## New Phytologist Supporting Information

Article title: Studies of moss reproductive development indicate that auxin biosynthesis in apical stem cells may constitute an ancestral function for focal growth control

Authors: Landberg Katarina, Šimura Jan, Ljung Karin, Sundberg Eva and Thelander Mattias

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Table S1 Constructs produced and used in the study

 Table S2 Primers used in study

**Table S3** Level of auxin metabolites in wildtype *P. patens* and in stated over-expressor (OE) and mutant lines

## Supplementary references

Method S1. Generation of overexpression (OE) constructs and lines. To produce the vector pMT258, a 1429 bp Rice actin promoter fragment amplified with primers SS596/598 was trimmed with *Hind*III/SalI and cloned between the same sites of plasmid pUK-Pp108+Hsp-GW+npt (gift from Michael Prigge and Mark Estelle). The resulting vector pMT258 carries a G418 selection cassette (G418R) and allows coding sequences to be cloned behind the Rice actin promoter for subsequent integration into the Pp108 locus. To produce the PpTARF OE construct pMT261, a 1488 bp PpTARF CDS fragment was amplified from cDNA with primers SS378/SS379, trimmed with AvrII/SalI, and cloned between the same sites of pMT258. To produce the PpYUCC OE construct pMT262, a 1317 bp PpYUCC CDS fragment was amplified from cDNA with primers SS372/373, trimmed with AvrII/SalI, and cloned between the same sites of pMT258. To produce the PpYUCA OE construct pMT266, a 1323 bp PpYUCA CDS fragment was amplified from cDNA with primers SS370/371, trimmed with AvrII/SalI, and cloned between the same sites of pMT258. To produce the OE vector pMT272 carrying a zeocin selection cassette (ZeoR), G418R in pMT258 was excised by AvrII/SalI and exchanged for ZeoR excised from plasmid 35S-Zeo by SpeI/XhoI. To produce the PpTARA OE construct pMT281, a 1554 bp PpTARA CDS fragment was amplified from cDNA with primers SS469/470, trimmed with XmaJI, and cloned into the same site of pMT272. All OE constructs were linearized with Sfil before transformation into WT. The PpTARA OE construct was also transformed into the Pptara-1 mutant background. Correct integration was confirmed by PCR and level of overexpression was determined by qPCR (Fig. S1, S2). Resulting constructs and sequences of primers used for cloning and genotyping are summarized in Tables S1 and S2, respectively.

Method S2. Generation of transcriptional reporter constructs and lines. To construct promoter-based reporters, the vector pMT211 carrying a hygromycin selection cassette (HygR) and allowing promoters to be cloned ahead of a GFP-GUS reporter gene for subsequent integration into the Pp108 locus was used (Thelander et al., 2019). To produce the PpTARA reporter construct pMT243, a 1808 bp PpTARA promoter fragment was amplified from gDNA with primers SS220/SS221, trimmed with BamHI/NcoI, and cloned between the same sites of pMT211. To produce the *PpTARB* reporter construct pMT241, a 2789 bp *PpTARB* promoter fragment was amplified from gDNA with primers SS222/223, trimmed with BspHI, and cloned into the same site of pMT211. To produce the *PpTARC* reporter construct pMT254, a 2987 bp *PpTARC* promoter fragment was amplified from gDNA with primers SS224/225, trimmed with BamHI/NcoI, and cloned between the same sites of pMT211. To produce the PpTARD reporter construct pMT237, a 2446 bp PpTARD promoter fragment was amplified from gDNA with primers SS226/227, trimmed with *Hind*III/NcoI, and cloned between the same sites of pMT211. To produce the *PpYUCF* reporter construct pMT246, a 2120 bp *PpYUCF* promoter fragment was amplified from gDNA with primers SS244/245, trimmed with BamHI/NcoI, and cloned between the same sites of pMT211. All reporter constructs were linearized with SfiI before transformation into WT. Correct integration was confirmed by PCR (Fig. S3). Resulting constructs and sequences of primers used for cloning and genotyping are summarized in Tables S1 and S2, respectively.

**Method S3. Generation of knockout (KO) constructs and lines.** All KO constructs were designed to delete the entire coding region of the gene of interest and genomic DNA was used as the template in all PCRs to amplify 5' and 3' flanking regions. Most KO constructs were produced by Gateway facilitated 3-fragment recombination (www.thermofisher.com). In each

such case, LR recombination was used to link a 5' flanking fragment (cloned in entry vector pDONR P1-P4), a selection cassette (cloned in entry vector pDONR P4r-P3r), and a 3' flanking fragment (cloned in entry vector pDONR P3-P2 by) in the destination vector pDEST14 (www.thermofisher.com). Three different selection cassette entry clones were produced and used: Primers SS265/266 were used to amplify and clone HygR from plasmid pMT123 (Thelander et al., 2004) to produce entry clone pMT222, primers SS611/612 were used to amplify and clone G418R from plasmid pMT164 (Thelander et al., 2007) to produce entry clone pDONR4r-3r-G418, and primers SS613/SS614 were used to amplify ZeoR from plasmid 35S-Zeo to produce entry clone pDONR4r-3r-Zeo. To produce the PpTARC KO construct pMT229 linearized with XhoI prior to transformation, a 1024 bp PpTARC 5' fragment amplified with primers SS269/270 was linked to G418R and a 1007 bp PpTARC 3' fragment amplified with primers SS271/SS272. To produce the PpYUCA KO construct pMT263 linearized with SalI prior to transformation, a 1136 bp *PpYUCA* 5' fragment amplified with primers SS325/326 was linked to ZeoR and a 906 bp PpYUCA 3' fragment amplified with primers SS368/369. To produce the PpYUCB KO construct pMT276 linearized with SalI prior to transformation, a 1081 bp PpYUCB 5' fragment amplified with primers SS424/425 was linked to ZeoR and a 1073 bp PpYUCB 3' fragment amplified with primers SS426/SS476. To produce the PpYUCC KO construct pMT232 linearized with XhoI prior to transformation, a 1055 bp PpYUCC 5' fragment amplified with primers SS281/282 was linked to G418R and a 1095 bp PpYUCC 3' fragment amplified with primers SS283/284. To produce the PpYUCD KO construct pMT236 linearized with XhoI prior to transformation, a 1009 bp PpYUCD 5' fragment amplified with primers SS285/286 was linked to ZeoR and a 960 bp PpYUCD 3' fragment amplified with primers SS287/288. To produce the *PpYUCE* KO construct pMT233 linearized with *Sal*I prior to transformation, a 938 bp *PpYUCE* 5' fragment amplified with primers SS290/292 was linked to G418R and a 984 bp PpYUCE 3' fragment amplified with primers SS293/294. To produce the *PpYUCF* KO construct pMT235 linearized with SalI prior to transformation, a 1007 bp PpYUCF 5' fragment amplified with primers SS295/296 was linked to HygR and a 815 bp *PpYUCF* 3' fragment amplified with primers SS298/300.

The PpTARA, PpTARB and PpTARD KO constructs were produced by traditional consecutive ligation steps. To produce the *PpTARA* HygR KO construct pMT210 linearized with *Sna*BI/SacI prior to transformation, a PpTARA 5' flanking fragment amplified with primers SS603/604 was trimmed to 1086 bp with Xhol/HindIII and ligated between the same sites of plasmid pMT123 where after a PpTARA 3' flanking fragment amplified with primers SS605/606 was trimmed to 952 bp with XbaI/SacI and ligated between the same sites of the product of the first ligation. To produce the *PpTARB* G418R KO construct pEP54 linearized with *BamHI/PacI* prior to transformation, a PpTARB 5' flanking fragment amplified with primers SS607/608 was trimmed to 1030 bp with *BamHI/XhoI* and ligated between the same sites of plasmid pMT164 where after a PpTARB 3' flanking fragment amplified with primers SS609/610 was trimmed to 894 bp with Spel/PacI and ligated between the same sites of the product of the first ligation. To produce the PpTARD HygR KO construct pMT207 linearized with Xhol/SacI prior to transformation, a PpTARD 5' flanking fragment amplified with primers SS599/600 was trimmed to 907 bp with XhoI/HindIII and ligated between the same sites of plasmid pMT123 where after a PpTARD 3' flanking fragment amplified with primers SS601/602 was trimmed to 1011 bp with SpeI/SacI and ligated between the same sites of the product of the first ligation.

All KO constructs were transformed into WT to produce a full set of *PpTARA-D* and *PpYUCA-F* single KO lines. The *PpTARB* KO construct pEP54 was also transformed into the confirmed *Pptara-1* mutant to produce *Pptaratarb* double KO lines. Other *PpTAR* double and triple mutants (*Pptaratarc*, *Pptarctard* and *Pptarbtarctard*) were produced by crosses from confirmed single mutant lines as described in Thelander et al., 2019. Lines resulting from new transformations were checked for correct construct integration by PCRs confirming the 5' junction, the 3' junction and the loss of internal gene sequences while the genotypes of lines resulting from crosses were confirmed only by a PCR demonstrating the loss of internal gene sequences (Fig. S4, S5). Constructs and sequences of primers used for cloning and genotyping are summarized in Tables S1 and S2, respectively.

**Method S4. Generation of knockout lines carrying the PpR2D2 reporter.** PpR2D2-2 and PpR2D2-3 (Thelander et al., 2019) were crossed to *Pptara-1* and *Pptaratarc-1* where after colonies from regenerating spores were screened for loss of *PpTARC*, resistance to selection agents, *Pptar* mutant phenotoypes, and PpR2D2 signals to identify mutant offspring carrying the PpR2D2 reporter construct (Fig. S6). Sequences of primers used for genotyping are summarized in Table S2.

Method S5. RT-qPCR to determine *PpTAR* transcript abundance. To determine *PpTARA-D* transcript abundance in various WT tissues material was harvested in triplicates, snap frozen and stored in -80°C awaiting RNA isolation. Chloronema-enriched protonema was harvested from cellophane-overlaid BCD media grown under standard conditions for 5 days since the last subcultivation by blending. To collect shoot apices and reproductive organs, colonies were grown on thick BCD plates in standard conditions for 45 days before transfer to inductive conditions. Shoot apices including only the youngest leaves were harvested before or 2, 10, 13 or 16 days after transfer to inductive conditions. Antheridia and archegonia bundles were separately harvested after 15-16 and 20 days in inductive conditions, respectively. At these time points, the most mature organs were typically at stage 6-7 and stage 9 (Landberg et al., 2013), respectively, but the bundles also contained a mix of younger organs. Total RNA was extracted from samples using the Picopure RNA extraction kit from Arcturus (Thermo Fisher Scientific). The manufacturer's protocol was followed with two additions: Tissue was homogenized with glass beads in a fast-prep machine for 60 s at full speed and an on-column DNase treatment step (Qiagen, 79254) was included. From each sample, 50 ng of total RNA was converted into cDNA and amplified using the Ovation PicoSL WTA System V2 from NuGen in accordance with instructions from the manufacturer. Quantitative real-time PCRs were based on Maxima SYBR Green/ROX qPCR master mix (Thermo Fisher Scientific, K0221) and 4 ng of amplified cDNA was consistently used in total reaction volumes of 25 µl. Reactions were run on an iQ5 Real-Time PCR system (Bio-Rad, Sundbyberg, Sweden) at 95°C for 10 min followed by 40 cycles of 95°C for 15 sec, 60° for 30 s and 72° for 30 s. To rule out amplification from non-specific targets and contaminating genomic DNA, *PpTARA-D* primers were designed to anneal to regions with limited sequence similarity and one primer in each pair also has an annealing site interrupted by an intron. For normalization, the three reference genes AdePRT, E2 and St-P2a were used. These three reference genes were selected among six candidates described in Le Bail et al., 2013 since they showed the most stable expression in antheridia and archegonia in our hands (data not shown). The primers used were: PpTARA, SS501/SS502; PpTARB, SS503/SS504; PpTARC, SS517/SS518, PpTARD, SS519/SS520; AdePRT, SS549/SS460; E2, SS455/SS456; ST-P2a,

SS463/SS464 (for sequences, see Table S2). Melt curve analysis, gel analysis and standard curve analysis confirmed that all primer pairs amplified a single product of the expected size with efficiencies of  $100 \pm 5$  % (data not shown). Fig. 2a,b and Fig. S10a show relative expression calculated with the 2– $\Delta\Delta$ CT method using the gene with the highest transcript abundance across the samples as the calibrator. Each data point is based on biological triplicates and error bars represent standard deviation.

To determine transcript abundance in *PpTARA, PpTARF, PpYUCA* and *PpYUCC* OE lines the RNeasy plant mini kit (Qiagen, 74903) was used to prepare total RNA from young protonemal tissue grown under standard conditions in duplicates or triplicates. On column DNAse treatment was performed for all samples (Qiagen, 79254). 1 µg RNA was used for cDNA synthesis using the Superscript III reverse transcript kit (Thermo Fisher Scientific, 18080051). Quantitative real-time PCRs were performed as described above, but with 1 µl cDNA as template per 25 µl reaction. For normalization, *AdePRT* (see above; for *PpTARA*) or actin (Prigge et al., 2010; for *PpTARF, PpYUCA* and *PpYUCC*) were used as reference genes. The primers used were: *PpTARA*, SS501/SS502; *PpTARF*, SS434/SS435; *PpYUCA*, SS430/SS431; *PpYUCC*, SS428/SS429; *ACT*, SS29/SS30; *AdePRT*, SS459/460 (for sequences, see Table S2). Fig. S1f-i and Fig. 2c show relative expression of 2-3 biological replicates for each line with the WT, or the OE line showing the lowest expression in cases when transcript were under detection level in WT, set to 1.

**Fig. S1.** *PpTARA*, *PpTARF*, *PpYUCA* and *PpYUCC* overexpressor lines in WT background: Construct design, PCR verification and expression levels. (A) Schematic view of overexpression constructs and the *Pp108* locus to which they were targeted. Arrows mark the approximate annealing sites of primers used for PCR verification in B-E. (**B-E**) PCR verification of 5' and 3' junctions to confirm correct integration in lines transformed with the *PpTARA* (B), *PpTARF* (C), *PpYUCA* (D) and *PpYUCC* (E) overexpressor constructs. Expected product sizes are indicated within parenthesis and the sequences of listed primers are shown in Table S2. (**F-I**) Relative *PpTARA* (F), *PpTARF* (G), *PpYUCA* (H) and *PpYUCC* (I) expression levels in selected overexpression lines as revealed by qPCR's using cDNA from young protonemal tissue as the template. For each line/gene combination the results from three (*PpTARA*) or two (*PpTARF*, *PpYUCA*, *PpYUC*) biological replicates are displayed as bars while the mean of replicates are indicated by a horizontal line and a number. In F (*PpTARA*) and I (*PpYUCC*) the mean WT expression is set to 1. For G and H the overexpressor line with the lowest expression is set to 1 since no expression could be detected for *PpTARF* and *PpYUCA* in the WT protonemal tissue sampled. For primers sequences, see Table S2.



**Fig. S2.** *PpTARA* overexpressor lines in *Pptara-1* mutant background: Construct design, PCR verification and expression levels. (A) Schematic view of overexpression construct and the *Pp108* locus to which it was targeted. Arrows mark the approximate annealing sites of primers used for PCR verification in B. (B) PCR verification of 5' and 3' junctions to confirm correct integration. Expected product sizes are indicated within parenthesis and the sequences of listed primers are shown in Table S2. (C) Relative *PpTARA* expression levels in selected overexpression lines as revealed by qPCR's using cDNA from young protonemal tissue as the template. For each line the results from three biological replicates are displayed as bars while the mean of replicates are indicated by a horizontal line and a number. The mean WT expression is set to 1. For primers sequences, see Table S2. For primers sequences, see Table S2.



**Fig. S3.** *PpTARA*, *PpTARB*, *PpTARC*, *PpTARD* and *PpYUCF* transcriptional reporter lines in WT background: Construct design and PCR verification. (A) Schematic view of constructs and the *Pp108* locus to which they were targeted. Arrows mark the approximate annealing sites of primers used for PCR verification in B-F. (**B-F**) PCR verification of 5' and 3' junctions to confirm correct integration. Expected product sizes are indicated within parenthesis. For primers sequences, see Table S2.



**Fig. S4.** *PpTARA-D* and *PpYUCA-F* single knockout lines in WT background: Principal construct design and PCR verification. (A) Schematic consensus view of constructs and loci of genes of interest (GOI) to which they were targeted. Arrows mark the approximate annealing sites of primers used for PCR reactions to confirm correct integration in B-K. (B-K) Results of PCR verification to confirm 5' junctions (5' PCR), 3' junctions (3' PCR) and loss of internal gene sequences (Int. PCR). For each genotype, primer names and expected product sizes are indicated for each of the three PCR types. For primers sequences, see Table S2. Note: Verification of the 3' junction in *PpTARD* KO lines was not possible due to the presence of an extended AT-rich region immediately downstream of the *PpTARD* coding region.



**Fig. S5. PCR verification of** *PpTAR* **double and triple knockout lines.** (A) PCR verification to confirm loss of *PpTARB* after transformation of the *Pptara-1* single mutant with the *PpTARB* KO construct pEP54. Primer names, expected product sizes and results are shown for PCRs confirming correct 5' junction, correct 3' junction, and the loss of internal gene sequences (see Fig. S4A for schematic explanation). (B-D) PCR verification to confirm the genotype of (A) *Pptaratarc* double mutants produced by a cross between *Pptara-1* and *Pptarc-4*, (B) *Pptarctard* double mutants produced by a cross between *Pptarc-4* and *Pptard-2*, and (C) *Pptarbtarctard* triple mutants produced by a cross between *Pptarb-2* and *Pptarctard-1*. In each case, primer names, expected product sizes and results are shown for a PCR confirming the loss of internal gene sequences (called Int. PCR in Fig. S4A). For primers sequences, see Table S2.



**Fig. S6. Confirmation of knockout lines carrying the PpR2D2 reporter.** Character matrix confirming that the selected meiotic offspring of crosses between the PpR2D2-2 and PpR2D2-3 auxin reporter lines (Thelander et al., 2019) and the *Pptara-1* and *Pptaratarc-1* lines, respectively, represent *Pptar* mutants carrying the PpR2D2 reporter. For primers sequences, see Table S2. Nd, not determined.

	otara-1	otara-1	otaratarc-1	otaratarc-1	Pa	Parent lines			
	PpR2D2-2 Pp	PpR2D2-3 Pµ	PpR2D2-2 Pµ	PpR2D2-3 Pµ	PpR2D2-2	PpR2D2-3	Pptara-1	Pptaratarc-1	WT
Pptara phenotype	+	+	-	-	-	-	+	-	-
Pptara Pptarc phenotype	-	-	+	+	-	-	+	-	-
PpR2D2 signals	+	+	+	+	+	+	-	-	-
Hyg R ( <i>PpTARA</i> KO construct)	+	+	+	+	-	-	+	+	-
G418 R ( <i>PpTARC</i> KO and R2D2 constructs)	+	+	+	+	+	+	-	+	-
<i>PpTARC</i> locus deleted (no PCR product with internal <i>PpTARC</i> primers SS150 and SS151 on gDNA)	nd	nd	+	+	nd	nd	nd	+	-

**Fig. S7. Intron positions in coding regions are conserved in Arabidopsis and** *P. patens TAR* **genes of both the TAA clade and the AtTAR3/4 clade**. The alignment was produced from amino acid sequences deduced from primary models of all Arabidopsis (black) and *P. patens* (green) *TAR* genes with Clustal Omega using the default settings. Positions of introns spliced out to generate the coding sequences from which amino acid sequences were deduced are marked in red.

AtTAA1 (AT1G70560.1)		0
AtTAR1 (AT1G23320.1)		0
AtTAR2 (AT4G24670.1)		41
AtTAR3 (AT1G34040.1)		37
AtTAR4 (AT1G34060.1)	IILNLVFTIHILYYSSTTWNPTWTNR	37
PpTARA(Pp3c21_15370V3.1)	MALEAER-IGRYERHORKKHLVAA-ALPNTSLSTKCSPSGNVOFTNWVSKSIPLIIGLLSTWLFQYSQSPHPATVDV-DTSAALS	82
PpTARB(Pp3c18_15140V3.1)	MGLEAER-IVTYGQSQRKKQLMAA-ALANSTLSTNCDPPGNAQSGHWSFKSTALAIFLLSTCFFQINKASNRDTVNVNDTSAMLI	83
PpTARC (Pp3c17_6500V3.1)	MDSNEGGAPTGSQDAMPVLSSPIMQRFSFENGHH-AQRMAA-VCPSVSSKGFMTNFATPVYIALLAVMLVLPSPAADWISKVHEFPLIKQMNGSSNDYFTNSRESMACFPHPES	112
PpTARD (Pp3c26_12520V3.1)		0
PpTARE (Pp3c25_6670V3.1)		0
PpTARF (Pp3c5_24670V3.1)	LVIVFHPIQGFLWTPPRSEQ	65
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AtTAA1 (AT1G70560.1)	BARNERWELENSREPEKISNENIPMSDFVVNLDH GDPTAYEEYWREMGDRCTVTIRGCDLMSYFSDMTNLCWFLEPELED	75
AtTAR1 (AT1G23320.1)	DTC	76
AtTAR2 (AT4G24670.1)	TAYVSIWPVVSTTASESSSLSSASCNYSKIEEDDDRIINLKFDDTVYERYWQENGEVTTMVIPGWQSLSYFSDENNLCWFLEPELAK	129
AtTAR3 (AT1G34040.1)	AALEAEAAASVSCSGHGRSYVDGLGVLDGHK-PCECHDCYTGKDCSVLLKDCPVDANSGDPLFLEPFWIRKAEESAVVESGWHRMSYTFNGYGLFMSAELEK	138
AtTAR4 (AT1G34060.1)	AAAEAETVASFSCSGHGRAFVDGLGVLDGQKPPCECNNCYIGKDCSVLLKDCPVDANSGDPLFLEPFWMRQAERSAILVSGWHRMSYIYEDGTYVSRELEK	138
PpTARA(Pp3c21_15370V3.1)	QLASQLAATNSLPCSGHGYMADFDTERSLGICKCYECFGGVDCSQVIDNCVIDLDH BDPTMFEEFWFRNAANTITVILGYQRMSYFAQSKH-VWFMENELEV	183
PpTARB(Pp3c18_15140V3.1)	QLATQIAATTTLPCSGHGYLEFGGTKQCVGTCKCYECFGGVDCSQVIHSCVIDLDHDDPTHPEEFWFRHEVSSITVILGYQRMSYFAQSKH-WFMENELEL	184
PpTARC (Pp3c17_6500V3.1)	PRLSSYASDHLQLCSGNGHYEIASHQERTTPDAGACHCYGCFSGKHCEHLNSDCDLMIFFBDPTLFEEYWLTQPDA-PTIIFSWQGLSYFAHRHNSYLFVDSFLEQ	217
PpTARD (Pp3c26_12520V3.1)	PRSLLTAAPPLLNCDHGDPTMPEAYWNARKDDRVKVGYANDTLSYFYXSKEQEGCPWFYSALLDD	95
PpTARE (Pp3c25_6670V3.1)		19
PPTARE (Pp3c5_24670V3.1)	PAAPUWAEAVUAAEKAASKWCSGNGNVFVDTVGIDADGSPSCECNDCFAGPDCSLFLPDCVADAISJDPLLFEATWKKNSDLGAVVIPAWYKNGTUTKUVTSHPYT-EALVA	176
		107
ALIAAI (AIIG/0500.1)	ALAD LING YO MARA I DAY I YVG I OS I QLUQAA WALAS LAK - SUPYS YAARAY I SA I YVE I TYYKSGIYKHEGDAWG? DKGGY I LLVTS YNNPDDT I KETYYNNPDDDEKK	185
ALIARI (A11023520.1)		100
ATTAR2 (AT4624670.1)	ETXVTRVVVRAVTUDRTTVVTGSTUDTALTALSFRDD-SOPTIVVSRTPTSTPTITDLEKSGLKRGGDAKTTKEUGPTELVTSFRNPDGEKESVVRTEUT	230
ALTARS (AT1034040.1)	TIRKULEVOIRAVIIARATITTOOGTIGUUDAD TIRUGUUS TASTEGOTATOTTOTTOTTOTTOTTOTTOTTOTTOTTOTTOTTOTT	255
D-TADA (D-2-21 1522002 1)	VIAKULEVIAKY LIKKY TITOOT OLU LAKTIKUU TIKUU TIKUU TIKUU SUPAKUU TIKUU KUUKU VUUKUTUU ALU KUUKUU LUUKUU VUUKUU KUUKUU KUUKUU KUUKUU KUUKUU KUUKUU	205
PoTADB (Po3e18 15140V3 1)	QUESTING VORAVISOR VISION CONTRACTOR AND A CONTRACT	295
PoTAPC (Po3c17 6500V3 1)	WIRAULEVOIRET DOURT I DOURT I VIEW STREET IN TRANSPORTER I INTERNET I DE LEVOIRE ANTONING STREET I DE LEVOIR AUTORIT AUTORI	328
PoTARD (Pp3c26 12520V3 1)	a de la revolución de la construction de la constru	205
PDTARE (PD3c25_6670V3_1)	TTEDLHCHVCHAVTKDRYTVVCTGSMDLTNAVVHSLALLNS-DEVSSVVAKAPVSYKVDTFYLDSDLFNFARDBARFTCN-ATGRANTELTASENNPDATGRVDDNTSFH	131
PDTARF (PD3c5 24670V3 1)	STRELHAMVCHAVTEGEVIAFCTGSTGLINAVIHSLALCOP-GRVTPVVSKAPYYNYYTOTEVFKSPFYSFSGEPDRKVGG-G-GADOTEVIASDANDOTOTOTOTOTOTO	286
· pratte (s poco - roioto)		
	* ;* ;***,* * ; * *; ** *; ;*; ; ;; * *; ; ; * *; ; **; ; **; ; **; ; **; ; **;	200
	* :* :**** * : .* *: .* *: .* *: .* : . * : : **: *	200
		200
AtTAA1 (AT1G70560.1)	* :* :**** * : .* *: ** * : .* : .* : .	275
AtTAA1 (AT1G70560.1) AtTAR1 (AT1G23320.1)	VINDLAYYWPHYTPITERODHDIMLFFFSKITGHAOSSICALVEDEVAKKNYFLITUSIOVSKESGVRTAKILUVLKETCK	275
AttAA1 (AT1G70560.1) AttAR1 (AT1G23320.1) AttAR2 (AT4G24670.1)	* :* :*** * : . * : : * : * : : : * : : : * : : : * : : * : : : * : : * :	275 272 325
AtTAA1 (AT1G70560.1) AtTAR1 (AT1G2320.1) AtTAR2 (AT4G24670.1) AtTAR3 (AT1G34040.1)	* :* :**** * : . * : : * : : * : : * : : * : : * : : * : * : * : : * : : * : : * : * : : * : * : : * : * : * : : * : : * : : * : : * : : * : : * : : * : : * : : * : : * : : * : : * : : * : : : * : : * : : : * : : * : : * : : * : : * : : * : : * : : * : : * : : * : : * : * : : : * : * : : * : : * : : * : : * : : * : : * : : * : : * : : * : :	275 272 325 336
A+TAR1 (AT1G70560.1) A+TAR1 (AT1G2320.1) A+TAR2 (AT4G24670.1) A+TAR3 (AT1G34040.1) A+TAR4 (AT1G34060.1)	*:*:****       *:::****       *:::****       *:::****       *:::****       *:::****       *:::****       *:::****       *:::****       *:::****       *:::****       *:::****       *:::****       *:::*****       *:::*****       *:::*****       *:::*****       *:::*****       *:::*****       *:::******       *:::*****       *:::******       *:::******       *:::******       *:::******       *:::******       *:::******       *:::*******       *:::******       *:::********       *:::*********************************	275 272 325 336 338
AtTAA1 (AT1G70560.1) AtTAR1 (AT1G23320.1) AtTAR2 (AT6224670.1) AtTAR2 (AT1G34040.1) AtTAR3 (AT1G34060.1) PpTARA (P33621_1537073.1)	* :* :*****       * :: :*****       * :: :****       * :: :****       * :: :****       * :: :****       * :: :****       * :: :****       * :: :****       * :: :*****       * :: :*****       * :: :*****       * :: :*****       * :: :*****       * :: :*****       * :: :*****       * :: :*****       * :: :******       * :: :******       * :: :******       * :: :********************************	275 272 325 336 338 396
AtTAA1 (AT1G70560.1) AtTAR1 (AT1G23320.1) AtTAR2 (AT4G24670.1) AtTAR4 (AT1G34040.1) AtTAR4 (AT1G34040.1) PpTAR8 (Pp3c1_1537073.1) PpTAR8 (Pp3c1_1537073.1)	VIHDFAYYWPHYTPITGADHAINLTFLSKSTGHADFIG GALLXDEXAKKMYKYLLINSIGVSKESGYRAATILKAYLGYLGYGG VINDLAYYWPHYTPITGADHAINLTFLSKSTGHADFIG GALXXDEFAKKMYKLLINSIGVSKESGYRAATILKETCK	275 272 325 336 338 396 404
AtTAA1 (AT1G70560.1) AtTAR1 (AT1G23320.1) AtTAR2 (AT4G24670.1) AtTAR2 (AT1G34040.1) AtTAR4 (AT1G34060.1) PpTAR8 (Pp3c21_1537073.1) PpTAR8 (Pp3c15_1534073.1) PpTAR8 (Pp3c17_650073.1)	* :* :**** * : *** * : ** : ** : ** :	275 272 325 336 338 396 404 416
AtTAA1 (AT1G70560.1) AtTAA2 (AT4G24670.1) AtTAA2 (AT4G24670.1) AtTAA2 (AT1G34040.1) AtTAA4 (AT1G34060.1) PpTABA (Pp3c1_1537073.1) PpTAB2 (Pp3c1_1534073.1) PpTAB2 (Pp3c1_650073.1) PpTAB2 (Pp3c2_1252073.1)	* :* :**** * : **** * : **** * : *****       * : **********************************	275 272 325 336 338 396 404 416 325
AtTAA1 (AT1G70560.1) AtTAA2 (AT1G23220.1) AtTAA2 (AT4G24670.1) AtTAA2 (AT4G24670.1) AtTAA2 (AT1G34060.1) PpTARA (Pp3c11_1537073.1) PpTARE (Pp3c11_5530073.1) PpTARE (Pp3c17_650073.1) PpTARE (Pp3c25_650073.1)	VIHD FAYYWPHYTPI TIRRQDHD IMLFTF SKITGHAGSRIG GALVKDKEVAKKMVEY I I VNSIGVSKESQVRTAKI LINVLKETCK	275 272 325 336 338 396 404 416 325 220
AtTAA1 (AT1070560.1) AtTAR1 (AT1023320.1) AtTAR2 (AT4024670.1) AtTAR2 (AT1034060.1) PpTAR8 (Pp3c21_15370V3.1) PpTAR8 (Pp3c21_15370V3.1) PpTAR8 (Pp3c25_12520V3.1) PpTAR8 (Pp3c25_12520V3.1) PpTAR8 (Pp3c5_24670V3.1)	* :*****       * :: :****       * :: :****       * :: :****       * :: :****         VIHDFAYYWPHYTPITRRQDHD INLFTFSKITGHAGSRIG KALVKDKEVAKKNVEYIIVNSIGVSKESQVRTAKILNVLKETCK-       TO-         VIHDFAYYWPHYTPITRRQDHD INLFTFSKITGHAGSRIG KALVKDKEVAKKNVEYIIVNSIGVSKESQVRTAKILNVLKETCK-       TO-         LINDLAYYWPHYTPITRRQDHD INLFTFSKITGHAGSRIG KALVKDKEVAKKNVEYIIVNSIGVSKESQVRTAKILNVLKETCK-       TO-         LINDLAYYWPHYTPITRRQDHD INLFTFSKITGHAGSRIG KALVKDKEVAKKNVEYIIVNSIGVSKESQURTAKILNVEKVSDSCG-       TO-         VINDLAYYWPYTSPITRADDEDLSLFSLSKTTGHAGSRIG KALVKEKTVEKORITISLSSMOSRDTQLIAULLKVVSDSCG-       TO-         VINDLAYYWPYTSPITRADDEDLSLFSLSKTTGHAGSRIG KALVKEKTVEKORITISLSSMOSRDTQLIKAVIEGVTSSEP-       OSG	275 272 325 336 338 396 404 416 325 220 375
AtTAA1 (AT1G70560.1) AtTAA1 (AT1G23320.1) AtTAA2 (AT4G24670.1) AtTAA2 (AT1G34040.1) AtTAA2 (AT1G34040.1) PpTAR8 (Pp3c1_1537073.1) PpTAR8 (Pp3c1_1537073.1) PpTAR8 (Pp3c2_1252073.1) PpTARE (Pp3c2_61252073.1) PpTARE (Pp3c2_647073.1) PpTARF (Pp3c5_2467073.1)	VIHOLAYYMPHYTPIITARQDHDIMLFTFSKITGHAOSIG (ALVXDKEVAKKMYEYIIVMSIGVSKESQURTAKILMVLKETCK	275 272 325 336 338 396 404 416 325 220 375
AtTAA1 (AT1G70560.1) AtTAR1 (AT1G23320.1) AtTAR2 (AT4G24670.1) AtTAR2 (AT4G24670.1) AtTAR4 (AT1G34060.1) PpTARA (Pp3c11_537073.1) PpTAR2 (Pp3c11_537073.1) PpTAR2 (Pp3c11_550073.1) PpTAR2 (Pp3c1_650073.1) PpTAR2 (Pp3c5_2467073.1)	VIND FAY YWPHYTPITREQDND INLEFTS KIT GRAADSRIG GALVKDKEVAKKRYEY I I UNSIGVSKESQYRTAKI LINVLKETCK SESE VIND LAYYWPYTPITREQDND INLEFTS KIT GRAADSRIG GALVKD IEVAKKRYEY I I UNSIGVSKESQYRTAKI LINVLKETCK SESE VIND LAYYWPYTPITREADND INLEFTS KIT GRAADSRIG GALVKD IEVAKKRYEY I I UNSIGVSKESQYRTAKI LINULKETCK SESE VIND LAYYWPYTPITREADND INLEFTS KIT GRAADSRIG GALVKD IEVAKKRYEY I UNSIGVSKESQYRTAKI LINULKETCK SESE VIND LAYYWPYTPITREADND INLEFTS KIT GRAADSRIG GALVKD KETVERKEI YI SLUSSKOSS KESQYRTAKI LINULKETCK SESE VIND LAYYWPYTPITREADND INLEFTS KIT GRAADSRIG GALVKD KETVERKEI YI SLUSSKOSS KESQYRTATU I UNSIGVSKESQYRTATU I UNSIGVSKESQYR	275 272 325 336 338 396 404 416 325 220 375
AtTAA1 (ATIG70560.1) AtTAA1 (ATIG70560.1) AtTAA2 (ATG24670.1) AtTAA2 (ATG24670.1) AtTAA2 (ATG34040.1) PpTAA8 (Pp3c1_1537073.1) PpTAA8 (Pp3c1_1534073.1) PpTAA8 (Pp3c1_650073.1) PpTAA8 (Pp3c2_6507073.1) PpTAAR (Pp3c5_2467073.1)	************************************	275 272 325 336 338 396 404 416 325 220 375
AtTAA1 (AT1G70560.1) AtTAR1 (AT1G23320.1) AtTAR2 (AT4G24670.1) AtTAR3 (AT1G34040.1) AtTAR4 (AT1G34040.1) PpTAR8 (Pp3c11_1537073.1) PpTAR6 (Pp3c11_1650073.1) PpTAR6 (Pp3c25_651073.1) PpTAR6 (Pp3c25_667073.1) PpTAR7 (Pp3c5_2467073.1) AtTAA1 (AT1G70560.1)	VIND LAYYMPHYTPITASDMD IMLIFILSKITCHADSSIC ALIXDEVAKMYEYILWSICOSHSQUAROLLERITSYN VIND LAYYMPHYTPITASDMD IMLIFISKITCHADSSIC ALIXDEVAKMYEYILWSICOSHSQUAROLLERITSYN SENFFKYGRENKURWEKLREVYKESDAFT LPKYPEAFCNYFGKSLESYF	275 272 325 336 338 396 404 416 325 220 375 387
AtTAR1 (AT1070560.1) AtTAR1 (AT1023320.1) AtTAR2 (AT4024670.1) AtTAR2 (AT1034040.1) AtTAR4 (AT1034060.1) PpTAR8 (Pp3c1_1537073.1) PpTAR0 (Pp3c1_1537073.1) PpTAR0 (Pp3c1_252073.1) PpTAR0 (Pp3c2_6507073.1) PpTARC (Pp3c5_2667073.1) PpTARC (Pp3c5_2467073.1) AtTAR1 (AT1070560.1) AtTAR1 (AT1070560.1)	Image:	275 272 325 336 396 404 416 325 220 375 387 384
AtTAA1 (AT1G70560.1) AtTAR1 (AT1G23320.1) AtTAR2 (AT4G24670.1) AtTAR2 (AT4G24670.1) AtTAR3 (AT1G34040.1) AtTAR4 (AT1G34060.1) PpTARE (Pp3c1_15370V3.1) PpTARE (Pp3c1_15500V3.1) PpTARE (Pp3c2_15250V3.1) PpTARE (Pp3c2_15250V3.1) PpTARE (Pp3c5_24670V3.1) PTARE (Pp3c5_24670V3.1) AtTAA1 (AT1G70560.1) AtTAR1 (AT1G70550.1)	VIHD LAYYMPHYTPI TIRAQDHD IMLFTFSKIT GHAOSSIC GALVXD KEVAKKAYEY I I IVNS I GVSKESGYRTAKI LINVLKETCK	275 272 325 336 338 396 404 416 325 220 375 387 384 439
AttAA1 (AT1G70560.1) AttAR2 (AT4G24670.1) AttAR2 (AT4G24670.1) AttAR2 (AT4G24670.1) AttAR4 (AT1G34060.1) PpTAR8 (Pp3c11_1537073.1) PpTARC (Pp3c11_550073.1) PpTARC (Pp3c12_650073.1) PpTARC (Pp3c2_625607073.1) PpTARF (Pp3c5_2467073.1) PATAR1 (AT1G70560.1) AttAA1 (AT1G70560.1) AttAR2 (AT4G24670.1) AttAR2 (AT4G24670.1)	VIND FAYYWPHYP JT FRAQDND INLFTF SKIT GHAOSSIG GALVKDKEVAKKAVEY JI UNSIGVSKESQVRTAKI LINVLKETCK	275 272 325 336 338 396 404 416 325 220 375 387 384 439 450
AtTAA1 (ATIG70560.1) AtTAR1 (ATIG70560.1) AtTAR2 (ATG24670.1) AtTAR2 (ATG24670.1) AtTAR2 (ATG34040.1) PpTAR4 (ATIG34060.1) PpTAR2 (Pp3c1_1537073.1) PpTAR2 (Pp3c1_154073.1) PpTAR2 (Pp3c2_1522073.1) PpTAR2 (Pp3c2_67073.1) PpTAR2 (Pp3c2_67073.1) PTAR2 (Pp3c2_67073.1) AtTAA1 (ATIG70560.1) AtTAA2 (ATIG70560.1) AtTAR2 (ATIG24670.1) AtTAR4 (ATIG34060.1)	VIND LAYYMPHY PITARQDHD INLFTFSKIT GHAOSSIG GALVKDKEVAKKAVEY I I IVNS I GVSKESGVRTAK I LNVLKETCK	275 272 325 336 338 396 404 416 325 220 375 387 384 439 450 452
AtTAA1 (AT1G70560.1) AtTAR1 (AT1G23320.1) AtTAR2 (AT4G24670.1) AtTAR2 (AT4G24670.1) AtTAR4 (AT1G34040.1) PpTAR8 (Pp3c1_1537073.1) PpTAR2 (Pp3c1_1537073.1) PpTAR2 (Pp3c2_252073.1) PpTAR2 (Pp3c2_2652073.1) PpTAR2 (Pp3c5_2667073.1) PpTAR2 (Pp3c5_2467073.1) AtTAR1 (AT1G70560.1) AtTAR2 (AT1G34060.1) AtTAR2 (AT1G34060.1) AtTAR2 (AT1G34060.1) PpTAR8 (Pp3c21_1537073.1)	VIND FAYYWPHYTPI TIRAQDHD INLFFT SKIT GHADSRIG GAUKKUKEVAKKMEY I I UNS I GYSKESQURTAKI LINULKETCK	275 272 325 336 338 404 416 325 220 375 387 384 439 450 452 508
AtTAA1 (AT1G70560.1) AtTAA2 (AT4G24670.1) AtTAA2 (AT4G24670.1) AtTAA2 (AT4G24670.1) AtTAA2 (AT4G24670.1) PpTAR2 (Pp3c11_5137073.1) PpTAR2 (Pp3c11_5137073.1) PpTAR2 (Pp3c11_550073.1) PpTAR2 (Pp3c1_650073.1) PpTAR2 (Pp3c5_667073.1) PpTAR2 (Pp3c5_647073.1) AtTAA1 (AT1G70560.1) AtTAA2 (AT4G24670.1) AtTAA2 (AT4G34060.1) PtTAR8 (Pp3c1_5137073.1) PpTAR8 (Pp3c1_5137073.1)	THE ATTERNATION AND AND AND AND AND AND AND AND AND AN	275 272 325 336 336 404 416 325 220 375 387 384 439 450 508 516
AtTAA1 (AT1G70560.1) AtTAA1 (AT1G23320.1) AtTAA2 (AT4G24670.1) AtTAR2 (AT4G24670.1) AtTAR2 (AT1G34040.1) AtTAR4 (AT1G34060.1) PpTARE (Pp3c1_1537073.1) PpTARE (Pp3c2_122073.1) PpTARE (Pp3c2_62122073.1) PpTARE (Pp3c2_627073.1) PTARE (Pp3c2_67073.1) PATAR1 (AT1G70560.1) AtTAA1 (AT1G70560.1) AtTAR2 (AT4G24670.1) AtTAR2 (AT4G24670.1) AtTAR2 (AT4G24670.1) AtTAR2 (AT4G24670.1) PpTARE (Pp3c1_1537073.1) PpTARE (Pp3c1_550773.1) PpTARE (Pp3c1_550773.1) PpTARE (Pp3c1_550773.1)	VIND LAYYMPHYTPITSRQDHD INLFFTSKITGHAOSIG (ALVXDKEVAKKNYEYI IVNSIGVSKESQTRAATI INNLKETCK	275 272 325 336 404 416 525 220 375 387 387 387 450 450 450 516 525
AtTAA1 (AT1670560.1) AtTAR1 (AT1670560.1) AtTAR2 (AT4624670.1) AtTAR2 (AT4624670.1) AtTAR3 (AT1634040.1) AtTAR3 (AT1634060.1) PpTAR2 (Pp3c15_1537073.1) PpTAR2 (Pp3c15_1537073.1) PpTAR2 (Pp3c25_657073.1) PpTAR2 (Pp3c5_67073.1) PpTAR2 (Pp3c5_2467073.1) PpTAR2 (Pp3c5_2467073.1) AtTAR1 (AT1670560.1) AtTAR2 (AT1634060.1) AtTAR2 (AT1634060.1) PpTAR8 (Pp3c1_1537073.1) PpTAR2 (Pp3c1_1537073.1) PpTAR2 (Pp3c1_1537073.1) PpTAR2 (Pp3c1_1537073.1) PpTAR2 (Pp3c1_1527073.1) PpTAR2 (Pp3c1_1527073.1) PpTAR2 (Pp3c2_1252073.1)	VIND FAYYWPHYTPITREQDND INLEFTESKIT GRAADSRIG GAUKUNKEVAKKAVEY I IVNS IGVSKESGVRTAK I LINULKETCK	275 272 325 336 338 396 404 416 325 220 375 387 384 439 450 452 508 516 525 442
AtTAA1 (ATIG70560.1) AtTAR1 (ATIG70560.1) AtTAR2 (ATG24670.1) AtTAR2 (ATG24670.1) AtTAR2 (ATG34040.1) PpTAR4 (ATIG34060.1) PpTAR2 (Pp3c1_1537073.1) PpTAR2 (Pp3c1_1537073.1) PpTAR2 (Pp3c2_1522073.1) PpTARE (Pp3c2_670703.1) PpTARE (Pp3c2_670703.1) AtTAA1 (ATIG70560.1) AtTAA1 (ATIG70560.1) AtTAR2 (ATG24670.1) AtTAR2 (ATG24670.1) AtTAR2 (ATG34060.1) PpTARE (Pp3c1_1537073.1) PpTARE (Pp3c2_670703.1) PpTARE (Pp3c2_670703.1) PpTARE (Pp3c2_670703.1) PpTARE (Pp3c2_670703.1) PpTARE (Pp3c2_670703.1)	VIND LAYYMPHY TPI TARADDH DINLFTFSKI TOHAOSIG (ALVXD KEVAKKAYEY I I TVNS I OYSKESQURATAKI LINULKETCK	275 272 325 336 338 396 404 416 325 220 375 387 384 439 450 508 516 525 5442 331
AtTAA1 (AT1G70560.1) AtTAR1 (AT1G23320.1) AtTAR2 (AT4G24670.1) AtTAR2 (AT4G24670.1) AtTAR4 (AT1G34040.1) PpTAR8 (Pp3c1_1537073.1) PpTAR2 (Pp3c1_550073.1) PpTARE (Pp3c2_52607073.1) PpTARE (Pp3c5_667073.1) PpTARE (Pp3c5_2467073.1) AtTAR1 (AT1G70560.1) AtTAR2 (AT4G24670.1) AtTAR2 (AT4G24670.1) AtTAR2 (AT4G24670.1) AtTAR2 (AT4G24670.1) AtTAR2 (AT4G24670.1) PpTARE (Pp3c1_5514073.1) PpTARE (Pp3c1_5514073.1) PpTARE (Pp3c2_6267073.1) PpTARE (Pp3c2_6267073.1) PpTARE (Pp3c2_647073.1)	VIND FAYYWPHY TPI TRRQDHD INLFTF SKIT ORIAOSSI O ALVXD KEVAKANYEY I I UNS I OYSKESQI TAXT I LNVLKETCK	275 272 325 336 338 396 404 416 325 220 375 387 384 452 439 450 452 508 516 525 508 516 525 331 489
AtTAA1 (AT1G70560.1) AtTAR1 (AT1G70560.1) AtTAR2 (AT4G24670.1) AtTAR2 (AT4G24670.1) AtTAR3 (AT1G34040.1) AtTAR3 (AT1G34060.1) PpTAR2 (Pp3c15_1537073.1) PpTAR2 (Pp3c1_650073.1) PpTAR2 (Pp3c25_667073.1) PpTAR2 (Pp3c5_647073.1) PTAR2 (Pp3c5_2467073.1) AtTAA1 (AT1G70560.1) AtTAR2 (AT1G34040.1) AtTAR2 (AT1G34040.1) AtTAR2 (AT1G34040.1) AtTAR2 (AT1G34040.1) PpTARE (Pp3c5_1537073.1) PpTARE (Pp3c5_267073.1) PpTARE (Pp3c5_267073.1) PpTARE (Pp3c5_2467073.1)	Sense is a set of the set of	275 272 325 336 336 338 396 404 416 325 220 375 387 387 384 419 450 452 508 508 525 516 525 5442 331 489
AtTAA1 (AT1G70560.1) AtTAR1 (AT1G23320.1) AtTAR2 (AT4G24670.1) AtTAR2 (AT4G24670.1) AtTAR3 (AT1G34040.1) AtTAR3 (AT1G34040.1) PpTARE (Pp3c1_1537073.1) PpTARE (Pp3c2_1525073.1) PpTARE (Pp3c2_6125073.1) PpTARE (Pp3c2_6125073.1) PTARE (Pp3c5_2467073.1) AtTAA1 (AT1G70560.1) AtTAR2 (AT4G24670.1) AtTAR2 (AT4G24670.1) AtTAR2 (AT4G24670.1) AtTAR2 (AT4G24670.1) AtTAR2 (AT4G24670.1) AtTAR2 (AT4G24670.1) PpTARE (Pp3c1_1537073.1) PpTARE (Pp3c1_1537073.1) PpTARE (Pp3c2_61252073.1) PpTARE (Pp3c2_62073.1) PpTARE (Pp3c2_62073.1) PpTARE (Pp3c5_2467073.1)	A STATE AND	275 272 325 336 336 404 416 325 220 375 387 439 450 508 516 452 508 516 452 508 516 452 531 489
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 PpTARF (Pp3c5\_24670V3.1)
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335 489 **Fig. S8. The number of introns in** *YUC* gene coding regions differ in both Arabidopsis and *P. patens* but the positions of introns that do exist are conserved. The alignment was produced from amino acid sequences deduced from primary models of all Arabidopsis (black) and *P. patens* (green) *YUC* genes with Clustal Omega using the default settings. Positions of introns spliced out to generate the coding sequences from which amino acid sequences were deduced are marked in red.



Fig. S9. The diameter of *Pptara* protonemal colonies is reduced. 21 day old colonies of three independent *Pptara* KO mutants and WT. Colony diameter is stated below each colony. Asterisks indicate statistically significant differences compared to WT, \*\* = p < 0.01 using Students t-test.



**Fig. S10. Relative expression of** *PpTAR* **genes in chloronema.** (A) Relative *PpTARA-D* transcript abundance in SPIA-amplified cDNA from chloronema-enriched protonema from the Reute ecotype. (B) Relative *PpTARA-D* transcript abundance in chloronema from the Gransden ecotype (eFP data from Ortiz-Ramirez et al., 2015). Error bars in (A) represent standard deviation of the mean of 3 biological replicates.



**Fig. S11.** *Pptaratarc* **shoots are dwarfed but otherwise develop normally**. Image shows representative adult shoots from WT, *Pptara-1*, *Pptarc-4*, *Pptaratarc-1*, *Pptaratarc-2* and WT grown for 30 days in standard growth conditions.



Fig. S12. Quantitative PpR2D2 output as a measure of auxin sensing during stage 2 antheridia development. Bar graphs showing average mDII-nVENUS:DII-nTdTOMATO signal ratios during stage 2 antheridia development as a measure of auxin sensing in (A) WT background (PpR2D2-3), (B) *Pptara* background (*PpR2D2-3 Pptara-1*) and (C) *Pptaratarc* background (*PpR2D2-3 Pptaratarc-1*). Errors bars indicate standard error of the mean. Asterisks indicate statistically significant difference between WT and mutant backgrounds (black) or between the two mutant backgrounds (red) in Student's t-tests (P < 0.05).



**Fig. S13. Complementation of** *Pptara* **reproductive organ phenotype by** *PpTARA* **OE.** The images show DIC micrographs of reproductive organs at comparable stages from the *Pptara-1* mutant and the *Pptara-1* mutant retransformed with the *ACT1pro::PpTARA* overexpressor construct. (A) *PpTARA* OE blocks the outgrowth of ectopic antheridia from the base of *Pptara* organs. Compare to Fig. 3e. (B) *PpTARA* OE blocks the formation of ectopic tip cells in *Pptara* antheridia. Compare to Fig. 4e. (C) *PpTARA* OE restores the formation of ectopic extra cells in the tip of *Pptara* archegonia. Compare to Fig. 6d.



Fig. S14. Quantitative PpR2D2 output as a measure of auxin sensing during stage 3 to 9 antheridia development. Bar graphs comparing average mDII-nVENUS:DII-nTdTOMATO signal ratios in WT background (PpR2D2-3), *Pptara* background (*PpR2D2-3 Pptara-1*) and *Pptaratarc* (*PpR2D2-3 Pptaratarc-1*) background during stage 3 to 9 antheridia development as a measure of auxin sensing. (A) Cells in organ tip (all cells above inner cells considered). (B) Jacket cells (8 representative cells from layer surrounding inner cell cavity considered for each organ). (C) Inner cells (6 representative cells along apical-basal axis considered from each organ). Errors bars indicate standard error of the mean. Asterisks indicate statistically significant difference between WT and mutant backgrounds (black) or between the two mutant backgrounds (red) in Student's t-tests (p < 0.05).



**Fig. S15. A sub-set of inner cells do not proliferate in the** *Pptaratarc* **double mutant.** The table summarizes the number of divisions that the six inner cells found in a stage 4 antheridium (see schematic organ drawing) have carried out when entering stage 6 in WT (right) and the *Pptaratarc-2* mutant (left). Each row represents an independent organ analyzed and each column represents a stage 4 inner cell of that organ (green numbers in column heading corresponds to green numbers in organ drawing and hence mark cell positions). Numbers shaded in pink report the number of divisions carried out by each stage 4 cell at the entrance of stage 6 development.



Fig. S16. Quantitative PpR2D2 output as a measure of auxin sensing during stage 1 and 2 archegonia development. Bar graphs showing average mDII-nVENUS:DII-nTdTOMATO signal ratios during stage 2 antheridia development as a measure of auxin sensing in (A) WT background (PpR2D2-2) and (B) *Pptara* background (*PpR2D2-2 Pptara-1*). Errors bars indicate standard error of the mean. Asterisks indicate statistically significant difference between WT and the mutant background in Student's t-tests (\*, p < 0.05; \*\*, p < 0.02).



Fig. S17. Quantitative PpR2D2 output as a measure of auxin sensing during stage 3 to 9 archegonia development. Bar graphs comparing average mDII-nVENUS:DII-nTdTOMATO signal ratios in WT background (PpR2D2-2) and *Pptara* background (*PpR2D2-2 Pptara-1*) background during stage 3 to 9 archegonia development as a measure of auxin sensing. (A) Cells in organ tip (8 apical-most cells of each organ considered). (B) Inner cells (see schematic drawing in Fig. 6a). (C) Neck cells (6 cells in basal part of neck considered for each organ). Errors bars indicate standard error of the mean. Asterisks indicate statistically significant difference between WT and the *Pptara* mutant backgrounds in Student's t-tests (p < 0.05).



Fig. S18. Archegonia neck lengths are reduced in *Pptar* mutants due to a cell elongation defect. (A) Bar graph showing average neck lengths in archegonia in different developmental stages from *Pptara-1*, *Pptaratarb-1*, *Pptaratarc-2* and WT. (B) Bar graph showing average number of cells in the outermost row of cells in the neck of archegonia in different developmental stages from *Pptara-1*, *Pptaratarb-1*, *Pptaratarb-1*, *Pptaratarc-2* and WT. (B) Bar graph showing average number of cells in the outermost row of cells in the neck of archegonia in different developmental stages from *Pptara-1*, *Pptaratarb-1*, *Pptaratarc-2* and WT. Error bars mark standard deviation and asterisks mark a statistically significant difference to WT in Student's t-tests (\* = p < 0.05; \*\* = p < 0.01).



Fig. S19. *PpYUC* expression patterns and knockout phenotype resemble those of *PpTAR* in reproductive organs. (A) Representative micrographs of the Ppyucb mutant showing a phenotype resembling that of *Pptar* mutants. The leftmost image shows a mature reproductive apex where antheridia and archegonia have been false colored in yellow and red, respectively. Compare to WT in Fig. 3c and note the hyperformation of antheridia and the stunted archegonia with fleshy tips. The middle image shows a close-up of a late stage antheridium with borders of tip cells marked for clarity. Compare to WT in Fig. 4e and note ectopic tip cells. The rightmost image shows a close-up of a stage 8 archegonium with inner cells and their borders shaded in yellow for clarity. Compare to stage 8 WT in Fig. 6d and note the stunted appearance of the organ, the extra outer cells in the organ tip and the wide and irregularly shaped apical cavity. (B) Representative examples of *PpYUCF::GFPGUS* reporter output in antheridia of various stages. For each stage, a merge of confocal channels detecting GFP (green) and chloroplast autofluorescence (red) is shown to the left and DIC image to the right. Compare to *PpTAR::GFPGUS* reporter output in Fig. 2f VII and Fig. 4b and note the largely overlapping expression pattern. (C) Representative examples of PpYUCF::GFPGUS reporter output in midstage archegonia. For each stage, a merge of confocal channels detecting GFP (green) and chloroplast autofluorescence (red) is shown to the left and DIC image to the right. Compare to PpTARA:: GFPGUS reporter output in Fig. 6b and note the largely overlapping expression pattern.





Fig. S20. Auxin sensing in the apical stem cell of young vegetative leaves is successively increased in a *PpTAR*-dependent manner. Bar graphs showing PpR2D2 output (average mDII-nVENUS:DII-nTdTOMATO signal ratios) as a measure of auxin sensing in cells along a single proximo-distal cell file of early vegetative leaves with different numbers of cells along the proximo-distal axis. (A) WT background (PpR2D2-3). (B) *Pptara* background (*PpR2D2-3 Pptara-1*). (C) *Pptaratarc* background (*PpR2D2-3 Pptaratarc-1*). The leftmost bar (darkest blue) in each cluster represents the apical cell. Errors bars indicate standard error of the mean. Asterisks indicate statistically significant difference between WT and the *Pptaratarc* mutant backgrounds in Student's t-tests (p < 0.05). The fact that both *PpTARA* and *PpTARC* must be deleted for reduced auxin sensing is in line with the observation that both genes are expressed in young leaves (Fig. 2d,f; Fig. 5b).



**Fig. S21**. *PpPIND* is expressed in spermatogenous cells of antheridia. Representative epifluorescence micrographs of signal output from the *PpPINDpro::GFP-1* transcriptional reporter (Viaene et al., 2014). (A) Antheridia bundle with organs in different developmental stages. (B) Mid-stage antheridium at high magnification. In both (A) and (B), a merge of channels detecting GFP (green) and chloroplast autofluorescence (magenta) as well as a DIC image are shown.



**Fig. S22**. Long *PpPINs* are expressed in the pre-egg / egg from around stage 5 of archegonia development. Representative micrographs of signal output from long *PpPIN* reporters in the body of archegonia at selected developmental stages. S3/5/6/7/8/9 indicate developmental stages (Fig. 6a; Landberg et al., 2013). (A) *PpPINB::GFPGUS-1* reporter output from stage 4 to stage 9. (B) *PpPINC::GFPGUS-1* reporter output from stage 6 to stage 9. (C) *PpPINA::PpPINA-GFP-2* reporter output from stage 6 to stage 8. In (A) and (B), a merge of confocal channels detecting GFP (green) and chloroplast autofluorescence (magenta) is shown on top and a DIC image is shown below for each stage. In (C), to better visualize the weak and dotty GFP signal produced by the translational reporter, the confocal channel detecting GFP (green) is shown on top and a DIC image is omitted. Instead, a long exposure of the confocal channel detecting GFP (green) is shown on top and a DIC image is shown below.



Name	Description
pDONR4r-3r-G418	G418R entry clone
pDONR4r-3r-Zeo	ZeoR entry clone
pEP54	PpTARB KO construct (G418R)
рМТ207	<i>PpTARD</i> KO construct (HygR)
pMT210	PpTARA KO construct (HygR)
рМТ222	HygR entry clone
рМТ229	PpTARC KO construct (G418R)
рМТ232	<i>PpYUCC</i> KO construct (G418R)
рМТ233	<i>PpYUCE</i> KO construct (G418R)
рМТ235	<i>PpYUCF</i> KO construct (HygR)
рМТ236	<i>PpYUCD</i> KO construct (ZeoR)
рМТ237	<i>PpTARD</i> trx reporter (HygR)
pMT241	<i>PpTARB</i> trx reporter (HygR)
рМТ243	<i>PpTARA</i> trx reporter (HygR)
pMT246	<i>PpYUCF</i> trx reporter (HygR)
рМТ254	<i>PpTARC</i> trx reporter (HygR)
pMT258	OE vector (pACT1, G418R)
pMT261	<i>PpTARF</i> OE construct (G418R)
pMT262	<i>PpYUCC</i> OE construct (G418R)
рМТ263	<i>PpYUCA</i> KO construct (ZeoR)
рМТ266	<i>PpYUCA</i> OE construct (G418R)
рМТ272	OE vector (pACT1, ZeoR)
рМТ276	<i>PpYUCB</i> KO construct (ZeoR)
pMT281	PpTARA OE construct (ZeoR)

Table S1. Constructs produced and used in the study

Table S2	<b>Primers</b>	used	in	this	study
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PCR p	rimers used to build constructs
Name	Sequence
SS220	CGCGGATCCATCAGGAGTTG
SS221	GAGCCATGGCGGAGTCGATAAGGCGACTCAG
SS222	TTGTCATGAGCTGCATCGAAGCCGCAC
SS223	GACTCATGATGGCATCGACGAAGTGAGAAAATG
SS224	AAGGGATCCGAGAGGGTGGTGGTGGTGG
SS225	TGTCCATGGTTGCAGACAGACAGTAGCTTGTGCG
SS226	TATAAGCTTGAGGGATCTTGGTTTGAATCTTGGT
SS227	CTGCCATGGTGATCAGTACCCGGGATGGTCC
SS244	CATGGATCCTCTTAATGTACAGCTGCTTTCATCTCC
SS245	TGACCATGGTGATCGATTGAGGTGTTCACCGA
SS265	GGGG ACA ACT TTT CTA TAC AAA GTT G ATGGCGCAGGGGATCAAGATCA
SS266	GGGG AC AAC TTT ATT ATA CAA AGT TGT CCCCCGAGGGGATCGA
SS269	GGGGACAAGTTTGTACAAAAAAGCAGGCTCTCGAGGTCGCCCCGCGTGGAGAGGT
SS270	GGGGACAACTTTGTATAGAAAAGTTGGGTGAATTTTATTCAAGAGGGCGTTCCTGA
SS271	GGGGACAACTTTGTATAATAAAGTTGCATCCAATGTACACAGATTTCAGTTCC
SS272	GGGGACCACTTTGTACAAGAAAGCTGGGTACTCGAGTAATTTTGAGGTTTTGGAGTAACACCA
SS281	GGGGACAAGTTTGTACAAAAAAGCAGGCTCTCGAGCATGAAGGGGATTTGAAAGCATAA
SS282	GGGGACAACTTTGTATAGAAAAGTTGGGTGGAATCGCTGGTCGCTGTGATGAAA
SS283	GGGGACAACTTTGTATAATAAAGTTGTGCCAGCCTTTAAAATCCCTCAAC
SS284	GGGGACCACTTTGTACAAGAAAGCTGGGTACTCGAGCTGGCAAGCGCGGTAACG
SS285	GGGGACAACTTTGTATAGAAAAGTTGGGTGCTGGCGAGTGGGAGAATGCAAAGTAG
SS286	GGGGACAAGTTTGTACAAAAAAGCAGGCTCTCGAGTCTAGACGCAATGAATG
SS287	GGGGACAACTTTGTATAATAAAGTTGCTGAATCCCCAGTCCGTCACTA
SS288	GGGGACCACTTTGTACAAGAAAGCTGGGTACTCGAGTTCGATGTTCCAATGTTGTTGTTTAC
SS290	GGGGACAAGTTTGTACAAAAAGCAGGCTGTCGACTTAGCCCTCACCGTTGTCAAGTCCTC
SS292	GGGGACAACTTTGTATAGAAAAGTTGGGTGAAGAGTAGTTCTAACCACCGAGATGG
SS293	GGGGACAACTTTGTATAATAAAGTTGCGCCCTCTGTGCAGCACCATTCC
SS294	GGGGACCACTTTGTACAAGAAAGCTGGGTAGTCGACCGAGCCATCGCTGTGTACCAAGACTG
SS295	GGGGACAACTTTGTATAGAAAAGTTGGGTGATCGCTGCAATGGGTCGTCTGAACC
SS296	GGGGACAAGTTTGTACAAAAAAGCAGGCTGTCGACCTCATTCAGGCCCGTGGTTTGGTG
SS298	GGGGACAACTTTGTATAATAAAGTTGTCGGCATTTGCGGAAGGAGTTTGAG
SS300	GGGGACCACTTTGTACAAGAAAGCTGGGTAGTCGACGGGCGGACGGTAGTGATGGTGGTT
SS325	GGGGACAAGTTTGTACAAAAAAGCAGGCTGTCGACGATGCCGAACCAGCCACAAG
SS326	GGGGACAACTTTGTATAGAAAAGTTGGGTGTGGTCAATTGTGCACCTACAAGC

SS368	GGGGACAACTTTGTATAATAAAGTTGGTATGCGGTCGGTTTCGGTAGGAA
SS369	GGGGACCACTTTGTACAAGAAAGCTGGGTAGTCGACTTGGCGTTTTTGGATAGAGCAGTGATT
SS370	CAACCTAGGATGTACCCCAGAAAGGATTCTTGG
SS371	TTTGTCGACTCAATAGGTCTTTTCATTATCTCTGTGG
SS372	ACTCCTAGGATGCCGCCCTACCTTGCTTC
SS373	CAGCCTAGGCTATCTAGACTGGAGCGGGGGAGATG
SS378	TCGCCTAGGATGGAGGCCGATGACACGTC
SS379	GAGGTCGACTCAAGATTGAGCGACGAGTTTGAG
SS424	GGGGACAAGTTTGTACAAAAAAGCAGGCTGTCGACAATGGCCCCCACAAAAGCAGTTA
SS425	GGGGACAACTTTGTATAGAAAAGTTGGGTGTGAGCAGAGGTTCTACCCCAGCATA
SS426	GGGGACAACTTTGTATAATAAAGTTGCCCGAGGGAGAACCCATCGTT
SS469	ATCCCTAGGATGGCTCTTGAAGCCGAGCG
SS470	CATCCTAGGCTAGTCGGGGGTTCTGGAAGCC
SS476	GGGGACCACTTTGTACAAGAAAGCTGGGTAGTCGACGTGAGAGGCTCTCTCT
SS596	AAGAAGCTTCGAGGTCATTCATATGCTTGAGAAG
SS598	CTAACTAGTGTCGACCCTAGGTCTACCTACAAAAAAGCTCCGCAC
SS599	ATCCTCGAGCTGTGAGACACAATGTTGTTCA
SS600	ATCTCAAGCTTCTTGATCAGTACCCGGGATGGT
SS601	ACAACTAGTGAAGATTAGCACGACTG
SS602	AAAGAGCTCAACAACAATAAGATATTA
SS603	CGCTATCTCGAGAAGTGGTGGACTTGATGAGTG
SS604	CGCTATAAAGCTTTCGGAGTCGATAAGGCGACT
SS605	CGCTATTCTAGACCCATGCCTCGCTTGTTGG
SS606	CGCTATTGAGCTCAATGTTGCTGCTGAGGCC
SS607	TCGCTATGGATCCTTTTGGCAGGTTGGGGACG
SS608	CGCTATCTCGAGATTGGCATCGACGAAGTGAGAAA
SS609	CGCTATACTAGTGCGTAGTTCTTCATGCCTCAAGTC
SS610	CGCTATATTAATTAAGCCAGGACGGTGATCATAGT
SS611	GGGGACAACTTTTCTATACAAAGTTGAATTCCCATGGAGTCAAAG
SS612	GGGGACAACTTTATTATACAAAGTTGTAATTCGAGCTCGGTACCCAC
SS613	GGGGACAACTTTTCTATACAAAGTTGAATTCCCTTTCAGAAAGAA
SS614	GGGGACAACTTTATTATACAAAGTTGTCCGTCACCGGTGTGAGGGAAC
Genoty	/ping primers
Name	Sequence
SS5	GAAACCTCCCAAGCTCTGACGA
SS37	CGGCTGAGTGGCTCCTTCAA
SS144	CGGCTGGCTGCGTTCCTAT
SS145	GAGGGCAATCATTTTCTGGAGTGG

SS146	TTCCGAAACGCAGCTAACACTATCAC
SS147	AACTTCGTCATCTTCTTCGCCACTCT
SS150	GTACGCCTTAACATCACCCGACTCC
SS151	GCTCATCCTGGCCCACCTATCT
SS152	GGTTTTCGCTCCATACTCTCGTCTA
SS154	GATCGTGGTCGGTAATGGAAGC
SS155	CCGAAAAAGTGCAAGTGGAAAAC
SS166	CGCGCCGCTTTGGAGATA
SS167	CAAGCGTAAGCCTGGAGAAGATGAC
SS158	TGAGCCTTCAACTTTAATCGAATAGACT
SS169	AGTGACCTAGTATGTGGCGGGGATTA
SS170	CGGCGTGCCTGGAGATGAA
SS171	GCCCGGGCACACCTTGATG
SS172	ACCCAGCCCACAACCTCACAT
SS173	GGATGACATTCTTGCACTTTTTACACA
SS174	CTACTTTCGTCGAGGGTGCCATTAT
SS175	CCAGAAGCGCGTCCGTGAA
SS176	GGCCCGCTCATCCTCTTTG
SS177	AGTTTCCCCACATGGTCGTCACA
SS178	GAGGGAGTACCGGGCGAAGTG
SS179	CAACCCGGCGATGTAGAGACC
SS180	GCGGAGGTCAGGGCTTAGG
SS181	GATCCATCAAGCACCACATTCCTA
SS182	GGGGTTTCGACAGGGTGGTTTA
SS183	ACAGGCGCGGGTCGTATGA
SS188	AGTCTTTACGGCGAGTTCTGTTAGGT
SS189	CATCTGTGGGTTAGCATTCTTTCTG
SS191	AGGCATGCCCGCTGAAATC
SS193	TCAAGATCAAAACTAGTTCCCTCACACC
SS194	ACGCGCAATAATGGTTTCTGAC
SS195	ACACCGAGCGGCGAACTAATAA
SS307	CGTCCGAGGGCAAAGAAATAGAGTA
SS308	GCTCGGCACAAAATCACCACTC
SS348	AGGCTGTGGTATGGGCTTGTCTAAC
SS354	GCGGCGCTTTATCCTTCCACTAC
SS355	GCTCGGTTCTCCTGGGGAAGTAGT
SS356	AGGCAGCGCTGAGGTTTCATTTA
SS357	TGCAGATTGTCCCTTTTCCTTCACTA

SS398	GGAGGGATCAAACGTAACAGAACAA
SS400	ACCTGCGCTTTCAAGCCTCACT
SS401	TTCACTTTGGGCCACCTTTTATTACC
SS402	CTGACCGCTTCCTCGTGCTTTAC
SS403	CGGGCAATCTTCCTCTTCTAC
SS404	ACTATGCTTGGGGATCTTGAAATGGA
SS407	ATATTGTCTCTGCCGCTCCGTTCTA
SS408	TCGCCACTTTCTCGTCTTTCAGG
SS413	GACTTGACCATGTGGAGGGACTTC
SS415	ATTTGGCAGGCGTGGAAGG
SS418	GAGGAAGGGTCTTGCGAAGGATAGTG
SS420	CTTCTTCATGCCCTCTTTCGGATAC
SS422	CACTTTAGTCGTAGGTTTCCGTCAGGTA
SS517 b	GGAAACCCAACAGGAGCACTTACTA
SS518 b	CCCCTCCTTCACTCCTGCTCTG
SS519	CCCACCGCCACCAGTTC
SS551	CGTGGCCGAGGAGCAGGAC
<b>qPCR</b>	primers
Name	Sequence
Name SS29	Sequence CGGAGAGGAAGTACAGTGTGTG
Name SS29 SS30	Sequence CGGAGAGGAAGTACAGTGTGTG ACCAGCCGTTAGAATTGAGCC
Name SS29 SS30 SS428	Sequence CGGAGAGGAAGTACAGTGTGTG ACCAGCCGTTAGAATTGAGCC AGTTTCGTGCGCAGTGGTTGG
Name SS29 SS30 SS428 SS429	Sequence CGGAGAGGAAGTACAGTGTGTG ACCAGCCGTTAGAATTGAGCC AGTTTCGTGCGCAGTGGTTGG ACTCGCTGCCCCTGGTAATGG
Name SS29 SS30 SS428 SS429 SS430	Sequence CGGAGAGGAAGTACAGTGTGTG ACCAGCCGTTAGAATTGAGCC AGTTTCGTGCGCAGTGGTTGG ACTCGCTGCCCCTGGTAATGG CCGACTCTCGTAGCTCGCAGTAA
Name SS29 SS30 SS428 SS429 SS430 SS431	Sequence CGGAGAGGAAGTACAGTGTGTG ACCAGCCGTTAGAATTGAGCC AGTTTCGTGCGCAGTGGTTGG ACTCGCTGCCCTGGTAATGG CCGACTCTCGTAGCTCGCAGTAA CGAGACCGGCAACACTTTCAAAA
Name SS29 SS30 SS428 SS429 SS430 SS431 SS434	Sequence CGGAGAGGAAGTACAGTGTGTG ACCAGCCGTTAGAATTGAGCC AGTTTCGTGCGCAGTGGTTGG ACTCGCTGCCCCTGGTAATGG CCGACTCTCGTAGCTCGCAGTAA CGAGACCGGCAACACTTTCAAAA GGGCATGCTGGGAGTCGTATT
Name SS29 SS30 SS428 SS429 SS430 SS431 SS434 SS435	Sequence CGGAGAGGAAGTACAGTGTGTG ACCAGCCGTTAGAATTGAGCC AGTTTCGTGCGCAGTGGTTGG ACTCGCTGCCCCTGGTAATGG CCGACTCTCGTAGCTCGCAGTAA CGAGACCGGCAACACTTTCAAAA GGGCATGCTGGGAGTCGTATT CCCTGCCTGAGTTGCCTTCC
Name SS29 SS30 SS428 SS429 SS430 SS431 SS431 SS435 SS435	Sequence CGGAGAGGAAGTACAGTGTGTG ACCAGCCGTTAGAATTGAGCC AGTTTCGTGCGCAGTGGTTGG ACTCGCTGCCCTGGTAATGG CCGACTCTCGTAGCTCGCAGTAA CGAGACCGGCAACACTTTCAAAA GGGCATGCTGGGAGTCGTATT CCCTGCCTGAGTTGCCTTCC TACGGACCCTAATCCAGATGAC
Name SS29 SS30 SS428 SS429 SS430 SS431 SS434 SS435 SS435 SS455	Sequence CGGAGAGGAAGTACAGTGTGTG ACCAGCCGTTAGAATTGAGCC AGTTTCGTGCGCAGTGGTTGG ACTCGCTGCCCCTGGTAATGG CCGACTCTCGTAGCTCGCAGTAA CGAGACCGGCAACACTTTCAAAA GGGCATGCTGGGAGTCGTATT CCCTGCCTGAGTTGCCTTCC TACGGACCCTAATCCAGATGAC CAACCCATTGCATACTTCTGAG
Name SS29 SS30 SS428 SS429 SS430 SS431 SS434 SS435 SS455 SS456 SS459	Sequence CGGAGAGGAAGTACAGTGTGTG ACCAGCCGTTAGAATTGAGCC AGTTTCGTGCGCAGTGGTTGG ACTCGCTGCCCTGGTAATGG CCGACTCTCGTAGCTCGCAGTAA CGAGACCGGCAACACTTTCAAAA GGGCATGCTGGGAGTCGTATT CCCTGCCTGAGTTGCCTTCC TACGGACCCTAATCCAGATGAC CAACCCATTGCATACTTCTGAG AGTATAGTCTAGAGTATGGTACCG
Name SS29 SS30 SS428 SS429 SS430 SS431 SS434 SS435 SS455 SS455 SS456 SS459 SS460	SequenceCGGAGAGGAAGTACAGTGTGTGACCAGCCGTTAGAATTGAGCCAGTTTCGTGCGCAGTGGTTGGACTCGCTGCCCTGGTAATGGCCGACTCTCGTAGCTCGCAGTAACGAGACCGGCAACACTTTCAAAAGGGCATGCTGGGAGTCGTATTCCCTGCCTGAGTTGCCTTCCTACGGACCCTAATCCAGATGACCAACCCATTGCATACTTCTGAGAGTATAGTCTAGAGTATGGTACCGTAGCAATTTGATGGCAGCTC
Name SS29 SS30 SS428 SS429 SS430 SS431 SS434 SS435 SS455 SS456 SS456 SS459 SS460 SS463	Sequence         CGGAGAGGAAGTACAGTGTGTG         ACCAGCCGTTAGAATTGAGCC         AGTTTCGTGCGCAGTGGTTGG         ACTCGCTGCCCCTGGTAATGG         CCGACTCTCGTAGCTCGCAGTAA         CGAGACCGGCAACACTTTCAAAA         GGGCATGCTGGGAGTCGTATT         CCCTGCCTGAGTTGCCTTCC         TACGGACCCTAATCCAGATGAC         CAACCCATTGCATACTTCTGAG         AGTATAGTCTAGAGTATGGTACCG         TAGCAATTTGATGGCAGCTC         GTCTAGTTAGTCCTTTGGTCCT
Name SS29 SS30 SS428 SS429 SS430 SS431 SS434 SS435 SS435 SS455 SS456 SS459 SS460 SS463 SS464	Sequence         CGGAGAGGAAGTACAGTGTGTG         ACCAGCCGTTAGAATTGAGCC         AGTTTCGTGCGCAGTGGTTGG         ACTCGCTGCCCCTGGTAATGG         CCGACTCTCGTAGCTCGCAGTAA         CGAGACCGGCAACACTTTCAAAA         GGGCATGCTGGGAGTCGTATT         CCCTGCCTGAGTGCCTTCC         TACGGACCCTAATCCAGATGAC         CAACCCATTGCATACTTCTGAG         AGTATAGTCTAGAGTATGGTACCG         TAGCAATTTGATGGCAGCTC         GTCTAGTTAGTCCTTTGGTCCT
Name SS29 SS30 SS428 SS429 SS430 SS431 SS434 SS435 SS455 SS455 SS456 SS459 SS460 SS463 SS464 SS501	Sequence         CGGAGAGGAAGTACAGTGTGTG         ACCAGCCGTTAGAATTGAGCC         AGTTTCGTGCGCAGTGGTTGG         ACTCGCTGCCCCTGGTAATGG         CCGACTCTCGTAGCTCGCAGTAA         CGAGACCGGCAACACTTTCAAAA         GGGCATGCTGGGAGTCGTATT         CCCTGCCTGAGTTGCCTTCC         TACGGACCCTAATCCAGATGAC         CAACCCATTGCATACTTCTGAG         AGTATAGTCTAGAGTATGGTACCG         TAGCAATTTGATGGCAGCTC         GTCTAGTTAGTCCTTGGTCCT         GCCTATTTCTATAATGACTCCGT         ACTCGAATTGGGTGGGCTATCTTGA
Name SS29 SS30 SS428 SS429 SS430 SS431 SS434 SS435 SS455 SS456 SS456 SS456 SS460 SS463 SS464 SS501 SS502	Sequence         CGGAGAGGAAGTACAGTGTGTG         ACCAGCCGTTAGAATTGAGCC         AGTTTCGTGCGCAGTGGTTGG         ACTCGCTGCCCCTGGTAATGG         CCGACTCTCGTAGCTCGCAGTAA         CGGAGCCGGCAACACTTTCAAAA         GGGCATGCTGGGAGTCGTATT         CCCTGCCTGAGTTGCCTTCC         TACGGACCCTAATCCAGATGAC         CAACCCATTGCATACTTCTGAG         AGTATAGTCTAGAGTATGGTACCG         TAGCAATTTGATGCCTTG         GTCTAGTTAGTCCTTTGGTCCT         GCCTATTTCTATAATGACTCCGT         ACTCGAATTGGGTGGGCTATCTTGA         CCTGAATTGGGTGGGCTATCTTGA
Name SS29 SS30 SS428 SS429 SS430 SS431 SS434 SS435 SS455 SS456 SS459 SS460 SS463 SS464 SS501 SS502 SS503	Sequence         CGGAGAGGAAGTACAGTGTGTG         ACCAGCCGTTAGAATTGAGCC         AGTTTCGTGCGCAGTGGTTGG         ACTCGCTGCCCTGGTAATGG         CCGACTCTCGTAGCTCGCAGTAA         CGGACCGGCAACACTTTCAAAA         GGGCATGCTGGGAGTGGTATT         CCCTGCCTGAGTTGCCTTCC         TACGGACCCTAATCCAGATGAC         CAACCCATTGCATACTTCTGAG         AGTATAGTCTAGAGTATGGTACCG         TAGCAATTTGATGGCAGCTC         GTCTAGTTAGTCCTTTGGTCCT         GCCTATTTCTATAATGACTCCGT         ACTCGAATTGGGTGGGGCTATCTTGA         CATCGGAATTGGTGGGGCTATCTTGA         CATTGGGTGGGGCTATCTTGA         CATTGGGTGGGGCTATCTGA

SS517 ACTCGCCTTGGTTGGGCTATTG

SS518 TCTCTGGCCGCGTGTTGTAACTA

SS519 ATGCCATCAGGGAGCTTCACTCAT

Table S3. Level of auxin metabolites in wildtype *P. patens* and in stated over-expressor (OE) and mutant lines, expressed as mmol per gram fresh weight. The mean values are based on 5-6 independent biological replicates, except for wildtype where 20 samples were analysed. UDL = under detection limit. Asterisks indicate statistically significant differences compared to WT, \* = p < 0.05 and \*\* = p < 0.01 using Students t-test. Error values represent standard deviation. The WT data presented here is the same data as in Table 1 in actual manuscript.

Abbreviation	Compound	WT	PpTARA OE-1	PpTARA OE-2	PpTARF OE-1	PpTARF OE-2	PpYUCA OE-1
TRP	Tryptophan	$21785 \pm 5712$	10855 ± 2421**	11659 ± 2193**	$22830 \pm 4694$	19387 ± 2922	14700 ± 2930*
TRA	Tryptamine	$11,77 \pm 3,56$	$10,67 \pm 2,74$	9,25 ± 1,95	8,81 ± 4,92	7,13 ± 3,83*	$10,22 \pm 5,42$
IAN	Indole-3-acetonitrile	UDL	UDL	UDL	UDL	UDL	UDL
IAM	Indol-3-acetamide	UDL	UDL	UDL	UDL	UDL	UDL
IPyA	Indole-3-pyruvic acid	82,99 ± 17,22	764,60 ± 152,30**	1583,90 ± 336,53**	99,21 ± 16,22	83,48 ± 20,79	48,74 ± 6,37**
IAA	Indol-3-acetic acid	8,50 ± 1,75	40,90 ± 7,75**	41,70 ± 2,53**	8,40 ± 2,26	6,65 ± 1,59*	13,25 ± 2,18**
oxIAA	2-oxoindole-3-acetic acid	$27,17 \pm 5,16$	55,45 ± 5,39**	59,78 ± 14,82**	23,29 ± 7,83	31,24 ± 7,28	46,17 ± 5,52**
OxIAA-Glc	oxIAA-glucose	46,69 ± 12,41	42,65 ± 11,85	72,15 ± 17,99**	32,86 ± 14,66*	41,98 ± 18,92	29,06 ± 12,39*
IAA-Glc	IAA-glucose	$7,84 \pm 2,08$	2,57 ± 1,08**	4,19 ± 1,78**	4,13 ± 0,82**	7,69 ± 1,17	8,21 ± 1,71
IAA-Asp	IAA-aspartate	$0,28 \pm 0,09$	UDL	$0,45 \pm 0,25$	$0,21 \pm 0,04$	$0,26 \pm 0,11$	0,16 ± 0,04*
IAA-Gly	IAA-glycine	$0,58 \pm 0,24$	$0,41 \pm 0,15$	0,47 ± 0,09	1,09 ± 0,29**	$1,01 \pm 0,11$ **	1,51 ± 0,28**
IAA-Glu	IAA-glutamate	$0,62 \pm 0,15$	0,39 ± 0,10*	0,47 ± 0,17	0,17±0,09**	$0,67 \pm 0,05$	1,29 ± 0,21**
IAA-Val	IAA-valine	UDL	UDL	UDL	UDL	UDL	UDL
IAA-Leu	IAA-leucine	0,08 ± 0,03	0,13 ± 0,02**	0,14 ± 0,03**	0,05 ± 0,01*	$0,05 \pm 0,02$	UDL
IAA-Phe	IAA-phenylalanine	UDL	UDL	UDL	UDL	UDL	UDL
IAA-Trp	IAA-tryptophan	UDL	UDL	UDL	UDL	UDL	UDL
Abbreviation	Compound	PpYUCA OE-2	PpYUCC OE-1	PpYUCC OE-2	Pptara-1	Pptarb-1	Pptaratarb-1
Abbreviation TRP	Compound Tryptophan	<b>PpYUCA OE-2</b> 12205 ± 2507**	<b>PpYUCC OE-1</b> 15188 ± 1680*	<b>PpYUCC OE-2</b> 12482 ± 1383**	<b>Pptara-1</b> 26461 ± 10518	<b>Pptarb-1</b> 16699 ± 2564	<b>Pptaratarb-1</b> 33330 ± 5050**
Abbreviation TRP TRA	Compound Tryptophan Tryptamine	<b>PpYUCA OE-2</b> 12205 ± 2507** 8,24 ± 4,44	<b>PpYUCC OE-1</b> 15188 ± 1680* 7,73 ± 4,07*	<i>PpYUCC OE-2</i> 12482 ± 1383** 8,89 ± 5,27	<b>Pptara-1</b> 26461 ± 10518 14,15 ± 5,17	<b>Pptarb-1</b> 16699 ± 2564 7,42 ± 1,55**	<b>Pptaratarb-1</b> 33330 ± 5050** 12,60 ± 5,73
Abbreviation TRP TRA IAN	Compound Tryptophan Tryptamine Indole-3-acetonitrile	<b>PpYUCA OE-2</b> 12205 ± 2507** 8,24 ± 4,44 UDL	PpYUCC OE-1 15188 ± 1680* 7,73 ± 4,07* UDL	PpYUCC OE-2 12482 ± 1383** 8,89 ± 5,27 UDL	Pptara-1 26461 ± 10518 14,15 ± 5,17 UDL	Pptarb-1 16699 ± 2564 7,42 ± 1,55** UDL	Pptaratarb-1 33330 ± 5050** 12,60 ± 5,73 UDL
Abbreviation TRP TRA IAN IAM	Compound Tryptophan Tryptamine Indole-3-acetonitrile Indol-3-acetamide	<i>PpYUCA OE-2</i> 12205 ± 2507** 8,24 ± 4,44 UDL UDL UDL	PpYUCC OE-1 15188 ± 1680* 7,73 ± 4,07* UDL UDL	PpYUCC OE-2 12482 ± 1383** 8,89 ± 5,27 UDL UDL UDL	Pptara-1 26461 ± 10518 14,15 ± 5,17 UDL UDL	Pptarb-1 16699 ± 2564 7,42 ± 1,55** UDL UDL	Pptaratarb-1 33330 ± 5050** 12,60 ± 5,73 UDL UDL
Abbreviation TRP TRA IAN IAM IPyA	Compound Tryptophan Tryptamine Indole-3-acetonitrile Indol-3-acetamide Indole-3-pyruvic acid	<b>PpYUCA OE-2</b> 12205 ± 2507** 8,24 ± 4,44 UDL UDL 29,45 ± 10,44**	PpYUCC OE-1           15188 ± 1680*           7,73 ± 4,07*           UDL           UDL           45,91 ± 12,15**	Pp YUCC OE-2           12482 ± 1383**           8,89 ± 5,27           UDL           UDL           28,70 ± 11,22**	Pptara-1 26461 ± 10518 14,15 ± 5,17 UDL UDL 15,88 ± 2,79**	Pptarb-1 16699 ± 2564 7,42 ± 1,55** UDL UDL UDL 62,88 ± 12,32*	Pptaratarb-1 33330 ± 5050** 12,60 ± 5,73 UDL UDL 13,34 ± 1,19**
Abbreviation TRP TRA IAN IAM IPyA IAA	Compound Tryptophan Tryptamine Indole-3-acetonitrile Indol-3-acetamide Indole-3-pyruvic acid Indol-3-acetic acid	PpYUCA OE-2 12205 ± 2507** 8,24 ± 4,44 UDL UDL 29,45 ± 10,44** 9,86 ± 3,00	$\begin{array}{c} \label{eq:pyucc of e-1} \\ 15188 \pm 1680^{*} \\ 7,73 \pm 4,07^{*} \\ UDL \\ UDL \\ 45,91 \pm 12,15^{**} \\ 15,99 \pm 3,67^{**} \end{array}$	PpYUCC OE-2           12482 ± 1383**           8,89 ± 5,27           UDL           UDL           28,70 ± 11,22**           10,52 ± 1,13*	$\begin{array}{c} Pptara-1\\ 26461\pm10518\\ 14,15\pm5,17\\ UDL\\ UDL\\ 15,88\pm2,79^{**}\\ 4,13\pm1,63^{**} \end{array}$	Pptarb-1 16699 ± 2564 7,42 ± 1,55** UDL UDL 62,88 ± 12,32* 6,04 ± 0,85**	Pptaratarb-1 33330 ± 5050** 12,60 ± 5,73 UDL UDL 13,34 ± 1,19** 2,71 ± 0,65**
Abbreviation TRP TRA IAN IAM IPyA IAA oxIAA	Compound Tryptophan Tryptamine Indole-3-acetonitrile Indol-3-acetamide Indol-3-acetic acid 2-oxoindole-3-acetic acid	PpYUCA OE-2 12205 ± 2507** 8,24 ± 4,44 UDL UDL 29,45 ± 10,44** 9,86 ± 3,00 60,95 ± 7,71**	$\begin{array}{c} \label{eq:pyucc of constraints} Pp YUCC OE-1 \\ 15188 \pm 1680^* \\ 7,73 \pm 4,07^* \\ UDL \\ UDL \\ 45,91 \pm 12,15^{**} \\ 15,99 \pm 3,67^{**} \\ 68,86 \pm 6,93^{**} \end{array}$	PpYUCC OE-2 12482 ± 1383** 8,89 ± 5,27 UDL UDL 28,70 ± 11,22** 10,52 ± 1,13* 70,38 ± 4,23**	$\begin{array}{c} Pptara-1\\ 26461\pm10518\\ 14,15\pm5,17\\ UDL\\ UDL\\ 15,88\pm2,79^{**}\\ 4,13\pm1,63^{**}\\ 15,70\pm2,44^{**} \end{array}$	Pptarb-1 16699 ± 2564 7,42 ± 1,55** UDL UDL 62,88 ± 12,32* 6,04 ± 0,85** 31,78 ± 10,69	$\begin{array}{c} \label{eq:ptaratarb-1} \\ 33330 \pm 5050^{**} \\ 12,60 \pm 5,73 \\ UDL \\ UDL \\ 13,34 \pm 1,19^{**} \\ 2,71 \pm 0,65^{**} \\ 6,54 \pm 1,92^{**} \end{array}$
Abbreviation TRP TRA IAN IAM IPyA IAA oxIAA OxIAA-Glc	Compound Tryptophan Tryptamine Indole-3-acetonitrile Indol-3-acetamide Indol-3-acetic acid 2-oxoindole-3-acetic acid oxIAA-glucose	PpYUCA OE-2 12205 ± 2507** 8,24 ± 4,44 UDL 29,45 ± 10,44** 9,86 ± 3,00 60,95 ± 7,71** 29,07 ± 10,66**	PpYUCC OE-1           15188 ± 1680*           7,73 ± 4,07*           UDL           45,91 ± 12,15**           15,99 ± 3,67**           68,86 ± 6,93**           28,97 ± 11,74**	PpYUCC OE-2           12482 ± 1383**           8,89 ± 5,27           UDL           28,70 ± 11,22**           10,52 ± 1,13*           70,38 ± 4,23**           34,76 ± 9,34	$\begin{array}{c} Pptara-1\\ 26461\pm10518\\ 14,15\pm5,17\\ UDL\\ UDL\\ 15,88\pm2,79^{**}\\ 4,13\pm1,63^{**}\\ 15,70\pm2,44^{**}\\ 42,44\pm17,62\\ \end{array}$	$\begin{array}{c} Pptarb-1\\ 16699 \pm 2564\\ 7,42 \pm 1,55^{**}\\ UDL\\ 02,88 \pm 12,32^{*}\\ 6,04 \pm 0,85^{**}\\ 31,78 \pm 10,69\\ 28,40 \pm 8,47^{*}\\ \end{array}$	$\begin{array}{c} \label{eq:ptaratarb-1} \\ 3330 \pm 5050^{**} \\ 12,60 \pm 5,73 \\ UDL \\ UDL \\ 13,34 \pm 1,19^{**} \\ 2,71 \pm 0,65^{**} \\ 6,54 \pm 1,92^{**} \\ 46,62 \pm 14,19 \end{array}$
Abbreviation TRP TRA IAN IAM IPyA IAA oxIAA OxIAA-Glc IAA-Glc	Compound Tryptophan Tryptamine Indole-3-acetonitrile Indole-3-acetamide Indol-3-acetic acid 2-oxoindole-3-acetic acid oxIAA-glucose IAA-glucose	PpYUCA OE-2 12205 ± 2507** 8,24 ± 4,44 UDL 29,45 ± 10,44** 9,86 ± 3,00 60,95 ± 7,71** 29,07 ± 10,66** 6,94 ± 2,07	PpYUCC OE-1 15188 ± 1680* 7,73 ± 4,07* UDL 45,91 ± 12,15** 15,99 ± 3,67** 68,86 ± 6,93** 28,97 ± 11,74** 8,65 ± 2,18	PpYUCC OE-2           12482 ± 1383**           8,89 ± 5,27           UDL           28,70 ± 11,22**           10,52 ± 1,13*           70,38 ± 4,23**           34,76 ± 9,34           9,27 ± 1,82	$\begin{array}{c} \hline Pptara-1\\ 26461 \pm 10518\\ 14,15 \pm 5,17\\ UDL\\ UDL\\ 15,88 \pm 2,79^{**}\\ 4,13 \pm 1,63^{**}\\ 15,70 \pm 2,44^{**}\\ 42,44 \pm 17,62\\ 5,78 \pm 2,05\\ \end{array}$	$\begin{array}{c} Pptarb-1\\ 16699 \pm 2564\\ 7,42 \pm 1,55^{**}\\ UDL\\ 028 \pm 12,32^{*}\\ 6,04 \pm 0,85^{**}\\ 31,78 \pm 10,69\\ 28,40 \pm 8,47^{*}\\ 4,85 \pm 1,56^{**}\\ \end{array}$	$\begin{array}{c} \hline Pptaratarb-1\\ 33330\pm 5050^{**}\\ 12,60\pm 5,73\\ UDL\\ UDL\\ 13,34\pm 1,19^{**}\\ 2,71\pm 0,65^{**}\\ 6,54\pm 1,92^{**}\\ 46,62\pm 14,19\\ 6,11\pm 0,78\\ \end{array}$
Abbreviation TRP TRA IAN IAM IPyA IAA oxIAA OxIAA-Glc IAA-Glc IAA-Asp	Compound Tryptophan Tryptamine Indole-3-acetonitrile Indole-3-acetic acid Indole-3-pyruvic acid Indole-3-acetic acid 2-oxoindole-3-acetic acid oxIAA-glucose IAA-glucose IAA-aspartate	$\begin{array}{c} \label{eq:pyuca observation} PpYUCA OE-2 \\ 12205 \pm 2507^{**} \\ 8,24 \pm 4,44 \\ UDL \\ UDL \\ 29,45 \pm 10,44^{**} \\ 9,86 \pm 3,00 \\ 60,95 \pm 7,71^{**} \\ 29,07 \pm 10,66^{**} \\ 6,94 \pm 2,07 \\ 0,15 \pm 0,07^{**} \end{array}$	$\begin{array}{c} \hline pp YUCC \ OE-1\\ 15188 \pm 1680^{*}\\ 7,73 \pm 4,07^{*}\\ UDL\\ UDL\\ 45,91 \pm 12,15^{**}\\ 15,99 \pm 3,67^{**}\\ 68,86 \pm 6,93^{**}\\ 28,97 \pm 11,74^{**}\\ 8,65 \pm 2,18\\ 0,21 \pm 0,07\\ \end{array}$	$\begin{array}{c} \hline pp YUCC \ OE-2 \\ 12482 \pm 1383^{**} \\ 8,89 \pm 5,27 \\ UDL \\ UDL \\ 28,70 \pm 11,22^{**} \\ 10,52 \pm 1,13^{*} \\ 70,38 \pm 4,23^{**} \\ 34,76 \pm 9,34 \\ 9,27 \pm 1,82 \\ 0,24 \pm 0,10 \end{array}$	$\begin{array}{c} \label{eq:ptara-1} \\ 26461 \pm 10518 \\ 14,15 \pm 5,17 \\ UDL \\ \ UDL \\ 15,88 \pm 2,79** \\ 4,13 \pm 1,63^{**} \\ 15,70 \pm 2,44^{**} \\ 42,44 \pm 17,62 \\ 5,78 \pm 2,05 \\ UDL \\ \end{array}$	$\begin{array}{c} \hline Pptarb-1 \\ 16699 \pm 2564 \\ 7,42 \pm 1,55^{**} \\ UDL \\ UDL \\ \hline 02,88 \pm 12,32^{*} \\ 6,04 \pm 0,85^{**} \\ 31,78 \pm 10,69 \\ 28,40 \pm 8,47^{*} \\ 4,85 \pm 1,56^{**} \\ UDL \\ \end{array}$	$\begin{array}{c} \hline Pptaratarb-1\\ 33330\pm 5050^{**}\\ 12,60\pm 5,73\\ UDL\\ UDL\\ 13,34\pm 1,19^{**}\\ 2,71\pm 0,65^{**}\\ 6,54\pm 1,92^{**}\\ 46,62\pm 14,19\\ 6,11\pm 0,78\\ UDL\\ \end{array}$
Abbreviation TRP TRA IAN IAM IPyA IAA OXIAA-Glc IAA-Glc IAA-Gly	Compound Tryptophan Tryptamine Indole-3-acetonitrile Indole-3-acetic acid Indole-3-pyruvic acid Indole-3-pyruvic acid 2-oxoindole-3-acetic acid oxIAA-glucose IAA-glucose IAA-aspartate IAA-glycine	$\begin{array}{c} \label{eq:pyuca observation} PpYUCA OE-2 \\ 12205 \pm 2507^{**} \\ 8,24 \pm 4,44 \\ UDL \\ \ UDL \\ 29,45 \pm 10,44^{**} \\ 9,86 \pm 3,00 \\ 60,95 \pm 7,71^{**} \\ 29,07 \pm 10,66^{**} \\ 6,94 \pm 2,07 \\ 0,15 \pm 0,07^{**} \\ 1,45 \pm 0,19^{**} \end{array}$	$\begin{array}{c} \label{eq:pyucc off-1} \\ 15188 \pm 1680^{*} \\ 7,73 \pm 4,07^{*} \\ UDL \\ UDL \\ 45,91 \pm 12,15^{**} \\ 15,99 \pm 3,67^{**} \\ 68,86 \pm 6,93^{**} \\ 28,97 \pm 11,74^{**} \\ 8,65 \pm 2,18 \\ 0,21 \pm 0,07 \\ 1,51 \pm 0,17^{**} \end{array}$	$\begin{array}{c} \hline pp YUCC \ OE-2 \\ 12482 \pm 1383^{**} \\ 8,89 \pm 5,27 \\ UDL \\ UDL \\ 28,70 \pm 11,22^{**} \\ 10,52 \pm 1,13^{*} \\ 70,38 \pm 4,23^{**} \\ 34,76 \pm 9,34 \\ 9,27 \pm 1,82 \\ 0,24 \pm 0,10 \\ 1,02 \pm 0,06^{**} \end{array}$	$\begin{array}{c} \label{eq:ptara-1} \\ 26461 \pm 10518 \\ 14,15 \pm 5,17 \\ UDL \\ \ UDL \\ 15,88 \pm 2,79^{**} \\ 4,13 \pm 1,63^{**} \\ 15,70 \pm 2,44^{**} \\ 42,44 \pm 17,62 \\ 5,78 \pm 2,05 \\ UDL \\ 0,48 \pm 0,11 \end{array}$	$\begin{array}{c} Pptarb-1\\ 16699\pm2564\\ 7,42\pm1,55^{**}\\ UDL\\ UDL\\ 62,88\pm12,32^{*}\\ 6,04\pm0,85^{**}\\ 31,78\pm10,69\\ 28,40\pm8,47^{*}\\ 4,85\pm1,56^{**}\\ UDL\\ 0,35\pm0,10^{*}\\ \end{array}$	$\begin{array}{c} \hline Pptaratarb-1\\ 33330\pm 5050^{**}\\ 12,60\pm 5,73\\ UDL\\ UDL\\ 13,34\pm 1,19^{**}\\ 2,71\pm 0,65^{**}\\ 6,54\pm 1,92^{**}\\ 46,62\pm 1,419\\ 6,11\pm 0,78\\ UDL\\ 0,45\pm 0,09\\ \end{array}$
Abbreviation TRP TRA IAN IAM IPyA IAA oxIAA OxIAA-Glc IAA-Glc IAA-Gly IAA-Glu	Compound Tryptophan Tryptamine Indole-3-acetonitrile Indole-3-acetinite Indole-3-acetic acid Indole-3-acetic acid 2-oxoindole-3-acetic acid oxIAA-glucose IAA-glucose IAA-aspartate IAA-glycine IAA-glutamate	$\begin{array}{c} \label{eq:pyuca observation} PpYUCA OE-2 \\ 12205 \pm 2507^{**} \\ 8,24 \pm 4,44 \\ UDL \\ UDL \\ 29,45 \pm 10,44^{**} \\ 9,86 \pm 3,00 \\ 60,95 \pm 7,71^{**} \\ 29,07 \pm 10,66^{**} \\ 6,94 \pm 2,07 \\ 0,15 \pm 0,07^{**} \\ 1,45 \pm 0,19^{**} \\ 0,99 \pm 0,15^{**} \end{array}$	$\begin{array}{c} \hline Pp YUCC \ OE-1\\ 15188 \pm 1680^{*}\\ 7,73 \pm 4,07^{*}\\ UDL\\ UDL\\ 45,91 \pm 12,15^{**}\\ 15,99 \pm 3,67^{**}\\ 68,86 \pm 6,93^{**}\\ 28,97 \pm 11,74^{**}\\ 8,65 \pm 2,18\\ 0,21 \pm 0,07\\ 1,51 \pm 0,17^{**}\\ 1,43 \pm 0,18^{**}\\ \end{array}$	$\begin{array}{c} \hline Pp YUCC \ OE-2 \\ 12482 \pm 1383^{**} \\ 8,89 \pm 5,27 \\ UDL \\ UDL \\ 28,70 \pm 11,22^{**} \\ 10,52 \pm 1,13^{*} \\ 70,38 \pm 4,23^{**} \\ 34,76 \pm 9,34 \\ 9,27 \pm 1,82 \\ 0,24 \pm 0,10 \\ 1,02 \pm 0,06^{**} \\ 1,25 \pm 0,27^{**} \end{array}$	$\begin{array}{c} \label{eq:ptara-1} \\ 26461 \pm 10518 \\ 14,15 \pm 5,17 \\ \mbox{UDL} \\ 15,88 \pm 2,79^{**} \\ 4,13 \pm 1,63^{**} \\ 15,70 \pm 2,44^{**} \\ 42,44 \pm 1,762 \\ 5,78 \pm 2,05 \\ \mbox{UDL} \\ 0,48 \pm 0,11 \\ \mbox{UDL} \\ \end{array}$	$\begin{array}{c} Pptarb-1\\ 16699\pm2564\\ 7,42\pm1,55^{**}\\ UDL\\ UDL\\ 62,88\pm12,32^{*}\\ 6,04\pm0,85^{**}\\ 31,78\pm10,69\\ 28,40\pm8,47^{*}\\ 4,85\pm1,56^{**}\\ UDL\\ 0,35\pm0,10^{*}\\ UDL\\ \end{array}$	$\begin{array}{c} \hline Pptaratarb-1\\ 33330\pm 5050^{**}\\ 12,60\pm 5,73\\ UDL\\ UDL\\ 13,34\pm 1,19^{**}\\ 2,71\pm 0,65^{**}\\ 6,54\pm 1,92^{**}\\ 46,62\pm 14,19\\ 6,11\pm 0,78\\ UDL\\ 0,45\pm 0,09\\ UDL\\ \end{array}$
Abbreviation TRP TRA IAN IAM IPyA IAA oxIAA OxIAA-Glc IAA-Glc IAA-Gly IAA-Glu IAA-Glu IAA-Val	Compound Tryptophan Tryptamine Indole-3-acetonitrile Indol-3-acetamide Indole-3-pyruvic acid Indol-3-acetic acid 2-oxoindole-3-acetic acid oxIAA-glucose IAA-glucose IAA-glucose IAA-glycine IAA-glytamate IAA-glutamate IAA-valine	$\begin{array}{c} \label{eq:pyuca observed} Pp YUCA OE-2 \\ 12205 \pm 2507^{**} \\ 8,24 \pm 4,44 \\ UDL \\ UDL \\ 29,45 \pm 10,44^{**} \\ 9,86 \pm 3,00 \\ 60,95 \pm 7,71^{**} \\ 29,07 \pm 10,66^{**} \\ 6,94 \pm 2,07 \\ 0,15 \pm 0,07^{**} \\ 1,45 \pm 0,19^{**} \\ 0,99 \pm 0,15^{**} \\ UDL \\ \end{array}$	$\begin{array}{c} \label{eq:pyucc oE-1} \\ 15188 \pm 1680^{*} \\ 7,73 \pm 4,07^{*} \\ UDL \\ UDL \\ 45,91 \pm 12,15^{**} \\ 15,99 \pm 3,67^{**} \\ 68,86 \pm 6,93^{**} \\ 28,97 \pm 11,74^{**} \\ 8,65 \pm 2,18 \\ 0,21 \pm 0,07 \\ 1,51 \pm 0,17^{**} \\ 1,43 \pm 0,18^{**} \\ UDL \\ \end{array}$	$\begin{array}{c} \hline Pp YUCC \ OE-2 \\ 12482 \pm 1383^{**} \\ 8,89 \pm 5,27 \\ UDL \\ UDL \\ 28,70 \pm 11,22^{**} \\ 10,52 \pm 1,13^{*} \\ 70,38 \pm 4,23^{**} \\ 34,76 \pm 9,34 \\ 9,27 \pm 1,82 \\ 0,24 \pm 0,10 \\ 1,02 \pm 0,06^{**} \\ 1,25 \pm 0,27^{**} \\ UDL \\ \end{array}$	$\begin{array}{c} \label{eq:ptara-1} \\ 26461 \pm 10518 \\ 14,15 \pm 5,17 \\ \mbox{UDL} \\ \mbox{UDL} \\ 15,88 \pm 2,79^{**} \\ 4,13 \pm 1,63^{**} \\ 15,70 \pm 2,44^{**} \\ 42,44 \pm 17,62 \\ 5,78 \pm 2,05 \\ \mbox{UDL} \\ 0,48 \pm 0,11 \\ \mbox{UDL} \\ \mbox{UDL} \\ \mbox{UDL} \\ \mbox{UDL} \\ \end{array}$	$\begin{array}{c} Pptarb-1\\ 16699\pm2564\\ 7,42\pm1,55^{**}\\ UDL\\ UDL\\ 62,88\pm12,32^{*}\\ 6,04\pm0,85^{**}\\ 31,78\pm10,69\\ 28,40\pm8,47^{*}\\ 4,85\pm1,56^{**}\\ UDL\\ 0,35\pm0,10^{*}\\ UDL\\ UDL\\ UDL\\ \end{array}$	$\begin{array}{c} \hline Pptaratarb-1\\ 33330\pm 5050^{**}\\ 12,60\pm 5,73\\ UDL\\ UDL\\ 13,34\pm 1,19^{**}\\ 2,71\pm 0,65^{**}\\ 6,54\pm 1,92^{**}\\ 46,62\pm 14,19\\ 6,11\pm 0,78\\ UDL\\ 0,45\pm 0,09\\ UDL\\ UDL\\ UDL\\ UDL\\ \end{array}$
Abbreviation TRP TRA IAN IAM IPyA IAA OxIAA-Glc IAA-Glc IAA-Gly IAA-Gly IAA-Glu IAA-Val IAA-Leu	Compound Tryptophan Tryptamine Indole-3-acetonitrile Indol-3-acetamide Indol-3-acetic acid 2-oxoindole-3-acetic acid oxIAA-glucose IAA-glucose IAA-glucose IAA-glycine IAA-glycine IAA-glytamate IAA-valine IAA-valine	$\begin{array}{c} \label{eq:pyUC4 OE-2} \\ 12205 \pm 2507^{**} \\ 8,24 \pm 4,44 \\ UDL \\ UDL \\ 29,45 \pm 10,44^{**} \\ 9,86 \pm 3,00 \\ 60,95 \pm 7,71^{**} \\ 29,07 \pm 10,66^{**} \\ 6,94 \pm 2,07 \\ 0,15 \pm 0,07^{**} \\ 1,45 \pm 0,19^{**} \\ 0,99 \pm 0,15^{**} \\ UDL \\ 0,03 \pm 0,00^{**} \end{array}$	$\begin{array}{c} \label{eq:pyucc of e-1} \\ 15188 \pm 1680^{*} \\ 7,73 \pm 4,07^{*} \\ UDL \\ UDL \\ 45,91 \pm 12,15^{**} \\ 15,99 \pm 3,67^{**} \\ 68,86 \pm 6,93^{**} \\ 28,97 \pm 11,74^{**} \\ 8,65 \pm 2,18 \\ 0,21 \pm 0,07 \\ 1,51 \pm 0,17^{**} \\ 1,43 \pm 0,18^{**} \\ UDL \\ 0,05 \pm 0,02^{*} \end{array}$	$\begin{array}{c} \label{eq:pyucc observed} Pp YUCC OE-2 \\ 12482 \pm 1383^{**} \\ 8,89 \pm 5,27 \\ UDL \\ UDL \\ 28,70 \pm 11,22^{**} \\ 10,52 \pm 1,13^{*} \\ 70,38 \pm 4,23^{**} \\ 34,76 \pm 9,34 \\ 9,27 \pm 1,82 \\ 0,24 \pm 0,10 \\ 1,02 \pm 0,06^{**} \\ 1,25 \pm 0,27^{**} \\ UDL \\ UDL \\ UDL \end{array}$	$\begin{array}{c} \label{eq:ptara-1} \\ 26461 \pm 10518 \\ 14,15 \pm 5,17 \\ UDL \\ UDL \\ 15,88 \pm 2,79^{**} \\ 4,13 \pm 1,63^{**} \\ 15,70 \pm 2,44^{**} \\ 42,44 \pm 17,62 \\ 5,78 \pm 2,05 \\ UDL \\ 0,48 \pm 0,11 \\ UDL \\ UDL \\ 0,10 \pm 0,04 \\ \end{array}$	$\begin{array}{c} Pptarb-1\\ 16699 \pm 2564\\ 7,42 \pm 1,55^{**}\\ UDL\\ UDL\\ 62,88 \pm 12,32^{*}\\ 6,04 \pm 0,85^{**}\\ 31,78 \pm 10,69\\ 28,40 \pm 8,47^{*}\\ 4,85 \pm 1,56^{**}\\ UDL\\ 0,35 \pm 0,10^{*}\\ UDL\\ 0,07 \pm 0,02\\ \end{array}$	$\begin{array}{c} \hline Pptaratarb-1\\ 33330\pm 5050^{**}\\ 12,60\pm 5,73\\ UDL\\ UDL\\ 13,34\pm 1,19^{**}\\ 2,71\pm 0,65^{**}\\ 6,54\pm 1,92^{**}\\ 46,62\pm 14,19\\ 6,11\pm 0,78\\ UDL\\ 0,45\pm 0,09\\ UDL\\ UDL\\ 0,11\pm 0,03\\ \end{array}$
Abbreviation TRP TRA IAN IAM IPyA IAA OxIAA-Glc IAA-Glc IAA-Glc IAA-Gly IAA-Glu IAA-Calu IAA-Calu IAA-Leu IAA-Phe	Compound Tryptophan Tryptamine Indole-3-acetonitrile Indole-3-aceticatide Indole-3-pyruvic acid Indol-3-acetic acid 2-oxoindole-3-acetic acid oxIAA-glucose IAA-glucose IAA-glucose IAA-glycine IAA-glycine IAA-glytine IAA-glutamate IAA-valine IAA-valine IAA-valine	$\begin{array}{c} \label{eq:pyUC4 OE-2} \\ 12205 \pm 2507^{**} \\ 8,24 \pm 4,44 \\ UDL \\ UDL \\ 29,45 \pm 10,44^{**} \\ 9,86 \pm 3,00 \\ 60,95 \pm 7,71^{**} \\ 29,07 \pm 10,66^{**} \\ 6,94 \pm 2,07 \\ 0,15 \pm 0,07^{**} \\ 1,45 \pm 0,19^{**} \\ 0,99 \pm 0,15^{**} \\ UDL \\ 0,03 \pm 0,00^{**} \\ UDL \\ \end{array}$	$\begin{array}{c} \label{eq:pyucc observation} Pp YUCC OE-1\\ 15188 \pm 1680^*\\ 7,73 \pm 4,07^*\\ UDL\\ UDL\\ 45,91 \pm 12,15^{**}\\ 15,99 \pm 3,67^{**}\\ 68,86 \pm 6,93^{**}\\ 28,97 \pm 11,74^{**}\\ 8,65 \pm 2,18\\ 0,21 \pm 0,07\\ 1,51 \pm 0,17^{**}\\ 1,43 \pm 0,18^{**}\\ UDL\\ 0,05 \pm 0,02^*\\ UDL\\ \end{array}$	$\begin{array}{c} \label{eq:pyucc observed} Pp YUCC OE-2 \\ 12482 \pm 1383^{**} \\ 8,89 \pm 5,27 \\ UDL \\ UDL \\ 28,70 \pm 11,22^{**} \\ 10,52 \pm 1,13^{*} \\ 70,38 \pm 4,23^{**} \\ 34,76 \pm 9,34 \\ 9,27 \pm 1,82 \\ 0,24 \pm 0,10 \\ 1,02 \pm 0,06^{**} \\ 1,25 \pm 0,27^{**} \\ UDL \\ UDL \\ UDL \\ UDL \\ UDL \\ \end{array}$	$\begin{array}{c} Pptara-1\\ 26461 \pm 10518\\ 14,15 \pm 5,17\\ UDL\\ UDL\\ 15,88 \pm 2,79^{**}\\ 4,13 \pm 1,63^{**}\\ 15,70 \pm 2,44^{**}\\ 42,44 \pm 17,62\\ 5,78 \pm 2,05\\ UDL\\ 0,48 \pm 0,11\\ UDL\\ 0,10 \pm 0,04\\ UDL\\ \end{array}$	$\begin{array}{c} Pptarb-1\\ 16699 \pm 2564\\ 7,42 \pm 1,55^{**}\\ UDL\\ UDL\\ 62,88 \pm 12,32^{*}\\ 6,04 \pm 0,85^{**}\\ 31,78 \pm 10,69\\ 28,40 \pm 8,47^{*}\\ 4,85 \pm 1,56^{**}\\ UDL\\ 0,35 \pm 0,10^{*}\\ UDL\\ UDL\\ 0,07 \pm 0,02\\ UDL\\ \end{array}$	$\begin{array}{c} \hline Pptaratarb-1\\ 33330 \pm 5050^{**}\\ 12,60 \pm 5,73\\ UDL\\ UDL\\ 13,34 \pm 1,19^{**}\\ 2,71 \pm 0,65^{**}\\ 6,54 \pm 1,92^{**}\\ 46,62 \pm 14,19\\ 6,11 \pm 0,78\\ UDL\\ 0,45 \pm 0,09\\ UDL\\ UDL\\ 0,11 \pm 0,03\\ UDL\\ \end{array}$

## **Supplementary references**

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