

### *Supplementary Information*

## **Large-scale meta-analysis across East Asian and European populations updated genetic architecture and variant-driven biology of rheumatoid arthritis, identifying 11 novel susceptibility loci**

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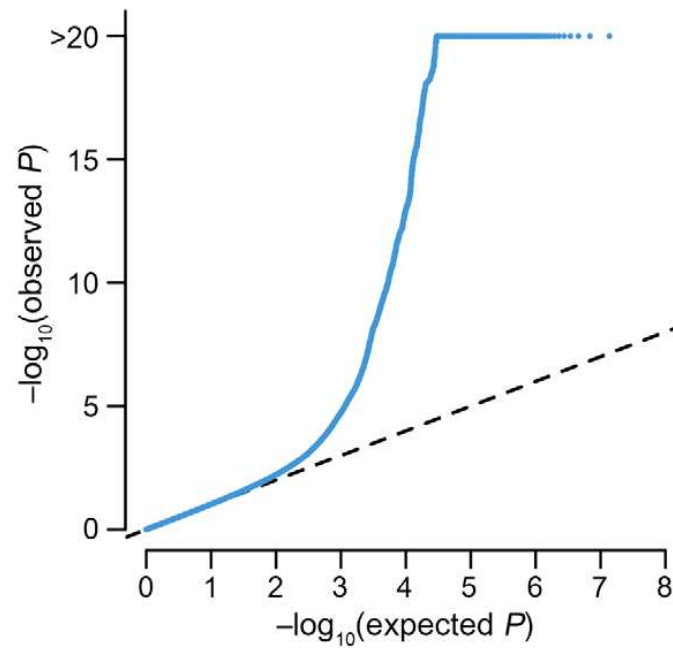
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#### Supplementary Figure 1 | Quantile-quantile (QQ) plot

Quantile-quantile (QQ) plot for comparing expected and observed RA association significance levels for 13,693,845 non-MHC variants in minus  $\log_{10}$  scale (inflation factor  $\lambda = 1.01$ ). The diagonal line of equality is shown by a black dash line.

Supplementary Table 1 | RA associations in 82 non-MHC loci

Variant*	Chr:Position*	Gene	EA	NEA	East Asian			European			Meta-analysis		
					Freq <sup>§</sup>	OR (95%CI)	P	Freq <sup>§</sup>	OR (95%CI)	P	OR (95%CI)	P <sub>meta</sub>	P <sub>het</sub>
rs2258734	1:2483961	TNFRSF14-MMEL1	A	G	0.44	0.92 (0.89-0.95)	1.2.E-06	0.17	0.91 (0.88-0.94)	6.0.E-09	0.91 (0.89-0.93)	6.0E-14	0.95
rs2301888	1:17672730	PADI4	A	G	0.59	0.86 (0.83-0.89)	5.1.E-20	0.17	0.90 (0.87-0.94)	5.5.E-09	0.88 (0.86-0.90)	3.8E-06	0.77
rs28411352	1:38278579	MTF1-INPP5B	T	C	0.24	1.08 (1.03-1.12)	2.0.E-04	0.13	1.11 (1.07-1.16)	5.2.E-09	1.10 (1.07-1.13)	1.7E-11	0.85
rs6679677	1:114303808	PTPN22	A	C	0.00	NA	NA	0.06	1.81 (1.73-1.89)	3.1.E-149	1.81 (1.73-1.89)	1.4E-145	NA
rs12126142	1:154425456	IL6R	A	G	0.41	0.92 (0.89-0.96)	3.8.E-06	0.20	0.93 (0.90-0.96)	4.5.E-06	0.93 (0.91-0.95)	1.0E-10	0.98
rs3761959	1:157669278	FCRL3	T	C	0.40	1.09 (1.05-1.12)	1.2.E-06	0.23	1.07 (1.04-1.10)	1.2.E-05	1.08 (1.05-1.10)	9.6E-11	0.94
rs12026490	1:160417157	SLAMF6	T	C	0.93	0.80 (0.75-0.85)	1.1.E-12	1.00	NA	NA	0.80 (0.75-0.85)	1.1E-12	NA
rs1234313	1:173166247	LOC100506023	A	G	0.73	0.92 (0.88-0.96)	3.6.E-05	0.15	0.93 (0.90-0.96)	9.3.E-06	0.92 (0.90-0.95)	1.9E-09	0.96
rs10911902	1:186632317	SMG7, NCF2	T	C	0.16	0.92 (0.88-0.96)	3.5.E-04	0.09	0.92 (0.88-0.95)	1.4.E-05	0.92 (0.89-0.95)	2.4E-08	0.99
rs1355208	2:30445322	LBH	A	G	0.55	0.92 (0.89-0.96)	3.3.E-06	0.18	0.92 (0.89-0.95)	3.1.E-07	0.92 (0.90-0.94)	6.8E-12	0.97
rs56095903	2:61072664	REL	T	G	0.02	0.93 (0.78-1.12)	4.5.E-01	0.19	1.12 (1.09-1.16)	7.1.E-14	1.12 (1.08-1.15)	8.7E-13	0.55
rs1858037	2:65598300	SPRED2	A	T	0.83	0.90 (0.86-0.94)	2.4.E-06	0.17	0.90 (0.88-0.93)	5.9.E-10	0.90 (0.88-0.93)	1.1E-14	0.99
<b>rs6705628</b>	<b>2:74208362</b>	<b>DGUOK-AS1</b>	<b>T</b>	<b>C</b>	<b>0.18</b>	<b>0.88 (0.84-0.92)</b>	<b>2.1.E-08</b>	<b>0.01</b>	<b>0.90 (0.79-1.03)</b>	<b>1.2.E-01</b>	<b>0.88 (0.85-0.92)</b>	<b>6.7E-09</b>	<b>0.95</b>
rs11123811	2:100760172	AFF3	T	C	0.47	1.11 (1.07-1.14)	1.5.E-09	0.25	1.10 (1.07-1.14)	1.3.E-10	1.10 (1.08-1.13)	2.0E-18	0.98
rs11889341	2:191943742	STAT4	T	C	0.31	1.18 (1.14-1.23)	1.1.E-20	0.12	1.13 (1.09-1.17)	6.5.E-12	1.16 (1.13-1.19)	4.3E-30	0.83
rs3087243	2:204738919	CTLA4	A	G	0.24	0.90 (0.87-0.94)	7.0.E-07	0.22	0.87 (0.84-0.90)	9.2.E-20	0.88 (0.86-0.90)	3.3E-24	0.83
rs4602367	3:17053499	PLCL2	A	G	0.38	0.94 (0.91-0.98)	6.7.E-04	0.24	0.92 (0.89-0.94)	2.0.E-08	0.93 (0.91-0.95)	1.8E-10	0.87
rs3806624	3:27764623	EOMES	A	G	0.17	0.92 (0.88-0.96)	1.0.E-04	0.27	0.92 (0.89-0.95)	6.1.E-08	0.92 (0.89-0.94)	3.9E-11	0.99
rs13103285	4:10726520	CLNK	T	C	0.52	1.11 (1.07-1.15)	1.1.E-09	0.24	1.09 (1.05-1.14)	5.4.E-06	1.10 (1.08-1.13)	4.3E-14	0.94
rs34046593	4:26111593	C4orf52	A	G	0.01	1.37 (0.97-1.93)	7.5.E-02	0.16	1.15 (1.11-1.19)	9.2.E-17	1.15 (1.12-1.19)	7.2E-17	0.71
rs117605225	4:78508197	CXCL13	T	C	0.96	1.54 (1.34-1.77)	1.9.E-09	1.00	NA	NA	1.54 (1.34-1.77)	1.9E-09	NA
<b>rs2918392</b>	<b>5:10704797</b>	<b>DAP</b>	<b>T</b>	<b>G</b>	<b>0.29</b>	<b>0.95 (0.91-0.98)</b>	<b>3.9.E-03</b>	<b>0.32</b>	<b>0.93 (0.90-0.96)</b>	<b>1.6.E-06</b>	<b>0.94 (0.91-0.96)</b>	<b>4.6E-08</b>	<b>0.89</b>
rs7731626	5:55444683	ANKRD55	A	G	0.09	0.81 (0.74-0.89)	1.2.E-05	0.18	0.82 (0.79-0.86)	7.9.E-23	0.82 (0.79-0.85)	1.9E-26	0.94
rs403214	5:102603701	C5orf30	A	G	0.74	1.06 (1.00-1.12)	3.8.E-02	0.34	1.11 (1.07-1.14)	9.4.E-10	1.10 (1.06-1.13)	4.0E-10	0.82
rs244685	5:133423890	IL3-CSF2	T	G	0.31	1.09 (1.05-1.13)	1.3.E-05	0.07	1.10 (1.06-1.15)	7.1.E-06	1.09 (1.06-1.12)	6.0E-10	0.93
rs9405192	6:382537	IRF4	A	G	0.57	0.91 (0.88-0.94)	1.8.E-07	0.14	0.92 (0.88-0.96)	9.5.E-05	0.91 (0.89-0.94)	9.3E-11	0.97
rs12530098	6:14107197	CD83	T	C	0.15	1.15 (1.10-1.21)	6.3.E-10	0.03	1.13 (1.04-1.23)	4.9.E-03	1.15 (1.10-1.20)	1.4E-11	0.94
rs2233424	6:44233921	NFKBIE	T	C	0.22	1.20 (1.16-1.25)	4.1.E-20	0.02	1.33 (1.20-1.47)	3.3.E-08	1.22 (1.17-1.26)	6.5E-26	0.71
rs62422878	6:106676470	ATG5	T	C	0.05	1.19 (1.10-1.28)	7.3.E-06	0.10	1.09 (1.05-1.13)	1.1.E-05	1.11 (1.07-1.15)	3.6E-09	0.73
rs7749323	6:138230389	TNFAIP3	A	G	0.07	1.28 (1.20-1.37)	2.9.E-14	0.02	1.40 (1.30-1.52)	1.4.E-17	1.33 (1.26-1.40)	3.5E-29	0.73
rs212389	6:159489791	TAGAP	A	G	0.92	1.14 (1.07-1.22)	5.2.E-05	0.31	1.10 (1.07-1.14)	1.1.E-09	1.11 (1.08-1.14)	6.7E-13	0.86
rs1571878	6:167540842	CCR6	T	C	0.54	0.83 (0.80-0.85)	5.0.E-29	0.28	0.89 (0.86-0.91)	4.9.E-15	0.86 (0.84-0.88)	4.1E-40	0.70
rs740122	7:28166442	JAZF1	A	G	0.74	0.94 (0.90-0.97)	7.9.E-04	0.11	0.91 (0.88-0.95)	7.5.E-07	0.92 (0.90-0.95)	5.4E-09	0.89
rs113066392	7:74026152	GTF2IRD1	A	AC	0.12	1.43 (1.33-1.55)	1.3.E-20	0.10	NA	NA	1.43 (1.33-1.55)	1.3E-20	NA
rs42034	7:92239144	CDK6	A	G	0.90	0.93 (0.88-0.98)	5.5.E-03	0.37	0.91 (0.88-0.95)	4.4.E-07	0.92 (0.89-0.94)	1.3E-08	0.94
rs3757387	7:128576086	IRF5	T	C	0.88	0.85 (0.80-0.89)	1.2.E-10	0.27	0.90 (0.87-0.93)	2.0.E-11	0.88 (0.86-0.91)	1.9E-19	0.78
rs9693589	8:11348961	BLK	A	G	0.70	1.15 (1.10-1.19)	2.1.E-13	0.13	1.10 (1.06-1.13)	2.0.E-07	1.12 (1.09-1.15)	1.5E-18	0.83
rs11574914	9:34710338	CCL19-CCL21	A	G	0.05	1.10 (1.03-1.19)	8.5.E-03	0.17	1.13 (1.09-1.16)	1.5.E-13	1.12 (1.09-1.16)	9.9E-15	0.92
rs10435844	9:123668199	TRAF1-C5	T	G	0.73	0.93 (0.89-0.96)	3.4.E-05	0.32	0.92 (0.90-0.95)	4.8.E-07	0.92 (0.90-0.95)	9.7E-11	0.99
rs3134883	10:6100725	IL2RA	A	G	0.27	1.11 (1.07-1.15)	6.9.E-08	0.15	1.10 (1.07-1.14)	3.5.E-09	1.10 (1.08-1.13)	2.0E-15	0.98
rs502919	10:6517167	PRKCQ	T	C	0.71	0.91 (0.88-0.94)	1.6.E-07	0.40	0.93 (0.90-0.97)	4.4.E-04	0.92 (0.90-0.94)	6.2E-10	0.86
rs2275806	10:8095340	GATA3	A	G	0.63	0.95 (0.92-0.98)	3.6.E-03	0.28	0.91 (0.89-0.94)	4.2.E-08	0.93 (0.91-0.95)	2.5E-09	0.86
rs1538981	10:31411355	ZNF438	T	C	0.46	1.07 (1.03-1.10)	1.5.E-04	0.27	1.07 (1.04-1.11)	5.6.E-06	1.07 (1.05-1.09)	4.4E-09	0.97
rs7097397	10:50025396	WDFY4	A	G	0.66	0.89 (0.86-0.92)	2.4.E-11	0.19	0.95 (0.92-0.97)	3.9.E-04	0.92 (0.90-0.94)	1.4E-12	0.71
rs71508903	10:63779871	ARID5B	T	C	0.24	1.17 (1.12-1.21)	5.9.E-14	0.11	1.15 (1.11-1.20)	3.8.E-13	1.16 (1.13-1.19)	3.1E-25	0.95
rs9943599	11:9752741	SWAP70	T	C	0.40	1.10 (1.06-1.14)	4.8.E-08	0.29	1.07 (1.03-1.11)	7.8.E-04	1.09 (1.06-1.11)	2.7E-10	0.90
<b>rs660442</b>	<b>11:64042997</b>	<b>BAD</b>	<b>A</b>	<b>G</b>	<b>0.08</b>	<b>0.84 (0.79-0.89)</b>	<b>3.9.E-08</b>	<b>0.10</b>	<b>0.93 (0.89-0.96)</b>	<b>2.0.E-04</b>	<b>0.90 (0.87-0.93)</b>	<b>1.1E-09</b>	<b>0.67</b>
<b>rs59578717</b>	<b>11:68859848</b>	<b>TPCN2</b>	<b>Ins1<sup>†</sup></b>	<b>C</b>	<b>0.51</b>	<b>0.91 (0.88-0.94)</b>	<b>4.3.E-08</b>	<b>0.86</b>	<b>NA</b>	<b>NA</b>	<b>0.91 (0.88-0.94)</b>	<b>4.3E-08</b>	<b>NA</b>
rs79145843	11:72404893	ARAP1	T	C	0.26	0.88 (0.84-0.91)	1.3.E-10	0.00	NA	NA	0.88 (0.84-0.91)	1.3E-10	NA
rs4409785	11:95311422	CEP57	T	C	0.93	0.88 (0.83-0.94)	8.0.E-05	0.41	0.92 (0.88-0.95)	1.2.E-05	0.91 (0.88-0.94)	7.8E-09	0.87
rs28361986	11:118693161	CXCR5	A	T	0.14	0.93 (0.86-1.00)	6.0.E-02	0.10	0.86 (0.82-0.89)	2.1.E-14	0.87 (0.84-0.90)	5.1E-14	0.74
<b>rs12795702</b>	<b>11:128156314</b>	<b>LOC107984408</b>	<b>A</b>	<b>G</b>	<b>0.77</b>	<b>1.11 (1.06-1.15)</b>	<b>5.8.E-07</b>	<b>0.18</b>	<b>1.07 (1.03-1.11)</b>	<b>8.5.E-04</b>	<b>1.09 (1.06-1.12)</b>	<b>4.1E-09</b>	<b>0.89</b>
rs73013527	11:128496952	ETS1	T	C	0.28	0.92 (0.89-0.96)	3.3.E-05	0.25	0.92 (0.89-0.95)	2.0.E-06	0.92 (0.90-0.95)	3.8E-10	0.99
<b>rs4963581</b>	<b>12:24813281</b>	<b>LOC105369698</b>	<b>A</b>	<b>G</b>	<b>0.75</b>	<b>1.09 (1.05-1.13)</b>	<b>6.6.E-06</b>	<b>0.09</b>	<b>1.09 (1.03-1.14)</b>	<b>1.4.E-03</b>	<b>1.09 (1.06-1.12)</b>	<b>3.8E-08</b>	<b>0.98</b>

rs4622308	12:56469185	<i>CDK2</i>	T	C	0.73	1.11 (1.07-1.16)	6.9.E-08	0.29	1.08 (1.04-1.11)	2.2.E-06	1.09 (1.07-1.12)	2.2E-12	0.86
rs77465633	12:111933545	<i>SH2B3-PTPN11</i>	A	C	0.07	1.32 (1.20-1.45)	3.8.E-09	0.00	NA	NA	1.32 (1.20-1.45)	3.8E-09	NA
rs9532434	13:40355913	<i>COG6</i>	T	C	0.25	0.88 (0.85-0.91)	5.8.E-11	0.17	0.90 (0.87-0.93)	2.1.E-10	0.89 (0.87-0.91)	1.9E-19	0.91
rs1950897	14:68760141	<i>RAD51B</i>	T	C	0.87	1.16 (1.10-1.22)	8.6.E-09	0.36	1.09 (1.06-1.13)	2.5.E-07	1.11 (1.08-1.14)	1.0E-13	0.77
rs3825568	14:69260588	<i>ZFP36L1</i>	T	C	0.69	1.10 (1.06-1.14)	1.6.E-07	0.24	1.07 (1.04-1.11)	3.7.E-06	1.08 (1.06-1.11)	6.1E-12	0.88
rs2841275	14:105388182	<i>PLD4-AHNAK2</i>	A	C	0.38	0.85 (0.82-0.88)	1.7.E-19	0.40	NA	NA	0.85 (0.82-0.88)	1.7E-19	NA
rs8032939	15:38834033	<i>RASGRP1</i>	T	C	0.40	0.88 (0.85-0.91)	1.5.E-13	0.37	0.89 (0.86-0.92)	2.4.E-12	0.88 (0.86-0.90)	4.5E-24	0.98
rs7170107	15:70010647	<i>LOC145837</i>	T	C	0.05	1.10 (1.02-1.18)	1.2.E-02	0.14	1.16 (1.12-1.20)	2.7.E-17	1.15 (1.11-1.18)	6.1E-18	0.83
<b>rs199894206</b>	<b>15:91038883</b>	<b><i>IQGAP1</i></b>	<b>CT</b>	<b>C</b>	<b>0.36</b>	<b>1.12 (1.08-1.16)</b>	<b>1.5.E-10</b>	<b>0.19</b>	<b>NA</b>	<b>NA</b>	<b>1.12 (1.08-1.16)</b>	<b>1.5E-10</b>	<b>NA</b>
rs7206670	16:11833886	<i>TXNDC11</i>	T	G	0.48	1.06 (1.02-1.09)	7.6.E-04	0.30	1.09 (1.05-1.12)	6.0.E-07	1.07 (1.05-1.10)	4.1E-09	0.91
<b>rs149041927<sup>†</sup></b>	<b>16:23871206</b>	<b><i>PRKCB</i></b>	<b>A</b>	<b>Ins2<sup>‡</sup></b>	<b>0.38</b>	<b>0.91 (0.88-0.94)</b>	<b>2.2.E-08</b>	<b>0.44</b>	<b>NA</b>	<b>NA</b>	<b>0.91 (0.88-0.94)</b>	<b>2.2E-08</b>	<b>NA</b>
<b>rs12918327</b>	<b>16:30626616</b>	<b><i>ZNF689</i></b>	<b>T</b>	<b>C</b>	<b>0.10</b>	<b>1.09 (1.03-1.16)</b>	<b>1.6.E-03</b>	<b>0.12</b>	<b>1.09 (1.05-1.13)</b>	<b>3.9.E-06</b>	<b>1.09 (1.06-1.12)</b>	<b>3.0E-08</b>	<b>0.98</b>
rs9927316	16:86016401	<i>IRF8</i>	C	G	0.59	0.93 (0.90-0.96)	4.4.E-05	0.88	0.89 (0.86-0.93)	2.8.E-08	0.91 (0.89-0.94)	2.3E-11	0.32
rs59716545	17:38031857	<i>IKZF3-CSF3</i>	T	G	0.73	0.95 (0.92-0.99)	5.8.E-03	0.27	0.91 (0.88-0.94)	2.0.E-09	0.93 (0.91-0.95)	2.7E-10	0.83
rs2847297	18:12797694	<i>PTPN2</i>	A	G	0.66	0.91 (0.88-0.94)	8.5.E-08	0.33	0.92 (0.89-0.95)	4.1.E-08	0.91 (0.89-0.94)	2.6E-14	0.98
rs34536443	19:10463118	<i>TYK2</i>	C	G	0.00	NA	NA	0.52	0.68 (0.62-0.75)	4.6.E-16	0.68 (0.62-0.75)	1.1E-15	NA
rs147622113	19:10771941	<i>ILF3</i>	T	C	0.00	NA	NA	0.01	0.68 (0.60-0.77)	8.7.E-10	0.68 (0.60-0.77)	1.4E-09	NA
rs1883832	20:44746982	<i>CD40</i>	T	C	0.37	0.92 (0.89-0.96)	8.0.E-06	0.12	0.87 (0.84-0.91)	1.1.E-13	0.90 (0.88-0.92)	1.1E-16	0.77
<b>rs6011186</b>	<b>20:62484008</b>	<b><i>C20orf181</i></b>	<b>T</b>	<b>C</b>	<b>0.38</b>	<b>0.90 (0.87-0.93)</b>	<b>3.7.E-09</b>	<b>0.04</b>	<b>0.90 (0.82-0.99)</b>	<b>2.6.E-02</b>	<b>0.90 (0.87-0.93)</b>	<b>3.2E-10</b>	<b>0.99</b>
rs8126756	21:34775444	<i>IFNGR2</i>	T	C	0.47	1.06 (1.03-1.10)	2.7.E-04	0.42	1.13 (1.08-1.18)	1.1.E-07	1.09 (1.06-1.12)	1.8E-09	0.78
rs8133843	21:36738242	<i>RUNX1-LOC100506403</i>	A	G	0.51	1.06 (1.02-1.10)	6.7.E-04	0.31	1.10 (1.06-1.14)	6.0.E-09	1.08 (1.06-1.11)	8.8E-11	0.82
rs1893592	21:43855067	<i>UBASH3A</i>	A	C	0.76	1.10 (1.06-1.14)	2.0.E-06	0.36	1.11 (1.07-1.15)	9.8.E-09	1.10 (1.07-1.13)	1.5E-13	0.97
rs7278257	21:45653764	<i>ICOSLG-AIRE</i>	C	G	0.18	0.90 (0.86-0.94)	5.0.E-06	0.63	0.92 (0.89-0.96)	1.1.E-05	0.91 (0.89-0.94)	4.3E-10	0.35
rs5754104	22:21916361	<i>UBE2L3-YDJC</i>	A	G	0.34	1.09 (1.05-1.13)	1.5.E-06	0.10	1.09 (1.05-1.14)	1.7.E-05	1.09 (1.06-1.12)	1.4E-10	NA
rs2069235	22:39747780	<i>SYNGR1</i>	A	G	0.85	1.20 (1.14-1.26)	2.1.E-13	0.15	1.11 (1.08-1.15)	3.0.E-10	1.14 (1.11-1.17)	1.7E-20	0.70
<b>rs35156883</b>	<b>22:45746152</b>	<b><i>SMC1B</i></b>	<b>A</b>	<b>AT</b>	<b>0.52</b>	<b>1.10 (1.06-1.13)</b>	<b>1.9.E-08</b>	<b>0.63</b>	<b>NA</b>	<b>NA</b>	<b>1.10 (1.06-1.13)</b>	<b>1.9E-08</b>	<b>NA</b>
rs6619397	X:78366127	<i>P2RY10</i>	A	T	0.46	1.11 (1.08-1.15)	1.0.E-11	0.01	1.11 (0.91-1.34)	3.0.E-01	1.11 (1.08-1.15)	5.9E-12	0.99
rs5987194	X:153301467	<i>IRAK1</i>	C	G	0.75	1.14 (1.09-1.18)	7.6.E-12	0.57	1.16 (1.12-1.21)	2.8.E-12	1.15 (1.12-1.18)	3.6E-22	0.16

\*Novel variants in bold; position based on hg19

<sup>†</sup>CGGCTAAGGGGAGAGAGCCCGAAGCCACGCACACCGGCGCAAGGGGCGGATA

<sup>‡</sup>AAGGGAG

<sup>§</sup>Frequency data not available in the association summary statistics were retrieved from statistics in the 1000 Genomes Project phase 3.

<sup>¶</sup>or rs59279623

Chr, chromosome; EA, effect allele; NEA, non-effect allele; Freq, frequency of EA; OR, odds ratio; CI, confidence interval; P<sub>het</sub>, p value from a Cochrane's Q test for heterogeneity in effect sizes.

**Supplementary Table 2 | RA associations of the newly identified loci in East Asians**

Variant	Chr:Position <sup>†</sup>	Nearest gene	EA/NEA	Korean*					Japanese			East Asian		
				Freq <sub>KOR</sub>	OR <sub>KOR1</sub>	OR <sub>KOR2</sub>	OR <sub>KOR</sub> (95%CI)	P <sub>KOR</sub>	Freq	OR (95%CI)	P	OR (95%CI)	P	P <sub>HET</sub>
rs6705628	2:74208362	<i>DGUOK-AS1</i>	T/C	0.19	0.86	0.89	0.87 (0.81-0.92)	1.6.E-05	0.17	0.89 (0.84-0.95)	2.0.E-04	0.88 (0.84-0.92)	2.1.E-08	0.91
rs2918392	5:10704797	<i>DAP</i>	T/C	0.26	0.97	0.85	0.95 (0.89-1.00)	4.9.E-02	0.31	0.95 (0.91-1.00)	3.1.E-02	0.95 (0.91-0.98)	3.9.E-03	0.68
rs660442	11:64042997	<i>BAD</i>	A/G	0.08	0.80	0.89	0.82 (0.74-0.90)	4.8.E-05	0.08	0.86 (0.79-0.93)	1.2.E-04	0.84 (0.79-0.89)	3.9.E-08	0.89
rs59578717	11:68859848	<i>TPCN2</i>	Ins1 <sup>‡</sup> /C	0.51	0.89	0.91	0.90 (0.85-0.94)	1.6.E-05	0.51	0.92 (0.88-0.96)	4.0.E-04	0.91 (0.88-0.94)	4.3.E-08	0.88
rs12795702	11:128156314	<i>LOC107984408</i>	A/G	0.76	1.14	1.15	1.14 (1.08-1.21)	6.3.E-06	0.77	1.07 (1.02-1.13)	6.6.E-03	1.11 (1.06-1.15)	5.8.E-07	0.39
rs4963581	12:24813281	<i>LOC105369698</i>	A/G	0.74	1.09	1.10	1.09 (1.03-1.16)	2.4.E-03	0.75	1.09 (1.04-1.15)	6.8.E-04	1.09 (1.05-1.13)	6.6.E-06	1.00
rs199894206	15:91038883	<i>IQGAP1</i>	CT/C	0.38	1.10	1.21	1.12 (1.07-1.18)	7.9.E-06	0.34	1.12 (1.07-1.17)	2.7.E-06	1.12 (1.08-1.16)	1.5.E-10	0.97
rs149041927 <sup>§</sup>	16:23871206	<i>PRKCB</i>	A/Ins2 <sup>¶</sup>	0.39	0.89	0.92	0.90 (0.85-0.94)	3.1.E-05	0.36	0.91 (0.87-0.96)	1.2.E-04	0.91 (0.88-0.94)	2.2.E-08	0.38
rs12918327	16:30626616	<i>ZNF689</i>	T/C	0.09	1.04	1.12	1.06 (0.97-1.15)	1.9.E-01	0.11	1.12 (1.04-1.20)	2.0.E-03	1.09 (1.03-1.16)	1.6.E-03	0.85
rs6011186	20:62484008	<i>C20orf181</i>	T/C	0.37	0.87	0.87	0.87 (0.82-0.91)	1.5.E-07	0.38	0.92 (0.88-0.97)	1.0.E-03	0.90 (0.87-0.93)	3.7.E-09	0.78
rs35156883	22:45746152	<i>SMC1B</i>	A/AT	0.49	1.12	1.10	1.12 (1.06-1.17)	9.4.E-06	0.54	1.08 (1.04-1.13)	2.8.E-04	1.10 (1.06-1.13)	1.9.E-08	0.38

\*The Korean population consists of two independent case-control collections (KOR1 and KOR2; Kwon et al., Ann Rheum Dis. 2020; PMID: 32723749). The sample sizes of the KOR1 and KOR2 are 35,997 and 4,488, respectively.

<sup>†</sup>Based on hg19

<sup>‡</sup>CGGCTAAGGGGAGAGAGCCCGGAAGCCACGCACACCGGCGCAAGGGGCGGATA

<sup>¶</sup>AAGGGAG

<sup>§</sup>or rs59279623

Chr, chromosome; EA, effect allele; NEA, non-effect allele; Freq, frequency of EA; OR, odds ratio; CI, confidence interval; P<sub>HET</sub>, p value from a Cochran's Q test for heterogeneity in effect sizes.

Supplementary Table 3 | Functional annotations of lead variants and their proxies ( $r^2 \geq 0.9$ ) in novel loci

Locus No	Chr	Position (hg19)	rs number	$r^2$ with a lead variant		Annotations in RA-associated tissues									
				CHB+JPT	EUR	RegulomeDB	Conserved	Promoter histone marks	Enhancer histone marks	TF	eGenes	RegulomeDB QTL	Nearest gene	Location	
1	2	74207634	rs371092749	1.00	1.00	N.A.	N.A.	N.A.	N.A.	N.A.	N.A.	N.A.	DGUOK-AS1	Intron	
1	2	74207645	rs2421690	1.00	1.00	<b>2b</b>	-	Yes	Yes	-	-	-	DGUOK-AS1	Intron	
1	2	74208362	<b>rs6705628</b>	self	self	4	-	Yes	Yes	CMYC, HEY1, MAX, POL2, POL24H8	-	-	DGUOK-AS1	Non Coding Transcript Variant	
1	2	74213245	rs2272165	1.00	1.00	<b>1b</b>	Yes	Yes	Yes	ZBTB7A	-	Yes	TET3	5'UTR	
1	2	74215701	rs12328448	1.00	1.00	4	-	Yes	Yes	-	-	-	TET3	Intron	
1	2	74216755	rs10197238	1.00	1.00	4	-	-	-	-	-	-	TET3	Intron	
1	2	74216764	rs10208256	1.00	1.00	4	-	-	-	-	-	-	TET3	Intron	
1	2	74216775	rs67919009	1.00	1.00	N.A.	-	Yes	Yes	-	-	N.A.	TET3	Intron	
1	2	74217856	rs6546883	1.00	1.00	5	-	-	Yes	-	-	-	TET3	Intron	
1	2	74219306	rs4852999	1.00	1.00	4	-	-	Yes	-	-	-	TET3	Intron	
1	2	74219948	rs10207365	1.00	1.00	6	-	-	-	-	-	-	TET3	Intron	
2	5	10682230	rs7715399	0.91	0.91	3a	-	-	Yes	-	-	-	DAP	Intron	
2	5	10687002	rs6881964	0.93	0.91	5	-	-	-	-	-	-	DAP	Intron	
2	5	10689562	rs3776414	0.93	0.94	4	-	-	-	CTCF, MAFK, NFE2	-	-	DAP	Intron	
2	5	10689768	rs3822412	0.93	0.94	4	-	-	-	CTCF	-	-	DAP	Intron	
2	5	10690749	rs5745271	0.93	0.91	<b>1f</b>	-	-	-	-	-	Yes	DAP	Intron	
2	5	10691118	rs5745264	0.92	0.93	5	-	-	-	-	-	-	DAP	Intron	
2	5	10695526	rs2930047	0.92	0.94	<b>1f</b>	-	-	Yes	YY1	-	Yes	DAP	Intron	
2	5	10698569	rs2930048	1.00	0.95	5	-	-	-	-	-	-	DAP	Intron	
2	5	10699878	rs3842028	0.93	0.96	<b>2a</b>	-	-	Yes	-	-	-	DAP	Intron	
2	5	10704797	<b>rs2918392</b>	self	self	5	-	Yes	Yes	-	-	-	DAP	Intron	
3	11	64042997	<b>rs660442</b>	self	self	3a	-	-	-	-	-	-	AP003774.1, AP003774.6, CCDC88B, NUDT22, PRDX5, RPS6KA4	BAD	Intron
4	11	68859848	<b>rs59578717</b>	self		4	-	-	-	-	-	-	TPCN2	Intergenic	
5	11	128156314	<b>rs12795702</b>	self	self	5	-	-	Yes	-	-	-	ETS1	Intergenic	
6	12	24809818	rs11494744	0.96	1.00	6	-	-	-	-	-	-	C12orf67	Intergenic	
6	12	24810552	rs11494745	0.99	1.00	7	-	-	-	-	-	-	C12orf67	Intergenic	
6	12	24813281	<b>rs4963581</b>	self	self	7	-	-	-	-	-	-	C12orf67	Intergenic	
7	15	91038883	<b>rs199894206</b>	self		6	-	-	-	-	-	-	IQGAP1	Intron	
8	16	23871206	<b>rs149041927</b>	self		5	-	Yes	Yes	-	-	-	PRKCB	Intron	
8	16	23873919	rs8052865	0.91		3a	-	Yes	Yes	-	PRKCB	-	PRKCB	Intron	
8	16	23873921	rs12923695	0.91		3a	-	Yes	Yes	-	PRKCB	-	PRKCB	Intron	
8	16	23874549	rs62030652	0.95		5	-	-	Yes	-	-	-	PRKCB	Intron	
8	16	23875683	rs11862363	0.98		4	-	Yes	Yes	-	PRKCB	-	PRKCB	Intron	
8	16	23876030	rs8063402	0.98		4	-	Yes	Yes	-	PRKCB	-	PRKCB	Intron	
8	16	23877175	rs3826261	0.98		5	-	-	Yes	-	PRKCB	-	PRKCB	Intron	
8	16	23877342	rs9806904	0.98		<b>2b</b>	-	-	Yes	-	PRKCB	-	PRKCB	Intron	
8	16	23877489	rs3826259	0.98		<b>1f</b>	Yes	-	Yes	-	PRKCB	Yes	PRKCB	Intron	
8	16	23878119	rs8044722	0.98		4	-	-	Yes	-	DCTN5	-	PRKCB	Intron	
8	16	23878688	rs12920718	0.98		5	-	-	Yes	-	PRKCB	-	PRKCB	Intron	
8	16	23878751	rs11645733	0.98		5	-	-	Yes	-	-	-	PRKCB	Intron	
8	16	23879382	rs6497692	0.98		4	-	-	Yes	-	-	-	PRKCB	Intron	
8	16	23880064	rs8055985	0.98		3a	-	-	Yes	-	-	-	PRKCB	Intron	
8	16	23880076	rs8056286	0.97		4	-	-	Yes	-	-	-	PRKCB	Intron	
8	16	23880097	rs8056423	0.98		3a	-	-	Yes	-	-	-	PRKCB	Intron	
8	16	23880477	rs7404819	0.98		3a	-	Yes	Yes	-	-	-	PRKCB	Intron	
8	16	23880480	rs35030326	0.98		3a	-	Yes	Yes	-	PRKCB	-	PRKCB	Intron	
8	16	23880873	rs12931116	0.98		5	-	-	Yes	-	PRKCB	-	PRKCB	Intron	

8	16	23880943	rs11648799	0.98		5	-	-	Yes	-	-	-	-	PRKCB	Intron	
8	16	23881080	rs55881781	0.98		5	-	-	Yes	-	-	-	-	PRKCB	Intron	
8	16	23881091	rs12931600	0.98		5	-	-	Yes	-	-	-	PRKCB	PRKCB	Intron	
8	16	23881203	rs56098067	0.96		6	-	-	Yes	-	-	-	-	PRKCB	Intron	
8	16	23881297	rs56405227	0.96		5	-	-	Yes	-	-	-	-	PRKCB	Intron	
8	16	23881428	rs7405331	0.98		5	-	-	Yes	-	-	-	-	PRKCB	Intron	
8	16	23881976	rs8046693	0.98		4	-	-	Yes	-	-	-	PRKCB	PRKCB	Intron	
8	16	23882044	rs8047317	0.98		1f	-	-	Yes	-	-	Yes	-	PRKCB	Intron	
8	16	23882332	rs11644964	0.96		3a	-	-	Yes	-	-	-	-	PRKCB	Intron	
8	16	23882548	rs1468130	0.96		1f	-	-	Yes	-	-	Yes	PRKCB	PRKCB	Intron	
8	16	23882763	rs7189228	0.96		5	-	-	Yes	-	-	-	-	PRKCB	Intron	
8	16	23882921	rs7194054	0.96		3a	-	-	Yes	-	-	-	-	PRKCB	Intron	
8	16	23883010	rs57803503	0.96		4	-	-	Yes	-	-	-	PRKCB	PRKCB	Intron	
8	16	23884122	rs12929938	0.96		5	-	-	Yes	-	-	-	PRKCB	PRKCB	Intron	
8	16	23885286	rs12934555	0.96		5	Yes	-	Yes	-	-	-	PRKCB	PRKCB	Intron	
9	16	30584430	rs34114657	0.92	0.94	5	-	-	Yes	-	-	-	KAT8	-	ZNF688	Intergenic
9	16	30603521	rs34699226	0.97	0.98	6	-	-	-	-	-	-	KAT8, RNF40	-	ZNF785	Intergenic
9	16	30610876	rs35661204	1.00	0.99	4	-	-	-	-	-	-	KAT8	-	ZNF689	Intergenic
9	16	30619601	rs374903175	0.90	0.96	N.A.	N.A.	N.A.	N.A.	N.A.	N.A.	N.A.	N.A.	-	ZNF689	Intergenic
9	16	30626616	rs12918327	self	self	1e	-	Yes	Yes	-	-	Yes	RNF40	-	ZNF689	Intergenic
10	20	62481460	rs6062547	0.91	0.98	4	-	-	Yes	BCL3	-	-	LIME1, TPD52L2, ZGPAT	-	ABHD16B	Intergenic
10	20	62481686	rs73624755	0.91	0.98	5	-	-	Yes	-	-	-	-	-	ABHD16B	Intergenic
10	20	62482220	rs12624502	0.91	0.98	2b	-	-	Yes	EBF1, SP1, USF1, USF2, ZEB1	-	-	-	-	ABHD16B	Intergenic
10	20	62482223	rs12624434	0.91	0.98	3a	-	-	Yes	EBF1, SP1, USF1, USF2, ZEB1	-	-	-	-	ABHD16B	Intergenic
10	20	62482273	rs12624512	0.91	0.98	4	-	-	Yes	CHD2, EBF1, MAX, NFKB, P300, POL24H8, PU1, SP1, TCF12, USF1, USF2, ZEB1	-	-	-	-	ABHD16B	Intergenic
10	20	62483066	rs6011184	0.92	1.00	2c	-	-	Yes	-	-	-	-	-	ABHD16B	Intergenic
10	20	62484008	rs6011186	self	self	5	-	-	Yes	-	-	-	-	-	ABHD16B	Intergenic
11	22	45714937	rs6006984	0.93		1d	-	Yes	Yes	-	-	Yes	FAM118A, RIBC2, SMC1B, UPK3A	Yes	FAM118A	Intron
11	22	45715608	rs6519922	0.93		1f	-	Yes	Yes	-	-	Yes	FAM118A, RIBC2, SMC1B, UPK3A	Yes	FAM118A	Intron
11	22	45715624	rs6519923	0.93		4	-	Yes	Yes	-	-	-	FAM118A, RIBC2	-	FAM118A	Intron
11	22	45716397	rs8138866	0.93		5	-	Yes	Yes	-	-	-	FAM118A, RIBC2, SMC1B	-	FAM118A	Intron
11	22	45717524	rs6007587	0.93		5	-	-	Yes	-	-	-	FAM118A, RIBC2, SMC1B	-	FAM118A	Intron
11	22	45717859	rs720682	0.93		1d	-	-	Yes	EBF1	-	Yes	FAM118A, RIBC2, SMC1B, UPK3A	Yes	FAM118A	Intron
11	22	45718041	rs1473953	0.93		1f	-	-	Yes	EBF1	-	Yes	FAM118A, RIBC2, SMC1B, UPK3A	Yes	FAM118A	Intron
11	22	45723116	rs6006985	0.97		5	-	-	-	-	-	-	FAM118A, RIBC2, SMC1B	-	FAM118A	Intron
11	22	45723320	rs6006987	0.97		4	-	-	-	-	-	-	FAM118A, RIBC2, SMC1B	-	FAM118A	Intron
11	22	45723807	rs11556482	0.97		4	Yes	-	-	-	-	-	FAM118A, RIBC2, SMC1B	-	FAM118A	Missense
11	22	45723842	rs17851057	0.97		3a	Yes	-	-	-	-	-	FAM118A, RIBC2, SMC1B	-	FAM118A	Synonymous
11	22	45724513	rs34080495	0.94		5	-	-	-	-	-	-	-	-	FAM118A	Intron
11	22	45724727	rs6007592	0.97		3a	-	-	-	-	-	-	FAM118A, RIBC2, SMC1B	-	FAM118A	Intron
11	22	45724999	rs736037	0.96		2c	-	-	-	-	-	-	FAM118A, RIBC2	-	FAM118A	Intron
11	22	45725106	rs6006988	0.96		1d	-	-	-	-	-	Yes	FAM118A, RIBC2	Yes	FAM118A	Intron
11	22	45725276	rs2350628	0.96		1f	-	-	-	-	-	Yes	FAM118A, RIBC2, UPK3A	Yes	FAM118A	Intron
11	22	45725392	rs742013	0.96		1b	-	-	-	-	-	Yes	FAM118A, RIBC2, UPK3A	Yes	FAM118A	Intron
11	22	45725524	rs742014	0.96		1f	-	-	-	-	-	Yes	FAM118A, RIBC2, UPK3A	Yes	FAM118A	Intron
11	22	45725600	rs736702	0.95		1f	-	-	-	-	-	Yes	FAM118A, RIBC2, UPK3A	Yes	FAM118A	Intron
11	22	45727565	rs1569414	0.92		1f	-	-	-	-	-	Yes	FAM118A, RIBC2, UPK3A	Yes	FAM118A	Intron
11	22	45727688	rs1569415	0.92		7	-	-	-	-	-	-	FAM118A, RIBC2	-	FAM118A	Intron
11	22	45727778	rs138809539	0.92		7	-	-	-	-	-	-	-	-	FAM118A	Intron
11	22	45728163	rs10592722	0.92		2b	-	-	-	-	-	-	-	-	FAM118A	Intron
11	22	45728370	rs6007594	0.92		1f	Yes	-	-	-	-	Yes	FAM118A, RIBC2, UPK3A	Yes	FAM118A	Missense

11	22	45729382	rs7284348	0.96		7	-	-	-	-	-	FAM118A, RIBC2	-	FAM118A	Intron
11	22	45729424	rs6006989	0.92		7	-	-	-	-	-	FAM118A, RIBC2	-	FAM118A	Intron
11	22	45743242	rs12160956	0.99		1f	-	-	-	-	-	FAM118A, RIBC2, SMC1B, UPK3A	Yes	SMC1B	Intron
11	22	45745229	rs9614460	0.99		6	-	-	-	-	-	FAM118A, RIBC2, SMC1B	-	SMC1B	Intron
11	22	45745948	rs6006733	1.00		1b	-	-	-	-	-	FAM118A, RIBC2, SMC1B, UPK3A	Yes	SMC1B	Intron
11	22	45746152	rs35156883	self		6	-	-	-	-	-	FAM118A, RIBC2, SMC1B	-	SMC1B	Intron
11	22	45746579	rs6006994	1.00		1f	-	-	-	-	-	FAM118A, RIBC2, SMC1B	Yes	SMC1B	Intron
11	22	45748812	rs6006995	1.00		4	-	-	-	-	-	FAM118A, RIBC2, SMC1B	-	SMC1B	Intron
11	22	45750250	rs6006996	0.96		5	-	-	Yes	-	-	FAM118A	-	SMC1B	Intron
11	22	45764165	rs7291368	0.93		6	-	-	-	-	-	FAM118A, RIBC2, SMC1B	Yes	SMC1B	Intron
11	22	45764617	rs11323907	0.95		5	-	-	-	-	-	FAM118A, RIBC2, SMC1B	-	SMC1B	Intron
11	22	45768749	rs6007002	0.95		5	-	-	-	-	-	FAM118A, RIBC2, SMC1B	-	SMC1B	Intron
11	22	45769906	rs6006736	0.99		6	-	-	-	-	-	FAM118A, RIBC2, SMC1B	-	SMC1B	Intron
11	22	45774080	rs6007005	0.95		7	-	-	Yes	-	-	FAM118A, RIBC2, SMC1B	Yes	SMC1B	Intron
11	22	45778382	rs6519847	0.94		5	-	-	-	-	-	FAM118A, RIBC2, SMC1B	-	SMC1B	Intron
11	22	45779170	rs2350929	0.94		6	-	-	-	-	-	FAM118A, RIBC2, SMC1B	-	SMC1B	Intron
11	22	45779553	rs11090629	0.94		6	-	-	-	-	-	FAM118A, RIBC2, SMC1B	-	SMC1B	Intron
11	22	45780282	rs2350930	0.94		5	-	-	-	-	-	FAM118A, RIBC2, SMC1B	-	SMC1B	Intron
11	22	45781388	rs6007007	0.94		6	-	-	-	-	-	FAM118A, RIBC2, SMC1B	-	SMC1B	Intron
11	22	45781508	rs6007009	0.94		7	Yes	-	-	-	-	FAM118A, RIBC2, SMC1B, UPK3A	Yes	SMC1B	Intron
11	22	45782903	rs6007010	0.94		7	Yes	-	-	-	-	FAM118A, RIBC2, SMC1B, UPK3A	Yes	SMC1B	Synonymous
11	22	45783093	rs6006737	0.93		7	-	-	-	-	-	FAM118A, RIBC2, SMC1B	-	SMC1B	Intron
11	22	45783352	rs34741782	0.94		6	-	-	-	-	-	-	-	SMC1B	Intron
11	22	45783924	rs6007011	0.94		5	-	-	-	-	-	FAM118A, RIBC2, SMC1B	-	SMC1B	Intron
11	22	45784172	rs6007012	0.94		7	-	-	-	-	-	FAM118A, RIBC2, SMC1B	Yes	SMC1B	Intron
11	22	45784799	rs6006739	0.93		6	-	-	-	-	-	FAM118A, RIBC2, SMC1B	-	SMC1B	Intron
11	22	45785840	rs8138001	0.94		6	-	-	-	-	-	FAM118A, RIBC2, SMC1B, UPK3A	-	SMC1B	Intron
11	22	45786123	rs8136997	0.94		7	-	-	-	-	-	FAM118A, RIBC2, SMC1B, UPK3A	Yes	SMC1B	Intron
11	22	45787512	rs6007017	0.93		7	-	-	-	-	-	FAM118A, RIBC2, SMC1B, UPK3A	Yes	SMC1B	Intron
11	22	45787521	rs6007018	0.93		7	-	-	-	-	-	FAM118A, RIBC2, SMC1B	-	SMC1B	Intron
11	22	45788155	rs2350931	0.94		6	-	-	-	-	-	FAM118A, RIBC2, SMC1B	Yes	SMC1B	Intron
11	22	45788896	rs7284306	0.94		7	-	-	-	-	-	FAM118A, RIBC2, SMC1B, UPK3A	Yes	SMC1B	Intron
11	22	45790132	rs6007020	0.94		7	-	-	-	-	-	FAM118A, RIBC2, SMC1B	-	SMC1B	Intron
11	22	45793010	rs10717441	0.94		7	Yes	-	-	-	-	FAM118A	-	SMC1B	Intron
11	22	45794723	rs2882538	0.94		6	-	-	-	-	-	FAM118A, RIBC2, SMC1B	-	SMC1B	Intron
11	22	45800569	rs374660472	0.95		N.A.	N.A.	N.A.	N.A.	N.A.	N.A.	N.A.	N.A.	SMC1B	Intron
11	22	45801245	rs6007021	0.95		5	-	-	-	-	-	FAM118A, RIBC2, SMC1B	-	SMC1B	Intron
11	22	45801432	rs6006742	0.95		5	-	-	-	-	-	FAM118A, RIBC2, SMC1B	-	SMC1B	Intron
11	22	45804414	rs1569437	0.95		7	-	-	-	-	-	FAM118A, RIBC2, SMC1B, UPK3A	Yes	SMC1B	Intron
11	22	45805134	rs6007023	0.95		6	-	-	-	-	-	FAM118A, RIBC2, SMC1B	Yes	SMC1B	Intron
11	22	45805523	rs6006743	0.95		1f	-	-	-	-	-	FAM118A, RIBC2, SMC1B, UPK3A	Yes	SMC1B	Intron
11	22	45806310	rs6006744	0.95		7	-	-	-	-	-	FAM118A, RIBC2, SMC1B	-	SMC1B	Intron
11	22	45807907	rs6007025	0.95		6	-	-	-	-	-	FAM118A, RIBC2, SMC1B	-	SMC1B	Intron

All data were retrieved from HaploReg v4.1 and RegulomeDB v2.0. LD values were calculated from the 1000 Genomes Project phase 3 data in ethnicity-matched populations [for East Asian, Han Chinese in Beijing (CHB) and Japanese in Tokyo (JPT)]; for European, all European sub-populations. For the eight loci where we identified the RA association of lead variants using both East Asian and European populations, proxies were extracted only when the proxies are in high LD ( $r^2 > 0.9$ ) with a lead variant in both populations. Proxies in the other four loci (Locus No. 4, 7, 8, & 11; where the lead variants were tested only in East Asians) were extracted based on  $r^2$  values in CHB+JPT.

RegulomeDB category 1 and 2 are marked in red.

Conserved: defined as conserved by either GERP or SiPhy algorithm

Promoter histone marks: promoter-specific ChromHMM chromatin states (1\_TssA, 2\_TssAFlnk, 10\_TssBiv, and 11\_BivFlnk).

Enhancer histone marks: enhancer-specific ChromHMM chromatin states (6\_EnhG, 7\_Enh, and 12\_EnhBiv).

TF: proteins detected in ENCODE ChIP-seq experiments

eGenes: eGenes regulated by the variant

RegulomeDB\_QTL: QTLs listed in RegulomeDB

"-": no hits, N.A.: missing annotations





**Supplementary Table 4 | Additional association signals in RA loci**

Index variant	Chr:Position (hg19)	Signal	Conditioned variant	EA/NEA	East Asian				European				Meta-analysis			
					Freq	bC	bC_se	pC	Freq	bC	bC_se	pC	bMETA	bMETA_se	pMETA	pHET
rs2235909	1:17429774	secondary	rs2301888	T/G	0.522	-0.080	0.018	5.50E-06	0.326	-0.084	0.022	1.00.E-04	-0.081	0.014	2.24E-09	0.86
rs2558210	2:204636190	secondary	rs3087243	A/G	0.565	0.085	0.017	4.06E-07	0.263	0.079	0.017	4.04E-06	0.082	0.012	7.69E-12	0.80
rs17264332	6:138005515	secondary	rs7749323	A/G	0.000	NA	NA	NA	0.779	-0.128	0.018	1.36E-12		NA		
rs11594656	10:6122009	secondary	rs3134883	A/T	0.009	-0.144	0.051	4.82.E-03	0.320	-0.095	0.018	1.65E-07	-0.100	0.017	4.21E-09	0.36
rs502919	10:6393260	secondary	rs4750316	C/G	0.087	-0.054	0.028	4.90.E-02	0.180	-0.111	0.020	2.02E-08	-0.092	0.016	1.17E-08	0.09
rs35576264	10:63959929	secondary	rs71508903	T/C	0.085	0.146	0.028	2.40E-07	0.221	0.074	0.023	1.32.E-03	0.103	0.018	8.76E-09	0.05
rs10152590	15:70048116	secondary	rs7170107	A/T	0.965	0.105	0.042	1.25.E-02	0.900	0.155	0.028	5.55E-08	0.139	0.024	3.68E-09	0.33
rs9373203	6:138289848	tertiary	rs7749323, rs17264332	T/C	0.394	0.073	0.018	3.72E-05	0.618	0.072	0.016	1.18E-05	0.073	0.012	1.78E-09	0.94

EA/NEA: effect allele / non-effect allele

Freq: frequency of the effect allele

bC, bC\_se, pC: beta (=effect size), standard error and p-value from conditional analyses

bMETA, bMETA\_se, pMETA: beta (=effect size), standard error and p-value from meta-analyses with two conditional results

pHET: p value from a Cochran's Q test for heterogeneity in effect sizes from conditional analyses

Supplementary Table 5 | Enrichment of partitioned RA heritability in transcription factor binding sites

TF	meta			East Asians							Europeans						
	t	p	p adj	Prop. SNPs	Prop. h <sup>2</sup>	Prop. h <sup>2</sup> SD	Enrichment	Enrichment SD	Enrichment p	Prop. SNPs	Prop. h <sup>2</sup>	Prop. h <sup>2</sup> SD	Enrichment	Enrichment SD	Enrichment p		
ARID3A	3.5	4.8E-01	7.2E-01	0.29%	2.68%	3.88%	9.3	13.4	5.3E-01	0.29%	4.35%	4.24%	14.8	14.5	3.4E-01		
ATF1	10.5	3.3E-02	1.1E-01	0.13%	-5.25%	1.89%	-41.3	14.9	6.1E-03	0.13%	0.53%	2.39%	4.2	18.7	8.7E-01		
<b>ATF2</b>	40.8	2.9E-08	5.8E-07	0.41%	19.03%	4.71%	46.5	11.5	2.2E-05	0.41%	19.06%	4.50%	46.5	11.0	6.2E-05		
ATF3	0.7	9.5E-01	9.9E-01	0.25%	-0.78%	3.34%	-3.2	13.6	7.6E-01	0.25%	-0.08%	3.18%	-0.3	12.9	9.2E-01		
BACH1	5.9	2.1E-01	4.4E-01	0.14%	4.28%	2.36%	29.5	16.3	9.0E-02	0.15%	1.45%	2.41%	9.9	16.4	5.9E-01		
<b>BATF</b>	26.2	2.9E-05	2.9E-04	0.22%	13.69%	4.63%	61.9	21.0	3.0E-03	0.22%	18.98%	5.38%	85.1	24.1	7.0E-04		
BCL11A	15.7	3.4E-03	1.6E-02	0.16%	9.55%	3.23%	58.6	19.8	3.4E-03	0.16%	5.96%	3.67%	36.6	22.5	1.1E-01		
<b>BCL3</b>	19.8	5.5E-04	4.2E-03	0.32%	10.21%	3.64%	32.2	11.5	5.8E-03	0.32%	12.60%	4.63%	39.5	14.5	8.7E-03		
BCLAF1	9.4	5.3E-02	1.6E-01	0.13%	5.38%	3.40%	42.0	26.6	1.1E-01	0.13%	6.39%	3.66%	49.8	28.5	8.7E-02		
BDP1	0.1	1.0E+00	1.0E+00	0.01%	-0.01%	0.70%	-0.5	65.4	9.8E-01	0.01%	0.02%	0.53%	2.1	49.5	9.8E-01		
<b>BHLHE40</b>	16.3	2.6E-03	1.5E-02	0.44%	15.05%	5.41%	34.2	12.3	8.9E-03	0.44%	10.74%	4.81%	24.4	10.9	3.2E-02		
BRCA1	2.1	7.2E-01	8.9E-01	0.10%	-1.64%	2.12%	-16.3	21.1	4.2E-01	0.10%	-0.37%	2.11%	-3.6	20.9	8.2E-01		
BRF1	4.9	2.9E-01	5.4E-01	0.01%	0.61%	0.63%	118.4	122.1	3.3E-01	0.01%	-0.36%	0.32%	-68.0	60.5	2.5E-01		
BRF2	3.5	4.8E-01	7.2E-01	0.01%	-0.45%	0.51%	-35.1	39.4	3.6E-01	0.01%	-0.45%	0.66%	-35.1	51.9	4.8E-01		
CBX3	7.6	1.1E-01	2.7E-01	0.31%	4.97%	3.11%	15.9	9.9	1.4E-01	0.31%	4.70%	3.17%	15.0	10.1	1.6E-01		
CCNT2	7.0	1.3E-01	3.1E-01	0.27%	14.69%	6.98%	54.7	26.0	4.3E-02	0.27%	-1.19%	3.80%	-4.4	14.1	7.0E-01		
CEBPB	5.2	2.6E-01	5.2E-01	1.35%	12.70%	1.51%	9.4	5.5	1.1E-01	1.36%	4.54%	7.07%	3.3	5.2	6.5E-01		
CEBPD	3.2	5.2E-01	7.3E-01	0.11%	3.06%	2.57%	29.0	24.3	2.3E-01	0.11%	-0.39%	2.61%	-3.6	24.5	8.5E-01		
CHD1	16.5	2.4E-03	1.4E-02	0.30%	14.76%	4.70%	48.4	15.4	2.2E-03	0.31%	6.61%	4.02%	21.5	13.1	1.2E-01		
CHD2	13.1	1.1E-02	4.3E-02	0.45%	16.90%	5.61%	37.8	12.5	3.2E-03	0.45%	4.14%	5.11%	9.3	11.5	4.6E-01		
CREB1	3.5	4.8E-01	7.2E-01	0.16%	-1.26%	3.04%	-8.0	19.3	6.4E-01	0.16%	-3.18%	3.02%	-20.0	19.0	2.8E-01		
CTBP2	4.0	4.1E-01	6.7E-01	0.13%	0.49%	1.54%	3.8	12.1	8.2E-01	0.13%	2.72%	1.86%	20.8	14.3	1.7E-01		
CTCF	7.8	9.9E-02	2.7E-01	2.11%	18.15%	7.39%	8.6	3.5	4.5E-02	2.10%	7.27%	6.71%	3.5	3.2	4.4E-01		
CTCF1	3.5	4.8E-01	7.2E-01	0.07%	2.58%	4.23%	36.8	60.3	5.5E-01	0.07%	2.68%	2.63%	38.7	38.0	3.2E-01		
E2F1	5.1	2.8E-01	5.3E-01	0.38%	6.41%	3.70%	16.7	9.6	9.5E-02	0.38%	1.30%	4.25%	3.4	11.1	8.3E-01		
E2F4	0.4	9.8E-01	1.0E+00	0.22%	0.79%	3.21%	3.6	14.4	8.6E-01	0.22%	-0.03%	3.35%	-0.1	15.0	9.4E-01		
E2F6	7.5	1.1E-01	2.7E-01	0.35%	4.98%	4.29%	14.1	12.2	2.8E-01	0.35%	7.65%	4.22%	21.7	12.0	8.3E-02		
<b>EBF1</b>	49.6	4.3E-10	1.4E-08	0.48%	25.31%	5.23%	52.3	10.8	1.2E-05	0.49%	29.29%	5.80%	59.9	11.9	1.4E-06		
EGR1	15.8	3.3E-03	1.6E-02	0.38%	18.97%	5.63%	49.6	14.7	2.0E-03	0.39%	6.33%	4.52%	16.4	11.7	1.9E-01		
ELF1	14.5	5.8E-03	2.5E-02	0.50%	11.08%	4.05%	22.0	8.0	7.0E-03	0.51%	8.33%	4.82%	16.5	9.5	9.9E-02		
<b>ELK1</b>	17.0	1.9E-03	1.2E-02	0.11%	7.11%	2.91%	61.9	25.3	1.3E-02	0.11%	7.06%	2.90%	62.1	25.5	1.5E-02		
ELK4	3.3	5.0E-01	7.3E-01	0.10%	-0.22%	1.82%	-2.2	18.1	8.6E-01	0.10%	2.60%	2.06%	26.2	20.8	2.2E-01		
<b>EP300</b>	40.0	4.3E-08	7.7E-07	1.59%	36.07%	7.88%	22.7	5.0	2.7E-06	1.60%	28.42%	8.18%	17.8	5.1	7.6E-04		
ESR1	6.8	1.5E-01	3.3E-01	0.27%	3.72%	2.80%	14.0	10.6	2.2E-01	0.27%	5.06%	3.40%	19.0	12.7	1.5E-01		
ESRRA	2.4	6.7E-01	8.4E-01	0.01%	0.26%	0.96%	17.6	65.3	8.0E-01	0.02%	0.82%	0.92%	54.1	60.7	3.8E-01		
ETS1	3.7	4.4E-01	7.1E-01	0.19%	4.54%	3.25%	23.4	16.7	1.6E-01	0.19%	0.14%	3.05%	0.7	15.7	9.9E-01		
<b>EZH2</b>	14.8	5.2E-03	2.3E-02	0.46%	5.68%	2.65%	12.2	5.7	4.3E-02	0.47%	7.57%	2.84%	16.0	6.0	1.4E-02		
FAM48A	1.6	8.0E-01	9.3E-01	0.03%	-0.28%	0.49%	-9.0	15.8	5.3E-01	0.03%	0.19%	0.77%	6.2	25.1	8.3E-01		
FOS	14.3	6.3E-03	2.7E-02	1.32%	19.66%	6.35%	14.9	4.8	3.3E-03	1.32%	8.17%	5.76%	6.2	4.4	2.3E-01		
FOSL1	4.9	3.0E-01	5.5E-01	0.09%	1.33%	2.19%	15.3	25.2	5.7E-01	0.09%	4.44%	3.08%	50.0	34.6	1.6E-01		
FOSL2	4.9	3.0E-01	5.4E-01	0.45%	3.68%	3.87%	8.2	8.6	4.0E-01	0.46%	-4.53%	4.08%	-9.9	8.9	2.1E-01		
FOXA1	1.8	7.6E-01	9.2E-01	0.77%	-2.62%	6.57%	-3.4	8.5	5.9E-01	0.77%	-1.47%	5.27%	-1.9	6.8	6.7E-01		
FOXA2	2.1	7.1E-01	8.9E-01	0.33%	3.08%	4.83%	9.3	14.6	5.7E-01	0.33%	-1.55%	3.73%	-4.7	11.2	6.1E-01		
<b>FOXM1</b>	43.7	7.4E-09	1.7E-07	0.34%	16.86%	4.21%	50.0	12.5	4.0E-05	0.34%	21.05%	4.61%	62.2	13.6	8.1E-06		
FOXP2	5.0	2.9E-01	5.3E-01	0.29%	5.71%	3.41%	19.5	11.7	9.6E-02	0.29%	0.92%	3.23%	3.2	11.0	8.4E-01		
GABPA	4.6	3.3E-01	5.9E-01	0.37%	6.76%	5.21%	18.3	14.1	2.3E-01	0.37%	3.56%	4.17%	9.6	11.2	4.4E-01		
GATA1	7.1	1.3E-01	3.1E-01	0.38%	7.63%	3.96%	19.9	10.3	4.4E-02	0.39%	2.04%	3.55%	5.2	9.1	6.4E-01		
GATA2	2.4	6.6E-01	8.4E-01	0.99%	4.37%	5.05%	4.4	5.1	5.0E-01	0.99%	3.24%	4.25%	3.3	4.3	6.0E-01		
GATA3	5.1	2.8E-01	5.3E-01	0.70%	-4.21%	3.61%	-6.1	5.2	1.7E-01	0.70%	3.88%	4.36%	5.5	6.2	4.6E-01		
GRp20	1.7	7.9E-01	9.3E-01	0.01%	-0.29%	0.48%	-37.6	63.0	5.4E-01	0.01%	-0.17%	0.64%	-22.9	87.4	7.8E-01		
GTF2B	0.7	9.6E-01	9.9E-01	0.04%	0.12%	1.37%	3.4	37.9	9.5E-01	0.04%	0.62%	1.90%	16.8	51.2	7.6E-01		
GTF2F1	3.8	4.4E-01	7.1E-01	0.23%	4.47%	3.60%	19.4	15.6	2.2E-01	0.23%	1.38%	2.91%	6.0	12.6	6.9E-01		
GTF3C2	3.3	5.1E-01	7.3E-01	0.05%	-1.27%	1.25%	-27.1	26.5	2.9E-01	0.05%	-0.43%	1.10%	-8.8	22.7	6.6E-01		
HDAC1	0.6	9.6E-01	9.9E-01	0.18%	1.14%	3.99%	6.2	21.6	8.1E-01	0.19%	-0.08%	2.72%	-0.4	14.4	9.2E-01		
HDAC2	4.8	3.1E-01	5.6E-01	0.33%	2.71%	4.61%	8.1	13.8	6.0E-01	0.34%	-4.58%	3.42%	-13.6	10.2	1.5E-01		
HDAC6	2.7	6.1E-01	8.1E-01	0.01%	0.82%	0.81%	64.0	63.4	3.2E-01	0.01%	-0.14%	0.64%	-11.0	50.5	8.1E-01		
HDAC8	8.8	6.6E-02	2.0E-01	0.03%	3.18%	2.27%	95.4	68.0	1.8E-01	0.03%	1.83%	1.00%	57.6	31.4	7.0E-02		
HMG3	5.8	2.1E-01	4.5E-01	0.22%	5.52%	3.21%	24.8	14.4	8.8E-02	0.23%	1.90%	3.48%	8.4	15.4	6.3E-01		
HNF4A	0.7	9.5E-01	9.9E-01	0.20%	-0.73%	2.88%	-3.5	14.1	7.5E-01	0.21%	-0.02%	3.04%	-0.1	14.7	9.4E-01		
HNF4G	3.6	4.6E-01	7.2E-01	0.18%	-1.01%	2.64%	-5.6	14.6	6.5E-01	0.18%	3.82%	3.15%	21.1	17.4	2.5E-01		
HSF1	7.1	1.3E-01	3.1E-01	0.02%	2.13%	1.13%	123.6	65.6	5.8E-02	0.02%	-0.57%	0.87%	-31.8	48.5	4.9E-01		
IKZF1	15.8	3.3E-03	1.6E-02	0.16%	3.46%	2.72%	21.9	17.2	2.3E-01	0.16%	11.46%	3.56%	72.7	22.6	1.6E-03		

IRF1	3.7	4.5E-01	7.2E-01	0.27%	0.43%	3.53%	1.6	13.3	9.6E-01	0.27%	5.84%	3.96%	21.7	14.7	1.6E-01
IRF3	3.5	4.9E-01	7.2E-01	0.02%	-0.99%	0.81%	-50.5	41.3	2.2E-01	0.02%	-0.23%	1.02%	-11.3	50.9	8.1E-01
IRF4	19.6	5.9E-04	4.3E-03	0.18%	6.52%	2.84%	36.8	16.1	2.4E-02	0.18%	11.63%	3.78%	65.3	21.2	2.2E-03
JUN	1.4	8.4E-01	9.5E-01	0.60%	2.50%	4.27%	4.2	7.2	6.5E-01	0.60%	-0.84%	4.41%	-1.4	7.4	7.4E-01
JUNB	0.2	9.9E-01	1.0E+00	0.15%	0.12%	2.51%	0.8	16.3	9.9E-01	0.15%	-0.14%	2.51%	-0.9	16.2	9.1E-01
JUND	7.6	1.1E-01	2.7E-01	1.08%	13.84%	6.07%	12.8	5.6	2.6E-02	1.09%	-0.17%	6.61%	-0.2	6.1	8.5E-01
KAP1	6.3	1.8E-01	3.9E-01	0.65%	7.34%	6.25%	11.3	9.6	2.8E-01	0.66%	6.19%	3.93%	9.4	6.0	1.6E-01
KDM5A	1.7	8.0E-01	9.3E-01	0.02%	-0.41%	0.76%	-27.3	50.9	5.8E-01	0.02%	0.34%	1.03%	22.2	66.2	7.5E-01
KDM5B	1.8	7.8E-01	9.2E-01	0.23%	3.49%	4.41%	15.1	19.0	4.5E-01	0.23%	0.55%	3.70%	2.4	15.8	9.3E-01
MAFF	4.1	3.9E-01	6.7E-01	0.44%	-3.96%	4.28%	-9.1	9.8	3.1E-01	0.44%	-2.90%	4.16%	-6.7	9.5	4.2E-01
MAFK	2.1	7.2E-01	8.9E-01	0.77%	-0.70%	5.18%	-0.9	6.7	7.8E-01	0.77%	-3.10%	5.34%	-4.0	6.9	4.6E-01
MAX	19.3	6.9E-04	4.8E-03	1.16%	23.85%	6.87%	20.5	5.9	1.3E-03	1.17%	12.51%	5.77%	10.7	4.9	5.0E-02
MAZ	21.6	2.4E-04	2.3E-03	0.67%	21.50%	6.19%	32.1	9.2	2.4E-04	0.68%	10.39%	5.74%	15.4	8.5	8.7E-02
MBD4	8.6	7.3E-02	2.1E-01	0.10%	3.20%	1.78%	32.3	18.0	7.3E-02	0.10%	3.09%	2.25%	30.1	22.0	1.9E-01
MEF2A	9.9	4.2E-02	1.3E-01	0.18%	0.31%	3.89%	1.7	21.7	9.7E-01	0.18%	7.95%	2.94%	44.4	16.4	7.2E-03
MEF2C	19.2	7.3E-04	4.9E-03	0.08%	4.05%	2.81%	49.4	34.3	1.4E-01	0.08%	8.50%	2.27%	105.5	28.2	5.1E-04
MTA3	46.5	1.9E-09	5.2E-08	0.21%	22.14%	3.99%	107.0	19.3	4.0E-07	0.21%	14.16%	3.77%	67.3	17.9	2.0E-04
MXI1	15.8	3.4E-03	1.6E-02	0.53%	20.34%	6.10%	38.1	11.4	6.3E-04	0.54%	3.28%	5.38%	6.1	10.0	6.1E-01
MYBL2	8.5	7.5E-02	2.1E-01	0.31%	5.08%	3.12%	16.4	10.1	1.3E-01	0.31%	5.68%	3.35%	18.2	10.7	1.1E-01
MYC	16.1	2.8E-03	1.5E-02	1.31%	15.02%	6.21%	11.5	4.7	1.9E-02	1.31%	15.39%	6.10%	11.7	4.6	1.6E-02
NANOG	1.3	8.5E-01	9.6E-01	0.04%	0.19%	1.14%	4.6	26.9	8.9E-01	0.04%	-0.67%	1.28%	-15.5	29.5	5.7E-01
NFATC1	34.3	6.5E-07	9.5E-06	0.20%	13.38%	3.00%	66.1	14.8	3.6E-05	0.20%	10.96%	3.27%	53.9	16.1	9.8E-04
NFE2	3.6	4.7E-01	7.2E-01	0.03%	-0.14%	1.13%	-5.6	45.1	8.8E-01	0.02%	-1.21%	0.93%	-48.5	37.6	1.9E-01
NFIC	60.7	2.0E-12	8.2E-11	0.63%	29.38%	5.26%	46.4	8.3	2.4E-09	0.64%	24.21%	5.61%	38.1	8.8	2.7E-05
NFYA	3.8	4.3E-01	7.1E-01	0.10%	3.32%	2.52%	32.7	24.9	1.9E-01	0.10%	0.71%	2.32%	7.0	22.7	7.9E-01
NFYB	5.3	2.6E-01	5.1E-01	0.26%	5.15%	3.26%	20.0	12.6	1.4E-01	0.26%	2.17%	2.96%	8.5	11.6	5.2E-01
NR2C2	0.8	9.3E-01	9.9E-01	0.07%	0.93%	2.16%	13.6	31.6	6.8E-01	0.07%	0.00%	1.63%	0.0	23.8	9.7E-01
NR2F2	0.4	9.9E-01	1.0E+00	0.20%	0.71%	2.82%	3.5	14.0	8.6E-01	0.20%	0.09%	3.39%	0.4	16.8	9.7E-01
NR3C1	4.3	3.7E-01	6.5E-01	0.36%	4.46%	3.31%	12.3	9.1	2.0E-01	0.37%	-1.36%	3.19%	-3.7	8.7	5.9E-01
NRF1	3.2	5.3E-01	7.4E-01	0.09%	2.67%	3.03%	31.3	35.5	3.9E-01	0.09%	1.37%	2.01%	16.1	23.7	5.2E-01
PAX5	29.9	5.2E-06	5.6E-05	0.35%	16.87%	4.09%	48.4	11.7	1.4E-04	0.35%	14.54%	4.71%	41.6	13.5	2.3E-03
PBX3	1.0	9.2E-01	9.9E-01	0.08%	-0.54%	1.82%	-7.1	23.9	7.3E-01	0.08%	-0.27%	1.77%	-3.5	23.0	8.4E-01
PHF8	9.6	4.7E-02	1.5E-01	0.32%	10.16%	4.25%	31.3	13.1	1.7E-02	0.33%	2.75%	3.55%	8.4	10.8	4.9E-01
PML	36.0	2.9E-07	4.7E-06	0.44%	16.88%	4.11%	38.5	9.4	4.2E-05	0.44%	17.45%	4.69%	39.8	10.7	3.7E-04
POLR2A	111.1	4.3E-23	6.9E-21	2.98%	55.45%	6.69%	18.6	2.2	1.8E-15	2.99%	39.64%	5.49%	13.3	1.8	4.2E-10
POLR3G	1.1	9.0E-01	9.9E-01	0.01%	0.30%	0.67%	32.8	73.0	6.6E-01	0.01%	0.13%	0.89%	13.9	93.7	8.9E-01
POU2F2	13.2	1.0E-02	4.2E-02	0.30%	14.73%	6.27%	49.3	21.0	1.5E-02	0.30%	8.72%	5.00%	29.4	16.8	9.0E-02
POU5F1	2.4	6.6E-01	8.4E-01	0.03%	-0.18%	1.16%	-5.7	36.7	8.5E-01	0.03%	-0.86%	0.96%	-27.3	30.6	3.6E-01
PPARGC1A	2.5	6.4E-01	8.3E-01	0.02%	1.19%	1.25%	61.0	64.3	3.5E-01	0.02%	-0.17%	0.82%	-8.9	41.7	8.1E-01
PRDM1	16.2	2.7E-03	1.5E-02	0.04%	-2.72%	0.77%	-70.8	20.0	1.0E-03	0.04%	1.18%	1.10%	30.8	28.8	3.0E-01
RAD21	1.5	8.3E-01	9.5E-01	1.06%	-2.63%	6.49%	-2.5	6.1	5.6E-01	1.06%	-0.13%	6.09%	-0.1	5.7	8.4E-01
RBBP5	8.6	7.3E-02	2.1E-01	0.47%	9.95%	4.86%	21.1	10.3	3.6E-02	0.48%	4.92%	5.11%	10.3	10.7	3.8E-01
RCOR1	20.2	4.6E-04	3.7E-03	0.58%	21.59%	7.89%	37.2	13.6	7.2E-03	0.58%	14.95%	5.01%	25.8	8.7	5.7E-03
RDBP	4.2	3.8E-01	6.6E-01	0.01%	-0.49%	0.58%	-54.0	64.6	4.0E-01	0.01%	-0.60%	0.60%	-68.2	68.2	3.1E-01
RELA	83.1	3.9E-17	3.1E-15	0.54%	47.50%	6.65%	87.2	12.2	4.6E-12	0.55%	39.43%	7.30%	72.3	13.4	2.0E-07
REST	6.9	1.4E-01	3.3E-01	0.69%	10.10%	4.69%	14.7	6.8	3.9E-02	0.69%	1.80%	4.99%	2.6	7.3	8.2E-01
RFX5	3.4	4.9E-01	7.2E-01	0.29%	3.03%	3.95%	10.3	13.4	4.8E-01	0.30%	3.51%	3.73%	11.8	12.6	3.8E-01
RPC155	0.9	9.3E-01	9.9E-01	0.06%	-0.50%	1.30%	-9.1	23.5	6.7E-01	0.06%	0.00%	1.99%	0.0	35.4	9.8E-01
RUNX3	75.0	2.0E-15	1.1E-13	0.66%	34.85%	6.14%	52.6	9.3	1.8E-10	0.66%	26.73%	5.37%	40.3	8.1	2.9E-07
RXRA	0.8	9.4E-01	9.9E-01	0.18%	-1.08%	3.07%	-6.0	17.1	6.8E-01	0.18%	0.22%	2.91%	1.2	16.2	9.9E-01
SAP30	0.9	9.3E-01	9.9E-01	0.14%	0.79%	2.97%	5.6	21.2	8.3E-01	0.14%	-0.69%	2.98%	-4.9	20.9	7.8E-01
SETDB1	0.5	9.7E-01	9.9E-01	0.55%	0.46%	2.93%	0.8	5.3	9.8E-01	0.55%	-0.47%	3.77%	-0.8	6.8	7.9E-01
SIN3A	20.7	3.6E-04	3.0E-03	0.42%	14.27%	5.50%	34.0	13.1	6.2E-03	0.42%	13.83%	4.77%	32.6	11.3	5.0E-03
SIN3AK20	6.8	1.5E-01	3.3E-01	0.55%	11.57%	5.65%	21.2	10.4	5.6E-02	0.55%	3.26%	5.35%	5.9	9.7	6.1E-01
SIRT6	5.5	2.4E-01	5.0E-01	0.03%	1.18%	1.06%	41.0	36.8	2.8E-01	0.03%	-1.16%	0.99%	-40.8	34.8	2.3E-01
SIX5	2.9	5.8E-01	7.9E-01	0.10%	1.02%	2.02%	10.3	20.4	6.4E-01	0.10%	2.40%	2.60%	24.4	26.4	3.7E-01
SMARCA4	1.9	7.6E-01	9.2E-01	0.07%	0.80%	1.46%	11.0	20.0	6.1E-01	0.07%	-0.75%	1.76%	-10.0	23.7	6.4E-01
SMARCB1	7.5	1.1E-01	2.7E-01	0.19%	7.27%	3.16%	39.1	17.0	2.9E-02	0.19%	0.79%	2.81%	4.2	14.8	8.3E-01
SMARCC1	16.5	2.4E-03	1.4E-02	0.17%	6.29%	2.69%	36.9	15.8	1.7E-02	0.17%	6.00%	2.43%	35.1	14.2	1.6E-02
SMARCC2	2.6	6.3E-01	8.3E-01	0.04%	-0.98%	1.16%	-23.3	27.5	3.8E-01	0.04%	-0.36%	1.13%	-8.6	26.9	7.2E-01
SMC3	8.9	6.5E-02	2.0E-01	0.55%	5.40%	5.90%	9.9	10.8	4.1E-01	0.55%	10.86%	4.73%	19.8	8.6	2.9E-02
SP1	11.0	2.7E-02	9.6E-02	0.53%	16.00%	6.24%	30.0	11.7	1.5E-02	0.54%	5.69%	4.66%	10.6	8.7	2.7E-01
SP2	3.1	5.4E-01	7.4E-01	0.05%	1.77%	1.73%	32.3	31.7	3.1E-01	0.06%	0.69%	1.51%	12.5	27.4	6.7E-01
SP4	2.8	6.0E-01	8.0E-01	0.11%	2.19%	2.29%	19.5	20.5	3.6E-01	0.11%	-0.66%	2.05%	-5.9	18.4	7.1E-01
SP11	33.6	8.9E-07	1.2E-05	0.53%	22.24%	5.00%	41.7	9.4	1.4E-05	0.54%	15.64%	5.09%	29.2	9.5	3.6E-03
SREBP1	3.0	5.5E-01	7.5E-01	0.03%	-0.70%	1.30%	-20.7	38.5	5.8E-01	0.03%	-0.89%	1.05%	-26.4	31.1	3.8E-01

SRF	2.4	6.6E-01	8.4E-01	0.12%	0.13%	2.87%	1.1	23.6	1.0E+00	0.12%	3.45%	3.22%	28.5	26.5	3.0E-01
STAT1	7.0	1.3E-01	3.1E-01	0.29%	1.68%	3.46%	5.7	11.7	6.8E-01	0.30%	8.73%	4.07%	29.6	13.8	4.4E-02
STAT2	5.1	2.8E-01	5.3E-01	0.05%	1.07%	1.56%	22.7	33.1	5.0E-01	0.05%	1.93%	1.35%	41.1	28.9	1.6E-01
STAT3	10.4	3.4E-02	1.1E-01	0.74%	7.68%	4.22%	10.4	5.7	1.1E-01	0.74%	11.41%	5.47%	15.4	7.4	5.2E-02
<b>STAT5A</b>	16.7	2.2E-03	1.4E-02	0.24%	7.06%	2.94%	29.3	12.2	2.3E-02	0.24%	8.47%	3.13%	35.3	13.1	1.0E-02
SUZ12	3.2	5.3E-01	7.4E-01	0.11%	1.17%	1.23%	10.7	11.3	3.8E-01	0.11%	0.94%	1.38%	8.4	12.5	5.5E-01
TAF1	10.8	2.9E-02	1.0E-01	0.63%	22.95%	9.10%	36.7	14.5	1.7E-02	0.63%	6.49%	5.31%	10.3	8.4	2.6E-01
TAF7	1.9	7.6E-01	9.2E-01	0.15%	1.66%	2.36%	10.8	15.4	5.2E-01	0.15%	0.99%	2.62%	6.5	17.0	7.5E-01
TAL1	7.7	1.0E-01	2.7E-01	0.22%	2.48%	2.51%	11.3	11.5	3.7E-01	0.22%	5.55%	2.76%	25.1	12.5	5.8E-02
<b>TBL1XR1</b>	32.3	1.7E-06	1.9E-05	0.30%	21.06%	4.71%	69.8	15.6	2.9E-05	0.30%	14.43%	4.77%	48.0	15.9	3.3E-03
<b>TBP</b>	32.9	1.3E-06	1.6E-05	0.63%	26.85%	5.69%	42.7	9.0	7.1E-06	0.63%	13.15%	5.01%	20.8	7.9	1.0E-02
TCF12	12.0	1.8E-02	6.5E-02	0.52%	12.71%	4.66%	24.3	8.9	6.8E-03	0.53%	4.69%	4.72%	8.9	8.9	3.7E-01
<b>TCF3</b>	12.9	1.2E-02	4.6E-02	0.17%	9.39%	4.52%	56.1	27.0	4.4E-02	0.17%	9.25%	4.33%	55.7	26.1	3.7E-02
TCF7L2	8.3	8.1E-02	2.2E-01	0.78%	9.39%	5.63%	12.1	7.2	1.1E-01	0.78%	7.77%	4.71%	9.9	6.0	1.4E-01
TEAD4	7.7	1.0E-01	2.7E-01	0.64%	5.17%	5.69%	8.1	8.9	4.3E-01	0.64%	11.35%	5.28%	17.6	8.2	4.9E-02
TFAP2A	13.4	9.4E-03	3.9E-02	0.30%	7.57%	5.07%	25.2	16.9	1.6E-01	0.30%	11.11%	4.08%	37.1	13.6	7.6E-03
TFAP2C	6.4	1.7E-01	3.7E-01	0.39%	7.15%	4.41%	18.1	11.2	1.3E-01	0.40%	4.31%	3.95%	10.9	10.0	3.2E-01
THAP1	1.0	9.1E-01	9.9E-01	0.04%	0.22%	1.43%	5.8	38.0	9.0E-01	0.04%	0.62%	1.39%	16.5	36.9	6.7E-01
TRIM28	0.7	9.5E-01	9.9E-01	0.17%	1.52%	3.42%	8.9	20.1	6.9E-01	0.17%	0.16%	2.61%	1.0	15.5	1.0E+00
UBTF	5.4	2.5E-01	5.0E-01	0.21%	5.04%	3.11%	24.1	14.9	1.2E-01	0.21%	1.95%	3.14%	9.2	14.9	5.8E-01
USF1	1.4	8.4E-01	9.5E-01	0.55%	0.88%	5.85%	1.6	10.7	9.5E-01	0.55%	-2.76%	5.06%	-5.0	9.2	5.1E-01
USF2	4.0	4.0E-01	6.7E-01	0.24%	4.80%	3.01%	20.1	12.6	1.4E-01	0.24%	0.46%	3.69%	1.9	15.5	9.5E-01
WRNIP1	12.1	1.7E-02	6.3E-02	0.18%	16.25%	8.07%	89.4	44.4	5.5E-02	0.18%	7.09%	3.41%	38.6	18.6	4.4E-02
<b>YY1</b>	21.2	2.8E-04	2.5E-03	0.85%	19.26%	6.29%	22.8	7.4	5.5E-03	0.85%	16.81%	5.60%	19.9	6.6	4.4E-03
ZBTB33	1.8	7.8E-01	9.2E-01	0.17%	-1.22%	2.92%	-7.0	16.8	6.3E-01	0.17%	1.57%	3.07%	9.0	17.6	6.5E-01
ZBTB7A	10.8	2.9E-02	1.0E-01	0.27%	9.51%	4.13%	35.3	15.3	1.9E-02	0.27%	4.63%	3.70%	17.0	13.6	2.4E-01
ZEB1	8.7	6.9E-02	2.0E-01	0.05%	3.19%	2.32%	59.1	43.1	1.6E-01	0.05%	4.00%	2.23%	74.2	41.3	8.0E-02
ZKSCAN1	3.3	5.1E-01	7.3E-01	0.05%	1.35%	1.79%	26.3	34.7	4.6E-01	0.05%	1.15%	1.38%	22.1	26.4	4.2E-01
ZNF143	2.8	5.9E-01	7.9E-01	0.49%	1.62%	6.40%	3.3	13.0	8.6E-01	0.49%	6.53%	5.64%	13.3	11.5	2.8E-01
ZNF217	4.0	4.0E-01	6.7E-01	0.18%	1.70%	1.48%	9.3	8.0	3.1E-01	0.18%	1.71%	1.95%	9.4	10.7	4.3E-01
ZNF263	5.7	2.2E-01	4.6E-01	0.53%	5.19%	4.64%	9.9	8.8	2.9E-01	0.53%	5.71%	4.05%	10.8	7.6	2.0E-01
ZNF274	0.6	9.6E-01	9.9E-01	0.06%	-0.18%	1.21%	-3.0	20.4	8.4E-01	0.06%	0.27%	1.25%	4.5	21.3	8.7E-01
ZZZ3	3.5	4.9E-01	7.2E-01	0.01%	0.40%	0.52%	32.5	41.9	4.5E-01	0.01%	-0.47%	0.57%	-39.2	47.5	3.9E-01

\*TFs (with p for heritability  $h^2$  enrichment < 0.05 in both populations and FDR-corrected  $p_{meta}$  < 0.05) are marked in bold. Large-enrichment TFs (enrichment > 40 in both population) are colored in red. Prop.\_SNPs: Proportion of SNPs in TFBSs; Prop.\_h2: Proportion of  $h^2$  in TFBS; SD: standard error.

**Supplementary Table 6 | Gene-set enrichment analysis results for 12 transcription factors with  $h^2$  enrichment > 40 in BioCarta pathways**

GeneSet	N_genes	N_overlap	P	P_adj	Genes	Link
FMLP PATHWAY	34	3	1.09E-06	0.000315328	RELA:NFATC1:ELK1	<a href="http://www.gsea-msigdb.org/gsea/msigdb/cards/BIOCARTA_FMLP_PATHWAY">http://www.gsea-msigdb.org/gsea/msigdb/cards/BIOCARTA_FMLP_PATHWAY</a>
TCR PATHWAY	44	3	2.41E-06	0.000347727	RELA:NFATC1:ELK1	<a href="http://www.gsea-msigdb.org/gsea/msigdb/cards/BIOCARTA_TCR_PATHWAY">http://www.gsea-msigdb.org/gsea/msigdb/cards/BIOCARTA_TCR_PATHWAY</a>
MAPK PATHWAY	80	3	1.47E-05	0.001420057	RELA:ATF2:ELK1	<a href="http://www.gsea-msigdb.org/gsea/msigdb/cards/BIOCARTA_MAPK_PATHWAY">http://www.gsea-msigdb.org/gsea/msigdb/cards/BIOCARTA_MAPK_PATHWAY</a>
PCAF PATHWAY	13	2	2.76E-05	0.001994539	RELA:ATF2	<a href="http://www.gsea-msigdb.org/gsea/msigdb/cards/BIOCARTA_PCAF_PATHWAY">http://www.gsea-msigdb.org/gsea/msigdb/cards/BIOCARTA_PCAF_PATHWAY</a>
41BB PATHWAY	18	2	5.41E-05	0.003124482	RELA:ATF2	<a href="http://www.gsea-msigdb.org/gsea/msigdb/cards/BIOCARTA_41BB_PATHWAY">http://www.gsea-msigdb.org/gsea/msigdb/cards/BIOCARTA_41BB_PATHWAY</a>
RAS PATHWAY	22	2	8.15E-05	0.003925694	RELA:ELK1	<a href="http://www.gsea-msigdb.org/gsea/msigdb/cards/BIOCARTA_RAS_PATHWAY">http://www.gsea-msigdb.org/gsea/msigdb/cards/BIOCARTA_RAS_PATHWAY</a>
TOLL PATHWAY	24	2	9.73E-05	0.003969805	RELA:ELK1	<a href="http://www.gsea-msigdb.org/gsea/msigdb/cards/BIOCARTA_TOLL_PATHWAY">http://www.gsea-msigdb.org/gsea/msigdb/cards/BIOCARTA_TOLL_PATHWAY</a>
VIP PATHWAY	26	2	0.000114509	0.003969805	RELA:NFATC1	<a href="http://www.gsea-msigdb.org/gsea/msigdb/cards/BIOCARTA_VIP_PATHWAY">http://www.gsea-msigdb.org/gsea/msigdb/cards/BIOCARTA_VIP_PATHWAY</a>
AT1R PATHWAY	27	2	0.000123627	0.003969805	ATF2:ELK1	<a href="http://www.gsea-msigdb.org/gsea/msigdb/cards/BIOCARTA_AT1R_PATHWAY">http://www.gsea-msigdb.org/gsea/msigdb/cards/BIOCARTA_AT1R_PATHWAY</a>
GPCR PATHWAY	30	2	0.000153054	0.004423267	NFATC1:ELK1	<a href="http://www.gsea-msigdb.org/gsea/msigdb/cards/BIOCARTA_GPCR_PATHWAY">http://www.gsea-msigdb.org/gsea/msigdb/cards/BIOCARTA_GPCR_PATHWAY</a>
BCR PATHWAY	33	2	0.000185583	0.004875784	NFATC1:ELK1	<a href="http://www.gsea-msigdb.org/gsea/msigdb/cards/BIOCARTA_BCR_PATHWAY">http://www.gsea-msigdb.org/gsea/msigdb/cards/BIOCARTA_BCR_PATHWAY</a>
P38MAPK PATHWAY	36	2	0.000221205	0.005327358	ATF2:ELK1	<a href="http://www.gsea-msigdb.org/gsea/msigdb/cards/BIOCARTA_P38MAPK_PATHWAY">http://www.gsea-msigdb.org/gsea/msigdb/cards/BIOCARTA_P38MAPK_PATHWAY</a>
FCER1 PATHWAY	39	2	0.00025991	0.00577799	NFATC1:ELK1	<a href="http://www.gsea-msigdb.org/gsea/msigdb/cards/BIOCARTA_FCER1_PATHWAY">http://www.gsea-msigdb.org/gsea/msigdb/cards/BIOCARTA_FCER1_PATHWAY</a>

**Supplementary Table 7 | Enrichment of RA variants in histone marks of selected tissues**

Epigenome	Epigenome_name (Standardized Epigenome_name)	Anatomy (Group)	Histone mark	P meta	P meta adj	Variants in East Asians			Variants in Europeans		
						N <sub>Obs</sub>	N <sub>Exp</sub>	P	N <sub>Obs</sub>	N <sub>Exp</sub>	P
E029	CD14_Primary_Cells (Primary monocytes from peripheral blood)	BLOOD (Myeloid)	H3K27ac	3.9E-05	1.1E-04	9	3.9	9.5E-03	13	4.8	3.0E-04
			H3K27me3	4.9E-01	6.2E-01	4	4.0	5.8E-01	6	4.6	3.1E-01
			H3K36me3	5.2E-03	1.1E-02	10	5.3	2.2E-02	12	7.0	2.8E-02
			H3K4me1	1.4E-11	9.7E-11	16	7.6	6.0E-04	27	9.4	8.0E-10
			H3K4me3	6.0E-03	1.3E-02	5	2.9	1.6E-01	9	3.5	4.6E-03
E030	CD15_Primary_Cells (Primary neutrophils from peripheral blood)	BLOOD (Myeloid)	H3K9me3	9.9E-01	1.0E+00	4	6.9	9.5E-01	6	9.2	9.4E-01
			H3K27me3	8.4E-01	9.2E-01	6	7.1	7.5E-01	8	8.5	6.5E-01
			H3K36me3	7.0E-03	1.5E-02	10	4.8	1.2E-02	10	6.3	7.4E-02
			H3K4me1	1.2E-11	8.9E-11	10	6.8	1.2E-01	28	8.3	3.4E-12
			H3K4me3	1.5E-04	3.7E-04	7	4.2	1.1E-01	14	5.0	1.1E-04
E032	CD19_Primary_Cells_Peripheral_UW (Primary B cells from peripheral blood)	BLOOD (B)	H3K9me3	6.1E-01	7.2E-01	5	5.7	7.2E-01	9	7.8	3.6E-01
			H3K27ac	4.4E-14	6.6E-13	15	3.7	1.5E-07	18	4.3	8.3E-09
			H3K27me3	4.5E-01	5.8E-01	6	4.8	3.4E-01	6	5.4	4.7E-01
			H3K36me3	1.4E-05	4.1E-05	14	5.6	1.8E-04	14	7.2	5.0E-03
			H3K4me1	1.5E-14	2.5E-13	19	7.6	4.8E-06	28	9.4	8.6E-11
E034	CD3_Primary_Cells_Peripheral_UW (Primary T cells from peripheral blood)	BLOOD (T)	H3K4me3	3.9E-07	1.5E-06	8	3.2	8.5E-03	14	3.7	2.5E-06
			H3K9me3	4.1E-01	5.4E-01	3	3.7	7.5E-01	7	4.8	1.8E-01
			H3K27ac	1.2E-11	8.9E-11	13	4.1	3.8E-05	19	4.9	1.1E-08
			H3K27me3	3.1E-01	4.4E-01	13	10.2	1.8E-01	13	12.5	5.0E-01
			H3K36me3	2.5E-04	6.1E-04	9	5.4	6.8E-02	16	7.0	3.1E-04
E035	CD34_Primary_Cells (Primary hematopoietic stem cells)	BLOOD (HSC or PBMC)	H3K4me1	3.6E-16	1.1E-14	20	7.5	5.4E-07	28	8.8	1.7E-11
			H3K9me3	9.1E-01	9.6E-01	2	3.9	9.3E-01	5	5.4	6.5E-01
			H3K27me3	4.1E-01	5.4E-01	1	1.3	7.4E-01	3	1.5	1.9E-01
			H3K36me3	7.1E-02	1.2E-01	6	3.4	1.1E-01	7	4.4	1.3E-01
			H3K4me1	8.6E-10	5.2E-09	15	5.1	1.4E-05	18	6.1	2.5E-06
E036	CD34_Cultured_Cells (Primary hematopoietic stem cells short term culture)	BLOOD (HSC or PBMC)	H3K4me3	2.0E-02	3.9E-02	7	3.7	5.9E-02	8	4.3	5.1E-02
			H3K9me3	4.0E-01	5.4E-01	4	2.6	2.7E-01	4	3.6	5.0E-01
			H3K27me3	5.8E-01	6.9E-01	5	5.3	6.3E-01	8	6.8	3.7E-01
			H3K36me3	7.1E-05	1.8E-04	12	5.3	2.0E-03	14	6.8	2.8E-03
			H3K4me1	1.1E-09	6.3E-09	14	7.6	6.6E-03	26	9.5	6.8E-09
E037	CD4_Memory_Primary_Cells (Primary T helper memory cells from peripheral blood 2)	BLOOD (T)	H3K4me3	2.4E-03	5.2E-03	6	3.9	1.8E-01	12	4.9	1.4E-03
			H3K9me3	7.8E-01	8.8E-01	6	5.4	4.7E-01	5	7.1	8.8E-01
			H3K27ac	2.9E-07	1.1E-06	12	4.8	7.8E-04	16	5.7	2.0E-05
			H3K27me3	5.0E-01	6.2E-01	1	1.5	7.9E-01	3	1.7	2.3E-01
			H3K36me3	5.7E-04	1.3E-03	6	2.7	4.4E-02	10	3.6	1.2E-03
E038	CD4_Naive_Primary_Cells (Primary T helper naive cells from peripheral blood)	BLOOD (T)	H3K4me1	1.1E-17	1.0E-15	17	6.8	2.5E-05	30	8.2	1.0E-14
			H3K9me3	1.0E+00	NA	1	1.8	8.5E-01	0	NA	NA
			H3K27ac	6.1E-05	1.6E-04	9	3.6	4.4E-03	11	4.1	1.0E-03
			H3K27me3	6.5E-01	7.5E-01	3	2.2	3.7E-01	2	2.8	7.9E-01
			H3K36me3	1.5E-02	2.9E-02	7	4.1	9.1E-02	10	5.2	2.2E-02
E039	CD4+_CD25-_CD45RA+_Naive_Primary_Cells (Primary T helper naive cells from peripheral blood)	BLOOD (T)	H3K4me3	2.1E-05	6.0E-05	10	3.8	2.0E-03	12	4.6	7.1E-04
			H3K9me3	1.0E+00	NA	0	NA	NA	0	NA	NA
			H3K27me3	6.2E-06	2.1E-05	11	4.2	1.1E-03	13	4.8	3.6E-04
			H3K36me3	7.5E-03	1.6E-02	6	5.3	4.4E-01	14	6.6	2.1E-03
			H3K4me1	1.2E-12	1.4E-11	17	6.9	2.8E-05	25	8.1	1.4E-09
E039	CD4+_CD25-_CD45RA+_Naive_Primary_Cells (Primary T helper naive cells from peripheral blood)	BLOOD (T)	H3K4me3	6.8E-06	2.2E-05	11	4.2	1.0E-03	13	5.0	4.3E-04
			H3K9me3	8.2E-01	9.2E-01	3	2.7	5.2E-01	2	3.5	8.9E-01

E040	CD4+ CD25- CD45RO+ Memory_Primary_Cells (Primary T helper memory cells from peripheral blood 1)	BLOOD (T)	H3K27ac	5.3E-08	2.2E-07	10	3.6	1.4E-03	15	4.1	1.9E-06
			H3K27me3	3.6E-02	6.4E-02	7	3.0	2.2E-02	5	3.5	2.6E-01
			H3K36me3	2.6E-05	7.1E-05	7	3.8	6.3E-02	14	4.6	2.9E-05
			H3K4me1	3.3E-17	2.0E-15	18	6.9	5.0E-06	29	8.3	1.5E-13
			H3K4me3	1.2E-08	5.5E-08	9	3.8	6.8E-03	17	4.5	7.7E-08
E041	CD4+ CD25- IL17- PMA- lonomycin_stimulated_MACS_purified_Th_Primary_Cells (Primary T helper cells PMA-I stimulated)	BLOOD (T)	H3K27ac	7.2E-15	1.5E-13	16	5.4	4.5E-06	24	6.4	4.4E-11
			H3K27me3	4.7E-01	6.0E-01	8	6.1	2.6E-01	7	7.5	6.6E-01
			H3K36me3	1.2E-08	5.6E-08	12	5.3	2.2E-03	20	6.7	2.5E-07
			H3K4me1	1.3E-19	2.4E-17	20	7.8	9.6E-07	32	9.3	2.8E-15
			H3K4me3	5.4E-12	5.2E-11	12	4.5	4.3E-04	21	5.3	4.1E-10
E042	CD4+_CD25- IL17+ PMA-lonomycin_stimulated_Th17_Primary_Cells (Primary T helper 17 cells PMA-I stimulated)	BLOOD (T)	H3K27ac	1.0E+00	1.0E+00	1	2.8	9.5E-01	1	3.6	9.8E-01
			H3K27me3	3.5E-13	4.7E-12	12	4.0	1.3E-04	21	5.0	8.3E-11
			H3K36me3	7.8E-02	1.3E-01	7	4.2	1.2E-01	8	5.1	1.3E-01
			H3K4me1	1.4E-06	5.1E-06	10	5.1	1.7E-02	18	6.5	5.0E-06
			H3K4me3	2.5E-16	8.9E-15	17	6.5	1.2E-05	28	7.9	5.3E-13
E043	CD4+_CD25- IL17+ PMA-lonomycin_stimulated_Th17_Primary_Cells (Primary T helper 17 cells PMA-I stimulated)	BLOOD (T)	H3K27ac	2.2E-10	1.4E-09	12	4.1	1.5E-04	18	4.9	5.5E-08
			H3K27me3	9.7E-01	9.9E-01	1	2.2	9.1E-01	2	3.0	8.2E-01
			H3K36me3	1.4E-07	5.8E-07	10	3.5	9.2E-04	14	4.0	7.7E-06
			H3K4me1	4.9E-01	6.2E-01	7	5.1	2.4E-01	5	6.2	7.8E-01
			H3K4me3	2.2E-04	5.6E-04	8	5.6	1.7E-01	17	7.2	1.1E-04
E044	CD4+_CD25- Th_Primary_Cells (Primary T helper cells from peripheral blood)	BLOOD (T)	H3K27ac	1.2E-14	2.1E-13	19	7.4	2.7E-06	27	8.8	1.2E-10
			H3K27me3	3.5E-08	1.6E-07	12	4.0	1.4E-04	15	4.8	1.2E-05
			H3K36me3	9.1E-01	9.6E-01	3	3.8	7.6E-01	4	5.3	8.1E-01
			H3K4me1	6.0E-13	7.2E-12	15	4.2	1.1E-06	19	5.1	1.7E-08
			H3K4me3	4.5E-01	5.8E-01	7	6.0	3.9E-01	8	7.0	4.0E-01
E045	CD4+_CD25+_CD127- Treg_Primary_Cells (Primary T regulatory cells from peripheral blood)	BLOOD (T)	H3K27ac	2.4E-05	6.6E-05	10	5.4	2.6E-02	17	6.9	6.3E-05
			H3K27me3	5.5E-16	1.4E-14	18	6.3	1.2E-06	26	7.4	1.2E-11
			H3K36me3	6.0E-12	5.5E-11	15	4.3	1.2E-06	18	5.2	1.7E-07
			H3K4me1	9.9E-01	1.0E+00	2	3.7	9.1E-01	2	4.7	9.6E-01
			H3K4me3	9.3E-11	6.2E-10	13	3.9	1.8E-05	17	4.6	1.9E-07
E046	CD4+_CD25int_CD127+_Tmem_Primary_Cells (Primary T cells effector/memory enriched from peripheral blood)	BLOOD (T)	H3K27ac	1.7E-01	2.6E-01	6	3.3	1.0E-01	5	4.1	4.0E-01
			H3K27me3	3.5E-04	8.2E-04	7	4.7	1.7E-01	15	6.1	1.8E-04
			H3K36me3	1.6E-15	3.6E-14	17	5.2	3.3E-07	23	6.1	1.2E-10
			H3K4me1	1.1E-08	5.2E-08	10	3.9	2.6E-03	17	4.7	1.8E-07
			H3K4me3	9.0E-01	9.6E-01	2	2.3	6.9E-01	2	3.1	8.5E-01
E047	CD56_Primary_Cells (Primary Natural Killer cells from peripheral blood)	BLOOD (NK)	H3K27ac	2.3E-09	1.2E-08	13	4.1	3.7E-05	16	4.8	2.6E-06
			H3K27me3	6.1E-01	7.2E-01	2	3.2	8.5E-01	5	3.7	3.0E-01
			H3K36me3	4.4E-04	1.0E-03	7	4.7	1.7E-01	15	6.2	2.3E-04
			H3K4me1	2.2E-16	8.9E-15	19	7.4	2.5E-06	29	8.9	2.1E-12
			H3K4me3	9.6E-06	3.1E-05	8	3.1	7.2E-03	12	3.7	8.8E-05
E048	CD8_Naive_Primary_Cells (Primary T CD8+ naive cells from peripheral blood)	BLOOD (T)	H3K27ac	1.0E+00	1.0E+00	2	4.9	9.7E-01	2	6.8	1.0E+00
			H3K27me3	4.6E-06	1.5E-05	9	3.2	2.3E-03	12	3.8	1.2E-04
			H3K36me3	8.3E-01	9.2E-01	3	4.0	7.9E-01	5	5.1	6.0E-01
			H3K4me1	3.5E-02	6.3E-02	3	3.6	7.3E-01	10	4.5	7.7E-03
			H3K4me3	2.2E-12	2.2E-11	17	7.1	4.4E-05	25	8.2	1.6E-09
E048	CD8_Memory_Primary_Cells (Primary T CD8+ memory cells from peripheral blood)	BLOOD (T)	H3K27ac	3.6E-05	9.9E-05	9	3.4	3.1E-03	11	4.0	8.6E-04
			H3K27me3	6.3E-01	7.3E-01	3	2.7	5.2E-01	4	3.7	5.3E-01
			H3K36me3	1.1E-05	3.4E-05	10	4.0	3.0E-03	13	4.8	2.4E-04
			H3K4me1	4.5E-01	5.8E-01	1	1.4	7.6E-01	3	1.6	2.1E-01
			H3K4me3	1.3E-02	2.6E-02	5	3.6	2.7E-01	10	4.4	6.2E-03
E048	CD8_Memory_Primary_Cells (Primary T CD8+ memory cells from peripheral blood)	BLOOD (T)	H3K27ac	3.6E-13	4.7E-12	14	5.8	3.4E-04	25	7.0	3.2E-11
			H3K27me3	1.5E-08	7.0E-08	12	3.6	4.6E-05	14	4.3	1.5E-05
			H3K36me3	1.5E-08	7.0E-08	12	3.6	4.6E-05	14	4.3	1.5E-05
			H3K4me1	8.7E-01	9.4E-01	1	1.6	8.2E-01	2	2.1	6.5E-01
			H3K4me3	8.7E-01	9.4E-01	1	1.6	8.2E-01	2	2.1	6.5E-01



E050	Mobilized_CD34_Primary_Cells_Female (Primary hematopoietic stem cells G-CSF-mobilized Female)	BLOOD (HSC or PBMC)	H3K27ac	1.4E-05	4.1E-05	10	5.1	1.7E-02	16	6.2	5.6E-05
			H3K27me3	5.8E-01	6.9E-01	2	4.9	9.7E-01	8	6.0	2.4E-01
			H3K36me3	1.5E-01	2.3E-01	8	5.8	2.0E-01	10	7.3	1.7E-01
			H3K4me1	3.1E-10	2.0E-09	19	9.9	2.8E-04	28	11.9	4.3E-08
			H3K4me3	7.8E-07	2.8E-06	11	4.6	2.2E-03	16	5.7	2.0E-05
			H3K9me3	9.1E-01	9.6E-01	4	6.0	9.0E-01	7	7.6	6.7E-01
E051	Mobilized_CD34_Primary_Cells_Male (Primary hematopoietic stem cells G-CSF-mobilized Male)	BLOOD (HSC or PBMC)	H3K27me3	4.9E-01	6.2E-01	3	4.6	8.6E-01	8	5.8	2.1E-01
			H3K36me3	3.2E-02	6.0E-02	9	6.3	1.5E-01	13	8.0	3.4E-02
			H3K4me1	1.0E-11	8.2E-11	18	9.3	4.3E-04	29	11.1	8.1E-10
			H3K4me3	1.5E-09	8.4E-09	13	5.7	1.1E-03	21	6.8	5.5E-08
			H3K9me3	8.5E-01	9.2E-01	5	8.2	9.6E-01	11	10.7	5.2E-01
			H3K27ac	3.8E-07	1.5E-06	8	2.6	2.1E-03	12	3.0	9.6E-06
E062	Peripheral_Blood_Mononuclear_Primary_Cells (Primary mononuclear cells from peripheral blood)	BLOOD (HSC or PBMC)	H3K27me3	4.0E-01	5.4E-01	5	5.3	6.4E-01	9	6.7	2.1E-01
			H3K36me3	2.4E-05	6.6E-05	12	5.6	3.2E-03	16	7.3	5.1E-04
			H3K4me1	1.4E-05	4.1E-05	10	3.8	2.0E-03	12	4.4	4.7E-04
			H3K4me3	5.5E-04	1.3E-03	7	3.5	4.4E-02	11	4.2	1.2E-03
			H3K9me3	9.6E-01	9.9E-01	2	3.9	9.2E-01	4	5.2	7.9E-01
			H3K27ac	3.5E-01	4.9E-01	5	4.3	4.4E-01	7	5.2	2.5E-01
E065	Aorta (Aorta)	VASCULAR	H3K27me3	6.6E-01	7.6E-01	3	2.9	5.8E-01	4	3.7	5.2E-01
			H3K36me3	4.1E-01	5.4E-01	4	2.5	2.2E-01	3	3.1	6.1E-01
			H3K4me1	5.4E-01	6.6E-01	1	4.1	9.9E-01	7	5.0	2.1E-01
			H3K4me3	1.3E-01	2.1E-01	2	2.7	7.7E-01	7	3.3	3.8E-02
			H3K9me3	5.2E-01	6.5E-01	4	2.7	2.8E-01	3	3.6	7.2E-01
			H3K27ac	1.2E-01	1.9E-01	7	6.9	5.6E-01	13	8.2	4.4E-02
E066	Adult_Liver (Liver)	LIVER	H3K27me3	4.0E-01	5.4E-01	4	2.7	2.8E-01	4	3.5	4.7E-01
			H3K36me3	2.8E-01	4.0E-01	8	6.0	2.3E-01	9	7.6	3.3E-01
			H3K4me1	6.3E-02	1.1E-01	10	8.8	3.7E-01	16	10.5	3.2E-02
			H3K4me3	1.0E-01	1.7E-01	5	4.7	5.2E-01	10	5.7	4.0E-02
			H3K9me3	8.9E-01	9.6E-01	5	5.4	6.5E-01	5	7.2	8.9E-01
			H3K27ac	1.7E-01	2.7E-01	2	2.9	8.1E-01	7	3.5	5.1E-02
E087	Pancreatic_Islets (Pancreatic Islets)	PANCREAS	H3K27me3	2.7E-02	5.1E-02	5	2.0	4.3E-02	5	2.5	9.5E-02
			H3K36me3	2.5E-01	3.6E-01	3	2.9	5.7E-01	6	3.5	1.2E-01
			H3K4me1	9.3E-01	9.7E-01	4	5.8	8.7E-01	6	6.9	7.3E-01
			H3K4me3	1.9E-02	3.7E-02	5	3.3	2.3E-01	9	4.0	1.2E-02
			H3K9me3	2.4E-01	3.6E-01	1	0.9	6.2E-01	3	1.1	1.0E-01
			H3K27ac	1.3E-02	2.7E-02	9	6.4	1.6E-01	14	7.8	1.1E-02
E096	Lung (Lung)	LUNG	H3K4me1	1.7E-03	3.7E-03	13	7.7	2.1E-02	16	9.2	8.4E-03
			H3K4me3	2.2E-01	3.3E-01	5	3.8	3.3E-01	7	4.7	1.7E-01
			H3K9me3	9.6E-01	9.9E-01	7	8.5	8.1E-01	8	11.1	9.3E-01
			H3K27me3	4.3E-02	7.5E-02	4	2.1	1.6E-01	6	2.7	4.5E-02
			H3K36me3	9.1E-02	1.5E-01	8	5.4	1.4E-01	10	6.9	1.3E-01
			H3K27ac	2.1E-01	3.2E-01	3	4.4	8.5E-01	9	5.3	6.5E-02
E097	Ovary (Ovary)	OVARY	H3K27me3	3.1E-02	5.7E-02	4	2.8	3.0E-01	8	3.4	1.6E-02
			H3K36me3	7.6E-01	8.6E-01	6	5.4	4.7E-01	5	6.6	8.3E-01
			H3K4me1	2.6E-01	3.8E-01	6	6.2	6.2E-01	11	7.7	1.2E-01
			H3K4me3	1.7E-01	2.7E-01	3	3.6	7.2E-01	8	4.4	5.7E-02
			H3K9me3	5.9E-01	7.0E-01	4	2.7	2.7E-01	2	3.7	9.1E-01
			H3K27ac	1.8E-01	2.7E-01	5	3.6	2.9E-01	7	4.5	1.5E-01
E098	Pancreas (Pancreas)	PANCREAS	H3K27me3	8.5E-01	9.2E-01	1	1.0	6.6E-01	1	1.3	7.5E-01
			H3K36me3	3.1E-01	4.4E-01	8	5.5	1.6E-01	7	7.1	5.8E-01
			H3K4me1	1.3E-01	2.1E-01	10	7.9	2.3E-01	13	9.5	1.2E-01
			H3K4me3	2.0E-02	3.9E-02	4	3.5	4.7E-01	10	4.3	6.3E-03
			H3K9me3	3.6E-01	5.0E-01	8	5.8	2.0E-01	8	8.0	5.7E-01

E109	Small_Intestine (Small Intestine)	GI_INTESTINE	H3K27ac	1.5E-06	5.3E-06	10	6.5	8.2E-02	21	7.8	1.1E-06
			H3K27me3	3.2E-01	4.6E-01	7	4.5	1.5E-01	5	5.4	6.5E-01
			H3K36me3	6.9E-02	1.2E-01	6	3.5	1.1E-01	7	4.3	1.1E-01
			H3K4me1	3.1E-04	7.4E-04	10	5.9	4.3E-02	15	6.6	6.2E-04
			H3K4me3	5.7E-04	1.3E-03	7	3.1	2.5E-02	10	3.8	2.1E-03
			H3K9me3	1.0E+00	NA	2	2.3	6.8E-01	0	NA	NA
E113	Spleen (Spleen)	SPLEEN	H3K27ac	9.7E-09	4.9E-08	17	6.0	3.5E-06	17	7.1	1.2E-04
			H3K27me3	3.4E-02	6.2E-02	5	1.6	2.1E-02	3	1.8	2.7E-01
			H3K36me3	1.4E-01	2.2E-01	10	6.1	5.7E-02	8	7.8	5.3E-01
			H3K4me1	5.8E-07	2.2E-06	18	8.4	1.1E-04	20	10.0	3.0E-04
			H3K4me3	1.3E-02	2.7E-02	9	6.2	1.3E-01	13	7.1	1.3E-02
			H3K9me3	5.4E-01	6.6E-01	6	6.5	6.7E-01	10	8.4	3.2E-01
E124	Monocytes-CD14+_RO01746 (Monocytes-CD14+ RO01746 Primary Cells)	BLOOD (Myeloid)	H3K27ac	1.1E-09	6.3E-09	13	6.7	5.8E-03	24	8.1	7.7E-09
			H3K27me3	5.3E-01	6.5E-01	6	5.9	5.6E-01	8	6.8	3.7E-01
			H3K36me3	4.0E-02	7.1E-02	10	6.0	5.2E-02	11	7.8	1.3E-01
			H3K4me1	1.0E-11	8.2E-11	17	8.7	8.9E-04	29	10.8	3.8E-10
			H3K4me3	3.1E-06	1.1E-05	11	6.1	2.4E-02	19	7.3	7.9E-06
			H3K9me3	8.5E-01	9.2E-01	5	5.7	7.1E-01	7	7.8	7.0E-01

**Supplementary Table 8 | Potential effector genes in RA loci**

Gene	Positional mapping	Gene-level RA association (MAGMA)		eQTL mapping		Chromatin interaction mapping
	posMap SNPs	Z	P	eqtlMap SNPs	eqtlMapts	ciMapts
PLCH2	0	2.28	1.13E-02	1	Whole Blood	NA
RP3-395M20.8	2	NA	NA	1	Whole Blood	NA
TNFRSF14	4	5.96	1.23E-09	1	LCL, Whole Blood	NA
RP3-395M20.9	26	NA	NA	1	Spleen	NA
FAM213B	50	6.87	3.29E-12	1	T-cell, monocyte CD14, Whole Blood, Lung, Spleen	NA
MMEL1	123	6.97	1.62E-12	1	T-cell, T CD8 naive, Whole Blood, Lung, Small Intestine Terminal Ileum, Spleen	NA
RP13-436F16.1	26	NA	NA	1	Whole Blood	NA
TTC34	53	4.94	3.98E-07	1	T-cell, LCL, T CD8 naive activated, Whole Blood, Cells EBV-transformed lymphocytes, Spleen	NA
NBPF1	0	0.39	3.49E-01	0	NA	GM12878
RP5-1182A14.5	0	NA	NA	0	NA	GM12878
MST1P2	0	NA	NA	6	Whole Blood, Lung, Spleen	NA
CROCC	7	0.97	1.67E-01	7	monocyte, T-cell, Whole Blood, Lung, Small Intestine Terminal Ileum, Spleen	NA
CROCCP4	0	NA	NA	4	Whole Blood	NA
MST1L	0	NA	NA	7	T CD8 naive activated, T CD4 TH17, Whole Blood, Cells EBV-transformed lymphocytes, Lung, Spleen	NA
U1	0	NA	NA	1	Whole Blood	NA
RP11-108M9.4	0	NA	NA	1	LCL, Whole Blood	NA
RP11-108M9.5	0	NA	NA	2	Whole Blood, Lung	NA
MFAP2	15	5.64	8.57E-09	7	Lung, Spleen	NA
RP1-37C10.3	23	NA	NA	1	Lung	NA
ATP13A2	32	6.89	2.86E-12	6	blood, Whole Blood	NA
SDHB	76	6.09	5.68E-10	0	NA	NA
PADI2	177	7.47	4.11E-14	9	monocyte, neutrophil CD15, LCL, T-cell, LCL, neutrophil CD16, macrophage naive, monocyte naive, Monocyte classical, Monocyte non classical, Whole Blood, Lung, Spleen	NA
PADI1	0	1.93	2.69E-02	1	Whole Blood	NA
PADI3	15	5.71	5.61E-09	0	NA	NA
MIR3972	12	NA	NA	0	NA	Spleen
PADI4	182	10.72	4.08E-27	7	monocyte, T-cell, monocyte CD14, T CD4 naive, T CD8 naive, Monocyte classical, Monocyte non classical, T CD4 naive TREG, Whole Blood, Lung, Spleen	Spleen
AC004824.2	121	9.54	7.41E-22	6	Whole Blood	NA
EPHA10	18	4.43	4.65E-06	4	Whole Blood	Spleen
MANE1	18	5.64	8.51E-09	4	macrophage naive, Whole Blood	Spleen, GM12878
RP11-109P14.9	12	NA	NA	1	Whole Blood	NA
YRDC	15	3.96	3.71E-05	4	B-cell CD19, monocyte naive	Spleen, GM12878
C1orf122	14	4.84	6.57E-07	5	monocyte, monocyte naive, Monocyte classical, Monocyte non classical, Whole Blood	Spleen, GM12878
MTF1	34	6.01	9.02E-10	4	macrophage naive, monocyte naive	GM12878
RP11-109P14.8	4	NA	NA	1	Whole Blood	NA
RP11-109P14.10	10	NA	NA	4	Whole Blood	GM12878
INPP5B	62	6.60	2.01E-11	7	monocyte, neutrophil, T-cell, neutrophil CD15, T-cell CD4, T-cell CD8, B-cell CD19, LCL, neutrophil CD16, macrophage naive, monocyte naive, B cell naive, T CD4 naive, T CD4 naive activated, T CD8 naive, T CD8 naive activated, Monocyte classical, Monocyte non classical, NK, T CD4 TFH, T CD4 TH1, T CD4 TH17, T CD4 TH1 17, T CD4 TH2, T CD4 memory TREG, T CD4 naive TREG, Cells EBV-transformed lymphocytes, Whole Blood, Lung, Small Intestine Terminal Ileum, Spleen	NA
SNORA63	18	NA	NA	4	Whole Blood	NA
RNU6-584P	18	NA	NA	3	Whole Blood	NA
SF3A3	0	3.61	1.55E-04	5	neutrophil, B-cell CD19, monocyte CD14, neutrophil CD15, T-cell CD4, T-cell CD8, neutrophil CD16, LCL, Monocyte classical, NK, T CD4 memory TREG, Cells EBV-transformed lymphocytes, Whole Blood, Lung, Small Intestine Terminal Ileum, Spleen	NA
RNU6-510P	0	NA	NA	4	Whole Blood	NA
FHL3	0	2.51	5.97E-03	5	monocyte, neutrophil, T-cell, neutrophil CD15, T-cell CD4, T-cell CD8, LCL, neutrophil CD16, LCL, T CD4 naive, T CD4 naive activated, T CD8 naive, T CD4 TFH, T CD4 TH1, T CD4 TH17, T CD4 TH2, T CD4 TH1 17, T CD4 TH2, T CD4 memory TREG, T CD4 naive TREG, Whole Blood, Lung, Small Intestine Terminal Ileum, Spleen	NA
UTP11L	0	-0.45	6.74E-01	5	monocyte, T-cell CD4, T-cell CD8, Whole Blood, Lung	NA
RRAGC	0	0.43	3.35E-01	0	NA	GM12878
RP5-864K19.4	0	NA	NA	0	NA	GM12878
CTTNBP2NL	0	-0.73	7.66E-01	0	NA	GM12878
ST1L	0	-1.47	9.29E-01	0	NA	GM12878
CAPZA1	0	-1.33	9.09E-01	0	NA	GM12878
MAGI3	325	10.48	5.51E-26	5	Whole Blood	GM12878
PHTF1	74	12.40	1.36E-35	4	monocyte CD14, monocyte naive, Whole Blood	NA
RP4-730K3.3	10	NA	NA	3	Whole Blood	GM12878
RSBN1	58	12.96	1.05E-38	0	NA	GM12878
RP5-1073O3.2	31	NA	NA	3	Whole Blood	GM12878
PTPN22	75	11.51	6.04E-31	20	neutrophil, B-cell CD19, T-cell CD4, T-cell CD8, B cell naive, Whole Blood, Small Intestine Terminal Ileum	GM12878
AP4B1-AS1	73	NA	NA	18	Whole Blood, Lung, Spleen	NA
BCL2L15	36	9.87	2.77E-23	20	LCL, B cell naive, T CD4 TH17, T CD4 TH2, T CD4 naive TREG, Whole Blood	NA
AP4B1	32	11.40	2.23E-30	19	monocyte, neutrophil, neutrophil CD15, B-cell CD19, Whole Blood, Spleen	Spleen, GM12878
DCLRE1B	20	9.68	1.84E-22	12	monocyte, monocyte CD14, monocyte naive, Whole Blood	Spleen, GM12878
RP5-1073O3.7	7	NA	NA	0	NA	Spleen, GM12878
HIPK1	17	6.12	4.83E-10	0	NA	NA
OLFML3	12	4.62	1.96E-06	0	NA	NA
DENND2C	0	-1.53	9.37E-01	0	NA	GM12878
NRAS	0	0.50	3.09E-01	0	NA	GM12878
CSDE1	0	0.45	3.25E-01	0	NA	GM12878
AQP10	0	0.58	2.82E-01	0	NA	GM12878
ATP8B2	0	1.49	6.83E-02	1	Whole Blood	GM12878
RNU7-57P	0	NA	NA	0	NA	GM12878
IL6R	35	6.95	1.87E-12	1	Whole Blood	NA
TDRD10	0	3.39	3.44E-04	1	Lung	NA
FCRL3	13	6.73	8.33E-12	0	NA	NA
FCRL2	9	5.78	3.65E-09	0	NA	NA
FCRL1	34	6.43	6.26E-11	0	NA	GM12878
KCNJ10	0	-0.42	6.22E-01	0	NA	GM12878
IGSF8	0	0.45	3.26E-01	0	NA	GM12878
PEA15	0	1.63	5.12E-02	0	NA	GM12878
AL121987.1	0	NA	NA	0	NA	GM12878
RP11-574F21.2	0	NA	NA	0	NA	GM12878
SLAMF6	4	4.03	2.83E-05	0	NA	Spleen, GM12878
CD84	0	2.67	3.81E-03	0	NA	Spleen, GM12878
SLAMF1	0	2.30	1.06E-02	0	NA	GM12878
CD48	0	-0.13	5.52E-01	0	NA	GM12878
SLAMF7	0	2.31	1.06E-02	0	NA	GM12878
LY9	0	0.15	4.42E-01	0	NA	GM12878
CD244	0	0.45	3.28E-01	0	NA	GM12878
ITLN1	0	-0.09	5.38E-01	0	NA	GM12878
RP11-544M22.13	0	-0.95	8.30E-01	0	NA	GM12878
TSTD1	0	-0.61	7.30E-01	0	NA	GM12878
USF1	0	-0.46	6.76E-01	0	NA	GM12878
ARHGAP30	0	-0.05	5.20E-01	0	NA	GM12878
SUCO	0	0.65	2.59E-01	0	NA	GM12878
FASLG	0	-0.02	5.09E-01	0	NA	GM12878
RP3-395P12.2	0	NA	NA	0	NA	GM12878
TNFSF4	2	5.00	2.93E-07	0	NA	GM12878
PRDX6	0	1.37	8.55E-02	0	NA	GM12878
ANKRD45	0	1.09	1.39E-01	0	NA	GM12878
KLHL20	0	0.78	2.18E-01	0	NA	GM12878
CENPL	0	0.73	2.32E-01	0	NA	GM12878

DARS2	0	0.85	1.99E-01	0	NA	GM12878
GAS5	0	NA	NA	0	NA	GM12878
SNORD78	0	NA	NA	0	NA	GM12878
ZBTB37	0	0.41	3.41E-01	0	NA	GM12878
RC3H1	0	0.57	2.86E-01	0	NA	GM12878
RP11-160H22.3	0	NA	NA	0	NA	GM12878
RP11-160H22.5	0	NA	NA	0	NA	GM12878
RABGAP1L	0	-0.32	6.24E-01	0	NA	GM12878
LBH	8	1.96	2.50E-02	1	neutrophil, neutrophil CD15, neutrophil CD16, Monocyte non classical, Whole Blood	NA
AC104698.1	0	NA	NA	1	Whole Blood	NA
LCAT1	0	-0.10	5.39E-01	0	NA	Spleen, GM12878
ATP1B3P1	0	NA	NA	0	NA	Spleen, GM12878
PAPOLG	15	2.51	6.08E-03	0	NA	Spleen, GM12878
AC010733.4	26	NA	NA	0	NA	GM12878
REL	25	5.70	5.84E-09	1	monocyte	GM12878
RP11-373L24.1	9	NA	NA	1	Whole Blood	NA
NONOP2	8	NA	NA	0	NA	GM12878
PUS10	14	3.88	5.25E-05	1	monocyte naive, LCL, Whole Blood, Lung, Spleen	GM12878
PEX13	3	4.18	1.44E-05	0	NA	GM12878
KIAA1841	1	1.87	3.09E-02	0	NA	GM12878
AC016747.3	0	NA	NA	0	NA	GM12878
C2orf74	0	2.20	1.38E-02	0	NA	GM12878
AHSA2	0	2.40	8.26E-03	1	Whole Blood	GM12878
VPS54	0	2.58	4.93E-03	0	NA	GM12878
SERTAD2	0	1.36	8.70E-02	0	NA	GM12878
AC007365.3	0	NA	NA	0	NA	GM12878
CEP68	0	-0.54	7.04E-01	0	NA	GM12878
RAB1A	0	-0.79	7.86E-01	0	NA	GM12878
ACTR2	0	2.76	2.88E-03	1	Whole Blood	GM12878
SPRED2	154	7.71	6.14E-15	11	Whole Blood	Lung, Spleen, GM12878
AC074391.1	31	NA	NA	0	NA	Lung, Spleen, GM12878
RP11-474G23.3	0	NA	NA	0	NA	GM12878
DGUOK	0	3.86	5.60E-05	3	T-cell CD4	NA
MOB1A	0	0.40	3.43E-01	0	NA	GM12878
MTHFD2	0	0.29	3.84E-01	0	NA	GM12878
AFF3	103	5.53	1.64E-08	11	B-cell CD19, T-cell CD4, LCL, Whole Blood	NA
LONRF2	5	1.09	1.39E-01	4	Whole Blood	NA
ASNSD1	0	-1.51	9.35E-01	0	NA	GM12878
ANKAR	0	-0.91	8.20E-01	0	NA	GM12878
ORMDL1	0	-1.55	9.39E-01	0	NA	GM12878
PMS1	0	-1.96	9.75E-01	0	NA	GM12878
HIBCH	0	1.28	1.01E-01	0	NA	GM12878
INPP1	0	0.54	2.93E-01	0	NA	GM12878
TMEM194B	0	-0.04	5.15E-01	0	NA	GM12878
AC093388.3	0	NA	NA	0	NA	GM12878
NAB1	0	5.09	1.77E-07	0	NA	GM12878
AC005540.3	0	NA	NA	0	NA	Spleen, GM12878
GLS	0	2.30	1.07E-02	0	NA	Spleen, GM12878
STAT1	11	4.47	3.87E-06	0	NA	GM12878
AC067945.2	11	NA	NA	0	NA	GM12878
AC067945.4	15	NA	NA	0	NA	GM12878
STAT4	73	10.24	6.91E-25	0	NA	GM12878
AC092614.2	0	NA	NA	0	NA	GM12878
MYO1B	0	-0.95	8.29E-01	0	NA	GM12878
NABP1	0	-0.95	8.29E-01	0	NA	GM12878
FAM117B	0	0.71	2.38E-01	0	NA	GM12878
CARF	0	1.42	7.77E-02	0	NA	GM12878
RAPH1	0	1.12	1.32E-01	0	NA	Spleen, GM12878
CD28	60	6.70	1.01E-11	3	T CD4 naive, T CD4 TFH, T CD4 TH17, T CD4 TH1 17, T CD4 TH2, T CD4 memory TREG, T CD4 naive TREG, Whole Blood	GM12878
KRT18P39	38	NA	NA	5	T CD4 naive, T CD4 naive activated, T CD8 naive, T CD8 naive activated, T CD4 TFH, T CD4 TH1, T CD4 TH17, T CD4 TH1 17, T CD4 TH2, T CD4 memory TREG, T CD4 naive TREG, Whole Blood, Lung, Small Intestine Terminal Ileum, Spleen	NA
AC125238.1	36	NA	NA	5	Whole Blood	NA
NPM1P33	40	NA	NA	3	T CD4 naive, T CD8 naive, T CD4 TFH, T CD4 TH1, T CD4 TH17, T CD4 TH2, T CD4 memory TREG, T CD4 naive TREG, Whole Blood	NA
CTLA4	25	6.82	4.70E-12	4	T-cell CD4, T-cell CD8	GM12878
ICOS	14	5.04	2.28E-07	0	NA	NA
INO80D	0	3.33	4.39E-04	0	NA	GM12878
AC007383.3	0	NA	NA	0	NA	GM12878
RFTN1	0	-1.74	9.59E-01	0	NA	GM12878
AC091493.1	0	NA	NA	0	NA	GM12878
PLCL2	89	6.19	3.10E-10	0	NA	NA
RP11-222K16.2	5	NA	NA	1	Lung	NA
EOMES	7	5.68	6.60E-09	1	Whole Blood	NA
AZ12	0	0.05	4.81E-01	0	NA	GM12878
ZCWPW2	0	0.51	3.04E-01	0	NA	GM12878
CLNK	0	2.29	1.10E-02	1	B-cell CD19, T CD4 TH17, T CD4 TH2, T CD4 memory TREG, T CD4 naive TREG	GM12878
RP11-61G19.1	2	NA	NA	0	NA	GM12878
HS3ST1	0	-1.62	9.48E-01	1	LCL	Spleen, GM12878
FAM173B	0	-0.93	8.23E-01	0	NA	GM12878
CTD-2256P15.1	0	NA	NA	0	NA	GM12878
CCT5	0	0.18	4.28E-01	0	NA	GM12878
ROPN1L-AS1	0	NA	NA	0	NA	GM12878
ROPN1L	0	1.11	1.34E-01	0	NA	GM12878
DAP	40	4.66	1.62E-06	1	monocyte, B-cell CD19, LCL, T-cell CD4, T-cell CD8, macrophage naive, T CD4 TFH, T CD4 TH1 17, T CD4 memory TREG, Whole Blood, Cells EBV-transformed lymphocytes, Lung, Small Intestine Terminal Ileum, Spleen	NA
IL6ST	0	-1.81	9.65E-01	1	monocyte, T-cell, Whole Blood	Spleen, GM12878
CTD-2031P19.5	0	NA	NA	1	Whole Blood	NA
CTD-2031P19.3	0	NA	NA	0	NA	Spleen, GM12878
ANKRD55	23	6.06	6.67E-10	1	T-cell CD4, Whole Blood	NA
CTC-236F12.4	0	-0.24	5.94E-01	0	NA	Spleen, GM12878
MAP3K1	0	0.85	1.99E-01	0	NA	Spleen, GM12878
AC008937.3	0	NA	NA	0	NA	GM12878
SETD9	0	0.15	4.41E-01	0	NA	GM12878
PAM	0	2.45	7.06E-03	2	monocyte CD14, neutrophil CD15, LCL, neutrophil CD16, Whole Blood	GM12878
EIF3KP1	0	NA	NA	2	Whole Blood, Lung, Spleen	NA
GIN1	0	3.24	5.89E-04	2	neutrophil, T-cell CD4, T-cell CD8, B-cell CD19	NA
PPIP5K2	2	3.29	5.02E-04	2	monocyte, neutrophil, T-cell, monocyte naive, LCL, Whole Blood, Spleen	NA
C5orf30	62	5.82	2.98E-09	2	T-cell, T CD4 memory TREG	NA
NUDT12	0	-0.55	7.08E-01	0	NA	GM12878
SKP1	0	5.01	2.71E-07	0	NA	GM12878
DUSP22	0	-0.69	7.54E-01	0	NA	GM12878
IRF4	6	4.64	1.78E-06	0	NA	NA
TBC1D7	0	-0.06	5.24E-01	0	NA	GM12878
RANBP9	0	-0.28	6.09E-01	0	NA	GM12878
RNF182	0	0.01	4.96E-01	0	NA	GM12878
CD83	10	5.95	1.38E-09	0	NA	NA
RP11-560J1.2	0	NA	NA	0	NA	GM12878
JARID2	0	1.28	1.00E-01	0	NA	GM12878
JARID2-AS1	0	NA	NA	0	NA	GM12878
DTNBP1	0	0.00	4.99E-01	0	NA	GM12878
RP5-1120P11.1	0	NA	NA	0	NA	Spleen, GM12878
RP5-1120P11.3	0	NA	NA	0	NA	Spleen, GM12878
RP1-302G2.5	17	NA	NA	1	Whole Blood	NA
HSP90AB1	17	5.67	7.23E-09	0	NA	NA
SLC35B2	22	4.97	3.32E-07	0	NA	NA
NFKBIE	26	9.62	3.36E-22	2	Whole Blood	NA

TMEM151B	63	7.37	8.28E-14	6	Whole Blood	NA
RP11-444E17.6	64	8.25	8.21E-17	0	NA	NA
TCTE1	40	6.59	2.24E-11	6	Whole Blood, Small Intestine Terminal Ileum, Spleen	NA
AARS2	40	8.77	9.10E-19	7	LCL, T CD4 naive TREG, Whole Blood	Spleen
SPATS1	0	2.39	8.35E-03	0	NA	Spleen
BVES	0	0.84	2.00E-01	0	NA	GM12878
BVES-AS1	0	NA	NA	0	NA	GM12878
PREP	0	-0.42	6.63E-01	0	NA	GM12878
PRDM1	0	4.18	1.47E-05	0	NA	GM12878
RP11-134E15.3	0	NA	NA	0	NA	GM12878
AIM1	0	0.99	1.61E-01	0	NA	GM12878
IL20RA	0	-0.91	8.17E-01	0	NA	GM12878
IL22RA2	0	0.39	3.47E-01	0	NA	GM12878
RP11-356I2.4	55	NA	NA	0	NA	GM12878
TNFAIP3	23	8.80	6.76E-19	0	NA	GM12878
RSPH3	0	1.18	1.19E-01	0	NA	GM12878
TAGAP	14	3.08	1.05E-03	0	NA	Spleen,GM12878
RP11-13P5.1	0	NA	NA	0	NA	GM12878
RPS6KA2	0	0.16	4.37E-01	2	neutrophil, neutrophil CD15, Whole Blood	Spleen
RPS6KA2-IT1	0	NA	NA	1	neutrophil	NA
FAM103A2P	0	NA	NA	1	neutrophil	NA
RP11-514O12.4	68	5.33	4.89E-08	2	Whole Blood	GM12878
RPS6KA2-AS1	0	NA	NA	1	T CD8 naive	NA
RNASET2	74	8.54	6.97E-18	2	monocyte, neutrophil, T-cell, neutrophil CD15, T-cell CD4, T-cell CD8, neutrophil CD16, T CD4 naive, T CD4 naive activated, T CD8 naive, T CD8 naive activated, NK, T CD4 TFH, T CD4 TH1, T CD4 TH17, T CD4 TH1 17, T CD4 TH2, T CD4 naive TREG, Whole Blood, Lung	GM12878
AL133458.1	22	NA	NA	2	T CD4 naive, T CD4 naive activated, T CD8 naive, T CD8 naive activated, NK, T CD4 TFH, T CD4 TH1, T CD4 TH17, T CD4 TH1 17, T CD4 TH2, T CD4 naive TREG, Whole Blood	NA
RP1-167A14.2	189	NA	NA	2	Whole Blood	GM12878
MIR3939	81	NA	NA	1	Whole Blood	GM12878
FGFR1OP	210	6.78	6.17E-12	2	Whole Blood, Lung	GM12878
RP11-517H2.6	349	NA	NA	0	NA	GM12878
CCR6	66	15.08	1.04E-51	2	B-cell CD19, T CD4 TFH, T CD4 TH17, T CD4 TH1 17, Whole Blood, Spleen	GM12878
HNRNP2B1	0	-0.76	7.75E-01	0	NA	GM12878
CBX3	0	0.40	3.45E-01	0	NA	GM12878
HOUA7	0	0.37	3.54E-01	0	NA	GM12878
RP1-170O19.21	0	NA	NA	0	NA	GM12878
HOUA9	0	-1.56	9.41E-01	0	NA	GM12878
HOUA10-AS	0	NA	NA	0	NA	GM12878
MIR196B	0	NA	NA	0	NA	GM12878
HOUA11	0	-1.20	8.86E-01	0	NA	GM12878
HOUA11-AS	0	NA	NA	0	NA	GM12878
RP1-170O19.14	0	NA	NA	0	NA	GM12878
HOUA13	0	-2.04	9.79E-01	0	NA	GM12878
HOTTIP	0	NA	NA	0	NA	GM12878
JAZF1	15	4.42	4.95E-06	1	T-cell CD4, T-cell, T CD4 naive, T CD4 naive activated, T CD4 naive TREG, Whole Blood	NA
JAZF1-AS1	0	NA	NA	1	Whole Blood, Lung	NA
GTF2IRD1	9	4.63	1.83E-06	0	NA	NA
PEX1	0	2.90	1.88E-03	0	NA	GM12878
RBM48	0	1.72	4.26E-02	0	NA	GM12878
FAM133B	0	3.27	5.35E-04	0	NA	GM12878
CDK6	12	5.73	4.94E-09	0	NA	Spleen,GM12878
AC002454.1	0	NA	NA	0	NA	Spleen,GM12878
SAMD9	0	2.61	4.47E-03	0	NA	GM12878
SAMD9L	0	2.21	1.35E-02	0	NA	GM12878
CCDC132	0	1.17	1.21E-01	0	NA	GM12878
IMPDH1	0	-0.47	6.83E-01	0	NA	GM12878
RP11-212P7.3	0	NA	NA	0	NA	GM12878
HILPDA	0	-1.17	8.78E-01	0	NA	GM12878
RP11-155G14.6	0	NA	NA	0	NA	GM12878
METTL2B	0	-0.18	5.72E-01	0	NA	GM12878
AC018638.1	0	NA	NA	1	Lung	NA
CAUJ	0	-0.14	5.54E-01	0	NA	GM12878
RN7SL81P	0	NA	NA	2	NK	NA
KCP	0	NA	NA	1	LCL	NA
RP11-309L24.6	0	NA	NA	0	NA	GM12878
IRF5	25	7.63	1.17E-14	4	monocyte CD14, neutrophil CD15, B-cell CD19, LCL, T-cell CD4, T-cell CD8, neutrophil CD16, macrophage naive, Whole Blood, Lung, Small Intestine Terminal Ileum, Spleen	GM12878
TNPO3	73	5.84	2.61E-09	4	monocyte, neutrophil, B-cell CD19, monocyte CD14, neutrophil CD15, B-cell CD19, T-cell CD4, T-cell CD8, NK, Whole Blood	GM12878
ODCP	10	NA	NA	1	Monocyte non classical	NA
TPI1P2	8	NA	NA	0	NA	GM12878
RP11-286H14.2	2	NA	NA	0	NA	GM12878
RP11-286H14.1	2	NA	NA	0	NA	GM12878
TSPAN33	0	1.30	9.61E-02	0	NA	GM12878
RP11-286H14.6	0	NA	NA	0	NA	GM12878
SMO	0	2.47	6.67E-03	0	NA	GM12878
CTC-493P15.2	0	NA	NA	0	NA	GM12878
MTMR9	0	1.11	1.33E-01	0	NA	GM12878
FAM167A	15	5.36	4.25E-08	0	NA	NA
BLK	45	6.35	1.08E-10	0	NA	GM12878
NEIL2	0	-1.08	8.61E-01	0	NA	GM12878
RP11-297N6.4	0	0.76	2.23E-01	0	NA	GM12878
CTSB	0	-1.24	8.92E-01	0	NA	GM12878
RP11-589N15.1	0	NA	NA	0	NA	GM12878
CCL21	7	5.78	3.68E-09	0	NA	NA
FAM205A	13	4.96	3.58E-07	0	NA	NA
MEGF9	0	4.30	8.62E-06	4	monocyte CD14, T-cell CD4, B-cell CD19, LCL	NA
FBXW2	0	3.61	1.56E-04	3	T-cell	Spleen,GM12878
RP11-271I.4	0	NA	NA	0	NA	Spleen,GM12878
PSMD5	0	3.97	3.56E-05	4	monocyte CD14, B-cell CD19, Whole Blood	Spleen,GM12878
PSMD5-AS1	0	NA	NA	4	B cell naive, T CD4 naive, T CD4 naive activated, T CD8 naive, T CD8 naive activated, Monocyte classical, Monocyte non classical, NK, T CD4 TFH, T CD4 TH1, T CD4 TH17, T CD4 TH1 17, T CD4 TH2, T CD4 memory TREG, T CD4 naive TREG, Whole Blood, Cells EBV-transformed lymphocytes, Lung, Small Intestine Terminal Ileum, Spleen	NA
PHF19	25	4.84	6.36E-07	4	T-cell CD4, T-cell CD8, Whole Blood	Spleen,GM12878
TRAF1	83	7.22	2.55E-13	4	monocyte, blood, T CD4 naive, T CD4 TFH, T CD4 TH17, T CD4 memory TREG, T CD4 naive TREG	Spleen,GM12878
C5	12	3.90	4.86E-05	4	neutrophil, Whole Blood	NA
CNTRL	0	2.86	2.09E-03	4	monocyte, Whole Blood	NA
RN7SL181P	0	NA	NA	0	NA	GM12878
GSN	0	0.56	2.86E-01	3	monocyte, LCL	NA
GGTA1P	0	NA	NA	4	Whole Blood	NA
FAM208B	0	-0.08	5.30E-01	0	NA	GM12878
RP11-318E3.9	0	NA	NA	0	NA	GM12878
ANKRD16	0	2.49	6.35E-03	0	NA	GM12878
FBXO18	0	3.03	1.21E-03	0	NA	GM12878
IL2RA	38	7.42	6.07E-14	0	NA	GM12878
RBM17	0	3.50	2.33E-04	0	NA	Spleen,GM12878
PKF3B	0	1.77	3.86E-02	1	T-cell, monocyte naive	Spleen,GM12878
MIR3155A	0	NA	NA	0	NA	Spleen,GM12878
RP11-414H17.5	0	NA	NA	0	NA	Spleen
DKFZP67F071.1	15	4.13	1.81E-05	1	Whole Blood	NA
PRKCC	17	6.93	2.10E-12	0	NA	NA
SFMBT2	0	0.86	1.94E-01	0	NA	GM12878

GATA3	16	6.49	4.36E-11	0	NA	NA
ZNF438	0	4.74	1.07E-06	1	Whole Blood	GM12878
ZEB1-AS1	0	NA	NA	0	NA	GM12878
ZEB1	0	-0.73	7.68E-01	0	NA	GM12878
SPTLC1P1	0	NA	NA	0	NA	GM12878
ARHGAP12	0	1.89	2.93E-02	0	NA	GM12878
ARHGAP22	0	-0.83	7.98E-01	1	T CD4 TH2	GM12878
WDFY4	99	7.19	3.24E-13	0	NA	NA
RP11-563N6.6	31	NA	NA	2	B cell naive, Whole Blood, Lung, Spleen	NA
ARID5B	38	8.89	2.93E-19	7	Whole Blood	Spleen,GM12878
RTKN2	188	6.89	2.85E-12	13	T-cell CD4, monocyte naive, T CD4 naive, T CD4 TH1, T CD4 TH2, T CD4 memory TREG, Whole Blood, Spleen	GM12878
RP11-120C12.3	41	NA	NA	5	macrophage naive, monocyte naive	NA
ZNF365	0	2.05	2.03E-02	8	monocyte naive, Lung	GM12878
NRBF2	0	1.95	2.56E-02	0	NA	GM12878
WEE1	0	0.86	1.96E-01	1	Whole Blood	Spleen,GM12878
snoU13	0	NA	NA	0	NA	Spleen,GM12878
SWAP70	29	6.01	9.26E-10	2	B-cell CD19, LCL, Whole Blood, Spleen	GM12878
SBF2-AS1	17	NA	NA	2	Whole Blood	NA
SBF2	9	3.61	1.55E-04	2	Whole Blood	NA
RP11-351I24.1	0	NA	NA	0	NA	Spleen,GM12878
ADM	0	0.16	4.38E-01	0	NA	Spleen,GM12878
AMPD3	0	0.80	2.11E-01	0	NA	Spleen,GM12878
RP11-783K16.14	0	NA	NA	1	Whole Blood	NA
DNAJC4	0	3.45	2.85E-04	1	Whole Blood	NA
VEGFB	0	3.16	7.87E-04	5	T-cell, Whole Blood	NA
PPP1R14B	0	3.64	1.36E-04	5	Whole Blood	NA
RP11-783K16.5	0	NA	NA	5	Whole Blood	NA
RP11-783K16.13	0	NA	NA	5	Whole Blood	NA
BAD	3	3.28	5.15E-04	2	Whole Blood	NA
ESRRA	3	0.51	3.06E-01	5	Whole Blood	NA
TRMT112	2	1.70	4.49E-02	5	Whole Blood	NA
PRDX5	3	2.96	1.54E-03	5	blood, LCL, Whole Blood monocyte, neutrophil, T-cell, LCL, B cell naive, T CD4 naive, T CD4 naive activated, T CD8 naive, T CD8 naive activated, Monocyte classical, Monocyte non classical, NK, T CD4 TFH, T CD4 TH1, T CD4 TH17, T CD4 TH17, T CD4 TH17, T CD4 TH2, T CD4 memory TREG, T CD4 naive TREG, Whole Blood, Cells EBV-transformed lymphocytes, Lung, Spleen	NA
AP003774.1	8	NA	NA	5	monocyte, neutrophil CD15, B-cell CD19, neutrophil CD16, Whole Blood, Spleen	NA
CCDC88B	31	6.68	1.19E-11	5	monocyte, neutrophil CD15, B-cell CD19, neutrophil CD16, Whole Blood, Spleen	NA
RPS6KA4	35	6.01	9.10E-10	5	Whole Blood	NA
AP003774.6	0	NA	NA	2	Whole Blood	NA
NRXN2	20	5.03	2.49E-07	1	Lung	NA
MEN1	18	6.80	5.13E-12	1	Whole Blood	NA
TPCN2	22	4.31	8.07E-06	1	B cell naive, T CD4 naive, T CD4 naive activated, T CD8 naive, T CD8 naive activated, Monocyte classical, Monocyte non classical, T CD4 TFH, T CD4 TH1, T CD4 TH17, T CD4 TH17, T CD4 TH2, T CD4 memory TREG, T CD4 naive TREG, Whole Blood, Lung, Spleen	NA
CLPB	0	1.67	4.77E-02	0	NA	Spleen,GM12878
PDE2A	28	5.23	8.67E-08	3	neutrophil, Whole Blood	NA
RP11-169D4.2	0	NA	NA	2	Whole Blood	NA
RP11-31L22.3	17	NA	NA	2	Whole Blood	NA
ARAP1	38	5.15	1.32E-07	3	Whole Blood	NA
ARAP1-AS1	32	NA	NA	3	Whole Blood	NA
ARAP1-AS2	29	NA	NA	3	Whole Blood	NA
STARD10	0	2.33	9.94E-03	3	neutrophil, neutrophil CD1, Whole Blood	NA
ATG16L2	0	1.39	8.21E-02	3	Whole Blood	NA
FCHSD2	0	3.10	9.66E-04	3	Whole Blood	NA
CWC15	0	0.02	4.94E-01	0	NA	GM12878
KDM4D	0	-0.22	5.89E-01	0	NA	GM12878
SRSF8	0	NA	NA	0	NA	GM12878
SRSF8	0	NA	NA	0	NA	GM12878
ENDOD1	0	-1.82	9.66E-01	0	NA	GM12878
RP11-712B9.2	0	NA	NA	0	NA	GM12878
RP11-770J1.5	0	3.01	1.31E-03	0	NA	GM12878
ATP9L	0	2.95	1.61E-03	0	NA	GM12878
RP11-770J1.7	0	NA	NA	0	NA	GM12878
RP11-770J1.4	0	1.00	1.59E-01	0	NA	GM12878
KMT2A	0	2.15	1.59E-02	0	NA	GM12878
IFT46	0	2.67	3.79E-03	0	NA	GM12878
ARCN1	1	2.79	2.67E-03	0	NA	GM12878
PHLDB1	20	5.66	7.67E-09	0	NA	NA
TREH	13	3.07	1.07E-03	6	Small Intestine Terminal Ileum	NA
AP002954.6	11	NA	NA	0	NA	GM12878
AP002954.4	101	NA	NA	9	Whole Blood	NA
DDX6	43	6.33	1.26E-10	10	Whole Blood, Lung	GM12878
BCL9L	0	3.15	8.26E-04	0	NA	Spleen,GM12878
MIR4492	0	NA	NA	0	NA	Spleen,GM12878
UPK2	1	2.49	6.37E-03	0	NA	Spleen,GM12878
RN7SL688P	0	NA	NA	0	NA	Spleen,GM12878
RP11-1007G5.2	0	NA	NA	0	NA	Spleen,GM12878
RP11-744N12.3	16	NA	NA	0	NA	Spleen,GM12878
FLI1	0	3.64	1.34E-04	0	NA	Spleen,GM12878
SENCR	0	NA	NA	0	NA	Spleen,GM12878
KCNJ5	0	-0.42	6.64E-01	0	NA	Spleen,GM12878
ITGA7	0	0.48	3.16E-01	0	NA	GM12878
RP11-644F5.10	0	-0.44	6.71E-01	0	NA	GM12878
BLOC1S1	0	0.39	3.47E-01	0	NA	GM12878
RDH5	0	-0.78	7.82E-01	0	NA	GM12878
GDF11	0	1.84	3.31E-02	1	Whole Blood	NA
WIBG	0	1.68	4.66E-02	0	NA	GM12878
DGKA	0	1.82	3.47E-02	0	NA	GM12878
PMEL	7	5.01	2.66E-07	0	NA	NA
CDK2	7	4.85	1.70E-06	0	NA	GM12878
RP11-973D8.4	2	NA	NA	0	NA	GM12878
RAB5B	20	6.52	3.58E-11	0	NA	NA
SUOX	11	6.13	4.26E-10	2	monocyte, T-cell, B-cell CD19, T-cell CD4, T-cell CD8, LCL, Monocyte classical, T CD4 TH17, T CD4 TH17, T CD4 TH2, T CD4 memory TREG, T CD4 naive TREG, Whole Blood, Lung, Small Intestine Terminal Ileum, Spleen	NA
IKZF4	4	6.33	1.22E-10	2	LCL, T CD4 memory TREG, Whole Blood	GM12878
RP11-603J24.4	1	NA	NA	0	NA	GM12878
RPS26	1	5.94	1.42E-09	2	monocyte, neutrophil, T-cell, monocyte CD14, neutrophil CD15, T-cell CD4, T-cell CD8, B-cell CD19, T-cell, LCL, neutrophil CD16, macrophage naive, monocyte naive, LCL, scRNA eQTLs/B cell, scRNA eQTLs/DC, scRNA eQTLs/NK, scRNA eQTLs/Monocyte, scRNA eQTLs/Classical Monocyte, scRNA eQTLs/Non classical Monocyte, scRNA eQTLs/T CD4, scRNA eQTLs/T CD8, scRNA eQTLs/PBMC, T CD8 naive activated, Whole Blood, Cells EBV-transformed lymphocytes, Lung, Small Intestine Terminal Ileum, Spleen	GM12878
ERBB3	13	7.06	8.61E-13	2	T-cell, T CD8 naive, T CD4 TH17, T CD4 naive TREG, Whole Blood	NA
RP11-603J24.9	0	3.43	3.00E-04	2	Whole Blood	NA
PA2G4	0	2.82	2.41E-03	0	NA	GM12878
RP11-603J24.17	0	NA	NA	0	NA	GM12878
RPL41	0	2.29	1.11E-02	0	NA	GM12878
ZC3H10	0	1.64	5.04E-02	0	NA	GM12878
ESYT1	0	3.68	1.16E-04	1	Whole Blood	GM12878
RP11-603J24.6	0	NA	NA	0	NA	GM12878
RP11-603J24.5	0	NA	NA	0	NA	GM12878
MYL6	0	1.87	3.09E-02	1	Whole Blood	NA
RP11-977G19.5	0	NA	NA	0	NA	GM12878
SMARCC2	0	2.73	3.20E-03	1	Whole Blood	GM12878

COG6	286	7.63	1.19E-14	8	monocyte, neutrophil, T-cell, monocyte CD14, T-cell CD4, B-cell CD19, macrophage naive, monocyte naive, LCL, B cell naive, T CD4 TFH, T CD4 TH1, T CD4 TH17, T CD4 TH17, T CD4 TH2, T CD4 naive TREG, Whole Blood, Lung	GM12878
FOXO1	0	1.51	6.51E-02	0	NA	Spleen,GM12878
MRPS31	0	2.36	9.17E-03	0	NA	Spleen,GM12878
SLC25A15	0	0.67	2.50E-01	0	NA	Spleen
TPTE2P5	0	NA	NA	0	NA	GM12878
SUGT1P3	0	NA	NA	0	NA	GM12878
TMEM229B	0	0.73	2.33E-01	1	Lung	NA
RDIH1	0	-1.62	9.47E-01	0	NA	GM12878
RN7SL369P	0	NA	NA	0	NA	GM12878
RAD51B	15	5.79	3.58E-09	0	NA	NA
CTD-2325P2.4	0	NA	NA	0	NA	Lung,Spleen,GM12878
ZFP36L1	34	6.92	2.18E-12	0	NA	Lung,Spleen,GM12878
LINC00638	0	NA	NA	2	Whole Blood	NA
CEP170B	0	0.89	1.86E-01	2	blood	NA
CTD-3051D23.3	0	NA	NA	0	NA	Spleen
PLD4	43	6.97	1.62E-12	2	monocyte, LCL, Whole Blood	Spleen
AHNAK2	80	8.89	3.18E-19	2	LCL, Lung	NA
C14orf79	0	2.01	2.20E-02	2	Whole Blood, Lung	NA
CDCA4	0	1.76	3.93E-02	2	T-cell CD4, T-cell CD8, Whole Blood	NA
RP11-1008C21.2	0	NA	NA	0	NA	GM12878
FAM98B	0	3.65	1.31E-04	0	NA	GM12878
RASGRP1	31	7.68	7.85E-15	0	NA	GM12878
RP11-19J5.1	0	NA	NA	0	NA	Spleen
TLE3	0	0.98	1.64E-01	0	NA	Spleen,GM12878
CIB1	0	0.83	2.03E-01	4	monocyte, neutrophil, T-cell, Whole Blood, Lung	NA
GDPGP1	0	0.66	2.54E-01	2	Whole Blood	NA
NGRN	0	1.02	1.54E-01	0	NA	GM12878
RP11-697E2.7	0	NA	NA	3	Whole Blood	NA
RP11-697E2.9	0	NA	NA	0	NA	GM12878
GABARAPL3	30	6.09	5.61E-10	0	NA	NA
ZNF774	31	6.35	1.04E-10	4	Lung	Lung,Spleen,GM12878
IQGAP1	93	6.70	1.03E-11	4	monocyte, T-cell, macrophage naive, Whole Blood, Lung, Small Intestine Terminal Ileum, Spleen	GM12878
CRTC3	0	4.90	4.84E-07	4	B-cell CD19, T CD8 naive, T CD8 naive activated, Whole Blood	Spleen,GM12878
RP11-387D10.2	0	NA	NA	0	NA	GM12878
BLM	0	0.43	3.34E-01	0	NA	GM12878
AC068831.6	0	NA	NA	0	NA	GM12878
RCCD1	0	0.27	3.93E-01	0	NA	GM12878
DEXI	0	0.65	2.57E-01	0	NA	GM12878
RP11-876N24.5	0	NA	NA	0	NA	GM12878
RP11-876N24.4	0	NA	NA	0	NA	GM12878
CLEC16A	0	2.33	9.99E-03	0	NA	GM12878
SOCS1	0	0.75	2.26E-01	0	NA	GM12878
RP11-485G7.5	0	NA	NA	0	NA	Spleen,GM12878
LITAF	0	0.18	4.28E-01	0	NA	GM12878
SNN	17	5.90	1.78E-09	0	NA	GM12878
TXNDC11	36	6.32	1.31E-10	0	NA	GM12878
RP11-490O6.2	8	NA	NA	0	NA	GM12878
ZC3H7A	2	2.71	3.37E-03	0	NA	GM12878
RSL1D1	0	-0.26	6.03E-01	0	NA	GM12878
RP11-166B2.8	0	NA	NA	0	NA	GM12878
PRKCB	51	4.64	1.76E-06	1	neutrophil, monocyte CD14, neutrophil CD15, LCL, Monocyte classical, Whole Blood	GM12878
FAM57B	0	0.81	2.08E-01	0	NA	GM12878
ALDOA	0	1.46	7.28E-02	0	NA	GM12878
PPP4C	0	0.63	2.65E-01	0	NA	GM12878
TBX6	0	0.03	4.89E-01	0	NA	GM12878
YPEL3	0	0.57	2.85E-01	0	NA	GM12878
RP11-455F5.3	0	NA	NA	0	NA	GM12878
CD2BP2	0	2.43	7.47E-03	0	NA	GM12878
RP11-347C12.10	0	NA	NA	0	NA	GM12878
TBC1D10B	0	3.26	5.52E-04	0	NA	GM12878
MYLPF	0	2.49	6.43E-03	0	NA	GM12878
ZNF48	0	2.51	5.96E-03	0	NA	GM12878
44075	0	2.55	5.44E-03	0	NA	GM12878
44075	0	1.40	8.05E-02	0	NA	Spleen,GM12878
ZNF771	0	2.42	7.77E-03	0	NA	GM12878
DCTPP1	0	0.55	2.91E-01	0	NA	Spleen,GM12878
SEPHS2	0	3.45	2.82E-04	0	NA	GM12878
ZNF768	0	0.87	1.92E-01	0	NA	GM12878
ZNF747	2	0.10	4.59E-01	0	NA	GM12878
ZNF747	2	0.28	3.89E-01	0	NA	GM12878
AC002310.12	2	NA	NA	1	Whole Blood	GM12878
ZNF689	4	4.88	5.24E-07	0	NA	NA
PRR14	2	3.57	1.81E-04	1	Whole Blood	GM12878
FBR3	2	5.18	1.10E-07	0	NA	GM12878
RP11-146F11.1	1	NA	NA	0	NA	GM12878
SRCAP	1	6.25	2.10E-10	0	NA	GM12878
C16orf93	0	3.83	6.33E-05	1	monocyte CD14	NA
RNF40	0	3.49	2.38E-04	1	monocyte, neutrophil, neutrophil CD15, Whole Blood, Lung	NA
BCL7C	19	5.11	1.58E-07	0	NA	GM12878
MIR4519	6	NA	NA	0	NA	GM12878
MIR4519	3	NA	NA	0	NA	GM12878
AC106782.20	6	NA	NA	0	NA	GM12878
MIR762	3	NA	NA	0	NA	GM12878
CTF1	3	2.37	8.98E-03	0	NA	GM12878
RP11-196G11.2	0	NA	NA	1	Whole Blood, Lung, Spleen	NA
ZNF668	0	1.56	5.91E-02	1	Whole Blood	NA
VKORC1	0	1.18	1.19E-01	1	Whole Blood	NA
KAT8	0	1.26	1.03E-01	1	Lung	NA
C16orf74	0	-0.49	6.87E-01	0	NA	GM12878
MIR1910	0	NA	NA	0	NA	GM12878
RP11-566J23.4	0	NA	NA	0	NA	GM12878
EMC8	0	0.18	4.30E-01	0	NA	GM12878
RNU1-103P	0	NA	NA	0	NA	GM12878
COX411	0	0.62	2.68E-01	0	NA	GM12878
IRF8	0	1.53	6.34E-02	0	NA	Spleen,GM12878
RP11-542M13.3	0	NA	NA	0	NA	Spleen,GM12878
FBXL20	159	5.65	7.87E-09	10	neutrophil, Small Intestine Terminal Ileum	GM12878
CTB-131K11.1	28	NA	NA	8	Whole Blood	GM12878
MED1	65	5.14	1.35E-07	10	Whole Blood	GM12878
CDK12	115	5.51	1.80E-08	9	monocyte CD14, T-cell CD4	GM12878
PPP1R1B	0	3.00	1.35E-03	17	Whole Blood	NA
STARD3	0	1.04	1.50E-01	12	T-cell, Whole Blood	NA
TCAP	0	2.49	6.47E-03	2	monocyte	NA
PNMT	0	3.71	1.02E-04	17	Whole Blood, Lung	NA
PGAP3	0	4.85	6.33E-07	26	B-cell CD19, T-cell CD4, T-cell CD8, Whole Blood, Lung, Small Intestine Terminal Ileum	NA
MIEN1	0	0.93	1.77E-01	0	NA	GM12878
RP11-94L15.2	8	NA	NA	20	T CD4 TFH, T CD4 naive TREG, Whole Blood	NA
IKZF3	35	1.58	5.67E-02	14	T-cell CD8, B-cell CD19, T-cell CD4, T CD4 naive TREG, Whole Blood, Cells EBV-transformed lymphocytes	GM12878
ZBP2	46	6.03	8.34E-10	14	B-cell CD19, LCL, B cell naive, Whole Blood, Spleen	GM12878
GSDMB	55	5.87	2.21E-09	26	T-cell, B-cell CD19, T-cell, LCL, T-cell CD4, T-cell CD8, B cell naive, T CD4 naive, T CD4 naive activated, T CD8 naive, T CD8 naive activated, NK, T CD4 TFH, T CD4	NA

Gene	posMap SNPs	eqtlMap SNPs	ciMMapts	cell types	Z	P	Gene-level disease association p-value from MAGMA	Gene-level association from MAGMA
ORMDL3	34	5.91	1.72E-09	26			TH1, T CD4 TH17, T CD4 TH1 17, T CD4 TH2, T CD4 memory TREG, T CD4 naive TREG, Cells EBV-transformed lymphocytes, Whole Blood, Lung, Small Intestine Terminal Ileum, Spleen	NA
GSDMA	0	2.54	5.49E-03	17			T-cell, T-cell CD4, macrophage naive, T CD4 naive, T CD8 naive, T CD4 TFH, T CD4 TH17, T CD4 TH2, T CD4 memory TREG, T CD4 naive TREG, Whole Blood, Lung, Small Intestine Terminal Ileum	NA
PSMD3	0	1.99	2.32E-02	0			NA	GM12878
MED24	0	2.02	2.16E-02	4			blood	NA
NR1D1	0	1.47	7.06E-02	0			NA	GM12878
MSL1	0	2.06	1.99E-02	10			Whole Blood, Lung	GM12878
CASC3	0	2.23	1.27E-02	1			Whole Blood	NA
KRT24	0	1.56	5.97E-02	2			T CD4 naive activated	NA
RP5-1110E20.1	0	NA	NA	1			T CD4 naive activated	NA
RP11-64C12.8	0	NA	NA	0			NA	GM12878
RNU6-170P	0	NA	NA	0			NA	GM12878
TUBB6	0	-1.12	8.69E-01	0			NA	GM12878
SLMO1	0	-1.79	9.63E-01	0			NA	GM12878
CEP76	0	-0.12	5.48E-01	0			NA	Spleen,GM12878
RP11-973H7.5	0	NA	NA	1			Whole Blood	NA
RP11-973H7.4	0	NA	NA	1			NK, Whole Blood, Lung, Spleen	NA
RP11-973H7.1	39	NA	NA	1			NK, Whole Blood, Lung, Spleen	Spleen,GM12878
PTPN2	127	7.68	8.14E-15	1			Whole Blood	NA
RP11-773H22.1	0	NA	NA	0			NA	Spleen,GM12878
RP11-773H22.2	0	NA	NA	0			NA	Spleen,GM12878
SEH1L	0	0.42	3.38E-01	0			NA	GM12878
RP11-773H22.4	0	NA	NA	0			NA	GM12878
CEP192	0	0.94	1.73E-01	1			Whole Blood	GM12878
C19orf66	0	-0.35	6.36E-01	1			Whole Blood	NA
TYK2	2	3.21	6.67E-04	2			Whole Blood	Spleen,GM12878
MIR1181	0	NA	NA	0			NA	Spleen,GM12878
ILF3	1	5.86	2.36E-09	0			NA	NA
PLTP	0	0.23	4.10E-01	4			Whole Blood	NA
RP11-465L10.10	0	NA	NA	3			Whole Blood	NA
SLC12A5	7	2.53	5.63E-03	4			Whole Blood, Lung	NA
CD40	6	7.31	1.29E-13	4			monocyte, monocyte CD14, Whole Blood, Lung	NA
ZBTB46	34	5.48	2.15E-08	0			NA	NA
SYNJ1	0	0.52	3.02E-01	0			NA	GM12878
PAXBP1-AS1	0	NA	NA	0			NA	GM12878
PAXBP1	0	-0.23	5.93E-01	0			NA	GM12878
C21orf49	0	-1.52	9.36E-01	0			NA	GM12878
IFNAR2	0	1.42	7.77E-02	0			NA	Spleen,GM12878
IL10RB-AS1	0	NA	NA	0			NA	Spleen,GM12878
IL10RB	0	0.39	3.47E-01	0			NA	Spleen,GM12878
IFNAR1	0	0.45	3.28E-01	0			NA	Spleen,GM12878
IFNGR2	39	5.36	4.27E-08	0			NA	GM12878
TMEM50B	15	4.57	2.50E-06	0			NA	NA
DONSON	0	5.16	1.27E-07	0			NA	GM12878
ZBTB21	0	3.85	5.84E-05	0			NA	GM12878
ZNF295-AS1	0	NA	NA	0			NA	GM12878
RNA5SP492	0	NA	NA	0			NA	Spleen,GM12878
AP001623.1	0	NA	NA	0			NA	Spleen,GM12878
TFF2	0	1.31	9.59E-02	0			NA	GM12878
UBASH3A	4	5.45	2.59E-08	0			NA	Spleen,GM12878
PWP2	0	1.77	3.87E-02	0			NA	Spleen
C21orf33	0	2.37	8.99E-03	0			NA	Spleen
AP001055.6	0	NA	NA	0			NA	GM12878
ICOSLG	47	7.24	2.17E-13	0			NA	GM12878
DNMT3L	30	7.33	1.19E-13	0			NA	NA
AP001059.5	20	NA	NA	0			NA	GM12878
AIRE	16	7.14	4.63E-13	0			NA	NA
UBE2L3	109	7.05	9.05E-13	3			monocyte, neutrophil, monocyte CD14, neutrophil CD15, T-cell CD4, T-cell CD8, B-cell CD19, neutrophil CD16, Whole Blood	NA
YDJC	23	6.36	1.02E-10	3			Whole Blood	NA
CCDC116	17	1.79	3.67E-02	3			T CD4 TH2, Whole Blood, Lung, Small Intestine Terminal Ileum, Spleen	NA
KB-1440D3.14	0	NA	NA	3			Lung	NA
PPIL2	0	0.12	4.54E-01	3			Whole Blood	NA
YPEL1	0	1.24	1.07E-11	3			Whole Blood	NA
RPL3	38	6.64	1.57E-11	0			NA	NA
SYNGR1	36	6.14	4.07E-10	0			NA	NA
TAB1	8	3.30	4.88E-04	0			NA	Spleen,GM12878
MGAT3	0	4.28	9.30E-06	0			NA	GM12878
ATF4	0	2.79	2.61E-03	0			NA	Spleen,GM12878
UPK3A	4	3.95	3.97E-05	2			monocyte CD14, Whole Blood	NA
FAM118A	43	5.63	8.82E-09	2			monocyte, monocyte CD14, T-cell CD4, T-cell CD8, B-cell CD19, LCL, T-cell, macrophage naive, monocyte naive, scRNA eQTLs/T CD4, scRNA eQTLs/PBMC, B cell naive, T CD4 naive, T CD4 naive activated, T CD8 naive activated, Monocyte classical, Monocyte non classical, T CD4 memory TREG, T CD4 naive TREG, Whole Blood, Cells EBV-transformed lymphocytes, Lung, Small Intestine Terminal Ileum, Spleen	NA
SMC1B	52	5.21	9.39E-08	2			LCL, T CD8 naive activated, Whole Blood, Lung	NA
RIBC2	10	3.60	1.59E-04	2			monocyte, LCL, T CD8 naive activated, T CD4 TH1 17, Whole Blood, Lung	NA
FBLN1	0	-0.28	6.10E-01	2			Whole Blood	NA
P2RY10	12	5.88	2.07E-09	0			NA	GM12878
GPR174	31	5.16	1.21E-07	0			NA	NA
FAM58A	0	-0.05	5.19E-01	1			T CD4 TH2	NA
PDZD4	0	1.79	3.66E-02	3			Whole Blood	NA
L1CAM	2	5.28	6.44E-08	0			NA	NA
ARHGAP4	21	7.61	1.34E-14	0			NA	NA
NAI10	19	7.28	1.62E-13	0			NA	NA
RENBP	25	7.31	1.36E-13	0			NA	NA
HCFC1	38	8.12	2.34E-16	0			NA	NA
TMEM187	27	7.43	5.25E-14	5			Monocyte classical, Whole Blood, Lung, Small Intestine Terminal Ileum, Spleen	NA
IRAK1	17	8.50	9.09E-18	0			NA	Spleen
MIR718	11	NA	NA	0			NA	Spleen
MECP2	40	7.03	1.04E-12	1			Lung	GM12878
PLXNA3	0	3.19	7.03E-04	2			Whole Blood, Lung	NA
FAM3A	0	3.15	8.03E-04	2			Lung	NA

Z: Z-value for the gene-level association from MAGMA  
P: gene-level disease association p-value from MAGMA  
posMap SNPs: the number of SNPs mapped to gene based on positional mapping  
eqtlMap SNPs: the number of SNPs mapped to the gene based on eQTL mapping  
eqtlMapts: cell types with mapped eQTL effects  
ciMapts: cell types with mapped chromatin interactions



**Supplementary Table 9 | Three ATC groups significantly enriching RA-relevant genes as drug targets**

Group name	Odds ratio	Fisher Exact P	Padj	TargetGene:DrugNames
ANTINEOPLASTIC AGENTS	2.40	1.82E-05	1.54E-03	BTK:ibrutinib; CCND1:arsenic trioxide; CD19:blinatumomab; CDK4:palbociclib; CDK6:palbociclib; CTLA4:ipilimumab; DCK:fludarabine; FGFR4:lenvatinib; FLT1:sunitinib,sorafenib,pazopanib,axitinib,regorafenib,lenvatinib,nintedanib,tivozanib; HDAC1:vorinostat,romidepsin,panobinostat,belinostat; HDAC11:panobinostat,belinostat; HDAC3:vorinostat,panobinostat,belinostat; HDAC8:panobinostat,belinostat; HDAC9:panobinostat,belinostat; IL2RA:denileukin diftitox; IL2RB:denileukin diftitox; IL2RG:denileukin diftitox; JAK1:ruxolitinib; JAK2:ruxolitinib; LCK:dasatinib; MAPK11:regorafenib; MAPK3:arsenic trioxide; MET:crizotinib,cabozantinib; PARP2:olaparib; POLB:cytarabine; PRKCA:midostaurin; PSMB1:bortezomib,carfilzomib; PSMB2:carfilzomib; PSMB5:bortezomib,carfilzomib; RAF1:sorafenib,regorafenib,dabrafenib; RARG:tretinoin,alitretinoin; RPL3:omacetaxine mepesuccinate; RXRA:alitretinoin,bexarotene; RXRG:tretinoin,alitretinoin,bexarotene; SLAMF7:elotuzumab; SMO:vismodegib; TEK:regorafenib; TOP2A:etoposide,teniposide,doxorubicin,daunorubicin,epirubicin,aclarubicin,idarubicin,mitoxantrone,valrubicin,pixantrone,amsacrine; TOP2B:etoposide,teniposide,doxorubicin,daunorubicin,epirubicin,aclarubicin,idarubicin,mitoxantrone,valrubicin,pixantrone,amsacrine; VEGFA:bevacizumab,afibercept; VEGFB:afibercept
IMMUNOSTIMULANTS	6.35	3.34E-04	9.45E-03	IFNA2:interferon alfa-2b,peginterferon alfa-2b,peginterferon alfa-2a,albinterferon alfa-2b; IFNAR1:interferon alfa-n1,interferon beta-1a,interferon beta-1b,interferon alfacon-1,peginterferon alfa-2b,peginterferon alfa-2a; IFNAR2:interferon alfa-n1,interferon beta-1a,interferon beta-1b,interferon alfacon-1,peginterferon alfa-2b,peginterferon alfa-2a; IFNB1:interferon beta-1a; IL11RA:oprelvekin; IL2RA:aldesleukin; IL2RB:aldesleukin; IL2RG:aldesleukin; PMEL:melanoma vaccine
IMMUNOSUPPRESSANTS	3.57	9.16E-05	3.89E-03	C5:eculizumab; CD2:alefacept; CD28:belatacept; CD80:abatacept; CD86:abatacept; IL2RA:daclizumab,basiliximab; IL2RB:daclizumab; IL6:siltuximab; IL6R:tocilizumab,sarilumab; IL6ST:tocilizumab,sarilumab; IMPDH1:mycophenolic acid,azathioprine; IMPDH2:mycophenolic acid; JAK1:tofacitinib,baricitinib; JAK2:tofacitinib,baricitinib; JAK3:tofacitinib; NFKB1:thalidomide; TNF:etanercept,infliximab,adalimumab,certolizumab pegol,golimumab,thalidomide,lenalidomide,pomalidomide; TNFSF11:lenalidomide