

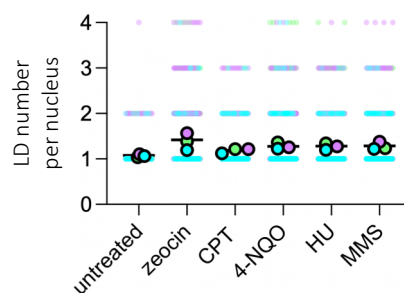
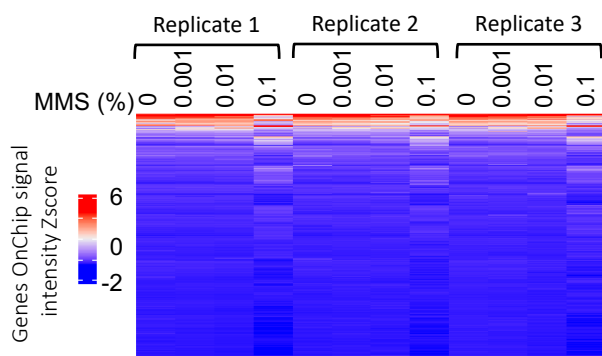
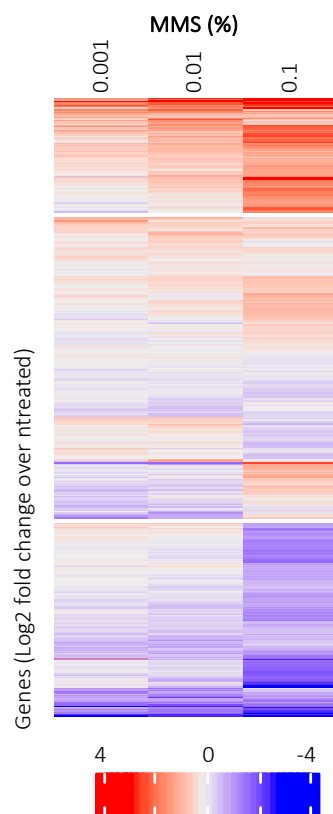
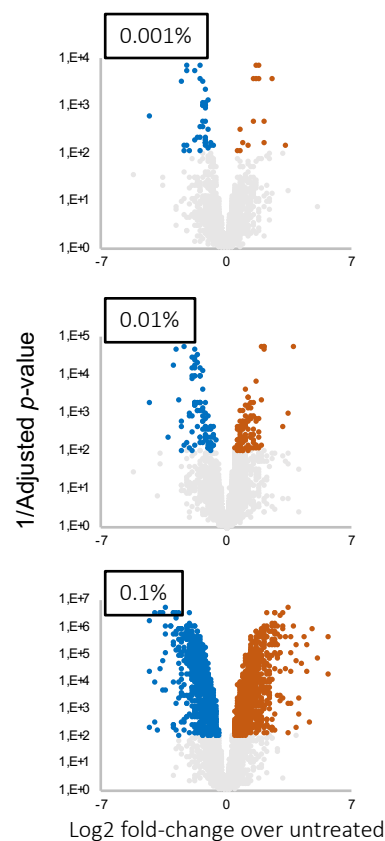
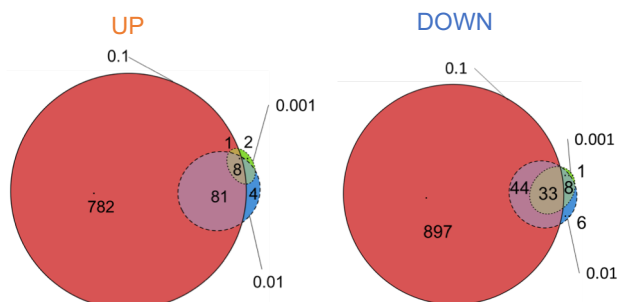
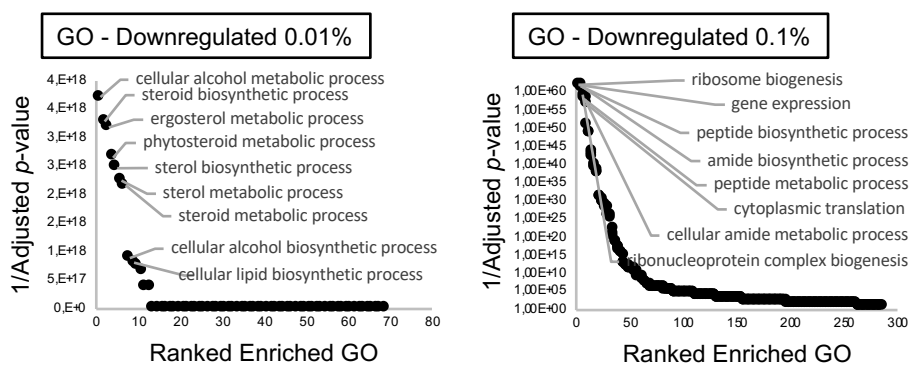
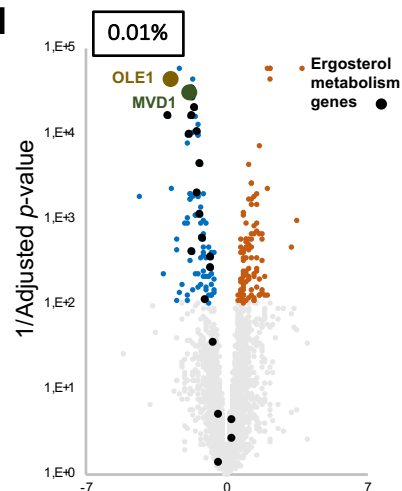
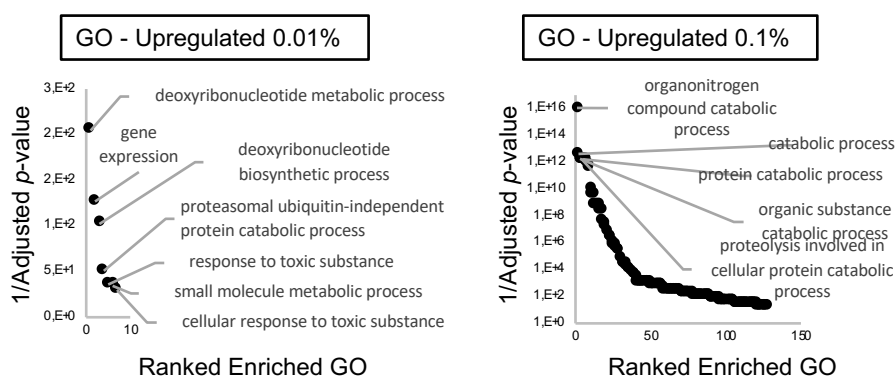
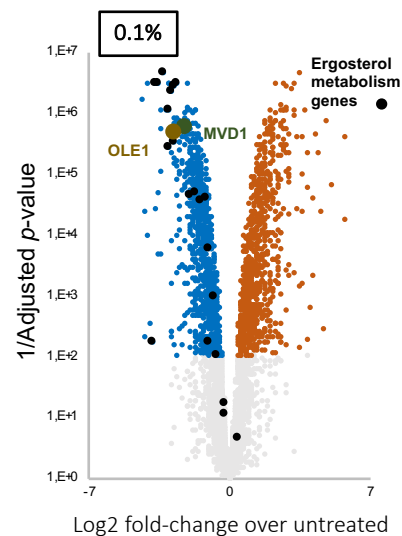
A**B****C****D****E****F****H****G****I**

Figure S1. MMS treatment triggers a downregulation of the fatty acid unsaturation and sterol transcriptional network

A. The number of lipid droplets in individual nuclei of *S. cerevisiae* cells treated as indicated was counted and plotted. Each dot of a light color refers to one nucleus. At least 300 nuclei were considered per condition and experiment. Three independent experiments were performed. To account for reproducibility, each experiment is shown in a different color. Darker, bigger dots indicate the mean of each experiment. The horizontal black line indicates the mean of the means.

B. Heatmaps of chip average signal intensity for every gene after normalization and filtering to visualize the three replicates. See also [Table S1](#).

C. Heatmaps of gene expression upon MMS treatment. Scale represents the averaged Log2 fold-change over untreated samples of the three considered independent experiments. See also [Table S2-4](#).

D. Volcano plots of all genes in response of the three doses of MMS. Fold-changes were computed from the average RNA signal of MMS-treated samples *versus* the average RNA signal of untreated samples. Adjusted *p*-values were computed with the Limma software [9] and corrected for multiple tests. Genes with significant changes according to Adjusted *p*-value are depicted in color, with upregulated ones in orange and downregulated ones in blue. The considered MMS dose is indicated above each graph.

E. Venn Diagrams representing the overlap between the three doses of MMS in absolute numbers. Left: upregulated genes. Right: downregulated genes.

F, G. Overrepresentation test on downregulated genes (F) or the upregulated ones (G) upon 0.01%- and 0.1%-MMS treatment. Enrichment is computed with Fisher's test and corrected for multiple testing by false discovery rate. $1/\text{Adjusted } p\text{-values}$ for all enriched pathways are represented. The top pathways are annotated. See also [Table S5-9](#).

H, I. Volcano plots of all genes in response to 0.01% MMS and 0.1% MMS. Fold-changes are computed from the average RNA signal of MMS-treated samples versus the average RNA signal of untreated ones. Adjusted *p*-values were computed with the Limma software [9] and corrected for multiple tests. Genes with significant changes according to the adjusted *p*-values are depicted in color, where upregulated ones are shown in orange and downregulated ones in blue. Genes annotated as related to ergosterol metabolism are annotated and depicted in black. *OLE1* and *MVD1* are represented in brown and green, respectively. See also [Table S2-4](#).