

43398775		TAGTGAGGGC	TGGAGGCTGC	GCAGACCTCG	ACGGGCCCTA	CATGACGTCA
43398825		CAAAGGGGCC	AGACCAAGTG	GGGCAGCACC	CTGCGACCCT	GCGATCCTGC
43398875		CTGGCTCAGC	CGCCTTCATA	TATCTGCTTC	CTTAAGTCCA	CTCTTGCCCA
43398925		GATAGCTTTC	AGTTAAAAC	AAAGAATGAA	AGCACTAGGT	TGAGAGCCCA
43398975	CpG1-6	CGCGGCTACA	CCC CGT TCTA	CTCCCCCACT	CT CGCC AGGC	AAC CGCG CCC
43399025	CpG7-11	CC CGC CTGCA	GTGGCAT CGT	CGGCCA CGC	CCAGTGGCAG	GGTTTCCAG C
43399075	CpG12-15	GCGAGC CTGC	AGGCAGG CGG	GGAAGG CGGA	GCCAGG CGG	CCTAGAGTCA
43399125	CpG16-18	CTTCTCCCC CG	CCCCTGACTG	GG CGGG GAGC	CGGGG CTGG	TCTCTAAGAG
43399175		TGGGTACCGA	G AACAGCCTG	ACCGTGGAGA	AG GGCTGCGG	GAAGCAGAAC
43399225		ACCGCCCCCA	GCGCCCAGCG	TGCTCCAGAA	ACATGAGCAC	AAACGCCTCA
43399275		GCCTCCTTCC	CCGGCCGGC	CGGCACCGGC	ACCAGTACCC	GCACCAGTAC
43399325		CGGCACCGGC	ACCAGTACCC	GCACCAGTAC	CGGCACCGGC	ACCAGTACCC
43399375		GCACCAGTAC	CGGCACCGGC	ACCGAGCGCA	AGGCGGAGGG	CCCGCCCGAA
43399425	CpG19-21	GCCGGGGGCA	CAACTGCCCA	GGTCC CGAAC	CGGACT CCA	GCTTGGA CGA
43399475	CpG22-26	CACCTCCTAC	AGCCTG TCCG	AATGGAG CGT	CGTT CTGAG	TGG CGGTCCG
43399525	CpG27-30	TCT CGGATCC	G CTAGCCAGT	TCCCAGTGGA	GCA CGT CCTC	AACTGC CGAG
43399575	CpG31-32	GC CGC CTCCT	GGAGCTCCAG	CATACTACTCC	CCAATCAGCA	CTAC CGGT TCT
43399625	CpG33-36	TAG CGAGAGT	ACTGACT CGG	ACTCCAAGAG	TGGCCT CGG	GGTTT CAGCG
43399675	CpG37-39	CTTACAACCC	GAGCAGT CGG	ATCCCCAAGT	CTACCACCAG	CT CGA ACTCC
43399725	CpG40-42	T CCGAT GGGG	CGT CACAGC	CTCCAATCAG	GACAC CGG CA	TTCCCTGGGT
43399775	CpG43-45	ATTAGTAACA	GGACCTACCC	CGCCCG TAAA	CTCCCC CGT A	GAGTCATTGC
43399825	CpG46	AAGGGTCTGC	CTTCTCCTCA	GGGTT CAGCA	CCCCA CGGGG	TTTGGTAAAA
43399875	CpG47-49	GGAC CGACCC	TGCCCC CGGA	TTCCAACCTG	ACCTCAGTGT	CGGACT TACAC
43399925	CpG50-51	TTGGATATTT	GT ACGGGG AC	CTCCTATAACC	CAATGACCTT	T CGAAGTGT
43399975	CpG52	CAATACAAGC	ACCTCCTACA	CCCAGTAACA	CCCC CGAGT G	TCAGTACAAG
43400025	CpG53	GGTCTGC CGC	ATCCTCAGTG	TCCAGCTTCC	CCTGGGGTTT	GGTACCAGGA
43400075	CpG54	CCACCTCTAC	CCAATAACAT	TTCCCCAGTG	T CGCCACAAG	CACCTCCTGC
43400125	CpG55	ACCCCATAAC	ATCCCCCAG	TGTCAAGGCA	GG CGT CTACC	CCCACCTCAG
43400175	CpG56-57	TGCCTGACAC	T CCGCG GGGT	TCAATACAAG	AACTCCTGC	ACCCAGTAAT
43400225	CpG58-60	CCTTTCCAGC	TGC CGAC ACA	AGGACATTCT	AAACCTAATA	ACTCT CGCG
43400275	CpG61-63	AGTGT CAGTA	CAAGGGT CG	CCC CGCT CTC	AGTGCCCAGC	TCCCC CGGG
43400325	CpG64-66	TATCAGCTGA	AACATCAGCT	CGCCCC Tgg	gCGctccCGg	agtatcagca
43400375	CpG67-70	aaagggttCG	cccCG ccac	agtgccCGgc	tccccCGgg	tatcaaaaga
43400425	CpG71-74	aggatCGgct	cCG cccc CGg	gctcccCGgg	ggagttgata	gaagggctct
43400475	CpG75-77	tcccaccctt	tgcCG tcccc	actcctgtgc	ctaCG accca	ggagCG tgtc
43400525	CpG78-80	agccaaagca	tggagaatca	agagaaggCG	agtatCGCGg	gccacatggt
43400575	CpG81-86	CGaCG tagt C	G tgat CG gag	gtggcatttc	agGTCAGTGT	GGACCGTAGC
43400625		GGTGGC CTGG	GGGACCCTGG	CCAGTGAGGG	GTAGGGGAAC	CTACAGTAGC
43400675	CpG87	TCTTGTGGTG	TTTGGGGGTC	TCTCATGCAT	GCG AGAGTGT	AGTGTAGCCA
43400725	CpG88	TGGCTTGGCC	CCATATCCTG	CGAGGT AGGA	GTGGGGGTTG	TGCCAGTTTT
43400775		GCTGGTGGTG	TGACTGGGGG	AGGCAGACAC	AATAATTTTA	CTACTACTAC

Figure 1. The sequence and structure of the *MAOA* promoter region. The first CpG island begins at bp 43398975 and contains 18 CpG residues. A second CpG island begins at bp 43399493 and contains 70 CpG residues. The position of each of the CpG residues is noted in the figure. The first exon of *MAOA* is denoted by small blue letters and is wholly contained within the second island. The positions of the primers used to amplify the *MAOA* VNTR are denoted by boxed letters. The transcription start site (TSS) is at bp43400353 between CpG residues 64 and 65.