

Selective chemical labeling reveals the genome-wide distribution of 5-hydroxymethylcytosine in rice

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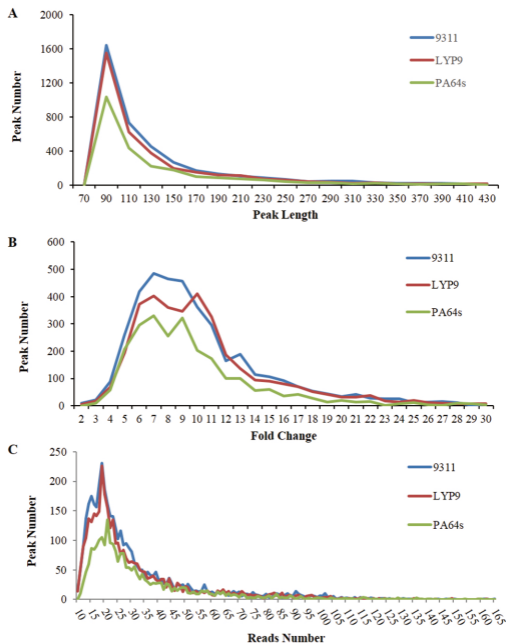
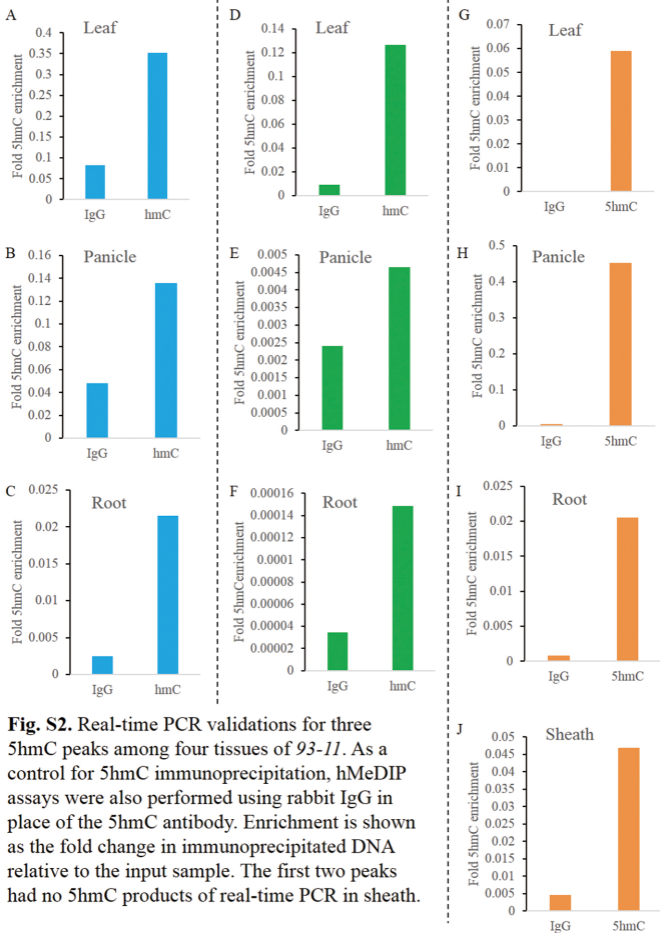


Fig. S1. Statistical properties of regions enriched for 5hmC modification. (A) Number of 5hmC peaks in various length; (B) Number of 5hmC peaks of a given fold-increase over background; (C) Number of reads distributed in 5hmC peaks.

P1:chr01_39121226_39121540

P2:chr04_30960643_30961018

P3:chr09_4722881_4723306



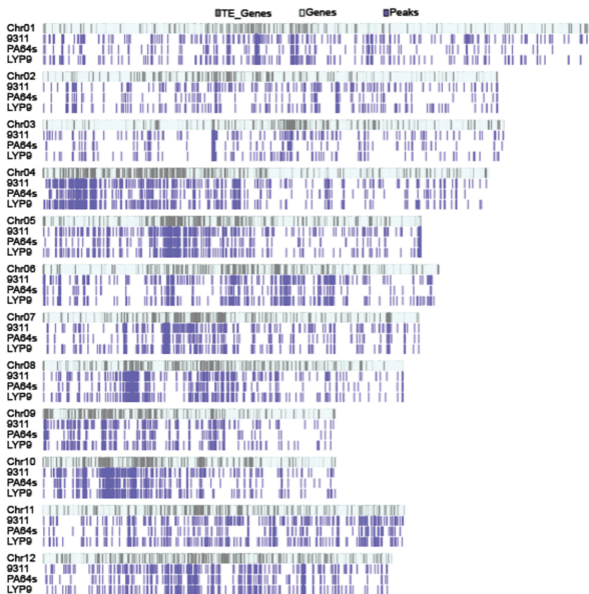


Fig. S3. Comparative whole genome distribution of 5hmC peaks among three cultivars.

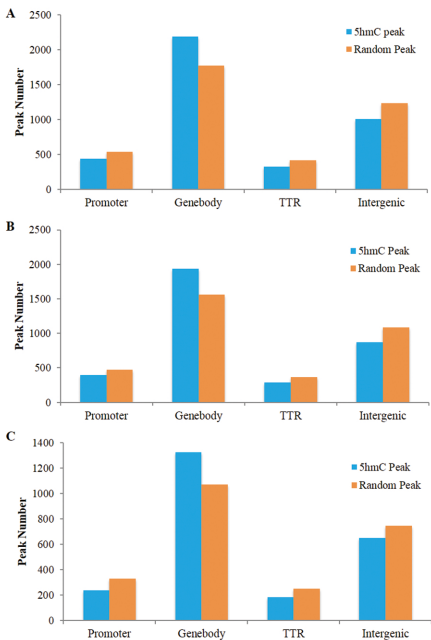


Fig. S4. Genome-wide distribution of those detected 5hmC peaks compared with 1000 times randomly simulated dataset in *93-11* (A), *LYP9* (B) and *PA64s* (C), respectively.

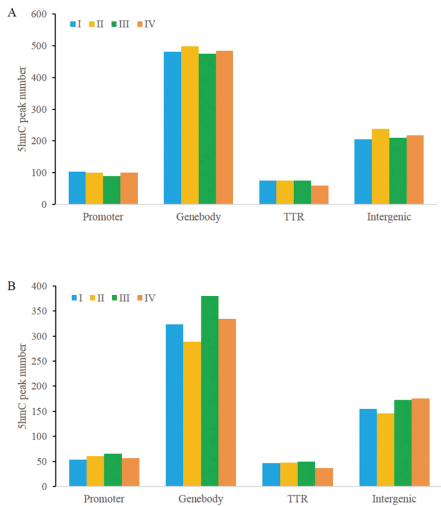


Fig. S5. Distribution of 5hmC peaks in each class for *LYP9* (A) and *PA64s* (B) in the whole genome.

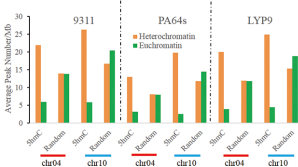


Fig. S6. Average number of 5hmC peaks per million bases in heterochromatin and euchromatin of chromosomes four and ten compared with random dataset.

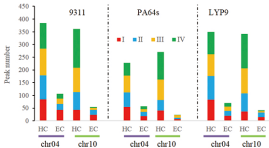


Fig. S7. Enrichment of 5hmC in heterochromatin (HC) over euchromatin (EC) of chromosomes four and ten in each class for three cultivars.

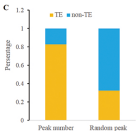
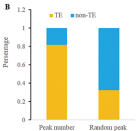
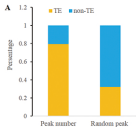


Fig. S8. Distribution of 5hmC peaks in TE genes and non-TE genes compared with a random dataset for *93-11* (A), *PA64s* (B) and *LYP9* (C), respectively.

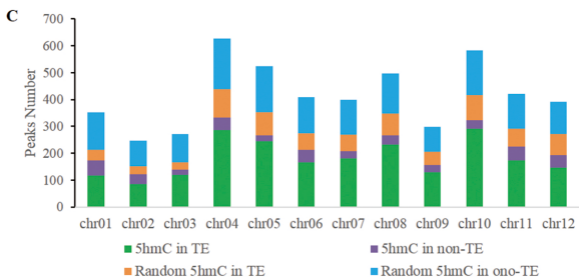
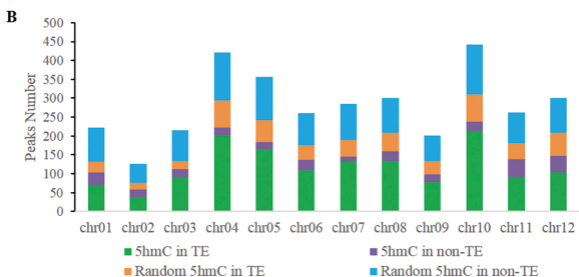
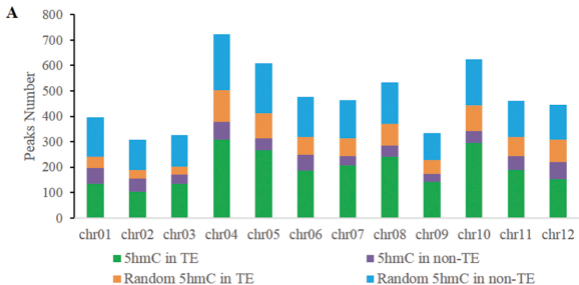


Fig. S9. Distribution of 5hmC peaks in TE genes and non-TE genes in every chromosome of *93-11* (A), *PA64s* (B) and *LYP9* (C) compared with a random dataset, respectively.

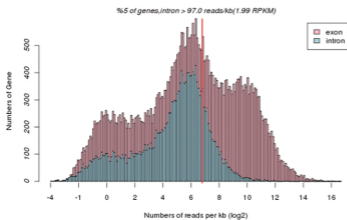
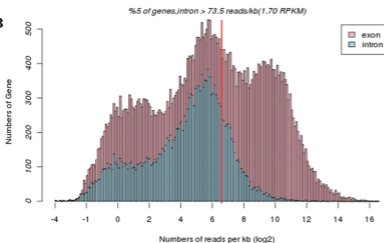
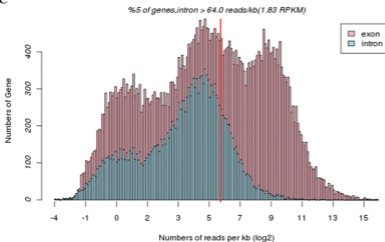
A**B****C**

Fig. S10. Detection of gene expression in rice by mRNA-Seq. Distribution of mRNA-Seq reads in exons and introns. About 5% of genes contained > 97.0 reads, 73.5 reads and 64.0 reads per kilobase intron for *93-11* (A), *LYP9* (B) and *PA64s* (C), respectively. Accordingly, 97.0 reads, 73.5 reads and 64.0 reads per kilobase exon was arbitrarily used as a cutoff to detect gene expression for *93-11*, *LYP9* and *PA64s*, respectively.

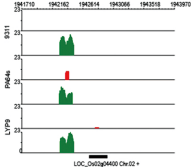
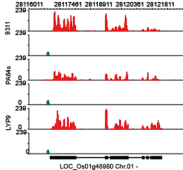


Fig. S11. Typical examples for expressed and silent genes with 5hmC peaks in read-level among three cultivars.

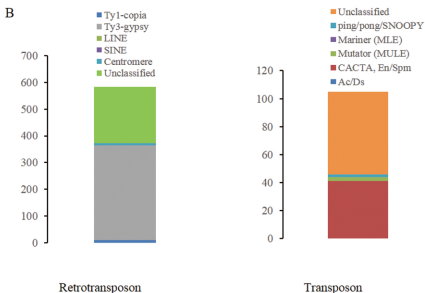
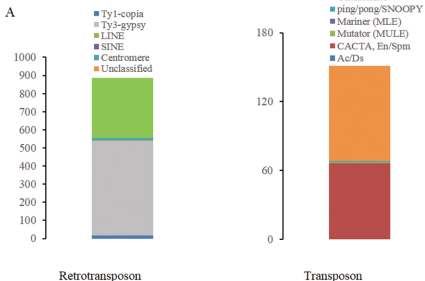


Fig. S12. Number of retrotransposons and transposons with MRPs for *LYP9* (A) and *PA64s* (B), respectively.