

## Benchmarking data for HiDi Taq DNA polymerase (#9201)

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

target sequence: 5' . . . ATAGGTGATTTTGGTCTAGCTACAGT / AGAAATCTCGATG . . .  
 forward primer: 5' -GGTGATTTTGGTCTAGCTACAGA-3'  
 reverse primer: 5' -ACCATCCACAAAATGGATCCA-3'  
 taqman-probe: 5' -ROX-TCGATGGAGTGGGTCCCATCAGTTTG-BMNQ590-3'

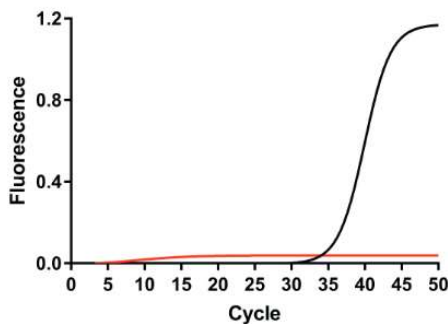
PCR protocol:

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

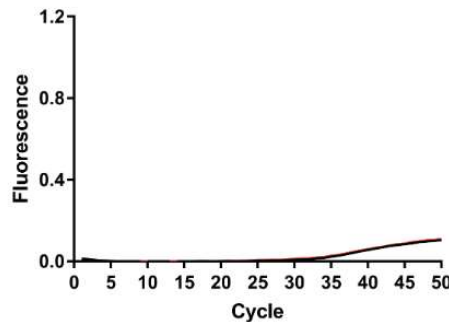
Reaction buffers and final DNA polymerase concentrations were applied according to manufacturer recommendations.

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

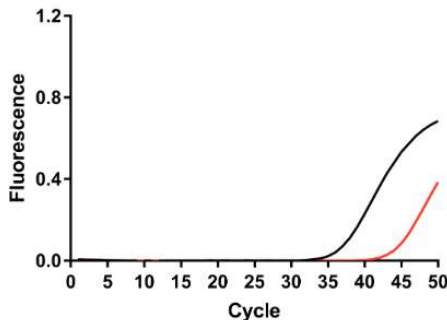
HiDi Taq DNA polymerase  
(myPOLS Biotec, #9201)



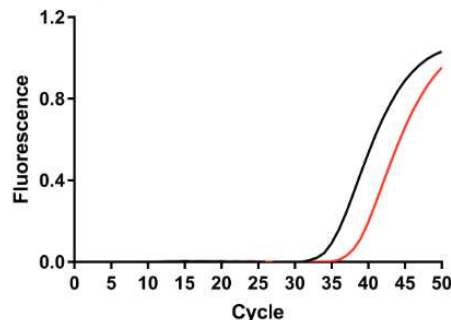
Taq DNA Polymerase (NEB, #M0267)



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 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.