Clara® **HRM Mix**

- SNP genotyping
- Methylation studies
- Gene scanning

Clara® HRM Mix is our next generation qPCR mix developed to give maximum specificity to your high resolution melt (HRM) curve analyses. Accurately detect genetic mutations, quickly identify genotypes based on SNPs, or reliably calculate percent methylation of a target region with HRM analysis.

Features

- Accurate distinction of SNP classes I-IV
- Reliably quantify methylation of target sequences
- Super-senstitive product melt curves for distinct allele profiles
- Compatible with all HRM-suitable real-time instruments
- Powered by PCRBIO Taq DNA Polymerase

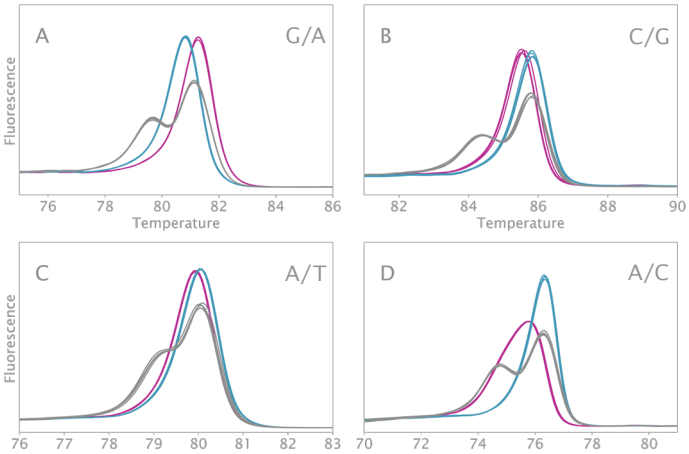

Figure 1. High resolution melting analysis of 4 SNPs using Clara® HRM Mix

A. SNP rs12913832 (G/A) associated with the expression of the OCA2 gene; B. SNP rs2230199 (C/G) associated with the expression of the C3 gene; C. SNP rs641805 (A/T) associated with the expression of the DPYD gene; D. SNP rs9903378 (A/C) associated with the expression of the TP53 gene. Reactions include 0.4 µM of each primer and 5 ng of human genomic DNA. Cycling conditions were 95˚C 2 min followed by 45 cycles of 95 ˚C 5 s and 60 ˚C 20 s.

Super senstitive melt curve separation allows accurate distinction of class I to class IV SNPs with Clara® HRM Mix.

Applications

- Accurate SNP genotyping
- Gene scanning
- CpG methylation analysis

PCRBIOSYSTEMS
simplifying research

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Superior HRM mix

Clara® HRM Mix is our latest high performance qPCR mix for high resolution melt curve (HRM) analysis. The mix contains our PCRBIO Taq DNA Polymerase, dNTPs, $MgCl_2$ and our third-generation, DNA interacalating dye, SyGreen 2. This non-inhibitory DNA binding dye allows the highly senstitive melt curve profile generation for superior HRM analysis.

SNP detection

Proprietary smart screen technology has enabled the development of an enzyme buffer with novel composition that guarantees excellent SNP differentiation capabilities. Use Clara® HRM Mix to distinguish all classes of SNP:

- Class I: C to T and G to A
- Class II: C to A and G to T
- Class III: C to G
- Class IV: A to T

Methylation studies

Clara® HRM Mix can also be used to quantify CpG methylation in a target sequence by combining HRM qPCR with bisulfite sequencing. HRM analysis on the bisulfite treated versus a corresponding, untreated, control sample allows the estimation of the target's cytosine methylation percentage, because methylated sequences will have a higher CG content compared to unmethylated targets following bisulfite treatment.

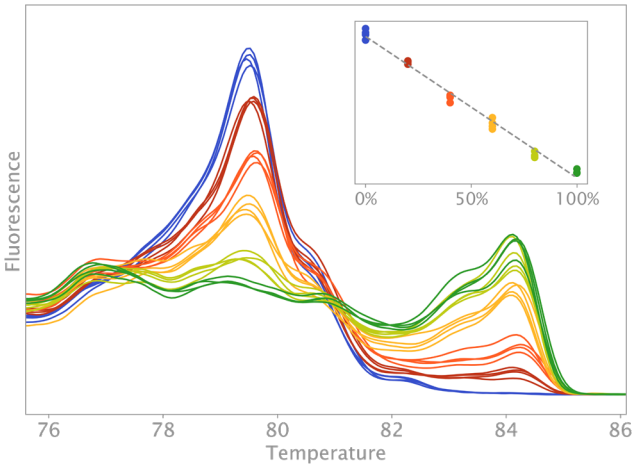

Figure 2. DNA Methylation analysis of FN3K gene by high resolution melting

Human genomic DNA with different levels of methylation (0%-100%) was treated with bisulfite prior to qPCR amplification. Clara® HRM Mix was used in qPCR reactions which included 0.4 µM of each primer and 5 ng of human genomic DNA. Cycling conditions were 95˚C 2 min followed by 45 cycles of 95 ˚C 15 s, 60 ˚C 20 s, and 72 ˚C 10 s on a Roche Applied Science Lightcycler® 96.

Clara® HRM Mix enables accurate estimation of CpG methylation in DNA targets.

Catalogue Number	Product Name	Pack Size	Presentation
PB20.32-01	Clara® HRM Mix	100 reactions	1 x 1 mL
PB20.32-05		500 reactions	5 x 1 mL
PB20.32-20		2000 reactions	20 x 1 mL

PCR Biosystems Ltd. | Aztec House | 397-405 Archway Road | London, N6 4ER
T: +44 (0) 203 930 8101 | E: info@pcrbio.com | Orders: sales@pcrbio.com
www.pcrbio.com