

## DNA methylation control package V2

Cat. No. **C02040019**

Format: 48 rxns

### Product content

Component	Quantity	Concentration	Storage
Methylated spike-in control	70 µl	0.1 ng/µl	-20°C/-4°F
Unmethylated spike-in control	70 µl	0.1 ng/µl	-20°C/-4°F
Primer pair for methylated spike-in ctrl	144 µl	5 µM each	-20°C/-4°F
Primer pair for unmethylated spike-in ctrl	144 µl	5 µM each	-20°C/-4°F

### Product description

The DNA methylation control package V2 includes one methylated and one unmethylated spike-in controls together with their corresponding qPCR primer sets that can be added to the DNA sample of interest for any methylation profiling experiment.

Those spike-in controls have been produced using synthetic oligonucleotides and are not homologous to any model species. They will not interfere with the DNA sample of interest.

### Applications

*For bisulfite sequencing (e.g. RRBS - Reduced Representation Bisulfite Sequencing)*

The spike-in controls must be added to the DNA sample of interest before bisulfite conversion and library preparation to monitor the efficiency of bisulfite conversion. Because their methylation status is known, they can be used to assess the conversion rate, i.e. in the case where you sequence the fully methylated control, all reads should align only to the methylated reference sequence if the conversion ratio is 100%. The sequences of these controls are shown in Table 1.

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Table 1. Sequences of the methylated and unmethylated spike-in controls

Spike-in control	Strand	Sequence (5'→3')
Unmethylated	Forward	TCGAACGCCCGGTGCGCGTGTGGAGGATGTCGGTGCTGCAGGGGGCGTTGGAGCCGA AGTAGACCGCGCCGAACGTACGAACGGTCGTTTCATATTAGTTATACTGGTTGTCTTGA TGTTGCTTCTCCTAATTT
	Reverse	AAATTAGGAGAAGCAACATCAAGACAACCAAGTATAACTAATATGAACGACGACCGTTTCGTA CGTTCGGCGCGGTCTACTTCGGCTCCAACGCCCCCTGCAGCACCGACATCCTCCACAC GCGCGACCGGGCGTTTCA
Methylated	Forward	T <b>mCG</b> GAGAGG <b>mC</b> AGTGGGT <b>mC</b> TGT <b>mCGGmCG</b> AAGTAGGGGTTGA <b>mCG</b> AT <b>mCmCGGAmCmC</b> GTT <b>mCGTAmCGTAmCGmCGmCGAmCmCGmCTAmCT</b> AATTTTAGT TGTGTTT <b>mCTGGTmCmCT</b> ATTGAT <b>mCATTATmCT</b> TTGC
	Reverse	<b>GmCA</b> AGATAATGATCAATAGG <b>AmCmC</b> AGAAACACA <b>mCT</b> AAAATTAGTAG <b>mCGGTmCG</b> <b>mCGmCGTAmCGTAmCGAAmCGGTmCmCGGmCATmCGTCAAmCCCCTAmCCTTmCGCmCG</b> ACAG <b>mCAmCmCmCmCTGmCmCTmCTmCGA</b>

For more details on the analysis of those spike-in controls after bisulfite sequencing, please download our Premium RRBS spike-in controls manual.

*For capture of methylated DNA (e.g. MeDIP - Methylated DNA Immunoprecipitation)*

The spike-in controls must be added to the DNA sample of interest before the capture. The package also includes primer pairs targeting respectively the methylated and unmethylated spike-in controls, allowing to check the success of the capture by qPCR. The size of the expected amplicons is described in Table 2.

Table 2. Expected PCR product size

Region	Amplicon size
Unmethylated spike-in control	110 bp
Methylated spike-in control	103 bp

**Storage conditions:** Store at -20°C/-4°F. For long storage, store at -80°C /-112°F. Avoid multiple freeze-thaw cycles.

**Precautions:** This product is for research use only. Not for use in diagnostic or therapeutic procedures.