

Additional file 1.

Combines Table S1 and Figure S1-S4

Table S1. Putative metabolic genes from *Myceliophthora thermophila* based on homology to genes from *A. niger*. Induction of the *M. thermophila* genes is indicated in the last column (see Additional file 4 for more information).

Protein	Homolog in <i>A. niger</i> :	Putative function in <i>M. thermophila</i>	Transcript levels are induced on:
Pentose Catabolic Pathway (PCP)			
62052	LadA (An01g10920)	L-arabitol dehydrogenase	L-arabinose
2302811	LxrA (An08g01930)	L-xylulose reductase	L-arabinose
2293953	XdhA (An12g00030)	Xylitol dehydrogenase	L-arabinose, D-xylose, arabinoxylan
67060	XkiA (An07g03140)	Xylulose kinase	L-arabinose, D-xylose, arabinoxylan
43671	XyrA (An01g03740)	D-xylose reductase	L-arabinose, D-xylose, arabinoxylan
D-galacturonic acid and L-rhamnose pathway			
87557	GaaC (An02g07720)	2-keto-3-deoxy-L_galactonate aldolase	L-arabinose
103080	LraB (An13g00940)	L-KDR aldolase	arabinoxylan
Pentose Phosphate Pathway (PPP)			
89872	RpiB (An02g02930)	Ribose 5-phosphate isomerase	L-arabinose, D-xylose, arabinoxylan
2300643	TktA (An08g06570)	Transketolase	arabinoxylan
Glycolysis			
112014	An14g02160	Alcohol dehydrogenase	L-arabinose
57502	An02g09090	Aldose-1-epimerase (or mutarotase)	L-arabinose
55576	AdhA (An17g01530)	Alcohol dehydrogenase	L-arabinose
2315623	AcuF (An11g02550)	Phosphoenolpyruvate carboxykinase	L-arabinose, D-xylose, arabinoxylan
39694	An02g02920	Triose-phosphate isomerase	D-xylose
84302	An16g02510	Alcohol dehydrogenase	D-xylose
2082283	An11g10890	Aldose 1-epimerase (or mutarotase)	D-xylose, arabinoxylan
2298452	An14g04410	Fructose-bisphosphate aldolase	D-xylose, arabinoxylan
TCA cycle			
2309210	Lpd1 (An07g06840)	Dihydrolipoamide dehydrogenase	L-arabinose, arabinoxylan
2295514	IdpA (An18g06760)	Isocitrate dehydrogenase	L-arabinose, arabinoxylan
Ethanol utilization pathway			
2140820	AldA (An08g07290)	Aldehyde dehydrogenase	L-arabinose, arabinoxylan

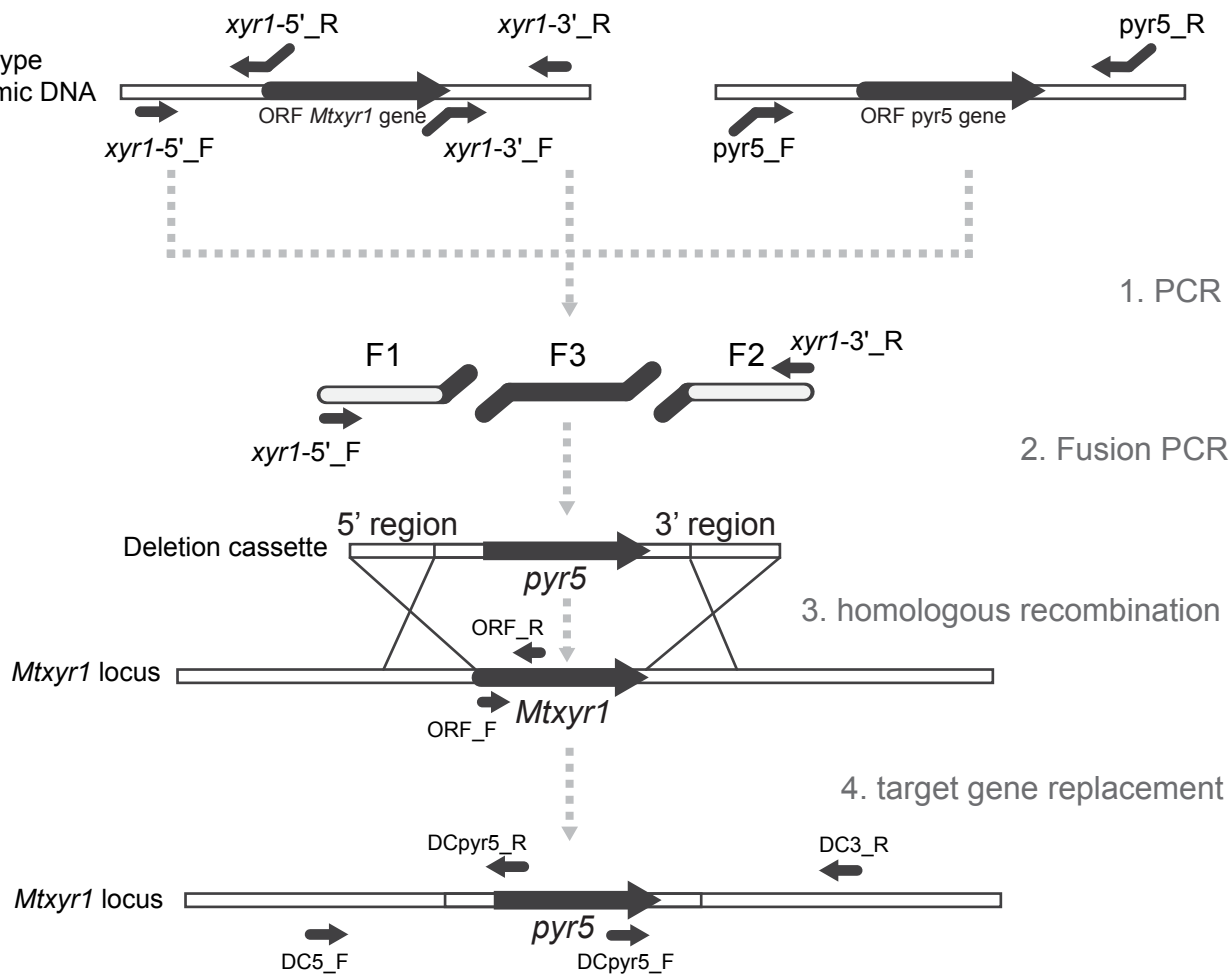
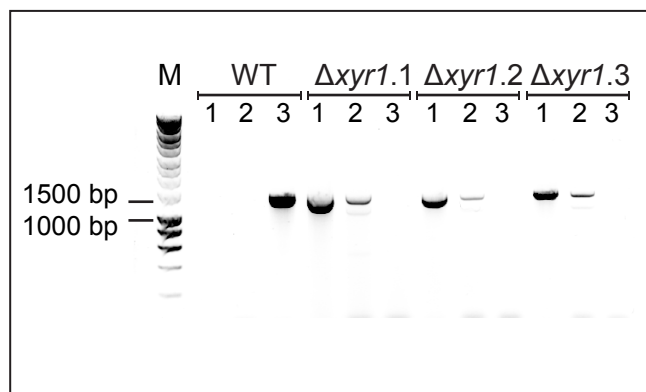
A**B**

Figure S1. Deletion of the *Mtxyr1* gene in the *M. thermophila* C1 strain. A) Graphic representation of the deletion strategy (see the Materials and Methods section for the primer sequences). B) PCR screening of the wild-type (WT) strain and three independent transformants ($\Delta xlr1.1-3$) that were obtained after transformation of *M. thermophila* WT with the *xlr1* deletion cassette. The lanes marked with 1: amplification of the 5' flanking region with primers DC5_F and DCpyr5_R. Lanes marked with 2: amplification of the 3' flanking region with primers DCpyr5_F and DC3_R. Lanes marked with 3: amplification inside the ORF of the *Mtxlr1* gene with primers ORF_F and ORF_R.

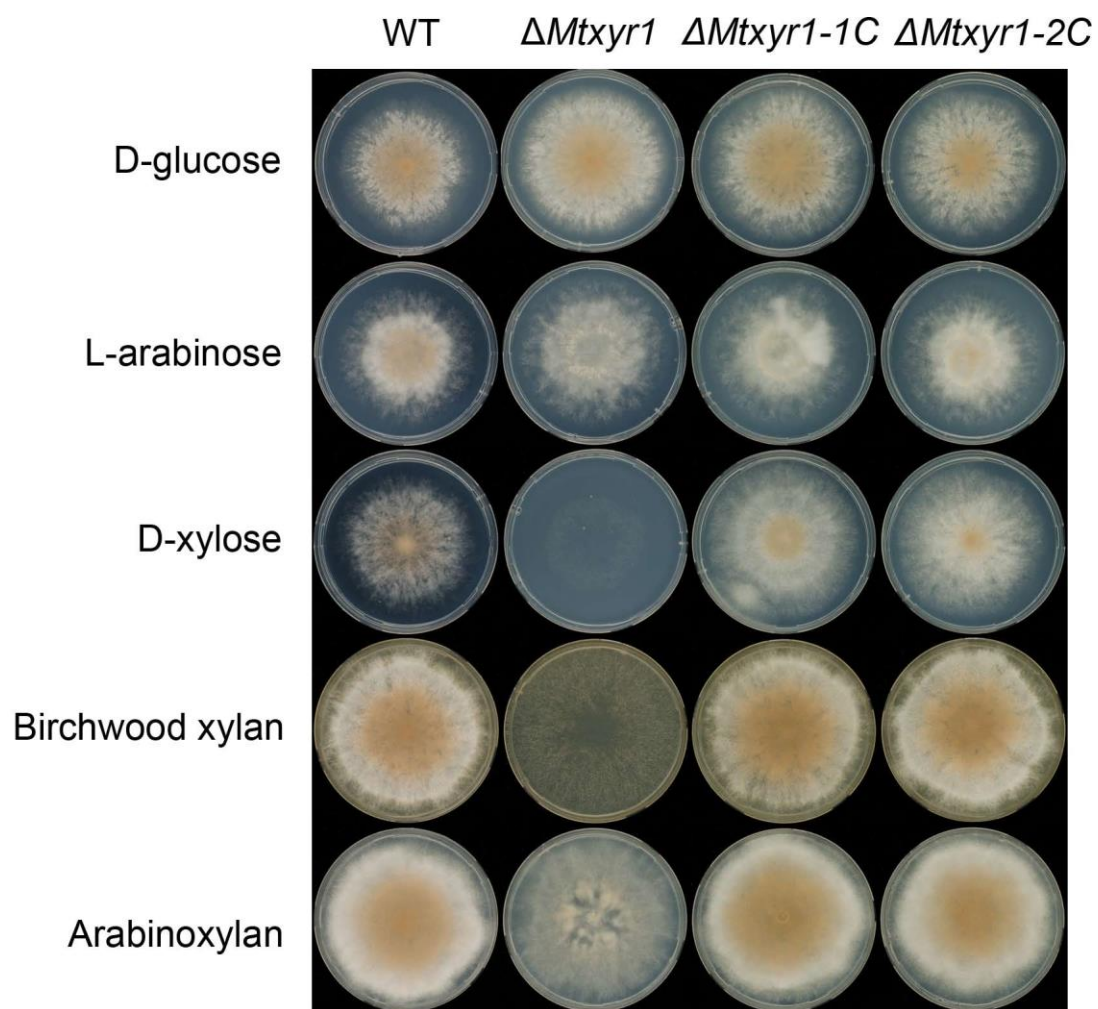
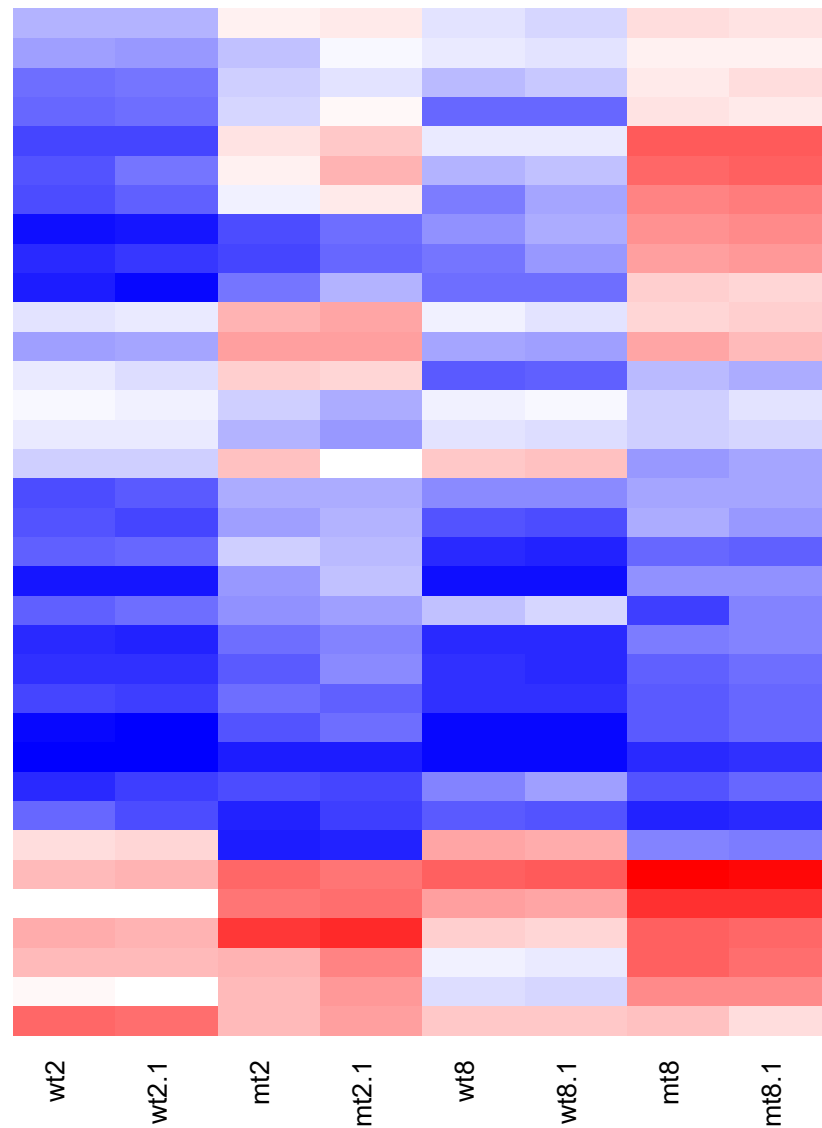
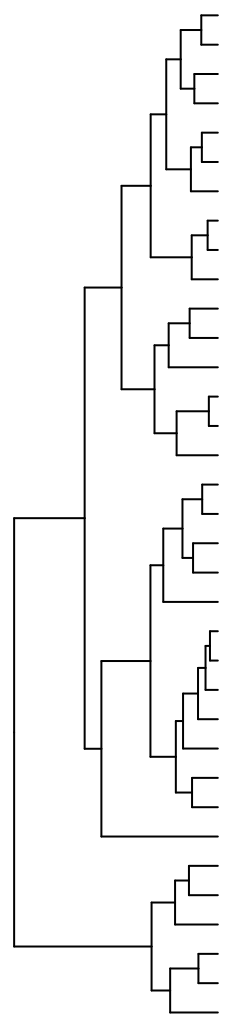
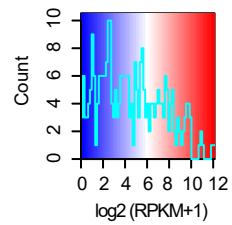


Figure S2. Growth phenotype of the *M. thermophila* wild type, $\Delta xyr1$ and complemented strains on agar plates. The wild-type strain, *Mtxyr1* deletion mutant ($\Delta Mtxyr1$) and complemented strains ($\Delta Mtxyr1-1C$ and $\Delta Mtxyr1-2C$; two independent transformants) were grown for 5 days at 37°C on solid media containing minimal medium with D-glucose, L-arabinose, D-xylose, birchwood xylan or wheat arabinoxylan.



Arabinosyln

Gene	Clade	(putative) function
2295230	A(i)	glucose/pentoses transporters
98222	A(i)	glucose/pentoses transporters
2307233	B	quinic acid and D-galacturonic acid transporters
38796	H	lactose/cellodextrin, melizitose and turanose (weakly) transporters
2305795	G	D-glucose or some oligosaccharides weakly transporters
108044	A(ii)	glucose/pentoses transporters
58642	D	oligosaccharide transporters
2299846	D	oligosaccharide transporters
43941	H	lactose/cellodextrin, melizitose and turanose (weakly) transporters
104673	G	D-glucose or some oligosaccharides weakly transporters
2076976	D	oligosaccharide transporters
2302949	F	glycerol/mannitol/pentose and some oligosaccharide transporters
2303090	D	oligosaccharide transporters
2297070	E(i)	phosphate transporters
2299773		UDP-galactose transmembrane transporter activity
2312740	C(iii)	inositol/fructose and some oligosaccharides
2306135	F	glycerol/mannitol/pentose and some oligosaccharide transporters
2309559	G	D-glucose or some oligosaccharides weakly transporters
2295444	F	glycerol/mannitol/pentose and some oligosaccharide transporters
50903	D	oligosaccharide transporters
112491	A(i)	glucose/pentoses transporters
2310790	H	lactose/cellodextrin, melizitose and turanose (weakly) transporters
2311167	D	oligosaccharide transporters
2309054	B	quinic acid and D-galacturonic acid transporters
103797	D	oligosaccharide transporters
53860		
108924	A(i)	glucose/pentoses transporters
2057386	D	oligosaccharide transporters
96047	A(iii)	glucose/pentoses transporters
2308157	A(i)	glucose/pentoses transporters
95427	A(ii)	glucose/pentoses transporters
2308979	C(iii)	inositol/fructose and some oligosaccharides
84164	H	lactose/cellodextrin, melizitose and turanose (weakly) transporters
108890	B	quinic acid and D-galacturonic acid transporters
114107	H	lactose/cellodextrin, melizitose and turanose (weakly) transporters

Figure S3. Hierarchical clustering of significantly differentially expressed putative sugar transporter genes in the $\Delta Mtxy1$ strain. The wild type and $\Delta Mtxy1$ strain were grown for 2 and 8 h on wheat arabinosyln. The color code represents the logged expression values (RPKM+1) of both biological duplicates (named 2 and 2.1 or 8 and 8.1). Behind the JGI protein numbers, the corresponding transporter clade according to de Vries et al., 2017 [54] is given, while the third column contains a prediction of function of the putative *M. thermophila* transporter gene (see Additional file 3 for more information).

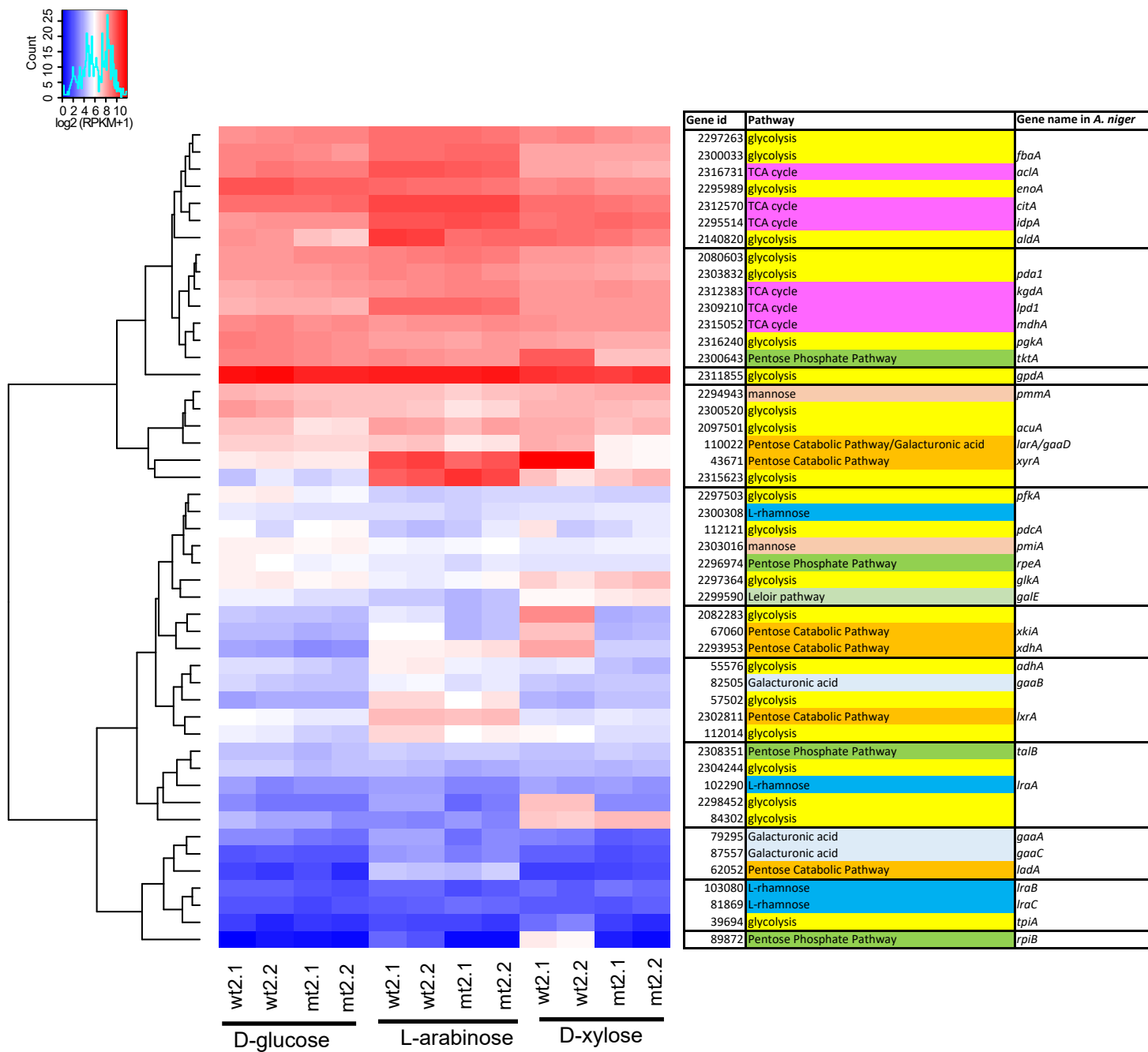


Figure S4. Hierarchical clustering of significantly differentially expressed putative metabolic genes in the $\Delta Mtxy1$ strain. The wild type and $\Delta Mtxy1$ strain were grown for 2 h on D-glucose, L-arabinose and D-xylose. The color code represents the logged expression values (RPKM+1) of both biological duplicates (named 2.1 and 2.2). Behind the JGI protein numbers, the pathway the gene is putatively involved in is given, while the third column contains the gene name of the ortholog from *A. niger*.