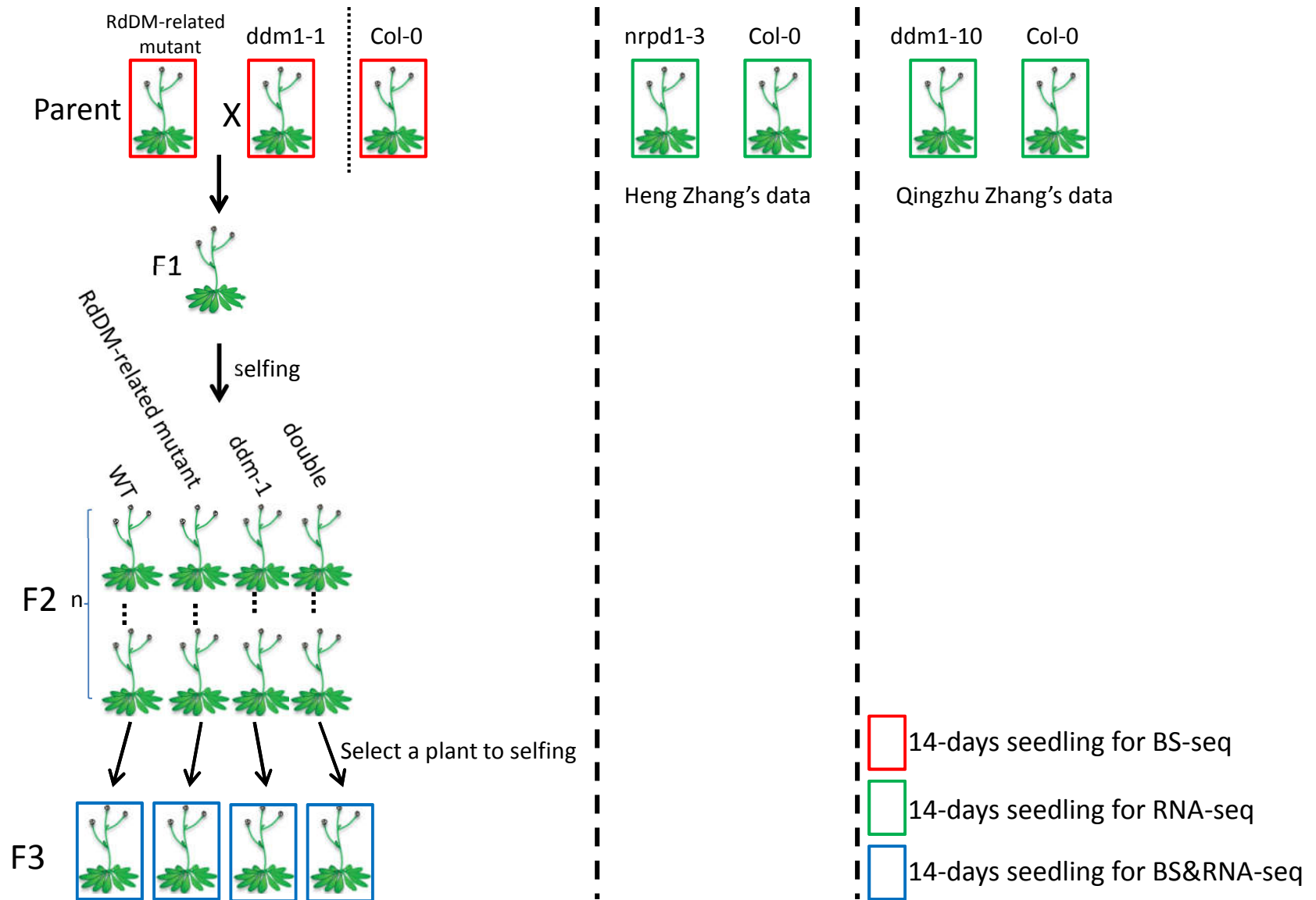
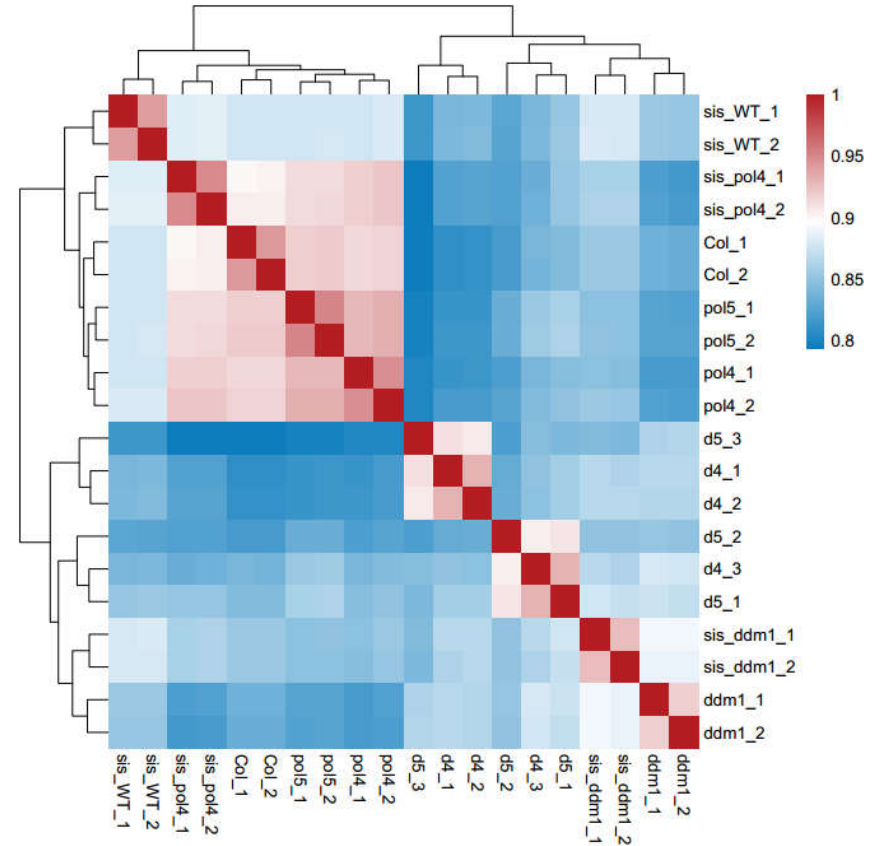
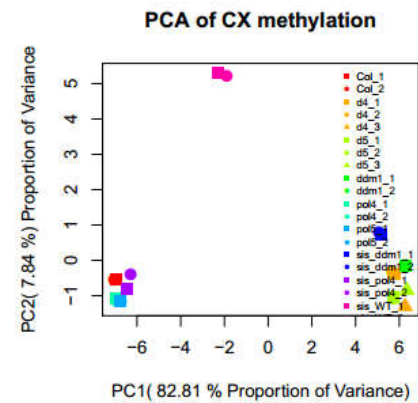
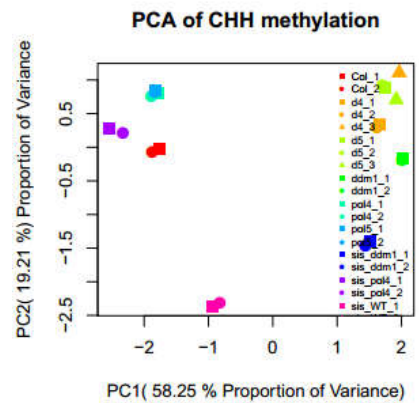
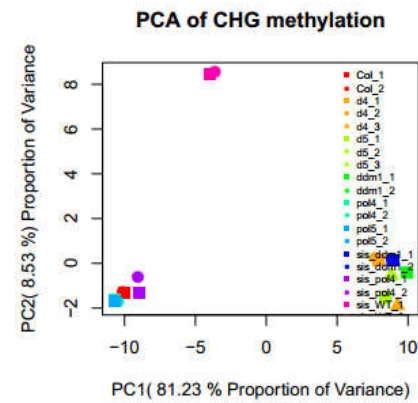
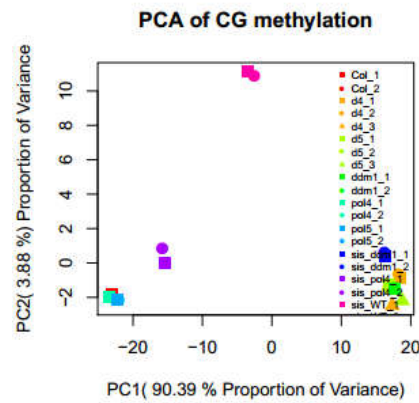


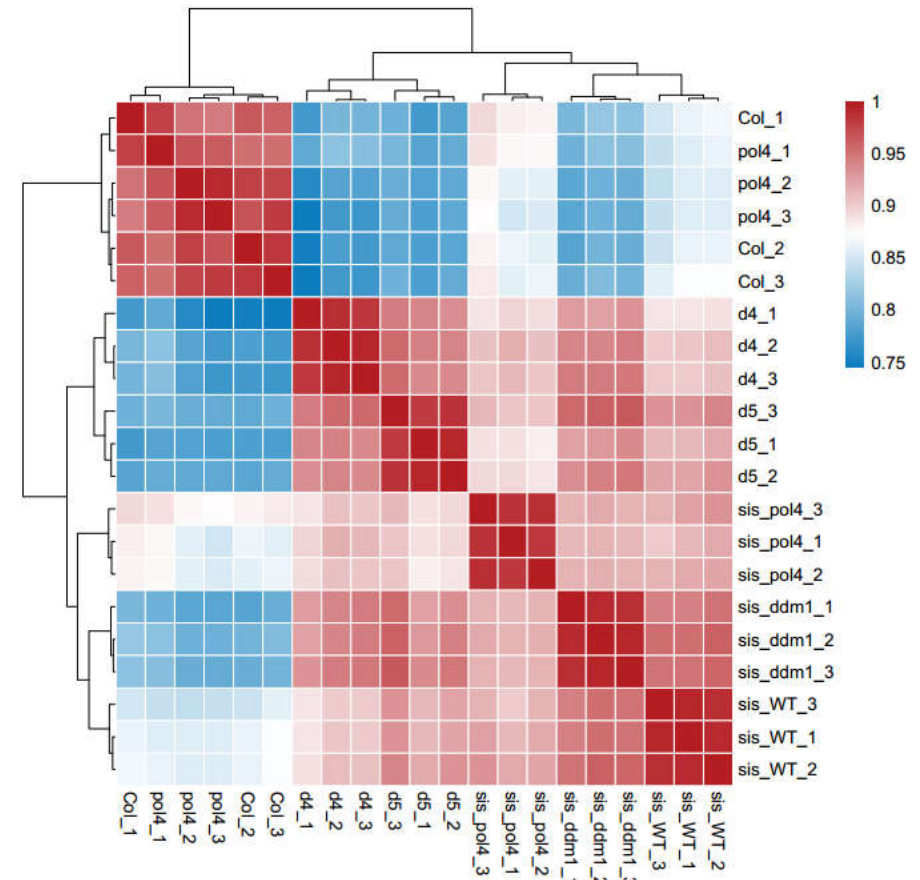
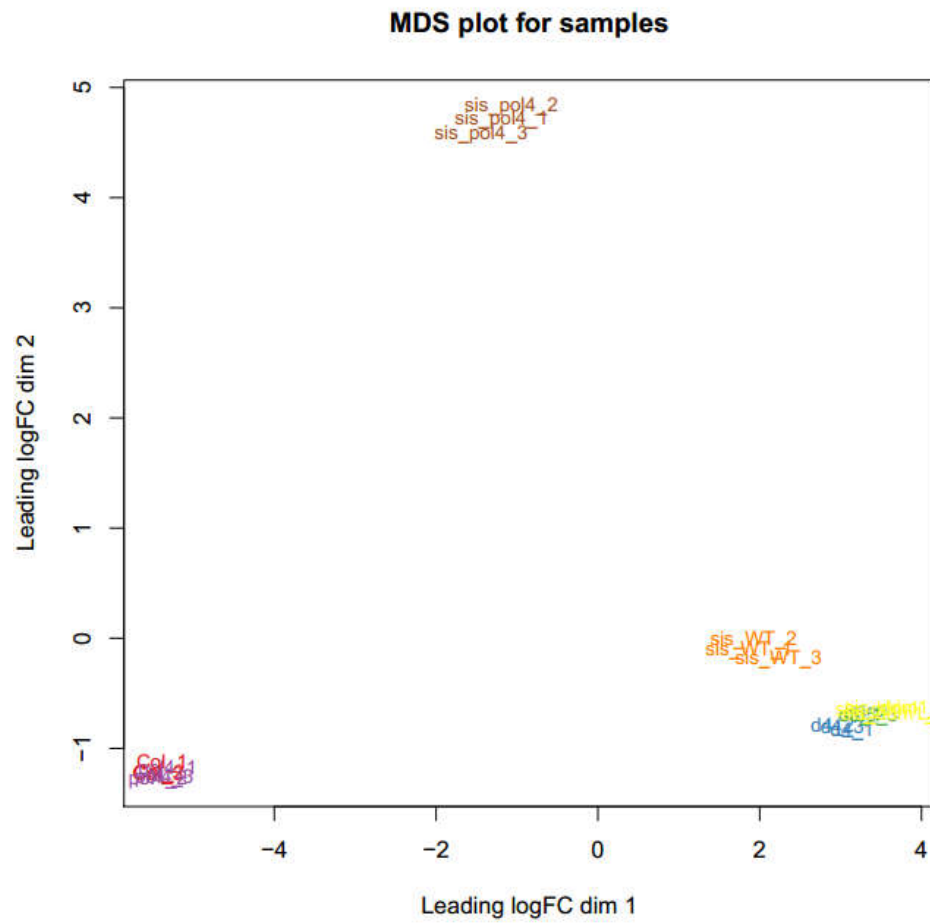
# Materials were used to BS and RNA sequencing



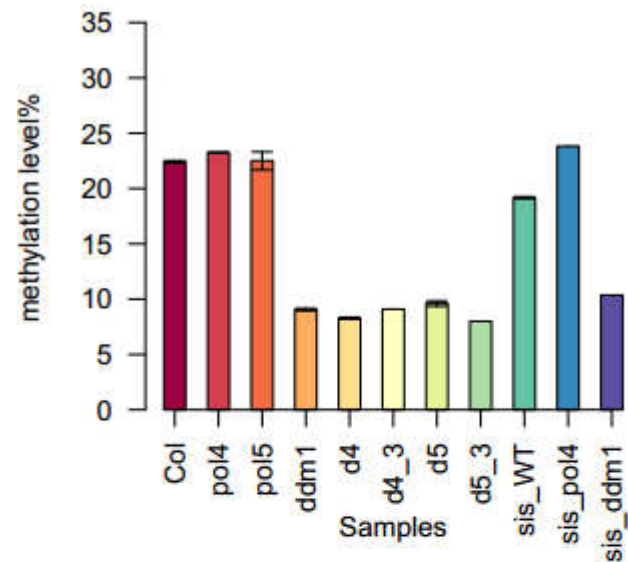
# PCA of BS-Seq samples



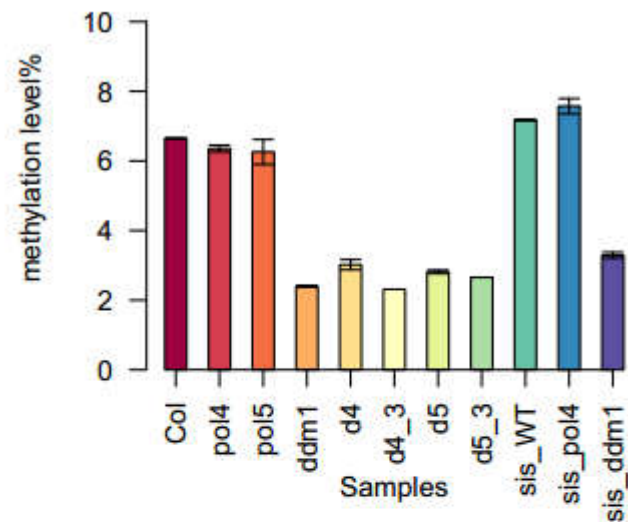
## PCA of BS-Seq samples



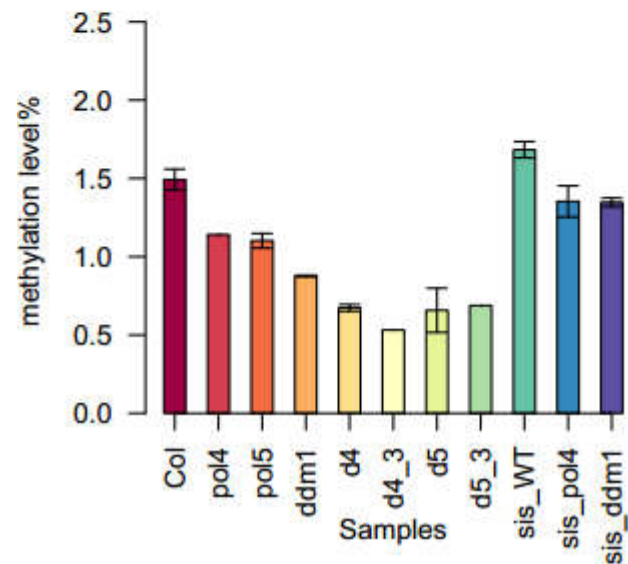
**Total\_region\_CG\_methylation**



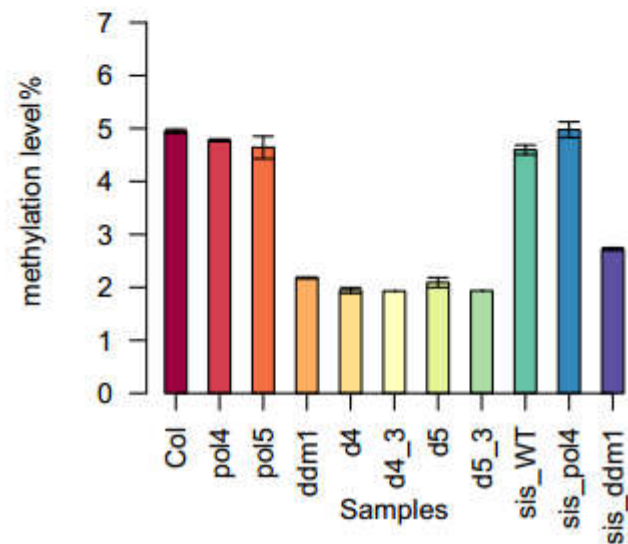
**Total\_region\_CHG\_methylation**



**Total\_region\_CHH\_methylation**

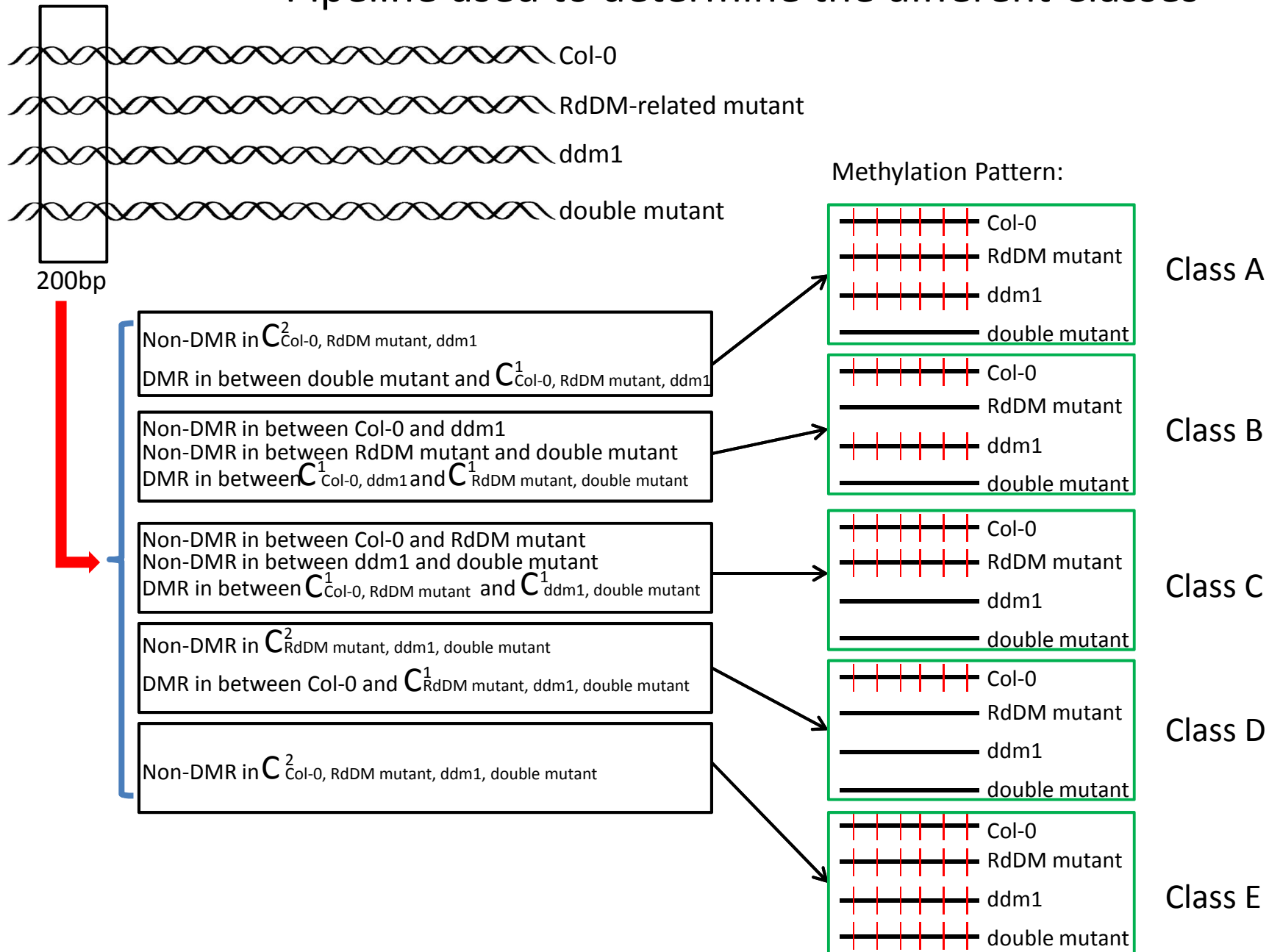


**Total\_region\_CX\_methylation**

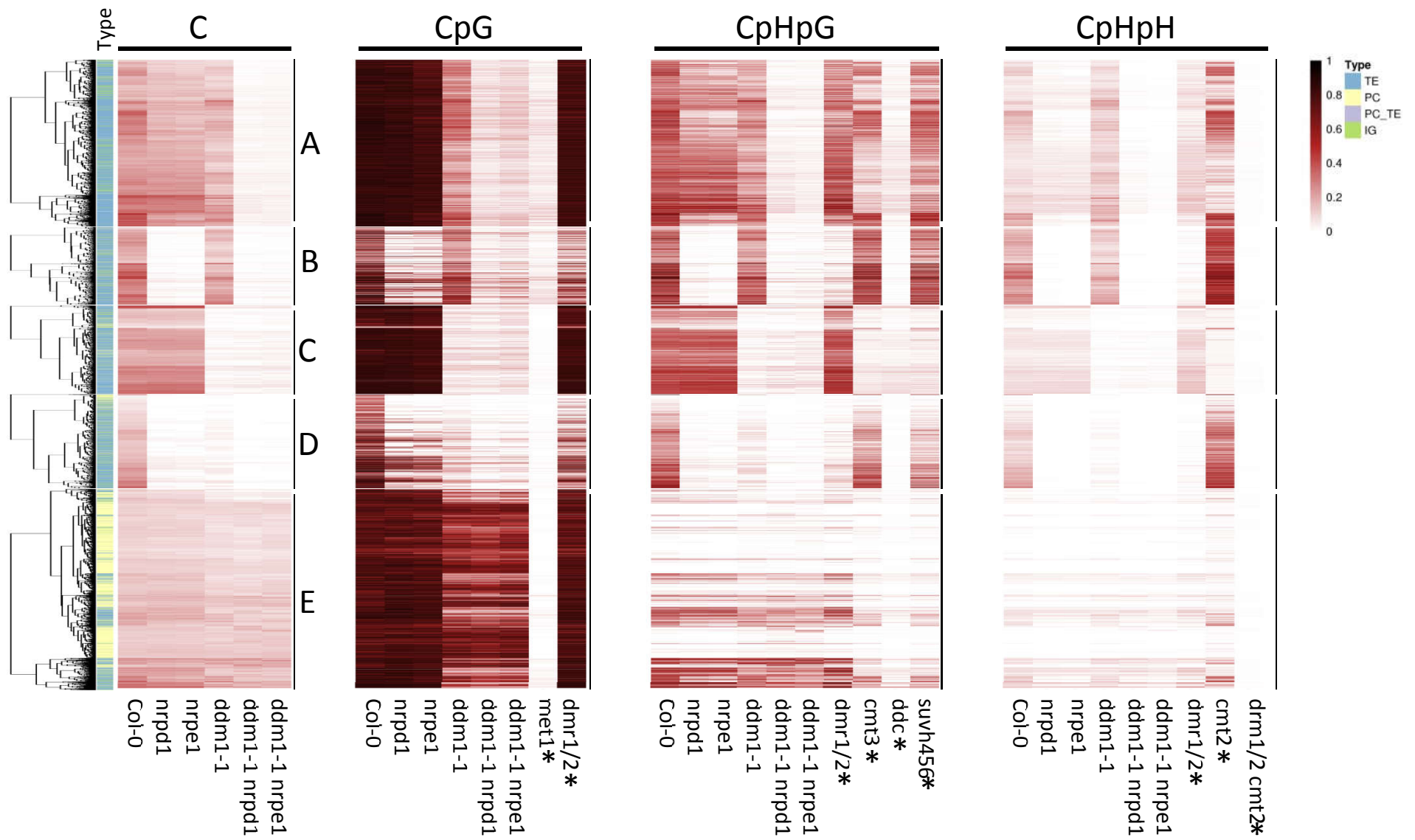


| sample     | average_depth |
|------------|---------------|
| Col_1      | 16.909        |
| Col_2      | 16.767        |
| d4_1       | 13.711        |
| d4_2       | 12.01         |
| d4_3       | 12.017        |
| d5_1       | 11.489        |
| d5_2       | 17.357        |
| d5_3       | 13.632        |
| ddm1_1     | 14.699        |
| ddm1_2     | 15.995        |
| pol4_1     | 13.476        |
| pol4_2     | 16.889        |
| pol5_1     | 18.122        |
| pol5_2     | 15.821        |
| sis_WT_1   | 13.001        |
| sis_WT_2   | 12.512        |
| sis_ddm1_1 | 13.195        |
| sis_ddm1_2 | 12.557        |
| sis_pol4_1 | 12.589        |
| sis_pol4_2 | 13.183        |

# Pipeline used to determine the different Classes



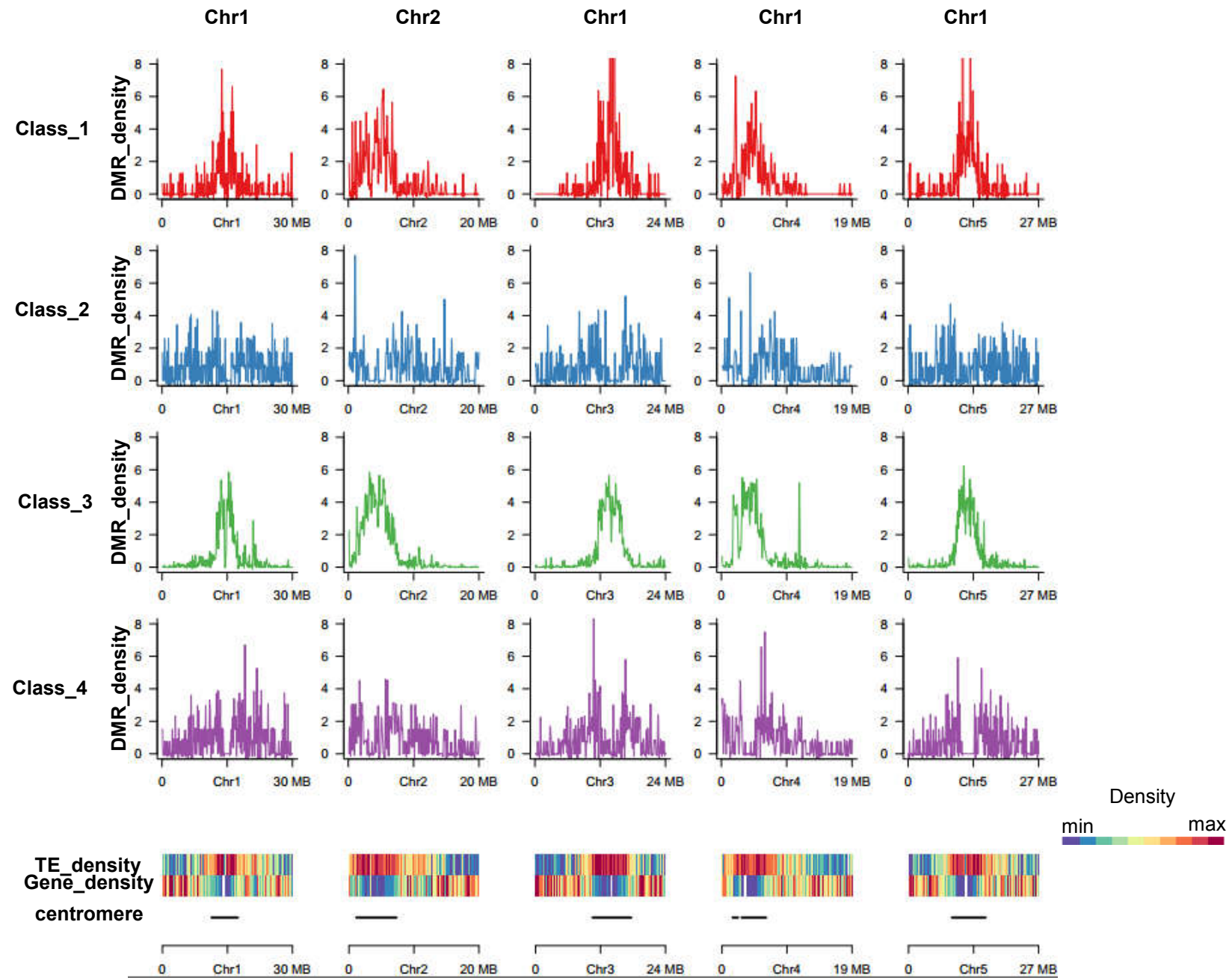
## Characterization of different Classes



\* : Jacobsen's data

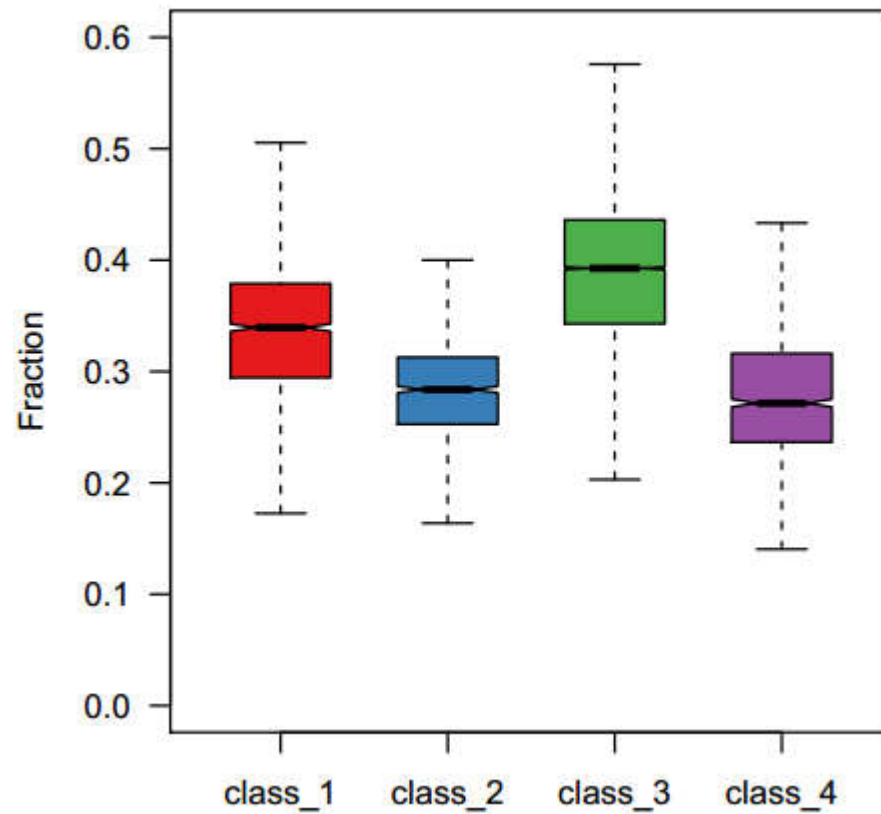


# Distribution of the region density of different Classes over chromosomes

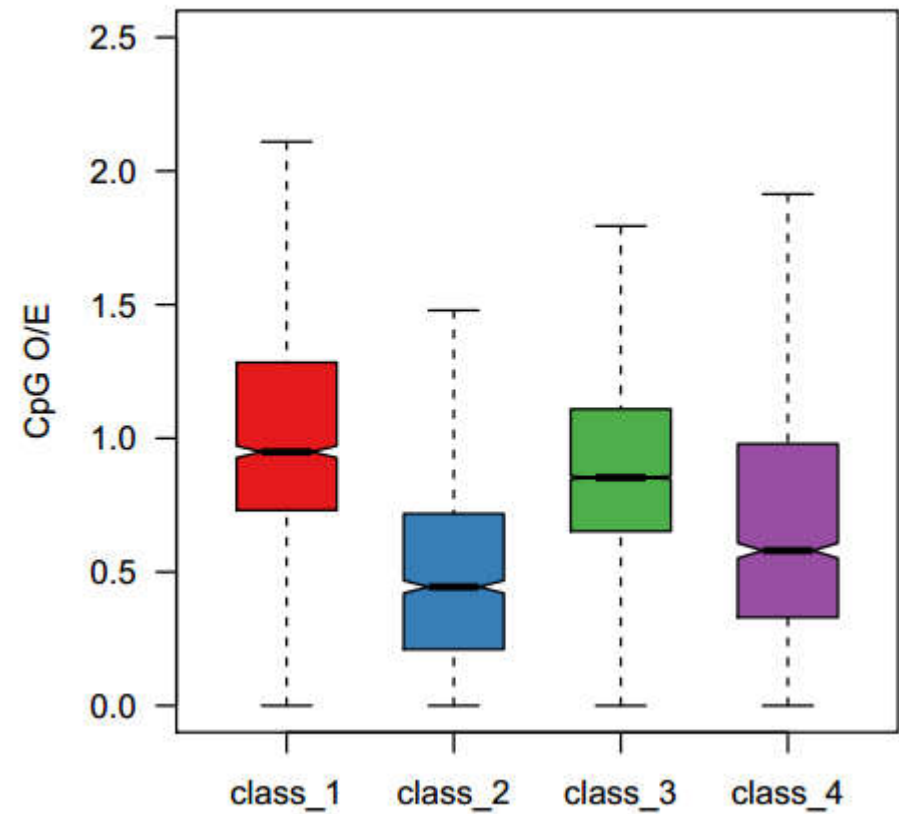


## Features of Classes

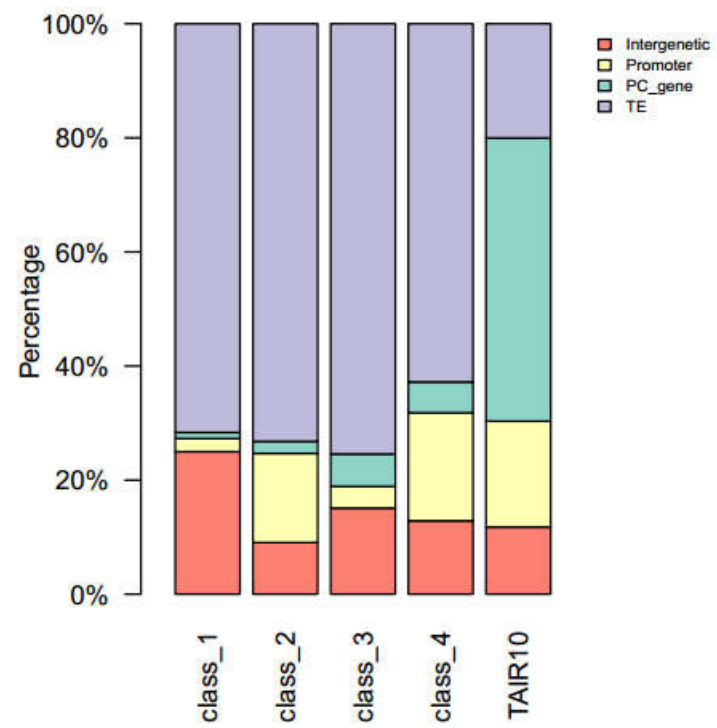
**G+C content in DMR**

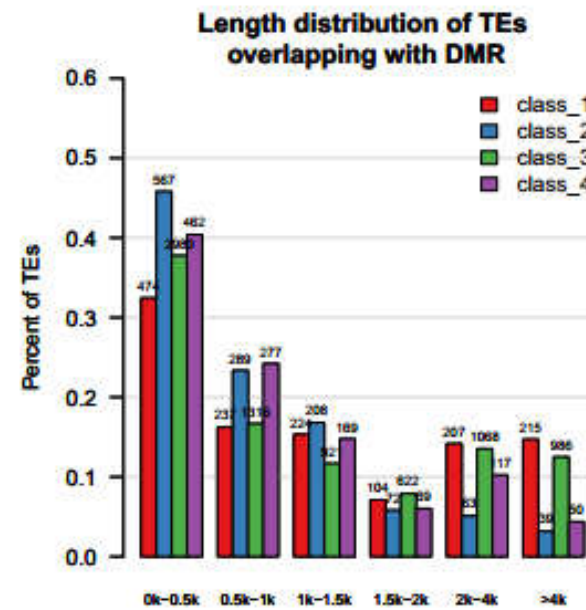
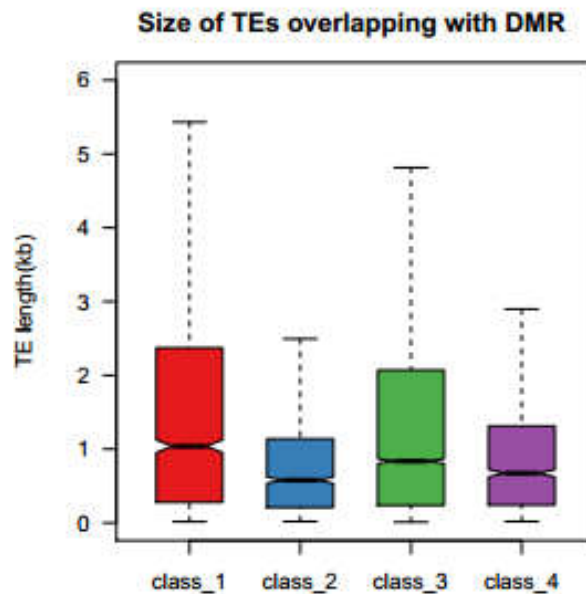
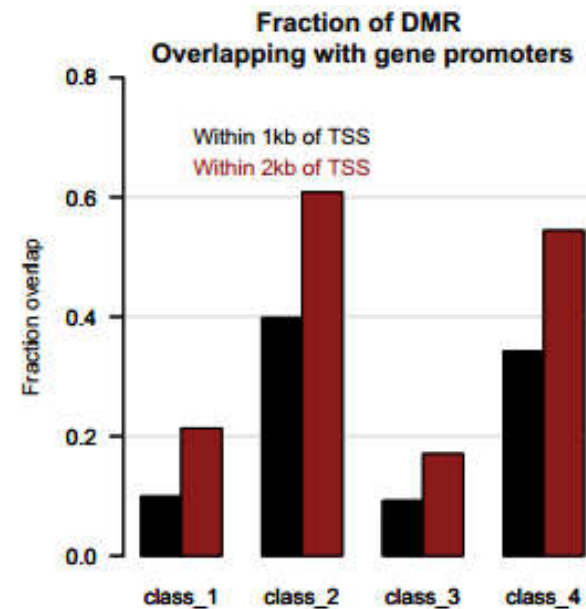
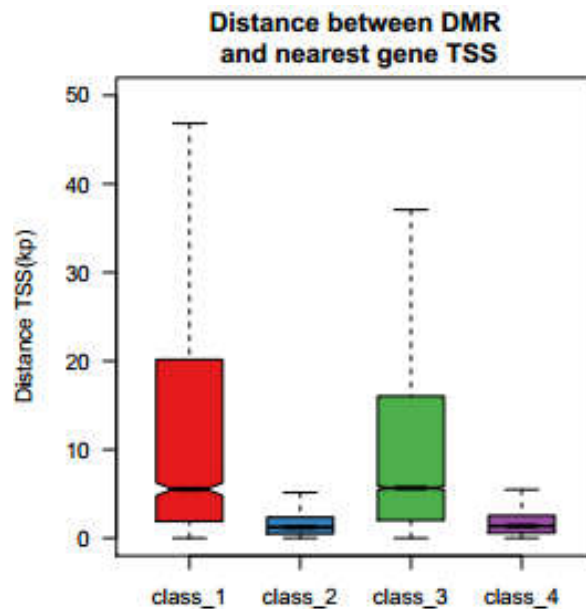


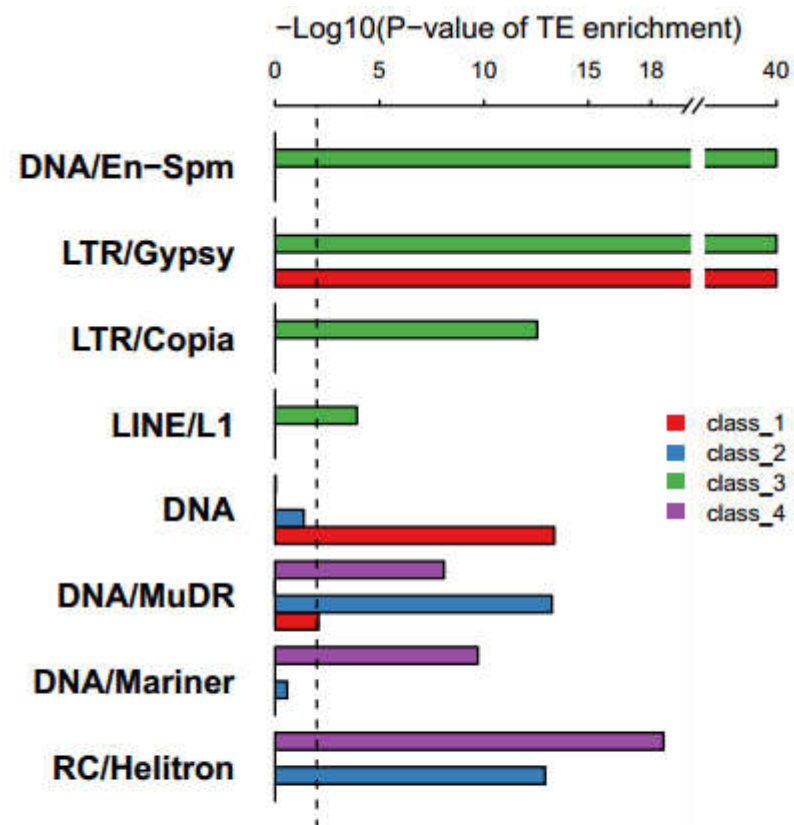
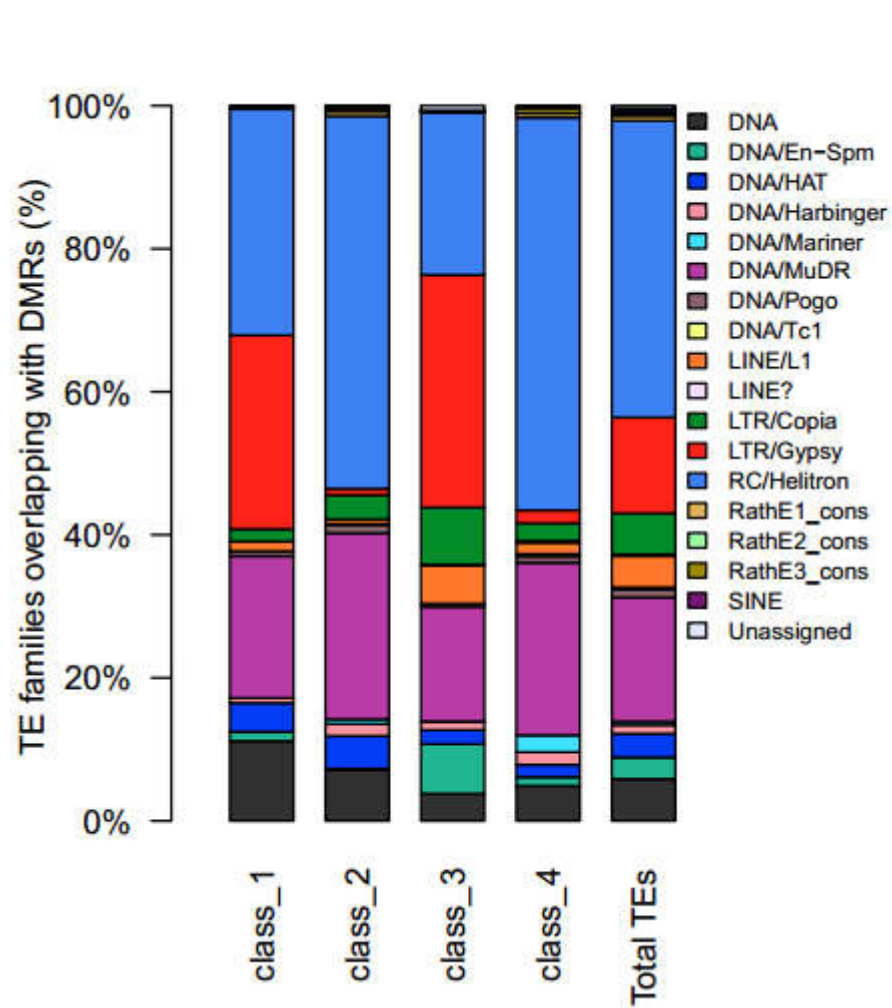
**CpG content in DMR**



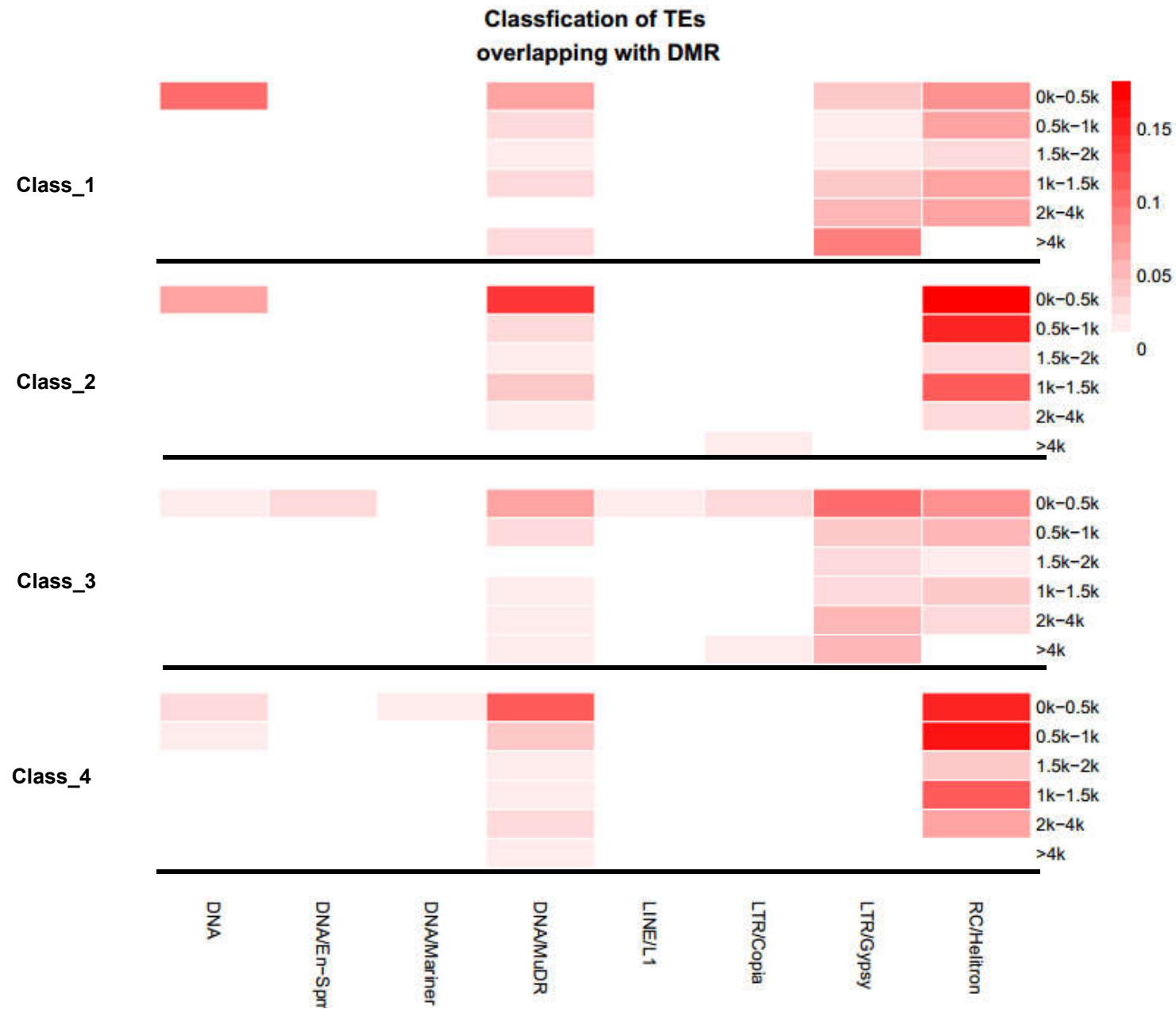




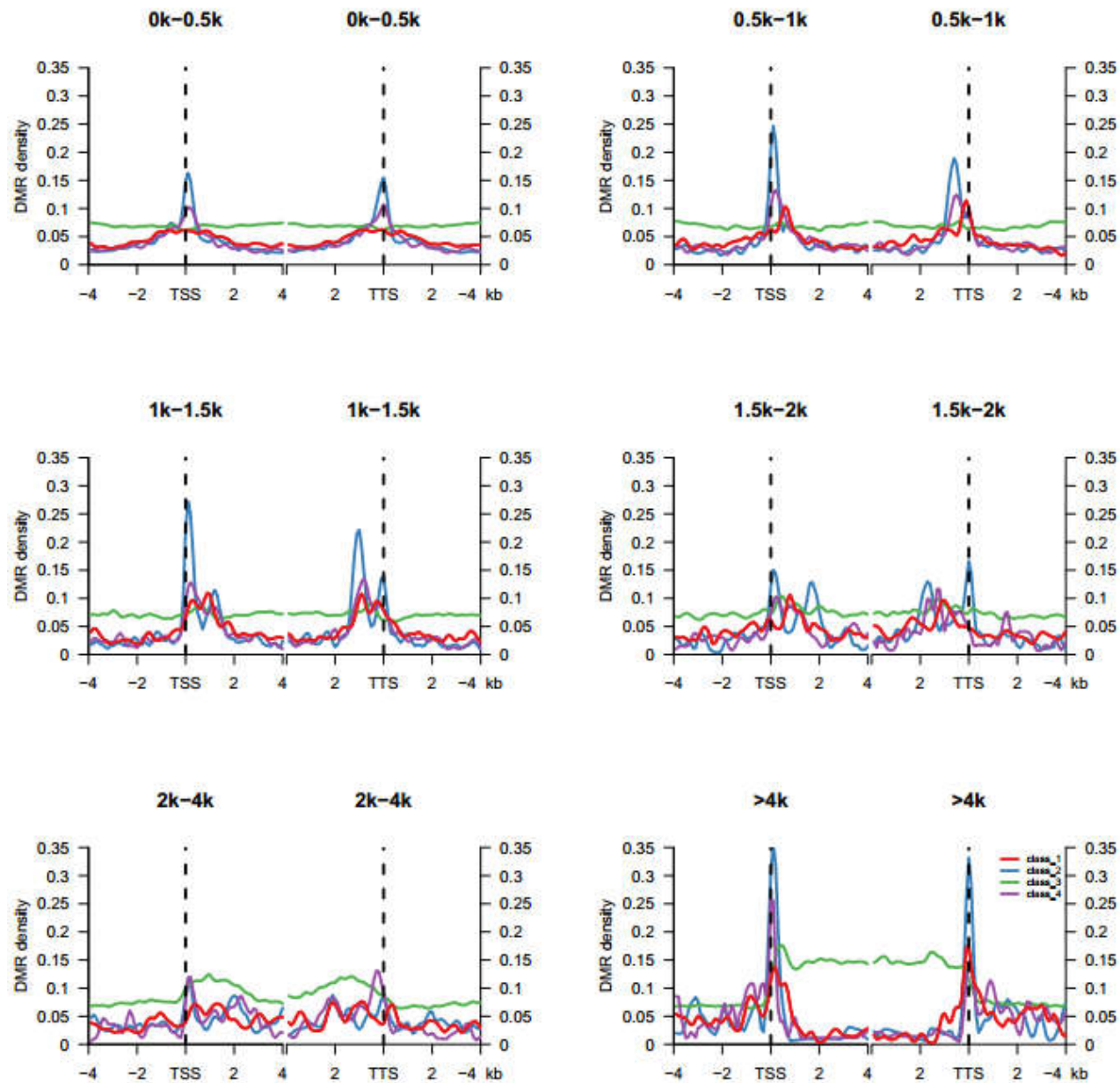




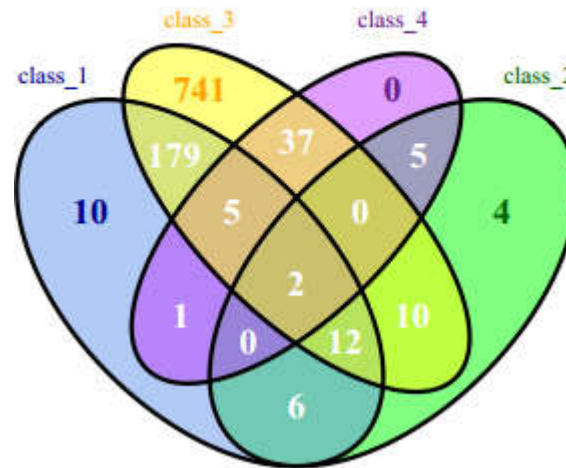
## Distribution of classes density over different TE element of length



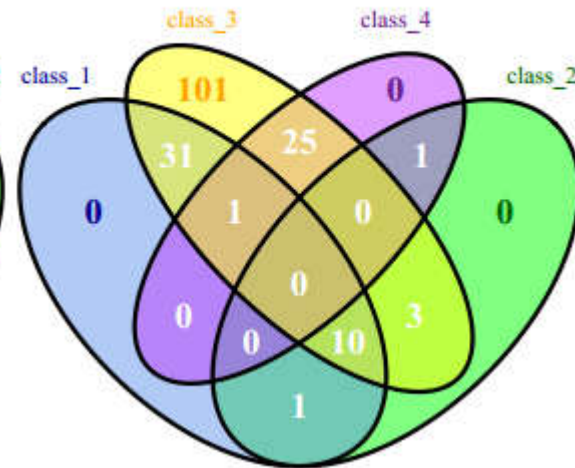
## Distribution of classes density over different TE element of length



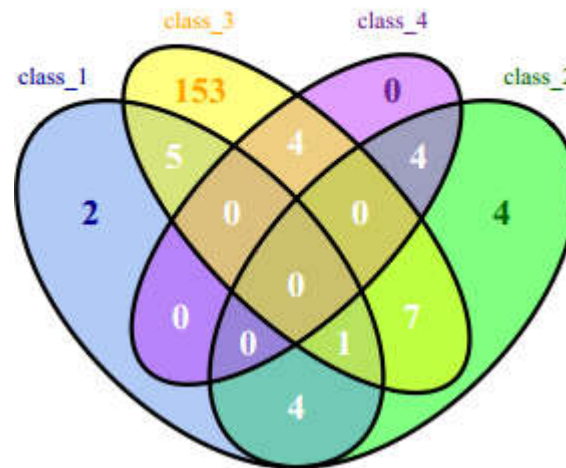
Overlaps of  
associated TEs(>4kb)



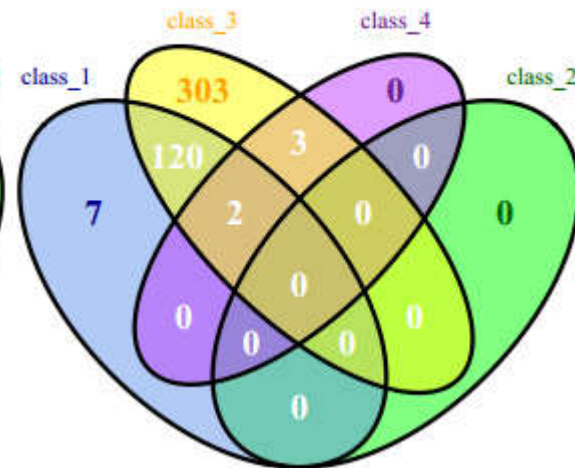
DNA/MuDR, Overlaps of  
associated TEs(>4kb)



LTR/Copia, Overlaps of  
associated TEs(>4kb)

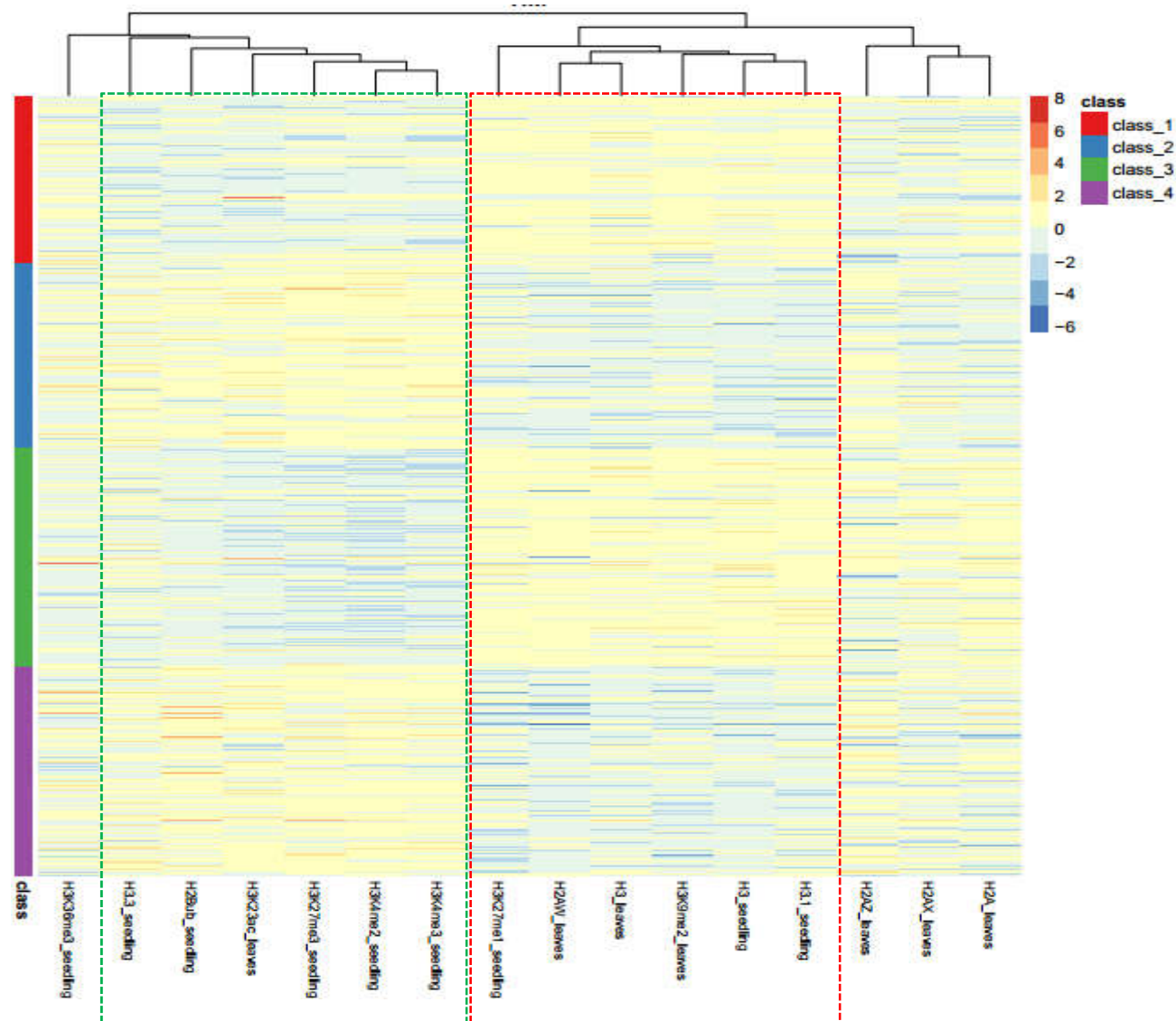


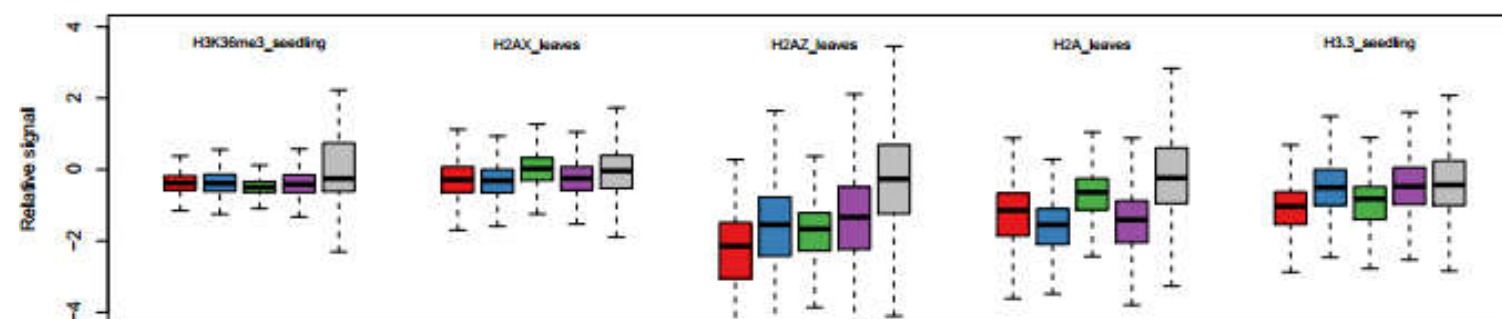
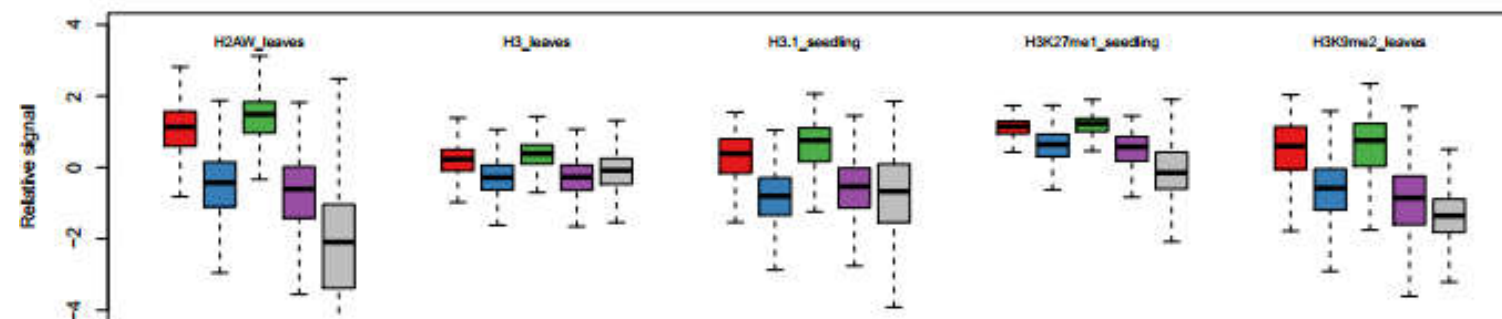
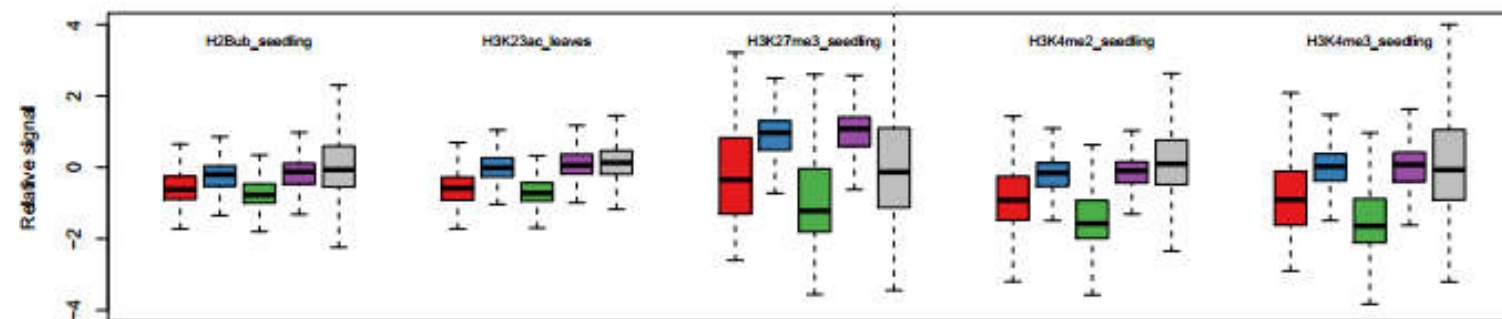
LTR/Gypsy, Overlaps of  
associated TEs(>4kb)





## Hierarchical clustering of histone modification signals from genomic regions of different classes

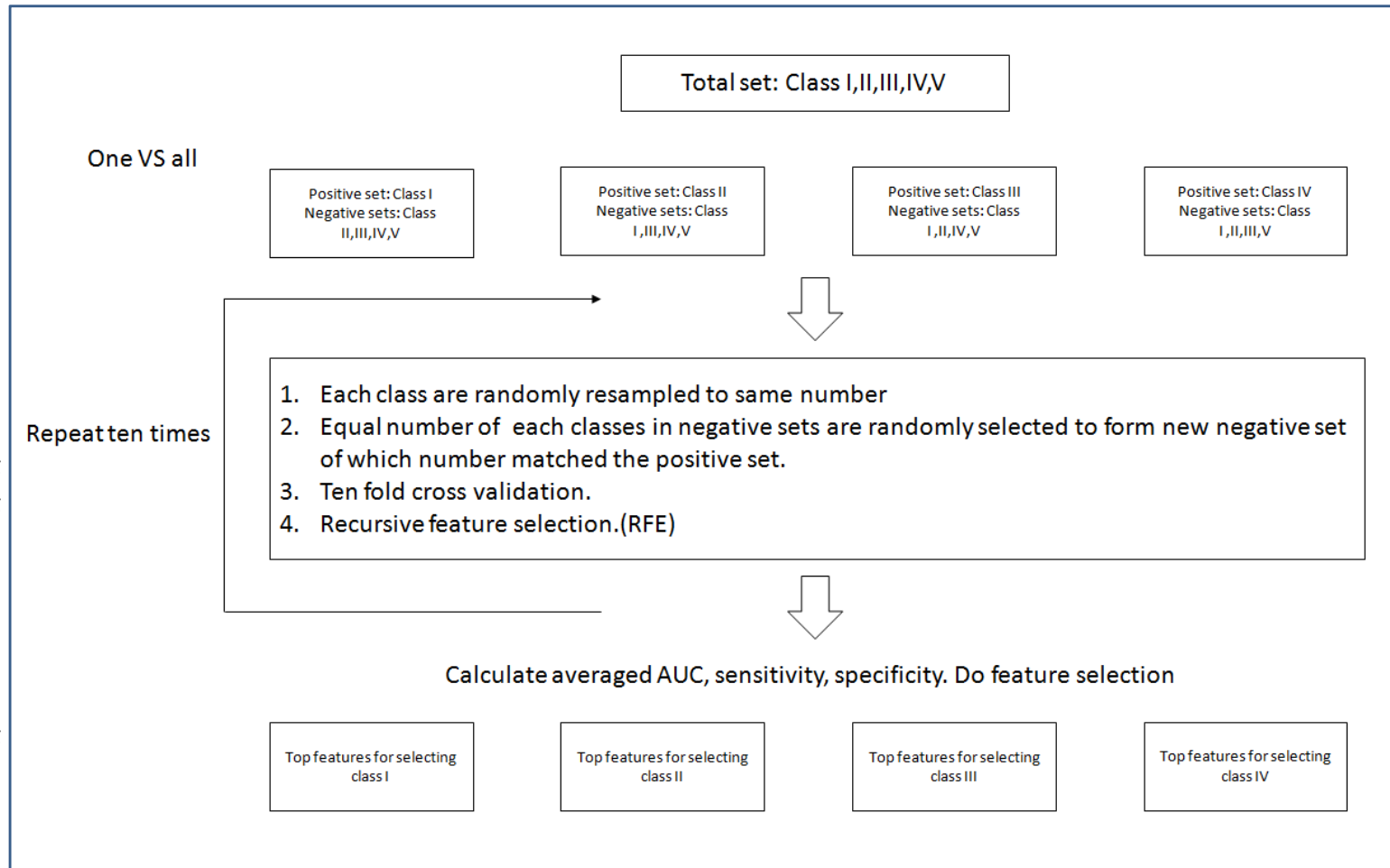




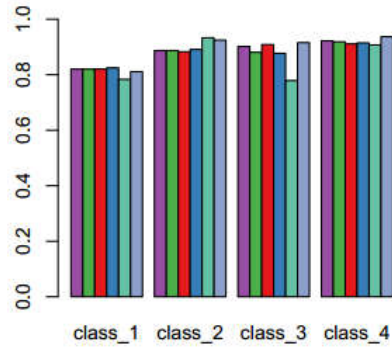
class\_1 class\_2 class\_3 class\_4 Simulation

# Pipeline used to machine learning

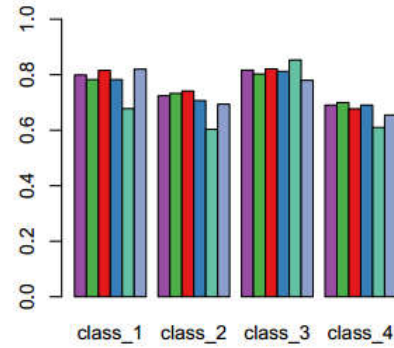
H3K23ac\_leaves  
 H3K9Ac\_aerial  
 H3.3\_seedling  
 H2Bub\_seedling  
 H3K4me2\_seedling  
 WT\_H2AZ\_leaves  
 H3K36me2\_aerial  
 H3K18Ac\_aerial  
 H3K4me3\_seedling  
 WT\_H2AX\_leaves  
 WT\_H2A\_leaves  
 H3K27me3\_seedling  
 H3K36me3\_seedling  
 G+C\_content  
  
 H3\_seedling  
 CpG\_0\_E  
 H3.1\_seedling  
 H3K27me1\_seedling  
 WT\_H2AW\_leaves  
 H3K9me2\_leaves  
 H3K9me2\_aerial.1



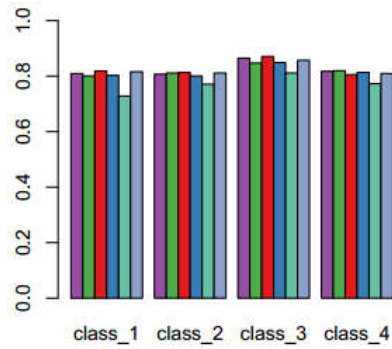
**Sensitivity statistic of predictor**



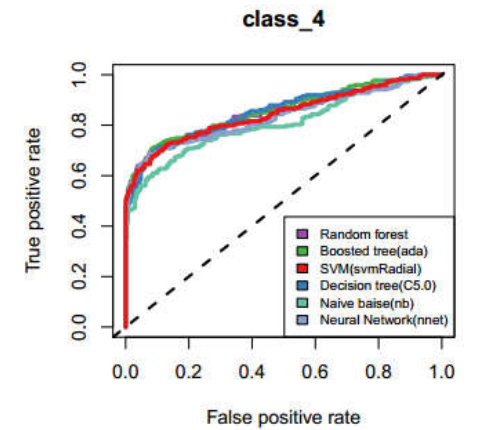
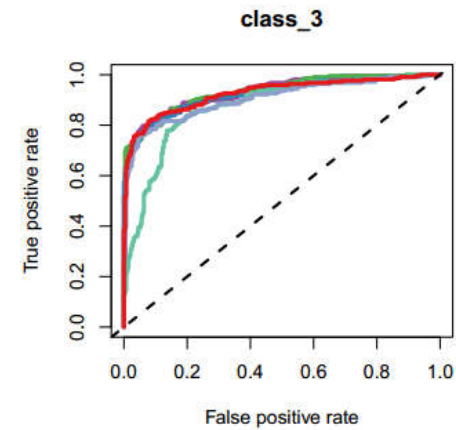
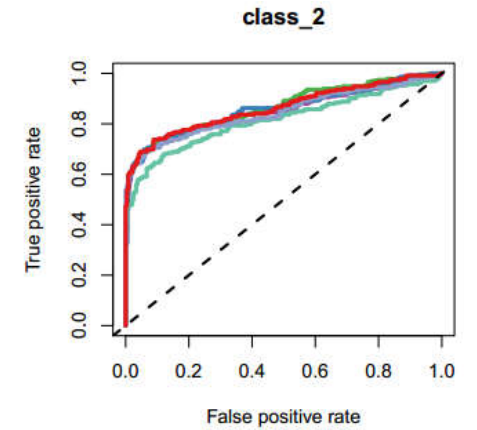
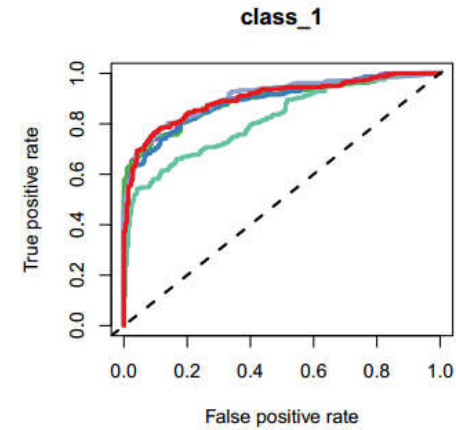
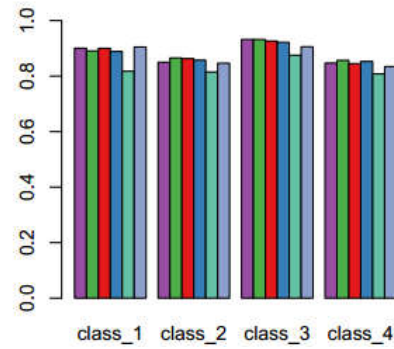
**Specificity statistic of predictor**



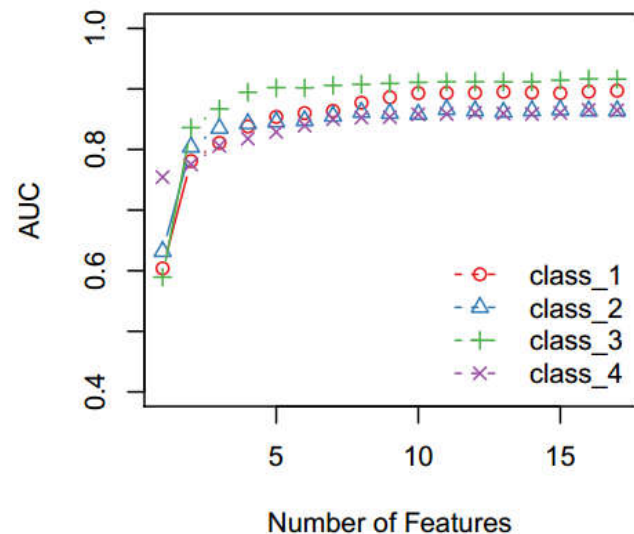
**Accuracy statistic of predictor**



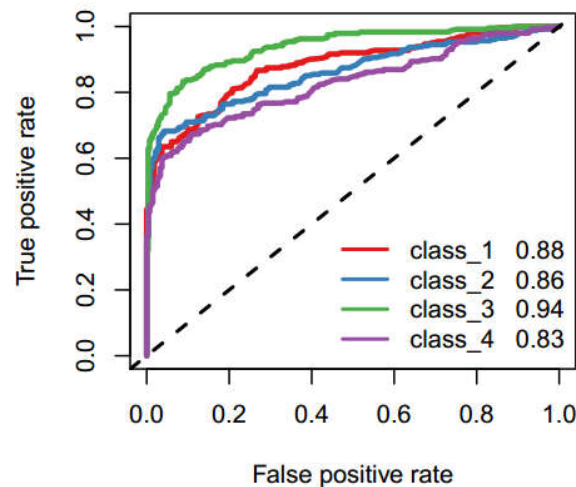
**AUC statistic of predictor**



# Different classes were predicted by various group of features



ROC curve for SVM(svmRadial,RFE)



AUC: area under receiver operating characteristic curve

| ID                | class_1_rank | class_2_rank | class_3_rank | class_4_rank |
|-------------------|--------------|--------------|--------------|--------------|
| CpG               | 1            | 1            | 1            | 7            |
| H2AW_leaves       | 2            | 3            | 2            | 1            |
| H3.1_seedling     | 3            | 2            | 3            | 16           |
| H2AZ_leaves       | 4            | NA           | 12           | 2            |
| H3K9me2_leaves    | 5            | 10           | 16           | 5            |
| H3K27me1_seedling | 6            | NA           | 14           | 3            |
| H3.3_seedling     | 7            | 4            | 8            | 10           |
| H3K4me2_seedling  | 8            | NA           | 4            | 8            |
| GC_contend        | 9            | 6            | 5            | 6            |
| H3K23ac_leaves    | 10           | 7            | 10           | 4            |
| H3_seedling       | 11           | 5            | 7            | 9            |
| H3K27me3_seedling | 12           | 9            | 11           | 11           |
| H2AX_leaves       | 13           | NA           | 9            | 15           |
| H3K4me3_seedling  | 14           | 11           | 6            | 13           |
| H2A_leaves        | 15           | 8            | 13           | 14           |
| H3K36me3_seedling | 16           | NA           | 15           | NA           |
| H2Bub_seedling    | 17           | NA           | NA           | 12           |

## Top 5 feature

### Class 1

CpG  
H2AW  
H3.1  
H2AZ  
H3K9me2

### Class 2

CpG  
H3.1  
H2AW  
H3.3  
H3

### Class 3

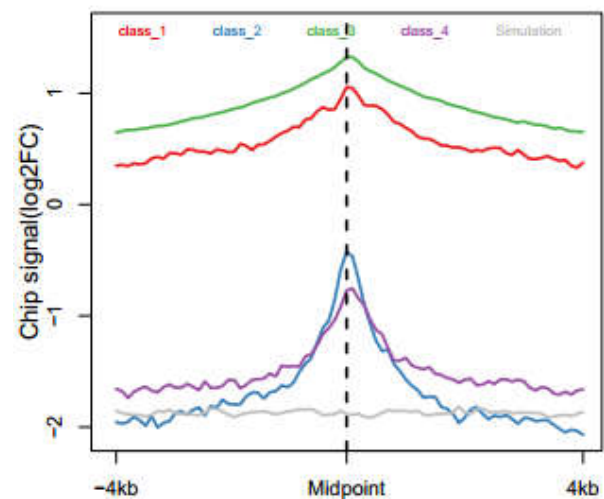
CpG  
H2AW  
H3.1  
H3K4me2  
GC\_contend

### Class 4

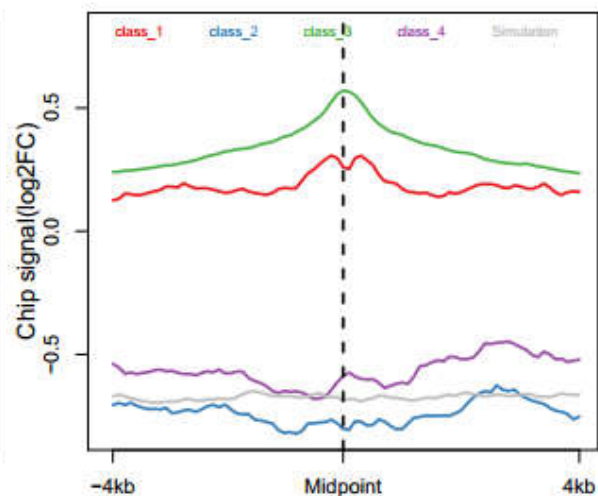
H2A.W  
H2AZ  
H3K27me1  
H3K23ac  
H3K9me2



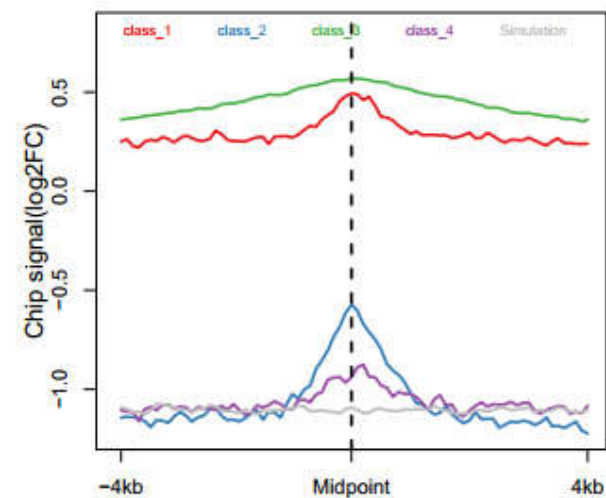
H2AW\_leaves



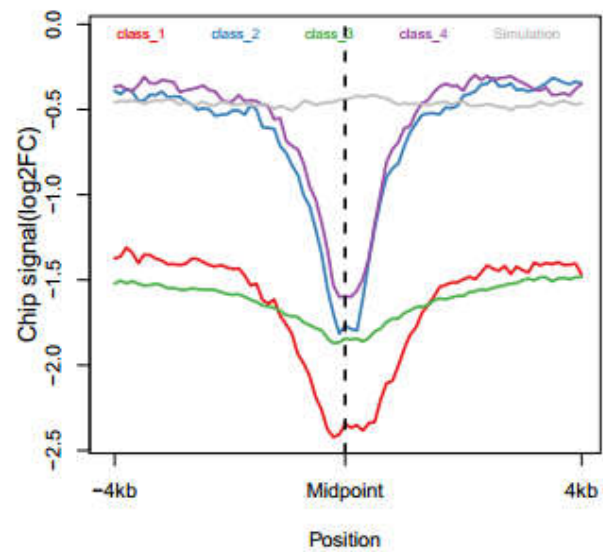
H3.1\_seedling



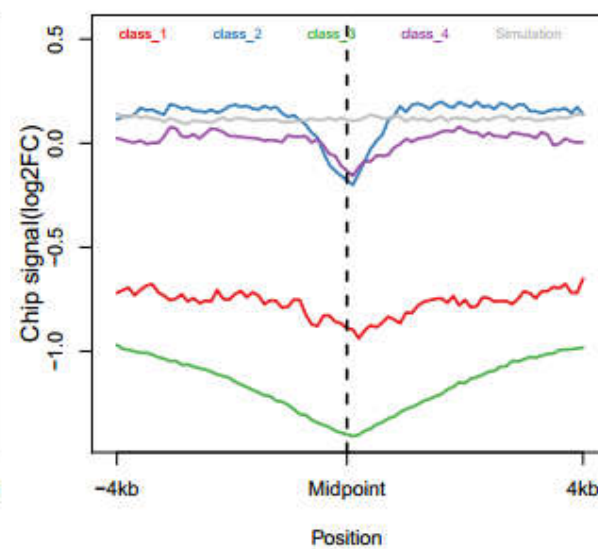
H3K9me2\_leaves



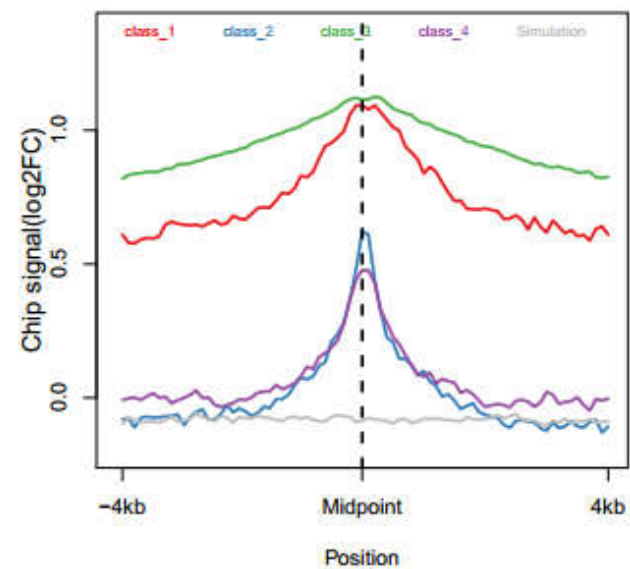
H2AZ\_leaves



H3K4me2\_seedling

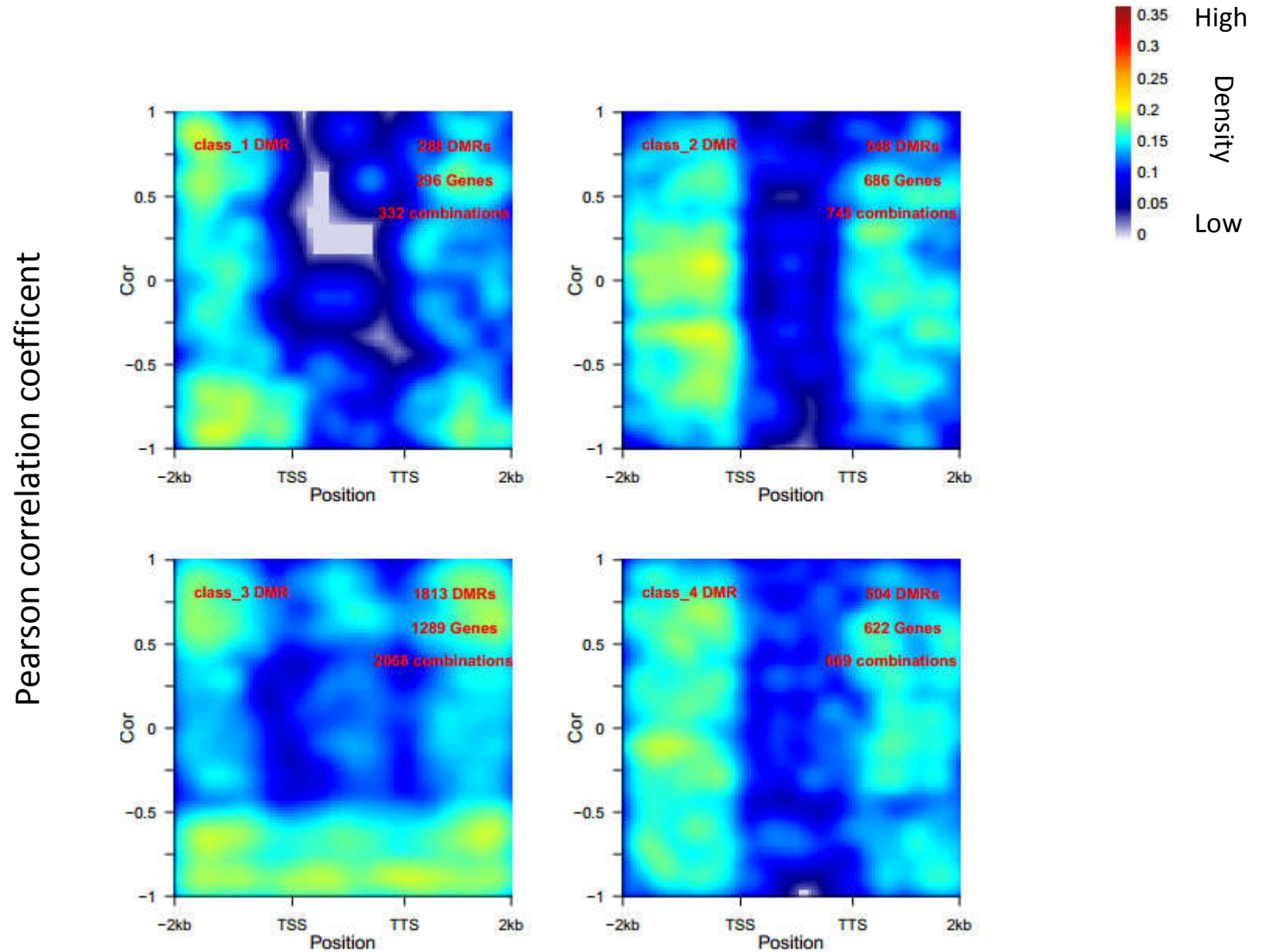


H3K27me1\_seedling

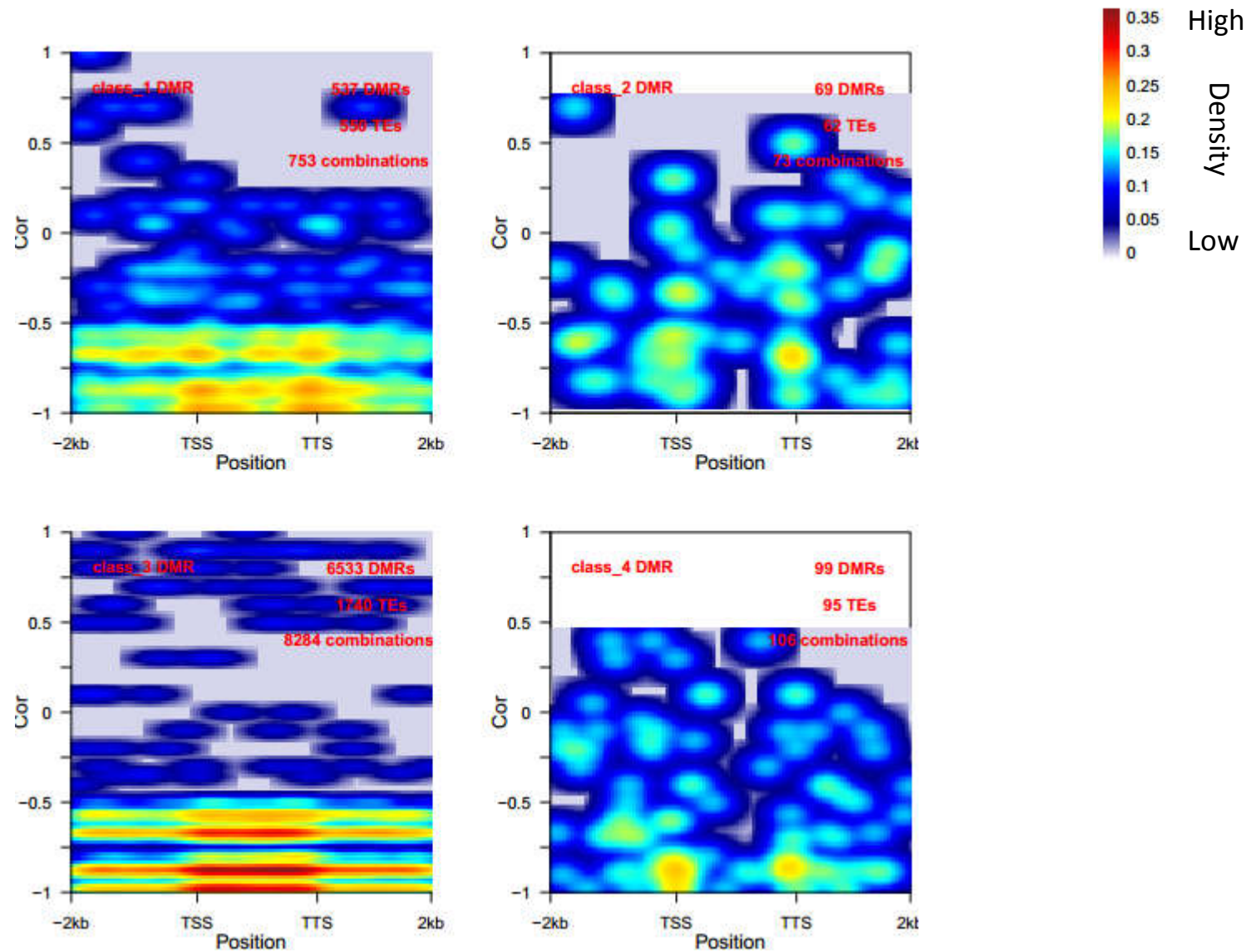




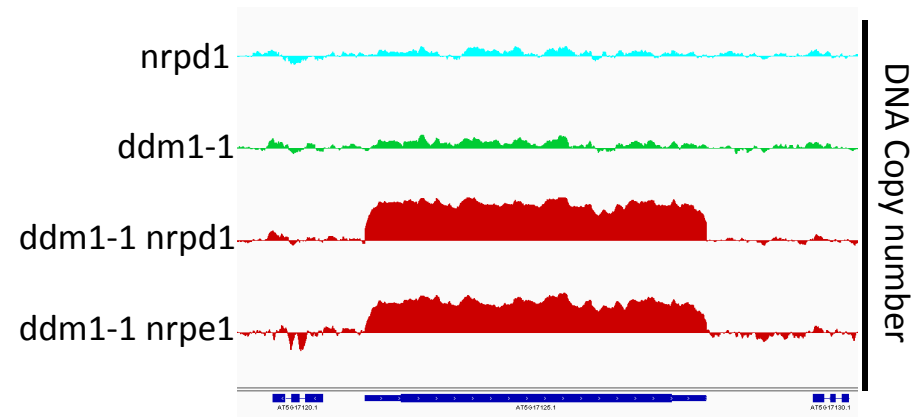
## Correlation between the methylation in DMRs and gene/TE expression levels



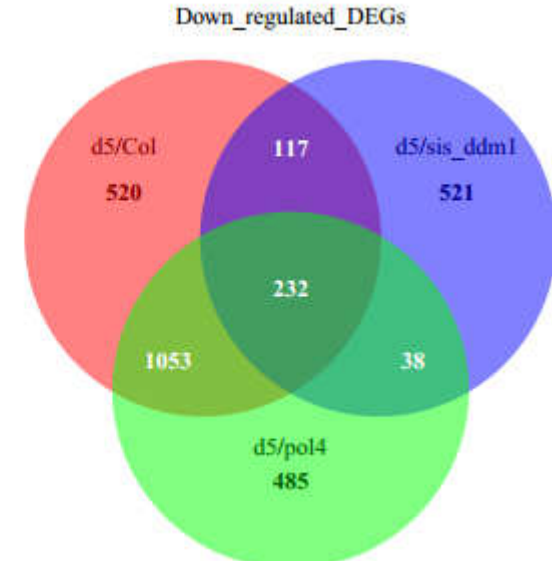
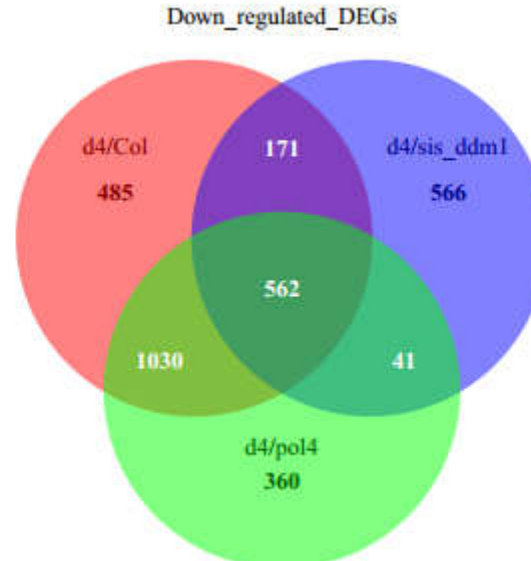
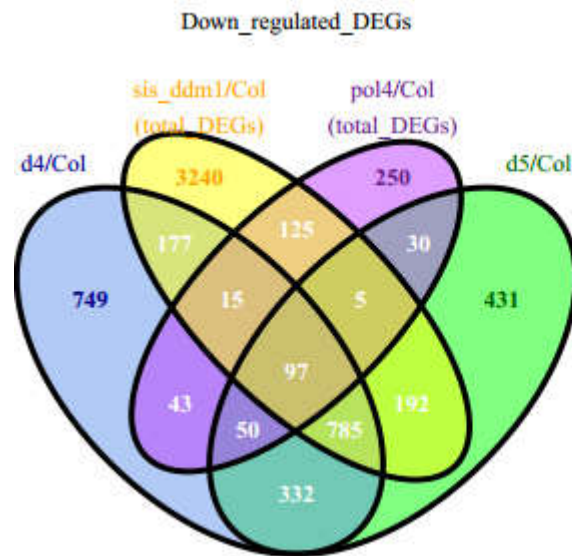
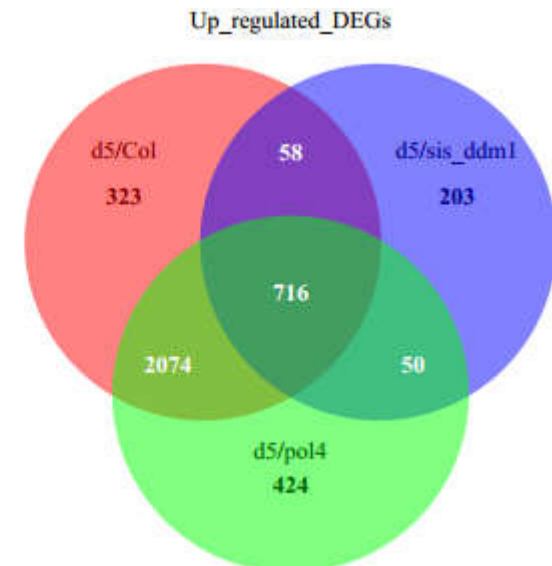
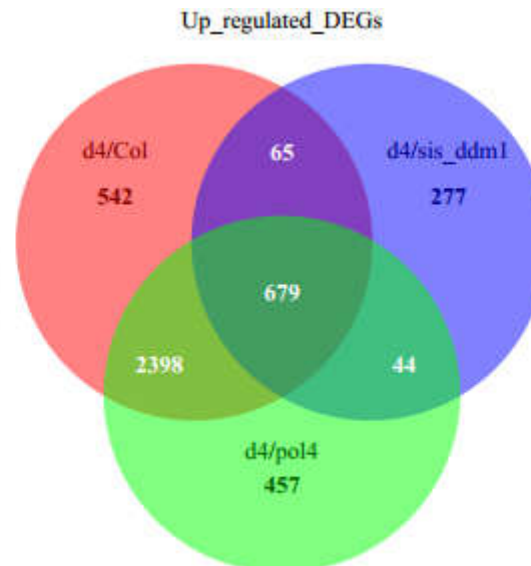
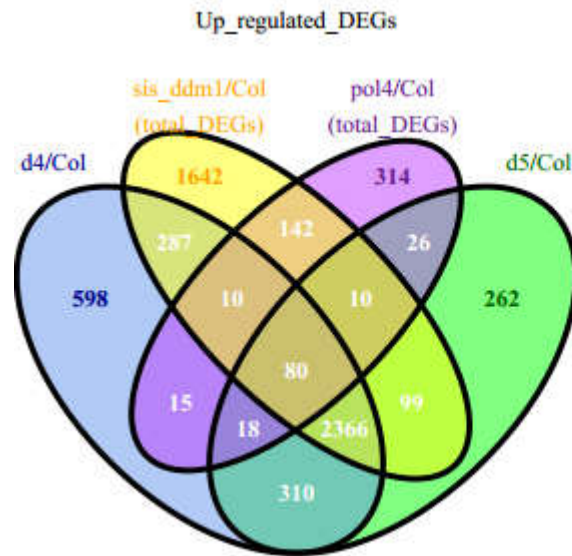
Pearson correlation coefficient



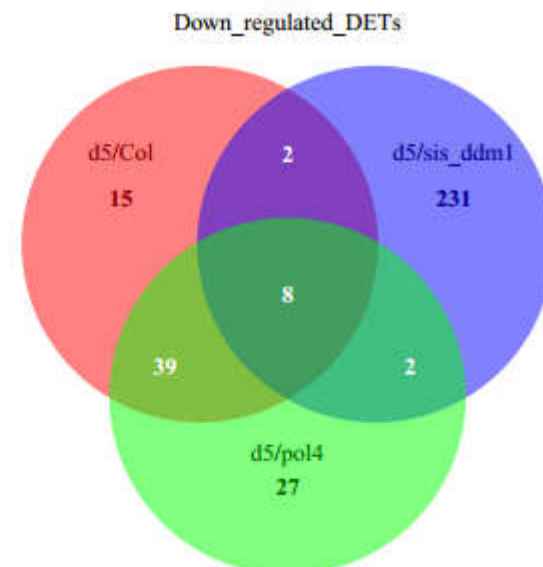
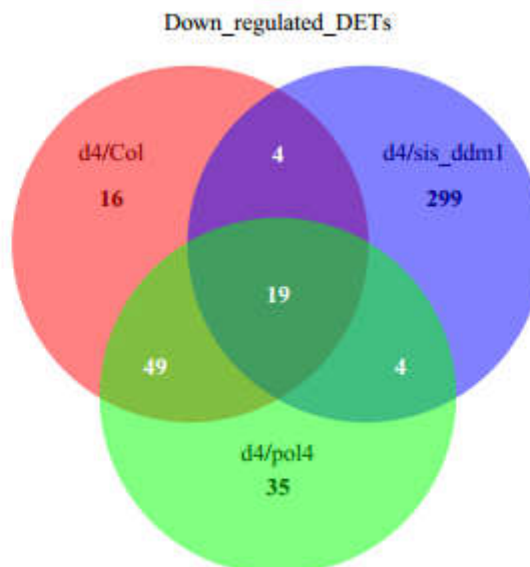
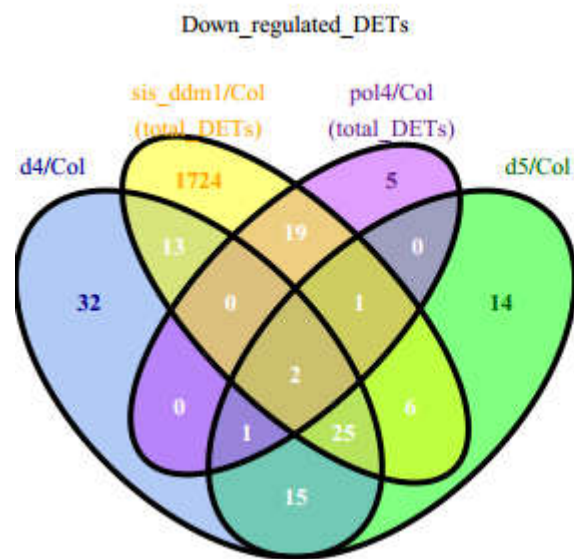
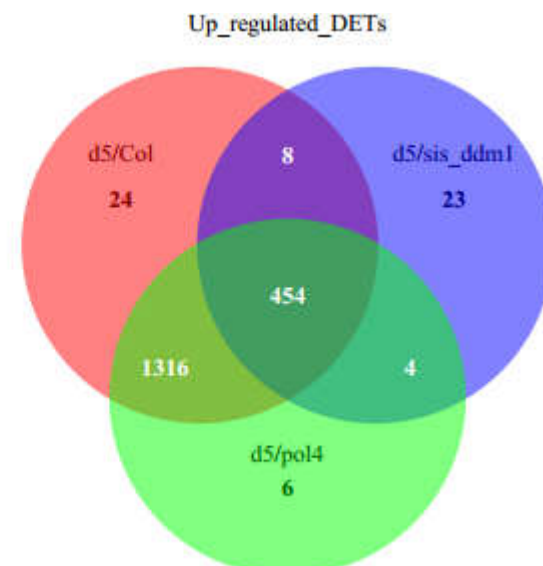
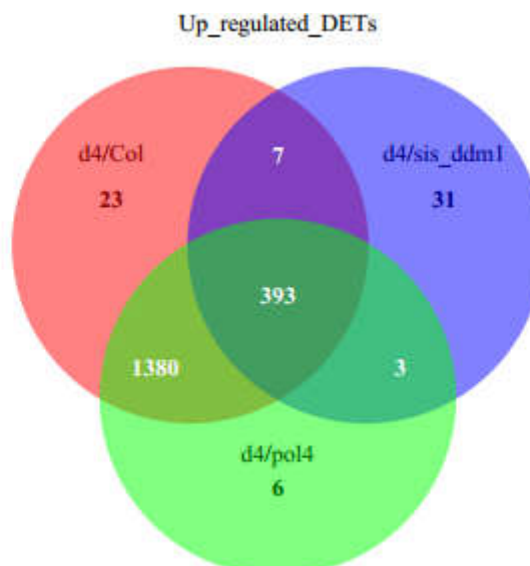
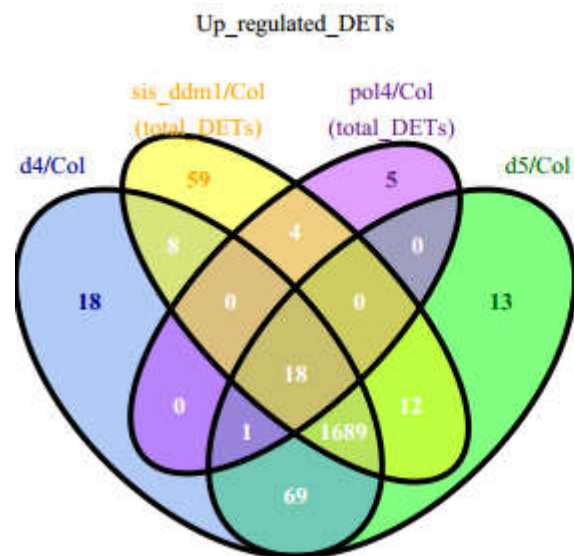
# DDM1 and RdDM Collaborate to Repress TE Expression and Transposition



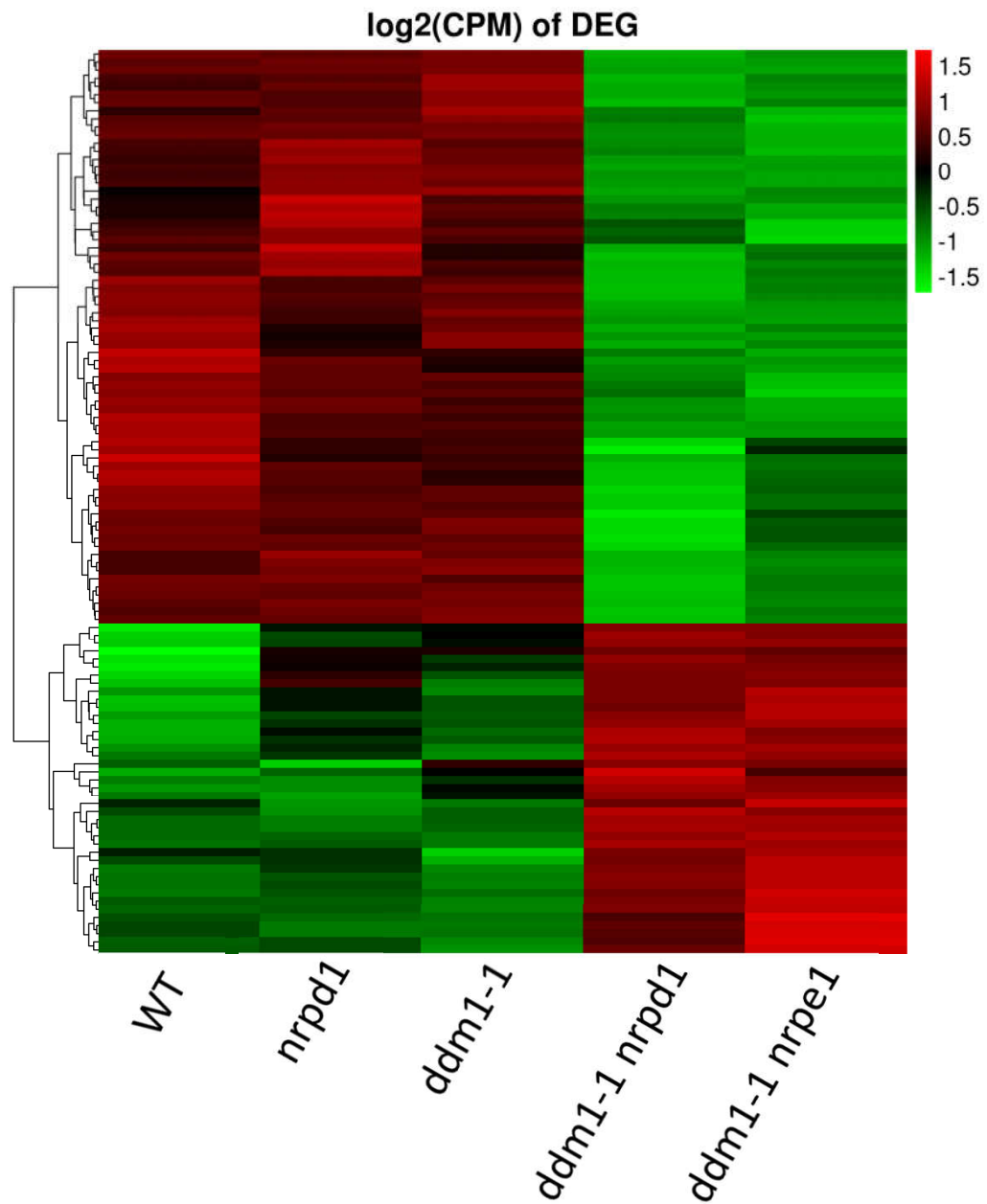
# RNA-Seq analysis







## DDM1 and RdDM Synergistically Regulate Gene Expression





*Thanks for your patience and time!*