S1 Table. Primer sequences and TaqMan IDs used in this study

Experiment	Gene	Primer Sequence (5'-3') [a]	Annealing (°C)
TaqMan Assay	*GAPDH*	Hs02758991_g1	60
	Gapdh	Rn01775763_g1	60
Fragmentation PCR	*Tp53* 301 bp	CCTCAATAAGCTGTTCTGCC AGTCTGCCTGTCGTCCAGAT	60
	Tp53 952 bp	CCTCAATAAGCTGTTCTGCC GCCTCCACCTTCTTTGTCCT	60
Sanger Sequencing	*CHEK2*	CCCAGGAGTGGTAGGTCTCA GCCTCTCTTGCTGAACCAAT	60/65 [c]
	FGFR3	ACTGTCTGGGTCAAGGATGG AGCTGTAGGCCCCGGAGT	60
	MAGI1	CAGCCACATCAACAGGAAGA CTCAGATTTCACCCCATGCT	60
SYBR Green Allele-specific qPCR	*ERCC2*	GCTCATGCTTCCGTCTG(C/G) [b] TTACCTTTGGCGTAGGTGCT	65
	CARD11	CCAAATCTCTCTTGGCCTG(T/A) GAGGGGACCTTTCAGCAGTT	65
	EPHA3	GGTTGGGCCACAGAAGAAG CCACCACTTCCGTCCAG(A/G)	65
	MTOR	TCTATCCAGGCCACTCTCTGA(C/T) ATGCGGATCTCCTTGTGCT	66
	FLT4	CAAGTGTTCCACCCAAAGAAA CTCCTGCACAGCTACCC(C/A)	65
	FANCD2	TAAAACAAGGAAAGCAAAGTGG(A/G) TATGTCAATCCCCAGAAGCA	65
	BCYRN1 / TAF1	AGAAATGGGTGAGTGGAGGA CCTCAAACAAAAAAAAGTGAGACT(C/A)	65
	*Kras*_ref	TCCACAAAGTGATTCTGAATT CGTAGGATCATATTCATCCACAAA	62

SYBR Green Allele-specific qPCR	*Kras* (c.34)	ACTTGTGGTAGTTGGAGCT(G/A) TCCACAAAGTGATTCTGAATT	62
	Kras (c.35)	CTTGTGGTAGTTGGAGCTG(G/A) CCACCAAGTGATTCTGAATTA	62
	Kras (c.38)	GTGGTAGTTGGAGCTGGTG(G/A) TCCACAAAGTGATTCTGAATT	65
TaqMan Mutation Detection Assay	*KRAS*_ref	Hs00000174_rf	58 (5), 60 (45) [d]
	KRAS (c.34)	Hs00000115_mu	
	KRAS (c.35)	Hs00000121_mu	
	KRAS (c.38)	Hs00000131_mu	

[a] Upper, forward primer; lower, reverse primer.

[b] The first nucleotide in parentheses is the wild-type allele, and the second is the mutant allele.

[c] PCR was performed using 2 annealing temperatures appropriate for each sample: 60°C for fresh-frozen tissue DNA and 65°C for FFPE DNA due to better PCR condition for Sanger Sequencing.

[d] MDA was performed using 2 annealing temperatures: 58°C for an initial 5 cycles and 60°C for the ensuing 45 cycles.