

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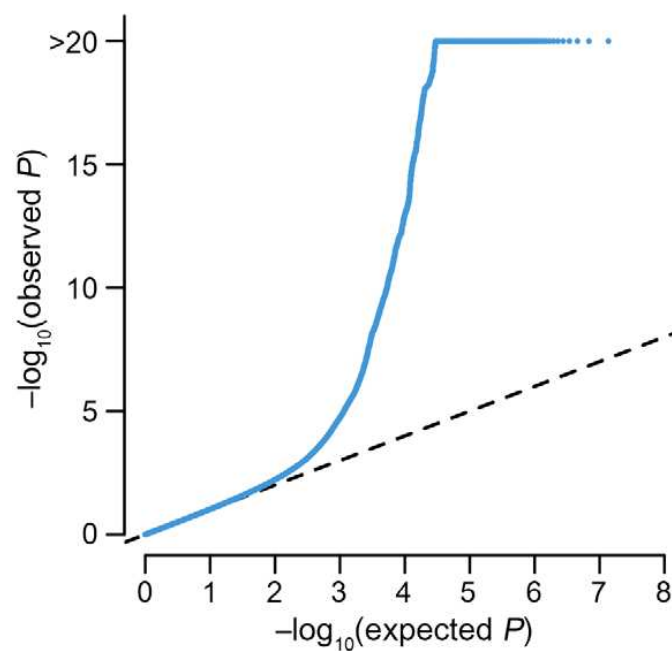
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#### Supplementary Figure 1 | Quantile-quantile (QQ) plot

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.



|                                |                    |                           |           |                         |             |                         |                 |             |                         |                 |                         |                |             |
|--------------------------------|--------------------|---------------------------|-----------|-------------------------|-------------|-------------------------|-----------------|-------------|-------------------------|-----------------|-------------------------|----------------|-------------|
| 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 |           |                        |                        |                                |        |       |      |   |            | RegulomeDB QTL                | Nearest gene | Location |
|----------|-----|-----------------|--------------------|---------------------------|------|--------------------------------------|-----------|------------------------|------------------------|--------------------------------|--------|-------|------|---|------------|-------------------------------|--------------|----------|
|          |     |                 |                    | CHB+JPT                   | EUR  | RegulomeDB                           | Conserved | Promoter histone marks | Enhancer histone marks | TF                             | eGenes |       |      |   |            |                               |              |          |
| 1        | 2   | 74207634        | rs371092749        | 1.00                      | 1.00 | N.A.                                 | N.A.      | 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   | -    | DAP   | Intron     |                               |              |          |
| 2        | 5   | 10687002        | rs6881964          | 0.93                      | 0.91 | 5                                    | -         | -                      | -                      | -                              | -      | DAP   | -    | DAP   | Intron     |                               |              |          |
| 2        | 5   | 10689562        | rs3776414          | 0.93                      | 0.94 | 4                                    | -         | -                      | -                      | CTCF, MAFK, NFE2               | -      | DAP   | -    | DAP   | Intron     |                               |              |          |
| 2        | 5   | 10689768        | rs3822412          | 0.93                      | 0.94 | 4                                    | -         | -                      | -                      | CTCF                           | -      | DAP   | -    | DAP   | Intron     |                               |              |          |
| 2        | 5   | 10690749        | rs5745271          | 0.93                      | 0.91 | <b>1f</b>                            | -         | -                      | -                      | -                              | -      | DAP   | Yes  | DAP   | Intron     |                               |              |          |
| 2        | 5   | 10691118        | rs5745264          | 0.92                      | 0.93 | 5                                    | -         | -                      | -                      | -                              | -      | DAP   | -    | DAP   | Intron     |                               |              |          |
| 2        | 5   | 10695526        | rs2930047          | 0.92                      | 0.94 | <b>1f</b>                            | -         | -                      | Yes                    | YY1                            | -      | DAP   | Yes  | DAP   | Intron     |                               |              |          |
| 2        | 5   | 10698569        | rs2930048          | 1.00                      | 0.95 | 5                                    | -         | -                      | -                      | -                              | -      | DAP   | -    | DAP   | Intron     |                               |              |          |
| 2        | 5   | 10699878        | rs3842028          | 0.93                      | 0.96 | <b>2a</b>                            | -         | -                      | Yes                    | -                              | -      | DAP   | -    | DAP   | Intron     |                               |              |          |
| 2        | 5   | 10704797        | <b>rs2918392</b>   | self                      | self | 5                                    | -         | Yes                    | Yes                    | -                              | -      | DAP   | -    | 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. | 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 | -     | FAM118A | Intron     |
| 11 | 22 | 45715608 | rs6519922   | 0.93 |      | 1f   | -    | Yes  | Yes  | -   | -    | -    | Yes  | FAM118A, RIBC2, SMC1B, UPK3A | -     | 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 | -     | FAM118A | Intron     |
| 11 | 22 | 45718041 | rs1473953   | 0.93 |      | 1f   | -    | -    | Yes  | EBF1  | -    | -    | Yes  | FAM118A, RIBC2, SMC1B, UPK3A | -     | 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               | -     | FAM118A | Intron     |
| 11 | 22 | 45725276 | rs2350628   | 0.96 |      | 1f   | -    | -    | -    | -   | -    | -    | Yes  | FAM118A, RIBC2, UPK3A        | -     | FAM118A | Intron     |
| 11 | 22 | 45725392 | rs742013    | 0.96 |      | 1b   | -    | -    | -    | -   | -    | -    | Yes  | FAM118A, RIBC2, UPK3A        | -     | FAM118A | Intron     |
| 11 | 22 | 45725524 | rs742014    | 0.96 |      | 1f   | -    | -    | -    | -   | -    | -    | Yes  | FAM118A, RIBC2, UPK3A        | -     | FAM118A | Intron     |
| 11 | 22 | 45725600 | rs736702    | 0.95 |      | 1f   | -    | -    | -    | -   | -    | -    | Yes  | FAM118A, RIBC2, UPK3A        | -     | FAM118A | Intron     |
| 11 | 22 | 45727565 | rs1569414   | 0.92 |      | 1f   | -    | -    | -    | -   | -    | -    | Yes  | FAM118A, RIBC2, UPK3A        | -     | 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        | -     | 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%               | 7.51%                   | 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      |  |  |
| CTCFL          | 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      |  |  |
| HMGN3          | 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<br>(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<br>(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<br>(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<br>(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<br>(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<br>(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<br>(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<br>(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<br>(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 |
|           |  |                     | H3K4me3      | 2.2E-07 | 8.7E-07    | 9                       | 3.6              | 5.4E-03 | 15                    | 4.3              | 2.1E-06 |
|           |  |                     | 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 |
| E039      | CD4+_CD25-_CD45RA+_Naive_Primary_Cells<br>(Primary T helper naive cells from peripheral blood) | BLOOD (T)           | H3K36me3     | 1.5E-02 | 2.9E-02    | 7                       | 4.1              | 9.1E-02 | 10                    | 5.2              | 2.2E-02 |
|           |  |                     | H3K4me1      | 1.5E-12 | 1.6E-11    | 16                      | 6.4              | 4.6E-05 | 24                    | 7.3              | 1.0E-09 |
|           |  |                     | 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      |
|           |  |                     | H3K27ac      | 6.2E-06 | 2.1E-05    | 11                      | 4.2              | 1.1E-03 | 13                    | 4.8              | 3.6E-04 |
| E039      | CD4+_CD25-_CD45RA+_Naive_Primary_Cells<br>(Primary T helper naive cells from peripheral blood) | BLOOD (T)           | H3K27me3     | 6.3E-01 | 7.3E-01    | 4                       | 3.8              | 5.4E-01 | 5                     | 4.7              | 5.1E-01 |
|           |  |                     | 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 |
|           |  |                     | 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<br>(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-<br>lonomycin_stimulated_MACS_purified_Th_Primary_Cells<br>(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<br>(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<br>(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<br>(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<br>(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<br>(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<br>(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<br>(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<br>(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<br>(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 | 8.7E-01 | 9.4E-01 | 1  | 1.6 | 8.2E-01 | 2  | 2.1 | 6.5E-01 |
|      |   |            | H3K4me1  | 1.5E-08 | 7.0E-08 | 12 | 3.6 | 4.6E-05 | 14 | 4.3 | 1.5E-05 |
|      |   |            | 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<br>(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 |
| E051 | Mobilized_CD34_Primary_Cells_Male<br>(Primary hematopoietic stem cells G-CSF-mobilized Male)     | BLOOD (HSC or PBMC) | H3K9me3  | 9.1E-01 | 9.6E-01 | 4  | 6.0 | 9.0E-01 | 7  | 7.6  | 6.7E-01 |
|      |  |                     | 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 |
| E062 | Peripheral_Blood_Mononuclear_Primary_Cells<br>(Primary mononuclear cells from peripheral blood)  | BLOOD (HSC or PBMC) | 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 |
|      |  |                     | 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 |
| E065 | Aorta<br>(Aorta)   | VASCULAR            | 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 |
|      |  |                     | 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 |
| E066 | Adult_Liver<br>(Liver)   | LIVER               | H3K4me1  | 5.4E-01 | 6.6E-01 | 1  | 4.1 | 9.9E-01 | 7  | 5.0  | 2.1E-01 |
|      |  |                     | H3K9me3  | 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 |
|      |  |                     | H3K27me3 | 4.0E-01 | 5.4E-01 | 4  | 2.7 | 2.8E-01 | 4  | 3.5  | 4.7E-01 |
| E087 | Pancreatic_Islets<br>(Pancreatic Islets)   | PANCREAS            | 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 |
| E096 | Lung<br>(Lung)   | LUNG                | 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 |
| E097 | Ovary<br>(Ovary)   | OVARY               | H3K27ac  | 1.3E-02 | 2.7E-02 | 9  | 6.4 | 1.6E-01 | 14 | 7.8  | 1.1E-02 |
|      |  |                     | 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 |
| E098 | Pancreas<br>(Pancreas)   | PANCREAS            | 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 |
|      |  |                     | 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 |
| E098 | Pancreas<br>(Pancreas)   | PANCREAS            | 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 |
|      |  |                     | H3K27me3 | 8.5E-01 | 9.2E-01 | 1  | 1.0 | 6.6E-01 | 1  | 1.3  | 7.5E-01 |
| E098 | Pancreas<br>(Pancreas)   | PANCREAS            | 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<br>(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<br>(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<br>(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 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                             | 6.62E-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                    |
| LCLAT1        | 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 TH1 17, 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        |
| RP1-134E15.3  | 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        |
| HOXA7         | 0   | 0.37  | 3.54E-01 | 0 | NA   | GM12878        |
| RP1-170O19.21 | 0   | NA    | NA       | 0 | NA   | GM12878        |
| HOXA9         | 0   | -1.56 | 9.41E-01 | 0 | NA   | GM12878        |
| HOXA10-AS     | 0   | NA    | NA       | 0 | NA   | GM12878        |
| MIR196B       | 0   | NA    | NA       | 0 | NA   | GM12878        |
| HOXA11        | 0   | -1.20 | 8.86E-01 | 0 | NA   | GM12878        |
| HOXA11-AS     | 0   | NA    | NA       | 0 | NA   | GM12878        |
| RP1-170O19.14 | 0   | NA    | NA       | 0 | NA   | GM12878        |
| HOXA13        | 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             |
| TP1P2         | 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 |
| RP11-27I1.4   | 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                  |

|                |     |       |          |    |  |                |
|----------------|-----|-------|----------|----|--|----------------|
|                |     |       |          |    | 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  |                |
| ORMDL3         | 34  | 5.91  | 1.72E-09 | 26 | monocyte, T-cell, T-cell CD4, T-cell CD8, B-cell CD19, LCL, scRNA eQTLs/PBMC, B cell naive, 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 memory TREG, T CD4 naive TREG, Whole Blood, Cells EBV-transformed lymphocytes, 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

eqtlMaps: cell types with mapped eQTL effects

ciMaps: 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, aflibercept; VEGFB:aflibercept |
| 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  |