Additional file 2

<u>Figure S1</u> - Co-regulation of cel6a/cbh2 (data obtained from microarrays) and cel7a/cbh1 (data obtained from qPCR) in QM9414 and $\Delta blr1$, $\Delta blr2$, $\Delta env1$, $\Delta gnb1$, $\Delta gng1$ and $\Delta phlp1$.

<u>Figure S2</u> – PCA analysis of replicate datasets of different mutants and conditions.

<u>Table S1</u> - Regulation of glycoside hydrolase genes in QM9414 and the deletion strains $\Delta env1$, $\Delta blr1$ and $\Delta blr2$ and comparison with regulations in $\Delta phlp1$, $\Delta gnb1$ and $\Delta gng1$.

Table S2 – Genes coregulated with cbh2/cel6a in QM9414 and $\Delta blr1$, $\Delta blr2$ and $\Delta env1$.

<u>Table S3</u> - Sequences of oligonucleotides used in this study.

Supplementary Figures

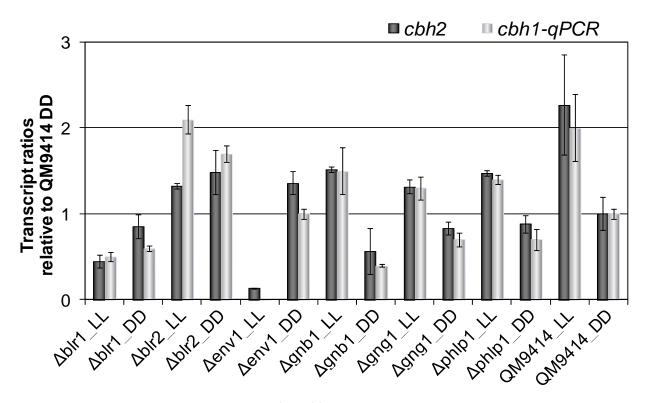
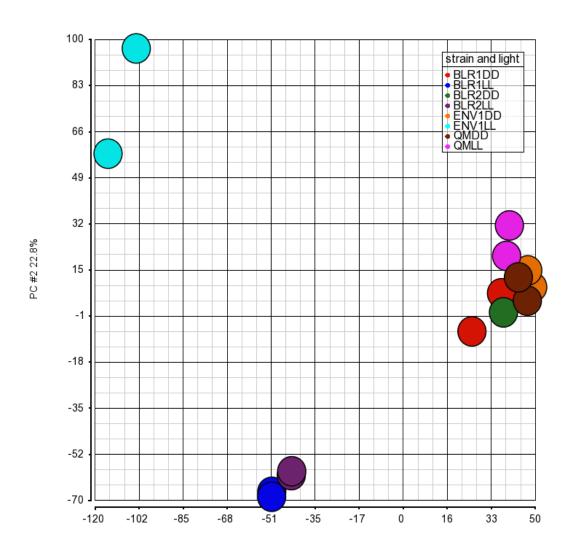


Figure S1 - Co-regulation of cel6a/cbh2 (data obtained from microarrays) and cel7a/cbh1 (data obtained from qRT-PCR) in QM9414 and $\Delta blr1$, $\Delta blr2$, $\Delta env1$, $\Delta gnb1$, $\Delta gng1$ and $\Delta phlp1$. Strains were grown on 1 % (w/v) microcrystalline cellulose as carbon source for 72 hours in constant light (LL) or darkness (DD). $\Delta gnb1$, $\Delta gng1$ and $\Delta phlp1$ were included in the analysis as additional controls for coregulation of cbh1 and cbh2 in different strains.

Supplementary Figure S2 – PCA analysis of replicate datasets of different mutants and conditions.

PCA Mapping (59.8%)



PC #1 37%

Supplementary Tables

Supplementary Table S1 Regulation of glycoside hydrolase genes in QM9414 and the deletion strains $\Delta env1$, $\Delta blr1$ and $\Delta blr2$ and comparison with regulations in $\Delta phlp1$, $\Delta gnb1$ and $\Delta gng1$.

If all genes of a glycoside hydrolase family are potentially light responsive, members of this family are given in bold

OFNE ID	0	December 1	On a Mile of land	Glycoside Hydrolase	all*	h**			u	pregulatio	on					do	wnregulati	ion			PhLP1-GNB1-	ENV1-BLR1-	shared
GENE_ID	Gene name	Description	Specification	Family	all	here**	WT	∆phlp1	∆gnb1	∆gng1	∆env1	∆blr1	∆blr2	WT	∆phlp1	∆gnb1	∆gng1	∆env1	∆blr1	∆blr2	GNG1 target	BLR2 target	target
22197	cel1B	b-glucosidase CEL1b (GenBank acc. No. AAP57758)		1	2	2												х					
120749	cel1A	b-glucosidase (GenBank acc. No. BAA74959)	cellulolytic enzyme	1	2	2			х									х					
120229		candidate xylanase	hemicellulolytic enzyme	10	1	1	Х	Х	Х	Х								Х					
57179		candidate glycosidase distantly related to unsaturated rhamnogalactuonyl hydrolase		105	1	1												х	х				
74223		xylanase 1 (EC 3.2.1.8)	hemicellulolytic enzyme	11	3	3		<u> </u>							Х	X		.,					
112392 123818		candidate xylanase xylanase 2 (EC 3.2.1.8)	hemicellulolytic enzyme hemicellulolytic enzyme	11 11	3	3	х	Х	х	Х						Х		X			Х	х	
77284		candidate b-glycosidase distantly related to endoglucanase	nemicentiolytic enzyme	12	2	2												х				A	
123232	cel12A	endoglucanase	cellulolytic enzyme	12	2	2	Х	Х	Х	Х								Х	Х				
57128		candidate glycogen-debranching enzyme		13	5	5									х		х	х	х			х	
59578		candidate oligo-1,6-glucosidase		13	5	5										Х							
105956		candidate a-amylase		13	5	5												Х					
108477		candidate oligo-1,6-glucosdiase		13	5	5												х					
123368		candidate glycogen branching enzyme		13	5	5												х					
65333		candidate a-glycosidase distantly related to glucoamylase and a,a- trehalase		15	1	1			х		х												
38536		candidate b-glycosidase related to b-1,3- 1,4-glucanase		16	16	13										Х		Х		Х	х		
41768		candidate b-glycosidase related to cell- wall modifying enzymes		16	16	13									Х	Х		Х		Х	х	х	х
49274		candidate b-glycosidase related to b-1,3- 1,4-glucanase		16	16	13								Х	Х	Х	Х						
50215		candidate b-glycosidase distantly related to endo-1,3-b-D-glucanase		16	16	13			Х									Х					
55886		candidate b-glycosidase related to b-1,3- 1,4-glucanase		16	16	13									Х	Х		Х	Х	Х	х		
65406		candidate b-glycosidase related to cell- wall modifying enzymes		16	16	13										Х							
66843		candidate b-glycosidase related to cell- wall modifying enzymes		16	16	13												Х					
70542		candidate b-glycosidase distantly related to b-1,3-1,4-glucanase/lichenase		16	16	13					Х						Х						
71399		candidate b-glycosidase distantly related to b-1,3-glucanase		16	16	13											Х						
73101		candidate b-glycosidase distantly related to b-1,3-1,4-glucanase		16	16	13									Х	Х	Х	Х		Х	х	Х	х
121294		candidate b-glycosidase realted to b-1,3- 1,4-glucanase		16	16	13			V		Х											Х	
122511 123726		candidate endo-1,3(4)-b-glucanase candidate endo-1,3(4)-b-glucanase		16 16	16 16	13 13	1	1	Х	-	1	1			-	Х			X	Х	1		
39942		candidate endo-1,3(4)-b-glocariase candidate b-glycosidase distantly related to exo-1,3-glucanase		17	4	3					Х								^	^			
49193		candidate b-glycosidase distantly related to exo-1,3-glucanase		17	4	3												Х					
66792		candidate b-glycosidase distantly related to exo-1,3-glucanase		17	4	3												Х					
2735		chitinase; fungal subgroup A chitinase		18	20	16										Х	Х			Х			
56448	chit18-11	chitinase; fungal subgroup A chitinase		18	20	16										Х		Х					$\perp =$
56894		candidate b-glycosidase related to chitinase; fungal subgroup C chitinase		18	20	16													Х				
59082	chi18-2	candidate b-glycosidase related to chitinase; fungal subgroup A chitinase		18	20	16									Х		Х	Х					<u> </u>

^{*} total number of genes belonging to this GH family in *T. reesei*

^{**} number of genes of this GH family being potentially regulated by light, as described in this study

									u	pregulatio	n					do	wnregulat		500/4 PL P4	aharad			
GENE_ID	Gene name	Description	Specification	Glycoside Hydrolase Family	ali*	here**	WT	∆phlp1	∆gnb1	∆gng1	∆env1	∆blr1	∆blr2	wT	∆phlp1	∆gnb1	∆gng1	∆env1	∆blr1	∆blr2	PhLP1-GNB1- GNG1 target	ENV1-BLR1- BLR2 target	shared target
		candidate chitinase related to bacterial																					
59791	chi18-15	chitinases, does not belong to a fungal subgroup		18	20	16									Х	х							
62704	chi18-3	chitinase; fungal subgroup A chitinase		18	20	16										Х							
65162		candidate b-glycosidase related to chitinase		18	20	16										х		×					
71245	chi18-1	chitinase, precursor protein, extracellular, contains chitin binding domain, type 1		18	20	16									х	х	х	х	х	х	х	х	х
72339	chi18-9	candidate b-glycosidase related to chitinase; CHI18-9 (GenBank acc. No. CDAA05857); fungal subgroup C chitinase		18	20	16			х		х												
80833	chi18-5	chitinase, fungal subgroup A chitinase; known as ECH42 in other <i>Trichoderma</i> species		18	20	16		х			х												
81598	chi18-7	chitinase; fungal subgroup A chitinase		18	20	16												Х					
108346	chi18-8	candidate b-glycosidase related to chitinase; CHI18-8 (GenBank acc. No. DAA05856); fungal subgroup C chitinase		18	20	16									Х	х	х		х	х	х		
110317	chi18-17	chitinase; C-terminal CBM1 module; fungal subgroup B chitinase		18	20	16										х		Х		Х			
119859	chi18-13	chitinase; fungal subgroup B chitinase		18	20	16										Х		Х					
121355		candidate b-glycosidase distantly related to chitinase		18	20	16					Х												1
124043	chi18-14	chitinase; fungal subgroup B chitinase		18	20	16									Χ	Х	Х	Х	Х	Х			
5836 57857		candidate b-mannosidase candidate b-mannosidase		2 2	7	7												l x					
59689		candidate b-mannosidase		2	7	7									Х		Х						
62166 69245		candidate b-mannosidase candidate b-mannosidase		2 2	7	7	Х		Х									Х					
76852		candidate b-glycosidase distantly related to b-galactosidase		2	7	7					х												
77299		exo-b-D-glucosaminidase GLS93 (GenBank acc. No. BAD99604)		2	7	7												х					
105931		candidate b-glycosidase distantly related to N-acetyl-b-D-glucosaminidase		20	3	1									х	х		х	х	х			
109278		candidate b-glycosidase distantly related to lysozyme		24	1	1					х					х							
103458		candidate b-glycosidase related to lysozyme		25	1	1										Х		х		х			
27219		candidate a-glycosidase related to a- galactosidase		27	8	6									Х	Х	х		х	Х	х	х	х
27259		candidate a-glycosidase related to a- galactosidase		27	8	6										Х							
55999		candidate a-galactosidase		27	8	6												Х	Х				
59391 65986		candidate a-galactosidase candidate a-galactosidase		27 27	8	6									X	Х	X	X		Х	х		
75015		candidate a-glycosidase related to a-		27	8	6										X	~	~		~	^		
70186		galactosidase candidate a-glycosidase related to exo-		28	4	3										^	Х				х		
103049		polygalacturonase candidate a-glycosidase related to exo-		28	4	3	 								Х						х		
122780		polygalacturonase candidate a-glycosidase related to exo-		28	4	3	1											Х	<u> </u>				
		polygalacturonase b-glucosidase (GenBank acc. No.																					
46816	cel3D	AAP57759)	cellulolytic enzyme	3	13	9			Х									Х					
47268		candidate b-glucosidase		3	13	9					X	Х											
58450		cadidate b-glycosidase distantly related to a-L-arabinofuanosidase / b-xylosidase		3	13	9												Х					
69557		candidate b-glycosidase related to b-N- acetylglucosaminidase b-glucosidase (genBank acc. No.		3	13	9												Х					
76227	cel3E	AAP57760)	cellulolytic enzyme	3	13	9											Х	Х					
76672		b-glucosidase b-glucosidase (GenBank acc. No.		3	13	9												Х	Х				
82227	cel3C	AAP57756)		3	13	9												Х					
108671		candidate b-glycosidase related to b- xylosidase		3	13	9													Х			х	
121127	bxl1	b-xylosidase (GenBank acc. No.CAA93248)		3	13	9	Х		Х									Х					
3094		candidate b-1,6-glucanase; similar to T. harzianum BGN16.3 (GenBank acc no Q8J0l9)		30	2	2									х	x	х	х	х	х	х	х	х

total number of genes belonging to this GH family in *T. reesei* number of genes of this GH family being potentially regulated by light, as described in this study

									u	pregulation	on					do	wnregulat						
GENE_ID	Gene name	Description	Specification	Glycoside Hydrolase Family	all*	here**	wt	∆phlp1	∆gnb1	∆gng1	∆env1	∆blr1	∆blr2	WT	∆phip1	∆gnb1	∆gng1	∆env1	∆bir1	∆blr2	PhLP1-GNB1- GNG1 target	ENV1-BLR1- BLR2 target	shared target
69736		candidate b-1,6-glucanase		30	2	2	1	 	 	 	1	 	 	-		х	 	х	 	 	 		
60085		candidate a-glycosidase distantly related to a-glucosidase		31	4	4												х					
69944		candidate a-xylosidase		31	4	4	Х		х									х					
82235		candidate a-glucosidase (required for normal cell wall synthesis)		31	4	4		х	х	х								х					
121351		a-glucosidase II from RutC30(GenBank acc. No. AAU87850.1)(EC 3.2.1)		31	4	4												х					
124016	agız	a-galactosidase(GenBank acc. No. CAA93245) (EC 3.2.1.22)		36	2	1			Х		х												
120676 123226		candidate neutral trehalase candidate trehalase		37 37	2	2					х							Х					
3196		candidate irenalase		38	1	1					_ ^							х					
73102		candidate b-glycosidase		39	1	1									Х			Х	Х		X		
3739		candidate b-xylosidase	hemicellulolytic enzyme	43	2	2			Х										Х				
68064		candidate b-glycosidase distantly related to b-xylosidase / a-L- arabinofuranosidase	hemicellulolytic enzyme	43	2	2												х					
49976	cel45A	endoglucanase V EGL5 (CEL45A)	cellulolytic enzyme	45	1	1												х	х				
79960		candidate a-mannosidase		47	8	1												Х					
56996	man5A	mannan endo-1,4-b-mannosidase (EC 3.2.1.78); C-terminal CBM1 module		5	11	7	Х		Х									Х	Х				
64375		candidate exo-b-1,3-glucanase		5	11	7										Х		Х					
64906		candidate b-1,6-glucanase; similar to <i>T. harzianum</i> B16-2 (GenBank acc. No. CAA55789) and <i>T. virens</i> BGN3 (AAL84696)		5	11	7									х	х	х	х	х	х	х	х	х
69276		candidate b-glycosidase distantly related to xylanase		5	11	7	Х	Х	Х	Х									Х				
71554		candidate b-glycosidase distantly related to b-mannanase		5	11	7			V							Х		V					
111849		xylanase 4	cellulolytic enzyme	5 5	11	7	X		X									X	X				
120312		endo-1,4-glucanase EGL2 a-L-arabinofuranosidase ABF1		-			^		^									^	^				
123283 55319	aprı	(GenBand acc. No. CAA93243) candidate a-L-arabinofuranosidase	hemicellulolytic enzyme	54 54	2	2	х	х		х	х							х				x	
55319		candidate b-1,3-exoglucanase; related	hemicellulolytic enzyme	54	2		^	^		^								^				^	
121746		to GLUC78 (GenBank acc. No. AAF80600) of T. atroviride		55	6	6												х					
54242		candidate b-glycosidase related to b- 1,3-glucanase		55	6	6										х		х					
56418		candidate b-1,3-exoglucanase candidate b-1,3 glucanase; similar to		55	6	6									Х	Х	Х	Х	Х	Х	Х	х	Х
70845		T. virens BGN1 (GenBank acc. No. AAL84694)		55	6	6										х		X			x		
73248		candidate b-1,3-exoglucanase		55	6	6										Х	Х	Х	1		X		
108776		candidate b-1,3-glucanase; similar to T. harzianum BGN13.1 (GenBank acc.no.CAA58889) and T. virens BGN2 (AAL84695)		55	6	6										x	х						
72567	cel6A;cbh2	cellobiohydrolase	cellulolytic enzyme	6	1	1	х		х							1		х	1				1
73643		endo-1,4-glucanase EGL4	cellulolytic enzyme	61	3	2			Х					Х				Х					
120961		endo-1,4-glucanase	cellulolytic enzyme	61	3	2			X									X	Х				
76210	abf2	a-L-arabinofuranosidase (GenBand acc. No. AAP57750)	hemicellulolytic enzyme	62	1	1	х		х	х			х						х				
22072		candidate a-glucosidase		63	2	2									,,			Х					
75036		candidate a-glucosidase		63	2	2									Х								
65137		candidate b-glycosidase distantly related to b-1,3-glucanase		64	3	3									х	х	х	х	х	х	х	x	х
123639		candidate b-glycosidase distantly related to b-1,3-glucanase		64	3	3			х		х								х				
124175		candidate b-glycosidase distantly related to b-1,3-glucanase		64	3	3					х	х				х					х		
123456		candidate acid trehalase		65	2	1												X					
72526	glr1	a-glucuronidase (GenBand acc.no. CAA92949)	hemicellulolytic enzyme	67	1	1	х		х	х								х				х	<u> </u>
122081	cel7B	endo-1,4-glucanase EGL1; C-terminal CBM1	cellulolytic enzyme	7	2	2			х									х	х				

total number of genes belonging to this GH family in *T. reesei* number of genes of this GH family being potentially regulated by light, as described in this study

				Chronoido Hudrologo	Glycoside Hydrolase				downregulation							ENV1-BLR1-	shared						
GENE_ID	Gene name	Description	Specification	Family	all*	here**	WT	∆phlp1	∆gnb1	∆gng1	∆env1	∆blr1	∆blr2	WT	∆phlp1	∆gnb1	∆gng1	∆env1	∆blr1	∆blr2	PhLP1-GNB1- GNG1 target	BLR2 target	target
123989	cel7A; cbh1	cellobiohydrolase		7	2	2	х	х	х	х								х					
71532		candidate a-glycosidase distantly related to a-1,3-glucanase		71	4	3			Х														
108672		candidate a-1,3-glucanase		71	4	3										Х		Х	X	Х	Х		
120873		candidate a-1,3-glucanase		71	4	3												Х	X				
22914		candidate b-1,3- glucanosyltransglycosylase		72	5	5												х					
77942		candidate b-1,3- glucanosyltransglycosylase		72	5	5												х					
78713		candidate b-1,3- glucanosyltransglycosylase		72	5	5	х		х										х				
82633		candidate b-1,3- glucanosyltransglycosylase		72	5	5												х					
123538		candidate b-1,3- glucanosyltransglycosylase		72	5	5												х					
49081	cel74A	candidate xyloglucanase; EGL6	hemicellulolytic enzyme	74	1	1	Х		Х									Х					
42152		candidate b-glycosidase related to chitosanase		75	3	3									х	х					х		
66789		candidate b-glycosidase related to chitosanase		75	3	3									х	х		х		х	х	х	х
70341		candidate b-glycosidase related to chitosanase		75	3	3										х	х			х	х		
27395		candidate a-glycosidase		76	7	2					Х												
55802		candidate a-glycosidase		76	7	2					X												
58887		candidate a-glycosidase distantly related to a-L-rhamnosidase		78	1	1												х	х			x	
71394		candidate b-glycosidase related to b- glucuronidase		79	4	3									х	х	Х	Х	х	х	х	х	х
72568		candidate b-glycosidase distantly related to b-glucuronidase		79	4	3													Х				
106575		candidate b-glucuronidase		79	4	3													X				
73256		candidate b-glycosidase related to endo-b-1,3-glucanase		81	2	2										х		х	х	х		х	
79602		candidate b-glycosidase related to endo-b-1,3-glucanase		81	2	2									х	х	х						
58117		candidate a-glycosidase related to a-N- acetylglucosaminidase		89	2	2												х					
69700		candidate a-glycosidase related to a-N- acetylglucosaminidase		89	2	2												х					
57098		candidate a-glycosidase distantly related to a-1,2-mannosidase		92	7	6												Х					
60635		candidate a-glycosidase distantly related to a-1,2-mannosidase		92	7	6									х	х	х	х	х				
69493		candidate a-glycosidase distantly related to a-1.2-mannosidase		92	7	6										х							
74198		candidate a-glycosidase		92	7	6									Х			Х					
79921		candidate a-glycosidase distantly related to a-1,2-mannosidase		92	7	6									Х	Х		х					
111733		candidate a-glycosidase distantly related to a-1,2-mannosidase		92	7	6									х				х				
5807		candidate a-glycosidase distantly related to a-1,2-L-fucosidase	hemicellulolytic enzyme	95	4	2											х		х				
58802		candidate a-glycosidase distantly related to a-1,2-L-fucosidase	hemicellulolytic enzyme	95	4	2										Х		х		х		х	

total number of genes belonging to this GH family in *T. reesei* number of genes of this GH family being potentially regulated by light, as described in this study

Supplementary Table S2 List of genes coregulated with *cel6a/cbh2*.

TRE	Gene name	Description	Specification	Group	Topic
TR_72567	cel6A;cbh2	cellobiohydrolase CBH2	cellulolytic enzyme	Glycoside Hydrolase Family 6 protein	Glycoside hydrolases
TR_102743					
TR_103041					
TR_103064		Uncharacterized conserved protein			
TR_103555					
TR_105275					
TR_108477		candidate oligo-1,6-glucosdiase		Glycoside Hydrolase Family 13 protein	Glycoside hydrolases
TR_112328					
TR_120120					
TR_120229		candidate xylanase	hemicellulolytic enzyme	Glycoside Hydrolase Family 10 protein	Glycoside hydrolases
TR_120311		unique protein			
TR_120312	cel5A	endo-1,4-glucanase EGL2	cellulolytic enzyme	Glycoside Hydrolase Family 5 protein	Glycoside hydrolases
TR_120504					
TR_120877					
TR_120961	cel61B	endo-1,4-glucanase; CEL61B	cellulolytic enzyme	Glycoside Hydrolase Family 61 protein	Glycoside hydrolases
TR_121127	bxl1	b-xylosidase BXL1 (GenBank acc. No.CAA93248)		Glycoside Hydrolase Family 3 protein	Glycoside hydrolases
TR_121189					
TR_121418					
TR_122208	xyr1	xylanase regulatator 1		cellulase transcription factor	Transcription factors
TR_123473		MFS, 12 TMs			
TR_123940		CIP2			
TR_123992		swollenin			
TR_23146					
TR_3739		candidate b-xylosidase	hemicellulolytic enzyme	Glycoside Hydrolase Family 43 protein	Glycoside hydrolases
TR_49081		candidate xyloglucanase; EGL6 (CEL74A)	hemicellulolytic enzyme	Glycoside Hydrolase Family 74 protein	Glycoside hydrolases
TR_52438					
TR_53238		TRE456, hypothetical G-protein coupled receptor, family 2, secretin like, related to Magnaporthe grisea MG00532 (GPCR with homology to rat growth hormone releasing factor)		G-proteins	signal trans- duction
TR_53331					
TR_53722					
TR_54086					
TR_54219					

TR_56999 Candidate a-galactosidase Family 27 protein hydrol TR_56684 hypothetical sugar transporter family protein TR_61763 TR_63001 TR_69276 Candidate b-glycosidase distantly related to xylanase Glycoside Hydrolase Family 5 protein hydrol TR_69316 unknown conserved protein TR_69375 unknown hypothetical protein TR_69375 Candidate a-xylosidase Glycoside Hydrolase Family 31 protein TR_70098 Amino acid transporters TR_70520 TR_72526 Candidate a-glucuronidase GLR1 (GenBand acc.no. CAA92949) enzyme Glycoside Hydrolase Family 67 protein TR_73632 AXE1 TR_73638 CIP1 TR_73634 The basic-leucine zipper (bZIP) transcription factors are proteins that contain a basic region mediating sequence-specific DNA-binding followed by a leucine zipper region (see IPR002158) required for		Gene name	Description	Specification	Group	Topic
TR_63064 TR_61763 TR_63001 TR_69276 Candidate b-glycosidase distantly related to xylanase TR_69316 TR_69375 Unknown conserved protein TR_69375 TR_69944 Candidate a-xylosidase Glycoside Hydrolase Family 5 protein TR_70098 Amino acid transporters TR_70520 TR_72526 Candidate a-glucuronidase GLR1 (GenBand acc.no. CAA92949) TR_73632 TR_73638 CIP1 The basic-leucine zipper (bZIP) transcription factors are proteins that contain a basic region mediating sequence-specific DNA-binding followed by a leucine zipper region (see IPR002158) required for	TR_55999	9	candidate a-galactosidase		Glycoside Hydrolase Family 27 protein	Glycoside hydrolases
TR_63001 TR_69276 Candidate b-glycosidase distantly related to xylanase TR_69316 Unknown conserved protein TR_69375 Unknown hypothetical protein TR_69944 Candidate a-xylosidase Glycoside Hydrolase Family 5 protein Glycoside Hydrolase Family 31 protein Glycoside Hydrolase Family 31 protein TR_70098 Amino acid transporters TR_70520 TR_72526 Candidate a-glucuronidase GLR1 (GenBand acc.no. CAA92949) TR_73632 AXE1 TR_73632 TR_73638 CIP1 The basic-leucine zipper (bZIP) transcription factors are proteins that contain a basic region mediating sequence-specific DNA-binding followed by a leucine zipper region (see IPR002158) required for	TR_56684	4				Transport
TR_69276	TR_61763	3				
TR_69316	TR_63001	1				
TR_69375 unknown hypothetical protein TR_69944 candidate a-xylosidase Glycoside Hydrolase Family 31 protein hydrol TR_70098 Amino acid transporters TR_70520 TR_72526 candidate a-glucuronidase GLR1 (GenBand acc.no. CAA92949) TR_73632 AXE1 TR_73638 CIP1 The basic-leucine zipper (bZIP) transcription factors are proteins that contain a basic region mediating sequence-specific DNA-binding followed by a leucine zipper region (see IPR002158) required for	TR_69276	6				Glycoside hydrolases
TR_69944 candidate a-xylosidase Glycoside Hydrolase Family 31 protein Pydrol. TR_70098 Amino acid transporters TR_70520 TR_72526 candidate a-glucuronidase GLR1 (GenBand acc.no. CAA92949) hemicellulolytic enzyme Glycoside Hydrolase Family 67 protein Pydrol. TR_73632 AXE1 TR_73638 CIP1 The basic-leucine zipper (bZIP) transcription factors are proteins that contain a basic region mediating sequence-specific DNA-binding followed by a leucine zipper region (see IPR002158) required for	TR_69316	6	unknown conserved protein			
TR_70098 Amino acid transporters TR_70520 TR_72526 Candidate a-glucuronidase GLR1 (GenBand acc.no. CAA92949) TR_73632 AXE1 TR_73638 CIP1 The basic-leucine zipper (bZIP) transcription factors are proteins that contain a basic region mediating sequence-specific DNA-binding followed by a leucine zipper region (see IPR002158) required for	TR_69375	5	unknown hypothetical protein			
TR_70520 TR_72526 Candidate a-glucuronidase GLR1 (GenBand acc.no. CAA92949) Family 67 protein TR_73632 AXE1 TR_73638 CIP1 The basic-leucine zipper (bZIP) transcription factors are proteins that contain a basic region mediating sequence-specific DNA-binding followed by a leucine zipper region (see IPR002158) required for IR_73654 TR_73654 CIP1 The basic-leucine zipper domain-containing/DNA binding domain protein	TR_69944	4	candidate a-xylosidase			Glycoside hydrolases
TR_72526	TR_70098	8	Amino acid transporters			
TR_73632	TR_70520	0				
TR_73638 CIP1 The basic-leucine zipper (bZIP) transcription factors are proteins that contain a basic region mediating sequence-specific DNA-binding followed by a leucine zipper region (see IPR002158) required for The basic-leucine zipper domain-containing/DNA binding domain protein Transcription factors are proteins that contain a basic region domain-containing/DNA binding domain protein	TR_72526	6				Glycoside hydrolases
The basic-leucine zipper (bZIP) transcription factors are proteins that contain a basic region mediating sequence-specific DNA-binding followed by a leucine zipper region (see IPR002158) required for The basic-leucine zipper domain- containing/DNA binding domain protein Transcription	TR_73632	2	AXE1			
transcription factors are proteins that contain a basic region mediating sequence-specific DNA-binding followed by a leucine zipper region (see IPR002158) required for IPR002158 transcription factors are proteins basic-leucine zipper domain-containing/DNA binding domain protein	TR_73638	8	CIP1			
dimerization.	TR_73654	4	transcription factors are proteins that contain a basic region mediating sequence-specific DNA-binding followed by a leucine zipper region (see	domain- containing/DNA binding domain		Transcription factors
TR 76215 T Sultide dehydrogenase T	TR_76215	5	Sulfide dehydrogenase			Sulfur meta- bolism
TR_76696 Flavin-containing monooxygenase	TR_76696	6				
TR_76722 flavohemoglobin	TR_76722	2	, and the second			
TR_77154 binding Homeobox Nuclear like protein cription factor-	TR_77154	4	binding Homeobox Nuclear protein			Trans- cription factors
D-xylulose 5-phosphate/D- fructose 6-phosphate phosphoketolase	TR_77481	1	fructose 6-phosphate			
	TR_80240	0 bga1	b-galactosidase (GenBank acc. No. CAD70669) (EC 3.2.1.23)			Glycoside hydrolases
TR_81148	TR_81148	8				

Supplementary Table S3 - Sequences of oligonucleotides used in this study.

fragment	oligonucleotide	study	sequence
cbh1	RTcbh1F	Tisch et al ., 2011a	5' ACCGTTGTCACCCAGTTCG 3'
CONT	RTcbh1R	Tisch et al ., 2011a	5' ATCGTTGAGCTCGTTGCCAG 3'
m16 o	RTL6eF1	Tisch et al ., 2011a	5' GATACGTCATCGCCACCTCC 3'
rpl6e	RTL6eR1	Tisch <i>et al</i> ., 2011a	5' CTTCTCCTTGGCCTTCTCG 3'
xyl1	RT_xyl1_fw1	This study	5' CATCTACGCCCGCATCAAGC 3'
xyt1	RT_xyl1_rev1	This study	5' CAAAGGACGAGTAGGCGGTGAC 3'
lad1	RT_lad1_fw1	This study	5' CTTGCCCGCTTGTCATCAC 3'
iaai	RT_lad1_rev1	This study	5' CCGTTTCCTCAGCCGACTTG 3'
xdh l	RT_xdh1_fw1	This study	5' CTCCACCATTGTCAGCGTC 3'
xanı	RT_xdh1_rev1	This study	5' CCTTTGCGTTGTCCTCAGC 3'
lxr3	RT_lxr3_fw1	This study	5' AGGAGGCACGACGATTGAC 3'
ixis	RT_lxr3_rev1	This study	5' GCCTTGGAGCTGTTGTACACG3'
lxr4	RT_lxr4_fw1	This study	5' GGCAAGAAGTTCCAGGTCG3'
13.74	RT_lxr4_rev1	This study	5' CAGCACGTTGATGGCGTAG 3'
xki1	RT_xki1_fw1	This study	5' TGTCAGATCACGCCCTTCAC 3'
λκιΙ	RT_xki1_rev1	This study	5' GGTTGAAGAAGTGGTACGAGC 3'