**Table s4.** association test for functional variants located in MED12L (Fine chip)

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **CHR** | **SNP** | **BP** | **A1** | **F\_A** | **F\_U** | **A2** | **CHISQ** | **P** | **OR** | **SE** | **L95** | **U95** | **p-hwe** | **call-rate** |
| **3** | rs17290219 | 150881774 | C | 0.0010 | 0.0017 | A | 0.5846 | 4.45E-01 | 0.6221 | 0.6266 | 0.1822 | 2.1240 | 1.00E+00 | 0.9998 |
| **3** | rs200591060 | 150883678 | A | 0.0003 | 0.0003 | G | 0.0198 | 8.88E-01 | 1.1760 | 1.1550 | 0.1223 | 11.3100 | 1.00E+00 | 1 |
| **3** | rs34501514 | 150908578 | A | 0 | 0.0002 | C | 0.5669 | 4.52E-01 | 0 | inf | 0 | nan | 1.00E+00 | 1 |
| **3** | rs199730852 | 150908656 | A | 0 | 0.0001 | G | 0.2834 | 5.95E-01 | 0 | inf | 0 | nan | 1.00E+00 | 1 |
| **3** | rs140793301 | 151105949 | G | 0 | 0.0001 | A | 0.2834 | 5.95E-01 | 0 | inf | 0 | nan | 1.00E+00 | 1 |
| **3** | **rs199780529** | **151107788** | **G** | **0.0010** | **0.0042** | **A** | **6.2380** | **1.25E-02** | **0.2512** | **0.5980** | **0.0778** | **0.8111** | **8.19E-02** | **1** |
| **3** | rs140281524 | 151129121 | A | 0 | 0.0001 | G | 0.2834 | 5.95E-01 | 0 | inf | 0 | nan | 1.00E+00 | 1 |
| **3** | rs200120968 | 151134191 | A | 0.0004 | 0.0005 | T | 0.1050 | 7.46E-01 | 0.7025 | 1.0960 | 0.0820 | 6.0150 | 1.00E+00 | 0.9924 |

CHR: chromosome; SNP: single nucleotide polymorphism; OR: odds ratio; SE: standard error; L95= the lower limit of 95%confidence interval; U95: the upper limit of 95% confidence interval;