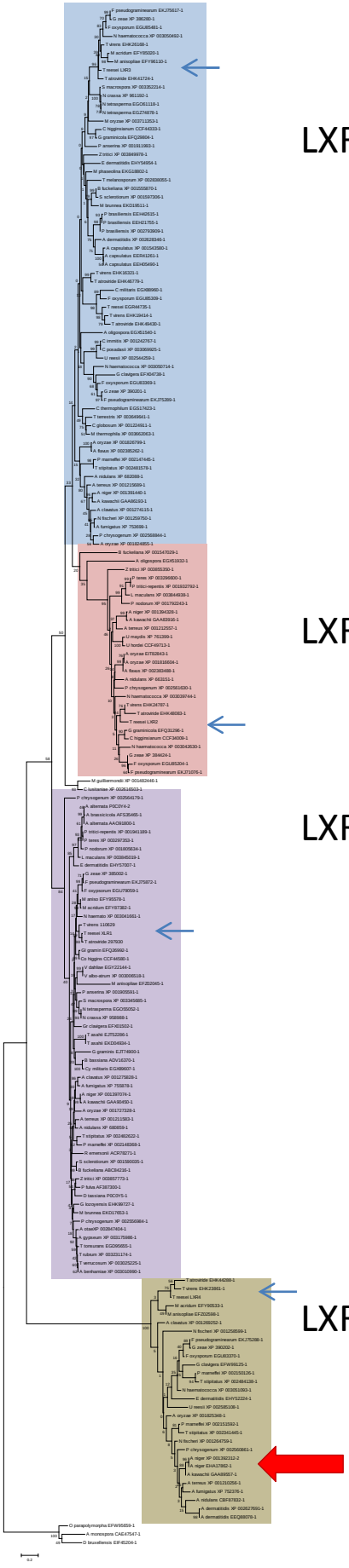
Supplementary Table S1 Summary of the analysis of twenty LXR candidates of the 117 SDRs of the *T. reesei* genome against the NCBI database, the NCBI *T. reesei* EST database and the *Candida guilliermondi* database.

Protein ID	NCBI (BLASTP	*T. reesei* ESTs	*C. guillermondi*	RT PCR		
				Gal	Ara	Glu
123265	+	+	+	-	-	-
81553	+	+	+	+/-	+/-	-
52718	+	+	+	-	-	-
77202	+	+	+	-	-	-
65433	+	+	+	-	-	-
46936	+	+	+	+	+	++
108201	+	+	+	-	-	-
22512	+	+	+	-	-	-
76114	+	+	+	-	-	-
69840	-	-	+	-	-	-
54086	+	-	+	++	++	+
120288	+	-	+	-	-	-
60033 *(lxr3)*	+	-	+	+++	+++	+/-
65588	+	-	+	-	-	-
62439	+	-	+	+	+	+
66175	+	-	+	-	-	-
122079	+	+	+	+/-	+++	+/-
123553	-	+	+	-	-	-
69502	+	-	+	-	-	-
54991	+	-	+	+/-	+/-	+/-

*Sequences were analyzed by BLASTP against the NCBI database (+ corresponds to e value < $1e^{-80}$) or *C. guilliermondi* genome database (+corresponds to e value < 10^{-30}) or for the presence (+) or absence (-) in the NCBI EST database of *T. reesei*. Expression was tested by RT PCR after replacement to the indicated carbon source (1 %; Ara, L-arabinose; D-galactose, Gal; and D-glucose, Glu) after 4 hours. Results indicated the relative level of transcription from high (+++) to absent (-).

Supplementary Figure 1. Growth test of *T. reesei* Δ*lxr3* and RE Δ*lxr3,* a Δ*lxr3* strain retransformed with *lxr3* on agar plates. Both strains were grown under the same conditions as in Fig. 3 on different carbon sources (1 % w/v) for 3 d.


LXR3
LXR2
LXR1
LXR4

Supplementary Figure 2. Phylogenetic analysis of L-xylulose reductases and related proteins. The four *T. reesei* LXR proteins LXR1 (D-mannitol 2-dehydrogenase), LXR2, LXR3 (L-xylulose reductase) and LXR4 (L-xylo-3-hexulose reductase), and *A. niger* LxrA were used as a query in a BLASTP search against the NCBI database and subjected to a neighbour joining analysis. Numbers below nodes indicate the bootstrap value. The bar marker indicates the genetic distance, which is proportional to the number of amino acid substitutions. GenBank Accession numbers of the respective proteins are indicated.