

miRNAting control of DNA methylation

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Supplementary material

Supplementary figure 1. Enrichment analysis of the genes methylated in the presence of IDN11 and/or IDN12 for molecular function and biological process

Supplementary figure 2. Enrichment analysis of the genes methylated by DRM2 for molecular function and biological process

Supplementary table 1. List of the locus IDs and its description for the genes found methylated in the presence of IDN2, IDN11 and/or IDN12 and DRM2 genes

Supplementary table 2. Expression correlation between the methylated genes and miRNAs, calculated using NGS RPKM data

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Supplementary table 4. Identification of transcription factors on known target sequences, downloaded from AGRIS database with expression correlation between the targets and the associated transcription factors calculated using RPKM and Microarray expression data

Supplementary table 5. The list of TFBS identified on the upstream genomic regions of IDN2, IDN11, IDN12, DRM2, and miRNA genes

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Supplementary table 8. The target genes of miRNAs and gene enrichment analysis of the target genes based on GO slim ID for the molecular function and biological process categories