

# MLH1 Promotor Hypermethylation REQUEST FORM

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## FOR LABORATORY USE ONLY

SCMD No:	Received by:	Prepared by:	Received: (Date/Time)
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## INDIVIDUAL AUTHORISING REQUEST (e.g. Clinician / Pathologist)

Name:	Address:
Phone:	

## DESTINATION FOR ANALYSIS REPORT (ESSENTIAL – Results may be delayed if not completed)

Name:	Address:
Phone:	
Note: If as above please tick here <input type="checkbox"/>	

Required Method(s) for Report Delivery (please tick all that apply): Post  Fax  Email

Results Fax number(s):	Results e-mail(s):
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## INVOICING DETAILS (ESSENTIAL – Results may be delayed if not completed in full)

Contact name:	Full Organisation Name and Postal Address:
Phone:	
Email:	
Note: An authorisation code is mandatory if providing private medical insurance details	

## PATIENT DETAILS (At least 3 unique identifiers are mandatory)

Surname:	Forename:	DOB (DD/MM/YYYY):	Gender: M <input type="checkbox"/> F <input type="checkbox"/>
Hospital Name:	Surgical Case ID: including block number(s)	Hospital Number:	Requester Ref: (if applicable)

## SAMPLE / PATHOLOGY DETAILS (Please provide as much information as possible)

**NOTE: This assay requires both tumour and normal tissue for comparative purposes. Single blocks/slides may be accepted if suitable for macro-dissection (i.e. yield sufficient normal and tumour components with >20% tumour nuclei in the latter).**

Material Supplied: (see website for tissue requirements)	Estimated % of tumour nuclei in tumour component		
FFPE Single Block <input type="checkbox"/>	FFPE Paired Blocks <input type="checkbox"/>	< 20% (reject)	51-75%
Unstained Slides <input type="checkbox"/>		21-50%	>75%
Primary Tumour Site: (e.g. Colorectal)	Tumour Sub-Type: (e.g. Adenocarcinoma)	Tissue Sample(s) Supplied: (e.g. colon biopsy)	

Address for return of FFPE block or other unused material:

Note: If left blank, material will be returned to the same address as specified for the analysis report.

## Microsatellite / Mismatch Repair / BRAF Mutation Status (if known)

<input type="checkbox"/> MSI-High	<input type="checkbox"/> MMR Defective (by IHC)	<input type="checkbox"/> BRAF codon 600 wild-type
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