Table S3: Top 100 signals in the CEU population using the T_2 test statistic.

Rank	Gene name	Chromosome	T_2	Rank	Gene name	Chromosome	T_2
1	***HLA-DPB1***[14]	6	405.3	51	***WFDC8***[83]	20	204.2
2	***HLA-DPA1***[76]	6	363.5	52	*USP20*	9	203.7
3	***SLC2A9***[15]	4	350.0	53	*CCDC146*	7	201.5
4	*FANK1*	10	330.0	54	***HLA-DRB1***[14,75]	6	197.9
5	*CPE*	4	317.9	55	*POLR1E*	9	197.1
6	***HLA-C***[75]	6	317.7	56	*ADH4*	4	196.5
7	*DMBT1*	10	312.2	57	*OR5W2*	11	195.8
8	***HLA-A***[74,75]	6	309.6	58	*ASB18*	2	195.0
9	*ARPC5*	1	297.8	59	*BICC1*	10	194.3
10	*CCDC169*	13	286.0	60	*SH3RF3*	2	192.6
11	*CCDC169-SOHLH2*	13	286.0	61	*BMPR1B*	4	192.1
12	***LGALS8***[15]	1	277.0	62	*NUP88*	17	190.9
13	*APBB1IP*	10	274.0	63	*ADAMTS12*	5	190.1
14	*RGL1*	1	268.4	64	*ADH1C*	4	188.7
15	*TEKT4*	2	261.8	65	*APOBEC4*	1	187.8
16	*STK32A*	5	259.2	66	*SNX31*	8	187.5
17	*CEP112*	17	257.7	67	*SGCZ*	8	187.1
18	*CPNE4*	3	253.0	68	*PANK1*	10	187.0
19	*RNF144B*	6	252.0	69	*ANK3*	10	186.9
20	*C4orf37*	4	245.2	70	*PKD1L1*	7	186.8
21	*MLF1IP*	4	244.1	71	*ZNF717*	3	186.5
22	***HLA-B***[15,74,75]	6	237.0	72	*KLHL14*	18	184.2
23	*RGS6*	14	236.1	73	*FXN*	9	184.0
24	*ARHGAP42*	11	234.8	74	*MAPT*	17	182.6
25	*POLN*	4	233.4	75	*TYW1*	7	182.0
26	*SLC15A2*	3	232.8	76	*BCAS1*	20	180.4
27	*KALRN*	3	227.2	77	*NTN4*	12	179.8
28	*FOPNL*	16	227.1	78	*THSD7B*	2	177.7
29	*KIAA1267*	17	226.7	79	*COL5A2*	2	177.6
30	*ZNF568*	19	226.4	80	*LRP1B*	2	175.6
31	*HEATR1*	1	225.7	81	*SNX19*	11	175.4
32	*KIAA1324L*	7	223.4	82	*OR4C3*	11	174.7
33	*MSH3*	5	222.5	83	*KRT83*	12	173.5
34	*FRAS1*	4	221.2	84	*LRRC16A*	6	171.5
35	*EMR1*	19	221.1	85	*C18orf1*	18	170.3
36	*GRIN2A*	16	220.1	86	*HLA-DRA*	6	169.8
37	*BNC2*	9	220.1	87	*PTPN14*	1	169.5
38	***HLA-DQA1***[14,75]	6	220.1	88	*CNBD1*	8	167.1
39	*KDM4C*	9	217.8	89	*GPC5*	13	166.6
40	*AXDND1*	1	217.1	90	*MAP2K3*	17	164.6
41	*MYRIP*	3	215.8	91	*CSMD1*	8	164.5
42	*SPEF2*	5	214.2	92	*CADM2*	3	162.8
43	*PLCB4*	20	212.3	93	*MYO1B*	2	162.6
44	*SLC38A9*	5	210.2	94	*MYLK4*	6	162.0
45	*ART3*	4	209.3	95	***OR5I1***[55]	11	162.0
46	*CTNNA3*	10	208.3	96	***FHIT***[77]	3	161.9
47	***ERAP1***[81]	5	207.6	97	*CUBN*	10	161.8
48	***HLA-DQB1***[14,75]	6	206.8	98	*ULK4*	3	161.8
49	*EMID2*	7	206.1	99	*ASTN2*	9	161.6
50	*ADCY5*	3	205.4	100	*PGLYRP4*	1	161.3

Previously-hypothesized genes are indicated in bold. Genes overlapping with Table S4 are highlighted in gray.

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