

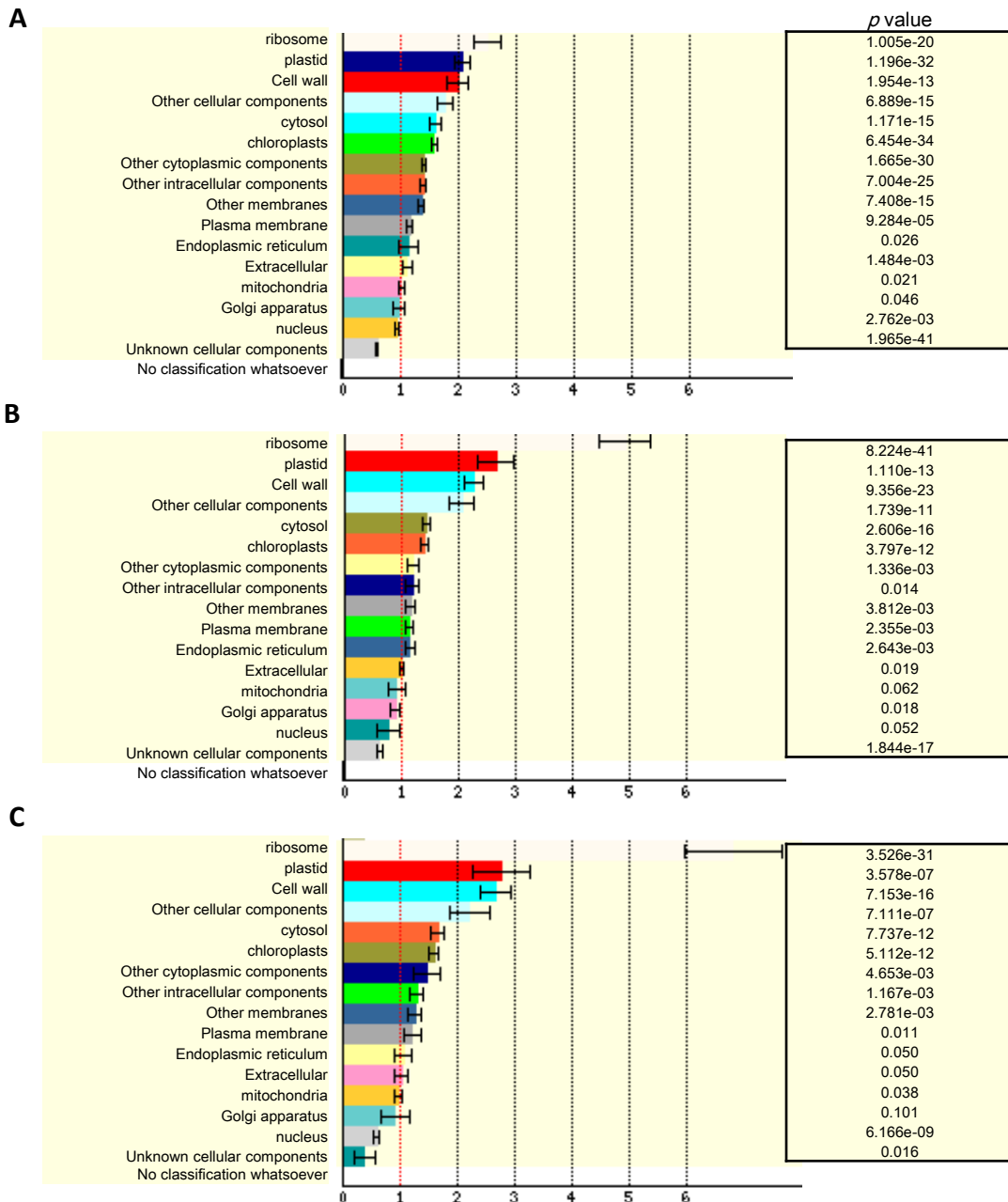
**Supplemental Figure 1: Dark grown phenotype of ABP1 knockdown lines**

**(A)** Hypocotyl length of 4-d-old dark grown seedlings grown in the presence of ethanol vapors. Length differences between WT and each ABP1 knockdown line are significant p value <0.01

**(B)** Phenotype of knockdown lines for ABP1 grown in darkness for 4 days, EtOH induction since germination

**(C)** Experimental disposal for ethanol induction via ethanol vapor

**(D)** Samples used for the transcriptomic analysis and real time PCR. After 8h of exposure to ethanol very subtle phenotypes are observed for SS12K. Bar represents 1cm



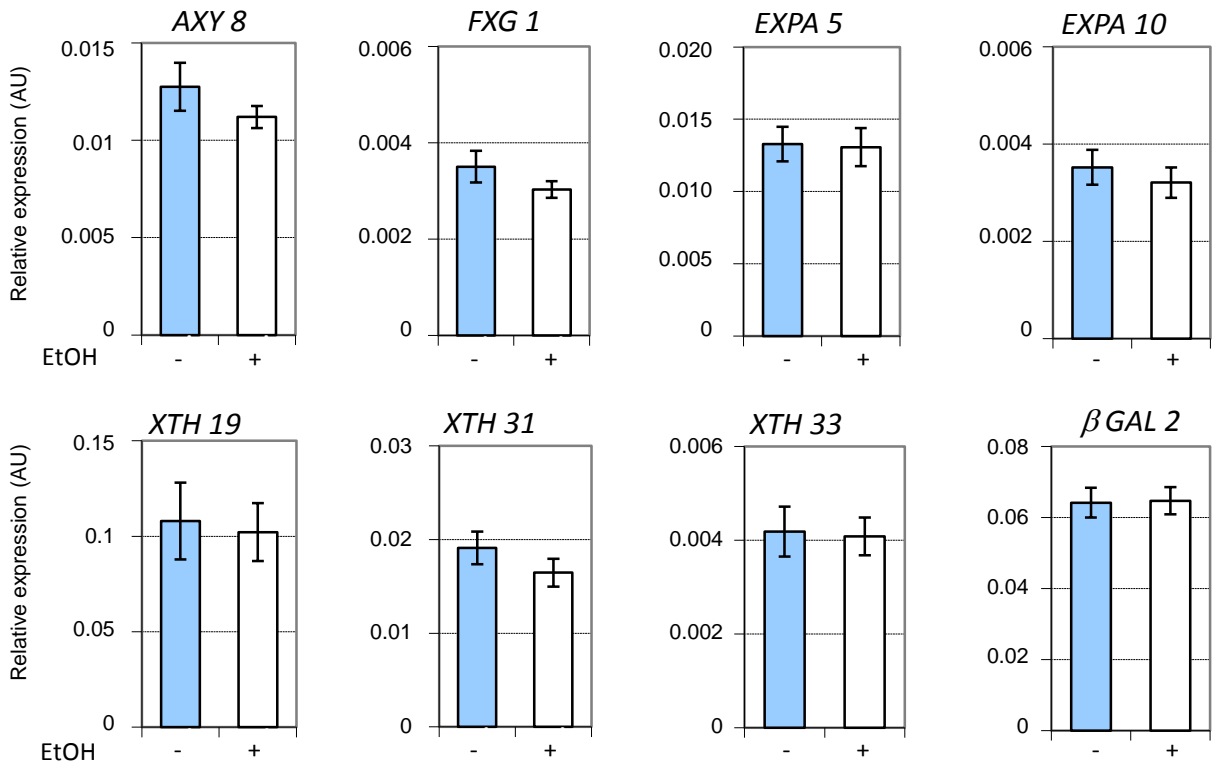
**Supplemental Figure 2: Overview of classes of genes differentially expressed after ABP1 inactivation in dark grown seedlings ordered by cellular component.**

**(A)** Comparison between SS12K and WT ethanol induced since germination (96h).

**(B)** Comparison between SS12K and WT ethanol induced only 8 h before harvesting.

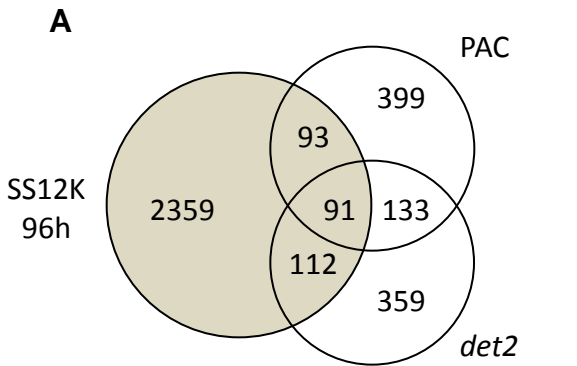
**(C)** Genes in common between short- and long- term ABP1 inactivation

Analysis were performed using Functional Classification Super Viewer available at (<http://bar.utoronto.ca>) (Winter et al., 2007)

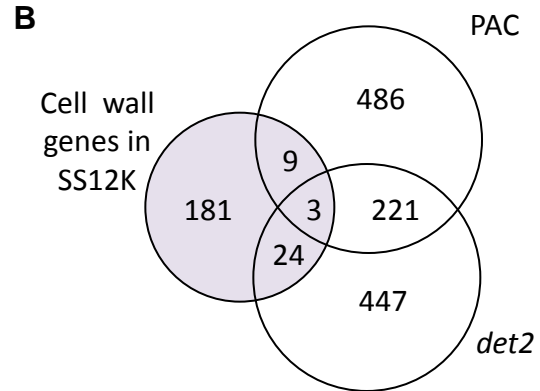


**Supplemental Figure 3: Expression of cell wall related genes after EtOH induction in WT**

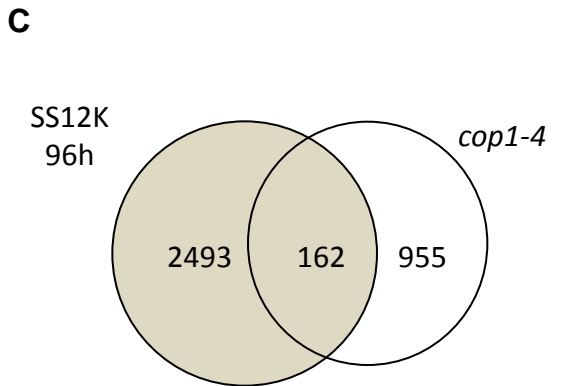
RNA accumulation of a selection of XyG related genes was analysed by RT-PCR. All data were normalized with respect to *ACTIN2-8* and expressed in relative units. Data are means  $\pm$ SD (biological repeats n=9). None of the differences are statistically significant.



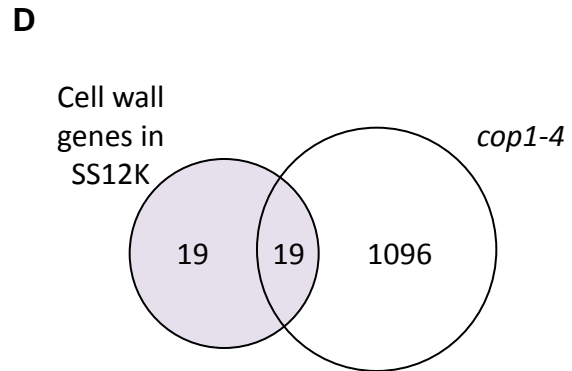
All genes affected by ABP1 knockdown (96h)  
vs  
all genes affected by PAC or by *det2* in darkness



All Cell-wall genes affected by ABP1 knockdown  
vs  
all genes affected by PAC or by *det2* in darkness



All genes affected by ABP1 knockdown (96h)  
vs  
all genes affected by *cop1-4* in darkness



Cell-wall genes affected by ABP1 knockdown  
vs  
genes affected in *cop1-4* in darkness

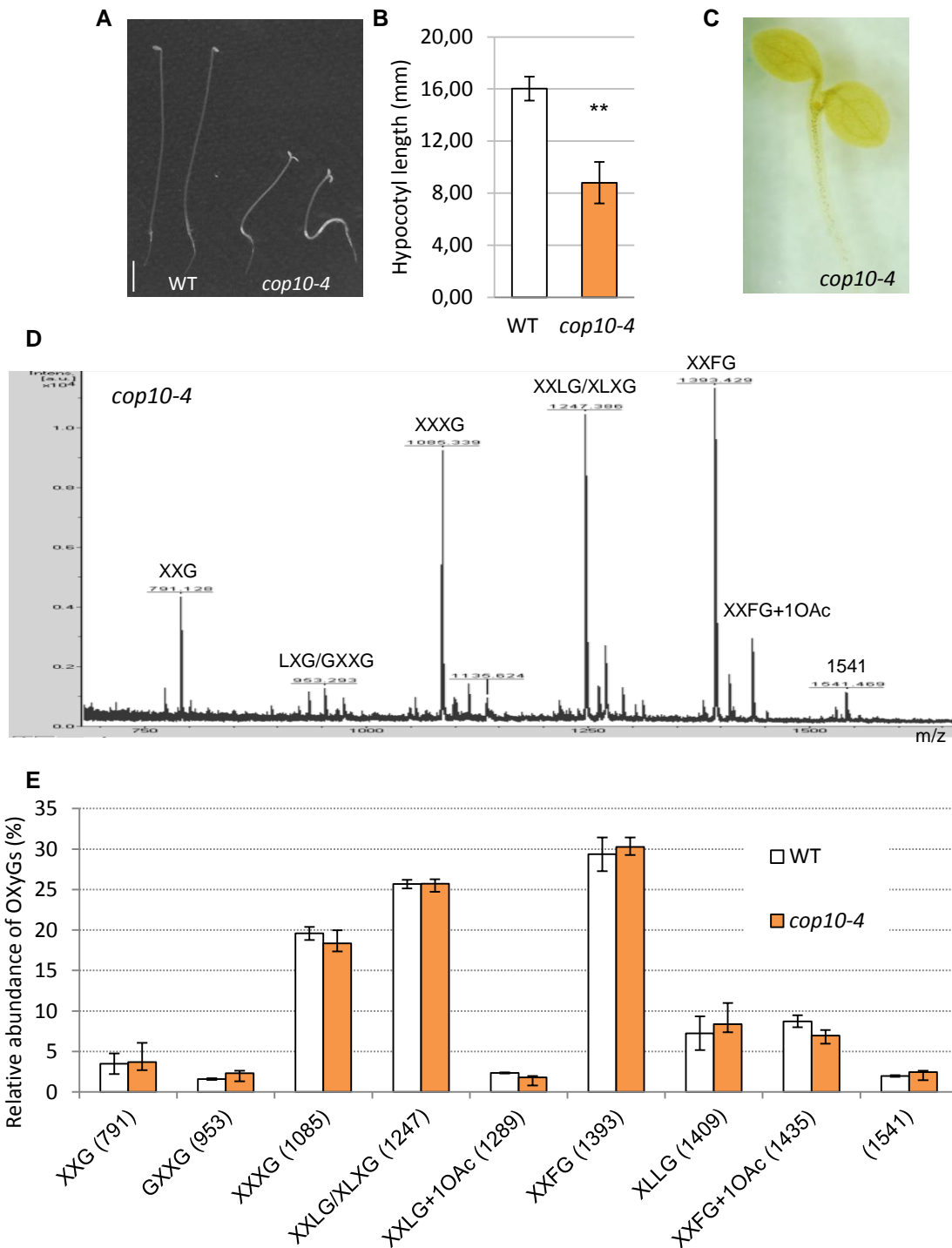
**Supplemental Figure 4: Venn diagram resulting from meta-analysis comparing genes affected in ABP1 knockdown with genes affected in de-etiolated seedlings resulting from alteration in GA, BR or light signalling**

**(A)** Comparison between all genes affected in SS12K inactivated since germination (96h) with genes affected in Col0 treated with PAC or in *det2* mutant grown in darkness

**(B)** Comparison between cell wall related genes affected in ABP1 knockdown and genes affected in Col0 treated with PAC or in *det2* mutant grown in darkness

**(C)** Comparison between all genes affected in SS12K inactivated since germination (96h) with genes affected in dark grown *cop1-4*.

**(D)** Comparison between cell wall related genes affected in ABP1 knockdown and genes affected in dark grown *cop1-4*.



**Supplemental Figure 5: Comparison of xyloglucan composition of dark grown hypocotyls *cop10-4* de-etiolated mutant with WT**

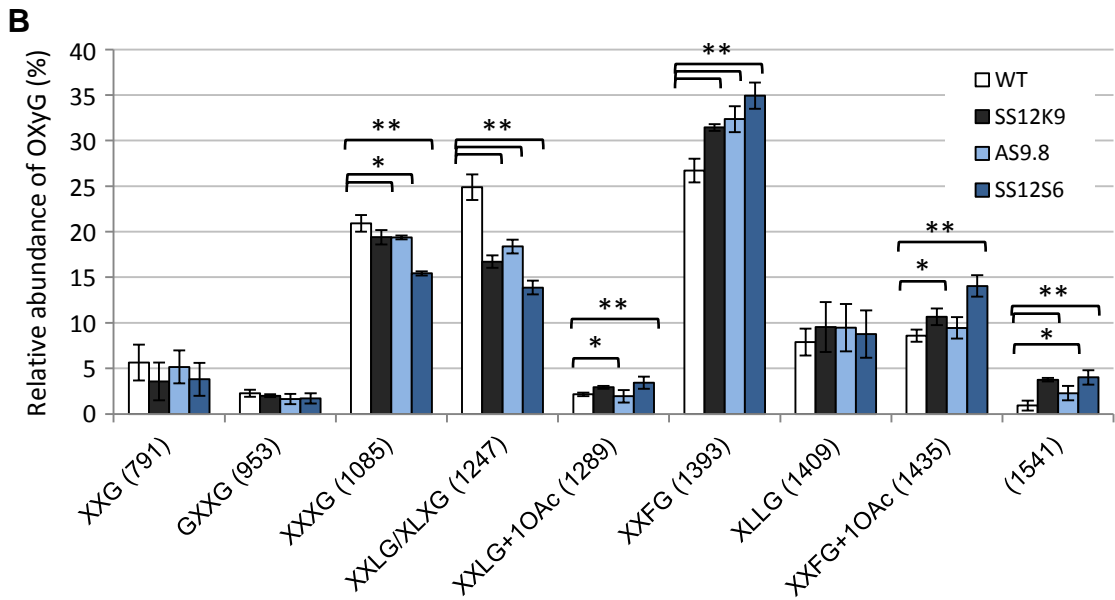
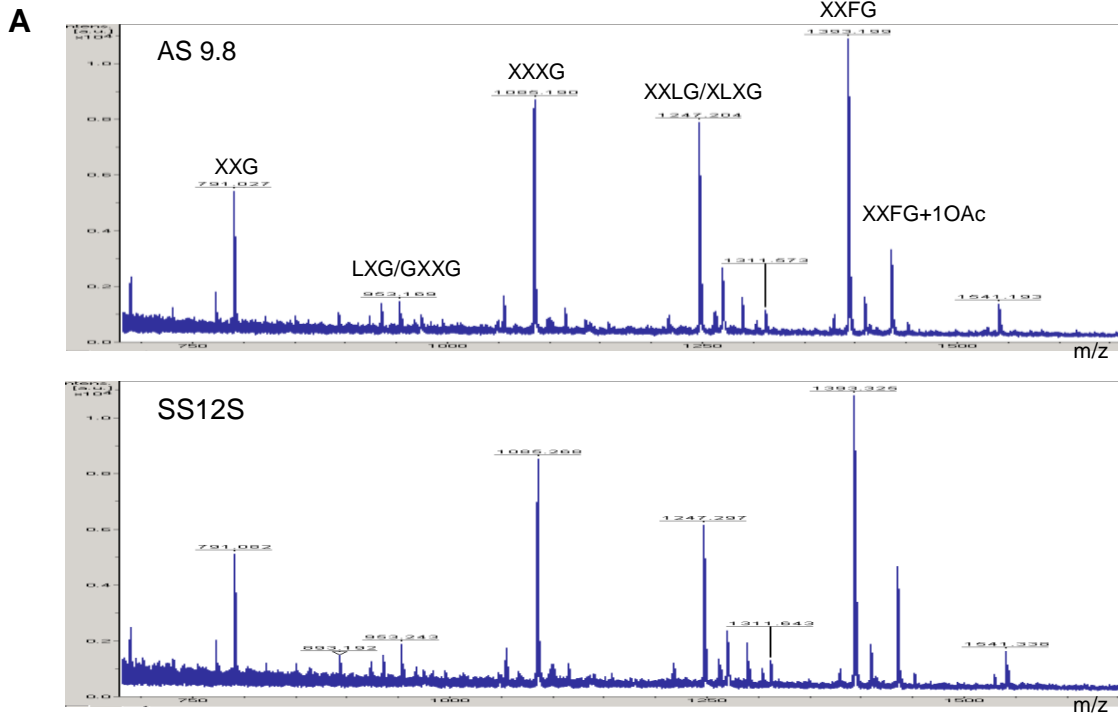
(A) Phenotype of *cop10-4*, bar represents 25 mm

(B) Hypocotyl length of 4 day-old dark grown seedlings; p value \*\* <0.01 (n= 4 x 25)

(C) Lugol staining of *cop10-4*. Bar represents

(D) Representative spectrum of oligosaccharide mass profiling of OXGs of ethanol induced *cop10-4* hypocotyls grown in darkness for 4 days.

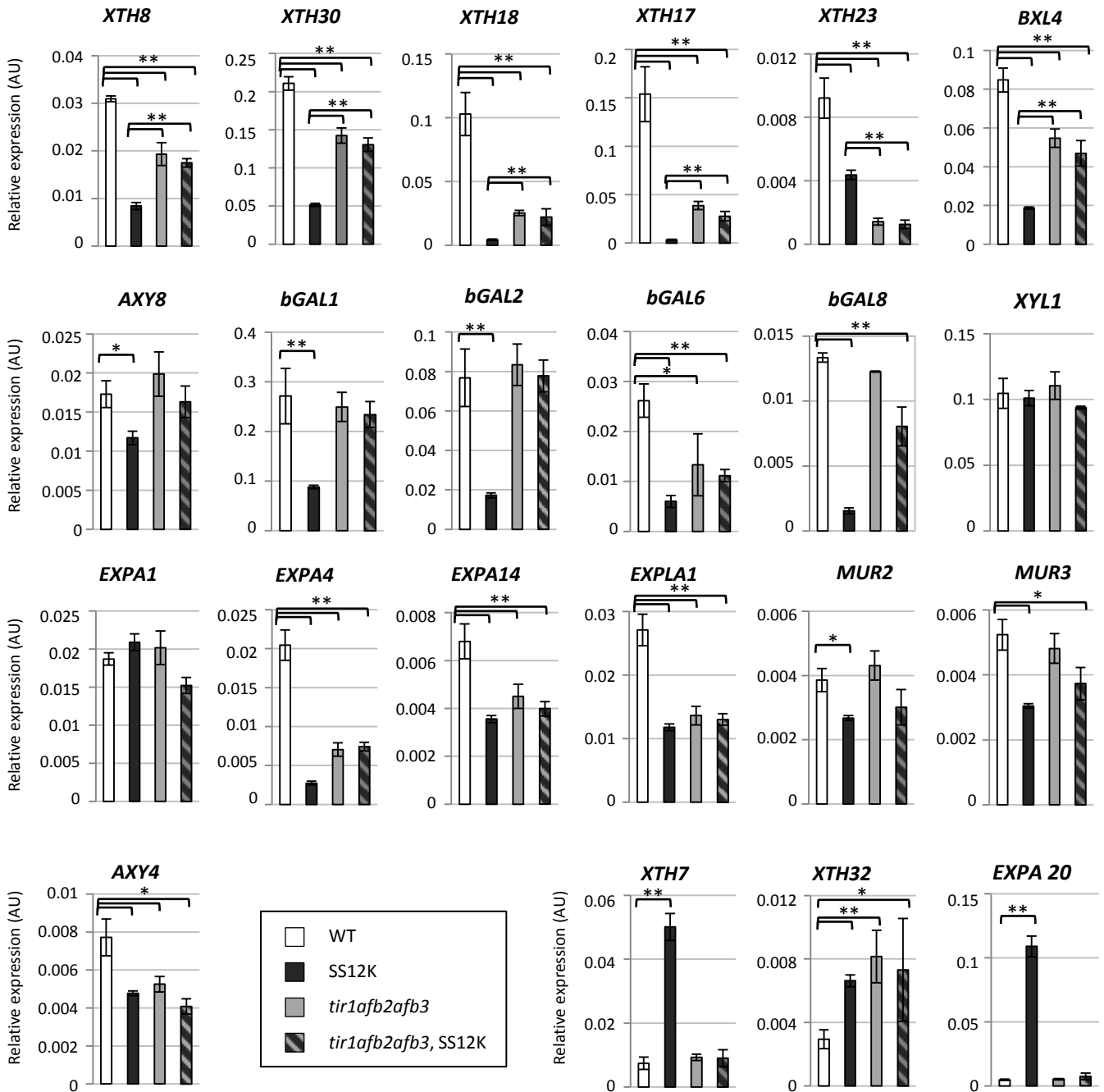
(E) Quantitative statistical analysis of OLIMP data for ethanol induced *cop10-4*. Data are compared with WT; Data are means  $\pm$ SD (biological replicates n=4). None of the differences are statistically significant



**Supplemental Figure 6: Xyloglucan composition in dark grown hypocotyls of various lines inactivated for ABP1**

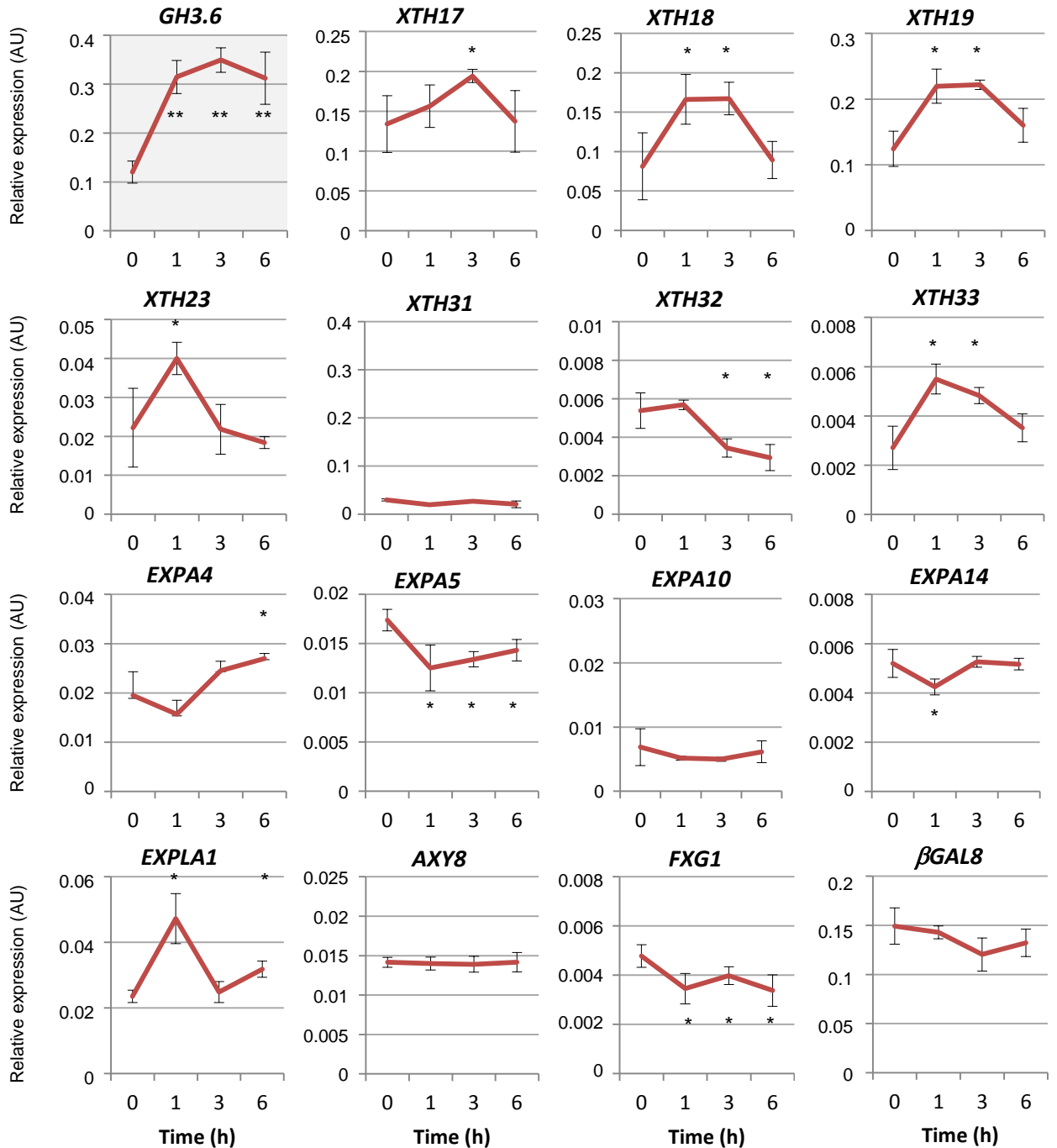
**(A)** Representative spectrum of oligosaccharide mass profiling of OXGs of ethanol induced hypocotyls grown in the dark for 4 days of SS12S and AS9.8 lines.

**(B)** Quantitative statistical analysis of OLIMP data for ethanol induced SS12S and AS9.8 and comparison with WT and SS12K; data are means  $\pm$ SD (biological replicates n=4). P values \* < 0.05 and \*\* < 0.01



**Supplemental Figure 7: XyG gene expression analysed by real-time RT-PCR**

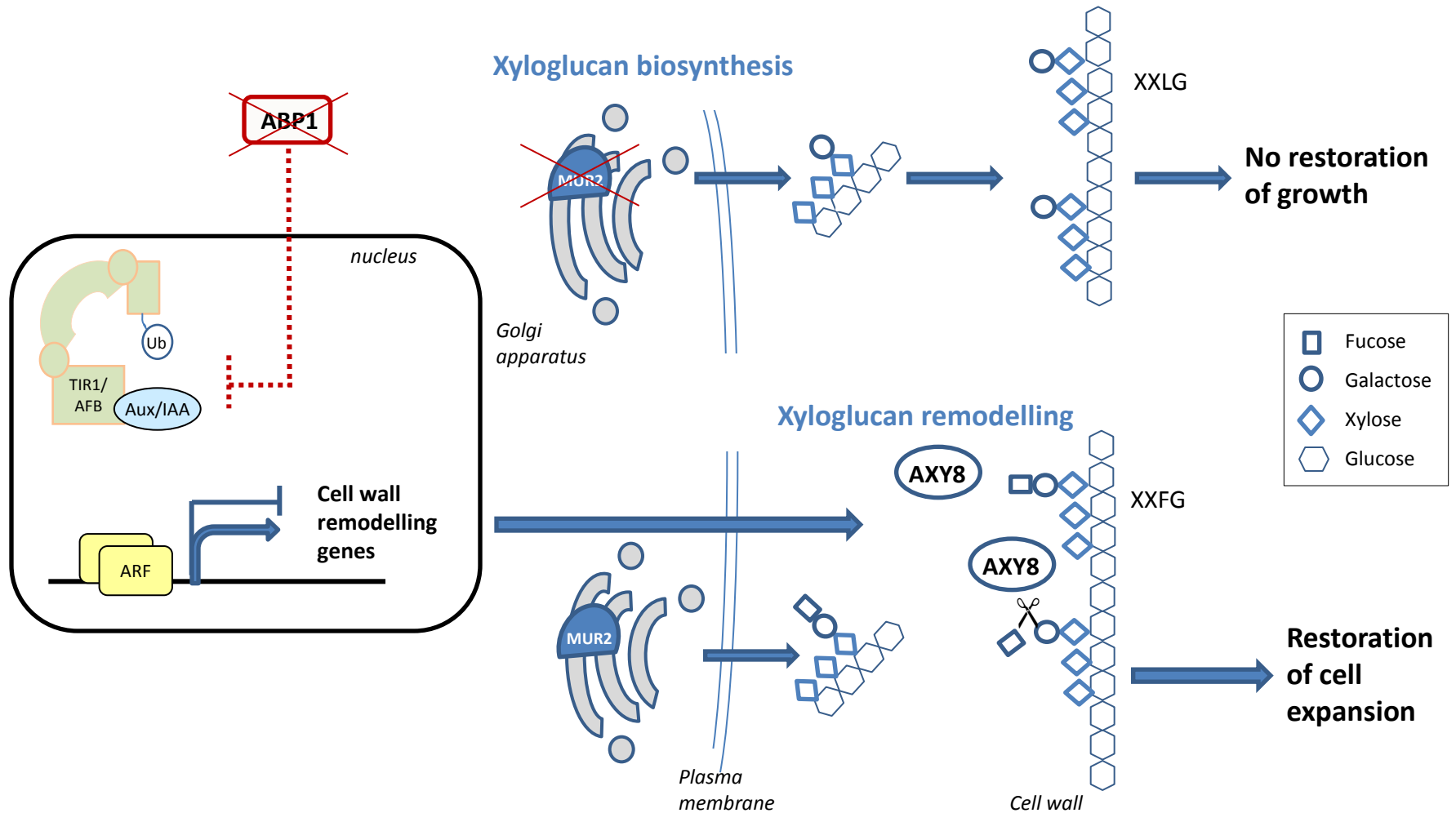
RNA accumulation of a selection of XyG related genes in the distinct genotypes as indicated. All data were normalized with respect to *ACTIN2-8* and expressed in relative units. Data are means  $\pm$ SD (biological repeats  $n=3$ , and two technical repeats for each). Statistical analysis was performed by comparing WT with other genotypes or SS12K with the triple mutants as indicated. \*  $p<0.05$  and \*\*  $p<0.01$



**Supplemental Figure 8: Auxin effect on expression of XyG remodelling genes**

Kinetics of mRNA accumulation of a selection of XyG related genes after 10 $\mu$ M IAA treatment of dark grown WT seedlings. All data were normalized with respect to *ACTIN2-8* and expressed in relative units. bars represent SD (biological repeats n=3, and two technical repeats for each). The early auxin response gene *GH3.6* was used as a positive control for auxin treatment. Statistical analysis was performed by comparing WT seedlings before and after auxin treatment \* p<0.05 and \*\* p<0.001





**Supplemental Figure 9: ABP1 acts on *in muro* xyloglucan composition to modulate cell expansion through an SCF<sup>TIR1/AFBs</sup> dependent pathway**

ABP1 is required for expression of cell wall remodelling genes. Cell expansion results from ABP1-dependent xyloglucan (XyG) remodelling. XyG fucosylation followed by *in muro* defucosylation are critical for cell expansion.

**Supplemental Table 1: Primer list**

Gene name	AGI	Forward primers	Revers primers	From
AXY4	At1g70230	5'-ACCGTCTCTAGCCCTGATCTCGTCT	5'-CGCATGTCCAAGTCCAGACCTTCT	Gilles et al., (2011)
AXY8	At4g34260	5'-TGATCTTGTGGATCCGTTGA	5'-GTGCCGAGCAAATATAGA	Günl et al., (2011)
bGAL1	At3g13750	5'-GAATGGCAATCAACGCTGGTGAAC	5'-GTGCTACAGTTACAGAACACCAGTTCTGC	Iglesias et al., (2006)
bGAL2	At3g52840	5'-TGATACACCGAGAGGCAACGAACC	5'-CAAGAGAGATTCCACTTGGATCACCACC	Iglesias et al., (2006)
bGAL6	At5g63800	5'-CCTGCTGGACAACCTTCTCAATCTATAT	5'-GAATTGAGATTGAGCTTGACTCGAACC	Iglesias et al., (2006)
bGAL8	At2g28470	5'-AACAGAACCAGGCCGTTTC	5'-GAAGCTTCAACAGCTAAGCTCTTGACGAC	Iglesias et al., (2006)
BXL4	At5g64570	5'-TGAATGGTGGTCTGAAGCAC	5'-TATAACCTGCGGGAAACTCG	
EXPA1	At1g69530	5'-AAGGCTATGGAACCAACACG	5'-GCCAGGAAGACACCATTTTC	
EXPA10	At1g26770	5'-CCTTGCTCAGCCTGTTTTTC	5'-GCTTGCCACACTGTTCTTGA	
EXPA14	At5g56320	5'-CAATACCGGAGAGTGGCTTGCC	5'-TTGTTAGATATAACTGTACGGCC	
EXPA20	At4g38210	5'-AAAGTGAAGGGCCACACAAC	5'-TTGCCGCCTTTGAGAGTAAC	
EXPA4	At2g39700	5'-AAAGGATCACGGACTGGTTG	5'-GCTTGACCAACCAAAACAGC	
EXPA5	At3g29030	5'-ATAGAAGGGTTCGGTGCAAG	5'-TCCTCGACCCTTTCATTGAG	
EXPAL1	At3g45970	5'-GCGATTACGGCAACAAGAAC	5'-GACTTGAGCAATGTGCGATGG	
FXG1	At1g67830	5'-ATGTTGCCTGAATCCGACAGC	5'-TTAGCGAAGTAACCTGCTGTG	
MUR2	At2g03220	5'-TGGAGGTTTAAAGCCTTGGA	5'-TGTCAAAAGCACAAAATTGACTT	
MUR3	At2g20370	5'-CTTTGTGCCGTTCTATGCTG	5'-ATGAGCCAATCGACCAACTC	
XTH17	At4g37800	5'-GGGAAGCCGAGCATTGGGCA	5'-ACCATGGGGAATTCGCGGAACA	
XTH18	At1g11545	5'-AATGAGGCTTTACGCGAGTC	5'-AGGAGCCTTTGACCAATCTG	
XTH19	At4g30290	5'-TGACCAACCGCTAACTTTC	5'-CTTTGTTGGGAATGGGACTC	
XTH23	At4g25810	5'-GCTGGAAGTGTACCCGCTTAC	5'-TCAAAGTCAATCTCGTCCCATGT	Lee et al., (2004)
XTH30	At1g32170	5'-GCTCTTACGCCACCATTTG	5'-ATAGGATCAACGGAGCAACC	
XTH31	At3g44990	5'-GGATGCATCGGACTGGGCCAC	5'-GCCATCTGCTGCCGGCTCAA	
XTH32	At2g36870	5'-CTCGGCTGCACCGCCTACTC	5'-TCCTAACGCCAACATTCCGGC	
XTH33	At1g10550	5'-CAATTCAGTAAGATCGCCATTG	5'-TTTGACACCAACCCAGCTC	
XTH7	At4g37800	5'-GATTCTGCCGGGACTGTCA	5'-CGTCTCGTACCGAATCGGTATC	Lee et al., (2004)
XTH8	At1g11545	5'-ATAACGACACCGGATGTGGATT	5'-TTTAGCTTCATACTAAACCATCCGAAT	Lee et al., (2004)
XYL1	At1g68560	5'-GGACATTAAGTAAGCCCTTGTGAGTTGCG	5'-ATCCCTGAAGGAAAGCAGTGTCCAAGTG	

**Supplemental reference:**

**Winter, D., Vinegar, B., Nahal, H., Ammar, R., Wilson, G.V., and Provat, N.J.** (2007). An "electronic fluorescent pictograph" browser for exploring and analyzing large-scale biological data sets. PLoS ONE **2**, e718.