

Human High Methylated Genomic DNA Control



Product Highlights

- ▶ Human High Methylated Genomic DNA is derived from whole blood and *in vitro* enzymatically methylated resulting in greater than 80% methylation in all regions of the genome. Most regions show more than 90% in methylation.
- ▶ Ideal for use as control in bisulfite methylation analysis procedures including Pyrosequencing, targeted NGS, and MS-HRM.
- ▶ Tested on gene specific and global methylation assays for consistent performance.
- ▶ Requires bisulfite modification prior to use.

Product Contents

1 vial Human High Methylated Genomic DNA (5 µg at 100 ng/µL, > 80% Methylation)

Ordering Information

CATALOG NUMBER	PRODUCT	PRICE
80-8061-HGHM5	Human high methylated genomic DNA (5 µg at 100 ng/ µL)	\$242.83

Related Products

CATALOG NUMBER	PRODUCT	PRICE
80-8063-MGHM5	Mouse high methylated genomic DNA (5 µg at 100 ng/ µL)	\$252.56
80-8065-RGHM5	Rat high methylated genomic DNA (5 µg at 100 ng/ µL)	\$252.56
80-8067-PMGHM5	Monkey (<i>Macaca mulatta</i>) high methylated genomic DNA (5 µg at 100 ng/ µL)	\$281.63
80-8062-HGUM5	Human low methylated genomic DNA (5 µg at 100 ng/ µL)	\$242.83
80-8064-MGUM5	Mouse low methylated genomic DNA (5 µg at 100 ng/ µL)	\$252.56
80-8066-RGUM5	Rat low methylated genomic DNA (5 µg at 100 ng/ µL)	\$252.56
80-8068-PMGUM5	Monkey (<i>Macaca mulatta</i>) low methylated genomic DNA (5 µg at 100 ng/ µL)	\$281.63
80-8060H-PREMIX	Human Premixed Calibration Standard (1 µg per vial, 20 µL volume)	\$386.56
80-8060M-PREMIX	Mouse Premixed Calibration Standard (1 µg per vial, 20 µL volume)	\$402.40
80-8060R-PREMIX	Rat Premixed Calibration Standard (1 µg per vial, 20 µL volume)	\$402.40
80-8060PM-PREMIX	Monkey (<i>Macaca mulatta</i>) Premixed Calibration Standard (1 µg per vial, 20 µL volume)	\$412.46

Example Protocol

- ▶ Bisulfite modification of controls and sample(s) of interest.
 - Zymo Research EZ Methylation kit (Cat.#D5002 or D5004) with 200 - 500 ng of input DNA following manufacturers recommended protocol.
- ▶ PCR amplification Protocol:

Component	Per 30µl reaction
10X PCR buffer (Contains 15mM MgCl ₂)	3 µl (1x)
25 mM MgCl ₂	1.8 µl (3.0 mM final conc.)
10 mM dNTPs	0.6 µl (200 µM of each)
10 µM Fwd primer	0.6 µl (6 pmol)
10 µM Rev primer	0.6 µl (6 pmol)
HotStar Taq Polymerase (5 U/µl)	0.15 µl (0.75 U)
DNA	1 µl of bisulfite treated DNA
Water	Adjust to 30 µl

- HotStar Taq Polymerase Qiagen (Cat. #203205) recommended with the following PCR cycling conditions:
 - 95°C 15 min; 45 x (95°C 30 s; Ta°C 30 s; 72°C 30 s); 72°C 5 min; 4°C ∞
- Additional optimization is needed if different PCR system is used in analysis.
- ▶ Sequencing Analysis: Pyrosequencing, NGS, or MS-HRM.

Technical Specifications

- ▶ 5µg DNA in TE buffer (10mM Tris-HCl, 1mM EDTA, pH 8.0)
- ▶ Store at -20°C, in aliquots, for 2 years. For best results, do not freeze/thaw an individual aliquot more than three times. For longer term storage -70°C is recommended.

Example Quality Control Results

Figure: High Methylated Control DNA Tested on a Human MGMT Promoter Methylation Assay via Pyrosequencing

Pyrogram showing approximately 90% methylation at all CpG sites

