**Parameter**

Workdir

Input

Genome

**Alignment Results**

Alignment rate ---- samtools

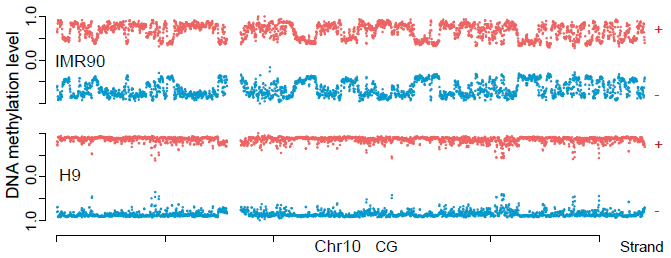
**DNA methylation level**

+

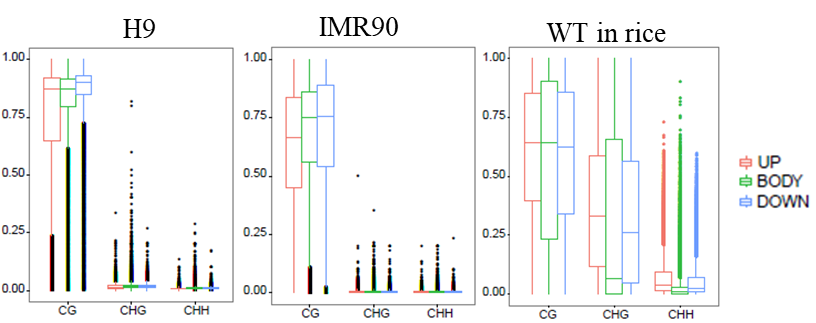
-

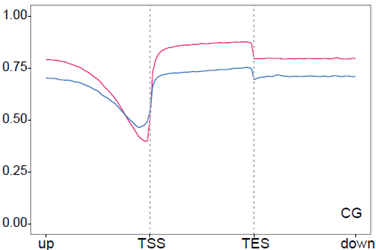
Count ….

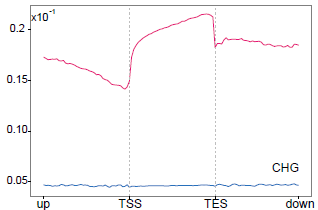
**DNA methylation distribution on genome**

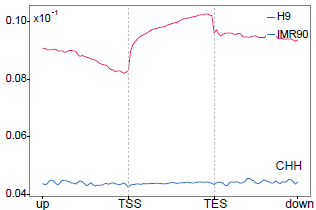


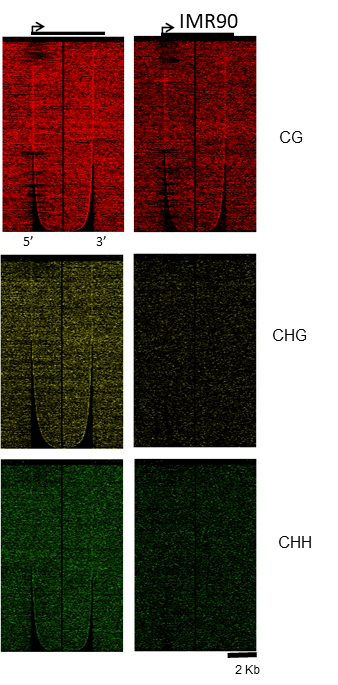
**DNA methylation distribution on function elements**



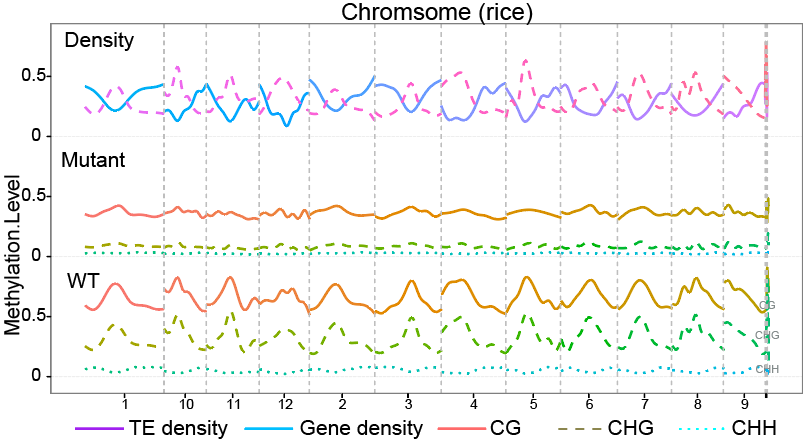








**DNA methylation distribution with function elements density**



**Differential methylation**

DMC

DMR

DMP

DMB

DMC annotation:

