**Table s6.** association test for 5 overlap functional variants located in MED12L

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **CHR** | **SNP** | **BP** | **A1** | **F\_A** | **F\_U** | **A2** | **CHISQ** | **P** | **OR** | **SE** | **L95** | **U95** | **p-hwe** | **call-rate** |
| **3** | rs17290219 | 150881774 | C | 0.0006 | 0.0014 | A | 2.1720 | 1.41E-01 | 0.4170 | 0.6126 | 0.1255 | 1.3850 | 1 | 0.9998 |
| **3** | rs200591060 | 150883678 | A | 0.0002 | 0.0004 | G | 0.5017 | 4.79E-01 | 0.4770 | 1.0690 | 0.0587 | 3.8780 | 1 | 1 |
| **3** | rs34501514 | 150908578 | A | 0 | 0.0002 | C | 1.1980 | 2.74E-01 | 0 | inf | 0 | nan | 1 | 1 |
| **3** | rs199730852 | 150908656 | A | 0 | 0.0001 | G | 0.2995 | 5.84E-01 | 0 | inf | 0 | nan | 1 | 1 |
| **3** | **rs199780529** | **151107788** | **G** | **0.0012** | **0.0044** | **A** | **10.6700** | **1.09E-03** | **0.2736** | **0.4250** | **0.1189** | **0.6293** | **0.1471** | **1** |

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;