

SUPPLEMENTARY TABLE 1D: gBlock sequences used to test ddPCR kits used in this study

APC (c.2626C>T (p.Arg876Ter))
TAGTTCTCGTTCTGAAAAAGATAGAAGTTTGGAGAGAGAACGCGGAATTGGTCTAGGCAACTACCATTCAGCAACGAAAAATCAGGAAGTCTTCTCAAAGTGAGGTTTGCAGATCTCCACCCTGCAGCCAGATGCCAAAGTCATGGAGAAGTGTCAGCATTACACTCTCAGGAAGACAGAAGTTCTGGGTCTA

APC (c.4348C>T; (p.R1450Ter))
CATTATAAGCCCCAGTGATCTTCAGATAGCCCTGGACAAACCATGCCACCAAGCAGAAGTAAACACCTCCACCACCTCTCAACAGCTCAAAACCAAGTGAGAAGTACCTAAAAATAAAGCACCTACTGCTGAAAAGAGAGAGAGTGGACCTAAGCAAGCTGCAGTAAATGCTGCAGTTTCAGAGGGTCCAGGTTCTTC

APC (c.3871C>T; (p.Gln1291Ter))
CCAAGAAACAATACAGACTTATTGTGTAGAAGATACTCCAATATGTTTTTCAAGATGTAGTTCATTATCATCTTTGTATCAGCTGAAGATGAAATAGGATGTAATTAGACGACACAGGAAGCAGATTCTGCTAATACCCTGCAATAGCAGAAATAAAAGAAAAGATTGGAAGTGGTCAGCTGAAGATCCTGTGAGCG

APC (c.4037C>A; p.(Ser1346Ter))
GGAACTAGGTCAGCTGAAGATCCTGTGAGCGAAGTTCAGCAGTGTACAGCACCTGAGACCAAAATCAGCAGACTGCAGGGTCTAGTTTATCTTCAGAATAAGCCAGGCACAAAGCTGTTGAATTTTCTTCAGGAGCGAAATCTCCCTCCAAAAGTGGTCTCAGACACCCAAAAGTCCACCTGAACACTATGTTCA

APC (c.4099C>T; p.(Gln1367Ter))
AATCCAGCAGACTGCAGGGTTCTAGTTTATCTTCAGAATCAGCCAGGCACAAAGCTGTTGAATTTCTTCAGGAGCGAAATCTCCCTCCAAAAGTGGTCTTAGACACCCAAAAGTCCCACTGAACACTATGTTTCAGGAGACCCCACTCATGTTTAGCAGATGTACTTCTGTCAAGTTCACTGTAGATGTTTGGAGAGTCGTTTCA

APC (c.4132C>T; p.(Q1378Ter))
AGAATCAGCCAGGCACAAAGCTGTTGAATTTCTTCAGGAGCGAAATCTCCCTCCAAAAGTGGTCTCAGACACCCAAAAGTCCACCTGAACACTATGTTTAGGAGACCCCACTCATGTTTAGCAGATGTACTTCTGCAGTTCAGTTGATAGTTTTGAGAGTCGTTTCGATTGCCAGCTCCGTTCAAGTGAACCATGCA

APC (c.4135G>T; p.(Glu1379Ter))
ATCAGCCAGGCACAAAGCTGTTGAATTTCTTCAGGAGCGAAATCTCCCTCCAAAAGTGGTCTCAGACACCCAAAAGTCCCACTGAACACTATGTTTCAGTAGACCCCACTCATGTTTAGCAGATGTACTTCTGCAGTTCAGTTGATAGTTTTGAGAGTCGTTTCGATTGCCAGCTCCGTTTCAGAGTGAACCATGCAGTG

BRAF (c.1799T>A; p.(Val600Glu))
GGAAAAATGAGATCTACTGTTTCTTACTACTACACCTCAGATATATTTCTTCATGAAGACCTCAGACAAAAATAGGTGATTTTGGTCTAGCTACAGAGAAATCTCGATGGAGTGGTCCCATCAGTTTGACAGTTGTCTGATCCATTTTGTGATGGTAAGAATTGAGGCTATTTTCCACTGATTAATTTTT

FBXW7 (c.1393C>T; p.(Arg465Cys))
CAACATCATCTTAGTGGATCTACAGATCGGACACTCAAAGTGTGGAATGCAGAGACTGGAGAATGTATACACACCTATATGGGCATACTCCACTGTGTGTTGTATGCATCTTCATGAAAAAGGTAAGGGAAAATCTGTATGGTTGGGACTTCTTCTCTATTATTGGTGAATTTGGGCCCTTCTGTGTAGAGT

FBXW7 (c.1273C>T; p.(Arg425Cys))
TGCAGAGTTGTTAGCGGTTCTCAGAGATGCCACTCTTAGGGTTTGGGATATTGAGACAGGCCAGTGTTTACATGTTTTGATGGGTGATGTTGCAGCAGTCTGCTGTTTCAATATGATGGCAGGAGGTTGTTAGTGGAGCATATGATTTTATGGTAAAGGTGTGGGATCCAGAGACTGAAACCTGTCTACACACGTTGCA

GNAS (c.602G>A; (p.Arg201His))
CTACTCCAGACCTTTGCTTTAGATTGGCAATTACTGTTTCGGTTGGCTTTGGTGAGATCATTGACCTCAATTTTGTTCAGGACGCTGTTCTGCTGCCATGTCTTGAACTTTTGAGACCAAGTTCAGGTGGACAAAGTCAACTCCAGTAAGCCAACTGTTACTTTTTATATAACAGAGATCATGGT

KRAS (c.35G>A; p.(Gly12Asp))
GTGTGACATGTTCTAATATAGTCACATTTTCATTATTTTATTATAAGGCCTGCTGAAAAAGTGAATATAAACTGTGGTAGTTGGAGCTGATGGCGTAGGCAAGAGTGCCTTGACGATACAGCTAATTCAGAATCATTTTGTGGACGAATATGATCCAACAATAGAGGTAATCTTGTTTAAATATGC

KRAS (c.35G>T; p.(Gly12Val))
GTGTGACATGTTCTAATATAGTCACATTTTCATTATTTTATTATAAGGCCTGCTGAAAAAGTGAATATAAACTGTGGTAGTTGGAGCTGTGGCGTAGGCAAGAGTGCCTTGACGATACAGCTAATTCAGAATCATTTTGTGGACGAATATGATCCAACAATAGAGGTAATCTTGTTTAAATATGC

KRAS (c.38G>A; p.(Gly13Asp))
GTGTGACATGTTCTAATATAGTCACATTTTCATTATTTTATTATAAGGCCTGCTGAAAAAGTGAATATAAACTGTGGTAGTTGGAGCTGTGGCGTAGGCAAGAGTGCCTTGACGATACAGCTAATTCAGAATCATTTTGTGGACGAATATGATCCAACAATAGAGGTAATCTTGTTTAAATATGC

KRAS (c.34G>T; p.(Gly12Cys))
GTGTGACATGTTCTAATATAGTCACATTTTCATTATTTTATTATAAGGCCTGCTGAAAAAGTGAATATAAACTGTGGTAGTTGGAGCTGTGGCGTAGGCAAGAGTGCCTTGACGATACAGCTAATTCAGAATCATTTTGTGGACGAATATGATCCAACAATAGAGGTAATCTTGTTTAAATATGC

KRAS (c.180_181delinsAA; p.(Gln61Lys))
GTAATAATCCAGACTGTGTTTCTCCCTCTCAGGATCTACAGGAAGCAAGTAGTAATTGATGGAGAAACCTGTCTCTGGATATTCTCGACACAGCAGG**AA**AGAGAGGTACAGTGCAATGAGGGACCAAGTACATGAGGACTGGGAGGGCTTCTTTGTGATTTGCCATAAAATACTAAATCATTTGAAGATAT

KRAS (c.351A>T; p.(Lys117Asn))
GTTACTAATGACTGTGCTATAACTTTTTTCTTTCCAGAGACAATAAATAAGAGTTAAGGACTCTGAAGATGTACTATGGTCTAGTAGGAAATAATTGTGATTTGCTCTAGAACAGTAGACACAAAACAGGCTCAGGACTTAGCAAGAAGTTAGGAATTCCTTTTATTGAAACATCAGCAAAGACAAAGACAG

KRAS c.35G>C (p.(Gly12Ala))
GTGTGACATGTTCTAATATAGTCACATTTTCATTATTTTATTATAAGGCCTGCTGAAAAAGTGAATATAAACTGTGGTAGTTGGAGCTGTGGCGTAGGCAAGAGTGCCTTGACGATACAGCTAATTCAGAATCATTTTGTGGACGAATATGATCCAACAATAGAGGTAATCTTGTTTAAATATGC

MET (c.3029C>T (p.Thr1010Ile))
TCTCTGTTTTAAGATCTGGGCGAGTGAATTAGTCGCTACGATGCAAGAGTACACACTCTCATTTGGATAGGCTTGTAAAGTGCCGAAAGTTAAGCCCAATTACAGAAATGGTTTCAAATGAATCTGTAGACTACCGAGCTACTTTCTCAGAAGGTATATTTCAAGTTATTGTTCTGAGAAATACCTATACATATACCTC

PIK3CA (c.263G>A; (p.Arg88Gln))
AATACCCCTCCATCAACTTCTTCAAGATGAATCTTCTACATTTTCGTAAGTGTACTCAAGAAGCAGAAAGGGAAGAATTTTGTATGAAACAAGACAACCTTTGTGACCTTCGGCTTTTTCAACCTTTTTTAAAGTAATTGAACCAAGTAGGCAACCGTGAAAGATCCTCAATCGAGAAATTGGTATGATACAATATCCTATTCTAAATGCAAAATACCAATAAGCTTAAGCTTGTGCCCTTTCTAAAATATTTCTG

PIK3CA (c.3019G>C; (p.G1007R))
GTTCTTATTACTTATAGGTTTCAGGAGATGTGTACAAGCTTATCTAGCTATTTCGACAGCATGCCAATCTCTCATAAATCTTTTCTCAATAGTCTGCTGCTGGAATGCCAGAACTACAATCTTTGATGACATTGCATACATTGAAAGACCTAGCCTTAGATAAAAAGTGAAGAGGCTTTGGAGTATTTCA

PIK3CA (c.325_327delGAA; p.(Glu109del))
AGAAGCAGAAAGGGAAGAATTTTTGATGAAACAAGACGACTTTGTGACCTTCGGCTTTTTCAACCTTTTTAAAGTAATTGAACCAAGTAGGCAACCGTGAAAGATCCTCAATCGAGAAATTGGTATGATACAATATCCTATTCTAAATGCAAAATACCAATAAGCTTAAGCTTGTGCCCTTTCTAAAATATTTCTG

PTEN (c.1003C>T (p.Arg335Ter))
TAGCATTTGCAGTATAGAGCGTGCAGATAATGACAAGGAATATCTAGTACTTACTTTAACAAAAATGATCTTGACAAAGCAATAAAGACAAAGCCAAGTACTACTTTTCTCAAATTTTAAAGTCAGTTAAATTAACATTTTGTGGGGTGTGTGACTGTATGTATGTATGTGTGTGTTTAACTTAGGAGTACAG

PTEN (c.650T>A; (p.Val217Asp))

TATTAATCATTAATAAATCGTTTTTGACAGTTTGACAGTTAAAGGCATTTCTGTGAAATAATACTGGTATGTATTTAAACCATGCAGATCCTCAGTTTGTGGACTGCCAGCTAAAGGTGAAGATATATCTCCAATTCAGGACCCACACGACGGGAAGACAAGTTTCATGTACTTTGAGTTCCTCAGCCGTTACCTGTGTG

SMAD4 (c.403C>T; p.(Arg135Ter))

GGCCTGATCTTCACAAAAATGAACATAAACATGTTAAATATTGTCAGTATGCGTTTGACTTAAATGTGATAGTGTCTGTGTGAATCCATACCTACGAATGAGTTGATACCTGGAATTTGTAAGTAGACTTTGCTTTCACTCTAAGAAACATAAAGGGAAAAGGATCTCAATAGTGTTCATTTTGTAAAGTTAA

SMAD4 (c.1082G>A; p.Arg361His)

ACTTTGAAATGGATGTTTCAGTAGGAGAGACATTAAGGTTCTTCAAGCTGCCATTGTTACTGTTGATGGATACGTGGACCCCTCTGGAGGAGATCACTTTTGTGGTCAACTCTCCAATGTCCACAGGACAGAAGCCATTGAGAGAGCAAGGTATTGATTGTATAGTCAGATAGTTACTTTAAAAAATTGAGCA

SMAD4 (c.1572G>T; p.(Trp524Cys))

GTGTTGATGACCTTCGTCGCTTATGCATACTCAGGATGAGTTTTGTGAAAGGCTGGGACCGGATTACCAAGACAGAGCATCAAAGAAACACCTTGTCTGATTGAAATTCACCTACACCGGCCCTCCAGCTCTAGACGAAGTACTTCATACCATGCCGATTGCAGACCCACAACCTTTAGACTGAGGTCTTTTACCG

TP53 (c.524G>A; p.(Arg175His))

TTTTGCCAACTGGCCAAGACCTGCCCTGTGCAGCTGTGGTTGATTCCACACCCCGCCCGCACCCGCGTCCGCGCATGGCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCACTGCCCCACCATGAGCGCTGCTCAGATAGCGATGGTGAGCAGCTGGGGCTGGAGAGACGACAGGGGCTGTTGCCAGGGTCCCCAGGCCTCTGATTCTCACTGATT

TP53 (c.586C>T; p.Arg196Ter)

GCTGGGGCTGGAGAGACGACAGGGCTGTTGCCAGGGTCCCCAGGCCTCTGATTCTCACTGATTGCTCTTAAAGTCTGCGCCCTCTCAGCATCTTATCTGAGTGAAGGAAATTTGCGTGTGGAGTATTTGATGACAGAAACACTTTTCGACATAGTGTGGTGGTGCCTATGAGCCGCTGAGGTCTGGTTTGCAA

TP53 (c.817C>T; p.(Arg273Cys))

TAAATGGGACAGGTAGGACCTGATTTCTTACTGCCTCTGCTCTTTTCTATCTCTGAGTAGTGGTAATCTACTGGGACGGAAACAGCTTTGAGGTGTGTTTGTGCTGTCTCTGGGAGAGACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACACGAGCTGCCCCAGGGAGCACTAAGCG

TP53 (c.818G>A; p.(Arg273His))

TAAATGGGACAGGTAGGACCTGATTTCTTACTGCCTCTTGCTTCTTTTCTATCTCTGAGTAGTGGTAATCTACTGGGACGGAAACAGCTTTGAGGTGCATGTTTGTGCTGTCTCTGGGAGAGACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACACGAGCTGCCCCAGGGAGCACTAAGCG

TP53 (c.844C>T; p.(Arg282Trp))

CCTACTGCCTCTTGCTTCTTTTCTATCTCTGAGTAGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTGCTGCTCTGGGAGAGACTGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACACGAGCTGCCCCAGGGAGCACTAAGCGAGGTAAAGCAAGCAGGACAAGAACGCGT

TP53 (c.422G>A; p.(Cys141Tyr))

TATCTGTTCACTTGTGCCCTGACTTTCAACTCTGTCTCTTCTCTTCTACAGTACTCCCTGCCCTCAACAAGATTTTTGCCAACTGGCCAAGACTACCTGTGCAGCTGTGGGTTGATTCCACACCCCGCCGGCACCCGCGTCCGCGCATGGCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAG

TP53 (c.701A>G; p.Tyr234Cys))

AAGGCTCTCCCTGCTTGCCACAGGTCTCCCCAAGGCGCACTGGCCTCATCTTGGGCTGTGTTATCTCTAGGTTGGCTGACTGTACCACCATCCACTGCAACTACATGTGTAACAGTTTCTGCATGGGCGGCATGAACCGGAGGCCATCTCACCATCATCACTGGAAGACTCCAGGTGAGGCCACTTGCCA

TP53 (c.711G>A; p.Met237Ile))

CTGCTTGCCACAGGTCTCCCCAAGGCGCACTGGCCTCATCTTGGGCTGTGTTATCTCTAGGTTGGCTGACTGTACCACCATCCACTACAACATATGTAACAGTTTCTGCATGGGCGGCATGAACCGGAGGCCATCTCACCATCATCACTGGAAGACTCCAGGTGAGGCCACTTGCCACCTGCACAC

TP53 (c.857A>T; p.Glu286Val))

GCTTCTCTTTTCTATCTCTGAGTAGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTGCTGCTCTGGGAGAGACCGGCGCACAGAGGTAGAGAATCTCCGCAAGAAAGGGGAGCCTCACACGAGCTGCCCCAGGGAGCACTAAGCGAGGTAAGCAAGCAGGACAAGACGGTGGAGGAGACCAA

TP53 c.560-1G>A splice variant

CGCTGCTCAGATAGCGATGGTGAGCAGCTGGGGCTGGAGAGACGACAGGGCTGTTGCCAGGGTCCCCAGGCCTCTGATTCTCACTGATTGCTCTTAAGTCTGGCCCTCTCAGCATCTTATCCGAGTGAAGGAAATTTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTGGTGGTCCCC