1	Cortical microtubule remodelling during strigolactone- and light-mediated
2	growth inhibition of Arabidopsis hypocotyls
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4	Running title: Strigolactones and light regulate plant microtubules
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28 Highlight

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- 30 Strigolactones regulate organization and dynamics of cortical microtubules in hypocotyl cells,
- 31 which contributes to the light-mediated inhibition of hypocotyl growth in Arabidopsis seedlings.

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34 Abstract

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36 Strigolactones are phytohormones involved in shoot branching and hypocotyl elongation. The latter phenomenon was addressed herein by the exogenous application of a synthetic 37 strigolactone GR24 and an inhibitor of strigolactone biosynthesis TIS108 on hypocotyls of wild 38 type Arabidopsis and a strigolactone signalling mutant max2-1 (more axillary growth 2-1). 39 40 Owing to the interdependence between light and strigolactone signalling, the present work was extended to seedling cultivation under a standard light/dark regime, or under continuous 41 darkness. Given the essential role of the cortical microtubules in cell elongation, their 42 organization and dynamics were characterized under the conditions of altered strigolactone 43 signalling using fluorescence microscopy methods with different spatiotemporal capacities such 44 as confocal laser scanning microscopy and structured illumination microscopy. It was found that 45 the strigolactone-dependent inhibition of hypocotyl elongation correlated with changes in 46 47 cortical microtubule organization and dynamics, visualized in living wild type and max2-1 seedlings stably expressing genetically-encoded fluorescent molecular markers for microtubules. 48 49 Quantitative analysis of microscopic datasets revealed that chemical and/or genetic manipulation 50 of strigolactone signalling affected microtubule remodelling, especially under light conditions. The application of GR24 and TIS108 in dark conditions partially alleviated cytoskeletal 51 52 rearrangement, suggesting a new mechanistic connection between the cytoskeletal behaviour and 53 the light-dependence of strigolactone signalling.

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55 **Key words:** cortical microtubules, GR24, kymographs, *max2-1* mutant, light, microtubule 56 organization, microtubule dynamics, strigolactone, structured illumination microscopy, TIS108

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- 58

Abbreviations: BZR1 - BRASSINAZOLE-RESISTANT 1; CLSM - confocal laser scanning 59 confocal microscopy; COP1 - CONSTITUTIVE PHOTOMORPHOGENIC 1; CRY1/2 -60 61 CRYPTOCHROMES 1 and 2; CUL - CULLIN; DDB1 - DAMAGE-BINDING PROTEIN 1; MAX2 - MORE AXILLARY GROWTH2; MBD - MT-binding domain of mammalian non-62 neuronal MICROTUBULE ASSOCIATED PROTEIN4; MDP40 - MICROTUBULE 63 DESTABILIZING PROTEIN40; MS - Murashige and Skoog; MT - microtubules; PHYA/B -64 65 PHYTOCHROME A and B; RBX1 – RING-BOX1; SCF complex – SKP1-CULLIN-F-BOX complex; SIM – structured illumination microscopy; Skp1 – S-phase kinase-associated protein 1; 66 SL - strigolactone(s); SMLX - SUPPRESSOR OF MORE AXILLARY GROWTH2-LIKE; 67 TUA6 – α-TUBULIN 6; WDL3 – WAVE-DAMPENED 2-LIKE 3. 68 69

71 Introduction

Strigolactones (SL), the carotenoid-derived plant hormones and rhizosphere signaling 72 73 molecules, were discovered in exogenous allelochemical responses as germination stimulants of Orobanchaceae root parasitic weed (Striga, Orobanche, Phelipanche, and Alectra spp.) (Cook et 74 75 al., 1966; Gomez-Roldan et al., 2008; Koltai, 2014). SL induce hyphal branching of arbuscular mycorrhizal fungi (Akiyama et al., 2005), promote nodulation in the legume-rhizobium 76 77 symbiosis (Soto et al., 2009), and enhance plant resistance to drought, salt and osmotic stresses, and to low soil phosphate and nitrate content (Yoneyama et al., 2007; Foo et al., 2013; Ha et al., 78 79 2014). The physiological effects of SL on the aboveground plant part include the regression of plant height and hypocotyl length (Stirnberg et al., 2002; de Saint Germain et al., 2013), 80 regulation of shoot branching by modulating auxin transport (Kapulnik et al., 2011; Shinohara et 81 al., 2013), increased expansion of cotyledons in etiolated Arabidopsis seedlings (Stirnberg et al., 82 2002; Tsuchiya et al., 2010), suppression of the preformed axillary bud outgrowths (Gomez-83 Roldan et al., 2008; Umehara et al., 2008; Domagalska and Leyser, 2011), rescue of the dark-84 induced elongation of rice mesocotyls (Hu et al., 2010), promotion of the secondary growth and 85 86 cell divisions in cambium, and stimulation of leaf senescence (Agusti et al., 2011; Koren et al., 2013; Koltai, 2014). Furthermore, synthetic SL GR24 acts synergistically with auxins and it is 87 used in potato tuber formation, the outgrowth of the axillary stolon buds, and above-ground 88 shoot branching (Roumeliotis et al., 2012). Not only parasitic plant seeds undergo enhanced 89 90 maturation in SL presence, but also Arabidopsis seeds germinate faster (Tsuchiya et al., 2010).

SL are perceived by the α/β-hydrolase receptor DWARF14 (Seto *et al.*, 2019) via a
specific receptor system, while subsequent signalling requires the SKP1-CULLIN-F-BOX (SCF)
complex and proteasome-mediated degradation of target proteins (reviewed by Kumar *et al.*,
2015a; Yoneyama *et al.*, 2020). At physiological and molecular levels, SL have been suggested
to affect auxin efflux (Koltai, 2014) through PIN1 efflux carrier in the root (Ruyter-Spira *et al.*,
2011) but also to dampen auxin transport in the shoot (Domagalska and Leyser, 2011).

Plant cytoskeleton is involved in many processes regulated by SL, e.g. the switch from
the cell division to expansion (Ruan and Wasteneys, 2014), the cell elongation and
differentiation (Ivakov and Persson, 2013; Ambrose and Wasteneys, 2014; Sampathkumar *et al.*,
2014), as well as in plant responses to salt (Shoji *et al.*, 2006) and osmotic stresses (Komis *et al.*,
2002; Wang *et al.*, 2010).

102 It is presumed that SL, as a new class of phytohormones, indirectly regulate cytoskeleton 103 organization together with well-studied phytohormones such as auxins, cytokinins, giberellins 104 and abscisic acid. Through the indirect regulation of microtubules (MT) and actin filaments, SL should orchestrate morphogenesis of both above- and underground plant parts (Blume et al., 105 106 2017). Previously, it was reported that SL affect architecture and dynamics of actin filaments in Arabidopsis root cells (Pandya-Kumar et al., 2014). GR24 reduces F-actin filament bundling in a 107 108 MORE AXILLARY GROWTH2 (MAX2)-dependent manner and, at the same time, enhances 109 actin dynamics, affects endosome trafficking and PIN2 localization in the plasma membrane 110 (Pandya-Kumar et al., 2014). Moreover, plant response to low phosphorus conditions involves MAX2-dependent reduction of PIN2 and endosome trafficking, plasma membrane polarization, 111 112 and increased actin filament bundling in epidermal root cells (Kumar et al., 2015b). Concerning MT, the other fundamental cytoskeletal component, SL analogues MEB55 and ST362 were 113 found to compromise the integrity of the MT network in animal cells (Mayzlish-Gati et al., 114 2015). Moreover, SL analogues also affect the MT regulation by activating apoptotic p38 115 (mitogen-activated protein kinase) cascade and inhibiting cyclin B expression (Pollock et al., 116 2014). 117

However, there are no reports on the effects of SL on plant MT so far. This study shows 118 effects of exogenously applied synthetic SL GR24 and inhibitor of SL biosynthesis TIS108 on 119 120 the organization and dynamics of cortical MT in epidermal cells of light-exposed and etiolated 121 hypocotyls of wild type plants and SL-insensitive Arabidopsis mutant max2-1. Our results suggest that strigolactones affect mainly MT cytoskeleton under light conditions and this effect 122 123 can be alleviated by darkness. From the methodological point of view, we have used combination of confocal laser scanning confocal microscopy (CLSM) and super-resolution 124 125 structured illumination microscopy (SIM) to obtain these results.

- 126
- 127 Materials and methods
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129 *Plant material and growth conditions*

Wild-type *Arabidopsis thaliana* plants ecotype Columbia-0 (Col-0), and the SLinsensitive *A. thaliana max2-1* mutant (EMS mutant in Col-0-background; Stirnberg *et al.*, 2002)
kindly provided by Prof. H. Koltai, were used in this study. MT dynamics were recorded in

133 seedlings stably expressing a 35S::GFP-MBD (MT-binding domain of mammalian non-neuronal 134 MICROTUBULE ASSOCIATED PROTEIN4), or a 35S::TUA6-GFP construct (α -TUBULIN 6) 135 (Marc *et al.*, 1998; Shaw *et al.*, 2003). Mutant plants of *max2-1* were crossed with lines carrying 136 35S::GFP-MBD or 35S::TUA6-GFP constructs. For microscopy studies the F3 generation of the 137 progenies was used. Homozygous *max2-1* seedlings expressing the above MT markers were 138 selected according to fluorescence detection under epifluorescence microscope.

Prior to germination, seeds were sterilized in 1% v/v sodium hypochlorite solution supplemented with 0.1% v/v Tween-20 for 10 min, short-spin vortexed, immersed to 70% v/v ethanol for 5 s, thoroughly rinsed 5 times by MilliQ water and placed to 0.6% w/v agarosesolidified ½ Murashige and Skoog medium (½ MS; Duchefa, the Netherlands) with 10% w/v sucrose with or without exogenous synthetic SL and/or inhibitors of endogenous SL biosynthesis.

145

146 *Chemical treatment*

147 Unless stated otherwise, all common chemicals were from Sigma-Aldrich (the USA) and 148 were of analytical grade. A synthetic specific SL cis-GR24 consisting only of D14-perceived 149 GR24+ was synthesized according to Zwanenburg et al., 2013 was dissolved ex tempore in pure 150 anhydrous acetone to prepare a 10 mM stock solution from which working concentrations of 3 151 and 25 µM were prepared. Four-day-old seedlings were taken from 0.6% w/v agarose-solidified 152 media, treated with GR24 and prepared for microscopy. A triazole-type SL biosynthesis inhibitor designated as TIS108 (Chiralix, the Netherlands) was dissolved in pure anhydrous acetone prior 153 154 to use to obtain 10 mM stock solution further diluted to 3 μ M final concentration and added to agarose-solidified ¹/₂ MS medium or used for short-time treatment in liquid MS. Petri dishes with 155 156 seeds were stored at 4°C for 1 day to synchronize germination and then germinated at a vertical position in Phytotron at 22°C under long-day conditions (16 h light/8 h darkness, photosynthetic 157 photon flux (PPF): 150 μ mol m⁻² s⁻¹) for 4 or 7 days prior to imaging. For the etiolation 158 experiment, Petri dishes were wrapped in aluminum foil after seeding, stratified at 4°C for 2–4 159 160 days, and germinated as such under the same environmental conditions.

161

162 Hypocotyl growth analysis

Petri dishes with 3-7 day old seedlings were placed in scanner (Image Scanner III, Seiko Epson, Japan) and scanned at transmitted light mode in order to document and subsequently quantify hypocotyl length. For hypocotyl width measurements, seedlings were documented with differential interference contrast of a widefield microscope (Axio Imager M2, Carl Zeiss, Germany) equipped with a polarizer and a Wollaston prism at three distinct parts of the hypocotyl: the upper part – situated right beneath the cotyledon petiole; the middle part – at the mid-plane of hypocotyl, and the lower part– at the border with the primary root.

For the detailed morphological studies 4- and 7-days old seedlings were captured using Axio Zoom.V16 Stereo Zoom system (Carl Zeiss, Germany) in bright field illumination (objective lenses PlanApo Z 1.5x, FWD = 30mm). The measurements were done using the default Measure application of ImageJ (Schneider et al. 2012) by tracking hypocotyls with the segmented line tool after appropriate scale calibration using the Set Scale tool of the Analyze menu.

176

177 Microscopy

For live imaging of MTs four different Zeiss microscopy platforms (Zeiss Microscopy, 178 Germany) were used (Komis et al., 2014; 2015). For deciphering MT organization, GFP-MBD 179 or TUA6-GFP molecular markers were visualized by means of CLSM with the LSM710 system 180 181 (Carl Zeiss, Germany) equipped with a $63 \times$ Plan-Apochromat oil-immersion objective (1.4 NA) 182 under excitation 488/543 nm, emission 510/540 nm. Laser excitation intensity did not exceed 2% of the laser intensity range available. Range of the Z-stack was always set up to 0.61 µm. GFP-183 labelled MT were imaged using excitation laser line 488 nm and emission spectrum 493-630 nm 184 for GFP fluorescence detection and with excitation laser line 405 nm and emission spectrum 185 186 410-495 nm for DAPI fluorescence detection.

Microscopy platform enabling SIM (ELYRA PS.1, Carl Zeiss, Germany) with $63 \times$ Plan-Apochromat oil-immersion objective was used for the time-lapse observations of MT dynamics. 4-days old seedlings were mounted between a microscope slide and a coverslip in 30 µL of liquid MS medium spaced by double-sided sticky tape, narrow Parafilm stripes and extra sealed using liquid petroleum jelly (nail polish) to form a chamber prior to imaging for sample stabilization. This prevented dislocation of the plantlets during liquid exchange and allowed the observation of the same area during 2 h. Seedlings were grown at solidified GR24/TIS108containing media for 4 d.

All preparations with the etiolated seedlings were done quickly in dark room using dim red or green light to prevent disturbances of MT by visible light.

197

198 *Post-acquisition image processing*

Raw SIM images were processed automatically by the respective add-on of the licensed Zen software (Black version; Carl Zeiss, Germany) coupled to the Elyra PS.1, according to standards thoroughly described before (Komis et al., 2014; 2015).

Kymographs of MT time series recordings were generated using the Kymograph add-on of the licensed Zen software (Blue version; Carl Zeiss, Germany), using the arrow tool to delineate individual or bundled MT of interest.

205

206 *Quantitative analysis of microtubule organization*

207 MT organization was quantitatively addressed by assessing the extend of MT bundling as the skewness of fluorescence distribution of GFP-MBD expressing cells. Skewness was 208 extrapolated from values provided by the Histogram add-on of licensed Zen software (Blue 209 version). Additionally, cortical MT ordering was quantitatively assessed by measuring MT 210 211 organization anisotropy. This anisotropy was demonstrated in full frames of CSLM images of 212 hypocotyl cells expressing GFP-MBD, which were analyzed with Cytospectre freeware 213 (Kartasalo et al., 2015) to extrapolate their angular distribution in the cortical cytoplasm. 214 Quantitatively, the ordering of cortical MT was measured through the FibrilTool macro as described previously (Boudaoud et al., 2014). Briefly, the FibrilTool macro was applied on 215 216 regions of interests drawn using the Polygon tool of Image J delineating the circumference of fully visible cells. Care was taken, to avoid cell edges, where frequently the signal is saturated. 217 218 Theoretically the numerical result ranges between 0 (complete isotropy) to 1 (perfect 219 anisotropy).

220

221 *Quantitative analysis of microtubule dynamics*

222 Kymographs from recordings of dynamic MT were used to extrapolate the following 223 parameters of MT dynamics: growth and shrinkage rates, catastrophe and rescue frequencies. Kymograph analysis was done manually using the Image J angle measure tool after size calibration of kymographs. Angles were acquired in degrees and converted to radians in MS Excel (Microsoft, the USA) prior to calculations of tangential values. Briefly, the equations used were as follows:

For growth rate, the equation was: $G = \tan \varphi \times pixel size \times fps$; where \tan_{φ} is the tangential of the growth slope, pixel size is in μ m and fps is the frame rate of the acquisition (frames×sec⁻¹). The final output is converted to μ m×min⁻¹ by multiplying the original value with 60 sec×min⁻¹.

For shrinkage rate, the equation was: $S = \tan \theta \times pixel size \times fps$; \tan_{θ} is the tangential of the shrinkage slope, pixel size is in μ m and fps is the frame rate of the acquisition (frames×sec⁻¹). The final output is converted to μ m×min⁻¹ by multiplying the original value with 60 sec×min⁻¹.

For catastrophe frequency the following equation was applied:

237
$$f_{cat} = \frac{N_{cat}}{\Sigma t_{growth}},$$

where f_{cat} is the catastrophe frequency, N_{cat} is the total number of catastrophe events and Σt_{growth} is the total time spent in growth, regarding all the growth events taken into account.

For rescue frequency the following equation was applied:

241
$$f_{res} = \frac{N_{res}}{\Sigma t_{shrinkage}},$$

where f_{res} is the rescue frequency, N_{res} is the total number of rescue events and Σt_{growth} is the total time spent in shrinkage, regarding all the shrinkage events taken into account.

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245 Statistics

246 Statistical analysis of all datasets was performed in the software STATISTICA (version 13.4.0.14; Statsoft, the USA). All datasets were first subjected to Shapiro-Wilk W test and 247 248 Levene's tests to test the normality and homogeneity. Frequently, the datasets failed to pass these 249 tests. On several representative datasets, following tests were calculated: (i) one-way ANOVA, 250 (ii) Welch's ANOVA, (iii) Tukey's post hoc test corrected for unequal sample size, (iv) Scheffé's post hoc test, (v) Kruskal-Wallis test. Based on results of these preliminary analysis, and in 251 252 agreement with previous reports (Liu, 2015), Welch's ANOVA followed by Scheffé's test was used as it exhibited higher stringency compared to other tests. Statistical significance was 253

determined based on the calculated p-values, were for Welch's ANOVA the probability level was 0.05 and for Scheffé's test the probability level was 0.01. For comparing two different experimental conditions (light-dark and inhibitor treatment), two-way ANOVA followed by Scheffé's test was used. In this case, the probability level set for Scheffé's test was 0.001.

258

259 **Results**

260 Strigolactone treatment affects hypocotyl growth in Arabidopsis

Col-0 and max2-1 mutant seedlings were germinated and cultivated on medium 261 containing different concentrations of GR24 or TIS108, either in the standard light/dark regime 262 of the phytotron or in the dark. Under the light/dark regime, GR24 used at two different 263 264 concentrations (3 and 25 µM), stalled hypocotyl elongation and induced mild radial swelling as compared to mock-treated Col-0 (Fig. 1A,I cf. Fig. 1B,C,J,K). Growth inhibition of the 265 hypocotyl was also evident after treatment with the inhibitor TIS108 tested in two concentrations 266 267 (Fig. 1D,L). In quantitative terms, the hypocotyl length of mock treated Col-0 seedlings was 2.05±0.145 mm (mean±SD; Fig. 1Q; N=75; Supplementary Table S1). After treatment with 3 268 269 uM GR24, the hypocotyl length was significantly reduced to 1.28±0.158 mm (mean±SD; Fig. 270 1Q; p=0.0000; N=60), while after treatment with 25 µM the hypocotyl length comprised 271 1.307±0.178 (mean±SD; Fig. 1Q; N=56), which was significantly different compared to mocktreated Col-0, but not to the effect of 3 µM GR24 (p=0.0000 and p=0.9992, respectively). In 272 273 turn, TIS108 treatment resulted in the most severe hypocotyl growth inhibition measured to 0.783±0.160 mm (mean±SD; Fig. 1Q; N=61), being significantly different from all other 274 conditions tested (p=0.0000 as compared to treatment with 3 and 25 µM GR24). Hypocotyl 275 width was only slightly affected by any of the treatments used herein. Briefly the width of mock-276 treated Col-0 hypocotyls was 0.309±0.04 mm (Fig. 1R; N=58; Supplementary Table S2), 277 0.325±0.07 mm after treatment with 3 µM GR24 (Fig. 1R; N=89), 0.290±0.08 mm after 278 treatment with 25 µM GR24 (Fig. 1R; N=90) and 0.323±0.05 mm after treatment with 3 µM 279 280 TIS108.

Subsequently we characterized hypocotyl growth in light-exposed *max2-1* mutants. In such mock-treated mutants (Fig. 1E) as well as after the treatment with both 3 (Fig. 1F) and 25 μ M GR24 (Fig. 1G), the hypocotyl length was comparable to mock-treated Col-0 seedlings. The hypocotyl length of *max2-1* mutant seedlings was only responsive to treatment with 3 μ M 285 TIS108 (Fig. 1H). Meanwhile, hypocotyl width does not show any noticeable changes at any 286 treatment used (Fig. 1M–P). In quantitative terms, the hypocotyl length of mock-treated max2-1 mutants was 2.16±0.19 mm (mean±SD; N=78), 2.06±0.17 mm after 3 µM GR24 (mean±SD; 287 288 N=69), 1.98±0.17 mm after 25 µM GR24 (mean±SD; N=80), and 0.74±0.16 mm after 3 µM TIS108 (mean±SD; N=59) treatments. The hypocotyl length of *max2-1* mutants was significantly 289 290 different at all GR24 and TIS108 treatments as compared to the treated Col-0 seedlings (Fig. 10; p=0.185 after mock treatment, p=0.9999 after 3 µM GR24, p=0.2333 after 25 µM GR24, and 291 292 p=0.0000 after 3 μ M TIS108 treatments). Within the max2-1 population, GR24 treatments did not affect hypocotyl length (Fig. 1Q) and only treatment with 3 µM TIS108 brought about its 293 294 significant shortening (Fig. 1Q). In terms of hypocotyl width, no changes were discerned (Fig. 295 1R).

296

297 Strigolactone effects are modulated in dark-grown seedlings

There have been reports of a synergy between exogenous application of SL and the illumination conditions during seedling growth. Therefore, the experimental regime of the treatment of Col-0 and *max2-1* seedlings with two different concentrations of GR24 (3 and 25 μ M) and with 3 μ M TIS108 grown under persistent darkness was tested.

As expected, hypocotyl length elongation of etiolated seedlings exceeds that of light-302 grown seedlings (Fig. 2A). By combining visual documentation and quantitative analysis, it 303 304 became evident that etiolated seedlings were also responsive to treatments with 3 (Fig. 2B,I) and 305 $25 \,\mu\text{M}$ GR24 (Fig. 2C,I), but were the most sensitive to $3 \,\mu\text{M}$ TIS108 (Fig. 2D,I). The length of mock-treated etiolated Col-0 seedlings was 15.45±1.77 mm (mean±SE; N=78), 14.09±1.22 mm 306 307 after treatment with 3 µM GR24 (mean±SE; N=75), 11.23±1.54 mm after 25 µM GR24 308 (mean±SE; N=77), and 2.55±0.72 mm after 3 µM TIS108 (N=13). All the treatments caused significant reduction of the etiolated hypocotyl length as compared to the mock treatment (Fig. 309 310 2I; p=0.0000 for 3 µM GR24; p=0.0000 for 25 µM GR24; p=0.0000 for 3 µM TIS108; Supplementary Table S3). 311

The same line of experiments was applied in the case of *max2-1* mutants (Fig. 2E-H), which also proved to be prone to either the application of exogenous SL, or to the metabolic inhibition of SL biosynthesis. Compared to mock treated *max2-1* seedlings (Fig. 2E,I), which exhibited length of 15.95 ± 1.64 mm (mean \pm SD; N=23), those treated with 3 μ M GR24 (Fig. 2F,I) were 15.72±1.12 mm (mean±SD; N=30), those treated with 25 μ M GR24 (Fig. 2G,I) were 10.05±1.66 mm (mean±SD; N=22), while those treated with 3 μ M TIS108 (Fig. 2H,I) were 3.07±0.66 mm (mean±SD; N=19). The effect of most treatments on hypocotyl length of etiolated *max2-1* seedlings was deemed to be significant by comparison to the mock treatment except for 3 μ M GR24 (Fig. 2I; p=0.9998 for 3 μ M GR24; and p=0.0000 for both 25 μ M GR24 and 3 μ M TIS108).

Such preliminary deductions make the assessment of whether light plays a crucial role on 322 323 the modulation of SL effects. For this reason, we examined the extent of its effect on the percentage of hypocotyl reduction of either light- or dark-grown Col-0 or max2-1 mutant 324 325 seedlings by comparison to the mock treatment. Thus, under the light exposure combined with 3 326 µM GR24 treatment the reduced hypocotyl length was observed, comprising 63.33±9.68% in 327 Col-0 (Supplementary Fig. 1A) and 93.01±12.48% in etiolated seedlings (Supplementary Fig. 328 1B) as compared to mock-treated seedlings. Similarly, the treatment with 25 μ M GR24 caused 329 the reduction of hypocotyl length up to $64.35\% \pm 9.63\%$ of mock-treated seedlings under light exposure, but this reduction was less pronounced in dark (cf. 74.00%±13.69% of mock treated 330 331 seedlings). TIS108 treatment caused hypocotyl length reduction in light up to $38.55\% \pm 8.17\%$ of mock-treated seedlings, and even more pronounced reduction in the dark, since the treated 332 333 etiolated hypocotyls were $23.90\% \pm 4.61\%$ of the mock-treated counterparts.

Regarding the light-exposed *max2-1* mutant, hypocotyl length of seedlings treated with 3 μ M GR24 (Supplementary Fig. 1C) was 96.65%±11.09% of mock-treated seedlings, of those treated with 25 μ M GR24 – 91.88%±10.55%, and of those treated with 3 μ M TIS108 – 34.72%±8.02%, respectively. Moreover, hypocotyl length of etiolated *max2-1* seedlings (Supplementary Fig. 1D) after the treatment with 3 μ M GR24 was 97.38%±6.92% of mocktreated seedlings, of those treated with 25 μ M GR24 – 63.18%±6.39%, and of those treated with 3 μ M TIS108 – 19.74%±3.19%, respectively.

These results revealed the extent of GR24 and TIS108 effects on hypocotyl elongation, showing that etiolated Col-0 seedlings are less responsive to GR24 as compared to light-grown ones, while at the same time they were more sensitive to TIS108 treatment. In addition, *max2-1* mutants were equally unresponsive to 3 μ M GR24, however, both 25 μ M GR24 and 3 μ M TIS108 caused much stronger inhibitory effect in etiolated seedlings.

346

347 Strigolactone affects microtubule organization in light-dependent manner

Inducible growth alterations following extrinsic stimulation as, e.g., with hormonal treatments, has been repeatedly shown to be preceded and supported by conditional rearrangements of cortical MT, which tend to keep the predominant orientation (e.g., Lindeboom *et al.*, 2013; True and Shaw, 2020). Such conditions favouring the parallel arrangement of cortical MT can be documented by showing the patterns of their angular distribution and quantified by measuring the degree of anisotropy within the cortical array.

In light-grown, mock-treated Col-0 seedlings expressing a GFP-MBD MT marker, cortical MT exhibit a more or less random distribution (Fig. 3A,E) with the tendency of more biased reorganization after treatment with 3 (Fig. 3B,F) and 25 μ M GR24 (Fig. 3C,G), and 3 μ M TIS108 (Fig. 3D,H). By contrast, *max2-1* mutants expressing the same MT marker appeared to have more organized cortical MT as compared to Col-0 either after mock treatment (Fig. 3I,M) and treatments with 3 (Fig. 3J,N) and 25 μ M GR24 (Fig. 3K,O), and 3 μ M TIS108 (Fig. 3L,P).

The qualitative observations mentioned above were quantitatively corroborated by 360 361 measuring changes in the anisotropy of MT organization. In mock-treated Col-0 anisotropy was 0.12 ± 0.06 (Fig. 3Q; mean \pm SD; N=54), after treatment with 3 μ M GR24 it became 0.17 ±0.08 362 (Fig. 3Q; mean±SD; N=71), and 0.016±0.08 (Fig. 3Q; mean±SD; N=54) and 0.15±0.07 (Fig. 363 3Q; mean±SD; N=75) after 25 µM GR24 and 3 µM TIS108 treatments, respectively. In light-364 365 grown Col-0 seedlings all treatments significantly promoted anisotropy within the cortical MT array as compared to the mock treatment (Fig. 3Q; p=0.005 for 3 µM GR24; p=0.0375 for 25 366 367 µM GR24; p=0.2381 for 3 µM TIS108).

368 Oppositely, light-grown mock-treated max2-1 seedlings exhibited more biased arrays as compared to mock-treated Col-0 seedlings (e.g., Fig. 3I,M), but all treatments (Fig. 3J-P) caused 369 anisotropy reduction to values comparable to those of Col-0, again at significant values (Fig. 3R; 370 371 p=0.0000 for 3 μ M GR24; and p=0.0000 for both 25 μ M GR24 and 3 μ M TIS108). In this case cortical MT anisotropy was 0.31±0.1 after mock treatment (Fig. 3R; mean±SD; N=35), but was 372 significantly reduced to 0.17±0.07 after treatment with 3 µM GR24 (Fig. 3R; mean±SD; N=31), 373 to 0.14±0.07 after 25 µM of GR25 (Fig. 3R; mean±SD; N=61), and to 0.13±0.06 for 3 µM 374 TIS108 (Fig. 3R; mean±SD; N=79). 375

376 In Col-0 etiolated seedlings the degree of cortical MT organization is much more pronounced as compared to light-grown seedlings. In mock-treated seedlings (Fig. 4A,E), 377 378 cortical MT are largely parallel to each other at variable orientations to the main cell axis, and this pattern seems to be unaffected in seedlings treated with 3 µM GR24 (Fig. 4B,F), 25 µM 379 380 GR24 (Fig. 4C,G) and 3 µM TIS108 (Fig. 4D,H). Similarly, etiolated seedlings of max2-1 mutant exhibit highly organized systems of parallel MT, at seemingly the same level of 381 382 organization comparing to mock-treatment (Fig. 4I,M) or treatments with 3 µM GR24 (Fig. 4J,N), 25 µM GR24 (Fig. 4K,O) and 3 µM TIS108 (Fig. 4L,P). Indeed, this observation was 383 reflected to the level of cortical MT anisotropy, which in Col-0 was statistically similar between 384 385 all cases (Fig. 4Q; 0.29±0.11, N=27 for mock-treated Col-0; 0.33±0.15, N=42 for Col-0 treated with 3 µM GR24; 0.27±0.12, N=47 for Col-0 treated with 25 µM GR24; and 0.34±0.09 for Col-386 0 treated with 3 µM TIS108; mean±SD). In all cases, anisotropy of cortical MT organization was 387 388 equally high in etiolated seedlings of the max2-1 mutant with minor variations within this group 389 of treatments (Fig. 4R). Thus, anisotropy values were 0.29±0.08 for mock-treated seedlings (mean±SD; N=29), 0.31±0.14 (mean±SD; N=54) after treatment with 3 µM GR24, 0.31±0.12 390 (mean±SD; N=51) after 25 µM GR24, and 0.32±0.11 (mean±SD) after 3 µM TIS108 (Fig. 4R). 391 Next, in max2-1 seedlings only the anisotropy of those treated with 3 µM GR24 was found to be 392 393 different compared to mock-treated ones (p=0.0280), but not compared to the other treatments, which were similar to the mock. In both cases, it seems that etiolation promotes the biased 394 395 organization of cortical MT irrespectively of treatments modulating SL activity.

396

397 Strigolactone content alterations interfere with microtubule bundling

From the putative mechanisms underlying MT reorganization, bundling is one of the possibilities and it can be related to changes in the distribution of fluorescence intensity frequencies. Uniform labelling results in somewhat normal distribution, while clustered labelling is linked to increasingly skewed distribution, depending on the degree of non-uniformity of the signal. We quantified skewness of fluorescence distribution in hypocotyl cells of either Col-0 or max2-1 untreated or treated with 3 and 25 μ M GR24 or 3 μ M TIS108 under light or darkness.

In light-grown Col-0 cells all treatments induced significantly higher skewness of the
fluorescent signal as compared to mock-treated cells. In such mock-treated cells (Fig. 5A),
skewness was 0.80±0.34 (Fig. 5I; mean±SD; N=32), while after treatment with 3 µM GR24 (Fig.

407 5B) it was 1.73 \pm 0.23 (Fig. 5I; mean \pm SD; N=31), and after treatments with 25 μ M GR24 (Fig. 5C) and 3 µM TIS108 (Fig. 5D) it was 1.74±0.34 (Fig. 5I; mean±SD; N=17) and 1.78±0.26 (Fig. 408 409 5I; mean \pm SD; N=51), respectively. It is noteworthy that the effects of all treatments were significantly different compared to the mock treatment (Fig. 5I; p=0.0000 for 3 µM GR24, 25 410 μ M GR24, and 3 μ M TIS108), though comparable to each other. The skewness of fluorescent 411 412 signal from GFP-MBD lines in *max2-1* mutant background was significantly higher compared to Col-0 (Fig. 5E-H,J; p=0.0000 for all treatments), but at comparable levels within all treatments in 413 414 the max2-1 group (Fig. 5K). The increase of skewness in the Col-0 group might be relevant to the inducible increase of cortical MT anisotropy and may also underlie the intrinsically higher 415 416 order of cortical MT organization of the max2-1 mutant compared to Col-0. At the same time, it 417 does not seem to correlate with the loosening of MT organization within the max2-1 group after the interference with either SL signalling or biosynthesis. 418

In dark-grown seedlings of either Col-0 or max2-1 mutants, skewness of fluorescence 419 420 distribution of GFP-MBD-labelled cortical MT was comparable between both groups with no 421 statistically significant difference (Fig. 6). In detail, mock-treated Col-0 cells showed a skewness 422 value of 1.49±0.3 (Fig. 6A,I; mean±SD; N=57), while 1.52±0.3 (Fig. 6B,I; mean±SD; N=58) -423 after the treatment with 3 µM GR24, 1.58±0.36 (Fig. 6C,I; mean±SD; N=24) – after 25 µM GR24, and 1.55±0.31 (Fig. 6D,I; mean±SD; N=22) – after 3 µM TIS108. Similarly, etiolated 424 425 mock-treated max2-1 seedlings (Fig. 6E) showed fluorescence skewness of 1.71±0.31 (Fig. 6J; 426 mean±SD; N=31), 1.71±.30 (Fig. 6J; mean±SD; N=39) after treatment with 3 µM GR24 (Fig. 6F), 1.73±0.29 (Fig. 6J; mean±SD; N=34) after 25 μM GR24 (Fig. 6G), and 1.71±0.35 (Fig. 6J; 427 mean±SD; N=47) after 3 µM TIS108 (Fig. 6H). Although skewness values of max2-1 etiolated 428 429 seedlings were consistently higher than those of the Col-0 group, the differences inferred were 430 not significant (Fig. 6K). These results are partially consistent with the mild effects of exogenous 431 SL or SL biosynthesis inhibitor on the anisotropy of MT organization in etiolated seedlings.

432

433 Strigolactones are involved in the regulation of cortical microtubule dynamics

MT dynamics were followed by means of time-lapsed SIM in hypocotyl cells of darkgrown Col-0 or *max2-1* mutants both stably expressing the GFP-MBD MT marker. Using a frame rate of ca. 0.4 frames per second (fps) it was possible to record time series of end-wise length excursions of individual or bundled MT and quantify measures of plus end dynamicinstability using appropriately generated kymographs.

439 In mock-treated Col-0 hypocotyl epidermal cells expressing GFP-MBD (Fig. 7A,B; Supplementary Movie 1) plus end growth and shrinkage rates as well as catastrophe and rescue 440 frequencies measured from appropriate kymographs (Fig. 7C,D) were within previously 441 published values. Briefly, the average growth rate was 5.46±2.76 µm×min-¹ (mean±SD; N=53 442 MT ends), while the average shrinkage rate was 16.48 ± 6.25 m×min⁻¹ (mean±SD: N=50 MT 443 ends). Furthermore, catastrophe frequency was 0.0122 events×sec⁻¹, while rescue frequency was 444 0.0512 events×sec⁻¹. In both cases of GR24 treatment (3 and 25 µM) plus end MT dynamics 445 446 were considerably slowed during both growth and shrinkage. At the concentration of 3 µM (Fig. 7E-H, Supplementary Movie 2) the average growth rate was 2.05±0.96 µm×min⁻¹ (mean±SD: 447 N=50 MT ends), and the average shrinkage rate was $12\pm8 \ \mu m \times min^{-1}$ (mean \pm SD; N=50 MT 448 ends). Catastrophe frequency was 0.0082 events×sec⁻¹, while rescue frequency was 0.0332449 events×sec⁻¹. At 25 µM (Fig. 7I-L, Supplementary Movie 3) the average growth rate was 450 $2.01\pm1.23 \text{ }\mu\text{m}\times\text{min}^{-1}$ (mean \pm SD; N=59 MT ends) and the average shrinkage rate was 6.23 ± 5.46 451 μ m×min⁻¹ (mean±SD; N=42 MT ends). Catastrophe frequency was 0.0078 events×sec⁻¹, while 452 rescue frequency was 0.0288 events×sec⁻¹. The biosynthetic inhibitor TIS108 (Fig. 7M–P, 453 Supplementary Movie 4) strongly inhibited MT plus end dynamic parameters. In general, the 454 average growth rate was $0.70\pm0.32 \ \mu m \times min^{-1}$ (mean \pm SD; N=33 MT ends) and the average 455 shrinkage rate was 4.59±5.42 µm×min⁻¹ (mean±SD; N=28 MT ends). Catastrophe frequency was 456 0.0077 events×sec⁻¹ while rescue frequency was 0.0255 events×sec⁻¹. 457

By comparison to mock-treated cells, both parameters of MT dynamics were in most cases significantly reduced in all treatments tested (Fig. 7Q for growth rate and Fig. 7R for shrinkage rate). In terms of growth rate (Fig. 7Q) both concentrations of GR24 showed comparable reduction as compared to mock treatment, while growth rates were even more reduced in the case of treatment with TIS108 (Fig. 7Q; p=0.0000 for 3 μ M GR24; 25 μ M GR24 and 3 μ M TIS108). Shrinkage rates were also reduced in all treatments (Fig. 7R; p=0.0108 for 3 μ M GR24; and p=0.0000 for both 25 μ M GR24 and 3 μ M TIS108).

The most striking feature of GFP-MBD MT in the *max2-1* mutant was the significantly lower growth rate and most importantly the long-sustained growth periods of nearly every MT

467 examined. The prolonged elongation of cortical MT was clearly evident in mock-treated max2-1 seedlings (Fig. 8A–E, Supplementary Movie 5) with the average growth rate being 2.09±1.27 468 μ m×min⁻¹ (mean±SD; N= 32 MT ends) and the average shrinkage rat being 8.48±7.06 μ m×min⁻¹ 469 (mean±SD; N= 54 MT ends). In such seedlings, the catastrophe frequency was 0.0087 470 events \times sec⁻¹ and the rescue frequency was 0.0266 events \times sec⁻¹. However, the exogenous 471 application of GR24 at either 3 or 25 µM, or the treatment with TIS108, had no effect on any 472 473 parameter of MT dynamics compared to mock-treated max2-1 cells. Briefly, in max2-1 seedlings treated with 3 µM GR24 (Fig. 8F-K, Supplementary Movie 6), the average growth rate was 474 $2.25\pm1.35 \,\mu\text{m}\times\text{min}^{-1}$ (mean \pm SD; N=134 MT ends) and the average shrinkage rate was 9.03 ± 7.38 475 μ m×min⁻¹ (mean±SD; N=87 MT ends). In turn, catastrophe frequency was 0.0071 events×sec⁻¹ 476 while rescue frequency was 0.0301 events \times sec⁻¹. Similar was the situation of *max2-1* seedlings 477 treated with 25 µM (Fig. 8L-P, Supplementary Movie 7) were average growth was measured at 478 $2.02\pm1.73 \text{ }\mu\text{m}\times\text{min}^{-1}$ (mean \pm SD; N=167 MT ends), and average shrinkage rate was calculated to 479 be 9.34±6.76 µm×min⁻¹ (mean±SD; N=92 MT ends). Catastrophe and rescue frequencies were 480 0.0081 events×sec⁻¹ and 0.0264 events×sec⁻¹, respectively. As in the case of GR24, max2-1 481 mutants were relatively insensitive to TIS108 treatment as well (Fig. 80-U, Supplementary 482 Movie 8). Therefore, the growth rate was $2.13\pm1.24 \,\mu\text{m}\times\text{min}^{-1}$ (mean \pm SD; N=41 MT ends) and 483 the shrinkage rate was $10.84\pm7.70 \text{ }\mu\text{m}\times\text{min}^{-1}$ (mean \pm SD; N=20 MT ends). Catastrophe and 484 rescue frequencies were 0.0083 events×sec⁻¹ and 0.0222 events×sec⁻¹, respectively. As 485 mentioned before, treatments had no significant effect on neither growth (Fig. 8V), nor shrinkage 486 487 (Fig. 8W) within the *max2-1* group.

Uniformly, growth rates in Col-0 group were reduced compared to mock treatment in a similar manner to the growth rates of *max2-1* (Supplementary Fig. 2A; p=0.0000 for 3 μ M GR24, 25 μ M GR24, and 3 μ M TIS108). Reductions of shrinkage rates showed higher variability either comparing different experimental conditions within the Col-0 group, or by comparing the Col-0 group with the *max2-1* group (Supplementary Fig. 2B; p=0.1732 for 3 μ M GR24; and p=0.0000 for both 25 μ M GR24 and 3 μ M TIS108).

494 Conclusively, the aforementioned results suggest that alterations in SL signaling either by 495 chemical (GR24 and TIS108 treatments) or genetic (*max2-1* mutant) interference, uniformly

reduce MT dynamicity and likely promote MT longevity, as evidenced by the considerably lowercatastrophe frequencies observed.

498

499 Discussion

500 Being produced mainly in the roots (Foo et al., 2013) SL adjust both shoot (Gomez-Roldan et al., 2008; Umehara et al., 2008) and root (Ruyter-Spira et al., 2011) development in 501 502 vascular plants as well as in moss caulonema (Hoffman et al., 2014) to changing environmental 503 conditions. Early grafting experiments showed that SL are transported from roots to shoot in the 504 xylem of Arabidopsis and tomato, which provided insight into SL signalling regulation via localization and transport (Kohlen et al., 2011). SL may enhance and inhibit organ size and 505 506 number depending upon the organ (rhizoid or caulonema; Hoffmann et al., 2014). In this study, 507 the role of SL in shaping shoot architecture via microtubular cytoskeleton rearrangement was addressed. However, the detailed mechanisms governing their regulation of plant development 508 509 still remain to be elucidated.

The exogenous application of a synthetic SL (GR24; Umehara et al., 2008) and an 510 511 inhibitor of endogenous SL production (TIS108; a potent triazole-containing inhibitor of cytochrome P450 monooxygenases; Ito et al., 2010; 2011; 2013), resulted in hypocotyl growth 512 alterations in both Col-0 and a SL perception mutant in MAX2, a gene encoding a member of the 513 514 F-box leucine-rich repeat protein family which is likely the substrate recognition subunit of SCF 515 ubiquitin E3 ligase for targeted proteolysis at the proteasome (Stirnberg et al., 2002; Wang Y et al., 2013; Wang L et al., 2015). Alleles of max2 mutant are rendered insensitive to exogenous SL 516 517 application in phenomena such as SL-induced inhibition of hypocotyl elongation (Jia et al., 518 2014; Wang L et al., 2020), suppression of shoot branching (Wang Y et al., 2013; Liu et al., 519 2014; Li et al., 2016) and lateral root formation (Ruyter-Spira et al., 2011; Li et al., 2016). 520 Moreover, recent works associated the function of MAX2 with photomorphogenesis (Lopez-521 Obando et al., 2018).

Previous studies on the effects of exogenous SL on vegetative growth have shown that compounds such as GR24 exert an inhibitory role on the skotomorphogenic elongation of the hypocotyl and on branching processes of either the shoot or the root culminating in the reduction of tilling and lateral root formation among others (Ruyter-Spira *et al.*, 2013; Jiang *et al.*, 2016; Sun *et al.*, 2019). 527 The effects of SL signalling manipulation were conspicuously evident in light-grown and, to lesser extent, in etiolated seedlings. Indeed, previous studies have shown that exogenous SL 528 529 application halts hypocotyl elongation of light-grown seedlings in a dose-dependent manner, being notable at even lower concentrations as the ones used herein (e.g., at 100 nM; Jia et al., 530 531 2014). Importantly, max2 mutant alleles show negligible response at low concentrations of exogenous SL and exhibited inhibition of hypocotyl elongations at concentrations exceeding 25 532 533 µM (Jia et al., 2014). These results corroborate the previous studies on the synergy between SL and light perception (Brewer et al., 2013) involving a correlation of SL perception with both 534 phytochrome and cryptochrome light-dependent signalling (Jia et al., 2014). 535

Diffuse organ growth (i.e., elongation or lateral expansion) is conditionally regulated by 536 physical or hormonal signals and involves the positional control of cellulose microfibril 537 deposition. In this sense, cortical MT have been repeatedly shown to underlie cell and organ 538 growth rate and directionality as shown in the case of light (e.g., Sambade et al., 2012; 539 540 Lindeboom et al., 2013; Ma et al., 2018), mechanical stimulation (Louveaux et al., 2016; Takatani et al., 2020), and hormonal cues including ethylene (Ma et al., 2018; Wang X et al., 541 542 2020), auxin (True and Shaw, 2020) and gibberellins (Vineyard et al., 2013; Locascio et al., 543 2013).

In light of the above, the present study was extended to address whether manipulation of 544 545 SL signalling could be related to cytoskeletal remodelling, thus, the organization and the 546 dynamics of cortical MT were studied in appropriate fluorescent marker lines of both Col-0 and max2-1 mutants. In terms of organization, exogenous SL application and inhibition of 547 endogenous SL biosynthesis under standard light/dark exposure did not affect significantly 548 549 cortical MT orientation in Col-0 but had a prominent effect in max2-1 mutants, promoting 550 randomization of the cortical array. By contrast, MT bundling was enhanced after all treatments 551 in Col-0 but remained unchanged in *max2-1* mutants, which seemingly exhibited a higher level 552 of bundling than Col-0 in all circumstances. Notably, such MT organization features as ordering 553 and bundling remained fairly unresponsive to the chemical treatments in etiolated seedlings of 554 both Col-0 and max2-1. MT dynamics were considerably lowered after chemical manipulation of SL signalling in Col-0, while the inherently lower MT dynamics of max2-1 remained 555 556 unresponsive to GR24 and TIS108.

557 Owing to the previous connection of SL with phytochrome and cryptochrome light 558 perception pathways, the differential responses of cortical MT to SL content alterations under 559 light or dark growth conditions is expected. Earlier studies have already demonstrated the 560 interdependence between phytochromes and light-induced MT reorientation (Fischer and 561 Schopfer, 1997), while more recently, the reorientation of cortical MT under blue light 562 stimulation was attributed to the stimulation of KATANIN-mediated MT severing via the 563 activation of the PHOT1 and PHOT2 phototropin photoreceptors (Lindeboom *et al.*, 2013).

564 At present, the molecular components responsible for SL-mediated suppression of MT dynamics in Arabidopsis remain unknown. Its putative mechanisms are summarized in the 565 hypothetical model of the interplay of light- and SL-induced pathways, which regulates the 566 567 organization and dynamics of cortical microtubules resulting in the subsequent changes of hypocotyl growth and morphology (Fig. 9). The initial perception of SL in karrikin-independent 568 569 pathway is provided by α/β hydrolase AtD14 (Seto et al., 2019), being activated by its binding 570 with the ligand and able to form complex with one of the F-box protein MAX2 (reviewed by Kumar et al., 2015a; Wang L et al., 2020; Yoneyama et al., 2020). Upon the assembly of the SCF 571 572 complex including CULLIN1 (CUL1), Skp1 (S-phase kinase-associated protein 1) and E3 573 ubiquitin-protein ligase RING-BOX1 (RBX1) it directs ubiquitin transfer from an E2 ligase onto target proteins, which leads to their proteasome degradation. SCF complex containing MAX2 is 574 575 known to affect plant development via the degradation of SUPPRESSOR OF MORE 576 AXILLARY GROWTH2-LIKE (SMLX) proteins (Wang L et al., 2020). Another putative target protein for MAX2-mediated ubiquitination is one the key transcription factors of the 577 brassinosteroid pathway, namely BRASSINAZOLE-RESISTANT 1 (BZR1), which directly 578 579 targets and upregulates MICROTUBULE DESTABILIZING PROTEIN40 (MDP40), a positive 580 regulator of hypocotyl cell elongation by altering the stability of cortical microtubules (Wang et al., 2012). The more pronounced randomization of cortical MT array, increased MT bundling 581 and stabilization as well as reduced MT dynamicity and likely promoted MT longevity leading to 582 583 the stalled hypocotyl elongation and mild radial swelling of epidermal cells might be regulated 584 by this BZR1- MDP40 pathway branch as well.

Alternatively, SL pathway might interplay with the light-induced one via the different type of an E3 ligase complex consisting of CUL4, DAMAGE-BINDING PROTEIN 1 (DDB1) and CONSTITUTIVE PHOTOMORPHOGENIC 1 (COP1). The COP1 is subjected to regulation

588 PHYTOCHROME A and B (PHYA/B), photoreceptors of red light, bv and CRYPTOCHROMES 1 and 2 (CRY1/2), photoreceptors of blue light (Podolec and Ulm, 2018). 589 590 It has been previously proposed that COP1 might be regulated by the SCF complex containing MAX2 (Jia et al., 2014). Moreover, E3 ligase complex including COP1 might target tubulin 591 592 (Khanna et al., 2014) as well as the proteins involved in cytoskeleton regulation such as phototropin-stimulated microtubule severing protein katanin (Lindeboom et al., 2013) and 593 594 microtubule-associated protein WAVE-DAMPENED 2-LIKE 3 (WDL3) that binds to, bundles and stabilizes microtubules (Liu et al., 2013; Lian et al., 2017). Future studies should elucidate 595 596 the relationship between these two complexes.

However, another plausible explanation may refer to the physiological differences 597 between hypocotyls and roots, especially in relation to the interplay between SL signalling and 598 light perception. As mentioned previously, light-induced MT reorientations in aboveground 599 600 tissues have been shown to correlate with phytochrome (Zandomeni and Schopfer, 1993; Fischer 601 and Schopfer, 1997) and phototropin (Lindeboom *et al.*, 2013) signalling. The roots are also not indifferent to light, since dim light gradients may form at shallow depths of the soil and probably 602 603 express specialized photoreceptors responsive to low illumination rates especially at the blue wavelength range (Galen et al., 2007 and references therein). Differences in photoreception 604 between aboveground and soil-residing plant parts may explain discrepancies in the cellular 605 606 responses to SL or SL inhibitors and this is a matter that deserves to be followed up.

Although TIS108 is an inhibitor of P450 cytochrome monooxygenases and thus antagonist of SL function, previous reports have confirmed its inhibitory effect to hypocotyl elongation (Kawada *et al.*, 2019). On this basis, the follow-up effects of TIS108 on cortical microtubules organization and dynamics are in line with its observed effects on hypocotyl growth. Since the effects of TIS108 are also differentiated between light-grown and etiolated seedlings, it is likely that the TIS108-induced cytoskeletal remodelling is also associated to imbalances in SL signalling.

In conclusion, SL have robust effects on several aspects of plant development including size regulation and growth directionality of both the hypocotyl and the root. Moreover, SL reportedly act in concert with other environmental and intrinsic factors, exerting effects in the same aspects of plant development. In the search of cellular mechanisms underlying developmental implications of SL signalling, the present study highlights the significance of

619 cytoskeletal remodelling in the process of SL-mediated inhibition of hypocotyl growth and 620 reveals the differential regulation of both MT organization and dynamics by SL at different 621 illumination regimes. It is reasonable to assume that SL signalling will diversely affect the 622 growth of different plant parts with exposure to different light conditions.

623

624 Supplementary data

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626 Supplementary data are available at *JXB* online.

627

Fig. S1. Quantitative extent of the effect of strigolactone interference in hypocotyl elongation of light-grown Col-0 (A), etiolated Col-0 (B), light-grown max2-1 (C), and etiolated max2-1 (D) seedlings. *, p<0.05; ***, p<0.001 according to Student's t-test.

Fig. S2. Pairwise comparison of Col-0 and max2-1 microtubule plus end growth (A; 631 (N≥33; two-way ANOVA was followed with Scheffé's test, statistical comparison is shown 632 within groups sharing the same genotype; letters in the graph are shared by groups without 633 statistically significant differences at the 0.001 probability level; results are in Table S12) and 634 shrinkage (B; $N \ge 20$; two-way ANOVA was followed with Scheffé's test, statistical comparison 635 is shown within groups sharing the same genotype; letters in the graph are shared by groups 636 637 without statistically significant differences at the 0.001 probability level; results are in Table 638 S13) under all experimental conditions used herein. In all box plots, average is presented by \times , median by the middle line, 1st quartile by the bottom line, 3rd quartile by the top line; the 639 whiskers lie within the 1.5^{\times} interquartile range (defined from the 1st to the 3rd quartile) while 640 641 outliers are omitted.

642 *Supplementary Movie S1.* SIM time series corresponding to Fig. 7A. Microtubule 643 dynamics of etiolated, mock-treated Col-0 hypocotyl epidermal cells expressing the GFP-MBD 644 marker.

Supplementary Movie S2. SIM time series corresponding to Fig. 7E. Microtubule
 dynamics of etiolated Col-0 hypocotyl epidermal cells expressing the GFP-MBD marker treated
 with 3 μM GR24.

Supplementary Movie S3. SIM time series corresponding to Fig. 7I. Microtubule
 dynamics of etiolated Col-0 hypocotyl epidermal cells expressing the GFP-MBD marker treated
 with 25 μM GR24.

Supplementary Movie S4. SIM time series corresponding to Fig. 7M. Microtubule
 dynamics of etiolated Col-0 hypocotyl epidermal cells expressing the GFP-MBD marker treated
 with 3 μM TIS108.

654 *Supplementary Movie S5.* SIM time series corresponding to Fig. 8A. Microtubule 655 dynamics of etiolated, mock-treated max2-1 hypocotyl epidermal cells expressing the GFP-MBD 656 marker.

Supplementary Movie S6. SIM time series corresponding to Fig. 8F. Microtubule
 dynamics of etiolated max2-1 hypocotyl epidermal cells expressing the GFP-MBD marker
 treated with 3 μM GR24.

660 *Supplementary Movie S7.* SIM time series corresponding to Fig. 8L. Microtubule 661 dynamics of etiolated *max2-1* hypocotyl epidermal cells expressing the GFP-MBD marker 662 treated with $25 \mu M$ GR24.

Supplementary Movie S8. SIM time series corresponding to Fig. 8Q. Microtubule
 dynamics of etiolated max2-1 hypocotyl epidermal cells expressing the GFP-MBD marker
 treated with 3 μM TIS108.

- *Table S1*. Statistical analysis for Fig. 1Q.
- *Table S2.* Statistical analysis for Fig. 1R.
- *Table S3*. Statistical analysis for Fig. 2I.
- *Table S4*. Statistical analysis for Fig. 3Q.
- 670 *Table S5.* Statistical analysis for Fig. 3R.
- 671 *Table S6*. Statistical analysis for Fig. 4R.
- *Table S7.* Statistical analysis for Fig. 5I.
- 673 *Table S8.* Statistical analysis for Fig. 5K.
- 674 *Table S9.* Statistical analysis for Fig. 6K.
- 675 *Table S10.* Statistical analysis for Fig. 7Q.
- 676 *Table S11*. Statistical analysis for Fig. 7R.
- 677 *Table S12.* Statistical analysis for Fig. S2A.
- 678 *Table S13*. Statistical analysis for Fig. S2B.

679

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681

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689

690 Author contributions

691

YK and JŠ designed experiments with contribution from GK. YK and SH carried out all image acquisitions with the help of GK and MO. YK, SH and GK carried out all post-acquisition image processing. YK and SH carried out all hypocotyl length and width measurements. GK acquired all necessary measurements and analyzed all data related to microtubule organization and dynamics. TV carried out statistical analyses. TP synthesized GR24. YK and GK drafted the manuscript. GK compiled all figures with input from YK, TV, and JŠ. JŠ provided funding and infrastructure.

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700 Data Availability Statement

701

All data supporting the findings of this study are available within the paper and within itssupplementary materials published online.

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- 923
- 924 **Figure legends**
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Fig. 1. Hypocotyl development of light-grown seedlings of Arabidopsis Col-0 or the max2-1 926 927 mutant in the presence or absence of GR24 synthetic strigolactone (3 and 25 µM) or the biosynthetic inhibitor of strigolactone production TIS108 (3 µM). (A-D). Overview of 928 hypocotyl of Col-0 seedlings treated with solvent alone (mock; A); 3 µM GR24 (B); 25 µM 929 930 GR24 (C); 3 µM TIS108 (D). (E–H) Similar overview of hypocotyls of light-grown max2-1 mutant seedlings in the presence of solvent alone (mock; E), 3 µM GR24 (F); 25 µM GR24 (G); 931 3 µM TIS108 (H). (I-L) Magnified views of hypocotyls of Col-0 treated with solvent alone 932 (mock; I); 3 µM GR24 (J); 25 µM GR24 (K); 3 µM TIS108 (L) showing mild cell swelling in all 933 treatments (J-L) compared to control (I). (M-P) Similar comparison of max2-1 hypocotyl 934 935 epidermal cells treated with solvent alone (mock; M); 3 µM GR24 (N); 25 µM GR24 (O); 3 µM 936 TIS108 (P). (Q) Quantitative assessment of Col-0 and max2-1 hypocotyl length comparing pairwise mock treatment and treatments with 3 µM GR24, 25 µM GR24, and 3 µM TIS108 937 938 (N≥59; two-way ANOVA was followed with Scheffé's test, statistical comparison is shown within groups sharing the same genotype; letters in the graph are shared by groups without 939 940 statistically significant differences at the 0.001 probability level; results are in Table S1). (R) Quantitative assessment of Col-0 and max2-1 hypocotyl width comparing pairwise mock 941 treatment and treatments with 3 µM GR24, 25 µM GR24 and 3 µM TIS108 (N≥27; two-way 942 ANOVA was followed with Scheffé's test, statistical comparison is shown within groups sharing 943 944 the same genotype; letters in the graph are shared by groups without statistically significant differences at the 0.001 probability level; results are in Table S2). In all box plots, average is 945 presented by \times , median by the middle line, 1st quartile by the bottom line, 3rd quartile by the top 946

947 line; the whiskers lie within the $1.5 \times$ interquartile range (defined from the 1st to the 3rd quartile) 948 while outliers are omitted. Scale bars: 5 mm (A–H); 5 µm (I–P).

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Fig. 2. Hypocotyl development of dark-grown seedlings of Arabidopsis Col-0 or the max2-1 950 951 mutant in the presence or absence of GR24 synthetic strigolactone (3 µM and 25 µM) or 952 the biosynthetic inhibitor of strigolactone production TIS108 (3 µM). (A–E). Overview of 953 etiolated hypocotyl of Col-0 seedlings treated with solvent alone (mock; A); 3 µM GR24 (B); 25 954 µM GR24 (C); 3 µM TIS108 (D). (E-H) Similar overview of hypocotyls of etiolated max2-1 955 mutant seedlings in the presence of solvent alone (mock; E); 3 µM GR24 (F); 25 µM GR24 (G); 3 µM of TIS108 (H). (I) Quantitative assessment of etiolated Col-0 and max2-1 hypocotyl length 956 957 comparing pairwise mock treatment and treatments with 3 µM GR24, 25 µM GR24, and 3 µM 958 TIS108 (N≥22; two-way ANOVA was followed with Scheffé's test, statistical comparison is shown within groups sharing the same genotype; letters in the graph are shared by groups 959 without statistically significant differences at the 0.001 probability level; results are in Table S3). 960 In all box plots, average is presented by \times , median by the middle line, 1st quartile by the bottom 961 line, 3^{rd} quartile by the top line; the whiskers lie within the 1.5^{\times} interquartile range (defined from 962 the 1st to the 3rd quartiles) while outliers are omitted. Scale bars: 10 mm (A–H). 963

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965 Fig. 3. Assessment of microtubule organization in epidermal hypocotyl cells of light-grown 966 seedlings of Arabidopsis Col-0 or the max2-1 mutant in the presence or absence of GR24 synthetic strigolactone (3 and 25 µM) or the biosynthetic inhibitor of strigolactone 967 production TIS108 (3 µM). (A–D). Overview of hypocotyl of Col-0 seedlings treated with 968 969 solvent alone (mock; A), 3 µM GR24 (B); 25 µM GR24 (C); 3 µM TIS108 (D). (E-H) 970 Cytospectre graphs of cortical microtubule distribution where (E) corresponds to (A), (F) to (B), 971 (G) to (C), and (H) to (D). (I-L) Overview of hypocotyl of max2-1 seedlings treated with solvent 972 alone (mock; I); 3 µM GR24 (J); 25 µM GR24 (K); 3 µM TIS108 (L). (M–P) Cytospectre graphs of cortical microtubule distribution where (M) corresponds to (I), (N) to (J), (O) to (K), and (P) 973 974 to (L). (Q) Quantitative assessment of anisotropy of cortical microtubule organization in lightgrown Col-0 after mock treatment and treatments with 3 µM GR24; 25 µM GR24 and 3 µM 975 976 TIS108 (N≥54; Welch's ANOVA was followed with Scheffé's test, statistical comparison is shown within groups sharing the same genotype; letters in the graph are shared by groups 977

978 without statistically significant differences at the 0.01 probability level; results are in Table S4). 979 (R) Quantitative assessment of anisotropy of cortical microtubule organization in light-grown 980 max2-1 after mock treatment and treatments with 3 µM GR24, 25 µM GR24, and 3 µM TIS108 (N≥31; Welch's ANOVA was followed with Scheffé's test, statistical comparison is shown 981 982 within groups sharing the same genotype; letters in the graph are shared by groups without 983 statistically significant differences at the 0.01 probability level; results are in Table S5). In all 984 box plots, average is presented by \times , median by the middle line, 1st quartile by the bottom line, 3^{rd} quartile by the top line; the whiskers lie within the 1.5^{\times} interquartile range (defined from the 985 1^{st} to the 3^{rd} quartile) while outliers are omitted. Scale bars: 20 µm. 986

987 Fig. 4. Assessment of microtubule organization in epidermal hypocotyl cells of etiolated 988 seedlings of Arabidopsis Col-0 or the max2-1 mutant in the presence or absence of GR24 synthetic strigolactone (3 and 25 µM) or the biosynthetic inhibitor of strigolactone 989 production TIS108 (3 µM). (A-D). Overview of hypocotyl of Col-0 seedlings treated with 990 solvent alone (mock; A); 3 µM GR24 (B); 25 µM GR24 (C); 3 µM TIS108 (D). (E-H) 991 992 Cytospectre graphs of cortical microtubule distribution where (E) corresponds to (A), (F) to (B), (G) to (C), and (H) to (D). (I-L) Overview of hypocotyl of max2-1 seedlings treated with solvent 993 994 alone (mock; I); 3 µM GR24 (J); 25 µM GR24 (K); 3 µM TIS108 (L). (M–P) Cytospectre graphs of cortical microtubule distribution where (M) corresponds to (I), (N) to (J), (O) to (K), and (P) 995 996 to (L). (Q) Quantitative assessment of anisotropy of cortical microtubule organization in light-997 grown Col-0 after mock treatment and treatments with 3 μ M GR24, 25 μ M GR24 and 3 μ M 998 TIS108 (N≥27; Welch's ANOVA showed no statistically significant difference within the 999 dataset; F (3, 143)=3.1416, p=0.030; Supplementary Table S4). (R). Quantitative assessment of 1000 anisotropy of cortical microtubule organization in light-grown max2-1 after mock treatment and treatments with 3 µM GR24, 25 µM GR24 and 3 µMTIS108 (N≥29; Welch's ANOVA was 1001 1002 followed with Scheffé's test, but there was no statistically significant difference at the 0.01 probability level; results are in Table S6). In all box plots, average is presented by \times , median by 1003 the middle line, 1st quartile by the bottom line, 3rd quartile by the top line; the whiskers lie within 1004 the $1.5 \times$ interquartile range (defined from the 1st to the 3rd quartile) while outliers are omitted. 1005 Scale bars: 20 µm. 1006

1007 Fig. 5. Skewness of fluorescence distribution of GFP-MBD-labelled microtubules of lightgrown Arabidopsis Col-0 and max2-1 epidermal hypocotyl cells in the presence or absence 1008 1009 of GR24 synthetic strigolactone (3 and 25 µM) or the biosynthetic inhibitor of strigolactone 1010 production TIS108 (3 μ M). (A-D) Overviews of hypocotyl of Col-0 seedlings treated with 1011 solvent alone (mock; A); 3 µM GR24 (B); 25 µM GR24 (C); 3 µM TIS108 (D). (E-H) Overview 1012 of hypocotyl of max2-1 seedlings treated with solvent alone (mock; E); 3 µM GR24 (F); 25 µM 1013 GR24 (G); 3 µM TIS108 (H). (I, J) Quantitative assessment of fluorescence distribution skewness, comparing Col-0 (I; N≥17; Welch's ANOVA was followed with Scheffé's test, 1014 1015 statistical comparison is shown within groups sharing the same genotype; letters in the graph are shared by groups without statistically significant differences at the 0.01 probability level; results 1016 1017 are in Table S7) and max2-1 (J; N \geq 34; Welch's ANOVA showed no statistically significant difference within the dataset; F (3, 161)=0.0777, p=0.9719). (K) Collective quantification of 1018 fluorescence skewness comparing Col-0 and max2-1 in a pairwise manner in all experimental 1019 1020 conditions (N \geq 17; two-way ANOVA was followed with Scheffé's test, statistical comparison is shown within groups sharing the same genotype; letters in the graph are shared by groups 1021 without statistically significant differences at the 0.001 probability level; results are in Table S8). 1022 In all box plots, average is presented by \times , median by the middle line, 1st quartile by the bottom 1023 line, 3^{rd} quartile by the top line; the whiskers lie within the 1.5^{\times} interquartile range (defined from 1024 the 1^{st} to the 3^{rd} quartiles) while outliers are omitted. Scale bars: 20 µm. 1025

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1027 Fig. 6. Skewness of fluorescence distribution of GFP-MBD-labelled microtubules of etiolated Arabidopsis Col-0 and max2-1 epidermal hypocotyl cells in the presence or 1028 1029 absence of GR24 synthetic strigolactone (3 and 25 µM) or the biosynthetic inhibitor of 1030 strigolactone production TIS108 (3 µM). (A–D) Overviews of hypocotyl of Col-0 seedlings 1031 treated with solvent alone (mock; A); 3 µM GR24 (B); 25 µM GR24 (C); 3 µM TIS108 (D). (E-1032 H) Overview of hypocotyl of max2-1 seedlings treated with solvent alone (mock; E); 3 μ M GR24 (F); 25 µM GR24 (G); 3 µM TIS108 (H). (I, J) Quantitative assessment of fluorescence 1033 1034 distribution skewness comparing Col-0 (I; N≥22; Welch's ANOVA showed no statistically significant difference within the dataset; F (3, 161)=0.4564, p=0.7138) and max2-1 (J; N \geq 31; 1035 1036 Welch's ANOVA showed no statistically significant difference within the dataset; F (3, 151)=0.0161, p=0.9972). (K) Collective quantification of fluorescence skewness comparing Col-1037

1038 0 and *max2-1* in a pairwise manner in all experimental conditions (N \ge 22; two-way ANOVA was 1039 followed with Scheffé's test, but there was no statistically significant difference at the 0.001 1040 probability level; results are in Table S9). In all box plots, average is presented by ×, median by 1041 the middle line, 1st quartile by the bottom line, 3rd quartile by the top line; the whiskers lie within 1042 the 1.5[×] interquartile range (defined from the 1st to the 3rd quartile) while outliers are omitted. 1043 Scale bars: 20 µm.

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Fig. 7. Analysis of microtubule dynamics of Arabidopsis Col-0 expressing the GFP-MBD 1045 microtubule marker in the presence or absence of GR24 synthetic strigolactone (3 µM and 1046 25 μ M) or the biosynthetic inhibitor of strigolactone production TIS108 (3 μ M). (A, B) 1047 1048 Overview (A) and color-coded projection (B) of the time series corresponding to mock-treated Col-0 (see Supplementary Movie 1). (C, D) Two kymographs showing length fluctuations of the 1049 left (C) and the right (D) boxed areas of (A, B). (E, F) Overview (E) and color-coded projection 1050 1051 (F) of the time series corresponding to Col-0 treated with $3 \mu M$ GR24 (Supplementary Movie 2). (G, H) Two representative kymographs from boxed areas 1 and 2 of (E, F) showing decelerated 1052 1053 and sustainable growth and shrinkage. (I, J) Overview (I) and color-coded projection (J) of the 1054 time series corresponding to Col-0 treated with 25 µM GR24 (Supplementary Movie 3). (K, L) Two representative kymographs from boxed areas 1 and 2 of (I, J) showing prolonged growth 1055 1056 and shrinkage at lower rates compared to mock-treated cells. (M, N) Overview (M) and color-1057 coded projection (N) of the time series corresponding to Col-0 treated with 3 µM TIS108 (Supplementary Movie 4). (O, P) Two representative kymographs from boxed areas 1 and 2 of 1058 1059 (M, N) showing prolonged growth and shrinkage at lower rates compared to mock-treated cells. 1060 (Q, R) Quantitative assessment of microtubule growth $(Q; N \ge 33;$ Welch's ANOVA was followed 1061 with Scheffé's test, statistical comparison is shown within groups sharing the same genotype; 1062 letters in the graph are shared by groups without statistically significant differences at the 0.01 1063 probability level; results are in Table S10) and shrinkage (R; $N \ge 28$; Welch's ANOVA was 1064 followed with Scheffé's test, statistical comparison is shown within groups sharing the same 1065 genotype; letters in the graph are shared by groups without statistically significant differences at the 0.01 probability level; results are in Table S11) of Col-0 GFP-MBD labeled microtubule in 1066 1067 all experimental conditions. In all box plots, average is presented by \times , median by the middle line, 1st quartile by the bottom line, 3rd quartile by the top line; the whiskers lie within the 1.5^{\times} 1068

1069 interquartile range (defined from the 1st to the 3rd quartile) while outliers are omitted. Scale bars: 1070 $10 \mu m$ (A, B, E, F, I, J, M, N); 5 μm (C, D, G, H, K, L, O, P). All time bars correspond to 2 min. 1071

- Fig. 8. Analysis of microtubule dynamics of Arabidopsis max2-1 mutant expressing the 1072 1073 GFP-MBD microtubule marker in the presence or absence of GR24 synthetic strigolactone (3 and 25 μ M) or the biosynthetic inhibitor of strigolactone production TIS108 (3 μ M). (A, 1074 1075 B) Overview (A) and color-coded projection (B) of the time series corresponding to mocktreated max2-1 (Supplementary Movie 5). (C, D, E) Three kymographs showing microtubule 1076 1077 length fluctuations corresponding to boxed areas 1,2,3 of (A, B), indicative of slower and prolonged growth and shrinkage compared to Col-0. (F, G) Overview (F) and color-coded 1078 1079 projection (G) of the time series corresponding to max2-1 treated with 3 µM GR24 (Supplementary Movie 6). (H–K) Four representative kymographs from boxed areas 1,2,3 and 4 1080 1081 of (F, G) showing similar microtubule dynamics as in mock-treated cells. (L, M) Overview (L) and color-coded projection (M) of the time series corresponding to max2-1 treated with 25 μ M 1082 GR24 (Supplementary Movie 7). (N–P) Three representative kymographs from boxed areas 1,2 1083 and 3 of (L, M) showing comparable growth and shrinkage to mock-treated cells. (Q, R) 1084 1085 Overview (Q) and color-coded projection (R) of the time series corresponding to max2-1 treated 1086 with 3 μ M TIS108 (Supplementary Movie 8). (S-U) Three representative kymographs from boxed areas 1,2 and 3 of (Q, R). (V,W) Quantitative assessment of microtubule growth (Q; 1087 1088 N \geq 41; Welch's ANOVA showed no statistically significant difference within the dataset; F (3, 601)=0.6081, p=0.6106) and shrinkage (R; N≥20; Welch's ANOVA showed no statistically 1089 significant difference within the dataset; F (3, 333)=80.2659, p=0.6649) of GFP-MBD labelled 1090 1091 microtubule in all experimental conditions. In all box plots, average is presented by \times , median by the middle line, 1st quartile by the bottom line, 3rd quartile by the top line; the whiskers lie within 1092 the $1.5 \times$ interquartile range (defined from the 1st to the 3rd quartiles) while outliers are omitted. 1093 1094 Scale bars: 10 µm (A, B, F, G, L, M, Q, R); 5 µm (H–K, N–P, S–U); 2 µm (C–E). All time bars 1095 correspond to 2 min.
- 1096

Fig. 9. Hypothetical model of light-dependent strigolactone effects on microtubules in Arabidopsis. (A) Red and blue light is perceived by PHYTOCHROMES A and B (PHYA/B) and CRYPTOCHROMES 1 and 2 (CRY1/2), respectively, which inhibit the E3 ligase complex 1100 consisting of CONSTITUTIVE PHOTOMORPHOGENIC 1 (COP1), CULLIN4 (CUL4) and DAMAGE-BINDING PROTEIN 1 (DDB1). This E3 ligase complex directs the transfer of 1101 1102 ubiquitin (U) from an E2 ligase onto targets, which generally leads to their degradation by proteasomes. Bellow the complex, known (solid line) and putative (dotted line) targets are 1103 1104 shown, specifically TUBULIN (TUB), KATANIN 60 (KAT60) and WAVE-DAMPENED 2-LIKE 3 (WDL3). The function of this E3 ligase complex is more prominent under darkness, 1105 1106 when it is not inhibited by PHYA/B and CRY1/2. It has been previously proposed that COP1 might be regulated by the SKP1-CULLIN-F-BOX (SCF) complex containing an F-box protein 1107 MORE AUXILARY GROWTH 2 (MAX2). This SCF complex consists of MAX2, hydrophobic 1108 scaffold protein CULLIN1 (CUL1), S-phase kinase-associated protein 1 (SKP1), and E3 1109 1110 ubiquitin-protein ligase RING-BOX1 (RBX1), it also functions as an E3 ligase, known (solid line) and putative (dotted line) targets are shown, namely SUPPRESSOR OF MORE 1111 AXILLARY **GROWTH2-LIKE** (SMLX) proteins transcriptional 1112 and repressor BRASSINAZOLE-RESISTANT 1 (BZR1), which is involved in regulation of microtubules via 1113 the MICROTUBULE DESTABILIZING PROTEIN40 (MDP40). SCF complex is activated by 1114 1115 artificial strigolactones GR24+ binding to an α/β -hydrolase D14, strigolactone-specific receptor. 1116 (B) In light-grown seedlings the treatment with GR24, or an inhibitor of strigolactone biosynthesis (TIS108) leads to changes in microtubule organisation and dynamics: (1) more 1117 1118 pronounced randomization of cortical microtubule array; (2) increased microtubule bundling and 1119 stabilization; (3) reduced microtubule dynamicity and likely promoted microtubule longevity. On the other hand, no significant microtubule changes were noted after similar treatments in 1120 1121 etiolated seedlings as the trend is to maintain highly organized systems of parallel microtubules. (C) Regarding the overall hypocotyl phenotype, the strigolactone treatment inhibits hypocotyl 1122 1123 growth and cause slight radial swelling of epidermal cells in light-grown seedlings; however, the dark-grown ones were more resistant to the changes of strigolactone content. 1124

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1126 **Conflict of Interest Statement:** The authors declare that the research was conducted in the 1127 absence of any commercial or financial relationships that could be construed as a potential 1128 conflict of interest.

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3 µM GR24

25 µM GR24

d

3 µM TIS108

15

10

5

0

mock

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3 μM GR24 $\,$ 25 μM GR24 3 μM TIS108 $\,$ mock

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Figure 9

