**Table S2.** **Analysis of Population Admixture with 21 Ancestry Informative Markersa**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **#** | **Chrom** | **rs #** | **HWE** | **IFN-** | **IL-2** | **IL-13** |
|  |  |  |  | **Low** | **High** | **χ2** | **P** | **Low** | **High** | **χ2** | **P** | **Low** | **High** | **χ2** | **P** |
|  |  |  |  | **MAF** | **MAF** |  |  | **MAF** | **MAF** |  |  | **MAF** | **MAF** |  |  |
| 1 | 2 | 1028184 | 0.013 | 0.34 | 0.37 | 1.03 | 0.31 | 0.34 | 0.37 | 0.71 | 0.40 | 0.35 | 0.37 | 0.36 | 0.55 |
| 2 | 19 | 11672183 | 0.241 | 0.13 | 0.12 | 0.35 | 0.55 | 0.11 | 0.13 | 0.63 | 0.43 | 0.13 | 0.11 | 0.76 | 0.38 |
| 3 | 6 | 12665321 | 0.099 | 0.14 | 0.14 | 0.06 | 0.81 | 0.12 | 0.15 | 1.31 | 0.25 | 0.13 | 0.15 | 0.70 | 0.40 |
| 4 | 11 | 12785524 | 0.428 | 0.42 | 0.35 | 3.51 | 0.06 | 0.41 | 0.37 | 1.04 | 0.31 | 0.38 | 0.39 | 0.07 | 0.79 |
| 5 | 16 | 1364198 | 0.082 | 0.24 | 0.18 | 3.83 | 0.05 | 0.22 | 0.20 | 0.56 | 0.45 | 0.21 | 0.21 | 0.01 | 0.91 |
| 6 | 8 | 1380229 | 0.468 | 0.33 | 0.33 | 0.01 | 0.91 | 0.35 | 0.32 | 0.95 | 0.33 | 0.36 | 0.31 | 1.93 | 0.16 |
| 7 | 15 | 1433456 | 0.764 | 0.22 | 0.22 | 0.00 | 0.98 | 0.21 | 0.23 | 0.39 | 0.53 | 0.21 | 0.22 | 0.10 | 0.75 |
| 8 | 5 | 1479067 | 0.213 | 0.26 | 0.28 | 0.40 | 0.53 | 0.26 | 0.28 | 0.61 | 0.43 | 0.26 | 0.28 | 0.66 | 0.42 |
| 9 | 9 | 1566838 | 0.040 | 0.49 | 0.47 | 0.41 | 0.52 | 0.48 | 0.47 | 0.04 | 0.84 | 0.48 | 0.47 | 0.01 | 0.94 |
| 10 | 16 | 1582598 | 0.852 | 0.33 | 0.31 | 0.47 | 0.49 | 0.34 | 0.29 | 2.28 | 0.13 | 0.32 | 0.31 | 0.07 | 0.79 |
| 11 | 21 | 169479 | 0.945 | 0.14 | 0.13 | 0.10 | 0.75 | 0.16 | 0.11 | 3.14 | 0.08 | 0.12 | 0.15 | 1.25 | 0.26 |
| 12 | 20 | 2024628 | 0.006 | 0.48 | 0.45 | 0.66 | 0.42 | 0.47 | 0.47 | 0.01 | 0.94 | 0.48 | 0.46 | 0.47 | 0.50 |
| 13 | 4 | 2048022 | 0.185 | 0.39 | 0.41 | 0.33 | 0.56 | 0.38 | 0.41 | 0.82 | 0.37 | 0.37 | 0.42 | 2.06 | 0.15 |
| 14 | 7 | 327747 | 0.654 | 0.30 | 0.27 | 0.57 | 0.45 | 0.29 | 0.28 | 0.04 | 0.84 | 0.27 | 0.30 | 0.62 | 0.43 |
| 15 | 10 | 650389 | 0.566 | 0.14 | 0.16 | 1.01 | 0.31 | 0.14 | 0.16 | 0.68 | 0.41 | 0.15 | 0.15 | 0.01 | 0.94 |
| 16 | 12 | 695982 | 0.921 | 0.27 | 0.27 | 0.03 | 0.87 | 0.28 | 0.26 | 0.25 | 0.62 | 0.28 | 0.26 | 0.16 | 0.69 |
| 17 | 15 | 708682 | 0.389 | 0.13 | 0.10 | 1.09 | 0.30 | 0.12 | 0.11 | 0.21 | 0.65 | 0.12 | 0.11 | 0.23 | 0.63 |
| 18 | 17 | 807131 | 0.051 | 0.34 | 0.36 | 0.31 | 0.58 | 0.37 | 0.33 | 1.08 | 0.30 | 0.37 | 0.33 | 1.76 | 0.18 |
| 19 | 14 | 876287 | 0.733 | 0.44 | 0.44 | 0.00 | 0.99 | 0.45 | 0.43 | 0.29 | 0.59 | 0.40 | 0.48 | 4.18 | 0.04 |
| 20 | 13 | 914904 | 0.841 | 0.26 | 0.29 | 0.81 | 0.37 | 0.26 | 0.28 | 0.31 | 0.58 | 0.27 | 0.28 | 0.06 | 0.81 |
| 21 | 13 | 975423 | 0.480 | 0.39 | 0.37 | 0.19 | 0.66 | 0.36 | 0.40 | 0.98 | 0.32 | 0.38 | 0.38 | 0.02 | 0.89 |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

**a**At each locus, χ2 represents Pearson’s χ2 value for comparison of allele frequencies in groups of low (less than median) and high

(greater than median) cytokine responses in the South African Mixed Ancestry Group. A global p value was calculated for the mean

χ2 value for the 21 SNPs for each cytokine. For IFN-γ, IL-2, and IL-13, the global p values were 0.40, 0.38, and 0.39, respectively.

Chrom, chromosomal location of SNP; Low, group of individuals with cytokine value below median; High, group of individuals with

cytokine value above the median; HWE, Hardy-Weinberg Equilibrium; MAF, minor allele frequency.