

Methylation patterns in CD34 positive chronic myeloid leukemia blast crisis cells

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Online Supplementary Table S1. Recognition sequences for MS-MLPA. Eighteen genes are represented by two probes, each recognizing a different HhaI restriction site. Probe mixes were purchased from MRC-Holland (Amsterdam, The Netherlands).

gene	sequence	Distance between HhaI site and startcodon TSG*
APC	CAGCTGTGTAATCCGCTGGATGCGGACCAGGGCGCTCCCATCCCGTCGGGAGCCCGC	17110
ATM-1	GGAGGGAGGAGGCGAGAGGAGTCCGGATCTGCGCTGCAGCCACCGCCGCGTTGATACTACTTT	4487
ATM-2	GCGGAGACCCGCTGATACTGGATGCGCATGGGCATACCGTCTCGCGCTGCTTGCC	4657
BRCA1-1	TTCTCAGATAACTGGGCCCTGCGCTCAGGAGGCTTACCCCTGCTGCTGGGTAAGG	1211
BRCA1-2	CCCTTGGTTCCGTTGCAACGAAAAGCGCGGGAATTCAGATAAATAAACTGCCACT	1317
BRCA2-1	CGGGAGAAGCGTGAGGGGACAGATTTGTGCGGCGCGGTTTTTTGTGAGCTTACTCCGGCCAAAAAAGA	848
BRCA2-2	CGGGTTAGTGGTGGTGGTGGTGGGACGAGCGCTTCCGAGTCCAGTCCAGCGTGG	763
CASP8	CTTTCCAATAAAGCATGTCCAGCGCTCGGGCTTTAGTTTGACAGTCCATGAATGTCTGCCACA	307
CD44-1	CTCCTTTGCGCCGCGCCCTCCGTTCCGTCGGACACCATGACAAGTTTTGGTGG	25
CD44-2	GGAGAAGAAAGCCAGTGCCTCTGCGCGCAGGGGCCAGTGGGGTCCGGAGGCACAGG	409
CDH13-1	TTCTGTGCTTCTCTGTCGCCAGTAGGGAAGAGGGGCTGCCGGCGCGCTCTG	221496
CDH13-2	CGTGCATGAATGAAAACGCCCGCGCGCTTCTAGTCGACAAAATGACAGCCGAG	221581
CDKN1B	AGCCCCGCGCTCCTAGAGCTCGGGCCGTGGCTCGTGGGGTCTGTGTCTTT	169
CDKN2A-1	CAGAGGGGAAGGAAAGAGGAAGAGCGCTCAGATGCTCCCGCGGTGCTGAAAGTTAAAACCGAAAATAAAATGG	20543
CDKN2A-2	GCAGGTTCTTGGTGAACCTCCGGATTCGGCGCGGTGCGGCCCGCCGCGAGTGAG	19513
CDKN2B	CTGCGACAGCTCCTGGAAGCGCGCGGATCCCAACGGAGTCAACCGTTTCGGGAGG	66
CHFR-1	CGAGAGTAGGCGGTGGAGGGCGCTCGGCCATCTTTGATCCTGACCAGGCGACTTCGT	358
CHFR-2	CGCAGAGTAGGCGGTGGAGGGCGCTCGGCCATCTTTGATCCTGACCAGGCGACTTCGT	361
DAPK1	CGCAGGATCTGGAGCGAAGTGTGCGCTCGGTGGCGCTCCCTTCCCTCCCT	712
ESR1-1	CGCCCCCGTGTACAACACCCCGAGGGCGCGCTACGAGTTCAACGCGCGCGC	113
ESR1-2	GCTCGCGTGTGCGGGGACATGCGCTGCGTCCCTTAACTCGGGTGTGCTCTTTTCC	117
FHIT	CBCGGTCTGGGTTTCCACGCGGTCAGGTCATACCCCGGAGCCAGTGGG	157
GATA5	GCTTGGCGACAAGGACGACGACAGGGCGCGCCAGCGCGGAGCCCGGACAGTGCATG	603
GSTP1-1	GGCAGGCTGCGCTCACCGCGCTTGGCATCTCCCGGGCTCCAGCAAACTTTCTTTGTTCCG	269
GSTP1-2	CGAAGAGCGGCGCGCTGACTCAGCACTGGGGCGGAGCGGGCGGGGACC	102
HIC1	CCGCTCCAGATAAGAGTGTGCGGAAAGCGCGGGGCTGAGACGCGACAGGAC	1050
IGSF4-1	CCTGGAGCCGAGTCTTGCACGCCAGGCGCCGGGAGAACACTTTTTCTTGATCCGGGGAAGCA	304
IGSF4-2	CTCCGCTCCAGCGCATGTATTAGCATCTATTAGCTGTCCGCTCGGGCTC	86
MGMT-1	CCAGCGTAGCCCGCCGAGCAGGACCGGGATTCTCACTAAGCGGGCGCCGTC	474
MGMT-2	GGCAAACTAAGCACAGAGCCTCAGGCGAAGCTGGGAGCGCGCCCGGCTTGTAC	329
MLH1-1	CGTTGAGCATAGAGCTTTCCTTGGCTTCTGCGGCCAAAATGTCGTTGTCGTCAGGGGTTAATC	7
MLH1-2	CTGCTGAGGTGATCTGCGCGACAGCGGAGGAGTGTGCGGCTTCTCAGGCTCCTCCTCT	343
MSH6	CGGCTGTGCGTATGTCGCGACAGACCCCTGTACAGCTTCTTCCCAAGTCTCCGCGCTGAG	-45
PAX5	GCGCTCGTCAAGCAGCGGGTTTGCACATGAGATGTCACAGCCCGCGCACAGCGCAG	636
PAX6	GGAGATGCGCGCGCCGAGGAGGCGCGGCTTTCATAAAGCAATATTTGTGTGA	4911
PTEN-1	CATGCTCAGTAGAGCTGCGGCTTGGGACTCTGCGCTCGCACCCAGAGTACCCTCTGC	1090
PTEN-2	CACCGAGCGGGCGCAGGAGGCGCTGCGGGTGCCTCCACTCACAGGGAT	1847
PYCARD	CCAAGTGTGACGTTCTACTGAGACCTACGGCGCGAGCTACCGCTAACGTGCTGCG	128
RARB-1	GGCGGGAGGCGAGCGGCGCAGGCGGAACCGTTTTCCAAAGCTAAGCCCGCAATAAA	828
RARB-2	CCGCCGCTTGTGCGCTGCTGCTGCTCTGCTGCTGCTTTTGCAGGGCTGCT	650
RASSF1-1	CAGTCCCTGCACCCAGGTTTCCATTGCGCGGCTCTCCTCAGTCTTCCCGCCCGC	137
RASSF1-2	GTCCACAGGGCGGGCCCGACTTACAGCGCTCCCGAGGATCCAGACTG	35
RB1-1	GGATGCTCCTGGAAGGCGCTGGACCCAGCCAGGTTTCCAGTTTAATTCCTCATGACTTAGCGTCCC	331
RB1-2	CAAGGAGGAGAGTGGCGCTCCCGCGAGGTTGCACTAGCCAGATATCCCTGCG	526
STK11	GTGGGATGGCGCGCCCGAGGAAAGACTGCGCTCGGCCGTGTCATACTTGTCCGTGGCG	421
THBS1	CCGCCGCCATTGGCCGAGGAATCCCGAAGTGCAGCGCCCTTTAAAA	816
TIMP3	TCCAGCGCCGAGGCGCTGCTGCGCCCATCCGTCGCCCGGGCACTCGG	169
TP53	CGGTGGCTCTAGACTTTTGAAGCTCAAACTTTTAGCGCCAGTCTTGAGCACATGGGAGGGAAAAACC	10819
TP73-1	GGAGTTGGATCGGCCCTGGGACTTGGCGCTCGCGAGAGGCTGGAGCGCCAGAG	29545
TP73-2	CGCCCCGAAAGGGAGCAGCGAAACCGGGGCCCGCCAGGCCAGCCCGGA	29776
VHL-1	CAGACGGAAGTGGGACGAGGCGGAGTAGGCGCGGAGGAGGCGGTCGAAGAGTACGG	-18
VHL-2	GCGAAGACTACGAGGTCGACTCGGGAGCGCGACGAGCTCCGCCCGCTCCGACC	78
WT1	GGAGGGTTGTGCCACCCCGCAGCTGAGAGCGGCTGTTGGGTTAAGAGGAGGGTGTCTCCGA	409

*TSG= tumor suppressor gene