**Appendix 3. MAF values for identified SNPs**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Gene | Chr1 position (hg38) | Nt change | SNP ID | MAF in the  Caucasian populationa | MAF in the  American populationb | Context |
| *NADK* | [1,753,551](http://genome-euro.ucsc.edu/cgi-bin/hgTracks?hgsid=220504662_0XSug9AjRvlpdNRc0eZ7VukKYAJj&db=hg38&position=chr1%3A1753551-1753551) | G/A | rs138146152 | 0.001380 | 0.0008 | Intron |
| *NADK* | [1,759,507](http://genome-euro.ucsc.edu/cgi-bin/hgTracks?hgsid=220504662_0XSug9AjRvlpdNRc0eZ7VukKYAJj&db=hg38&position=chr1%3A1759507-1759507) | A/G | rs560222331 | 0.001268 | 0.0008 | Intron |
| *GNB1* | [1,847,942](http://genome-euro.ucsc.edu/cgi-bin/hgTracks?hgsid=220504662_0XSug9AjRvlpdNRc0eZ7VukKYAJj&db=hg38&position=chr1%3A1847942-1847942) | G/A | rs146652180 | 0.001533 | 0.0008 | Intron |
| *GNB1* | [1,879,388](http://genome-euro.ucsc.edu/cgi-bin/hgTracks?hgsid=220504662_0XSug9AjRvlpdNRc0eZ7VukKYAJj&db=hg38&position=chr1%3A1879388-1879388) | C/A | rs768509593 | 0.001334 | 0.0008 | Intron |
| *RP1-140A9.1* | 1,891,852 | G/C | [rs763295804](https://www.ncbi.nlm.nih.gov/SNP/snp_ref.cgi?type=rs&rs=rs763295804" \t "_blank) | 0.001335 | 0.0008 | Splice donor variant |

a MAF data for the non-Finnish Europeans population is from the gnomAD browser (https://gnomad.broadinstitute.org/).

b MAF data for the American population is from TOPMed/dbSNP. The American population is very heterogeneous and the TOPMed population represents >144k participants posing 40% Europeans, 32% Africans, 16% Hispanic/Latinos, 10% Asians etc. (<https://www.nhlbiwgs.org/>)