

Additional file 1, The target promoter CpG islands and the primers for MSP

Gene Name	GeneBank No.	Sense 5'-3'	Antisense 5'-3'	Amplicon ligation relative to transcription start	Size (bp)
ABL (M)	U07563	CGAGGATCGTTATTTGGTTCG	TAACCGAAAACCGCCTATTA	-368 to -172	197
ABL (U)		TTGTTATTTGGTTTGGGTTGG	TAACCCACAACCACATCTCCAC	-362 to -150	213
APAF1 (M)	AB070829	AGGTTTAGTTACGTTTCGTTTCG	CGTCCACTCGCTACCTCTTC	-348 to -99	217
APAF1 (U)		GAGGTTTAGTTAAGTTTGTGTGG	CCACTCACTACCTCTCTCTCC	-348 to -102	215
APC (M)	U02509	TATTGCGGAGTCCGGGTC	TCGACGAATCCCGACGA	-17147 to -17050	97
APC (U)		GTGTTTTATTTGGAGTTGGGGT	CCAATCAACAACTCCCAACAA	-17153 to -17046	108
AR (M)	M58158	TTTCGAGATTTCCGGGAG	ACAACCTCCGAAACGACGAC	-3 to +210	214
AR (U)		TTTGTAGATTTTGGGGAGTTAG	CCAAACAACAACCTCAAAACCA	-3 to +204	208
BRCA1 (M)	L78833	GGTTAATTTAGAGTTTCGAGAGACG	TCAACGAACCTCACGGCGCAATCG	-320 to -138	182
BRCA1 (U)		GGTTAATTTAGAGTTTTCGAGAGATG	TCAACAAACTCACACACAAATCA	-320 to -138	182
CAV (M)	NT_007933	TTAGGGCGAGAGCGATTTC	GCCGCCAAAATCAAAAAC	+1320 to +1482	163
CAV (U)		AGTGTTTAGGGTTCGAGTATTG	CCACCCACCACAAAAT	+1315 to +1488	174
CDH1 (M)	L34545	GTTGGCGGGTTCGTTAGTTTC	CTCACAATACTTTACAATCCGACG	-265 to -93	172
CDH1 (U)		GGTGGGTGGGTTGTAGTTTGT	AACCTACAATACTTTACAATCCAAC	-266 to -93	172
CDH13 (M)	AB001090	TCGCGGGGTTTCGTTTTCGC	GACGTTTTCATTATACACCGG	-267 to -24	243
CDH13 (U)		TTGTGGGGTTTGTTTTTGT	AACCTTTCATTATACACACA	-267 to -24	243
CSPG2(M)	AC026696	AGTTTCGGGGGACGTTT	TTTCTACCCCGCTCTCC	+1350 to +1525	176
CSPG2(U)		GAGTTTTCGGGGAGTTT	AACCAACCAACCACTCCA	+1349 to +1500	152
eyelin a1 (M)	AF124143	TCGTCGGGTTTAGTCGT	ACCCTGTTCCCAACAAC	-755 to -550	206
eyelin a1 (U)		GGGTAGTTTGTGTGTTTAGTTG	AACCACTAACAACCCCTCT	-762 to -565	199
DAPK1 (M)	NM_004938	GGATAGTCGGATCGAGTTAACGTC	CCCTCCAAACGCCGA	-332 to -234	98
DAPK1 (U)		GGATAGTTGGATTGAGTTAATGTC	CAAACTCCCTCCAAACACAA	-332 to -229	103
DBCCR1 (M)	AL138894	CGGGTGTAGCGTTTCGTA	CAAAAACCCCTCCCTAA	+396 to +561	166
DBCCR1(U)		GGTGTGTTGGGTTGATG	CAAAAACCCCTCCCTAA	+388 to +561	174
EPO (M)	NT_007933	TTACGTTTCGGCGAGTT	CGAACGACCGAAAATAACC	-212 to -28	185
EPO (U)		TTTGTTTATGTTTGGTTCGAGTTTA	ACCCCAATCCAACCTCAA	-217 to +17	236
hMLH1 (M)	AB017806	ACGTAGACGTTTATAGGGTCGC	CCTCATCGTAATACCCCGG	-531 to -655	124
hMLH1 (U)		TTTGTAGTTAGATGTTTATAGGGTGT	ACCACCTCATATAACTCCACA	-526 to -654	118
IRF 7(M)	NT_008953.8	GTTTCGGGAGTTGAGAATC	TATAACCTGACGGCGACAC	+161 to +356	196
IRF 7 (U)		GGTGGGGTTTGTGGAGT	TACAAATATAACCAACACACACAT	+155 to +362	208
LKB1 (M)	XM_012913	GGTGTTCGTCGGTTCGTA	TTCCGACTTCCCTCTCC	-253 to -68	168
LKB1(U)		TTTGTGTTTGTGTGTTTGTGA	TATATCCAACCTCCCTCTCC	-238 to -64	175
MAGEA1 (M)	U82670	GTTTCGGTCGAAGGAATTTGA	CCACAACCTCCCTCTTAAA	+24 to +345	322
MAGEA1 (U)		GTTTGGTTGAAGGAATTTGA	ACCACAACCTCCCTCTTAA	+24 to +347	324
MGMT(M)	AL355531	AGCGTCGTTGTTTGTGC	CGCTTCAAAAACCACTCG	-451 to -266	186
MGMT(U)		TTGTAGTGTGTTGTTTGTGT	CATCTACAACCCCCACA	-469 to -261	209
MT1A (M)	K01383	TAAGGTTGGGTTTCGGAAC	AAATACGACACCAGAAAACCA	-421 to -258	164
MT1A (U)		TAAGGTTGGGTTTTCGGAAT	CTCCCTAATAACAAAACACA	-421 to -251	171
MYOD1 (M)	AF027148	GACGTTTTCGACGGT	GCCCGAAAACCGAATACAC	+210 to +393	184
MYOD1 (U)		ATTGTAGTGGTTTGTGATGGTT	CACACACATACTCATCTCACA	+206 to +418	213
OCT6 (M)	L26494	ACGAGGATCGGTTAGTTCG	GAATCGATCTCTCCAACCA	+727 to +955	229
OCT6 (U)		GGATGAGGATGTTGTTAGTTG	TCAATCTCTCCAACCACTT	+725 to +952	228
p14 ^{ARF} (M)	L41934	GTCGAGTTCGGTTTGGAGG	AAAACCAACAACGACGAAACG	+95 to +255	160
p14 ^{ARF} (U)		TGAGTTTGGTTTTGGAGGTGG	AACCAACAACAACCAACCCCT	+97 to +262	165
p15 ^{INK4b} (M)	NM_004936	CGCTTCGATTTTCGCGTT	CGTACAATAACCGAACGACCGA	-312 to -165	147
p15 ^{INK4b} (U)		TGTGATGTTGTTGATTTTGGGTT	CCATAAATAACCAACCAACCA	-318 to -164	154
p16 ^{INK4a} (M)	NM_000077	TTATTAGAGGTTGGGCGGATCGC	ACCCCGAACCCGACCGTAA	-80 to +69	149
p16 ^{INK4a} (U)		TTATTAGAGGGTGGGGTGGATTGT	CAACCCCAACCAACCAATAA	-80 to +71	151
p27 ^{KIP1} (M)	AB003688	CGACGTCGGTAAGGTTG	AAACGCGCAAAAACCTACG	-355 to -163	193
p27 ^{KIP1} (U)		TGTGATTTGATGTTGGTAAGGT	CAAAACCAACCCAACTCT	-363 to -141	223
p53 ^{KIP2} (M)	HSU48869	GGGTCGCGGCTATAAA	ATACGAAAAACGGACGA	-70 to +118	205
p53 ^{KIP2} (U)		GGGTGGGGTTTGTGTGAT	AAACACAACAACCTACCTAACTTCCA	-79 to +111	203
p73 (M)	AB031234	GCGTTCGGTTCGTAGGT	CTCAACTCCAAAACCCAA	-1722 to -1511	212
p73 (U)		TGGGTGTTGGTTGTAGGT	CCAATCTCAACTCCAAA	-1725 to -1505	221
PTEN (M)	NM_000314	GGTTTTTCGAGCGCTTCG	CGCTCACAACCTCAACT	-978 to -786	192
PTEN (U)		TGGTTTTTTGAGGTGTTG	TTCCATCATAACTACAACCTCCA	-979 to -812	167
RASSF1A (M)	XM_040961	GTTGTTAACGCGTTCGCTATC	AAACCCCGGAACATAAAAACGA	+82 to +176	94
RASSF1A(U)		TTTGGTTGGAGTGTGTAATGTG	CAAAACCCCAACAATAAAAACAA	+70 to +178	108
RASSF1C(M)	NT_006014.7	AGTTGGATTGTCGGTTTCG	TCAAAAACCCCACTACCAC	-370 to -137	187
RASSF1C(U)		GGAGTTTGGATTGTTGGTTTGG	CACCCCAAAAATAACCTCAT	-370 to -137	187
RBI (M)	L11910	GGGAGTTTCGCGGACGTGAC	ACGTGGAACACGCCCGG	-90 to 74	163
RBI (U)		GGGAGTTTTCGTTGATGTGAT	ACATCAAAAACACACCCCA	-90 to 74	163
SURVIVIN (M)	U75285	GCGCGGAGGATATAAATTTTCG	CCGCCACCTCTACCAACG	-171 to -7	163
SURVIVIN (U)		GGTGGGAGGATATAAATTTTTCG	CCACCAACCAACCTCTAC	-171 to -7	163
VHL (M)	AF010238	TGGAGGATTTTTTTCGGTACCG	GAACCGAAGCCCGCGGAA	-183 to -25	158
VHL (U)		GTTGGAGGATTTTTTGTGATGT	CCAAAACCAACCAACCAAA	-185 to -20	165
WT1(M)	X74840	GTTAGGCGTCGTCGAGGTTA	AAAACGCAAAAATCAACACC	+321 to +526	206
WT1 (U)		TGGGATTTGGTGGTATTG	CACCAACACCACTACACCA	+295 to +510	216