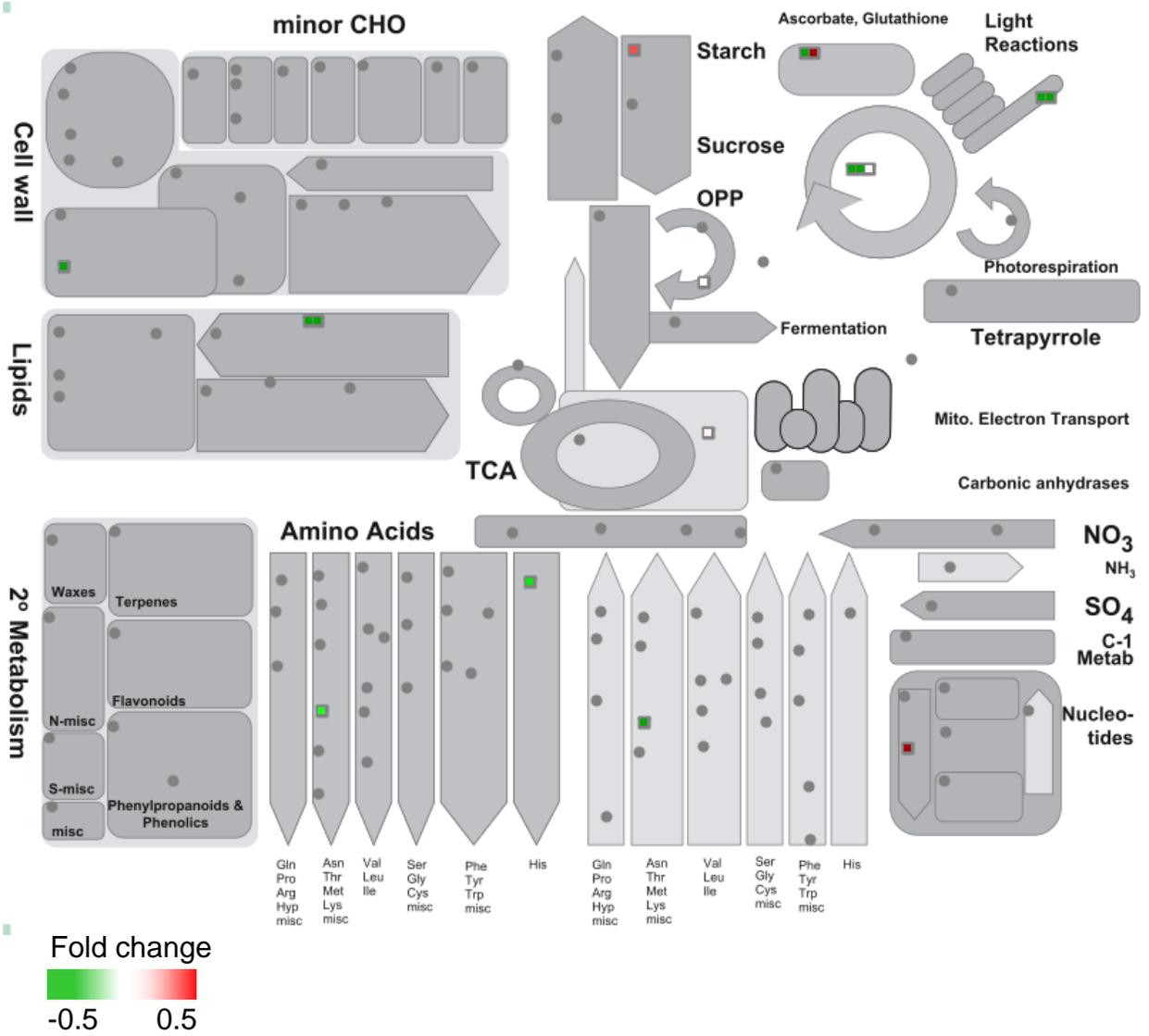


Supplementary Fig. 1

GO categories of proteins with differential abundance in maize treated with plant-derived smoke. Seeds were treated without or with 2000 ppm plant-derived smoke for 4 days. Proteins were extracted from shoot and identified using a gel-free/label-free proteomic technique. Proteins with differential abundance were classified as biological, cellular, and molecular function by WEGO according to the GO terms. A total of 69 proteins identified in maize were analyzed by WEGO. The x-axis indicates the number of proteins. Categories that contained zero proteins are marked with (-).



Supplementary Fig. 2

Metabolic pathway of proteins identified in maize treated with plant-derived smoke. Maize seeds were treated without or with 2000 ppm plant-derived smoke for 4 days. The abundance changes of proteins grouped into functional categories related to primary metabolism were visualized using MapMan software. Each square and color indicate the fold change value of a differentially changed protein. Green and red colors indicate a decrease and increase, respectively, in fold change values compared with untreated one. Abbreviations are follows: CHO, carbohydrate; TCA, tricarboxylic acid cycle; OPP, pyrophosphate.