

Table 1: Distribution of five hundred most strongly COMT-correlated genes (ranked by p-value) by sign of correlation and chromosome. Chromosomes 1, 3, and 7 are most discrepant from the expected ratio of positively correlated to negative correlated genes of 1.92.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	X	Total
negative	7	5	4	18	5	3	2	12	5	19	21	4	5	6	4	5	13	3	4	4	4	9	9	171
positive	49	6	20	23	6	8	10	20	7	15	18	9	12	14	13	18	12	9	6	14	9	22	9	329
prop. neg.	0.12	0.45	0.17	0.44	0.45	0.27	0.17	0.38	0.42	0.56	0.54	0.31	0.29	0.30	0.24	0.22	0.52	0.25	0.40	0.22	0.31	0.29	0.50	0.34

Pearson’s Chi-squared test of independence

$$\chi^2 = 44.6, df = 23, p - value = 0.0044$$

The most strongly positively and negatively *COMT* – correlated genes are distributed proportionately unequally across the 22 autosomes and the X chromosome. There are significantly ( $p = 0.00034$ ) fewer negatively correlated than positively correlated genes on Chromosome 1 than would be expected from the overall proportion of negatively *COMT* – correlated genes across the 500 most strongly correlated genes. The *COMT* gene is located on Chromosome 22.