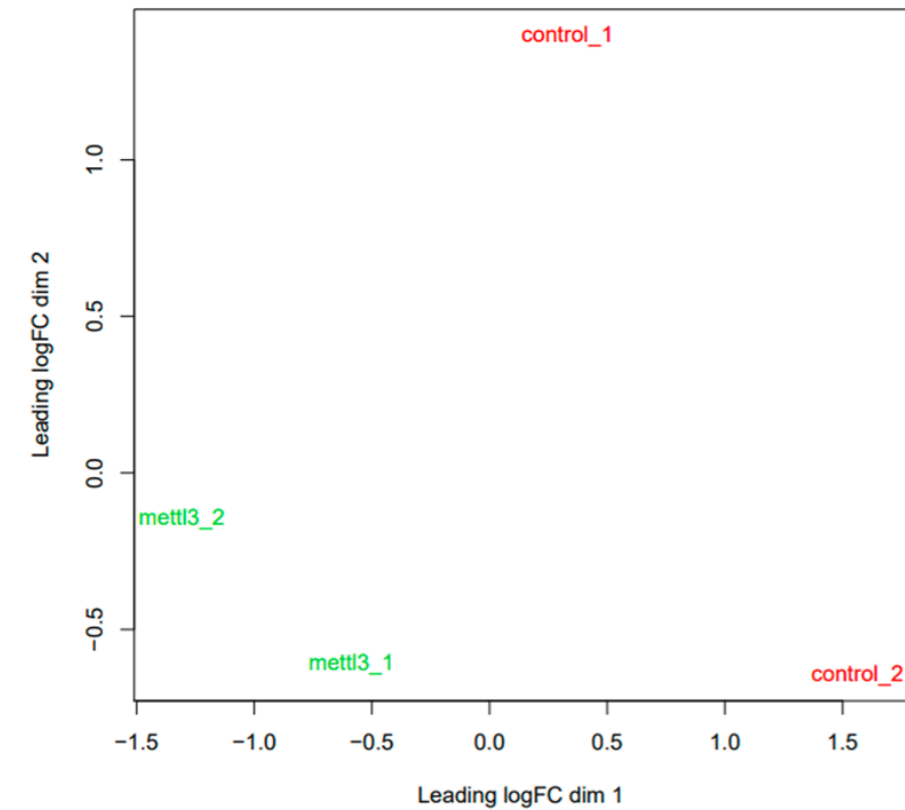
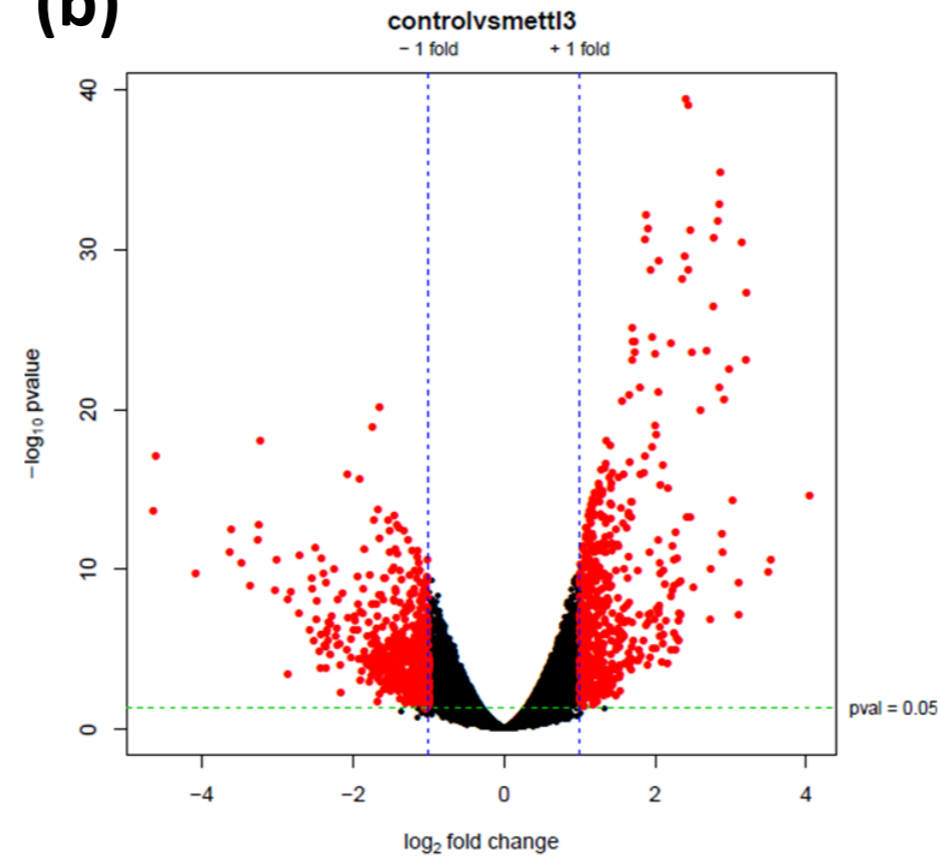
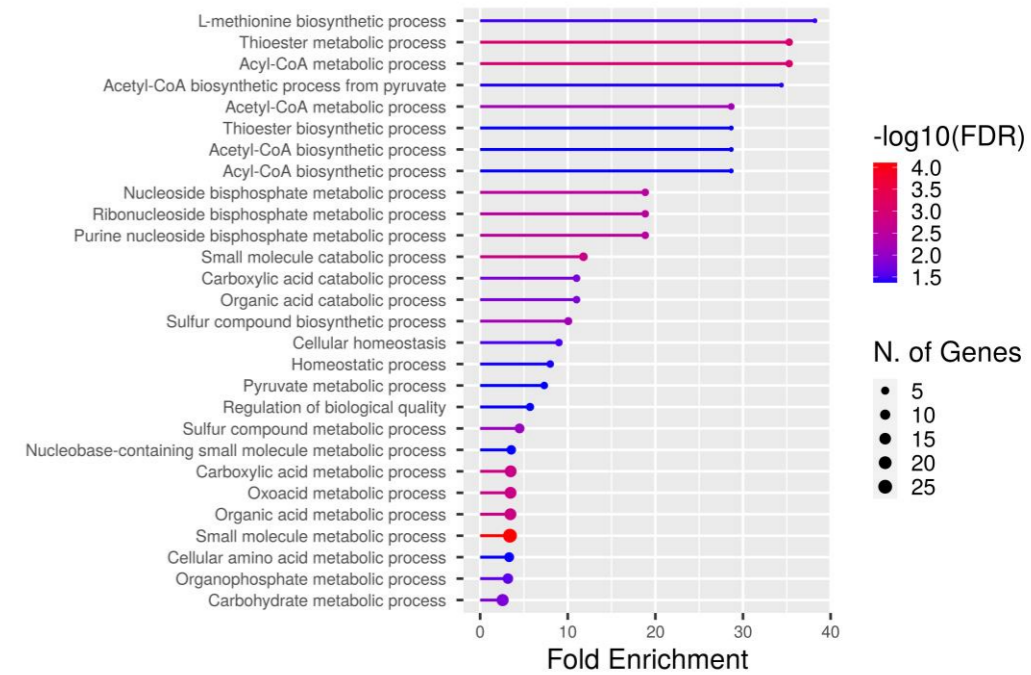


**(a)****(b)****(c)**

**Figure S6. Analysis of RNA-seq data obtained from *Ppmta* and wild type plants.**

(a) Principal Component Analysis showing the similarity among sequencing libraries, control (in red) and *mettl3* (*Ppmta*, in green), replicate libraries 1 and 2 are indicated.

(b) Volcano plots showing differentially expressed genes (DEGs) between *Ppmta* and wild type plants. Red dots represent significant DEGs. Negative  $\log^2$  fold change values represent down-regulation, and positive values, up-regulation.

(c) DEGs identified in the RNA-seq analysis were used to identify GO categories using the shinyGO program. Categories are enlisted according to the fold enrichment, and the false discovery rate (FDR, in  $-\log^{10}$ ) is shown in a color scale as indicated in the figure. Number of genes included in each GO category are represented by the size of the circle.