Supplementary Table1. Description of the studies included in PanC4 Case-Control Consortium

Study	Cases	Controls	Accrual Years	Source of cases	Source of Controls	Control Matching	Age of Diagnosis for Cases (SD)[a]	Age of Controls (SD)	Male (%)	Cauc (%)[b]
IARC	448	456	2006-2010	Academic hospitals	General practitioners;	Age; sex; region	63.84 (11.16)	61.88 (11.88)	57	100
Johns Hopkins Hospital	315	81	2007-2011	Clinic	Spouse in-law	None (in-law)	64.29 (11.53)	63.45 (14.73)	51	93
Mayo Clinic	1104	1027	2000-2010	Clinic	Primary care patients	Age; sex; race; residence	65.92 (11.09)	63.34 (10.58)	56	93
MD Anderson	616	509	1997-2007	Hospital	Friends and spouses of non-pancreatic cancer patients	Age; race; sex	62.6 (9.69)	59.2 (10.6)	59	100
Memorial Sloan Kettering	317	139	2000-2008	Clinic	Patient Spouses and patient visitors	None	64.03 (10.39)	61.68 (10.98)	64	87
Toronto	402	401	2003-2012	Population-based cancer registry	Family medicine clinic database	Age; sex; ethnicity	64.92 (11.03)	62.95 (11.73)	50	85
Queensland	559	604	2007-2011	Population-based hospitals & cancer registry	Electoral rolls	Age; sex	66.64 (11.26)	67.51 (10.91)	60	96
UCSF	253	248	2006-2010	Two UCSF Clinics	Three UCSF Clinics	Frequency matched by age and sex	62.52 (10.35)	60.4 (10.96)	54	82
YALE	156	366	2005-2009	Population-based hospitals & cancer registry	Enhanced RDD	Frequency matched by age and sex	67.02 (10.43)	65.15 (10.6)	59	93
Total[c]	4170	3831					64.76	63.09	58	95

							(10.92)	(11.33)		

a- SD- Standard Deviation

b- Percent self-identifying as Caucasian

c- Table excludes the 31 failed samples and 20 samples with unresolved identity issues (See Supplementary Table 2)

Supplementary Table 2. Quality control steps applied to PanC4 Samples and SNPs

Filters Applied	**N**
Samples	
Total Samples Genotyped	8,052
Failed samples	31
Unresolved identity issues	20
Relatedness issues	45
Total Samples Analyzed	**7,956**
SNPs	
Total SNPs Genotyped	951,117
MAF<= 0.005	244,744
Technical failures or missing call rate greater than 2%	22,865
HWE p-value $<10^{-6}$	9,477
Positional duplicates	18,699
More than 1 Mendelian error in HapMap control trios	755
More than two discordant calls in study duplicates	102
Sex difference in allele frequency greater than 0.2	5
Total SNPs Analyzed	**654,470**

Supplementary Table 3. Association results for ten loci previously identified in pancreatic cancer GWASs

Chr	Gene[a]	SNP	Position[b]	Study[c]	Reported OR (CI)[d]	Reported P-value[e]	PanC4 OR (CI)[f]	PanC4 P-value [g]
9q34	*ABO*	rs505922	136149229	PanScan 1	1.2 (1.12 - 1.28)	5.37×10^{-8}	1.27 (1.19 - 1.35)	1.72×10^{-13}
13q22.1	*KLF5 AND KLF12*	rs9543325	73916628	PanScan 2	1.26 (1.18 - 1.35)	3.27×10^{-11}	1.24 (1.16 - 1.32)	2.26×10^{-10}
1q32.1	*NR5A2*	rs3790844	200007432	PanScan 2	0.77 (0.71 - 0.84)	2.45×10^{-10}	0.83 (0.77 - 0.90)	3.05×10^{-6}
5p15.33	*CLPTM1L*	rs401681	1322087	PanScan 2	1.19 (1.11 - 1.27)	3.66×10^{-7}	1.20 (1.13 -1.28)	2.70×10^{-8}
5p15.33	*TERT*	rs2736098	1294086	PanScan 3	0.80 (0.76 - 0.85)	9.78×10^{-14}	0.85 (0.78 - 0.93)	2.31×10^{-5}
7q32.3	*LINC-PINT*	rs6971499	130680521	PanScan 3	0.79 (0.74 - 0.84)	2.98×10^{-12}	0.81 (0.74 - 0.88)	7.10×10^{-6}
16q23.1	*BCAR1*	rs7190458	75263661	PanScan 3	1.46 (1.3 - 1.65)	1.13×10^{-10}	1.40 (1.22 - 1.60)	1.01×10^{-4}
13q12.2	*PDX1*	rs9581943	28493997	PanScan 3	1.15 (1.1 - 1.2)	2.35×10^{-9}	1.17 (1.10 - 1.24)	1.94×10^{-7}
22q12.1	*ZNRF3*	rs16986825	29300306	PanScan 3	1.18 (1.12 - 1.25)	1.18×10^{-8}	1.14 (1.04 - 1.24)	2.72×10^{-3}
8q24.21	*MIR1208*	rs1561927	129568078	PanScan 3	0.87 (0.83 - 0.92)	1.3×10^{-7}	0.92 (0.85-0.99)	2.20×10^{-2}
2p13.3	*ETAA1*	rs2035565	67,619,656	China	1.33 (1.19 - 1.49)	$5.46 x 10^{-7}$	1.15 (1.07 - 1.25)	$2.69 x 10^{-4}$

a. RefSeq Gene symbol of the closest gene to the listed SNP. For SNPs not intragenic to the listed gene, the gene is listed in grey.
b. Position of the SNP according to NCBI Human Genome Build 37
c. GWAS where the SNP was first found to be associated with Pancreatic Cancer
d. Odds ratio and Confidence Interval for the SNP in publication listed in the Study column
e. P-value listed in the original study
f. OR and CI from a test for association of this SNP with pancreatic cancer in the PanC4 Study
g. P-value from a test for association of this SNP with pancreatic cancer in the PanC4 Study

Supplementary Table 4. Quality control steps applied to PanScan 1 and PanScan 2 Samples and SNPs

Filters Applied	PanScan 1 N	PanScan 2 N
Samples		
Total Samples Genotyped	3,937	3,484
Failed samples	3	38
Unresolved identity issues	27	9
Replicated subjects	152	137
Relatedness issues	9	0
Total Samples Analyzed	**3,746**	**3,300**
SNPs		
Total SNPs Genotyped	561,466	620,901
MAF<= 0.005	13,701	43,531
Technical failures or missing call rate greater than 2%	12,443	16,131
HWE p-value $<10^{-6}$	7,143	3,682
Missingness varying by phenotype (p<0.00001)	0	2
Total SNPs Analyzed	**528,179**	**557,555**

Supplementary Table 5. Association results for 25 SNPs in Stages 1 and 2

			Stage 1					Stage 2			
Chr[a] SNP Position[b] Gene	**Effect Allele (Minor)/ Reference Allele**	**Statistic**	**PanC4**	**PanScan 1**	**PanScan 2**	**All Stage 1[c]**	**Heterogeneity[d]**	**PANDoRA**	**Heterogeneity[e]**	**Combined Stage 1&2[f]**	**Heterogeneity[g]**
17q25.1	T/C	maf[h] cases;controls	0.146; 0.11	0.139; 0.129	0.149; 0.116			0.135; 0.114			
rs11655237		info[i]	0.963	g	g						
70400166		OR (CI)[j]	1.38 (1.26 - 1.52)	1.09 (0.96 - 1.25)	1.34 (1.16 - 1.55)	1.27 (1.19 - 1.36)		1.24 (1.1 - 1.4)		1.26 (1.19 - 1.34)	
LINC00673		p-value	1.38E-10	1.95E-01	2.95E-04	6.74E-12	2.29E-02	6.40E-04	2.49E-01	1.42E-14	7.34E-02
17q25.1	T/C	maf cases;controls	0.148; 0.112	0.140; 0.133	0.150; 0.117			0.139; 0.117			
rs7214041		info	g	0.966	0.96						
70401476		OR (CI)	1.38 (1.26 - 1.51)	1.07 (0.93 - 1.22)	1.33 (1.15 - 1.53)	1.26 (1.18 - 1.35)		1.25 (1.11 - 1.41)		1.26 (1.19 - 1.34)	
LINC00673		p-value	1.95E-10	3.36E-01	3.69E-04	2.67E-11	1.46E-02	3.37E-04	3.69E-01	2.88E-14	8.52E-02
13q12.2	T/C	maf cases;controls	0.440; 0.399	0.428; 0.416	0.437; 0.405			0.450; 0.424			
rs9554197		info	g	g	g						
28476978		OR (CI)	1.18 (1.11 - 1.26)	1.05 (0.96 - 1.15)	1.14 (1.03 - 1.26)	1.15 (1.1 - 1.21)		1.11 (1.03 - 1.2)		1.14 (1.1 - 1.19)	
PDX1-AS1		p-value	4.22E-08	3.20E-01	1.05E-03	1.93E-09	6.25E-02	1.03E-02	8.35E-01	8.89E-11	4.12E-01
2p13.3	G/T	maf cases;controls	0.302; 0.275	0.305; 0.292	0.305; 0.276			0.292; 0.273			
rs1486134		info	g	g	g						
67639769		OR (CI)	1.14 (1.06 - 1.22)	1.06 (0.96 - 1.18)	1.15 (1.03 - 1.28)	1.13 (1.08 - 1.19)		1.16 (1.06 - 1.27)		1.14 (1.09 - 1.19)	
ETAA1 (2236 bp on 3')		p-value	5.96E-05	1.57E-01	5.18E-03	8.35E-07	4.54E-01	9.42E-04	3.32E-02	3.36E-09	8.32E-02
2p13.3	C/T	maf cases;controls	0.407; 0.379	0.401; 0.391	0.406; 0.371			0.386; 0.31			
rs962856		info	g	g	g						
67593803		OR (CI)	1.12 (1.06 -1.20)	1.04 (0.95 - 1.14)	1.16 (1.05 - 1.28)	1.12 (1.07 - 1.18)		1.12 (1.03 - 1.22)		1.12 (1.08 - 1.17)	
		p-value	4.58E-05	3.40E-01	1.37E-03	8.30E-07	1.82E-01	8.05E-03	1.87E-01	2.21E-08	2.08E-01
7p13	A/C	maf cases;controls	0.241; 0.263	0.218; 0.254	0.237; 0.268			0.254; 0.277			
rs17688601		info	g	g	g						
40866663		OR (CI)	0.89 (0.83 - 0.96)	0.82 (0.73 - 0.91)	0.85 (0.76 - 0.94)	0.87 (0.82 - 0.91)		0.91 (0.83 - 1)		0.88 (0.84 - 0.92)	
SUGCT		p-value	1.98E-03	1.66E-04	8.72E-03	9.77E-08	3.99E-01	3.93E-02	7.25E-02	1.41E-08	1.23E-01
3q29	A/G	maf cases;controls	0.328; 0.362	0.336; 0.366	0.325; 0.356			0.341; 0.356			
rs9854771		info	g	0.998	0.998						
189508471		OR (CI)	0.86 (0.81 - 0.92)	0.88 (0.80 - 0.97)	0.87 (0.79 - 0.97)	0.87 (0.83 - 0.92)		0.93 (0.86 - 1.01)		0.89 (0.85 - 0.93)	
TP63		p-value	3.10E-05	7.94E-03	1.55E-02	4.08E-08	9.71E-01	1.01E-01	8.15E-01	2.35E-08	8.61E-01
18q21.2	T/C	maf cases;controls	0.172; 0.182	0.170; 0.195	0.164; 0.189			0.168; 0.187			
rs1517037		info	g	g	g						
56878274		OR (CI)	0.93 (0.86 - 1.01)	0.85 (0.75 - 0.95)	0.84 (0.74 - 0.95)	0.87 (0.82 - 0.93)		0.87 (0.79 - 0.97)		0.87 (0.83 - 0.92)	
GRP (9126 bp on 5')		p-value	3.39E-02	3.82E-03	1.82E-03	9.93E-06	2.56E-01	1.17E-02	7.73E-02	3.17E-07	1.24E-01
12q24.31	A/G	maf cases;controls	0.407; 0.386	0.423; 0.375	0.421; 0.392			0.426; 0.415			
rs7310409		info	g	g	g						
121424861		OR (CI)	1.09 (1.02 - 1.16)	1.22 (1.11 - 1.34)	1.13 (1.02 - 1.24)	1.12 (1.07 - 1.18)		1.07 (0.98 - 1.16)		1.11 (1.06 - 1.15)	
HNF1A		p-value	1.80E-02	5.35E-05	1.76E-02	1.24E-06	1.45E-01	1.26E-01	9.95E-01	6.34E-07	7.08E-01
1p13.1	T/C	maf cases;controls	0.228; 0.257	0.24; 0.254	0.239; 0.258			0.229; 0.248			
rs351365		info	g	0.891	0.889						
113046395		OR (CI)	0.85 (0.79 - 0.92)	0.93 (0.84 - 1.03)	0.91 (0.81 - 1.01)	0.88 (0.83 - 0.93)		0.92 (0.83 - 1.01)		0.89 (0.85 - 0.93)	
WNT2B		p-value	3.08E-05	1.62E-01	4.45E-02	2.72E-06	5.21E-01	8.02E-02	3.97E-01	7.39E-07	5.33E-01
20q13.11	A/G	maf cases;controls	0.415; 0.381	0.429; 0.411	0.411; 0.384			0.413; 0.403			
rs6073450		info	g	g	g						
43086648		OR (CI)	1.15 (1.08 - 1.23)	1.08 (0.98 - 1.18)	1.12 (1.02 - 1.24)	1.12 (1.06 - 1.17)		1.09 (1 - 1.18)		1.11 (1.06 - 1.15)	
		p-value	1.82E-04	1.20E-01	2.62E-02	6.01E-06	6.79E-01	4.92E-02	9.03E-01	9.21E-07	9.52E-01
17q25.1	G/A	maf cases;controls	0.312; 0.282	0.292; 0.281	0.317; 0.29			0.289; 0.272			
rs11652288		info	g	0.892	0.802						
70405340		OR (CI)	1.15 (1.08 - 1.23)	1.05 (0.95 - 1.16)	1.14 (1.02 - 1.26)	1.13 (1.07 - 1.18)		1.07 (0.98 - 1.17)		1.11 (1.06 - 1.16)	
LINC00673		p-value	1.04E-04	2.42E-01	2.56E-02	8.90E-06	4.98E-01	1.52E-01	5.59E-01	4.53E-06	6.11E-01
1p31.3	C/A	maf cases;controls	0.222; 0.233	0.207; 0.233	0.220; 0.243			0.230; 0.237			
rs1747924		info[g]	g	g	g						
64538961		OR (CI)[h]	0.94 (0.87 - 1.01)	0.86 (0.77 - 0.96)	0.88 (0.78 - 0.98)	0.88 (0.84 - 0.93)		0.94 (0.85 - 1.03)		0.9 (0.86 - 0.94)	
ROR1		p-value	2.38E-02	4.06E-03	3.13E-03	9.16E-06	3.33E-01	1.94E-01	1.94E-01	6.74E-06	2.12E-01
21q11.2	A/G	maf cases;controls	0.494; 0.464	0.234; 0.227	0.247; 0.209			0.253; 0.252			
rs1822660		info	0.619	g	g						
22658894		OR (CI)	1.13 (1.06 -1.20)	1.04 (0.93 -1.16)	1.24 (1.11 - 1.40)	1.15 (1.09 - 1.22)		1.02 (0.93 - 1.11)		1.11 (1.06 - 1.17)	
NCAM2		p-value	2.19E-05	5.61E-01	6.53E-04	8.86E-07	6.72E-02	7.41E-01	9.29E-02	1.08E-05	1.01E-02
4q26	G/A	maf cases;controls	0.111; 0.098	0.117; 0.099	0.117; 0.088			0.117; 0.116			
rs1380376		info	0.999	g	g						
118636270		OR (CI)	1.15 (1.03 - 1.27)	1.20 (1.04 - 1.39)	1.38 (1.17 - 1.62)	1.19 (1.11 - 1.28)		1.05 (0.93 - 1.2)		1.15 (1.08 - 1.23)	
		p-value	2.35E-02	9.52E-03	3.64E-04	4.38E-06	1.91E-01	4.04E-01	1.46E-01	1.22E-05	7.74E-02
9q31.3	C/T	maf cases;controls	0.407; 0.366	0.391; 0.371	0.390; 0.388			0.365; 0.364			
rs10991043		info	g	g	g						
106797388		OR (CI)	1.19 (1.12 - 1.27)	1.09 (0.99 - 1.2)	1 (0.91 - 1.11)	1.13 (1.08 - 1.18)		1 (0.92 - 1.08)		1.1 (1.05 - 1.14)	
		p-value	7.00E-08	5.18E-02	7.09E-01	5.10E-07	2.56E-02	9.19E-01	3.02E-01	1.35E-05	1.05E-02
15q22.32	C/T	maf cases;controls	0.376; 0.354	0.383; 0.357	0.400; 0.356			0.352; 0.341			
rs8024986		info	g	0.999	0.999						
73024868		OR (CI)	1.10 (1.03 - 1.17)	1.12 (1.02 - 1.23)	1.21 (1.09 - 1.33)	1.12 (1.06 - 1.17)		1.04 (0.95 - 1.13)		1.1 (1.05 - 1.14)	
BBS4		p-value	1.25E-02	9.68E-03	2.30E-03	6.30E-06	1.00E+00	4.13E-01	2.28E-01	1.37E-05	2.11E-01
6q25.2	C/T	maf cases;controls	0.300; 0.268	0.288; 0.261	0.290; 0.285			0.286; 0.288			
rs7762516		info	g	0.776	0.744						
154806742		OR (CI)	1.17 (1.09 - 1.25)	1.15 (1.04 - 1.27)	1.02 (0.92 - 1.14)	1.14 (1.08 - 1.2)		1.02 (0.94 - 1.12)		1.11 (1.06 - 1.16)	
CNKSR3		p-value	1.90E-05	3.17E-03	8.81E-01	2.21E-06	1.04E-01	6.29E-01	2.11E-01	1.82E-05	4.34E-02
1p22.3	G/A	maf cases;controls	0.448; 0.481	0.472; 0.493	0.449; 0.474			0.450; 0.452			
rs318405		info	g	g	g						
83014374		OR (CI)	0.88 (0.82 - 0.93)	0.92 (0.84 - 1)	0.91 (0.82 - 1)	0.9 (0.86 - 0.94)		0.99 (0.91 - 1.07)		0.92 (0.88 - 0.95)	
		p-value	5.69E-05	5.69E-02	6.22E-02	2.15E-06	6.88E-01	8.10E-01	2.66E-02	2.19E-05	2.13E-02
12q24.21	G/A	maf cases;controls	0.436; 0.408	0.439; 0.414	0.452; 0.42			0.422; 0.408			
rs10850078		info	g	g	g						
113209519		OR (CI)	1.12 (1.05 - 1.2)	1.11 (1.01 - 1.21)	1.14 (1.03 - 1.25)	1.11 (1.06 - 1.17)		1.02 (0.94 - 1.11)		1.09 (1.05 - 1.13)	
		p-value	1.56E-03	1.63E-02	2.85E-02	6.29E-06	9.80E-01	6.26E-01	1.79E-01	2.98E-05	2.11E-01
1q42.2	G/T	maf cases;controls	0.484; 0.465	0.491; 0.465	0.480; 0.465			0.469; 0.455			
rs1317764		info	g	g	g						
230877400		OR (CI)	1.08 (1.01 - 1.15)	1.11 (1.01 - 1.21)	1.06 (0.96 - 1.17)	1.12 (1.07 - 1.17)		0.98 (0.9 - 1.06)		1.09 (1.04 - 1.13)	
		p-value	1.79E-04	2.37E-02	2.88E-02	1.12E-06	9.62E-01	6.53E-01	6.43E-01	5.72E-05	1.87E-01
5q35.2	A/G	maf cases;controls	0.208; 0.224	0.199; 0.213	0.204; 0.24			0.210; 0.211			
rs6894235		info	g	g	g						
173285545		OR (CI)	0.91 (0.84 - 0.98)	0.92 (0.82 - 1.03)	0.81 (0.72 - 0.91)	0.88 (0.83 - 0.93)		1.01 (0.91 - 1.11)		0.91 (0.87 - 0.95)	
		p-value	8.44E-03	1.27E-01	1.29E-04	7.23E-06	1.64E-01	9.20E-01	5.39E-02	1.10E-04	1.14E-02
10q26.3	C/T	maf cases;controls	0.101; 0.085	0.1; 0.088	0.114; 0.091			0.082; 0.086			
rs7086546		info	g	g	g						
130347966		OR (CI)	1.21 (1.09 - 1.35)	1.16 (0.99 - 1.36)	1.3 (1.11 - 1.52)	1.2 (1.11 - 1.29)		0.88 (0.76 - 1.02)		1.12 (1.04 - 1.2)	
		p-value	2.37E-03	5.63E-02	5.82E-03	8.23E-06	7.82E-01	9.31E-02	6.14E-01	1.84E-03	2.94E-02
8q22.3	C/T	maf cases;controls	0.431; 0.391	0.383; 0.397	0.420; 0.420			0.408; 0.403			
rs16867971		info	g	0.99	0.99						
102609456		OR (CI)	1.18 (1.11 - 1.26)	0.94 (0.86 - 1.03)	1 (0.91 - 1.1)	1.05 (1.01 - 1.1)		1.06 (0.98 - 1.16)		1.06 (1.01 - 1.1)	
GRHL2		p-value	6.85E-06	2.13E-01	4.12E-01	2.64E-02	2.52E-04	1.47E-01	7.04E-01	8.15E-03	8.92E-03
2p11.2	A/G	maf cases;controls	0.440; 0.478	0.471; 0.445	0.474; 0.457			0.465; 0.459			
rs6706539		info	g	0.773	0.758						
84381680		OR (CI)	0.86 (0.80 - 0.91)	1.11 (1.01 - 1.22)	1.07 (0.97 - 1.18)	0.96 (0.92 - 1.01)		1.06 (0.98 - 1.15)		0.99 (0.95 - 1.03)	
		p-value	3.44E-06	8.63E-03	4.71E-02	1.29E-01	3.05E-07	1.52E-01	1.68E-01	5.69E-01	1.46E-06

[a] Cytogenetic regions according to NCBI Human Genome Build 37

[b] SNP position according to NCBI Human Genome Build 37

[c] Results from the meta-analysis of Stage 1: PanC4, PanScan 1, and PanScan 2

[d] P-value from test of heterogeneity of the Stage 1 studies (PanC4, PanScan 1, and PanScan 2)

[e] P-value from test of heterogeneity of the PANDoRA countries

[f] Results from the meta-analysis of Stage1 and Stage 2: PanC4, PanScan 1, PanScan 2, and PANDoRA

[g] P-value from test of heterogeneity of the Stage 1 and Stage 2 studies (PanC4, PanScan 1, PanScan 2, and PANDoRA)

[h] Minor allele frequency

[i] Quality of imputation metric. See online methods for more detail. If snp is genotyped and not imputed, a 'g' is reported

[j] Allelic Odds Ratio and corresponding 95% Confidence Interval

Supplementary Table 6. PANDoRA features

	Pre Quality Control Filters		**Post Quality Control Filters**	
	Cases	**Controls**	**Cases**	**Controls**
By Country				
Germany	1166	1800	1071	1729
Italy	983	1702	914	1448
Czech Republic	60	542	57	531
Lithuania	58	192	57	174
Poland	106	207	90	173
Greece	124	168	98	150
By Gender				
Men	1392	2415	1307	2265
Women	1066	2126	980	1940
Missing (%)	1.56	1.52	0	0
By Age				
Mean (SD)	59.81 (10.35)	53.53 (11.21)	59.87 (10.39)	53.56 (11.19)
Missing (%)	2.36	6.96	0	0
Total	**2497**	**4611**	**2287**	**4205**

Supplementary Table 7. Association results for loci highly suggestive ($P<1x10^{-6}$) for pancreatic cancer

			Stage 1				**Stage 2**	
Chr[a] **SNP** **Position[b]** **Gene**	**Effect Allele (Minor)/ Reference Allele**	**Statistic**	**PanC4** 4,164 cases 3,792 controls	**PanScan 1** 1,856 cases, 1,890 controls	**PanScan 2** 1,618 cases and 1,682 controls	**Combined Stage 1[c]** 7,638 cases 7,364 controls	**PANDoRA** 2497 cases 4611 controls	**Combined Stage 1&2[d]** 9,925 cases 11,569 controls
18q21.2 rs1517037 56,878,274 *GRP* (9126bp 5')	T/C	maf cases;controls	0.172; 0.182	0.170; 0.195	0.164; 0.189		0.168; 0.187	
		info	g	g	g			
		OR (CI)	0.93 (0.86 - 1.01)	0.85 (0.75 - 0.95)	0.84 (0.74 - 0.95)	0.87 (0.82 - 0.93)	0.87 (0.79 - 0.97)	0.87 (0.83 - 0.92)
		p-value	3.39 X 10^{-2}	3.82 X 10^{-3}	1.82 X 10^{-3}	9.93 X 10^{-6}	1.17 X 10^{-2}	3.17 X 10^{-7}
12q24.31 rs7310409 121,424,861 *HNF1A*	A/G	maf cases;controls	0.407; 0.386	0.423; 0.375	0.421; 0.392		0.426; 0.415	
		info	g	g	g			
		OR (CI)	1.09 (1.02 - 1.16)	1.22 (1.11 - 1.34)	1.13 (1.02 - 1.24)	1.12 (1.07 - 1.18)	1.07 (0.98 - 1.16)	1.11 (1.06 - 1.15)
		p-value	1.80 X 10^{-2}	5.35 X 10^{-5}	1.76 X 10^{-2}	1.24 X 10^{-6}	1.26 X 10^{-1}	6.34 X 10^{-7}
1p13.1 rs351365 113,046,395 *WNT2B*	T/C	maf cases;controls	0.228; 0.257	0.240; 0.254	0.239; 0.258		0.229; 0.248	
		info	g	0.891	0.889			
		OR (CI)	0.85 (0.79 - 0.92)	0.93 (0.84 - 1.03)	0.91 (0.81 - 1.01)	0.88 (0.83 - 0.93)	0.92 (0.83 - 1.01)	0.89 (0.85 - 0.93)
		p-value	3.08 X 10^{-5}	1.62 X 10^{-1}	4.45 X 10^{-2}	2.72 X 10^{-6}	8.02 X 10^{-2}	7.39 X 10^{-7}
20q13.11 rs6073450 43,086,648	A/G	maf cases;controls	0.415; 0.381	0.429; 0.411	0.411; 0.384		0.413; 0.403	
		info	g	g	g			
		OR (CI)	1.15 (1.08 - 1.23)	1.08 (0.98 - 1.18)	1.12 (1.02 - 1.24)	1.12 (1.06 - 1.17)	1.09 (1.00 - 1.18)	1.11 (1.06 - 1.15)
		p-value	1.82 X 10^{-4}	1.20 X 10^{-1}	2.62 X 10^{-2}	6.01 X 10^{-6}	4.92 X 10^{-2}	9.21 X 10^{-7}

9q31.3 rs6073450 106797388	C/T	maf cases;controls	0.407; 0.366	0.391; 0.371	0.390; 0.388		0.365; 0.364	
		info	g	g	g			
		OR (CI)	1.19 (1.12 - 1.27)	1.09 (0.99 - 1.2)	1.00 (0.91 - 1.11)	1.13 (1.08 - 1.18)	1.00 (0.92 - 1.08)	1.10 (1.05 - 1.14)
		p-value	7.00 X 10^{-8}	5.18 X 10^{-2}	7.09 X 10^{-1}	5.10 X 10^{-7}	9.19 X 10^{-1}	1.35 X 10^{-5}

[a] Cytogenetic regions according to NCBI Human Genome Build 37 and NCBI's Map Viewer

[b] SNP position according to NCBI Human Genome Build 37

[c] Results from the Combined Stage 1 meta-analysis of PanC4, PanScan 1, and PanScan 2

[d] Results from the Combined Stage 1 and 2 meta-analysis of PanC4, PanScan 1, PanScan 2, and PANDoRA

[e] MAF- minor allele frequency

[f] Quality of imputation metric. See online methods for more detail. If snp is genotyped and not imputed, a 'g' is reported

[g] Allelic Odds Ratio and corresponding 95% Confidence Interval

[h] R^2>0.95

Supplementary Figure 1. Quantile-Quantile (Q-Q) plot of association results from PanC4 analysis

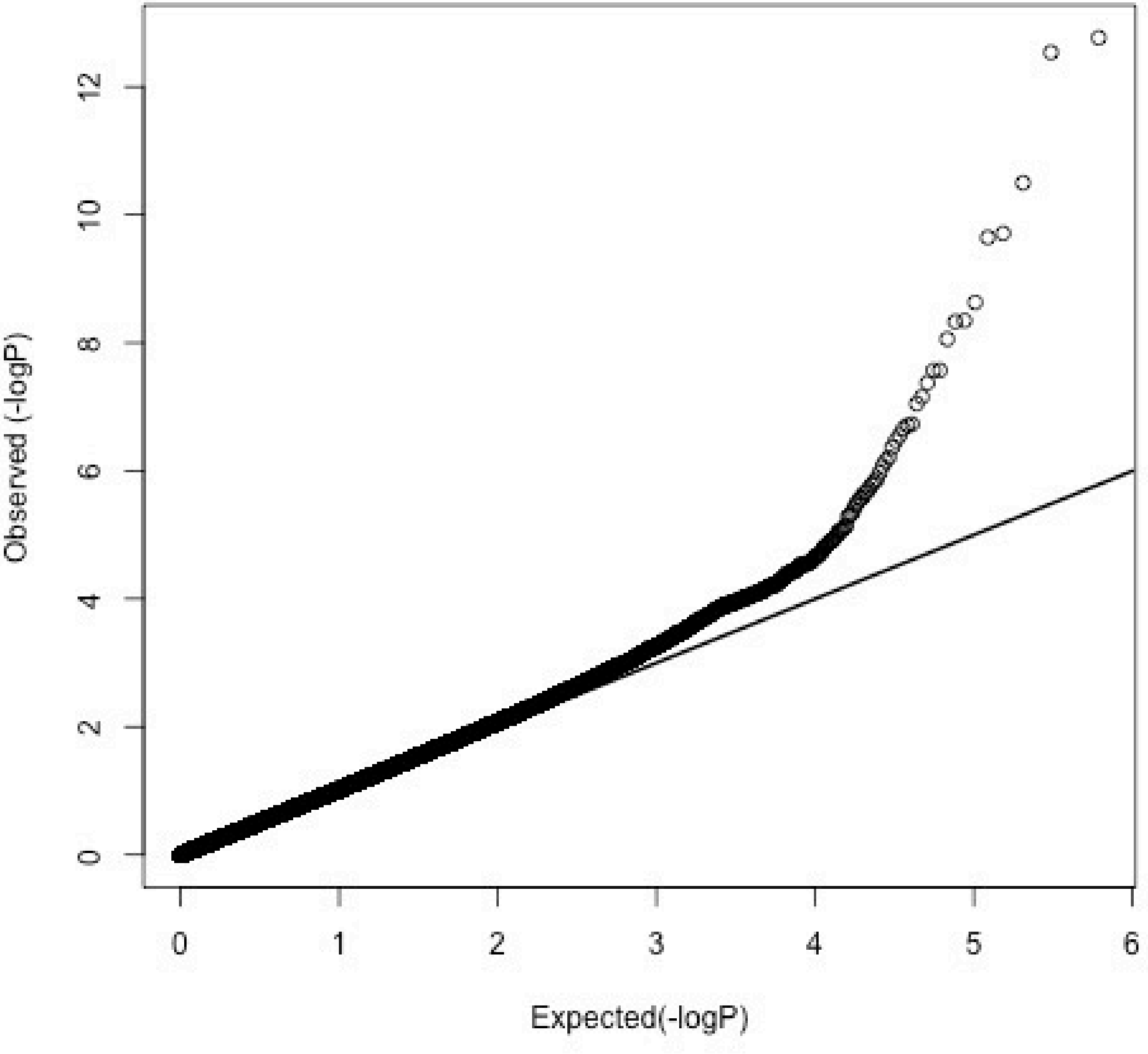
Supplementary Figure 2. Quantile-Quantile (Q-Q) plot of association results from the Combined Stage 1 analysis

Supplementary Figure 3. Regional association and linkage disequilibrium (LD) plots for five suggestive loci: (a) 12q24.31 (b) 18q21.2, (c) 1p13.1, (d) 20q13.11, and (e) 9q31.3. Association p-values are shown for three analyses: PanC4 only (black circles), Combined Stage 1 (PanC4, PanScan 1, and PanScan 2) (grey circles), and Combined Stage 1 and 2 (PanC4, PanScan 1, PanScan 2, and PANDoRA) (red circles). LD plots are based on 1000 Genomes European samples

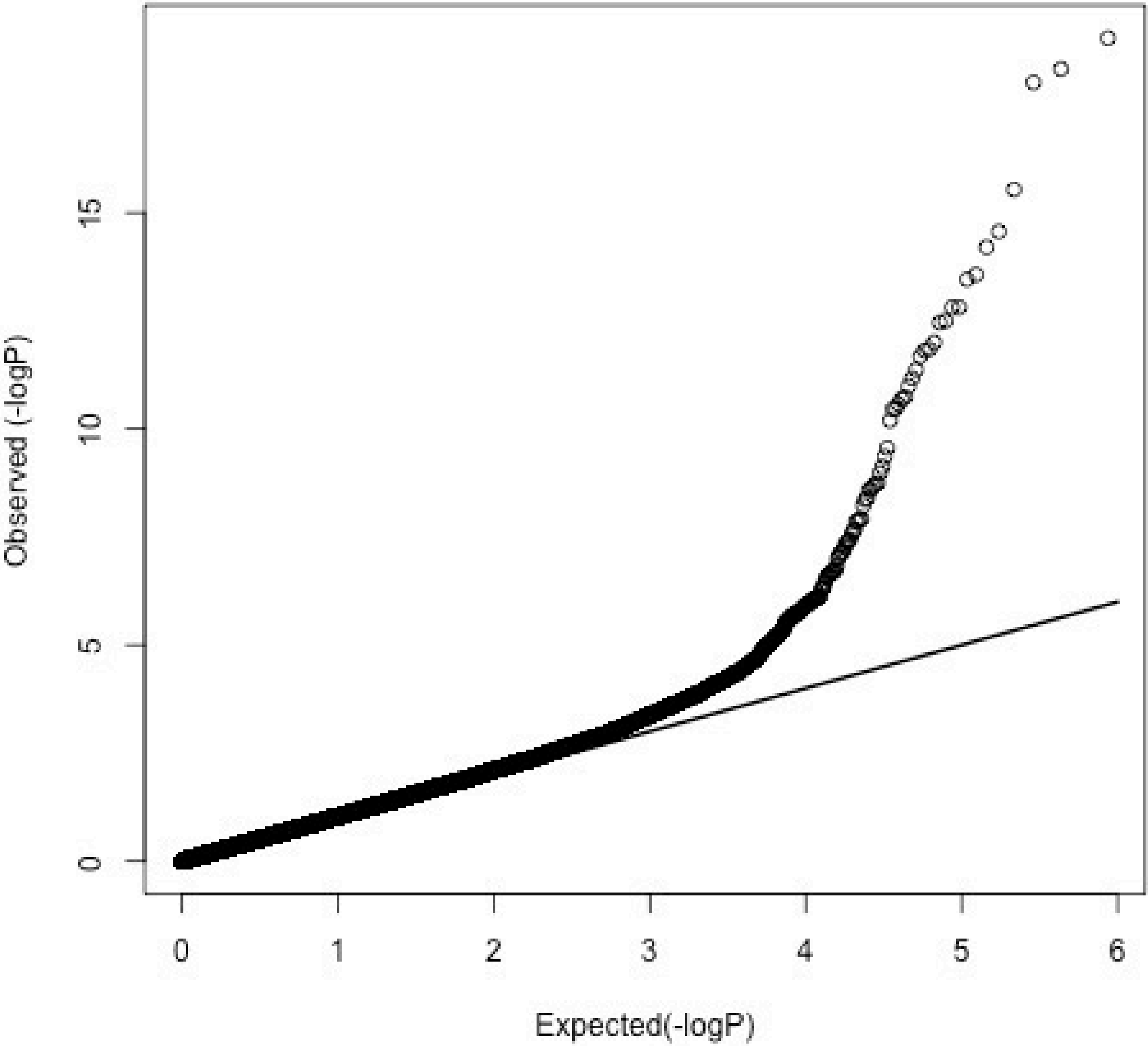
Supplementary Figure 4. Plot of the first two eigenvectors from a principal components analysis of PanC4

Supplementary Figure 5a-5i. Forest plots for the nine top associations reported

Supplementary Figure 1

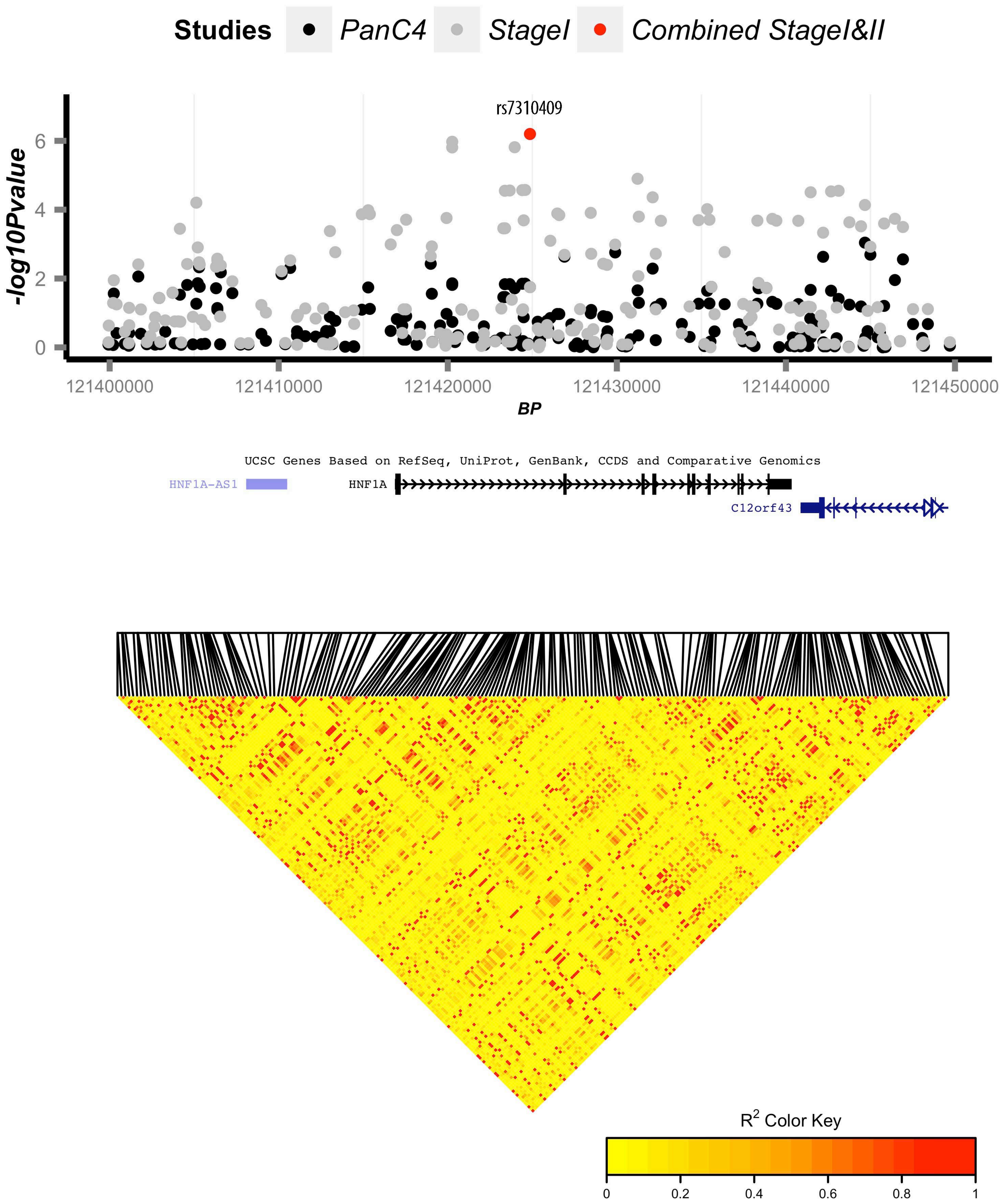


Supplementary Figure 2

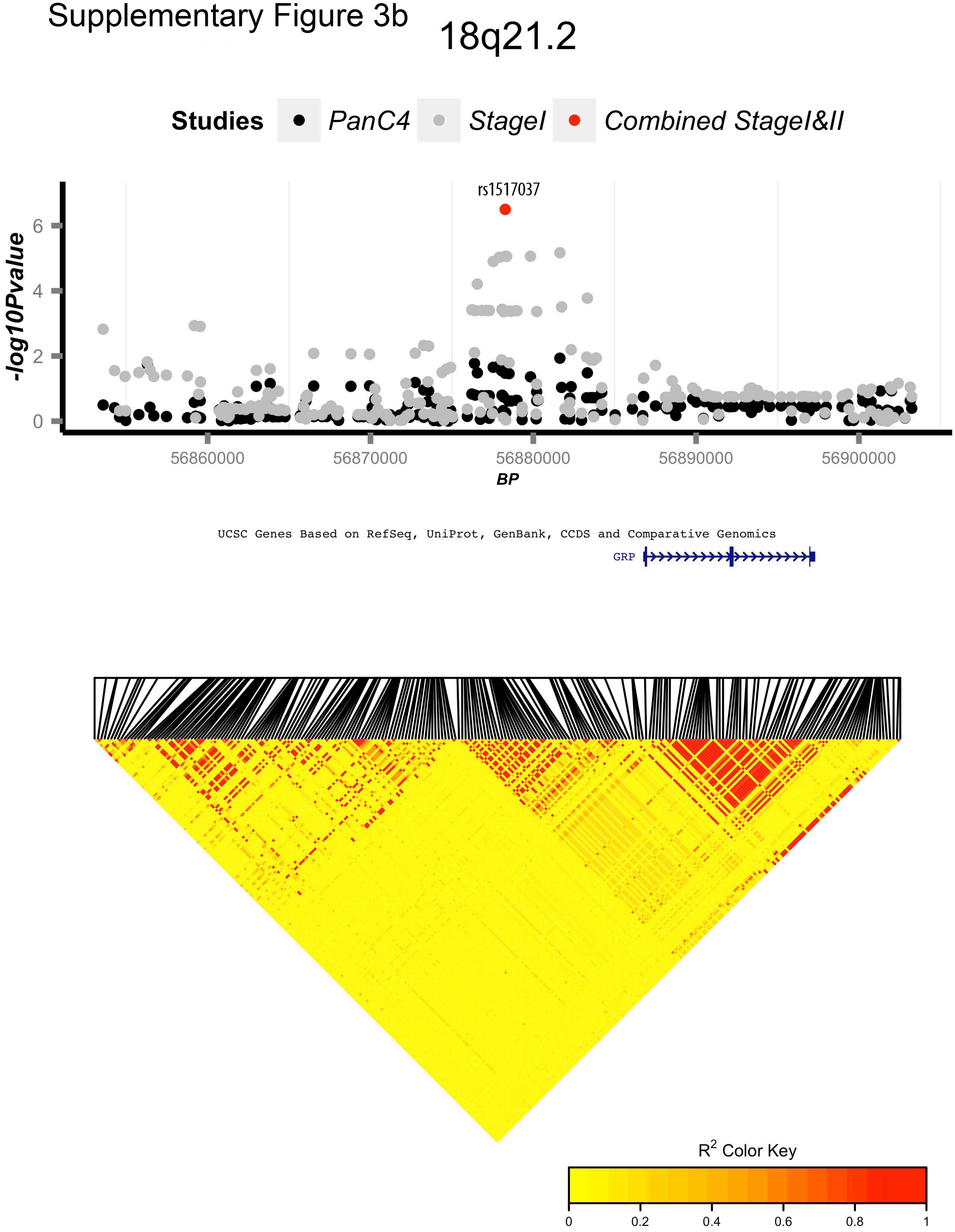


Supplementary Figure 3a

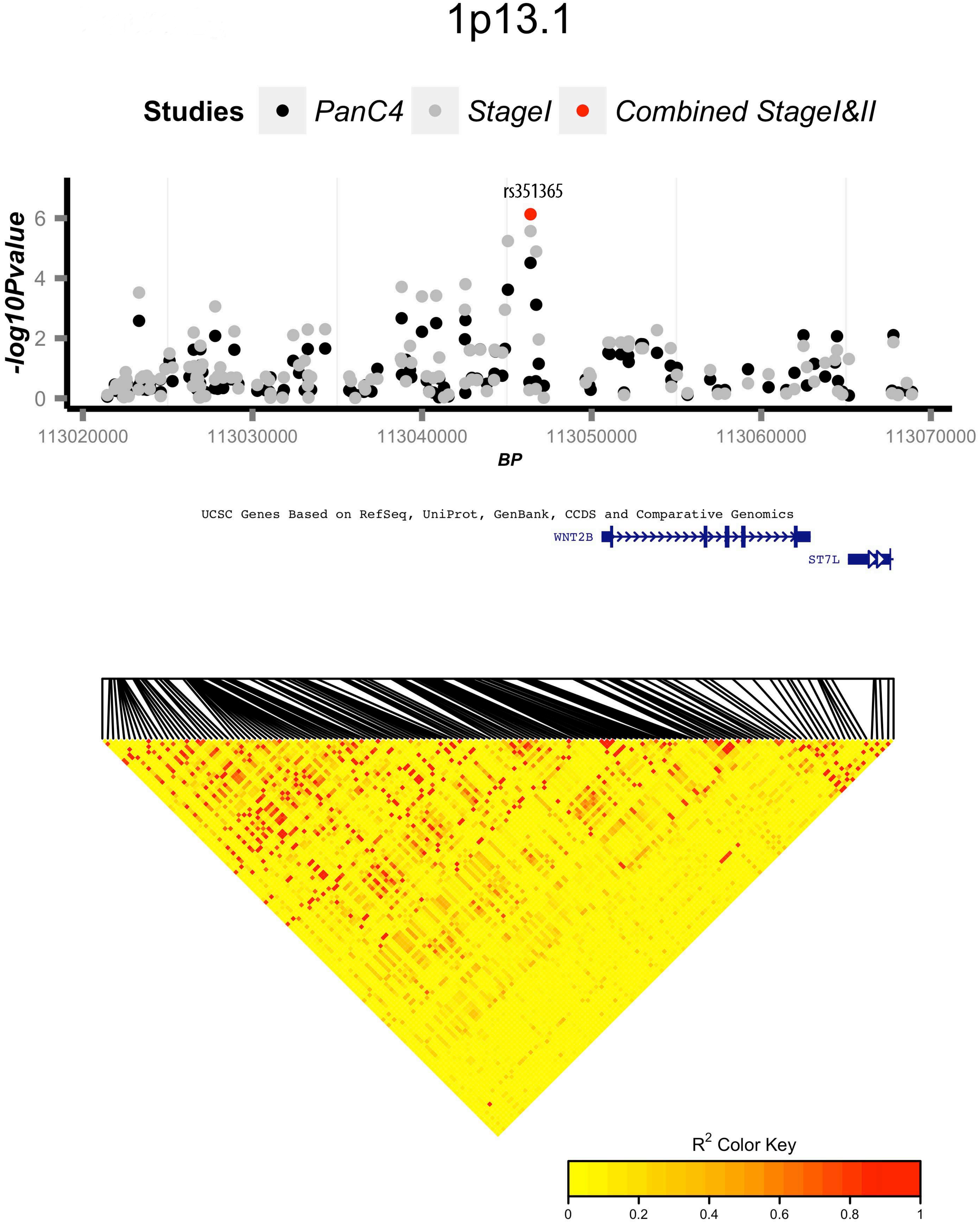
12q24.31



Supplementary Figure 3b

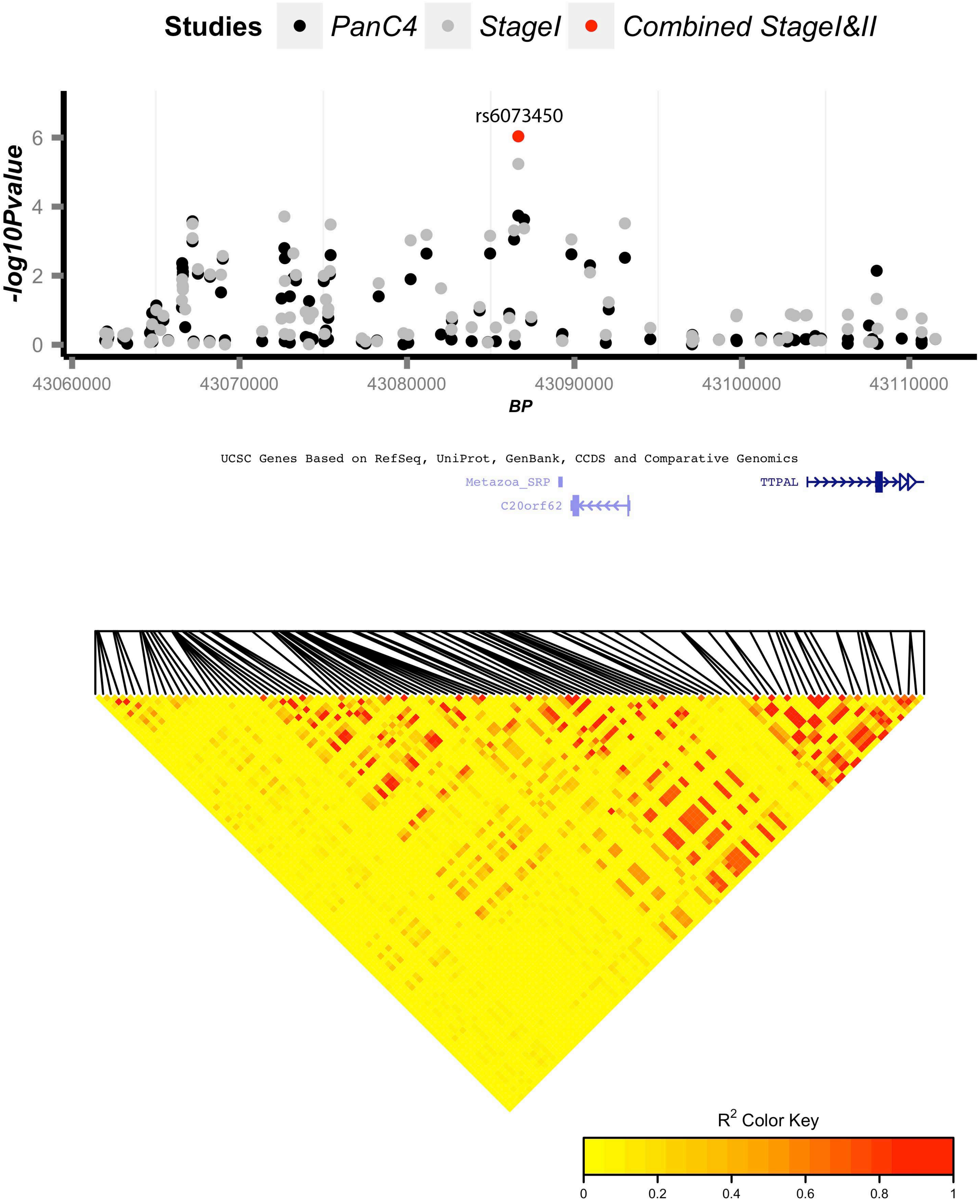


Supplementary Figure 3c

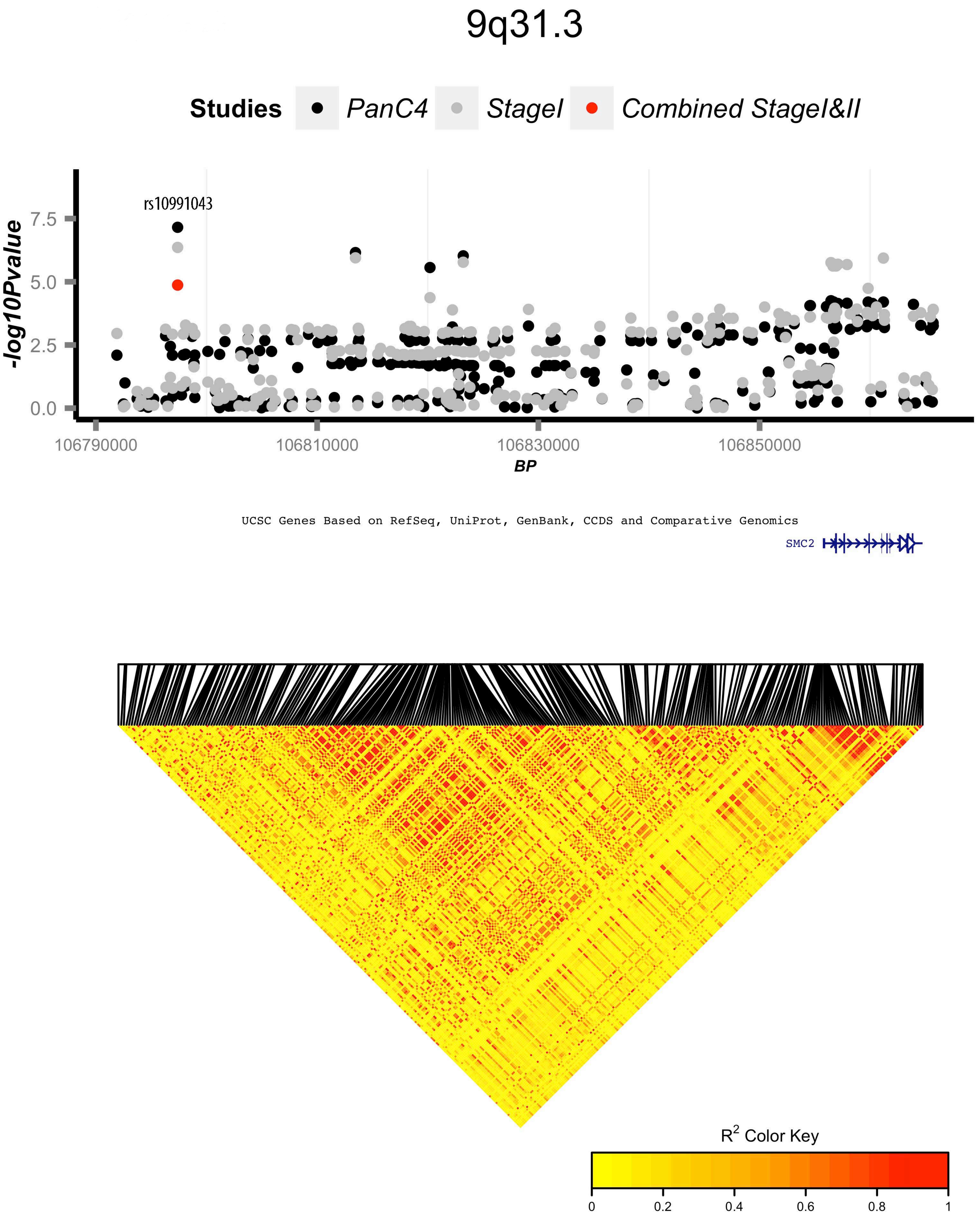


Supplementary Figure 3d

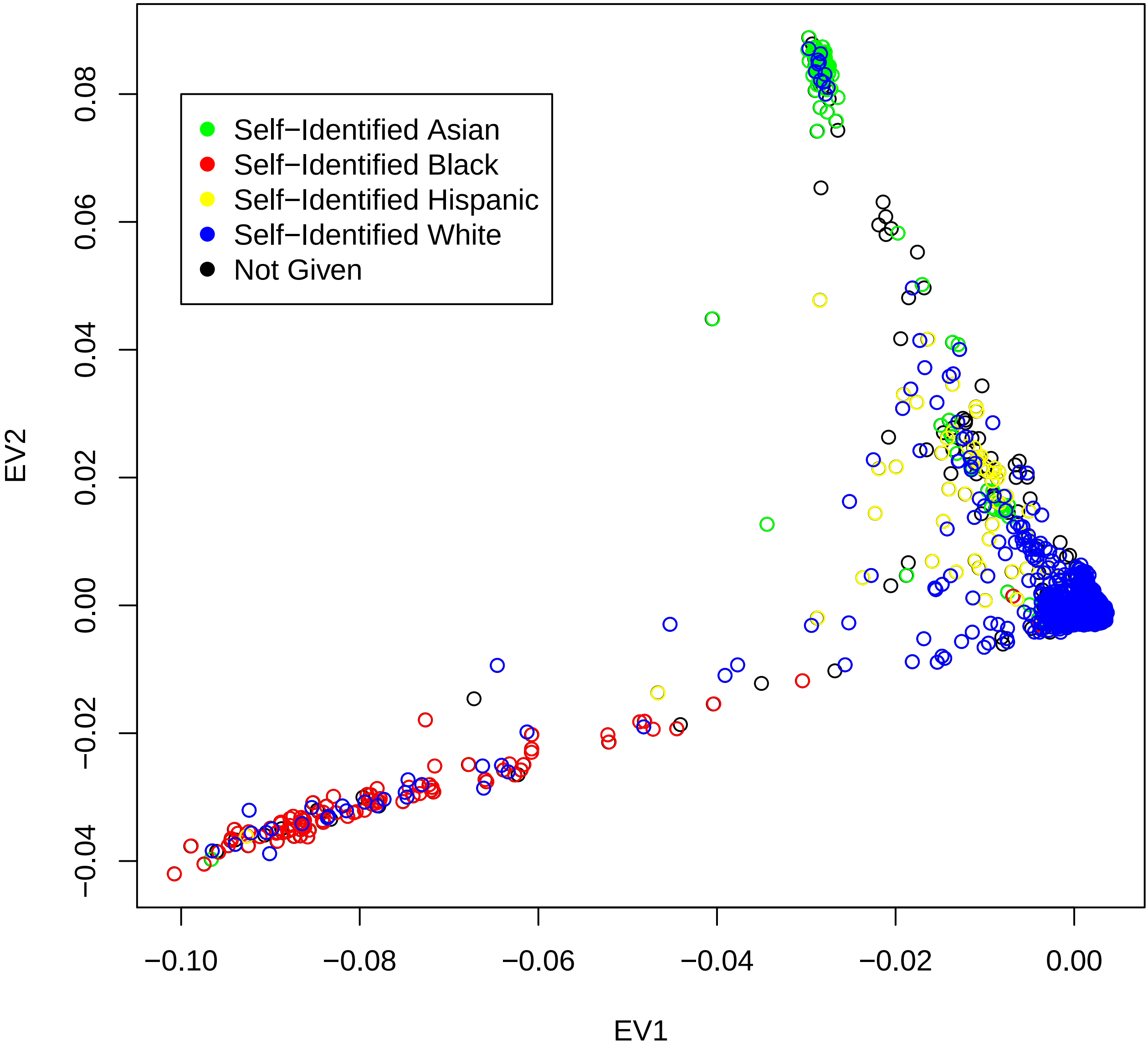
20q13.11



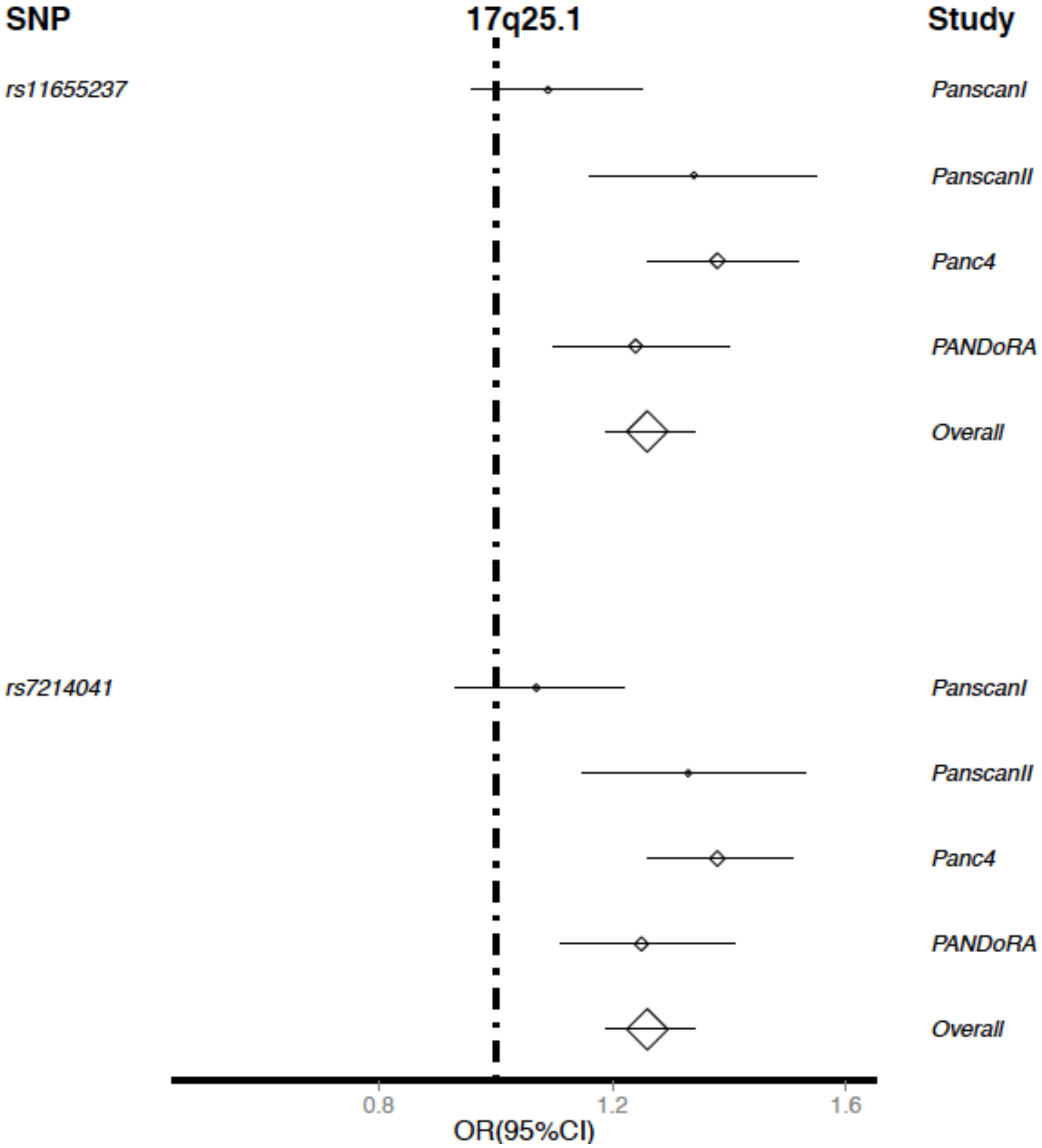
Supplementary Figure 3e



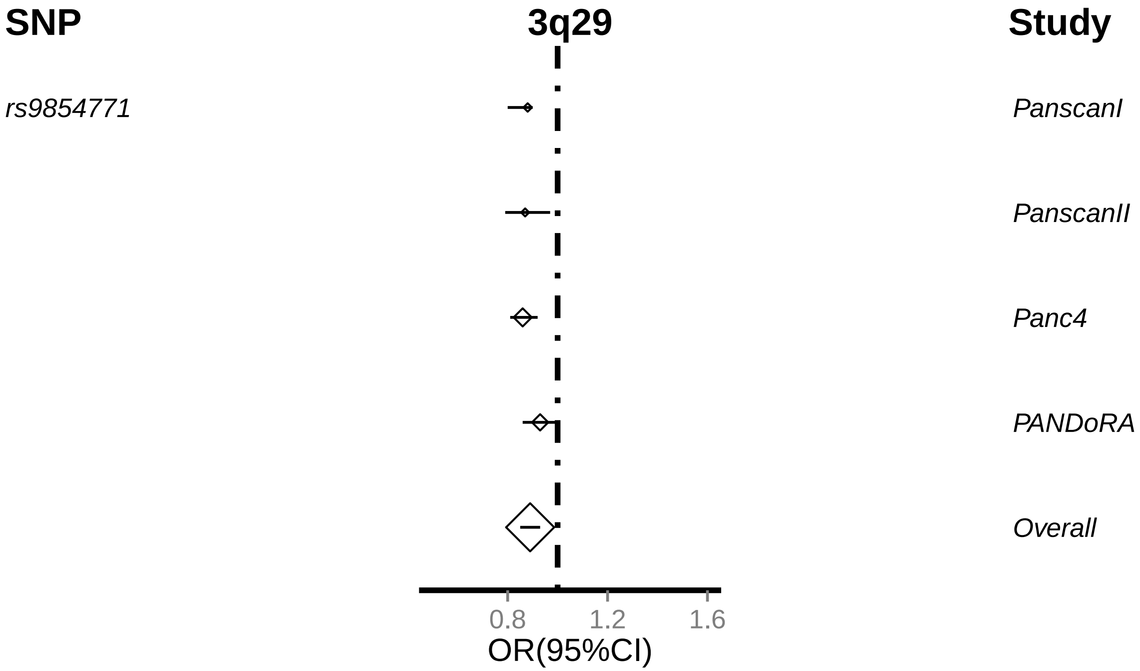
Supplementary Figure 4



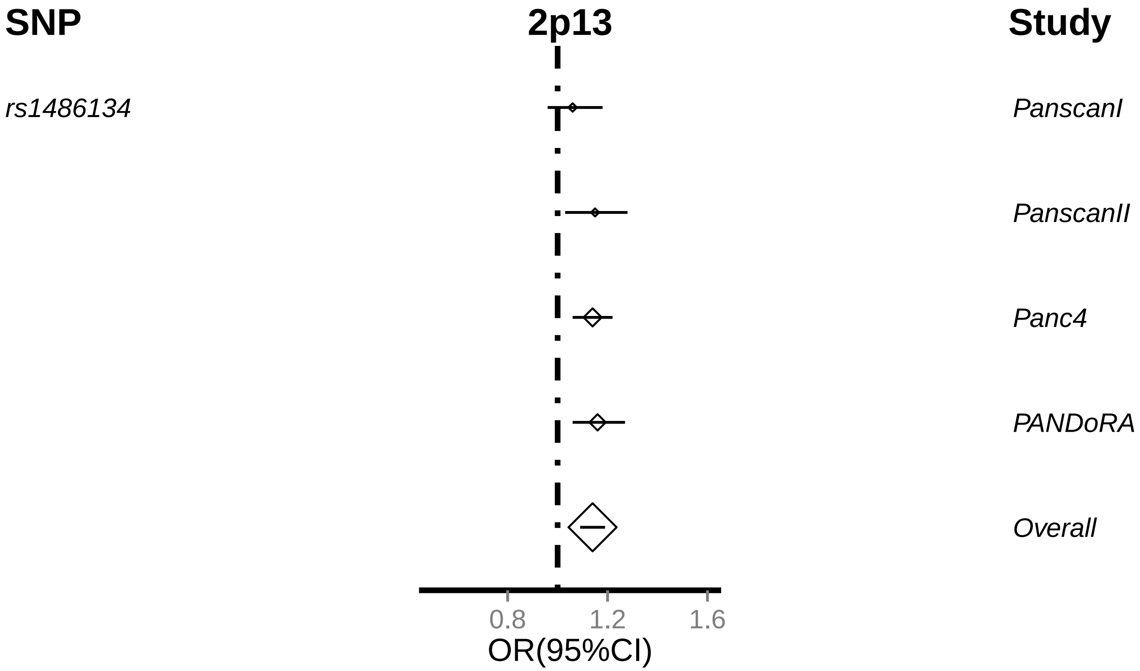
Supplementary Figure 5a



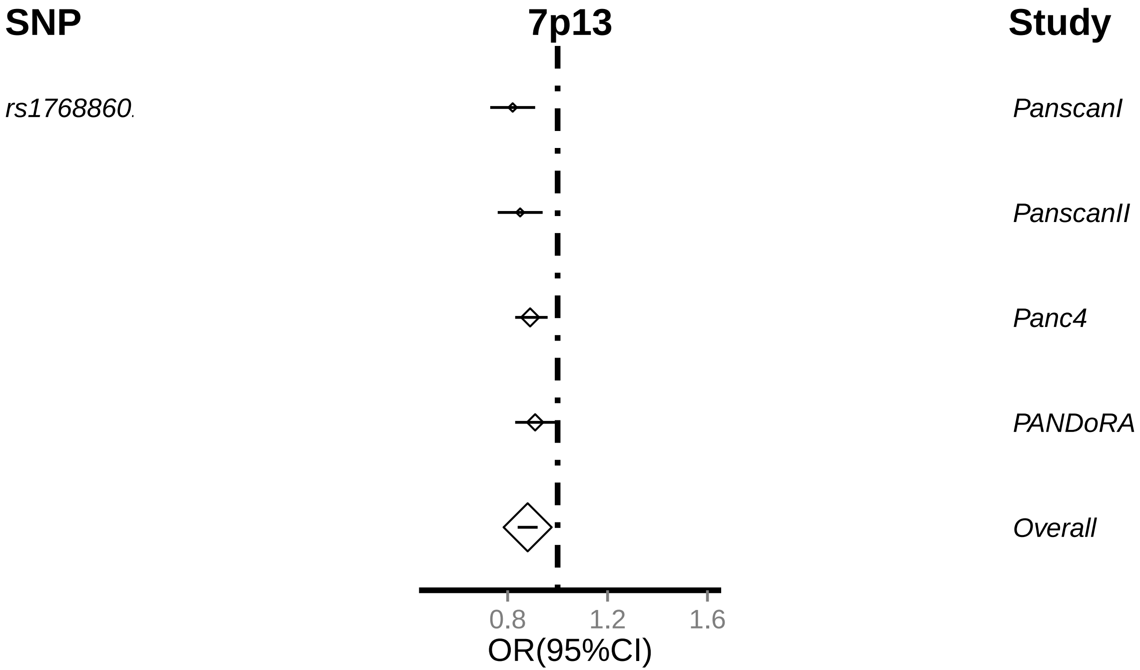
Supplementary Figure 5b



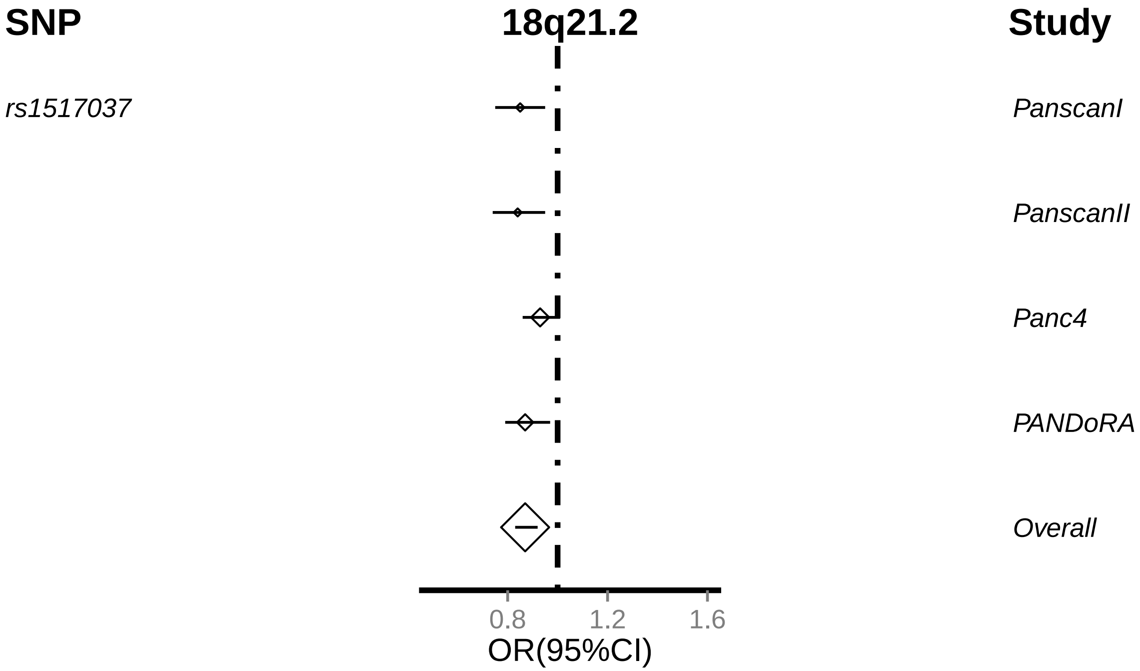
Supplementary Figure 5c



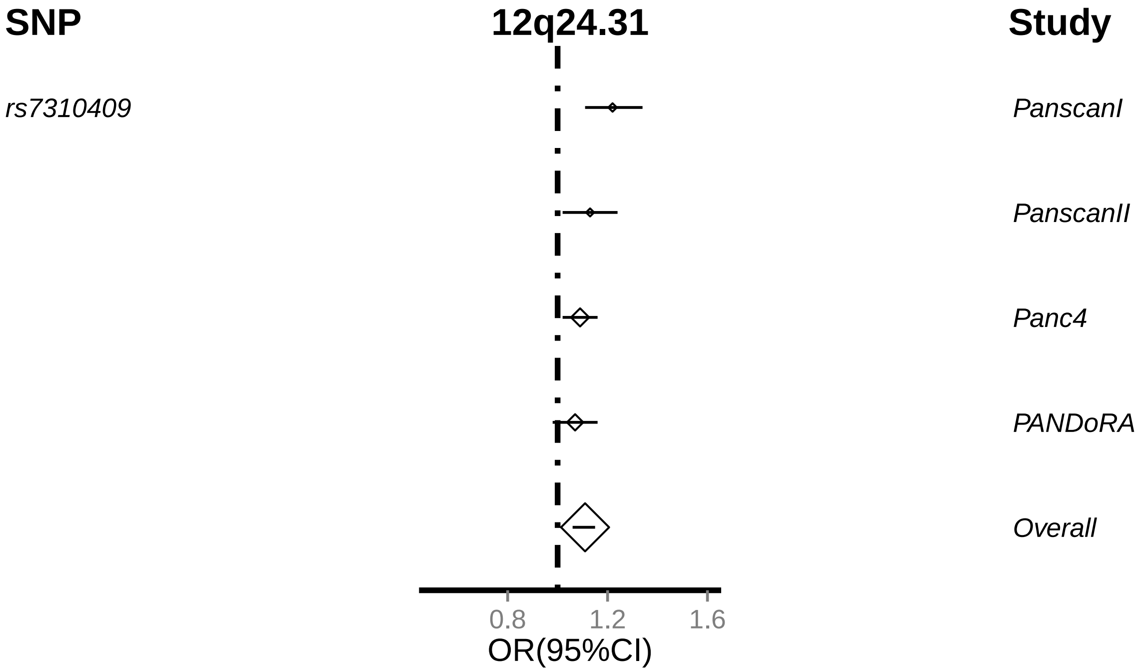
Supplementary Figure 5d



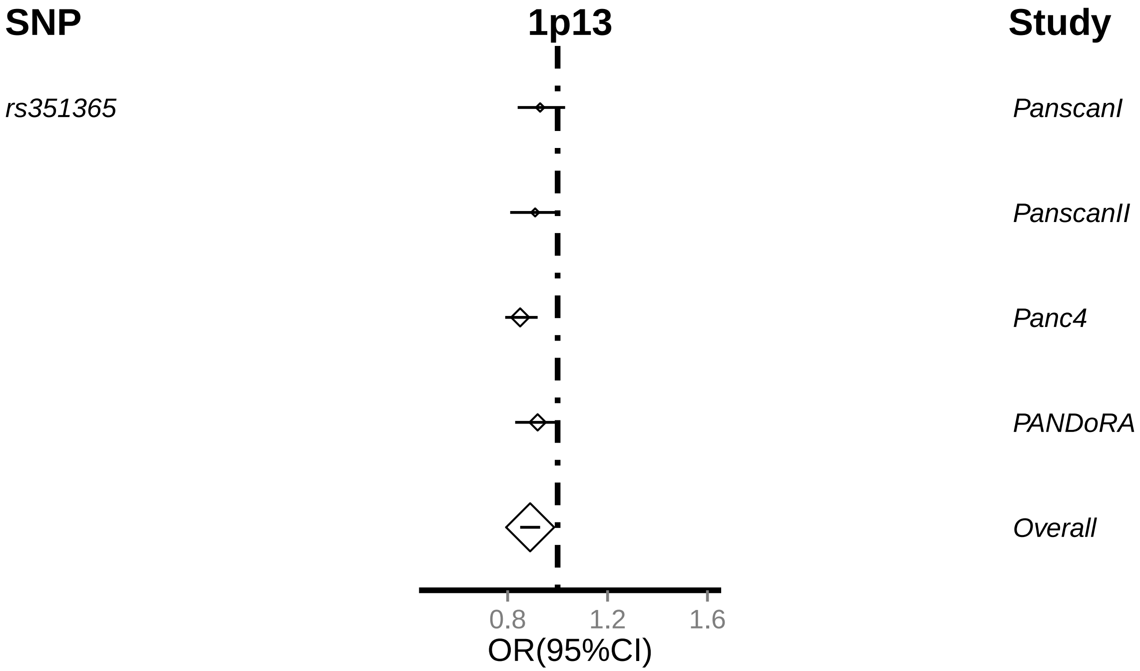
Supplementary Figure 5e



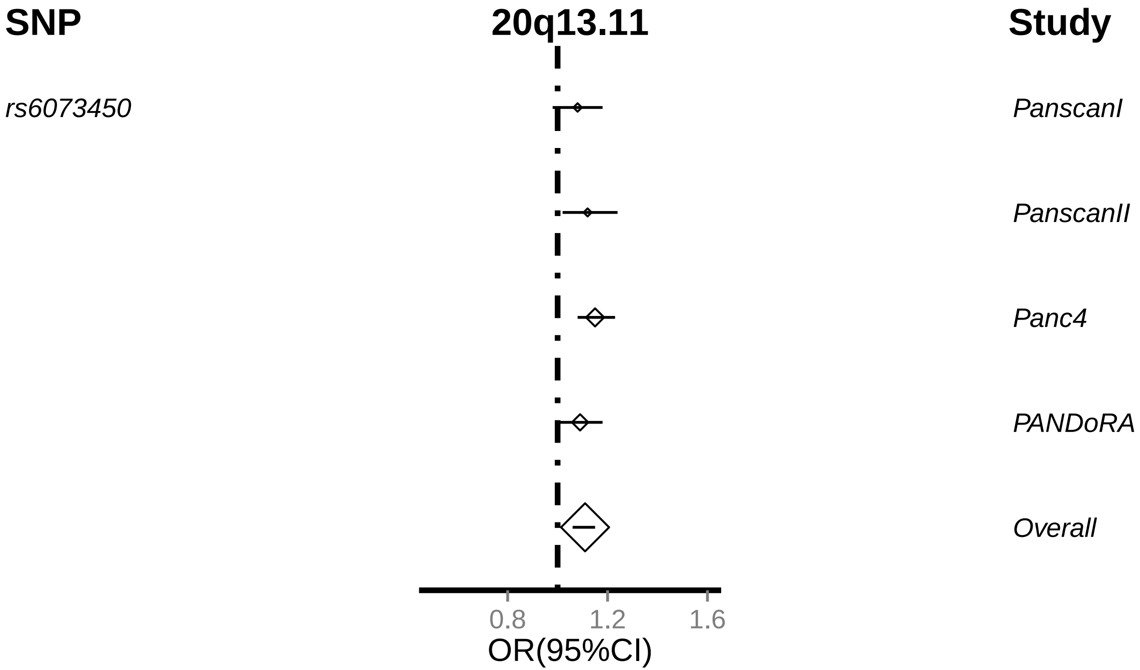
Supplementary Figure 5f



Supplementary Figure 5g



Supplementary Figure 5h



Supplementary Figure 5i