**Supplemental Table 2.** Age at natural menopause single nucleotide polymorphisms in relation to age at natural menopause (ANM) in the Nurses’ Health Study (N=7143) and primary open-angle glaucoma (POAG) in the NEIGHBORHOOD (N=2160 cases and 29,110 controls)

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **RSID**a | **chr** | **position** | **Gene** | **A0** | **A1** | **ANM** | | **POAG** | |
|  |  |  |  |  |  | ***beta*** | ***P-value*** | ***OR*** | ***P-value*** |
| rs4246511 | 1 | 39,152,972 | *RHBDL2* | T | C | 0.22 | 5.1E-21 | 1.041 | 0.42 |
| rs12142240 | 1 | 46,519,888 | *LRRC41* | C | T | 0.13 | 6.6E-09 | 0.987 | 0.78 |
| rs1411478 | 1 | 179,228,905 | *STX6* | G | A | 0.13 | 1.4E-10 | 0.989 | 0.80 |
| rs2236918 | 1 | 240,084,449 | *EXO1* | G | C | 0.15 | 8.3E-14 | 1.029 | 0.53 |
| rs704795 | 2 | 27,569,998 | *FNDC4* | G | A | 0.16 | 2.1E-15 | 1.032 | 0.48 |
| rs1800932 | 2 | 47,871,585 | *MSH6* | G | A | 0.17 | 3.2E-11 | 0.904 | 0.078 |
| rs7598194 | 2 | 171,479,657 | *GORASP2* | G | C | 0.15 | 6.2E-12 | 0.970 | 0.52 |
| rs930036 | 2 | 171,649,264 | *TLK1* | G | A | 0.19 | 3.1E-19 | 0.970 | 0.50 |
| rs7573003 | 2 | 172,449,661 | *SLC25A12* | T | A | 0.12 | 3.9E-08 | 0.966 | 0.46 |
| rs16858210 | 3 | 185,106,704 | *ABCC5* | A | G | 0.14 | 3.1E-09 | 0.923 | 0.12 |
| rs4693089 | 4 | 84,592,646 | *HELQ* | G | A | 0.2 | 9.2E-23 | 1.013 | 0.77 |
| rs6856693 | 4 | 185,985,800 | *ACSL1* | G | A | 0.16 | 9.8E-15 | 0.974 | 0.57 |
| rs427394 | 5 | 6,798,875 | *PAPD7* | A | G | 0.13 | 3.8E-09 | 1.003 | 0.96 |
| rs11738223 | 5 | 171,867,097 | *SH3PXD2B* | G | A | 0.12 | 2.0E-08 | 0.935 | 0.16 |
| rs365132 | 5 | 176,311,180 | *UIMC1* | T | G | 0.24 | 1.4E-33 | 1.011 | 0.81 |
| rs6899676 | 6 | 11,003,246 | *SYCP2L* | G | A | 0.23 | 2.2E-19 | 0.972 | 0.60 |
| rs3094222 | 6 | 31,189,413 | *C6orf15* | A | G | 0.18 | 7.8E-09 | 0.944 | 0.39 |
| rs1046089 | 6 | 31,710,946 | *PRRC2A* | G | A | 0.22 | 3.7E-21 | 1.041 | 0.52 |
| rs3134942 | 6 | 32,276,749 | *NOTCH4* | G | T | 0.2 | 2.9E-09 | 1.024 | 0.79 |
| rs12196873 | 6 | 111,704,751 | *KIAA1919* | C | A | 0.16 | 2.8E-08 | 0.993 | 0.91 |
| rs2720044 | 8 | 38,099,744 | *ASH2L* | C | A | 0.29 | 7.3E-22 | 1.020 | 0.77 |
| rs10957156 | 8 | 61,791,955 | *CHD7* | G | A | 0.14 | 4.5E-09 | 1.048 | 0.36 |
| rs4879656 | 9 | 33,002,382 | *APTX* | C | A | 0.12 | 2.0E-08 | 0.971 | 0.51 |
| rs10905065 | 10 | 5,809,833 | *FAM208B* | G | A | 0.11 | 3.9E-08 | 1.034 | 0.45 |
| rs11031006 | 11 | 30,183,104 | *FSHB* | A | G | 0.22 | 8.5E-14 | 0.941 | 0.35 |
| rs10734411 | 11 | 32,498,360 | *EIF3M* | G | A | 0.12 | 2.6E-09 | 1.040 | 0.38 |
| rs2277339 | 12 | 55,432,336 | *PRIM1* | T | G | 0.31 | 1.8E-19 | 1.020 | 0.80 |
| rs12371165 | 12 | 65,101,815 | *GRIP1* | T | C | 0.18 | 7.0E-10 | 1.015 | 0.81 |
| rs551087 | 12 | 119,693,576 | *SPPL3* | A | G | 0.13 | 3.9E-08 | 1.009 | 0.86 |
| rs1727326 | 12 | 122,166,039 | *PITPNM2* | G | C | 0.19 | 1.7E-09 | 1.005 | 0.94 |
| rs12824058 | 12 | 129,370,287 | *PIWIL1* | A | G | 0.14 | 6.1E-11 | 1.116 | 0.014 |
| rs4886238 | 13 | 60,011,740 | *TDRD3* | A | G | 0.18 | 2.5E-16 | 1.062 | 0.20 |
| rs1713460 | 14 | 20,003,455 | *PNP* | A | G | 0.14 | 2.4E-10 | 0.951 | 0.30 |
| rs9796 | 15 | 39,058,739 | *INO80* | A | T | 0.13 | 1.3E-10 | 1.047 | 0.30 |
| rs1054875 | 15 | 87,680,130 | *POLG* | A | T | 0.19 | 1.7E-19 | 0.978 | 0.63 |
| rs9039 | 16 | 9,112,864 | *C16orf72* | T | C | 0.12 | 3.3E-08 | 0.982 | 0.71 |
| rs10852344 | 16 | 11,924,420 | *GSPT1* | C | T | 0.16 | 1.3E-15 | 1.011 | 0.80 |
| rs12599106 | 16 | 34,355,526 | *UBE2MP1* | T | A | 0.12 | 3.1E-08 | 1.010 | 0.83 |
| rs8070740 | 17 | 5,272,620 | *RPAIN* | G | A | 0.15 | 1.5E-09 | 1.050 | 0.34 |
| rs2941505 | 17 | 35,086,230 | *PGAP3* | G | A | 0.13 | 1.9E-09 | 1.022 | 0.64 |
| rs1799949 | 17 | 38,498,992 | *BRCA1* | A | G | 0.14 | 8.4E-11 | 0.932 | 0.13 |
| rs349306 | 19 | 901,694 | *ARID3A* | A | G | 0.23 | 1.7E-10 | 1.084 | 0.32 |
| rs7259376 | 19 | 22,299,545 | *ZNF729* | G | A | 0.11 | 4.2E-08 | 0.994 | 0.88 |
| rs11668344 | 19 | 60,525,476 | *TMEM150B* | A | G | 0.41 | 5.5E-85 | 1.000 | 0.99 |
| rs16991615 | 20 | 5,896,227 | *MCM8* | A | G | 0.88 | 1.6E-89 | 1.107 | 0.27 |
| rs13040088 | 20 | 61,019,647 | *DIDO1* | A | G | 0.16 | 2.4E-10 | 0.971 | 0.58 |
| rs5762534 | 22 | 26,963,571 | *MIR548AM* | C | T | 0.16 | 6.1E-09 | 1.009 | 0.88 |
| rs763121 | 22 | 37,209,886 | *DDX17* | A | G | 0.16 | 2.3E-13 | 1.009 | 0.86 |
|  |  |  |  |  |  |  |  |  |  |
| *uGRS* |  |  |  |  |  |  |  | 1.001 | 0.87 |
| *wGRS* |  |  |  |  |  |  |  | 1.033 | 0.42 |

*a The variants were extracted from the supplementary table S2 of Day et al. [*[*Day, et al. 2015*](#_ENREF_1)*]*

*b These variants were not included in the derivation of the genetic risk score (GRS) p-value because of their potential correlation with other SNPs in the same locus.*

*Other abbreviations used: RS ID= rs identification; chr=chromosome; uGRS= un-weighted genetic risk score; wGRS= weighted genetic risk score; OR=odds ratio; A0 and A1 correspond to the reference and coded allele, where the coded allele is associated later ANM.*

**References**

*Day FR, Ruth KS, Thompson DJ, Lunetta KL, Pervjakova N, Chasman DI, Stolk L, Finucane HK, Sulem P, Bulik-Sullivan B and others. 2015. Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nat Genet 47(11):1294-303.*