

Table S4. Primer sequences and optimal PCR conditions for MassARRAY.

Gene symbol	ID of CpG units	Size of amplicon (bp)	Primer sequences		Target Sequence (Examined CpG units are marked in yellow. Examined CpG sites in each CpG unit are underlined. CpG sites which were present, but could not be evaluated by MassARRAY, are indicated by dotted underlining.)	Optimized PCR condition	
			Forward primer	Reverse primer		Annealing temperature (°C)	Polymerase
FAM150A	1-17	455	aggaagag agGGGA GGATTTA GTAGGG TAATTGT	cagtaatac gactcactat aggagaa ggctTTTC ACCTAAA AAAACAC TAAAACC	GGGAGGACCCAGTAGGGTAACCTGCCGCTCGCCCCGGCGGTTCTCCCTGGGC TCTGTCTCCCGCCGCTCCACCCCGAGCCTCGGGGTCCGTACCGGCTTCC CCTGGCTGGCGGGGTCAGTAGAACC <u>CGCGGC</u> CCTAGGTCCGGACGGAAAA AGCAGGGC <u>CGGGGTGCG</u> GCCTGGATGAGCGGAGATCTC <u>CGCG</u> CCTTGGGCTC AAAGGTGCGGGGTGCGCTCTGCTGCCGAGCCCTGCT <u>CGCT</u> CAGGAACACTG GCCA <u>CGCCG</u> TCA <u>CG</u> CCAGC <u>CG</u> CCCCCTGCCCCAGGTCTGGAGGCC <u>CG</u> ACCTGC TCTCCTAGG <u>CG</u> CAGCACCGCGTCTCTTCCGCGTGGGGAG <u>CGGCGGGCG</u> GA AGAGGTCTGGGGCTGGGCAC <u>CG</u> GGGACA <u>CGCG</u> CCCAGCTCCCCTGGCCTCCC TGGGGGAGTGGC <u>CG</u> GTTTCAGTGCCTCCCAGGTGAAA	60	TaKaRa Taq HS DNA polymerase (Takara Bio, Shiga, Japan)
GRM6	18,19	188	aggaagag agGGTTT AGGATAA GTTTGTG ATAGATG	cagtaatac gactcactat aggagaa ggctAAAA CAAAAAA ACAAACC CAAAAAT	GGTTCAGGACAAGTCTGTGACAGATG <u>CGGCCC</u> AGGCCCTGAGCGAGAGAGGA TTTAAGGATTCTAGGGAGGGATGAGAGAC <u>CGTCTCCG</u> AGGGTGGAGACCCCTCC TGAGTGTGGGGGTGGCGGTGCTGGCTCTCCCGCATCTCCTCCCCTCCCTC TCCAATCTCTGGGTCTGTTTTCTGTTTT	56	HotStar Taq DNA polymerase (QIAGEN GmbH, Hilden, Germany)
ZFP42	20-25	196	aggaagag agGAGTT GATGGG TGGTTGT AGTTT	cagtaatac gactcactat aggagaa ggctCCCA TTTAAAA AAAATTC CATAAAA CAAAA	GAGCTGATGGGTGGCTGTAGCCTGATTAGAC <u>CGCGT</u> CAGTC <u>CG</u> GAGGGTGGG TCTTGGGAGGGGG <u>CG</u> CAGGGCAGTCCA <u>CG</u> TTTCCACTGCAGTTTCTCCTTTGT TTTA <u>CG</u> TTTTGGGAGGAGGTGGCATTGGAAATAGCAGAGTGCTT <u>CGCG</u> GTAACA GGGGTGAGTCTTGTTCATGGAACCTTTTTTCAAATGGG	56	HotStar Taq DNA polymerase (QIAGEN)

ZNF540	26-42	463	aggaagag agGGGTA GGGTAG AATTAGG TTAAAGA AA	cagtaatac gactcactat aggagaa ggctACTA AAATCAA TAACCCC CAAAAAA	GGGCAGGGCAGAACCAGGCTAAAGAAA CG TCCAG CG TAGCTTCAAGGATGCAC CGCG TGATCCCTAT CG GATCTCCC CGA CGCG TCAGGCCCTGCCTAGA CG GTGCT GGGAG CGCG TCTCCTTGAAC CGTTGTCCCG CCTGGGATTG CG AGGTAGGTAC CG GC CTGCCTGTGTGTAC CGGGGCTGCTGTCTCCG GGGAGGGGCTTCTGG CG GA CAGGAGAACCAAGCAGCCTCAGGAGCTGCCTGGGTGTGTGTGTTTCTGTGC CG GA GTGTTGCATATCTCTGTGTGTGTTTCTGTGCAAGTGTGTCATGTCTGTGTGTGT GGGGGGGGTGGTGTCTGGTGAAAAGAATGTGTCT CGTGCG GTGGAG CGCG T TTCTCTGTAGT CGCG GGCTCTCTTATG CG CCCTCTTGGTCCCAAGTGTGCT TTCTTGTTTTT CG CTTTCTTGGGGGTCATTGATTTACG	58	TaKaRa Taq HS DNA polymerase (Takara)
ZNF154	43-48	279	aggaagag agGGTGA ATATATT TTAGAGA AGTTAAA ATGG	cagtaatac gactcactat aggagaa ggctTCCC TCCACTA CCCTAAA ACTTAAA	GGTGAACACACCTCAGAGAAGCTAAAATGGC CG CCACGAAGAGGCCCCCCCAA AAGTCC CG TCCTTTCTTTTTGTGACTCTCAAGGAAAGT CG GTTTTCTGAGCTCTT ACTGGCTTAGTAG CGTGCG TTCAACGCAGAGCATTCTAGGTAATGTAGTTTTTC ATAGATCC CG AGGTGGGTGC CG GGGACCTTTGCACCAACCTCTTGAGTAAA AGCCAGCTCCAGGG CGCTGGGCG ATGAGAAATGGCTTATCCAAGTCTAGGG CAGTGGAGGGA	54	HotStar Taq DNA polymerase (QIAGEN)
RISM4	49-59	404	aggaagag agGGAGT TTTAGTT TATGAG GGAAGG A	cagtaatac gactcactat aggagaa ggctAAAC CCCAAAA TCTCAA AATAC	GGAGCCCCAGCCCATGAGGGAAGGAGAGGAGAGATAAATGGGG CG CTCAAG GCCTGGGG CGCG GGCAGGGGTCTTGGGCAGGGATCCTTGATGTGGCCAA GACAAAGATGGAGAGGTAAGGTCTG CGCG CCACCTCCAATGG CGGGGGCG GTCC GAGCCCCAGGGGTGGGA CG GCCAAAGCCAGGGCTTGAAGAGTGGC ACATTCAAGGAGACTCAGGGAGGTGGCAGGT CG GCTCCAGGGACGAGGCAAG GGGCCTCCAATAG CGCG GGTGAGGAGGAGATGGGTCTGG CG ACCCAAG GGCCACCTG CG GGAAAGGTGAATGCAGACAATCT CG GGGTCCCTGGGGGAG AAGGCCAGAAGGTAG CG CATCCTGGAGACCCTGGGGTCC	54	HotStar Taq DNA polymerase (QIAGEN)
PCDHAC1	60-73	362	aggaagag agTGGTA GTTTTTG GGATATA AGAGGG	cagtaatac gactcactat aggagaa ggctAAAC TACCCAA ATCTTAA CCTCCA C	TGGCAGCTCCTGGGATACAGAGGGTGCAGGACAGACTTCAACC CG CAGCAG GATCCAG CGCG GAAAGCTCTGCAGCAGGATCCAG CGCG GAAAGCCCC CG CA GCATTTCTTT CGGGGG CTCCTGTTTCTTAAGCCTAGAAGGTGTGGT CG CTCA CG TTACCGTCCCGCCTCTCGCCGCCTCCGCTCGGCAGCTCCA CG CTGAGTCC CGCCCTCTCCCGCG GAGAGGTG CGCG GGGTGAGAG CGCG GGACC CGA CG CGCG GCTCCCAAAGGG CG GCAGGAAGAGCCCAGCTGGGCTCAGCCACAGTTA TCAGCAATCTG CG GGCAGAGGATGTGGAGTTAAGATCTGGGCAGCCT	56	HotStar Taq DNA polymerase (QIAGEN)

PRAC	74-78	264	aggaagag agGGTGA AAGTTTG TTGTTTA TTTTTT T	cagtaatac gactcactat agggagaa ggctCAAA CTAAATT CTAATCC CCACCTT	GGTGAAAGCCTGCTGCTCACCCCTTCCCTTGTTCCTCCAAAACCTTCTGAAGGCTCC CAAATTCCTGGGAGACCCTCTCCAGGGCCTCCTGATGCAGCTACCATACTGA GCGATC_CGTCCGATAA_CGCCCTTGGCCACCGATCAGTTTACCTTATTAGAGAGA AAAGCACTTTGGAGGTAGTAAGATGGGC_CCGTCCTTGATCTGAGAAATGGGC _CACAAACAT_CCGCTGTTCTCTGCAAAGGTGGGGACCAGAATCCAGCTTG	58	HotStar Taq DNA polymerase (QIAGEN)
TRH	79-97	414	aggaagag agAATAG ATTTTAA GAGGTG GTGTAG AAA	cagtaatac gactcactat agggagaa ggctAAAA AACTCCC TTTCCAA TACTCC	AACAGATCTCCAGAGGTGGTGCAGAAACGACCC_CGCGCCCGGGCC_CCCCATCCT G_CCGGCCAGTGCTCCCGCGCCCGGCTCCGGTCCCCAC_CGTCCCCG_CCCCAGA TTTC_CCGGAGGAGCAGGCGGGCGGGGTCCCGCGGGGCGGGTGCCTGACAGCG CCCCTTCCCGCGGGCGCGACCCCTCC_CCGCTGACCTACT_CGAGC_CGCGCG _CTGGCG_CAGATATAAG_CGGCG_GCCCATCTGAAGAGGGCT_CGCGCAGG_CGCCCC GGTCTCAG_CCGCTGCAGACTCCTGACCTGC_CGACTG_CCGATCC_CGAGTCCC _CGGATCC_CCGACCCATCCTGTGGAGCCCACTCCTGGCAGGTAAC_CGCCCCAA CCCCTCTCCTT_CCGCAGA_CGGTGTCCG_GGAGCACTGGAAGGGAGCCCTCT	54	HotStar Taq DNA polymerase (QIAGEN)
SLC13A5	98-114	500	aggaagag agGAAGG ATTTGAA TTTGAG ATATAGT TT	cagtaatac gactcactat agggagaa ggctAAAA AACCCAA AAACCTA CAAAAA	GAAGGACTTGAACCTGGAGACATAGCTCAG_CGCGCAGGCCAT_CGCGCGGGAG GGAGACTGG_CGGGGCAGACGAGTGAGGGCAGCTAGAGG_CGCGCGGGCTT AAGAAGGGGCCACAGTCCC_CGGGGATTGGGGAGGGGG_CGCTGACAACCT_CG _CCCCC_CACGGGGGGCCTCCCGCGGCCCTGGGGCGGGGCCACCCCT_CGGG GTCTGTGGGA_CGCGCCTGCCCCCAATTCTGCCACC_CGGCGGGCGGTGGGAGGC _GTCTTTGGACTCAA_CGCTTCGGGCCAGCCCTTAGGGGCAGCCTGGGCCCTA GCATCT_CGCGCCTGTCCAAGCCTCTCCTG_CGCTGCGCAGGCAGAGGTG_CGTCC _CGGGGCTGCCAAG_CGGGGCGTGTTTTGGTCACTGGTGTGCCCGCTTTGGCG TAAGG_CGCCCCCTCCCGCGTCC_CATCTGCTCTTTCTGGGCTCTGAAGGGTCC _GGATGAAACTCTCTGCAGGCCCTCTGGGTCTCTC	54	HotStar Taq DNA polymerase (QIAGEN)
SLC13A5	115-130	463	aggaagag agTTTTTT TGGGTTT TGAAGG GTT	cagtaatac gactcactat agggagaa ggctTTAT ATCCCTT CCTCTCT AAAACCT C	CTTTCCTGGGCTCTGAAGGGTCC_CCGATGAACTCTCTGCAGGCCTCTGGGTC TCTCAGGTCTATCTCCC_CGATCTCCCTCTCCTTTCCATCTCCTTACTTCCGCCCC TCCGGTGTCTCTCCGAGAGGTGTCCCCCA_CGCCCCCGGCCCTCCG_CACCGC GGCCCTCGCTTCCCGGTCCCCCTGGCTTCTCCTCGCCA_CGTCCG_CCCCACTCTA GGTGCAGGACCCCTTTTCCC_CGCTCGCACTCTC_CGGCCCGGAGCTCCTGGGC _GAT_CG_CACAGGGAAGCGAGGCCACTGTCTCCTCTGTCCCAGGGGCTGT_CGC _CTCCAGTGGAG_CGCTGCACCC_CG_CAGA_CGCCCCGGCG_GGCAGATG_CGGACAC _CGCTTTGGAGGGGCCCCACCGAGCCTCAGCAGC_CG_CAGCTGCC_CGCCCCGAC CCAGGTCAGAGGGAAACCGGAGCTCTAGAGAGGAAGGGACACAA	58	HotStar Taq DNA polymerase (QIAGEN)

SLC13A5	123-135	384	aggaagag agTTTTTT TTGTTTT AGGGGT TGT	cagtaatac gactcactat aggagaa ggctCCAC CAACATA AATAAAA CTCCCC	CCTCCTCTGTCCCAGGGGCTGT CGCG CTCCAGTGGA CG CTGCACCC CG CAGA CGCCCGGCG GGCAGATG CG GACAC CGCG TCTTGGAGGGGCCACCGAGCCT CAGCAGC CG CAGCTGCC CGCCCG ACCCAGGTGAGAGGGAAACGGAGCTCTAG AGAGGAAGGGACACAACCTAAGG CG ACACTGAGACAGT CG CCCATGTATTTCATT CAGCC CG CCAGGCAACAGACAGGTGC CG AGCACCTCTTCTC CGCG AGGCCCT GTTTTGGGCACTGGAGACACACGGATGCAAAGACATCCCCACCTCTGTGATTTT CTTCTTTCCTCTCCTCTGCCTGCCTCTCATTCTGCAGTTCCTTTTGGGGAGTCT CATCCATGCTGGTGG	58	HotStar Taq DNA polymerase (QIAGEN)
ZNF671	136-156	428	aggaagag agTGGGA TATAGG GGTTGTA GGTATTT	cagtaatac gactcactat aggagaa ggctATAA AAACCAC ACTCTAC CCACAAA	TGGGACACAGGGGCTGCAGGCACCTTACGATT CG GAGT CG GAGAAAGGGTGA CTGAGGGCC CG GAGGACGCAGCACCCACC CGCGCG GAGTCC CG TTAGCTC CG C CATAGGAC CGTGGGCGCG GACAGCTGC CG GGAG CG GCAGG CGTCTCG AT CG GGGACGCAGGCACCTTC CGTCCCTGCAGAGCATCAGA CGCGTCTCG GGACACT GGGGACAACATCTCCTC CGCG CTTTCCCAACACCTCCACCTG CG GCCACACA AG CG TTACAGAACCC CG GCCAGGGACAGCCTGACAGAAACAAAATGTC CG CTA CAAGGAGGAGC CG GAAGTCC CG CCCA _{CG} GCACCCCC CG CAGGCACTGAAACAC CCCTCTCCTGGGCCCTCATTGGGTATGCAAC _{CG} TATAGGTTTGTGGGTAGAGTGT GGTCCAC	58	HotStar Taq DNA polymerase (QIAGEN)
WNT3A	157-165	348	aggaagag agGTTTA TTTGGTA ATGAGG GGTTGTT	cagtaatac gactcactat aggagaa ggctTTCC TCAATCT TAAACAT CTCAAAA	GTCCACCTGGCAATGAGGGGCTGCTGTAGAGAGAGTTAAGGGTGAGTTAAGCA CG GGGTGTGAGGGGCTCCAGGACCCTCAATCAGAAAG CGCTGTGCTGCG CCC TCCACACCAGAAAAG CGCGTTCCG TGAGACCCTCCCCAGCCTGG CG ATGGAA GTGCAGATAAACCAAAGGAAGGGTCC CG AAAGTCTCTCAGGCCTCCACC TCCATGCACATATCCTGTGGGAGGGGGAA CG GTGGCCACACTTT CG CCAGGG CTTGATCCCTCAGAGCCCTCACCAGCAAGGATCACCCAGTTC CG AATTA GGG CG CTCTGAGATGCCAAGATTGAGGAA	58	HotStar Taq DNA polymerase (QIAGEN)
KHDRBS2	166-181	422	aggaagag agTTTGG TATTATT ATTAATG AGTGGTT GG	cagtaatac gactcactat aggagaa ggctAACA AATCCTA CCTTCTA CCAAAA A	CCTGGCACCAACCAATGAGTGGTTGG CG GAGGTGGGCCGCGTCTGTTCC CG CCTCTCCAGTTAAGGC CG CTGGTGTGAGC CGGGGCTCTGCGCG AGCGAGG GACGACGGAAGGGA CG GGCAGGTGTGGG CGCG GGGCCACGCAGCC CG A CGG CG GGAGT CG CAGGTGCTGGGTGCATGGGCCAGTGAAGGACGCACAGAGATCCC T CGCCGCGCG GAGGAGGAGCAG CGCG GGAGCCAGGCGCTGCCCAAGACCC TGCCTG CGTCCG AGCGAGCGGAACCT CGCGCTTCGCGCG GGGACAATC CG AA GTC CGCG CTATGGAAGAGGAGAAATATTTGCCTGAGCTGATGGCAGAGAAAGA TAGCCTGGATCCATCTTTTGTGCATG CGTCCCG CCTTTTGGCAGAAGGTAGGAC TTGCC	56	HotStar Taq DNA polymerase (QIAGEN)
ASCL2	182-193	339	aggaagag agGTTAA TAAAGTT GGGTTTT TGTTGG	cagtaatac gactcactat aggagaa ggctAATA CAAACCT CCAAAC CCTCC	GCTAACAAAGCTGGGTTCTGCTGGGCCCGCCCTGCTCCTCGCCCCGCGA CTGGGCTGGGCGCGCTGTCCCCTAG CG CAGCTATGTCC CG AG CGCG CCCCCA CCTGTG CG TAAATCTACTGGGAATGGGGGTGGACTG CG CCTTACCTGGGG CG G GGTGGGCTTAAGGAGTGGT CG GAGACTGAGG CG GGGTGGGAGGTTTCAGGTTT C CGGGGCG CCTTCCCCAACCCGCCCCGCTTTCCCGTCCCTCCA CGCG CACC CTGCCTGTGTTTTCCGTGC _{CG} CCCCCGCCTGAGGGCTCTGGG CG GCACCTTA ACC CG GAGGGCCTGGAGGTCTGCACC	58	HotStar Taq DNA polymerase (QIAGEN)