Supplementary files

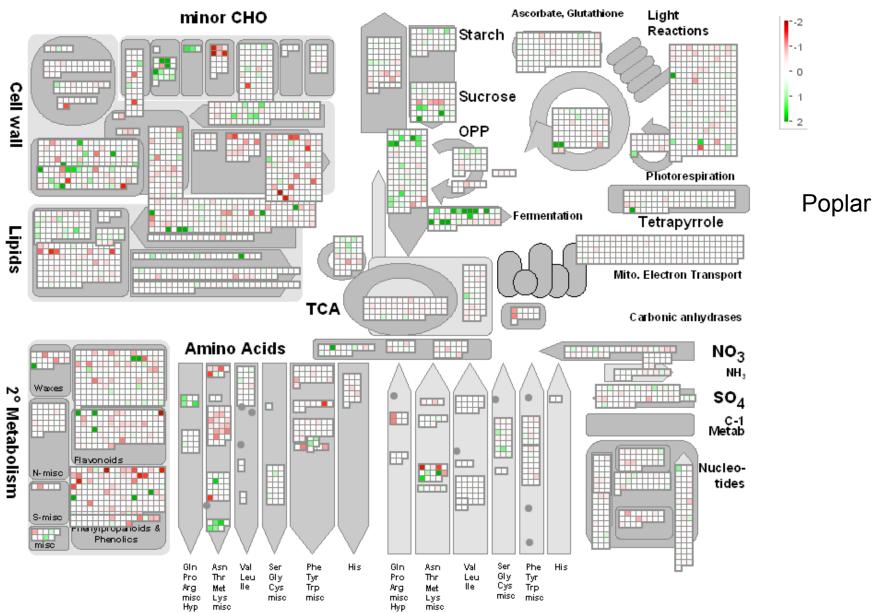
Supplemental Table 1. Genes commonly up-regulated or down-regulated in response to hypoxic stress in cotton, Arabidopsis and Poplar.

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 verview 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.

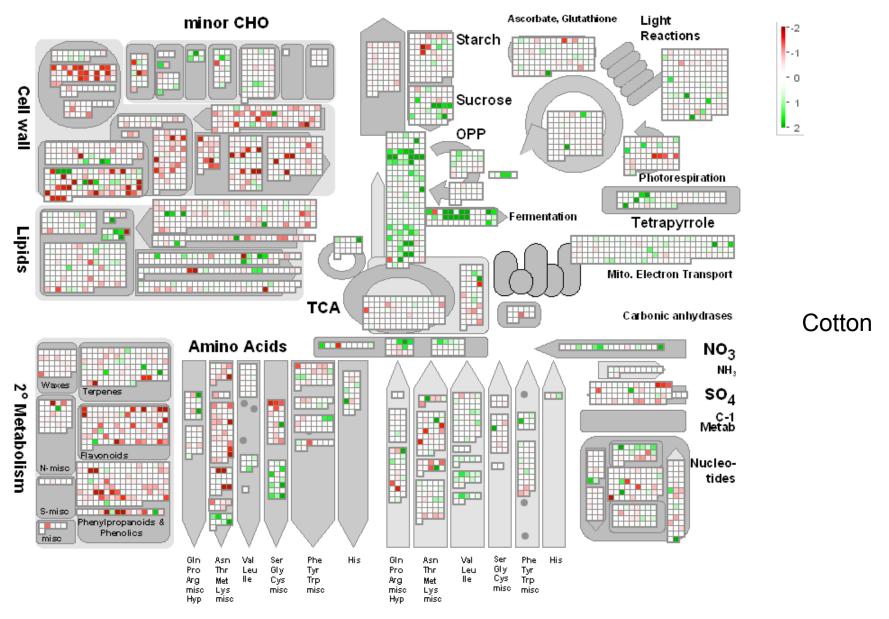
Supplemental Figure 2. Cross species PageMan comparison. Microarray data from each species were analysed in PageMan (Usadel et al. 2006) to identify annotation bins with more or less upregulated or downregulated (> 2-fold) than would be expected by chance. Each box represents an annotation bin and the 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.

PS.photorespiration.serine hydroxymethyltransferase 3.0053844
Imajor CHO metabolism.degradation.sucrose 2.441182
Imajor CHO metabolism.degradation.sucrose.hexokinase 3.410077
Imajor CHO metabolism.degradation.starch.starch.cleavage 2.5655777
Imajor CHO metabolism.tedabose 6.32918267
Imajor CHO metabolism.tedabose 6.32918267 minnor CHO metabolism.trehalose 6.3291826
minnor CHO metabolism.trehalose.TPP 3.410077
minnor CHO metabolism.trehalose.potential TPS/TPP 2.289435
minnor CHO metabolism.myo-inosikof 5.0493073
minnor CHO ■fermentation.ADH
■TCA / org. transformation.other organic acid transformaitons.atp-citrate lyase TICA / org. transformation.other organic acid transformations.4 cell wall precursor synthesis. Cell wall precursor synthesis. UGD cell wall precursor synthesis. UGD cell wall precursor synthesis. GAE cell wall precursor synthesis. RHM cell wall cellulose synthesis. Cell wall cell wall proteins cell wall cell wall proteins cell wall cell wall proteins. AGPs cell wall cell wall proteins. Cell wall cell wall proteins. Cell wall cell wall degradation. Cell w cell wall degradation pectale lyases and polygalacturonases cell wall modification cell wall pectin'esterases lipid metabolism.FA synthesis and FA elongation.acyl coa ligase lipid metabolism.FA synthesis and FA elongation.acyl coa ligase lipid metabolism.FA desaturation.omega 3 desaturase lipid metabolism.A desaturation.omega 3 desaturase lipid metabolism.Agvolipid synthesis amino acid metabolism synthesis amino acid metabolism synthesis central amino acid metabolism synthesis central amino acid metabolism amino acid metabolism.synthesis dutamate family proline amino acid metabolism.synthesis agaratate family amino acid metabolism.synthesis aspartate family amino acid metabolism.synthesis aspartate family amino acid metabolism.synthesis aspartate family asparagine amino acid metabolism synthesis asparate family' amino acid metabolism synthesis asparate family asparagine amino acid metabolism synthesis asparate family asparagine amino acid metabolism synthesis asparate family misc mino acid metabolism synthesis asparate family misc homoserine amino acid metabolism synthesis serine-glycine-oysteine group amino acid metabolism synthesis serine-glycine-oysteine group glycine amino acid metabolism synthesis serine-glycine-oysteine group glycine amino acid metabolism synthesis serine-glycine-oysteine group cysteine. OASTL amino acid metabolism synthesis serine-glycine-oysteine group cysteine. OASTL amino acid metabolism synthesis aromate as phenylalanine amino acid metabolism.degradation amino acid metabolism.degradation branched-chain group shared amino acid metabolism degradation branched-chain group shared amino acid metabolism degradation branched-chain group leucine secondary metabolism scorperondis non-mevalonate pathway secondary metabolism sphenyloropanoids secondary metabolism phenyloropanoids lignin biosynthesis secondary metabolism phenyloropanoids lignin biosynthesis C4H secondary metabolism phenyloropanoids lignin biosynthesis C4H secondary metabolism sphenyloropanoids lignin biosynthesis C4L secondary metabolism sulfur containing secondary me secondary metabolism sulfur-containing secondary metabolism sulfur-containing glucosinolates secondary metabolism flavonoids secondary metabolism flavonoids anthocyanins secondary metabolism flavonoids chalcones secondary metabolism flavonoids dihydroflavonois secondary metabolism flavonoids isoflavonoids secondary metabolism simple phenois secondary metabolism simple phenois flavonome metabolism simple phenois hormone metabolism.auxin 4.315735 nomone metabolism entylene signal transduction nomone metabolism ethylene signal transduction nomone metabolism gibberelin induced-regulated-responsive-activated 4.1796584 nomone metabolism gismonate nomone metabolism gismonate synthesis-degradation siress abotic drought/salt siress abotic unspecified polyamine metabolism inucleotide metabolism salvage_phosphoribosyltransferases inucleotide metabolism salvage_phosphoribosyltransferases.aprt inucleotide metabolism.aphosphoriansfer and pyrophosphatases.misc C1-metabolism misc.glutathione S transf misc.cytochrome P450 misc.envidases
misc.acid and other phosphatases
misc.invertase/pectin methylesterase inhibitor family protein RNA-regulation of transcription
RRNA-regulation of transcription
R DNA.synthesis/chromatin structure
DNA.synthesis/chromatin structure.histone protein protein.synthesis -3.0885968 protein.synthesis.chloroplast/mito - plastid ribosomal protein protein synthesis mitscribosomal protein protein synthesis mitscribososomal protein protein postranslational modification protein postranslational modification.kinase.receptor like cytoplasmatic kinase VII protein degradation ignalling ignalling.receptor kinases signalling receptor kinases signalling receptor kinases signalling receptor kinases leucine rich repeat III signalling receptor kinases leucine rich repeat VII signalling receptor kinases leucine rich repeat IVI signalling receptor kinases leucine rich repeat IVI signalling receptor kinases leucine rich repeat XI signalling receptor kinases Catharanthus roseus-lik signalling receptor kinases DIIF 26 signalling receptor kinases wall associated kinase development development.unspecified development.unspecined transport **transport amino acids** 2.9921196 transport.metabolite transporters at the envelope membrane transport.peptides and oligopeptides transport.Major intrinsic Proteins transport.Major intrinsic Proteins.TIP not assigner. not assigned not assigned.no ontology not assigned no ontology pentatricopeptide (PPR) repeat-containing protein assigned no ontology proline rich family and assigned no ontology.

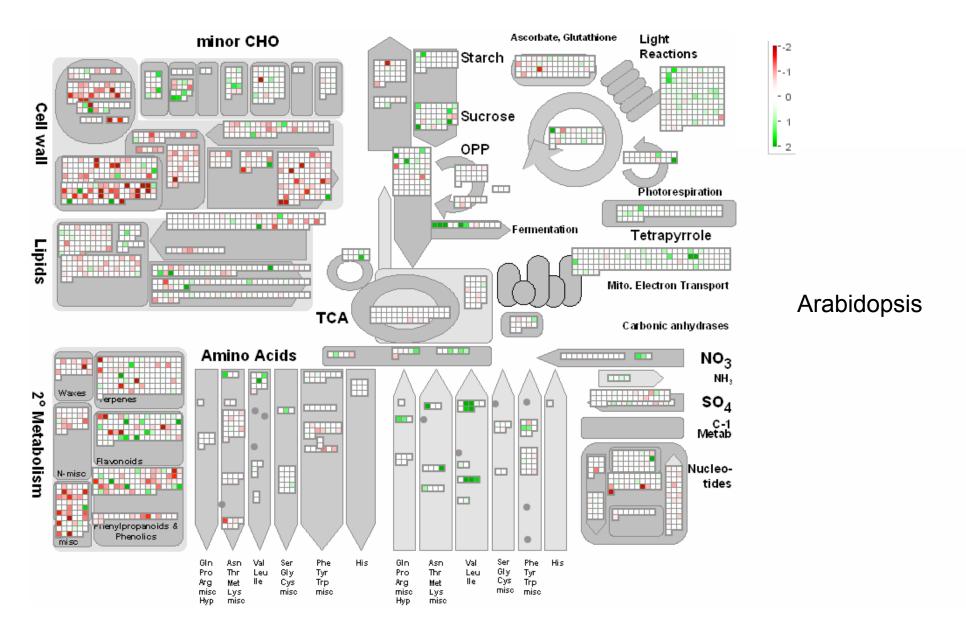
Supplemental Figure 2. Cross species PageMan comparison. Microarray data from each species were analysed in PageMan (Usadel et al. 2006) to identify annotation bins with more or less upregulated or downregulated (> 2-fold) than would be expected by chance. Each box represents an annotation bin and the 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 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