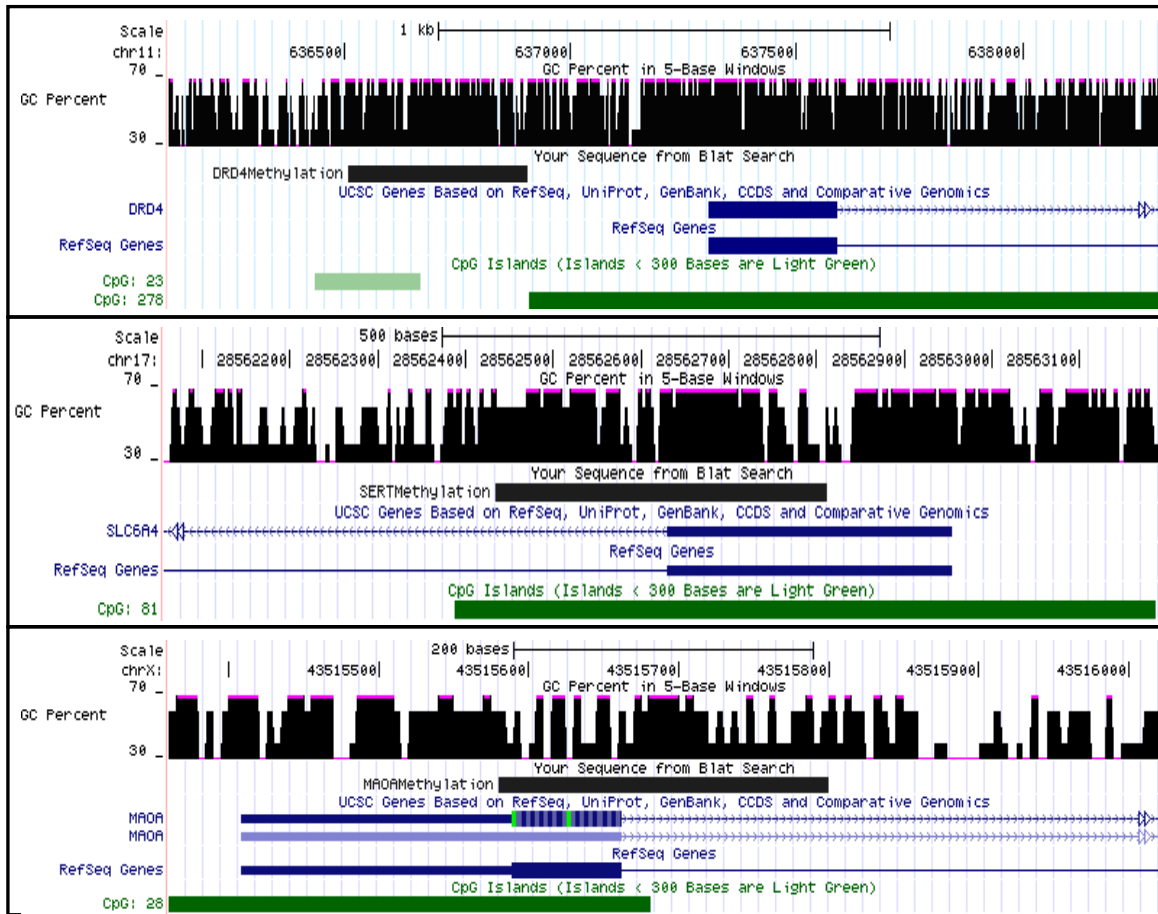
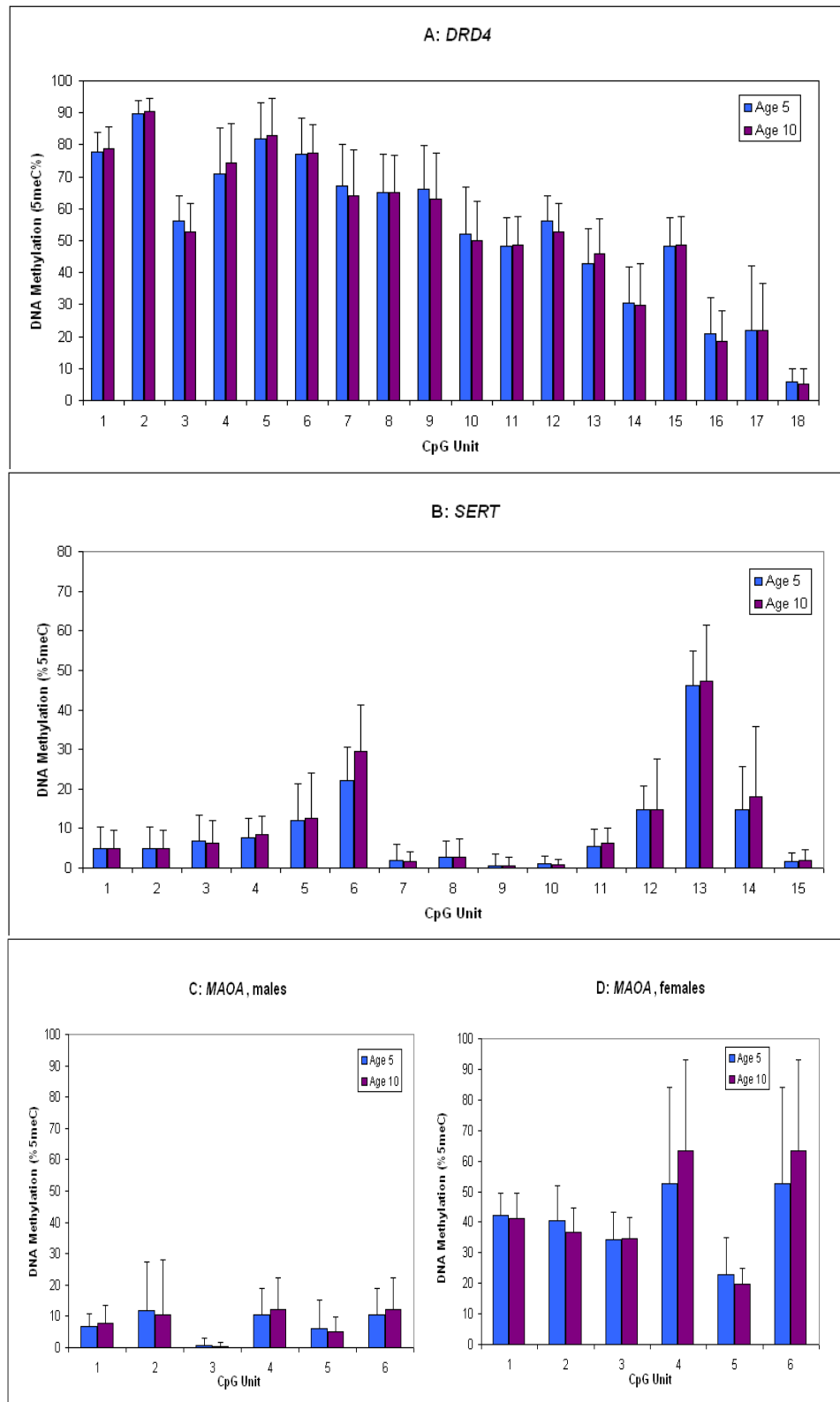


**SUPPLEMENTARY FIGURE 1.** The genomic locations of the *DRD4*, *SERT* and *MAOA* DNA methylation assays utilized in this study (adapted from UCSC GRCH39 Genome Browser).



**SUPPLEMENTARY FIGURE 2.** Average DNA methylation level at specific CpG units for A) *DRD4*, B) *SERT*, C) *MAOA* male and D) *MAOA* female amplicons at age 5 and age 10. Error bars represent the standard deviation of the mean.



**SUPPLEMENTARY TABLE 1.** Summary of primer sequences for PCR amplification and the total number of twin-pairs included in the analyses for each gene. \*UCSC March GRCH39 Genomic Assembly. \*\*Primers were ordered with the standard Sequenom MassCLEAVE tails (F: aggaagagag, R:cagtaatcgcactactatagggagaaggct).

Gene	Genomic Region *	Number of CpG units assessed	Primer Sequences** (5' to 3')	Age 5		Age 10		Both	
				MZ	DZ	MZ	DZ	MZ	DZ
Dopamine D4 Receptor ( <i>DRD4</i> )	chr11:636508-636904	18 CpG units (30 CpG sites)	F: GGGATTTTTTGTAGGGTTAGAGG R: CACCCTAATCCACCTAATATCTAACA	45	43	41	42	40	40
Serotonin Transporter ( <i>SERT</i> )	chr17:28562435-28562812	15 CpG units (27 CpG sites)	F: GGTTAGTTTTAGTTTTGGTTTTTGTT R: CAAAATTCTTCAAAAACCTTTAAC	44	44	43	39	41	38
Monamine Oxidase A ( <i>MAOA</i> )	chrX: 43515581-43515800	6 CpG units (7 CpG sites)	F: GTTAAAGTATGGAGAATTAAGAGAAGG R: CAAAATATAAAACCAAACCATAACTACA	Male					
				19	21	20	22	17	21
				Female					
				22	21	21	20	20	19