Supplement S6. Overview of Reported Genetic Variants in Chromosomes in Genome-wide Association Studies on Aggression

Chromosome	N variants at suggestive significance (P<1E^{-05})	Number of SNPs at genome-wide significance (P<5.0E^{-08})	Genes with nearby or inside location of SNPS at genome-wide significance (P<5.0E^{-08})
1	53	1	
2	81	2	*HTR2B; PSMD1*
3	40		
4	35	2	*C1QTNF7*
5	52		
6	54	1	*LINC00915*
7	79		
8	25		
9	49		
10	56		
11	62	2	
12	34		
13	8	1	
14	15		
15	9		
16	27		
17	19		
18	21		
19	6		
20	44		
21	26		
22	8		
X	4	1	
	817	10	4

Note. $N_{studies}$=17