# Identification of ten variants associated with risk of estrogen receptor negative breast cancer

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Most common breast cancer susceptibility variants have been identified through genome-wide association studies (GWASs) of predominantly estrogen receptor (ER)-positive disease<sup>1</sup>. We conducted a GWAS using 21,468 ERnegative cases and 100,594 controls combined with 18,908 *BRCA1* mutation carriers (9,414 with breast cancer), all of European origin. We identified independent associations at  $P<5x10^{-8}$  with 10 variants at nine novel loci. At P<0.05, we replicated associations with 10 of 11 variants previously reported in ER-negative or *BRCA1* mutation carrier GWASs, and observed consistent associations with ER-negative disease for 105 susceptibility variants identified by other breast cancer GWASs. These 125 variants explain approximately 16% of the familial risk of this breast cancer subtype. There was high genetic correlation (0.72) between risk of ER-negative breast cancer and breast cancer risk for *BRCA1* carriers. These findings will likely lead to improved risk prediction and inform further fine-mapping and functional work to better understand the biological basis of ER-negative breast cancer.

GWASs have identified 107 single nucleotide polymorphisms (SNPs) that are independently associated with breast cancer risk<sup>2-32</sup>. Association studies focused on ER-negative disease, or *BRCA1* mutation carriers, who are more likely to develop ER-negative disease (70-80% of cases)<sup>33</sup>, have identified 11 of these SNPs<sup>3,9,12,19,29,30</sup>. We aimed to discover additional ER-negative breast cancer susceptibility variants by performing a GWAS in women of European origin.

New genotyping data were generated for 9,655 ER-negative cases and 45,494 controls from 68 Breast Cancer Association Consortium (BCAC) studies and 15,566 BRCA1 mutation carriers (7,784 with breast cancer) from 58 Consortium of Investigators of Modifiers of BRCA1/2 (CIMBA) studies (Supplementary Tables 1 and 2) using the Illumina OncoArray beadchip, a 570K SNP custom array with genome-wide coverage<sup>34</sup>. Imputation was used to derive estimated genotypes for ~21M SNPs, using the 1000 Genomes Project (Phase 3) as reference; ~11.5M of those with imputation  $r^2$ >0.3 and minor allele frequency (MAF)>0.005 were included in further analyses. For BCAC data, we estimated per-allele odds ratios (ORs) using logistic regression, adjusting for country and principal components. For CIMBA data, we estimated per-allele hazard ratios (HR) using a retrospective cohort analysis framework, modelling time to breast cancer and stratifying on country. Ashkenazi Jewish origin and birth cohort<sup>35,36</sup> (see Online Methods). These analyses were also applied to an independent set of previously generated data from other genome-wide genotyping of additional European participants in 44 BCAC studies (11,813 ERnegative cases and 55,100 controls)<sup>9,12,16,20,37,38</sup> and 54 CIMBA studies (3,342 BRCA1 mutation carriers, 1,630 with breast cancer) (Supplementary Tables 1 and 2). Fixed-effects meta-analysis was used to combine results across genotyping initiatives within consortia and, assuming that the OR and HR estimates approximate the same underlying relative risk, across consortia<sup>39</sup>.

Results from the combined meta-analysis are summarised in Supplementary Figures 1 and 2. There was minimal inflation of test statistics (lambda1000=1.004;

Supplementary Figure 3). We identified 10 variants at nine novel loci that were independently associated with risk of ER-negative breast cancer at  $P<5x10^{-8}$  (Table 1; Supplementary Table 3; Supplementary Figures 4-11). Two independent signals were observed within 12kb at 11q22.3, for rs74911261 (MAF=0.02) and rs11374964 (MAF=0.42); OR estimates and statistical significance were largely unchanged when each variant was adjusted for the other (Supplementary Table 4). The association with 8p23.3-rs66823261 was not observed for *BRCA1* mutation carriers (P=0.32, P-heterogeneity=0.030).

For each of these 10 novel signals, we identified candidate causal SNPs analytically<sup>40,41</sup> (see Online Methods) and combined multiple sources of *in silico* functional annotation from public databases<sup>42-52</sup> to identify likely functional variants and target genes. Results are summarised in Supplementary Table 5 (including UCSC Genome Browser links; see also Supplementary Note), Figure 1 and Supplementary Figures 4-11 (data sources in Supplementary Table 6). Many candidate causal SNPs lie in predicted regulatory regions and are associated with expression of nearby genes in blood or other tissues. At 2p23, the predicted target genes include ADCY3 and NCOA1 (Supplementary Figure 4). At 6q23.1 (Supplementary Figure 5), the most plausible target gene is L3MBTL3<sup>53</sup>. A predicted target at 8q24.13 is FBXO32, which is expressed in ER-negative HMECs but not ERpositive MCF7 breast cancer cells (Supplementary Figure 7) and has a known role in cancer cachexia<sup>54</sup>. At 11q22.3 (Figure 1), a predicted target gene of common riskassociated variants is NPAT<sup>55</sup>. The rarer SNPs underlying the other 11g22.3 signal are predicted to target ATM, a known breast cancer susceptibility gene<sup>56</sup>. Three rare coding variants (MAF≤0.03) in ATM, NPAT and KDELC2, are also among the candidate causal SNPs at this locus. At 16p13, predicted target genes include ADCY9 and CREBBP (Supplementary Figure 8). At 19g12 (Supplementary Figure 11), a potential target gene encodes cyclin E1 which is involved in cell cycle control and phosphorylation of NPAT<sup>57</sup>.

Expression QTL associations were assessed between each candidate causal variant and genes within 1Mb using 79 ER-negative breast tumours from TCGA and 135 normal breast tissue samples from METABRIC<sup>58-60</sup>. The strongest associations identified were 6q23.1-rs6569648-*L3MBTL3* (P=4.3x10<sup>-6</sup>) and 18q12.1-rs12965632-*CDH2* (P=1.0x10<sup>-4</sup>), both in METABRIC (Supplementary Table 5). SNP rs6569648 was the top *cis*-eQTL (of all imputed variants within 1 Mb) for *L3MBTL3* while the pvalue for the rs12965632-*CDH2* eQTL was within two orders of magnitude of the top *cis*-eQTLs for this gene (Supplementary Figures 12-13).

For 10 of the 11 variants previously identified through GWASs of ER-negative disease or overall disease in *BRCA1* mutation carriers<sup>3,9,12,18,19,30,31</sup>, or reported as more strongly associated with ER-negative breast cancer<sup>29</sup>, associations with ER-negative disease were replicated (P<0.05) using OncoArray data from BCAC, which does not overlap with any of the discovery studies (Table 2). Effect sizes were generally similar to those originally reported. Using all available CIMBA data, six of these 11 variants were associated with breast cancer risk (P<0.05) for *BRCA1* mutation carriers (Table 2). No evidence of association was observed for 20q11-rs2284378<sup>12</sup> in either BCAC or CIMBA (P≥0.46).

Based on estimated ORs using BCAC data for all cases with known ER status (16,988 ER-negative; 65,275 ER-positive), all 10 new and 10 previously reported

and replicated ER-negative disease susceptibility SNPs were more strongly associated with risk of ER-negative than ER-positive subtype (P-heterogeneity<0.05, except for novel hit 19p13.2-rs322144; Supplementary Table 7). Two variants (1q32.1-rs4245739 and 19p13.11-rs67397200) were not associated with ER-positive disease. For four variants (11q22.3- rs11374964, 11q22.3-rs74911261, 1q32.1-rs6678914 and 2p23.2-rs4577244), the risk-associated allele for ER-negative disease was associated with reduced risk of ER-positive disease (P<0.05).

For these 20 ER-negative breast cancer susceptibility SNPs, we also assessed associations by triple-negative (TN) status (negative for ER, progesterone receptor and HER2; Table 3), tumour grade (Table 4) and age at diagnosis (Supplementary Table 8) using BCAC data only. Five, including the novel susceptibility variants 11q22.3-rs11374964 and 11q22.3-rs74911261, were more strongly associated with risk of both TN and higher-grade disease (P<0.05), although after adjustment for TN status, heterogeneity by grade was observed only for 11q22.3-rs74911261 and 1q32.1-rs4245739 (P<0.05). For 2p23.3-rs4577244, heterogeneity was observed for grade only, while 6q25.2-rs2747652 was more strongly associated with risk of other (non-TN) ER-negative breast cancer subtypes (P<0.05). At younger ages, associations appeared to be stronger for two variants (5p15.33-rs10069690 and 19p13.11-rs67397200), and weaker for one (6q25.2-rs2747652) (P<0.05).

Elsewhere we report 65 novel susceptibility loci for overall breast cancer<sup>1</sup>. Three of these overlap within 500kb with the novel ER-negative disease-associated loci reported here (variants 2p23.3-rs200648189, 6q23.1-rs6569648 and 8q24.13-rs17350191). We assessed associations with risk of ER-negative disease, and with risk of overall breast cancer for *BRCA1* mutation carriers, for SNPs at the remaining 62 loci, as well as for the 96 previously reported breast cancer susceptibility variants that were not ER-negative specific. Of these 158 SNPs, 105 were associated (P<0.05) with risk of ER-negative breast cancer, and 24 with risk for *BRCA1* mutation carriers (Supplementary Tables 9-10). Results for *BRCA2* mutation carriers are presented in Supplementary Table 11.

Pathway analysis based on mapping each SNP to the nearest gene was performed using summary association statistics from the meta-analysis of BCAC and CIMBA data combined<sup>61-64</sup> (see Online Methods). This identified several pathways implicated in ER-negative disease (enrichment score [ES] $\geq$ 0.41; Supplementary Figure 14; Supplementary Tables 12-13), including a subset that was not enriched in susceptibility to ER-positive disease (ES<0; Supplementary Table 14). One of the latter subsets was the adenylate cyclase (AC) activating pathway (ES=0.62; Supplementary Figure 15). Two of the predicted target genes for the 10 novel ER-negative breast cancer susceptibility variants, based on the eQTL analysis (Supplementary Table 5), *ADCY3* (P[TCGA]=6.7x10<sup>-3</sup>] and *ADCY9* (P[METABRIC]=1.3x10<sup>-4</sup>), are part of this pathway, and their association signals were critical to the elevated ES observed (Supplementary Figure 14). ADCY9 is stimulated by  $\beta$ 2 adrenergic receptor ( $\beta$ 2AR) signalling<sup>65</sup> in ER-negative breast cancer<sup>66</sup>, which in turn drives AC-cAMP signalling, including for example mitogenic signalling through  $\beta$ -arrestin-Src-ERK<sup>67</sup>.

To further explore the functional properties of the genome that contribute to ERnegative breast cancer heritability, we conducted a partitioned heritability analysis using linkage disequilibrium (LD) score regression<sup>68</sup>. Considering 52 "baseline" genomic features, we observed the greatest enrichment for super-enhancers (2.5fold,  $p=2x10^{-7}$ ) and the H3K4me3 histone mark (2.4-fold, p=0.0005), with 33% depletion (p=0.0002) observed for repressed regions (Supplementary Table 15). No differences in enrichment for these features were observed between susceptibility to ER-negative and ER-positive breast cancer, but baseline genomic features are not specific to cell type<sup>68</sup>. The estimated correlation between ER-negative and ERpositive breast cancer based on ~1M common genetic variants<sup>69,70</sup> was 0.60 (standard error [SE], 0.03) indicating that, although these two breast cancer subtypes have a shared genetic component, a substantial proportion is distinct. The estimated correlation between ER-negative disease in the general population and overall breast cancer for *BRCA1* mutation carriers was 0.72 (SE, 0.11).

In summary, in this study of women of European origin, we have identified 10 novel susceptibility variants for ER-negative breast cancer and replicated associations with ER-negative disease for 10 SNPs identified by previous GWASs. Most of these were not associated, or more weakly associated, with ER-positive disease, consistent with the findings from pathway and partitioned heritability analyses showing that ERnegative breast cancer has a partly distinct genetic aetiology. We also observed consistent associations with ER-negative disease for a further 105 overall breast cancer susceptibility SNPs. Together, these 125 variants explain ~14% of an assumed 2-fold increased risk of developing ER-negative disease for the first degree female relatives of women affected with this subtype (the newly identified SNPs explain ~1.5%); Supplementary Table 16) and ~40% of the estimated familial risk that is attributable to all variants imputable from the Oncoarray (see Online Methods). We have also identified nine novel breast cancer susceptibility variants for BRCA1 mutation carriers and confirmed associations for a further 30 previously reported SNPs; these 39 variants explain ~8% of the variance in polygenic risk for carriers of these mutations (Supplementary Table 17). However, the lower number of BRCA1 risk-associated variants may merely be a consequence of the smaller sample size, since the genetic correlation with ER-negative breast cancer is high. These findings will likely inform improved risk prediction, both for the general population and for *BRCA1* mutation carriers<sup>30,71,72</sup>. Further investigation is required for other populations of non-European origin. Fine-mapping and functional studies should lead to a better understanding of the biological basis of ER-negative breast cancer, and perhaps inform the design of more effective preventive interventions, early detection and treatments for this disease.

#### **Data availability**

A subset of the data that support the findings of this study is publically available via dbGaP (see URLs section; accession number phs001265.v1.p1). The complete dataset will not be made publically available due to restraints imposed by the ethics committees of individual studies; requests for data can be made to the corresponding author or the Data Access Coordination Committees (DACCs) of BCAC (see URLs section) and CIMBA (see URLs section). BCAC DACC approval is required to access data from studies ABCFS, ABCS, ABCTB, BBCC, BBCS, BCEES, BCFR-NY, BCFR-PA, BCFR-UT, BCINIS, BSUCH, CBCS, CECILE, CGPS, CTS, DIETCOMPLYF, ESTHER, GC-HBOC, GENICA, GEPARSIXTO, GESBC, HABCS, HCSC, HEBCS, HMBCS, HUBCS, KARBAC, KBCP, LMBC, MABCS,

MARIE, MBCSG, MCBCS, MISS, MMHS, MTLGEBCS, NC-BCFR, OFBCR, ORIGO, pKARMA, POSH, PREFACE, RBCS, SKKDKFZS, SUCCESSB, SUCCESSC, SZBCS, TNBCC, UCIBCS, UKBGS and UKOPS (see Supplementary Table 1). CIMBA DACC approval is required to access data from studies BCFR-ON, CONSIT TEAM, DKFZ, EMBRACE, FPGMX, GC-HBOC, GEMO, G-FAST, HEBCS, HEBON, IHCC, INHERIT, IOVHBOCS, IPOBCS, MCGILL, MODSQUAD, NAROD, OCGN, OUH and UKGRFOCR (see Supplementary Table 2).

# URLs

dbGaP: <u>https://www.ncbi.nlm.nih.gov/gap</u> BCAC: <u>http://bcac.ccge.medschl.cam.ac.uk/</u> CIMBA: <u>http://cimba.ccge.medschl.cam.ac.uk/</u> PCcalc software: <u>http://ccge.medschl.cam.ac.uk/software/pccalc/</u> SNPTEST: <u>https://mathgen.stats.ox.ac.uk/genetics\_software/snptest/snptest.html</u> GeneSets: <u>http://baderlab.org/GeneSets</u> GenGen package: <u>http://gengen.openbioinformatics.org/en/latest/</u>

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# **Competing Financial Interests**

The authors confirm that they have no competing financial interests

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#### **Figure legends**

Figure 1. Genomic region around independent ER negative risk associated variants, 11\_108345515\_G\_A (rs11374964) and 11\_108357137\_G\_A (rs74911261). One Mb region showing statistical significance of all genotyped and imputed SNPs and positions of candidate causal variants for two independent signals (shown below as red or blue ticks) in relation to RefSeg genes. Missense variants are labelled with asterisks. Breast cell enhancers overlapping candidate SNPs predicted to target nearby genes by IM-PET<sup>46</sup> are depicted as black bars. Chromatin interactions from ENCODE ChIA-PET in MCF7 cells overlapping candidate variants are shaded to reflect interaction confidence scores. Epigenomic features (derived from publicly available ChIP-seq and DNase-seq) that overlap candidate variants are shown as red or blue segments, depending on the intersected signal. Density tracks show the summed occurrence of ChIP-seg and DNase-seg peak signals at each position. Roadmap Epigenomics Project chromatin state models for HMEC and myoepithelial cells grouped into enhancer, promoter or transcribed annotations are shown as yellow, red or green segments, respectively. Transcript levels in MCF7 and HMEC cells are represented by histograms depicting mean normalised RNA-seq expression. All MCF7 ChIA-PET (ENCODE) and HMEC Hi-C<sup>47</sup> chromatin interactions are represented by black and blue arcs, respectively. NHGRI catalog GWAS SNPs are shown as green ticks. All Oncoarray SNPs (genotyped or imputed) are shown as black ticks and uninterrogated, common SNPs (dbSNP138, EUR MAF > 1%) as red ticks. Features may be examined in detail via exploration of a custom UCSC Genome Browser session accessible via hyperlinks within Supplementary Table 5.

Table 1: Ten novel loci associated with risk of estrogen receptor (ER)-negative breast cancer using meta-analysis of BCAC and
CIMBA data

	<u></u>	~			Nearest			BCAC ER-negati	ve <sup>†</sup>	CIMBA	A BRCA1 mutation	carriers <sup>*</sup>	Meta-analysis	Heterogeneity
Location	SNP	Chr	Position	gene	Alleles"	MAF	OR (95%CI)	P-value	MAF	HR (95%CI)	P-value	P-value	P-value <sup>¥</sup>	
2p23.3	rs200648189	2	24739694	NCOA1	CT/C	0.19	0.94 (0.91-0.97)	4.7x10 <sup>-4</sup>	0.20	0.88 (0.84-0.92)	3.3x10 <sup>-7</sup>	9.7x10 <sup>-9</sup>	2.0x10 <sup>-2</sup>	
6q23.1	rs6569648	6	130349119	L3MBTL3	T/C	0.23	0.93 (0.90-0.95)	4.3x10 <sup>-8</sup>	0.22	0.94 (0.90-0.98)	5.4x10 <sup>-3</sup>	8.3x10 <sup>-10</sup>	0.64	
8p23.3	rs66823261	8	170692	RPL23AP53	T/C	0.23	1.09 (1.06-1.12)	5.6x10 <sup>-9</sup>	0.22	1.02 (0.98-1.07)	0.32	3.3x10 <sup>-8</sup>	3.0x10 <sup>-2</sup>	
8q24.13	rs17350191	8	124757661	ANXA13	C/T	0.34	1.07 (1.04-1.09)	2.0x10 <sup>-8</sup>	0.34	1.08 (1.04-1.12)	1.9x10 <sup>-4</sup>	1.7x10 <sup>-11</sup>	0.81	
11q22.3	rs11374964	11	108345515	KDELC2	G/GA	0.42	0.94 (0.92-0.96)	3.6x10 <sup>-8</sup>	0.43	0.91 (0.88-0.95)	1.3x10 <sup>-6</sup>	4.1x10 <sup>-13</sup>	0.26	
11q22.3	rs74911261	11	108357137	KDELC2	G/A	0.02	0.82 (0.75-0.89)	2.3x10 <sup>-6</sup>	0.02	0.74 (0.65-0.84)	2.0x10 <sup>-6</sup>	5.4x10 <sup>-11</sup>	0.17	
16p13.3	rs11076805	16	4106788	ADCY9	C/A	0.25	0.92 (0.90-0.95)	2.2x10 <sup>-8</sup>	0.25	0.96 (0.92-1.00)	0.073	1.4x10 <sup>-8</sup>	0.14	
18q12.1	rs36194942	18	25401204	CDH2	A/AT	0.30	0.94 (0.91-0.96)	2.5x10 <sup>-7</sup>	0.31	0.95 (0.91-0.99)	1.4x10 <sup>-2</sup>	1.4x10 <sup>-8</sup>	0.50	
19p13.2	rs322144	19	11423703	TSPAN16	C/G	0.47	0.95 (0.93-0.97)	2.4x10 <sup>-5</sup>	0.46	0.92 (0.89-0.96)	3.7x10⁻⁵	7.4x10 <sup>-9</sup>	0.23	
19q12	rs113701136	19	30277729	CCNE1	C/T	0.32	1.07 (1.04-1.09)	1.7x10 <sup>-7</sup>	0.32	1.05 (1.01-1.09)	1.2x10 <sup>-2</sup>	6.8x10 <sup>-9</sup>	0.57	

<sup>#</sup>More common allele listed first, minor allele second; <sup>†</sup>Combined data from 21,468 ER-negative cases and 100,594 controls of European ancestry from the Breast Cancer Association Consortium (BCAC); <sup>‡</sup>Combined data from 18,908 *BRCA1* mutation carriers from the Consortium of Investigators of Modifiers of BRCA1/2 (CIMBA), 9,414 of whom had developed breast cancer; <sup>¥</sup>Test for heterogeneity in effect size for ER-negative disease and overall disease for *BRCA1* mutation carriers

Chr, chromosome; MAF, minor allele frequency; OR, odds ratio per copy of the minor allele; Cl, confidence interval; HR, hazard ratio per copy of the minor allele

Table 2: Previously reported estrogen receptor	(ER)-negative hits: replication using independent data from BCAC and comb	ined
results using all BCAC and CIMBA data		

	SNP				••		IND	EPENDENT REPL	ICATION		ALL A	VAILABLE D		
Location		Chr	Position	Ref	Nearest	Alleles <sup>#</sup>	BCAC	ER-negative (On	coArray)*	В	CAC ER-negati	ve <sup>†</sup>	CIMBA BRCA1 <sup>‡</sup>	
					gene		MAF	OR (95%CI)	P-value	0	PR (95%CI)	P-value	HR (95%CI)	P-value
1q32.1	rs6678914	1	202187176	19	LGR6	G/A	0.41	0.94 (0.91-0.97)	1.1x10 <sup>-4</sup>	0	.92 (0.90-0.94)	2.6x10 <sup>-12</sup>	0.98 (0.95-1.02)	0.31
1q32.1	rs4245739	1	204518842	19	MDM4	A/C	0.26	1.12 (1.09-1.17)	9.2x10 <sup>-11</sup>	1	.14 (1.11-1.16)	3.1x10 <sup>-23</sup>	1.09 (1.04-1.13)	7.3x10⁻⁵
2p24.1	rs12710696	2	19320803	19	MIR4757	C/T	0.37	1.04 (1.00-1.07)	2.5x10 <sup>-2</sup>	1	.06 (1.04-1.09)	6.5x10 <sup>-8</sup>	1.01 (0.98-1.05)	0.49
2p23.2	rs4577244 <sup>‡</sup>	2	29120733	30	WDR43	C/T	0.34	0.93 (0.89-0.96)	9.6x10 <sup>-⁵</sup>	0	.92 (0.90-0.95)	1.5x10 <sup>-9</sup>	0.92 (0.88-0.96)	1.3x10 <sup>-₄</sup>
5p15.33	rs10069690	5	1279790	9,18	TERT	C/T	0.26	1.19 (1.14-1.23)	3.8x10 <sup>-21</sup>	1	.18 (1.15-1.21)	1.5x10 <sup>-35</sup>	1.18 (1.14-1.23)	3.7x10 <sup>-16</sup>
6q25.1	rs3757322 <sup>‡</sup>	6	151942194	29	ESR1	T/G	0.32	1.14 (1.10-1.18)	5.5x10 <sup>-14</sup>	1	.15 (1.12-1.18)	2.8x10 <sup>-31</sup>	1.14 (1.10-1.19)	2.9x10 <sup>-12</sup>
6q25.2	rs2747652 <sup>‡</sup>	6	152437016	29	ESR1	C/T	0.48	0.92 (0.89-0.95)	1.1x10 <sup>-7</sup>	0	.91 (0.89-0.93)	1.9x10 <sup>-18</sup>	1.00 (0.97-1.04)	0.96
13q22.1	rs6562760 <sup>‡</sup>	13	73957681	30	KLF5	G/A	0.24	0.92 (0.88-0.95)	5.0x10 <sup>-6</sup>	0	.92 (0.90-0.95)	8.7x10 <sup>-10</sup>	0.89 (0.86-0.93)	3.5x10 <sup>-7</sup>
16q12.2	rs11075995	16	53855291	19	FTO	T/A	0.30	1.07 (1.03-1.11)	3.3x10 <sup>-4</sup>	1	.09 (1.06-1.12)	1.0x10 <sup>-10</sup>	1.01 (0.97-1.06)	0.49
19p13.11	rs67397200	19	17401404	3,31	ANKLE1	C/G	0.32	1.17 (1.13-1.21)	7.0x10 <sup>-20</sup>	1	.17 (1.14-1.19)	2.7x10 <sup>-37</sup>	1.18 (1.14-1.23)	2.7x10 <sup>-17</sup>
20q11.21	rs2284378	20	32588095	12	RALY	C/T	0.32	0.99 (0.95-1.02)	0.46	1	.03 (1.01-1.06)	1.7x10 <sup>-2</sup>	1.00 (0.97-1.04)	0.81

<sup>#</sup>More common allele listed first, minor allele second; \*Includes Breast Cancer Association Consortium (BCAC) OncoArray data from 9,655 ER-negative cases and 45,494 controls cases and controls not included in previously published studies; <sup>†</sup>Combined data from 21,468 ER-negative cases and 100,594 controls of European ancestry from BCAC, which includes overlapping samples with previous publications for all SNPs; <sup>‡</sup>Combined data from 18,908 *BRCA1* mutation carriers from the Consortium of Investigators of Modifiers of BRCA1/2 (CIMBA), 9,414 of whom had developed breast cancer - includes overlapping samples with previous publications for SNPs rs4577244, rs3757322, rs2747652 and rs6562760

Chr, chromosome; Ref, publication(s) in reference list in which the association was identified; MAF, minor allele frequency; OR, odds ratio per copy of the minor allele; CI, confidence interval; HR, hazard ratio per copy of the minor allele

#### Table 3: Associations for 10 novel and 10 previously reported (and replicated) ERnegative breast cancer susceptibility loci, by triple-negative status (BCAC data only: ER-negative cases<sup>\*</sup>, all controls))

		Triple-neg	ative	Other ER-ne	Heterogeneity	
Location	SNP	OR (95%CI)	P-value	OR (95%CI)	P-value	P-value*
Loci ident	ified by the prese	ent study				
2p23.3	rs200648189	0.95 (0.90-1.00)	4.8x10 <sup>-2</sup>	0.96 (0.91-1.03)	0.24	0.36
6q23.1	rs6569648	0.93 (0.89-0.97)	1.4x10 <sup>-3</sup>	0.93 (0.88-0.98)	5.6x10 <sup>-3</sup>	0.91
8p23.3	rs66823261	1.11 (1.05-1.16)	3.3x10 <sup>-5</sup>	1.12 (1.07-1.19)	2.4x10 <sup>-5</sup>	0.91
8q24.13	rs17350191	1.07 (1.03-1.11)	7.9x10 <sup>-4</sup>	1.07 (1.02-1.12)	4.0x10 <sup>-3</sup>	0.67
11q22.3	rs11374964	0.88 (0.85-0.91)	1.9x10 <sup>-11</sup>	0.99 (0.95-1.04)	0.75	1.5x10 <sup>-5</sup>
11q22.3	rs74911261	0.76 (0.66-0.87)	1.1x10 <sup>-4</sup>	0.98 (0.84-1.13)	0.76	3.0x10 <sup>-2</sup>
16p13.3	rs11076805	0.91 (0.87-0.96)	1.5x10 <sup>-4</sup>	0.95 (0.90-1.00)	4.5x10 <sup>-2</sup>	0.20
18q12.1	rs36194942	0.93 (0.89-0.96)	2.4x10 <sup>-4</sup>	0.92 (0.88-0.97)	9.9x10 <sup>-4</sup>	0.94
19p13.2	rs322144	0.94 (0.91-0.98)	5.9x10 <sup>-3</sup>	0.94 (0.90-0.98)	9.7x10 <sup>-3</sup>	0.68
19q12	rs113701136	1.10 (1.06-1.15)	9.1x10 <sup>-7</sup>	1.07 (1.02-1.12)	4.4x10 <sup>-3</sup>	0.12
Previously	y reported loci (as	ssociations replicat	ed by the pre	esent study)		
1q32.1	rs6678914	0.94 (0.91-0.98)	2.1x10 <sup>-3</sup>	0.91 (0.87-0.95)	2.0x10 <sup>-5</sup>	0.45
1q32.1	rs4245739	1.18 (1.13-1.23)	4.3x10 <sup>-15</sup>	1.04 (1.00-1.10)	7.5x10 <sup>-2</sup>	6.5x10 <sup>-4</sup>
2p24.1	rs12710696	1.07 (1.03-1.11)	1.1x10 <sup>-3</sup>	1.04 (1.00-1.09)	6.1x10 <sup>-2</sup>	0.52
2p23.2	rs4577244	0.90 (0.86-0.94)	5.3x10 <sup>-6</sup>	0.94 (0.89-0.99)	1.9x10 <sup>-2</sup>	0.15
5p15.33	rs10069690	1.28 (1.23-1.33)	2.4x10 <sup>-33</sup>	1.07 (1.02-1.12)	5.4x10 <sup>-3</sup>	5.6x10 <sup>-8</sup>
6q25.1	rs3757322	1.15(1.10-1.19)	4.3x10 <sup>-12</sup>	1.14(1.10-1.20)	4.8x10 <sup>-9</sup>	0.35
6q25.2	rs2747652	0.93(0.89-0.96)	5.7x10 <sup>-5</sup>	0.87(0.83-0.91)	2.9x10 <sup>-10</sup>	9.6x10 <sup>-3</sup>
13q22.1	rs6562760	0.94 (0.90-0.98)	$2.8 \times 10^{-3}$	0.92 (0.87-0.96)	8.8x10⁻⁴	0.46
16q12.2	rs11075995	1.06 (1.02-1.11)	6.5x10 <sup>-3</sup>	1.08 (1.03-1.13)	3.1x10 <sup>-3</sup>	0.81
19p13.11	rs67397200	1.27 (1.22-1.32)	2.0x10 <sup>-32</sup>	1.05 (1.01-1.10)	2.7x10 <sup>-2</sup>	4.7x10 <sup>-10</sup>

<sup>\*</sup>Combined Breast Cancer Association Consortium (BCAC) data from 6,877 triple-negative and 4,467 other ER-negative cases and 83,700 controls; \*ER-negative case-only analysis, by triple-negative status; OR, odds ratio per copy of the minor allele; CI, confidence interval

Legation	CND	Grade	1	Grade	2	Grade	Grade 3		
Location	5NP	OR (95%CI)	P-value	OR (95%CI)	P-value	OR (95%CI)	P-value	P-value*	
Loci ident	ified by the prese	nt study							
2p23.3	rs200648189	1.11 (0.92-1.33)	0.28	0.95 (0.88-1.03)	0.23	0.96 (0.91-1.00)	6.8x10 <sup>-2</sup>	0.70	
6q23.1	rs6569648	0.93 (0.79-1.09)	0.37	0.93 (0.87-0.99)	1.6x10 <sup>-2</sup>	0.94 (0.91-0.98)	3.8x10 <sup>-3</sup>	0.34	
8p23.3	rs66823261	1.13 (0.96-1.34)	0.14	1.12 (1.04-1.19)	1.2x10 <sup>-3</sup>	1.10 (1.05-1.15)	1.3x10 <sup>-₅</sup>	0.11	
8q24.13	rs17350191	1.16 (1.01-1.34)	3.0x10 <sup>-2</sup>	1.05 (0.99-1.11)	0.10	1.09 (1.05-1.12)	4.1x10 <sup>-6</sup>	0.94	
11q22.3	rs11374964	0.91 (0.79-1.04)	0.16	0.99 (0.94-1.05)	0.85	0.93 (0.90-0.96)	1.3x10 <sup>-5</sup>	3.0x10 <sup>-2</sup>	
11q22.3	rs74911261	1.22 (0.81-1.84)	0.35	0.89 (0.73-1.07)	0.21	0.74 (0.65-0.85)	7.4x10 <sup>-6</sup>	6.7x10 <sup>-4</sup>	
16p13.3	rs11076805	0.90 (0.76-1.06)	0.21	0.93 (0.87-0.99)	3.2x10 <sup>-2</sup>	0.92 (0.88-0.95)	4.5x10 <sup>-5</sup>	0.71	
18q12.1	rs36194942	0.97 (0.84-1.13)	0.73	0.93 (0.88-0.99)	2.2x10 <sup>-2</sup>	0.96 (0.92-0.99)	$2.3 \times 10^{-2}$	0.98	
19p13.2	rs322144	0.94 (0.81-1.08)	0.38	0.95 (0.90-1.01)	0.11	0.96 (0.93-1.00)	6.4x10 <sup>-2</sup>	0.48	
19q12	rs113701136	1.02 (0.89-1.18)	0.77	1.06 (1.01-1.13)	3.0x10 <sup>-2</sup>	1.10 (1.06-1.14)	2.5x10 <sup>-7</sup>	0.12	
Previously	/ reported loci (as	sociations replicat	ed by the pr	resent study)					
1q32.1	rs6678914	0.95 (0.83-1.09)	0.46	0.90 (0.85-0.95)	9.3x10⁻⁵	0.92 (0.89-0.95)	1.2x10 <sup>-6</sup>	0.75	
1q32.1	rs4245739	1.02 (0.88-1.19)	0.75	1.05 (0.99-1.12)	8.7x10 <sup>-2</sup>	1.18 (1.14-1.22)	2.5x10 <sup>-18</sup>	4.3x10 <sup>-5</sup>	
2p24.1	rs12710696	1.08 (0.94-1.23)	0.28	1.10 (1.04-1.16)	9.6x10 <sup>-4</sup>	1.04 (1.01-1.08)	1.6x10 <sup>-2</sup>	0.28	
2p23.2	rs4577244	1.02 (0.88-1.20)	0.77	0.95 (0.89-1.01)	9.4x10 <sup>-2</sup>	0.90 (0.86-0.93)	1.2x10 <sup>-7</sup>	4.0x10 <sup>-2</sup>	
5p15.33	rs10069690	0.96 (0.83-1.12)	0.64	1.07 (1.01-1.14)	2.2x10 <sup>-2</sup>	1.21 (1.17-1.26)	1.5x10 <sup>-24</sup>	7.3x10 <sup>-4</sup>	
6q25.1	rs3757322	1.16 (1.01-1.34)	0.04	1.13 (1.07-1.20)	7.5x10 <sup>-6</sup>	1.18 (1.14-1.22)	4.5x10 <sup>-20</sup>	0.16	
6q25.2	rs2747652	0.86 (0.75-0.98)	0.02	0.92 (0.87-0.97)	1.9x10 <sup>-3</sup>	0.90 (0.87-0.93)	1.6x10 <sup>-9</sup>	0.61	
13q22.1	rs6562760	0.98 (0.84-1.15)	0.82	0.92 (0.87-0.98)	$1.4 \times 10^{-2}$	0.91 (0.88-0.95)	1.2x10 <sup>-5</sup>	0.52	
16q12.2	rs11075995	1.16 (1.00-1.35)	4.7x10 <sup>-2</sup>	1.09 (1.02-1.15)	$7.5 \times 10^{-3}$	1.08 (1.04-1.13)	$5.2 \times 10^{28}$	0.42	
19p13.11	rs67397200	1.01 (0.87-1.16)	0.91	1.08 (1.02-1.14)	9.8x10 <sup>-3</sup>	1.22 (1.18-1.26)	5.3x10 <sup>-37</sup>	1.3x10 <sup>-3</sup>	

Table 4: Associations for 10 novel and 10 previously reported (and replicated) ER-negative breast cancer susceptibility loci, by grade (BCAC data only: ER-negative cases<sup>‡</sup>, all controls)

\*Combined Breast Cancer Association Consortium (BCAC) data from 492 grade 1, 3,243 grade 2 and 8,568 grade 3 cases and 82,347 controls; \* ER-negative case-only analysis of BCAC data, by grade (trend test, 1df); OR, odds ratio per copy of the minor allele; CI, confidence interval

# **Online Methods**

#### Study subjects

Supplementary Table 1 summarises the studies from the Breast Cancer Association Consortium (BCAC) that contributed data. The majority were case-control studies. Sixty-eight BCAC studies participated in the ER-negative breast cancer component of the OncoArray, contributing 9,655 cases and 45,494 controls. All studies provided core data on disease status and age at diagnosis/observation, and the majority provided information on clinico-pathological and lifestyle factors, which have been curated and incorporated into the BCAC database (version 6). Estrogen receptor status for most (~70%) cases was obtained from clinical records. After removal of overlapping participants, genotype data were also available from eight GWASs<sup>9,12,16,37,38</sup> (4,480 ER-negative cases and 12,632 controls) and 40 studies previously genotyped using the Illumina iCOGS custom array<sup>20</sup> (7,333 ER-negative cases and 42,468 controls).

A total of 21,468 ER-negative cases were included in the combined analyses. Of those 5,793 had tumours that were also negative for progesterone receptor (PR) and human epidermal growth factor receptor 2 (HER2) and were defined as triple-negative (TN). PR and HER2 status was also obtained predominantly from clinical records. A further 4,217 were positive for PR or HER and were considered non-TN. The remainder had unknown PR or HER status. All participating studies were approved by their appropriate ethics review boards and all subjects provided informed consent.

Subjects included from the Consortium of Investigators of Modifiers of BRCA1/2 (CIMBA) were women of European ancestry aged 18 years or older with a pathogenic variant in *BRCA1*. The majority of the participants were sampled through cancer genetics clinics. Multiple members of the same families were included in some instances. Fifty-eight studies from 24 countries contributed Oncoarray genotype data. After quality control (see below) and removal of overlapping participants with the BCAC OncoArray study, data were available on 15,566 *BRCA1* mutation carriers, of whom 7,784 were affected with breast cancer (Supplementary Table 2). We also obtained iCOGS genotype data on 3,342 *BRCA1* mutation carriers (1,630 with breast cancer) from 54 studies through CIMBA. All mutation carriers provided written informed consent and participated under ethically approved protocols.

#### OncoArray SNP selection

Approximately 50% of the SNPs for the OncoArray were selected as a "GWAS backbone" (Illumina HumanCore), which aimed to provide high coverage for the majority of common variants through imputation. The remaining allocation was selected from lists supplied by each of six disease-based consortia, together with a seventh lists of SNPs of interest to multiple disease groups. Approximately 72k SNPs were selected specifically for their relevance to breast cancer, based on prior evidence of association with overall or subtype-specific disease, with breast density or with breast tissue specific gene expression. Lists were merged, as described previously<sup>34</sup>.

#### Genotype calling and quality control

Details of the genotype calling and quality control (QC) for the iCOGS and GWAS are described elsewhere<sup>19,20,23,30</sup>, and those for OncoArray are described in the Supplementary Note.

#### **Imputation**

Genotypes for ~21M SNPs were imputed for all samples using the October 2014 (Phase 3) release of the 1000 Genomes Project data as the reference panel and Nhap=800. The iCOGS, OncoArray and six of the GWAS datasets were imputed using a two-stage imputation approach, using SHAPEIT<sup>73</sup> for phasing and IMPUTEv2<sup>74</sup> for imputation. The imputation was performed in 5Mb non-overlapping intervals. All subjects were split into subsets of ~10,000 samples, with subjects from the same grouped in the subset. The Breast and Prostate Cancer Cohort Consortium (BPC3) and Breast Cancer Family Registry (BCFR) GWAS performed the imputation separately using MACH and Minimac<sup>75,76</sup>. We imputed genotypes for all SNPs that were polymorphic (MAF>0.1%) in either European or Asian samples. For the BCAC GWAS, data were included in the analysis for all SNPs with MAF>0.01 and imputation r<sup>2</sup>>0.3. For iCOGS and OncoArray we included data for all SNPs with imputation r<sup>2</sup>>0.3 and MAF>0.005.

#### Statistical analyses of BCAC data

Per-allele odds ratios and standard errors were generated for the Oncoarray, iCOGS and each GWAS, adjusting for principal components using logistic regression. The Oncorray and iCOGS analyses were additionally adjusted for country and study, respectively. For the OncoArray dataset, principal components analysis was performed using data for 33,661 SNPs (which included the 2,318 markers of continental ancestry) with a MAF≥0.05 and maximum correlation of 0.1, using purpose-written software (PCcalc; see URLs section) to allow standard calculations to be performed sufficiently rapidly on a very large dataset. We used the first 10 principal components, as additional components did not further reduce inflation in the test statistics. We used nine principal components for the iCOGS and up to 10 principal components for the other GWAS, where this was found to reduce inflation.

OR estimates were derived using MACH for the BCFR GWAS, ProbABEL<sup>77</sup> for the BPC3 GWAS, SNPTEST (see URLs section) for the remaining GWAS and purpose written software for the iCOGS and Oncoarray datasets. OR estimates and standard errors were combined by a fixed effects inverse variance meta-analysis using METAL<sup>39</sup>. This was first done across the eight GWAS, applying genomic control, as described previously<sup>20</sup>. It was then applied (without genomic control) to combine findings from the three BCAC genotyping initiatives (GWAS, iCOGS, OncoArray).

The independence of signals from two variants at 11q22.3 was by fitting the logistic regression models described above with both variants as covariates. This was done separately for iCOGS and OncoArray data and results for each variant combined by meta-analysis.

For selected SNPs we estimated per-allele ORs by ER-status using all available BCAC data for 82,263 cases with known ER status and 87,962 controls from the iCOGS and OncoArray studies. We also estimated the per-allele ORs by TN status (TN versus other ER-negative subtypes) and tumour grade, using available BCAC data for ER-negative cases and corresponding controls. Tests for heterogeneity by subtype were derived by applying logistic regression to cases only. This was done separately for the iCOGS and Oncoarray datasets, adjusted as before, and then combined in a fixed-effects meta-analysis. Multinomial regression was applied to cases only to test a linear trend for grade, with the model constrained so that the difference between grade 1 and 3 was double that for the difference between grade 2 and 3; this method was also used to test for a linear trend with age with ordinal values 1, 2, 3 and 4 representing ages <40, 40-49, 50-59 and  $\geq$ 60, respectively.

#### Statistical analyses of CIMBA data

Associations between genotypes and breast cancer risk for *BRCA1* mutation carriers were evaluated using a 1*df* per allele trend-test (*P*-trend), based on modeling the retrospective likelihood of the observed genotypes conditional on breast cancer phenotypes<sup>36</sup>. This was done separately for iCOGS and OncoArray data. To allow for the non-independence among related individuals, an adjusted test statistic was used which took into account the correlation in genotypes<sup>3</sup>. All analyses were stratified by country of residence and, for countries where strata were sufficiently large (USA and Canada), by Ashkenazi Jewish ancestry. The results from the iCOGS and OncoArray datasets were then pooled using fixed effects meta-analysis. We repeated these analyses modelling ovarian cancer as a competing risk and observed no substantial difference in the results obtained.

The independence of signals from two variants at 11q22.3 was assessed using OncoArray data only, fitting a Cox regression model with per-allele effects for both variants, adjusting for birth cohort, stratified by country of residence and using robust standard errors and clustered observations for relatives. This approach provides valid significance tests of associations, although the HR estimates can be biased<sup>35</sup>.

#### Meta-analysis of BCAC and CIMBA

A fixed effects meta-analysis of results from BCAC and CIMBA was conducted using an inverse variance approach assuming fixed effects, as implemented in METAL<sup>39</sup>. The effect estimates used were the logarithm of the per-allele hazard ratio (HR) estimate for the association with breast cancer risk in *BRCA1* mutation carriers from CIMBA and the logarithm of the per-allele OR estimate for the association with risk of ER-negative breast cancer based on BCAC data, both of which were assumed to approximate the same relative risk. We assessed genomic inflation using common (MAF>1%) GWAS backbone variants. As lambda is influenced by sample size, we calculated lambda1000 to be comparable with other studies.

All statistical tests conducted were two-sided.

#### Definition of known hits

We identified all associations previously reported from genome-wide or candidate analysis at a significance level  $P < 5 \times 10^{-8}$  for overall breast cancer, ER-negative or ER-positive breast cancer, in *BRCA1* or *BRCA2* carriers, or in meta-analyses of these categories. We included only one SNP in any 500kb interval, unless joint analysis provided genome-wide significant evidence (conditional  $P < 5 \times 10^{-8}$ ) of more than one independent signal. Where multiple studies reported associations in the same region, we considered the first reported association unless a later study identified a different variant in the same region that was more strongly associated with breast cancer risk. One hundred and seven previously reported hits were identified, 11 of these through GWAS of ER-negative disease or of breast cancer in *BRCA1* mutation carriers, or reported as more strongly associated with ER-negative breast cancer. These are listed in Table 2. The other 96 previously reported hits are listed in Supplementary Table 10.

# Definition of new hits

To search for novel loci, we assessed all SNPs excluding those within 500kb of a known hit. This identified 206 SNPs in nine regions that were associated with disease risk at  $P < 5x10^{-8}$  in the meta-analysis of BCAC ER-negative breast cancer and CIMBA *BRCA1* mutation carriers. The SNP with lowest p-value from this analysis was considered the lead SNP. No additional loci were detected from the analysis of BCAC data only. Imputation quality, as assessed by the IMPUTE2 imputation r<sup>2</sup> in the Oncoarray dataset, was ≥0.89 for the 10 lead SNPs reported (Supplementary Table 3).

# Candidate causal SNPs

To define the set of potentially causal variants at each of the novel susceptibility loci, we selected all variants with p-values within two orders of magnitude of the most significant SNP at each of the 10 novel loci. This is approximately equivalent to selecting variants whose posterior probability of causality is within two orders of magnitude of the most significant SNP<sup>40,41</sup>. This approach was applied to identify potentially causal variants for the signal given by the more frequent lead SNP at 11q22.3 (rs11374964). A similar approach was applied for the rarer lead SNP at this locus (rs74911261), but based on p-values from analyses adjusted for rs11374964.

#### Proportion of familial risk explained

The relative risk of ER-negative breast cancer for the first degree female relative of a woman with ER-negative disease has not been estimated. We therefore assumed that the 2-fold risk observed for overall disease also applied to ER-negative disease. In order to estimate the proportion of this explained by the 125 variants associated with ER-negative disease, we used minor allele frequency and OR estimates from the OncoArray-based genotype data and applied the formula:  $\sum_{i=1}^{n} \frac{(1-n_i)(\beta_i^2 - \tau_i^2)}{(1-n_i)}$ where *n* is the minor allele frequency for variant *i*. *B* is

 $\sum_i p_i (1 - p_i)(\beta_i^2 - \tau_i^2)/\ln(\lambda))$ , where  $p_i$  is the minor allele frequency for variant *i*,  $\beta_i$  is the log(OR) estimate for variant *i*,  $\tau_i$  is the standard error of  $\beta_i$  and  $\lambda$ =2 is the assumed overall familial relative risk.

The corresponding estimate for the FRR due to all variants is the *frailty scale* heritability, defined as  $h_f^2 = \sum_i 2p_i(1-p_i)\gamma_i^2$ , where the sum over all variants and  $\gamma_i$  is the true relative risk conferred by variant *i*, assuming a log-additive model. We first obtained the estimated heritability based on the full set of summary estimates using LD Score Regression<sup>68</sup>, which derives a heritability estimate on the observed scale. We then converted this to an estimate on the fraility scale using the formula  $h_f^2 = \frac{h_{obs}^2}{P(1-P)}$ , where *P* is the proportion of samples in the population that are cases.

Proportion of polygenic risk-modifying variance explained for *BRCA1* carriers. The proportion of the variance in the polygenic frailty modifying risk in BRCA1

carriers explained by the set of associated SNPs was estimated by  $\sum_i \ln c_i / \sigma^2$ , where

c<sub>i</sub> is the squared estimated coefficient of variation in incidences associated with  $SNP_i^{78}$  and  $\sigma^2$  is the total polygenic variance, estimated from segregation data<sup>79</sup>.

# In Silico Annotation of Candidate Causal variants

We combined multiple sources of *in silico* functional annotation from public databases to help identify potential functional SNPs and target genes, based on previous observations that breast cancer susceptibility alleles are enriched in cisregulatory elements and alter transcriptional activity<sup>28,80-82</sup>. The influence of candidate causal variants on transcription factor binding sites was determined using the ENCODE-Motifs resource<sup>43</sup>. To investigate functional elements enriched across the region encompassing the strongest candidate causal SNPs, we analysed chromatin biofeatures data from the Encyclopedia of DNA Elements (ENCODE) Project<sup>42</sup>, Roadmap Epigenomics Projects<sup>44</sup> and other data obtained through the National Center for Biotechnology Information (NCBI) Gene Expression Omnibus (GEO) namely: Chromatin State Segmentation by Hidden Markov Models (chromHMM), DNase I hypersensitive and histone modifications of epigenetic markers H3K4, H3K9, and H3K27 in Human Mammary Epithelial (HMEC) and myoepithelial (MYO) cells. T47D and MCF7 breast cancer cells and transcription factor ChIP-seg in a range of breast cell lines (Supplementary Table 6). To identify the SNPs most likely to be functional we used RegulomeDB<sup>45</sup>, and to identify putative target genes, we examined potential functional chromatin interactions between distal and proximal regulatory transcription-factor binding sites and the promoters at the risk regions, using Hi-C data generated in HMECs<sup>47</sup> and Chromatin Interaction Analysis by Paired End Tag (ChiA-PET) in MCF7 cells. This detects genome-wide interactions brought about by, or associated with, CCCTCbinding factor (CTCF), DNA polymerase II (POL2), and Estrogen Receptor (ER), all involved in transcriptional regulation<sup>47</sup>. Annotation of putative *cis*-regulatory regions and predicted target genes used the Integrated Method for Predicting Enhancer Targets (IM-PET)<sup>46</sup>, the "Predicting Specific Tissue Interactions of Genes and Enhancers" (PreSTIGE) algorithm<sup>48</sup>, Hnisz<sup>51</sup> and FANTOM<sup>49</sup>. Intersections between candidate causal variants and regulatory elements were identified using Galaxy, BedTools v2.24 and HaploReg v4.1, and visualised in the UCSC Genome Browser. Publically available eQTL databases including Gene-Tissue Expression (GTEx;<sup>50</sup> version 6, multiple tissues) and Westra<sup>52</sup> (blood), were queried for candidate causal variants.

#### eQTL analyses

Expression quantitative trait loci (eQTL) analyses were performed using data from The Cancer Genome Atlas (TCGA) and Molecular Taxonomy of Breast Cancer International Consortium (METABRIC) projects<sup>59,60</sup>.

The TCGA eQTL analysis was based on 79 ER-negative breast tumors that had matched gene expression, copy number, and methylation profiles together with the corresponding germline genotypes available. All 79 individuals were of European ancestry as ascertained using the genotype data and the Local Ancestry in adMixed Populations (LAMP) software package (LAMP estimate cut-off >95% European)<sup>83</sup>. Germline genotypes were imputed into the 1000 Genomes reference panel (October 2014 release) using IMPUTE2<sup>75,84</sup>. Gene expression had been measured on the Illumina HiSeq 2000 RNA-Seq platform (gene-level RSEM normalized counts<sup>85</sup>), copy number estimates were derived from the Affymetrix SNP 6.0 (somatic copy
number alteration minus germline copy number variation called using the GISTIC2 algorithm<sup>86</sup>), and methylation beta values measured on the Illumina Infinium HumanMethylation450, as previously described<sup>59</sup>. Primary TCGA eQTL analysis focused on all potentially causal variants in the 10 new regions associated with breast cancer risk in the meta-analysis of ER-negative cases and controls from BCAC and *BRCA1* mutation carriers from CIMBA. We considered all genes located up to 1 Mb on either side of each of these variants. The effects of tumor copy number and methylation on gene expression were first removed using a method described previously<sup>58</sup>, and eQTL analysis was performed by linear regression as implemented in the R package Matrix eQTL<sup>87</sup>.

The METABRIC eQTL analysis was based on 135 normal breast tissue samples resected from breast cancer patients of European ancestry. Germline genotyping for the METABRIC study was also done on the Affymetrix SNP 6.0, and ancestry estimation and imputation for this data set was conducted as described for TCGA. Gene expression in the METABRIC study had been measured using the Illumina HT12 microarray platform and we used probe-level estimates. As for TCGA, we considered all genes in 10 regions using Matrix eQTL.

We also performed additional eQTL analyses using the METABRIC data set for all variants within 1 Mb of *L3MBTL3* and *CDH2* and the expression of these specific genes.

#### **Global Genomic Enrichment Analyses**

We performed stratified LD score regression analyses<sup>68</sup> for ER- breast cancer using the summary statistics based on the meta-analyses of OncoArray, GWAS, iCOGS and CIMBA. We used all SNPs in the 1000 Genomes Project phase 1 v3 release that had a minor allele frequency > 1% and an imputation quality score R<sup>2</sup>>0.3 in the OncoArray data. LD scores were calculated using the 1000 Genomes Project Phase 1 v3 EUR panel. Further details are provided in the Supplementary Note.

We tested the differences in functional enrichment between ER-positive and ERnegative subsets for individual features through a Wald test, using the regression coefficients and standard errors for the two subsets based on the models described above. Finally, we assessed the heritability due to genotyped and imputed SNPs<sup>70</sup> and estimated the genetic correlation between ER-positive and ER-negative breast cancer<sup>69</sup>. The genetic correlation analysis was restricted to the ~1M SNPs included in HapMap 3.

# Pathway Enrichment Analyses (see also the Supplementary Note)

#### The pathway gene set database

Human\_GOBP\_AllPathways\_no\_GO\_iea\_January\_19\_2016\_symbol.gmt (GeneSets; see URLs section)<sup>61</sup>, was used for all analyses. Pathway size was determined by the total number of genes in the pathway to which SNPs in the imputed GWAS dataset could be mapped. To provide more biologically meaningful results, and reduce false positives, only pathways that contained between 10 and 200 genes were considered.

SNPs were mapped to the nearest gene within 500kb; those that were further than 500 kb away from any gene were excluded. Gene significance was calculated by

assigning the lowest p-value observed across all SNPs assigned to a gene<sup>63,64</sup>, based on the meta-analysis of BCAC and CIMBA data described above.

The gene set enrichment analysis (GSEA)<sup>61</sup> algorithm, as implemented in the GenGen package (see URLs section)<sup>62,63</sup> was used to perform pathway analysis. Briefly, the algorithm calculates an enrichment score (ES) for each pathway based on a weighted Kolmogorov-Smirnov statistic<sup>62</sup>. Pathways that have most of their genes at the top of the ranked list of genes obtain higher ES values.

We defined an ES threshold (ES≥0.41) to yield a true-positive rate (TPR) of 0.20 and a false-positive rate (FPR) of 0.14, with true-positive pathways defined as those observed with false discovery rate (FDR)<0.05 in a prior analysis carried out using the analytic approach defined above applied to iCOGS data for ER-negative disease.

To visualize the pathway enrichment analysis results, an enrichment map was created using the Enrichment Map (EM) v 2.1.0  $app^{61}$  in Cytoscape v3.30<sup>88</sup>, applying an edge-weighted force directed layout. To measure the contribution of each gene to enriched pathways and annotate the map, we reran the pathway enrichment analysis multiple times, each time excluding one gene. A gene was considered to drive the enrichment if the ES dropped to zero or less (pathway enrichment driver) after it was excluded. Pathways were grouped in the map if they shared >70% of their genes or their enrichment was driven by a shared gene.

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rowser	variant chron 2_24739694_C_CT	n position locus 2 24739694 2_24739694_C_CT	rsID rs200648189	TF_motifs(delta TF-ChIP Historie_modific ChromHMM_enhChromHMM_pro Open_chromatinRegu	6	scGWAS_traits	Overlapping_Re	NCOA1 67651	INTERGENIC	nceQTL_target_all eQTL_GTEx.breaeQTL_TCGA	eQTL_METABRIC Predicted_target_gene DNA/C27.CT:-:0.0154745 NCOA1:MCF7:ChIA-PET
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rowser	2_25085268_T_A	2 25085268 2_24739694_C_CT 2 26086277 2_24739694_C_CT	rs2384055	AridSal+, Foxa_disc2 - Next_t1_RPDNt_dect1_T2E51=Med21+	7		ADCY3	ADCY3 56787	INTRON	ADCY3, DNAJC27, DNAJC27-AS1, RPADCY3-A0.0147104, MFSD2 ADCY3, CENEO, DNAJC27, DNAJC27, ADCY3, do 015242, MFSD2	8: NCDA1:A0.0045141
rowser	2_25089594_C_A	2 25089594 2_24739694_C_CT 2 25089594 2_24739694_C_CT	rs35177510	Not-Ipprovi_decip.tor1::Nerg+	7		ADCY3	ADCY3/52461	INTRON	ADC Y3, CENPO, DNAJC27, DNAJC27 ADC Y3C: -0.015543, MYSD28 ADC Y3, DNAJC27, DNAJC27 -AS1, RPADC Y3:A: -0.015643, MYSD28	INCOALC:-0.0045199 ADCY3/MCF7:CNA-PET
rowser :	2_25001721_T_TA 2_25001869_A_G	2 25091721 2_24739694_C_CT 2 25091869 2_24739694_C_CT	rs35609705 rs11683929	Mrg_1 -,2ID +	6		ADCY3 ADCY3	ADCY3 50334 ADCY3 50186	INTRON	ADCY3.TA:-:0.018074,MF5D2 ADCY3,DNAJC27,DNAJC27-AS1,RPADCY3:G:-:0.0158047,MF5D2	8: NCD41:TA:-0.0048031 8: NCD41:G:-0.0045227
rowser	2_25003151_C_T	2 25093151 2_24739694_C_CT 2 25094003 2 24739694 C_CT	rs13019149 rs11433494	Zbitdj-	6		ADCY3 ADCY3	ADCY3 48904 ADCY3 48952	INTRON	ADCY3,DNAJC27,DNAJC27-AS1,RPADCY3.T0.0158397,MF5D21 C2vr644-ATT-+-0.0057104-AD	B:NCDA1:T:-0.0045227 CNCDA1:4T:-0.0065397
rowser	2_25096892_A_T	2 25096692 2_24739694_C_CT	rs11892869	TCF12_disc5 +,Z MCF_10A;E2F4,J BRST.MYOEP;H;BRST.MYOEP;Enhanoar	4		ADCY3	ADCY3 45363	INTRON	ADCY3,CENPOJADCY3,DNAJC27,DNAJC27-AS1,RP11-443B20.1	NC0A1:T:-0.0082746,DNM1EFR3B:HCC1954:IM-PET_CENPO:HCC1954
rowser	2_25098062_1_C 2_25097072_G_C	2 25096952 2_24739694_C_CT 2 25097072 2_24739694_C_CT	rs7580081	NF-kappaB_discsMCF_10A;FOS;MCF_10A;MYC;MCBRS1.MYOEP[cnhancer] ATF4]+,AhR::AmMCF_10A;FOS;MCF_10A;MYC;MCBRS1.HMEC;Enhancer;BRS1.vHM HMEC;dnase;HM	4		ADCY3 ADCY3	ADCY3 45103 ADCY3 44983	INTRON	ADCY3,CENPOJADCY3,DNAJC27,DNAJC27-AS1,RP11-443820.1 ADCY3,CENPOJADCY3,DNAJC27,DNAJC27-AS1,RP11-443820.1	NCDA1:C-30.0083688,0NM/CENPOHCC1954/Hist2,,EPR38/HCC1954/M NCDA1:C-30.0078969,0NM/EFR38/HCC1954/M-PETCENPO/HCC1954
rowser	2_25097644_A_G 2_25097939 T_C	2 25097644 2_24739694_C_CT 2 25097939 2 24739694 C CT	rs13407913 rs13410999	CAC-binding-prot MCF-7;ERbata, MCF-7;SPDEF GR knownfil-HDAC2 disc3i+, Pax-8 2i+	1d 5		ADCY3 ADCY3	ADCY3 44411 ADCY3 44116	INTRON	ADCY3,CENPOJADCY3,DNAJC27,DNAJC27-AS1,RP11-443B20.1 ADCY3,CENPOJADCY3,DNAJC27,DNAJC27-AS1,RP11-443B20.1	NCOA1:G:-0.0082746,DNM EFR3B:HCC1954;IM-PET_CENPO:HCC1954 NCOA1:C:-0.0082746,DNM1CENPO:HCC1954;Hrisz
rowser	2_25098859_A_G	2 25098859 2_24739694_C_CT	196722022	First dark Die bereite De bereite De bereite Orte dark 1800 in di 1800 in di De			ADCY3	ADCY3 43196	INTRON		NCDA1:G-0.0175907,DNM CENPO HCC1954 Hrisz
rowser	2_25100167_C_G	2 25100167 2_24739694_C_CT 2 25100167 2_24739694_C_CT	rs2384057	Egr-1_mac2, Ets, Ets, ets, ets, ets, ets, ets, ets, ets, e	2b		ADCY3	ADCY3 41888	INTRON	ADCY3,DNAJC27,DNAJC27-AS1,RPADCY36:-0.0179219	NCDA1:C-0.0082746,0NM1343C-0.0356562,08A0243C-0.0446517 NCDA1:G-0.0038145
rowser	2_25100338_C_T 2_25100738_C_A	2 25100338 2_24739694_C_CT 2 25100738 2_24739694_C_CT	rs2384059 rs10865315	MCF-7;SPDEF MCF-7;H3K4me1 AP-4_1 -,AP-4_3 MCF_10A,FOS	5 3a		ADCY3 ADCY3	ADCY3 41717 ADCY3 41317	INTRON	ADCY3,CENPO(ADCY3,DNAJC27,DNAJC27-AS1,RP11-443B20.1 ADCY3,CENPO,DNAJC27,DNAJC27 ADCY3:A:-0.0176854	NCDA1:T:-0.0082631,DNM1ADCY3:MCF7:CNA-PET NCDA1:A:-0.0045205 ADCY3:MCF7:CNA-PET
rowser	2_25101092_G_A	2 25101092 2_24739694_C_CT 2 25103957 2 24739694_C_CT	rs2033855 rs7591460	Hoxb13 +,Hoxd10 + HDAC2 disc3la NRSE known2la NRSE known3la Rhov111a TATA known6l, TATA known6l, TEIM,	1f 5		ADCY3 ADCY3	ADCY3 40963 ADCY3 38088	INTRON	ADCY3,CENPO,DNAJC27,DNAJC27 ADCY3:A:-0.0178972 ADCY3 AS31 2 CENPO DNA IC27 DNADCY3:C:-0.0167899 MFSD21	NCDA1:A:-0.0045227 ADCY3:MCF7:CNA-PET 8:NCDA1:C:-0.0042332
rowser	2_25104679_AGT_A	2 25104679 2_24739694_C_CT	rs3037312	fibroblaat_of_marBRST.MYOEP.H3K4ma1 MCF-7;dnase			ADCY3	ADCY3 37376	INTRON	ADCY3:A:-0.0069134,MFSD2	8: NCDA1:A0.0045227
rowser	2_25105021_C_1 2_25107589_G_C	2 25105921 2_24739694_C_C1 2 25107589 2_24739694_C_CT	rs11675198	DMR(5)+ TATA_diao4 +	6		ADCY3 ADCY3	ADCY3/36134 ADCY3/34466	INTRON	ADCY3,ASXL2,DNAJC27,DNAJC27-ADCY3:1:-0.006/162,MISD2 ADCY3,DNAJC27,DNAJC27-AS1,RPADCY3:C:-0.0068633,MISD2	B:NCDA1:1:-0.0045227 B:NCDA1:C:-0.0045227
rowser	2_25107712_CT_C 2_25107759_C_T	2 25107712 2_24739694_C_CT 2 25107759 2_24739694_C_CT	rs36007978 rs11688663	Irf_known0 -,RXRA_diac4 -,TR4_diac2 +,p300_diac5 - GLI -HEY1_diac2 -,KIH -,NRSF_diac9 - HMEC;dnase	5		ADCY3 ADCY3	ADCY3 34343 ADCY3 34296	INTRON	ADCY3.C::0.0068569,MF5D21 ADCY3.ASXL2,CENPO,DNAJC27,DNADCY3.T::0.0068569,MF5D21	8:NCDA1:C:-0.0045227 8:NCDA1:T:-0.0045227
rowser	2_25108197_T_C 2_25109317_G_A	2 25108197 2_24739694_C_CT 2 25109317 2 24739694 C CT	rs1865689 rs7605335	MCF-7;SPDEF BDP1 disc3i-Foxi1+Foxi1-Foxi1 11+Pax-4 11-RREB-1 21+.SP1 disc3i-UF1H3BETAI-	7		ADCY3 ADCY3	ADCY3 33858 ADCY3 32738	INTRON	ADCY3,ASXL2,CENPO,DNAJC27,DNADCY3;C::0.0068505,MF5021 ADCY3,ASXL2,DNAJC27,DNAJC27,ADCY3;A::0.0067226,MF5021	8:NCDA1:C:-:0.0045227 8:NCDA1:A:-:0.0045279
rowser :	2_25115243_A_G 2_25117215_A_G	2 25115243 2 24739694 C CT 2 25117215 2 24739694 C CT	rs10165451 rs28836469	BDP1_disc3 +,LUN-1 - MCF-7H3K4me1	6		ADCY3 ADCY3	ADCY3 26812 ADCY3 26840	INTRON	ADCY3, DNAJC27, DNAJC27-AS1, RP11-443820.1 ADCY3, DNAJC27, DNAJC27-AS1, RP11-443820.1	NCDA1:G:-:0.0116802,UBXN2A:G:+:0.0305978 NCDA1:G:-:0.0116913,UBXN2A:G:+:0.03057
rowser	2_25118885_C_T	2 25118885 2_24739694_C_CT	rs6545800	Foxa_diac5[+,Pou212_known2]-,TATA_known2[+,TATA_known4]+,TATA_known5[+	6	Inflammatory_bo	ADCY3	ADCY3 23170	INTRON	ADCY3,CENPO(ADCY3,DNAJC27,DNAJC27-AS1,RP11-443B20.1	NCDA1:T0.0116913,UBXN2A:T:+:0.03057
rowser	2_25120086_C_1 2_25120713_G_C	2 25120086 2_24739694_C_CT 2 25120713 2_24739694_C_CT	rs6723803	LXR_3(-NRSF_dMCF-7;SPDEF	5		ADCY3	ADCY3 21369 ADCY3 21342	INTRON	ADC Y3, CENPO(ADC Y3, DNAJC27, DNAJC27, AS1, RP11-443820.1 ADC Y3, CENPO(ADC Y3, DNAJC27, DNAJC27, AS1, RP11-443820.1	NCDA1:1-00116913,088424:1+0.03057 NCDA1:C0.0116913,UBXN24:C++0.03057
rowser	2_25121125_C_A 2_25122323_A_C	2 25121125 2_24739694_C_C1 2 25122323 2_24739694_C_CT	rs6718510	ERapha-a_disc4 MCF-7/SPDEF ERapha-a_known4 +,Ear2 +,GR_disc1 +	5		ADCY3 ADCY3	ADCY3/20030 ADCY3/19732	INTRON	ADCY3, CENPOJADCY3, UNAJC27, UNAJC27-AS1, RP11-443820.1 ADCY3, DNAJC27, DNAJC27-AS1, RP11-443820.1	NCDA1:A0.0992671,UBKN2A:A+0.0330707,H08P18:A0.046318 NCDA1:C0.0116939,UBKN2A:C+0.0305716
rowser	2_25122324_A_G 2_25122840_C_G	2 25122324 2_24739694_C_CT 2 25122840 2_24739694_C_CT	rs6718511 rs4077678	NRSF_diac3 +,NRSF_known1 +,Pax-5_diac1 + KAP1_diac2 -	5 7		ADCY3 ADCY3	ADCY3 19731 ADCY3 19215	INTRON	ADCY3,DNAJC27,DNAJC27-AS1,RP11-443820.1 ADCY3,CENPO(ADCY3,DNAJC27,DNAJC27-AS1,RP11-443820.1	NCDA1:G:-0.0116939,UBXN2A:G:+:0.0305716 NCDA1:G:-0.0116939,UBXN2A:G:+:0.0305716
rowser	2_25123463_C_G	2 25123463 2_24739694_C_CT 2 25124348 2 24739694_C_CT	rs3903070 rs6545806	MCF-7;CTCF HMCLIV 2/4 Nev2 11/4 Nev2 8/4 Nev3 4/4	5		ADCY3 ADCY3	ADCY3 18592 ADCY317707	INTRON	ADCY3,CENPO(ADCY3,DNAJC27,DNAJC27-AS1,RP11-443820.1 ADCY3,DNAJC27,DNAJC27-AS1,RP11-443820.1	NCDA1:G:-0.0116939,UBXN2A:G:+:0.0305716 NCDA1:A:-0.0117273,UBXN2A:A:+:0.0304589
rowser :	2_25124563_T_C 2_25125075_T_G	2 25124563 2_24739694_C_CT 2 25125075 2 24739694_C_CT	rs1550110 rs7563204	LUN-1 +,Mui1_diac1 -	5		ADCY3 ADCY3	ADCY3 17492 ADCY3 16980	INTRON	ADCY3, DNAJC27, DNAJC27-AS1, RP11-443820.1 ADCY3, DNAJC27, DNAJC27-AS1, RP11-443820.1	NCDA1:C:-0.0116891,UBXN2A:C:+0.0305697 NCDA1:G:-0.0116913 UBXN2A:C:+0.03057
rowser	2_25125585_C_T	2 25125585 2_24739694_C_CT	rs876186	Hmx_2 -Nkx3_3 -,PRDM1_disc1 +,PU.1_disc1 +	6		ADCY3	ADCY3 16470	INTRON	ADCY3,DNAJC27,DNAJC27-AS1,RP11-443820.1	NCOA1:T:-:0.0116913,UBXN2A:T:+:0.03057
rowser	2_25126230_A_G 2_25126328_G_C	2 25126230 2_24739694_C_CT 2 25126328 2_24739694_C_CT	rs6726199	BHLHE40_disc2[+,ELF1_disc3]+,NRSF_disc9]+	11		ADCY3	ADCY3 15825 ADCY3 15727	INTRON	ADCY3,CENPO(ADCY3,DNAJC27,DNAJC27,AS1,RP11-443820.1 ADCY3,CENPO(ADCY3,DNAJC27,DNAJC27,AS1,RP11-443820.1	NCOA1:0:-0.0116913;0800 DNAG227-85130CP7-CHA-PE1,,DNAG22730 NCOA1:C:-0.0116913;08XN DNAJC27:MCF7:CHA-PET,,DNAJC27-AS130
rowser	2_25126715_C_1 2_25127006_CAGAG_C	2 25120715 2_24739694_C_CT 2 25127006 2_24739694_C_CT	rs10566562	HDAC2_disc6]-,Irf_disc3[-,Nanog_disc2]+,p300_disc5[-			ADCY3	ADCY3 15049	INTRON	ADC13,CENPORDC13,DIAADC27,0R43C27-463,RP11-4438201 ADCY3:C::0.0074356,MF5D21	B:NCDA1::-:-:0.0055166 DNAJC27:MCF7:CHA-PET,,,DNAJC27-AS1M B:NCDA1:C:-:0.0055166 DNAJC27:MCF7:CHA-PET,,,DNAJC27-AS1M
rowser	2_25127394_A_G 2_25127614_A_G	2 25127394 2_24739694_C_CT 2 25127614 2_24739694_C_CT	rs34697209 rs6717671	Evi-1_4 +,Foxp1 -HDAC2_disc6 +,Irf_disc3 +,Irf_known6 -,Pax-5_disc3 +,RXRA_disc4 -,2(p106)-,p300_dis HNF4_known6 +	6 7		ADCY3 ADCY3	ADCY3 14661 ADCY3 14441	INTRON	ADCY3,DNAJC27,DNAJC27-AS1,RPADCY3;6:-0.0078437,MFSD2 ADCY3,DNAJC27,DNAJC27-AS1,RP11-443820.1	B NCDA1:6:-0.0065119 DNAJC27-AS1:MCF7:ChiA-PET,,,DNAJC27-M NCDA1:6:-0.0116913,UBXN DNAJC27:MCF7:ChiA-PET,,,DNAJC27-AS1:M
rowser	2_25128351_C_G 2_25128719_A_G	2 25128351 2_24739694_C_CT 2 25128719 2 24739694 C CT	rs6706316 rs6721750	Arid3a_2(+.Dobox4(+.Fox(Fox(1)+.HNF1_5(HNF1_6(HNF1_7)- TR4_disc3(+	6		ADCY3 ADCY3	ADCY3 13704 ADCY3 13336	INTRON	ADCY3,CENPO(ADCY3,DNAJC27,DNAJC27-AS1,RP11-443820.1 ADCY3,CENPO(ADCY3,DNAJC27,DNAJC27-AS1,RP11-443820.1	NCDA1:G:-0.0116913,UBXN2A:G:+:0.03057 NCDA1:G:-0.0116913,UBXN2A:G:+:0.03057
rowser	2_25128730_T_C 2_25129166 A_ACT	2 25128730 2_24739694_C_CT 2 25129166 2 24739694 C CT	rs6724772 rs10651478	AP-4_2 +AP-4_3 +Ascl2 +,E2A_2 +,LBP-1_2 +,Nanog_disc3 +Nix3_3 -,RREB-1_2 -,TCF12_known1 +	6		ADCY3 ADCY3	ADCY3 13325 ADCY3 12889	INTRON	ADCY3,CENPOJADCY3,DNAJC27,DNAJC27-AS1,RP11-443B20.1	NCDA1:C:-:0.0116913,UBXN2A:C:+:0.03057 NCDA1:ACT:-:0.0112739.UBXN2A:ACT:+:0.0268574
rowser	2_25129473_A_G	2 25129473 2_24739694_C_CT	rs6725517	AP-2_known1)+,BCL_disc10(+,BDP1_disc3)-,CAC-binding-protein(-,CCNT2_disc2)-,CTCF_disc5)+,Egr-1_d	5		ADCY3	ADCY3 12582	INTRON	ADCY3,DNAJC27,DNAJC27-AS1,RPADCY3:6:-0.0080013,MFSD2	B NCOA1:G0.0065119
rowser	2_25130073_C_T	2 25130073 2_24739694_C_CT 2 25130073 2_24739694_C_CT	rs7585460	CTCF_dsc4+_EEMCF_10AFOS.NBRST.HMEC;H3K4me1 HMEC;dnase	5		ADCY3	ADCY3 12288 ADCY3 11982	INTRON	ADCY3, DNAJC27, DNAJC27-AS1, P11-443820.1	NCDA1:T-:0.0117488,UBNA2A:T+:0.0311296
rowser rowser	z_25130440_A_T 2_25130451_A_G	z 25130440 2_24739694_C_CT 2 25130451 2_24739694_C_CT	rs11689543 rs11689546	CICE_dsc10+,EMCF_10A;STAT3 BDP1_dsc1+,G/MCF_10A;STAT3	5 1f		ADCY3 ADCY3	ADCY3 11615 ADCY3 11604	INTRON	ADCY3, DNAJC27, DNAJC27-AS1, RPMFSD28:T:+:0.0459888 ADCY3, CENPOJADCY3, DNAJC27, DMFSD28:G:+:0.0459888	NCDA1:T:-0.0117109,UBXN2A:T:+:0.0304424 NCDA1:G:-0.0117109,UBXN2A:G:+:0.0304424
rowser	2_25130462_T_G 2_25130542_A_C	2 25130462 2_24739694_C_CT 2 25130542 2_24739694 C CT	rs10200566 rs10198275	Bach1 -,GATA_diMCF_104;STAT3 Anrt_1 +,Anrt_2 +,BHLHE40_disc1 +,BHLHE40_known1 +,HMG-IY_21+.Hoxd101Irf known5iMw <sup>-</sup> known	1f 1f		ADCY3 ADCY3	ADCY3 11593 ADCY3 11513	INTRON	ADCY3,CENPOJADCY3,DNAJC27,DNAJC27-AS1,RP11-443820.1 ADCY3,CENPOJADCY3,DNAJC27,DNAJC27-AS1,RP11-443820.1	NCDA1:G:0.0116913,UBXN2A:G:+:0.03057 NCDA1:C:-0.0116913,UBXN2A:C:+:0.03057
rowser rowser	2_25130502_A_G 2_25130684_C_T	2 25130592 2_24739694_C_CT 2 25130684 2 24739694_C_CT	rs10198356 rs10188242	Ets_disc7(+ZP)161_2(+ GR_disc4)_TATA_disc1.THAP1_disc2.VV1_risc1L_VV1_risc2L_VV446*C_7.docsauce	7		ADCY3 ADCY3	ADCY3 11463 ADCY3 11974	INTRON	ADCY3, DNAJC27, DNAJC27-AS1, RP11-443820.1 ADCY3, DNAJC27, DNAJC27-AS1, RP11-443820.1	NCDA1:G:-0.0116913,UBXN2A:G:+0.03057 NCDA1:T:-0.0116913,UBXN2A:T:+0.03057
rowser	2_25130907_T_C	2 25130907 2_24739894_C_CT 2 25130907 2_24739694_C_CT	rs6733224	Pars 5 (Kound) - MCF-7 Promoter	1f		ADCY3	ADCY3[113/1 ADCY3[11148	INTRON	ADCY3, CENPO(ADCY3, DNAJC27, NB), RF11-443820.1 ADCY3, CENPO(ADCY3, DNAJC27, AS1, RP11-443820.1	NCDA1C0.0116913,UBN2A:C+0.03057
rowser rowser	z_25130920_A_G 2_25131161_T_C	z 25130920 2_24739694_C_CT 2 25131161 2_24739694_C_CT	rs6730191 rs6736210	MCF-7;Promoter ELF1_disc3(+,HNF4_disc1)-,RXRA_known8)-,Ztx(+ MCF-7;Promoter	7 6		ADCY3 ADCY3	ADCY3 11135 ADCY3 10894	INTRON	ADCY3, DNAJC27, DNAJC27-AS1, RP11-443820.1 ADCY3, DNAJC27, DNAJC27-AS1, RP11-443820.1	NCDA1:6:0.0116913,UBXN2A:6:+:0.03057 NCDA1:C:-0.0116913,UBXN2A:C:+:0.03057
rowser	2_25131170_C_G 2_25131287_C_T	2 25131170 2_24739694_C_CT 2 25131287 2_24739694 C_CT	rs6718628 rs6545813	AP-2_known1 + MCF-7;Promoter DMRT2 -,DMRT3 -,DMRT4 -,Pou212_known2 +,Sox_;MCF-7;Enhancer HMF:dnpse	7 5		ADCY3 ADCY3	ADCY3 10885 ADCY3 10768	INTRON	ADCY3, DNAJC27, DNAJC27-AS1, RP11-443820.1 ADCY3, DNAJC27, DNAJC27-AS1, RP11-443820.1	NCDA1:G:-0.0116913,UBXN2A:S:+0.03057 NCDA1:T:-0.0116913,UBXN2A:T:+0.03057
rowser	2_25131316_A_G	2 25131316 2_24739694_C_CT 2 25131986 2 24739694_C_CT	rs6545814	AP-1_disc4(+Jk-2_3)+.NF-AT)+.Sox_1)+ MCF-7;Enhancer HMF;dnase Exxe_disc5(a	1f	Body_mass_inde	ADCY3	ADCY3 10739	INTRON	ADCY3, CENPOJADCY3, DNAJC27, DNAJC27-AS1, RP11-443B20.1 ADCY3, CENPOJADCY3, DNAJC27, DNAJC27-AS1, RP11-443B20.1	NCDA1:G:-0.0116913,UBXN2A:G:+0.03057 NCDA1:C:-0.0116913,UBXN2A:G:+0.03057
rowser	2_25132192_C_A	2 25132192 2_24739694_C_CT 2 25132192 2_24739694_C_CT	16722587	E2A_2}-E2A_5}-Gm397}+ Nanog_disc1+, Pou212_disc1+, Pou212_known10+, Pou212_known6+, Pou212_k	6		ADCY3	ADCY39863	INTRON	ADCY3, CENPO(ADCY3, DNAJC27, DNAJC27, AS1, RP11-443820.1 ADCY3, CENPO(ADCY3, DNAJC27, DNAJC27, AS1, RP11-443820.1	NCOA1:A0.0116913,UEX02A:A+-0.03057
rowser	z_z5133148_T_C 2_25133630_CTT_C	∠ 25133148 2_24739694_C_CT 2 25133530 2_24739694_C_CT	rs6/44205 rs59644324	owoni (+,cBPD)-Myc_discb)-/Hix-6_known3]-Rad21_disc6]+	1		ADCY3 ADCY3	ADCY3 8907 ADCY3 8525	INTRON	ADC 13, UNAJC27, UNAJC27-AS1, RP11-443820.1 ADCY3:C:-:0.0083468, MFSD21	NCDA1:C:-0.011bN13,UBNN2A:C:+0.03057 B:NCDA1:C:-0.0077432
rowser	2_25133750_G_A 2_25134009_T_C	2 25133750 2_24739694_C_CT 2 25134009 2_24739694 C_CT	rs6754997 rs13035244	AP-1_disc1 +,CTCF_disc6 -,ERalpha-a_known1 -,RXRA_known3 +,RXRA_known4 + HES1 + MCF-7;GATA3	5 5		ADCY3 ADCY3	ADCY3 8305 ADCY3 8046	INTRON	ADCY3, DNAJC27, DNAJC27-AS1, RPMFSD28:A:+:0.0488246 ADCY3, DNAJC27, DNAJC27-AS1, RPMFSD28:C:+:0.047935	NCDA1:A:-:0.0116913,UBXN2A:A:+:0.03057 NCDA1:C:-:0.0116913,UBXN2A:C:+:0.03057
rowser	2_25134344_T_C	2 25134344 2_24739694_C_CT	rs13003430		7		ADCY3	ADCY3/7711	INTRON	ADCY3,DNAJC27,DNAJC27-AS1,RPMFSD28:C++0.0468104	NCDA1:C:-0.0116913,UBXN2A:C:+0.03057
rowser	2_25134497_A_C 2_25135620_G_A	2 25135620 2_24739694_C_CT 2 25135620 2_24739694_C_CT	rs2384061	HNF4_disc1 +,HNF4_disc3 +,HNF4_disc5 -	11		ADCY3	ADCY3[6435	INTRON	ADCY3,ASXL2,CENPO(ADCY3,DNA ADCY3:A:-0.0068505,MFSD2	8:NCOA1:C-300116915,06AN2AC-90005057 8:NCOA1:A:-0.0065119 ADCY3:MCF7:CNA-PET
rowser	2_25136866_T_A 2_25136916_T_C	2 25136866 2_24739694_C_CT 2 25136916 2_24739694_C_CT	rs10203386 rs10203482	MZF1::14_2[+,MZF1::14_3[+,SP1,BRST.MYOEP;H3K4ma1,MCF-7;H3K4ma1 CAC-binding-protein]+,CCNT2_discBRST.MYOEP;H3K4ma1,BRST.MYOEP;H3K9ac,MCF-7;H3K4ma1	5		ADCY3 ADCY3	ADCY3 5189 ADCY3 5139	INTRON	ADCY3,CENPO(ADCY3,DNAJC27,D MFSD28:A:+:0.0408796 ADCY3,DNAJC27,DNAJC27-AS1,RPMFSD28:C:+:0.0279945	NCDA1:A:-:0.0075481,UBXN ADCY3:MCF7:CMA-PET NCDA1:C:-:0.00755,UBXN2A ADCY3:MCF7:CMA-PET
rowser	2_25137323_T_C 2_25138040_A_C	2 25137323 2_24739694_C_CT 2 25138040 2 24739694 C CT	rs10206196 rs6737082	Crx_2)-GATA_Inown11 +LXR_2 +BRST.MYOEP;H:MCF-7;Enhancer Exr-1 disc4i+.IN:MCF-7:SPDEF BRST.MYOEP;H3K9ac HMEC:dnase	6 1f		ADCY3 ADCY3	ADCY3 4732 ADCY3 4015	INTRON	ADCY3, DNAJC27, DNAJC27-AS1, RPMFSD28;C;+:0.0378157 ADCY3, CENPO(ADCY3, DNAJC27, DNAJC27-AS1, RP11-443820, 1	NCDA1:C:-0.0044577,UBXN ADCY3:MCF7:CNA-PET FK8P18:C:-0.0187241.POMI ADCY3:MCF7:CNA-PET
rowser	2_25156773_T_C	2 25156773 2_24739694_C_CT	rs2384054	RXRA_known4 -	6			ADCY3 14718	INTERGENIC	ADCY3,CENPOJADCY3,DNAJC27,DNAJC27-AS1,POMC,RP11-44	I3 FK8P18:C0.0352998,NCDA1:C0.0427467,NCDA1:C0.0486829
rowser	2_25159172_1_C 2_25159501_G_C	2 25159172 2_24739694_C_CT 2 25159501 2_24739694_C_CT	rs6738433	Dtx3[+Hoxa10]-Met2_known1]-Met2_known4[-Nox_2]-	6			ADCY3 17446	INTERGENIC	ADCY3,DNAJC27,DNAJC27-AS1,POMC,RP11-443620.1 ADCY3,DNAJC27,DNAJC27-AS1,POMC,RP11-443620.1	NCDA1:C:-0.0235036,FKBP18:C:-0.0243267,NCDA1:C:-0.0355645
rowser	2_25159/80_A_G 2_25159855_T_C	2 25159780 2_24739894_C_C1 2 25159855 2_24739694_C_CT	rs10865320 rs10865321	E2A_2(,E2A_5),HEN1_1(,ZEB1_known3)+ Pax-4_1)+	7			ADCY3 17725 ADCY3 17800	INTERGENIC	ADCY3, DNAUC27, DNAUC27-AS1, POMC, RP11-443820.1 ADCY3, DNAUC27, DNAUC27-AS1, RP11-443820.1	NCDA1:G-0.0216102;FK8P18:G-0.024305;NCDA1:G-0.0358081 NCDA1:C0.0210955;FK8P18:C0.0242307;NCDA1:C0.0358254
rowser	2_25159858_A_G 2_25161236_A_G	2 25159858 2_24739694_C_CT 2 25161238 2_24739694_C_CT	rs10865322 rs4343432	Maf_disc2 ,Ni2i2 +,Pax-4_1 + Nicc2_4 ,TFII-I +	7			ADCY3 17803 ADCY3 19181	INTERGENIC	ADCY3,DNAJC27,DNAJC27-AS1,RP11-443B20.1 ADCY3,DNAJC27,DNAJC27-AS1,POMC,RP11-443B20.1	NCDA1:G0.0210781,FK8P18:G0.0242269,NCDA1:G0.035826 NCDA1:G0.0166212,FK8P18:G0.0249794,NCDA1:G0.0367388
rowser	2_25161265_G_T 2_25161386_C_T	2 25161265 2_24739694_C_CT 2 25161386 2 24739694 C CT	rs4459693 rs4430895	CTCF_disc8[-,CTCF_known1]-,Ets_disc5[+,Irf_disc5[-,Myf_1]-,Nanog_disc3[-,Ni2f2]+,Rad21_disc1]-,Rad21	6 7			ADCY3 19210 ADCY3 19331	INTERGENIC	ADCY3,DNAJC27,DNAJC27-AS1,POMC,RP11-443820.1 ADCY3,DNAJC27,DNAJC27-AS1,POMC,RP11-443820.1	NCDA1:T:-0.0166212,FK8P18:T:-0.0249794,NCDA1:T:-0.0367388 NCDA1:T:-0.0166212,FK8P18:T:-0.0249794,NCDA1:T:-0.0367388
rowser	6_130341728_C_CT	6 130341728 6_130349119_C_T	rs55941023	mammary_epithe BRST.HMEC;H3K4me3,BRST.MYCBRST.HMEC;Promoter,BRST.MYOEP;Pr	romoter,B	RST.vHMEC;Promo	ter,MCF-7;Promot	Nr Long To Long A	INTRON	TMEM200ACT: 0.0139554	L3MBTL3:CT-:0.0077711
rowser	6_130346105_G_A	6 130346105 6_130349119_C_T	rs7740188	YY1_diac2 -	6		L3MBTL3	L3MBTL3(6378	INTRON	L3MBTL3.RP11-73 L3MBTL3.RP11-7TMEM200A:A::0.0489309	L3MBTL3:A:0.0070517 L3MBTL3:MCF7:ChIA-PET
rowser	6_130349119_C_1 6_130350294_G_A	6 130340119 6_130340119_C_1 6 130350204 6_130340119_C_T	rs6926186	DMRT1 +,p300_diac7 -	7	Haight	L3MBTL3 L3MBTL3	L3MB1L3 9392 L3MBTL3 10567	INTRON	L3MBTL3,RP11-73 L3MBTL3,RP11-7TMEM200A;T:-30.0448786 L3MBTL3,RP11-73 L3MBTL3,RP11-7TMEM200A;A:-30.0172537	L3MBTL3:T::4.25E-06 L3MBTL3:A::0.0043689
rowser rowser	6_130352025_T_TA 6_130353612_T_C	6 130352025 6_130340119_C_T 6 130353612 6_130340119_C_T	rs11390217 rs9402211		7		L3MBTL3 L3MBTL3	L3MBTL3 12298 L3MBTL3 13885	INTRON	TMEM200A:TA:-0.017267 L3MBTL3,RP11-73 L3MBTL3,RP11-7TMEM200A:C:-0.0171127	L3MBTL3:TA0.0045989 L3MBTL3:C-:0.0048717
rowser	6_130354855_T_C 6 130356608 G A	6 130354855 6_130349119_C_T 6 130356608 6 130349119 C T	rs9388766 rs9375694	Evi-1_4 - RXR:LXRi+.c300 disc7i+	6 1d		L3MBTL3 L3MBTL3	L3MBTL3 15128 L3MBTL3 16881	INTRON	L3MBTL3.RP11-73 L3MBTL3.RP11-7TMEM200A.C:-0.0176176 L3MBTL3.RP11-73 L3MBTL3.RP11-7TMEM200A.A:-0.017281	L3M8TL3:C:-0.0050839 L3M8TL3:A:-0.0056388
rowser	6_130357553_G_A	6 130357553 6_130349119_C_T	rs9388767	Found is NE 1.31 Residues of managers, aloud CTCS managers, subbalat cell CTCE MCS 2/CTCE	6	Moleka	L3MBTL3	L3MBTL3/17826	INTRON	L3MBTL3,RP11-73 L3MBTL3,RP11-7TMEM200A-A0.0176738	L3M8TL3:A:-:0.0056388
rowser	6_130358944_G_T	6 130358944 6_130349119_C_T	rs9375695	Hoxa7_1 +,Smad3_1 -	6	reign	L3MBTL3	L3MBTL3 19217	INTRON	L3MBTL3,RP11-73 L3MBTL3,RP11-7TMEM2004;8:-0.01270084 L3MBTL3,RP11-73 L3MBTL3,RP11-7TMEM2004;1:-0.0150127	L3MB1L326-30.0056388
rowser rowser	6_130367725_T_G 6_130372984_A_G	6 130367725 6_130349119_C_T 6 130372984 6_130349119_C_T	rs7744830 rs6914670	Barhi1 +,En-1_3 +,Foxo_3 +,Nix4_8 +,Nix6-1_3 +,Pax-8_1 +,Pou611_1 -,Sox_15 +,Sox_2 +,Sox_7 + HEN1_2 +,Nix3_5 +	6 7		L3MBTL3 L3MBTL3	L3MBTL3/27998 L3MBTL3/33257	INTRON	L3MBTL3,RP11-73 L3MBTL3,RP11-7TMEM200A-G0.0244252 L3MBTL3,RP11-73 L3MBTL3,RP11-7TMEM200A-G0.0247459	L3MBTL3:6:-:0.0074777 L3MBTL3:6:-:0.0074764
rowser	6_130373648_C_G 6_130375810_A_G	6 130373648 6_130349119_C_T 6 130375810 6_130349119_C_T	rs7756870 rs6900473	FXR_2 -,HNF4_known5 +,RXRA_known3 - E2F_diac6 -,HNF1_6 +,HNF1_7 +,Mal_diac2 -,Mal_known3 -,Mal_known4 -,Pou511_diac1 -,Pou511_known	7		L3MBTL3 L3MBTL3	L3MBTL3/33921 L3MBTL3/36083	INTRON	L3MBTL3, RP11-73 L3MBTL3, RP11-7TMEM200A-G: -0.0244362 L3MBTL3, RP11-73 L3MBTL3, RP11-7TMEM200A-G: -0.0247465	L3MBTL3:6:-0.0074764 L3MBTL3:6:-0.0074764
rowser	6_130377843_C_T	6 130377843 6_130349119_C_T	rs11759018	HDAC2_disc6)+.If_disc3}- Id_disc01_SPEEP_incom01a	6		L3MBTL3	L3MBTL3/38116	INTRON	L3MBTL3,RP11-73 L3MBTL3,RP11-7TMEM200A-T:-0.0247452	L3M8TL3:T:-0.0074764
rowser	6_130378833_T_C	6 130378833 6_130340119_C_T	rs12661188	Egr-1_known1}-EMCF-7/MYC	7		L3MBTL3	L3MBTL3/39106	INTRON	L3MBTL3,RP11-73 L3MBTL3,RP11-7TMEM2004CC:0.0247452 L3MBTL3,RP11-73 L3MBTL3,RP11-7TMEM2004:C:-0.0242921	L3MBTL3:C:-0.0075615
rowser	6_130379160_T_C 6_130379282_A_G	6 130379160 6_130349119_C_T 6 130379282 6_130349119_C_T	rs12661232 rs12201492	CTCF_disc8i-,ELF1_disc3)+,Ets_disc7)+,NRSF_disc9)-,Rad21_disc6i-,YY1_disc4[+,2n/143_disc3]+,p300_c Pax-5_disc1 +	7		L3MBTL3 L3MBTL3	L3MBTL3/39433 L3MBTL3/39555	INTRON	L3MBTL3,RP11-7506.3 TMEM200A:C:-0.024747 L3MBTL3,RP11-73 L3MBTL3 TMEM200A:G:-0.0247452	L3M8TL3:C:-0.0074764 L3M8TL3:G:-0.0074764
rowser rowser	6_130379852_A_G 6_130379854_T_C	6 130379852 6_130349119_C_T 6 130379854 6_130349119_C_T	rs7760760 rs9375700	DMRT2 - MCF-7;SPDEF DMRT2 -ERalph MCF-7;SPDEF	7		L3MBTL3 L3MBTL3	L3MBTL3 40125 L3MBTL3 40127	INTRON	L3MBTL3, RP11-73 L3MBTL3, RP11-7TMEM200A-G: -0.0248784 L3MBTL3, RP11-73 L3MBTL3, RP11-7TMEM200A-C: -0.0248602	L3MBTL3:6:-:0.0075712 L3MBTL3:C:-:0.0075712
rowser	6_130381246_T_C 6_130384187_C_T	6 130381246 6_130349119_C_T 6 130384187 6 130349119_C_T	rs7451021 rs9375702	CONT2 discilla Exit 3ia GATA knownidia TAL1 discilla	6		L3MBTL3 L3MBTL3	L3MBTL3 41519	EXON	L3MBTL3,RP11-73 L3MBTL3,RP11-7TMEM200A;C::0.0244209 L3MBTL3,RP11-73 L3MBTL3,RP11-7TMEM200A;T::0.0242219	L3M8TL3:C:-0.0074764 L3M8TL3:T:-0.0126009
rowser 1	8_163366_T_C	8 163366 8_170592_T_C	rs34810249		4		RPL23AP53	ZNF596 18833	SUTR, EXON	RP5-855021.1,RP5-855D21.2,RPL23AP53,ZNF596	
rowser	8_163654_C_T	8 163654 8_170692_T_C 8 163654 8_170692_T_C	rs2906362	AP-1_disc4 +,HNF4_known3 +,HNF4_known4 -,lrf_disc3 +,Jrf_known1 +,Irf_known2 +,Jrf_known3 +,PLZF +	7		RPL23AP53 RPL23AP53	ZNF596 18545	3UTR,EXON	RP5-855D21.1,RP5-855D21.2,RPL23AP53,ZNF596 RP5-855D21.1,RP5-855D21.2,RPL23AP53,ZNF596	
rowser I	8_170692_T_C 8_172477_T_C	8 170692 8_170692_T_C 8 172477 8_170692_T_C	rs66823261 rs3008281	Mal_disc1 +,Mal_known1 +,NF-E2_disc1 +,Nf-2_2 +,Nf-2_3 +,TCF11::MalG +,p300_disc7 + CACD_2 -,ERalpha-a_disc1 +,Ear2 +,KIR +,KIR +,Pax-5_known2 +,RFX5_disc1 +,SP1_known4 +,SREBP_	6		RPL23AP53 RPL23AP53	ZNF596(11507 ZNF596(9722	INTRON	RP5-855D21.1, RP5-855D21.2, RPL23AP53, ZNF596 RP5-855D21.1, RP5-855D21.2, RP5-855D21.3, RPL23AP53, ZNF596	3
rowser I	8_174284_A_T 8 174546 G A	8 174284 8_170692_T_C 8 174546 8 170692 T C	rs3008282 rs2906324	Mat2_disc1 +.Mat2_known2 + NF-E2_disc4 -	7		RPL23AP53 RPL23AP53	ZNF596(7915 ZNF596(7653	INTRON	RP5-855D21.1, RP5-855D21.2, RP5-855D21.3, RPL23AP53, ZNF598 RP5-855D21.1, RP5-855D21.2, RP5-855D21.3, RPL23AP53, ZNF598	8
rowser I	8_177093_G_C 8 184919 G C	8 177093 8_170692_T_C 8 184919 8 170692 T C	rs10099411 rs2286140	AP-1_disc1 .CTCF_disc4 .E2F_disc1 .Nr2f2 - Nanog_disc1 +.Pax-5_disc4 .Pou2f2_known2 +.Pou2f2_known5 Pou3f3 +	7		RPL23AP53 ZNF596	ZNF596(5108 ZNF596(2538	INTRON	RP5-855D21.1,RP5-855D21.2,RPL23AP53,ZNF596 RP5-855D21.1,RP5-855D21.2,RPL23RPL23AP53.C:+0.0396912	0R4F21:C0.0275255,2NF596:C0.0376048 0R4F21:C0.0210876 RP5-855D21.2:MCF7:CNA-PET., RP5-855D21
rowser	8_189364_T_C	8 189364 8_170692_T_C	rs3008276	Foxa_diac5(+.MeIMCF_10A;POLR2A	6		ZNF596	ZNF596(6981	INTRON	RP11-585F1.10,RP5-855D21.1,RP5-RPL23AP53:C+0.0398809	OR4F21:C-0.0191729,2NF596:C-0.0464847
rowser I	8_191746_A_C 8_124737769_C_T	8 191746 8_170692_1_C 8 124737769 8_124757661_C_T	rs4401839	Eomesi- HP1-site-factori- mammary_spithe BRST.MYOEP;H3K4me1;BRST.vHMEC;H3K4me1;mammary_spithelia	7		ANXA13	2NF596 9363 ANXA13 11878	INTRON	HP11-585F1.10, HP5-855021.1, HP5- RP225AP533C+0.0421935 ANXA13	0R4F211C-0.0237581 HP5-855021.23MCF7/ChiA-PE1RP5-855022 MTSS17:+:0.0414242
rowser I	8_124738098_G_A 8_124738449_T_A	8 124738098 8_124757661_C_T 8 124738449 8_124757661_C_T	rs4509301 rs970820	Crx_1MOVD-B(mammary_epithe BRST.HMEC;H3FBRST.vHMEC;Enhancer BRST.HMEC;dna CEBPD -Mal_kni mammary_epithe BRST.MYOEP;H3K4me1,mammary_epithelial_call;H3K4me1,mammary	2b 5		ANXA13 ANXA13	ANXA13 11549 ANXA13 11198	INTRON	ANXA13 ANXA13	
rowser I	8_124738618_C_T 8_124738742_C_T	8 124738618 8_124757661_C_T 8 124738742 8_124757661_C_T	rs970821 rs970822	FAC1 + mammary_apithe BRST.MYOEP;H3K4me1_mammary_apithelial_call;H3K4me1 INSM1 +,Smad4  mammary_apithe BRST.MYOEP;H3K4me1_mammary_apithelial_call;H3K4me1_MCF-7:H	4		ANXA13 ANXA13	ANXA13 11029 ANXA13 10905	INTRON	ANXA13 ANXA13	MTSS1:T:+:0.0414389 ANXA13:MCF7:CNA-PET MTSS1:T:+:0.041432 ANXA13:MCF7:CNA-PET
rowser rowser	8_124739287_T_C 8_124739293 G A	8 124739287 8_124757661_C_T 8 124739293 8 124757661_C_T	rs4871410 rs4871411	Myc_dsc9(+,RXRmammary_spithe BRST.MYOEP;H3K4me1_mammary_spithelial_cell;H3K4me1 SP1_dsc3)-STA'mammary_spithe BRST.MYOEP;H3K4me1_mammary_enitedial_cell;H3K4me1	7		ANXA13 ANXA13	ANXA13 10360 ANXA13 10354	INTRON	ANXA13	ANXA13:MCF7:CNA-PET MTSS1:A:+:0.0414071 ANXA13:MCF7:CNA-PFT
rowser	8_124739556_G_A 8_124739709_G_^	8 124739556 8_124757661_C_T 8 124739709 8 124757661_C_T	rs7820718	Esr2 -,RXR:LXR mammary_spithe BRST.MYOEP;H:BRST.MYOEP;Enhancer mammary_spithe BRST.HMEC;HUPPET MYOED Enhancer	7		ANXA13 ANXA19	ANXA13[10091	INTRON	ANXA13	MTSS1:A:+0.0414044 ANXA13:MCF7:CNA-PET ANXA13:MCF7:CNA-PET
rowser	8_124730913_T_G	8 124739913 8_124757661_C_T 8 124740499 9 124757661_C_T	rs7842619	Barx1)-Bax +.Dtr mammary_optime BRST_MYOEP,H:BRST_MYOEP,Enhancer Fis_digeNr001 mammary_optime BRST_MYOEP,H:BRST_MYOEP,Enhancer	5		ANXA13	ANXA13(9734	INTRON	ANXA13 ANXA13	MTSS1:6:+:0.0414671 ANXA13:MCF7:CNA-PET MTSS1:6:+:0.0414675 EAMMAA:UPC7:CNA-PET
rowser I	8_124741789_T_C	8 124741789 8_124757681_C_T	rs13281094	<ul> <li></li></ul>	5		ANXA13	ANXA13/7858	INTRON	ANXA13	PANNELA LINE F. MARANEL ANXA13 MCF7: CNA-PE1, FAM91A1:MCF7: C
rowser	8_124742320_G_A 8_124743332_G_A	8 124742320 8_124757661_C_1 8 124743332 8_124757661_C_T	rs4549748	DMR11 -Sox_13 mammary_epithe BRS1.MYOEP;H38451.MYOEP;Enhancer Arrt_1 -Jrf_know.mammary_epithe BRST.MYOEP;H384me1,mammary_epithelial_cell;H384me1,MCF-7;H	5		ANXA13 ANXA13	ANXA13(7327 ANXA13(6315	INTRON	ANDA13 ANDA13	MTSS1A+LURUS956 ANXA133MCF7.CNA-PE1,,FBXO323MCF7.CN MTSS1A+L0.0392256 FBX0323MCF7.CNA-PET,,ANXA133MCF7.CF
rowser	o_124746417_G_G 8_124746417_C_G	e 124744912 8_124757661_C_T 8 124746417 8_124757661_C_T	rs4418323 rs17349815	rwc+p-rose_exenomenmenty_epithe BRS1.MYUEPIH3K4me1_mammary_epithelial_cell;H3K4me1 SP2_disc2[+ mammary_epithe BRST.MYOEPIH3K4me1_mammary_epithelial_cell;H3K4me1	б 5		ANXA13 ANXA13	ANXA13 4735 ANXA13 3230	INTRON	ANXA13	MTSS1:6:+:0.0209763 MTSS1:6:+:0.0391251 ANXA13:MCF7:CNA-PET
rowser I	8_124746618_C_T 8_124750451_G_A	8 124746618 8_124757661_C_T 8 124750451 8_124757661 C T	rs17258588 rs4617136	Foxm1 + mammary_apithe BRST.MYOEP;H3K4me1 mammary_apithelial_oal;H3K4me1 Mal_known3 + mammary_apithelial_oal;CTCF	4		ANXA13	ANXA13 3029 ANXA13 804	INTRON 2kbUPSTREAM	ANDIA13 (JANDIA13	MTSS1:T:+:0.0391251 ANXA13:MCF7:CNA-PET MTSS1:A:+:0.0391251 FAM91A1:MCF7:CNA-PETANXA13:MCF7:C
rowser I	8_124750521_C_T 8_124750585_G, A	8 124750521 8_124757661_C_T 8 124750585 8_124757661 C T	rs13279803 rs1946584	PouSI2_2 -Sox_1mammary_apithelial_cell;CTCF Ets_disc0(-,MOV/mammary_apithelMCF-7;H3K4me3	5 7			ANXA13 874 ANXA13 938	2kbUPSTREAM 2kbUPSTREAM	(LANXA13 (LANXA13	MTSS1:T:+:0.0391251 FAM01A1:MCF7:CNA-PET., ANXA13:MCF7:C MTSS1:A:+:0.0391251 ANXA13:MCF7:CNA-PET., FAM01A1:MCF7:C
rowser	8_124750741_A_G 8_124754567 T C	8 124750741 8_124757681_C_T 8 124754567 8 124757681_C_T	rs1946585 rs2008198	Btx - mammary_spithelial_cell/CTCF.MCF-7;ERelpha Nix3_1 - mammary_spithe BRST.MYOEP.H3K4me1	5 7			ANXA13 1094 ANXA13 4920	265UPSTREAM	ALIANDIA13 ANDIA13	MTSS1:G++0.0391279 ANXA13:MCF7:CNA-PET, FAM91A1:MCF7:C ANXA13:MCF7:CNA-PET
rowser	8_124755190_G_GA	8 124755190 8_124757661_C_T 8 124755313 9 124757661_C_T	rs71289608	Inf_disc3)+,2lp10tmammary_epithe BRST.MYOEP;H3K4me1 mammary_epithe BRST.MYOED;H3K4me1	7			ANXA13/5543	INTERGENIC	ANYA13	ZHX2:GA:+:0.0486941
rowser	24/50313_C_1 8_124757021_CAA_C	<ul> <li>.24/55/661_C_T</li> <li>8 124757021 8_124757661_C_T</li> <li>4 04757021 8_124757661_C_T</li> </ul>	ra1009/319 rs34838484	mammary_spine BhS1.HWCE/H3K4ma1 EWSR1-FL11;_Gumanmary_spine BhS1.HMEC/H3K4ma3	2			ANAA13(0666 ANXA13(7374	INTERGENIC	AND(A13	ANXA13:MCF7:CNA-PET
rowser	0_124/5/881_C_T 11_108043535_T_TAGA 1	e 124757661_C_T 1 108043535 11_108357137_A_G	rs17350191 rs141989202	cor_wows2+,Gmammaty_epithe BRS1.MYUEP;HSK4me1 HNF1_6(+,HNF1_mammaty_epithelial_cell;CTCF	5		NPAT	ANXA13 8014 NPAT 49830	EXON	SLC35F2:T:-0.0293648,C11or	ANXA13:MCF7:CNA-PET 165:T:+:0.0347634,ATM:T:+:0.0495976
rowser rowser	11_108044995_A_G 1 11_108055198_C_CAA 1	1 108044995 11_108345515_G_A 1 108055198 11_108345515_G A	rs7129627	GACU_2-KI4-MCF-7FoxA1MCF-7GATA3	6		NPAT	NPAT 48370	INTRON	ACA11,ATM,KDELC2	SLC35Y2-G++0.0010141,SLC35F2-G++0.0348472,L0C643923-G-+0.0452348 SLC35F2-CAA++0.0010519,SLC35F2-CAA++0.0366358
rowser	11_106087847_G_T 1 11_10608459 TAA T	1 108087847 11_108345515_G_A 1 108098459 11 108345515_C_A	rs228606 rs2066734	Gm397(+,SRF_krfibroblast_of_marBRST.HMEC/H3K4me1,BRST.vHMEC/H3K4me1,BRST.vHMEC/H3K4re1,BRST.vHMEC/H3	4		NPAT ATM	NPAT 5518 ATMI4901	INTRON	ACAT1,ATM,CUL5,KDELC2,NPAT ACAT1,ATM,KDELC2	SLC35F2:T:+:0.0010235,SLC35F2:T:+:0.0349345,L0C643923:T:-0.0453462 SLC35F2:T:+:0.0005916.L0D ATM/MCF2 CMAPET NPAT/MCF2 CMAPET
rowser rowser	11_108105593_G_A 1 11_108141701_G_T	1 108105593 11_108345515_G_A 1 108141701 11 108945515_C_A	rs228595 rs651/090	Fourth-Fourth- E2A 21-LBP-1 31+TBX5 31-ZEB1 digr11.7FR1 invested.	6		ATM ATM	ATM 12035 ATM 48149	INTRON	ACAT1,ATM,KDELC2 ACAT1,ATM,KDELC2	SLC35F2:A++0.000899,SLC35F2:A++0.034903,L0C643923:A-+0.0432518 SLC35F2:T++0.0007461.SLC35F2:T++0.0357162.207653923:T++0.0452518
rowser	11_108143456_C_G 1	1 108143456 11_108345515_G_A	rs1800057	Pou22_know8(k-Pou32_1)+Pou31_know1(+,4E01_know1(+,THAP1_diac1)-	7		ATM	ATM/49898	EXON	· · · · · · · · · · · · · · · · · · ·	ALKENBIG-0.0148008
rowser	11_108177097_T_G 1	1 108149207 11_108345515_G_A 1 108177097 11_108345515_G_A	rs141379009 rs611646	munuc_swidt), Nkkt-1_1-,dp105 - DMRT2 ,GATA_known1 ,GATA_known2 +,GATA_known4 -	394 6		ATM	A1M/55649 ATM/83539	INTRON	ACAT1,ATM,CULS,KDELC2,NPAT	ALADMS'UU.0148008 SLC35F2:A:+:0.0007372,SLC35F2:A:+:0.0358342,L00643923:A:-:0.0403296
rowser rowser	11_108210258_T_C 1 11_108267402_C_CA 1	1 108210258 11_108345515_G_A 1 108267402 11_108345515_G A	rs227069 rs199504893	Osl2_2 - MCF-7;FoxA1 BRST.vHMEC;dn	6		ATM C11orf85	ATM 116700 C11or/65 70856	INTRON	ACAT1,ATM,KDELC2	SLC35F2:C:+:0.0007372,SLC35F2:C:+:0.0358342,L0C643923:C:-:0.0403296 SLC35F2:CA:+:0.001005,L0C643923:CA:-:0.0402809,SLC35F2:CA:+:0.04481
rowser	11_108288808_G_T 1 11_108290959_A_G 1	1 108288808 11_108345515_G_A 1 108290959 11_108345515 G A	rs10431061 rs11212620	Nix3_2 +,Pou111_2 + T47D,dnase AP-3 -,PRDM1_d T47D,ER	5 6		C11orf85 C11orf85	C11or/65(49450 C11or/65)47299	INTRON	ACAT1,ATM,KDELC2 ACAT1,ATM,KDELC2	SLC35F2:T:+:0.0007372,SLC35F2:T:+:0.0358342,L0C543923:T:-0.0403296 SLC35F2:G:+:0.0007372,SLC35F2:G:+:0.0358342,L0C543923:G:-0.0403296
rowser	11_108294107_А_G 1 11_108295315 С Т 1	1 108294107 11_108345515_G_A 1 108295315 11 108345515_C_A	rs1960006 rs4250067	BCL_dsc3 -ERalpha-a_dsc4 -LXR_3 -ZBRK1 + Arid5a +.Brachuury 1 +.Fora disc2 +.Mto 1 +.Tol/1 2!+	7		C11orf65 C11orf65	C11or85(44151 C11or85(42949	INTRON	ACAT1,ATM,KDELC2 ACAT1,ATM,KDELC2	SLC35F2-G++0.0007372,SLC35F2-G++0.0358342,L0C643923-G-+0.0403296 SLC35F2-T++0.0007372,SLC35F2-T++0.0358842,L0C643923-T-+0.0403296
rowser	11_108296680_C_T 1	1 108296880 11_108345515_G_A 1 108297408 11_108345515_G_A	rs7952492	NERF1al, Soc_14 AIRF 11, FAC11a Growtla HMG, IV 21a PDAD 31. Dox 4.41	7		C11orf85	C11or85 41578	INTRON	ACAT1,ATM,KDELC2 ACAT1,ATM,KDELC2	SLC35F2:T++0.0007372;SLC35F2:T++0.0358342;LC05643923:T-+0.0403296 SLC35F2:T++0.0007372;SLC35F2:T++0.0358342;LC05643923:T-+0.0403296
rowser	11_108298019_C_G 1	1 108298019 11_108345515_G_A	rs11212624		6 7		C11orf85	C11orf65(40850	INTRON	ACAT1,ATM,NDELC2	sccss zcc+uuou737z,scc397zC+UU398542,L0C643923;C-0.0403296 ScC55F2:6:+0.0007372,ScC55F2:6:+0.0358342,L0C643923;6:-0.0403296
rowser	11_108298213_G_T 1 11_108298263_G_A 1	1 108298213 11_108345515_G_A 1 108298263 11_108345515_G_A	rs11212625 rs11212626		7		C11orf85 C11orf85	C11or/65/40045 C11or/65/39995	INTRON	ACA11,KDELC2 ACAT1,ATM,KDELC2	stc35r2:T:+:0.0007372,StC35F2:T:+:0.0358342,L0C643923:T:-:0.0403296 StC35F2:A:+:0.0007375,StC35F2:A:+:0.0358448,L0C643923:A:-:0.0403251
rowser rowser	11_108298323_T_C 1 11_108298374_G_A 1	1 108298323 11_108345515_G_A 1 108298374 11_108345515 G A	rs28861227 rs28810151	E2F_known8 +,GZF1 -Zlp161_3 + BDP1_disc1 -,CTCF_disc8 +,Ets_disc9 +,Irf_disc4 +,RXRA_known3 +,Rad21_disc10 +,Rad21_disc71+_RM	6		C11orf85 C11orf85	C11or/65/39/935 C11or/65/39/884	INTRON	ACAT1,KDELC2 ACAT1,KDELC2	SLC35F2:C:+:0.0007372,SLC35F2:C:+:0.0358342,L0C643923:C:-:0.0403296 SLC35F2:A:+:0.0007372,SLC35F2:A:+:0.0358342,L0C643923:A:-:0.0403296
rowser rowser	11_108298482_T_C 1	1 108298482 11_108345515_G_A 1 108298581 11 108946646 0	rs111612688 rs112588389	Pax-4_4 +,Pax-4_5 + DMRTSI-	6 7		C11or/85 C11or/85	C11or85(39776	INTRON	ACAT1,ATM,KDELC2	SLC35F2-C+0.0007367,SLC35F2-C+0.0358129,L0C643923:C-0.0403225 SLC35F2-G+0.0007372,SLC35F2-G+0.0358129,L0C643923:C-0.0403225
rowser	11_108298852_A_G 1	1 108298852 11_108345515_G_A	rs61913875	CHD2_disc3(+,E2F_disc7)+,Egr-1_disc1)+,Egr-1_disc6)-,GLI]-,NRSF_disc0)-,Nif1_disc1)+,Nif1_disc3(+,Sin	6		C11orf85	C11or/65/39406	INTRON	ACAT1,ATM,KDELC2	SLC35F2-G++0.0007372,SLC35F2-G++0.0358342,L0C643923-G-+0.0403296 SLC35F2-G++0.0007872,SLC35F2-G++0.0358342,L0C643923-G-+0.0403296
rowser	11_108306238_C_A 1	1 108306238 11_108345515_G_A	rs10890839	INSM1-	7		C11orf85	C110/85/37404 C110/85/32022	INTRON	ACAT1,ATM,KDELC2	ACLAN 21C+100008303,0068439221C-10.0588861,51C35F2:C+0.0389152 StC35F2:A+10.0007372,51C35F2:A+10.0358342,10C643923:A0.0403296
rowser rowser	11_108308175_G_A 1 11_108308510_G_A 1	1 108308175 11_108345515_G_A 1 108308510 11_108345515_G A	rs10789662 rs7129816	Crx_1 +,Pix2 - Hoxe7_1 -	6 7		C11orf85 C11orf85	C11orf65 30083 C11orf65 29748	INTRON	ACAT1,ATM,KDELC2 ACAT1,ATM,KDELC2	SLC35F2:A++0.0007372,SLC35F2:A++0.0358342,L0C643923:A-+0.0403296 SLC35F2:A++0.0007057,SLC35F2:A++0.0351832,L0C643923:A-+0.0408943
rowser	11_108311606_G_C 1 11_108311655 T C	1 108311606 11_108345515_G_A 1 108311655 11 108345515_C A	rs4753842 rs4754322	CEBPD)-My(_4)+,NF-kappaB_disc3 -,SREBP_known41+.ZEB1_known41-	5 6		C11orf85 C11orf85	C11or85(26852 C11or85(268/P	INTRON	ACAT1,ATM,KDELC2 ACAT1,ATM,KDELC2	SLC35F2-C+0.0007372,SLC35F2-C+0.0358342,L0C643923:C-0.0403296 SLC35F2-C+0.0007415,SLC35F2-C+0.0359714100643973-C-0.0403296
rowser	11_108311965_G_A 1	1 108311965 11_108345515_G_A	rs11212636	AP-1_disc7[-,GCNF]-,Pax-6_2[- F] F1_disc7[-,Dax-5_mman33, Sin34k.20_45-44	7		C11or/85	C11or85 26293	INTRON	ACAT1,ATM,KDELC2 ACAT1 ATM KDELC2	SLC35F2-A++0.0007372,SLC35F2-A++0.0358342,L00543923-A-+0.0403296 SLC35F2-A++0.0005488,SLC35F2-A++0.03588342,L00543923-A+-0.0403296
rowser	11_108312080_T_C 1	1 108312080 11_108345515_G_A	rs11212638	ERalpha-a_known3(+,RXRA_known2)-,VDR_4)-	6		C11orf85	C11or/65 26178	INTRON	ACAT1,ATM,KDELC2	SLC35F2:C:+0.0007372,SLC35F2:C:+0.0358342,L0C643923:C:-0.0403296
rowser	11_108314128_C_G 1	1 108314128 11_108345515_G_A	rai 16201292 ra6589018	Brachyury_1 +,Foxa_known3 -	7		C11orf85	C110/05/24659 C110/05/24130	INTRON	ACAT1,ATM,KDELC2	SLC3572-G++0.0007493,SLC3572:C++0.0559886,L0C643923:C-+0.0401561 SLC3572-G++0.0007335,SLC3572:G++0.0358354,L0C643923:G-+0.0404882
rowser	11_108314382_A_C 1 11_108314383_C_A 1	1 108314362 11_108345515_G_A 1 108314363 11_108345515_G_A	rs4255510 rs4460776	E2P_disc1)-Eir2 -Pbx1_4 +,Pbx3_known1 + E2F_disc1)-Eir2 -Jif_known5 +	7		C11orf65 C11orf65	C11or/65 23896 C11or/65 23895	INTRON		sLc35r2-C++0.0006334,L0C643923-C++0.034378,SLC35F2-C++0.0396955 SLC35F2-A++0.0006334,L0C643923-A++0.034378,SLC35F2-A++0.0396955
rowser	11_108314694_T_A 1 11_108314886 A G 4	1 108314694 11_108345515_G_A 1 108314886 11 108345515_C A	rs7111091 rs13968578n	HNF4_diac2 -,Hoxa5_1 +,Pax-1 -	7		C11or/85 C11or/85	C11or/65/23564 C11or/65/2%379	INTRON	ACAT1,ATM,KDELC2	SLC35F2-A++0.0007372,SLC35F2-A++0.0358342,L00643923-A0.0403296 SLC35F2-G++0.0007372,SLC35F2-G++0.0358342,L00643923-A0.0403296
rowser	11_108315463_C_G 1	1 108315463 11_108345515_G_A	rs2118308	Pax-5_known4 + CTCR: deetL-P2a St. HMCLIV 21a Hands St. TALS Income21 TCCP2. doi:10.	7 P		C11orf85	C11or85j22795	INTRON	ACAT1,ATM,KDELC2	SLC35F2-G:+:0.0007372,SLC35F2-G:+:0.0358342,LOC543923-G:-:0.0403296 4/KBH8-T:-0.0146579
rowser	11_108315606_C_T 1	1 108315606 11_108345515_G_A	rs149934734	CTCFL_diac1 ,E2A_5 ,HMG-IY_2 +,Hand1_1 +,TAL1_known2 ,TCF12_diac1 -	6		C11orf85	C11or865/22852	INTRON		ALKBH8:T0.0146579
rowser	11_108333974_AAGAC_A 1	1 108333974 11_108345515_G_A	rs78462478	CEBPB_known6 +,Nanog_disc2 -,SP1_disc2 +			C11orf85	C11or85/4284	INTRON	ACAT1,ATM,KDELC2	SLC35F2.A+0.0007373,SLC 110/f65/MCF7.CNA.PET
rowser	11_108338907_C_A 1	1 108338907 11_108345515_G_A 1 108341554 11_108345515_G_A	rs/943063 rs10749917	uumiz_cosc1;-UATA_known14;-,Tteroblast_of_mammary_gland;H3K4me3,mammary_epithelial_cell;H3K	5		u110f85	C11or85 1351 C11or85 3298	INTERGENIC	AGAT1,AIM,KDELC2 ACAT1,ATM,KDELC2	sucasrz:A+30.0007372,5LC C11of65:HMEC3M-PET,,KDELC2:HCC1954: SLC35F2:A+30.000741,5LC3:AP005718.13MCF7:CNA-PET
rowser	11 109241964 C T	1 108341864 11 108345515 G A	rs7934719	Lhu4 -,Lhu8 -Myf_1 -Pmc1 +,ZBRK1 -	6		KDELC2	C11or85(3606 C11or85(5822	INTERGENIC SUTR.EXON	ACAT1,ATM,KDELC2 ACAT1,ATM,KDELC2	SLC35F2:T:+:0.0007416,SLC3AP005718.1:MCF7:CNA-PET SLC35F2:4:+:0.000743 SLC35F2:4:+:0.0555170.1:0C543822:4:-:0.0404921
rowser	11_108344081 G A 1	1 108344081 11 108345515 0 ^	rs7943203	Zbtb3 -	~				10000	and the second se	
rowser rowser	11_108344081_G_A 1 11_108345515_G_A 1 11_108345515_G_A 1	1 108344081 11_108345515_G_A 1 108345515 11_108345515_G_A 1 108345515 11 108345515_G_A	rs7943203 rs201942465 rs201942465	2bts3i DMRT1 + DMRT1 +	5		KDELC2 KDELC2	C11or85/7257 C11or85/7257	SUTR, EXON SUTR, EXON		SLC35F2-GA:+:0.0007442,SLC35F2:A:+:0.0261269,SLC35F2-GA:+:0.0355693 SLC35F2-GA:+:0.0007442,SLC35F2:A:+:0.0261269 SLC35F2-GA:+:0.0955693

rowser	11_108349506_A_C	11 1	08349526 11_108345515_G_A	112419828 112419828	Add: Add: Add: Add: Add: Add: Add: Add:	147D)dhase	• 6	KDELC2	C11or85/1268 C11or85/11268	INTRON	ACAT1,ATM,KDELC2 ACAT1,ATM,KDELC2 ACAT1,ATM,KDELC2		SLC35F2:C5+0.00124/9,L02 C1088580.077.C104/PET SLC35F2:C5+0.001629,SLC3 AP005718.130CF7.C104/PET SLC35F2:C5+0.001629,SLC3 AP005718.130CF7.C104/PET
rowser	11_108354102_C_T	11 1	08350451 11_108345515_G_A	s12223381 s12223381	Discol+, brachysey_1+, connest-, nose+(+, Pac+_2(+, Pac+_2(+, S1A1_shown))+ Nanog_disc2(+, PMCF_10A;FOS, Mmammary_epithelial_cell;H3K4me1 DEVE_disc101	BRST.HMEC;dna	4	KDELC2	KDELC2 15057	INTRON	ACAT1,ATM,KDELC2 ACAT1,ATM,KDELC2		SLC35F2T1+0.001521+3LC3 AP00516.138CF7C08+PE1_KDELC288CF1 SLC35F2T1+0.0012018,SLC35F2T1+0.0266562 SLC35F2C1+0.0012018,SLC35F2T1+0.0266562
rowser	11_108356680_T_C	11 1	08356680 11_108345515_G_A	10789665	AP-2_disc2[-TCF12_disc6]-,TLX1:NFIC]-,Zix]+		7	KDELC2	KDELC2 12479	INTRON	ACAT1,ATM,KDELC2		SLC35F2:C:+0.0010514,SLC:KDELC2:MCF7:ChiA-PET
rowser	11_108367137_A_G	11 1	06361278 11_108345515_G_A	10890848	Dimad3_2(+ MCF-7/F0041,McMcF-7/F3K27ac MCF-7/ER/MCF-1MCF-7/H3K27ac MCF-7/Enhancer	107 3 4	7	KDELC2	KDELC2(7881	INTRON	ACAT1,ATM,KDELC2	510357254-30.0313088	SLC35F2-G:+:0.0010151,SLC35F2:G:+:0.0492218
rowser	11_108381578_G_A 11_108385182_C_T	11 1	06365182 11_108345515_G_A	111212676 19893279	ELF1_disc1[+;EL MCF-7;ER,MCF-7]H3R27ac,MCF-7]H3R4ma1 Gmeb1[+;RC300MDA-MB-231;FOXM1	MCF-7)dnase 3	5 5	KDELC2 KDELC2	KDELC2(7581 KDELC2(3977	INTRON	ACAT1,ATM,KDELC2 ACAT1,ATM,KDELC2		SLC35F2:A:+:0.0010152 SLC35F2:T:+:0.0010152
vowser	11_108366449_A_C 11_108406943_A_G	11 1 11 1	08366449 11_108345515_G_A 08406943 11_108357137_A_G	rs751343 rs117706999	Pou3(2_1)-2(D)+2(bb3)+ MCF-7(H3K4me1 CEBPB_known4(+,lk-1_2)-SD(5_diac2)-STAT_known5(-,2nf143_diac1)-		5 7	KDELC2 EXPH5	KDELC2 2710 KDELC2 37784	INTRON	ACAT1,ATM,KDELC2	SLC35F2:A:-:0.026571	SLC35F2:C:+:0.0010044,SLC:KDELC2:MCF7:ChiA-PET ALX8H8:A:-:0.0130292
rowser	16_4012480_T_C 16_4015046_G_A	16 16	4012480 16_4106788_C_A 4015046 16_4106788_C_A	1962038942 19879619	AFP1 +,FAC1 +,Foxa_known4 +,FoMCF-7;H3K4me1 HES1 -,Hic1_1 - MCF-7;ER.MCF-7;ERalpha,MCF-7;ERbeta,MCF-7;SPDEF		6 5	ADCY9	CREBBP 82359 CREBBP 84925	INTERGENIC 3UTR,EXON	RP11-462G12.1	VASN:C:-0.0036798,TFAP4:C:- VASN:A:-0.0033684,TFAP4:A:-	IL32:C-:0.0104076,ADCY9:C CREBBP:MCF7:ChiA-PET IL32:A::0.0093752,ADCY9:A TFAP4:MCF7:ChiA-PET
rowser	16_4106788_C_A 16_4108158_TA_T	16 16	4106788 16_4106788_C_A 4108158 16_4106788_C_A	11076805 1156278937	MCF-7;PBX1 MCF-7;H3K4me1MCF-7;Enhancer MCF-7;Promoter		5	ADCY9 ADCY9	ADCY9(59398 ADCY9(58028	INTRON		MMP25:T:::0.0020061,0R2C1:	2NF75A:A:+:0.009638,ADCY9:A:-:0.0213383,2NF174:A:+:0.0366211,VASN:# HM0X2:T:+:0.030937,DNASI ADCY9:MCF7:CNA-PET
vowser	16_4109828_G_C	16 16	4109828 16_4106788_C_A	1572762799 159347038	ERalpha-a_disc2[+,ERalpha-a_known1]+,NF-kappaB_disc4[+ ATE4L_CERPGIa_HEV1_disc1[a_HNF1_7L_Pxr(92_1]a		7	ADCY9 ADCY9	ADCY9(56358 ADCY9(54661	INTRON	ADCY9	GLYR1:C:-:0.0060267 CULAP1:A:-:0.042371	2NF75A:C++0.0095536;VASN:C-+0.0131072;DNAIA3:C++0.0221999;UBN1:C
rowser	16_4126201_C_T	16	4126201 16_4106788_C_A	12283498			- 6	ADCY9	ADCY9/39985	INTRON	ADCY9	ZNF174:T:-:0.0321264	ADCY9:T:-0.0126716,ZNF75A:T:+0.0140913,VASN:T:-0.0350573,ZNF174:T
rowser	16_4133033_G_A	16	4133033 16_4106788_C_A	197192040	Mxi1_disc2 -Myc_disc2 -Myc_known3 -Myc_known4 -Myc_known6 -Myc_known7 -My	yc_known8(-,Myc_	5	ADCY9	ADCY9/33153	INTRON			2NF263:A:+ 0.0195678, CREE ADCY9:MCF7: PreSTIGE
rowser	16_4133076_C_A 16_4134162_G_A	16	4134162 16_4106788_C_A	134826380	HEN _1 ,Razz_casov,S1A1_know11 - SIX5_disc1 +,TEF-1_2 -Zbtb3 -Zhf143_disc2 +		8	ADCY9	ADCY9[32024	INTRON			2NF263:A:+0.019546,CREEADC193MCF7.PN8511GE 2NF263:A:+0.0194706,CREERP11-95P2.3:MCF7.CNA-PET
rowser	16_4134246_G_A 16_4134522_A_T	16 16	4134246 16_4106788_C_A 4134522 16_4106788_C_A	1934040332 198059483	LUN-1 -,Pis2 -		5 7	ADCY9 ADCY9	ADCY9 31940 ADCY9 31664	INTRON			2NF263:A:+ 0.0237075,2NF5 RP11-95P2.3:MCF7:ChiA-PET 2NF263:T:+ 0.023674,2NF50 RP11-95P2.3:MCF7:ChiA-PET
rowser	16_4171880_A_G 16_4172061_G_C	16 16	4171880 16_4106788_C_A 4172061 16_4106788_C_A	196500680 196500681	AP-1_diac7 +,Hic MCF-7;SPDEF ATF3_diac2 +,HNMCF-7;SPDEF		7 B		ADCY9 5694 ADCY9 5875	INTERGENIC INTERGENIC		C16orf71:G:+:0.0127987 C16orf71:C:+:0.0139172	ADCY9.5:+:0.0001307,CREBIADCY9:MCF7:CNA-PET ADCY9.C:+:0.0001301,CREBIADCY9:MCF7:CNA-PET
rowser	16_4172887_C_A 16_4172966_G_A	16 16	4172887 16_4106788_C_A 4172968 16 4106788 C_A	1966881004 1966803611	Ptx3_diac3 + Pax5_diac2 -		5		ADCY9/6701 ADCY9/6780	INTERGENIC		C16orf71:A:+:0.0140314 C16orf71:A:+:0.0140284	ADCY9:A:+:0.0001307,CREBI ADCY9:MCF7:CNA-PET ADCY9:A:+:0.0001307,CREBI ADCY9:MCF7:CNA-PET
rowser	18_25367257_TAAGAG_Ci	18	25367257 18_25401204_AT_A	1934026214	ERabha-a knowntia PRDM1 knowntia Pro212 knowntill-		7		CDH2 390188 CDH2 389369	INTERGENIC	CDH2		CDH2:CAAGAG:+:0.0119402 CDH2:C+:0.0194579
rowser	18_25368846_G_A	18	25368846 18_25401204_AT_A	11872300	mammary_epithelial_cell;H3K4me1	BOST HMEC day	7		CDH2 388599	INTERGENIC	CDH2		CDH2:A:-0.0140461 CDH2:A:-0.0140461
rowser	18_25371514_A_G	18	25371514 18_25401204_AT_A	1962100742	CEBPA_1 +.Evi-1_2 Evi-1_4 Pou2t2_known2 +	CHOT THE COURSE	7		CDH2 385931	INTERGENIC			CDH2:6:+0.0177234
rowser	18_25372386_G_A 18_25374914_T_C	18	25372386 18_25401204_AT_A 25374914 18_25401204_AT_A	ni 10853677 ni 4273126	DMM12(+,Foxa_known2(+,Foxa_known4(+,Foxq1_2),Foxq2_1)+,Foxk1(-,Foxp1)+,1CF4_k Bbx(-,Foxq1)-,Hoxb8(-,RXRA_known2)-	ingen1 +	6 6		CDH2/385050 CDH2/382531	INTERGENIC	CDH2		
rowser	18_25376473_C_1 18_25377105_A_T	18 18	25376473 18_25401204_A1_A	194800820 199951088	STAT_known15 - Dbx1 +,Hoxa10 -,Hoxd10 -,Nox_2 +,Pou2f2_known2 -,Pou2f2_known8 +,Sox_5 +,TATA_	known1 -,21p106 +	6		CDH2/380972 CDH2/380340	INTERGENIC	CDH2 CDH2		
vowser vowser	18_25377196_G_A 18_25377513_T_C	18 18	25377196 18_25401204_AT_A = 25377513 18_25401204_AT_A =	19961475 198096576	Smad3_2 + AIRE_1 ,Barhi1 ,Bax ,Eax1 ,Hmx_2 ,Max2 ,Nkx2_10 ,Nobox_1 ,OTX ,Obox6 ,Ob2	2 -,Vax2 -	5		CDH2 380249 CDH2 379932	INTERGENIC	CDH2		
rowser	18_25377563_G_A 18_25379003 T_G	18 18	25377563 18_25401204_AT_A 25379003 18 25401204 AT_A	19091387 19085358	Hand1_1 +,Smad3_2 + GR_known10 +,Irf_known5 -,Irf_known9 -,PRDM1_disc1 -,RORalpha1_1 -,RORalpha1_2	2-THAP1 disc1-	5		CDH2 379882 CDH2 378442	INTERGENIC	CDH2		
vowser	18_25379275_A_G	18	25379275 18_25401204_AT_A	s11875525 s9957708	ZEB1_known2 + CTCF_disc101a.HMG.IV_21a.HNF1_11a.HNF1_61a.Ltv3_21.OTXL_Pov.4_21a.TCF12_kn	mentia	7		CDH2 378170 CDH2 378055	INTERGENIC	CDH2 CDH2		CDH2:G:+:0.006796
rowser	18_25380364_T_C	18	25380364 18_25401204_AT_A	16508502	lf_known6 +		7		CDH2 377081	INTERGENIC	CDH2		
rowser	18_25383465_G_A 18_25383770_T_C	18	25383465 16_25401204_AT_A 25383770 18_25401204_AT_A	14270255	Faxj1_1]-, Foxq1 +,Htt]-,Met2_known1 +,Nkx3_1]-,Pou2t2_known2 +,Pou2t2_known6 +		6 B		CDH2 373675	INTERGENIC			CDH2:C:+:0.006796
rowser	18_25383952_C_T 18_25384041_TA_T	18 18	25383952 18_25401204_A1_A = 1 25384041 18_25401204_AT_A = 1	181893947 1900238522	CHX10(+,E2F_)khMCF_10A;FOS Cdx2_1(+,Dbx1)-,MCF_10A;FOS	BRST.vHMEC;dnase,HME	ia EC;dnase		CDH2 373493 CDH2 373404	INTERGENIC	CDH2		CDH2:1:+:0.0442163 CDH2:T:+:0.0442163
rowser	18_25385055_G_A 18_25385221_C_A 1	18 18	25385055 18_25401204_AT_A = 25385221 18_25401204_AT_A =	rs4275930 rs4506992	Aad2 -,HEN1_1 +ZR751;ER		5		CDH2 372390 CDH2 372224	INTERGENIC			CDH2:A:+:0.0442163 CDH2:A:+:0.0442163
vowser vowser	18_25385760_C_T 18_25386439_A_G	18 18	25385760 18_25401204_AT_A 25386439 18_25401204_AT_A	194508491 1960877454	Dbx1 +,Fox -,FoxMCF_10A;FOS,MCF_10A;MYC,MCF_10A;STAT3 CACD_2 +,TCF12_disc1 -,ZEB1_disc1 -,ZEB1_known3 -		5		CDH2 371685 CDH2 371006	INTERGENIC			CDH2:T:+:0.0442163 CDH2:G:+:0.006796
rowser	18_25386727_G_GAAAAA 18_25387937_A_G	18	25386727 18_25401204_AT_A 25387937 18_25401204_AT_A	1910628611 1956300506	DMRT3I+.DMRT4I+.Nanog diso4I+.Pou5/1 disc1I+.Z/o187I+.c300 disc2I+		7		CDH2 370718 CDH2 369508	INTERGENIC			CDH2:GAAAAA:+:0.0022748 CDH2:G:+:0.0039924
rowser	18_25388628_C_T	18	25388628 18_25401204_AT_A	s11663001	BCL_disc3 +.Mtl1_1 +.NRSF_disc2 +.NRSF_disc4 +.NRSF_known3 +.Sin3Ak-20_disc3  Rev 6 disc9 _TATA_disc9], x200_disc6	•	7		CDH2 368817	INTERGENIC	CDH2		CDH2:T:-0.0442163 CDH2:4:-0.0441163
rowser	18_25389124_T_A	18	25388704 18_25401204_AT_A	14800822	EBF_disct - mammary_epithelial_cell;CTCF		7		CDH2 368321	INTERGENIC	CDH2		CDH2A+0.0442163 CDH2A+0.0442163
rowser	18_25390102_T_G	18	25380314 18_25401204_AT_A	rs16944207	Hitte_1]+ Hoxa4 -,RORalpha1_2 -		7		CDH2 367343	INTERGENIC	CDH2		CDH2:4:+0.0040705
rowser	18_25390181_A_G 18_25390278_G_A	18 18	25390181 18_25401204_AT_A 25390278 18_25401204_AT_A	is16944210 is16944213	Foxa_disc2[-,Foxa_known2]- AP-1_disc8[+,CTIMCF_10A;MYC		6 6		CDH2 367264 CDH2 367167	INTERGENIC	CDH2		CDH2:6:+:0.0040705 CDH2:A:+:0.0040705
vowser vowser	18_25390333_G_A 18_25390652_A_G	18 18	25390333 18_25401204_AT_A 25390652 18_25401204_AT_A	is10438924 is11874471	EBF_known3}NMCF_10A;MYC MCF_10A;FOS,MCF_10A;MYC,MCF_10A;STAT3		4		CDH2 367112 CDH2 366793	INTERGENIC	CDH2		CDH2:A:+:0.0040705 CDH2:G:+:0.0040705
rowser	18_25390938_C_A	18	25390938 18_25401204_AT_A 25391263 18 25401204 AT_A	ni11873567 ni62102182	Poutf1_1 - GATA known11 Obox6 Pitx2 Pitx3 -		7		CDH2 366507 CDH2 366182	INTERGENIC	CDH2		CDH2:G:+:0.0040705
rowser	18_25393153_C_A	18	25393153 18_25401204_AT_A	162102184	Nr2f2 -		6		CDH2 364292	INTERGENIC			CDH2:A:+:0.0040442 CDH2:A: -: 0.0096528
rowser	18_25400833_CT_C	18	25400833 18_25401204_AT_A	1379186737	Dtx1 -Evi-1_4 -Foxk1 -Foxp1 -HDAC2_disc6 -Mef2_known4 +,Nanog_disc2 +.Ncx_2	-,PLZF +,Sax_13 +,Sax_2 -	Zfp105 -,p300_disc5 -		CDH2 356612	INTERGENIC			CDH2:C:+0.0096997
rowser	18_25401204_A1_A 18_25401397_G_T	18	25401204 18_25401204_A1_A	1936194942 1936194692	Cdtz_1 ,CdxZ_2 +,Homa2 +,Hoxa10 ,Hoxa2 +,Hoxb8 ,Hoxb8 -,Hoxb8 +,IA1A_khown5 - AIRE_1 +,Maf_disc1 +,Maf_known1 +,RORalpha1_3 +,THAP1_disc1 -,Zlp410 -		в		CDH2/356241 CDH2/356048	INTERGENIC			CDH2:A:-0.0039993
rowser	18_25402557_G_GT 18_25406525_T_TTA	18 18	25402557 18_25401204_AT_A 25406525 18_25401204_AT_A	19201689215 1935875783	BAF156_disc2 -,EBF_known3 +,Ets_disc1 -,SDX5_disc1 +,SIX5_disc4 +,Znf143_disc2 -				CDH2 354888 CDH2 350920	INTERGENIC			CDH2:GT:+:0.0011533 CDH2:TTA:-:0.0285914
vowser vowser	18_25406855_C_T 18_25406866_C_T	18 18	25406855 18_25401204_AT_A 25406866 18_25401204_AT_A	19959491 1967108301	E2A_1 +,E2A_3 -,EBF_disc2 -,LUN-1 +,NF-kappaB_disc4 +		6 7		CDH2 350590 CDH2 350579	INTERGENIC	CDH2		CDH2:T:-:0.001208 CDH2:T:+:0.0012083
nowser	18_25407513_C_G	18	25407513 18_25401204_AT_A	198092192	Arid5a -,Dbx1 -,Foxa_known1 -,Foxd3 -,Foxi1 -,Foxj1_1 -,Foxj1_2 -,Foxj2_1 -,Mel2_know	m2 +,Mef2_known!	5		CDH2 349932 CDH2 349599	INTERGENIC	CDH2		CDH2:G:=0.001242 CDH2:G:=0.0091194 CDH2:T:=0.0091194
rowser	18_25407846_A_T	18	25407846 18_25401204_AT_A	190093178			7		CDH2 349599	INTERGENIC			CDH2:G:+0.0091194,CDH2:T:-0.0091194 CDH2:T:-0.0092502
rowser	18_25408642_T_C	18	25408642 18_25401204_AT_A	11662671	CDP_7 +,Hdx +,Hoxa3_1 +,Pou2t2_known9 -,Sox_5 -		5		CDH2 348803	INTERGENIC	CDH2		CDH2:C:+:0.0012649
rowser	18_25410803_A_G 18_25411773_A_C	18	25410603 18_25401204_A1_A	s2002401	Barhi1 -,CDP_1 +,CDP_4 +,E2F_disc4 +,En-1_3 -,Foxa_known2 -,Foxj2_1 -,Hix1 -,Hoxa	5_1 +,Hoxd8 +,Irf_1	6		CDH2 346842 CDH2 345672	INTERGENIC	CDH2 CDH2		CDH2:6:+0.0012979 CDH2:C:+0.0005314
rowser	18_25442301_T_C 18_25442412_T_G	18 18	25442301 18_25401204_AT_A = 25442412 18_25401204_AT_A =	197231957 197232124	MCF-7;FOXM1,MCF-7;GATA3 CDP_6[-,Zlp106]+MCF-7;FOXM1,MCF-7;GATA3		4 5		CDH2 315144 CDH2 315033	INTERGENIC	CDH2		CDH2:C:=0.0001084 CDH2:G:=0.0001084
vowser vowser	18_25444712_A_G 18_25446224_A_ACT	18 18	25444712 18_25401204_AT_A = 25446224 18_25401204_AT_A =	rs3924216 rs79858006	BDP1_disc2]+,Maf_disc2[-,Nr212]+		7		CDH2 312733	INTERGENIC			CDH2:6:-:0.000107 CDH2:ACT:-:0.0001056
rowser	18_25447072_T_C 18_25459346 ATTTTT A	18 18	25447072 18_25401204_AT_A 25450346 18 25401204 AT_A	112965632 11201680130			7		CDH2 310373 CDH2 298099	INTERGENIC			CDH2:C:-0.0001048 CDH2:A:+:0.0001524
vowser	18_25460298_C_T 18_25460372_C_T	18	25460208 18_25401204_AT_A	1935149382	Foxa_diac3(+,Pou212_known2(+ Mrs11:Hora0 11_Nix2_dia_Nix2_Ria_Nix3_dia		7		CDH2 297147 CDH2 297073	INTERGENIC			CDH2:T:+0.0002615 CDH2:T:+0.0002618
rowser	18_25462046_T_TAAC	18	25462046 18_25401204_AT_A	s140077604		050 4 41	-		CDH2 295399	INTERGENIC			CDH2:TAAC:+:0.0037265
rowser	18_25462222_T_C	18	25462138 18_25401204_AT_A	s12970390	GATA_DECH_GATA_DOMINIO_GATA_DOMINIC_GATA_DOMINIC_AFA_D	RED-1_1 +	7		CDH2(295223	INTERGENIC			CDH2:C:+0.0004118 CDH2:C:+0.0004118
rowser	18_25462858_C_T	18 18	25462380 18_25401204_A1_A = 1 25462858 18_25401204_AT_A = 1	is12970571 is12968914	AP-1_disc8[,ELF1_known1]+,ElB]-,H_known7[-,NF-A1]+,PU.1_disc1[+,Pax-5_disc3]+,H Banx1]+,Bsn(-,Dtx2]-,Fonj2_2]-,GR_known4]-,Pou2f2_known3[+,Rhox11]-,Ztp187]-	CKKA_disc4 +,SPIt	6		CDH2j295065 CDH2j294587	INTERGENIC			CDH2:C:+0.0004119 CDH2:T:+0.0004122
rowser	18_25463154_C_G 18_25464267_A_G	18 18	25463154 18_25401204_AT_A = 25464267 18_25401204_AT_A =	199355765 199347975	CTCF_disc1 .RaMCF-7;SPDEF COMP1 +,EWSR1-FLI1 -,GATA_disc3 -,GR_known1 +,HDAC2_disc6 -,STAT_disc6 +,p3	100_disc10 -,p300_	7 B		CDH2 294291 CDH2 293178	INTERGENIC			CDH2:G:+0.0004153 CDH2:G:+0.0004089
rowser	18_25465844_A_G	18	25465844 18_25401204_AT_A 25466016 18 25401204 AT A	n 17467487 n 17467494	Foxd1_1 +,HDAC2_disc2 + Mef2_known5i+		7		CDH2 291601 CDH2 291429	INTERGENIC	CDH2 CDH2		CDH2:G:+:0.0004008 CDH2:A:+:0.0003954
vowser	18_25466367_G_T 19_11420160_G_A	18	25466367 18_25401204_AT_A	1317445112	Ma(2_known1 +,PEBP -,p300_disc8 + CHD2_disc3L_F2E_disc5L_NRSE_disc10Le_Pro/22_disc2Le	HMECvinase	7	TSPAN16	CDH2 291078 TSPAN16 13337	INTERGENIC	AC024575 6-2 C19vd39 CTC-510E1	TMFM205-4-+-0 0288047 7NF4	CDH2:T:+0.0003722 (2NE135:4:+0.0005093 2NE433:4:-0.0182658 2NE44:4:-0.0226724
rowser	19_11421239_T_C	19	11421239 19_11423703_C_G	19322146	BDP1_disc1 +		7	TSPAN16	TSPAN16 14416	INTRON	AC024575.6-2,C19orf39,CTC-510F1	TMEM205:C:+:0.0280174,2NF4	2NF136.C:+0.0003985,2NF4 CTC-510F12.8:MCF7:CNA-PET, CTC-510F12
rowser	19_11423703_C_G	19	11423703 19_11423703_C_G	1322144	Evi-1_H;+,HNF1_6 ,HNF1_7 ,Hoxa7_2 +,Hoxa9],Hoxb3 +,Nox6-1_1 ,Nox6-1_3 ,OTX	+,Pax-6_3 -,Pdx1_	5	TSPAN16	TSPAN16 16880	INTRON	AC024575.6-2,C19orf39,CTC-510F1	TMEM205:G:+:0.0298398,ZNF	2NF136.G + 0.0003752,2NF4 CTC-510F12.8:MCF7:CNA-PET
rowser	19_11426182_A_G	19	11426182 19_11423703_C_G	19322142	RXRA_known7]-STAT_disc6]-		2	TSPAN16	TSPAN16 10274	INTRON	CTC-510F12.4,TSPAN16	TMEM205:G:+:0.0288978,2NF	2NF136:6:+0.0003938,2NF4 CTC-510F12.6:MCF7:CNA-PET
rowser	19_11426639_C_A 19_30265235_G_A	19 19	11428639 19_11423703_C_G 30265235 19_30277729_C_T	19322141 1912461902	BUZ_dbdbl+,ENAMUF_10A/POLR2A Mrg_1 ,Pdx1_2 +,Tgl1_2 -		5	ISPAN16	ISPAN16 19816 CCNE1 37665	SUTR, SUTR, EXC INTERGENIC	AL0245/5.6-2,C19orf39,CTC-510F1 C19orf12,CCNE1	TMEM205:A:+:0.0269175,2NF	2NP13b:A:+0.0005123,2NF44:A:-0.0155147,2NF433:A:-0.0194137,ELOF1:
vowser vowser	19_30266706_G_A 19_30272202_G_A	19 19	30266706 19_30277729_C_T 30272202 19_30277729_C_T	1962107106 1912462975	ATF4]+,CTCF_dtMCF-7;CTCF BDP1_disc3]+	MCF-7;dnase 2	5		CCNE1 38194 CCNE1 30698	INTERGENIC	CCNE1 C19orf12,CCNE1		
vowser	19_30277729_C_T 19_30284882_G_GTA	19	30277729 19_30277729_C_T 30284882 19_30277729_C_T	s113701136 s149892244	ELF1_disc3 .Egr1_disc4 .Myc_disc10 .NRSF_disc9 .2b - Poutf1_2la_TATA_konum1la		в		CCNE1 25171 CCNE1 18018	INTERGENIC	CCNE1	ZNF536:T:+:0.0292298 ZNF536:GTA:+:0.01618	2NF536/T0.0231483 2NF536/GTA0.0486063
rowser	19_30285548_C_T	19	30285548 19_30277729_C_T	112000024	Nanog_disc2 +		7		CCNE1 17352	INTERGENIC	CCNE1	ZNF536:T:+:0.0202404	ZNF536:T:-0.0435014
rowser	19_30286245_A_G	19	30286037 19_30277729_C_T 30286245 19_30277729_C_T	1113090034	84 1_2(-, nat-0_010413)-, P102(+ BDP1_diac2)+, GCNF(-, N/212)-		в		CCNE1 16655	INTERGENIC	CCNE1	2NF536:G:+:0.0206124	2NF536:6:-0.0438311
rowser	19_30286822_T_C	19 19	30286450 19_30277729_C_1 30286822 19_30277729_C_T	ni145999282 ni17513613	HDAC2_diad5 +.If_diad3 20105 + Foxa_diad5 -		5		CCNE1 16450 CCNE1 16078	INTERGENIC	C19orf12,CCNE1	ZNF536:C+:0.0205261	ZNF536:C:-0.0437663
rowser	19_30287988_A_AAC 19_30288177_G_A	19 19	3028/988 19_30277729_C_T 30288177 19_30277729_C_T	is112020302 is8111686	+AC1 +,Foxa_known2 +,Foxd3 +,Foxk1 +,Foxo_2 +,Foxp1 +,HDAC2_diac8 -,Irf_diac3 -,N BCL_diac10 -,BD MCF-7;POLR2A	vanog_disc2 +,Sox	5 6		CCNE1 14912 CCNE1 14723	INTERGENIC	CCNE1	ZNF536:AAC:+:0.0191332 ZNF536:A:+:0.0201659	ZNP536:AAC:-0.0442486 CCNE1:MCF7:ChIA-PET ZNP536:A:-0.0445983 CCNE1:MCF7:ChIA-PET
rowser	19_30288488_C_T 19_30288545 T_C	19 19	30288488 19_30277729_C_T 30288545 19_30277729_C_T	192161516 1960560217	HNF4_known6 +,RXRA_diac2 -,SETDB1_diac1 -,Znf143_diac3 - E2F_diac3 +.Mvc_diac10 +,TATA_diac1 -,YY1_known2 -,ZBTB33_diac2 +,Znf143_diac3	+	7		CCNE1 14412 CCNE1 14355	INTERGENIC	CCNE1 CCNE1	ZNF536:T:+:0.0201096 ZNF536:C:+:0.020071	2NF536/T0.0367992 CCNE1:MCF7:ChIA-PET 2NF536/C0.0447923 CCNE1:MCF7:ChIA-PET
rowser	19_30289630_G_A	19	30289630 19_30277729_C_T	162107115	RXRA incentia		7		CCNE1 13270	INTERGENIC	CONE1 CONE1	ZNF536:A:+:0.0200859 ZNF536:T:+:0.0198184	2NF536-A0.0450312 CCNE1:MCF7-ChiA-PET 2NF536-T0.045269 CCNE1:MCF7-ChiA-PET
vowser	19_30290357_G_C	19	30290357 19_30277729_C_T 30290811 19_30277729_C_T	s111640872	NRSF_disc9(-ZEB1_known6)- BRST_MYOEP;H3K4me1 FRahhaus_knownMCF_7/FR_MCF_3/HCF_7/H3K4me1	MCE-7 vinase	5		CCNE1 12543 CCNE1 12089	INTERGENIC	CONE1 CONE1	ZNF536:C:+:0.0175784 ZNF536:G:+:0.0174535	2NF536.C0.0470261 CCNE1:MCF7.ChiA-PET 2NF536.G0.047258 CCNE1:MCF7.ChiA-PET
rowser	19_30290890_A_G	19	30290890 19_30277729_C_T	1979576418	Foxa_diac3 +,OR MCF-7;ER,MCF-7;H3K27ac,MCF-7;H3K4ma1,MCF-7;H3K4ma2	MCF-7;dnase	5		CCNE1 12010	INTERGENIC	CCNE1	ZNF536:6:+:0.0174321	ZNF536.G-0.0472474
vowser vowser	19_30291869_AAATAATA4 19_30292557_A_AAT	19 19	30291869 19_30277729_C_T 30292557 19_30277729_C_T	is146397219 is140500237	CUP_7-,Pou2f2_known2 -,Sox_5 - Foxp1 +,Pou2f2_known2 +				CCNE1 11031 CCNE1 10343	INTERGENIC		ZNF536:A:+:0.0172722 ZNF536:AAT:+:0.0154937	ZNF536:A-3L04544 ZNF536:AAT:-:0.0443114
rowser	19_30292701_G_A 19_30293267_C_T	19 19	30292701 19_30277729_C_T 30293267 19_30277729_C_T	1962104475 198111487	BHLHE40_disc2 +,CTCF_disc5 +,CTCF_disc9 +,LBP-1_2 +,Mt1_1 -,Nanog_disc3 +,SRI Ets_disc6 ,Gt1_2 -,NF-kappaB_known3 -	F_diac2 -,Sin3Ak-2	5		CCNE1 10199 CCNE1 9633	INTERGENIC	CONE1 CONE1	ZNF536:A:+:0.0357322 ZNF536:T:+:0.0170755	2NF536:A0.0260607 2NF536:T0.0432732
rowser	19_30293462_G_A 19_30294716_G_A	19 19	30293462 19_30277729_C_T 30294716 19_30277729 C T	157894940 1962104476	Evi-1_4 +,GATA_known8 -,HDAC2_diac6 +,RREB-1_2 +,STAT_diac6 - E2F_known3 -		7		CCNE1 9438 CCNE1 8184	INTERGENIC	CCNE1 CCNE1	ZNF536:A:+:0.0170503 ZNF536:A:+:0.0168866	2NF536:A:-0.0429795 2NF536:A:-0.0410456 CCNE1:MCF7:ChiA-PET
rowser	19_30294991_G_T	19	30294991 19_30277729_C_T	1962104477	AFP1 ,Arid3a_2 +,Lhx3_1 +,OTX +,Sox_1 +,TCF4_known1 +		5		CCNE1/7909	INTERGENIC	CONE1	ZNF536:T:+:0.0194845	CCNE1:MCF7.ChiA-PET
- certer Yowser	19_30296853_T_C	19	30296853 19_30277729_C_T	104476 198102137	PLAG1 -,Smad4 + BRST.HMEC;Enhanoar,BRST.MYG	DEP;Enhancer	5 Bladder_cancer		CCNE1/594 CCNE1/6047	INTERGENIC	C19orf12,CCNE1	ZNF536.C+0.0165371	ZNESSEC-0.0382064 CCNE1:MCF7:CNA-PET
yowser yowser	19_30297516_A_G 19_30297577_G_A	19 19	3029/516 19_30277729_C_T 30297577 19_30277729_C_T	1959592823 1959868991	OTX +,Otx2 + BRST.MYOEP;Enhancer		4		CCNE1 5384 CCNE1 5323	INTERGENIC INTERGENIC	CCNE1	ZNF536:A:+:0.0164808 ZNF536:A:+:0.0164734	ZNP536/G-30.0374045 CCNE1:MCF7.Ch/A-PET ZNP536:A0.0373386 CCNE1:MCF7.Ch/A-PET
vowser	19_30297919_G_C 19_30298800_A_G	19 19	30297919 19_30277729_C_T 30298800 19_30277729_C_T	197247779 1962104480	HNF4_diac2 + BRST.MYOEP;Enhancer GR1_1 -2BTB7A MCF-7;SPDEF		8 5		CCNE1 4981 CCNE1 4100	INTERGENIC	CONE1 CONE1	ZNF536:C:+:0.0164586 ZNF536:S:+:0.0163471	2NF536:C:-0.0369452 CCNE1:MCF7:ChIA-PET 2NF536:G:-0.0359188 CCNE1:MCF7:ChIA-PET
rowser	19_30299634_A_C	19	30299634 19_30277729_C_T	1566400371	DMRT3)-EIIS- CDP 11-CDP 71a Cartil, Dhytia Dhytia Econoli Churti Lioune 11-Lioune 11-L	tower a	5		CCNE1 3266	INTERGENIC	CONE1 CONE1	ZNF536:C:+:0.0162757 7NF536:T:+:0.0162757	2NF536-C0.0350057 CCNE1:MCF7-ChiA-PET 2NF536-T0.0352728 CCNE1:MCF7-ChiA-PET
rowser	19_30300017_G_A	19	30300017 19_30277729_C_T	1962104483	BCL_disc10 .ERabha-a_known3 +,if_disc4 .SP1_disc3 .SP1_known1 ,ZBRK1 +	(97) mod0),5	- 7 98 Amerik menumenan	W CONE1	CCNE1 2883	INTERGENIC	CONE1	ZNF536:A:+:0.0161801	2NF536:A-:0.0334678 CCNE1:MCF7:Chi4-PET
rowser	19_30305684_G_A	19	30305684 19_30277729_C_T	13218036	Myc_known7 -TCMCF_10A;E2F4		5	CCNE1	CCNE1 2784	INTRON	C19orf12,CCNE1	ZNF536:A:+:0.0162527	ZNF536-A0.0186491

IM-PET, KDELC2 HMEC3MPET, C11or85MCF7-CMA-PET, KDELC2 MCF7-CMA-PET, C11or85 HCC19543M-PET

,L0C643923:GA:-:0.0405219 ,L0C643923:GA:-:0.0405219

:Hnia A-PE' :Hnia :Hnia

ICF7:ChIA-PE1 ICF7:ChIA-PE1 ICF7:ChIA-PE1 ICF7:ChIA-PE1 ICF7:ChIA-PE1 ICF7:ChIA-PE1

1.1.MCF7:CNA-PET

:MA-PET IA-PET, FAM91A1:MCF7:CNA-PE1 IA-PET

NA-PET NA-PET NA-PET NA-PET

T

35

10MAPET

L=0.0410264 ==-0.0120156,CLUAP1:C==0.0477839,IL32:C==0.048916 ==-0.0233509 ==-0.0418819

2.4:MCF7:CNA-PET A:+:0.0297273

#### Supplementary Table 4: Results for the two novel ER-negative susceptibility loci on 11q22.3

SND	Chr	Position	Allalaa <sup>#</sup>	_	BCAC ER-negativ	e <sup>†</sup>	CIME	CIMBA BRCA1 mutation carriers <sup>‡</sup>						
SINF	CIII	POSICION	Alleles	MAF	OR (95%CI)	P-value	MAF	HR (95%CI)	P-value					
Each SNP mo	delled	individually												
rs11374964	11	108345515	G/GA	0.42	0.94 (0.92-0.96)	3.6x10 <sup>-7</sup>	0.43	0.92 (0.89-0.95)	1.6x10 <sup>-7</sup>					
rs74911261	11	108357137	G/A	0.02	0.81 (0.74-0.89)	3.7x10 <sup>-6</sup>	0.02	0.78 (0.70-0.87)	1.1x10 <sup>-5</sup>					
Both SNPs modelled together														
rs11374964	11	108345515	G/GA	0.42	0.95 (0.93-0.97)	3.5x10 <sup>-5</sup>	0.43	0.93 (0.90-0.96)	5.1x10 <sup>-6</sup>					
rs74911261	11	108357137	G/A	0.02	0.84 (0.76-0.91)	8.6x10 <sup>-5</sup>	0.02	0.81 (0.73-0.91)	3.3x10 <sup>-4</sup>					

<sup>#</sup>More common allele listed first, minor allele second; <sup>†</sup>Combined data from 16,988 ER-negative cases and 87,962 controls of European ancestry from the Breast Cancer Association Consortium (BCAC) - results differ from those in Table 1 as GWAS data were excluded (unit record data was not available to run the models with both SNPs together); <sup>†</sup>Combined OncoArray data from 15,566 *BRCA1* mutation carriers from the Consortium of Investigators of Modifiers of BRCA1/2 (CIMBA), 7,784 of whom had developed breast cancer - estimates from multivariable Cox regression; Chr, chromosome; MAF, minor allele frequency; OR, odds ratio per copy of the minor allele; CI, confidence interval; HR, hazard ratio per copy of the minor allele

ER-negative breast cancer (BCAC)								BRCA1 mutation carriers (CIMBA)																				
Location SNP Chr Position Alleles <sup>7</sup> N		MAF	GWAS				iCOGS			OncoArray			,2	D(hat )	iCOGS			OncoArray										
					OR(95%CI)	P-value	1 <sup>2</sup> (5)	P (het <sub>s</sub> )	r <sup>2</sup> (imp)	OR(95%CI)	P -value	1 <sup>2</sup> (9)	P (het;)	r <sup>2</sup> (imp)	OR(95%CI)	P-value	1 <sup>2</sup> (5)	P (het <sub>s</sub> )	(G)	P(neta)	r <sup>2</sup> (imp)	HR(95%CI)	P-value	r <sup>2</sup> (imp)	HR(95%CI)	P-value	r <sup>2</sup> (0)	P (het <sub>c</sub> )
2p23.3 rs200648189	2	24739694	CT/C	0.19	0.96 (0.88-1.06)	4.1x10 <sup>-1</sup>	0	0.93	0.57	0.93 (0.87-0.99)	2.3x10 <sup>-2</sup>	0	0.58	0.90	0.94 (0.90-0.99)	9.3x10 <sup>-3</sup>	0	0.95	0	0.83	0.52	0.93 (0.81-1.08)	3.5x10 <sup>-1</sup>	0.89	0.87 (0.83-0.92)	3.5x10 <sup>-7</sup>	0.09	0.34
6q23.1 rs6569648	6	130349119	T/C	0.23	0.88 (0.83-0.94)	1.4x10 <sup>-4</sup>	0	0.96	1.00	0.94 (0.89-0.98)	3.3x10 <sup>-3</sup>	0	0.79	1.00	0.94 (0.91-0.98)	1.8x10 <sup>-3</sup>	0	0.88	0.31	0.24	1.00	0.96 (0.86-1.06)	4.2x10 <sup>-1</sup>	1.00	0.94 (0.89-0.98)	7.0x10 <sup>-3</sup>	0	0.61
8p23.3 rs66823261	8	170692	T/C	0.23	1.02 (0.96-1.09)	4.7x10 <sup>-1</sup>	0	0.49	0.74	1.13 (1.08-1.19)	1.0x10 <sup>-6</sup>	0	0.71	0.92	1.08 (1.04-1.13)	8.2x10 <sup>-5</sup>	0	0.85	0.66	0.05	0.72	1.14 (1.01-1.29)	4.0x10 <sup>-2</sup>	0.92	1.01 (0.96-1.06)	8.2x10 <sup>-1</sup>	0.33	0.06
8q24.13 rs17350191	8	124757661	C/T	0.34	1.07 (1.01-1.13)	3.1x10 <sup>-2</sup>	0.43	0.09	1.00	1.06 (1.02-1.11)	1.9x10 <sup>-2</sup>	0.12	0.27	1.00	1.07 (1.04-1.11)	3.2x10 <sup>-5</sup>	0	0.71	0	0.94	1.00	1.03 (0.95-1.13)	4.6x10 <sup>-1</sup>	1.00	1.08 (1.04-1.13)	1.6x10 <sup>-6</sup>	0.22	0.16
11q22.3 rs11374964	11	108345515	G/GA	0.42	0.94 (0.88-1.00)	6.0x10 <sup>-2</sup>	0	0.69	1.00	0.97 (0.94-1.01)	1.4x10 <sup>-1</sup>	0.26	0.07	1.00	0.91 (0.88-0.94)	2.7x10 <sup>-8</sup>	0	0.66	0.68	0.04	1.00	0.96 (0.88-1.05)	4.1x10 <sup>-1</sup>	1.00	0.90 (0.87-0.94)	7.8x10 <sup>-7</sup>	0.18	0.24
11q22.3 rs74911261	11	108357137	G/A	0.02	0.88 (0.70-1.10)	2.6x10 <sup>-1</sup>	0	0.88	0.90	0.79 (0.68-0.92)	2.6x10 <sup>-3</sup>	0	0.86	1.00	0.82 (0.73-0.91)	4.0x10 <sup>-4</sup>	0.01	0.44	0	0.75	0.87	0.82 (0.58-1.15)	2.5x10 <sup>-1</sup>	1.00	0.73 (0.63-0.83)	3.3x10 <sup>-6</sup>	0	0.74
16p13.3 rs11076805	16	4106788	C/A	0.25	0.91 (0.86-0.97)	2.8x10 <sup>-3</sup>	0.40	0.11	0.72	0.94 (0.89-0.99)	1.9x10 <sup>-2</sup>	0	0.80	0.97	0.92 (0.89-0.96)	2.9x10 <sup>-5</sup>	0.18	0.24	0	0.76	0.72	1.02 (0.90-1.16)	7.3x10 <sup>-1</sup>	0.97	0.95 (0.91-1.00)	4.1x10 <sup>-2</sup>	0.09	0.34
18q12.1 rs36194942	18	25401204	A/AT	0.30	0.92 (0.85-0.99)	1.9x10 <sup>-2</sup>	0	0.52	0.95	0.96 (0.92-1.00)	5.1x10 <sup>-2</sup>	0	0.48	0.95	0.92 (0.89-0.96)	9.6x10 <sup>-6</sup>	0	0.99	0.15	0.31	0.94	0.96 (0.87-1.06)	4.5x10 <sup>-1</sup>	0.94	0.95 (0.91-0.99)	1.8x10 <sup>-2</sup>	0	0.65
19p13.2 rs322144	19	11423703	C/G	0.47	0.94 (0.89-0.99)	2.1x10 <sup>-2</sup>	0	0.73	0.51	0.96 (0.91-1.01)	1.0x10 <sup>-1</sup>	0	0.92	0.99	0.95 (0.92-0.98)	1.5x10 <sup>-3</sup>	0.29	0.11	0	0.86	0.50	0.89 (0.79-1.01)	7.2x10 <sup>-2</sup>	0.99	0.93 (0.89-0.96)	1.7x10 <sup>-6</sup>	0	0.48
19q12 rs113701136	19	30277729	C/T	0.32	1.04 (0.98-1.10)	1.6x10 <sup>-1</sup>	0	0.89	0.97	1.06 (1.02-1.10)	4.0x10 <sup>-3</sup>	0.26	0.07	0.98	1.08 (1.04-1.12)	2.1x10 <sup>-5</sup>	0	0.48	0	0.61	0.96	1.11 (1.01-1.22)	3.0x10 <sup>-2</sup>	0.98	1.04 (1.00-1.09)	7.7x10 <sup>-2</sup>	0.21	0.18

Supplementary Table 2: CIMBA studies contributing data on BRCA1 mutation carriers, by genotyping initiati	tary Table 2: CIMBA studies contributing data on BRCA1 mutation carriers, by gence	otyping intiative
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• · · · · ·			Onco	Array	iCOGS			
Acronym	Study Name	Country	Unaffected	Breast cancer	Unaffected	Breast cancer		
BCFR-AU	Australian site of the Breast Cancer Family Registry	AUSTRALIA	13	25	0	2		
BCFR-NC	Northern California site of the Breast Cancer Family Registry	USA	3	12	1	1		
BCFR-NY	New York site of the Breast Cancer Family Registry	USA	24	37	4	5		
BCFR-ON	Ontario site of the Breast Cancer Family Registry	CANADA	34	86	2	7		
BCFR-PA	Philadelphia site of the Breast Cancer Family Registry	USA	26	17	14	16		
BCFR-UT	Utah site of the Breast Cancer Family Registry	USA	135	64	1	0		
BFBOCC	Baltic Familial Breast Ovarian Cancer Consortium	LITHUANIA/LATVIA	133	111	16	8		
BIDMC	Beth Israel Deaconess Medical Center	USA	41	44	1	1		
BMBSA	BRCA-gene mutations and breast cancer in South African women	SOUTH AFRICA	21	37	2	1		
BRICOH	Beckman Research Institute of the City of Hope	USA	96	50	11	9		
CBCS	Rigshospitalet	DENMARK	110	75	80	57		
CNIO	Spanish National Cancer Centre	SPAIN	32	31	49	44		
СОН	City of Hope Cancer Center	USA	84	141	6	8		
CONSIT TEAM	CONsorzio Studi ITaliani sui Tumori Ereditari Alla Mammella	ITALY	265	271	217	234		
DEMOKRITOS	National Centre for Scientific Research Demokritos	GREECE	85	132	12	20		
DFCI	Dana-Farber Cancer Institute	USA	82	65	3	4		
DKFZ	German Cancer Research Center	GERMANY	19	36	0	2		
EMBRACE	Epidemiological Study of Familial Breast Cancer	UK/IRELAND	907	785	14	13		
FCCC	Fox Chase Cancer Center	USA	49	26	20	19		
FPGMX	Fundación Pública Galega de Medicina Xenómica	SPAIN	40	61				
GC-HBOC	German Familial Breast Group	GERMANY	673	1145	54	111		
GEMO	Genetic Modifiers of cancer risk in BRCA1/2 mutation carriers	FRANCE/USA	630	842	114	111		
GEORGETOWN	Georgetown University	USA	6	5	1	2		
G-FAST	Ghent University Hospital	BELGIUM	69	121	91	42		
HCSC	Hospital Clinico San Carlos	SPAIN	85	55	5	6		
HEBCS	Helsinki Breast Cancer Study	FINLAND	67	53	3	5		
HEBON	Genen Omgeving studie van de werkgroep Hereditiair Borstkanker Onderzoek Nederland	NETHERLANDS	500	372	220	202		
HUNBOCS	Molecular Genetic Studies of Breast- and Ovarian Cancer in Hungary	HUNGARY	101	179				
HVH	University Hospital Vall d'Hebron	SPAIN	56	62	0	1		
ICO	Institut Català d'Oncologia	SPAIN	150	130	5	1		
IHCC	International Hereditary Cancer Centre	POLAND	121	77	279	223		
INHERIT	INterdisciplinary HEalth Research Internal Team BReast CAncer susceptibility	CANADA (QUEBEC)	52	37	6	2		
IOVHBOCS	Istituto Oncologico Veneto	ITALY	93	111	5	4		
IPOBCS	Portuguese Oncology Institute-Porto Breast Cancer Study	PORTUGAL	79	36	1	2		
KCONFAB	Kathleen Cuningham Consortium for Research into Familial Breast Cancer	AUSTRALIA	355	366	24	26		
KUMC	University of Kansas Medical Center	USA	3	11				
MAYO	Mayo Clinic	USA	126	121	12	10		
MCGILL	McGill University	CANADA (QUEBEC)	30	24				
MODSQUAD	Modifier Study of Quantitative Effects on Disease	CZECH REPUBLIC			68	106		
MSKCC	Memorial Sloane Kettering Cancer Center	USA	193	185	32	59		
MUV	General Hospital Vienna	AUSTRIA	266	268	11	11		
NAROD	Women's College Research Institute Hereditary Breast and Ovarian Cancer Study	CANADA			100	46		
NCI	National Cancer Institute	USA	108	42	6	1		
NNPIO	N.N. Petrov Institute of Oncology	RUSSIA	22	44	1	4		
NORTHSHORE	NorthShore University HealthSystem	USA	40	40		-		
NRG_UNCOLUGY	NKG Uncology	USA/AUSTRALIA	153	166	4	/		
OCGN	Untario Cancer Genetics Network	LICA	133	71	0	4		
	Ine Unio State University Comprenensive Cancer Center	DENMARK	34	39	8	10		
DRCS	Università di Disa		300	192	10	10		
SMC	Shaha Madical Centre	ISPACI	39	49	57	41		
SIVIC	Swedich Breast Cancer Study	SWEDEN	39	199	57	29		
	Juniversity of Chicago	USA	51	43	7	0		
LICSE	University of California San Francisco	USA	60	32	16	15		
UKGREOCR	UK and Gilda Radner Familial Ovarian Cancer Registries	UK	40	13	5	0		
UPFNN	University of Pennsylvania	USA	218	239	11	22		
UPITT	Cancer Family Registry University of Pittsburg	USA	77	77				
UTMDACC	University of Texas MD Anderson Cancer Center	USA	18	25	27	45		
VFCTG	Victorian Familial Cancer Trials Group	AUSTRALIA	104	103	2	1		
WCP	Women's Cancer Program at Cedars-Sinai Medical Center	USA	137	50	10	6		

Supplementary	Table 1: BCAC studies contributing data on estrogen receptor negative cases and controls, by genotyping intiative †		OncoA		icoc	¢	GWASs		
Acronym	Study Name	Country	Study design	Controls	Cases	Controls	Cases	Controls	Cases
ABCFS	Australian Breast Cancer Family Study	Australia	Case-control study	188	62	551	204	285	72
ABCS	Amsterdam Breast Cancer Study	Netherlands	Case-control study	4	27	1815	154		
ABCTB	Australian Breast Cancer Tissue Bank	Australia	Case-control study	374	290				
BBCC	Bavarian Breast Cancer Cases and Controls	Germany	Case-control study	248	354	458	67		
BBCS	British Breast Cancer Study	UK	Case-control study	442	18	1397	108		
BCEES	Breast Cancer Employment and Environment Study	Australia USA Capada Australia	Case-control study	834	115			2251	022
BCFR-NY	New York site of the Reast Carrer Family Registry	USA, canada, Austrana	Case-control study	27	60			2251	322
BCFR-PA	Philadelphia site of the Breast Cancer Family Registry	USA	Case-control study	0	27				
BCFR-UT	Utah site of the Breast Cancer Family Registry	USA	Case-control study	0	13				
BCINIS	Breast Cancer in Northern Israel Study	Israel	Case-control study	723	262				
BIGGS	Breast Cancer in Galway Genetic Study	Ireland	Case-control study			719	154		
BPC3	Breast and Prostate Cancer Cohort Consortium	International	Prospective cohorts: nested case-control studies					2305	1998
BREOGAN	Breast Oncology Galicia Network	Spain	Case-control study	725	246				
BSUCH	Breast Cancer Study of the University of Heidelberg	Germany	Case-control study	167	42	954	157		
CBCS	Canadian Breast Cancer Study	Canada	Case-control study	81/	119				
CECILE	CFCIE Breast Cancer Study	France	Case-control study	332	1//	999	144		
CGPS	Conenhagen General Ponulation Study	Denmark	Case-control study	712	160	4534	357		
CNIO-BCS	Spanish National Cancer Centre Breast Cancer Study	Spain	Case-control study			876	88		
CPSII	Cancer Prevention Study-II Nutrition Cohort	USA	Prospective cohort: nested case-control study	3025	99				
CTS	California Teachers Study	USA	Prospective cohort: nested case-control study	577	126	71	68		
DEMOKRITOS	Demokritos	Greece	Case-control study			95	413		
DIETCOMPLYF	DietCompLyf Breast Cancer Survival Study	UK	Prospective cohort: nested case-control study	0	104				
EPIC	European Prospective Investigation Into Cancer and Nutrition	International (Europe)	Prospective cohort: nested case-control study	3522	179				
ESTHER	ESTHER Breast Cancer Study	Germany	Case-control study	3	1	502	98		
GC-HBOC*	German Consortium for Hereditary Breast & Ovarian Cancer	Germany	Case-control study	1593	358	168			
GENICA	Gene Environment Interaction and Breast Cancer in Germany	Germany	Case-control study	284	78	427	104		
GEPARSIATO	Kanoomized phase II thai Gonatic Enidemicians Study of Proact Cancer by Are 50	Germany	Case-only study	190	122				
HABOS	Genetic chicemonogy study of breast cancer by Age 50 Hannower Repart Cancer Study	Germany	Case-control study	865	147				
HCSC	Hospital Clinico San Carlos	Spain	Case-control study	0	109				
HEBCS	Helsinki Breast Cancer Study	Finland	Case-control study	2	14	1233	235	1012	145
HMBCS	Hannover-Minsk Breast Cancer Study	Belarus	Case-control study	214	7	130	8		
HUBCS	Hannover-Ufa Breast Cancer Study	Russia	Case-control study	131	18				
KARBAC	Karolinska Breast Cancer Study	Sweden	Case-control study	0	3	662	63		
KBCP	Kuopio Breast Cancer Project	Finland	Case-control study	182	23	250	97		
KConFab/AOCS	Kathleen Cuningham Foundation Consortium for research into Familial Breast Cancer/Australian Ovarian Cancer Study	Australia and New Zeland	Case-control study	425	145	897	55		
LIVIDE	Leuven mututiscipinary breast centre	Macadonia	Case-control study	435	145	1300	5/6		
MARIE	Mammary Carcinoma Risk Eactor Investigation	Germany	Case-control study	288	8	1778	346	470	76
MBCSG	Milan Breast Cancer Study Group	Italy	Case-control study	366	75	400	42		
MCBCS	Mayo Clinic Breast Cancer Study	USA	Case-control study	179	84	1931	269		
MCCS	Melbourne Collaborative Cohort Study	Australia	Prospective cohort: nested case-control study	712	77	511	110		
MEC	Multiethnic Cohort	USA	Prospective cohort: nested case-control study	127	3	741	87		
MISS	Melanoma Inquiry of Southern Sweder	Sweden	Prospective cohort: nested case-control study	1523	79				
MMHS	Mayo Mammography Health Study	USA	Prospective cohort: nested case-control study	1605	50	426	<i>C</i> 4		
NILGEBUS	Monumeral generativity	Nonway	Case-control study	29	2	430	200		
NBHS	Notwegian breast Cancer Study	LISA	Case-control study	613	163	118	125		
NC-BCFR	Northern California Breast Cancer Family Registry	USA	Case-control study	149	261	110	125		
NHS	Nurses Health Study	USA	Prospective cohort: nested case-control study	1804	203				
NHS2	Nurses Health Study 2	USA	Prospective cohort: nested case-control study	1905	224				
OBCS	Oulu Breast Cancer Study	Finland	Case-control study			414	100		
OFBCR	Ontario Familial Breast Cancer Registry	Canada	Case-control study	217	259	511	269		
ORIGO	Leiden University Medical Centre Breast Cancer Study	Netherlands	Prospective conort: nested case-control study	660	230	327	207		
PRCS	On Date Onversity	Poland	Case-control study	1658	547	205	207		
pKARMA	Karolinska Mammography Project for Risk Prediction of Breast Cancer - Case-Control Study	Sweden	Case-control study	6042	166	5568	701		
PLCO	The Prostate, Lung, Colorectal and Ovarian (PLCO) Cancer Screening Trial	USA	Prospective cohort: nested case-control study	858	184				
POSH	Prospective Study of Outcomes in Sporadic Versus Hereditary Breast Cancer	UK	Case-only study	0	207				
PREFACE	Evaluation of Predictive Factors regarding the Effectivity of Aromatase Inhibitor Therapy	Germany	Case-only study	0	15				
RBCS	Rotterdam Breast Cancer Study	Netherlands	Case-control study	231	87	699	124		
RPCI	Roswell Park Cancer Institute	USA	Case-control study			126	136	75.0	400
SASBAC	Singapore and Sweden Breast Cancer Study Shaffiold Breast Cancer Study	Sweden	Case-control study			849	43	/56	109
SEARCH	Sinch of Enidemiology and Risk factors in Cancer Heredity	UK	Case-control study	989	420	8068	1173		
SISTER	The Siter Study	USA	Prospective cohort: nested case-control study	1560	282	0000	11/5		
2SISTER	The Two Sister Study	USA	Case-only study	0	204				
SKKDKFZS*	Städtisches Klinikum Karlsruhe Deutsches Krebsforschungszentrum Study	Germany	Case-only study	0	298	0	135		
SMC	Swedish Mammography Cohort	Sweden	Prospective cohort: nested case-control study	708	195				
SUCCESSB	Simultaneous Study of Gemcitabine-Docetaxel Combination adjuvant treatment	Germany	Case-only study	0	159				
SUCCESSC	Simultaneous Study of Docetaxel Based Anthracycline Free Adjuvant Treatment Evaluation	Germany	Case-only study	0	204	24-			
SZBCS	IHLL-Szczecin Breast Cancer Study	Poland	Case-control study	157	72	315	60	2800	000
LICIPCS	Inpre-wegative preasilitation consortium	international	Case control studies	259	288			2890	998
UK2	LIK2 GWAS	UK	Case-control study	200	/3			2663	160
UKBGS	UK Breakthrough Generations Study	UK	Prospective cohort: nested case-control study	567	78	470	22	2005	100
UKOPS	UK Ovarian Cancer Population Study	UK	Case-control study	974	0				
WHI	Women's Health Initiative	LISA	Brospostivo cohort: ported caro control study	4612	659				

WHI Women's Health Initiative TStudies participated in one or more of the following genotyping initiatives: OncoArray, ICOGS or one of eight genome-wide association studies (GWASs) \*For the analysis of ICOGS data, cases from SKORVETS and controls from GC-HBOC included as one study

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## In Silico Annotation of Candidate Causal Variants

Guide to results table (Supplementary Table 5) and UCSC Genome Browser session Each candidate causal SNP has been annotated with publicly available genomic data in order to highlight potentially functional variants, prioritise experimental validation, and predict target genes. Annotations fall into categories relating to putative effects on transcription factors, regulatory element activities, expression quantitative trait loci (eQTL) and target gene prediction. For each variant, a link to the UCSC Genome Browser is provided that shows a 1 Mb region with relevant genomic data.

## Transcription factors

Information regarding potential effects on transcription factor recognition sequences was obtained from the ENCODE-Motifs resource (http://compbio.mit.edu/encodemotifs)<sup>1</sup> using VCFtools v0.1.11 to access the downloaded HaploReg v4.0 database<sup>2</sup>. The impact each variant has on the position weight matrix for specific transcription factors is expressed as '+' or '-' for strengthened or weakened motifs relative to elements carrying the reference allele, respectively. Processed transcription factor ChIP-seq peak data for breast cell types were downloaded from ENCODE and other publications via NCBI GEO, in BED or NarrowPeak format, converted to the hg19 assembly using LiftOver if required, and given a standardised naming system (format = *"celltype;target"* in Supplementary Table 5). More details about the overlapping binding sites may be found within browser session track "TF-chip peaks overlapping candidate SNP" where TF-ChIP-seq peaks are named in the format *"Biosample\_term\_name, Experiment\_target, Biosample\_treatments, Biological\_replicate(s), File\_accession"*. All ChIP-seq datasets are listed in Supplementary Table 6. Variants were assessed for overlap with ChIP-seq peaks using BedTools v2.25.0<sup>3</sup>.

### **Regulatory features**

Histone signatures derived from histone modification ChIP-seg experiments on breast cell types carried out by ENCODE, NIH Roadmap Epigenomics, and other published studies were obtained and formatted as for ChIP-seq data. Histone modification peaks overlapping candidate causal variants are represented as "celltype; histone mark" in Supplementary Table 5 and "Biosample\_term\_name, Experiment\_target, *Biosample\_treatments, Biological\_replicate(s), File\_accession*" in the browser track "Histone modification ChIP-seq peaks overlapping candidate SNP". BedTools was used to intersect variants with histone signatures including commonly used marks associated with enhancers (H3K4me1, H3K4me2 and H3K27ac) and promoters (H3K4me3 and H3K9ac). Chromatin Hidden Markov Modelling (ChromHMM) states were obtained for breast cells from Roadmap (HMEC and myoepithelial cells) and published MCF7 data<sup>4</sup> and filtered for states corresponding to 'enhancers' (Roadmap 25-state E13, E14, E15, E16, E17, E18) or 'promoters' (Roadmap 25-state E1, E2, E3, E4, E22, E23). Chromatin state features containing candidate variants are represented as "celltype;chromatin\_state". Chromatin accessibility data obtained from ENCODE, Roadmap and other published sources via NCBI GEO measured using DNase-seg and FAIRE-seq for relevant breast cell types were also tested for overlap with candidate causal variants. Intersected regions are reported in the format "celltype;method". Scores based on RegulomeDB<sup>5</sup> are presented for available SNPs (based on dbSNP141), where lower scores are increasingly likely to be functional (http://regulomedb.org/help#score).

## <u>eQTL</u>

Genes showing expression levels correlated with query SNPs are shown in the column headed 'eQTL\_target\_all'. All genes reported to be associated with genotype in studies including GTEx version 6<sup>6</sup> (expression is any GTEx tissue, *P* value cutoff 10<sup>-6</sup>) and Westra *et al.*,<sup>7</sup> (expression in whole blood). Genes associated with genotype in GTEx breast samples (N=186) are listed in the column "eQTL\_GTEx.breast". eQTL data from TCGA and METABRIC studies for relevant variants are also presented (format "*Associated\_gene:EffectAllele:EffectDirection:P\_value*").

### Other genomic features

Chromosomal position, the lead variant for the associated locus, and potentially conflicting rsIDs (assessed as overlapping at the query position) are given for each variant. GWAS tagSNPs were downloaded from the UCSC Table Browser (December 2015) and associated traits are listed if the tagSNP is within a 10 kb window of the candidate causal variant. NCBI RefSeq gene annotations were downloaded from the UCSC Table Browser and BedTools was used to determine overlapping genes ("Overlapping\_RefGene"). The nearest RefGene transcription start site is also presented, given in the format "RefGeneTSS|distance". Basic genomic annotations such as intergenic, intronic, exonic, and untranslated regions based on RefSeq gene annotations were determined for each variant.

#### Target Gene Prediction

The column headed "Predicted target gene" lists genes predicted by various methods to be targets of, or the expression of which is associated with, regulatory elements in which the candidate causal variant lies. The reported gene is listed with cell type and method in the format "target:cell:method". A database was created comprising publicly available data based on various methods aiming to link enhancers with target genes (Annex to Supplementary Table 5). Laboratory based experimental approaches include genome-wide Chromatin Interaction Analysis with Paired-End-Tag sequencing (ChIA-PET)<sup>8</sup>, Hi-C<sup>9</sup>, and other Chromosome conformation capture (3C)-based techniques. Computational resources designed to predict target promoters by correlation of gene expression with ChIP-seq signals at specific regulatory elements including IM-PET<sup>10</sup>, PreSTIGE<sup>11</sup> and data from Hnisz et al.<sup>12</sup> are also included. These methods associate enhancers defined by histone modification ChIP-seq for H3K4me1 (PreSTIGE), H3K27ac (Hnisz), H3K4me1, H3K4me3 and H3K27ac (IM-PET) with gene expression signals measured by RNA-seq. FANTOM5<sup>13</sup> data representing enhancer-promoter cap analysis of gene expression (CAGE) expression correlation from all cell types were downloaded from http://enhancer.binf.ku.dk/. Target genes have been predicted for multiple cell types and all data were included in the database, and filtered for breast derived cell types for this analysis (see Key to Supplementary Table 5).

The following strategy was used to assign potential target genes to regulatory elements. The published computational methods (Hnisz, PreSTIGE and IM-PET) included target gene annotation in the reported data. For ChIA-PET and Hi-C data, interaction peaks were mapped to promoters defined as -1.0 kb to +0.1 kb around GENCODE (v19) transcription start sites. Enhancer definitions were used as reported for computational methods while for ChIA-PET and Hi-C were interpreted as any region interacting with a promoter (regardless of other enhancer annotation information such as histone modification or open chromatin). FANTOM5 target promoters were predefined and

tissue specificity was determined by intersecting "TSS associated enhancers" with tissue-specific sets of enhancers.

All data were formatted to enable intersection of test variants with "enhancers" as defined by each method using the Galaxy "intersect" tool<sup>14</sup>. Each enhancer-promoter assignment or interaction was represented as a single record along with details about potential target promoter, cell type, method, scoring and confidence statistics from the original publication. A set of query SNPs (or any loci with genomic positional information in BED format) could be queried into a custom Galaxy workflow leading to generation of a table of predicted gene targets and a link to the UCSC Genome Browser for visualisation.

## UCSC Genome Browser session

A custom session has been uploaded to UCSC Genome Browser<sup>15</sup> to facilitate exploration of breast cancer risk associated variation and implicated regulatory features. This can be accessed via the hyperlink (ie. "browser") in the functional annotation *xlsx* file. All standard Genome Browser data and functions are then available, including track display options (eg. right click on a particular track to activate visualisation options), highlighting regions (shift and mouse over region of interest), and the table browser (eg. to intersect or export data).

Within the session, Oncoarray candidate causal variants are shown in red, and names can be shown by activating "pack" mode (as for all tracks). Target gene prediction data from Hnisz, PreSTIGE and IM-PET shows enhancers depicted as black bars. The segment name revealed in 'pack' mode lists predicted target gene and cell-type (eg "WNT7B.MCF7"). ChIA-PET interactions, represented in BED12 format, have been filtered to remove duplicates and *trans*-chromosomal interactions. The interactions are shaded to reflect statistical confidence based on enrichment in the original experiment. ChIA-PET interaction names show the genomic co-ordinates of either-end of the interaction, the cell type (restricted to MCF7 for this analysis), the immunoprecipitation target, and the experimental replicate. Depicted interactions are restricted to those for which a candidate variant lies within an interaction "end" with the opposite end overlapping a TSS. All other interactions may be visualised by activating the standard ENCODE ChIA-PET track (\Regulation\ENCODE Chromatin Interactions Tracks\ChIA-PET from ENCODE/GIS-Ruan).

Chromatin interactions based on *in situ* Hi-C data from HMEC cells were downloaded from NCBI GEO (accession GSE63525)<sup>9</sup>. Annotated loops (representing potential enhancer-promoter interactions) processed by HiCCUPS were reformatted as BED files and tested for overlap with RefSeq promoters to assign potential target genes. Opposing ends of TSS-overlap loops were then annotated as 'potential enhancers'. Specific loop regions which overlap BC risk candidate causal variants are depicted as black segments and named "*TSS\_target.Celltype*".

Various classes of genomic data representing regulatory features which harbour candidate variants are shown as separate tracks:

- Histone modification ChIP-seq peaks overlapping candidate SNP
- DNase HS and FAIRE-seq peaks overlapping candidate SNP
- TF-chip peaks overlapping candidate SNP

As mentioned above, changing the track display to 'pack' mode will show details of the overlapping peak in the format:

"Biosample\_term\_name, Experiment\_target, Biosample\_treatments, Biological\_replicate(s), File\_accession".

A representation of all TF and histone ChIP-seq, DNase-seq, and FAIRE-seq data tested for overlap with candidate variants is shown in three histogram tracks (computed with BedTools genomeCoverageBed). These show the summed peak density at each genomic position and allow simple visualisation of loci with relative abundance of regulatory features.

Tracks for Roadmap Epigenomics Chromatin state models (based on imputed data - 25 state, 12 marks, 127 epigenomes) were generated for breast Myoepithelial and HMEC cells. Chromatin states were separated and colour coded for states related to enhancers, promoters, and transcribed regions.

The bottom track ("Oncoarray SNPs") shows all directly genotyped and imputed SNPs passing quality control (imputation  $r^2>0.3$ ) as black ticks. SNPs from dbSNP build 138 with a MAF > 0.01 in European samples which were not informative are shown in red.

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### OncoArray genotype calling and quality control

Of the 568,712 variants selected for genotyping on OncoArray, 533,631 were successfully manufactured on the array (including 778 duplicate probes). OncoArray genotyping of BCAC and CIMBA samples was conducted at six sites. Details of the genotyping calling for the OncoArray are described in more detail elsewhere<sup>16</sup>. Briefly, we developed a single calling pipeline that was applied to more than 500,000 samples. An initial cluster file was generated using from 56,284 samples, selected over all the major genotyping centres and ethnicities, using the Gentrain2 algorithm. Variants likely to have problematic clusters were selected for manual inspection using the following criteria: call rate below 99%, minor allele frequency (MAF) <0.001, poor Illumina intensity and clustering metrics, deviation from the MAF observed in the 1000 Genomes Project using the criterion:  $\frac{(|p_1-p_0|-0.01)^2}{((p_1+p_0)(2-p_1-p_0))} > C,$ where  $p_0$  and  $p_1$  are the minor frequencies in the 1000 Genome Project and Oncoarray datasets, respectively, and C=0.008. (This latter criterion is approximately equivalent to excluding SNPs on the basis of a Chi-square statistic of 16 for the difference in allele frequencies, assuming 1,000 samples in each group). This resulted in manual adjustment of the cluster file for 3,964 variants, and the exclusion of 16,526 variants. The final cluster file was then applied to the full dataset.

We excluded SNPs with a call rate <95% in any consortium, not in Hardy-Weinberg equilibrium (P<10<sup>-7</sup> in controls, or P<10<sup>-12</sup> in cases) or with concordance <98% among 5,280 duplicate pairs. For the imputation, we additionally excluded SNPs with a MAF<1% and a call rate <98% in any consortium, SNPs that could not be linked to the 1000 Genomes Project reference, those with MAF for Europeans that differed from that for the 1000 Genomes Project and a further 1,128 SNPs where the cluster plot was judged to be not ideal. Of the 533,631 SNPs which were manufactured on the array, 494,763 passed the initial QC and 469,364 were used in the imputation (see below).

For BCAC, we excluded probable duplicate samples and close relatives within each study, and probable duplicates between studies. These were identified by identity by state (IBS) analysis using a set of approximately 38,000 uncorrelated ( $r^2$ <0.1) SNPs for OncoArray and iCOGS and 16,000 SNPs for GWAS. Based on inspection of the distribution of IBS values, we identified first-degree relative pairs using the criterion 0.82<IBS<0.90 for OncoArray and 0.85<IBS<0.90 for iCOGS; similar criteria were used for each GWAS (with limits depending on the IBS distribution in that study).

We applied LD score regression to the summary results from GWAS, iCOGS and OncoArray to assess the evidence of overlap in individuals between the three datasets. We conducted three pair-wise cross-trait regression analyses (GWAS-iCOGS, GWAS-OncoArray and iCOGS-OncoArray) and used the intercept from the regression analysis to estimate the amount of overlap<sup>17</sup>. Assuming that the phenotypic correlation is 1 (that is, a case is a case in all datasets and a control is a control in all datasets), we found that for GWAS-iCOGS, the estimated overlap was 1.5% of individuals, for GWAS-OncoArray, the estimated overlap was 0.2% of individuals. It is unlikely that this degree of overlap would have influenced the results obtained from our analyses.

We also excluded samples with a call rate <95% and samples with extreme heterozygosity (>4.9 standard deviations from the mean for the reported ethnicity). Ancestry analysis was performed using a standardized approach in which 2,318 ancestry informative markers with minor allele frequencies of 0.05 on a subset of ~66,000 samples including 505 Hapmap 2 samples. The contribution of each of the three major continental ancestry groups (European, Asian and African) was estimated by mapping each individual to regions of a triangle based on the first two principal components, as implemented in the software package FastPop (<u>http://sourceforge.net/projects/fastpop/</u>)<sup>18</sup>. Individuals were thus classified into 4 groups: European (defined as >80% European ancestry), East Asian (>40% Asian ancestry), African (>20% African ancestry) and other (not fulfilling any of the above criteria)<sup>16</sup>. Of the 152,492 samples genotyped, the final dataset consisted of 142,072 samples, of which 9,655 ER-negative cases and 45,494 controls of European origin had not been included in a previous GWAS and had not been genotyped using iCOGS and were included in this analysis.

For the CIMBA samples we excluded individuals of non-European ancestry using multi-dimensional scaling. For this purpose we selected 30,733 uncorrelated autosomal SNPs (pair-wise  $r^2 < 0.10$ ) to compute the genomic kinship between all pairs of *BRCA1* and *BRCA2* carriers, along with 267 HapMap samples (CHB, JPT,

YRI and CEU). These were converted to distances and subjected to multidimensional scaling. Using the first two components, we calculated the proportion of European ancestry for each individual and excluded samples with >27% non-European ancestry to ensure that samples of Ashkenazi Jewish ancestry were included in the final sample.

## **Global Genomic Enrichment Analyses (further details)**

We created a "full baseline model" as previously described<sup>19</sup> that included 52 "baseline" genomic features (24 non-cell-type specific publicly available annotations, a 500-bp window around each of the 24 annotations and a 100-bp window around each of four ChIP-seq peaks) and one category containing all SNPs. We estimated the enrichment for these 53 functional categories in a single multivariable LD score regression analysis.

We subsequently performed analyses using cell-type specific annotations for the four histone marks H3K4me1, H3K4me3, H3K9ac and H3K27ac across 27-81 cell types, depending on histone mark, giving a total of 220 cell-type specific marks<sup>19</sup>. We estimated the enrichment for each of these marks after adjusting for the baseline annotations by running 220 LD score regressions, each adding a different histone mark to the baseline model. We observed no associations after adjusting for 220 tests

# Pathway Enrichment Analyses (further details)

Pathway enrichment analysis was performed to identify pathways associated with ER-negative breast cancer risk, pointing to biological hypotheses that can be further tested experimentally.

The pathway gene set database used contains pathway gene sets from Reactome<sup>20</sup>, NCI Pathway Interaction Database<sup>21</sup>, GO (Gene Ontology) biological process<sup>22</sup>, HumanCyc<sup>23</sup>, MSigdb<sup>24</sup>, NetPath<sup>25</sup> and Panther<sup>26</sup>. GO pathways inferred from electronic annotation terms were excluded. Some manual annotation was performed on the pathway gene set database where annotation errors from public data were discovered. In particular, in several pathways, the PDPK1 gene was mistakenly entered as PDK1 gene and was manually corrected. The same pathway (e.g. apoptosis) may be defined in two or more databases with potentially different sets of genes, and all versions of these duplicate/overlapping pathways were included.

Gene information (hg19) was downloaded from the ANNOVAR<sup>27</sup> website (http://www.openbioinformatics.org/annovar/). Some pathways include genes that are also grouped closely together in the genome and are thus are likely to share the significance of a single SNP, which would artificially increase the pathway significance in our analysis. This was the case for pathways including histone genes. Thus, we selected representative SNP-gene associations to control for this effect (chr6:26055031 for HIST1, chr1:120904839, 149864043 for HIST2, chr1: 228615251 for HIST3 and chr12: 14919727 for HIST4). Although there are several methods for pathway enrichment analysis, we chose the GSEA approach as it is one of the most established methods that is threshold free; many other methods such as SRT, ALIGATOR and Plink set-based test require an arbitrary p-value threshold to be defined for SNPs and applied before pathway analysis.

To focus on pathway enrichment analysis results about which we were most confident, we implemented a number of filters. First, only pathways with positive ES and containing at least one gene linked to a significant SNP ( $P<5x10^{-8}$ ) were retained for subsequent analysis. Second, we defined an ES threshold (ES≥0.41) based on a comparison with a gold standard pathway enrichment analysis we previously performed on the iCOGS data alone and where we were able to analytically compute FDR values by shuffling case/control labels (this was not computationally feasible with the more complex meta-analysis scheme used in this paper).

We chose the true positive rate (TPR) threshold by varying the TPR in steps of 0.1 and observing how the FPR changed. A TPR of 0.1 resulted in a very low FPR (0.02), but we considered this to be unduly conservative as it resulted in a small number of pathways (37, clustered into 8 themes) and excluded many pathways known to be involved in breast cancer. A TPR of 0.20 (FPR = 0.14) gave a reasonable balance between the true and false positive rates, while including pathways known to be involved in breast cancer. Thus this threshold was chosen for this study. A TPR of 0.3 gave an FPR of 0.30, which we considered high; further, the resulting additional pathways included (in addition to those included at TPR=0.2) were weaker (i.e. they had worse enrichment scores [ES<0.41] and had relatively very few genes included) than pathways appearing at lower FPRs (and TPRs). We rejected TPR thresholds >0.3 because each gave an FPR that was larger than the TPR.

Finally, we performed an in depth literature search on all resulting pathways to confirm their relevance to breast cancer biology, applying the following criteria: 1) reported in at least one of five published breast cancer pathway analyses<sup>28-32</sup>; or 2) reported elsewhere in the literature to be involved in breast cancer. We also removed pathways that were significant due to incorrect gene function annotation.

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## In Silico Annotation of Candidate Causal Variants

Guide to results table (Supplementary Table 5) and UCSC Genome Browser session Each candidate causal SNP has been annotated with publicly available genomic data in order to highlight potentially functional variants, prioritise experimental validation, and predict target genes. Annotations fall into categories relating to putative effects on transcription factors, regulatory element activities, expression quantitative trait loci (eQTL) and target gene prediction. For each variant, a link to the UCSC Genome Browser is provided that shows a 1 Mb region with relevant genomic data.

## Transcription factors

Information regarding potential effects on transcription factor recognition sequences was obtained from the ENCODE-Motifs resource (http://compbio.mit.edu/encodemotifs)<sup>1</sup> using VCFtools v0.1.11 to access the downloaded HaploReg v4.0 database<sup>2</sup>. The impact each variant has on the position weight matrix for specific transcription factors is expressed as '+' or '-' for strengthened or weakened motifs relative to elements carrying the reference allele, respectively. Processed transcription factor ChIP-seq peak data for breast cell types were downloaded from ENCODE and other publications via NCBI GEO, in BED or NarrowPeak format, converted to the hg19 assembly using LiftOver if required, and given a standardised naming system (format = *"celltype;target"* in Supplementary Table 5). More details about the overlapping binding sites may be found within browser session track "TF-chip peaks overlapping candidate SNP" where TF-ChIP-seq peaks are named in the format *"Biosample\_term\_name, Experiment\_target, Biosample\_treatments, Biological\_replicate(s), File\_accession"*. All ChIP-seq datasets are listed in Supplementary Table 6. Variants were assessed for overlap with ChIP-seq peaks using BedTools v2.25.0<sup>3</sup>.

### **Regulatory features**

Histone signatures derived from histone modification ChIP-seg experiments on breast cell types carried out by ENCODE, NIH Roadmap Epigenomics, and other published studies were obtained and formatted as for ChIP-seq data. Histone modification peaks overlapping candidate causal variants are represented as "celltype; histone mark" in Supplementary Table 5 and "Biosample\_term\_name, Experiment\_target, *Biosample\_treatments, Biological\_replicate(s), File\_accession*" in the browser track "Histone modification ChIP-seq peaks overlapping candidate SNP". BedTools was used to intersect variants with histone signatures including commonly used marks associated with enhancers (H3K4me1, H3K4me2 and H3K27ac) and promoters (H3K4me3 and H3K9ac). Chromatin Hidden Markov Modelling (ChromHMM) states were obtained for breast cells from Roadmap (HMEC and myoepithelial cells) and published MCF7 data<sup>4</sup> and filtered for states corresponding to 'enhancers' (Roadmap 25-state E13, E14, E15, E16, E17, E18) or 'promoters' (Roadmap 25-state E1, E2, E3, E4, E22, E23). Chromatin state features containing candidate variants are represented as "celltype;chromatin\_state". Chromatin accessibility data obtained from ENCODE, Roadmap and other published sources via NCBI GEO measured using DNase-seg and FAIRE-seq for relevant breast cell types were also tested for overlap with candidate causal variants. Intersected regions are reported in the format "celltype;method". Scores based on RegulomeDB<sup>5</sup> are presented for available SNPs (based on dbSNP141), where lower scores are increasingly likely to be functional (http://regulomedb.org/help#score).

## <u>eQTL</u>

Genes showing expression levels correlated with query SNPs are shown in the column headed 'eQTL\_target\_all'. All genes reported to be associated with genotype in studies including GTEx version 6<sup>6</sup> (expression is any GTEx tissue, *P* value cutoff 10<sup>-6</sup>) and Westra *et al.*,<sup>7</sup> (expression in whole blood). Genes associated with genotype in GTEx breast samples (N=186) are listed in the column "eQTL\_GTEx.breast". eQTL data from TCGA and METABRIC studies for relevant variants are also presented (format "*Associated\_gene:EffectAllele:EffectDirection:P\_value*").

### Other genomic features

Chromosomal position, the lead variant for the associated locus, and potentially conflicting rsIDs (assessed as overlapping at the query position) are given for each variant. GWAS tagSNPs were downloaded from the UCSC Table Browser (December 2015) and associated traits are listed if the tagSNP is within a 10 kb window of the candidate causal variant. NCBI RefSeq gene annotations were downloaded from the UCSC Table Browser and BedTools was used to determine overlapping genes ("Overlapping\_RefGene"). The nearest RefGene transcription start site is also presented, given in the format "RefGeneTSS|distance". Basic genomic annotations such as intergenic, intronic, exonic, and untranslated regions based on RefSeq gene annotations were determined for each variant.

#### Target Gene Prediction

The column headed "Predicted target gene" lists genes predicted by various methods to be targets of, or the expression of which is associated with, regulatory elements in which the candidate causal variant lies. The reported gene is listed with cell type and method in the format "target:cell:method". A database was created comprising publicly available data based on various methods aiming to link enhancers with target genes (Annex to Supplementary Table 5). Laboratory based experimental approaches include genome-wide Chromatin Interaction Analysis with Paired-End-Tag sequencing (ChIA-PET)<sup>8</sup>, Hi-C<sup>9</sup>, and other Chromosome conformation capture (3C)-based techniques. Computational resources designed to predict target promoters by correlation of gene expression with ChIP-seq signals at specific regulatory elements including IM-PET<sup>10</sup>, PreSTIGE<sup>11</sup> and data from Hnisz et al.<sup>12</sup> are also included. These methods associate enhancers defined by histone modification ChIP-seq for H3K4me1 (PreSTIGE), H3K27ac (Hnisz), H3K4me1, H3K4me3 and H3K27ac (IM-PET) with gene expression signals measured by RNA-seq. FANTOM5<sup>13</sup> data representing enhancer-promoter cap analysis of gene expression (CAGE) expression correlation from all cell types were downloaded from http://enhancer.binf.ku.dk/. Target genes have been predicted for multiple cell types and all data were included in the database, and filtered for breast derived cell types for this analysis (see Key to Supplementary Table 5).

The following strategy was used to assign potential target genes to regulatory elements. The published computational methods (Hnisz, PreSTIGE and IM-PET) included target gene annotation in the reported data. For ChIA-PET and Hi-C data, interaction peaks were mapped to promoters defined as -1.0 kb to +0.1 kb around GENCODE (v19) transcription start sites. Enhancer definitions were used as reported for computational methods while for ChIA-PET and Hi-C were interpreted as any region interacting with a promoter (regardless of other enhancer annotation information such as histone modification or open chromatin). FANTOM5 target promoters were predefined and

tissue specificity was determined by intersecting "TSS associated enhancers" with tissue-specific sets of enhancers.

All data were formatted to enable intersection of test variants with "enhancers" as defined by each method using the Galaxy "intersect" tool<sup>14</sup>. Each enhancer-promoter assignment or interaction was represented as a single record along with details about potential target promoter, cell type, method, scoring and confidence statistics from the original publication. A set of query SNPs (or any loci with genomic positional information in BED format) could be queried into a custom Galaxy workflow leading to generation of a table of predicted gene targets and a link to the UCSC Genome Browser for visualisation.

## UCSC Genome Browser session

A custom session has been uploaded to UCSC Genome Browser<sup>15</sup> to facilitate exploration of breast cancer risk associated variation and implicated regulatory features. This can be accessed via the hyperlink (ie. "browser") in the functional annotation *xlsx* file. All standard Genome Browser data and functions are then available, including track display options (eg. right click on a particular track to activate visualisation options), highlighting regions (shift and mouse over region of interest), and the table browser (eg. to intersect or export data).

Within the session, Oncoarray candidate causal variants are shown in red, and names can be shown by activating "pack" mode (as for all tracks). Target gene prediction data from Hnisz, PreSTIGE and IM-PET shows enhancers depicted as black bars. The segment name revealed in 'pack' mode lists predicted target gene and cell-type (eg "WNT7B.MCF7"). ChIA-PET interactions, represented in BED12 format, have been filtered to remove duplicates and *trans*-chromosomal interactions. The interactions are shaded to reflect statistical confidence based on enrichment in the original experiment. ChIA-PET interaction names show the genomic co-ordinates of either-end of the interaction, the cell type (restricted to MCF7 for this analysis), the immunoprecipitation target, and the experimental replicate. Depicted interactions are restricted to those for which a candidate variant lies within an interaction "end" with the opposite end overlapping a TSS. All other interactions may be visualised by activating the standard ENCODE ChIA-PET track (\Regulation\ENCODE Chromatin Interactions Tracks\ChIA-PET from ENCODE/GIS-Ruan).

Chromatin interactions based on *in situ* Hi-C data from HMEC cells were downloaded from NCBI GEO (accession GSE63525)<sup>9</sup>. Annotated loops (representing potential enhancer-promoter interactions) processed by HiCCUPS were reformatted as BED files and tested for overlap with RefSeq promoters to assign potential target genes. Opposing ends of TSS-overlap loops were then annotated as 'potential enhancers'. Specific loop regions which overlap BC risk candidate causal variants are depicted as black segments and named "*TSS\_target.Celltype*".

Various classes of genomic data representing regulatory features which harbour candidate variants are shown as separate tracks:

- Histone modification ChIP-seq peaks overlapping candidate SNP
- DNase HS and FAIRE-seq peaks overlapping candidate SNP
- TF-chip peaks overlapping candidate SNP

As mentioned above, changing the track display to 'pack' mode will show details of the overlapping peak in the format:

"Biosample\_term\_name, Experiment\_target, Biosample\_treatments, Biological\_replicate(s), File\_accession".

A representation of all TF and histone ChIP-seq, DNase-seq, and FAIRE-seq data tested for overlap with candidate variants is shown in three histogram tracks (computed with BedTools genomeCoverageBed). These show the summed peak density at each genomic position and allow simple visualisation of loci with relative abundance of regulatory features.

Tracks for Roadmap Epigenomics Chromatin state models (based on imputed data - 25 state, 12 marks, 127 epigenomes) were generated for breast Myoepithelial and HMEC cells. Chromatin states were separated and colour coded for states related to enhancers, promoters, and transcribed regions.

The bottom track ("Oncoarray SNPs") shows all directly genotyped and imputed SNPs passing quality control (imputation  $r^2>0.3$ ) as black ticks. SNPs from dbSNP build 138 with a MAF > 0.01 in European samples which were not informative are shown in red.

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### OncoArray genotype calling and quality control

Of the 568,712 variants selected for genotyping on OncoArray, 533,631 were successfully manufactured on the array (including 778 duplicate probes). OncoArray genotyping of BCAC and CIMBA samples was conducted at six sites. Details of the genotyping calling for the OncoArray are described in more detail elsewhere<sup>16</sup>. Briefly, we developed a single calling pipeline that was applied to more than 500,000 samples. An initial cluster file was generated using from 56,284 samples, selected over all the major genotyping centres and ethnicities, using the Gentrain2 algorithm. Variants likely to have problematic clusters were selected for manual inspection using the following criteria: call rate below 99%, minor allele frequency (MAF) <0.001, poor Illumina intensity and clustering metrics, deviation from the MAF observed in the 1000 Genomes Project using the criterion:  $\frac{(|p_1-p_0|-0.01)^2}{((p_1+p_0)(2-p_1-p_0))} > C,$ where  $p_0$  and  $p_1$  are the minor frequencies in the 1000 Genome Project and Oncoarray datasets, respectively, and C=0.008. (This latter criterion is approximately equivalent to excluding SNPs on the basis of a Chi-square statistic of 16 for the difference in allele frequencies, assuming 1,000 samples in each group). This resulted in manual adjustment of the cluster file for 3,964 variants, and the exclusion of 16,526 variants. The final cluster file was then applied to the full dataset.

We excluded SNPs with a call rate <95% in any consortium, not in Hardy-Weinberg equilibrium (P<10<sup>-7</sup> in controls, or P<10<sup>-12</sup> in cases) or with concordance <98% among 5,280 duplicate pairs. For the imputation, we additionally excluded SNPs with a MAF<1% and a call rate <98% in any consortium, SNPs that could not be linked to the 1000 Genomes Project reference, those with MAF for Europeans that differed from that for the 1000 Genomes Project and a further 1,128 SNPs where the cluster plot was judged to be not ideal. Of the 533,631 SNPs which were manufactured on the array, 494,763 passed the initial QC and 469,364 were used in the imputation (see below).

For BCAC, we excluded probable duplicate samples and close relatives within each study, and probable duplicates between studies. These were identified by identity by state (IBS) analysis using a set of approximately 38,000 uncorrelated ( $r^2$ <0.1) SNPs for OncoArray and iCOGS and 16,000 SNPs for GWAS. Based on inspection of the distribution of IBS values, we identified first-degree relative pairs using the criterion 0.82<IBS<0.90 for OncoArray and 0.85<IBS<0.90 for iCOGS; similar criteria were used for each GWAS (with limits depending on the IBS distribution in that study).

We applied LD score regression to the summary results from GWAS, iCOGS and OncoArray to assess the evidence of overlap in individuals between the three datasets. We conducted three pair-wise cross-trait regression analyses (GWAS-iCOGS, GWAS-OncoArray and iCOGS-OncoArray) and used the intercept from the regression analysis to estimate the amount of overlap<sup>17</sup>. Assuming that the phenotypic correlation is 1 (that is, a case is a case in all datasets and a control is a control in all datasets), we found that for GWAS-iCOGS, the estimated overlap was 1.5% of individuals, for GWAS-OncoArray, the estimated overlap was 0.2% of individuals. It is unlikely that this degree of overlap would have influenced the results obtained from our analyses.

We also excluded samples with a call rate <95% and samples with extreme heterozygosity (>4.9 standard deviations from the mean for the reported ethnicity). Ancestry analysis was performed using a standardized approach in which 2,318 ancestry informative markers with minor allele frequencies of 0.05 on a subset of ~66,000 samples including 505 Hapmap 2 samples. The contribution of each of the three major continental ancestry groups (European, Asian and African) was estimated by mapping each individual to regions of a triangle based on the first two principal components, as implemented in the software package FastPop (<u>http://sourceforge.net/projects/fastpop/</u>)<sup>18</sup>. Individuals were thus classified into 4 groups: European (defined as >80% European ancestry), East Asian (>40% Asian ancestry), African (>20% African ancestry) and other (not fulfilling any of the above criteria)<sup>16</sup>. Of the 152,492 samples genotyped, the final dataset consisted of 142,072 samples, of which 9,655 ER-negative cases and 45,494 controls of European origin had not been included in a previous GWAS and had not been genotyped using iCOGS and were included in this analysis.

For the CIMBA samples we excluded individuals of non-European ancestry using multi-dimensional scaling. For this purpose we selected 30,733 uncorrelated autosomal SNPs (pair-wise  $r^2 < 0.10$ ) to compute the genomic kinship between all pairs of *BRCA1* and *BRCA2* carriers, along with 267 HapMap samples (CHB, JPT,

YRI and CEU). These were converted to distances and subjected to multidimensional scaling. Using the first two components, we calculated the proportion of European ancestry for each individual and excluded samples with >27% non-European ancestry to ensure that samples of Ashkenazi Jewish ancestry were included in the final sample.

## **Global Genomic Enrichment Analyses (further details)**

We created a "full baseline model" as previously described<sup>19</sup> that included 52 "baseline" genomic features (24 non-cell-type specific publicly available annotations, a 500-bp window around each of the 24 annotations and a 100-bp window around each of four ChIP-seq peaks) and one category containing all SNPs. We estimated the enrichment for these 53 functional categories in a single multivariable LD score regression analysis.

We subsequently performed analyses using cell-type specific annotations for the four histone marks H3K4me1, H3K4me3, H3K9ac and H3K27ac across 27-81 cell types, depending on histone mark, giving a total of 220 cell-type specific marks<sup>19</sup>. We estimated the enrichment for each of these marks after adjusting for the baseline annotations by running 220 LD score regressions, each adding a different histone mark to the baseline model. We observed no associations after adjusting for 220 tests

# Pathway Enrichment Analyses (further details)

Pathway enrichment analysis was performed to identify pathways associated with ER-negative breast cancer risk, pointing to biological hypotheses that can be further tested experimentally.

The pathway gene set database used contains pathway gene sets from Reactome<sup>20</sup>, NCI Pathway Interaction Database<sup>21</sup>, GO (Gene Ontology) biological process<sup>22</sup>, HumanCyc<sup>23</sup>, MSigdb<sup>24</sup>, NetPath<sup>25</sup> and Panther<sup>26</sup>. GO pathways inferred from electronic annotation terms were excluded. Some manual annotation was performed on the pathway gene set database where annotation errors from public data were discovered. In particular, in several pathways, the PDPK1 gene was mistakenly entered as PDK1 gene and was manually corrected. The same pathway (e.g. apoptosis) may be defined in two or more databases with potentially different sets of genes, and all versions of these duplicate/overlapping pathways were included.

Gene information (hg19) was downloaded from the ANNOVAR<sup>27</sup> website (http://www.openbioinformatics.org/annovar/). Some pathways include genes that are also grouped closely together in the genome and are thus are likely to share the significance of a single SNP, which would artificially increase the pathway significance in our analysis. This was the case for pathways including histone genes. Thus, we selected representative SNP-gene associations to control for this effect (chr6:26055031 for HIST1, chr1:120904839, 149864043 for HIST2, chr1: 228615251 for HIST3 and chr12: 14919727 for HIST4). Although there are several methods for pathway enrichment analysis, we chose the GSEA approach as it is one of the most established methods that is threshold free; many other methods such as SRT, ALIGATOR and Plink set-based test require an arbitrary p-value threshold to be defined for SNPs and applied before pathway analysis.

To focus on pathway enrichment analysis results about which we were most confident, we implemented a number of filters. First, only pathways with positive ES and containing at least one gene linked to a significant SNP ( $P<5x10^{-8}$ ) were retained for subsequent analysis. Second, we defined an ES threshold (ES≥0.41) based on a comparison with a gold standard pathway enrichment analysis we previously performed on the iCOGS data alone and where we were able to analytically compute FDR values by shuffling case/control labels (this was not computationally feasible with the more complex meta-analysis scheme used in this paper).

We chose the true positive rate (TPR) threshold by varying the TPR in steps of 0.1 and observing how the FPR changed. A TPR of 0.1 resulted in a very low FPR (0.02), but we considered this to be unduly conservative as it resulted in a small number of pathways (37, clustered into 8 themes) and excluded many pathways known to be involved in breast cancer. A TPR of 0.20 (FPR = 0.14) gave a reasonable balance between the true and false positive rates, while including pathways known to be involved in breast cancer. Thus this threshold was chosen for this study. A TPR of 0.3 gave an FPR of 0.30, which we considered high; further, the resulting additional pathways included (in addition to those included at TPR=0.2) were weaker (i.e. they had worse enrichment scores [ES<0.41] and had relatively very few genes included) than pathways appearing at lower FPRs (and TPRs). We rejected TPR thresholds >0.3 because each gave an FPR that was larger than the TPR.

Finally, we performed an in depth literature search on all resulting pathways to confirm their relevance to breast cancer biology, applying the following criteria: 1) reported in at least one of five published breast cancer pathway analyses<sup>28-32</sup>; or 2) reported elsewhere in the literature to be involved in breast cancer. We also removed pathways that were significant due to incorrect gene function annotation.

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## In Silico Annotation of Candidate Causal Variants

Guide to results table (Supplementary Table 5) and UCSC Genome Browser session Each candidate causal SNP has been annotated with publicly available genomic data in order to highlight potentially functional variants, prioritise experimental validation, and predict target genes. Annotations fall into categories relating to putative effects on transcription factors, regulatory element activities, expression quantitative trait loci (eQTL) and target gene prediction. For each variant, a link to the UCSC Genome Browser is provided that shows a 1 Mb region with relevant genomic data.

## Transcription factors

Information regarding potential effects on transcription factor recognition sequences was obtained from the ENCODE-Motifs resource (http://compbio.mit.edu/encodemotifs)<sup>1</sup> using VCFtools v0.1.11 to access the downloaded HaploReg v4.0 database<sup>2</sup>. The impact each variant has on the position weight matrix for specific transcription factors is expressed as '+' or '-' for strengthened or weakened motifs relative to elements carrying the reference allele, respectively. Processed transcription factor ChIP-seq peak data for breast cell types were downloaded from ENCODE and other publications via NCBI GEO, in BED or NarrowPeak format, converted to the hg19 assembly using LiftOver if required, and given a standardised naming system (format = *"celltype;target"* in Supplementary Table 5). More details about the overlapping binding sites may be found within browser session track "TF-chip peaks overlapping candidate SNP" where TF-ChIP-seq peaks are named in the format *"Biosample\_term\_name, Experiment\_target, Biosample\_treatments, Biological\_replicate(s), File\_accession"*. All ChIP-seq datasets are listed in Supplementary Table 6. Variants were assessed for overlap with ChIP-seq peaks using BedTools v2.25.0<sup>3</sup>.

### **Regulatory features**

Histone signatures derived from histone modification ChIP-seg experiments on breast cell types carried out by ENCODE, NIH Roadmap Epigenomics, and other published studies were obtained and formatted as for ChIP-seq data. Histone modification peaks overlapping candidate causal variants are represented as "celltype; histone mark" in Supplementary Table 5 and "Biosample\_term\_name, Experiment\_target, *Biosample\_treatments, Biological\_replicate(s), File\_accession*" in the browser track "Histone modification ChIP-seq peaks overlapping candidate SNP". BedTools was used to intersect variants with histone signatures including commonly used marks associated with enhancers (H3K4me1, H3K4me2 and H3K27ac) and promoters (H3K4me3 and H3K9ac). Chromatin Hidden Markov Modelling (ChromHMM) states were obtained for breast cells from Roadmap (HMEC and myoepithelial cells) and published MCF7 data<sup>4</sup> and filtered for states corresponding to 'enhancers' (Roadmap 25-state E13, E14, E15, E16, E17, E18) or 'promoters' (Roadmap 25-state E1, E2, E3, E4, E22, E23). Chromatin state features containing candidate variants are represented as "celltype;chromatin\_state". Chromatin accessibility data obtained from ENCODE, Roadmap and other published sources via NCBI GEO measured using DNase-seg and FAIRE-seq for relevant breast cell types were also tested for overlap with candidate causal variants. Intersected regions are reported in the format "celltype;method". Scores based on RegulomeDB<sup>5</sup> are presented for available SNPs (based on dbSNP141), where lower scores are increasingly likely to be functional (http://regulomedb.org/help#score).

## <u>eQTL</u>

Genes showing expression levels correlated with query SNPs are shown in the column headed 'eQTL\_target\_all'. All genes reported to be associated with genotype in studies including GTEx version 6<sup>6</sup> (expression is any GTEx tissue, *P* value cutoff 10<sup>-6</sup>) and Westra *et al.*,<sup>7</sup> (expression in whole blood). Genes associated with genotype in GTEx breast samples (N=186) are listed in the column "eQTL\_GTEx.breast". eQTL data from TCGA and METABRIC studies for relevant variants are also presented (format "*Associated\_gene:EffectAllele:EffectDirection:P\_value*").

### Other genomic features

Chromosomal position, the lead variant for the associated locus, and potentially conflicting rsIDs (assessed as overlapping at the query position) are given for each variant. GWAS tagSNPs were downloaded from the UCSC Table Browser (December 2015) and associated traits are listed if the tagSNP is within a 10 kb window of the candidate causal variant. NCBI RefSeq gene annotations were downloaded from the UCSC Table Browser and BedTools was used to determine overlapping genes ("Overlapping\_RefGene"). The nearest RefGene transcription start site is also presented, given in the format "RefGeneTSS|distance". Basic genomic annotations such as intergenic, intronic, exonic, and untranslated regions based on RefSeq gene annotations were determined for each variant.

#### Target Gene Prediction

The column headed "Predicted target gene" lists genes predicted by various methods to be targets of, or the expression of which is associated with, regulatory elements in which the candidate causal variant lies. The reported gene is listed with cell type and method in the format "target:cell:method". A database was created comprising publicly available data based on various methods aiming to link enhancers with target genes (Annex to Supplementary Table 5). Laboratory based experimental approaches include genome-wide Chromatin Interaction Analysis with Paired-End-Tag sequencing (ChIA-PET)<sup>8</sup>, Hi-C<sup>9</sup>, and other Chromosome conformation capture (3C)-based techniques. Computational resources designed to predict target promoters by correlation of gene expression with ChIP-seq signals at specific regulatory elements including IM-PET<sup>10</sup>, PreSTIGE<sup>11</sup> and data from Hnisz et al.<sup>12</sup> are also included. These methods associate enhancers defined by histone modification ChIP-seq for H3K4me1 (PreSTIGE), H3K27ac (Hnisz), H3K4me1, H3K4me3 and H3K27ac (IM-PET) with gene expression signals measured by RNA-seq. FANTOM5<sup>13</sup> data representing enhancer-promoter cap analysis of gene expression (CAGE) expression correlation from all cell types were downloaded from http://enhancer.binf.ku.dk/. Target genes have been predicted for multiple cell types and all data were included in the database, and filtered for breast derived cell types for this analysis (see Key to Supplementary Table 5).

The following strategy was used to assign potential target genes to regulatory elements. The published computational methods (Hnisz, PreSTIGE and IM-PET) included target gene annotation in the reported data. For ChIA-PET and Hi-C data, interaction peaks were mapped to promoters defined as -1.0 kb to +0.1 kb around GENCODE (v19) transcription start sites. Enhancer definitions were used as reported for computational methods while for ChIA-PET and Hi-C were interpreted as any region interacting with a promoter (regardless of other enhancer annotation information such as histone modification or open chromatin). FANTOM5 target promoters were predefined and

tissue specificity was determined by intersecting "TSS associated enhancers" with tissue-specific sets of enhancers.

All data were formatted to enable intersection of test variants with "enhancers" as defined by each method using the Galaxy "intersect" tool<sup>14</sup>. Each enhancer-promoter assignment or interaction was represented as a single record along with details about potential target promoter, cell type, method, scoring and confidence statistics from the original publication. A set of query SNPs (or any loci with genomic positional information in BED format) could be queried into a custom Galaxy workflow leading to generation of a table of predicted gene targets and a link to the UCSC Genome Browser for visualisation.

## UCSC Genome Browser session

A custom session has been uploaded to UCSC Genome Browser<sup>15</sup> to facilitate exploration of breast cancer risk associated variation and implicated regulatory features. This can be accessed via the hyperlink (ie. "browser") in the functional annotation *xlsx* file. All standard Genome Browser data and functions are then available, including track display options (eg. right click on a particular track to activate visualisation options), highlighting regions (shift and mouse over region of interest), and the table browser (eg. to intersect or export data).

Within the session, Oncoarray candidate causal variants are shown in red, and names can be shown by activating "pack" mode (as for all tracks). Target gene prediction data from Hnisz, PreSTIGE and IM-PET shows enhancers depicted as black bars. The segment name revealed in 'pack' mode lists predicted target gene and cell-type (eg "WNT7B.MCF7"). ChIA-PET interactions, represented in BED12 format, have been filtered to remove duplicates and *trans*-chromosomal interactions. The interactions are shaded to reflect statistical confidence based on enrichment in the original experiment. ChIA-PET interaction names show the genomic co-ordinates of either-end of the interaction, the cell type (restricted to MCF7 for this analysis), the immunoprecipitation target, and the experimental replicate. Depicted interactions are restricted to those for which a candidate variant lies within an interaction "end" with the opposite end overlapping a TSS. All other interactions may be visualised by activating the standard ENCODE ChIA-PET track (\Regulation\ENCODE Chromatin Interactions Tracks\ChIA-PET from ENCODE/GIS-Ruan).

Chromatin interactions based on *in situ* Hi-C data from HMEC cells were downloaded from NCBI GEO (accession GSE63525)<sup>9</sup>. Annotated loops (representing potential enhancer-promoter interactions) processed by HiCCUPS were reformatted as BED files and tested for overlap with RefSeq promoters to assign potential target genes. Opposing ends of TSS-overlap loops were then annotated as 'potential enhancers'. Specific loop regions which overlap BC risk candidate causal variants are depicted as black segments and named "*TSS\_target.Celltype*".

Various classes of genomic data representing regulatory features which harbour candidate variants are shown as separate tracks:

- Histone modification ChIP-seq peaks overlapping candidate SNP
- DNase HS and FAIRE-seq peaks overlapping candidate SNP
- TF-chip peaks overlapping candidate SNP

As mentioned above, changing the track display to 'pack' mode will show details of the overlapping peak in the format:

"Biosample\_term\_name, Experiment\_target, Biosample\_treatments, Biological\_replicate(s), File\_accession".

A representation of all TF and histone ChIP-seq, DNase-seq, and FAIRE-seq data tested for overlap with candidate variants is shown in three histogram tracks (computed with BedTools genomeCoverageBed). These show the summed peak density at each genomic position and allow simple visualisation of loci with relative abundance of regulatory features.

Tracks for Roadmap Epigenomics Chromatin state models (based on imputed data - 25 state, 12 marks, 127 epigenomes) were generated for breast Myoepithelial and HMEC cells. Chromatin states were separated and colour coded for states related to enhancers, promoters, and transcribed regions.

The bottom track ("Oncoarray SNPs") shows all directly genotyped and imputed SNPs passing quality control (imputation  $r^2>0.3$ ) as black ticks. SNPs from dbSNP build 138 with a MAF > 0.01 in European samples which were not informative are shown in red.

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### OncoArray genotype calling and quality control

Of the 568,712 variants selected for genotyping on OncoArray, 533,631 were successfully manufactured on the array (including 778 duplicate probes). OncoArray genotyping of BCAC and CIMBA samples was conducted at six sites. Details of the genotyping calling for the OncoArray are described in more detail elsewhere<sup>16</sup>. Briefly, we developed a single calling pipeline that was applied to more than 500,000 samples. An initial cluster file was generated using from 56,284 samples, selected over all the major genotyping centres and ethnicities, using the Gentrain2 algorithm. Variants likely to have problematic clusters were selected for manual inspection using the following criteria: call rate below 99%, minor allele frequency (MAF) <0.001, poor Illumina intensity and clustering metrics, deviation from the MAF observed in the 1000 Genomes Project using the criterion:  $\frac{(|p_1-p_0|-0.01)^2}{((p_1+p_0)(2-p_1-p_0))} > C,$ where  $p_0$  and  $p_1$  are the minor frequencies in the 1000 Genome Project and Oncoarray datasets, respectively, and C=0.008. (This latter criterion is approximately equivalent to excluding SNPs on the basis of a Chi-square statistic of 16 for the difference in allele frequencies, assuming 1,000 samples in each group). This resulted in manual adjustment of the cluster file for 3,964 variants, and the exclusion of 16,526 variants. The final cluster file was then applied to the full dataset.

We excluded SNPs with a call rate <95% in any consortium, not in Hardy-Weinberg equilibrium (P<10<sup>-7</sup> in controls, or P<10<sup>-12</sup> in cases) or with concordance <98% among 5,280 duplicate pairs. For the imputation, we additionally excluded SNPs with a MAF<1% and a call rate <98% in any consortium, SNPs that could not be linked to the 1000 Genomes Project reference, those with MAF for Europeans that differed from that for the 1000 Genomes Project and a further 1,128 SNPs where the cluster plot was judged to be not ideal. Of the 533,631 SNPs which were manufactured on the array, 494,763 passed the initial QC and 469,364 were used in the imputation (see below).

For BCAC, we excluded probable duplicate samples and close relatives within each study, and probable duplicates between studies. These were identified by identity by state (IBS) analysis using a set of approximately 38,000 uncorrelated ( $r^2$ <0.1) SNPs for OncoArray and iCOGS and 16,000 SNPs for GWAS. Based on inspection of the distribution of IBS values, we identified first-degree relative pairs using the criterion 0.82<IBS<0.90 for OncoArray and 0.85<IBS<0.90 for iCOGS; similar criteria were used for each GWAS (with limits depending on the IBS distribution in that study).

We applied LD score regression to the summary results from GWAS, iCOGS and OncoArray to assess the evidence of overlap in individuals between the three datasets. We conducted three pair-wise cross-trait regression analyses (GWAS-iCOGS, GWAS-OncoArray and iCOGS-OncoArray) and used the intercept from the regression analysis to estimate the amount of overlap<sup>17</sup>. Assuming that the phenotypic correlation is 1 (that is, a case is a case in all datasets and a control is a control in all datasets), we found that for GWAS-iCOGS, the estimated overlap was 1.5% of individuals, for GWAS-OncoArray, the estimated overlap was 0.2% of individuals. It is unlikely that this degree of overlap would have influenced the results obtained from our analyses.

We also excluded samples with a call rate <95% and samples with extreme heterozygosity (>4.9 standard deviations from the mean for the reported ethnicity). Ancestry analysis was performed using a standardized approach in which 2,318 ancestry informative markers with minor allele frequencies of 0.05 on a subset of ~66,000 samples including 505 Hapmap 2 samples. The contribution of each of the three major continental ancestry groups (European, Asian and African) was estimated by mapping each individual to regions of a triangle based on the first two principal components, as implemented in the software package FastPop (<u>http://sourceforge.net/projects/fastpop/</u>)<sup>18</sup>. Individuals were thus classified into 4 groups: European (defined as >80% European ancestry), East Asian (>40% Asian ancestry), African (>20% African ancestry) and other (not fulfilling any of the above criteria)<sup>16</sup>. Of the 152,492 samples genotyped, the final dataset consisted of 142,072 samples, of which 9,655 ER-negative cases and 45,494 controls of European origin had not been included in a previous GWAS and had not been genotyped using iCOGS and were included in this analysis.

For the CIMBA samples we excluded individuals of non-European ancestry using multi-dimensional scaling. For this purpose we selected 30,733 uncorrelated autosomal SNPs (pair-wise  $r^2 < 0.10$ ) to compute the genomic kinship between all pairs of *BRCA1* and *BRCA2* carriers, along with 267 HapMap samples (CHB, JPT,

YRI and CEU). These were converted to distances and subjected to multidimensional scaling. Using the first two components, we calculated the proportion of European ancestry for each individual and excluded samples with >27% non-European ancestry to ensure that samples of Ashkenazi Jewish ancestry were included in the final sample.

## **Global Genomic Enrichment Analyses (further details)**

We created a "full baseline model" as previously described<sup>19</sup> that included 52 "baseline" genomic features (24 non-cell-type specific publicly available annotations, a 500-bp window around each of the 24 annotations and a 100-bp window around each of four ChIP-seq peaks) and one category containing all SNPs. We estimated the enrichment for these 53 functional categories in a single multivariable LD score regression analysis.

We subsequently performed analyses using cell-type specific annotations for the four histone marks H3K4me1, H3K4me3, H3K9ac and H3K27ac across 27-81 cell types, depending on histone mark, giving a total of 220 cell-type specific marks<sup>19</sup>. We estimated the enrichment for each of these marks after adjusting for the baseline annotations by running 220 LD score regressions, each adding a different histone mark to the baseline model. We observed no associations after adjusting for 220 tests

# Pathway Enrichment Analyses (further details)

Pathway enrichment analysis was performed to identify pathways associated with ER-negative breast cancer risk, pointing to biological hypotheses that can be further tested experimentally.

The pathway gene set database used contains pathway gene sets from Reactome<sup>20</sup>, NCI Pathway Interaction Database<sup>21</sup>, GO (Gene Ontology) biological process<sup>22</sup>, HumanCyc<sup>23</sup>, MSigdb<sup>24</sup>, NetPath<sup>25</sup> and Panther<sup>26</sup>. GO pathways inferred from electronic annotation terms were excluded. Some manual annotation was performed on the pathway gene set database where annotation errors from public data were discovered. In particular, in several pathways, the PDPK1 gene was mistakenly entered as PDK1 gene and was manually corrected. The same pathway (e.g. apoptosis) may be defined in two or more databases with potentially different sets of genes, and all versions of these duplicate/overlapping pathways were included.

Gene information (hg19) was downloaded from the ANNOVAR<sup>27</sup> website (http://www.openbioinformatics.org/annovar/). Some pathways include genes that are also grouped closely together in the genome and are thus are likely to share the significance of a single SNP, which would artificially increase the pathway significance in our analysis. This was the case for pathways including histone genes. Thus, we selected representative SNP-gene associations to control for this effect (chr6:26055031 for HIST1, chr1:120904839, 149864043 for HIST2, chr1: 228615251 for HIST3 and chr12: 14919727 for HIST4). Although there are several methods for pathway enrichment analysis, we chose the GSEA approach as it is one of the most established methods that is threshold free; many other methods such as SRT, ALIGATOR and Plink set-based test require an arbitrary p-value threshold to be defined for SNPs and applied before pathway analysis.

To focus on pathway enrichment analysis results about which we were most confident, we implemented a number of filters. First, only pathways with positive ES and containing at least one gene linked to a significant SNP ( $P<5x10^{-8}$ ) were retained for subsequent analysis. Second, we defined an ES threshold (ES≥0.41) based on a comparison with a gold standard pathway enrichment analysis we previously performed on the iCOGS data alone and where we were able to analytically compute FDR values by shuffling case/control labels (this was not computationally feasible with the more complex meta-analysis scheme used in this paper).

We chose the true positive rate (TPR) threshold by varying the TPR in steps of 0.1 and observing how the FPR changed. A TPR of 0.1 resulted in a very low FPR (0.02), but we considered this to be unduly conservative as it resulted in a small number of pathways (37, clustered into 8 themes) and excluded many pathways known to be involved in breast cancer. A TPR of 0.20 (FPR = 0.14) gave a reasonable balance between the true and false positive rates, while including pathways known to be involved in breast cancer. Thus this threshold was chosen for this study. A TPR of 0.3 gave an FPR of 0.30, which we considered high; further, the resulting additional pathways included (in addition to those included at TPR=0.2) were weaker (i.e. they had worse enrichment scores [ES<0.41] and had relatively very few genes included) than pathways appearing at lower FPRs (and TPRs). We rejected TPR thresholds >0.3 because each gave an FPR that was larger than the TPR.

Finally, we performed an in depth literature search on all resulting pathways to confirm their relevance to breast cancer biology, applying the following criteria: 1) reported in at least one of five published breast cancer pathway analyses<sup>28-32</sup>; or 2) reported elsewhere in the literature to be involved in breast cancer. We also removed pathways that were significant due to incorrect gene function annotation.

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Supplementary	ementary Table 1: BCAC studies contributing data on estrogen receptor negative cases and controls, by genotyping intiative †					0				
Acronym	Study Name	Country	Study design	Controls	Cases	Controls	Cases	Controls	Cases	
ABCFS	Australian Breast Cancer Family Study	Australia	Case-control study	188	62	551	204	285	72	
ABCS	Amsterdam Breast Cancer Study	Netherlands	Case-control study	4	27	1815	154			
ABCTB	Australian Breast Cancer Tissue Bank	Australia	Case-control study	374	290					
BBCC	Bavarian Breast Cancer Cases and Controls	Germany	Case-control study	248	354	458	67			
BBCS	British Breast Cancer Study	UK	Case-control study	442	18	1397	108			
BCEES	Breast Cancer Employment and Environment Study	Australia USA Capada Australia	Case-control study	834	115			2251	022	
BCFR-NY	Diedos Cancer Failing Registry New York site of the Report Cancer Family Registry	USA, canada, Austrana	Case-control study	27	60			2251	322	
BCFR-PA	Philadelphia site of the Breast Cancer Family Registry	USA	Case-control study	0	27					
BCFR-UT	Utah site of the Breast Cancer Family Registry	USA	Case-control study	0	13					
BCINIS	Breast Cancer in Northern Israel Study	Israel	Case-control study	723	262					
BIGGS	Breast Cancer in Galway Genetic Study	Ireland	Case-control study			719	154			
BPC3	Breast and Prostate Cancer Cohort Consortium	International	Prospective cohorts: nested case-control studies					2305	1998	
BREOGAN	Breast Oncology Galicia Network	Spain	Case-control study	725	246					
BSUCH	Breast Cancer Study of the University of Heidelberg	Germany	Case-control study	167	42	954	157			
CBCS	Canadian Breast Cancer Study	Canada	Case-control study	81/	119					
CECILE	CFCIE Breast Cancer Study	France	Case-control study	332	1//	999	144			
CGPS	Conenhagen General Ponulation Study	Denmark	Case-control study	712	160	4534	357			
CNIO-BCS	Spanish National Cancer Centre Breast Cancer Study	Spain	Case-control study			876	88			
CPSII	Cancer Prevention Study-II Nutrition Cohort	USA	Prospective cohort: nested case-control study	3025	99					
CTS	California Teachers Study	USA	Prospective cohort: nested case-control study	577	126	71	68			
DEMOKRITOS	Demokritos	Greece	Case-control study			95	413			
DIETCOMPLYF	DietCompLyf Breast Cancer Survival Study	UK	Prospective cohort: nested case-control study	0	104					
EPIC	European Prospective Investigation Into Cancer and Nutrition	International (Europe)	Prospective cohort: nested case-control study	3522	179					
ESTHER	ESTHER Breast Cancer Study	Germany	Case-control study	3	1	502	98			
GC-HBOC*	German Consortium for Hereditary Breast & Ovarian Cancer	Germany	Case-control study	1593	358	168				
GENICA	Gene Environment Interaction and Breast Cancer in Germany	Germany	Case-control study	284	78	427	104			
GEPARSIATO	Kanoomized phase in that Genetic Enidemicial Carport Carport Mars E0	Germany	Case-only study	190	122					
HARCS	Genetic chicemonogy study of breast cancer by Age 50	Germany	Case-control study	865	147					
HCSC	Hospital Clinico San Carlos	Spain	Case-control study	0	109					
HEBCS	Helsinki Breast Cancer Study	Finland	Case-control study	2	14	1233	235	1012	145	
HMBCS	Hannover-Minsk Breast Cancer Study	Belarus	Case-control study	214	7	130	8			
HUBCS	Hannover-Ufa Breast Cancer Study	Russia	Case-control study	131	18					
KARBAC	Karolinska Breast Cancer Study	Sweden	Case-control study	0	3	662	63			
KBCP	Kuopio Breast Cancer Project	Finland	Case-control study	182	23	250	97			
KConFab/AOCS	Kathleen Cuningham Foundation Consortium for research into Familial Breast Cancer/Australian Ovarian Cancer Study	Australia and New Zeland	Case-control study	425	145	897	55			
LIVIDE	Leuven mutuliscipinary breast Centre	Macadonia	Case-control study	435	145	1300	5/6			
MARIE	Mammary Carcinoma Risk Eactor Investigation	Germany	Case-control study	288	8	1778	346	470	76	
MBCSG	Milan Breast Cancer Study Group	Italy	Case-control study	366	75	400	42			
MCBCS	Mayo Clinic Breast Cancer Study	USA	Case-control study	179	84	1931	269			
MCCS	Melbourne Collaborative Cohort Study	Australia	Prospective cohort: nested case-control study	712	77	511	110			
MEC	Multiethnic Cohort	USA	Prospective cohort: nested case-control study	127	3	741	87			
MISS	Melanoma Inquiry of Southern Sweder	Sweden	Prospective cohort: nested case-control study	1523	79					
MMHS	Mayo Mammography Health Study	USA	Prospective cohort: nested case-control study	1605	50	426	<i>C</i> 4			
NILGEBUS	Monumeral generativity	Nonway	Case-control study	29	2	430	200			
NBHS	Notwegian breast Cancer Study	LISA	Case-control study	613	163	118	125			
NC-BCFR	Northern California Breast Cancer Family Registry	USA	Case-control study	149	261	110	125			
NHS	Nurses Health Study	USA	Prospective cohort: nested case-control study	1804	203					
NHS2	Nurses Health Study 2	USA	Prospective cohort: nested case-control study	1905	224					
OBCS	Oulu Breast Cancer Study	Finland	Case-control study			414	100			
OFBCR	Ontario Familial Breast Cancer Registry	Canada	Case-control study	217	259	511	269			
ORIGO	Leiden University Medical Centre Breast Cancer Study	Netherlands	Prospective conort: nested case-control study	660	230	327	207			
PRCS	On Date Onversity	Poland	Case-control study	1658	547	205	207			
pKARMA	Karolinska Mammography Project for Risk Prediction of Breast Cancer - Case-Control Study	Sweden	Case-control study	6042	166	5568	701			
PLCO	The Prostate, Lung, Colorectal and Ovarian (PLCO) Cancer Screening Trial	USA	Prospective cohort: nested case-control study	858	184					
POSH	Prospective Study of Outcomes in Sporadic Versus Hereditary Breast Cancer	UK	Case-only study	0	207					
PREFACE	Evaluation of Predictive Factors regarding the Effectivity of Aromatase Inhibitor Therapy	Germany	Case-only study	0	15					
RBCS	Rotterdam Breast Cancer Study	Netherlands	Case-control study	231	87	699	124			
RPCI	Roswell Park Cancer Institute	USA	Case-control study			126	136	750	400	
SASBAC	Singapore and Sweden Breast Cancer Study Shaffiold Breast Cancer Study	Sweden	Case-control study			849	43	/56	109	
SEARCH	Sinch of Enidemiology and Risk factors in Cancer Heredity	UK	Case-control study	989	420	8068	1173			
SISTER	The Sister Study	USA	Prospective cohort: nested case-control study	1560	282					
2SISTER	The Two Sister Study	USA	Case-only study	0	204					
SKKDKFZS*	Städtisches Klinikum Karlsruhe Deutsches Krebsforschungszentrum Study	Germany	Case-only study	0	298	0	135			
SMC	Swedish Mammography Cohort	Sweden	Prospective cohort: nested case-control study	708	195					
SUCCESSB	Simultaneous Study of Gemcitabine-Docetaxel Combination adjuvant treatmen	Germany	Case-only study	0	159					
SUCCESSC	Simultaneous Study of Docetaxel Based Anthracycline Free Adjuvant Treatment Evaluation	Germany	Case-only study	0	204	24-				
SZBCS	IHLL-Szczecin Breast Cancer Study	Poland	Case-control study	157	72	315	60	2000	000	
LICIPCS	Inple-wegative breast caller Consortium	international	Case control studies	259	288			2890	998	
UK2	LIK2 GWAS	UK	Case-control study	200	/5			2663	160	
UKBGS	UK Breakthrough Generations Study	UK	Prospective cohort: nested case-control study	567	78	470	22	2005	100	
UKOPS	UK Ovarian Cancer Population Study	UK	Case-control study	974	0					
WHI	Women's Health Initiative	LISA	Brospostivo cohort: ported caro control study	4612	659					

WHI Women's Health Initiative TStudies participated in one or more of the following genotyping initiatives: OncoArray, ICOGS or one of eight genome-wide association studies (GWASs) \*For the analysis of ICOGS data, cases from SKORVETS and controls from GC-HBOC included as one study
Supplementary Table 2: CIMBA studies contributing data on BRCA1 mutation carriers, by genotyping initiati	CIMBA studies contributing data on BRCA1 mutation carriers, by genotyping intiative
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• · · · · ·			Onco	Array	iC	OGS
Acronym	Study Name	Country	Unaffected	Breast cancer	Unaffected	Breast cancer
BCFR-AU	Australian site of the Breast Cancer Family Registry	AUSTRALIA	13	25	0	2
BCFR-NC	Northern California site of the Breast Cancer Family Registry	USA	3	12	1	1
BCFR-NY	New York site of the Breast Cancer Family Registry	USA	24	37	4	5
BCFR-ON	Ontario site of the Breast Cancer Family Registry	CANADA	34	86	2	7
BCFR-PA	Philadelphia site of the Breast Cancer Family Registry	USA	26	17	14	16
BCFR-UT	Utah site of the Breast Cancer Family Registry	USA	135	64	1	0
BFBOCC	Baltic Familial Breast Ovarian Cancer Consortium	LITHUANIA/LATVIA	133	111	16	8
BIDMC	Beth Israel Deaconess Medical Center	USA	41	44	1	1
BMBSA	BRCA-gene mutations and breast cancer in South African women	SOUTH AFRICA	21	37	2	1
BRICOH	Beckman Research Institute of the City of Hope	USA	96	50	11	9
CBCS	Rigshospitalet	DENMARK	110	75	80	57
CNIO	Spanish National Cancer Centre	SPAIN	32	31	49	44
СОН	City of Hope Cancer Center	USA	84	141	6	8
CONSIT TEAM	CONsorzio Studi ITaliani sui Tumori Ereditari Alla Mammella	ITALY	265	271	217	234
DEMOKRITOS	National Centre for Scientific Research Demokritos	GREECE	85	132	12	20
DFCI	Dana-Farber Cancer Institute	USA	82	65	3	4
DKFZ	German Cancer Research Center	GERMANY	19	36	0	2
EMBRACE	Epidemiological Study of Familial Breast Cancer	UK/IRELAND	907	785	14	13
FCCC	Fox Chase Cancer Center	USA	49	26	20	19
FPGMX	Fundación Pública Galega de Medicina Xenómica	SPAIN	40	61		
GC-HBOC	German Familial Breast Group	GERMANY	673	1145	54	111
GEMO	Genetic Modifiers of cancer risk in BRCA1/2 mutation carriers	FRANCE/USA	630	842	114	111
GEORGETOWN	Georgetown University	USA	6	5	1	2
G-FAST	Ghent University Hospital	BELGIUM	69	121	91	42
HCSC	Hospital Clinico San Carlos	SPAIN	85	55	5	6
HEBCS	Helsinki Breast Cancer Study	FINLAND	67	53	3	5
HEBON	Genen Omgeving studie van de werkgroep Hereditiair Borstkanker Onderzoek Nederland	NETHERLANDS	500	372	220	202
HUNBOCS	Molecular Genetic Studies of Breast- and Ovarian Cancer in Hungary	HUNGARY	101	179		
HVH	University Hospital Vall d'Hebron	SPAIN	56	62	0	1
ICO	Institut Català d'Oncologia	SPAIN	150	130	5	1
IHCC	International Hereditary Cancer Centre	POLAND	121	77	279	223
INHERIT	INterdisciplinary HEalth Research Internal Team BReast CAncer susceptibility	CANADA (QUEBEC)	52	37	6	2
IOVHBOCS	Istituto Oncologico Veneto	ITALY	93	111	5	4
IPOBCS	Portuguese Oncology Institute-Porto Breast Cancer Study	PORTUGAL	79	36	1	2
KCONFAB	Kathleen Cuningham Consortium for Research into Familial Breast Cancer	AUSTRALIA	355	366	24	26
KUMC	University of Kansas Medical Center	USA	3	11		
MAYO	Mayo Clinic	USA	126	121	12	10
MCGILL	McGill University	CANADA (QUEBEC)	30	24		
MODSQUAD	Modifier Study of Quantitative Effects on Disease	CZECH REPUBLIC			68	106
MSKCC	Memorial Sloane Kettering Cancer Center	USA	193	185	32	59
MUV	General Hospital Vienna	AUSTRIA	266	268	11	11
NAROD	Women's College Research Institute Hereditary Breast and Ovarian Cancer Study	CANADA			100	46
NCI	National Cancer Institute	USA	108	42	6	1
NNPIO	N.N. Petrov Institute of Oncology	RUSSIA	22	44	1	4
NORTHSHORE	NorthShore University HealthSystem	USA	40	40		-
NRG_UNCOLUGY	NKG Uncology	USA/AUSTRALIA	153	166	4	/
OCGN	Untario Cancer Genetics Network	LICA	133	71	0	4
OSO CCG	Ine Unio State University Comprenensive Cancer Center	DENMARK	34	39	8	10
DRCS	Università di Disa		300	192	10	10
SMC	Shaha Madical Centre	ISPACI	39	49	57	41
SIVIC	Swedich Breast Cancer Study	SWEDEN	39	199	57	29
	Juniversity of Chicago	USA	51	43	7	0
UCSE	University of California San Francisco	USA	60	32	16	15
UKGREOCR	UK and Gilda Radner Familial Ovarian Cancer Registries	UK	40	13	5	0
UPFNN	University of Pennsylvania	USA	218	239	11	22
UPITT	Cancer Family Registry University of Pittsburg	USA	77	77		
UTMDACC	University of Texas MD Anderson Cancer Center	USA	18	25	27	45
VFCTG	Victorian Familial Cancer Trials Group	AUSTRALIA	104	103	2	1
WCP	Women's Cancer Program at Cedars-Sinai Medical Center	USA	137	50	10	6

											ER-negativ	e breast	cancer (BCAC	:)									BRC	41 mutati	on carriers (CIMBA	)		
Location SNP	Chr	Position	Alleles	MAF		GWAS				ii ii	COGS				One	oArray			,2	D(hat )		icogs				OncoArray		
					OR(95%CI)	P-value	1 <sup>2</sup> (5)	P (het <sub>s</sub> )	r <sup>2</sup> (imp)	OR(95%CI)	P -value	1 <sup>2</sup> (9)	P(het;)	r <sup>2</sup> (imp)	OR(95%CI)	P-value	1 <sup>2</sup> (5)	P (het <sub>s</sub> )	(6)	P(neta)	r <sup>2</sup> (imp)	HR(95%CI)	P-value	r <sup>2</sup> (imp)	HR(95%CI)	P-value	r <sup>2</sup> (0)	P (het <sub>c</sub> )
2p23.3 rs200648189	2	24739694	CT/C	0.19	0.96 (0.88-1.06)	4.1x10 <sup>-1</sup>	0	0.93	0.57	0.93 (0.87-0.99)	2.3x10 <sup>-2</sup>	0	0.58	0.90	0.94 (0.90-0.99)	9.3x10 <sup>-3</sup>	0	0.95	0	0.83	0.52	0.93 (0.81-1.08)	3.5x10 <sup>-1</sup>	0.89	0.87 (0.83-0.92)	3.5x10 <sup>-7</sup>	0.09	0.34
6q23.1 rs6569648	6	130349119	T/C	0.23	0.88 (0.83-0.94)	1.4x10 <sup>-4</sup>	0	0.96	1.00	0.94 (0.89-0.98)	3.3x10 <sup>-3</sup>	0	0.79	1.00	0.94 (0.91-0.98)	1.8x10 <sup>-3</sup>	0	0.88	0.31	0.24	1.00	0.96 (0.86-1.06)	4.2x10 <sup>-1</sup>	1.00	0.94 (0.89-0.98)	7.0x10 <sup>-3</sup>	0	0.61
8p23.3 rs66823261	8	170692	T/C	0.23	1.02 (0.96-1.09)	4.7x10 <sup>-1</sup>	0	0.49	0.74	1.13 (1.08-1.19)	1.0x10 <sup>-6</sup>	0	0.71	0.92	1.08 (1.04-1.13)	8.2x10 <sup>-5</sup>	0	0.85	0.66	0.05	0.72	1.14 (1.01-1.29)	4.0x10 <sup>-2</sup>	0.92	1.01 (0.96-1.06)	8.2x10 <sup>-1</sup>	0.33	0.06
8q24.13 rs17350191	8	124757661	C/T	0.34	1.07 (1.01-1.13)	3.1x10 <sup>-2</sup>	0.43	0.09	1.00	1.06 (1.02-1.11)	1.9x10 <sup>-2</sup>	0.12	0.27	1.00	1.07 (1.04-1.11)	3.2x10 <sup>-5</sup>	0	0.71	0	0.94	1.00	1.03 (0.95-1.13)	4.6x10 <sup>-1</sup>	1.00	1.08 (1.04-1.13)	1.6x10 <sup>-6</sup>	0.22	0.16
11q22.3 rs11374964	11	108345515	G/GA	0.42	0.94 (0.88-1.00)	6.0x10 <sup>-2</sup>	0	0.69	1.00	0.97 (0.94-1.01)	1.4x10 <sup>-1</sup>	0.26	0.07	1.00	0.91 (0.88-0.94)	2.7x10 <sup>-8</sup>	0	0.66	0.68	0.04	1.00	0.96 (0.88-1.05)	4.1x10 <sup>-1</sup>	1.00	0.90 (0.87-0.94)	7.8x10 <sup>-7</sup>	0.18	0.24
11q22.3 rs74911261	11	108357137	G/A	0.02	0.88 (0.70-1.10)	2.6x10 <sup>-1</sup>	0	0.88	0.90	0.79 (0.68-0.92)	2.6x10 <sup>-3</sup>	0	0.86	1.00	0.82 (0.73-0.91)	4.0x10 <sup>-4</sup>	0.01	0.44	0	0.75	0.87	0.82 (0.58-1.15)	2.5x10 <sup>-1</sup>	1.00	0.73 (0.63-0.83)	3.3x10 <sup>-6</sup>	0	0.74
16p13.3 rs11076805	16	4106788	C/A	0.25	0.91 (0.86-0.97)	2.8x10 <sup>-3</sup>	0.40	0.11	0.72	0.94 (0.89-0.99)	1.9x10 <sup>-2</sup>	0	0.80	0.97	0.92 (0.89-0.96)	2.9x10 <sup>-5</sup>	0.18	0.24	0	0.76	0.72	1.02 (0.90-1.16)	7.3x10 <sup>-1</sup>	0.97	0.95 (0.91-1.00)	4.1x10 <sup>-2</sup>	0.09	0.34
18q12.1 rs36194942	18	25401204	A/AT	0.30	0.92 (0.85-0.99)	1.9x10 <sup>-2</sup>	0	0.52	0.95	0.96 (0.92-1.00)	5.1x10 <sup>-2</sup>	0	0.48	0.95	0.92 (0.89-0.96)	9.6x10 <sup>-6</sup>	0	0.99	0.15	0.31	0.94	0.96 (0.87-1.06)	4.5x10 <sup>-1</sup>	0.94	0.95 (0.91-0.99)	1.8x10 <sup>-2</sup>	0	0.65
19p13.2 rs322144	19	11423703	C/G	0.47	0.94 (0.89-0.99)	2.1x10 <sup>-2</sup>	0	0.73	0.51	0.96 (0.91-1.01)	1.0x10 <sup>-1</sup>	0	0.92	0.99	0.95 (0.92-0.98)	1.5x10 <sup>-3</sup>	0.29	0.11	0	0.86	0.50	0.89 (0.79-1.01)	7.2x10 <sup>-2</sup>	0.99	0.93 (0.89-0.96)	1.7x10 <sup>-6</sup>	0	0.48
19q12 rs113701136	19	30277729	C/T	0.32	1.04 (0.98-1.10)	1.6x10 <sup>-1</sup>	0	0.89	0.97	1.06 (1.02-1.10)	4.0x10 <sup>-3</sup>	0.26	0.07	0.98	1.08 (1.04-1.12)	2.1x10 <sup>-5</sup>	0	0.48	0	0.61	0.96	1.11 (1.01-1.22)	3.0x10 <sup>-2</sup>	0.98	1.04 (1.00-1.09)	7.7x10 <sup>-2</sup>	0.21	0.18

## Supplementary Table 4: Results for the two novel ER-negative susceptibility loci on 11q22.3

SND	Chr	Position	Alleles <sup>#</sup> -	_	BCAC ER-negativ	e	CIMBA BRCA1 mutation carriers <sup>‡</sup>				
SINF	CIII	rosition	Alleles	MAF	OR (95%CI)	P-value	MAF	HR (95%CI)	P-value		
Each SNP mo	delled	individually									
rs11374964	11	108345515	G/GA	0.42	0.94 (0.92-0.96)	3.6x10 <sup>-7</sup>	0.43	0.92 (0.89-0.95)	1.6x10 <sup>-7</sup>		
rs74911261	11	108357137	G/A	0.02	0.81 (0.74-0.89)	3.7x10 <sup>-6</sup>	0.02	0.78 (0.70-0.87)	1.1x10 <sup>-5</sup>		
Both SNPs m	odelled	d together									
rs11374964	11	108345515	G/GA	0.42	0.95 (0.93-0.97)	3.5x10 <sup>-5</sup>	0.43	0.93 (0.90-0.96)	5.1x10 <sup>-6</sup>		
rs74911261	11	108357137	G/A	0.02	0.84 (0.76-0.91)	8.6x10 <sup>-5</sup>	0.02	0.81 (0.73-0.91)	3.3x10 <sup>-4</sup>		

<sup>#</sup>More common allele listed first, minor allele second; <sup>†</sup>Combined data from 16,988 ER-negative cases and 87,962 controls of European ancestry from the Breast Cancer Association Consortium (BCAC) - results differ from those in Table 1 as GWAS data were excluded (unit record data was not available to run the models with both SNPs together); <sup>†</sup>Combined OncoArray data from 15,566 *BRCA1* mutation carriers from the Consortium of Investigators of Modifiers of BRCA1/2 (CIMBA), 7,784 of whom had developed breast cancer - estimates from multivariable Cox regression; Chr, chromosome; MAF, minor allele frequency; OR, odds ratio per copy of the minor allele; CI, confidence interval; HR, hazard ratio per copy of the minor allele

rowser	variant chrom 2_24739694_C_CT :	n position locus 2 24739694 2_24739694_C_CT	rsID rs200648189	TF_motifs(delta TF-ChIP Historne_modific ChromHMM_enhChromHMM_pro Open_chromatinRegu	formeDB_s 6	icGWAS_traits	Overlapping_Re	KRefGeneTSSjdist NCOA1 67651	INTERGENIC	sceQTL_target_all eQTL_GTEx.breaeQTL_TCGA	DNA/C27.CT:-:0.0154745 NCOA1:MCF7:ChIA-PET
rowser	2_25079770_C_T 2_25082414_G_A	2 25079770 2_24739694_C_CT 2 25082414 2_24739694_C_CT	rs11675457 rs1541984	AP-3 + BRST.MYOEP,Enhancer Nkx2,2(+,Pax-5_known2)+	1f 1f		ADCY3 ADCY3	ADCY3(62285 ADCY3(59641	INTRON	ADCY3,CENPO,DNAJC27,DNAJC27ADCY3:T::0.014376,MFSD28: ADCY3,CENPO,DNAJC27,DNAJC27ADCY3:A::0.0143482,MFSD21	T NCOA1:T:-0.0045227 8: NCOA1:A:-0.0045227
rowser	2_25082926_T_C	2 25082926 2_24739694_C_CT 2 25083310 2 24739694_C_CT	rs11687089 rs7576788	YY1_disc5(+ HMEC;dnase MCE.7/ER	5		ADCY3 ADCY3	ADCY3 59129 ADCY3 58745	INTRON	ADCY3,CENPO,DNAJC27,DNAJC27ADCY3;C-:0.0280437 ADCY3,DNAJC27,DNAJC27,451,PDADCY3;C-:0.0093761	NC041:C0.0032996 NC041:C0.0166227 SEB14:C+-0.040135
rowser	2_25085268_T_A	2 25085268 2_24739694_C_CT 2 25085268 2_24739694_C_CT	rs2384055	AridSal+, Foxa_disc2 - Next_til_DDDMt_disc1_T2ES1_Mat21_	7		ADCY3	ADCY3 56787	INTRON	ADCY3, DNAJC27, DNAJC27-AS1, RPADCY3:A:-0.0147104, MFSD2 ADCY3, CEMPO, DMA, IC27, DNA, IC27, ADCY3, GL, 0.015343, MFSD2	8.NCDA1:A:-0.0045141
rowser	2_25089594_C_A	2 25089594 2_24739694_C_CT 2 25089594 2_24739694_C_CT	rs35177510	Not-Ipprovi_decip.tor1::Wataj+	7		ADCY3	ADCY3 52461	INTRON	ADCY3, DNAJC27, DNAJC27, ADCY3, 0: 0015343, MY5028 ADCY3, DNAJC27, DNAJC27, AS1, RPADCY3, A:-0.015643, MF5028	ANCOA1:0:-0.0045177 ADCY3:MCF7:CNA-PET
rowser :	2_25091721_T_TA 2_25091869_A_G	2 25091721 2_24739694_C_CT 2 25091869 2_24739694_C_CT	rs35609705 rs11683929	Mrg_1 -,2ID)+	6		ADCY3 ADCY3	ADCY3 50334 ADCY3 50186	INTRON	ADCY3;TA:-:0.018074,MF5D2 ADCY3,DNAJC27,DNAJC27-AS1,RPADCY3;G:-:0.0158047,MF5D2	8:NCDA1:TA0.0048031 8:NCDA1:G0.0045227
rowser	2_25093151_C_T	2 25093151 2_24739694_C_CT 2 25094003 2 24739694_C_CT	rs13019149 rs11433494	Zbitdj-	6		ADCY3 ADCY3	ADCY3 48904 ADCY3 48052	INTRON	ADCY3,DNAJC27,DNAJC27-AS1,RPADCY3.T0.0158397,MF5D21 C2vr44.4TT-+-0.0057104.4D	3: NCDA1:T:-0.0045227 CNCDA1:AT:-0.0065397
rowser	2_25096892_A_T	2 25096692 2_24739694_C_CT	rs11892889	TCF12_diac5(+,Z MCF_10A,E2F4,) BRST.MYOEP.H:BRST.MYOEP.Enhancer	4		ADCY3	ADCY3 45363	INTRON	ADCY3,CENPOJADCY3,DNAJC27,DNAJC27-AS1,RP11-443B20.1	NC0A1:T:-0.0082746,DNM1EFR3B:HCC1964;IM-PETCENPO:HCC1954
rowser	2_25096952_1_C 2_25097072_G_C	2 25096952 2_24739694_C_CT 2 25097072 2_24739694_C_CT	rs7580081	NF-kappaB_discsMCF_10A;FOS;MCF_10A;MYC;MCBHS1;MYOEP[Enhancer] ATF4]+,AhR::Am/MCF_10A;FOS;MCF_10A;MYC;MCBRST;HMEC;Enhancer;BRST;VHMHMEC;dnase,HM	4		ADCY3 ADCY3	ADCY3 45103 ADCY3 44983	INTRON	ADCY3, CENPOJADCY3, DNAJC27, DNAJC27-AS1, HP11-443820.1 ADCY3, CENPOJADCY3, DNAJC27, DNAJC27-AS1, RP11-443820.1	NCDA1:C0.0083698,0NMICENPOHCC1954;Hnitz,,EFR3B;HCC1954;M NCOA1:C0.0078969,0NMIEFR3B;HCC1954;IM-PET_,CENPO;HCC1954
rowser	2_25097644_A_G 2_25097939 T_C	2 25097644 2_24739694_C_CT 2 25097939 2 24739694 C CT	rs13407913 rs13410999	CAC-binding-prot MCF-7;ERbata, MCF-7;SPDEF GR known/0-HDAC2 disc3i+.Pax-8 2i+	1d 5		ADCY3 ADCY3	ADCY3 44411 ADCY3 44116	INTRON	ADCY3,CENPO(ADCY3,DNAJC27,DNAJC27-AS1,RP11-443820.1 ADCY3,CENPO(ADCY3,DNAJC27,DNAJC27-AS1,RP11-443820.1	NC0A1:G:-0.0082746,DNM EFR3B:HCC1954:IM-PETCENPO:HCC1954 NC0A1:C:-0.0082746,DNMI CENPO:HCC1954:Hnisz
rowser	2_25098859_A_G	2 25098859 2_24739694_C_CT	156722022	First dark Die besteht De besteht De besteht Offic dark 1940 in di 1940 in di De			ADCY3	ADCY3 43196	INTRON		NC0A1:G0.0175907,DNM CENPO HCC1954 Hrisz
rowser	2_25100167_C_G	2 25100167 2_24739694_C_CT	rs2384057	Egr-1_mac2+, Ets_, Ets_, Ets_, Houring+, Ets_, Houring+, Ets_, Houring+, GAT A_ats_3+, Hard-11_, I-, Hard-11_, 2), Par CAC-binding-prot MCF-7;SPDEF MCF-7;H3K4ma1	2b		ADCY3	ADCY3 41888	INTRON	ADCY3, DNAJC27, DNAJC27, AD1, RPADCY3;6::0.0179219	NCDA1:C-0.0082746,0NM13ACC-0.0336562,0BAN2AC-0.0446517 NCDA1:C-0.0038145
rowser	2_25100338_C_T 2_25100738_C_A	2 25100338 2_24739694_C_CT 2 25100738 2_24739694_C_CT	rs2384059 rs10865315	MCF-7;SPDEF MCF-7;H3K4me1 AP-4_1 -AP-4_3 MCF_10A;FOS	5 3a		ADCY3 ADCY3	ADCY3 41717 ADCY3 41317	INTRON	ADCY3,CENPO(ADCY3,DNAJC27,DNAJC27-AS1,RP11-443B20.1 ADCY3,CENPO,DNAJC27,DNAJC27 ADCY3:A:-0.0176854	NCOA1:T:-0.0082631,DNM1ADCY3:MCF7:CNA-PET NCOA1:A:-0.0045205 ADCY3:MCF7:CNA-PET
rowser	2_25101092_G_A	2 25101092 2_24739694_C_CT 2 25103957 2 24739694 C_CT	rs2033855 rs7591460	Hoxb13 +,Hoxd10 + HDAC2 disc3la NRSE known2la NRSE known3la Rhow11 a TATA known4l, TATA known5l, TEIIAL	11		ADCY3 ADCY3	ADCY3 40963 ADCY3 38088	INTRON	ADCY3,CENPO,DNAJC27,DNAJC27ADCY3:A:-0.0178972 ADCY3,AS312,CENPO,DNAJC27,DNAJCY3:C:-0.0167899 MFSD2	NC0A1:A-:0.0045227 ADCY3:MCF7:CNA-PET
rowser	2_25104679_AGT_A	2 25104679 2_24739694_C_CT	rs3037312	fibroblast_of_marBRST.MYOEP.H3K4me1 MCF-7;dnase			ADCY3	ADCY3 37376	INTRON	ADCY3:A:-0.0069134,MFSD2	B NCDA1:A:-0.0045227
rowser	2_25105921_C_1 2_25107589_G_C	2 25105921 2_24739894_C_C1 2 25107589 2_24739694_C_CT	rs11675198	DMR(5)+ TATA_diao4 +	6		ADCY3 ADCY3	ADCY3 36134 ADCY3 34466	INTRON	ADCY3,ASXE2,DNAJC27,DNAJC27-ADCY3:T>-0.006/162,MISD2 ADCY3,DNAJC27,DNAJC27-AS1,RPADCY3:C>-0.0068633,MISD2	s:NCDA1:1:-0:0045227 3:NCDA1:C:-0:0045227
rowser	2_25107712_CT_C 2_25107759_C_T	2 25107712 2_24739694_C_CT 2 25107759 2_24739694_C_CT	rs36007978 rs11686663	Irf_known0 -,RXRA_diac4 -,TR4_diac2 +,p300_diac5 - GLI -HEY1_diac2 -,KIH -,NRSF_diac9 - HMEC;dnase	5		ADCY3 ADCY3	ADCY3 34343 ADCY3 34296	INTRON	ADCY3.C::0.0068569,MF5D21 ADCY3,ASXL2,CENPO,DNAJC27,DNADCY3.T::0.0068569,MF5D21	3:NCOA1:C0.0045227 3:NCOA1:T0.0045227
rowser	2_25108197_T_C 2_25109317_G_A	2 25108197 2_24739694_C_CT 2 25109317 2 24739694 C CT	rs1865689 rs7605335	MCF-7;SPDEF BDP1 disc3i-Foxi1+Foxi1-Foxi1 11+Pax-4 11-RREB-1 2i+.SP1 disc3i-UF1H3BETAI-	7		ADCY3 ADCY3	ADCY3 33858 ADCY3 32738	INTRON	ADCY3,ASXL2,CENPO,DNAJC27,DNADCY3;C:-0.0068505,MF5021 ADCY3,ASXL2,DNAJC27,DNAJC27- ADCY3;A:-0.0067226,MF5021	3: NCDA1:C0.0045227 3: NCDA1:A0.0045279
rowser :	2_25115243_A_G	2 25115243 2_24739694_C_CT 2 25117215 2 24739694_C_CT	rs10165451 rs28836469	BDP1_disc3 +,LUN-1 - MCF-7+H%4me1	6		ADCY3 ADCY3	ADCY3 26812 ADCY3 24840	INTRON	ADCY3, DNAJC27, DNAJC27-AS1, RP11-443820.1 ADCY3, DNAJC27, DNAJC27-AS1, RP11-443820.1	NC041:G0.0116802,UBXN24:G+:0.0305978 NC041:G0.0116913 UBXN24:G+:0.03057
rowser	2_25118885_C_T	2 25118885 2_24739694_C_CT	rs6545800	Foxa_disc5[+,Pou212_known2]+,TATA_known4]+,TATA_known4]+,TATA_known5[+	6	Inflammatory_bo	ADCY3	ADCY3 23170	INTRON	ADCY3,CENPOJADCY3,DNAJC27,DNAJC27-AS1,RP11-443B20.1	NCOA1:T:-0.0116913,UBX0247:+:0.08057
rowser	2_25120086_C_1 2_25120713_G_C	2 25120088 2_24739894_C_CT 2 25120713 2_24739894_C_CT	rs6723803	LXR_3(-NRSF_dMCF-7;SPDEF	5		ADCY3	ADCY3 21342	INTRON	ADCY3,CENPO(ADCY3,DNAJC27,DNAJC27-AS1,RP11-443820.1 ADCY3,CENPO(ADCY3,DNAJC27,DNAJC27-AS1,RP11-443820.1	NCDA1:C0.0116913,08AN24:C++0.03057 NCDA1:C0.0116913,U8KN24:C++0.03057
rowser	2_25121125_C_A 2_25122323_A_C	2 25121125 2_24/39894_C_CT 2 25122323 2_24739694_C_CT	rs6718510	ERapha-a_disc4 MCF-7/SPDEF ERapha-a_known4 +,Eat2 +,GR_disc1 +	5		ADCY3 ADCY3	ADCY3[20930 ADCY3]19732	INTRON	ADCY3, CENPO(ADCY3, DNAJC27, DNAJC27-AS1, RP11-443820.1 ADCY3, DNAJC27, DNAJC27-AS1, RP11-443820.1	NCDA1:A:-0.0902671,080N2A:A:+0.0330707,90918:A:-0.046318 NCDA1:C:-0.0116939,08XN2A:C:+0.0305716
rowser	2_25122324_A_G 2_25122840_C_G	2 25122324 2_24739694_C_CT 2 25122840 2_24739694_C_CT	rs6718511 rs4077678	NRSF_diac3 +,NRSF_known1 +,Pax-6_diac1 + KAP1_diac2 -	5		ADCY3 ADCY3	ADCY3 19731 ADCY3 19215	INTRON	ADCY3, DNAJC27, DNAJC27-AS1, RP11-443820.1 ADCY3, CENPO(ADCY3, DNAJC27, DNAJC27-AS1, RP11-443820.1	NCDA1:G:-0.0116939,UB/N2A:G:+:0.0305716 NCDA1:G:-0.0116939,UB/N2A:G:+:0.0305716
rowser	2_25123463_C_G	2 25123463 2_24739694_C_CT 2 25124348 2 24739694_C_CT	rs3903070 rs6545806	MCF-7;CTCF HMCLIV 2/4 Nev2 11/4 Nev2 6/4 Nev3 4/4	5		ADCY3 ADCY3	ADCY3 18592 ADCY3 17707	INTRON	ADCY3,CENPO(ADCY3,DNAJC27,DNAJC27-AS1,RP11-443820.1 ADCY3,DNAJC27,DNAJC27,AS1,RP11-443820.1	NC0A1:6:-0.0116939,UBXN2A:6:+:0.0305716 NC0A1:4:-0.0117273 UBXN2A:4:+0.0304589
rowser :	2_25124563_T_C	2 25124563 2_24739694_C_CT 2 25125075 2 24739694_C_CT	rs1550110 rs7563204	LUN-1 +,Mui1_diac1 -	5		ADCY3 ADCY3	ADCY3 17492 ADCY3 16980	INTRON	ADCY3, DNAJC27, DNAJC27-AS1, RP11-443820.1 ADCY3, DNAJC27, DNAJC27-AS1, RP11-443820.1	NCOA1:C:-:0.0116891,UBXN2A:C:+:0.0305697 NCOA1:G:-0.0116913 UBXN2A:G:+:0.03057
rowser	2_25125585_C_T	2 25125585 2_24739694_C_CT	rs876186	Hmx_2 -Nkx3_3 -,PRDM1_disc1 +,PU.1_disc1 +	6		ADCY3	ADCY3 16470	INTRON	ADCY3, DNAJC27, DNAJC27-AS1, RP11-443820.1	NCOA1:T0.0116913,UBX24:T-+0.03057
rowser	2_25126230_A_G 2_25126328_G_C	2 25126230 2_24739694_C_CT 2 25126328 2_24739694_C_CT	rs6726199	BHLHE40_disc2[+,ELF1_disc3]+,NRSF_disc9]+	11		ADCY3	ADCY3 15825 ADCY3 15727	INTRON	ADC13;CENPO(ADC13;DIA4C22;DIA4C22;AS1;RP11=443820;1 ADC13;CENPO(ADC13;DIA4C22;DIA4C22;AS1;RP11=443820;1	NCDA1:C0.0116913/0BM DNAJC27-AS1:MCP7.CHA-PET.,,DNAJC27:M NCDA1:C0.0116913/UBXN DNAJC27:MCP7.CHA-PET.,,DNAJC27-AS1:M
rowser	2_25126/15_C_1	2 25126715 2_24739694_C_CT 2 25127006 2_24739694_C_CT	rs10566562	HDAC2_disc6]-,Irf_disc3]-,Nanog_disc2]+,p300_disc5]-			ADCY3	ADCY3 15040 ADCY3 15040	INTRON	ADC13,CENPO(ADC13,DIAADC27,DIAADC27,483,RP11-4438201 ADCY3:C-:0.0074356,MF5D21	8:NC0A1:C:-0.0065166 DNAJC27:MCP7:CHA-PET_DNAJC27-A51M
rowser	2_25127394_A_G 2_25127614_A_G	2 25127394 2_24739694_C_CT 2 25127614 2_24739694_C_CT	rs34697209 rs6717671	Evi-1_4 +,Foxp1 -HDAC2_disc6 +,Irf_disc3 +,Irf_known0 -Pax-5_disc3 +,RXRA_disc4 -,2[p106]-,p300_dis HNF4_known5 +	6 7		ADCY3 ADCY3	ADCY3 14661 ADCY3 14441	INTRON	ADCY3, DNAJC27, DNAJC27-AS1, RPADCY3:6:-0.0078437, MFSD2 ADCY3, DNAJC27, DNAJC27-AS1, RP11-443820.1	8 NC0A1:6:-0.0065119 DNAJC27-AS1:MCF7:ChiA-PET,,,DNAJC27:M NC0A1:6:-0.0116913,UBIN DNAJC27:MCF7:ChiA-PET,,,DNAJC27-AS1:M
rowser	2_25128351_C_G	2 25128351 2_24739694_C_CT 2 25128719 2 24739694 C CT	rs6706316 rs6721750	Arid3a_2(+.Dobox4(+,Fox(-,Fox(1)+,HNF1_5(-,HNF1_6(-,HNF1_7)- TR4_disc3(+	6		ADCY3 ADCY3	ADCY3 13704 ADCY3 13336	INTRON	ADCY3,CENPO(ADCY3,DNAJC27,DNAJC27-AS1,RP11-443820.1 ADCY3,CENPO(ADCY3,DNAJC27,DNAJC27-AS1,RP11-443820.1	NCDA1:G:-0.0116913,UBXN2A:G:+0.03057 NCDA1:G:-0.0116913,UBXN2A:G:+0.03057
rowser	2_25128730_T_C 225129166 A ACT 2	2 25128730 2_24739694_C_CT 2 25129168 2 24739694 C CT	rs6724772 rs10651478	AP-4_2 +,AP-4_3 +,Ascl2 +,E2A_2 +,LBP-1_2 +,Nanog_disc3 +,Nix3_3 -,RREB-1_2 -,TCF12_known1 +	6		ADCY3 ADCY3	ADCY3 13325 ADCY3 12889	INTRON	ADCY3,CENPO(ADCY3,DNAJC27,DNAJC27-AS1,RP11-443B20.1	NCDA1:C:-:0.0116913,UBXN2A:C:+:0.03057 NCDA1:ACT:-:0.0112739.UBXN2A:ACT:+:0.0268574
rowser	2_25129473_A_G	2 25129473 2_24739694_C_CT	rs6725517	AP-2_known1 +,BCL_disc10 +,BDP1_disc3 -,CAC-binding-protein -,CCNT2_disc2 -,CTCF_disc5 +,Egr-1_d	5		ADCY3	ADCY3 12582	INTRON	ADCY3,DNAJC27,DNAJC27-AS1,RPADCY3:G:-0.0080013,MFSD2	B NCDA1:G:-0.0065119
rowser	2_25130073_C_T	2 25130073 2_24739694_C_CT	rs7585460	CTCF_dsc4+_EEMCF_10A_FOR_NBRST_HMEC;H3K4me1 HMEC;dnase	5		ADCY3	ADCY3 12268	INTRON	ADCY3, DNAJ227, DNAJ227-AS1, RP11-443820.1	NCDA1T-0.0117488,UBW2AT:+0.0311296
rowser rowser	2_25130440_A_T 2_25130451_A_G	z 25130440 2_24739694_C_CT 2 25130451 2_24739694_C_CT	rs11689543 rs11689546	CICE_dsc10+,EMCF_10A;STAT3 BDP1_dsc1+,G/MCF_10A;STAT3	5 1f		ADCY3 ADCY3	ADCY3 11615 ADCY3 11604	INTRON	AUCY3, DNAJC27, DNAJC27-AS1, RPMFSD28:T:+:0.0459888 ADCY3, CENPO(ADCY3, DNAJC27, D MFSD28:G:+:0.0459888	NCDA1:f:-0.0117109,UBXN2A:T:+:0.0304424 NCOA1:G:-0.0117109,UBXN2A:G:+:0.0304424
rowser	2_25130462_T_G 2_25130542_A_C	2 25130462 2_24739694_C_CT 2 25130542 2_24739694_C_CT	rs10200566 rs10198275	Bach1 ,GATA_diMCF_10A;STAT3 Armt_1 +.Armt_2 +.BHLHE40_disc1 +.BHLHE40_known1 +.HMG-IY_2 +.Hoxd10 Irf_known5 Myc_known1	1f 1f		ADCY3 ADCY3	ADCY3 11593 ADCY3 11513	INTRON	ADCY3,CENPO(ADCY3,DNAJC27,DNAJC27-AS1,RP11-443820.1 ADCY3,CENPO(ADCY3,DNAJC27,DNAJC27-AS1,RP11-443820.1	NCDA1:6:-0.0116913,UB/N2A:6:+:0.03057 NCDA1:C:-0.0116913,UB/N2A:C:+:0.03057
rowser	2_25130592_A_G 2_25130684 C_T	2 25130592 2_24739694_C_CT 2 25130684 2 24739694_C_CT	rs10198356 rs10188242	Ets_disc7[+2/p161_2]+ GR_disc4[-TATA_disc1]-THAP1_disc2[-VV1_r/scr1]_VV1_r/scr2]_VV444CC_7.5	7		ADCY3 ADCY3	ADCY3 11463 ADCY3 11974	INTRON	ADCY3, DNAJC27, DNAJC27-AS1, RP11-443820.1 ADCY3, DNAJC27, DNAJC27-AS1, RP11_443820.1	NCOA1:G:~0.0116913,UBXN2A:G:+:0.03057 NCOA1:T:~0.0116913,UBXN2A:T:+-0.03057
rowser	2_25130907_T_C	2 25130907 2_24739694_C_CT	rs6733224	Pax-5_known2 - MCF-7/Promoter	11		ADCY3	ADCY3[11148	INTRON	ADCY3,CENPO(ADCY3,DNAJC27,DNAJC27,AS1,RP11-443B20.1	NCDA1:C:-:0.0116913,UBXNZA:C:+:0.08057
rowser	2_25131161_T_C	∠ 25130920 2_24739694_C_CT 2 25131161 2_24739694_C_CT	ra6/30191 ra6/36210	rskr-o_krowth2 -∠kic + MCF-7/Promoter ELF1_disc5 +,HNF4_disc1 -,RXRA_known8 -,2tx + MCF-7/Promoter	6		ADCY3 ADCY3	ADCY3[11135 ADCY3[10894	INTRON	AUX: 13,UNAJC27,UNAJC27-AS1,RP11-443820.1 ADCY3,DNAJC27,DNAJC27-AS1,RP11-443820.1	NCDA1:C-0.0116913,UBN2A:C+0.03057 NCDA1:C-0.0116913,UBN2A:C+0.03057
rowser	2_25131170_C_G 2_25131287_C_T	2 25131170 2_24739694_C_CT 2 25131287 2_24739694_C_CT	rs6718628 rs6545813	AP-2_known1 + MCF-7;Promoter DMRT2 ;DMRT3 ;DMRT4 :Pou212_known2 +.Sox_:MCF-7;Enhancar HMF;dnase	7		ADCY3 ADCY3	ADCY3 10885 ADCY3 10768	INTRON	ADCY3, DNAJC27, DNAJC27-AS1, RP11-443820.1 ADCY3, DNAJC27, DNAJC27-AS1, RP11-443820.1	NCDA1:6:-0.0116913,UB9N2A:6:+:0.03057 NCDA1:T:-0.0116913,UB9N2A:T:+:0.03057
rowser	2_25131316_A_G 2_25131986_A_C	2 25131316 2_24739694_C_CT 2 25131986 2 24739694_C_CT	rs6545814 rs11900505	AP-1_disc4 +,Jk-2_3 +,NF-AT +,Sox_1 + MCF-7;Enhancer HMF;dnase Foxa_disc5 +	1f 1f	Body_mass_inde	ADCY3 ADCY3	ADCY3 10739 ADCY3 10049	INTRON	ADCY3,CENPO(ADCY3,DNAJC27,DNAJC27,AS1,RP11-443820.1 ADCY3,CENPO(ADCY3,DNAJC27,DNAJC27,AS1,RP11-443820.1	NCOA1:G:-0.0116913,UBXN2A:G:+0.03057 NCOA1:C:-0.0116913,UBXN2A:C:+0.03057
rowser	2 25132192 C A	2 25132192 2_24739694_C_CT 2 25133149 2 24739694_C_CT	rs6722587	E2A_2 .E2A_5 .Gm397 +.Nanog_disc1 +.Pou212_disc1 +.Pou212_known10(+.Pou212_known6(+.Pou212_k Bachtla CEBPDI. Mar. discRi	6		ADCY3	ADCY3 9863	INTRON	ADCY3,CENPO(ADCY3,DNAJC27,DNAJC27,AS1,RP11-443820.1 ADCY3,CENPO(ADCY3,DNAJC27,DNAJC27,AS1,RP11-443820.1 ADCY4,DNA_C27,DNA_C27,DNAJC27,AS1,RP11-443820.1	NCDA1:A0.0116913,UB(N2A:A+-0.03057 NCDA1:A0.0116913,UB(N2A:A+-0.03057
rowser	2_25133530_CTT_C	2513314d 2_24739694_C_CT 2 25133530 2_24739694_C_CT	rati/+4205 ra59644324	umun (+,-udbru)-wyc_smcb(-,rem-o_molent3)-,Na321_disc6)4	<u></u>		ADC13 ADCY3	ADC Y3(8907 ADC Y3(8525	INTRON	ADCY3.C:-0.0083468,MFSD21	NCA4:C-300110915,00ANZAC:+30.05057 3:NCA4:C-30.0077432
rowser	z_z5133750_G_A 2_25134009_T_C	z 25133750 2_24739694_C_CT 2 25134009 2_24739694_C_CT	rs6754997 rs13035244	AM-1_dsc1 +,CTCF_disd6 ,ERalpha-a_known1 ,RXRA_known3 +,RXRA_known4 + HES1 + MCF-7;GATA3	5		ADCY3 ADCY3	ADCY3 8305 ADCY3 8046	INTRON	AUCY3, DNAJC27, DNAJC27-AS1, RPMFSD28:A++:0.0488246 ADCY3, DNAJC27, DNAJC27-AS1, RPMFSD28:C++:0.047935	NCDA1:A-:0.0116913,UB(N2A:A:+0.03057 NCDA1:C-:0.0116913,UB(N2A:C:+0.03057
rowser :	2_25134344_T_C	2 25134344 2_24739694_C_CT 2 25134497 2 24739694_C_CT	rs13003430 rs12713422	AbR 11a Pax.6 innun31a Smarth 11.	7		ADCY3 ADCY3	ADCY3/7711 ADCY3/7558	INTRON	ADCY3, DNAJC27, DNAJC27-AS1, RPMFSD28;C++0.0468104 ADCY3, DNAJC27, DNAJC27-AS1, RPMFSD28;C++0.0464535	NCOA1:C0.0116913,UBXN2A:C+-0.03057 NCOA1:C0.0116913,UBXN2A:C+-0.03057
rowser	2_25135620_G_A	2 25135620 2_24739694_C_CT	rs2384061	HNF4_disc1[+,HNF4_disc3[+,HNF4_disc5]-	11		ADCY3	ADCY3(6435	INTRON	ADCY3,ASXL2,CENPO(ADCY3,DNA ADCY3,A:-0.0068505,MFSD2)	R NCOA1:A0.0055119 ADCY3MCF7:CNA-PET
rowser	2_25136006_T_A	2 25136916 2_24739694_C_CT 2 25136916 2_24739694_C_CT	rs10203482	CAC-binding-protein(+,CCNT2_discBRST.MYOEP;H3K4ma1,BRST.MYOEP;H3K9ac,MCF-7;H3K4ma1 CAC-binding-protein(+,CCNT2_discBRST.MYOEP;H3K4ma1,BRST.MYOEP;H3K9ac,MCF-7;H3K4ma1	4		ADCY3	ADCY3j5139	INTRON	ADCY3,DNAJC27,DNAJC27-AS1,RPMFSD28:C+0.0279945	NCDA1:C0.00755, UBXN2A ADCY3:MCF7:ChiA-PET
rowser	2_25137323_T_C 2_25138040_A_C	2 25137323 2_24739694_C_CT 2 25138040 2_24739694_C_CT	rs10206196 rs6737082	Crx_2 ,GATA_known1 +,LXR_2 +BRST.MYOEP,H:MCF-7;Erhancer Egr-1_diso4 +,INEMCF-7;SPDEF BRST.MYOEP,H3K9ac HMEC;dnase	6 1f		ADCY3 ADCY3	ADCY3 4732 ADCY3 4015	INTRON	ADCY3, DNAJC27, DNAJC27-AS1, RPMFSD28:C:+:0.0378157 ADCY3, CENPOJADCY3, DNAJC27, DNAJC27-AS1, RP11-443B20.1	NCOA1:C:-0.0044577,UBXN ADCY3:MCF7:CNA-PET FK8P18:C:-0.0187241,POMI ADCY3:MCF7:CNA-PET
rowser :	2_25156773_T_C	2 25156773 2_24739694_C_CT 2 25159172 2 24739694_C_CT	rs2384054 rs6728219	RXRA_known4 - HNF1 7i, Mat2 known5i,	6			ADCY3 14718 ADCY3 17117	INTERGENIC	ADCY3,CENPO(ADCY3,DNAJC27,DNAJC27-AS1,POMC,RP11-44 ADCY3,DNAJC27,DNAJC27,AS1,POMC,RP11-44382011	3 FK8P18:C0.0352998,NCDA1:C0.0427467,NCDA1:C0.0486829 FK8P18:C0.0244445 NCDA1:C0.0260209 NCDA1:C0.0355845
rowser	2_25159501_G_C	2 25159501 2_24739694_C_CT	rs6738433	Dtx1;+Hoxa10;-Mat2_known1;-Mat2_known4;-Nox_2;-	6			ADCY3 17446	INTERGENIC	ADCY3, DNAJC27, DNAJC27-AS1, POMC, RP11-443820.1	NCDA1:C0.0235036,FKBP1B:C0.0243267,NCDA1:C0.0356658
rowser	2_25159/80_A_G	2 25159760 2_24739694_C_CT 2 25159855 2_24739694_C_CT	rs10865321	Pax4_1 +	7			ADCY3 17725 ADCY3 17800	INTERGENIC	ADCY3,DNAJC27,DNAJC27-AS1,POIntC,RP11-443620.1 ADCY3,DNAJC27,DNAJC27-AS1,RP11-443820.1	NCOA1:C0.0210102/MBP18:C0.024305,MCOA1:C0.0358061 NCOA1:C0.0210955,FKBP1B:C0.0242307,NCOA1:C0.0358254
rowser	2_25159858_A_G 2_25161236_A_G	2 25159858 2_24739694_C_CT 2 25161238 2_24739694_C_CT	rs10865322 rs4343432	Maf_disc2 -,Ni2l2 +,Pax-4_1 + Nkc2_4 -,TFII-I +	7			ADCY3 17803 ADCY3 19181	INTERGENIC	ADCY3,DNAJC27,DNAJC27-AS1,RP11-443B20.1 ADCY3,DNAJC27,DNAJC27-AS1,POMC,RP11-443B20.1	NCOA1:G0.0210781,FK8P18:G0.0242269,NCOA1:G0.035826 NCOA1:G0.0166212,FK8P18:G0.0249794,NCOA1:G0.0367388
rowser	2_25161265_G_T	2 25161265 2_24739694_C_CT 2 25161386 2 24739694 C CT	rs4459693 rs4430895	CTCF_disc8[-,CTCF_known1]-,Ets_disc5[+,Irf_disc5[-,Myf_1]-,Nanog_disc3[-,Nt2f2]+,Rad21_disc1]-,Rad21	6 7			ADCY3 19210 ADCY3 19331	INTERGENIC	ADCY3,DNAJC27,DNAJC27-AS1,POMC,RP11-443820.1 ADCY3,DNAJC27,DNAJC27-AS1,POMC,RP11-443820.1	NCOA1:T:-0.0166212,FK8P18:T:-0.0240794,NCOA1:T:-0.0367388 NCOA1:T:-0.0166212,FK8P18:T:-0.0240794,NCOA1:T:-0.0367388
rowser	5_130341728_C_CT	6 130341728 6_130349119_C_T 6 130345791 6 130349119_C_T	rs55941023 rs1415700	mammary_apithe BRST.HMEC;H3K4ma3,BRST.MY(BRST.HMEC;Promoter,BRST.MYOEP;Pr MCF_10A;STAT3	omoter,BR	ST.vHMEC;Promo	ter MCF-7;Promot 1 3MRTL3	er I SMRTI SIEDE4	INTRON	TMEM200A-CT0.0139554 13MBTI 3 RP11.7313MBTI 3 RP11.7TMEM200A-40.0169898	L3MBTL3:CT:-0.0077711 J3MBTL3:A:-0.0070491 J3MBTL3:MCF7:CN4.PET
rowser (	5_130346105_G_A	6 130346105 6_130349119_C_T	rs7740188	YY1_disc2 -	6		L3MBTL3	L3MBTL3(6378	INTRON	L3MBTL3,RP11-73 L3MBTL3,RP11-7TMEM200A:A:-0.0489309	L3MBTL3:A:-:0.0070517 L3MBTL3:MCF7:ChIA-PET
rowser	5_130349119_C_1 5_130350294_G_A	6 130349119 6_130349119_C_1 6 130350294 6_130349119_C_T	rs6926186	DMRT1 +,p300_diac7 -	7	Height	L3MBTL3 L3MBTL3	L3MB1L3 9392 L3MBTL3 10567	INTRON	L3MBTL3;RP11-73 L3MBTL3;RP11-7TMEM2004;T::0.0448786 L3MBTL3;RP11-73 L3MBTL3;RP11-7TMEM2004;A::0.0172537	L3MBTL3:1:-4.25E-06 L3MBTL3:A:-:0.0043689
rowser rowser	8_130352025_T_TA 8_130353612_T_C	6 130352025 6_130340119_C_T 6 130353612 6_130340119_C_T	rs11390217 rs9402211		7		L3MBTL3 L3MBTL3	L3MBTL3 12298 L3MBTL3 13885	INTRON	TMEM200A:TA:-0.017267 L3MBTL3,RP11-73 L3MBTL3,RP11-7TMEM200A:C:-0.0171127	L3M8TL3:TA:-0.0045989 L3M8TL3:C:-0.0048717
rowser	5_130354855_T_C	6 130354855 6_130349119_C_T 6 130356608 6 130349119 C T	rs9388766 rs9375694	Evi-1_4 - RXR:LXRi+.c300 disc7 +	6 1d		L3MBTL3 L3MBTL3	L3MBTL3 15128 L3MBTL3 16881	INTRON	L3MBTL3,RP11-73 L3MBTL3,RP11-7TMEM200A;C:-0.0176176 L3MBTL3,RP11-73 L3MBTL3,RP11-7TMEM200A;A:-0.017281	L3M8TL3:C:-0.0050839 L3M8TL3:A:-0.0056388
rowser	8_130357553_G_A	6 130357553 6_130340119_C_T	rs9388767	Found is NE 1.31 Resident of managers and CTCE managers without out CTCE MCE 2/CTCE	6	Molake	L3MBTL3	L3MBTL3 17826	INTRON	L3MBTL3,RP11-73 L3MBTL3,RP11-7TMEM200A-A 0.0176738	L3M8TL3:A:-0.0056388
rowser	5_1303589426_G_A	6 130358944 6_130349119_C_T	rs9375695	Hoxa7_1 +,Smad3_1 -	6	neign:	L3MBTL3	L3MBTL3 19217	INTRON	L3MBTL3,RP11-73 L3MBTL3,RP11-71MEM2004;3:-0.0120084 L3MBTL3,RP11-73 L3MBTL3,RP11-71MEM2004;1:-0.0150127	L3MBTL37:-0.0056388
rowser rowser	8_130367725_T_G 8_130372984_A_G	6 130367725 6_130349119_C_T 6 130372984 6_130349119_C_T	rs7744830 rs6914670	Barhi1 +,En-1_3 +,Foxo_3 +,Nix2_8 +,Nix6=1_3 +,Pax-8_1 +,Pou6f1_1 -,Sox_15 +,Sox_2+,Sox_7 + HEN1_2 +,Nix3_5 +	6 7		L3MBTL3 L3MBTL3	L3MBTL3 27998 L3MBTL3 33257	INTRON	L3MBTL3,RP11-73 L3MBTL3,RP11-7TMEM200A-G:-0.0244252 L3MBTL3,RP11-73 L3MBTL3,RP11-7TMEM200A-G:-0.0247459	L3MBTL3:6:-0.0074777 L3MBTL3:6:-0.0074764
rowser	5_130373648_C_G 5_130375810_A_G	6 130373648 6_130349119_C_T 6 130375810 6_130349119_C_T	rs7756870 rs6900473	FXR_2 -,HNF4_known5 +,RXRA_known3 - E2F_diac6 -,HNF1_6 +,HNF1_7 +,Mal_diac2 -,Mal_known3 -,Mal_known4 -,Pou5f1_diac1 -,Pou5f1_known	7		L3MBTL3 L3MBTL3	L3MBTL3 33021 L3MBTL3 36083	INTRON	L3MBTL3,RP11-73 L3MBTL3,RP11-7TMEM200A:G:-:0.0244362 L3MBTL3,RP11-73 L3MBTL3,RP11-7TMEM200A:G:-:0.0247465	L3MBTL3:6:-:0.0074764 L3MBTL3:6:-:0.0074764
rowser	5_130377843_C_T	6 130377843 6_130349119_C_T	rs11759018	HDAC2_disc6)+.If_disc3}- Id_disc91_SPEEP_incom21a	6		L3MBTL3	L3MBTL3 38116	INTRON	L3MBTL3,RP11-73 L3MBTL3,RP11-7TMEM200A-T0.0247452	L3M8TL3:T:-0.0074764
rowser	5_130377847_1_C 5_130378833_T_C	6 130378833 6_130340119_C_T	rs12661188	Egr-1_known1}-EMCF-7/MYC	7		L3MBTL3	L3MBTL3[39106	INTRON	L3MBTL3,RP11-73 L3MBTL3,RP11-7TMEM2004CC:0.0247452 L3MBTL3,RP11-73 L3MBTL3,RP11-7TMEM2004-CC:0.0242921	L3MBTL3:C:0.0075615
rowser	5_130379160_T_C 5_130379282_A_G	6 130379160 6_130349119_C_T 6 130379282 6_130349119_C_T	rs12661232 rs12201492	CTCF_disc8 -,ELF1_disc3 +,Ets_disc7 +,NRSF_disc9 -,Rad21_disc6 -,YY1_disc4 +,Znf143_disc3 +,p300_c Pax-5_disc1 +	7		L3MBTL3 L3MBTL3	L3MBTL3 39433 L3MBTL3 39555	INTRON	L3MBTL3,RP11-7306.3 TMEM200A:C:-0.024747 L3MBTL3,RP11-73 L3MBTL3 TMEM200A:C:-0.0247452	L3MBTL3:C:-0.0074764 L3MBTL3:G:-0.0074764
rowser rowser	8_130379852_A_G 8_130379854_T_C	6 130379852 6_130349119_C_T 6 130379854 6_130349119_C_T	rs7760760 rs9375700	DMRT2 - MCF-7;SPDEF DMRT2 -ERaiph MCF-7;SPDEF	7		L3MBTL3 L3MBTL3	L3MBTL3 40125 L3MBTL3 40127	INTRON	L3MBTL3,RP11-73 L3MBTL3,RP11-7TMEM200A-G:-0.0248784 L3MBTL3,RP11-73 L3MBTL3,RP11-7TMEM200A-C:-0.0248602	L3MBTL3:6:-0.0075712 L3MBTL3:C:-0.0075712
rowser	8_130381246_T_C	6 130381246 6_130349119_C_T 6 130384187 6 130349119_C_T	rs7451021 rs9375702	CONT2 discilla Exist Na GATA knowntalla TAL1 discilla	6		L3MBTL3	L3MBTL3 41519	EXON INTRON	L3MBTL3, RP11-73 L3MBTL3, RP11-7TMEM200A-C -: 0.0244209 L3MBTL3, RP11-73 L3MBTL3, RP11-7TMEM200A-T -: 0.0242219	L3MBTL3:C:-0.0074764 J3MBTL3:T:-0.0126009
rowser 1	8_163366_T_C	8 163366 8_170692_T_C	rs34810249		4		RPL23AP53	ZNF596 18833	SUTR, EXON	RP5-855021.1,RP5-855021.2,RPL23AP53,ZNF596	
rowser	5_163853_1_C 8_163854_C_T	8 163654 8_170692_T_C 8 163654 8_170692_T_C	rs2906362	AP-1_disc4 +,HNF4_known3 +,HNF4_known4 -,Irf_disc3 +,Irf_known1 +,Irf_known2 +,Irf_known3 +,PLZF +	7		RPL23AP53 RPL23AP53	ZNF596 18545	3UTR,EXON	RP5-855D21.1, RP5-855D21.2, RPL23AP53, ZNF596 RP5-855D21.1, RP5-855D21.2, RPL23AP53, ZNF596	
rowser I	3_170692_T_C I 3_172477_T_C I	8 170692 8_170692_T_C 8 172477 8_170692_T_C	rs66823261 rs3008281	Maf_disc1 +,Maf_known1 +,NF-E2_disc1 +,Nf-2_2 +,Nf-2_3 +,TCF11:MafG +,p300_disc7 + CACD_2 -,ERalpha-a_disc1 +,Ear2 +,Klf4 -,Klf7 +,Pax-5_known2 +,RFX5_disc1 +,SP1_known4 +,SREBP_	6		RPL23AP53 RPL23AP53	ZNF596 11507 ZNF596 9722	INTRON	RP5-855D21.1, RP5-855D21.2, RPL23AP53, ZNF596 RP5-855D21.1, RP5-855D21.2, RP5-855D21.3, RPL23AP53, ZNF596	
rowser I	8_174284_A_T I 8 174546 G A	8 174284 8_170692_T_C 8 174546 8 170692 T C	rs3008282 rs2906324	Mat2_disc1 +.Mat2_known2 + NF-E2_disc4 -	7		RPL23AP53 RPL23AP53	ZNF596(7915 ZNF596(7653	INTRON	RP5-855D21.1, RP5-855D21.2, RP5-855D21.3, RPL23AP53, ZNF598 RP5-855D21.1, RP5-855D21.2, RP5-855D21.3, RPL23AP53, ZNF598	
rowser I	8_177093_G_C 8 8 184919 G C	8 177093 8_170692_T_C 8 184919 8 170692 T C	rs10099411 rs2286140	AP-1_disc1).CTCF_disc4).E2F_disc1).Nr2f2 - Nanoo_disc1]+.Pax-5_disc4].Pou2f2_known2]+.Pou2f2_known5]Pou3f3]+	7		RPL23AP53 ZNF596	ZNF596(5106 ZNF596(2536	INTRON	RP5-855D21.1,RP5-855D21.2,RPL23AP53,ZNF596 RP5-855D21.1,RP5-855D21.2,RPL23RPL23AP53;C:+0.0396912	0R4F21:C:-0.0275255,2NF596-C:-0.0376048 0R4F21:C:-0.0210876 RP5-855D21.2:MCF7:CNA-PET., RP5-855D2
rowser	3_189364_T_C	8 189364 8_170692_T_C	rs3008276	Foxa_diac5(+,MeIMCF_10A;POLR2A	6		ZNF596	ZNF596(6981	INTRON	RP11-585F1.10,RP5-855D21.1,RP5-RPL23AP53:C++0.0398899	OR4F21:C-0.0191729,2NF596:C-0.0464847
rowser I	5_191746_A_C I 5_124737769_C_T I	8 191746 8_170692_1_C 8 124737769 8_124757661_C_T	rs4401839	Eomesi- HP1-site-factori- mammary_spithe BRST.MYOEP;H3K4me1;BRST.vHMEC;H3K4me1;mammary_spithelia	7		ANXA13	2NF596(9363 ANXA13(11878	INTRON	NP11-685F1.10,NP5-855021.1,NP5-RPL25AP53:C+0.0421935 ANXA13	0K4F213C-30.0237581 KP5-855021 2:MCF7/ChiA-PE1KP5-855021 MTSS1:T:+:0.0414242
rowser I	8_124738098_G_A I 8_124738449_T_A I	8 124738098 8_124757661_C_T 8 124738449 8_124757661_C_T	rs4509301 rs970820	Crx_1MOVO-8(mammary_epithe BRST.HMEC;H3FBRST.vHMEC;Enhancer BRST.HMEC;dna CEBPD\-Mal_kmmammary_epithe BRST.MYOEP;H3K4me1_mammary_epithelial_cell;H3K4me1_mammary_	2b 5		ANXA13 ANXA13	ANXA13 11549 ANXA13 11198	INTRON	ANXA13 ANXA13	
rowser I	8_124738618_C_T 8_124738742_C_T	8 124738618 8_124757661_C_T 8 124738742 8_124757661_C_T	rs970821 rs970822	FAC1 + mammary_apithe BRST.MYOEP;H3K4me1,mammary_apithelial_call;H3K4me1 INSM1 +,Smad4  mammary_apithe BRST.MYOEP;H3K4me1 mammary_apithelial_call;H3K4me1.MCF-7;H	4		ANXA13 ANXA13	ANXA13 11029 ANXA13 10905	INTRON	ANXA13 ANXA13	MTSS1:T:+:0.0414389 ANXA13:MCF7:CNA-PET MTSS1:T:+:0.041432 ANXA13:MCF7:CNA-PET
rowser rowser	8_124739287_T_C 8_124739293 G A	8 124739287 8_124757661_C_T 8 124739293 8 124757661_C_T	rs4871410 rs4871411	Myc_dsc9(+,RXRmammary_spithe BRST.MYOEP;H3K4me1_mammary_spithelial_call;H3K4me1 SP1_dsc3)-STA'mammary_spithe BRST.MYOEP;H3K4me1_mammary_spithelial_call;H3K4me1	7		ANXA13 ANXA13	ANXA13 10360 ANXA13 10354	INTRON	ANXA13	ANXA13:MCF7:CNA-PET MTSS1:A:+:0.0414071 ANXA13:MCF7:CNA-PFT
rowser	8_124739558_G_A	8 124739556 8_124757661_C_T 8 124739700 9 124757661_C_T	rs7820718	Esr2), RXR:LXR(mammary, spithe BRST.MYOEP,H:BRST.MYOEP,Enhancer mammary, anithe BRST.MYOEP,H:BRST.MYOEP,Chinacer	7		ANXA13 ANXA*9	ANXA13 10091	INTRON	ANXA13	MTSS1:A:+:0.0414044 ANXA13:MCF7:CNA-PET
rowser	5_124739709_G_A 8_124739913_T_G	8 124730700 8_124757661_C_T 8 124730913 8_124757661_C_T	rs7842619	Banx1 -Bax +.Dtx mammary_spithe BRST.MYOEP;H;BRST.MYOEP;Enhancer	5		ANXA13 ANXA13	ANXA13(9734	INTRON	ANXA13	MTSS1:6:+:0.0414671 ANXA13:MCF7:CHA-PET
rowser	aereneral_G_A I 8_124741789_T_C I	.247404081 8_124757661_C_T 8 124741789 8_124757661_C_T	ra1391695 ra13281094	Cit2, view, poor, mammary, spime BRS1.HMEC/EXHMS1.HMEC/Enhancer Cit2, VDAC2_dia mammary_spine BRST.MVOEP.H:BRST.HMEC/Enhancer,BRST.vHMEC/Enhancer	5		ANXA13	ANXA13/0148 ANXA13/7858	INTRON	ANXA13	ANXA13MCF7:CNA-PET ANXA13MCF7:CNA-PET
rowser I	8_124742320_G_A I 8_124743332_G_A I	8 124742320 8_124757661_C_T 8 124743332 8_124757661_C_T	rs7014939 rs4549748	DMRT1 -Sox_13 mammary_epithe BRST.MYOEP,H:BRST.MYOEP,Enhancer Arnt_1 -Jrf_knowmammary_epithe BRST.MYOEP,H3K4me1,mammary_epithelial_cell;H3K4me1,MCF-7;H	5		ANXA13 ANXA13	ANXA13 7327 ANXA13 6315	INTRON	ANXA13 ANXA13	MTSS1:A:+:0.0403596 ANXA13:MCF7:CNA-PET,,FBX032:MCF7:Ch MTSS1:A:+:0.0392256 FBX032:MCF7:CNA-PET,,ANXA13:MCF7:Ch
rowser 1	8_124744912_G_T 8_124746417_C_G	8 124744912 8_124757661_C_T 8 124746417 8_124757661 C T	rs4418323 rs17349815	FAC1 -Foxa_knomammary_epithe BRST.MYOEP;H3K4me1_mammary_epithelial_call;H3K4me1 SP2_disc2 + mammary_epithe BRST.MYOEP;H3K4me1_mammary_epithelial_call;H3K4me1	6 5		ANXA13 ANXA13	ANXA13 4735 ANXA13 3230	INTRON	ANXA13	FAM83A:T:+:0.0209763 MTSS1:6:+:0.0391251 ANXA13:MCF7:CNA-PET
rowser I	8_124746618_C_T 8_124750451_G_A	8 124746618 8_124757661_C_T 8 124750451 8_124757661_C_T	rs17258588 rs4617138	Foxm1 + mammary_apithe BRST.MYOEP;H3K4me1,mammary_apithelial_cell;H3K4me1 Mal_known3 + mammary_apithelial_cell;CTCF	4		ANXA13	ANXA13 3029 ANXA13 804	INTRON 2kbUPSTREAM	ANKA13 U ANKA13	MTSS1:T:+:0.0391251 ANXA13:MCF7:CNA-PET MTSS1:A:+0.0391251 FAM91A1:MCF7:CNA-PETANXA13:MCF7:C
rowser	8_124750521_C_T	8 124750521 8_124757661_C_T 8 124750585 8 124757661_C_T	rs13279803 rs1946584	Pou392_2 -,8xx_5mammary_apithelial_cell;CTCF Ets_dlsc/0i-MOV(mammary_apithelMCF-7;H3K4me3	5 7			ANXA13 874 ANXA13038	2kbUPSTREAM 2kbUPSTREAM	U ANKA13	MTSS1:T:+:0.0391251 FAM01A1:MCF7:CNA-PET_ANXA13:MCF7:C MTSS1:A:+:0.0391251 ANXA13:MCF7:CNA-PET_FAM01a+MCF7C
rowser rowser	8_124750741_A_G	8 124750741 8_124757661_C_T 8 124754567 8 124757661_C_T	rs1946585 rs2008198	Bitx - mammary_spithelial_cell;CTCF,MCF-7;ERalpha Nix3 11- mammary_spithelial_cell;CTCF,MCF-7;ERalpha	5			ANXA13 1094 ANXA13 4030	260UPSTREAM	U ANXA13 ANXA13	MTSS1:6:+:0.0391279 ANXA13:MCF7:CNA-PET.,FAM91A1:MCF7:C ANXA13:MCF7:CNA-PET.
rowser I	3_124755190_G_GA	8 124755190 8_124757661_C_T	rs71289608	Inf_disc3]+,2[p10f mammary_epithe BRST_MYOEP;H3K4ma1				ANXA13 5543	INTERGENIC		2HX2:GA++0.0486941
rowser	a_1447500313_U_1 I	<ul> <li>.24/35313 8_124/57661_C_T</li> <li>8 124757021 8_124757661_C_T</li> <li>4 04757021</li></ul>	ra1003/319 ra34838484	mammary_spine bhb1.MYUEPH384ma1 EWSR1-FL11;_Gumammary_spine BRS1.HIEC;H3K4ma3				ANXA13(5666 ANXA13(7374	INTERGENIC	ANDKA13	ANXA13:MCF7:CNA-PET
rowser	5_12+757881_C_T I 11_108043535_T_TAGA 1	e 124757661 8_124757661_C_T 1 106043535 11_108357137_A_G	rs17350191 rs141989202	cor_wows2+,4mammaty_spithe BHS1.MYUEP/HSK4me1 HNF1_6(+,HNF1_mammaty_spithelial_cell/CTCF	5		NPAT	ANXA13 8014 NPAT 49830	INTEMGENIC EXON	SLC35F2:T:-:0.0293648,C11or	ANXA13:MCF7:CNA-PET 165:T:+:0.0347634,ATM:T:+:0.0495976
rowser rowser	11_108044995_A_G 1 11_108055198_C_CAA 1	1 108044995 11_108345515_G_A 1 108055198 11_108345515_G A	rs7129627	GACU_2-KI4-MCF-7/FoxA1/MCF-7/GATA3	6		NPAT	NPAT 48370	INTRON	AUA I 1,ATM,KDELC2	SLC3592:G:+:0.0010141;SLC35F2:G:+:0.0348472;L0C643923:G:-:0.0452348 SLC35F2:C4A:+:0.0010519;SLC35F2:C4A:+:0.0366358
rowser	11_108087847_G_T 1	1 108087847 11_108345515_G_A 1 108098459 11 108345515_C_A	rs228606 rs2066734	Gm397(+,SRF_kr/fibroblast_of_marBRST.HMEC;H3K4ma1,BRST.vHMEC;H	4		NPAT ATM	NPAT 5518 ATM 4901	INTRON	ACAT1,ATM,CUL5,KDELC2,NPAT ACAT1,ATM,KDELC2	SLC35F2:T:+:0.0010235;SLC35F2:T:+:0.0349345;L0C643923:T:-:0.0453462 SLC35F2:T:+:0.0005936;L0D ATM/MCF7 CMA.PET NPAT/MCF7 CMA.PET
rowser rowser	11_108105593_G_A 1	1 108105593 11_108345515_G_A 1 108141701 11 108345515_C_A	rs228595 rs651030	Fouril-Fouril- E2A 2LLBP-1 3ixTBXS 3LZEB1 digr1L 7FR1 invested.	6		ATM ATM	ATM 12035 ATM 48149	INTRON	ACAT1,ATM,KDELC2 ACAT1,ATM,KDELC2	SLC35F2:A++0.000899.SLC35F2:A++0.034903;0C643923:A-+0.0432518 SLC35F2:T++0.0007461.SLC35F2:T++0.0357631006643923:T+0.04432518
rowser	11_108143456_C_G 1	1 108143456 11_108345515_G_A	rs1800057	Pou22_Interv88(+Pou22_1+Pou21_interv1+,iten/	7		ATM	ATM/49898	EXON		ALXBH8:G:-0.0148008
rowser	11_108149207_T_G 1 11_108177097_T_A 1	1 10814920/ 11_108345515_G_A 1 108177097 11_108345515_G_A	rs141379009 rs611646	munuc_swidt), Nkitt-1_1-,dp105 - DMRT2 ,GATA_known1 ,GATA_known2 +,GATA_known4 -	39 6		ATM	ATM(55649 ATM(83539	INTRON	ACAT1,ATM,CUL5,KDELC2,NPAT	ALADROSUS-U.UL48008 SLC35F2:A:+10.0007372,SLC35F2:A:+10.0358342,LOC643923:A:-0.0403296
rowser rowser	11_108210258_T_C 1 11_108267402_C_CA 1	1 108210258 11_108345515_G_A 1 108267402 11_108345515_G A	rs227069 rs199504893	Osl2_2 - MCF-7;FoxA1 BRST.vHMEC;dn	6		ATM C11orf85	ATM 116700 C11or/65 70856	INTRON	ACAT1,ATM,KDELC2	SLC35F2:C.+.0.0007372,SLC35F2:C:+.0.0358342,L0C643923:C0.0403296 SLC35F2:CA:+.0.001005,L0C643923:CA:-0.0402809,SLC35F2:CA:+.0.04481
rowser rowser	11_108288808_G_T 1 11_108290959_A_G 1	1 108288808 11_108345515_G_A 1 108290959 11_108345515_G A	rs10431061 rs11212620	Nex3_2(+;Mou111_2(+ T47D)dnase AP-3(-,PRDM1_dT47D;ER	5 6		C11orf85 C11orf85	C11or85(49450 C11or85)47299	INTRON	AGA11,ATM,KDELC2 ACAT1,ATM,KDELC2	sLc359z.T.+:0.0007372,SLC35F2.T.+:0.0358342,L0C643923.T:0.0403296 SLC35F2:G:+:0.0007372,SLC35F2:G:+:0.0358342,L0C643923:G:-:0.0403296
rowser	11_108294107_A_G 1	1 108294107 11_108345515_G_A 1 108295315 11 108345515_C A	rs1960006 rs4250067	BCL_disc3 -ERalpha-a_disc4 -LXR_3 -ZBRK1 + Arid5a +.Brachuury 1 +.Fora disc2 +.Mto 1 +.Tol11_2 +	7		C11orf65 C11orf65	C11or85(44151 C11or85(42942	INTRON	ACAT1,ATM,KDELC2 ACAT1,ATM,KDELC2	SLC35F2:G:+:0.0007372;SLC35F2:G:+:0.0358342;L0C643923:G:-:0.0403296 SLC35F2:T:+:0.0007372;SLC35F2:T:+:0.0358342;L0C643923:G:-:0.0403296
rowser	11_108296680_C_T 1	1 108296680 11_108345515_G_A 1 108297409 11 108245515_G_A	rs7952492	NERF1al, Sox_14 AIRF 11, FAC11a Growtla HMGJY 21a PDAD 31a David 41a	7		C11orf85	C110/85/41578	INTRON	ACATI,ATM,KDELC2	SLC35F2:T++0.0007372;SLC35F2:T+10.0358342;LOC643923:T-10.0403296 SLC35F2:T+0.0007372;SLC35F2:T+10.0358342;LOC643923:T-10.0403296 SLC35F2:T+0.0007372;SLC35F2:T+0.0358342;LOC643923:T-10.0403296
rowser	11_108298019_C_G 1	1 108298019 11_108345515_G_A	m11212624	TAL1_known1 +	7		C11or(85	C11or/65/40850	INTRON	ACATI,ATM,KDELC2	SLC35F2-G++0.0007372_SLC35F2-G++0.0358342_L0C643923-G-+0.0403296
rowser	11_108298213_G_T 1 11_108298263_G_A 1	1 108298213 11_108345515_G_A 1 108298263 11_108345515_G_A	rs11212625 rs11212626		7		C11orf85 C11orf85	C11arl65 40045 C11arl65 39995	INTRON	ALA I 1,KDELC2 ACAT1,ATM,KDELC2	stc35r2:T++0.0007372,StC35F2:T++0.0358342,L0C643923:T-+0.0403296 StC35F2:A++0.0007375,StC35F2:A++0.0358448,L0C643923:A-+0.0403251
rowser rowser	11_108298323_T_C 1 11_108298374_G_A 1	1 108298323 11_108345515_G_A 1 108298374 11_108345515 G A	rs28861227 rs28810151	E2F_known3 +,GZF1 -Zlp161_3 + BDP1_disc1 -,CTCF_disc8 +,Ets_disc9 +,Irf_disc4 +,RXRA_known3 +,Rad21_disc10 +,Rad21_disc71+_RM	6		C11orf85 C11orf85	C11or/65/39935 C11or/65/39884	INTRON	ACAT1,KDELC2 ACAT1,KDELC2	SLC35F2-C++0.0007372_SLC35F2-C++0.0358342_L0C643923:C-+0.0403296 SLC35F2-A++0.0007372_SLC35F2-A++0.0358342_L0C643923:A-+0.0403296
rowser rowser	11_108298482_T_C 1	1 108298482 11_108345515_G_A 1 108298581 11 108345515_G_A	rs111612686 rs1125683F9	Pax-4_4 +,Pax-4_5 + DMRTSI-	6 7		C11or/85 C11or/85	C11or85(39776	INTRON	ACAT1,ATM,KDELC2	SLC35F2-C+0.0007367,SLC35F2-C+0.0358129,L0C643923:C-0.0403225 SLC35F2-G+0.0007372,SLC35F2-G+0.0358129,L0C643923:C-0.0403225
rowser	11_108298852_A_G 1	1 108298852 11_108345515_G_A	rs61913875	CHD2_disc3(+,E2F_disc7)+,Egr-1_disc1)+,Egr-1_disc6)-,OLI -,NRSF_disc9(-,Nrf1_disc1)+,Nrf1_disc3)+,Sin	6		C11orf85	C11or/65/39406	INTRON	ACAT1,ATM,KDELC2	SLC35F2-G++0.0007372_SLC35F2-G++0.0358342_L0C643923-G0.0403296 SLC35F2-G++0.0007372_SLC35F2-G++0.0358342_L0C643923-G0.0403296
rowser	11_108306236_C_A 1	1 108306238 11_108345515_G_A	rs3+00562/ rs10890839	INSM1 -	7		C11orf85	C110/85/37404 C110/85/32022	INTRON	ACAT1,ATM,KDELC2	accoracc+successus,coc643922C-sucs88861,SLC35F2:C+s0.0389152 SLC35F2:A+s0.0007372,SLC35F2:A+s0.0358342,L0C643923:A-s0.0403296
rowser rowser	11_108308175_G_A 1 11_108308510_G_A 1	1 108308175 11_108345515_G_A 1 108308510 11_108345515_G A	rs10789682 rs7129816	Cnx_1 +,Pix2 - Hoxe7_1 -	6 7		C11orf85 C11orf85	C11or(65)30083 C11or(65)29748	INTRON	ACAT1,ATM,KDELC2 ACAT1,ATM,KDELC2	SLC35F2:A++:0.0007372,SLC35F2:A++:0.0358342,LOC643923:A+-:0.0403296 SLC35F2:A++:0.0007057,SLC35F2:A++:0.0351832,LOC643923:A:0.0408943
rowser	11_108311606_G_C 1 11_108311655 T C 4	1 108311606 11_108345515_G_A 1 108311655 11 108345515_C_A	rs4753842 rs4754322	CEBPD)-My[_4]+,NF-kappaB_disc3]-,SREBP_known4I+,ZEB1_known4I-	5 6		C11orf85 C11orf85	C11or85 26652 C11or85 26679	INTRON	ACAT1,ATM,KDELC2 ACAT1,ATM,KDELC2	SLC35F2-C+0.0007372,SLC35F2-C+0.0358342,L0C643923-C-0.0403296 SLC35F2-C+0.0007415,SLC35F2-C+0.0359714J,0C643973-C-0.0403296
rowser	11_108311965_G_A 1	1 108311965 11_108345515_G_A	rs11212636	AP-1_disc7[-,GCNF]-,Pax-6_2[- F] F1_disc7[-,Bax-6_anews33,Sin3da.20_disc41.	7		C11orf85	C11or85 26293	INTRON	ACAT1,ATM,KDELC2 ACAT1 ATM KDELC2	SLC35F2-A++0.0007372,5LC35F2-A++0.0358342,L0C643923-A-+0.0403296 SLC35F2-A++0.006488 SLC25F2-A++0.0358342,L0C643923-A-+0.0403296
rowser	11_108312080_T_C 1	1 106312080 11_108345515_G_A	rs11212638	ERalpha-a_known3(+.RXRA_known2(-,VDR_4)-	6		C11orf65	C11or/65 26178	INTRON	ACAT1,ATM,KDELC2	SLC35F2-C+0.0007372_SLC35F2-C+0.0358342_L0C643923_C-0.0403296
rowser	1_108314128_C_G 1	1 108314128 11_108345515_G_A	rai r6201292 ra6589018	Brachyury_1 +.Foxa_known3 -	7		C11orf85	C110/85/24659 C110/85/24130	INTRON	ACAT1,ATM,KDELC2	SLC25F2.G++0.0007493,5LC35F2C++0.0359856,L0C643923:C-+0.0401561 SLC25F2.G++0.0007335,SLC35F2.G++0.0358354,L0C643923.G-+0.0404882
rowser	11_108314362_A_C 1 11_108314363_C_A 1	1 108314362 11_108345515_G_A 1 108314363 11_108345515_G_A	rs4255510 rs4460776	E2P_disc1)-Esr2 -Pbx1_4 +,Pbx3_known1 + E2F_disc1)-Esr2 -Jif_known5 +	7		C11orf85 C11orf85	C11or65 23896 C11or65 23895	INTRON		stc35r2:C+0.0006334,L0C643923:C-0.034378,StC35F2:C+0.0396955 StC35F2:A+0.0006334,L0C643923:A-0.034378,StC35F2:A+0.0396955
rowser	11_108314694_T_A 1 11_108314886 A G 4	1 108314694 11_108345515_G_A 1 108314886 11 108345515_C A	rs7111091 rs139685780	HNF4_diac2 -,Hoxa5_1 +,Pax-1 -	7		C11orf85 C11orf85	C11or85j23564 C11or85j23322	INTRON	ACAT1,ATM,KDELC2	SLC35F2-A++0.0007372,SLC35F2-A++0.0358342,L00643923-A0.0403296 SLC35F2-G++0.0007372,SLC35F2-G++0.0358342,L00643923-G0.0403296
rowser	11_108315463_C_G 1	1 108315463 11_108345515_G_A	m2118308	Pax-5_known4j+	7		C11orf85	C11or/65/22795	INTRON	ACAT1,ATM,KDELC2	SLC35F2:G:+:0.0007372,SLC35F2:G:+:0.0358342,L0C643923:G:-0.0403296
rowser	uuruut0_1_t_t 1		rs149934734	CTCFL_disc1],E2A_S[-;HMG-IY_2]+;Hard1_1]+;TAL1_known2];TCF12_disc1]-	6		C11or(85	C11or/65/22652	INTRON		ALKBH8:T0.0146579
rowser 1	11_108315606_C_T 1	1 108315606 11_108345515_G_A			7		u11orf85	G110/85 21085	INTRON		THE REPORT OF A DESCRIPTION OF A DESCRIP
rowser	11_108315606_C_T 1 11_108317173_C_G 1 11_10833974_AAGAC_A 1	1 108315606 11_108345515_G_A 1 108317173 11_108345515_G_A 1 108333974 11_108345515_G_A	rs199528050 rs78462478	CEBPB_known6 +,Nanog_disc2 -,SP1_disc2 +			C11orf85	C11orf65 4284	INTRON	ACAT1,ATM,KDELC2	SLC35F2:A:+:0.0007373,SLC: C11of65:MCF7:CNA-PET
rowser rowser rowser	11_108315606_C_T 1 11_108317173_C_G 1 11_108333974_AAGAC_A 1 11_108338907_C_A 1 11_108341554_C_A 1	1 108315006 11_108345515_G_A 1 108317173 11_108345515_G_A 1 10833974 11_108345515_G_A 1 108349507 11_108345515_G_A 1 108341554 11_108345515_G_A	rs199528050 rs78462478 rs7943063 rs10749917	CEBPB_known8j+Nanog_disc2j-SP1_disc2j+ CCNT2_disc1j-,GATA_known14j-TfBroblast_of_mammany_gland;HSK4me3,mammany_spithelial_cell;HSK	5 7		C11orf85 C11orf85	C11or/65/4284 C11or/65/1351 C11or/65/3296	INTRON INTRON INTERGENIC	ACAT1,ATM,KDELC2 ACAT1,ATM,KDELC2 ACAT1,ATM,KDELC2	SLC35F2.4x+0.0007373,SLC1C116/I65/MCF7-CNA-PET SLC35F2.4x+0.0007373,SLC1C116/I65/MCF7-CNA-PET SLC35F2.4x+0.0007372,SLC1C116/I65/MCF2-CNA-PET SLC35F2.4x+0.000741,SLC3:AP005718.1:MCF7-CNA-PET
rowser rowser rowser	111_108315606_C_T 11 11_1083157073_C_G 11 11_108338007_C_A 11 11_108338007_C_A 11 11_108341554_C_A 11 11_108341864_C_T 11 11_1083	1 108315606 11_105345515_G_A 1 108337173 11_108345515_G_A 1 108336907 11_108345515_G_A 1 108345554 11_108345515_G_A 1 108341884 11_108345515_G_A	ns199528050 ns78462478 ns7943063 ns10742917 ns7934719 ns7934719	CEBPB_Invertile+Nanog_disc2[+SP1_disc2[+ CCNT2_disc1]-GATA_invertil4;Tifterbiset_cf_mammary_gland H3K4ms3_mammary_spithelial_cell;H3K Linke[Luba]:Luba]:Luba]:Laba]:ABTK1]- Zma1	5 7 6		C11orf85 C11orf85	C11or85/4284 C11or85/1351 C11or85/3296 C11or85/3806	INTRON INTRON INTERGENIC INTERGENIC	ACAT1,ATM/KDELC2 ACAT1,ATM/KDELC2 ACAT1,ATM/KDELC2 ACAT1,ATM/KDELC2	SECSIFICATION CONTROL
rowser rowser rowser rowser rowser	11_106315606_C_T 1 11_106315606_C_T 1 11_10633974_AAGAC_A 1 11_106338207_C_A 1 11_106345654_C_A 1 11_106341684_C_T 1 11_106344061_C_A 1 11_106346515_C_A 1 11_106346515_C_A 1 11_106346515_C_A 1 11_106346551_C_A 1 11_106345551_C_A 1 11_1063455551_C_A 1 11_1063455551_C_A 1 11_1063455551_C_A 1 11_1063455551_C_A 1 11_1063455551_C_A 1 11_1063455555_C_A 1 11_105555555555555555555555555555555555	1 10831506 11.108345515_0_A 1 10833907 11.108345515_0_A 1 10833907 11.108345515_0_A 1 10833907 11.108345515_0_A 1 10834564 11.108345515_0_A 1 108344081 11.108345515_0_A 1 108345615 11.108345515_0_A	m199528050 m78462478 m7943063 m10749917 m7934719 m7943203 m201942465	CEBPB, Jonovsky, Hung, Sacki, 20 M. Sacki) CONT2, Sacki, DATA, Smorth, Titerates of mannary, sland;HSK4mc3,mannary, spithelial, cell;HSK Links, Links, My, 1, Amori, a, 280K1; Zacki).	5 7 6 5 5		C11orR5 C11orR5 KDELC2 KDELC2	C11or85)4284 C11or85)3296 C11or85)3296 C11or85)3606 C11or85)5823 C11or85)7257	INTRON INTRON INTERGENIC INTERGENIC SUTR,EXON SUTR,EXON	ACAT1, ATM KOELC2 ACAT1, ATM KOELC2 ACAT1, ATM KOELC2 ACAT1, ATM, KOELC2 ACAT1, ATM, KOELC2	LCSSF2A-4.0007373,SLCCTref65M2F7.04A-PET SCSSF2A-4.0007373,SLCCTref65M2F7.04A-PET SCSSF2A-4.0007373,SLCCTref65MECIMPET, MCRELC2+CCT64- SCSSF2A-4.0007373,SLCSF2A06771,SLCF7.04A-PET SCSSF2A-4.000745,SLCSF2A-6.005579,0LC64922A-4.00494921 SCSF2A-64.0007445,SLCSF2A-4.0055593,SLCSF2A64-4.0055593 SCSF2A-64.0007445,SLCSF2A-4.0055593,SLCSF2A64-4.0055593

rowser	11_108346103_A_G 11_108340526_A_C	11 1	08340526 11_108345515_G_A 08340526 11_108345515_G_A	112419828 112419828	Addisond Physics (1970)	147D)dhase		KDELC2 KDELC2	C110/85/7845 C110/85/11268	INTRON	ACAT1,ATM,KDELC2 ACAT1,ATM,KDELC2 ACAT1,ATM,KDELC2		SLC35F2:C5+0.00124/9,L02 C1088580.077.C104/PET SLC35F2:C5+0.001629,SLC3 AP005718.130CF7.C104/PET SLC35F2:C5+0.001629,SLC3 AP005718.130CF7.C104/PET
rowser	11_108354102_C_T 11_108354102_C_T	11 1	08350451 11_108345515_G_A 08354102 11_108345515_G_A	s12223381 s12223381	Bobbi+, Bractrysty_i), connect, noxe+(+,Pax+_2)+,Pax+_2+(+,S1A1_k100m1)+ Nanog_disc2)+,PiMCF_10A;FOS,Mmammary_epithelial_cell;H3K4me1 PEVe_disc21+	BRST.HMEC;dna		KDELC2 KDELC2	KDELC2 15057	INTRON	ACAT1,ATM,KDELC2 ACAT1,ATM,KDELC2		SLC35F2T1+0.001521+3LC3 AP00516.138CF7C08+PE1_KDELC288CF1 SLC35F2T1+0.0012018,SLC35F2T1+0.0266562 SLC35F2C1+0.0012018,SLC35F2T1+0.0266562
rowser	11_108356680_T_C	11 1	08356680 11_108345515_G_A	10789665	AP-2_diac2 .TCF12_diac6 .TLX1:NFIC .2h)+			KDELC2	KDELC2 12479	INTRON	ACAT1,ATM,KDELC2		SLC35F2:C:+0.0010514,SLC:KDELC2:MCF7:ChiA-PET
rowser	11_108367137_A_G 11_108361278_A_G	11 1	06361278 11_108345515_G_A	s10890848	MCF-7/EDX1,MCF-7/H3K27ac MCF-7/ER/MCF-1MCF-7/H3K27ac, MCF-7/Enhancar	107 3 4	-	KDELC2	KDELC2/7881	INTRON	ACAT1,ATM,KDELC2	510357254-30.0313088	SLC35F2-G:+:0.0010151,SLC35F2:G:+:0.0492218
rowser	11_108361578_G_A 11_108365182_C_T	11 1	06361578 11_108345515_G_A 06365182 11_108345515_G_A	111212676 19893279	ELP1_disc1 +,EL MCF-7;ER MCF-1MCF-7;H3K27ac,MCF-7;H3K4ma1 Gmab1 +,IRC000MDA-MB-231;FOXM1	MCF-7)dnase 3	a 5	KDELC2 KDELC2	KDELC2 7581 KDELC2 3977	INTRON	ACAT1,ATM,KDELC2 ACAT1,ATM,KDELC2		SLC35F2:A:+:0.0010152 SLC35F2:T:+:0.0010152
vowser	11_108366449_A_C 11_108406943_A_G	11 1	08386449 11_108345515_G_A 08406943 11_108357137_A_G	rs751343 rs117706999	Pou3f2_1 -ZID +,Zbtb3 + MCF-7;H3K4me1 CEBPB_known4 +,Ik-1_2 -,SDK5_diac2 -,STAT_known9 -,Znf143_diac1 -		5	KDELC2 EXPH5	KDELC2 2710 KDELC2 37784	INTRON	ACAT1,ATM,KDELC2	SLC35F2:A:-:0.026571	SLC35F2:C:+:0.0010044,SLC:KDELC2:MCF7:ChiA-PET ALX8H8:A:-:0.0130292
rowser	16_4012480_T_C 16_4015046_G_A	16 16	4012480 16_4106788_C_A 4015046 16_4106788_C_A	1962038942 19879619	AFP1 +,FAC1 +,Foxa_known4 +,FoMCF-7;H3K4me1 HES1 -,Hic1_1 - MCF-7;ER.MCF-7;ERalpha,MCF-7;ERbeta,MCF-7;SPDEF		5	ADCY9	CREBBP 82359 CREBBP 84925	INTERGENIC 3UTR,EXON	RP11-462G12.1	VASN:C:-:0.0036798,TFAP4:C:- VASN:A:-:0.0033684,TFAP4:A:-	IL32:C-:0.0104076,ADCY9:C CREBBP:MCF7:ChiA-PET IL32:A::0.0093752,ADCY9:A TFAP4:MCF7:ChiA-PET
rowser	16_4106788_C_A 16_4108158_TA_T	16 16	4106788 16_4106788_C_A 4108158 16_4106788_C_A	11076805 1156278937	MCF-7;PBX1 MCF-7;H3K4me1MCF-7;Enhancer MCF-7;Promoter		5	ADCY9 ADCY9	ADCY9(59398 ADCY9(58028	INTRON		MMP25:T:-:0.0020061,0R2C1:	2NF75A:A:+:0.009638,ADCY9:A:-:0.0213383,2NF174:A:+:0.0366211,VASN:# HM0X2:T:+:0.030937,DNASI ADCY9:MCF7:CNA-PET
vowser	16_4109828_G_C	16 16	4109828 16_4106788_C_A 4111525 16_4106788_C_A	1572762799 159347038	ERalpha-a_disc2[+,ERalpha-a_known1]+,NF-kappaB_disc4]+ ATE4L CERPOLA HEV1_disc11a HNE1_7L Prov02_11a		r 5	ADCY9	ADCY9(56358 ADCY9(54861	INTRON	ADCY9	GLYR1:C:-0.0060267 CULAP1:A:-0.042371	2NF75A:C++0.0095536;VASN:C-+0.0131072;DNAIA3:C++0.0221999;UBN1:C
rowser	16_4126201_C_T	16	4126201 16_4106788_C_A	12283498	11000 11000 11000 11000 11000 11000 11000 11000 11000 11000 11000 11000 11000 11000 11000 11000 11000 11000 11000		3	ADCY9	ADCY9/39/85	INTRON	ADCY9	ZNF174:T:-:0.0321264	ADCY9:T:-0.0126716,ZNF75A:T:+0.0140913,VASN:T:-0.0350573,ZNF174:T
rowser	16_4133033_G_A	16	4133033 16_4106788_C_A	197192040	Mri1_disc2 -Myc_disc2 -Myc_known3 -Myc_known4 -Myc_known6 -Myc_known7 -My	yc_known8(-,Myc_	5	ADCY9	ADCY9 33153	INTRON			2NF263:A:+ 0.0195678, CREE ADCY9:MCF7: PreSTIGE
rowser	16_4134162_G_A	16	4134162 16_4106788_C_A	134826380	HEN(_1,_Nub2(_0000),S(A(_0000))) SIX5_disc1 +,TEF-1_2 -Zbtb3 -Znl143_disc2 +		3	ADCY9	ADCY9[32024	INTRON			2NF263:A:+0.019546,CREEADC193MCF7.PN8511GE 2NF263:A:+0.0194706,CREERP11-95P2.3:MCF7.CNA-PET
rowser	16_4134246_G_A 16_4134522_A_T	16 16	4134246 16_4106788_C_A 4134522 16_4106788_C_A	1934040332 198059483	LUN-1 .,Pis2 -		5	ADCY9 ADCY9	ADCY9 31940 ADCY9 31664	INTRON			2NF263:A:+ 0.0237075,2NF5 RP11-95P2.3:MCF7:ChiA-PET 2NF263:T:+ 0.023674,2NF50 RP11-95P2.3:MCF7:ChiA-PET
rowser	16_4171880_A_G 16_4172061_G_C	16 16	4171880 16_4106788_C_A 4172061 16_4106788_C_A	196500680 196500681	AP-1_disc7 +,Hic MCF-7;SPDEF ATF3_disc2 +,HNMCF-7;SPDEF		r 3		ADCY9)5694 ADCY9)5875	INTERGENIC INTERGENIC		C16orf71:G:+:0.0127987 C16orf71:C:+:0.0139172	ADCY9.5:+:0.0001307,CREBIADCY9:MCF7:CNA-PET ADCY9.C:+:0.0001301,CREBIADCY9:MCF7:CNA-PET
rowser	16_4172887_C_A 16_4172966_G_A	16 16	4172887 16_4106788_C_A 4172968 16 4106788 C A	1966881004 1966803611	Ptx3_disc3 + Pax-5_disc2 -		5		ADCY9)6701 ADCY9)6780	INTERGENIC		C16orf71:A:+:0.0140314 C16orf71:A:+:0.0140284	ADCY9:A:+:0.0001307,CREBI ADCY9:MCF7:CNA-PET ADCY9:A:+:0.0001307,CREBI ADCY9:MCF7:CNA-PET
nowser	18_25367257_TAAGAG_Ci	18	25367257 18_25401204_AT_A 25368078 18_25401204_AT_A	1534026214	ERabha-a knowntia PROM1 knowntia Pro212 known10.		,		CDH2 390188 CDH2 389369	INTERGENIC	CDH2		CDH2:CAAGAG:+:0.0119402 CDH2:C:+0.0194579
rowser	18_25368846_G_A	18	25368846 18_25401204_AT_A	11872300	mammary_epithelial_cell;H3K4me1	BOST HMEC day			CDH2/388599	INTERGENIC	CDH2		CDH2:A:-0.0140461 CDH2:A:-0.0140461
rowser	18_25371514_A_G	18	25371514 18_25401204_AT_A	1962100742	CEBPA_1 +,Evi-1_2 -,Evi-1_4 -,Pou2t2_known2 +	CHOT THE COULD			CDH2 385931	INTERGENIC			CDH2:6:+0.0177234
rowser	18_25372388_G_A 18_25374914_T_C	18	25372386 18_25401204_AT_A 25374914 18_25401204_AT_A	ni 10853677 ni 4273126	DMM12(+,Foxa_sroum2(+,Foxa_sroum4(+,Foxq1_2(-,Foxp2_1)+,Foxs1)-,Foxp1(+,1CF4_st Bbx(-,Foxq1)-,Hoxb8(-,RXRA_sroum2)-	ingen1 +	5		CDH2/385050 CDH2/382531	INTERGENIC	CDH2		
rowser	18_25376473_C_1 18_25377105_A_T	18	25376473 18_25401204_AT_A 25377105 18_25401204_AT_A	194800820 199951088	STAT_known15 - Dbx1 +,Hoxa10 -,Hoxd10 -,Nox_2 +,Pou2f2_known2 -,Pou2f2_known8 +,Sox_5 +,TATA_	known1 -,21p106 +	5		CDH2/380972 CDH2/380340	INTERGENIC	CDH2 CDH2		
vowser vowser	18_25377196_G_A 18_25377513_T_C	18 18	25377196 18_25401204_AT_A 25377513 18_25401204_AT_A	19961475 198096576	Smad3_2 + AIRE_1 -Barhi1 -Bax -Eax1 -Hmx_2 -Max2 -Nkx2_10 -Nobox_1 -OTX -Obox6 -Otx2	2 -,Vax2 -	5		CDH2 380249 CDH2 379932	INTERGENIC	CDH2		
rowser	18_25377563_G_A 18_25379003_T_G	18 18	25377563 18_25401204_AT_A 25379003 18_25401204_AT_A	198091387 198088358	Hand1_1 +,Smad3_2 + GR_known10 +,Jrf_known5 -,Jrf_known9 -,PRDM1_disc1 -,RORalpha1_1 -,RORalpha1_2	2 -,THAP1_disc1 -	5		CDH2 379882 CDH2 378442	INTERGENIC	CDH2		
vowser	18_25379275_A_G 18_25379390_A_G	18	25379275 18_25401204_AT_A 25379390 18_25401204_AT_A	s11875525 s9957708	ZEB1_known2j+ CTCF_dise10ia_HMG_IV_2ia_HNF1_1ia_HNF1_6ia_Lbv3_2i_OTXi_Pav_4_2ia_TCF12_kn	mentia	r		CDH2 378170 CDH2 378055	INTERGENIC	CDH2 CDH2		CDH2:G:+:0.006796
rowser	18_25380364_T_C	18	25380364 18_25401204_AT_A	16508502	If_known6 +				CDH2 377081	INTERGENIC	CDH2		
rowser	18_25383770_T_C	18	25383465 18_25401204_AT_A 25383770 18_25401204_AT_A	14270255	Foxj1_1 .Foxq1 +.Hitl Met2_known1 +.Nkx3_1 Pox2t2_known2 +.Pox2t2_known6 +		3		CDH2 373675	INTERGENIC			CDH2:C:+:0.006796
rowser	18_25384041_TA_T	18	25383952 18_25401204_AT_A 25384041 18_25401204_AT_A	181893947 1980238522	CHX10[+,E2F_knMCF_10A;FOS Cdx2_1[+,Dbx1]-,MCF_10A;FOS	BRST.vHMEC;dnase,HME	a C;dnase		CDH2 373493 CDH2 373404	INTERGENIC	CDH2		CDH2:1:+:0.0442163 CDH2:T:+:0.0442163
rowser	18_25385055_G_A 18_25385221_C_A	18 18	25385055 18_25401204_AT_A 25385221 18_25401204_AT_A	rs4275930 rs4506992	Aad2 -,HEN1_1 +ZR751;ER		5		CDH2 372390 CDH2 372224	INTERGENIC			CDH2:A:+:0.0442163 CDH2:A:+:0.0442163
vowser vowser	18_25385760_C_T 18_25386439_A_G	18 18	25385760 18_25401204_AT_A 25386439 18_25401204_AT_A	194508491 1960877454	Dtx1 +,Fox -,FoxMCF_10A;FOS,MCF_10A;MYC,MCF_10A;STAT3 CACD_2 +,TCF12_disc1 -,ZEB1_disc1 -,ZEB1_known3 -		5		CDH2 371685 CDH2 371006	INTERGENIC			CDH2:T:+:0.0442163 CDH2:G:+:0.006796
rowser	18_25386727_G_GAAAAA 18_25387937_A_G	18 18	25386727 18_25401204_AT_A 25387937 18_25401204_AT_A	1910628611 1956300506	DMRT3I+.DMRT4I+.Nanog diso4I+.Pou5/1 disc1I+.Z/p187I+.p300 disc2I+		,		CDH2 370718 CDH2 369508	INTERGENIC			CDH2:GAAAAA:+:0.0022748 CDH2:G:+:0.0039924
rowser	18_25388628_C_T	18	25388628 18_25401204_AT_A	s11663001	BCL_dsc3 +.Mt1_1 +.NRSF_disc2 +.NRSF_dsc4 +.NRSF_known3 +.Sin3Ak-20_disc3 - Bay 6_dsc4 _TATA_dsc71_s200_dsc4 _	•	r		CDH2 368817	INTERGENIC	CDH2		CDH2:T:-0.0442163 CDH2:4:-0.0441163
rowser	18_25389124_T_A	18	25388704 18_25401204_AT_A 25380124 18_25401204_AT_A	14800822	EBF_disc1 - mammary_spithelial_cell;CTCF				CDH2[368321	INTERGENIC	CDH2		CDH2A+0.0442163 CDH2A+0.0442163
rowser	18_25390102_T_G	18	25380314 18_25401204_AT_A 25390102 18_25401204_AT_A	rs16944207	Aine_1)+ Hoxa4 -,RORalpha1_2 -				CDH2 367343	INTERGENIC	CDH2		CDH2:4:+0.0040705
rowser	18_25390181_A_G 18_25390278_G_A	18 18	25390181 18_25401204_AT_A 25390278 18_25401204_AT_A	is16944210 is16944213	Foxa_disc2 -,Foxa_known2 - AP-1_disc8 +,CTIMCF_10A;MYC		8		CDH2 367264 CDH2 367167	INTERGENIC	CDH2		CDH2:6:+:0.0040705 CDH2:A:+:0.0040705
vowser vowser	18_25390333_G_A 18_25390652_A_G	18 18	25390333 18_25401204_AT_A 25390652 18_25401204_AT_A	is10438924 is11874471	EBF_known3 -,NMCF_10A;MYC MCF_10A;FOS,MCF_10A;MYC,MCF_10A;STAT3		r 1		CDH2 367112 CDH2 366793	INTERGENIC	CDH2		CDH2:A:+:0.0040705 CDH2:G:+:0.0040705
rowser	18_25390938_C_A 18_25391263_C_G	18 18	25390938 18_25401204_AT_A 25391263 18 25401204 AT A	ni11873567 ni62102182	Poutf1_1 - GATA known11 -ObaxBI-Pitx2 -Pitx3 -		r 3		CDH2 366507 CDH2 366182	INTERGENIC	CDH2		CDH2:G:+:0.0040705
rowser	18_25393153_C_A	18	25393153 18_25401204_AT_A	162102184	Nr212 -		3		CDH2 364292	INTERGENIC			CDH2:A:+:0.0040442 CDH2:A: -: 0.0096528
rowser	18_25400833_CT_C	18	25400833 18_25401204_AT_A	1379186737	Dtx1 -Evi-1_4 -Foxk1 -Foxp1 -HDAC2_disc6 -Mef2_known4 +,Nanog_disc2 +,Ncx_2	-,PLZF +,Sax_13 +,Sax_2 -	Zfp105 -,p300_disc5 -		CDH2 356612	INTERGENIC			CDH2:C:+0.0096997
rowser	18_25401204_A1_A 18_25401397_G_T	18	25401204 18_25401204_AT_A 25401397 18_25401204_AT_A	1936194942 1936194692	Cdt2_1 -Cdtc2_2(+,Homa2)+,Hoxa10 -,Hoxa0(+,Hox88)+,Hox88(+,Hox88)+,IA1A_known5)- AIRE_1(+,Ma[_disc1)+,Ma[_known1]+,RORalpha1_3(+,THAP1_disc1)-,Zlp410]-		8		CDH2/356241 CDH2/356048	INTERGENIC			CDH2:A:-0.0039993
rowser	18_25402557_G_GT 18_25406525_T_TTA	18 18	25402557 18_25401204_AT_A 25406525 18_25401204_AT_A	19201689215 1935875783	BAF155_disc2 -,EBF_known3 +,Ets_disc1 -,SU5_disc1 +,SIX5_disc4 +,Znf143_disc2 -				CDH2 354888 CDH2 350920	INTERGENIC			CDH2:GT:+:0.0011533 CDH2:TTA:-:0.0285914
vowser vowser	18_25406855_C_T 18_25406866_C_T	18 18	25406855 18_25401204_AT_A 25406866 18_25401204_AT_A	19959491 1967108301	E2A_1 +,E2A_3 -,EBF_disc2 -,LUN-1 +,NF-kappaB_disc4 +		5		CDH2 350590 CDH2 350579	INTERGENIC	CDH2		CDH2:T:-:0.001208 CDH2:T:+:0.0012083
nowser	18_25407513_C_G	18	25407513 18_25401204_AT_A 25407848 18 25401204_AT_A	198092192	Arid5a -,Dbx1 -,Foxa_known1 -,Foxd3 -,Foxi1 -,Foxj1_1 -,Foxj1_2 -,Foxj2_1 -,Mel2_know	m2 +,Mef2_known!	5		CDH2 349932 CDH2 349599	INTERGENIC	CDH2		CDH2:G:=0.001242 CDH2:G:=0.0091194 CDH2:T:=0.0091194
rowser	18_25407846_A_T	18	25407846 18_25401204_AT_A	190093178			·		CDH2/349599	INTERGENIC			CDH2:G:+0.0091194,CDH2:T:-0.0091194 CDH2:T:-0.0092502
rowser	18_25408642_T_C	18	25408642 18_25401204_AT_A	11662671	CDP_7]+;Hdx]+;Hoxa3_1]+;Pou212_known9]-;Sox_5]-		5		CDH2 348803	INTERGENIC	CDH2		CDH2:C:+:0.0012649
rowser	18_25410603_A_G 18_25411773_A_C	18	25410603 18_25401204_A1_A 25411773 18_25401204_AT_A	s2002401	Barhi1 -,CDP_1 +,CDP_4 +,E2F_diac4 +,En-1_3 -,Foxa_known2 -,Foxj2_1 -,Hix1 -,Hoxa5	5_1 +,Hoxd8 +,Irf_1	3		CDH2/346842 CDH2/345672	INTERGENIC	CDH2 CDH2		CDH2:6:+0.0012979 CDH2:C:+0.0005314
rowser	18_25442301_T_C 18_25442412_T_G	18 18	25442301 18_25401204_AT_A 25442412 18_25401204_AT_A	197231957 197232124	MCF-7;FOXM1,MCF-7;GATA3 CDP_6 ,-Zlp106 -MCF-7;FOXM1,MCF-7;GATA3		5		CDH2 315144 CDH2 315033	INTERGENIC	CDH2		CDH2:C:=0.0001084 CDH2:G:=0.0001084
vowser vowser	18_25444712_A_G 18_25446224_A_ACT	18 18	25444712 18_25401204_AT_A 25446224 18_25401204_AT_A	rs3924216 rs79858006	BDP1_disc2 +,Maf_disc2 -,Nr212 +		,		CDH2 312733	INTERGENIC			CDH2:6:-:0.000107 CDH2:ACT:-:0.0001056
rowser	18_25447072_T_C 18_25459346_ATTTTT_A	18 18	25447072 18_25401204_AT_A 25459346 18 25401204 AT A	112965632 11201680130			r		CDH2 310373 CDH2 298099	INTERGENIC			CDH2:C:-0.0001048 CDH2:A:+:0.0001524
vowser	18_25460298_C_T 18_25460372_C_T	18	25460208 18_25401204_AT_A 25460372 18_25401204_AT_A	1935149382	Foxa_disc3(+,Pou292_known2)+ Mrs11:Howe0_1L_Nex2_dia_Nex2_dia_Nex3_dia		r 3		CDH2 297147 CDH2 297073	INTERGENIC			CDH2:T:+0.0002615 CDH2:T:+0.0002618
rowser	18_25462046_T_TAAC	18	25462046 18_25401204_AT_A	s140077604		050 4 41			CDH2;295399	INTERGENIC			CDH2:TAAC:+:0.0037265
rowser	18_25462222_T_C	18	25462138 18_25401204_AT_A 25462222 18_25401204_AT_A	s12970390	GATA_date4_,GATA_known10,,GATA_known2,,GATA_known3,-AP-kappab_date3, R Hsf_dat1;-	RED-1_1 +			CDH2 295223	INTERGENIC			CDH2:C:+0.0004118 CDH2:C:+0.0004118
rowser	18_25462380_1_C 18_25462858_C_T	18	25462380 18_25401204_AT_A 25462858 18_25401204_AT_A	is12970571 is12968914	AP-1_dsid8j-,ELF1_known1j+,ElBj-,M_known7j-,NF-ATj+,PU.1_dsid1j+,Pix-5_dsid3j+,R Barx1j+,Bsx(-,Dtx2j-,Fxxj2_2)-,GR_known4j-,Pou2t2_known5j+,Rhox11j-,Zlp187j-	CKHA_disc4(+,SPIt	5		CDH2/296065 CDH2/294587	INTERGENIC			CDH2:C:+0.0004119 CDH2:T:+0.0004122
rowser	18_25463154_C_G 18_25464267_A_G	18 18	25463154 18_25401204_AT_A 25464267 18_25401204_AT_A	19965765 19947975	CTCF_disc1 .RaMCF-7;SPDEF COMP1 +,EWSR1-FLI1 -,GATA_disc3 -,GR_known1 +,HDAC2_disc6 -,STAT_disc6 +,p3	100_disc10[-p300_	r 3		CDH2 294291 CDH2 293178	INTERGENIC			CDH2:G:+0.0004153 CDH2:G:+0.0004089
rowser	18_25465844_A_G 18_25466016 T_A	18 18	25465844 18_25401204_AT_A 25466016 18 25401204 AT A	n 17467487 n 17467494	Foxd1_1 +,HDAC2_disc2 + Mel2_known5 +		r -		CDH2 291601 CDH2 291429	INTERGENIC	CDH2 CDH2		CDH2:G:+:0.0004008 CDH2:A:+:0.0003954
vowser	18_25466367_G_T 19_11420160_G_A	18	25466367 18_25401204_AT_A 11420160 19_11423703_C_G	1317445112	Mar2_known1 +,PEBP -,p300_disc6 + CHD2_disc2 _E2E_disc5 _NRSE_disc10 _EPu;212_disc2 _E	HMECvinase	r 5	TSPAN16	CDH2 291078 TSPAN16 13337	INTERGENIC	AC024575 6-2 C19vd39 CTC-510E1	TMFM205-4-+-0.0288047.7NFr	CDH2:T:+0.0003722 (2NE135:4:+0.0005093 2NE433:4:-0.0182658 2NE44:4:-0.0226724
rowser	19_11421239_T_C	19	11421239 19_11423703_C_G	19322146	BDP1_disc1 +			TSPAN16	TSPAN16 14416	INTRON	AC024575.6-2,C19orf39,CTC-510F1	TMEM205-C+0.0280174,2NF4	2NF136.C:+0.0003985,2NF4 CTC-510F12.8:MCF7:CNA-PET, CTC-510F12
rowser	19_11423703_C_G	19	11423703 19_11423703_C_G	1322144	Evi-1.4(+,HNF1_6),HNF1_7),Hoxa7_2(+,Hoxa8),Hoxb3(+,Nxx8-1_1),Nxx8-1_3),OTX(-	+,Pax-6_3 -,Pdx1_	5	TSPAN16	TSPAN16 16880	INTRON	AC024575.6-2,C19orf39,CTC-510F1	TMEM205-G:+:0.0298398,ZNF-	2NF136.G + 0.0003752,2NF4 CTC-510F12.8:MCF7:CNA-PET
rowser	19_11426182_A_G	19	11426182 19_11423703_C_G	19322142	RXRA_known71,STAT_diad6j-			TSPAN16	TSPAN16 19359	INTRON	CTC-510F12.4,TSPAN16	TMEM205:G:+:0.0288978,2NF	2NF136:6:+0.0003938,2NF4 CTC-510F12.6:MCF7:CNA-PET
rowser	19_11426639_C_A 19_30265235_G_A	19 19	11426639 19_11423703_C_G 30265235 19_30277729_C_T	15322141 1512461902	BCL_disc6 +,ER#MCF_10A;POLR2A Mrg_1 -,Pdx1_2 +,Tgi1_2 -		5	TSPAN16	TSPAN16 19816 CCNE1 37665	SUTR, SUTR, EXC INTERGENIC	AC024575.6-2,C19orf39,CTC-510F1 C19orf12,CCNE1	2TMEM205:A:+:0.0269175,2NF4	2NP136:A:+0.0005123,2NF44:A:-0.0155147,2NF433:A:-0.0194137,ELDF1:
vowser vowser	19_30266706_G_A 19_30272202_G_A	19 19	30266706 19_30277729_C_T 30272202 19_30277729_C_T	1962107106 1912462975	ATF4(+,CTCF_dtMCF-7;CTCF BDP1_disc3)+	MCF-7;dnase 2	a 5		CCNE1 36194 CCNE1 30698	INTERGENIC	CCNE1 C19orf12,CCNE1		
rowser	19_30277729_C_T 19_30284882_G_GTA	19 19	30277729 19_30277729_C_T 30284882 19_30277729 C_T	ni113701136 ni149892244	ELF1_disc3 -,Egr-1_disc4 -,Myc_disc10 -,NRSF_disc9 -,20x - Pou111_2 +,TATA_known1 +		8		CCNE1 25171 CCNE1 18018	INTERGENIC	CCNE1	2NF536:T:+:0.0292298 2NF536:STA:+:0.01618	ZNF536:T:-0.0231483 ZNF536:GTA:-0.0486063
rowser	19_30285548_C_T	19	30285548 19_30277729_C_T	112000021	Nanog_disc2 +		r		CCNE1 17352	INTERGENIC	CCNE1	2NF536:T:+:0.0202404	ZNF536.T 0.0435014
rowser	19_30286245_A_G	19	30286245 19_30277729_C_T	12151208	BDP1_diac2 +,GCNF -,N/2f2 -		8		CCNE1 16655	INTERGENIC	CCNE1	ZNF536:G:+:0.0206124	ZNF536:G0.0438311
rowser	19_30286822_T_C	19	30286450 19_30277729_C_T 30286822 19_30277729_C_T	1417513613	HDAL2_dac6 +,II_dac5 -20105 + Foxa_dic5 -		5		CCNE1 16078	INTERGENIC	C19orf12,CCNE1	2NF536:C+0.0205261	ZNF536:C0.0437663
rowser	19_30267988_A_AAC 19_30288177_G_A	19	30288177 19_30277729_C_T 30288177 19_30277729_C_T	na 112920392 na8111686	rwu 11+,runa_xnownu(+,rund3(+,runx1)+,runu_2)+,runp1(+,HUAG2_disc6(-,Irf_disc3)-,N BCL_disc10(-,BD MCF-7;POLR2A	verrog_disc2[+,Sox	5		CCNE1 14912 CCNE1 14723	INTERGENIC	CCNE1	2NF536:A:+:0.0201659	2NF35004C-0.0442486 CCNE1:MCF7ChIA-PET 2NF536:A0.0445983 CCNE1:MCF7.ChIA-PET
vowser vowser	19_30288488_C_T 19_30288545_T_C	19 19	30288488 19_30277729_C_T 30288545 19_30277729_C_T	192161516 1980560217	HNF4_known6 +,RXRA_diac2 -,SETDB1_diac1 -,Znf143_diac3 - E2F_diac3 +,Myc_diac10 +,TATA_diac1 -,YY1_known2 -,ZBTB33_diac2 +,Znf143_diac3 -	+	8		CCNE1 14412 CCNE1 14355	INTERGENIC	CCNE1 CCNE1	2NF536:T:+:0.0201096 2NF536:C:+:0.020071	2NF536:T:-0.0367992 CCNE1:MCF7:ChIA-PET 2NF536:C:-0.0447923 CCNE1:MCF7:ChIA-PET
rowser	19_30289630_G_A 19_30289779_C T	19 19	30289630 19_30277729_C_T 30289779 19_30277729 C T	1962107115 1962104473	RXRA_known7)+		5		CCNE1 13270 CCNE1 13121	INTERGENIC	CONE1 CONE1	2NF536:A:+:0.0200859 2NF536:T:+:0.0198184	2NF536:A-:0.0450312 CCNE1:MCF7:ChIA-PET 2NF536:T:-0.045269 CCNE1:MCF7:ChIA-PET
rowser	19_30290357_G_C 19_30290811_A_G	19 19	30290357 19_30277729_C_T 30290811 19_30277729_C_T	s111640872 s17513752	NRSF_diac9(-ZEB1_known6)- BRST.MYOEP;H3K4me1 ERalpha-a_knownMCF-7;ER,MCF-1MCF-7;H3K4me1	MCF-7;dnase	5		CCNE1 12543 CCNE1 12089	INTERGENIC	CCNE1 CCNE1	ZNF536:C:+:0.0175784 ZNF536:G:+:0.0174535	2NF536:C:-0.0470261 CCNE1:MCF7:ChIA-PET 2NF536:G:-0.0473768 CCNE1:MCF7:ChIA-PET
rowser	19_30290890_A_G	19	30290890 19_30277729_C_T 30291860 19_30277729_C_T	1979576418 19146397210	Foxa_disc3(+,GR MCF-7;ER MCF-1MCF-7;H3K27ac,MCF-7;H3K4ma1,MCF-7;H3K4ma2 CDP_71, Pro/02 Innum21, Sox 51,	MCF-7;dnase	5		CCNE1 12010	INTERGENIC	CONE1	2NF536:6:+:0.0174321 2NF536:4:+:0.0172322	2NF536:G:-0.0472474 2NF536:G:-0.04544
- certer Yowser	19_30292557_A_AAT	19	30292557 19_30277729_C_T	s140500237	Foxp11+Pox222 known21+				CCNE1/1031 CCNE1/10343	INTERGENIC	00151	2NF536:AAT:+0.0154937	ZNF556-AAT0.0443114
yowser yowser	19_30292701_G_A 19_30293267_C_T	19 19	30292701 19_30277729_C_T 30293267 19_30277729_C_T	istz104475 is8111487	BHLHE40_dsc2(+,CTCF_disc5)+,CTCF_disc9)+,LBP-1_2)+,Mif1_1)-Nanog_disc3)+,SRF Ets_disc6(-,Gfi1_2)-,NF-kappaB_known3)-	F_disc2 -,Sin3Ak-2	, ,		CCNE1 10199 CCNE1 9633	INTERGENIC INTERGENIC	CONE1	ZNF536:A:+:0.0357322 ZNF536:T:+:0.0170755	ZNF536:AU.0260607 ZNF536:T0.0432732
vowser vowser	19_30293462_G_A 19_30294716_G_A	19 19	30293462 19_30277729_C_T 30294716 19_30277729_C_T	157894940 1562104476	Evi-1_4 +,GATA_known8 -,HDAC2_disc6 +,RREB-1_2 +,STAT_disc6 - E2F_known3 -		, ,		CCNE1 9438 CCNE1 8184	INTERGENIC	CCNE1 CCNE1	ZNF536:A:+:0.0170503 ZNF536:A:+:0.0168866	2NF536:A0.0429795 2NF536:A0.0410456 CCNE1:MCF7:ChIA-PET
rowser	19_30294991_G_T 19_30295306_G_A	19 19	30294991 19_30277729_C_T 30295306 19_30277729_C_T	1962104477	AFP1 -Arid3a_2 +,Lhx3_1 +,OTX +,Sox_1 +,TCF4_known1 + Zbtt3i-		5		CCNE1/7909 CCNE1/7594	INTERGENIC	CCNE1 CCNE1	ZNF536:T:+:0.0194845 ZNF536:A:+:0.0167213	CCNE1:MCF7:ChiA-PET 2NF536:A:-0.0401817 CCNE1:MCF7:ChiA-PET
rowser	19_30296853_T_C	19	30296853 19_30277729_C_T 30297516 19_30277729_C_T	188102137	PLAG1 -,Smad4 + BRST.HMEC;Enhanoar,BRST.MYC DOOT MV/CD External	DEP;Enhancer	6 Bladder_cancer		CCNE1 6047	INTERGENIC	C19orf12,CCNE1	2NF536:C:+:0.0165371 2NF536:G:+:0.0165371	2NF536.C0.0382064 CCNE1:MCF7.Chi4-PET 2NF536.C0.0320045 CCNE1:MCF7.Chi4-PET
rowser	19_30297577_G_A	19	30297577 19_30277729_C_T	159868991	OTX +,Otx2 + BRST.MYOEP.Enhancer				CCNE1 5323	INTERGENIC	CCNE1	ZNF536:A:+:0.0164734	ZNF536:A-0.0373386 CCNE1:MCF7:ChIA-PET
vowser vowser	19_30297919_G_C 19_30298800_A_G	19 19	3029/919 19_30277729_C_T 30298800 19_30277729_C_T	19.7247779 1962104480	HNF4_dsc2 + BRST.MYOEP,Enhancer Gf1_1]-2BTB7A,MCF-7;SPDEF		5		CCNE1 4981 CCNE1 4100	INTERGENIC	CONE1	ZNF536:C:+:0.0164586 ZNF536:G:+:0.0163471	ZNP536.C:-3.0369452 CCNE1:MCF7:ChiA-PET ZNF536.G:-0.0359188 CCNE1:MCF7:ChiA-PET
rowser	19_30299634_A_C 19_30299796_A_T	19 19	30299634 19_30277729_C_T 30299796 19_30277729_C_T	156400371 158989684	DMRT3 .Ell5 - CDP_1 -,CDP_7 +,Cart1 -,Dbx1 +,Dbx2 +,Foxp1 -,Gbx1 -,Hoxa5_1 -,Hoxb13 +.Hoxb7 H	A(8bxdf)+,Hoxd	5		CCNE1 3266 CCNE1 3104	INTERGENIC	CONE1 CONE1	ZNF536:C:+:0.0162757 ZNF536:T:+:0.0161851	2NF536:C:-0.0350057 CCNE1:MCF7:ChIA-PET 2NF536:T:-0.0352728 CCNE1:MCF7:ChIA-PET
rowser	19_30300017_G_A 19_30304254_CAGTT_C	19 19	30300017 19_30277729_C_T 30304254 19_30277729_C_T	1962104483 1972010703	BCL_disc10 .ERalpha-a_known3 +.lrl_disc4 .SP1_disc3 .SP1_known1 .ZBRK1 + ELF1_known1 .GATA_disc3 +.HD/BRST.MYOEP.H3K4ma1.fibroblast_dfmammarv_nli	and H3K4me3.HDC2157 H	r 3K4me2,mammarv enithi	I CCNE1	CCNE1 2883 CCNE1 1354	INTERGENIC	CCNE1 CCNE1	ZNF536:A:+:0.0162011 ZNF536:C:+:0.0161848	2NF536:A:-0.0334678 CCNE1:MCF7:ChiA-PET 2NF536:C:-0.0195011
rowser	19_30305684_G_A	19	30305684 19_30277729_C_T	193218036	Myc_known7 -,TCMCF_10A;E2F4		5	CCNE1	CCNE1 2784	INTRON	C19orf12,CCNE1	ZNF536:A:+:0.0162527	ZNF536:A0.0186491

IM-PET, KDELC2 HMEC3MPET, C11or85MCF7-CMA-PET, KDELC2 MCF7-CMA-PET, C11or85 HCC19543M-PET

,L0C643923:GA:-:0.0405219 ,L0C643923:GA:-:0.0405219

:Hnia A-PE' :Hnia :Hnia

ICF7:ChIA-PE1 ICF7:ChIA-PE1 ICF7:ChIA-PE1 ICF7:ChIA-PE1 ICF7:ChIA-PE1 ICF7:ChIA-PE1

1.1.MCF7:CNA-PET

:MA-PET IA-PET, FAM91A1:MCF7:CNA-PE1 IA-PET

NA-PET NA-PET NA-PET NA-PET

T

35

10MAPET

L=0.0410264 ==-0.0120156,CLUAP1:C==0.0477839,IL32:C==0.048916 ==-0.0233509 ==-0.0418819

2.4:MCF7:CNA-PET A:+:0.0297273

Key (Supplementary Table 5)	
Field	Description
browser	hyperlink to UCSC Genome Browser showing 1 Mb around variant
variant	Oncoarray variant ID
chrom	Chromosome
position	Chromosome position, hg19/GRCh37 build
locus	Oncoarray variant ID for top snp at locus
rsID	dnSNP rsID: multiple IDs may be listed if several rsIDs (dbSNP 138) overlap the same position
rsID_at.same.pos	rsID(s) overlapping this position
TF_motifs delta	ENCODE_PWM alteration. The delta shown as "+" (PWM strengthened) or "-" (weakened)
TF-ChIP	Transcription factor ChIP-seq from ENCODE and GEO datasets. Format = celltype;target,celltype;target,celltype;target,c
Histone_modifications	Histone modification ChIP-seq. Format = celltype;histonemark,celltype;histonemark,celltype;histonemark,
ChromHMM_enhancer	Enhancers from 25-state chromatin state segmentation HMM modeling from Roadmap Epigenomics Project. Breast cell types = myoepithelial, HMEC, variant HMEC and MCF7
ChromHMM_promoter	Promoters from 25-state chromatin state segmentation HMM modeling from Roadmap Epigenomics Project. Breast cell types = myoepithelial, HMEC, variant HMEC and MCF7
Open_chromatin	Regions identified by DNase-seq and FAIRE-seq. Data from ENCODE, Roadmap, GEO
RegulomeDB_score	RegulomeDB score. Score (http://regulomedb.org/help#score). Scale: 1 is most ilkely to be functional, to 7 = least likely.
GWAS_traits	A GWAS signal within 5 kb either direction
Overlapping_RefGene	SNP falls within an annotated RefGene (within transcribed sequence)
RefGeneTSS distance	Distance to nearest refseq transcription start site
Functional_annotation	RefGene functional annotation
eQTL_target_all	SNP reported to be associated with expression in studies including GTEx.v6, GEUVADIS, Westra Nat Genetics. All tissue types included.
eQTL_GTEx.breast	SNP is associated with expression in GTEx breast samples (N =186)
eQTL_TCGA	Significant eGene from TCGA. Format = Gene1:EffectAllele:Direction:Pvalue1,Gene2:EffectAllele:Direction:Pvalue2 (*+* denotes the effect allele is associated with increased expression)
eQTL_METABRIC	Significant eGene from METABRIC. Format = Gene1:EffectAllele:Direction:Pvalue1,Gene2:EffectAllele:Direction:Pvalue2 (*+* denotes the effect allele is associated with increased expression)
Predicted_target_gene	SNP lies in a putative regulatory element predicted to regulated the listed gene, reported by methods IM-PET, Hnisz, PreSTIGE, Chia-PET, Hi-C, 3C, 4C, 5C, FANTOM5. Format = target.cell.method., target.cell

## Summary of chromatin interaction and enhancer-promoter annotation methods

Method	PMID	Experimental basis	N cell types assayed	Data source	Breast cells	Target annotation
ChIA-PET	22265404	NGS of immunoprecipitated chromatin interactions	5	ENCODE, https://www.encodeproject.org/	MCF7	Intersection of TSS and chromatin interaction
Hi-C	25497547	Genome-wide chromatin interactions	6	NCBI GEO, http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE63525	HMEC	Intersection of TSS and chromatin interaction
Hnisz	24119843	Correlation of H3K27ac levels at enhancers and RNA-seq signals	82	Original publication	MCF7, HMEC, HCC1954	Reported in original publication
PreSTIGE	24196873	Correlation of cell type-specific H3K4me1 levels at enhancers and RNA-seq signals	14	PreSTIGE web resource, http://genetics.case.edu/prestige/	MCF7, HMEC	Reported in original publication
IM-PET	24821768	Correlation of combined H3K4me1, H3K4me3 and H3K27ac levels at enhancers and RNA-seq signals	31	4DGenome web resource, http://4dgenome.int-med.uiowa.edu/	MCF7, HMEC, HCC1954	Reported in original publication and 4DGenome web resource.
FANTOM5	24670763	Correlation of expression at enhancers and promoters by CAGE analysis	113	FANTOM5 web resource, http://enhancer.binf.ku.dk/presets/	Primary breast	TSS reported

ell:method,,,target:cell:method1,method2,,,.....

## Supplementary Table 6: Data Sources for in silico analyses of the 10 novel ER-negative breast cancer susceptibility loci

Supplementary Table 6: Data Sources for	in silico anal	yses of the 10 nov	el ER-negative br	east cancer susce	ptibility loci		
Filename	Class	Biosample_term	Experiment_tar	gBiosample_trea	t Biological_repl	ic Accession	BrowserName_(cell,target,treatment,note,accession)
GSE41995 AR.bed.gz	tf	MCF-7	AR	none	GFPtagged	GSE41995	MCF-7,AR,none,GFPtagged,GSE41995
GSE74069 AR ChIP DHT 4brs strigent	tf	MDA-MB-453	AR	DHT	x	GSE74069	MDA-MB-453 AB DHT x GSE74069
CCE740C0 AD CHID MDA Abra atriaant	4	MDA MD 450		MDA		00271000	
GSE74069_AR_ChiP_MPA_4hrs_strigent_	u	WDA-WB-453	AR	IVIPA	x	GSE74069	MDA-MB-453,AR,MPA,X,G5E/4069
GSE74069_AR_ChIP_Veh_4hrs_strigent_	r tf	MDA-MB-453	AR	Veh	х	GSE74069	MDA-MB-453,AR,Veh,x,GSE74069
GSM1099030_AR-peak.bed.gz	tf	MDA-MB-453	AR	none	х	GSM1099030	MDA-MB-453,AR,none,x,GSM1099030
GSE41995 ATF1.bed.gz	tf	MCF-7	ATF1	none	GFPtagged	GSE41995	MCF-7,ATF1,none,GFPtagged,GSE41995
ENCEE001UM Lbed az	tf	MCE-7	CEBPB	none	ren1	ENCEE001UM I	MCE-7 CEBPB pone ren1 ENCEE001UMU
ENOFFOOTUNIS.bed.gz		MOE 7	OEDPD	none	lepi	ENGEFOOTUNI	
ENCFF001UMK.bed.gz	tt	MCF-7	CEBPB	none	rep2	ENCFF001UMK	MCF-7,CEBPB,none,rep2,ENCFF001UMK
GSE57498_MCF7_ChromHMM.bed.gz	chromhmm	MCF-7	chromhmm	none	х	GSE57498	MCF-7,chromhmm,none,x,GSE57498
E027_25_imputed12marks_segments.bed.	chromhmm	BRST.MYOEP	chromhmm	none	х	RM_E027_25_in	BRST.MYOEP,chromhmm,none,x,RM_E027_25_imputed12marks
E028 25 imputed12marks segments.bed	chromhmm	BRST.HMEC	chromhmm	none	x	RM E119 25 in	BRST.HMEC.chromhmm.none.x.RM_E119_25_imputed12marks
E110 25 imputed12marks accoments had	obromhmm	PRETULINEC	obrombmm			DM E029 25 im	BBST vHMEC obsombran pope v BM E029, 25 imputed12moska
E119_25_Imputed12Inarks_segments.bed.	CHIOMINI	BR31.VHIVEC		none	X	KIVI_E026_25_III	TBRST.VHWEC,CHIOHINIHI,HOHE,X,RWI_E026_25_IIIIpule012Harks
GSE46166_Peaks_cJun_reff_IgG_200.bec	tf	BT549	cJUN	lgG	х	GSE46166	BT549,cJUN,IgG,x,GSE46166
GSE46166_Peaks_cJun_reff_input_200.be	ŧť	BT549	cJUN	input	х	GSE46166	BT549,cJUN,input,x,GSE46166
GSE41995 CREB1.bed.gz	tf	MCF-7	CREB1	none	GFPtagged	GSE41995	MCF-7.CREB1.none.GFPtagged.GSE41995
ENCEE001UTP bod az	+f	MCE-7	CTCE	nono	ron1	ENICEE001UTP	MCE-7 CTCE pope rep1 ENCEE001UTP
ENCIT 001011X.bed.gz	u	101-7		none	lepi	LINCITOTIO	
ENCFF002DBL.bed.gz	tf	MCF-7	CTCF	none	х	ENCFF002DBL	MCF-7,CTCF,none,x,ENCFF002DBL
ENCFF001UML.bed.gz	tf	MCF-7	CTCF	none	rep1	ENCFF001UML	MCF-7,CTCF,none,rep1,ENCFF001UML
ENCFF001UMN.bed.gz	tf	MCF-7	CTCF	none	rep2	ENCFF001UMN	MCF-7,CTCF,none,rep2,ENCFF001UMN
ENCEE001UBB bed gz	tf	T47D	CTCE	dimethyl sulfoxid	d ren1	ENCEE001UBB	T47D CTCE dimethyl sulfoxide rep1 ENCEE001UBB
		T 47D	CTOF	dimethyl_cultoria	d 100 1	ENGEE004UDG	TATE OTOF dimethal sulfavide read ENGEF001UEC
ENCFF0010RC.bed.gz	u	1470	CICF	dimethyi_sulloxid	j repz	ENCFFUUTURC	147D,CTCF,dimethyl_sulloxide,rep2,ENCFF0010RC
ENCFF002CNT.bed.gz	tf	T47D	CTCF	dimethyl_sulfoxid	d x b	ENCFF002CNT	T47D,CTCF,dimethyl_sulfoxide,x,ENCFF002CNT
ENCFF001SWS.bed.gz	tf	mammary_epithe	CTCF	none	х	ENCFF001SWS	mammary_epithelial_cell,CTCF,none,x,ENCFF001SWS
ENCEF002CEB.bed.gz	tf	mammary epithe	CTCF	none	x	ENCFF002CEB	mammary epithelial cell.CTCF.none.x.ENCFF002CEB
ENCEE001UTO bod gz	+f	MCE-7	CTCE	nono	ron1	ENCEEDO1UTO	MCE-7 CTCE pope rep1 ENCEE001UTO
ENCFF00101Q.bed.gz	u	WGF-7	CTCF	none	lepi	ENCFFUUIUIQ	
ENCFF002DBK.bed.gz	π	MCF-7	GTCF	none	x	ENCFF002DBK	MCF-7,CTCF,none,x,ENCFF002DBK
ENCFF001UTO.bed.gz	tf	MCF-7	CTCF	17b-estradiol	х	ENCFF001UTO	MCF-7,CTCF,17b-estradiol,x,ENCFF001UTO
ENCFF002DBJ.bed.az	tf	MCF-7	CTCF	17b-estradiol	x	ENCFF002DBJ	MCF-7,CTCF,17b-estradiol,x,ENCFF002DBJ
ENCEE001UTB bed an	#	MCE-7	CTCE	0000	×	ENICEEDDUITE	MCE-7 CTCE pope x ENCEE001UTP
	u v	NOF-	OTOF	none	^	ENGFFUUIUIP	NOT TOTOT, NOT OF, NOT TOTOTOTOTO
ENCFF002DBM.bed.gz	π	MCF-7	GTCF	none	х	ENCFF002DBM	MUE-1, CICE, none, x, ENCEF002DBM
ENCFF001UTS.bed.gz	tf	MCF-7	CTCF	none	х	ENCFF001UTS	MCF-7,CTCF,none,x,ENCFF001UTS
ENCEE002DBN bed az	tf	MCE-7	CTCE	none	x	ENCEE002DBN	MCE-7 CTCE none x ENCEE002DBN
ENCEE001XS\/ bod gz	#	MCE-7	CTCE	0000	ren1	ENCEEDOAYON	MCE-7 CTCE pope rep1 ENCEE004VSV/
ENCFF001X5V.bed.gz	u	WGF-7		none	repi	ENCFFUUIXSV	MCF-7,CTCF,none,rep1,ENCFF001XSV
ENCFF001XSW.bed.gz	tf	MCF-7	CTCF	none	rep1	ENCFF001XSW	MCF-7,CTCF,none,rep1,ENCFF001XSW
ENCFF001XSX.bed.gz	tf	MCF-7	CTCF	none	rep2	ENCFF001XSX	MCF-7,CTCF,none,rep2,ENCFF001XSX
ENCFE001XSY.bed.gz	tf	MCF-7	CTCF	none	rep2	ENCFF001XSY	MCE-7.CTCE.none.rep2.ENCEE001XSY
ENCEE002DDK bod gz	+f	MCE-7	CTCE	none	·		
ENGEROUSELLE		101-7	0101	none	^ .	ENCITOUZDDIK	
ENCFF001XRL.bed.gz	tt	mammary_epithe	CICF	none	rep1	ENCFF001XRL	mammary_epithelial_cell,CTCF,none,rep1,ENCFF001XRL
ENCFF001XRM.bed.gz	tf	mammary_epithe	CTCF	none	rep2	ENCFF001XRM	mammary_epithelial_cell,CTCF,none,rep2,ENCFF001XRM
ENCFF001XRN.bed.gz	tf	mammary_epithe	CTCF	none	rep1	ENCFF001XRN	mammary_epithelial_cell,CTCF,none,rep1,ENCFF001XRN
ENCFF001XRO.bed.gz	tf	mammary_epithe	CTCF	none	rep2	ENCFF001XRO	mammary_epithelial_cell,CTCF,none,rep2,ENCFF001XRO
ENCFF002DDB.bed.gz	tf	mammary epithe	CTCF	none	x	ENCFF002DDB	mammary epithelial cell.CTCF.none.x.ENCFF002DDB
GSM1122667_CTCE-SUM159-ba19-sd-a	tf	SUM159	CTCE	none	v	GSM1122667	SUM159 CTCE none x GSM1122667
ENCEE001//BX had az	.u .f	MCE 10A	5754	ofimovifono	~	ENCEEDD1//DV	MCE 104 E2E4 of movifore v ENCEE001\/BX
ENCFFOUTVFA.bed.gz	u	NICF_TOA	EZF4	alimoxilene	X	ENCFFUUIVEA	
ENCFF002CZB.bed.gz	tt	MCF_10A	E2F4	atimoxitene	х	ENCFF002CZB	MCF_10A,E2F4,afimoxifene,x,ENCFF002CZB
GSM1462477_EgIn2_peaks.bed.gz	tf	T47D	Egln2	hypoxia	х	GSM1462477	T47D,EgIn2,hypoxia,x,GSM1462477
ENCFF001UMM.bed.gz	tf	MCF-7	EGR1	none	rep1	ENCFF001UMM	MCF-7,EGR1,none,rep1,ENCFF001UMM
ENCFF001UMO.bed.gz	tf	MCF-7	EGR1	none	rep2	ENCFF001UMO	MCF-7,EGR1,none,rep2,ENCFF001UMO
ENCFF001UMP.bed.gz	tf	MCF-7	ELF1	none	rep1	ENCFF001UMP	MCF-7,ELF1,none,rep1,ENCFF001UMP
ENCEE001UMO bed az	tf	MCF-7	ELE1	none	ren2	ENCEE001UMO	MCE-7 ELE1 pope rep2 ENCEE001LIMO
	u 4	MOE 7		none	CEDterrard		MCF 7 EL K4 mana CEDtanard CCE 44005
GSE41995_ELK1.bed.gz	u	NICF-7	ELKI	none	GFFlagged	G3E41993	MCF-7,ELK1,IUIIE,GFFlaggeu,GSE41995
ENCFF001URP.bed.gz	tt	147D	EP300	dimethyl_sulfoxid	d rep1	ENCFF001URP	147D,EP300,dimethyl_sulfoxide,rep1,ENCFF0010RP
ENCFF001URQ.bed.gz	tf	T47D	EP300	dimethyl_sulfoxid	d rep2	ENCFF001URQ	T47D,EP300,dimethyl_sulfoxide,rep2,ENCFF001URQ
ENCFF002CNZ.bed.gz	tf	T47D	EP300	dimethyl_sulfoxid	x b	ENCFF002CNZ	T47D,EP300,dimethyl_sulfoxide,x,ENCFF002CNZ
ENCFF001UNJ.bed.gz	tf	MCF-7	EP300	none	rep1	ENCFF001UNJ	MCF-7,EP300,none,rep1,ENCFF001UNJ
ENCEE001UNK.bed.gz	tf	MCF-7	EP300	none	rep2	ENCFF001UNK	MCF-7.EP300.none.rep2.ENCFE001UNK
CSM1187116 c01 MCE7 EP rop1 macs	. ff	MCE-7	EP	E2	rop2	GSM1187116	MCE-7 ER E2 ron1 GSM1187116
COM1107110_301_MOL7_ER_rep1_mada		MOE 7		52		CCM4407447	MOF 7,ER,E2,ICP1,COM1107110
GSWI187117_SU2_WCF7_ER_rep2_macs	i u	NICF-7	ER	EZ	repz	GSIVITIO/TT/	MCF-7,ER,E2,Iep2,GSM1187117
GSM118/118_s03_MCF7_ER_rep3_macs	tt	MCF-7	ER	E2	rep3	GSM1187118	MCF-7,ER,E2,rep3,GSM1187118
GSM1669078_jc2334MCF7ERVehRep1.br	tf	MCF-7	ER	vehicle	rep1	GSM1669078	MCF-7,ER,vehicle,rep1,GSM1669078
GSM1669079_jc2335MCF7ERE2Rep1.bw	; tf	MCF-7	ER	E2	rep1	GSM1669079	MCF-7,ER,E2,rep1,GSM1669079
GSM1669080_jc2336MCF7ERPGRep1.bw	tf	MCF-7	ER	PG	rep1	GSM1669080	MCF-7,ER,PG,rep1,GSM1669080
GSM1669081_ic2337MCF7ERE2+PGRep	٠tf	MCF-7	ER	E2+PG	rep1	GSM1669081	MCF-7,ER,E2+PG,rep1,GSM1669081
GSM1669082_ic2338MCE7ERVebRep2.bt	tf	MCE-7	FR	vehicle	ren2	GSM1669082	MCE-7 ER vehicle rep2 GSM1669082
GSM1669083 io2330MCE7EBE3Boco Lui	ff	MCE-7	FR	F2		GSM1660092	MCF-7 FR F2 ren2 GSM1660083
COMICODEA in2240MCE7EDDODan2 hu		MCE 7		L2 DC	16p2	GSIM1003003	MCF 7 ED DC
COMICCOORE CONTRACTOR	/ U	NOT 7		F G	iepz	000000000000000000000000000000000000000	NOL 7 LD LO
GSIVI 1009U05_JC2341MCF /ERE2+PGRep	. U	WIGE-/		EZ+PG	repz	GOIVI1009085	NOF-1, EK, E2+PG, 16P2, GSM1009085
GSM1669086_jc2342MCF7ERVehRep3.br	tf	MCF-7	ER	vehicle	rep3	GSM1669086	MCF-7,ER,vehicle,rep3,GSM1669086
GSM1669087_jc2343MCF7ERE2Rep3.bw	tf	MCF-7	ER	E2	rep3	GSM1669087	MCF-7,ER,E2,rep3,GSM1669087
GSM1669088_jc2344MCF7ERPGRep3.bv	tf	MCF-7	ER	PG	rep3	GSM1669088	MCF-7,ER,PG,rep3,GSM1669088
GSM1669089_ic2345MCF7ERE2+PGRep	tf	MCF-7	ER	E2+PG	rep3	GSM1669089	MCF-7,ER,E2+PG,rep3,GSM1669089
GSM1669102 ic2358T47DER\/ehRen1 bv	tf	T47D	ER	vehicle	rep1	GSM1669102	T47D.ER.vehicle.rep1.GSM1669102
CSM1660103 ic2350T47DEPE2Pop1 bw	. tf	T47D	EP	E2	rop1	GSM1660102	T47D ER E2 rop1 GSM1660103
COMPOSITION CONTRACTOR		1470		L2	lepi	00111009103	T47D,ER,E2,Iep1,G3M1009103
GSM1669104_JC2360147DERPGRep1.bw	α	147D	ER	PG	repi	GSM1669104	147D,ER,PG,rep1,GSM1669104
GSM1669105_jc2361T47DERE2+PGRep1	tf	T47D	ER	E2+PG	rep1	GSM1669105	T47D,ER,E2+PG,rep1,GSM1669105
GSM1669106_jc2362T47DERVehRep2.bv	tf	T47D	ER	vehicle	rep2	GSM1669106	T47D,ER,vehicle,rep2,GSM1669106
GSM1669107_jc2363T47DERE2Rep2.bwa	tf	T47D	ER	E2	rep2	GSM1669107	T47D,ER,E2,rep2,GSM1669107
GSM1669108_ic2364T47DERPGRep2.bw	atf	T47D	ER	PG	rep2	GSM1669108	T47D,ER,PG,rep2,GSM1669108
GSM1669109 ic2365T47DERE2+PGPop	Ptf	T47D	ER	E2+PG	rep2	GSM1669109	T47D.ER.E2+PG.rep2.GSM1669109
GSM1669110 is2366T47DEDVobBa-2 bit		T47D	ER ER	vehicle	ren3	GSM1660110	T47D FR vehicle ren3 GSM1660110
COMACCOLAL COOCTATER VERREP3.DV	1 U . 46	14/D			iepo	0000000110	
GSIV1069111_JC236/14/DERE2Rep3.bwa	u	14/D	EK	E2	терз	GSM1669111	14/D,EK,EZ,FEP3,GSM1669111
GSM1669112_jc2368T47DERPGRep3.bw	atf	147D	ER	PG	rep3	GSM1669112	14/D,ER,PG,rep3,GSM1669112
GSM1669113_jc2369T47DERE2+PGRep3	Btf	T47D	ER	E2+PG	rep3	GSM1669113	T47D,ER,E2+PG,rep3,GSM1669113
GSM986059_JC349_ER_siNT E2 1 mac	tf	MCF-7	ER	E2	siNT	GSM986059	MCF-7,ER,E2,siNT,GSM986059
GSM986060 JC350 ER siGATA F2 1 n	rtf	MCF-7	ER	E2	SIGATA	GSM986060	MCF-7.ER.E2.siGATA.GSM986060
GSM086061 10406 ED -:NT E0 0		MCE-7	ED	E2	siNT	COMORCOCA	MCE-7 ED E2 ciNT CCM096064
COM00000 1_JC400_ER_SIN1_E2_2_MAC	(U) .45	MOF-/		L'2 F2		COMOGOGIC	
GSIM986062_JC407_ER_siGATA_E2_2_n	π	MCF-7	EK	E2	SIGATA	GSM986062	MUF-7,EK,E2,SIGATA,GSM986062
GSM986063_JC471_ER_siNT_E2_3_mac	tf	MCF-7	ER	E2	siNT	GSM986063	MCF-7,ER,E2,siNT,GSM986063
GSM986064_JC472_ER_siGATA_E2_3_n	rtf	MCF-7	ER	E2	siGATA	GSM986064	MCF-7,ER,E2,siGATA,GSM986064
GSM986089_JC589_ER_siNT_E2_1 mac	ŧť	ZR751	ER	E2	siNT	GSM986089	ZR751,ER,E2,siNT,GSM986089
GSM986090_JC590 ER siGATA E2 1 n	rtf	ZR751	ER	E2	siGATA	GSM986090	ZR751,ER,E2,siGATA,GSM986090
GSM1038222 ERalphainERacells hed or	tf	MCF-7	ERalpha	E2	ERa.cells	GSM1038222	MCF-7, ERalpha, E2, ERa, cells, GSM1038222
GSM1038223 ERalphainERabcells bod an	tf	MCE-7	FRainha	F2	ERab cells	GSM1038222	MCF-7 FRainha F2 FRah cells GSM1038223
CCM060470 to superior to SE 111		MCE 7	EDolota	+0	-1100.0003	COM000470	MCE 7 EBolaho 10 v CSM000470
GSIVIOO2170_U_export.txt_unique.EE_W1	u u	MOF-/	⊑rkaipna	10	x	GON0021/8	NOF-7, CRaipha, U, X, GOMODOLTO
GSIN862179_t1_export.txt_unique.EE_W1	π	MCF-7	ERalpha	ti .	х	GSM862179	MUE-7, EKalpha, t1, x, GSM862179
GSM862180_t4_export.txt_unique.EE_W1	τ	MCF-7	⊾Ralpha	τ4	х	GSM862180	MCF-7,ERalpha,t4,x,GSM862180

CCM1029224 EBhotoinEBohoollo had an	u	MCF-7	ERalpha	t24	х	GSM862181	MCF-7,ERalpha,t24,x,GSM862181
GSIVI1036224_ERDetaillERabcells.beu.yz	tf	MCF-7	ERbeta	E2	ERab.cells	GSM1038224	MCF-7,ERbeta,E2,ERab.cells,GSM1038224
GSM1038225_ERbetainERbCells.bed.gz	tf	MCF-7	ERbeta	E2	ERb.cells	GSM1038225	MCF-7,ERbeta,E2,ERb.cells,GSM1038225
ENCFF001URF.bed.gz	tf	T47D	ESR1	genistein	rep1	ENCFF001URF	T47D,ESR1,genistein,rep1,ENCFF001URF
ENCFF001URG.bed.gz	tf	T47D	ESR1	genistein	rep2	ENCFF001URG	T47D,ESR1,genistein,rep2,ENCFF001URG
ENCFF002CNV.bed.gz	tf	T47D	ESR1	genistein	х	ENCFF002CNV	T47D,ESR1,genistein,x,ENCFF002CNV
ENCFF001URD.bed.gz	tf	T47D	ESR1	bisphenol_A	rep1	ENCFF001URD	T47D,ESR1,bisphenol_A,rep1,ENCFF001URD
ENCFF001URE.bed.gz	tf	T47D	ESR1	bisphenol_A	rep2	ENCFF001URE	T47D,ESR1,bisphenol_A,rep2,ENCFF001URE
ENCFF002CNU.bed.gz	tf	T47D	ESR1	bisphenol_A	х	ENCFF002CNU	T47D,ESR1,bisphenol_A,x,ENCFF002CNU
ENCFF001URH.bed.gz	tf	T47D	ESR1	estradiol	rep1	ENCFF001URH	T47D,ESR1,estradiol,rep1,ENCFF001URH
ENCFF001URI.bed.gz	tf	T47D	ESR1	estradiol	rep2	ENCFF001URI	T47D,ESR1,estradiol,rep2,ENCFF001URI
ENCFF002CNW.bed.gz	tf	T47D	ESR1	estradiol	х	ENCFF002CNW	T47D,ESR1,estradiol,x,ENCFF002CNW
GSE41995_ESR1.bed.gz	tf	MCF-7	ESR1	none	GFPtagged	GSE41995	MCF-7,ESR1,none,GFPtagged,GSE41995
ENCFF001VPR.bed.gz	tf	MCF_10A	FOS	ethanol	х	ENCFF001VPR	MCF_10A,FOS,ethanol,x,ENCFF001VPR
ENCFF002CYV.bed.gz	tf	MCF_10A	FOS	ethanol	х	ENCFF002CYV	MCF_10A,FOS,ethanol,x,ENCFF002CYV
ENCFF001VPT.bed.gz	tf	MCF_10A	FOS	afimoxifene	х	ENCFF001VPT	MCF_10A,FOS,afimoxifene,x,ENCFF001VPT
ENCFF001SWW.bed.gz	histone	mammary_epithe	H3K27ac	none	х	ENCFF001SWW	mammary_epithelial_cell,H3K27ac,none,x,ENCFF001SWW
ENCFF001VCU.bed.gz	histone	MCF-7	H3K27ac	none	х	ENCFF001VCU	MCF-7,H3K27ac,none,x,ENCFF001VCU
GSE49651_MDAMB231.H3K27Ac.hg19.al	histone	MDA-MB-231	H3K27ac	none	х	GSE49651	MDA-MB-231,H3K27ac,none,x,GSE49651
ENCFF002CYX.bed.gz	tf	MCF_10A	FOS	afimoxifene	х	ENCFF002CYX	MCF_10A,FOS,afimoxifene,x,ENCFF002CYX
ENCFF001VPU.bed.gz	tf	MCF_10A	FOS	afimoxifene	x	ENCFF001VPU	MCF_10A,FOS,afimoxifene,x,ENCFF001VPU
ENCFF002CYY.bed.gz	tf	MCF_10A	FOS	afimoxifene	х	ENCFF002CYY	MCF_10A,FOS,afimoxifene,x,ENCFF002CYY
ENCFF001VPS.bed.gz	tf	MCF_10A	FOS	afimoxifene	x	ENCFF001VPS	MCF_10A,FOS,afimoxifene,x,ENCFF001VPS
GSM986077_JC622_H3K27ac_siNT_E2_N	histone	MCF-7	H3K27ac	E2	siNT	GSM986077	MCF-7,H3K27ac,E2,siNT,GSM986077
ENCFF002CYW.bed.gz	tf	MCF_10A	FOS	afimoxifene	x	ENCFF002CYW	MCF_10A,FOS,afimoxifene,x,ENCFF002CYW
GSE41995 FOS.bed.gz	tf	MCF-7	FOS	none	GFPtagged	GSE41995	MCF-7,FOS,none,GFPtagged,GSE41995
GSE41995 FOSB.bed.az	tf	MCF-7	FOSB	none	GFPtagged	GSE41995	MCF-7.FOSB.none.GFPtagged.GSE41995
GSE41995 FOSI 1 bed az	tf	MCF-7	FOSI 1	none	GEPtagged	GSE41995	MCE-7 FOSI 1 none GEPtagged GSE41995
ENCEE001UMR bed az	tf	MCF-7	FOSL2	none	ren1	ENCEE001UMR	MCF-7 FOSL2 none ren1 ENCEF0011 IMR
CSM086078 IC624 H3K27ac siGATA E	histopo	MCE-7	H3K27ac	E2	SIGATA	CSM086078	MCE-7 H3K27ac E2 siGATA GSM086078
ENCEE0011 IMS bod az	#	MCF-7		EZ	SIGATA	GSIVI960076	MCF-7, H3K27 dC, E2, SIGATA, G3W9800078
ENCFF0010MS.bed.gz	u 	MCF-7	FUSL2	none	CEDtenand	ENCFF0010MS	MCF-7,FOSL2,none,rep2,ENCFF0010MS
GSE41995_FUSL2.Ded.gZ	u	IVICE-/	FUBLZ	none	Greiagged	GSE41995	NICF-7, FUSLZ, NONE, GFPTagged, GSE41995
ENGFF0010KJ.bed.gz	π	14/0	FUXA1	aimethyl_sulfoxid	rep1	ENCEF001URJ	14/D,FOXA1,dimethyl_sulfoxide,rep1,ENCFF001URJ
ENCFF001URK.bed.gz	tt	147D	FUXA1	dimethyl_sulfoxid	rep2	ENCFF001URK	14/D,FOXA1,dimethyl_sulfoxide,rep2,ENCFF001URK
ENCFF002CNX.bed.gz	tf	T47D	FOXA1	dimethyl_sulfoxid	х	ENCFF002CNX	T47D,FOXA1,dimethyl_sulfoxide,x,ENCFF002CNX
GSM986079_JC621_H3K27ac_siNT_Veh_	histone	MCF-7	H3K27ac	Veh	siNT	GSM986079	MCF-7,H3K27ac,Veh,siNT,GSM986079
GSM986080_JC623_H3K27ac_siGATA_V	histone	MCF-7	H3K27ac	Veh	siGATA	GSM986080	MCF-7,H3K27ac,Veh,siGATA,GSM986080
GSE41995_FOXA1.bed.gz	tf	MCF-7	FOXA1	none	GFPtagged	GSE41995	MCF-7,FOXA1,none,GFPtagged,GSE41995
GSM1099031_FOXA1-peak.bed.gz	tf	MDA-MB-453	FOXA1	none	x	GSM1099031	MDA-MB-453,FOXA1,none,x,GSM1099031
GSM986065 JC731 FoxA1 siNT Veh NA	tf	MCF-7	FoxA1	Veh	siNT	GSM986065	MCF-7,FoxA1,Veh,siNT,GSM986065
GSM986066 JC732 FoxA1 siGATA Veh	tf	MCF-7	FoxA1	Veh	siGATA	GSM986066	MCF-7.FoxA1.Veh.siGATA.GSM986066
E119-H3K27ac narrowPeak oz	histone	BRST VHMEC	H3K27ac	none	x	RM E119-H3K27	BRST vHMEC H3K27ac none x RM_E119-H3K27ac
ENCEE001UMT bed az	tf	MCF-7	FOXM1	none	ren1	ENCEE001UMT	MCE-7 FOXM1 pone rep1 ENCEF001UMT
ENCEE001UMU bed gz	tf	MCE-7	FOYM1	none	rop?	ENCEE001UMU	MCE-7 EOXM1, none, rep1, ENCEE0011 IMU
CSM100000E do001 met7 dmoo mooo n	4	MCE 7	FOXM1	dmaa	iepz	CSM1000005	MCE 7 EOXM1, hone, rep2, ENCI 1 0010M0
COM1000995_ds001_mci7_dmso.macs_p	u 4	MOF 7	FOXIMI	umso te	*	GSIM1000995	MCF-7,FOXM1,dttsu,2004000000
GSM1000996_ds002_mci7_ts.macs_peak	u	MCF-7	FUXIMI	is .	x	GSIVI1000996	MCF-7,FOXMIT,IS,X,GSMI1000996
GSM1000997_ds003_mcf7_dmso.macs_p	tf	MCF-7	FOXM1	dmso	х	GSM1000997	MCF-7,FOXM1,dmso,x,GSM1000997
GSM1000998_ds004_mcf7_ts.macs_peak	tf	MCF-7	FOXM1	ts	х	GSM1000998	MCF-7,FOXM1,ts,x,GSM1000998
GSM1000999_ds005_mda231_dmso.macs	tf	MDA-MB-231	FOXM1	dmso	х	GSM1000999	MDA-MB-231,FOXM1,dmso,x,GSM1000999
GSM1001000_ds006_mda231_ts.macs_pe	tf	MDA-MB-231	FOXM1	ts	х	GSM1001000	MDA-MB-231,FOXM1,ts,x,GSM1001000
GSM1001001_ds007_mda231_dmso.macs	tf	MDA-MB-231	FOXM1	dmso	х	GSM1001001	MDA-MB-231,FOXM1,dmso,x,GSM1001001
GSM1001002_ds008_mda231_ts.macs_pe	tf	MDA-MB-231	FOXM1	ts	х	GSM1001002	MDA-MB-231,FOXM1,ts,x,GSM1001002
GSM1001003_ds011_mcf7_dmso.macs_p	tf	MCF-7	FOXM1	dmso	x	GSM1001003	MCF-7,FOXM1,dmso,x,GSM1001003
GSM1001004 ds012 mcf7 ts.macs peak	tf	MCF-7	FOXM1	ts	x	GSM1001004	MCF-7,FOXM1,ts,x,GSM1001004
GSM1001005 ds017 mcf7 dmso.macs p	tf	MCF-7	FOXM1	dmso	x	GSM1001005	MCF-7.FOXM1.dmso.x.GSM1001005
GSM1001006 ds018 mcf7 ts macs peak	tf	MCF-7	FOXM1	ts	x	GSM1001006	MCF-7 FOXM1 ts x GSM1001006
Common Topo _ doo to_mon _ tom doo_pour		inor i	i ozani	10	~	00111001000	
CSE46166 Poaks fra1 roff IgG 200 bod	+f	BT5/0	EDA1	InC.	v	GSE46166	BT540 EPA1 InC x CSE46166
GSE46166_Peaks_fra1_reff_IgG_200.bed	tf +f	BT549	FRA1	lgG	x	GSE46166	BT549,FRA1,IgG,x,GSE46166
GSE46166_Peaks_fra1_reff_lgG_200.bed. GSE46166_Peaks_fra1_reff_input_200.bed	tf tf	BT549 BT549	FRA1 FRA1	IgG input	x x	GSE46166 GSE46166	BT549,FRA1,IgG,x,GSE46166 BT549,FRA1,input,x,GSE46166 MCE Z CAPPA page reg1 ENCEE0011 MV
GSE46166_Peaks_fra1_reff_IgG_200.bed. GSE46166_Peaks_fra1_reff_input_200.bed ENCFF001UMV.bed.gz	tf tf tf	BT549 BT549 MCF-7	FRA1 FRA1 GABPA	IgG input none	x rep1	GSE46166 GSE46166 ENCFF001UMV	BT549,FRA1.IgG.x,GSE46166 BT549,FRA1.input,x,GSE46166 MCF-7,GABPA,none.rep1,ENCFF001UMV
GSE46166_Peaks_fra1_reff_IgG_200.bed. GSE46166_Peaks_fra1_reff_input_200.bed ENCFF001UMV.bed.gz ENCFF001UMW.bed.gz	tf tf tf tf	BT549 BT549 MCF-7 MCF-7	FRA1 FRA1 GABPA GABPA	IgG input none none	x rep1 rep2	GSE46166 GSE46166 ENCFF001UMV ENCFF001UMW	BT549,FRA1,IgG.x,GSE46166 BT549,FRA1,input,x,GSE46166 MCF-7,GABPA,none,rep1,ENCFF001UMV MCF-7,GABPA,none,rep2,ENCFF001UMW
GSE46166_Peaks_fra1_reff_lgG_200.bed. GSE46166_Peaks_fra1_reff_input_200.bed ENCFF001UMV.bed.gz ENCFF001UMW.bed.gz ENCFF001UQG.bed.gz	tf tf tf tf	BT549 BT549 MCF-7 MCF-7 MCF-7	FRA1 FRA1 GABPA GABPA GATA3	IgG input none none	x x rep1 rep2 x	GSE46166 GSE46166 ENCFF001UMV ENCFF001UMW ENCFF001VQG	BT549,FRA1.IgG.x,GSE46166 BT549,FRA1.inputx,GSE46166 MCF-7,GABPA,none,rep1,ENCFF001UMV MCF-7,GABPA,none,rep2,ENCFF001UMW MCF-7,GATA3,none,x,ENCFF001VQG
GSE46166_Peaks_fra1_reff_lgG_200.bed. GSE46166_Peaks_fra1_reff_input_200.bed ENCFF001UMV.bed.gz ENCFF001UMW.bed.gz ENCFF001UQG.bed.gz ENCFF002CZK.bed.gz	tf tf tf tf tf	BT549 BT549 MCF-7 MCF-7 MCF-7 MCF-7	FRA1 FRA1 GABPA GABPA GATA3 GATA3	lgG input none none none	x rep1 rep2 x x	GSE46166 GSE46166 ENCFF001UMV ENCFF001UQG ENCFF001VQG	BT549,FRA1.IgG.x,GSE46166 BT549,FRA1.input,x,GSE46166 MCF-7,GABPA,none.rep1,ENCFF001UMV MCF-7,GABPA,none,rep2,ENCFF001UMW MCF-7,GATA3,none,x,ENCFF001VQG MCF-7,GATA3,none,x,ENCFF002CZK
GSE46166_Peaks_fra1_reff_lgG_200.bed GSE46166_Peaks_fra1_reff_input_200.bed ENCFF001UMV.bed.gz ENCFF001UMV.bed.gz ENCFF001VQB.bed.gz ENCFF002CZK.bed.gz ENCFF002CZK.bed.gz	tf tf tf tf tf tf	BT549 BT549 MCF-7 MCF-7 MCF-7 MCF-7 T47D	FRA1 FRA1 GABPA GABPA GATA3 GATA3 GATA3	IgG input none none none dimethyl_sulfoxid	x x rep1 rep2 x x rep1	GSE46166 GSE46166 ENCFF001UMV ENCFF001UMW ENCFF001VQG ENCFF002CZK ENCFF001URL	BT549,FRA1.IgG.x,GSE46166 BT549,FRA1.input,x,GSE46166 MCF-7,GABPA,none.rep1,ENCFF001UMV MCF-7,GABPA,none.rep2,ENCFF001UMW MCF-7,GATA3,none.x,ENCFF001VGG MCF-7,GATA3,none.x,ENCFF002CZK T47D,GATA3,dmethyl_sulfoxide.rep1,ENCFF001URL
GSE46166_Peaks_fra1_reff_lgG_200.bed. GSE46166_Peaks_fra1_reff_input_200.bed ENCFF001UMV.bed.gz ENCFF001UMV.bed.gz ENCFF001UQG.bed.gz ENCFF001URL.bed.gz ENCFF001URL.bed.gz ENCFF001URL.bed.gz	tf tf tf tf tf tf tf	BT549 BT549 MCF-7 MCF-7 MCF-7 MCF-7 T47D T47D	FRA1 FRA1 GABPA GATA3 GATA3 GATA3 GATA3 GATA3	IgG input none none none dimethyl_sulfoxid dimethyl_sulfoxid	x x rep1 rep2 x x rep1 rep2	GSE46166 GSE46166 ENCFF001UMV ENCFF001UQG ENCFF001VQG ENCFF002CZK ENCFF001URL ENCFF001URM	BT549,FRA1.IgG.x,GSE46166 BT549,FRA1.inputx,GSE46166 MCF-7,GABPA,none,rep1,ENCFF001UMV MCF-7,GABPA,none,rep2,ENCFF001UMW MCF-7,GATA3,none,x,ENCFF001VQG MCF-7,GATA3,none,x,ENCFF002CZK T47D,GATA3,dimethyl_sulfoxide,rep1,ENCFF001URL T47D,GATA3,dimethyl_sulfoxide,rep2,ENCFF001URM
GSE46166_Peaks_fra1_reff_lgG_200.bed. GSE46166_Peaks_fra1_reff_input_200.bed ENCFF001UMV.bed.gz ENCFF001UMW.bed.gz ENCFF001VQG.bed.gz ENCFF002CZK.bed.gz ENCFF001URL.bed.gz ENCFF001URM.bed.gz ENCFF001URM.bed.gz	ឋ ឋ ឋ ឋ ឋ ឋ ឋ ឋ	BT549 BT549 MCF-7 MCF-7 MCF-7 MCF-7 T47D T47D T47D	FRA1 FRA1 GABPA GATA3 GATA3 GATA3 GATA3 GATA3	IgG input none none none dimethyl_sulfoxid dimethyl_sulfoxid dimethyl_sulfoxid	x rep1 rep2 x x rep1 rep2 x	GSE46166 GSE46166 ENCFF001UMV ENCFF001UMW ENCFF001VQG ENCFF002CZK ENCFF001URL ENCFF001URM ENCFF002CNY	BT549,FRA1.IgG.x,GSE46166 BT549,FRA1.input,x,GSE46166 MCF-7,GABPA,none,rep2,ENCFF001UMV MCF-7,GABPA,none,rep2,ENCFF001UMW MCF-7,GATA3,none,x,ENCFF001VQG MCF-7,GATA3,none,x,ENCFF002CZK T47D,GATA3,dimethy1_sulfoxide,rep1,ENCFF001URL T47D,GATA3,dimethy1_sulfoxide,rep2,ENCFF001URM T47D,GATA3,dimethy1_sulfoxide,rep2,ENCFF001URM
GSE46166_Peaks_fra1_reff_lgG_200.bed. GSE46166_Peaks_fra1_reff_input_200.bed ENCFF001UMV.bed.gz ENCFF001UMV.bed.gz ENCFF001VQG.bed.gz ENCFF002CK.bed.gz ENCFF001URL.bed.gz ENCFF001URL.bed.gz ENCFF001URM.bed.gz ENCFF001UMX.bed.gz	tf tf tf tf tf tf tf tf tf tf tf	BT549 BT549 MCF-7 MCF-7 MCF-7 T47D T47D T47D T47D MCF-7	FRA1 FRA1 GABPA GATA3 GATA3 GATA3 GATA3 GATA3 GATA3 GATA3	IgG input none none none dimethyl_sulfoxid dimethyl_sulfoxid none	x x rep1 rep2 x x rep1 x rep2 x rep2 x rep1	GSE46166 GSE46166 ENCFF001UMV ENCFF001UMW ENCFF001VQG ENCFF001URL ENCFF001URM ENCFF002CNY ENCFF001UMX	BT549,FRA1.IgG.x,GSE46166 BT549,FRA1.input,x,GSE46166 MCF-7,GABPA,none,rep1,ENCFF001UMV MCF-7,GATA3,none,x,ENCFF001UMW MCF-7,GATA3,none,x,ENCFF001VQG MCF-7,GATA3,dimethyl_sulfoxide,rep1,ENCFF001URL T47D,GATA3,dimethyl_sulfoxide,rep2,ENCFF001URM T47D,GATA3,dimethyl_sulfoxide,x,ENCFF002CNY MCF-7,GATA3,none,rep1,ENCFF002UNY
GSE46166_Peaks_fra1_reff_lgG_200.bed. GSE46166_Peaks_fra1_reff_input_200.bed ENCFF001UMV.bed.gz ENCFF001UMV.bed.gz ENCFF001URG.bed.gz ENCFF001URL.bed.gz ENCFF001URL.bed.gz ENCFF001URM.bed.gz ENCFF001URM.bed.gz ENCFF001UMX.bed.gz ENCFF001UMX.bed.gz	ឋ ឋ ឋ ឋ ឋ ឋ ឋ ឋ ឋ ឋ	BT549 BT549 MCF-7 MCF-7 MCF-7 T47D T47D T47D T47D MCF-7 MCF-7	FRA1 FRA1 GABPA GATA3 GATA3 GATA3 GATA3 GATA3 GATA3 GATA3 GATA3	IgG input none none none dimethyl_sulfoxid dimethyl_sulfoxid dimethyl_sulfoxid none none	x x rep1 rep2 x x rep1 rep2 x rep1 rep1 rep2 rep1 rep2	GSE46166 GSE46166 ENCFF001UMV ENCFF001UMW ENCFF001UQG ENCFF001URL ENCFF001URL ENCFF001URL ENCFF001UMX ENCFF001UMX	BT549,FRA1.IgG.x,GSE46166 BT549,FRA1.inputx,GSE46166 MCF-7,GABPA,none,rep1,ENCFF001UMV MCF-7,GABPA,none,rep2,ENCFF001UMW MCF-7,GATA3,none,x,ENCFF001VQG MCF-7,GATA3,none,x,ENCFF002CZK T47D,GATA3,dimethyl_sulfoxide,rep1,ENCFF001URL T47D,GATA3,dimethyl_sulfoxide,rep2,ENCFF001URL T47D,GATA3,dimethyl_sulfoxide,x,ENCFF002CNY MCF-7,GATA3,none,rep1,ENCFF001UMX MCF-7,GATA3,none,rep2,ENCFF001UMZ
GSE46166_Peaks_fra1_reff_lgG_200.bed. GSE46166_Peaks_fra1_reff_input_200.bed ENCFF001UMV.bed.gz ENCFF001UMV.bed.gz ENCFF001UQG.bed.gz ENCFF001URL.bed.gz ENCFF001URL.bed.gz ENCFF001URM.bed.gz ENCFF001URX.bed.gz ENCFF001UMX.bed.gz ENCFF001UMX.bed.gz ENCFF001UMZ.bed.gz ENCFF001UMZ.bed.gz	ឋ ឋ ឋ ឋ ឋ ឋ ឋ ឋ ឋ ឋ ឋ ឋ ឋ ឋ ឋ	BT549 BT549 MCF-7 MCF-7 MCF-7 T47D T47D T47D T47D MCF-7 MCF-7 MCF-7	FRA1 FRA1 GABPA GATA3 GATA3 GATA3 GATA3 GATA3 GATA3 GATA3 GATA3 GATA3	IgG input none none none dimethyl_sulfoxid dimethyl_sulfoxid none none none	x x rep1 rep2 x x rep1 rep2 x rep1 rep2 x x rep1 x	GSE46166 GSE46166 ENCFF001UMV ENCFF001UMW ENCFF001VQG ENCFF001URL ENCFF001URL ENCFF001URM ENCFF001UMX ENCFF001UMZ ENCFF001VQF	BT549,FRA1.IgG.x,GSE46166 BT549,FRA1.input,x,GSE46166 MCF-7,GABPA,none,rep2,ENCFF001UMV MCF-7,GABPA,none,rep2,ENCFF001UMW MCF-7,GATA3,none,x,ENCFF002C2K T47D,GATA3,dimethyl_sulfoxide,rep1,ENCFF001URL T47D,GATA3,dimethyl_sulfoxide,rep2,ENCFF001URM T47D,GATA3,dimethyl_sulfoxide,rep2,ENCFF001URM MCF-7,GATA3,none,rep1,ENCFF001UMX MCF-7,GATA3,none,rep2,ENCFF001UMZ MCF-7,GATA3,none,rep2,ENCFF001UMZ
GSE46166_Peaks_fra1_reff_lgG_200.bed. GSE46166_Peaks_fra1_reff_input_200.bed ENCFF001UMV.bed.gz ENCFF001UMV.bed.gz ENCFF001VQC.bed.gz ENCFF001ZCK.bed.gz ENCFF001URL.bed.gz ENCFF001URL.bed.gz ENCFF001UMX.bed.gz ENCFF001UMX.bed.gz ENCFF001UMZ.bed.gz ENCFF001UMZ.bed.gz ENCFF001UMZ.bed.gz ENCFF001VQF.bed.gz	ឋ ឋ ឋ ឋ ឋ ឋ ឋ ឋ ឋ ឋ ឋ ឋ ឋ ឋ ឋ ឋ ឋ ឋ	BT549 BT549 MCF-7 MCF-7 MCF-7 T47D T47D T47D T47D MCF-7 MCF-7 MCF-7 MCF-7	FRA1 FRA1 GABPA GATA3 GATA3 GATA3 GATA3 GATA3 GATA3 GATA3 GATA3 GATA3 GATA3	IgG input none none none dimethyl_sulfoxid dimethyl_sulfoxid dimethyl_sulfoxid none none none none	x x rep1 rep2 x x rep1 rep2 x rep1 rep2 x x x x	GSE46166 GSE46166 ENCFF001UMW ENCFF001UMW ENCFF0012CZ ENCFF002CZK ENCFF001URL ENCFF001URL ENCFF001UMX ENCFF001UMX ENCFF001UMZ ENCFF0012CZJ	BT549,FRA1.IgG.x,GSE46166 BT549,FRA1.input,x,GSE46166 MCF-7,GABPA,none,rep1,ENCFF001UMV MCF-7,GATA3,none,x,ENCFF001UMW MCF-7,GATA3,none,x,ENCFF002CZK T47D,GATA3,dimethyl_sulfoxide,rep1,ENCFF001URL T47D,GATA3,dimethyl_sulfoxide,rep2,ENCFF001URM T47D,GATA3,dimethyl_sulfoxide,x,ENCFF002CNY MCF-7,GATA3,none,rep1,ENCFF001UMX MCF-7,GATA3,none,rep2,ENCFF001UMZ MCF-7,GATA3,none,rep2,ENCFF001UQF MCF-7,GATA3,none,x,ENCFF001UQF
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GSE46166_Peaks_fra1_reff_ipgC_200.bed GSE46166_Peaks_fra1_reff_input_200.bed ENCFF001UMV.bed.gz ENCFF001UMV.bed.gz ENCFF001URL.bed.gz ENCFF001URL.bed.gz ENCFF001URL.bed.gz ENCFF001UMX.bed.gz ENCFF001UMX.bed.gz ENCFF001UMX.bed.gz ENCFF001UMZ.bed.gz ENCFF001UMZ.bed.gz ENCFF001UMZ.bed.gz ENCFF001UMZ.bed.gz ENCFF001UMZ.bed.gz GSM986068_JC1315_GATA3_E2_1_macs. GSM986068_JC1315_GATA3_E2_1_macs. GSM986068_JC1314_GATA3_Veh_1_macs GSM986068_JC134_GATA3_Veh_2_macs. GSM986071_JC485_GATA3_E2_1_macs. GSM986071_JC485_GATA3_E2_1_macs. GSM986071_JC485_GATA3_E2_1_macs. GSM986071_JC485_GATA3_E2_1_macs. GSM986071_JC485_GATA3_E2_1_macs. GSM986071_JC485_GATA3_Veh_2_macs GSM986071_JC555_GATA3_E2_1_macs. GSM986071_JC555_GATA3_Veh_1_macs GSM986071_JC555_GATA3_Veh_1_macs GSM986071_JC555_GATA3_Veh_1_macs GSM986071_JC555_GATA3_Veh_1_macs GSM986071_JC555_GATA3_Veh_1_macs GSM986071_JC555_GATA3_Veh_1_macs GSM986071_JC555_GATA3_Veh_1_macs GSM986071_JC555_GATA3_Veh_1_macs GSM986071_JC555_GATA3_Veh_1_macs GSM986071_JC555_GATA3_Veh_1_macs GSM986071_JC555_GATA3_Veh_1_macs GSM986071_JC555_GATA3_Veh_1_macs GSM986082_JC620_H3K4me1_siNT_E2_ GSM9806082_JC620_H3K4me1_siNT_Veh GSM986083_JC617_H3K4me1_siNT_Veh GSM986083_JC619_H3K4me1_siGATA_V GSE42617_H3K4Me1_narrowPeak.gz E119-H3K4me1_narrowPeak.gz E119-H3K4me1_narrowPeak.gz ENCFF696NQUed.gz ENCFF476WFLbed.gz ENCFF457GJC.bed.gz	tf tt tf t	BT549 BT549 MCF-7 MCF-7 MCF-7 T47D MCF-7 T47D MCF-7 MC	FRA1 FRA1 GABPA GABPA GATA3 GA	IgG         input           input         none           none         none           none         dimethyL_sulfoxid           dimethyL_sulfoxid         none           none         2           Veh         E2           Veh         E2           Veh         E2           Veh         E2           Veh         E2           Veh         None           none         none      none <td>x x rep1 rep2 x rep1 rep2 x rep1 rep2 x x x x x x x x x x x x x</td> <td>GSE46166 GSE46166 ENCFF001UMV ENCFF001UMV ENCFF001UMV ENCFF001URL ENCFF001URL ENCFF001URL ENCFF001URL ENCFF001URZ ENCFF001URZ ENCFF001VQF ENCFF001VQF GSM986067 GSM986070 GSM986070 GSM986070 GSM986070 GSM986073 GSM986070 GSM986070 GSM986070 GSM986073 GSM986073 GSM986074 GSM986073 GSM986074 GSM977 GSM9777 GSM977777 GSM9777777777777777777777777777777777777</td> <td>BT549,FRA1.JgG.x,GSE46166           BT549,FRA1.JgG.x,GSE46166           MCF-7,GABPA,none,rep1,ENCFF001UMV           MCF-7,GATA3,none,x,ENCFF001UMV           MCF-7,GATA3,none,x,ENCFF001UMV           MCF-7,GATA3,none,x,ENCFF001UMV           MCF-7,GATA3,none,x,ENCFF001UMX           MCF-7,GATA3,none,x,ENCFF001UMX           T47D,GATA3,dimethyl_sulfoxide,rep1,ENCFF001URL           T47D,GATA3,dimethyl_sulfoxide,rep2,ENCFF001URL           T47D,GATA3,dimethyl_sulfoxide,rep2,ENCFF001UMX           MCF-7,GATA3,none,rep1,ENCFF001UMX           MCF-7,GATA3,none,rep1,ENCFF001UMX           MCF-7,GATA3,none,rep1,ENCFF001UMZ           MCF-7,GATA3,none,rENCFF002CJJ           MCF-7,GATA3,Nene,X,ENCFF001VQF           MCF-7,GATA3,Nene,X,GSM986068           MCF-7,GATA3,Veh,x,GSM986070           MCF-7,GATA3,Veh,x,GSM986071           MCF-7,GATA3,Veh,x,GSM986072           MCF-7,GATA3,Veh,x,GSM986073           MCF-7,GATA3,Veh,x,GSM986074           MCF-7,GATA3,Veh,x,GSM986075           MCF-7,GATA3,Veh,x,GSM986076           mammary_epithelial_cell,H3K4me1,none,x,ENCFF001SWZ           MDA-MB-231,H3K4me1,none,x,GSE49651           MCF-7,H3K4me1,E2,siGATA,GSM986084           MCF-7,H3K4me1,Ny,Hy,SiGATA,GSM986084           MCF-7,H3K4me1,none,x,GSE42617           BRST.MMEC,H3K4me1,none</td>	x x rep1 rep2 x rep1 rep2 x rep1 rep2 x x x x x x x x x x x x x	GSE46166 GSE46166 ENCFF001UMV ENCFF001UMV ENCFF001UMV ENCFF001URL ENCFF001URL ENCFF001URL ENCFF001URL ENCFF001URZ ENCFF001URZ ENCFF001VQF ENCFF001VQF GSM986067 GSM986070 GSM986070 GSM986070 GSM986070 GSM986073 GSM986070 GSM986070 GSM986070 GSM986073 GSM986073 GSM986074 GSM986073 GSM986074 GSM977 GSM9777 GSM977777 GSM9777777777777777777777777777777777777	BT549,FRA1.JgG.x,GSE46166           BT549,FRA1.JgG.x,GSE46166           MCF-7,GABPA,none,rep1,ENCFF001UMV           MCF-7,GATA3,none,x,ENCFF001UMV           MCF-7,GATA3,none,x,ENCFF001UMV           MCF-7,GATA3,none,x,ENCFF001UMV           MCF-7,GATA3,none,x,ENCFF001UMX           MCF-7,GATA3,none,x,ENCFF001UMX           T47D,GATA3,dimethyl_sulfoxide,rep1,ENCFF001URL           T47D,GATA3,dimethyl_sulfoxide,rep2,ENCFF001URL           T47D,GATA3,dimethyl_sulfoxide,rep2,ENCFF001UMX           MCF-7,GATA3,none,rep1,ENCFF001UMX           MCF-7,GATA3,none,rep1,ENCFF001UMX           MCF-7,GATA3,none,rep1,ENCFF001UMZ           MCF-7,GATA3,none,rENCFF002CJJ           MCF-7,GATA3,Nene,X,ENCFF001VQF           MCF-7,GATA3,Nene,X,GSM986068           MCF-7,GATA3,Veh,x,GSM986070           MCF-7,GATA3,Veh,x,GSM986071           MCF-7,GATA3,Veh,x,GSM986072           MCF-7,GATA3,Veh,x,GSM986073           MCF-7,GATA3,Veh,x,GSM986074           MCF-7,GATA3,Veh,x,GSM986075           MCF-7,GATA3,Veh,x,GSM986076           mammary_epithelial_cell,H3K4me1,none,x,ENCFF001SWZ           MDA-MB-231,H3K4me1,none,x,GSE49651           MCF-7,H3K4me1,E2,siGATA,GSM986084           MCF-7,H3K4me1,Ny,Hy,SiGATA,GSM986084           MCF-7,H3K4me1,none,x,GSE42617           BRST.MMEC,H3K4me1,none
GSE46166_Peaks_fra1_reff_ipgC_200.bed GSE46166_Peaks_fra1_reff_input_200.bed ENCFF001UMV.bed.gz ENCFF001UMV.bed.gz ENCFF001UML.bed.gz ENCFF001URL.bed.gz ENCFF001UML.bed.gz ENCFF001UML.bed.gz ENCFF001UMZ.bed.gz ENCFF001UMZ.bed.gz ENCFF001UMZ.bed.gz ENCFF001UMZ.bed.gz ENCFF001UMZ.bed.gz ENCFF001UMZ.bed.gz ENCFF001UMZ.bed.gz GSM986068_UC31_GATA3_E2_1_macs. GSM986068_UC31_GATA3_Veh_1_macs GSM986068_UC31_GATA3_Veh_2_macs GSM986067_UC426_GATA3_Veh_2_macs GSM986071_UC485_GATA3_E2_1_macs. GSM986073_UC556_GATA3_Veh_2_macs GSM986075_UC633_GATA3_E2_4_macs. GSM986075_UC633_GATA3_E2_4_macs. GSM986075_UC633_GATA3_E2_4_macs. GSM986075_UC633_GATA3_E2_4_macs. GSM986075_UC633_GATA3_E2_4_macs. GSM986075_UC633_GATA3_E2_4_macs. GSM986075_UC633_GATA3_E2_5_macs. GSM986075_UC633_GATA3_E2_5_macs. GSM986075_UC633_GATA3_E2_5_macs. GSM986075_UC633_GATA3_E2_5_macs. GSM986075_UC633_GATA3_E2_5_macs. GSM986081_UC618_H3K4me1_siNT_E2_ GSM986081_UC618_H3K4me1_siGATA_E GSM986081_UC618_H3K4me1_siGATA_E GSM986084_UC619_H3K4me1_siGATA_E GSM986084_UC619_H3K4me1_siGATA_E GSM986084_UC619_H3K4me1_siGATA_E GSM986084_UC619_H3K4me1_siGATA_E GSM986084_UC619_H3K4me1_siGATA_E GSM986084_UC619_H3K4me1_siGATA_E GSM986084_UC619_H3K4me1_siGATA_E GSM986084_UC619_H3K4me1_siGATA_E GSM986084_UC619_H3K4me1_siGATA_E GSM986084_UC619_H3K4me1_siGATA_E GSM986084_UC619_H3K4me1_siGATA_E GSM986084_UC619_H3K4me1_siGATA_E GSM1122655_H3K4me2-MCF7-hg19-sd-q GSM1122655_H3K4me2-SUJM159-hg19-sd-q GSM1122654_H3K4me2-MCF7-hg19-sd-q GSM1122654_H3K4me2-SUJM159-hg19-sd-q GSM1122654_H3K4me2-SUJM159-hg19-sd-q GSM1122654_H3K4me2-HCF7-hg19-sd-q GSM1122654_H3K4me2-HCF7-hg19-sd-q GSM1122654_H3K4me2-HCF7-hg19-sd-q GSM1122654_H3K4me2-HCF7-hg19-sd-q GSM1122654_H3K4me2-HCF7-hg19-sd-q	tf t	BT549 BT549 MCF-7 MCF-7 MCF-7 T47D T47D MCF-7 MC	FRA1 FRA1 GABPA GABPA GATA3 GA	IgG	x x rep1 rep2 x rep1 rep2 x rep1 rep2 x rep1 rep2 x x rep1 rep2 x x x x x x x x x x x x x	GSE46166 GSE46166 ENCFF001UMV ENCFF001UMV ENCFF001UMV ENCFF001URL ENCFF002CX ENCFF001URL ENCFF002CX ENCFF001UMX ENCFF001UMX ENCFF001UMZ ENCFF001UMZ ENCFF001VQF GSM986067 GSM986067 GSM986070 GSM986070 GSM986071 GSM986071 GSM986071 GSM986071 GSM986071 GSM986073 GSM986074 GSM977 GSM9777 GSM97777 GSM9777777 GSM9777777777777777777777777777777777777	BT549,FRA1.JgG.x,GSE46166           BT549,FRA1.JgG.x,GSE46166           MCF-7,GABPA,none,rep1,ENCFF001UMV           MCF-7,GATA3,none,x,ENCFF001UMV           MCF-7,GATA3,none,x,ENCFF001UMV           MCF-7,GATA3,none,x,ENCFF001VQG           MCF-7,GATA3,none,x,ENCFF002CK           TA7D,GATA3,dimethyl_sulfoxide,rep2,ENCFF001URL           T47D,GATA3,dimethyl_sulfoxide,rep2,ENCFF001URM           T47D,GATA3,none,rep1,ENCFF001UMX           MCF-7,GATA3,none,rep1,ENCFF001UMX           MCF-7,GATA3,none,rep2,ENCFF001UMX           MCF-7,GATA3,none,rep2,ENCFF001UMX           MCF-7,GATA3,none,rep2,ENCFF001UMX           MCF-7,GATA3,none,KENCFF002CJJ           MCF-7,GATA3,none,GFPtagged,GSE41995           MCF-7,GATA3,L2x,GSM986067           MCF-7,GATA3,Vehx,GSM986070           MCF-7,GATA3,Vehx,GSM986071           MCF-7,GATA3,Vehx,GSM986073           MCF-7,GATA3,Vehx,GSM986074           MCF-7,GATA3,Vehx,GSM986075           MCF-7,GATA3,Z2x,GSM986074           MCF-7,GATA3,Vehx,GSM986075           MCF-7,GATA3,Vehx,GSM986074           MCF-7,GATA3,Vehx,GSM986074           MCF-7,H3K4me1,E2,siGATA,GSM986081           MCF-7,H3K4me1,E2,siGATA,GSM986083           MCF-7,H3K4me1,Neh,siGATA,GSM986084           MCF-7,H3K4me1,Neh,siNT,GSM986083           M
GSE46166_Peaks_fra1_reff_ipgC200.bed GSE46166_Peaks_fra1_reff_input_200.bed ENCFF001UMV.bed.gz ENCFF001UMV.bed.gz ENCFF001UMV.bed.gz ENCFF001URL.bed.gz ENCFF001URL.bed.gz ENCFF001UMZ.bed.gz ENCFF001UMZ.bed.gz ENCFF001UMZ.bed.gz ENCFF001UMZ.bed.gz ENCFF001UMZ.bed.gz ENCFF001UMZ.bed.gz ENCFF001UMZ.bed.gz GSM986069_JC427_GATA3_E2_1_macs. GSM986069_JC427_GATA3_E2_1_macs. GSM986072_JC484_GATA3_Veh_2_macs GSM986072_JC484_GATA3_Veh_2_macs GSM986072_JC484_GATA3_Veh_2_macs. GSM986072_JC484_GATA3_Veh_4_macs. GSM986072_JC484_GATA3_Veh_4_macs. GSM986072_JC484_GATA3_Veh_4_macs. GSM986072_JC484_GATA3_Veh_4_macs. GSM986072_JC484_GATA3_Veh_4_macs. GSM986081_JC556_GATA3_E2_4_macs. GSM986081_JC618_H3X4me1_siNT_E2_ GSM986081_JC618_H3X4me1_siGATA_V GSE42651_MDAMB231.H3K4me1.siNT_Veh GSM986084_JC619_H3X4me1_siGATA_V GSE42617_H3K4ME1.bed.gz E027-H3K4me1.narrowPeak.gz E119-H3K4me1.narrowPeak.gz E119-H3K4me1.narrowPeak.gz ENCFF00SX2.bed.gz ENCFF2580SE.be	tf t	BT549 BT549 MCF-7 MCF-7 MCF-7 T47D T47D T47D MCF-7 MCF	FRA1 FRA1 GABPA GABPA GABPA GATA3 GA	IgG	x x rep1 rep2 x rep1 rep2 x rep1 rep2 x x GFPtagged x x x x x x x x x x x x x x x x x x x	GSE46166 GSE46166 ENCFF001UMV ENCFF001UMV ENCFF001UMV ENCFF001UML ENCFF001URL ENCFF002CXF ENCFF001UMX ENCFF001UMX ENCFF001UMX ENCFF001UMX ENCFF001UMZ ENCFF001VGT GSM986067 GSM986068 GSM986070 GSM986071 GSM986071 GSM986072 GSM986073 GSM986073 GSM986073 GSM986074 GSM986074 GSM986075 GSM986075 GSM986075 GSM986075 GSM986074 GSM986074 GSM986074 GSM986074 GSM986074 GSM986075 GSM986074 GSM9	BT549,FRA1.JgG.x,GSE46166           BT549,FRA1.JgG.x,GSE46166           MCF-7,GABPA,none,rep1,ENCFF001UMV           MCF-7,GATA3,none,x,ENCFF001UMV           MCF-7,GATA3,none,x,ENCFF001UMV           MCF-7,GATA3,none,x,ENCFF001UQG           MCF-7,GATA3,none,x,ENCFF001UQG           MCF-7,GATA3,dimethyl_sulfoxide,rep2,ENCFF001URL           T47D,GATA3,dimethyl_sulfoxide,rep2,ENCFF001URM           T47D,GATA3,none,rep1,ENCFF001UMX           MCF-7,GATA3,none,rep1,ENCFF001UMX           MCF-7,GATA3,none,rep1,ENCFF001UMZ           MCF-7,GATA3,none,rep1,ENCFF001UMZ           MCF-7,GATA3,none,x,ENCFF002CJJ           MCF-7,GATA3,none,X,ENCFF002CJJ           MCF-7,GATA3,None,X,ENCFF002CJ           MCF-7,GATA3,None,X,ENCFF002CJ           MCF-7,GATA3,Neh,X,GSM986070           MCF-7,GATA3,Yeh,X,GSM986071           MCF-7,GATA3,Yeh,X,GSM986072           MCF-7,GATA3,Yeh,X,GSM986073           MCF-7,GATA3,Yeh,X,GSM986074           MCF-7,GATA3,Veh,X,GSM986075           MCF-7,GATA3,Yeh,X,GSM986074           MCF-7,GATA3,Yeh,X,GSM986075           MCF-7,GATA3,Yeh,X,GSM986074           MCF-7,H3K4me1,L2,SiGATA,GSM986081           MCF-7,H3K4me1,L2,SiGATA,GSM986081           MCF-7,H3K4me1,L2,SiGATA,GSM986083           MCF-7,H3K4me1,Nen,X,R_E027-H3K4me1

GSM2037450_HAUSP_MDA_MB_231_CI	tf	MDA-MB-231	HAUSP	none	x	GSM2037450	MDA-MB-231,HAUSP,none,x,GSM2037450
ENCFF001UMY.bed.gz	tf	MCF-7	HDAC2	none	rep1	ENCFF001UMY	MCF-7,HDAC2,none,rep1,ENCFF001UMY
ENCFF001UNA.bed.gz	tt	MCF-7	HDAC2	none	rep2	ENCFF001UNA	MCF-7,HDAC2,none,rep2,ENCFF001UNA
CSM1462475_HIFTaipna_peaks.bed.gz	u +f	147D T47D	HIF Taipna	hypoxia	x	GSM1462475	T47D,FIFTalpha,hypoxia,x,GSM1462475
GSE47164 AE1 HOXB7 MACS peaks b	u ⊧tf	BT474	HOXB7	none	ren1	GSE47164	BT472 HOXB7 none ren1 GSE47164
GSE47164 AF2 HOXB7 MACS peaks.b	etf	BT474	HOXB7	none	rep1	GSE47164	BT474.HOXB7.none.rep1.GSE47164
GSM1122651 JARID1B-MCF7-hg19-sd-g	tf	MCF-7	JARID1B	none	x	GSM1122651	MCF-7, JARID1B, none, x, GSM1122651
GSM1122652_JARID1B-MCF7-siJARID1E	B tf	MCF-7	JARID1B	siJARID1B	x	GSM1122652	MCF-7, JARID1B, si JARID1B, x, GSM1122652
GSM1122653_JARID1B-MCF7-siCTCF-hg	g tf	MCF-7	JARID1B	siCTCF	х	GSM1122653	MCF-7, JARID1B, siCTCF, x, GSM1122653
GSM1122659_JARID1B-T47D-hg19-sd-q_	tf	T47D	JARID1B	none	х	GSM1122659	T47D,JARID1B,none,x,GSM1122659
GSM1122661_JARID1B-SUM185-hg19-sc	l tf	SUM185	JARID1B	none	х	GSM1122661	SUM185, JARID1B, none, x, GSM1122661
GSM1122662_JARID1B-SUM185-siCTCF	-tf	SUM185	JARID1B	siCTCF	х	GSM1122662	SUM185, JARID1B, siCTCF, x, GSM1122662
GSM1122664_JARID1B-SUM159-hg19-sc	l tf	SUM159	JARID1B	none	х	GSM1122664	SUM159,JARID1B,none,x,GSM1122664
GSM1122669_JARID1B-MDA231-ng19-sc	1 UT	MDA231		none	x	GSM1122669	MDA231,JARID1B,none,X,GSM1122669
GSE41995 IIIN bed az	ff	MCE-7	ILIN	none	x GEPtagged	GSE41995	MCE-7 IIIN none GEPtagged GSE41995
GSE66081 MDA-MB-231 JUN IDB 0.01	tf	MDA-MB-231	JUN	none	x	GSE66081	MDA-MB-231 JUN none x GSE66081
GSM1848883 36noTNFJun 35lgG peaks	tf	BT549	JUN	noTNF	laG	GSM1848883	BT549.JUN.noTNF.laG.GSM1848883
GSM1848883_noTNFJun36_Input38_pea	ctf	BT549	JUN	noTNF	input	GSM1848883	BT549,JUN,noTNF,input,GSM1848883
GSM1848885_39TNFJun_35IgG_peaks.b	e tf	BT549	JUN	TNF	lgG	GSM1848885	BT549,JUN,TNF,IgG,GSM1848885
GSM1848885_TNFJun39_Input38_peaks.	t tf	BT549	JUN	TNF	input	GSM1848885	BT549,JUN,TNF,input,GSM1848885
GSE41995_JUNB.bed.gz	tf	MCF-7	JUNB	none	GFPtagged	GSE41995	MCF-7, JUNB, none, GFPtagged, GSE41995
ENCFF001UNB.bed.gz	tf	MCF-7	JUND	none	rep1	ENCFF001UNB	MCF-7,JUND,none,rep1,ENCFF001UNB
ENCFF001UNC.bed.gz	tf	MCF-7	JUND	none	rep2	ENCFF001UNC	MCF-7,JUND,none,rep2,ENCFF001UNC
ENCFF001URN.bed.gz	tf	T47D	JUND	none	rep1	ENCFF001URN	T47D,JUND,none,rep1,ENCFF001URN
ENCFF001URO.bed.gz	tf	T47D	JUND	none	rep2	ENCFF001URO	T47D,JUND,none,rep2,ENCFF001URO
GSE41995_JUND.bed.gz	tf	MCF-7	JUND	none	GFPtagged	GSE41995	MCF-7, JUND, none, GFPtagged, GSE41995
ENCFF001UND.bed.gz	tt	MCF-7	MAX	none	rep1	ENCFF001UND	MCF-7,MAX,none,rep1,ENCFF001UND
ENCFF001UNE.bed.gz	tt 	MCF-7	MAX	none	rep2	ENCFF001UNE	MCF-7, MAX, none, rep2, ENCFF001UNE
ENCFF00101L.bed.gz	u ++	MCF-7	MYC	none	repi	ENCEE002DBC	MCF-7,MTC, none, rep1,ENCFF00101L
ENCFF002DBG.bed.gz	u 	MCF-7	MYC	none	x	ENCFF002DBG	MCF-7,MTC,NONE,X,ENCFF002DBG
ENCFF00101N.bed.gz	π	MCF-7	MYC	none	x	ENCFF00101N	MCF-7,MYC,none,X,ENCFF00101N
ENCFF002DBI.Ded.gz	π #	MCF-7	MYC	none	x	ENCFF002DBI	MCF-1,MYC,none,X,ENCFF002DBI
ENCFF001VPW.bed.gz	u +f	MCF_10A	MYC	alimoxilene	x	ENCEE002CZA	MCF_10A,MYC,allmoxilene,x,ENCFF001VPW
ENCFF002CZA.bed.gz	u ff	MCF_TOA	MYC	annoxiene	x rep1	ENCEE001UTM	MCF_T0A,MTC,annoxiene,x,ENCFF002C2A
ENCEF002DBH bod gz	u ++	MCE 7	MYC	none	iepi	ENCEE002DBH	MCF-7,MTC, NOTE, TEPT, ENCEFOOTOTM
ENCFF002DBH.bed.gz	u +f	MCF-7	MYC	17b ostradial	X rop1	ENCEE001UTK	MCF-7, MTC, NOTE, X, ENCFF002DBH
ENCEE002DBE bed az	u tf	MCF-7	MYC	17b-estradiol	v	ENCEE002DBE	MCF-7 MYC 17b-estradiol x ENCEE002DBE
ENCEE001VPV bed gz	u tf	MCF 10A	MYC	ethanol	x	ENCEE001//PV	MCF 104 MYC ethanol x ENCEF001//PV
ENCEE002CVZ bed az	u ff	MCE 10A	MYC	othanol	~	ENCEE002CV7	MCE_10A,MYC ethanol x ENCEE002CVZ
GSM1099029 MYC-peak bed az	u tf	MDA-MB-453	MYC	none	x	GSM1099029	MDA-MB-453 MYC none x GSM1099029
GSE41995 NR1D1 bed gz	tf	MCF-7	NR1D1	none	GEPtagged	GSE41995	MCE-7 NR1D1 none GEPtaged GSE41995
GSE41995 NR1D2.bed.gz	tf	MCF-7	NR1D2	none	GFPtagged	GSE41995	MCF-7,NR1D2,none,GEPtagged,GSE41995
GSE41995 NR1H3.bed.gz	tf	MCF-7	NR1H3	none	GFPtagged	GSE41995	MCF-7.NR1H3.none.GFPtagged.GSE41995
GSE41995 NR2C1-L bed.gz	tf	MCF-7	NR2C1-L	none	GFPtagged	GSE41995	MCE-7 NR2C1-L none GEPtagged GSE41995
GSE41995 NR2C1-S.bed.az	tf	MCF-7	NR2C1-S	none	GFPtagged	GSE41995	MCF-7.NR2C1-S.none.GFPtagged,GSE41995
GSE41995 NR2C2.bed.az	tf	MCF-7	NR2C2	none	GFPtagged	GSE41995	MCF-7,NR2C2,none,GFPtagged,GSE41995
GSE41995 NR2F1.bed.gz	tf	MCF-7	NR2F1	none	GFPtagged	GSE41995	MCF-7,NR2F1,none,GFPtagged,GSE41995
ENCFF001UNF.bed.gz	tf	MCF-7	NR2F2	none	rep1	ENCFF001UNF	MCF-7,NR2F2,none,rep1,ENCFF001UNF
ENCFF001UNG.bed.gz	tf	MCF-7	NR2F2	none	rep2	ENCFF001UNG	MCF-7,NR2F2,none.rep2,ENCFF001UNG
GSE41995 NR2F2.bed.gz	tf	MCF-7	NR2F2	none	GFPtagged	GSE41995	MCF-7,NR2F2,none,GFPtagged,GSE41995
GSE41995_NR3C1.bed.gz	tf	MCF-7	NR3C1	none	GFPtagged	GSE41995	MCF-7,NR3C1,none,GFPtagged,GSE41995
GSE41995_NR4A1.bed.gz	tf	MCF-7	NR4A1	none	GFPtagged	GSE41995	MCF-7,NR4A1,none,GFPtagged,GSE41995
GSE41995_NR4A2.bed.gz	tf	MCF-7	NR4A2	none	GFPtagged	GSE41995	MCF-7,NR4A2,none,GFPtagged,GSE41995
GSM1462478_NRF1_peaks.bed.gz	tf	T47D	NRF1	hypoxia	x	GSM1462478	T47D,NRF1,hypoxia,x,GSM1462478
wgEncodeAwgDnaseDukeMcf7hypoxiaUn	dnase	MCF-7	open-chrom	hypoxia	х	ENC_dnase	MCF-7,open-chrom,hypoxia,x,ENC_dnase
wgEncodeAwgDnaseDukeT47dUniPk.nam	dnase	T47D	open-chrom	none	х	ENC_dnase	T47D,open-chrom,none,x,ENC_dnase
wgEncodeAwgDnaseUwdukeHmecUniPk.	dnase	HMEC	open-chrom	none	х	ENC_dnase	HMEC,open-chrom,none,x,ENC_dnase
wgEncodeAwgDnaseUwdukeMcf7UniPk.n	adnase	MCF-7	open-chrom	none	х	ENC_dnase	MCF-7,open-chrom,none,x,ENC_dnase
GSE42617_FAIRE.bed.gz	faire	MCF-7	open-chrom	none	х	GSE42617	MCF-7,open-chrom,none,x,GSE42617
GSM1122847_HMEC_FAIRE_1.peaksMo	sfaire	HMEC	open-chrom	none	х	GSM1122847	HMEC,open-chrom,none,x,GSM1122847
GSM1122848_HMEC_FAIRE_2.peaksMo	faire	HMEC	open-chrom	none	х	GSM1122848	HMEC,open-chrom,none,x,GSM1122848
GSM925735_FAIRE_H19_LTED_rep1.be	faire	MCF-7-LTED	open-chrom	none	rep1	GSM925735	MCF-7-LTED, open-chrom, none, rep1, GSM925735
GSM925736_FAIRE_H19_LTED_rep2.be	faire	MCF-7-LTED	open-chrom	none	rep2	GSM925736	MCF-7-LTED,open-chrom,none,rep2,GSM925736
E028-DNase.hotspot.all.peaks.bed.gz	dnase	BRST.HMEC	open-chrom	none	all	RM_E028-DNase	BRST.HMEC,open-chrom,none,all,RM_E028-DNase
E028-DNase.hotspot.fdr0.01.peaks.bed.gz	dnase	BRST.HMEC	open-chrom	none	fdr0.01	RM_E028-DNase	BRST.HMEC,open-chrom,none,fdr0.01,RM_E028-DNase
E028-DNase.macs2.narrowPeak.gz	dnase	BRST.HMEC	open-chrom	none	x	RM_E028-DNase	BRST.HMEC.open-chrom,none,x,RM_E028-DNase
E119-DNase.macs2.narrowPeak.gz	dnase	BRST.VHMEC	open-chrom	none	X	RM_E119-DNase	BRST.vHMEC,open-chrom,none,x,RM_E119-DNase
GSM986085_JC476_p300_siN1_E2_2_III	- U - 4	MCF-7	-200	E2	SINT	GSIM986085	MCF-7, p300, E2, SIN 1, GSM980085
GSM986086_JC478_p300_siGATA_E2_2	_ U	MCF-7	p300	EZ Voh	SIGATA	CSM0960085	MCE 7 p200,E2,SIGATA,GSM986086
CSM986087_JC475_p300_silv1_ven_2_r	ru *#	MCF-7	p300	Ven	SINT	CSM086087	MCF-7,p300,Veh,SIN1,GSM980087
CSM692743 PBX1 MCE7 rod m16 10	2 U F #f	MCE-7	PBV1	pope	SIGATA	GSM602743	MCE-7 PBX1 pope x GSM692743
GSM082743_FBX1_MCI7_Ied_III10_10_	. u (#f		PBX1	none	~	GSM092743	MCE-7-I TED DBY1 pope x CSM080353
GSE41995 PGR bod gz	:u +f	MCE-7	PCP	none	A GEDtaggod	GSM909355	MCE-7 PCP pope CEPtagged CSE41905
ENCEE001UNL bed az	u tf	MCF-7	PMI	none	ren1	ENCEE001UNI	MCF-7 PML none ren1 ENCEE001UNI
ENCEE001UNM bed gz	tf	MCF-7	PMI	none	ren2	ENCEF001UNM	MCE-7 PML none rep2 ENCEE001UNM
ENCFE001VPZ.bed.gz	tf	MCF 10A	POLR2A	afimoxifene	x	ENCFF001VPZ	MCF 10A POLR2A afimoxifene x ENCEF001VPZ
ENCFE002CZD.bed.gz	tf	MCF 10A	POLR2A	afimoxifene	x	ENCFF002CZD	MCF_10A_POLR2A_afimoxifene_x_ENCFE002CZD
ENCEF001UTT.bed.gz	tf	MCE-7	DOL DOA				
ENCFF002DBQ.bed.gz	u		FULKZA	none	X	ENCFF001UTT	MCF-7.POLR2A.none.x.ENCFF001UTT
ENCFF001UTU.bed.az	tf	MCF-7	POLR2A POLR2A	none	x	ENCFF001UTT ENCFF002DBQ	MCF-7,POLR2A,none,x,ENCFF001UTT MCF-7,POLR2A,none,x,ENCFF002DBQ
ENCFF002DBO.bed.gz	tf tf	MCF-7 MCF-7	POLR2A POLR2A POLR2A	none none none	x x rep1	ENCFF001UTT ENCFF002DBQ ENCFF001UTU	MCF-7,POLR2A,none,x,ENCFF001UTT MCF-7,POLR2A,none,x,ENCFF002DBQ MCF-7,POLR2A,none.rep1.ENCFF001UTU
	tf tf tf	MCF-7 MCF-7 MCF-7	POLR2A POLR2A POLR2A POLR2A	none none none	x rep1 x	ENCFF001UTT ENCFF002DBQ ENCFF001UTU ENCFF002DBO	MCF-7, POLR2A, none, x, ENCFF001UTT MCF-7, POLR2A, none, x, ENCFF002DBQ MCF-7, POLR2A, none, x, ENCFF001UTU MCF-7, POLR2A, none, x, ENCFF002DBO
ENCFFUUTVPT.bed.gz	tf tf tf tf	MCF-7 MCF-7 MCF-7 MCF-7 MCF_10A	POLR2A POLR2A POLR2A POLR2A POLR2A	none none none ethanol	x rep1 x x	ENCFF001UTT ENCFF002DBQ ENCFF001UTU ENCFF002DBO ENCFF001VPY	MCF-7,POLR2A,none,x,ENCFF001UTT MCF-7,POLR2A,none,x,ENCFF002DBQ MCF-7,POLR2A,none,rep1,ENCFF001UTU MCF-7,POLR2A,none,x,ENCFF002DB0 MCF_10A,POLR2A,ethanol,x,ENCFF001VPY
ENCFF0010P1.bed.gz	tf tf tf tf tf	MCF-7 MCF-7 MCF-7 MCF_10A MCF_10A	POLR2A POLR2A POLR2A POLR2A POLR2A	none none none ethanol ethanol	x rep1 x x x	ENCFF001UTT ENCFF002DBQ ENCFF001UTU ENCFF002DBO ENCFF001VPY ENCFF002CZC	MCF-7,POLR2A,none,x,ENCFF001UTT MCF-7,POLR2A,none,x,ENCFF002DBQ MCF-7,POLR2A,none,rep1,ENCFF001UTU MCF-7,POLR2A,none,x,ENCFF001UTU MCF_10A,POLR2A,ethanol,x,ENCFF001VPY MCF_10A,POLR2A,ethanol,x,ENCFF002C2C
ENCFF001VP1.bed.gz ENCFF002CZC.bed.gz ENCFF001UTV.bed.gz	tf tf tf tf tf tf	MCF-7 MCF-7 MCF-7 MCF_10A MCF_10A MCF_10A	POLR2A POLR2A POLR2A POLR2A POLR2A POLR2A	none none none ethanol ethanol none	x rep1 x x x rep1	ENCFF001UTT ENCFF002DBQ ENCFF001UTU ENCFF002DBO ENCFF001VPY ENCFF002CZC ENCFF001UTV	MCF-7,POLR2A,none,x,ENCFF001UTT MCF-7,POLR2A,none,x,ENCFF002DBQ MCF-7,POLR2A,none,rep1,ENCFF001UTU MCF-7,POLR2A,none,x,ENCFF002DBO MCF_10A,POLR2A,ethanol,x,ENCFF001VPY MCF_10A,POLR2A,ethanol,x,ENCFF002CZC MCF-7,POLR2A,none,rep1,ENCFF001UTV
ENCFF001VF1.bed.gz ENCFF002CZC.bed.gz ENCFF001UTV.bed.gz ENCFF002DBP.bed.gz	tf tf tf tf tf tf tf	MCF-7 MCF-7 MCF-7 MCF_10A MCF_10A MCF_10A MCF-7 MCF-7	POLR2A POLR2A POLR2A POLR2A POLR2A POLR2A POLR2A	none none none ethanol ethanol none none	x rep1 x x x x rep1 x	ENCFF001UTT ENCFF002DBQ ENCFF001UTU ENCFF002DBO ENCFF001VPY ENCFF002CZC ENCFF001UTV ENCFF002DBP	MCF-7,POLR2A,none,x,ENCFF001UTT MCF-7,POLR2A,none,x,ENCFF002DBQ MCF-7,POLR2A,none,rep1,ENCFF001UTU MCF-7,OLR2A,none,x,ENCFF001UTU MCF_10A,POLR2A,ethanol,x,ENCFF001VPY MCF_10A,POLR2A,ethanol,x,ENCFF002CZC MCF-7,POLR2A,none,rep1,ENCFF001UTV MCF-7,POLR2A,none,x,ENCFF001DBP
ENCFF001VP1.08d.gz ENCFF002CC.bed.gz ENCFF001UTV.bed.gz ENCFF002DBP.bed.gz GSE41995_PPARA.bed.gz	tf tf tf tf tf tf tf	MCF-7 MCF-7 MCF-7 MCF_10A MCF_10A MCF_10A MCF-7 MCF-7 MCF-7	POLR2A POLR2A POLR2A POLR2A POLR2A POLR2A POLR2A POLR2A PPARA	none none none ethanol ethanol none none none	x rep1 x x x rep1 x GFPtagged	ENCFF001UTT ENCFF002DBQ ENCFF001UTU ENCFF002DBO ENCFF001VPY ENCFF002CZC ENCFF002CZC ENCFF002DBP GSE41995	MCF-7, POLR2A, none, x, ENCFF001UTT MCF-7, POLR2A, none, x, ENCFF002DBQ MCF-7, POLR2A, none, x, ENCFF001UTU MCF-7, POLR2A, none, x, ENCFF002DB0 MCF_10A, POLR2A, ethanol, x, ENCFF001VPY MCF_10A, POLR2A, ethanol, x, ENCFF002C2C MCF-7, POLR2A, none, rep1, ENCFF001UTV MCF-7, POLR2A, none, x, ENCFF002DBP MCF-7, PPARA, none, x, ENCFF002DBP
ENCFF002CZC.bed.gz ENCFF002CZC.bed.gz ENCFF001UTV.bed.gz ENCFF002DBP.bed.gz GSE41995_PPARD.bed.gz GSE41995_PPARD.bed.gz	tf tf tf tf tf tf tf tf tf	MCF-7 MCF-7 MCF-7 MCF_10A MCF_10A MCF_10A MCF-7 MCF-7 MCF-7	POLR2A POLR2A POLR2A POLR2A POLR2A POLR2A POLR2A PPARA PPARD	none none none ethanol ethanol none none none none	x rep1 x x x rep1 x GFPtagged GFPtagged	ENCFF001UTT ENCFF002DBQ ENCFF001UTU ENCFF002DBO ENCFF002DBO ENCFF002DZC ENCFF002DBP GSE41995 GSE41995	MCF-7,POLR2A,none,x,ENCFF001UTT MCF-7,POLR2A,none,x,ENCFF002DBQ MCF-7,POLR2A,none,rep1,ENCFF001UTU MCF-7,POLR2A,none,x,ENCFF001UTV MCF-10A,POLR2A,ethanol,x,ENCFF001VPY MCF-10A,POLR2A,ethanol,x,ENCFF002D2C MCF-7,POLR2A,none,rep1,ENCFF001UTV MCF-7,POLR2A,none,x,ENCFF002DBP MCF-7,PPARD,none,GFPtagged,GSE41995
ENCFF002CZC.bed.gz ENCFF002CZC.bed.gz ENCFF001UTV.bed.gz ENCFF002DBP.bed.gz GSE41995_PPARD.bed.gz GSE41995_PPARG.bed.gz	t tf tf tf tf tf tf tf	MCF-7 MCF-7 MCF-7 MCF_10A MCF_10A MCF_10A MCF-7 MCF-7 MCF-7 MCF-7	POLR2A POLR2A POLR2A POLR2A POLR2A POLR2A POLR2A POLR2A POLR2A PPARA PPARD PPARG	none none none ethanol ethanol none none none none none none	x rep1 x x x rep1 x GFPtagged GFPtagged GFPtagged	ENCFF001UTT ENCFF002DBQ ENCFF001UTU ENCFF002DBO ENCFF002DBO ENCFF002DBP GSE41995 GSE41995 GSE41995	MCF-7,POLR2A,none,x,ENCFF001UTT MCF-7,POLR2A,none,x,ENCFF002DBQ MCF-7,POLR2A,none,xep1,ENCFF001UTU MCF-7,POLR2A,none,xENCFF002DB0 MCF_10A,POLR2A,ethanol,x,ENCFF001VPY MCF_10A,POLR2A,ethanol,x,ENCFF001VPY MCF-7,POLR2A,none,xep1,ENCFF001UTV MCF-7,POLR2A,none,GPTagged,GSE41995 MCF-7,PPARG,none,GFPtagged,GSE41995
ENCFF001VP1.bed.gz ENCFF001UTV.bed.gz ENCFF001UTV.bed.gz ENCFF002DBP.bed.gz GSE41995_PPAR.bed.gz GSE41995_PPARD.bed.gz GSE41995_PPARG.bed.gz GSE41995_PPARG.bed.gz	tf tf tf tf tf tf tf tf	MCF-7 MCF-7 MCF-7 MCF_10A MCF_10A MCF-7 MCF-7 MCF-7 MCF-7 MCF-7 MCF-7 MCF-7	POLR2A POLR2A POLR2A POLR2A POLR2A POLR2A POLR2A POLR2A PPARA PPARD PPARG PR	none none none ethanol ethanol none none none none vehicle	x rep1 x x rep1 x GFPtagged GFPtagged GFPtagged rep1	ENCFF001UTT ENCFF002DBQ ENCFF001UTU ENCFF002DBO ENCFF001VPY ENCFF002DBP GSE41995 GSE41995 GSE41995 GSE41995 GSE41995	MCF-7,POLR2A,none,x,ENCFF001UTT MCF-7,POLR2A,none,x,ENCFF001DTU MCF-7,POLR2A,none,x,ENCFF001UTU MCF-7,POLR2A,none,x,ENCFF001UTU MCF_10A,POLR2A,ethanol,x,ENCFF001VPY MCF_10A,POLR2A,ethanol,x,ENCFF001VTV MCF-7,POLR2A,none,rep1,ENCFF001UTV MCF-7,POLR2A,none,x,ENCFF002DBP MCF-7,PPARA,none,GFPtagged,GSE41995 MCF-7,PPARA,none,GFPtagged,GSE41995 MCF-7,PPARG,none,GFPtagged,GSE41995 MCF-7,PPARG,none,GFPtagged,GSE41995
ENCFF002CZC.bed.gz ENCFF002CZC.bed.gz ENCFF002DBP.bed.gz GSE41995_PPARb.bed.gz GSE41995_PPARb.bed.gz GSE41995_PPARb.bed.gz GSE41995_PPARb.dg.gz GSM1660901_jc2347MCF7PREJRep1.bv	4 ff ff ff ff ff ff ff ff ff f	MCF-7 MCF-7 MCF-7 MCF-10A MCF-10A MCF-10A MCF-7 MCF-7 MCF-7 MCF-7 MCF-7 MCF-7 MCF-7	POLR2A POLR2A POLR2A POLR2A POLR2A POLR2A POLR2A PPARA PPARA PPARG PR PR	none none none ethanol ethanol none none none none none vehicle E2	x rep1 x x x x GFPtagged GFPtagged GFPtagged rep1 rep1 rep1	ENCFF001UTT ENCFF002DBQ ENCFF001UTU ENCFF002DBO ENCFF001VPY ENCFF002CZC ENCFF001UTV ENCFF002DBP GSE41995 GSE41995 GSE41995 GSE41995 GSE41995 GSM1669091	MCF-7,POLR2A,none,x,ENCFF001UTT MCF-7,POLR2A,none,x,ENCFF002DBQ MCF-7,POLR2A,none,xep1,ENCFF001UTU MCF-7,POLR2A,none,x,ENCFF001UTV MCF_10A,POLR2A,ethanol,x,ENCFF001VPY MCF_10A,POLR2A,ethanol,x,ENCFF002DB2 MCF-7,POLR2A,none,rep1,ENCFF001UTV MCF-7,POLR2A,none,x,ENCFF002DBP MCF-7,PPARA,none,GFPtagged,GSE41995 MCF-7,PPARD,none,GFPtagged,GSE41995 MCF-7,PPARD,none,GFPtagged,GSE41995 MCF-7,PRARD,none,GFPtagged,GSE41995 MCF-7,PRARD,none,GFNtagged,GSE41995 MCF-7,PRARD,none,GFNtagged,GSE41995 MCF-7,PRARD,none,GFNtagged,GSE41995 MCF-7,PRARD,none,GFNtagged,GSE41995 MCF-7,PR,Vehicle,rep1,GSM1669091
ENCFF002CZC.bed.gz ENCFF002CZC.bed.gz ENCFF001UTV.bed.gz ENCFF002DBP.bed.gz GSE41995_PPARD.bed.gz GSE41995_PPARD.bed.gz GSE41995_PPARG.bed.gz GSM1669090_jc2346MCF7PRVehRep1.b GSM1669092_jc2346MCF7PRPCRep1.bx	4 ff ff ff ff ff ff ff ff ff f	MCF-7 MCF-7 MCF-7 MCF-10A MCF-10A MCF-10A MCF-7 MCF-7 MCF-7 MCF-7 MCF-7 MCF-7 MCF-7	POLR2A POLR2A POLR2A POLR2A POLR2A POLR2A POLR2A POLR2A POLR2A PPARA PPARA PPARA PPARG PR PR	none none none ethanol ethanol none none none none vehicle E2 PG	x rep1 x x x rep1 x GFPtagged GFPtagged GFPtagged rep1 rep1 rep1	ENCFF001UTT ENCFF002DBQ ENCFF001UTU ENCFF001VPV ENCFF001VPV ENCFF002DBP GSE41995 GSE41995 GSE41995 GSM1669091 GSM1669092	MCF-7,POLR2A,none,x,ENCFF001UTT MCF-7,POLR2A,none,x,ENCFF002DBQ MCF-7,POLR2A,none,xep1,ENCFF001UTU MCF-7,POLR2A,ethanol,x,ENCFF001VPY MCF_10A,POLR2A,ethanol,x,ENCFF001VPY MCF-10A,POLR2A,ethanol,x,ENCFF001UTV MCF-7,POLR2A,none,x,ENCFF001UTV MCF-7,POLR2A,none,x,ENCFF001UTV MCF-7,PPARD,none,GFPtagged,GSE41995 MCF-7,PPARD,none,GFPtagged,GSE41995 MCF-7,PPARD,none,GFPtagged,GSE41995 MCF-7,PRARD,none,GFPtagged,GSE41995 MCF-7,PRARD,none,GFPtagged,GSE41995 MCF-7,PRARD,none,GFPtagged,GSE41995 MCF-7,PRARD,none,GFPtagged,GSE41995 MCF-7,PRARD,none,GFPtagged,GSE41995 MCF-7,PR,PARD,none,GFPtagged,GSE41995 MCF-7,PR,PARD,none,GFPtagged,GSE41995
ENCFF002CZC bed.gz ENCFF002CZC bed.gz ENCFF001UTV.bed.gz ENCFF002DBP.bed.gz GSE41995_PPARb.bed.gz GSE41995_PPARb.bed.gz GSE41995_PPARb.bed.gz GSM1669090_jc2346MCF7PRVehRep1.b GSM1669092_jc2346MCF7PRE2Rep1.bw GSM1669092_jc2348MCF7PRE2+PGRep1.bt	5 tf tf tf tf tf tf tf tf tf tf tf tf tf	MCF-7 MCF-7 MCF-10A MCF_10A MCF-10A MCF-7 MCF-7 MCF-7 MCF-7 MCF-7 MCF-7 MCF-7 MCF-7 MCF-7 MCF-7	POLR2A POLR2A POLR2A POLR2A POLR2A POLR2A POLR2A POLR2A PPARA PPARA PPARG PR PR PR PR	none none none ethanol ethanol none none none none vehicle E2 PG E2+PG	x rep1 x x x rep1 x GFPtagged GFPtagged GFPtagged GFPtagged rep1 rep1 rep1 rep1	ENCFF001UTU ENCFF001DTU ENCFF001UTU ENCFF001UTU ENCFF001UTU ENCFF001UTV ENCFF001UTV ENCFF002DBP GSE41995 GSE41995 GSE41995 GSM1669091 GSM1669091 GSM1669093	MCF-7,PCLR2A,none,x,ENCFF001UTT MCF-7,POLR2A,none,x,ENCFF001DTU MCF-7,POLR2A,none,x,ENCFF001UTU MCF-7,POLR2A,none,x,ENCFF001UTU MCF-1,POLR2A,ethanol,x,ENCFF001VPY MCF_10A,POLR2A,ethanol,x,ENCFF001VPY MCF-7,POLR2A,none,rep1,ENCFF001UTV MCF-7,POLR2A,none,GP1agged,GSE41995 MCF-7,PPARQ,none,GFP1agged,GSE41995 MCF-7,PPARQ,none,GFP1agged,GSE41995 MCF-7,PRARQ,none,GFP1agged,GSE41995 MCF-7,PRARQ,none,GFP1agged,GSE41995 MCF-7,PR,RQ,etp1,GSM1669091 MCF-7,PR,E2+P0,rep1,GSM1669093
ENCFF001VP1/bed.gz ENCFF002CZC.bed.gz ENCFF002DBP.bed.gz GSE41995_PPARb.bed.gz GSE41995_PPARb.bed.gz GSE41995_PPARb.bed.gz GSM166900_jc2346MCF7PRVehRep1.b GSM1669091_jc2347MCF7PRE2Rep1.bw GSM1669093_jc2348MCF7PRPCRep1.bu GSM1669093_jc2348MCF7PRPCRep1.bu	5 tf tf tf tf tf tf tf tf tf tf tf tf tf	MCF-7 MCF-7 MCF_10A MCF_10A MCF_10A MCF-7 MCF-7 MCF-7 MCF-7 MCF-7 MCF-7 MCF-7 MCF-7 MCF-7 MCF-7 MCF-7	POLR2A POLR2A POLR2A POLR2A POLR2A POLR2A POLR2A POLR2A POLR2A PDARD PPARD PPARD PR PR PR PR PR	none none none ethanol ethanol none none none none vehicle E2 PG E2+PG vehicle	x rep1 x x x x GFPtagged GFPtagged GFPtagged GFPtagged rep1 rep1 rep1 rep1 rep2	ENCFF001UTT ENCFF002DBQ ENCFF001UTU ENCFF001VPY ENCFF001VPY ENCFF002DBP GSE41995 GSE41995 GSE41995 GSE41995 GSM1669090 GSM1669091 GSM1669094	MCF-7,PCLR2A,none,x,ENCFF001UTT MCF-7,POLR2A,none,x,ENCFF002DBQ MCF-7,POLR2A,none,x,eP1,ENCFF001UTU MCF-7,POLR2A,none,x,ENCFF001UTU MCF_10A,POLR2A,ethanol,x,ENCFF001VPY MCF_10A,POLR2A,ethanol,x,ENCFF002D2D MCF-7,POLR2A,none,rep1,ENCFF001UTV MCF-7,POLR2A,none,cFP1agged,GSE41995 MCF-7,PPARD,none,GFP1agged,GSE41995 MCF-7,PPARD,none,GFP1agged,GSE41995 MCF-7,PPARD,none,GFP1agged,GSE41995 MCF-7,PRARD,none,GFP1agged,GSE41995 MCF-7,PR,Neihele,rep1,GSM1669090 MCF-7,PR,E2,rep1,GSM1669091 MCF-7,PR,Yehicle,rep1,GSM1669094
ENCFF002CZC.bed.gz ENCFF002CZC.bed.gz ENCFF002DBP.bed.gz GSE41995_PPARD.bed.gz GSE41995_PPARD.bed.gz GSE41995_PPARD.bed.gz GSM1669091_ic2347MCF7PRE2Rep1.bv GSM1669091_ic2347MCF7PRE2Rep1.bv GSM1669091_ic2347MCF7PRE2PGRep SM1669093_ic2349MCF7PRPE2PGRep2.bv GSM1669095_ic2351MCF7PRE2Rep2.bv	2 4 4 4 4 4 4 4 4 4 4 4 4 4	MCF-7 MCF-7 MCF-10A MCF_10A MCF-10A MCF-7 MCF-7 MCF-7 MCF-7 MCF-7 MCF-7 MCF-7 MCF-7 MCF-7 MCF-7 MCF-7 MCF-7 MCF-7 MCF-7	POLR2A POLR2A POLR2A POLR2A POLR2A POLR2A POLR2A POLR2A POLR2A PPARD PPARD PPARD PR PR PR PR PR PR	none none enone ethanol ethanol none none none none vehicle E2 PG E2+PG vehicle E2	x rep1 x x x rep1 GFPtagged GFPtagged GFPtagged GFPtagged GFPtagged rep1 rep1 rep1 rep1 rep2 rep2	ENCFF001UTT ENCFF002DBQ ENCFF001UTU ENCFF002DBQ ENCFF001VPY ENCFF002CZC ENCFF001UTV ENCFF002DBP GSE41995 GSE41995 GSE41995 GSE41995 GSM1669091 GSM1669091 GSM1669094 GSM1669094 GSM1669095	MCF-7, POLR2A, none, x, ENCFF001UTT MCF-7, POLR2A, none, x, ENCFF001UTU MCF-7, POLR2A, none, rep1, ENCFF001UTU MCF-7, POLR2A, none, rep1, ENCFF001VPY MCF_10A, POLR2A, ethanol, x, ENCFF002C2C MCF-7, POLR2A, none, rep1, ENCFF001UTV MCF-7, POLR2A, none, c, FPCF002DBP MCF-7, PPARD, none, c, FPTagged, GSE41995 MCF-7, PPARD, none, GFPTagged, GSE41995 MCF-7, PPARD, none, GFPTagged, GSE41995 MCF-7, PRARD, none, GFPTagged, GSE41995 MCF-7, PRARD, none, GFPTagged, GSE41995 MCF-7, PRARD, none, GFPTagged, GSE41995 MCF-7, PR, E2, rep1, GSM1669091 MCF-7, PR, E2, rep1, GSM1669093 MCF-7, PR, E2, rep1, GSM1669094 MCF-7, PR, E2, rep2, GSM1669095
ENCFF002CZC.bed.gz ENCFF002CZC.bed.gz ENCFF002DBP.bed.gz GSE41995_PPARb.bed.gz GSE41995_PPARb.bed.gz GSE41995_PPARb.bed.gz GSM1669090_ic2346MCF7PRVehRep1.b GSM1669092_ic2346MCF7PRE2Rep1.bw GSM1669093_ic2349MCF7PRE2+PGRep GSM1669094_ic2350MCF7PRE2+PGRep GSM1669094_ic2350MCF7PRE2+PGRep2.bw GSM1669096_ic2352MCF7PRPReP2.bw	a u u u u u u u u u u u u u u u u u u u	MCF-7 MCF-7 MCF-7 MCF_10A MCF_10A MCF-10A MCF-7 MCF-7 MCF-7 MCF-7 MCF-7 MCF-7 MCF-7 MCF-7 MCF-7 MCF-7 MCF-7 MCF-7 MCF-7	POLR2A POLR2A POLR2A POLR2A POLR2A POLR2A POLR2A POLR2A POLR2A PPARA PPARA PPARA PPARG PR PR PR PR PR PR	none none none ethanol none ethanol none none none none vehicle E2 PG E2+PG vehicle E2 PG	x rep1 x x x rep1 x GFPtagged GFPtagged GFPtagged GFPtagged rep1 rep1 rep1 rep1 rep2 rep2 rep2	ENCFF001UTT ENCFF002DBQ ENCFF001UTU ENCFF001UTU ENCFF001UPY ENCFF002DBP GSE41995 GSE41995 GSE41995 GSM1669091 GSM1669092 GSM1669093 GSM1669093 GSM1669095 GSM1669095	MCF-7, PCLR2A,none, x, ENCFF001UTT MCF-7, POLR2A,none, x, ENCFF001UTU MCF-7, POLR2A,none, x, ENCFF001UTU MCF-7, POLR2A, ethanol, x, ENCFF001VPY MCF_10A, POLR2A, ethanol, x, ENCFF001VPY MCF-7, POLR2A, none, x, ENCFF001UTV MCF-7, POLR2A, none, x, ENCFF001UTV MCF-7, POLR2A, none, x, ENCFF001UTV MCF-7, POLR2A, none, x, ENCFF002DBP MCF-7, PPARD, none, GFPtagged, GSE41995 MCF-7, PPARD, none, GFPtagged, GSE41995 MCF-7, PPARD, none, GFPtagged, GSE41995 MCF-7, PRARD, none, GFPtagged, GSE41995 MCF-7, PRARD, none, GFPtagged, GSE41995 MCF-7, PR, experi, GSM1669091 MCF-7, PR, R2, rep1, GSM1669093 MCF-7, PR, vehicle, rep2, GSM1669094 MCF-7, PR, Vehicle, rep2, GSM1669095 MCF-7, PR, PG, rep2, GSM1669095
ENCFF002CZC bed.gz ENCFF002CZC bed.gz ENCFF002DBP.bed.gz GSE41995_PPARb.bed.gz GSE41995_PPARb.bed.gz GSE41995_PPARb.bed.gz GSM1660090_ic2346MCF7PRVehRep1.b GSM1660092_ic2346MCF7PRVehRep1.b GSM1660093_ic2349MCF7PR2eP.b GSM1660093_ic2349MCF7PR2eP.b GSM1660093_ic2350MCF7PRVehRep2.b GSM1660096_ic2352MCF7PRVehRep2.b GSM1660096_ic2352MCF7PRPE2Rep2.by GSM1660096_ic2353MCF7PRE2+PGRep2.b	2 <b>0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0</b>	MCF-7 MCF-7 MCF-10A MCF_10A MCF-10A MCF-7 MCF-7 MCF-7 MCF-7 MCF-7 MCF-7 MCF-7 MCF-7 MCF-7 MCF-7 MCF-7 MCF-7 MCF-7 MCF-7 MCF-7 MCF-7	POLR2A POLR2A POLR2A POLR2A POLR2A POLR2A POLR2A POLR2A POLR2A PPARA PPARA PPARA PR PR PR PR PR PR PR PR PR	none none none ethanol ethanol none none none none vehicle E2 PG E2+PG E2+PG	x rep1 x x rep1 x x GFPtagged GFPtagged GFPtagged GFPtagged rep1 rep1 rep1 rep1 rep1 rep2 rep2 rep2 rep2	ENCFF001UTT ENCFF002DBQ ENCFF001UTU ENCFF002DBQ ENCFF001VPY ENCFF002CZC ENCFF001UTV ENCFF002DBP GSE41995 GSE41995 GSE41995 GSM1669091 GSM1669093 GSM1669093 GSM1669094 GSM1669096 GSM1669096	MCF-7, PCLR2A,none, x, ENCFF001UTT MCF-7, POLR2A,none, x, ENCFF001UTU MCF-7, POLR2A,none, x, ENCFF001UTU MCF-7, POLR2A, ethanol, x, ENCFF001VPY MCF_10A, POLR2A, ethanol, x, ENCFF001VPY MCF-7, POLR2A, none, rep1, ENCFF001UTV MCF-7, POLR2A, none, cep1, ENCFF001UTV MCF-7, POLR2A, none, GPTagged, GSE41995 MCF-7, PPARQ, none, GPTagged, GSE41995 MCF-7, PPARQ, none, GPTagged, GSE41995 MCF-7, PPARQ, none, GPTagged, GSE41995 MCF-7, PRARQ, none, GPTagged, GSE41995 MCF-7, PRARQ, none, GPTagged, GSE41995 MCF-7, PRARQ, none, GPTagged, GSE41995 MCF-7, PR, Rep1, GSM1669090 MCF-7, PR, Grep1, GSM1669091 MCF-7, PR, Rep1, GSM1669093 MCF-7, PR, Rep1, GSM1669094 MCF-7, PR, Rep2, GSM1669095 MCF-7, PR, Rep2, GSM1669096 MCF-7, PR, PG, rep2, GSM1669097

GSM1669099_jc2355MCF7PRE2Rep3.bv	v; tf	MCF-7	PR	E2	rep3	GSM1669099	MCF-7,PR,E2,rep3,GSM1669099
GSM1669100_jc2356MCF7PRPGRep3.b	w tf	MCF-7	PR	PG	rep3	GSM1669100	MCF-7,PR,PG,rep3,GSM1669100
GSM1669101_jc2357MCF7PRE2+PGRep	ottf	MCF-7	PR	E2+PG	rep3	GSM1669101	MCF-7,PR,E2+PG,rep3,GSM1669101
GSM1669114_jc2370T47DPRVehRep1.b	w tf	T47D	PR	vehicle	rep1	GSM1669114	T47D,PR,vehicle,rep1,GSM1669114
GSM1669115_JC2371147DPRE2Rep1.bw	20. ##	T47D	PR	EZ BG	rep i	GSM1009115	147D,PR,E2,IEP1,GSM1009115
GSM1669117 ic2373T47DPRE2+PGRep	1tf	T47D	PR	E2+PG	rep1	GSM1669117	T47D,PR,E2+PG,rep1,GSM1669117
GSM1669118 jc2374T47DPRVehRep2.b	w tf	T47D	PR	vehicle	rep2	GSM1669118	T47D,PR,vehicle,rep2,GSM1669118
GSM1669119_jc2375T47DPRE2Rep2.bw	atf	T47D	PR	E2	rep2	GSM1669119	T47D,PR,E2,rep2,GSM1669119
GSM1669120_jc2376T47DPRPGRep2.bv	/atf	T47D	PR	PG	rep2	GSM1669120	T47D,PR,PG,rep2,GSM1669120
GSM1669121_jc2377T47DPRE2+PGRep	2tf	T47D	PR	E2+PG	rep2	GSM1669121	T47D,PR,E2+PG,rep2,GSM1669121
GSM1669122_jc2378T47DPRVehRep3.b	n tf	T47D	PR	vehicle	rep3	GSM1669122	T47D,PR,vehicle,rep3,GSM1669122
GSM1669123_jc2379T47DPRE2Rep3.bw	a tf	T47D	PR	E2	rep3	GSM1669123	T47D,PR,E2,rep3,GSM1669123
GSM1669124_jc2380T47DPRPGRep3.bv	/atf	T47D	PR	PG	rep3	GSM1669124	T47D,PR,PG,rep3,GSM1669124
GSM1669125_jc2381T47DPRE2+PGRep	3tf	T47D	PR	E2+PG	rep3	GSM1669125	T47D,PR,E2+PG,rep3,GSM1669125
ENCEF001UNN.bed.gz	τ ++	MCF-7	RAD21	none	rep1	ENCFF001UNN	MCF-7, KAD21, none, rep1, ENCFF001UNN
CSE41005 BABA bod gz	u ++	MCF-7	RADZI	none	CEDtoggod	CSE41005	MCF-7, KAD21, none, rep2, ENCFF0010NO
GSE41995_RARG bed gz	u tf	MCF-7	RARG	none	GEPtagged	GSE41995	MCF-7 RARG none GEPtagged, GSE41995
ENCEE001UNH bed az	tf	MCF-7	REST	none	ren1	ENCEE001UNH	MCF-7 REST none ren1 ENCEF001UNH
ENCFF001UNI.bed.az	tf	MCF-7	REST	none	rep2	ENCFF001UNI	MCF-7.REST.none.rep2.ENCFF001UNI
GSM1038229_RIP140inERacells.bed.gz	tf	MCF-7	RIP140	E2	ERa.cells	GSM1038229	MCF-7,RIP140,E2,ERa.cells,GSM1038229
GSM1038230_RIP140inERabcells.bed.gz	tf	MCF-7	RIP140	E2	ERab.cells	GSM1038230	MCF-7,RIP140,E2,ERab.cells,GSM1038230
GSM1038231_RIP140inERbcells.bed.gz	tf	MCF-7	RIP140	E2	ERb.cells	GSM1038231	MCF-7,RIP140,E2,ERb.cells,GSM1038231
GSE41995_RORA.bed.gz	tf	MCF-7	RORA	none	GFPtagged	GSE41995	MCF-7,RORA,none,GFPtagged,GSE41995
GSE41995_RORC.bed.gz	tf	MCF-7	RORC	none	GFPtagged	GSE41995	MCF-7,RORC,none,GFPtagged,GSE41995
GSE41995_RXRA.bed.gz	tf	MCF-7	RXRA	none	GFPtagged	GSE41995	MCF-7,RXRA,none,GFPtagged,GSE41995
GSE41995_RXRB.bed.gz	tf	MCF-7	RXRB	none	GFPtagged	GSE41995	MCF-7,RXRB,none,GFPtagged,GSE41995
ENCFF001UNP.bed.gz	tf	MCF-7	SIN3A	none	rep1	ENCFF001UNP	MCF-7,SIN3A,none,rep1,ENCFF001UNP
ENCFF001UNQ.bed.gz	tf	MCF-7	SIN3A	none	rep2	ENCFF001UNQ	MCF-7,SIN3A,none,rep2,ENCFF001UNQ
GSE41995_SPDEF.bed.gz	tf	MCF-7	SPDEF	none	GFPtagged	GSE41995	MCF-7,SPDEF,none,GFPtagged,GSE41995
GSM1187119_s04_MCF7_SPDEF_rep1_	ntf	MCF-7	SPDEF	none	rep1	GSM1187119	MCF-7,SPDEF,none,rep1,GSM1187119
GSM1187120_s05_MCF7_SPDEF_rep2_	ntf	MCF-7	SPDEF	none	rep2	GSM1187120	MCF-7,SPDEF,none,rep2,GSM1187120
GSM118/121_s06_MCF7_SPDEF_rep3_	ntt	MCF-7	SPDEF	none	rep3	GSM1187121	MUE-7,SPDEF,none,rep3,GSM1187121
GSIVITU38226_SRC3inERacells.bed.gz	(T +f	MCF-7	SRU3	E2 E2	ERat cells	GSM1038226	MCF-7, SKU3, E2, EKa.Cells, GSM1038226
GSM1038227_SRC3inERabcells.bed.gz	tt	MCF-7	SRC3	E2	ERab.cells	GSM1038227	MCF-7,SRC3,E2,ERab.cells,GSM1038227
GSM1038228_SRC3inERbcells.bed.gz	tt	MCF-7	SRC3	E2	ERb.cells	GSM1038228	MCF-7,SRC3,E2,ERb.cells,GSM1038228
ENCFF001UNR.bed.gz	tt	MCF-7	SRF	none	rep1	ENCFF001UNR	MCF-7,SRF,none,rep1,ENCFF001UNR
ENCFF001UNS.bed.gz	ti 	MCF-7	SKF	none	repz	ENCFF001UNS	MCF-7,SRF,none,rep2,ENCFF001UNS
ENCEE002CZH bod az	u ++	MCF_10A	STATS	alimoxilene	x	ENCEE002CZH	MCF_10A,STAT3,alimoxilene,X,ENCFF001VQD
ENCEF00202FLbed.gz	u ++	MCF_10A	STATS	athonal	x	ENCEE001VOA	MCF_10A,STAT2,athmoxIlene,x,ENCFF00202F
ENCEE002CZE bod az	u ff	MCF_10A	STATS	ethanol	x	ENCEE002CZE	MCF_10A,STAT3,ethanol,x,ENCFF001VQA
ENCEE002CZG bed az	u tf	MCF 10A	STATS	ethanol	x	ENCEE002CZG	MCF_10A_STAT3 ethanol x_ENCEF002CZG
ENCEE002CZE.bed.gz	tf	MCF 10A	STAT3	ethanol	x	ENCFF002CZF	MCF_10A,STAT3.ethanol.x.ENCFF002CZF
ENCFE001VQE.bed.gz	tf	MCF 10A	STAT3	afimoxifene	x	ENCFF001VQE	MCF 10A STAT3 afimoxifene x ENCEF001VQE
ENCEE002CZI.bed.gz	tf	MCF 10A	STAT3	afimoxifene	x	ENCFF002CZI	MCE 10A STAT3 afimoxifene x ENCEF002CZI
ENCFF001UNT.bed.gz	tf	MCF-7	TAF1	none	rep1	ENCFF001UNT	MCF-7.TAF1.none.rep1.ENCFF001UNT
ENCFF001UNU.bed.gz	tf	MCF-7	TAF1	none	rep2	ENCFF001UNU	MCF-7, TAF1, none, rep2, ENCFF001UNU
GSE66081_MDA-MB-231_TAZ_IDR_0.01	. tf	MDA-MB-231	TAZ	none	x	GSE66081	MDA-MB-231,TAZ,none,x,GSE66081
ENCFF001UNV.bed.gz	tf	MCF-7	TCF12	none	rep1	ENCFF001UNV	MCF-7,TCF12,none,rep1,ENCFF001UNV
ENCFF001UNW.bed.gz	tf	MCF-7	TCF12	none	rep2	ENCFF001UNW	MCF-7,TCF12,none,rep2,ENCFF001UNW
ENCFF001VQI.bed.gz	tf	MCF-7	TCF7L2	none	х	ENCFF001VQI	MCF-7,TCF7L2,none,x,ENCFF001VQI
ENCFF002CZM.bed.gz	tf	MCF-7	TCF7L2	none	х	ENCFF002CZM	MCF-7,TCF7L2,none,x,ENCFF002CZM
GSM1099032_TCF7L2-DHT-peak.bed.gz	tf	MDA-MB-453	TCF7L2	DHT	x	GSM1099032	MDA-MB-453,TCF7L2,DHT,x,GSM1099032
GSM1099033_TCF7L2-vehicle-peak.bed.	g tf	MDA-MB-453	TCF7L2	vehicle	x	GSM1099033	MDA-MB-453,TCF7L2,vehicle,x,GSM1099033
ENCFF001UNX.bed.gz	tf	MCF-7	TEAD4	none	rep1	ENCFF001UNX	MCF-7,TEAD4,none,rep1,ENCFF001UNX
ENCFF001UNY.bed.gz	tf	MCF-7	TEAD4	none	rep2	ENCFF001UNY	MCF-7,TEAD4,none,rep2,ENCFF001UNY
GSE66081_MDA-MB-231_TEAD4_IDR_0	.)tf	MDA-MB-231	TEAD4	none	х	GSE66081	MDA-MB-231,TEAD4,none,x,GSE66081
GSE41995_THRA.bed.gz	tf	MCF-7	THRA	none	GFPtagged	GSE41995	MCF-7,THRA,none,GFPtagged,GSE41995
GSE66753_MACS_peaks_minus_est.bed	.(tf	MCF-7	TOP2B	minus_estrogen	x	GSE66753	MCF-7,TOP2B,minus_estrogen,x,GSE66753
GSE66753_MACS_peaks_plus_est.bed.g	ztf	MCF-7	TOP2B	plus_estrogen	x	GSE66753	MCF-7,TOP2B,plus_estrogen,x,GSE66753
GSE41995_VDR.bed.gz	tf	MCF-7	VDR	none	GFPtagged	GSE41995	MCF-7,VDR,none,GFPtagged,GSE41995
GSE41995_XBP1.bed.gz	tt	MCF-7	XBP1	none	GFPtagged	GSE41995	MCF-7,XBP1,none,GFPtagged,GSE41995
GSE66081_MDA-MB-231_YAP_IDR_0.01		MDA-MB-231	YAP ZNE04Z	none	x	GSE66081	MDA-MB-231, YAP, none, X, GSE66081
ENCEF0020ZN bod an	u 	MCF-7	ZINF217	none	x	ENCFF001VQJ	MCF-7,ZNF217,none,x,ENCFF0017QJ
ENCEF002CZN.bed.gz	li biotono	MCF-7	ZINFZ17	none	x	ENCEF0018VP	mcF-7,ZINF217,IIOIIe,X,EINCFF002CZIN
ENCEE001XHB bed az	histone	MCE-7	H3K4me3	none	x ron2	ENCEEDO1XHB	MCE-7 H3K4mo3 pope rep2 ENCEE001YHB
ENCEE001XHC bed az	histone	MCF-7	H3K4me3	none	rep2	ENCEE001XHC	MCF-7 H3K4me3 none rep2 ENCEE001XHC
ENCFF001XHD.bed.gz	histone	MCF-7	H3K4me3	none	rep1	ENCFF001XHD	MCF-7,H3K4me3,none,rep1,ENCFF001XHD
ENCFF001XHE.bed.gz	histone	MCF-7	H3K4me3	none	rep1	ENCFF001XHE	MCF-7,H3K4me3,none,rep1,ENCFF001XHE
ENCFF001XDR.bed.gz	histone	mammary_epithe	H3K4me3	none	rep1	ENCFF001XDR	mammary_epithelial_cell,H3K4me3,none,rep1,ENCFF001XDR
ENCFF001XDS.bed.gz	histone	mammary_epithe	H3K4me3	none	rep2	ENCFF001XDS	mammary_epithelial_cell,H3K4me3,none,rep2,ENCFF001XDS
ENCFF001XDT.bed.gz	histone	mammary_epithe	H3K4me3	none	rep1	ENCFF001XDT	mammary_epithelial_cell,H3K4me3,none,rep1,ENCFF001XDT
ENCFF001XDU.bed.gz	histone	mammary_epithe	H3K4me3	none	rep2	ENCFF001XDU	mammary_epithelial_cell,H3K4me3,none,rep2,ENCFF001XDU
GSE49651_MDAMB231.H3K4me3.hg19./	A histone	MDA-MB-231	H3K4me3	none	х	GSE49651	MDA-MB-231,H3K4me3,none,x,GSE49651
GSM1122656_H3K4me3-MCF7-hg19-sd-	q histone	MCF-7	H3K4me3	none	х	GSM1122656	MCF-7,H3K4me3,none,x,GSM1122656
GSM1122657_H3K4me3-siJarid1b-MCF7	-I histone	MCF-7	H3K4me3	siJarid1b	х	GSM1122657	MCF-7,H3K4me3,siJarid1b,x,GSM1122657
GSM1122666_H3K4me3-SUM159-hg19-s	chistone	SUM159	H3K4me3	none	х	GSM1122666	SUM159,H3K4me3,none,x,GSM1122666
GSM1402463_H3K4me3-HCC2157-hg19	histone	HCC2157	H3K4me3	none	x	GSM1402463	HCC2157,H3K4me3,none,x,GSM1402463
GSE42617_H3K4ME3.bed.gz	histone	MCF-7	H3K4me3	none	х	GSE42617	MCF-7,H3K4me3,none,x,GSE42617
EU27-H3K4me3.narrowPeak.gz	histone	BRST.MYOEP	H3K4me3	none	x	RM_E027-H3K4	BRST.MYOEP,H3K4me3,none,x,RM_E027-H3K4me3
EU28-H3K4me3.narrowPeak.gz	nistone	BRST.HMEC	H3K4me3	none	x	KM_E028-H3K4	BRST. HMEC, H3K4me3, none, x, RM_E028-H3K4me3
E 119-H3K4me3.narrowPeak.gz	nistone	BRSI.VHMEC	H3K4Me3	rione	x	KM_E119-H3K4	IDRST MYOED H3K4me3, none, X, KM_E119-H3K4me3
EU21-H3K9ac.narrowPeak.gz	nistone	BRST.MYOEP	H3K98C	none	x	KM_E027-H3K9a	PRSTUNITOEP,H3K9ac,none,x,KM_E027-H3K9ac
EITSTUSTUS	nisione #	BROI.VHMEC	HJNYBC	none	x ron1	KIM_E119-H3K98	fibroblast of mammany closed CTCE sone and ENCEE004YDD
ENCEF001XRO bod az	u tf	fibroblast of man	CTCF	none	rep:	ENCEE001XRP	fibroblast_of_mammary_gland,CTCE.pone.rep1,ENCFF001XRP
ENCEE001XRR bed az	u tf	fibroblast of mor	CTCF	none	ren1	ENCEE001XRQ	fibroblast of mammary gland CTCE none rep1 ENCEE001YPP
ENCEE001XRS bed az	tf	fibroblast of mor	CTCF	none	ren2	ENCEE001YPC	fibroblast of mammary gland CTCE none rop2 ENCEE0012PS
ENCEF002DDC bed az	tf	fibroblast of mar	CTCF	none	. ор <i>2</i> х	ENCEEU02DDC	fibroblast of mammary gland CTCE none v ENCEF00120DC
ENCFF001XDV.bed.gz	histone	fibroblast of mar	H3K4me3	none	rep1	ENCFF001XDV	fibroblast of mammary gland, BIK4me3.none ren1 ENC.FE001YDV
ENCFF001XDW.bed.az	histopo	fibroblast of mar	H3K4me3	none	rep2	ENCFF001XDW	fibroblast of mammary gland,H3K4me3.none.rep2.ENCFF001XDW
ENCFF001XDX.bed.gz	11ISLUIIC		LI2K4mo2	none	ren1	ENCEF001XDX	fibroblast of mammary gland,H3K4me3,none,rep1.ENCFF001XDX
	histone	fibroblast of mar	H3K4IIIe3	none	i op i		
ENCFF001XDY.bed.gz	histone	fibroblast_of_mar fibroblast_of_mar	H3K4me3	none	rep2	ENCFF001XDY	fibroblast_of_mammary_gland,H3K4me3,none.rep2.ENCFF001XDY
ENCFF001XDY.bed.gz ENCFF001VQH.bed.gz	histone histone tf	fibroblast_of_mar fibroblast_of_mar MCF-7	H3K4me3 HA-E2F1	none none	rep2 x	ENCFF001XDY ENCFF001VQH	fibroblast_of_mammary_gland,H3K4me3,none,rep2,ENCFF001XDY MCF-7,HA-E2F1,none,x,ENCFF001VQH
ENCFF001XDY.bed.gz ENCFF001VQH.bed.gz ENCFF002CZL.bed.gz	histone histone tf	fibroblast_of_mar fibroblast_of_mar MCF-7 MCF-7	H3K4me3 H3K4me3 HA-E2F1 HA-E2F1	none none none	rep2 x x	ENCFF001XDY ENCFF001VQH ENCFF002CZL	fibroblast_of_mammary_gland,H3K4me3,none,rep2,ENCFF001XDY MCF-7,HA-E2F1,none,x,ENCFF001VQH MCF-7,HA-E2F1,none,x,ENCFF002CZL
ENCFF001XDY.bed.gz ENCFF001VQH.bed.gz ENCFF002CZL.bed.gz GSM2037451_HAUSP_H1299_CHIP_pea	histone histone tf tf	fibroblast_of_mar fibroblast_of_mar MCF-7 MCF-7 H1299	H3K4me3 H3K4me3 HA-E2F1 HA-E2F1 HAUSP	none none none none	rep2 x x x	ENCFF001XDY ENCFF001VQH ENCFF002CZL GSM2037451	fibroblast_of_mammary_gland,H3K4me3,none,rep2,ENCFF001XDY MCF-7,HA-E2F1,none x,ENCFF001VOH MCF-7,HA-E2F1,none x,ENCFF002CZL H1299,HAUSP,none x,GM2037451
ENCFF001XDY.bed.gz ENCFF001VQH.bed.gz ENCFF002C2L.bed.gz GSM2037451_HAUSP_H1299_CHIP_pec GSM2037452_H1299_HIF_hg19_rmdup_	histone histone tf tf al tf p tf	fibroblast_of_mar fibroblast_of_mar MCF-7 MCF-7 H1299 H1299	H3K4me3 HA-E2F1 HA-E2F1 HAUSP HIF	none none none none none	rep2 x x x x x	ENCFF001XDY ENCFF001VQH ENCFF002CZL GSM2037451 GSM2037452	fibroblast_of_mammary_gland,H3K4me3,none,rep2,ENCFF001XDY MCF-7,HA-E2F1,none,x,ENCFF001VOH MCF-7,HA-E2F1,none,x,ENCFF002CZL H1299,H4USP,none,x,GSM2037451 H1299,HIF,none,x,GSM2037452

	Location	ER-negat	ive <sup>†</sup>	ER-positi	Heterogeneity P-	
SINP	Location	OR (95%CI)	P-value	OR (95%CI)	P-value	value*
Loci identified	by the prese	nt study				
rs200648189	2p23.3	0.94 (0.91-0.97)	4.7x10 <sup>-4</sup>	0.99 (0.97-1.01)	0.49	4.7x10 <sup>-3</sup>
rs6569648	6q23.1	0.93 (0.90-0.95)	4.3x10 <sup>-8</sup>	0.96 (0.94-0.97)	2.0x10 <sup>-7</sup>	$2.5 \times 10^{-2}$
rs66823261	8p23.3	1.09 (1.06-1.12)	5.6x10 <sup>-9</sup>	1.02 (1.01-1.04)	9.6x10 <sup>-3</sup>	1.3x10 <sup>-5</sup>
rs17350191	8q24.13	1.07 (1.04-1.09)	2.0x10 <sup>-8</sup>	1.03 (1.02-1.05)	6.3x10 <sup>-5</sup>	$1.1 \times 10^{-3}$
rs11374964	11q22.3	0.94 (0.92-0.96)	3.6x10 <sup>-8</sup>	1.02 (1.01-1.04)	5.9x10 <sup>-3</sup>	2.8x10 <sup>-12</sup>
rs74911261	11q22.3	0.82 (0.75-0.89)	2.3x10 <sup>-6</sup>	1.05 (1.00-1.10)	5.0x10 <sup>-2</sup>	5.7x10 <sup>-9</sup>
rs11076805	16p13.3	0.92 (0.90-0.95)	2.2x10 <sup>-8</sup>	0.98 (0.97-1.00)	4.9x10 <sup>-2</sup>	$1.2 \times 10^{-4}$
rs36194942 18q12.1		0.94 (0.91-0.96)	2.5x10 <sup>-7</sup>	0.98 (0.96-0.99)	2.9x10 <sup>-3</sup>	2.0x10 <sup>-3</sup>
rs322144 19p13.2		0.95 (0.93-0.97)	2.4x10 <sup>-5</sup>	4x10 <sup>-5</sup> 0.98 (0.96-1.00)		0.12
rs113701136	19q12	1.07 (1.04-1.09)	1.7x10 <sup>-7</sup>	1.02 (1.00-1.04)	1.6x10 <sup>-2</sup>	9.8x10 <sup>-4</sup>
Previously repo	orted loci (as	sociations replicat	ted by the pr	resent study)		
rs6678914	1q32.1	0.92 (0.90-0.94)	2.6x10 <sup>-12</sup>	1.02 (1.00-1.03)	2.4x10 <sup>-2</sup>	8.1x10 <sup>-16</sup>
rs4245739	1q32.1	1.14 (1.11-1.16)	3.1x10 <sup>-23</sup>	1.00 (0.98-1.02)	0.87	5.0x10 <sup>-19</sup>
rs12710696	2p24.1	1.06 (1.04-1.09)	6.5x10 <sup>-8</sup>	1.01 (1.00-1.03)	7.7x10 <sup>-2</sup>	1.3x10 <sup>-4</sup>
rs4577244	2p23.2	0.92 (0.90-0.95)	1.5x10 <sup>-9</sup>	1.02 (1.01-1.04)	1.1x10 <sup>-2</sup>	2.8x10 <sup>-14</sup>
rs10069690	5p15.33	1.18 (1.15-1.21)	1.5x10 <sup>-35</sup>	1.03 (1.01-1.04)	1.1x10 <sup>-3</sup>	7.3x10 <sup>-25</sup>
rs3757322	6q25.1	1.15 (1.12-1.18)	2.8x10 <sup>-31</sup>	1.07 (1.05-1.08)	5.4x10 <sup>-17</sup>	1.1x10 <sup>-9</sup>
rs2747652	6q25.2	0.91 (0.89-0.93)	1.9x10 <sup>-18</sup>	0.95 (0.93-0.96)	1.5x10 <sup>-13</sup>	3.0x10 <sup>-5</sup>
rs6562760	13q22.1	0.92 (0.90-0.95)	8.7x10 <sup>-10</sup>	0.96 (0.94-0.98)	2.3x10 <sup>-6</sup>	2.7x10 <sup>-3</sup>
rs11075995	16q12.2	1.09 (1.06-1.12)	$1.0 \times 10^{-10}$	1.02 (1.00-1.04)	2.2x10 <sup>-2</sup>	$4.2 \times 10^{-6}$
rs67397200	19p13.11	1.17 (1.14-1.19)	2.7x10 <sup>-37</sup>	0.99 (0.98-1.01)	0.52	6.7x10 <sup>-36</sup>

Supplementary Table 7: Associations for ten novel and ten previously reported (and replicated) ER-negative breast cancer susceptibility loci, by ER status (BCAC data only)

<sup>†</sup>Combined Breast Cancer Association Consortium (BCAC) data from 16.988 cases and 87,962 controls

<sup>+</sup>Combined BCAC data from 65,275 cases and 87,962 controls \*ER-negative case-only analysis of BCAC data (N=82,263), by ER status

OR, odds ratio per copy of the minor allele; CI, confidence interval

Supplementary Table 8: Associations for ten novel and ten previously reported (and replicated) ER-negative breast cancer susceptibility loci, by age in years (BCAC data only<sup>†</sup>)

SND	Location	•	Heterogeneity P-			
SINP	Location	< 40	40-49	50-59	≥ 60	value*
Loci identified	by the preser	nt study				
rs200648189	2p23.3	0.98 (0.9-1.07)	0.96 (0.9-1.03)	0.94 (0.89-1.01)	0.93 (0.87-0.98)	0.060
rs6569648	6q23.1	0.93 (0.87-1.00)	0.91 (0.86-0.96)	0.95 (0.90-1.00)	0.95 (0.91-1.00)	0.16
rs66823261	8p23.3	1.16 (1.08-1.25)	1.15 (1.08-1.22)	1.11 (1.05-1.17)	1.06 (1.01-1.11)	0.15
rs17350191	8q24.13	1.09 (1.03-1.16)	1.08 (1.03-1.13)	1.05 (1.01-1.10)	1.09 (1.04-1.13)	0.84
rs11374964	11q22.3	0.89 (0.83-0.94)	0.93 (0.89-0.98)	0.95 (0.91-0.99)	0.95 (0.91-0.99)	0.16
rs74911261	11q22.3	0.72 (0.57-0.91)	0.78 (0.65-0.93)	0.86 (0.74-1.01)	0.83 (0.72-0.96)	0.12
rs11076805	16p13.3	0.92 (0.85-0.99)	0.95 (0.9-1.01)	0.92 (0.87-0.97)	0.93 (0.88-0.97)	0.68
rs36194942	18q12.1	0.95 (0.89-1.01)	0.92 (0.87-0.97)	0.94 (0.90-0.99)	0.93 (0.89-0.97)	0.95
rs322144	19p13.2	0.97 (0.91-1.04)	0.96 (0.91-1.02)	0.93 (0.89-0.98)	0.95 (0.91-1.00)	0.98
rs113701136	19q12	1.06 (1.00-1.13)	1.05 (1.00-1.11)	1.10 (1.05-1.15)	1.06 (1.02-1.11)	0.33
Previously rep	orted loci (as	sociations replicated	d by the present stu	ıdy)		
rs6678914	1q32.1	0.95 (0.89-1.00)	0.97 (0.92-1.01)	0.92 (0.88-0.96)	0.92 (0.88-0.96)	0.28
rs4245739	1q32.1	1.15 (1.08-1.23)	1.11 (1.06-1.17)	1.16 (1.11-1.21)	1.12 (1.07-1.17)	0.63
rs12710696	2p24.1	1.05 (0.99-1.12)	1.10 (1.05-1.16)	1.05 (1.01-1.10)	1.06 (1.02-1.11)	0.62
rs4577244	2p23.2	0.87 (0.81-0.94)	0.96 (0.90-1.01)	0.93 (0.89-0.98)	0.90 (0.86-0.95)	0.65
rs10069690	5p15.33	1.25 (1.17-1.34)	1.20 (1.14-1.27)	1.20 (1.15-1.26)	1.10 (1.06-1.15)	$1.2 \times 10^{-3}$
rs3757322	6q25.1	1.21 (1.14-1.29)	1.18 (1.13-1.24)	1.16 (1.11-1.21)	1.12 (1.08-1.17)	0.065
rs2747652	6q25.2	0.97 (0.91-1.03)	0.91 (0.87-0.96)	0.87 (0.83-0.91)	0.90 (0.87-0.94)	$1.0 \times 10^{-2}$
rs6562760	13q22.1	0.92 (0.86-0.99)	0.87 (0.82-0.92)	0.93 (0.89-0.98)	0.95 (0.91-1.00)	0.052
rs11075995	16q12.2	1.12 (1.04-1.20)	1.08 (1.02-1.14)	1.06 (1.01-1.11)	1.08 (1.04-1.13)	0.75
rs67397200	19p13.11	1.26 (1.18-1.34)	1.18 (1.13-1.25)	1.14 (1.09-1.19)	1.14 (1.10-1.19)	3.8x10 <sup>-2</sup>

<sup>+</sup>Combined Breast Cancer Association Consortium (BCAC) data from 1954, 3487, 4179 and 5116 cases aged <40, 40-49, 50-59 and ≥60 years, respectively, and 82,347 controls; \*ER-negative case-only analysis, by age (trend test, 1df)

OR, odds ratio per copy of the minor allele; CI, confidence interval

Supplementary ruble stricter over an breast cancer successionly room mentandou et an (2017) rus	Supplementary	y Table 9: Novel overal	I breast cancer suceptibilit	y loci from Michailidou e	t al. (2017)*: ass
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GWAS		
(95%CI)	P-value	
(0.93-1.04)	5.8x10 <sup>-01</sup>	
(0.92-1.03)	3.2x10 <sup>-01</sup>	
(0.81-1.11)	5.2x10 <sup>-01</sup>	
(0.96-1.07)	6.9x10 <sup>-01</sup>	
(0.87-0.99)	3.4x10 <sup>-02</sup>	
(0.92-1.07)	8.2x10 <sup>-01</sup>	
(0.97-1.11)	2.9x10 <sup>-01</sup>	
(0.97-1.09)	3.6x10 <sup>-01</sup>	
(0.88-1.15)	9.8x10 <sup>-01</sup>	
(0.86-0.99)	1.7x10 <sup>-02</sup>	
(0.98-1.17)	1.3x10 <sup>-01</sup>	
(0.97-1.26)	1.4x10 <sup>-01</sup>	
(0.87-1.00)	3.8x10 <sup>-02</sup>	
(0.92-1.03)	3.2x10 <sup>-01</sup>	
(0.82-1.07)	3.2x10 <sup>-01</sup>	
(0.96-1.09)	4.9x10 <sup>-01</sup>	
(0.93-1.06)	8.7x10 <sup>-01</sup>	
(0.96-1.09)	4.8x10 <sup>-01</sup>	
(0.97-1.09)	3.9x10 <sup>-01</sup>	
(0.99-1.13)	1.1x10 <sup>-01</sup>	
(0.99-1.10)	1.3x10 <sup>-01</sup>	
, (0.83-0.99)	2.3x10 <sup>-02</sup>	
(1.01-1.27)	3.5x10 <sup>-02</sup>	
(0.84-1.06)	3.2x10 <sup>-01</sup>	
(0.92-1.07)	8.2x10 <sup>-01</sup>	
(0.87-0.98)	8.1x10 <sup>-03</sup>	
(0.95-1.07)	7.7x10 <sup>-01</sup>	
(0.98-1.10)	$2.6 \times 10^{-01}$	
(0.90-1.02)	$2.2 \times 10^{-01}$	
(0.99-1.10)	$1.5 \times 10^{-01}$	
(0.85-1.05)	2.9x10 <sup>-01</sup>	
(0.89-0.99)	$1.7 \times 10^{-02}$	
(0.97-1.08)	3.8x10 <sup>-01</sup>	
(1.04-1.27)	$5.3 \times 10^{-03}$	
(0.99-1.11)	1.2x10 <sup>-01</sup>	
(0.90-1.06)	5.0x10 <sup>-01</sup>	
(0.98-1.10)	$1.8 \times 10^{-01}$	
(0.89-1.07)	$5.9 \times 10^{-01}$	
(0.94-1.05)	9.0x10 <sup>-01</sup>	
(1.02-1.13)	$1.3 \times 10^{-02}$	
(1.00-1 18)	$5.1 \times 10^{-02}$	
(0.94-1.15)	$4.3 \times 10^{-01}$	
(0.93-1.13)	$7.2 \times 10^{-01}$	
(0.91-1.02)	$1.7 \times 10^{-01}$	
	GWAS           (95%CI)           (0.93-1.04)           (0.92-1.03)           (0.81-1.11)           (0.96-1.07)           (0.97-1.09)           (0.97-1.09)           (0.97-1.09)           (0.98-1.17)           (0.97-1.26)           (0.87-1.00)           (0.92-1.03)           (0.98-1.17)           (0.97-1.26)           (0.87-1.00)           (0.92-1.03)           (0.92-1.03)           (0.92-1.03)           (0.92-1.03)           (0.92-1.03)           (0.93-1.06)           (0.99-1.09)           (0.99-1.09)           (0.99-1.09)           (0.99-1.09)           (0.99-1.00)           (0.83-0.99)           (1.01-1.27)           (0.84-1.06)           (0.92-1.07)           (0.88-0.99)           (0.99-1.10)           (0.98-1.07)           (0.98-1.07)           (0.99-1.10)           (0.99-1.10)           (0.99-1.10)           (0.99-1.10)           (0.99-1.10)           (0.99-1.10)           (0.99-1.10)           (0.99-1.10)	

12q21.31	12:85009437:T:C	12	85009437	T/C	0.34	0.99 (0.93-1.05)	7.2x10 <sup>-01</sup>
12q24.31	12:120832146:C:T	12	120832146	C/T	0.16	1.06 (0.98-1.15)	1.6x10 <sup>-01</sup>
14q32.33	rs10623258	14	105212261	C/CTT	0.45	1.01 (0.93-1.10)	8.1x10 <sup>-01</sup>
16q12.2	rs28539243	16	54682064	G/A	0.49	1.06 (1.00-1.12)	3.4x10 <sup>-02</sup>
16q13	rs2432539	16	56420987	G/A	0.40	1.03 (0.97-1.08)	3.5x10 <sup>-01</sup>
16q24.2	rs4496150	16	87085237	C/A	0.25	0.93 (0.87-0.99)	1.7x10 <sup>-02</sup>
17q21.2	rs72826962	17	40836389	C/T	0.01	0.86 (0.58-1.26)	4.3x10 <sup>-01</sup>
17q21.31	17:44252468:G:A	17	44252468	G/A	0.19	0.94 (0.87-1.01)	1.1x10 <sup>-01</sup>
18q12.1	rs117618124	18	29977689	T/C	0.05	0.88 (0.77-1.01)	7.2x10 <sup>-02</sup>
19p13.13	rs78269692	19	13158277	T/C	0.05	1.08 (0.95-1.23)	2.3x10 <sup>-01</sup>
19p13.12	rs2594714	19	13954571	G/A	0.23	0.97 (0.91-1.03)	$3.4 \times 10^{-01}$
19p13.11	rs2965183	19	19545696	G/A	0.35	1.03 (0.98-1.09)	$2.4 \times 10^{-01}$
19q13.22	rs71338792	19	46183031	A/AT	0.23	1.02 (0.94-1.11)	6.0x10 <sup>-01</sup>
20p12.3	rs16991615	20	5948227	G/A	0.06	1.15 (1.03-1.29)	1.4x10 <sup>-02</sup>
20q13.13	rs6122906	20	48945911	A/G	0.18	1.07 (1.00-1.14)	6.8x10 <sup>-02</sup>
22q13.1	rs738321	22	38568833	C/G	0.38	0.97 (0.92-1.02)	2.8x10 <sup>-01</sup>
22q13.2	rs73161324	22	42038786	C/T	0.06	1.19 (1.03-1.36)	$1.7 \times 10^{-02}$
22q13.31	rs28512361	22	46283297	G/A	0.11	1.01 (0.90-1.13)	9.2x10 <sup>-01</sup>

\*Michailidou, K. et al. Identification of more than 70 new breast cancer susceptibility loci for breast cancer and definitic <sup>†</sup>Results for 2p23.3-rs6725517, 6q23.1-rs6569648 and 8q24.13-rs58847541 are not reported because they represent the Chr, chromosome; MAF, minor allele frequency; BCAC, Breast Cancer Association Consortium; CIMBA, Consortium of Inv <sup>¥</sup>21 base-pair deletion; <sup>‡</sup>36 base-pair deletion

BCAC results were based on GWAS data for 4,480 cases and 12,632 controls, iCOGS data for 7,333 cases and 42,468 con CIMBA results were based on data for 18,908 *BRCA1* mutation carriers (9,414 with breast cancer)

Associations observed with ER-negative breast cancer based on P<0.05 in meta-analysis of all BCAC data Associations observed with breast cancer for *BRCA1* mutation carriers based on P<0.05 in meta-analysis of

ER-negative breast	cancer (BCAC	2)			BRCA1 mutation
iCOGS		OncoArr	ау	Combined	All CIMBA data co
OR (95%CI)	P-value	OR (95%CI)	P -value	P -value	HR (95%CI)
1.01 (0.97-1.06)	$4.8 \times 10^{-01}$	1.03 (1.00-1.07)	$4.2 \times 10^{-02}$	1.1x10 <sup>-01</sup>	1.01 (0.97-1.04)
0.95 (0.91-1.00)	4.7x10 <sup>-02</sup>	0.97 (0.94-1.00)	6.6x10 <sup>-02</sup>	$4.4 \times 10^{-03}$	0.95 (0.92-0.99)
0.92 (0.83-1.03)	1.4x10 <sup>-01</sup>	0.89 (0.98-1.07)	6.2x10 <sup>-01</sup>	1.4x10 <sup>-01</sup>	0.96 (0.87-1.06)
1.00 (0.96-1.04)	8.8x10 <sup>-01</sup>	1.01 (0.98-1.04)	$5.4 \times 10^{-01}$	5.7x10 <sup>-01</sup>	0.99 (0.95-1.03)
0.98 (0.94-1.02)	3.1x10 <sup>-01</sup>	0.96 (0.93-0.99)	2.3x10 <sup>-02</sup>	2.9x10 <sup>-03</sup>	1.03 (0.99-1.06)
1.00 (0.95-1.05)	9.6x10 <sup>-01</sup>	1.04 (0.99-1.08)	$1.2 \times 10^{-01}$	3.4x10 <sup>-01</sup>	1.04 (0.99-1.09)
1.07 (1.02-1.11)	$4.0 \times 10^{-03}$	1.05 (1.02-1.09)	$5.8 \times 10^{-03}$	$4.8 \times 10^{-05}$	1.03 (0.99-1.08)
0.97 (0.94-1.01)	1.6x10 <sup>-01</sup>	1.03 (1.00-1.07)	5.7x10 <sup>-02</sup>	$4.2 \times 10^{-01}$	0.99 (0.96-1.03)
1.05 (0.96-1.14)	3.0x10 <sup>-01</sup>	1.15 (1.08-1.23)	3.2x10 <sup>-05</sup>	3.3x10 <sup>-04</sup>	1.02 (0.94-1.10)
1.03 (0.98-1.08)	1.9x10 <sup>-01</sup>	0.98 (0.95-1.02)	$3.9 \times 10^{-01}$	3.7x10 <sup>-01</sup>	0.94 (0.90-0.98)
1.02 (0.96-1.09)	5.1x10 <sup>-01</sup>	1.06 (1.01-1.12)	$1.8 \times 10^{-02}$	$7.4 \times 10^{-03}$	0.99 (0.94-1.05)
1.04 (0.96-1.13)	3.0x10 <sup>-01</sup>	1.05 (0.99-1.12)	$1.2 \times 10^{-01}$	$3.2 \times 10^{-02}$	1.01 (0.94-1.09)
1.01 (0.96-1.05)	8.1x10 <sup>-01</sup>	1.00 (0.96-1.04)	$9.8 \times 10^{-01}$	4.3x10 <sup>-01</sup>	0.96 (0.92-1.01)
0.94 (0.90-0.97)	8.9x10 <sup>-04</sup>	1.00 (0.97-1.03)	8.6x10 <sup>-01</sup>	$9.9 \times 10^{-03}$	0.97 (0.93-1.00)
0.95 (0.89-1.01)	1.2x10 <sup>-01</sup>	0.96 (0.91-1.02)	$1.8 \times 10^{-01}$	$2.4 \times 10^{-02}$	0.96 (0.90-1.02)
1.01 (0.97-1.06)	6.2x10 <sup>-01</sup>	1.01 (0.98-1.05)	$5.1 \times 10^{-01}$	$2.5 \times 10^{-01}$	1.00 (0.96-1.04)
1.01 (0.97-1.05)	6.6x10 <sup>-01</sup>	1.03 (1.00-1.07)	5.5x10 <sup>-02</sup>	$1.1 \times 10^{-01}$	1.03 (0.99-1.07)
0.99 (0.94-1.03)	5.3x10 <sup>-01</sup>	1.00 (0.96-1.04)	9.5x10 <sup>-01</sup>	8.5x10 <sup>-01</sup>	0.98 (0.94-1.03)
1.01 (0.97-1.06)	5.3x10 <sup>-01</sup>	1.06 (1.02-1.10)	2.9x10 <sup>-03</sup>	$4.9 \times 10^{-03}$	0.99 (0.95-1.03)
1.08 (1.04-1.13)	3.9x10 <sup>-05</sup>	1.03 (1.00-1.06)	7.9x10 <sup>-02</sup>	2.9x10 <sup>-05</sup>	0.99 (0.96-1.03)
1.04 (1.00-1.08)	5.3x10 <sup>-02</sup>	1.01 (0.98-1.05)	$4.2 \times 10^{-01}$	$2.3 \times 10^{-02}$	0.98 (0.94-1.01)
0.92 (0.87-0.98)	6.9x10 <sup>-03</sup>	0.94 (0.90-0.99)	$1.4 \times 10^{-02}$	1.3x10 <sup>-05</sup>	1.03 (0.97-1.09)
1.15 (1.06-1.25)	$5.8 \times 10^{-04}$	1.03 (0.96-1.11)	$3.5 \times 10^{-01}$	$5.2 \times 10^{-04}$	1.01 (0.93-1.09)
0.91 (0.84-0.99)	$2.1 \times 10^{-02}$	0.99 (0.94-1.04)	6.5x10 <sup>-01</sup>	5.2x10 <sup>-02</sup>	0.99 (0.93-1.05)
0.97 (0.93-1.02)	$2.0 \times 10^{-01}$	0.96 (0.93-1.00)	$4.4 \times 10^{-02}$	$1.5 \times 10^{-02}$	1.00 (0.96-1.04)
0.98 (0.94-1.02)	$3.0 \times 10^{-01}$	0.98 (0.94-1.01)	1.7x10 <sup>-01</sup>	7.9x10 <sup>-03</sup>	0.99 (0.95-1.03)
1.01 (0.96-1.06)	6.6x10 <sup>-01</sup>	0.95 (0.92-0.99)	8.4x10 <sup>-03</sup>	1.2x10 <sup>-01</sup>	0.97 (0.93-1.01)
1.03 (0.99-1.07)	$2.1 \times 10^{-01}$	1.02 (0.99-1.05)	2.8x10 <sup>-01</sup>	5.9x10 <sup>-02</sup>	0.98 (0.95-1.02)
0.99 (0.95-1.04)	$8.3 \times 10^{-01}$	0.97 (0.94-1.00)	$5.4 \times 10^{-02}$	$3.5 \times 10^{-02}$	0.98 (0.94-1.02)
1.00 (0.96-1.04)	8.9x10 <sup>-01</sup>	1.02 (0.99-1.05)	2.4x10 <sup>-01</sup>	2.1x10 <sup>-01</sup>	0.98 (0.95-1.02)
0.98 (0.91-1.06)	$6.2 \times 10^{-01}$	0.91 (0.84-0.98)	$1.0 \times 10^{-02}$	1.7x10 <sup>-02</sup>	1.07 (0.99-1.16)
0.97 (0.94-1.01)	$1.5 \times 10^{-01}$	0.96 (0.93-0.99)	$1.8 \times 10^{-02}$	$6.1 \times 10^{-04}$	0.95 (0.92-0.98)
0.96 (0.92-0.99)	$2.7 \times 10^{-02}$	0.96 (0.93-0.99)	$2.0 \times 10^{-02}$	8.3x10 <sup>-03</sup>	1.02 (0.98-1.06)
1.07 (1.01-1.13)	$2.5 \times 10^{-02}$	1.05 (1.00-1.10)	$5.8 \times 10^{-02}$	3.3x10 <sup>-04</sup>	1.01 (0.95-1.07)
1.02 (0.98-1.06)	3.9x10 <sup>-01</sup>	1.02 (0.98-1.05)	$4.0 \times 10^{-01}$	1.0x10 <sup>-01</sup>	1.02 (0.98-1.07)
0.96 (0.90-1.02)	2.0x10 <sup>-01</sup>	0.95 (0.90-1.00)	3.5x10 <sup>-02</sup>	1.7x10 <sup>-02</sup>	0.99 (0.93-1.05)
1.00 (0.97-1.05)	8.2x10 <sup>-01</sup>	1.01 (0.98-1.05)	$4.2 \times 10^{-01}$	1.8x10 <sup>-01</sup>	1.02 (0.98-1.06)
0.95 (0.89-1.03)	$2.0 \times 10^{-01}$	0.98 (0.93-1.03)	$4.4 \times 10^{-01}$	1.3x10 <sup>-01</sup>	0.98 (0.92-1.05)
0.96 (0.92-1.00)	3.1x10 <sup>-02</sup>	0.93 (0.90-0.96)	7.8x10 <sup>-06</sup>	1.4x10 <sup>-05</sup>	0.95 (0.92-0.99)
1.04 (1.00-1.08)	$2.8 \times 10^{-02}$	1.05 (1.02-1.08)	$3.0 \times 10^{-03}$	$1.4 \times 10^{-05}$	1.01 (0.97-1.05)
1.01 (0.96-1.06)	$7.2 \times 10^{-01}$	1.05 (1.01-1.09)	$1.3 \times 10^{-02}$	8.0x10 <sup>-03</sup>	1.02 (0.98-1.07)
1.03 (0.97-1.09)	3.0x10 <sup>-01</sup>	1.08 (1.03-1.14)	8.7x10 <sup>-04</sup>	8.4x10 <sup>-04</sup>	0.96 (0.90-1.01)
1.03 (0.98-1.09)	$2.3 \times 10^{-01}$	1.04 (0.99-1.08)	$9.7 \times 10^{-02}$	$4.0 \times 10^{-02}$	1.00 (0.95-1.05)
0.95 (0.92-0.99)	$1.4 \times 10^{-02}$	0.94 (0.91-0.97)	3.8x10 <sup>-∪4</sup>	9.9x10 <sup>-06</sup>	0.97 (0.94-1.01)

ciations with risk of ER-negative breast cancer and breast cancer for BRCA1 mutation carriers

0.96 (0.92-1.01)	$9.2 \times 10^{-02}$	0.93 (0.90-0.96)	6.1x10 <sup>-05</sup>	1.1x10 <sup>-04</sup>	1.02 (0.98-1.06)
1.06 (1.00-1.12)	$5.1 \times 10^{-02}$	1.04 (1.00-1.09)	$5.4 \times 10^{-02}$	2.5x10 <sup>-03</sup>	1.06 (1.00-1.11)
1.03 (0.99-1.07)	$9.4 \times 10^{-02}$	1.03 (1.00-1.06)	$6.8 \times 10^{-02}$	1.5x10 <sup>-02</sup>	1.00 (0.97-1.04)
1.01 (0.98-1.05)	4.8x10 <sup>-01</sup>	1.05 (1.01-1.08)	$4.1 \times 10^{-03}$	1.1x10 <sup>-03</sup>	0.97 (0.94-1.01)
1.02 (0.98-1.06)	3.1x10 <sup>-01</sup>	1.02 (0.99-1.06)	1.9x10 <sup>-01</sup>	5.5x10 <sup>-02</sup>	0.98 (0.94-1.02)
0.98 (0.94-1.02)	$3.8 \times 10^{-01}$	0.96 (0.92-0.99)	$1.9 \times 10^{-02}$	1.7x10 <sup>-03</sup>	0.97 (0.93-1.01)
1.03 (0.85-1.25)	$7.5 \times 10^{-01}$	1.13 (0.98-1.30)	$9.0 \times 10^{-02}$	2.0x10 <sup>-01</sup>	1.06 (0.87-1.27)
0.96 (0.91-1.02)	$1.6 \times 10^{-01}$	0.95 (0.91-0.99)	$1.3 \times 10^{-02}$	1.7x10 <sup>-03</sup>	0.99 (0.94-1.04)
0.92 (0.83-1.01)	$8.9 \times 10^{-02}$	0.84 (0.77-0.91)	2.7x10 <sup>-05</sup>	5.0x10 <sup>-06</sup>	0.89 (0.81-0.98)
1.05 (0.94-1.17)	$4.2 \times 10^{-01}$	1.09 (1.02-1.17)	$1.4 \times 10^{-02}$	6.2x10 <sup>-03</sup>	1.02 (0.94-1.12)
0.98 (0.93-1.02)	$2.8 \times 10^{-01}$	1.00 (0.96-1.04)	$8.7 \times 10^{-01}$	3.3x10 <sup>-01</sup>	1.00 (0.95-1.04)
1.05 (1.01-1.09)	9.3x10 <sup>-03</sup>	1.05 (1.02-1.09)	$2.2 \times 10^{-03}$	2.3x10 <sup>-05</sup>	1.02 (0.98-1.05)
1.03 (0.98-1.09)	3.0x10 <sup>-01</sup>	1.03 (0.99-1.07)	$1.0 \times 10^{-01}$	2.3x10 <sup>-02</sup>	0.99 (0.95-1.04)
1.08 (1.00-1.17)	$3.7 \times 10^{-02}$	1.10 (1.04-1.18)	$2.2 \times 10^{-03}$	1.7x10 <sup>-05</sup>	0.98 (0.91-1.05)
1.00 (0.95-1.05)	$9.2 \times 10^{-01}$	1.08 (1.03-1.12)	$4.5 \times 10^{-04}$	2.9x10 <sup>-03</sup>	0.98 (0.94-1.03)
0.98 (0.95-1.02)	3.7x10 <sup>-01</sup>	0.99 (0.96-1.02)	5.7x10 <sup>-01</sup>	1.9x10 <sup>-01</sup>	1.03 (0.99-1.06)
1.10 (1.01-1.19)	$2.5 \times 10^{-02}$	1.10 (1.03-1.18)	2.8x10 <sup>-03</sup>	1.2x10 <sup>-05</sup>	1.04 (0.96-1.12)
1.12 (1.05-1.21)	1.3x10 <sup>-03</sup>	1.09 (1.04-1.14)	8.3x10 <sup>-04</sup>	1.5x10 <sup>-05</sup>	1.04 (0.98-1.10)

on of risk-associated genomic features, Reference 1 in the main text

e same signals as those reported for these regions for ER-negative disease

vestigators of Modifiers of BRCA1/2; <sup>\*</sup>More common allele listed first, minor allele second

trols and OncoArray data 9,655 cases and 45,494 controls

all CIMBA data

carriers								
mbined								
P-value								
7.5x10 <sup>-01</sup>								
$1.5 \times 10^{-02}$								
$4.4 \times 10^{-01}$								
$6.9 \times 10^{-01}$								
1.8x10 <sup>-01</sup>								
$1.6 \times 10^{-01}$								
$1.6 \times 10^{-01}$								
$7.0 \times 10^{-01}$								
$7.0 \times 10^{-01}$								
$4.6 \times 10^{-03}$								
8.0x10 <sup>-01</sup>								
$7.9 \times 10^{-01}$								
$1.1 \times 10^{-01}$								
7.8x10 <sup>-02</sup>								
$1.7 \times 10^{-01}$								
9.9x10 <sup>°1</sup>								
1.5x10 <sup>-01</sup>								
$4.1 \times 10^{-01}$								
$7.5 \times 10^{-01}$								
$7.7 \times 10^{-01}$								
$2.0 \times 10^{-01}$								
$2.9 \times 10^{-01}$								
8.9x10 <sup>°°</sup>								
$6.4 \times 10^{-01}$								
$9.7 \times 10^{-01}$								
$4.8 \times 10^{-01}$								
$1.7 \times 10^{-01}$								
$3.9 \times 10^{-01}$								
$3.3 \times 10^{-01}$								
$4.0 \times 10^{-02}$								
$8.4 \times 10^{-03}$								
$5.4 \times 10^{-01}$								
2.0000								
$7.70^{-01}$								
2.0010								
7.3710 1.2v10 <sup>-01</sup>								
4.210								
8 0v10 <sup>-03</sup>								
$6.1 \times 10^{-01}$								
3.0v10 <sup>-01</sup>								
$1.0 \times 10^{-01}$								
9 3x10 <sup>-01</sup>								
$1.4 \times 10^{-01}$								
···								

3.4x10 <sup>-01</sup>
$3.8 \times 10^{-02}$
9.3x10 <sup>-01</sup>
1.7x10 <sup>-01</sup>
2.8x10 <sup>-01</sup>
1.6x10 <sup>-01</sup>
5.7x10 <sup>-01</sup>
6.7x10 <sup>-01</sup>
$1.5 \times 10^{-02}$
5.9x10 <sup>-01</sup>
8.4x10 <sup>-01</sup>
$4.2 \times 10^{-01}$
7.3x10 <sup>-01</sup>
6.2x10 <sup>-01</sup>
4.5x10 <sup>-01</sup>
$1.8 \times 10^{-01}$
3.2x10 <sup>-01</sup>
1.9x10 <sup>-01</sup>

Suppleme	Supplementary Table 10: Other previously reported (non ER-negative disease-specific) breast cancer suceptibility loci: associations with risk of ER-negative breast cancer * and breast cancer for BRCA1 mutation carr													
Location	SNP	Reference	Chr	Position	Alleles	MAF	GWAS		ER-negative breas iCOGS	st cancer (BCA S	AC) OncoArr	ay	Combined	BRCA1 mutation All CIMBA data co
							OR (95%CI)	P-value	OR (95%CI)	P-value	OR (95%CI)	P-value	P-value	HR (95%CI)
1p36.22	rs616488	[1]	1	10566215	A/G	0.33	0.91 (0.86-0.96)	7.3x10 <sup>-04</sup>	0.91 (0.87-0.95)	3.9x10 <sup>-06</sup>	0.89 (0.86-0.92)	4.8x10 <sup>-11</sup>	4.1x10 <sup>-18</sup>	0.96 (0.92-1.00)
1p13.2 1p11 2	rs11552449 rs11249433	[1]	1	114448389	C/T A/G	0.17	1.10 (1.02-1.18)	9.4x10 <sup>-0</sup> 7.8x10 <sup>-01</sup>	1.04 (0.99-1.10)	8.3x10 <sup></sup> 9.4x10 <sup>-01</sup>	1.04 (1.00-1.08)	7.3x10 <sup>-01</sup>	8.4x10 <sup>-01</sup>	1.02 (0.97-1.07)
1q21.1	rs12405132	[3]	1	145644984	с/т	0.37	0.95 (0.90-1.01)	1.1x10 <sup>-01</sup>	0.98 (0.95-1.02)	3.9x10 <sup>-01</sup>	1.00 (0.96-1.03)	7.8x10 <sup>-01</sup>	1.8x10 <sup>-01</sup>	0.99 (0.96-1.03)
1q21.2	rs12048493	[3]	1	149927034	A/C	0.38	1.03 (0.96-1.11)	3.5x10 <sup>-01</sup>	1.02 (0.98-1.07)	2.5x10 <sup>-01</sup>	1.05 (1.02-1.09)	2.3x10 <sup>-03</sup>	1.3x10 <sup>-03</sup>	1.03 (1.00-1.07)
1q32.1	rs4951011	[4]	1	203766331	A/G	0.16	1.03 (0.96-1.11)	4.0x10 <sup>-01</sup>	1.03 (0.98-1.09)	2.8x10 <sup>-01</sup>	1.07 (1.02-1.11)	2.8x10 <sup>-03</sup>	1.9x10 <sup>-03</sup>	1.04 (0.99-1.09)
2014.1	rs4849887	[3]	2	242034263	A/G C/T	0.03	0.93 (0.70-1.23)	6.1X10 6.7x10 <sup>-01</sup>	1.20 (1.08-1.33)	4.4X10 2.2x10 <sup>-03</sup>	1.09 (1.00-1.19)	5.6X10 1.7x10 <sup>-08</sup>	3.9X10 4.1x10 <sup>-09</sup>	1.13 (1.02-1.25)
2q31.1	rs2016394	[1]	2	172972971	G/A	0.10	1.06 (1.00-1.11)	3.9x10 <sup>-02</sup>	1.00 (0.96-1.03)	8.2x10 <sup>-01</sup>	1.00 (0.97-1.03)	9.8x10 <sup>-01</sup>	4.5x10 <sup>-01</sup>	1.03 (0.99-1.07)
2q31.1	rs1550623	[1]	2	174212894	A/G	0.15	0.99 (0.92-1.06)	7.6x10 <sup>-01</sup>	0.95 (0.91-1.01)	7.8x10 <sup>-02</sup>	1.00 (0.95-1.04)	8.5x10 <sup>-01</sup>	2.0x10 <sup>-01</sup>	0.99 (0.94-1.04)
2q33.1	rs1830298	[5],[6]	2	202181247	T/C	0.28	1.09 (1.03-1.16)	3.3x10 <sup>-03</sup>	1.03 (0.99-1.07)	1.5x10 <sup>-01</sup>	1.08 (1.04-1.12)	3.0x10 <sup>-05</sup>	7.4x10 <sup>-07</sup>	1.08 (1.04-1.13)
2q35 2q35	rs44005590	[7]	2	217963060	C/A G/T	0.05	0.86 (0.72-1.02)	7.9X10 8.9x10 <sup>-02</sup>	0.93 (0.85-1.02)	9.6x10 <sup>-03</sup>	0.98 (0.91-1.05)	5.4X10 4.9x10 <sup>-04</sup>	3.4x10 <sup>-06</sup>	0.99 (0.91-1.08)
2q35	rs16857609	[0],[5]	2	218296508	C/T	0.26	1.07 (1.01-1.14)	2.6x10 <sup>-02</sup>	1.09 (1.04-1.13)	1.0x10 <sup>-04</sup>	1.07 (1.03-1.10)	5.2x10 <sup>-04</sup>	1.8x10 <sup>-08</sup>	1.04 (1.00-1.09)
3p26.1	rs6762644	[1]	3	4742276	A/G	0.38	0.97 (0.92-1.03)	3.0x10 <sup>-01</sup>	1.02 (0.98-1.06)	2.8x10 <sup>-01</sup>	1.04 (1.01-1.08)	1.2x10 <sup>-02</sup>	5.3x10 <sup>-02</sup>	1.03 (0.99-1.07)
3p24.1	rs4973768	[10]	3	27416013	C/T	0.47	1.03 (0.98-1.08)	3.0x10 <sup>-01</sup>	1.05 (1.01-1.09)	9.0x10 <sup>-03</sup>	1.04 (1.01-1.07)	1.4x10 <sup>-02</sup>	2.4x10 <sup>-04</sup>	1.01 (0.98-1.05)
3p.24.1 3n21 31	rs12493607	[1]	3	30682939	G/C	0.34	0.99 (0.93-1.04)	6.1x10 <sup></sup> 3.9x10 <sup>-01</sup>	1.02 (0.98-1.06)	3./x10 <sup></sup> 1.0x10 <sup>-01</sup>	1.00 (0.96-1.03)	7.9x10 <sup>-03</sup>	9.0x10 <sup>-04</sup>	1.00 (0.96-1.04)
3p14.1	rs1053338	[11]	3	63967900	A/G	0.10	1.01 (0.93-1.09)	8.3x10 <sup>-01</sup>	1.06 (1.00-1.12)	3.7x10 <sup>-02</sup>	1.03 (0.99-1.08)	1.8x10 <sup>-01</sup>	2.5x10 <sup>-02</sup>	1.00 (0.95-1.05)
4q24	rs9790517	[1]	4	106084778	C/T	0.23	1.09 (1.02-1.16)	8.3x10 <sup>-03</sup>	1.03 (0.98-1.07)	2.8x10 <sup>-01</sup>	0.98 (0.94-1.02)	2.3x10 <sup>-01</sup>	3.5x10 <sup>-01</sup>	1.01 (0.96-1.05)
4q34.1	rs6828523	[1]	4	175846426	C/A	0.12	0.94 (0.87-1.02)	1.6x10 <sup>-01</sup>	1.02 (0.96-1.08)	4.8x10 <sup>-01</sup>	1.00 (0.95-1.05)	9.3x10 <sup>-01</sup>	9.3x10 <sup>-01</sup>	1.04 (0.98-1.10)
5p15.33	rs3215401	[12]	5	1296255	A/AG	0.31	0.89 (0.81-0.98)	1.7x10 <sup>-02</sup>	0.89 (0.85-0.92)	8.4x10 <sup>-03</sup>	0.88 (0.85-0.91)	2.3x10 <sup>-12</sup>	6.4x10 <sup>-21</sup>	0.90 (0.87-0.94)
5p15.1 5p13.3	rs2012709	[3]	5	32567732	C/T	0.45	1.00 (0.95-1.00)	9.2x10 <sup>-01</sup>	1.03 (0.93-1.00)	9.8x10	0.98 (0.95-1.01)	2.1x10 1.5x10 <sup>-01</sup>	9.9x10 <sup>-01</sup>	1.00 (0.96-1.03)
5p12	rs10941679	[13]	5	44706498	A/G	0.25	1.04 (0.98-1.11)	1.9x10 <sup>-01</sup>	1.03 (0.99-1.08)	1.5x10 <sup>-01</sup>	1.03 (1.00-1.07)	8.5x10 <sup>-02</sup>	9.4x10 <sup>-03</sup>	1.01 (0.96-1.05)
5q11.2	rs62355902	[14],[15]	5	56053723	A/T	0.16	1.06 (0.99-1.14)	1.0x10 <sup>-01</sup>	1.10 (1.05-1.15)	2.3x10 <sup>-04</sup>	1.06 (1.02-1.11)	6.7x10 <sup>-03</sup>	2.1x10 <sup>-06</sup>	1.02 (0.97-1.07)
5q11.2	rs10472076	[1]	5	58184061	T/C	0.38	1.04 (0.99-1.10)	1.3x10 <sup>-01</sup>	1.06 (1.02-1.10)	4.6x10 <sup>-03</sup>	1.03 (1.00-1.07)	4.0x10 <sup>-02</sup>	2.0x10 <sup>-04</sup>	1.02 (0.98-1.05)
5q11.2	rs1353747	[1]	5	58337481	T/G	0.09	0.97 (0.88-1.06)	4.8x10 <sup></sup>	0.92 (0.86-0.98)	8.4x10 <sup>-01</sup>	0.98 (0.92-1.03)	3.8x10 <sup>-02</sup>	1.5x10 <sup>-02</sup>	0.97 (0.91-1.04)
5q14.2	rs10474352	[4]	5	90732225	C/T	0.16	0.96 (0.90-1.04)	3.4x10 <sup>-01</sup>	1.00 (0.94-1.06)	9.8x10 <sup>-01</sup>	0.98 (0.94-1.03)	4.1x10 <sup>-01</sup>	3.1x10 <sup>-01</sup>	0.99 (0.94-1.04)
5q33.3	rs1432679	[1]	5	158244083	T/C	0.43	1.05 (1.00-1.11)	6.3x10 <sup>-02</sup>	1.08 (1.04-1.13)	2.4x10 <sup>-05</sup>	1.08 (1.04-1.11)	4.0x10 <sup>-06</sup>	1.1x10 <sup>-10</sup>	1.04 (1.01-1.08)
6p25.3	rs11242675	[1]	6	1318878	T/C	0.37	0.93 (0.88-0.98)	6.8x10 <sup>-03</sup>	0.96 (0.92-0.99)	2.2x10 <sup>-02</sup>	0.99 (0.96-1.02)	5.1x10 <sup>-01</sup>	3.3x10 <sup>-03</sup>	0.96 (0.93-1.00)
6p24.3	rs9348512	[16]	6	10456706	C/A	0.33	1.02 (0.96-1.08)	5.3x10 <sup>-01</sup>	0.99 (0.95-1.03)	6.7x10 <sup>-01</sup>	1.01 (0.98-1.05)	5.1x10 <sup>-01</sup>	6.5x10 <sup>-01</sup>	1.01 (0.97-1.05)
6p23	rs9257408	[1]	6	28926220	A/G	0.44	1.08 (1.03-1.14)	3.5X10 2.0x10 <sup>-02</sup>	1.01 (0.97-1.04)	7.4x10 1.4x10 <sup>-02</sup>	1.00 (0.97-1.03)	5.9x10	2.0x10 <sup>-04</sup>	1.01 (0.97-1.05)
6q14.1	rs17529111	[17]	6	82128386	T/C	0.22	1.12 (1.05-1.19)	5.3x10 <sup>-04</sup>	1.05 (1.00-1.09)	4.7x10 <sup>-02</sup>	1.06 (1.02-1.10)	1.5x10 <sup>-03</sup>	1.6x10 <sup>-06</sup>	1.01 (0.96-1.05)
6q25.1	rs9485372	[18]	6	149608874	G/A	0.19	1.02 (0.95-1.09)	5.9x10 <sup>-01</sup>	0.95 (0.91-1.00)	6.4x10 <sup>-02</sup>	0.99 (0.95-1.03)	5.1x10 <sup>-01</sup>	1.9x10 <sup>-01</sup>	1.00 (0.95-1.04)
6q25	rs9397437	[19],[20]	6	151952332	G/A	0.07	1.35 (1.22-1.49)	7.4x10 <sup>-09</sup>	1.29 (1.20-1.38)	6.5x10 <sup>-13</sup>	1.32 (1.25-1.40)	8.3x10 <sup>-22</sup>	2.8x10 <sup>-40</sup>	1.20 (1.12-1.28)
7q21.2	rs6964587	[11]	7	91630620	G/T	0.39	1.02 (0.96-1.07)	5.5x10 <sup>-02</sup>	1.04 (1.00-1.08)	6.0x10 <sup>-01</sup>	1.02 (0.98-1.05)	3.5x10 <sup>-02</sup>	4.5x10 <sup>-02</sup>	1.00 (0.97-1.04)
7q32.5	rs11977670	[3]	7	139942304	G/A	0.55	1.03 (0.97-1.19)	$3.4 \times 10^{-01}$	0.98 (0.95-1.03)	5.9x10 <sup>-01</sup>	1.02 (0.99-1.05)	5.5x10 <sup>-01</sup>	2.1x10 <sup>-01</sup>	1.06 (1.02-1.10)
7q35	rs720475	[1]	7	144074929	G/A	0.25	1.04 (0.97-1.11)	2.8x10 <sup>-01</sup>	0.99 (0.95-1.03)	6.9x10 <sup>-01</sup>	1.00 (0.96-1.03)	8.0x10 <sup>-01</sup>	9.8x10 <sup>-01</sup>	0.98 (0.94-1.02)
8p12	rs9693444	[1]	8	29509616	C/A	0.32	1.02 (0.96-1.08)	5.4x10 <sup>-01</sup>	1.09 (1.04-1.13)	4.7x10 <sup>-05</sup>	1.02 (0.98-1.05)	2.9x10 <sup>-01</sup>	6.4x10 <sup>-04</sup>	1.00 (0.96-1.04)
8p11.23	rs13365225	[3]	8	36858483	A/G	0.18	0.89 (0.83-0.96)	1.7x10 <sup>-03</sup>	0.93 (0.88-0.98)	3.5x10 <sup>-03</sup>	0.90 (0.86-0.94)	1.1x10 <sup>-00</sup>	1.4x10 <sup>-10</sup>	0.95 (0.91-1.00)
8q21.11 8q21.11	rs2943559	[1]	8	76230301	A/G	0.17	1 17 (1 06-1 29)	2.0x10 <sup>-03</sup>	0.94 (0.89-0.99)	1.3X10 5 5x10 <sup>-02</sup>	0.96 (0.92-1.00)	$1.2 \times 10^{-03}$	3.7X10 3.1x10 <sup>-06</sup>	1.07 (1.00-1.14)
8q23.3	rs13267382	[3]	8	117209548	G/A	0.36	1.05 (1.00-1.12)	7.3x10 <sup>-02</sup>	1.06 (1.02-1.10)	4.8x10 <sup>-03</sup>	1.02 (0.98-1.05)	3.0x10 <sup>-01</sup>	1.8x10 <sup>-03</sup>	0.97 (0.94-1.01)
8q24.21	rs13281615	[14]	8	128355618	A/G	0.41	1.07 (1.01-1.13)	1.9x10 <sup>-02</sup>	1.03 (0.99-1.07)	2.0x10 <sup>-01</sup>	1.07 (1.03-1.10)	9.5x10 <sup>-05</sup>	8.8x10 <sup>-06</sup>	1.03 (0.99-1.07)
8q24.21	rs11780156	[1]	8	129194641	C/T	0.17	1.04 (0.97-1.11)	2.9x10 <sup>-01</sup>	1.06 (1.00-1.11)	3.2x10 <sup>-02</sup>	1.05 (1.01-1.10)	1.8x10 <sup>-02</sup>	8.5x10 <sup>-04</sup>	0.95 (0.91-0.99)
9p21.3	rs1011970	[21]	9	22062134	G/I C/A	0.16	1.09 (1.02-1.17)	1.5x10 <sup>-03</sup>	1.11 (1.06-1.17)	1.4x10 <sup>-01</sup>	1.05 (1.00-1.09)	3./x10 <sup>-01</sup>	4./x10 <sup>-02</sup>	1.05 (1.00-1.10)
9q31.2 9q31.2	rs676256	[22].[23]	9	110300113	T/C	0.23	0.98 (0.93-1.04)	5.1x10 <sup>-01</sup>	0.98 (0.94-1.01)	2.3x10 <sup>-01</sup>	0.98 (0.94-1.01)	1.5x10 <sup>-01</sup>	4.6x10 <sup>-02</sup>	0.99 (0.95-1.02)
9q31.2	rs10816625	[23]	9	110837073	A/G	0.06	1.13 (0.99-1.29)	6.7x10 <sup>-02</sup>	1.05 (0.97-1.13)	2.3x10 <sup>-01</sup>	1.07 (1.01-1.14)	2.8x10 <sup>-02</sup>	3.2x10 <sup>-03</sup>	0.99 (0.92-1.07)
9q31.2	rs13294895	[23]	9	110837176	C/T	0.18	1.00 (0.93-1.08)	9.9x10 <sup>-01</sup>	1.04 (0.99-1.09)	1.3x10 <sup>-01</sup>	0.99 (0.95-1.04)	7.5x10 <sup>-01</sup>	4.9x10 <sup>-01</sup>	1.03 (0.98-1.08)
10p15.1	rs2380205	[21]	10	5886734	C/T	0.44	0.98 (0.93-1.04)	5.6x10 <sup>-01</sup>	1.01 (0.97-1.05)	7.2x10 <sup>-01</sup>	0.97 (0.94-1.00)	8.6x10 <sup>-02</sup>	2.2x10 <sup>-01</sup>	1.02 (0.99-1.06)
10p12.31	rs11814448	[1]	10	22032942	A/C	0.29	1.29 (1.02-1.63)	3.4x10 <sup>-02</sup>	1.20 (1.06-1.37)	4.0x10 <sup>-03</sup>	1.04 (0.95-1.02)	4.5x10 <sup>-01</sup>	$2.7 \times 10^{-03}$	1.13 (1.00-1.28)
10q21.2	rs10995201	[21],[24]	10	64299890	A/G	0.16	0.92 (0.85-1.00)	4.2x10 <sup>-02</sup>	0.87 (0.82-0.91)	1.0x10 <sup>-07</sup>	0.93 (0.89-0.98)	3.0x10 <sup>-03</sup>	1.6x10 <sup>-09</sup>	0.98 (0.94-1.03)
10q22.3	rs704010	[21]	10	80841148	C/T	0.38	1.07 (1.01-1.13)	1.6x10 <sup>-02</sup>	1.03 (0.99-1.07)	9.7x10 <sup>-02</sup>	1.06 (1.03-1.09)	5.8x10 <sup>-04</sup>	1.3x10 <sup>-05</sup>	1.01 (0.97-1.05)
10q25.2	rs7904519	[1]	10	114773927	A/G	0.46	1.12 (1.06-1.18)	5.3x10 <sup>-05</sup>	1.04 (1.01-1.08)	2.1x10 <sup>-02</sup>	1.08 (1.04-1.11)	7.4x10 <sup>-00</sup>	8.2x10 <sup>-10</sup>	1.08 (1.04-1.12)
10q26.12	rs11199914	[1]	10	123093901	6/60	0.32	0.99 (0.93-1.04)	6.2x10 1.9x10 <sup>-01</sup>	1.02 (0.98-1.06)	4.0x10 <sup>-01</sup>	0.98 (0.95-1.02)	3.3x10 1.5x10 <sup>-04</sup>	7.1x10 1.4x10 <sup>-04</sup>	1.01 (0.97-1.05)
10q26.13	rs45631563	[25]	10	123349324	A/T	0.05	1.02 (0.89-1.17)	7.6x10 <sup>-01</sup>	1.06 (0.97-1.15)	2.2x10 <sup>-01</sup>	0.93 (0.86-1.00)	5.2x10 <sup>-02</sup>	6.2x10 <sup>-01</sup>	1.04 (0.95-1.13)
10q26.13	rs2981578	[25]	10	123340311	T/C	0.47	1.04 (0.99-1.10)	1.1x10 <sup>-01</sup>	1.04 (1.00-1.08)	4.7x10 <sup>-02</sup>	1.04 (1.00-1.07)	2.5x10 <sup>-02</sup>	7.1x10 <sup>-04</sup>	1.00 (0.97-1.04)
11p15.5	rs3817198	[14]	11	1909006	T/C	0.32	1.07 (1.01-1.13)	2.5x10 <sup>-02</sup>	1.06 (1.02-1.11)	2.8x10 <sup>-03</sup>	1.02 (0.99-1.06)	2.0x10 <sup>-01</sup>	3.4x10 <sup>-04</sup>	1.06 (1.02-1.10)
11q13.1	rs3903072	[1]	11	65583066	G/T	0.47	0.93 (0.89-0.99)	1.2x10	0.97 (0.94-1.01)	1.7x10	0.99 (0.96-1.02)	5.6x10 <sup>-01</sup>	2.5x10 <sup>-01</sup>	0.99 (0.95-1.02)
11q13.3	rs75915166	[21],[20]	11	69379161	C/G C/A	0.15	- 1.04 (0.93-1.18)	- 4.8x10 <sup>-01</sup>	- 1.06 (0.98-1.14)	- 1.6x10 <sup>-01</sup>	0.98 (0.94-1.03)	4.6x10 7.6x10 <sup>-01</sup>	4.6x10 3.6x10 <sup>-01</sup>	1.02 (0.96-1.07)
11q24.3	rs11820646	[1]	11	129461171	C/T	0.40	0.92 (0.87-0.97)	1.6x10 <sup>-03</sup>	0.96 (0.92-1.00)	3.0x10 <sup>-02</sup>	0.94 (0.91-0.97)	2.0x10 <sup>-04</sup>	2.4x10 <sup>-07</sup>	0.94 (0.90-0.97)
12p13.1	rs12422552	[1]	12	14413931	G/C	0.26	1.12 (1.05-1.19)	3.4x10 <sup>-04</sup>	1.05 (1.00-1.09)	3.4x10 <sup>-02</sup>	1.04 (1.01-1.08)	1.8x10 <sup>-02</sup>	1.3x10 <sup>-05</sup>	1.00 (0.96-1.04)
12p11.22	rs7297051	[27],[28]	12	28174817	C/T	0.24	0.86 (0.81-0.92)	8.4x10 <sup>-06</sup>	0.87 (0.83-0.91)	1.3x10 <sup>-09</sup>	0.87 (0.84-0.91)	2.4x10 <sup>-12</sup>	8.5x10 <sup>-25</sup>	0.88 (0.85-0.92)
12q22 12q24 21	rs1292011	[1]	12	96027759	A/G	0.30	0.88 (0.83-0.93)	2.4X10 4.1x10 <sup>-01</sup>	0.95 (0.91-0.99)	1.0x10 4.2x10 <sup>-01</sup>	0.94 (0.91-0.97)	7.5X10 1.5x10 <sup>-01</sup>	2.3X10 6.8x10 <sup>-02</sup>	0.97 (0.93-1.00)
13q13.1	rs11571833	[1]	13	32972626	A/T	0.01	2.50 (0.92-6.79)	7.3x10 <sup>-02</sup>	1.48 (1.24-1.77)	1.6x10 <sup>-05</sup>	1.58 (1.35-1.84)	5.8x10 <sup>-09</sup>	1.5x10 <sup>-13</sup>	1.07 (0.88-1.30)
14q13.3	rs2236007	[1]	14	37132769	G/A	0.21	1.01 (0.94-1.08)	8.1x10 <sup>-01</sup>	0.96 (0.92-1.00)	7.8x10 <sup>-02</sup>	0.95 (0.91-0.99)	1.4x10 <sup>-02</sup>	8.0x10 <sup>-03</sup>	0.97 (0.93-1.01)
14q24.1	rs2588809	[1]	14	68660428	C/T	0.17	0.96 (0.89-1.05)	3.9x10 <sup>-01</sup>	1.01 (0.96-1.07)	6.1x10 <sup>-01</sup>	0.99 (0.95-1.03)	6.8x10 <sup>-01</sup>	7.6x10 <sup>-01</sup>	0.96 (0.92-1.01)
14q24.1	rs999737	[2]	14	69034682	C/T	0.23	0.91 (0.85-0.97)	3.4x10 <sup>-03</sup>	0.94 (0.90-0.98)	7.3x10 <sup>-03</sup>	0.92 (0.89-0.96)	7.2x10 <sup>-05</sup>	2.9x10 <sup>-06</sup>	0.96 (0.92-1.00)
14a32.12	rs11627032	[3]	14	93104072	T/C	0.55	0.92 (0.87-0.98)	1.1x10 <sup>-02</sup>	0.93 (0.89-0.97)	4.5x10	0.95 (0.92-0.99)	8.5x10 <sup>-03</sup>	2.4x10 <sup>-06</sup>	0.96 (0.92-1.00)
15q26.1	rs2290203	[4]	15	91512067	G/A	0.21	0.94 (0.88-1.01)	9.9x10 <sup>-02</sup>	0.94 (0.90-0.99)	1.2x10 <sup>-02</sup>	0.96 (0.92-1.00)	5.5x10 <sup>-02</sup>	4.7x10 <sup>-04</sup>	0.98 (0.93-1.02)
16q12.1	rs4784227	[14],[29]	16	52599188	C/T	0.24	1.12 (1.06-1.19)	2.3x10 <sup>-04</sup>	1.16 (1.11-1.21)	6.3x10 <sup>-12</sup>	1.14 (1.10-1.19)	2.8x10 <sup>-13</sup>	1.7x10 <sup>-26</sup>	1.05 (1.00-1.09)
16q12.2	rs17817449	[1]	16	53813367	T/G	0.41	0.97 (0.92-1.02)	2.5x10 <sup>-01</sup>	0.91 (0.87-0.94)	3.4x10 <sup>-07</sup>	0.93 (0.90-0.96)	3.0x10 <sup>-05</sup>	1.8x10 <sup>-10</sup>	0.94 (0.91-0.98)
16q23.2	r\$13329835 chr17.202205	[1]	16	29230520	A/G GGT/G	0.23	1.06 (0.99-1.13)	9.1x10 <sup>°°</sup> 8.1x10 <sup>-01</sup>	1.02 (0.98-1.07)	4.0x10 <sup>°°</sup> 1.3x10 <sup>°02</sup>	1.06 (1.02-1.10)	3./x10 <sup>00</sup> 7.9x10 <sup>03</sup>	1.4x10 <sup>-04</sup>	1.06 (1.01-1.10)
17q22	rs2787486	[10].[28]	17	53209774	A/C	0.30	0.96 (0.92-1.07)	1.8x10 <sup>-01</sup>	0.96 (0.92-1.00)	6.6x10 <sup>-02</sup>	0.96 (0.93-1.00)	3.9x10 <sup>-02</sup>	2.2x10 <sup>-03</sup>	1.01 (0.97-1.05)
17q25.3	rs745570	[3]	17	77781725	G/A	0.50	1.08 (1.03-1.14)	4.0x10 <sup>-03</sup>	1.05 (1.01-1.09)	8.4x10 <sup>-03</sup>	1.04 (1.01-1.07)	1.6x10 <sup>-02</sup>	1.0x10 <sup>-05</sup>	1.03 (1.00-1.07)
18q11.2	rs527616	[1]	18	24337424	G/C	0.38	0.93 (0.88-0.99)	1.5x10 <sup>-02</sup>	0.98 (0.94-1.02)	3.3x10 <sup>-01</sup>	1.00 (0.97-1.03)	9.7x10 <sup>-01</sup>	1.3x10 <sup>-01</sup>	0.99 (0.96-1.03)
18q11.2	rs1436904	[1]	18	24570667	T/G	0.40	0.98 (0.92-1.03)	3.7x10 <sup>-01</sup>	1.00 (0.97-1.04)	8.2x10 <sup>-01</sup>	0.99 (0.96-1.03)	7.1x10 <sup>-01</sup>	6.2x10 <sup>-01</sup>	0.99 (0.95-1.02)
18012.3 19p13.11	rs4808801	[3]	18	42399590	A/G	0.07	0.96 (0.86-1.07)	4.5X10 3.0x10 <sup>-01</sup>	0.97 (0.90-1.04)	2.8x10 <sup>-05</sup>	0.97 (0.91-1.03)	1.9x10 <sup>-02</sup>	5.7x10 <sup>-06</sup>	0.99 (0.92-1.06) 0.98 (0.94-1.02)
19q13.31	rs3760982	[1]	19	44286513	G/A	0.46	1.05 (1.00-1.11)	5.4x10 <sup>-02</sup>	1.04 (1.00-1.08)	3.8x10 <sup>-02</sup>	1.08 (1.05-1.12)	7.8x10 <sup>-07</sup>	5.3x10 <sup>-08</sup>	1.02 (0.99-1.06)
21q21.1	rs2823093	[27]	21	16520832	G/A	0.27	1.03 (0.97-1.09)	4.1x10 <sup>-01</sup>	0.97 (0.93-1.01)	1.3x10 <sup>-01</sup>	1.00 (0.96-1.04)	9.9x10 <sup>-01</sup>	5.9x10 <sup>-01</sup>	0.97 (0.93-1.01)
22q12.1	rs17879961	[1]	22	29121087	A/G	0.005	1.10 (0.73-1.66)	6.4x10 <sup>-01</sup>	1.01 (0.78-1.31)	9.3x10 <sup>-01</sup> 5.1×10 <sup>-02</sup>	0.86 (0.68-1.09)	2.2x10 <sup>-01</sup>	5.5x10 <sup>-01</sup>	0.78 (0.59-1.05)
22Y12.2	13137320	11	22	290214//	1/0	0.10	T'TT (0'AT-T'2A)	2.0710	1.10(1.00-1.21)	J.1VT0	T.01 (0.92-1.09)	0.3410	1.0710	0.32 (0.80-1.02)
22q13.1	chr22:39359355	[30]	22	39359355	I/D <sup>9</sup>	0.04	1.01 (0.90-1.13)	9.2x10 <sup>-01</sup>	1.12 (1.05-1.21)	1.3x10 <sup>-03</sup>	1.09 (1.04-1.14)	8.3x10 <sup>-04</sup>	1.5x10 <sup>-05</sup>	1.01 (0.94-1.08)
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22q13.1	rs6001930	[1]	22	40876234	T/C	0.10	1.15 (1.06-1.25)	1.3x10 <sup>-03</sup>	1.10 (1.04-1.17)	8.7x10 <sup>-04</sup>	1.14 (1.08-1.19)	6.8x10 <sup>-07</sup>	1.6x10 <sup>-11</sup>	1.06 (1.00-1.13)
*results for	ER-negative disease als	so reported	d in Mi	chailidou, K. e	t al. Identi	ification o	of more than 70 new br	east cancer sus	ceptibility loci for bre	east cancer and	definition of risk-associ	ated genomic fea	atures, Reference	e 1 in the main text
Chr, chrom	Chr, chromosome; MAF, minor allele frequency; BCAC, Breast Cancer Association Consortium; CIMBA, Consortium of Investigators of Modifiers of BRCA1/2; <sup>7</sup> More common allele listed first, minor allele second; <sup>§</sup> 31kb deletion													
BCAC resul	3CAC results were based on GWAS data for 4,480 cases and 12,632 controls, iCOGS data for 7,333 cases and 42,468 controls and OncoArray data 9,655 cases and 45,494 controls													

CIMBA results were based on data for 18,908 BRCA1 mutation carriers (9,414 with breast cancer)

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Associations observed with ER-negative breast cancer based on P<0.05 in meta-analysis of all BCAC data Associations observed with breast cancer for *BRCA1* mutation carriers based on P<0.05 in meta-analysis of all CIMBA data

# Supplementary Table 11: Associations of 179 breast cancer susceptibility loci with risk for BRCA2 mutation carriers

How identified	Location	SNP	Alleles <sup>₹</sup>	MAF	HR (95%CI)	P-value
Other previous hit for breast cancer	1p36.22	rs616488	A/G	0.32	0.95 (0.91-1.00)	6.3x10 <sup>-2</sup>
New hit for overall breast cancer	1p36.13	rs2992756	C/T	0.50	1.00 (0.96-1.05)	9.2x10 <sup>-1</sup>
New hit for overall breast cancer	1p34.2	rs4233486	T/C	0.36	0.95 (0.90-1.00)	3.6x10 <sup>-2</sup>
New hit for overall breast cancer	1p34.2	rs79724016	T/G	0.04	0.93 (0.82-1.06)	3.0x10 <sup>-1</sup>
New hit for overall breast cancer	1p34.1	rs1707302	G/A	0.32	1.03 (0.98-1.09)	1.9x10 <sup>-1</sup>
New hit for overall breast cancer	1p32.3	rs140850326	$I/D^{\dagger}$	0.46	0.99 (0.94-1.03)	5.5x10 <sup>-1</sup>
New hit for overall breast cancer	1p22.3	rs17426269	G/A	0.16	1.01 (0.94-1.07)	8.2x10 <sup>-1</sup>
Other previous hit for breast cancer	1p13.2	rs11552449	C/T	0.17	1.04 (0.98-1.11)	2.1x10 <sup>-1</sup>
New hit for overall breast cancer	1p12	rs7529522	T/C	0.24	1.01 (0.96-1.07)	6.0x10 <sup>-1</sup>
Other previous hit for breast cancer	1p11.2	rs11249433	A/G	0.41	1.04 (0.99-1.09)	9.6x10 <sup>-2</sup>
Other previous hit for breast cancer	1q21.1	rs12405132	C/T	0.35	1.02 (0.97-1.07)	$4.9 \times 10^{-1}$
Other previous hit for breast cancer	1q21.2	rs12048493	A/C	0.38	1.00 (0.95-1.05)	8.6x10 <sup>-1</sup>
New hit for overall breast cancer	1q22	rs4971059	G/A	0.34	1.01 (0.96-1.06)	$7.5 \times 10^{-1}$
New hit for overall breast cancer	1q32.1	rs35383942	C/T	0.06	1.13 (1.02-1.25)	1.7x10 <sup>-2</sup>
Previous hit for ER-negative disease	1q32.1	rs6678914	G/A	0.41	0.99 (0.94-1.04)	5.8x10 <sup>-1</sup>
Other previous hit for breast cancer	1q32.1	rs4951011	A/G	0.16	1.02 (0.95-1.08)	6.5x10 <sup>-1</sup>
Previous hit for ER-negative disease	1q32.1	rs4245739	A/C	0.28	0.96 (0.91-1.01)	$1.2 \times 10^{-1}$
New hit for overall breast cancer	1q41	rs11117758	G/A	0.22	0.94 (0.89-1.00)	3.7x10 <sup>-2</sup>
Other previous hit for breast cancer	1q43	rs72755295	A/G	0.03	1.17 (1.02-1.34)	2.5x10 <sup>-2</sup>
New hit for overall breast cancer	2p25.1	rs113577745	C/G	0.10	1.01 (0.93-1.09)	8.7x10 <sup>-1</sup>
Previous hit for ER-negative disease	2p24.1	rs12710696	C/T	0.38	1.00 (0.95-1.05)	9.3x10 <sup>-1</sup>
New hit for ER-negative breast cancer	2p23.3	rs200648189	CT/C	0.19	1.00 (0.94-1.07)	9.2x10 <sup>-1</sup>
Previous hit for ER-negative disease	2p23.2	rs4577244‡	C/T	0.22	0.99 (0.93-1.04)	6.2x10 <sup>-1</sup>
New hit for overall breast cancer	2q13	rs71801447	CTTATGTT/C	0.07	1.09 (0.99-1.20)	6.8x10 <sup>-2</sup>
Other previous hit for breast cancer	2q14.1	rs4849887	C/T	0.11	1.00 (0.93-1.08)	9.9x10 <sup>-1</sup>
Other previous hit for breast cancer	2q31.1	rs2016394	G/A	0.46	0.99 (0.94-1.04)	6.0x10 <sup>-1</sup>
Other previous hit for breast cancer	2q31.1	rs1550623	A/G	0.15	1.00 (0.94-1.07)	9.7x10 <sup>-1</sup>
Other previous hit for breast cancer	2q33.1	rs1830298	T/C	0.30	1.02 (0.97-1.07)	4.9x10 <sup>-1</sup>
Other previous hit for breast cancer	2q35	rs4442975	G/T	0.49	0.98 (0.94-1.03)	4.7x10 <sup>-1</sup>
Other previous hit for breast cancer	2q35	rs34005590	C/A	0.04	0.98 (0.88-1.11)	7.9x10 <sup>-1</sup>
Other previous hit for breast cancer	2q35	rs16857609	C/T	0.27	0.97 (0.92-1.02)	1.9x10 <sup>-1</sup>
New hit for overall breast cancer	2q36.3	rs12479355	A/G	0.21	0.94 (0.89-1.00)	5.0x10 <sup>-2</sup>
Other previous hit for breast cancer	3p26.1	rs6762644	A/G	0.37	0.99 (0.94-1.04)	5.9x10 <sup>-1</sup>
Other previous hit for breast cancer	3p24.1	rs4973768	C/T	0.50	1.07 (1.02-1.12)	4.1x10 <sup>-3</sup>
Other previous hit for breast cancer	3p.24.1	rs12493607	G/C	0.33	1.01 (0.96-1.06)	7.5x10 <sup>-1</sup>
Other previous hit for breast cancer	3p21.31	rs6796502	G/A	0.10	1.03 (0.95-1.11)	4.8x10 <sup>-1</sup>
Other previous hit for breast cancer	3p14.1	rs1053338	A/G	0.14	1.02 (0.96-1.09)	4.9x10 <sup>-1</sup>
New hit for overall breast cancer	3p13	rs6805189	T/C	0.47	1.03 (0.98-1.08)	2.1x10 <sup>-1</sup>
New hit for overall breast cancer	3p12.1	rs13066793	A/G	0.09	0.91 (0.84-0.99)	3.6x10 <sup>-2</sup>
New hit for overall breast cancer	3p12.1	rs9833888	G/T	0.22	1.04 (0.98-1.10)	2.2x10 <sup>-1</sup>
New hit for overall breast cancer	3q23	rs34207738	CTT/C	0.40	0.98 (0.94-1.03)	$4.4 \times 10^{-1}$
New hit for overall breast cancer	3q26.31	rs58058861	G/A	0.21	1.03 (0.97-1.09)	3.5x10 <sup>-1</sup>
New hit for overall breast cancer	4p14	rs6815814	A/C	0.28	0.96 (0.91-1.01)	1.3x10 <sup>-1</sup>
New hit for overall breast cancer	4q21.23	4:84370124	ΤΑ/ΤΑΑ	0.49	0.98 (0.94-1.03)	4.8x10 <sup>-1</sup>
New hit for overall breast cancer	4q22.1	rs10022462	C/T	0.45	0.99 (0.94-1.04)	6.3x10 <sup>-1</sup>
Other previous hit for breast cancer	4q24	rs9790517	C/T	0.22	0.98 (0.93-1.04)	5.4x10 <sup>-1</sup>
New hit for overall breast cancer	4q28.1	rs77528541	G/T	0.12	0.94 (0.87-1.02)	1.3x10 <sup>-1</sup>
Other previous hit for breast cancer	4q34.1	rs6828523	C/A	0.11	0.97 (0.90-1.04)	4.0x10 <sup>-1</sup>
New hit for overall breast cancer	5p15.33	rs116095464	T/C	0.06	1.04 (0.93-1.15)	5.0x10 <sup>-1</sup>
Previous hit for ER-negative disease	5p15.33	rs10069690	C/T	0.27	1.06 (1.01-1.12)	2.7x10 <sup>-2</sup>
Other previous hit for breast cancer	5p15.33	rs3215401	A/AG	0.31	0.94 (0.89-0.98)	$1.0 \times 10^{-2}$
Other previous hit for breast cancer	5p15.1	rs13162653	G/T	0.44	1.05 (1.00-1.10)	6.4x10 <sup>-2</sup>
Other previous hit for breast cancer	5p13.3	rs2012709	C/T	0.49	1.01 (0.96-1.05)	8.0x10 <sup>-1</sup>
Other previous hit for breast cancer	5p12	rs10941679	A/G	0.24	1.09 (1.03-1.15)	1.9x10 <sup>-3</sup>
New hit for overall breast cancer	5q11.1	rs72749841	T/C	0.16	0.98 (0.91-1.06)	6.5x10 <sup>-1</sup>
New hit for overall breast cancer	5q11.1	rs35951924	A/AT	0.32	0.96 (0.91-1.02)	1.9x10 <sup>-1</sup>
Other previous hit for breast cancer	5q11.2	rs62355902	A/T	0.16	1.10 (1.03-1.17)	4.0x10 <sup>-3</sup>
Other previous hit for breast cancer	5q11.2	rs10472076	T/C	0.38	1.02 (0.97-1.07)	4.9x10 <sup>-1</sup>
Other previous hit for breast cancer	5q11.2	rs1353747	T/G	0.09	0.94 (0.86-1.01)	1.0x10 <sup>-1</sup>
Other previous hit for breast cancer	5q14.2	rs7707921	A/T	0.25	1.00 (0.95-1.05)	9.4x10 <sup>-1</sup>
Other previous hit for breast cancer	5q14.3	rs10474352	C/T	0.15	0.98 (0.91-1.04)	4.6x10 <sup>-1</sup>

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New hit for overall breast cancer	5q22.1	rs6882649	T/G	0.32	0.97 (0.92-1.02)	2.5x10 <sup>-1</sup>
New hit for overall breast cancer	5q31.1	rs6596100	C/T	0.23	0.97 (0.91-1.02)	2.4x10 <sup>-1</sup>
Other previous hit for breast cancer	5q33.3	rs1432679	T/C	0.45	1.03 (0.98-1.08)	2.0x10 <sup>-1</sup>
New hit for overall breast cancer	5q35.1	rs4562056	G/T	0.36	1.01 (0.96-1.06)	7.4x10 <sup>-1</sup>
Other previous hit for breast cancer	6p25.3	rs11242675	T/C	0.35	1.01 (0.96-1.06)	7.4x10 <sup>-1</sup>
Other previous hit for breast cancer	6p24.3	rs9348512	C/A	0.34	0.87 (0.83-0.91)	1.9x10 <sup>-8</sup>
Other previous hit for breast cancer	6p23	rs204247	A/G	0.45	1.08 (1.03-1.13)	1.1x10 <sup>-3</sup>
New hit for overall breast cancer	6p22.3	rs3819405	C/T	0.34	0.97 (0.92-1.02)	2.0x10 <sup>-1</sup>
New hit for overall breast cancer	6p22.3	rs2223621	C/T	0.37	1.03 (0.98-1.08)	2.8x10 <sup>-1</sup>
New hit for overall breast cancer	6p22.2	rs71557345	G/A	0.07	1.02 (0.93-1.13)	6.5x10 <sup>-1</sup>
Other previous hit for breast cancer	6p22.1	rs9257408	G/C	0.43	1.00 (0.95-1.05)	9.9x10 <sup>-1</sup>
New hit for overall breast cancer	6a14.1	rs12207986	A/G	0.46	0.97 (0.93-1.02)	$2.3 \times 10^{-1}$
Other previous hit for breast cancer	6q14 1	rs17529111	т/С	0.22	1 06 (1 00-1 12)	$2.5 \times 10^{-2}$
New hit for FR-negative breast cancer	6q23 1	rs6569648	τ/C	0.23	0.97(0.92-1.02)	$3.5\times10^{-1}$
Other previous hit for breast cancer	6q25.1	rc0/85372	G/A	0.23	0.07 (0.52 1.02)	2.0X10 8.0v10 <sup>-3</sup>
Dravious bit for EP pogative disease	6q25.1	rc2757272	5/A T/C	0.15	1 07 (1 02 1 12)	0.0X10
Other provious hit for broast concer	0q23.1	155757522+	1/G	0.55	1.07 (1.02 - 1.12)	5.9X10
Other previous hit for breast cancer	6q25	159397437	G/A	0.08	1.12 (1.03-1.22)	8.6X10
Previous nit for ER-negative disease	6q25.2	rs2/4/652‡	C/1	0.48	0.98 (0.93-1.02)	3.3x10 <sup>-</sup>
New hit for overall breast cancer	7p15.3	rs/9/1	A/G	0.35	0.96 (0.91-1.01)	9.4x10 <sup>-</sup>
New hit for overall breast cancer	7p15.1	rs17156577	T/C	0.12	1.03 (0.95-1.10)	4.9x10
Other previous hit for breast cancer	7q21.2	rs6964587	G/T	0.41	1.05 (1.00-1.10)	6.9x10 <sup>-2</sup>
New hit for overall breast cancer	7q21.3	rs17268829	T/C	0.28	1.00 (0.95-1.05)	8.8x10 <sup>-1</sup>
New hit for overall breast cancer	7q22.1	rs71559437	G/A	0.12	1.09 (1.01-1.18)	2.0x10 <sup>-2</sup>
Other previous hit for breast cancer	7q32.3	rs4593472	C/T	0.33	1.03 (0.98-1.08)	2.8x10 <sup>-1</sup>
Other previous hit for breast cancer	7q34	rs11977670	G/A	0.44	1.02 (0.98-1.07)	3.5x10 <sup>-1</sup>
Other previous hit for breast cancer	7q35	rs720475	G/A	0.26	0.99 (0.94-1.04)	6.2x10 <sup>-1</sup>
New hit for ER-negative breast cancer	8p23.3	rs66823261	T/C	0.22	1.02 (0.96-1.08)	5.5x10 <sup>-1</sup>
Other previous hit for breast cancer	8p12	rs9693444	C/A	0.33	0.99 (0.94-1.04)	6.0x10 <sup>-1</sup>
Other previous hit for breast cancer	8p11.23	rs13365225	A/G	0.18	0.98 (0.92-1.04)	4.6x10 <sup>-1</sup>
Other previous hit for breast cancer	8q21.11	rs6472903	T/G	0.17	0.95 (0.89-1.02)	1.3x10 <sup>-1</sup>
Other previous hit for breast cancer	8a21.11	rs2943559	A/G	0.09	1.08 (0.99-1.17)	$7.0 \times 10^{-2}$
New hit for overall breast cancer	8g22.3	rs514192	T/A	0.33	1.01 (0.96-1.06)	6.4x10 <sup>-1</sup>
New hit for overall breast cancer	8g23.1	rs12546444	А/Т	0.10	0.97 (0.90-1.05)	4 8x10 <sup>-1</sup>
Other previous hit for breast cancer	8q23 3	rs13267382	G/A	0.35	1 00 (0 96-1 05)	8.6v10 <sup>-1</sup>
New hit for FR-negative breast cancer	8q23.3	rs17350191	С/Т	0.35	1.00 (0.95-1.05)	$0.010^{-1}$
Other previous hit for breast cancer	8q24.13	rs13281615	۵/G	0.33	1.05 (1.00-1.10)	$5.2\times10^{-2}$
Other previous hit for breast cancer	8q24.21	rc117001E6	С/Т	0.42	1.03(1.00-1.10)	0.1X10
Other previous hit for breast cancer	0y24.21	rs1011070	C/T	0.19	0.99 (0.95-1.03)	7.7X10
Other previous hit for breast cancer	9p21.5	rs10750242		0.17	1.04 (0.96-1.11)	2.1X10
Other previous hit for breast cancer	9451.2	1510759245		0.29	1.05 (1.00-1.10)	7.6X10
Other previous hit for breast cancer	9431.2	1510816625	A/G	0.07	0.96 (0.88-1.06)	4.3x10
Other previous hit for breast cancer	9q31.2	rs13294895	C/1 T/0	0.17	1.04 (0.98-1.11)	1.8x10 <sup>-</sup>
Other previous hit for breast cancer	9q31.2	rs6/6256	1/C	0.36	1.00 (0.95-1.05)	9.3x10 <sup>+</sup>
New hit for overall breast cancer	9q33.1	rs1895062	A/G	0.40	1.00 (0.95-1.05)	9.9x10 <sup>-1</sup>
New hit for overall breast cancer	9q33.3	rs10760444	A/G	0.44	0.98 (0.94-1.03)	4.9x10 <sup>-1</sup>
New hit for overall breast cancer	9q34.2	rs587745765	I/D <sup>+</sup>	0.21	1.01 (0.95-1.07)	8.1x10 <sup>-1</sup>
Other previous hit for breast cancer	10p15.1	rs2380205	C/T	0.43	0.99 (0.95-1.04)	7.1x10 <sup>-1</sup>
New hit for overall breast cancer	10p14	rs67958007	TG/T	0.13	1.10 (1.03-1.18)	6.6x10 <sup>-3</sup>
Other previous hit for breast cancer	10p12.31	rs7072776	G/A	0.30	1.03 (0.98-1.08)	2.8x10 <sup>-1</sup>
Other previous hit for breast cancer	10p12.31	rs11814448	A/C	0.02	1.03 (0.88-1.21)	6.8x10 <sup>-1</sup>
Other previous hit for breast cancer	10q21.2	rs10995201	A/G	0.15	0.95 (0.89-1.01)	$1.0 \times 10^{-1}$
Other previous hit for breast cancer	10q22.3	rs704010	C/T	0.38	1.02 (0.98-1.07)	3.3x10 <sup>-1</sup>
New hit for overall breast cancer	10q23.33	rs140936696	C/CAA	0.17	1.01 (0.94-1.07)	8.3x10 <sup>-1</sup>
Other previous hit for breast cancer	10q25.2	rs7904519	A/G	0.47	1.01 (0.96-1.06)	$6.5 \times 10^{-1}$
Other previous hit for breast cancer	10a26.12	rs11199914	C/T	0.33	0.94 (0.89-0.98)	9 3x10 <sup>-3</sup>
Other previous hit for breast cancer	10a26.13	rs2981578	T/C	0.51	1.20 (1.14-1.25)	1.1x10 <sup>-13</sup>
Other previous hit for breast cancer	10q26.13	rs35054928	G/GC	0.31	1 23 (1 17-1 29)	$5.8 \times 10^{-18}$
Other previous hit for breast cancer	10g20.13	rc/5631562	а/т	0.44	1.23(1.17-1.23) 0.84(0.75-0.04)	1.0×10 <sup>-3</sup>
New bit for overall breast cancer	110420.13	rc6507091		0.05		1.9X10
Other provious hit for breast same	11~1C C	13037/701		0.50	0.30 (0.32-1.01) 1 10 (1 04 4 45)	1.3X1U
Other previous hit for breast cancer	11~12.5	122011178		0.33	1.10(1.04-1.15)	2.8X10
Other previous nit for breast cancer	11013.1	153903072		0.47	0.97 (0.92-1.02)	2.0x10 <sup>+</sup>
Other previous hit for breast cancer	11q13.3	rs554219	C/G	0.13	1.07 (1.00-1.15)	4.4x10 <sup>-2</sup>
Other previous hit for breast cancer	11q13.3	rs/5915166	C/A	0.06	1.04 (0.94-1.15)	4.1x10 <sup>-1</sup>
New hit for ER-negative breast cancer	11q22.3	rs11374964	G/GA	0.43	1.02 (0.97-1.07)	3.8x10 <sup>-1</sup>

New

New

New

New

New hit for ER-negative breast cancer Other previous hit for breast cancer Other previous hit for breast cancer Other previous hit for breast cancer

New hit for overall breast cancer Other previous hit for breast cancer Other previous hit for breast cancer

New hit for overall breast cancer Other previous hit for breast cancer Previous hit for ER-negative disease Other previous hit for breast cancer 
New hit for overall breast cancer Other previous hit for breast cancer New hit for ER-negative breast cancer Other previous hit for breast cancer Other previous hit for breast cancer Previous hit for ER-negative disease New hit for overall breast cancer New hit for overall breast cancer Other previous hit for breast cancer New hit for overall breast cancer Other previous hit for breast cancer New hit for overall breast cancer New hit for overall breast cancer Other previous hit for breast cancer New hit for ER-negative breast cancer New hit for overall breast cancer Other previous hit for breast cancer New hit for ER-negative breast cancer New hit for overall breast cancer New hit for overall breast cancer Previous hit for ER-negative disease Other previous hit for breast cancer New hit for overall breast cancer New hit for ER-negative breast cancer

Other previous hit for breast cancer New hit for overall breast cancer New hit for overall breast cancer Previous hit for ER-negative disease New hit for overall breast cancer Other previous hit for breast cancer Other previous hit for breast cancer Other previous hit for breast cancer New hit for overall breast cancer Other previous hit for breast cancer New hit for overall breast cancer

New hit for overall breast cancer

	11q22.3	rs74911261	G/A	0.02	0.94 (0.80-1.09)	4.2x10 <sup>-1</sup>
	11q24.3	rs11820646	C/T	0.39	0.92 (0.88-0.97)	1.2x10 <sup>-3</sup>
	12p13.1	rs12422552	G/C	0.28	0.99 (0.94-1.04)	7.3x10 <sup>-1</sup>
	12p11.22	rs7297051	C/T	0.23	0.92 (0.87-0.97)	2.5x10 <sup>-3</sup>
	12q21.31	12:85009437:T:C	T/C	0.32	1.04 (0.98-1.09)	2.0x10 <sup>-1</sup>
	12q22	rs17356907	A/G	0.30	1.01 (0.96-1.07)	6.0x10 <sup>-1</sup>
	12a24.21	rs1292011	A/G	0.41	0.95 (0.90-0.99)	3.0x10 <sup>-2</sup>
	12a24.31	12:120832146:C:T	С/Т	0.15	1.02 (0.95-1.09)	6.0x10 <sup>-1</sup>
	13a13.1	rs11571833	A/T	0.03	0.99 (0.85-1.14)	8 4x10 <sup>-1</sup>
	13a22.1	rs6562760±	G/A	0.25	0.96 (0.91-1.01)	$1.1 \times 10^{-1}$
	14a13 3	rs2236007	G/A	0.21	0.97 (0.92-1.03)	3.9x10 <sup>-1</sup>
	14a24.1	rs2588809	C/T	0.20	1.05(0.99-1.11)	$1.1 \times 10^{-1}$
	14a24.1	rs999737	C/T	0.22	0.95 (0.90-1.00)	6.9x10 <sup>-2</sup>
	14a32.11	rs941764	A/G	0.34	1.02 (0.97-1.07)	$5.1 \times 10^{-1}$
	14a32.12	rs11627032	T/C	0.26	1.01 (0.96-1.07)	$7.5 \times 10^{-1}$
	14a32.33	rs10623258	C/CTT	0.46	1.00 (0.95-1.05)	9.2x10 <sup>-1</sup>
	15g26.1	rs2290203	G/A	0.21	0.95 (0.90-1.01)	$1.1 \times 10^{-1}$
	16n13 3	rs11076805	C/A	0.21	0.93 (0.88-0.99)	$1.1\times10^{-2}$
	16g12 1	rs4784227	C/T	0.20	1 21 (1 15-1 28)	$6.8 \times 10^{-13}$
	16q12.2	rs17817449	T/G	0.40	0.97 (0.93-1.02)	$2.5 \times 10^{-1}$
	16q12.2	rs11075995	Τ/Δ	0.10	1 03 (0 98-1 09)	$2.5 \times 10^{-1}$
	16q12.2	rs28539243	G/A	0.29	1 01 (0 96-1 06)	$6.4 \times 10^{-1}$
	16q12.2	rs2432539	G/A	0.40	1.04 (0.99-1.09)	$1.1 \times 10^{-1}$
	16g23 2	rs13329835	A/G	0.10	1.05 (0.99-1.10)	$1.1\times10^{-1}$
	16q23.2	rs4496150	C/A	0.26	0.97 (0.92-1.02)	$2.2 \times 10^{-1}$
	17a11 2	chr17·29230520	GGT/G	0.20	0.92 (0.87-0.97)	$2.5 \times 10^{-3}$
	17a21 2	rs72826962	с/т	0.01	1 21 (0 98-1 50)	$7.4\times10^{-2}$
	17a21.31	17:44252468:G:A	G/A	0.20	0.90 (0.85-0.96)	$6.1 \times 10^{-4}$
	17a22	rs2787486	A/C	0.29	1.02 (0.97-1.07)	$5.1 \times 10^{-1}$
	17a25.3	rs745570	G/A	0.50	1.03 (0.98-1.08)	$2.2 \times 10^{-1}$
	18a11.2	rs527616	G/C	0.37	0.98 (0.93-1.03)	$4.2 \times 10^{-1}$
	18a11.2	rs1436904	T/G	0.39	0.98 (0.93-1.02)	3.3x10 <sup>-1</sup>
	18a12.1	rs36194942	A/AT	0.31	0.99 (0.94-1.04)	$6.2 \times 10^{-1}$
	18q12.1	rs117618124	T/C	0.04	0.93 (0.83-1.06)	2.9x10 <sup>-1</sup>
	18q12.3	rs6507583	A/G	0.07	0.9 (0.82-0.99)	$2.2 \times 10^{-2}$
	19p13.2	rs322144	C/G	0.45	0.98 (0.93-1.03)	$4.2 \times 10^{-1}$
	19p13.13	rs78269692	т/с	0.05	0.98 (0.87-1.10)	6 9x10 <sup>-1</sup>
	19p13.12	rs2594714	G/A	0.22	0.99 (0.93-1.05)	$7.3 \times 10^{-1}$
	19p13.11	rs67397200	C/G	0.30	1.00 (0.95-1.05)	8.6x10 <sup>-1</sup>
	19p13.11	rs4808801	A/G	0.33	0.97 (0.92-1.02)	$1.8 \times 10^{-1}$
	19p13.11	rs2965183	G/A	0.36	1.06 (1.01-1.12)	$1.6 \times 10^{-2}$
	19q12	rs113701136	C/T	0.32	1.06 (1.01-1.12)	1.7x10 <sup>-2</sup>
	19q13.31	rs3760982	G/A	0.46	1.02 (0.97-1.07)	3.7x10 <sup>-1</sup>
	19q13.22	rs71338792	A/AT	0.23	1.04 (0.98-1.10)	$2.3 \times 10^{-1}$
	20p12.3	rs16991615	, G/A	0.07	1.00 (0.92-1.10)	9.3x10 <sup>-1</sup>
	20a11.21	rs2284378	C/T	0.31	1.02 (0.97-1.07)	4.9x10 <sup>-1</sup>
	20q13.13	rs6122906	A/G	0.19	1.06 (1.00-1.12)	7.0x10 <sup>-2</sup>
	21a21.1	rs2823093	G/A	0.27	0.94 (0.89-0.99)	$1.4 \times 10^{-2}$
	22q12.1	rs17879961	A/G	0.004	1.83 (1.23-2.71)	$2.7 \times 10^{-3}$
	22a12.2	rs132390	T/C	0.03	1.09 (0.96-1.24)	1.9x10 <sup>-1</sup>
	22q13.1	rs738321	C/G	0.38	0.97 (0.92-1.02)	2.1x10 <sup>-1</sup>
	22q13.1	chr22:39359355	I/D <sup>§</sup>	0.004	1.67 (0.97-2.88)	6.3x10 <sup>-2</sup>
	22q13.1	rs6001930	, т/с	0.10	1.02 (0.95-1.11)	$5.5 \times 10^{-1}$
	22a13.2	rs73161324	, - С/Т	0.05	1.01 (0.91-1.13)	$7.8 \times 10^{-1}$
	22a13.31	rs28512361	G/A	0.11	0.98 (0.91-1.06)	$6.3 \times 10^{-1}$
Ŧ				0.11	2.33 (0.31 1.00)	0.3710

Chr, chromosome; MAF, minor allele frequency; <sup>\*</sup>More common allele listed first, minor allele second;

<sup>†</sup>21 base-pair deletion; <sup>‡</sup>36 base-pair deletion; <sup>¥</sup>14 base-pair insertion; <sup>§</sup>31 kb deletion

Results based on OncoArray data for 10,988 BRCA2 mutation carriers (5,611 with breast cancer) and iCOGS data for 1,418 BRCA2

mutation carriers (755 with breast cancer), all from the Consortium of Investigators of Modifiers of BRCA1/2 (CIMBA)

## Supplementary Table 12: Detailed informat

#### Theme

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**APOPTOSIS** APOPTOSIS **APOPTOSIS APOPTOSIS APOPTOSIS** APOPTOSIS **APOPTOSIS APOPTOSIS APOPTOSIS APOPTOSIS APOPTOSIS APOPTOSIS** APOPTOSIS **APOPTOSIS APOPTOSIS APOPTOSIS APOPTOSIS APOPTOSIS APOPTOSIS** APOPTOSIS **CELL AGING/TELOMERE CELL AGING/TELOMERE CELL AGING/TELOMERE CELL AGING/TELOMERE CELL AGING/TELOMERE** CELL AGING/TELOMERE **CELL AGING/TELOMERE CELL AGING/TELOMERE** CELL AGING/TELOMERE **CELL AGING/TELOMERE CELL AGING/TELOMERE** CELL AGING/TELOMERE CELL AGING/TELOMERE **CELL AGING/TELOMERE CELL AGING/TELOMERE CELL AGING/TELOMERE CELL AGING/TELOMERE CELL AGING/TELOMERE** CELL AGING/TELOMERE **CELL AGING/TELOMERE CELL AGING/TELOMERE** CELL AGING/TELOMERE **CELL AGING/TELOMERE CELL AGING/TELOMERE CELL AGING/TELOMERE** CELL CYCLE/DNA DAMAGE RESPONSE DNA DEMETHYLATION/DEALKYLATION DNA DEMETHYLATION/DEALKYLATION DOUBLE STRAND BREAK REPAIR **EPITHELIAL-MESENCHYMAL INTERACTIONS EPITHELIAL-MESENCHYMAL INTERACTIONS** EPITHELIAL-MESENCHYMAL INTERACTIONS **EPITHELIAL-MESENCHYMAL INTERACTIONS** ESTROGEN RECEPTOR SIGNALING 
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OTHER-NOT CLUSTERED OTHER-NOT CLUSTERED

<sup>†</sup>Standardized Enrichment Score is the actual val

### Pathway

ACTIVATION OF NMDA RECEPTOR UPON GLUTAMATE BINDING AND POSTSYNAPTIC EVENT: ACTIVATION OF PROTEIN KINASE A ACTIVITY ACTIVATION OF PROTEIN KINASE A ACTIVITY ADENYLATE CYCLASE ACTIVATING PATHWAY ADENYLATE CYCLASE ACTIVATING PATHWAY ADENYLATE CYCLASE INHIBITORY PATHWAY ADENYLATE CYCLASE INHIBITORY PATHWAY ADENYLATE CYCLASE-ACTIVATING ADRENERGIC RECEPTOR SIGNALING PATHWAY ADENYLATE CYCLASE-ACTIVATING ADRENERGIC RECEPTOR SIGNALING PATHWAY ADENYLATE CYCLASE-ACTIVATING G-PROTEIN COUPLED RECEPTOR SIGNALING PATHWAY ADENYLATE CYCLASE-INHIBITING G-PROTEIN COUPLED RECEPTOR SIGNALING PATHWAY ADRENERGIC RECEPTOR SIGNALING PATHWAY ADRENERGIC RECEPTOR SIGNALING PATHWAY **CA-DEPENDENT EVENTS CA-DEPENDENT EVENTS** CALMODULIN INDUCED EVENTS CALMODULIN INDUCED EVENTS CAM PATHWAY CAM PATHWAY CAMP BIOSYNTHETIC PROCESS CAMP BIOSYNTHETIC PROCESS CAMP METABOLIC PROCESS CAMP METABOLIC PROCESS CAMP METABOLIC PROCESS CAMP METABOLIC PROCESS CAMP-MEDIATED SIGNALING CAMP-MEDIATED SIGNALING CAMP-MEDIATED SIGNALING CYCLIC NUCLEOTIDE METABOLIC PROCESS CYCLIC NUCLEOTIDE METABOLIC PROCESS CYCLIC NUCLEOTIDE METABOLIC PROCESS CYCLIC NUCLEOTIDE METABOLIC PROCESS CYCLIC-NUCLEOTIDE-MEDIATED SIGNALING CYCLIC-NUCLEOTIDE-MEDIATED SIGNALING CYCLIC-NUCLEOTIDE-MEDIATED SIGNALING DAG AND IP3 SIGNALING DAG AND IP3 SIGNALING EGFR INTERACTS WITH PHOSPHOLIPASE C-GAMMA EGFR INTERACTS WITH PHOSPHOLIPASE C-GAMMA ENDOTHELIN SIGNALING PATHWAY ENDOTHELIN SIGNALING PATHWAY

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CIRCADIAN CLOCK

INTRACELLULAR ESTROGEN RECEPTOR SIGNALING PATHWAY INTRACELLULAR STEROID HORMONE RECEPTOR SIGNALING PATHWAY INTRACELLULAR STEROID HORMONE RECEPTOR SIGNALING PATHWAY INTRACELLULAR STEROID HORMONE RECEPTOR SIGNALING PATHWAY NUCLEAR RECEPTOR TRANSCRIPTION PATHWAY NUCLEAR RECEPTOR TRANSCRIPTION PATHWAY NUCLEAR RECEPTOR TRANSCRIPTION PATHWAY NUCLEAR SIGNALING BY ERBB4 **RESPONSE TO ESTRADIOL** RORA ACTIVATES GENE EXPRESSION SIGNALING EVENTS MEDIATED BY HDAC CLASS II SIGNALING MEDIATED BY P38-ALPHA AND P38-BETA CELLULAR RESPONSE TO DSRNA CELLULAR RESPONSE TO DSRNA CELLULAR RESPONSE TO EXOGENOUS DSRNA **DSRNA FRAGMENTATION** NEGATIVE REGULATION OF GENE SILENCING POSTTRANSCRIPTIONAL GENE SILENCING BY RNA POSTTRANSCRIPTIONAL GENE SILENCING BY RNA POSTTRANSCRIPTIONAL GENE SILENCING POSTTRANSCRIPTIONAL GENE SILENCING PRODUCTION OF SMALL RNA INVOLVED IN GENE SILENCING BY RNA **REGULATION OF GENE SILENCING BY RNA REGULATION OF GENE SILENCING REGULATION OF POSTTRANSCRIPTIONAL GENE SILENCING RNA INTERFERENCE** POSITIVE REGULATION OF MONOOXYGENASE ACTIVITY POSITIVE REGULATION OF MONOOXYGENASE ACTIVITY POSITIVE REGULATION OF NITRIC OXIDE BIOSYNTHETIC PROCESS POSITIVE REGULATION OF NITRIC OXIDE METABOLIC PROCESS POSITIVE REGULATION OF NITRIC-OXIDE SYNTHASE ACTIVITY POSITIVE REGULATION OF NITRIC-OXIDE SYNTHASE ACTIVITY POSITIVE REGULATION OF OXIDOREDUCTASE ACTIVITY POSITIVE REGULATION OF OXIDOREDUCTASE ACTIVITY POSITIVE REGULATION OF REACTIVE OXYGEN SPECIES BIOSYNTHETIC PROCESS **REGULATION OF MONOOXYGENASE ACTIVITY REGULATION OF MONOOXYGENASE ACTIVITY REGULATION OF NITRIC-OXIDE SYNTHASE ACTIVITY REGULATION OF NITRIC-OXIDE SYNTHASE ACTIVITY** ACTIVIN RECEPTOR SIGNALING PATHWAY DEVELOPMENT OF PRIMARY FEMALE SEXUAL CHARACTERISTICS FEMALE GONAD DEVELOPMENT NEGATIVE REGULATION OF CYTOKINE BIOSYNTHETIC PROCESS NEGATIVE REGULATION OF INSULIN SECRETION NEGATIVE REGULATION OF PEPTIDE HORMONE SECRETION NEGATIVE REGULATION OF PEPTIDE SECRETION **OVARIAN FOLLICLE DEVELOPMENT OVULATION CYCLE PROCESS OVULATION CYCLE** POSITIVE REGULATION OF REPRODUCTIVE PROCESS

**REGULATION OF ENDOCRINE PROCESS** SIGNALING BY ACTIVIN CELLULAR RESPONSE TO CATECHOLAMINE STIMULUS **CELLULAR RESPONSE TO MONOAMINE STIMULUS RESPONSE TO CATECHOLAMINE RESPONSE TO MONOAMINE** FORMATION OF THE BETA-CATENIN:TCF TRANSACTIVATING COMPLEX FORMATION OF THE BETA-CATENIN:TCF TRANSACTIVATING COMPLEX **REPRESSION OF WNT TARGET GENES** ACROSOME REACTION ACTIN CYTOSKELETON REORGANIZATION AMINO ACID AND OLIGOPEPTIDE SLC TRANSPORTERS AMINO ACID TRANSPORT ACROSS THE PLASMA MEMBRANE **BIOCARTA DNAFRAGMENT PATHWAY** BIOCARTA\_RARRXR\_PATHWAY BIOCARTA\_SET\_PATHWAY **BIOCARTA VDR PATHWAY CELL RECOGNITION** CHROMOSOME SEPARATION **GLYCOPROTEIN HORMONES** INSULIN IGF PATHWAY-PROTEIN KINASE B SIGNALING CASCADE MICROTUBULE ANCHORING MITOCHONDRIAL RNA PROCESSING MITOCHONDRIAL RNA PROCESSING MYOBLAST DIFFERENTIATION N-CADHERIN SIGNALING EVENTS NEGATIVE REGULATION OF ESTABLISHMENT OF PROTEIN LOCALIZATION TO PLASMA MEME NEURONAL STEM CELL POPULATION MAINTENANCE **P38MAPK EVENTS** PEPTIDE HORMONE BIOSYNTHESIS PHOSPHATIDYLINOSITOL 3-KINASE SIGNALING PHOSPHATIDYLINOSITOL-3-PHOSPHATE BIOSYNTHETIC PROCESS PHOSPHATIDYLINOSITOL-3-PHOSPHATE BIOSYNTHETIC PROCESS POSITIVE REGULATION OF ANTIGEN RECEPTOR-MEDIATED SIGNALING PATHWAY POSITIVE REGULATION OF GLYCOPROTEIN BIOSYNTHETIC PROCESS POSITIVE REGULATION OF GLYCOPROTEIN METABOLIC PROCESS POSITIVE REGULATION OF PROTEIN EXPORT FROM NUCLEUS PROTEIN IMPORT INTO PEROXISOME MATRIX **PROTEIN K63-LINKED DEUBIQUITINATION PROTEIN KINASE C SIGNALING RAP PROTEIN SIGNAL TRANSDUCTION REGULATION OF CELLULAR EXTRAVASATION REGULATION OF HORMONE METABOLIC PROCESS REGULATION OF MYOBLAST FUSION REGULATION OF PROTEIN EXPORT FROM NUCLEUS REGULATION OF PROTEIN EXPORT FROM NUCLEUS REGULATION OF PROTEIN HOMOOLIGOMERIZATION** SIGNALING EVENTS MEDIATED BY THE HEDGEHOG FAMILY SMOOTH MUSCLE CELL DIFFERENTIATION **TISSUE REGENERATION** TRNA THREONYLCARBAMOYLADENOSINE METABOLIC PROCESS

## TRNA THREONYLCARBAMOYLADENOSINE METABOLIC PROCESS YAP1- AND WWTR1 (TAZ)-STIMULATED GENE EXPRESSION

ue used to create the enrichment map in Supplementary Figure 14. This value is (ES-min(ES))/(max(ES

# es 14-15)

Database	Pathway ID	Enrichment Score (ES)	Standardized ES†	Gene
REACTOME DATABASE ID RELEASE 55	442755	0.4343	0.0554	ADCY3
GOBP	GO:0034199	0.5247	0.2721	ADCY3
GOBP	GO:0034199	0.5247	0.2721	ADCY9
REACTOME DATABASE ID RELEASE 55	170660	0.6199	0.5003	ADCY3
REACTOME DATABASE ID RELEASE 55	170660	0.6199	0.5003	ADCY9
REACTOME	R-HSA-170670.1	0.5521	0.3376	ADCY3
REACTOME	R-HSA-170670.1	0.5521	0.3376	ADCY9
GOBP	GO:0071880	0.4217	0.0252	ADCY9
GOBP	GO:0071880	0.4217	0.0252	PDE4D
GOBP	GO:0007189	0.4122	0.0024	PTHLH
GOBP	GO:0007189	0.4122	0.0024	ADCY3
GOBP	GO:0007189	0.4122	0.0024	ADCY9
GOBP	GO:0007189	0.4122	0.0024	PDE4D
GOBP	GO:0007193	0.4223	0.0266	MCHR1
GOBP	GO:0007193	0.4223	0.0266	ADCY3
GOBP	GO:0007193	0.4223	0.0266	ADCY9
GOBP	GO:0007193	0.4223	0.0266	CORT
GOBP	GO:0071875	0.4217	0.0252	ADCY9
GOBP	GO:0071875	0.4217	0.0252	PDE4D
REACTOME	R-HSA-111996.1	0.4310	0.0474	ADCY3
REACTOME	R-HSA-111996.1	0.4310	0.0474	ADCY9
REACTOME	R-HSA-111933.1	0.4216	0.0250	ADCY3
REACTOME	R-HSA-111933.1	0.4216	0.0250	ADCY9
REACTOME	R-HSA-111997.1	0.4216	0.0250	ADCY3
REACTOME	R-HSA-111997.1	0.4216	0.0250	ADCY9
GOBP	GO:0006171	0.4718	0.1453	ADCY3
GOBP	GO:0006171	0.4718	0.1453	ADCY9
GOBP	GQ:0046058	0.5935	0.4371	PTHIH
GOBP	GO:0046058	0.5935	0.4371	ADCY3
GOBP	GO:0046058	0.5935	0.4371	ADCY9
GOBP	GO:0046058	0.5935	0.4371	PDF4D
GOBP	GO:0019933	0.4832	0.1726	ADCY3
GOBP	GO:0019933	0.4832	0 1726	ADCY9
GOBP	GO:0019933	0.4832	0.1726	PDF4D
GOBP	GO:0009187	0.4588	0 1141	PTHIH
GOBP	GO:0009187	0.4588	0.1141	ADCY3
GOBP	GO:0009187	0.4588	0.1141	ADCY9
GOBP	GQ:0009187	0.4588	0.1141	PDF4D
GOBP	GO:0019935	0.4454	0.0819	ADCY3
GOBP	GO:0019935	0.4454	0.0819	ADCY9
GOBP	GO:0019935	0.4454	0.0819	PDF4D
REACTOME DATABASE ID RELEASE 55	1489509	0.4559	0.1072	ADCY3
REACTOME DATABASE ID RELEASE 55	1489509	0.4559	0.1072	ADCY9
REACTOME DATABASE ID RELEASE 55	212718	0 4683	0.1369	ADCY3
REACTOME DATABASE ID RELEASE 55	212718	0 4683	0.1369	ADCY9
PANTHER PATHWAY	P00019	0 4392	0.0670	
PANTHER PATHWAY	P00019	0.4392	0.0670	ADCY9

REACTOME DATABASE ID RELEASE 55	112040	0.4310	0.0474	ADCY3
REACTOME DATABASE ID RELEASE 55	112040	0.4310	0.0474	ADCY9
REACTOME DATABASE ID RELEASE 55	997269	0.5521	0.3376	ADCY3
REACTOME DATABASE ID RELEASE 55	997269	0.5521	0.3376	ADCY9
PATHWAY INTERACTION DATABASE NCI-	NA LPA4-MEDIATED S	0.5537	0.3415	ADCY3
PATHWAY INTERACTION DATABASE NCI-	NA LPA4-MEDIATED S	0.5537	0.3415	ADCY9
GOBP	GO:1903523	0.4744	0.1515	PDE4D
REACTOME	R-HSA-5654219.1	0.4569	0.1094	ADCY3
REACTOME	R-HSA-5654219.1	0.4569	0.1094	ADCY9
REACTOME	R-HSA-5654221.1	0.4192	0.0193	ADCY3
REACTOME	R-HSA-5654221.1	0.4192	0.0193	ADCY9
REACTOME	R-HSA-5654227.1	0.4425	0.0750	ADCY3
REACTOME	R-HSA-5654227.1	0.4425	0.0750	ADCY9
REACTOME DATABASE ID RELEASE 55	5654228	0.4150	0.0091	ADCY3
REACTOME DATABASE ID RELEASE 55	5654228	0.4150	0.0091	ADCY9
REACTOME	R-HSA-164378.1	0.4943	0.1992	ADCY3
REACTOME	R-HSA-164378.1	0.4943	0.1992	ADCY9
REACTOME DATABASE ID RELEASE 55	163615	0.4478	0.0877	ADCY3
REACTOME DATABASE ID RELEASE 55	163615	0.4478	0.0877	ADCY9
REACTOME DATABASE ID RELEASE 55	111931	0.4419	0.0737	ADCY3
REACTOME DATABASE ID RELEASE 55	111931	0.4419	0.0737	ADCY9
REACTOME	R-HSA-112043.1	0.4219	0.0255	ADCY3
REACTOME	R-HSA-112043.1	0.4219	0.0255	ADCY9
REACTOME DATABASE ID RELEASE 55	167021	0.4450	0.0810	ADCY3
REACTOME DATABASE ID RELEASE 55	167021	0.4450	0.0810	ADCY9
REACTOME DATABASE ID RELEASE 55	1251932	0.4736	0.1496	ADCY3
REACTOME DATABASE ID RELEASE 55	1251932	0.4736	0.1496	ADCY9
GOBP	GO:0032743	0.4614	0.1202	PDE4D
REACTOME DATABASE ID RELEASE 55	438064	0.4256	0.0346	ADCY3
GOBP	GO:0009154	0.5344	0.2953	PDE4D
GOBP	GO:0072523	0.4459	0.0831	AOX1
GOBP	GO:0072523	0.4459	0.0831	PDE4D
GOBP	GO:0086004	0.4661	0.1315	PDE4D
GOBP	GO:0010649	0.4786	0.1615	PDE4D
GOBP	GO:0010880	0.4741	0.1507	PDE4D
GOBP	GO:0009261	0.5100	0.2368	PDE4D
GOBP	GO:0034332	0.4359	0.0593	CDH2
REACTOME	R-HSA-418990.2	0.5433	0.3166	CDH2
GOBP	GO:0097296	0.4650	0.1290	CASP8
GOBP	GO:0097296	0.4650	0.1290	CFLAR
GOBP	GO:0006309	0.4490	0.0906	DFFA
MSIGDB C2	BIOCARTA CASPA	0.4325	0.0510	DFFA
MSIGDB C2	BIOCARTA CASPA	0.4325	0.0510	CASP8
MSIGDB C2	BIOCARTA DEATH	0.4502	0.0934	DFFA
MSIGDB C2	BIOCARTA DEATH	0.4502	0.0934	CASP8
MSIGDB C2	BIOCARTA DEATH	0.4502	0.0934	CFLAR
MSIGDB C2	BIOCARTA FAS P	0.4661	0.1315	DFFA
MSIGDB C2	BIOCARTA FAS P	0.4661	0.1315	CASP8
MSIGDB C2	BIOCARTA FAS P	0.4661	0.1315	CFLAR
MSIGDB C2	BIOCARTA SODD	0.4379	0.0640	CASPR
REACTOME DATABASE ID RELEASE 55	5218900	0.4860	0.1793	CASP8

REACTOME DATABASE ID RELEASE 55	69416	0.4860	0.1793	CASP8
GOBP	GO:0001701	0.4212	0.0239	CASP8
GOBP	GO:0030225	0.5281	0.2802	CASP8
GOBP	GO:2001240	0.5273	0.2784	TERT
GOBP	GO:0010832	0.4220	0.0260	CFLAR
GOBP	GO:1901099	0.5273	0.2784	TERT
GOBP	GO:0051154	0.4127	0.0035	CFLAR
GOBP	GO:2001269	0.4279	0.0401	CASP8
GOBP	GO:2001269	0.4279	0.0401	CFLAR
REACTOME	R-HSA-3371378.1	0.4860	0.1793	CASP8
GOBP	GO:1900117	0.4943	0.1993	DFFA
GOBP	GO:1900117	0.4943	0.1993	CDKN2A
GOBP	GO:2001239	0.4922	0.1941	TERT
GOBP	GO:0045649	0.4404	0.0701	CASP8
MSIGDB C2	SA CASPASE CAS	0.5552	0.3451	DFFA
MSIGDB C2	SA CASPASE CAS	0.5552	0.3451	CASP8
REACTOME	R-HSA-5357786.2	0.4783	0.1608	CASP8
PATHWAY INTERACTION DATABASE NCI-NA	TRAIL SIGNALING	0.4312	0.0480	CASP8
PATHWAY INTERACTION DATABASE NCI-NA	TRAIL SIGNALING	0.4312	0.0480	CELAR
REACTOME DATABASE ID RELEASE 55	2562578	0.4260	0.0353	CASP8
MSIGDB C2	BIOCARTA ACH F	0.5688	0.3778	TFRT
MSIGDB_C2	BIOCARTA TEL P	0.6706	0.6217	TERT
GOBP	GO:0007569	0 4542	0.1031	TERT
GOBP	GO:0007569	0.4542	0 1031	
GOBP	GO:0007569	0.4542	0 1031	ATM
GOBP	GO:0070199	0.6937	0.6773	TFRT
GOBP	GO:0070199	0.6937	0.6773	BRCA2
REACTOME DATABASE ID RELEASE 55	180786	0.4875	0.1829	TERT
GOBP	GO:0070828	0.5417	0.1029	
GOBP	GO:0090344	0.6567	0.5120	TERT
GOBP	GO:0070198	0.6490	0.5701	TERT
GOBP	GO:0070198	0.6490	0.5701	BRCA2
GOBP	GO:0090342	0.5290	0.2824	TERT
GOBP	GO:0090342	0.5290	0.2824	
GOBP	GO:2000772	0.5250	0.2024	TERT
GOBP	GO:2000772	0.5862	0.4195	
GOBP	GO:1902893	0.6356	0.5379	TERT
GOBP	GO:1002000	0.8284	1 0000	TERT
GOBP	GO:0090399	0.8284	1.0000	
GOBP	GO:0090399	0.8284	1.0000	
GOBP	GO:0006278	0.5204	0.4150	TERT
GOBP	GO:0006278	0.5843	0.4150	ΔΤΜ
GOBP	GO:0007004	0.5045	0.4130	TERT
GORP	GO:0007004	0.6456	0.5618	
REACTOME DATABASE ID RELEASE 55	157570	0.0430	0.00155	TERT
MSIGDB C2	BIOCARTA G1 D/	0.4177	0.0133	
MSIGDB_C2	BIOCARTA G1 P/	0.4355	0.0581	
MSIGDB_C2		0.4355	0.0581	
MSIGDB_C2		0.4555	0.1300	
MSIGDB_C2		0.4658	0.1309	
PANTHER PATHWAY	P00012	0.4000	0.1305	
	1 00010	0.4130	0.0200	CONLI

PATHWAY INTERACTION DATABASE NCI-	NA FOXM1 TRANSCRI	0.4407	0.0708	ESR1
PATHWAY INTERACTION DATABASE NCI-	NA FOXM1 TRANSCRI	0.4407	0.0708	CDKN2A
PATHWAY INTERACTION DATABASE NCI-	NA FOXM1 TRANSCRI	0.4407	0.0708	BRCA2
PATHWAY INTERACTION DATABASE NCI-	NA FOXM1 TRANSCRI	0.4407	0.0708	CCNE1
GOBP	GO:0031572	0.5234	0.2690	BABAM1
GOBP	GO:0031572	0.5234	0.2690	ATM
GOBP	GO:0044818	0.4708	0.1428	ATM
GOBP	GO:0050869	0.4305	0.0463	CDKN2A
GOBP	GO:0050869	0.4305	0.0463	ATM
GOBP	GO:0010972	0.4125	0.0031	ATM
GOBP	GO:1902751	0.4123	0.0026	RAD51B
GOBP	GO:0043517	0.5451	0.3210	CDKN2A
GOBP	GO:0043517	0.5451	0.3210	ATM
GOBP	GO:0010971	0.4602	0.1173	RAD51B
GOBP	GO:1901798	0.4790	0.1625	CDKN2A
GOBP	GO:1901798	0.4790	0.1625	ATM
MSIGDB C2	SA REG CASCADI	0.5062	0.2278	CDKN2A
MSIGDB_C2	SA REG CASCADI	0.5062	0.2278	CCNF1
GOBP	GO:0048103	0.4686	0 1377	
GOBP	GO:0035510	0 4665	0 1324	FTO
GOBP	GO:0080111	0.4312	0.0478	FTO
MSIGDB C2	BIOCARTA ATRRE	0.4567	0 1090	ΔΤΜ
MSIGDB_C2	BIOCARTA ATRRE	0.4567	0.1090	BRCA2
GOBP	GO:0071/80	0.4696	0.1000	
REACTOME DATABASE ID RELEASE 55	5693606	0.4050	0.0577	BABAM1
REACTOME DATABASE ID RELEASE 55	5693606	0.4353	0.0577	
GORD	GO:0045003	0.4303	0.0317	
CORP	GO:0045003	0.4201	0.0214	
CORP	GO:0045003	0.4201	0.0214	
REACTOME	D-HSA-60472 2	0.4201	0.0214	
REACTOME	P-HSA-60472 2	0.4241	0.0300	
REACTOME	P-HSA-5602571 1	0.4241	0.0305	
REACTOME	R-HSA-5603571.1	0.4039	0.1204	
CORD	GO:0045720	0.4039	0.1204	
	D-HSA-5602565 1	0.4394	0.0073	BABANI1 BABANI1
	R-HSA-5603565 1	0.4405	0.0703	
REACTOME DATABASE ID RELEASE 55	5603557	0.4405	0.0703	
	5603554	0.4355	0.0583	
	5095554	0.4355	0.0585	
COPD	CO:0061027	0.4333	0.0363	
CORP	GO:0001037	0.5213	0.2045	
GOBP	GO:0052551	0.3077	0.2514	
GOBP	GO:0001055	0.4675	0.1629	
GOBP		0.4995	0.2117	
		0.4456	0.0781	
		0.4021	0.1098	
		0.4656	0.1741	
	N-1124-1200100.1	0.3209	0.2030	
	GU.UU9/500 CO:0071202	0.4101	0.000	
	GO.0071392	0.3/80	0.3998	ESKT
		0.4033	0.1728	ESK1
REACIONE	К-ПЗА-400253.1	0.4437	0.0779	NCUAL

REACTOME	R-HSA-400253.1	0.4437	0.0779	PPP1CB
GOBP	GO:0030520	0.5593	0.3550	ESR1
GOBP	GO:0030518	0.4217	0.0251	ESR1
GOBP	GO:0030518	0.4217	0.0251	CCNE1
GOBP	GO:0030518	0.4217	0.0251	NCOA1
REACTOME	R-HSA-383280.1	0.4767	0.1569	ESR1
REACTOME	R-HSA-383280.1	0.4767	0.1569	NR2F6
REACTOME	R-HSA-383280.1	0.4767	0.1569	HNF4G
REACTOME DATABASE ID RELEASE 55	1251985	0.4518	0.0973	ESR1
GOBP	GO:0032355	0.4796	0.1640	ESR1
REACTOME	R-HSA-1368082.1	0.5497	0.3319	NCOA1
PATHWAY INTERACTION DATABASE NCI-	-NA SIGNALING EVEN	0.5074	0.2305	ESR1
PATHWAY INTERACTION DATABASE NCI-	NA SIGNALING MEDI/	0.4406	0.0705	ESR1
GOBP	GO:0071359	0.4562	0.1079	TFRT
GOBP	GO:0071359	0.4562	0.1079	RALB
GOBP	GO:0071360	0.4569	0 1096	RAIR
GOBP	GO:0071900	0.5095	0.2356	TERT
GOBP	GO:0051050	0.5055	0.2350	TERT
CORP	GO:0000000	0.0052	0.0004	TEDT
CORP	CO:0025194	0.4124	0.0028	
CORP	GO:0035194	0.4124	0.0028	TEDT
GOBP	GO.0016441	0.4112	0.0000	
GOBP	GO:0016441	0.4112	0.0000	
GOBP	GO:0070918	0.5095	0.2356	
GOBP	GO:0060966	0.6605	0.5975	
GOBP	GO:0060968	0.5325	0.2909	
GOBP	GO:0060147	0.6605	0.5975	
GOBP	GO:0016246	0.6554	0.5855	IERI
GOBP	GO:0032770	0.6466	0.5642	TERT
GOBP	GO:0032770	0.6466	0.5642	ESR1
GOBP	GO:0045429	0.4481	0.0885	ESR1
GOBP	GO:1904407	0.4481	0.0885	ESR1
GOBP	GO:0051000	0.7346	0.7752	TERT
GOBP	GO:0051000	0.7346	0.7752	ESR1
GOBP	GO:0051353	0.5059	0.2270	TERT
GOBP	GO:0051353	0.5059	0.2270	ESR1
GOBP	GO:1903428	0.4215	0.0247	ESR1
GOBP	GO:0032768	0.4148	0.0086	TERT
GOBP	GO:0032768	0.4148	0.0086	ESR1
GOBP	GO:0050999	0.4699	0.1406	TERT
GOBP	GO:0050999	0.4699	0.1406	ESR1
GOBP	GO:0032924	0.5005	0.2140	INHBB
GOBP	GO:0046545	0.4333	0.0530	INHBB
GOBP	GO:0008585	0.4333	0.0530	INHBB
GOBP	GO:0042036	0.5133	0.2446	INHBB
GOBP	GO:0046676	0.4505	0.0941	INHBB
GOBP	GO:0090278	0.4322	0.0504	INHBB
GOBP	GO:0002792	0.4126	0.0034	INHBB
GOBP	GO:0001541	0.4579	0.1120	INHBB
GOBP	GO:0022602	0.4414	0.0724	INHBB
GOBP	GO:0042698	0.4182	0.0167	INHBB
GOBP	GO:2000243	0.4991	0.2106	INHBB

GOBP	GO:0044060	0.4149	0.0088	INHBB
REACTOME DATABASE ID RELEASE 55	1502540	0.5210	0.2631	INHBB
GOBP	GO:0071870	0.4291	0.0429	PDE4D
GOBP	GO:0071868	0.4291	0.0429	PDE4D
GOBP	GO:0071869	0.4291	0.0429	PDE4D
GOBP	GO:0071867	0.4291	0.0429	PDE4D
REACTOME	R-HSA-201722.2	0.4371	0.0620	TERT
REACTOME	R-HSA-201722.2	0.4371	0.0620	TCF7L2
REACTOME DATABASE ID RELEASE 55	4641265	0.4123	0.0027	TCF7L2
GOBP	GO:0007340	0.4709	0.1432	ADCY3
GOBP	GO:0031532	0.4347	0.0564	FRY
REACTOME	R-HSA-425374 1	0 4182	0.0167	SI C6A18
REACTOME DATABASE ID RELEASE 55	352230	0 5339	0 2940	SI C6A18
MSIGDB C2		0.5028	0.2340	
MSIGDB_C2		0.3028	0.2150	
MSIGDB_C2		0.4704	0.1302	
		0.4000	0.1100	
		0.4843	0.1751	
GOBP	GO:0008037	0.4248	0.0325	KCNU1
GOBP	GO:0051304	0.4932	0.1966	APIID1
REACTOME DATABASE ID RELEASE 55	209822	0.4456	0.0825	INHBB
PANTHER PATHWAY	P00033	0.4207	0.0227	MDM4
GOBP	GO:0034453	0.4252	0.0336	PEX14
GOBP	GO:0000963	0.5413	0.3119	GTPBP3
GOBP	GO:0000963	0.5413	0.3119	TRMT61B
GOBP	GO:0045445	0.5165	0.2523	TCF7L2
PATHWAY INTERACTION DATABASE NCI-NA	N-CADHERIN SIGN	0.4122	0.0024	CDH2
GOBP	GO:0090005	0.4264	0.0363	ANXA13
GOBP	GO:0097150	0.5715	0.3843	CDH2
REACTOME DATABASE ID RELEASE 55	171007	0.4664	0.1323	RALB
REACTOME DATABASE ID RELEASE 55	209952	0.4670	0.1338	INHBB
GOBP	GO:0014065	0.4647	0.1281	PIK3C2B
GOBP	GO:0036092	0.6415	0.5520	PIK3C2B
GOBP	GO:0036092	0.6415	0.5520	ATM
GOBP	GO:0050857	0.4366	0.0608	KCNN4
GOBP	GO:0010560	0.4915	0.1924	TCF7L2
GOBP	GO:1903020	0.4440	0.0786	TCF7L2
GOBP	GO:0046827	0.5167	0.2529	TCF7L2
GOBP	GO:0016558	0.4646	0.1280	PEX14
GOBP	GO:0070536	0.5459	0.3228	BABAM1
GOBP	GO:0070528	0.4710	0.1434	PLVAP
GOBP	GO:0032486	0.4819	0.1695	SGSM3
GOBP	GO:0002691	0 5444	0 3194	PLVAP
GOBP	GO:0032350	0 4184	0.0172	TCF712
GOBP	GO:1901739	0.4467	0.0172	
GOBP	GO:00/6825	0.5059	0.0002	
CORP	GO:0046825	0.5059	0.2271	
CORP	GO:0040823	0.5039	0.2271	
		0.3224	0.2000	
CODD		0.4890	0.1000	PIHLH
GOBP	GU:0051145	0.4252	0.0336	
GOBP	GU:0042246	0.4795	0.1637	CFLAR
GOBP	GO:0070525	0.5931	0.4360	GTPBP3

GOBP	GO:0070525	0.5931	0.4360	TRMT61B	
REACTOME DATABASE ID RELEASE 55	2032785	0.4338	0.0543	NCOA1	
$\sum_{i=1}^{n} (\Gamma C)$					

)-min(ES))

Number of	SNID with		Distance to gene	Appears in
SNDs in gene	lowest P-value	P-value	from SNP (bp)	Supplementary
SINFS III gene	iowest r-value		nom sive (bp)	Figure 14
836	2_25129473_A_G	1.3x10 <sup>-8</sup>	0	Yes
836	2_25129473_A_G	1.3x10 <sup>-8</sup>	0	Yes
1,630	16_4106788_C_A	1.4x10 <sup>-8</sup>	0	Yes
836	2_25129473_A_G	1.3x10 <sup>-8</sup>	0	Yes
1,630	16_4106788_C_A	1.4x10 <sup>-8</sup>	0	Yes
836	2_25129473_A_G	1.3x10 <sup>-8</sup>	0	Yes
1,630	16_4106788_C_A	1.4x10 <sup>-8</sup>	0	Yes
1,630	16_4106788_C_A	1.4x10 <sup>-8</sup>	0	Yes
8,270	5_58429733_C_T	1.7x10 <sup>-8</sup>	0	Yes
1,366	12_28174817_C_T	2.3x10 <sup>-31</sup>	49901	Yes
836	2_25129473_A_G	1.3x10 <sup>-8</sup>	0	Yes
1,630	16_4106788_C_A	1.4x10 <sup>-8</sup>	0	Yes
8,270	5_58429733_C_T	1.7x10 <sup>-8</sup>	0	Yes
427	22_41059171_A_G	7.7x10 <sup>-12</sup>	16010	Yes
836	2_25129473_A_G	1.3x10 <sup>-8</sup>	0	Yes
1,630	16_4106788_C_A	1.4x10 <sup>-8</sup>	0	Yes
56	1_10506667_G_A	1.7x10 <sup>-8</sup>	0	Yes
1,630	16_4106788_C_A	1.4x10 <sup>-8</sup>	0	Yes
8,270	5_58429733_C_T	1.7x10 <sup>-8</sup>	0	Yes
836	2_25129473_A_G	1.3x10 <sup>-8</sup>	0	Yes
1,630	16_4106788_C_A	1.4x10 <sup>-8</sup>	0	Yes
836	2_25129473_A_G	1.3x10 <sup>-8</sup>	0	Yes
1,630	16_4106788_C_A	1.4x10 <sup>-8</sup>	0	Yes
836	2_25129473_A_G	1.3x10 <sup>-8</sup>	0	Yes
1,630	16_4106788_C_A	1.4x10 <sup>-8</sup>	0	Yes
836	2_25129473_A_G	1.3x10 <sup>-8</sup>	0	Yes
1,630	16_4106788_C_A	1.4x10 <sup>-8</sup>	0	Yes
1,366	12_28174817_C_T	2.3x10 <sup>-31</sup>	49901	Yes
836	2_25129473_A_G	1.3x10 <sup>-8</sup>	0	Yes
1,630	16_4106788_C_A	1.4x10 <sup>-8</sup>	0	Yes
8,270	5_58429733_C_T	1.7x10 <sup>-8</sup>	0	Yes
836	2_25129473_A_G	1.3x10 <sup>-8</sup>	0	Yes
1,630	16_4106788_C_A	1.4x10 <sup>-8</sup>	0	Yes
8,270	5_58429733_C_T	1.7x10 <sup>-8</sup>	0	Yes
1,366	 12_28174817_C_T	2.3x10 <sup>-31</sup>	49901	Yes
836	2_25129473_A_G	1.3x10 <sup>-8</sup>	0	Yes
1,630	16_4106788_C_A	1.4x10 <sup>-8</sup>	0	Yes
8,270	5_58429733_C_T	1.7x10 <sup>-8</sup>	0	Yes
836	2_25129473_A_G	1.3x10 <sup>-8</sup>	0	Yes
1,630	16_4106788_C_A	1.4x10 <sup>-8</sup>	0	Yes
8,270	5_58429733_C_T	1.7x10 <sup>-8</sup>	0	Yes
836	2_25129473_A_G	1.3x10 <sup>-8</sup>	0	Yes
1,630	16_4106788_C_A	1.4x10 <sup>-8</sup>	0	Yes
836	2_25129473_A_G	1.3x10 <sup>-8</sup>	0	Yes
1,630	 16_4106788_C_A	1.4x10 <sup>-8</sup>	0	Yes
836	2_25129473_A_G	1.3x10 <sup>-8</sup>	0	Yes
1,630	16_4106788_C_A	1.4x10 <sup>-8</sup>	0	Yes

836	2_25129473_A_G	1.3x10 <sup>-8</sup>	0	Yes
1,630	 16_4106788_C_A	1.4x10 <sup>-8</sup>	0	Yes
836	2_25129473_A_G	1.3x10 <sup>-8</sup>	0	Yes
1,630	16_4106788_C_A	1.4x10 <sup>-8</sup>	0	Yes
836	2_25129473_A_G	1.3x10 <sup>-8</sup>	0	Yes
1,630	16_4106788_C_A	1.4x10 <sup>-8</sup>	0	Yes
8,270	5_58429733_C_T	1.7x10 <sup>-8</sup>	0	Yes
836	2_25129473_A_G	1.3x10 <sup>-8</sup>	0	Yes
1,630	16_4106788_C_A	1.4x10 <sup>-8</sup>	0	Yes
836	2_25129473_A_G	1.3x10 <sup>-8</sup>	0	Yes
1,630	16_4106788_C_A	1.4x10 <sup>-8</sup>	0	Yes
836	2_25129473_A_G	1.3x10 <sup>-8</sup>	0	Yes
1,630	16_4106788_C_A	1.4x10 <sup>-8</sup>	0	Yes
836	2_25129473_A_G	1.3x10 <sup>-8</sup>	0	Yes
1,630	16_4106788_C_A	1.4x10 <sup>-8</sup>	0	Yes
836	2_25129473_A_G	1.3x10 <sup>-8</sup>	0	Yes
1,630	16_4106788_C_A	1.4x10 <sup>-8</sup>	0	Yes
836	2_25129473_A_G	1.3x10 <sup>-8</sup>	0	Yes
1,630	16_4106788_C_A	1.4x10 <sup>-8</sup>	0	Yes
836	2_25129473_A_G	1.3x10 <sup>-8</sup>	0	Yes
1,630	16_4106788_C_A	1.4x10 <sup>-8</sup>	0	Yes
836	2_25129473_A_G	1.3x10 <sup>-8</sup>	0	Yes
1,630	16_4106788_C_A	$1.4 \times 10^{-8}$	0	Yes
836	2_25129473_A_G	1.3x10 <sup>-8</sup>	0	Yes
1,630	16_4106788_C_A	$1.4 \times 10^{-8}$	0	Yes
836	2_25129473_A_G	1.3x10 <sup>-8</sup>	0	Yes
1,630	16_4106788_C_A	1.4x10 <sup>-8</sup>	0	Yes
8,270	5_58429733_C_T	1.7x10 <sup>-8</sup>	0	Yes
836	2_25129473_A_G	1.3x10 <sup>-8</sup>	0	Yes
8,270	5_58429733_C_T	$1.7 \times 10^{-8}$	0	Yes
570	2_201524267_A_C	5.4x10 <sup>-10</sup>	0	Yes
8,270	5_58429733_C_T	1.7x10 <sup>-°</sup>	0	Yes
8,270	5_58429733_C_T	1.7x10 <sup>-</sup> °	0	Yes
8,270	5_58429733_C_T	1.7x10 <sup>-°</sup>	0	Yes
8,270	5_58429733_C_T	1.7x10 <sup>-°</sup>	0	Yes
8,270	5_58429733_C_T	1.7x10 <sup>-°</sup>	0	Yes
5,742	18_25401204_AT_A	1.4x10 <sup>-°</sup>	129725	
5,742	18_25401204_AT_A	1.4x10 <sup>-o</sup>	129725	
321	2_202122995_A_G	3.2x10 <sup>-11</sup>	0	
323	2_202004837_G_C	3.1x10 <sup>-9</sup>	0	
112	1_10537437_C_G	2.0x10 <sup>-20</sup>	0	
112	1_10537437_C_G	2.0x10 <sup>20</sup>	0	
321	2_202122995_A_G	3.2x10 <sup>11</sup>	0	
112	1_10537437_C_G	2.0x10 <sup>20</sup>	0	
321	2_202122995_A_G	3.2x10 <sup>-1</sup>	0	
323	2_202004837_G_C	3.1x10 <sup>-20</sup>	U	
112	1_1053/43/_C_G	$2.0 \times 10^{-11}$	U	
321	2_202122995_A_G	$3.2 \times 10^{-11}$	U	
323	2_202004837_G_C	$3.1 \times 10^{-11}$	U	
321	2_202122995_A_G	$3.2 \times 10^{-11}$	U	
321	2_202122995_A_G	3.2x10	U	

321	2_202122995_A_G	3.2x10 <sup>-11</sup>	0	
321	2_202122995_A_G	3.2x10 <sup>-11</sup>	0	
321	2_202122995_A_G	3.2x10 <sup>-11</sup>	0	
381	5_1279790_C_T	1.9x10 <sup>-49</sup>	0	
323	2_202004837_G_C	3.1x10 <sup>-9</sup>	0	
381	5_1279790_C_T	1.9x10 <sup>-49</sup>	0	
323	2_202004837_G_C	3.1x10 <sup>-9</sup>	0	
321	2_202122995_A_G	3.2x10 <sup>-11</sup>	0	
323	2_202004837_G_C	3.1x10 <sup>-9</sup>	0	
321	2_202122995_A_G	3.2x10 <sup>-11</sup>	0	
112	 1_10537437_C_G	2.0x10 <sup>-20</sup>	0	
170	9_21963048_C_T	4.3x10 <sup>-15</sup>	0	
381	 5 1279790 С Т	$1.9 \times 10^{-49}$	0	
321	2 202122995 A G	$3.2 \times 10^{-11}$	0	
112		$2.0 \times 10^{-20}$	0	
321	2 202122995 A G	$3.2 \times 10^{-11}$	0	
321	2 202122995 A G	$3.2 \times 10^{-11}$	0	
321	2 202122995 A G	$3.2 \times 10^{-11}$	0	
323	2 202004837 G C	$3.1 \times 10^{-9}$	0	
323	2 202122995 A G	$2.2 \times 10^{-11}$	0	
381	5 1279790 C T	3.2×10 1 0×10 <sup>-49</sup>	0	
381	5 1279790 C T	$1.9\times10^{-49}$	0	
381	5 1279790 C T	1.9X10	0	
170	9 219630/8 C T	1.900	0	
701	$5_21505048_C_1$	$4.3 \times 10^{-12}$	0	
201	5 1270700 C T	$2.5 \times 10^{-49}$	0	
70E	5_12/9/90_C_1	1.900	0	
400	13_329/2020_A_1	2.5X10	0	
301 170	5_12/9/90_C_1	$1.9 \times 10^{-15}$	0	
201	9_21963048_C_1	$4.3 \times 10^{-49}$	0	
201	5_1279790_C_1	$1.9 \times 10^{-49}$	0	
381	5_12/9/90_C_1	$1.9 \times 10^{-11}$	0	
485	13_32972626_A_1	$2.5 \times 10^{-49}$	0	
381	5_12/9/90_C_1	1.9x10 <sup>-15</sup>	0	
170	9_21963048_C_1	4.3x10 <sup>13</sup>	0	
381	5_12/9/90_C_1	1.9x10 <sup>45</sup>	0	
170	9_21963048_C_I	$4.3 \times 10^{13}$	0	
381	5_1279790_C_1	1.9x10 <sup>-49</sup>	0	
381	5_1279790_C_T	$1.9 \times 10^{-49}$	0	
170	9_21963048_C_T	$4.3 \times 10^{-13}$	0	
701	11_108098459_TAA_T	$2.5 \times 10^{-12}$	0	
381	5_1279790_C_T	$1.9 \times 10^{-49}$	0	
701	11_108098459_TAA_T	$2.5 \times 10^{-12}$	0	
381	5_1279790_C_T	1.9x10 <sup>-49</sup>	0	
701	11_108098459_TAA_T	$2.5 \times 10^{-12}$	0	
381	5_1279790_C_T	$1.9 \times 10^{-49}$	0	
170	9_21963048_C_T	$4.3 \times 10^{-15}$	0	
701	11_108098459_TAA_T	$2.5 \times 10^{-12}$	0	
755	19_30277729_C_T	6.8x10 <sup>-9</sup>	25171	
701	11_108098459_TAA_T	2.5x10 <sup>-12</sup>	0	
755	19_30277729_C_T	6.8x10 <sup>-9</sup>	25171	
755	19_30277729_C_T	6.8x10 <sup>-9</sup>	25171	

2,783	6_151985574_T_C	8.9x10 <sup>-39</sup>	26056
170	9_21963048_C_T	4.3x10 <sup>-15</sup>	0
485	13_32972626_A_T	2.5x10 <sup>-11</sup>	0
755	19_30277729_C_T	6.8x10 <sup>-9</sup>	25171
141	19_17393925_C_A	4.7x10 <sup>-53</sup>	0
701	11_108098459_TAA_T	2.5x10 <sup>-12</sup>	0
701	11_108098459_TAA_T	2.5x10 <sup>-12</sup>	0
170	9_21963048_C_T	4.3x10 <sup>-15</sup>	0
701	 11_108098459_TAA_T	$2.5 \times 10^{-12}$	0
701	11_108098459_TAA_T	2.5x10 <sup>-12</sup>	0
4,358	14_69029203_C_T	1.1x10 <sup>-10</sup>	0
170	9_21963048_C_T	4.3x10 <sup>-15</sup>	0
701	11_108098459_TAA_T	2.5x10 <sup>-12</sup>	0
4,358	14_69029203_C_T	1.1x10 <sup>-10</sup>	0
170	9_21963048_C_T	4.3x10 <sup>-15</sup>	0
701	11_108098459_TAA_T	2.5x10 <sup>-12</sup>	0
170	9_21963048_C_T	4.3x10 <sup>-15</sup>	0
755	19_30277729_C_T	6.8x10 <sup>-9</sup>	25171
170	9_21963048_C_T	$4.3 \times 10^{-15}$	0
3,106	16_53809123_C_T	$6.0 \times 10^{-14}$	0
3,106	16_53809123_C_T	$6.0 \times 10^{-14}$	0
701	11_108098459_TAA_T	$2.5 \times 10^{-12}$	0
485	13_32972626_A_T	$2.5 \times 10^{-11}$	0
701	11_108098459_TAA_T	$2.5 \times 10^{-12}$	0
141	 19 17393925 C A	$4.7 \times 10^{-53}$	0
701	 11_108098459_TAA_T	$2.5 \times 10^{-12}$	0
701	11 108098459 TAA T	$2.5 \times 10^{-12}$	0
485	13_32972626_A_T	2.5x10 <sup>-11</sup>	0
4,358	14_69029203_C_T	1.1x10 <sup>-10</sup>	0
141	19_17393925_C_A	$4.7 \times 10^{-53}$	0
701	 11_108098459_TAA_T	$2.5 \times 10^{-12}$	0
141	19_17393925_C_A	$4.7 \times 10^{-53}$	0
701	 11_108098459_TAA_T	$2.5 \times 10^{-12}$	0
141	19_17393925_C_A	$4.7 \times 10^{-53}$	0
141	19_17393925_C_A	$4.7 \times 10^{-53}$	0
701	11_108098459_TAA_T	2.5x10 <sup>-12</sup>	0
701	11_108098459_TAA_T	2.5x10 <sup>-12</sup>	0
485	13_32972626_A_T	2.5x10 <sup>-11</sup>	0
4,358	14_69029203_C_T	1.1x10 <sup>-10</sup>	0
1,366	12_28174817_C_T	2.3x10 <sup>-31</sup>	49901
1,366	12_28174817_C_T	2.3x10 <sup>-31</sup>	49901
1,366	12_28174817_C_T	2.3x10 <sup>-31</sup>	49901
1,366	12_28174817_C_T	2.3x10 <sup>-31</sup>	49901
2,783	6_151985574_T_C	8.9x10 <sup>-39</sup>	26056
2,783	6_151985574_T_C	8.9x10 <sup>-39</sup>	26056
2,783	6_151985574_T_C	8.9x10 <sup>-39</sup>	26056
1,426	2_24739694 C CT	9.7x10 <sup>-9</sup>	67651
2,783	6_151985574 T C	8.9x10 <sup>-39</sup>	26056
2,783	6_151985574 T C	8.9x10 <sup>-39</sup>	26056
2,783	6_151985574 T C	8.9x10 <sup>-39</sup>	26056
1,426	2_24739694_C_CT	9.7x10 <sup>-9</sup>	67651

575	2_28956786_G_A	1.2x10 <sup>-8</sup>	17827
2,783	6_151985574_T_C	8.9x10 <sup>-39</sup>	26056
2,783	6_151985574_T_C	8.9x10 <sup>-39</sup>	26056
755	19_30277729_C_T	6.8x10 <sup>-9</sup>	25171
1,426	2_24739694_C_CT	9.7x10 <sup>-9</sup>	67651
2,783	6 151985574 T C	8.9x10 <sup>-39</sup>	26056
187	19 17359535 C T	$9.4 \times 10^{-32}$	0
3,619		$1.2 \times 10^{-8}$	91565
2,783	6 151985574 T C	$8.9 \times 10^{-39}$	26056
2,783	 6 151985574 T C	$8.9 \times 10^{-39}$	26056
, 1,426	2 24739694 C CT	$9.7 \times 10^{-9}$	67651
, 2,783	6 151985574 T C	$8.9 \times 10^{-39}$	26056
2.783		8 9x10 <sup>-39</sup>	26056
381	5 1279790 C T	$1.9 \times 10^{-49}$	0
447	2 121077184 A G	$1.3 \times 10^{-13}$	24898
447	2 121077184 A G	$1.2 \times 10^{-13}$	24898
381	5 1279790 C T	$1.2\times10^{-49}$	0
381	5_1279790_C_T	$1.9 \times 10^{-49}$	0
381	5_1279790_C_T	$1.9 \times 10^{-49}$	0
1 327	22 40734189 G GA	$2.9\times10^{-11}$	0
381	5 1279790 C T	0.5X10 1.0x10 <sup>-49</sup>	0
1 3 2 7	22 /073/189 G GA	1.9X10	0
381	5 1279790 C T	0.5X10 1.0x10 <sup>-49</sup>	0
381	5_1279790_C_T	$1.9 \times 10^{-49}$	0
381	5_1279790_C_T	$1.9 \times 10^{-49}$	0
381	5_1279790_C_T	$1.9 \times 10^{-49}$	0
201	5_1279790_C_T	$1.9 \times 10^{-49}$	0
201	5_1279790_C_T	$1.9 \times 10^{-49}$	0
201 2722	5_1279790_C_1 6 151085574 T C	$1.9 \times 10^{-39}$	26056
2,705	0_131985574_1_C	8.9X10	20050
2,705	0_131985574_1_C	8.9X10	20050
2,705	5 1270700 C T	8.9X10	20050
201 2702	5_1279790_C_1 6_151095574_T_C	$1.9 \times 10^{-39}$	26056
2,705	5 1270700 C T	8.9X10	20050
201 2702	5_12/9/90_C_1 6_151095574_T_C	$1.9 \times 10^{-39}$	26056
2,705	0_131983374_1_C	8.9X10	20030
2,705	5 1270700 C T	8.9X10	20050
201 2702	5_1279790_C_1 6 151095574 T C	$1.9 \times 10^{-39}$	26056
2,705	0_131903374_1_C 5_1270700_C_T	8.9X10	20030
201 207 C	5_1279790_C_1 6_161096674_T_C	$1.9 \times 10^{-39}$	26056
2,705	0_101960074_1_C	8.9x10	20050
605 605	2_121079515_A_C	$9.3 \times 10^{-18}$	24203
605 605	2_121079515_A_C	$9.3 \times 10^{-18}$	24203
605 605	2_121079515_A_C	$9.3 \times 10^{-18}$	24203
605 605	2_121079515_A_C	$9.3 \times 10^{-18}$	24203
005	2_121079515_A_C	$9.3 \times 10^{-18}$	24203
	2_121070515_A_C	$9.3 \times 10^{-18}$	24203
	2_1210/9515_A_C	$9.3 \times 10^{-18}$	24203
	2_1210/9515_A_C	9.3x10 <sup>10</sup>	24203
005 605	2_1210/9515_A_C	9.3x10 <sup>10</sup>	24203
6U5	2_1210/9515_A_C	9.3x10 <sup>10</sup>	24203
605	Z_1Z10/9515_A_C	9.3x10 <sup>10</sup>	24203

605	2_121079515_A_C	9.3x10 <sup>-18</sup>	24203
605	2_121079515_A_C	9.3x10 <sup>-18</sup>	24203
8,270	5_58429733_C_T	1.7x10 <sup>-8</sup>	0
8,270	5_58429733_C_T	1.7x10 <sup>-8</sup>	0
8,270	5_58429733_C_T	1.7x10 <sup>-8</sup>	0
8,270	5_58429733_C_T	1.7x10 <sup>-8</sup>	0
381	5_1279790_C_T	1.9x10 <sup>-49</sup>	0
2,437	10_114782803_T_C	6.5x10 <sup>-15</sup>	0
2,437	10_114782803_T_C	6.5x10 <sup>-15</sup>	0
836	2_25129473_A_G	1.3x10 <sup>-8</sup>	0
1,573	927 CAATAAATAAATA C/	$2.0 \times 10^{-12}$	0
290	5 1241565 A G	8.4x10 <sup>-13</sup>	0
290	5 1241565 A G	8.4x10 <sup>-13</sup>	0
112	1_10537437_C_G	$2.0 \times 10^{-20}$	0
1,426	2 24739694 C CT	9.7x10 <sup>-9</sup>	67651
112		$2.0 \times 10^{-20}$	0
1,426	2	9.7x10 <sup>-9</sup>	67651
, 3,952		$2.8 \times 10^{-12}$	56303
, 154	 L0491895 A AGCGAGAC1	$4.6 \times 10^{-9}$	0
605	2 121079515 A C	9 $3 \times 10^{-18}$	24203
527	1 204518842 C A	$7.0 \times 10^{-26}$	0
813	1 10566272 C T	$9.7 \times 10^{-22}$	0
118	19 17456375 TCTC T	$1.4 \times 10^{-23}$	0
217	2 29094032 C A	8.6x10 <sup>-9</sup>	0
2.437	10 114782803 T C	$6.5 \times 10^{-15}$	0
5.742	18 25401204 AT A	$1.4 \times 10^{-8}$	129725
541	8 124757661 C T	$1.7 \times 10^{-11}$	8014
5.742	18 25401204 AT A	$1.7 \times 10^{-8}$	129725
447	2 121077184 A G	$1.1 \times 10^{-13}$	24898
605	2 121079515 A C	9 $3 \times 10^{-18}$	24203
533	1 204464181 C T	$1.0 \times 10^{-24}$	0
533	1 204464181 C T	$1.0 \times 10^{-24}$	0
701	11 108098459 TAA T	$2.5 \times 10^{-12}$	0
182	19 44281824 C CTCTT	$2.3\times10^{-9}$	0
2.437	10 114782803 T C	$6.5 \times 10^{-15}$	0
2.437	10 114782803 T C	$6.5 \times 10^{-15}$	0
2.437	10 114782803 T C	$6.5 \times 10^{-15}$	0
813	1 10566272 C T	$9.5 \times 10^{-22}$	0
141	19 17393925 C A	$1.7 \times 10^{-53}$	0
308	19 17462094 T G	$1.7 \times 10^{-26}$	0
196	22 40810946 T C	$1.5 \times 10^{-11}$	0
308	19 17462094 T G	1.010	0
2 437	10 114782803 T C	6.5v10 <sup>-15</sup>	0
323	2 202004837 G C	$2.1 \times 10^{-9}$	0
170	9 21963048 C T	$4.2 \times 10^{-15}$	0
2 437	10 114782803 T C	4.3X10 6 5v10 <sup>-15</sup>	0
813	1 10566272 C T	0.3×10 0.7×10 <sup>-22</sup>	0
1.366	<u></u> 12 28174817 С Т	$2.7 \times 10^{-31}$	49901
1 176	22 40904707 CT C	2.3×10 1 0×10 <sup>-13</sup>	0
373	2 202004837 G C	3.1v10-9	0
118	2_20200-037_0_0 19 17456375 ΤΟΤΟ Τ	1 /v10 <sup>-23</sup>	0
110	13_1, 1303/3_1010_1	T'4YTO	0

217	2_29094032_C_A	8.6x10 <sup>-9</sup>	0	
1,426	2_24739694_C_CT	9.7x10 <sup>-9</sup>	67651	

Supplementary Table 13: Detailed information about themes and unique genes appearing in the enrichment maps (Supplementar	y Fi
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Supplementary Table 13: Detailed information about themes and unique genes appearing in the enrichment maps (Supplementary Fig								
		Number of	SNP with		Distance to			
Theme	Gene	SNPs in gene	lowest P-value	P-value	gene from			
ΔΟΕΝΥΙ ΔΤΕ ΓΥΓΙ ΔSE	РТНІ Н	1 366	12 28174817 C T	2 3x10 <sup>-31</sup>	49901			
	MCHR1	427	22 41059171 A G	$7.6 \times 10^{-12}$	16010			
		570	$22_41035171_A_G$	$5.4 \times 10^{-10}$	0			
	ADCY3	836	2_201324207_A_C	1 3x10 <sup>-8</sup>	0			
	ADCY9	1 630	16 4106788 C A	$1.3 \times 10^{-8}$	0			
	PDF4D	8 270	5 58429733 C T	$1.7 \times 10^{-8}$	0			
	CORT	56	1 10506667 G A	$1.7 \times 10^{-8}$	0			
ADHERENS JUNCTION	CDH2	5,742	18 25401204 AT A	$1.4 \times 10^{-8}$	129725			
APOPTOSIS	TFRT	381	5 1279790 C T	1.9x10 <sup>-49</sup>	0			
APOPTOSIS	DFFA	112	1 10537437 C G	2.0x10 <sup>-20</sup>	0			
APOPTOSIS	CDKN2A	170	9 21963048 C T	4.3x10 <sup>-15</sup>	0			
APOPTOSIS	CASP8	321	2 202122995 A G	3.2x10 <sup>-11</sup>	0			
APOPTOSIS	CFLAR	323	2 202004837 G C	3.1x10 <sup>-9</sup>	0			
CELL AGING/TELOMERE	TERT	381	5 1279790 C T	1.9x10 <sup>-49</sup>	0			
CELL AGING/TELOMERE	CDKN2A	170	9 21963048 C T	4.3x10 <sup>-15</sup>	0			
CELL AGING/TELOMERE	ATM	701	11 108098459 TAA T	2.5x10 <sup>-12</sup>	0			
CELL AGING/TELOMERE	BRCA2	485	13 32972626 A T	2.5x10 <sup>-11</sup>	0			
CELL CYCLE/DNA DAMAGE RESPONSE	BABAM1	141	19 17393925 C A	4.7x10 <sup>-53</sup>	0			
CELL CYCLE/DNA DAMAGE RESPONSE	ESR1	2.783	6 151985574 T C	8.9x10 <sup>-39</sup>	26056			
CELL CYCLE/DNA DAMAGE RESPONSE	CDKN2A	170	9 21963048 C T	4.3x10 <sup>-15</sup>	0			
CELL CYCLE/DNA DAMAGE RESPONSE	ATM	701	11 108098459 TAA T	2.5x10 <sup>-12</sup>	0			
CELL CYCLE/DNA DAMAGE RESPONSE	BRCA2	485	13 32972626 A T	2.5x10 <sup>-11</sup>	0			
CELL CYCLE/DNA DAMAGE RESPONSE	RAD51B	4.358	14 69029203 C T	1.1x10 <sup>-10</sup>	0			
CELL CYCLE/DNA DAMAGE RESPONSE	CCNE1	755	19 30277729 C T	6.8x10 <sup>-9</sup>	25171			
DNA DEMETHYLATION/DEALKYLATION	FTO	3.106	16 53809123 C T	$6.0 \times 10^{-14}$	0			
DOUBLE STRAND BREAK REPAIR	BABAM1	141	19 17393925 C A	4.7x10 <sup>-53</sup>	0			
DOUBLE STRAND BREAK REPAIR	ATM	701	11 108098459 TAA T	2.5x10 <sup>-12</sup>	0			
DOUBLE STRAND BREAK REPAIR	BRCA2	485	13 32972626 A T	2.5x10 <sup>-11</sup>	0			
DOUBLE STRAND BREAK REPAIR	RAD51B	4,358	14 69029203 C T	1.1x10 <sup>-10</sup>	0			
EPITHELIAL-MESENCHYMAL INTERACTIONS	PTHLH	1,366	 12 28174817 С Т	2.3x10 <sup>-31</sup>	49901			
ESTROGEN RECEPTOR SIGNALING	ESR1	2,783	6 151985574 T C	8.9x10 <sup>-39</sup>	26056			
ESTROGEN RECEPTOR SIGNALING	NR2F6	187	19 17359535 C T	9.4x10 <sup>-32</sup>	0			
ESTROGEN RECEPTOR SIGNALING	CCNE1	755	19_30277729_C_T	6.8x10 <sup>-9</sup>	25171			
ESTROGEN RECEPTOR SIGNALING	NCOA1	1,426	2_24739694_C_CT	9.7x10 <sup>-9</sup>	67651			
ESTROGEN RECEPTOR SIGNALING	HNF4G	3,619	8_76360637_A_G	1.2x10 <sup>-8</sup>	91565			
ESTROGEN RECEPTOR SIGNALING	PPP1CB	575	2_28956786_G_A	1.2x10 <sup>-8</sup>	17827			
GENE SILENCING	TERT	381	5_1279790_C_T	1.9x10 <sup>-49</sup>	0			
GENE SILENCING	RALB	447	2_121077184_A_G	1.2x10 <sup>-13</sup>	24898			
GENE SILENCING	TNRC6B	1,327	22_40734189_G_GA	8.3x10 <sup>-11</sup>	0			
REGULATION OF NITRIC OXIDE METABOLISM	TERT	381	5_1279790_C_T	1.9x10 <sup>-49</sup>	0			
REGULATION OF NITRIC OXIDE METABOLISM	ESR1	2,783	6_151985574_T_C	8.9x10 <sup>-39</sup>	26056			
REPRODUCTIVE SYSTEM	INHBB	605	2_121079515_A_C	9.3x10 <sup>-18</sup>	24203			
RESPONSE TO CATECHOLAMINE	PDE4D	8,270	5_58429733_C_T	1.7x10 <sup>-8</sup>	0			
WNT/BETA CATENIN	TERT	381	5_1279790_C_T	1.9x10 <sup>-49</sup>	0			
WNT/BETA CATENIN	TCF7L2	2,437	10_114782803_T_C	6.5x10 <sup>-15</sup>	0			
OTHER-NOT CLUSTERED	BABAM1	141	19_17393925_C_A	4.7x10 <sup>-53</sup>	0			
OTHER-NOT CLUSTERED	PTHLH	1,366	12_28174817_C_T	2.3x10 <sup>-31</sup>	49901			
OTHER-NOT CLUSTERED	PLVAP	308	19_17462094_T_G	1.3x10 <sup>-26</sup>	0			
OTHER-NOT CLUSTERED	MDM4	527	1_204518842_C_A	7.0x10 <sup>-26</sup>	0			
OTHER-NOT CLUSTERED	PIK3C2B	533	1_204464181_C_T	1.0x10 <sup>-24</sup>	0			
OTHER-NOT CLUSTERED	GTPBP3	118	19_17456375_TCTC_T	1.3x10 <sup>-23</sup>	0			
OTHER-NOT CLUSTERED	PEX14	813	1_10566272_C_T	9.7x10 <sup>-22</sup>	0			
OTHER-NOT CLUSTERED	DFFA	112	1_10537437_C_G	2.0x10 <sup>-20</sup>	0			
OTHER-NOT CLUSTERED	INHBB	605	2_121079515_A_C	9.3x10 <sup>-18</sup>	24203			
OTHER-NOT CLUSTERED	CDKN2A	170	9_21963048_C_T	4.3x10 <sup>-15</sup>	0			
OTHER-NOT CLUSTERED	TCF7L2	2,437	10_114782803_T_C	6.5x10 <sup>-15</sup>	0			
OTHER-NOT CLUSTERED	RALB	447	2_121077184_A_G	1.2x10 <sup>-13</sup>	24898			

OTHER-NOT CLUSTERED	MKL1	1,176	22_40904707_CT_C	4.0x10 <sup>-13</sup>	0
OTHER-NOT CLUSTERED	SLC6A18	290	5_1241565_A_G	8.4x10 <sup>-13</sup>	0
OTHER-NOT CLUSTERED	FRY	1,573	27_CAATAAATAAATA_C	2.0x10 <sup>-12</sup>	0
OTHER-NOT CLUSTERED	ATM	701	11_108098459_TAA_T	2.5x10 <sup>-12</sup>	0
OTHER-NOT CLUSTERED	KCNU1	3,952	8_36849946_C_G	2.8x10 <sup>-12</sup>	56303
OTHER-NOT CLUSTERED	ANXA13	541	8_124757661_C_T	1.7x10 <sup>-11</sup>	8014
OTHER-NOT CLUSTERED	KCNN4	182	19_44281824_C_CTCTT	2.7x10 <sup>-9</sup>	0
OTHER-NOT CLUSTERED	CFLAR	323	2_202004837_G_C	3.1x10 <sup>-9</sup>	0
OTHER-NOT CLUSTERED	APITD1	154	0491895_A_AGCGAGAC	4.6x10 <sup>-9</sup>	0
OTHER-NOT CLUSTERED	TRMT61B	217	2_29094032_C_A	8.6x10 <sup>-9</sup>	0
OTHER-NOT CLUSTERED	NCOA1	1,426	2_24739694_C_CT	9.7x10 <sup>-9</sup>	67651
OTHER-NOT CLUSTERED	ADCY3	836	2_25129473_A_G	1.3x10 <sup>-8</sup>	0
OTHER-NOT CLUSTERED	CDH2	5,742	18_25401204_AT_A	1.4x10 <sup>-8</sup>	129725

;ures 14-15)

#### Supplementary Table 14: Pathways enri

#### Theme

ADENYLATE CYCLASE ADENYLATE CYCLASE ADENYLATE CYCLASE ADENYLATE CYCLASE ADENYLATE CYCLASE ADENYLATE CYCLASE ADENYLATE CYCLASE ADENYLATE CYCLASE ADENYLATE CYCLASE ADENYLATE CYCLASE ADENYLATE CYCLASE ADENYLATE CYCLASE ADHERENS JUNCTION ADHERENS JUNCTION APOPTOSIS CELL CYCLE/DNA DAMAGE RESPONSE CELL CYCLE/DNA DAMAGE RESPONSE CELL CYCLE/DNA DAMAGE RESPONSE CELL CYCLE/DNA DAMAGE RESPONSE DOUBLE STRAND BREAK REPAIR DOUBLE STRAND BREAK REPAIR **GENE SILENCING** WNT/BETA CATENIN **OTHER-NOT CLUSTERED OTHER-NOT CLUSTERED OTHER-NOT CLUSTERED OTHER-NOT CLUSTERED OTHER-NOT CLUSTERED OTHER-NOT CLUSTERED OTHER-NOT CLUSTERED** OTHER-NOT CLUSTERED **OTHER-NOT CLUSTERED OTHER-NOT CLUSTERED** OTHER-NOT CLUSTERED OTHER-NOT CLUSTERED **OTHER-NOT CLUSTERED OTHER-NOT CLUSTERED OTHER-NOT CLUSTERED OTHER-NOT CLUSTERED OTHER-NOT CLUSTERED**
# Pathway

ACTIVATION OF PROTEIN KINASE A ACTIVITY ADENYLATE CYCLASE ACTIVATING PATHWAY ADENYLATE CYCLASE INHIBITORY PATHWAY **CA-DEPENDENT EVENTS** CALMODULIN INDUCED EVENTS CAM PATHWAY CAMP BIOSYNTHETIC PROCESS INHIBITION OF ADENYLATE CYCLASE PATHWAY LPA4-MEDIATED SIGNALING EVENTS PKA-MEDIATED PHOSPHORYLATION OF CREB PKA ACTIVATION PKA ACTIVATION IN GLUCAGON SIGNALLING ADHERENS JUNCTION ORGANIZATION ADHERENS JUNCTIONS INTERACTIONS APOPTOTIC DNA FRAGMENTATION CELL CYCLE **G2 DNA DAMAGE CHECKPOINT** MITOTIC G2/M TRANSITION CHECKPOINT NEGATIVE REGULATION OF G2/M TRANSITION OF MITOTIC CELL CYCLE CELLULAR RESPONSE TO GAMMA RADIATION NONHOMOLOGOUS END-JOINING (NHEJ) CELLULAR RESPONSE TO EXOGENOUS DSRNA **REPRESSION OF WNT TARGET GENES** ACROSOME REACTION AMINO ACID TRANSPORT ACROSS THE PLASMA MEMBRANE BIOCARTA\_DNAFRAGMENT\_PATHWAY **BIOCARTA RARRXR PATHWAY** BIOCARTA\_SET\_PATHWAY BIOCARTA\_VDR\_PATHWAY CHROMOSOME SEPARATION INSULIN IGF PATHWAY-PROTEIN KINASE B SIGNALING CASCADE MITOCHONDRIAL RNA PROCESSING MYOBLAST DIFFERENTIATION N-CADHERIN SIGNALING EVENTS NEGATIVE REGULATION OF ESTABLISHMENT OF PROTEIN LOCALIZATION TO PLASMA NEURONAL STEM CELL POPULATION MAINTENANCE **P38MAPK EVENTS** POSITIVE REGULATION OF GLYCOPROTEIN BIOSYNTHETIC PROCESS POSITIVE REGULATION OF GLYCOPROTEIN METABOLIC PROCESS **PROTEIN KINASE C SIGNALING REGULATION OF CELLULAR EXTRAVASATION REGULATION OF HORMONE METABOLIC PROCESS REGULATION OF MYOBLAST FUSION TISSUE REGENERATION** TRNA THREONYLCARBAMOYLADENOSINE METABOLIC PROCESS YAP1- AND WWTR1 (TAZ)-STIMULATED GENE EXPRESSION

## not ER-positive breast cancer (ES<0)

### Database

GOBP **REACTOME DATABASE ID RELEASE 55** REACTOME REACTOME REACTOME REACTOME GOBP **REACTOME DATABASE ID RELEASE 55** PATHWAY INTERACTION DATABASE NCI-NATURE CURATED DATA **REACTOME DATABASE ID RELEASE 55 REACTOME DATABASE ID RELEASE 55** REACTOME GOBP REACTOME GOBP PANTHER PATHWAY GOBP GOBP GOBP GOBP REACTOME GOBP **REACTOME DATABASE ID RELEASE 55** GOBP **REACTOME DATABASE ID RELEASE 55** MSIGDB\_C2 MSIGDB\_C2 MSIGDB\_C2 MSIGDB\_C2 GOBP PANTHER PATHWAY GOBP GOBP PATHWAY INTERACTION DATABASE NCI-NATURE CURATED DATA GOBP GOBP **REACTOME DATABASE ID RELEASE 55** GOBP GOBP GOBP GOBP GOBP GOBP GOBP GOBP **REACTOME DATABASE ID RELEASE 55** 

Pathway ID	Enrichment	Number of	Conoc	
	Score	Genes	Genes	
GO:0034199	0.52	16	ADCY3,ADCY9,F	
170660	0.62	10	ADCY3,ADCY9,(	
R-HSA-170670.1	0.55	14	ADCY3,ADCY9,(	
R-HSA-111996.1	0.43	30	ADCY3,ADCY9,F	
R-HSA-111933.1	0.42	28	ADCY3,ADCY9,F	
R-HSA-111997.1	0.42	28	ADCY3,ADCY9,F	
GO:0006171	0.47	16	ADCY3,ADCY9,(	
997269	0.55	14	ADCY3,ADCY9,(	
LPA4-MEDIATED SIGNALING EVENTS	0.55	15	ADCY3,ADCY9,(	
111931	0.44	20	ADCY3,ADCY9,F	
163615	0.45	19	ADCY3,ADCY9,F	
R-HSA-164378.1	0.49	17	ADCY3,ADCY9,F	
GO:0034332	0.44	60	CDH2,SORBS1,(	
R-HSA-418990.2	0.54	29	CDH2,CDH8,CA	
GO:0006309	0.45	13	DFFA,CECR2,DI	
P00013	0.42	14	CCNE1,RPA3,PS	
GO:0031572	0.52	29	BABAM1.ATM.	
GO:0044818	0.47	15	ATM,HUS1B,FA	
GO:0010972	0.41	17	ATM.HUS1B.FA	
GO:0071480	0.47	11	ATM.XRCC6.AT	
R-HSA-5693571.1	0.46	36	BABAM1.ATM.	
GO:0071360	0.46	10	RALB.COLEC12.	
4641265	0.41	13	TCF7L2.AES.TLE	
GO:0007340	0.47	10	ADCY3.STX2.SY	
352230	0.53	30	SLC6A18.SLC6A	
BIOCARTA DNAFRAGMENT PATHWAY	0.50	10	DFFA.CASP3.GZ	
BIOCARTA RARRXR PATHWAY	0.48	15	NCOA1.NCOA3	
BIOCARTA SET PATHWAY	0.46	11	DFFA.CRFBBP.A	
BIOCARTA VDR PATHWAY	0.48	12	NCOA1.NCOA3.	
GO:0051304	0.49	15	APITD1.SMARC	
P00033	0.42	22		
GC:0000963	0.54	14	GTPBP3 TRMT6	
GO:0045445	0.52	20	TCF7L2 MYOCD	
N-CADHERIN SIGNALING EVENTS	0.41	36	CDH2.PTPN1.RI	
GO:0090005	0.43	12	ANXA13.PID1.L	
GO:0097150	0.57	10	CDH2,DLL1,HES	
171007	0.47	12	RALB, MAPKAPK	
GO:0010560	0.49	14	TCF7L2,PLCB1,F	
GO:1903020	0.44	16	TCF7L2,PLCB1,F	
GO:0070528	0.47	13	PLVAP,SLC26A6	
GO:0002691	0.54	13	PLVAP,PLCB1,P	
GO:0032350	0.42	17	TCF7L2,GATA3,	
GO:1901739	0.45	10	CFLAR,CD53,M۱	
GO:0042246	0.48	13	CFLAR,EYS,IGF1	
GO:0070525	0.59	12	GTPBP3,TRMT6	
2032785	0.43	29	NCOA1,HIPK1,T	

'RKAR1A,PRKAR2B,ADCY1,PRKACB,ADCY2,ADCY8,PRKACA,PRKAR2A,PRKACG,PRKAR1B,ADCY5,ADCY7,ADCY4,A 3NAL,ADCY1,ADCY2,ADCY8,ADCY5,ADCY7,ADCY4,ADCY6

3NAL,ADCY1,ADCY2,GNAI3,ADCY8,GNAT3,GNAI1,GNAI2,ADCY5,ADCY7,ADCY4,ADCY6 'DE1C,PRKAR1A,PRKAR2B,ADCY1,PRKACB,PLA2G4A,CAMK4,ADCY2,ADCY8,PRKACA,PDE1A,PRKAR2A,CREB1,CA DE1C,PRKAR1A,PRKAR2B,ADCY1,PRKACB,CAMK4,ADCY2,ADCY8,PRKACA,PDE1A,PRKAR2A,CREB1,CALM3,PRK 'DE1C,PRKAR1A,PRKAR2B,ADCY1,PRKACB,CAMK4,ADCY2,ADCY8,PRKACA,PDE1A,PRKAR2A,CREB1,CALM3,PRK CALCRL, ADCY1, ADCY2, RAMP2, ADCY10, ADM, NPR3, UCN2, GNAS, ADCY5, TAAR1, ADORA2A, ADCY4, ADCY6 3NAL, ADCY1, ADCY2, GNAI3, ADCY8, GNAT3, GNAI1, GNAI2, ADCY5, ADCY7, ADCY4, ADCY6 3NAL,ADCY1,RPS6KA5,ADCY2,ADCY8,PRKACA,PRKCE,CREB1,LPAR4,ADCY5,ADCY7,ADCY4,ADCY6 >RKAR1A,PRKAR2B,ADCY1,PRKACB,ADCY2,ADCY8,PRKACA,PRKAR2A,CREB1,CALM3,PRKACG,PRKAR1B,ADCY5,F 'RKAR1A, PRKAR2B, ADCY1, PRKACB, ADCY2, ADCY8, PRKACA, PRKAR2A, CALM3, PRKACG, PRKAR1B, ADCY5, ADCY7, ( 'RKAR1A, PRKAR2B, ADCY1, PRKACB, ADCY2, ADCY8, PRKACA, PRKAR2A, PRKACG, PRKAR1B, GNAS, ADCY5, ADCY7, AI CDH8,CADM2,ACTN2,PVR,CDH10,CDH11,CDH13,CDH4,TBCD,JUP,CTNND1,PVRL1,DLC1,CDH18,CDH12,RAMP2, DM2,PVR,CDH10,CDH11,CDH13,CDH4,JUP,CTNND1,PVRL1,CDH18,CDH12,CTNNA1,CDH6,CDH7,CADM1,CDH1, CER1,KPNA1,CASP3,H1F0,DNASE1L3,HMGB2,KPNB1,HMGB1,DFFB,FOXL2,ENDOG ME3,CCNE2,PSMD11,PSMD12,CCND2,CINP,PSMD14,PSMD7,PSMD3,PSMD13,PSMD4,CCND3 3RE,BRCA1,FANCI,FOXN3,DTL,FAM175A,PLK1,HMGA2,TAOK1,CHEK1,BRSK1,NBN,NEK6,TAOK2,MAPKAPK2,TAC NCI,FOXN3,NAE1,HMGA2,NBN,TAOK3,CLSPN,BLM,TICRR,CDK5RAP3,CCNA2,HUS1,ZNF830 NCI,FOXN3,NAE1,HMGA2,NBN,TAOK3,FHL1,USP47,CLSPN,BLM,TICRR,CDK5RAP3,CCNA2,HUS1,ZNF830 R,XRCC5,WRN,TLK2,YAP1,TSPYL5,KDM1A,CRYAB,TMEM109 FP53BP1,XRCC6,BRE,BRCA1,FAM175A,XRCC5,SUMO1,LIG4,POLM,UBE2V2,BARD1,TDP2,RNF8,NHEJ1,HERC2,NE IFNB1,MB21D1,TMEM173,CAV1,MAVS,MUL1,IFIT1,FLOT1 1,CTNNB1,CTBP2,HDAC1,TLE3,TLE4,LEF1,TCF7L1,TLE2,TCF7,CTBP1 T6,ZP4,ACR,ROPN1B,TNP2,PKDREJ,SPESP1,AKAP3 19,SLC38A1,SLC38A2,SLC43A1,SLC6A14,SLC3A2,SLC7A8,SLC43A2,SLC38A4,SLC7A6,SLC36A1,SLC7A9,SLC6A15, MB,HMGB2,TOP2A,HMGB1,DFFB,TOP2B,CASP7,ENDOG .POLR2A,NCOR2,GTF2E1,NCOA2,HDAC3,RXRA,KAT2B,GTF2F1,TBP,GTF2A1,GTF2B,RARA,ERCC3 NP32A,GZMA,GZMB,HMGB2,PRF1,DFFB,NME1,APEX1,SET NCOA2, TSC2, RXRA, CREBBP, MED1, HDAC1, EP300, CARM1, KAT2B, NCOR1 AD1, ERCC4, M1AP, RECQL5, FANCM, TEX14, ESPL1, STRA13, NCAPD3, MEIOB, DIS3L2, TOP2A, TOP2B, NCAPD2 IGF1,IGF1R,INSRR,TSC2,IGF2,GSK3B,IRS2,TSC1,INSR,PTEN,IRS1,PIK3CA,IGF2R,FOXO3,GSK3A,INPPL1,PDPK1,MD 1B,TRNT1,PNPT1,ELAC2,KIAA0391,HSD17B10,MTO1,SUPV3L1,TRIT1,TRMU,PUS1,TRMT10C,FASTKD5 ,IGF1,NRG1,IFRD1,EPAS1,JAG1,GREM1,MBNL1,SDC1,RBPJ,SRF,NOTCH1,RB1,SOX15,T,REST,HINFP,MAPK12,TB) +OA,PTPN11,ROCK1,MYL2,JUP,CTNND1,GSN,AXIN1,GAP43,MAPK8,PIK3R1,FER,CTNNA1,CNR1,DCTN1,CTNNB1 RRC15,GOPC,PPP2R5A,PKDCC,RHOQ,BCL2L1,PPFIA1,TMEM59,CSK,TMBIM1 5,MMP24,JAG1,HES1,PROX1,NOTCH1,SOX2,SRRT (3,KRAS,RALA,HRAS,MAPKAPK2,MAPK11,RALGDS,NRAS,MAPK14,MAPK13,MAPK12 'XYLP1,IGF1,CTNNB1,RAMP1,CCR7,ARFGEF1,CCL19,CCL21,SOAT1,CHP1,SLC51B,GOLGA2 'XYLP1,IGF1,RAB1A,CTNNB1,RAMP1,CCR7,ARFGEF1,CCL19,CCL21,SOAT1,CHP1,SLC51B,RAB1B,GOLGA2 i,AVP,MAS1,ZP4,PLEK,AZU1,DGKQ,ZP3,PDGFB,HTR2B,FLOT1,ADAM15 TGER4,CXCL12,OLFM4,CCL25,CCR2,RIPK3,FADD,ADAM8,CCL28,CCL21,ICAM1 BMP2,ARNT,DKK3,STC2,TRERF1,BMP6,HIF1A,BMP5,FFAR3,PAX8,WNT4,REST,STUB1,AKR1C3,HPN YOD1,EHD1,MYF5,EHD2,MYOG,FLOT1,MYF6,MAPK14 ,LARGE,ERBB4,TEC,CPQ,TXK,NOV,APOD,KLK6,NACA,APOA5 1B,HSD17B10,MTO1,OSGEPL1,TRIT1,TRMU,TP53RK,OSGEP,PUS1,TRMT10C,YRDC

EAD4,TBL1XR1,CHD9,TBL1X,NCOA6,HELZ2,NCOA2,SMARCD3,RXRA,CREBBP,MED1,TEAD1,HIPK2,GATA4,RUNX

**\DCY6** 

\LM3,PRKCD,PRKCG,MAPK1,PRKCA,PRKACG,PRKAR1B,ADRBK1,ADCY5,ADCY7,CALM2,PDE1B,CALM1,ADCY4,AL CD,PRKCG,PRKCA,PRKACG,PRKAR1B,ADRBK1,ADCY5,ADCY7,CALM2,PDE1B,CALM1,ADCY4,ADCY6 CD,PRKCG,PRKCA,PRKACG,PRKAR1B,ADRBK1,ADCY5,ADCY7,CALM2,PDE1B,CALM1,ADCY4,ADCY6

ADCY7,CALM2,CALM1,ADCY4,ADCY6 CALM2,CALM1,ADCY4,ADCY6 DCY4,ADCY6 CTNNA1,LAMA5,ACTN1,CDH6,CDH7,ACTB,CADM1,CDH1,RCC2,PVRL3,ZNF703,CTNNB1,PTPRK,RHOD,FERMT2,F PVRL3,PVRL4,CDH3,CDH9,CDH17,CDH5,PVRL2,CADM3,CDH24,ANG,CDH15

)K3,FZR1,NEK11,RBBP8,PLK5,CDC14B,UIMC1,CLSPN,BLM,BRCC3,CDK5RAP3,CCNA2

3N,PIAS4,XRCC4,RIF1,WHSC1,KAT5,PAXIP1,RAD50,PRKDC,MRE11A,UIMC1,RNF168,H2AFX,DCLRE1C,UBE2N,MI

SLC16A10,SLC1A4,SLC7A11,SLC7A1,SLC38A5,SLC1A5,SLC7A3,SLC7A5,SLC7A10,SLC7A7,SLC6A20,SLC36A2,SLC3,

)M2,IRS4,INS

X2

,LRP5,CALM3,PIP5K1C,GJA1,GRIA2,CDC42,CTTN,FGFR1,PIK3CA,DAGLB,MAPRE1,CAMK2G,DAGLA,CALM2,RAC1

CY6

AB8B,PKP2,PVRL4,SMAD7,CDH3,PIP5K1C,CDH9,CDH17,CDH5,TAOK2,PIP5K1A,ARHGEF7,ACTG1,PVRL2,VCL,CT

DC1,BRCC3,TDP1,POLL

A1,SLC6A12,SLC6A6,SLC38A3

L,KIF5B,CALM1,PLCG1

TN,MLLT4,WHAMM,ACTN3,CADM3,TRIP6,TESK2,CDH24,ANG,CSK,CDH15,THY1

Supplementary Table 15: Enrichments* for ER- breast cancer based on summary statistic	ics for c
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Annotation <sup>¥</sup>	Proportion	Proportion	Enrichment	P-value		
Amotation	SNPs	heritability	Linternet	· value		
SuperEnhancers, extended 500bp	0.17	0.43	2.48	2x10 <sup>-7</sup>		
SuperEnhancers	0.17	0.40	2.36	1x10 <sup>-5</sup>		
H3K4me3, extended 500 bp	0.26	0.60	2.35	5x10 <sup>-4</sup>		
H3K4me1	0.43	1.00	2.35	3x10 <sup>-4</sup>		
H3K27ac <sup>†</sup> extended 500 bp	0.42	0.98	2.31	1x10 <sup>-12</sup>		
H3K27ac <sup>†</sup>	0.39	0.81	2.07	2x10 <sup>-7</sup>		
H3K27ac <sup>‡</sup> extended 500 bp	0.34	0.67	1.98	5x10 <sup>-4</sup>		
DGF, extended 500 bp	0.54	1.03	1.90	7x10 <sup>-5</sup>		
H3K4me1, extended 500 bp	0.61	0.91	1.49	2x10 <sup>-4</sup>		
Introns, extended 500 bp	0.40	0.57	1.43	9x10 <sup>-4</sup>		
Repressed, extended 500 bp	0.72	0.48	0.67	2x10 <sup>-4</sup>		
Of the 52 baseline genomic features described in Finucane, H.K. et al. Partitioning heritability by functiona *Statistically significant after Bonferroni correction for 52 tests Hinks, D. et al. Super-enhancers in the control of cell identity and disease. Cell 155, 934-47 (2013) <sup>†</sup> Schizophrenia Working Group of the Psychiatric Genomics Consortium. Biological insights from 108 schize						

#### ombined analysis of BCAC (ER-negative) and CIMBA (BRCA1 mutation carrier

al annotation using genome-wide association summary statistics. Nat Genet 47, 1228

ophrenia-associated genetic loci. Nature 511, 421-7 (2014).

rs) data

### -35 (2015).

Supplementary Table 16: List of 125 SNPs associated with risk of ER-negative breast
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How identified	Location	SNP	MAF	OR	%FRR
Previous hit for breast cancer	1p36.22	rs616488	0.33	0.89	0.424
New hit for overall breast cancer	1p34.2	rs4233486	0.36	0.97	0.023
New hit for overall breast cancer	1p32.3	rs140850326	0.49	0.96	0.051
Previous hit for breast cancer	1p13.2	rs11552449	0.17	1.04	0.023
New hit for overall breast cancer	1p12	rs7529522	0.23	1.05	0.053
Previous hit for breast cancer	1q21.2	rs12048493	0.38	1.05	0.071
Previous hit for breast cancer	1q32.1	rs6678914	0.41	0.94	0.124
Previous hit for breast cancer	1q32.1	rs4245739	0.26	1.12	0.347
Previous hit for breast cancer	1a32.1	rs4951011	0.16	1.07	0.080
New hit for overall breast cancer	1a32.1	rs35383942	0.06	1.15	0.150
Previous hit for breast cancer	1a43	rs72755295	0.03	1.09	0.023
New hit for overall breast cancer	2n25.1	rs113577745	0.10	1.06	0.035
Previous hit for breast cancer	2p24.1	rs12710696	0.36	1.04	0.041
New hit for FR-negative breast cancer	2p23.3	rs200648189	0.19	0.94	0.072
Previous hit for breast cancer	2p23.2	rs4577244	0.23	0.93	0.072
New hit for overall breast cancer	2a13	rs71801447	0.06	1.05	0.110
Previous hit for breast cancer	2q13 2q14 1	rs/18/19887	0.00	0.85	0.33/
Previous hit for breast cancer	2q1 2a33 1	rs1830298	0.10	1.08	0.554
Previous hit for breast cancer	2935.1	rs/1/2075	0.20	0.04	0.102
Previous hit for breast cancer	2935 2035	rs16857609	0.30	1.07	0.120
Provious hit for breast cancer	2q33 3n2/ 1	rs/1072768	0.20	1.07	0.115
Previous hit for breast cancer	3p24.1 3n21.31	rs6706502	0.47	0.02	0.047
Previous hit for breast cancer	2n1/11	rc10E2229	0.10	1.02	0.000
New bit for everall breast concer	3p14.1	151053538	0.14	1.03	0.007
New hit for everall breast cancer	3p13	150805189	0.48	1.00	0.008
New hit for overall breast cancer	3p12.1	1513066793	0.09	0.96	0.010
New hit for overall breast cancer	4p14	rs6815814	0.26	1.06	0.084
New hit for overall breast cancer	4q21.23	4:84370124	0.47	1.03	0.023
New hit for overall breast cancer	4q22.1	rs10022462	0.44	1.01	0.007
New hit for overall breast cancer	4q28.1	rs//528541	0.13	0.94	0.053
Previous hit for breast cancer	5p15.33	rs10069690	0.26	1.19	0.830
Previous hit for breast cancer	5p15.33	rs3215401	0.31	0.88	0.495
New hit for overall breast cancer	5p15.33	rs116095464	0.05	1.03	0.003
Previous hit for breast cancer	5p15.1	rs13162653	0.45	0.98	0.006
Previous hit for breast cancer	5p12	rs10941679	0.25	1.03	0.016
New hit for overall breast cancer	5q11.1	rs35951924	0.32	0.96	0.042
Previous hit for breast cancer	5q11.2	rs62355902	0.16	1.06	0.057
Previous hit for breast cancer	5q11.2	rs104/20/6	0.38	1.03	0.020
Previous hit for breast cancer	5q11.2	rs1353/4/	0.09	0.98	0.005
Previous nit for breast cancer	5q14.2	rs//0/921	0.25	0.97	0.016
New hit for overall breast cancer	5q22.1	rs6882649	0.34	0.98	0.002
Previous hit for breast cancer	5q33.3	rs1432679	0.43	1.08	0.200
Previous nit for breast cancer	6p25.3	rs11242675	0.37	0.99	0.005
New hit for overall breast cancer	op22.3	153819405	0.33	0.97	0.022
Drovious bit for broast concer	op22.2	15/105/345	0.07	1.02	0.009
Previous fill for breast cancer	op22.1	15920/408	0.41	1.03	0.020
Now bit for overall broast cancer	0414.1 6α14-1	151/529111 rc12207096	0.22	1.00	0.075
new nit for overall preast cancer	0Y14.1	121220/200	0.47	0.90	0.051

New hit for ER-negative breast cancer	6q23.1	rs6569648	0.23	0.94	0.089
Previous hit for breast cancer	6q25	rs9397437	0.07	1.32	0.716
Previous hit for breast cancer	6q25.1	rs3757322	0.32	1.14	0.529
Previous hit for breast cancer	6q25.2	rs2747652	0.47	0.92	0.240
New hit for overall breast cancer	7p15.3	rs7971	0.35	0.96	0.046
New hit for overall breast cancer	7p15.1	rs17156577	0.11	1.05	0.025
Previous hit for breast cancer	7q21.2	rs6964587	0.39	1.02	0.003
New hit for overall breast cancer	7q22.1	rs71559437	0.12	0.95	0.029
Previous hit for breast cancer	7q32.3	rs4593472	0.35	0.97	0.019
New hit for ER-negative breast cancer	, 8p23.3	rs66823261	0.23	1.08	0.140
Previous hit for breast cancer	, 8p12	rs9693444	0.32	1.02	0.003
Previous hit for breast cancer	, 8p11.23	rs13365225	0.18	0.90	0.225
Previous hit for breast cancer	8g21.11	rs6472903	0.17	0.96	0.025
Previous hit for breast cancer	8g21.11	rs2943559	0.08	1.10	0.088
Previous hit for breast cancer	8q23.3	rs13267382	0.36	1.02	0.003
New hit for ER-negative breast cancer	8q24.13	rs17350191	0.34	1.07	0.139
Previous hit for breast cancer	8q24.21	rs13281615	0.41	1.07	0.150
Previous hit for breast cancer	8q24.21	rs11780156	0.17	1.05	0.039
Previous hit for breast cancer	9p21.3	rs1011970	0.16	1.05	0.037
Previous hit for breast cancer	9q31.2	rs10759243	0.29	1.02	0.003
Previous hit for breast cancer	9q31.2	rs676256	0.38	0.98	0.002
Previous hit for breast cancer	9q31.2	rs10816625	0.06	1.07	0.029
New hit for overall breast cancer	9q33.1	rs1895062	0.41	0.93	0.174
New hit for overall breast cancer	9q33.3	rs10760444	0.43	1.05	0.077
New hit for overall breast cancer	9q34.2	rs587745765	0.20	1.05	0.046
New hit for overall breast cancer	10p14	rs67958007	0.12	1.08	0.080
Previous hit for breast cancer	10p12.31	rs11814448	0.02	1.04	0.004
Previous hit for breast cancer	10q21.2	rs10995201	0.16	0.93	0.090
Previous hit for breast cancer	10q22.3	rs704010	0.38	1.06	0.108
New hit for overall breast cancer	10q23.33	rs140936696	0.18	1.04	0.022
Previous hit for breast cancer	10q25.2	rs7904519	0.46	1.08	0.202
Previous hit for breast cancer	10q26.13	rs35054928	0.40	1.06	0.108
Previous hit for breast cancer	10q26.13	rs2981578	0.47	1.04	0.045
Previous hit for breast cancer	11p15.5	rs3817198	0.32	1.02	0.003
New hit for overall breast cancer	11p15	rs6597981	0.48	0.94	0.128
Previous hit for breast cancer	11q13.1	rs3903072	0.47	0.99	0.005
New hit for ER-negative breast cancer	11q22.3	rs11374964	0.42	0.91	0.303
New hit for ER-negative breast cancer	11q22.3	rs74911261	0.02	0.82	0.102
Previous hit for breast cancer	11q24.3	rs11820646	0.40	0.94	0.123
Previous hit for breast cancer	12p13.1	rs12422552	0.26	1.04	0.035
Previous hit for breast cancer	12p11.22	rs7297051	0.24	0.87	0.499
New hit for overall breast cancer	12q21.31	12:85009437:T:C	0.34	0.93	0.162
Previous hit for breast cancer	12q22	rs17356907	0.30	0.94	0.108
New hit for overall breast cancer	12q24.31	12:120832146:C:T	0.16	1.04	0.020
Previous hit for breast cancer	13q13.1	rs11571833	0.01	1.58	0.290
Previous hit for breast cancer	13q22.1	rs6562760	0.23	0.92	0.168
Previous hit for breast cancer	14q13.3	rs2236007	0.21	0.95	0.052
Previous hit for breast cancer	14q24.1	rs999737	0.23	0.92	0.168
Previous hit for breast cancer	14q32.12	rs11627032	0.25	0.95	0.062
New hit for overall breast cancer	14q32.33	rs10623258	0.45	1.03	0.023
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Previous hit for breast cancer	15q26.1	rs2290203	0.21	0.96	0.029
New hit for ER-negative breast cancer	16p13.3	rs11076805	0.25	0.92	0.178
Previous hit for breast cancer	16q12.1	rs4784227	0.24	1.14	0.441
Previous hit for breast cancer	16q12.2	rs11075995	0.24	1.07	0.111
Previous hit for breast cancer	16q12.2	rs17817449	0.41	0.93	0.174
New hit for overall breast cancer	16q12.2	rs28539243	0.49	1.05	0.075
Previous hit for breast cancer	16q23.2	rs13329835	0.23	1.06	0.077
New hit for overall breast cancer	16q24.2	rs4496150	0.25	0.96	0.036
Previous hit for breast cancer	17q11.2	chr17:29230520	0.27	0.95	0.065
New hit for overall breast cancer	17q21.31	17:44252468:G:A	0.19	0.95	0.048
Previous hit for breast cancer	17q22	rs2787486	0.30	0.96	0.040
Previous hit for breast cancer	17q25.3	rs745570	0.50	1.04	0.048
New hit for ER-negative breast cancer	18q12.1	rs36194942	0.30	0.92	0.199
New hit for overall breast cancer	18q12.1	rs117618124	0.05	0.84	0.196
New hit for overall breast cancer	19p13.13	rs78269692	0.05	1.09	0.042
Previous hit for breast cancer	19p13.11	rs67397200	0.30	1.17	0.738
Previous hit for breast cancer	19p13.11	rs4808801	0.34	0.96	0.046
New hit for overall breast cancer	19p13.11	rs2965183	0.35	1.05	0.069
New hit for ER-negative breast cancer	19p13.2	rs322144	0.47	0.95	0.085
New hit for ER-negative breast cancer	19q12	rs113701136	0.32	1.08	0.175
New hit for overall breast cancer	19q13.22	rs71338792	0.23	1.03	0.012
Previous hit for breast cancer	19q13.31	rs3760982	0.46	1.08	0.203
New hit for overall breast cancer	20p12.3	rs16991615	0.06	1.10	0.065
New hit for overall breast cancer	20q13.13	rs6122906	0.18	1.08	0.116
Previous hit for breast cancer	22q13.1	chr22:39359355	0.04	1.09	0.038
Previous hit for breast cancer	22q13.1	rs6001930	0.10	1.14	0.215
New hit for overall breast cancer	22q13.2	rs73161324	0.06	1.10	0.064
New hit for overall breast cancer	22q13.31	rs28512361	0.11	1.09	0.097

MAF, minor allele frequency; OR, odds ratio pero copy of the minor allele, estimated based on OncoArray data %FRR, percentage explained of an assumed 2-fold increased risk of ER-negative breast cancer to the first-degree female relative of a woman with ER-negative breast cancer

Supplementary Table 17: List of 39 SNPs associated with breast cancer risk for BRCA1 mutation c					
How identified	Location	SNP	MAF	HR	
Previous hit for breast cancer	1p36.22	rs616488	0.33	0.96	
New hit for overall breast cancer	1p34.2	rs4233486	0.36	0.95	
Previous hit for breast cancer	1q32.1	rs4245739	0.26	1.09	
New hit for overall breast cancer	1q41	rs11117758	0.21	0.94	
Previous hit for breast cancer	1q43	rs72755295	0.03	1.13	
New hit for ER-negative breast cancer	2p23.3	rs200648189	0.19	0.88	
Previous hit for breast cancer	2p23.2	rs4577244	0.23	0.92	
Previous hit for breast cancer	2q33.1	rs1830298	0.28	1.08	
Previous hit for breast cancer	2q35	rs16857609	0.26	1.04	
Previous hit for breast cancer	5p15.33	rs10069690	0.26	1.18	
Previous hit for breast cancer	5p15.33	rs3215401	0.31	0.90	
Previous hit for breast cancer	5q33.3	rs1432679	0.43	1.04	
New hit for overall breast cancer	6q14.1	rs12207986	0.47	0.95	
New hit for ER-negative breast cancer	6q23.1	rs6569648	0.23	0.94	
Previous hit for breast cancer	6q25	rs9397437	0.07	1.20	
Previous hit for breast cancer	6q25.1	rs3757322	0.32	1.14	
New hit for overall breast cancer	7q34	rs11977670	0.43	1.06	
Previous hit for breast cancer	8p11.23	rs13365225	0.18	0.95	
Previous hit for breast cancer	8q21.11	rs2943559	0.08	1.07	
New hit for ER-negative breast cancer	8q24.13	rs17350191	0.34	1.08	
New hit for overall breast cancer	9q33.1	rs1895062	0.41	0.95	
Previous hit for breast cancer	10q25.2	rs7904519	0.46	1.08	
Previous hit for breast cancer	11p15.5	rs3817198	0.32	1.06	
New hit for ER-negative breast cancer	11q22.3	rs11374964	0.42	0.91	
New hit for ER-negative breast cancer	11q22.3	rs74911261	0.02	0.74	
Previous hit for breast cancer	11q24.3	rs11820646	0.40	0.94	
Previous hit for breast cancer	12p11.22	rs7297051	0.24	0.88	
New hit for overall breast cancer	12q24.31	12:120832146:C:T	0.16	1.06	
Previous hit for breast cancer	13q22.1	rs6562760	0.23	0.89	
New hit for ER-negative breast cancer	16p13.3	rs11076805	0.25	0.96	
Previous hit for breast cancer	16q12.1	rs4784227	0.24	1.05	
Previous hit for breast cancer	16q12.2	rs17817449	0.41	0.94	
Previous hit for breast cancer	16q23.2	rs13329835	0.23	1.06	
New hit for ER-negative breast cancer	18q12.1	rs36194942	0.30	0.95	
New hit for overall breast cancer	18q12.1	rs117618124	0.05	0.89	
Previous hit for breast cancer	19p13.11	rs67397200	0.30	1.18	
New hit for ER-negative breast cancer	19p13.2	rs322144	0.47	0.92	
New hit for ER-negative breast cancer	19q12	rs113701136	0.32	1.05	
Previous hit for breast cancer	<b>22</b> a13.1	rs6001930	0.10	1.06	

MAF, minor allele frequency; HR, hazard ratio pero copy of the minor allele, estimated based on all available CI %VPR, percentage explained of the variance in polygenic risk of breast cancer for *BRCA1* mutation carriers

