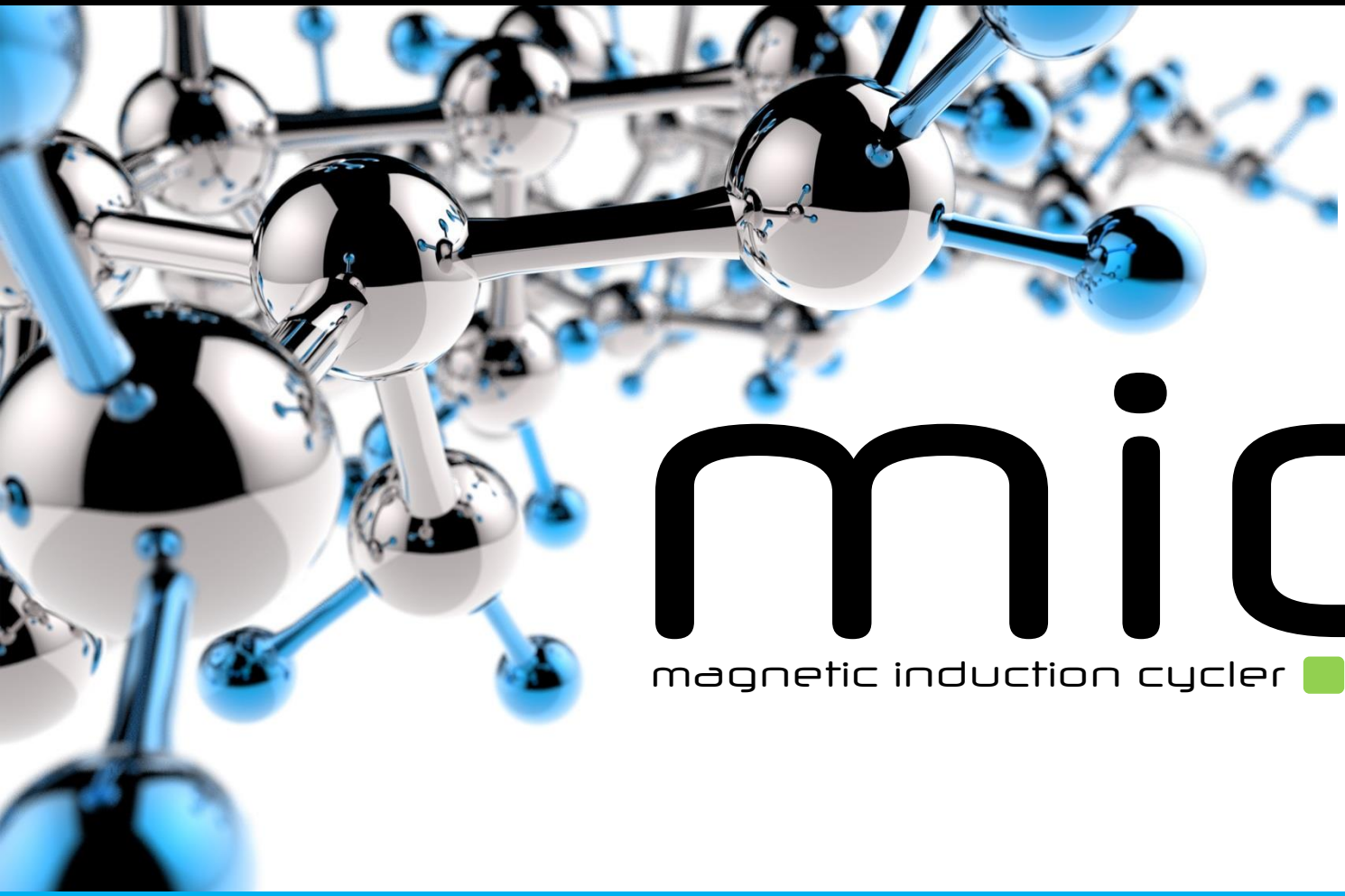


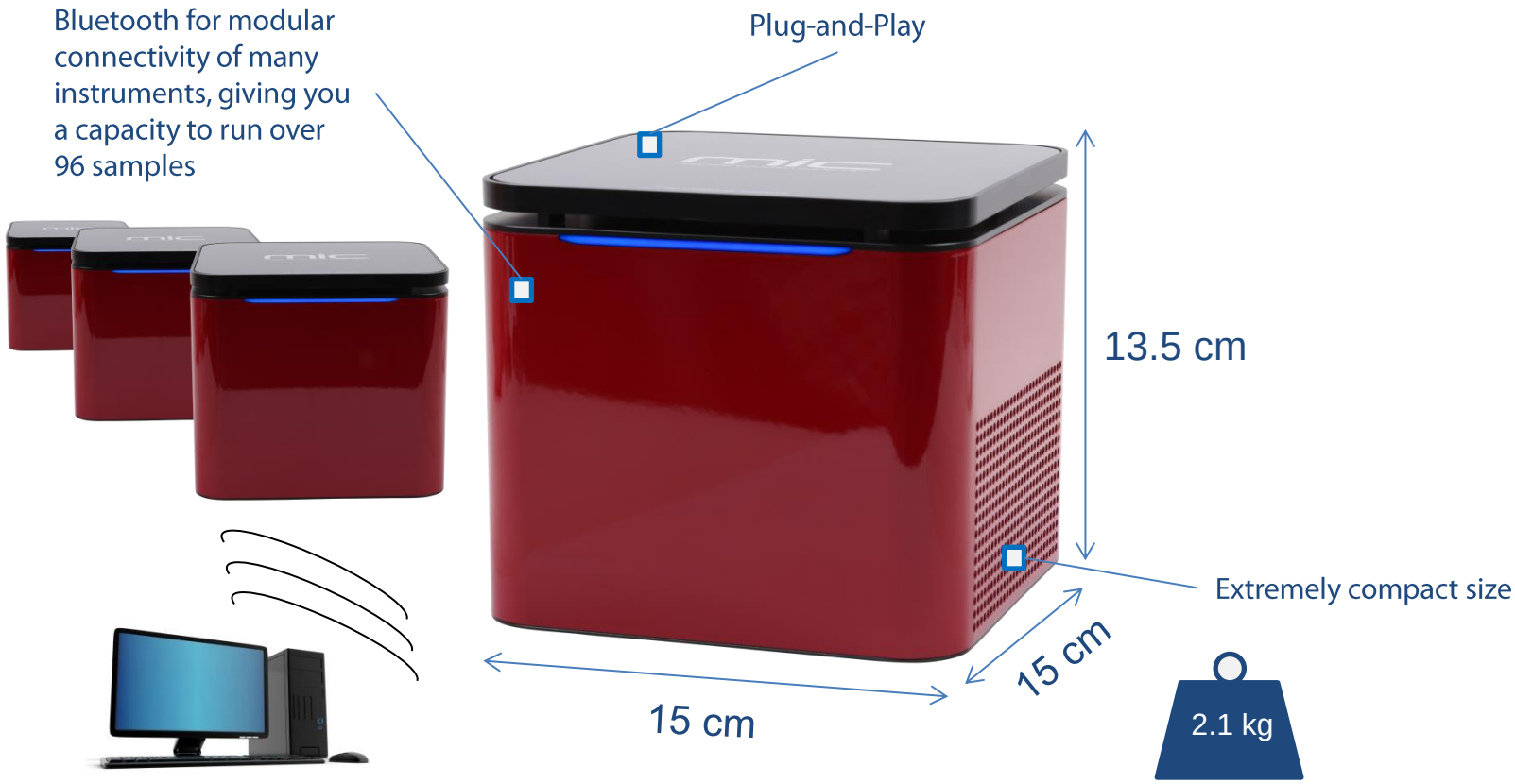
mic

magnetic induction cycler

All information within this presentation is preliminary and is subject to change.

bms
bio molecular systems

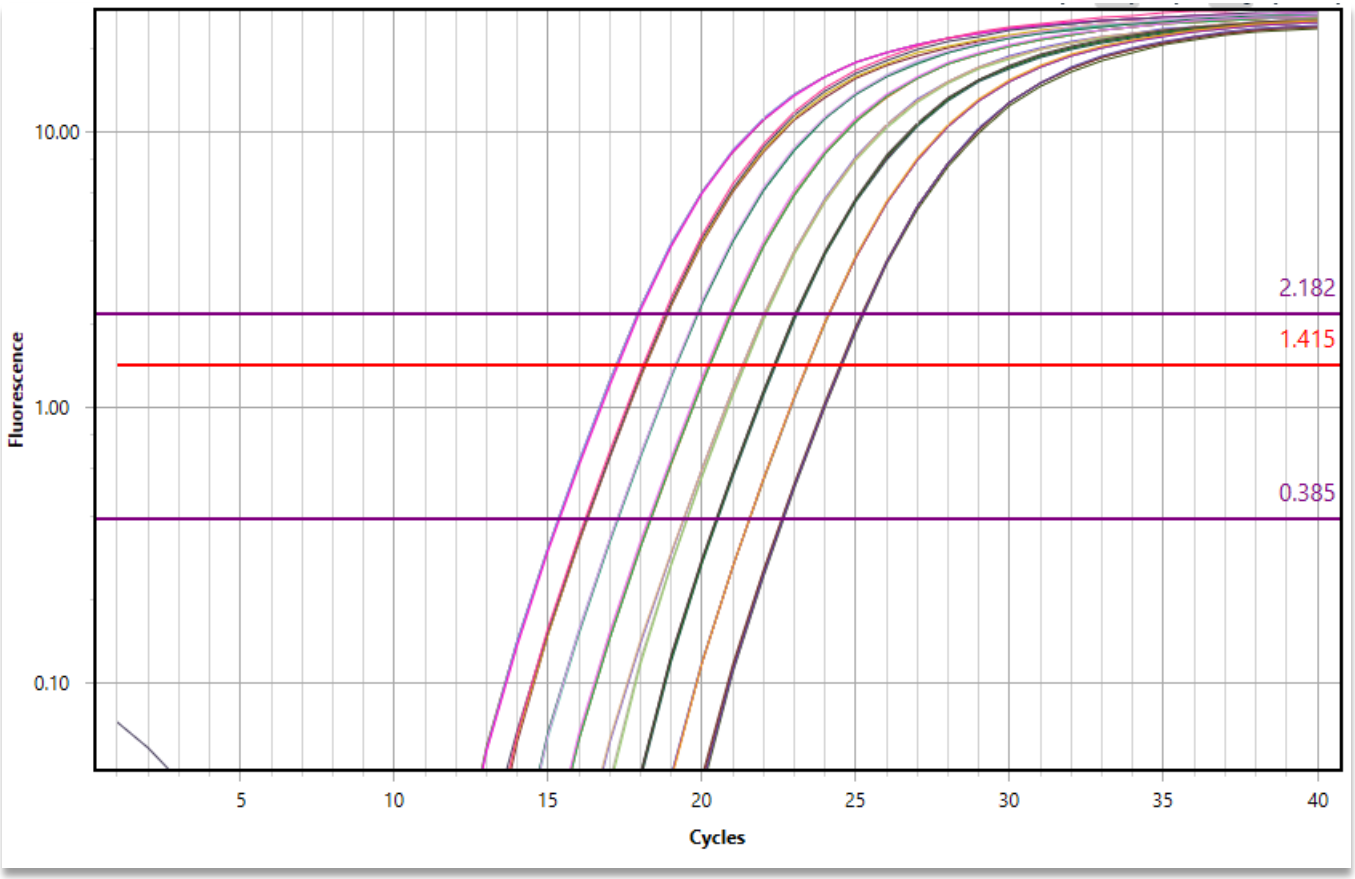
Compact , light , fast, and precise



- 2 or 4 channel
- HRM option

High level of quantitative precision

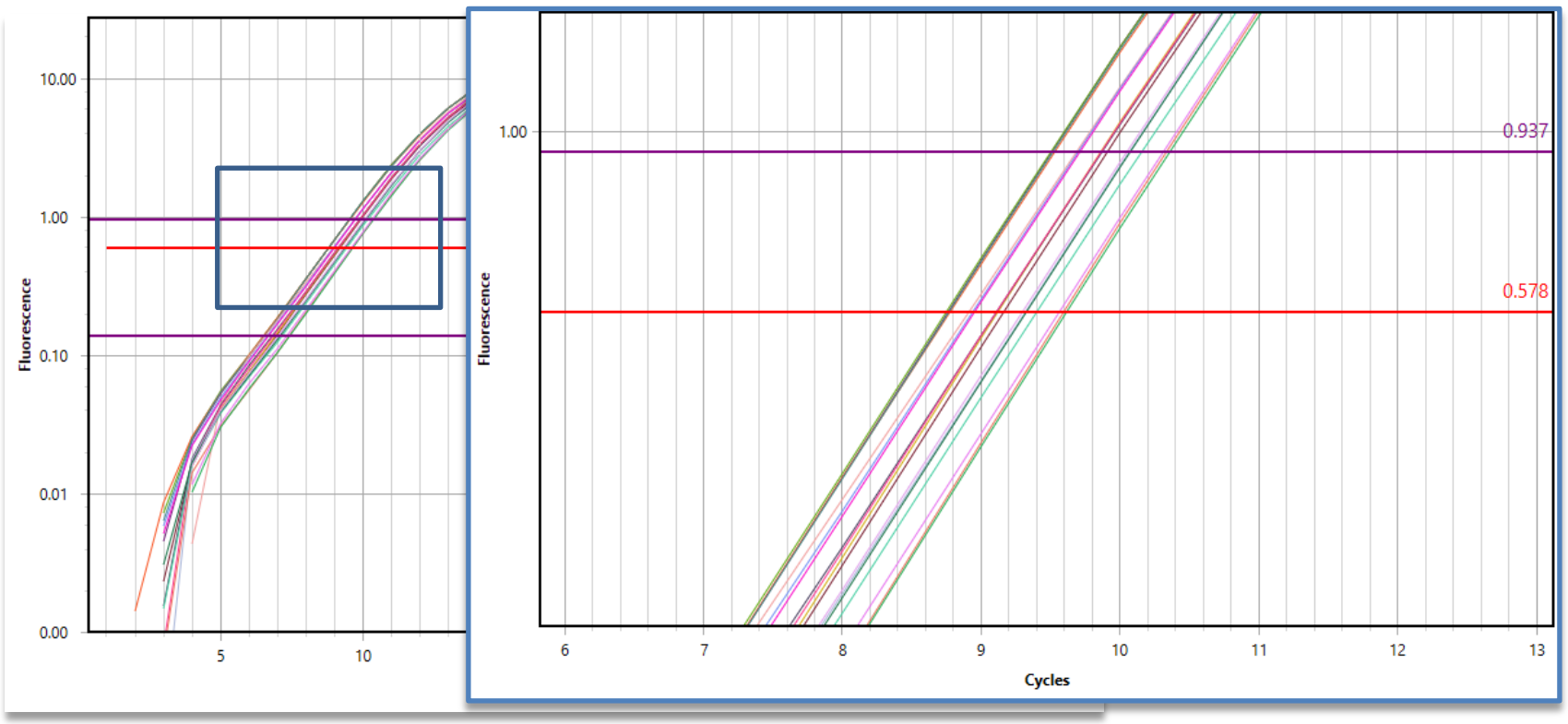
Confidently detect 2 fold differences in gene expression levels



- Manganese superoxide dismutase (MnSOD) gene
- Eight point, 1:2 dilution of human genomic DNA (*n* = 4 each)
- Efficiency = 97%
- $r^2 = 0.999$

Extreme level of quantitative precision

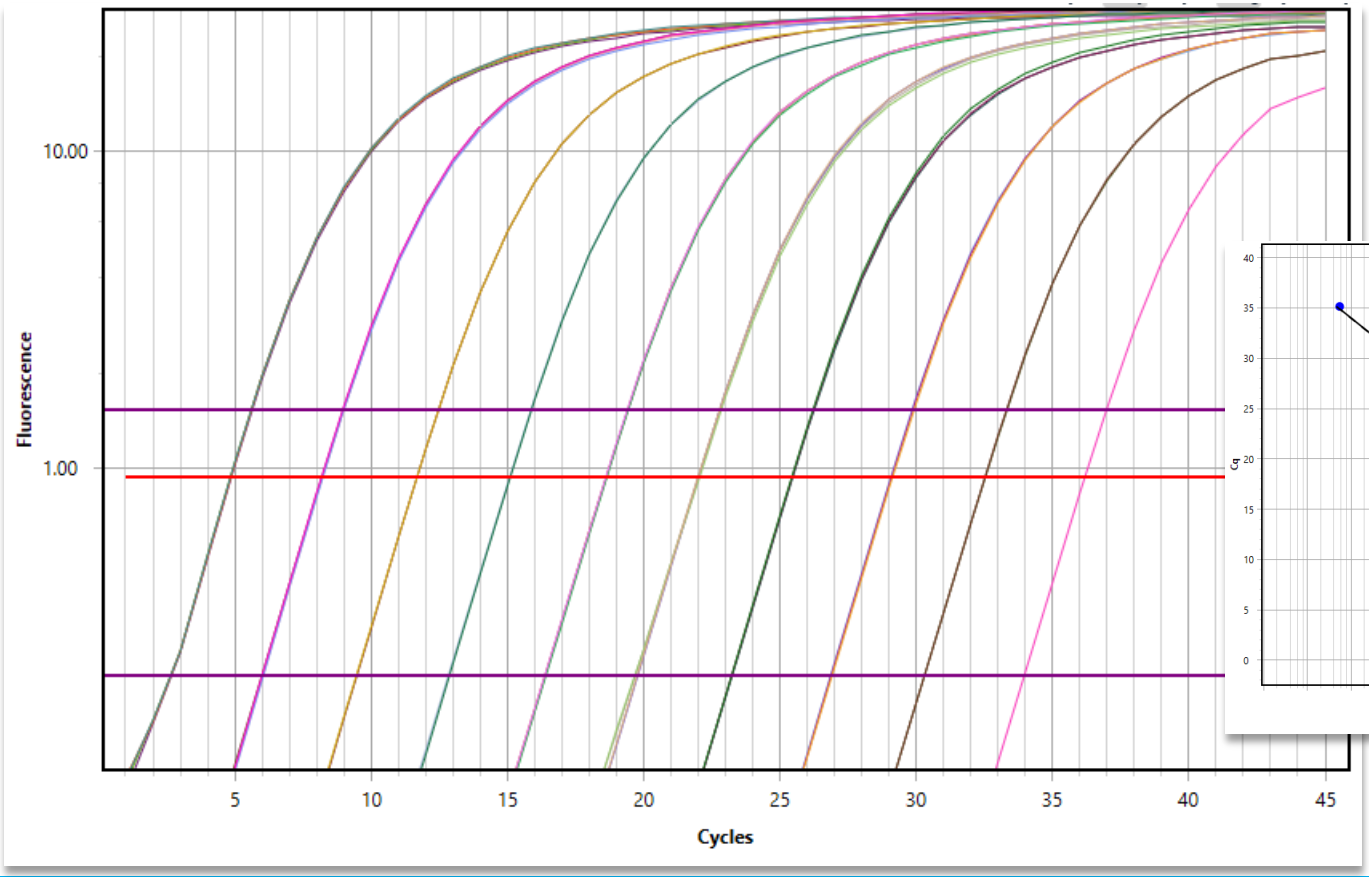
Detect differences within one cycle

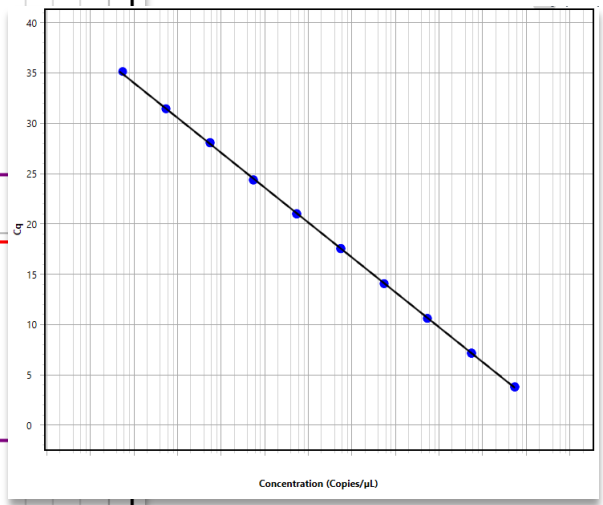


- HBM plasmid cDNA
- Five point, 0.2x dilution of human genomic DNA ($n = 4$ each)
- Efficiency = 95%
- $r^2 = 0.999$
- 5 pg difference between standards.

A wide linear dynamic range,

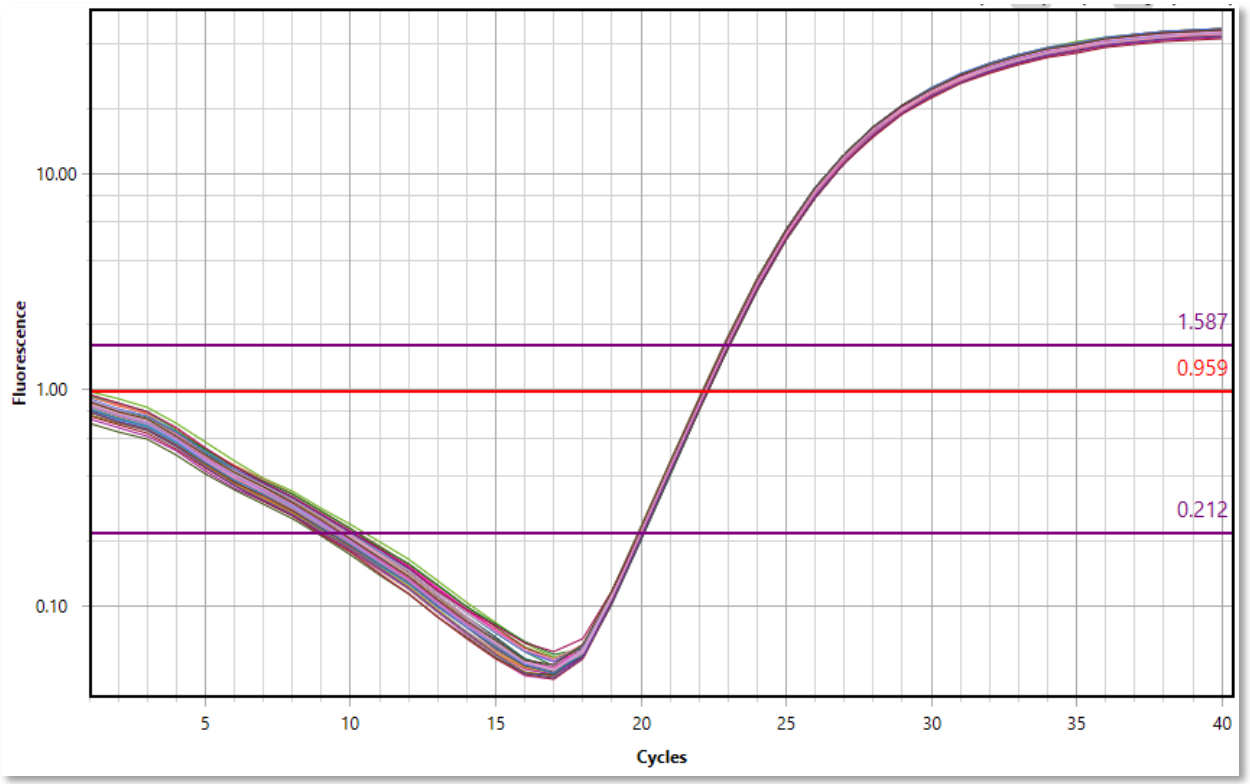
Down to 1 copy of DNA





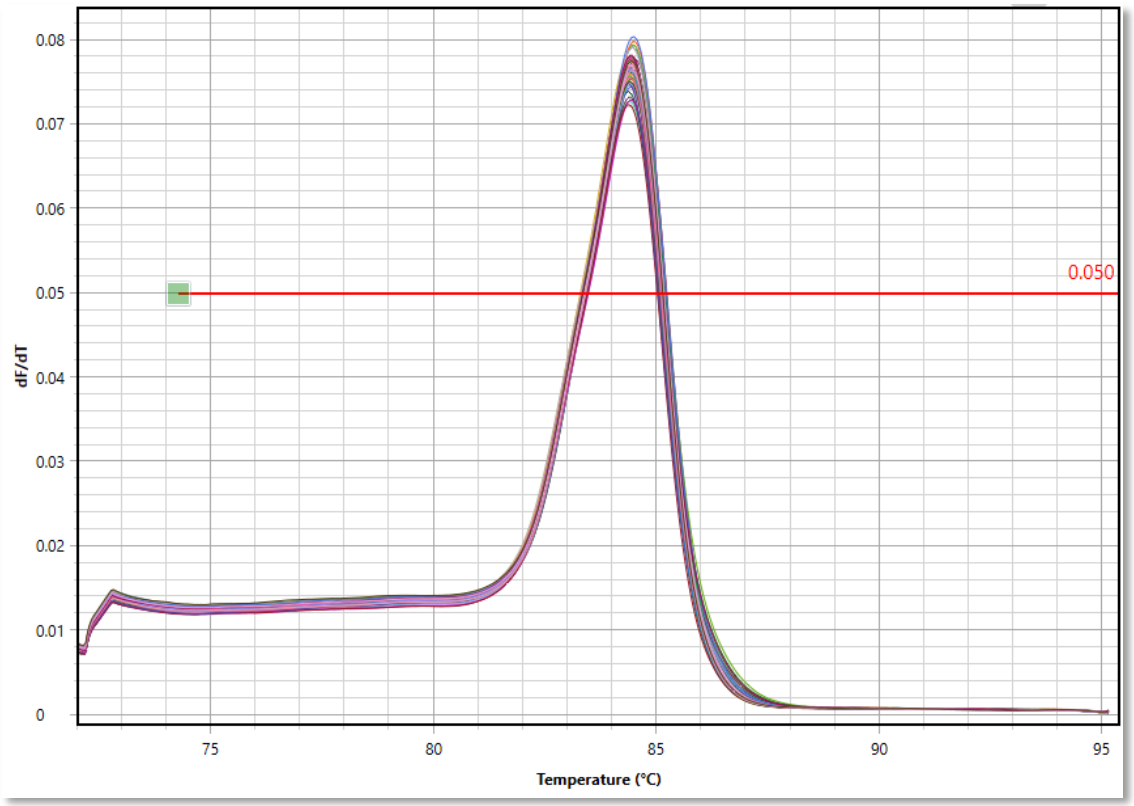
- Hepatitis B virus (HBV) plasmid cDNA template
- 10 point, 1:10 dilution starting amount of $3x10^9$ copies ($n = 3$ each).
- Efficiency = 95%
- $r^2 = 0.998$.

Amazing Reproducibility



- Manganese superoxide dismutase (MnSOD) gene ($n = 48$)
- Standard deviation = 0.03
- Efficiency = 98%.

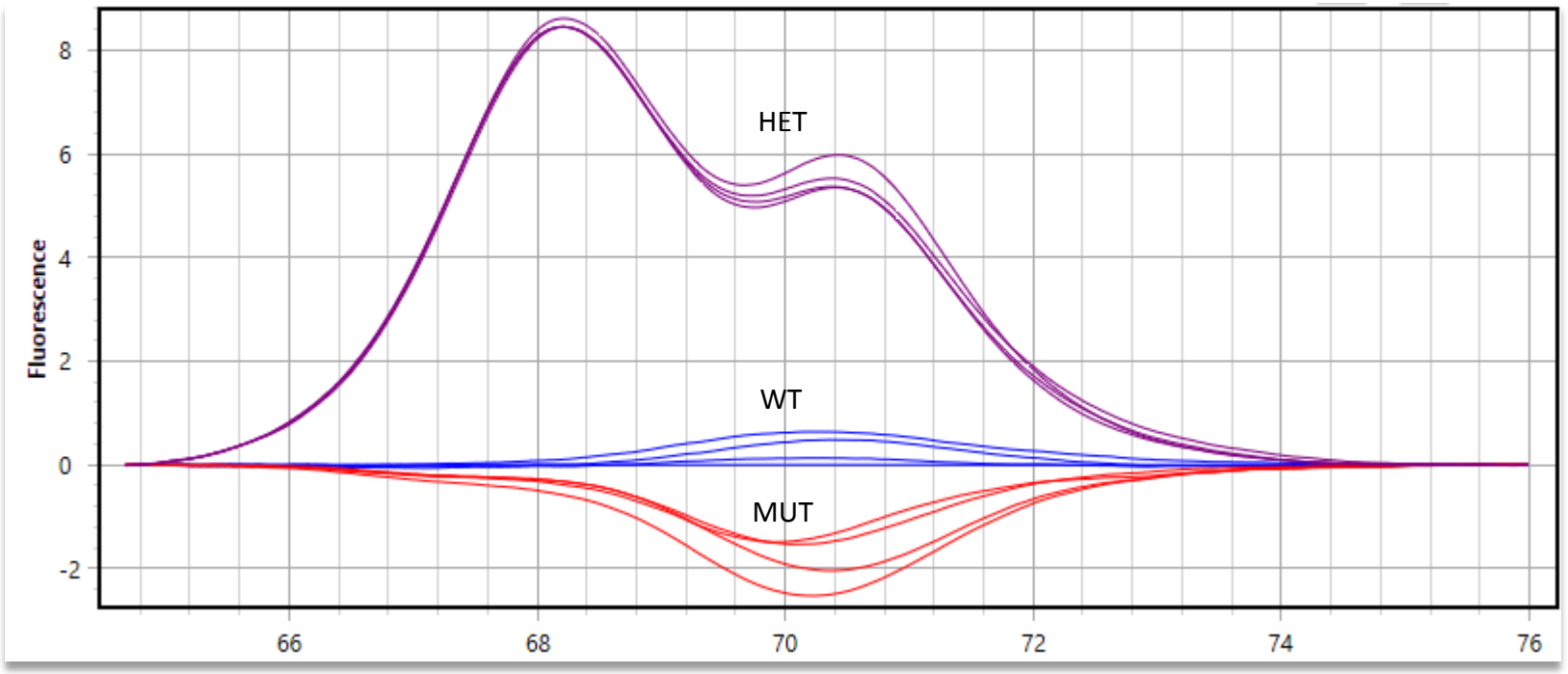
First class temperature uniformity



- Melt cure analysis of the MnSOD gene amplification product ($n = 48$)
- Melt peak range = 84.44 – 84.52°C
- Tm delta of 0.08°C.
- Uniformity measure of < ±0.05°C

High Resolution Melting (optional)

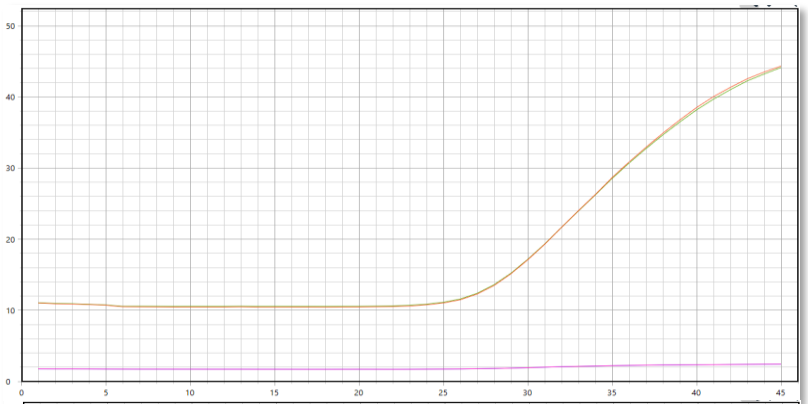
Class IV SNP with HRM (Optional)

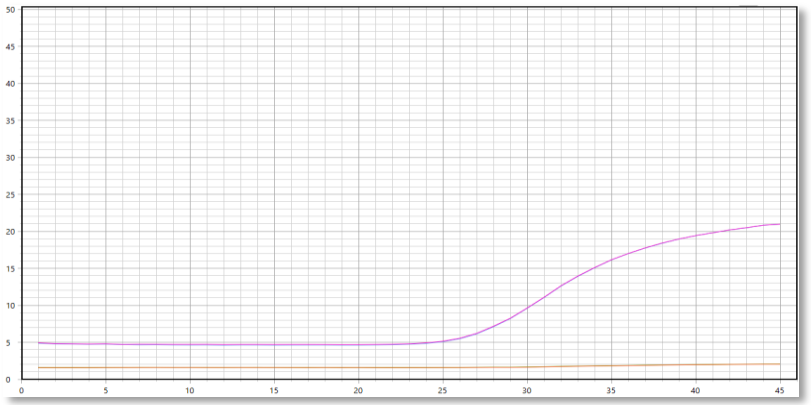


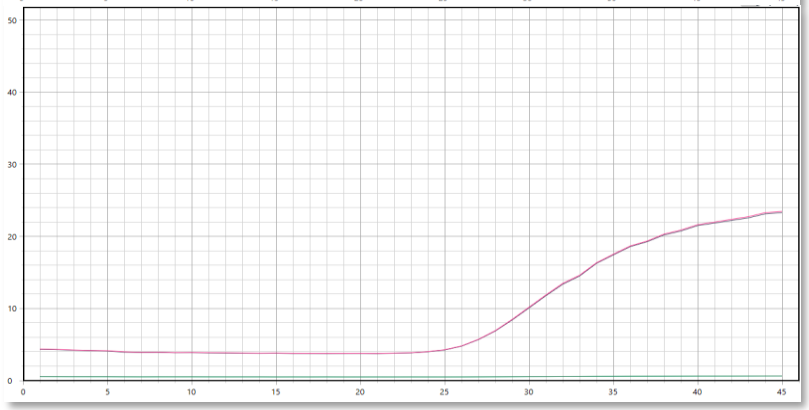
- Class IV SNP (A to T)
- Temperature difference between alleles < 0.1°C

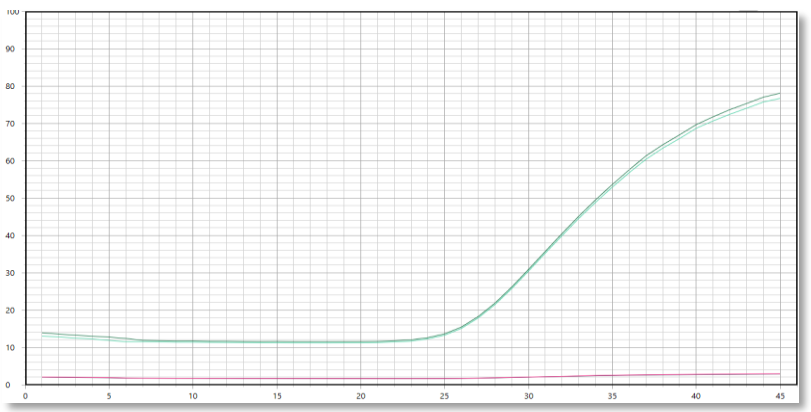
Four colours

Minimal cross talk









- Individual colour high power LEDs
- Individual colour detectors
- Cross talk < 2% across all channels

Analysis Note

Cycling analysis was achieved using the Constant Efficiency baseline normalisation method (Ruijter et al. 2009) combined with LinReg (Ramakers et al. 2003) to determine a window of linearity (purple lines); from which individual reaction efficiencies could be calculated and a cycle threshold (red line) could be set automatically.

Calculated Cq values were plotted against known concentrations to generate standard curves. Efficiency was calculated from the gradient of the curve and the linearity measured as the r-squared value.

- Ruijter JM, Ramakers C, Hoogaars MH, Karlen Y, Bakker O, van den Hoff MJB, and Moorman AFM. (2009) Amplification efficiency: linking baseline and bias in the analysis of quantitative PCR data. Nucleic Acids Research, e45.
- Ramakers C, Ruijter JM, Lakanne Deprez RH, and Moorman AFM. (2003) Assumption-free analysis of quantitative real-time polymerase chain reaction (PCR) data. Neuroscience Letters, 339; 62-66.

Specifications

Specification	Value
Physical	
Dimensions	W: 150mm, L: 150mm, H: 130 mm (265 mm lid open)
Weight	2.1 kg
Electrical	
AC Input	100-240 VAC, 50/60 Hz 4.0 A
Thermal Performance	
Temperature Accuracy	± 0.25°C
Temperature Uniformity	± 0.05°C
Ramp Rates	Heating: 4°C/s Cooling: 3°C/s
Temperature Input Range	40 – 99°C
Optical	
Detectors	Photodiode per channel
Excitation Sources	High energy light emitting diodes for each channel
Channels	Green: Ex 470 Em 510
	Yellow: Ex 530 Em 555
	Orange: Ex 585 Em 610
	Red: Ex 625 Em 660
Acquisition time	1 s
Reaction Vessels	
Samples per Instrument	48
Reaction Volumes	10 - 25 µL
Operating Environment	
Temperature	18 – 30°C
Relative Humidity	20 – 80%