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(54) Title: DETECTION OF METHYLATION STATUS

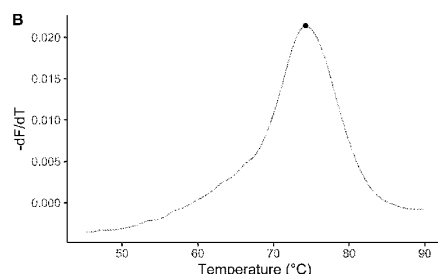
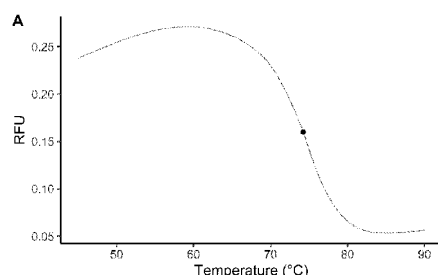


Fig 1

(57) Abstract: The present invention relates to a method for determining epigenetic modification status of at least one nucleotide of interest (NOI) in a target nucleic acid sequence of interest. The invention is based on the finding that certain oligonucleotides comprising hydrophobic nucleotides have significant differences in melting temperature to epigenetically modified target nucleic acids compared to unmodified target nucleic acids. The methods have multiple applications for example in diagnosis. The invention also provides oligonucleotides, in particular BasePrimers for use in such methods.

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