Table 1 Suppl. Primer sequences used in the experiment (F - forward primer, R - reverse primer).

Name	Primer sequences
3' outer	GAAACCATAGCAGACGCAAAG
3' inner	GAAAGGAGTGGACTTCAAGGG
5' outer	GTCAAGAGTCTCATCGAGGAGTT
5' inner	ATCTCGGTTCCGTACTCGTT
BoCYP83B1-F	GGCTTAAUATGGATCTCTTATTGATTATAGCCG
BoCYP83B1-R	GGTTTAAUTCAAATGTGCGTCCTTGGTG
BoCYP83B1-pro-F	GGCTTAAUAAAGATTGTATGATGGATCACCG
BoCYP83B1-pro-R	GGTTTAAUTCTACCAATGCAAGTGATGGTCT
TSB1-F	AGCCTCAGGCACCTCTGCTACTT
TSB1-R	GGAGACGGAGAAGGATGATGACTT
CYP79B2-F	AACAAAAAGAAACCGTATCTGCCAC
CYP79B2-R	TCCTAACTTCACGCATGCTATCTC
CYP79B3-F	CTCCTTCTTCCTTGCAAATGGA
CYP79B3-R	GAGAATCATCAAGAAGCAAAGGG
CYP83B1-F	ATAGCCGGTTTAGTAGCGGCT
CYP83B1-R	GCCGTATAGCTTGGAGAGACGGAAA
SUR1-F	CAGGCATATCTAAGGGATGGGTTG
SUR1-R	AATTATTGTGGCAGGGTCAGGAG
SOT16-F	CGAAGTCGTCGAACTCACAGAGTT
SOT16-R	AAAGACCTTCGAGGAGACATTCTTG
CYP81F2-F	GTCACAGGGAGACGCTACTACGG
CYP81F2-R	GAGCAGTCGTTGTAAGAAAGCGTCC
PEN2-F	CTGAAAACGGGTATGGTGAAGTAGC
PEN2-R	TCCACTCGAAGTTATCTAGCAATGACC
BCAT4-F	CATCACAATCACAAAGATCAGAGAC
BCAT4-R	GCCAGGGCTGAAAGTTGA
MAM1-F	CCGCAGAAGCTAGAGATTG
MAM1-R	TCCTCATCCACCTCATTCC
MYB28-F	GCAGATTCGCAATGAAGAGGATAGT
MYB28-R	GACTTCTTGGGAAACATCGGACATA
CYP79F1-F	CTTGACGTACTGTCGTTTGTTG
CYP79F1-R	GCTACTCCGAATGTTTGATCG
CYP79F2-F	TGATGTGTTTCGACGCTTTG
CYP79F2-R	TATAGCGTTTTCGGGCAATG
CYP83A1-F	ATACGGTCCAATCTTGTCATACAGGAT
CYP83A1-R	TAATGCCATGTCACGCCTGC
UGT74C1-F	CCGAGAGAAGCAAACTACCC
UGT74C1-R	CTCTAACCCCAATCTTCCAC
$FMO_{GS\text{-}OX1}$-F	TCTGGAACTACTCATCTAAAGCTGACTCTG
$FMO_{GS\text{-}OX1}$-R	ATGTCATGAATGCGTGGCACG
TGG1-F	GACTTTGAGAAGGCTACTGCCGATTA
TGG1-R	CCATTTGCCAGATGCTTTGAGGT
AtACTIN2-F	CCATCCTCCGTCTTGACCTT
AtACTIN2-R	ACTTGCCCATCGGGTAATTC
BoCYP83B1-QRT-F	CTCGATGAGACTCTTGACCCTAGCC
BoCYP83B1-QRT-R	CGCAGTGTCAGTTCCCGGTAC
BoACTIN2-F	CGTATTGCTCCTGAAGAACACCC
BoACTIN2-R	AGAAACCCTCGTAGATTGGGACAG

Table 2 Suppl. Physicochemical properties of BoCYP83B1 predicted by *Protparam*.

Properties	BoCYP83B1
Number of amino acids	499
Formula	$C_{2582}H_{4068}N_{672}O_{716}S_{27}$
Molecular mass [Da]	56846.40
Total number of atoms	8065
Theoretical pI	8.54
Most abundant amino acids	Leu
Total number of positively charged residues (Arg + Lys)	62
Total number of negatively charged residues (Asp + Glu)	58
Aliphatic index	92.46
Instability index	36.56
Types of protein	stable protein
Grand average of hydropathicity	-0.110

Table 3 Suppl. Predicted *cis*-elements in the promoter of *BoCYP83B1*.

Name	Sequence 5' to 3'	Position	Function
TCA-element	CCATCTTTTT, TCAGAAGAGG	-1345, -529	*cis*-acting element involved in salicylic acid responsiveness
GARE-motif	TCTGTTG	-1304	gibberellin-responsive element
TC-rich repeats	ATTTTCTTCA	-661, -454, -246	*cis*-acting element involved in defense and stress responsiveness
CCAAT-box	CAACGG	-1488	MYBHv1 binding site
CGTCA-motif (TGACG)	CGTCA	-1612, -1452, -1438, -925, -131	*cis*-acting regulatory element involved in MeJA-responsiveness
ACE	GACACGTATG	-1725	*cis*-acting element involved in light responsiveness
ACE	AAAACGTTTA	-1545, -235	*cis*-acting element involved in light responsiveness
ERE	ATTTCAAA	-1368, -913	ethylene-responsive element
MBS	TAACTG	-811, -634	MYB binding site involved in drought-inducibility
WUN-motif	AAATTTCCT	-1446	wound-responsive element

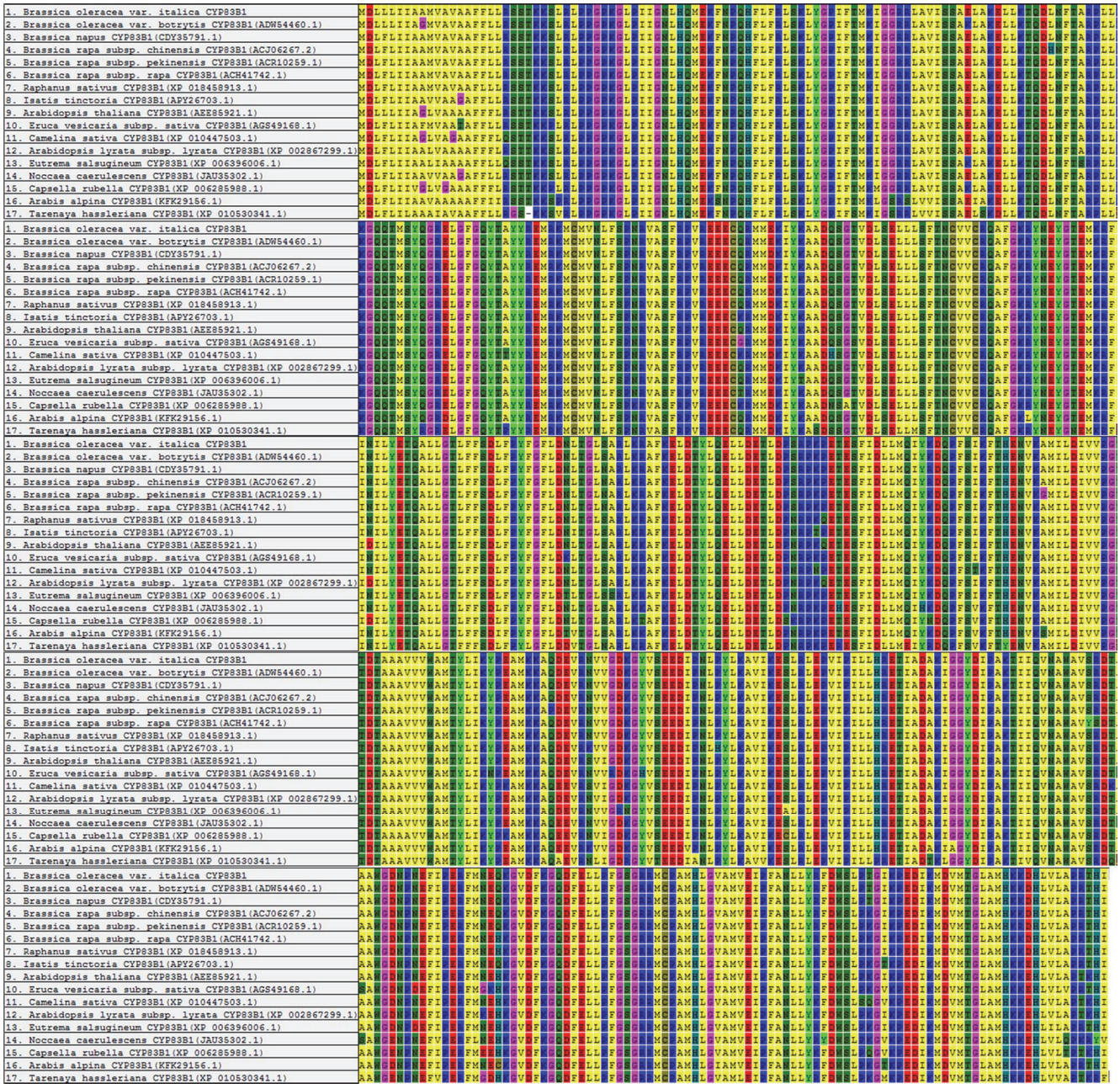

Fig. 1 Suppl. Multiple alignment of deduced BoCYP83B1 with its orthologs from *Brassicaceae* plants. Multiple alignment was performed using *MEGA5.0*. Different shaded boxes show identical and similar amino acids, respectively.

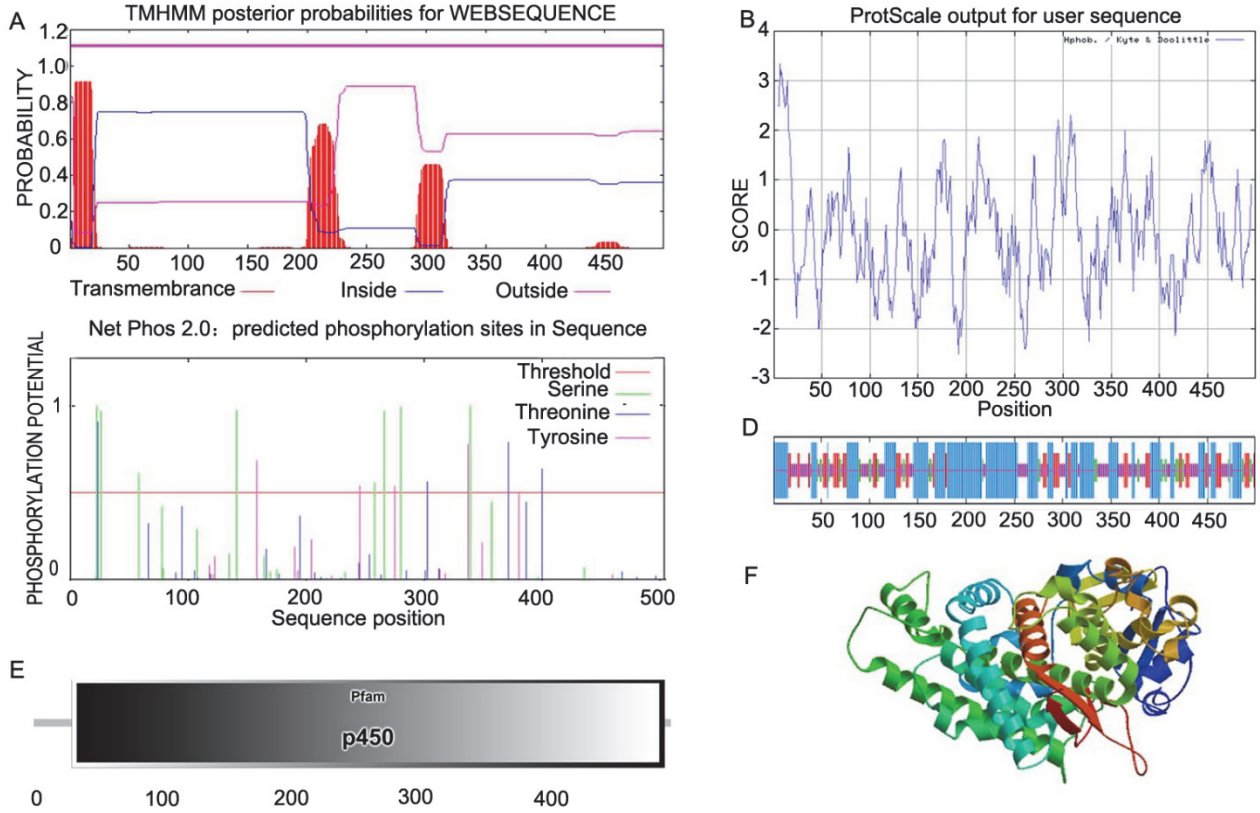

Fig. 2 Suppl. Bioinformatics analysis of BoCYP83B1 proteins. *A* - Transmembrane prediction. *B* - Hydrophobicity prediction. *C* - Translational modification of amino acids. *D* - Secondary structure of the protein. *E* - Functional domain of the protein. *F* - Three-dimensional structure of the protein.

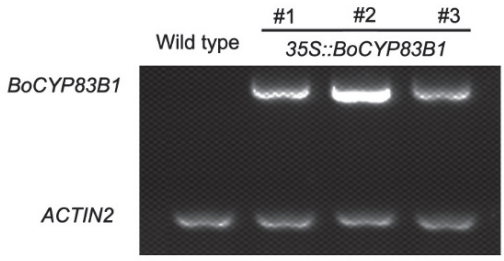

Fig. 3 Suppl. *BoCYP83B1* expression in *35S::BoCYP83B1* transgenic *Arabidopsis* plants. RT-PCR analysis was performed on RNA extracted from 4-week-old rosette leaves. One representative plant from each line is shown. *AtACTIN2* was used as an internal control.

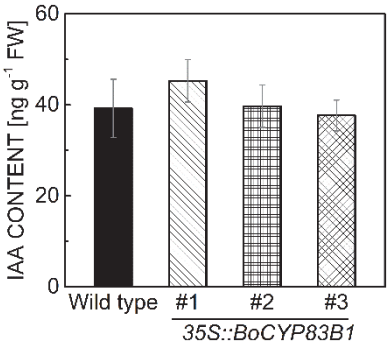

Fig. 4 Suppl. Content of indole-3-acetic acid (IAA) in *35S::BoCYP83B1* transgenic *Arabidopsis* seedlings and the respective wild type. The experiment included three biological repeats, and five technical repeats. Data were analyzed statistically using the *t*-test, and no significant difference was detected compared with wild type.

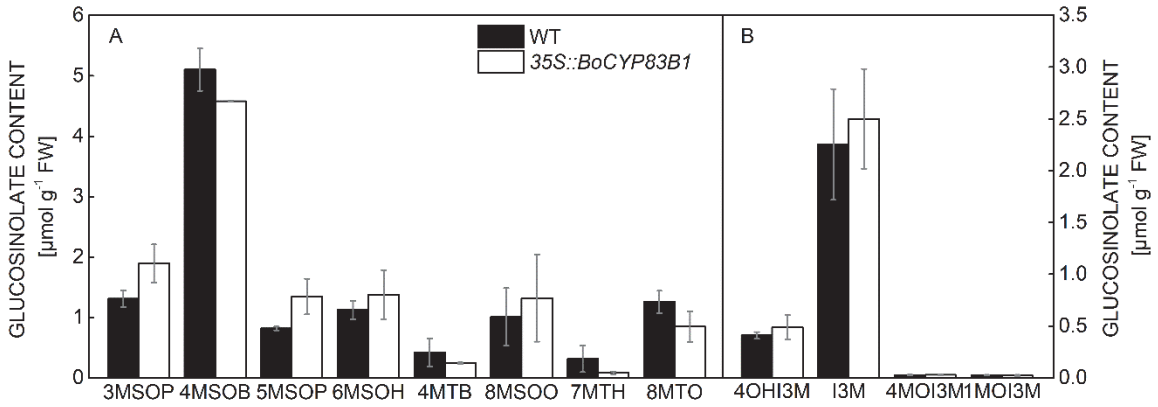

Fig. 5 Suppl. Glucosinolate content in *35S::BoCYP83B1*. *A* - Aliphatic glucosinolate profile in leaves. *B* - Indolic glucosinolate profile in leaves. Glucosinolates were analyzed by HPLC. Three independent transgenic lines with high expression of *BoCYP83B1* and clear phenotype were used for glucosinolate analysis. The experiment included three biological repeats, and three technical repeats. Data were analyzed statistically using the *t*-test and no significant differences between transgenic plants and wild-type were found. 3MSOP - 3-methylsulphinylpropyl glucosinolate; 4MSOB - 4-methylsulphinylbutyl glucosinolate; 4MTB - 4-methylthiobutyl glucosinolate; 5MSOP - 5-methylsulphinylpentyl glucosinolate; 6MSOH - 6-methylsulphinylhexyl glucosinolate; 7MTH - 7-methylthiohepthyl glucosinolate; 8MSOO - 8-methylsulphinyloctyl glucosinolate; 8MTO - 8-methylthiooctyl glucosinolate; 4OHI3M - 4-hydroxyindol-3-ylmethyl glucosinolate; I3M - indol-3-ylmethyl glucosinolate; 4MOI3M - 4-methoxyindol-3-ylmethyl glucosinolate; 1MOI3M - 1-methoxyindol-3-ylmethyl glucosinolate.

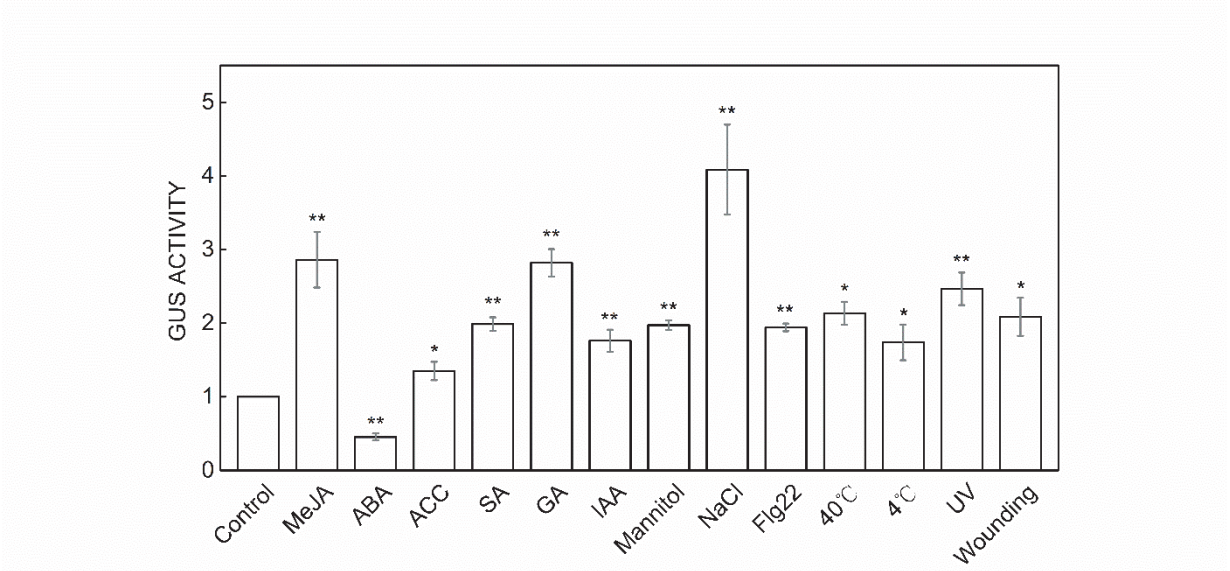

Fig. 6 Suppl. Changes of β-glucuronidase (GUS) activity in response to exogenous hormones and stresses in $P_{BoCYP83B1}$::*GUS*. Activities of GUS were measured quantitatively in 5-d-old $P_{BoCYP83B1}$::*GUS* seedlings treated with 25 μM methyl jasmonate (MeJA), 200 μM salicylic acid (SA), 10 μM abscisic acid (ABA), 20 μM 1-amino-1-cyclopropanecarboxylic acid (ACC), 10 μM gibberellic acid (GA), 5 μM indole-3-acetic acid (IAA), 200 mM mannitol, 150 mM NaCl, and 1 μM Flagelin 22 (Flg22) for 3 d. For the other stress treatments, 5-d-old seedlings were exposed under UV radiation for 1.5 h, 40 °C for 2 h, and 4 °C for 2 h. The wounding treatment was performed by cutting the cotyledons in half. Seedlings without any treatment were used as control. The fold change of GUS activity in comparison with the control was calculated. The experiment included three biological repeats, and three technical repeats and the mean values (±SEs) are shown. Data were analyzed statistically using the *t*-test, * and ** indicate significant differences from the corresponding control at $0.01 < P < 0.05$ and $P < 0.01$, respectively.

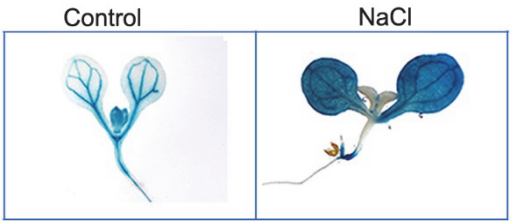

Fig. 7 Suppl. *BoCYP83B1* expression in response to NaCl in 5-d-old plants treated with 150 mM NaCl for 4 d.