Table S2: Top 100 signals in the YRI population using the $T_1$ test statistic.

| Rank | Gene name | Chromosome | $T_1$ | Rank | Gene name | Chromosome | $T_1$ |
|---|---|---|---|---|---|---|---|
| 1 | ***HLA-A*** [74,75] | 6 | 307.4 | 51 | *WWTR1* | 3 | 119.9 |
| 2 | *FANK1* | 10 | 302.2 | 52 | *WDR75* | 2 | 119.4 |
| 3 | ***HLA-B*** [15,74,75] | 6 | 272.3 | 53 | *C1orf130* | 1 | 118.2 |
| 4 | *TEKT4* | 2 | 271.7 | 54 | *FOPNL* | 16 | 118.1 |
| 5 | ***HLA-DPA1*** [76] | 6 | 267.1 | 55 | *SGCG* | 13 | 117.6 |
| 6 | ***HLA-C*** [75] | 6 | 262.7 | 56 | *ZNF568* | 19 | 117.0 |
| 7 | *MLL3* | 7 | 240.3 | 57 | *FRAS1* | 4 | 116.1 |
| 8 | *HLA-DRB5* | 6 | 227.2 | 58 | *SLC39A12* | 10 | 116.0 |
| 9 | *OR4C3* | 11 | 209.3 | 59 | *KANK1* | 9 | 115.5 |
| 10 | ***HLA-DQA1*** [14,75] | 6 | 205.4 | 60 | *EMID2* | 7 | 114.7 |
| 11 | *FRG2C* | 3 | 189.5 | 61 | *MYRIP* | 3 | 114.7 |
| 12 | ***HLA-DQB1*** [14,75] | 6 | 186.7 | 62 | ***PRIM2*** [79] | 6 | 114.4 |
| 13 | ***HLA-DPB1*** [14] | 6 | 180.2 | 63 | *ASB18* | 2 | 114.3 |
| 14 | *SNTG2* | 2 | 170.8 | 64 | *HLA-DRA* | 6 | 114.2 |
| 15 | *ZNF717* | 3 | 170.3 | 65 | *ARHGAP24* | 4 | 113.8 |
| 16 | *POLR1E* | 9 | 167.8 | 66 | *KCNAB1* | 3 | 113.8 |
| 17 | *DMBT1* | 10 | 166.4 | 67 | ***TRIM40*** [78] | 6 | 111.9 |
| 18 | *CPE* | 4 | 166.0 | 68 | *LUZP2* | 11 | 111.8 |
| 19 | *RNF144B* | 6 | 163.2 | 69 | *ABCD4* | 14 | 111.7 |
| 20 | *CTNNA3* | 10 | 160.1 | 70 | ***LGALS8*** [15] | 1 | 111.1 |
| 21 | ***HLA-DRB1*** [14,75] | 6 | 157.2 | 71 | *BNC2* | 9 | 109.4 |
| 22 | *OR4C45* | 11 | 156.4 | 72 | *PTPRB* | 12 | 109.3 |
| 23 | *AXDND1* | 1 | 151.8 | 73 | *RBFOX1* | 16 | 109.1 |
| 24 | ***SLC2A9*** [15] | 4 | 150.8 | 74 | *KL* | 13 | 106.6 |
| 25 | *ZNF85* | 19 | 150.4 | 75 | *HEATR1* | 1 | 106.3 |
| 26 | *MAP2K3* | 17 | 150.3 | 76 | *POLN* | 4 | 105.5 |
| 27 | *KCNJ12* | 17 | 150.1 | 77 | *PDE11A* | 2 | 105.1 |
| 28 | *SORD* | 15 | 148.5 | 78 | *VWDE* | 7 | 103.9 |
| 29 | *ARHGAP42* | 11 | 146.6 | 79 | *SPATA13* | 13 | 103.7 |
| 30 | *KCNJ18* | 17 | 146.3 | 80 | *SPATA16* | 3 | 103.6 |
| 31 | *ARPC5* | 1 | 143.7 | 81 | *APBB1IP* | 10 | 103.0 |
| 32 | *MCM9* | 6 | 141.1 | 82 | *MPHOSPH6* | 16 | 102.0 |
| 33 | *C18orf1* | 18 | 139.5 | 83 | *CES5A* | 16 | 101.9 |
| 34 | *SLC38A9* | 5 | 132.0 | 84 | *PARP4* | 13 | 100.9 |
| 35 | *GRIN2A* | 16 | 131.9 | 85 | *KRT83* | 12 | 100.9 |
| 36 | *MYOM2* | 8 | 131.7 | 86 | *MOSC2* | 1 | 100.9 |
| 37 | *GBA3* | 4 | 127.8 | 87 | *PACRG* | 6 | 99.1 |
| 38 | *STK32A* | 5 | 125.2 | 88 | ***RCBTB1*** [15] | 13 | 97.8 |
| 39 | *CSMD1* | 8 | 125.2 | 89 | *FAM55A* | 11 | 96.5 |
| 40 | ***FHIT*** [77] | 3 | 125.0 | 90 | *GALC* | 14 | 96.0 |
| 41 | *ART3* | 4 | 124.5 | 91 | *LRPPRC* | 2 | 95.6 |
| 42 | *RGS6* | 14 | 123.7 | 92 | *SLC24A4* | 14 | 95.3 |
| 43 | *CEP112* | 17 | 123.7 | 93 | *ADCY5* | 3 | 95.0 |
| 44 | *IGSF5* | 21 | 123.6 | 94 | *ULK4* | 3 | 94.9 |
| 45 | *GRHL1* | 2 | 122.8 | 95 | *FYB* | 5 | 94.3 |
| 46 | *RGL1* | 1 | 121.9 | 96 | *KIAA0748* | 12 | 93.8 |
| 47 | *SNX19* | 11 | 121.8 | 97 | *COL4A3* | 2 | 93.7 |
| 48 | *SPEF2* | 5 | 121.2 | 98 | *CCDC169* | 13 | 93.6 |
| 49 | *FXN* | 9 | 121.0 | 99 | *CCDC169-SOHLH2* | 13 | 93.6 |
| 50 | *PTCHD3* | 10 | 120.3 | 100 | *PLEKHG1* | 6 | 93.3 |

Previously-hypothesized genes are indicated in bold. Genes overlapping with Table S1 are highlighted in gray.

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