

Table 1: Distribution of the top 200 positively *COMT*-correlated genes by Chromosome: Prefrontal Cortex

Chromosome	Frequency	Expected	Enrichment	P value
1	28	20.9	1.34	0.10
2	13	12.6	1.03	0.91
3	12	10.8	1.11	0.71
4	4	7.6	0.52	0.18
5	9	8.7	1.04	0.92
6	12	11.0	1.09	0.76
7	7	9.1	0.77	0.48
8	6	6.8	0.88	0.75
9	10	7.9	1.26	0.45
10	1	7.5	0.13	0.02
11	12	13.2	0.91	0.73
12	8	10.8	0.74	0.38
13	5	3.3	1.51	0.35
14	2	6.2	0.32	0.09
15	12	5.7	2.09	0.01
16	6	8.3	0.72	0.41
17	12	11.7	1.03	0.93
18	2	2.8	0.71	0.63
19	15	13.6	1.11	0.69
20	5	5.8	0.86	0.74
21	5	2.6	1.91	0.14
22	8	4.6	1.75	0.11
X	6	7.9	0.75	0.49

Table 1: (*Top 200 positively correlated genes by chromosome continued*)

Chromosome	Frequency	Expected	Enrichment	P value
Y**	0	--	--	--

\*\*There were no genes on the Y chromosome that fell within the 200 most strongly positively *COMT*-correlated genes in Prefrontal Cortex

A chi-square test on the observed distribution of the 200 most strongly positively *COMT* – correlated genes in Prefrontal Cortex using the proportion of genes on each chromosome across the entire sample to derive the expected frequencies showed that this distribution did not differ significantly from the expected distribution,  $\chi^2 = 28.874$ ,  $df = 22$ ,  $p = 0.16$ .