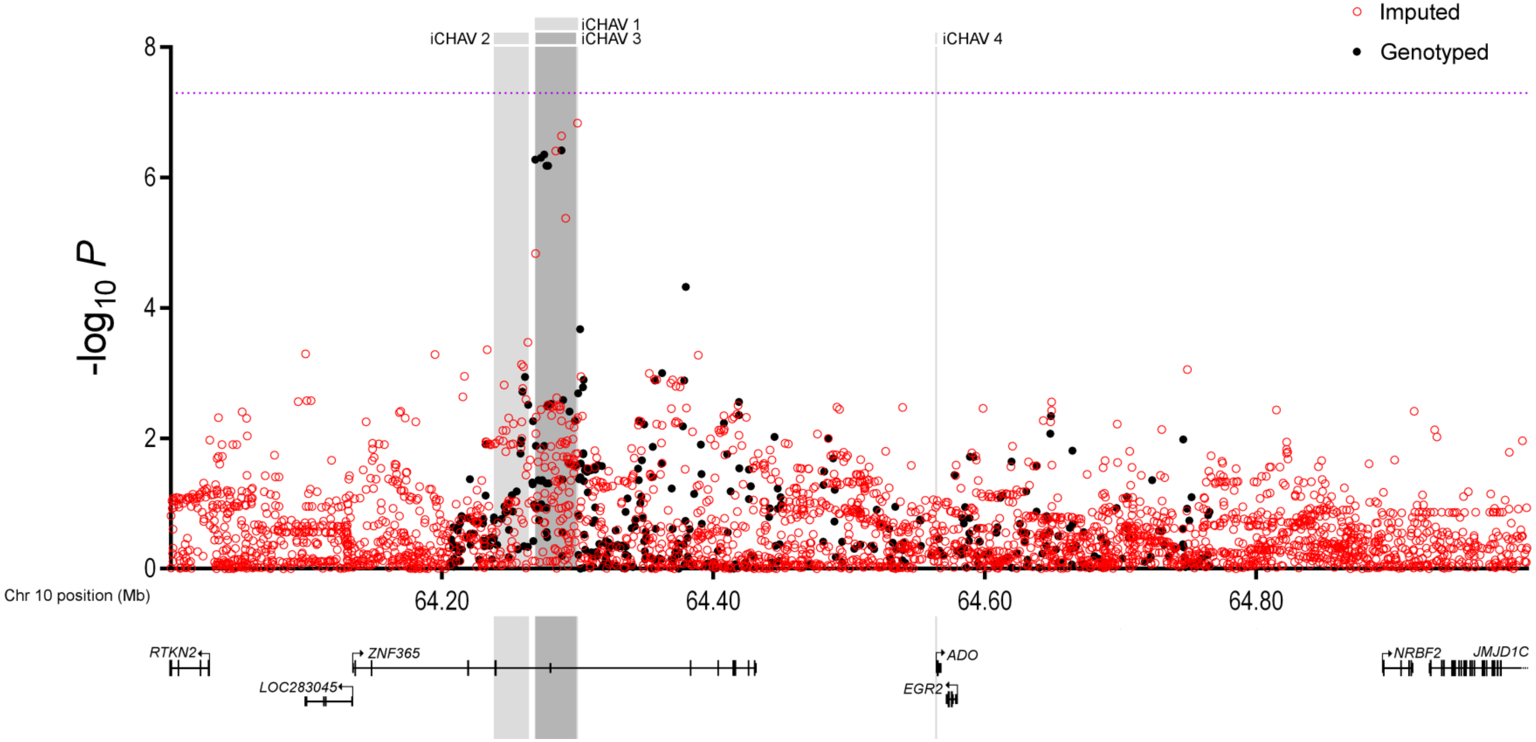

Figure S3. Association results for mammographic dense area. Directly genotyped SNPs are shown as filled black circles and imputed SNPs (r^2 >0.3, MAF >0.02) are shown as open red circles, plotted as the negative log of the P value against relative position across teh locus. A schematic of the gene structures is shown. Association peaks are labelled and are shown as grey regions.

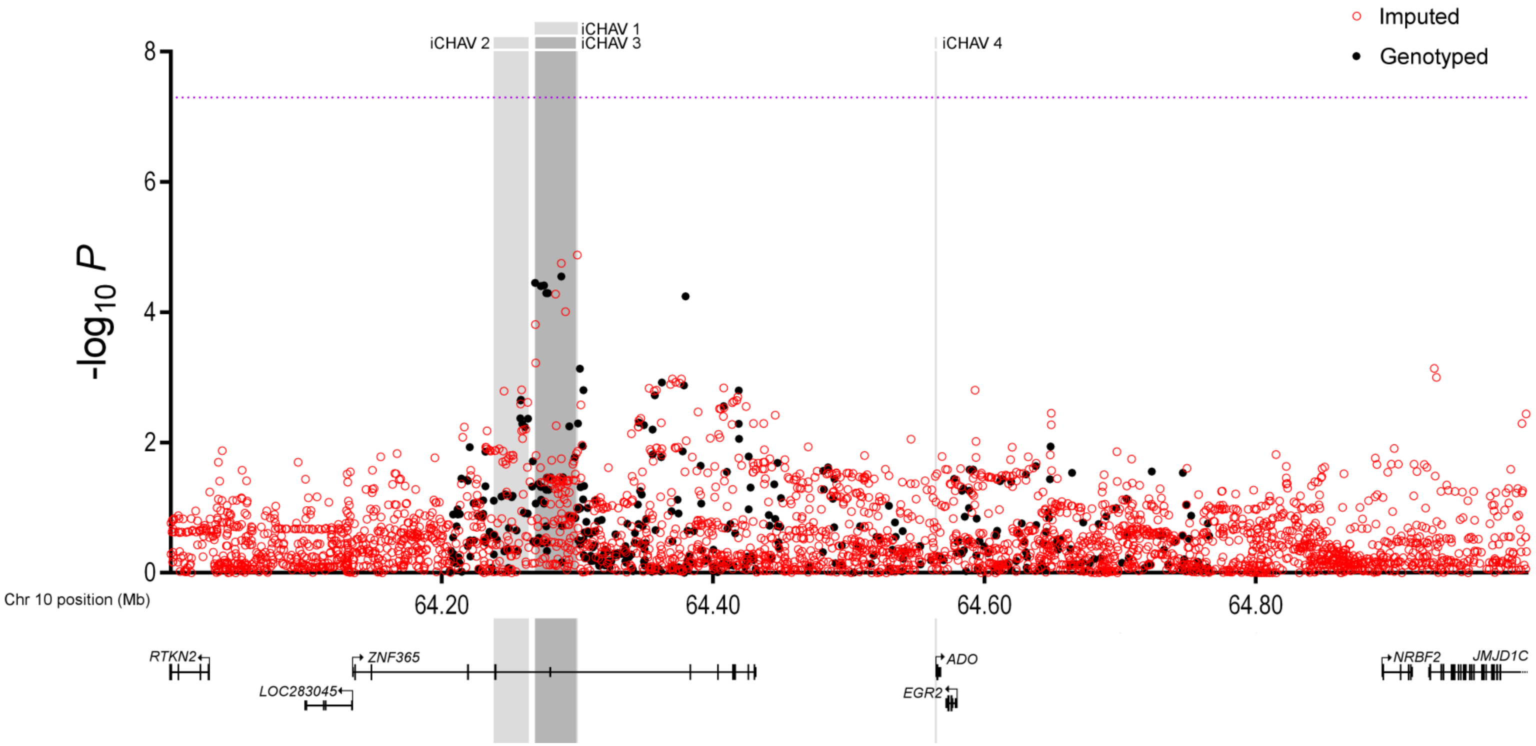

Figure S4. Association results for percent density. Directly genotyped SNPs are shown as filled black circles and imputed SNPs (r^2 >0.3, MAF >0.02) are shown as open red circles, plotted as the negative log of the P value against relative position across the locus. A schematic of the gene structures is shown. Association peaks, shown as grey bars, are labelled.

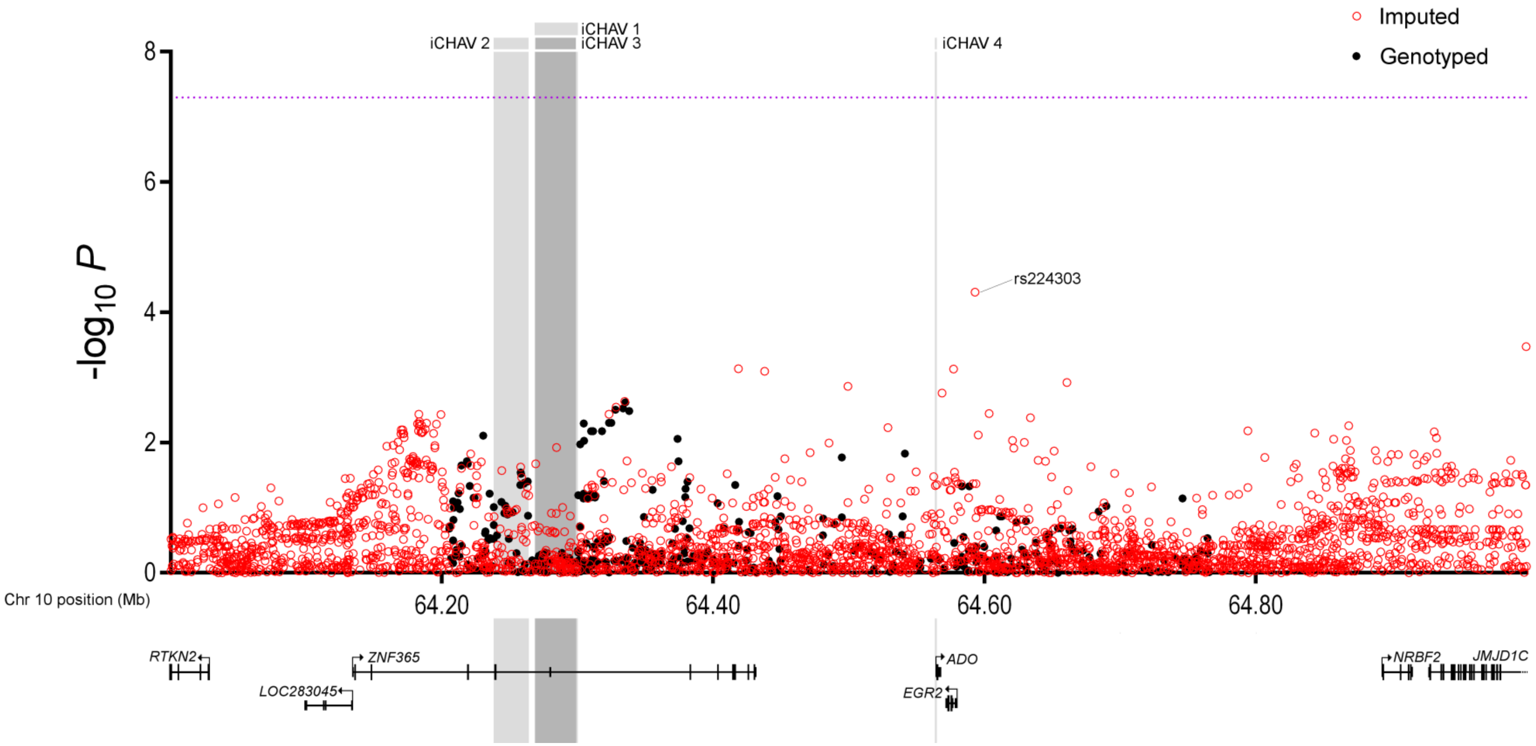

Figure S5. Association results for non-dense area. Directly genotyped SNPs are shown as filled black circles and imputed SNPs (r^2 >0.3, MAF >0.02) are shown as open red circles, plotted as the negative log of the P value against relative position across the locus. A schematic of the gene structures is shown. Association peaks, shown as grey bars, are labelled.

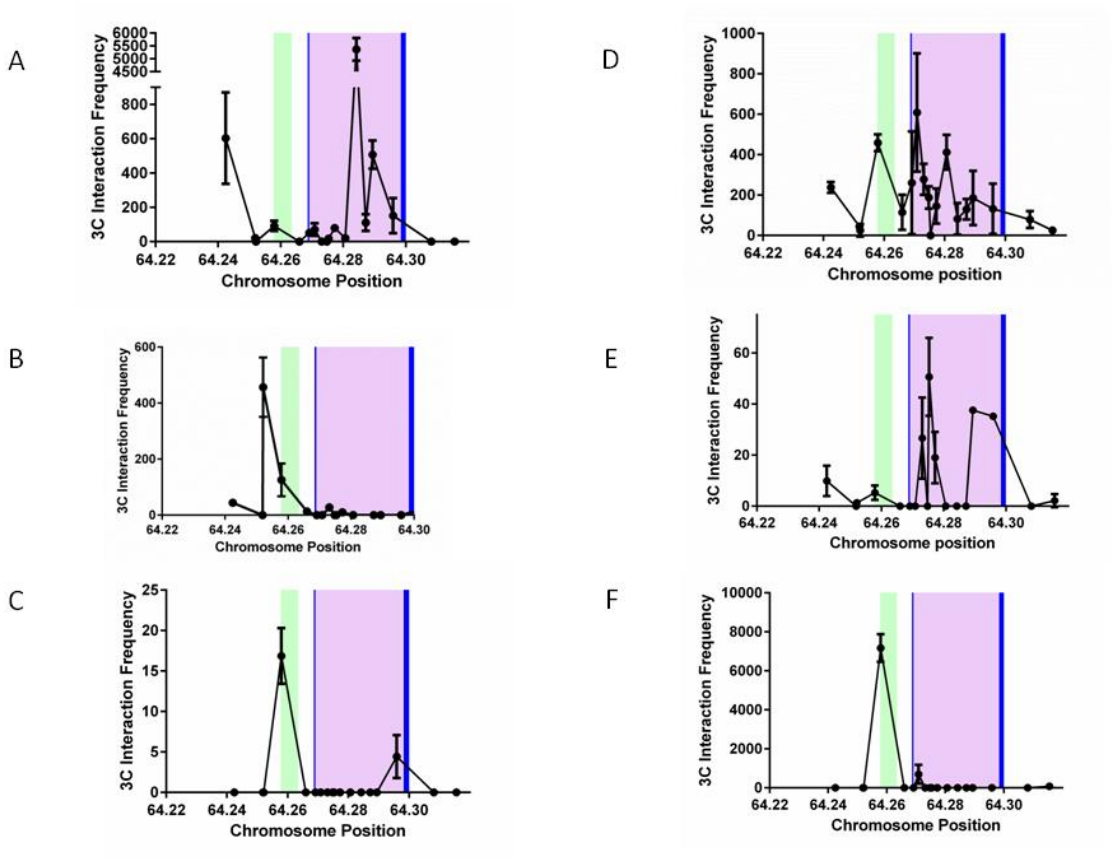

Figure S6. Chromatin interactions with the *ZNF365* and *NRBF2* promoters at the 10q21.2 locus. Chromatin interaction frequencies were plotted at the corresponding position for MCF7 (A and D), MCF10A (B and E) and Bre80 (C and F) for the *ZNF365*and *NRBF2* promoters, respectively. iCHAV2 is marked in green, iCHAV1 (which physically overlaps iCHAV3) in blue and iCHAV3 in purple. Error bars denote SD.

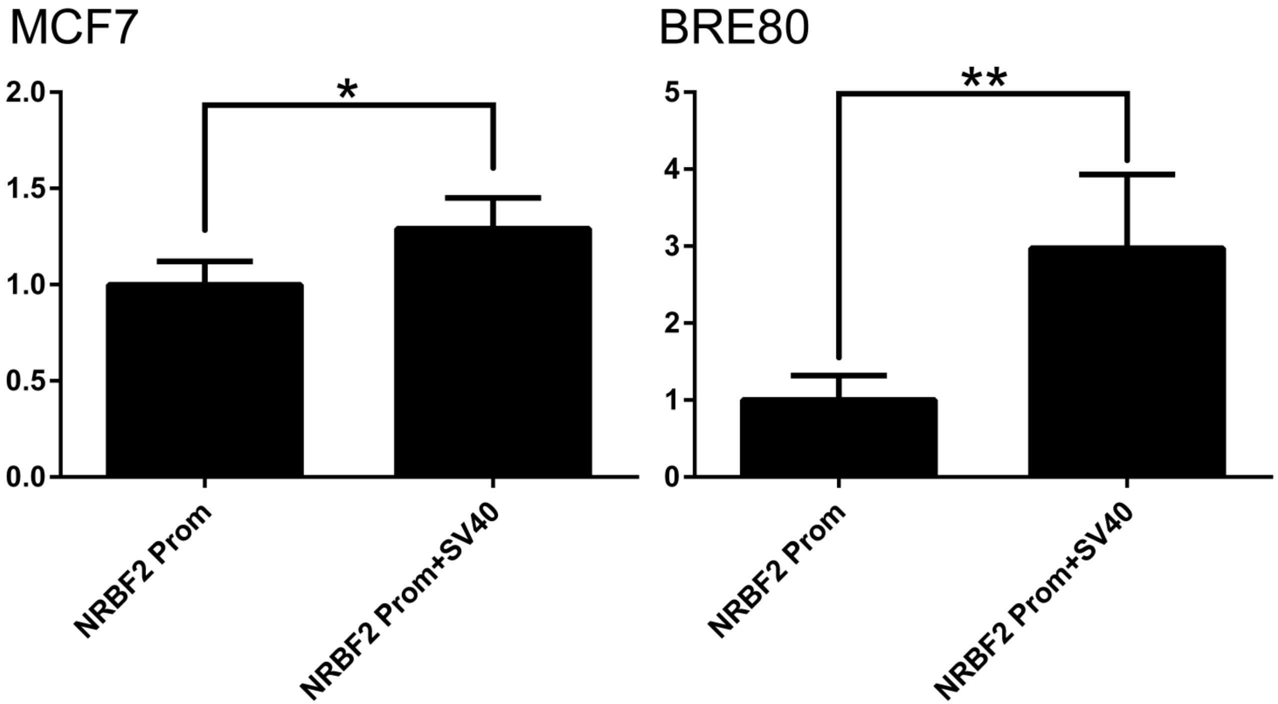

Figure S7. ***NRBF2* promoter activity is up-regulated by the positive control SV40 enhancer.** Presence of the SV40 enhancer increases luciferase activity in MCF7 and BRE80 breast cell lines (P=0.0205 and 0.0070, respectively).

SUPPLEMENTAL TABLES

Table S1: Summary of available mammographic density data from nine different studies.

Study Acronym	ABCFS	BBCC	MCBCS	MCCS	MEC	NBCS	OFBCR	SASBAC	SEARCH	All
Number of Cases/Controls	106/0	512/367	677/864	68/28	110/101	0/40	86/0	869/783	86/2329	2514/4512
Mean Age years (Sd)	39.1 (6.3)	58.9 (11.6)	59.5 (11.5)	58.6 (7.0)	58.5 (8.9)	64.4 (5.5)	54 (6.9)	62.8 (6.3)	61.8 (6.9)	60.6 (9.3)
Mean Body Mass Index (Sd)	23.7 (3.8)	26.3 (5.1)	28.0 (5.6)	27.3 (4.9)	25.6 (5.9)	27.1 (4.8)	26.6 (4.8)	25.6 (4.0)	27.4 (5)	26.8 (5.1)
% Premenopausal	60.4	19.5	22.7	17.7	17.1	12.5	18.6	2.5	5.8	82.6
% Postmenopausal	29.2	74.3	75.7	78.1	82.5	87.5	81.4	97.5	82.2	11.9
% HRT User	4.7	11	10.1	13.5	54	0	1.2	21.6	16.7	17.2
Mammogram View MLO/CC	1/105	0/879	0/1541	0/96	0/211	0/40	0/86	1652/0	2415/0	4068/2958
Mean PD (Sd)	44.2 (23.1)	36.5 (19.6)	17.3 (12.4)	16.8 (15.5)	31.2 (24.8)	15.3 (10)	33.9 (18)	16.1 (14.1)	17.6 (14.2)	20.5 (17.0)
Mean DA (Sd)	47.3 (30.1)	67.9 (38.4)	23.7 (16.9)	21.6 (20)	36.3 (34.3)	24.7 (16.4)	47.1 (30.5)	25.5 (23.2)	26.8 (20.9)	31.7 (28.2)
Mean nDA (Sd)	67.5 (48)	141.3 (89.9)	133.4 (66.3)	122.9 (53.7)	103.6 (76.8)	152.8 (62.4)	105.9 (60.4)	145.1 (56.7)	148.1 (69.5)	140 (69.9)

Data from ABCFS, BBCC, MCBCS, MCCS, MEC, NBCS, OFBCR, SASBAC and SEARCH

HRT - hormone replacement therapy
MLO - medio-lateral oblique
CC - craniocaudal
PD – percent density
DA – dense area
nDA – non-dense area

Table S2: 3C and cloning primers

Fragment	Sequence 5´….3´
ZNF365_1_A-New Bait	GCCAACATCTCTGGGCTTCATGTCTTCG
ZNF365_1_B-New Bait	CCTGTACTTGAGGATAGGTCCTGAGCTTGC
NRBF2_1_A-Bait	AGCTGAGACCAATCACACCACTGCATTCC
NRBF2_1_B-Bait	TCACAGGTTTGCAATTCATTTGCGATGG
ZNF365_23_B	GGCAGATTTCATTTGCCATAGGCAAGGC
ZNF365_24_B	GAAGGGACATCAAAATGTTCATGGAAGATGC
ZNF365_25_B	GACCCATGTCTCTCAACACTTCTGTCCAGG
ZNF365_26_A	CAGCTTGTGGGAAAAGGAGGATGTGAATAGC
ZNF365_28_B	AACCTATGTGCCTTTTGAATTTTATGCCAGATGC
ZNF365_29_A	CCAAGTTTGTTCACAACGCATTTTCTTGTGC
ZNF365_29_B	CAGGTGATGCCAGGAATCACCAAGTAGTATCG
ZNF365_30_B	GGCCAGCTCTCTTCTCATCAACCAGTGC
ZNF365_31_A	ACCATAGCAAGCACCGTGGAAGATATGAGC
ZNF365_32_A	GCTGCCATACTGGACAGCAGTCACTGG
ZNF365_33_B	CTATGTGCCGAAGTGGTGGTCAGAGAATAGC
ZNF365_34_B	CAAAGTGAAAATTTGAACCAGATCTTGCTGGC
ZNF365_35_B	AACAGTTTTGTTGCTTTGATGCCTCCAGC
ZNF365_36_A	AAGAAGAAAACAGGAGAGACAGAGCCTGAGAAGG
ZNF365_38_B	AAGAATAGCTACCCCTGCTTGTTTTTGGTGCC
ZNF365_39_B	GAACTAATGATGGCCAATGAAATTATCACTTGGG
ZNF365_40_B	GAAGTGGCAATTGTACAGTGATGACAGTGGTAGC
ZNF365_41_A	CATGGGCCTCCAGCTAGGAAGTTGAAGC
NRBF2_1_A-Bait	AGCTGAGACCAATCACACCACTGCATTCC
NRBF2_1_B-Bait	TCACAGGTTTGCAATTCATTTGCGATGG
ZNF365 promoter -forward	AAAGGTACCAGCACATTCGATCCACCGCTATATTAAG
ZNF365 promoter- reverse	TTTAGATCTAGCGGTTTTCAGCAGAGCCGTA
NRBF2 promoter- forward	AAAGGTACCCCGCCTTTAGAGTTGAGGCATAA
NRBF2 promoter- reverse	TTTAGATCTAAGGGAGCTCGACGCAGC
iCHAV-2putative enhancer forward	AAAGGATCCCCTCTTCCCACTTGCGTATATC
iCHAV-2 putative enhancer forward	TTTGTCGACGAAAACCCAATGAGGAAATTCA

Table S3: Based on data from all European studies, genotyped or imputed variants associated with overall risk of breast cancer (P-values $1x10^{-3}$ to 10^{-29})

						Overall Risk [e]		ER+ [f]		ER- [g]		Heterogeneity
SNP	Position [a]	Type	Info [b]	Major/Minor [c]	MAF [d]	P-value	OR (95%CI)	P-value	OR (95%CI)	P-value	OR (95%CI)	P-value [h]
rs10995201	64299890	Imputed	0.95	A/G	0.15	1.05E-29	0.85 (0.83,0.88)	2.51E-23	0.85 (0.82,0.88)	9.60E-08	0.87 (0.82,0.91)	0.34
rs10995193	64288082	Imputed	0.99	A/T	0.15	3.67E-29	0.86 (0.83,0.88)	4.28E-22	0.86 (0.83,0.88)	2.26E-07	0.87 (0.83,0.92)	0.367
rs10995194	64288130	Genotyped	1	G/C	0.15	3.77E-29	0.86 (0.84,0.88)	3.79E-22	0.86 (0.83,0.88)	2.79E-07	0.87 (0.83,0.92)	0.342
rs11524313	64283656	Imputed	0.97	G/A	0.14	4.16E-29	0.85 (0.83,0.88)	6.13E-22	0.85 (0.83,0.88)	2.41E-07	0.87 (0.82,0.92)	0.432
rs4746419	64275261	Genotyped	1	C/G	0.15	4.43E-29	0.86 (0.84,0.88)	3.28E-22	0.86 (0.83,0.88)	3.62E-07	0.87 (0.83,0.92)	0.332
rs10995190	64278682	Genotyped	1	G/A	0.15	5.61E-29	0.86 (0.84,0.88)	4.07E-22	0.86 (0.83,0.88)	2.78E-07	0.87 (0.83,0.92)	0.351
rs10995189	64278181	Genotyped	1	G/A	0.15	6.04E-29	0.86 (0.84,0.88)	4.20E-22	0.86 (0.83,0.88)	2.79E-07	0.87 (0.83,0.92)	0.352
rs10995191	64278874	Genotyped	1	G/A	0.15	6.04E-29	0.86 (0.84,0.88)	4.41E-22	0.86 (0.83,0.88)	2.82E-07	0.87 (0.83,0.92)	0.352
rs34511355	64276964	Genotyped	1	A/C	0.15	6.22E-29	0.86 (0.84,0.88)	4.93E-22	0.86 (0.83,0.88)	2.79E-07	0.87 (0.83,0.92)	0.36
rs10995187	64273026	Genotyped	1	G/A	0.15	6.66E-29	0.86 (0.84,0.88)	7.14E-22	0.86 (0.83,0.88)	3.18E-07	0.87 (0.83,0.92)	0.369
rs10995182	64268764	Imputed	0.92	T/C	0.12	3.42E-28	0.84 (0.82,0.87)	8.68E-22	0.84 (0.81,0.87)	6.68E-08	0.85 (0.8,0.9)	0.535
rs10995181	64268659	Genotyped	1	T/A	0.14	5.07E-28	0.86 (0.84,0.88)	1.86E-21	0.86 (0.83,0.88)	5.94E-07	0.88 (0.83,0.92)	0.389
chr10:64291099:I	64291099	Imputed	0.94	T/TA	0.11	6.38E-27	0.84 (0.82,0.87)	5.57E-23	0.83 (0.8,0.86)	1.08E-06	0.86 (0.81,0.92)	0.189
rs16917398	64301817	Genotyped	1	G/A	0.1	1.48E-16	0.87 (0.85,0.9)	9.28E-13	0.87 (0.84,0.91)	4.71E-06	0.87 (0.81,0.92)	0.968
c10_pos64304197	64304197	Genotyped	1	A/G	0.1	4.12E-15	0.88 (0.85,0.91)	2.34E-11	0.88 (0.85,0.92)	4.49E-06	0.87 (0.82,0.92)	0.791
chr10:64258684:D	64258684	Imputed	0.98	T/TGAA	0.47	4.24E-14	0.93 (0.91,0.95)	8.01E-11	0.93 (0.91,0.95)	0.0055	0.95 (0.91,0.98)	0.291
rs2393886	64258343	Genotyped	1	G/A	0.47	4.50E-14	0.93 (0.91,0.95)	6.68E-11	0.93 (0.91,0.95)	0.00334	0.95 (0.91,0.98)	0.34
rs10995176	64257971	Imputed	0.99	G/A	0.47	7.17E-14	0.93 (0.91,0.95)	4.62E-11	0.93 (0.91,0.95)	0.00704	0.95 (0.92,0.99)	0.235
c10_pos64258017	64258017	Genotyped	1	A/G	0.47	1.03E-13	0.93 (0.91,0.95)	7.02E-11	0.93 (0.91,0.95)	0.00576	0.95 (0.92,0.99)	0.273
c10_pos64288411	64288411	Genotyped	0.33	A/G	0.01	1.65E-13	0.69 (0.63,0.77)	3.07E-10	0.7 (0.63,0.78)	6.50E-08	0.6 (0.49,0.73)	0.29
rs10509168	64257828	Genotyped	1	G/A	0.46	2.22E-13	0.93 (0.91,0.95)	1.03E-10	0.93 (0.91,0.95)	0.00576	0.95 (0.92,0.99)	0.288
chr10:64258692:D	64258692	Imputed	0.86	AAGC/A	0.48	8.51E-13	1.08 (1.06,1.1)	1.62E-09	1.08 (1.05,1.1)	0.0166	1.05 (1.01,1.09)	0.226
rs7100995	64249139	Imputed	0.85	T/C	0.06	9.13E-13	0.86 (0.82,0.89)	1.12E-10	0.85 (0.81,0.89)	3.19E-05	0.84 (0.77,0.91)	0.925
rs4746409	64263402	Genotyped	1	C/G	0.49	3.06E-12	0.93 (0.92,0.95)	1.08E-09	0.93 (0.91,0.95)	0.00751	0.95 (0.92,0.99)	0.407
c10_pos64254983	64254983	Genotyped	1	G/A	0.09	3.81E-12	0.89 (0.86,0.92)	5.33E-11	0.88 (0.84,0.91)	0.00019	0.88 (0.82,0.94)	0.622
rs35816896	64300340	Genotyped	1	C/A	0.07	4.77E-12	0.88 (0.84,0.91)	1.09E-08	0.88 (0.84,0.92)	0.00894	0.91 (0.84,0.98)	0.419

rs1955331	64232042	Genotyped	1	A/G	0.45	7.99E-11	0.94 (0.92,0.96)	1.96E-09	0.93 (0.91,0.95)	0.0432	0.96 (0.93,1)	0.12
chr10:64247954:I	64247954	Imputed	0.86	A/AT	0.2	8.00E-11	0.92 (0.9,0.94)	3.51E-09	0.91 (0.89,0.94)	0.0122	0.94 (0.89,0.99)	0.28
rs10822013	64251977	Genotyped	1	A/G	0.47	8.81E-11	0.94 (0.92,0.96)	2.32E-09	0.93 (0.91,0.96)	0.0665	0.97 (0.93,1)	0.157
rs10995173	64246575	Genotyped	1	A/T	0.48	3.89E-10	0.94 (0.92,0.96)	6.49E-09	0.94 (0.92,0.96)	0.0829	0.97 (0.93,1)	0.151
rs10761637	64247585	Imputed	0.99	G/A	0.48	3.92E-10	0.94 (0.92,0.96)	5.42E-09	0.94 (0.92,0.96)	0.0951	0.97 (0.93,1.01)	0.133
rs10822012	64247568	Imputed	0.99	C/T	0.48	3.93E-10	0.94 (0.92,0.96)	5.42E-09	0.94 (0.92,0.96)	0.0952	0.97 (0.93,1.01)	0.133
rs12245332	64260847	Genotyped	1	A/G	0.37	3.95E-10	0.94 (0.92,0.96)	3.95E-09	0.93 (0.91,0.95)	0.0176	0.95 (0.92,0.99)	0.221
rs12243471	64260410	Genotyped	0.99	A/G	0.37	4.00E-10	0.94 (0.92,0.96)	3.33E-09	0.93 (0.91,0.95)	0.017	0.95 (0.92,0.99)	0.22
rs12098307	64248099	Imputed	0.99	T/C	0.48	4.16E-10	0.94 (0.92,0.96)	6.08E-09	0.94 (0.92,0.96)	0.0989	0.97 (0.93,1.01)	0.134
rs2393887	64263093	Genotyped	1	C/G	0.37	6.94E-10	0.94 (0.92,0.96)	6.80E-09	0.93 (0.91,0.96)	0.0225	0.96 (0.92,0.99)	0.207
rs4282885	64243828	Genotyped	0.99	A/G	0.48	8.51E-10	0.94 (0.92,0.96)	1.36E-08	0.94 (0.92,0.96)	0.106	0.97 (0.94,1.01)	0.149
rs4489633	64238333	Genotyped	0.96	G/A	0.48	1.45E-09	0.94 (0.93,0.96)	2.22E-08	0.94 (0.92,0.96)	0.104	0.97 (0.93,1.01)	0.147
rs4745820	64253044	Imputed	0.98	T/C	0.35	8.44E-09	0.94 (0.92,0.96)	1.11E-08	0.93 (0.91,0.96)	0.146	0.97 (0.94,1.01)	0.0372
rs35972160	64347963	Genotyped	1	A/C	0.04	1.19E-08	0.86 (0.82,0.91)	2.65E-08	0.84 (0.79,0.89)	0.104	0.92 (0.83,1.02)	0.0678
chr10:64352628:D	64352628	Imputed	0.97	AGCATTCATCT/A	0.11	1.70E-08	0.92 (0.89,0.94)	1.21E-05	0.92 (0.89,0.96)	0.000392	0.9 (0.85,0.95)	0.484
rs1955332	64231895	Genotyped	1	G/A	0.4	1.75E-08	0.95 (0.93,0.96)	3.14E-08	0.94 (0.92,0.96)	0.202	0.98 (0.94,1.01)	0.0338
chr10:64293571:D	64293571	Imputed	0.88	AAAGG/A	0.3	1.94E-08	1.07 (1.04,1.09)	7.63E-06	1.06 (1.03,1.09)	0.000406	1.08 (1.03,1.13)	0.632
rs10822017	64296420	Imputed	0.99	T/C	0.33	2.07E-08	1.06 (1.04,1.08)	3.55E-07	1.06 (1.04,1.09)	0.00201	1.06 (1.02,1.11)	0.892
rs7072167	64231739	Genotyped	1	G/C	0.4	2.20E-08	0.95 (0.93,0.96)	3.60E-08	0.94 (0.92,0.96)	0.208	0.98 (0.94,1.01)	0.0357
c10_pos64357440	64357440	Genotyped	1	C/G	0.04	2.34E-08	0.86 (0.82,0.91)	3.89E-08	0.84 (0.79,0.9)	0.117	0.92 (0.84,1.02)	0.0637
rs78697955	64376479	Imputed	0.97	G/A	0.11	2.48E-08	0.92 (0.89,0.95)	2.05E-05	0.93 (0.89,0.96)	0.000337	0.9 (0.85,0.95)	0.4
c10_pos64378296	64378296	Genotyped	1	A/G	0.11	2.58E-08	0.92 (0.89,0.95)	1.12E-05	0.92 (0.89,0.96)	0.000655	0.9 (0.85,0.96)	0.529
rs9633558	64293805	Imputed	0.99	C/T	0.33	2.62E-08	1.06 (1.04,1.08)	4.72E-07	1.06 (1.04,1.09)	0.00192	1.06 (1.02,1.11)	0.909
rs1914182	64294817	Imputed	0.99	T/C	0.33	2.62E-08	1.06 (1.04,1.08)	4.56E-07	1.06 (1.04,1.09)	0.00209	1.06 (1.02,1.11)	0.924
rs7915519	64293843	Imputed	0.99	C/T	0.33	2.63E-08	1.06 (1.04,1.08)	4.63E-07	1.06 (1.04,1.09)	0.00207	1.06 (1.02,1.11)	0.91
rs6479823	64294020	Imputed	1	C/T	0.33	2.66E-08	1.06 (1.04,1.08)	4.63E-07	1.06 (1.04,1.09)	0.00208	1.06 (1.02,1.11)	0.91
rs10995196	64292344	Imputed	0.98	A/G	0.32	2.70E-08	1.06 (1.04,1.08)	1.77E-06	1.06 (1.04,1.09)	0.000979	1.07 (1.03,1.11)	0.834
rs7901573	64297378	Imputed	0.99	G/C	0.33	2.93E-08	1.06 (1.04,1.08)	4.77E-07	1.06 (1.04,1.09)	0.00207	1.06 (1.02,1.11)	0.921
rs12258134	64297521	Imputed	0.99	T/A	0.33	2.94E-08	1.06 (1.04,1.08)	4.76E-07	1.06 (1.04,1.09)	0.00209	1.06 (1.02,1.11)	0.919
rs4746428	64293118	Genotyped	1	G/A	0.33	3.24E-08	1.06 (1.04,1.08)	6.08E-07	1.06 (1.04,1.09)	0.00194	1.06 (1.02,1.11)	0.961

rs10822011	64240648	Genotyped	1	A/G	0.4	3.29E-08	0.95 (0.93,0.97)	4.21E-08	0.94 (0.92,0.96)	0.224	0.98 (0.94,1.01)	0.0362
rs78499789	64372231	Imputed	0.98	A/T	0.11	3.46E-08	0.92 (0.89,0.95)	2.42E-05	0.93 (0.89,0.96)	0.000427	0.9 (0.85,0.95)	0.422
rs1914191	64362223	Genotyped	1	A/G	0.11	3.51E-08	0.92 (0.89,0.95)	2.11E-05	0.93 (0.89,0.96)	0.000471	0.9 (0.85,0.96)	0.441
rs77439234	64375399	Imputed	0.98	C/T	0.11	3.54E-08	0.92 (0.89,0.95)	2.51E-05	0.93 (0.89,0.96)	0.000433	0.9 (0.85,0.95)	0.423
rs1949356	64298273	Genotyped	1	A/G	0.33	3.61E-08	1.06 (1.04,1.08)	5.68E-07	1.06 (1.04,1.09)	0.00227	1.06 (1.02,1.1)	0.931
rs78969820	64369858	Imputed	0.98	C/A	0.11	3.72E-08	0.92 (0.89,0.95)	2.63E-05	0.93 (0.9,0.96)	0.000421	0.9 (0.85,0.95)	0.415
rs10995192	64286975	Imputed	0.99	G/T	0.36	3.75E-08	1.06 (1.04,1.08)	5.67E-07	1.06 (1.04,1.09)	0.000234	1.07 (1.03,1.12)	0.621
rs7070565	64278512	Genotyped	1	C/A	0.36	3.76E-08	1.06 (1.04,1.08)	6.67E-07	1.06 (1.04,1.09)	0.000176	1.08 (1.04,1.12)	0.596
rs10740082	64281167	Imputed	0.99	G/A	0.36	3.82E-08	1.06 (1.04,1.08)	6.43E-07	1.06 (1.04,1.09)	0.000181	1.08 (1.04,1.12)	0.597
rs4746423	64281259	Imputed	0.99	C/T	0.36	3.82E-08	1.06 (1.04,1.08)	6.44E-07	1.06 (1.04,1.09)	0.000181	1.08 (1.04,1.12)	0.597
rs7073475	64284370	Imputed	0.99	C/T	0.36	3.87E-08	1.06 (1.04,1.08)	6.59E-07	1.06 (1.04,1.09)	0.00018	1.08 (1.04,1.12)	0.594
rs77317045	64358198	Imputed	0.99	G/A	0.11	3.89E-08	0.92 (0.89,0.95)	2.28E-05	0.93 (0.89,0.96)	0.000491	0.9 (0.85,0.96)	0.449
rs16917477	64356405	Imputed	0.99	C/T	0.11	3.90E-08	0.92 (0.89,0.95)	2.22E-05	0.93 (0.89,0.96)	0.000529	0.9 (0.85,0.96)	0.463
rs1914198	64279556	Imputed	0.99	G/A	0.36	4.04E-08	1.06 (1.04,1.08)	6.41E-07	1.06 (1.04,1.09)	0.000188	1.08 (1.04,1.12)	0.6
rs7895055	64278217	Imputed	0.99	A/G	0.36	4.19E-08	1.06 (1.04,1.08)	6.23E-07	1.06 (1.04,1.09)	0.000203	1.08 (1.03,1.12)	0.57
rs7082733	64286215	Imputed	0.99	A/C	0.36	4.19E-08	1.06 (1.04,1.08)	7.77E-07	1.06 (1.04,1.09)	0.000173	1.08 (1.04,1.12)	0.609
rs1914197	64280647	Imputed	0.99	G/A	0.36	4.24E-08	1.06 (1.04,1.08)	6.96E-07	1.06 (1.04,1.09)	0.000188	1.08 (1.04,1.12)	0.596
rs1914196	64287434	Imputed	0.99	T/C	0.36	4.25E-08	1.06 (1.04,1.08)	8.00E-07	1.06 (1.04,1.08)	0.000171	1.08 (1.04,1.12)	0.565
rs7350397	64289214	Genotyped	1	C/G	0.36	4.33E-08	1.06 (1.04,1.08)	6.84E-07	1.06 (1.04,1.09)	2.00E-04	1.08 (1.03,1.12)	0.601
rs12413429	64368352	Imputed	0.98	C/T	0.11	4.52E-08	0.92 (0.89,0.95)	2.81E-05	0.93 (0.9,0.96)	0.000436	0.9 (0.85,0.96)	0.407
rs1949359	64356993	Genotyped	1	G/A	0.11	4.53E-08	0.92 (0.89,0.95)	2.66E-05	0.93 (0.9,0.96)	0.000547	0.9 (0.85,0.96)	0.438
rs2176291	64277372	Genotyped	1	C/A	0.36	4.58E-08	1.06 (1.04,1.08)	7.65E-07	1.06 (1.04,1.09)	0.000197	1.08 (1.03,1.12)	0.598
rs10733779	64280182	Genotyped	1	G/C	0.36	5.44E-08	1.06 (1.04,1.08)	9.09E-07	1.06 (1.04,1.08)	0.000202	1.07 (1.03,1.12)	0.581
rs2393894	64291065	Imputed	0.98	C/G	0.33	5.95E-08	1.06 (1.04,1.08)	2.23E-06	1.06 (1.03,1.08)	0.000295	1.08 (1.03,1.12)	0.568
rs7073867	64284517	Imputed	0.99	G/A	0.35	6.07E-08	1.06 (1.04,1.08)	2.15E-06	1.06 (1.03,1.08)	0.000338	1.07 (1.03,1.12)	0.614
rs1878253	64269210	Genotyped	1	G/A	0.32	6.54E-08	1.06 (1.04,1.08)	5.14E-06	1.06 (1.03,1.08)	0.000554	1.07 (1.03,1.11)	0.658
rs7901318	64290213	Imputed	0.98	A/T	0.32	7.26E-08	1.06 (1.04,1.08)	5.14E-06	1.06 (1.03,1.08)	0.00057	1.07 (1.03,1.12)	0.644
chr10:64407678:D	64407678	Imputed	0.9	C/CACAT	0.28	7.36E-08	0.94 (0.92,0.96)	1.40E-05	0.94 (0.92,0.97)	0.000132	0.92 (0.88,0.96)	0.0764
rs7912431	64280616	Imputed	0.98	C/T	0.36	8.59E-08	1.06 (1.04,1.08)	8.16E-07	1.06 (1.04,1.09)	0.00076	1.07 (1.03,1.11)	0.862
rs3847337	64208433	Genotyped	1	G/A	0.25	9.15E-08	0.94 (0.92,0.96)	1.40E-06	0.94 (0.91,0.96)	0.0919	0.96 (0.92,1.01)	0.309

rs10740081	64280059	Imputed	0.99	T/C	0.31	9.17E-08	1.06 (1.04,1.08)	5.48E-06	1.06 (1.03,1.08)	0.000753	1.07 (1.03,1.11)	0.689
rs10761639	64286938	Imputed	0.98	T/C	0.31	1.01E-07	1.06 (1.04,1.08)	6.41E-06	1.06 (1.03,1.08)	0.000704	1.07 (1.03,1.11)	0.665
rs1914200	64275340	Genotyped	1	A/G	0.32	1.03E-07	1.06 (1.04,1.08)	7.15E-06	1.06 (1.03,1.08)	0.000673	1.07 (1.03,1.11)	0.64
rs10761655	64418179	Imputed	0.99	C/A	0.27	1.07E-07	0.94 (0.92,0.96)	4.02E-05	0.95 (0.92,0.97)	0.000317	0.93 (0.89,0.97)	0.0683
rs7083350	64249170	Genotyped	0.99	G/A	0.36	1.17E-07	0.95 (0.93,0.97)	1.03E-07	0.94 (0.92,0.96)	0.223	0.98 (0.94,1.01)	0.0412
rs6479831	64418946	Genotyped	1	G/A	0.27	1.26E-07	0.94 (0.92,0.96)	3.19E-05	0.95 (0.92,0.97)	0.000314	0.93 (0.89,0.97)	0.0752
rs2393885	64238342	Genotyped	1	A/G	0.26	1.28E-07	0.95 (0.93,0.97)	9.12E-08	0.94 (0.92,0.96)	0.262	0.98 (0.94,1.02)	0.0717
rs10822047	64424284	Imputed	0.98	G/T	0.36	1.28E-07	0.94 (0.92,0.96)	2.90E-05	0.95 (0.92,0.97)	0.000297	0.93 (0.89,0.97)	0.0302
rs10822041	64404706	Imputed	0.99	C/T	0.26	1.29E-07	0.94 (0.92,0.96)	2.90E-05	0.95 (0.92,0.97)	0.000191	0.92 (0.88,0.96)	0.0607
rs7071642	64414060	Imputed	0.99	A/G	0.26	1.30E-07	0.94 (0.92,0.96)	2.76E-05	0.95 (0.92,0.97)	0.000276	0.92 (0.89,0.96)	0.0705
rs7089612	64414164	Imputed	0.99	C/T	0.26	1.30E-07	0.94 (0.92,0.96)	2.76E-05	0.95 (0.92,0.97)	0.000277	0.92 (0.89,0.96)	0.0705
rs10761652	64397656	Imputed	0.98	A/G	0.26	1.33E-07	0.94 (0.92,0.96)	2.99E-05	0.95 (0.92,0.97)	0.00028	0.92 (0.89,0.96)	0.0693
rs10761654	64405646	Imputed	0.99	G/A	0.26	1.35E-07	0.94 (0.92,0.96)	2.99E-05	0.95 (0.92,0.97)	0.000198	0.92 (0.89,0.96)	0.0618
rs753518	64235506	Genotyped	1	G/A	0.26	1.39E-07	0.95 (0.93,0.97)	1.01E-07	0.94 (0.92,0.96)	0.253	0.98 (0.94,1.02)	0.0705
rs7076156	64415184	Imputed	0.99	G/A	0.36	1.39E-07	0.94 (0.92,0.96)	2.88E-05	0.95 (0.92,0.97)	0.000284	0.93 (0.89,0.96)	0.0343
rs10761636	64233999	Genotyped	1	A/C	0.36	1.41E-07	0.95 (0.93,0.97)	1.07E-07	0.94 (0.92,0.96)	0.275	0.98 (0.94,1.02)	0.03
rs7086072	64417289	Imputed	0.99	T/C	0.26	1.42E-07	0.94 (0.92,0.96)	2.92E-05	0.95 (0.92,0.97)	0.000305	0.93 (0.89,0.97)	0.0732
rs4237304	64407845	Genotyped	1	A/G	0.27	1.44E-07	0.94 (0.92,0.96)	2.92E-05	0.95 (0.92,0.97)	0.000283	0.93 (0.89,0.97)	0.0756
rs4237305	64407851	Imputed	0.99	A/T	0.26	1.47E-07	0.94 (0.92,0.96)	3.16E-05	0.95 (0.92,0.97)	0.000216	0.92 (0.89,0.96)	0.0646
rs12782013	64225299	Imputed	0.98	C/T	0.29	1.51E-07	0.95 (0.93,0.97)	5.01E-07	0.94 (0.92,0.96)	0.0746	0.96 (0.93,1)	0.13
rs1996318	64236820	Genotyped	1	G/A	0.36	1.57E-07	0.95 (0.93,0.97)	1.22E-07	0.94 (0.92,0.96)	0.247	0.98 (0.94,1.02)	0.0366
rs34316596	64399622	Imputed	0.95	T/C	0.04	1.58E-07	0.87 (0.83,0.92)	1.53E-07	0.85 (0.8,0.9)	0.137	0.93 (0.84,1.03)	0.0771
rs2393883	64226323	Imputed	0.99	G/A	0.29	1.64E-07	0.95 (0.93,0.97)	5.95E-07	0.94 (0.92,0.96)	0.0785	0.96 (0.93,1)	0.139
rs7922449	64291308	Imputed	0.86	C/T	0.3	1.68E-07	1.06 (1.04,1.08)	6.70E-06	1.06 (1.03,1.09)	0.000268	1.08 (1.04,1.13)	0.484
rs12781954	64225130	Imputed	0.99	G/A	0.29	1.93E-07	0.95 (0.93,0.97)	6.54E-07	0.94 (0.92,0.96)	0.0762	0.96 (0.93,1)	0.145
rs10995205	64304083	Genotyped	1	G/A	0.24	1.96E-07	1.06 (1.04,1.08)	1.77E-06	1.07 (1.04,1.09)	0.0124	1.06 (1.01,1.1)	0.537
rs2393906	64379118	Imputed	0.93	G/A	0.05	2.05E-07	0.89 (0.85,0.93)	8.79E-06	0.89 (0.84,0.94)	5.94E-05	0.84 (0.77,0.91)	0.239
rs2393905	64379119	Imputed	0.93	C/T	0.05	2.06E-07	0.89 (0.85,0.93)	8.83E-06	0.89 (0.84,0.94)	5.96E-05	0.84 (0.77,0.91)	0.239
rs10995204	64304060	Genotyped	1	A/C	0.24	2.41E-07	1.06 (1.04,1.08)	2.64E-06	1.06 (1.04,1.09)	0.0155	1.05 (1.01,1.1)	0.471
rs10995170	64223383	Genotyped	1	A/G	0.29	2.51E-07	0.95 (0.93,0.97)	7.60E-07	0.94 (0.92,0.96)	0.0852	0.97 (0.93,1)	0.137

rs2393907	64407359	Imputed	0.99	G/C	0.27	2.52E-07	0.95 (0.93,0.97)	7.93E-05	0.95 (0.93,0.97)	0.000142	0.92 (0.88,0.96)	0.0385
rs6479815	64224100	Genotyped	1	A/G	0.29	2.54E-07	0.95 (0.93,0.97)	7.57E-07	0.94 (0.92,0.96)	0.0869	0.97 (0.93,1.01)	0.134
rs7086948	64292836	Imputed	0.98	T/A	0.36	3.16E-07	1.05 (1.03,1.07)	3.17E-06	1.06 (1.03,1.08)	0.00247	1.06 (1.02,1.1)	0.982
rs10740085	64395795	Imputed	0.98	C/T	0.21	3.18E-07	0.94 (0.92,0.96)	1.90E-05	0.94 (0.92,0.97)	6.19E-05	0.91 (0.87,0.95)	0.0307
rs7094985	64211810	Genotyped	1	A/G	0.41	3.34E-07	0.95 (0.93,0.97)	3.79E-06	0.95 (0.93,0.97)	0.227	0.98 (0.94,1.01)	0.151
rs6479832	64419102	Genotyped	1	A/G	0.22	3.89E-07	0.94 (0.92,0.96)	1.72E-05	0.94 (0.92,0.97)	0.000105	0.92 (0.87,0.96)	0.0427
rs10822007	64208221	Genotyped	1	A/G	0.41	4.21E-07	0.95 (0.93,0.97)	3.88E-06	0.95 (0.93,0.97)	0.265	0.98 (0.94,1.02)	0.124
rs145426092	64061106	Imputed	0.48	T/A	0.01	4.34E-07	0.75 (0.67,0.84)	5.45E-06	0.73 (0.64,0.84)	0.0102	0.75 (0.59,0.94)	0.978
rs10822008	64213069	Genotyped	0.99	A/G	0.42	4.89E-07	0.95 (0.93,0.97)	2.93E-06	0.95 (0.93,0.97)	0.298	0.98 (0.94,1.02)	0.129
rs2893906	64387934	Imputed	0.98	C/T	0.22	5.44E-07	0.94 (0.92,0.96)	3.09E-05	0.94 (0.92,0.97)	0.000265	0.92 (0.88,0.96)	0.0623
chr10:64345167:D	64345167	Imputed	0.98	CT/C	0.19	7.40E-07	0.94 (0.92,0.96)	4.42E-07	0.93 (0.9,0.96)	0.0209	0.95 (0.9,0.99)	0.485
rs7907439	64346650	Genotyped	1	G/A	0.19	9.27E-07	0.94 (0.92,0.96)	5.29E-07	0.93 (0.9,0.96)	0.0246	0.95 (0.9,0.99)	0.473
rs2138555	64220494	Genotyped	1	A/G	0.41	1.04E-06	0.95 (0.93,0.97)	8.11E-06	0.95 (0.93,0.97)	0.143	0.97 (0.94,1.01)	0.135
rs35306388	64478832	Imputed	0.98	C/G	0.04	1.21E-06	0.88 (0.84,0.93)	2.92E-07	0.85 (0.8,0.91)	0.24	0.94 (0.85,1.04)	0.0377
rs4746123	64214402	Genotyped	1	G/A	0.44	1.33E-06	0.95 (0.94,0.97)	1.47E-05	0.95 (0.93,0.97)	0.166	0.97 (0.94,1.01)	0.18
rs7477501	64348374	Imputed	0.98	C/T	0.19	1.33E-06	0.94 (0.92,0.96)	5.78E-07	0.93 (0.9,0.96)	0.0287	0.95 (0.9,0.99)	0.427
rs34284450	64480783	Genotyped	1	G/A	0.04	1.55E-06	0.88 (0.84,0.93)	2.75E-07	0.86 (0.81,0.91)	0.212	0.94 (0.85,1.04)	0.041
rs2138556	64214282	Imputed	0.99	G/A	0.44	2.25E-06	0.95 (0.94,0.97)	2.11E-05	0.95 (0.93,0.97)	0.23	0.98 (0.94,1.01)	0.149
rs1949355	64218423	Genotyped	1	A/G	0.44	2.58E-06	0.96 (0.94,0.97)	2.11E-05	0.95 (0.93,0.97)	0.208	0.98 (0.94,1.01)	0.17
rs12220488	64219000	Genotyped	1	A/G	0.44	2.62E-06	0.96 (0.94,0.97)	2.06E-05	0.95 (0.93,0.97)	0.208	0.98 (0.94,1.01)	0.168
rs2393881	64205643	Genotyped	1	G/A	0.26	2.80E-06	0.95 (0.93,0.97)	1.79E-05	0.95 (0.92,0.97)	0.0823	0.96 (0.92,1)	0.781
rs61259183	64225914	Imputed	0.99	A/C	0.44	3.06E-06	0.96 (0.94,0.97)	2.61E-05	0.95 (0.93,0.97)	0.219	0.98 (0.94,1.01)	0.18
rs7918077	64202391	Imputed	0.98	G/T	0.26	3.99E-06	0.95 (0.93,0.97)	2.94E-05	0.95 (0.92,0.97)	0.062	0.96 (0.92,1)	0.977
chr10:64206361:D	64206361	Imputed	0.96	A/AT	0.26	4.13E-06	0.95 (0.93,0.97)	3.09E-05	0.95 (0.92,0.97)	0.102	0.97 (0.93,1.01)	0.78
rs10822009	64221290	Imputed	0.95	T/G	0.46	4.24E-06	0.96 (0.94,0.97)	3.33E-05	0.95 (0.93,0.97)	0.171	0.97 (0.94,1.01)	0.25
rs77606114	64221291	Imputed	0.95	T/A	0.46	4.24E-06	0.96 (0.94,0.97)	3.33E-05	0.95 (0.93,0.97)	0.171	0.97 (0.94,1.01)	0.25
rs10761643	64303351	Imputed	0.91	C/T	0.29	4.51E-06	1.05 (1.03,1.07)	9.99E-06	1.06 (1.03,1.09)	0.0164	1.05 (1.01,1.1)	0.486
rs7074870	64205327	Genotyped	1	G/A	0.26	4.54E-06	0.95 (0.93,0.97)	2.44E-05	0.95 (0.92,0.97)	0.0935	0.96 (0.93,1.01)	0.846
chr10:64221291:I	64221291	Imputed	0.93	ATT/A	0.47	4.65E-06	0.96 (0.94,0.97)	5.69E-05	0.95 (0.93,0.98)	0.158	0.97 (0.94,1.01)	0.271
rs10822006	64205492	Genotyped	1	A/G	0.29	5.81E-06	0.95 (0.93,0.97)	2.31E-05	0.95 (0.92,0.97)	0.106	0.97 (0.93,1.01)	0.0878

rs10160102	64390647	Genotyped	1	A/G	0.26	5.81E-06	0.95 (0.93,0.97)	0.000712	0.96 (0.94,0.98)	0.00291	0.94 (0.9,0.98)	0.823
rs224120	64445760	Imputed	0.98	C/T	0.28	5.89E-06	0.95 (0.93,0.97)	9.78E-05	0.95 (0.93,0.98)	0.00411	0.94 (0.9,0.98)	0.243
rs4745874	64413809	Imputed	0.99	A/T	0.29	6.19E-06	0.95 (0.93,0.97)	0.000645	0.96 (0.93,0.98)	0.00112	0.93 (0.9,0.97)	0.0452
rs6479830	64418739	Genotyped	1	G/A	0.29	6.43E-06	0.95 (0.93,0.97)	0.000689	0.96 (0.93,0.98)	0.00137	0.94 (0.9,0.97)	0.0473
rs16917317	64270771	Genotyped	1	A/G	0.42	6.63E-06	1.05 (1.03,1.07)	1.47E-05	1.05 (1.03,1.08)	0.00126	1.06 (1.02,1.1)	0.67
rs10761640	64298025	Imputed	0.99	G/T	0.4	6.67E-06	1.05 (1.03,1.07)	1.12E-05	1.05 (1.03,1.08)	0.0119	1.05 (1.01,1.09)	0.818
rs10761653	64404034	Imputed	0.99	A/T	0.29	6.73E-06	0.95 (0.93,0.97)	0.000753	0.96 (0.93,0.98)	0.000781	0.93 (0.89,0.97)	0.0359
rs16917312	64270701	Imputed	1	T/C	0.43	6.97E-06	1.04 (1.03,1.07)	1.61E-05	1.05 (1.03,1.07)	0.00122	1.06 (1.02,1.1)	0.658
rs7895082	64270919	Genotyped	1	C/A	0.42	7.15E-06	1.04 (1.03,1.07)	1.59E-05	1.05 (1.03,1.07)	0.00127	1.06 (1.02,1.1)	0.66
rs4237288	64269110	Genotyped	1	A/G	0.42	7.23E-06	1.04 (1.03,1.07)	1.60E-05	1.05 (1.03,1.07)	0.00129	1.06 (1.02,1.1)	0.677
rs1955328	64269387	Genotyped	1	A/G	0.42	7.26E-06	1.04 (1.03,1.07)	1.65E-05	1.05 (1.03,1.07)	0.00113	1.06 (1.02,1.1)	0.649
rs11523825	64285985	Imputed	0.99	G/T	0.43	7.40E-06	1.04 (1.02,1.07)	1.80E-05	1.05 (1.03,1.07)	0.00141	1.06 (1.02,1.1)	0.656
rs7900998	64287981	Imputed	0.99	C/T	0.43	7.58E-06	1.04 (1.02,1.07)	1.86E-05	1.05 (1.03,1.07)	0.00141	1.06 (1.02,1.1)	0.652
rs7923316	64270846	Genotyped	1	G/A	0.42	8.03E-06	1.04 (1.02,1.06)	1.76E-05	1.05 (1.03,1.07)	0.00125	1.06 (1.02,1.1)	0.646
rs79829650	64380124	Imputed	0.96	G/T	0.09	8.30E-06	0.93 (0.9,0.96)	0.000449	0.93 (0.9,0.97)	0.00977	0.92 (0.86,0.98)	0.679
rs737314	64274177	Genotyped	1	A/G	0.42	8.38E-06	1.04 (1.02,1.06)	1.90E-05	1.05 (1.03,1.07)	0.00131	1.06 (1.02,1.1)	0.636
rs10509169	64276759	Genotyped	1	A/G	0.42	8.44E-06	1.04 (1.02,1.06)	1.69E-05	1.05 (1.03,1.07)	0.00155	1.06 (1.02,1.1)	0.677
rs17221319	64206712	Genotyped	1	C/A	0.49	8.77E-06	1.04 (1.02,1.06)	1.19E-05	1.05 (1.03,1.07)	0.149	1.03 (0.99,1.07)	0.358
rs10822042	64404827	Imputed	0.98	T/A	0.29	1.01E-05	0.95 (0.93,0.97)	0.00102	0.96 (0.94,0.98)	0.00102	0.93 (0.9,0.97)	0.0374
rs12766269	64205248	Imputed	0.7	G/A	0.03	1.02E-05	0.86 (0.8,0.92)	0.000576	0.87 (0.8,0.94)	0.0827	0.89 (0.78,1.02)	0.826
rs1878262	64273879	Genotyped	0.99	C/A	0.43	1.02E-05	1.04 (1.02,1.06)	2.10E-05	1.05 (1.03,1.07)	0.00147	1.06 (1.02,1.1)	0.632
rs224121	64447352	Genotyped	1	C/A	0.23	1.02E-05	0.95 (0.93,0.97)	8.29E-05	0.95 (0.92,0.97)	0.000551	0.92 (0.88,0.97)	0.0698
rs10822015	64268345	Genotyped	1	A/T	0.43	1.03E-05	1.04 (1.02,1.06)	2.04E-05	1.05 (1.03,1.07)	0.00159	1.06 (1.02,1.1)	0.707
rs10995180	64267743	Genotyped	1	G/A	0.43	1.04E-05	1.04 (1.02,1.06)	1.93E-05	1.05 (1.03,1.07)	0.00164	1.06 (1.02,1.1)	0.705
rs10995157	64202451	Imputed	0.96	G/T	0.49	1.14E-05	1.04 (1.02,1.06)	2.30E-05	1.05 (1.03,1.07)	0.142	1.03 (0.99,1.07)	0.458
rs77051803	64384640	Imputed	0.95	G/A	0.09	1.21E-05	0.93 (0.9,0.96)	0.00109	0.94 (0.9,0.97)	0.00649	0.91 (0.86,0.98)	0.509
rs1914188	64312627	Genotyped	1	C/A	0.47	1.41E-05	1.04 (1.02,1.06)	7.62E-06	1.05 (1.03,1.08)	0.0167	1.05 (1.01,1.09)	0.534
c10_pos64593869	64593869	Genotyped	0.97	G/A	0.03	1.45E-05	0.89 (0.85,0.94)	5.51E-07	0.85 (0.8,0.91)	0.441	0.96 (0.87,1.06)	0.0175
rs35997229	64957591	Imputed	0.53	T/C	0.03	1.46E-05	0.85 (0.79,0.91)	9.51E-07	0.8 (0.74,0.88)	0.967	1 (0.87,1.15)	0.00332
rs35661318	64935520	Imputed	0.53	T/A	0.03	1.47E-05	0.85 (0.79,0.91)	9.81E-07	0.8 (0.74,0.88)	0.954	1 (0.87,1.14)	0.00355

rs6479826	64314760	Genotyped	1	G/A	0.25	1.48E-05	1.05 (1.03,1.07)	5.08E-05	1.06 (1.03,1.08)	0.0765	1.04 (1,1.08)	0.326
rs12243155	64306395	Genotyped	1	A/T	0.25	1.56E-05	1.05 (1.03,1.07)	5.18E-05	1.05 (1.03,1.08)	0.0716	1.04 (1,1.09)	0.341
rs6479827	64317700	Genotyped	1	G/A	0.25	1.57E-05	1.05 (1.03,1.07)	5.37E-05	1.05 (1.03,1.08)	0.0729	1.04 (1,1.09)	0.342
rs7911140	64317150	Imputed	0.99	A/T	0.47	1.61E-05	1.04 (1.02,1.06)	9.45E-06	1.05 (1.03,1.08)	0.0167	1.05 (1.01,1.09)	0.55
rs2138564	64307317	Imputed	0.99	C/T	0.47	1.62E-05	1.04 (1.02,1.06)	8.76E-06	1.05 (1.03,1.08)	0.0155	1.05 (1.01,1.09)	0.57
rs34922281	64680751	Genotyped	1	C/A	0.04	1.75E-05	0.9 (0.86,0.94)	1.70E-06	0.87 (0.82,0.92)	0.639	0.98 (0.89,1.07)	0.0205
rs147709318	64809464	Imputed	0.77	C/T	0.03	1.76E-05	0.87 (0.82,0.93)	5.00E-06	0.84 (0.78,0.91)	0.466	0.96 (0.85,1.08)	0.0438
rs34942900	64817375	Imputed	0.77	C/T	0.03	1.76E-05	0.87 (0.82,0.93)	4.99E-06	0.84 (0.78,0.91)	0.467	0.96 (0.85,1.08)	0.0437
rs10822025	64311098	Genotyped	1	G/A	0.47	1.85E-05	1.04 (1.02,1.06)	8.86E-06	1.05 (1.03,1.08)	0.019	1.05 (1.01,1.08)	0.521
rs34632941	64414265	Imputed	0.97	C/T	0.07	2.29E-05	0.92 (0.89,0.96)	4.11E-06	0.9 (0.87,0.94)	0.633	0.98 (0.92,1.06)	0.0196
rs10822019	64303915	Genotyped	1	C/A	0.31	2.53E-05	0.96 (0.94,0.98)	0.000906	0.96 (0.94,0.98)	0.0316	0.96 (0.92,1)	0.931
chr10:64313970:I	64313970	Imputed	0.96	A/AT	0.28	2.56E-05	1.05 (1.03,1.07)	1.46E-05	1.06 (1.03,1.08)	0.122	1.03 (0.99,1.08)	0.217
c10_pos64599839	64599839	Genotyped	1	G/A	0.02	3.00E-05	1.15 (1.08,1.22)	1.16E-05	1.18 (1.1,1.28)	0.535	1.04 (0.92,1.18)	0.0403
rs4746518	64429595	Imputed	0.98	A/G	0.25	3.17E-05	0.95 (0.93,0.98)	0.00086	0.96 (0.93,0.98)	0.00148	0.93 (0.89,0.97)	0.0395
rs729738	64430265	Imputed	0.98	C/A	0.25	3.23E-05	0.95 (0.93,0.98)	0.000877	0.96 (0.93,0.98)	0.00152	0.93 (0.89,0.97)	0.0399
rs729739	64430302	Imputed	0.98	G/A	0.25	3.23E-05	0.95 (0.93,0.98)	0.000877	0.96 (0.93,0.98)	0.00152	0.93 (0.89,0.97)	0.0399
rs34146356	64721200	Genotyped	1	G/A	0.04	3.28E-05	0.9 (0.86,0.95)	3.73E-06	0.87 (0.82,0.93)	0.642	0.98 (0.89,1.07)	0.0263
c10_pos64489095	64489095	Genotyped	1	A/G	0.03	3.45E-05	0.88 (0.83,0.94)	1.31E-05	0.86 (0.8,0.92)	0.0699	0.9 (0.8,1.01)	0.471
rs7393302	64437054	Imputed	0.98	T/G	0.25	3.72E-05	0.95 (0.93,0.98)	0.000982	0.96 (0.93,0.98)	0.00161	0.93 (0.89,0.97)	0.0408
rs7921139	64312533	Imputed	0.97	G/A	0.28	4.59E-05	1.05 (1.02,1.07)	0.000125	1.05 (1.02,1.08)	0.14	1.03 (0.99,1.08)	0.316
c10_pos64403240	64403240	Genotyped	1	A/G	0.07	4.90E-05	0.93 (0.89,0.96)	5.48E-06	0.91 (0.87,0.95)	0.72	0.99 (0.92,1.06)	0.0145
rs11812737	64429319	Imputed	0.98	G/A	0.21	5.20E-05	0.95 (0.93,0.98)	0.000723	0.95 (0.93,0.98)	0.000244	0.92 (0.88,0.96)	0.00946
rs1980663	64619338	Imputed	0.97	G/A	0.06	5.20E-05	0.92 (0.88,0.96)	0.000586	0.92 (0.88,0.97)	0.0536	0.93 (0.86,1)	0.987
rs35419901	64063451	Imputed	0.43	A/T	0.02	5.26E-05	0.82 (0.74,0.9)	1.30E-05	0.77 (0.69,0.87)	0.156	0.87 (0.72,1.06)	0.341
chr10:64593676:D	64593676	Imputed	0.94	AAATG/A	0.06	5.47E-05	0.92 (0.88,0.96)	0.000236	0.91 (0.87,0.96)	0.0221	0.91 (0.84,0.99)	0.931
rs4746524	64437797	Imputed	0.97	C/T	0.21	5.80E-05	0.95 (0.93,0.98)	0.000785	0.95 (0.93,0.98)	0.000258	0.92 (0.88,0.96)	0.00987
rs7394165	64437018	Imputed	0.97	C/T	0.21	5.82E-05	0.95 (0.93,0.98)	0.000787	0.95 (0.93,0.98)	0.000259	0.92 (0.88,0.96)	0.00989
rs12765365	64848937	Imputed	0.56	T/C	0.03	5.99E-05	0.86 (0.8,0.93)	1.53E-05	0.82 (0.75,0.9)	0.744	0.98 (0.85,1.12)	0.0142
rs1914190	64305244	Genotyped	1	A/G	0.27	6.39E-05	1.04 (1.02,1.07)	7.03E-05	1.05 (1.03,1.08)	0.127	1.03 (0.99,1.08)	0.311
rs9971363	64563702	Imputed	0.97	A/G	0.13	6.54E-05	0.94 (0.92,0.97)	1.26E-05	0.93 (0.9,0.96)	0.776	0.99 (0.94,1.05)	0.0102

rs1949358	64306130	Genotyped	1	C/A	0.27	6.55E-05	1.04 (1.02,1.07)	7.90E-05	1.05 (1.03,1.08)	0.126	1.03 (0.99,1.08)	0.326
rs1914189	64309377	Genotyped	1	T/A	0.27	6.56E-05	1.04 (1.02,1.07)	7.50E-05	1.05 (1.03,1.08)	0.129	1.03 (0.99,1.08)	0.311
rs10159722	64390776	Imputed	0.73	G/A	0.49	6.57E-05	0.96 (0.94,0.98)	0.000827	0.96 (0.93,0.98)	0.0184	0.95 (0.91,0.99)	0.609
rs7090365	64564428	Imputed	0.97	A/C	0.13	6.59E-05	0.94 (0.92,0.97)	1.32E-05	0.93 (0.9,0.96)	0.777	0.99 (0.94,1.05)	0.0102
rs2138562	64317335	Imputed	0.98	T/A	0.47	6.73E-05	1.04 (1.02,1.06)	2.71E-05	1.05 (1.03,1.07)	0.0394	1.04 (1,1.08)	0.447
rs1914187	64312794	Genotyped	1	A/G	0.27	6.75E-05	1.04 (1.02,1.07)	8.36E-05	1.05 (1.03,1.08)	0.129	1.03 (0.99,1.08)	0.323
rs16917421	64308304	Genotyped	1	A/T	0.27	6.83E-05	1.04 (1.02,1.07)	8.17E-05	1.05 (1.03,1.08)	0.13	1.03 (0.99,1.08)	0.319
rs2138563	64307474	Genotyped	1	A/G	0.27	6.86E-05	1.04 (1.02,1.07)	8.20E-05	1.05 (1.03,1.08)	0.131	1.03 (0.99,1.08)	0.319
rs16917442	64313404	Genotyped	1	A/T	0.27	6.87E-05	1.04 (1.02,1.07)	8.46E-05	1.05 (1.03,1.08)	0.131	1.03 (0.99,1.08)	0.318
rs61865880	64556134	Imputed	0.96	G/A	0.06	6.94E-05	0.92 (0.89,0.96)	0.000127	0.91 (0.87,0.96)	0.0369	0.92 (0.85,1)	0.958
rs16917441	64313211	Genotyped	1	G/A	0.27	6.99E-05	1.04 (1.02,1.07)	8.53E-05	1.05 (1.03,1.08)	0.132	1.03 (0.99,1.08)	0.319
rs1955335	64310267	Genotyped	1	A/G	0.27	7.00E-05	1.04 (1.02,1.07)	8.20E-05	1.05 (1.03,1.08)	0.134	1.03 (0.99,1.08)	0.311
rs2176288	64307657	Imputed	1	A/C	0.27	7.03E-05	1.04 (1.02,1.07)	8.67E-05	1.05 (1.03,1.08)	0.129	1.03 (0.99,1.08)	0.326
rs16917422	64309822	Genotyped	1	G/A	0.27	7.06E-05	1.04 (1.02,1.07)	8.40E-05	1.05 (1.03,1.08)	0.134	1.03 (0.99,1.08)	0.315
rs1949357	64306569	Genotyped	1	G/A	0.27	7.12E-05	1.04 (1.02,1.07)	8.44E-05	1.05 (1.03,1.08)	0.131	1.03 (0.99,1.08)	0.316
rs7906421	64312647	Imputed	0.99	T/C	0.27	7.13E-05	1.04 (1.02,1.07)	8.43E-05	1.05 (1.03,1.08)	0.13	1.03 (0.99,1.08)	0.316
rs2138565	64307302	Genotyped	1	G/A	0.27	7.17E-05	1.04 (1.02,1.07)	8.58E-05	1.05 (1.03,1.08)	0.132	1.03 (0.99,1.08)	0.319
rs7082053	64268772	Imputed	0.96	A/C	0.44	7.21E-05	1.04 (1.02,1.06)	0.000159	1.04 (1.02,1.07)	0.00194	1.06 (1.02,1.1)	0.535
rs12242302	64310992	Genotyped	1	A/G	0.27	7.25E-05	1.04 (1.02,1.07)	8.40E-05	1.05 (1.03,1.08)	0.137	1.03 (0.99,1.08)	0.307
rs1955334	64310533	Genotyped	1	G/A	0.27	7.32E-05	1.04 (1.02,1.07)	8.40E-05	1.05 (1.03,1.08)	0.137	1.03 (0.99,1.08)	0.307
rs12761892	64803386	Imputed	0.76	C/T	0.03	7.35E-05	0.89 (0.83,0.94)	1.56E-05	0.85 (0.8,0.92)	0.453	0.96 (0.85,1.07)	0.0614
rs10509171	64306881	Genotyped	1	G/A	0.27	8.13E-05	1.04 (1.02,1.07)	9.25E-05	1.05 (1.03,1.08)	0.138	1.03 (0.99,1.08)	0.322
rs16917743	64603659	Imputed	0.96	T/C	0.02	8.27E-05	1.14 (1.07,1.21)	1.54E-05	1.18 (1.09,1.27)	0.624	1.03 (0.91,1.17)	0.048
rs34106588	64852335	Imputed	0.58	G/T	0.03	8.61E-05	0.86 (0.8,0.93)	1.18E-05	0.82 (0.75,0.9)	0.94	0.99 (0.86,1.15)	0.00635
rs4481919	64933236	Imputed	0.52	C/T	0.02	8.73E-05	0.84 (0.77,0.92)	0.00214	0.85 (0.77,0.94)	0.0682	0.85 (0.72,1.01)	0.886
rs16917407	64304454	Genotyped	1	G/A	0.27	9.46E-05	1.04 (1.02,1.07)	0.000101	1.05 (1.03,1.08)	0.159	1.03 (0.99,1.07)	0.279
rs10822027	64344371	Genotyped	1	C/A	0.44	0.000101	0.96 (0.94,0.98)	3.29E-05	0.95 (0.93,0.98)	0.699	0.99 (0.96,1.03)	0.00927
chr10:64553557:D	64553557	Imputed	0.96	GA/G	0.12	0.000102	0.94 (0.92,0.97)	4.79E-06	0.92 (0.89,0.95)	0.504	0.98 (0.93,1.04)	0.024
rs9971328	64561869	Imputed	0.98	A/G	0.06	0.000102	0.94 (0.92,0.97)	5.15E-06	0.92 (0.89,0.95)	0.515	0.98 (0.93,1.04)	0.907
rs61865900	64582482	Imputed	0.98	T/C	0.12	0.000102	0.92 (0.89,0.96)	0.000179	0.91 (0.87,0.96)	0.0457	0.92 (0.85,1)	0.022

chr10:64931557:D	64931557	Imputed	0.52	GA/G	0.02	0.000103	0.84 (0.77,0.92)	0.0033	0.86 (0.77,0.95)	0.0515	0.84 (0.71,1)	0.969
rs10995309	64560878	Imputed	0.99	G/A	0.12	0.000107	0.94 (0.92,0.97)	5.19E-06	0.92 (0.89,0.95)	0.517	0.98 (0.93,1.04)	0.0225
chr10:64562931:D	64562931	Imputed	0.91	AC/A	0.1	0.000109	0.94 (0.9,0.97)	1.78E-05	0.92 (0.88,0.95)	0.179	0.96 (0.9,1.02)	0.224
rs9990	64567938	Imputed	0.99	C/T	0.12	0.000109	0.94 (0.92,0.97)	2.18E-05	0.93 (0.9,0.96)	0.85	0.99 (0.94,1.05)	0.0121
rs12262796	64558740	Imputed	0.99	T/C	0.12	0.000112	0.94 (0.92,0.97)	5.51E-06	0.92 (0.89,0.96)	0.52	0.98 (0.93,1.04)	0.0227
rs7922917	64559027	Imputed	0.99	G/C	0.12	0.000113	0.94 (0.92,0.97)	5.53E-06	0.92 (0.89,0.96)	0.521	0.98 (0.93,1.04)	0.0117
rs60033636	64559641	Imputed	0.99	G/A	0.12	0.000113	0.94 (0.92,0.97)	5.52E-06	0.92 (0.89,0.96)	0.521	0.98 (0.93,1.04)	0.0226
rs1509964	64567364	Imputed	0.99	C/T	0.12	0.000113	0.94 (0.92,0.97)	2.14E-05	0.93 (0.9,0.96)	0.851	0.99 (0.94,1.05)	0.0227
rs2077316	64225448	Imputed	0.77	A/C	0.05	0.000118	1.1 (1.05,1.16)	0.00116	1.1 (1.04,1.17)	0.0034	1.15 (1.05,1.26)	0.137
rs10995312	64566572	Genotyped	1	A/G	0.13	0.000138	0.95 (0.92,0.97)	2.43E-05	0.93 (0.9,0.96)	0.835	0.99 (0.94,1.05)	0.0121
rs1444418	64560470	Genotyped	1	A/G	0.12	0.000142	0.94 (0.92,0.97)	5.49E-06	0.92 (0.89,0.96)	0.573	0.98 (0.93,1.04)	0.0179
rs2138560	64336729	Genotyped	1	A/G	0.46	0.000155	1.04 (1.02,1.06)	4.86E-05	1.05 (1.02,1.07)	0.0396	1.04 (1,1.08)	0.511
rs117874299	64083271	Imputed	0.46	T/C	0.02	0.000158	0.83 (0.75,0.91)	0.000424	0.81 (0.73,0.91)	0.0208	0.8 (0.65,0.97)	0.603
rs10761656	64426243	Genotyped	1	G/A	0.27	0.000163	0.96 (0.94,0.98)	0.00442	0.96 (0.94,0.99)	0.00697	0.94 (0.91,0.98)	0.0535
rs61864670	64620357	Imputed	0.91	T/C	0.05	0.00017	0.91 (0.87,0.96)	0.00237	0.92 (0.87,0.97)	0.0388	0.91 (0.83,1)	0.801
c10_pos64277369	64277369	Genotyped	1	G/A	0.08	0.000186	1.07 (1.03,1.11)	0.000432	1.08 (1.03,1.12)	0.22	1.04 (0.98,1.12)	0.212
rs10995341	64636079	Imputed	0.98	T/C	0.07	0.000199	0.93 (0.89,0.97)	0.00187	0.93 (0.89,0.97)	0.053	0.93 (0.86,1)	0.881
rs10509174	64637908	Genotyped	1	G/A	0.07	0.000223	0.93 (0.89,0.97)	0.00198	0.93 (0.89,0.97)	0.0532	0.93 (0.86,1)	0.9
chr10:64562930:D	64562930	Imputed	0.9	AAC/A	0.09	0.00023	0.94 (0.91,0.97)	3.94E-05	0.92 (0.88,0.96)	0.227	0.96 (0.9,1.03)	0.204
rs7393734	64389552	Imputed	0.86	C/T	0.35	0.000239	0.96 (0.94,0.98)	0.00541	0.97 (0.94,0.99)	0.0146	0.95 (0.91,0.99)	0.139
rs10509175	64637989	Imputed	0.99	G/C	0.06	0.000253	0.93 (0.89,0.97)	0.00208	0.93 (0.89,0.97)	0.0548	0.93 (0.86,1)	0.892
rs9651304	64671764	Genotyped	1	G/A	0.21	0.000277	0.96 (0.94,0.98)	0.000234	0.95 (0.92,0.98)	0.136	0.97 (0.92,1.01)	0.635
rs10128333	64570038	Genotyped	1	G/A	0.17	0.000287	0.95 (0.93,0.98)	0.000345	0.95 (0.92,0.98)	0.696	0.99 (0.94,1.04)	0.0864
rs4746523	64437748	Imputed	0.89	G/A	0.06	0.00031	0.92 (0.88,0.96)	0.00439	0.93 (0.88,0.98)	0.00132	0.87 (0.8,0.95)	0.216
rs17314489	64273892	Genotyped	0.97	G/A	0.43	0.000332	1.04 (1.02,1.06)	0.0072	1.03 (1.01,1.06)	0.583	1.01 (0.97,1.05)	0.273
rs9633559	64293978	Genotyped	1	G/A	0.45	0.000345	1.04 (1.02,1.06)	0.00969	1.03 (1.01,1.05)	0.209	1.02 (0.99,1.06)	0.649
rs184101200	64130546	Imputed	0.31	C/T	0.11	0.000346	0.9 (0.86,0.96)	0.000157	0.88 (0.83,0.94)	0.0759	0.91 (0.82,1.01)	0.46
rs7921946	64299868	Imputed	0.92	G/A	0.24	0.000349	1.04 (1.02,1.07)	0.00351	1.04 (1.01,1.07)	0.00565	1.06 (1.02,1.11)	0.335
rs10995321	64591612	Imputed	0.98	C/A	0.07	0.000367	0.93 (0.9,0.97)	0.000219	0.92 (0.88,0.96)	0.0785	0.94 (0.87,1.01)	0.649
rs10995188	64276804	Genotyped	1	C/A	0.43	0.000376	1.04 (1.02,1.06)	0.00792	1.03 (1.01,1.05)	0.575	1.01 (0.97,1.05)	0.288

rs10995186	64273023	Genotyped	1	G/A	0.43	0.000382	1.04 (1.02,1.06)	0.00776	1.03 (1.01,1.05)	0.612	1.01 (0.97,1.05)	0.27
rs1878261	64273942	Genotyped	1	A/G	0.43	0.000395	1.04 (1.02,1.06)	0.00788	1.03 (1.01,1.05)	0.621	1.01 (0.97,1.05)	0.263
rs12782363	64283247	Imputed	0.98	A/G	0.23	0.000399	1.04 (1.02,1.07)	0.005	1.04 (1.01,1.07)	0.00366	1.07 (1.02,1.11)	0.235
rs10509170	64278634	Genotyped	1	G/A	0.43	0.000435	1.04 (1.02,1.06)	0.00844	1.03 (1.01,1.05)	0.595	1.01 (0.97,1.05)	0.278
rs10995316	64580430	Imputed	0.98	T/C	0.07	0.000437	0.93 (0.9,0.97)	0.000216	0.92 (0.88,0.96)	0.097	0.94 (0.87,1.01)	0.609
rs10995317	64582766	Imputed	0.99	G/A	0.07	0.000442	0.93 (0.9,0.97)	0.00023	0.92 (0.88,0.96)	0.0958	0.94 (0.87,1.01)	0.617
rs61865885	64579059	Imputed	0.98	C/T	0.07	0.000449	0.93 (0.9,0.97)	0.00022	0.92 (0.88,0.96)	0.102	0.94 (0.87,1.01)	0.596
rs7916322	64612824	Genotyped	0.89	G/A	0.07	0.000449	0.94 (0.9,0.97)	0.000814	0.93 (0.89,0.97)	0.131	0.95 (0.88,1.02)	0.683
rs12415752	64620876	Imputed	0.98	A/G	0.07	0.000453	0.94 (0.9,0.97)	0.000879	0.93 (0.89,0.97)	0.174	0.95 (0.89,1.02)	0.602
rs7905654	64562524	Imputed	0.97	G/A	0.12	0.000467	0.95 (0.92,0.98)	1.91E-05	0.93 (0.89,0.96)	0.526	0.98 (0.93,1.04)	0.0372
rs61866264	64287241	Imputed	0.99	T/C	0.43	0.000471	1.03 (1.02,1.06)	0.00863	1.03 (1.01,1.05)	0.573	1.01 (0.97,1.05)	0.293
chr10:64286199:D	64286199	Imputed	0.99	CA/C	0.43	0.000478	1.03 (1.02,1.06)	0.00875	1.03 (1.01,1.05)	0.578	1.01 (0.97,1.05)	0.29
rs114669910	64285152	Imputed	0.99	C/T	0.43	0.000481	1.03 (1.02,1.06)	0.00862	1.03 (1.01,1.05)	0.585	1.01 (0.97,1.05)	0.289
rs80353807	64319539	Imputed	0.96	G/A	0.1	0.000485	1.06 (1.03,1.09)	0.00736	1.05 (1.01,1.09)	0.0263	1.07 (1.01,1.14)	0.461
rs61744064	64565011	Imputed	0.96	G/A	0.07	0.000487	0.93 (0.9,0.97)	0.000232	0.92 (0.88,0.96)	0.168	0.95 (0.88,1.02)	0.44
rs143919493	64368863	Imputed	0.92	A/T	0.01	0.000499	0.83 (0.75,0.92)	0.00302	0.83 (0.73,0.94)	0.047	0.81 (0.66,1)	0.662
rs141742451	64406084	Imputed	0.43	A/T	0.01	0.000503	1.44 (1.17,1.76)	0.00138	1.47 (1.16,1.87)	0.00981	1.67 (1.15,2.43)	0.992
rs2893901	64283205	Imputed	0.99	G/A	0.43	0.000515	1.03 (1.01,1.05)	0.00933	1.03 (1.01,1.05)	0.582	1.01 (0.97,1.05)	0.297
chr10:64563699:D	64563699	Imputed	0.96	ACT/A	0.07	0.000529	0.93 (0.9,0.97)	0.000249	0.92 (0.88,0.96)	0.165	0.95 (0.88,1.02)	0.469
rs11817939	64588680	Genotyped	1	A/G	0.07	0.000529	0.94 (0.9,0.97)	0.000239	0.92 (0.88,0.96)	0.094	0.94 (0.87,1.01)	0.623
rs12257509	64302504	Imputed	0.93	T/A	0.17	0.000531	1.05 (1.02,1.07)	0.00111	1.05 (1.02,1.08)	0.485	1.02 (0.97,1.07)	0.0858
rs2297489	64575360	Imputed	0.97	C/G	0.07	0.000532	0.93 (0.9,0.97)	0.000241	0.92 (0.88,0.96)	0.122	0.94 (0.88,1.02)	0.54
rs7922314	64538279	Imputed	0.94	C/T	0.07	0.000537	0.94 (0.9,0.97)	0.00016	0.92 (0.88,0.96)	0.132	0.95 (0.88,1.02)	0.63
rs10995184	64271051	Genotyped	1	G/A	0.43	0.000538	1.03 (1.01,1.05)	0.0089	1.03 (1.01,1.05)	0.697	1.01 (0.97,1.05)	0.25
rs2297488	64575245	Imputed	0.97	G/A	0.07	0.000544	0.93 (0.9,0.97)	0.000247	0.92 (0.88,0.96)	0.12	0.94 (0.87,1.02)	0.545
rs75902654	64687050	Imputed	0.97	C/T	0.1	0.000548	0.94 (0.91,0.98)	0.00194	0.94 (0.91,0.98)	0.0272	0.93 (0.88,0.99)	0.661
rs10995315	64574571	Imputed	0.97	G/A	0.07	0.000552	0.93 (0.9,0.97)	0.00025	0.92 (0.88,0.96)	0.121	0.94 (0.88,1.02)	0.544
rs11817773	64593743	Imputed	0.96	T/C	0.07	0.000558	0.93 (0.9,0.97)	0.000405	0.92 (0.88,0.96)	0.0635	0.93 (0.87,1)	0.737
c10_pos64583263	64583263	Genotyped	1	G/A	0.07	0.000559	0.94 (0.9,0.97)	0.000257	0.92 (0.88,0.96)	0.1	0.94 (0.87,1.01)	0.612
rs12219294	64618478	Imputed	0.98	G/A	0.07	0.000561	0.94 (0.9,0.97)	0.00109	0.93 (0.89,0.97)	0.161	0.95 (0.88,1.02)	0.639

rs7074237	64545572	Imputed	0.96	G/T	0.07	0.000565	0.94 (0.9,0.97)	2.00E-04	0.92 (0.88,0.96)	0.141	0.95 (0.88,1.02)	0.586
rs11818600	64548854	Imputed	0.96	G/A	0.07	0.000567	0.94 (0.9,0.97)	2.00E-04	0.92 (0.88,0.96)	0.142	0.95 (0.88,1.02)	0.583
rs1509960	64620689	Imputed	0.97	C/A	0.07	0.000581	0.94 (0.9,0.97)	0.00106	0.93 (0.89,0.97)	0.173	0.95 (0.89,1.02)	0.616
rs2393892	64288592	Genotyped	1	A/G	0.24	0.00059	1.04 (1.02,1.06)	0.00791	1.04 (1.01,1.06)	0.00336	1.07 (1.02,1.11)	0.197
rs138309605	64706734	Imputed	0.72	C/G	0.05	0.000598	0.91 (0.86,0.96)	0.00394	0.91 (0.86,0.97)	0.0991	0.92 (0.82,1.02)	0.832
rs61865882	64572093	Imputed	0.97	T/C	0.07	0.000609	0.93 (0.9,0.97)	0.000324	0.92 (0.88,0.96)	0.159	0.95 (0.88,1.02)	0.451
rs61865883	64572680	Imputed	0.97	A/T	0.07	0.000613	0.93 (0.9,0.97)	0.000321	0.92 (0.88,0.96)	0.158	0.95 (0.88,1.02)	0.45
chr10:64288396:I	64288396	Imputed	0.98	A/AG	0.42	0.000623	1.03 (1.01,1.05)	0.00986	1.03 (1.01,1.05)	0.535	1.01 (0.97,1.05)	0.324
rs2295814	64571276	Imputed	0.97	G/A	0.07	0.000626	0.93 (0.9,0.97)	0.000335	0.92 (0.88,0.96)	0.161	0.95 (0.88,1.02)	0.451
chr10:64617871:D	64617871	Imputed	0.96	AAAAATCTATAC/A	0.07	0.000641	0.94 (0.9,0.97)	0.0011	0.93 (0.89,0.97)	0.16	0.95 (0.88,1.02)	0.646
rs150486911	64999283	Imputed	0.67	C/A	0.01	0.000679	0.83 (0.74,0.92)	0.0127	0.85 (0.75,0.97)	0.0184	0.77 (0.61,0.96)	0.425
rs61865884	64578483	Imputed	0.98	C/T	0.07	0.000681	0.94 (0.9,0.97)	0.00033	0.92 (0.88,0.96)	0.119	0.94 (0.88,1.02)	0.571
rs16917747	64615626	Imputed	0.98	C/T	0.07	0.000693	0.94 (0.9,0.97)	0.00129	0.93 (0.89,0.97)	0.164	0.95 (0.88,1.02)	0.656
rs11818583	64616476	Imputed	0.98	A/G	0.07	0.000696	0.94 (0.9,0.97)	0.00131	0.93 (0.89,0.97)	0.16	0.95 (0.88,1.02)	0.656
rs7915693	64612523	Imputed	0.99	C/T	0.07	0.000726	0.94 (0.9,0.97)	0.00145	0.93 (0.89,0.97)	0.157	0.95 (0.88,1.02)	0.677
rs74422190	64344728	Imputed	0.98	A/G	0.08	0.00076	0.94 (0.91,0.97)	0.0166	0.95 (0.91,0.99)	0.192	0.96 (0.89,1.02)	0.62
rs76406857	64344800	Imputed	0.98	T/C	0.08	0.000765	0.94 (0.91,0.97)	0.0168	0.95 (0.91,0.99)	0.191	0.96 (0.89,1.02)	0.622
rs190985765	64390795	Imputed	0.68	G/T	0.03	0.000767	0.89 (0.83,0.95)	0.00472	0.89 (0.82,0.97)	0.00304	0.81 (0.71,0.93)	0.316
rs12253072	64346501	Imputed	0.98	A/G	0.08	0.000779	0.94 (0.91,0.98)	0.0153	0.95 (0.91,0.99)	0.242	0.96 (0.9,1.03)	0.504
rs77555161	64609174	Imputed	0.98	T/C	0.07	0.000779	0.94 (0.9,0.97)	0.00168	0.93 (0.89,0.97)	0.158	0.95 (0.88,1.02)	0.683
chr10:64588179:D	64588179	Imputed	0.97	AT/A	0.07	0.000784	0.94 (0.9,0.97)	0.000295	0.92 (0.88,0.96)	0.108	0.94 (0.88,1.01)	0.631
rs61865905	64605987	Imputed	0.97	C/T	0.07	0.000811	0.94 (0.9,0.97)	0.00157	0.93 (0.89,0.97)	0.157	0.95 (0.88,1.02)	0.68
c10_pos64349002	64349002	Genotyped	1	G/A	0.08	0.000818	0.94 (0.91,0.98)	0.0171	0.95 (0.91,0.99)	0.213	0.96 (0.89,1.03)	0.569
rs12249410	64301941	Genotyped	1	C/A	0.11	0.000821	1.05 (1.02,1.09)	0.000604	1.07 (1.03,1.11)	0.223	1.04 (0.98,1.1)	0.193
rs61865904	64604548	Imputed	0.97	G/C	0.07	0.000823	0.94 (0.9,0.97)	0.00147	0.93 (0.89,0.97)	0.159	0.95 (0.88,1.02)	0.672
rs61865903	64598118	Imputed	0.97	G/A	0.07	0.000826	0.94 (0.9,0.97)	0.00135	0.93 (0.89,0.97)	0.147	0.95 (0.88,1.02)	0.678
rs10995329	64605284	Imputed	0.97	C/A	0.07	0.00083	0.94 (0.9,0.97)	0.00155	0.93 (0.89,0.97)	0.157	0.95 (0.88,1.02)	0.68
rs10822063	64599100	Imputed	0.97	A/G	0.07	0.000831	0.94 (0.9,0.97)	0.00139	0.93 (0.89,0.97)	0.149	0.95 (0.88,1.02)	0.679
rs10509172	64603279	Imputed	0.97	C/T	0.07	0.000832	0.94 (0.9,0.97)	0.00146	0.93 (0.89,0.97)	0.159	0.95 (0.88,1.02)	0.672
rs75877907	64602562	Imputed	0.97	A/C	0.07	0.000846	0.94 (0.9,0.97)	0.00153	0.93 (0.89,0.97)	0.158	0.95 (0.88,1.02)	0.678

rs10822061	64597189	Imputed	0.97	T/C	0.07	0.000862	0.94 (0.9,0.97)	0.00157	0.93 (0.89,0.97)	0.141	0.95 (0.88,1.02)	0.732
rs10995177	64266512	Genotyped	1	A/G	0.43	0.000875	1.03 (1.01,1.05)	0.0128	1.03 (1.01,1.05)	0.688	1.01 (0.97,1.05)	0.306
rs74423982	64345155	Imputed	0.99	G/A	0.08	0.000877	0.94 (0.91,0.98)	0.0179	0.95 (0.91,0.99)	0.21	0.96 (0.89,1.03)	0.591
rs911609	64611477	Genotyped	1	G/A	0.07	0.000916	0.94 (0.91,0.97)	0.00168	0.93 (0.89,0.97)	0.174	0.95 (0.89,1.02)	0.662
rs4746522	64437684	Imputed	0.97	G/A	0.28	0.00094	0.96 (0.94,0.99)	0.0135	0.97 (0.94,0.99)	0.00665	0.94 (0.91,0.98)	0.027
chr10:64569708:D	64569708	Imputed	0.96	GT/G	0.15	0.000972	0.96 (0.93,0.98)	0.00107	0.95 (0.92,0.98)	0.663	0.99 (0.94,1.04)	0.129
rs56699626	64633733	Imputed	0.94	C/T	0.02	0.00103	1.13 (1.05,1.21)	0.00117	1.15 (1.06,1.25)	0.217	1.09 (0.95,1.25)	0.422
rs12266041	64634409	Imputed	0.94	G/T	0.02	0.00103	1.13 (1.05,1.21)	0.00117	1.15 (1.06,1.25)	0.217	1.09 (0.95,1.25)	0.423
rs10995178	64266748	Genotyped	1	G/A	0.43	0.00107	1.03 (1.01,1.05)	0.0138	1.03 (1.01,1.05)	0.72	1.01 (0.97,1.05)	0.302
rs74158908	64202077	Imputed	0.69	T/C	0.06	0.00108	1.08 (1.03,1.13)	0.00164	1.09 (1.03,1.16)	0.0202	1.11 (1.02,1.22)	0.262
rs141867094	64073846	Imputed	0.39	C/T	0.06	0.00109	1.18 (1.07,1.31)	0.0217	1.15 (1.02,1.29)	0.14	1.16 (0.95,1.4)	0.274
c10_pos64301873	64301873	Genotyped	1	G/A	0.08	0.00109	1.07 (1.03,1.11)	0.0066	1.07 (1.02,1.12)	0.0108	1.1 (1.02,1.19)	0.632
c10_pos64345050	64345050	Genotyped	1	A/C	0.02	0.00109	0.94 (0.91,0.98)	0.0216	0.95 (0.91,0.99)	0.201	0.96 (0.89,1.02)	0.405
rs78530715	64361480	Imputed	0.89	T/C	0.06	0.00124	1.07 (1.03,1.12)	0.00154	1.09 (1.03,1.14)	0.0946	1.07 (0.99,1.17)	0.982
rs12359549	64649423	Imputed	0.83	G/A	0.11	0.00128	0.95 (0.92,0.98)	0.000862	0.94 (0.9,0.97)	0.142	0.95 (0.89,1.02)	0.486
rs12242530	64627906	Imputed	0.95	T/C	0.02	0.00131	1.12 (1.05,1.2)	0.00208	1.14 (1.05,1.24)	0.232	1.09 (0.95,1.24)	0.465
rs10995335	64623533	Imputed	0.97	C/T	0.07	0.0014	0.94 (0.91,0.98)	0.00273	0.94 (0.9,0.98)	0.122	0.95 (0.88,1.02)	0.844
rs10995340	64632908	Imputed	0.98	G/A	0.07	0.0014	0.94 (0.91,0.98)	0.00298	0.94 (0.9,0.98)	0.143	0.95 (0.88,1.02)	0.75
rs10995337	64626026	Imputed	0.98	G/A	0.07	0.00142	0.94 (0.91,0.98)	0.00258	0.94 (0.9,0.98)	0.131	0.95 (0.88,1.02)	0.793
rs12217462	64628755	Imputed	0.98	T/C	0.07	0.00152	0.94 (0.91,0.98)	0.00286	0.94 (0.9,0.98)	0.138	0.95 (0.88,1.02)	0.781
rs4746461	64344998	Genotyped	0.99	C/A	0.46	0.00158	0.97 (0.95,0.99)	0.000663	0.96 (0.94,0.98)	0.938	1 (0.96,1.04)	0.0163
rs10995336	64623708	Imputed	0.97	C/A	0.08	0.00163	0.94 (0.91,0.98)	0.00307	0.94 (0.9,0.98)	0.123	0.95 (0.88,1.02)	0.839
chr10:64680148:D	64680148	Imputed	0.99	AAC/A	0.1	0.00165	0.95 (0.92,0.98)	0.00349	0.95 (0.91,0.98)	0.0288	0.93 (0.88,0.99)	0.588
rs12267821	64625919	Genotyped	1	A/G	0.02	0.00166	1.12 (1.04,1.2)	0.00354	1.13 (1.04,1.22)	0.223	1.09 (0.95,1.24)	0.51
rs61863379	64129685	Imputed	0.31	T/C	0.21	0.00167	1.07 (1.03,1.12)	0.00333	1.08 (1.02,1.13)	0.373	1.04 (0.96,1.13)	0.142
rs12220702	64628704	Imputed	0.98	G/A	0.07	0.00168	0.94 (0.91,0.98)	0.00307	0.94 (0.9,0.98)	0.143	0.95 (0.88,1.02)	0.781
rs61863949	64514564	Imputed	0.81	G/A	0.03	0.00174	0.9 (0.85,0.96)	0.00356	0.89 (0.83,0.96)	0.059	0.89 (0.78,1.01)	0.733
chr10:64624163:D	64624163	Imputed	0.89	AAAGG/A	0.1	0.00181	0.95 (0.92,0.98)	0.00425	0.94 (0.91,0.98)	0.0366	0.93 (0.87,1)	0.981
c10_pos64508238	64508238	Genotyped	1	A/G	0.02	0.00183	1.12 (1.04,1.2)	0.00256	1.14 (1.05,1.23)	0.558	1.04 (0.91,1.2)	0.132
c10_pos64684113	64684113	Genotyped	1	G/A	0.1	0.00183	0.95 (0.92,0.98)	0.0044	0.95 (0.91,0.98)	0.0297	0.93 (0.88,0.99)	0.591

rs61865902	64597721	Imputed	0.94	G/A	0.08	0.00189	0.94 (0.91,0.98)	0.00325	0.94 (0.9,0.98)	0.157	0.95 (0.88,1.02)	0.79
c10_pos64219094	64219094	Genotyped	1	A/G	0.01	0.00192	1.14 (1.05,1.24)	0.000332	1.19 (1.08,1.31)	0.0401	1.18 (1.01,1.38)	0.766
chr10:64293697:I	64293697	Imputed	0.55	A/AAT	0.02	0.00192	0.87 (0.79,0.95)	0.053	0.9 (0.81,1)	0.0303	0.82 (0.69,0.98)	0.513
rs10822145	64934548	Imputed	0.48	C/T	0.45	0.00211	0.96 (0.93,0.98)	0.0012	0.95 (0.92,0.98)	0.458	0.98 (0.93,1.03)	0.103
rs10822074	64630538	Genotyped	1	G/A	0.08	0.00212	0.95 (0.91,0.98)	0.00445	0.94 (0.9,0.98)	0.17	0.95 (0.89,1.02)	0.761
rs7068164	64401056	Imputed	0.98	C/A	0.44	0.00215	0.97 (0.95,0.99)	0.0477	0.98 (0.96,1)	0.0271	0.96 (0.92,1)	0.22
rs10219104	64420972	Imputed	0.98	A/C	0.43	0.00216	0.97 (0.95,0.99)	0.0468	0.98 (0.96,1)	0.0404	0.96 (0.93,1)	0.214
chr10:64624176:D	64624176	Imputed	0.92	AAGGG/A	0.12	0.0022	0.95 (0.92,0.98)	0.00381	0.95 (0.92,0.98)	0.217	0.96 (0.91,1.02)	0.51
c10_pos64339833	64339833	Genotyped	1	A/C	0.09	0.00228	1.05 (1.02,1.09)	0.0015	1.07 (1.02,1.11)	0.169	1.05 (0.98,1.12)	0.361
rs16917829	64650618	Imputed	0.98	C/A	0.1	0.00231	0.95 (0.92,0.98)	0.00436	0.95 (0.91,0.98)	0.0522	0.94 (0.88,1)	0.75
rs4746697	64644428	Imputed	0.96	C/T	0.1	0.00234	0.95 (0.92,0.98)	0.00456	0.95 (0.91,0.98)	0.0516	0.94 (0.88,1)	0.736
rs10995112	64069740	Imputed	0.36	T/C	0.23	0.00242	1.06 (1.02,1.1)	0.0419	1.05 (1,1.09)	0.0555	1.07 (1,1.15)	0.587
rs868914	64340802	Genotyped	1	A/G	0.3	0.00249	1.03 (1.01,1.05)	0.00509	1.04 (1.01,1.06)	0.0247	1.05 (1.01,1.09)	0.741
rs3864807	64070219	Imputed	0.4	A/G	0.25	0.00258	1.05 (1.02,1.09)	0.0171	1.05 (1.01,1.09)	0.107	1.06 (0.99,1.13)	0.744
rs4746780	64743728	Imputed	0.95	C/T	0.18	0.00259	0.96 (0.94,0.99)	0.00355	0.96 (0.93,0.99)	0.264	0.97 (0.93,1.02)	0.634

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a: Build 37 coordinates
b: IMPUTE2 info score
c: Major and Minor Allele
d: Minor Allele Frequency in controls.
e-g: P-value, Odds ratio (OR) and 95% Confidence Interval (CI) for association with Overall Breast Cancer Risk, Estrogen Positive (ER+) and Estrogen Negative (ER-) disease.
h: Case-only analysis, treating subtype status as a dependent variable, models adjusted for principal components and per-study fixed-effects .

Table S4: iCHAV1 - eleven markers correlated ($r^2 > 0.6$) with, and likelihood ratio (RL) of >1:100 relative to rs10995201

								Overall Risk [g]		ER+ [h]		ER- [i]		Heterogeneity
SNP	Position [a]	Type	Maj/Min [b]	MAF [c]	Info [d]	Rsq [e]	RL [f]	P-value	OR (95% CI)	P-value	OR (95% CI)	P-value	OR (95% CI)	P-value [j]
rs10995181	64268659	Genotyped	T/A	0.14	1	0.91	0.02	5.07E-28	0.86 (0.84,0.88)	1.86E-21	0.86 (0.83,0.88)	5.94E-07	0.88 (0.83,0.92)	0.39
rs10995182	64268764	Imputed	T/C	0.12	0.92	0.77	0.03	3.42E-28	0.84 (0.82,0.87)	8.68E-22	0.84 (0.81,0.87)	6.68E-08	0.85 (0.8,0.9)	0.54
rs10995187	64273026	Genotyped	G/A	0.15	1	0.94	0.16	6.66E-29	0.86 (0.84,0.88)	7.14E-22	0.86 (0.83,0.88)	3.18E-07	0.87 (0.83,0.92)	0.37
rs4746419	64275261	Genotyped	C/G	0.15	1	0.94	0.24	4.43E-29	0.86 (0.84,0.88)	3.28E-22	0.86 (0.83,0.88)	3.62E-07	0.87 (0.83,0.92)	0.33
rs34511355	64276964	Genotyped	A/C	0.15	1	0.94	0.17	6.22E-29	0.86 (0.84,0.88)	4.93E-22	0.86 (0.83,0.88)	2.79E-07	0.87 (0.83,0.92)	0.36
rs10995189	64278181	Genotyped	G/A	0.15	1	0.94	0.18	6.04E-29	0.86 (0.84,0.88)	4.20E-22	0.86 (0.83,0.88)	2.79E-07	0.87 (0.83,0.92)	0.35
rs10995190	64278682	Genotyped	G/A	0.15	1	0.94	0.19	5.61E-29	0.86 (0.84,0.88)	4.07E-22	0.86 (0.83,0.88)	2.78E-07	0.87 (0.83,0.92)	0.35
rs10995191	64278874	Genotyped	C/T	0.15	1	0.94	0.18	6.04E-29	0.86 (0.84,0.88)	4.41E-22	0.86 (0.83,0.88)	2.82E-07	0.87 (0.83,0.92)	0.35
rs11524313	64283656	Imputed	G/A	0.14	0.97	0.93	0.26	4.16E-29	0.85 (0.83,0.88)	6.13E-22	0.85 (0.83,0.88)	2.41E-07	0.87 (0.82,0.92)	0.43
rs10995193	64288082	Imputed	A/T	0.15	0.99	0.95	0.29	3.67E-29	0.86 (0.83,0.88)	4.28E-22	0.86 (0.83,0.88)	2.26E-07	0.87 (0.83,0.92)	0.37
rs10995194	64288130	Genotyped	G/C	0.15	1	0.95	0.28	3.77E-29	0.86 (0.84,0.88)	3.79E-22	0.86 (0.83,0.88)	2.79E-07	0.87 (0.83,0.92)	0.34
rs10995201	64299890	Imputed	A/G	0.15	0.95			1.05E-29	0.85 (0.83,0.88)	2.51E-23	0.85 (0.82,0.88)	9.60E-08	0.87 (0.82,0.91)	0.34

a: Build 37 coordinates
b: Major and Minor Allele
c: Minor Allele Frequency in controls.
d: IMPUTE2 info score
e: LD R-Squared (Rsq) with independent variant identified with forward stepwise regression (rs10995201).
f: relative likelihood ratio in comparison to rs10995201.
g-i: P-value, Odds ratio (OR) and 95% Confidence Interval (CI) for association with Overall Breast Cancer Risk, Estrogen Positive (ER+) and Estrogen Negative (ER-) disease.
j: Case-only analysis, treating subtype status as a dependent variable, models adjusted for principal components and per-study fixed-effects .

Table S5: iCHAV2 - sixteen markers correlated ($r^2 > 0.6$) with, and a likelihood ratio (RL) of >1:100 in relative to chr10:64258684:D

														Adjusted for lead SNP of iCHAV1		
							Overall Risk [f]		ER+ [g]		ER- [h]		Heterogeneity	Overall Risk [j]		
SNP	Position [a]	Type	Maj/Min [b]	MAF [c]	Info [d]	Rsq [e]	P-value	OR (95% CI)	P-value	OR (95% CI)	P-value	OR (95% CI)	P-value [i]	P-value	OR (95% CI)	RL
rs4489633	64238333	Genotyped	C/T	0.48	0.96	0.68	1.45E-09	0.94 (0.93,0.96)	2.22E-08	0.94 (0.92,0.96)	0.104	0.97 (0.93,1.01)	0.15	0.00228	0.97 (0.95,0.99)	0.05
rs4282885	64243828	Genotyped	A/G	0.48	0.99	0.68	8.51E-10	0.94 (0.92,0.96)	1.36E-08	0.94 (0.92,0.96)	0.106	0.97 (0.94,1.01)	0.15	0.00142	0.97 (0.95,0.99)	0.07
rs10995173	64246575	Genotyped	T/A	0.48	1	0.69	3.89E-10	0.94 (0.92,0.96)	6.49E-09	0.94 (0.92,0.96)	0.0829	0.97 (0.93,1)	0.15	0.00115	0.97 (0.95,0.99)	0.09
rs10822012	64247568	Imputed	C/T	0.48	0.99	0.69	3.93E-10	0.94 (0.92,0.96)	5.42E-09	0.94 (0.92,0.96)	0.0952	0.97 (0.93,1.01)	0.13	0.00117	0.97 (0.95,0.99)	0.08
rs10761637	64247585	Imputed	G/A	0.48	0.99	0.69	3.92E-10	0.94 (0.92,0.96)	5.42E-09	0.94 (0.92,0.96)	0.0951	0.97 (0.93,1.01)	0.13	0.00116	0.97 (0.95,0.99)	0.08
rs12098307	64248099	Imputed	T/C	0.48	0.99	0.69	4.16E-10	0.94 (0.92,0.96)	6.08E-09	0.94 (0.92,0.96)	0.0989	0.97 (0.93,1.01)	0.13	0.00118	0.97 (0.95,0.99)	0.08
rs10822013	64251977	Genotyped	T/C	0.47	1	0.71	8.81E-11	0.94 (0.92,0.96)	2.32E-09	0.93 (0.91,0.96)	0.0665	0.97 (0.93,1)	0.16	0.000639	0.97 (0.95,0.99)	0.15
rs10509168	64257828	Genotyped	C/T	0.46	1	0.96	2.22E-13	0.93 (0.91,0.95)	1.03E-10	0.93 (0.91,0.95)	0.00576	0.95 (0.92,0.99)	0.29	0.00021	0.96 (0.94,0.98)	0.42
rs10995176	64257971	Imputed	G/A	0.47	0.99	0.98	7.17E-14	0.93 (0.91,0.95)	4.62E-11	0.93 (0.91,0.95)	0.00704	0.95 (0.92,0.99)	0.24	0.000118	0.96 (0.94,0.98)	0.72
c10_pos64258017	64258017	Genotyped	A/G	0.47	1	0.98	1.03E-13	0.93 (0.91,0.95)	7.02E-11	0.93 (0.91,0.95)	0.00576	0.95 (0.92,0.99)	0.27	0.000131	0.96 (0.94,0.98)	0.65
rs2393886	64258343	Genotyped	C/T	0.47	1	0.99	4.50E-14	0.93 (0.91,0.95)	6.68E-11	0.93 (0.91,0.95)	0.00334	0.95 (0.91,0.98)	0.34	8.48E-05	0.96 (0.94,0.98)	0.98
chr10:64258684:D	64258684	Imputed	T/TGAA	0.47	0.98		4.24E-14	0.93 (0.91,0.95)	8.01E-11	0.93 (0.91,0.95)	0.0055	0.95 (0.91,0.98)	0.29	8.34E-05	0.96 (0.94,0.98)	
chr10:64258692:D	64258692	Imputed	AAGC/A	0.48	0.86	0.91	8.51E-13	1.08 (1.06,1.1)	1.62E-09	1.08 (1.05,1.1)	0.0166	1.05 (1.01,1.09)	0.23	0.000289	1.04 (1.02,1.06)	0.31
rs12243471	64260410	Genotyped	T/C	0.37	0.99	0.66	4.00E-10	0.94 (0.92,0.96)	3.33E-09	0.93 (0.91,0.95)	0.017	0.95 (0.92,0.99)	0.22	0.000906	0.97 (0.95,0.99)	0.11
rs12245332	64260847	Genotyped	T/C	0.37	1	0.66	3.95E-10	0.94 (0.92,0.96)	3.95E-09	0.93 (0.91,0.95)	0.0176	0.95 (0.92,0.99)	0.22	0.000903	0.97 (0.95,0.99)	0.11
rs2393887	64263093	Genotyped	G/C	0.37	1	0.65	6.94E-10	0.94 (0.92,0.96)	6.80E-09	0.93 (0.91,0.96)	0.0225	0.96 (0.92,0.99)	0.21	0.00115	0.97 (0.95,0.99)	0.09
rs4746409	64263402	Genotyped	C/G	0.49	1	0.73	3.06E-12	0.93 (0.92,0.95)	1.08E-09	0.93 (0.91,0.95)	0.00751	0.95 (0.92,0.99)	0.41	0.000638	0.97 (0.95,0.99)	0.15

a: Build 37 coordinates
b: Major and Minor Allele
c: Minor Allele Frequency in controls.
d: IMPUTE2 info score
e: LD R-Squared (Rsq) with independent variant identified with forward stepwise regression (chr10:64258684:D).
f-h: P-value, Odds ratio (OR) and 95% Confidence Interval (CI) for association with Overall Breast Cancer Risk, Estrogen Positive (ER+) and Estrogen Negative (ER-) disease.
i: Case-only analysis, treating subtype status as a dependent variable, models adjusted for principal components and per-study fixed-effects .
j: P-value and OR for association with Overall Breast Cancer Risk and relative likelihood ratio after adjusting for lead SNP of iCHAV1 (rs10995201)

Table S6: iCHAV 3 - Seventeen markers correlated ($r^2 > 0.6$) with, and a likelihood ratio of >1:100 relative to rs7922449

														Adjusted for lead SNP of iCHAV1 and iCHAV2		
							Overall Risk [f]		ER+ [g]		ER- [h]		Heterogeneity	Overall Risk [j]		
SNP	Position [a]	Type	Maj/Min [b]	MAF [c]	Info [d]	Rsq [e]	P-value	OR (95% CI)	P-value	OR (95% CI)	P-value	OR (95% CI)	P-value [i]	P-value	SNP	RL
rs1878253	64269210	Genotyped	G/A	0.32	1	0.63	6.54E-08	1.06 (1.04.1.08)	5.14E-06	1.06 (1.03.1.08)	0.000554	1.07 (1.03.1.11)	0.66	0.0103	1.03 (1.01.1.05)	0.02
rs1914200	64275340	Genotyped	T/C	0.32	1	0.63	1.03E-07	1.06 (1.04.1.08)	7.15E-06	1.06 (1.03.1.08)	0.000673	1.07 (1.03.1.11)	0.64	0.0133	1.03 (1.01.1.05)	0.02
rs10740081	64280059	Imputed	T/C	0.31	0.99	0.63	9.17E-08	1.06 (1.04.1.08)	5.48E-06	1.06 (1.03.1.08)	0.000753	1.07 (1.03.1.11)	0.69	0.0127	1.03 (1.01.1.05)	0.02
rs10761639	64286938	Imputed	T/C	0.31	0.98	0.63	1.01E-07	1.06 (1.04.1.08)	6.41E-06	1.06 (1.03.1.08)	0.000704	1.07 (1.03.1.11)	0.67	0.0133	1.03 (1.01.1.05)	0.02
rs7901318	64290213	Imputed	A/T	0.32	0.98	0.64	7.26E-08	1.06 (1.04.1.08)	5.14E-06	1.06 (1.03.1.08)	0.00057	1.07 (1.03.1.12)	0.64	0.0122	1.03 (1.01.1.05)	0.02
rs2393894	64291065	Imputed	C/G	0.33	0.97	0.68	5.95E-08	1.06 (1.04.1.08)	2.23E-06	1.06 (1.03.1.08)	0.000295	1.08 (1.03.1.12)	0.57	0.0156	1.03 (1.1.05)	0.01
rs7922449	64291308	Imputed	C/T	0.3	0.86		1.68E-07	1.06 (1.04.1.08)	6.70E-06	1.06 (1.03.1.09)	0.000268	1.08 (1.04.1.13)	0.48	0.000154	1.05 (1.02.1.07)	
rs10995196	64292344	Imputed	A/G	0.32	0.98	0.66	2.70E-08	1.06 (1.04.1.08)	1.77E-06	1.06 (1.04.1.09)	0.000979	1.07 (1.03.1.11)	0.83	0.00725	1.03 (1.01.1.05)	0.03
rs4746428	64293118	Genotyped	G/A	0.33	1	0.68	3.24E-08	1.06 (1.04.1.08)	6.08E-07	1.06 (1.04.1.09)	0.00194	1.06 (1.02.1.11)	0.96	0.0108	1.03 (1.01.1.05)	0.02
chr10:64293571:D	64293571	Imputed	AAAGG/A	0.3	0.88	0.7	1.94E-08	1.07 (1.04.1.09)	7.63E-06	1.06 (1.03.1.09)	0.000406	1.08 (1.03.1.13)	0.63	0.00139	1.04 (1.01.1.06)	0.13
rs9633558	64293805	Imputed	C/T	0.33	0.99	0.68	2.62E-08	1.06 (1.04.1.08)	4.72E-07	1.06 (1.04.1.09)	0.00192	1.06 (1.02.1.11)	0.92	0.00946	1.03 (1.01.1.05)	0.02
rs7915519	64293843	Imputed	C/T	0.33	0.99	0.68	2.63E-08	1.06 (1.04.1.08)	4.63E-07	1.06 (1.04.1.09)	0.00207	1.06 (1.02.1.11)	0.91	0.00951	1.03 (1.01.1.05)	0.02
rs6479823	64294020	Imputed	C/T	0.33	0.99	0.68	2.66E-08	1.06 (1.04.1.08)	4.63E-07	1.06 (1.04.1.09)	0.00208	1.06 (1.02.1.11)	0.91	0.00954	1.03 (1.01.1.05)	0.02
rs1914182	64294817	Imputed	T/C	0.33	0.99	0.68	2.62E-08	1.06 (1.04.1.08)	4.56E-07	1.06 (1.04.1.09)	0.00209	1.06 (1.02.1.11)	0.91	0.00952	1.03 (1.01.1.05)	0.02
rs10822017	64296420	Imputed	T/C	0.33	0.99	0.68	2.07E-08	1.06 (1.04.1.08)	3.55E-07	1.06 (1.04.1.09)	0.00201	1.06 (1.02.1.11)	0.89	0.0085	1.03 (1.01.1.05)	0.02
rs7901573	64297378	Imputed	G/C	0.33	0.99	0.68	2.93E-08	1.06 (1.04.1.08)	4.77E-07	1.06 (1.04.1.09)	0.00207	1.06 (1.02.1.11)	0.92	0.00988	1.03 (1.01.1.05)	0.02
rs12258134	64297521	Imputed	T/A	0.33	0.99	0.68	2.94E-08	1.06 (1.04.1.08)	4.76E-07	1.06 (1.04.1.09)	0.00209	1.06 (1.02.1.11)	0.92	0.00992	1.03 (1.01.1.05)	0.02
rs1949356	64298273	Genotyped	A/G	0.33	1	0.68	3.61E-08	1.06 (1.04.1.08)	5.68E-07	1.06 (1.04.1.09)	0.00227	1.06 (1.02.1.1)	0.93	0.0115	1.03 (1.01.1.05)	0.02

a: Build 37 coordinates
b: Major and Minor Allele
c: Minor Allele Frequency in controls.
d: IMPUTE2 info score
e: LD R-Squared (Rsq) with independent variant identified with forward stepwise regression (rs7922449).
f-h: P-value. Odds ratio (OR) and 95% Confidence Interval (CI) for association with Overall Breast Cancer Risk. Estrogen Positive (ER+) and Estrogen Negative (ER-) disease.
i: Case-only analysis; treating subtype status as a dependent variable; models adjusted for principal components and per-study fixed-effects .
j: P-value and OR for association with overall breast cancer risk and relative likelihood ratio after adjusting for lead SNP of iCHAV1 (rs10995201) and iCHAV2 (chr10:64258684:D).

Table S7: iCHAV 4 - marker correlated ($r^2 > 0.6$) with, and likelihood ratio of >1:100 relative to rs9971363

							Overall Risk [f]		ER+ [g]		ER- [h]		Heterogeneity	Adjusted for lead SNP of iCHAV1, iCHAV2 and iCHAV3 Overall Risk [j]		
SNP	Position [a]	Type	Maj/Min [b]	MAF [c]	Info [d]	Rsq [e]	P-value	OR (95% CI)	P-value	OR (95% CI)	P-value	OR (95% CI)	P-value [i]	P-value	SNP	RL
rs9971363	64563702	Imputed	A/G	0.13	0.97		6.54E-05	0.94 (0.92,0.97)	1.26E-05	0.93 (0.9,0.96)	0.776	0.99 (0.94,1.05)	0.0102	3.96E-04	0.95 (0.92,0.98)	
rs7090365	64564428	Imputed	A/C	0.13	0.97	1	6.59E-05	0.94 (0.92,0.97)	1.32E-05	0.93 (0.9,0.96)	0.777	0.99 (0.94,1.05)	0.0102	3.98E-04	0.95 (0.92,0.98)	1

a: Build 37 coordinates
b: Major and Minor Allele
c: Minor Allele Frequency in controls.
d: IMPUTE2 info score
e: LD R-Squared (Rsq) with independent variant identified with forward stepwise regression (rs9971363).
f-h: P-value. Odds ratio (OR) and 95% Confidence Interval (CI) for association with Overall Breast Cancer Risk. Estrogen Positive (ER+) and Estrogen Negative (ER-) disease.
i: Case-only analysis; treating subtype status as a dependent variable; models adjusted for principal components and per-study fixed-effects .
j: P-value and OR for association with overall breast cancer risk and relative likelihood ratio after adjusting for lead SNP of iCHAV1 (rs10995201) , iCHAV2 (chr10:64258684:D) and iCHAV3(rs7922449).

Table S8: Per-allele odds ratios (OR) for overall breast cancer, and for ER-positive and ER-negative breast cancer, in nine Asian BCAC studies for genotyped markers with minor allele frequency among Asians ≥0.01

				Overall Risk[d]		ER+[e]		ER-[f]		Heterogeneity[g]
SNP	Position[a]	A0/A1[b]	A1_F[c]	P-value	OR (95%CI)	P-value	OR (95%CI)	P-value	OR (95%CI)	P-value
rs7914770	64323230	A/G	0.50	0.00598	0.93 (0.89,0.98)	0.093	0.95 (0.89,1.01)	4.83e-03	0.89 (0.82,0.97)	0.286
rs4746446	64321407	A/G	0.47	0.0089	0.93 (0.89,0.98)	0.182	0.96 (0.9,1.02)	4.34e-03	0.89 (0.82,0.96)	0.198
c10_pos64266932	64266932	G/A	0.21	0.00905	0.92 (0.86,0.98)	0.06	0.93 (0.86,1)	3.37e-02	0.9 (0.81,0.99)	0.442
rs4746449	64322494	G/A	0.47	0.00937	0.93 (0.89,0.98)	0.191	0.96 (0.9,1.02)	3.95e-03	0.89 (0.82,0.96)	0.172
rs10822026	64320658	A/G	0.47	0.0104	0.94 (0.89,0.98)	0.225	0.96 (0.9,1.02)	3.13e-03	0.89 (0.82,0.96)	0.134
rs10740084	64336783	T/A	0.49	0.0104	0.94 (0.89,0.98)	0.102	0.95 (0.89,1.01)	7.08e-03	0.9 (0.83,0.97)	0.301
rs10761645	64320150	C/G	0.47	0.0109	0.94 (0.89,0.98)	0.207	0.96 (0.9,1.02)	3.99e-03	0.89 (0.82,0.96)	0.165
rs7901648	64327791	A/G	0.45	0.011	0.94 (0.89,0.98)	0.168	0.96 (0.9,1.02)	6.34e-03	0.89 (0.82,0.97)	0.21
rs7089578	64335310	G/A	0.45	0.0116	0.94 (0.89,0.99)	0.134	0.95 (0.9,1.01)	6.84e-03	0.89 (0.82,0.97)	0.245
rs7916322	64612824	G/A	0.18	0.0122	1.09 (1.02,1.16)	0.078	1.08 (0.99,1.17)	0.12	1.09 (0.98,1.21)	0.544
rs7074979	64323303	A/G	0.47	0.0124	0.94 (0.89,0.99)	0.181	0.96 (0.9,1.02)	5.87e-03	0.89 (0.82,0.97)	0.222
rs10509174	64637908	G/A	0.15	0.0124	1.09 (1.02,1.17)	4.95e-02	1.09 (1,1.19)	0.092	1.1 (0.99,1.23)	0.719
rs7903566	64315820	G/A	0.46	0.0125	0.94 (0.89,0.99)	0.236	0.96 (0.91,1.02)	8.9e-03	0.9 (0.83,0.97)	0.208
rs7067850	64584617	A/G	0.31	0.0145	0.93 (0.88,0.99)	2.28e-02	0.92 (0.86,0.99)	0.235	0.95 (0.87,1.04)	0.466
rs868913	64340599	G/A	0.5	0.0151	0.94 (0.89,0.99)	0.169	0.96 (0.9,1.02)	9.1e-03	0.9 (0.83,0.97)	0.255
rs11592442	64533904	T/A	0.18	0.0157	1.08 (1.02,1.16)	0.092	1.07 (0.99,1.16)	0.203	1.07 (0.96,1.19)	0.743
rs10822057	64520151	G/A	0.19	0.0184	1.08 (1.01,1.15)	0.128	1.06 (0.98,1.15)	0.154	1.08 (0.97,1.19)	0.968
rs7911225	64588535	C/A	0.31	0.0192	0.94 (0.88,0.99)	3.41e-02	0.93 (0.87,0.99)	0.264	0.95 (0.87,1.04)	0.492
rs868914	64340802	A/G	0.48	0.0198	0.94 (0.89,0.99)	0.251	0.96 (0.91,1.03)	6.02e-03	0.89 (0.82,0.97)	0.162
rs911609	64611477	G/A	0.19	0.0205	1.08 (1.01,1.15)	0.097	1.07 (0.99,1.16)	0.062	1.1 (1,1.22)	0.291
rs224087	64532193	G/A	0.15	0.0212	0.92 (0.85,0.99)	3.64e-02	0.91 (0.83,0.99)	0.164	0.92 (0.82,1.03)	0.601
rs2136613	64594164	A/G	0.62	0.0218	0.94 (0.89,0.99)	3.31e-02	0.93 (0.88,0.99)	0.241	0.95 (0.88,1.03)	0.865
rs10995202	64300893	G/A	0.22	0.0225	0.93 (0.88,0.99)	0.058	0.93 (0.86,1)	0.223	0.94 (0.85,1.04)	0.896
c10_pos64345050	64345050	A/C	0.15	0.0228	0.92 (0.86,0.99)	0.074	0.93 (0.85,1.01)	4.44e-02	0.89 (0.79,1)	0.575
rs9943383	64429757	A/T	0.31	0.0248	0.94 (0.89,0.99)	0.087	0.94 (0.88,1.01)	0.135	0.93 (0.86,1.02)	0.864

rs10822019	64303915	C/A	0.48	0.0262	0.94 (0.9,0.99)	0.126	0.95 (0.9,1.01)	2.57e-02	0.91 (0.84,0.99)	0.411
rs7922576	64300637	A/T	0.55	0.0265	0.94 (0.9,0.99)	0.214	0.96 (0.9,1.02)	0.125	0.94 (0.87,1.02)	0.724
c10_pos64349002	64349002	G/A	0.15	0.0272	0.92 (0.86,0.99)	0.083	0.93 (0.85,1.01)	0.073	0.9 (0.8,1.01)	0.721
rs10822018	64302195	A/C	0.22	0.0276	0.93 (0.88,0.99)	0.058	0.93 (0.86,1)	0.204	0.94 (0.85,1.04)	0.911
rs224278	64580575	G/A	0.6	0.0303	0.94 (0.9,0.99)	3.92e-02	0.94 (0.88,1)	0.204	0.95 (0.87,1.03)	0.809
rs7079501	64428129	G/C	0.25	0.0309	0.94 (0.88,0.99)	4.64e-02	0.93 (0.87,1)	0.197	0.94 (0.86,1.03)	0.76
rs224277	64580061	A/G	0.6	0.031	0.94 (0.9,0.99)	4.06e-02	0.94 (0.88,1)	0.192	0.95 (0.87,1.03)	0.841
rs10128333	64570038	G/A	0.47	0.0337	0.95 (0.9,1)	0.107	0.95 (0.89,1.01)	0.234	0.95 (0.88,1.03)	0.781
rs7905412	64297969	C/G	0.22	0.0348	0.94 (0.88,1)	0.156	0.95 (0.88,1.02)	0.071	0.91 (0.83,1.01)	0.368
rs4746409	64263402	C/G	0.47	0.0351	1.06 (1,1.11)	0.168	1.04 (0.98,1.11)	0.086	1.07 (0.99,1.16)	0.431
rs10761660	64516306	A/G	0.18	0.0358	1.07 (1,1.14)	0.073	1.07 (0.99,1.16)	0.599	1.03 (0.93,1.14)	0.433
rs10509168	64257828	G/A	0.52	0.0368	0.95 (0.9,1)	0.108	0.95 (0.89,1.01)	0.174	0.95 (0.87,1.02)	0.913
c10_pos64258017	64258017	A/G	0.52	0.038	0.95 (0.9,1)	0.136	0.95 (0.9,1.01)	0.184	0.95 (0.87,1.03)	0.881
rs1914188	64312627	C/A	0.63	0.0397	0.95 (0.9,1)	0.423	0.97 (0.91,1.04)	0.119	0.94 (0.86,1.02)	0.501
rs2393886	64258343	G/A	0.51	0.04	0.95 (0.9,1)	0.133	0.95 (0.9,1.01)	0.167	0.95 (0.87,1.02)	0.816
rs12263972	64749082	C/A	0.03	0.0423	0.86 (0.74,1)	0.182	0.88 (0.74,1.06)	0.17	0.85 (0.67,1.08)	0.445
rs224036	64522439	A/G	0.15	0.0424	0.93 (0.86,1)	0.086	0.93 (0.85,1.01)	0.203	0.93 (0.83,1.04)	0.912
rs10822025	64311098	G/A	0.63	0.0429	0.95 (0.9,1)	0.434	0.97 (0.91,1.04)	0.13	0.94 (0.86,1.02)	0.518
rs10995194	64288130	G/C	0.02	0.0435	1.18 (1,1.39)	0.308	1.11 (0.91,1.35)	0.264	1.16 (0.9,1.49)	0.712
rs224136	64470675	G/A	0.31	0.0473	0.95 (0.9,1)	0.056	0.94 (0.88,1)	0.996	1 (0.92,1.09)	0.114
rs224034	64522390	G/A	0.15	0.0481	0.93 (0.87,1)	0.089	0.93 (0.85,1.01)	0.186	0.93 (0.83,1.04)	0.864
rs2393887	64263093	C/G	0.34	0.0494	0.95 (0.9,1)	0.128	0.95 (0.89,1.01)	0.546	0.97 (0.9,1.06)	0.577
rs7082182	64349321	G/C	0.15	0.051	0.93 (0.87,1)	0.156	0.94 (0.86,1.02)	0.195	0.93 (0.83,1.04)	0.873
rs10822074	64630538	G/A	0.17	0.051	1.07 (1,1.14)	0.113	1.07 (0.98,1.16)	0.124	1.09 (0.98,1.21)	0.543
rs2138560	64336729	A/G	0.65	0.052	0.95 (0.9,1)	0.423	0.97 (0.91,1.04)	0.072	0.93 (0.85,1.01)	0.419
rs10822038	64385224	G/A	0.38	0.053	0.95 (0.9,1)	3.1e-02	0.93 (0.87,0.99)	0.433	0.97 (0.89,1.05)	0.45
rs1848797	64552934	A/G	0.16	0.053	1.07 (1,1.14)	0.144	1.06 (0.98,1.15)	0.311	1.06 (0.95,1.18)	0.758
rs10995181	64268659	T/A	0.02	0.055	1.17 (1,1.38)	0.429	1.08 (0.89,1.32)	0.242	1.16 (0.91,1.5)	0.537
rs10995245	64391375	G/A	0.35	0.056	0.95 (0.9,1)	4.54e-02	0.94 (0.88,1)	0.352	0.96 (0.88,1.05)	0.55
rs34511355	64276964	A/C	0.02	0.057	1.17 (1,1.38)	0.401	1.09 (0.89,1.33)	0.29	1.15 (0.89,1.48)	0.652

rs10995189	64278181	G/A	0.02	0.057	1.17 (1,1.38)	0.401	1.09 (0.89,1.33)	0.29	1.15 (0.89,1.48)	0.652
rs10995190	64278682	G/A	0.02	0.057	1.17 (1,1.38)	0.401	1.09 (0.89,1.33)	0.29	1.15 (0.89,1.48)	0.652
rs10995191	64278874	G/A	0.02	0.057	1.17 (1,1.38)	0.401	1.09 (0.89,1.33)	0.29	1.15 (0.89,1.48)	0.652
rs4746419	64275261	C/G	0.02	0.061	1.17 (0.99,1.38)	0.429	1.08 (0.89,1.32)	0.283	1.15 (0.89,1.48)	0.609
rs224308	64602767	A/G	0.4	0.061	0.95 (0.9,1)	0.165	0.96 (0.9,1.02)	0.403	0.97 (0.89,1.05)	0.932
rs7923316	64270846	G/A	0.53	0.063	0.95 (0.91,1)	0.695	0.99 (0.93,1.05)	0.121	0.94 (0.87,1.02)	0.319
rs10995312	64566572	A/G	0.46	0.063	0.95 (0.91,1)	0.23	0.96 (0.91,1.02)	0.159	0.94 (0.87,1.02)	0.854
rs10995263	64424538	G/A	0.25	0.065	0.95 (0.89,1)	0.114	0.94 (0.88,1.01)	0.458	0.97 (0.88,1.06)	0.557
rs16917317	64270771	A/G	0.53	0.067	0.95 (0.91,1)	0.683	0.99 (0.93,1.05)	0.133	0.94 (0.87,1.02)	0.351
rs2393881	64205643	G/A	0.35	0.068	0.95 (0.9,1)	0.175	0.96 (0.9,1.02)	0.089	0.93 (0.85,1.01)	0.581
c10_pos64596362	64596362	C/G	0.4	0.069	0.95 (0.91,1)	0.128	0.95 (0.89,1.01)	0.499	0.97 (0.9,1.06)	0.893
rs7895082	64270919	C/A	0.53	0.07	0.95 (0.91,1)	0.707	0.99 (0.93,1.05)	0.135	0.94 (0.87,1.02)	0.345
rs10822013	64251977	A/G	0.5	0.075	0.96 (0.91,1)	0.129	0.95 (0.9,1.01)	0.315	0.96 (0.89,1.04)	0.815
rs10995180	64267743	G/A	0.52	0.075	0.96 (0.91,1)	0.701	0.99 (0.93,1.05)	0.172	0.95 (0.87,1.02)	0.431
rs1955328	64269387	A/G	0.52	0.076	0.96 (0.91,1)	0.681	0.99 (0.93,1.05)	0.152	0.94 (0.87,1.02)	0.4
rs10995173	64246575	A/T	0.5	0.077	0.96 (0.91,1)	0.12	0.95 (0.9,1.01)	0.376	0.96 (0.89,1.04)	0.74
rs4537656	64406802	G/A	0.26	0.078	0.95 (0.9,1.01)	0.097	0.94 (0.88,1.01)	0.589	0.97 (0.89,1.07)	0.431
rs224117	64443139	C/A	0.25	0.079	0.95 (0.89,1.01)	0.085	0.94 (0.87,1.01)	0.388	0.96 (0.87,1.05)	0.545
rs7074870	64205327	G/A	0.35	0.08	0.95 (0.9,1.01)	0.155	0.95 (0.9,1.02)	0.093	0.93 (0.86,1.01)	0.62
rs4282885	64243828	A/G	0.5	0.08	0.96 (0.91,1.01)	0.116	0.95 (0.9,1.01)	0.39	0.97 (0.89,1.05)	0.723
rs16917994	64740148	G/A	0.27	0.081	1.05 (0.99,1.11)	0.09	1.06 (0.99,1.14)	0.18	1.06 (0.97,1.16)	0.807
rs4237288	64269110	A/G	0.52	0.082	0.96 (0.91,1.01)	0.715	0.99 (0.93,1.05)	0.159	0.94 (0.87,1.02)	0.395
rs2893907	64382359	C/A	0.47	0.082	1.05 (0.99,1.1)	0.067	1.06 (1,1.13)	0.349	1.04 (0.96,1.13)	0.759
rs371774	64484682	T/A	0.17	0.083	0.94 (0.88,1.01)	0.112	0.94 (0.86,1.02)	0.823	0.99 (0.89,1.1)	0.339
rs10509169	64276759	A/G	0.52	0.084	0.96 (0.91,1.01)	0.717	0.99 (0.93,1.05)	0.219	0.95 (0.88,1.03)	0.483
rs12245332	64260847	A/G	0.34	0.085	0.95 (0.9,1.01)	0.177	0.96 (0.9,1.02)	0.592	0.98 (0.9,1.06)	0.582
rs10822015	64268345	A/T	0.52	0.086	0.96 (0.91,1.01)	0.768	0.99 (0.93,1.05)	0.172	0.95 (0.87,1.02)	0.37
rs737314	64274177	A/G	0.53	0.087	0.96 (0.91,1.01)	0.796	0.99 (0.93,1.05)	0.143	0.94 (0.87,1.02)	0.315
rs4746508	64408208	G/A	0.26	0.088	0.95 (0.9,1.01)	0.106	0.94 (0.88,1.01)	0.625	0.98 (0.89,1.07)	0.425
rs2393909	64412544	G/C	0.25	0.088	0.95 (0.9,1.01)	0.104	0.94 (0.88,1.01)	0.631	0.98 (0.89,1.07)	0.401

rs2893905	64381124	A/G	0.47	0.089	1.05 (0.99,1.1)	0.063	1.06 (1,1.13)	0.421	1.03 (0.95,1.12)	0.628
rs4746493	64399617	C/G	0.26	0.093	0.95 (0.9,1.01)	0.097	0.94 (0.88,1.01)	0.662	0.98 (0.89,1.07)	0.376
rs7068751	64697148	G/A	0.03	0.095	0.88 (0.76,1.02)	0.335	0.91 (0.76,1.1)	0.208	0.86 (0.68,1.09)	0.371
rs12243471	64260410	A/G	0.34	0.097	0.96 (0.9,1.01)	0.212	0.96 (0.9,1.02)	0.546	0.97 (0.89,1.06)	0.646
rs10822006	64205492	A/G	0.4	0.101	0.96 (0.91,1.01)	0.31	0.97 (0.91,1.03)	0.109	0.94 (0.86,1.02)	0.527
rs4745873	64413468	G/C	0.26	0.101	0.95 (0.9,1.01)	0.113	0.94 (0.88,1.01)	0.667	0.98 (0.89,1.08)	0.399
rs1888967	64579460	A/T	0.19	0.101	1.06 (0.99,1.13)	0.22	1.05 (0.97,1.14)	0.496	1.04 (0.94,1.15)	0.71
rs1955331	64232042	A/G	0.5	0.107	0.96 (0.91,1.01)	0.127	0.95 (0.9,1.01)	0.521	0.97 (0.9,1.05)	0.603
rs9633559	64293978	G/A	0.43	0.107	1.04 (0.99,1.1)	0.678	1.01 (0.95,1.08)	0.186	1.06 (0.97,1.15)	0.447
rs7086136	64410072	A/G	0.34	0.109	0.96 (0.91,1.01)	0.106	0.95 (0.89,1.01)	0.722	0.98 (0.9,1.07)	0.321
rs2176289	64350533	A/G	0.46	0.11	0.96 (0.91,1.01)	0.18	0.96 (0.9,1.02)	0.204	0.95 (0.87,1.03)	0.952
rs4523588	64750796	G/A	0.2	0.115	0.95 (0.89,1.01)	0.145	0.94 (0.87,1.02)	0.201	0.94 (0.85,1.04)	0.53
rs7083350	64249170	G/A	0.34	0.117	0.96 (0.91,1.01)	0.24	0.96 (0.9,1.03)	0.861	0.99 (0.91,1.08)	0.409
rs7094985	64211810	A/G	0.49	0.122	0.96 (0.91,1.01)	0.43	0.98 (0.92,1.04)	0.112	0.94 (0.87,1.02)	0.32
rs10822043	64415031	G/A	0.25	0.125	0.96 (0.9,1.01)	0.132	0.95 (0.88,1.02)	0.731	0.98 (0.9,1.08)	0.361
rs10995170	64223383	A/G	0.32	0.127	0.96 (0.91,1.01)	0.662	0.99 (0.92,1.05)	0.186	0.94 (0.87,1.03)	0.381
rs1878262	64273879	C/A	0.53	0.129	0.96 (0.91,1.01)	0.994	1 (0.94,1.06)	0.179	0.95 (0.87,1.03)	0.275
rs10822008	64213069	A/G	0.49	0.13	0.96 (0.92,1.01)	0.449	0.98 (0.92,1.04)	0.089	0.93 (0.86,1.01)	0.294
rs17314489	64273892	G/A	0.45	0.131	1.04 (0.99,1.09)	0.692	1.01 (0.95,1.08)	0.172	1.06 (0.98,1.15)	0.446
rs224285	64584810	C/A	0.19	0.135	1.05 (0.98,1.12)	0.259	1.05 (0.97,1.13)	0.536	1.03 (0.93,1.15)	0.701
rs4746516	64426056	C/A	0.28	0.137	0.96 (0.9,1.01)	0.118	0.95 (0.88,1.01)	0.773	0.99 (0.9,1.08)	0.423
rs2138566	64355339	A/G	0.46	0.138	0.96 (0.91,1.01)	0.196	0.96 (0.9,1.02)	0.21	0.95 (0.88,1.03)	0.957
rs10995253	64401650	A/C	0.26	0.14	0.96 (0.9,1.01)	0.144	0.95 (0.88,1.02)	0.735	0.98 (0.9,1.08)	0.398
rs7907439	64346650	G/A	0.01	0.142	1.17 (0.95,1.44)	0.342	1.13 (0.88,1.47)	0.206	1.23 (0.9,1.69)	0.541
rs7072167	64231739	G/C	0.34	0.144	0.96 (0.91,1.01)	0.266	0.96 (0.9,1.03)	0.886	0.99 (0.91,1.08)	0.403
rs10761636	64233999	A/C	0.33	0.148	0.96 (0.91,1.01)	0.256	0.96 (0.9,1.03)	0.97	1 (0.92,1.09)	0.355
rs753518	64235506	G/A	0.33	0.151	0.96 (0.91,1.01)	0.273	0.96 (0.9,1.03)	0.93	1 (0.92,1.08)	0.389
rs1996318	64236820	G/A	0.33	0.154	0.96 (0.91,1.01)	0.259	0.96 (0.9,1.03)	0.903	0.99 (0.91,1.08)	0.399
rs7075349	64427649	A/G	0.36	0.157	0.96 (0.91,1.01)	0.173	0.96 (0.9,1.02)	0.555	0.97 (0.9,1.06)	0.777
rs6479815	64224100	A/G	0.32	0.159	0.96 (0.91,1.02)	0.718	0.99 (0.93,1.05)	0.236	0.95 (0.87,1.03)	0.42

rs17316874	64360090	A/G	0.01	0.159	1.16 (0.94,1.43)	0.124	1.22 (0.95,1.56)	0.276	1.19 (0.87,1.63)	0.88
rs1955332	64231895	G/A	0.34	0.161	0.96 (0.91,1.02)	0.287	0.97 (0.9,1.03)	0.908	1 (0.91,1.08)	0.41
rs10822011	64240648	A/G	0.34	0.163	0.96 (0.91,1.02)	0.307	0.97 (0.91,1.03)	0.897	0.99 (0.91,1.08)	0.422
rs35816896	64300340	C/A	0.02	0.163	1.12 (0.95,1.33)	0.497	1.07 (0.88,1.31)	0.472	1.1 (0.85,1.43)	0.787
rs10822007	64208221	A/G	0.49	0.165	0.97 (0.92,1.01)	0.564	0.98 (0.92,1.04)	0.114	0.94 (0.87,1.02)	0.28
rs2138555	64220494	A/G	0.52	0.167	0.97 (0.92,1.01)	0.691	0.99 (0.93,1.05)	4.51e-02	0.92 (0.85,1)	0.123
rs35770602	64371206	A/C	0.01	0.169	1.16 (0.94,1.42)	0.127	1.21 (0.95,1.55)	0.27	1.19 (0.87,1.63)	0.893
c10_pos64373686	64373686	A/G	0.01	0.171	1.16 (0.94,1.42)	0.143	1.21 (0.94,1.54)	0.247	1.21 (0.88,1.65)	0.843
rs2393885	64238342	A/G	0.33	0.172	0.96 (0.91,1.02)	0.298	0.97 (0.9,1.03)	0.984	1 (0.92,1.09)	0.378
rs35123851	64354263	G/A	0.01	0.173	1.15 (0.94,1.42)	0.152	1.2 (0.94,1.54)	0.262	1.2 (0.88,1.64)	0.794
rs1949359	64356993	G/A	0.16	0.173	0.95 (0.89,1.02)	0.241	0.95 (0.88,1.03)	0.124	0.92 (0.82,1.02)	0.485
rs10822027	64344371	C/A	0.42	0.175	0.97 (0.92,1.02)	0.545	0.98 (0.92,1.04)	3.31e-02	0.92 (0.84,0.99)	0.336
rs4746725	64673830	A/G	0.2	0.184	0.96 (0.9,1.02)	0.217	0.95 (0.88,1.03)	0.316	0.95 (0.86,1.05)	0.584
rs2136614	64701286	A/G	0.31	0.196	1.04 (0.98,1.09)	0.127	1.05 (0.99,1.12)	0.24	1.05 (0.97,1.15)	0.885
rs12252317	64646868	G/A	0.03	0.199	0.91 (0.78,1.05)	0.49	0.94 (0.78,1.13)	0.386	0.9 (0.71,1.14)	0.515
rs10995186	64273023	G/A	0.45	0.203	1.03 (0.98,1.09)	0.86	1.01 (0.95,1.07)	0.228	1.05 (0.97,1.14)	0.428
rs1914191	64362223	A/G	0.16	0.207	0.96 (0.89,1.02)	0.237	0.95 (0.88,1.03)	0.185	0.93 (0.83,1.04)	0.614
rs10995184	64271051	G/A	0.45	0.216	1.03 (0.98,1.09)	0.889	1 (0.94,1.07)	0.236	1.05 (0.97,1.14)	0.428
rs1878261	64273942	A/G	0.45	0.218	1.03 (0.98,1.09)	0.906	1 (0.94,1.07)	0.226	1.05 (0.97,1.14)	0.401
rs10822031	64361700	A/G	0.4	0.219	0.97 (0.92,1.02)	0.474	0.98 (0.92,1.04)	0.1	0.93 (0.86,1.01)	0.653
c10_pos64583263	64583263	G/A	0.18	0.224	1.04 (0.98,1.11)	0.105	1.07 (0.99,1.16)	0.324	1.05 (0.95,1.17)	0.892
rs7082801	64349735	G/A	0.01	0.226	1.13 (0.92,1.39)	0.13	1.21 (0.95,1.54)	0.318	1.17 (0.86,1.61)	0.974
rs10995260	64410580	G/A	0.56	0.227	1.03 (0.98,1.09)	0.19	1.04 (0.98,1.11)	0.932	1 (0.93,1.09)	0.442
rs1040875	64588209	G/A	0.2	0.227	1.04 (0.98,1.11)	0.454	1.03 (0.95,1.11)	0.694	1.02 (0.92,1.13)	0.786
c10_pos64277369	64277369	G/A	0.14	0.232	1.05 (0.97,1.12)	0.448	1.03 (0.95,1.13)	0.081	1.11 (0.99,1.24)	0.219
rs2176290	64349979	G/A	0.52	0.233	1.03 (0.98,1.09)	0.351	1.03 (0.97,1.1)	0.321	1.04 (0.96,1.13)	0.934
rs9988771	64704647	C/G	0.45	0.235	1.03 (0.98,1.08)	0.284	1.03 (0.97,1.1)	0.41	1.03 (0.95,1.12)	0.997
rs10995177	64266512	A/G	0.45	0.236	1.03 (0.98,1.08)	0.83	1.01 (0.95,1.07)	0.344	1.04 (0.96,1.13)	0.62
rs12249410	64301941	C/A	0.15	0.238	1.04 (0.97,1.12)	0.298	1.05 (0.96,1.14)	0.148	1.09 (0.97,1.22)	0.582
rs911610	64620042	G/A	0.19	0.238	1.04 (0.97,1.11)	0.094	1.07 (0.99,1.16)	0.738	0.98 (0.89,1.09)	0.072

c10_pos64339833	64339833	A/C	0.14	0.244	1.04 (0.97,1.12)	0.336	1.04 (0.96,1.14)	0.066	1.11 (0.99,1.25)	0.345
c10_pos64449549	64449549	C/A	0.15	0.244	1.04 (0.97,1.12)	0.179	1.06 (0.97,1.16)	0.881	1.01 (0.9,1.13)	0.309
rs10995178	64266748	G/A	0.45	0.247	1.03 (0.98,1.08)	0.91	1 (0.94,1.07)	0.312	1.04 (0.96,1.13)	0.524
rs7083045	64539964	G/A	0.66	0.25	0.97 (0.92,1.02)	0.389	0.97 (0.91,1.04)	0.271	0.95 (0.88,1.04)	0.909
rs10995188	64276804	C/A	0.45	0.253	1.03 (0.98,1.08)	0.899	1 (0.94,1.07)	0.377	1.04 (0.96,1.12)	0.599
rs4746445	64321261	G/A	0.27	0.257	0.97 (0.91,1.02)	0.697	0.99 (0.92,1.06)	0.106	0.93 (0.85,1.02)	0.321
rs2500953	64764512	A/G	0.03	0.259	0.91 (0.78,1.07)	0.523	0.94 (0.76,1.15)	0.522	0.92 (0.72,1.18)	0.692
rs10509176	64638049	G/A	0.21	0.26	0.96 (0.9,1.03)	0.22	0.95 (0.88,1.03)	0.81	0.99 (0.89,1.09)	0.487
rs10822021	64305389	A/G	0.25	0.261	0.97 (0.91,1.03)	0.724	0.99 (0.92,1.06)	4.08e-02	0.91 (0.83,1)	0.112
rs2393884	64230266	G/A	0.49	0.266	0.97 (0.92,1.02)	0.546	0.98 (0.92,1.04)	0.262	0.96 (0.88,1.03)	0.546
rs2138561	64335087	A/G	0.14	0.267	1.04 (0.97,1.12)	0.347	1.04 (0.96,1.14)	0.063	1.11 (0.99,1.25)	0.321
rs10509170	64278634	G/A	0.45	0.275	1.03 (0.98,1.08)	0.948	1 (0.94,1.07)	0.39	1.04 (0.96,1.12)	0.606
rs2944542	64369999	G/C	0.52	0.277	1.03 (0.98,1.08)	0.406	1.03 (0.96,1.09)	0.375	1.04 (0.96,1.12)	0.93
c10_pos64317869	64317869	A/G	0.02	0.289	0.91 (0.76,1.08)	0.131	0.85 (0.68,1.05)	0.92	0.99 (0.75,1.29)	0.343
rs11817939	64588680	A/G	0.18	0.289	1.04 (0.97,1.11)	0.141	1.06 (0.98,1.15)	0.389	1.05 (0.94,1.16)	0.9
rs4746443	64313836	G/A	0.25	0.295	0.97 (0.91,1.03)	0.821	0.99 (0.92,1.06)	4.38e-02	0.91 (0.83,1)	0.106
c10_pos64672836	64672836	G/A	0.39	0.299	1.03 (0.98,1.08)	0.761	1.01 (0.95,1.08)	0.556	1.03 (0.94,1.11)	0.525
rs2393892	64288592	A/G	0.17	0.301	0.96 (0.9,1.03)	0.622	1.02 (0.94,1.11)	0.205	0.93 (0.84,1.04)	0.234
rs10995207	64311054	A/G	0.25	0.302	0.97 (0.91,1.03)	0.829	0.99 (0.92,1.06)	4.38e-02	0.91 (0.83,1)	0.104
c10_pos64361513	64361513	G/A	0.04	0.308	0.94 (0.82,1.06)	0.17	0.9 (0.76,1.05)	0.658	1.04 (0.86,1.27)	0.461
rs2393898	64348899	G/C	0.43	0.312	1.03 (0.98,1.08)	0.726	1.01 (0.95,1.08)	0.316	1.04 (0.96,1.13)	0.665
rs4745849	64313875	A/C	0.25	0.315	0.97 (0.91,1.03)	0.839	0.99 (0.93,1.07)	4.52e-02	0.91 (0.83,1)	0.104
rs4746441	64310034	A/G	0.25	0.323	0.97 (0.92,1.03)	0.841	0.99 (0.93,1.07)	4.54e-02	0.91 (0.83,1)	0.104
rs7078554	64595034	T/A	0.19	0.326	1.03 (0.97,1.1)	0.195	1.05 (0.97,1.14)	0.655	0.98 (0.88,1.08)	0.111
c10_pos64324858	64324858	C/G	0.02	0.327	0.92 (0.77,1.09)	0.172	0.86 (0.7,1.07)	0.955	0.99 (0.76,1.29)	0.372
c10_pos64323123	64323123	T/A	0.02	0.329	0.92 (0.77,1.09)	0.171	0.86 (0.7,1.07)	0.96	0.99 (0.76,1.3)	0.367
rs10740102	64756872	C/A	0.19	0.335	0.97 (0.91,1.03)	0.347	0.96 (0.89,1.04)	0.774	0.99 (0.89,1.09)	0.942
c10_pos64304569	64304569	A/C	0.02	0.337	0.92 (0.77,1.09)	0.158	0.86 (0.69,1.06)	0.999	1 (0.77,1.3)	0.34
rs10740092	64629705	A/C	0.4	0.339	0.98 (0.93,1.03)	0.534	0.98 (0.92,1.04)	0.729	0.99 (0.91,1.07)	0.977
c10_pos64325337	64325337	G/A	0.02	0.344	0.92 (0.77,1.09)	0.18	0.86 (0.7,1.07)	0.984	1 (0.76,1.3)	0.368

rs12220488	64219000	A/G	0.49	0.345	0.98 (0.93,1.03)	0.868	0.99 (0.94,1.06)	0.057	0.93 (0.86,1)	0.101
rs11812404	64259322	A/G	0.17	0.346	0.97 (0.91,1.04)	0.498	0.97 (0.9,1.05)	0.158	0.93 (0.83,1.03)	0.334
c10_pos64338079	64338079	G/A	0.02	0.347	0.92 (0.77,1.09)	0.134	0.85 (0.69,1.05)	0.904	1.02 (0.78,1.32)	0.239
c10_pos64333511	64333511	G/A	0.02	0.35	0.92 (0.77,1.09)	0.146	0.85 (0.69,1.06)	0.965	0.99 (0.76,1.29)	0.305
rs12259030	64412618	G/A	0.04	0.351	1.06 (0.93,1.21)	0.962	1 (0.85,1.17)	0.242	1.12 (0.93,1.37)	0.429
c10_pos64609200	64609200	G/A	0.21	0.351	0.97 (0.91,1.03)	0.273	0.96 (0.89,1.03)	0.838	0.99 (0.89,1.09)	0.467
c10_pos64684113	64684113	G/A	0.42	0.353	1.02 (0.97,1.08)	0.69	1.01 (0.95,1.08)	0.455	1.03 (0.95,1.12)	0.425
rs12766377	64381013	G/A	0.01	0.354	1.1 (0.9,1.36)	0.236	1.16 (0.91,1.49)	0.295	1.19 (0.86,1.65)	0.923
c10_pos64311302	64311302	A/G	0.02	0.358	0.92 (0.77,1.1)	0.16	0.86 (0.69,1.06)	0.949	1.01 (0.77,1.32)	0.313
rs10822065	64610932	A/C	0.2	0.359	1.03 (0.97,1.1)	0.194	1.05 (0.97,1.14)	0.529	0.97 (0.87,1.07)	0.093
c10_pos64335212	64335212	T/A	0.02	0.361	0.92 (0.78,1.1)	0.162	0.86 (0.69,1.06)	0.983	1 (0.77,1.3)	0.327
rs7096842	64583441	G/A	0.01	0.361	0.89 (0.7,1.14)	0.265	0.85 (0.63,1.14)	0.29	0.81 (0.55,1.2)	0.874
rs17470703	64481684	A/G	0.01	0.363	1.12 (0.88,1.44)	0.447	0.88 (0.63,1.23)	3.43e-02	1.47 (1.04,2.09)	0.063
rs1949355	64218423	A/G	0.49	0.368	0.98 (0.93,1.03)	0.898	1 (0.94,1.06)	0.064	0.93 (0.86,1)	0.104
rs10761664	64607061	A/G	0.2	0.375	1.03 (0.97,1.1)	0.226	1.05 (0.97,1.13)	0.479	0.96 (0.87,1.07)	0.073
rs16917424	64309992	A/G	0.02	0.376	0.92 (0.78,1.1)	0.14	0.85 (0.69,1.06)	0.999	1 (0.77,1.3)	0.313
rs11817265	64654102	A/G	0.42	0.378	1.02 (0.97,1.08)	0.674	1.01 (0.95,1.08)	0.593	1.02 (0.94,1.11)	0.547
rs6479827	64317700	G/A	0.15	0.382	1.03 (0.96,1.11)	0.265	1.05 (0.96,1.14)	0.143	1.09 (0.97,1.22)	0.667
c10_pos64327928	64327928	A/G	0.02	0.39	0.93 (0.78,1.1)	0.181	0.87 (0.7,1.07)	0.983	1 (0.77,1.3)	0.359
rs12243155	64306395	A/T	0.15	0.392	1.03 (0.96,1.11)	0.338	1.04 (0.96,1.14)	0.153	1.09 (0.97,1.21)	0.605
rs224082	64566258	G/A	0.36	0.394	1.02 (0.97,1.08)	0.384	1.03 (0.97,1.1)	0.498	1.03 (0.95,1.12)	0.919
rs4746123	64214402	G/A	0.48	0.397	0.98 (0.93,1.03)	0.956	1 (0.94,1.06)	0.071	0.93 (0.86,1.01)	0.106
rs4746447	64321478	C/A	0.28	0.4	0.98 (0.92,1.03)	0.979	1 (0.93,1.07)	0.105	0.93 (0.85,1.02)	0.207
rs10995213	64320735	A/G	0.28	0.401	0.98 (0.92,1.03)	0.908	1 (0.93,1.07)	0.107	0.93 (0.85,1.02)	0.24
rs2393935	64656038	G/A	0.42	0.401	1.02 (0.97,1.08)	0.719	1.01 (0.95,1.08)	0.593	1.02 (0.94,1.11)	0.525
rs6479826	64314760	G/A	0.15	0.404	1.03 (0.96,1.11)	0.334	1.04 (0.96,1.14)	0.155	1.08 (0.97,1.21)	0.61
rs4746444	64314689	G/A	0.27	0.407	0.98 (0.92,1.03)	0.972	1 (0.93,1.07)	3.42e-02	0.91 (0.83,0.99)	0.065
rs10995187	64273026	G/A	0.01	0.409	1.13 (0.85,1.51)	0.967	0.99 (0.67,1.47)	0.464	1.18 (0.76,1.83)	0.397
rs10995212	64320620	G/A	0.28	0.409	0.98 (0.92,1.03)	0.997	1 (0.93,1.07)	0.105	0.93 (0.85,1.02)	0.203
rs12781740	64377967	G/A	0.01	0.417	1.09 (0.88,1.36)	0.207	1.18 (0.91,1.53)	0.606	1.09 (0.78,1.53)	0.781

rs10740083	64309726	C/G	0.27	0.44	0.98 (0.92,1.04)	0.964	1 (0.93,1.07)	3.92e-02	0.91 (0.83,1)	0.071
rs16917302	64261198	A/C	0.18	0.443	0.97 (0.91,1.04)	0.641	0.98 (0.91,1.06)	0.197	0.93 (0.84,1.04)	0.327
rs10995208	64311230	A/G	0.27	0.446	0.98 (0.92,1.04)	0.953	1 (0.94,1.07)	3.78e-02	0.91 (0.83,0.99)	0.069
rs6479860	64745865	A/G	0.17	0.455	0.97 (0.91,1.04)	0.381	0.96 (0.89,1.05)	0.453	0.96 (0.86,1.07)	0.681
rs10761646	64331214	G/A	0.25	0.46	0.98 (0.92,1.04)	0.818	1.01 (0.94,1.08)	0.121	0.93 (0.84,1.02)	0.129
rs9651304	64671764	G/A	0.5	0.466	1.02 (0.97,1.07)	0.696	1.01 (0.95,1.08)	0.437	1.03 (0.95,1.12)	0.414
rs1444418	64560470	A/G	0.32	0.468	0.98 (0.93,1.03)	0.4	0.97 (0.91,1.04)	0.902	0.99 (0.91,1.08)	0.616
rs7917222	64326912	A/G	0.25	0.474	0.98 (0.92,1.04)	0.743	1.01 (0.94,1.09)	0.109	0.93 (0.84,1.02)	0.1
rs4746461	64344998	C/A	0.42	0.475	0.98 (0.93,1.03)	0.951	1 (0.94,1.06)	0.135	0.94 (0.86,1.02)	0.459
rs12764150	64664180	A/G	0.06	0.475	1.04 (0.93,1.16)	0.768	1.02 (0.9,1.16)	0.241	1.11 (0.94,1.31)	0.44
rs953026	64654202	G/A	0.16	0.477	0.98 (0.91,1.04)	0.332	0.96 (0.88,1.04)	0.651	0.98 (0.87,1.09)	0.916
c10_pos64378296	64378296	A/G	0.15	0.487	0.98 (0.91,1.05)	0.47	0.97 (0.89,1.06)	0.202	0.93 (0.83,1.04)	0.468
rs4745851	64341951	G/A	0.25	0.492	0.98 (0.92,1.04)	0.811	1.01 (0.94,1.08)	0.108	0.93 (0.84,1.02)	0.11
rs3847337	64208433	G/A	0.27	0.496	0.98 (0.93,1.04)	0.937	1 (0.94,1.07)	0.488	0.97 (0.88,1.06)	0.505
rs16917407	64304454	G/A	0.18	0.497	1.02 (0.96,1.09)	0.502	1.03 (0.95,1.12)	0.216	1.07 (0.96,1.19)	0.623
rs4497277	64329298	A/G	0.25	0.497	0.98 (0.92,1.04)	0.778	1.01 (0.94,1.08)	0.128	0.93 (0.85,1.02)	0.127
rs4489633	64238333	G/A	0.5	0.498	0.98 (0.93,1.04)	0.558	0.98 (0.92,1.05)	0.807	1.01 (0.93,1.1)	0.607
rs4508090	64329247	G/A	0.25	0.5	0.98 (0.92,1.04)	0.702	1.01 (0.95,1.09)	0.118	0.93 (0.84,1.02)	0.1
rs10822078	64642355	C/G	0.25	0.51	0.98 (0.92,1.04)	0.465	0.97 (0.91,1.05)	0.87	0.99 (0.9,1.09)	0.985
rs10995218	64334119	G/A	0.25	0.523	0.98 (0.93,1.04)	0.773	1.01 (0.94,1.08)	0.144	0.93 (0.85,1.02)	0.138
rs10160102	64390647	A/G	0.19	0.524	1.02 (0.96,1.09)	0.611	1.02 (0.94,1.1)	0.507	1.04 (0.93,1.15)	0.747
rs7900283	64332495	G/A	0.25	0.529	0.98 (0.93,1.04)	0.776	1.01 (0.94,1.08)	0.13	0.93 (0.85,1.02)	0.129
rs7087449	64648813	G/A	0.02	0.53	0.94 (0.76,1.15)	0.852	1.02 (0.79,1.32)	0.994	1 (0.73,1.38)	0.655
rs11817964	64208276	G/A	0.18	0.532	0.98 (0.92,1.05)	0.435	0.97 (0.9,1.05)	0.37	0.95 (0.86,1.06)	0.715
rs10995204	64304060	A/C	0.15	0.534	1.02 (0.95,1.1)	0.28	1.05 (0.96,1.14)	0.492	1.04 (0.93,1.16)	0.847
rs7900579	64332738	C/A	0.25	0.539	0.98 (0.93,1.04)	0.721	1.01 (0.94,1.09)	0.122	0.93 (0.84,1.02)	0.104
rs7920642	64342362	G/C	0.27	0.548	0.98 (0.93,1.04)	0.985	1 (0.93,1.07)	0.101	0.93 (0.84,1.02)	0.172
rs10822109	64765654	G/A	0.64	0.55	1.02 (0.96,1.07)	0.586	1.02 (0.95,1.09)	0.94	1 (0.92,1.08)	0.424
rs12784493	64755609	G/A	0.21	0.557	0.98 (0.92,1.05)	0.262	0.96 (0.89,1.03)	0.847	0.99 (0.9,1.09)	0.445
rs7073406	64335377	A/G	0.25	0.564	0.98 (0.93,1.04)	0.753	1.01 (0.94,1.09)	0.154	0.93 (0.85,1.03)	0.142

rs953027	64654109	A/G	0.54	0.568	1.02 (0.96,1.07)	0.66	1.01 (0.95,1.08)	0.482	1.03 (0.95,1.12)	0.576
rs16917521	64393646	A/G	0.04	0.572	1.04 (0.91,1.19)	0.768	0.98 (0.82,1.15)	0.345	1.1 (0.9,1.36)	0.466
rs10995185	64271398	G/A	0.01	0.574	0.92 (0.68,1.24)	0.97	1.01 (0.7,1.44)	0.346	0.79 (0.48,1.31)	0.328
rs2842282	64765220	A/C	0.4	0.579	1.01 (0.96,1.07)	0.708	1.01 (0.95,1.08)	0.983	1 (0.92,1.09)	0.745
rs10822077	64639899	A/G	0.67	0.582	0.99 (0.93,1.04)	0.264	0.96 (0.9,1.03)	0.948	1 (0.92,1.09)	0.359
rs12244675	64400052	A/G	0.14	0.594	1.02 (0.95,1.1)	0.742	0.98 (0.9,1.08)	0.138	1.09 (0.97,1.23)	0.118
rs7100329	64349667	A/G	0.24	0.595	0.98 (0.93,1.04)	0.832	0.99 (0.92,1.07)	0.553	0.97 (0.88,1.07)	0.773
c10_pos64304197	64304197	A/G	0.02	0.6	0.96 (0.81,1.13)	0.297	0.9 (0.73,1.1)	0.801	1.03 (0.8,1.34)	0.397
rs4746428	64293118	G/A	0.33	0.606	0.99 (0.93,1.04)	0.618	1.02 (0.95,1.09)	0.825	0.99 (0.91,1.08)	0.874
rs10822073	64627636	C/G	0.38	0.606	1.01 (0.96,1.07)	0.97	1 (0.94,1.07)	0.39	1.04 (0.95,1.13)	0.294
c10_pos64489257	64489257	A/G	0.15	0.607	0.98 (0.91,1.05)	0.407	0.96 (0.88,1.05)	0.495	1.04 (0.93,1.17)	0.213
rs4746790	64757342	A/G	0.49	0.611	1.01 (0.96,1.07)	0.873	1.01 (0.95,1.07)	0.723	1.01 (0.94,1.1)	0.641
c10_pos64210669	64210669	A/G	0.03	0.613	0.96 (0.82,1.12)	0.141	0.86 (0.71,1.05)	0.596	1.07 (0.84,1.36)	0.073
c10_pos64391054	64391054	G/A	0.01	0.618	1.09 (0.77,1.55)	0.851	1.04 (0.67,1.63)	0.638	1.13 (0.69,1.84)	0.661
rs35078125	64591640	C/G	0.02	0.618	1.05 (0.87,1.27)	0.598	1.07 (0.83,1.37)	0.337	1.16 (0.86,1.56)	0.988
rs12256499	64381009	G/A	0.13	0.62	0.98 (0.91,1.06)	0.319	0.95 (0.87,1.05)	0.842	1.01 (0.9,1.14)	0.602
rs2393904	64379326	G/A	0.15	0.622	1.02 (0.95,1.09)	0.528	1.03 (0.94,1.12)	0.923	0.99 (0.89,1.12)	0.552
rs1509966	64552607	G/A	0.31	0.622	0.99 (0.93,1.04)	0.771	0.99 (0.93,1.06)	0.863	0.99 (0.91,1.08)	0.901
rs34331523	64619588	G/A	0.02	0.624	1.05 (0.86,1.28)	0.428	1.11 (0.86,1.43)	0.613	1.09 (0.79,1.49)	0.574
rs1914189	64309377	T/A	0.17	0.626	1.02 (0.95,1.09)	0.687	1.02 (0.94,1.1)	0.155	1.08 (0.97,1.2)	0.374
rs10509171	64306881	G/A	0.17	0.63	1.02 (0.95,1.09)	0.715	1.02 (0.94,1.1)	0.145	1.08 (0.97,1.2)	0.341
rs16917421	64308304	A/T	0.17	0.632	1.02 (0.95,1.09)	0.707	1.02 (0.94,1.1)	0.153	1.08 (0.97,1.2)	0.357
rs7919182	64643001	G/A	0.17	0.632	0.98 (0.92,1.05)	0.452	0.97 (0.89,1.05)	0.705	0.98 (0.88,1.09)	0.849
rs2138563	64307474	A/G	0.17	0.634	1.02 (0.95,1.09)	0.707	1.02 (0.94,1.1)	0.155	1.08 (0.97,1.2)	0.363
rs1949358	64306130	C/A	0.17	0.635	1.02 (0.95,1.09)	0.71	1.02 (0.94,1.1)	0.155	1.08 (0.97,1.2)	0.36
rs7088266	64481048	G/A	0.03	0.635	1.04 (0.89,1.22)	0.67	1.04 (0.86,1.27)	0.875	1.02 (0.8,1.3)	0.762
rs1949357	64306569	G/A	0.17	0.639	1.02 (0.95,1.09)	0.717	1.02 (0.94,1.1)	0.155	1.08 (0.97,1.2)	0.354
rs2138565	64307302	G/A	0.17	0.639	1.02 (0.95,1.09)	0.717	1.02 (0.94,1.1)	0.155	1.08 (0.97,1.2)	0.354
rs1955335	64310267	A/G	0.17	0.64	1.02 (0.95,1.09)	0.691	1.02 (0.94,1.1)	0.164	1.08 (0.97,1.2)	0.385
rs1955334	64310533	G/A	0.17	0.64	1.02 (0.95,1.09)	0.691	1.02 (0.94,1.1)	0.164	1.08 (0.97,1.2)	0.385

rs12242302	64310992	A/G	0.17	0.64	1.02 (0.95,1.09)	0.691	1.02 (0.94,1.1)	0.164	1.08 (0.97,1.2)	0.385
rs16917422	64309822	G/A	0.17	0.648	1.02 (0.95,1.09)	0.713	1.02 (0.94,1.1)	0.159	1.08 (0.97,1.2)	0.369
rs1949356	64298273	A/G	0.33	0.654	0.99 (0.94,1.04)	0.651	1.02 (0.95,1.08)	0.96	1 (0.92,1.09)	0.998
rs1914190	64305244	A/G	0.18	0.654	1.02 (0.95,1.09)	0.686	1.02 (0.94,1.1)	0.166	1.08 (0.97,1.2)	0.389
rs224121	64447352	C/A	0.15	0.664	1.02 (0.95,1.09)	0.586	0.98 (0.89,1.07)	0.391	1.05 (0.94,1.18)	0.24
rs9633562	64647504	C/A	0.58	0.668	1.01 (0.96,1.06)	0.794	0.99 (0.93,1.06)	0.82	1.01 (0.93,1.1)	0.59
c10_pos64231994	64231994	A/G	0.16	0.67	0.99 (0.92,1.05)	0.435	0.97 (0.89,1.05)	0.45	0.96 (0.86,1.07)	0.748
rs34533699	64251268	A/T	0.16	0.676	0.99 (0.92,1.05)	0.447	0.97 (0.89,1.05)	0.396	0.95 (0.86,1.06)	0.708
rs224067	64506971	A/G	0.53	0.677	1.01 (0.96,1.06)	0.254	1.04 (0.97,1.1)	0.338	0.96 (0.89,1.04)	0.087
rs17221319	64206712	C/A	0.56	0.686	1.01 (0.96,1.06)	0.741	0.99 (0.93,1.05)	0.599	1.02 (0.94,1.11)	0.56
rs10822092	64704741	A/G	0.66	0.686	1.01 (0.96,1.07)	0.936	1 (0.93,1.06)	0.68	1.02 (0.94,1.11)	0.598
c10_pos64395977	64395977	G/A	0.01	0.688	1.04 (0.84,1.29)	0.628	1.07 (0.82,1.38)	0.393	1.16 (0.83,1.62)	0.681
rs950214	64667404	C/A	0.45	0.688	1.01 (0.96,1.06)	0.887	1 (0.94,1.07)	0.825	1.01 (0.93,1.09)	0.689
rs10822100	64722406	A/G	0.31	0.688	1.01 (0.96,1.07)	0.532	1.02 (0.96,1.09)	0.862	1.01 (0.92,1.1)	0.808
rs6479830	64418739	G/A	0.09	0.691	1.02 (0.93,1.11)	0.906	0.99 (0.89,1.11)	0.431	1.06 (0.92,1.22)	0.343
rs1914187	64312794	A/G	0.18	0.696	1.01 (0.95,1.08)	0.718	1.02 (0.94,1.1)	0.179	1.08 (0.97,1.2)	0.396
rs10822099	64722032	A/G	0.31	0.696	1.01 (0.96,1.07)	0.532	1.02 (0.96,1.09)	0.862	1.01 (0.92,1.1)	0.808
c10_pos64529379	64529379	G/A	0.03	0.701	1.03 (0.88,1.21)	0.733	1.03 (0.85,1.26)	0.911	0.99 (0.77,1.27)	0.519
rs3939306	64631119	A/G	0.78	0.701	0.99 (0.93,1.05)	0.544	0.98 (0.91,1.05)	0.399	1.04 (0.95,1.15)	0.163
rs12413946	64431206	A/G	0.06	0.702	0.98 (0.88,1.09)	0.671	1.03 (0.9,1.17)	0.58	0.95 (0.79,1.14)	0.313
rs7921433	64666428	A/G	0.45	0.707	1.01 (0.96,1.06)	0.899	1 (0.94,1.07)	0.844	1.01 (0.93,1.09)	0.688
rs6479832	64419102	A/G	0.09	0.71	1.02 (0.93,1.11)	0.746	0.98 (0.88,1.1)	0.409	1.06 (0.92,1.22)	0.273
rs16917441	64313211	G/A	0.18	0.712	1.01 (0.95,1.08)	0.736	1.01 (0.93,1.1)	0.176	1.08 (0.97,1.2)	0.374
rs224313	64616940	A/G	0.28	0.713	0.99 (0.94,1.05)	0.862	0.99 (0.93,1.06)	0.815	0.99 (0.9,1.08)	0.701
rs16917442	64313404	A/T	0.18	0.716	1.01 (0.95,1.08)	0.771	1.01 (0.93,1.1)	0.167	1.08 (0.97,1.2)	0.335
rs4746475	64358685	G/A	0.24	0.716	0.99 (0.93,1.05)	0.854	1.01 (0.94,1.08)	0.434	0.96 (0.87,1.06)	0.92
rs7096063	64730894	A/G	0.66	0.72	1.01 (0.96,1.06)	0.917	1 (0.93,1.06)	0.724	1.02 (0.93,1.11)	0.638
rs1914200	64275340	A/G	0.3	0.721	1.01 (0.96,1.07)	0.235	1.04 (0.97,1.11)	0.716	1.02 (0.93,1.11)	0.889
rs1949064	64735477	A/G	0.31	0.725	1.01 (0.96,1.07)	0.554	1.02 (0.95,1.09)	0.914	1 (0.92,1.1)	0.792
c10_pos64589030	64589030	T/A	0.02	0.728	1.03 (0.85,1.26)	0.695	1.05 (0.82,1.35)	0.394	1.14 (0.85,1.53)	0.964

rs10761677	64652606	A/G	0.67	0.729	1.01 (0.96,1.06)	0.839	0.99 (0.93,1.06)	0.627	1.02 (0.94,1.11)	0.484
rs10822029	64354452	G/A	0.24	0.74	0.99 (0.93,1.05)	0.897	1 (0.93,1.08)	0.583	0.97 (0.88,1.07)	0.897
rs1878253	64269210	G/A	0.3	0.742	1.01 (0.95,1.07)	0.249	1.04 (0.97,1.11)	0.727	1.02 (0.93,1.11)	0.897
rs1397028	64728198	G/A	0.66	0.756	1.01 (0.96,1.06)	0.876	0.99 (0.93,1.06)	0.744	1.01 (0.93,1.1)	0.626
rs2944540	64369924	A/G	0.31	0.759	0.99 (0.94,1.05)	0.875	0.99 (0.93,1.06)	0.972	1 (0.91,1.09)	0.587
rs6479831	64418946	G/A	0.09	0.759	1.01 (0.93,1.11)	0.734	0.98 (0.88,1.1)	0.423	1.06 (0.92,1.22)	0.247
c10_pos64585387	64585387	A/C	0.03	0.773	0.98 (0.84,1.14)	0.63	0.95 (0.79,1.16)	0.86	0.98 (0.77,1.24)	0.832
rs949566	64631605	G/C	0.28	0.792	1.01 (0.95,1.07)	0.745	1.01 (0.94,1.08)	0.833	1.01 (0.92,1.1)	0.709
rs10995307	64552242	A/G	0.32	0.829	0.99 (0.94,1.05)	0.662	0.99 (0.92,1.05)	0.672	0.98 (0.9,1.07)	0.94
rs10822082	64677307	A/G	0.3	0.836	1.01 (0.95,1.06)	0.523	1.02 (0.96,1.09)	0.816	0.99 (0.91,1.08)	0.537
rs224053	64494790	C/A	0.01	0.837	0.98 (0.78,1.22)	0.885	1.02 (0.77,1.35)	0.372	0.84 (0.58,1.23)	0.143
rs10995392	64764692	G/A	0.33	0.847	0.99 (0.94,1.05)	0.746	0.99 (0.93,1.06)	0.756	1.01 (0.93,1.1)	0.359
rs35713824	64220842	C/A	0.19	0.849	0.99 (0.93,1.06)	0.929	1 (0.92,1.08)	0.256	0.94 (0.85,1.04)	0.315
rs10761659	64445564	G/A	0.27	0.858	1.01 (0.95,1.07)	0.412	0.97 (0.9,1.04)	0.404	1.04 (0.95,1.14)	0.321
rs16917269	64223632	T/A	0.19	0.862	0.99 (0.93,1.06)	0.937	1 (0.92,1.08)	0.264	0.94 (0.85,1.04)	0.322
rs16917398	64301817	G/A	0.04	0.863	1.01 (0.89,1.15)	0.599	0.96 (0.82,1.12)	0.721	1.04 (0.85,1.26)	0.479
rs10761656	64426243	G/A	0.1	0.867	1.01 (0.92,1.1)	0.51	0.96 (0.87,1.07)	0.32	1.07 (0.94,1.23)	0.175
rs224122	64447418	T/A	0.06	0.876	1.01 (0.91,1.12)	0.839	1.01 (0.89,1.15)	0.742	1.03 (0.87,1.22)	0.9
rs10822036	64374360	G/A	0.23	0.878	1 (0.94,1.06)	0.683	1.02 (0.94,1.09)	0.589	0.97 (0.88,1.07)	0.922
rs7923418	64230159	G/A	0.16	0.879	1.01 (0.94,1.08)	0.621	0.98 (0.9,1.06)	0.887	0.99 (0.89,1.1)	0.909
rs11595021	64663270	C/A	0.08	0.893	0.99 (0.91,1.09)	0.921	1.01 (0.9,1.12)	0.617	1.04 (0.9,1.2)	0.747
rs7070565	64278512	C/A	0.31	0.895	1 (0.95,1.06)	0.295	1.04 (0.97,1.11)	0.846	1.01 (0.92,1.1)	0.885
rs192007	64586395	G/A	0.29	0.904	1 (0.95,1.06)	0.907	1 (0.94,1.07)	0.865	0.99 (0.91,1.08)	0.647
rs2176291	64277372	C/A	0.31	0.916	1 (0.95,1.06)	0.305	1.04 (0.97,1.11)	0.846	1.01 (0.92,1.1)	0.895
c10_pos64267265	64267265	C/A	0.04	0.921	1.01 (0.89,1.14)	0.775	0.98 (0.84,1.14)	0.218	1.13 (0.93,1.36)	0.115
rs16917275	64230324	A/G	0.16	0.926	1 (0.94,1.07)	0.62	0.98 (0.9,1.06)	0.838	0.99 (0.89,1.1)	0.969
rs10733779	64280182	G/C	0.31	0.926	1 (0.95,1.06)	0.309	1.04 (0.97,1.11)	0.85	1.01 (0.92,1.1)	0.893
c10_pos64449989	64449989	C/G	0.03	0.927	1.01 (0.86,1.18)	0.836	1.02 (0.84,1.24)	0.901	0.98 (0.77,1.26)	0.654
rs10995205	64304083	G/A	0.14	0.93	1 (0.93,1.08)	0.88	1.01 (0.92,1.1)	0.477	1.04 (0.93,1.17)	0.653
rs4237304	64407845	A/G	0.08	0.931	1 (0.91,1.09)	0.685	0.98 (0.87,1.1)	0.799	1.02 (0.88,1.18)	0.477

rs224150	64488087	G/A	0.68	0.944	1 (0.94,1.05)	0.568	1.02 (0.95,1.09)	0.577	0.98 (0.89,1.06)	0.351
rs7917418	64577689	G/A	0.02	0.953	0.99 (0.82,1.21)	0.828	0.97 (0.76,1.25)	0.559	1.09 (0.81,1.47)	0.77
rs10509173	64611889	G/A	0.59	0.96	1 (0.95,1.05)	0.953	1 (0.94,1.06)	0.465	1.03 (0.95,1.12)	0.393
rs4141617	64614068	G/A	0.59	0.963	1 (0.95,1.05)	0.953	1 (0.94,1.06)	0.474	1.03 (0.95,1.12)	0.404
c10_pos64662596	64662596	G/A	0.03	0.971	1 (0.86,1.17)	0.562	1.06 (0.88,1.27)	0.611	1.06 (0.84,1.35)	0.732
c10_pos64664879	64664879	G/A	0.03	0.971	1 (0.86,1.17)	0.562	1.06 (0.88,1.27)	0.611	1.06 (0.84,1.35)	0.732
rs2393902	64369001	A/G	0.25	0.975	1 (0.94,1.06)	0.587	1.02 (0.95,1.09)	0.695	0.98 (0.89,1.08)	0.97
rs7901870	64226948	A/G	0.2	0.976	1 (0.94,1.07)	0.921	1 (0.93,1.08)	0.306	0.95 (0.86,1.05)	0.313
rs7350397	64289214	C/G	0.31	0.997	1 (0.95,1.06)	0.338	1.03 (0.97,1.1)	0.944	1 (0.92,1.09)	0.857

a: Build 37 coordinates.

b: A0: Allele coded as major in Europeans, A1: Allele coded as minor in Europeans.

c: Frequency of allele A1 in Asian population.

d-f: P-value. Odds ratio (OR) and 95% Confidence Interval (CI) for association with Overall Breast Cancer Risk, Estrogen Positive (ER+) and Estrogen Negative (ER-) disease.

g: Case-only analysis, treating subtype status as a dependent variable models adjusted for principal components and per-study fixed-effects.

Table S9: Analysis utilizing the four lead SNPs for each iCHAV: iCHAV1 - rs10995201, iCHAV2 - chr10:64258684:D, iCHAV3 - rs7922449, iCHAV4 - rs9971363

Risk	All/Ctrl/Case [a]	OR (95%CI) [b]	P-value [b]	**ER+**	All/Ctrl/Case [a]	OR (95%CI) [b]	P-value [b]	**ER-**	All/Ctrl/Case [a]	OR (95%CI) [b]	P-value [b]
H6: 1010	0.08/0.08/0.08	0.86 (0.82,0.90)	8.52e-10	H6: 1010	0.08/0.08/0.08	0.88 (0.84,0.94)	3.75e-05	H6: 1010	0.08/0.08/0.07	0.83 (0.75,0.91)	0.000126
H14: 0010	0.01/0.02/0.01	0.80 (0.71,0.90)	0.000304	H5: 1011	0.01/0.01/0.01	0.68 (0.56,0.82)	4.75e-05	H14: 0010	0.02/0.02/0.01	0.68 (0.52,0.87)	0.0022
H5: 1011	0.01/0.01/0.01	0.77 (0.66,0.89)	0.000456	H11: 0101	0.02/0.02/0.02	1.20 (1.04,1.39)	0.0116	H8: 1000	0.17/0.18/0.17	0.9 (0.83,0.97)	0.00774
H7: 1001	0.03/0.03/0.03	0.87 (0.80,0.95)	0.00226	H7: 1001	0.03/0.03/0.03	0.88 (0.79,0.98)	0.0162	H15: 0001	0.03/0.03/0.03	0.86 (0.72,1.03)	0.111
H8: 1000	0.18/0.18/0.17	0.96 (0.92,1.00)	0.0286	H3: 1101	0.03/0.03/0.03	0.89 (0.80,1.00)	0.0419	H11: 0101	0.02/0.02/0.02	1.14 (0.91,1.43)	0.261
H3: 1101	0.03/0.03/0.03	0.91 (0.83,1.00)	0.0396	H14: 0010	0.02/0.02/0.02	0.88 (0.77,1.01)	0.067	H7: 1001	0.03/0.03/0.03	0.94 (0.79,1.11)	0.447
H11: 0101	0.02/0.02/0.02	1.13 (1.00,1.28)	0.0553	H12: 0100	0.12/0.12/0.12	1.03 (0.98,1.09)	0.23	H3: 1101	0.03/0.03/0.03	0.96 (0.81,1.15)	0.682
H15: 0001	0.03/0.03/0.03	0.91 (0.83,1.00)	0.0574	H15: 0001	0.03/0.03/0.03	0.94 (0.84,1.05)	0.268	H5: 1011	0.01/0.01/0.01	0.96 (0.73,1.26)	0.758
H4: 1100	0.12/0.12/0.12	0.98 (0.94,1.02)	0.256	H8: 1000	0.18/0.18/0.17	0.98 (0.93,1.02)	0.287	H12: 0100	0.12/0.12/0.12	1.01 (0.92,1.10)	0.864
H12: 0100	0.12/0.12/0.12	1.03 (0.98,1.07)	0.261	Hrare: ****	0.01/0/0.0	0.94 (0.71,1.25)	0.681	H4: 1100	0.12/0.12/0.12	1.00 (0.93,1.09)	0.907
Hrare: ****	0.01/0/0.01	0.92 (0.73,1.16)	0.481	H4: 1100	0.12/0.12/0.12	0.99 (0.94,1.04)	0.691	Hrare: ****	0.01/0/0.02	1.02 (0.66,1.58)	0.933
0000	0.37/0.36/0.37	**Reference**		0000	0.36/0.36/0.37	**Reference**		0000	0.36/0.36/0.37	**Reference**	

a: Haplotype frequency among all subjects, cases and respectively controls only, rounded to two decimal points; grouped haplotypes with a frequency < 0.01 into one (rare) group.

b: P-value and OR of association for overall Risk, Estrogen positive (ER+) and Estrogen negative (ER-); adjusted for study and principal components.

Table S10: Association statistics for breast density phenotypes, for variants ranked by P-values for association with overall risk of breast cancer in European studies

			Overall Risk	PD[c]		DA[d]		nDA[e]	
SNP	Position[a]	Type	P-value[b]	P-value	Beta (SE)	P-value	Beta (SE)	P-value	Beta (SE)
rs10995201	64299890	Imputed	1.05e-29	1.32E-05	-0.15 (0.04)	1.45E-07	-0.25 (0.05)	0.787	0.01 (0.05)
rs10995193	64288082	Imputed	3.67e-29	1.77E-05	-0.15 (0.03)	2.28E-07	-0.24 (0.05)	0.85	0.01 (0.05)
rs10995194	64288130	Genotyped	3.77e-29	2.82E-05	-0.14 (0.03)	3.81E-07	-0.24 (0.05)	0.898	0.01 (0.05)
rs11524313	64283656	Imputed	4.16e-29	5.22E-05	-0.14 (0.04)	3.91E-07	-0.24 (0.05)	0.842	-0.01 (0.05)
rs4746419	64275261	Genotyped	4.43e-29	3.86E-05	-0.14 (0.03)	4.41E-07	-0.24 (0.05)	0.949	0 (0.05)
rs10995190	64278682	Genotyped	5.61e-29	5.08E-05	-0.14 (0.03)	6.55E-07	-0.23 (0.05)	0.972	0 (0.05)
rs10995189	64278181	Genotyped	6.04e-29	5.08E-05	-0.14 (0.03)	6.55E-07	-0.23 (0.05)	0.972	0 (0.05)
rs10995191	64278874	Genotyped	6.04e-29	5.08E-05	-0.14 (0.03)	6.55E-07	-0.23 (0.05)	0.972	0 (0.05)
rs34511355	64276964	Genotyped	6.22e-29	5.08E-05	-0.14 (0.03)	6.55E-07	-0.23 (0.05)	0.972	0 (0.05)
rs10995187	64273026	Genotyped	6.66e-29	3.93E-05	-0.14 (0.03)	4.95E-07	-0.23 (0.05)	0.919	0.01 (0.05)
rs10995182	64268764	Imputed	3.42e-28	0.000153	-0.15 (0.04)	1.46E-05	-0.23 (0.05)	0.781	0.02 (0.06)
rs10995181	64268659	Genotyped	5.07e-28	3.51E-05	-0.15 (0.04)	5.27E-07	-0.24 (0.05)	0.896	0.01 (0.05)
chr10:64291099:I	64291099	Imputed	6.38e-27	9.76E-05	-0.16 (0.04)	4.19E-06	-0.25 (0.05)	0.855	-0.01 (0.06)
rs16917398	64301817	Genotyped	1.48e-16	0.000733	-0.14 (0.04)	0.000211	-0.21 (0.06)	0.192	0.08 (0.06)
c10_pos64304197	64304197	Genotyped	4.12e-15	0.00156	-0.13 (0.04)	0.00127	-0.18 (0.06)	0.0721	0.11 (0.06)
chr10:64258684:D	64258684	Imputed	4.24e-14	0.00155	-0.08 (0.02)	0.00555	-0.09 (0.03)	0.034	0.08 (0.04)
rs2393886	64258343	Genotyped	4.50e-14	0.00221	-0.08 (0.02)	0.0107	-0.08 (0.03)	0.03	0.08 (0.04)
rs10995176	64257971	Imputed	7.17e-14	0.00256	-0.07 (0.02)	0.014	-0.08 (0.03)	0.0237	0.08 (0.04)
c10_pos64258017	64258017	Genotyped	1.03e-13	0.00225	-0.08 (0.02)	0.0119	-0.08 (0.03)	0.0289	0.08 (0.04)
c10_pos64288411	64288411	Genotyped	1.65e-13	0.687	-0.03 (0.08)	0.629	-0.05 (0.11)	0.556	0.07 (0.12)
rs10509168	64257828	Genotyped	2.22e-13	0.00423	-0.07 (0.02)	0.017	-0.08 (0.03)	0.0445	0.07 (0.04)
chr10:64258692:D	64258692	Imputed	8.51e-13	0.0066	0.07 (0.03)	0.01	0.09 (0.04)	0.217	-0.05 (0.04)
rs7100995	64249139	Imputed	9.13e-13	0.317	-0.05 (0.05)	0.0898	-0.12 (0.07)	0.247	-0.09 (0.08)
rs4746409	64263402	Genotyped	3.06e-12	0.00429	-0.07 (0.02)	0.00307	-0.1 (0.03)	0.133	0.05 (0.03)
c10_pos64254983	64254983	Genotyped	3.81e-12	0.224	-0.05 (0.04)	0.0649	-0.11 (0.06)	0.496	-0.04 (0.06)
rs35816896	64300340	Genotyped	4.77e-12	0.00511	-0.14 (0.05)	0.00204	-0.2 (0.06)	0.457	0.05 (0.07)

rs1955331	64232042	Genotyped	7.99e-11	0.0467	-0.05 (0.02)	0.075	-0.06 (0.03)	0.232	0.04 (0.04)
chr10:64247954:I	64247954	Imputed	8.00e-11	0.275	-0.04 (0.03)	0.183	-0.06 (0.04)	0.897	0.01 (0.05)
rs10822013	64251977	Genotyped	8.81e-11	0.0659	-0.05 (0.02)	0.133	-0.05 (0.03)	0.117	0.05 (0.04)
rs10995173	64246575	Genotyped	3.89e-10	0.0623	-0.05 (0.02)	0.137	-0.05 (0.03)	0.0935	0.06 (0.04)
rs10761637	64247585	Imputed	3.92e-10	0.0575	-0.05 (0.02)	0.115	-0.05 (0.03)	0.103	0.06 (0.03)
rs10822012	64247568	Imputed	3.93e-10	0.0575	-0.05 (0.02)	0.115	-0.05 (0.03)	0.103	0.06 (0.03)
rs12245332	64260847	Genotyped	3.95e-10	0.121	-0.04 (0.03)	0.457	-0.03 (0.03)	0.0412	0.08 (0.04)
rs12243471	64260410	Genotyped	4.00e-10	0.119	-0.04 (0.03)	0.448	-0.03 (0.03)	0.0426	0.07 (0.04)
rs12098307	64248099	Imputed	4.16e-10	0.0645	-0.05 (0.02)	0.131	-0.05 (0.03)	0.113	0.06 (0.03)
rs2393887	64263093	Genotyped	6.94e-10	0.123	-0.04 (0.03)	0.458	-0.03 (0.03)	0.0396	0.08 (0.04)
rs4282885	64243828	Genotyped	8.51e-10	0.067	-0.04 (0.02)	0.172	-0.04 (0.03)	0.0812	0.06 (0.04)
rs4489633	64238333	Genotyped	1.45e-09	0.0781	-0.04 (0.02)	0.181	-0.04 (0.03)	0.0976	0.06 (0.04)
rs4745820	64253044	Imputed	8.44e-09	0.208	-0.03 (0.03)	0.277	-0.04 (0.03)	0.259	0.04 (0.04)
rs35972160	64347963	Genotyped	1.19e-08	0.19	-0.08 (0.06)	0.167	-0.12 (0.09)	0.593	-0.05 (0.09)
chr10:64352628:D	64352628	Imputed	1.70e-08	0.00147	-0.13 (0.04)	0.00101	-0.18 (0.05)	0.596	0.03 (0.06)
rs1955332	64231895	Genotyped	1.75e-08	0.315	-0.03 (0.03)	0.441	-0.03 (0.03)	0.245	0.04 (0.04)
chr10:64293571:D	64293571	Imputed	1.94e-08	0.342	0.03 (0.03)	0.0674	0.07 (0.04)	0.392	0.03 (0.04)
rs10822017	64296420	Imputed	2.07e-08	0.14	0.04 (0.03)	0.0253	0.08 (0.03)	0.689	0.01 (0.04)
rs7072167	64231739	Genotyped	2.20e-08	0.322	-0.02 (0.03)	0.448	-0.03 (0.03)	0.246	0.04 (0.04)
c10_pos64027446	64357440	Genotyped	2.34e-08	0.22	-0.08 (0.06)	0.244	-0.1 (0.09)	0.53	-0.06 (0.09)
rs78697955	64376479	Imputed	2.48e-08	0.00105	-0.13 (0.04)	0.00131	-0.17 (0.05)	0.378	0.05 (0.06)
c10_pos64378296	64378296	Genotyped	2.58e-08	0.00132	-0.13 (0.04)	0.00129	-0.17 (0.05)	0.423	0.04 (0.06)
rs1914182	64294817	Imputed	2.62e-08	0.134	0.04 (0.03)	0.0245	0.08 (0.03)	0.691	0.01 (0.04)
rs9633558	64293805	Imputed	2.62e-08	0.134	0.04 (0.03)	0.0254	0.08 (0.03)	0.702	0.01 (0.04)
rs7915519	64293843	Imputed	2.63e-08	0.134	0.04 (0.03)	0.0246	0.08 (0.03)	0.691	0.01 (0.04)
rs6479823	64294020	Imputed	2.66e-08	0.134	0.04 (0.03)	0.0247	0.08 (0.03)	0.691	0.01 (0.04)
rs10995196	64292344	Imputed	2.70e-08	0.0849	0.05 (0.03)	0.0108	0.09 (0.04)	0.753	0.01 (0.04)
rs7901573	64297378	Imputed	2.93e-08	0.131	0.04 (0.03)	0.0239	0.08 (0.03)	0.699	0.01 (0.04)
rs12258134	64297521	Imputed	2.94e-08	0.131	0.04 (0.03)	0.0238	0.08 (0.03)	0.699	0.01 (0.04)
rs4746428	64293118	Genotyped	3.24e-08	0.132	0.04 (0.03)	0.0239	0.08 (0.03)	0.692	0.01 (0.04)

rs10822011	64240648	Genotyped	3.29e-08	0.309	-0.03 (0.03)	0.428	-0.03 (0.03)	0.265	0.04 (0.04)
rs78499789	64372231	Imputed	3.46e-08	0.00118	-0.13 (0.04)	0.00158	-0.17 (0.05)	0.379	0.05 (0.06)
rs1914191	64362223	Genotyped	3.51e-08	0.00119	-0.13 (0.04)	0.000994	-0.17 (0.05)	0.497	0.04 (0.06)
rs77439234	64375399	Imputed	3.54e-08	0.00122	-0.13 (0.04)	0.00162	-0.17 (0.05)	0.387	0.05 (0.06)
rs1949356	64298273	Genotyped	3.61e-08	0.144	0.04 (0.03)	0.026	0.08 (0.03)	0.688	0.01 (0.04)
rs78969820	64369858	Imputed	3.72e-08	0.00105	-0.13 (0.04)	0.00127	-0.17 (0.05)	0.403	0.05 (0.06)
rs10995192	64286975	Imputed	3.75e-08	0.0346	0.05 (0.03)	0.00362	0.1 (0.03)	0.779	0.01 (0.04)
rs7070565	64278512	Genotyped	3.76e-08	0.0352	0.05 (0.03)	0.00313	0.1 (0.03)	0.672	0.02 (0.04)
rs10740082	64281167	Imputed	3.82e-08	0.0373	0.05 (0.03)	0.00323	0.1 (0.03)	0.652	0.02 (0.04)
rs4746423	64281259	Imputed	3.82e-08	0.0374	0.05 (0.03)	0.00323	0.1 (0.03)	0.651	0.02 (0.04)
rs7073475	64284370	Imputed	3.87e-08	0.0375	0.05 (0.03)	0.00323	0.1 (0.03)	0.652	0.02 (0.04)
rs77317045	64358198	Imputed	3.89e-08	0.00156	-0.13 (0.04)	0.00127	-0.17 (0.05)	0.538	0.04 (0.06)
rs16917477	64356405	Imputed	3.90e-08	0.00162	-0.13 (0.04)	0.00123	-0.17 (0.05)	0.563	0.03 (0.06)
rs1914198	64279556	Imputed	4.04e-08	0.0364	0.05 (0.03)	0.00318	0.1 (0.03)	0.658	0.02 (0.04)
rs7082733	64286215	Imputed	4.19e-08	0.0384	0.05 (0.03)	0.00325	0.1 (0.03)	0.652	0.02 (0.04)
rs7895055	64278217	Imputed	4.19e-08	0.0348	0.05 (0.03)	0.00305	0.1 (0.03)	0.661	0.02 (0.04)
rs1914197	64280647	Imputed	4.24e-08	0.0357	0.05 (0.03)	0.0033	0.1 (0.03)	0.683	0.01 (0.04)
rs1914196	64287434	Imputed	4.25e-08	0.0386	0.05 (0.03)	0.00325	0.1 (0.03)	0.653	0.02 (0.04)
rs7350397	64289214	Genotyped	4.33e-08	0.0341	0.05 (0.03)	0.00258	0.1 (0.03)	0.621	0.02 (0.04)
rs12413429	64368352	Imputed	4.52e-08	0.00128	-0.13 (0.04)	0.00142	-0.17 (0.05)	0.432	0.04 (0.06)
rs1949359	64356993	Genotyped	4.53e-08	0.00187	-0.12 (0.04)	0.00129	-0.17 (0.05)	0.605	0.03 (0.06)
rs2176291	64277372	Genotyped	4.58e-08	0.0343	0.05 (0.03)	0.00321	0.1 (0.03)	0.708	0.01 (0.04)
rs10733779	64280182	Genotyped	5.44e-08	0.0339	0.05 (0.03)	0.00296	0.1 (0.03)	0.671	0.02 (0.04)
rs2393894	64291065	Imputed	5.95e-08	0.056	0.05 (0.03)	0.0121	0.09 (0.04)	0.855	-0.01 (0.04)
rs7073867	64284517	Imputed	6.07e-08	0.0422	0.05 (0.03)	0.00237	0.1 (0.03)	0.476	0.03 (0.04)
rs1878253	64269210	Genotyped	6.54e-08	0.0865	0.04 (0.03)	0.013	0.09 (0.04)	0.841	0.01 (0.04)
rs7901318	64290213	Imputed	7.26e-08	0.0745	0.05 (0.03)	0.0117	0.09 (0.04)	0.896	0 (0.04)
chr10:64407678:D	64407678	Imputed	7.36e-08	0.00145	-0.09 (0.03)	0.00451	-0.11 (0.04)	0.143	0.06 (0.04)
rs7912431	64280616	Imputed	8.59e-08	0.0437	0.05 (0.03)	0.00442	0.1 (0.03)	0.681	0.01 (0.04)
rs3847337	64208433	Genotyped	9.15e-08	0.512	-0.02 (0.03)	0.703	-0.01 (0.04)	0.154	0.06 (0.04)

rs10740081	64280059	Imputed	9.17e-08	0.0881	0.04 (0.03)	0.0133	0.09 (0.04)	0.835	0.01 (0.04)
rs10761639	64286938	Imputed	1.01e-07	0.0869	0.05 (0.03)	0.0125	0.09 (0.04)	0.843	0.01 (0.04)
rs1914200	64275340	Genotyped	1.03e-07	0.0865	0.04 (0.03)	0.013	0.09 (0.04)	0.841	0.01 (0.04)
rs10761655	64418179	Imputed	1.07e-07	0.00198	-0.09 (0.03)	0.00313	-0.11 (0.04)	0.211	0.05 (0.04)
rs7083350	64249170	Genotyped	1.17e-07	0.204	-0.03 (0.03)	0.252	-0.04 (0.03)	0.301	0.04 (0.04)
rs6479831	64418946	Genotyped	1.26e-07	0.00158	-0.09 (0.03)	0.00277	-0.11 (0.04)	0.224	0.05 (0.04)
rs10822047	64424284	Imputed	1.28e-07	0.0028	-0.08 (0.03)	0.00476	-0.11 (0.04)	0.253	0.05 (0.04)
rs2393885	64238342	Genotyped	1.28e-07	0.267	-0.03 (0.03)	0.339	-0.03 (0.03)	0.3	0.04 (0.04)
rs10822041	64404706	Imputed	1.29e-07	0.00303	-0.08 (0.03)	0.00735	-0.1 (0.04)	0.206	0.05 (0.04)
rs7071642	64414060	Imputed	1.30e-07	0.00244	-0.08 (0.03)	0.00509	-0.1 (0.04)	0.217	0.05 (0.04)
rs7089612	64414164	Imputed	1.30e-07	0.00243	-0.08 (0.03)	0.00506	-0.1 (0.04)	0.217	0.05 (0.04)
rs10761652	64397656	Imputed	1.33e-07	0.00852	-0.07 (0.03)	0.0101	-0.1 (0.04)	0.36	0.04 (0.04)
rs10761654	64405646	Imputed	1.35e-07	0.00303	-0.08 (0.03)	0.00738	-0.1 (0.04)	0.205	0.05 (0.04)
rs7076156	64415184	Imputed	1.39e-07	0.00234	-0.08 (0.03)	0.00472	-0.11 (0.04)	0.218	0.05 (0.04)
rs753518	64235506	Genotyped	1.39e-07	0.263	-0.03 (0.03)	0.337	-0.03 (0.03)	0.292	0.04 (0.04)
rs10761636	64233999	Genotyped	1.41e-07	0.28	-0.03 (0.03)	0.35	-0.03 (0.03)	0.312	0.04 (0.04)
rs7086072	64417289	Imputed	1.42e-07	0.00224	-0.08 (0.03)	0.00424	-0.11 (0.04)	0.221	0.05 (0.04)
rs4237304	64407845	Genotyped	1.44e-07	0.00276	-0.08 (0.03)	0.0058	-0.1 (0.04)	0.207	0.05 (0.04)
rs4237305	64407851	Imputed	1.47e-07	0.00292	-0.08 (0.03)	0.0072	-0.1 (0.04)	0.198	0.05 (0.04)
rs12782013	64225299	Imputed	1.51e-07	0.0966	-0.05 (0.03)	0.2	-0.05 (0.04)	0.0872	0.07 (0.04)
rs1996318	64236820	Genotyped	1.57e-07	0.258	-0.03 (0.03)	0.329	-0.03 (0.03)	0.3	0.04 (0.04)
rs34316596	64399622	Imputed	1.58e-07	0.264	-0.07 (0.07)	0.273	-0.1 (0.09)	0.612	-0.05 (0.1)
rs2393883	64226323	Imputed	1.64e-07	0.0852	-0.05 (0.03)	0.19	-0.05 (0.04)	0.0699	0.07 (0.04)
rs7922449	64291308	Imputed	1.68e-07	0.634	0.01 (0.03)	0.308	0.04 (0.04)	0.547	0.02 (0.04)
rs12781954	64225130	Imputed	1.93e-07	0.0838	-0.05 (0.03)	0.186	-0.05 (0.04)	0.0702	0.07 (0.04)
rs10995205	64304083	Genotyped	1.96e-07	0.0709	0.05 (0.03)	0.0175	0.09 (0.04)	0.742	0.01 (0.04)
rs2393906	64379118	Imputed	2.05e-07	0.0281	-0.13 (0.06)	0.0298	-0.17 (0.08)	0.804	0.02 (0.08)
rs2393905	64379119	Imputed	2.06e-07	0.0281	-0.13 (0.06)	0.0298	-0.17 (0.08)	0.804	0.02 (0.08)
rs10995204	64304060	Genotyped	2.41e-07	0.0743	0.05 (0.03)	0.0169	0.09 (0.04)	0.665	0.02 (0.04)
rs10995170	64223383	Genotyped	2.51e-07	0.0848	-0.05 (0.03)	0.189	-0.05 (0.04)	0.0703	0.07 (0.04)

rs2393907	64407359	Imputed	2.52e-07	0.00397	-0.08 (0.03)	0.00769	-0.1 (0.04)	0.223	0.05 (0.04)
rs6479815	64224100	Genotyped	2.54e-07	0.0848	-0.05 (0.03)	0.189	-0.05 (0.04)	0.0703	0.07 (0.04)
rs7086948	64292836	Imputed	3.16e-07	0.412	0.02 (0.03)	0.145	0.05 (0.03)	0.714	0.01 (0.04)
rs10740085	64395795	Imputed	3.18e-07	0.029	-0.07 (0.03)	0.0604	-0.08 (0.04)	0.272	0.05 (0.04)
rs7094985	64211810	Genotyped	3.34e-07	0.126	-0.04 (0.03)	0.233	-0.04 (0.03)	0.0841	0.06 (0.04)
rs6479832	64419102	Genotyped	3.89e-07	0.0088	-0.08 (0.03)	0.0289	-0.09 (0.04)	0.165	0.06 (0.04)
rs10822007	64208221	Genotyped	4.21e-07	0.126	-0.04 (0.03)	0.23	-0.04 (0.03)	0.0794	0.06 (0.04)
rs145426092	64061106	Imputed	4.34e-07	0.883	-0.02 (0.15)	0.79	0.05 (0.2)	0.792	0.06 (0.22)
rs10822008	64213069	Genotyped	4.89e-07	0.125	-0.04 (0.02)	0.201	-0.04 (0.03)	0.105	0.06 (0.04)
rs2893906	64387934	Imputed	5.44e-07	0.0271	-0.07 (0.03)	0.054	-0.08 (0.04)	0.231	0.05 (0.04)
chr10:64345167:D	64345167	Imputed	7.40e-07	0.336	-0.03 (0.03)	0.0725	-0.08 (0.04)	0.528	-0.03 (0.05)
rs7907439	64346650	Genotyped	9.27e-07	0.355	-0.03 (0.03)	0.0779	-0.08 (0.04)	0.538	-0.03 (0.05)
rs2138555	64220494	Genotyped	1.04e-06	0.0117	-0.06 (0.02)	0.0424	-0.07 (0.03)	0.0463	0.07 (0.04)
rs35306388	64478832	Imputed	1.21e-06	0.556	-0.04 (0.07)	0.476	-0.06 (0.09)	0.289	-0.1 (0.09)
rs4746123	64214402	Genotyped	1.33e-06	0.0356	-0.05 (0.02)	0.156	-0.05 (0.03)	0.0224	0.08 (0.04)
rs7477501	64348374	Imputed	1.33e-06	0.38	-0.03 (0.03)	0.0972	-0.07 (0.04)	0.557	-0.03 (0.05)
rs34284450	64480783	Genotyped	1.55e-06	0.483	-0.05 (0.06)	0.382	-0.08 (0.09)	0.265	-0.1 (0.09)
rs2138556	64214282	Imputed	2.25e-06	0.0434	-0.05 (0.02)	0.174	-0.05 (0.03)	0.0247	0.08 (0.04)
rs1949355	64218423	Genotyped	2.58e-06	0.0372	-0.05 (0.02)	0.167	-0.05 (0.03)	0.0193	0.08 (0.04)
rs12220488	64219000	Genotyped	2.62e-06	0.0384	-0.05 (0.02)	0.169	-0.05 (0.03)	0.0211	0.08 (0.04)
rs2393881	64205643	Genotyped	2.80e-06	0.994	0 (0.03)	0.856	0.01 (0.04)	0.199	0.05 (0.04)
rs61259183	64225914	Imputed	3.06e-06	0.0364	-0.05 (0.02)	0.155	-0.05 (0.03)	0.0226	0.08 (0.04)
rs7918077	64202391	Imputed	3.99e-06	0.93	0 (0.03)	0.884	0.01 (0.04)	0.261	0.05 (0.04)
chr10:64206361:D	64206361	Imputed	4.13e-06	0.984	0 (0.03)	0.856	0.01 (0.04)	0.193	0.05 (0.04)
rs10822009	64221290	Imputed	4.24e-06	0.0321	-0.05 (0.03)	0.162	-0.05 (0.03)	0.0149	0.09 (0.04)
rs77606114	64221291	Imputed	4.24e-06	0.0321	-0.05 (0.03)	0.162	-0.05 (0.03)	0.0149	0.09 (0.04)
rs10761643	64303351	Imputed	4.51e-06	0.011	0.07 (0.03)	0.00453	0.11 (0.04)	0.342	-0.04 (0.04)
rs7074870	64205327	Genotyped	4.54e-06	0.975	0 (0.03)	0.876	0.01 (0.04)	0.209	0.05 (0.04)
chr10:64221291:I	64221291	Imputed	4.65e-06	0.0267	-0.06 (0.03)	0.132	-0.05 (0.03)	0.0225	0.08 (0.04)
rs10160102	64390647	Genotyped	5.81e-06	0.0226	-0.06 (0.03)	0.0124	-0.09 (0.04)	0.538	0.02 (0.04)

rs10822006	64205492	Genotyped	5.81e-06	0.935	0 (0.03)	0.809	0.01 (0.04)	0.192	0.05 (0.04)
rs224120	64445760	Imputed	5.89e-06	0.0038	-0.08 (0.03)	0.0328	-0.08 (0.04)	0.0342	0.08 (0.04)
rs4745874	64413809	Imputed	6.19e-06	0.00524	-0.08 (0.03)	0.00503	-0.1 (0.04)	0.365	0.04 (0.04)
rs6479830	64418739	Genotyped	6.43e-06	0.00515	-0.08 (0.03)	0.00437	-0.1 (0.04)	0.386	0.03 (0.04)
rs16917317	64270771	Genotyped	6.63e-06	0.342	0.02 (0.02)	0.114	0.05 (0.03)	0.71	0.01 (0.04)
rs10761640	64298025	Imputed	6.67e-06	0.756	0.01 (0.03)	0.383	0.03 (0.03)	0.695	0.01 (0.04)
rs10761653	64404034	Imputed	6.73e-06	0.00743	-0.07 (0.03)	0.00744	-0.1 (0.04)	0.387	0.03 (0.04)
rs16917312	64270701	Imputed	6.97e-06	0.34	0.02 (0.02)	0.116	0.05 (0.03)	0.73	0.01 (0.04)
rs7895082	64270919	Genotyped	7.15e-06	0.342	0.02 (0.02)	0.114	0.05 (0.03)	0.71	0.01 (0.04)
rs4237288	64269110	Genotyped	7.23e-06	0.346	0.02 (0.02)	0.118	0.05 (0.03)	0.712	0.01 (0.04)
rs1955328	64269387	Genotyped	7.26e-06	0.335	0.02 (0.02)	0.111	0.05 (0.03)	0.717	0.01 (0.04)
rs11523825	64285985	Imputed	7.40e-06	0.348	0.02 (0.02)	0.118	0.05 (0.03)	0.733	0.01 (0.04)
rs7900998	64287981	Imputed	7.58e-06	0.349	0.02 (0.02)	0.117	0.05 (0.03)	0.733	0.01 (0.04)
rs7923316	64270846	Genotyped	8.03e-06	0.344	0.02 (0.02)	0.113	0.05 (0.03)	0.701	0.01 (0.04)
rs79829650	64380124	Imputed	8.30e-06	0.00936	-0.11 (0.04)	0.00344	-0.17 (0.06)	0.957	0 (0.06)
rs737314	64274177	Genotyped	8.38e-06	0.342	0.02 (0.02)	0.114	0.05 (0.03)	0.71	0.01 (0.04)
rs10509169	64276759	Genotyped	8.44e-06	0.341	0.02 (0.02)	0.116	0.05 (0.03)	0.729	0.01 (0.04)
rs17221319	64206712	Genotyped	8.77e-06	0.461	0.02 (0.02)	0.356	0.03 (0.03)	0.589	-0.02 (0.04)
rs10822042	64404827	Imputed	1.01e-05	0.00835	-0.07 (0.03)	0.00817	-0.1 (0.04)	0.395	0.03 (0.04)
rs12766269	64205248	Imputed	1.02e-05	0.181	-0.12 (0.09)	0.264	-0.13 (0.12)	0.922	0.01 (0.13)
rs1878262	64273879	Genotyped	1.02e-05	0.35	0.02 (0.02)	0.116	0.05 (0.03)	0.71	0.01 (0.04)
rs224121	64447352	Genotyped	1.02e-05	0.0204	-0.07 (0.03)	0.12	-0.06 (0.04)	0.0665	0.08 (0.04)
rs10822015	64268345	Genotyped	1.03e-05	0.332	0.02 (0.02)	0.111	0.05 (0.03)	0.738	0.01 (0.04)
rs10995180	64267743	Genotyped	1.04e-05	0.317	0.02 (0.02)	0.103	0.05 (0.03)	0.74	0.01 (0.04)
rs10995157	64202451	Imputed	1.14e-05	0.51	0.02 (0.02)	0.36	0.03 (0.03)	0.685	-0.01 (0.04)
rs77051803	64384640	Imputed	1.21e-05	0.0167	-0.1 (0.04)	0.00792	-0.15 (0.06)	0.921	-0.01 (0.06)
rs1914188	64312627	Genotyped	1.41e-05	0.375	0.02 (0.02)	0.179	0.04 (0.03)	0.426	0.03 (0.04)
c10_pos64593869	64593869	Genotyped	1.45e-05	0.537	-0.04 (0.07)	0.629	-0.04 (0.09)	0.674	-0.04 (0.1)
rs35997229	64957591	Imputed	1.46e-05	0.285	0.1 (0.09)	0.384	0.11 (0.12)	0.105	-0.21 (0.13)
rs35661318	64935520	Imputed	1.47e-05	0.291	0.1 (0.09)	0.388	0.11 (0.12)	0.106	-0.21 (0.13)

rs6479826	64314760	Genotyped	1.48e-05	0.161	0.04 (0.03)	0.0256	0.08 (0.04)	0.333	0.04 (0.04)
rs12243155	64306395	Genotyped	1.56e-05	0.164	0.04 (0.03)	0.0286	0.08 (0.04)	0.351	0.04 (0.04)
rs6479827	64317700	Genotyped	1.57e-05	0.154	0.04 (0.03)	0.0267	0.08 (0.04)	0.365	0.04 (0.04)
rs7911140	64317150	Imputed	1.61e-05	0.412	0.02 (0.02)	0.191	0.04 (0.03)	0.388	0.03 (0.04)
rs2138564	64307317	Imputed	1.62e-05	0.377	0.02 (0.02)	0.176	0.04 (0.03)	0.412	0.03 (0.04)
rs34922281	64680751	Genotyped	1.75e-05	0.613	-0.03 (0.06)	0.637	-0.04 (0.08)	0.8	-0.02 (0.09)
rs147709318	64809464	Imputed	1.76e-05	0.513	0.05 (0.08)	0.525	0.07 (0.11)	0.32	-0.11 (0.11)
rs34942900	64817375	Imputed	1.76e-05	0.513	0.05 (0.08)	0.525	0.07 (0.11)	0.321	-0.11 (0.11)
rs10822025	64311098	Genotyped	1.85e-05	0.407	0.02 (0.02)	0.196	0.04 (0.03)	0.397	0.03 (0.04)
rs34632941	64414265	Imputed	2.29e-05	0.864	-0.01 (0.05)	0.426	-0.05 (0.07)	0.0839	-0.12 (0.07)
rs10822019	64303915	Genotyped	2.53e-05	0.0113	-0.07 (0.03)	0.00163	-0.11 (0.04)	0.894	-0.01 (0.04)
chr10:64313970:I	64313970	Imputed	2.56e-05	0.0845	0.05 (0.03)	0.0198	0.09 (0.04)	0.308	0.04 (0.04)
c10_pos64599839	64599839	Genotyped	3.00e-05	0.395	-0.07 (0.09)	0.602	-0.06 (0.12)	0.396	0.1 (0.12)
rs4746518	64429595	Imputed	3.17e-05	0.00508	-0.08 (0.03)	0.0223	-0.09 (0.04)	0.0715	0.07 (0.04)
rs729738	64430265	Imputed	3.23e-05	0.00506	-0.08 (0.03)	0.0224	-0.09 (0.04)	0.071	0.07 (0.04)
rs729739	64430302	Imputed	3.23e-05	0.00506	-0.08 (0.03)	0.0224	-0.09 (0.04)	0.071	0.07 (0.04)
rs34146356	64721200	Genotyped	3.28e-05	0.719	-0.02 (0.06)	0.71	-0.03 (0.08)	0.805	-0.02 (0.09)
c10_pos64489095	64489095	Genotyped	3.45e-05	0.199	-0.1 (0.08)	0.189	-0.13 (0.1)	0.902	0.01 (0.11)
rs7393302	64437054	Imputed	3.72e-05	0.00507	-0.08 (0.03)	0.0242	-0.09 (0.04)	0.0618	0.08 (0.04)
rs7921139	64312533	Imputed	4.59e-05	0.193	0.04 (0.03)	0.0155	0.09 (0.04)	0.0484	0.08 (0.04)
c10_pos64403240	64403240	Genotyped	4.90e-05	0.974	0 (0.05)	0.531	-0.04 (0.06)	0.0855	-0.12 (0.07)
rs11812737	64429319	Imputed	5.20e-05	0.0204	-0.07 (0.03)	0.0884	-0.07 (0.04)	0.095	0.07 (0.04)
rs1980663	64619338	Imputed	5.20e-05	0.0183	-0.12 (0.05)	0.0272	-0.15 (0.07)	0.246	0.08 (0.07)
rs35419901	64063451	Imputed	5.26e-05	0.873	-0.02 (0.13)	0.577	-0.1 (0.18)	0.424	-0.15 (0.19)
chr10:64593676:D	64593676	Imputed	5.47e-05	0.0096	-0.14 (0.05)	0.0213	-0.16 (0.07)	0.142	0.11 (0.08)
rs4746524	64437797	Imputed	5.80e-05	0.0201	-0.07 (0.03)	0.0943	-0.07 (0.04)	0.082	0.08 (0.04)
rs7394165	64437018	Imputed	5.82e-05	0.02	-0.07 (0.03)	0.0941	-0.07 (0.04)	0.082	0.08 (0.04)
rs12765365	64848937	Imputed	5.99e-05	0.246	0.11 (0.09)	0.253	0.14 (0.13)	0.149	-0.19 (0.13)
rs1914190	64305244	Genotyped	6.39e-05	0.239	0.03 (0.03)	0.0307	0.08 (0.04)	0.0687	0.07 (0.04)
rs9971363	64563702	Imputed	6.54e-05	0.629	-0.02 (0.04)	0.634	-0.02 (0.05)	0.549	0.03 (0.05)

rs1949358	64306130	Genotyped	6.55e-05	0.237	0.03 (0.03)	0.0305	0.08 (0.04)	0.0686	0.07 (0.04)
rs1914189	64309377	Genotyped	6.56e-05	0.251	0.03 (0.03)	0.0309	0.08 (0.04)	0.0621	0.07 (0.04)
rs10159722	64390776	Imputed	6.57e-05	0.693	-0.01 (0.03)	0.315	-0.04 (0.04)	0.261	-0.05 (0.04)
rs7090365	64564428	Imputed	6.59e-05	0.628	-0.02 (0.04)	0.628	-0.02 (0.05)	0.556	0.03 (0.05)
rs2138562	64317335	Imputed	6.73e-05	0.511	0.02 (0.02)	0.21	0.04 (0.03)	0.276	0.04 (0.04)
rs1914187	64312794	Genotyped	6.75e-05	0.236	0.03 (0.03)	0.0302	0.08 (0.04)	0.0693	0.07 (0.04)
rs16917421	64308304	Genotyped	6.83e-05	0.237	0.03 (0.03)	0.0305	0.08 (0.04)	0.0686	0.07 (0.04)
rs2138563	64307474	Genotyped	6.86e-05	0.237	0.03 (0.03)	0.0305	0.08 (0.04)	0.0686	0.07 (0.04)
rs16917442	64313404	Genotyped	6.87e-05	0.234	0.03 (0.03)	0.0273	0.08 (0.04)	0.0635	0.07 (0.04)
rs61865880	64556134	Imputed	6.94e-05	0.0385	-0.11 (0.05)	0.0892	-0.12 (0.07)	0.147	0.11 (0.07)
rs16917441	64313211	Genotyped	6.99e-05	0.226	0.03 (0.03)	0.0273	0.08 (0.04)	0.0654	0.07 (0.04)
rs1955335	64310267	Genotyped	7.00e-05	0.237	0.03 (0.03)	0.0305	0.08 (0.04)	0.0686	0.07 (0.04)
rs2176288	64307657	Imputed	7.03e-05	0.231	0.03 (0.03)	0.0292	0.08 (0.04)	0.0716	0.07 (0.04)
rs16917422	64309822	Genotyped	7.06e-05	0.237	0.03 (0.03)	0.0305	0.08 (0.04)	0.0686	0.07 (0.04)
rs1949357	64306569	Genotyped	7.12e-05	0.228	0.03 (0.03)	0.0294	0.08 (0.04)	0.0716	0.07 (0.04)
rs7906421	64312647	Imputed	7.13e-05	0.232	0.03 (0.03)	0.0274	0.08 (0.04)	0.0643	0.07 (0.04)
rs2138565	64307302	Genotyped	7.17e-05	0.237	0.03 (0.03)	0.0305	0.08 (0.04)	0.0686	0.07 (0.04)
rs7082053	64268772	Imputed	7.21e-05	0.443	0.02 (0.02)	0.175	0.05 (0.03)	0.727	0.01 (0.04)
rs12242302	64310992	Genotyped	7.25e-05	0.237	0.03 (0.03)	0.0305	0.08 (0.04)	0.0686	0.07 (0.04)
rs1955334	64310533	Genotyped	7.32e-05	0.237	0.03 (0.03)	0.0305	0.08 (0.04)	0.0686	0.07 (0.04)
rs12761892	64803386	Imputed	7.35e-05	0.376	0.07 (0.08)	0.475	0.07 (0.1)	0.235	-0.13 (0.11)
rs10509171	64306881	Genotyped	8.13e-05	0.247	0.03 (0.03)	0.0326	0.08 (0.04)	0.0682	0.07 (0.04)
rs16917743	64603659	Imputed	8.27e-05	0.337	-0.08 (0.09)	0.412	-0.09 (0.11)	0.516	0.08 (0.12)
rs34106588	64852335	Imputed	8.61e-05	0.41	0.08 (0.1)	0.436	0.1 (0.13)	0.152	-0.2 (0.14)
rs4481919	64933236	Imputed	8.73e-05	0.001	-0.37 (0.11)	0.0095	-0.4 (0.15)	0.00844	0.43 (0.16)
rs16917407	64304454	Genotyped	9.46e-05	0.314	0.03 (0.03)	0.0452	0.07 (0.04)	0.0608	0.07 (0.04)
rs10822027	64344371	Genotyped	1.01e-04	0.0888	-0.04 (0.02)	0.0291	-0.07 (0.03)	0.714	-0.01 (0.04)
chr10:64553557:D	64553557	Imputed	1.02e-04	0.678	-0.02 (0.04)	0.706	-0.02 (0.05)	0.531	0.04 (0.06)
rs61865900	64582482	Imputed	1.02e-04	0.0252	-0.12 (0.05)	0.0581	-0.13 (0.07)	0.114	0.12 (0.07)
rs9971328	64561869	Imputed	1.02e-04	0.567	-0.02 (0.04)	0.575	-0.03 (0.05)	0.527	0.04 (0.06)

chr10:64931557:D	64931557	Imputed	1.03e-04	0.000728	-0.39 (0.11)	0.00738	-0.41 (0.15)	0.0068	0.45 (0.16)
rs10995309	64560878	Imputed	1.07e-04	0.57	-0.02 (0.04)	0.585	-0.03 (0.05)	0.52	0.04 (0.06)
chr10:64562931:D	64562931	Imputed	1.09e-04	0.211	-0.06 (0.04)	0.357	-0.05 (0.06)	0.176	0.09 (0.06)
rs9990	64567938	Imputed	1.09e-04	0.584	-0.02 (0.04)	0.568	-0.03 (0.05)	0.602	0.03 (0.05)
rs12262796	64558740	Imputed	1.12e-04	0.58	-0.02 (0.04)	0.593	-0.03 (0.05)	0.524	0.04 (0.06)
rs1509964	64567364	Imputed	1.13e-04	0.573	-0.02 (0.04)	0.558	-0.03 (0.05)	0.603	0.03 (0.05)
rs60033636	64559641	Imputed	1.13e-04	0.578	-0.02 (0.04)	0.591	-0.03 (0.05)	0.524	0.04 (0.06)
rs7922917	64559027	Imputed	1.13e-04	0.579	-0.02 (0.04)	0.592	-0.03 (0.05)	0.524	0.04 (0.06)
rs2077316	64225448	Imputed	1.18e-04	0.56	-0.04 (0.06)	0.931	0.01 (0.08)	0.0321	0.19 (0.09)
rs10995312	64566572	Genotyped	1.38e-04	0.561	-0.02 (0.04)	0.529	-0.03 (0.05)	0.631	0.03 (0.05)
rs1444418	64560470	Genotyped	1.42e-04	0.636	-0.02 (0.04)	0.617	-0.03 (0.05)	0.603	0.03 (0.06)
rs2138560	64336729	Genotyped	1.55e-04	0.175	0.03 (0.02)	0.0831	0.06 (0.03)	0.751	0.01 (0.04)
rs117874299	64083271	Imputed	1.58e-04	0.352	-0.12 (0.13)	0.431	-0.14 (0.17)	0.6	0.1 (0.19)
rs10761656	64426243	Genotyped	1.63e-04	0.0164	-0.07 (0.03)	0.0302	-0.08 (0.04)	0.235	0.05 (0.04)
rs61864670	64620357	Imputed	1.70e-04	0.0117	-0.15 (0.06)	0.0131	-0.2 (0.08)	0.321	0.09 (0.09)
c10_pos64277369	64277369	Genotyped	1.86e-04	0.458	0.03 (0.04)	0.326	0.06 (0.06)	0.711	0.02 (0.06)
rs10995341	64636079	Imputed	1.99e-04	0.0244	-0.11 (0.05)	0.0265	-0.15 (0.07)	0.419	0.06 (0.07)
rs10509174	64637908	Genotyped	2.23e-04	0.0228	-0.11 (0.05)	0.0268	-0.15 (0.07)	0.342	0.07 (0.07)
chr10:64562930:D	64562930	Imputed	2.30e-04	0.169	-0.06 (0.04)	0.287	-0.06 (0.06)	0.138	0.09 (0.06)
rs7393734	64389552	Imputed	2.39e-04	0.0553	-0.05 (0.03)	0.0518	-0.07 (0.04)	0.498	0.03 (0.04)
rs10509175	64637989	Imputed	2.53e-04	0.0208	-0.11 (0.05)	0.0264	-0.15 (0.07)	0.32	0.07 (0.07)
rs9651304	64671764	Genotyped	2.77e-04	0.693	-0.01 (0.03)	0.857	0.01 (0.04)	0.692	0.02 (0.04)
rs10128333	64570038	Genotyped	2.87e-04	0.638	0.02 (0.03)	0.622	0.02 (0.05)	0.866	0.01 (0.05)
rs4746523	64437748	Imputed	3.10e-04	0.0432	-0.12 (0.06)	0.123	-0.12 (0.08)	0.38	0.07 (0.08)
rs17314489	64273892	Genotyped	3.32e-04	0.0472	0.05 (0.02)	0.0439	0.07 (0.03)	0.668	-0.02 (0.04)
rs9633559	64293978	Genotyped	3.45e-04	0.00566	0.07 (0.02)	0.00386	0.1 (0.03)	0.592	-0.02 (0.04)
rs184101200	64130546	Imputed	3.46e-04	0.911	-0.01 (0.07)	0.762	-0.03 (0.09)	0.625	-0.05 (0.1)
rs7921946	64299868	Imputed	3.49e-04	0.101	0.05 (0.03)	0.017	0.09 (0.04)	0.91	0 (0.04)
rs10995321	64591612	Imputed	3.67e-04	0.0353	-0.1 (0.05)	0.118	-0.1 (0.07)	0.0425	0.14 (0.07)
rs10995188	64276804	Genotyped	3.76e-04	0.0527	0.05 (0.02)	0.0489	0.07 (0.03)	0.707	-0.01 (0.04)

rs10995186	64273023	Genotyped	3.82e-04	0.0479	0.05 (0.02)	0.0446	0.07 (0.03)	0.678	-0.01 (0.04)
rs1878261	64273942	Genotyped	3.95e-04	0.0478	0.05 (0.02)	0.0445	0.07 (0.03)	0.676	-0.01 (0.04)
rs12782363	64283247	Imputed	3.99e-04	0.173	0.04 (0.03)	0.0311	0.08 (0.04)	0.858	0.01 (0.04)
rs10509170	64278634	Genotyped	4.35e-04	0.0527	0.05 (0.02)	0.0489	0.07 (0.03)	0.707	-0.01 (0.04)
rs10995316	64580430	Imputed	4.37e-04	0.0445	-0.1 (0.05)	0.142	-0.1 (0.07)	0.0428	0.14 (0.07)
rs10995317	64582766	Imputed	4.42e-04	0.0477	-0.1 (0.05)	0.15	-0.1 (0.07)	0.043	0.14 (0.07)
rs61865885	64579059	Imputed	4.49e-04	0.0389	-0.1 (0.05)	0.128	-0.1 (0.07)	0.0394	0.15 (0.07)
rs7916322	64612824	Genotyped	4.49e-04	0.0362	-0.1 (0.05)	0.0756	-0.11 (0.06)	0.135	0.1 (0.07)
rs12415752	64620876	Imputed	4.53e-04	0.0321	-0.1 (0.05)	0.0722	-0.12 (0.06)	0.117	0.11 (0.07)
rs7905654	64562524	Imputed	4.67e-04	0.41	-0.03 (0.04)	0.454	-0.04 (0.05)	0.471	0.04 (0.06)
rs61866264	64287241	Imputed	4.71e-04	0.0464	0.05 (0.02)	0.0422	0.07 (0.03)	0.725	-0.01 (0.04)
chr10:64286199:D	64286199	Imputed	4.78e-04	0.0471	0.05 (0.02)	0.0428	0.07 (0.03)	0.724	-0.01 (0.04)
rs114669910	64285152	Imputed	4.81e-04	0.0509	0.05 (0.02)	0.0464	0.07 (0.03)	0.725	-0.01 (0.04)
rs80353807	64319539	Imputed	4.85e-04	0.837	0.01 (0.04)	0.247	0.06 (0.05)	0.147	0.08 (0.06)
rs61744064	64565011	Imputed	4.87e-04	0.0302	-0.11 (0.05)	0.106	-0.11 (0.07)	0.044	0.14 (0.07)
rs143919493	64368863	Imputed	4.99e-04	0.0821	-0.23 (0.13)	0.00351	-0.51 (0.17)	0.166	-0.26 (0.19)
rs141742451	64406084	Imputed	5.03e-04	0.555	-0.18 (0.3)	0.412	-0.33 (0.4)	0.794	0.11 (0.42)
rs2893901	64283205	Imputed	5.15e-04	0.051	0.05 (0.02)	0.045	0.07 (0.03)	0.72	-0.01 (0.04)
chr10:64563699:D	64563699	Imputed	5.29e-04	0.0328	-0.11 (0.05)	0.115	-0.11 (0.07)	0.0458	0.14 (0.07)
rs11817939	64588680	Genotyped	5.29e-04	0.0548	-0.09 (0.05)	0.166	-0.09 (0.07)	0.0467	0.14 (0.07)
rs12257509	64302504	Imputed	5.31e-04	0.00263	0.1 (0.03)	0.00113	0.14 (0.04)	0.284	-0.05 (0.05)
rs2297489	64575360	Imputed	5.32e-04	0.0439	-0.1 (0.05)	0.134	-0.1 (0.07)	0.0534	0.14 (0.07)
rs7922314	64538279	Imputed	5.37e-04	0.0892	-0.08 (0.05)	0.257	-0.07 (0.07)	0.0846	0.12 (0.07)
rs10995184	64271051	Genotyped	5.38e-04	0.043	0.05 (0.02)	0.0435	0.07 (0.03)	0.608	-0.02 (0.04)
rs2297488	64575245	Imputed	5.44e-04	0.0438	-0.1 (0.05)	0.133	-0.1 (0.07)	0.0531	0.14 (0.07)
rs75902654	64687050	Imputed	5.48e-04	0.189	-0.05 (0.04)	0.779	-0.02 (0.06)	0.0997	0.1 (0.06)
rs10995315	64574571	Imputed	5.52e-04	0.0427	-0.1 (0.05)	0.13	-0.1 (0.07)	0.0535	0.14 (0.07)
rs11817773	64593743	Imputed	5.58e-04	0.0168	-0.12 (0.05)	0.0683	-0.12 (0.07)	0.0427	0.14 (0.07)
c10_pos64583263	64583263	Genotyped	5.59e-04	0.0548	-0.09 (0.05)	0.166	-0.09 (0.07)	0.0467	0.14 (0.07)
rs12219294	64618478	Imputed	5.61e-04	0.0328	-0.1 (0.05)	0.0728	-0.11 (0.06)	0.12	0.11 (0.07)

rs7074237	64545572	Imputed	5.65e-04	0.0428	-0.1 (0.05)	0.134	-0.1 (0.07)	0.0557	0.13 (0.07)
rs11818600	64548854	Imputed	5.67e-04	0.0428	-0.1 (0.05)	0.134	-0.1 (0.07)	0.0556	0.13 (0.07)
rs1509960	64620689	Imputed	5.81e-04	0.0473	-0.09 (0.05)	0.0958	-0.11 (0.06)	0.146	0.1 (0.07)
rs2393892	64288592	Genotyped	5.90e-04	0.188	0.04 (0.03)	0.0426	0.08 (0.04)	0.979	0 (0.04)
rs138309605	64706734	Imputed	5.98e-04	0.132	-0.1 (0.07)	0.0158	-0.22 (0.09)	0.428	-0.08 (0.1)
rs61865882	64572093	Imputed	6.09e-04	0.026	-0.11 (0.05)	0.0963	-0.11 (0.07)	0.0395	0.15 (0.07)
rs61865883	64572680	Imputed	6.13e-04	0.0259	-0.11 (0.05)	0.0957	-0.11 (0.07)	0.0392	0.15 (0.07)
chr10:64288396:I	64288396	Imputed	6.23e-04	0.0629	0.05 (0.03)	0.0548	0.06 (0.03)	0.682	-0.01 (0.04)
rs2295814	64571276	Imputed	6.26e-04	0.0256	-0.11 (0.05)	0.095	-0.11 (0.07)	0.04	0.15 (0.07)
chr10:64617871:D	64617871	Imputed	6.41e-04	0.0427	-0.1 (0.05)	0.0931	-0.11 (0.06)	0.132	0.1 (0.07)
rs150486911	64999283	Imputed	6.79e-04	0.0036	-0.41 (0.14)	0.116	-0.3 (0.19)	0.000337	0.72 (0.2)
rs61865884	64578483	Imputed	6.81e-04	0.0399	-0.1 (0.05)	0.14	-0.1 (0.07)	0.0345	0.15 (0.07)
rs16917747	64615626	Imputed	6.93e-04	0.0313	-0.1 (0.05)	0.0703	-0.12 (0.06)	0.116	0.11 (0.07)
rs11818583	64616476	Imputed	6.96e-04	0.0327	-0.1 (0.05)	0.072	-0.11 (0.06)	0.121	0.11 (0.07)
rs7915693	64612523	Imputed	7.26e-04	0.0322	-0.1 (0.05)	0.0705	-0.12 (0.06)	0.119	0.11 (0.07)
rs74422190	64344728	Imputed	7.60e-04	0.00572	-0.13 (0.05)	0.00621	-0.17 (0.06)	0.5	0.04 (0.07)
rs76406857	64344800	Imputed	7.65e-04	0.00573	-0.13 (0.05)	0.00622	-0.17 (0.06)	0.5	0.04 (0.07)
rs190985765	64390795	Imputed	7.67e-04	0.0637	-0.18 (0.09)	0.128	-0.19 (0.13)	0.413	0.11 (0.14)
rs12253072	64346501	Imputed	7.79e-04	0.00425	-0.13 (0.05)	0.00549	-0.17 (0.06)	0.439	0.05 (0.07)
rs77555161	64609174	Imputed	7.79e-04	0.0368	-0.1 (0.05)	0.0819	-0.11 (0.06)	0.115	0.11 (0.07)
chr10:64588179:D	64588179	Imputed	7.84e-04	0.0497	-0.1 (0.05)	0.129	-0.1 (0.07)	0.0701	0.13 (0.07)
rs61865905	64605987	Imputed	8.11e-04	0.0344	-0.1 (0.05)	0.0787	-0.11 (0.06)	0.109	0.11 (0.07)
c10_pos64349002	64349002	Genotyped	8.18e-04	0.00539	-0.13 (0.05)	0.00611	-0.17 (0.06)	0.495	0.04 (0.07)
rs12249410	64301941	Genotyped	8.21e-04	0.102	0.06 (0.04)	0.0396	0.11 (0.05)	0.744	0.02 (0.06)
rs61865904	64604548	Imputed	8.23e-04	0.0342	-0.1 (0.05)	0.0792	-0.11 (0.06)	0.107	0.11 (0.07)
rs61865903	64598118	Imputed	8.26e-04	0.0338	-0.1 (0.05)	0.0781	-0.11 (0.06)	0.106	0.11 (0.07)
rs10995329	64605284	Imputed	8.30e-04	0.0343	-0.1 (0.05)	0.0787	-0.11 (0.06)	0.109	0.11 (0.07)
rs10822063	64599100	Imputed	8.31e-04	0.0338	-0.1 (0.05)	0.0783	-0.11 (0.06)	0.106	0.11 (0.07)
rs10509172	64603279	Imputed	8.32e-04	0.0342	-0.1 (0.05)	0.0793	-0.11 (0.06)	0.107	0.11 (0.07)
rs75877907	64602562	Imputed	8.46e-04	0.0342	-0.1 (0.05)	0.0789	-0.11 (0.06)	0.108	0.11 (0.07)

rs10822061	64597189	Imputed	8.62e-04	0.0314	-0.1 (0.05)	0.0704	-0.12 (0.06)	0.107	0.11 (0.07)
rs10995177	64266512	Genotyped	8.75e-04	0.0473	0.05 (0.02)	0.0475	0.07 (0.03)	0.641	-0.02 (0.04)
rs74423982	64345155	Imputed	8.77e-04	0.00459	-0.13 (0.05)	0.00541	-0.17 (0.06)	0.459	0.05 (0.07)
rs911609	64611477	Genotyped	9.16e-04	0.0391	-0.1 (0.05)	0.0812	-0.11 (0.06)	0.135	0.1 (0.07)
rs4746522	64437684	Imputed	9.40e-04	0.0129	-0.07 (0.03)	0.0295	-0.08 (0.04)	0.138	0.06 (0.04)
chr10:64569708:D	64569708	Imputed	9.72e-04	0.706	0.01 (0.04)	0.625	0.02 (0.05)	0.76	0.02 (0.05)
rs12266041	64634409	Imputed	1.03e-03	0.192	-0.12 (0.09)	0.155	-0.18 (0.13)	0.632	0.07 (0.14)
rs56699626	64633733	Imputed	1.03e-03	0.192	-0.12 (0.09)	0.155	-0.18 (0.13)	0.632	0.07 (0.14)
rs10995178	64266748	Genotyped	1.07e-03	0.0487	0.05 (0.02)	0.0506	0.07 (0.03)	0.639	-0.02 (0.04)
rs74158908	64202077	Imputed	1.08e-03	0.403	-0.05 (0.06)	0.684	-0.03 (0.08)	0.0553	0.17 (0.09)
c10_pos64301873	64301873	Genotyped	1.09e-03	0.365	-0.04 (0.05)	0.997	0 (0.07)	0.0106	0.18 (0.07)
c10_pos64345050	64345050	Genotyped	1.09e-03	0.00492	-0.13 (0.05)	0.00552	-0.17 (0.06)	0.471	0.05 (0.07)
rs141867094	64073846	Imputed	1.09e-03	0.794	-0.03 (0.12)	0.512	0.11 (0.16)	0.0497	0.35 (0.18)
rs78530715	64361480	Imputed	1.24e-03	0.514	-0.04 (0.06)	0.905	-0.01 (0.08)	0.0339	0.17 (0.08)
rs12359549	64649423	Imputed	1.28e-03	0.407	-0.04 (0.04)	0.625	-0.03 (0.06)	0.553	0.04 (0.06)
rs12242530	64627906	Imputed	1.31e-03	0.295	-0.1 (0.09)	0.213	-0.16 (0.13)	0.855	0.02 (0.13)
rs10995335	64623533	Imputed	1.40e-03	0.0284	-0.1 (0.05)	0.0616	-0.12 (0.06)	0.166	0.09 (0.07)
rs10995340	64632908	Imputed	1.40e-03	0.0257	-0.1 (0.05)	0.0525	-0.12 (0.06)	0.152	0.1 (0.07)
rs10995337	64626026	Imputed	1.42e-03	0.0299	-0.1 (0.05)	0.0662	-0.12 (0.06)	0.151	0.1 (0.07)
rs12217462	64628755	Imputed	1.52e-03	0.0294	-0.1 (0.05)	0.0655	-0.12 (0.06)	0.151	0.1 (0.07)
rs4746461	64344998	Genotyped	1.58e-03	0.178	-0.03 (0.02)	0.0439	-0.07 (0.03)	0.493	-0.02 (0.04)
rs10995336	64623708	Imputed	1.63e-03	0.0385	-0.1 (0.05)	0.0735	-0.11 (0.06)	0.206	0.08 (0.07)
chr10:64680148:D	64680148	Imputed	1.65e-03	0.205	-0.05 (0.04)	0.75	-0.02 (0.06)	0.136	0.09 (0.06)
rs12267821	64625919	Genotyped	1.66e-03	0.246	-0.11 (0.09)	0.204	-0.16 (0.12)	0.763	0.04 (0.13)
rs61863379	64129685	Imputed	1.67e-03	0.11	0.09 (0.05)	0.421	0.06 (0.07)	0.0683	-0.14 (0.08)
rs12220702	64628704	Imputed	1.68e-03	0.0298	-0.1 (0.05)	0.0657	-0.12 (0.06)	0.152	0.1 (0.07)
rs61863949	64514564	Imputed	1.74e-03	0.042	-0.16 (0.08)	0.0276	-0.24 (0.11)	0.533	0.07 (0.11)
chr10:64624163:D	64624163	Imputed	1.81e-03	0.229	-0.05 (0.04)	0.309	-0.06 (0.06)	0.708	0.02 (0.06)
c10_pos64508238	64508238	Genotyped	1.83e-03	0.193	-0.12 (0.09)	0.426	-0.1 (0.13)	0.392	0.11 (0.13)
c10_pos64684113	64684113	Genotyped	1.83e-03	0.178	-0.06 (0.04)	0.699	-0.02 (0.05)	0.115	0.09 (0.06)

rs61865902	64597721	Imputed	1.89e-03	0.0295	-0.1 (0.05)	0.0666	-0.12 (0.06)	0.116	0.11 (0.07)
c10_pos64219094	64219094	Genotyped	1.92e-03	0.387	-0.09 (0.11)	0.332	-0.14 (0.14)	0.74	0.05 (0.15)
chr10:64293697:I	64293697	Imputed	1.92e-03	0.624	-0.06 (0.12)	0.583	-0.09 (0.16)	0.49	-0.12 (0.17)
rs10822145	64934548	Imputed	2.11e-03	0.398	-0.03 (0.03)	0.467	-0.03 (0.05)	0.646	0.02 (0.05)
rs10822074	64630538	Genotyped	2.12e-03	0.0309	-0.1 (0.05)	0.0649	-0.11 (0.06)	0.16	0.09 (0.07)
rs7068164	64401056	Imputed	2.15e-03	0.0233	-0.06 (0.02)	0.0127	-0.08 (0.03)	0.602	0.02 (0.04)
rs10219104	64420972	Imputed	2.16e-03	0.0224	-0.06 (0.02)	0.0129	-0.08 (0.03)	0.634	0.02 (0.04)
chr10:64624176:D	64624176	Imputed	2.20e-03	0.172	-0.05 (0.04)	0.141	-0.08 (0.05)	0.993	0 (0.06)
c10_pos64339833	64339833	Genotyped	2.28e-03	0.52	0.03 (0.04)	0.239	0.07 (0.06)	0.858	0.01 (0.06)
rs16917829	64650618	Imputed	2.31e-03	0.326	-0.04 (0.04)	0.838	-0.01 (0.06)	0.218	0.07 (0.06)
rs4746697	64644428	Imputed	2.34e-03	0.316	-0.04 (0.04)	0.781	-0.02 (0.06)	0.238	0.07 (0.06)
rs10995112	64069740	Imputed	2.42e-03	0.481	0.03 (0.05)	0.113	0.1 (0.06)	0.171	0.09 (0.07)
rs868914	64340802	Genotyped	2.49e-03	0.935	0 (0.03)	0.934	0 (0.04)	0.861	-0.01 (0.04)
rs3864807	64070219	Imputed	2.58e-03	0.709	0.02 (0.04)	0.259	0.07 (0.06)	0.26	0.07 (0.06)
rs4746780	64743728	Imputed	2.59e-03	0.846	-0.01 (0.03)	0.86	-0.01 (0.04)	0.647	-0.02 (0.05)

a: Build 37 coordinates
b: P-value for association with Overall Breast Cancer Risk.
c-e: P-value, beta and standard error (SE) for association with percentage density (PD), dense area (DA) and non-dense area (nDA) after adjustment for study and principal components, age, body mass index, hormone replacement therapy, mammographic view, menopausal status, and case-control status.

Table S11: iCHAV1 - eleven markers correlated ($r^2 > 0.6$) with, and a likelihood ratio of >1:100 relative to rs10995201, and their association with density phenotypes

			PD [b]		DA [c]		nDA [d]	
SNP	Position [a]	Type	P-value	β (SE)	P-value	β (SE)	P-value	β (SE)
rs10995181	64268659	Genotyped	3.51E-05	-0.15 (0.04)	5.27E-07	-0.24 (0.05)	0.896	0.01 (0.05)
rs10995182	64268764	Imputed	0.000153	-0.15 (0.04)	1.46E-05	-0.23 (0.05)	0.781	0.02 (0.06)
rs10995187	64273026	Genotyped	3.93E-05	-0.14 (0.03)	4.95E-07	-0.23 (0.05)	0.919	0.01 (0.05)
rs4746419	64275261	Genotyped	3.86E-05	-0.14 (0.03)	4.41E-07	-0.24 (0.05)	0.949	0 (0.05)
rs34511355	64276964	Genotyped	5.08E-05	-0.14 (0.03)	6.55E-07	-0.23 (0.05)	0.972	0 (0.05)
rs10995189	64278181	Genotyped	5.08E-05	-0.14 (0.03)	6.55E-07	-0.23 (0.05)	0.972	0 (0.05)
rs10995190	64278682	Genotyped	5.08E-05	-0.14 (0.03)	6.55E-07	-0.23 (0.05)	0.972	0 (0.05)
rs10995191	64278874	Genotyped	5.08E-05	-0.14 (0.03)	6.55E-07	-0.23 (0.05)	0.972	0 (0.05)
rs11524313	64283656	Imputed	5.22E-05	-0.14 (0.04)	3.91E-07	-0.24 (0.05)	0.842	-0.01 (0.05)
rs10995193	64288082	Imputed	1.77E-05	-0.15 (0.03)	2.28E-07	-0.24 (0.05)	0.85	0.01 (0.05)
rs10995194	64288130	Genotyped	2.82E-05	-0.14 (0.03)	3.81E-07	-0.24 (0.05)	0.898	0.01 (0.05)
rs10995201	64299890	Imputed	1.32E-05	-0.15 (0.04)	1.45E-07	-0.25 (0.05)	0.787	0.01 (0.05)

a: Build 37 coordinates

b-d: P-value, beta and standard error (SE) for association with percentage density (PD), dense area (DA) and non-dense area (nDA) after adjustment for study, principal components, age, body mass index, hormone replacement therapy, mammographic view, menopausal status, and case-control status.

Table S12: iCHAV2 - sixteen markers correlated (r2 > 0.6) with, and a likelihood ratio of >1:100 relative to chr10:64258684:D, and their association statistics for breast density phenotypes

			PD [b]		DA [c]		nDA [d]	
SNP	Position [a]	Type	P-value	β (SE)	P-value	β (SE)	P-value	β (SE)
rs4489633	64238333	Genotyped	0.0781	-0.04 (0.02)	0.181	-0.04 (0.03)	0.0976	0.06 (0.04)
rs4282885	64243828	Genotyped	0.067	-0.04 (0.02)	0.172	-0.04 (0.03)	0.0812	0.06 (0.04)
rs10995173	64246575	Genotyped	0.0623	-0.05 (0.02)	0.137	-0.05 (0.03)	0.0935	0.06 (0.04)
rs10822012	64247568	Imputed	0.0575	-0.05 (0.02)	0.115	-0.05 (0.03)	0.103	0.06 (0.03)
rs10761637	64247585	Imputed	0.0575	-0.05 (0.02)	0.115	-0.05 (0.03)	0.103	0.06 (0.03)
rs12098307	64248099	Imputed	0.0645	-0.05 (0.02)	0.131	-0.05 (0.03)	0.113	0.06 (0.03)
rs10822013	64251977	Genotyped	0.0659	-0.05 (0.02)	0.133	-0.05 (0.03)	0.117	0.05 (0.04)
rs10509168	64257828	Genotyped	0.00423	-0.07 (0.02)	0.017	-0.08 (0.03)	0.0445	0.07 (0.04)
rs10995176	64257971	Imputed	0.00256	-0.07 (0.02)	0.014	-0.08 (0.03)	0.0237	0.08 (0.04)
c10_pos64258017	64258017	Genotyped	0.00225	-0.08 (0.02)	0.0119	-0.08 (0.03)	0.0289	0.08 (0.04)
rs2393886	64258343	Genotyped	0.00221	-0.08 (0.02)	0.0107	-0.08 (0.03)	0.03	0.08 (0.04)
chr10:64258684:D	64258684	Imputed	0.00155	-0.08 (0.02)	0.00555	-0.09 (0.03)	0.034	0.08 (0.04)
chr10:64258692:D	64258692	Imputed	0.0066	0.07 (0.03)	0.01	0.09 (0.04)	0.217	-0.05 (0.04)
rs12243471	64260410	Genotyped	0.119	-0.04 (0.03)	0.448	-0.03 (0.03)	0.0426	0.07 (0.04)
rs12245332	64260847	Genotyped	0.121	-0.04 (0.03)	0.457	-0.03 (0.03)	0.0412	0.08 (0.04)
rs2393887	64263093	Genotyped	0.123	-0.04 (0.03)	0.458	-0.03 (0.03)	0.0396	0.08 (0.04)
rs4746409	64263402	Genotyped	0.00429	-0.07 (0.02)	0.00307	-0.1 (0.03)	0.133	0.05 (0.03)

a: Build 37 coordinates

b-d: P-value, beta and standard error (SE) for association with percentage density (PD), dense area (DA) and non-dense area (nDA) after adjustment for study, principal components, age, body mass index, hormone replacement therapy, mammographic view, menopausal status, and case-control status.

Table S13: iCHAV3 - seventeen markers correlated (r2 > 0.6) with, and a likelihood ratio of >1:100 relative to rs7922449, and their association statistics with density phenotypes

			PD [b]		DA [c]		nDA [d]	
SNP	Position [a]	Type	P-value	β (SE)	P-value	β (SE)	P-value	β (SE)
rs1878253	64269210	Genotyped	0.0865	0.04 (0.03)	0.013	0.09 (0.04)	0.841	0.01 (0.04)
rs1914200	64275340	Genotyped	0.0865	0.04 (0.03)	0.013	0.09 (0.04)	0.841	0.01 (0.04)
rs10740081	64280059	Imputed	0.0881	0.04 (0.03)	0.0133	0.09 (0.04)	0.835	0.01 (0.04)
rs10761639	64286938	Imputed	0.0869	0.05 (0.03)	0.0125	0.09 (0.04)	0.843	0.01 (0.04)
rs7901318	64290213	Imputed	0.0745	0.05 (0.03)	0.0117	0.09 (0.04)	0.896	0 (0.04)
rs2393894	64291065	Imputed	0.056	0.05 (0.03)	0.0121	0.09 (0.04)	0.855	-0.01 (0.04)
rs7922449	64291308	Imputed	0.634	0.01 (0.03)	0.308	0.04 (0.04)	0.547	0.02 (0.04)
rs10995196	64292344	Imputed	0.0849	0.05 (0.03)	0.0108	0.09 (0.04)	0.753	0.01 (0.04)
rs4746428	64293118	Genotyped	0.132	0.04 (0.03)	0.0239	0.08 (0.03)	0.692	0.01 (0.04)
chr10:64293571:D	64293571	Imputed	0.342	0.03 (0.03)	0.0674	0.07 (0.04)	0.392	0.03 (0.04)
rs9633558	64293805	Imputed	0.134	0.04 (0.03)	0.0254	0.08 (0.03)	0.702	0.01 (0.04)
rs7915519	64293843	Imputed	0.134	0.04 (0.03)	0.0246	0.08 (0.03)	0.691	0.01 (0.04)
rs6479823	64294020	Imputed	0.134	0.04 (0.03)	0.0247	0.08 (0.03)	0.691	0.01 (0.04)
rs1914182	64294817	Imputed	0.134	0.04 (0.03)	0.0245	0.08 (0.03)	0.691	0.01 (0.04)
rs10822017	64296420	Imputed	0.14	0.04 (0.03)	0.0253	0.08 (0.03)	0.689	0.01 (0.04)
rs7901573	64297378	Imputed	0.131	0.04 (0.03)	0.0239	0.08 (0.03)	0.699	0.01 (0.04)
rs12258134	64297521	Imputed	0.131	0.04 (0.03)	0.0238	0.08 (0.03)	0.699	0.01 (0.04)
rs1949356	64298273	Genotyped	0.144	0.04 (0.03)	0.026	0.08 (0.03)	0.688	0.01 (0.04)

a: Build 37 coordinates

b-d: P-value, beta and standard error (SE) for association with percentage density (PD), dense area (DA) and non-dense area (nDA) after adjustment for study, principal components, age, body mass index, hormone replacement therapy, mammographic view, menopausal status, and case-control status.

Table S14: iCHAV4 - marker correlated ($r^2 > 0.6$) with, and a likelihood ratio of >1:100 relative to rs9971363, and their association statistics with density phenotypes

			PD [b]		DA [c]		nDA [d]	
SNP	Position [a]	Type	P-value	β (SE)	P-value	β (SE)	P-value	β (SE)
rs9971363	64563702	Imputed	0.629	-0.02 (0.04)	0.634	-0.02 (0.05)	0.549	0.03 (0.05)
rs7090365	64564428	Imputed	0.628	-0.02 (0.04)	0.628	-0.02 (0.05)	0.556	0.03 (0.05)

a: Build 37 coordinates

b-d: P-value, beta and standard error (SE) for association with percentage density (PD), dense area (DA) and non-dense area (nDA) after adjustment for study, principal components, age, body mass index, hormone replacement therapy, mammographic view, menopausal status, and case-control status.

Table S15 – Risk association for the four lead SNPs for each iCHAV: iCHAV1-rs10995201, iCHAV2-chr10:64258684:D, iCHAV3-rs7922449, iCHAV4-rs9971363 and known risk variant rs10995190

Full Data - Case/Control 46450/42600

SNP	P-value [a]	OR (95%CI) [a]
rs10995201	1.05E-29	0.85 (0.83,0.88)
chr10:64258684:D	4.24E-14	0.93 (0.91,0.95)
rs7922449	1.68E-07	1.06 (1.04,1.08)
rs9971363	6.54E-05	0.94 (0.92,0.97)
rs10995190	5.61E-29	0.86 (0.84,0.88)

Subset of samples with density data (2379 cases and 4507 controls)

			+ Adjusted for PD		+ Adjusted for DA		+ Adjusted for nDA	
SNP	P-value [a]	OR (95%CI) [a]	P-value [b]	OR (95%CI) [b]	P-value [b]	OR (95%CI) [b]	P-value [b]	OR (95%CI) [b]
rs10995201	0.02	0.87 (0.77,0.98)	0.05	0.88 (0.78,1.00)	0.06	0.89 (0.79,1.01)	0.02	0.87 (0.77,0.98)
chr10:64258684:D	0.07	0.92 (0.85,1.01)	0.11	0.93 (0.86,1.02)	0.10	0.93 (0.85,1.01)	0.08	0.93 (0.95,1.01)
rs7922449	0.07	1.09 (0.99,1.20)	0.11	1.08 (0.98,1.19)	0.11	1.08 (0.98,1.20)	0.08	1.09 (0.99,1.20)
rs9971363	0.27	0.93 (0.82,1.06)	0.31	0.94 (0.82,1.06)	0.32	0.94 (0.82,1.06)	0.28	0.93 (0.82,1.06)
rs10995190	0.006	0.85 (0.75,0.95)	0.01	0.86 (0.77,0.97)	0.02	0.87 (0.77,0.98)	0.006	0.85 (0.75,0.95)

a: P-value, Odds ratio (OR) and 95% Confidence Interval (CI) for association with Overall Breast Cancer Risk adjusted for principal components and per-study fixed-effects..

b: P-value, Odds ratio (OR) and 95% Confidence Interval (CI) for association with Overall Breast Cancer Risk adjusted for principal components and per-study fixed-effects plus additional variables indicated.

Table S16 – eQTL analysis for *ZNF365* and *NRBF2* in three normal breast data sets for each iCHAV (FDR-adjusted P values)

	NBI				**NBII**				**METABRIC**			
	iCHAV1	**iCHAV2**	**iCHAV3**	**iCHAV4**	**iCHAV1**	**iCHAV2**	**iCHAV3**	**iCHAV4**	**iCHAV1**	**iCHAV2**	**iCHAV3**	**iCHAV4**
Representative SNP	**rs10995181**	**rs4489633**	**rs1878253**	**rs9971363**	**rs10995181**	**rs4489633**	**rs1878253**	**rs9971363**	**rs10995201**	**chr10: 64258684:D**	**rs7922449**	**rs9971363**
ADO	0.996	0.996	0.996	0.996	0.995	0.995	0.995	0.995	0.997	1.000	0.858	0.997
ARID5B	0.996	0.996	0.996	0.996	0.995	0.995	0.995	0.995	0.997	0.997	0.997	0.997
c10orf107	0.996	0.996	0.996	n.d.	0.995	0.991	0.995	n.d.	0.997	0.997	0.997	0.997
EGR2	0.996	0.996	0.996	0.996	0.995	0.995	0.995	0.995	0.766	0.997	0.995	0.997
JMJD1C	0.996	0.996	0.996	0.996	0.995	0.995	0.995	0.995	0.997	0.997	0.997	0.987
JMJD1C-AS1	n.d.	n.d.	n.d.	n.d.	0.961	0.995	0.995	0.995	n.d.	n.d.	n.d.	n.d.
NRBF2	0.836	0.996	0.996	0.996	0.995	0.995	0.997	0.995	0.997	0.997	1.000	0.997
REEP3	n.d.	n.d.	n.d.	0.996	n.d.	n.d.	n.d.	0.995	0.917	0.997	0.997	0.997
RTKN2	0.996	0.996	0.996	0.996	0.995	0.997	0.995	0.995	1.000	0.997	0.997	0.997
ZNF365	0.996	0.996	0.996	0.996	0.995	0.995	0.995	0.995	1.000	0.997	0.999	0.997

ZNF365 probe = A_23_P86610 in NBI and NBII and ilmn_1691022 in METABRIC

*JMJD1C pr*obe = A_23_P427217 in NBI; ilmn_1764970 in METABRIC

ARID5B probe = A_23_P97871 in NBI

RTKN2 probe = A_23_P52410 in NBI

REEP3 probe = A_23_P423543 in NBI

n.d. = not done because SNP is >1Mb from the transcript

Table S17 – eQTL analysis for *ZNF365* and *NRBF2* in two breast tumour data sets for each iCHAV (FDR-adjusted P values)

	BCI				**BCII**			
	iCHAV1	**iCHAV2**	**iCHAV3**	**iCHAV4**	**iCHAV1**	**iCHAV2**	**iCHAV3**	**iCHAV4**
representative SNP	**rs10995181**	**rs4489633**	**rs1878253**	**rs9971363**	**rs10995181**	**rs4489633**	**rs1878253**	**rs9971363**
ADO	0.933	0.990	0.981	0.990	0.834	0.877	0.947	0.883
ARID5B	0.997	0.996	0.970	0.820	0.949	0.992	0.666	0.974
c10orf107	0.814	0.958	0.933	n.d.	0.883	0.789	0.780	n.d.
EGR2	0.990	0.995	0.990	0.990	0.996	0.982	0.939	0.943
JMJD1C	0.974	0.970	0.972	0.895	0.996	0.951	0.949	0.510
JMJD1C-AS1	n.d.	n.d.	n.d.	n.d.	0.948	0.902	0.949	0.974
NRBF2	0.997	0.981	0.820	0.980	0.985	0.985	0.949	0.378
REEP3	n.d.	n.d.	n.d.	0.899	n.d.	n.d.	n.d.	0.536
RTKN2	0.953	0.789	0.995	0.990	0.949	0.997	0.949	0.919
ZNF365	0.820	0.904	0.974	0.919	0.950	0.739	0.946	0.955

ZNF365 probe = A_23_P86610

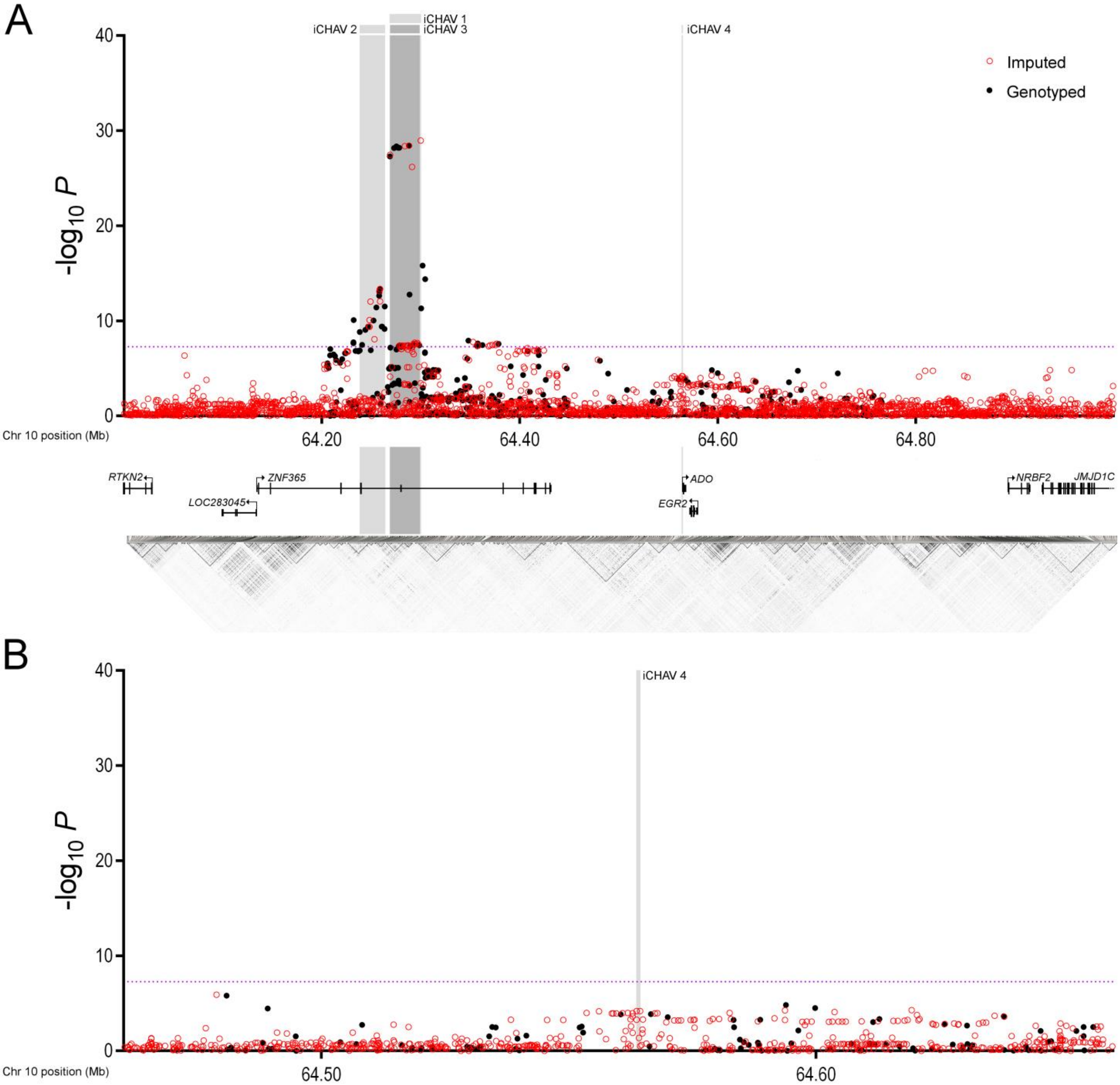
RTKN2 probe = A_23_P52410 in BCI

JMJD1C probe = A_23_P427217 in BCI

ARID5B probe = A_23_P97871 in BCI

REEP3 probe = A_23_P75028

n.d. = not done because SNP is >1Mb from the transcript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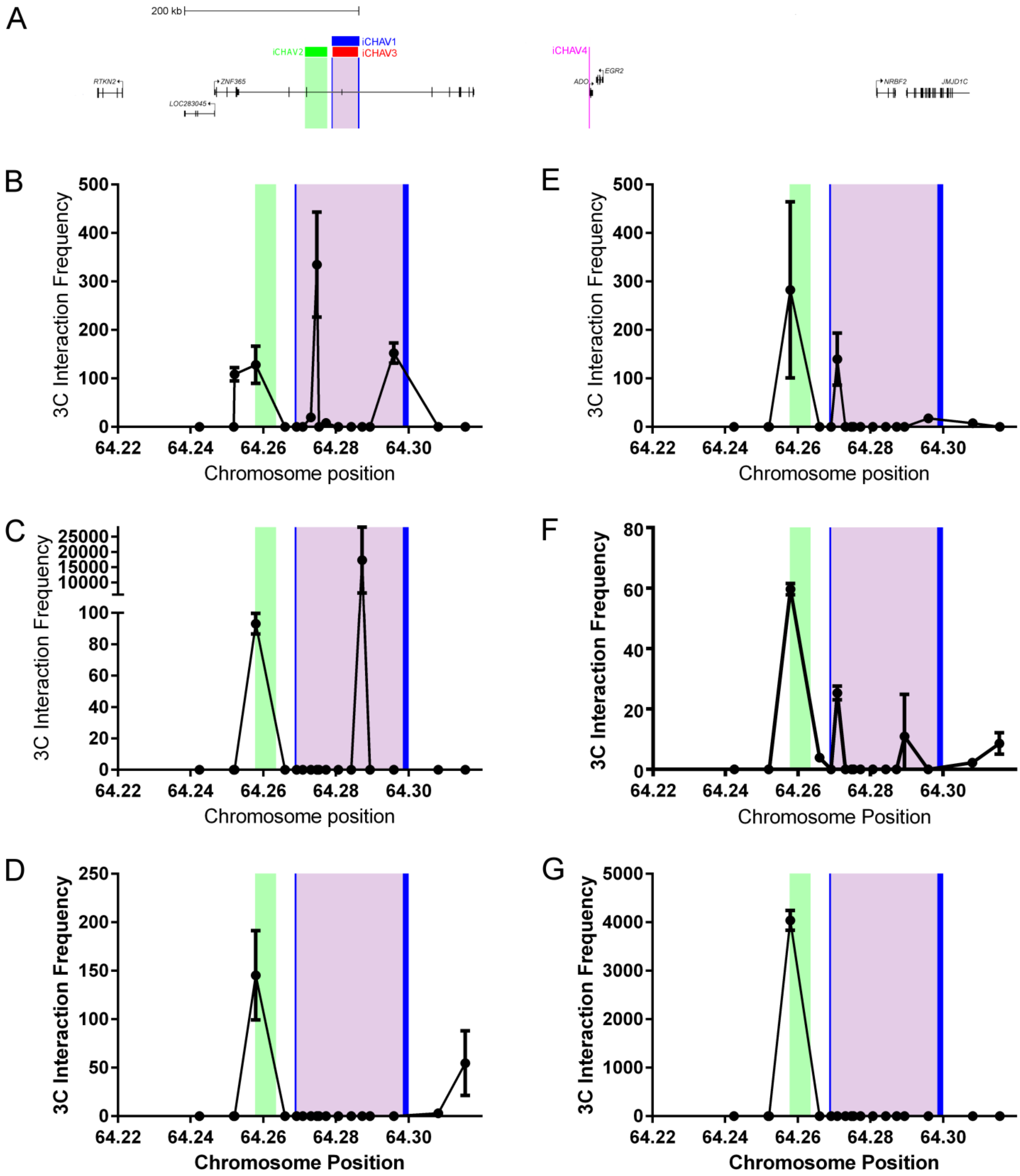
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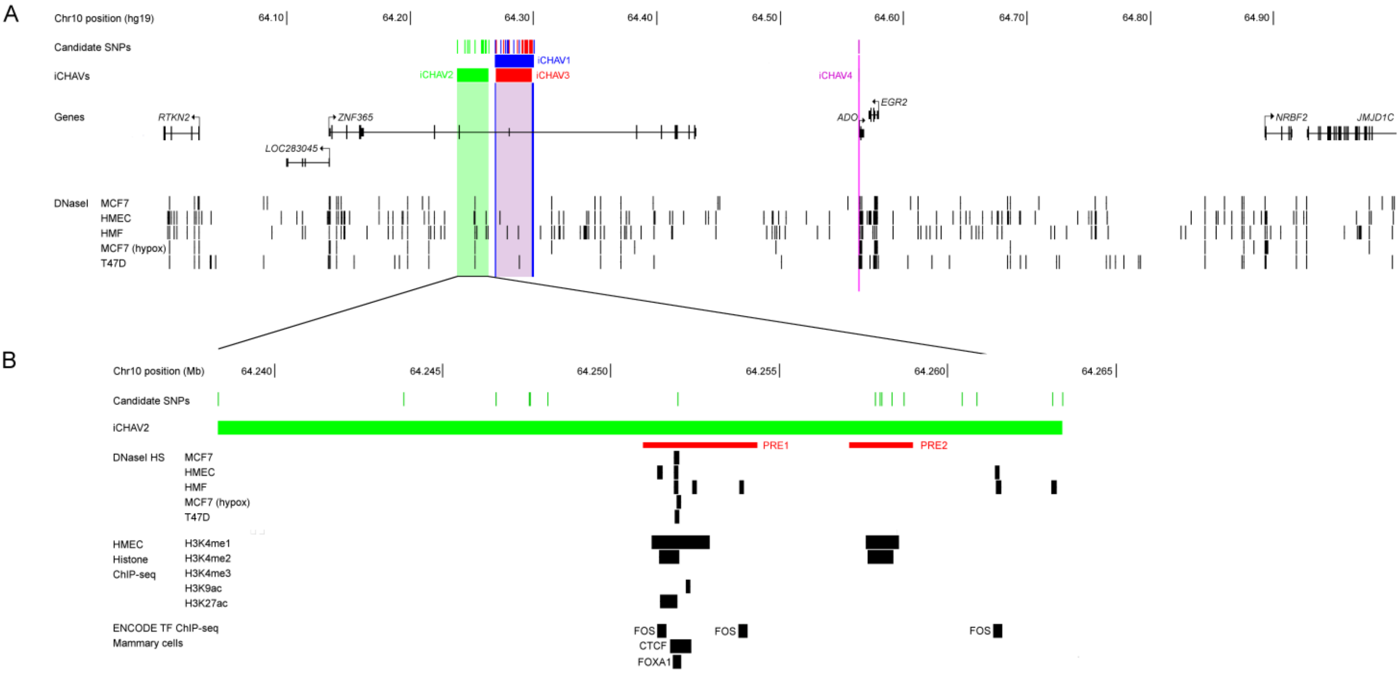
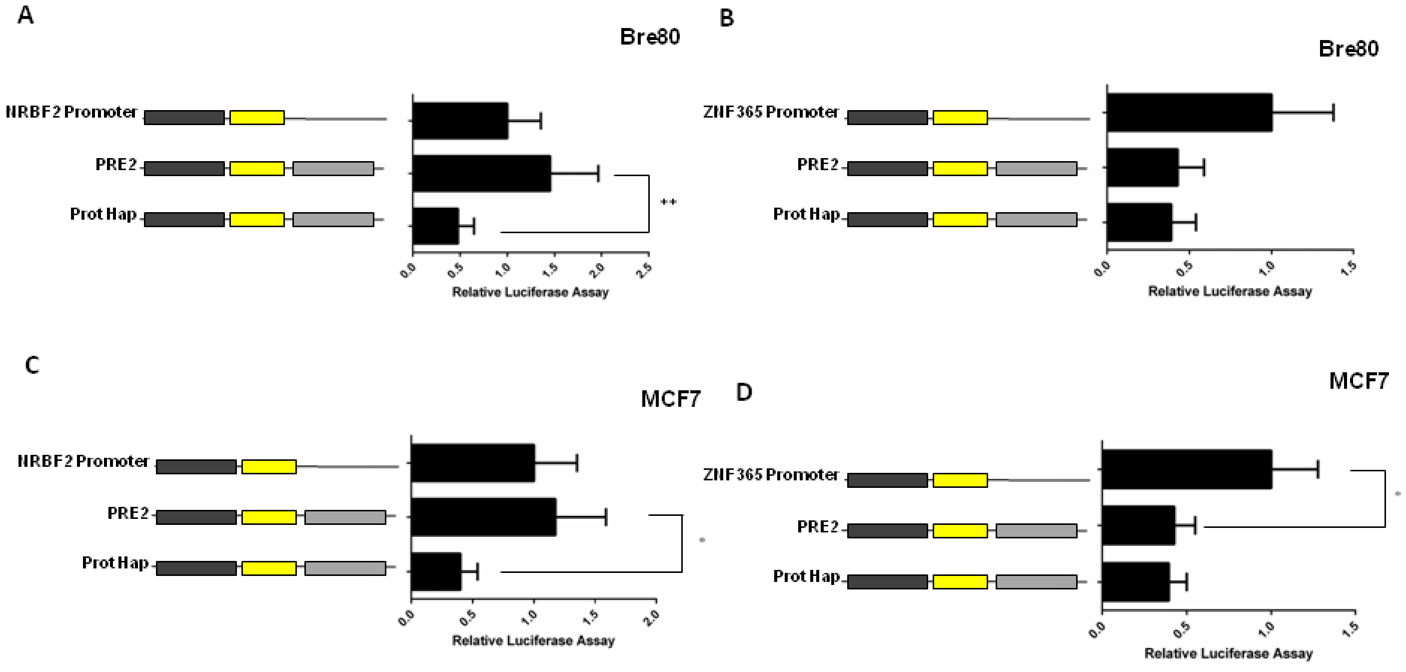
64.30
Chromosome Position


A
Chr10 position (hg19)
64.10
64.20
64.30
64.40
64.50
64.60
64.70
64.80
64.90
Candidate SNPs
iCHAVs
iCHAV1
iCHAV2
iCHAV3
iCHAV4
Genes
RTKN2
ZNF365
LOC283045
ADO
EGR2
NRBF2
JMJD1C
DNaseI
MCF7
HMEC
HMF
MCF7 (hypox)
T47D
B
Chr10 position (Mb)
64.240
64.245
64.250
64.255
64.260
64.265
Candidate SNPs
iCHAV2
PRE1
PRE2
DNaseI HS
MCF7
HMEC
HMF
MCF7 (hypox)
T47D
HMEC
Histone
ChIP-seq
H3K4me1
H3K4me2
H3K4me3
H3K9ac
H3K27ac
ENCODE TF ChIP-seq
Mammary cells
FOS
FOS
FOS
CTCF
FOXA1


A
Bre80
NRBF2 Promoter
PRE2
Prot Hap
**
0.0
0.5
1.0
1.5
2.0
2.5
Relative Luciferase Assay
B
Bre80
ZNF365 Promoter
PRE2
Prot Hap
0.0
0.5
1.0
1.5
Relative Luciferase Assay
C
MCF7
NRBF2 Promoter
PRE2
Prot Hap
*
0.0
0.5
1.0
1.5
2.0
Relative Luciferase Assay
D
MCF7
ZNF365 Promoter
PRE2
Prot Hap
*
0.0
0.5
1.0
1.5
Relative Luciferase Assay