mic

magnetic induction cycler

bio molecular systems

Performance Data

All information within this presentation is subject to change.

Meet Mic

Fast

Accurate

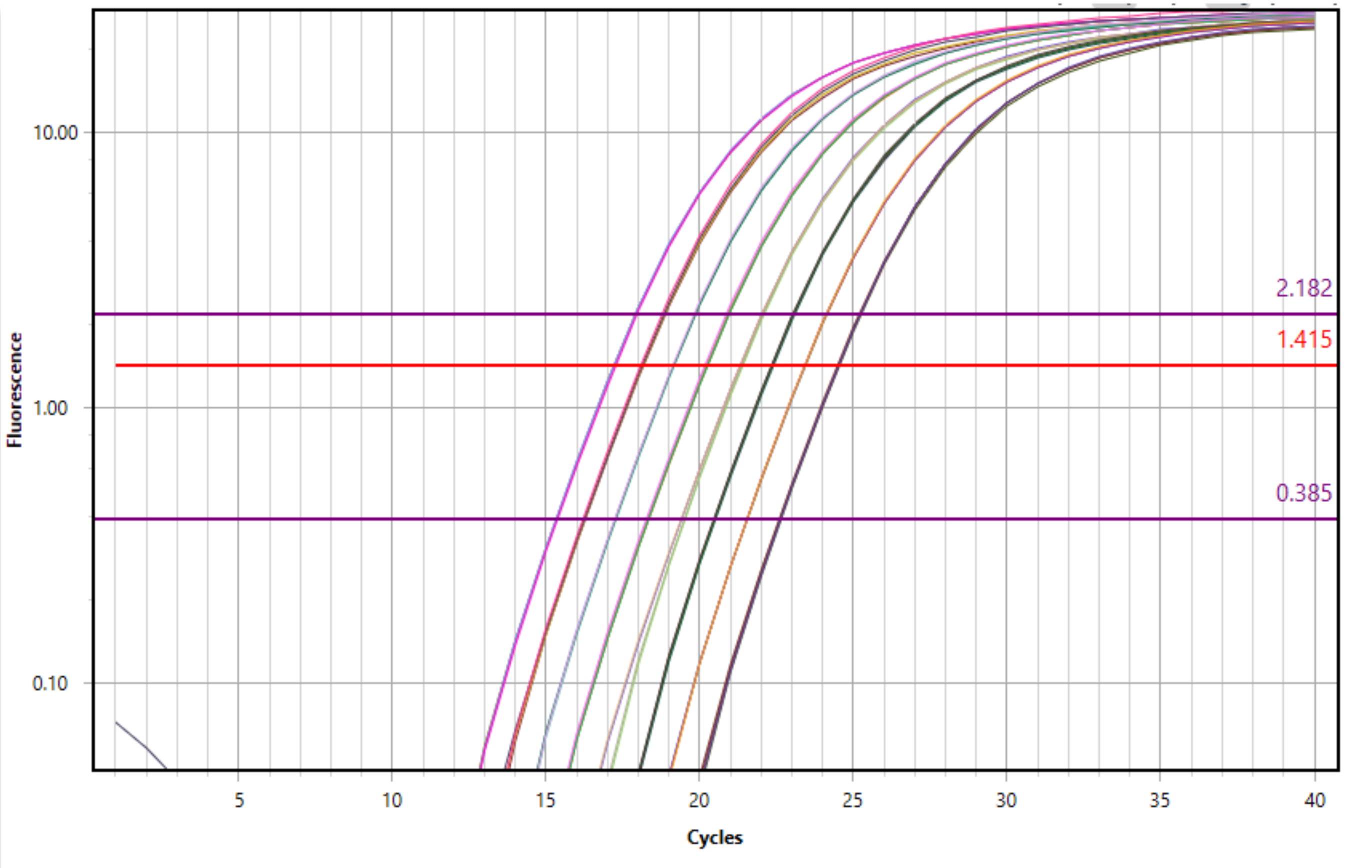
Compact

2-Channel (Green & Yellow) or 4-Channel
HRM option
Bluetooth / USB connectivity

Contact
sales@biomolecularsystems.com
www.mic-qpcr.com

High level of quantitative precision

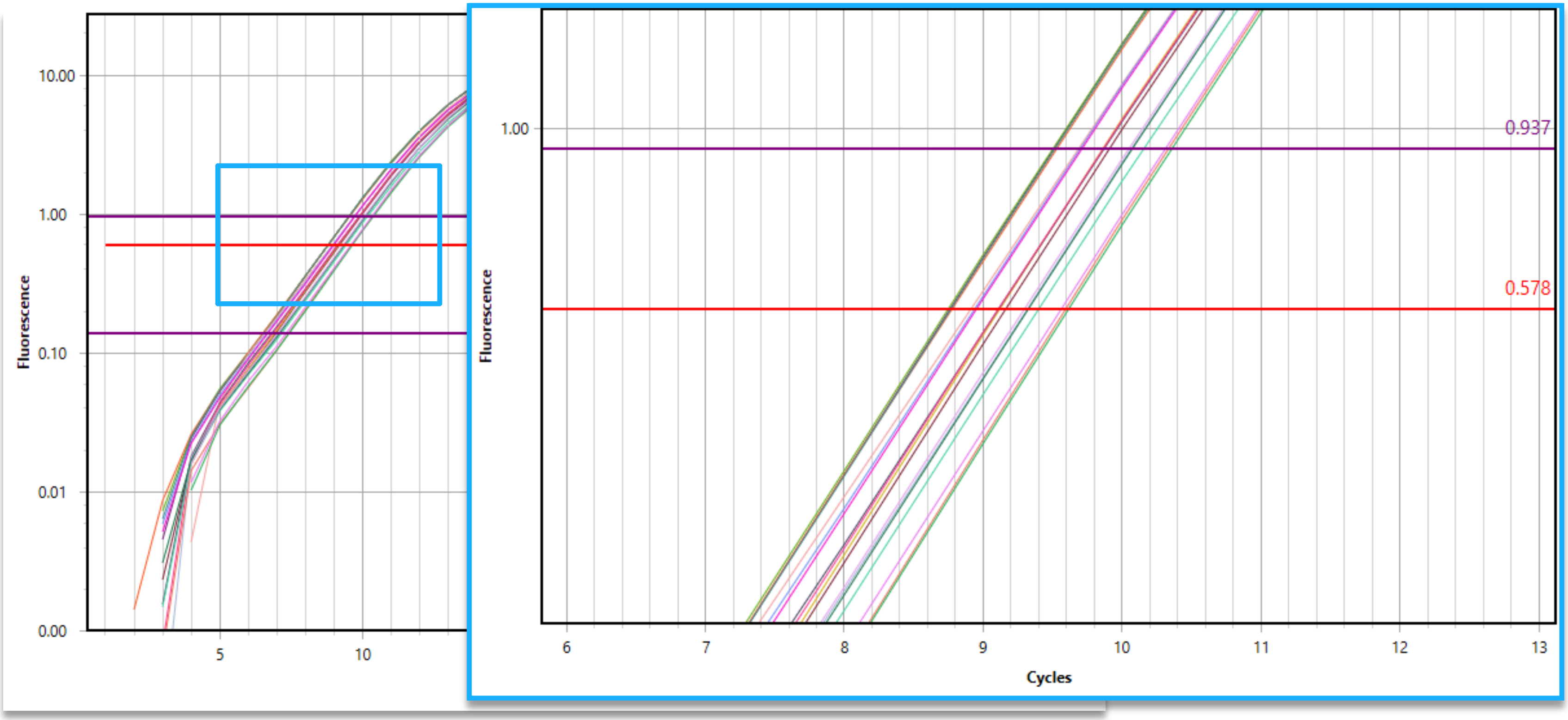
Confidently detect 2 fold differences in gene expression levels



- Manganese superoxide dismutase gene (MnSOD)
- Eight point, 2x dilution series of human genomic DNA (*n* = 4 each)
- Efficiency = 98% (standard curve method)
- $R^2 = 1.00$

Extreme level of quantitative precision

Detect differences within one cycle



- Five point, 0.2x dilution series of HBV plasmid cDNA template (*n* = 4 each)
- 5 pg difference between standards
- Efficiency = 98% (standard curve method)
- $R^2 = 0.99$

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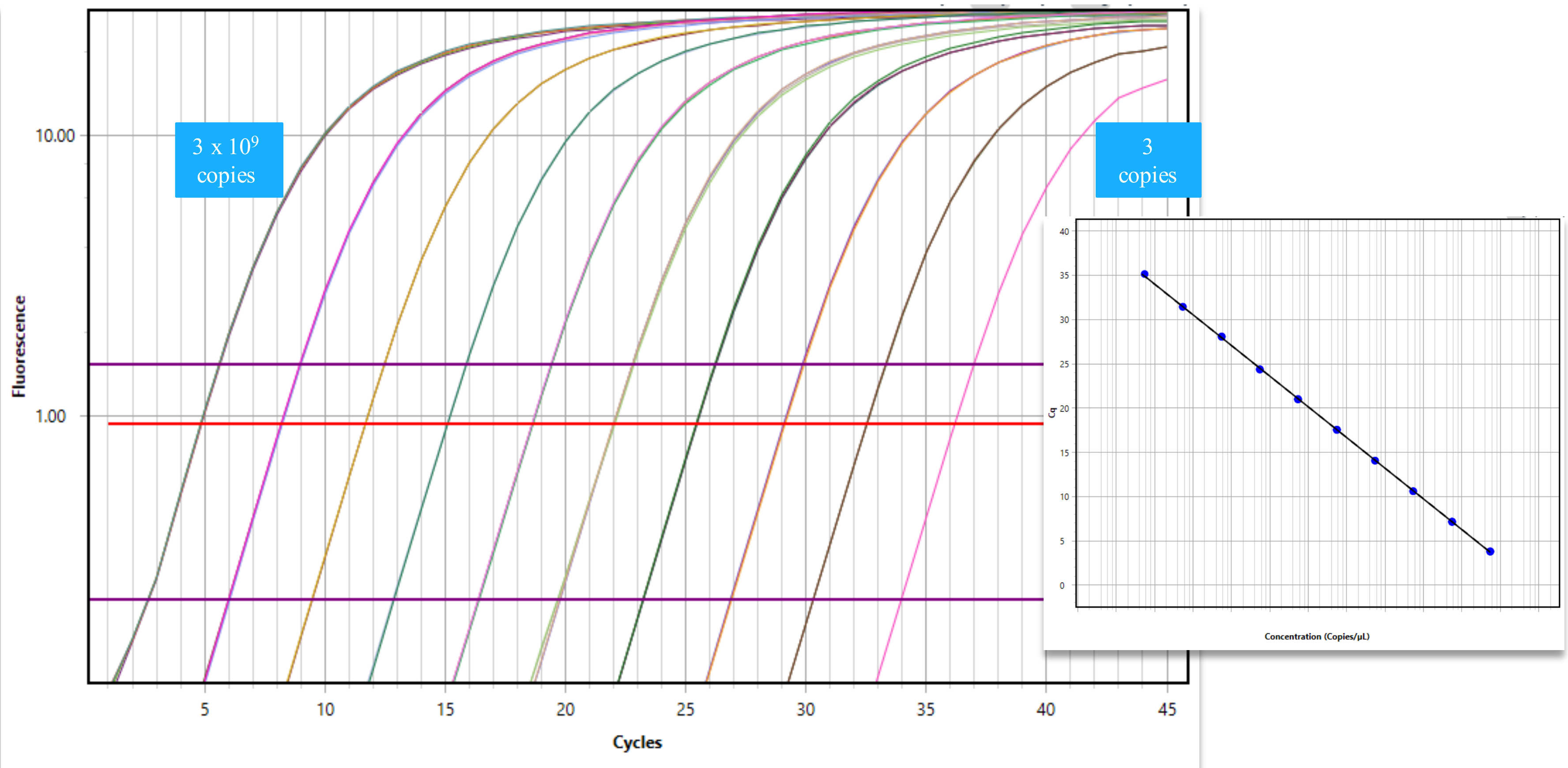
A wide linear dynamic range

Down to single digit copies of DNA



3×10^9 copies

3 copies

- 10 point, 10x dilution series of Hepatitis B virus (HBV) cDNA template
- Starting amount of 3×10^9 copies ($n = 3$ each) over 10 logs
- Efficiency = 95% (standard curve method)
- $R^2 = 0.99$

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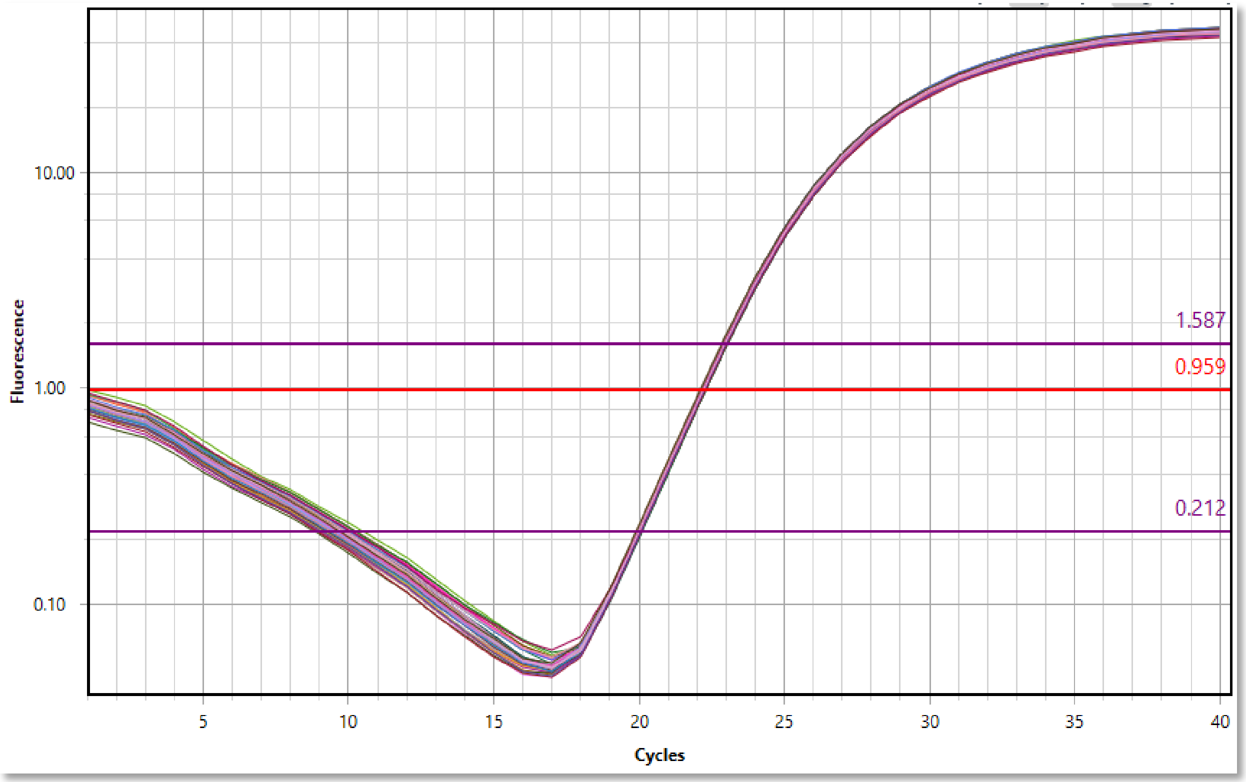
Amazing Repeatability



- Manganese superoxide dismutase gene (MnSOD) (*n* = 48)
- Standard deviation = 0.03
- C_q range =
- Efficiency = 98% (LinRegPCR method)

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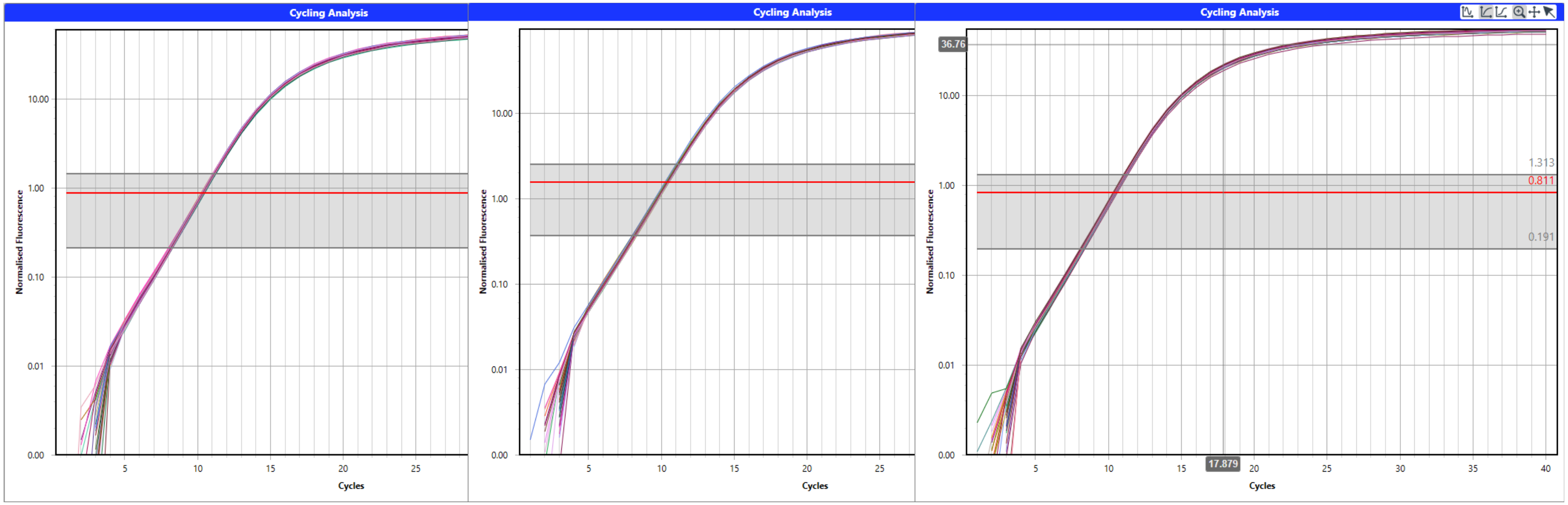
Outstanding Reproducibility

Minimal variation between instruments



Instrument	C_q Range	Range Δ	C_q Mean	C_q S.D.
M0000002	10.22 – 10.49	0.27	10.33	0.06
M0000005	10.16 – 10.43	0.27	10.34	0.05
M0000008	10.21 – 10.42	0.21	10.32	0.06

- Hepatitis B virus (HBV) cDNA template
- Template amount was 3 x 10^6 copies/µL ($n = 48$).
- Three different instruments and three different experiments set up at different times
- Max spread of C_q across three instruments = 0.33

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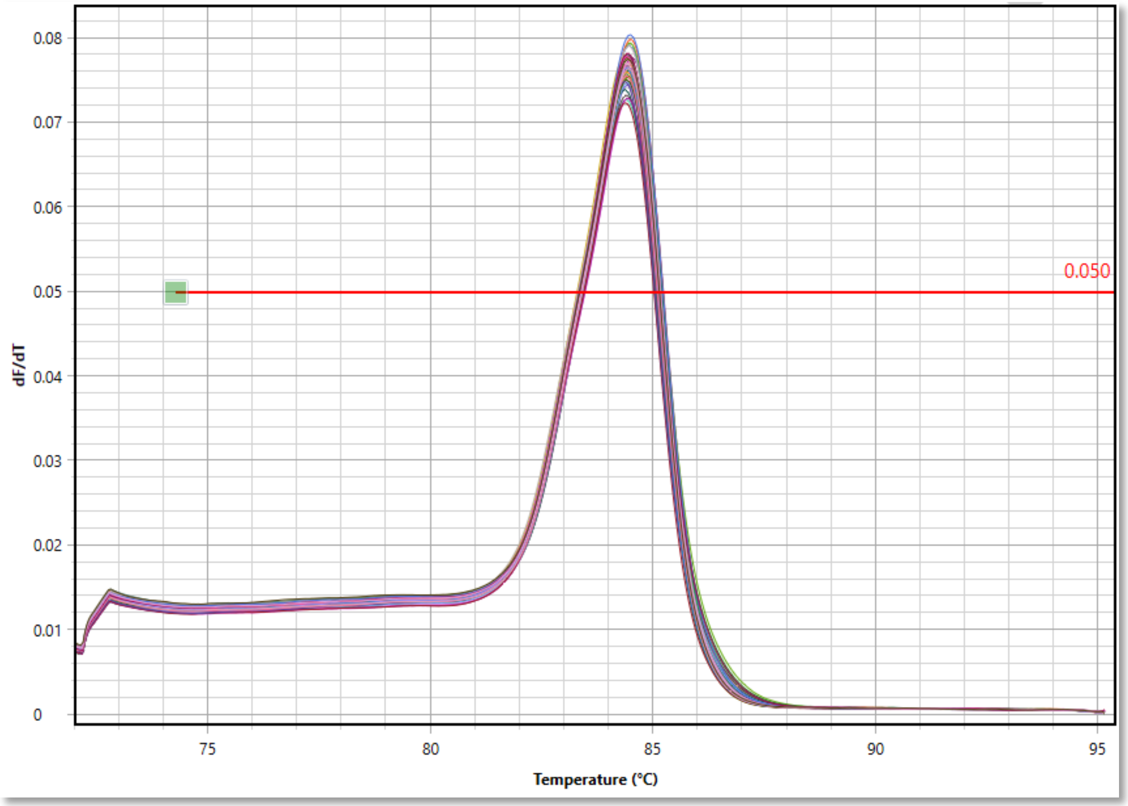
First class temperature uniformity



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

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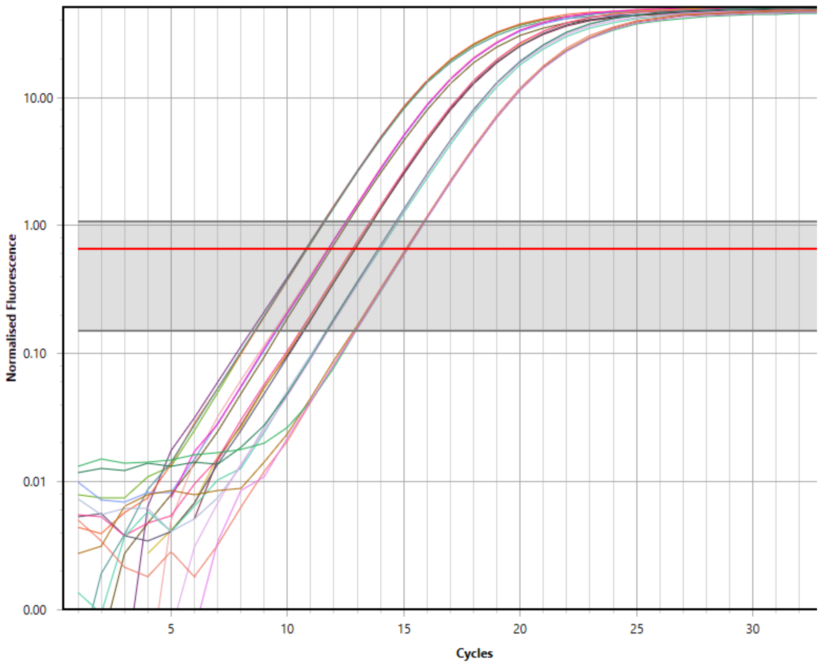
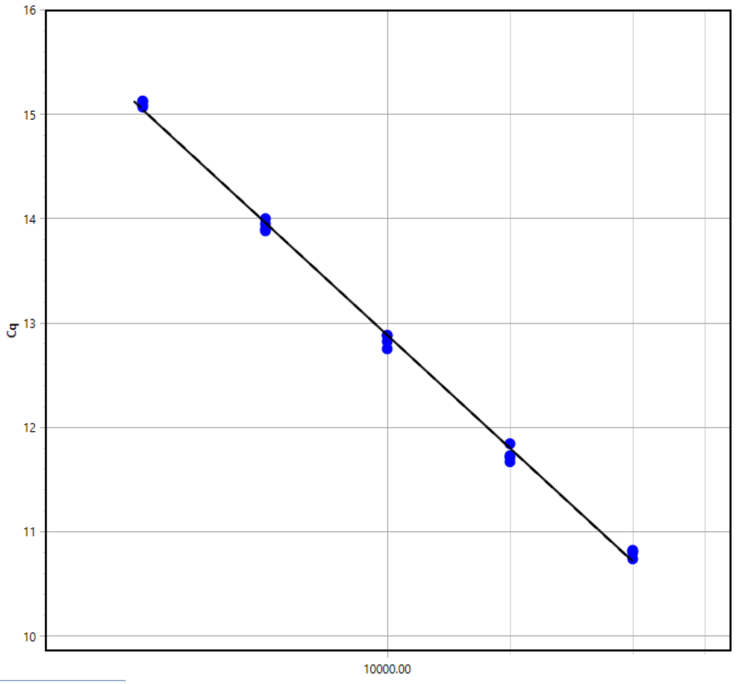
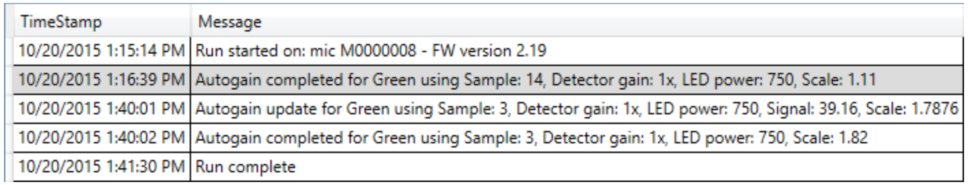
Fast Cycling

Maintain assay performance even at speed







TimeStamp	Message
10/20/2015 1:15:14 PM	Run started on: mic M0000008 - FW version 2.19
10/20/2015 1:16:39 PM	Autogain completed for Green using Sample: 14, Detector gain: 1x, LED power: 750, Scale: 1.11
10/20/2015 1:40:01 PM	Autogain update for Green using Sample: 3, Detector gain: 1x, LED power: 750, Signal: 39.16, Scale: 1.7876
10/20/2015 1:40:02 PM	Autogain completed for Green using Sample: 3, Detector gain: 1x, LED power: 750, Scale: 1.82
10/20/2015 1:41:30 PM	Run complete

- 5 point, 2x dilution series of Hepatitis B virus (HBV) cDNA template
- Starting amount of 3×10^6 copies ($n = 4$ each)
- Efficiency = 90% (standard curve method) ; $R^2 = 0.99$
- Time to complete run (including melt) = 26 min.

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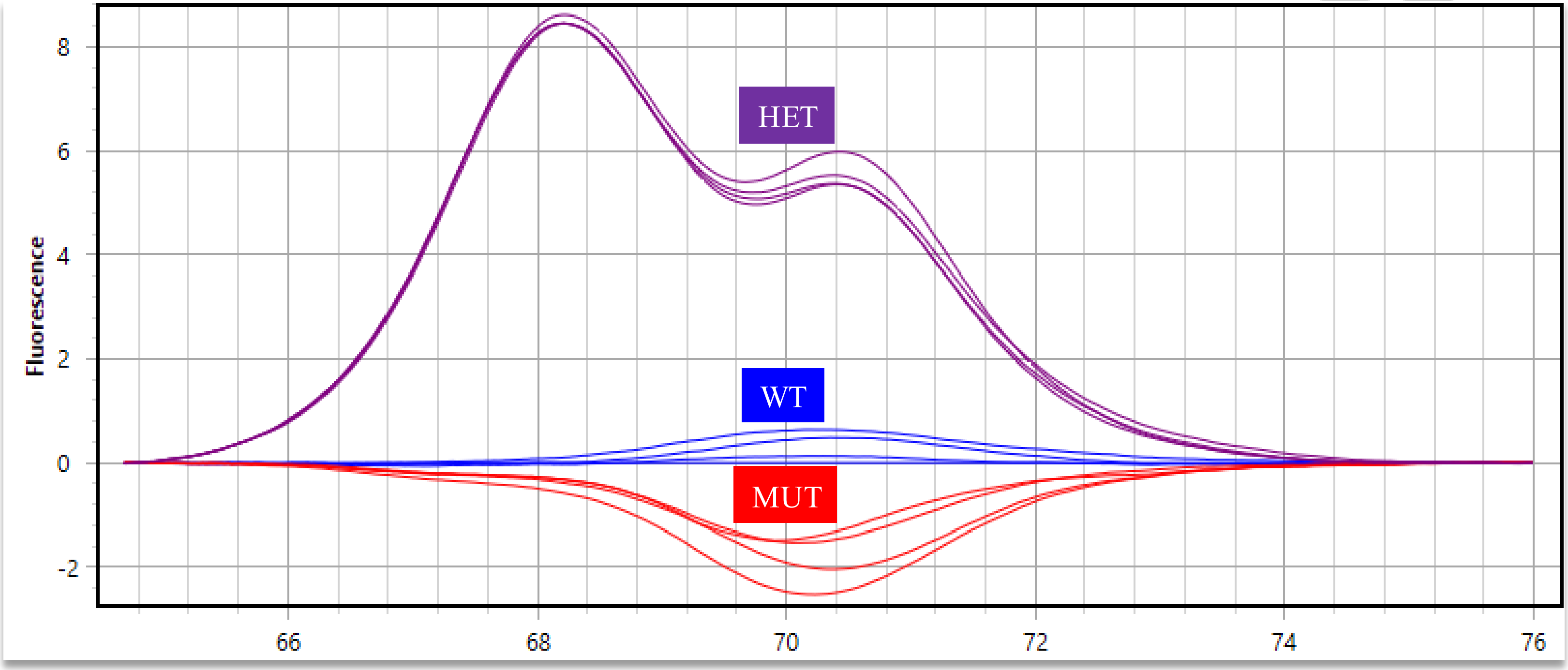
High Resolution Melting (optional)

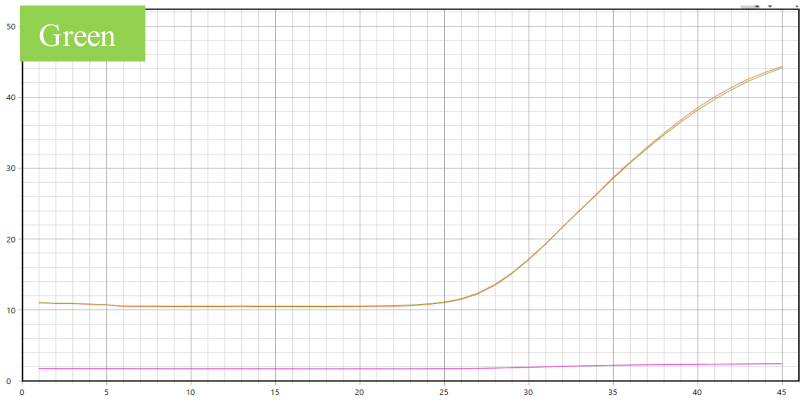
Classify difficult Class IV SNPs

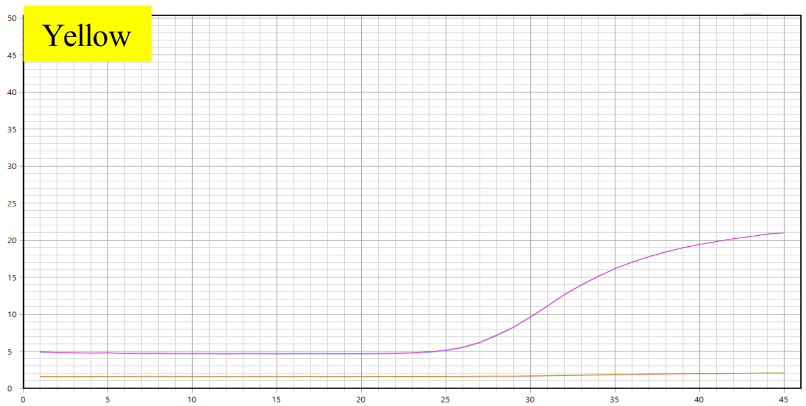


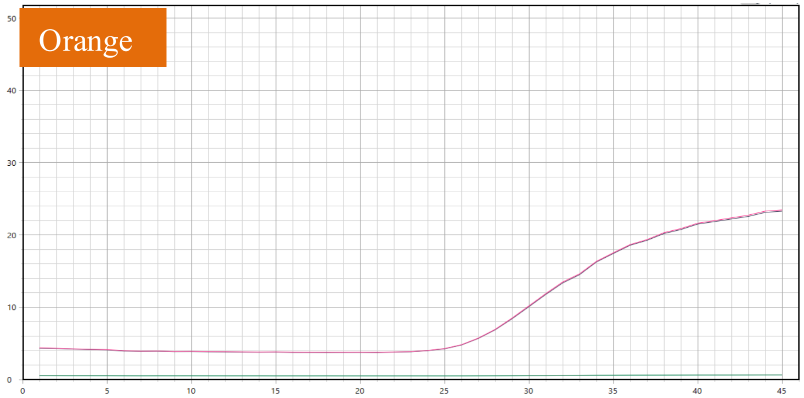
- Class IV SNP (A to T)
- Temperature difference between alleles < 0.10°C

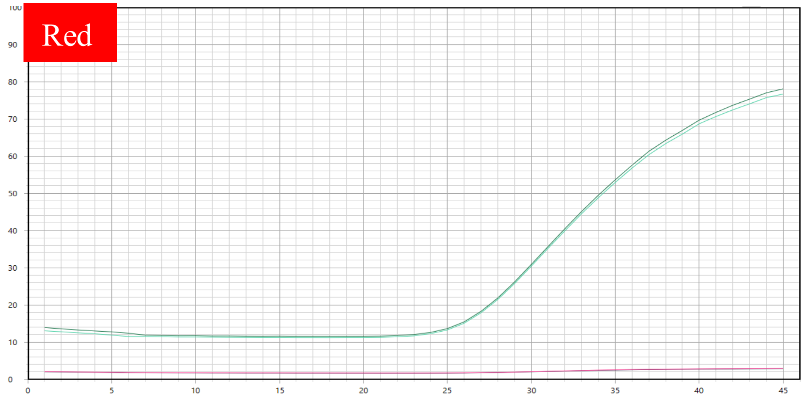
Four colours

Minimal cross talk









- Individual channel high power LEDs
- Individual channel detectors
- Cross talk < 3% across all channels

Analysis Note

Cycling analysis was achieved using the LinRegPCR method (Ramakers et al. 2003[2], Ruijter et al. 2009[1]) 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 C_q 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.

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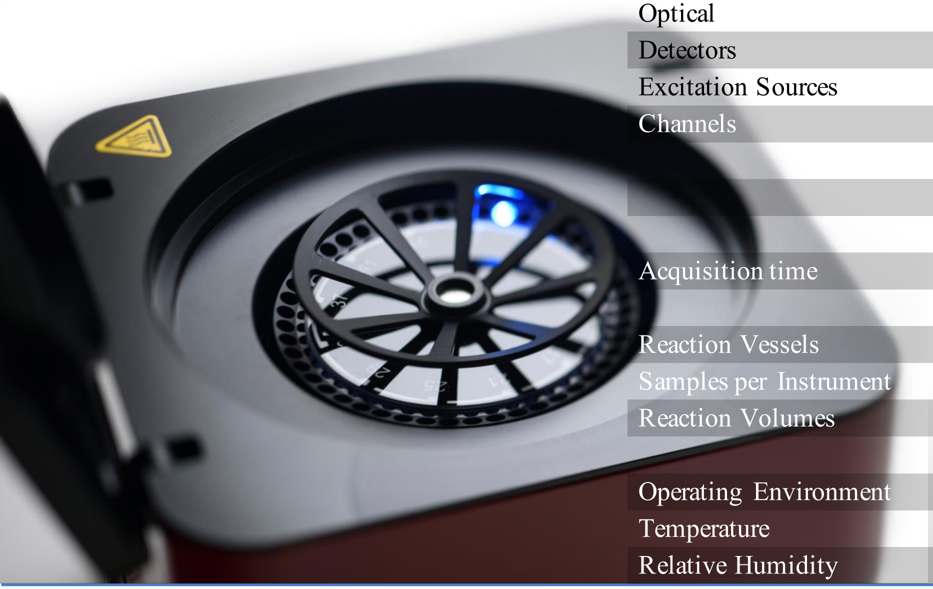
[1] Ruijter JM, Ramakers C, Hoogaars MH, Karlen Y, Bakker O, van den Hoff MJB, and Moorman AFM. (2009) Amplification efficiency: linking baseline and bias in the analysis of quantitative PCR data. Nucleic Acids Research, e45.

[2] 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
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 nm Em. 510 nm
	Yellow: Ex. 530 nm Em. 555 nm
	Orange: Ex. 585 nm Em. 610 nm
	Red: Ex. 625 nm Em. 660 nm
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%

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