

Supplementary Materials

Table S1. Comparison of nucleotide sequence obtained following rapid amplification of cDNA ends (RACE) PCR using gene specific primers.

Description	Identity (%)	Accession Number
β -Glucosidase 2 (<i>Trichoderma asperellum</i>)*	100	ARW78142.1
<i>Trichoderma virens</i> beta-1,4-glucosidase (bgl2) gene, complete cds	98.64	KM052276.1
<i>Trichoderma virens</i> bgl1 (BGL1) mRNA, complete cds	98.61	KU535892.1
<i>Trichoderma asperellum</i> CBS 433.97 glycoside hydrolase family 1 protein	98.57	XM_024909259.1
<i>Trichoderma gamsii</i> beta-glucosidase (TGAM01_v203663), partial mRNA	91.85	XM_018806048.2
<i>Trichoderma atroviride</i> IMI 206040 glycoside hydrolase family 1 protein partial mRNA	91.70	XM_014084068.1

* This study

Table S2. Comparison of predicted TaBgl2 amino acid sequence to selected β -glucosidases from several *Trichoderma* spp.

Description	Length (amino acid)	Molecular Weight (Daltons, D)	Identity (%)	Accession Number
β -Glucosidase 2 (<i>Trichoderma asperellum</i>) *	465	52,798.31	100	ARW78142.1
Glycoside hydrolase family 1 protein (<i>Trichoderma asperellum</i> CBS 433.97)	465	52,784.24	99	XP_024766195.1
β -Glucosidase (<i>Trichoderma gamsii</i>)	465	52,899.28	97	XP_018660766.2
Glycoside hydrolase family 1 protein (<i>Trichoderma atroviride</i> IMI 206040)	465	52,956.42	97	XP_013939543.1
β -1,4-Glucosidase (<i>Trichoderma virens</i>)	455	51,612.88	99	AJW67427.1
GH1 β -glucosidase BGL2/CEL1a (<i>Trichoderma guizhouense</i>)	465	52,950.44	92	OPB39337.1
β -Glucosidase (<i>Trichoderma harzianum</i>)	465	52,982.50	92	KKP02477.1
β -Glucosidase (<i>Trichoderma reesei</i>)	466	52,240.56	90	BAA74959.1

* This study

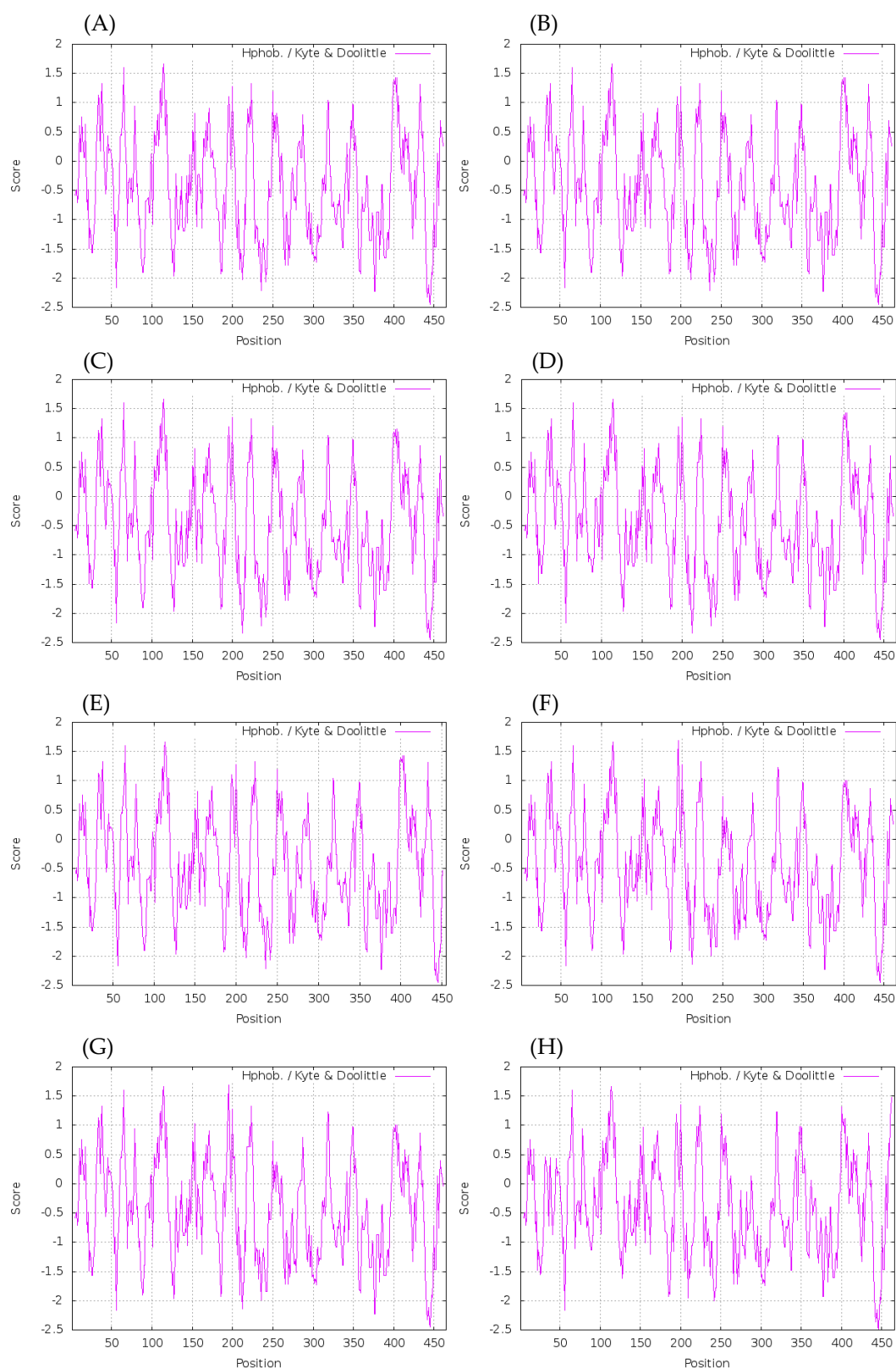


Figure S1. Kyte and Doolittle Plots for β -glucosidases from different *Trichoderma* sp. (A: *T. asperellum* UPM1 Bgl 2 – ARW78142.1; B: *T. asperellum* CBS 433.97 glycoside hydrolase family 1 – XP_024766195.1; C: *T. gamsii* beta-glucosidase – XP_018660766.2; D: *T. atroviride* IMI 206040 glycoside hydrolase family 1 – XP_013939543.1; E: *T. virens* beta-1,4-glucosidase – AJW67427.1; F: *T. guizhouense* GH1 beta-glucosidase Bgl2 – OPB339337.1; G: *T. harzianum* beta-glucosidase – KKP02477.1; H: *T. reesei* beta-glucosidase – BAA74959.1). Dashed lines in red indicate threshold value of 1.6.

Table S3. Subcellular localization of TaBgl2 following prediction from (A) PSORT II and (B) DeepLoc 1.0 servers (including protein solubility).

(A)

Localization	Probability (%)
Cytoplasmic	56.5
Nuclear	17.4
Cytoskeletal	17.4
Endoplasmic reticulum	4.3
Peroxisomal	4.3

(B)

Localization	Probability	Solubility
Cytoplasm	0.6021	Soluble
Peroxisome	0.1255	
Plastid	0.0810	
Mitochondrion	0.0734	
Lysosome/Vacuole	0.0455	
Extracellular	0.0349	
Endoplasmic reticulum	0.0226	
Cell membrane	0.0080	
Nucleus	0.0059	
Golgi apparatus	0.0010	