

Product Highlights

- ▶ Rat High Methylated Genomic DNA is derived from whole blood and *in vitro* enzymatically methylated resulting in greater than 85% 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 Rat High Methylated Genomic DNA (5 µg at 100 ng/µL, > 85% Methylation)

Ordering Information

CATALOG NUMBER	PRODUCT	PRICE
80-8065-RGHM5	Rat high methylated genomic DNA (5 µg at 100 ng/ µL)	\$229.99

Related Products

CATALOG NUMBER	PRODUCT	PRICE
80-8061-HGHM5	Human high methylated genomic DNA (5 µg at 100 ng/ µL)	\$219.99
80-8063-MGHM5	Mouse high methylated genomic DNA (5 µg at 100 ng/ µL)	\$229.99
80-8067-PMGHM5	Monkey (<i>Macaca mulatta</i>) high methylated genomic DNA (5 µg at 100 ng/ µL)	\$250.00
80-8062-HGUM5	Human low methylated genomic DNA (5 µg at 100 ng/ µL)	\$219.99
80-8064-MGUM5	Mouse low methylated genomic DNA (5 µg at 100 ng/ µL)	\$229.99
80-8066-RGUM5	Rat low methylated genomic DNA (5 µg at 100 ng/ µL)	\$229.99
80-8068-PMGUM5	Monkey (<i>Macaca mulatta</i>) low methylated genomic DNA (5 µg at 100 ng/ µL)	\$250.00
80-8060H-PREMIX	Human Premixed Calibration Standard (1 µg per vial, 20 µL volume)	\$359.96
80-8060M-PREMIX	Mouse Premixed Calibration Standard (1 µg per vial, 20 µL volume)	\$359.96
80-8060R-PREMIX	Rat Premixed Calibration Standard (1 µg per vial, 20 µL volume)	\$353.96
80-8060PM-PREMIX	Monkey (<i>Macaca mulatta</i>) Premixed Calibration Standard (1 µg per vial, 20 µL volume)	\$359.96

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 Rat NR3C1 Methylation Assay via Pyrosequencing

Pyrogram showing approximately 90% methylation at all CpG sites

