Benchmarking data for HiDi Taq DNA polymerase (#9201)

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

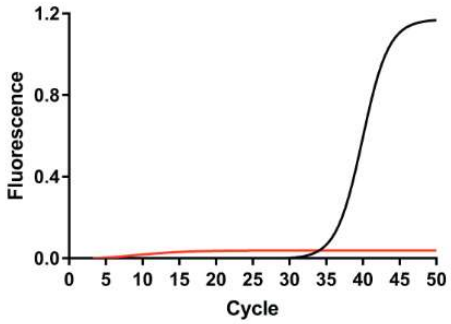
target sequence:	5'...ATAGGTGATTTTGGTCTAGCTACAG**T/A**GAAATCTCGATG...
forward primer:	5'-GGTGATTTTGGTCTAGCTACAGA-3'
reverse primer:	5'-ACCATCCACAAAATGGATCCA-3'
taqman-probe:	5'-ROX-TCGATGGAGTGGGTCCCATCAGTTTG-BMNQ590-3'

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

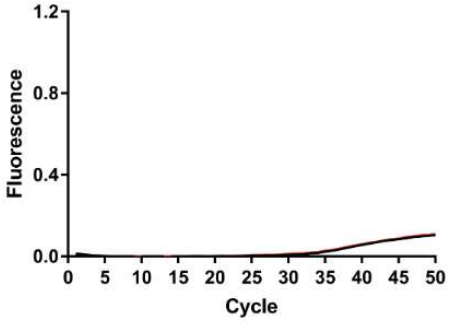
Reaction buffers and final DNA polymerase concentrations were applied according to manufacturer recommendations.

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

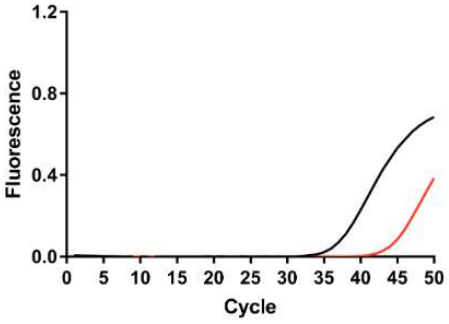
HiDi Taq DNA polymerase (myPOLS Biotec, #9201)



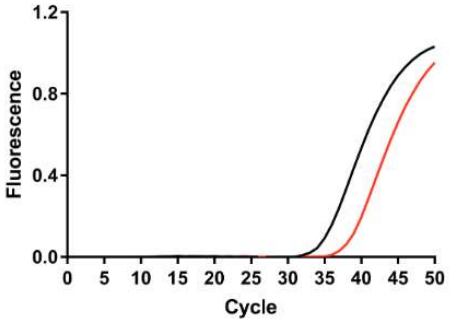
Taq DNA Polymerase (NEB, #M0267)



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



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



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