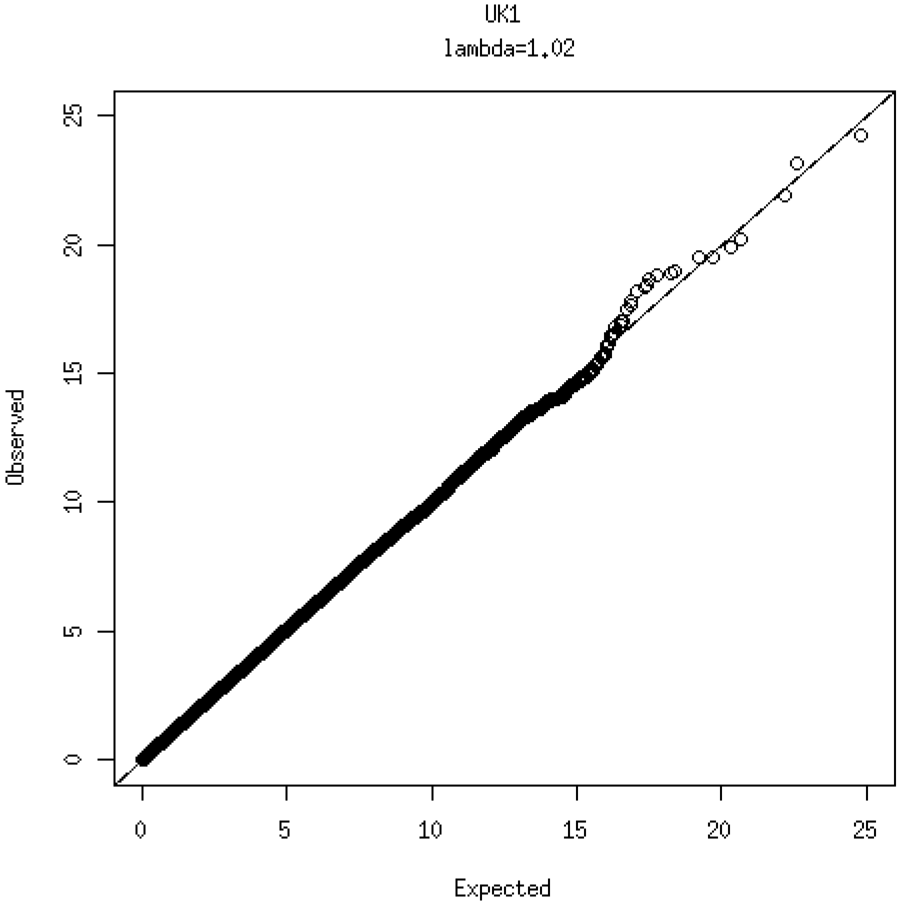
	UK1	UK2	Scotland1	Scotland2	VQ58
pre-QC	940 cases 965 controls	2,873 cases 2,871 controls	1,012 cases 1,012 controls	2,057 cases 2,111 controls	1,800 cases 2,690 controls
Call rate	15	30	15	22	0
Ethnicity	54	6	9	7	0
Relatedness	26	197*	9	30*	9
Sex discrepancy	3	45	15	22	1
Other	17	9	5	5	0
post-QC	**890 cases** **900 controls**	**2,659 cases** **2,798 controls**	**973 cases** **998 controls**	**2,007 cases** **2,075 controls**	**1,794 cases** **2,686 controls**

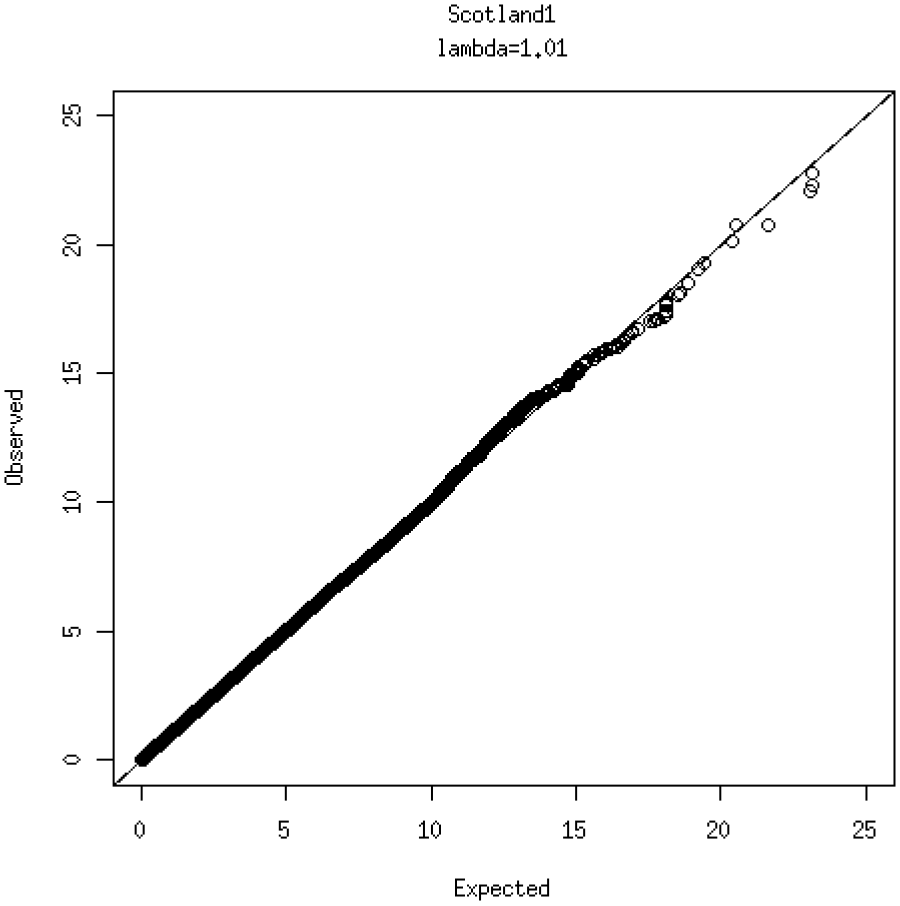
Supplementary Figure 1: Details of the quality control filters applied to each GWAS. Samples were excluded - call rate (<95%), Ethnicity (principle components analysis or self-reported not to be of European descent), relatedness (duplicates or related within or between each case-control series), sex discrepancy, other (cases found to carry a high-risk CRC mutation, controls with a 1st degree relative with CRC, low concordance of genotypes in duplicates, subjects withdrawn from the study). *samples preferentially removed from these data-sets over GWAS datasets.

Supplementary Figure 2: Quantile-Quantile (Q-Q) plots of observed and expected χ^2 values of association between SNP genotype and colorectal cancer risk. (a) UK1, (b) Scotland1, (c) UK2, (d) Scotland2 and (e) VQ58

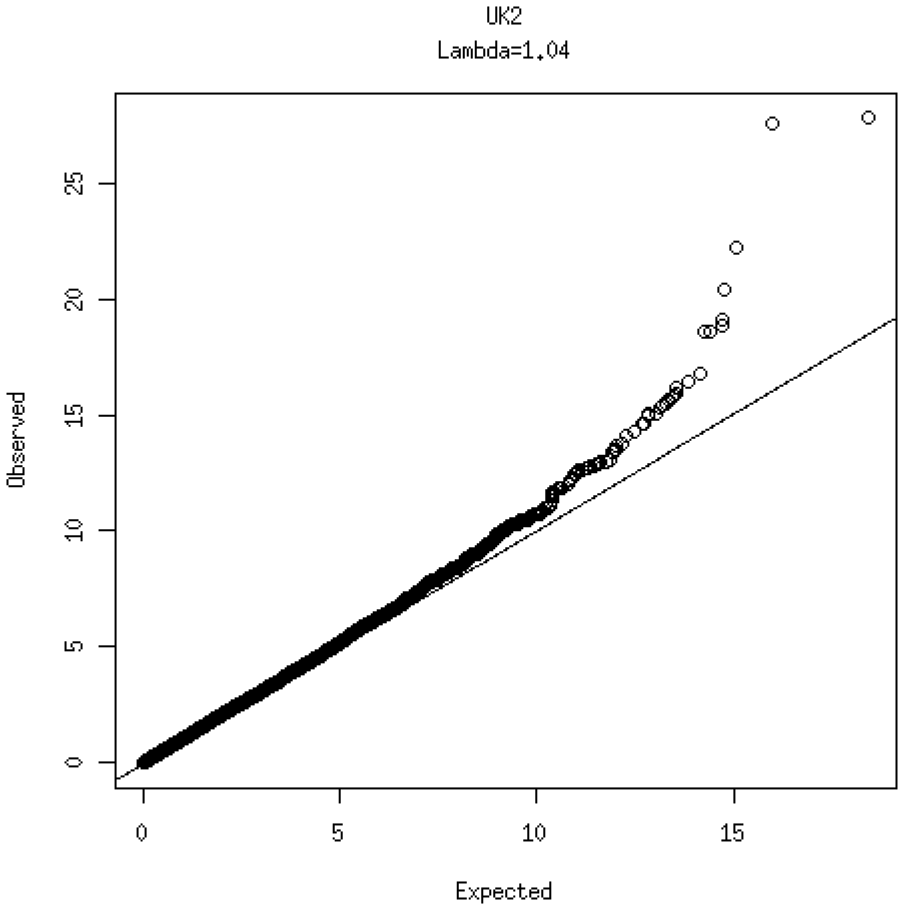
(a)



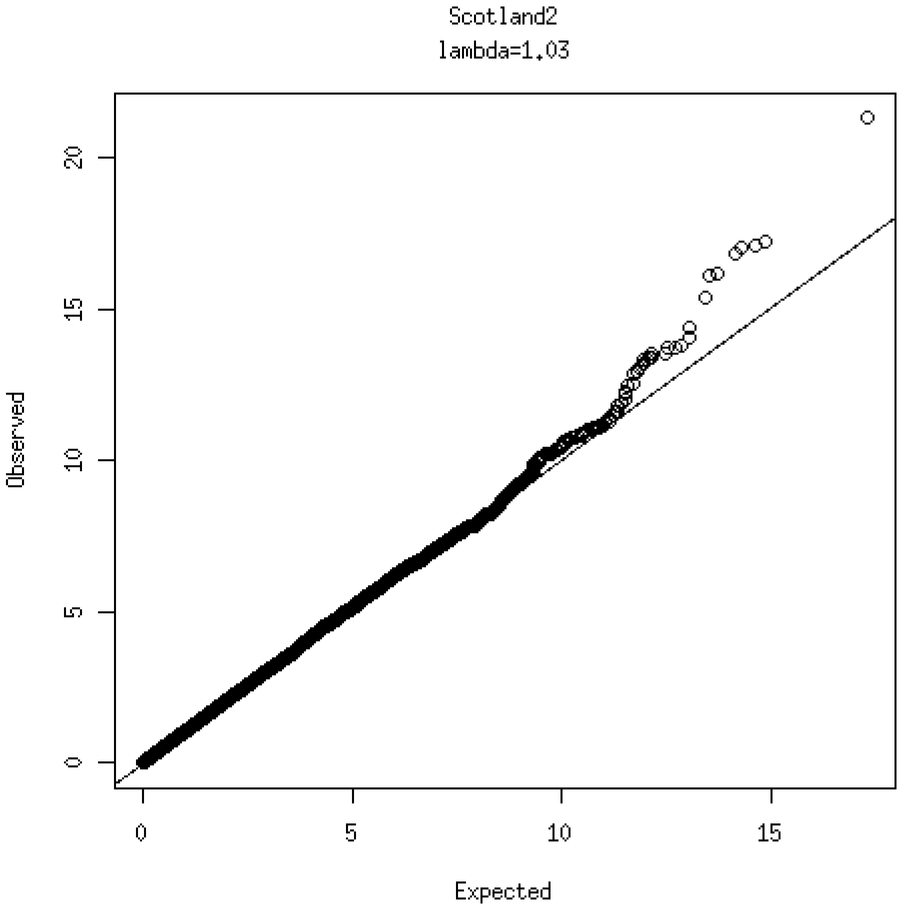
(b)



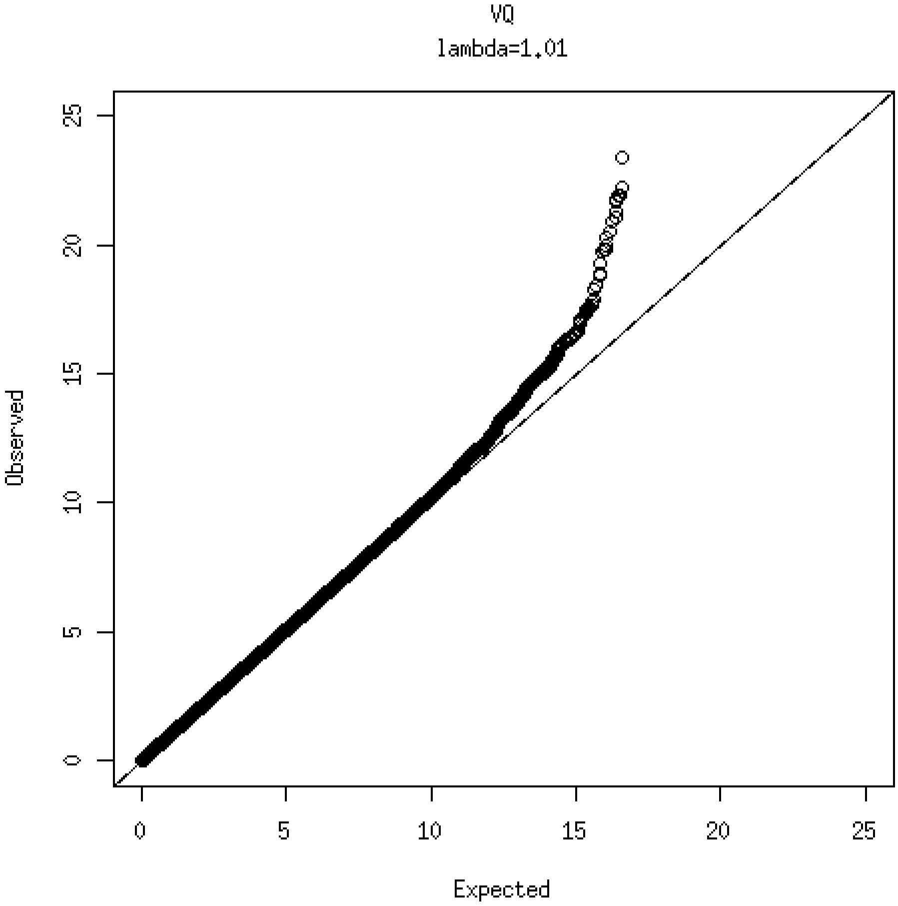
(c)


UK2
Lambda=1.04
Observed
Expected
0
5
10
15
20
25
0
5
10
15

(d)

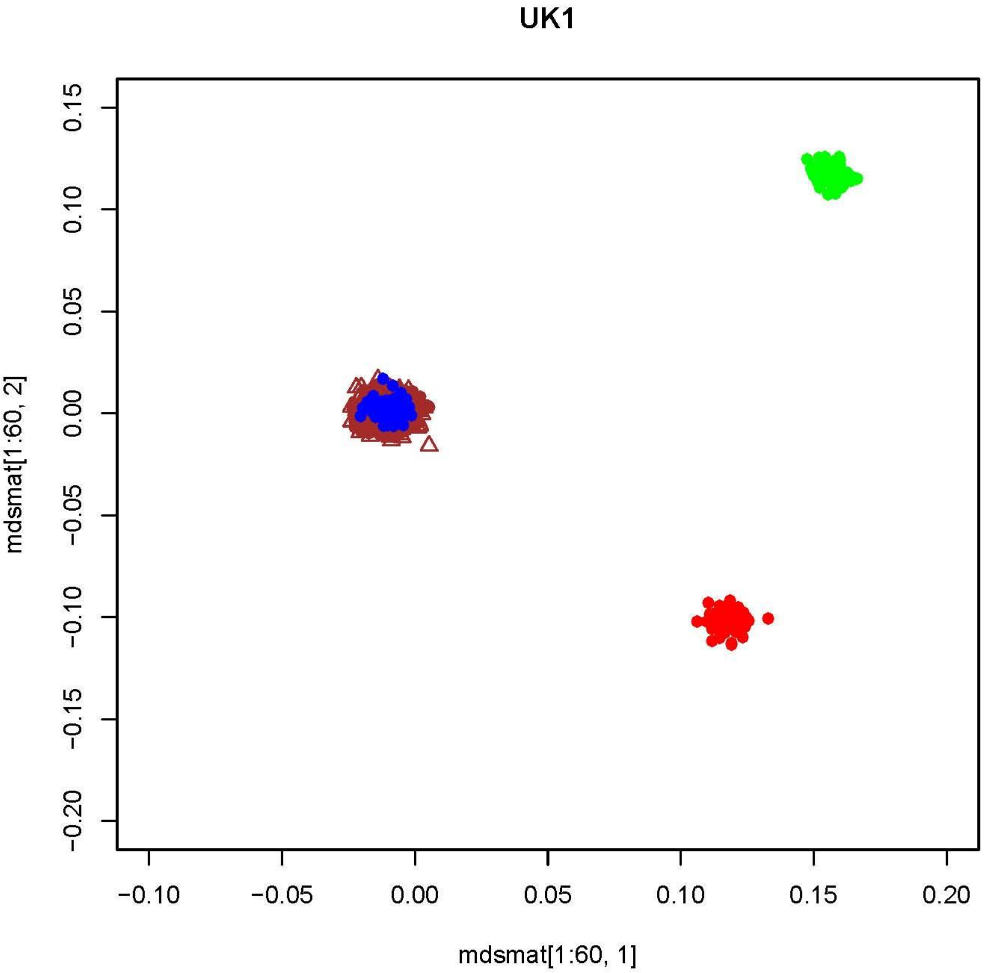

Scotland2
lambda=1.03
Observed
Expected
0
5
10
15
20
0
5
10
15

(e)

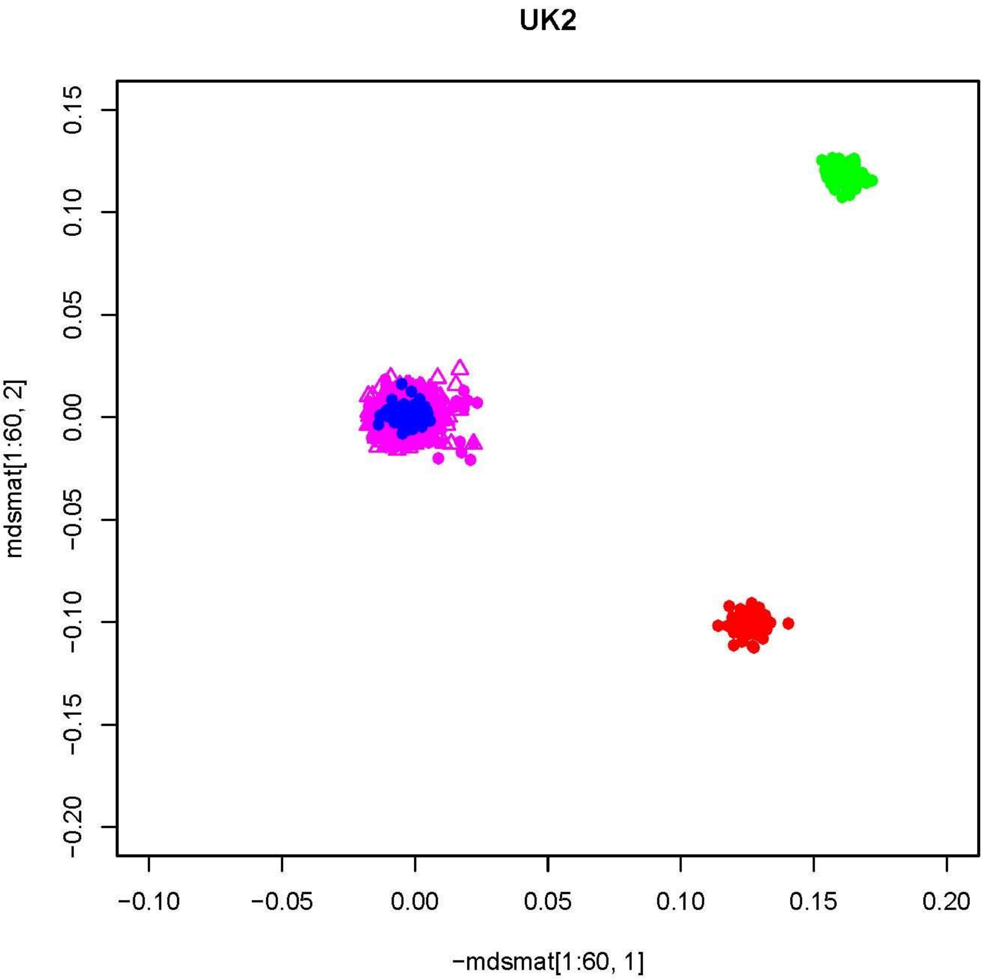


Supplementary Figure 3: **Identification of individuals in the GWAS of non-European ancestry in cases and controls.** The first two principal components of the analysis are plotted, before exclusions, for the (a) UK1, (b) UK2, (c) Scotland1, (d) Scotland2 and (e) VQ58 cases and controls. HapMap CEU individuals are plotted in blue; CHB+JPT individuals are plotted in green; YRI individuals are plotted in red; GWAS cases are plotted as circles and controls as triangles.

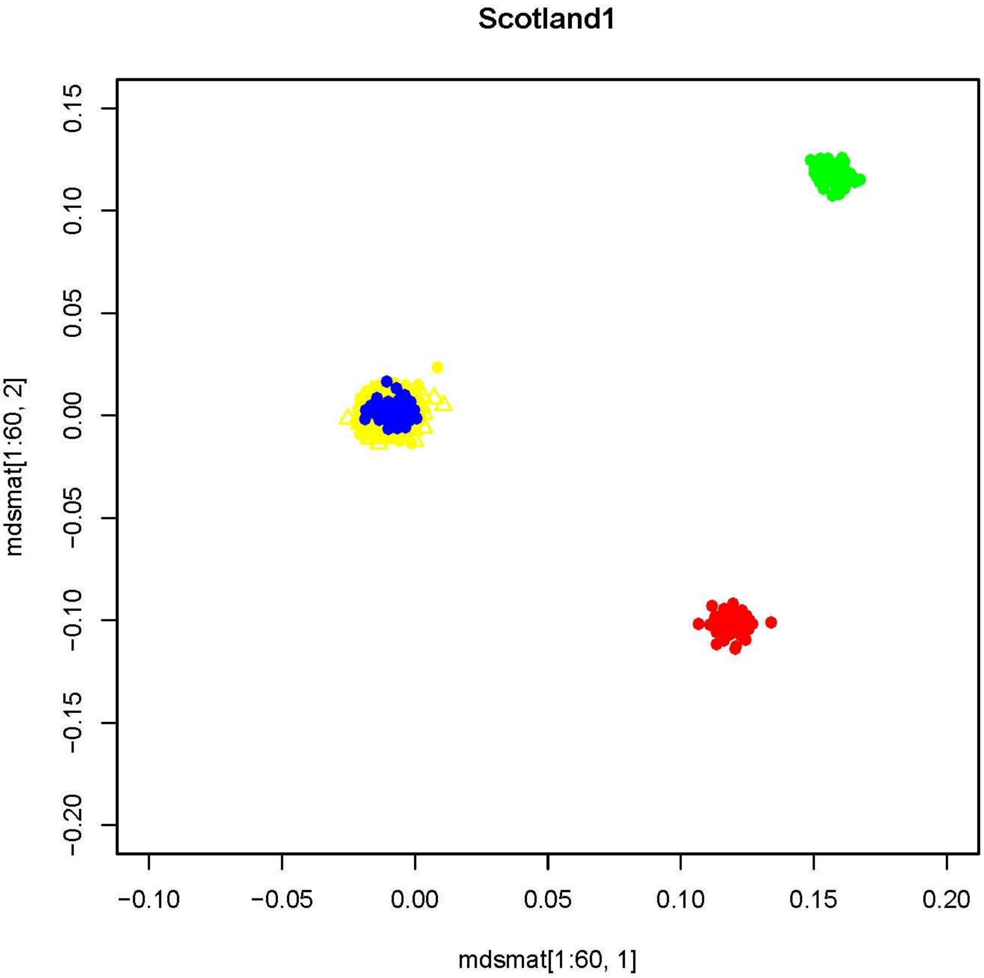
(a)



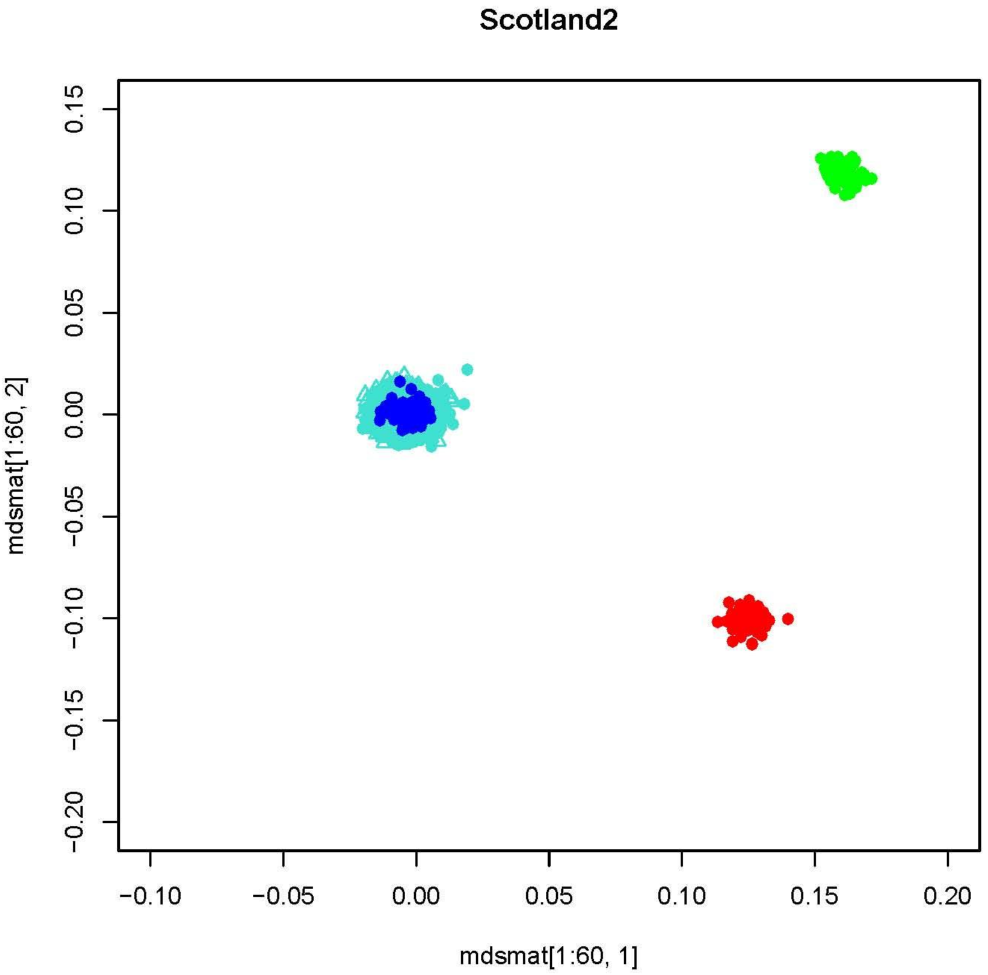
(b)


UK2
mdsmat[1:60, 2]
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
−0.20
−0.10
−0.05
0.00
0.05
0.10
0.15
0.20
−mdsmat[1:60, 1]

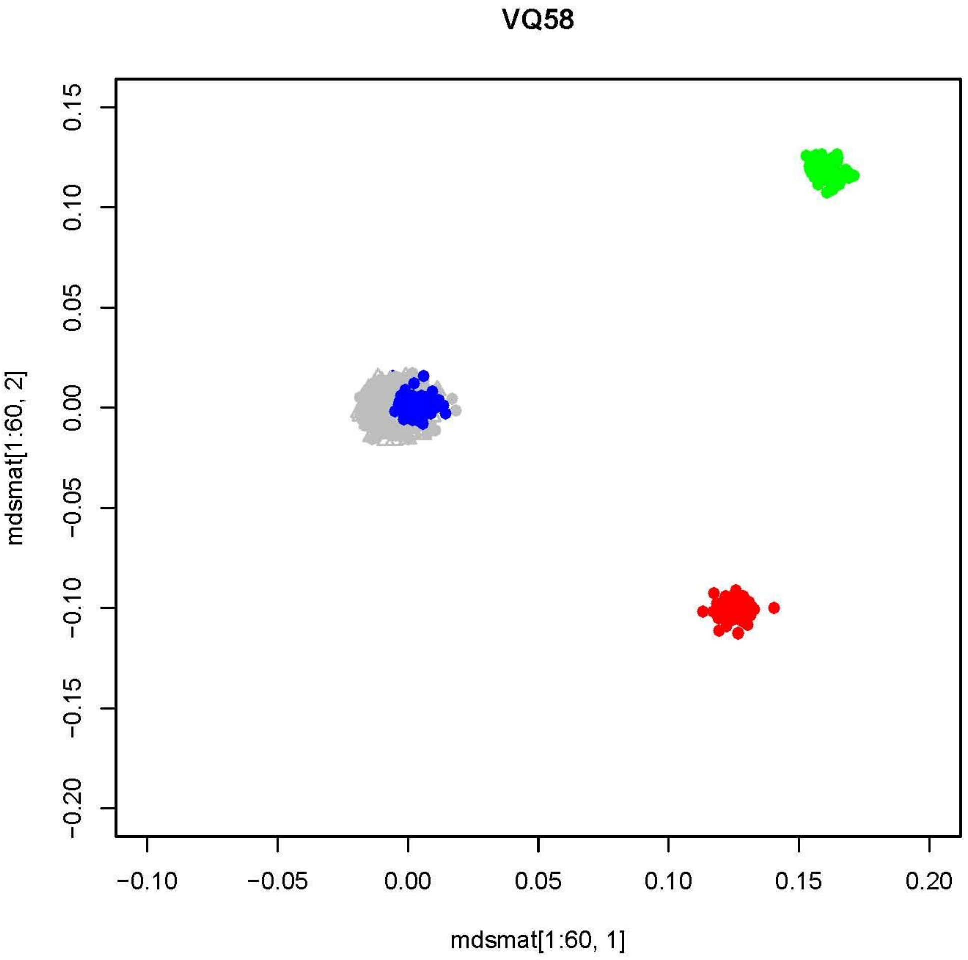
(c)


Scotland1
mdsmat[1:60, 2]
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
−0.20
−0.10
−0.05
0.00
0.05
0.10
0.15
0.20
mdsmat[1:60, 1]

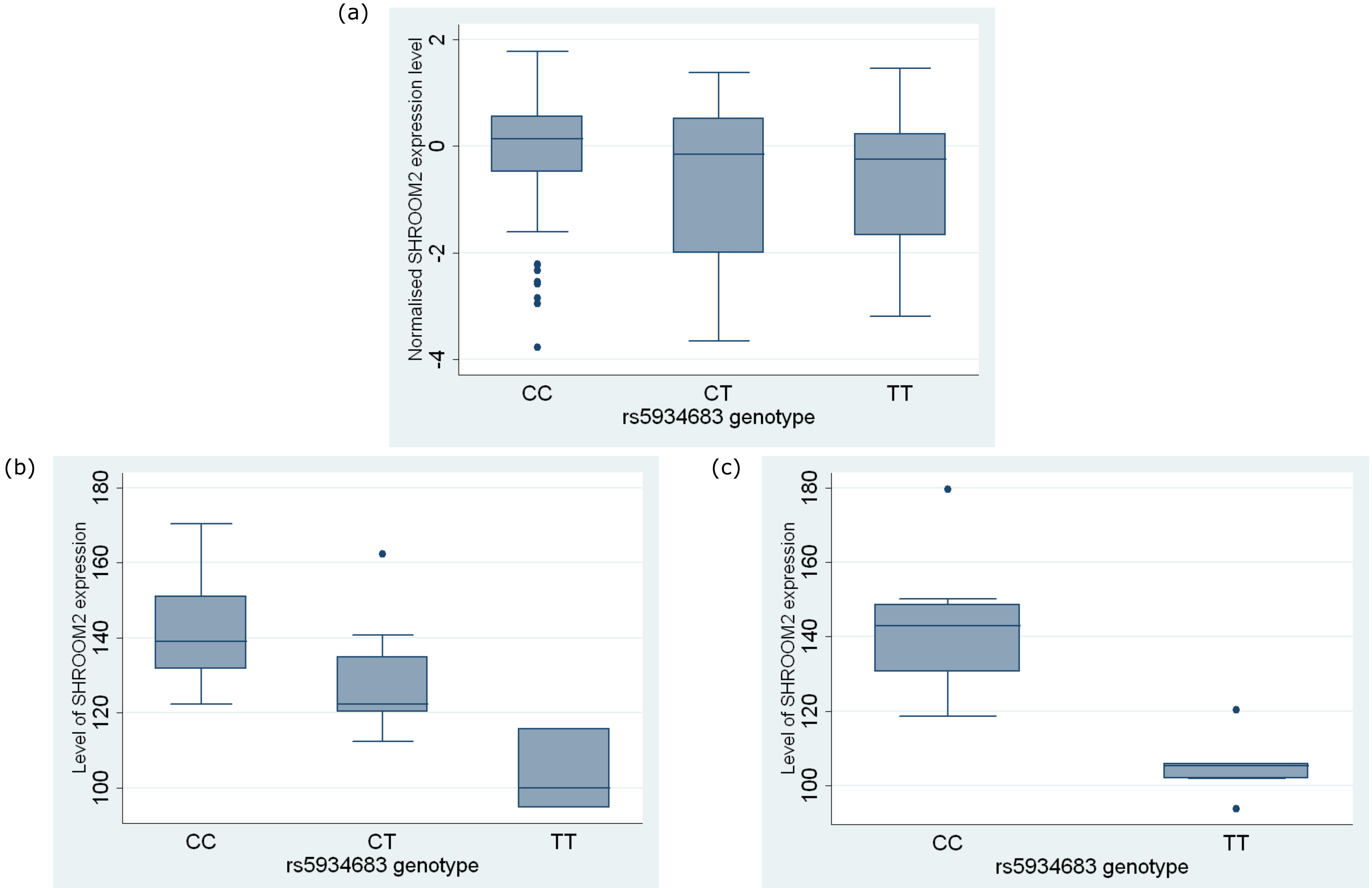
(d)


Scotland2
mdsmat[1:60, 2]
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
−0.20
−0.10
−0.05
0.00
0.05
0.10
0.15
0.20
mdsmat[1:60, 1]

(e)


VQ58
mdsmat[1:60, 2]
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
−0.20
−0.10
−0.05
0.00
0.05
0.10
0.15
0.20
mdsmat[1:60, 1]

Supplementary Figure 4 : Relationship between rs5934683 genotype and *SHROOM2* expression. Differences in the distribution of expression by SNP (a) 154 CRCs from The Cancer Genome Atlas (TCGA) project, (b-c) 42 colon tissue samples, (b) females and (c) males.



Supplementary Table 1: Summary of the sample sets used in the study.

Series	Study setting	Study centre	Sampling	Genotyping platform	No. cases	No. controls
GWAS studies						
UK1	CORGI (Colorectal Tumour Gene Identification Consortium)	Oxford University	Cases enriched for family history of CRC ascertained through clinical genetics centres in the UK. Spouse controls with no personal family history of CRC.	Illumina HumanHap550	940	965
UK2	NSCCG (National study of Colorectal Cancer). http://www.icr.ac.uk/research/research_divisions/Genetics_and_Epidemiology/index.shtml	Institute of Cancer Research	Population-based UK study. Spouse controls from NSCCG and GELCAPS (Genetic Lung Cancer Predisposition Study).	Illumina iSelect and Goldengate	2,873	2,871
SCOTLAND1	COGS (Colorectal Cancer Genetics Susceptibility Study)	Edinburgh University	Population-based incident case series aged <55 at diagnosis; Scotland. Population-based controls frequency matched by area of residence within Scotland	Illumina HumanHap300 Illumina HumanHap240S	1,012	1,012
SCOTLAND2	SOCCS (Scottish Colorectal Cancer Study)	Edinburgh University	Population-based incident case series; Scotland. Population-based controls frequency matched by area of residence within Scotland.	Illumina iSelect and Goldengate	2,057	2,111
VQ58	Cases: VICTOR, post treatment stage of a phase III, randomised controlled trial of rofecoxib (VIOXX) in CRC patients after potentially curative therapy. QUASAR2, multicentre study if capecitibine +/- bevacizumab as adjuvant CRC treatment. hhttp://www.octo-oxford.org.uk/alltrials. Controls: 58BC (UK 1958 Birth Cohort) http://www.b58cgene.sgul.ac.uk	Oxford University	Cases recruited as a clinical-based series and controls as population-based series.	Illumina HumanHap300 Illumina HumanHap370 Illumina Human 1.2MDuo Custom_V1	1,800	2,690
TOTAL	**GWAS Sets**				**8,682**	**9,649**
Non-GWAS studies						
COINNBS	COIN, COIN-B http://public.ukcrn.org.uk NBS UK National Blood Service Blood Donor samples) http://www.wtccc.org.uk	University of Cardiff	Multicentre study of cetuximab and other therapies in metastatic CRC. Controls were unselected UK blood donors	Illumina Goldengate Illumina Human 1.2MDuo Custom_V1	2,183	2,501
CCFR1	CCFR (Colon Cancer Family Registry) http://epi.grants.cancer.gov/CFR	University of Southern California	Recently diagnosed CRC cases reported to population complete cancer registries in the USA (Seattle Familial Colorectal Cancer Registry), Canada (Ontario Familial Cancer Registry) and Australia (Australasian Colorectal Cancer Family Study). Population based controls.	Illumina HumanHap 550	1,290	1,055

UK3	NSCCG (National study of Colorectal Cancer). http://www.icr.ac.uk/research/research_divisions/Genetics_and_Epidemiology/index.shtml	Institute of Cancer Research	Population-based UK study. Spouse controls from NSCCG and GELCAPS (Genetic Lung Cancer Predisposition Study).	KASPar	7,862	4,431
UK4	CORGI (Colorectal Tumour Gene Identification Consortium)	Oxford University	Cases enriched for family history of CRC ascertained through clinical genetics centres in the UK. Spouse controls with no personal family history of CRC.	KASPar	589	1,087
SCOTLAND3	SOCCS3 Study	Edinburgh University	CRC cases arising within the Lothian region of Scotland. Cancer free population controls from Lothian born 1921 and 1936 (LBC1921 and LBC1936).	Taqman	736	1,522
CAMBRIDGE	UKSEARCH (Studies of Epidemiology and Risk Factors in Cancer Heredity) http://www.srl.cam.ac.uk/search	Cambridge University	Population-based case-control study	Kaspar	2,248	2,288
CROATIA	Croatian Colorectal Cancer Genetic Study	University Hospital Centre 'Sestre milosrdnice', Zagreb	Hospital based recruited from University Hospital in Zagreb, Croatia. Urban Croatian population from Split, Croatia.	Taqman	375	1,051
HELSINKI	FCCPS (Finnish Colorectal Cancer Predisposition Study) http://research.med.helsinki.fi/gsb/aaltonen	University of Helsinki, Finland	Population-based study, south-eastern Finland	KASPar	1,013	827
SWEDEN	Swedish Low Risk Colorectal Cancer Study	Karolinska Institute	Cases ascertained from 14 different surgical clinics in Sweden between 2004 and 2006. Controls were blood donors or healthy volunteers from Uppsala.	Taqman	3,217	2,895
JAPAN	Biobank Japan project	The University of Tokyo	Cases and controls were ascertained from 66 hospitals in Japan. Controls included subjects with non-cancer diseases or healthy volunteers.	Illumina Human 10Quad, Illumina HumanHap550v3	1,583	1,898
TOTAL	**Non-GWAS Studies**		**Various populations**		**21,096**	**19,555**
TOTAL	**COMBINED STUDIES**				**29,778**	**29,204**

Supplementary Table 2: Summary results for the SNPS: rs1321311 (6p21), rs3824999 (11q13.4) and rs5934683 (Xp22.2) associated with CRC risk. [a]Risk allele frequency (RAF), genotype counts are given in brackets. [b]Odds ratio. [c]95% Confidence Interval.

rs1321311 (6p21.31)

STUDY	**Cases**	**Controls**	**OR[b]**	**95% CI[c]**	***P*-value**
	RAF[a] (AA / AC / CC)	**RAF (AA / AC /CC)**			
UK1	0.26 (53/363/473)	0.23 (49/317/534)	1.20	1.03-1.40	2.00×10^{-2}
UK2	0.25 (169/970/1519)	0.23 (149/996/1652)	1.08	0.99-1.18	7.23×10^{-2}
SCOTLAND1	0.25 (65/356/552)	0.22 (53/331/614)	1.18	1.02-1.37	2.45×10^{-2}
SCOTLAND2	0.24 (109/741/1157)	0.23 (110/736/1229)	1.05	0.95-1.16	3.60×10^{-1}
VQ58	0.24 (108/634/1052)	0.23 (141/955/1588)	1.04	0.94-1.14	4.80×10^{-1}
COINNBS	0.25 (135/810/1201)	0.23 (128/892/1481)	1.13	1.03-1.24	1.26×10^{-2}
			1.09	***1.05-1.14***	***4.79 x10^{-5}***
CCFR1	0.27 (89/449/644)	0.24 (65/352/575)	1.12	0.98-1.28	9.83×10^{-2}
UK3	0.24 (449/2836/4368)	0.23 (227/1531/2541)	1.08	1.01-1.14	2.26×10^{-2}
UK4	0.23 (29/217/343)	0.24 (35/264/397)	0.96	0.8-1.16	6.94×10^{-1}
SCOTLAND3	0.25 (49/267/404)	0.23 (82/535/905)	1.14	0.98-1.31	8.17×10^{-2}
CAMBRIDGE	0.25 (143/826/1279)	0.23 (116/789/1338)	1.11	1.01-1.23	2.86×10^{-2}
CROATIA	0.27 (25/156/194)	0.25 (67/374/594)	1.16	0.96-1.41	1.16×10^{-1}
HELSINKI	0.21 (44/334/621)	0.17 (20/245/550)	1.27	1.07-1.50	5.63×10^{-3}
SWEDEN	0.22 (132/1092/1900)	0.21 (128/872/1705)	1.05	0.96-1.15	2.61×10^{-1}
			1.09	***1.06-1.13***	***1.12x10^{-9}***
JAPAN	0.14 (26/390/1167)	0.12 (38/380/1479)	1.18	1.03-1.36	1.71×10^{-2}
Combined			***1.10***	***1.07-1.13***	***1.14x10^{-10}***

rs3824999 (11q13.4)

STUDY	Cases	Controls	OR[b]	95% CI[c]	P-value
	RAF[a] (AA / AC / CC)	RAF (AA / AC / CC)			
UK1	0.53 (194/443/253)	0.50 (231/438/231)	1.14	1.00-1.30	4.90x10^{-2}
UK2	0.52 (624/1310/724)	0.50 (699/1423/676)	1.10	1.02-1.18	1.66x10^{-2}
SCOTLAND1	0.53 (216/489/268)	0.50 (244/516/238)	1.13	1.00-1.28	5.94x10^{-2}
SCOTLAND2	0.50 (505/998/504)	0.51 (486/1045/544)	0.94	0.87-1.03	1.99x10^{-1}
VQ58	0.53 (376/920/498)	0.49 (704/1318/653)	1.19	1.09-1.30	5.48x10^{-5}
COINNBS	0.52 (519/1063/601)	0.50 (627/1241/633)	1.07	0.99-1.16	9.21x10^{-2}
			1.08	***1.05-1.13***	***1.77 x10^{-5}***
CCFR1	0.54 (241/606/326)	0.50 (242/510/247)	1.15	1.02-1.30	2.45x10^{-2}
UK3	0.51 (1789/3857/2005)	0.51 (1061/2211/1117)	1.03	0.98-1.09	2.46x10^{-1}
UK4	0.52 (133/288/156)	0.50 (259/540/252)	1.10	0.95-1.27	2.00x10^{-1}
SCOTLAND3	0.52 (162/373/195)	0.49 (385/774/361)	1.13	1.00-1.29	5.32x10^{-2}
CAMBRIDGE	0.52 (499/1121/584)	0.51 (523/1074/560)	1.04	0.96-1.14	3.15x10^{-1}
CROATIA	0.53 (80/188/101)	0.52 (239/536/276)	1.05	0.88-1.24	6.08x10^{-1}
HELSINKI	0.48 (261/460/228)	0.48 (235/395/196)	1.02	0.90-1.17	7.16x10^{-1}
SWEDEN	0.53 (741/1546/904)	0.49 (713/1509/673)	1.14	1.06-1.22	3.41x10^{-4}
			1.08	***1.05-1.10***	***1.65x10^{-9}***
JAPAN	0.45 (490/761/331)	0.43 (630/908/360)	1.09	0.99-1.19	8.46x10^{-2}
Combined			***1.08***	***1.05-1.10***	***3.65x10^{-10}***

rs5934683 (Xp22.2)

STUDY	Cases		Controls		OR[b]	95% CI[c]	*P*-value
	Male	Female	Male	Female			
	RAF[a] (TT / CT / CC)	RAF (TT / CT / CC)	RAF (TT / CT / CC)	RAF (TT / CT / CC)			
UK1	0.37 (153/-/258)	0.38 (65/235/180)	0.30 (123/-/284)	0.31 (50/205/237)	1.23	1.10-1.38	3.32x10^{-4}
UK2	0.36 (398/-/708)	0.35 (180/723/648)	0.35 (393/-/733)	0.33 (198/702/770)	1.05	0.99-1.13	1.23x10^{-2}
SCOTLAND1	0.36 (177/-/317)	0.35 (57/226/196)	0.35 (181/-/331)	0.34 (55/219/212)	1.03	0.93-1.15	5.75x10^{-1}
SCOTLAND2	0.38 (459/-/754)	0.35 (106/347/341)	0.34 (412/-/808)	0.35 (109/382/364)	1.07	1.00-1.15	6.44x10^{-2}
VQ58	0.34 (299/-/592)	0.35 (64/245/223)	0.31 (427/-/958)	0.33 (132/586/581)	1.07	0.99-1.16	8.31x10^{-2}
					1.08	***1.04-1.12***	***8.19x10^{-5}***
CCFR1	0.36 (218/-/392)	0.37 (77/267/220)	0.33 (158/-/320)	0.33 (49/245/227)	1.11	1.00-1.23	4.66x10^{-2}
UK3	0.36 (1763/-/3097)	0.34 (318/1216/1178)	0.31 (496/-/1089)	0.33 (297/1199/1243)	1.11	1.06-1.16	1.87x10^{-5}
UK4	0.39 (106/-/168)	0.34 (36/132/129)	0.35 (158/-/291)	0.32 (69/206/269)	1.10	0.97-1.25	1.38x10^{-1}
SCOTLAND3	0.33 (138/-/278)	0.33 (34/129/133)	0.33 (233/-/477)	0.35 (87/383/327)	0.98	0.88-1.09	7.01x10^{-1}
CAMBRIDGE	0.36 (443/-/804)	0.34 (104/423/395)	0.34 (304/-/591)	0.35 (160/572/535)	1.01	0.94-1.08	8.23x10^{-1}
CROATIA	0.39 (68/-/106)	0.36 (18/62/58)	0.41 (118/-/172)	0.34 (67/203/231)	1.04	0.89-1.21	6.48x10^{-1}
HELSINKI	0.43 (182/-/246)	0.41 (70/197/144)	0.38 (159/-/257)	0.40 (86/111/158)	1.08	0.96-1.20	2.02x10^{-1}
SWEDEN	0.34 (573/-/1099)	0.35 (204/601/632)	0.32 (423/-/894)	0.33 (144/632/624)	1.07	1.00-1.13	4.67x10^{-2}
					1.07	***1.05-1.10***	***7.46x10^{-10}***
JAPAN	0.88 (850/-/111)	0.87 (470/131/12)	0.87 (1041/-/150)	0.87 (516/160/6)	1.04	0.93-1.16	5.38x10^{-1}
Combined					***1.07***	***1.04-1.10***	***7.30x10^{-10}***

Supplementary Table 3: Relationship between rs1321311 (6p21), rs3824999 (11q13.4), and rs5934683 (Xp22.2) genotypes and sex, age at diagnosis of CRC, tumor site (rectal [ICD9:154], colonic [ICD9:153]), stage, family history of CRC (presence of 1+ first degree relative) and MSI status. *OR>1.0 indicative of over-representation of rectal disease.

	rs1321311			**rs3824999**			**rs5934683**		
	OR (95% CI)	***p*-value**	**Sample size**	**OR (95% CI)**	***p*-value**	**Sample size**	**OR (95% CI)**	***p*-value**	**Sample size**
Sex	0.99 (0.95-1.03)	0.61	23,280[a]	1.04 (1.00-1.08)	0.03	24,313[a]	-	-	-
Age	0.97 (0.92-1.02)	0.19	22,924[b]	0.99 (0.95-1.03)	0.75	22,956[b]	1.00 (0.99-1.01)	0.68	20,667[c]
Site*	1.02 (0.98-1.08)	0.26	19,843[d]	0.97 (0.93-1.01)	0.12	19,889[d]	1.00 (0.98-1.01)	0.70	17,589[e]
Family History	0.97 (0.89-1.04)	0.39	11,867[f]	0.97 (0.90-1.03)	0.32	11,909[f]	1.00 (0.97-1.02)	0.81	11,782[f]
MSI	0.96 (0.81-1.14)	0.67	4,453[g]	1.06 (0.92-1.23)	0.41	4,462[g]	0.99 (0.98-1.04)	0.66	3,060[h]
Stage	0.96 (0.88-1.05)	0.37	5,681[i]	1.02 (0.95-1.10)	0.55	5,726[i]	1.00 (0.98-1.04)	0.66	5,679[i]

a: UK1, SCOTLAND 1, SCOTLAND 2, VQ58, CCFR1, UK2, UK3, SCOTLAND 3 , COINNBS, SWEDEN, UK4, HELSINKI

b: UK1, SCOTLAND 1, SCOTLAND 2, VQ58, UK2, UK3, SCOTLAND 3 , COINNBS, SWEDEN, UK4, HELSINKI

c: UK1, SCOTLAND 1, SCOTLAND 2, VQ58, UK2, UK3, SCOTLAND 3 , SWEDEN, UK4, HELSINKI

d: SCOTLAND 2, VQ58, UK2, UK3, SCOTLAND 3 , COINNBS, SWEDEN, HELSINKI

e: SCOTLAND 2, VQ58, UK2, UK3, SCOTLAND 3 , SWEDEN, HELSINKI

f: UK2, UK3, SCOTLAND 3, HELSINKI

g: UK1, UK2, UK3, COINNBS

h: UK1, UK2, UK3

i: UK1, SCOTLAND 2, SCOTLAND 3, SWEDEN, HELSINKI

Supplementary Table 4: Details of transcription factor binding sites (TFBSs) and regulatory regions as predicted by Transfac Matrix Database (v7), ENCODE CHIP-Seq and ENCODE UW DNAaseI Hypersensitivity (HS) data. "Score" refers to the confidence value assigned to each predicted binding region by the three different programs; regions of DNaseI HS are highlighted. For comparison, the observed and imputed SNPs and associated SNP-Test *P*-values are shown. The genotyped SNP with the most significant association is highlighted in blue; imputed SNPs showing a more significant association are highlighted in red with the SNP showing the most significant association highlighted in purple. Also shown are gene regions with exons highlighted in grey.

6p21 (rs1321311)

Gene region	rsID	SNP type	P-value	TF type	Source	Score	Chrom start	Chrom end
	rs10214849	Genotyped	0.632				36709423	
	rs9296193	Imputed	0.667				36709434	
DNaseI HS					ENCODE	1000	36709820	36710050
	rs6937430	Imputed	0.629				36709875	
DNaseI HS					ENCODE	173	36710260	36710430
DNaseI HS					ENCODE	95	36710560	36710770
	rs4713989	Genotyped	0.645				36712176	
DNaseI HS					ENCODE	153	36712200	36712510
				EBF	ENCODE ChIP-seq	799	36712201	36712641
				CEBPB	ENCODE ChIP-seq	388	36714395	36714711
DNaseI HS					ENCODE	143	36715220	36715510
				RXRA	ENCODE ChIP-seq	178	36717292	36717668
				p300	ENCODE ChIP-seq	303	36717324	36717624
				HNF4A	ENCODE ChIP-seq	403	36717355	36717660
				BAF155	ENCODE ChIP-seq	1000	36718400	36719560
				BAF170	ENCODE ChIP-seq	861	36718451	36719233
				FOSL2	ENCODE ChIP-seq	240	36718572	36719302
DNaseI HS					ENCODE	394	36718580	36718770
				HEY1	ENCODE ChIP-seq	37	36718705	36719185
				Ini1	ENCODE ChIP-seq	259	36718791	36719580
				GR	ENCODE ChIP-seq	170	36718796	36719242
				JunD	ENCODE ChIP-seq	119	36718884	36719160
DNaseI HS					ENCODE	768	36718900	36719370
				NRSF	ENCODE ChIP-seq	206	36718923	36719167
	rs9368944	Genotyped	0.567				36719846	
				GR	ENCODE ChIP-seq	258	36720272	36720793
				Ini1	ENCODE ChIP-seq	189	36720328	36720885
				BAF155	ENCODE ChIP-seq	469	36720355	36720906
				JunD	ENCODE ChIP-seq	312	36720381	36720626
DNaseI HS					ENCODE	1000	36720400	36720610
				CEBPB	ENCODE ChIP-seq	310	36720626	36720906
DNaseI HS					ENCODE	401	36720700	36720950
				PU.1	ENCODE ChIP-seq	1000	36720908	36721324
DNaseI HS					ENCODE	110	36721060	36721250
				Pbx1a	TransFac	1.89	36725309	36725318
				NFKB	ENCODE ChIP-seq	126	36725374	36725592
				NRSF	ENCODE ChIP-seq	174	36725389	36725761
				EBF	ENCODE ChIP-seq	241	36725392	36725813
DNaseI HS					ENCODE	97	36725440	36725650

				BAF155	ENCODE ChIP-seq	628	36725508	36725699
				MZF-1	TransFac	1.69	36725591	36725599
	rs12207916	Imputed	5.16E-03				36725630	
				CEBPB	ENCODE ChIP-seq	108	36725640	36725912
DNaseI HS					ENCODE	159	36725660	36725930
				c-Jun	ENCODE ChIP-seq	426	36725832	36725949
	rs6457932	Imputed	0.349				36726118	
	rs6457933	Imputed	0.108				36726246	
				IRF4	ENCODE ChIP-seq	497	36726514	36727028
				PU.1	ENCODE ChIP-seq	1000	36726517	36727130
				SP1	ENCODE ChIP-seq	208	36726586	36727062
				BCL11A	ENCODE ChIP-seq	784	36726596	36727038
				NFKB	ENCODE ChIP-seq	46	36726612	36727087
				TCF12	ENCODE ChIP-seq	427	36726630	36726960
DNaseI HS					ENCODE	753	36726660	36727130
				PAX5-N19	ENCODE ChIP-seq	241	36726670	36727012
	rs1321313	Genotyped	0.013				36726799	
	rs9349003	Imputed	0.340				36727368	
	rs7742159	Imputed	5.39E-03				36727430	
				EBF	ENCODE ChIP-seq	118	36727550	36727878
				CEBPB	ENCODE ChIP-seq	166	36727704	36727910
DNaseI HS					ENCODE	102	36727720	36727890
	rs9366912	Imputed	0.407				36727861	
	rs12524435	Imputed	0.339				36728126	
				CEBPB	ENCODE ChIP-seq	341	36728145	36728376
				RXRA	ENCODE ChIP-seq	114	36728199	36728477
	rs10947616	Imputed	0.338				36728477	
	rs9470358	**Imputed**	**4.60E-03**				**36728480**	
	rs4713993	Imputed	0.338				36728720	
	rs7382183	Imputed	0.338				36728853	
	rs6915170	Imputed	0.338				36729017	
	rs4568449	Imputed	0.108				36729121	
	rs4464789	Genotyped	0.329				36729156	
	rs10456441	Imputed	0.338				36729337	
	rs10456442	Imputed	0.338				36729389	
	rs10456443	Imputed	0.338				36729425	
	rs4713994	Imputed	0.409				36729511	
	rs12210094	Imputed	0.337				36730291	
	rs12528913	Imputed	0.326				36730527	
	rs9918353	Imputed	5.41E-03				36730655	
DNaseI HS					ENCODE	417	36730800	36731230
	rs1321312	Imputed	0.325				36730852	
	rs1321311	**Genotyped**	**6.25E-03**				**36730878**	
	rs12530170	Genotyped	0.824				36731061	
				NRSF	ENCODE ChIP-seq	95	36731099	36731443
	rs1321310	Imputed	7.42E-03				36731102	
	rs4331968	Imputed	8.08E-03				36731221	
DNaseI HS					ENCODE	357	36731260	36731450
	rs9470361	Imputed	7.73E-03				36731357	
	rs7774130	Imputed	8.06E-03				36731734	
				EBF	ENCODE ChIP-seq	110	36731903	36732220
	rs7740181	Imputed	0.117				36732089	
				c-Jun	ENCODE ChIP-seq	514	36732176	36732506
				c-Fos	ENCODE ChIP-seq	305	36732201	36732497

DNaseI HS					ENCODE	1000	36732300	36732490
				USF-1	ENCODE ChIP-seq	817	36732353	36732453
	rs12203953	Imputed	0.350				36732400	
	rs9470362	Imputed	0.123				36732627	
	rs9470363	Imputed	0.124				36732691	
	rs6907437	Imputed	0.128				36732999	
DNaseI HS					ENCODE	182	36733120	36733310
	rs6907793	Imputed	0.131				36733184	
	rs6930671	Imputed	0.132				36733250	
	rs11969445	Imputed	0.130				36733360	
	rs9470366	Imputed	0.031				36733540	
DNaseI HS					ENCODE	1000	36733840	36734250
				PAX5-N19	ENCODE ChIP-seq	121	36733879	36734419
				BATF	ENCODE ChIP-seq	163	36733913	36734308
				EBF	ENCODE ChIP-seq	493	36733933	36734256
				NFKB	ENCODE ChIP-seq	120	36733980	36734419
				PAX5-C20	ENCODE ChIP-seq	251	36734000	36734333
	rs6936598	Imputed	0.130				36734074	
				Arnt	TransFac	2.76	36734095	36734115
				c-Myc	TransFac	2.13	36734095	36734115
				SREBP-1a	TransFac	2.67	36734099	36734110
	rs6936993	Imputed	0.132				36734300	
	rs9470367	Imputed	0.326				36734910	
	rs7756236	Imputed	7.85E-03				36735031	
DNaseI HS					ENCODE	1000	36735140	36735390
				BCL3	ENCODE ChIP-seq	119	36735264	36735564
				NFKB	ENCODE ChIP-seq	1000	36735422	36735425
	rs6920453	Imputed	0.319				36735461	
	rs9462207	Imputed	7.85E-03				36735577	
	rs9368950	Genotyped	0.347				36735850	
	rs9462208	Imputed	0.133				36735868	
	rs9462209	Genotyped	0.141				36736020	
				HEY1	ENCODE ChIP-seq	42	36736470	36736845
				STAT2	ENCODE ChIP-seq	161	36736508	36736967
				c-Myc	ENCODE ChIP-seq	354	36736511	36737120
				c-Jun	ENCODE ChIP-seq	107	36736539	36736941
				STAT1	ENCODE ChIP-seq	274	36736555	36737050
DNaseI HS					ENCODE	387	36736600	36736890
				Max	ENCODE ChIP-seq	498	36736621	36737110
				BCL3	ENCODE ChIP-seq	1000	36736634	36737717
				PAX5-N19	ENCODE ChIP-seq	113	36736644	36737199
	rs6926780	Imputed	0.386				36736650	
				PAX5-C20	ENCODE ChIP-seq	164	36736721	36737085
				NFKB	ENCODE ChIP-seq	91	36736774	36737107
				Pbx3	ENCODE ChIP-seq	200	36736781	36737169
	rs9462210	Imputed	7.82E-03				36736931	
				Pbx3	ENCODE ChIP-seq	98	36737344	36737584
	rs10807170	Genotyped	0.031				36737422	
	rs4713996	Imputed	0.067				36737692	
	rs4713997	Imputed	0.384				36737811	
DNaseI HS					ENCODE	340	36738100	36738530
				NFKB	ENCODE ChIP-seq	119	36738149	36739005
				BATF	ENCODE ChIP-seq	63	36738245	36738550
				BAF155	ENCODE ChIP-seq	427	36738311	36739440

				Ini1	ENCODE ChIP-seq	227	36738314	36739025
	rs9380585	Imputed	0.383				36738346	
	rs9394368	Imputed	0.066				36738503	
				BAF170	ENCODE ChIP-seq	868	36738562	36738905
DNaseI HS					ENCODE	244	36738580	36738750
				CEBPB	ENCODE ChIP-seq	899	36738716	36739111
				HNF4A	ENCODE ChIP-seq	211	36738720	36739058
DNaseI HS					ENCODE	336	36738780	36739050
				AREB6	TransFac	2.6	36738824	36738837
				TBP	TransFac	1.65	36739239	36739254
				NF-E2	ENCODE ChIP-seq	281	36739301	36739527
DNaseI HS					ENCODE	83	36739320	36739510
	rs9380586	Imputed	0.372				36739542	
				PU.1	ENCODE ChIP-seq	126	36739583	36739874
				IRF4	ENCODE ChIP-seq	134	36739602	36740231
DNaseI HS					ENCODE	233	36739640	36739930
				NFKB	ENCODE ChIP-seq	110	36739800	36740167
				JunD	ENCODE ChIP-seq	352	36739844	36740258
				BATF	ENCODE ChIP-seq	325	36739856	36740214
DNaseI HS					ENCODE	138	36739940	36740110
				POU2F2	ENCODE ChIP-seq	796	36740309	36740962
				HEY1	ENCODE ChIP-seq	160	36740336	36740644
				EBF	ENCODE ChIP-seq	285	36740385	36740865
	rs4711456	Imputed	0.080				36740460	
DNaseI HS					ENCODE	297	36740460	36740830
				NFKB	ENCODE ChIP-seq	164	36740478	36740942
				TCF12	ENCODE ChIP-seq	113	36740535	36740811
	rs13196885	Imputed	0.365				36740666	
	rs4713999	Genotyped	0.072				36741047	
	rs4711457	Imputed	0.065				36741138	
DNaseI HS					ENCODE	132	36741240	36741390
	rs1969701	Imputed	0.379				36741676	
DNaseI HS					ENCODE	99	36742080	36742270
	rs6930083	Imputed	0.063				36742134	
	rs6931097	Imputed	0.166				36742437	
				NFKB	ENCODE ChIP-seq	193	36742534	36743469
				HNF4A	ENCODE ChIP-seq	172	36742679	36743175
				BAF155	ENCODE ChIP-seq	666	36742715	36743228
				FOSL2	ENCODE ChIP-seq	125	36742720	36743263
				TAF1	ENCODE ChIP-seq	447	36742738	36743359
				POU2F2	ENCODE ChIP-seq	728	36742754	36743292
				SP1	ENCODE ChIP-seq	682	36742760	36743311
				BCL11A	ENCODE ChIP-seq	699	36742763	36743257
				EBF	ENCODE ChIP-seq	1000	36742768	36743364
				PAX5-N19	ENCODE ChIP-seq	1000	36742780	36743370
				HSF1	ENCODE ChIP-seq	241	36742785	36743114
				CEBPB	ENCODE ChIP-seq	1000	36742789	36743242
				p300	ENCODE ChIP-seq	704	36742808	36743203
				IRF4	ENCODE ChIP-seq	555	36742808	36743390
				JunD	ENCODE ChIP-seq	492	36742809	36743180
				BATF	ENCODE ChIP-seq	732	36742809	36743196
				TCF12	ENCODE ChIP-seq	509	36742813	36743187
				c-Myc	ENCODE ChIP-seq	351	36742816	36743217
				PAX5-C20	ENCODE ChIP-seq	1000	36742816	36743384

				c-Jun	ENCODE ChIP-seq	173	36742841	36743140
				Ini1	ENCODE ChIP-seq	232	36742843	36743217
				HEY1	ENCODE ChIP-seq	161	36742853	36743331
				BAF170	ENCODE ChIP-seq	647	36742862	36743206
				BCL3	ENCODE ChIP-seq	119	36742877	36743190
DNaseI HS					ENCODE	1000	36742880	36743150
				PU.1	ENCODE ChIP-seq	822	36742890	36743338
				NRSF	ENCODE ChIP-seq	168	36742933	36743246
				Egr-2	TransFac	2.35	36742947	36742959
				p53	TransFac	4.55	36743012	36743032
				POU3F2	TransFac	2.06	36743479	36743489
				Rad21	ENCODE ChIP-seq	139	36743573	36743630
	rs66761782	Imputed	6.94E-03				36744058	
				AP-1	TransFac	2.21	36744277	36744290
				Max	ENCODE ChIP-seq	639	36744338	36744565
				EBF	ENCODE ChIP-seq	53	36744369	36744656
DNaseI HS					ENCODE	112	36744380	36744570
	rs6457934	Imputed	0.178				36745303	
DNaseI HS					ENCODE	140	36745480	36745650
	rs4714000	Genotyped	0.636				36745575	
DNaseI HS					ENCODE	384	36746040	36746310
	rs4714001	Imputed	0.035				36746153	
	rs1321309	Imputed	0.209				36746614	
	rs1321308	Imputed	0.222				36746669	
				HNF4A	ENCODE ChIP-seq	209	36747420	36747819
				USF-1	ENCODE ChIP-seq	55	36747495	36747701
	rs58714705	Imputed	0.213				36747591	
DNaseI HS					ENCODE	148	36747820	36748070
	rs11758192	Imputed	0.213				36747946	
				STAT1	ENCODE ChIP-seq	50	36748055	36748275
	rs10947618	Imputed	0.213				36748110	
	rs10947619	Imputed	0.210				36748135	
	rs10947620	Imputed	0.213				36748166	
	rs7452626	Imputed	0.602				36748219	
	rs10947621	Imputed	0.209				36748250	
	rs9349005	Imputed	0.226				36748346	
	rs9380587	Imputed	0.623				36748461	
	rs12174270	Imputed	0.213				36748647	
	rs7747146	Imputed	0.181				36748968	
	rs7764973	Imputed	0.213				36749014	
	rs6457935	Imputed	0.213				36749116	
	rs12199346	Imputed	6.11E-03				36749524	
				LCR-F1	TransFac	1.71	36749563	36749576
				XBP-1	TransFac	2.35	36749614	36749631
DNaseI HS					ENCODE	69	36749680	36749910
				SRF	TransFac	1.99	36749730	36749745
	rs1977172	Imputed	0.622				36749732	
	rs1010424	Imputed	0.213				36749763	
	rs1010423	Imputed	0.213				36749769	
				CUTL1	TransFac	1.94	36749900	36749910
	rs4711458	Imputed	0.213				36749919	
	rs4711459	Imputed	0.213				36750002	
	rs4711460	Imputed	0.213				36750106	
	rs4711461	Imputed	0.230				36750146	

	rs4714002	Imputed	0.213				36750164	
	rs4711462	Imputed	0.213				36750168	
	rs4714003	Imputed	0.213				36750238	
				POU2F1	TransFac	2.41	36750348	36750367
				SRF	TransFac	1.88	36750354	36750368
	rs10947622	Imputed	0.213				36750380	
				p53	TransFac	2.34	36750494	36750514
	rs12214686	Imputed	0.206				36750529	
				Arnt	TransFac	1.96	36750663	36750683
				c-Myc	TransFac	1.77	36750663	36750683
DNaseI HS					ENCODE	588	36750800	36750990
				c-Jun	ENCODE ChIP-seq	428	36750808	36750975
	rs10947623	Imputed	0.206				36750814	
				POU3F2	TransFac	1.7	36750883	36750899
				Lmo2	TransFac	2.23	36750942	36750951
	rs12192827	Imputed	0.213				36750949	
	rs12192877	Imputed	0.213				36750977	
	rs72853370	Imputed	0.213				36751200	
	rs11962192	Imputed	0.213				36751215	
	rs113041051	Imputed	0.213				36751224	
	rs9357222	Imputed	0.213				36751338	
	rs9368953	Imputed	0.213				36751444	
				STAT1	ENCODE ChIP-seq	155	36751645	36752569
				NFKB	ENCODE ChIP-seq	148	36751723	36752524
	rs9394371	Imputed	0.213				36751733	
				PU.1	ENCODE ChIP-seq	823	36751757	36752165
				HEY1	ENCODE ChIP-seq	616	36751779	36752604
				TAF1	ENCODE ChIP-seq	304	36751788	36752505
				POU2F2	ENCODE ChIP-seq	181	36751815	36752543
DNaseI HS					ENCODE	308	36751840	36751990
				SRF	TransFac	2.46	36751897	36751911
				p300	ENCODE ChIP-seq	106	36751941	36752370
				CEBPB	ENCODE ChIP-seq	83	36752026	36752491
DNaseI HS					ENCODE	537	36752060	36752510
				p53	TransFac	3.3	36752203	36752223
CDKN1A Exon 1							36752245	36752279
CDKN1A Intron 1							36752280	36753656
	rs3829963	Genotyped	0.252				36752364	
DNaseI HS					ENCODE	110	36752520	36752790
				FOXC1	TransFac	2.98	36752741	36752757
				FOXD1	TransFac	3.72	36752741	36752757
				FOXF2	TransFac	2.77	36752741	36752757
				FOXI1	TransFac	1.73	36752743	36752756
DNaseI HS					ENCODE	432	36752860	36753210
				NFKB	ENCODE ChIP-seq	233	36752897	36755402
				p53	TransFac	3.36	36753085	36753105
				SRF	TransFac	1.73	36753093	36753111
				p53	TransFac	2.58	36753095	36753105
				STAT3	TransFac	1.85	36753095	36753116
				HEY1	ENCODE ChIP-seq	1000	36753132	36755082
				SRF	ENCODE ChIP-seq	1000	36753401	36753987
				p300	ENCODE ChIP-seq	247	36753453	36753966
DNaseI HS					ENCODE	376	36753460	36753830
				CEBPB	ENCODE ChIP-seq	86	36753482	36753903

	JunD	ENCODE ChIP-seq	113	36753483	36753923
	HNF4A	ENCODE ChIP-seq	195	36753496	36754726
	Sin3Ak-20	ENCODE ChIP-seq	302	36753532	36753841
	SREBP1	ENCODE ChIP-seq	12	36753532	36754042
	USF-1	ENCODE ChIP-seq	164	36753628	36753872
CDKN1A Exon 2				36753657	36753688
CDKN1A Intron 2				36753689	36759851
	BAF170	ENCODE ChIP-seq	310	36753819	36755474
	STAT1	ENCODE ChIP-seq	414	36753877	36755452
	PAX5-N19	ENCODE ChIP-seq	216	36754015	36755157
	EBF	ENCODE ChIP-seq	453	36754026	36754594
	Ini1	ENCODE ChIP-seq	282	36754031	36756991
	GR	ENCODE ChIP-seq	1000	36754051	36756479
	Nrf1	ENCODE ChIP-seq	237	36754070	36754496
	Max	ENCODE ChIP-seq	415	36754074	36756527
	BAF155	ENCODE ChIP-seq	414	36754074	36756900
	SREBP1	ENCODE ChIP-seq	331	36754076	36755259
	FOSL2	ENCODE ChIP-seq	300	36754077	36754697
	JunD	ENCODE ChIP-seq	713	36754088	36754658
	SP1	ENCODE ChIP-seq	162	36754089	36754806
	c-Myc	ENCODE ChIP-seq	434	36754093	36755452
	SREBP2	ENCODE ChIP-seq	45	36754109	36754121
	PU.1	ENCODE ChIP-seq	303	36754112	36754350
	GABP	ENCODE ChIP-seq	45	36754114	36754341
	p300	ENCODE ChIP-seq	372	36754115	36754767
	PAX5-C20	ENCODE ChIP-seq	553	36754116	36754746
	TAF1	ENCODE ChIP-seq	864	36754125	36755421
	TCF12	ENCODE ChIP-seq	1000	36754131	36754984
	POU2F2	ENCODE ChIP-seq	1000	36754138	36756424
	Sin3Ak-20	ENCODE ChIP-seq	1000	36754146	36754621
	NRSF	ENCODE ChIP-seq	183	36754146	36754743
DNaseI HS		ENCODE	1000	36754160	36754590
	CEBPB	ENCODE ChIP-seq	88	36754168	36754884
	ERRA	ENCODE ChIP-seq	372	36754185	36754832
	FOXP2	ENCODE ChIP-seq	380	36754241	36754341
	Pbx3	ENCODE ChIP-seq	487	36754282	36754684
	c-Jun	ENCODE ChIP-seq	185	36754286	36755391
	BCL3	ENCODE ChIP-seq	124	36754308	36754654
	SREBP2	ENCODE ChIP-seq	38	36754348	36754534
	BCL11A	ENCODE ChIP-seq	101	36754368	36754774
	PU.1	ENCODE ChIP-seq	97	36754369	36754576
	E47	TransFac	1.93	36754671	36754687
	AREB6	TransFac	1.88	36754673	36754685
	MyoD	TransFac	1.72	36754689	36754699
	Sin3Ak-20	ENCODE ChIP-seq	134	36754751	36755010
DNaseI HS		ENCODE	430	36754780	36755610
	FOSL2	ENCODE ChIP-seq	335	36754819	36755646
	Input	ENCODE ChIP-seq	362	36754858	36755348
	BCL11A	ENCODE ChIP-seq	210	36754992	36755313
	JunD	ENCODE ChIP-seq	249	36755001	36755385
	Sin3Ak-20	ENCODE ChIP-seq	237	36755016	36755312
	EBF	ENCODE ChIP-seq	135	36755035	36755321
	ATF	TransFac	2.01	36755114	36755128
	Bach1	TransFac	2.57	36755186	36755201

	AP-1	TransFac	2.47	36755187	36755200
	E2F	TransFac	2.41	36755330	36755342
	HEY1	ENCODE ChIP-seq	326	36755648	36756385
	EBF	ENCODE ChIP-seq	215	36755651	36756499
	TAF1	ENCODE ChIP-seq	325	36755663	36756186
DNaseI HS		ENCODE	260	36755680	36755870
	STAT1	ENCODE ChIP-seq	162	36755702	36756840
	NFKB	ENCODE ChIP-seq	175	36755709	36757018
	FOSL2	ENCODE ChIP-seq	602	36755738	36756475
	BAF170	ENCODE ChIP-seq	411	36755741	36755958
	c-Myc	ENCODE ChIP-seq	641	36755769	36756511
	STAT2	ENCODE ChIP-seq	96	36755798	36756529
	c-Jun	ENCODE ChIP-seq	334	36755806	36756545
	c-Fos	ENCODE ChIP-seq	424	36755821	36756491
	JunD	ENCODE ChIP-seq	269	36755826	36756530
	PAX5-C20	ENCODE ChIP-seq	926	36755836	36756546
	Brg1	ENCODE ChIP-seq	555	36755838	36756729
	GABP	ENCODE ChIP-seq	39	36755840	36756203
DNaseI HS		ENCODE	1000	36755880	36756370
	IRF4	ENCODE ChIP-seq	611	36755912	36756604
	RSRFC4	TransFac	1.96	36755955	36755971
	CEBPB	ENCODE ChIP-seq	353	36755963	36756421
	Bach1	TransFac	2.6	36755976	36755991
	BCL3	ENCODE ChIP-seq	501	36755976	36756551
	AP-1	TransFac	2.54	36755977	36755990
	Arnt	TransFac	1.87	36755981	36756001
	BATF	ENCODE ChIP-seq	636	36755984	36756497
	NRSF	ENCODE ChIP-seq	45	36755999	36756484
	PAX5-N19	ENCODE ChIP-seq	456	36756018	36756516
	TCF12	ENCODE ChIP-seq	661	36756022	36756393
	SP1	ENCODE ChIP-seq	165	36756065	36756506
	BCL11A	ENCODE ChIP-seq	442	36756086	36756505
	p300	ENCODE ChIP-seq	168	36756094	36756573
	LUN-1	TransFac	2.34	36756132	36756149
	Rad21	ENCODE ChIP-seq	200	36756184	36756781
	CTCF	ENCODE ChIP-seq	680	36756191	36756542
	CREB	TransFac	2.19	36756229	36756244
	HNF4A	ENCODE ChIP-seq	406	36756233	36756422
	E2F	TransFac	2.21	36756256	36756264
	FOXP2	ENCODE ChIP-seq	543	36756271	36756371
	Bach1	TransFac	2.14	36756283	36756298
	AP-1	TransFac	1.86	36756284	36756297
	BAF170	ENCODE ChIP-seq	774	36756285	36756485
	Egr-1	ENCODE ChIP-seq	638	36756290	36756390
	Egr-2	TransFac	1.95	36756322	36756334
	Egr-3	TransFac	2.01	36756322	36756334
DNaseI HS		ENCODE	251	36756560	36757010
	EBF	ENCODE ChIP-seq	173	36756693	36757001
	POU2F2	ENCODE ChIP-seq	99	36756756	36756932
DNaseI HS		ENCODE	139	36757180	36757330
	PAX5-C20	ENCODE ChIP-seq	114	36757186	36757378
	NFKB	ENCODE ChIP-seq	102	36757305	36757343
	NFKB	ENCODE ChIP-seq	287	36757720	36759504
DNaseI HS		ENCODE	97	36757780	36757930

	FOSL2	ENCODE ChIP-seq	877	36757904	36758525
	RXRA	ENCODE ChIP-seq	761	36757938	36758419
	JunD	ENCODE ChIP-seq	396	36757957	36759002
	c-Jun	ENCODE ChIP-seq	495	36757984	36758961
	BAF155	ENCODE ChIP-seq	789	36757991	36758995
	c-Fos	ENCODE ChIP-seq	277	36757997	36759031
	Max	ENCODE ChIP-seq	363	36758006	36758905
	STAT1	ENCODE ChIP-seq	36	36758019	36758873
	p300	ENCODE ChIP-seq	171	36758048	36758305
	EBF	ENCODE ChIP-seq	1000	36758052	36758953
	HNF4A	ENCODE ChIP-seq	274	36758055	36758427
	BAF170	ENCODE ChIP-seq	593	36758074	36758806
	c-Myc	ENCODE ChIP-seq	437	36758080	36758940
	Ini1	ENCODE ChIP-seq	234	36758116	36758944
DNaseI HS		ENCODE	1000	36758140	36758490
	POU2F2	ENCODE ChIP-seq	959	36758141	36759262
	AP-4	TransFac	2.12	36758267	36758277
	TCF12	ENCODE ChIP-seq	1000	36758339	36758987
	PAX5-N19	ENCODE ChIP-seq	100	36758431	36759049
	BCL11A	ENCODE ChIP-seq	224	36758514	36759042
DNaseI HS		ENCODE	828	36758560	36758890
	PU.1	ENCODE ChIP-seq	396	36758595	36759031
	MIF-1	TransFac	2	36758600	36758618
	BATF	ENCODE ChIP-seq	146	36758649	36759000
	SREBP-1a	TransFac	1.94	36758655	36758666
	Arnt	TransFac	1.74	36758780	36758800
	E47	TransFac	1.79	36758782	36758798
	MyoD	TransFac	2.14	36758785	36758795
	Meis-1	TransFac	2.24	36758787	36758799
	TGIF	TransFac	2.12	36758788	36758799
DNaseI HS		ENCODE	215	36759000	36759270
	HNF4A	ENCODE ChIP-seq	659	36759144	36759793
	CEBPB	ENCODE ChIP-seq	468	36759299	36759882
	RXRA	ENCODE ChIP-seq	1000	36759311	36759804
	JunD	ENCODE ChIP-seq	169	36759355	36759751
	ERRA	ENCODE ChIP-seq	493	36759356	36760283
	POU2F2	ENCODE ChIP-seq	535	36759357	36760199
	p300	ENCODE ChIP-seq	348	36759367	36759716
	ZBTB33	ENCODE ChIP-seq	400	36759378	36759715
DNaseI HS		ENCODE	237	36759540	36760190
	NFKB	ENCODE ChIP-seq	42	36759589	36759715
	Ini1	ENCODE ChIP-seq	181	36759686	36760016
CDKN1A Exon 3				36759852	36760301
	c-Myc	TransFac	2.58	36760176	36760196
	c-Myc	TransFac	3.17	36760179	36760193
	POU2F2	ENCODE ChIP-seq	225	36760249	36760695
	E2F	TransFac	2.37	36760267	36760282
CDKN1A Intron 3				36760302	36761505
DNaseI HS		ENCODE	201	36760440	36760590
DNaseI HS		ENCODE	143	36761140	36761330
DNaseI HS		ENCODE	291	36761440	36761610
	POU2F2	ENCODE ChIP-seq	1000	36761442	36763056
CDKN1A Exon 4				36761506	36763095
	Cart-1	TransFac	1.98	36761641	36761659

				Cdc5	TransFac	1.99	36761658	36761670
DNaseI HS					ENCODE	390	36761820	36762090
				LCR-F1	TransFac	2.17	36762093	36762106
DNaseI HS					ENCODE	143	36762180	36762590
				NF-kappaB1	TransFac	1.66	36762253	36762263
DNaseI HS					ENCODE	125	36762680	36762830
				NFKB	ENCODE ChIP-seq	32	36762791	36763034
DNaseI HS					ENCODE	226	36762840	36763070
				FOXF2	TransFac	2.02	36762918	36762934
				POU2F2	ENCODE ChIP-seq	603	36763148	36763609
				Input	ENCODE ChIP-seq	172	36763218	36763437
DNaseI HS					ENCODE	187	36763300	36763570
	rs876581	Genotyped	0.594				36763423	
				POU2F2	ENCODE ChIP-seq	704	36763633	36764117
				PAX5-N19	ENCODE ChIP-seq	94	36763718	36764126
DNaseI HS					ENCODE	369	36763740	36764730
				POU2F2	ENCODE ChIP-seq	525	36764132	36764788
				NFKB	ENCODE ChIP-seq	101	36764148	36764798
	rs12207548	Genotyped	0.740				36764234	
DNaseI HS					ENCODE	51	36765000	36765150
				NFKB	ENCODE ChIP-seq	92	36765558	36765674
DNaseI HS					ENCODE	115	36766880	36767090
				NFKB	ENCODE ChIP-seq	87	36767820	36768456
				PAX5-N19	ENCODE ChIP-seq	139	36767846	36768332
				PU.1	ENCODE ChIP-seq	1000	36767880	36768436
				PAX5-C20	ENCODE ChIP-seq	92	36768009	36768254
DNaseI HS					ENCODE	1000	36768020	36768270
				Hlf	TransFac	2.4	36768262	36768272
				ATF-2	TransFac	2.5	36768263	36768271
DNaseI HS					ENCODE	112	36768660	36768810
DNaseI HS					ENCODE	128	36768960	36769170
	rs2395656	Genotyped	0.656				36770149	

11q13.4 (rs3824999)

Gene region	rsID	SNP type	P-value	TF type	Source	Score	Chrom start	Chrom end
	rs11236148	Genotyped	9.17E-03				73941983	
DNaseI HS					ENCODE	91	73942260	73942510
	rs1655483	Genotyped	0.034				73942425	
	rs1783200	Imputed	2.81E-03				73942542	
	rs7930294	Imputed	0.745				73942862	
	rs1791495	Imputed	6.62E-05				73943628	
	rs2887046	Genotyped	0.379				73943674	
	rs4044287	Imputed	0.133				73944835	
				PU.1	ENCODE ChIP-seq	355	73946169	73946357
	rs12795302	Imputed	1.50E-03				73946320	
	rs12801229	Imputed	9.35E-04				73946819	
	rs1292504	Genotyped	1.56E-06				73947278	
	rs3902018	Genotyped	1.52E-03				73947465	
	rs10793091	Imputed	0.195				73947740	
DNaseI HS					ENCODE	98	73947940	73948230
	rs10501416	Imputed	1.40E-03				73947977	

				p300	ENCODE ChIP-seq	730	73948212	73948661
				RXRA	ENCODE ChIP-seq	218	73948221	73948637
				FOSL2	ENCODE ChIP-seq	157	73948226	73948906
DNaseI HS					ENCODE	385	73948300	73948670
				c-Jun	ENCODE ChIP-seq	200	73948379	73948973
				Elk-1	TransFac	2.38	73948476	73948492
				CREB	TransFac	2.2	73948667	73948679
				ATF-2	TransFac	2	73948669	73948677
DNaseI HS					ENCODE	356	73948700	73948930
				JunD	ENCODE ChIP-seq	647	73948853	73948869
	rs4315111	Imputed	0.173				73949244	
	rs7947451	Imputed	0.172				73949417	
	rs11236152	Imputed	0.171				73949906	
	rs7130461	Imputed	0.170				73950487	
	rs7941941	Genotyped	0.180				73951606	
	rs7929392	Imputed	0.168				73951655	
	rs4439539	Imputed	0.174				73951677	
	rs10899007	Imputed	0.134				73952433	
DNaseI HS					ENCODE	182	73953120	73953410
				FAC1	TransFac	2.72	73953403	73953417
				FOXL1	TransFac	2.39	73953420	73953436
				NFKB	ENCODE ChIP-seq	332	73953472	73953835
				USF-1	ENCODE ChIP-seq	119	73953534	73953681
	rs6592568	Imputed	0.026				73953542	
DNaseI HS					ENCODE	150	73953760	73953930
	rs10899009	Imputed	3.50E-07				73953815	
	rs11604752	Imputed	3.48E-07				73954792	
DNaseI HS					ENCODE	280	73955180	73955510
				NFKB	ENCODE ChIP-seq	107	73955296	73955593
DNaseI HS					ENCODE	208	73955660	73955810
	rs4944047	Imputed	0.011				73955738	
	rs1433969	Imputed	0.029				73956081	
DNaseI HS					ENCODE	173	73956160	73956310
				MRF-2	TransFac	1.97	73956182	73956196
				CUTL1	TransFac	1.8	73956343	73956358
				Cdc5	TransFac	1.65	73956353	73956365
	rs10793092	Imputed	4.91E-07				73956355	
				Pbx1a	TransFac	1.71	73956355	73956370
	rs11826567	Imputed	8.74E-03				73956941	
	rs7943504	Imputed	8.72E-03				73957654	
	rs7121958	Imputed	3.42E-07				73957660	
	rs4944903	Genotyped	0.203				73957984	
	rs6592570	Imputed	1.13E-03				73958558	
	rs1971114	Imputed	0.026				73959054	
				Rad21	ENCODE ChIP-seq	734	73959143	73959606
				CTCF	ENCODE ChIP-seq	1000	73959184	73959578
				NFKB	ENCODE ChIP-seq	51	73959261	73959526
DNaseI HS					ENCODE	352	73959280	73959570
	rs7952661	Imputed	0.026				73959425	
	rs7937232	Imputed	0.025				73959558	
	rs72991606	Imputed	3.16E-05				73959768	
	rs1433972	Imputed	1.59E-03				73960574	
	rs10751238	Imputed	0.036				73960645	
	rs10751239	Imputed	0.026				73960646	
	rs11236154	Imputed	0.026				73960818	
	rs7113533	Genotyped	0.064				73961919	
	rs4944904	Imputed	0.026				73963540	
	rs10899010	Imputed	0.026				73963794	

				MyoD	TransFac	1.93	73965508	73965518
	rs4944048	Imputed	0.027				73965974	
				Sox9	TransFac	3.43	73966031	73966045
	rs12290016	Imputed	1.26E-03				73966297	
				BCL3	ENCODE ChIP-seq	412	73966348	73966661
	rs36005373	Imputed	7.91E-03				73966365	
				Pbx3	ENCODE ChIP-seq	151	73966379	73966589
	rs9665746	Imputed	2.47E-03				73966534	
	rs9667597	Imputed	2.47E-03				73966555	
	rs4944906	Imputed	2.47E-03				73966570	
DNaseI HS					ENCODE	497	73966780	73966990
	rs35165052	Imputed	0.083				73967273	
	rs11236158	Imputed	3.44E-07				73967376	
				CUTL1	TransFac	2.63	73968423	73968438
	rs9919665	Imputed	1.32E-03				73968469	
				FOXD1	TransFac	1.76	73968479	73968495
				FOXO4	TransFac	2.34	73968481	73968495
	rs9919666	Genotyped	8.52E-03				73968529	
	rs10793093	Genotyped	2.10E-04				73968600	
	rs4944907	Imputed	2.85E-03				73969005	
	rs11236161	Imputed	2.41E-07				73969361	
				PU.1	ENCODE ChIP-seq	502	73969746	73970154
				IRF4	ENCODE ChIP-seq	674	73969799	73970284
				SP1	ENCODE ChIP-seq	189	73969821	73970217
DNaseI HS					ENCODE	468	73969840	73970190
				PAX5-N19	ENCODE ChIP-seq	221	73969851	73970326
				BATF	ENCODE ChIP-seq	1000	73969858	73970236
				BCL11A	ENCODE ChIP-seq	380	73969874	73970202
				NFKB	ENCODE ChIP-seq	85	73969904	73970215
				PAX5-C20	ENCODE ChIP-seq	98	73969975	73970268
	rs60085010	Imputed	2.39E-07				73970261	
	rs9919663	Imputed	7.40E-03				73970373	
	rs7935260	Imputed	0.024				73971187	
	rs7938931	Imputed	0.024				73971868	
	rs7939930	Genotyped	8.57E-03				73972014	
	rs12292725	Imputed	4.82E-03				73972273	
	rs7929876	Imputed	0.024				73972419	
	rs11236164	Genotyped	1.13E-04				73972614	
				Rad21	ENCODE ChIP-seq	228	73972786	73972969
				AP-2rep	TransFac	2.23	73972888	73972895
	rs12364155	Imputed	5.60E-03				73973383	
	rs7934776	Imputed	4.91E-03				73974498	
				FOXC1	TransFac	2.12	73975129	73975145
	rs34222102	Imputed	3.16E-03				73975606	
	rs4417306	Imputed	4.98E-03				73975658	
	rs4573702	Imputed	4.99E-03				73977147	
	rs4627114	Imputed	0.024				73977466	
	rs4335575	Imputed	5.01E-03				73977488	
	rs34835838	Imputed	0.046				73977658	
	rs10899012	Imputed	3.11E-03				73977882	
	rs72977282	**Imputed**	**1.34E-07**				**73978089**	
	rs7944514	Imputed	3.46E-03				73978840	
DNaseI HS					ENCODE	199	73979320	73979490
	rs11236165	Imputed	5.09E-03				73979918	
	rs12362729	Imputed	0.053				73979965	
DNaseI HS					ENCODE	120	73980260	73980410
				STAT1	ENCODE ChIP-seq	921	73980589	73980597
				BAF170	ENCODE ChIP-seq	441	73980630	73980941

DNaseI HS					ENCODE	121	73980800	73981050
				NFKB	ENCODE ChIP-seq	185	73981001	73981966
				STAT1	ENCODE ChIP-seq	60	73981011	73982132
				c-Myc	ENCODE ChIP-seq	365	73981018	73981981
				FOSL2	ENCODE ChIP-seq	126	73981022	73981396
				TAF1	ENCODE ChIP-seq	829	73981049	73981862
				HEY1	ENCODE ChIP-seq	233	73981052	73981611
				JunD	ENCODE ChIP-seq	97	73981059	73981355
				Sin3Ak-20	ENCODE ChIP-seq	1000	73981062	73981399
				SP1	ENCODE ChIP-seq	240	73981065	73981433
				HNF4A	ENCODE ChIP-seq	388	73981065	73981400
				TCF12	ENCODE ChIP-seq	177	73981072	73981400
				CEBPB	ENCODE ChIP-seq	153	73981079	73981941
				USF-1	ENCODE ChIP-seq	66	73981080	73981338
				Max	ENCODE ChIP-seq	528	73981082	73982034
				IRF4	ENCODE ChIP-seq	301	73981084	73981496
				Ini1	ENCODE ChIP-seq	207	73981085	73982092
				POU2F2	ENCODE ChIP-seq	378	73981086	73981577
				NRSF	ENCODE ChIP-seq	684	73981099	73981423
				BAF155	ENCODE ChIP-seq	622	73981104	73982086
				BATF	ENCODE ChIP-seq	73	73981111	73981345
DNaseI HS					ENCODE	1000	73981120	73981350
				HSF1	ENCODE ChIP-seq	274	73981126	73981546
				p300	ENCODE ChIP-seq	183	73981127	73981365
POLD3 Exon 1							73981277	73981411
				E2F	TransFac	2.57	73981281	73981289
				BAF170	ENCODE ChIP-seq	572	73981296	73982112
POLD3 Intron 1							73981412	73982753
	rs2298572	Imputed	0.025				73981489	
DNaseI HS					ENCODE	489	73981520	73981950
DNaseI HS					ENCODE	106	73981958	73982150
	rs7939226	Genotyped	0.082				73982157	
				p300	ENCODE ChIP-seq	105	73982168	73982433
DNaseI HS					ENCODE	107	73982260	73982450
				BAF170	ENCODE ChIP-seq	643	73982322	73982497
				NFKB	ENCODE ChIP-seq	164	73982329	73982375
POLD3 Exon 2							73982754	73982809
POLD3 Intron 2							73982810	73993384
				PAX5-C20	ENCODE ChIP-seq	83	73983298	73983567
	rs4944049	Imputed	0.024				73984058	
	rs4944050	Imputed	0.024				73984142	
	rs7125480	Imputed	5.47E-03				73984436	
	rs4944911	Imputed	0.024				73985706	
DNaseI HS					ENCODE	82	73986160	73986330
	rs61901537	Imputed	3.05E-03				73986667	
	rs10899013	Genotyped	6.19E-03				73987190	
	rs61901538	Imputed	5.86E-03				73988107	
	rs7934321	Imputed	0.024				73988327	
	rs7934742	Imputed	0.023				73988699	
	rs12801024	Imputed	6.10E-03				73989133	
	rs34702292	Imputed	3.35E-03				73989272	
	rs34060848	Imputed	0.091				73989315	
	rs7932731	Imputed	6.17E-03				73989436	
				BAF170	ENCODE ChIP-seq	1000	73989805	73989986
				POU3F2	TransFac	2.6	73989932	73989942
	rs6592573	Imputed	6.49E-03				73990610	
	rs7925556	Imputed	0.025				73990935	
				POU2F1	TransFac	1.82	73991924	73991937

DNaseI HS					ENCODE	68	73991960	73992210
	rs61901540	Imputed	0.051				73992513	
				RSRFC4	TransFac	1.77	73993128	73993144
POLD3 Exon 3							73993385	73993487
				HSF1	TransFac	1.79	73993417	73993427
				E47	TransFac	3.26	73993450	73993466
POLD3 Intron 3							73993488	74000191
				PU.1	ENCODE ChIP-seq	470	73994088	73994445
				EBF	ENCODE ChIP-seq	266	73994134	73994456
DNaseI HS					ENCODE	63	73994700	73994850
	rs7940880	Imputed	1.54E-06				73995062	
	rs11236171	Imputed	0.051				73995166	
	rs61901541	Imputed	0.080				73995633	
	rs7124188	Imputed	1.28E-06				73995994	
				CEBPB	ENCODE ChIP-seq	890	73998625	73998873
				RXRA	ENCODE ChIP-seq	225	73998635	73998801
	rs4944912	Imputed	1.36E-03				73998929	
	rs4944913	Imputed	6.69E-03				73998997	
	rs4944914	Imputed	1.37E-03				73999053	
	rs12296094	Imputed	0.027				73999348	
	rs4944915	Imputed	0.018				73999612	
	rs4944916	Imputed	0.018				73999688	
				CTCF	ENCODE ChIP-seq	155	73999999	74000392
DNaseI HS					ENCODE	866	74000080	74000590
				Rad21	ENCODE ChIP-seq	267	74000105	74000338
				Ini1	ENCODE ChIP-seq	786	74000156	74000372
POLD3 Exon 4							74000192	74000231
POLD3 Intron 4							74000232	74001570
	rs6592574	Genotyped	5.43E-04				74000610	
	rs6592575	Imputed	0.019				74000654	
	rs7122710	Imputed	0.052				74000823	
	rs4944917	Imputed	0.049				74000929	
				CREB	TransFac	1.67	74001330	74001345
				E47	TransFac	1.93	74001341	74001357
POLD3 Exon 5							74001571	74001703
				LUN-1	TransFac	1.92	74001577	74001594
DNaseI HS					ENCODE	259	74001640	74001850
				AP-2rep	TransFac	2.23	74001640	74001647
				MRF-2	TransFac	2.29	74001650	74001664
				TBP	TransFac	1.92	74001672	74001682
POLD3 Intron 5							74001704	74007229
				Nkx3-1	TransFac	1.74	74001839	74001851
	rs10219203	Genotyped	3.66E-04				74002571	
	rs10899014	Imputed	0.057				74002757	
	rs4944051	Imputed	0.053				74002983	
	rs7120069	Imputed	0.018				74003036	
	rs7130839	Imputed	3.05E-03				74003231	
	rs7101472	Imputed	3.06E-03				74003265	
	rs4584608	Imputed	0.018				74003296	
	rs4996254	Imputed	1.66E-03				74003306	
				Input	ENCODE ChIP-seq	252	74003652	74003836
				PU.1	ENCODE ChIP-seq	473	74004062	74004339
DNaseI HS					ENCODE	356	74004080	74004310
	rs6592576	Imputed	0.018				74004469	
	rs7932194	Imputed	0.027				74005026	
	rs6592577	Genotyped	0.021				74005262	
				AP-2rep	TransFac	2.23	74005292	74005299
				E47	TransFac	1.81	74005614	74005630

	rs10899015	Imputed	1.71E-03				74006732	
POLD3 Exon 6							74007230	74007497
	rs4944052	Imputed	1.67E-03				74007263	
				CUTL1	TransFac	2.36	74007355	74007370
				E47	TransFac	1.78	74007367	74007382
POLD3 Intron 6							74007498	74008709
	rs7943085	Imputed	1.59E-03				74007856	
	rs7944208	Imputed	1.62E-03				74008042	
	rs11236172	Imputed	0.050				74008536	
	rs10501417	Imputed	1.53E-03				74008628	
DNaseI HS					ENCODE	70	74008680	74008850
POLD3 Exon 7							74008710	74008782
POLD3 Intron 7							74008783	74014100
DNaseI HS					ENCODE	211	74009340	74009530
	rs4145953	Genotyped	0.042				74009527	
	rs10899016	Imputed	0.018				74009849	
	rs11236173	Imputed	1.38E-03				74009910	
	rs12288519	Imputed	1.45E-03				74010227	
	rs12288525	Imputed	0.026				74010237	
	rs12287097	Imputed	0.050				74010312	
	rs12280434	Imputed	0.026				74010475	
	rs59768581	Imputed	1.55E-06				74010784	
	rs10899017	Imputed	0.050				74010945	
	rs12807398	Imputed	0.046				74011387	
	rs11236174	Imputed	0.050				74011849	
	rs11236175	Imputed	1.30E-03				74011992	
	rs11236176	Imputed	1.30E-03				74011996	
	rs10899018	Imputed	1.28E-03				74012303	
	rs10899019	Imputed	0.026				74012810	
				RSRFC4	TransFac	1.92	74013247	74013263
	rs10899020	Imputed	1.14E-06				74013417	
	rs10793094	Imputed	1.14E-06				74013473	
POLD3 Exon 8							74014101	74014266
POLD3 Intron 8							74014267	74017909
				Input	ENCODE ChIP-seq	184	74014337	74014513
				FOXO4	TransFac	2.11	74014658	74014672
				Lmo2	TransFac	2.18	74014830	74014839
				AP-2rep	TransFac	2.23	74014929	74014936
	rs2117222	Imputed	9.76E-07				74015333	
	rs10899021	Imputed	0.056				74015702	
	rs57796856	Imputed	9.24E-07				74016003	
				BATF	ENCODE ChIP-seq	80	74016179	74016359
	rs59830047	Imputed	9.09E-07				74016183	
				NFKB	ENCODE ChIP-seq	152	74016209	74016400
	rs11236177	Imputed	0.027				74016715	
	rs1433970	Imputed	0.035				74016841	
	rs10899022	Imputed	0.027				74017034	
	rs2155935	Imputed	8.04E-07				74017225	
	rs2298792	Imputed	7.40E-07				74017844	
				Nkx3-1	TransFac	2.13	74017852	74017864
POLD3 Exon 9							74017910	74018016
				IRF-7A	TransFac	2.56	74017943	74017961
POLD3 Intron 9							74018017	74023275
				PU.1	ENCODE ChIP-seq	164	74018799	74019095
	rs11236178	Imputed	7.22E-07				74018984	
	rs4944053	Imputed	8.30E-04				74019358	
				NFKB	ENCODE ChIP-seq	281	74020374	74020707
				BATF	ENCODE ChIP-seq	135	74020409	74020651

DNaseI HS					ENCODE	877	74020440	74020630
	rs11236180	Genotyped	0.329				74020576	
				E47	TransFac	2.02	74020704	74020720
				STAT3	TransFac	2.09	74020898	74020919
DNaseI HS					ENCODE	95	74021640	74021790
				IRF-7A	TransFac	2.23	74022227	74022245
				POU2F1	TransFac	1.74	74022231	74022243
DNaseI HS					ENCODE	83	74022240	74022430
				AREB6	TransFac	2.31	74022258	74022270
				AML1a	TransFac	1.68	74022307	74022313
				Lmo2	TransFac	2.05	74022507	74022516
				JunD	ENCODE ChIP-seq	173	74023143	74023635
				c-Jun	ENCODE ChIP-seq	176	74023188	74023487
	rs3824999	**Genotyped**	**1.49E-06**				**74023198**	
DNaseI HS					ENCODE	1000	74023200	74023570
				ISGF-3	TransFac	2.26	74023258	74023273
POLD3 Exon 10							74023276	74023388
				CTCF	ENCODE ChIP-seq	564	74023287	74023633
				Meis-1	TransFac	1.97	74023377	74023389
				Rad21	ENCODE ChIP-seq	133	74023382	74023636
POLD3 Intron 10							74023389	74024889
				STAT1	ENCODE ChIP-seq	130	74023407	74023461
	rs11236181	Genotyped	0.072				74023471	
				AREB6	TransFac	1.9	74023555	74023568
	rs11236182	Imputed	5.40E-07				74024170	
DNaseI HS					ENCODE	144	74024180	74024370
	rs10899023	Imputed	1.42E-03				74024340	
	rs3741127	Imputed	0.173				74024581	
POLD3 Exon 11							74024890	74024968
POLD3 Intron 11							74024969	74029256
	rs4944920	Imputed	0.011				74025082	
				c-Jun	ENCODE ChIP-seq	1000	74025218	74025717
				JunD	ENCODE ChIP-seq	569	74025265	74025736
				c-Fos	ENCODE ChIP-seq	386	74025373	74025674
				Max	ENCODE ChIP-seq	578	74025392	74025689
				BAF170	ENCODE ChIP-seq	464	74025399	74025592
DNaseI HS					ENCODE	1000	74025420	74025690
				BAF155	ENCODE ChIP-seq	405	74025425	74025592
				c-Myc	ENCODE ChIP-seq	179	74025452	74025654
	rs7112384	Imputed	0.068				74025853	
	rs7112664	Imputed	0.068				74026074	
	rs7936385	Imputed	1.59E-03				74027598	
DNaseI HS					ENCODE	237	74027680	74027870
				Input	ENCODE ChIP-seq	293	74027778	74027875
				CUTL1	TransFac	2.32	74028066	74028081
				Oct-B1	TransFac	2.32	74028147	74028160
DNaseI HS					ENCODE	101	74028240	74028570
				c-Jun	ENCODE ChIP-seq	217	74028384	74028672
	rs7925747	Genotyped	0.012				74028431	
	rs7925341	Imputed	9.97E-03				74028736	
	rs12282266	Imputed	8.52E-07				74028972	
				AP-1	TransFac	1.95	74029254	74029265
POLD3 Exon 12							74029257	74031413
				CUTL1	TransFac	2.4	74029428	74029440
				ZIC2	TransFac	2.18	74029487	74029496
				Pax-2	TransFac	1.72	74029489	74029508
				c-Jun	ENCODE ChIP-seq	480	74029621	74029821
	rs1051058	Imputed	0.038				74029849	

DNaseI HS					ENCODE	712	74030040	74030330
				Brg1	ENCODE ChIP-seq	1000	74030082	74030465
				c-Jun	ENCODE ChIP-seq	250	74030124	74030426
DNaseI HS					ENCODE	533	74030700	74030930
				CREB	TransFac	2.28	74030919	74030934
				Bach1	TransFac	2.36	74030922	74030937
	rs10857	Imputed	9.91E-03				74031019	
	rs1051076	Genotyped	0.435				74031247	
DNaseI HS					ENCODE	175	74031380	74031590
				c-Jun	ENCODE ChIP-seq	329	74031685	74032027
DNaseI HS					ENCODE	62	74031760	74031937
	rs7947345	Imputed	9.80E-03				74031875	
	rs59958321	Imputed	0.052				74032262	
	rs7935057	Imputed	9.52E-03				74032431	
				SRF	TransFac	2.84	74032881	74032896
				CUTL1	TransFac	2.36	74032935	74032947
				FOXC1	TransFac	1.85	74033117	74033133
				p300	TransFac	1.66	74033199	74033213
				LCR-F1	TransFac	2.43	74033208	74033221
				ZIC2	TransFac	1.85	74033270	74033279
				ZIC2	TransFac	2.33	74033284	74033293
				E47	TransFac	1.89	74033440	74033456
	rs7123887	Imputed	0.033				74033737	
	rs4944921	Imputed	9.30E-03				74034319	
	rs4944922	Imputed	0.033				74034353	
	rs4944923	Imputed	0.033				74034638	
	rs12293317	Imputed	0.105				74034815	
DNaseI HS					ENCODE	168	74034980	74035130
	rs10793095	Imputed	0.010				74035012	
	rs1893362	Imputed	9.21E-03				74035085	
	rs11236183	Genotyped	0.414				74035494	
DNaseI HS					ENCODE	75	74035740	74035910
	rs7102084	Imputed	0.108				74035780	
	rs4944054	Imputed	9.11E-03				74036143	
DNaseI HS					ENCODE	264	74036200	74036410
	rs10899024	Imputed	6.81E-05				74036330	
	rs7130195	Imputed	0.034				74036574	
	rs61900635	Imputed	0.111				74036658	
	rs7106219	Imputed	0.034				74036714	
	rs4944924	Imputed	9.05E-03				74036946	
				PU.1	ENCODE ChIP-seq	95	74037088	74037275
	rs4944925	Genotyped	0.052				74037177	
	rs61900636	Imputed	0.113				74037239	
	rs4944926	Imputed	8.71E-03				74037464	
	rs7932922	Genotyped	3.64E-03				74037678	
DNaseI HS					ENCODE	374	74037720	74037890
				CREB	TransFac	2.32	74037876	74037891
	rs7110993	Imputed	8.68E-03				74037961	
				Nrf1	ENCODE ChIP-seq	635	74038002	74038122
	rs7122810	Imputed	8.88E-03				74038283	
				FOXL1	TransFac	1.78	74039225	74039241
DNaseI HS					ENCODE	1000	74039260	74039470
	rs1944933	Imputed	1.19E-06				74039262	
				ITF-2	TransFac	1.77	74039308	74039324
				AML1a	TransFac	1.68	74039352	74039358
				POU2F1	TransFac	1.69	74039353	74039368
				ARP-1	TransFac	1.7	74039464	74039480
				p53	TransFac	2	74039518	74039528

				AP-4	TransFac	1.81	74039605	74039615
				FOXI1	TransFac	1.97	74039634	74039647
				FOXD1	TransFac	3.29	74039637	74039653
				FOXC1	TransFac	4.02	74039637	74039653
				FOXF2	TransFac	2.77	74039637	74039653
				FOXO4	TransFac	2.77	74039637	74039651
				NRSF	ENCODE ChIP-seq	93	74039732	74039965
	rs11236185	Imputed	1.01E-06				74040179	
	rs11236186	Imputed	0.116				74040513	
	rs4145954	Imputed	6.58E-05				74040814	
	rs7934301	Imputed	0.033				74041304	
				IRF-7A	TransFac	2.19	74041350	74041368
	rs7924706	Imputed	6.53E-05				74041492	
	rs7935426	Imputed	0.116				74041538	
				NRSF	TransFac	2.25	74041665	74041686
	rs7924701	Imputed	8.65E-03				74041686	
				POU2F1	TransFac	2.41	74041782	74041797
				FOXO4	TransFac	1.85	74041803	74041817
	rs7937753	Imputed	1.08E-04				74041841	
				CUTL1	TransFac	2.07	74041920	74041935
	rs6592578	Imputed	0.033				74042175	
	rs11236187	Imputed	1.09E-06				74042214	
	rs11236188	Imputed	1.09E-06				74042378	
	rs11236189	Imputed	1.15E-06				74042418	
	rs55719957	Imputed	0.097				74042693	
	rs12421418	Imputed	8.54E-03				74042787	
	rs12421429	Imputed	1.14E-06				74042833	
	rs9651760	Imputed	8.50E-03				74043104	
	rs9651761	Imputed	8.48E-03				74043242	
	rs9651762	Imputed	8.41E-03				74043298	
	rs9651763	Imputed	8.40E-03				74043387	
DNaseI HS					ENCODE	152	74043780	74043970
	rs6592579	Genotyped	8.13E-03				74043979	
	rs6592580	Imputed	8.35E-03				74044106	
	rs6592581	Imputed	8.33E-03				74044162	
	rs11236190	Imputed	0.145				74044403	
	rs6592582	Imputed	9.92E-03				74044512	
	rs7933770	Imputed	9.94E-03				74044557	
	rs10899025	Imputed	0.134				74044688	
	rs7118314	Imputed	0.010				74044932	
	rs7128944	Imputed	0.010				74045032	
	rs7128944	Imputed	6.55E-05				74045033	
	rs58659624	Imputed	1.53E-06				74045135	
	rs4944928	Imputed	0.010				74045235	
	rs12271394	Imputed	0.010				74045291	
	rs4944055	Imputed	0.011				74045814	
	rs4944929	Imputed	0.011				74045853	
	rs11236193	Imputed	0.140				74045955	
	rs4944056	Imputed	0.011				74046068	
	rs4944930	Imputed	0.011				74046089	
	rs61621556	Imputed	0.028				74046227	
	rs7103197	Imputed	6.70E-05				74046364	
	rs7126573	Imputed	0.011				74046743	
	rs10793098	Imputed	6.79E-05				74046995	
	rs7106984	Imputed	0.011				74047007	
	rs7126957	Imputed	0.011				74047023	
	rs7127628	Imputed	0.011				74047532	
	rs7127630	Imputed	0.011				74047537	

	rs7127668	Imputed	0.011				74047800	
	rs7111251	Imputed	0.012				74047839	
	rs7111273	Imputed	0.012				74047879	
	rs7131096	Imputed	0.012				74048004	
	rs4514450	Imputed	0.012				74048604	
	rs4644667	Imputed	7.01E-05				74048721	
	rs4944931	Imputed	0.012				74049014	
	rs11236198	Imputed	0.201				74049848	
DNaseI HS					ENCODE	168	74049940	74050110
	rs11236199	Imputed	2.29E-06				74050133	
				USF-1	ENCODE ChIP-seq	223	74051271	74051480
				HNF4A	ENCODE ChIP-seq	813	74051446	74051817
				p300	ENCODE ChIP-seq	120	74051524	74051741
DNaseI HS					ENCODE	68	74051540	74051730
				ERRA	ENCODE ChIP-seq	783	74051545	74051816
	rs11236200	Imputed	2.60E-06				74051588	
	rs10219168	Imputed	0.122				74052101	
	rs4420291	Imputed	2.83E-06				74052598	
	rs2186955	Imputed	0.110				74053123	
	rs11236201	Imputed	0.177				74053281	
	rs7948555	Imputed	0.023				74053444	
	rs11236202	Imputed	0.183				74054340	
DNaseI HS					ENCODE	154	74054880	74055030
	rs10899029	Imputed	3.59E-06				74055159	
	rs10793101	Imputed	2.45E-05				74055394	
	rs11236203	Genotyped	1.04E-03				74055648	
	rs4944057	Imputed	0.011				74056151	
	rs11825804	Imputed	3.88E-06				74056519	
	rs7109940	Imputed	3.89E-06				74056548	
	rs4944933	Imputed	0.094				74056594	
				PU.1	ENCODE ChIP-seq	78	74056773	74056895
	rs1944935	Imputed	0.016				74056814	
				E47	TransFac	1.78	74058089	74058105
				Lmo2	TransFac	1.65	74058091	74058103
				AREB6	TransFac	2.1	74058091	74058103
				MyoD	TransFac	1.7	74058092	74058102
				c-Myb	TransFac	3.21	74058145	74058155
				SRF	TransFac	1.75	74058350	74058365
	rs6592590	Genotyped	3.86E-05				74058677	
	rs7129492	Imputed	3.65E-05				74058829	
				BAF155	ENCODE ChIP-seq	632	74060407	74060857
				Ini1	ENCODE ChIP-seq	458	74060450	74060526
DNaseI HS					ENCODE	645	74060500	74060770
	rs7933422	Imputed	7.65E-03				74060954	
DNaseI HS					ENCODE	80	74061120	74061330
				BAF155	ENCODE ChIP-seq	752	74061293	74062255
				c-Myc	ENCODE ChIP-seq	255	74061351	74062396
				Ini1	ENCODE ChIP-seq	191	74061390	74062244
				BAF170	ENCODE ChIP-seq	623	74061390	74062314
				USF-1	ENCODE ChIP-seq	84	74061437	74062359
				GR	ENCODE ChIP-seq	916	74061480	74062381
				JunD	ENCODE ChIP-seq	206	74061504	74062392
				c-Jun	ENCODE ChIP-seq	161	74061556	74062388
				NRSF	ENCODE ChIP-seq	127	74061572	74061938
				TAF1	ENCODE ChIP-seq	64	74061591	74061997
	rs11236207	Imputed	7.47E-03				74061645	
DNaseI HS					ENCODE	1000	74061680	74061950
				AP-4	TransFac	1.87	74061714	74061724

DNaseI HS					ENCODE	1000	74061960	74062330
				Brg1	ENCODE ChIP-seq	623	74062123	74062456
DNaseI HS					ENCODE	581	74062340	74062610
	rs10793102	Imputed	0.206				74062485	
DNaseI HS					ENCODE	317	74062660	74062910
				BAF155	ENCODE ChIP-seq	688	74062695	74062888
	rs11822234	Imputed	2.04E-05				74062794	
	rs11602237	Imputed	1.95E-05				74063339	
				PU.1	ENCODE ChIP-seq	154	74063350	74063581
	rs7104259	Genotyped	0.015				74064089	
	rs7104675	Imputed	9.61E-03				74064380	
	rs7104802	Genotyped	3.66E-03				74064448	
DNaseI HS					ENCODE	471	74064580	74064730
	rs7127935	Imputed	6.92E-03				74064655	
DNaseI HS					ENCODE	387	74065840	74066170
				ARP-1	TransFac	1.97	74066489	74066505
DNaseI HS					ENCODE	95	74067040	74067190
				Ini1	ENCODE ChIP-seq	244	74067226	74067389
	rs7940591	Imputed	5.78E-03				74067530	
				c-Jun	ENCODE ChIP-seq	264	74067531	74067852
DNaseI HS					ENCODE	267	74067620	74067850
	rs11236208	Imputed	0.020				74067969	
DNaseI HS					ENCODE	175	74068840	74069050
				Ini1	ENCODE ChIP-seq	203	74068891	74069051
				Arnt	TransFac	1.85	74069611	74069631
DNaseI HS					ENCODE	53	74069880	74070030
				p53	TransFac	1.67	74070525	74070535
DNaseI HS					ENCODE	127	74070560	74070710
				c-Myc	TransFac	1.86	74070594	74070614
				RSRFC4	TransFac	3.51	74070621	74070637
				POU3F2	TransFac	2.06	74070652	74070662
DNaseI HS					ENCODE	95	74071080	74071330
	rs12282262	Genotyped	0.013				74071586	
	rs10793104	Genotyped	0.530				74071663	

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Gene region	rsID	SNP type	P-value	TF type	Source	Score	Chrom start	Chrom end
	rs2521579	Genotyped	0.991				9493090	
				FAC1	TransFac	1.83	9493996	9494010
TBL1X Exon 18							9493996	9497516
				HSF1	TransFac	2.36	9494556	9494566
				E4BP4	TransFac	2.29	9494941	9494953
				ATF-2	TransFac	2.31	9494943	9494951
				Nkx3-1	TransFac	2.03	9494989	9495001
				Ini1	ENCODE ChIP-seq	274	9495217	9495357
				POU2F1	TransFac	1.89	9496114	9496126
				ZID	TransFac	3.28	9497097	9497110
				FAC1	TransFac	2.21	9497431	9497445
	rs5979160	Imputed	0.012				9499933	
				FOSL2	ENCODE ChIP-seq	211	9500429	9501193
	rs734253	Genotyped	3.83E-03				9501246	
DNaseI HS					ENCODE	307	9502576	9502806

	rs1476510	Genotyped	0.010				9503079	
GPR143 Exon 9							9503190	9503616
	rs3044	Genotyped	0.013				9503388	
GPR143 Intron 8							9503617	9517260
				FOSL2	ENCODE ChIP-seq	170	9503876	9504268
	rs6640489	Imputed	0.013				9504607	
				FOSL2	ENCODE ChIP-seq	920	9504930	9506097
				PU.1	ENCODE ChIP-seq	1000	9505984	9506393
	rs5978337	Imputed	0.013				9506038	
	rs5979162	Imputed	0.013				9506243	
				USF-1	ENCODE ChIP-seq	236	9507026	9507200
DNaseI HS					ENCODE	112	9507096	9507306
DNaseI HS					ENCODE	152	9507336	9507586
DNaseI HS					ENCODE	206	9507816	9507966
DNaseI HS					ENCODE	125	9508116	9508306
				EBF	ENCODE ChIP-seq	54	9508520	9508867
				PAX5-N19	ENCODE ChIP-seq	106	9508543	9508819
				BCL11A	ENCODE ChIP-seq	181	9508550	9508870
				BATF	ENCODE ChIP-seq	425	9508591	9508878
				NFKB	ENCODE ChIP-seq	339	9508610	9508782
DNaseI HS					ENCODE	546	9508616	9508850
	rs6530311	Genotyped	0.015				9509233	
				POU2F1	TransFac	3.29	9514099	9514111
				Oct-B1	TransFac	2.44	9514100	9514113
DNaseI HS					ENCODE	137	9515216	9515426
DNaseI HS					ENCODE	106	9515956	9516186
	rs6654731	Genotyped	0.717				9516373	
				PU.1	ENCODE ChIP-seq	1000	9516943	9517222
				Pbx3	ENCODE ChIP-seq	491	9516959	9517187
				BCL11A	ENCODE ChIP-seq	338	9516972	9517208
GPR143 Exon 8							9517261	9517495
				AP-2rep	TransFac	2.23	9517392	9517399
				SRF	TransFac	3.07	9517444	9517459
GPR143 Intron 7							9517496	9519113
GPR143 Exon 7							9519114	9519231
				c-Myc	TransFac	2.29	9519119	9519133
				AML1a	TransFac	1.68	9519125	9519131
				CUTL1	TransFac	1.92	9519206	9519221
GPR143 Intron 6							9519232	9521340
GPR143 Exon 6							9521341	9521449
GPR143 Intron 5							9521450	9523819
				Cart-1	TransFac	2.06	9523181	9523199
				c-Jun	ENCODE ChIP-seq	444	9523207	9523574
				PU.1	ENCODE ChIP-seq	219	9523238	9523542
DNaseI HS					ENCODE	649	9523296	9523546
				GABP	ENCODE ChIP-seq	45	9523301	9523445
DNaseI HS					ENCODE	179	9523596	9523746
				GR	ENCODE ChIP-seq	48	9523613	9523926
				c-Jun	ENCODE ChIP-seq	328	9523819	9524657
GPR143 Exon 5							9523820	9523929
				CREB	TransFac	2.13	9523886	9523898
				GATA-2	TransFac	1.79	9523898	9523908
				XBP-1	TransFac	1.95	9523899	9523916
				PU.1	ENCODE ChIP-seq	315	9523912	9524106

GPR143 Intron 4							9523930	9526349
DNaseI HS					ENCODE	576	9523936	9524286
				TBP	TransFac	2.45	9524181	9524191
DNaseI HS					ENCODE	255	9524356	9524626
GPR143 Exon 4							9526350	9526442
GPR143 Intron 3							9526443	9537107
DNaseI HS					ENCODE	131	9527040	9527310
				PU.1	ENCODE ChIP-seq	103	9527835	9528075
	rs6640499	Genotyped	0.588				9530781	
	rs6638961	Imputed	0.603				9531752	
DNaseI HS					ENCODE	78	9532016	9532206
				EBF	ENCODE ChIP-seq	132	9533232	9533473
DNaseI HS					ENCODE	149	9533260	9533446
				NFKB	ENCODE ChIP-seq	152	9533290	9533506
	rs11796366	Genotyped	0.012				9533879	
DNaseI HS					ENCODE	664	9535216	9535426
GPR143 Exon 3							9537108	9537202
				USF-1	ENCODE ChIP-seq	78	9537125	9537510
				RP58	TransFac	2.05	9537183	9537195
GPR143 Intron 2							9537203	9538492
	rs2732872	Genotyped	0.511				9538257	
GPR143 Exon 2							9538493	9538602
GPR143 Intron 1							9538603	9543343
				EBF	ENCODE ChIP-seq	148	9542734	9542962
				TAF1	ENCODE ChIP-seq	490	9542793	9543804
DNaseI HS					ENCODE	207	9542836	9543326
GPR143 Exon 1							9543344	9543653
				AP-4	TransFac	2.19	9543531	9543541
DNaseI HS					ENCODE	367	9543636	9543846
				Arnt	TransFac	1.71	9543643	9543663
				c-Myc	TransFac	2.09	9543762	9543776
DNaseI HS					ENCODE	286	9545180	9545486
				HNF4A	ENCODE ChIP-seq	578	9545222	9545451
DNaseI HS					ENCODE	56	9546096	9546270
				EBF	ENCODE ChIP-seq	79	9546112	9546331
DNaseI HS					ENCODE	550	9548156	9548506
				c-Jun	ENCODE ChIP-seq	374	9548204	9548563
	rs2521651	Imputed	0.141				9550636	
	rs2521655	Genotyped	0.143				9551779	
DNaseI HS					ENCODE	740	9553736	9554070
				CEBPB	ENCODE ChIP-seq	463	9558164	9558367
DNaseI HS					ENCODE	61	9559596	9559826
	rs2521661	Genotyped	0.499				9559988	
	rs5934683	**Genotyped**	**5.11E-04**				**9561210**	
				c-Fos	ENCODE ChIP-seq	398	9562194	9562419
DNaseI HS					ENCODE	72	9563096	9563530
				AREB6	TransFac	1.82	9563681	9563693
DNaseI HS					ENCODE	95	9563736	9563946
				HEY1	ENCODE ChIP-seq	209	9563946	9564280
DNaseI HS					ENCODE	170	9563960	9564466
SHROOM2 Exon 1							9564232	9564486
				Egr-1	TransFac	2.03	9564282	9564294
				Egr-2	TransFac	2.17	9564282	9564294
				Egr-3	TransFac	2.2	9564282	9564294

				Pax-5	TransFac	2.29	9564415	9564443
SHROOM2 Intron 1							9564487	9651427
DNaseI HS					ENCODE	95	9564600	9564846
				AP-1	TransFac	1.78	9564607	9564618
				Arnt	TransFac	1.68	9564607	9564627
				MZF-1	TransFac	2.98	9564710	9564723
				AREB6	TransFac	1.82	9564785	9564797
				Lmo2	TransFac	1.7	9564785	9564797
DNaseI HS					ENCODE	136	9564936	9565306
	rs2521662	Imputed	0.347				9566359	
				p300	ENCODE ChIP-seq	123	9566723	9566997
				CEBPB	ENCODE ChIP-seq	413	9566740	9567025
DNaseI HS					ENCODE	718	9566776	9566990
				POU2F1	TransFac	1.65	9566881	9566904
				FOXC1	TransFac	3.27	9566883	9566899
	rs757018	Genotyped	0.355				9567034	
DNaseI HS					ENCODE	1000	9567416	9567586
				AP-4	TransFac	1.78	9567467	9567477
				c-Myb	TransFac	3.21	9568555	9568565
	rs2040621	Imputed	0.345				9568681	
DNaseI HS					ENCODE	1000	9568716	9568946
				POU2F1	TransFac	2.33	9569008	9569021
				Oct-B1	TransFac	2.53	9569150	9569163
DNaseI HS					ENCODE	240	9569316	9569486
				AP-4	TransFac	1.76	9573639	9573649
				Nkx3-1	TransFac	2.34	9575362	9575374
DNaseI HS					ENCODE	171	9575856	9576006
				CEBPB	ENCODE ChIP-seq	496	9575891	9576124
	rs6530318	Genotyped	0.020				9575936	
				CUTL1	TransFac	1.64	9576134	9576149
DNaseI HS					ENCODE	107	9576756	9576906
				c-Myb	TransFac	1.72	9577823	9577833
				NRSF	ENCODE ChIP-seq	29	9579754	9579922
	rs7059068	Genotyped	9.92E-03				9581936	
DNaseI HS					ENCODE	83	9582076	9582246
				Pax-2	TransFac	1.7	9583461	9583480
DNaseI HS					ENCODE	298	9583796	9584026
DNaseI HS					ENCODE	112	9584796	9584946
				PU.1	ENCODE ChIP-seq	236	9585578	9585791
DNaseI HS					ENCODE	333	9585736	9585906
DNaseI HS					ENCODE	264	9587756	9587946
DNaseI HS					ENCODE	142	9588056	9588286
DNaseI HS					ENCODE	301	9594216	9594446
				AREB6	TransFac	1.64	9595165	9595174
				Hlf	TransFac	3.1	9595642	9595652
				RP58	TransFac	1.74	9595754	9595766
				FOXL1	TransFac	1.96	9595791	9595807
				RSRFC4	TransFac	2.35	9595791	9595807
				TBP	TransFac	1.97	9595795	9595803
				ISGF-3	TransFac	1.72	9596058	9596073
				HSF1	TransFac	1.93	9596134	9596144
				CUTL1	TransFac	2.38	9596180	9596195
				AP-4	TransFac	1.76	9596235	9596245
				Pbx1a	TransFac	2.37	9596519	9596534

				CUTL1	TransFac	1.64	9596520	9596535
				Elk-1	TransFac	1.66	9596564	9596580
				POU2F1	TransFac	1.91	9596618	9596641
				ARP-1	TransFac	2.05	9596654	9596670
				Pax-2	TransFac	1.72	9596881	9596900
				p53	TransFac	1.95	9596888	9596898
				AREB6	TransFac	2.2	9596959	9596968
				CUTL1	TransFac	1.7	9597043	9597053
				CREB	TransFac	2.42	9597223	9597238
				FOXL1	TransFac	2.19	9597328	9597344
				ATF-2	TransFac	1.76	9597329	9597337
				FOXO4	TransFac	2.13	9597330	9597344
				MRF-2	TransFac	1.93	9597417	9597431
DNaseI HS					ENCODE	118	9599036	9599186
DNaseI HS					ENCODE	532	9602336	9602610
				MRF-2	TransFac	2.56	9602458	9602472
DNaseI HS					ENCODE	171	9602916	9603186
				FOXO4	TransFac	1.8	9603308	9603322
DNaseI HS					ENCODE	371	9603336	9603546
				RelA	TransFac	1.81	9603407	9603417
				HNF4A	ENCODE ChIP-seq	233	9603448	9604073
				p300	ENCODE ChIP-seq	114	9603882	9604083
				Ini1	ENCODE ChIP-seq	230	9606971	9607151
				TCF12	ENCODE ChIP-seq	122	9607009	9607324
DNaseI HS					ENCODE	177	9607120	9607270
				IRF4	ENCODE ChIP-seq	940	9607193	9607690
				NFKB	ENCODE ChIP-seq	172	9607253	9607719
				BCL11A	ENCODE ChIP-seq	1000	9607272	9607706
				p300	ENCODE ChIP-seq	234	9607275	9607687
				PAX5-N19	ENCODE ChIP-seq	603	9607291	9607678
				JunD	ENCODE ChIP-seq	672	9607308	9607728
				BATF	ENCODE ChIP-seq	1000	9607310	9607704
				EBF	ENCODE ChIP-seq	70	9607320	9607599
				TAF1	ENCODE ChIP-seq	90	9607336	9607669
				TCF12	ENCODE ChIP-seq	778	9607336	9607682
				c-Jun	ENCODE ChIP-seq	357	9607338	9607742
DNaseI HS					ENCODE	1000	9607351	9607626
				PAX5-C20	ENCODE ChIP-seq	324	9607381	9607661
				BAF155	ENCODE ChIP-seq	1000	9607385	9607622
				POU2F2	ENCODE ChIP-seq	235	9607387	9607640
	rs5934697	Imputed	0.427				9608931	
				Max	ENCODE ChIP-seq	1000	9610157	9610486
DNaseI HS					ENCODE	41	9610316	9610426
DNaseI HS					ENCODE	982	9610460	9610906
	rs5933761	Imputed	0.456				9613230	
	rs2405940	Genotyped	0.391				9613280	
				p53	TransFac	1.79	9613419	9613439
	rs1859013	Imputed	0.463				9613481	
	rs6530329	Imputed	0.491				9614078	
	rs6638967	Imputed	0.627				9615667	
DNaseI HS					ENCODE	331	9616136	9616306
	rs4830660	Imputed	0.646				9617325	
	rs4830661	Genotyped	0.285				9617429	
	rs6530331	Imputed	0.788				9617838	

	rs5933762	Genotyped	0.668				9618602	
				FOXD1	TransFac	1.87	9620267	9620283
				NFKB	ENCODE ChIP-seq	63	9620303	9620527
DNaseI HS					ENCODE	562	9620336	9620686
	rs6530332	Imputed	0.710				9620377	
				MZF-1	TransFac	1.66	9620411	9620424
	rs960417	Genotyped	0.604				9620831	
DNaseI HS					ENCODE	112	9622756	9622906
				HEY1	ENCODE ChIP-seq	47	9622907	9623250
DNaseI HS					ENCODE	107	9622976	9623270
				CEBPB	ENCODE ChIP-seq	595	9623275	9623740
				p300	ENCODE ChIP-seq	221	9623298	9623670
DNaseI HS					ENCODE	628	9623336	9623666
	rs2405942	Genotyped	0.825				9623871	
DNaseI HS					ENCODE	264	9624416	9624706
	rs6530333	Genotyped	0.637				9624668	
				BAF155	ENCODE ChIP-seq	539	9624923	9625160
				c-Jun	ENCODE ChIP-seq	321	9624941	9625255
				CEBPB	ENCODE ChIP-seq	355	9624963	9625294
				FOSL2	ENCODE ChIP-seq	100	9624969	9625203
				JunD	ENCODE ChIP-seq	143	9624971	9625303
DNaseI HS					ENCODE	1000	9624976	9625226
	rs5933763	Imputed	0.580				9625101	
	rs5933764	Imputed	0.565				9625257	
	rs5933765	Genotyped	0.538				9625538	
DNaseI HS					ENCODE	141	9626956	9627166
	rs5934702	Genotyped	0.365				9627249	
	rs5934703	Imputed	0.359				9627315	
	rs16985744	Imputed	0.696				9627419	
	rs4830418	Imputed	0.357				9627483	
	rs4830419	Imputed	0.353				9627715	
DNaseI HS					ENCODE	1000	9629736	9629966
	rs5934705	Genotyped	0.294				9631135	
DNaseI HS					ENCODE	186	9631136	9631346
	rs12395804	Genotyped	0.634				9632657	
DNaseI HS					ENCODE	212	9633356	9633726
DNaseI HS					ENCODE	269	9633816	9634026
				Max	ENCODE ChIP-seq	713	9634448	9634827
DNaseI HS					ENCODE	113	9634456	9634606
	rs7051365	Genotyped	0.096				9634583	
DNaseI HS					ENCODE	44	9635456	9635606
DNaseI HS					ENCODE	394	9635856	9636166
				GR	ENCODE ChIP-seq	181	9635934	9636308
				MZF-1	TransFac	2.27	9635995	9636008
				c-Rel	TransFac	1.82	9636084	9636094
				FOXI1	TransFac	1.83	9636096	9636109
				ISGF-3	TransFac	1.67	9636150	9636165
	rs7062290	Genotyped	0.094				9637173	
	rs5979192	Imputed	0.107				9637705	
DNaseI HS					ENCODE	334	9637716	9637906
				Bach1	TransFac	2.5	9637766	9637781
DNaseI HS					ENCODE	597	9637996	9638206
DNaseI HS					ENCODE	165	9638676	9638946
				CTCF	ENCODE ChIP-seq	88	9640324	9640554

				CEBPB	ENCODE ChIP-seq	948	9640446	9640612
	rs1016625	Genotyped	0.047				9640837	
	rs1016626	Imputed	0.428				9641162	
	rs1016627	Genotyped	0.078				9641307	
DNaseI HS					ENCODE	296	9641756	9642106
				XBP-1	TransFac	1.67	9643244	9643261
				Ini1	ENCODE ChIP-seq	235	9643639	9643851
DNaseI HS					ENCODE	108	9643640	9643790
				NFKB	ENCODE ChIP-seq	993	9643732	9644277
				GR	ENCODE ChIP-seq	424	9643749	9644173
				BAF155	ENCODE ChIP-seq	663	9643809	9644371
				c-Jun	ENCODE ChIP-seq	354	9643858	9644367
				JunD	ENCODE ChIP-seq	466	9643868	9644599
				BAF170	ENCODE ChIP-seq	653	9643905	9644706
DNaseI HS					ENCODE	435	9643916	9644186
				AP-1	TransFac	1.72	9644019	9644028
	rs5934708	Genotyped	0.115				9644055	
				E47	TransFac	1.76	9644156	9644172
				AP-1	TransFac	1.79	9644166	9644175
DNaseI HS					ENCODE	366	9644356	9644786
				Ini1	ENCODE ChIP-seq	376	9644429	9644840
				p300	TransFac	1.82	9644532	9644546
	rs12007032	Imputed	0.353				9644753	
DNaseI HS					ENCODE	159	9644856	9645006
	rs5979195	Imputed	0.355				9644975	
	rs5933773	Imputed	0.399				9645028	
	rs6640534	Genotyped	0.317				9645430	
DNaseI HS					ENCODE	471	9645556	9645886
	rs4830665	Imputed	0.195				9645855	
	rs5934710	Imputed	0.442				9647321	
	rs723259	Genotyped	0.498				9648934	
DNaseI HS					ENCODE	107	9649136	9649306
	rs723261	Imputed	0.466				9649446	
				NFKB	ENCODE ChIP-seq	101	9649584	9649750
	rs5933775	Genotyped	0.459				9649608	
DNaseI HS					ENCODE	287	9649716	9649946
DNaseI HS					ENCODE	59	9650676	9650886
	rs763375	Imputed	0.484				9651274	
SHROOM2 Exon 2							9651428	9651579
				CUTL1	TransFac	1.92	9651487	9651497
SHROOM2 Intron 2							9651580	9668752
				Rad21	ENCODE ChIP-seq	152	9651725	9652121
				CTCF	ENCODE ChIP-seq	364	9651740	9652075
				NFKB	ENCODE ChIP-seq	78	9651784	9652122
DNaseI HS					ENCODE	284	9651816	9652026
	rs2239416	Imputed	0.497				9652249	
DNaseI HS					ENCODE	516	9652336	9652586
DNaseI HS					ENCODE	150	9654096	9654266
DNaseI HS					ENCODE	333	9655976	9656206
				Pbx1a	TransFac	2.07	9656058	9656073
				RP58	TransFac	2.12	9656424	9656436
	rs6640537	Imputed	0.430				9657453	
	rs17280844	Genotyped	0.407				9657652	
				Elk-1	TransFac	1.8	9658008	9658024

	rs2051687	Genotyped	0.213				9659037	
	rs2239427	Imputed	0.472				9659259	
				Max	ENCODE ChIP-seq	696	9660400	9661200
				c-Jun	ENCODE ChIP-seq	1000	9660503	9660980
DNaseI HS					ENCODE	437	9660536	9660926
	rs1858883	Genotyped	0.511				9660624	
				TBP	TransFac	1.92	9660651	9660661
DNaseI HS					ENCODE	195	9661896	9662126
				IRF4	ENCODE ChIP-seq	496	9662910	9663280
				CTCF	ENCODE ChIP-seq	882	9662948	9663277
				Rad21	ENCODE ChIP-seq	249	9662959	9663389
				NFKB	ENCODE ChIP-seq	194	9662995	9663300
DNaseI HS					ENCODE	514	9662996	9663226
	rs13340753	Genotyped	0.505				9663006	
				Ini1	ENCODE ChIP-seq	141	9663024	9663233
	rs6640541	Imputed	0.537				9664230	
	rs12557532	Genotyped	0.819				9664501	
DNaseI HS					ENCODE	62	9664956	9665106
	rs5979199	Genotyped	0.654				9665537	
				NRSF	ENCODE ChIP-seq	832	9666720	9667086
DNaseI HS					ENCODE	310	9666896	9667086
	rs6638974	Imputed	0.575				9666988	
	rs6640542	Imputed	0.577				9667110	
DNaseI HS					ENCODE	101	9667416	9667606
SHROOM2 Exon 3							9668753	9668884
				p300	TransFac	2.6	9668773	9668787
	rs6640543	Imputed	0.915				9668834	
SHROOM2 Intron 3							9668885	9672133
	rs6640544	Genotyped	0.929				9668933	
	rs17327524	Genotyped	0.515				9671845	
	rs17327531	Imputed	0.593				9671904	
DNaseI HS					ENCODE	84	9671916	9672106
SHROOM2 Exon 4							9672134	9674474
				NRSF	TransFac	2.77	9672197	9672218
				E47	TransFac	2.17	9672273	9672289
				c-Myc	TransFac	1.94	9672274	9672288
				ZID	TransFac	1.65	9672313	9672326
				AML1a	TransFac	1.68	9672345	9672351
				HSF1	TransFac	1.87	9672381	9672391
				SRF	TransFac	1.76	9672568	9672582
				Arnt	TransFac	1.8	9673051	9673071
				AREB6	TransFac	2.65	9673055	9673068
				SREBP-1a	TransFac	1.86	9673056	9673067
				TBP	TransFac	2.21	9673720	9673735
				XBP-1	TransFac	2.01	9673759	9673776
SHROOM2 Intron 4							9674475	9675965
DNaseI HS					ENCODE	1000	9675556	9675946
SHROOM2 Exon 5							9675966	9676066
SHROOM2 Intron 5							9676067	9709950
	rs2073944	Imputed	0.817				9676156	
DNaseI HS					ENCODE	97	9676476	9676686
				Nkx6-1	TransFac	2.03	9676544	9676557

				Cdc5	TransFac	2.24	9676565	9676577
	rs2012821	Genotyped	0.360				9676743	
				IRF4	ENCODE ChIP-seq	763	9677186	9677753
				POU2F2	ENCODE ChIP-seq	180	9677274	9677751
				BCL11A	ENCODE ChIP-seq	902	9677277	9677666
				PAX5-N19	ENCODE ChIP-seq	130	9677301	9677708
				EBF	ENCODE ChIP-seq	158	9677333	9677881
				BATF	ENCODE ChIP-seq	309	9677355	9677620
				TCF12	ENCODE ChIP-seq	797	9677361	9677714
				FOXL1	TransFac	2.31	9677369	9677385
DNaseI HS					ENCODE	914	9677376	9677766
				E4BP4	TransFac	2.03	9677437	9677449
				NFKB	ENCODE ChIP-seq	344	9677438	9677624
				c-Myc	TransFac	2.28	9677563	9677583
				Arnt	TransFac	2.62	9677563	9677583
				SREBP-1a	TransFac	2.19	9677567	9677578
				c-Myc	TransFac	2.52	9677567	9677579
				FOXL1	TransFac	1.67	9680386	9680402
DNaseI HS					ENCODE	171	9680536	9680746
DNaseI HS					ENCODE	94	9680996	9681246
	rs6640551	Genotyped	0.639				9681893	
	rs6640552	Genotyped	0.609				9682157	
DNaseI HS					ENCODE	597	9683016	9683386
DNaseI HS					ENCODE	612	9684776	9685086
				FOSL2	ENCODE ChIP-seq	117	9685347	9685592
				JunD	ENCODE ChIP-seq	244	9685350	9685626
				CEBPB	ENCODE ChIP-seq	694	9685351	9685631
				c-Jun	ENCODE ChIP-seq	271	9685355	9685660
DNaseI HS					ENCODE	780	9685416	9685726
DNaseI HS					ENCODE	813	9685756	9686066
DNaseI HS					ENCODE	528	9689336	9689626
				c-Jun	ENCODE ChIP-seq	296	9689399	9689707
				POU3F2	TransFac	2.82	9689532	9689548
DNaseI HS					ENCODE	793	9690116	9690366
				RP58	TransFac	2.25	9690235	9690247
				Sox9	TransFac	1.97	9690561	9690575
				FOXF2	TransFac	2.09	9690563	9690579
				FOXL1	TransFac	1.68	9690563	9690579
				Oct-B1	TransFac	2.77	9690596	9690609
				p53	TransFac	1.82	9690906	9690916
DNaseI HS					ENCODE	529	9690916	9691126
				FOXC1	TransFac	1.89	9691403	9691419
				LCR-F1	TransFac	1.74	9691405	9691427
				AP-1	TransFac	2.34	9691411	9691424
				POU2F1	TransFac	2.23	9692075	9692090
	rs6640557	Genotyped	0.826				9692207	
	rs2239419	Genotyped	0.700				9694918	
	rs2239420	Imputed	0.677				9695076	
	rs2239421	Genotyped	0.345				9695788	
	rs2239422	Genotyped	0.398				9695900	
	rs2239423	Imputed	0.352				9695930	
				BCL3	ENCODE ChIP-seq	173	9697480	9697840
DNaseI HS					ENCODE	54	9697556	9697746
DNaseI HS					ENCODE	165	9697776	9697926

DNaseI HS					ENCODE	189	9698856	9699026
				CEBPB	ENCODE ChIP-seq	1000	9699190	9699552
				HNF4A	ENCODE ChIP-seq	686	9699231	9699486
	rs2283703	Genotyped	0.523				9700159	
DNaseI HS					ENCODE	86	9701216	9701426
				AML1a	TransFac	1.68	9701666	9701672
				c-Myc	TransFac	2.21	9701831	9701843
DNaseI HS					ENCODE	99	9703916	9704086
DNaseI HS					ENCODE	195	9705496	9705746
				TAF1	ENCODE ChIP-seq	35	9705871	9706089
DNaseI HS					ENCODE	1000	9705996	9706226
				Nkx6-1	TransFac	2.08	9706894	9706907
				FOXO4	TransFac	1.87	9708946	9708957
SHROOM2 Exon 6							9709951	9710646
				NRSF	ENCODE ChIP-seq	52	9710472	9710647
SHROOM2 Intron 6							9710647	9714909
DNaseI HS					ENCODE	171	9711196	9711346
	rs2238886	Genotyped	0.989				9712112	
DNaseI HS					ENCODE	65	9713276	9713446
				CUTL1	TransFac	1.88	9714909	9714919
SHROOM2 Exon 7							9714910	9715461
				MRF-2	TransFac	2.09	9714925	9714939
				FAC1	TransFac	1.76	9714925	9714939
				ZID	TransFac	2.14	9714942	9714955
SHROOM2 Intron 7							9715462	9716970
SHROOM2 Exon 8							9716971	9717142
				XBP-1	TransFac	1.8	9717024	9717041
				CREB	TransFac	1.88	9717028	9717043
SHROOM2 Intron 8							9717143	9722416
	rs4830676	Genotyped	0.933				9717327	
	rs4830677	Imputed	0.981				9717408	
	rs3788949	Genotyped	0.901				9718077	
				c-Jun	ENCODE ChIP-seq	287	9718122	9718532
				Max	ENCODE ChIP-seq	617	9718167	9718668
	rs3788950	Genotyped	0.782				9718173	
DNaseI HS					ENCODE	1000	9718196	9718466
	rs3788951	Imputed	0.620				9718313	
DNaseI HS					ENCODE	263	9718960	9719466
				NRSF	ENCODE ChIP-seq	1000	9719025	9719285
				POU2F2	ENCODE ChIP-seq	219	9719081	9719535
				EBF	ENCODE ChIP-seq	124	9719213	9719527
				NFKB	ENCODE ChIP-seq	136	9719215	9719495
				BATF	ENCODE ChIP-seq	324	9719224	9719494
				PAX5-C20	ENCODE ChIP-seq	1000	9719717	9720249
				p300	ENCODE ChIP-seq	890	9719748	9720412
				TCF12	ENCODE ChIP-seq	1000	9719769	9720334
				NFKB	ENCODE ChIP-seq	373	9719775	9720393
				IRF4	ENCODE ChIP-seq	985	9719783	9720382
				PAX5-N19	ENCODE ChIP-seq	1000	9719786	9720294
				EBF	ENCODE ChIP-seq	983	9719795	9720338
				BCL11A	ENCODE ChIP-seq	1000	9719799	9720337
				SP1	ENCODE ChIP-seq	450	9719821	9720356

				PU.1	ENCODE ChIP-seq	221	9719823	9720227
				BCL3	ENCODE ChIP-seq	1000	9719828	9720318
				POU2F2	ENCODE ChIP-seq	440	9719847	9720327
				BATF	ENCODE ChIP-seq	1000	9719859	9720273
				Max	ENCODE ChIP-seq	425	9719901	9720280
	rs5934722	Genotyped	0.476				9719918	
DNaseI HS					ENCODE	724	9719920	9720166
				Pbx3	ENCODE ChIP-seq	543	9719975	9720240
				EBF	ENCODE ChIP-seq	364	9721122	9721539
				IRF4	ENCODE ChIP-seq	299	9721138	9721546
				POU2F2	ENCODE ChIP-seq	211	9721144	9721542
				BCL11A	ENCODE ChIP-seq	517	9721173	9721533
				PAX5-N19	ENCODE ChIP-seq	467	9721180	9721503
				NFKB	ENCODE ChIP-seq	143	9721201	9721606
				PAX5-C20	ENCODE ChIP-seq	523	9721212	9721497
				TCF12	ENCODE ChIP-seq	701	9721240	9721552
				BATF	ENCODE ChIP-seq	405	9721248	9721530
				Pbx3	ENCODE ChIP-seq	112	9721288	9721445
DNaseI HS					ENCODE	329	9721296	9721570
	rs4830679	Genotyped	0.721				9722022	
	rs3815015	Imputed	0.561				9722222	
				POU2F1	TransFac	1.81	9722274	9722293
	rs3815016	Genotyped	0.626				9722278	
SHROOM2 Exon 9							9722417	9722689
				E47	TransFac	2.39	9722444	9722460
				Lmo2	TransFac	2.01	9722446	9722458
				RP58	TransFac	1.95	9722567	9722579
				Pax-5	TransFac	1.87	9722607	9722635
SHROOM2 Intron 9							9722690	9724446
	rs2238887	Imputed	0.847				9723258	
	rs2238888	Genotyped	0.926				9723489	
	rs2238889	Imputed	0.878				9724026	
	rs2073940	Imputed	0.758				9724075	
	rs2073941	Genotyped	0.715				9724403	
SHROOM2 Exon 10							9724447	9727217
				Pax-5	TransFac	1.71	9724604	9724632
	rs2073942	Imputed	0.937				9724683	
				EBF	ENCODE ChIP-seq	52	9724919	9725203
				Pbx3	ENCODE ChIP-seq	136	9724982	9725197
DNaseI HS					ENCODE	127	9725016	9725306
				BCL11A	ENCODE ChIP-seq	447	9725157	9725532
				NFKB	ENCODE ChIP-seq	47	9725161	9725519
				LCR-F1	TransFac	1.7	9725217	9725239
				BATF	ENCODE ChIP-seq	118	9725221	9725509
				TCF12	ENCODE ChIP-seq	288	9725245	9725470
	rs1858884	Genotyped	0.553				9725585	
DNaseI HS					ENCODE	182	9726296	9726486
DNaseI HS					ENCODE	98	9727256	9727406
				BCL3	ENCODE ChIP-seq	127	9727338	9727577
	rs2188384	Genotyped	0.275				9729314	

Supplementary Table 5: Relationship between SNP genotype and gene expression in colonic tissue, CRC, lymphoblastoid cell lines (LCL), fibroblasts, T-cells and adipocytes. Box plots are shown only for selected associations.

Variant	**Gene/probe**	**Colonic epithelium[¥]** ***P*-value**	**CRC[$]** ***P*-value**	**LCL** ***P*-value** **Twin1** **Twin2** **Geneva [1,2]**	**Fibroblast** ***P*-value** **Twin1** **Twin2** **Geneva[1,2]**	**Adipose** ***P*-value** **Twin1** **Twin2[1,2]**	**T-cell** ***P*-value** **Geneva[1]**
rs1321311 (6p21)	*CDKN1A* ILMN_1784602	0.28	-	0.91 0.98 0.15	0.97 0.95 0.42	0.53 0.38	0.0001
rs1321311 (6p21)	*CDKN1A* ILMN_1787212	-	-	4.0x10^{-5} 0.008 0.002	0.14 0.37 0.16	0.73 0.17	0.46
rs1321310* (6p21)	*CDKN1A* A_24_P89457	-	0.46	- - -	- - -	- - -	-
rs3824999 (11q13.4)	*POLD3* ILMN_1751773	0.25	-	0.73 0.79 0.18	0.37 0.72 0.04	0.24 0.64	0.17
rs3824999 (11q13.4)	*POLD3* ILMN_2233552	-	-	0.16 0.06 0.12	0.43 0.33 0.02	0.54 0.49	0.56
rs11236187** (11q13.4)	*POLD3* A_32_P182439		0.12	- - -	- - -	- -	-
rs5934683 (Xp22.2)	*SHROOM2* ILMN_1681777	1.28x10^{-7} Male–0.0003 Female–0.0004		- - -	- - -	- -	-
rs5934683 (Xp22.2)	*SHROOM2* A_23_P217753	-	0.015 Male-0.77 Female-0.0037	- - -	- - -	- -	-
rs5934683 (Xp22.2)	*GPR143* ILMN_1756261	0.47 Male-0.89 Female-0.24		- - -	- - -	- - -	-

¥Illumina analysis of 42 colon tissue samples

$Data on AgilentG4502A_07_3 custom gene expression platform derived from the analysis of 154 CRCs as part of the Cancer Genome Atlas project: http://cancergenome.nih.gov

Geneva: Fibroblast, LCL and T-cells derived from the umbilical cords of 75 Geneva GenCord individuals[1]

Twin1 and Twin 2: 166 adipose, 156 LCL and 160 skin samples derived from a subset of healthy female twins of the MuTHER resource[2]

*Linkage disequilibrium between rs1321311 and rs1321310 – r^2=1.0, D'=1.0.

**Linkage disequilibrium between rs3824999 and rs11236187 – r^2=1.0, D'=1.0.

REFERENCES

1. Dimas, A.S. et al. Common regulatory variation impacts gene expression in a cell type-dependent manner. *Science* **325**, 1246-50 (2009).
2. Nica, A.C. et al. The architecture of gene regulatory variation across multiple human tissues: the MuTHER study. *PLoS Genet* **7**, e1002003 (2011).

SUPPLEMENTARY NOTE

1. Subjects and datasets

Scotland1 (COGS)[8] included 1,012 CRC cases (51% male; mean age at diagnosis 49.6 years, SD±6.1) and 1,012 cancer-free population controls (51% male; mean age 51.0 years; SD±5.9). Cases were for early age at onset (age ≤55 years). Known dominant polyposis syndromes, HNPCC/Lynch syndrome or bi-allelic *MYH* mutation carriers were excluded. Control subjects were sampled from the Scottish population NHS registers, matched by age (±5 years), gender and area of residence within Scotland.

Scotland2 (SOCCS)[8] comprised 2,057 CRC cases (61% male; mean age at diagnosis 65.8 years, SD±8.4) and 2,111 population controls (60% males; mean age 67.9 years, SD±9.0) ascertained in Scotland. Cases were taken from an independent, prospective, incident CRC case series and aged <80 years at diagnosis. Control subjects were population controls matched by age (±5 years), gender and area of residence within Scotland.

UK1 (CORGI)[8] comprised 940 cases with colorectal neoplasia (47% male) ascertained through the Colorectal Tumour Gene Identification (CoRGI) consortium. All had at least one first-degree relative affected by CRC and one or more of the following phenotypes: CRC at age 75 or less; any colorectal adenoma (CRAd) at age 45 or less; ≥3 colorectal adenomas at age 75 or less; or a large (>1 cm diameter) or aggressive (villous and/or severely dysplastic) adenoma at age 75 or less. The 965 controls (45% males) were spouses or partners unaffected by cancer and without a personal family history (to 2nd degree relative level) of colorectal neoplasia. Known dominant polyposis syndromes, HNPCC/Lynch syndrome or bi-allelic *MYH* mutation carriers were excluded. All cases and controls were of white UK ethnic origin.

UK2 (NSCCG)[8] consisted of 2,873 CRC cases (58% male, mean age at diagnosis 59.3 years; SD±8.7) ascertained through two ongoing initiatives at the Institute of Cancer Research/Royal Marsden Hospital NHS Trust (RMHNHST) from 1999 onwards - The National Study of Colorectal Cancer Genetics (NSCCG)[29] and the Royal Marsden Hospital Trust/Institute of Cancer Research Family History and DNA Registry. The 2,871 controls (41% males; mean age 59.8 years; SD±10.8) were the spouses or unrelated friends of patients with malignancies. None had a personal history of malignancy at time of ascertainment. All cases and controls had self-reported European ancestry, and there were no obvious differences in the demography of cases and controls in terms of place of residence within the UK.

VQ58 comprised 1,800 CRC cases (1,099 males, mean age of diagnosis 62.5 years; SD±10.9) from the VICTOR[30] and QUASAR2 (www.octo-oxford.org.uk/alltrials/trials/q2.html) trials. There were 2,690 population control genotypes (1,391 males,) from the Wellcome Trust Case-Control Consortium 2 (WTCCC2) 1958 birth cohort (also known as the National Child Development Study), which included all births in England, Wales and Scotland during a single week in 1958[31].

The COIN samples were 2,183 cases derived from the COIN and COIN-B clinical trials of metastatic CRC[32]. Median age was 63 years. COIN cases were compared against genotypes from 2,501 population controls (1,237 males,) from the WTCCC2 National Blood Service (NBS) cohort (50% male; mean age at diagnosis 53.2 years, SD±15.4).

The Colon Cancer Family Registry (CCFR1) data set comprised 1,290 familial CRC cases and 1,055 controls Colon Cancer Family Registry (Colon-CFR) (http://epi.grants.cancer.gov/CFR/about_colon.html)[33]. The cases were recently diagnosed CRC cases reported to population complete cancer registries in the USA (Puget Sound, Washington State) who were recruited by the Seattle Familial Colorectal Cancer Registry; in Canada (Ontario) who were recruited by the Ontario Familial Cancer Registry; and in Australia (Melbourne, Victoria) who were recruited by the Australasian

Colorectal Cancer Family Study. Controls were population-based and for this analysis were restricted to those without a family history of colorectal cancer.

UK3 (NSCCG)[8] comprised 7,862 CRC cases (65% male; mean age at diagnosis 59 years, SD±8.2) and 4,431 controls (40% male; mean age 62 years, SD±11.5) ascertained through NSCCG post-2005[29].

UK4 (CORGI2BCD)[8] consisted of 589 CRC cases (46% male; mean age at diagnosis 58.3 years; SD±14.1) and 1,087 cancer-free population or spouse controls (45% male; mean age 45.1 years, SD±15.9).

Scotland3 (SOCCS)[8] comprised 736 CRC cases (50% male; mean age at diagnosis 53.2 years, SD±15.4) and 1,522 cancer-free population controls (47% male; mean age 51.8 years, SD±11.5). Controls comprised cancer-free participants in the Lothian Birth Cohort 1921 and Lothian Birth Cohort 1936.

Cambridge/SEARCH consisted of 2,248 CRC cases (56% male; mean age at diagnosis 59.2 years, SD±8.1) and 2,288 controls (42% males; mean age 57.6 years; SD±15.1. Samples were ascertained through the SEARCH (Studies of Epidemiology and Risk Factors in Cancer Heredity, http://www.cancerhelp.org.uk/trials/a-study-looking-at-genetic-causes-of-cancer) study based in Cambridge, UK. Recruitment started in 2000; initial patient contact was though the general practitioner. Control samples were collected post-2003. Eligible individuals were sex- and frequency-matched in five-year age bands to cases.

In Croatia, the cases (n=375) were recruited during preoperative work-up and individuals coming for a regular follow-up after the surgery for colorectal cancer, at the surgical unit of the University hospital “Sestre Milosrdnice” in Zagreb, Croatia, in the period between 2008-2010. Only individuals with adenocarcinoma were included in this study. Although all recruited cases come to Zagreb for treatment, a substantial proportion were resident elsewhere in Croatia. Controls (N=1,051) comprised individuals with no malignant disease recruited from the surgical unit of the same hospital and healthy subjects from Split, Croatia. Both Zagreb and Split represent urban centres that attract immigration from other parts of Croatia. Hence both populations are mixed and comprise diverse Croatian subpopulations. Nevertheless, we acknowledge there may be population substructure within Croatian population.

The Helsinki (FCCPS) study (http://research.med.helsinki.fi/gsb/aaltonen/) comprised 1,013 cases from a population-based collection centred on south-eastern Finland and 827 population controls from the same collection.

The Swedish study comprised 3,217 CRC patients were recruited within a Swedish national study conducted by the Swedish Low-Risk Colorectal Cancer Study Group. Samples were obtained during 2004-2009 from 14 different surgical clinics in central Sweden. All CRC patients during the study period were eligible for recruitment and were invited to participate. Only those too ill or too frail to consent were excluded. Controls (n=2,895) comprised blood donors from Stockholm and Uppsala. Fully informed consent was obtained in accordance with the Swedish law concerning ethical approval of research on human subjects (refs:2002:489,2003:198,2010:1213-31/4).

The Japanese study comprised 1,583 colorectal cancer cases and 1,898 control subjects as described previously[34]. All cases and controls were obtained from Biobank Japan. These samples were genotyped using the Illumina Human610-QuadBeadChip in cases and the Illumina HumanHap550v3 BeadChip in controls. Exclusion criteria: Samples with a call rate of <0.98, SNP quality call rates <0.95, Hardy-Weinberg $P<1.0\times10^{-7}$ in controls.

In all cases CRC was defined according to the ninth revision of the International Classification of Diseases (ICD) by codes 153–154.

2. ADDITIONAL PCA BASED ANALYSIS

Although no substantial population structure was indicated by analysis of the QQ plots, the Eigenstrat software was utilised to check for the effect of any substructure on the results for the SNPs reported in this paper. Adjusting along the lowest ten principal components and recalculating *p*-values showed minimal changes in the association statistics (shown below). It should be noted that the eigenstrat software does not facilitate proper testing of the x-chromosome and the results reported here are based on males being treated as female homozygotes.

Table of Eigenstrat adjusted p-values for implicated SNPs (10PCs)

	Inflation (λ)		**rs1321311**		**rs3824999**		**rs5934683**	
	PRE	**POST**	**PRE**	**POST**	**PRE**	**POST**	**PRE**	**POST**
LP1	1.02	1.01	$2.0x10^{-2}$	$1.8x10^{-2}$	$4.9x10^{-2}$	$7.3x10^{-2}$	$3.3x10^{-4}$	$4.9x10^{-4}$
SP1	1.01	1.00	$2.4x10^{-2}$	$1.6x10^{-2}$	$5.9x10^{-2}$	$4.4x10^{-2}$	$5.8x10^{-1}$	$5.8x10^{-1}$
LP2	1.04	1.03	$7.2x10^{-2}$	$6.6x10^{-2}$	$1.7x10^{-2}$	$1.4x10^{-2}$	$1.2x10^{-1}$	$1.2x10^{-1}$
SP2	1.03	1.04	$3.6x10^{-1}$	$3.4x10^{-1}$	$2.0x10^{-1}$	$2.2x10^{-1}$	$6.5x10^{-2}$	$8.3x10^{-2}$
VQ	1.01	1.01	$4.8x10^{-1}$	$5.2x10^{-1}$	$5.4x10^{-5}$	$9.2x10^{-5}$	$9.0x10^{-2}$	$1.1x10^{-1}$
CFR1	1.02	1.01	$1.4x10^{-1}$	$9.7x10^{-2}$	$1.9x10^{-2}$	$2.4x10^{-2}$	$5.4x10^{-2}$	$4.6x10^{-2}$