# Integration of Brassinosteroid and Phytosulfokine Signalling Controls Vascular Cell Fate in the Arabidopsis Root

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#### 34 Abstract

Multicellularity arose independently in plants and animals, but invariably requires robust 35 determination and maintenance of cell fate. This is exemplified by the highly specialized water-36 and nutrient-conducting cells of the plant vasculature, which are specified long before their 37 commitment to terminal differentiation. Here, we show that the hormone receptor 38 39 BRASSINOSTEROID INSENSITIVE 1 (BRI1) is required for root vascular cell fate maintenance, as BRI1 mutants show ectopic xylem in procambial position. However, this 40 phenotype is unrelated to classical brassinosteroid signalling outputs. Instead, BRI1 is 41 42 required for the expression and function of its interaction partner RECEPTOR-LIKE PROTEIN 43 44 (RLP44), which, in turn, associates with the receptor for the peptide hormone phytosulfokine (PSK). We show that PSK signalling is required for the maintenance of 44 45 procambial cell identity and is quantitatively controlled by RLP44, which promotes complex formation between the receptor for PSK and its co-receptor. Mimicking the loss of RLP44, 46 PSK-related mutants show ectopic xylem in the position of procambium, whereas *rlp44* can 47 be rescued by exogenous PSK. Based on these findings, we propose that RLP44 controls cell 48 49 fate by connecting BRI1 and PSK signalling, providing a mechanistic framework for the 50 integration of signalling mediated by the plethora of plant receptor-like kinases at the plasma

51 membrane.

#### 52 Introduction

A key function of signalling networks in multicellular organisms is to ensure robust 53 determination and maintenance of cell fate. In plants, extreme specialization is displayed by 54 the cells of the vascular tissues, vital for the distribution of water, nutrients, and signalling 55 molecules. Xylem tracheary elements are characterized by lignified secondary cell wall 56 57 thickenings that protect against collapse and provide mechanical support for vertical growth. Positioned between xylem and the nutrient-transporting phloem are the cells of the 58 procambium, which give rise to the lateral meristems during secondary growth (1). Root 59 60 vascular tissue patterning is set up in the embryo and maintained in the post-embryonic root by mutual antagonism of auxin and cytokinin signalling domains (2-5). After xylem precursor 61 cells are displaced from the root meristem, an intricate gene-regulatory network connected to 62 patterning mechanisms by HD-ZIP III transcription factors mediates differentiation into 63 tracheary elements (6-9). Thus, primary root xylem cell fate can be traced back to early 64 specification events in the embryo. In contrast, during secondary growth, (pro)cambial cells 65 66 adjacent to the existing tracheary elements acquire xylem cell fate dependent on positional 67 information (10).

Brassinosteroid (BR) hormone signalling (11, 12) has been implicated in xylem differentiation 68 and vascular patterning (13, 14). BRs are perceived by BRASSINOSTEROID INSENSITIVE 69 1 (BRI1) (15) which belongs to the large group of plant receptor-like kinases (RLK) with a 70 71 leucine-rich repeat (LRR) extracellular domain, a transmembrane domain, and a cytosolic kinase domain related to animal Irak and Pelle kinases (16). Upon ligand binding, BRI1 72 73 heterodimerizes with members of the SOMATIC EMBRYGENESIS RECEPTOR KINASE 74 (SERK) LRR-RLK family such as BRI1-ASSOCIATED KINASE 1 (BAK1)(17, 18), and 75 activates a signalling cascade that negatively regulates BRASSINOSTEROID INSENSITIVE 2 (BIN2)(19), a GSK3-like kinase that phosphorylates the BR-responsive transcription factors 76 BRASSINAZOLE RESISTANT 1 (BZR1)(20) and BRI1 EMS SUPPRESSOR 1 (BES1)/BZR2. 77 78 Inhibition of BIN2 activity allows BZR1 and BES1 to translocate to the nucleus, where they 79 mediate BR-responsive control of transcription (21-23). A so far somewhat enigmatic 80 relationship exists between BR and PHYTOSULFOKINE (PSK) signalling. PSKs are small secreted peptide growth factors that have been implicated in a variety of fundamental 81 processes and are perceived by two close relatives of BRI1, PHYTOSULFOKINE RECEPTOR 82 83 1 and 2 (24-27). PSK activity depends on proteolytic processing of the precursor peptides, the sulfation of two tyrosine residues in the mature pentapeptide (YIYTQ) by TYROSYLPROTEIN 84 85 SULFOTRANSFERASE (TPST) (28), and functional BR signalling (29-31). At present, it is not clear how BR and PSK signalling interact but the receptors for both growth factors share the 86 requirement for a SERK co-receptor (32, 33). 87

88 Recently, we demonstrated that feedback information from the cell wall is integrated with BR signalling at the level of the receptor complex through RECEPTOR-LIKE PROTEIN (RLP) 44 89 90 (34). RLP44 is genetically required for the BR-mediated response to impaired cell wall 91 modification and is sufficient to elevate BR signalling when overexpressed. RLP44 was shown 92 to be in a complex with BRI1 and BAK1 and to directly interact with BAK1. Thus, we hypothesized that RLP44 modulates BR signalling strength in response to cues from the cell 93 wall (34). However, it is not clear whether the RLP44-BR signalling module plays additional 94 roles in plant physiology, besides a possible mechanism for cell wall homeostasis (35). Here, 95 we show that RLP44 is required for the maintenance of cell fate in the root vasculature by 96 97 connecting components of the BR and PSK signalling pathways. RLP44 directly interacts with BRI1 and controls xylem differentiation in a BRI1-dependent manner, but independently of BR 98 99 signalling outputs. In addition, RLP44 can directly interact with PSKR1, and the rlp44 100 phenotype can be rescued by application of the PSK peptide. Moreover, mutants affected in 101 PSK signalling show an *rlp44*-like xylem phenotype, suggesting that RLP44 has a positive 102 effect on PSK signalling, which, in turn, promotes procambial identity.

### 103 **Results**

#### 104 RLP44 directly interacts with the brassinosteroid receptor BRI1

We previously demonstrated that RLP44 is present in a complex with both BRI1 and its co-105 receptor BAK1 and is able to promote BR signalling upon cues from the cell wall or when 106 107 overexpressed. In addition, we provided evidence for direct interaction with BAK1 (34). To 108 assess whether RLP44 can also directly interact with BRI1, we performed a mating-based split ubiquitin assay in yeast (36). Under selective conditions, interaction of BRI1 and RLP44 109 enabled yeast growth, similar to what was observed before with BAK1-RLP44 and BAK1-BRI1 110 (34) (Fig. 1A). In addition, Foerster resonance energy transfer-fluorescence lifetime imaging 111 microscopy (FRET-FLIM) analysis after transient expression in *Nicotiana benthamiana* leaves 112 confirmed that BRI1 and RLP44 are able to interact directly (Fig. 1B and Fig. S1A). 113 Furthermore, endogenous BRI1 and BAK1 were detected in immunoprecipitates of RLP44-114 GFP expressed under the control of its own promoter in the *rlp44*<sup>cnu2</sup> mutant background (Fig. 115 S1B). In summary, RLP44 and BRI1 form complexes in yeast and in planta through a direct 116 117 interaction. To assess the potential role of the RLP44-BRI1 signalling modules we sought to identify the tissues in which it might be active. As BRI1 is ubiquitously expressed, we thus 118 investigated the expression pattern of RLP44. 119

#### 120 RLP44 is expressed in the developing root vasculature

To study the function of RLP44, we generated transgenic plants expressing a translational 121 GFP fusion of RLP44 under control of the RLP44 promoter (pRLP44:RLP44-GFP). These 122 123 plants displayed elongated, narrow leaf blades and elongated petioles, reminiscent of BRI1 overexpressing plants (Fig. 2A and B) (37), and as previously observed with RLP44 124 overexpression (34). We crossed a *pRLP44:RLP44-GFP* line with the *RLP44* loss-of-function 125 mutant rlp44<sup>cnu2</sup> derived from comfortably numb 2 (34), which resulted in plants with a wildtype-126 like appearance (Fig. 1C), demonstrating that the fusion protein is functional, and confirming 127 that the additional transgenic RLP44 expression was causative for the observed 128 morphological effects (Fig. S2A). In the root apical meristem of pRLP44:RLP44-GFP and 129 pRLP44:RLP44-GFP (rlp44<sup>cnu2</sup>), fluorescence was present in most tissues, but markedly 130 enriched in epidermis and lateral root cap (Fig. 2D-F and Fig. S2B-E); slightly enhanced 131 expression was also observed in xylem precursor cells (Fig. S2B). A strong increase of GFP 132 fluorescence in the stele was observed towards the more mature part of the root (Fig. 2D-G 133 and Fig. S2B-D), in accordance with previously published transcriptome data (38) and  $\beta$ -134 glucuronidase reporter activity under control of the RLP44 promoter (Fig. S2F, G). In the 135 differentiating part of the root stele, RLP44-GFP fluorescence was relatively weak in the 136 phloem, intermediate in xylem, and highest in the undifferentiated procambial cells (Fig. 1H, I, 137 and Fig. S1C and D, compare Fig. 3A for vascular anatomy). 138

# RLP44 controls xylem cell fate in a BRI1-dependent manner, but independently of BR signalling outputs

The prevalence of *pRLP44:RLP44-GFP* fluorescence in the stele prompted us to study the 141 role of RLP44 in vascular development. To this end, we visualized lignified secondary cell 142 walls in rlp44 loss-of-function mutants through basic fuchsin staining and observed 143 supernumerary metaxylem-like cells, frequently outside the primary xylem axis in the position 144 of the procambium (Fig. 3A and B), a phenomenon we never observed in wildtype roots. 145 Quantification of metaxylem cells in seedling roots of both *rlp44<sup>cnu2</sup>* and the T-DNA insertion 146 line rlp44-3 six days after germination (dag) showed a significant increase (Fig. 3C). 147 148 suggesting that RLP44 controls xylem cell fate. Expression of RLP44 under control of its own

149 promoter complemented this phenotype (Fig. S3). Since we had previously identified RLP44 as an activator of BR signalling, we also included *bri1<sup>cnu1</sup>*, a hypomorphic *bri1* allele (39) in the 150 analysis. Surprisingly, primary root xylem number in bri1<sup>cnu1</sup> was indistinguishable from 151 wildtype, suggesting that the ectopic xylem in *rlp44* mutants might be unrelated to the outputs 152 153 of BR signalling. We therefore analysed the root xylem of a number of BR-related mutants 154 spanning a broad range of growth phenotypes. Hypomorphic bri1 mutants such as bri1-301 (19) and bri1-5 (40), the more severe signalling mutant bin2-1 (19), and the BR-deficient 155 biosynthetic mutant constitutive photomorphogenic dwarf (cpd) (41) did not show a 156 pronounced increase in xylem cell number (Fig. 3D). In sharp contrast, bri1 null alleles such 157 158 as a previously characterized T-DNA mutant (termed bri1-null) (42) and the bri1 brl1 brl3 triple mutant (called bri triple from hereon) (43) displayed a marked increase in the number of 159 160 differentiated xylem cells (Fig. 3D), whereas expression of BRI1 under the control of its own promoter in *bri1-null* resulted in wildtype-like xylem (Figure 3E). Taken together, our results 161 162 show that the xylem differentiation phenotype does not correlate with the severity of BR deficiency-related growth phenotypes (Fig. 3F). This is best exemplified by the comparison 163 between the cpd and bri1 null mutants, with cpd displaying wildtype-like or even slightly 164 decreased xylem cell numbers, despite exhibiting a *bri1-null*-like growth phenotype. Thus, the 165 166 control of xylem cell number, is largely independent of BR signalling outputs, but requires the presence of both BRI1 and RLP44. Interestingly, the expression of RLP44 was reduced in the 167 bri1-null mutant but not in bri1 hypomorphs or cpd, suggesting that reduced RLP44 levels 168 could partially explain the xylem phenotype of bri1-null (Fig. S4A, B). Consistent with this, 169 170 uncoupling RLP44 transcription from BRI1 control through the 35S promoter could alleviate 171 the bri1-null xylem phenotype (Fig. S4C), suggesting that BRI1 and RLP44 indeed act in the same pathway regulating xylem cell fate. In contrast, overexpression of RLP44 had no effect 172 on growth BL-insensitivity of bri1-null (Fig. S5). Taken together, our findings demonstrate that 173 174 the phenotype of bri1 loss-of-function mutants is partially independent from BR signalling 175 outputs and suggest that RLP44 exerts its function downstream of BRI1 through other, yet 176 unidentified signalling components.

177 It has been previously reported that root vascular development is responsive to environmental 178 conditions (7). We compared xylem cell numbers of plants grown on standard medium (0.9% 179 agar) and those that experienced increased mechanical force by growth on reclined hard agar 180 plates (2% agar) (44). Interestingly, the number of xylem cells in the wildtype increased 181 substantially under those conditions, whereas it did not further increase in *rlp44-3* (Fig. S6).

# Vascular cell fate determination by RLP44 and BRI1 is independent of BR signalling mediated control of cell proliferation

We next asked whether the increase in xylem cell number observed in the rlp44 mutant is 184 reflected in enhanced cell proliferation in the root and therefore quantified vascular cell number 185 of the seedling roots 6 dag. In rlp44-3, vascular cell number was indistinguishable from 186 wildtype in the differentiation zone, suggesting normal cell proliferation in the root meristem 187 (Fig. 4A). The *bri1<sup>cnu1</sup>* mutant, which did not display ectopic xylem cells, showed a significant 188 189 increase in total vascular cell number (Fig. 4A), consistent with the recently described role of BR signalling in controlling formative cell divisions (45). These results suggest that increased 190 191 xylem and increased proliferation in the vasculature are independent phenomena, and confirm a role for BR signalling in controlling formative cell divisions in the root meristem (Fig. 4A). In 192 line with this, depletion of BRs in wildtype roots by application of the BR biosynthesis inhibitor 193 194 PPZ (46) resulted in pronounced increase of vascular cell number (Fig. 4B, C). When PPZtreated roots were supplemented with a low dose (0.5 nM) of BL, both root growth and vascular 195 196 cell number were fully recovered (Fig. 4B, C). A higher-than-optimal dose of BL (5 nM) suppressed root growth and led to a strongly decreased vascular cell number (Fig. 4C). The 197 198 rlp44<sup>cnu2</sup> mutant displayed a wildtype-like response to the manipulation of BR levels in terms

of cell number (Fig. 4C), further supporting the independence of the xylem cell fate phenotypefrom the BR-signalling mediated control of cell proliferation (45).

#### 201 RLP44 controls xylem cell fate by promoting phytosulfokine signalling

202 The results described so far suggested that the maintenance of procambial cell identity in the root requires the presence of both BRI1 and RLP44. In addition, RLP44 seems to act 203 204 downstream of BRI1 in controlling vascular cell fate. As it could be ruled out that RLP44 exerts 205 its effect on xylem differentiation through BR signalling, we reasoned that in the absence of a kinase domain. RLP44 is required to interact with and influence the activity of another 206 signalling component which, in turn, controls xylem cell fate. Interestingly, besides BRI1 and 207 its close homologues BRL1, BRL2, and BRL3, the LRR X clade of RLKs harbours the 208 209 receptors for the peptide growth factor PSK, PSKR1 and 2 (16). As PSK signalling has also 210 been implicated in promoting the trans-differentiation of Zinnia elegans mesophyll cells into tracheary elements (31, 47) and depends on functional BR signalling (29), we tested the 211 association of RLP44 with PSKR1. Co-immunoprecipitation experiments in N. benthamiana 212 213 showed that *PSKR1-GFP* (33) was present in RLP44-RFP immunoprecipitates (Fig. 5A). In addition, FRET-FLIM analysis showed a pronounced reduction in fluorescence lifetime when 214 PSKR1-GFP was co-expressed with RLP44-RFP, suggesting a direct interaction (Fig. 5B) that 215 216 was not affected by exogenous application of PSK (Fig. S7A and B). Moreover, exogenous application of PSK peptide reverted *rlp44* xylem back to the stereotypical wildtype pattern of 217 mostly two protoxylem and three metaxylem cells in one axis (Fig. 5C). Further supporting a 218 219 role of PSK signalling in the control of xylem cell fate, the pskr1-3 pskr2-1 double mutant (48) showed an increased number of xylem cells reminiscent of the rlp44 mutant (Fig. 6D and E). 220 A similar phenotype was observed in the double mutant of *pskr1-3* and the related RLK *psy1r1*, 221 as well as in the tpst-1 mutant, impaired in the biosynthesis of PSK and other sulfated peptides 222 (Fig. 5D and E) (28, 49). We then asked how RLP44 might promote PSK signalling. As RLP44 223 is a direct interaction partner of both PSKR1 and its co-receptor BAK1, we assessed whether 224 presence of RLP44 could increase association of receptor and co-receptor. Indeed, more 225 226 BAK1 was detected in immunoprecipitates of PSKR1-GFP expressed in *N. benthamiana* when 227 RLP44-RFP was co-expressed (Fig. 5F), suggesting that RLP44 might act as a scaffold in the complex. Supporting these results, BAK1 levels in immunoprecipitates of PSKR1-GFP were 228 reduced in the *rlp44<sup>cnu2</sup>* mutant (Fig. 5G). Notably, presence of PSKR1-GFP had a negative 229 effect on the amount of RLP44 in immunoprecipitates of BRI1-RFP (Fig. S7C), suggesting that 230 231 the two pathways might compete for RLP44. Taken together, our data suggest that RLP44 interacts with, and stabilizes a complex between, PSKR1 and BAK1 to promote PSK 232 233 signalling, which, in turn, suppresses the progression from procambial to xylem identity (Fig. 234 5H).

### 235 **Discussion**

#### 236 RLP44 controls vascular cell fate in a BRI1-dependent manner

Cell fate determination in plants mainly relies on positional information provided by perception 237 of hormone gradients and non-cell autonomous factors (50-52). The expanded family of plant 238 RLK proteins and their ligands play central roles in intercellular communication, cell identity 239 240 maintenance, and the regulation of cell expansion and proliferation (53). Currently, our view of these pathways is evolving to appreciate the extensive cross-talk and interdependence of 241 diverse signalling pathways (54). The response to BRs, mediated by what is probably the best-242 243 characterized plant signalling cascade (11), is found to be integrated with a growing number of other pathways at two cross-talk "hot spots", namely the GSK3-like kinase BIN2 (55-57) 244 and the BR-responsive transcription factors BZR1 and BES1 (58-61). Here, we report that BR 245 and PSK signalling are coupled at the level of the plasma membrane receptors through RLP44 246 247 and that this signalling module is required to control xylem cell fate. Our genetic and

248 biochemical analyses support a scenario where PSK signalling strength is quantitatively controlled by RLP44, which itself is dependent on the presence of BRI1. While we do not rule 249 out post-translational control of RLP44 by BRI1, for example through phosphorylation of the 250 cytoplasmic domain or because the presence of BRI1 is required for correct receptor complex 251 252 assembly, this dependency is at least partially based on transcriptional regulation. The bri1-253 null loss-of-function mutant, but not hypomorphs or the BR biosynthetic mutant cpd, showed reduced RLP44 expression. Consistent with this, uncoupling RLP44 from its native 254 transcriptional regulation by constitutive expression could rescue the bri1-null xylem 255 phenotype. Conversely, the novel bri1 loss-of-function phenotype of ectopic xylem in 256 257 procambial position is unrelated to BR-signalling. In line with this, only limited overlap of differentially expressed genes in *bri1-116* and the morphologically similar BR biosynthetic 258 259 mutant dwf4 was observed, potentially indicating additional brassinosteroid-independent 260 functions of BRI1 (21).

261 More work will be needed to mechanistically understand the interaction between RLP44 and RLKs. External application of PSK (this study) or BR (34) ligands had no influence on the 262 association between RLP44 and PSKR1 or BRI1, respectively, in line with ligand-263 independence of many, but not all, RLP-RLK interactions (62, 63). BRI1 and PSKR1/2 belong 264 265 to the LRR X subfamily of LRR-RLKs (16) and share the requirement for interaction with SERK co-receptors to form an active, heteromeric signalling complex (32, 33, 64). With the exception 266 267 of the ligand binding domain, the SERK-bound BRI1 and PSKR1 complex structures are very similar (32, 64), therefore it is conceivable that RLP44 binds both receptors through the same 268 269 mechanism. These results are in line with the emerging theme of dynamic, promiscuous, and 270 flexible interactions of plasma membrane proteins to integrate signalling information and finetune cellular responses to external cues (65-67). Interestingly, the mechanism by which RLPs 271 influence signalling seems to differ widely, ranging from direct participation in ligand binding 272 273 (62, 68), to the control of signalling specificity through blocking access of RLK ligands (68), to 274 the guarding of extracellular proteins targeted by pathogens (69). Here, we propose a scaffolding function of RLP44 for the interaction between PSKR1 and its co-receptor BAK1, 275 276 expanding the mechanistic diversity of RLPs. We have previously reported that RLP44 is 277 involved in the response to cell wall state; along those lines, it will be interesting to see whether cues from the cell wall are able to influence the balance between the two known roles of 278 279 RLP44 by shifting its interaction with BRI1 or PSKR1.

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# 281 **PSK signalling likely promotes procambial identity**

282 Alongside classical plant hormones, signalling peptides have been revealed to play major roles in plant development and stress responses (70, 71). The sulfated pentapeptide PSK has 283 been implicated in a number of diverse processes (24, 71). Here, we propose that PSK 284 signalling controls xylem cell fate through promoting the maintenance of procambial identity. 285 A number of observations support this hypothesis. First, PSK treatment rescued the ectopic 286 xylem phenotype in *rlp44* mutants. Second, PSK-related mutants showed increased xylem 287 differentiation in procambial position and PSK genes are co-expressed with RLP44 in 288 289 procambial cells (Fig. S7D)(38). Third, PSK expression is transiently increased prior to the acquisition of a procambial intermediate state by cells trans-differentiating into tracheary 290 elements (31, 72), which could explain why PSK promotes tracheary element formation in Z. 291 elegans only when applied early to the cell culture (31, 47). Finally, PSK signalling promotes 292 293 callus growth and longevity, in line with a role in the maintenance of cell identity (27). Accordingly, it has been proposed that PSK signalling maintains the responsiveness to 294 intrinsic and extrinsic cues to tune proliferation or differentiation (27). However, it is unclear 295 296 how PSK signalling affects cellular behaviour, in part due to a lack of knowledge about potential downstream targets. It will be interesting to see how the BRI1-RLP44-PSK signalling 297

298 module described here integrates with the fundamental patterning processes and the gene 299 regulatory networks controlling xylem differentiation (2, 7).

#### 300 The role of BR signalling in vascular development

301 It has long been described that BR signalling plays an important role in the development of vascular tissue (13, 14). In addition, it has been reported that BR signalling is kept at low levels 302 in procambial cells of leaf and hypocotyl to prevent their differentiation into xylem cells (57). 303 304 Our results suggest that in the primary xylem of the root, BR signalling only plays a minor role in controlling differentiation, in marked contrast to the strong patterning defects of BR 305 signalling and biosynthetic mutants in the shoot (14). Conversely, at least in the root, presence 306 of BRI1 has a negative effect on xylem cell fate through RLP44 and PSK signalling-mediated 307 308 maintenance of procambial identity. Therefore, our results identify a novel role of BRI1 in root 309 development which is independent of its role as BR receptor.

310

# 311 Materials and Methods

312 Details of materials and methods are provided in the Supplemental Information file. Mutants

- and transgenic lines used in this study are listed in Table S1.
- 314

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# 499 Figure Legends

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Fig. 2. RLP44 is expressed in the root vascular tissue. (A-C) Effect of expressing RLP44 as a 508 translational fusion to GFP under control of its native 5' regulatory sequence (pRLP44:RLP44-509 510 GFP). (A) Col-0. (B) pRLP44:RLP44-GFP in wildtype background shows a growth phenotype reminiscent of enhanced BR signalling. (C) Mutation of endogenous RLP44 in 511 pRLP44:RLP44-GFP (rlp44<sup>cnu2</sup>) reconstitutes wildtype-like phenotype. (D-F) pRLP44:RLP44-512 GFP expression (D) in root meristem counterstained with propidium iodide (E) and merged 513 (F). e = epidermis, c = cortex, st = stele, en = endodermis. Scale bars = 100 µm. (G) Projection 514 515 of a confocal stack through the differentiation zone of a pRLP44:RLP44-GFP root showing fluorescence predominantly in the stele. (H and I) Optical section through the stele of a 516 pRLP44:RLP44-GFP expressing root in the differentiation zone (H), counterstained with 517 518 propidium iodide (I) indicating differentiated phloem (ph) and protoxylem (p) as well as yet undifferentiated metaxylem (m). Scale bar =  $10 \mu m$ . 519

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521 Fig. 3. RLP44 and BRI1 are required for the control of xylem cell fate. (A) Overview over xylem differentiation in the Arabidopsis root and schematic representation of the stele. Arrow marks 522 point of xylem observation. (B) Basic fuchsin staining of 6 day old Arabidopsis root. DIC image 523 524 shows secondary cell wall thickenings of protoxylem and metaxylem (left panel), basic fuchsin labels lignified secondary cell walls (middle panel). Confocal stacks allow xylem number 525 quantification of the indicated genotypes in orthogonal view (right panel). Note ectopic 526 527 metaxylem in procambial position (arrows). Left panel is a median plane image, middle panel is a maximum projection of a confocal stack. (C and D) Frequency of roots with the indicated 528 529 number of metaxylem cells in rlp44 and bri1 mutants (C) and BR-related mutants (D) after basic fuchsin staining as in (B). Right panel in (D) shows orthogonal view and maximum 530 projection of a confocal stack obtained with fuchsin stained bri triple mutant. Note metaxylem 531 532 in procambial position (arrows) and disrupted protoxylem (arrowhead). Asterisks indicate statistically significant difference from Col-0 based on Dunn's post-hoc test with Benjamini-533 Hochberg correction after Kruskal-Wallis modified U-test (\*p < 0.05; \*\*\*p < 0.001). (E) 534 535 Transgenic expression of BRI1 under control of its own regulatory 5' sequence rescues the ectopic xylem phenotype of bri1-null. (F) Overview over ectopic xylem phenotypes of rlp44 536 537 and BR-related mutants. Note the absence of correlation between severity of BR signalling 538 deficiency (x-axis) and frequency of ectopic xylem phenotype (y-axis). Based on (C) and (D). 539

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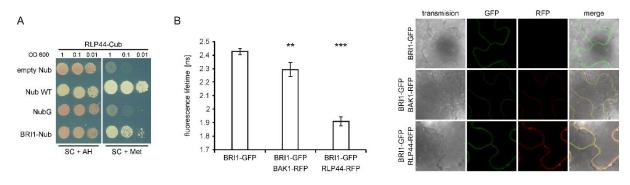
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554 Fig. 5. RLP44 interacts with PSKR1 to promote PSK signalling and procambial identity. (A) Co-immunoprecipitation after transient expression in *Nicotiana benthamiana* leaves 555 demonstrates presence of RLP44-RFP in PSKR1-GFP immunoprecipitates, in contrast to 556 immunoprecipitates of the Lti6b-GFP control. (B) FRET-FLIM analysis of the PSKR1-557 558 GFP/RLP44-RFP interaction in Nicotiana benthamiana leaves. Bars denote average of 9 measurements ± SD. Asterisks indicate statistically significant difference from PSKR1-GFP 559 according to pairwise t-test (\*\*\*p < 0.001). (C) Application of PSK peptide rescues the ectopic xylem phenotype of *rlp44<sup>cnu2</sup>*. Asterisks indicate statistically significant difference according to 560 561 562 Mann-Whitney U-test (\*p < 0.05). (D and E) Quantification of metaxylem (D) and total xylem (E) cell number in Col-0 and PSK signalling-related mutants. Asterisks indicate statistically 563 significant difference from Col-0 based on Dunn's post-hoc test with Benjamini-Hochberg 564 correction after Kruskal-Wallis modified U-test (\*p < 0.05). (F) Co-immunoprecipitation 565 566 analysis after transient expression in Nicotiana benthamiana leaves demonstrates increased amount of BAK1-HA in PSKR1-GFP immunoprecipitates in the presence of RLP44-RFP. 567 568 RLP44 levels were adjusted through increasing the density of Agrobacteria (denoted by + or ++). (G) BAK1-HA is decreased in immunoprecipitates of PSKR1-GFP in the rlp44<sup>cnu2</sup> 569 background. (H) Model of RLP44-mediated integration of PSK and BR signalling. 570 571

### 572 Figures



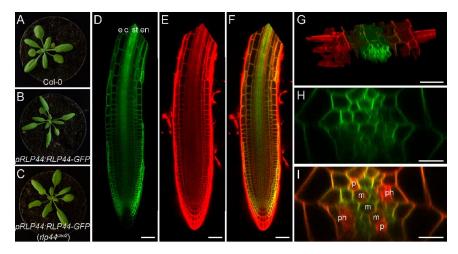
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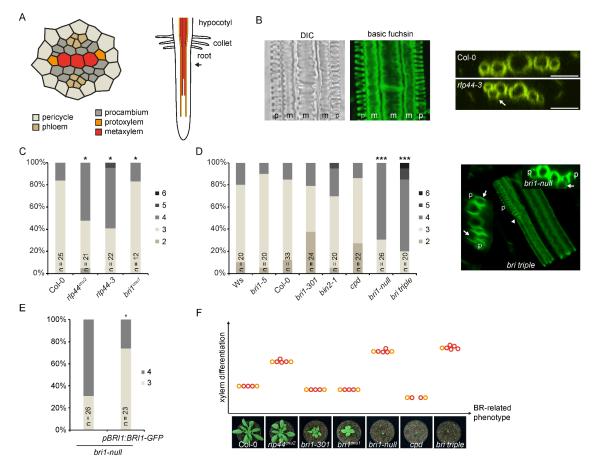


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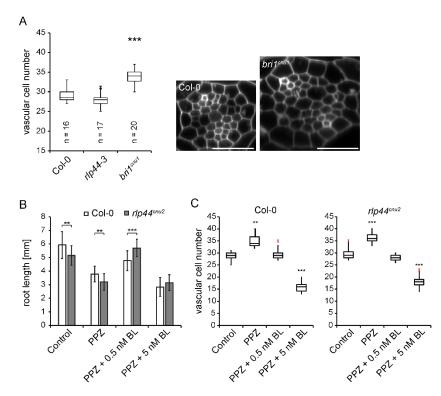
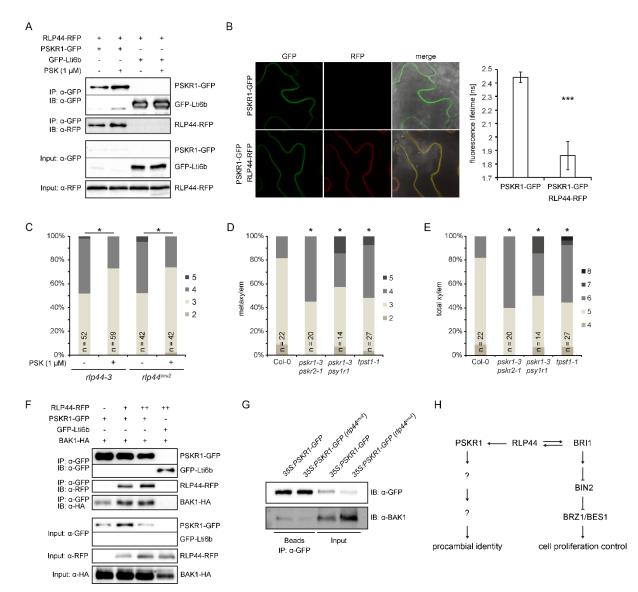




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