



Comparison of MED1 Glycosylase in Detection of Mutations/Polymorphisms

Features	MED1 glycosylase	S1 nuclease method	DNA mismatch glycosylases	MutS binding assay	Chemical cleavage method	T4 endo-nuclease VII	RNase nicking mismatched RNA:DNA	Automated DNA sequencing	ddNTP SSCP finger-printing	CEL I mismatch endonuclease
Assay at neutral pH	yes	no	yes	yes	yes	yes	yes	yes	yes	yes
Applicable to mutations of unknown positions	no	yes	no	yes	yes	yes	yes	yes	yes	yes
Applicable to all basepair substitutions	with difficulty	unknown	with difficulty	with difficulty	with difficulty	yes	no	yes	yes	yes
Applicable to DNA loops	no	yes	no	with difficulty	multiple bands	yes	unknown	yes	yes	yes
Provides single major band in loop detection	no	no	no	yes	no	yes	no	no	no	yes
Advantage of little influence by sequence specificity	unknown	no	unknown	yes	unknown	cuts w/o mismatch	unknown	no	with difficulty	yes
Advantage of no RNA instability	yes	yes	yes	yes	yes	yes	no	yes	yes	yes
Ability to show the position of a detectable mutation	yes	yes	yes	no	yes	yes	yes	yes	with difficulty	yes
Ability to lower background w/ DNA polymerase & DNA ligase recycling reaction	no	no	no	no	no	with difficulty	no	no	no	yes
Ability to multiplex samples of the same	no	unknown	no	with difficulty	yes	unknown	no	no	no	yes

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color										
Ability to analyze targets of 1 Kbp to 3 Kbp	unknown	unknown	unknown	with difficulty	yes, up to 1 Kbp	unknown	no	no	no	yes
Preference for G:T mismatches	yes	no	no	slight	no	no	no	no	no	no
Preference for methylated or unmethylated CpG sites	yes	no	no	no	no	no	no	no	no	no