Table 1: Hexamer motifs in the promoter regions of genes in Prefrontal Cortex for which the proportion of positively $COMT-$correlated genes containing that motif differed significantly (after Bonferroni correction) from the proportion of negatively $COMT-$correlated genes containing that motif (ordered by p value). Motifs were only tested for significance if the proportion of promoters containing at least one instance of that motif in both positively and negatively correlated genes exceeded 20%.

Motif	Prop. Positive	Prop. Negative	p
TTTAAA	0.61	**0.84**[a]	0.00000024057
AATTTA	0.34	**0.59**	0.00000030031
AAATTT	0.44	**0.69**	0.00000030277
TATATT	0.32	**0.57**	0.00000031028
TTTATT	0.54	**0.78**	0.00000040966
ATGTAA	0.28	**0.50**	0.00000129787
TAATCT	0.23	**0.44**	0.00000144207
CCAGCC	**0.74**	0.52	0.00000164385
GTAAAA	0.28	**0.51**	0.00000211174
ATCTTT	0.36	**0.59**	0.00000244105
TTATTC	0.30	**0.52**	0.00000372026
ATTTAT	0.41	**0.63**	0.00000633234
TGATAT	0.20	**0.39**	0.00000725867
AATCTT	0.31	**0.52**	0.00000738220
AATGAA	0.41	**0.63**	0.00000861035
CTGTAT	0.28	**0.49**	0.00000891989
GCCTCT	**0.52**	0.30	0.00000983746
AATTTG	0.34	**0.55**	0.00001512169

[a] The significantly larger of the two proportions is indicated in bold. For 16 of the 18 hexamer motifs, the motif appeared at least once in the promoter region of the set of negatively $COMT-$correlated genes proportionately more often than in the set of positively $COMT-$correlated genes. When the greater proportion of genes containing at least one instance of these motifs fell to the negatively correlated genes, the motifs tended to be [A,T]$-$enriched.