

**GENOMICS OF HUMAN AGGRESSION: Current state of genome-wide studies and an automated systematic review tool**

Odintsova V.V., Roetman P.J., Ip H.F., Pool R., Van der Laan C.M., Tona K.D., Vermeiren R.R.J.M., Boomsma D.I.

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

Chromosome	N variants at suggestive significance ( $P<1E^{-5}$ )	Number of SNPs at genome-wide significance ( $P<5.0E^{-8}$ )	Genes with nearby or inside location of SNPs at genome-wide significance ( $P<5.0E^{-8}$ )
1	53	1	
2	81	2	<i>HTR2B; PSMD1</i>
3	40		
4	35	2	<i>C1QTNF7</i>
5	52		
6	54	1	<i>LINC00915</i>
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<sub>studies</sub>=17