Table S1: Top 100 signals in the CEU population using the T_1 test statistic.

Rank	Gene name	Chromosome	T_1	Rank	Gene name	Chromosome	T_1
1	***HLA-A***[74,75]	6	375.3	51	*ZNF568*	19	137.9
2	***HLA-B***[15,74,75]	6	366.3	52	*MYRIP*	3	136.8
3	*FANK1*	10	357.9	53	*IGSF5*	21	136.2
4	***HLA-C***[75]	6	320.9	54	*KIAA1267*	17	135.0
5	*TEKT4*	2	307.8	55	*CCDC169-SOHLH2*	13	134.9
6	***HLA-DPB1***[14,75]	6	262.0	56	*CCDC169*	13	134.9
7	*OR4C3*	11	246.8	57	*KIAA1324L*	7	134.5
8	***HLA-DPA1***[76]	6	244.4	58	*RNF150*	4	133.9
9	***HLA-DQA1***[14,75]	6	240.9	59	*OR51F1*	11	130.1
10	*RNF144B*	6	237.8	60	*DLG2*	11	130.0
11	*CPE*	4	216.3	61	*KDM4C*	9	129.7
12	*AXDND1*	1	206.9	62	*HLA-DRA*	6	129.0
13	*ARPC5*	1	205.5	63	***FHIT***[77]	3	128.3
14	***HLA-DQB1***[14]	6	204.0	64	*ANO3*	11	128.1
15	*DMBT1*	10	199.2	65	***CDSN***[15]	6	127.5
16	*ARHGAP42*	11	198.9	66	***PSORS1C1***[78]	6	127.5
17	*ZNF717*	3	196.6	67	*SH3RF3*	2	127.3
18	*CTNNA3*	10	195.8	68	*CCDC146*	7	127.1
19	*RGS6*	14	193.9	69	*L1TD1*	1	126.0
20	***HLA-DRB1***[14,75]	6	189.4	70	*FMO5*	1	125.9
21	*CPNE4*	3	184.1	71	*CEP112*	17	125.0
22	*RGL1*	1	181.3	72	*TRPC6*	11	124.8
23	*STK32A*	5	179.7	73	*C4orf37*	4	124.7
24	*POLN*	4	175.3	74	***PRIM2***[79]	6	124.2
25	*KALRN*	3	172.3	75	*ADH1C*	4	124.0
26	*SNX31*	8	171.7	76	***MYO3A***[80]	10	123.4
27	*MAP2K3*	17	169.0	77	*IGFBP7*	4	123.0
28	***SLC2A9***[15]	4	166.7	78	*HLA-DRB5*	6	122.7
29	*KCNJ12*	17	159.8	79	*CSMD1*	8	122.0
30	*KCNJ18*	17	159.8	80	*EMID2*	7	121.9
31	***ERAP1***[81]	5	159.2	81	*LRP1B*	2	121.7
32	*APBB1IP*	10	156.1	82	*CHRNB3*	8	121.6
33	*BNC2*	9	154.5	83	*KRT83*	12	121.4
34	*FRAS1*	4	151.1	84	*PTPRB*	12	121.3
35	*WWTR1*	3	150.9	85	*LGALS8*	1	120.9
36	*ART3*	4	150.3	86	*GCOM1*	15	120.9
37	*SLC38A9*	5	150.3	87	*SNX19*	11	120.1
38	*FXN*	9	150.0	88	*SCP2*	1	119.8
39	*FOPNL*	16	148.8	89	*ANK3*	10	119.4
40	***MAGI2***[82]	7	146.8	90	*OR51B6*	11	119.4
41	*POLR1E*	9	146.0	91	*OR5W2*	11	119.0
42	*BCAS1*	20	145.6	92	*RIMBP2*	12	118.9
43	*USP20*	9	145.3	93	*ADH4*	4	118.6
44	*GRIN2A*	16	145.2	94	*ITGA1*	5	118.5
45	*OR4C45*	11	145.0	95	*EMR1*	19	118.2
46	*SPEF2*	5	143.6	96	*PACRG*	6	118.1
47	*MSH3*	5	143.3	97	*KANK1*	9	117.9
48	*LUZP2*	11	141.1	98	*APOBEC4*	1	117.8
49	*COL4A3*	2	139.3	99	*ZDHHC7*	16	117.5
50	*MLF1IP*	4	138.1	100	*ANK2*	4	117.4

Previously-hypothesized genes are indicated in bold. Genes overlapping with Table S2 are highlighted in gray.

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