

Table 1: Number (proportion) of the positive subset of the 500 most highly *COMT* – correlated genes in each brain area having three different consensus initiator element (Inr) sequences on either DNA strand

	Inr1 ^a	Inr2 ^b	Inr3 ^c	Number of Strands
Prefrontal Cortex	9 (.014)	10 (.016)	534 (.837)	638
Cerebellum	10 (.013)	8 (.011)	645 (.860)	750
Temporal Cortex	18 (.022)	11 (.014)	683 (.852)	802
Pons	19 (.022)	9 (.011)	710 (.839)	846

TSS +1 locus underlined

a. Inr: BBCABW

b. Inr: YYANWYY

c. Inr: YR