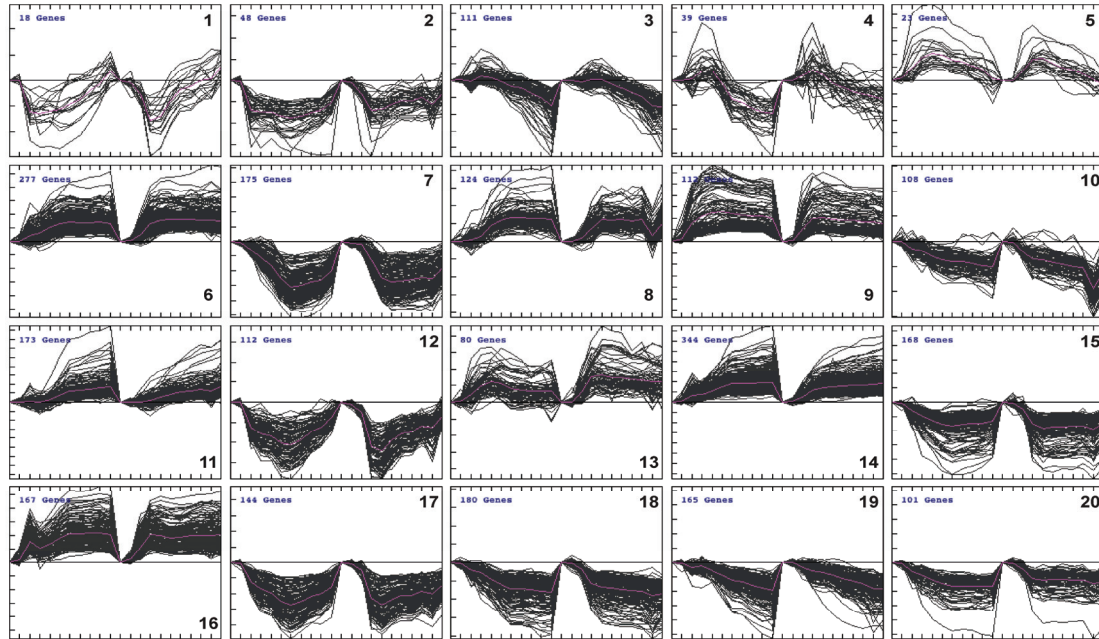


SUPPLEMENTARY FIGURE LEGENDS

A.



B.

Cluster 3

Cell cycle; S phase; Cell wall organization; M phase; Interphase; Cytokinesis. TF binding sites: Ndd1, Fkh1, Fkh2, Mbp, Tec1, Swi5, Swi4, Swi6, Ste1, Ash1

Cluster 4

Nucleosome assembly; Chromatin assembly; Histidine biosynthesis; Rho signal transduction; Methionine biosynthesis; Histone methylation; Establishment of cellular polarity. TF binding sites: Swi4, Swi6, Gcn4

Cluster 5

Pheromone response; Translational elongation; Serine family amino acid biosynthesis; Sulfur metabolism. TF binding sites: Ste12, Dig1

Cluster 6

Response to stress; Response to pH; Response to heat; Fatty acid metabolism; Regulation of Ras GTPase activity; Response to toxin; Autophagy.

Cluster 9

Sulfur amino acid metabolism; Methionine metabolism; Aspartate family metabolism; Serine family metabolism; Cysteine metabolism; Response to hydrogen peroxide; Response to cadmium; Oxidation-reduction; Response to oxidative stress; Autophagy. TF binding sites: Fkh1, Gcn4, Cbf1, Met31, Met32

Cluster 10

DNA packaging; Chromosome condensation; DNA replication; Mitochondrial translation; Chromatin modification; Histone methylation.

Cluster 11

Protein folding; Generation of precursor metabolites and energy (TCA cycle); Glucose metabolism; Oxidation-reduction; ATP synthesis-coupled electron transport; Iron-sulfur cluster assembly; Electron transport chain. TF binding sites: Msn2, Msn4, Hap4.

Cluster 13

Amino acid biosynthesis; Pheromone response; GPCR signaling. TF binding sites: Ste12, Gcn4.

Cluster 14

Autophagy; Response to heat; Mitochondrion degradation; Negative regulation of gluconeogenesis; Sporulation; Lactate metabolism.

Cluster 16

Response to heat; Metabolism of energy reserves; Glycogen biosynthesis; Glucose metabolism; Generation of precursor metabolites and energy; Trehalose metabolism; Oxidation-reduction; Autophagy; Phosphate metabolism; Response to oxidative stress. TF binding sites: Msn2, Msn4.

Cluster 19

Cell cycle; Mitosis; DNA replication; Chromosome segregation; Cell polarity; DNA repair. TF binding sites: Mbp1, Swi4, Swi6, Stb1.

Cluster 20

Amino acid catabolism; Divalent metal ion transport; Electron transport (cytochrome c to oxygen); Mitosis; DNA synthesis during DNA repair; fermentation.

Figure S1. *k*-means clustering of Met-dependent genes in two biosynthetic mutants. A) *k*-means clustering and B) Gene Ontology (GO) term enrichment for genes that are similarly expressed in *met6Δ* and *met13Δ* during Met starvation. Each cluster shows data for *met6Δ* (left) and *met13Δ* (right).

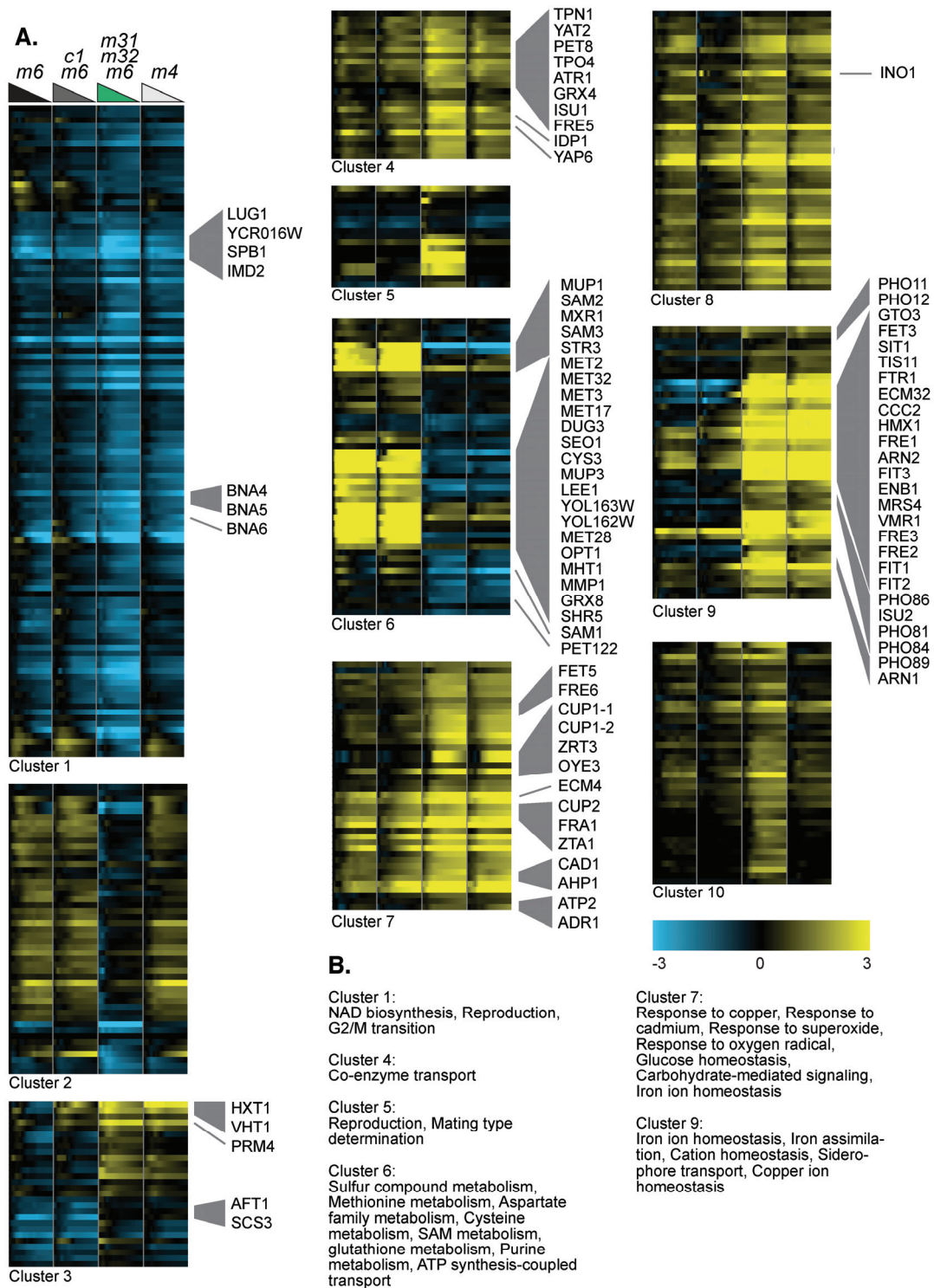
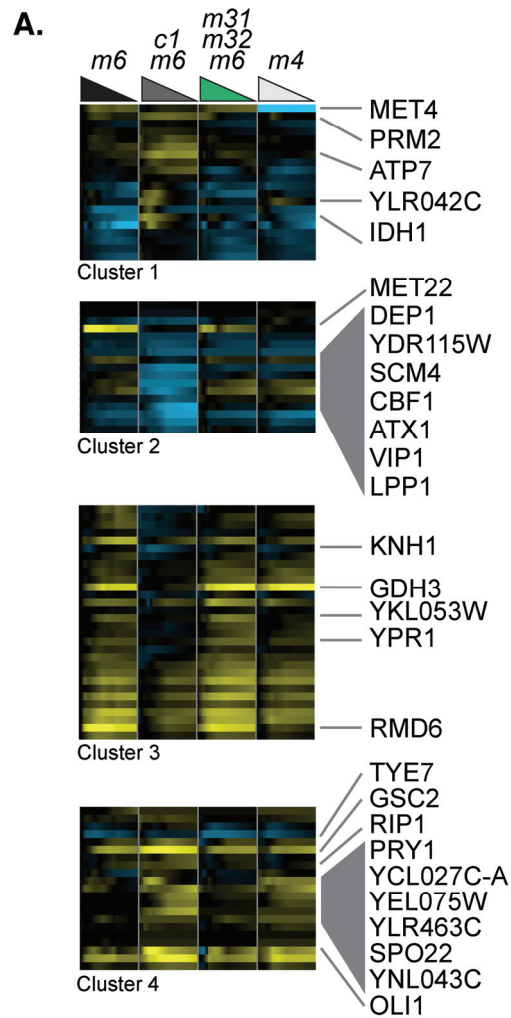


Figure S2. All genes whose expression depends on *MET31/MET32*. A) All genes that depend statistically significantly on *MET31/MET32* but not *CBF1*. Strain order is *met6Δ*, *cbf1Δmet6Δ*, *met31Δmet32Δmet6Δ*, *met4Δ*. Genes of particular interest are shown. B) GO term enrichment.



B. Cluster 1:
Deoxyribonucleotide metabolism

Cluster 2:
Sulfate assimilation

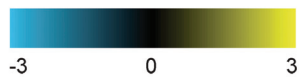


Figure S3. All genes whose expression depends on *CBF1*. A) All genes that depend statistically significantly on *CBF1* but not *MET31/MET32*. Strain order is *met6Δ*, *cbf1Δmet6Δ*, *met31Δmet32Δmet6Δ*, *met4Δ*. Genes of particular interest are shown. B) GO term enrichment.

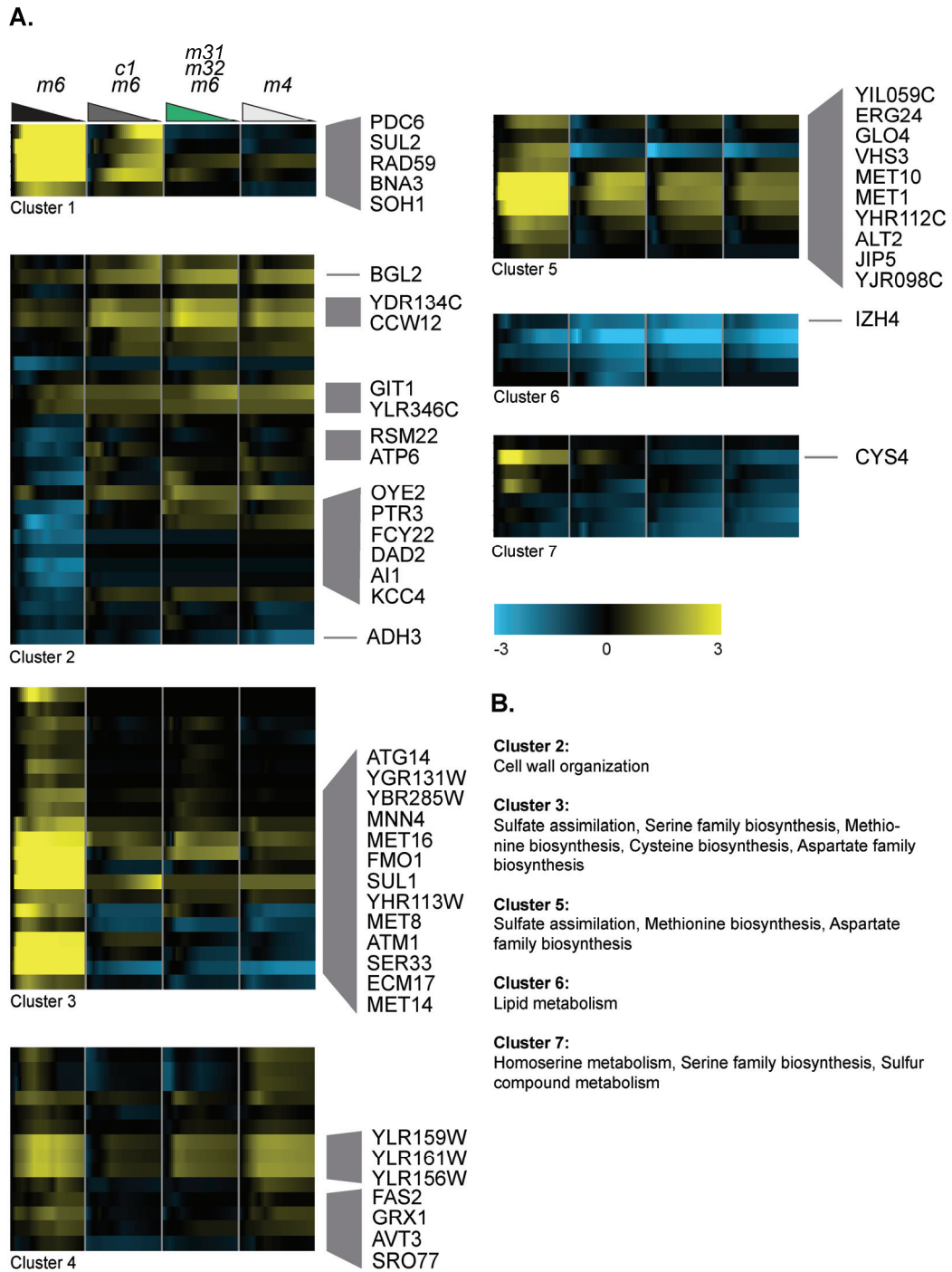


Figure S4. All genes whose expression depends on *MET31/MET32* and *CBF1*. A) All genes that depend statistically significantly on *MET31/MET32* and *CBF1*. Strain order is *met6* Δ , *cbf1* Δ *met6* Δ , *met31* Δ *met32* Δ *met6* Δ , *met4* Δ . Genes of particular interest are shown. B) GO term enrichment.

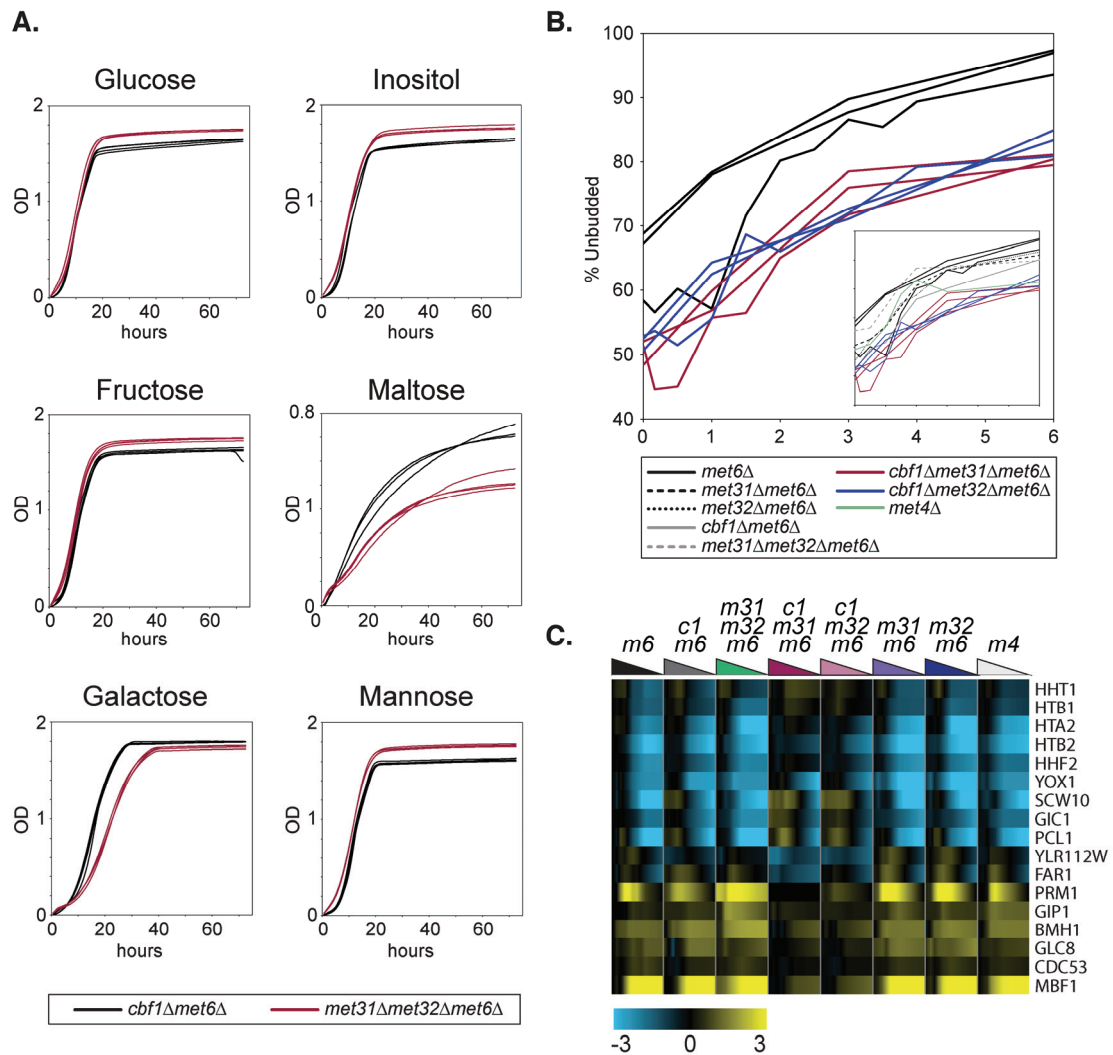


Figure S6. Growth rate and cell cycle arrest phenotypes. A) Comparison of *cbf1Δmet6Δ* (black) and *met31Δmet32Δmet6Δ* (red) growth rates in different carbon sources. B) Cell cycle arrest phenotypes. Percent unbudded cells (*i.e.* bud index) measured during six hours of Met starvation for three replicates each of *met6Δ*, which arrests efficiently, and *cbf1Δmet31Δmet6Δ* and *cbf1Δmet32Δmet6Δ*, which do not arrest efficiently. Inset: Bud index for all strains. C) Potentially Met-dependent cell cycle genes.

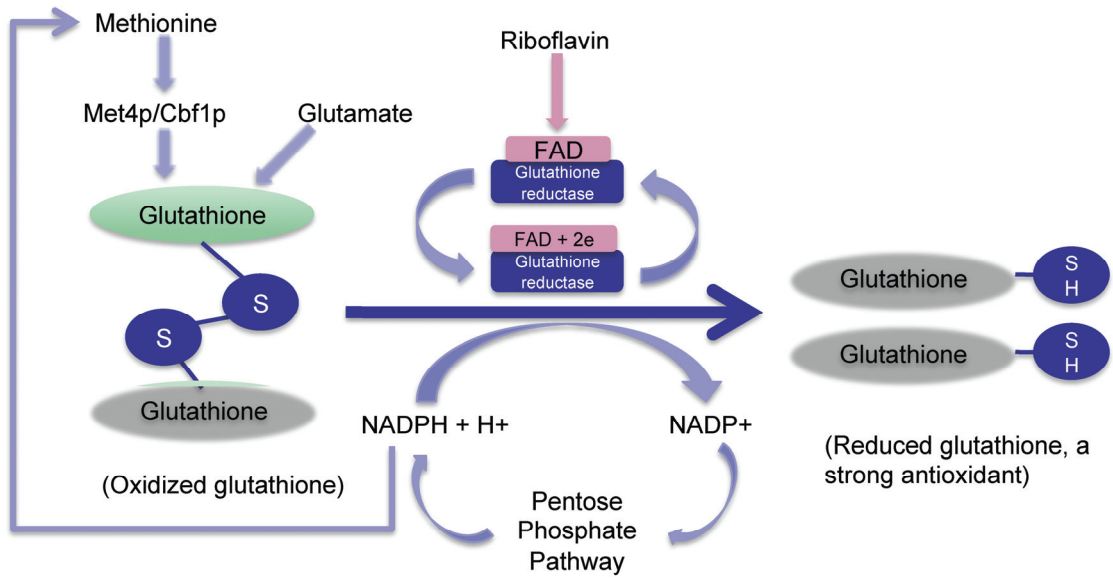


Figure S7. Relationship between antioxidants and Met-regulated metabolites.