

**Supplementary Table 1** Age and sex composition of the GWAS and replication studies

Study population	Cases <sup>*</sup>			Controls <sup>†</sup>			Ethnicity	Genotyping Platform
	Sample size	Age (mean±s.d.)	Sex ratio (M/F)	Sample size	Age (mean±s.d.)	Sex ratio (M/F)		
<b>GWAS groups</b>								
Children	246	4.4±4.1	169/77	108	9.5±3.1	49/59	Korean	Axiom
Adults	NA	NA	NA	551	65.0±8.4	211/340	Korean	5.0
<b>Replication group<sup>13</sup></b>								
Adults	1,472	28.6±9.2	807/665	7,966	49.1±17.6	4,588/3,378	Japanese	Illumina Human OmniExpress-12

\* Cases included children with both moderate to severe AD (SCORAD  $\geq$  30; mean  $\pm$  SD,  $59.9 \pm 14.4$ ), and allergic sensitization (positive specific IgE to  $\geq 1$  food or airborne allergen).

† Controls included subjects without history of allergic diseases or evidence of allergic sensitization (negative skin prick tests or negative specific IgE to common allergens).

Children cases and adult controls were used for the GWAS analysis.

Children controls were used for the association studies of selected SNPs with total serum IgE.

**Supplementary Table2** Summary of association results from the discovery GWAS and replication stage

Genes or nearby genes	Location	SNP ID	Position	Alleles (risk/alt)	Discovery GWAS					Replication stage (Japanese group)			
					RAF Case	RAF Control	P	OR	95% CI	RAF	Beta	SE	P
<i>NBAS</i>	2p24.3	rs13403179	15482752	C/G	0.131	0.054	8.07E-08	2.947	(1.989-4.386)	0.032	0.043	0.113	0.705
		rs13428288	15482611	G/A	0.131	0.054	8.20E-08	2.946	(1.988-4.385)	0.032	0.043	0.113	0.704
		rs16862519	15481752	T/C	0.131	0.054	9.03E-08	2.943	(1.984-4.384)	0.032	0.043	0.113	0.704
		rs75790198	15481366	T/C	0.130	0.054	1.00E-07	2.936	(1.978-4.375)	0.032	0.043	0.113	0.703
		rs13398948	15481147	A/G	0.129	0.055	1.54E-07	2.903	(1.952-4.334)	0.032	0.044	0.114	0.701
		rs13409223	15480569	C/T	0.129	0.055	1.67E-07	2.898	(1.948-4.328)	0.032	0.044	0.114	0.701
		rs147759857	15485351	A/T	0.125	0.054	4.55E-07	2.826	(1.890-4.243)	0.032	0.043	0.113	0.705
<i>THEMIS</i>	6q22.33	rs675531	128040839	C/T	0.205	0.113	6.82E-07	2.193	(1.610-2.994)	0.164	-0.017	0.054	0.755
		rs35766269	9023815	A/T	0.717	0.580	9.61E-08	1.946	(1.529-2.494)	0.654	-0.013	0.043	0.767
<i>GATA3</i>	10p14	rs12253258	9024290	T/C	0.717	0.580	9.72E-08	1.946	(1.529-2.494)	0.654	-0.012	0.043	0.778
		rs34385685	9007216	T/A	0.689	0.557	4.49E-07	1.843	(1.458-2.342)	0.630	-0.022	0.042	0.604
<i>PCDH9</i>	13q21.31	rs9540294	65564031	G/T	0.181	0.083	1.01E-08	2.655	(1.904-3.717)	0.117	-0.047	0.064	0.454
		rs9540299	65568331	T/C	0.178	0.083	2.24E-08	2.614	(1.869-3.669)	0.117	-0.048	0.064	0.453
		rs9540298	65567319	T/C	0.186	0.088	2.97E-08	2.515	(1.818-3.493)	0.122	-0.058	0.063	0.354
		rs9598920	65569199	T/G	0.184	0.088	4.06E-08	2.499	(1.804-3.474)	0.122	-0.058	0.063	0.353
		rs9598921	65569216	T/C	0.184	0.088	4.12E-08	2.498	(1.804-3.473)	0.122	-0.058	0.063	0.353
		rs9540302	65571257	G/A	0.172	0.083	8.66E-08	2.536	(1.806-3.573)	0.117	-0.048	0.064	0.451
		rs4600354	65574724	G/A	0.170	0.083	1.58E-07	2.498	(1.776-3.525)	0.117	-0.048	0.064	0.452
		rs7993759	65575511	G/A	0.178	0.088	1.79E-07	2.415	(1.736-3.370)	0.122	-0.058	0.063	0.353
		rs9540309	65575966	C/T	0.178	0.088	1.86E-07	2.413	(1.735-3.368)	0.122	-0.058	0.063	0.352
		rs9598922	65577047	G/C	0.169	0.083	1.96E-07	2.484	(1.765-3.507)	0.117	-0.048	0.063	0.451
		rs9528865	65564293	A/G	0.267	0.160	3.35E-07	2.044	(1.555-2.695)	0.214	-0.023	0.049	0.629
<i>SCAPER</i>	15q24.3	rs4293255	65562307	T/C	0.265	0.160	5.49E-07	2.022	(1.536-2.667)	0.214	-0.022	0.049	0.653
		rs9564212	65566594	C/T	0.265	0.160	5.56E-07	2.020	(1.535-2.665)	0.214	-0.024	0.049	0.626
		rs7987130	65557327	T/C	0.164	0.083	8.42E-07	2.380	(1.687-3.368)	0.117	-0.047	0.064	0.456
		rs3099143	77104856	C/A	0.239	0.137	3.02E-07	2.126	(1.594-2.841)	0.123	-0.072	0.063	0.252
		rs2046415	77085253	G/A	0.235	0.134	4.31E-07	2.096	(1.575-2.798)	0.122	-0.066	0.063	0.291
		rs1114717	77086078	A/G	0.235	0.134	4.36E-07	2.096	(1.574-2.797)	0.121	-0.066	0.063	0.291
		rs3110379	77095175	G/A	0.235	0.135	4.56E-07	2.094	(1.573-2.795)	0.121	-0.067	0.063	0.288
		rs901008	77097018	A/C	0.235	0.135	4.64E-07	2.093	(1.572-2.794)	0.121	-0.067	0.063	0.288
		rs3110381	77099665	T/A	0.235	0.135	4.70E-07	2.092	(1.571-2.793)	0.121	-0.067	0.063	0.287
		rs3106380	77104377	A/G	0.235	0.135	4.84E-07	2.091	(1.570-2.792)	0.121	-0.067	0.063	0.287
<i>SCAPER</i>	15q24.3	rs3099142	77104909	T/C	0.235	0.135	4.95E-07	2.090	(1.570-2.791)	0.121	-0.067	0.063	0.287
		rs4886831	77106801	T/C	0.235	0.135	4.98E-07	2.090	(1.569-2.791)	0.121	-0.067	0.063	0.286
		rs78020233	77107050	G/T	0.235	0.135	5.00E-07	2.090	(1.569-2.790)	0.121	-0.067	0.063	0.286
		rs3102712	77058926	A/G	0.235	0.136	5.68E-07	2.097	(1.570-2.807)	0.122	-0.063	0.063	0.312
		rs3102710	77061148	C/T	0.235	0.136	5.69E-07	2.097	(1.570-2.807)	0.122	-0.064	0.063	0.311
		rs280024	77034518	C/A	0.235	0.136	6.03E-07	2.096	(1.569-2.808)	0.122	-0.060	0.062	0.337

rs280028	77031466	G/A	0.235	0.136	6.14E-07	2.096	(1.568-2.807)	0.122	-0.059	0.062	0.338
rs280029	77031235	G/A	0.235	0.136	6.16E-07	2.095	(1.568-2.807)	0.122	-0.059	0.062	0.338
rs3102709	77072260	T/C	0.235	0.136	6.24E-07	2.088	(1.564-2.793)	0.122	-0.065	0.063	0.303
rs3106378	77110524	C/A	0.235	0.136	6.39E-07	2.077	(1.559-2.774)	0.121	-0.070	0.064	0.272
rs111406539	77076517	C/T	0.235	0.136	6.45E-07	2.084	(1.562-2.787)	0.122	-0.065	0.063	0.302
rs3099140	77111012	A/G	0.235	0.136	6.53E-07	2.076	(1.558-2.773)	0.121	-0.070	0.064	0.272
rs3099139	77112291	G/A	0.235	0.136	6.54E-07	2.076	(1.558-2.773)	0.121	-0.070	0.064	0.272
rs3099138	77115524	A/G	0.235	0.136	6.68E-07	2.075	(1.557-2.772)	0.121	-0.070	0.064	0.268
rs4886832	77121196	G/A	0.235	0.136	6.89E-07	2.074	(1.556-2.770)	0.121	-0.071	0.064	0.263
rs3099137	77123626	A/G	0.235	0.137	6.92E-07	2.073	(1.556-2.769)	0.121	-0.071	0.064	0.263
rs111908804	77123773	G/C	0.235	0.137	6.94E-07	2.073	(1.556-2.769)	0.121	-0.071	0.064	0.263
rs3099134	77133168	G/T	0.235	0.137	7.48E-07	2.069	(1.553-2.764)	0.121	-0.071	0.064	0.261
rs141545456	77014367	T/C	0.228	0.132	8.82E-07	2.078	(1.554-2.787)	0.118	-0.066	0.065	0.307
rs3110378	77127983	A/G	0.234	0.137	9.57E-07	2.059	(1.544-2.753)	0.121	-0.071	0.064	0.263

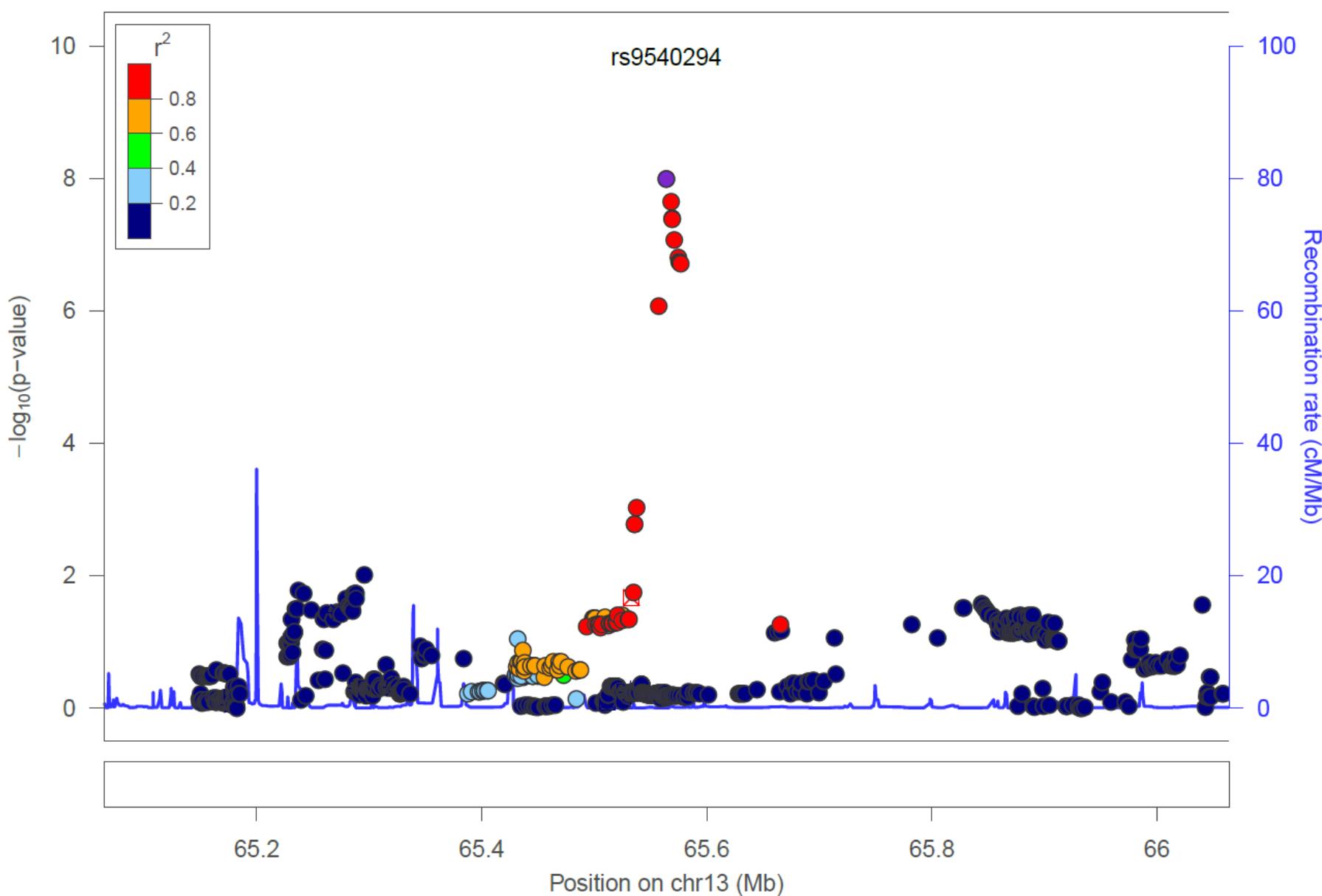
RAF, risk allele frequency; OR, odds ratio; CI, confidence interval; SE, standard error.

**Supplementary Figure 1** Regional association plots at the 13q21.31 (a), 2p24.3 (b), 6q22.33 (c), and 10p14 (d) loci for recalcitrant atopic dermatitis. For each plot, the  $-\log_{10} P$  value (left y axis) of each SNP is shown according to its chromosomal position (x axis). Genetic recombination rates are shown by the blue line, and horizontal arrows indicate the locations of genes and direction of transcription. The most associated SNP (labeled by rs number) is shown as a purple circle, and its LD ( $r^2$ ) with all other SNPs is indicated by color.

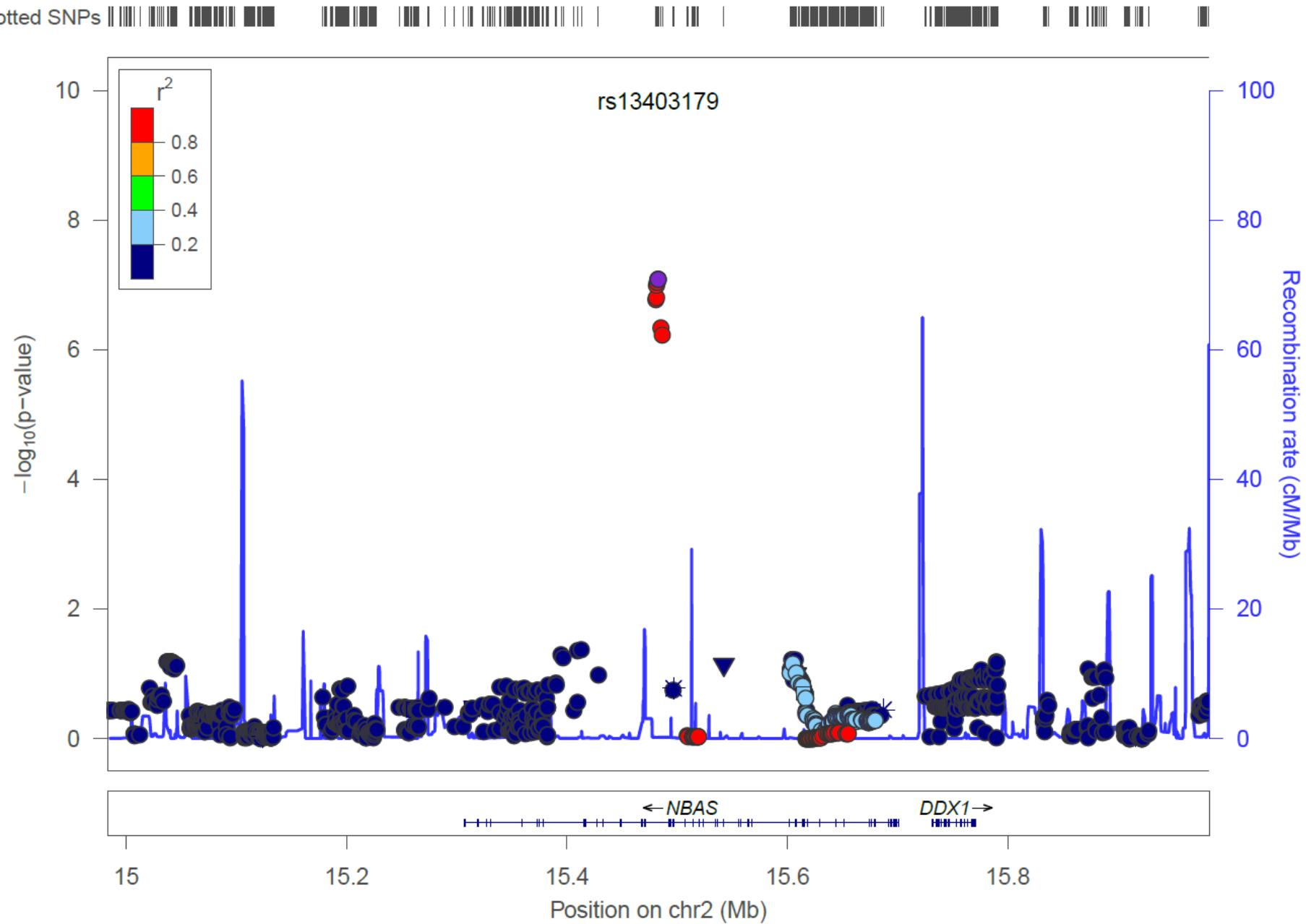
**Supplementary Figure 2** Box plots comparing total serum IgE between cases and controls in children. Total serum IgE levels are higher in cases than in controls ( $6.443 \pm 1.449$  vs.  $3.260 \pm 0.941$  ln kU/l, respectively,  $P = 2.2 \times 10^{-16}$ ).

Supplementary Figure 1a

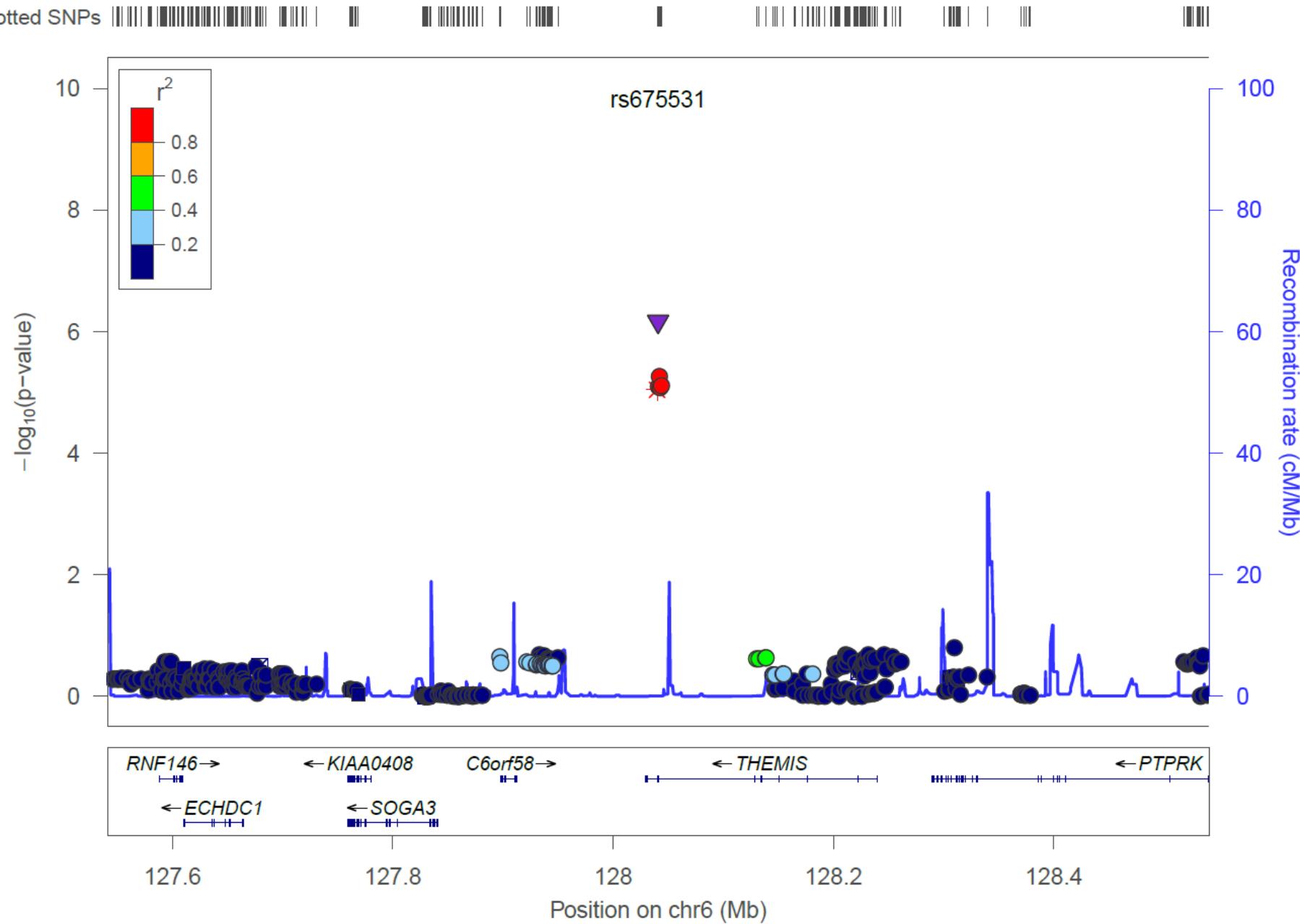
Plotted SNPs



Supplementary Figure 1b

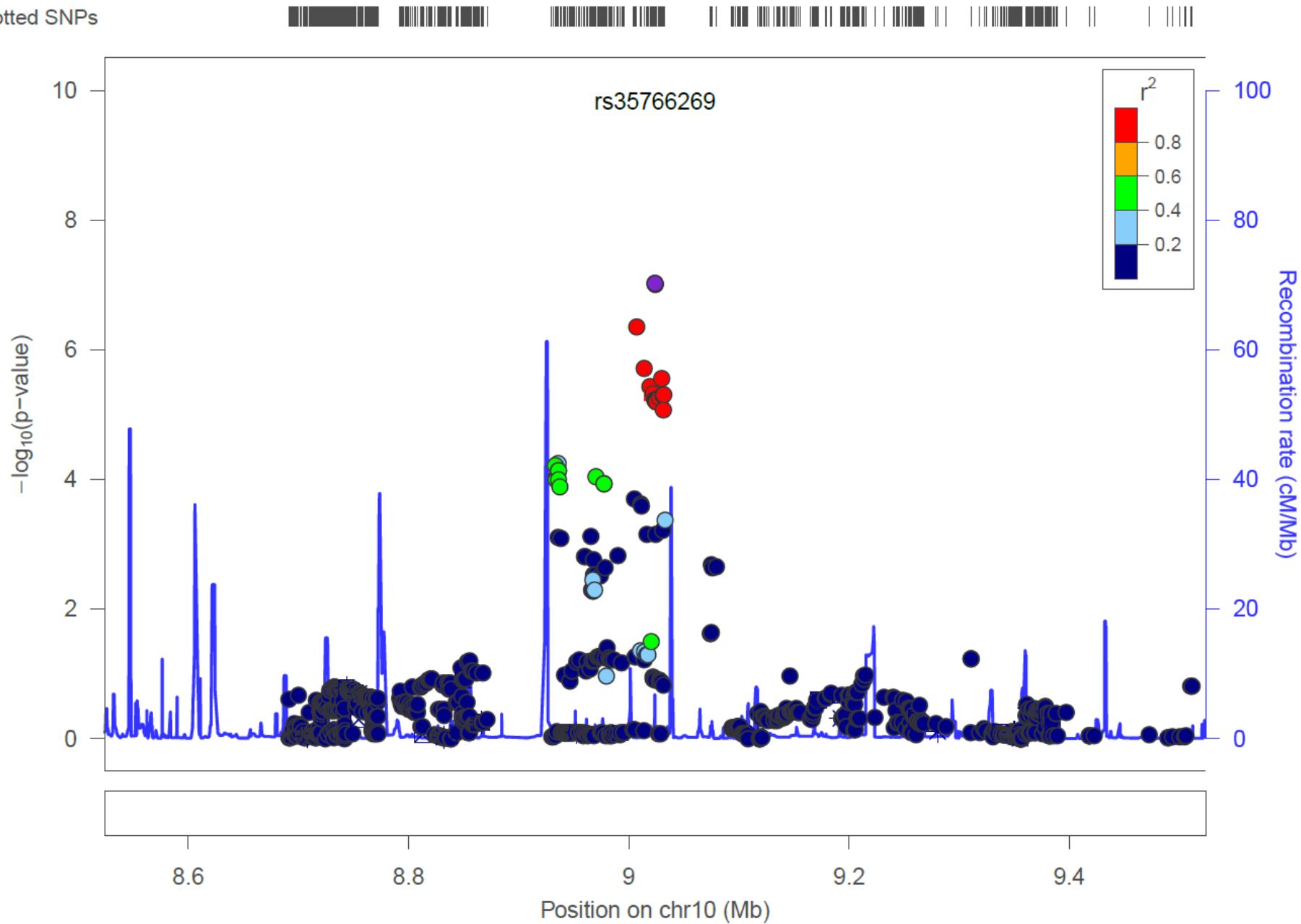


Supplementary Figure 1c



Supplementary Figure 1d

Plotted SNPs



Supplementary Figure 2

