

MegaMix HRM 2X Mastermix

P. Code	Reactions (20 µl)	Tubes	Component	Description	Lot Number	Expiry
2MM-HRM-1	100	1 ml	2X MegaMix HRM Mastermix	Hot Start Taq, 0.2 mM dNTPs, 3 mM MgCl ₂ and microGREEN dye in optimised buffer (concentrations are final).		

Applications

High Resolution Melt (HRM) analysis:

- Single Nucleotide Polymorphism (SNP) genotyping
- Methylation analysis
- Mutation scanning
- Detection of sequence variations

Key Features

- Save Time and Money—quickly and efficiently identify sequence variations.
- Specificity—Hot Start Taq DNA Polymerase in optimised buffer eliminates non-specific amplification and the formation of primer dimers.
- Sensitivity—detect class 4 SNP.
- Versatile— compatible with standard and fast cycling conditions, GC/AT rich templates.
- Reproducibility and convenience—ready to use 2X format.
- Third generation intercalating dye— no inhibition of PCR, even at high concentrations, suitable for High Resolution Melting.

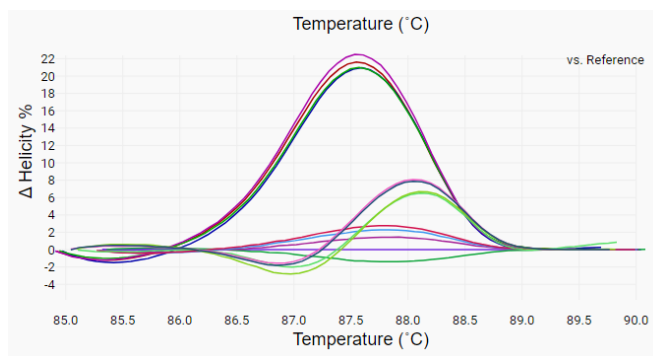
Product Description

HRM quick as quick and simple process that allows detection of variations in DNA sequences. It enables the detection of the single nucleotide polymorphisms by distinguishing minor differences in melting curves.

megaMix HRM contains all the components needed to perform HRM-PCR swiftly and reliably. The 2X mix contains chemically modified Hot Start Taq DNA polymerase and microGREEN intercalating dye in enhancing buffer optimised for HRM analysis. microGREEN is a third generation, saturating, intercalating fluorescent dye that binds to double stranded DNA without inhibiting PCR; making MegaMix HRM the perfect choice for HRM.

The Hot Start Taq polymerase is chemically inactivated until heating to 95°C, providing excellent sensitivity and specificity; eliminating the formation of non-specific amplification and primer-dimers.

This mastermix performs excellently when amplifying from GC rich templates, proving reproducible and reliable results with little or no optimisation.



HRM analysis by exponential difference plot showing detection of the rs414833 SNP amplified and melted using MegaMix HRM. Clear differentiation between curves allow identification of the wild type, homozygous and heterozygous genotypes.

Protocol

This products is to be used as follows.

Thaw all reagents completely and mix well before use.

Prepare a master mix as described in the table below. This reaction can be scaled according to the quantity of reactions required.

Mix gently, avoiding bubbles, centrifuge if necessary.

Include a no template control and positive control as required.

Components	Volume
2X MegaMix HRM Mastermix	10 µl
Primer mix	x µl
Template	y µl
Just Water (Molecular grade water)	make up to 20 µl

Thermocycling

Transfer the reactions to the thermal cycler and set as follows.

Cycles	Temperature	Time
1	95°C	2 min
40	95°C	15 sec
	60°C	30 sec

Follow instrument guidelines for melt instructions.

Annealing temperature (60°C) may require optimisation depending on the specific primers in use.

The run time can be shortened by optimising the steps of the thermocycling profile.

The included dye has an absorption wavelength of 488 nm and a excitation wavelength of 510 nm, therefore acquisition can be performed in the FAM/SYBR channel of any compatible thermal cycler.

For research use only

Product Handling

Storage

To ensure the quality of the product until the expiry date keep at the recommended storage temperature and limit exposure to light.

Contamination Control

To prevent erroneous results ensure work environment is free of contamination by cleaning your workstation and equipment with a DNA decontaminant daily, wear gloves, use sterile tubes and filter pipette tips.

Simple | Effective | Efficient