Comparison data for SNP PolTaq DNA polymerase

Mutation detection test: BRAF c.1799**T>A** (V600E), rs113488022, homo sapiens

target sequence: 5'...ATAGGTGATTTTGGTCTAGCTACAG**T/A**GAAATCTCGATG...
forward primer: 5'-GGTGATTTTGGTCTAGCTACAGA-3'

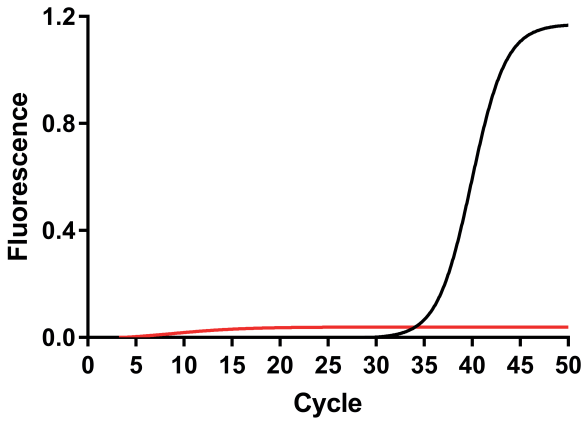
reverse primer: 5'-ACCATCCACAAAATGGATCCA-3'
taqman-probe: 5'-ROX-TCGATGGAGTGGGTCCCATCAGTTTG-BMNQ590-3'

PCR protocol:
95°C - 2 min (initial denaturation)
95°C - 10 sec
59°C - 10 sec
72°C - 30 sec (50 cycles)

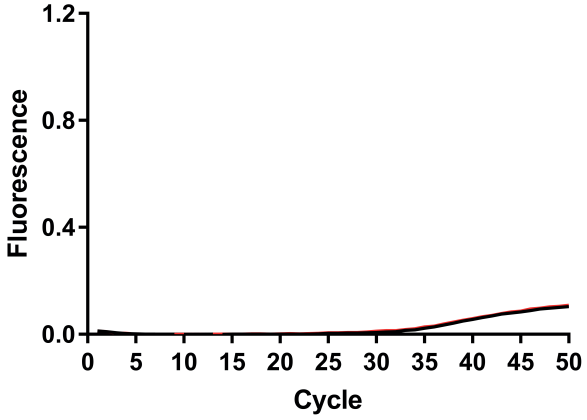
Reaction buffers and final DNA polymerase concentrations were applied according to manufacturer recommendations.

black curve - positive mutation
red curve - wildtype (mismatching primer at 3'-end)

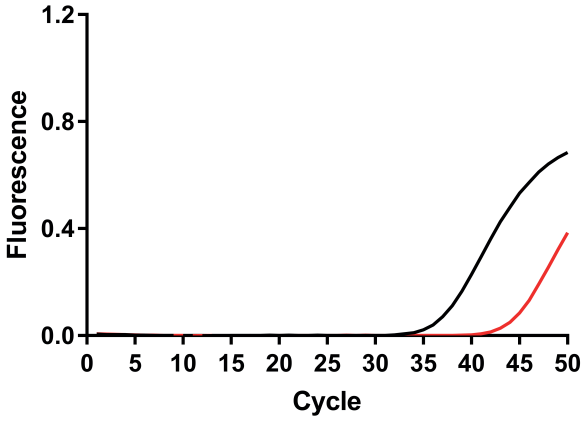
SNP PolTaq DNA polymerase M3025



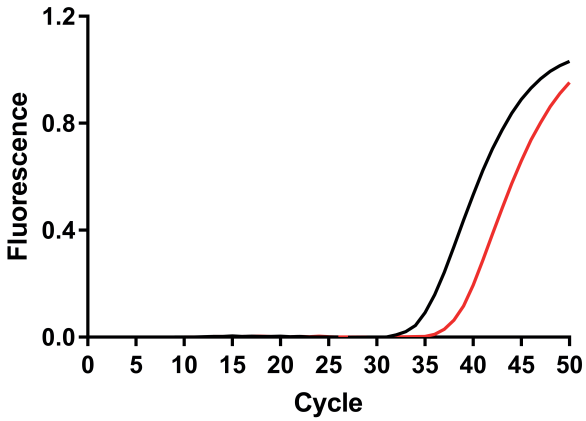
Taq DNA Polymerase (NEB, #M0267)



Taq DNA Polymerase
Hot Start Version (TaKaRa, #R007)



GoTaq® hot start
DNA Polymerase (Promega, #M5001)



SNP PolTaq DNA polymerase is a highly selective DNA polymerase variant, specially evolved for all assays in which high single nucleotide discrimination is required.
HiDi efficiently discriminates primers, which have a mismatch at the 3'-end. Competitor products yield lower fluorescence signals and result in poor discrimination between absence and presence of mutation.