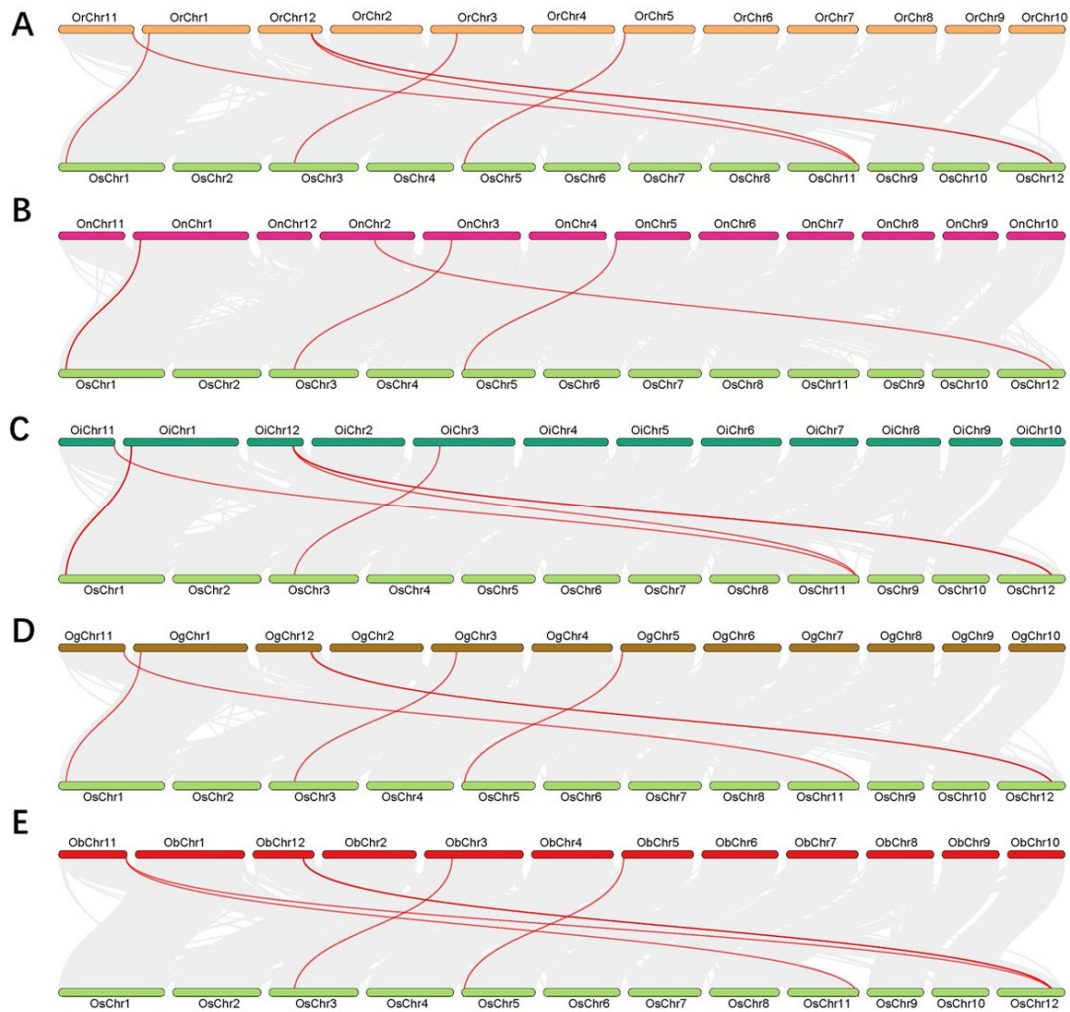


**Supplementary Figure S1.** (A-F) Chromosome mapping of *MT* genes in the six *Oryza* genomes. Chromosome numbers are indicated at the bottom of each bar. Scale is represented in mega bases (Mb) and lines in the background chromosome indicate all genes within the genomes.



**Supplementary Figure S2.** Collinearity relationships of MT genes in *O. sativa ssp. japonica* and *O. rufipogon* (A), *Oryza nivara* (B), *Oryza sativa ssp. indica* (C), *Oryza glumaepatula* (D), *Oryza barthii* (E)



**Supplementary Figure S3.** Identification of cis-regulatory elements in all *MT* genes of *Oryza sativa* ssp. *japonica*. (A) The different bars represent different primary categories; different characters represent different secondary categories; different colors in the histogram represent the number of different promoter elements in each secondary category. (B) Pie charts of different sizes indicate the ratio of each primary/secondary category. (C) Cis-regulatory elements of all *OsMT* genes in the phylogenetic tree. The differently colored boxes represent the different secondary categories