

## **Supplementary Information for**

Application of 5-methylcytosine DNA glycosylase to the quantitative analysis of DNA methylation

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Supplementary Table S1

**Table S1.** List of primers for PCR amplification

Primer	Sequence (5'→3')	Region of interest
<b>DME-PCR of <i>Hpa</i> II-methylated yeast genomic DNA</b>		
F1a	TACTCATCTATGGCAATTCTGAGG	
F1b	GGACTACAGATTACAGGTCCTTC	<i>Hpa</i> II site-methylated region
R1	CAGAAATATCATTTCAGTTTGACC	
F2	CAGCCAAAAAAGTCCTTATCACC	
R2	TCAGATGATCTATTTGAATCCTCTG	<i>Hpa</i> II site-deficient region
<b>DME-qPCR of methylated pUC19 plasmid</b>		
DG1764	TAAGGGATTTTGGTCATGAGATTATC	
DG1882	GGTAACTGTCAGACCAAGTTTACTC	CG site-deficient UMR
DG1883	CACATTAATTGCGTTGCGCTCAC	
DG1884	GGATAACCGTATTACCGCCTTTGAG	<i>M.Sss</i> I-methylated HMR
DG1915	GATACGGGAGGGCTTACCATC	
DG1916	ACTGGCGAACTACTTACTCTAGCTTC	<i>Hpa</i> II-methylated LMR
<b>Bisulfite sequencing of <i>FWA</i> allele in <i>Arabidopsis</i></b>		
DG662	TAAGAGAATTTAAATGYAAAYTTTGYAAATA	
DG663	CCTAACAATRCAATCTRTTTCRAAAATRAC	Unmethylated gene <i>ASAI</i>
5'- <i>FWA</i> F	GGTTYTATAYTAATATYAAAGAGTTATGGGYGGAAG	
5'- <i>FWA</i> R	CAAARTACTTTACACATAARCRAAAAACARACAAATC	5'-regulatory region upstream from start codon of <i>FWA</i> gene [1]
<b>DME-qPCR of <i>FWA</i> allele in <i>Arabidopsis</i></b>		
DG1287	GAACCCTTTTAAAGGACTAGCCCA	
DG1288	CGAAAATGACTGTTAAGAGCTCGTTG	Unmethylated gene <i>ASAI</i>
DG1289	CATACGAGCACCGCTTACGG	
DG1290	GAACCAAATCATTCTCTAAACAAAGTGT	5'-regulatory region 0.7 kb upstream from the start codon of the <i>FWA</i> gene
<b>CAPS marker</b>		
DG660	CCAGCCAAATATCAGATCTTGCGCC	
DG661	CCTTAAACAACCAAATAGCASTCCGACCAATG	5'-regulatory region from the start codon of the <i>FWA</i> gene

(Continued)

Primer	Sequence (5'→3')	Region of interest
<b>Bisulfite sequencing of <i>Cnr</i> epiallele</b>		
ATP1-1 F	TGAAYGAGATTYAAGYTGGGGAAATGGT	Unmethylated gene <i>ATP 1</i> [2]
ATP1-1 R	CCCCCTTCCATCAATARRTACTCCCA	
DG1680	TTYTAAGYTGYTAYAGAGATATTGGAAGAG	<i>Cnr</i> epiallele 2.5 kb upstream from the start codon of the <i>CNR</i> gene [3]
DG1682	CARATTA AACACTTCATCAATTRAACAA	
<b>DME-qPCR of <i>Cnr</i> epiallele</b>		
DG1801	GAATGAGAATGTAGGGATTGTTGTC	Unmethylated gene <i>ATP 1</i>
DG1802	CCCTTCCATCAATAGGTACTCCC	
DG1803	CAACAGCTATCATTTATTATGTTACCTC	<i>Cnr</i> epiallele 2.5 kb upstream from the start codon of the <i>CNR</i> gene
DG1804	AAATCATGTAATATAGCTAGGCAGAGG	
<b>RT-qPCR of <i>CNR</i></b>		
CAC F	CCTCCGTTGTGATGTAAGTGG	SGN-U314153 ( <i>CAC</i> ) gene [4]
CAC R	ATTGGTGGAAAGTAACATCATCG	
TIP41 F	ATGGAGTTTTTGAGTCTTCTGC	SGN-U321250 ( <i>TIP41</i> ) gene [4]
TIP41 R	GCTGCGTTTCTGGCTTAGG	
QRT-PCR forward primer	TCCGGGAATTGACAGAAGATAGAGAG	<i>CNR</i> gene [3]
QRT-PCR reverse primer	TTCTGTCAGCAATGTAGCAGATTCA	
<b>Bisulfite sequencing of the DMR in the <i>CNR</i> promoter</b>		
DG2395	AGTGGAAGGAYAATTYTAAATTATTTYTGA	Unmethylated gene <i>Actin</i> (Solyc01g066800)
DG2396	CTAAATCCAACRAAATRCCTAARCCCTATAC	
DG2364	GAGGAGTTGTGYAAYYATAGAYYAAAGYYAGTGG	DMR 0.7 kb upstream from the start codon of the <i>CNR</i> gene [5]
DG2365	CACTCTACTRRACCRACATRRACA ACTRARARACCAAC	
<b>DME-qPCR of the DMR in the <i>CNR</i> promoter</b>		
DG2397	CATTATAACTTGTTCAATCTTGAATCAAG	Unmethylated gene <i>Actin</i> (Solyc01g066800)
DG2398	TATACACGACCCCCTCCGATGTAC	
DG2399	GTTTAGTCGACTCCCTTCGGAATC	DMR 0.7 kb upstream from the start codon of the <i>CNR</i> gene
DG2401	CTCTTTTCTCTAGCTTTGGAGGGATC	

## References

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