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- I. Contributing authors participating in the RACI consortium
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*: Microsoft Excel source files for Supplementary Tables 2-6 are available at www.nature.com/nature.

Section 1. Supplementary Tables

Supplementary Table 1. Associations of the 101 RA risk loci

SNP	Chr.	Position (bp)	Gene	A1/A2	Population	GWAS meta-analysis (Stage 1)				Replication study (Stages 2-3)				Combined (Stages 1-2-3)				Ref								
						Freq. (A1)	No. subjects	Control	Case	OR (95%CI)	P	No. subjects	Control	Case	Freq. (A1)	OR (95%CI)	P		No. subjects	Control	Case	Freq. (A1)	OR (95%CI)	P		
chr1:2523811	1	2,523,811	TNFRSF14-MMEL1	G/A	Trans-ethnic	-	18435	60813	0.70	0.67	1.13 (1.09-1.16)	3.3E-14	3566	5312	0.68	0.67	1.05 (0.97-1.13)	2.2E-01	22001	66125	0.69	0.67	1.11 (1.08-1.15)	7.8E-14		
-	-	-	-	-	European	0.71	14361	43923	0.72	0.70	1.12 (1.08-1.16)	2.2E-10	2638	4477	0.69	0.68	1.01 (0.93-1.09)	8.9E-01	16999	48400	0.72	0.70	1.10 (1.07-1.14)	4.8E-09		
-	-	-	-	-	Asian	0.61	4074	16890	0.61	0.58	1.15 (1.08-1.22)	2.1E-05	928	835	0.64	0.60	1.32 (1.09-1.59)	4.1E-03	5002	17725	0.61	0.58	1.16 (1.09-1.23)	7.8E-07		
rs227163	1	7,961,206	TNFRSF9	C/T	Trans-ethnic	-	19234	61564	0.42	0.42	1.03 (1.01-1.06)	1.5E-02	8661	10211	0.44	0.42	1.06 (1.02-1.11)	4.6E-03	27895	17775	0.42	0.42	1.04 (1.02-1.06)	3.9E-04		
-	-	-	-	-	European	0.41	14361	43923	0.42	0.42	1.00 (0.97-1.03)	9.4E-01	2780	4700	0.43	0.42	0.99 (0.92-1.06)	6.9E-01	17141	48623	0.42	0.42	1.00 (0.97-1.03)	9.3E-01		
-	-	-	-	-	Asian	0.33	4873	17641	0.43	0.42	1.12 (1.07-1.18)	5.0E-06	5881	5511	0.44	0.42	1.11 (1.05-1.17)	1.4E-04	10754	23152	0.44	0.42	1.11 (1.08-1.16)	3.1E-09		
rs2301888	1	17,672,730	PADI4	G/A	Trans-ethnic	-	19234	61564	0.62	0.58	1.13 (1.10-1.17)	2.2E-18	928	835	0.45	0.43	1.10 (0.93-1.29)	2.7E-01	20162	62399	0.61	0.58	1.13 (1.10-1.16)	1.3E-18		
-	-	-	-	-	European	0.65	14361	43923	0.67	0.65	1.11 (1.07-1.14)	5.5E-09	-	-	-	-	-	-	14361	43923	0.67	0.65	1.11 (1.07-1.14)	5.5E-09		
-	-	-	-	-	Asian	0.42	4873	17641	0.46	0.41	1.20 (1.14-1.26)	8.9E-13	928	835	0.45	0.43	1.10 (0.93-1.29)	2.7E-01	5801	18476	0.46	0.41	1.19 (1.14-1.25)	8.0E-13		
rs28411352	1	38,278,579	MTF1-INPP5B	T/C	Trans-ethnic	-	19234	61564	0.27	0.24	1.12 (1.08-1.15)	3.6E-12	3355	4894	0.29	0.28	1.06 (0.98-1.14)	1.4E-01	22589	66458	0.27	0.25	1.11 (1.08-1.14)	2.8E-12		
-	-	-	-	-	European	0.26	14361	43923	0.27	0.25	1.11 (1.07-1.16)	5.2E-09	2427	4059	0.31	0.30	1.05 (0.97-1.14)	2.4E-01	16788	47982	0.28	0.25	1.10 (1.07-1.14)	5.9E-09		
-	-	-	-	-	Asian	0.23	4873	17641	0.25	0.23	1.13 (1.06-1.20)	1.3E-04	928	835	0.22	0.21	1.10 (0.91-1.32)	3.2E-01	5801	18476	0.25	0.23	1.12 (1.06-1.19)	7.8E-05		
rs12140275	1	38,633,879	LOC339442	A/T	Trans-ethnic	-	17574	58919	0.81	0.81	1.10 (1.06-1.14)	2.7E-07	3681	5486	0.84	0.79	1.16 (1.06-1.26)	1.1E-03	21255	64405	0.82	0.81	1.11 (1.07-1.14)	2.0E-09		
-	-	-	-	-	European	0.78	14361	43923	0.77	0.75	1.10 (1.06-1.14)	3.6E-07	2753	4651	0.80	0.76	1.15 (1.05-1.25)	2.2E-03	17114	48574	0.77	0.75	1.11 (1.07-1.14)	4.4E-09		
-	-	-	-	-	Asian	0.99	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
rs2476601	1	114,377,568	PTPN22	A/G	Trans-ethnic	-	14361	43923	0.16	0.10	1.81 (1.74-1.90)	1.0E-149	2780	4700	0.17	0.09	1.72 (1.54-1.91)	3.0E-22	17141	48623	0.16	0.09	1.80 (1.73-1.88)	6.6E-170		
-	-	-	-	-	European	0.09	14361	43923	0.16	0.10	1.81 (1.73-1.90)	1.6E-149	2780	4700	0.17	0.09	1.72 (1.54-1.91)	3.0E-22	17141	48623	0.16	0.09	1.80 (1.73-1.88)	8.9E-170		
-	-	-	-	-	Asian	0.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
rs624988	1	117,263,790	CD2	T/C	Trans-ethnic	-	19234	61564	0.42	0.41	1.06 (1.03-1.09)	3.3E-05	3708	5535	0.42	0.40	1.05 (0.98-1.12)	1.5E-01	22942	67099	0.42	0.40	1.06 (1.03-1.08)	1.2E-05		
-	-	-	-	-	European	0.40	14361	43923	0.42	0.40	1.09 (1.06-1.12)	4.6E-08	2780	4700	0.42	0.39	1.11 (1.03-1.20)	4.3E-03	17141	48623	0.42	0.40	1.09 (1.06-1.12)	8.0E-10		
-	-	-	-	-	Asian	0.42	4873	17641	0.42	0.43	0.98 (0.93-1.02)	3.2E-01	928	835	0.43	0.48	0.81 (0.70-0.95)	8.3E-03	5801	18476	0.43	0.43	0.96 (0.92-1.01)	8.1E-02		
rs2228145	1	154,426,970	IL6R	A/C	Trans-ethnic	-	19234	61564	0.62	0.60	1.08 (1.05-1.11)	3.5E-09	3708	5535	0.62	0.60	1.04 (0.97-1.11)	2.7E-01	22942	67099	0.62	0.60	1.08 (1.05-1.10)	3.7E-09		
-	-	-	-	-	European	0.64	14361	43923	0.62	0.60	1.07 (1.04-1.11)	4.5E-06	2780	4700	0.63	0.61	1.03 (0.96-1.11)	3.8E-01	17141	48623	0.62	0.60	1.07 (1.04-1.10)	4.8E-06		
-	-	-	-	-	Asian	0.64	4873	17641	0.61	0.60	1.10 (1.05-1.16)	1.0E-04	928	835	0.58	0.59	1.06 (0.91-1.23)	4.8E-01	5801	18476	0.61	0.60	1.10 (1.05-1.15)	9.2E-05		
rs2317230	1	157,674,997	FCRL3	T/G	Trans-ethnic	-	19234	61564	0.44	0.42	1.08 (1.05-1.11)	2.1E-08	3557	5222	0.40	0.41	1.00 (0.93-1.07)	9.1E-01	22791	66786	0.43	0.42	1.07 (1.04-1.09)	2.2E-07		
-	-	-	-	-	European	0.46	14361	43923	0.45	0.43	1.07 (1.04-1.10)	1.0E-05	2629	4387	0.40	0.42	0.97 (0.90-1.04)	3.6E-01	16990	48310	0.44	0.43	1.06 (1.03-1.09)	1.9E-04		
-	-	-	-	-	Asian	0.40	4873	17641	0.41	0.39	1.10 (1.04-1.16)	3.1E-04	928	835	0.40	0.38	1.14 (0.97-1.33)	1.0E-01	5801	18476	0.41	0.39	1.10 (1.05-1.16)	8.3E-05		
rs4656942	1	160,831,048	LY9-CD244	G/A	Trans-ethnic	-	19234	61564	0.75	0.75	1.03 (1.00-1.06)	6.9E-02	928	835	0.70	0.71	0.97 (0.82-1.15)	7.4E-01	20162	62399	0.75	0.75	1.03 (1.00-1.06)	8.4E-02		
-	-	-	-	-	European	0.74	14361	43923	0.77	0.77	1.01 (0.98-1.05)	4.8E-01	-	-	-	-	-	-	14361	43923	0.77	0.77	1.01 (0.98-1.05)	4.8E-01		
-	-	-	-	-	Asian	0.70	4873	17641	0.71	0.70	1.06 (1.01-1.12)	2.6E-02	928	835	0.70	0.71	0.97 (0.82-1.15)	7.4E-01	5801	18476	0.71	0.70	1.05 (1.00-1.11)	4.4E-02		
rs72717009	1	161,405,053	FCGR2A	T/C	Trans-ethnic	-	16775	58168	0.11	0.10	1.13 (1.08-1.19)	2.3E-07	2590	4331	0.10	0.10	1.09 (0.96-1.24)	1.9E-01	19365	62499	0.11	0.10	1.13 (1.08-1.18)	1.1E-07		
-	-	-	-	-	European	0.13	14361	43923	0.12	0.12	1.13 (1.08-1.19)	1.1E-06	2590	4331	0.10	0.10	1.09 (0.96-1.24)	1.9E-01	16951	48254	0.12	0.12	1.12 (1.07-1.18)	5.2E-07		
-	-	-	-	-	Asian	0.03	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
chr1:161644258	1	161,644,258	FCGR2B	C/G	Trans-ethnic	-	4873	17641	0.31	0.30	1.15 (1.08-1.22)	4.5E-06	928	835	0.18	0.20	0.75 (0.58-0.96)	2.4E-02	5801	18476	0.29	0.29	1.12 (1.06-1.19)	8.2E-05		
-	-	-	-	-	European	0.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
-	-	-	-	-	Asian	0.21	4873	17641	0.31	0.30	1.15 (1.08-1.22)	3.3E-06	928	835	0.18	0.20	0.75 (0.58-0.96)	2.4E-02	5801	18476	0.29	0.29	1.12 (1.06-1.19)	6.0E-05		
rs2105325	1	173,349,725	LOC100506023	C/A	Trans-ethnic	-	19234	61564	0.80	0.79	1.11 (1.08-1.15)	3.1E-10	3568	5319	0.82	0.77	1.17 (1.07-1.27)	2.9E-04	22802	66883	0.81	0.79	1.12 (1.08-1.15)	6.9E-13		
-	-	-	-	-	European	0.76	14361	43923	0.76	0.74	1.11 (1.07-1.15)	1.0E-08	2640	4484	0.78	0.74	1.17 (1.07-1.28)	3.9E-04	17001	48407	0.77	0.74	1.12 (1.08-1.15)	3.3E-11		
-	-	-	-	-	Asian	0.92	4873	17641	0.93	0.92	1.13 (1.03-1.24)	7.6E-03	928	835	0.93	0.92	1.12 (0.85-1.48)	4.1E-01	5801	18476	0.93	0.92	1.13 (1.04-1.23)	5.2E-03		
rs17688708	1	198,640,488	PTPRC	C/T	Trans-ethnic	-	14361	43923	0.91	0.89	1.12 (1.06-1.18)	1.7E-05	-	-	-	-	-	-	-	-	14361	43923	0.91	0.89	1.12 (1.06-1.18)	1.7E-05
-	-	-	-	-	European	0.89	14361	43923	0.91	0.89	1.12 (1.06-1.18)	1.7E-05	-	-	-	-	-	-	-	-	14361	43923	0.91	0.89	1.12 (1.06-1.18)	1.8E-05
-	-	-	-	-	Asian	1.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
rs10175798	2	30,449,594	LBH	A/G	Trans-ethnic	-	19234	61564	0.57	0.54	1.09 (1.06-1.12)	5.4E-09	3608	5												

rs13385025	2	62,461,120	B3GN72	A/G	Trans-ethnic	-	13748	47008	0.18	0.17	1.11 (1.06-1.16)	2.1E-06	928	835	0.21	0.20	1.16 (0.94-1.43)	1.7E-01	14676	47843	0.18	0.17	1.11 (1.07-1.16)	8.8E-07
-	-	-	-	-	European	0.13	8875	29367	0.13	0.12	1.08 (1.02-1.15)	1.0E-02	-	-	-	-	-	-	8875	29367	0.13	0.12	1.08 (1.02-1.15)	1.0E-02
-	-	-	-	-	Asian	0.23	4873	17641	0.28	0.27	1.13 (1.07-1.20)	3.0E-05	928	835	0.21	0.20	1.16 (0.94-1.43)	1.7E-01	5801	18476	0.27	0.26	1.14 (1.07-1.20)	1.2E-05
rs1858037	2	65,598,300	SPRED2	T/A	Trans-ethnic	-	19234	61564	0.55	0.51	1.12 (1.09-1.15)	1.2E-14	3691	5505	0.56	0.58	1.07 (1.00-1.15)	5.6E-02	22925	67069	0.55	0.52	1.11 (1.08-1.14)	3.3E-15
-	-	-	-	-	European	0.68	14361	43923	0.68	0.65	1.11 (1.07-1.14)	5.9E-10	2763	4670	0.67	0.65	1.03 (0.95-1.11)	4.8E-01	17124	48593	0.68	0.65	1.09 (1.06-1.13)	2.0E-09
-	-	-	-	-	Asian	0.22	4873	17641	0.19	0.16	1.17 (1.10-1.25)	4.7E-07	928	835	0.23	0.19	1.36 (1.13-1.63)	1.2E-03	5801	18476	0.20	0.16	1.19 (1.12-1.26)	1.0E-08
rs9653442	2	100,825,367	AFF3	C/T	Trans-ethnic	-	19234	61564	0.49	0.46	1.11 (1.08-1.14)	9.9E-15	3589	5300	0.47	0.44	1.16 (1.08-1.24)	1.6E-05	22823	68864	0.48	0.46	1.11 (1.09-1.14)	1.6E-18
-	-	-	-	-	European	0.46	14361	43923	0.49	0.46	1.11 (1.08-1.15)	3.6E-12	2661	4465	0.48	0.46	1.14 (1.06-1.23)	5.7E-04	17022	48388	0.49	0.46	1.12 (1.09-1.15)	9.8E-15
-	-	-	-	-	Asian	0.41	4873	17641	0.49	0.47	1.09 (1.04-1.15)	4.8E-04	928	835	0.43	0.38	1.24 (1.06-1.44)	5.5E-03	5801	18476	0.48	0.47	1.10 (1.05-1.16)	2.7E-05
rs6732565	2	111,607,832	ACOXL	A/G	Trans-ethnic	-	13748	47008	0.63	0.61	1.08 (1.04-1.11)	2.8E-06	10588	12138	0.62	0.61	1.06 (1.02-1.10)	5.0E-03	24336	59146	0.62	0.61	1.07 (1.05-1.10)	2.8E-08
-	-	-	-	-	European	0.63	8875	29367	0.64	0.62	1.08 (1.04-1.13)	8.8E-05	3770	5756	0.64	0.61	1.16 (1.09-1.24)	4.3E-06	12645	35123	0.64	0.62	1.10 (1.07-1.14)	9.4E-09
-	-	-	-	-	Asian	0.60	4873	17641	0.61	0.59	1.07 (1.02-1.12)	8.7E-03	6818	6382	0.60	0.60	1.00 (0.95-1.05)	9.7E-01	11691	24023	0.61	0.59	1.04 (1.00-1.08)	4.0E-02
rs11889341	2	191,943,742	STAT4	T/C	Trans-ethnic	-	19234	61564	0.27	0.25	1.14 (1.11-1.18)	6.7E-19	3670	5466	0.28	0.25	1.07 (1.00-1.16)	6.0E-02	22904	67030	0.27	0.25	1.13 (1.10-1.17)	3.6E-19
-	-	-	-	-	European	0.23	14361	43923	0.25	0.23	1.13 (1.09-1.17)	6.5E-12	2742	4631	0.25	0.23	1.09 (1.00-1.18)	5.2E-02	17103	48554	0.25	0.23	1.12 (1.09-1.16)	1.4E-12
-	-	-	-	-	Asian	0.33	4873	17641	0.33	0.30	1.17 (1.11-1.24)	6.3E-09	928	835	0.36	0.34	1.03 (0.88-1.21)	7.3E-01	5801	18476	0.34	0.30	1.16 (1.10-1.22)	2.0E-08
rs6715284	2	202,154,397	CFLAR-CASP8	G/C	Trans-ethnic	-	14361	43923	0.11	0.10	1.14 (1.08-1.20)	2.9E-07	3672	5501	0.10	0.09	1.20 (1.08-1.35)	1.1E-03	18033	49424	0.11	0.10	1.15 (1.10-1.20)	1.8E-09
-	-	-	-	-	European	0.11	14361	43923	0.11	0.10	1.14 (1.08-1.20)	2.9E-07	2744	4666	0.13	0.10	1.20 (1.07-1.34)	1.6E-03	17105	48589	0.11	0.10	1.15 (1.10-1.20)	2.5E-09
-	-	-	-	-	Asian	0.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
rs1980422	2	204,610,396	CD28	C/T	Trans-ethnic	-	19234	61564	0.21	0.19	1.12 (1.09-1.16)	6.4E-12	3606	5366	0.22	0.22	1.14 (1.06-1.24)	1.0E-03	22840	66930	0.21	0.19	1.12 (1.09-1.16)	3.0E-14
-	-	-	-	-	European	0.26	14361	43923	0.25	0.23	1.12 (1.08-1.16)	6.0E-11	2678	4531	0.26	0.24	1.16 (1.07-1.27)	5.7E-04	17039	48454	0.25	0.24	1.13 (1.09-1.17)	1.9E-13
-	-	-	-	-	Asian	0.09	4873	17641	0.08	0.06	1.11 (1.01-1.23)	3.4E-02	928	835	0.12	0.11	1.01 (0.80-1.28)	9.1E-01	5801	18476	0.08	0.07	1.10 (1.00-1.20)	4.6E-02
rs3087243	2	204,738,919	CTLA4	G/A	Trans-ethnic	-	19234	61564	0.64	0.60	1.14 (1.11-1.17)	1.7E-22	3669	5454	0.65	0.59	1.13 (1.06-1.21)	4.0E-04	22903	67018	0.64	0.60	1.14 (1.11-1.17)	3.1E-25
-	-	-	-	-	European	0.55	14361	43923	0.59	0.55	1.15 (1.12-1.19)	9.2E-20	2741	4619	0.59	0.54	1.13 (1.05-1.22)	8.7E-04	17102	48542	0.59	0.55	1.15 (1.12-1.18)	3.6E-22
-	-	-	-	-	Asian	0.76	4873	17641	0.77	0.74	1.11 (1.05-1.18)	2.2E-04	928	835	0.83	0.82	1.13 (0.93-1.37)	2.3E-01	5801	18476	0.78	0.74	1.12 (1.06-1.18)	1.0E-04
rs4452313	3	17,047,032	PLCL2	T/A	Trans-ethnic	-	19234	61564	0.36	0.35	1.09 (1.06-1.12)	8.2E-10	3618	5422	0.37	0.34	1.07 (1.00-1.14)	6.1E-02	22852	66986	0.37	0.35	1.09 (1.06-1.12)	1.6E-10
-	-	-	-	-	European	0.30	14361	43923	0.30	0.29	1.12 (1.08-1.15)	2.7E-10	2690	4587	0.32	0.30	1.08 (1.00-1.17)	5.2E-02	17051	48510	0.31	0.29	1.11 (1.08-1.15)	5.2E-11
-	-	-	-	-	Asian	0.53	4873	17641	0.54	0.53	1.04 (0.99-1.10)	9.7E-02	928	835	0.54	0.53	1.03 (0.89-1.19)	7.4E-01	5801	18476	0.54	0.53	1.04 (0.99-1.09)	9.2E-02
rs3806624	3	27,764,623	EOMES	G/A	Trans-ethnic	-	19234	61564	0.57	0.57	1.09 (1.05-1.12)	1.9E-08	3376	5023	0.53	0.48	1.06 (0.98-1.14)	1.5E-01	22610	66587	0.57	0.56	1.08 (1.05-1.11)	8.6E-09
-	-	-	-	-	European	0.47	14361	43923	0.48	0.46	1.09 (1.06-1.12)	6.1E-08	2448	4188	0.42	0.42	1.06 (0.98-1.14)	1.6E-01	16809	48111	0.47	0.46	1.08 (1.05-1.12)	2.8E-08
-	-	-	-	-	Asian	0.84	4873	17641	0.84	0.84	1.06 (0.99-1.14)	1.0E-01	928	835	0.81	0.81	1.03 (0.79-1.34)	8.1E-01	5801	18476	0.84	0.84	1.06 (0.99-1.14)	1.0E-01
rs73081554	3	58,302,935	DNASE1L3-ABHD6-PYK	T/C	Trans-ethnic	-	14361	43923	0.08	0.07	1.18 (1.11-1.25)	4.6E-08	-	-	-	-	-	-	14361	43923	0.08	0.07	1.18 (1.11-1.25)	4.6E-08
-	-	-	-	-	European	0.06	14361	43923	0.08	0.07	1.18 (1.11-1.25)	4.7E-08	-	-	-	-	-	-	14361	43923	0.08	0.07	1.18 (1.11-1.25)	4.7E-08
-	-	-	-	-	Asian	0.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
rs9826828	3	136,402,060	IL20RB	A/G	Trans-ethnic	-	10269	31898	0.02	0.02	1.42 (1.25-1.62)	9.0E-08	2774	4690	0.02	0.02	1.51 (1.16-1.97)	2.4E-03	13043	36588	0.02	0.02	1.44 (1.28-1.61)	8.6E-10
-	-	-	-	-	European	0.02	10269	31898	0.02	0.02	1.42 (1.25-1.62)	9.2E-08	2774	4690	0.02	0.02	1.51 (1.16-1.97)	2.4E-03	13043	36588	0.02	0.02	1.44 (1.28-1.61)	8.7E-10
-	-	-	-	-	Asian	0.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
rs13142500	4	10,727,357	CLNK	C/T	Trans-ethnic	-	13748	47008	0.51	0.49	1.10 (1.07-1.14)	5.0E-09	928	835	0.62	0.60	1.08 (0.92-1.27)	3.3E-01	14676	47843	0.51	0.49	1.10 (1.07-1.13)	3.0E-09
-	-	-	-	-	European	0.50	8875	29367	0.47	0.45	1.10 (1.06-1.15)	2.4E-06	-	-	-	-	-	-	8875	29367	0.47	0.45	1.10 (1.06-1.15)	2.4E-06
-	-	-	-	-	Asian	0.53	4873	17641	0.58	0.56	1.10 (1.04-1.16)	4.6E-04	928	835	0.62	0.60	1.08 (0.92-1.27)	3.3E-01	5801	18476	0.58	0.56	1.10 (1.04-1.15)	2.8E-04
rs1933540	4	26,120,001	C4orf52	C/T	Trans-ethnic	-	14361	43923	0.34	0.31	1.15 (1.11-1.19)	8.8E-17	-	-	-	-	-	-	14361	43923	0.34	0.31	1.15 (1.11-1.19)	8.8E-17
-	-	-	-	-	European	0.31	14361	43923	0.34	0.31	1.15 (1.11-1.19)	9.2E-17	-	-	-	-	-	-	14361	43923	0.34	0.31	1.15 (1.11-1.19)	9.5E-17
-	-	-	-	-	Asian	0.01	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
rs2664035	4	48,220,839	TEC	A/G	Trans-ethnic	-	19234	61564	0.39	0.37	1.06 (1.03-1.09)	1.2E-05	4335	5995	0.39	0.37	1.11 (1.04-1.18)	8.6E-04	23569	67559	0.39	0.37	1.07 (1.04-1.10)	9.5E-08
-	-	-	-	-	European	0.40	14361	43923	0.42	0.40	1.08 (1.04-1.11)	2.5E-06	3407	5160	0.41	0.38	1.11 (1.04-1.18)	2.9E-03	17768	49083	0.42	0.40	1.08 (1.05-1.11)	3.3E-08
-	-	-	-	-	Asian	0.34	4873	17641	0.29	0.29	1.01 (0.96-1.07)	6.0E-01	928	835	0.34	0.30	1.13 (0.96-1.33)	1.3E-01	5801	18476	0.30	0.29	1.03 (0.97-1.08)	3.3E-01
rs10028001	4	79,502,972	ANXA3	T/A	Trans-ethnic	-	13748	47008	0.41	0.40	1.06 (1.03-1.09)	3.1E-04	928	835	0.40	0.38	1.02 (0.86-1.21)	8.4E-01	14676	47843	0.41	0.40	1.06 (1.03-1.09)	3.4E-04
-	-	-	-	-	European	0.34	8875	29367	0.38	0.37	1.02 (0.98-1.06)	2.7E-01	-	-	-	-	-	-	8875	29367	0.38	0.37	1.02 (0.98-1.06)	2.7E-01
-	-	-	-	-	Asian	0.41	4873	17641	0.47	0.45	1.12 (1.07-1.18)	6.9E-06	928	835	0.40	0.38	1.02 (0.86-1.21)	8.4E-01	5801	18476	0.46	0.44	1.11 (1.06-1.17)	1.2E-05
rs4547595	4	123,399,491	IL2-IL21	G/A	Trans-ethnic	-	14361	43923	0.08	0.07	1.14 (1.08-1.20)	3.5E-06	-	-	-	-	-	-	14361	43923	0.09	0.07	1.14 (1.08-1.20)	3.5E-06
-	-	-	-	-	European	0.08	14361	43923	0.08	0.07	1.14 (1.08-1.20)	3.5E-06	-	-	-	-	-	-	14361	43923	0.08	0.07	1.14 (1.08-1.20)	3.5E-06
-	-	-	-	-	Asian	0.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	

rs7731626	5	55,444,683	ANKRD55	G/A	Trans-ethnic	-	15255	47661	0.70	0.71	1.21 (1.17-1.26)	7.3E-24	15255	47661	0.70	0.71	1.21 (1.17-1.26)	7.3E-24
-	-	-	-	-	European	0.63	12841	33416	0.67	0.63	1.21 (1.17-1.26)	7.9E-23	12841	33416	0.67	0.63	1.21 (1.17-1.26)	8.2E-23
-	-	-	-	-	Asian	0.91	-	-	-	-	-	-	-	-	-	-	-	-
rs2561477	5	102,608,924	C5orf30	G/A	Trans-ethnic	-	19234	61564	0.71	0.69	1.09 (1.06-1.12)	1.9E-09	3608	5352	0.72	0.70	1.09 (1.02-1.18)	1.6E-02
-	-	-	-	-	European	0.68	14361	43923	0.70	0.68	1.11 (1.07-1.15)	5.2E-10	2880	4517	0.70	0.69	1.11 (1.02-1.20)	1.3E-02
-	-	-	-	-	Asian	0.76	4873	17641	0.73	0.72	1.04 (0.98-1.10)	2.0E-01	928	835	0.76	0.75	1.03 (0.87-1.23)	7.1E-01
rs657075	5	131,430,118	IL3-CSF2	A/G	Trans-ethnic	-	19234	61564	0.17	0.17	1.09 (1.05-1.13)	1.1E-06	928	835	0.25	0.24	1.08 (0.90-1.29)	3.9E-01
-	-	-	-	-	European	0.13	14361	43923	0.10	0.10	1.07 (1.01-1.12)	1.1E-02	-	-	-	-	-	-
-	-	-	-	-	Asian	0.31	4873	17641	0.37	0.35	1.12 (1.07-1.18)	8.9E-06	928	835	0.25	0.24	1.08 (0.90-1.29)	3.9E-01
rs9378815	6	426,155	IRF4	C/G	Trans-ethnic	-	19234	61564	0.60	0.58	1.10 (1.07-1.13)	5.9E-11	3399	4979	0.57	0.59	1.03 (0.96-1.11)	4.4E-01
-	-	-	-	-	European	0.64	14361	43923	0.67	0.66	1.09 (1.06-1.13)	1.6E-07	2471	4144	0.67	0.65	1.05 (0.96-1.13)	2.7E-01
-	-	-	-	-	Asian	0.36	4873	17641	0.40	0.38	1.11 (1.06-1.17)	6.0E-05	928	835	0.30	0.32	0.96 (0.81-1.13)	6.2E-01
chr6:14103212	6	14,103,212	CD83	T/C	Trans-ethnic	-	13748	47008	0.10	0.09	1.15 (1.09-1.21)	1.8E-07	3698	5499	0.09	0.07	1.05 (0.93-1.19)	4.1E-01
-	-	-	-	-	European	0.07	8875	29367	0.06	0.05	1.13 (1.04-1.23)	4.6E-03	2770	4664	0.05	0.05	0.99 (0.84-1.17)	9.2E-01
-	-	-	-	-	Asian	0.19	4873	17641	0.17	0.15	1.17 (1.09-1.25)	7.3E-06	928	835	0.21	0.19	1.13 (0.94-1.36)	1.8E-01
rs9268839	6	32,428,772	H1A-DRB1	G/A	Trans-ethnic	-	19234	61564	0.65	0.45	2.30 (2.23-2.36)	<1.0E-250	928	835	0.55	0.42	1.78 (1.52-2.07)	4.8E-13
-	-	-	-	-	European	0.45	14361	43923	0.66	0.45	2.47 (2.39-2.55)	<1.0E-250	-	-	-	-	-	-
-	-	-	-	-	Asian	0.39	4873	17641	0.60	0.44	1.91 (1.81-2.01)	3.5E-134	928	835	0.55	0.42	1.78 (1.52-2.07)	4.8E-13
rs2234067	6	36,355,654	ETV7	C/A	Trans-ethnic	-	19234	61564	0.90	0.90	1.15 (1.10-1.20)	1.6E-09	-	-	-	-	-	-
-	-	-	-	-	European	0.88	14361	43923	0.88	0.87	1.14 (1.09-1.19)	4.1E-08	-	-	-	-	-	-
-	-	-	-	-	Asian	0.96	4873	17641	0.97	0.96	1.22 (1.06-1.41)	7.0E-03	-	-	-	-	-	-
rs2233424	6	44,233,921	NFKBIE	T/C	Trans-ethnic	-	12852	40405	0.13	0.12	1.26 (1.20-1.33)	7.6E-19	928	835	0.18	0.15	1.23 (0.99-1.52)	6.4E-02
-	-	-	-	-	European	0.04	7979	22764	0.05	0.04	1.33 (1.20-1.47)	3.3E-08	-	-	-	-	-	-
-	-	-	-	-	Asian	0.16	4873	17641	0.25	0.21	1.24 (1.17-1.31)	9.3E-13	928	835	0.18	0.15	1.23 (0.99-1.52)	6.4E-02
rs9372120	6	106,667,535	ATG5	G/T	Trans-ethnic	-	19234	61564	0.18	0.16	1.10 (1.06-1.14)	2.1E-07	3606	5363	0.17	0.16	1.18 (1.08-1.29)	3.1E-04
-	-	-	-	-	European	0.19	14361	43923	0.22	0.20	1.09 (1.05-1.13)	1.2E-05	2678	4548	0.21	0.18	1.20 (1.09-1.31)	1.2E-04
-	-	-	-	-	Asian	0.02	4873	17641	0.06	0.05	1.19 (1.07-1.31)	1.2E-03	928	835	0.04	0.05	0.91 (0.63-1.32)	6.1E-01
rs17264332	6	138,005,515	TNFAIP3	G/A	Trans-ethnic	-	14361	43923	0.24	0.21	1.17 (1.13-1.22)	6.7E-19	2699	4591	0.22	0.20	1.12 (1.03-1.23)	1.1E-02
-	-	-	-	-	European	0.17	14361	43923	0.24	0.21	1.17 (1.13-1.22)	7.1E-19	2699	4591	0.22	0.20	1.12 (1.03-1.23)	1.1E-02
-	-	-	-	-	Asian	0.00	-	-	-	-	-	-	-	-	-	-	-	-
rs7752903	6	138,227,364	TNFAIP3	G/T	Trans-ethnic	-	19234	61564	0.05	0.04	1.38 (1.30-1.46)	2.7E-26	3687	5488	0.04	0.03	1.42 (1.18-1.70)	1.5E-04
-	-	-	-	-	European	0.02	14361	43923	0.04	0.03	1.40 (1.30-1.52)	1.4E-17	2759	4653	0.03	0.03	1.49 (1.20-1.84)	2.5E-04
-	-	-	-	-	Asian	0.07	4873	17641	0.09	0.07	1.35 (1.23-1.48)	1.4E-10	928	835	0.06	0.05	1.25 (0.89-1.77)	2.0E-01
rs9373594	6	149,834,574	PPL4	T/C	Trans-ethnic	-	13748	47008	0.68	0.66	1.10 (1.06-1.14)	7.7E-07	9562	10952	0.48	0.53	1.08 (1.03-1.13)	1.8E-03
-	-	-	-	-	European	0.85	8875	29367	0.85	0.85	1.07 (1.01-1.13)	1.2E-02	2721	4578	0.85	0.85	1.06 (0.96-1.17)	2.8E-01
-	-	-	-	-	Asian	0.25	4873	17641	0.36	0.34	1.13 (1.07-1.19)	5.3E-06	6841	6374	0.32	0.31	1.08 (1.03-1.14)	3.1E-03
rs2451258	6	159,505,600	TAGAP	T/C	Trans-ethnic	-	19234	61564	0.75	0.74	1.11 (1.07-1.14)	2.0E-10	3624	5386	0.75	0.70	1.08 (1.00-1.17)	4.1E-02
-	-	-	-	-	European	0.64	14361	43923	0.67	0.64	1.11 (1.07-1.14)	6.6E-10	2696	4551	0.69	0.65	1.07 (0.99-1.16)	7.4E-02
-	-	-	-	-	Asian	0.95	4873	17641	0.98	0.98	1.15 (0.97-1.37)	1.1E-01	928	835	0.94	0.93	1.28 (0.90-1.81)	1.7E-01
rs1571878	6	167,540,842	CCR6	C/T	Trans-ethnic	-	19234	61564	0.49	0.45	1.17 (1.14-1.20)	6.1E-30	3607	5345	0.48	0.44	1.18 (1.11-1.27)	1.3E-06
-	-	-	-	-	European	0.42	14361	43923	0.47	0.44	1.13 (1.10-1.16)	4.9E-15	2679	4510	0.48	0.44	1.16 (1.08-1.25)	8.0E-05
-	-	-	-	-	Asian	0.45	4873	17641	0.53	0.48	1.28 (1.22-1.35)	1.1E-20	928	835	0.49	0.44	1.28 (1.09-1.50)	2.7E-03
rs67250450	7	28,174,986	JAZF1	T/C	Trans-ethnic	-	19234	61564	0.60	0.57	1.09 (1.05-1.13)	1.8E-06	4675	6593	0.65	0.68	1.16 (1.07-1.25)	1.2E-04
-	-	-	-	-	European	0.79	14361	43923	0.80	0.79	1.10 (1.05-1.14)	1.9E-06	3747	5758	0.80	0.78	1.16 (1.07-1.25)	1.5E-04
-	-	-	-	-	Asian	0.02	4873	17641	0.01	0.01	0.99 (0.80-1.22)	9.3E-01	928	835	0.03	0.03	1.15 (0.74-1.76)	5.4E-01
rs4272	7	92,236,829	CDK6	G/A	Trans-ethnic	-	19234	61564	0.20	0.18	1.10 (1.06-1.13)	1.9E-07	3708	5535	0.20	0.19	1.12 (1.03-1.21)	7.3E-03
-	-	-	-	-	European	0.23	14361	43923	0.23	0.21	1.10 (1.06-1.14)	3.4E-07	2780	4700	0.23	0.21	1.12 (1.03-1.23)	9.6E-03
-	-	-	-	-	Asian	0.11	4873	17641	0.12	0.12	1.06 (0.97-1.15)	1.7E-01	928	835	0.13	0.11	1.09 (0.87-1.37)	4.8E-01
chr7:128580042	7	128,580,042	IRF5	G/A	Trans-ethnic	-	19234	61564	0.42	0.39	1.12 (1.09-1.15)	1.1E-14	-	-	-	-	-	-
-	-	-	-	-	European	0.46	14361	43923	0.48	0.46	1.12 (1.08-1.15)	4.2E-12	-	-	-	-	-	-
-	-	-	-	-	Asian	0.15	4873	17641	0.25	0.23	1.11 (1.05-1.18)	5.4E-04	-	-	-	-	-	-

rs2736337	8	11,341,880	BLK	C/T	Trans-ethnic	-	19234	61564	0.38	0.37	1.11 (1.08-1.14)	4.8E-12	3529	5211	0.37	0.31	1.12 (1.02-1.22)	2.0E-02	22763	66775	0.38	0.36	1.11 (1.08-1.14)	3.1E-13
-	-	-	-	-	European	0.25	14361	43923	0.27	0.25	1.10 (1.06-1.14)	1.6E-07	2601	4376	0.24	0.24	1.07 (0.96-1.20)	2.1E-01	16962	48299	0.26	0.25	1.09 (1.06-1.13)	7.6E-08
-	-	-	-	-	Asian	0.70	4873	17641	0.70	0.67	1.15 (1.08-1.21)	2.0E-06	928	835	0.73	0.68	1.24 (1.04-1.47)	1.8E-02	5801	18476	0.71	0.67	1.15 (1.09-1.22)	1.5E-07
rs938731	8	81,095,395	TPD52	T/C	Trans-ethnic	-	19234	61564	0.57	0.57	1.07 (1.04-1.11)	7.9E-07	3708	5534	0.46	0.40	1.11 (1.03-1.20)	4.8E-03	22942	67098	0.55	0.56	1.08 (1.05-1.11)	1.9E-08
-	-	-	-	-	European	0.49	14361	43923	0.47	0.46	1.09 (1.05-1.12)	1.3E-07	2780	4699	0.34	0.33	1.10 (1.02-1.19)	1.5E-02	17141	48622	0.45	0.44	1.09 (1.06-1.12)	6.6E-09
-	-	-	-	-	Asian	0.80	4873	17641	0.85	0.86	1.01 (0.94-1.08)	8.0E-01	928	835	0.81	0.80	1.25 (0.97-1.62)	8.9E-02	5801	18476	0.85	0.85	1.02 (0.96-1.10)	4.9E-01
rs678347	8	102,463,602	GRHL2	G/A	Trans-ethnic	-	19234	61564	0.42	0.42	1.08 (1.05-1.11)	6.2E-07	3617	5388	0.41	0.34	1.11 (1.03-1.20)	5.6E-03	22851	66952	0.42	0.42	1.08 (1.05-1.11)	1.6E-08
-	-	-	-	-	European	0.23	14361	43923	0.29	0.27	1.09 (1.06-1.13)	1.4E-07	2689	4553	0.28	0.27	1.10 (1.02-1.20)	1.6E-02	17050	48476	0.29	0.27	1.10 (1.06-1.13)	7.3E-09
-	-	-	-	-	Asian	0.77	4873	17641	0.80	0.80	1.02 (0.96-1.09)	4.7E-01	928	835	0.77	0.74	1.13 (0.95-1.35)	1.6E-01	5801	18476	0.80	0.80	1.03 (0.98-1.10)	2.6E-01
rs1516971	8	129,542,100	PVT1	T/C	Trans-ethnic	-	17574	58919	0.90	0.90	1.12 (1.07-1.17)	1.4E-06	2777	4697	0.90	0.87	1.36 (1.22-1.53)	1.2E-07	20351	63616	0.90	0.89	1.15 (1.10-1.20)	1.3E-10
-	-	-	-	-	European	0.90	14361	43923	0.88	0.87	1.13 (1.08-1.18)	5.3E-07	2777	4697	0.90	0.87	1.36 (1.22-1.53)	1.2E-07	17138	48620	0.88	0.87	1.16 (1.11-1.21)	3.2E-11
-	-	-	-	-	Asian	0.97	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
rs11574914	9	34,710,338	CCL19-CC121	A/G	Trans-ethnic	-	17997	59477	0.30	0.26	1.12 (1.09-1.16)	2.1E-13	2780	4700	0.35	0.32	1.12 (1.04-1.21)	3.3E-03	20777	64177	0.31	0.26	1.12 (1.09-1.15)	2.8E-15
-	-	-	-	-	European	0.32	14361	43923	0.36	0.33	1.13 (1.09-1.16)	1.5E-13	2780	4700	0.35	0.32	1.12 (1.04-1.21)	3.3E-03	17141	48623	0.36	0.33	1.13 (1.09-1.16)	1.8E-15
-	-	-	-	-	Asian	0.06	3636	15554	0.05	0.05	1.05 (0.92-1.19)	5.0E-01	-	-	-	-	-	-	3636	15554	0.05	0.05	1.05 (0.92-1.19)	5.0E-01
rs10985070	9	123,636,121	TRAF1-C5	C/A	Trans-ethnic	-	19234	61564	0.48	0.46	1.08 (1.05-1.11)	2.1E-09	3677	5490	0.39	0.35	1.10 (1.03-1.18)	5.9E-03	22911	67054	0.46	0.45	1.08 (1.06-1.11)	5.0E-11
-	-	-	-	-	European	0.43	14361	43923	0.46	0.43	1.09 (1.06-1.12)	1.7E-08	2749	4655	0.35	0.33	1.07 (0.99-1.15)	8.7E-02	17110	48578	0.44	0.42	1.09 (1.06-1.12)	4.2E-09
-	-	-	-	-	Asian	0.50	4873	17641	0.54	0.52	1.06 (1.01-1.11)	2.4E-02	928	835	0.51	0.47	1.22 (1.06-1.42)	7.4E-03	5801	18476	0.53	0.52	1.08 (1.03-1.13)	2.7E-03
rs706778	10	6,098,949	IL2RA	T/C	Trans-ethnic	-	19234	61564	0.47	0.45	1.09 (1.06-1.12)	1.5E-10	3647	5435	0.48	0.43	1.16 (1.08-1.24)	1.4E-05	22881	66939	0.47	0.45	1.10 (1.07-1.12)	4.8E-14
-	-	-	-	-	European	0.42	14361	43923	0.43	0.40	1.11 (1.08-1.15)	7.1E-12	2719	4600	0.45	0.40	1.16 (1.08-1.25)	8.0E-05	17080	48523	0.43	0.40	1.12 (1.09-1.15)	4.6E-15
-	-	-	-	-	Asian	0.56	4873	17641	0.57	0.56	1.03 (0.98-1.08)	2.9E-01	928	835	0.58	0.56	1.15 (0.99-1.33)	6.9E-02	5801	18476	0.57	0.56	1.04 (0.99-1.09)	1.2E-01
rs947474	10	6,390,450	PRKQ	A/G	Trans-ethnic	-	19234	61564	0.84	0.83	1.11 (1.07-1.15)	1.5E-08	3694	5506	0.84	0.82	1.13 (1.03-1.23)	7.8E-03	22928	67070	0.84	0.83	1.11 (1.07-1.15)	4.1E-10
-	-	-	-	-	European	0.82	14361	43923	0.83	0.81	1.13 (1.08-1.17)	2.8E-09	2766	4671	0.82	0.81	1.10 (1.01-1.21)	3.8E-02	17127	48594	0.83	0.81	1.12 (1.08-1.16)	3.3E-10
-	-	-	-	-	Asian	0.87	4873	17641	0.89	0.88	1.03 (0.95-1.11)	4.4E-01	928	835	0.89	0.88	1.26 (1.00-1.59)	4.9E-02	5801	18476	0.89	0.88	1.05 (0.98-1.13)	1.7E-01
rs3824660	10	8,104,722	GATA3	C/T	Trans-ethnic	-	19234	61564	0.40	0.38	1.08 (1.05-1.11)	5.4E-08	3437	5194	0.40	0.39	1.05 (0.98-1.13)	1.3E-01	22671	66758	0.40	0.38	1.08 (1.05-1.10)	2.0E-08
-	-	-	-	-	European	0.41	14361	43923	0.41	0.39	1.10 (1.07-1.14)	3.6E-09	2509	4359	0.40	0.39	1.05 (0.97-1.14)	1.9E-01	16870	48282	0.41	0.39	1.10 (1.06-1.13)	2.7E-09
-	-	-	-	-	Asian	0.35	4873	17641	0.36	0.35	1.02 (0.97-1.08)	4.3E-01	928	835	0.38	0.38	1.06 (0.91-1.24)	4.4E-01	5801	18476	0.36	0.35	1.03 (0.98-1.08)	3.2E-01
rs12413578	10	9,049,253	10p14	C/T	Trans-ethnic	-	8875	29367	0.91	0.90	1.20 (1.12-1.29)	3.2E-07	1923	1936	0.94	0.93	1.21 (1.00-1.47)	5.5E-02	10798	31303	0.92	0.90	1.20 (1.13-1.29)	4.8E-08
-	-	-	-	-	European	0.90	8875	29367	0.91	0.90	1.20 (1.12-1.29)	3.3E-07	995	1101	0.90	0.88	1.19 (0.97-1.45)	9.0E-02	9870	30468	0.91	0.90	1.20 (1.12-1.29)	7.5E-08
-	-	-	-	-	Asian	0.99	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
rs793108	10	31,415,106	ZNF438	T/C	Trans-ethnic	-	19234	61564	0.51	0.49	1.07 (1.04-1.10)	1.2E-07	3485	5195	0.52	0.49	1.11 (1.04-1.19)	1.6E-03	22719	66759	0.51	0.49	1.08 (1.05-1.10)	1.3E-09
-	-	-	-	-	European	0.48	14361	43923	0.52	0.50	1.07 (1.04-1.10)	8.2E-06	2557	4360	0.55	0.51	1.09 (1.01-1.18)	2.2E-02	16918	48283	0.52	0.50	1.07 (1.04-1.10)	6.1E-07
-	-	-	-	-	Asian	0.41	4873	17641	0.50	0.48	1.07 (1.02-1.13)	3.8E-03	928	835	0.43	0.39	1.22 (1.04-1.42)	1.3E-02	5801	18476	0.49	0.48	1.09 (1.04-1.14)	4.4E-04
rs2671692	10	50,097,819	WDFV4	A/G	Trans-ethnic	-	19234	61564	0.57	0.53	1.08 (1.05-1.11)	8.8E-08	7688	10599	0.47	0.47	1.06 (1.02-1.11)	8.5E-03	26902	72163	0.54	0.52	1.07 (1.05-1.10)	2.8E-09
-	-	-	-	-	European	0.61	14361	43923	0.65	0.63	1.07 (1.03-1.10)	6.6E-05	3775	5801	0.63	0.61	1.05 (0.98-1.12)	1.6E-01	18136	49724	0.65	0.63	1.06 (1.03-1.09)	2.6E-05
-	-	-	-	-	Asian	0.31	4873	17641	0.32	0.29	1.11 (1.05-1.17)	1.4E-04	3893	4798	0.31	0.29	1.08 (1.01-1.15)	2.1E-02	8766	22439	0.31	0.29	1.10 (1.05-1.14)	9.9E-06
rs71508903	10	63,779,871	ARID5B	T/C	Trans-ethnic	-	19234	61564	0.23	0.22	1.17 (1.13-1.21)	2.3E-20	3458	5134	0.21	0.20	1.13 (1.04-1.23)	4.0E-03	22692	66698	0.23	0.22	1.16 (1.13-1.20)	4.7E-22
-	-	-	-	-	European	0.24	14361	43923	0.22	0.21	1.15 (1.11-1.20)	3.8E-13	2530	4299	0.22	0.20	1.15 (1.05-1.26)	2.2E-03	16891	48222	0.22	0.21	1.15 (1.11-1.20)	3.3E-15
-	-	-	-	-	Asian	0.18	4873	17641	0.27	0.24	1.20 (1.13-1.27)	4.0E-09	928	835	0.18	0.18	1.02 (0.82-1.26)	8.7E-01	5801	18476	0.25	0.24	1.18 (1.12-1.25)	1.1E-08
rs6479800	10	64,036,881	RTKN2	C/G	Trans-ethnic	-	13748	47008	0.20	0.18	1.11 (1.06-1.15)	3.6E-07	3382	4927	0.20	0.19	1.10 (1.01-1.20)	3.4E-02	17130	51935	0.20	0.18	1.11 (1.07-1.15)	3.6E-08
-	-	-	-	-	European	0.22	8875	29367	0.24	0.23	1.07 (1.03-1.12)	2.2E-03	2454	4092	0.24	0.22	1.12 (1.02-1.22)	1.6E-02	11329	33459	0.24	0.23	1.08 (1.04-1.13)	1.4E-04
-	-	-	-	-	Asian	0.09	4873	17641	0.12	0.11	1.22 (1.13-1.32)	6.9E-07	928	835	0.08	0.09	0.94 (0.72-1.22)	6.3E-01	5801	18476	0.11	0.10	1.19 (1.11-1.29)	3.6E-06
rs726288	10	81,706,973	SFTPD	T/C	Trans-ethnic	-	13748	47008	0.09	0.09	1.13 (1.06-1.21)	9.3E-05	3676	5477	0.08	0.05	1.16 (0.99-1.36)	6.7E-02	17424	52485	0.09	0.08	1.14 (1.07-1.20)	1.6E-05
-	-	-	-	-	European	0.04	8875	29367	0.03	0.03	0.93 (0.82-1.05)	2.4E-01	2748	4642	0.03	0.03	1.05 (0.84-1.32)	6.4E-01	11623	34009	0.03	0.03	0.96 (0.86-1.06)	4.1E-01
-	-	-	-	-	Asian	0.21	4873	17641	0.21	0.18	1.22 (1.13-1.31)	8.2E-08	928	835	0.23	0.20	1.27 (1.02-1.58)	3.5E-02	5801	18476	0.21	0.18	1.22 (1.14-1.31)	8.8E-09
rs331463	11	36,501,787	TRAF6-RAG1/2	T/A	Trans-ethnic	-	19234	61564	0.88	0.87	1.09 (1.05-1.13)	1.8E-05	3565	5279	0.89	0.86	1.17 (1.06-1.30)	2.3E-03	22799	66843	0.88	0.87	1.10 (1.06-1.14)	3.4E-07
-	-	-	-	-	European	0.87	14361	43923	0.86	0.85	1.11 (1.06-1.15)	5.7E-06	2637	4444	0.87	0.85	1.18 (1.06-1.32)	3.1E-03	16998	48367	0.86	0.85	1.12 (1.07-1.16)	1.1E-07
-	-	-	-	-	Asian	0.93	4873	17641	0.92	0.92	1.02 (0.93-1.12)	6.9E-01	928	835	0.94	0.93	1.14 (0.82-1.58)	4.3E-01	5801	18476	0.93	0.92	1.03 (0.94-1.12)	5.5E-01
rs508970	11	60,906,450	CD5	A/G	Trans-ethnic	-	14361	43923	0.50	0.49	1.07 (1.04-1.11)	4.3E-06	2729	4568	0.48	0.48	1.05 (0.97-1.12)	2.4E-01	17090	48491	0.50	0.49	1.07 (1.04-1	

rs968567	11	61,595,564	FADS1-FADS2-FADS3	C/T	Trans-ethnic	-	14361	43923	0.84	0.82	1.11	(1.06-1.16)	7.3E-07	2680	4543	0.86	0.84	1.16	(1.04-1.28)	5.5E-03	17041	48466	0.84	0.83	1.12	(1.07-1.16)	1.8E-08
-	-	-	-	-	European	0.83	14361	43923	0.84	0.82	1.11	(1.06-1.16)	7.4E-07	2680	4543	0.86	0.84	1.16	(1.04-1.28)	5.5E-03	17041	48466	0.84	0.83	1.12	(1.07-1.16)	1.8E-08
-	-	-	-	-	Asian	1.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
rs11605042	11	72,411,664	ARAP1	G/A	Trans-ethnic	-	13748	47008	0.53	0.51	1.06	(1.03-1.10)	8.2E-05	928	835	0.68	0.66	1.09	(0.93-1.27)	3.1E-01	14676	47843	0.54	0.51	1.06	(1.03-1.10)	4.9E-05
-	-	-	-	-	European	0.56	8875	29367	0.52	0.51	1.05	(1.01-1.09)	1.4E-02	-	-	-	-	-	-	-	-	-	-	-	-	-	
-	-	-	-	-	Asian	0.64	4873	17641	0.54	0.50	1.09	(1.03-1.14)	9.7E-04	928	835	0.68	0.66	1.09	(0.93-1.27)	3.1E-01	14676	47843	0.54	0.51	1.06	(1.03-1.10)	4.9E-05
rs4403785	11	95,311,422	CEP57	C/T	Trans-ethnic	-	19234	61564	0.16	0.15	1.11	(1.07-1.15)	3.0E-08	3708	5535	0.18	0.16	1.21	(1.11-1.32)	1.5E-05	22942	67099	0.16	0.15	1.12	(1.09-1.16)	1.2E-11
-	-	-	-	-	European	0.19	14361	43923	0.19	0.17	1.09	(1.05-1.14)	1.2E-05	2780	4700	0.20	0.17	1.25	(1.14-1.37)	1.7E-06	17141	48623	0.19	0.17	1.12	(1.08-1.16)	3.6E-09
-	-	-	-	-	Asian	0.09	4873	17641	0.09	0.08	1.20	(1.09-1.31)	9.2E-05	928	835	0.10	0.10	0.94	(0.74-1.21)	6.4E-01	5801	18476	0.09	0.08	1.16	(1.07-1.27)	4.3E-04
chr11:107967350	11	107,967,350	ATM	A/G	Trans-ethnic	-	8875	29367	0.93	0.92	1.21	(1.12-1.30)	4.4E-07	3674	5448	0.95	0.94	1.21	(1.05-1.40)	1.0E-02	12549	34815	0.94	0.92	1.21	(1.13-1.29)	1.4E-08
-	-	-	-	-	European	0.91	8875	29367	0.93	0.92	1.21	(1.12-1.30)	4.5E-07	2746	4613	0.94	0.93	1.22	(1.05-1.42)	7.6E-03	11621	33980	0.93	0.92	1.21	(1.13-1.29)	1.1E-08
-	-	-	-	-	Asian	0.99	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
rs10790268	11	118,729,391	CXCR5	G/A	Trans-ethnic	-	19234	61564	0.82	0.81	1.15	(1.11-1.19)	6.2E-14	3635	5404	0.83	0.82	1.13	(1.04-1.24)	5.0E-03	22869	66968	0.82	0.81	1.14	(1.11-1.18)	1.1E-15
-	-	-	-	-	European	0.81	14361	43923	0.81	0.79	1.17	(1.13-1.21)	3.3E-15	2707	4569	0.82	0.81	1.17	(1.07-1.29)	1.1E-03	17068	48492	0.81	0.79	1.17	(1.13-1.22)	1.4E-17
-	-	-	-	-	Asian	0.85	4873	17641	0.85	0.85	1.04	(0.96-1.13)	3.2E-01	928	835	0.84	0.84	0.93	(0.74-1.18)	5.5E-01	5801	18476	0.85	0.85	1.03	(0.96-1.11)	4.5E-01
rs73013527	11	128,496,952	ETS1	C/T	Trans-ethnic	-	18837	61165	0.58	0.57	1.10	(1.07-1.13)	9.8E-11	3647	5433	0.53	0.50	1.04	(0.98-1.12)	2.1E-01	22484	66598	0.57	0.56	1.09	(1.06-1.12)	1.2E-10
-	-	-	-	-	European	0.46	13964	43524	0.52	0.50	1.08	(1.05-1.12)	2.0E-06	2719	4598	0.48	0.46	1.05	(0.98-1.13)	1.7E-01	16683	48122	0.51	0.50	1.08	(1.05-1.11)	1.0E-06
-	-	-	-	-	Asian	0.70	4873	17641	0.74	0.72	1.16	(1.09-1.23)	1.2E-06	928	835	0.70	0.71	1.00	(0.84-1.20)	1.0E-00	5801	18476	0.74	0.72	1.14	(1.08-1.21)	4.1E-06
rs773125	12	56,394,954	CDK2	A/G	Trans-ethnic	-	19234	61564	0.66	0.65	1.09	(1.06-1.12)	4.4E-10	3304	4815	0.69	0.66	1.07	(0.99-1.15)	8.5E-02	22538	66379	0.67	0.65	1.09	(1.06-1.12)	1.1E-03
-	-	-	-	-	European	0.62	14361	43923	0.61	0.59	1.09	(1.06-1.12)	8.5E-08	2376	3980	0.66	0.64	1.07	(0.99-1.16)	9.1E-02	16737	47903	0.62	0.60	1.09	(1.06-1.12)	2.1E-08
-	-	-	-	-	Asian	0.73	4873	17641	0.80	0.79	1.11	(1.04-1.18)	9.8E-04	928	835	0.77	0.76	1.04	(0.87-1.24)	6.5E-01	5801	18476	0.80	0.79	1.10	(1.04-1.17)	1.1E-03
rs1633360	12	58,108,052	CDK4	T/C	Trans-ethnic	-	19234	61564	0.51	0.48	1.07	(1.05-1.10)	1.9E-07	3647	5404	0.54	0.56	1.05	(0.98-1.12)	1.8E-01	22881	68968	0.51	0.49	1.07	(1.04-1.10)	9.8E-08
-	-	-	-	-	European	0.59	14361	43923	0.60	0.58	1.09	(1.05-1.12)	9.1E-08	2719	4569	0.60	0.60	1.05	(0.97-1.13)	2.4E-01	17080	48492	0.60	0.58	1.08	(1.05-1.11)	7.1E-08
-	-	-	-	-	Asian	0.34	4873	17641	0.25	0.24	1.03	(0.97-1.09)	2.9E-01	928	835	0.36	0.34	1.06	(0.90-1.24)	4.9E-01	5801	18476	0.27	0.24	1.03	(0.98-1.09)	2.2E-01
rs10774624	12	111,833,788	SH2B3-PTPN11	G/A	Trans-ethnic	-	14361	43923	0.51	0.49	1.09	(1.06-1.13)	2.3E-07	2271	3841	0.53	0.51	1.12	(1.03-1.21)	7.6E-03	16632	47764	0.51	0.50	1.09	(1.06-1.13)	6.8E-09
-	-	-	-	-	European	0.48	14361	43923	0.51	0.49	1.09	(1.06-1.13)	2.4E-07	2271	3841	0.53	0.51	1.12	(1.03-1.21)	7.6E-03	16632	47764	0.51	0.50	1.09	(1.06-1.13)	6.8E-09
-	-	-	-	-	Asian	0.01	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
rs9603616	13	40,365,069	COG6	C/T	Trans-ethnic	-	19234	61564	0.70	0.69	1.11	(1.07-1.14)	4.6E-12	3646	5417	0.69	0.68	1.07	(0.99-1.14)	8.5E-02	22880	66981	0.70	0.68	1.10	(1.07-1.13)	1.8E-12
-	-	-	-	-	European	0.67	14361	43923	0.68	0.66	1.11	(1.08-1.15)	8.4E-11	2718	4582	0.66	0.66	1.07	(0.99-1.16)	8.6E-02	17079	48505	0.68	0.66	1.11	(1.07-1.14)	2.8E-11
-	-	-	-	-	Asian	0.77	4873	17641	0.76	0.75	1.08	(1.02-1.14)	1.0E-02	928	835	0.78	0.76	1.03	(0.86-1.24)	7.1E-01	5801	18476	0.77	0.75	1.08	(1.02-1.14)	1.0E-02
rs3783782	14	61,940,675	PRKCH	A/G	Trans-ethnic	-	15010	49087	0.09	0.09	1.16	(1.10-1.23)	1.8E-07	8650	10214	0.16	0.12	1.11	(1.04-1.18)	1.5E-03	23660	59301	0.12	0.09	1.14	(1.09-1.18)	2.2E-09
-	-	-	-	-	European	0.01	10137	31446	0.01	0.01	1.07	(0.90-1.27)	4.5E-01	2768	4678	0.01	0.01	1.32	(0.96-1.82)	9.1E-02	12905	36124	0.01	0.01	1.12	(0.96-1.31)	1.4E-01
-	-	-	-	-	Asian	0.26	4873	17641	0.25	0.23	1.17	(1.11-1.25)	9.8E-08	5882	5536	0.23	0.22	1.10	(1.03-1.17)	3.7E-03	10755	23177	0.24	0.22	1.14	(1.09-1.19)	4.4E-09
rs1950897	14	68,760,141	RAD51B	T/C	Trans-ethnic	-	19234	61564	0.77	0.76	1.10	(1.07-1.14)	7.4E-10	3639	5437	0.77	0.73	1.09	(1.01-1.17)	3.5E-02	22873	67001	0.77	0.76	1.10	(1.07-1.13)	8.2E-11
-	-	-	-	-	European	0.67	14361	43923	0.73	0.71	1.09	(1.06-1.13)	2.5E-07	2711	4602	0.73	0.70	1.08	(0.99-1.17)	7.2E-02	17072	48525	0.73	0.71	1.09	(1.06-1.12)	5.0E-08
-	-	-	-	-	Asian	0.89	4873	17641	0.90	0.89	1.16	(1.07-1.26)	2.3E-04	928	835	0.88	0.85	1.14	(0.92-1.42)	2.2E-01	5801	18476	0.89	0.88	1.16	(1.08-1.25)	1.1E-04
rs2582532	14	105,392,837	PLD4-AHNAK2	C/T	Trans-ethnic	-	11082	35486	0.90	0.87	1.14	(1.08-1.17)	2.0E-05	928	835	0.75	0.71	1.39	(1.15-1.68)	5.3E-04	12010	36321	0.89	0.86	1.17	(1.10-1.24)	2.7E-07
-	-	-	-	-	European	0.99	7008	18596	0.99	0.99	0.93	(0.72-1.21)	5.9E-01	-	-	-	-	-	-	-	-	-	-	-	-	-	
-	-	-	-	-	Asian	0.72	4074	16890	0.75	0.73	1.16	(1.09-1.23)	4.4E-06	928	835	0.75	0.71	1.39	(1.15-1.68)	5.3E-04	5002	17725	0.75	0.73	1.18	(1.11-1.25)	4.9E-08
rs8032939	15	38,834,033	RASGRP1	C/T	Trans-ethnic	-	19234	61564	0.36	0.35	1.12	(1.09-1.16)	4.8E-16	3691	5504	0.36	0.30	1.13	(1.05-1.22)	9.3E-04	22925	67068	0.36	0.35	1.13	(1.10-1.16)	1.9E-18
-	-	-	-	-	European	0.25	14361	43923	0.28	0.25	1.13	(1.09-1.17)	2.4E-12	2763	4669	0.27	0.25	1.13	(1.04-1.23)	3.6E-03	17124	48592	0.28	0.25	1.13	(1.09-1.17)	3.2E-14
-	-	-	-	-	Asian	0.58	4873	17641	0.62	0.60	1.11	(1.06-1.17)	3.1E-05	928	835	0.61	0.56	1.14	(0.97-1.33)	1.2E-01	5801	18476	0.62	0.60	1.12	(1.06-1.17)	8.7E-06
rs8268898	15	69,991,417	LOC145837	A/G	Trans-ethnic	-	17997	59477	0.25	0.21	1.16	(1.12-1.19)	6.5E-19	3612	5412	0.23	0.24	1.08	(1.00-1.17)	5.5E-02	21609	64889	0.24	0.21	1.15	(1.11-1.18)	3.6E-19
-	-	-	-	-	European	0.29	14361	43923	0.29	0.27	1.16	(1.12-1.19)	2.4E-17	2684	4577	0.28	0.27	1.09	(1.00-1.18)	3.8E-02	17045	48500	0.29	0.27	1.15	(1.11-1.18)	5.9E-18
-	-	-	-	-	Asian	0.09	3636	15554	0.06	0.05	1.18	(1.05-1.33)	6.8E-03	928	835	0.08	0.09	0.97	(0.74-1.27)	8.2E-01	4564	16399	0.07	0.05	1.14	(1.02-1.27)	1.7E-02
rs4780401	16	11,839,326	TXNDC11	T/G	Trans-ethnic	-	19234	61564	0.57	0.56	1.07	(1.04-1.10)	5.5E-07	3208	4736	0.57	0.56	1.09	(1.01-1.17)	2.3E-02	22442	66300	0.57	0.56	1.07	(1.05-1.10)	4.1E-08
-	-	-	-	-	European	0.60	14361	43923	0.60	0.59	1.09	(1.05-1.12)	5.0E-07	2280	3901	0.62	0.59	1.13	(1.04-1.23)	3.5E-03	16641	47824	0.60	0.59	1.09	(1.06-1.13)	8.7E-09
-	-	-	-	-	Asian	0.44	4873	17641	0.49	0.49	1.04	(0.99-1.09)	1.5E-01	928	835	0.43	0.										

rs72634030	17	5,272,580	C10BP	A/C	Trans-ethnic	-	19234	61564	0.23	0.24	1.12 (1.07-1.16)	7.7E-08	3628	5407	0.21	0.15	1.17 (1.05-1.30)	3.8E-03	22862	68971	0.22	0.23	1.12 (1.08-1.17)	1.5E-09
-	-	-	-	-	European	0.10	14361	43923	0.07	0.07	1.11 (1.05-1.18)	4.7E-04	2700	4572	0.07	0.06	1.21 (1.04-1.40)	1.3E-02	17061	48495	0.07	0.07	1.12 (1.06-1.19)	2.9E-05
-	-	-	-	-	Asian	0.63	4873	17641	0.68	0.66	1.12 (1.06-1.18)	3.5E-05	928	835	0.62	0.60	1.13 (0.97-1.32)	1.2E-01	5801	18476	0.67	0.65	1.12 (1.07-1.18)	9.8E-06
rs1677030	17	37,740,161	MED1	C/T	Trans-ethnic	-	19234	61564	0.85	0.84	1.11 (1.07-1.15)	2.7E-08	10449	11881	0.84	0.83	1.05 (1.00-1.11)	6.4E-02	29683	73445	0.84	0.83	1.09 (1.06-1.12)	1.9E-08
-	-	-	-	-	European	0.84	14361	43923	0.85	0.84	1.10 (1.05-1.15)	1.5E-05	3614	5492	0.85	0.84	1.05 (0.96-1.14)	3.0E-01	17975	49415	0.85	0.84	1.09 (1.05-1.13)	1.3E-05
-	-	-	-	-	Asian	0.78	4873	17641	0.84	0.83	1.13 (1.06-1.21)	2.9E-04	6835	6389	0.83	0.82	1.05 (0.99-1.12)	1.2E-01	11708	24030	0.83	0.83	1.09 (1.04-1.14)	3.2E-04
chr17:38031857	17	38,031,957	#ZF3-CSF3	G/T	Trans-ethnic	-	19234	61564	0.43	0.40	1.10 (1.07-1.13)	1.2E-12	3700	5513	0.40	0.42	1.04 (0.97-1.11)	2.6E-01	22934	67077	0.43	0.40	1.09 (1.07-1.12)	2.3E-12
-	-	-	-	-	European	0.48	14361	43923	0.48	0.46	1.10 (1.06-1.13)	2.0E-09	9772	4678	0.45	0.44	1.07 (0.99-1.14)	8.8E-02	17133	48601	0.47	0.46	1.09 (1.06-1.12)	6.0E-10
-	-	-	-	-	Asian	0.32	4873	17641	0.28	0.26	1.12 (1.06-1.18)	9.5E-05	928	835	0.28	0.28	0.90 (0.76-1.07)	2.4E-01	5801	18476	0.28	0.26	1.09 (1.04-1.15)	7.7E-04
rs8083786	18	12,881,361	PTPN2	G/A	Trans-ethnic	-	19234	61564	0.22	0.21	1.14 (1.10-1.18)	1.0E-15	3664	5462	0.20	0.17	1.15 (1.05-1.25)	1.5E-03	22898	67026	0.22	0.21	1.14 (1.11-1.18)	6.3E-18
-	-	-	-	-	European	0.15	14361	43923	0.17	0.16	1.12 (1.07-1.16)	1.2E-07	2736	4627	0.16	0.15	1.12 (1.02-1.24)	2.4E-02	17097	48550	0.17	0.16	1.12 (1.08-1.16)	8.4E-09
-	-	-	-	-	Asian	0.32	4873	17641	0.38	0.34	1.18 (1.12-1.24)	2.4E-10	928	835	0.32	0.32	1.22 (1.03-1.43)	1.8E-02	5801	18476	0.37	0.34	1.18 (1.13-1.24)	1.5E-11
rs2469434	18	67,544,046	CD226	C/T	Trans-ethnic	-	19234	61564	0.41	0.40	1.06 (1.04-1.09)	5.5E-06	10495	11988	0.40	0.38	1.09 (1.05-1.13)	2.2E-05	29729	73552	0.41	0.40	1.07 (1.05-1.10)	8.9E-10
-	-	-	-	-	European	0.40	14361	43923	0.42	0.41	1.04 (1.01-1.07)	1.2E-02	3661	5603	0.42	0.41	1.09 (1.02-1.16)	9.4E-03	18022	49526	0.42	0.41	1.05 (1.02-1.08)	6.7E-04
-	-	-	-	-	Asian	0.35	4873	17641	0.40	0.37	1.14 (1.08-1.20)	1.8E-06	6834	6385	0.39	0.36	1.09 (1.04-1.15)	7.8E-04	11707	24026	0.39	0.37	1.11 (1.07-1.15)	1.2E-08
rs34536443	19	10,463,118	TYK2	G/C	Trans-ethnic	-	12358	31785	0.97	0.95	1.46 (1.33-1.60)	4.4E-16	-	-	-	-	-	-	-	-	-	-	-	-
-	-	-	-	-	European	0.97	12358	31785	0.97	0.95	1.46 (1.33-1.60)	4.4E-16	-	-	-	-	-	-	-	-	-	-	-	-
-	-	-	-	-	Asian	1.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
chr19:10771941	19	10,771,941	ILF3	C/T	Trans-ethnic	-	12841	33416	0.98	0.97	1.47 (1.30-1.67)	8.5E-10	-	-	-	-	-	-	-	-	-	-	-	-
-	-	-	-	-	European	0.98	12841	33416	0.98	0.97	1.47 (1.30-1.67)	8.7E-10	-	-	-	-	-	-	-	-	-	-	-	-
-	-	-	-	-	Asian	1.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
rs4239702	20	44,749,251	CD40	C/T	Trans-ethnic	-	19234	61564	0.72	0.69	1.12 (1.09-1.15)	9.0E-15	3586	5325	0.72	0.70	1.16 (1.08-1.25)	6.0E-05	22820	66889	0.72	0.69	1.13 (1.10-1.16)	4.0E-18
-	-	-	-	-	European	0.72	14361	43923	0.75	0.72	1.14 (1.10-1.18)	4.2E-14	2658	4490	0.74	0.71	1.16 (1.06-1.26)	6.2E-04	17019	48413	0.75	0.72	1.14 (1.11-1.18)	1.1E-16
-	-	-	-	-	Asian	0.60	4873	17641	0.64	0.62	1.07 (1.02-1.13)	7.2E-03	928	835	0.66	0.64	1.19 (1.01-1.39)	3.5E-02	5801	18476	0.65	0.62	1.08 (1.03-1.14)	1.4E-03
rs73194058	21	34,764,288	IFNGR2	C/A	Trans-ethnic	-	19234	61564	0.78	0.76	1.08 (1.05-1.12)	5.3E-06	3609	5383	0.81	0.83	1.08 (0.99-1.19)	9.3E-02	22843	66947	0.79	0.76	1.08 (1.05-1.12)	1.2E-06
-	-	-	-	-	European	0.85	14361	43923	0.88	0.87	1.14 (1.09-1.19)	7.1E-08	2681	4548	0.89	0.88	1.09 (0.97-1.23)	1.3E-01	17042	48471	0.89	0.87	1.13 (1.08-1.18)	2.6E-08
-	-	-	-	-	Asian	0.58	4873	17641	0.48	0.48	1.02 (0.97-1.08)	3.9E-01	928	835	0.59	0.58	1.06 (0.91-1.24)	4.4E-01	5801	18476	0.50	0.48	1.03 (0.98-1.08)	2.9E-01
chr21:35928240	21	35,928,240	RCAN1	C/T	Trans-ethnic	-	19234	61564	0.91	0.90	1.12 (1.07-1.17)	2.7E-07	3695	5514	0.91	0.89	1.05 (0.94-1.18)	3.5E-01	22929	67078	0.91	0.90	1.11 (1.07-1.16)	3.0E-07
-	-	-	-	-	European	0.86	14361	43923	0.89	0.88	1.13 (1.08-1.19)	2.9E-07	2767	4679	0.88	0.88	1.04 (0.93-1.16)	5.4E-01	17128	48402	0.89	0.88	1.12 (1.07-1.17)	7.1E-07
-	-	-	-	-	Asian	0.96	4873	17641	0.95	0.94	1.06 (0.95-1.19)	2.9E-01	928	835	0.99	0.98	1.76 (0.97-3.21)	6.4E-02	5801	18476	0.96	0.94	1.08 (0.97-1.21)	1.7E-01
rs8133843	21	36,738,242	RUNX1-LOC100506403	A/G	Trans-ethnic	-	19234	61564	0.61	0.59	1.09 (1.06-1.12)	1.3E-09	3428	5086	0.61	0.61	1.03 (0.96-1.11)	4.2E-01	22662	66650	0.61	0.59	1.08 (1.05-1.11)	2.7E-09
-	-	-	-	-	European	0.63	14361	43923	0.64	0.62	1.10 (1.06-1.14)	6.0E-09	2500	4251	0.63	0.62	1.02 (0.95-1.11)	5.6E-01	18681	48174	0.64	0.62	1.09 (1.06-1.12)	2.0E-08
-	-	-	-	-	Asian	0.52	4873	17641	0.52	0.50	1.06 (1.00-1.11)	3.3E-02	928	835	0.54	0.52	1.06 (0.89-1.25)	5.2E-01	5801	18476	0.52	0.50	1.06 (1.01-1.11)	2.6E-02
rs1893592	21	43,855,067	UBASH3A	A/C	Trans-ethnic	-	19234	61564	0.74	0.73	1.11 (1.08-1.15)	3.7E-12	928	835	0.74	0.74	1.00 (0.84-1.20)	9.6E-01	20162	62399	0.74	0.73	1.11 (1.08-1.14)	7.2E-12
-	-	-	-	-	European	0.72	14361	43923	0.73	0.72	1.11 (1.07-1.15)	9.8E-09	-	-	-	-	-	-	-	-	-	-	-	-
-	-	-	-	-	Asian	0.77	4873	17641	0.77	0.75	1.13 (1.06-1.19)	6.1E-05	928	835	0.74	0.74	1.00 (0.84-1.20)	9.6E-01	5801	18476	0.77	0.75	1.11 (1.07-1.15)	9.8E-09
rs2236668	21	45,650,009	ICOSLG-AIRE	C/T	Trans-ethnic	-	18435	60813	0.72	0.70	1.08 (1.05-1.11)	1.3E-07	2535	4278	0.71	0.70	1.00 (0.92-1.09)	9.6E-01	20970	65091	0.72	0.70	1.07 (1.04-1.10)	5.7E-07
-	-	-	-	-	European	0.72	14361	43923	0.73	0.71	1.08 (1.04-1.12)	1.2E-05	2535	4278	0.71	0.70	1.00 (0.92-1.09)	9.6E-01	16896	48201	0.73	0.71	1.07 (1.03-1.10)	4.8E-05
-	-	-	-	-	Asian	0.61	4074	16890	0.68	0.66	1.09 (1.03-1.16)	2.6E-03	-	-	-	-	-	-	-	-	-	-	-	-
rs11089637	22	21,979,096	UBE2L3-YDJC	C/T	Trans-ethnic	-	19234	61564	0.25	0.25	1.08 (1.05-1.12)	1.4E-06	10322	11732	0.37	0.32	1.08 (1.04-1.13)	4.3E-04	29556	73296	0.29	0.26	1.08 (1.05-1.11)	2.1E-09
-	-	-	-	-	European	0.18	14361	43923	0.18	0.16	1.11 (1.07-1.16)	5.6E-07	3480	5361	0.15	0.15	1.07 (0.98-1.18)	1.2E-01	17841	49284	0.17	0.16	1.10 (1.06-1.15)	2.0E-07
-	-	-	-	-	Asian	0.48	4873	17641	0.46	0.46	1.04 (0.99-1.09)	1.4E-01	6842	6371	0.49	0.47	1.08 (1.03-1.14)	1.6E-03	11715	24012	0.48	0.46	1.06 (1.02-1.10)	8.9E-04
rs3218251	22	37,545,505	IL2RB	A/T	Trans-ethnic	-	19234	61564	0.23	0.21	1.07 (1.03-1.10)	5.7E-05	3441	5092	0.22	0.23	1.06 (0.98-1.16)	1.6E-01	22675	66656	0.23	0.21	1.07 (1.04-1.10)	2.1E-05
-	-	-	-	-	European	0.27	14361	43923	0.28	0.27	1.08 (1.04-1.11)	2.0E-05	2513	4257	0.27	0.25	1.07 (0.98-1.17)	1.2E-01	18874	48180	0.28	0.27	1.08 (1.04-1.11)	5.7E-06
-	-	-	-	-	Asian	0.07	4873	17641	0.07	0.07	1.00 (0.91-1.10)	9.7E-01	928	835	0.10	0.10	0.93 (0.66-1.31)	6.8E-01	5801	18476	0.08	0.07	0.99 (0.90-1.09)	8.8E-01
rs098685	22	39,747,671	SYNGR1	A/T	Trans-ethnic	-	19234	61564	0.46	0.46	1.12 (1.09-1.16)	6.3E-14	3503	5270	0.46	0.37	1.14 (1.06-1.23)	5.0E-04	22737	66834	0.46	0.45	1.13 (1.10-1.16)	1.4E-16
-	-	-	-	-	European	0.31	14361	43923	0.32	0.30	1.11 (1.08-1.15)	3.1E-10	2575	4435	0.33	0.29	1.12 (1.03-1.21)	5.8E-03	16936	48358	0.32	0.30	1.11 (1.08-1.15)	6.4E-12
-	-	-	-	-	Asian	0.79	4873	17641	0.87	0.85	1.22 (1.12-1.33)	3.8E-06	928	835	0.82	0.79	1.26 (1.04-1.52)	1.7E-02	5801	18476	0.86	0.85	1.23 (1.14-1.33)	2.0E-07
chrX:78464616	X	78,464,616	P2RY10	A/C	Trans-ethnic	-	6557	22168	0.25	0.30	1.16 (1.09-1.22)	4.2E-07	5879	5508	0.50	0.48	1.08 (1.03-1.15)	3.5E-03	12436	27676	0.37	0.33	1.11 (1.07-1.15)	3.5E-08
-	-	-	-	-	European	0.01	2977	6771	0.01	0.01	1.16 (0.78-1.75)	4.6E-01	-	-	-	-	-	-	-	-	-	-	-	-
-	-	-	-	-	Asian	0.45	5592	15397	0.45	0.42	1.16 (1.09-1.22)	4.4E-07	5879	5508	0.50	0.48	1.08 (1.03-1.15)</							

Association results of 101 RA risk loci in the Stage 1 GWAS meta-analysis, the Stage 2 and 3 replication studies, and the combined analysis of the Stages 1-3 are indicated for the trans-ethnic (Europeans and Asians), European, and Asian populations, separately. SNP IDs, positions, and alleles are based on positive strand of NCBI build 37. A1 represent risk allele of RA. For known RA risk loci, representative studies reporting the associations of the loci are indicated as references.

Chr., chromosome; freq., frequency in the reference panel; OR, odds ratio; 95%CI, 95% confidence interval; GWAS, genome-wide association study; Ref., references.

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Supplementary Table 2. A list of primary immunodeficiency (PID) genes

Human primary immunodeficiency (PID) genes						
ACTB	CARD9	CXCR4	IKBKG	MASP1	PTPRC	TAZ
ADA	CASP10	CYBA	IKZF1	MASP2	RAB27A	TBK1
ADAM17	CASP8	CYBB	IL10	MCM4	RAC2	TBX1
AICDA	CD19	DCLRE1C	IL10RA	MEFV	RAG1/RAG2	TERC
AIRE	CD247	DKC1	IL10RB	MRE11A	RFX5	TERT
AK2	CD27	DNMT3B	IL12B	MS4A1	RFXANK	TICAM1
AP3B1	CD3D	DOCK8	IL12RB1	MVK	RFXAP	TINF2
APOL1	CD3E	ECI2	IL17F	MYD88	RHOH	TLR3
ATM	CD3G	ELANE	IL17RA	NBN	RMRP	TMC6
BLM	CD40	FADD	IL1RN	NCF1	RNF168	TMC8
BLNK	CD40LG	FAS	IL2RA	NCF2	SBDS	TNFRSF13B
BLOC1S6	CD46	FASLG	IL2RG	NCF4	SERPING1	TNFRSF13C
BTK	CD59	FCN3	IL36RN	NFKBIA	SH2D1A	TNFRSF1A
C1QA	CD79A	FERMT3	IL7R	NHEJ1	SLC35C1	TRA@
C1QB	CD79B	FOXP3	IRAK4	NKX2-5	SLC37A4	TRAF3
C1QC	CD81	FOXP3	IRF8	NLRP3	SMARCAL1	TYK2
C1R	CD8A	FPR1	ISG15	NOD2	SP110	UNC119
C1S	CEBPE	G6PC3	ITCH	NOP10	SPINK5	UNC13D
C2	CFD	GATA2	ITGB2	NRAS	STAT1	UNG
C3	CFH	GFI1	ITK	ORAI1	STAT3	USB1
C4A	CFI	HAX1	JAK3	PIGA	STAT5B	VPS13B
C4B	CFP	ICOS	LAMTOR2	PIK3R1	STIM1	WAS
C5	CIITA	IFNGR1	LCK	PLCG2	STK4	WIPF1
C6	COLEC11	IFNGR2	LIG4	PMS2	STX11	XIAP
C7	CORO1A	IGHG1	LPIN2	PNP	STXBP2	ZAP70
C8A	CR2	IGHM	LRBA	PRF1	TAP1	ZBTB24
C8B	CSF2RA	IGKC	LYST	PRKDC	TAP2	
C9	CTSC	IGLL1	MAGT1	PSTPIP1	TAPBP	

Supplementary Table 3. A list of cancer somatic mutation genes

Cancer somatic mutation genes											
ABI1	BIRC3	CDX2	EIF4A2	FNBP1	HOXD11	LCK	MPL	NUP214	PRRX1	SMARCB1	TLX1
ABL1	BRAF	CEBPA	ELF4	FOXO2	HOXD13	LCP1	MSH2	NUP98	PSIP1	SMO	TLX3
ABL2	BRCA1	CHCHD7	ELK4	FOXO1	HRAS	LHFP	MSH6	OLIG2	PTCH1	SNX29	TMPRSS2
ACSL3	BRCA2	CHIC2	ELL	FOXO3	HSP90AA1	LIFR	MSI2	OMD	PTEN	SOCS1	TNFAIP3
ACSL6	BRD3	CHN1	ELN	FOXO4	HSP90AB1	LMO1	MSN	P2RY8	PTPN11	SOX2	TNFRSF14
AFF1	BRD4	CIC	EML4	FOXP1	IDH1	LMO2	MTCP1	PAFAH1B2	RABEP1	SPECC1	TNFRSF17
AFF3	BTG1	CIITA	EP300	FSTL3	IDH2	LPP	MUC1	PATZ1	RAD51B	SRGAP3	TOP1
AFF4	C12orf9	CLP1	EPS15	FUBP1	IGH@	LRIG3	MYB	PAX3	RAF1	SRSF2	TP53
AKAP9	C15orf55	CLTC	ERBB2	FUS	IGK@	LYL1	MYC	PAX5	RALGDS	SRSF3	TPM3
AKT1	C2orf44	CLTCL1	ERC1	GAS7	IGL@	MAF	MYCL1	PAX7	RANBP17	SS18	TPM4
AKT2	CAMTA1	CNBP	ERG	GATA1	IKZF1	MAFB	MYCN	PAX8	RAP1GDS1	SS18L1	TPR
ALDH2	CANT1	CNTRL	ETV1	GATA2	IL2	MALAT1	MYD88	PBRM1	RARA	SSX1	TRA@
ALK	CARD11	COL1A1	ETV4	GATA3	IL21R	MALT1	MYH11	PBX1	RB1	SSX2	TRB@
APC	CARS	COX6C	ETV5	GMPS	IL6ST	MAML2	MYH9	PCM1	RBM15	SSX4	TRD@
ARHGAP26	CASC5	CREB1	ETV6	GNA11	IL7R	MAP2K4	NACA	PCSK7	REL	STIL	TRIM24
ARHGEF12	CBFA2T3	CREB3L1	EWSR1	GNAQ	IRF4	MDM2	NCKIPSD	PDCD1LG2	RET	STK11	TRIM27
ARID1A	CBFB	CREB3L2	EZH2	GNAS	ITK	MDM4	NCOA1	PDE4DIP	RHOH	STL	TRIM33
ARID2	CBL	CREBBP	EZR	GOLGA5	JAK1	MDS2	NCOA2	PDGFB	RM12	SUFU	TRIP11
ARNT	CBLB	CRLF2	FAM123B	GOPC	JAK2	MECOM	NCOA4	PDGFRA	RNF213	SUZ12	TSHR
ASPCR1	CBLC	CRTC1	FAM22A	GPHN	JAK3	MED12	NDRG1	PDGFRB	ROS1	SYK	TTL
ASXL1	CCDC6	CRTC3	FAM22B	H3F3A	JAZF1	MEN1	NF1	PER1	RPL22	TAF15	U2AF1
ATF1	CCNB1IP1	CTNNB1	FAM46C	HERPUD1	JUN	MET	NF2	PHF6	RPN1	TAL1	USP6
ATIC	CCND1	CXCR7	FAS	HEY1	KAT6A	MITF	NFE2L2	PHOX2B	RUNX1	TAL2	VHL
ATM	CCND2	CYLD	FBXO11	HIP1	KAT6B	MKL1	NFIB	PICALM	RUNX1T1	TCEA1	VTI1A
ATRX	CCND3	DAXX	FBXW7	HIST1H4I	KDM5A	MLF1	NFKB2	PIK3CA	SDC4	TCF12	WHSC1
BAP1	CCNE1	DDIT3	FCGR2B	HLF	KDM5C	MLH1	NIN	PIK3R1	SEPT5	TCF3	WHSC1L1
BCL10	CD274	DDX10	FCRL4	HMGA1	KDM6A	MLL	NKX2-1	PIM1	SEPT6	TCF7L2	WIF1
BCL11A	CD74	DDX5	FEV	HMGA2	KDR	MLL2	NONO	PLAG1	SEPT9	TCL1A	WT1
BCL11B	CD79A	DDX6	FGFR1	HMG2P46	KDSR	MLL3	NOTCH1	PML	SET	TCL6	WWTR1
BCL2	CD79B	DEK	FGFR1OP	HNF1A	KIAA1549	MLLT1	NOTCH2	POU2AF1	SETD2	TET1	XPO1
BCL3	CDC73	DICER1	FGFR2	HNRNPA2B1	KIF5B	MLLT10	NPM1	POU5F1	SF3B1	TET2	YWHAE
BCL5	CDH1	DNM2	FGFR3	HOOK3	KIT	MLLT11	NR4A3	PPARG	SFPQ	TFE3	ZBTB16
BCL6	CDH11	DNMT3A	FHIT	HOXA11	KLF6	MLLT3	NRAS	PPP2R1A	SH3GL1	TFEB	ZMYM2
BCL7A	CDK12	DUX4	FIP1L1	HOXA13	KLK2	MLLT4	NSD1	PRCC	SLC34A2	TFG	ZNF331
BCL9	CDK6	EBF1	FLI1	HOXA9	KRAS	MLLT6	NTRK1	PRDM1	SLC45A3	TFPT	ZNF384
BCOR	CDKN2A	ECT2L	FLJ27352	HOXC11	KTN1	MN1	NTRK3	PRDM16	SMAD4	TFRC	ZNF521
BCR	CDKN2C	EGFR	FLT3	HOXC13	LASP1	MNX1	NUMA1	PRKAR1A	SMARCA4	THRAP3	ZRSR2

Hematological cancer somatic mutation genes

ABI1	BCL7A	CDK6	ELN	FOXP1	IGK@	LMO1	MSI2	OLIG2	RABEP1	SOCS1	TNFRSF14
ABL1	BCL9	CDKN2C	EP300	FSTL3	IGL@	LMO2	MSN	P2RY8	RALGDS	SPECC1	TNFRSF17
ABL2	BCOR	CDX2	EPS15	FUS	IKZF1	LPP	MTCP1	PAFAH1B2	RANBP17	SRSF2	TOP1
ACSL6	BCR	CEBPA	ERG	GAS7	IL2	LYL1	MUC1	PAX5	RAP1GDS1	SRSF3	TPM3
AFF1	BIRC3	CHIC2	ETV6	GATA1	IL21R	MAF	MYC	PBX1	RARA	STIL	TPM4
AFF3	BTG1	CIITA	EWSR1	GATA2	IL7R	MAFB	MYD88	PCM1	RBM15	STL	TRA@
AFF4	CARD11	CLP1	EZH2	GMPS	IRF4	MALT1	MYH11	PCSK7	REL	SYK	TRB@
ALK	CARS	CLTC	FAM46C	GPHN	ITK	MDS2	MYH9	PDCD1LG2	RHOH	TAF15	TRD@
ARHGAP26	CASC5	CLTCL1	FAS	HIP1	JAK1	MECOM	NACA	PDE4DIP	RM12	TAL1	TRIM24
ARHGEF12	CBFA2T3	CNTRL	FBXO11	HIST1H4I	JAK2	MKL1	NCKIPSD	PDGFRB	RNF213	TAL2	TRIP11
ARNT	CBFB	CREBBP	FBXW7	HLF	JAK3	MLF1	NCOA2	PER1	RPL22	TCF3	TTL
ASXL1	CBL	CRLF2	FCGR2B	HOXA11	KAT6A	MLL	NFKB2	PHF6	RPN1	TCL1A	U2AF1
ATIC	CBLB	DDX10	FCRL4	HOXA13	KAT6B	MLLT1	NIN	PICALM	RUNX1	TCL6	WHSC1
ATM	CBLC	DDX6	FGFR1	HOXA9	KDM5A	MLLT10	NOTCH1	PIM1	RUNX1T1	TET1	WHSC1L1
BCL10	CCDC6	DEK	FGFR1OP	HOXC11	KDM6A	MLLT11	NOTCH2	PML	SEPT5	TET2	XPO1
BCL11A	CCND1	DNM2	FGFR3	HOXC13	KDSR	MLLT3	NPM1	POU2AF1	SEPT6	TFG	ZBTB16
BCL11B	CCND2	DNMT3A	FLJ27352	HOXD11	KIT	MLLT4	NRAS	PRDM1	SEPT9	TFPT	ZMYM2
BCL2	CCND3	ECT2L	FLT3	HOXD13	KRAS	MLLT6	NSD1	PRDM16	SET	TFRC	ZNF384
BCL3	CD274	EIF4A2	FNBP1	HSP90AA1	LASP1	MN1	NUMA1	PRRX1	SF3B1	TLX1	ZNF521
BCL5	CD79A	ELF4	FOXO3	HSP90AB1	LCK	MNX1	NUP214	PSIP1	SH3GL1	TLX3	ZRSR2
BCL6	CD79B	ELL	FOXO4	IGH@	LCP1	MPL	NUP98	PTPN11	SNX29	TNFAIP3	

Non-hematological cancer somatic mutation genes

CAMTA1	BRD4	CLTC	ELK4	FGFR3	HMG2P46	KTN1	MSH2	NTRK3	PRKAR1A	SS18	TPR
ACSL3	C12orf9	CNBP	EML4	FHIT	HNF1A	LHFP	MSH6	OMD	PTCH1	SS18L1	TRIM27
AKAP9	C15orf55	COL1A1	EP300	FIP1L1	HNRNPA2B1	LIFR	MYB	PATZ1	PTEN	SSX1	TRIM33
AKT1	C2orf44	COX6C	ERBB2	FLI1	HOOK3	LMO1	MYC	PAX3	RAD51B	SSX2	TSHR
AKT2	CANT1	CREB1	ERC1	FOXL2	HRAS	LPP	MYCL1	PAX7	RAF1	SSX4	USP6
ALDH2	CCDC6	CREB3L1	ERG	FOXO1	IDH1	LRIG3	MYCN	PAX8	RB1	STK11	VHL
ALK	CCNB1IP1	CREB3L2	ETV1	FUBP1	IDH2	MALAT1	NCOA1	PBRM1	RET	SUFU	VT1A
APC	CCND1	CRTC1	ETV4	FUS	IL6ST	MAML2	NCOA2	PBX1	ROS1	SUZ12	WIF1
ARID1A	CCNE1	CRTC3	ETV5	GATA3	JAZF1	MAP2K4	NCOA4	PCM1	SDC4	TAF15	WT1
ARID2	CD74	CTNNB1	ETV6	GNA11	JUN	MDM2	NDRG1	PDGFB	SETD2	TCEA1	WWTR1
ASPSCR1	CDC73	CXCR7	EWSR1	GNAQ	KDM5C	MDM4	NF1	PDGFRA	SFPQ	TCF12	YWHAE
ATF1	CDH1	CYLD	EZR	GNAS	KDM6A	MED12	NF2	PHOX2B	SLC34A2	TCF7L2	ZNF331
ATRX	CDH11	DAXX	FAM123B	GOLGA5	KDR	MEN1	NFE2L2	PIK3CA	SLC45A3	TFE3	
BAP1	CDK12	DDIT3	FAM22A	GOPC	KIAA1549	MET	NFIB	PIK3R1	SMAD4	TFEB	
BCOR	CDKN2A	DDX5	FAM22B	H3F3A	KIF5B	MITF	NKX2-1	PLAG1	SMARCA4	TFG	
BRAF	CDKN2C	DICER1	FAS	HERPUD1	KIT	MLH1	NONO	POU5F1	SMARCB1	THRAP3	
BRCA1	CHCHD7	DUX4	FBXW7	HEY1	KLF6	MLL2	NR4A3	PPARG	SMO	TMPRSS2	
BRCA2	CHN1	EBF1	FEV	HMGA1	KLK2	MLL3	NRAS	PPP2R1A	SOX2	TP53	
BRD3	CIC	EGFR	FGFR2	HMGA2	KRAS	MN1	NTRK1	PRCC	SRGAP3	TPM3	

Supplementary Table 4. A list of knockout mouse genes and phenotypes

(Microsoft Excel source file is available at www.nature.com/nature)

Supplementary Table 5. Biological scores of the genes in the RA risk loci

RA risk SNP (cytoband)	Gene	Score	Biological gene criteria								Nearest gene from RA risk SNP	Overlap with H3K4me3 peaks								Drug target gene	RA drug target gene	PPI with RA drug target gene																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						
			RA risk missense variant	Cis- eQTL	PubMed text-mining	Protein-protein interaction	Primary immunodeficiency	Hematological cancer	Knockout mouse phenotype	Molecular pathway		Treg primary cells	CD4+ memory primary cells	CD4+ naïve primary cells	CD8+ memory primary cells	CD8+ naïve primary cells	CD34+ primary cells	CD34+ cultured cells	Mobilized CD34+ primary cells				CD19+ primary cells	CD3+ primary cells																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
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RA risk SNP (cytoband)	Gene	Score	Biological gene criteria							Nearest gene from RA risk SNP	Overlap with H3K4me3 peaks								Drug target gene	RA drug target gene	PPI with RA drug target gene						
			RA risk missense variant	Cis- eQTL	PubMed text-mining	Protein-protein interaction	Primary immunodeficiency	Hematological cancer	Knockout mouse phenotype		Molecular pathway	Treg primary cells	CD4+ memory primary cells	CD4+ naive primary cells	CD8+ memory primary cells	CD8+ naive primary cells	CD34+ primary cells	CD34+ cultured cells				Mobilized CD34+ primary cells	CD19+ primary cells	CD3+ primary cells			
rs72717009 (1q23)	FCGR2A	3																									
rs72717009 (1q23)	HSPA6	2																									
rs72717009 (1q23)	FCGR3A	1																									
rs72717009 (1q23)	FCGR2C	1																									
chr1:161644258 (1q23)	HSPA7	0																									
chr1:161644258 (1q23)	FCGR3B	1																									
chr1:161644258 (1q23)	FCGR2B	5																									
chr1:161644258 (1q23)	RPL31P11	0																									
chr1:161644258 (1q23)	FCRLA	2																									
chr1:161644258 (1q23)	FCRLB	1																									
chr1:161644258 (1q23)	DUSP12	0																									
chr1:161644258 (1q23)	ATF6	0																									
rs2105325 (1q25)	LOC100506023	0																									
rs17668708 (1q31)	PTPRC	6																									
rs10175798 (2p23)	LBH	0																									
rs34695944 (2p16-p15)	FLJ16341	0																									
rs34695944 (2p16-p15)	REL	4																									
rs34695944 (2p16-p15)	PUS10	0																									
rs34695944 (2p16-p15)	PEX13	0																									
rs34695944 (2p16-p15)	KIAA1841	0																									
rs34695944 (2p16-p15)	LOC339803	0																									
rs34695944 (2p16-p15)	C2orf74	0																									
rs34695944 (2p16-p15)	AHSA2	1																									
rs34695944 (2p16-p15)	USP34	0																									
rs34695944 (2p16-p15)	SNORA70B	0																									
rs34695944 (2p16-p15)	XPO1	2																									
rs13385025 (2p15)	MIR5192	0																									
rs13385025 (2p15)	B3GNT2	1																									
rs1858037 (2p14)	SPRED2	0																									
rs9653442 (2q11)	AFF3	4																									
rs9653442 (2q11)	LONRF2	0																									
rs6732565 (2q13)	ACOXL	0																									
rs11889341 (2q32)	STAT4	3																									
rs6715284 (2q33)	CFLAR	3																									
rs6715284 (2q33)	CFLAR-AS1	0																									
rs6715284 (2q33)	CASP10	2																									
rs6715284 (2q33)	CASP8	2																									
rs6715284 (2q33)	ALS2CR12	1																									
rs6715284 (2q33)	TRAK2	0																									
rs6715284 (2q33)	STRADB	0																									
rs6715284 (2q33)	ALS2CR11	0																									
rs1980422 (2q33)	CD28	4																									
rs3087243 (2q33)	CTLA4	4																									
rs4452313 (3p24)	PLCL2	1																									
rs4452313 (3p24)	MIR3714	0																									
rs3806624 (3p24)	EOMES	1																									
rs73081554 (3p14)	FLNB	0																									
rs73081554 (3p14)	DNASE1L3	1																									
rs73081554 (3p14)	ABHD6	1																									
rs73081554 (3p14)	RPP14	0																									
rs73081554 (3p14)	PXK	1																									
rs73081554 (3p14)	PDHB	0																									
rs73081554 (3p14)	KCTD6	0																									
rs9826828 (3q22)	PCCB	0																									
rs9826828 (3q22)	STAG1	1																									

RA risk SNP (cytoband)	Gene	Score	Biological gene criteria							Overlap with H3K4me3 peaks										Drug target gene	RA drug target gene	PPI with RA drug target gene					
			RA risk missense variant	Cis- eQTL	PubMed text-mining	Protein-protein interaction	Primary immunodeficiency	Hematological cancer	Knockout mouse phenotype	Molecular pathway	Nearest gene from RA risk SNP	Treg primary cells	CD4+ memory primary cells	CD4+ naive primary cells	CD8+ memory primary cells	CD8+ naive primary cells	CD34+ primary cells	CD34+ cultured cells	Mobilized CD34+ primary cells				CD19+ primary cells	CD3+ primary cells			
rs9826828 (3q22)	SLC35G2	0																									
rs9826828 (3q22)	NCK1	1																									
rs9826828 (3q22)	IL20RB	3																									
rs13142500 (4p16)	CLNK	1																									
rs11933540 (4p15)	C4orf52	0																									
rs2664035 (4p12-p11)	TEC	2																									
rs10028001 (4q21)	ANXA3	1																									
rs10028001 (4q21)	LOC100505702	0																									
rs45475795 (4q26-q27)	KIAA1109	0																									
rs45475795 (4q26-q27)	ADAD1	1																									
rs45475795 (4q26-q27)	IL2	5																									
rs45475795 (4q26-q27)	IL21	3																									
rs7731626 (5q11)	ANKRD55	2																									
rs2561477 (5q21)	C5orf30	0																									
rs657075 (5q31)	CDC42SE2	0																									
rs657075 (5q31)	RAPGEF6	1																									
rs657075 (5q31)	FNIP1	1																									
rs657075 (5q31)	ACSL6	2																									
rs657075 (5q31)	IL3	4																									
rs657075 (5q31)	CSF2	4																									
rs657075 (5q31)	P4HA2	0																									
rs657075 (5q31)	PDLIM4	0																									
rs657075 (5q31)	SLC22A4	1																									
rs657075 (5q31)	MIR3936	0																									
rs657075 (5q31)	LOC553103	0																									
rs657075 (5q31)	SLC22A5	0																									
rs657075 (5q31)	C5orf56	0																									
rs9378815 (6p25)	IRF4	3																									
chr6:14103212 (6p23)	CD83	3																									
rs2234067 (6p21)	ETV7	1																									
rs2234067 (6p21)	PXT1	0																									
rs2233424 (6p21)	HSP90AB1	2																									
rs2233424 (6p21)	MIR4647	0																									
rs2233424 (6p21)	SLC35B2	0																									
rs2233424 (6p21)	NFKBIE	4																									
rs2233424 (6p21)	TMEM151B	0																									
rs2233424 (6p21)	TCTE1	2																									
rs2233424 (6p21)	AARS2	1																									
rs9372120 (6q21)	ATG5	1																									
rs17264332 (6q23)	LOC100130476	0																									
rs7752903 (6q23)	TNFAIP3	6																									
rs9373594 (6q25)	PPIL4	0																									
rs9373594 (6q25)	GINM1	0																									
rs2451258 (6q25)	TAGAP	2																									
rs1571878 (6q27)	FGFR1OP	1																									
rs1571878 (6q27)	CCR6	2																									
rs67250450 (7p15)	JAZF1	1																									
rs67250450 (7p15)	JAZF1-AS1	0																									
rs4272 (7q21)	FAM133B	0																									
rs4272 (7q21)	FAM133DP	0																									
rs4272 (7q21)	CDK6	4																									
chr7:128580042 (7q32)	IRF5	4																									
chr7:128580042 (7q32)	TNPO3	1																									
rs2736337 (8p23)	FAM167A	0																									
rs2736337 (8p23)	BLK	3																									

RA risk SNP (cytoband)	Gene	Score	Biological gene criteria							Overlap with H3K4me3 peaks										Drug target gene	RA drug target gene	PPI with RA drug target gene					
			RA risk missense variant	Cis- eQTL	PubMed text-mining	Protein-protein interaction	Primary immunodeficiency	Hematological cancer	Knockout mouse phenotype	Molecular pathway	Nearest gene from RA risk SNP	Treg primary cells	CD4+ memory primary cells	CD4+ naïve primary cells	CD8+ memory primary cells	CD8+ naïve primary cells	CD34+ primary cells	CD34+ cultured cells	Mobilized CD34+ primary cells				CD19+ primary cells	CD3+ primary cells			
rs998731 (8q21)	TPD52	0																									
rs678347 (8q22)	GRHL2	0																									
rs1516971 (8q24)	MIR1208	0																									
rs11574914 (9p13)	CCL19	2																									
rs11574914 (9p13)	CCL21	2																									
rs11574914 (9p13)	FAM205A	0																									
rs10985070 (9q33)	LOC253039	0																									
rs10985070 (9q33)	PHF19	1																									
rs10985070 (9q33)	TRAF1	4																									
rs10985070 (9q33)	C5	4																									
rs706778 (10p15)	IL2RA	5																									
rs947474 (10p15)	LOC399715	0																									
rs3824660 (10p14)	GATA3-AS1	0																									
rs3824660 (10p14)	GATA3	2																									
rs793108 (10p11)	ZNF438	0																									
rs2671692 (10q11)	WDFY4	2																									
rs2671692 (10q11)	LRRC18	0																									
rs71508903 (10q21)	ARID5B	2																									
rs6479800 (10q21)	RTKN2	1																									
rs726288 (10q22)	MBL1P	1																									
rs726288 (10q22)	LOC100288974	0																									
rs726288 (10q22)	SFTPD	2																									
rs331463 (11p12)	PRR5L	0																									
rs331463 (11p12)	TRAF6	4																									
rs331463 (11p12)	RAG1	4																									
rs331463 (11p12)	RAG2	3																									
rs331463 (11p12)	C11orf74	0																									
rs508970 (11q12)	CD5	4																									
rs508970 (11q12)	VPS37C	0																									
rs968567 (11q12)	MYRF	0																									
rs968567 (11q12)	TMEM258	0																									
rs968567 (11q12)	MIR611	0																									
rs968567 (11q12)	FEN1	1																									
rs968567 (11q12)	FADS1	3																									
rs968567 (11q12)	MIR1908	0																									
rs968567 (11q12)	FADS2	3																									
rs11605042 (11q13)	ARAP1	0																									
rs4409785 (11q21)	FAM76B	0																									
chr11:107967350 (11q22)	CUL5	1																									
chr11:107967350 (11q22)	ACAT1	0																									
chr11:107967350 (11q22)	NPAT	0																									
chr11:107967350 (11q22)	ATM	4																									
chr11:107967350 (11q22)	C11orf65	1																									
chr11:107967350 (11q22)	KDELC2	0																									
rs10790268 (11q23)	DDX6	1																									
rs10790268 (11q23)	CXCR5	2																									
rs73013527 (11q24)	ETS1	2																									
rs773125 (12q13)	CDK2	3																									
rs773125 (12q13)	RAB5B	0																									
rs773125 (12q13)	SUOX	2																									
rs773125 (12q13)	IKZF4	0																									
rs773125 (12q13)	RPS26	1																									
rs773125 (12q13)	ERBB3	2																									
rs1633360 (12q13-q14)	ARHGEF25	0																									
rs1633360 (12q13-q14)	SLC26A10	0																									

RA risk SNP (cytoband)	Gene	Score	Biological gene criteria							Overlap with H3K4me3 peaks										Drug target gene RA drug target gene PPI with RA drug target gene	
			RA risk missense variant	Cis- eQTL	PubMed text-mining	Protein-protein interaction	Primary immunodeficiency	Hematological cancer	Knockout mouse phenotype	Molecular pathway	Nearest gene from RA risk SNP	Treg primary cells	CD4+ memory primary cells	CD4+ naive primary cells	CD8+ memory primary cells	CD8+ naive primary cells	CD34+ primary cells	CD34+ cultured cells	Mobilized CD34+ primary cells		CD19+ primary cells
rs1633360 (12q13-q14)	B4GALNT1	1																			
rs1633360 (12q13-q14)	OS9	0																			
rs1633360 (12q13-q14)	AGAP2	0																			
rs1633360 (12q13-q14)	LOC100130776	0																			
rs1633360 (12q13-q14)	TSPAN31	1																			
rs1633360 (12q13-q14)	CDK4	3																			
rs1633360 (12q13-q14)	MARCH9	0																			
rs1633360 (12q13-q14)	CYP27B1	2																			
rs1633360 (12q13-q14)	METTL1	0																			
rs1633360 (12q13-q14)	METTL21B	1																			
rs1633360 (12q13-q14)	TSMF	0																			
rs1633360 (12q13-q14)	AVIL	0																			
rs10774624 (12q24)	CORO1C	0																			
rs10774624 (12q24)	SSH1	0																			
rs10774624 (12q24)	DAO	0																			
rs10774624 (12q24)	SVOP	0																			
rs10774624 (12q24)	USP30	0																			
rs10774624 (12q24)	USP30-AS1	0																			
rs10774624 (12q24)	ALKBH2	0																			
rs10774624 (12q24)	UNG	2																			
rs10774624 (12q24)	ACACB	0																			
rs10774624 (12q24)	FOXN4	0																			
rs10774624 (12q24)	MYO1H	0																			
rs10774624 (12q24)	KCTD10	0																			
rs10774624 (12q24)	UBE3B	0																			
rs10774624 (12q24)	MMAB	0																			
rs10774624 (12q24)	MVK	2																			
rs10774624 (12q24)	FAM222A	0																			
rs10774624 (12q24)	FAM222A-AS1	0																			
rs10774624 (12q24)	TRPV4	1																			
rs10774624 (12q24)	MIR4497	0																			
rs10774624 (12q24)	GLTP	0																			
rs10774624 (12q24)	TCHP	0																			
rs10774624 (12q24)	GIT2	1																			
rs10774624 (12q24)	ANKRD13A	0																			
rs10774624 (12q24)	C12orf76	0																			
rs10774624 (12q24)	IFT81	0																			
rs10774624 (12q24)	ATP2A2	0																			
rs10774624 (12q24)	ANAPC7	0																			
rs10774624 (12q24)	ARPC3	0																			
rs10774624 (12q24)	GPN3	1																			
rs10774624 (12q24)	FAM216A	0																			
rs10774624 (12q24)	VPS29	0																			
rs10774624 (12q24)	RAD9B	0																			
rs10774624 (12q24)	PPTC7	0																			
rs10774624 (12q24)	TCTN1	0																			
rs10774624 (12q24)	HVCN1	0																			
rs10774624 (12q24)	PPP1CC	0																			
rs10774624 (12q24)	CCDC63	1																			
rs10774624 (12q24)	MYL2	0																			
rs10774624 (12q24)	LOC100131138	0																			
rs10774624 (12q24)	CUX2	1																			
rs10774624 (12q24)	FAM109A	0																			
rs10774624 (12q24)	SH2B3	5																			
rs10774624 (12q24)	ATXN2	0																			

RA risk SNP (cytoband)	Gene	Score	Biological gene criteria							Overlap with H3K4me3 peaks							Drug target gene	RA drug target gene	PPI with RA drug target gene								
			RA risk missense variant	Cis- eQTL	PubMed text-mining	Protein-protein interaction	Primary immunodeficiency	Hematological cancer	Knockout mouse phenotype	Molecular pathway	Nearest gene from RA risk SNP	Treg primary cells	CD4+ memory primary cells	CD4+ naive primary cells	CD8+ memory primary cells	CD8+ naive primary cells				CD34+ primary cells	CD34+ cultured cells	Mobilized CD34+ primary cells	CD19+ primary cells	CD3+ primary cells			
rs10774624 (12q24)	BRAP	0																									
rs10774624 (12q24)	ACAD10	0																									
rs10774624 (12q24)	ALDH2	1																									
rs10774624 (12q24)	MAPKAPK5	1																									
rs10774624 (12q24)	MAPKAPK5-AS1	0																									
rs10774624 (12q24)	ADAM1A	0																									
rs10774624 (12q24)	TMEM116	0																									
rs10774624 (12q24)	ERP29	0																									
rs10774624 (12q24)	NAA25	0																									
rs10774624 (12q24)	TRAFD1	2																									
rs10774624 (12q24)	HECTD4	0																									
rs10774624 (12q24)	RPL6	1																									
rs10774624 (12q24)	PTPN11	3																									
rs9603616 (13q14)	COG6	1																									
rs9603616 (13q14)	MIR4305	0																									
rs3783782 (14q23)	PRKCH	2																									
rs1950897 (14q24)	RAD51B	0																									
rs2582532 (14q32)	PLD4	1																									
rs2582532 (14q32)	AHNAK2	1																									
rs8032939 (15q14)	RASGRP1	2																									
rs8026898 (15q23)	LOC145837	0																									
rs4780401 (16p13)	SNN	0																									
rs4780401 (16p13)	TXNDC11	1																									
rs4780401 (16p13)	ZC3H7A	0																									
rs13330176 (16q24)	IRF8	3																									
rs72634030 (17p13)	ZNF232	0																									
rs72634030 (17p13)	USP6	0																									
rs72634030 (17p13)	ZNF594	2																									
rs72634030 (17p13)	SCIMP	0																									
rs72634030 (17p13)	LOC100130950	0																									
rs72634030 (17p13)	RABEP1	1																									
rs72634030 (17p13)	NUP88	1																									
rs72634030 (17p13)	C1QBP	2																									
rs72634030 (17p13)	RPAIN	0																									
rs72634030 (17p13)	DHX33	0																									
rs1877030 (17q12)	FBXL20	2																									
rs1877030 (17q12)	MED1	2																									
rs1877030 (17q12)	CDK12	0																									
rs1877030 (17q12)	NEUROD2	0																									
rs1877030 (17q12)	PPP1R1B	1																									
rs1877030 (17q12)	STARD3	2																									
chr17:38031857 (17q12-q21)	IKZF3	4																									
chr17:38031857 (17q12-q21)	ZBPB2	2																									
chr17:38031857 (17q12-q21)	GSDMB	2																									
chr17:38031857 (17q12-q21)	ORMDL3	2																									
chr17:38031857 (17q12-q21)	LRRC3C	0																									
chr17:38031857 (17q12-q21)	GSDMA	1																						</			

RA risk SNP (cytoband)	Gene	Score	Biological gene criteria							Overlap with H3K4me3 peaks										Drug target gene	RA drug target gene	PPI with RA drug target gene					
			RA risk missense variant	Cis- eQTL	PubMed text-mining	Protein-protein interaction	Primary immunodeficiency	Hematological cancer	Knockout mouse phenotype	Molecular pathway	Nearest gene from RA risk SNP	Treg primary cells	CD4+ memory primary cells	CD4+ naive primary cells	CD8+ memory primary cells	CD8+ naive primary cells	CD34+ primary cells	CD34+ cultured cells	Mobilized CD34+ primary cells				CD19+ primary cells	CD3+ primary cells			
rs34536443 (19p13)	ICAM5	0																									
rs34536443 (19p13)	ZGLP1	0																									
rs34536443 (19p13)	FDX1L	0																									
rs34536443 (19p13)	RAVER1	0																									
rs34536443 (19p13)	ICAM3	2																									
rs34536443 (19p13)	TYK2	6																									
chr19:10771941 (19p13)	AP1M2	0																									
chr19:10771941 (19p13)	SLC44A2	0																									
chr19:10771941 (19p13)	ILF3-AS1	0																									
chr19:10771941 (19p13)	ILF3	1																									
rs4239702 (20q13)	SLC12A5	1																									
rs4239702 (20q13)	NCOA5	0																									
rs4239702 (20q13)	CD40	6																									
rs73194058 (21q22)	IFNGR2	6																									
rs73194058 (21q22)	TMEM50B	1																									
rs73194058 (21q22)	DNAJC28	0																									
rs73194058 (21q22)	GART	0																									
chr21:35928240 (21q22)	RCAN1	1																									
rs8133843 (21q22)	LOC100506403	0																									
rs1893592 (21q22)	UBASH3A	2																									
rs2236668 (21q22)	ICOSLG	5																									
rs2236668 (21q22)	DNMT3L	0																									
rs2236668 (21q22)	AIRE	4																									
rs11089637 (22q11)	UBE2L3	0																									
rs11089637 (22q11)	YDJC	1																									
rs11089637 (22q11)	CCDC116	0																									
rs11089637 (22q11)	SDF2L1	0																									
rs3218251 (22q12)	IL2RB	3																									
rs909685 (22q13)	RPL3	1																									
rs909685 (22q13)	SNORD83B	1																									
rs909685 (22q13)	SNORD83A	1																									
rs909685 (22q13)	RNU86	1																									
rs909685 (22q13)	SNORD43	1																									
rs909685 (22q13)	SYNGR1	1																									
chrX:78464616 (Xq21)	MIR4328	0																									
chrX:78464616 (Xq21)	P2RY10	0																									
chrX:78464616 (Xq21)	GPR174	0																									
rs5987194 (Xq28)	ARHGAP4	0																									
rs5987194 (Xq28)	NAA10	0																									
rs5987194 (Xq28)	RENBP	0																									
rs5987194 (Xq28)	HCFC1	0																									
rs5987194 (Xq28)	MIR3202-2	0																									
rs5987194 (Xq28)	MIR3202-1	0																									
rs5987194 (Xq28)	TMEM187	0																									
rs5987194 (Xq28)	IRAK1	3																									
rs5987194 (Xq28)	MIR718	0																									
rs5987194 (Xq28)	MECP2	0																									

Biological candidate gene prioritization criteria and related information flags for all 377 genes included in the 100 RA risk loci outside of the MHC region (indexed by SNP and chromosomal location). For each, we list the summary score derived from individual criterion (filled red box indicates criterion satisfied). Filled blue box indicates that the gene is the nearest gene to the RA risk SNP. Filled green boxes indicate overlap with H3K4me3 peaks in immune-related cells. Filled purple boxes indicate overlap with drug target genes.

Supplementary Table 6. A list of drug target genes.

All drug target genes										
TNFRSF4	ADORA1	RAF1	GLRB	PDE7B	TOP1MT	TPH1	ACVRL1	CYP19A1	PRKCA	TUBB1
SCNN1D	REN	THRB	NPY1R	IFNGR1	DGAT1	CAT	ITGB7	APH1B	CACNG1	HRH3
MMP23A	AVPR1B	RARB	NPY5R	GRM1	SLC52A2	CHRM4	RARG	PPIB	SSTR2	NTSR1
GABRD	IKBKE	TOP2B	GLRA3	ESR1	JAK2	F2	ITGA5	CYP11A1	GRIN2C	CHRNA4
MTOR	HSD11B1	CCR4	SLC25A4	OPRM1	TEK	FOLH1	PDE1B	MPI	SPHK1	KCNQ2
EPHA2	KCNK2	SCN5A	TLR3	PLG	CNTFR	MS4A2	MMP19	CHRNA3	BIRC5	APP
HTR6	ESRRG	SCN10A	KLKB1	PDE10A	SIGMAR1	MS4A1	CDK2	CHRNA4	GAA	GRIK1
PLA2G2A	TGFB2	SCN11A	F11	PSMB1	IL11RA	PTGDR2	ERBB3	PDE8A	GCGR	SOD1
ALPL	PARP1	VIPR1	MTNR1A	HDAC9	NPR2	PGA3	IL23A	IGF1R	FASN	IFNAR2
HTR1D	GGPS1	CCR1	SLC6A3	IL6	ANXA1	FADS1	CDK4	HBA2	TYMS	IFNAR1
CNR2	MTR	CCR3	SRD5A1	CRHR2	RFK	FADS2	AVPR1A	HBA1	YES1	IFNGR2
CD52	RYR2	CCR2	PRLR	GHRHR	SYK	FTH1	IFNG	SSTR5	MC2R	GART
PTAFR	CHRM3	CCR5	IL7R	PDE1C	FBP1	CHRM1	MDM2	CACNA1H	ROCK1	KCNE1
OPRD1	TPO	PTH1R	PTGER4	BLVRA	GABBR2	SLC22A6	METAP2	NOXO1	CDH2	CBS
HCRT1	ADAM17	IMPDH2	PRKAA1	GCK	GRIN3A	SLC22A8	LTA4H	MMP25	TTR	PDXK
LCK	RRM2	CACNA2D2	GHR	NPC1L1	PPP3R2	PRDX5	NR1H4	ABAT	FECH	COMT
HDAC1	ODC1	GRM2	IL6ST	PPIA	ABCA1	SLC22A11	IGF1	GRIN2A	MC4R	SERPIND1
PSMB2	NTSR2	TLR9	PDE4D	RAMP3	TXN	SLC22A12	PAH	ABCC1	BCL2	MAPK1
CSF3R	APOB	TNNC1	HTR1A	ADCY1	UGCG	PYGM	TXNRD1	SCNN1G	SERPINB2	MMP11
KCNQ4	KCNK3	PRKCD	CDK7	DDC	ALAD	CPT1A	ACACB	SCNN1B	MADCAM1	MIF
MPL	XDH	TKT	CARTPT	EGFR	POLE3	CCND1	ALDH2	PLK1	ELANE	ADORA2A
SLC6A9	SRD5A2	CACNA1D	HMGCR	VKORC1L1	TLR4	FOLR3	NOS1	PRKCB	CFD	CHEK2
AKR1A1	SLC8A1	UBA3	F2R	HSPB1	C5	FOLR2	PRKAB1	IL4R	KISS1R	SLC5A1
FAAH	PRKCE	HTR1F	PDE8B	HGF	PTGS1	P2RY2	PLA2G1B	CD19	GRIN3B	HMOX1
CPT2	EPAS1	PROS1	DHFR	CACNA2D1	CDK9	SLCO2B1	P2RX7	QPRT	GAMT	CSF2RB
DIO1	CALM2	GABRR3	CKMT2	GRM3	ABL1	DGAT2	ORAI1	MAPK3	TBXA2R	IL2RB
PCSK9	LHCGR	ATP6V1A	CHD1	ABCB4	DBH	GRM5	HPD	ITGAL	PLIN3	SSTR3
JUN	FSHR	DRD3	SLC12A2	CYP51A1	RXRA	TYR	HCAR2	VKORC1	PTPRS	PDXP
PDE4B	POLE4	CD80	IL13	CDK6	EGFL7	MTNR1B	HCAR3	SLC5A2	CD70	PLA2G6
PTGER3	TACR1	NR1I2	CAMLG	CALCR	GRIN1	PGR	MMP17	MMP2	C3	CACNA1I
PTGFR	GGCX	GSK3B	IL9	CYP3A4	TUBB4B	MMP7	POLE	SLC6A2	INSR	MCHR1
S1PR1	ADRA2B	CD86	HDAC3	EPHB4	CACNA1B	MMP20	FLT3	CES1	DNMT1	CYP2D6
AMY2A	IL1R2	CASR	FGF1	ACHE	AKR1C2	MMP27	FLT1	SLC12A3	ICAM1	TSPO
CSF1	IL1R1	ATP2C1	NR3C1	SERPINE1	IL2RA	MMP8	ALOX5AP	CETP	PDE4A	PPARA
ADORA3	IL1B	AGTR1	HTR4	PIK3CG	PRKCQ	MMP10	TNFSF11	MMP15	EPOR	MAPK12
KCND3	SCTR	P2RY12	ADRB2	MET	CACNB2	MMP1	CPB2	CA7	CACNA1A	CPT1B
ATP1A1	PROC	MME	CSF1R	IMPDH1	ITGB1	MMP3	HTR2A	AGRP	PTGER1	CHKB-CPT1B
CD2	SMPD4	IL12A	PDGFRB	SMO	NRP1	MMP12	CYSLTR2	SLC12A4	JAK3	CSF2RA
HSD3B2	CXCR4	SI	GLRA1	AKR1B1	RET	MMP13	MLNR	PDF	PDE4C	IL3RA

All drug target genes (continued)

HSD3B1	HNMT	BCHE	GRIA1	CHRM2	ALOX5	GUCY1A2	EDNRB	NQO1	SCN1B	SLC25A6
FCGR1B	CACNB4	GHSR	ADRA1B	AKR1D1	PPYR1	ACAT1	TPP2	DHODH	HPN	STS
GNRHR2	DPP4	PSMD2	GABRB2	TBXAS1	MAPK8	SDHD	TNFSF13B	DPEP1	CD22	TLR7
FCGR1A	SCN3A	CLCN2	GABRA6	BRAF	CDK1	IL18	F7	TUBB3	FFAR1	TLR8
SV2A	SCN2A	SST	GABRA1	MGAM	SIRT1	DRD2	F10	SERPINF1	ATP4A	GLRA2
CA14	SCN1A	FGFR3	GABRG2	TPK1	TACR2	HTR3B	TEP1	TRPV3	RYR1	ACE2
MCL1	SCN9A	ADRA2C	GABRP	KCNH2	EIF4EBP2	HTR3A	APEX1	TRPV1	BLVRB	GRPR
CTSS	ABCB11	DRD5	DRD1	NOS3	DDIT4	NNMT	PNP	TP53	EGLN2	SMS
CTSK	PDK1	CCKAR	HRH2	ANGPT2	PLAU	APOC3	MMP14	VAMP2	RAB4B-EGLN2	POLA1
NPR1	ITGA4	CHRNA9	FGFR4	FDFT1	ADK	BACE1	PSMB5	AURKB	CEACAM3	MAOA
IL6R	PDE1A	GABRG1	FLT4	LPL	VDAC2	FXSD2	BCL2L2	ADORA2B	PLAUR	MAOB
CHRNA2	ITGAV	GABRA2	NQO2	SLC18A1	KCNMA1	SCN4B	LTBR4	SHMT1	KCNN4	PORCN
GBA	CALCRL	GABRA4	SIRT5	ATP6V1B2	LIPF	SCN2B	CTSG	KCNJ12	CKM	HDAC6
FDPS	TFPI	GABRB1	TPMT	TNFRSF10B	HTR7	CD3E	SSTR1	NOS2	CALM3	CACNA1F
BGLAP	STAT1	PDGFRA	ALDH5A1	TNFRSF10A	IDE	CD3D	POLE2	SLC6A4	PTGIR	AR
NTRK1	PLCL1	KIT	GABBR1	ADRA1A	KIF11	CD3G	PTGDR	CCL2	GRIN2D	IL2RG
CD1A	AOX1	KDR	TUBB	CHRNA2	CYP26A1	HSPA8	PTGER2	MMP28	FTL	CXCR3
FCER1A	CD28	GNRHR	LTA	CLU	ABCC2	SCN3B	HIF1A	CACNB1	KLK2	CYSLTR1
CRP	CTLA4	DCK	TNF	GSR	CHUK	CHEK1	ESR2	ERBB2	CD33	GLA
KCNJ10	PTH2R	ALB	SLC44A4	ADRB3	SCD	DCPS	PGF	THRA	PRKCG	HTR2C
PVRL4	MAP2	CXCL2	C4A	FGFR1	NFKB2	KCNJ1	TSHR	RARA	AURKC	AGTR2
FCER1G	CPS1	HPSE	C4B	IDO1	CYP17A1	KCNJ5	CALM1	TOP2A	FKBP1A	SLC25A5
NR1I3	ERBB4	EIF4E	RXR8	PLAT	ADRA2A	CACNA1C	SERPINA6	STAT3	SMOX	XIAP
FCGR2A	ATIC	METAP1	ITPR3	IKKBK	ADRB1	KCNA1	SERPINA1	NAGLU	ADRA1D	GPR119
FCGR3A	FN1	ADH1A	PPARD	POLB	PNLIP	KCNA5	BDKRB2	HSD17B1	SLC23A2	HPRT1
FCGR2C	CXCR2	ADH1B	MAPK14	VDAC3	SLC18A2	VWF	HSP90AA1	TUBG1	SNAP25	F9
FCGR3B	CXCR1	ADH1C	GLP1R	FNTA	FGFR2	SCNN1A	MARK3	RAMP2	SSTR4	GABRE
FCGR2B	GPBAR1	MTPP	VEGFA	OPRK1	MMP21	VAMP1	CKB	AOC3	BCL2L1	GABRA3
RXRG	TUBA4A	NFKB1	PLA2G7	PDE7A	CALY	CD4	AKT1	ITGA2B	MMP24	GABRQ
CD247	PSMD1	CENPE	MUT	TRPA1	DRD4	PTPN6	GABRB3	CRHR1	SRC	SLC6A8
F5	HTR2B	TACR3	IL17A	CA1	TH	C1S	GABRA5	ITGB3	TGM2	AVPR2
SELP	ALPPL2	EGF	HTR1B	CA3	KCNQ1	M6PR	GABRG3	NPEPPS	TOP1	F8
SELE	TRPM8	PDE5A	CNR1	CA2	CHRNA10	GRIN2B	OCA2	NGFR	ADA	
SERPINC1	RAMP1	FGF2	GABRR1	MMP16	RRM1	GUCY2C	CHRFAM7A	CACNA1G	TNNC2	
ABL2	HDAC4	SLC7A11	GABRR2	RRM2B	MMP26	PDE3A	CHRNA7	MPO	MMP9	
SOAT1	IL5RA	IL15	FYN	ANGPT1	HBB	KCNJ8	RYR3	TUBD1	SLC12A5	
MR1	ITPR1	EDNRA	TUBE1	SQLE	CCKBR	ITPR2	CHRM5	RPS6KB1	CD40	
PTGS2	OXTR	NR3C2	HDAC2	MYC	WEE1	VDR	MAP1A	CA4	PTGIS	
PLA2G4A	SLC6A1	TLR2	CTGF	KCNQ3	CALCA	CACNB3	CKMT1A	ACE	PTPN1	
CACNA1S	HRH1	FGA	TAAR1	KCNK9	KCNJ11	TUBA1A	SLC12A1	SCN4A	MC3R	
SYT2	PPARG	NPY2R	MYB	CYP11B1	ABCC8	ASIC1	HDC	APOH	AURKA	

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