**S2 Table.** Maximum genotype counts for 12 previously reported monogenic causes of sleep and circadian conditions in unrelated individuals of European ancestry from the UK Biobank, FINRISK & Health 2000-2011 and MESA studies. Genotype counts are based on availability of sleep characteristics relevant to each gene.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  |  |  | **UK Biobank** |  **FINRISK & Health 2000-2011** | **MESA** |
| **Gene / Variant** | **Trait** | **REF/ALTd** | **REF/REFe** | **REF/ALTf** | **ALT/ALTg** | **REF/REFe** | **REF/ALTf** | **ALT/ALTg** | **REF/REFe** | **REF/ALTf** | **ALT/ALTg** |
| *GRM1* / S458A | FNSSa | T/G | 169,451 | 67 | - | 5,927 | <5 | 0 | - | - | - |
| *GRM1* / R889W | FNSSa | A/T | 169,513 | 3 | - | - | - | - | - | - | - |
| *NPSR1* / Y206H | FNSSa | T/C | - | - | - | - | - | - | - | - | - |
| *ADRB1* / A187V | FNSSa | C/T | 169,450 | 69 | - | - | - | - | - | - | - |
| *DEC2/BHLHE41* / P384R | FNSSa | G/C | 169,500 | 10 | - | - | - | - | 1,993 | 22 | - |
| *CRY1* / c.1657+3A>C | DSPDb | T/G | 168,586 | 1,480 | 9 | 2,838 | <5 | 0 | - | - | - |
| *PER3* / P415A | FASPc | C/G | 168,500 | 1,565 | 7 | 2,734 | 149 | <5 | 2,003 | 12 | - |
| *PER3* / H417R | FASPc | A/G | 168,500 | 1,567 | 7 | 2,734 | 149 | <5 | 2,003 | 12 | - |
| *PER2* / PER2S662G | FASPc | A/G | - | - | - | - | - | - | - | - | - |
| *CRY2* / A260T | FASPc | G/A | 170,038 | 38 | - | - | - | - | - | - | - |
| *TIMELESS* / R1081X | FASPc | G/A | 170,064 | 5 | - | - | - | - | - | - | - |
| *CSNK1D* / T44A | FASPc | T/C | 170,075 | 1 | - | - | - | - | - | - | - |

afamilial natural short sleep; bdelayed sleep phase disorder; cfamilial advanced sleep phase; dreference allele / alternate allele; enumber of homozygous carriers for reference allele; fnumber of heterozygous carriers; gnumber of homozygous carriers for alternate allele.