

Supplementary Material

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Supplementary Table S7. List of primers used for RNA-seq validations

Supplementary Table S8. Eggplant DNA methyltransferases and demethylases gene IDs and their level of transcription in EMP and TOR plants. Statistical significant p values (< 0.05) are highlighted. NA = not analysed/not significant/not expressed.

Supplementary Table S9. Output of enrichment analysis on up-regulated genes in *S. torvum* and 'Emperador RZ'. The analysis was conducted using a p-value cut-off of 0.05.

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Supplementary Table S11. List of transposable elements differentially expressed in at least one hetero-grafted condition (pvalue < 0.05)

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Supplementary Table S13. List of up-regulated LTRs in the two heterografted conditions (i.e. EMP and TOR; $P < 0.05$).

Supplementary Table S14. List of down-regulated LTRs in the two heterografted conditions (i.e. EMP and TOR; $P < 0.05$).

Supplementary Figure Legends

Figure S1. DNA methylation profile in eggplant leaves of not grafted plants. DNA methylation content in CG (red), CHG (blue) and CHH (yellow) contexts, represented in the 12 eggplant chromosomes. In dashed black is reported the gene density.

Figure S2. DNA methylation profiles in self-grafted and hetero-grafted eggplant. Distribution of DNA methylation at each cytosine context (mCG, mCHG and mCHH) along chromosomes 2 to 12, in eggplant scions self-grafted (Self), or grafted onto *S. torvum* (TOR) or tomato ‘Emperor RZ’ (EMP) rootstocks. The profiles in chromosome 1 are displayed in **Figure 2**.

Figure S3. DNA methylation distribution at the main TEs classes. Distribution of averaged DNA methylation (at CG, CHG and CHH contexts) at annotated TEs of main three groups in eggplant genome, in eggplant scions self-grafted (Self), grafted on *S. torvum* (TOR) or tomato ‘Emperor RZ’ (EMP).

Figure S4. DMR analysis. **a** Identified CHH DMRs in TOR and in EMP, using self-grafted scions replicates as common denominator. **b** Distribution of CHH DMRs in scions grafted on EMP rootstock compared to self-grafted scions. DMR density (axes on the left) in 5 million bp windows is plotted for each chromosome. For reference, the density of repeats and coding genes are also plotted (axes on the right). **c** Distribution of CHH DMRs in scions grafted on TOR rootstock compared to self-grafted scions. Description is as in **b**. **d** Proportion of CHH DMRs in TOR (N = 9,745) and in EMP (N = 16,304) that overlap with genomics features in comparison to randomly selected 300bp regions (Control). Promoters are defined as the DNA sequence located 1Kb upstream of each annotated gene. Significant enrichment calculated with one-tailed Fisher's exact test is marked with *** (p-value < 10⁻¹⁰⁰) and ** (p-value < 10⁻¹⁸).

Figure S5. Overlap among differentially expressed annotated genes and LTR-TEs. Venn-diagrams displaying up-regulated (**a**) and down-regulated (**b**) genes, or up-regulated (**c**) and down-regulated (**d**) annotated LTR-TEs, in eggplant scions grafted onto *S. torvum* (TOR) and tomato ‘Emperor RZ’ (EMP) compared to self-grafted control.

Figure S6. Validation of RNA-seq expression data. RNA accumulation was measured with qPCR for a subset of 11 genes randomly selected with $|\log_2FC| > 3$. Bars represent up/down-regulated genes in eggplant

scions grafted onto *S. torvum* (a) or tomato 'Emperador RZ' (b) rootstocks compared to self-grafted plants (Self). Both up-regulated (top line) and down-regulated (bottom line) genes were tested. Error bars represent SD of three replicates.

Figure S7. Gene enrichment analysis in self-grafted and hetero-grafted eggplants. Lists of enriched Gene ontology categories (with a p-value < 0.05) of differentially expressed genes shared in hetero-grafted compared to self-grafted scions. Different graphs display information for down-regulated (a) and up-regulated (b) genes. The number of genes belonging to each GO category is reported at the top of each bar. The specific p-values found for the enrichment of each GO category is reported in Tables S9 and S10.

Figure S8. Overlap among DMRs and differentially expressed genes. Venn-diagrams displaying promoters (1Kb DNA sequence located upstream of each gene) and coding sequences (CDS) from differentially expressed genes (DEGs) or overlapping DMRs in EMP (a,b) or in TOR conditions (c,d).

Figure S9. Hetero-grafted scions display similar LTR-TEs expression profiles. a Heatmap illustrating the expression (\log_2 FPKM) of differentially expressed *de novo*-annotated LTR TEs ($|\log_2| > 2$ and FDR < 0.05) in hetero-grafted plants and self-grafted controls. Each row represents one LTR TE ($n = 63$). Coloured bars on the top-left indicate the expression level. Each column represents an eggplant scion grafted on different rootstock (TOR = *S. torvum*, EMP = tomato 'Emperador RZ' and Self = self-grafted). Expression values were ordered according to hierarchical clustering (hclust and heatmap3 R software environment). The Euclidean distance dendrogram is presented on the left. b Scatter-plots of annotated LTR-TEs ($n = 6,583$) in Self and EMP conditions, each dot represents a gene and in red are displayed differentially expressed LTR-TEs between the two conditions. c Scatter-plots of annotated LTR-TEs ($n = 6,583$) in Self and TOR conditions. In purple are displayed differentially expressed LTR-TEs between the two conditions.

Figure S10. CHH hypomethylation in differentially expressed LTR-TEs. Box plots displaying the averaged mCHH methylation on downregulated (DOWN) and upregulated (UP) LTR-TEs in EMP (a) and in TOR (b) conditions, compared to self-grafted scions (self). Data are from both replicates.

Figure S1

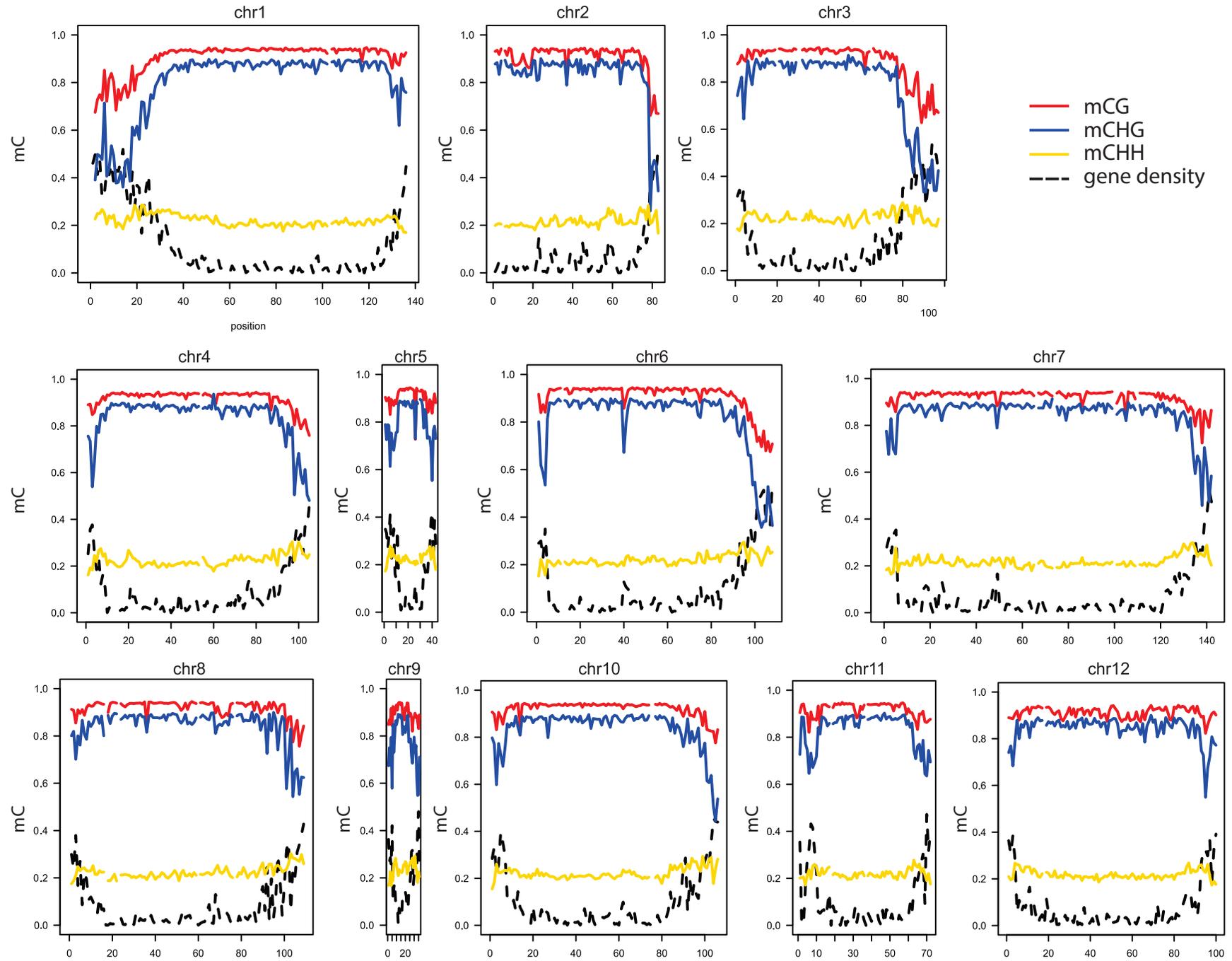
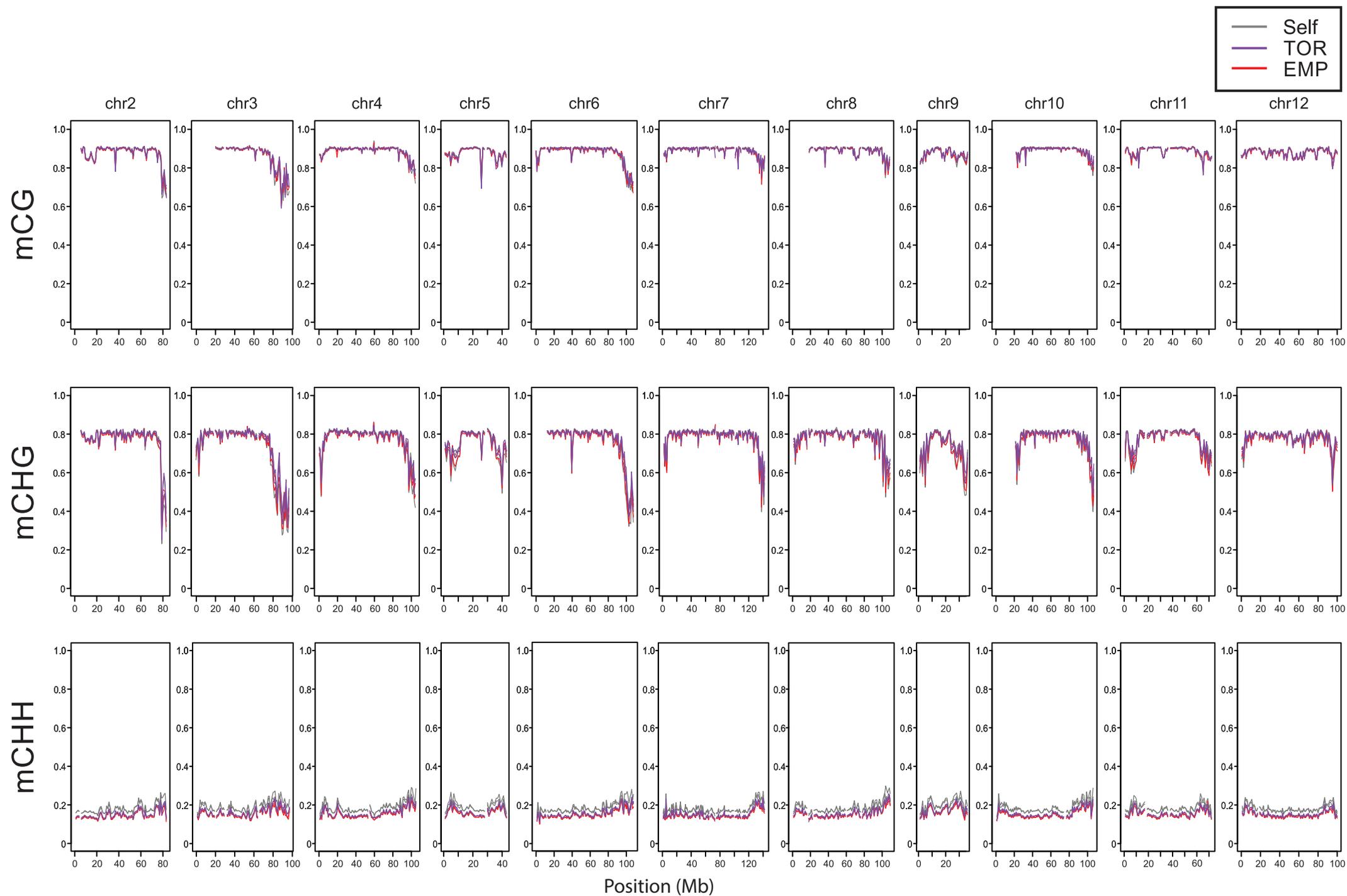


Figure S2



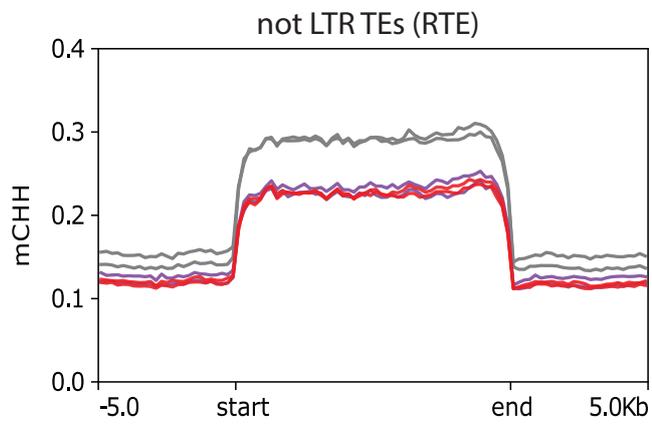
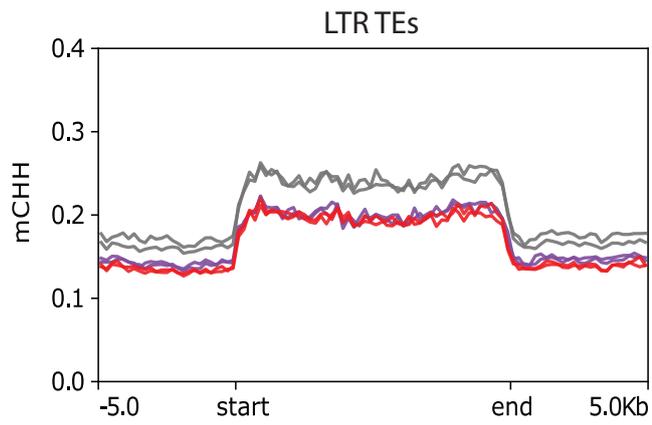
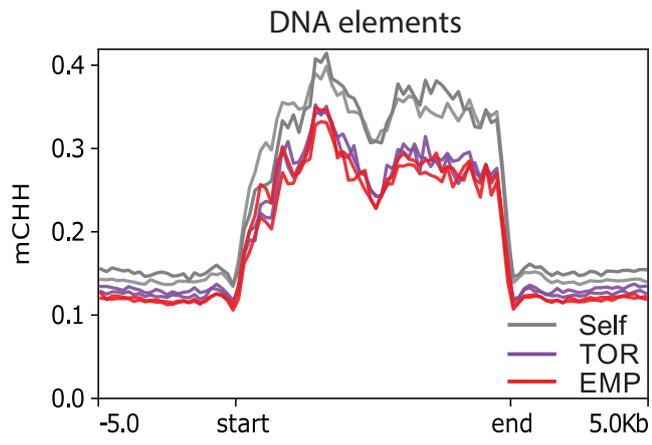


Figure S4

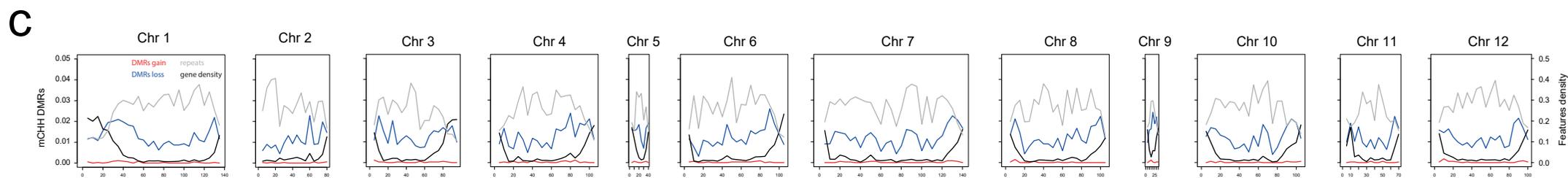
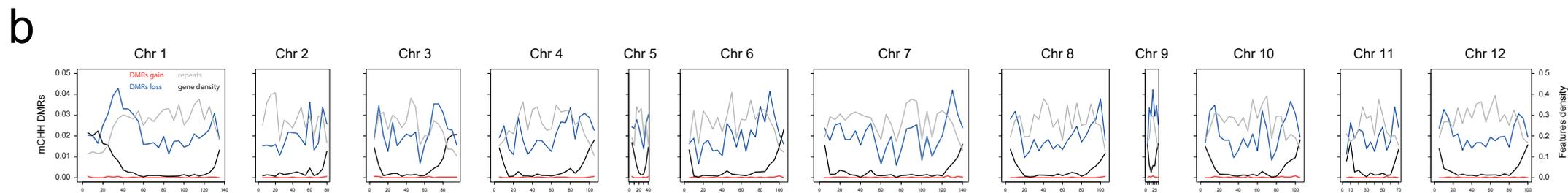
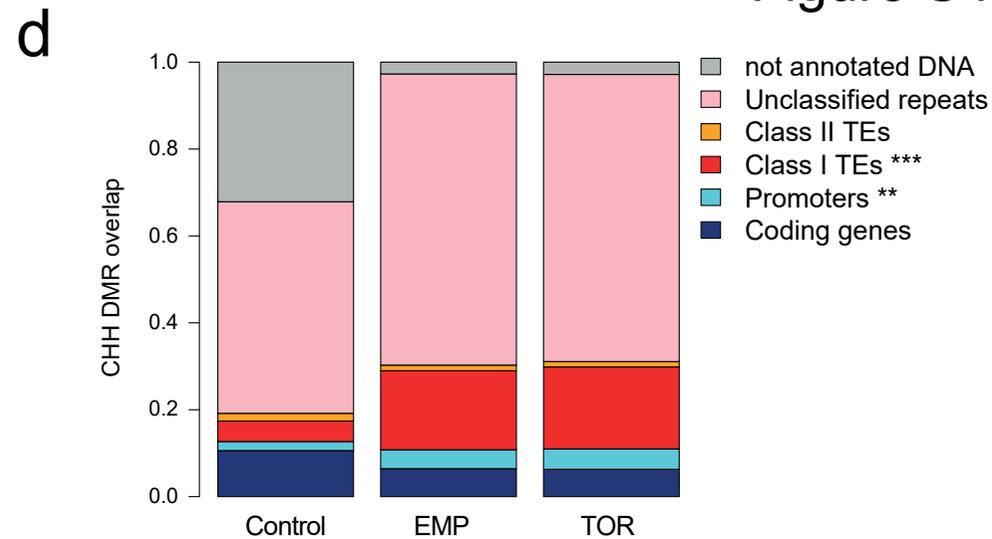
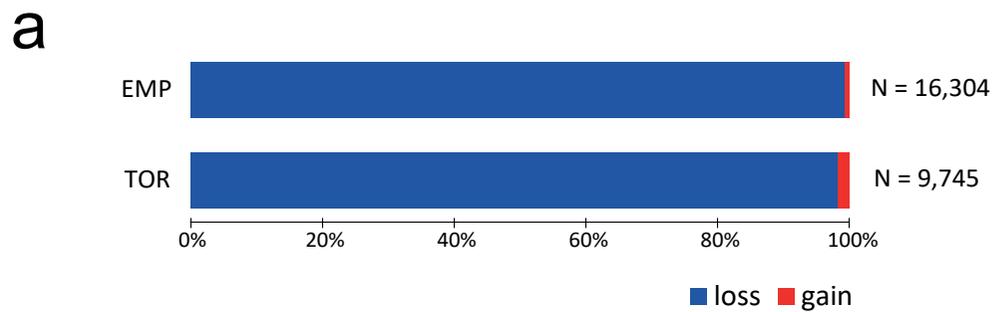


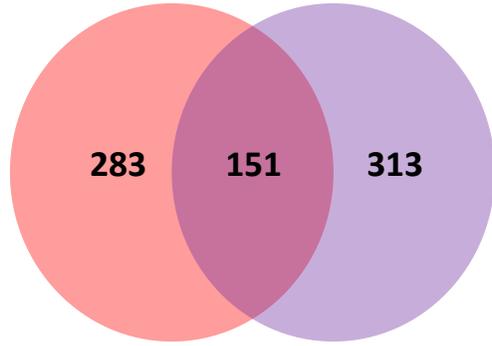
Figure S5

a

Up-regulated genes

EMP

TOR

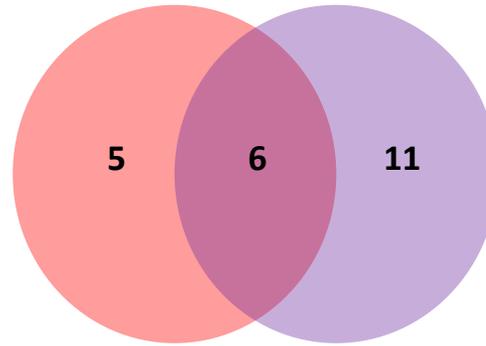


c

Up-regulated LTRs

EMP

TOR

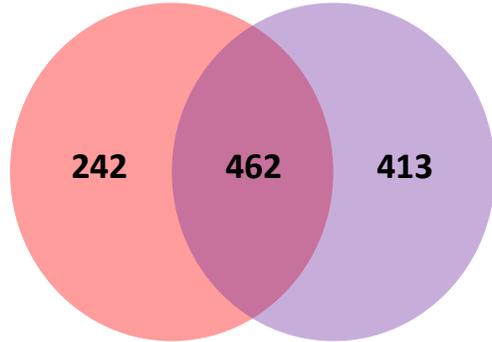


b

Down-regulated genes

EMP

TOR



d

Down-regulated LTRs

EMP

TOR

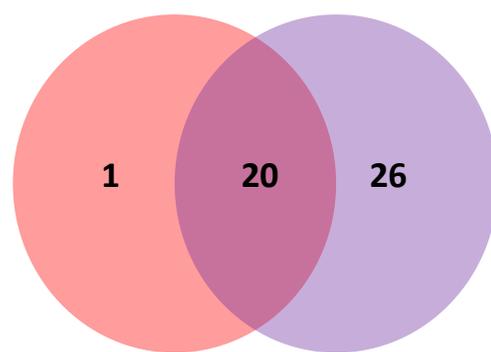
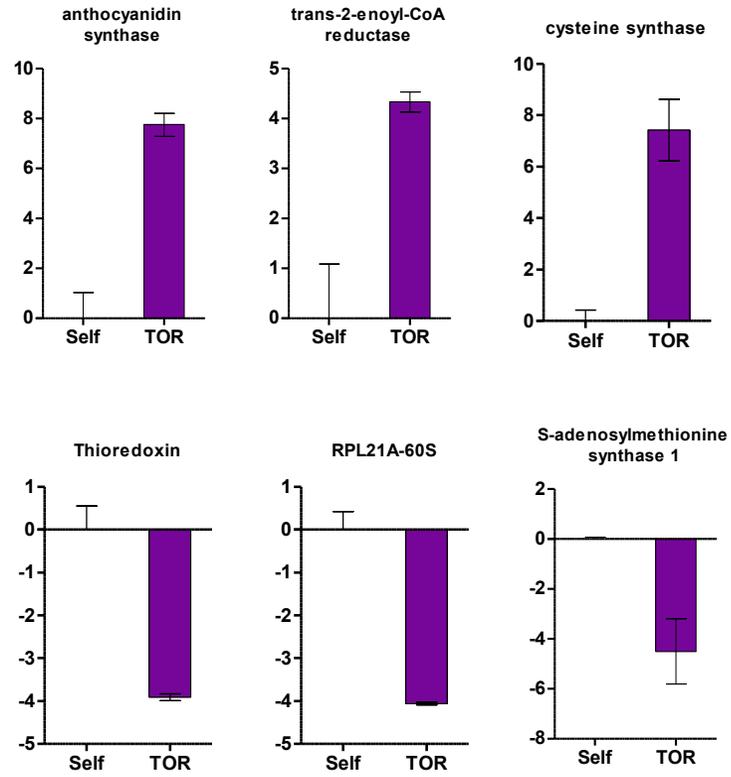


Figure S6

a



b

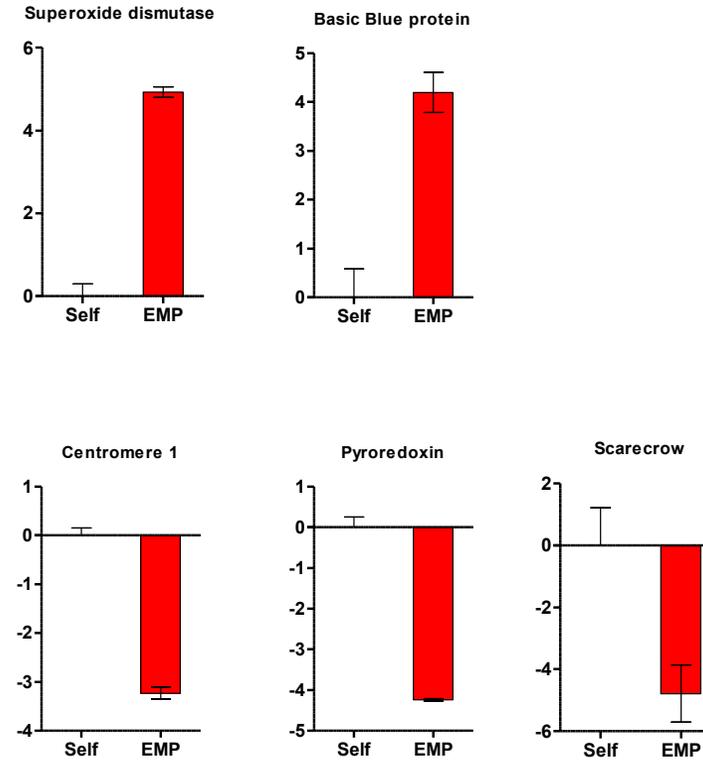


Figure S7

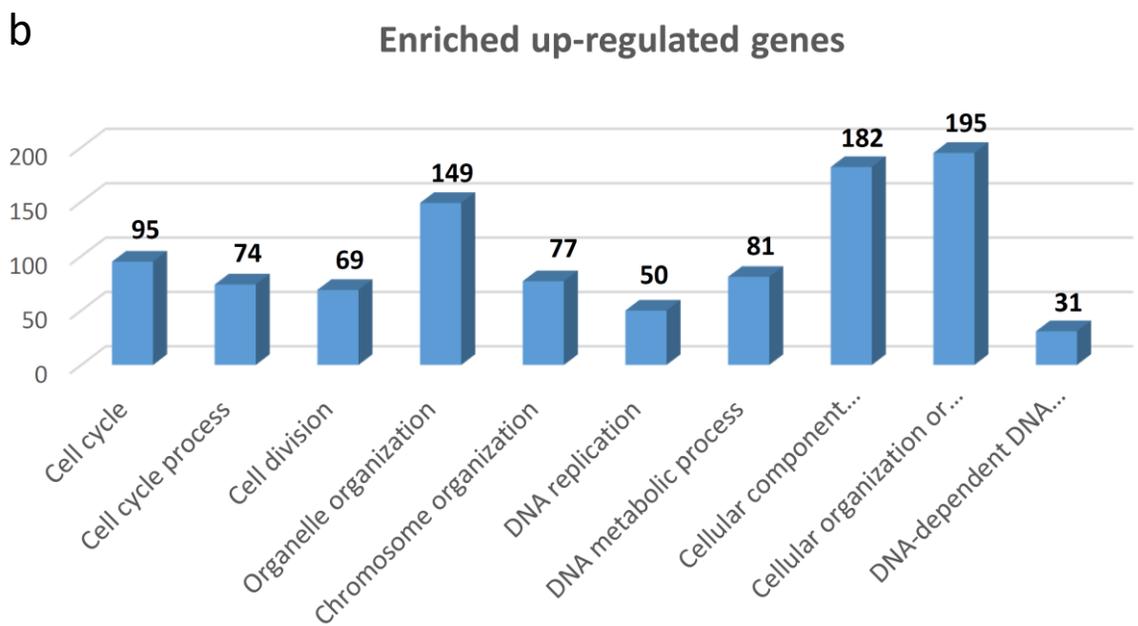
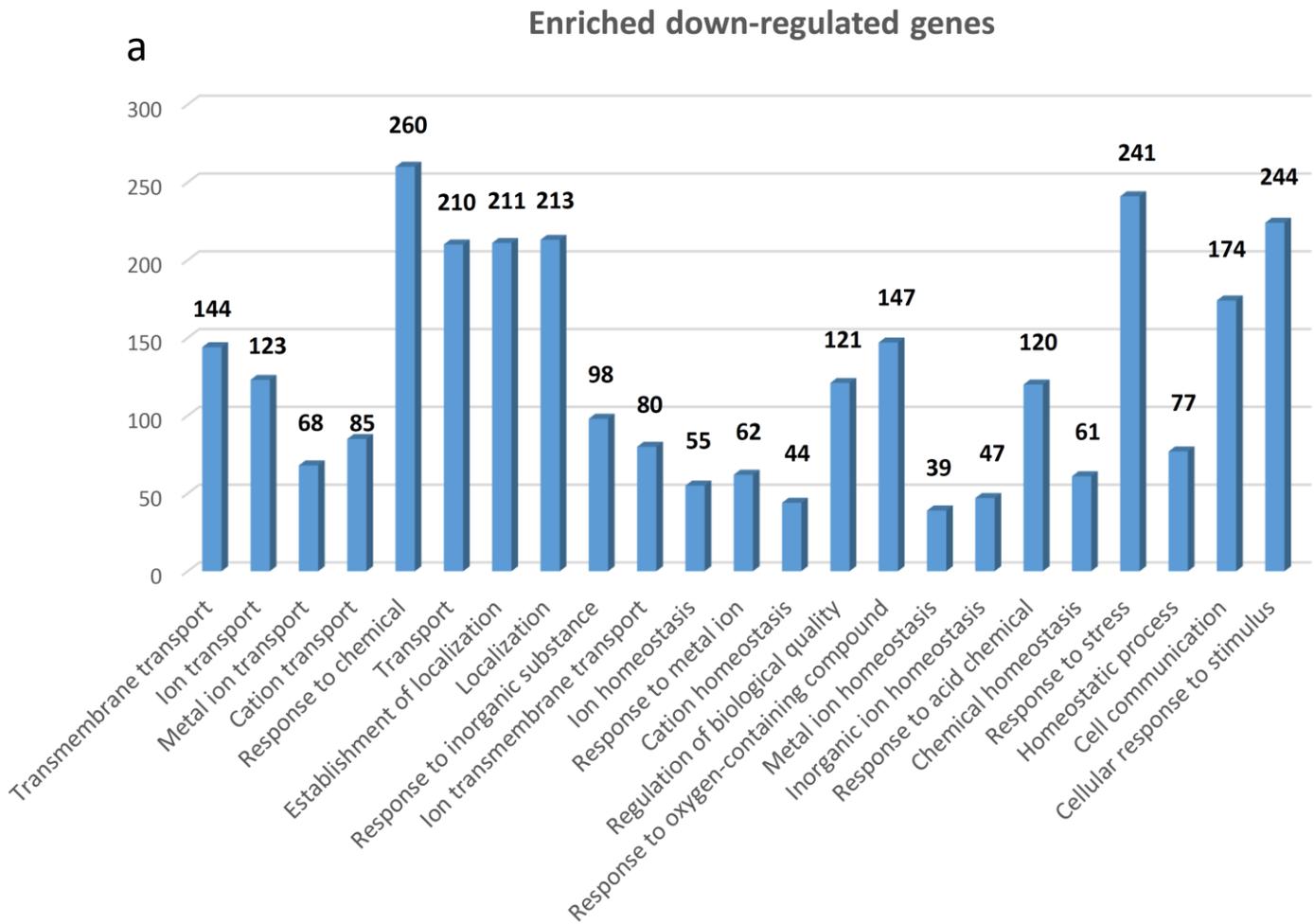
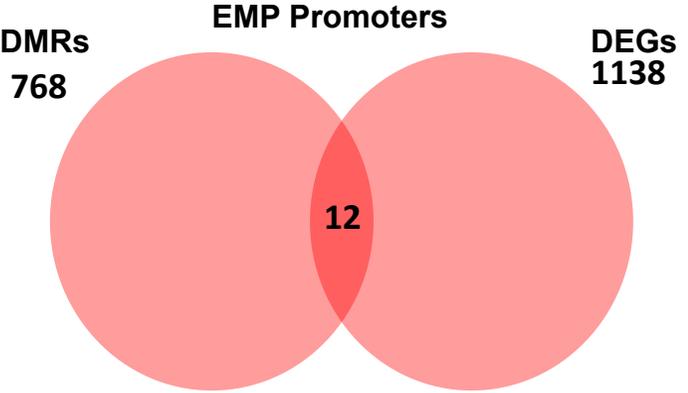
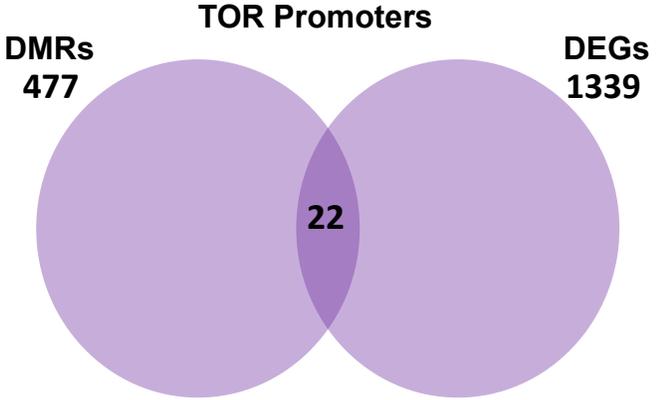


Figure S8

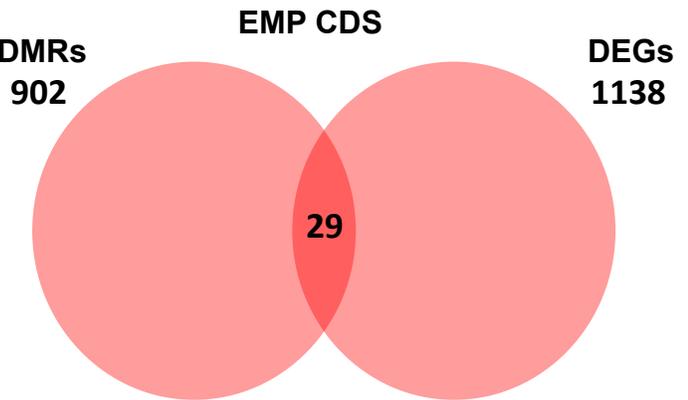
a



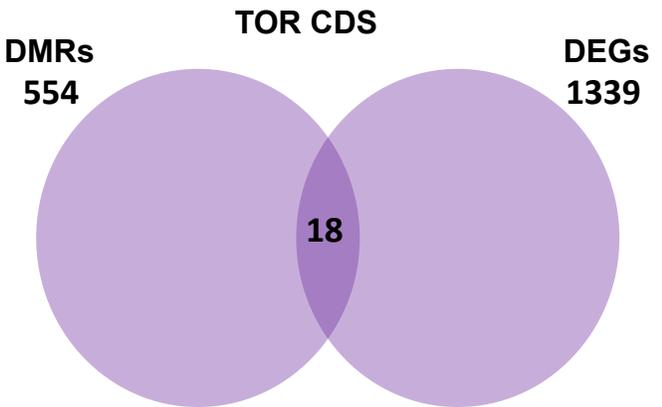
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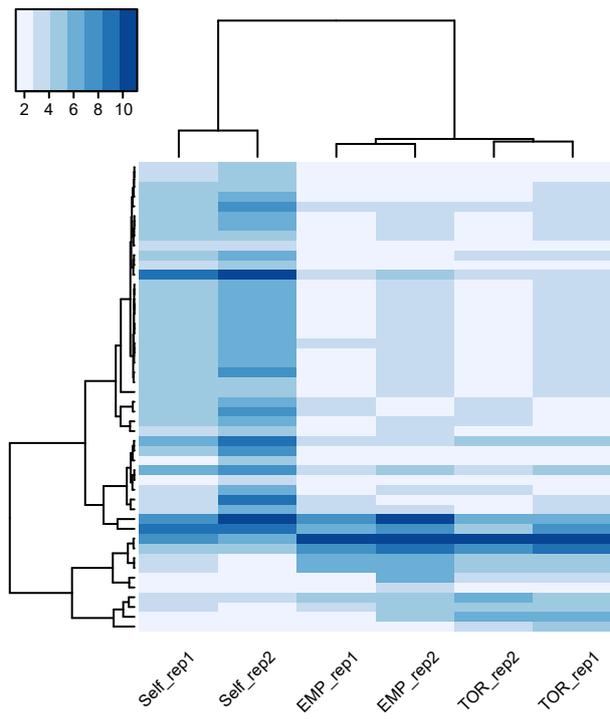
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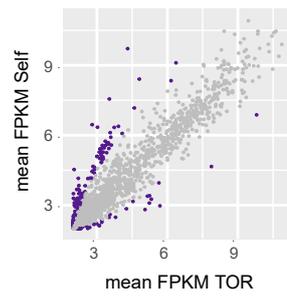
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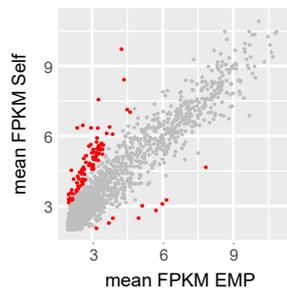
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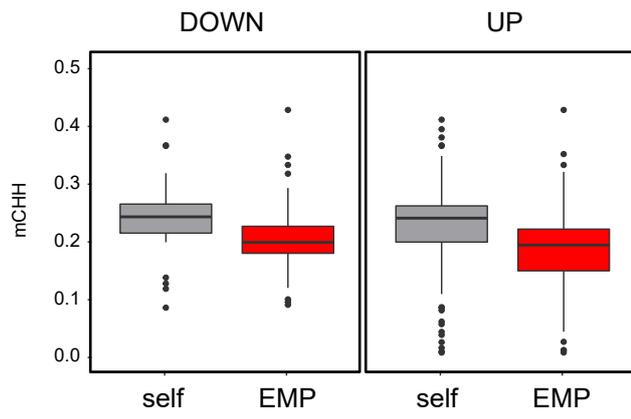
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c



a



b

