

**Supplementary Table 2.** Sequence and position of Primers Used for RT-QPCR analysis.

Primer	Forward primer	Reverse primer	Distance (to p-tel. (bp))
Set1: Primers used for deletion analysis of <i>KRIT1</i> gene			
KRIT1_CD1	tttagcctcaccagaagtccttca	cactccagaagggtagaaaataatga	91,712,366
KRIT1_CD2	ttattccgaccttctccttga	tgagtttctgtctgacctgattca	91,702,831
KRIT1_CD3	tcagtacaagtgaagggtgcagtaaaga	ggaatttcccagcaattctgtaag	91,680,620
KRIT1_CD4	tgcccactgaagaaattcatg	ttcacggaaaaaaactctgcat	91,667,987
KRIT1_FL1	cctaccaataatgagcatgataatttc	gggtagagtattgagccatgtgaa	91,717,972
KRIT1_FL2	gatcaatgtataaaaactcccacagact	cattgaggatgcatatgacatttattag	91,715,967
KRIT1_FL3	ctgagcaagtgatgcttgagttg	tccagctgtactgccttcaca	91,665,033
KRIT1_FL4	gcacagtgagaagcaagcaaaa	ggatgctttgtggattgtcctaa	91,662,288
Set2: Primers used for deletion analysis of up- and down-stream <i>KRIT1</i> flanking genes			
PFTK1_copyn1	ccatttgcatatgacaaatatacacgta	ccaagttcagccaccatca	90,176,465
PFTK1_copyn2	tgcaaccagaagctggagaa	tgtttgatagactttgccataactattg	90,585,349
FZD1_copyn	cagttctgcgtcggttcaa	cctcggaccggttcca	90,731,617
MTERF_copyn	aggcggaagtaaaagcgaacta	gcctcaccaccttccaat	91,347,929
AKAP9_copyn	ggctggagtgtagtgggcaa	gatcgcttgagcccaggaa	91,460,483
CYP51A1_copyn	tggagagaatctgcctcctttaa	tcaaagtcataaggcagcaatga	91,590,381
ANKIB1_copyn	gaggcctctgtgattggatttt	aacaccacaggctgcatcaa	91,855,450
GATAD1_copyn	tgctcggctcagaaacactaaa	tttctcttggtggagactttctt	91,916,028
ERVWE1_copyn	ccctccatgccgtgtat	gggacgctgcattctccata	91,937,536
PEX1_copyn	gcacacacaaaaacccaatca	gcctcagcctcccagtag	91,974,653
CDK6	gccacctaacttaacctcttgtttt	ggtttctctgtctgttcgtgacact	92,242,090

*Note:* Table lists primer sequences and absolute distances of amplicons to the telomere (kb). Amplicon name indicates the 7q21 genes.