Supplementary Data for

Meta-analysis of five genome-wide association studies identifies multiple new loci associated with testicular germ cell tumor

Zhaoming Wang[1†], Katherine A. McGlynn[1], Ewa Rajpert-De Meyts[2], D. Timothy Bishop[3], Charles Chung[1], Marlene D. Dalgaard[2,4], Mark H. Greene[1], Ramneek Gupta[4], Tom Grotmol[5], Trine B. Haugen[6], Robert Karlsson[7], Kevin Litchfield[8], Nandita Mitra[9], Kasper Nielsen[4], Louise C. Pyle[10,11], Stephen M. Schwartz[12], Vesteinn Thorsson[13], Saran Vardhanabhuti[14], Fredrik Wiklund[7], Clare Turnbull[8,15], Stephen J. Chanock[1], Peter A. Kanetsky[16,18], Katherine L. Nathanson[10,17,18] for the Testicular Cancer Consortium

Supplementary Tables:

Supplementary Figures:

Supplementary Table 1. Genome-wide scans included in the meta-analysis

Center	Cases	Controls	Total	Reference	Comment
Denmark	183	363	546	Dalgaard et al. *J Med Genet* , 2012	
NCI (STEED, FTCS)	582	1,055	1,637	Schumacher et al. *Hum Mol Genet* , 2013	
Norway/Sweden	1,326	6,687	8,013	Kristiansen et al. *Hum Mol Genet* , 2015	
Penn	481	919	1,400	Kanetsky et al. *Hum Mol Genet* , 2011	The sample set used in the meta-analysis includes an additional 132 previously unpublished case subjects.
UK	986	4,946	5,932	Litchfield et al. *Nat Commun* , 2015	The sample set used in the meta-analysis includes only Stage 1 cases and controls. Stage 2 and 3 sample sets were not genotyped on a genome-wide platform.
Combined	3,558	13,970	17,528		

Supplementary Table 2. Bayes false discovery probabilities for TGCT loci

Novel susceptibility loci

CYTOBAND	SNPID	PRIOR = 0.0001
2q14.2	rs2713206	3.87E-02
3q26.2	rs3755605	4.72E-03
4q35.2	rs6837349	3.22E-02
7q36.3	rs11769858	2.68E-02
9p24.3	rs55873183	3.95E-11
10q26.13	rs61408740	7.82E-01
15q21.3	rs12912292	3.16E-05
15q22.31	rs60180747	2.55E-04
19p12	rs58521262	1.11E-06
19p12	rs34601376	1.34E-04
19p12	rs73019876	2.03E-02
Xq28	rs17336718	3.50E-01

Previously published susceptibility loci

CYTOBAND	SNPID	PRIOR = 0.1
1q22	rs2072499	1.99E-06
1q24.1	rs3790672	1.16E-10
3p24.3	rs10510452	5.79E-07
3q23	rs11705932	8.75E-02
3q25.31	rs1510272	9.24E-06
4q22.3	rs17021463	7.29E-04
4q24	rs2720460	7.39E-13
5p15.33	rs2736100	9.33E-16
5p15.33	rs4635969	1.54E-21
5q31.1	rs3805663	3.94E-03
5q31.3	rs4624820	1.01E-39
6p21.31	rs210138	1.35E-27
7p22.3	rs12699477	3.45E-07
8q13.3	rs7010162	1.02E-04
9p24.3	rs7040024	2.22E-26
9p24.3	rs755383	1.45E-34
11q14.1	rs7107174	3.96E-03
12p13.1	rs2900333	2.49E-05
12q21.32	rs3782181	3.44E-63
16p13.13	rs4561483	2.76E-04
16q12.1	rs8046148	5.78E-06
16q23.1	rs4888262	9.47E-08
16q24.2	rs55637647	1.07E-04
17q12	rs7501939	5.65E-11
17q22	rs9905704	1.02E-10
19p12	rs2195987	2.32E-06
21q22.3	rs2839186	7.50E-03

Supplementary Table 3. Summary of genomic annotation by HaploReg and RegulomeDB of variants with pairwise r^2 >= 0.4 with index TGCT SNPs

chr	pos (hg38)	pos (hg19)	LD (r^2)	LD (D')	variant	Ref	Alt	GENCODE genes	dbSNP func annot	RegulomeDB Score	Promoter histone marks	Enhancer histone marks	DNAse	Proteins bound	Motifs changed	NHGRI/EBI GWAS hits	GRASP QTL hits	Selected eQTL hits
2	121218638	121976214	0.4	0.73	rs6541770	C	T	TFCP2L1	3'-UTR	5		ESDR, MUS, GI			GR,T3R,VDR			
2	121218978	121976554	0.4	0.73	rs6541772	G	A	TFCP2L1	3'-UTR	5		ESDR, IPSC, MUS, GI			SP2,ZBTB7A		1 hit	
2	121220033	121977609	0.42	0.73	rs34764243	C	A	TFCP2L1	3'-UTR	5		ESDR, GI						
2	121221644	121979220	0.53	-0.81	rs34639030	T	TACA	TFCP2L1	3'-UTR	5		BRST, SKIN			Bcl6b,STAT			
2	121221748	121979324	0.42	0.73	rs35883727	C	T	TFCP2L1	3'-UTR	6		BRST, SKIN			HDAC2,Pou3f2			
2	121222404	121979980	0.42	0.73	rs13004931	G	A	TFCP2L1	3'-UTR	7					Foxi1,Foxj2,Foxp1,Pbx-1,Pou1f1			
2	121222829	121980405	0.57	-0.82	rs35790307	TC	T	TFCP2L1	3'-UTR	7					BCL,GATA,Pax-5,RXRA,SPIB,p300			
2	121222889	121980465	0.61	-0.82	rs4848698	C	T	TFCP2L1	3'-UTR	6					CEBPB,SP2			
2	121226155	121983731	0.41	0.72	rs12994901	C	T	TFCP2L1	intronic	3a					Ik-1,RBP-Jkappa			
2	121228183	121985759	0.41	0.72	rs34773350	C	T	TFCP2L1	intronic	5		ESDR, ESC, IPSC, BRN, LIV, GI, KID, MUS, LNG, PANC	KID,LNG		Nanog,Pax-5,Pax-6			
2	121230815	121988391	0.41	0.72	rs74902775	C	T	TFCP2L1	intronic	6					Crx,TBX5			
2	121231308	121988884	0.41	0.72	rs11694902	G	A	TFCP2L1	intronic	5					COMP1,CTCF			
2	121232081	121989657	0.41	0.72	rs35847463	G	A	TFCP2L1	intronic	6					AP-1,BCL,E2F,EBF,ELF1,ERalpha-a,ETF,Egr-1,GR,HNF4,Hic1,NRSF,Pax-5,SP1,Sin3Ak-20,TCF12,YY1,Znf143,p300			
2	121233899	121991475	0.43	0.74	rs71424379	G	A	TFCP2L1	intronic	5		ESDR, GI			AP-1,CTCF,Nanog,Pax-5,YY1,Zbtb3,p300			
2	121234391	121991967	0.44	0.75	rs11677172	C	T	TFCP2L1	intronic	5		GI			ERalpha-a,RXRA		2 hits	
2	121235882	121993458	0.46	0.77	rs76512888	T	C	TFCP2L1	intronic	4		MUS, THYM			PU.1,Rad21			
2	121237489	121995065	0.46	0.77	rs13001348	G	A	TFCP2L1	intronic	5		ESC, ESDR, THYM, BRN	HRT		BHLHE40,DBP			
2	121238062	121995638	0.45	0.77	rs11689538	G	C	TFCP2L1	intronic	4		ESC, ESDR, BRN	ESDR,IPSC,MUS,MUS	CTCF	GR		1 hit	
2	121238301	121995877	0.45	0.76	rs11678466	A	C	TFCP2L1	intronic	5		ESC, ESDR			HNF4,RXRA			
2	121239356	121996932	0.55	0.88	rs755865	G	A	TFCP2L1	intronic	6	ESDR				NRSF,Sin3Ak-20			
2	121239754	121997330	0.65	0.86	rs11692478	C	G	TFCP2L1	intronic	3a	ESDR	PLCNT		ZNF263	E2A,SEF-1,ZEB1			
2	121241322	121998898	0.62	0.9	rs6757766	C	T	TFCP2L1	intronic	7		PLCNT			SZF1-1,Spz1,ZBTB33			
2	121243169	122000745	0.59	0.89	rs6723509	T	C	TFCP2L1	intronic	4		KID, MUS, PLCNT		CTCF	Nrf1		1 hit	
2	121248854	122006430	0.77	0.92	rs2252628	G	C	TFCP2L1	intronic	5		ESC			Ets,Myc,NF-kappaB,TR4,ZBTB33			
2	121249124	122006700	0.77	0.92	rs7562700	G	C	TFCP2L1	intronic	5		ESC	IPSC		ATF3,Glis2,LXR,MOVO-B,WT1			
2	121250282	122007858	0.78	0.91	rs2713207	G	A	TFCP2L1	intronic	5					Hoxb13,Hoxd10,PLZF,p300			
2	121250365	122007941	1	1	rs2713206	C	T	TFCP2L1	intronic	6					Foxp1,Pou2f2,RREB-1,TATA			
2	121264726	122022302	0.59	0.92	rs13035310	G	C	TFCP2L1	intronic	4		PLCNT, GI		CTCF	LXR			
2	121267075	122024651	0.59	0.92	rs7590374	G	A	TFCP2L1	intronic	6		GI			CACD,Klf4,Klf7,NRSF,SP1			
3	170013239	169731027	0.49	0.78	rs12636720	T	C	15kb 3' of SEC62		5	GI	STRM, GI, PANC			ERalpha-a,MIF-1,Mxi1,RFX5,SREBP		4 hits	
3	170014294	169732082	0.49	0.78	rs56710324	T	C	16kb 3' of SEC62		6					Foxo,Foxp1,Homez,Nanog,Pax-4,Sox			1 hit
3	170014489	169732277	0.49	0.8	rs7649136	C	A	16kb 3' of SEC62		7								1 hit
3	170014865	169732653	0.4	0.84	rs12634772	G	A	16kb 3' of SEC62		7					Foxl1			2 hits
3	170015062	169732850	0.42	0.87	rs7621439	T	G	17kb 3' of SEC62		6					DMRT2,DMRT5,RXRA			1 hit
3	170015775	169733563	0.42	0.86	rs9816960	A	G	17kb 3' of SEC62		7								2 hits
3	170015950	169733738	0.48	0.8	rs7622073	A	G	18kb 3' of SEC62		6					CDP,HNF1,HNF4,Lhx3,Pbx3			1 hit
3	170015951	169733739	0.5	0.8	rs7624470	T	C	18kb 3' of SEC62		6					CDP,HNF1,HNF4,Lhx3,Pbx3			1 hit
3	170016091	169733879	0.52	0.81	rs9878976	T	C	18kb 3' of SEC62		6					Hbp1,Pou1f1			
3	170016873	169734661	0.51	0.81	rs7635200	G	A	18kb 3' of SEC62		5		BLD						1 hit
3	170017494	169735282	0.41	0.86	rs16854744	C	T	19kb 3' of SEC62		4				USF1			2 hits	2 hits
3	170017584	169735372	0.42	0.87	rs28711732	C	T	19kb 3' of SEC62		5				USF1	Irf,Klf4,Klf7,SP1,TATA			1 hit
3	170017739	169735527	0.5	0.81	rs113042206	A	G	19kb 3' of SEC62		6					Brachyury,Mxi1,Pitx2			1 hit
3	170017823	169735611	0.49	0.81	rs57203320	T	C	19kb 3' of SEC62		7					HP1-site-factor,Zbtb3			1 hit
3	170018195	169735983	0.41	0.86	rs9861620	T	C	20kb 5' of GPR160		7					BAF155,Hsf,SIX5,Znf143			2 hits

Supplementary Table 3. Summary of genomic annotation by HaploReg and RegulomeDB of variants with pairwise r^2 >= 0.4 with index TGCT SNPs

chr	pos (hg38)	pos (hg19)	LD (r^2)	LD (D')	variant	Ref	Alt	GENCODE genes	dbSNP func annot	RegulomeDB Score	Promoter histone marks	Enhancer histone marks	DNAse	Proteins bound	Motifs changed	NHGRI/EBI GWAS hits	GRASP QTL hits	Selected eQTL hits
3	170018835	169736623	0.41	0.86	rs12054277	T	C	19kb 5' of GPR160		3a		GI, LIV			EWSR1-FLI1,Esx1,Hoxa5,Irf,Msx-1,Pax7,Prrx2,RXRA			2 hits
3	170019073	169736861	0.53	0.81	rs4955703	T	C	19kb 5' of GPR160		5		GI, LIV			Sox,TCF4,Zfp105			
3	170019237	169737025	0.53	0.81	rs4955704	C	G	19kb 5' of GPR160		3a		GI, LIV	LNG,GI		Irf,Pou2f2,Rad21,SP1,STAT,UF1H3BETA,Zfp281,Znf143			1 hit
3	170020490	169738278	0.53	0.82	rs7651441	C	T	17kb 5' of GPR160		5		BLD, GI			GATA,Pax-4		1 hit	1 hit
3	170020898	169738686	0.53	0.83	rs9853647	G	A	17kb 5' of GPR160		6		BLD			FXR,Spz1			1 hit
3	170021365	169739153	0.53	0.81	rs111883874	AT	A	17kb 5' of GPR160		2b		BLD, GI	BLD	CTCF,RAD21	Arid3a,Dbx1,Dbx2,Elf3,Evi-1,HDAC2,Hlx1,Hoxa10,Irf,Mef2,NF-AT,Otx2,Pou2f2,Pou4f3,Zfp105,p300			1 hit
3	170021686	169739474	0.46	0.72	rs7631843	G	A	16kb 5' of GPR160		7		BLD, GI			GATA,p53			2 hits
3	170023202	169740990	0.73	0.92	rs9868424	G	A	15kb 5' of GPR160		5		BLD, GI, LIV	GI,GI,GI,GI,GI	P300	AhR::Arnt,Arnt,Foxo			4 hits
3	170023300	169741088	0.73	0.92	rs9813102	T	A	15kb 5' of GPR160		4		BLD, GI, LIV	GI,GI,GI,GI,PANC,GI	CEBPB,HNF4A,P300			1 hit	4 hits
3	170023462	169741250	0.46	0.93	rs9868869	G	T	14kb 5' of GPR160		3a		BLD, GI, LIV	GI,GI,GI,GI	HNF4A,P300	Eomes,TBX5		1 hit	2 hits
3	170023503	169741291	0.73	0.92	rs9868633	C	T	14kb 5' of GPR160		3a		BLD, GI, LIV	GI,GI,GI,GI		Smad		3 hits	4 hits
3	170024039	169741827	0.73	0.92	rs9814241	T	C	14kb 5' of GPR160		5		BLD, GI			CIZ,Cdx,Evi-1,Foxa,Foxp1,HDAC2,Nanog,Pax-4,TATA,p300			3 hits
3	170024067	169741855	0.48	0.94	rs9873403	C	T	14kb 5' of GPR160		5		BLD, GI			BAF155,Nr2f2,SIX5,Znf143			2 hits
3	170024137	169741925	0.48	0.94	rs9818038	T	C	14kb 5' of GPR160		7		BLD, GI			RP58			2 hits
3	170025167	169742955	0.74	0.92	rs7636306	T	C	13kb 5' of GPR160		7	BLD	BLD, LIV			E2F,ERalpha-a			3 hits
3	170025538	169743326	0.48	0.94	rs9841623	A	C	12kb 5' of GPR160		5	BLD	BLD	BLD		DMRT3,DMRT4,Egr-1,Irx			1 hit
3	170026095	169743883	0.72	0.92	rs2018802	A	G	12kb 5' of GPR160		7	BLD	BLD			Zfx			3 hits
3	170027053	169744841	0.74	0.92	rs9810602	G	C	11kb 5' of GPR160		7		BLD			HDAC2,p300			4 hits
3	170027083	169744871	0.74	0.92	rs9861501	G	A	11kb 5' of GPR160		6		BLD			DMRT2,DMRT3,Hlx1,Sox			3 hits
3	170027166	169744954	0.74	0.92	rs9861394	C	T	11kb 5' of GPR160		5		BLD			STAT			4 hits
3	170027739	169745527	0.76	0.94	rs9824474	A	G	10kb 5' of GPR160		4		BLD, LIV			GR,TATA,YY1			3 hits
3	170027833	169745621	0.5	0.96	rs66515054	T	C	10kb 5' of GPR160		4		BLD, THYM, LIV			T3R			2 hits
3	170028335	169746123	0.82	0.98	rs9829025	A	G	9.6kb 5' of GPR160		7		BLD, LIV			BATF			3 hits
3	170028973	169746761	0.52	0.97	rs58934405	T	A	9kb 5' of GPR160		7					AP-1,Mef2,Mxi1,RFX5,SREBP			1 hit
3	170029066	169746854	0.82	0.98	rs7612214	G	A	8.9kb 5' of GPR160		6					Mrg1::Hoxa9,Myb			4 hits
3	170029638	169747426	0.82	0.98	rs7635413	C	T	8.3kb 5' of GPR160		6					Foxp1,GR,Irx			4 hits
3	170029908	169747696	0.82	0.98	rs9873412	G	T	8kb 5' of GPR160		7					Pdx1,TCF4			4 hits
3	170030150	169747938	0.77	0.98	rs9839296	A	G	7.8kb 5' of GPR160		6					ELF1,Elf3,Ets,Tel2,ZBRK1,ZEB1			4 hits
3	170030167	169747955	0.51	0.97	rs73178449	G	A	7.8kb 5' of GPR160		6					AIRE,ERalpha-a,HNF4,TLX1::NFIC			1 hit
3	170030762	169748550	0.82	0.98	rs9822939	T	C	7.2kb 5' of GPR160		5		BLD	BLD		CEBPG			3 hits
3	170031011	169748799	0.8	0.97	rs9823305	T	A	6.9kb 5' of GPR160		6		BLD			Foxo,Foxp1,HDAC2,HMG-IY,Mef2,Pax-4,Pou2f2,Zfp105			4 hits
3	170031186	169748974	0.81	0.98	rs11929428	C	A	6.7kb 5' of GPR160		7		BLD			Foxp1,Pax-4,ZEB1			3 hits
3	170031236	169749024	0.82	0.98	rs6791438	A	G	6.7kb 5' of GPR160		6		BLD						3 hits
3	170031368	169749156	0.82	0.98	rs6794118	T	C	6.6kb 5' of GPR160		5		BLD	THYM		HNF1			3 hits
3	170031401	169749189	0.82	0.98	rs6778873	C	G	6.5kb 5' of GPR160		5		BLD	KID,THYM		ERalpha-a,Esr2			3 hits
3	170031433	169749221	0.82	0.98	rs6778888	C	T	6.5kb 5' of GPR160		5		BLD			Foxp1,Hoxd8			3 hits
3	170031689	169749477	0.81	0.98	rs4955706	G	C	6.2kb 5' of GPR160		5		BLD	THYM		COMP1,Evi-1,PEBP,Sox,Zfp105			3 hits
3	170032776	169750564	0.8	0.98	rs4955707	A	C	5.2kb 5' of GPR160		7		ESDR, BLD, GI						4 hits
3	170033095	169750883	0.78	0.98	rs4955708	C	T	4.8kb 5' of GPR160		6		ESC, ESDR, BLD, GI, THYM	SKIN		CIZ,Ik-2,Irf			3 hits
3	170033149	169750937	0.52	0.97	rs4955709	G	A	4.8kb 5' of GPR160		7		ESC, ESDR, BLD, GI, THYM	SKIN		Dlx2,Evi-1,GR,Hoxa4,Hoxa5,Pou2f2,Pou3f2,Sox,TATA,Zfp187,p300			1 hit
3	170033387	169751175	0.52	0.97	rs4955710	G	A	4.5kb 5' of GPR160		5	BLD	ESC, ESDR, IPSC, BLD, SKIN, GI, THYM	BLD,THYM		Maf,Pax-4,ZBTB7A,ZNF219			1 hit

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chr	pos (hg38)	pos (hg19)	LD (r^2)	LD (D')	variant	Ref	Alt	GENCODE genes	dbSNP func annot	RegulomeDB Score	Promoter histone marks	Enhancer histone marks	DNAse	Proteins bound	Motifs changed	NHGRI/EBI GWAS hits	GRASP QTL hits	Selected eQTL hits
3	170033504	169751292	0.82	0.98	rs9838308	T	C,G	4.4kb 5' of GPR160		4	BLD	ESC, ESDR, IPSC, BLD, SKIN, GI, THYM	BLD,THYM					3 hits
3	170035163	169752951	0.82	0.98	rs2160901	C	T	2.8kb 5' of GPR160		7		BLD			GATA,UF1H3BETA,Zfp410			4 hits
3	170035782	169753570	0.54	0.97	rs4955711	A	G	2.1kb 5' of GPR160		5		BLD	BLD		BCL,Irf,Nkx2,Nrf1,PU.1,Pax-5,RXRA,STAT,TATA		2 hits	1 hit
3	170038109	169755897	0.54	0.91	rs11541853	A	T	GPR160	5'-UTR	4	ESC, ESDR, LNG, IPSC, FAT, STRM, BRST, BLD, MUS, BRN, SKIN, VAS, GI, ADRL, PANC, PLCNT, THYM, HRT, OVRY, SPLN, CRVX, LIV, BONE	BLD, LIV, BRN, MUS	ESC,ESDR,ESC,IPSC,BLD,BLD,BLD,BLD,GI,GI,KID,PLCNT,GI,THYM,GI,PANC,GI,LIV	POL2,ZEB1,USF1,HAE2F1,HEY1,TAF1,ZBTB7A	BCL,BHLHE40,CTCF,E2F,Ets,Irf,Znf143			3 hits
3	170038331	169756119	1	1	rs3755605	C	T	GPR160	intronic	4	ESC, ESDR, LNG, IPSC, FAT, STRM, BRST, BLD, SKIN, VAS, LIV, BRN, GI, KID, PANC, PLCNT, HRT, OVRY, MUS, SPLN, CRVX	BRN	ESC,ESDR,ESDR,ESDR,ESC,IPSC,BRST,BLD,BLD,BLD,SKIN,ADRL,BRN,HRT,GI,KID,LNG,PLCNT,GI,THYM,GI,LIV,BRST	POL2,HAE2F1	Ik-1,NRSF,Znf143			5 hits
3	170039974	169757762	0.99	1	rs67666682	G	A	GPR160	intronic	5	ESC, BLD, GI	BLD, KID			GR			4 hits
3	170042977	169760765	0.46	0.83	rs113170134	A	G	GPR160	intronic	7					BDP1,SP1			2 hits
3	170043935	169761723	0.51	0.84	rs7648495	C	T	GPR160	intronic	5	BLD	BLD, GI, BRN			INSM1,Ik-2,Mef2,RFX5,Znf143			4 hits
3	170044789	169762577	0.51	0.84	rs3755604	A	G	GPR160	intronic	2b	BLD, GI	BLD, GI, LNG, THYM, PANC, SPLN	BLD	POL2	BDP1,GR,MZF1::1-4,NRSF,PU.1,SP1,UF1H3BETA,ZNF219,Zfp281,Znf143			4 hits
3	170045527	169763315	0.45	0.78	rs11719255	T	G	GPR160	intronic	5	GI, BLD	BLD, FAT, GI, KID, THYM, PANC			CTCF,ERalpha-a,Mtf1,Rad21,Zbtb3,Zfp281			1 hit
3	170049233	169767021	0.85	0.98	rs6788950	T	C	GPR160	intronic	5	GI	IPSC, FAT, GI, LNG, PANC, MUS, VAS	GI		Maf			7 hits
3	170050496	169768284	0.49	0.83	rs73178452	T	C	GPR160	intronic	6		FAT, GI, ADRL, LNG			CTCF,E2A,Lmo2-complex,Pax-4,TAL1,THAP1			2 hits
3	170052169	169769957	0.49	0.83	rs7634463	G	A	GPR160	intronic	7					Sp4			2 hits
3	170052799	169770587	0.85	0.98	rs6784040	T	C	GPR160	intronic	7								5 hits
3	170052857	169770645	0.85	0.98	rs6784109	T	C	GPR160	intronic	7		GI						5 hits
3	170054726	169772514	0.49	0.83	rs10433356	C	T	GPR160	intronic	7					Nrf1,Smad			2 hits
3	170054937	169772725	0.85	0.98	rs1987540	C	G	GPR160	intronic	6		ESDR, BLD			CTCFL,CTCF,RXRA,Rad21,TAL1,YY1			5 hits
3	170055177	169772965	0.49	0.83	rs4955585	C	T	GPR160	intronic	4	BLD	ESDR, BLD	BLD	NFKB	DMRT7,Mef2,Pax-4,Pou1f1			3 hits
3	170056064	169773852	0.49	0.83	rs3772177	A	G	GPR160	intronic	5	BLD				AIRE,Foxp1,HMG-IY			3 hits
3	170057461	169775249	0.85	0.98	rs2241296	T	A	GPR160	intronic	5	BLD	ESC, IPSC, BLD, GI			BCL,COMP1,Dbx1,Evi-1,Foxp1,HDAC2,Hmx,Irf,Mef2,Nanog,Ncx,Pax-5,Pou3f2,Pou5f1,Zfp105,p300			5 hits
3	170059775	169777563	0.82	0.97	rs6789982	T	C	GPR160	intronic	5	ESC, IPSC	ESC, IPSC, GI, LNG, BLD						4 hits
3	170059784	169777572	0.83	0.97	rs6787266	A	G	GPR160	intronic	5	ESC, IPSC	ESC, IPSC, GI, LNG, BLD						4 hits
3	170059850	169777638	0.49	0.82	rs6774747	C	G	GPR160	intronic	5	ESC, IPSC	ESC, IPSC, LNG, BLD			CTCF,Ets,GR,MZF1::1-4,RREB-1,Rad21,SP1,Spz1,ZNF219,Zfp281,p300			3 hits
3	170059925	169777713	0.49	0.82	rs6790119	T	A	GPR160	intronic	7	ESC, IPSC	ESC, IPSC, LNG, BLD			Foxa,Nkx2,RAR,RXRA,SIX5,STAT,TCF4			3 hits
3	170059947	169777735	0.5	0.84	rs6787395	A	G	GPR160	intronic	7	ESC, IPSC	ESC, IPSC, LNG, BLD			CEBPG,STAT			3 hits
3	170060113	169777901	0.49	0.82	rs6444892	A	G	GPR160	intronic	6		ESC, IPSC	BRN,SKIN		GR,MIF-1,NF-I			3 hits
3	170060471	169778259	0.47	0.82	rs7621777	C	T	GPR160	intronic	7		GI			Arid5b		4 hits	4 hits
3	170060675	169778463	0.47	0.82	rs7643378	G	A	GPR160	intronic	7					NF-E2			3 hits

Supplementary Table 3. Summary of genomic annotation by HaploReg and RegulomeDB of variants with pairwise r^2 >= 0.4 with index TGCT SNPs

chr	pos (hg38)	pos (hg19)	LD (r^2)	LD (D')	variant	Ref	Alt	GENCODE genes	dbSNP func annot	RegulomeDB Score	Promoter histone marks	Enhancer histone marks	DNAse	Proteins bound	Motifs changed	NHGRI/EBI GWAS hits	GRASP QTL hits	Selected eQTL hits
3	170060837	169778625	0.83	0.97	rs7635670	A	G	GPR160	intronic	6					ATF3,BHLHE40,HEY1,Myc,NF-E2,RORalpha1,SIRT6,SREBP			6 hits
3	170061262	169779050	0.47	0.82	rs58311244	G	A	GPR160	intronic	7					TCF11::MafG			3 hits
3	170061587	169779375	0.47	0.82	rs16854825	G	A	GPR160	intronic	7					Hoxa4,Sox			4 hits
3	170062018	169779806	0.46	0.83	rs202106734	C	CA	GPR160	intronic	6					HDAC2,Hltf,Hoxa13,Hoxd10,SRF,Zfp105			3 hits
3	170062020	169779808	0.46	0.83	rs138968699	AGTTTT	A	GPR160	intronic	7					HDAC2,Hltf,Hoxa13,Hoxb13,Hoxd10,SRF,Zfp105			3 hits
3	170062336	169780124	0.46	0.8	rs2270442	A	G	GPR160	intronic	5		ESC			CHD2,NRSF,Rad21,UF1H3BETA			3 hits
3	170064098	169781886	0.62	0.85	rs35627980	T	TG	GPR160	intronic	5					Egr-1,FAC1,Foxo,Glis2,Ik-1,Irf,Myc,Nanog,Pax-4,RREB-1,SP1,SRF,Sox,UF1H3BETA,WT1,ZBRK1,ZBTB7A,ZNF219,Zfp740			4 hits
3	170064099	169781887	0.43	0.83	rs2302864	T	G	GPR160	intronic	5					AP-1,Glis2,MAZR,Pax-4,RREB-1,SP1,Spz1,UF1H3BETA,WT1,ZBTB7A,ZNF219,Zfp281,Zfp740			2 hits
3	170064371	169782159	0.74	0.89	rs6764015	G	A	GPR160	intronic	5					CCNT2		1 hit	6 hits
3	170064416	169782204	0.74	0.89	rs6804193	T	C	GPR160	intronic	5		IPSC			CCNT2,PPAR,SETDB1,STAT		1 hit	6 hits
3	170065245	169783033	0.75	0.9	rs57105084	C	G	GPR160	intronic	6					Foxa,Foxk1,Irf,NF-AT			5 hits
3	170065363	169783151	0.73	0.87	rs55802818	G	A	GPR160	intronic	5					EBF,Foxa,HP1-site-factor,STAT			4 hits
3	170066202	169783990	0.72	0.86	rs12637839	A	G	GPR160	intronic	7					E2F,SP1			4 hits
3	170066828	169784616	0.74	0.9	rs6798945	C	T	GPR160	intronic	7					Arid5a,Foxl1,GATA,HNF1,HP1-site-factor,PLZF,Pou3f2			5 hits
3	170067069	169784857	0.74	0.9	rs6762959	A	C	GPR160	intronic	6					BDP1,CEBPB,CEBPD,Gfi1,Hdx			5 hits
3	170067166	169784954	0.42	0.78	rs6763055	A	T	GPR160	intronic	6					ERalpha-a,Esr2,Foxa,NRSF,RXRA			3 hits
3	170067872	169785660	0.42	0.78	rs2287481	T	C	GPR160	intronic	5					Mef2		2 hits	4 hits
3	170068923	169786711	0.42	0.78	rs2287480	T	C	GPR160	intronic	5					Bbx,STAT			4 hits
3	170070765	169788553	0.74	0.9	rs17406322	A	G	GPR160	intronic	5		ESC			Foxd3,Foxj1,GR,Myf,Sox			5 hits
3	170071528	169789316	0.41	0.78	rs66909655	G	C	GPR160	intronic	7					ATF3,Maf			3 hits
3	170071847	169789635	0.74	0.9	rs6779244	G	T	GPR160	intronic	6					Mef2,PLZF			5 hits
3	170072109	169789897	0.69	0.86	rs2160900	T	C	GPR160	intronic	7					ERalpha-a,Nanog,Nrf-2,TCF11::MafG,ZID			5 hits
3	170073273	169791061	0.41	0.78	rs9682052	G	A	GPR160	intronic	6					Homez,STAT			4 hits
3	170075524	169793312	0.41	0.78	rs56761528	G	A	GPR160	intronic	4		GI, LIV, BLD			AP-1,BAF155,CTCF,PRDM1			2 hits
3	170080963	169798751	0.4	0.77	rs2241293	T	C	GPR160	intronic	7		ESDR, LNG, HRT, GI, LIV			GR,Ik-1			2 hits
3	170081702	169799490	0.68	0.86	rs6793019	G	T	GPR160	intronic	7		HRT, GI, BONE			CDP,CIZ,HDAC2,Sox			5 hits
3	170081757	169799545	0.69	0.87	rs12487269	A	G	GPR160	intronic	7		HRT, GI, BONE			ERalpha-a,Egr-1,NRSF,VDR			5 hits
3	170082613	169800401	0.68	0.86	rs60284850	C	T	GPR160	intronic	6		HRT			HDAC2			5 hits
3	170083749	169801537	0.69	0.86	rs7638448	T	A	GPR160	intronic	6		HRT			Dbx2,En-1,Foxp1,Hoxa7,Hoxb4,Hoxc6,Hoxd8,Isl2,Lhx3,Nkx6-1,Pou2f2,Pou3f2,Pou3f4,Pou4f3,Pou6f1,Prrx1			5 hits
3	170083870	169801658	0.69	0.86	rs6444895	G	A	GPR160	intronic	7		HRT			GATA,Mef2			5 hits
3	170085443	169803231	0.69	0.86	rs5854365	GGAA	G	39bp 3' of GPR160		5					CEBPB,HDAC2,RXRA,TATA,p300			5 hits

Supplementary Table 3. Summary of genomic annotation by HaploReg and RegulomeDB of variants with pairwise r^2 >= 0.4 with index TGCT SNPs

chr	pos (hg38)	pos (hg19)	LD (r^2)	LD (D')	variant	Ref	Alt	GENCODE genes	dbSNP func annot	RegulomeDB Score	Promoter histone marks	Enhancer histone marks	DNAse	Proteins bound	Motifs changed	NHGRI/EBI GWAS hits	GRASP QTL hits	Selected eQTL hits
3	170086549	169804337	0.69	0.86	rs61672237	G	A	182bp 3' of PHC3		7								5 hits
3	170089028	169806816	0.67	0.84	rs6808369	A	G	PHC3	3'-UTR	7					Pax-5,TCF12			5 hits
3	170089836	169807624	0.69	0.86	rs6444896	C	G	PHC3	3'-UTR	7		BLD			HNF4,Znf143			5 hits
3	170090051	169807839	0.69	0.87	rs6804888	G	T	PHC3	3'-UTR	3a		BLD	SKIN,LNG,BRST,SKIN		HNF4,Nkx2		1 hit	5 hits
3	170092135	169809923	0.68	0.87	rs7644857	A	G	PHC3	3'-UTR	7					E2A,LUN-1,Pitx2,Pou3f1,STAT			5 hits
3	170095552	169813340	0.54	0.81	rs7643249	C	T	PHC3	3'-UTR	7							1 hit	5 hits
3	170098722	169816510	0.69	0.86	rs1352204	C	T	PHC3	intronic	1f		FAT, BLD			GR		5 hits	7 hits
3	170107417	169825205	0.68	0.86	rs6788549	T	C	PHC3	intronic	7					Smad3,XBP-1			5 hits
3	170109966	169827754	0.66	0.86	rs61266926	TA	T	PHC3	intronic	3a		BLD, VAS		GATA2	AP-1,Evi-1,Hoxa9,Irf,Ncx,Nkx3,PLZF,Pou3f1,SIX5,STAT			5 hits
3	170112379	169830167	0.57	0.77	rs199779545	TTA	T	PHC3	intronic	6					Cdx,Foxd3,Foxp1			5 hits
3	170112394	169830182	0.61	0.8	rs58060142	TA	T	PHC3	intronic	6					Cdx,Evi-1,Foxp1,HDAC2,TATA,Zfp105			5 hits
3	170116132	169833920	0.68	0.86	rs56403328	G	C	PHC3	intronic	7					GATA,Irf,NRSF,Pou5f1			5 hits
3	170119731	169837519	0.68	0.86	rs6444900	C	T	PHC3	intronic	6					BCL,Irf,PRDM1,PU.1,Pax-5,Pou5f1,RXRA			5 hits
3	170120212	169838000	0.68	0.86	rs7638591	A	G	PHC3	intronic	5					HNF6			5 hits
3	170127086	169844874	0.62	0.82	rs10936612	T	A	PHC3	intronic	7					ELF1,RXRA			5 hits
3	170127145	169844933	0.63	0.83	rs10936613	T	C	PHC3	intronic	7					Foxa,Foxp1,HDAC2,Mef2,Smad3			5 hits
3	170136883	169854671	0.62	0.82	rs34124911	T	C	PHC3	intronic	7		BLD			GATA,HDAC2,p300			5 hits
3	170148225	169866013	0.6	0.8	rs58771861	T	C	PHC3	intronic	7					Zbtb3			5 hits
3	170155618	169873406	0.61	0.81	rs6799087	C	A	PHC3	intronic	6		LNG, BLD, SKIN, GI, THYM			GR,SP1,Sin3Ak-20			5 hits
3	170161570	169879358	0.61	0.82	rs11921468	A	G	PHC3	intronic	5		BLD, MUS			BDP1,Ets,Irf,SP1,TATA			5 hits
3	170162296	169880084	0.61	0.82	rs10936614	T	C	PHC3	intronic	5			SKIN		Cdx2		1 hit	5 hits
3	170163562	169881350	0.61	0.82	rs11915943	C	T	PHC3	intronic	7		BLD, STRM			Foxl1,Pou2f2,Pou3f2			5 hits
3	170163766	169881554	0.61	0.82	rs36029519	C	G	PHC3	intronic	6		BLD, STRM			BDP1,Bach2,Maf			5 hits
3	170174510	169892298	0.61	0.82	rs16847919	G	A	PHC3	intronic	5		BLD, BRN, GI			AIRE,Foxp1,Irf,Mef2			5 hits
3	170175610	169893398	0.61	0.82	rs6765667	C	G	PHC3	intronic	5		ESDR, BLD, GI			CTCFL,HDAC2,Nanog,RFX5			5 hits
3	170176555	169894343	0.61	0.82	rs2901549	C	G	PHC3	intronic	5		BRST, BLD, GI			HES1,Nr2f2		1 hit	5 hits
3	170176892	169894680	0.61	0.81	rs1386333	G	A	PHC3	intronic	5		BRST, BLD, SKIN, GI			Crx,Dmbx1,Nkx2,Obox3,Obox6,Otx2,PLAG1,Pitx3		1 hit	5 hits
3	170177230	169895018	0.61	0.81	rs6444902	G	C	PHC3	intronic	5		BRST, BLD, SKIN, LIV, GI			Fox			5 hits
3	170177236	169895024	0.61	0.81	rs6444903	A	G	PHC3	intronic	5		BRST, BLD, SKIN, LIV, GI			SIX5,YY1			5 hits
3	170183694	169901482	0.61	0.82	rs56772533	C	T	1.9kb 5' of PHC3		7								5 hits
3	170184291	169902079	0.61	0.82	rs17200223	C	T	2.5kb 5' of PHC3		7					HNF1,Pax-4			5 hits
3	170184973	169902761	0.61	0.82	rs11718963	C	T	3.2kb 5' of PHC3		7		LIV			CDP			6 hits
3	170188156	169905944	0.61	0.82	rs6766729	G	A	6.4kb 5' of PHC3		7					Mrg1::Hoxa9,Pou2f2,Pou5f1			5 hits
3	170189965	169907753	0.61	0.82	rs57184265	C	T	8.2kb 5' of PHC3		3a		ESC, ESDR, LNG, BLD, SKIN, BRN, GI, LIV, BONE	ESC	PU1	Ets,NERF1a,Pbx3			5 hits
3	170190333	169908121	0.58	0.81	rs12492192	C	T	8.6kb 5' of PHC3		6					Foxj2,GR,Nkx2,Nkx3,Nkx6-1,Zfp691			4 hits
3	170190991	169908779	0.58	0.81	rs6783660	C	T	9.2kb 5' of PHC3		7					LBP-1			4 hits
3	170192077	169909865	0.58	0.81	rs12493997	G	A	10kb 5' of PHC3		6								4 hits
3	170194728	169912516	0.57	0.8	rs141949597	CA	C	13kb 5' of PHC3		7					AP-1,BCL,E2F,Evi-1,Foxj1,Foxp1,Hoxd10,Irf,Pax-2,Pou2f2,Pou3f2,STAT,ZEB1			4 hits
3	170194821	169912609	0.58	0.81	rs6797319	C	T	13kb 5' of PHC3		7					Foxq1,Gm397			4 hits
3	170194960	169912748	0.58	0.81	rs6809704	A	G	13kb 5' of PHC3		7					ATF3,Brachyury,Lmo2-complex,NF-E2,TCF12			4 hits
3	170195044	169912832	0.58	0.81	rs6797517	C	A	13kb 5' of PHC3		7					GCNF			4 hits
3	170197165	169914953	0.58	0.81	rs1798239	T	G	15kb 5' of PHC3		4		ESC, IPSC, BRST, SKIN, CRVX, LIV	SKIN,CRVX,SKIN	CJUN,FOSL2,FOSL1	Sox			4 hits

Supplementary Table 3. Summary of genomic annotation by HaploReg and RegulomeDB of variants with pairwise r^2 >= 0.4 with index TGCT SNPs

chr	pos (hg38)	pos (hg19)	LD (r^2)	LD (D')	variant	Ref	Alt	GENCODE genes	dbSNP func annot	RegulomeDB Score	Promoter histone marks	Enhancer histone marks	DNAse	Proteins bound	Motifs changed	NHGRI/EBI GWAS hits	GRASP QTL hits	Selected eQTL hits
3	170199573	169917361	0.58	0.81	rs1705581	C	T	18kb 5' of PHC3		5					Pax-4,Pou2f2,Pou5f1,Sox			5 hits
3	170201897	169919685	0.58	0.81	rs73181240	T	C	20kb 5' of PHC3		4		LIV			GR			4 hits
3	170203619	169921407	0.58	0.81	rs1684883	A	G	19kb 5' of PRKCI		5		ESC, ESDR, STRM, GI, LIV			AP-1,Foxp1		2 hits	5 hits
3	170203653	169921441	0.58	0.81	rs1798231	G	A	19kb 5' of PRKCI		5		ESC, ESDR, STRM, GI, LIV						4 hits
3	170204727	169922515	0.4	0.68	rs201603188	GTT	G	18kb 5' of PRKCI		5		GI, OVRY, LIV			DMRT5,FAC1,Fox,Foxa,Foxd3,Foxi1,Foxj1,Foxj2,Foxk1,Foxl1,Foxo,Foxp1,Foxq1,HDAC2,Irf,Nanog,Pax-4,RREB-1,Sox,Zfp105,p300			1 hit
3	170204729	169922517	0.4	0.68	rs199737139	T	TTG	18kb 5' of PRKCI		5		GI, OVRY, LIV			DMRT5,FAC1,Fox,Foxa,Foxd3,Foxf1,Foxi1,Foxj1,Foxj2,Foxk1,Foxl1,Foxo,Foxp1,Foxq1,HDAC2,Irf,Nanog,Pax-4,RREB-1,Sox,Zfp105,p300			1 hit
3	170204732	169922520	0.4	0.68	rs67768524	TG	T	18kb 5' of PRKCI		5		GI, OVRY, LIV			DMRT5,FAC1,Foxa,Foxj1,Foxk1,Foxo,Foxp1,HDAC2,Irf,Nanog,Pax-4,RREB-1,Sox			1 hit
3	170205910	169923698	0.46	0.77	rs12491746	T	C	16kb 5' of PRKCI		6		GI, BLD, LIV			Hmx,Mxi1,Rad21,Sin3Ak-20,TCF12,ZEB1			1 hit
3	170206200	169923988	0.41	0.71	rs1798234	A	G	16kb 5' of PRKCI		7		ESDR, GI, BLD, LIV			ATF3,BCL,ELF1,ETF,Egr-1,Ets,NF-E2,NRSF,Nrf1,SRF,TATA,YY1,Zfp161			1 hit
3	170206461	169924249	0.46	0.74	rs907241	A	C	16kb 5' of PRKCI		2b	GI, LIV	LIV, GI	GI,GI		AP-1,Irf,PRDM1			1 hit
3	170206594	169924382	0.44	0.77	rs907240	A	C	16kb 5' of PRKCI		2b	GI, LIV	LIV, GI	GI,GI,GI,LIV	HEY1,HNF4A	Brachyury,Mtf1,Myb			1 hit
3	170210203	169927991	0.42	0.73	rs3928356	T	C	12kb 5' of PRKCI		6					BCL,CACD,Myc,NRSF,Pax-5,Rad21,YY1,p300			1 hit
3	170212080	169929868	0.44	0.72	rs1705585	A	G	10kb 5' of PRKCI		5				KAP1				1 hit
3	170212161	169929949	0.46	0.77	rs1798235	T	C	10kb 5' of PRKCI		5					E2A,HIF1::Arnt,Myc,Pax-5			1 hit
3	170212674	169930462	0.49	0.77	rs34710333	T	C	9.7kb 5' of PRKCI		5					Pou3f1			1 hit
3	170213932	169931720	0.42	0.73	rs59678208	G	A	8.4kb 5' of PRKCI		7					ATF3,CHD2,HNF4,PEBP			1 hit
3	170214308	169932096	0.43	0.75	rs67895649	T	G	8.1kb 5' of PRKCI		7					Mtf1,Smad3			1 hit
3	170214955	169932743	0.43	0.75	rs1705601	A	T	7.4kb 5' of PRKCI		6					FAC1,Foxf2,Foxj1,Foxo,Hoxc10			1 hit
3	170215127	169932915	0.47	0.75	rs1705602	A	G	7.2kb 5' of PRKCI		7					Arid5b,Evi-1,Foxp1,GATA			1 hit
3	170215346	169933134	0.43	0.75	rs1705603	C	T	7kb 5' of PRKCI		7					AP-1,Elf5,HMG-IY,Ik-1,Ik-2,Pou2f2,p300			1 hit
3	170217576	169935364	0.47	0.75	rs28857583	G	A	4.8kb 5' of PRKCI		7								1 hit
3	170217713	169935501	0.43	0.75	rs10049400	A	G	4.7kb 5' of PRKCI		7								1 hit
3	170217830	169935618	0.43	0.75	rs28812297	C	G	4.5kb 5' of PRKCI		7					LBP-1			1 hit
3	170218756	169936544	0.47	0.75	rs1705579	G	T	3.6kb 5' of PRKCI		5					HDAC2			1 hit
3	170219204	169936992	0.47	0.75	rs1082978	A	T	3.2kb 5' of PRKCI		7								2 hits
3	170220597	169938385	0.47	0.75	rs1082977	C	T	1.8kb 5' of PRKCI		7					GR			1 hit
3	170221102	169938890	0.48	0.75	rs1082976	G	A	1.3kb 5' of PRKCI		4			ESDR,LNG,BLD,BLD,SKIN,SKIN,SKIN,CRVX,BLD,SKIN,LNG	JUND	Hoxa13,Hoxc10,Mef2			2 hits
3	170221724	169939512	0.47	0.75	rs1082975	T	C	640bp 5' of PRKCI		4			ESC,SKIN,BLD		Myc,Pax-6,Pou5f1,p300			2 hits

Supplementary Table 3. Summary of genomic annotation by HaploReg and RegulomeDB of variants with pairwise r^2 >= 0.4 with index TGCT SNPs

chr	pos (hg38)	pos (hg19)	LD (r^2)	LD (D')	variant	Ref	Alt	GENCODE genes	dbSNP func annot	RegulomeDB Score	Promoter histone marks	Enhancer histone marks	DNAse	Proteins bound	Motifs changed	NHGRI/EBI GWAS hits	GRASP QTL hits	Selected eQTL hits
3	170222257	169940045	0.44	0.75	rs481781	T	C	107bp 5' of PRKCI		4	ESC, ESDR, LNG, IPSC, FAT, STRM, BRST, BLD, MUS, BRN, SKIN, VAS, LIV, GI, ADRL, HRT, KID, PANC, PLCNT, THYM, OVRY, SPLN, CRVX, BONE		ESC,ESDR,ESDR,ESDR,ESDR,ESC,LNG,IPSC,BRST,BLD,BLD,BLD,BLD,BLD,BLD,BLD,SKIN,SKIN,SKIN,SKIN,ADRL,BRN,BRN,HRT,GI,GI,KID,LNG,MUS,MUS,PLCNT,GI,THYM,GI,OVRY,PANC,MUS,GI,LNG,BLD,CRVX,LIV,BRST,MUS,MUS,VAS,BLD,BLD,BRN,SKIN,SKIN,LNG	FOXA1,ELF1,P300,PAX5N19,SIX5,SP1,NFKB,TCF4,BAF170,BRCA1,CEBPB,IRF3,JUND,STAT1,SREBP1,IRF1,POL2B,HAE2F1,GATA1,USF1,GATA3,KAP1			2 hits	2 hits
3	170223916	169941704	0.42	0.71	rs3842653	CT	C	PRKCI	intronic	6	ESC, ESDR, LNG, IPSC, STRM, BRST, SKIN, GI, BLD, CRVX	ESDR, FAT, BLD, STRM, MUS, BRN, HRT, PANC, GI, LNG, LIV			Dbx1,HDAC2,Hoxa10,Hoxd10,Irf,Sox,TATA,Zfp105			
3	170226157	169943945	0.47	0.75	rs998295	C	A	PRKCI	intronic	7		ESC, LNG, IPSC, STRM, BRST, SKIN, GI, CRVX			LXR			2 hits
3	170226312	169944100	0.47	0.75	rs546950	C	T	PRKCI	intronic	6		ESC, LNG, IPSC, FAT, STRM, BRST, SKIN, GI, CRVX, LIV, MUS, BRN, BONE			E2A,Lmo2-complex,Mtf1,Myf,ZEB1		1 hit	2 hits
3	170226356	169944144	0.43	0.75	rs579909	T	C	PRKCI	intronic	7		ESC, LNG, IPSC, FAT, STRM, BRST, SKIN, GI, CRVX, LIV, MUS, BRN, BONE						1 hit
4	187996404	188917558	0.72	0.94	rs6553123	G	A	ZFP42	intronic	5	ESC, ESDR, IPSC, SKIN, PLCNT	MUS			BCL,ERalpha-a,GR,HNF4,RXRA			
4	187996471	188917625	0.65	0.97	rs6851368	C	G	ZFP42	intronic	4	ESC, ESDR, IPSC, SKIN, PLCNT	MUS			LXR,SRF			
4	187997000	188918154	0.69	0.97	rs150847996	15-mer	A	ZFP42	intronic	4	ESC, ESDR, IPSC, SKIN, PLCNT, HRT	MUS, PLCNT	ESC,ESDR,ESC,IPSC,PLCNT	POL2,POL24H8,TAF1				
4	187997028	188918182	0.58	0.96	rs200342587	8-mer	A	ZFP42	intronic	4	ESC, ESDR, IPSC, SKIN, PLCNT, HRT	MUS, PLCNT	ESC,ESDR,ESC,IPSC,PLCNT	POL2,POL24H8,TAF1	Ets,NF-E2,NRSF,TCF12,YY1,ZBRK1			
4	187997035	188918189	0.71	0.96	rs73874769	G	A	ZFP42	intronic	4	ESC, ESDR, IPSC, SKIN, PLCNT, HRT	MUS, PLCNT	ESC,ESDR,ESC,IPSC,PLCNT	POL2,POL24H8,TAF1				
4	187999232	188920386	0.98	0.99	rs10031545	G	C	ZFP42		5			ESDR		AP-1,AhR,EBF,RREB-1			
4	188000201	188921355	1	1	rs6837349	G	T	ZFP42	intronic	5		ESC, ESDR, IPSC						
4	188000286	188921440	0.98	0.99	rs4862848	A	G	ZFP42	intronic	7		ESC, ESDR, IPSC			Ets,Hoxa5,NRSF			
4	188004295	188925449	0.42	0.87	rs6553124	T	A	ZFP42		5					DMRT2,Foxj1,Foxk1,Foxo,Foxp1,Homez,Mef2,Sox,Zfp105			
4	188004661	188925815	0.42	0.86	rs7665254	G	A	ZFP42	3'-UTR	7					E2A,ZEB1			
4	188006668	188927822	0.42	0.87	rs1388935	C	T	1.6kb 3' of ZFP42		4	ESDR	LNG		POL2,POL24H8				
4	188007130	188928284	0.4	0.87	rs10708435	TA	T	2.1kb 3' of ZFP42		6					Evi-1,GR			
4	188007454	188928608	0.47	0.79	rs6854509	G	A	2.4kb 3' of ZFP42		7					GR,NRSF,TATA,YY1			
4	188007658	188928812	0.47	0.8	rs6854867	G	A	2.6kb 3' of ZFP42		6								
7	158638215	158430907	0.42	0.73	rs877279	C	T	NCAPG2	intronic	1f		LIV	ESDR,LIV	CEBPB,FOXA1			4 hits	6 hits
7	158641040	158433732	0.4	0.7	rs4909245	T	C	NCAPG2	intronic	7					Hmbox1,Pou4f3			6 hits
7	158641259	158433951	0.4	0.7	rs6942491	A	G	NCAPG2	intronic	6					DMRT4,FAC1,Foxa,Foxp1,HDAC2,Sox,THAP1			6 hits
7	158642955	158435647	0.4	0.7	rs4909246	A	C	NCAPG2	intronic	6					AP-1,Dbx1,Foxo,Foxp1,HDAC2,HMG-IY,HNF1,Hoxa10,Irf,Mef2,Zfp105,p300			5 hits
7	158645494	158438186	0.4	0.7	rs2290393	G	A	NCAPG2	intronic	7					Mrg			6 hits
7	158647014	158439706	0.4	0.7	rs73165308	C	G	NCAPG2	intronic	4				FOXA1,P300,TCF4	Ets			6 hits
7	158647291	158439983	0.4	0.7	rs35348911	G	C	NCAPG2	intronic	4		LNG, GI, LIV	ESC,ESC,LNG,LIV	CTCF,RAD21,TCF4,EGR1,SMC3,CMYC	EBF			6 hits
7	158647583	158440275	0.4	0.7	rs3793177	T	C	NCAPG2	intronic	1f		SKIN, GI, LIV	ESC,BLD		E2A,ZEB1		4 hits	6 hits

Supplementary Table 3. Summary of genomic annotation by HaploReg and RegulomeDB of variants with pairwise r^2 >= 0.4 with index TGCT SNPs

chr	pos (hg38)	pos (hg19)	LD (r^2)	LD (D')	variant	Ref	Alt	GENCODE genes	dbSNP func annot	RegulomeDB Score	Promoter histone marks	Enhancer histone marks	DNAse	Proteins bound	Motifs changed	NHGRI/EBI GWAS hits	GRASP QTL hits	Selected eQTL hits
7	158648181	158440873	0.4	0.7	rs10282403	A	G	NCAPG2	intronic	6					Cdx,DMRT1,DMRT3,DMRT5,DMRT7,Dbx1,Evi-1,Foxa,Foxo,Foxp1,HNF1,Hoxd10,Mef2,Pou2f2,RFX5,Zfp105			6 hits
7	158649102	158441794	0.4	0.7	rs56654636	A	G	NCAPG2	intronic	2a	FAT, MUS, LIV, GI, BRN, SKIN, LNG, BONE	LNG, STRM, BRST, SKIN, GI, ADRL, PANC, PLCNT, CRVX, LIV, VAS	ESDR,SKIN,SKIN,GI,GI,MUS,LIV,MUS,MUS,BRN,SKIN,SKIN,LNG	FOXA1	Cdx2,Mrg1::Hoxa9			6 hits
7	158651319	158444011	0.4	0.7	rs35267207	A	G	NCAPG2	intronic	5		FAT, STRM, MUS, SKIN, BRN, LNG, BONE	SKIN,SKIN,MUS,MUS,BRN,SKIN					6 hits
7	158652788	158445480	0.4	0.7	rs28454061	T	C	NCAPG2	intronic	7		FAT						6 hits
7	158657693	158450385	0.43	-0.77	rs12670222	G	T	NCAPG2	intronic	5		ESDR, IPSC, BLD	ESDR		YY1			10 hits
7	158657877	158450569	0.42	0.73	rs60680627	A	T	NCAPG2	intronic	7		ESDR, IPSC			BATF,E2A,Irf,Myc,Myf			8 hits
7	158658273	158450965	0.47	0.77	rs12533939	A	T	NCAPG2	intronic	5		ESDR, ESC, IPSC			Arid3a,Evi-1,HNF1,Hbp1,Ncx,Pou1f1,Pou3f4,Pou4f3,Zfp187			8 hits
7	158659690	158452382	0.47	0.77	rs10949737	G	A	NCAPG2	intronic	6					CDP,Cart1,Dbx1,Foxp1,Hoxa10,Hoxd10,Mef2,Ncx,Pou2f2,Sox,Zfp105			8 hits
7	158660488	158453180	0.46	0.77	rs4909248	C	T	NCAPG2	intronic	7					RXRA			8 hits
7	158660573	158453265	0.46	0.77	rs4909249	A	G	NCAPG2	intronic	7		BLD			HNF4			8 hits
7	158660604	158453296	0.47	0.77	rs4909251	C	T	NCAPG2	intronic	7		BLD			STAT			8 hits
7	158660715	158453407	0.47	0.76	rs4909252	T	C	NCAPG2	intronic	6					AP-1,CEBPB,E2F,Hoxa5,Hoxb3,Irf,Lhx8,NF-Y,Nkx1-1,Pbx3,Pou6f1,RFX5,SP1,SP2			7 hits
7	158660896	158453588	0.44	-0.78	rs10233307	T	C	NCAPG2	intronic	7					Myb			6 hits
7	158661304	158453996	0.43	-0.77	rs13243036	C	T	NCAPG2	intronic	6					E2F,Gfi1,Gfi1b,Mef2,Osf2,TATA			6 hits
7	158661329	158454021	0.47	0.76	rs1377499	A	G	NCAPG2	intronic	6					Pou1f1,Pou2f2,TEF-1			6 hits
7	158663701	158456393	0.47	0.77	rs10949738	C	T	NCAPG2	intronic	5			SKIN		PLZF			8 hits
7	158664403	158457095	0.48	0.78	rs2290392	G	C	NCAPG2	intronic	6		LNG			Hdx,Mef2,Pax-5,STAT,TATA,TCF12			7 hits
7	158664766	158457458	0.44	-0.75	rs3816466	A	G	NCAPG2	intronic	5					HIF1,Pou3f3			6 hits
7	158665476	158458168	0.48	0.78	rs12537562	G	A	NCAPG2	intronic	5					AP-2,CAC-binding-protein,RREB-1,TATA			8 hits
7	158665888	158458580	0.49	0.78	rs35598457	G	A	NCAPG2	intronic	5					AP-2,EBF,Sin3Ak-20,TR4,Zic			8 hits
7	158666204	158458896	0.48	0.78	rs34171903	T	C	NCAPG2	intronic	5		THYM	VAS		Bach1,Pax-4			7 hits
7	158666355	158459047	0.44	-0.77	rs4909091	C	A	NCAPG2	intronic	4		MUS, THYM		GATA1	BHLHE40,CTCF,Rad21			7 hits
7	158666766	158459458	0.44	-0.77	rs3793178	A	T	NCAPG2	intronic	2b					Cdx,Dbx1,Foxa,Foxd3,Foxf1,Foxf2,Foxi1,Foxj1,Foxj2,Foxk1,Foxl1,Foxo,Foxp1,HDAC2,HMG-IY,Mef2,Ncx,Pou3f2,Pou3f4,TATA,Zfp105			5 hits
7	158669270	158461962	0.69	0.93	rs6961537	C	A	NCAPG2	intronic	7					EBF,Mef2,Pou1f1,Pou2f2,Pou5f1,Sox			8 hits
7	158670720	158463412	0.68	-0.95	rs6966396	G	A	NCAPG2	intronic	7								7 hits
7	158671292	158463984	0.68	-0.95	rs2290391	G	C	NCAPG2	intronic	7					Sox			7 hits
7	158672563	158465255	0.56	0.93	rs6976925	G	A	NCAPG2	intronic	7		ESDR			ZID			7 hits
7	158672795	158465487	0.69	0.93	rs6977288	G	A	NCAPG2	intronic	6		ESDR, LNG, IPSC, MUS, ADRL, BONE			AP-2,ELF1,RREB-1,SMC3			8 hits
7	158673236	158465928	0.68	-0.95	rs11767214	G	A	NCAPG2	intronic	4		ESDR, LNG, IPSC, FAT, BLD, MUS, SKIN, ADRL, BRN, BONE	ESDR,LNG,BLD,SKIN,SKIN,SKIN,LNG,MUS,BRN,SKIN,LNG		BDP1,ELF1,HDAC2,Irf,MAZ,Myc,PLAG1,PU.1,STAT,TATA,p300			4 hits
7	158673740	158466432	0.68	0.93	rs4909254	T	C	NCAPG2	intronic	5		ESDR, IPSC, MUS, SKIN, LNG, VAS			AP-4,CTCF,GATA,Myc,Nrf1,Rad21			8 hits
7	158675745	158468437	0.68	-0.95	rs1530967	G	A	NCAPG2	intronic	1f		MUS, SKIN, BONE	SKIN		SIX5,Znf143		4 hits	7 hits

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chr	pos (hg38)	pos (hg19)	LD (r^2)	LD (D')	variant	Ref	Alt	GENCODE genes	dbSNP func annot	RegulomeDB Score	Promoter histone marks	Enhancer histone marks	DNAse	Proteins bound	Motifs changed	NHGRI/EBI GWAS hits	GRASP QTL hits	Selected eQTL hits
7	158675870	158468562	0.69	0.93	rs12535671	T	C	NCAPG2	intronic	5		MUS, SKIN, BONE			BHLHE40,TFE			8 hits
7	158676504	158469196	0.68	-0.95	rs55669347	G	A	NCAPG2	intronic	3a		FAT, STRM, MUS, SKIN, BONE	BLD,SKIN		CDP,Dbx1,Dbx2,HNF1,Hdx,Homez,Lhx3,Pax-4,Pax-6,Pou2f2,Pou3f4,Pou4f3			6 hits
7	158677602	158470294	0.68	0.95	rs34525750	A	C	NCAPG2	intronic	6		SKIN			AP-3,Foxp1,GR,Pou1f1,Sox,TATA			8 hits
7	158678978	158471670	0.68	-0.95	rs2123658	C	T	NCAPG2	intronic	6					E2A,HEN1,Myf,Pax-4,ZEB1			5 hits
7	158680213	158472905	0.68	-0.95	rs2305469	T	C	NCAPG2	intronic	6		BLD, STRM			En-1,Hmx,XBP-1			7 hits
7	158680354	158473046	0.69	0.93	rs4909257	C	T	NCAPG2	intronic	5		STRM, BLD	BLD					8 hits
7	158681028	158473720	0.69	0.93	rs4909258	G	A	NCAPG2	intronic	1f		STRM, MUS, SKIN, LNG, BONE	MUS		Irf		3 hits	8 hits
7	158683579	158476271	0.68	-0.95	rs6956496	T	C	NCAPG2	intronic	4		LNG, FAT, STRM, MUS, SKIN, ADRL, VAS, BRN, BONE	BLD,ADRL,MUS					6 hits
7	158683645	158476337	0.68	0.93	rs35328933	TA	T	NCAPG2	intronic	4		LNG, FAT, STRM, MUS, SKIN, ADRL, VAS, BRN, BONE	SKIN,ADRL	RAD21	AP-3,SF1			8 hits
7	158683946	158476638	0.69	0.93	rs7803635	C	A	NCAPG2	intronic	6		ESDR, LNG, FAT, STRM, MUS, SKIN, HRT, PLCNT, VAS, BRN, BONE	SKIN		Zfx			8 hits
7	158684334	158477026	0.69	0.95	rs4909260	T	A	NCAPG2	intronic	5		LNG, FAT, STRM, MUS, SKIN, PLCNT, BRN, BONE	MUS		TATA			8 hits
7	158685719	158478411	0.69	0.93	rs7800022	T	C	NCAPG2	intronic	5		LNG, FAT, STRM, MUS, SKIN, BONE	BLD,ADRL		Cphx,Duxl,Pax-5,Pbx-1			8 hits
7	158687582	158480274	0.67	-0.94	rs41271193	T	C	NCAPG2	intronic	5				POL24H8,POL2	GR			5 hits
7	158689248	158481940	0.68	0.94	rs3793182	T	A	NCAPG2	intronic	5					Dbx1,Foxp1,GR,Hoxa13,Hoxb4,Hoxc9,Hoxd8,Isl2,Ncx,Nkx6-1,Pou2f2,Pou3f4,Pou4f3,Pou6f1,Sox,Zfp105			8 hits
7	158693907	158486599	0.69	0.95	rs61634093	A	G	NCAPG2	intronic	5		BLD	PLCNT		Hdx,Znf143			9 hits
7	158694230	158486922	0.68	-0.95	rs10225435	A	G	NCAPG2	intronic	6					Foxp1,Gfi1,HMG-IY,HNF6,Hdx,Tgif1			5 hits
7	158694507	158487199	0.68	-0.95	rs12666144	A	G	NCAPG2	intronic	4	BLD	BLD		POL2,POL24H8	p53			6 hits
7	158694661	158487353	0.68	-0.95	rs12668173	G	A	NCAPG2	intronic	5	BLD	BLD	BLD,BLD		Cdx,Cdx2,FXR,Hoxa10,Hoxa9,Hoxb9,Hoxc10,Hoxc9,Hoxd10,Mrg1::Hoxa9,RXRA,Tgif1			7 hits
7	158695562	158488254	0.69	0.94	rs59551278	T	A	NCAPG2	intronic	5		IPSC, BLD, SKIN	BLD		BCL,EWSR1-FLI1,Irf,NF-kappaB,Nkx2,PU.1,Pax-5,STAT			8 hits
7	158696072	158488764	0.7	0.95	rs11761779	A	G	NCAPG2	intronic	4		IPSC, FAT, BLD, STRM, SKIN, BRN, ADRL, GI, PANC, LNG	BLD,BLD,BLD,BLD,SKIN,LNG,VAS	CTCF	Nr2e3,Zec			8 hits
7	158696348	158489040	0.7	0.94	rs13242357	G	A	NCAPG2	intronic	1b	FAT, STRM, BLD, SKIN, GI, BONE	LNG, IPSC, FAT, BLD, MUS, SKIN, BRN, GI, ADRL, PANC, VAS	ESDR,ESDR,LNG,IPSC,BRST,BLD,BLD,BLD,BLD,BLD,BLD,BLD,SKIN,SKIN,SKIN,SKIN,ADRL,BRN,HRT,GI,GI,KID,LNG,MUS,MUS,PLCNT,GI,THYM,GI,OVRY,PANC,MUS,GI,LNG,BLD,CRVX,MUS,MUS,VAS,BLD,BLD,BRN,SKIN,LNG	CTCF,ELF1,PU1,SMC3,RAD21,POL24H8			4 hits	8 hits
7	158697744	158490435	0.55	-0.94	rs10215605	G	A	NCAPG2	intronic	7								7 hits
7	158698358	158491049	0.68	-0.95	rs10215422	G	T	NCAPG2	intronic	5			SKIN,SKIN,SKIN		FXR,GR			7 hits
7	158700983	158493674	0.69	0.94	rs12539199	C	G	NCAPG2	intronic	1d		ESC, ESDR, IPSC, LIV, BLD	LNG	POL24H8,POL2B	PPAR,PU.1,RXRA,SP1,SZF1-1		3 hits	8 hits
7	158701255	158493946	0.68	-0.95	rs1979195	A	G	NCAPG2	intronic	5		ESC, ESDR, IPSC, CRVX, LIV, BLD		POL2B	GR			5 hits

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chr	pos (hg38)	pos (hg19)	LD (r^2)	LD (D')	variant	Ref	Alt	GENCODE genes	dbSNP func annot	RegulomeDB Score	Promoter histone marks	Enhancer histone marks	DNAse	Proteins bound	Motifs changed	NHGRI/EBI GWAS hits	GRASP QTL hits	Selected eQTL hits
7	158704586	158497277	0.7	0.96	rs748949	C	T	NCAPG2	intronic	3a	ESC, ESDR, LNG, IPSC, FAT, STRM, BRST, BLD, MUS, BRN, SKIN, VAS, LIV, GI, ADRL, HRT, KID, PANC, PLCNT, THYM, OVRY, SPLN, CRVX, BONE		ESDR,ESDR,ESDR,ESC,IPSC,IPSC,BRST,BLD,BLD,BLD,BLD,BLD,SKIN,ADRL,KID,LNG,MUS,PLCNT,GI,THYM,GI,MUS,BLD,LIV,VAS,BLD,BRN	CTCF,POL2,POL24H8,POL2S2,CTCFL,HEY1,ZBTB7A	Ahr::Arnt::HIF1,HIF1,NRSF			8 hits
7	158707794	158500485	0.71	0.95	rs13238542	C	T	3kb 5' of NCAPG2		4	ESC, LIV	BLD	ESDR,ESDR,LNG,BLD,SKIN,SKIN,LNG,BLD,LIV,MUS,MUS,BLD,BRN,SKIN,LNG	ELF1,HEY1,POL2,NFYA,NFYB,PU1,USF1,KAP1,SETDB1	Nkx2,Rad21,Znf143			9 hits
7	158708801	158501492	1	1	rs11769858	T	C	4kb 5' of NCAPG2		6					GATA,LUN-1,Pitx2,SETDB1			5 hits
7	158709934	158502625	0.88	0.96	rs13225986	C	T	5.1kb 5' of NCAPG2		6	BLD	BLD, SKIN, MUS	PLCNT		EBF			5 hits
7	158710658	158503349	0.82	0.96	rs6974036	A	C	5.8kb 5' of NCAPG2		3a	STRM, BLD, BONE	ESDR, LNG, FAT, BLD, STRM, SKIN, MUS, CRVX, LIV, BRST, BRN	ESDR,BLD,BLD,BLD,SKIN,SKIN,MUS,MUS,MUS,BLD,BLD,BRN,LNG	PU1	BRCA1,Pax-4			8 hits
7	158711796	158504487	0.69	0.83	rs6960207	C	G	7kb 5' of NCAPG2		6		BLD			CTCF,HEN1,Maf,Nr2f2,RFX5,Rad21,T3R			9 hits
7	158712265	158504956	0.64	0.88	rs12533594	C	G	7.4kb 5' of NCAPG2		5	SKIN, BLD	BLD, PLCNT	BLD,BLD		GR			15 hits
7	158712276	158504967	0.64	0.88	rs12536788	T	C	7.4kb 5' of NCAPG2		5	SKIN, BLD	BLD, PLCNT	BLD,BLD		GR,Pbx3			15 hits
7	158712297	158504988	0.64	0.88	rs12538618	G	A	7.5kb 5' of NCAPG2		5	SKIN, BLD	BLD, PLCNT	BLD,BLD,PANC,BLD		Gfi1,Pou3f1			15 hits
7	158712671	158505362	0.49	0.96	rs142552473	C	T	7.8kb 5' of NCAPG2		6	BLD	BLD, PLCNT	BLD		CEBPD,GATA,Gfi1,Zbtb3			5 hits
7	158712694	158505385	0.52	0.89	rs111924232	T	C	7.9kb 5' of NCAPG2		6	BLD	BLD, PLCNT	BLD		BDP1,Irf,PU.1,SP1,ZBRK1			11 hits
7	158712729	158505420	0.57	0.88	rs112081908	T	C	7.9kb 5' of NCAPG2		6		BLD, PLCNT			LUN-1			9 hits
7	158712754	158505445	0.62	0.88	rs113666472	G	A	7.9kb 5' of NCAPG2		6		BLD, PLCNT			BCL,CTCF,Ets,INSM1,SMC3,ZBTB7A,Znf143,p300			13 hits
7	158712906	158505597	0.62	0.88	rs9801356	T	C	8.1kb 5' of NCAPG2		7		BLD, PLCNT	PLCNT		AP-1,HEY1,SP2,Sin3Ak-20			15 hits
7	158712976	158505667	0.62	0.88	rs111523321	G	13-mer	8.1kb 5' of NCAPG2		5		BLD, PLCNT	PLCNT		ERalpha-a,Esr2,GR,Myc,NRSF,Nanog,Pou2f2,RXRA,WT1,ZBTB33			12 hits
7	158713334	158506025	0.48	0.85	rs4909098	T	G	8.5kb 5' of NCAPG2		6		BLD			Mtf1,Zbtb3			15 hits
7	158713889	158506580	0.51	0.76	rs6459896	G	A	9.1kb 5' of NCAPG2		6					Mef2,TATA		2 hits	10 hits
7	158714242	158506933	0.51	0.85	rs7790167	A	T	9.4kb 5' of NCAPG2		7					Foxj1,HNF1,Hoxb8,Ncx,PRDM1			15 hits
7	158714263	158506954	0.51	0.85	rs7790283	A	T	9.4kb 5' of NCAPG2		6					CDP,Pdx1,Pou2f2			15 hits
7	158714400	158507091	0.46	0.86	rs13234425	T	C	9.6kb 5' of NCAPG2		7					SZF1-1,Spz1,ZBTB33			13 hits
7	158714870	158507561	0.51	0.76	rs10949740	G	A	10kb 5' of NCAPG2		7					OTX			14 hits
7	158714916	158507607	0.51	0.76	rs13235002	T	A	10kb 5' of NCAPG2		6		BLD			Evi-1,HDAC2			14 hits
7	158715049	158507740	0.47	0.68	rs11981184	T	C	10kb 5' of NCAPG2		7		BLD						10 hits
7	158715381	158508072	0.51	0.76	rs13221375	C	T	11kb 5' of NCAPG2		7		BLD			Pax-4,RFX5			15 hits
7	158715516	158508207	0.51	0.76	rs7799553	T	C	11kb 5' of NCAPG2		5		BLD			AP-1,Maf,NRSF			15 hits
7	158715550	158508241	0.48	0.84	rs13238369	T	G	11kb 5' of NCAPG2		5		BLD			Ik-1,Pax-6			14 hits
7	158715553	158508244	0.47	0.84	rs13247757	G	A	11kb 5' of NCAPG2		5		BLD			Ik-1			14 hits
7	158716363	158509054	0.52	0.85	rs34329117	C	A	12kb 5' of NCAPG2		5		BLD			AIRE,Foxj2,Foxl1,Foxp1,Mef2			16 hits
7	158716946	158509637	0.51	0.76	rs13224920	G	A	12kb 5' of NCAPG2		3a		BLD		PU1,ZNF263	Foxa,Foxd1,Foxi1,Foxk1,Foxl1,Foxo,Foxp1,Homez,Irf,Pax-4,Pou2f2,RREB-1,Zfp105,p300			15 hits
7	158717015	158509706	0.51	0.76	rs13225825	C	G	12kb 5' of NCAPG2		4		BLD	BLD,BLD,LNG	PU1,ZNF263	AP-1,GCM,Gfi1			15 hits
7	158717570	158510261	0.43	0.66	rs115918902	C	T	13kb 5' of NCAPG2		5					CCNT2,EWSR1-FLI1,Irf,Myf,PU.1,SP1,Sp4,TATA,TFII-I,ZNF263,Zfp281			7 hits
7	158718616	158511307	0.5	0.84	rs201487556	ATAAG	A	12kb 3' of ESYT2		5					Foxd1,GATA,HNF1,Sox			19 hits
7	158718740	158511431	0.5	0.84	rs11770112	C	T	12kb 3' of ESYT2		5					AP-1,BCL,Hoxa7			16 hits
7	158718937	158511628	0.5	0.83	rs10949741	C	T	12kb 3' of ESYT2		4					E2F			15 hits
7	158719250	158511941	0.49	0.74	rs12538001	T	C	12kb 3' of ESYT2		5					AhR::Arnt,Arnt,E2A,HEN1,Lmo2-complex,ZEB1			16 hits

Supplementary Table 3. Summary of genomic annotation by HaploReg and RegulomeDB of variants with pairwise r^2 >= 0.4 with index TGCT SNPs

chr	pos (hg38)	pos (hg19)	LD (r^2)	LD (D')	variant	Ref	Alt	GENCODE genes	dbSNP func annot	RegulomeDB Score	Promoter histone marks	Enhancer histone marks	DNAse	Proteins bound	Motifs changed	NHGRI/EBI GWAS hits	GRASP QTL hits	Selected eQTL hits
7	158719297	158511988	0.49	0.83	rs12539877	G	A	12kb 3' of ESYT2		5								19 hits
7	158719628	158512319	0.41	0.69	rs10266859	T	C	11kb 3' of ESYT2		3a				CEBPB	AP-1,Foxa,Pou1f1,Pou2f2,Pou3f2,Pou5f1			5 hits
7	158719664	158512355	0.44	0.82	rs34524453	AG	A	11kb 3' of ESYT2		4			PLCNT	CEBPB	EWSR1-FLI1,NERF1a,Pax-5			15 hits
7	158719831	158512522	0.43	0.67	rs12698276	A	G	11kb 3' of ESYT2		6		PLCNT	IPSC		BCL,TCF4			14 hits
7	158720203	158512894	0.42	0.78	rs2053993	G	C	11kb 3' of ESYT2		4		BLD			Cdx2,Pax-4			17 hits
7	158720205	158512896	0.42	0.78	rs2053992	C	A	11kb 3' of ESYT2		4		BLD			Cdx2,Hsf,Pax-4,SP1,Znf143			17 hits
9	870410	870410	0.96	1	rs55670979	A	G	DMRT1	intronic	5					FAC1,Foxo,Foxp1,IRC900814,Mef2,Pax-4,SIX5,Sox,Zfp105			
9	878563	878563	1	1	rs55873183	A	G	DMRT1	intronic	4		ESDR, ADRL, HRT, GI	IPSC,OVRY		BCL,KAP1,NRSF,SETDB1,Smad3			
10	124572567	126261136	0.57	1	rs182574087	G	T	LHPP	intronic	7					CTCF,Ets,RXRA,Rad21,SMC3,SP1			
10	124586043	126274612	1	1	rs61408740	C	G	LHPP	intronic	6		BLD, LIV			GLI,Ik-1,RXRA,Zic			
10	124827532	126516101	0.5	0.89	rs117674072	A	G	FAM175B	intronic	4			BLD		HNF1			
15	55640419	55932617	0.4	-0.65	rs4561398	T	C	PRTG	intronic	7		GI			GATA,GZF1,SIX5,Znf143			3 hits
15	55640791	55932989	0.4	0.66	rs1659296	C	G	PRTG	intronic	6					DEC,Nkx2			3 hits
15	55645164	55937362	0.41	0.65	rs8027131	G	A	PRTG	intronic	7					BCL,CHD2,E2F,Egr-1,Ets,HEY1,Mtf1,NRSF,Nrf1,SRF,Sin3Ak-20,YY1,Zfp161			3 hits
15	55645374	55937572	0.4	0.64	rs111622136	C	G	PRTG	intronic	7								3 hits
15	55654534	55946732	0.48	0.89	rs9920546	C	T	PRTG	intronic	4		ESDR, STRM, SKIN, LNG	SKIN,VAS		BCL,HDAC2,Hoxa10,Irf,Mef2,Pax-5,Pou5f1,RXRA,p300			1 hit
15	55659234	55951432	0.46	0.89	rs12438177	A	G	PRTG	intronic	6		ESDR, ESC, IPSC, ADRL	ADRL		Pou6f1,RORalpha1			2 hits
15	55666219	55958417	0.4	0.79	rs12903822	T	C	PRTG	intronic	5		ESDR	IPSC					1 hit
15	55671646	55963844	0.54	0.77	rs4412917	G	A	PRTG	intronic	7					HES1,SP1			2 hits
15	55680940	55973138	0.69	0.9	rs34303822	T	G	RP11-420M1.2	intronic	6		BLD			PRDM1,STAT			2 hits
15	55682756	55974954	0.7	0.91	rs12899647	T	C	PRTG	intronic	5								2 hits
15	55691589	55983787	0.78	0.9	rs11855737	A	G	PRTG	intronic	7					NF-E2,NRSF			2 hits
15	55692067	55984265	0.57	0.93	rs11852746	T	C	PRTG	intronic	6					Cdx,Evi-1,GR,HDAC2,p300		2 hits	2 hits
15	55692241	55984439	0.8	0.93	rs12899976	A	C	PRTG	intronic	6			BLD		HNF4,Nkx2,Nkx3			3 hits
15	55692407	55984605	0.58	0.94	rs687128	A	C	PRTG	intronic	7					AP-4,NF-E2,TR4			2 hits
15	55695300	55987498	0.81	0.94	rs1011061	A	G	PRTG	intronic	5				MAFK	PLZF			2 hits
15	55697741	55989939	0.8	0.92	rs10851590	C	T	PRTG	intronic	7					Zfx			3 hits
15	55704898	55997096	0.4	0.93	rs9672390	A	T	PRTG	intronic	7		ESDR	BLD		Foxl1,HNF6,RXRA			1 hit
15	55705346	55997544	0.81	0.93	rs3985768	A	T	PRTG	intronic	5		ESDR, IPSC, ESC			Bcl6b,STAT			2 hits
15	55706050	55998248	0.78	0.88	rs12908813	C	T	PRTG	intronic	7		ESDR			Ets,Gfi1,Mef2,NF-kappaB			3 hits
15	55706098	55998296	0.4	0.93	rs11857467	C	G	PRTG	intronic	7		ESDR			CTCF,ERalpha-a,RXRA			1 hit
15	55706397	55998595	0.41	0.94	rs11858195	A	C	PRTG	intronic	6		ESDR, ESC, SKIN, KID	IPSC		Pou3f1			1 hit
15	55708272	56000470	0.59	0.95	rs4774802	T	C	PRTG	intronic	6		ESDR, SKIN, CRVX	ESDR,THYM,CRVX		AP-1,EWSR1-FLI1,Foxa,Foxc1,Foxj1,Foxj2,Foxk1,Foxo,Foxp1,Irf,Nkx2,PU.1,TATA,TCF12			2 hits
15	55709218	56001416	0.41	0.94	rs200765984	T	TTTAG	PRTG	intronic	6					AFP1,Cdx2,Foxq1,HMG-IY,HNF1,Hlxb9,Hmbox1,Hoxa9,Hoxb7,Hoxc6,Irf,Lhx3,Pou3f1			1 hit
15	55709388	56001586	0.57	0.86	rs4598842	T	G	PRTG	intronic	6					TATA			2 hits
15	55709576	56001774	0.4	0.94	rs7162371	C	T	PRTG	intronic	6			BRST		Cdx,Irx,Pou1f1,Pou2f2,Pou3f3			1 hit
15	55710821	56003019	0.58	0.94	rs12907892	T	C	PRTG	intronic	5		ESDR, FAT, STRM, BONE	THYM		GATA,HDAC2,Irf,Nanog,TAL1,TCF4			2 hits
15	55711507	56003705	0.41	0.96	rs10851591	A	G	PRTG	intronic	7			LNG		Pax-6			1 hit

Supplementary Table 3. Summary of genomic annotation by HaploReg and RegulomeDB of variants with pairwise r^2 >= 0.4 with index TGCT SNPs

chr	pos (hg38)	pos (hg19)	LD (r^2)	LD (D')	variant	Ref	Alt	GENCODE genes	dbSNP func annot	RegulomeDB Score	Promoter histone marks	Enhancer histone marks	DNAse	Proteins bound	Motifs changed	NHGRI/EBI GWAS hits	GRASP QTL hits	Selected eQTL hits
15	55714389	56006587	0.81	0.94	rs12439011	C	T	PRTG	intronic	6		ESDR, ESC			BDP1,CACD,Egr-1,GR,Klf7,MOVO-B,NRSF,Pou2f2,RREB-1,Rad21,SP1,Spz1,WT1,ZNF219,Zfp281,Zfp740			2 hits
15	55714806	56007004	0.41	0.96	rs2008336	C	T	PRTG	intronic	6		ESDR, ESC, IPSC, SKIN			Foxa,Foxd1,Foxj1,Foxj2,Foxk1,Foxl1			1 hit
15	55717756	56009954	0.79	0.93	rs12908232	A	G	PRTG	intronic	7		ESDR			Pou3f2			3 hits
15	55720508	56012706	0.4	0.93	rs4774803	T	A	PRTG	intronic	7		IPSC	PANC		DMRT7,HNF1,Irf,Nrf-2			1 hit
15	55721723	56013921	0.41	0.95	rs8034414	C	T	PRTG	intronic	5	IPSC	ESC, IPSC	ESC,IPSC,IPSC		Gfi1,TCF12,Znf143			1 hit
15	55722407	56014605	0.82	0.95	rs137878193	7-mer	A	PRTG	intronic	6		ESC, IPSC			Foxp1,HNF1,HP1-site-factor,Mrg1::Hoxa9,Nrf1,Pbx3			
15	55722538	56014736	0.83	0.95	rs55874929	T	C	PRTG	intronic	7		ESC, IPSC			ZBTB7A			2 hits
15	55723569	56015767	0.59	0.95	rs12903239	T	C	PRTG	intronic	5		ESDR, ESC			Brachyury			2 hits
15	55724548	56016746	0.83	0.95	rs12442165	T	C	PRTG	intronic	7					BDP1,Nr2f2			2 hits
15	55727455	56019653	0.83	0.95	rs8028880	T	C	PRTG	intronic	6					Cdx,HDAC2,TATA,p300			3 hits
15	55728117	56020315	0.81	0.92	rs12915423	C	T	PRTG	intronic	6					Myc,NRSF,PLAG1,Sp4,Zfx			3 hits
15	55728523	56020721	0.81	0.91	rs200938361	C	CA	PRTG	intronic	7					CIZ,HMG-IY,Pou2f2			3 hits
15	55728808	56021006	0.59	0.95	rs12901963	T	C	PRTG	intronic	7		GI						2 hits
15	55730730	56022928	0.58	0.95	rs12912118	G	T	PRTG	intronic	6	GI				BDP1,CTCF,Ets,Irf,NF-I SP1 TATA			
15	55733214	56025412	0.83	0.95	rs11071203	T	C	PRTG	intronic	6					Mef2,Msx-1			3 hits
15	55735815	56028013	0.59	0.95	rs11630141	G	T	PRTG	intronic	4	ESDR	ESDR, ESC, IPSC, BLD, KID			CTCF,Eomes,Evi-1,HNF4,RORalpha1			2 hits
15	55736364	56028562	0.83	0.95	rs11853533	C	T	PRTG	intronic	6	ESDR	ESDR, ESC, BLD, SKIN, KID, PLCNT			DMRT2,DMRT4			2 hits
15	55737147	56029345	0.83	0.95	rs11857271	T	C	PRTG	intronic	6	ESDR	ESDR, ESC, BLD, SKIN, KID, PLCNT, CRVX, VAS	ESDR		CEBPB,Mef2,Pou1f1,TATA			2 hits
15	55737180	56029378	0.83	0.95	rs12907772	T	C	PRTG	intronic	6	ESDR	ESDR, ESC, BLD, SKIN, KID, PLCNT, CRVX, VAS	ESDR,ESDR		GR,HNF1			2 hits
15	55738345	56030543	0.88	0.98	rs12906885	G	A	PRTG	intronic	5	ESDR	ESDR, ESC, SKIN, GI, CRVX, VAS	ESDR,ESDR		Foxj1,Foxk1,Foxl1,Foxo,Mef2,Pou1f1,Pou4f3,TATA,Zfp105			2 hits
15	55738558	56030756	0.88	0.98	rs4774222	T	C	PRTG	intronic	4	ESDR	ESC, IPSC, SKIN, KID, GI, CRVX, VAS	ESDR	ZNF263	CTCF,Eomes			2 hits
15	55738828	56031026	0.84	-0.98	rs11071204	A	G	PRTG	intronic	3a	ESDR	ESDR, ESC, SKIN, GI, MUS, VAS	ESC,PLCNT	ZNF263	EWSR1-FLI1			3 hits
15	55739042	56031240	0.89	0.98	rs11857254	C	T	PRTG	intronic	5	ESDR	ESDR, SKIN, PLCNT, VAS			Ets			2 hits
15	55739473	56031671	0.64	0.99	rs6493814	G	A	PRTG	intronic	5	ESDR, ESC, IPSC	ESDR, KID, PLCNT, GI, LIV, VAS	ESDR,ESDR		Gfi1			2 hits
15	55739901	56032099	0.64	0.99	rs12442771	A	G	PRTG	intronic	5	ESDR, ESC, IPSC	ESDR, IPSC, KID, PLCNT, LIV	ESDR,ESDR,ESDR		CTCF,Hoxd10,Nkx6-1,PPAR,Rad21			2 hits
15	55740321	56032519	0.9	0.99	rs10152116	G	A	PRTG	intronic	5					Arid3a,Dbx1,Evi-1,Foxa,Foxp1,Hdx,Mef2,Ncx,PLZF,Pou2f2,Pou4f3,Pou6f1,TATA			2 hits
15	55740777	56032975	0.64	0.99	rs7182733	G	A	PRTG	intronic	5	ESDR, ESC, IPSC, GI, KID	ESDR, ESC, BLD, BRN, ADRL, LNG, GI, CRVX, LIV			Nrf1,Pax-4,Spz1			2 hits
15	55741649	56033847	0.9	0.99	rs12438394	G	A	PRTG	intronic	5	ESDR, ESC, FAT, STRM, BRST, BLD, BRN, SKIN, VAS, GI, ADRL, KID, LNG, PLCNT, OVRY, MUS, HRT, THYM, CRVX, LIV, BONE	LNG, IPSC, BRST, BLD, LIV, GI, HRT	ESC,ESDR,ESDR,ESDR,ESC,HRT,GI,LNG,MUS,MUS,GI,VAS		ELF1,ERalpha-a,Ets,PLAG1,PPAR,RREB-1,UF1H3BETA			2 hits

Supplementary Table 3. Summary of genomic annotation by HaploReg and RegulomeDB of variants with pairwise r^2 >= 0.4 with index TGCT SNPs

chr	pos (hg38)	pos (hg19)	LD (r^2)	LD (D')	variant	Ref	Alt	GENCODE genes	dbSNP func annot	RegulomeDB Score	Promoter histone marks	Enhancer histone marks	DNAse	Proteins bound	Motifs changed	NHGRI/EBI GWAS hits	GRASP QTL hits	Selected eQTL hits
15	55741909	56034107	0.9	0.99	rs12905693	T	C	PRTG	intronic	3a	ESC, ESDR, IPSC, STRM, BRST, BLD, BRN, SKIN, FAT, VAS, GI, ADRL, KID, PANC, LNG, PLCNT, HRT, OVRY, MUS, CRVX, LIV	LNG, IPSC, BRST, BLD, SKIN, LIV, GI, HRT, PANC, SPLN	ESC,ESDR,ESDR,ESC,IPSC,IPSC,BLD,BLD,BLD,SKIN,HRT,GI,KID,LNG,MUS,PLCNT,GI,THYM,LIV,VAS		AP-2rep,STAT,Zbtb3			2 hits
15	55742680	56034878	0.89	0.98	rs11632579	G	A	PRTG	intronic	4	ESC, ESDR, LNG, IPSC, FAT, STRM, BRST, BLD, MUS, BRN, SKIN, VAS, LIV, GI, ADRL, KID, PANC, PLCNT, THYM, HRT, OVRY, SPLN, CRVX, BONE	BLD	ESDR,ESDR,ESC,LNG,BLD,BLD,SKIN,SKIN,SKIN,ADRL,HRT,KID,LNG,MUS,MUS,PLCNT,GI,THYM,LIV,MUS,BLD,BRN	E2F1,HAE2F1	Smad3			2 hits
15	55742812	56035010	0.9	0.99	rs12910180	G	A	PRTG	intronic	4	ESC, ESDR, LNG, IPSC, FAT, STRM, BRST, BLD, MUS, BRN, SKIN, VAS, LIV, GI, ADRL, KID, PANC, PLCNT, THYM, HRT, OVRY, SPLN, CRVX, BONE	BLD	ESC,ESDR,ESDR,ESDR,ESC,LNG,IPSC,BRST,BLD,BLD,SKIN,SKIN,SKIN,SKIN,ADRL,BRN,BRN,HRT,GI,GI,KID,LNG,MUS,MUS,PLCNT,GI,THYM,OVRY,LNG,LIV,MUS,VAS,BLD,BRN,SKIN,LNG	CTCF,E2F1,HAE2F1	Irf,KAP1,TATA			2 hits
15	55743123	56035321	0.85	0.97	rs11632762	G	A	32bp 5' of PRTG		4	ESC, ESDR, LNG, IPSC, FAT, STRM, BRST, BLD, MUS, BRN, SKIN, VAS, LIV, GI, ADRL, KID, PANC, PLCNT, THYM, HRT, OVRY, SPLN, CRVX, BONE	BLD, GI	ESC,ESDR,ESDR,ESDR,ESDR,ESC,LNG,IPSC,BRST,SKIN,SKIN,SKIN,ADRL,BRN,HRT,KID,LNG,MUS,MUS,PLCNT,GI,THYM,OVRY,PANC,MUS,LNG,LIV,MUS,MUS,VAS,BLD,BRN,SKIN,LNG	POL2,NRSF,TAF1,BRCA1,CHD2,HEY1,TBP,ZBTB33,EGR1,RAD21,YY1	SP1			2 hits
15	55743484	56035682	0.9	0.99	rs11639086	T	A	393bp 5' of PRTG		4	ESC, ESDR, LNG, IPSC, FAT, STRM, BRST, BLD, MUS, BRN, SKIN, VAS, LIV, GI, ADRL, KID, PANC, PLCNT, THYM, HRT, OVRY, CRVX, BONE	BLD, BRN	ESDR,ESDR,ESDR,ESDR,ESC,IPSC,ADRL,BRN,HRT,KID,LNG,MUS,MUS,PLCNT,GI,OVRY,LIV,MUS,BRN	POL2	E2F			2 hits
15	55743537	56035735	0.9	0.99	rs12914863	A	G	446bp 5' of PRTG		2b	ESC, ESDR, LNG, IPSC, FAT, STRM, BRST, BLD, MUS, BRN, SKIN, VAS, LIV, GI, ADRL, KID, PANC, PLCNT, THYM, HRT, OVRY, CRVX, BONE	BLD, BRN	ESC,ESDR,ESDR,ESDR,ESDR,ESC,IPSC,SKIN,ADRL,BRN,HRT,KID,LNG,MUS,MUS,PLCNT,GI,OVRY,MUS,LIV,MUS,LNG	POL2	COMP1,HNF4,PRDM1			2 hits
15	55743569	56035767	0.87	0.97	rs12915092	C	A	478bp 5' of PRTG		2b	ESC, ESDR, LNG, IPSC, FAT, STRM, BRST, BLD, MUS, BRN, SKIN, VAS, LIV, GI, ADRL, KID, PANC, PLCNT, THYM, HRT, OVRY, CRVX, BONE	BLD, BRN	ESC,ESDR,ESDR,ESDR,ESDR,ESC,SKIN,ADRL,BRN,BRN,HRT,KID,LNG,MUS,MUS,PLCNT,GI,OVRY,MUS,LIV,MUS,LNG		AP-1,ATF3,Egr-1,Irf,Klf4,Klf7,MOVO-B,Myc,NRSF,Nrf1,PLAG1,RREB-1,SP1,SRF,Sp4,TATA,YY1			2 hits
15	55743870	56036068	0.9	0.99	rs12440103	A	G	779bp 5' of PRTG		5	ESC, ESDR, LNG, IPSC, FAT, STRM, BRST, BLD, MUS, BRN, SKIN, GI, ADRL, KID, OVRY, LIV, VAS	ESDR, BLD, HRT, PLCNT	ESDR,ESDR,ESDR,ESC,IPSC,SKIN,BRN,KID,LNG,MUS,MUS,PLCNT,GI		Gm397,TCF12,Zfp691			2 hits
15	55744616	56036814	0.9	0.99	rs66519039	A	G	1.5kb 5' of PRTG		5		ESDR, KID			Hoxa5,Pou6f1			2 hits
15	55746219	56038417	0.91	1	rs12907557	C	T	3.1kb 5' of PRTG		7		ADRL			CDP,Maf			2 hits
15	55746357	56038555	0.9	1	rs12911682	A	G	3.3kb 5' of PRTG		6		ADRL			CHD2,E2F,Egr-1,Ets,LBP-1,Mtf1,NRSF,Nrf1,SRF,Sin3Ak-20,Zfp161,Zfx			2 hits
15	55746427	56038625	0.84	1	rs67342368	CACCA	C	3.3kb 5' of PRTG		7		ADRL			CDP,Sin3Ak-20			2 hits
15	55746433	56038631	0.84	1	rs199561921	G	GA	3.3kb 5' of PRTG		7		ADRL			AP-1,Irf,SIX5,Sin3Ak-20			2 hits
15	55746509	56038707	1	1	rs12912292	G	A	3.4kb 5' of PRTG		6		ADRL			LUN-1			2 hits

Supplementary Table 3. Summary of genomic annotation by HaploReg and RegulomeDB of variants with pairwise r^2 >= 0.4 with index TGCT SNPs

chr	pos (hg38)	pos (hg19)	LD (r^2)	LD (D')	variant	Ref	Alt	GENCODE genes	dbSNP func annot	RegulomeDB Score	Promoter histone marks	Enhancer histone marks	DNAse	Proteins bound	Motifs changed	NHGRI/EBI GWAS hits	GRASP QTL hits	Selected eQTL hits
15	55747059	56039257	0.9	1	rs10152830	C	G	4kb 5' of PRTG		7					ERalpha-a,RXRA			2 hits
15	55755348	56047546	0.71	0.86	rs8036481	G	C	5.7kb 3' of AC009997.1		3a				FOXA1	AP-1			3 hits
15	55757827	56050025	0.65	0.82	rs12915888	T	C	3.2kb 3' of AC009997.1		6					Foxa,Foxd3,Foxp1,HDAC2,Hoxa4,Pax-4,Zfp105			3 hits
15	55758484	56050682	0.65	0.81	rs12900119	A	T	2.5kb 3' of AC009997.1		5		SKIN			Cdx,Foxp1,HDAC2,Pax-4,Pou2f2,TATA,Zfp105			3 hits
15	55761277	56053475	0.66	0.82	rs12916744	G	A	174bp 5' of AC009997.1		6								3 hits
15	55767363	56059561	0.59	-0.78	rs5812815	TATA	T	6.3kb 3' of AC009997.1		6					Cdx2,Hoxa10,Hoxa9,Hoxb13,Hoxb9,Hoxd10			4 hits
15	55771455	56063653	0.59	0.79	rs12438264	A	G	10kb 5' of AC009997.1		7		SKIN			BDP1			3 hits
15	66295243	66587581	0.78	0.94	rs80126717	G	A	DIS3L	intronic	4	ESC, ESDR, IPSC, FAT, STRM, BLD, MUS, SKIN, BRN, GI, KID, LNG, THYM, CRVX, LIV, BRST, VAS, BONE	ESC, ESDR, LNG, IPSC, BRST, BLD, BRN, SKIN, FAT, LIV, GI, ADRL, HRT, PANC, MUS, PLCNT, THYM	ESDR,IPSC,BLD,BLD	GATA2				10 hits
15	66301130	66593468	0.77	0.93	rs76095247	A	C	DIS3L	intronic	6					Evi-1,Foxa,Foxj2,Foxp1,Mef2,Pax-4,Pou3f1			12 hits
15	66307755	66600093	0.72	0.95	rs200782531	G	GAA	DIS3L	intronic	6		BRN			AP-1,MAZ,NRSF,PU.1,Rad21,STAT			8 hits
15	66307758	66600096	0.74	0.95	rs11639144	G	A	DIS3L	intronic	6		BRN			Rad21,STAT,ZEB1			8 hits
15	66307759	66600097	0.72	0.95	rs11639073	C	A	DIS3L	intronic	6		BRN			EBF,HDAC2,Rad21,STAT			8 hits
15	66308079	66600417	0.77	0.95	rs11639266	G	A	DIS3L	intronic	7		BRN			Maf,Myc,NF-E2,NRSF,ZNF263,p300			9 hits
15	66316393	66608731	0.92	0.98	rs11631625	A	G	DIS3L	intronic	5			LNG		BCL,MOVO-B,PU.1,Pax-4			5 hits
15	66317853	66610191	0.76	0.98	rs200140256	AAAAAG	A	DIS3L	intronic	6					Evi-1,FAC1,Foxd3,Foxk1,Foxo,Foxp1,Homez,Irf,Sox,Zfp105,p300			10 hits
15	66317854	66610192	0.76	0.98	rs200207760	AAAAG	A	DIS3L	intronic	6					Evi-1,FAC1,Foxd3,Foxk1,Foxo,Foxp1,Homez,Irf,Sox,Zfp105,p300			9 hits
15	66319741	66612079	0.93	0.98	rs35510028	C	G	DIS3L	intronic	7					Irf,NF-AT,RBP-Jkappa,YY1			7 hits
15	66320627	66612965	0.93	0.98	rs17851970	T	C	DIS3L	synonymous	5								7 hits
15	66321658	66613996	0.82	0.98	rs111712020	C	T	DIS3L	intronic	6					BDP1,LUN-1			6 hits
15	66330099	66622437	0.68	0.95	rs113238971	G	A	DIS3L	intronic	7		BLD	IPSC					10 hits
15	66333810	66626148	0.82	0.98	rs71827453	CAG	C	DIS3L	3'-UTR	5					CEBPG,DMRT5,GR,Hlxb9,Hoxa5,Hoxb3,Hoxb7,Pax-8,Vax2			8 hits
15	66336536	66628874	0.79	0.98	rs11637949	A	G	TIPIN		7					Pax-5			6 hits
15	66338231	66630569	0.51	-0.93	rs8042593	G	A	TIPIN	intronic	7								6 hits
15	66344180	66636518	0.82	0.98	rs2414902	C	T	TIPIN	intronic	7								9 hits
15	66345659	66637997	0.91	0.97	rs11633335	C	T	TIPIN	intronic	7					ERalpha-a			8 hits
15	66361108	66653446	0.95	0.98	rs112981358	G	A	TIPIN		7					EBF,NRSF,Pax-5,RFX5			8 hits
15	66362519	66654857	0.95	0.99	rs11632444	G	A	TIPIN		7		ESDR, BRST, BLD, SKIN, PLCNT			BDP1,GCNF,Nr2f2			8 hits
15	66370282	66662620	0.98	1	rs59718328	A	T	TIPIN		2b	FAT, STRM, BRST, BLD, MUS, SKIN, LIV, BRN, GI, ADRL, KID, PANC, LNG, PLCNT, HRT, THYM, VAS, BONE	ESC, ESDR, IPSC, BRST, BLD, BRN, SKIN, GI, THYM, CRVX	ESC,ESDR,ESC,IPSC,IPSC,BRST,BLD,BLD,BLD,BLD,BLD,BLD,SKIN,SKIN,SKIN,GI,KID,LNG,MUS,MUS,PLCNT,THYM,PANC,MUS,GI,LNG,BLD,CRVX,MUS,MUS,VAS,BLD,BLD,SKIN,LNG	BATF,MAX,POL2,POL24H8,CEBPB,JUND,CJUN,E2F6,TAF1	Egr-1,Elf3,Ets,FEV,LBP-1,Nrf-2,PU.1,Pax-5,STAT,Tel2			8 hits
15	66370923	66663261	1	1	rs60180747	A	C	TIPIN		5	BLD	BLD, MUS, THYM, LNG, LIV, VAS			NRSF			5 hits
15	66371763	66664101	0.98	1	rs113872287	C	T	TIPIN		7		BLD, LIV			ELF1,Maf,Myc,NRSF,Rad21,SETDB1			7 hits

Supplementary Table 3. Summary of genomic annotation by HaploReg and RegulomeDB of variants with pairwise r^2 >= 0.4 with index TGCT SNPs

chr	pos (hg38)	pos (hg19)	LD (r^2)	LD (D')	variant	Ref	Alt	GENCODE genes	dbSNP func annot	RegulomeDB Score	Promoter histone marks	Enhancer histone marks	DNAse	Proteins bound	Motifs changed	NHGRI/EBI GWAS hits	GRASP QTL hits	Selected eQTL hits
15	66385835	66678173	0.85	0.99	rs111584879	T	C	TIPIN		7	GI, BLD	ESDR, FAT, BRST, BLD, STRM, BRN, GI, HRT, MUS, PANC, CRVX, LIV	KID		AhR,Zbtb3			9 hits
15	66387263	66679601	0.85	0.99	rs112542693	G	C	MAP2K1	5'-UTR	4	ESC, ESDR, LNG, IPSC, FAT, STRM, BRST, BLD, MUS, BRN, SKIN, VAS, LIV, GI, ADRL, KID, PANC, PLCNT, THYM, HRT, OVRY, SPLN, CRVX, BONE		ESC,ESDR,ESDR,IPSC,BRST,BLD,BLD,BLD,BLD,BLD,BLD,BLD,SKIN,SKIN,SKIN,SKIN,BRN,BRN,HRT,GI,KID,LNG,MUS,MUS,PLCNT,GI,THYM,OVRY,MUS,GI,LNG,BLD,LIV,BRST,MUS,BLD,BRN,LNG		BCL,BHLHE40,ELF1,HEY1,HNF4,NRSF,Nanog,Pou2f2,SMC3,Sin3Ak-20,YY1			9 hits
15	66389064	66681402	0.97	0.99	rs112089092	G	T	MAP2K1	intronic	5	ESDR, BRST, BLD, STRM	ESDR, ESC, FAT, BRST, BLD, MUS, BRN, SKIN, GI, THYM, LNG, HRT, CRVX, LIV, VAS			Ets,LUN-1,TCF12,p53			8 hits
15	66394432	66686770	0.91	0.99	rs16953563	G	A	MAP2K1	intronic	5		BRST, BLD, GI	SKIN		STAT			2 hits
15	66396888	66689226	0.89	0.98	rs111500258	T	C	MAP2K1	intronic	7		BLD			GCM,GR,NRSF			4 hits
15	66396964	66689302	0.88	0.97	rs113513894	C	T	MAP2K1	intronic	7		BLD						4 hits
15	66397773	66690111	0.89	0.98	rs79065844	T	G	MAP2K1	intronic	5		BLD, VAS			MZF1::1-4			4 hits
15	66409162	66701500	0.87	0.97	rs74397736	G	A	MAP2K1	intronic	5	BLD	ESC, ESDR, IPSC, FAT, BLD, BRN, GI, ADRL, HRT, LNG, MUS, THYM, PANC, LIV	SKIN,HRT,MUS,BLD,BLD		Cdc5,Dobox4,Evi-1,GATA,Zfp410			4 hits
15	66410007	66702345	0.74	0.95	rs56913458	C	A	MAP2K1	intronic	4	BLD	ESC, ESDR, IPSC, BLD, BRN, SKIN, FAT, LIV, ADRL, HRT, MUS, THYM	HRT,BLD		Foxj2			5 hits
15	66412705	66705043	0.86	0.97	rs80326387	G	A	MAP2K1	intronic	7		BLD, FAT, LIV			GATA,Lmo2-complex,RREB-1			4 hits
15	66416601	66708939	0.87	0.97	rs77515996	C	A	MAP2K1	intronic	5	BLD	ESC, ESDR, IPSC, BLD, FAT, BRN, GI, HRT, MUS, THYM, LIV	MUS		GR,Pou2f2,RFX5			4 hits
15	66419981	66712319	0.87	0.97	rs34356923	AC	A	MAP2K1	intronic	6		BLD			E2A,Ik-1,NRSF,Pitx2,TBX5,ZEB1			4 hits
15	66422405	66714743	0.78	0.92	rs11635184	A	G	MAP2K1	intronic	5		BLD	BRN		Pou1f1,Pou2f2			4 hits
15	66423768	66716106	0.7	0.93	rs112747606	C	T	MAP2K1	intronic	6					Ets,Mef2,TCF12,p53			4 hits
15	66435972	66728310	0.69	0.92	rs78136741	A	G	MAP2K1	intronic	6					GATA,Irf,SETDB1,TATA			4 hits
15	66436613	66728951	0.77	0.91	rs11637556	A	C	MAP2K1	intronic	7								5 hits
15	66437589	66729927	0.76	0.91	rs11636809	T	C	MAP2K1	intronic	7		MUS			BDP1			4 hits
15	66437969	66730307	0.69	0.92	rs17200912	C	T	MAP2K1	intronic	7			BRN					5 hits
15	66438362	66730700	0.74	0.89	rs11632885	C	T	MAP2K1	intronic	5					Crx,Pitx2			4 hits
15	66438707	66731045	0.69	0.92	rs17200970	A	C	MAP2K1	intronic	5					Mtf1			5 hits
15	66446031	66738369	0.77	0.91	rs111458651	C	T	MAP2K1	intronic	5					BCL,NRSF,YY1,Zic			4 hits
15	66449049	66741387	0.69	0.92	rs11629783	C	G	MAP2K1	intronic	7					Foxj2,Pax-4,RREB-1			5 hits
15	66452799	66745137	0.77	0.91	rs11630608	T	C	MAP2K1	intronic	6		BRN, LIV, ADRL, BLD			CEBPB,Dbx1,Hlx1,Hoxa13,Mef2,Pou6f1,Sox,TATA			5 hits
15	66457115	66749453	0.76	0.91	rs149682516	TTTA	T	MAP2K1	intronic	6					CDP,Cart1,Cdx,Cdx2,Dbx1,Dbx2,Foxa,Foxo,Foxp1,HDAC2,Hlx1,Hoxa10,Hoxd8,Mef2,Ncx,Pou2f2,Pou3f2,Sox,TATA,Zfp105			3 hits
15	66457732	66750070	0.67	0.9	rs112064988	C	T	MAP2K1	intronic	7					Egr-1			5 hits
15	66460830	66753168	0.77	0.91	rs79809053	G	C	MAP2K1	intronic	6	SKIN, BRST	ESDR, BRST, BLD, SKIN, GI, CRVX, VAS			AP-1,CEBPB,HNF4,Myc,PPAR,p300			4 hits
15	66463585	66755923	0.77	0.89	rs111572611	C	T	MAP2K1	intronic	7		ESC, ESDR, IPSC			HNF4,Nkx2,RXRA			5 hits
15	66464674	66757012	0.69	0.92	rs112156518	C	T	MAP2K1	intronic	7		BLD			E2F,Myc,SIRT6,p53			7 hits
15	66465623	66757961	0.77	0.91	rs11631448	T	A	MAP2K1	intronic	4		BLD			Pax-4,Pou6f1			4 hits
15	66468642	66760980	0.76	0.9	rs74581464	T	A	MAP2K1	intronic	6					Arid3a,Zfp105			4 hits
15	66468953	66761291	0.52	0.79	rs111563723	C	CA	MAP2K1	intronic	6					FAC1,HDAC2,Zfp105			6 hits
15	66476691	66769029	0.69	0.92	rs78135660	G	A	MAP2K1	intronic	2b		ESC, ESDR, IPSC, BRN, MUS, PLCNT, BLD	MUS	NRSF	RXRA			4 hits

Supplementary Table 3. Summary of genomic annotation by HaploReg and RegulomeDB of variants with pairwise r^2 >= 0.4 with index TGCT SNPs

chr	pos (hg38)	pos (hg19)	LD (r^2)	LD (D')	variant	Ref	Alt	GENCODE genes	dbSNP func annot	RegulomeDB Score	Promoter histone marks	Enhancer histone marks	DNAse	Proteins bound	Motifs changed	NHGRI/EBI GWAS hits	GRASP QTL hits	Selected eQTL hits
15	66477826	66770164	0.69	0.92	rs11638268	G	A	MAP2K1	intronic	5		IPSC, BRN, MUS, LNG			CTCF,ELF1,Egr-1,Hic1,Rad21,SREBP			4 hits
15	66481637	66773975	0.67	0.91	rs41277720	G	A	MAP2K1	intronic	3a		ESDR, BRST, SKIN, PLCNT, BLD, BRN	MUS,BLD,SKIN	CTCF	Myc,RXRA,Rad21,SEF-1,ZNF219			4 hits
15	66483908	66776246	0.63	0.89	rs4287513	C	T	MAP2K1	intronic	5		BLD, LIV			CACD,NRSF,Pax-4			4 hits
15	66490923	66783261	0.75	0.9	rs14303	C	A	CTD-3185P2.1	3'-UTR	5		LIV			AP-1,HMG-IY			4 hits
15	66496322	66788660	0.67	0.9	rs11636407	C	G,T	SNAPC5	intronic	5	CRVX	ESC, BRST, BLD, SKIN, LIV, BRN, GI, MUS, PANC						4 hits
15	66499749	66792087	0.66	0.9	rs112095287	C	T	RPL4	intronic	5		SKIN, LNG, CRVX	BLD	POL2	Hic1			4 hits
15	66502014	66794352	0.66	0.9	rs74956204	G	A	RPL4	intronic	5	SKIN	ESDR, FAT, STRM, BRST, BLD, SKIN, GI, LIV, MUS, LNG, BONE	MUS,BLD,SKIN					4 hits
15	66502368	66794706	0.66	0.9	rs28684409	T	A,C	RPL4	intronic	5	SKIN	ESDR, IPSC, STRM, BRST, BLD, SKIN, LIV, GI, PANC, MUS, LNG						4 hits
15	66509324	66801662	0.66	0.9	rs79981875	T	C	RPL4	intronic	7					Pax-5			4 hits
15	66509599	66801937	0.74	0.89	rs79350921	G	T	RPL4	intronic	5			SKIN		COMP1,Cdx2,Hoxb9,Pou2f2			4 hits
15	66509870	66802208	0.44	0.81	rs12905354	T	G	RPL4	intronic	6					Dobox4,Hoxa13,Mef2,Pou2f2,TATA			6 hits
15	66510085	66802423	0.63	0.83	rs112020147	G	A	RPL4	intronic	7					Maf,NF-E2,p300			4 hits
15	66511723	66804061	0.66	0.9	rs4332695	C	G	RPL4	intronic	7					DEC			4 hits
15	66516710	66809048	0.73	0.88	rs8027892	T	C	RPL4	intronic	7								5 hits
15	66517256	66809594	0.66	0.9	rs150676795	CTT	C	RPL4	intronic	6					GATA,HDAC2,Ik-2,Irf,Nanog,PRDM1,TATA,p300			3 hits
15	66528117	66820455	0.7	0.86	rs8033122	T	A	ZWILCH	intronic	6					CDP,Cart1,Dbx1,Foxd3,Foxp1,HNF1,Hoxd8,Mef2,Ncx,Pou2f2,Sox,Zfp105			5 hits
15	66528912	66821250	0.71	0.86	rs11071896	A	G	ZWILCH	missense	7			ESDR		GCNF,GR		2 hits	6 hits
15	66533699	66826037	0.63	0.88	rs78921612	G	A	ZWILCH	intronic	7					Myf,RP58,TEF			4 hits
15	66534560	66826898	0.63	0.88	rs76549445	T	C	ZWILCH	intronic	6					Brachyury			4 hits
15	66535445	66827783	0.63	0.88	rs113631817	G	A	ZWILCH	intronic	6		PLCNT	PLCNT		BDP1,Maf,Smad3,Smad4			4 hits
15	66541006	66833344	0.71	0.86	rs112914414	G	A	ZWILCH	intronic	5					ELF1,LBP-1,NRSF,SETDB1			4 hits
15	66543366	66835704	0.71	0.86	rs74634457	A	G	ZWILCH	intronic	7								4 hits
15	66546944	66839282	0.7	0.86	rs76428668	T	G	ZWILCH	intronic	6					Evi-1,Foxd3,HDAC2,HMG-IY,Nkx2,Nkx3,Zfp105			4 hits
15	66552690	66845028	0.7	0.86	rs35244038	CATT	C	LCTL	intronic	6		BRST, SKIN			DMRT1,DMRT2,Foxd3,Foxj2,Foxp1,HDAC2,HMG-IY,HNF4,SIX5,Zfp105,Znf143			5 hits
15	66556600	66848938	0.4	0.78	rs12437980	C	T	LCTL	intronic	6					Foxa,Hic1			20 hits
19	21937561	22120363	0.52	-0.74	rs807951	C	T	29kb 3' of ZNF208		7					Foxa,GATA,Irf,PLZF,STAT			14 hits
19	21937728	22120530	0.5	-0.72	rs807950	A	C	28kb 3' of ZNF208		7					NRSF,Rad21			16 hits
19	21939533	22122335	0.62	-0.81	rs812673	C	T	27kb 3' of ZNF208		6					Foxp3,NF-I,TLX1::NFIC			20 hits
19	21940164	22122966	0.61	-0.8	rs34620362	AT	A	26kb 3' of ZNF208		7					Foxp1,GATA,HDAC2,Ik-1,p300			23 hits
19	21940615	22123417	0.62	-0.81	rs2522096	C	A	25kb 3' of ZNF208		7					BDP1,Rad21			21 hits
19	21941265	22124067	0.63	-0.83	rs2522095	T	G	25kb 3' of ZNF208		6					AP-1,Hoxa4,NF-I,Pax-4,Pou2f2,Pou3f2			21 hits
19	21942410	22125212	0.63	-0.83	rs2079062	T	G	24kb 3' of ZNF208		6					Cdx,DMRT1,DMRT5,Foxf1,Foxq1,Hoxa10,Hoxd10,Mef2,PLZF,TATA,ZEB1,Zfp105			21 hits
19	21942767	22125569	0.63	-0.83	rs2522094	A	G	23kb 3' of ZNF208		6					BCL,BDP1,Maf,SP1,VDR			20 hits
19	21942794	22125596	0.63	-0.83	rs2522093	A	G	23kb 3' of ZNF208		7					E2A,Gm397,Mtf1,RREB-1,ZEB1			19 hits

Supplementary Table 3. Summary of genomic annotation by HaploReg and RegulomeDB of variants with pairwise r^2 >= 0.4 with index TGCT SNPs

chr	pos (hg38)	pos (hg19)	LD (r^2)	LD (D')	variant	Ref	Alt	GENCODE genes	dbSNP func annot	RegulomeDB Score	Promoter histone marks	Enhancer histone marks	DNAse	Proteins bound	Motifs changed	NHGRI/EBI GWAS hits	GRASP QTL hits	Selected eQTL hits
19	21944078	22126880	0.63	-0.83	rs2666457	T	C	22kb 3' of ZNF208		6					Barhl1,FXR,Foxp3,Hmx,Lhx3,Maf,NRSF,Nkx6-1,Nrf-2			19 hits
19	21944190	22126992	0.63	-0.83	rs2522092	G	T	22kb 3' of ZNF208		7					BATF			19 hits
19	21944680	22127482	0.62	-0.81	rs2666456	C	T	21kb 3' of ZNF208		6					E2F,Mef2,ZBRK1			19 hits
19	21945379	22128181	0.6	-0.79	rs2136889	A	T	21kb 3' of ZNF208		6					AP-1,Foxp1,HMG-IY,HNF1,Lhx3,Pax-4,Sox,Zfp105			
19	21946485	22129287	0.63	-0.83	rs2666453	T	C	20kb 3' of ZNF208		6					Pou2f2			22 hits
19	21947509	22130311	0.63	-0.83	rs2097733	T	C	19kb 3' of ZNF208		7								19 hits
19	21947961	22130763	0.63	-0.83	rs1849001	C	G	18kb 3' of ZNF208		4			ESDR,ESC,IPSC,BLD,BLD,ADRL,MUS,PLCNT,GI,LNG,MUS,LNG	KAP1,USF1,SETDB1	NRSF			22 hits
19	21948503	22131305	0.63	-0.83	rs2522090	C	T	18kb 3' of ZNF208		5					SRF			
19	21948886	22131688	0.63	-0.83	rs2666450	G	A	17kb 3' of ZNF208		5					HDAC2,Ik-2,TATA			19 hits
19	21949122	22131924	0.63	-0.83	rs2666449	T	C	17kb 3' of ZNF208		6					Evi-1,Foxp3,IRC900814			19 hits
19	21949706	22132508	0.63	-0.83	rs2666448	G	A	16kb 3' of ZNF208		5					NF-kappaB			22 hits
19	21949885	22132687	0.63	-0.83	rs2522089	C	T	16kb 3' of ZNF208		5					CTCF,NRSF,Rad21			19 hits
19	21950978	22133780	0.63	-0.83	rs2214296	G	A	15kb 3' of ZNF208		7					Evi-1,Foxj2,HNF1			19 hits
19	21951250	22134052	0.62	-0.82	rs1849000	T	C	15kb 3' of ZNF208		6					CCNT2,CTCF,GATA,TAL1			22 hits
19	21951998	22134800	0.63	-0.82	rs2262908	C	T	14kb 3' of ZNF208		7					BCL,ZEB1			20 hits
19	21952467	22135269	0.53	-0.77	rs200284015	G	GC	14kb 3' of ZNF208		7					Foxa,HNF4,Pax-4,STAT			12 hits
19	21952470	22135272	0.5	-0.78	rs201410404	AT	A	14kb 3' of ZNF208		7					Barx1,Bsx,Dlx3,Foxa,HMG-IY,Hoxb8,Pax-4,STAT			13 hits
19	21952471	22135273	0.52	-0.78	rs1848999	T	A	14kb 3' of ZNF208		7					Foxa,HMG-IY,Pax-4			12 hits
19	21952478	22135280	0.55	-0.77	rs1848998	A	G	14kb 3' of ZNF208		7					Foxa			17 hits
19	21952961	22135763	0.65	-0.84	rs2666442	G	A	13kb 3' of ZNF208		6					PRDM1			21 hits
19	21953255	22136057	0.61	-0.79	rs2522086	A	T	13kb 3' of ZNF208		7					FXR,NF-I			23 hits
19	21953412	22136214	0.46	-0.79	rs61609732	A	10-mer	13kb 3' of ZNF208		6								10 hits
19	21954963	22137765	0.41	-0.78	rs2428382	C	G	11kb 3' of ZNF208		6					AP-4,CTCF,HEN1,Rad21			16 hits
19	21955181	22137983	0.67	-0.84	rs116027282	G	C	11kb 3' of ZNF208		7					BAF155,Ets,Foxa,SIX5,Znf143			
19	21955473	22138275	0.59	-0.77	rs150332127	C	T	11kb 3' of ZNF208		7					NF-Y,SIX5,SP1			
19	21956325	22139127	0.5	-0.76	rs71178796	CA	C	9.8kb 3' of ZNF208		7					BAF155,En-1,Pax-6			13 hits
19	21956428	22139230	0.4	-0.78	rs2666441	C	A	9.7kb 3' of ZNF208		5					CAC-binding-protein,CTCF,PPAR,Rad21,SP1,TATA			17 hits
19	21956543	22139345	0.65	-0.84	rs2666440	G	T	9.6kb 3' of ZNF208		5					AP-1,Hand1,Irf,Klf4,Klf7,MAZR,SP1,UF1H3BETA			22 hits
19	21957819	22140621	0.56	-0.76	rs2522106	T	A	8.3kb 3' of ZNF208		6					Arid3a,Dbx1,Evi-1,Foxp1,Hoxa10,Hoxd10,Mef2,PLZF,Pax-4,Pou2f2,TATA			24 hits
19	21958742	22141544	0.47	-0.79	rs138217248	TA	T	7.4kb 3' of ZNF208		7					MZF1::1-4,NRSF			20 hits
19	21959459	22142261	0.65	-0.84	rs1849003	C	T	6.6kb 3' of ZNF208		7					NRSF,PPAR,Pou2f2,Rhox11		1 hit	19 hits
19	21959941	22142743	0.42	-0.78	rs1849005	T	C	6.2kb 3' of ZNF208		6					Tgif1			16 hits
19	21959962	22142764	0.66	-0.85	rs1849006	A	C	6.1kb 3' of ZNF208		6					Dbx1,Foxl1,Pou1f1,Pou2f2,Pou3f2,Pou3f3,Pou4f3,Sox			20 hits
19	21960537	22143339	0.65	-0.84	rs1859093	T	G	5.6kb 3' of ZNF208		7							3 hits	22 hits
19	21960639	22143441	0.62	-0.8	rs1859092	A	G	5.5kb 3' of ZNF208		6					CTCF,ERalpha-a,HNF4,Nrf-2,RXRA,SREBP,TR4			18 hits
19	21961238	22144040	0.42	-0.79	rs12971688	G	A	4.9kb 3' of ZNF208		7					Myc			16 hits
19	21961377	22144179	0.66	-0.84	rs2522103	T	C	4.7kb 3' of ZNF208		7					SREBP			22 hits
19	21961457	22144259	0.65	-0.84	rs2666438	A	G	4.6kb 3' of ZNF208		7			ESDR,HRT					22 hits
19	21961493	22144295	0.65	-0.84	rs2522102	C	T	4.6kb 3' of ZNF208		5			ESDR,HRT		COMP1,Foxo			19 hits
19	21961508	22144310	0.65	-0.84	rs2522101	T	C	4.6kb 3' of ZNF208		5			HRT		Hoxa4			19 hits
19	21962128	22144930	0.65	-0.84	rs10408274	C	T	4kb 3' of ZNF208		7					GATA,PU.1,STAT			22 hits
19	21962345	22145147	0.42	-0.79	rs12608935	T	C	3.7kb 3' of ZNF208		7					GR,T3R			17 hits

Supplementary Table 3. Summary of genomic annotation by HaploReg and RegulomeDB of variants with pairwise r^2 >= 0.4 with index TGCT SNPs

chr	pos (hg38)	pos (hg19)	LD (r^2)	LD (D')	variant	Ref	Alt	GENCODE genes	dbSNP func annot	RegulomeDB Score	Promoter histone marks	Enhancer histone marks	DNAse	Proteins bound	Motifs changed	NHGRI/EBI GWAS hits	GRASP QTL hits	Selected eQTL hits
19	21962865	22145667	0.65	-0.84	rs7253518	C	T	3.2kb 3' of ZNF208		7					COMP1,DBP,Foxa,HNF4,PLZF		1 hit	22 hits
19	21963066	22145868	0.65	-0.84	rs6511303	C	T	3kb 3' of ZNF208		6					MZF1::1-4			19 hits
19	21963497	22146299	0.65	-0.84	rs58270321	G	A	2.6kb 3' of ZNF208		7					AP-1,AP-2,BAF155,BATF,Bach1,GATA,GR,HMGN3,Irf,KAP1,TCF4,p300			19 hits
19	21964535	22147337	0.65	-0.84	rs10410985	C	T	1.6kb 3' of ZNF208		6					HMG-IY,Sox			22 hits
19	21964648	22147450	0.64	-0.82	rs8108093	C	T	1.4kb 3' of ZNF208		7					AP-3,Cdc5,PLZF,Pou1f1			17 hits
19	21965150	22147952	0.65	-0.84	rs10418985	T	C	944bp 3' of ZNF208		7					Rad21		1 hit	22 hits
19	21965299	22148101	0.65	-0.84	rs10417673	A	T	795bp 3' of ZNF208		6					Foxd3,HLF,Sox,Zfp105			20 hits
19	21965780	22148582	0.65	-0.84	rs11085504	A	T	314bp 3' of ZNF208		7					Hbp1,Pax-4			19 hits
19	21965869	22148671	0.65	-0.84	rs11085505	G	C	225bp 3' of ZNF208		7					Rad21			19 hits
19	21966242	22149044	0.65	-0.84	rs1064170	T	A	ZNF208	3'-UTR	7					Pou3f2			19 hits
19	21966656	22149458	0.41	-0.78	rs2188972	A	G	ZNF208	3'-UTR	6					Mef2,Pou5f1,ZEB1			17 hits
19	21967560	22150362	0.65	-0.84	rs10412331	C	T	ZNF208	3'-UTR	6					DMRT2,Evi-1,Foxk1,HNF1,Mef2,Pax-6,TATA			19 hits
19	21968066	22150868	0.42	-0.79	rs12985553	C	T	ZNF208	3'-UTR	7					Pou3f3			16 hits
19	21968543	22151345	0.66	-0.85	rs2158107	T	G	ZNF208	3'-UTR	6					BHLHE40,DMRT2,DMRT3,DMRT7,TFE			20 hits
19	21968775	22151577	0.64	-0.82	rs35935777	A	AT	ZNF208	3'-UTR	6					CEBPB,Gfi1,Nanog,Pou2f2			15 hits
19	21969380	22152182	0.66	-0.85	rs2188971	T	C	ZNF208	3'-UTR	6							1 hit	23 hits
19	21969725	22152527	0.68	-0.86	rs2359810	G	A	ZNF208	3'-UTR	6					GR,Irx			23 hits
19	21969744	22152546	0.42	-0.78	rs34371812	CTT	C	ZNF208	3'-UTR	6					Arid5a,Bcl6b,Ets,Foxj2,Foxl1,Foxp1,Nkx2,TATA			18 hits
19	21970335	22153137	0.68	-0.86	rs1987570	A	C,G,T	ZNF208	3'-UTR	5								23 hits
19	21970693	22153495	0.67	-0.86	rs2359812	A	T	ZNF208	3'-UTR	5				ZNF274	SIX5		1 hit	20 hits
19	21970894	22153696	0.68	-0.86	rs4378732	G	A	ZNF208	3'-UTR	5					HNF1			23 hits
19	21971006	22153808	0.42	-0.79	rs4550595	C	T	ZNF208	3'-UTR	5					CEBPB			18 hits
19	21971930	22154732	0.62	-0.79	rs8108957	T	C	ZNF208	missense	5				ZNF274	DMRT4,Nrf-2			19 hits
19	21972152	22154954	0.68	-0.86	rs2214301	C	T	ZNF208	missense	5					CDP,Cart1,Esx1,HNF1,Hoxa5,Hoxd8,Nkx2,Pou2f2,Pou3f2,Pou5f1,Sox		1 hit	24 hits
19	21973680	22156482	0.42	-0.79	rs12975751	G	T	ZNF208	missense	6					KAP1,Pax-4,RFX5,Smad,Zec			20 hits
19	21974190	22156992	0.67	-0.85	rs2007506	C	T	ZNF208	missense	7					AP-1,KAP1,Pax-6,Pou1f1			24 hits
19	21974500	22157302	0.66	-0.84	rs10419899	G	A	ZNF208	synonymous	6					ATF3,Foxd1,XBP-1			22 hits
19	21975365	22158167	0.4	-0.76	rs10426971	G	A	ZNF208	intronic	7					NRSF,Nanog			24 hits
19	21975497	22158299	0.68	-0.86	rs1987975	C	A	ZNF208	intronic	7					Sox		1 hit	25 hits
19	21975600	22158402	0.68	-0.86	rs1987974	T	A	ZNF208	intronic	6					Sox		1 hit	21 hits
19	21975910	22158712	0.64	-0.81	rs10592430	AAC	A	ZNF208	intronic	6					Cdx,Foxd3,Foxo,Foxp1,HDAC2,Hmbox1,Irf,Mef2,Pax-4,STAT			
19	21975911	22158713	0.65	-0.81	rs57233797	AC	A	ZNF208	intronic	6					AP-1,Cdx,Foxd3,Foxo,Foxp1,HDAC2,Hmbox1,Irf,Mef2,Pax-4			
19	21976190	22158992	0.67	-0.86	rs8103214	C	T	ZNF208	intronic	6					HNF1,IRC900814,Pou1f1,Pou5f1		2 hits	25 hits
19	21977502	22160304	0.68	-0.86	rs8108535	T	G	ZNF208	intronic	7					NRSF,SF1			25 hits
19	21977736	22160538	0.68	-0.86	rs2079064	G	A	ZNF208	intronic	7					Foxp3,PRDM1,p300			25 hits
19	21977907	22160709	0.42	-0.79	rs12979885	C	T	ZNF208	intronic	6					Hand1,YY1			19 hits
19	21978688	22161490	0.68	-0.86	rs7247121	T	C	ZNF208	intronic	7							1 hit	24 hits
19	21980122	22162924	0.68	-0.86	rs6511305	G	A	ZNF208	intronic	7								25 hits
19	21980295	22163097	0.58	-0.79	rs199663483	C	CTTA	ZNF208	intronic	7					RXRA			19 hits
19	21980804	22163606	0.4	-0.76	rs2214298	T	C	ZNF208	intronic	6					Foxo,Sox			23 hits
19	21981046	22163848	0.69	-0.87	rs6511306	A	G	ZNF208	intronic	6					CDP,Irf			22 hits
19	21981355	22164157	0.69	-0.87	rs6511307	T	C	ZNF208	intronic	7								25 hits
19	21981527	22164329	0.69	-0.87	rs6511308	T	C	ZNF208	intronic	6					Hoxb8			22 hits
19	21982852	22165654	0.69	-0.87	rs146328811	C	G	ZNF208	intronic	6					HNF1,Hltf,Pax-4			

Supplementary Table 3. Summary of genomic annotation by HaploReg and RegulomeDB of variants with pairwise r^2 >= 0.4 with index TGCT SNPs

chr	pos (hg38)	pos (hg19)	LD (r^2)	LD (D')	variant	Ref	Alt	GENCODE genes	dbSNP func annot	RegulomeDB Score	Promoter histone marks	Enhancer histone marks	DNAse	Proteins bound	Motifs changed	NHGRI/EBI GWAS hits	GRASP QTL hits	Selected eQTL hits
19	21984199	22167001	0.68	-0.86	rs10401697	G	A	ZNF208	intronic	6					Dbx1,Dbx2,HMG-IY,HNF1,Hoxb13,Hoxb9,Ncx,Pax-6,Pou1f1,Pou2f2,Pou3f2,Pou3f4,Pou4f3,Pou6f1,Sox,TATA			25 hits
19	21985339	22168141	0.68	-0.86	rs2359813	C	T	ZNF208	intronic	7					TEF		1 hit	25 hits
19	21986000	22168802	0.68	-0.86	rs10416159	G	A	ZNF208	intronic	7							1 hit	25 hits
19	21986747	22169549	0.42	-0.79	rs12980606	A	G	ZNF208	intronic	7					SIX5			20 hits
19	21986971	22169773	0.68	-0.86	rs1988427	A	G	ZNF208	intronic	7								25 hits
19	21987749	22170551	0.68	-0.86	rs8101183	C	A	ZNF208	intronic	6					HDAC2,HMG-IY,Pax-4,Sin3Ak-20,Sox			22 hits
19	21988447	22171249	0.68	-0.86	rs11670558	T	A	ZNF208	intronic	6					Brachyury,FXR,Smad3,T3R,p300			25 hits
19	21989078	22171880	0.67	-0.85	rs4574045	C	T	ZNF208	intronic	6					Evi-1,GATA,HDAC2,Irf,TATA,p300			25 hits
19	21989145	22171947	0.68	-0.86	rs2359814	A	G	ZNF208	intronic	6					Dlx2,Dlx3,E4BP4,Hoxa3,Hoxa5,Hoxb4,Hoxb6,Hoxc6,Hoxc9,Lhx3,Pou2f2,Prx2			22 hits
19	21991434	22174236	0.68	-0.86	rs10402796	T	C	ZNF208	intronic	6					E4BP4,Foxc1,Foxk1,Mef2,Nkx2,Nkx3,Pbx-1,Pou5f1			25 hits
19	21991950	22174752	0.68	-0.86	rs8103163	A	C	ZNF208	intronic	6					Nkx3			25 hits
19	21992070	22174872	0.68	-0.86	rs8103368	A	G	ZNF208	intronic	6					Ik-2,Irf,Mef2,NF-AT,STAT,ZEB1			25 hits
19	21992764	22175566	0.68	-0.86	rs1988501	T	G	ZNF208	intronic	6					Foxd3,TATA		2 hits	25 hits
19	21994297	22177099	0.68	-0.87	rs2214297	A	G	ZNF208	intronic	7								25 hits
19	21994951	22177753	0.53	-0.84	rs200674456	T	TTC	ZNF208	intronic	6					DMRT5,Evi-1,Foxp1,HDAC2,Irf,Nanog,Pax-5,RXRA,Zfp105,p300			13 hits
19	21995012	22177814	0.69	-0.87	rs10418541	T	C	ZNF208	intronic	6					HNF4,SREBP			24 hits
19	21995883	22178685	0.69	-0.86	rs9304993	A	G	ZNF208	intronic	6					AP-1,PU.1,RXRA,SPIB,SRF,STAT		1 hit	24 hits
19	21997919	22180721	0.72	-0.89	rs4932723	C	G	ZNF208	intronic	7					GR		1 hit	25 hits
19	21998003	22180805	0.71	-0.88	rs1963300	A	G	ZNF208	intronic	7					AP-1,Pbx-1,Smad3			24 hits
19	21998683	22181485	0.57	-0.79	rs2078235	C	A	ZNF208	intronic	6					CACD,Glis2,PLAG1			14 hits
19	21999137	22181939	0.72	-0.89	rs11085506	A	G	ZNF208	intronic	7					Cdx,Sox			25 hits
19	21999251	22182053	0.43	-0.78	rs11668920	T	C	ZNF208	intronic	7					Nkx2			24 hits
19	22000658	22183460	0.72	-0.89	rs7249472	A	G	ZNF208	intronic	7					SP2			25 hits
19	22001240	22184042	0.72	-0.89	rs2106870	G	A	ZNF208	intronic	7								20 hits
19	22001286	22184088	0.7	-0.87	rs138857791	AAAAC	A	ZNF208	intronic	6					CIZ,Foxa,Foxd3,Foxf1,Foxp1,Foxq1,Irf,RREB-1,Sox			
19	22002440	22185242	0.73	-0.9	rs8108807	G	A	ZNF208	intronic	6					Pou5f1			25 hits
19	22002615	22185417	0.72	-0.89	rs8112395	T	C	ZNF208	intronic	6					Bcl6b,Evi-1,HDAC2,Sox			27 hits
19	22003908	22186710	0.45	-0.82	rs2158106	C	T	ZNF208	intronic	6					Hic1,XBP-1,p53			17 hits
19	22004958	22187760	0.72	-0.9	rs2359815	C	A	ZNF208	intronic	7					PRDM1,RXRA		1 hit	17 hits
19	22005475	22188277	0.72	-0.89	rs4592778	A	G	ZNF208	intronic	6								25 hits
19	22005907	22188709	0.73	-0.9	rs7248488	A	C	ZNF208	intronic	7					CIZ,Irf,NF-kappaB		2 hits	25 hits
19	22007277	22190079	0.73	-0.9	rs8108160	T	C	ZNF208	intronic	7					GR,Ik-1,NRSF			24 hits
19	22008163	22190965	0.72	-0.9	rs8111955	T	C	ZNF208	intronic	6					CACD,Ets,NRSF			22 hits
19	22009869	22192671	0.43	-0.79	rs10410114	C	T	ZNF208	intronic	7	IPSC, FAT, BLD, STRM, VAS, BRN, GI, PANC, HRT, OVRY, PLCNT	BLD	OVRY		HMG-IY,Maf,Pbx3,RFX5			2 hits
19	22010082	22192884	0.43	-0.79	rs10410914	G	A	ZNF208	intronic	5			LNG,IPSC,BLD,HRT,PLCNT,BLD		BDP1,LUN-1,Maf			24 hits
19	22010329	22193131	0.43	-0.79	rs8105991	T	C	ZNF208	intronic	7	IPSC, FAT, STRM, BLD, SKIN, VAS, BRN, GI, KID, PANC, HRT, OVRY, PLCNT, MUS	BLD			NRSF,Zfp410,Zic			24 hits

Supplementary Table 3. Summary of genomic annotation by HaploReg and RegulomeDB of variants with pairwise r^2 >= 0.4 with index TGCT SNPs

chr	pos (hg38)	pos (hg19)	LD (r^2)	LD (D')	variant	Ref	Alt	GENCODE genes	dbSNP func annot	RegulomeDB Score	Promoter histone marks	Enhancer histone marks	DNAse	Proteins bound	Motifs changed	NHGRI/EBI GWAS hits	GRASP QTL hits	Selected eQTL hits
19	22011184	22193986	0.46	-0.82	rs11085508	A	C	240bp 5' of ZNF208		5	BLD, STRM, SKIN, FAT, BRN, GI, HRT, OVRY, PLCNT		IPSC		BCL,HDAC2,Pax-5,Pou2f2,p300		1 hit	17 hits
19	22011802	22194604	0.42	-0.79	rs10424932	G	T	858bp 5' of ZNF208		6					Cart1,Foxp1,Hoxa10,Hoxa9,Pou2f2,RREB-1,Sox,Zfp105			18 hits
19	22011949	22194751	0.63	-0.84	rs10425160	G	C	1kb 5' of ZNF208		7					Rad21			17 hits
19	22014801	22197603	0.43	-0.83	rs4458136	C	T	3.9kb 5' of ZNF208		6					PLAG1,Pax-5,Rad21,ZBRK1,Zfx			17 hits
19	22015874	22198676	0.44	-0.83	rs2359816	G	A	4.9kb 5' of ZNF208		6					Ets,Zbtb3			16 hits
19	22022863	22205665	0.76	-0.89	rs1989119	T	G	12kb 5' of ZNF208		7					Nanog,PTF1-beta,STAT			20 hits
19	22022877	22205679	0.76	-0.9	rs1989118	A	G	12kb 5' of ZNF208		7					Evi-1,Mef2,PEBP			22 hits
19	22023327	22206129	0.43	-0.79	rs10854064	C	T	12kb 5' of ZNF208		7					BAF155,SIX5,TEF-1,Znf143			22 hits
19	22025730	22208532	0.45	-0.83	rs67520962	8-mer	G	15kb 5' of ZNF208		7					AP-1,YY1,ZEB1			19 hits
19	22025799	22208601	0.47	-0.83	rs1985744	G	T	15kb 5' of ZNF208		7					AP-2rep			17 hits
19	22027599	22210401	0.47	-0.83	rs10401339	A	T	17kb 5' of ZNF208		6					Nkx2,Zic			19 hits
19	22031109	22213911	0.47	-0.83	rs34190595	ACT	A	20kb 5' of ZNF208		7					TATA			19 hits
19	22031320	22214122	0.45	-0.8	rs441017	T	C	20kb 5' of ZNF208		7					Pax-4			23 hits
19	22033910	22216712	0.47	-0.83	rs452459	T	G	19kb 5' of ZNF257		7					CTCF,Hmx			17 hits
19	22036361	22219163	0.45	-0.81	rs1654509	C	T	16kb 5' of ZNF257		7								21 hits
19	22036708	22219510	0.47	-0.83	rs437192	C	G	16kb 5' of ZNF257		6					DMRT1,DMRT5,DMRT7,Fox,Foxa,Foxd3,Foxf1,Foxi1,Foxj1,Foxj2,Foxl1,Foxp1,Foxq1,HDAC2,Nanog,RREB-1,Sox,YY1,Zfp105			19 hits
19	22037741	22220543	0.47	-0.83	rs403997	T	C	15kb 5' of ZNF257		7					Pou2f2			19 hits
19	22040082	22222884	0.47	-0.83	rs424066	T	C	12kb 5' of ZNF257		7					AP-1,HNF6,Hmx			19 hits
19	22041228	22224030	0.47	-0.84	rs417947	G	A	11kb 5' of ZNF257		7					Spz1		1 hit	17 hits
19	22042535	22225337	0.45	-0.81	rs408124	A	G	9.9kb 5' of ZNF257		7								21 hits
19	22045289	22228091	0.73	-0.85	rs548059	A	G	7.2kb 5' of ZNF257		6					RXRA,ZID			23 hits
19	22045319	22228121	0.72	-0.85	rs7258834	A	G	7.1kb 5' of ZNF257		6					Foxp1,HDAC2,Irf,Nanog,STAT,TATA,Zfp105,p300			23 hits
19	22045413	22228215	0.81	-0.94	rs431346	T	C	7.1kb 5' of ZNF257		7							1 hit	22 hits
19	22045725	22228527	0.81	-0.94	rs436194	A	G	6.7kb 5' of ZNF257		6					Pdx1		3 hits	22 hits
19	22045990	22228792	0.81	-0.94	rs431474	A	G	6.5kb 5' of ZNF257		7					Ascl2,E2A,HEN1,Sin3Ak-20		3 hits	22 hits
19	22046473	22229275	0.81	-0.94	rs426299	G	A	6kb 5' of ZNF257		7								22 hits
19	22046705	22229507	0.74	-0.87	rs450641	A	C	5.8kb 5' of ZNF257		7					CIZ,Irf			22 hits
19	22046791	22229593	0.52	-0.88	rs403850	C	T	5.7kb 5' of ZNF257		7					ZEB1			14 hits
19	22047167	22229969	0.81	-0.94	rs450298	A	C	5.3kb 5' of ZNF257		6					CEBPB,Foxl1,LRH1,Mef2,TATA			22 hits
19	22047531	22230333	0.8	-0.94	rs35407365	CAT	C	4.9kb 5' of ZNF257		6					ATF3,BHLHE40,Myc,TFE			22 hits
19	22047626	22230428	0.81	-0.94	rs394457	G	T	4.8kb 5' of ZNF257		7					HDAC2,Hoxd10,Mef2,Pax-4,Zfp105		1 hit	22 hits
19	22047869	22230671	0.4	-0.95	rs409835	T	C	4.6kb 5' of ZNF257		5					ERalpha-a,Esr2,GATA,Hdx		8 hits	50 hits
19	22047992	22230794	0.81	-0.94	rs417628	C	A	4.5kb 5' of ZNF257		5					Brachyury,E2A,ERalpha-a,Esr2,Myf,RXRA,Rad21,SIX5,TBX5,Tgif1,p300		1 hit	22 hits
19	22048510	22231312	0.81	-0.94	rs402281	G	C	4kb 5' of ZNF257		7			IPSC		BCL,NRSF,THAP1		1 hit	22 hits
19	22049576	22232378	0.81	-0.94	rs423284	C	T	2.9kb 5' of ZNF257		6					ATF3,Myc,Obox6,SIRT6,SREBP,ZEB1			22 hits
19	22049774	22232576	0.8	-0.94	rs390852	T	C	2.7kb 5' of ZNF257		7					Foxa,Foxj2,GR			22 hits
19	22049994	22232796	0.81	-0.94	rs399990	G	A	2.5kb 5' of ZNF257		7					GR		1 hit	22 hits
19	22050054	22232856	0.75	-0.88	rs199539811	AAC	A	2.4kb 5' of ZNF257		7					BCL,Foxa,GATA,HDAC2,Irf,Pax-5,RXRA,Sin3Ak-20,p300			23 hits

Supplementary Table 3. Summary of genomic annotation by HaploReg and RegulomeDB of variants with pairwise r^2 >= 0.4 with index TGCT SNPs

chr	pos (hg38)	pos (hg19)	LD (r^2)	LD (D')	variant	Ref	Alt	GENCODE genes	dbSNP func annot	RegulomeDB Score	Promoter histone marks	Enhancer histone marks	DNAse	Proteins bound	Motifs changed	NHGRI/EBI GWAS hits	GRASP QTL hits	Selected eQTL hits
19	22050055	22232857	0.75	-0.88	rs150122872	ACAGG	A	2.4kb 5' of ZNF257		7					AP-1,BCL,Foxa,GATA,HDAC2,Irf,Pax-5,RXRA,Sin3Ak-20,p300			26 hits
19	22050232	22233034	0.81	-0.94	rs430614	C	T	2.2kb 5' of ZNF257		7					GR,Mrg,Myf			22 hits
19	22050257	22233059	0.81	-0.94	rs507994	G	C	2.2kb 5' of ZNF257		7								22 hits
19	22050294	22233096	0.52	-0.88	rs632709	T	C	2.2kb 5' of ZNF257		7								14 hits
19	22050456	22233258	0.81	-0.94	rs391422	G	A	2kb 5' of ZNF257		7					AIRE			22 hits
19	22050876	22233678	0.8	-0.94	rs424465	C	T	1.6kb 5' of ZNF257		7					BDP1,CTCF,HNF4,RXRA,Rad21			22 hits
19	22050890	22233692	0.8	-0.94	rs424460	C	T	1.6kb 5' of ZNF257		6					GR,RXRA,TATA,THAP1,YY1			22 hits
19	22050966	22233768	0.81	-0.94	rs440102	A	G	1.5kb 5' of ZNF257		6					Pax-4,Pou3f2,Pou3f4			22 hits
19	22051382	22234184	0.41	-0.84	rs8108146	A	C	1.1kb 5' of ZNF257		6					FAC1,Foxa,Foxd3,Foxj1,Foxk1,Foxo,Foxp1,HDAC2,Irf,Nanog,Pax-4,RREB-1,Sox,Zfp105,p300			13 hits
19	22051399	22234201	0.55	-0.83	rs8108152	A	C	1.1kb 5' of ZNF257		6	BLD	BLD			Foxa,Foxd3,Foxp1,HDAC2,HMG-IY,Pax-4,RREB-1,Sox,Zfp105		1 hit	16 hits
19	22051676	22234478	0.51	-0.87	rs417331	C	T	787bp 5' of ZNF257		7	BLD	BLD			STAT,TLX1::NFIC			14 hits
19	22051787	22234589	0.81	-0.94	rs417066	C	T	676bp 5' of ZNF257		7	BLD	BLD			Foxm1,Mef2,SIX5,Znf143			22 hits
19	22051986	22234788	0.81	-0.94	rs367280	T	G	477bp 5' of ZNF257		6	FAT, BLD	BLD, GI, MUS			AIRE,Cdx2,Ncx,Pdx1		1 hit	22 hits
19	22052126	22234928	0.75	-0.88	rs366863	T	C	337bp 5' of ZNF257		5	FAT, BRST, BLD, STRM, SKIN, BRN, GI, ADRL, KID, PANC, MUS, PLCNT, HRT, OVRY, THYM, VAS, LNG, BONE	BLD, GI			Ets,HNF4,Irf,Rad21,SMC3,SP1			21 hits
19	22052136	22234938	0.77	-0.9	rs416312	C	A	327bp 5' of ZNF257		5	FAT, BRST, BLD, STRM, SKIN, BRN, GI, ADRL, KID, PANC, MUS, PLCNT, HRT, OVRY, THYM, VAS, LNG, BONE	BLD, GI			HNF4,RXRA			21 hits
19	22052139	22234941	0.49	-0.87	rs366849	T	G	324bp 5' of ZNF257		5	FAT, BRST, BLD, STRM, SKIN, BRN, GI, ADRL, KID, PANC, MUS, PLCNT, HRT, OVRY, THYM, VAS, LNG, BONE	BLD, GI						11 hits
19	22052505	22235307	0.81	-0.94	rs415291	C	G	ZNF257	5'-UTR	4	ESDR, IPSC, FAT, STRM, BRST, BLD, MUS, SKIN, VAS, BRN, GI, ADRL, KID, PANC, LNG, PLCNT, HRT, OVRY, THYM, SPLN, BONE		IPSC,BRST,BLD,BLD,BLD,BLD,BLD,BLD,SKIN,SKIN,SKIN,SKIN,BRN,BRN,HRT,GI,GI,KID,LNG,MUS,MUS,PLCNT,GI,THYM,GI,OVRY,PANC,MUS,GI,LIV,BLD,BLD,SKIN,SKIN	POL2,ELF1,CFOS,HEY1,NFYA,NFYB,POL24H8,TAF1,TBP	NRSF,Sin3Ak-20,TCF12,Znf143		1 hit	22 hits
19	22052689	22235491	0.81	-0.94	rs387343	T	G	ZNF257	intronic	4	ESDR, IPSC, FAT, STRM, BRST, BLD, MUS, SKIN, VAS, BRN, GI, ADRL, KID, PANC, LNG, PLCNT, HRT, OVRY, THYM, SPLN, BONE		BLD,BLD,BLD,BLD,BLD,SKIN,BRN,BRN,HRT,GI,GI,LNG,MUS,PLCNT,GI,THYM,PANC	POL2	LBP-1,LBP-9,RBP-Jkappa		1 hit	22 hits
19	22052724	22235526	0.81	-0.94	rs387315	T	C	ZNF257	intronic	4	ESDR, IPSC, FAT, STRM, BRST, BLD, MUS, SKIN, VAS, BRN, GI, ADRL, KID, PANC, LNG, PLCNT, HRT, OVRY, THYM, SPLN, BONE		BLD,BLD,BLD,BLD,SKIN,BRN,BRN,HRT,GI,GI,LNG,MUS,PLCNT,GI	YY1	AP-1		1 hit	22 hits

Supplementary Table 3. Summary of genomic annotation by HaploReg and RegulomeDB of variants with pairwise r^2 >= 0.4 with index TGCT SNPs

chr	pos (hg38)	pos (hg19)	LD (r^2)	LD (D')	variant	Ref	Alt	GENCODE genes	dbSNP func annot	RegulomeDB Score	Promoter histone marks	Enhancer histone marks	DNAse	Proteins bound	Motifs changed	NHGRI/EBI GWAS hits	GRASP QTL hits	Selected eQTL hits
19	22052775	22235577	0.81	-0.94	rs408312	C	T	ZNF257	intronic	3a	ESDR, IPSC, FAT, STRM, BRST, BLD, MUS, SKIN, VAS, BRN, GI, ADRL, KID, PANC, LNG, PLCNT, HRT, OVRY, THYM, SPLN, BONE		BLD,BLD,BLD,BLD,BLD,SKIN,BRN,BRN,HRT,GI,LNG,MUS,PLCNT,GI	YY1	Zfx		1 hit	22 hits
19	22052818	22235620	0.81	-0.94	rs423926	G	C	ZNF257	intronic	4	ESDR, IPSC, FAT, STRM, BRST, BLD, MUS, SKIN, VAS, BRN, GI, ADRL, KID, PANC, LNG, PLCNT, HRT, OVRY, THYM, SPLN, BONE		BLD,BLD,BLD,SKIN,BRN,BRN,LNG,MUS,PLCNT,GI	YY1	EBF,Hic1,NRSF,YY1,ZBTB7A,p300		1 hit	22 hits
19	22056188	22238990	0.52	0.88	rs8107039	G	A	ZNF257	intronic	7								14 hits
19	22057117	22239919	0.52	0.88	rs4244913	A	T	ZNF257	intronic	6					Barhl1,Barx2,Dbx1,Dbx2,En-1,Foxc1,Foxk1,Foxo,Gbx1,Gbx2,HNF1,Hdx,Hlx1,Hlxb9,Hoxa3,Hoxb4,Hoxb7,Hoxd8,Irx,Msx-1,Ncx,Nkx6-1,Nkx6-2,Pax-6,Phox2a,Pou2f2,Pou3f2,Pou3f4,Prrx1			14 hits
19	22057678	22240480	0.51	0.87	rs7246619	T	C	ZNF257	intronic	7								14 hits
19	22058813	22241615	0.51	0.87	rs2043318	G	C	ZNF257	intronic	5					RREB-1			14 hits
19	22060910	22243712	0.48	0.84	rs60740351	G	GC	ZNF257	intronic	6					GATA,TAL1			14 hits
19	22062943	22245745	0.5	0.86	rs6511318	A	C	ZNF257	intronic	7					COMP1			14 hits
19	22065635	22248437	0.44	0.78	rs202098525	T	TTAA	ZNF257	intronic	6					Barx2,Dbx1,Dbx2,Foxi1,Foxj2,Foxl1,HNF1,Hlx1,Hoxa3,Hoxa7,Hoxb4,Hoxb8,Hoxc6,Hoxc9,Hoxd8,Maf,Ncx,Nkx6-1,Nkx6-2,Pax-6,Phox2a,Pou1f1,Pou2f2,Pou3f2,Pou3f4,Pou4f3,Prrx1,Prrx2,TATA			10 hits
19	22066114	22248916	0.79	0.93	rs9653156	C	A	ZNF257	intronic	6					GR,Hoxb13,Hoxd10,Mef2			22 hits
19	22066243	22249045	0.5	0.86	rs4932953	G	C	ZNF257	intronic	7					Smad			14 hits
19	22071890	22254692	0.53	0.88	rs28881618	G	A	ZNF257	intronic	6					Dmbx1,Elf5,Foxa,Foxd1,Foxj2,Foxo,Isl2,Obox3,PU.1,Pitx3			14 hits
19	22073594	22256396	0.53	0.88	rs3752163	G	A	ZNF257	intronic	6					RFX5,ZEB1			14 hits
19	22074246	22257048	0.53	0.88	rs7254363	C	T	ZNF257	intronic	6					DMRT1,Dbx1,E2F,Evi-1,Foxp1,HNF1,Hoxa9,Pou2f2,Pou3f2			14 hits
19	22074462	22257264	0.53	0.89	rs7255666	T	C	ZNF257	intronic	7					Maf,NF-E2,p300			14 hits
19	22074823	22257625	0.53	0.89	rs7258080	A	T	ZNF257	intronic	6					Homez,Mef2,TATA			14 hits
19	22075594	22258396	0.53	0.89	rs10403779	C	G	ZNF257	intronic	7								14 hits
19	22076665	22259467	0.4	0.97	rs11667209	A	G	ZNF257	intronic	7					Hoxa5,PU.1,SRF,p300			50 hits
19	22076864	22259666	0.4	0.97	rs11667274	A	G	ZNF257	intronic	6					Foxp1,Mef2			50 hits
19	22079074	22261876	0.41	0.98	rs112205850	G	A	ZNF257	intronic	7					ATF3			50 hits
19	22080097	22262899	0.41	0.98	rs55728714	A	G	ZNF257	intronic	6								50 hits
19	22081194	22263996	0.41	0.98	rs12609368	T	C	ZNF257	intronic	6					Foxk1,Foxl1,Irx,Pou2f2			50 hits
19	22081856	22264658	0.54	0.9	rs7258192	G	A	ZNF257	intronic	6					Barhl1,Barx1,Barx2,Bsx,CEBPA,CEBPB,DMRT1,Dbx2,Dlx2,Foxj1,Gbx1,Hmx,Hoxb3,Hoxb8,Hoxc6,Hoxd8,Msx-1,Ncx,Prrx2,Sox			13 hits
19	22083299	22266101	0.41	0.98	rs1978719	G	A	ZNF257	intronic	7					ZBTB33			50 hits
19	22083867	22266669	0.53	0.9	rs2116895	T	C	ZNF257	intronic	6								12 hits
19	22084320	22267122	0.54	0.9	rs6511320	C	T	ZNF257	intronic	6					Foxq1,Myc,XBP-1			12 hits

Supplementary Table 3. Summary of genomic annotation by HaploReg and RegulomeDB of variants with pairwise r^2 >= 0.4 with index TGCT SNPs

chr	pos (hg38)	pos (hg19)	LD (r^2)	LD (D')	variant	Ref	Alt	GENCODE genes	dbSNP func annot	RegulomeDB Score	Promoter histone marks	Enhancer histone marks	DNAse	Proteins bound	Motifs changed	NHGRI/EBI GWAS hits	GRASP QTL hits	Selected eQTL hits
19	22084383	22267185	0.41	0.98	rs56369285	T	C	ZNF257	intronic	6					DMRT2,DMRT7,Foxp1,Sox			50 hits
19	22085047	22267849	1	1	rs73019876	T	G	ZNF257	intronic	6					Foxp1,HDAC2,Irf,RREB-1,Sox,Zfp105,p300			18 hits
19	22085977	22268779	0.53	0.9	rs28456336	T	G	ZNF257	intronic	6					ERalpha-a,Egr-1,GCNF,SF1,p53			13 hits
19	22089652	22272454	0.53	0.9	rs4932954	T	A	ZNF257	3'-UTR	7					LBP-1,PU.1			11 hits
19	22089941	22272743	0.53	0.9	rs9304994	G	A	ZNF257	3'-UTR	7					Pou2f2			11 hits
19	22092960	22275762	0.4	0.96	rs34141566	TCTTA	T	1.9kb 3' of ZNF257		6					Pou1f1			50 hits
19	22093496	22276298	0.41	0.98	rs56073035	C	G	2.4kb 3' of ZNF257		7					NF-kappaB,STAT,TCF12			50 hits
19	22093635	22276437	0.41	0.98	rs55886600	G	A	2.5kb 3' of ZNF257		5					ELF1,NRSF,SETDB1,YY1,Zfx			50 hits
19	22094254	22277056	0.41	0.98	rs147695994	TG	T	3.2kb 3' of ZNF257		6					E2A,Ik-1,Mxi1,Myf,NRSF			49 hits
19	22095024	22277826	0.41	0.98	rs73019889	C	G	3.9kb 3' of ZNF257		6					Pbx3			50 hits
19	22095319	22278121	0.41	0.98	rs17459246	T	C	4.2kb 3' of ZNF257		7					GR,YY1		7 hits	50 hits
19	22096450	22279252	0.44	0.76	rs4932747	C	G	5.4kb 3' of ZNF257		7					EBF			4 hits
19	22096516	22279318	0.53	0.9	rs4932748	T	G	5.4kb 3' of ZNF257		7					GR,TCF4			10 hits
19	22096739	22279541	0.53	0.9	rs1036235	T	C	5.6kb 3' of ZNF257		6					BDP1,HNF4,LF-A1,Maf,Rad21			10 hits
19	22097258	22280060	0.53	0.9	rs2359995	C	T	6.2kb 3' of ZNF257		6					Barhl1,Barx2,Bsx,CDP,Dbx1,Dbx2,Dlx3,En-1,HNF1,Hlx1,Hmx,Hoxa7,Hoxb4,Hoxc6,Hoxc9,Hoxd8,Msx-1,Ncx,Nkx3,Nkx6-1,Pax-6,Pou2f2,Pou3f2,Pou3f4,Prrx1,Prrx2			10 hits
19	22098152	22280954	0.53	0.9	rs1019938	T	A	7.1kb 3' of ZNF257		6					DMRT2,p300			10 hits
19	22099112	22281914	0.53	0.9	rs6511323	T	C	8kb 3' of ZNF257		6					Hoxa10,Hoxa9,Hoxd10			10 hits
19	22099812	22282614	0.53	0.9	rs2099347	T	G	8.7kb 3' of ZNF257		7					BRCA1,CACD,Egr-1,FAC1,RFX5,Znf143			10 hits
19	22100390	22283192	0.41	0.97	rs140410292	TA	T	9.3kb 3' of ZNF257		6					Cdx,Dbx1,Evi-1,Foxp1,HDAC2,HMG-IY,Irf,Pou3f2,p300			50 hits
19	22101555	22284357	0.53	0.9	rs6511325	A	G	10kb 3' of ZNF257		6					HMG-IY,Hoxd10,Nanog,Pou2f2			10 hits
19	22102261	22285063	0.53	0.9	rs4553749	C	G	11kb 3' of ZNF257		6					LBP-1,Pbx-1			10 hits
19	22103648	22286450	0.4	0.95	rs62111035	G	C,T	13kb 3' of ZNF257		5								49 hits
19	22103877	22286679	0.47	0.82	rs6511326	T	C	13kb 3' of ZNF257		5								9 hits
19	22105059	22287861	0.45	0.8	rs8111771	A	G	14kb 3' of ZNF257		7					ATF3,BCL,ETF,Ets,YY1,Znf143			10 hits
19	22105103	22287905	0.41	0.74	rs6511329	T	C	14kb 3' of ZNF257		6					BDP1,LXR			10 hits
19	22109410	22292212	0.49	0.86	rs1560718	C	A	18kb 3' of ZNF257		7					RFX5			10 hits
19	22110324	22293126	0.49	0.86	rs1978718	T	C	19kb 3' of ZNF257		6					CDP,GATA,Maf			10 hits
19	22114141	22296943	0.47	0.82	rs55921217	C	A	23kb 3' of ZNF257		6					CDP,HEN1			10 hits
19	22115423	22298225	0.48	0.84	rs10408261	T	C	24kb 3' of ZNF257		7					TCF12			8 hits
19	22115520	22298322	0.48	0.83	rs8103088	G	C	24kb 3' of ZNF257		6					AP-2,GR,HEY1,Ik-1,Rad21,SETDB1			9 hits
19	22117205	22300007	0.48	0.85	rs987711	T	G	26kb 3' of ZNF257		7		LIV						11 hits
19	22118201	22301003	0.48	0.85	rs8100438	C	T	27kb 3' of ZNF257		7			PLCNT		TR4			12 hits
19	22121343	22304145	0.47	-0.84	rs452707	C	T	30kb 3' of ZNF257		6								10 hits
19	22839042	23021844	0.44	0.68	rs62123860	C	T	69kb 5' of ZNF99		7					AP-1,CACD,NRSF,Znf143			4 hits
19	22840945	23023747	0.44	0.68	rs11671459	G	A	71kb 5' of ZNF99		7								4 hits
19	22849568	23032370	0.44	0.68	rs7253127	T	A	80kb 5' of ZNF99		6					CIZ,Duxl,Pou2f2			4 hits
19	22851749	23034551	0.44	0.68	rs58604290	GT	G	82kb 5' of ZNF99		6					AFP1,CEBPG,FAC1,Foxo,Foxp1,Pax-4,Pou1f1			4 hits
19	22851778	23034580	0.44	0.68	rs57042530	G	A	82kb 5' of ZNF99		6					Arid3a,Dbx1,Irx,Pou1f1,Pou2f2,Pou3f3			4 hits
19	22855558	23038360	0.44	0.68	rs62120774	A	G	86kb 5' of ZNF99		6					Hbp1,Pou3f2			4 hits
19	22860508	23043310	0.44	0.68	rs62120778	G	A	91kb 5' of ZNF99		7					EBF,Pax-5			4 hits
19	22861789	23044591	0.43	0.67	rs56053588	A	C	92kb 5' of ZNF99		7					Smad3			4 hits

Supplementary Table 3. Summary of genomic annotation by HaploReg and RegulomeDB of variants with pairwise r^2 >= 0.4 with index TGCT SNPs

chr	pos (hg38)	pos (hg19)	LD (r^2)	LD (D')	variant	Ref	Alt	GENCODE genes	dbSNP func annot	RegulomeDB Score	Promoter histone marks	Enhancer histone marks	DNAse	Proteins bound	Motifs changed	NHGRI/EBI GWAS hits	GRASP QTL hits	Selected eQTL hits
19	22861792	23044594	0.43	0.67	rs56074892	A	G	92kb 5' of ZNF99		7								4 hits
19	22868506	23051308	0.44	0.68	rs62120789	A	C	99kb 5' of ZNF99		6					Foxa,Foxd1,Foxf2,Mrg,TCF12,p300			2 hits
19	22870656	23053458	0.43	0.68	rs11671261	C	T	101kb 5' of ZNF99		6					Ehf,Ets,HNF1,Spdef,p300			2 hits
19	22871699	23054501	0.44	0.68	rs143235804	G	A	102kb 5' of ZNF99		5					BCL,BDP1,E2F,ELF1,Ets,Hic1,MAZR,SP1,SREBP,Sin3Ak-20,TR4,WT1,YY1,Znf143			3 hits
19	22871897	23054699	0.43	0.68	rs146676454	C	T	102kb 5' of ZNF99		7								1 hit
19	22877293	23060095	0.49	0.73	rs7255375	C	G	107kb 5' of ZNF99		7					GATA,HDAC2,p300			4 hits
19	22877621	23060423	0.49	0.73	rs62120829	G	A	108kb 5' of ZNF99		7					Znf143,p300			4 hits
19	22879427	23062229	0.5	0.73	rs58977014	G	A	109kb 5' of ZNF99		7					Foxa,STAT			2 hits
19	22879889	23062691	0.49	0.73	rs11667539	C	A	110kb 5' of ZNF99		7					Dobox4,LUN-1,NF-kappaB			4 hits
19	22880924	23063726	0.49	0.73	rs7256784	A	C	111kb 5' of ZNF99		6					Irf,Mrg1::Hoxa9,Pax-2,Pax-8			3 hits
19	22881188	23063990	0.49	0.73	rs61567314	C	T	111kb 5' of ZNF99		7					SREBP			2 hits
19	22881330	23064132	0.49	0.73	rs11668871	G	C	111kb 5' of ZNF99		7					SZF1-1,Spz1			2 hits
19	22881596	23064398	0.49	0.73	rs11669667	A	G	112kb 5' of ZNF99		6					COMP1,Foxp1,HNF1,Pou2f2,TCF4			3 hits
19	22882321	23065123	0.49	0.73	rs7246529	C	T	112kb 5' of ZNF99		7					Foxc1,HNF1,Rhox11			3 hits
19	22884113	23066915	0.49	0.73	rs12608610	C	T	114kb 5' of ZNF99		7								3 hits
19	22884778	23067580	0.49	0.73	rs55925020	G	A	115kb 5' of ZNF99		7								3 hits
19	22889050	23071852	0.46	0.71	rs4932804	G	A	119kb 5' of ZNF99		7								2 hits
19	22891313	23074115	0.48	0.72	rs62120834	G	T	121kb 5' of ZNF99		7					AP-1,Pax-6,TCF4			2 hits
19	22891613	23074415	0.45	0.69	rs4932696	G	T	122kb 5' of ZNF99		6					HNF1,Hoxa4,Pax-4,Pou3f2			2 hits
19	22892977	23075779	0.46	0.71	rs12460438	C	A	122kb 3' of CTD-2291D10.2		7					AP-1,BCL,Dbx2,Foxj1,Foxo,HDAC2,HMG-IY,Hoxd8,Irf,Lhx3,Ncx,Nkx6-1,RXRA,STAT,p300			2 hits
19	22894300	23077102	0.46	0.71	rs56015704	T	G	121kb 3' of CTD-2291D10.2		4				CTCF				3 hits
19	22894375	23077177	0.48	0.72	rs142841751	AG	A	121kb 3' of CTD-2291D10.2		5				CTCF	FAC1,Foxo,HDAC2,PU.1,SPIB,Sox,TATA,Zfp105			3 hits
19	22896131	23078933	0.5	0.76	rs62122462	T	C	119kb 3' of CTD-2291D10.2		5					Foxj2,Smad3			2 hits
19	22896270	23079072	0.5	0.76	rs62122463	G	T	119kb 3' of CTD-2291D10.2		5					NF-kappaB,Pou2f2			3 hits
19	22896419	23079221	0.44	0.76	rs62122464	A	G	119kb 3' of CTD-2291D10.2		6					GR			2 hits
19	22896468	23079270	0.44	0.76	rs62122465	T	C	119kb 3' of CTD-2291D10.2		7					HP1-site-factor,ZID			3 hits
19	22896551	23079353	0.43	0.76	rs62122466	G	T	119kb 3' of CTD-2291D10.2		6					AIRE,EWSR1-FLI1,HDAC2,SP1,Smad4,Zfp105			3 hits
19	22897096	23079898	0.43	0.76	rs10408793	A	G	118kb 3' of CTD-2291D10.2		7								3 hits
19	22903215	23086017	0.51	-0.88	rs4497815	G	A	112kb 3' of CTD-2291D10.2		5								4 hits
19	22904135	23086937	0.45	0.88	rs10421901	G	A	111kb 3' of CTD-2291D10.2		7					ZBTB33			3 hits
19	22904706	23087508	0.75	0.87	rs57841869	CAA	C	110kb 3' of CTD-2291D10.2		6					Fox,Foxa,Foxd3,Foxi1,Foxj1,Foxj2,Foxk1,Foxl1,Foxo,Foxp1,Hoxa9,Pou3f2			3 hits
19	22911055	23093857	0.47	-0.9	rs1382353	T	C	104kb 3' of CTD-2291D10.2		6					Cdx,Foxf1,Foxl1,Mef2,Pou2f2,Pou3f2,TATA			4 hits
19	22911499	23094301	0.47	-0.9	rs1478458	C	T	104kb 3' of CTD-2291D10.2		6					Irx,Pou1f1,Pou2f2			4 hits
19	22912431	23095233	0.48	-0.93	rs1842018	T	C	103kb 3' of CTD-2291D10.2		6					AIRE,DMRT7,Sox,YY1		1 hit	4 hits
19	22912624	23095426	0.48	-0.93	rs10408398	A	G	102kb 3' of CTD-2291D10.2		6					E2A,Mxi1,Myf,NRSF,TAL1,TATA,Zfx			4 hits
19	22912881	23095683	0.88	0.95	rs62122471	A	G	102kb 3' of CTD-2291D10.2		7					HNF4,RAR,STAT			4 hits
19	22917652	23100454	0.42	-0.93	rs34876638	TCTC	T	97kb 3' of CTD-2291D10.2		7					CTCFL,Nrf-2			
19	22918353	23101155	0.46	-0.93	rs289280	G	A	97kb 3' of CTD-2291D10.2		7					AP-2			4 hits
19	22918885	23101687	0.46	-0.93	rs289281	T	C	96kb 3' of CTD-2291D10.2		7					Pou2f2			4 hits
19	22920680	23103482	0.48	-0.93	rs289282	T	C	94kb 3' of CTD-2291D10.2		6					Ets,NRSF,Nanog,Sin3Ak-20,Sox			4 hits
19	22921266	23104068	0.88	0.95	rs60907808	A	G	94kb 3' of CTD-2291D10.2		6					Ehf,Elf3,Elf5,Ets,Hoxb13,Hoxb9,PU.1,THAP1,YY1,p300			3 hits
19	22922807	23105609	0.45	-0.93	rs289283	T	G	92kb 3' of CTD-2291D10.2		7					PPAR			3 hits
19	22923950	23106752	0.88	0.95	rs62122474	G	C	91kb 3' of CTD-2291D10.2		7					Mtf1,Sin3Ak-20			3 hits

Supplementary Table 3. Summary of genomic annotation by HaploReg and RegulomeDB of variants with pairwise r^2 >= 0.4 with index TGCT SNPs

chr	pos (hg38)	pos (hg19)	LD (r^2)	LD (D')	variant	Ref	Alt	GENCODE genes	dbSNP func annot	RegulomeDB Score	Promoter histone marks	Enhancer histone marks	DNAse	Proteins bound	Motifs changed	NHGRI/EBI GWAS hits	GRASP QTL hits	Selected eQTL hits
19	22930362	23113164	0.46	-0.93	rs289372	C	T	85kb 3' of CTD-2291D10.2		6					DMRT3,DMRT4,DMRT5,NF-I			5 hits
19	22931336	23114138	0.47	-0.93	rs289371	A	G	84kb 3' of CTD-2291D10.2		7					Brachyury			5 hits
19	22931384	23114186	0.48	-0.93	rs289370	G	A	84kb 3' of CTD-2291D10.2		7								3 hits
19	22931428	23114230	0.46	-0.93	rs289369	T	A	84kb 3' of CTD-2291D10.2		6					Foxa,Foxp3,HDAC2,SP1			5 hits
19	22931626	23114428	0.48	-0.93	rs289368	C	A	83kb 3' of CTD-2291D10.2		7					AP-1,Foxd1			3 hits
19	22931728	23114530	0.48	-0.93	rs289367	A	T	83kb 3' of CTD-2291D10.2		6					BATF,Bach1,KAP1,Maf,NF-E2,TCF11::MafG			3 hits
19	22932082	23114884	0.46	-0.93	rs289366	G	A	83kb 3' of CTD-2291D10.2		7								3 hits
19	22934234	23117036	0.43	-0.84	rs289364	G	T	81kb 3' of CTD-2291D10.2		7					NF-kappaB			2 hits
19	22935597	23118399	0.47	-0.93	rs289362	T	C	79kb 3' of CTD-2291D10.2		7							1 hit	3 hits
19	22936129	23118931	0.47	-0.93	rs380541	C	T	79kb 3' of CTD-2291D10.2		7					NRSF,TATA			3 hits
19	22936372	23119174	0.46	-0.93	rs460636	G	A	79kb 3' of CTD-2291D10.2		6					DMRT1,Hoxd10,Myc,Pou2f2,Pou3f2			3 hits
19	22936379	23119181	0.46	-0.93	rs461762	A	G	79kb 3' of CTD-2291D10.2		6					Gm397,Nanog,Pou2f2,Pou3f3,Pou5f1,TATA			3 hits
19	22937336	23120138	0.47	-0.93	rs75395623	A	G	78kb 3' of CTD-2291D10.2		5					p53			
19	22937741	23120543	0.47	-0.93	rs5827541	CA	C	77kb 3' of CTD-2291D10.2		7					AP-1,CTCFL,Egr-1,Foxd3,Foxj1,GR,INSM1,Myc,Pou2f2			3 hits
19	22938025	23120827	0.87	0.94	rs56103105	A	T	77kb 3' of CTD-2291D10.2		7					HNF1,Pbx-1			4 hits
19	22938838	23121640	0.47	-0.93	rs453743	G	A	76kb 3' of CTD-2291D10.2		7					Foxo,Mef2,Pou2f2			3 hits
19	22938877	23121679	0.48	-0.93	rs440580	T	C	76kb 3' of CTD-2291D10.2		7					AP-1,Nanog,Pax-4,RXRA			3 hits
19	22939624	23122426	0.46	-0.93	rs424913	G	A	75kb 3' of CTD-2291D10.2		7					GR,HDAC2,Pou6f1			3 hits
19	22939845	23122647	0.44	-0.93	rs449210	C	A	75kb 3' of CTD-2291D10.2		7								3 hits
19	22940621	23123423	0.47	-0.93	rs460336	C	G	74kb 3' of CTD-2291D10.2		6					Cdx,Cdx2,Foxp1,HDAC2,HMG-IY,Hoxa9,Hoxb13,Hoxb9,Hoxd10,Irf,Isl2,Nkx6-1,Sox,Zfp105			5 hits
19	22940861	23123663	0.48	-0.93	rs462900	G	T	74kb 3' of CTD-2291D10.2		7					Myc,Pou2f2,RFX5			5 hits
19	22941943	23124745	0.47	-0.93	rs390911	A	C	73kb 3' of CTD-2291D10.2		6					STAT			5 hits
19	22942429	23125231	0.47	-0.93	rs456348	G	A	73kb 3' of CTD-2291D10.2		7					AP-4,TAL1			5 hits
19	22942542	23125344	0.46	-0.93	rs462446	T	G	73kb 3' of CTD-2291D10.2		7					DMRT2,HMG-IY,Irf,PTF1-beta,Pax-4,Pou2f2,SIX5,Sox			5 hits
19	22943284	23126086	0.47	-0.93	rs435715	G	C	72kb 3' of CTD-2291D10.2		6					Foxa,Foxp3			5 hits
19	22943434	23126236	0.46	-0.93	rs381403	C	T	72kb 3' of CTD-2291D10.2		7					Cdx,HMG-IY			5 hits
19	22944633	23127435	0.46	-0.93	rs452404	A	C	70kb 3' of CTD-2291D10.2		6					CHD2,E2F,Irf,PRDM1,RXR::LXR,SREBP			5 hits
19	22945046	23127848	0.47	-0.93	rs431585	C	A	70kb 3' of CTD-2291D10.2		7					FXR,Foxa,Foxd1,NF-kappaB,Pax-4,Spz1			5 hits
19	22945401	23128203	0.47	-0.93	rs465933	T	C	70kb 3' of CTD-2291D10.2		5								5 hits
19	22946757	23129559	0.48	-0.93	rs467101	C	T	68kb 3' of CTD-2291D10.2		7	HRT						1 hit	5 hits
19	22947311	23130113	0.48	-0.93	rs457149	A	C	68kb 3' of CTD-2291D10.2		6					GR,LBP-1			5 hits
19	22947593	23130395	0.48	-0.93	rs466223	T	C	67kb 3' of CTD-2291D10.2		7					GATA,Gfi1		1 hit	5 hits
19	22947617	23130419	0.47	-0.93	rs461390	G	C	67kb 3' of CTD-2291D10.2		7					ERalpha-a			5 hits
19	22948265	23131067	0.48	-0.93	rs464598	A	C	67kb 3' of CTD-2291D10.2		6					Mef2,TATA			5 hits
19	22948661	23131463	0.47	-0.93	rs465723	G	A	66kb 3' of CTD-2291D10.2		7								5 hits
19	22948981	23131783	0.47	-0.93	rs459820	C	T	66kb 3' of CTD-2291D10.2		7					TATA			5 hits
19	22949915	23132717	0.48	-0.93	rs457599	T	C	65kb 3' of CTD-2291D10.2		7					CTCF,NF-Y,Pou6f1,Rad21,Sox			5 hits
19	22952159	23134961	0.47	-0.93	rs146911305	C	G	63kb 3' of CTD-2291D10.2		7					HNF4,Nanog,Tel2			
19	22953030	23135832	0.88	0.95	rs58558372	C	T	62kb 3' of CTD-2291D10.2		6					Pbx-1,Rhox11,Zfp105			4 hits
19	22953272	23136074	0.43	-0.93	rs415849	C	T	62kb 3' of CTD-2291D10.2		6					Arid5a,CEBPA,Foxa,Hlx1,Hoxa10,Hoxb13			5 hits
19	22953310	23136112	0.45	-0.93	rs415650	C	T	62kb 3' of CTD-2291D10.2		7								5 hits
19	22954177	23136979	0.47	-0.93	rs462739	A	T	61kb 3' of CTD-2291D10.2		6					Irf,RAR,RXR::LXR,RXRA			5 hits
19	22954586	23137388	0.45	-0.93	rs464585	T	C	60kb 3' of CTD-2291D10.2		5								5 hits
19	22955209	23138011	0.9	0.96	rs61025974	G	A	60kb 3' of CTD-2291D10.2		6					Arnt,E2A,Gm397,Myc,TATA			4 hits
19	22955533	23138335	0.48	-0.94	rs380443	G	A	60kb 3' of CTD-2291D10.2		7					AP-2,BCL,BDP1,EBF,Irf,MAZ,PLAG1,Pax-5,STAT			5 hits
19	22957743	23140545	0.48	-0.94	rs460681	T	C	57kb 3' of CTD-2291D10.2		6					GATA			5 hits
19	22957777	23140579	0.48	-0.94	rs457741	A	G	57kb 3' of CTD-2291D10.2		7					STAT,TCF4			5 hits
19	22960289	23143091	0.42	-0.93	rs201581174	CA	C	55kb 3' of CTD-2291D10.2		6					CIZ,Dbx1,Evi-1,Foxo			3 hits
19	22960503	23143305	0.48	-0.94	rs289359	T	A	55kb 3' of CTD-2291D10.2		6					Dbx1,E2A,HNF1,Lhx3,Mef2,Pou1f1,Pou2f2			5 hits
19	22960568	23143370	0.48	-0.94	rs289358	G	C	55kb 3' of CTD-2291D10.2		7					BDP1,PU.1,ZEB1,p300			5 hits

Supplementary Table 3. Summary of genomic annotation by HaploReg and RegulomeDB of variants with pairwise r^2 >= 0.4 with index TGCT SNPs

chr	pos (hg38)	pos (hg19)	LD (r^2)	LD (D')	variant	Ref	Alt	GENCODE genes	dbSNP func annot	RegulomeDB Score	Promoter histone marks	Enhancer histone marks	DNAse	Proteins bound	Motifs changed	NHGRI/EBI GWAS hits	GRASP QTL hits	Selected eQTL hits
19	22961337	23144139	0.46	-0.94	rs34262155	AT	A	54kb 3' of CTD-2291D10.2		5					TATA			
19	22961349	23144151	0.47	-0.94	rs289357	A	C	54kb 3' of CTD-2291D10.2		5					Cdc5,TATA			5 hits
19	22961532	23144334	0.48	-0.94	rs289356	G	A	54kb 3' of CTD-2291D10.2		5					Maf,Pou3f3			5 hits
19	22961567	23144369	0.48	-0.94	rs289355	A	G	54kb 3' of CTD-2291D10.2		7					DMRT2,HNF1,PLZF			5 hits
19	22961666	23144468	0.48	-0.94	rs289354	C	G	53kb 3' of CTD-2291D10.2		7					Barx1,EWSR1-FLI1,Isl2			5 hits
19	22961787	23144589	0.48	-0.94	rs289353	C	T	53kb 3' of CTD-2291D10.2		6					CEBPB,Zec			5 hits
19	22962468	23145270	0.48	-0.94	rs289352	A	G	53kb 3' of CTD-2291D10.2		6					Bcl6b,GATA,LBP-9,NERF1a,STAT,TCF12,Tel2			5 hits
19	22962536	23145338	0.48	-0.94	rs289351	A	G	53kb 3' of CTD-2291D10.2		7					Foxp3			5 hits
19	22963530	23146332	0.47	-0.93	rs112451828	ATG	A	52kb 3' of CTD-2291D10.2		6					Foxa,Foxd3,Foxf1,Foxj1,Foxj2,Foxo,Foxp3			5 hits
19	22963533	23146335	0.42	-0.94	rs71163428	TG	T,TGT	52kb 3' of CTD-2291D10.2		6								5 hits
19	22963758	23146560	0.46	-0.94	rs289349	A	T	51kb 3' of CTD-2291D10.2		6					AP-1,Arid3a,Dbx1,Dbx2,Foxj1,Mef2,Ncx,Pou2f2,Pou6f1,TATA			5 hits
19	22964638	23147440	0.48	-0.94	rs289348	A	G	50kb 3' of CTD-2291D10.2		7					p300			5 hits
19	22965136	23147938	0.48	-0.94	rs289347	A	T	50kb 3' of CTD-2291D10.2		6					En-1,Foxc1,Nkx2,Pax-4			5 hits
19	22965198	23148000	0.48	-0.94	rs289346	T	G	50kb 3' of CTD-2291D10.2		6					AFP1,Dbx1,Foxp3,GR,HNF1,Hoxa5,Lhx3,Ncx,Pou1f1,Pou2f2,Sox			5 hits
19	22966079	23148881	0.48	-0.94	rs289345	G	A	49kb 3' of CTD-2291D10.2		6					Evi-1,GATA,Hoxa9,Mef2			5 hits
19	22966868	23149670	0.48	-0.94	rs289344	G	A	48kb 3' of CTD-2291D10.2		7					GR			5 hits
19	22967394	23150196	0.48	-0.94	rs289343	C	T	48kb 3' of CTD-2291D10.2		6					Hdx			5 hits
19	22967587	23150389	0.48	-0.94	rs289342	T	A	47kb 3' of CTD-2291D10.2		5				MAFK	GR,Irf,TATA			5 hits
19	22967653	23150455	0.48	-0.94	rs289341	T	G	47kb 3' of CTD-2291D10.2		5				MAFK	CDP,Foxd3,Mef2			5 hits
19	22967836	23150638	0.48	-0.94	rs289340	T	G	47kb 3' of CTD-2291D10.2		6					Pou1f1			5 hits
19	22968097	23150899	0.48	-0.94	rs289339	T	C	47kb 3' of CTD-2291D10.2		6					AIRE,AP-1,Cdx2,HNF1,Irf,Mef2,Pax-4,Pdx1,SIX5,STAT,Sox			5 hits
19	22968623	23151425	0.5	-0.94	rs289338	C	T	46kb 3' of CTD-2291D10.2		7					Evi-1,Foxl1,Pou2f2,Pou3f2			5 hits
19	22968765	23151567	0.5	-0.94	rs201098314	A	AAATT	46kb 3' of CTD-2291D10.2		7					AP-1,DMRT2,Dbx1,Hoxb7,Ik-2,NF-AT,NF-AT1,Ncx,Pax-4,Pou3f2,Sox,Zfp187			
19	22968988	23151790	0.48	-0.94	rs289337	G	A	46kb 3' of CTD-2291D10.2		7							1 hit	5 hits
19	22969433	23152235	0.48	-0.94	rs289336	G	C	46kb 3' of CTD-2291D10.2		7					Cdx,HMG-IY,Irx,SIX5			5 hits
19	22969561	23152363	0.47	-0.94	rs140013314	CCATA	C	46kb 3' of CTD-2291D10.2		7					Cdx,DMRT5,DMRT7,Foxd3,Foxj1,Foxp1,Irf,Pax-2,Sox,TCF11::MafG			5 hits
19	22969670	23152472	0.47	-0.94	rs289335	T	A	45kb 3' of CTD-2291D10.2		7					Evi-1,TATA			5 hits
19	22970162	23152964	0.48	-0.94	rs289334	T	C	45kb 3' of CTD-2291D10.2		7					AP-1,EBF,Nr2f2,RFX5,SETDB1		1 hit	5 hits
19	22970240	23153042	0.48	-0.94	rs289333	C	A	45kb 3' of CTD-2291D10.2		7			LNG		Pou2f2			5 hits
19	22970311	23153113	0.48	-0.94	rs10602378	GAA	G	45kb 3' of CTD-2291D10.2		7					Cdx2,HDAC2,HP1-site-factor,Sox			5 hits
19	22971634	23154436	0.48	-0.94	rs289331	T	C	43kb 3' of CTD-2291D10.2		6					HNF1,Irf			5 hits
19	22971906	23154708	0.43	-0.94	rs289330	C	A	43kb 3' of CTD-2291D10.2		7					Foxj1,Foxp1,Sox			5 hits
19	22972365	23155167	0.48	-0.94	rs289329	A	G	43kb 3' of CTD-2291D10.2		7					Pou5f1,p300			5 hits
19	22972746	23155548	0.48	-0.94	rs289328	G	C	42kb 3' of CTD-2291D10.2		6					Foxj1,Foxk1,Hoxa9,Pou3f2,Zfp105			5 hits
19	22973175	23155977	0.48	-0.94	rs289327	C	T	42kb 3' of CTD-2291D10.2		7					Evi-1,Hoxa4,Hoxa5			5 hits
19	22973460	23156262	0.48	-0.94	rs289326	G	A	42kb 3' of CTD-2291D10.2		6					GCNF,GR,Nr2f2,RXRA			5 hits
19	22973903	23156705	0.47	-0.94	rs289325	G	A	41kb 3' of CTD-2291D10.2		6					Eomes,Evi-1,Irf,Pax-3			5 hits
19	22974103	23156905	0.5	-0.94	rs289324	A	G	41kb 3' of CTD-2291D10.2		7					E2A,RP58,Znf143			5 hits
19	22974347	23157149	0.46	-0.94	rs200992356	TTTC	T	41kb 3' of CTD-2291D10.2		6					Dbx1,Dbx2,Evi-1,Hoxa10,Irf,Mef2,Ncx,Pou6f1			5 hits
19	22974413	23157215	0.48	-0.94	rs289323	T	C	41kb 3' of CTD-2291D10.2		6					BCL,Pdx1,Smad3			5 hits
19	22974468	23157270	0.48	-0.94	rs289322	G	T	41kb 3' of CTD-2291D10.2		6					DMRT3,Foxp1,Hoxa10,Hoxd10,PLZF,Pitx2,Pou2f2,Pou3f4			5 hits
19	22974479	23157281	0.48	-0.94	rs289321	T	C	41kb 3' of CTD-2291D10.2		6					Arid5a,CEBPB,Dbx1,Foxa,HNF1,Ncx,PLZF,Pou2f2,p300			5 hits

Supplementary Table 3. Summary of genomic annotation by HaploReg and RegulomeDB of variants with pairwise r^2 >= 0.4 with index TGCT SNPs

chr	pos (hg38)	pos (hg19)	LD (r^2)	LD (D')	variant	Ref	Alt	GENCODE genes	dbSNP func annot	RegulomeDB Score	Promoter histone marks	Enhancer histone marks	DNAse	Proteins bound	Motifs changed	NHGRI/EBI GWAS hits	GRASP QTL hits	Selected eQTL hits
19	22974997	23157799	0.5	-0.94	rs289320	A	T	40kb 3' of CTD-2291D10.2	3'-UTR*	7					Evi-1			5 hits
19	22975029	23157831	0.47	-0.94	rs289319	T	A	40kb 3' of CTD-2291D10.2	3'-UTR*	6					Barhl1,SRF,Tgif1			5 hits
19	22975918	23158720	0.91	0.97	rs1836017	A	T	39kb 3' of CTD-2291D10.2	synonymous*	5				KAP1,SETDB1	Cdx,Pax-6,Pax-8			4 hits
19	22976045	23158847	0.91	0.97	rs1433111	T	A	39kb 3' of CTD-2291D10.2	missense*	5					DMRT4			4 hits
19	22976684	23159486	0.5	0.94	rs289318	T	C	38kb 3' of CTD-2291D10.2	missense*	5								5 hits
19	22978495	23161297	0.48	0.94	rs289317	C	T	37kb 3' of CTD-2291D10.2	intronic*	7					CTCF,Rad21			5 hits
19	22978876	23161678	0.48	0.94	rs289316	G	A	36kb 3' of CTD-2291D10.2	intronic*	6								5 hits
19	22979171	23161973	0.48	0.94	rs289315	C	G	36kb 3' of CTD-2291D10.2	intronic*	5					ATF3,GR,NF-kappaB,Nrf1,SREBP,ZEB1			5 hits
19	22979629	23162431	0.48	0.94	rs142323343	C	CCA	35kb 3' of CTD-2291D10.2	intronic*	7					CEBPB,PEBP			5 hits
19	22979814	23162616	0.48	0.94	rs289314	G	T	35kb 3' of CTD-2291D10.2	intronic*	6					Gfi1,Maf,PTF1-beta			5 hits
19	22980541	23163343	0.48	0.94	rs289313	T	A	35kb 3' of CTD-2291D10.2	intronic*	7								5 hits
19	22982045	23164847	0.48	0.94	rs289311	A	C	33kb 3' of CTD-2291D10.2	intronic*	6					BCL,Cdx,HDAC2,Irf,Nanog,Pax-2,Pax-5,RXRA,STAT,Sox,p300			5 hits
19	22982612	23165414	0.48	0.94	rs289310	C	T	32kb 3' of CTD-2291D10.2	intronic*	7					SIX5			5 hits
19	22983501	23166303	0.48	0.94	rs289309	G	A	32kb 3' of CTD-2291D10.2	intronic*	7					Dobox4,Zfp410			5 hits
19	22983560	23166362	0.48	0.94	rs289308	C	T	32kb 3' of CTD-2291D10.2	intronic*	6					Cdx2,Foxl1,Hoxa10,Hoxb8,Nanog,Pou2f2,Pou3f2,Pou3f3,Pou5f1			5 hits
19	22984111	23166913	0.91	0.97	rs11670032	T	C	31kb 3' of CTD-2291D10.2	intronic*	6					FXR,Ik-2			4 hits
19	22984154	23166956	0.49	0.94	rs289307	C	T	31kb 3' of CTD-2291D10.2	intronic*	7					Zic			5 hits
19	22984164	23166966	0.49	0.94	rs176456	G	T	31kb 3' of CTD-2291D10.2	intronic*	7								5 hits
19	22984244	23167046	0.49	0.94	rs140897200	T	TACA	31kb 3' of CTD-2291D10.2	intronic*	7					DMRT7,Evi-1,Fox,Foxp1,HDAC2,Irf,Pou2f2,Sox,Zfp105			5 hits
19	22985486	23168288	0.48	0.94	rs289305	T	A	30kb 3' of CTD-2291D10.2	intronic*	7					Pax-5			5 hits
19	22985492	23168294	0.48	0.94	rs289304	T	A	30kb 3' of CTD-2291D10.2	intronic*	7					Pax-5			5 hits
19	22986213	23169015	0.48	0.94	rs289303	A	G	29kb 3' of CTD-2291D10.2	intronic*	6					AP-1,NF-AT,NF-AT1,SP2,TATA			5 hits
19	22986264	23169066	0.5	0.94	rs167034	C	T	29kb 3' of CTD-2291D10.2	intronic*	7					ATF3,Nkx2			5 hits
19	22987152	23169954	0.5	0.94	rs289302	G	A	28kb 3' of CTD-2291D10.2	intronic*	7					CTCF,Rad21,SMC3			5 hits
19	22988787	23171589	0.48	0.94	rs289301	C	T	26kb 3' of CTD-2291D10.2	intronic*	7								5 hits
19	22992528	23175330	0.48	0.94	rs289300	T	C	23kb 3' of CTD-2291D10.2	intronic*	6					AP-1,AP-2,BAF155,BATF,BCL,Bach1,GATA,GR,HMGN3,Irf,KAP1,Mef2,Myc,PRDM1,RXRA,STAT,TCF4,Zbtb3,p300			5 hits
19	22992949	23175751	0.48	0.94	rs289299	A	G	22kb 3' of CTD-2291D10.2	intronic*	7								5 hits
19	22993143	23175945	0.48	0.94	rs289298	G	T	22kb 3' of CTD-2291D10.2	intronic*	7								5 hits
19	22993338	23176140	0.48	0.94	rs289297	T	C	22kb 3' of CTD-2291D10.2	intronic*	7					ERalpha-a,Esr2,SRF			5 hits
19	22993565	23176367	0.48	0.94	rs289295	C	T	22kb 3' of CTD-2291D10.2	intronic*	7					Irf			5 hits
19	22993971	23176773	0.48	0.94	rs289294	A	G	21kb 3' of CTD-2291D10.2	intronic*	7								5 hits
19	22995042	23177844	0.5	0.94	rs289293	T	C	20kb 3' of CTD-2291D10.2	intronic*	7					Sox,TATA			5 hits
19	22995087	23177889	0.48	0.94	rs289291	T	C	20kb 3' of CTD-2291D10.2	intronic*	6					GR,Pou3f2,YY1			5 hits
19	22996071	23178873	0.48	0.94	rs289290	C	T	19kb 3' of CTD-2291D10.2	intronic*	7					DMRT4,DMRT5			5 hits
19	22996716	23179518	0.91	0.97	rs62124389	A	G	18kb 3' of CTD-2291D10.2	intronic*	6					AP-1,DMRT5,DMRT7,Foxo,Foxp3,Pou3f2,Sox			4 hits
19	22996758	23179560	0.49	0.93	rs71762313	7-mer	T	18kb 3' of CTD-2291D10.2	intronic*	6					Evi-1,Foxl1,Foxq1,Mef2,Nanog,Pou1f1,Pou2f2,TATA,TEF			5 hits
19	22997898	23180700	0.48	0.94	rs399132	C	A	17kb 3' of CTD-2291D10.2	intronic*	6					DMRT7,Foxa,RXRA,TCF4			5 hits
19	22998186	23180988	0.47	0.93	rs289288	C	T	17kb 3' of CTD-2291D10.2	intronic*	7					AhR::Arnt,Arnt			5 hits
19	22998445	23181247	0.46	0.92	rs289287	C	T	17kb 3' of CTD-2291D10.2	intronic*	7					GR			5 hits
19	22999578	23182380	0.91	0.97	rs2132818	T	C	15kb 3' of CTD-2291D10.2	intronic*	6		ESC			Dlx3,Hoxa5,Hoxa7,Hoxb6,Hoxc6,Lhx3,Nkx6-1,Pax-6,Pou2f2,Pou5f1		1 hit	3 hits
19	23000722	23183524	0.5	0.96	rs2453972	G	A	14kb 3' of CTD-2291D10.2	intronic*	7					DMRT1,DMRT7,HNF1,ZEB1			5 hits
19	23000739	23183541	0.5	0.96	rs2463795	G	A	14kb 3' of CTD-2291D10.2	intronic*	6					E2A,Ets,Lmo2-complex,Myf,ZEB1			5 hits
19	23001139	23183941	0.5	0.96	rs291769	T	C,G	14kb 3' of CTD-2291D10.2	intronic*	7								5 hits
19	23001275	23184077	0.5	0.96	rs2548897	T	G	14kb 3' of CTD-2291D10.2	intronic*	7								5 hits
19	23001307	23184109	0.5	0.96	rs1908942	A	G	14kb 3' of CTD-2291D10.2	intronic*	6					Arid5a,Foxj2,Pou2f2,Pou4f3,Pou6f1,TATA			5 hits

Supplementary Table 3. Summary of genomic annotation by HaploReg and RegulomeDB of variants with pairwise r^2 >= 0.4 with index TGCT SNPs

chr	pos (hg38)	pos (hg19)	LD (r^2)	LD (D')	variant	Ref	Alt	GENCODE genes	dbSNP func annot	RegulomeDB Score	Promoter histone marks	Enhancer histone marks	DNAse	Proteins bound	Motifs changed	NHGRI/EBI GWAS hits	GRASP QTL hits	Selected eQTL hits
19	23002209	23185011	0.5	0.96	rs291770	A	G	13kb 3' of CTD-2291D10.2	intronic*	6	ESC, GI, HRT				LUN-1			5 hits
19	23002361	23185163	0.5	0.96	rs10418414	G	A	13kb 3' of CTD-2291D10.2	intronic*	6					CIZ,HDAC2,PTF1-beta			5 hits
19	23003395	23186197	0.5	0.96	rs188343	G	A	12kb 3' of CTD-2291D10.2		4	STRM, FAT, VAS, BRN, GI, PANC, HRT, OVRY, MUS		ADRL,HRT,LIV		Cphx,Obox6			5 hits
19	23004765	23187567	0.5	0.96	rs771353	G	A	10kb 3' of CTD-2291D10.2		7					Crx,LBP-1			5 hits
19	23005103	23187905	0.5	0.96	rs771354	C	A	10kb 3' of CTD-2291D10.2		6					ERalpha-a,Esr2,Hic1			5 hits
19	23005706	23188508	0.51	0.96	rs1066011	C	A	9.4kb 3' of CTD-2291D10.2		7					AhR::Arnt,Arnt,Myb			5 hits
19	23005721	23188523	0.51	0.96	rs1066012	G	A	9.4kb 3' of CTD-2291D10.2		7					Klf4			5 hits
19	23005753	23188555	0.5	0.96	rs1066013	G	A	9.3kb 3' of CTD-2291D10.2		7					SZF1-1,Spz1,ZBTB33			5 hits
19	23006145	23188947	0.5	0.94	rs1066014	T	G	8.9kb 3' of CTD-2291D10.2		6					AIRE,Barhl1,Cdx,Fox,Foxa,Foxd3,Foxp1,HDAC2,HMG-IY,Hoxa9,Hoxb13,Hoxb9,Hoxd10,Pax-4,Pbx-1,SP2			5 hits
19	23006317	23189119	0.49	0.94	rs200585626	A	ATG	8.8kb 3' of CTD-2291D10.2		7					DMRT3,Pou1f1,Pou5f1			5 hits
19	23006318	23189120	0.49	0.96	rs35895462	T	TGC	8.8kb 3' of CTD-2291D10.2		7					DMRT3			5 hits
19	23006586	23189388	0.51	0.96	rs1066015	C	A	8.5kb 3' of CTD-2291D10.2		7					Foxp1,GR,HDAC2,HMG-IY,Irf,p300			5 hits
19	23007166	23189968	0.49	0.96	rs1676465	C	T	7.9kb 3' of CTD-2291D10.2		6					Evi-1,Foxp1,HDAC2,Irf,STAT,Zfp105,p300			5 hits
19	23007904	23190706	0.5	0.96	rs1729043	A	G	7.2kb 3' of CTD-2291D10.2		7					ERalpha-a,Mrg1::Hoxa9		1 hit	5 hits
19	23008188	23190990	0.5	0.96	rs1645772	A	G	6.9kb 3' of CTD-2291D10.2		6					DEC,LXR,Nkx2			5 hits
19	23008732	23191534	0.5	0.96	rs2927369	A	C	6.3kb 3' of CTD-2291D10.2		6					Hoxd10,STAT			5 hits
19	23008970	23191772	0.5	0.96	rs2935435	T	C	6.1kb 3' of CTD-2291D10.2		6					Obox3,Pax-8			5 hits
19	23009228	23192030	0.43	0.86	rs200103846	TCA	T	5.8kb 3' of CTD-2291D10.2		7					FAC1,Foxp1,RREB-1,Zfp105			4 hits
19	23009737	23192539	0.5	0.96	rs2963060	C	T	5.3kb 3' of CTD-2291D10.2		7			ESDR		GR,Pax-2,Pax-8,SRF			5 hits
19	23009876	23192678	0.43	0.88	rs2548894	T	G	5.2kb 3' of CTD-2291D10.2		7					AP-1,Myf			4 hits
19	23009909	23192711	0.51	0.96	rs2645875	T	A	5.2kb 3' of CTD-2291D10.2		6					Cdx,Dbx1,Fox,Foxp1,HNF1,Mef2,Nkx6-1,PLZF,Pou2f2,TATA			5 hits
19	23011661	23194463	0.5	0.96	rs2081175	T	C	3.4kb 3' of CTD-2291D10.2		6					ERalpha-a,HNF4,LXR,PPAR,RORalpha1			5 hits
19	23011785	23194587	0.49	0.96	rs2101921	T	A	3.3kb 3' of CTD-2291D10.2		7								5 hits
19	23012292	23195094	0.5	0.96	rs2173179	A	G	2.8kb 3' of CTD-2291D10.2		6					Pou2f2			5 hits
19	23013070	23195872	0.5	0.96	rs2548890	C	T	2kb 3' of CTD-2291D10.2		7								5 hits
19	23013654	23196456	0.5	0.96	rs2935437	A	C	1.4kb 3' of CTD-2291D10.2		7					GR			5 hits
19	23013871	23196673	0.51	0.96	rs2963064	T	C	1.2kb 3' of CTD-2291D10.2		6					Ets,Mxi1,Myf,Pitx2,ZEB1,Znf143			5 hits
19	23013894	23196696	0.5	0.96	rs2935438	C	T	1.2kb 3' of CTD-2291D10.2		6					CACD,Klf4,Pou2f2			5 hits
19	23014518	23197320	0.49	0.96	rs2935439	A	G	556bp 3' of CTD-2291D10.2		7								5 hits
19	23015301	23198103	0.5	0.96	rs290582	A	G	CTD-2291D10.2		6					ATF3,Myf,ZEB1		1 hit	5 hits
19	23015635	23198437	0.5	0.96	rs290583	A	G	CTD-2291D10.2		6					Nanog,SIX5			5 hits
19	23015674	23198476	0.49	0.94	rs290584	A	T	CTD-2291D10.2		7								5 hits
19	23016638	23199440	0.49	0.94	rs80225251	G	A	CTD-2291D10.2		6			PLCNT		Foxq1,ZEB1			
19	23016639	23199441	0.49	0.94	rs1645768	G	A	CTD-2291D10.2		6			PLCNT		Foxq1,PRDM1			5 hits
19	23016898	23199700	0.5	0.96	rs24833	A	G	CTD-2291D10.2		6					CDP,SRF			5 hits
19	23017251	23200053	0.5	0.96	rs158691	T	C	CTD-2291D10.2		7					Brachyury,RREB-1			5 hits
19	23017866	23200668	0.5	0.96	rs158692	C	T	CTD-2291D10.2		7					CACD,GLI			5 hits
19	23018005	23200807	0.51	0.96	rs158693	C	T	CTD-2291D10.2		7					CACD			5 hits
19	23018861	23201663	0.5	0.96	rs158577	T	G	CTD-2291D10.2		7					HNF4,RXRA			5 hits
19	23018982	23201784	0.43	0.88	rs290585	A	G	CTD-2291D10.2		6					Foxp1,HDAC2,Pax-4			5 hits
19	23019577	23202379	0.5	0.96	rs290586	G	A	CTD-2291D10.2		6					Evi-1			5 hits
19	23019974	23202776	0.51	0.96	rs158694	A	G	CTD-2291D10.2		7								5 hits
19	23020559	23203361	0.5	0.96	rs290587	A	G	CTD-2291D10.2		7					RFX5			5 hits
19	23020694	23203496	0.96	1	rs55774410	A	G	CTD-2291D10.2		6					HMG-IY,Hdx,PPAR,RFX5			4 hits
19	23020769	23203571	0.5	0.96	rs158695	C	T	CTD-2291D10.2		7					Cdx2,Hoxb9,Mef2			5 hits
19	23021289	23204091	0.96	1	rs62124391	G	C	CTD-2291D10.2		7					Brachyury,Egr-1,NRSF,Sin3Ak-20			3 hits
19	23022382	23205184	1	1	rs58521262	G	A	CTD-2291D10.2		7					Foxm1,Smad			3 hits
19	23024584	23207386	0.51	0.96	rs291772	T	C	886bp 5' of CTD-2291D10.2		7					TCF12		1 hit	5 hits
19	23025296	23208098	0.5	0.96	rs291773	T	C	1.6kb 5' of CTD-2291D10.2		5					Glis2,HNF4,TR4			5 hits
19	23025713	23208515	0.48	0.96	rs2645876	C	T	2kb 5' of CTD-2291D10.2		7					RREB-1			5 hits

Supplementary Table 3. Summary of genomic annotation by HaploReg and RegulomeDB of variants with pairwise r^2 >= 0.4 with index TGCT SNPs

chr	pos (hg38)	pos (hg19)	LD (r^2)	LD (D')	variant	Ref	Alt	GENCODE genes	dbSNP func annot	RegulomeDB Score	Promoter histone marks	Enhancer histone marks	DNAse	Proteins bound	Motifs changed	NHGRI/EBI GWAS hits	GRASP QTL hits	Selected eQTL hits
19	23026398	23209200	0.5	0.96	rs291774	T	C	2.7kb 5' of CTD-2291D10.2		6					Barhl1,Dlx5,Egr-1,En-1,Esx1,Gbx1,Gbx2,Hlxb9,Isx,Lhx4,Lhx8,Msx2,Nkx1-1,Nobox,Phox2a,Prrx2,Vax2			5 hits
19	23026435	23209237	0.5	0.96	rs1645767	A	G	2.7kb 5' of CTD-2291D10.2		7					Eomes,RBP-Jkappa			5 hits
19	23026439	23209241	0.51	0.96	rs1645766	C	A	2.7kb 5' of CTD-2291D10.2		6					Brachyury,DEC,Eomes,Nanog			5 hits
19	23026569	23209371	0.94	0.97	rs10421332	G	A	2.9kb 5' of CTD-2291D10.2		7					ZEB1,Znf143			2 hits
19	23026624	23209426	0.49	0.94	rs291775	T	C	2.9kb 5' of CTD-2291D10.2		5					CCNT2,HNF4,INSM1,Pou2f2,RXRA,Rad21,SMC3,SP1,ZNF219			5 hits
19	23026980	23209782	0.51	0.96	rs167101	A	T	3.3kb 5' of CTD-2291D10.2		7					Elf5,PU.1			5 hits
19	23027181	23209983	0.51	0.96	rs291776	A	G	3.5kb 5' of CTD-2291D10.2		7					NF-kappaB			5 hits
19	23027538	23210340	0.96	1	rs56397003	C	G	3.8kb 5' of CTD-2291D10.2		7					Smad			3 hits
19	23028009	23210811	0.51	0.96	rs2645877	G	A	4.3kb 5' of CTD-2291D10.2		7					Pou5f1			5 hits
19	23028144	23210946	0.51	0.96	rs2645878	G	A	4.4kb 5' of CTD-2291D10.2		7					Ets,Nanog,Pax-5,RFX5,STAT			5 hits
19	23028226	23211028	0.51	0.96	rs2548888	C	A	4.5kb 5' of CTD-2291D10.2		6					CDP,CEBPA,DMRT4,Maf,Pou2f2,TCF11::MafG,TCF12			5 hits
19	23028369	23211171	0.51	0.96	rs2935440	G	A	4.7kb 5' of CTD-2291D10.2		7					NF-I			5 hits
19	23028393	23211195	0.5	0.96	rs2935441	T	C	4.7kb 5' of CTD-2291D10.2		7					CDP,HNF1			5 hits
19	23028515	23211317	0.51	0.96	rs2548887	T	C	4.8kb 5' of CTD-2291D10.2		7					Egr-1,LUN-1			5 hits
19	23029760	23212562	0.5	0.96	rs2088374	A	G	6.1kb 5' of CTD-2291D10.2		7					EWSR1-FLI1,PPAR,RXRA			5 hits
19	23030131	23212933	0.51	0.96	rs2548898	G	A	6.4kb 5' of CTD-2291D10.2		7					STAT			5 hits
19	23030200	23213002	0.5	0.96	rs2645880	A	G	6.5kb 5' of CTD-2291D10.2		7					THAP1,ZBTB7A			5 hits
19	23030228	23213030	0.51	0.96	rs1645776	T	C	6.5kb 5' of CTD-2291D10.2		7					BDP1,Roaz			5 hits
19	23030612	23213414	0.49	0.96	rs2645881	C	G	6.9kb 5' of CTD-2291D10.2		7					Nr2f2			5 hits
19	23030632	23213434	0.5	0.96	rs1676468	T	C	6.9kb 5' of CTD-2291D10.2		7					Foxp1,Maf,TATA			5 hits
19	23031560	23214362	0.49	0.96	rs2963072	T	C	7.9kb 5' of CTD-2291D10.2		7					NRSF			5 hits
19	23031847	23214649	0.51	0.96	rs2935443	G	C	8.1kb 5' of CTD-2291D10.2		6					Arnt,BHLHE40,E2A,Myc,RAR,SIRT6			5 hits
19	23032558	23215360	0.49	0.96	rs12985585	G	A	8.9kb 5' of CTD-2291D10.2		6					ATF3,Nkx2,SREBP			5 hits
19	23032870	23215672	0.49	0.94	rs112982213	CATT	C	9.2kb 5' of CTD-2291D10.2		6					GR,LF-A1,Pax-4,Sox			
19	23033043	23215845	0.49	0.96	rs1645775	G	A	9.3kb 5' of CTD-2291D10.2		7		IPSC			CACD,NF-kappaB			5 hits
19	23033301	23216103	0.96	1	rs62121598	G	C	9.6kb 5' of CTD-2291D10.2		7		IPSC, ESC			Ets,Spdef,TFII-I			3 hits
19	23033654	23216456	0.51	0.96	rs12978716	C	T	10kb 5' of CTD-2291D10.2		7		IPSC			LXR			5 hits
19	23033865	23216667	0.48	0.94	rs1645774	C	T	10kb 5' of CTD-2291D10.2		5		IPSC	ESC		ATF2,Myc,Nanog,Pou2f2,Pou3f2,Pou3f3,Pou5f1,Sox,TATA			5 hits
19	23034189	23216991	0.48	0.94	rs10410470	T	C	10kb 5' of CTD-2291D10.2		7					HIF1,Hand1,Myc,Smad			5 hits
19	23037049	23219851	0.95	1	rs56025038	G	C	13kb 5' of CTD-2291D10.2		7					Evi-1,Foxo,GATA,Mef2			2 hits
19	23037106	23219908	0.48	0.94	rs11458122	C	CT	13kb 5' of CTD-2291D10.2		6					CCNT2,Cart1,GATA,HMG-IY,IRC900814,Maf,Nanog,Pou2f2,Sp100,TAL1			5 hits
19	23037515	23220317	0.49	0.94	rs290581	G	A	14kb 5' of CTD-2291D10.2		7		ESC, HRT			Mef2,Pou2f2,SRF,THAP1			5 hits
19	23037940	23220742	0.49	0.94	rs290580	T	C	14kb 5' of CTD-2291D10.2		6		HRT			AP-1,p53			5 hits
19	23038265	23221067	0.49	0.94	rs290579	T	C	15kb 5' of CTD-2291D10.2		5		ESC, HRT	HRT		AP-1,Gfi1,TATA			5 hits
19	23038687	23221489	0.49	0.94	rs290578	T	G	15kb 5' of CTD-2291D10.2		7			HRT					5 hits
19	23038977	23221779	0.49	0.94	rs290577	C	T	15kb 5' of CTD-2291D10.2		6					Maf,Zbtb3			5 hits
19	23039358	23222160	0.49	0.94	rs60241495	C	G,T	15kb 3' of CTD-2291D10.1		6								
19	23039618	23222420	0.49	0.94	rs1841805	T	G	15kb 3' of CTD-2291D10.1		6					DMRT3,Foxp3,Pou3f2			5 hits
19	23040422	23223224	0.49	0.94	rs2645883	T	C	14kb 3' of CTD-2291D10.1		6					ERalpha-a,SEF-1,SP1,TR4,ZBRK1			5 hits
19	23041690	23224492	0.49	0.94	rs918644	G	A	13kb 3' of CTD-2291D10.1		7			IPSC		LUN-1,Zfp410,p300			5 hits
19	23044455	23227257	0.95	1	rs11668185	A	T	10kb 3' of CTD-2291D10.1		7								2 hits
19	23044693	23227495	0.49	0.94	rs1676464	A	G	10kb 3' of CTD-2291D10.1		6					Brachyury,Mef2			5 hits
19	23045280	23228082	0.94	0.99	rs2017779	C	T	9.5kb 3' of CTD-2291D10.1		6			KID		AP-1,BHLHE40,GATA,Myc,Nrf1,RFX5,SIRT6			2 hits
19	23045287	23228089	0.49	0.94	rs2927365	C	T	9.5kb 3' of CTD-2291D10.1		6			KID		BHLHE40,Mxi1,RFX5			5 hits
19	23046125	23228927	0.49	0.94	rs1020912	A	C	8.7kb 3' of CTD-2291D10.1		7								5 hits
19	23046474	23229276	0.49	0.94	rs2935449	G	C	8.3kb 3' of CTD-2291D10.1		7					AP-4,E2A,LBP-1,ZEB1			4 hits
19	23047160	23229962	0.5	0.94	rs2927366	A	G	7.7kb 3' of CTD-2291D10.1		6					DMRT2,DMRT5,DMRT7,Foxp3,NF-AT,Pax-4			5 hits
19	23047317	23230119	0.49	0.94	rs2927367	A	G	7.5kb 3' of CTD-2291D10.1		7							1 hit	5 hits

Supplementary Table 3. Summary of genomic annotation by HaploReg and RegulomeDB of variants with pairwise r^2 >= 0.4 with index TGCT SNPs

chr	pos (hg38)	pos (hg19)	LD (r^2)	LD (D')	variant	Ref	Alt	GENCODE genes	dbSNP func annot	RegulomeDB Score	Promoter histone marks	Enhancer histone marks	DNAse	Proteins bound	Motifs changed	NHGRI/EBI GWAS hits	GRASP QTL hits	Selected eQTL hits
19	23047743	23230545	0.47	0.93	rs2935450	G	A	7.1kb 3' of CTD-2291D10.1		6					HDAC2,Irf,STAT			4 hits
19	23047905	23230707	0.48	0.94	rs2935451	C	T	6.9kb 3' of CTD-2291D10.1		6					Arnt,BHLHE40,HIF1::Arnt,Mxi1,Myc,SIRT6			4 hits
19	23048147	23230949	0.47	0.89	rs35598049	TGG	T	6.7kb 3' of CTD-2291D10.1		7					AP-1,PPAR,SRF			4 hits
19	23048597	23231399	0.48	0.94	rs1381880	A	C,G	6.2kb 3' of CTD-2291D10.1		6			MUS					4 hits
19	23049405	23232207	0.49	0.94	rs67098980	GT	G	5.4kb 3' of CTD-2291D10.1		6		PLCNT	PLCNT		Myb			3 hits
19	23049683	23232485	0.5	0.94	rs2927368	T	A	5.1kb 3' of CTD-2291D10.1		7		PLCNT	PLCNT					4 hits
19	23050245	23233047	0.95	1	rs2362806	G	A	4.6kb 3' of CTD-2291D10.1		7					ATF3,NRSF,Znf143			3 hits
19	23050313	23233115	0.94	1	rs1551844	A	G	4.5kb 3' of CTD-2291D10.1		6					EWSR1-FLI1,Foxp1,Irf			2 hits
19	23052965	23235767	0.77	1	rs58704317	C	T	1.9kb 3' of CTD-2291D10.1		7		PLCNT	BLD		HNF4			3 hits
19	23055889	23238691	0.77	1	rs55784046	G	A	CTD-2291D10.1		7		PLCNT			Cdx			3 hits
19	23056338	23239140	0.77	1	rs60836997	G	A	CTD-2291D10.1		7		PLCNT						2 hits
19	23058478	23241280	0.74	0.98	rs56231779	A	G	CTD-2291D10.1		7					ATF3,Brachyury,E2A,Lmo2-complex,Myf,NRSF,Sin3Ak-20,TCF12,TLX1::NFIC,ZEB1			2 hits
19	23058484	23241286	0.72	0.95	rs56221424	T	C	CTD-2291D10.1		7								2 hits
19	23724828	23907630	0.42	0.7	rs4449070	G	T	14kb 3' of ZNF681		7	ESDR, ESC	ESC, ESDR, IPSC, SKIN, PLCNT, BLD			CDP,LBP-1			7 hits
19	23856756	24039558	0.41	0.98	rs388939	G	A	29kb 3' of RPSAP58		7								
19	23860017	24042819	0.43	1	rs387560	C	T	32kb 3' of RPSAP58		6					DMRT2,SIX5			
19	23860095	24042897	0.43	1	rs450542	T	G	32kb 3' of RPSAP58		7					HP1-site-factor,RAR			
19	23860388	24043190	0.43	1	rs386273	C	T	32kb 3' of RPSAP58		6					HDAC2,NF-AT1,RBP-Jkappa			
19	23862907	24045709	0.42	0.94	rs251752	T	G	35kb 3' of RPSAP58		6					Evi-1,Fox,Foxa,Foxd3,Foxf1,Foxi1,Foxj1,Foxj2,Foxl1,Foxp1,HDAC2,Irf,RREB-1,Sox,p300			
19	23864558	24047360	0.43	1	rs251750	C	A	36kb 3' of RPSAP58		7					Pbx3,YY1			
19	23864700	24047502	0.43	1	rs251749	A	T	37kb 3' of RPSAP58		6					Cdx2,Dbx1,Foxa,Foxl1,Foxo,Hoxa5,Hoxa9,Mef2,Ncx,PLZF,Pou3f2,Sox,TATA,TEF			
19	23865187	24047989	0.43	1	rs251747	C	G	37kb 3' of RPSAP58		7		ESDR, PLCNT			HP1-site-factor			
19	23867246	24050048	0.43	1	rs251746	A	T	39kb 3' of RPSAP58		7					Otx2			
19	23868026	24050828	1	1	rs34601376	A	T	40kb 3' of RPSAP58		3a			IPSC,SKIN,PLCNT	CTCF,RAD21	NF-E2,Rad21			
19	23875776	24058578	0.43	0.97	rs36078717	G	A	39kb 5' of ZNF726		6					Foxq1,Maf			
19	23877904	24060706	0.42	0.88	rs34361340	C	A	37kb 5' of ZNF726		7					GATA,NRSF,p53			
19	23912368	24095170	0.56	0.79	rs35718556	C	T	2.5kb 5' of ZNF726		6		BRN			HNF4,Pitx2,SETDB1			
X	154307767	153536119	1	1	rs17336718	C	T	TKTL1	intronic	5		FAT, BLD, BRN, MUS	BLD,KID					

* This region corresponds to *ZNF728* as seen in the UCSD Genome Browser, assessed August 19, 2016.

Supplementary Table 4a. TGCT association results for conditional analyses among independent SNPs for 9p24.3 locus

SNP	LOCATION	GROUP	CATEGORY	INFO	CONTROLS	CASES	REFERENCE ALLELE	EFFECT ALLELE	FFECT ALLELE FREQUENC		OR	CI	P	P_{het}	I^2
									CONTROL	CASE					
rs755383[a]	863635	NCI	genotyped	1.00	1056	582	C	T	0.62	0.71	1.35	(1.12-1.64)	2.16E-03		
rs755383[a]	863635	UK	genotyped	1.00	4946	986	C	T	0.63	0.73	1.32	(1.16-1.49)	1.66E-05		
rs755383[a]	863635	Sweden	genotyped	1.00	6687	1326	C	T	0.60	0.69	1.26	(1.11-1.42)	3.39E-04		
rs755383[a]	863635	PENN	imputed	0.90	919	481	C	T	0.62	0.72	1.24	(1.00-1.54)	5.04E-02		
rs755383[a]	863635	Combined			13608	3375			0.61	0.71	1.29	(1.20-1.39)	3.28E-11	0.89	0.0
rs7040024[b]	845516	NCI	imputed	0.99	1055	582	A	C	0.25	0.19	0.81	(0.64-1.01)	6.49E-02		
rs7040024[b]	845516	UK	imputed	0.96	4945	985	A	C	0.24	0.16	0.71	(0.61-0.82)	8.93E-06		
rs7040024[b]	845516	Sweden	genotyped	1.00	6687	1326	A	C	0.25	0.19	0.91	(0.79-1.05)	2.12E-01		
rs7040024[b]	845516	PENN	imputed	1.00	919	481	A	C	0.27	0.17	0.68	(0.53-0.86)	1.67E-03		
rs7040024[b]	845516	Combined			13606	3374			0.25	0.18	0.79	(0.72-0.86)	1.97E-07	0.06	60.0
rs55873183[c]	878563	NCI	imputed	0.73	1055	581	A	G	0.06	0.07	1.10	(0.76-1.59)	6.03E-01		
rs55873183[c]	878563	UK	imputed	0.82	4945	985	A	G	0.06	0.09	1.43	(1.15-1.77)	1.16E-03		
rs55873183[c]	878563	Sweden	imputed	0.81	6687	1326	A	G	0.07	0.11	1.77	(1.44-2.16)	3.61E-08		
rs55873183[c]	878563	PENN	imputed	0.73	919	481	A	G	0.06	0.09	1.59	(1.10-2.30)	1.35E-02		
rs55873183[c]	878563	Combined			13606	3373			0.07	0.09	1.53	(1.34-1.74)	9.70E-11	0.15	44.4

[a] PMID: 20543847.

[b] PMID: 21551455.

[c] A teritiary signal for the known locus.

Supplementary Table 4b. Linkage disequilibrium among three independent TGCT SNPs in 9p24.3 locus

r^2	rs7040024	rs755383	rs55873183[a]
rs7040024[a]	1.00		
rs755383[b]	0.38	1.00	
rs55873183[c]	0.029	0.061	1.00

[a] PMID: 21551455.

[b] PMID: 20543847.

[c] A tertiary signal for the known region.

Supplementary Table 5a. TGCT association results for conditional analyses among independent SNPs for 19p12 locus

SNP	LOCATION	GROUP	CATEGORY	INFO	CONTROLS	CASES	REFERENCE ALLELE	EFFECT ALLELE	EFFECT ALLELE FREQUENCY		OR	CI	P	P_{het}	I^2
									CONTROL	CASE					
rs2194275*	24021327	NCI	imputed	0.82	1055	581	G	A	0.18	0.15	0.76	(0.60-0.94)	1.39E-02		
rs2194275*	24021327	UK	imputed	0.96	4946	985	G	A	0.18	0.15	0.82	(0.72-0.94)	4.87E-03		
rs2194275*	24021327	Sweden	imputed	0.87	6687	1326	G	A	0.17	0.14	0.72	(0.62-0.83)	3.55E-06		
rs2194275*	24021327	PENN	imputed	0.84	919	481	G	A	0.17	0.13	0.74	(0.58-0.93)	1.06E-02		
rs2194275*	24021327	Combined			13607	3373			0.17	0.14	0.76	(0.70-0.83)	2.57E-10	0.56	0.0
rs34601376	24050828	NCI	imputed	0.84	1055	581	A	T	0.22	0.22	0.97	(0.79-1.19)	7.60E-01		
rs34601376	24050828	UK	imputed	0.92	4945	985	A	T	0.20	0.24	1.18	(1.04-1.34)	8.85E-03		
rs34601376	24050828	Sweden	imputed	0.87	6687	1326	A	T	0.20	0.24	1.27	(1.12-1.45)	2.41E-04		
rs34601376	24050828	PENN	imputed	0.83	919	481	A	T	0.19	0.23	1.27	(1.02-1.58)	3.02E-02		
rs34601376	24050828	Combined			13606	3373			0.20	0.23	1.19	(1.10-1.28)	8.69E-06	0.15	44.0
rs58521262	23205184	NCI	imputed	0.99	1056	581	G	A	0.15	0.11	0.68	(0.55-0.85)	5.84E-04		
rs58521262	23205184	UK	imputed	1.00	4946	986	G	A	0.14	0.11	0.75	(0.65-0.87)	1.36E-04		
rs58521262	23205184	Sweden	imputed	0.99	6687	1326	G	A	0.17	0.14	0.75	(0.65-0.86)	2.11E-05		
rs58521262	23205184	PENN	imputed	0.98	919	481	G	A	0.15	0.12	0.80	(0.64-1.01)	5.60E-02		
rs58521262	23205184	Combined			13608	3374			0.16	0.12	0.75	(0.69-0.81)	7.10E-12	0.77	0.0
rs73019876	22267849	NCI	imputed	0.93	1055	581	T	G	0.45	0.42	0.89	(0.76-1.04)	1.35E-01		
rs73019876	22267849	UK	imputed	0.96	4945	985	T	G	0.45	0.41	0.85	(0.77-0.94)	1.07E-03		
rs73019876	22267849	Sweden	imputed	0.95	6687	1326	T	G	0.43	0.41	0.86	(0.78-0.95)	4.29E-03		
rs73019876	22267849	PENN	imputed	0.95	919	481	T	G	0.51	0.49	0.91	(0.78-1.06)	2.40E-01		
rs73019876	22267849	Combined			13606	3373			0.45	0.42	0.87	(0.82-0.92)	3.02E-06	0.88	0.0

[a] rs2194275 represents the previously published SNP rs2195987 (r^2=0.69) (PMID: 25877299).

Supplementary Table 5b. Linkage Disequilibrium among four TGCT independent SNPs in 19p12 locus

r^2	rs73019876	rs58521262	rs2194275[a]	rs34601376
rs73019876	1.00			
rs58521262	0.001	1.00		
rs2194275[a]	0.007	0.036	1.00	
rs34601376	0.010	0.030	0.044	1.00

[a] rs2194275 represents the previously published SNP rs2195987 (r^2=0.69) (PMID: 25877299).

Supplementary Table 6. Comparison of allele frequencies by population for all known and novel TGCT SNPs*

CYTOBAND	SNP	GENE NEIGHBORHOOD	Race	Allele 1	Allele 2	Allele Freq 1	Allele Freq 2	Global P-value	Pairwise P-values			
										AFR	AMR	ASN
1q22	rs2072499	*KIAA0446*	AFR	A	***G*** †	0.33	0.67	1.83E-66	AFR			
		SLC25A44	AMR	A	***G***	0.67	0.33		AMR	2.07E-23		
			ASN	A	***G***	0.85	0.15		ASN	2.14E-66	6.37E-10	
			EUR	A	***G***	0.64	0.36		EUR	3.07E-26	2.11E-01	1.66E-17
1q24.1	rs3790672	*UCK2*	AFR	***C***	T	0.07	0.93	9.77E-59	AFR			
			AMR	***C***	T	0.40	0.60		AMR	4.65E-31		
			ASN	***C***	T	0.53	0.47		ASN	2.04E-57	1.04E-04	
			EUR	***C***	T	0.28	0.72		EUR	4.85E-19	3.91E-05	7.73E-21
2q14.2	rs2713206	*TFCP2L1*	AFR	C	***T***	0.81	0.19	6.62E-18	AFR			
			AMR	C	***T***	0.83	0.17		AMR	4.79E-01		
			ASN	C	***T***	0.62	0.38		ASN	4.15E-11	3.52E-11	
			EUR	C	***T***	0.81	0.19		EUR	9.71E-01	4.25E-01	9.68E-14
3p24.3	rs10510452	*DAZL*	AFR	***A***	G	0.93	0.07	6.47E-27	AFR			
			AMR	***A***	G	0.78	0.22		AMR	6.05E-11		
			ASN	***A***	G	0.88	0.12		ASN	2.70E-03	5.85E-05	
			EUR	***A***	G	0.70	0.30		EUR	1.25E-22	7.95E-03	3.13E-14
3q23	rs11705932	*TFDP2*	AFR	***C***	T	0.76	0.24	1.25E-08	AFR			
		DKFZp434G222	AMR	***C***	T	0.85	0.15		AMR	5.87E-04		
			ASN	***C***	T	0.70	0.30		ASN	2.73E-02	5.80E-08	
			EUR	***C***	T	0.81	0.19		EUR	2.05E-02	9.12E-02	1.02E-06
3q25.31	rs1510272	*SSR3*	AFR	***C***	T	0.77	0.23	3.58E-02	AFR			
		TIPARP	AMR	***C***	T	0.78	0.22		AMR	7.12E-01		
			ASN	***C***	T	0.70	0.30		ASN	1.90E-02	1.22E-02	
			EUR	***C***	T	0.74	0.26		EUR	2.83E-01	1.72E-01	1.36E-01
3q26.2	rs3755605	*GPR160*	AFR	C	***T***	0.43	0.57	1.38E-26	AFR			
			AMR	C	***T***	0.46	0.54		AMR	4.09E-01		
			ASN	C	***T***	0.28	0.72		ASN	1.26E-07	1.02E-08	
			EUR	C	***T***	0.58	0.42		EUR	2.06E-07	1.30E-04	1.75E-28
4q22.3	rs17021463	*SMARCAD1*	AFR	G	***T***	0.50	0.50	1.55E-16	AFR			
		HPGDS	AMR	G	***T***	0.64	0.36		AMR	1.74E-05		
			ASN	G	***T***	0.74	0.26		ASN	7.32E-16	2.68E-03	
			EUR	G	***T***	0.55	0.45		EUR	5.47E-02	3.44E-03	5.01E-12
4q24	rs2720460	*CENPE*	AFR	***A***	G	0.69	0.31	1.51E-07	AFR			
		CENPE variant protein	AMR	***A***	G	0.65	0.35		AMR	2.53E-01		
			ASN	***A***	G	0.73	0.27		ASN	1.04E-01	7.34E-03	
			EUR	***A***	G	0.59	0.41		EUR	2.27E-04	3.39E-02	1.90E-08
4q35.2	rs6837349	*ZFP42*	AFR	***G***	T	0.32	0.68	2.59E-42	AFR			
			AMR	***G***	T	0.30	0.70		AMR	4.39E-01		
			ASN	***G***	T	0.04	0.96		ASN	8.36E-34	6.06E-28	
			EUR	***G***	T	0.36	0.64		EUR	1.51E-01	3.34E-02	8.79E-44
5p15.33	rs2736100	*TERT*	AFR	***A***	C	0.57	0.43	1.34E-03	AFR			
		hTERT	AMR	***A***	C	0.55	0.45		AMR	6.71E-01		
			ASN	***A***	C	0.61	0.39		ASN	1.91E-01	1.02E-01	
			EUR	***A***	C	0.50	0.50		EUR	2.03E-02	1.00E-01	1.10E-04
5p15.33	rs4635969	*CLPTM1L*	AFR	***A***	G	0.34	0.66	6.62E-21	AFR			
			AMR	***A***	G	0.13	0.87		AMR	9.03E-13		
			ASN	***A***	G	0.12	0.88		ASN	6.05E-18	7.70E-01	
			EUR	***A***	G	0.20	0.80		EUR	6.22E-09	4.80E-03	2.66E-04

Supplementary Table 6. Comparison of allele frequencies by population for all known and novel TGCT SNPs*

CYTOBAND	SNP	GENE NEIGHBORHOOD	Race	Allele 1	Allele 2	Allele Freq 1	Allele Freq 2	Global P-value	Pairwise P-values			
										AFR	AMR	ASN
5q31.1	rs3805663	*CATSPER3*	AFR	***A***	G	0.20	0.80	1.80E-44	AFR			
		PITX1	AMR	***A***	G	0.49	0.51		AMR	3.04E-19		
		AK026965	ASN	***A***	G	0.51	0.49		ASN	3.83E-25	6.33E-01	
			EUR	***A***	G	0.61	0.39		EUR	1.01E-45	1.96E-04	2.11E-04
5q31.3	rs4624820	*SPRY4*	AFR	***A***	G	0.59	0.41	5.82E-37	AFR			
			AMR	***A***	G	0.59	0.41		AMR	8.02E-01		
			ASN	***A***	G	0.25	0.75		ASN	2.23E-28	1.14E-25	
			EUR	***A***	G	0.54	0.46		EUR	1.33E-01	1.03E-01	2.04E-26
6p21.31	rs210138	*BAK1*	AFR	A	***G***	0.87	0.13	6.49E-35	AFR			
		AY383626	AMR	A	***G***	0.77	0.23		AMR	1.52E-04		
		C6orf227	ASN	A	***G***	0.57	0.43		ASN	2.76E-27	2.16E-10	
			EUR	A	***G***	0.82	0.18		EUR	1.53E-02	6.26E-02	1.49E-23
7p22.3	rs12699477	*MAD1L1*	AFR	***C***	T	0.04	0.96	1.10E-52	AFR			
			AMR	***C***	T	0.42	0.58		AMR	4.04E-44		
			ASN	***C***	T	0.44	0.56		ASN	1.68E-51	5.91E-01	
			EUR	***C***	T	0.37	0.63		EUR	8.25E-41	6.56E-02	5.58E-03
7q36.3	rs11769858	*NCAPG2*	AFR	C	***T***	0.35	0.65	6.58E-31	AFR			
			AMR	C	***T***	0.62	0.38		AMR	1.03E-14		
			ASN	C	***T***	0.52	0.48		ASN	7.58E-08	2.02E-03	
			EUR	C	***T***	0.68	0.32		EUR	5.66E-31	2.90E-02	3.84E-10
8q13.3	rs7010162	*PRDM14*	AFR	***C***	T	0.33	0.67	5.77E-88	AFR			
			AMR	***C***	T	0.36	0.64		AMR	4.33E-01		
			ASN	***C***	T	0.07	0.93		ASN	1.04E-26	5.08E-28	
			EUR	***C***	T	0.61	0.39		EUR	1.42E-21	4.13E-15	1.45E-88
9p24.3	rs7040024	*DMRT1*	AFR	***A***	C	0.73	0.27	3.25E-06	AFR			
			AMR	***A***	C	0.74	0.26		AMR	6.13E-01		
			ASN	***A***	C	0.84	0.16		ASN	3.08E-06	1.40E-04	
			EUR	***A***	C	0.74	0.26		EUR	7.40E-01	8.05E-01	2.14E-06
9p24.3	rs755383	*DMRT1*	AFR	C	***T***	0.65	0.35	4.20E-25	AFR			
			AMR	C	***T***	0.44	0.56		AMR	3.68E-10		
			ASN	C	***T***	0.35	0.65		ASN	1.94E-22	9.96E-03	
			EUR	C	***T***	0.39	0.61		EUR	2.10E-20	9.28E-02	2.37E-01
9p24.3	rs55873183	*DMRT1*	AFR	A	***G***	1.00	0.00	5.53E-15	AFR			
			AMR	A	***G***	0.97	0.03		AMR	3.85E-03		
			ASN	A	***G***	1.00	0.00		ASN	1.27E-01	6.43E-05	
			EUR	A	***G***	0.93	0.07		EUR	4.18E-08	5.03E-03	1.65E-10
10q26.13	rs61408740	*LHPP*	AFR	C	***G***	0.80	0.20	1.81E-28	AFR			
			AMR	C	***G***	0.95	0.05		AMR	1.80E-10		
			ASN	C	***G***	0.87	0.13		ASN	3.53E-03	2.61E-05	
			EUR	C	***G***	0.98	0.02		EUR	1.99E-27	6.56E-03	3.96E-16
11q14.1	rs7107174	*GAB2*	AFR	C	***T***	0.94	0.06	8.94E-42	AFR			
			AMR	C	***T***	0.75	0.25		AMR	5.08E-16		
			ASN	C	***T***	0.59	0.41		ASN	9.15E-40	1.38E-06	
			EUR	C	***T***	0.81	0.19		EUR	4.97E-11	1.35E-02	1.86E-18
12p13.1	rs2900333	*ATF7IP*	AFR	***C***	T	0.97	0.03	3.21E-46	AFR			
		PLBD1	AMR	***C***	T	0.58	0.42		AMR	7.22E-46		
			ASN	***C***	T	0.74	0.26		ASN	5.79E-25	2.27E-07	
			EUR	***C***	T	0.65	0.35		EUR	6.27E-41	3.57E-02	1.54E-04

Supplementary Table 6. Comparison of allele frequencies by population for all known and novel TGCT SNPs*

CYTOBAND	SNP	GENE NEIGHBORHOOD	Race	Allele 1	Allele 2	Allele Freq 1	Allele Freq 2	Global P-value	Pairwise P-values			
										AFR	AMR	ASN
12q21.32	rs3782181	*KITLG*	AFR	***A***	C	0.20	0.80	4.32E-121	AFR			
			AMR	***A***	C	0.85	0.15		AMR	5.98E-77		
			ASN	***A***	C	0.68	0.32		ASN	2.44E-55	3.13E-08	
			EUR	***A***	C	0.80	0.20		EUR	6.27E-95	5.19E-02	2.46E-06
15q21.3	rs12912292	*PRTG*	AFR	***A***	G	0.02	0.98	3.31E-130	AFR			
			AMR	***A***	G	0.44	0.56		AMR	1.64E-52		
			ASN	***A***	G	0.02	0.98		ASN	5.73E-01	4.61E-61	
			EUR	***A***	G	0.49	0.51		EUR	8.48E-69	1.60E-01	2.55E-79
15q22.31	rs60180747	*MAP2K1*	AFR	A	***C***	0.93	0.07	3.56E-18	AFR			
		TIPIN	AMR	A	***C***	0.78	0.22		AMR	4.64E-10		
			ASN	A	***C***	0.87	0.13		ASN	1.18E-03	5.83E-04	
			EUR	A	***C***	0.74	0.26		EUR	8.31E-17	1.45E-01	1.66E-08
16p13.13	rs4561483	*BCAR4*	AFR	***A***	G	0.25	0.75	2.88E-42	AFR			
		CATX-11	AMR	***A***	G	0.24	0.76		AMR	6.95E-01		
		RSL1D1	ASN	***A***	G	0.61	0.39		ASN	1.00E-31	2.54E-28	
			EUR	***A***	G	0.35	0.65		EUR	2.72E-04	2.29E-04	3.88E-21
16q12.1	rs8046148	*HEATR3*	AFR	A	***G***	0.30	0.70	1.53E-08	AFR			
		AF086132	AMR	A	***G***	0.24	0.76		AMR	5.84E-02		
			ASN	A	***G***	0.34	0.66		ASN	1.98E-01	1.93E-03	
			EUR	A	***G***	0.19	0.81		EUR	1.50E-05	6.57E-02	2.98E-09
16q23.1	rs4888262	*RFWD3*	AFR	***C***	T	0.17	0.83	9.43E-58	AFR			
			AMR	***C***	T	0.55	0.45		AMR	1.27E-31		
			ASN	***C***	T	0.22	0.78		ASN	2.93E-02	1.37E-24	
			EUR	***C***	T	0.53	0.47		EUR	1.10E-36	4.39E-01	4.37E-29
16q24.2	rs55637647	*ZFPM1*	AFR	C	***G***	0.27	0.73	7.62E-40	AFR			
			AMR	C	***G***	0.50	0.50		AMR	1.04E-11		
			ASN	C	***G***	0.47	0.53		ASN	6.11E-11	3.37E-01	
			EUR	C	***G***	0.66	0.34		EUR	1.66E-41	1.53E-07	8.11E-13
17q12	rs7501939	*HNF1B*	AFR	C	***T***	0.44	0.56	1.38E-21	AFR			
			AMR	C	***T***	0.65	0.35		AMR	1.99E-09		
			ASN	C	***T***	0.73	0.27		ASN	1.22E-22	4.30E-03	
			EUR	C	***T***	0.62	0.38		EUR	2.44E-10	4.17E-01	1.46E-05
17q22	rs9905704	*TEX14*	AFR	G	***T***	0.05	0.95	6.48E-249	AFR			
			AMR	G	***T***	0.22	0.78		AMR	1.41E-14		
			ASN	G	***T***	1.00	0.00		ASN	3.04E-213	3.93E-140	
			EUR	G	***T***	0.33	0.67		EUR	2.18E-31	3.79E-04	9.05E-138
19p12	rs2195987	*AK125686*	AFR	***C***	T	0.04	0.96	1.87E-17	AFR			
			AMR	***C***	T	0.15	0.85		AMR	1.34E-09		
			ASN	***C***	T	0.13	0.87		ASN	1.80E-07	2.12E-01	
			EUR	***C***	T	0.22	0.78		EUR	1.32E-18	1.51E-02	1.90E-05
19p12	rs34601376	*ZNF726*	AFR	A	***T***	0.98	0.02	2.08E-16	AFR			
			AMR	A	***T***	0.89	0.11		AMR	2.91E-08		
			ASN	A	***T***	0.90	0.10		ASN	2.89E-08	7.87E-01	
			EUR	A	***T***	0.82	0.18		EUR	1.17E-17	3.03E-03	1.47E-04
19p12	rs58521262	*LOC101929164*	AFR	A	***G***	0.12	0.88	8.35E-01	AFR			
			AMR	A	***G***	0.10	0.90		AMR	4.72E-01		
			ASN	A	***G***	0.12	0.88		ASN	8.91E-01	3.87E-01	
			EUR	A	***G***	0.12	0.88		EUR	9.64E-01	4.15E-01	9.16E-01

Supplementary Table 6. Comparison of allele frequencies by population for all known and novel TGCT SNPs*

CYTOBAND	SNP	GENE NEIGHBORHOOD	Race	Allele 1	Allele 2	Allele Freq 1	Allele Freq 2	Global P-value	Pairwise P-values			
										AFR	AMR	ASN
19p12	rs73019876	*ZNF257*	AFR	G	***T***	0.57	0.43	2.89E-07	AFR			
			AMR	G	***T***	0.46	0.54		AMR	1.59E-03		
			ASN	G	***T***	0.40	0.60		ASN	3.11E-08	6.70E-02	
			EUR	G	***T***	0.44	0.56		EUR	9.17E-06	5.47E-01	1.28E-01
21q22.3	rs2839186	*MCM3APAS* *MCM3AP*	AFR	C	***T***	0.69	0.31	7.59E-17	AFR			
			AMR	C	***T***	0.49	0.51		AMR	2.58E-09		
			ASN	C	***T***	0.74	0.26		ASN	1.22E-01	3.34E-14	
			EUR	C	***T***	0.57	0.43		EUR	7.83E-06	1.76E-02	2.21E-10
Xq28	rs17336718	*TKTL1*	AFR	C	***T***	0.99	0.01	7.13E-07	AFR			
			AMR	C	***T***	0.93	0.07		AMR	2.38E-06		
			ASN	C	***T***	0.98	0.02		ASN	5.52E-02	7.38E-04	
			EUR	C	***T***	0.94	0.06		EUR	7.77E-06	6.15E-01	1.30E-03

* From 1000 Genomes. Total observations for AFR = 492, AMR = 362, ASN = 572, EUR = 758.

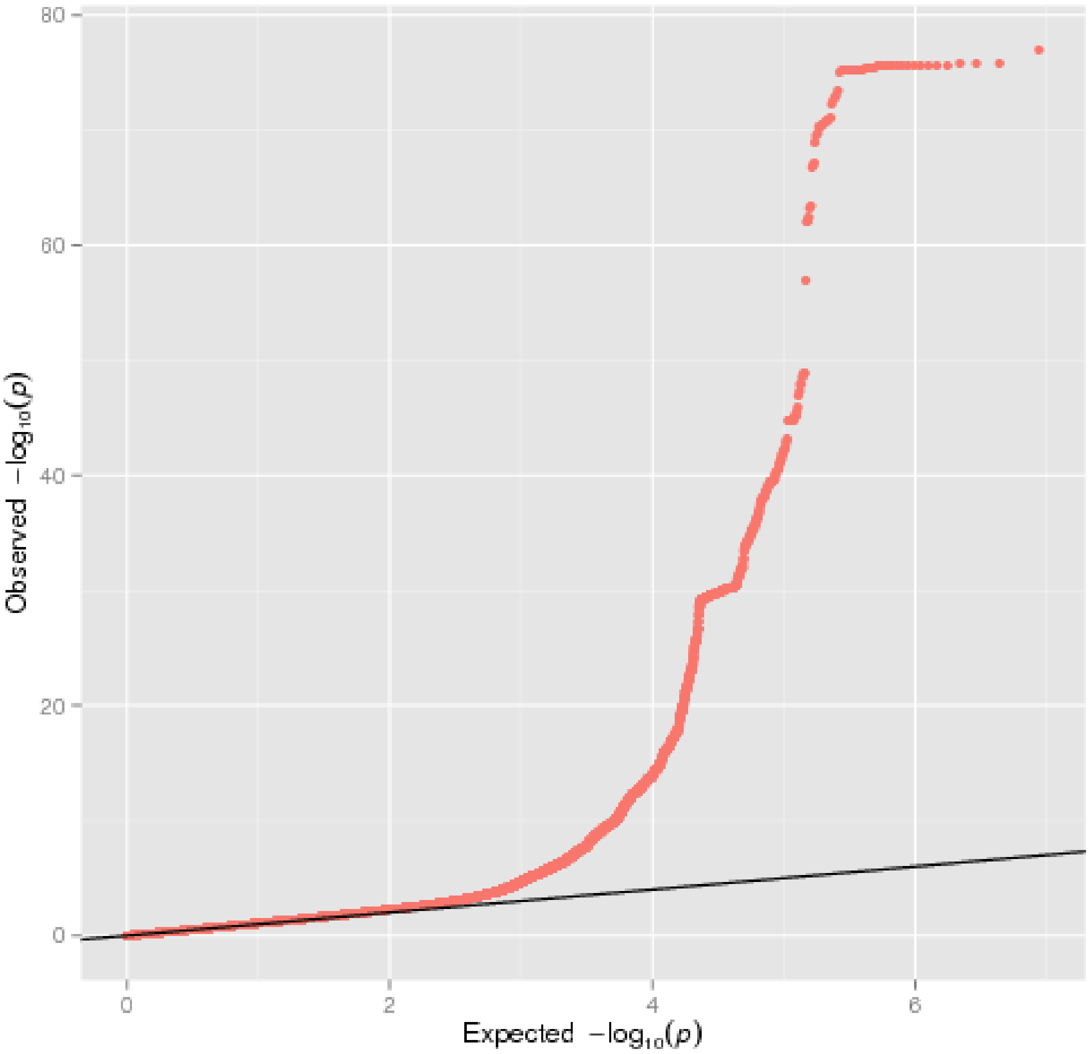
†Risk allele is bolded and underlined

Supplementary Table 7. Concordance between the imputed and TaqMan genotype

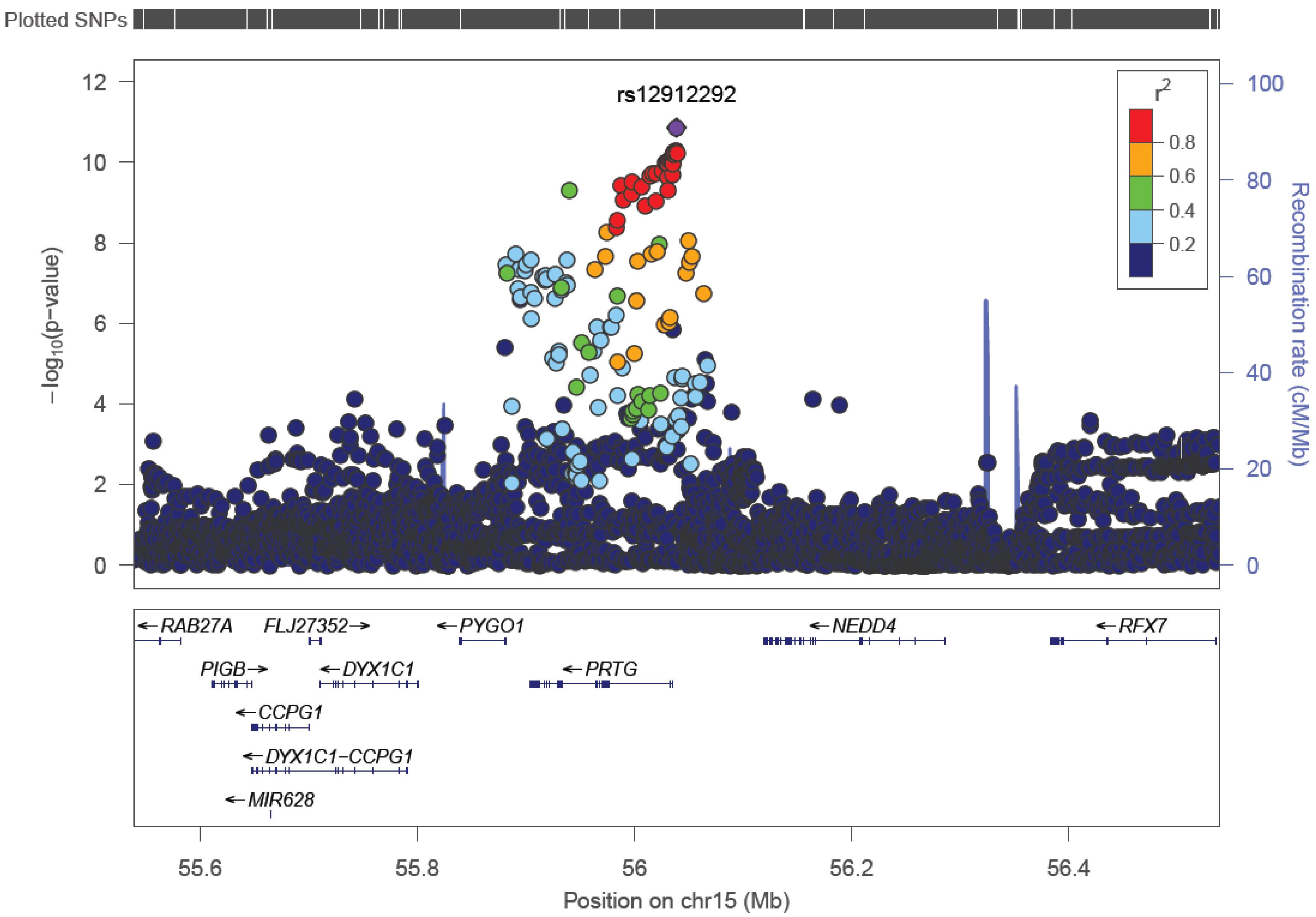
		NCI		Penn		Norway/Sweden	
SNP (target)	**TaqMan**	**# Sample**	**Concordance**	**# Sample**	**Concordance**	**# Sample**	**Concordance**
rs11769858	rs13225986*	284	0.92	311	0.95	298	0.86
rs12912292	rs12905693	318	0.99	365	0.99	343	0.93
rs17336718	rs17336718	311	1.00	358	0.90	-	-
rs2713206	rs2713207*	317	1.00	365	0.99	351	0.95
rs34601376	rs34601376	266	0.95	312	0.96	312	0.92
rs3755605	rs67666682*	309	1.00	349	0.98	345	0.92
rs55873183	rs55873183	286	0.93	324	0.90	316	0.92
rs58521262	rs62124391*	316	1.00	376	0.99	340	0.95
rs60180747	rs60180747	310	0.99	371	0.99	346	0.92
rs61408740	rs72837316*	316	1.00	367	0.99	356	0.94
rs6837349	rs6837349	315	0.99	186	0.76	348	0.93
rs73019876	rs436194*	317	1.00	373	0.99	346	0.91
Average		305	0.98	336	0.97	336	0.93

* LD surrogates used if target SNP failed assay design

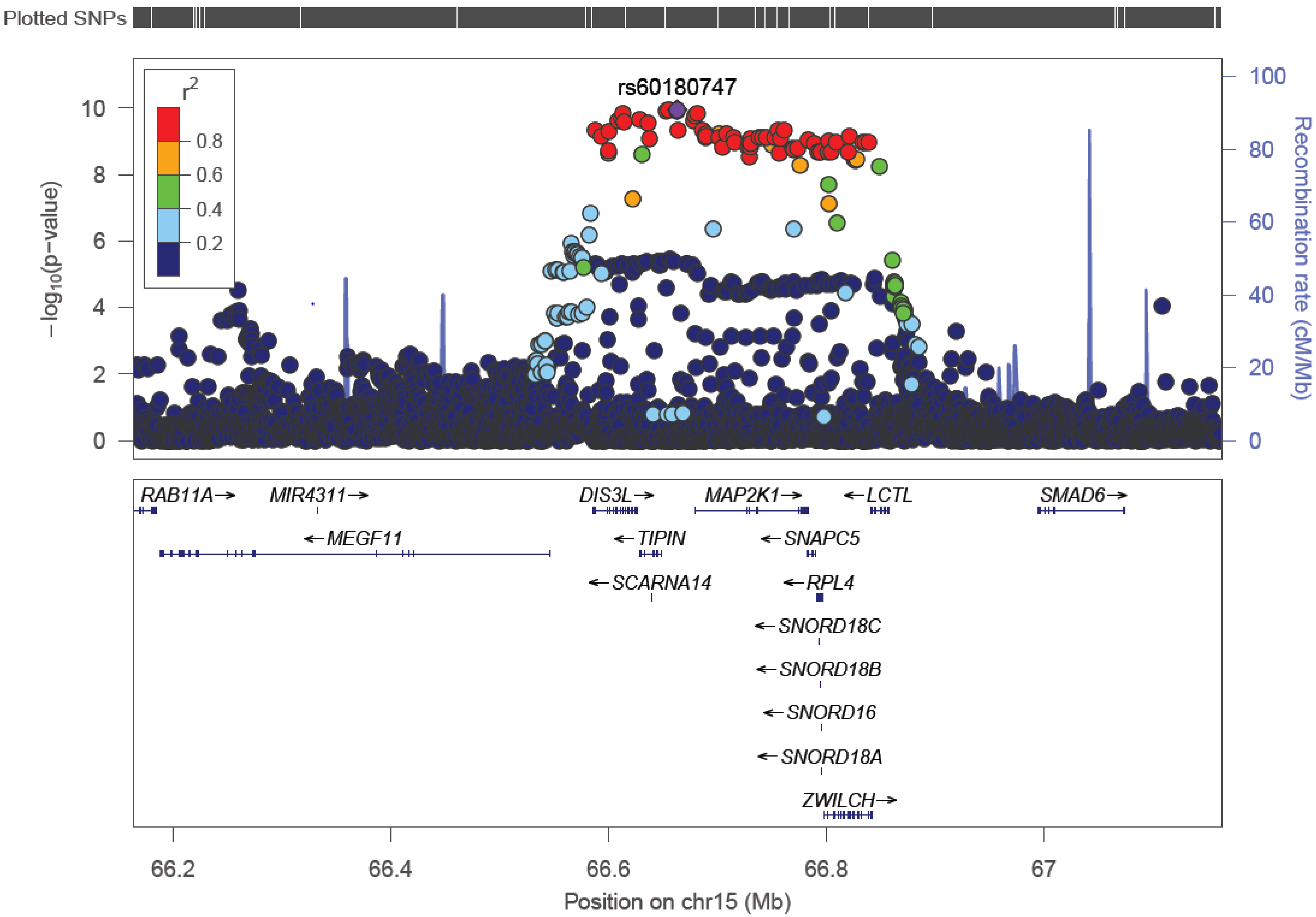
Supplementary Figure 1. Q-Q plot for meta-analysis



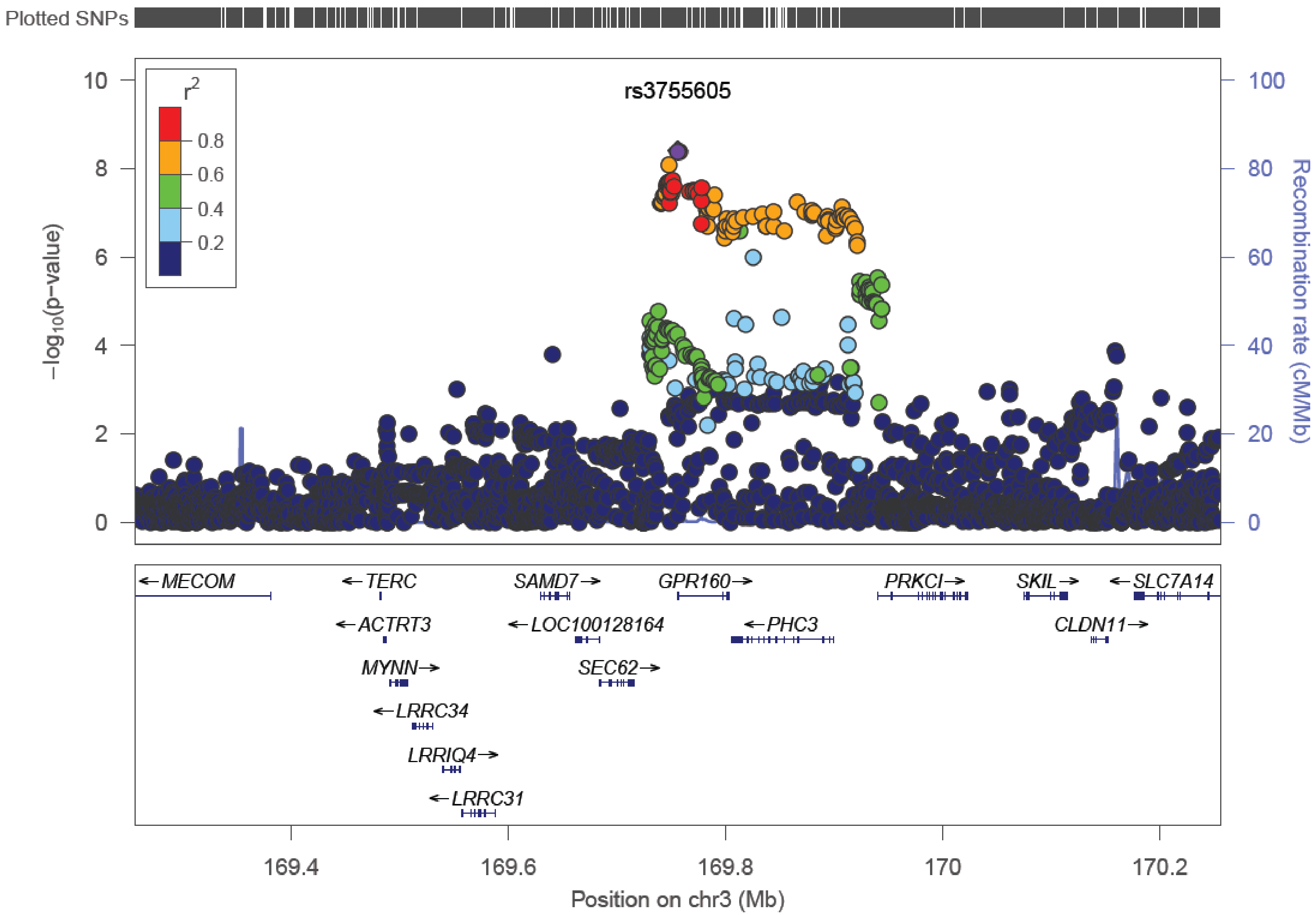
Supplementary Figure 2a. 500 kb region around rs12912292 imputed in Europeans



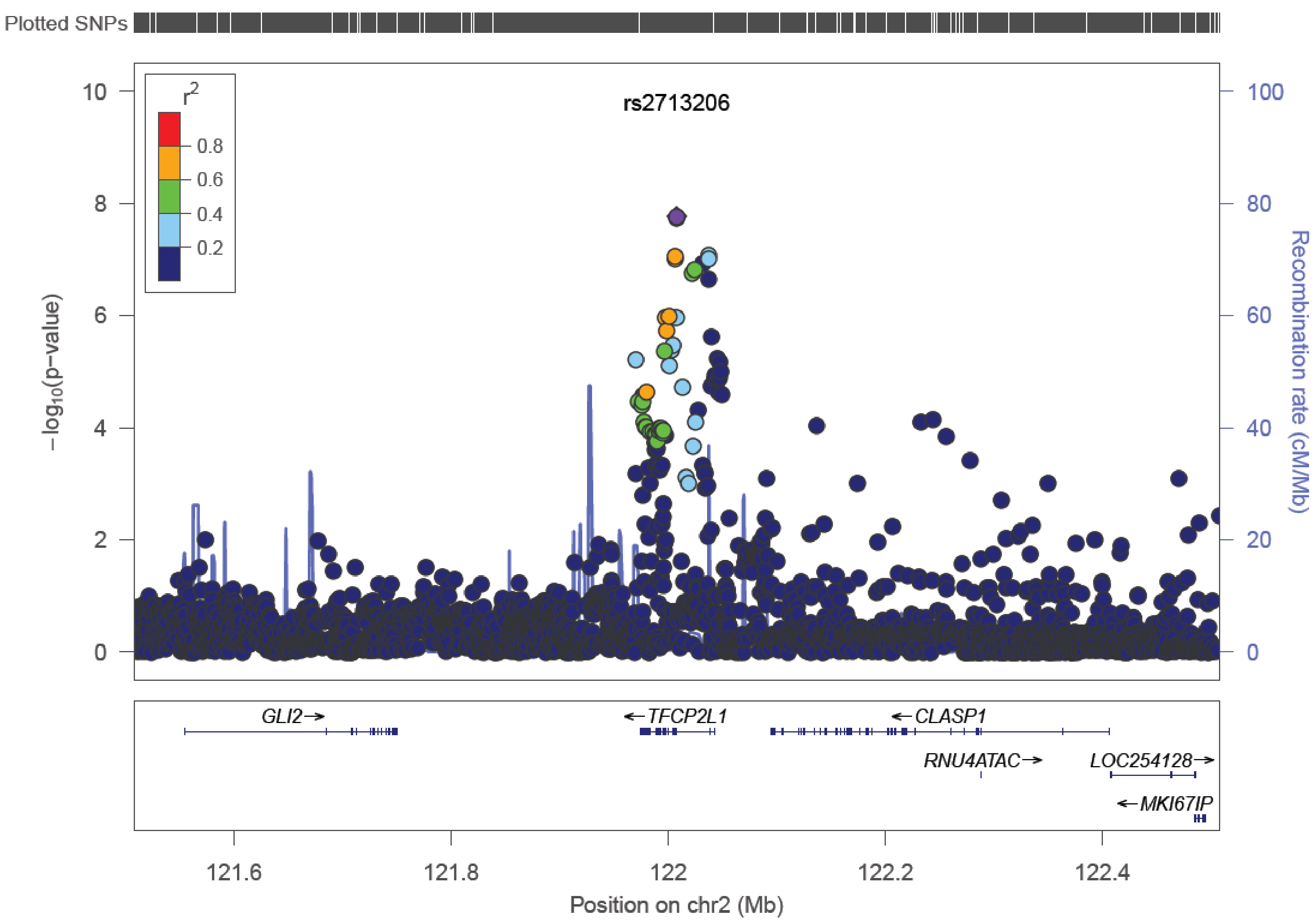
Supplementary Figure 2b. 500 kb region around rs60180747 imputed in Europeans



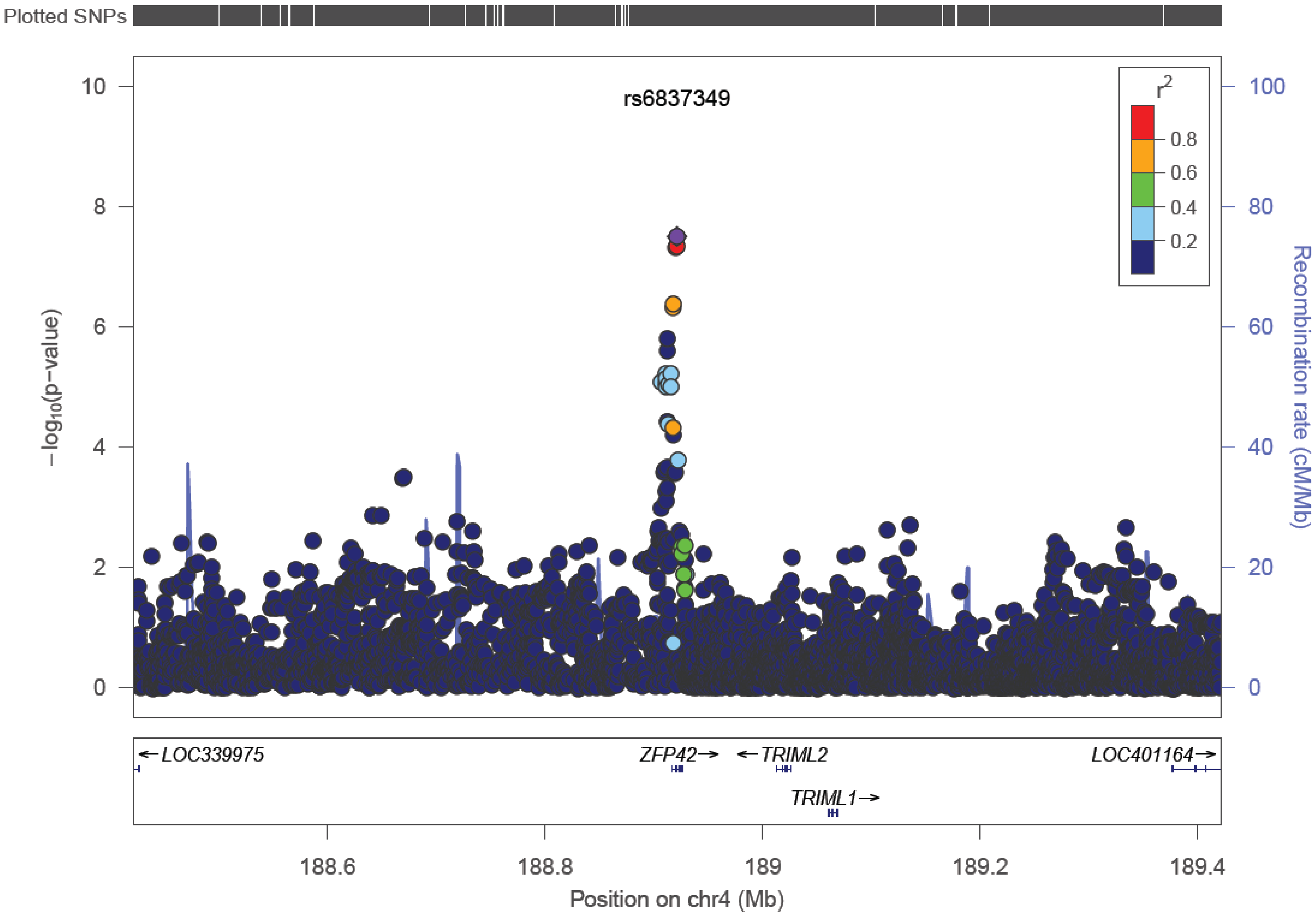
Supplementary Figure 2c. 500 kb region around rs3755605 imputed in Europeans



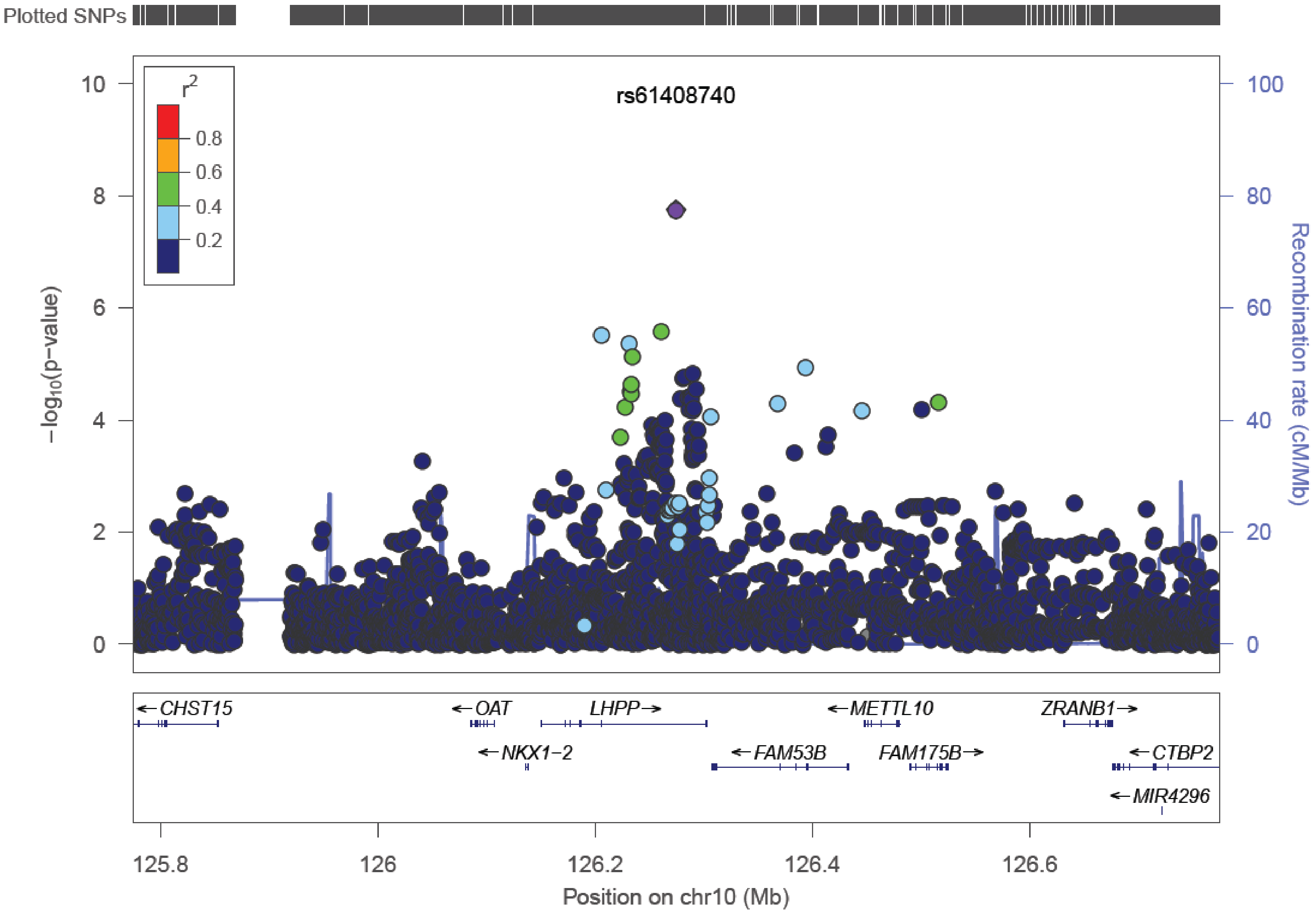
Supplementary Figure 2d. 500 kb region around rs2713206 imputed in Europeans



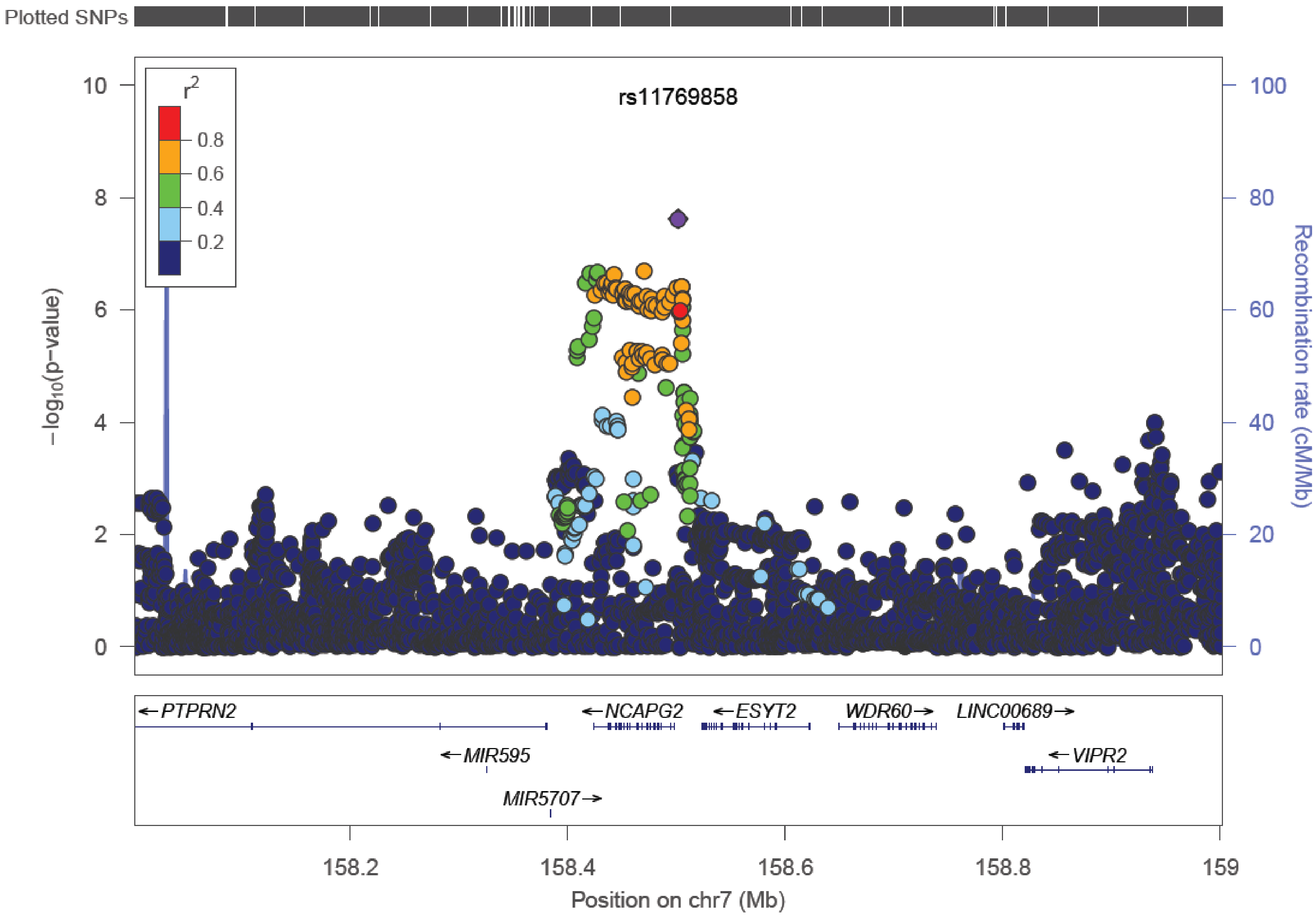
Supplementary Figure 2e. 500 kb region around rs6837349 imputed in Europeans



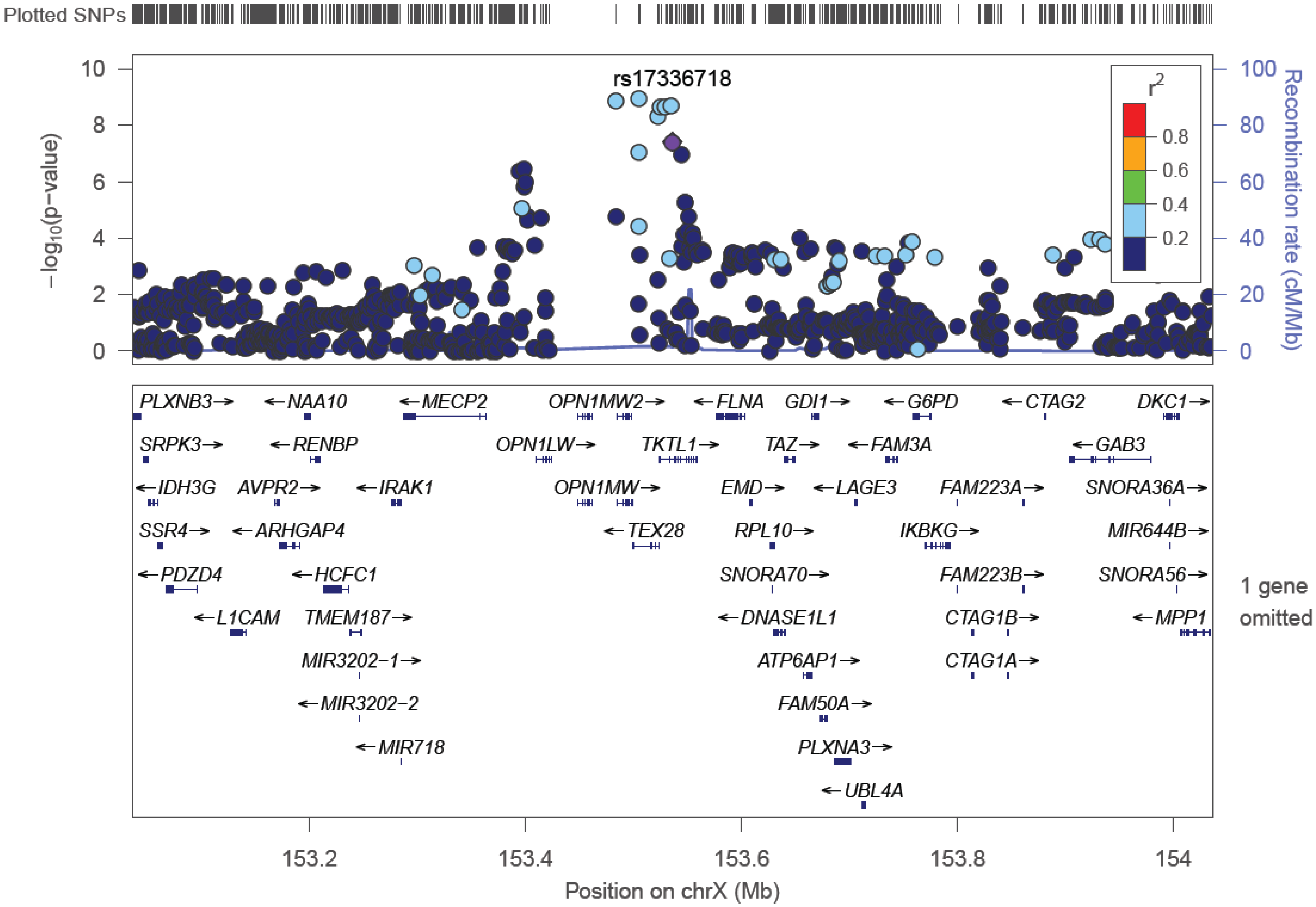
Supplementary Figure 2f. 500 kb region around rs61408740 imputed in Europeans



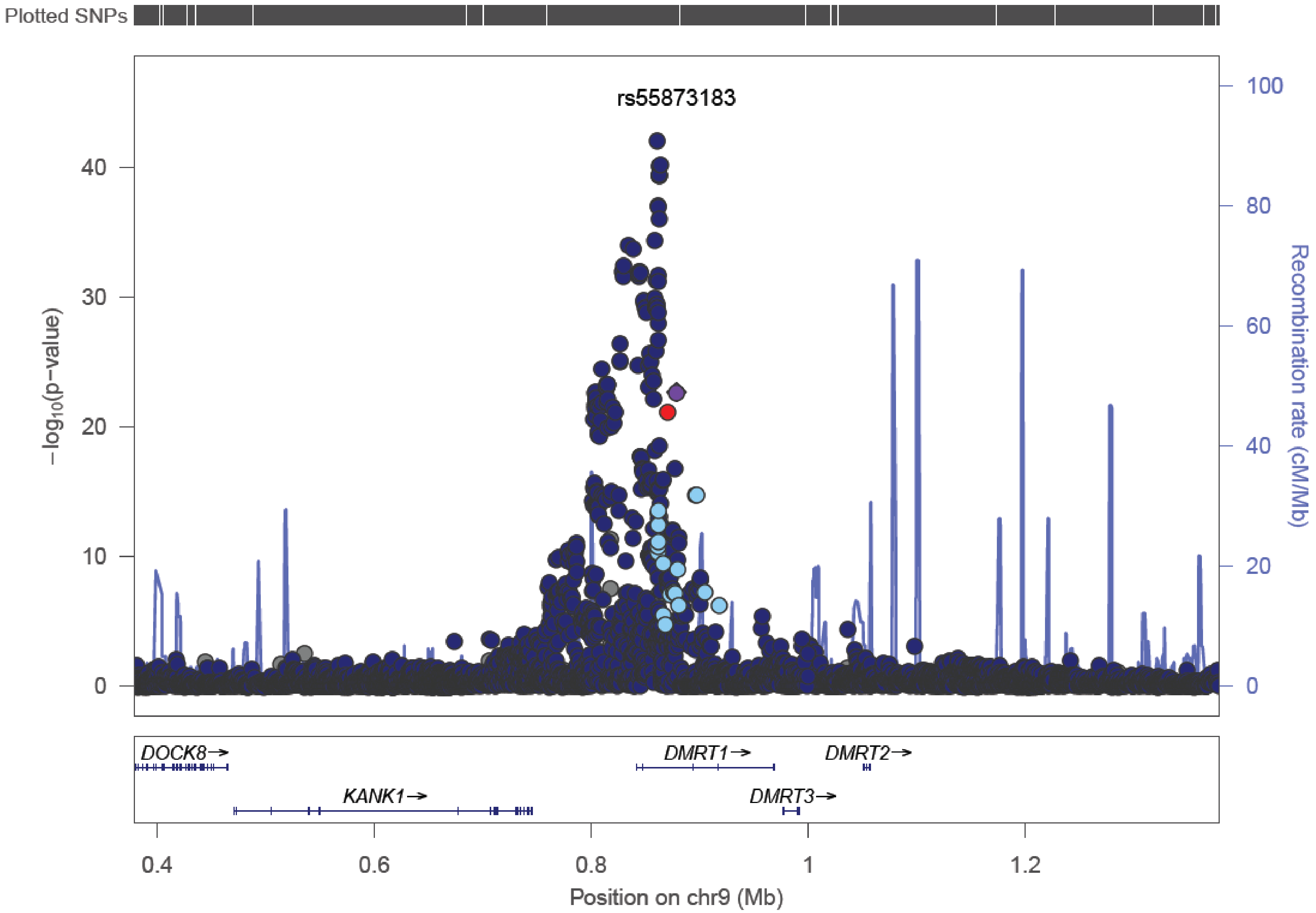
Supplementary Figure 2g. 500 kb region around rs11769858 imputed in Europeans



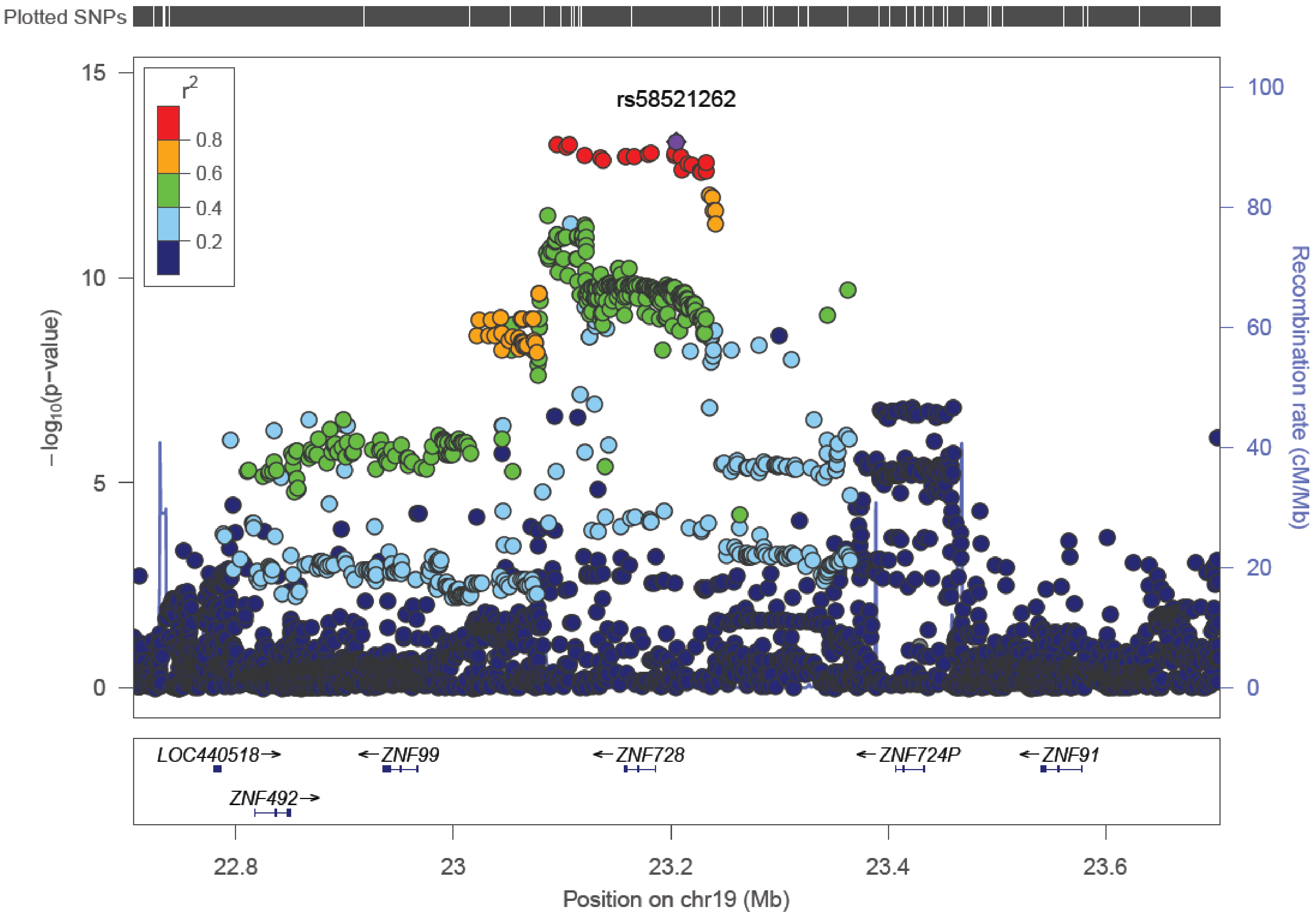
Supplementary Figure 2h. 500 kb region around rs17336718 imputed in Europeans



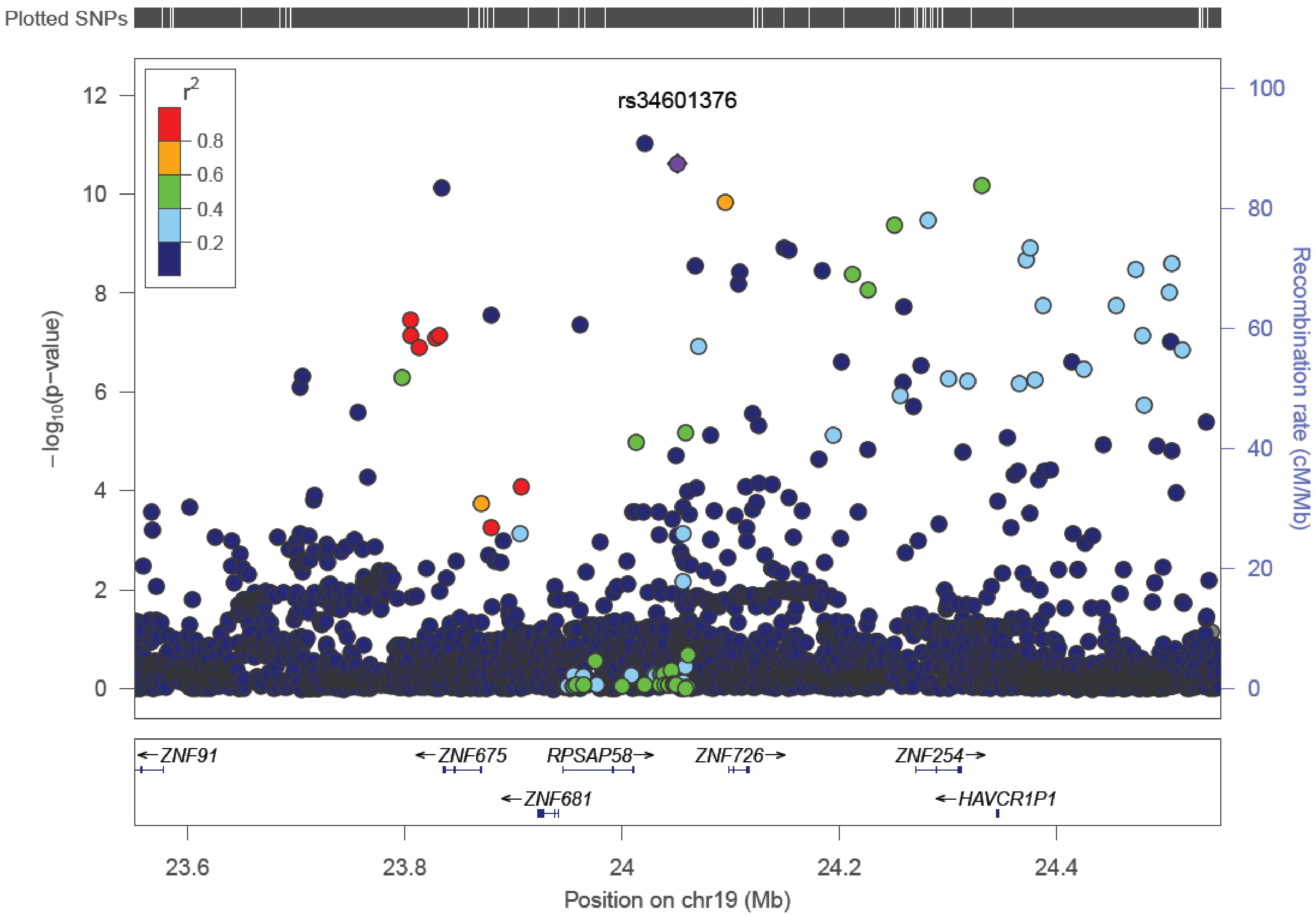
Supplementary Figure 2i. 500 kb region around rs55873183 imputed in Europeans



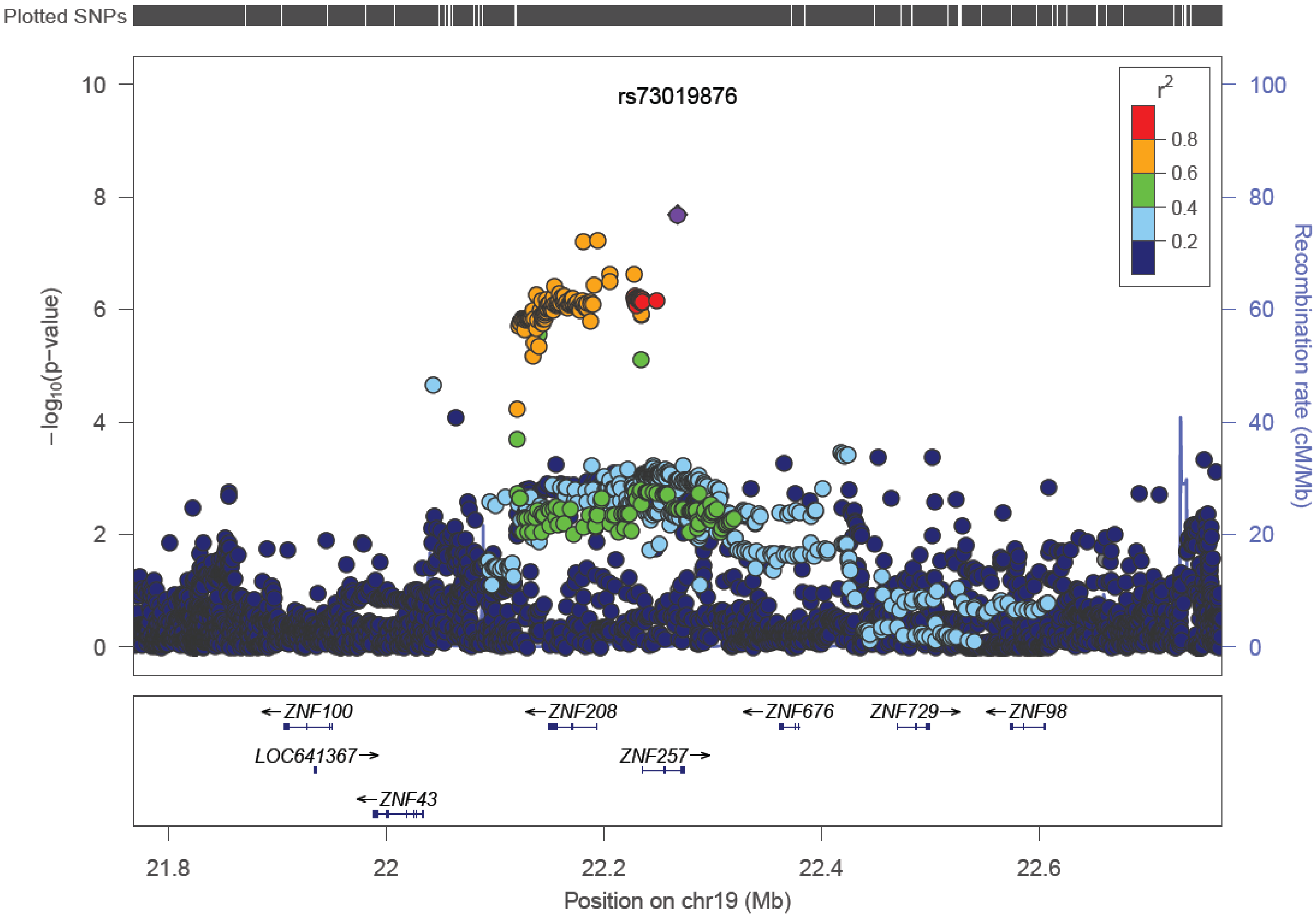
Supplementary Figure 2j. 500 kb region around rs58521262 imputed in Europeans



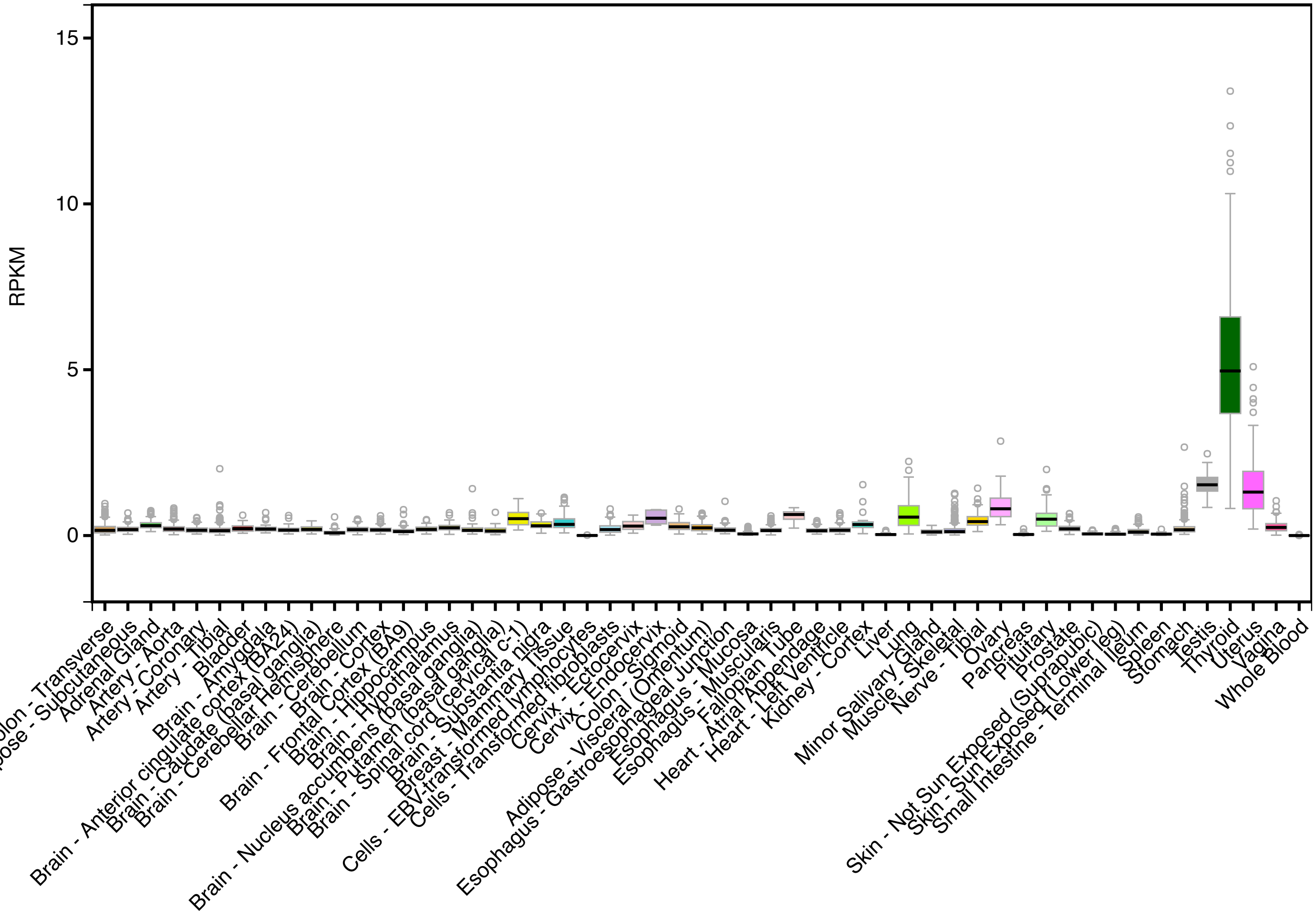
Supplementary Figure 2k. 500 kb region around rs34601376 imputed in Europeans



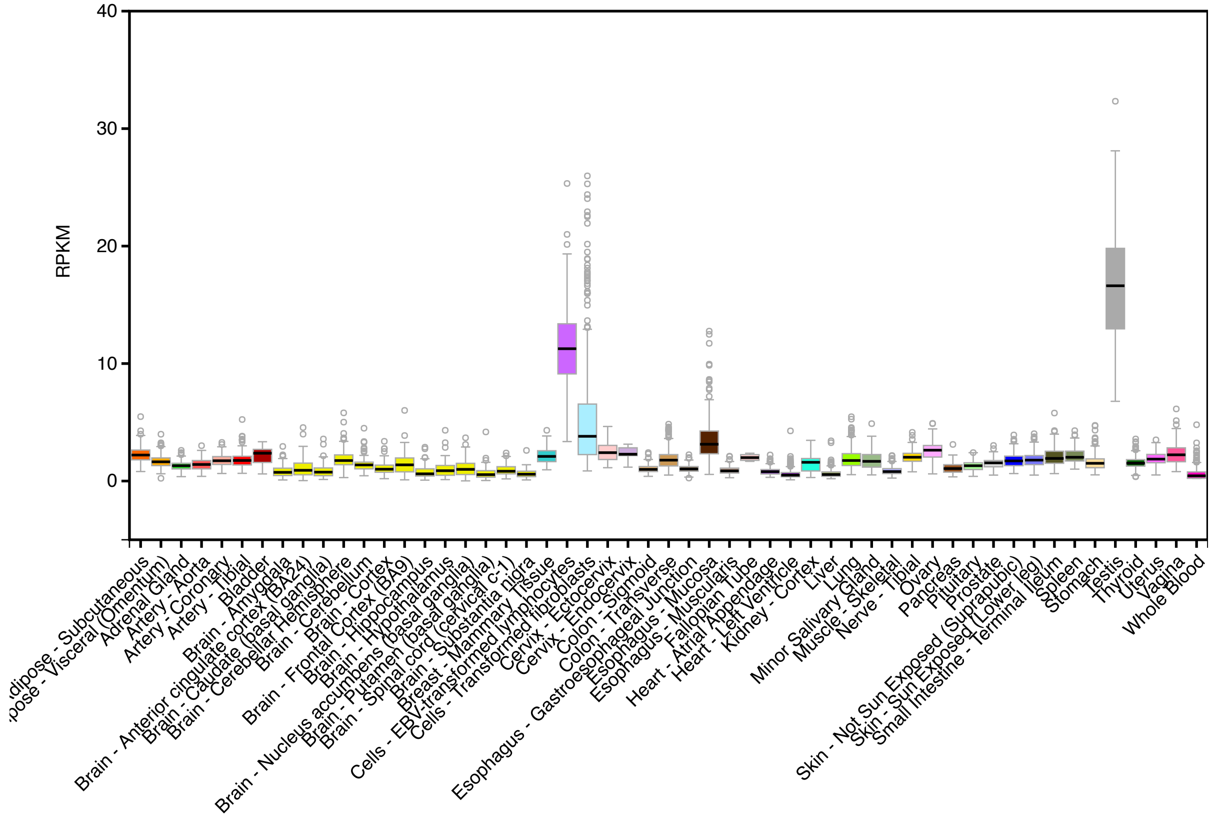
Supplementary Figure 2l. 500 kb region around rs73019876 imputed in Europeans



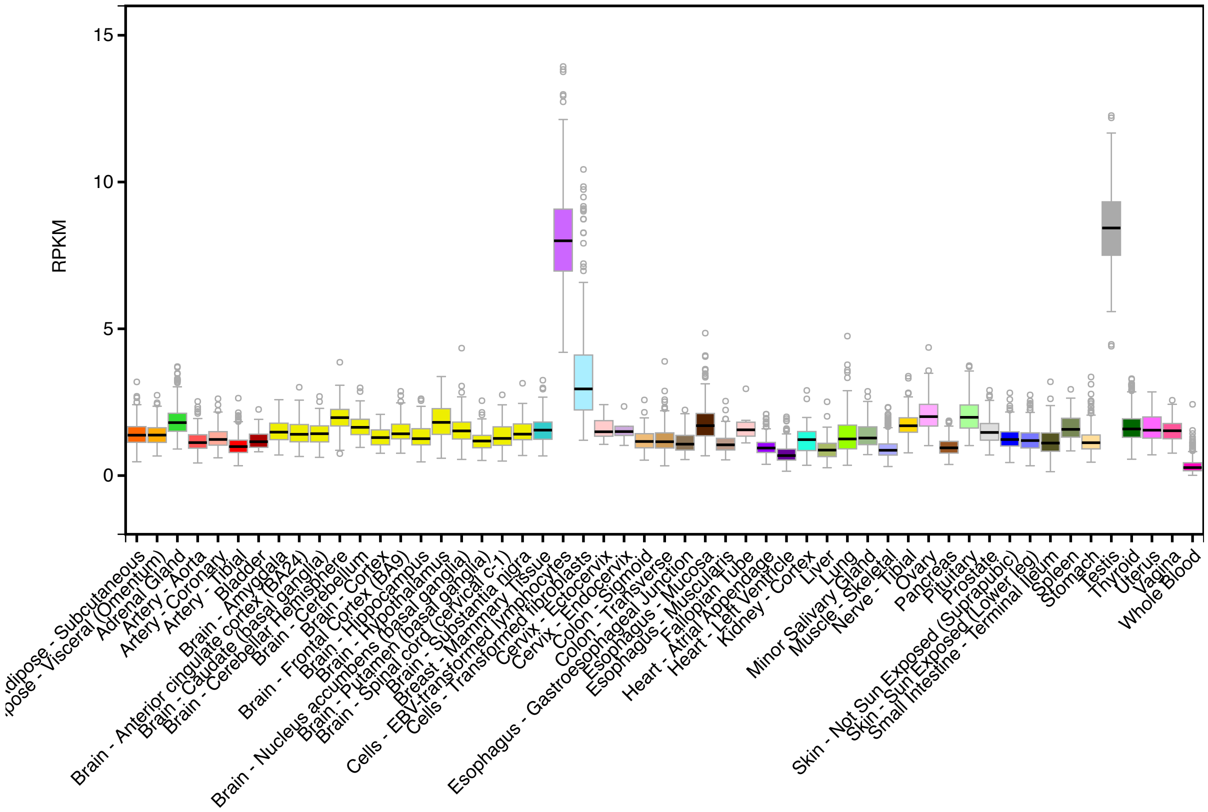
Supplementary Figure 3a. *PRTG* expression in the 53 normal tissues reported by GTEx



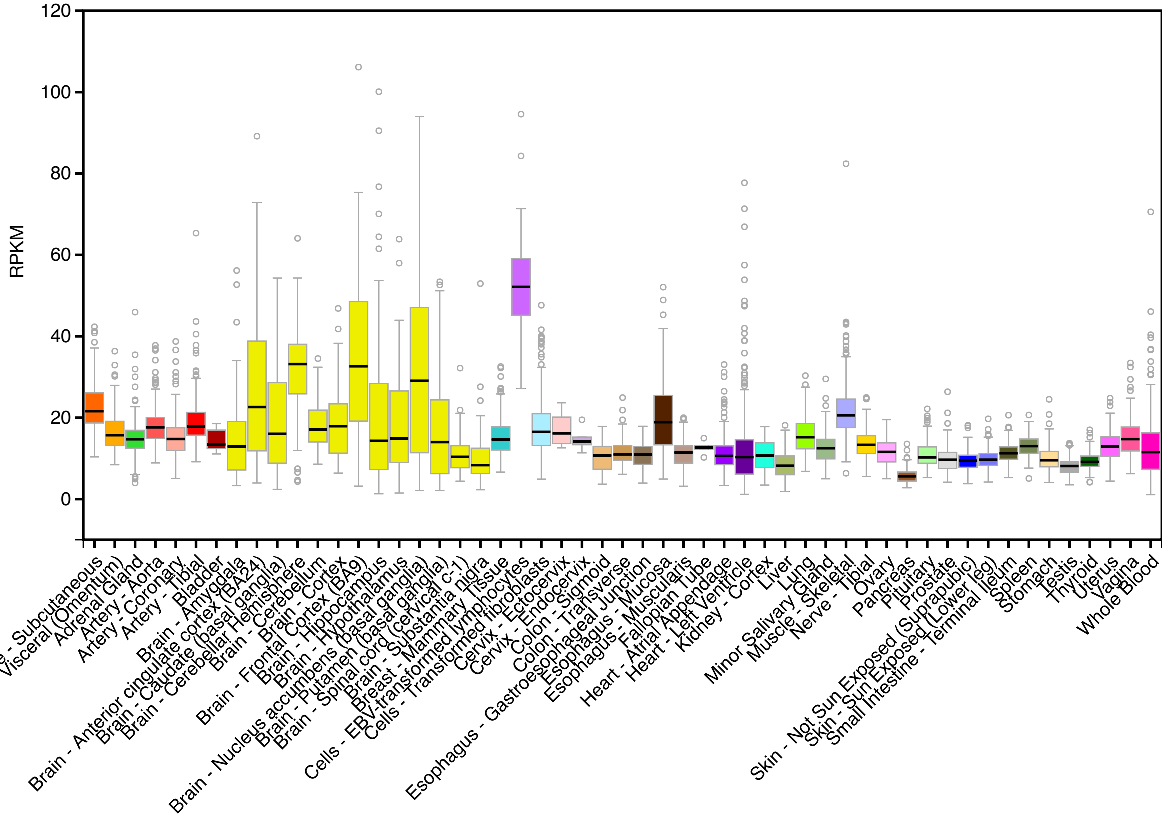
Supplementary Figure 3b. *ZWILCH* expression in the 53 normal tissues reported by GTEx



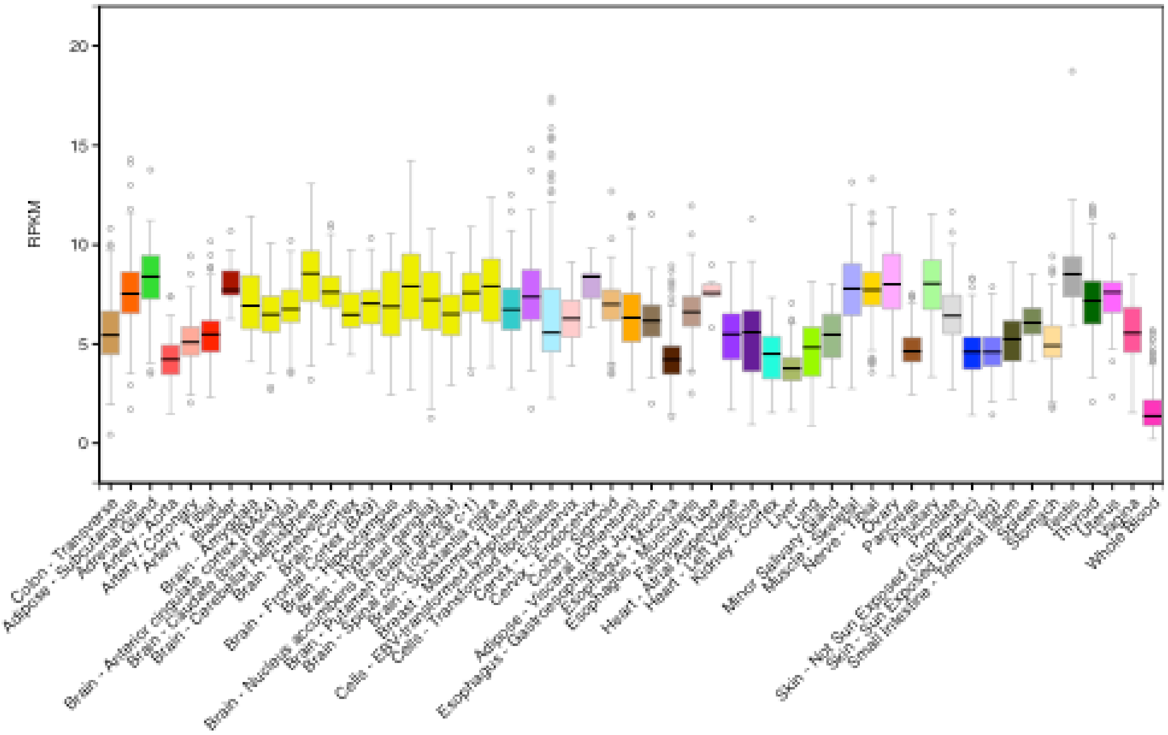
Supplementary Figure 3c. *TIPIN* expression in the 53 normal tissues reported by GTEx



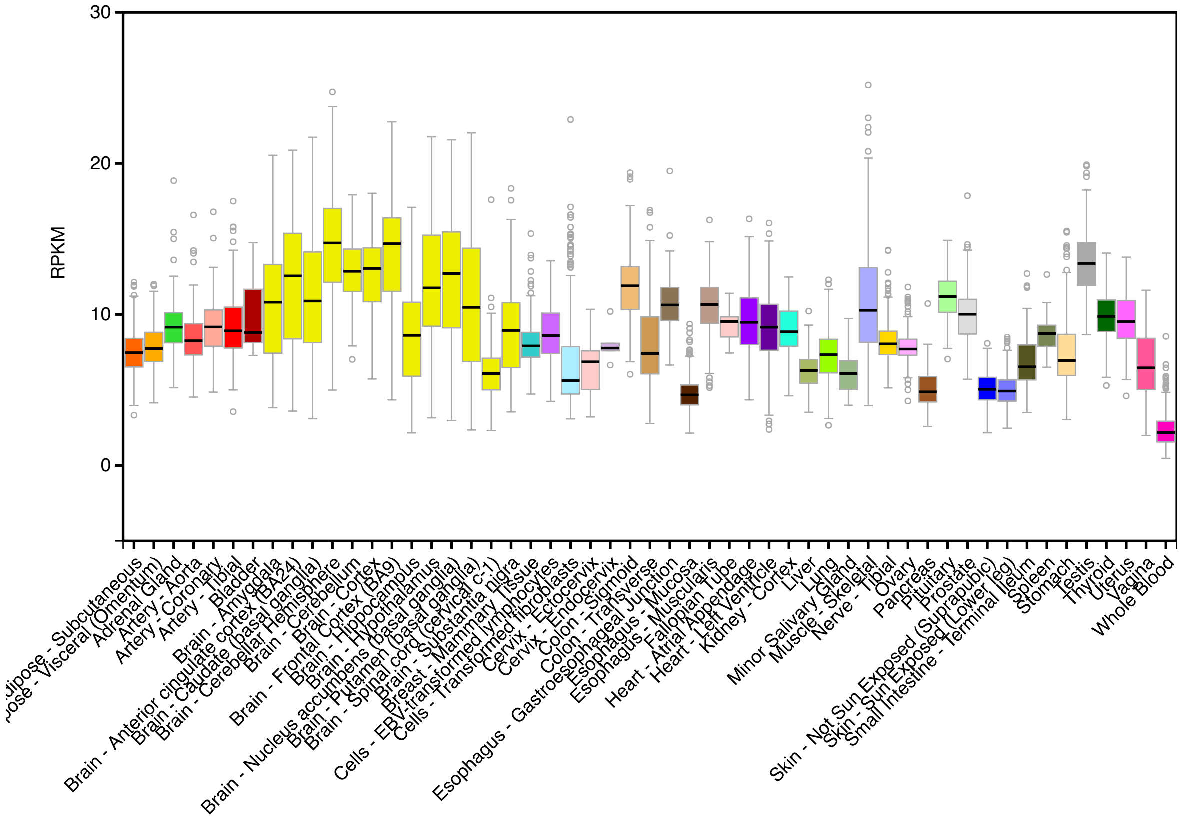
Supplementary Figure 3d. *MAP2K1* expression in the 53 normal tissues reported by GTEx



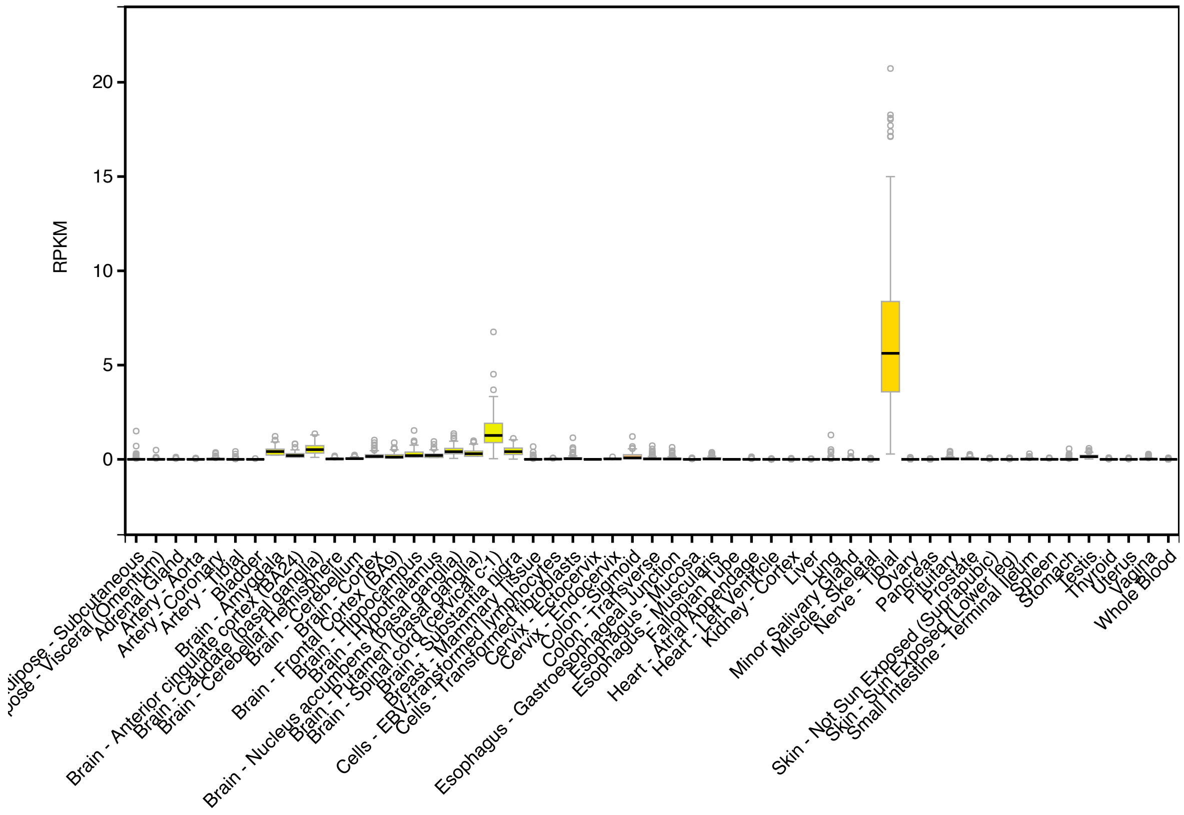
Supplementary Figure 3e. *DIS3L* expression in the 53 normal tissues reported by GTEx



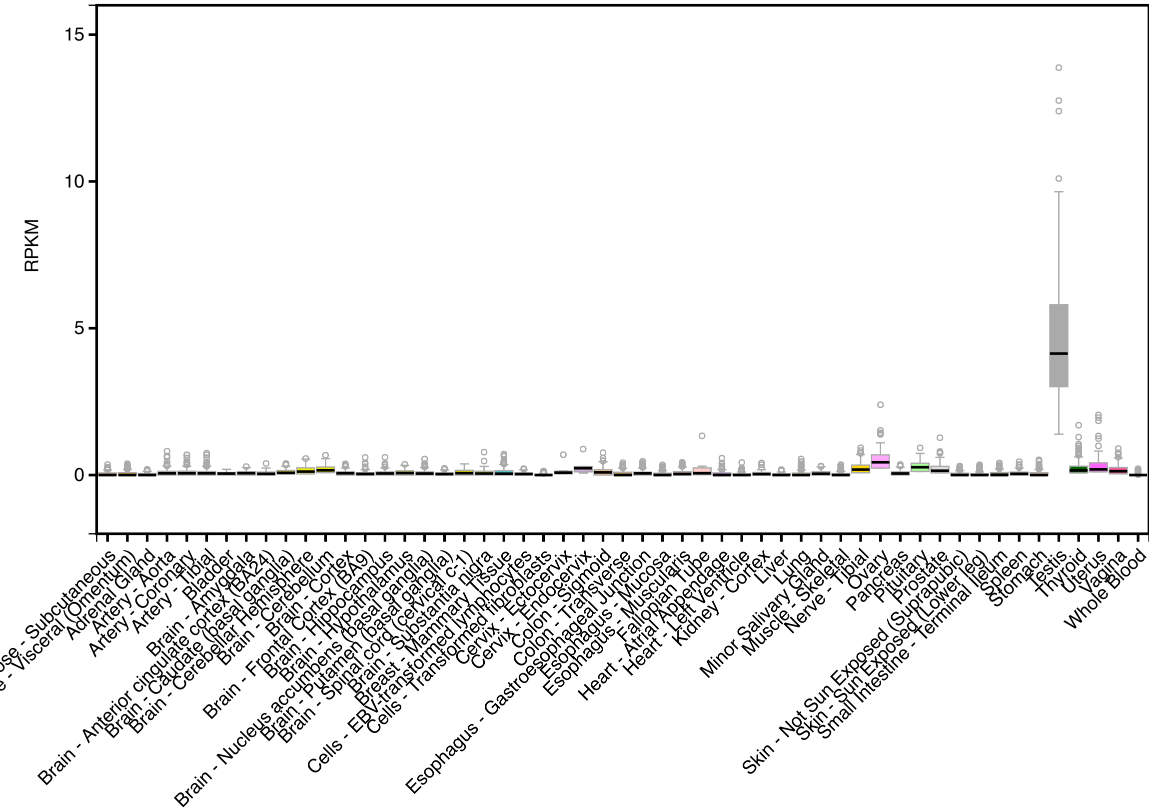
Supplementary Figure 3f. *SNAPC5* expression in the 53 normal tissues reported by GTEx



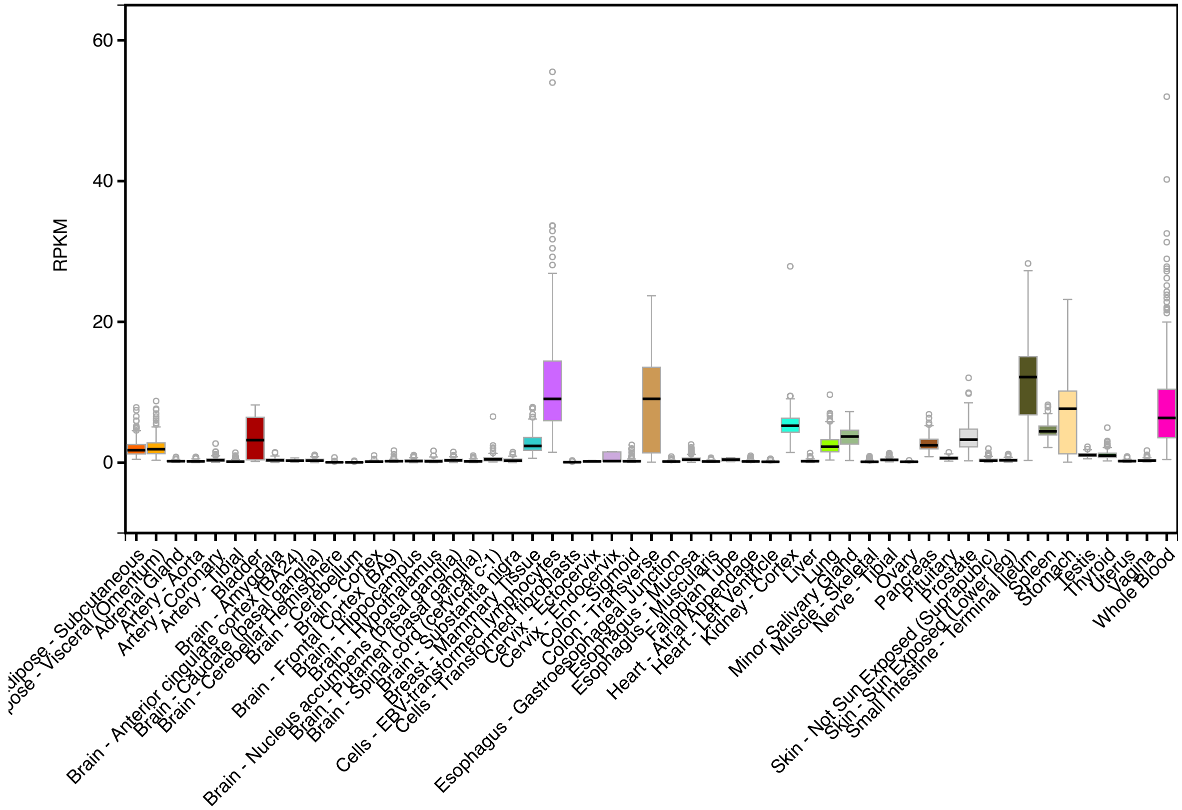
Supplementary Figure 3g. *LCTL* expression in the 53 normal tissues reported by GTEx



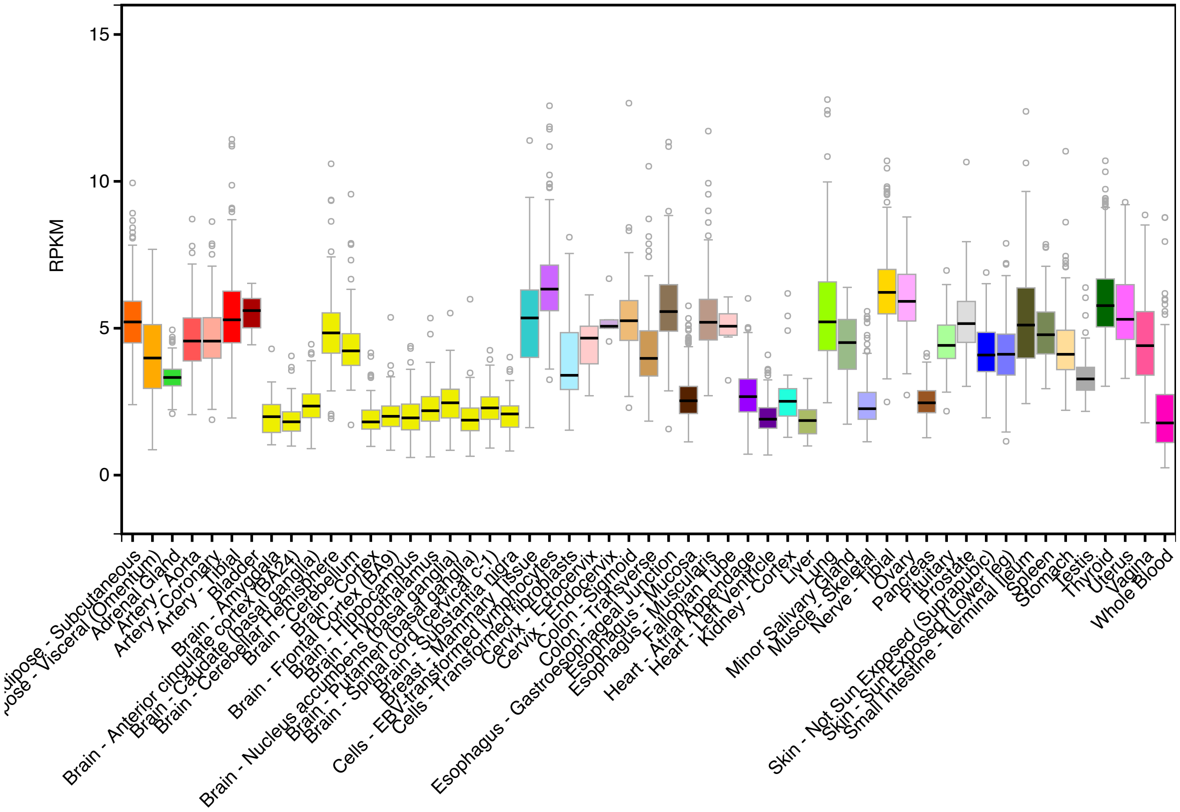
Supplementary Figure 3h. *RP11-653J6.1* expression in the 53 normal tissues reported by GTEx



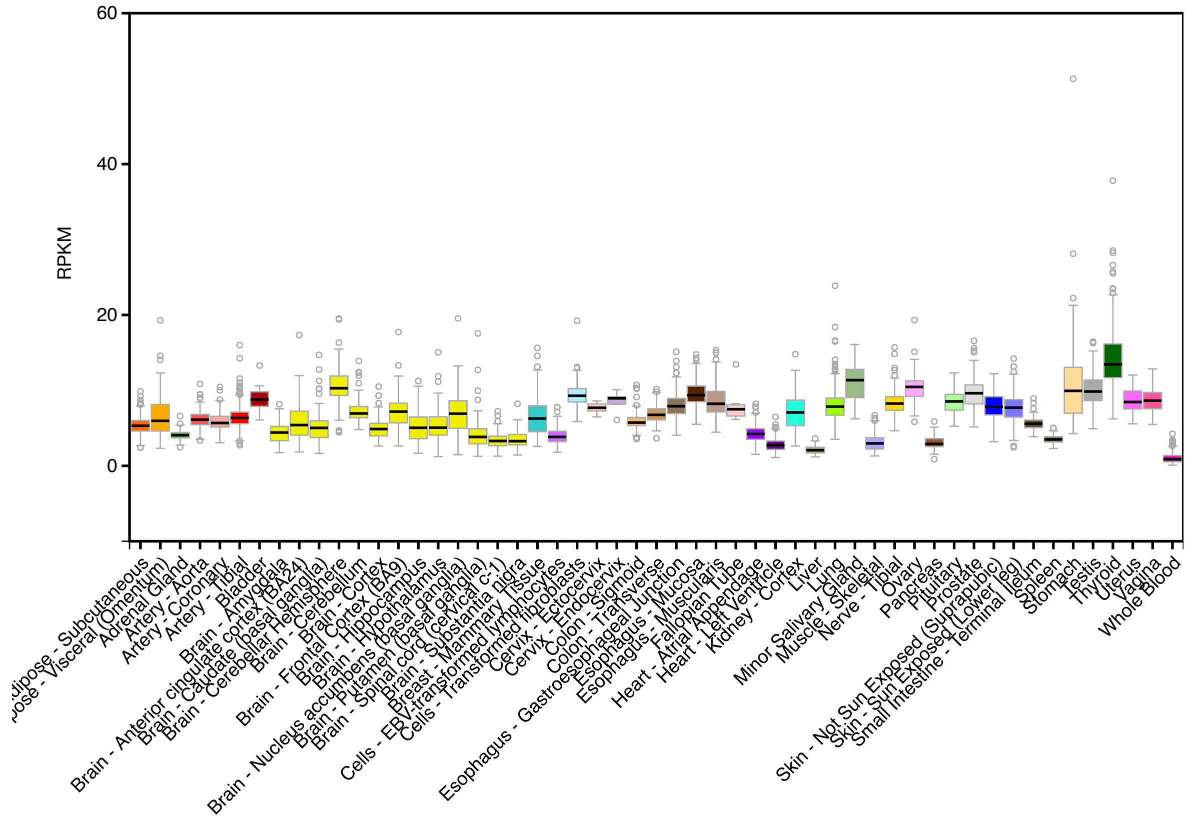
Supplementary Figure 3i. *GPR160* expression in the 53 normal tissues reported by GTEx



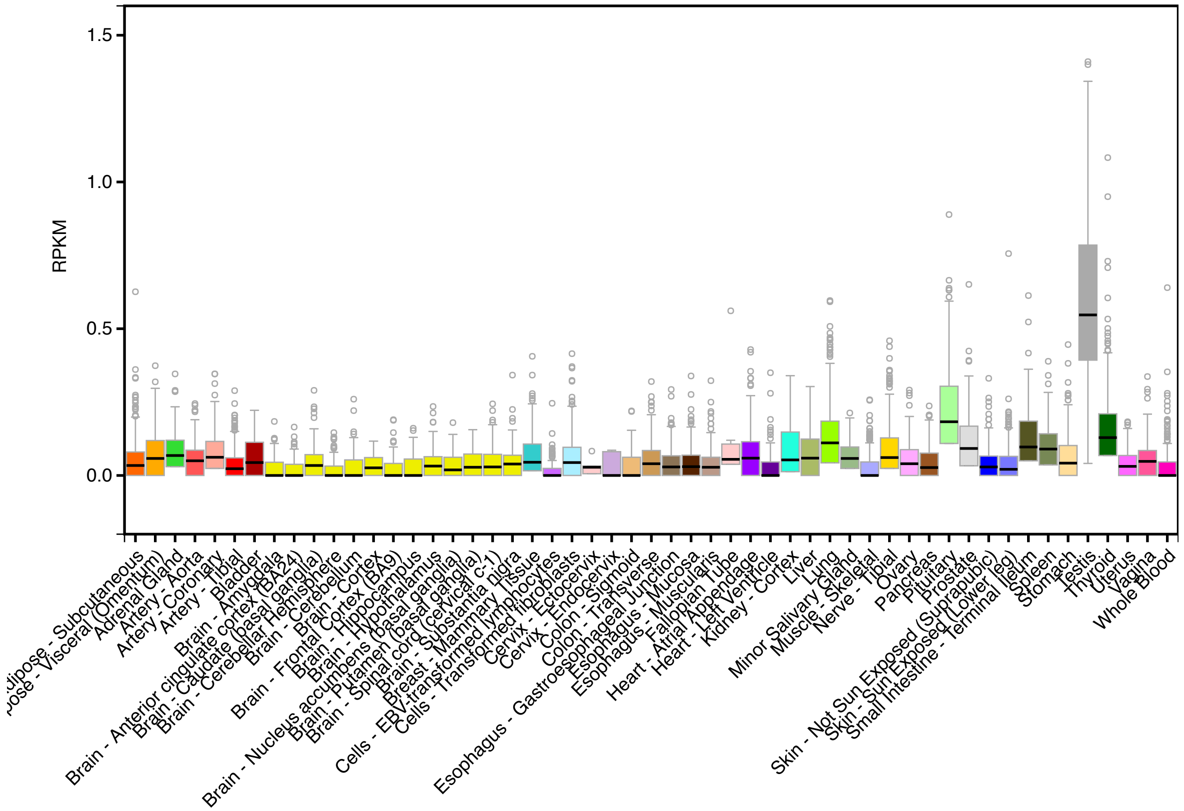
Supplementary Figure 3j. *PHC3* expression in the 53 normal tissues reported by GTEx



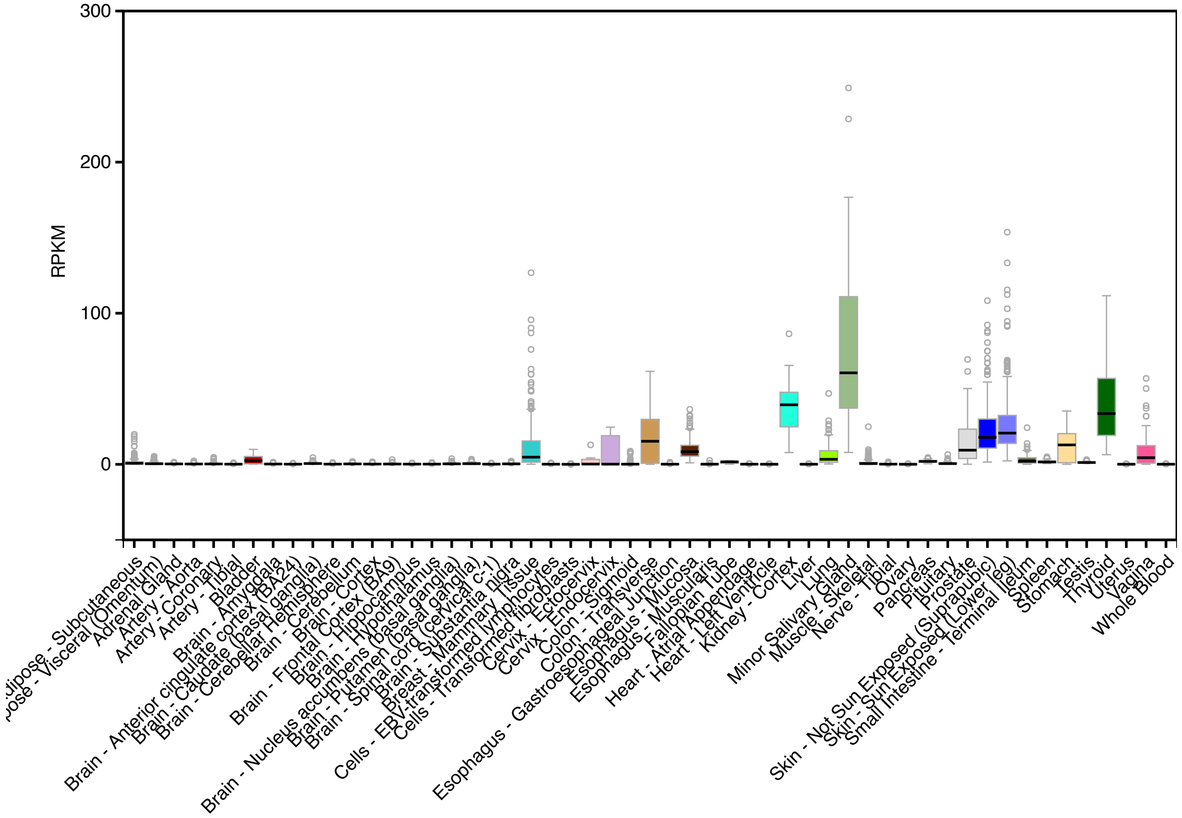
Supplementary Figure 3k. *PRKCI* expression in the 53 normal tissues reported by GTEx



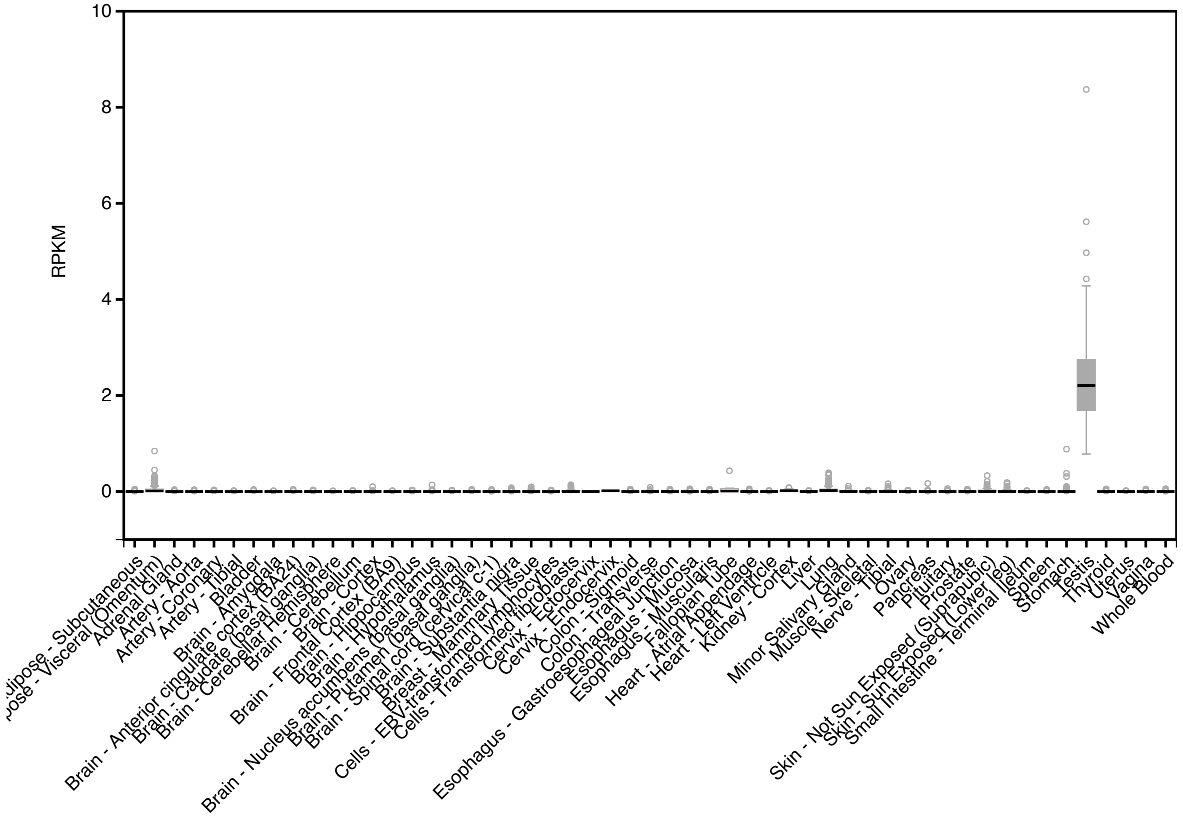
Supplementary Figure 3I. *RP11-469J4.3* expression in the 53 normal tissues reported by GTEx



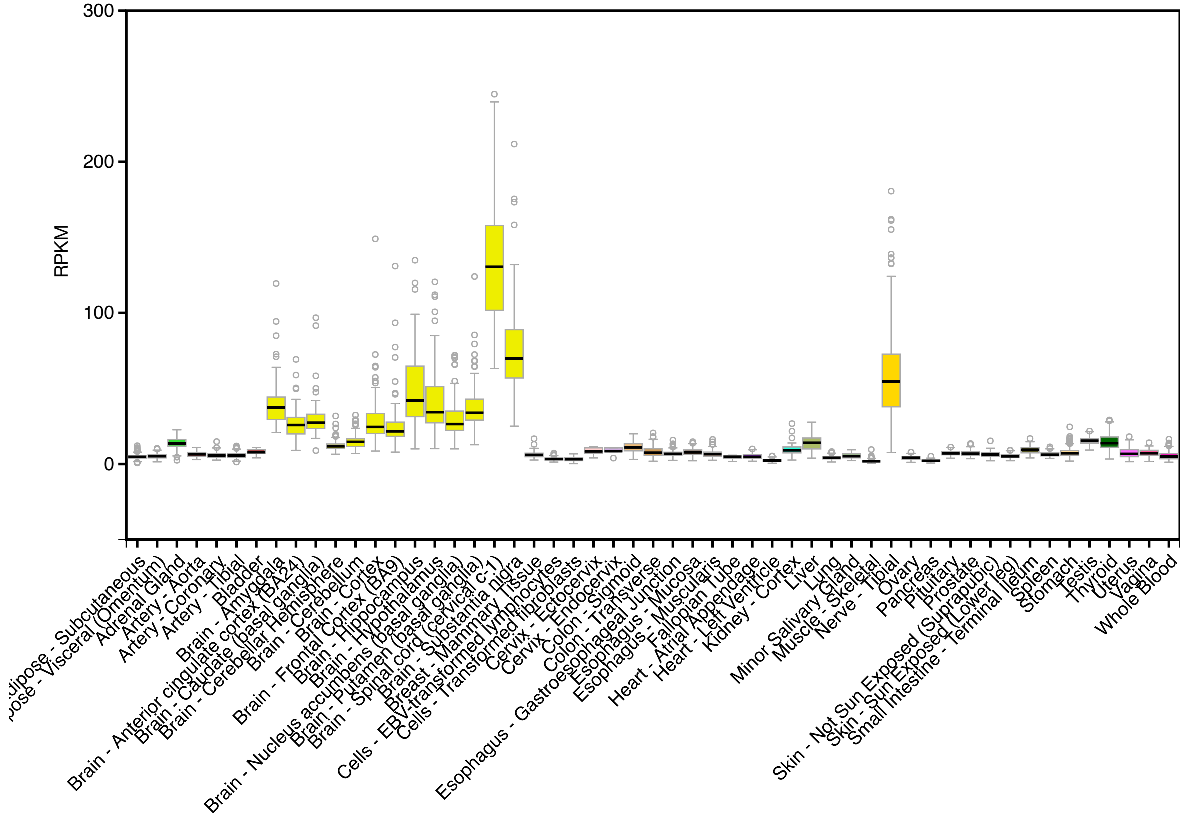
Supplementary Figure 3m. *TFCP2L1* expression in the 53 normal tissues reported by GTEx



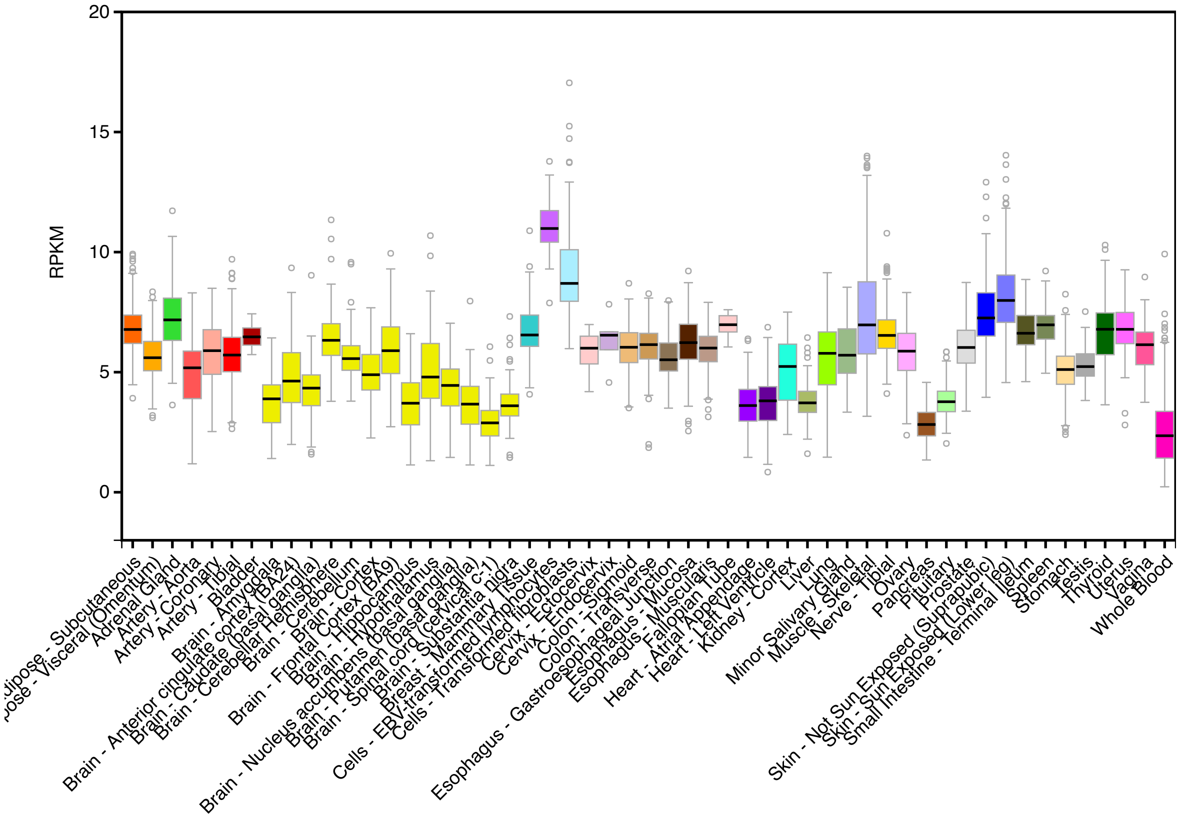
Supplementary Figure 3n. *ZFP42* expression in the 53 normal tissues reported by GTEx



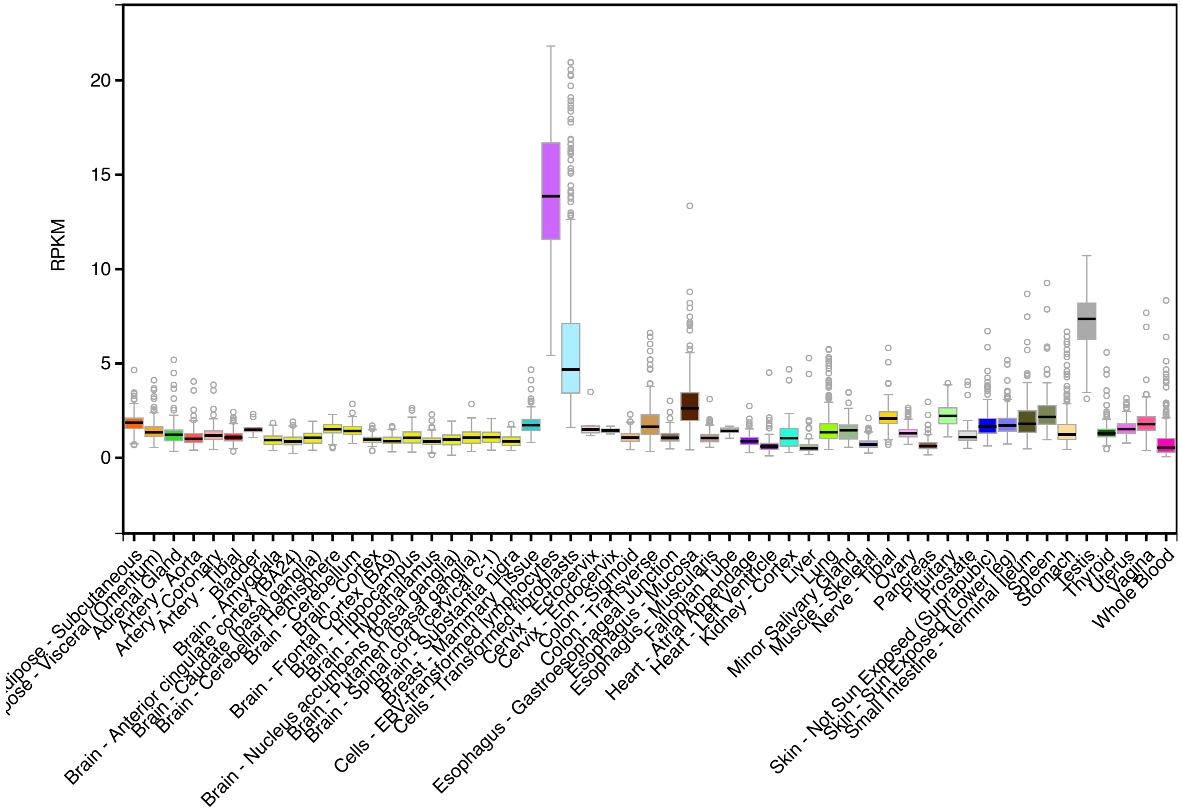
Supplementary Figure 3o. *LHPP* expression in the 53 normal tissues reported by GTEx



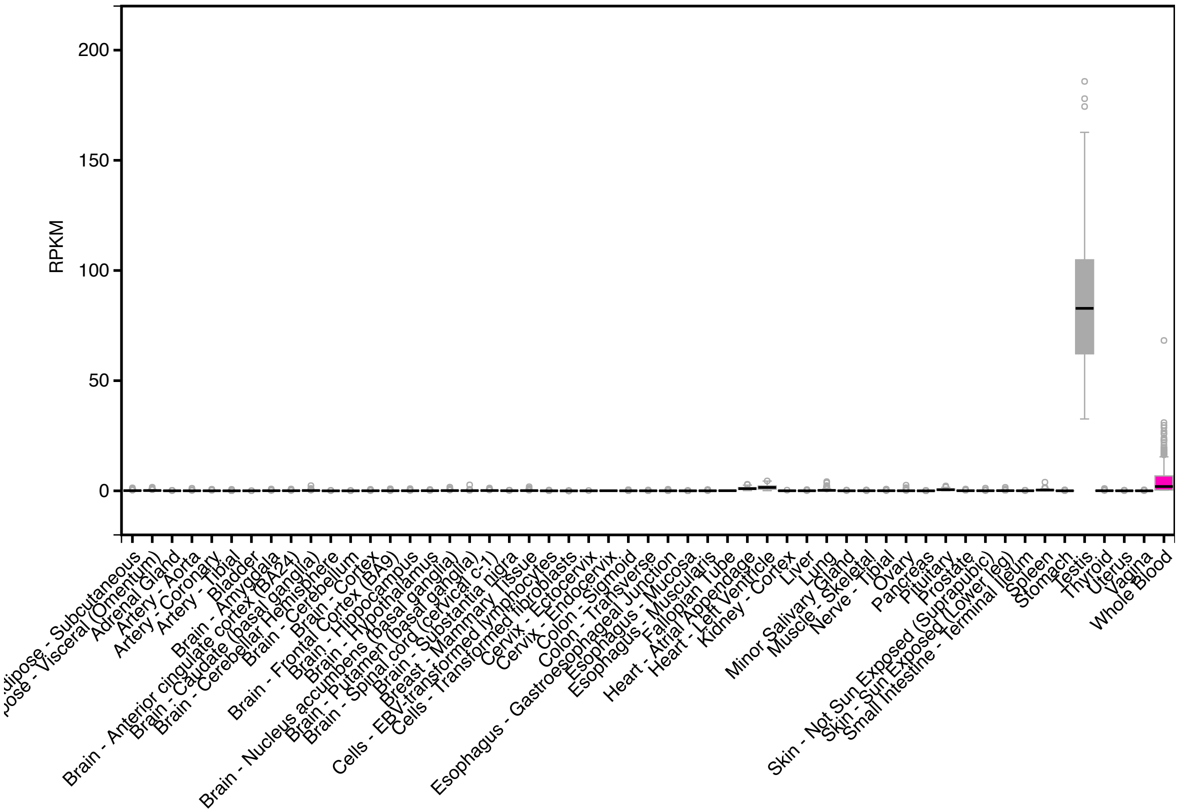
Supplementary Figure 3p. *LHPP* expression in the 53 normal tissues reported by GTEx



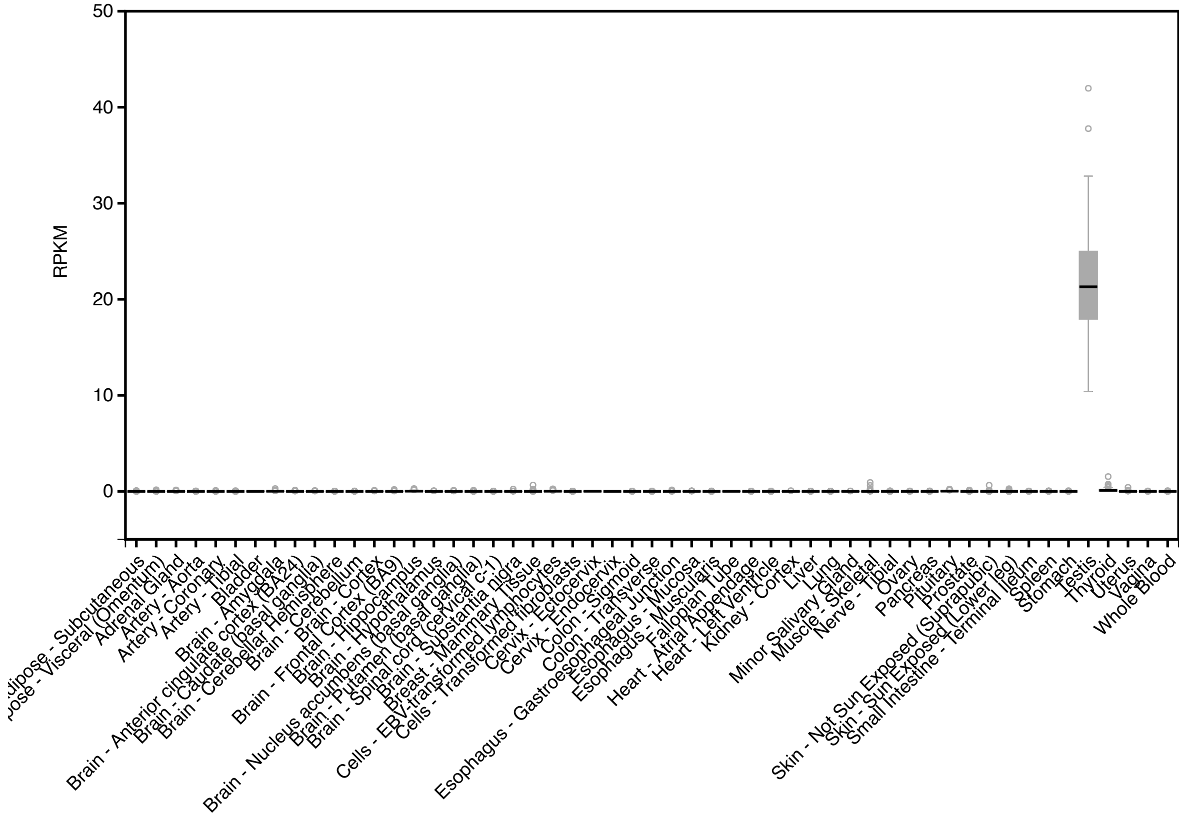
Supplementary Figure 3q. *NCAPG2* expression in the 53 normal tissues reported by GTEx



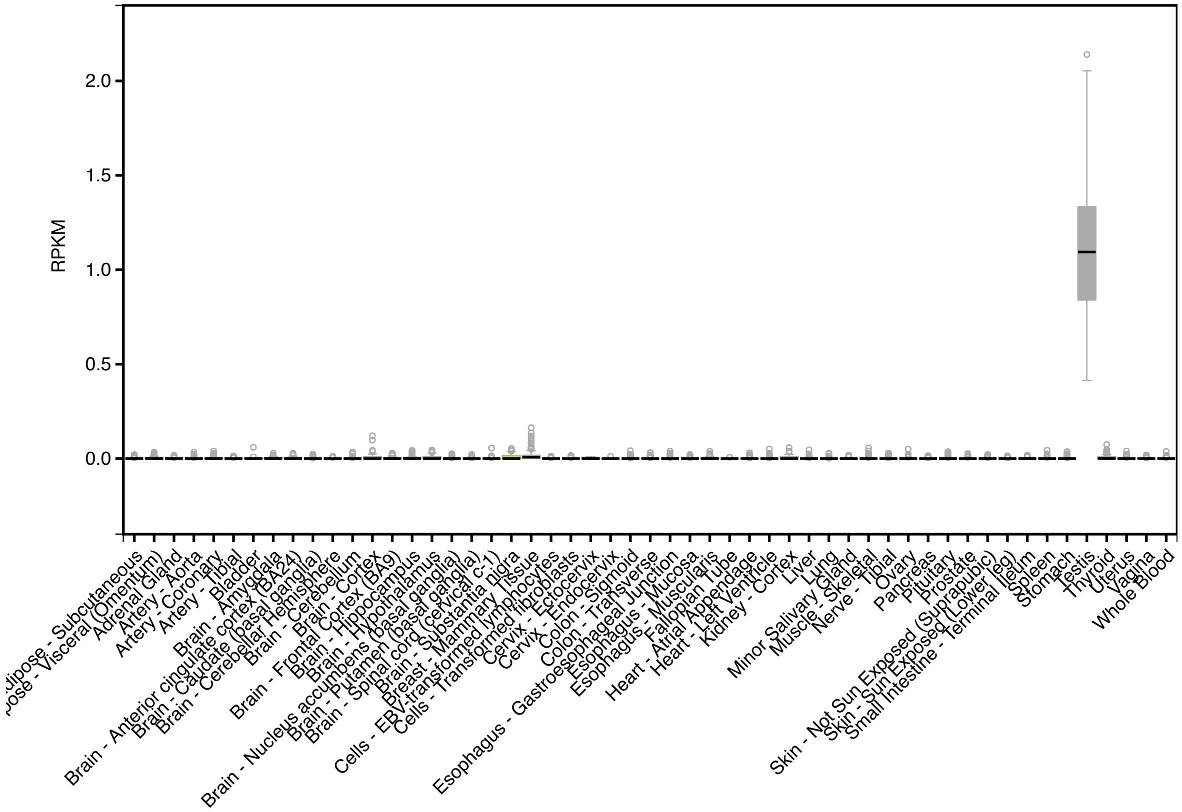
Supplementary Figure 3r. *TKTL1* expression in the 53 normal tissues reported by GTEx



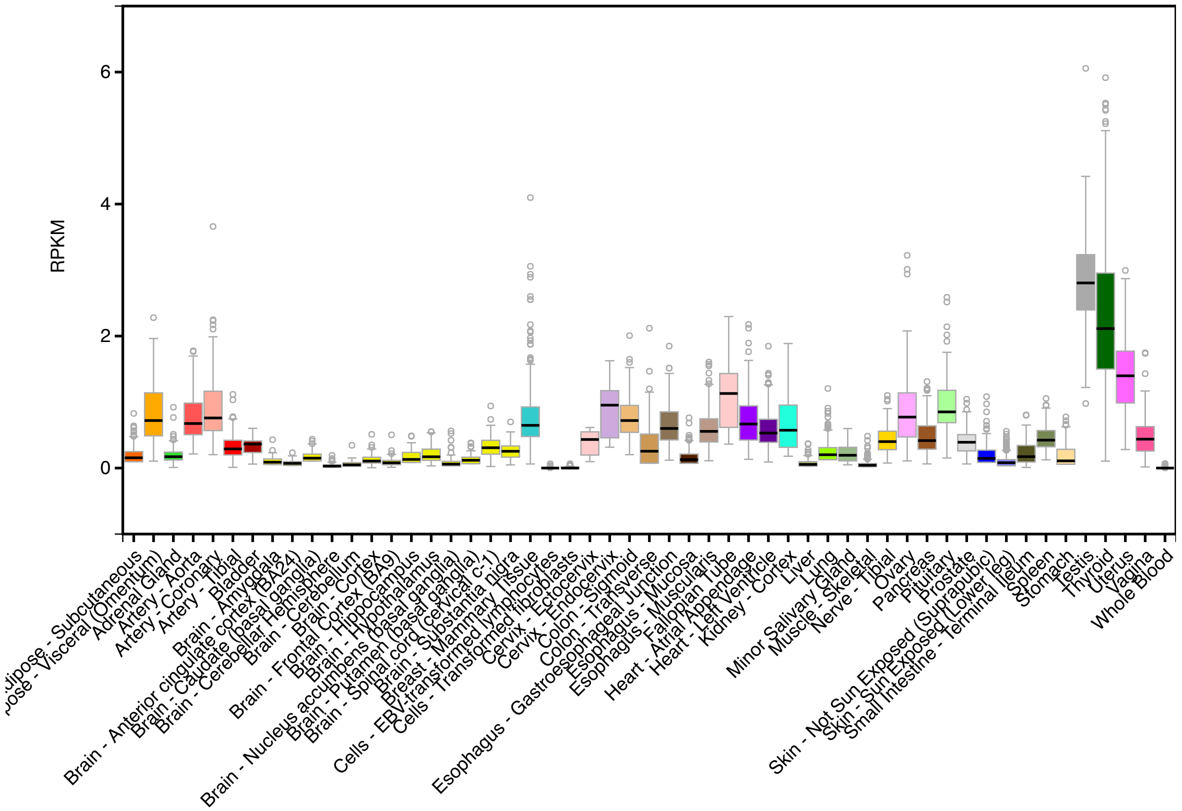
Supplementary Figure 3s. *DMRT1* expression in the 53 normal tissues reported by GTEx



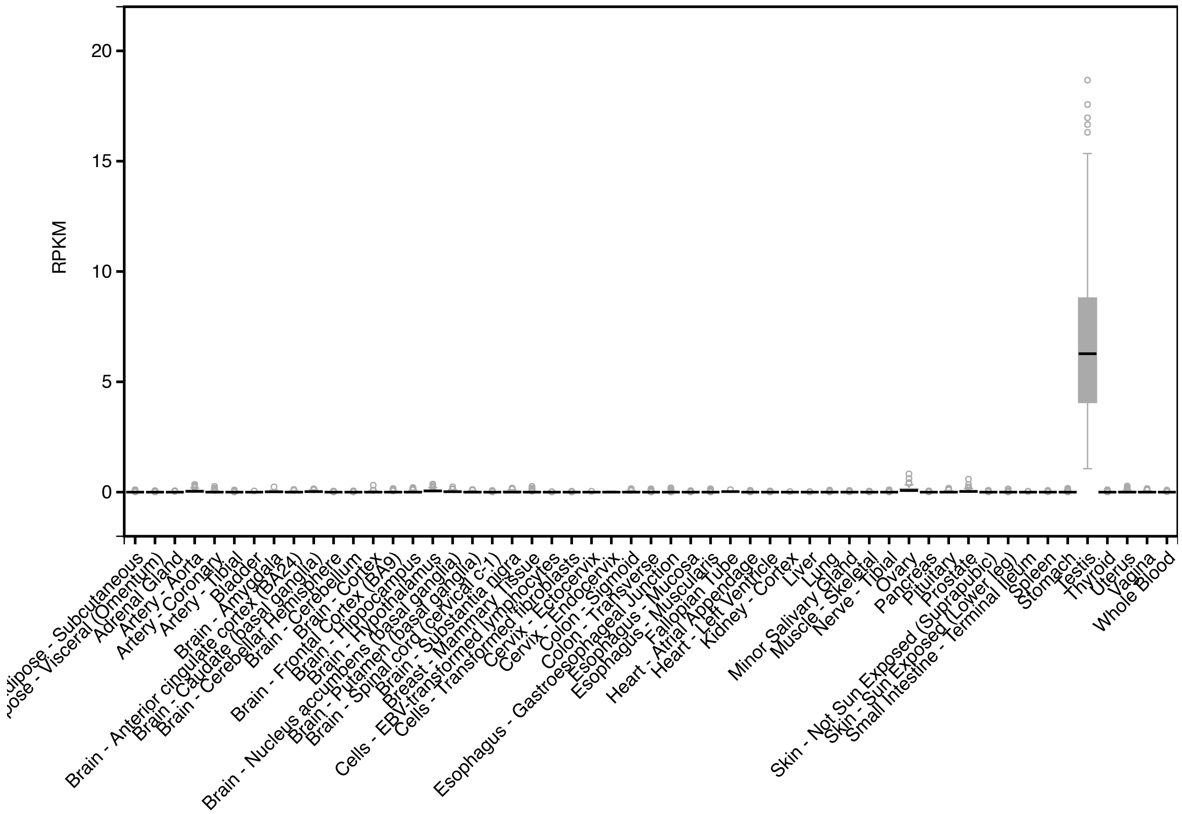
Supplementary Figure 3t. *ZNF729* expression in the 53 normal tissues reported by GTEx



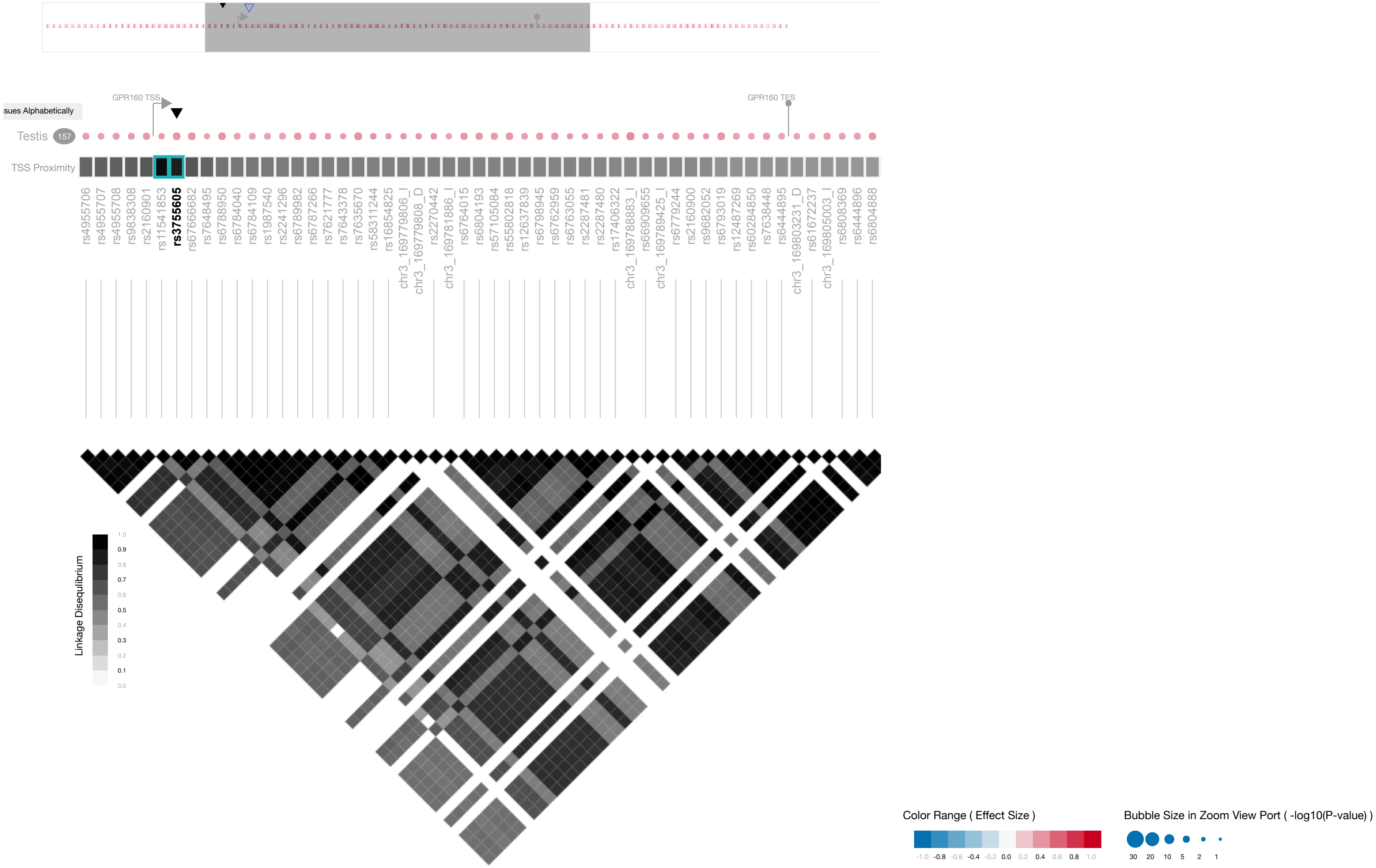
Supplementary Figure 3u. *ZNF676* expression in the 53 normal tissues reported by GTEx



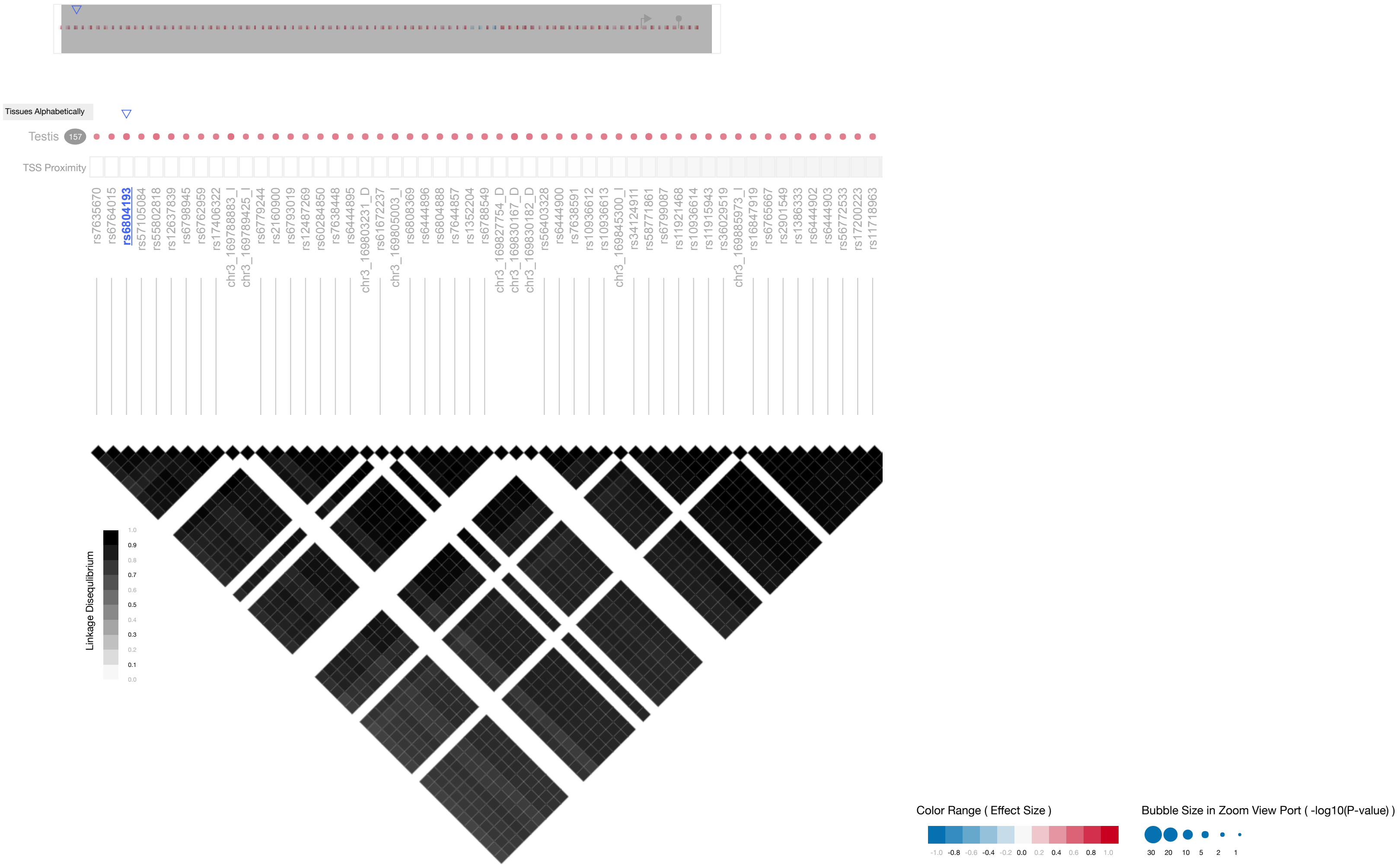
Supplementary Figure 3v. *CTD-2291D10.2* expression in the 53 normal tissues reported by GTEx



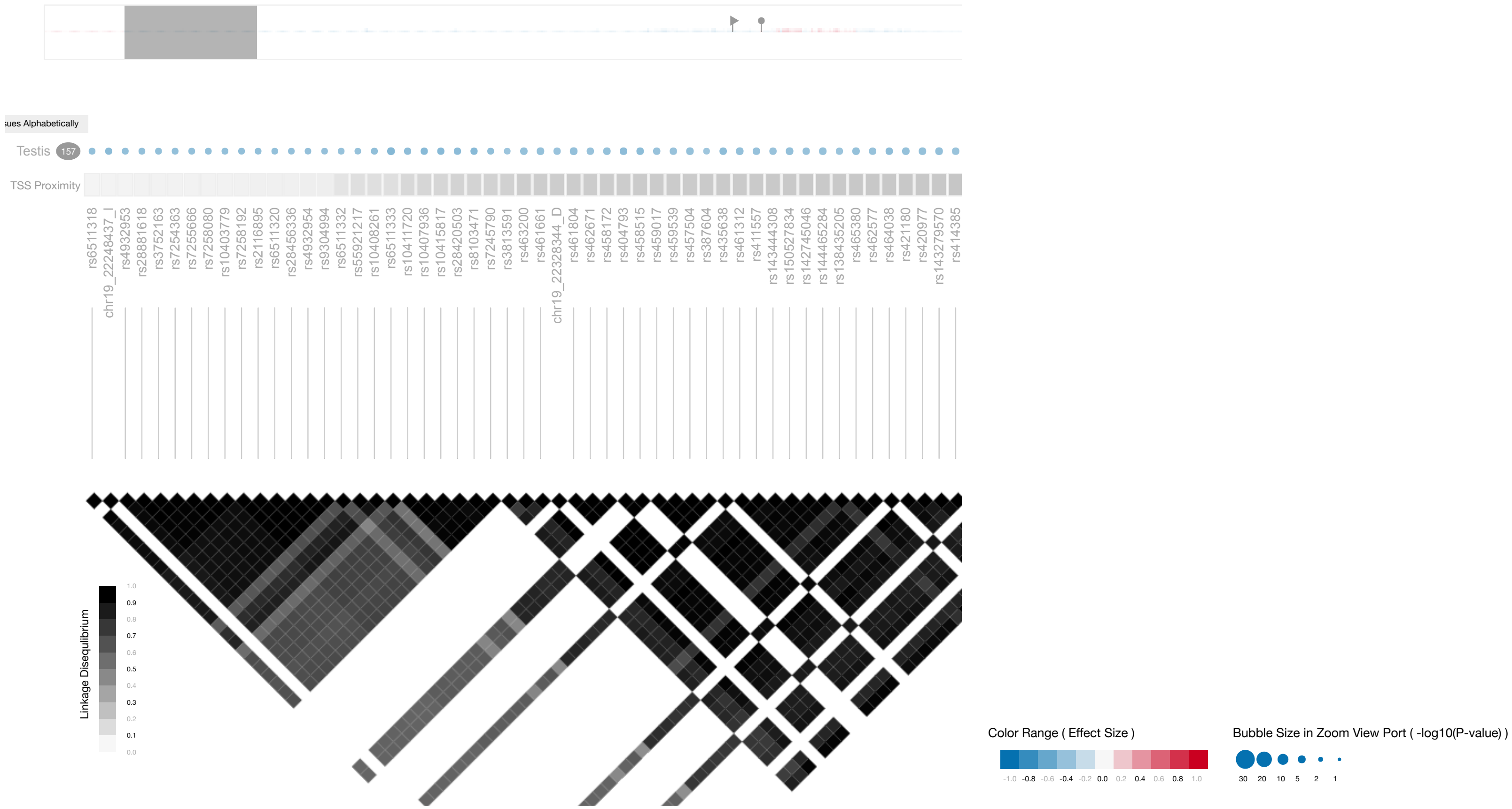
Supplementary Figure 4a. eQTL SNPs across the region of *GPR160* in normal testes (GTEx)



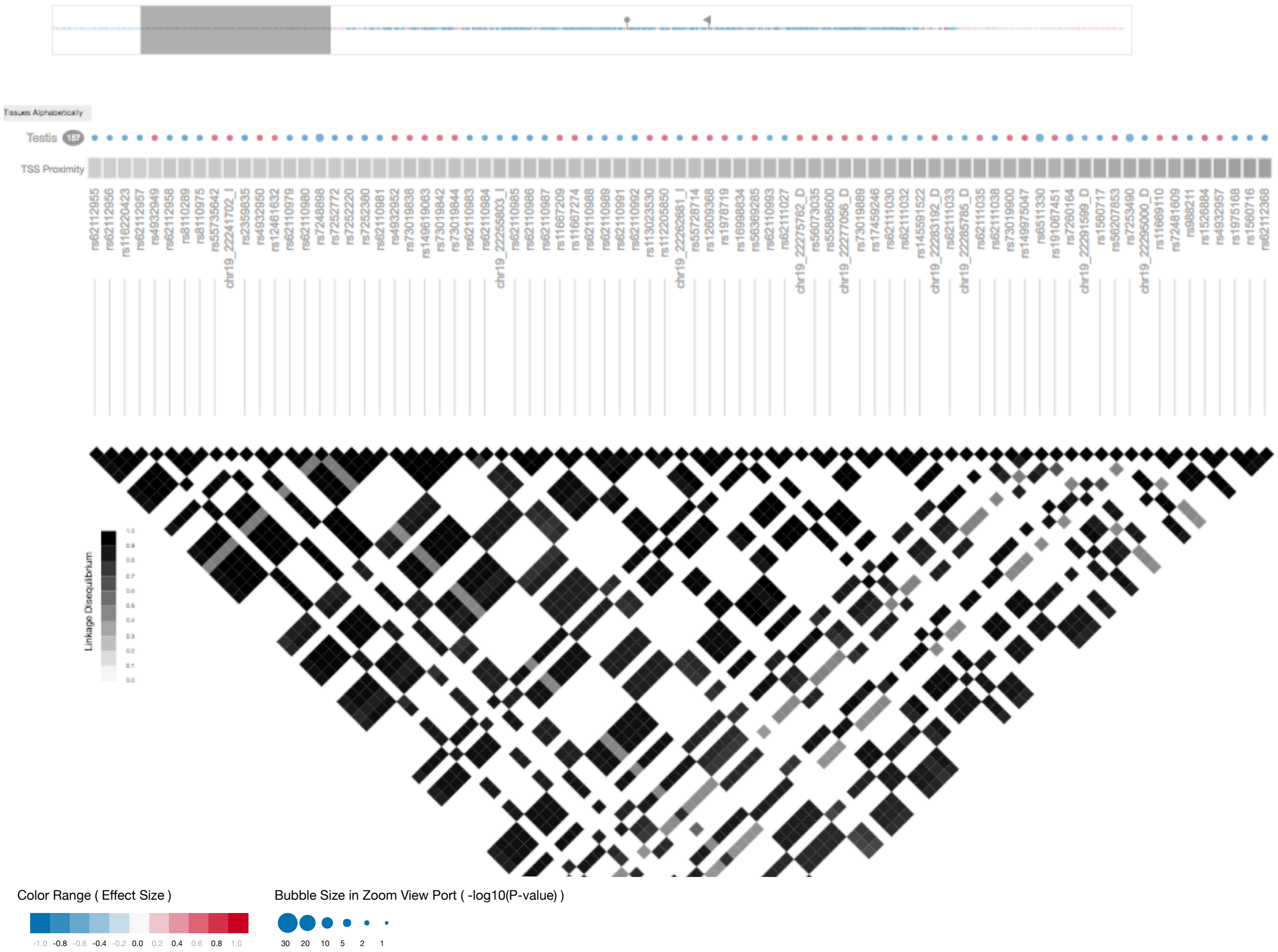
Supplementary Figure 4b. eQTL SNPs across the region of *RP11-469J4.3* in normal testes (GTEx)



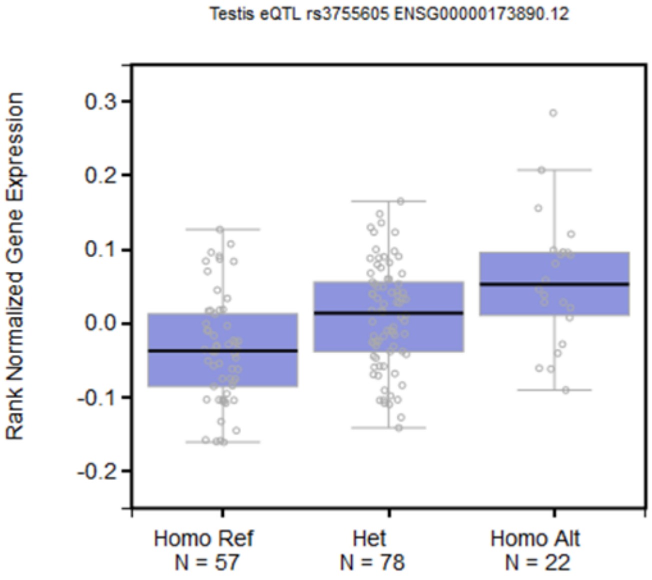
Supplementary Figure 4c. eQTL SNPs across the region of *ZNF729* in normal testes (GTEx)



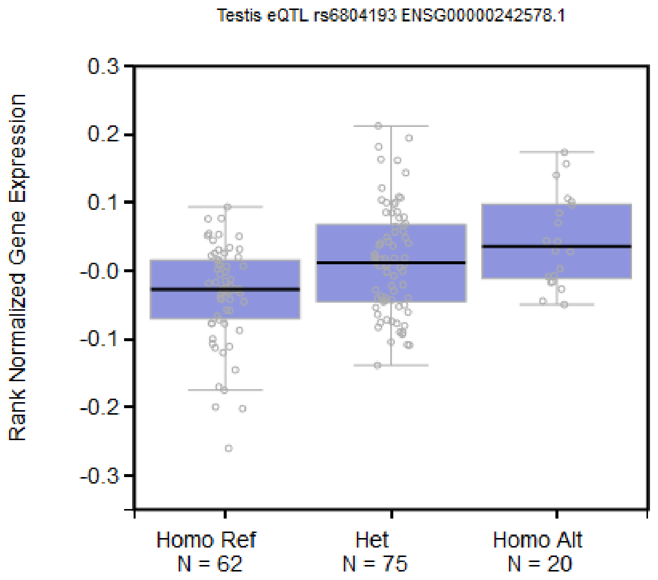
Supplementary Figure 4d. eQTL SNPs across the region of *ZNF676* in normal testes (GTEx)



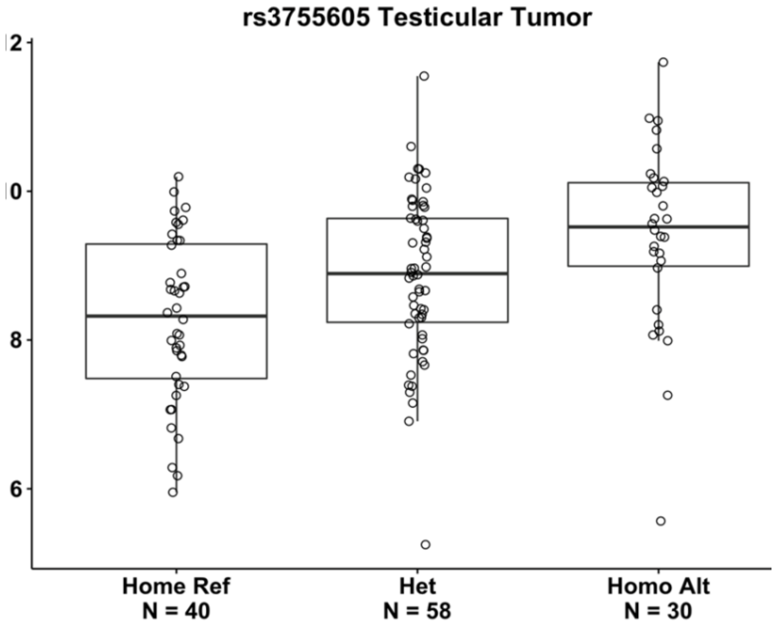
Supplementary Figure 5a. eQTL association of rs3755605 genotype status and GPR160 expression in normal testis (GTEx) – p-value – 3.4e-08



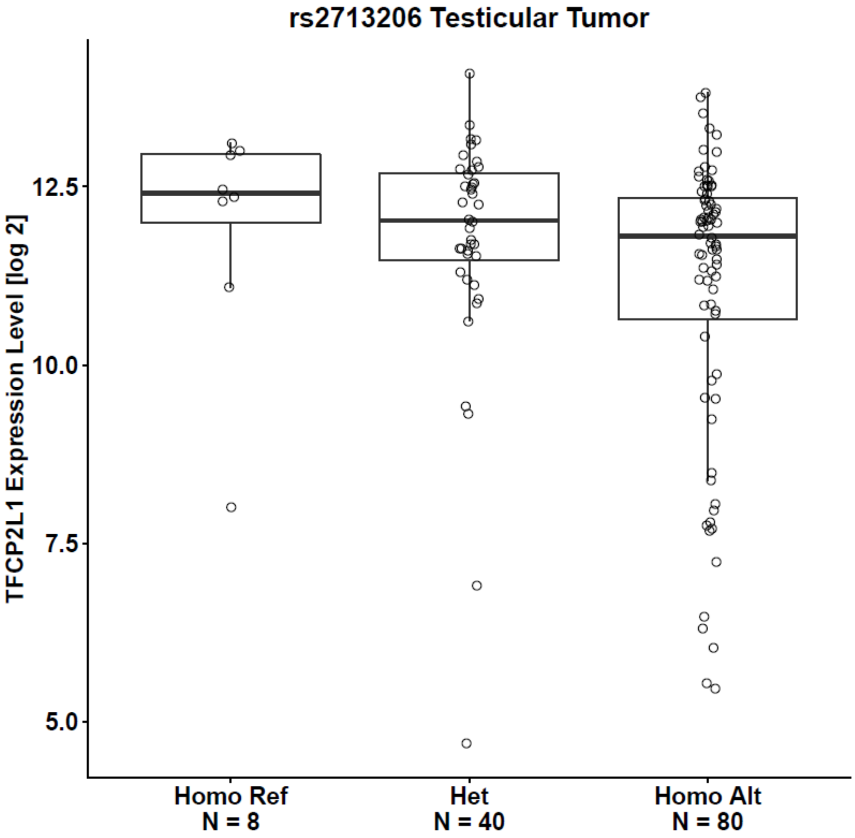
Supplementary Figure 5b. eQTL association of rs6804193 genotype status and RP11-469J4.3 expression in normal testis – p-value – 7.9e-07



Supplementary Figure 6a. eQTL association of rs3755605 genotype status and GPR160 expression in TGCT (TCGA) – p-value - 6.43e-05



Supplementary Figure 6b. eQTL association of rs2713206 genotype status and TFCP2L1 expression in TGCT (TCGA) – p-value 0.058 (p value 0.0047 with non-transformed expression values)



Supplementary Figure 6c. eQTL association of rs17336718 genotype status and TKTL1 expression in TGCT (TCGA) – p-value 0.037