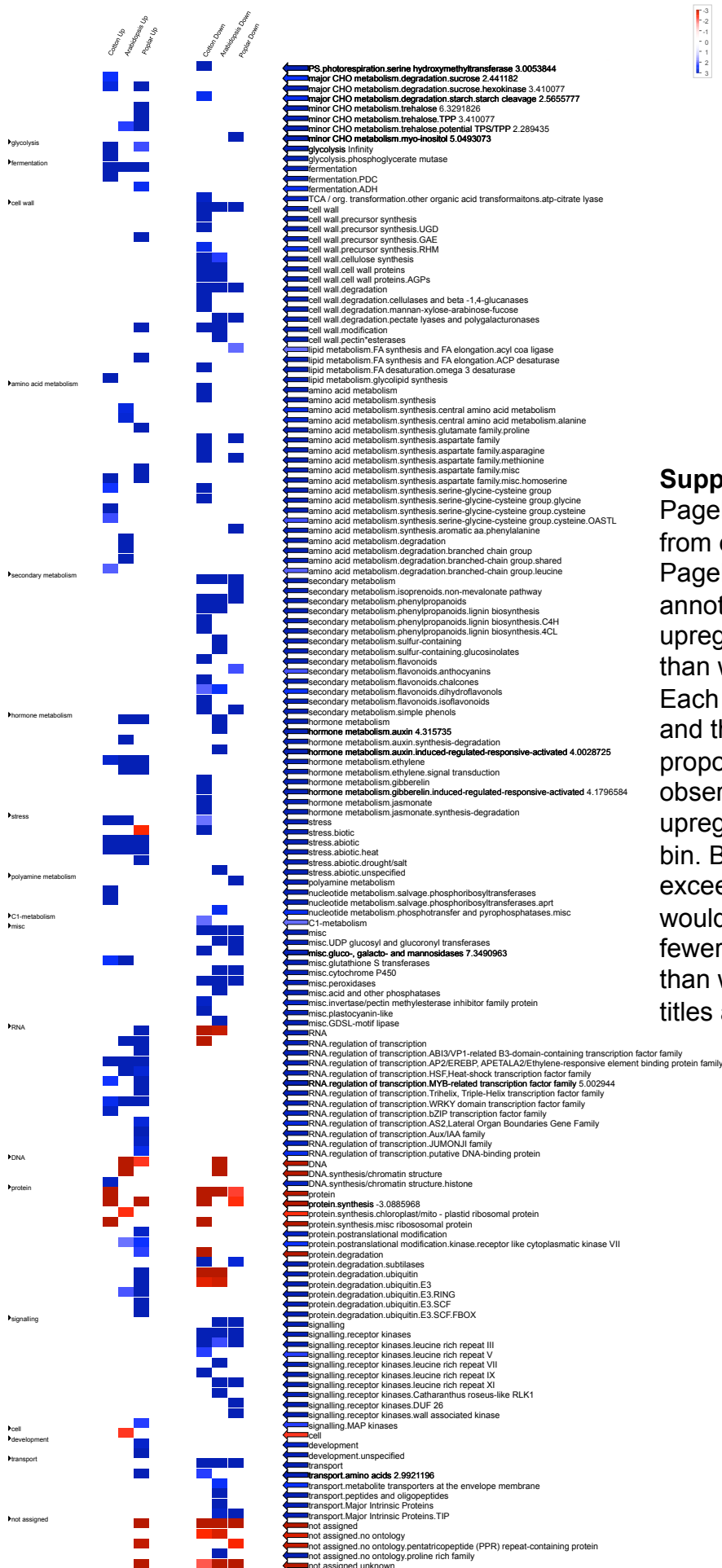


Supplementary files

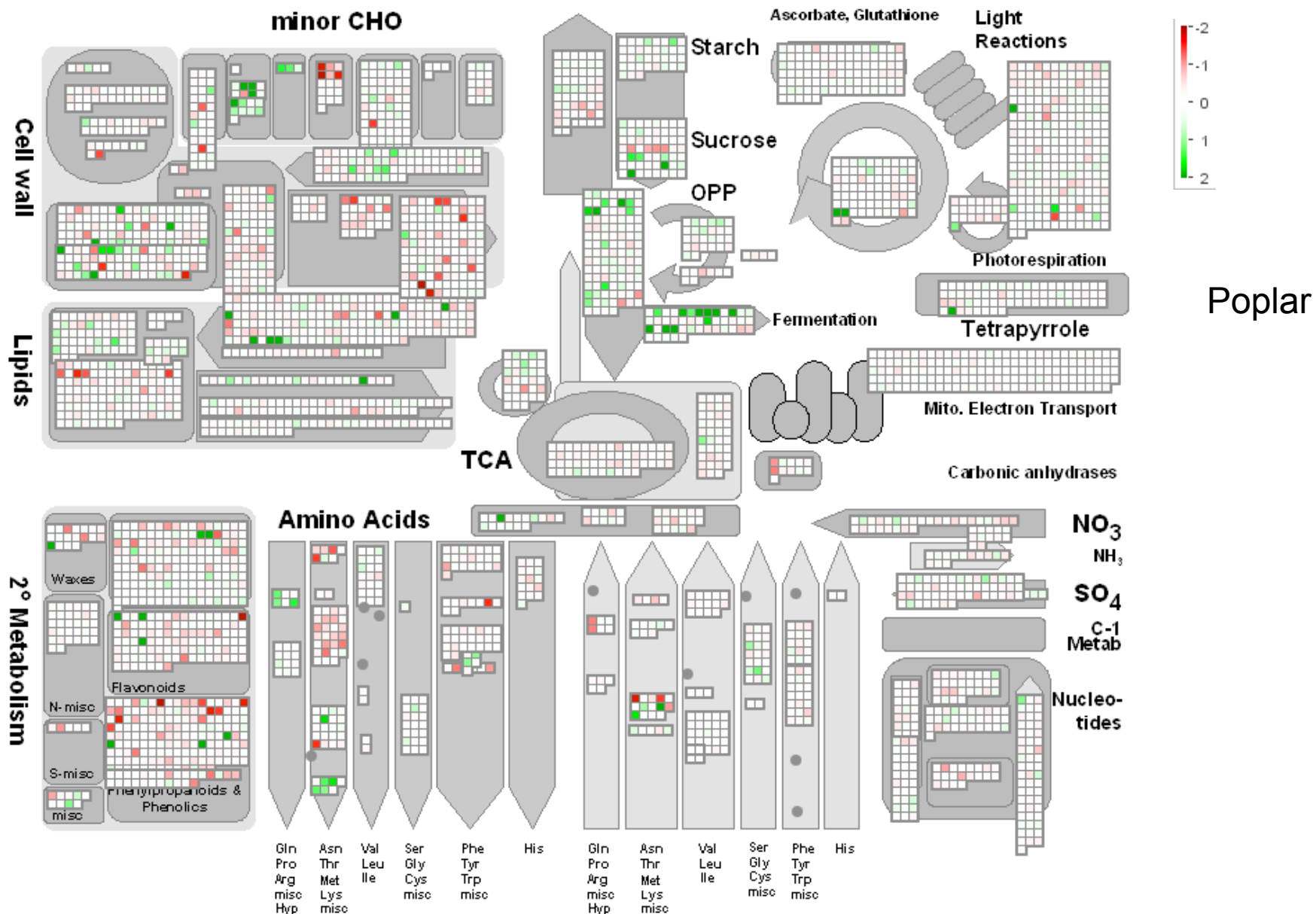
Supplemental Table 1. Genes commonly up-regulated or down-regulated in response to hypoxic stress in cotton, Arabidopsis and Poplar.

Supplemental Figure 1. Supplemental Figure S1. MapMan overviews of global transcriptional responses to hypoxia/waterlogging in poplar, cotton and Arabidopsis. Each box on the metabolic overview chart corresponds to a gene represented on the organisms Affymetrix array chip. Colours represent the log₂ value of transcript abundance difference between stressed and control arrays, where the colour intensity is proportional to the log₂ value. Green boxes indicate genes that are upregulated in response to the stress while red boxes indicate genes downregulated in response to the stress.

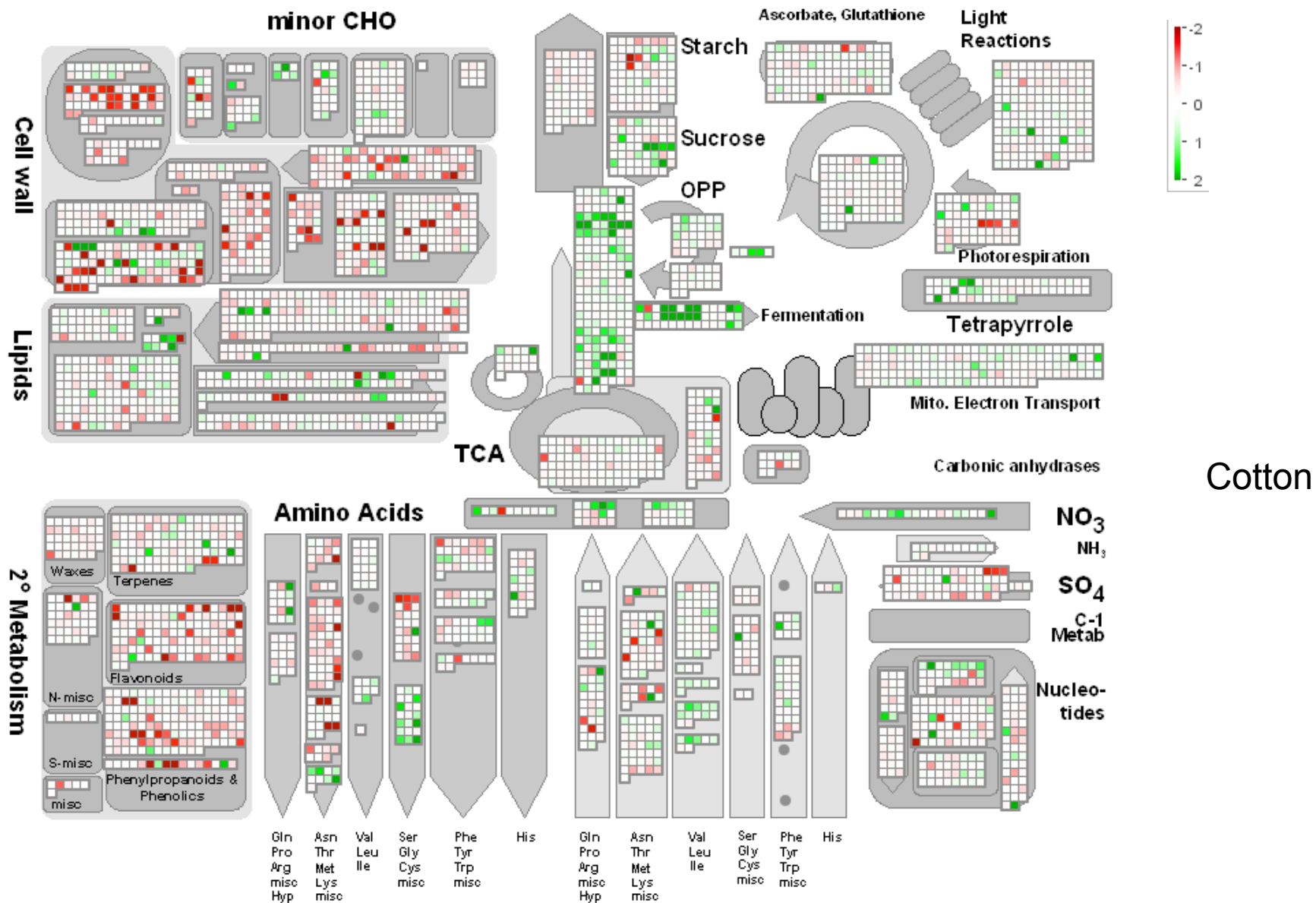
Supplemental Figure 2. Cross species PageMan comparison. Microarray data from each species were analysed in PageMan (Usadel et al. 2006) to identify annotation bins with more or less upregulated or downregulated (> 2-fold) than would be expected by chance. Each box represents an annotation bin and the colour intensity of the bin is proportional to the likelihood of observing the number of genes upregulated or downregulated in each bin. Blue indicates more genes exceeding the expression threshold than would be expected while red indicates fewer genes exceeding the threshold than would be expected. Bin annotation titles are listed to the right.



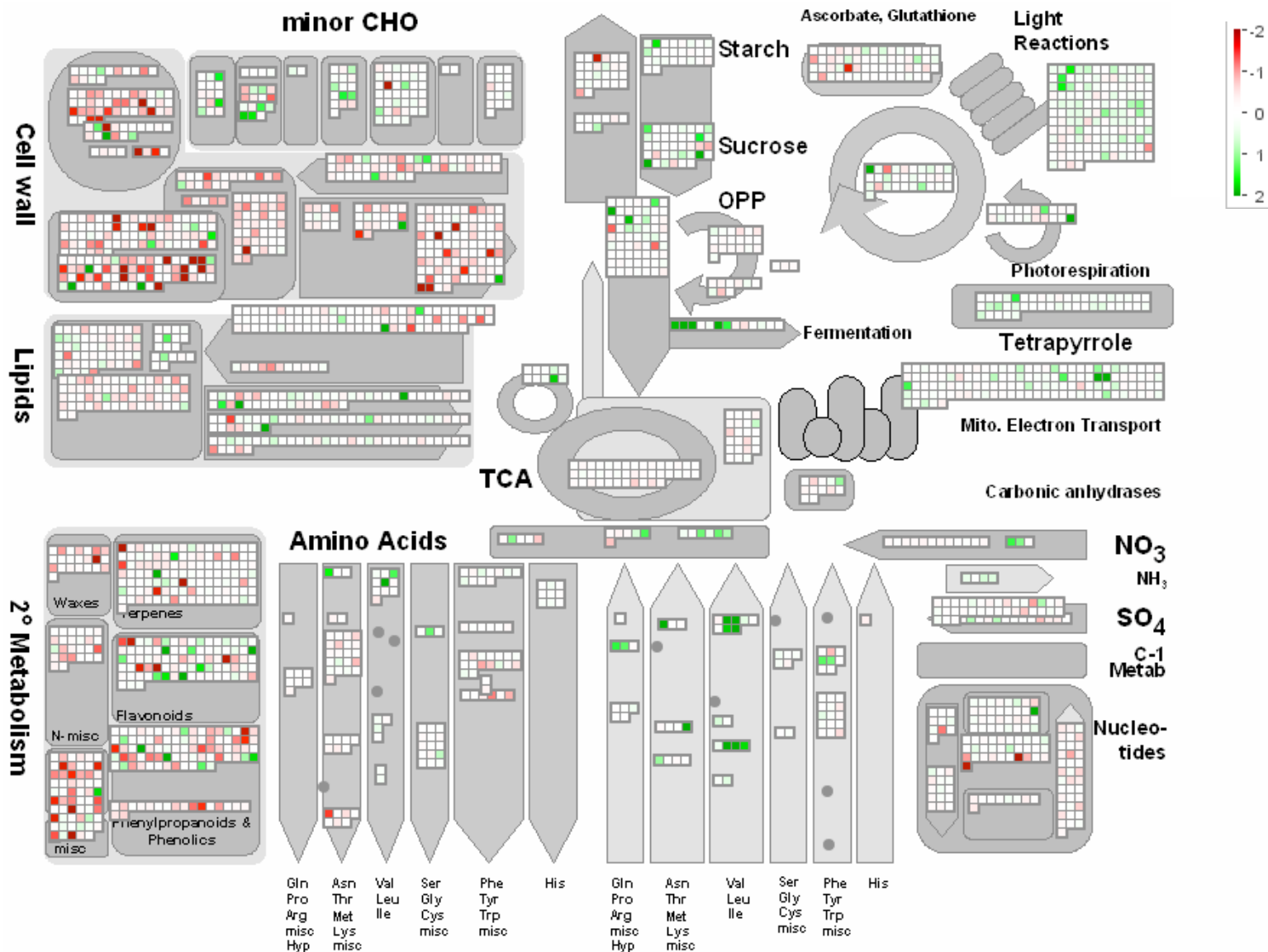
Supplemental Figure 2. Cross species PageMan comparison. Microarray data from each species were analysed in PageMan (Usadel et al. 2006) to identify annotation bins with more or less upregulated or downregulated (> 2 -fold) than would be expected by chance. Each box represents an annotation bin and the colour intensity of the bin is proportional to the likelihood of observing the number of genes exceeding the expression threshold than would be expected while red indicates fewer genes exceeding the threshold than would be expected. Bin annotation titles are listed to the right.



Supplemental Figure S1A. MapMan overviews of global transcriptional responses to hypoxia/waterlogging in poplar. Each box on the metabolic overview chart corresponds to a gene represented on the organisms Affymetrix array chip. Colors represent the \log_2 value of transcript abundance difference between stressed and control arrays, where the colour intensity is proportional to the \log_2 value. Green boxes indicate genes that are upregulated in response to the stress while red boxes indicate genes down-regulated in response to the stress



Supplemental Figure S1B. MapMan overviews of global transcriptional responses to hypoxia/waterlogging in cotton. Each box on the metabolic overview chart corresponds to a gene represented on the organisms Affymetrix array chip. Colors represent the \log_2 value of transcript abundance difference between stressed and control arrays, where the colour intensity is proportional to the \log_2 value. Green boxes indicate genes that are upregulated in response to the stress while red boxes indicate genes down-regulated in response to the stress



Supplemental Figure S1C. MapMan overviews of global transcriptional responses to hypoxia/waterlogging in Arabidopsis. Each box on the metabolic overview chart corresponds to a gene represented on the organisms Affymetrix array chip. Colors represent the \log_2 value of transcript abundance difference between stressed and control arrays, where the colour intensity is proportional to the \log_2 value. Green boxes indicate genes that are upregulated in response to the stress while red boxes indicate genes down-regulated in response to the stress

Table 1. Summary of Pageman functional bins affected by hypoxic stress in cotton, Arabidopsis and Poplar

Functional bin	Number of sub-bins with upregulated genes over-represented			Number of sub-bins with downregulated genes over-represented		
	Cotton	Arabidopsis	Poplar	Cotton	Arabidopsis	Poplar
major CHO metabolism	2	0	1	1	0	0
minor CHO metabolism	0	1	3	0	0	1
glycolysis	2	0	1	0	0	0
fermentation	2	1	2	0	0	0
cell wall	0	0	2	11	8	3
lipid metabolism	0	0	1	1	0	1
amino acid metabolism	5	5	3	7	0	3
secondary metabolism	0	0	0	10	6	5
hormone metabolism	1	4	3	4	3	0
stress	3	3	4	2	1	0
nucleotide metabolism	2	0	0	0	1	0
misc	1	1	0	5	6	5
RNA	4	4	12	2	1	0
DNA	1	2	1	0	2	0
Protein	3	3	9	7	3	3
signalling	0	0	1	4	6	6
development	0	0	2	0	0	0
transport	0	0	1	2	5	2
not assigned	0	0	3	3	4	3