

Table 1: Number (percentage) of the positive subset of the most highly *COMT* – correlated genes in each brain area having at least one instance of each of three different consensus initiator element (Inr) sequences in the region from -100 to + 50 nucleotides relative to the transcription start site TSS (adjacent to +1)

	Inr1 ^a	Inr2 ^b	Inr3 ^c	Number of Genes
Prefrontal Cortex	127 (39.8)	131 (41.1)	319 (100)	319
Cerebellum	170 (45.3)	178 (47.5)	375 (100)	375
Temporal Cortex	169 (42.1)	175 (43.6)	401 (100)	401
Pons	184 (43.5)	189 (44.7)	423 (100)	423

+1 TSS locus underlined

- a.** Inr: BBCABW — e.g., CTCAGT
- b.** Inr: YYANWYY — e.g., TCAGACC
- c.** Inr: YR — e.g., CA