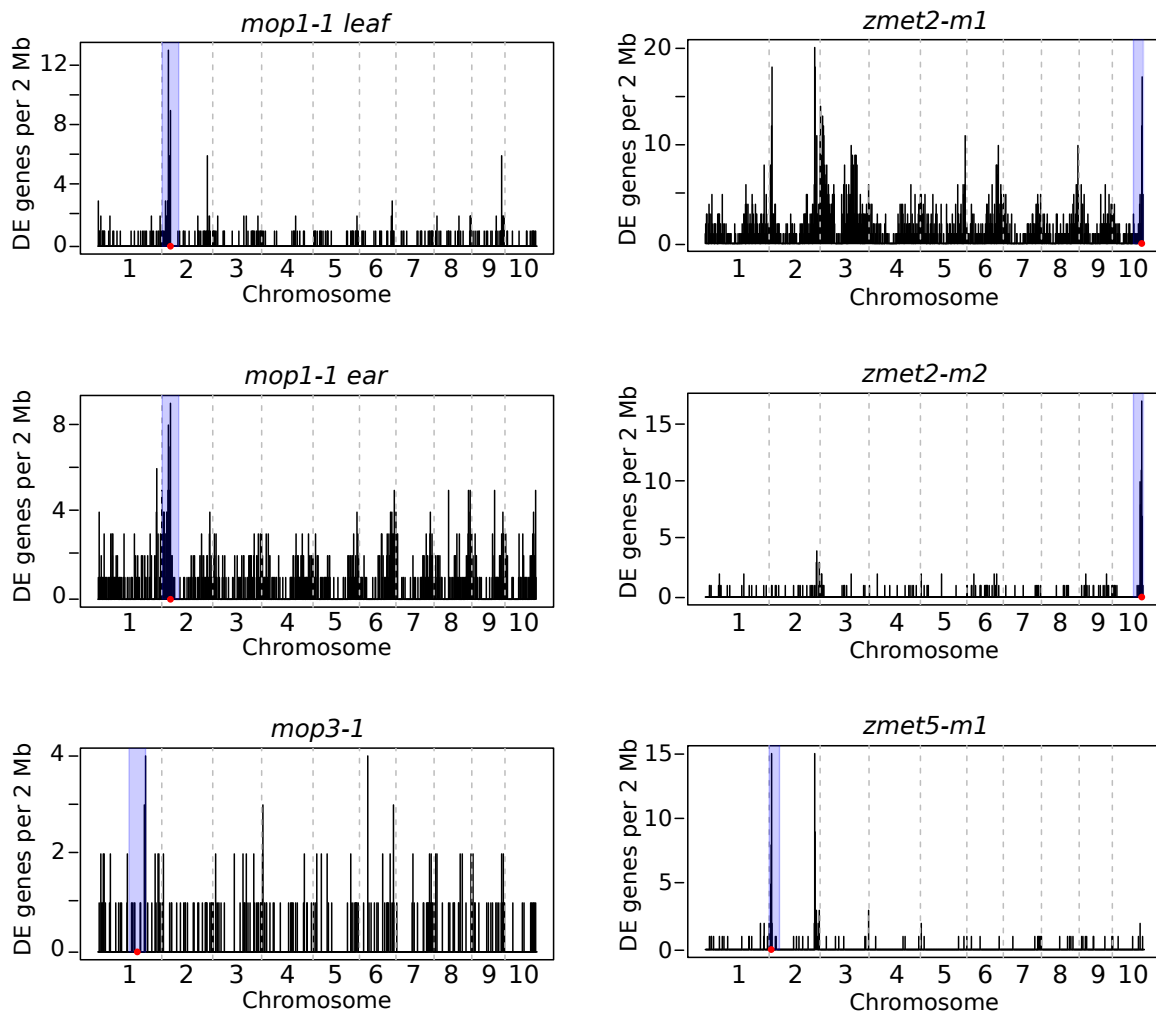**Figure S1**

Figure S1: Locations of DE genes along the chromosomes in mutants, with the location of mutant genes marked in red. DE genes in blue regions are excluded from analysis due to the possibility that differential expression could be derived from linkage to the mutant allele.
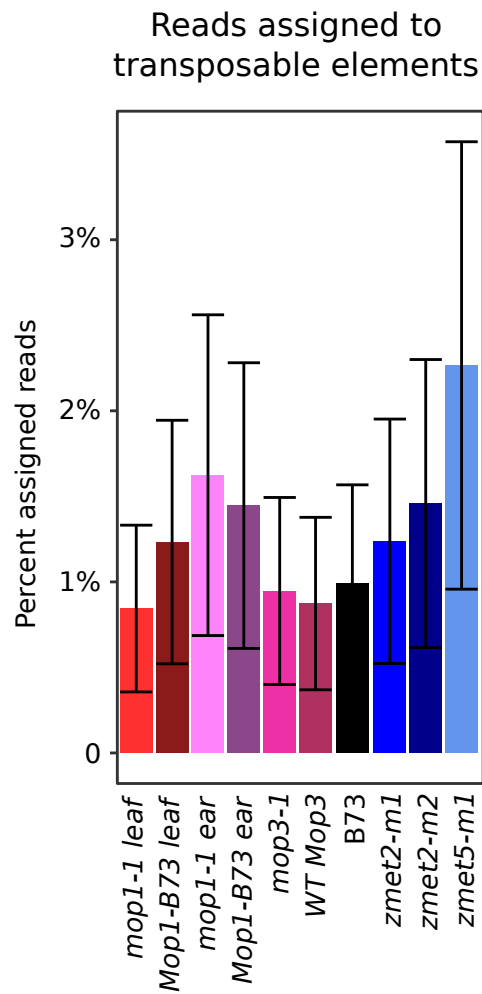
Figure S2

Figure S2: Percent of RNA-seq reads assigned to transposable element families in mutants and wild-type samples. Unique and multi-mapped reads mapping to an individual element or TE family were combined for per-family expression counts, and the percent of assigned reads was calculated by dividing TE-assigned reads by the sum of TE and gene reads. Error bars represent the standard error for three biological replicates per genotype.

Figure S3

A. RdDM Up-Regulated Genes

mop1-1 leaf

134(10) 22(4) 591(10)

3(2)

23(5) 9(1)

135(5)

mop3-1 *mop1-1 ear* (180)

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B. RdDM Down-Regulated Genes

mop1-1 leaf

57(1) 7 153(2)

4 3(2)

1

mop3-1 56(2) *mop1-1 ear* (63)

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C. CMT Up-Regulated Genes

zmet2-m1

zmet2-m2

802 65 28

21 5

21 16

zmet5-m1

D. CMT Down-Regulated Genes

zmet2-m1

zmet2-m2

915 19 3

7 2

25 16

zmet5-m1

E. RdDM Up-Regulated TE Families

mop1-1 leaf *mop1-1 ear*

18(3) 19(9) 128(23)

4 3(3)

6(4)

mop3-1 9(2)

(94)

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F. RdDM Down-Regulated TE Families

mop1-1 ear

mop1-1 leaf

12(1) 7 67(1)

mop3-1 3 (13)

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G. CMT Up-Regulated TE Families

zmet2-m1

zmet2-m2

124 27 15

10 7

7 47

zmet5-m1

H. CMT Down-Regulated TE Families

zmet2-m1
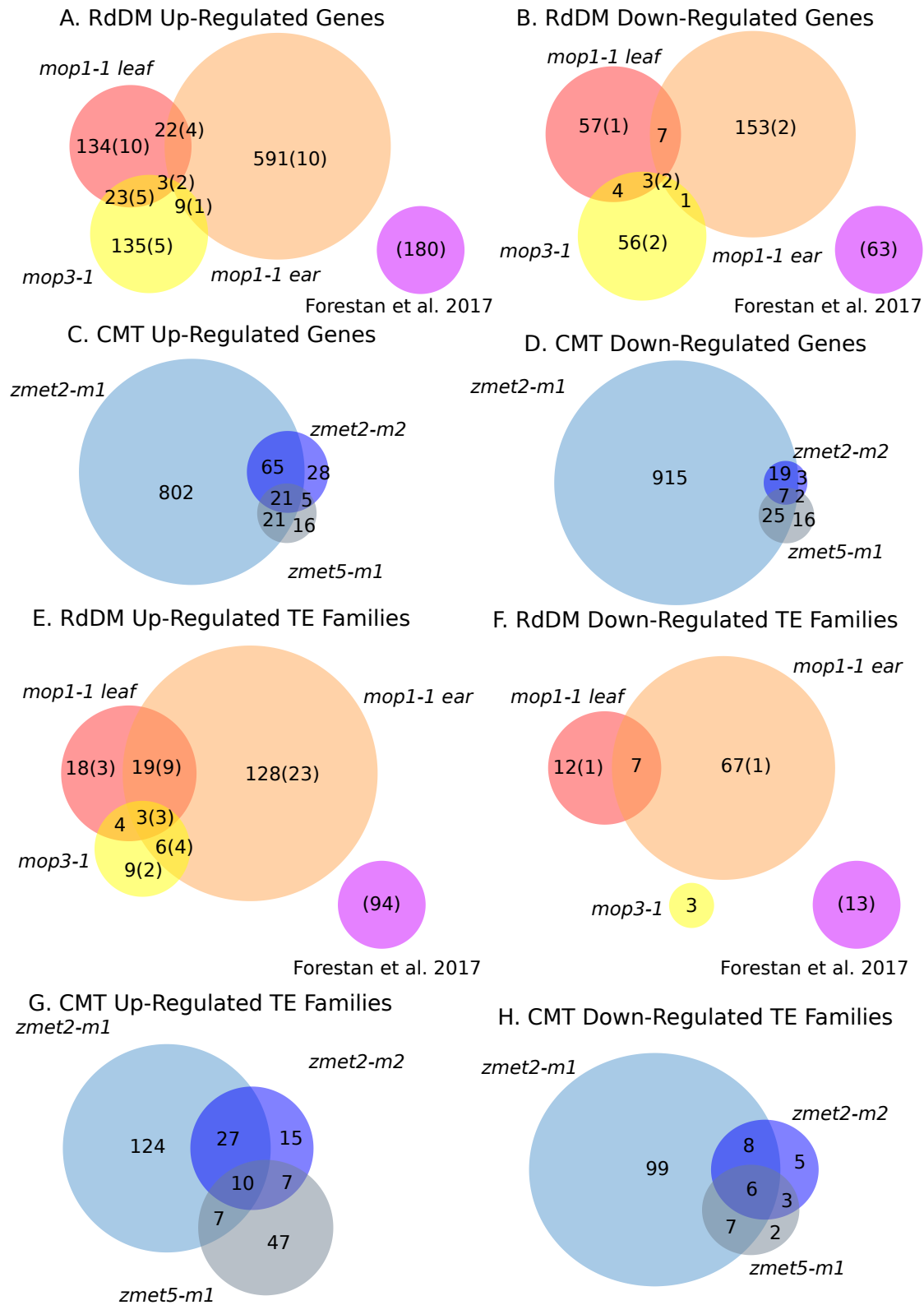
zmet2-m2

99 8 5

6 3

7 2

zmet5-m1

Figure S3: Overlap between differentially expressed genes (A-D) and TE families (E-H) in CMT and RdDM mutants. Only elements with consistent expression changes in at least two samples were retained for downstream analysis. All pairwise overlaps are significant (p-val < 0.01 using GeneOverlap package in R). Numbers in parentheses denote the number of DE genes or TE families that were also differentially expressed in *rmr6-1* mutants (Forestan et al. 2017).
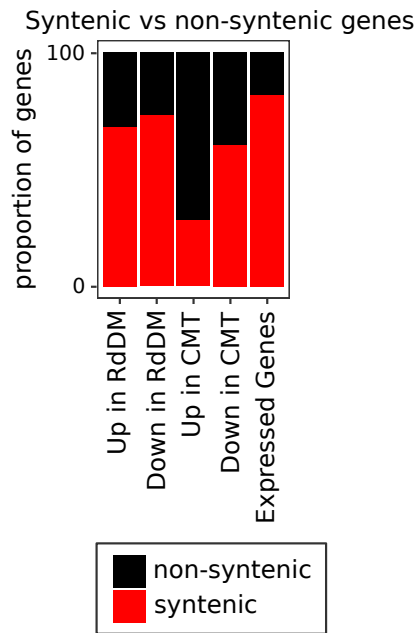
Figure S4

Figure S4. For each set of genes that are up- or down-regulated we determined the proportion that are located in syntenic genomic positions relative to rice or sorghum as defined by Brohammer et al. (2017). The proportion of all genes that are expressed (RPM >1) that are syntenic is also shown.
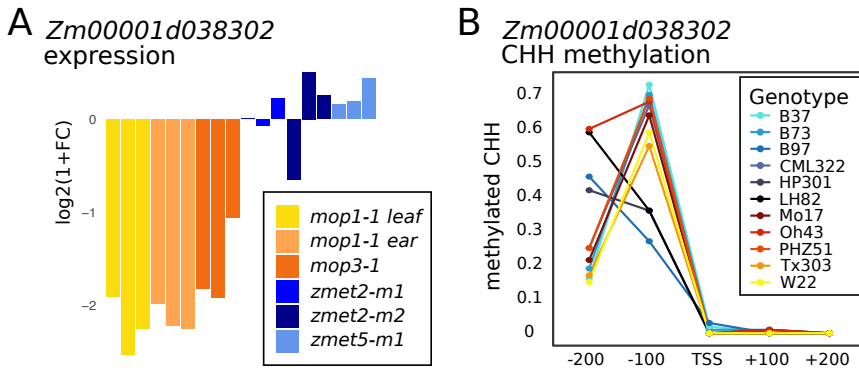
Figure S5

Figure S5: Conservation of mCHH island for DNA demethylase gene *Zm00001d038302*. A. The expression of *Zm00001d038302* in mutants, showing large loss of expression in RdDM mutants which lose CHH methylation. B. The CHH levels in the 500 bp surrounding the TSS of *Zm00001d038302* is shown for the eleven inbred lines with data for each bin.

Figure S6

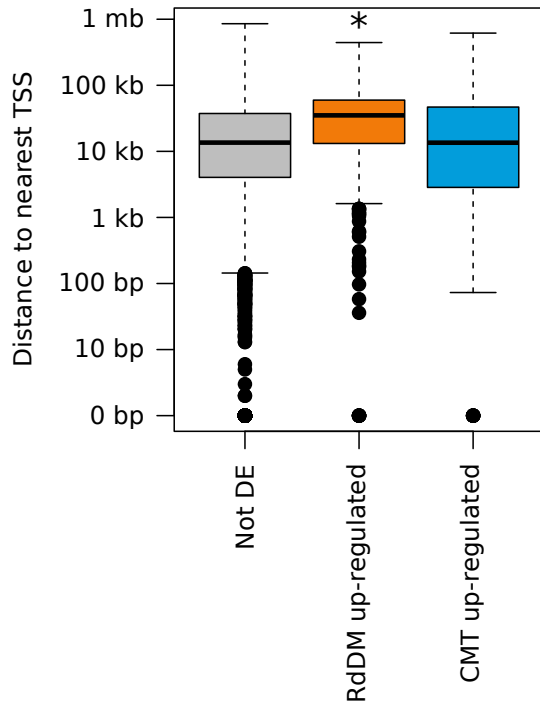Expressed TEs distance to nearest gene

Figure S6: Boxplot of the distance of expressed TEs to the nearest transcription start site (TSS). TEs are grouped by DE status of their family, and elements with at least one unique-mapping read in at least 3 libraries are included. Distance is plotted on a log scale. * denotes significant difference from the "Not DE" set (p.value < 0.01, t-test).