

Table 1: Observed, expected number of negative correlations and associated hypergeometric p-values by brain area for the 200 genes whose *COMT* expression correlations had the smallest p values.

	Prefrontal	Cerebellum	Temporal	Pons
Number of negative correlations	170	118	94	68
Expected number of negative correlations	310	316	327	302
Sample size	500	500	500	500
Proportion of negative correlations: sample	0.340	0.236	0.188	0.136
Total number of negative correlations	10341	10527	10875	10016
Total number of genes	16670	16685	16636	16616
Proportion negative correlations: total	0.620	0.631	0.654	0.603
Log10(probability)	-37.236	-73.854	-103.910	-106.137

Among the 500 most strongly *COMT* – correlated genes, the proportion of negatively correlated genes is significantly less in every brain area than would be expected given the proportion of negatively correlated genes in the full sample (gene as unit).

This is in keeping with previous work that has shown that the strongest co-expressed genes tend to have positive correlations (need ref).