# Analysis of Chromatin Regulators Reveals Specific Features of Rice DNA Methylation Pathways[1]

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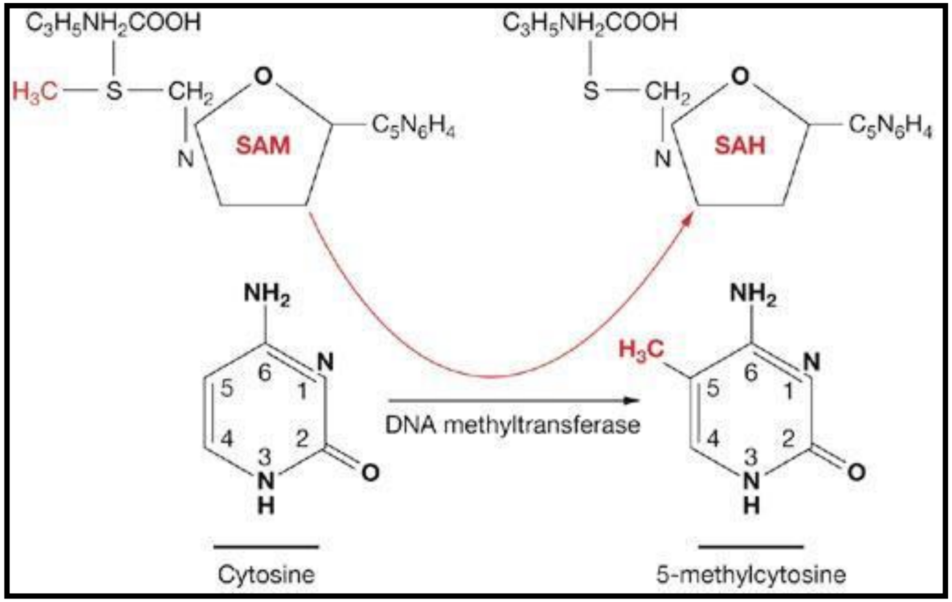
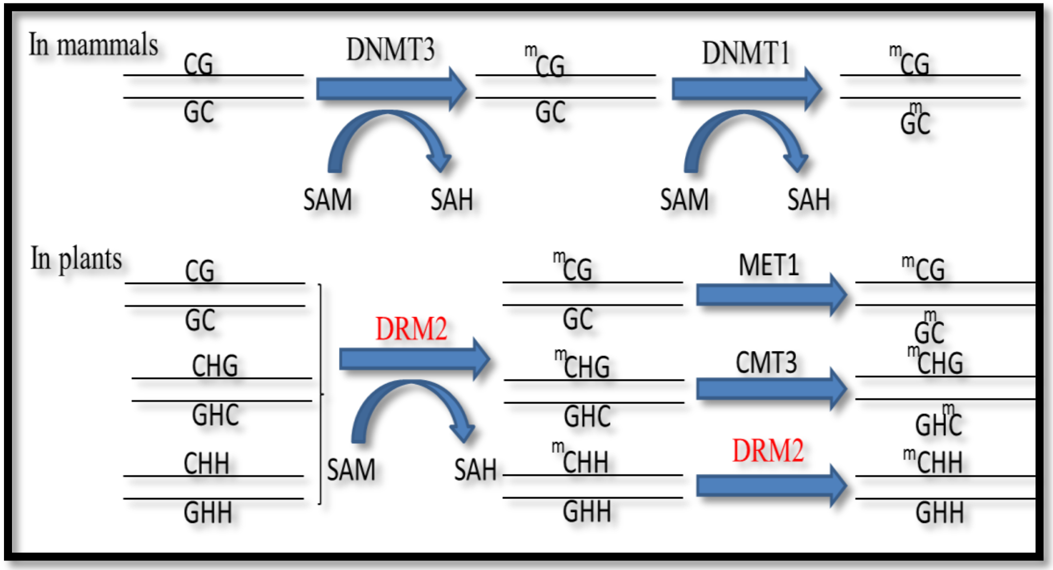
# Backgroud

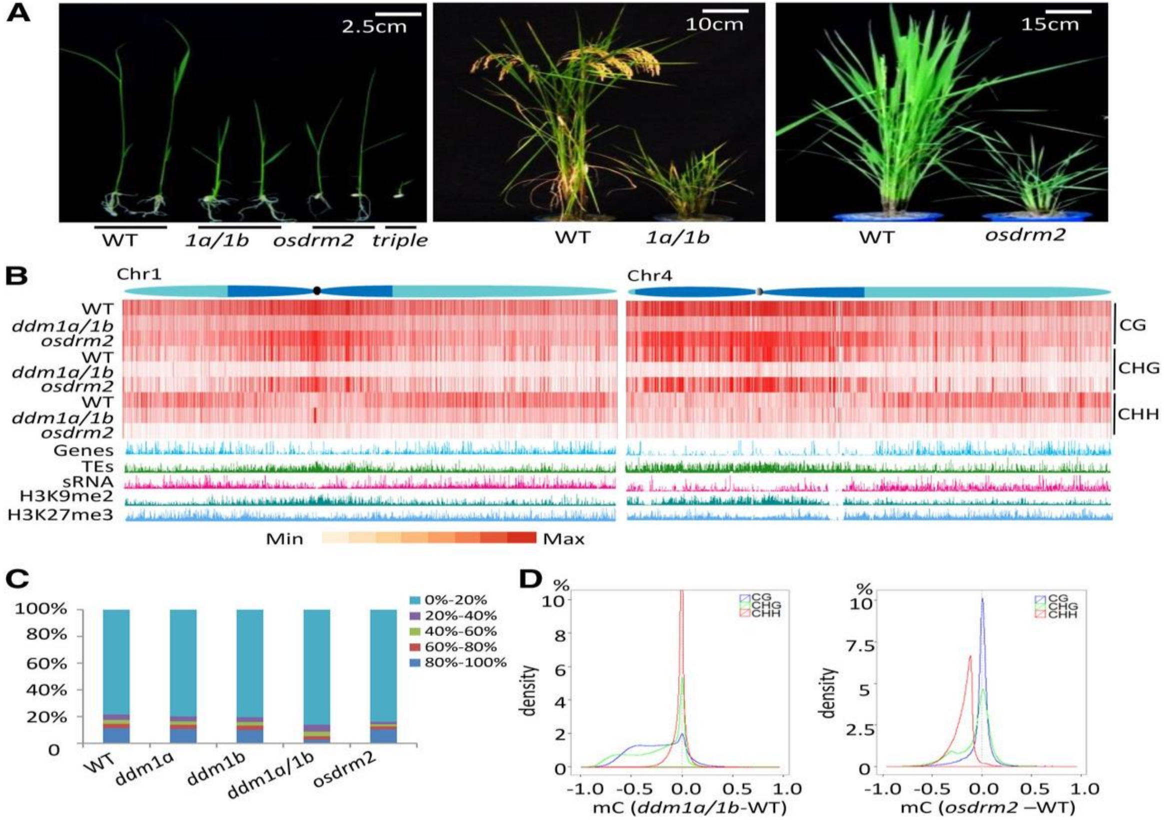




**Chan *et al*., 2005**

***Julie A. Law et al* ., 2010**

# Effects of the osddm1a/1b and osdrm2 mutations on plant growth and genome-wide cytosine methylation.



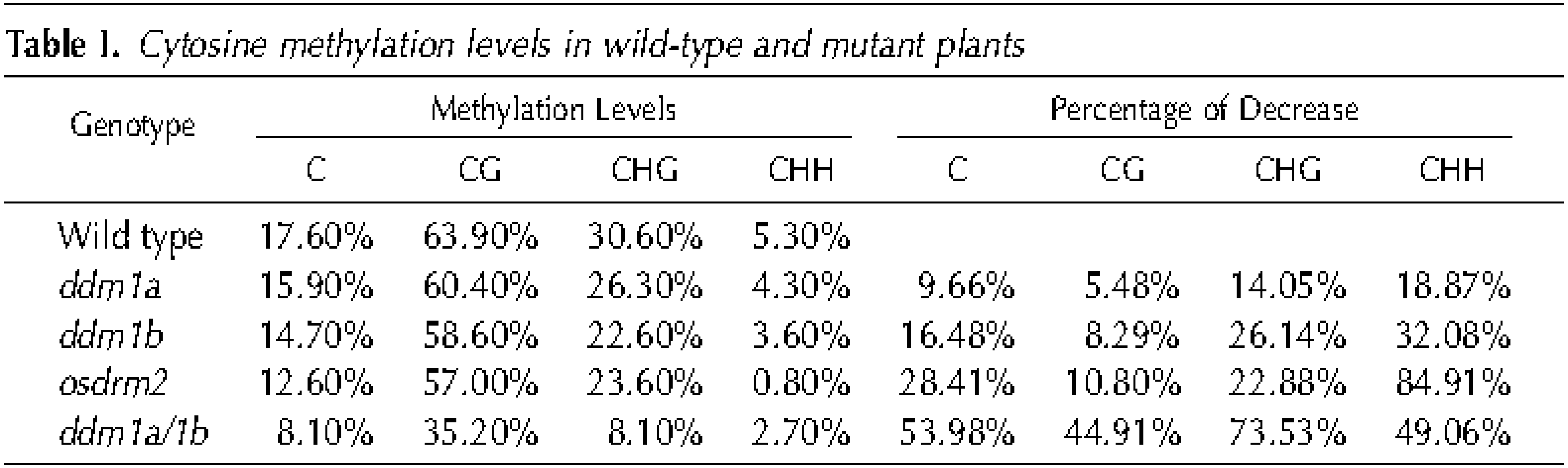
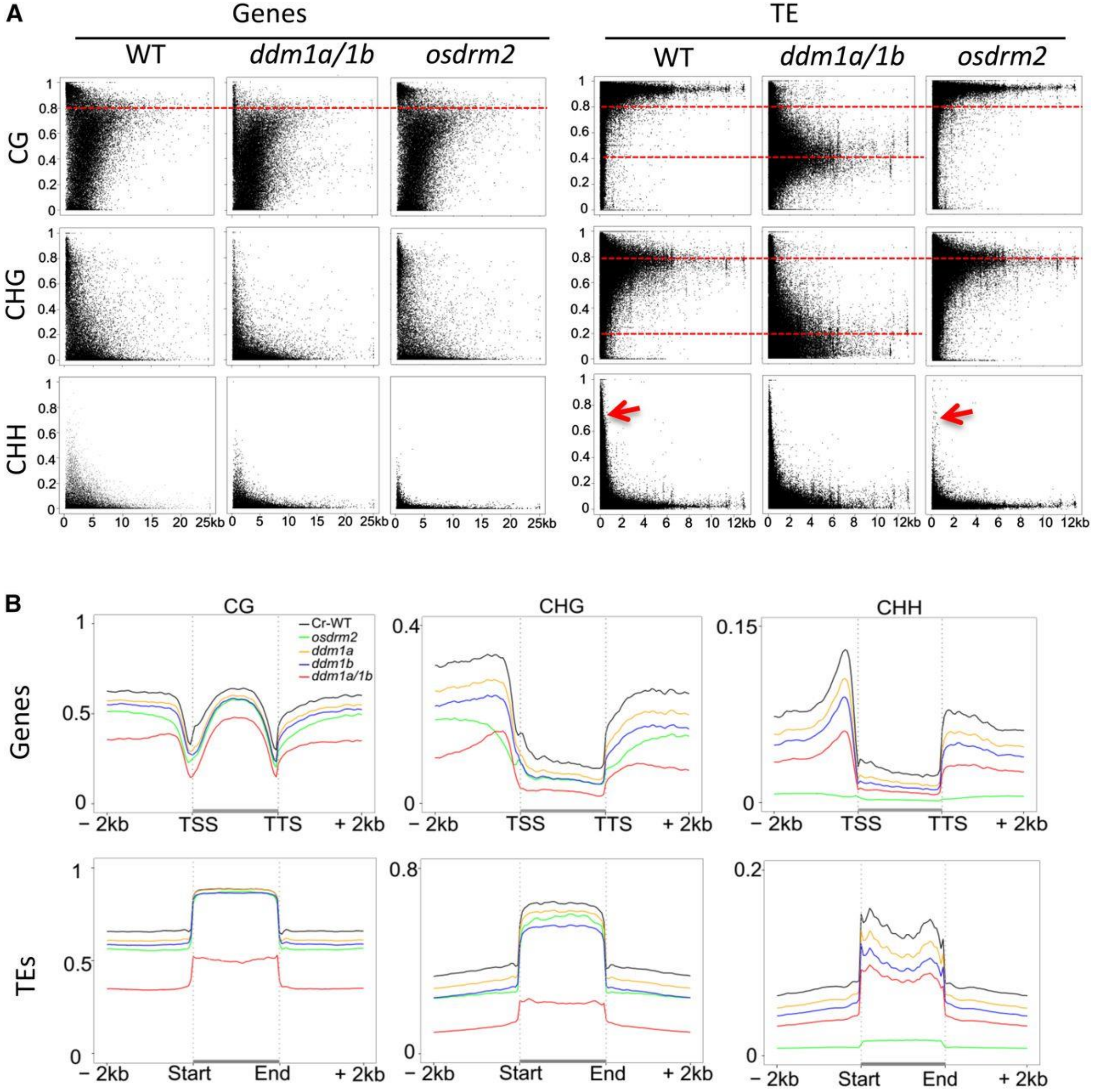


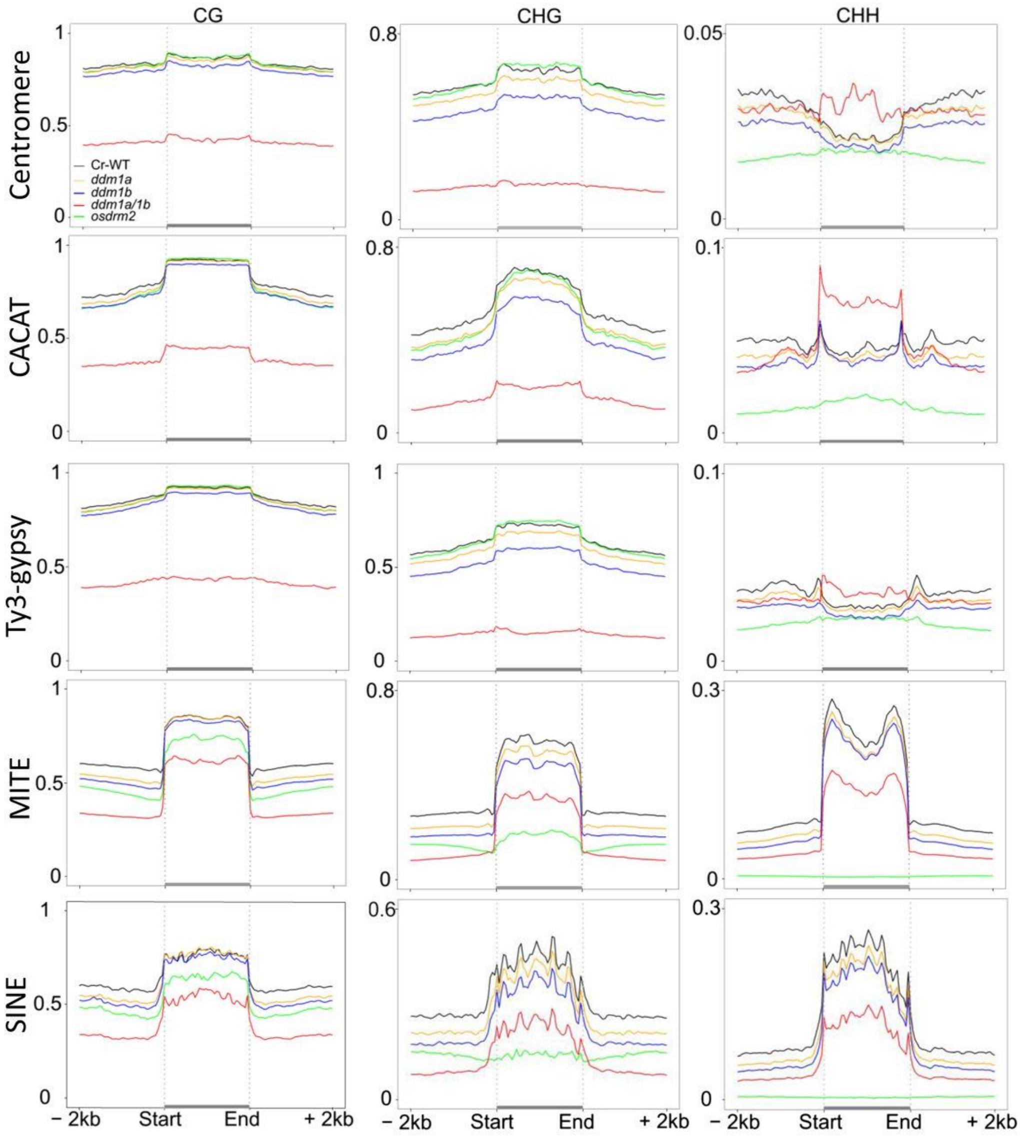
Table 1. *Cytosine methylation levels in wild-type and mutant plants*

| Genotype | Methylation Levels | | | | Percentage of Decrease | | | |
|---|---|---|---|---|---|---|---|---|
| | C | CG | CHG | CHH | C | CG | CHG | CHH |
| Wild type | 17.60% | 63.90% | 30.60% | 5.30% | | | | |
| *ddm1a* | 15.90% | 60.40% | 26.30% | 4.30% | 9.66% | 5.48% | 14.05% | 18.87% |
| *ddm1b* | 14.70% | 58.60% | 22.60% | 3.60% | 16.48% | 8.29% | 26.14% | 32.08% |
| *osdrm2* | 12.60% | 57.00% | 23.60% | 0.80% | 28.41% | 10.80% | 22.88% | 84.91% |
| *ddm1a/1b* | 8.10% | 35.20% | 8.10% | 2.70% | 53.98% | 44.91% | 73.53% | 49.06% |

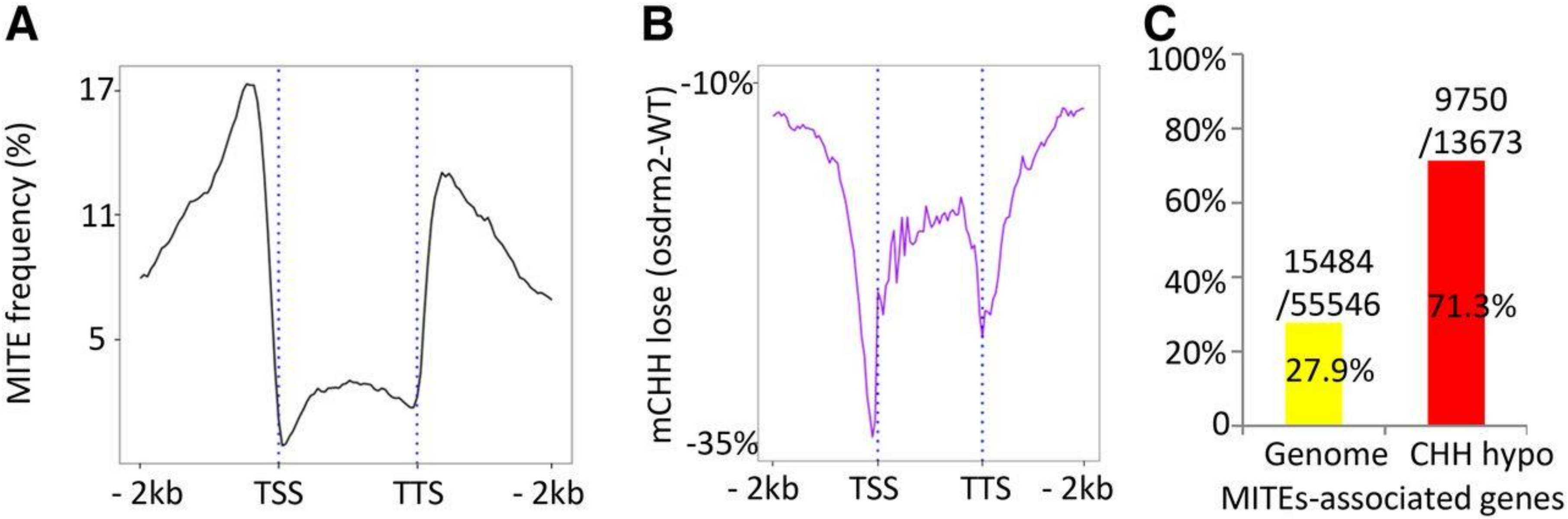
# Average cytosine methylation levels in all sequence contexts in genes and TEs. A, Average cytosine methylation levels in all sequence contexts plotted against gene (left) and TE (right) sizes.



# Genome-wide average levels of methylation in each sequence context of the indicated TE families and repeats in culture-regenerated wild-type (Cr WT) and mutant plants.



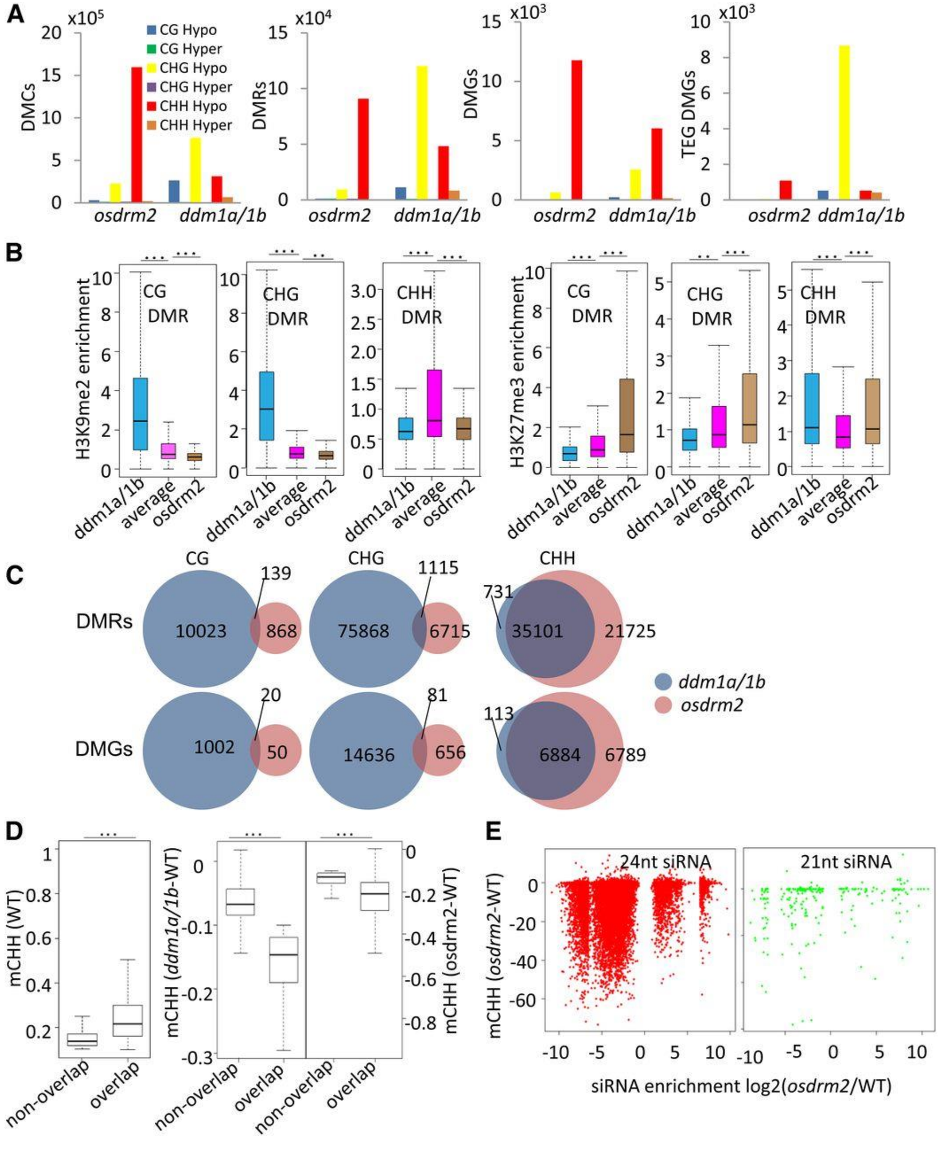
**The osdrm2 mutation reduces CHH methylation of MITEs that are located close to genes.**



TSS：Transcription start site

TTS: transcription terminal site

# Analysis of DMCs, DMRs, and DMGs detected in osddm1a/1b and osdrm2 mutants.

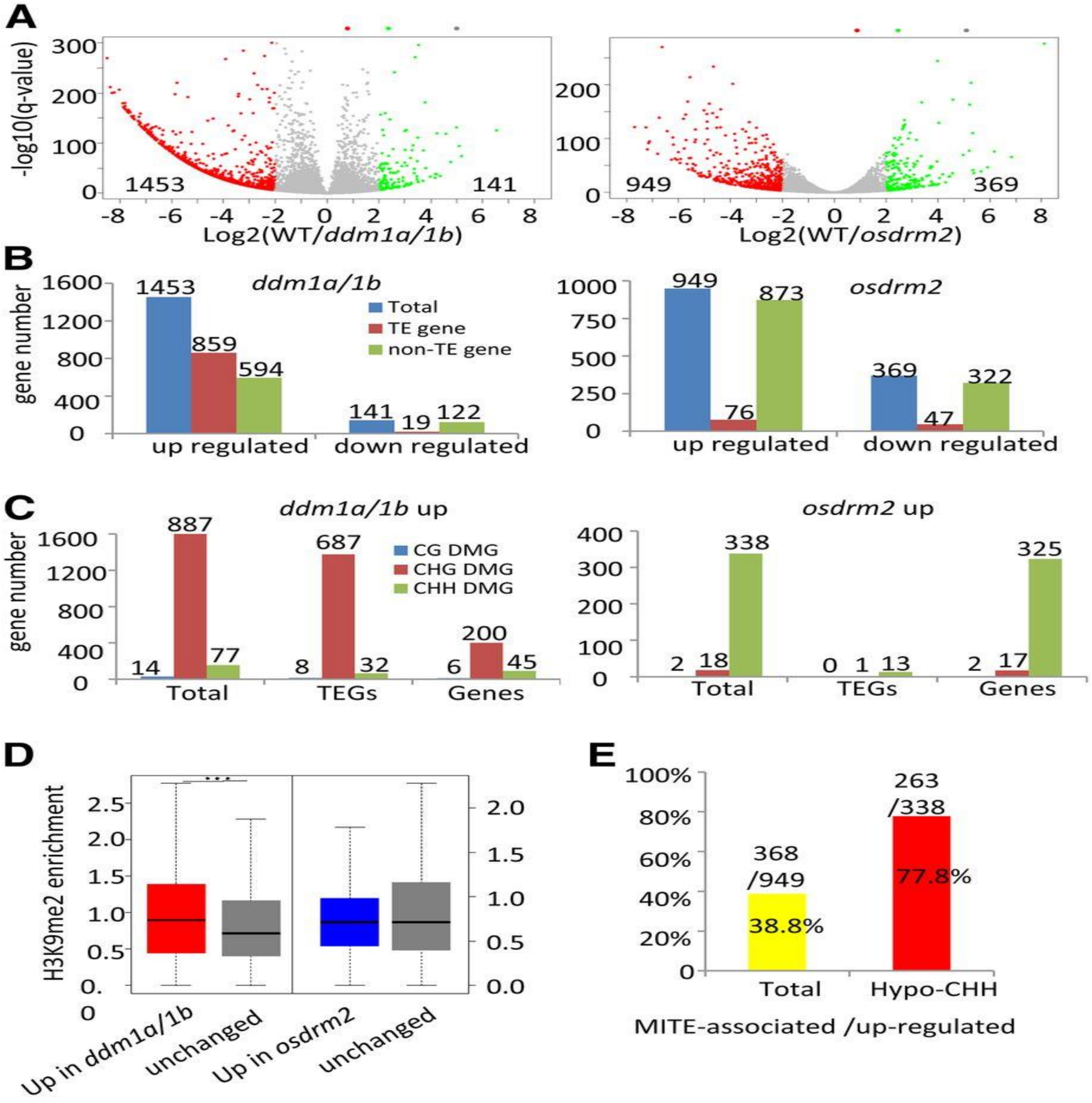


DMCs：differentially methylated cytosines

DMRs：differentially methylated regions

DMGs：differentially methylated genes

# **Differentially expressed protein-coding genes and TEGs in osddm1a/1b and osdrm2 mutants.**



总结：

*水稻中失去DDM1和DRM2基因，在初代会产生很严重的表型，而在拟南芥中初代并没有什么表型。*

未解决的问题：
CHH在常染色质中反而增加，这一点文中并没有解释为什么。

在后面研究与MITE相关的基因也没具体说哪些基因。

不足：
文章老围绕一个话题在那里反过来覆过去的讨论，图形比较单一。

# 谢谢