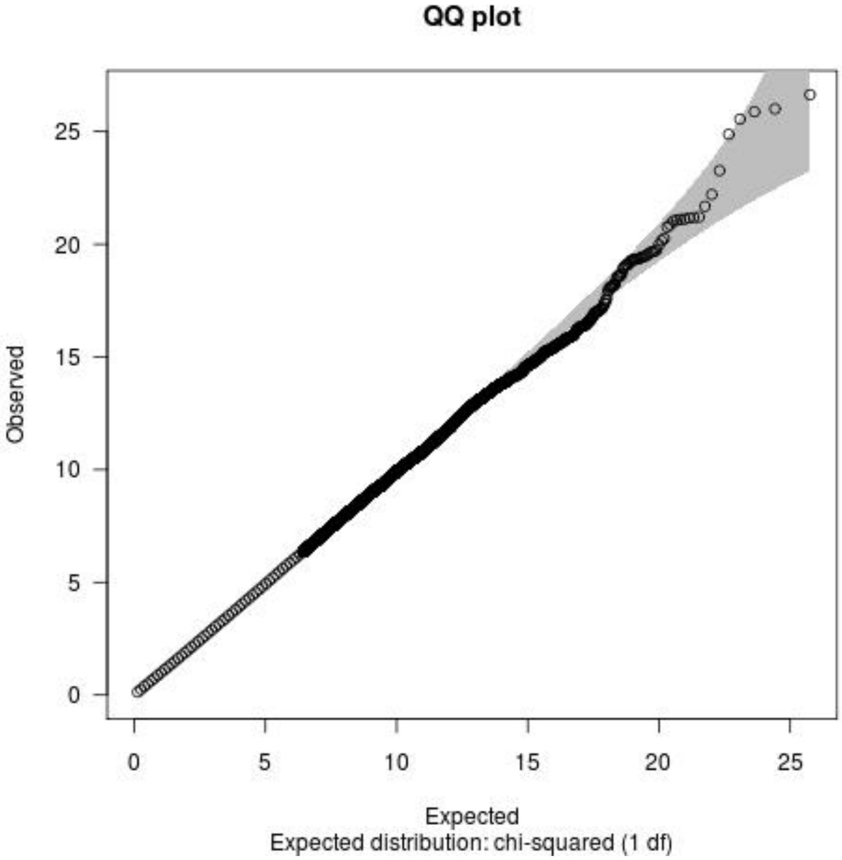
Supplementary Figure 1: QQ Plot of Association Statistics for the C-BCAC ER- GWAS. The observed versus expected score test statistics are shown for ~2.6M autosomal loci after QC exclusions and imputation to HapMap2 (λ=0.98).

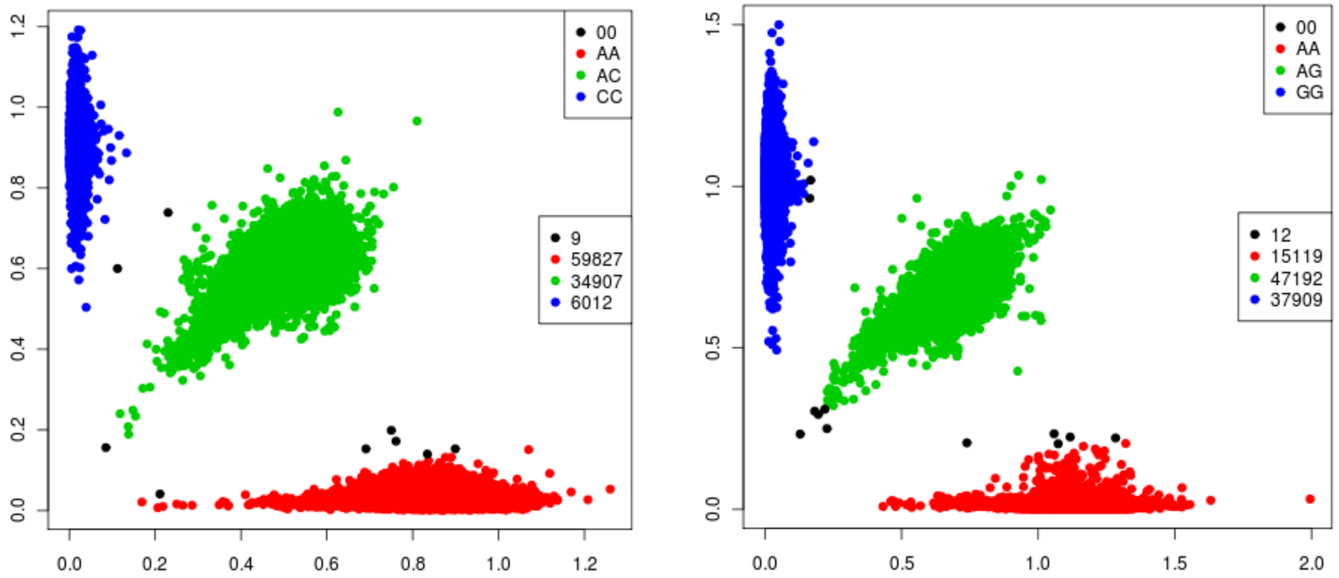


Nature Genetics: doi:10.1038/ng.2561

Supplementary Figure 2: Cluster plots for the normalized intensities of the two alleles, over all BCAC studies, for four SNPs achieving genome-wide significance.

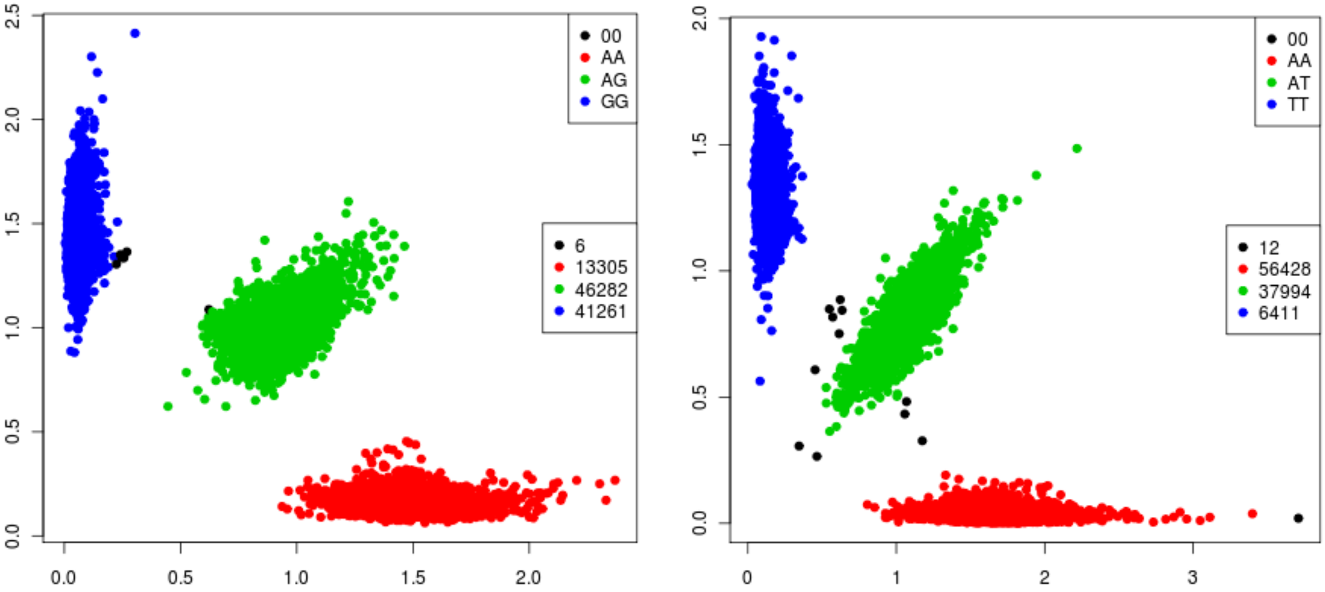
A. rs4245739 1q32.1/*MDM4*

B. rs6678914 1q32.1/*LGR6*



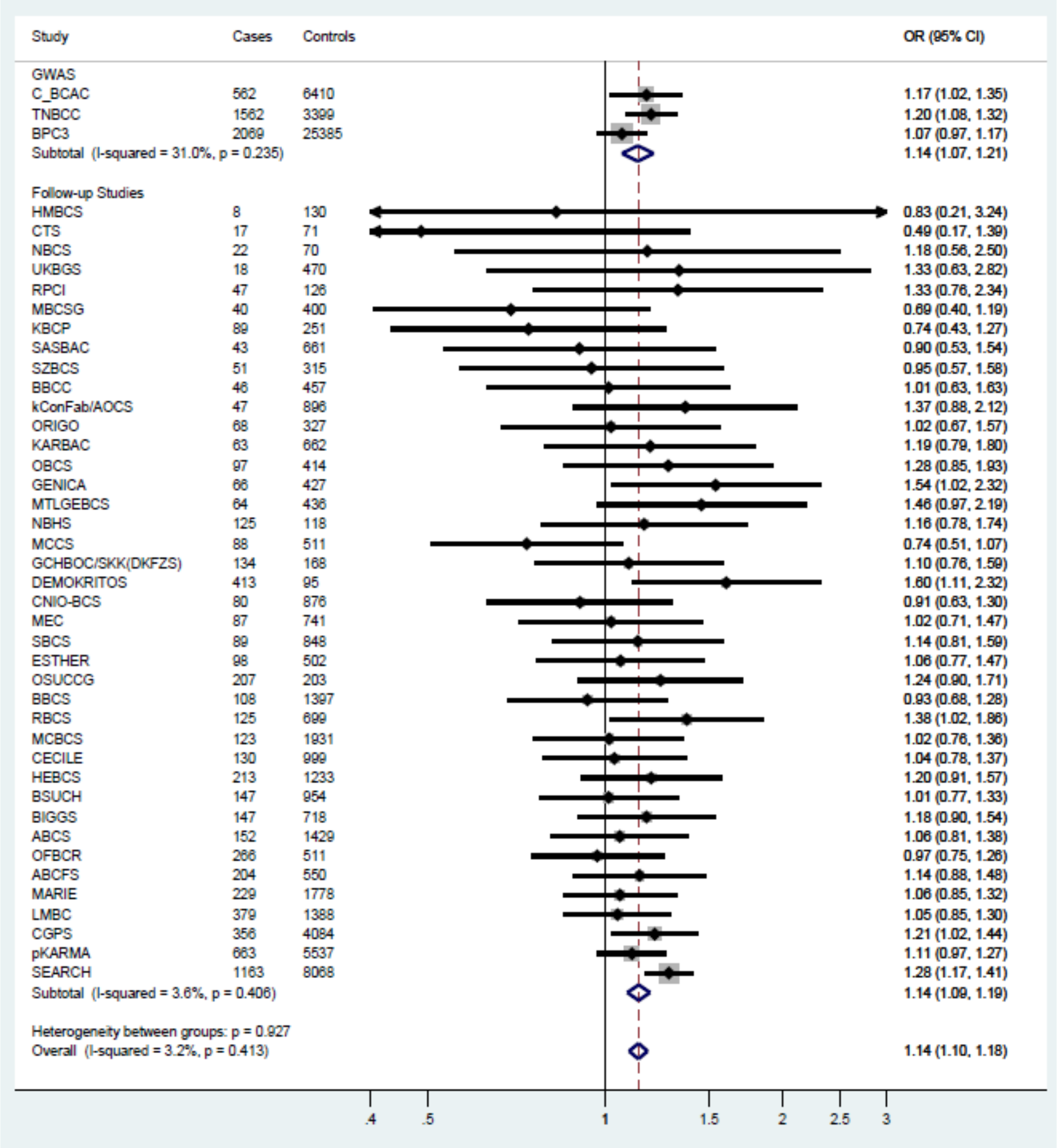
C. rs12710696 2p24

D. rs11075995 6q12/*FTO*

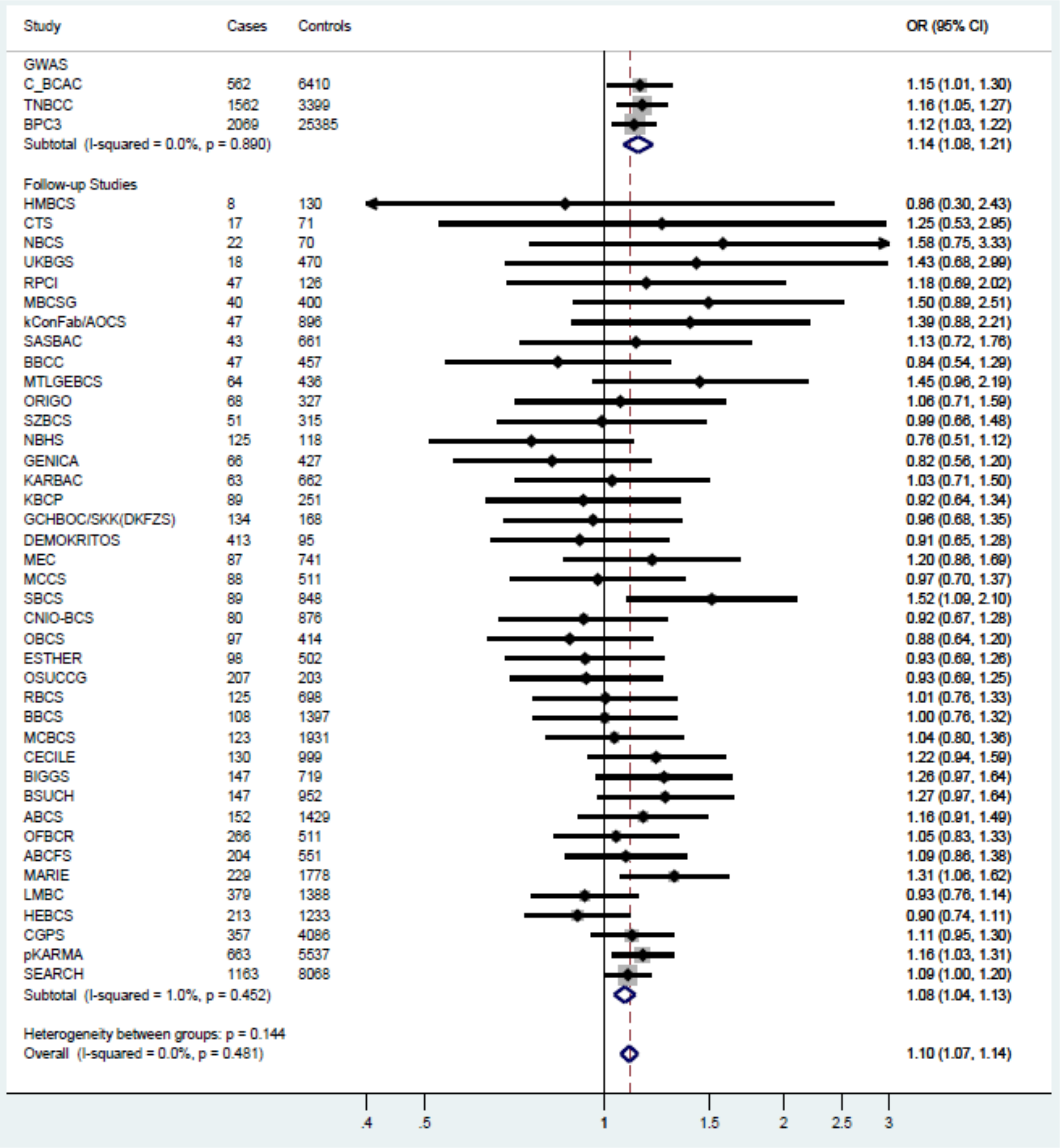


Supplementary Figure 3: Forest plots showing study-specific estimates and meta-analysis of ER- disease for 1q32.1/MDM4, 1q32.1/LGR6 , 2p24 and 6q12.2/FTO loci in women of European ancestry. Black circles denote the estimated per-allele OR for the risk allele in Europeans. The horizontal lines denote 95% confidence limits. The area of the grey squares is inversely proportional to the variance of the estimate. The diamond denotes the estimated per-allele OR and overall CI from the combined analyses. Estimates from combined analyses differ slightly from those shown in Table 1 because of different software used.

A. rs4245739 in 1q32.1/*MDM4*

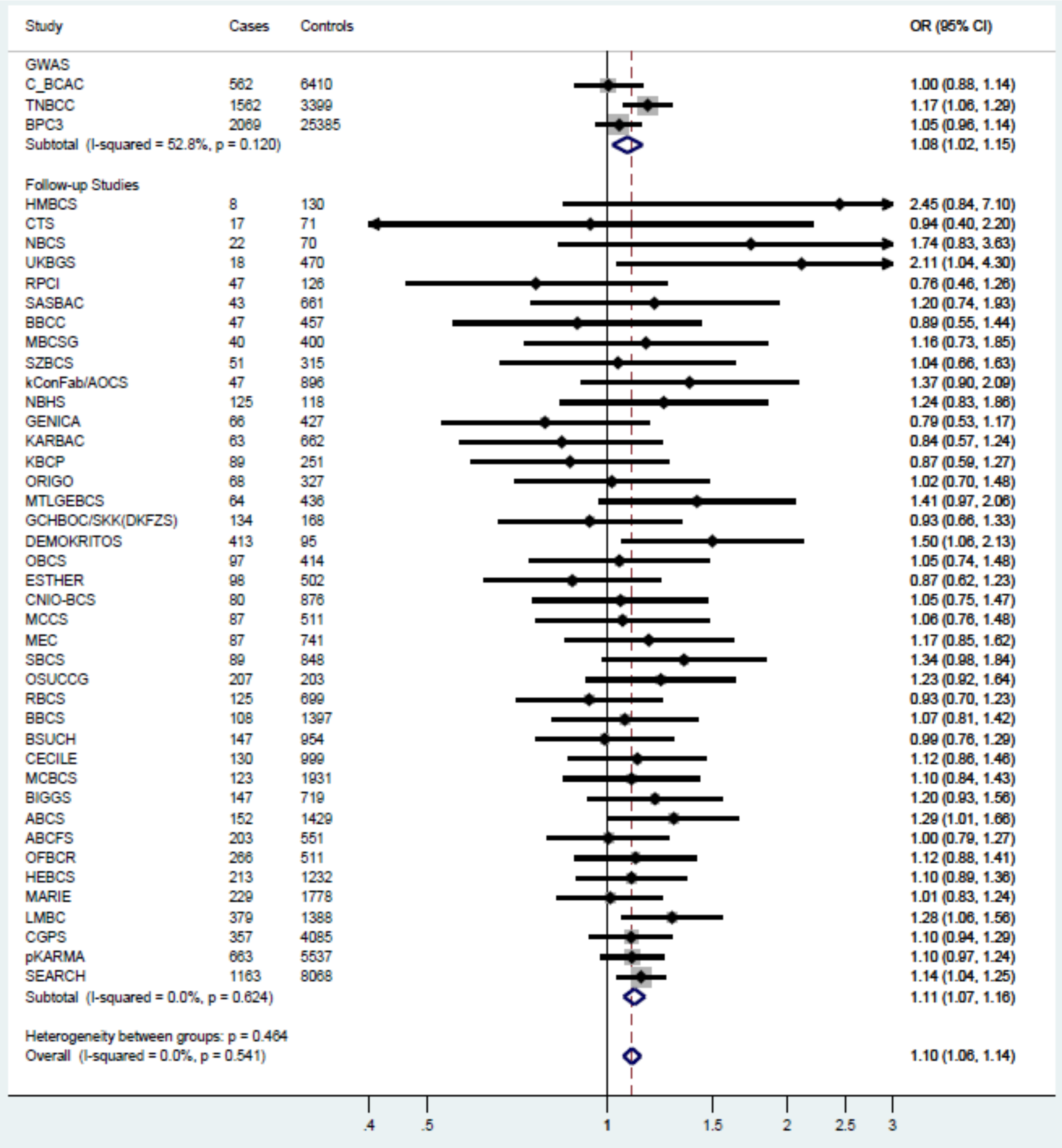


B. rs6678914 in 1q32.1/*LGR6*



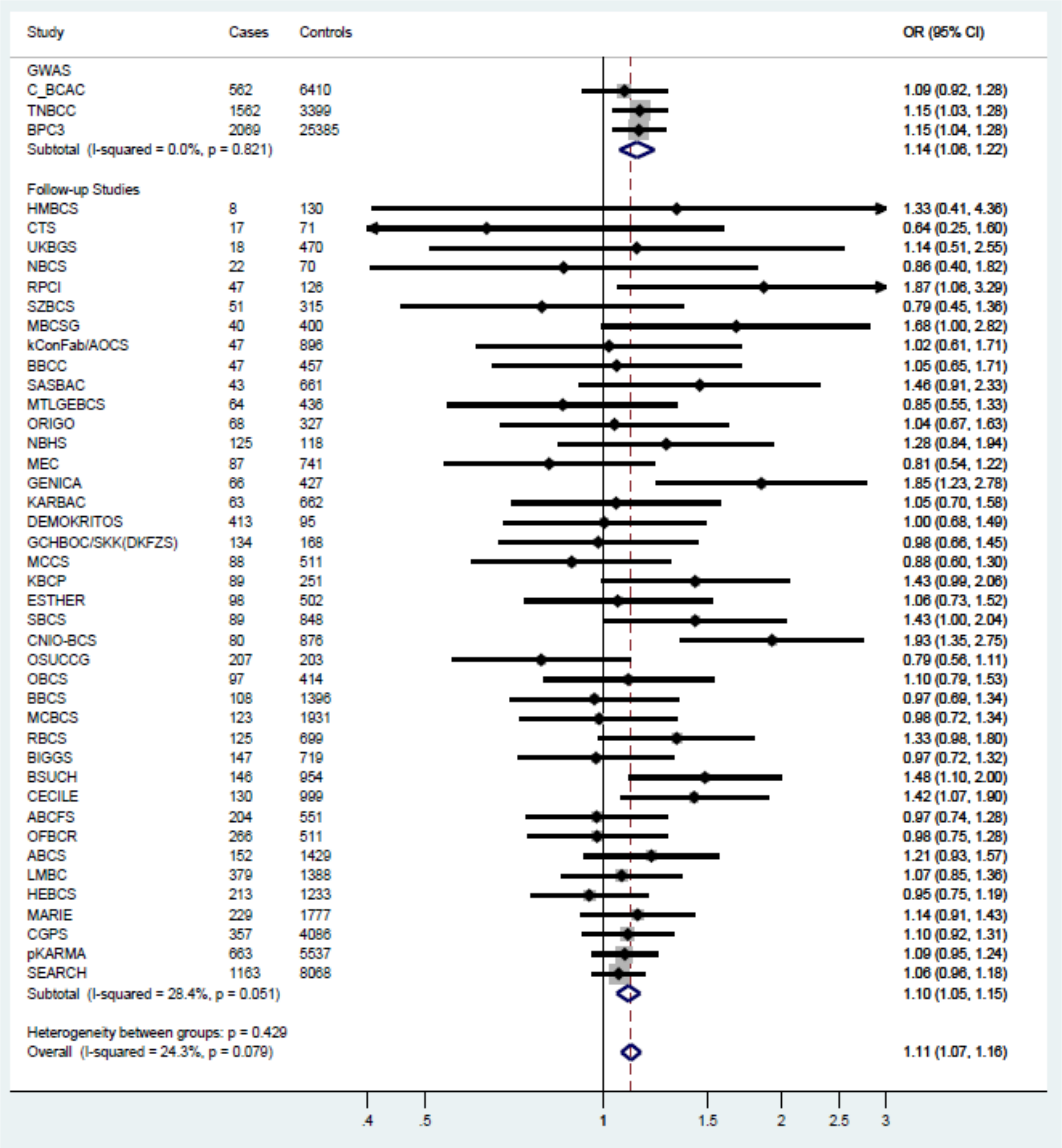
Study	Cases	Controls	OR (95% CI)
GWAS			
C_BCAC	562	6410	1.15 (1.01, 1.30)
TNBCC	1562	3399	1.16 (1.05, 1.27)
BPC3	2069	25385	1.12 (1.03, 1.22)
Subtotal (I-squared = 0.0%, p = 0.890)			1.14 (1.08, 1.21)
Follow-up Studies			
HMBCS	8	130	0.86 (0.30, 2.43)
CTS	17	71	1.25 (0.53, 2.95)
NBCS	22	70	1.58 (0.75, 3.33)
UKBGS	18	470	1.43 (0.68, 2.99)
RPCI	47	126	1.18 (0.69, 2.02)
MBCSG	40	400	1.50 (0.89, 2.51)
kConFab/AOCS	47	896	1.39 (0.88, 2.21)
SASBAC	43	661	1.13 (0.72, 1.76)
BBCC	47	457	0.84 (0.54, 1.29)
MTLGEBCS	64	436	1.45 (0.96, 2.19)
ORIGO	68	327	1.06 (0.71, 1.59)
SZBCS	51	315	0.99 (0.66, 1.48)
NBHS	125	118	0.76 (0.51, 1.12)
GENICA	66	427	0.82 (0.56, 1.20)
KARBAC	63	662	1.03 (0.71, 1.50)
KBCP	89	251	0.92 (0.64, 1.34)
GCHBOC/SKK(DKFZS)	134	168	0.96 (0.68, 1.35)
DEMOKRITOS	413	95	0.91 (0.65, 1.28)
MEC	87	741	1.20 (0.86, 1.69)
MCCS	88	511	0.97 (0.70, 1.37)
SBCS	89	848	1.52 (1.09, 2.10)
CNIO-BCS	80	876	0.92 (0.67, 1.28)
OBCS	97	414	0.88 (0.64, 1.20)
ESTHER	98	502	0.93 (0.69, 1.26)
OSUCCG	207	203	0.93 (0.69, 1.25)
RBCS	125	698	1.01 (0.76, 1.33)
BBCS	108	1397	1.00 (0.76, 1.32)
MCBCS	123	1931	1.04 (0.80, 1.36)
CECILE	130	999	1.22 (0.94, 1.59)
BIGGS	147	719	1.26 (0.97, 1.64)
BSUCH	147	952	1.27 (0.97, 1.64)
ABCS	152	1429	1.16 (0.91, 1.49)
OFBCR	266	511	1.05 (0.83, 1.33)
ABCFS	204	551	1.09 (0.86, 1.38)
MARIE	229	1778	1.31 (1.06, 1.62)
LMBC	379	1388	0.93 (0.76, 1.14)
HEBCS	213	1233	0.90 (0.74, 1.11)
CGPS	357	4086	1.11 (0.95, 1.30)
pKARMA	663	5537	1.16 (1.03, 1.31)
SEARCH	1163	8068	1.09 (1.00, 1.20)
Subtotal (I-squared = 1.0%, p = 0.452)			1.08 (1.04, 1.13)
Heterogeneity between groups: p = 0.144			
Overall (I-squared = 0.0%, p = 0.481)			1.10 (1.07, 1.14)

C. rs12710696 in 2p24



Study	Cases	Controls	OR (95% CI)
GWAS			
C_BCAC	562	6410	1.00 (0.88, 1.14)
TNBCC	1562	3399	1.17 (1.06, 1.29)
BPC3	2069	25385	1.05 (0.96, 1.14)
Subtotal (I-squared = 52.8%, p = 0.120)			1.08 (1.02, 1.15)
Follow-up Studies			
HMBCS	8	130	2.45 (0.84, 7.10)
CTS	17	71	0.94 (0.40, 2.20)
NBCS	22	70	1.74 (0.83, 3.63)
UKBGS	18	470	2.11 (1.04, 4.30)
RPCI	47	126	0.76 (0.46, 1.26)
SASBAC	43	661	1.20 (0.74, 1.93)
BBCC	47	457	0.89 (0.55, 1.44)
MBCSG	40	400	1.16 (0.73, 1.85)
SZBCS	51	315	1.04 (0.66, 1.63)
kConFab/AOCS	47	896	1.37 (0.90, 2.09)
NBHS	125	118	1.24 (0.83, 1.86)
GENICA	66	427	0.79 (0.53, 1.17)
KARBAC	63	662	0.84 (0.57, 1.24)
KBCP	89	251	0.87 (0.59, 1.27)
ORIGO	68	327	1.02 (0.70, 1.48)
MTLGEBCS	64	436	1.41 (0.97, 2.06)
GCHBOC/SKK(DKFZS)	134	168	0.93 (0.66, 1.33)
DEMOKRITOS	413	95	1.50 (1.06, 2.13)
OBCS	97	414	1.05 (0.74, 1.48)
ESTHER	98	502	0.87 (0.62, 1.23)
CNIO-BCS	80	876	1.05 (0.75, 1.47)
MCCS	87	511	1.06 (0.76, 1.48)
MEC	87	741	1.17 (0.85, 1.62)
SBCS	89	848	1.34 (0.98, 1.84)
OSUCCG	207	203	1.23 (0.92, 1.64)
RBCS	125	699	0.93 (0.70, 1.23)
BBCS	108	1397	1.07 (0.81, 1.42)
BSUCH	147	954	0.99 (0.76, 1.29)
CECILE	130	999	1.12 (0.86, 1.46)
MCBCS	123	1931	1.10 (0.84, 1.43)
BIGGS	147	719	1.20 (0.93, 1.56)
ABCS	152	1429	1.29 (1.01, 1.66)
ABCFS	203	551	1.00 (0.79, 1.27)
OFBCR	266	511	1.12 (0.88, 1.41)
HEBCS	213	1232	1.10 (0.89, 1.36)
MARIE	229	1778	1.01 (0.83, 1.24)
LMBC	379	1388	1.28 (1.06, 1.56)
CGPS	357	4085	1.10 (0.94, 1.29)
pKARMA	663	5537	1.10 (0.97, 1.24)
SEARCH	1163	8068	1.14 (1.04, 1.25)
Subtotal (I-squared = 0.0%, p = 0.624)			1.11 (1.07, 1.16)
Heterogeneity between groups: p = 0.464			
Overall (I-squared = 0.0%, p = 0.541)			1.10 (1.06, 1.14)

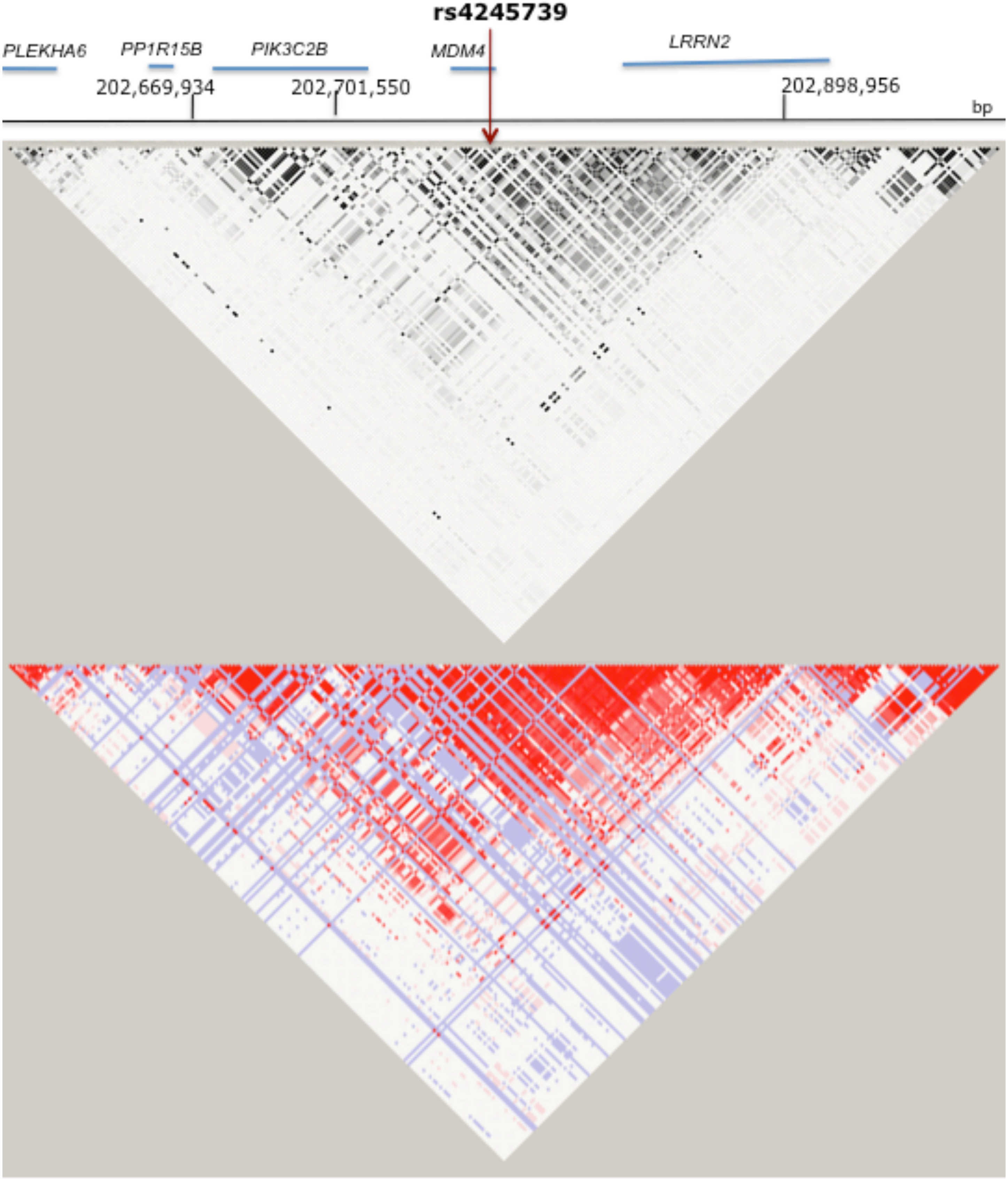
D. rs11075995 in 6q12.2/*FTO*



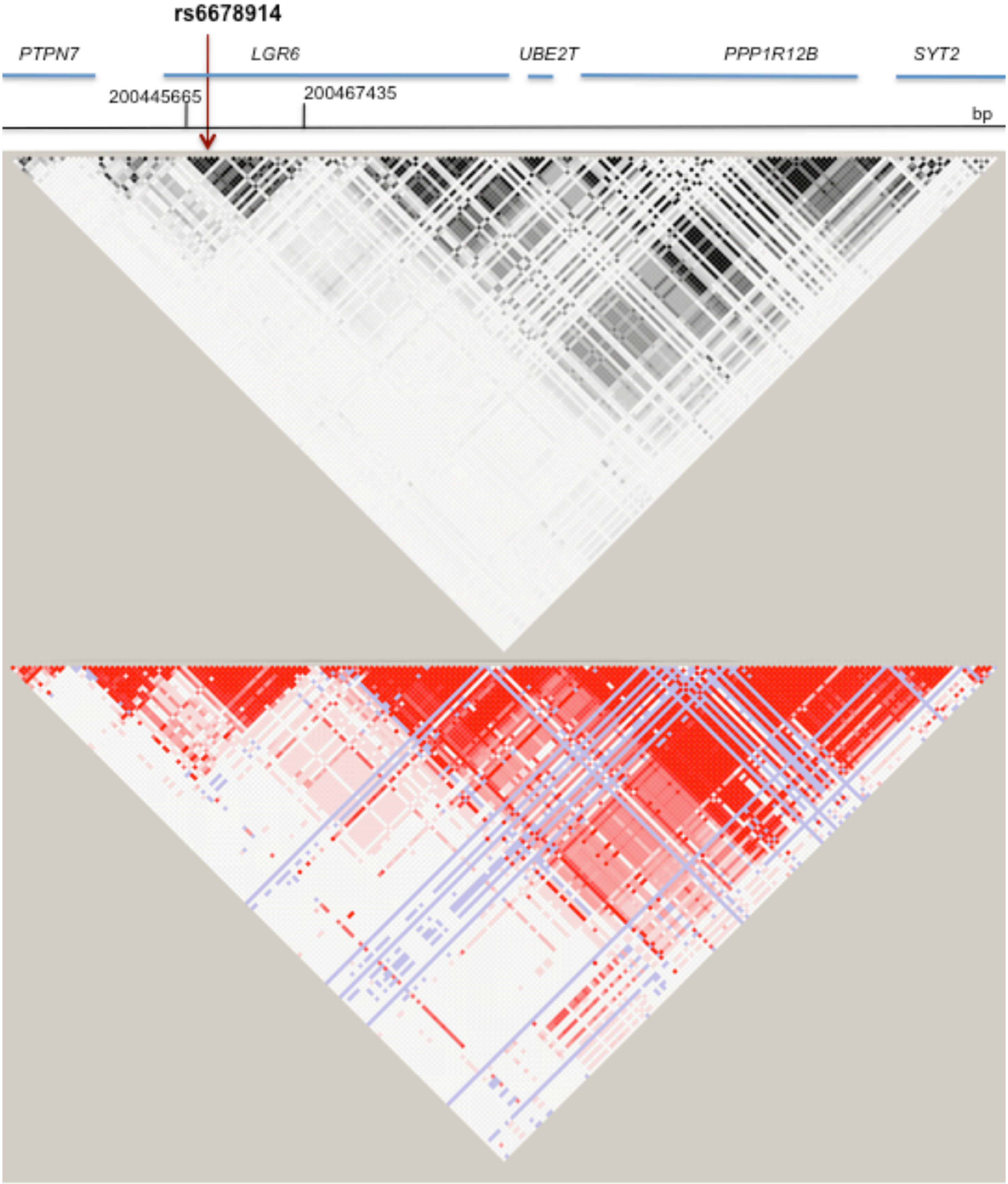
Study	Cases	Controls	OR (95% CI)
GWAS			
C_BCAC	562	6410	1.09 (0.92, 1.28)
TNBCC	1562	3399	1.15 (1.03, 1.28)
BPC3	2069	25385	1.15 (1.04, 1.28)
Subtotal (I-squared = 0.0%, p = 0.821)			1.14 (1.06, 1.22)
Follow-up Studies			
HMBCS	8	130	1.33 (0.41, 4.36)
CTS	17	71	0.64 (0.25, 1.60)
UKBGS	18	470	1.14 (0.51, 2.55)
NBCS	22	70	0.86 (0.40, 1.82)
RPCI	47	126	1.87 (1.06, 3.29)
SZBCS	51	315	0.79 (0.45, 1.36)
MBCSG	40	400	1.68 (1.00, 2.82)
kConFab/AOCS	47	896	1.02 (0.61, 1.71)
BBCC	47	457	1.05 (0.65, 1.71)
SASBAC	43	661	1.46 (0.91, 2.33)
MTLGEBCS	64	436	0.85 (0.55, 1.33)
ORIGO	68	327	1.04 (0.67, 1.63)
NBHS	125	118	1.28 (0.84, 1.94)
MEC	87	741	0.81 (0.54, 1.22)
GENICA	66	427	1.85 (1.23, 2.78)
KARBAC	63	662	1.05 (0.70, 1.58)
DEMOKRITOS	413	95	1.00 (0.68, 1.49)
GCHBOC/SKK(DKFZS)	134	168	0.98 (0.66, 1.45)
MCCS	88	511	0.88 (0.60, 1.30)
KBCP	89	251	1.43 (0.99, 2.06)
ESTHER	98	502	1.06 (0.73, 1.52)
SBCS	89	848	1.43 (1.00, 2.04)
CNIO-BCS	80	876	1.93 (1.35, 2.75)
OSUCCG	207	203	0.79 (0.56, 1.11)
OBCS	97	414	1.10 (0.79, 1.53)
BBCS	108	1396	0.97 (0.69, 1.34)
MCBCS	123	1931	0.98 (0.72, 1.34)
RBCS	125	699	1.33 (0.98, 1.80)
BIGGS	147	719	0.97 (0.72, 1.32)
BSUCH	146	954	1.48 (1.10, 2.00)
CECILE	130	999	1.42 (1.07, 1.90)
ABCFS	204	551	0.97 (0.74, 1.28)
OFBCR	266	511	0.98 (0.75, 1.28)
ABCS	152	1429	1.21 (0.93, 1.57)
LMBC	379	1388	1.07 (0.85, 1.36)
HEBCS	213	1233	0.95 (0.75, 1.19)
MARIE	229	1777	1.14 (0.91, 1.43)
CGPS	357	4086	1.10 (0.92, 1.31)
pKARMA	663	5537	1.09 (0.95, 1.24)
SEARCH	1163	8068	1.06 (0.96, 1.18)
Subtotal (I-squared = 28.4%, p = 0.051)			1.10 (1.05, 1.15)
Heterogeneity between groups: p = 0.429			
Overall (I-squared = 24.3%, p = 0.079)			1.11 (1.07, 1.16)

Supplementary Figure 4: Linkage Disequilibrium (LD) Structure at the 1q32.1/ *MDM4*, 1q32.1/*LGR6*, 2p24 and 16q12.2/*FTO* loci. rs3751812 is used as a surrogate for the obesity-related SNP rs9939609[14]. rs17817449 is ~5Kb from rs3751812 and has been associated with ER-positive and ER-negative disease[15]. Pairwise LD plots generated using data from the HapMap CEU population and estimated by r^2 (top panel) and D' (bottom panel). The positions of rs4245739, rs6678914 and rs6678914 are indicated. Gene positions are approximate. Genomic coordinates are from NCBI build 36.

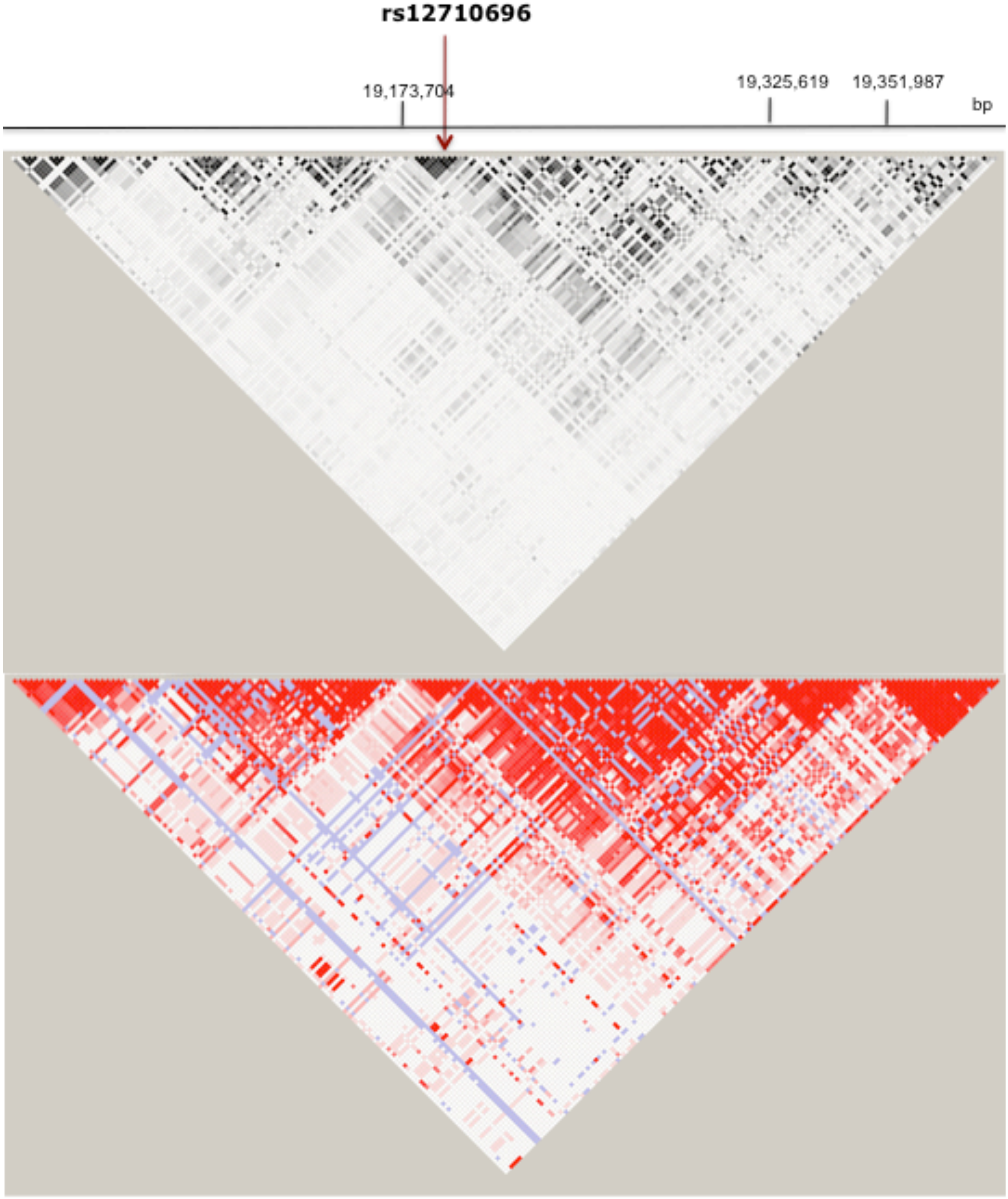
A. 1q32 (*MDM4*) from 202,585kb to 202,885kb



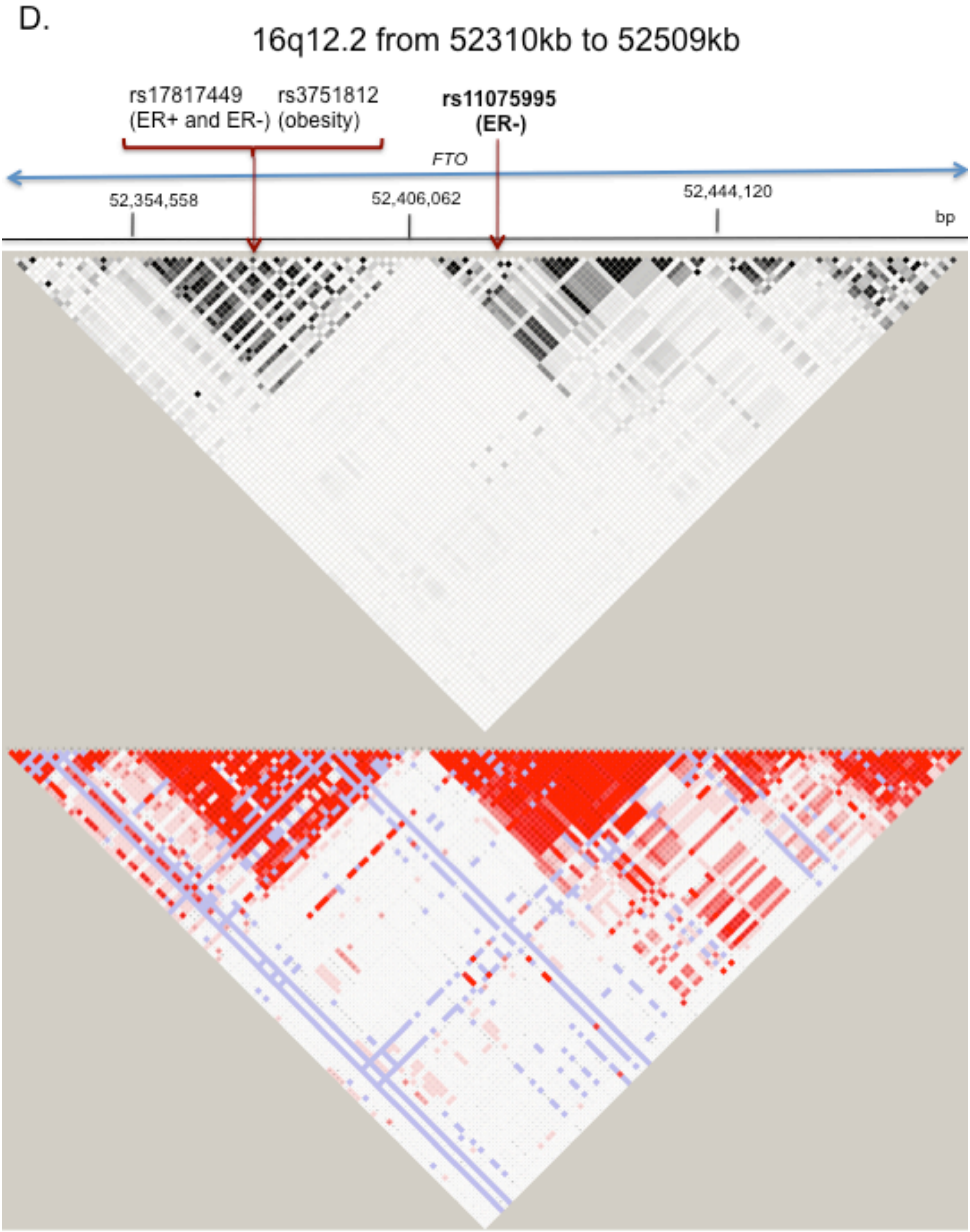
B. 1q32.1 (*LGR6*) from 200380kb to 200880kb



C.



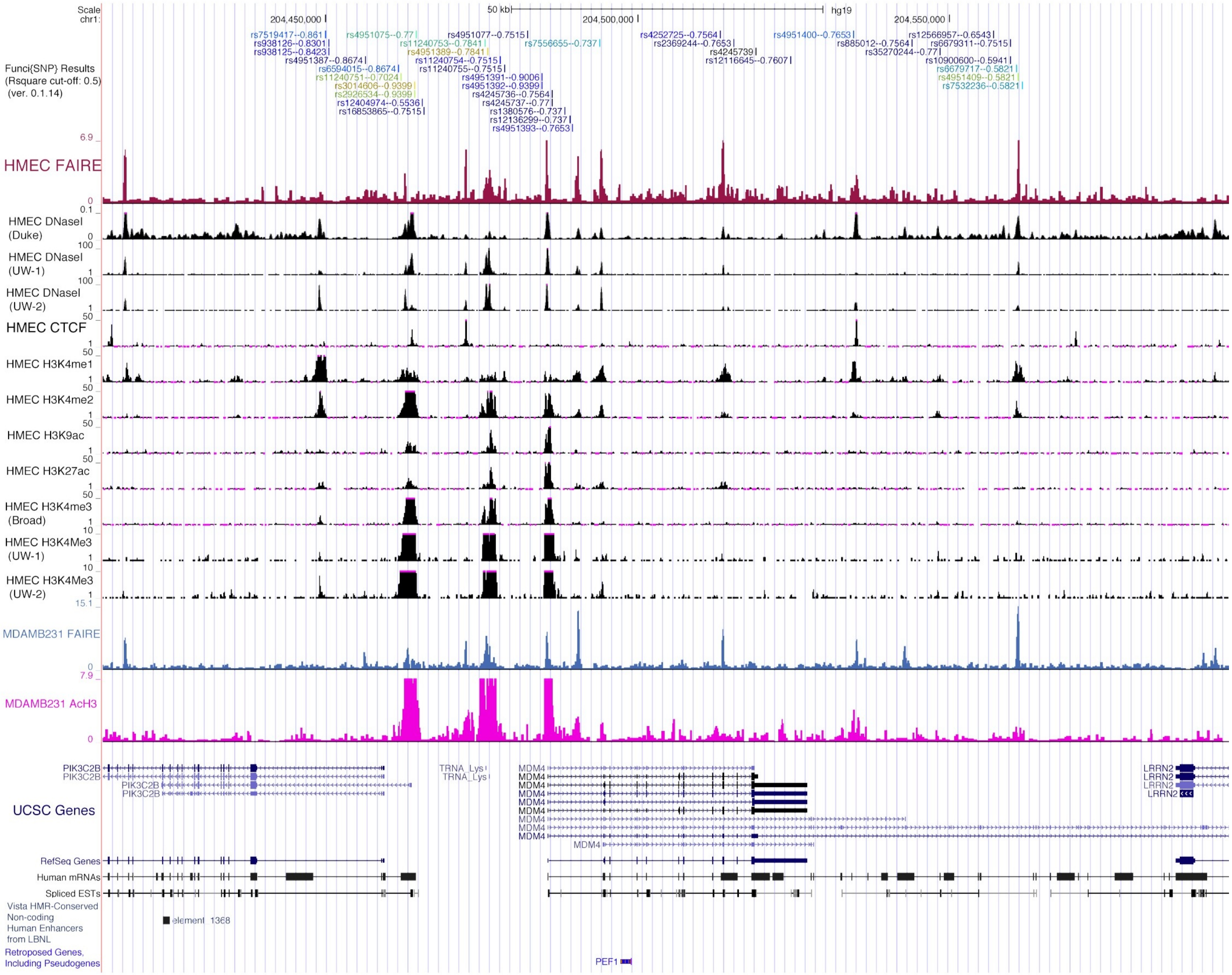
2p24 from 18984kb to 19284kb


D.
16q12.2 from 52310kb to 52509kb
rs17817449
(ER+ and ER-)
rs3751812
(obesity)
rs11075995
(ER-)
FTO
52,354,558
52,406,062
52,444,120
bp

Supplementary Figure 5: Chromatin features for 1q32.1/*MDM4*, 1q32.1/*LGR6*, 2p24 and 16q12.2/*FTO* regions in normal human mammary epithelial cells (HMEC) and triple negative breast cancer cells (MDAMB231).

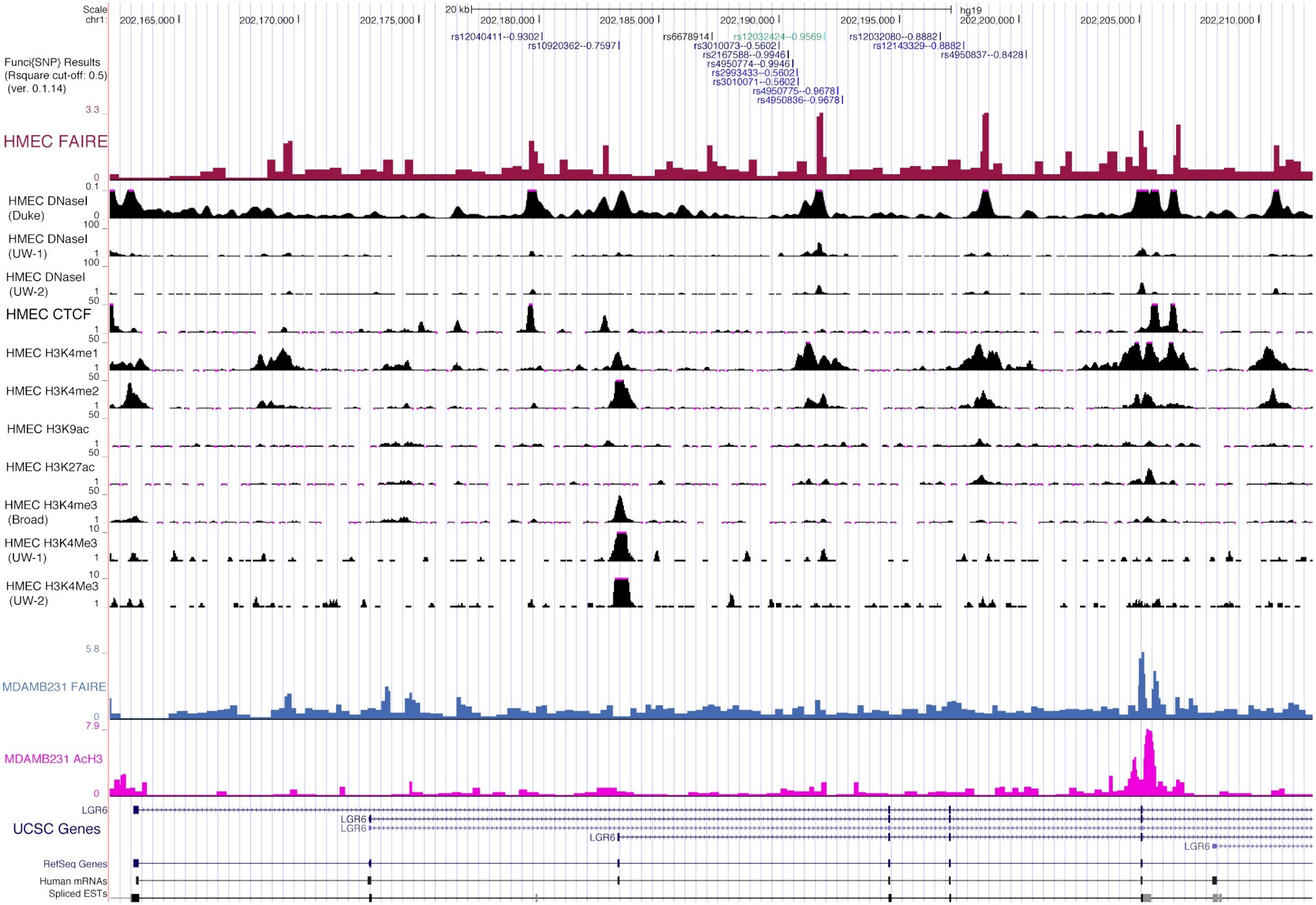
First track shows FunciSNP result. The name of correlated SNP (rsnumber – r^2 value) is shown and colour coded to indicate the number of biofeatures. The bottom tracks are biofeature tracks and RefSeq genes/mRNA/Pseudogene tracks. rsnumber colour code for number of biofeatures (dark blue:0, green:5 brown:10). We collected 9,893 SNPs, which coincided with one or more biofeatures, in a 1Mb window of each of the four tagSNP from the 1000 genome projects in European ethnic group. Among them, 64 SNPs had R^2 value ≥ 0.5 with the tagSNP. Among the 64 SNPs, 17 SNPs were coinciding with 5 or more biofeatures

A. rs4245739 in 1q32.1/*MDM4*

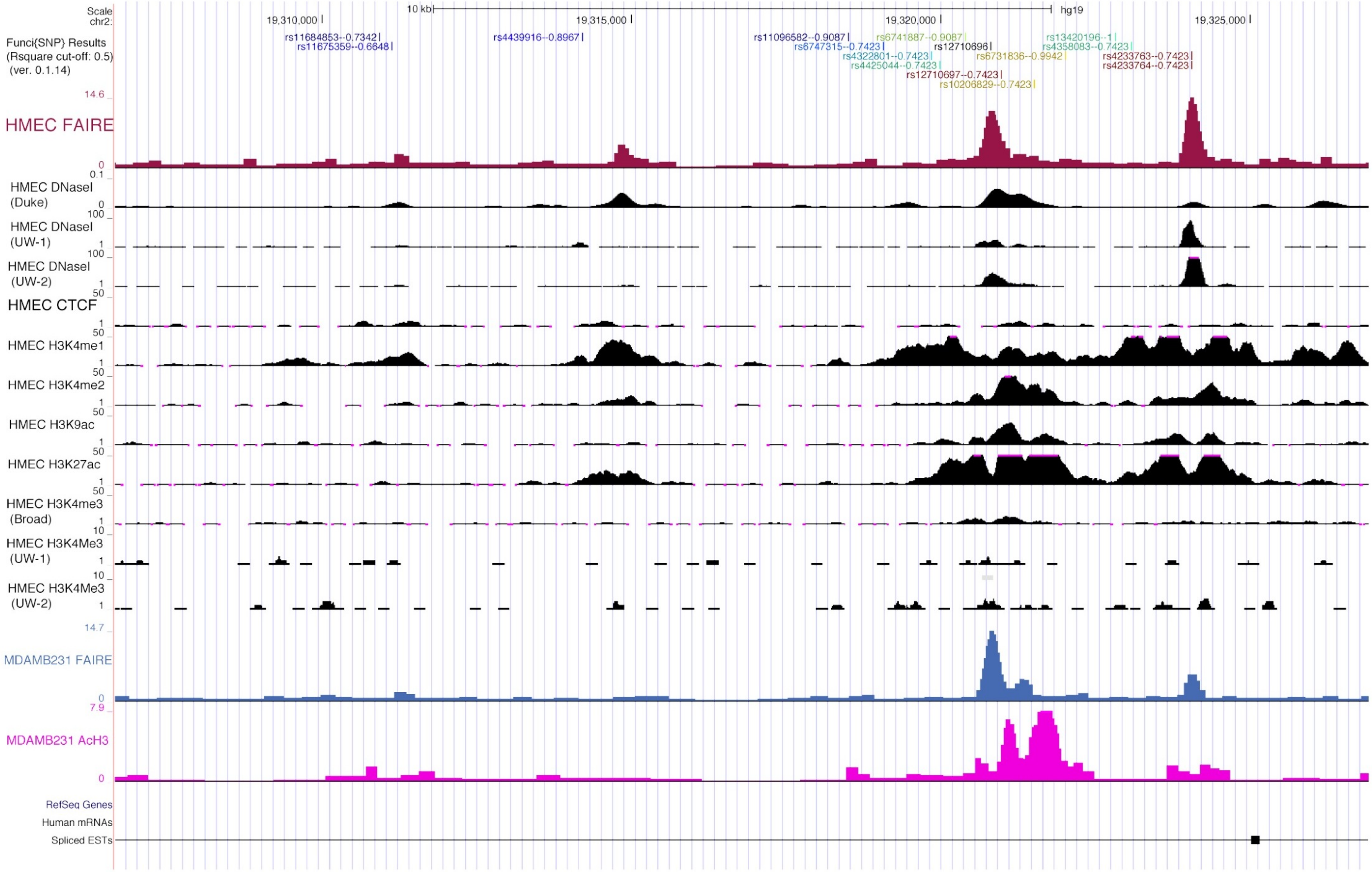


Nature Genetics: doi:10.1038/ng.2561

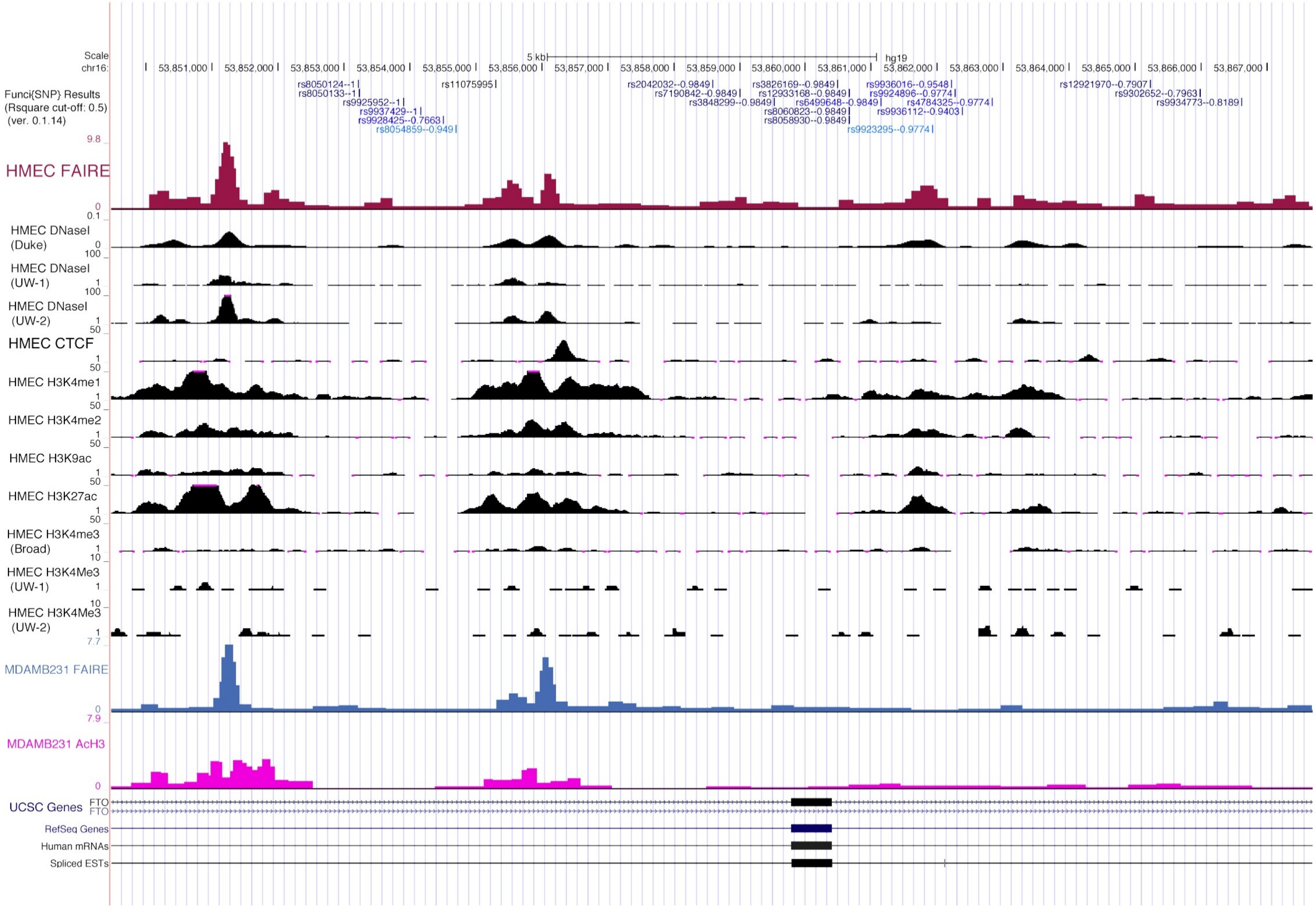
B. rs6678914 1q32.1/LGR6



C. rs12710696 2p24



D. rs11075995 6q12.2/*FTO*



Supplementary Table 1: Number of breast cancer cases and controls in each of the study populations. Numbers for BPC3, TNBCC, C-BCAC and BCAC replication in European populations exclude of subjects that overlapped between studies.

Consortium/Study	Study Abbreviation	Full Name	Country	Controls	ER + cases	ER - cases	TN cases
BPC3	CPS-II	Cancer Prevention Study II Nutrition Cohort	USA	295		293	66
Breast and Prostate Cancer	EPIC	European Prospective Investigation into Cancer and Nutrition	Europe	467		478	93
Cohort Consortium	NHS	The Nurses' Health Study	USA	184		234	86
	NHSII	The Nurses' Health Study II	USA	374		76	34
	PLCO	Prostate, Lung, Colorectal and Ovarian Cancer Screening Trial	USA	340		255	98
	PBCS	Polish Breast Cancer Study	Poland	511		543	229
	WGHS	Women's Genome Health Study	USA	23,214		190	NA
			TOTAL	**25,385**		**2,069**	**606**
TNBCC	ABCTB	Australian Breast Cancer Tissue Bank	Australia				144
Triple Negative	BBCC	Bavarian Breast Cancer Cases and Controls	Germany				218
Breast Cancer	CGEMS	Cancer Genetic Markers of Susceptibility	USA	947			
Consortium	DFCI	Harvard Breast Cancer SPORE Blood Repository	USA				246
	FCCC	Fox Chase Cancer Center	USA				120
	GENICA	Gene Environment Interaction and Breast Cancer in Germany	Germany				59
	HEBCS	Helsinki Breast Cancer Study	Finland	219			83
	KORA	Cooperative Health Research in the Region of Augsburg	Germany	215			
	MARIE	Mammary Carcinoma Risk Factor Investigation	Germany				198
	MCBCS	Mayo Clinic Breast Cancer Study	USA				147
	MCCS	Melbourne Collaborative Cohort Study	Australia				39
	POSH	Prospective Study of Outcomes in Sporadic Versus Hereditary Breast Cancer	UK				266
	QIMR	Australian Twin Cohort study from the Queensland Institute of Medical Research	Australia	650			
	SBCS	Sheffield Breast Cancer Study	UK				42
	WTCCC	Wellcome Trust Case Control Consortium	UK	1,368			
			TOTAL	**3,399**			**1,562**
C-BCAC	ABCFS	Northern California Australian Breast Cancer Family Study	Australia	285		72	
Breast Cancer Association	MARIE	Mammary Carcinoma Risk Factor Investigation	Germany	470		76	
Consortium	HEBCS	Helsinki Breast Cancer Study	Finland	1,012		145	
Combined GWAS	SASBAC	Singapore and Sweden Breast Cancer Study	Sweden	756		109	
	UK2	UK Familial Breast Cancer Study	UK	3,887		160	
			TOTAL	**6,410**		**562**	
AABC	CARE	The Los Angeles component of The Women's Contraceptive and Reproductive Experiences Study	USA	215		130	
African-American	CBCS	The Carolina Breast Cancer Study	USA	589		317	
Breast Cancer	MEC-AA	Multiethnic Cohort	USA	990		176	
Consortium	NBHS	The Nashville Breast Health Study	USA	182		65	
	NC-BCFR	The Northern California Breast Cancer Family Registry	USA	50		121	
	PLCO	Prostate, Lung, Colorectal and Ovarian Cancer Screening Trial	USA	116		6	
	SFBCS	The San Francisco Bay Area Breast Cancer Study	USA	220		50	
	WCHS	The Women's Circle of Health Study	USA	239		80	
	WFBC	Wake Forest University Breast Cancer Study	USA	144		43	
			TOTAL	**2,745**		**988**	
BCAC Replication	**European**						
	ABCFS	Australian Breast Cancer Family Study	Australia	551	382	204	
	ABCS	Amsterdam Breast Cancer Study	Netherlands	1,429	411	152	81
	BBCC	Bavarian Breast Cancer Study	Germany	457	454	47	24
	BBCS	British Breast Cancer Study	UK	1,397	493	108	29
	BIGGS	Breast Cancer In Galway Genetic Study	Ireland	719	476	147	35
	BSUCH	Breast Cancer Study of the University Clinic Heidelberg	Germany	954	479	147	75
	CECILE	CECILE Breast Cancer Study	France	999	743	130	67
	CGPS	Copenhagen General Population Study	Denmark	4,086	1,919	357	80
	CNIO-BCS	Spanish National Cancer Centre Breast Cancer Study	Spain	876	216	80	32

CTS*	California Teachers Study	USA	71		17	17
DEMOKRITOS*	Demokritos	Greece	95		413	413
ESTHER	ESTHER Breast Cancer Study	Germany	502	302	98	23
GC-HBOC[a]	German Consortium for Hereditary Breast & Ovarian Cancer, and Städtisches Klinikum Karlsruhe Deutsches Krebsforschungszentrum Study	Germany	139			
GENICA	Gene Environment Interaction and Breast Cancer in Germany	Germany	427	327	66	5
HEBCS	Helsinki Breast Cancer Study	Finland	1,233	1,231	213	82
HMBCS	Hannover-Minsk Breast Cancer Study	Belarus	130	35	8	
KARBAC	Karolinska Breast Cancer Study	Sweden	662	338	63	
KBCP	Kuopio Breast Cancer Project	Finland	251	288	89	60
LMBC	Leuven Multidisciplinary Breast Centre	Belgium	1,388	2,068	379	215
MARIE	Mammary Carcinoma Risk Factor Investigation	Germany	1,778	1,257	229	51
MBCSG	Milan Breast Cancer Study Group	Italy	400	128	40	9
MCBCS	Mayo Clinic Breast Cancer Study	USA	1,931	1,271	123	26
MCCS	Melbourne Collaborative Cohort Study	Australia	511	350	88	34
MEC	Multi-ethnic Cohort	USA	741	412	87	8
MTLGEBCS	Montreal Gene-Environment Breast Cancer Study	Canada	436	421	64	45
NBCS*	Norwegian Breast Cancer Study	Norway	70		22	21
NBHS*	The Nashville Breast Health Study	USA	118		125	125
OBCS	Oulu Breast Cancer Study	Finland	414	403	97	62
OFBCR	Ontario Familial Breast Cancer Registry	Canada	511	630	266	
ORIGO	Leiden University Medical Centre Breast Cancer Study	Netherlands	327	211	68	5
OSUCCG*	Ohio State University	USA	203		207	207
RBCS	Rotterdam Breast Cancer Study	Netherlands	699	366	125	11
RPCI*	Roswell Park Cancer Institute	USA	126		47	47
SASBAC	Singapore and Sweden Breast Cancer Study	Sweden	661	198	43	
SBCS	Sheffield Breast Cancer Study	UK	848	356	89	17
SEARCH	Study of Epidemiology and Risk factors in Cancer Heredity	UK	8,068	5,113	1,163	400
SKK(DKFZS)*[a]	Städtisches Klinikum Karlsruhe and Deutsches Krebsforschungszentrum Breast Cancer Study	Germany	29		134	134
SZBCS	IHCC-Szczecin Breast Cancer Study	Poland	315	149	51	6
UKBGS	UK Breakthrough Generations Study	UK	470	88	18	3
kConFab/AOCS	kConFab/AOCS	Australia	896	126	47	18
pKARMA	Karolinska Mammography Project for Risk Prediction of Breast Cancer - prevalent cases	Sweden	5,537	3,586	663	
		TOTAL	**41,455**	**25,227**	**6,514**	**2,467**
Asian						
ACP	Asia Cancer Program	Thailand	636	91	52	
HERPACC	Hospital-based Epidemiologic Research Program at Aichi Cancer Center	Japan	1,376	342	124	29
LAABC	Los Angeles County Asian-American Breast Cancer Case-Control Study	USA	990	527	138	
MYBRCA	Malaysian Breast Cancer Genetic Study	Malaysia	610	422	291	84
SBCGS	Shanghai Breast Cancer Genetic Study	China	892	498	271	
SEBCS	Seoul Breast Cancer Study	Korea	1,129	622	363	68
SGBCC	Singapore Breast Cancer Cohort	Singapore	502	261	103	41
TBCS	IARC-Thai Breast Cancer Study	Thailand	253	26	26	
TWBCS	Taiwanese Breast Cancer Study	Taiwan	236	395	179	12
		TOTAL	**6,624**	**3,184**	**1,547**	**234**
African-American						
NBHS	The Nashville Breast Health Study	USA	252	176	91	14
TOTAL ALL STUDIES			**86,270**	**28,587**	**11,771**	**4,883**

ER+: Estrogen receptor (ER) positive

ER-: Estrogen receptor (ER) negative

TN: triple-negative

* These four TNBCC studies only provided controls for other studies and are thus not counted as separate studies.

** These follow up studies were genotyped as part of the TNBCC.

[a] GC-HBOC contains controls only - to be used as controls for SKKDKFZS.

Supplementary Table 2: Conditional analyses of risk of ER-negative breast cancer for the two loci in 1q32.1 (*MDM4* and *LGR6*), and for the two 16q12.2/FTO loci (based on BCAC replication data only)

Locus	SNP	OR	95% CI		*P*		OR	95% CI		*P*
1q32.1	rs4245739	1.14	1.09	1.19	$7.0\text{x}10^{-9}$	rs6678914	1.08	1.04	1.12	$2.2\text{x}10^{-4}$
16q12.2	rs11075995	1.13	1.08	1.18	$2.3\text{x}10^{-7}$	rs17817449	1.13	1.09	1.18	$2.1\text{x}10^{-9}$

Supplementary Table 3: Genotype-specific odds ratios for the most significant SNPs in the 1q32.1/MDM4, 1q32.1/LGR6, 2p24 and 16q12.2/FTO loci and risk of ER-negative breast cancer (based on BCAC replication data only)

Rsnumber/cytoband/gene/ position (NCBI build 36) Genotypes	N Studies	Cases	Controls	OR	95% CI		P value
rs4245739 / 1q32.1 / 202785465 / MDM4							
AA	40	3,318	22,825	1.00			Ref.
AC		2,637	15,798	1.13	1.06	1.20	4.7x10^{-5}
CC		557	2,828	1.31	1.18	1.46	3.6x10^{-7}
Total		6,512	41,451				
				P for departure from log-additivity			0.666
rs6678914 / 1q32.1 / 200453799 / LGR6							
AA	40	1,008	7,036	1.00			Ref.
AG		3,078	20,201	1.02	0.96	1.11	0.545
GG		2,428	14,215	1.15	1.06	1.25	1.3x10^{-3}
Total		6,514	41,452				
				P for departure from log-additivity			0.138
rs12710696 / 2p24.1 / 19184284							
GG	40	2,427	17,123	1.00			Ref.
AG		3,102	19,092	1.10	1.03	1.17	0.002
AA		983	5,238	1.23	1.13	1.34	2.3x10^{-6}
Total		6,512	41,453				
				P for departure from log-additivity			0.744
rs11075995 /16q12.2 / 52412792 / FTO							
AA	40	3,624	23,826	1.00			Ref.
AT		2,443	15,290	1.06	1.00	1.12	0.061
TT		446	2,337	1.30	1.16	1.46	4.4x10^{-6}
Total		6,513	41,453				
				P for departure from log-additivity			0.039

Supplementary Table 4: Distribution of ER, PR, HER2 and triple-negative status in BCAC replication samples of invasive breast cancer cases of European ancestry with ER data

Study	Total	ER status			PR status				HER2 status				TN status in ER- cases			
		Negative	Positive	% neg	Negative	Positive	Missing	% neg	Negative	Positive	Missing	% neg	TN	non-TN	Missing	% TN
ABCFS	586	204	382	35	167	419	0	28	0	0	586		0	0	204	
ABCS	563	152	411	27	235	325	3	42	332	203	28	62	81	66	5	55
BBCC	501	47	454	9	115	386	0	23	433	51	17	89	24	22	1	52
BBCS	601	108	493	18	126	256	219	33	201	50	350	80	29	17	62	63
BIGGS	623	147	476	24	126	390	107	24	328	87	208	79	35	55	57	39
BSUCH	626	147	479	23	192	432	2	31	495	98	33	83	75	65	7	54
CECILE	873	130	743	15	249	613	11	29	560	84	229	87	67	29	34	70
CGPS	2,276	357	1,919	16	635	1,163	478	35	677	110	1,489	86	80	39	238	67
CNIO-BCS	296	80	216	27	127	158	11	45	153	42	101	78	32	22	26	59
CTS*	17	17	0		17	0	0		17	0	0		17	0	0	
DEMOKRITOS*	413	413	0		413	0	0		413	0	0		413	0	0	
ESTHER	400	98	302	25	135	257	8	34	126	49	225	72	23	18	57	56
GENICA	393	66	327	17	90	303	0	23	192	84	117	70	5	36	25	12
HEBCS	1,444	213	1,231	15	455	983	6	32	756	73	615	91	82	32	99	72
HMBCS	43	8	35	19	0	0	43		0	0	43		0	0	8	
KARBAC	401	63	338	16	83	267	51	24	0	0	401		0	0	63	
KBCP	377	89	288	24	139	236	2	37	346	23	8	94	60	27	2	69
LMBC	2,447	379	2,068	15	568	1,866	13	23	1,937	295	215	87	215	122	42	64
MARIE	1,486	229	1,257	15	412	1,073	1	28	1,035	285	166	78	51	148	30	26
MBCSG	168	40	128	24	51	117	0	30	60	57	51	51	9	17	14	35
MCBCS	1,394	123	1,271	9	263	1,130	1	19	970	190	234	84	26	71	26	27
MCCS	438	88	350	20	141	297	0	32	336	59	43	85	34	38	16	47
MEC	499	87	412	17	132	334	33	28	74	20	33	79	8	11	68	42
MTLGEBCS	485	64	421	13	127	357	1	26	422	49	14	90	45	17	2	73
NBCS*	22	22	0		22	0	0		21	0	1		21	0	1	
NBHS*	125	125	0		125	0	0		125	0	0		125	0	0	
OBCS	500	97	403	19	144	355	1	29	431	69	0	86	62	35	0	64
OFBCR	896	266	630	30	339	534	23	39	0	0	896		0	0	266	
ORIGO	279	68	211	24	85	144	50	37	9	0	270		5	0	63	
OSUCCG*	207	207	0		207	0	0		207	0	0		207	0	0	
RBCS	491	125	366	25	146	271	74	35	69	10	412	87	11	2	112	85
RPCI*	47	47	0		47	0	0		47	0	0		47	0	0	
SASBAC	241	43	198	18	67	168	6	29	0	0	241		0	0	43	
SBCS	445	89	356	20	65	109	271	37	188	4	253	98	17	14	58	55
SEARCH	6,276	1,163	5,113	19	898	2,138	3,240	30	2,730	107	3,439	96	400	169	594	70
SKK(DKFZS)*	134	134	0		134	0	0		134	0	0		134	0	0	
SZBCS	200	51	149	26	26	93	81	22	49	55	96	47	6	10	35	38
UKBGS	106	18	88	17	23	54	29	30	31	7	68	82	3	1	14	75
kConFab/AOCS	173	47	126	27	45	108	20	29	102	15	56	87	18	11	18	62
pKARMA	4,249	663	3,586	16	1,246	2,923	80	30	0	0	4,249		0	0	663	
Total	31,741	6,514	25,227		8,617	18,259	4,865		14,006	2,176	15,559		2,467	1,094	2,953	

Table includes only invasive breast cancer cases in iCOGS with data on ER status (i.e. 9,354 invasive breast cancer cases in iCOGS with missing ER data (21% of all cases) are excluded from this table. * Studies including only triple-negative cases (Part of TNBCC). GC-HBOC not shown because it has only controls to be used as controls for SKKDKFZS.

Supplementary Table 5: Association with risk of breast cancer for most significant SNPs in the 1q32.1/*MDM4*, 1q32.1/*LGR6*, 2p24 and 16q12.2/*FTO* loci, stratified by breast cancer tumour subtypes

rsnumber/cytoband/position /neighnourhood genes	Consortium	N Studies	Cases	Controls	OR	95% CI		P value
rs4245739/1q32.1/202785465/MDM4								
All cases vs controls	BCAC/iCOGS	40	41,090	41,451	1.02	1.00	1.04	0.080
ER+ cases vs controls	BCAC/iCOGS	33	25,225	40,600	0.99	0.97	1.02	0.563
ER- cases vs controls	BCAC/iCOGS	40	6,512	41,451	1.14	1.09	1.19	$5.6x10^{-9}$
ER- vs ER+ cases	BCAC/iCOGS	33	5,547	25,225	0.88	0.84	0.92	$2.8x10^{-8}$
TN cases vs controls	BCAC/iCOGS	34	2,465	33,400	1.17	1.09	1.26	$3.1x10^{-5}$
non-TN ER- cases vs controls	BCAC/iCOGS	26	1,094	32,222	1.02	0.92	1.12	0.711
TN cases vs non-TN ER- cases	BCAC/iCOGS	26	1,496	1,094	1.11	0.98	1.27	0.103
	BPC3	5	606	429	1.31	1.07	1.60	0.009
	Combined BCAC+BPC3	*31*	*2,102*	*1,523*	*1.17*	*1.05*	*1.30*	*0.005*
rs6678914 / 1q32.1 / 200453799 / LGR6								
All cases vs controls	BCAC/iCOGS	40	41,090	41,452	1.00	0.98	1.02	0.857
ER+ cases vs controls	BCAC/iCOGS	33	25,223	40,601	0.99	0.96	1.01	0.212
ER- cases vs controls	BCAC/iCOGS	40	6,514	41,452	1.08	1.04	1.12	$1.6x10^{-4}$
ER- vs ER+ cases	BCAC/iCOGS	33	5,549	25,223	0.90	1.00	0.94	$1.6x10^{-6}$
TN cases vs controls	BCAC/iCOGS	34	2,467	33,400	1.03	0.96	1.10	0.414
non-TN ER- cases vs controls	BCAC/iCOGS	26	1,094	32,222	1.11	1.01	1.21	0.027
TN cases vs non-TN ER- cases	BCAC/iCOGS	26	1,498	1,094	0.97	0.86	1.09	0.603
	BPC3	5	606	429	1.02	0.85	1.21	0.869
	Combined BCAC+BPC3	*31*	*2,104*	*1,523*	*0.98*	*0.89*	*1.09*	*0.734*
rs12710696 /2p24.1/19184284								
All cases vs controls	BCAC/iCOGS	40	41,090	41,453	1.04	1.01	1.06	$9.7x10^{-4}$
ER+ cases vs controls	BCAC/iCOGS	33	25,225	40,602	1.01	0.98	1.03	0.534
ER- cases vs controls	BCAC/iCOGS	40	6,512	41,453	1.11	1.06	1.15	$1.0x10^{-6}$
ER- vs ER+ cases	BCAC/iCOGS	33	5,547	25,225	0.91	0.87	0.95	$2.7x10^{-5}$
TN cases vs controls	BCAC/iCOGS	34	2,466	33,401	1.15	1.07	1.23	$6.7x10^{-5}$
non-TN ER- cases vs controls	BCAC/iCOGS	26	1,094	32,223	1.16	1.06	1.26	0.001
TN cases vs non-TN ER- cases	BCAC/iCOGS	26	1,497	1,094	0.98	0.87	1.11	0.802
	BPC3	5	606	429	0.91	0.76	1.10	0.342
	Combined BCAC+BPC3	*31*	*2,103*	*1,523*	*0.96*	*0.87*	*1.07*	*0.468*
rs11075995 /16q12.2 / 52412792 / FTO								
All cases vs controls	BCAC/iCOGS	40	41,085	41,453	1.04	1.02	1.06	$7.5x10^{-4}$
ER+ cases vs controls	BCAC/iCOGS	33	25,220	40,602	1.02	1.00	1.05	0.083
ER- cases vs controls	BCAC/iCOGS	40	6,513	41,453	1.10	1.05	1.15	$3.6x10^{-5}$
ER- vs ER+ cases	BCAC/iCOGS	33	5,548	25,220	0.93	0.89	0.98	0.003
TN cases vs controls	BCAC/iCOGS	34	2,466	33,401	1.11	1.03	1.20	0.007
non-TN ER- cases vs controls	BCAC/iCOGS	26	1,094	32,223	1.13	1.02	1.25	0.016
TN cases vs non-TN ER- cases	BCAC/iCOGS	26	1,497	1,094	1.04	0.91	1.19	0.547
	BPC3	5	606	429	1.14	0.93	1.41	0.210
	Combined BCAC+BPC3	*31*	*2,103*	*1,523*	*1.07*	*0.91*	*1.19*	*0.239*

Supplementary Table 6: Association with risk of ER-negative breast cancer for most significant SNPs in the 1q32.1/MDM4, 1q32.1/LGR6, 2p24 and 16q12.2/FTO loci in populations of Asian and African ancestry

Rsnumber /cytoband / gene / position (NCBI build 36) – risk allele/reference allele	T/I	Ethnicity	N Studies	Cases	Controls	RAF	OR	95% CI		*P*	*P* test for difference in OR compared to Europeans
rs4245739/1q32.1/*MDM4*/ 202,785,465 –C/A											
AABC	T	African	9	1,004	2,773	0.24	1.07	0.95	1.21	0.291	
BCAC	T	African	1	91	252	0.23	1.22	0.83	1.79	0.304	
Meta-analysis in Africans		***African***	***10***	***1095***	***3025***		***1.08***	***0.96***	***1.22***	***0.186***	***0.440***
BCAC	T	Asian	9	1547	6622	0.06	0.97	0.81	1.16	0.723	0.086
rs6678914 / 1q32.1/*LGR6* /200,453,799 – G/A											
AABC	T	African	9	1,004	2,773	0.67	1.00	0.89	1.12	0.988	
BCAC	T	African	1	91	252	0.67	0.90	0.62	1.31	0.573	
Meta-analysis in Africans		***African***	***10***	***1095***	***3025***		***0.99***	***0.89***	***1.10***	***0.882***	***0.076***
BCAC	T	Asian	9	1547	6623	0.76	1.04	0.95	1.15	0.385	0.330
rs12710696 /2p24.1/ 19,184,284 – T/C											
AABC	I	African	9	1,004	2,773	0.54	1.00	0.90	1.11	0.997	
BCAC	T	African	1	91	252	0.52	0.91	0.65	1.28	0.601	
Meta-analysis in Africans		***African***	***10***	***1095***	***3025***		***0.99***	***0.90***	***1.10***	***0.875***	***0.065***
BCAC/iCOGS	T	Asian	9	1547	6623	0.33	1.05	0.96	1.14	0.295	0.339
rs11075995 /16q12.2 / FTO, KIAA1752 / 52,412,792 –A/T											
AABC	I	African	9	1,004	2,773	0.19	1.13	0.98	1.29	0.087	
BCAC	T	African		21	252	0.15	1.32	0.81	2.14	0.262	
Meta-analysis in Africans		***African***	***9***	***1025***	***3025***		***1.14***	***1.00***	***1.30***	***0.050***	***0.688***
BCAC	T	Asian	9	1547	6623	0.30	1.03	0.94	1.13	0.489	0.135

I/T indicates imputed and typed SNPs. RAF: risk allele frequency. P-study het.: Q-test for study heterogeneity of estimated ORs.

Estimates for Europeans (meta-analysis) are shown in Table 1.

Supplementary Table 7: Association with risk of ER-negative breast cancer risk for most significant SNPs in the 1q32.1/MDM4, 1q32.1/LGR6, 2p24 and 16q12.2/FTO loci, stratified by 5-year age categories (based on BCAC replication data in studies of European ancestry).

RS number	ER- vs controls						
Age category, years	ER-	Controls	OR	95%CI		*P*	P-het
rs4245739							
<40	531	3,791	1.28	1.11	1.49	0.001	0.008
40-<45	526	3,433	1.15	0.99	1.34	0.076	0.138
45-<50	583	4,433	1.14	0.99	1.31	0.073	0.144
50-<55	775	6,354	1.17	1.04	1.32	0.010	0.055
55-<60	827	6,198	0.99	0.88	1.12	0.875	Ref.
60-<65	779	5,558	1.10	0.98	1.24	0.119	0.227
65-<70	567	4,529	1.19	1.04	1.37	0.014	0.049
>=70	582	3,732	1.00	0.87	1.16	0.977	0.902
Total	5,170	38,028		*P trend in ER- cases=0.314*			
rs6678914							
<40	532	3,791	1.00	0.87	1.15	0.382	0.063
40-<45	526	3,433	1.03	0.90	1.18	0.508	0.118
45-<50	583	4,434	1.11	0.98	1.27	0.900	0.469
50-<55	775	6,354	1.17	1.05	1.31	0.994	0.873
55-<60	827	6,197	1.19	1.06	1.32	0.998	Ref.
60-<65	779	5,558	1.05	0.94	1.17	0.670	0.125
65-<70	567	4,530	1.09	0.96	1.24	0.838	0.346
>=70	582	3,732	1.04	0.91	1.19	0.593	0.146
Total	5,171	38,029		*P trend in ER- cases=0.315*			
rs12710696							
<40	531	3,790	1.14	0.99	1.31	0.067	0.560
40-<45	526	3,433	1.09	0.95	1.25	0.225	0.916
45-<50	583	4,434	1.11	0.97	1.26	0.124	0.769
50-<55	774	6,354	1.15	1.03	1.29	0.014	0.427
55-<60	827	6,199	1.08	0.97	1.21	0.179	Ref.
60-<65	779	5,558	1.17	1.05	1.31	0.005	0.302
65-<70	567	4,529	1.06	0.93	1.21	0.417	0.807
>=70	582	3,732	1.06	0.93	1.21	0.392	0.832
Total	5,169	38,029		*P trend in ER- cases=0.694*			
rs11075995							
<40	532	3,791	1.07	0.91	1.25	0.423	0.852
40-<45	526	3,433	1.20	1.03	1.40	0.018	0.165
45-<50	582	4,433	0.95	0.82	1.10	0.502	0.327
50-<55	775	6,354	1.08	0.96	1.23	0.215	0.711
55-<60	827	6,199	1.05	0.93	1.18	0.468	Ref.
60-<65	779	5,558	1.11	0.98	1.26	0.115	0.537
65-<70	567	4,529	1.27	1.10	1.46	0.001	0.044
>=70	582	3,732	1.19	1.03	1.37	0.020	0.193
Total	5,170	38,029		*P trend in ER- cases=0.841*			

Supplementary Table 8: Association with risk of ER-negative breast cancer risk for most significant SNPs in the 1q32.1/MDM4, 1q32.1/LGR6, 2p24 and 16q12.2/FTO loci, stratified by family history (FH) of breast cancer in first degree relatives (based on iCOGS data from studies of European ancestry)

	ER + vs controls							ER- vs controls						FH+ vs FH- in ER- cases			
Family History	ER+	Controls	OR	95%CI		*P*	P-het	ER-	Controls	OR	95%CI		*P*	OR	95%CI		*P*
rs4245739																	
No	8,783	15,317	0.99	0.95	1.03	0.575	Ref.	2,121	15,440	1.21	1.12	1.30	3.1x10^{-7}				Ref.
Yes	2,403	1,891	0.95	0.86	1.05	0.305	0.473	490	1,919	1.01	0.86	1.19	0.885	0.91	0.80	1.04	0.172
Total	*11,186*	*17,208*						*2,611*	*17,359*								
rs6678914																	
No	8,783	15,318	1.00	0.96	1.03	0.809	Ref.	2,121	15,441	1.13	1.06	1.21	2.7x10^{-4}				Ref.
Yes	2,403	1,891	0.98	0.89	1.07	0.632	0.731	491	1,919	0.97	0.84	1.12	0.684	0.89	0.79	1.00	0.049
Total	*11,186*	*17,209*						2,612	17,360								
rs12710696																	
No	8,782	15,318	1.01	0.97	1.05	0.758	Ref.	2,120	15,441	1.13	1.05	1.21	0.001				Ref.
Yes	2,403	1,891	1.04	0.95	1.14	0.408	0.523	491	1,919	1.12	0.97	1.30	0.134	0.98	0.87	1.10	0.719
Total	*11,185*	*17,209*						*2,611*	*17,360*								
rs12710696																	
No	8,783	15,316	1.05	1.00	1.10	0.043	Ref.	2,121	15,439	1.12	1.04	1.21	0.003				Ref.
Yes	2,403	1,891	1.04	0.94	1.15	0.478	0.886	491	1,919	1.10	0.93	1.30	0.283	0.98	0.86	1.12	0.773
Total	*11,186*	*17,207*						*2,612*	*17,358*								

Supplementary Table 9: Association with risk of ER-negative breast cancer for known breast cancer risk loci in populations of European ancestry (meta-analysis of BPC3, TNBCC, Combined ER-negative GWAS and BCAC replication data in studies of European ancestry). SNPs with P<0.05 are shown in bold.

Cytoband	Locus	RS number	Position	Minor Allele	Other Allele	MAF	OR	(95% C.I)		P
Previously reported loci[1]										
1p11.2		rs11249433	120982136	G	A	0.405	1.00	0.97	1.04	0.796
2q33.1	***CASP8***	**rs1045485**	**201857834**	C	G	**0.115**	**0.94**	**0.89**	**0.98**	**0.008**
2q35		**rs13387042**	**217614077**	G	A	**0.489**	**0.95**	**0.92**	**0.98**	**0.002**
3p24.1	***SLC4A7***	**rs4973768**	**27391017**	T	C	**0.472**	**1.04**	**1.01**	**1.07**	**0.018**
5p15.33	***TERT***	**rs10069690**	**1332790**	T	C	**0.321**	**1.15**	**1.11**	**1.20**	**4.5x10^{-12}**
5p12		**rs10941679**	**44742255**	G	A	**0.338**	**1.04**	**1.00**	**1.08**	**0.029**
5q11.2	***MAP3K1***	**rs889312**	**56067641**	C	A	**0.334**	**1.05**	**1.01**	**1.09**	**0.006**
6q14.1		**rs17530068**	**82249828**	C	T	**0.237**	**1.09**	**1.05**	**1.13**	**3.3x10^{-6}**
6q25.1	***ESR1***	**rs3757318**	**151955806**	A	G	**0.071**	**1.22**	**1.15**	**1.30**	**2.5x10^{-11}**
6q25.1	***ESR1***	**rs2046210**	**151990059**	A	G	**0.423**	**1.15**	**1.11**	**1.19**	**4.9x10^{-16}**
8q24.21		rs13281615	128424800	G	A	0.411	1.03	0.99	1.06	0.113
9p21.3	***CDKN2A/B***	**rs1011970**	**22052134**	T	G	**0.169**	**1.09**	**1.05**	**1.14**	**3.9x10^{-5}**
9q31.2		rs865686	109928299	G	T	0.377	0.98	0.95	1.02	0.325
10p15.1	*ANKRD16*	rs2380205	5926740	T	C	0.440	1.00	0.97	1.03	0.903
10q21.2	***ZNF365***	**rs10995190**	**63948688**	A	G	**0.154**	**0.89**	**0.85**	**0.93**	**1.3x10^{-7}**
10q22.3	***ZMIZ1***	**rs704010**	**80511154**	T	C	**0.383**	**1.05**	**1.01**	**1.08**	**0.006**
10q26.13	*FGFR2*	rs2981579	123327325	A	G	0.410	1.02	0.99	1.05	0.273
11p15.5	***LSP1***	**rs3817198**	**1865582**	G	A	**0.312**	**1.06**	**1.02**	**1.09**	**0.002**
11q13.3		rs614367	69037945	T	C	0.150	1.03	0.98	1.07	0.224
12p11.22	***PTHLH***	**rs10771399**	**28046347**	C	T	**0.105**	**0.83**	**0.79**	**0.87**	**2.4x10^{-12}**
12q24.21		rs1292011	114320905	G	A	0.420	0.99	0.96	1.02	0.443
14q24.1	***RAD51L1***	**rs999737**	**68104435**	A	G	**0.234**	**0.94**	**0.91**	**0.98**	**0.001**
16q12.1	***TOX3***	**rs3803662**	**51143842**	T	C	**0.267**	**1.14**	**1.10**	**1.18**	**5.5x10^{-13}**
17q22	***COX11***	**rs6504950**	**50411470**	A	G	**0.364**	**0.96**	**0.93**	**0.99**	**0.024**
19p13.11	***MERIT40***	**rs8170**	**17250704**	A	G	**0.191**	**1.15**	**1.11**	**1.20**	**9.3x10^{-13}**
21q21.1	*NRIP1*	rs2823093	15442703	A	G	0.268	0.99	0.96	1.03	0.595
Newly identified loci (Michailidou, K. et al. Nature Genetics, In Press)										
1p13.2	***PTPN22:BCL2L15: AP4B1:DCLRE1B: HIPK1***	**rs11552449**	**114249912**	T	C	**0.266**	**1.06**	**1.01**	**1.10**	**0.009**
1p36.22	***PEX14***	**rs616488**	**10488802**	G	A	**0.335**	**0.91**	**0.88**	**0.94**	**1.0x10^{-8}**
2q14.2		**rs4849887**	**120961592**	T	C	**0.099**	**0.93**	**0.88**	**0.99**	**0.013**
2q31.1	*METAP1D:DLX1:DLX2*	rs2016394	172681217	A	G	0.475	1.00	0.97	1.04	0.854
2q31.1	*CDCA7*	rs1550623	173921140	G	A	0.160	0.96	0.92	1.00	0.051
2q35	***DIRC3***	**rs16857609**	**218004753**	T	C	**0.229**	**1.07**	**1.04**	**1.11**	**1.0x10^{-4}**
3p26.1	*ITPR1:EGOT*	rs6762644	4717276	G	A	0.395	1.01	0.98	1.04	0.572
3p24.1	*TGFBR2*	rs12493607	30657943	C	G	0.422	1.00	0.97	1.04	0.830
4q24	***TET2***	**rs9790517**	**106304227**	T	C	**0.316**	**1.04**	**1.00**	**1.08**	**0.028**
4q34.1	*ADAM29*	rs6828523	176083001	A	C	0.216	0.99	0.95	1.04	0.774
5q11.2	***RAB3C***	**rs10472076**	**58219818**	C	T	**0.332**	**1.04**	**1.01**	**1.08**	**0.015**
5q11.2	***PDE4D,PDE4DN2***	**rs1353747**	**58373238**	G	T	**0.096**	**0.95**	**0.90**	**1.00**	**0.046**
5q33.3	***EBF1***	**rs1432679**	**158176661**	C	T	**0.435**	**1.08**	**1.04**	**1.11**	**6.7x10^{-6}**
6p25.3	***FOXQ1***	**rs11242675**	**1263878**	C	T	**0.382**	**0.95**	**0.91**	**0.98**	**0.001**
6p23	*RABBP9*	rs204247	13830502	G	A	0.439	1.02	0.99	1.06	0.134
7q35	*ARHGEF5:NOBOX*	rs720475	143705862	A	G	0.255	1.01	0.97	1.05	0.587
8p12		**rs9693444**	**29565535**	A	C	**0.324**	**1.06**	**1.02**	**1.09**	**0.001**
8q21.11		**rs6472903**	**76392856**	G	T	**0.277**	**0.95**	**0.91**	**0.99**	**0.016**
8q21.11	***HNF4G***	**rs2943559**	**76580492**	G	A	**0.194**	**1.12**	**1.05**	**1.18**	**2.5x10^{-4}**
8q24.21	***MIR1208***	**rs11780156**	**129263823**	T	C	**0.167**	**1.05**	**1.00**	**1.09**	**0.037**
9q31.2		rs10759243	109345936	A	C	0.262	1.04	1.00	1.07	0.057
10p12.31	*MLLT10:DNAJC1*	rs7072776	22072948	A	G	0.285	0.98	0.95	1.02	0.322
10p12.31	***DNAJC1***	**rs11814448**	**22355849**	C	A	**0.132**	**1.20**	**1.08**	**1.35**	**0.001**
10q25.2	***TCF7L2***	**rs7904519**	**114763917**	G	A	**0.462**	**1.06**	**1.03**	**1.09**	**2.9x10^{-4}**
10q26.12		rs11199914	123083891	T	C	0.320	1.01	0.97	1.04	0.741
11q13.1	***DKFZp761E198:OVOL1:SNX32:CFL1:MUS81***	**rs3903072**	**65339642**	T	G	**0.414**	**0.97**	**0.94**	**1.00**	**0.027**
11q24.3		**rs11820646**	**128966381**	T	C	**0.479**	**0.94**	**0.91**	**0.97**	**2.3x10^{-4}**
12p13.1		**rs12422552**	**14305198**	C	G	**0.344**	**1.05**	**1.02**	**1.09**	**0.005**
12q22	***NTN4***	**rs17356907**	**94551890**	G	A	**0.298**	**0.92**	**0.89**	**0.96**	**9.3x10^{-6}**
13q13.1	***BRCA2,N4BP2L1***	**rs11571833**	**31870626**	T	A	**0.496**	**1.52**	**1.31**	**1.77**	**6.0x10^{-6}**
14q13.3	*PAX9:SLC25A21*	rs2236007	36202520	A	G	0.291	0.97	0.94	1.02	0.218
14q24.1	*RAD51L1*	rs2588809	67730181	T	C	0.248	1.00	0.96	1.05	0.940
14q32.11	*CCDC88C*	rs941764	90910822	G	A	0.415	1.03	0.99	1.06	0.117
16q12.2	***MIR1972-2:FTO***	**rs17817449**	**52370868**	G	T	**0.474**	**0.92**	**0.89**	**0.95**	**6.2x10^{-7}**
16q23.2	*CDYL2*	rs13329835	79208306	G	A	0.223	1.02	0.98	1.06	0.269
18q11.2		**rs527616**	**22591422**	C	G	**0.447**	**0.95**	**0.92**	**0.99**	**0.006**
18q11.2	*CHST9*	rs1436904	22824665	G	T	0.399	1.00	0.97	1.03	0.995
19p13.11	***SSBP4:ISYNA1:ELL***	**rs4808801**	**18432141**	G	A	0.349	0.93	0.90	0.96	**5.1x10^{-5}**
19q13.31	***C19orf61:KCNN4:LYPD5:ZNF283***	**rs3760982**	**48978353**	A	G	**0.466**	**1.04**	**1.01**	**1.07**	**0.016**
22q12.2	*EMID1:RHBDD3:EWSR1*	rs132390	27951477	C	T	0.035	1.08	0.98	1.19	0.117
22q13.1	***MKL1***	**rs6001930**	**39206180**	C	T	**0.107**	**1.14**	**1.08**	**1.20**	**1.6x10^{-6}**

[1] rs2284378 at 20q11 previously reported by Siddiq, A. et al. (ref. 7) is not included because it was not well tagged in the iCOGS array used for BCAC replication.

Supplementary Note

Consortia membership:

The GENICA Network Dr. Margarete Fischer-Bosch-Institute of Clinical Pharmacology, Stuttgart and University of Tübingen, Germany (Christina Justenhoven, Hiltrud Brauch); Molecular Genetics of Breast Cancer, Deutsches Krebsforschungszentrum (DKFZ), Heidelberg, Germany (Ute Hamann); Department of Internal Medicine, Evangelische Kliniken Bonn gGmbH, Johanniter Krankenhaus, Bonn, Germany (Yon-Dschun Ko, Christian Baisch); Institute of Pathology, University of Bonn, Bonn, Germany (Hans-Peter Fischer); Institute for Prevention and Occupational Medicine of the German Social Accident Insurance (IPA), Bochum, Germany (Thomas Brüning, Beate Pesch, Sylvia Rabstein, Anne Lotz); Institute and Outpatient Clinic of Occupational Medicine, Saarland University Medical Center and Saarland University Faculty of Medicine, Homburg, Germany (Volker Harth).

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The Familial Breast Cancer Study (FBCS): Julian W Adlard (Yorkshire Regional Genetics Service, Chapel Allerton Hospital, Leeds), Julian Barwell (Leicestershire Genetics Centre, Leicester Royal Infirmary, Leicester), Jonathan Berg (Human genetics, Division of Medical Sciences, University of Dundee), Angela F Brady (NW Thames Regional Genetics Service, Kennedy Galton Centre, London), Carole Brewer (Peninsula Regional Genetics Service, Royal Devon & Exeter Hospital, Exeter), Glen Brice (SW Thames Regional Genetics Service, St George's Hospital, London), Cyril Chapman (West Midlands Regional Genetics Service, Birmingham Women's Hospital, Birmingham), Jackie Cook (Sheffield Regional Genetics Service, Sheffield Children's NHS Foundation Trust), Rosemarie Davidson (West of Scotland Regional Genetics Service, Laboratory Medicine, Southern General Hospital, Glasgow), Alan Donaldson (South Western Regional Genetics Service, University Hospitals of Bristol NHS Foundation Trust), Fiona Douglas (Northern Genetics Service, Newcastle upon Tyne Hospitals NHS Foundation Trust), Diana Eccles (Faculty of Medicine, University of Southampton, Southampton University Hospitals NHS Trust,), D. Gareth Evans (Genetic Medicine, Manchester Academic Health Science Centre, St. Mary's Hospital, Manchester), Lynn Greenhalgh (Merseyside and Cheshire Clinical Genetics Service, Liverpool Women's NHS Foundation Trust, Liverpool), Helen Hanson (Dept of Cancer Genetics, Royal Marsden NHS Foundation Trust, Sutton), Alex Henderson (Northern Genetics Service Cumbria), Louise Izatt (SE Thames Regional Genetics Service, Guy's and St Thomas NHS Foundation Trust, London), Ajith Kumar (NE Thames Regional Genetics Service, Great Ormond St Hospital, London), Fiona Lalloo (University Dept of Medical Genetics & Regional Genetics Service, St Mary's Hospital, Manchester), Zosia Miedzybrodzka (University of Aberdeen and North of Scotland Clinical Genetics Service, Aberdeen Royal Infirmary), Patrick J Morrison (Northern Ireland Regional Genetics Service, Belfast HSC Trust, Department of Medical Genetics, Queen's University Belfast), Joan Paterson (East Anglian Regional Genetics Service, Cambridge University Hospitals NHS Foundation Trust), Mary Porteous (South East of Scotland Clinical Genetics Service, Western General Hospital, Edinburgh), Mark T Rogers (All Wales Medical Genetics Service, University Hospital of Wales, Cardiff), Lisa Walker (Oxford Regional Genetics Service, Oxford University Hospitals NHS Trust, Oxford).

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