

Table 1: Number (percentage) of the negative subset, positive subset, and all of the *COMT* – correlated genes in each brain area having at least one instance of the TATA8 motif^a in the region from -250 to +150 nucleotides relative to the transcription start site TSS (adjacent to +1). The p-values are derived from hypergeometric tests on the negative and positive subsets given the statistics for all the genes shown in the same rows of last two columns.

	Negative	Number of Genes	p-value	Positive	Number of Genes	p-value	All <i>COMT</i> Genes	Number of Genes
Prefrontal Cortex	10 (6.0)	168	0.285	21 (6.6)	319	0.321	1192 (7.5)	15998
Cerebellum	8 (6.9)	116	0.517	20 (5.3)	375	0.074	1176 (7.3)	16008
Temporal Cortex	4 (4.3)	94	0.169	27 (6.7)	401	0.355	1176 (7.4)	15967
Pons	1 (1.5)	68	0.034	25 (5.9)	423	0.137	1179 (7.4)	15950

a. TATA8 consensus motif TATAWAWN: e.g.,TATAAATC (-30 TSS locus underlined)