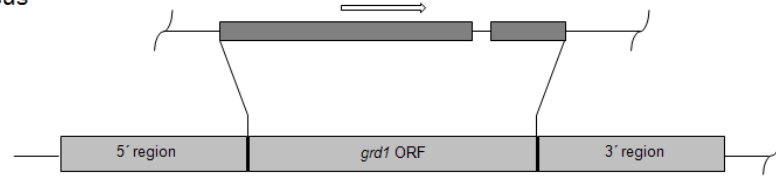


Supplementary table S1

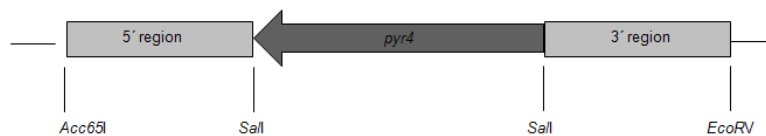
Sophorose specific cDNA fragments									
Clone	equal	frequency	best hit	expect	length	TRIRE cDNA	protein ID	InterPro domains	putative function
STCD4	STCD16 STCD22 STCD39	4	hypothetical protein NECHADRAFT_89138 [<i>Nectria haematococca</i> mpVI 77-13-4] XP_003039507.1	2e-158	113 bp	CF885793 CF882297 CF881092 CB908798 CB907879	tr_3405	IPR003663 IPR005828 IPR005829 IPR007114	probable sugar transporter of the major facilitator superfamily
STCD12	STCD13 STCD18 STCD24	4	G-protein beta like WD repeat protein [<i>Fusarium oxysporum</i>] BAD44728.1	3e-76	123 bp	CF933888 CF933394 CF933320 CF933194 CF932925	tr_45736 (<i>cpc2</i>)	IPR001680 IPR011046 IPR015943 IPR017986 IPR019775 IPR019781 IPR019782 IPR020472	cross pathway control protein CPC2, involved in general amino acid control
STCD21	STCD41 STCD47 STCD68 STCD70 STCD85 STCD91 STCD96	8	NADP(+)-dependent dehydrogenase, putative [<i>Aspergillus clavatus</i>] XP_001269058.1	2e-117	174 bp	CF869945 CB900101 CF935099 CF879699 CF935625 CF935683	tr_123946	IPR002347 IPR002198	GRD1
STCD27		1	FAD binding domain protein	5e-96			tr_73631	IPR006094	probable isoamyl
STCD43	STCD65 STCD73	3	QJ74 protein [<i>Hypocrea lixii</i>] CAA64974.1	0.0	162 bp	CF886467 CF882327 CF881368 CF879527 CF878972	tr_74282	IPR009030	inducible cell wall protein
STCD55		1	NADP(+)-dependent dehydrogenase, putative [<i>Aspergillus clavatus</i>] XP_001269058.1	2e-117	107 bp	CF935625 CF869945 CF653652 CB900101 CF935099	tr_123946	IPR002347 IPR002198	GRD1
STCD67		1	glycosyltransferase family 35 [<i>Nectria haematococca</i> mpVI 77-13-4] XP_003046680.1	0.0	278 bp	CF944364 BM076494 CB867726 CF881803 CF908472	tr_120198 (<i>gph1</i>)	IPR000811	glycogen phosphorylase GPH1, glycosyl transferase family 35, carbohydrate metabolism
STCD76		1	ATP synthase beta chain, mitochondrial precursor [<i>Chaetomium globosum</i> CBS 148.51]	0.0	134 bp	CF876408 CF876393 CF874883 CF870779 CF870633	tr_123071 (<i>atp2</i>)	IPR000194 IPR005722 IPR003593 IPR000793 IPR004100	ATP synthase beta chain, mitochondrial precursor, associated to cellulase signal transduction (PMID:
STCD82		1	ATP carrier protein [<i>Neurospora crassa</i> OR74A] XP_963201.1	8e-131	146 bp	CF944425 CF944116 CF883491 CF883338 CF881386	tr_121834	IPR002113 IPR002067 IPR001993	mitochondrial carrier protein
STCD89		1	Pc12g07300 [<i>Penicillium chrysogenum</i> Wisconsin 54-1255] XP_002557565.1	3e-11	230 bp	CF945334 BM077096 CF935759 CF935269 CF935219	tr_71851	IPR011058	unkown

A

wild type *grd1* locus

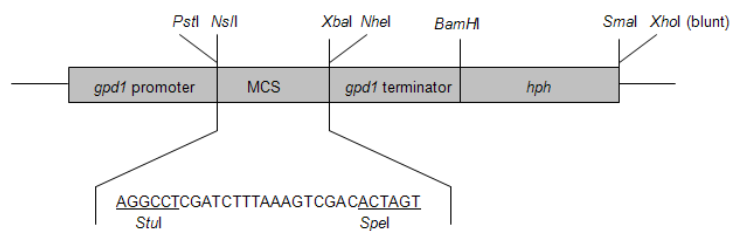


deletion cassette

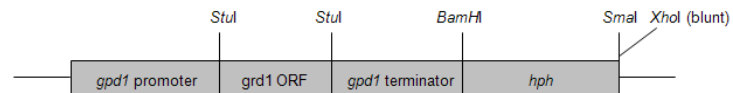


B

pLH1mcsHPH



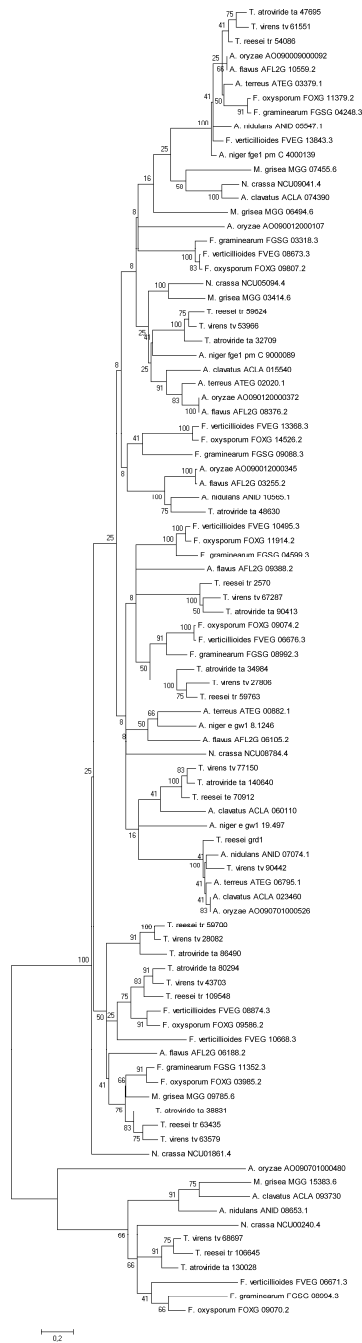
paGPD1hph



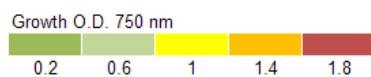
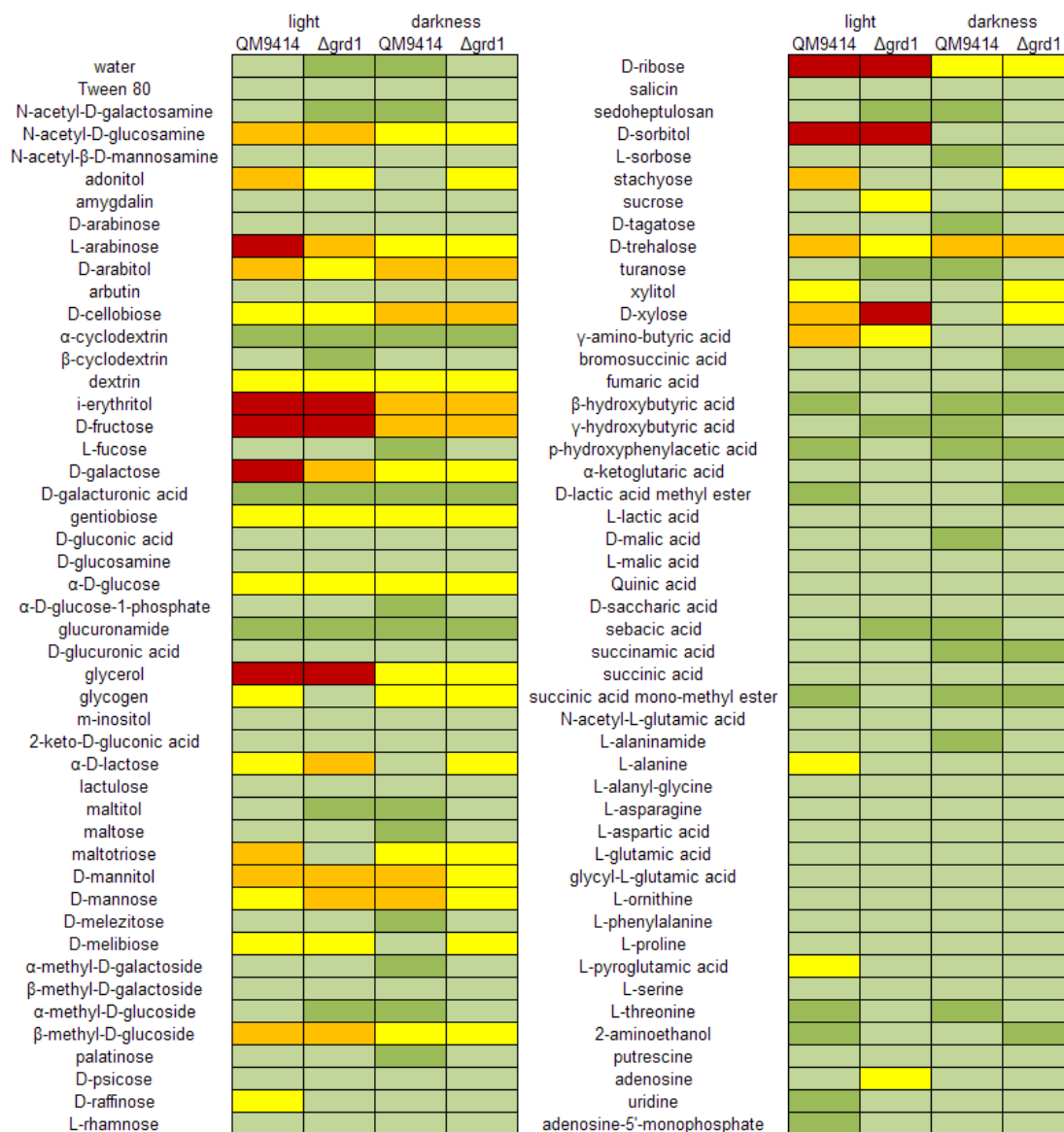
Supplementary figure S1: Gene structure of *grd1*, deletion cassette (A), constitutive expression cassette and constitutive *grd1* expression cassette (B)

(A) construction of a transformation cassette for deletion of *grd1* by replacing its open reading frame with the *pyr4* gene as a selection marker

(B) construction of a constitutive expression cassette under control of *gpd1* promoter and terminator, multiple cloning side was cloned into the *Pst*I - *Xba*I site with *Nsi*I - *Nhe*I. The hygromycin B resistance gen (*hph*) was cloned into the *Bam*HI – *Sma*I site (*Bam*HI – *Xho*I, blunt)



Supplementary figure S2: Phylogenetic analysis of short chain dehydrogenases. Analysis was done using the Minimum evolution method and 500 Bootstrap replications as test of phylogeny. Phylogenetic tree obtained by MEGA 4.0.2 and the sequences were obtained from the JGI *T. reesei* genome database V 2.0 (<http://genome.jgi-psf.org/Trire2/Trire2.home.html>) and the BROAD Database (<http://www.broadinstitute.org/scientific-community/data>).



Supplementary figure S3: Light stimulation of growth of *T. reesei* wild type QM9414 and Δ grd1 on all 96 BIOLOG carbon sources. Biomass equivalents (OD750) after 72 hrs of growth in constant darkness and constant illumination (1800 lux) are given.