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## A method to visualize cellular gibberellin levels using the nlsGPS1 FRET biosensor

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**Cover letter for**

“A method to visualize cellular gibberellin levels using the nlsGPS1 FRET biosensor”

Rizza A, Walia A, Tang B, Jones AM, 3 July 2018 JoVE 2018

Dear Editors,

We would like to submit for evaluation a protocol focused on gibberellin patterning in plant development. This manuscript was prepared as the documentary support for a video article in JoVE as invited by editors Indrani Mukherjee and Lyndsay Troyer.

Thank you kindly for the invitation and for consideration of this manuscript.

Best regards,

A handwritten signature in black ink that reads "Alexander M. Jones". The script is cursive and fluid, with the first letters of the first and last names being capitalized and prominent.

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**TITLE:**

Visualizing Cellular Gibberellin Levels Using the nlsGPS1 Förster Resonance Energy Transfer (FRET) Biosensor

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**SUMMARY:**

Gibberellin Perception Sensor 1 (GPS1) is the first Förster resonance energy transfer-based biosensor for measuring the cellular levels of gibberellin phytohormones with a high spatiotemporal resolution. This protocol reports on the method to visualize and quantify cellular gibberellin levels using the genetically encoded nlsGPS1 biosensor in *Arabidopsis* hypocotyls and root tips.

**ABSTRACT:**

The phytohormone gibberellin (GA) is a small, mobile signaling molecule that plays a key role in seed germination, cellular elongation, and developmental transitions in plants. Gibberellin Perception Sensor 1 (GPS1) is the first Förster resonance energy transfer (FRET)-based biosensor that allows monitoring of cellular GA levels *in vivo*. By measuring a fluorescence emission ratio of nuclear localized-GPS1 (nlsGPS1), spatiotemporal mapping of endogenously and exogenously supplied GA gradients in different tissue types is feasible at a cellular scale. This protocol will describe how to image nlsGPS1 emission ratios in three example experiments: steady-state, before-and-after exogenous gibberellin A<sub>4</sub> (GA<sub>4</sub>) treatments, and over a treatment time-course. We also provide methods to analyze nlsGPS1 emission ratios using both Fiji and a commercial three-dimensional (3-D) micrograph visualization and analysis software and explain the limitations and likely pitfalls of using nlsGPS1 to quantify gibberellin levels.

**INTRODUCTION:**

Plant hormones play a fundamental role in plant growth and development. These small, mobile signaling molecules are typically regulated at several levels, such as biosynthesis, catabolism, and short- and long-distance transport<sup>1-4</sup>. The understanding of hormone signaling pathways and downstream transcriptional responses has sharpened over the years. However, to link the diverse cellular responses of the hormone signaling pathways with the regulatory inputs directing hormone distributions, we require a spatiotemporal quantification of hormone levels at a cellular

scale. FRET-based biosensors that can detect phytohormones can advance scientists' ability to quantify hormone levels at a cellular scale. FRET-based biosensors consist of a FRET pair (donor and acceptor fluorescent proteins) linked to a sensory domain that binds a specific ligand or responds to a biological stimulus. For small molecule biosensors, ligand binding triggers a conformational change of the sensory domain that results in a change of distance and/or orientation between the two fluorescent proteins of the FRET pair. A ratiometric analysis of a FRET biosensor is accomplished by exciting the donor and measuring the fluorescence emission ratio of acceptor over donor<sup>5,6</sup>. Ligand binding is detectable as a change in this emission ratio<sup>7</sup>.

We recently developed a FRET-based biosensor for the plant hormone GA. GAs are a class of hormones that can promote seed germination, cellular elongation, and the developmental transition from vegetative to flowering phases. The nlsGPS1 biosensor is nuclear localized and provides spatiotemporal insights into GA dynamics in diverse plant tissues. In *Arabidopsis* cells, GA binds to soluble receptors, gibberellin-insensitive dwarf (GID), and the complex induces the degradation of DELLA proteins that act as negative regulators of GA signalling<sup>2</sup>. The GA sensory domain of nlsGPS1 consists of the *Arabidopsis* GA receptor (AtGID1C) linked to a 74-amino acid truncation of a DELLA protein (AtGAI) and a FRET pair consisting of enhanced dimerization variants of Cerulean as the donor fluorescent protein and Aphrodite (a codon-diversified Venus) as the acceptor fluorescent protein<sup>8</sup>. The nlsGPS1 biosensor is a high-affinity sensor for the bioactive GA<sub>4</sub> ( $K_d = 24$  nM for GA<sub>4</sub>) and it can be utilized in diverse tissue-types to map and quantify GA gradients. To avoid misinterpretation of the *Arabidopsis* GA levels *in vivo*, we have also developed a nonresponsive variant of nlsGPS1 (nlsGPS1-NR) to use as a negative control. The nlsGPS1-NR protein carries mutations in the GA-binding pocket that disrupt the binding of GA and mutations in the DELLA protein that disrupt the interaction with GID receptor proteins<sup>7,9</sup>. Emission ratio patterns or changes observed in both nlsGPS1 and nlsGPS1-NR lines can be considered artefacts not directly related to GA-binding events. It is also important to note that nlsGPS1 binding to GA<sub>4</sub> is not rapidly reversible, and therefore, cellular nlsGPS1 emission ratios should be interpreted as representing the highest recent concentration of GA in a given nucleus rather than the real-time steady-state levels. As a consequence, an analysis of falling GA levels is not possible with nlsGPS1.

Here we provide a detailed protocol for utilizing a nlsGPS1 biosensor in cells of the model plant *Arabidopsis*, using confocal imaging-based approaches at a high-resolution. The protocol provides information on imaging plant roots and hypocotyls both at steady state and over time-courses. The nlsGPS1 sensor could potentially be utilized in diverse tissue-types, as well as across plant species, to map and quantify GA distributions.

## PROTOCOL:

### 1. Preparations

1.1. Prepare ½ Murashige and Skoog agar pH 5.7 with no sucrose (1 L).



1.1.1. Dissolve 2.2 g of Murashige and Skoog (MS) basal medium in 950 mL of ultrapure water. Adjust pH to 5.7 with 5 M KOH.

1.1.2. Make up the solution to a final volume of 1 L with ultrapure water. Divide it into two 500 mL bottles, each containing 1% plant agar. Autoclave at 121 °C for 20 min.

1.2. Prepare ¼ MS liquid at pH 5.7 with no sucrose (1 L).

1.2.1. Dissolve 1.1 g of MS in 950 mL of ultrapure water. Adjust pH to 5.7 with 5 M KOH. Make up the solution to a final volume of 1 L with ultrapure water. Divide it into two 500 mL bottles. Autoclave at 121 °C for 20 min.

1.3. Prepare GA<sub>4</sub>.

1.3.1. Dissolve the GA<sub>4</sub> in ethanol 70% to make a final concentration of 100 mM GA<sub>4</sub> stock.

1.3.2. To prepare working solution, dilute the GA<sub>4</sub> stock to 0.1 - 1 µM in ¼ MS liquid pH 5.7.

## 2. Plant Growth

2.1. Sterilize the *Arabidopsis* seeds.

2.1.1. Work using a chemical hood. Aliquot seeds (approximately 200 seeds) into 2 mL microcentrifuge tubes. Use a marker with chlorine-resistant ink and place the tubes with open lids inside the sterilization vessel (a large box that can be sealed).

2.1.2. Place a 250 mL beaker containing 50 mL of ultrapure water and 50 mL of sodium hypochlorite solution inside the sterilization vessel.

2.1.3. Add 3 mL of concentrated hydrochloric acid (HCl) to the beaker. Immediately seal the vessel and allow sterilization by chlorine gas for 6 - 16 h.

2.1.4. After unsealing the vessel, close the lids of all the microcentrifuge tubes in the seed rack. Sterilized seeds can be stored dry until the time of plating.

2.2. Sow approximately 20 sterilized *Arabidopsis* seeds on ½ MS agar square plates. Seal the plates with porous surgical tape and wrap them with aluminum foil. Incubate them at 4 °C for 1 - 3 d for stratification.

2.3. For root imaging, transfer the plates to the growth chamber in a vertical position for 3 d with the following growth conditions: long-day conditions (LD, 16 h of light/8 h of dark); intensity light of 120 µmol/m<sup>2</sup>s; temperature of 22 °C (during the light cycle) or 18 °C (during the dark cycle), 65% relative humidity (RH).

2.4. For dark-grown hypocotyl: transfer the plates to the growth chamber for a light pulse of 1 - 4 h to synchronize the germination. Wrap the plates with aluminum foil and place them into the growth chamber in a vertical position for 3 d.

### 3. Sample Preparation

#### 3.1. Steady-state measurements (Figure 1A)

3.1.1. On a clean microscope slide, add 50  $\mu$ L of  $\frac{1}{4}$  MS liquid (from now on termed as mock solution). Gently transfer seedlings expressing nlsGPS1 from the plate to the slide.

3.1.2. Take a clean coverslip and spot a drop of vacuum grease on each corner of the coverslip. Gently place the coverslip over the seedlings and carefully add extra mock solution to remove any air bubbles.

#### 3.2. GA<sub>4</sub> treatment: chemical exchange experiment (Figure 1B).

3.2.1. Before the GA<sub>4</sub> treatment, use a 20 mL syringe filled with vacuum grease (attached to a pipet tip) to draw a rectangle (length: 3.5 cm, height: 2.5 cm) with a uniform layer of vacuum grease on a clean glass slide (Figure 1B). To allow for a fine line of vacuum grease, the pipet tip should be cut to have an opening of 1 mm in diameter.

3.2.2. Add 50  $\mu$ L of mock solution to the glass slide. With clean forceps, pick the nlsGPS1 seedlings and gently place them on the mock solution. To prevent any damage, transfer the seedlings by supporting the undersides of the cotyledons without grasping the seedling with the forceps.

3.2.3. Take a clean coverslip and spot a drop of vacuum grease on each corner of the coverslip. Using the forceps, place the coverslip in the center of the vacuum grease rectangle. Now the coverslip is sealed on the two sides corresponding to the long edges of the vacuum grease rectangle.

3.2.4. Carefully add extra mock solution to fill up the reservoir and remove any air bubbles within the reservoir without disturbing the seedling(s) inside.

3.2.5. Acquire the images before the GA<sub>4</sub> treatment using a confocal microscope. Follow the instructions as described in section 4 of this protocol.

3.2.6. For the GA<sub>4</sub> treatment, remove the microscope slide from the confocal stage. Set a timer for 20 min.

3.2.7. After starting the timer, exchange the buffer solution with  $\frac{1}{4}$  MS liquid containing 1  $\mu$ M GA<sub>4</sub>. Add the GA<sub>4</sub> solution (approximately 50  $\mu$ L) from the left side of the coverslip and remove the previous (mock) solution from the right side. Keep on exchanging the solution to replace the mock solution completely, which takes approximately 10 min (Figure 1B).

3.2.8. Place the glass slide back on the microscope stage. Wait another 10 min before acquiring the after-GA image.

### 3.3. Set up of a time course for the tissue of interest

Note: The tissue of interest might be, for instance, hypocotyls or roots. We routinely perform time courses for imaging nlsGPS1 biosensor using a commercial perfusion system (**Figure 1C**, see **Table of Materials**) or a RootChip<sup>7,10,11</sup>.

3.3.1. Add 200 µL of mock solution to the center of the perfusion channel of the sticky-slide (see **Table of Materials**). Gently pick nlsGPS1 seedlings and place them on the mock solution in the sticky-slide.

3.3.2. Using forceps, gently place the glass coverslip and, using the backside of the forceps, press gently on the outer edges of the coverslip so that it forms a strong bond with the sticky material on the periphery of the sticky-slide.

3.3.3. Using two elbow Luer connectors (with an inner diameter [ID] of 0.8 mm) and the silicone tubing (with an ID of 0.8 mm), connect the sticky-slide to a 20 mL syringe and to an outlet container collecting the outflow solution. Use the Luer lock connector (with an ID of 0.8 mm) to connect the syringe to the silicone tubing.

3.3.4. Gently press the syringe containing the mock solution manually to let enough solution pass through the chamber so that there are no air bubbles left in the chamber. Place and hold the syringe on the programmable syringe pump.

3.3.5. Set the pump parameters specific to the syringe used (*i.e.*, diameter and volume) along with the flow rate according to the manual provided with the pump.

Note: In this protocol, a flow rate of 1 - 3 mL/h was used, and this can be changed according to the experimental demands. Initiate the time course by starting the pump.

3.3.6. For GA<sub>4</sub> treatment during a time course (**Figure 1C**), stop the perfusion by pausing the pump and change the syringe with a new one containing ¼ MS liquid supplemented with GA<sub>4</sub>.

## 4. Microscopy

Note: We perform confocal laser microscopy.

4.1. Acquire images using a confocal microscope equipped with lasers to perform FRET imaging.

Note: For nlsGPS1, variants of cyan fluorescent protein (CFP) and yellow fluorescent protein (YFP) are imaged. In this protocol, commercial microscopes (see **Table of Materials**, listed as microscope 1 and 2) are used with 10X or 20X dry 0.70 harmonic compound PLAN APO objectives.

4.2. For microscope 1, use 448 nm and 514 nm wavelength lasers to excite CFP and YFP, respectively. Acquire sequential scans. Set detectors (*e.g.*, HyD SMD) to detect 460 - 500 nm for CFP (donor emission) and 525 - 560 nm for YFP (FRET emission) after the excitation of CFP. Using a second sequence, set a detector to detect 525 - 560 nm for YFP (YFP emission) after the excitation of YFP.

Note: This YFP fluorescence is used as an expression control, as well as in segmenting nuclei, to generate surfaces using a commercial 3-D micrograph visualization and analysis software.

4.3. For microscope 2, use 440 nm and 514 nm wavelength laser lines to excite CFP and YFP, respectively. Acquire two tracks. For track 1, set detectors (*e.g.*, ChS) to detect 464 - 500 nm for CFP (donor emission) and 526 - 562 nm for YFP (FRET emission) after the excitation of CFP. For track 2, set a detector to detect 526 - 562 nm for YFP (YFP emission) after the excitation of YFP.

Note: This YFP fluorescence is used as an expression control, as well as in segmenting nuclei, to generate surfaces in the 3-D visualization and analysis software.

4.4. Acquire images using a format of 512 x 512 pixels and a resolution of 12 bits.

4.5. The gain needs to be adjusted to an empirically determined value that allows for a good signal while not saturating pixels. The gain should not be changed between CFP and FRET emission over the experiment. Set the pinhole to 1 airy unit (AU).

4.6. In the microscope 1 software, while in an active live scan, utilize **Glow over/under** located on the top left side of the image screen to determine the underexposure and saturation of the region of interest. In the microscope 2 software, utilize **Range Indicator** located on the bottom side of the image screen to determine the underexposure and saturation of the region of interest. For any quantitative image analysis, there should be no pixel saturation.

4.7. Set the z-stacks with a step size of 1  $\mu\text{m}$ . The step size can be reduced for an increased z-resolution or increased for an increased speed of acquisition or to increase the number of positions/samples that can be imaged. For the automated time course, set the time along with the z-stacks (xyzt mode from the acquisition mode tab) to acquire the images at set time intervals.

## 5. Image Analysis Using Fiji

Note: Using ImageJ (Fiji) it is possible to process imaging data and produce two-dimensional (2-D) images of the nlsGPS1 emission ratio in *Arabidopsis* seedlings. For examples of images, see

**Figures 2A, 2C, 2E, 2G, and 3A.** In ImageJ, it is possible to find each command of this protocol using the search function. Press the **space bar and L** on the computer keyboard. A new window will open; type the required command in the search field.

5.1. Drag the file (either .lif or .ism files) into Fiji (Image J) and open the images as hyper-stack.

5.2. From the main menu, select **Image > Stack > Z project** and select **Sum slices** to capture all pixels rather than only the brightest pixels as in **Max projection**.

5.3. From the main menu, select **Process > Subtract background** and set the rolling ball radius to 50 pixels. Unselect any other options and process all three images. This step removes background using the “rolling ball” algorithm.

Note: 50 pixels was empirically determined to include nuclei as foreground.

5.4. From the main menu, select **Image > Color > Split channels**. Three new windows will open: **C1-SUM** (CFP channel); **C2-SUM** (FRET channel), and **C3-SUM** (YFP channel).

5.5. Select the **C3-SUM** window and, from the main menu, select **Process > Filters > Gaussian Blur** and apply a Gaussian Blur of 1 to reduce the image noise.

5.6. From the main menu, select **Image > Adjust > Brightness/Contrast** and select auto.

5.7. From the main menu, select **Process > Enhance Contrast**, and set **saturated** = 0.35.

5.8. From the main menu, select **Image > Type > 8-bit** and convert the stacks into an 8-bit image.

5.9. From the main menu, select **Image > Adjust > Auto-Local Threshold**. In the **Auto-Local Threshold**, select the following parameters: **Phansalkar method**, **radius = 15**, **parameter 1 = 0**, **parameter 2 = 0**, and **white stack**. In this step, YFP stacks are used to make a binary mask.

5.10. Select the **C2-SUM** window and, from the main menu, select **Process > Filters > Gaussian Blur** and apply a Gaussian Blur of 1.

5.11. Select the **C1-SUM** window and, from the main menu, select **Process > Filters > Gaussian Blur** and apply a Gaussian Blur of 1.

5.12. To create the emission ratio stack from the two channels, from the main menu, select **Process > Image Calculator**. In the new window that will appear, select **C2-SUM** as image 1, select **Divide** as operator, and select **C1 sum** as image 2.

5.13. Make sure to select **Create a new window** and the 32-bit format. A new window will appear named **Result of C2-SUM**.

5.14. From the main menu, select **Image > Lookup table > LUT 16\_colors**.

5.15. From the main menu, select **Process > Image Calculator**. In the new window that will appear, select **Result of C2-SUM** as image 1, select **Multiply** as operator, and select **C3-SUM** as image 2. In this step, the YFP binary mask is multiplied with the YFP/CFP stack to show only pixels present in the YFP control channel.

5.16. From the main menu, select **Process > Math > Divide** and set the value to 255. In the new window that opens, select **Yes** to analyze all images in the stack. A new image will appear named **Result of Result of C2-SUM**.

5.17. From the main menu, select **Image > Adjust > Brightness/Contrast** and select **Auto**.

5.18. From the main menu, select **Process > Enhance Contrast**, and select **Type saturated = 0.35**.

5.19. From the main menu, select **Image > Adjust > Brightness/Contrast**, and set minimum and maximum values to capture the GA distribution. Optional step: from the main menu, select **Analyze > Tools > Calibration Bar** and **Show LUT-calibration bar**, and save the **Result of Result of C2-SUM** as a .tiff file.

5.20. To obtain values of the emission ratios, from the main menu, select **Analyze > Set measurement** and select **Mean gray value** and **Standard deviation**.

5.21. Select the rectangle shape from the toolbar and draw a region of interest (ROI). From the main menu, select **Analyze > Measure**. A new window will report the mean value from the selected ROI.

5.22. Copy and paste the obtained values into spreadsheet software (*e.g.*, Excel or OriginPro) and make either a histogram for a before-and-after GA<sub>4</sub> treatment experiment or a line graph for a time course experiment.

## 6. Image Analysis Using 3-D Visualization and Analysis Software

Note: The advantage of using the selected software (see **Table of Materials**) is to segment objects (*e.g.*, nuclei) and create 3-D images from a confocal z-stack. For examples of images, see **Figures 2B, 2D, 2F, 2H, and 3B**.

6.1. Open the software and import the file (either .lif or .ism files).

6.2. Segment nuclei based on the control YFP emission channel using the **Surfaces wizard**. The segmented objects are termed “surfaces”. This segmentation step permits the analysis of all voxels in a nucleus as one object while eliminating background from voxels outside of the nucleus.

6.3. In the **Surfaces wizard**, set the background subtraction (local contrast) to 3  $\mu\text{m}$  and the thresholding to default. Mask the CFP emission (donor excitation donor emission [DxDm]) and FRET emission (donor excitation acceptor emission [DxA<sub>m</sub>]) channels based on the surfaces created using the YFP emission (acceptor excitation acceptor emission [Ax<sub>A<sub>m</sub></sub>]) channel.

6.4. Use the extension **XT Mean Intensity Ratio** to compute a ratio of donor excitation acceptor emission divided by donor excitation donor emission (DxA<sub>m</sub>/DxD<sub>m</sub>) between the mean intensity values of the individual surfaces in the two channels.

Note: This extension is available online for download.

6.5. To color the individual surfaces with the nlsGPS1 emission ratio, select **Color coding with statistics**, which is represented as a color wheel icon. Select **Mean intensity ratio** as statistics type.

6.6. Export the ratios of individual values from the table, which is found under the **Statistics** icon.

6.7. Copy and paste the values into a spreadsheet and make either a histogram for before-and-after GA<sub>4</sub> treatment experiments or a linear graph for time course experiments.

## 7. Statistical Analysis

Note: See **Figure 3D** for a beeswarm and box plot of nlsGPS1 emission ratios.

7.1. Open the software and paste the emission ratio of the nuclei surfaces as Y columns.

7.2. Select the columns of interest and select **Statistics > Statistics Description > Normality test** to know whether the samples are normally distributed. Run the Normality test and a new window will open and report the results.

7.3. If the samples are normally distributed, use the *t*-test as statistical test. Select **Statistics > Hypothesis testing > Two-Sample t-test on Rows** and run the *t*-test.

7.4. If the samples are not normally distributed, select **Statistics > Statistics Hypothesis testing > Two-Sample test for variance** to know whether the variance between the samples is not significantly different.

7.5. If the variance is not significantly different, use the **Mann-Whitney U test** as statistical test. Select **Statistics > Nonparametric Test > Mann-Whitney test** and run the test.

7.6. If the variance is significantly different, use **Kruskal Wallis ANOVA test** as statistical test. Select **Statistics > Nonparametric Test > Kruskal Wallis ANOVA test** and run the test.

## REPRESENTATIVE RESULTS:

Using nlsGPS1, it is possible to measure cellular GA<sub>4</sub> levels in tissues amenable to fluorescence imaging, including root tips and dark-grown hypocotyls (**Figure 2**). In the *Arabidopsis* root, the nlsGPS1 emission ratio gradient is indicative of low GA levels in the meristematic and division zones and high GA levels in the late elongation zone (**Figures 2A and 2B**). In contrast, an emission ratio gradient was not observed in nlsGPS1-NR roots, suggesting that the endogenous GA gradient is not an artefact (**Figures 2C and 2D**). A nlsGPS1 emission ratio gradient was also formed in dark-grown hypocotyls, with low levels in the cotyledons and the apical hook and high levels in the rapidly elongating basal region of the hypocotyl (**Figures 2E and 2F**). In contrast, an emission ratio gradient was not observed in the nlsGPS1-NR hypocotyls (**Figures 2G and 2H**). In both *Arabidopsis* roots and dark-grown hypocotyl cells, endogenous GA accumulation correlated with cellular elongation rate.

Furthermore, exogenously supplied GA<sub>4</sub> accumulates preferentially in the elongation zone compared to the division zone of the *Arabidopsis* root (**Figure 3**), indicating that nlsGPS1 can be used to study endogenous and exogenous GA patterning.

During time course experiments, nlsGPS1 seedlings were placed in sticky-slide chambers and perfused with ¼ MS liquid, followed by a treatment with 0.1 µM GA<sub>4</sub> for 30 min. The video shows a faster accumulation of exogenous GA<sub>4</sub> in the root elongation zone compared to the division zone (**Video 1**).

#### FIGURE LEGENDS:

**Figure 1: Sample preparation for confocal imaging.** These panels show a schematic representation of the sample preparation for (A) a steady-state experiment, (B) before-and-after exogenous GA<sub>4</sub> treatments, and for (C) a treatment time course experiment using sticky-slides (C).

**Figure 2: The GA gradient in *Arabidopsis* roots and dark-grown hypocotyls.** Two-dimensional images of (A) nlsGPS1 and (C) nlsGPS1-NR roots were analyzed using ImageJ software, and three-dimensional images of (B) nlsGPS1 and (D) nlsGPS1-NR were analyzed using a commercial three-dimensional image analysis software. Both analyses showed an endogenous GA<sub>4</sub> gradient in *Arabidopsis* roots. Two-dimensional images of (E) nlsGPS1 and (G) nlsGPS1-NR dark-grown hypocotyl were analyzed using ImageJ software, and three-dimensional images of (F) nlsGPS1 and (H) nlsGPS1-NR were analyzed using the commercial three-dimensional image analysis software. Both analyses showed an endogenous GA<sub>4</sub> gradient in dark-grown hypocotyls. The LUT bar displays the false coloration of nlsGPS1 emission ratios. YFP images are reported as expression controls. Hypocotyl images were acquired using two stage positions.

**Figure 3: The exogenous GA gradient in roots.** The first two panels show (A) two-dimensional and (B) three-dimensional images of a nlsGPS1 root before and 20 min after the treatment of exogenous GA<sub>4</sub> (1 µM). YFP images are reported as expression controls. The last two panels show (C) the mean and standard deviation and (D) beeswarm and box plot of nlsGPS1 emission ratios for nuclei of the elongation zone (the region which is defined with a white frame). In the



elongation zone, the nlsGPS1 emission ratio was significantly higher after GA<sub>4</sub> treatment (Mann-Whitney U test, \*\*\* *P*-value < 0.0001).

**Video 1: Perfusion experiment of nlsGPS1 root using sticky-slide.** This video shows three-dimensional images of nlsGPS1 perfused with ¼ MS liquid and treated with 0.1 µM GA<sub>4</sub> for 30 min. In the time course, imaging was acquired every 10 min for 3 h with the following intervals: 30 min of mock solution (frame *t* = 1, *t* = 2, *t* = 3), 30 min of GA<sub>4</sub> treatment (frame *t* = 4, *t* = 5, *t* = 6), 2 h of mock solution (frame *t* = 7 to *t* = 18) solution. Prior to the acquisition, the sample was perfused with mock solution for 2 h.

## DISCUSSION:

The FRET-based GA biosensor nlsGPS1 provides a quantitative method to report and measure GA hormone gradients in multicellular plants. FRET-based biosensors can quantify dynamics with an improved spatiotemporal resolution over direct detection by mass spectrometry and indirect measurement by transcriptional reporters or signaling-protein-degradation-based methods<sup>12,13</sup>. High-resolution cellular imaging in diverse tissue-types can yield meaningful insights into GA biology and spark new hypotheses regarding the regulation and function of GA accumulations in a multicellular context. For example, monitoring changes in the nlsGPS1 biosensor in specific GA biosynthetic, catabolic, and transport mutants, as well as during spatiotemporally induced perturbations, could be very informative to test specifically how GA gradients are established in the root and address root cell responses to GA gradients. The sensor could be used in other model and crop species to test the conservation of the mechanisms that control the GA-mediated control of seed germination, cellular elongation, and flowering.

The critical steps in the FRET-based imaging of the nlsGPS1 biosensor are that, 1) the pixels should not be saturated during the quantitative FRET analysis, 2) imaging parameters such as “detector gain” should be kept constant for the donor emission (DxDm) and acceptor emission (DxA<sub>m</sub>) acquisitions, 3) control nlsGPS1-NR lines should be used to rule out artefacts, and 4) samples should be prepared to minimize drift and focal-change issues. Additionally, the environmental conditions in which samples are grown are important to control since GA levels are sensitive to environmental conditions such as light duration and light intensity<sup>14-17</sup>. A key limitation of this type of analysis is that a high signal-to-noise ratio is required for imaging due to the increase in noise inherent in ratiometric imaging. Thus, nlsGPS1 imaging will not be useful for tissues and organs that are not amenable to ratiometric fluorescence microscopy using cyan and yellow fluorescent proteins—for example, deeper tissues where fluorescent proteins are poorly detected. On the other hand, ratiometric readouts are often preferred over intensimetric readouts, because an internal control is helpful to rule out artefacts stemming from changes in biosensor expression, stability, brightness, or detectability in a given cell, tissue, or condition. For example, FRET biosensor imaging and image analyses have also been used to study a variety of ligands in a variety of tissues<sup>5,6,18,19,20</sup>. The imaging experiments and image analyses reported here can be modified to suit new imaging methods, such as light sheet microscopy, that could yield novel insights in, for example, deeper root tissue-types.

The first-generation nlsGPS1 biosensor is a high-affinity sensor that provides a high-resolution map of GA gradients that can also report on intracellular increases in GA following exogenous GA treatments. One of the current limitations of nlsGPS1 is that the sensor is not rapidly reversible and, thus, reports not on steady-state GA levels but, likely, on the maximum recent GA concentration in the solution of interest. The precise turnover rate for the sensor is also not known and this, combined with low reversibility, precludes detection of endogenous GA depletions that might be happening within a minutes to few a hours in some tissue-types. It is also important to note that nlsGPS1 has a high affinity for GA<sub>4</sub> ( $K_d$  = 24 nM) compared to other GA forms (GA<sub>3</sub>  $K_d$  = 240 nM, GA<sub>1</sub>  $K_d$  = 110 nM) when imaging other bioactive GAs<sup>7</sup>. Future generations of GA biosensors can be engineered to increase reversibility while maintaining high affinity or to exhibit different specificities for the various precursor, bioactive, or catabolite GAs.

#### ACKNOWLEDGMENTS:

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#### DISCLOSURES:

The authors have nothing to disclose.

#### REFERENCES:

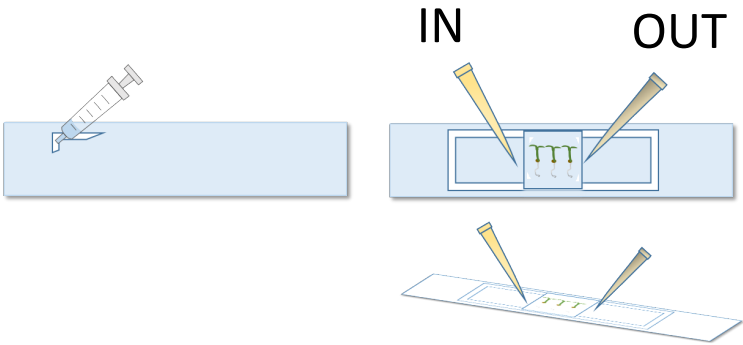
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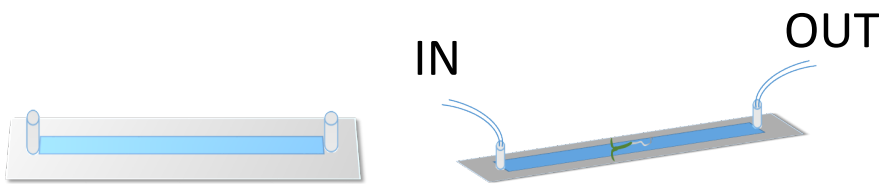
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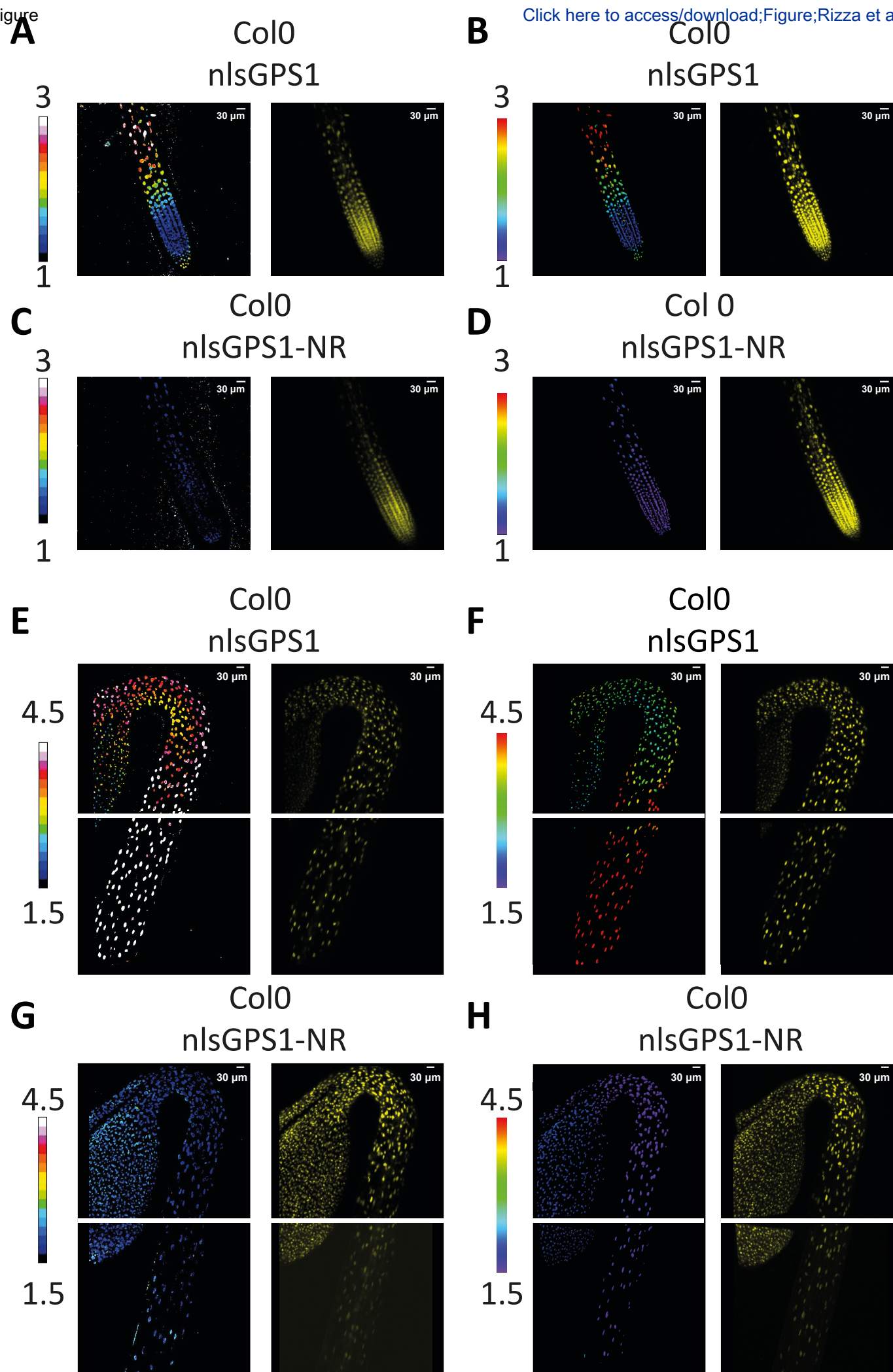


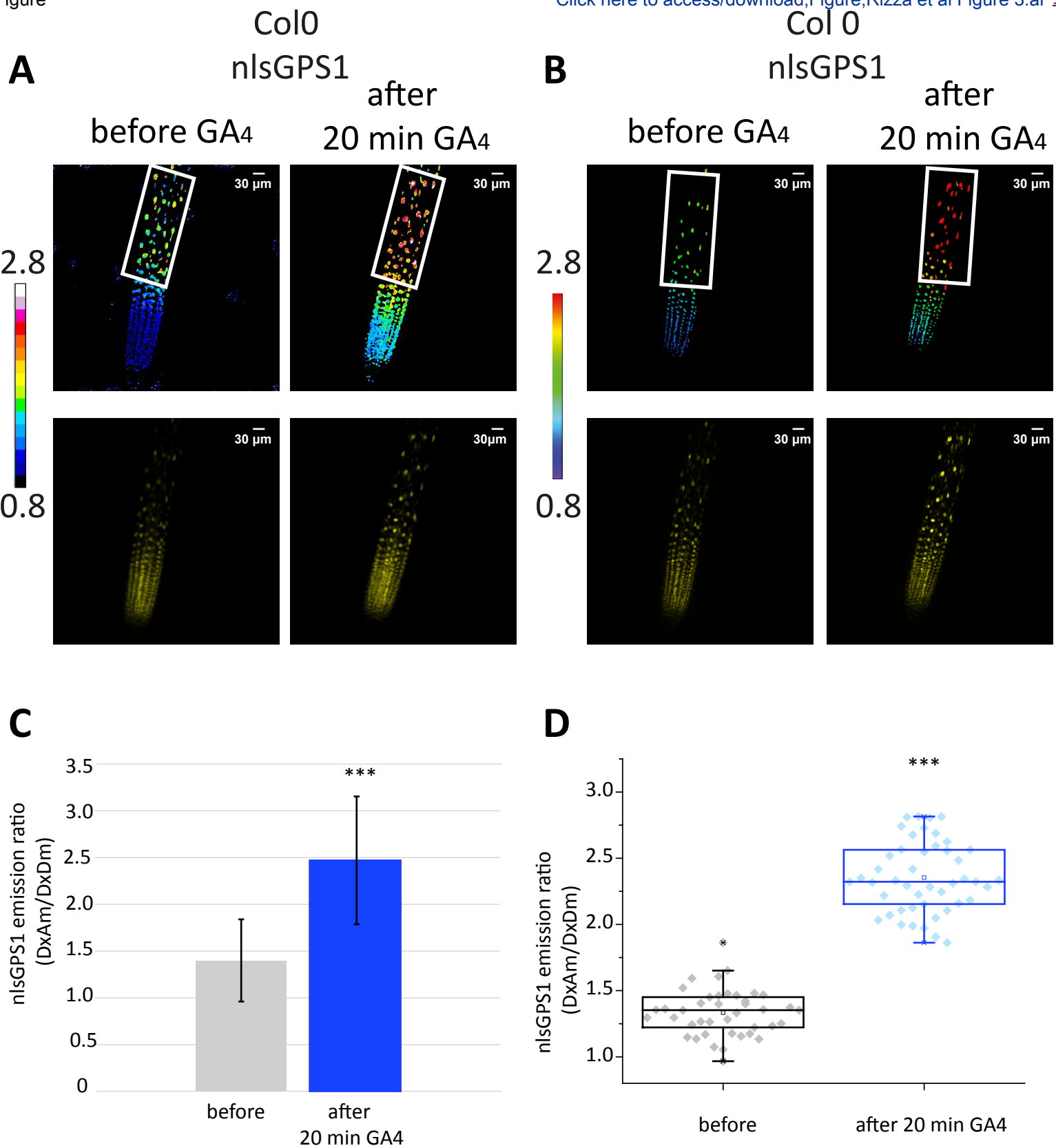
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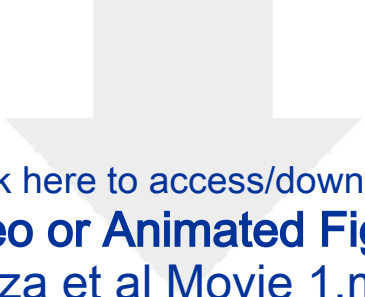


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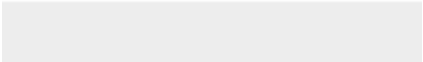









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Name of Material/ Equipment	Company	Catalog Number	Comments/Description
nlsGPS1 Col0 Arabidopsis seeds	NASC	N2107734	
nlsGPS-NR Col0 Arabidopsis seeds	NASC	N2107735	
Gibberellin A <sub>4</sub> (GA <sub>4</sub> )	Sigma	G7276	dissolve in EtH70 % , and keep at -20°
sodium hypochlorite solution (Bleach)	Fisher S/5040	HSRA 064	
Hydrogen chloride HCl	Sigma	31434	
Micropore tape	3M	1530-1	
ibidi sticky-slide	Ibidi	81128	Luer 0.1 for root imaging
ibidi sticky-slide	Ibidi	80168	Luer 0.2 for hypocotyl imaging
glass coverslip for sticky slides	Ibidi	10812	
Elbow Luer Connectors	Ibidi	10802	
silicone tubing	Ibidi	108401	
Luer Lock Connector	Ibidi	10826	
programmable syringe pump	World Precision Instruments	AL-1000	
Vacuum grease	Sigma	18405	
Murashige and Skoog Basal Salts	Duchefa	M0221	
Agar plant, 1kg	Melford	P1001	
Microscope slide ground edges, 76mm x 26mm, 1.0mm to 1.2mm thick	Fisher Scientific	12383118	
Cover slip No.1 1/2 glass 22mm x 22mm	Fisher Scientific	12363138	
Luer-slip Syringe 20 ml	Fisher Scientific	10785126	
3M Micropor Surgical Paper Tape	Fisher Scientific	12787597	
Potassium Hydroxide, 500g	Sigma Aldrich	221473-500G-D	
Absolute Ethanol	Fisher Scientific	10428671	
	Scientific Laboratory		
Forceps Watchmaker 5 StSteel	Supplies	INS4340	
Scissors, 125mm, stainless steel	Fisher Scientific	12338099	
Fitting reducer 0.5 to 1.6	Ibidi	10829	
Leica SP8			Confocal laser microscope 1
Zeiss LSM 780			Confocal laser microscope 2



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9. Please revise the protocol text to avoid the use of any personal pronouns (e.g., "we", "you", "our" etc.).

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10. Please revise the protocol to contain only action items that direct the reader to do something (e.g., "Do this," "Ensure that," etc.). The actions should be described in the imperative tense in complete sentences wherever possible. Avoid usage of phrases such as "could be," "should be," and "would be" throughout the Protocol. Any text that cannot be written in the imperative tense may be added as a "Note." Please include all safety procedures and use of hoods, etc. Please move the discussion about the protocol to the Discussion.

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11. Please add more details to your protocol steps. There should be enough detail in each step to supplement the actions seen in the video so that viewers can easily replicate the protocol. Please ensure you answer the "how" question, i.e., how is the step performed? Alternatively, add references to published material specifying how to perform the protocol action. Some examples:

Line 69: Please specify the final volume.

Line 84: How many seeds are sown per plate?

Line 98: How many seedlings are placed on each slide? Please specify throughout.

Line 107: Please specify the growth conditions.

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12. The Protocol should be made up almost entirely of discrete steps without large paragraphs of text between sections. Please simplify the Protocol so that individual steps contain only 2-3 actions per step and a maximum of 4 sentences per step. Use sub-steps as necessary. Please move the discussion about the protocol to the Discussion.

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## **Reviewers' comments:**

### **Reviewer #1:**

Manuscript Summary:

The article "A method to visualize cellular gibberellin levels using the nlsGPS1 FRET biosensor" by Rizza et al. describes protocols for the use of the GA biosensor GPS1. The



protocol to analyze steady state GA levels and GA uptake and distribution in vivo using confocal microscopy are comprehensively described, and controls and critical steps are included.

#### Major Concerns:

There are three major points that could be improved

1) Improve the description of the sample mounting by adding a new figure with images or schematic presentation of the different sample mountings.

We thank the reviewer for the suggestion. We have now included a new Figure (Figure 1) with schematic presentation of the different sample mountings.

3) Improve the description of the microscopy settings.

We have added the improved description now.

3) Besides image processing, also include image data analyses. How to get quantitative data from the images, and how to present them in a graph?

We thank the reviewer for the suggestion. We have now included the quantitative analysis of the images.

#### Minor Concerns:

Minor points: typing errors in ()

We have corrected it.

line 18) locali(s)ed

We have corrected it.

line 52) The nlsGPS1-NR carries mutations in the GA binding pocket (mutations) that disrupt...

We have corrected it.

line 54) Maybe cite here also original publication about GA receptor structure ...

We have corrected it.

lines 66 & 72) maybe spell out MS

We have corrected it.

line 79) E(T)OH

We have corrected it.

line 81) Working solution: Dilute the GA4 stock in 1/4 MS liquid pH:5.7 to 1  $\mu$ M as working concentration

We have corrected it.

lines 86-89) add relative humidity conditions for the growth chamber

We have corrected it.

line 91) Wrap the plates in aluminum foil...

We have corrected it.

line 100) add schematic picture for glass slide preparation or cite [4]?

We have corrected it.

line 106) Maybe cite original publication for root chip, or cite [4]

We have corrected it.

line 138) Using (your) forceps

We have corrected it.

lines 148-150) Explain how to remove the mock solution from the left side

We have corrected it.

line 169) SP8-FLIM(an) ?

We have corrected it.

line 163) better separate microscope settings for LEICA SP8 and Zeiss LSM 780. Better to use new headers for each microscope

We have clarified the different settings for the different microscopes.

line 176) and separate excitation/emission scan?

We have corrected it.

lines 171-189) Add more microscope settings: Objective, pixel resolution, scan frequency, bit-depth of images, bidirectional scan? zoom? HyD mode? How many z-steps? Sequential scanning for Ex CFP / Em, CFP/FRET and Ex YFP / Em YFP? pinhole size? Inverted or upright microscope?

We have included more details following your instructions

line 194: with the; the detector?

We have corrected it.

line 200) add more microscope settings?

We have corrected it.

line 202) add Fiji WWW link

We have added it.

line 205) explain why Sum is better to use than Max

We have corrected it. The “Sum” function is better because it includes all the pixels while the “Max” function only takes the brightest pixel.

lines 224-226) not sure what this means and if this is correct?

We have improved the text of the protocol to explain these steps of the Fiji analysis.

line 249) Description of quantitative data analyses is missing (Extraction of numbers/values from the pictures)

We have now included the quantitative data analyses.

line 260) seedlings were placed (into?) "Ibidi sticky slide"

We have corrected it.

Video 1: scale bar, calibration bar and time scale are missing

Comments/Description: 70% EtOH? For what is this description good for?

We have corrected it.

## **Reviewer #2:**

### **Manuscript Summary:**

The ability to measure hormone levels *in situ* at the cellular level is an important advance: the very high resolution enabled by these methods will undoubtedly improve understanding of hormone-regulated processes. The development and application of a FRET-based sensor for gibberellin A4 was described in a recent publication in *Nature Plants* and has stimulated considerable interest. Although the scope for the method is at present quite limited, the detailed protocols for its use in *Arabidopsis* seedlings under defined conditions will be helpful for those wishing to follow up this work and have access to the plants or the constructs. Some of the protocols, for example the perfusion method, have more general application. The methods are clearly described and accessible to most plant scientists with access to a confocal fluorescence microscope.

### **Major Concerns:**

There is no discussion of calibrating the method for absolute quantitation. Can the units on the LUT bars be translated into GA concentration?

The emission ratio of the sensor cannot be directly translated into GA concentration. Since the range of the nlsGPS1 biosensor is between ~2 nM to 200 nM *in vitro*, the range of nlsGPS1 emission ratio values *in vivo* likely falls in the same range.

However, as it is not currently possible to establish the *in vivo* minimum ratio for apo-sensor and maximum ratio for saturated sensor, we cannot confidently translate ratios

to exact concentrations. Nevertheless, we can be more confident that strong biosensor ratio changes are indicative of GA concentration changes around the  $K_d$  of 24 nM.

**Minor Concerns:**

Line 84: For imaging roots on vertical plates, should square plates be specified?

We have corrected it.

Line 106: For the RootChip, why not refer to the original publication, Grossmann et al Plant Cell 2012

We have added the reference now.

Line 288: sample prep (jargon)

We have corrected it.

The figure legends do not mention the second of the pairs of images in each subfigure. Are these of YFP emission?

We have corrected it.

**Reviewer #3:**

Manuscript Summary:

Clear and concise.

We thank the reviewer.

**Major Concerns:**

No major concerns

**Minor Concerns:**

\*Line 41. The authors may specify already at the beginning of the protocol which is the bioactive GA primarily sensed by the sensor.

We have corrected it

\*Line 47. It would be more consistent with the rest of the paper to report "edCerulean" instead of "Cerulean".

We have corrected it

\*Line 52. I would slightly modified the following sentence: "The nlsGPS1-NR carries mutations in the GA binding pocket mutations that disrupt....." by removing the word "mutations" after "pocket".

We have corrected it

\*Line 67. From Duchefa there are several MS media with or without Vitamins. For the sake of clarity, the authors might also report the code, e.g. M0221.

We have added the Cat N.

\*Line 70. Also, in this case if the authors want be really precise, they can indicate from which company they order the "Plant Agar" or specify if any agar can be used.

We have added the Cat N

\*Line 84. The authors may also report that the seeds need to be sterilized before being plated on agar plates. They could add a sentence in which report the method of sterilization they use.

We have now added the sterilization method.

\*Line 166. The authors might report if the microscope they use is inverted or upright.

We have corrected. In this protocol we used upright confocal microscope.

\*Line 172. Please, revise the following sentence: "A 3% laser power is used to excite the 448nm and 1-2% power to excite 514nm laser." It does not sounds really good.

We have corrected it following your suggestion.

\*Line 179. The authors report: "The detector gain is set to 110 to capture CFP (excited donor) and YFP (FRET emission). For the FRET-imaging, it is very important that the gain is kept constant while collecting the donor and FRET-emission. We use a line average of 4 for the majority of our experiments".

The authors may just report that the gain needs to be adjusted to a given value and not changed. Indeed, the gain value depends on the used objective, the transgenic line (e.g. the nlsGPS1 expressed in a mutant could have a lower or higher expression level) and other parameters. They can report that in their case the gain used was 110 but I would avoid to provide a fixed number.

Thank you for your suggestion. We have now corrected the text accordingly.

\*Lines 183-185. To avoid pixel saturation the operator has to change parameters such as laser power and gain, thus I would avoid being so strict in reporting the settings routinely used by the authors.

Thank you for your suggestion. We have now corrected the text accordingly.

\*Line 194. There are two "the".

We have corrected it.

\*Line 218. A technical issue comes from how the authors have suggested to calculate the ratio. The authors calculate the maximum projection of the stack (#2. Select "Z project" and run Z projection, selection type Sum slices) and, later, the fluorescence ratio obtained from the stack. However Maximum Intensity Projection (MIP) is a non-linear process: for each pixel of the image, the maximum value within the stack is visualized. This means that the ratio is calculated between voxels that are randomly chosen within the stack. Hence, to be precise they should have first calculated the ratio and eventually later show the MIP. The introduced error it is probably not dramatic, but for the sake of clarity I wanted to mention it.

Thank you for your suggestion. However, we did not use the MIP in our calculation. We have used the Sum slice projection method that incorporates all the pixels in the stack.

\*Line 243. Please explain the meaning of "(DxAm/DxDm)".

We have included the explanation. DxAm/DxDm means: Dx is donor excitation, Am is the acceptor emission and Dm is donor emission.

#### **Reviewer #4:**

This protocol is Important and timely as GPS1 represents the first GA responsive biosensor that has been made. Aiding the community in its effective use is an important goal. The protocol is well written but I have a few suggestions that might make it easier to follow for the non-specialist reader.

In the introduction, some more references might be useful in helping the reader understand the background to the work. For example:

Line 41: Should there be a reference to the original GPS1 paper here?

We have now included the reference.

Line 43: Referencing some recent reviews on GA here would greatly help the reader who is not an expert in the GA field.

We thank the reviewer. We have now included more references.

Line 45-46: Add a short description of normal GA sensing and how this makes the GID1C/GAI partnership a key part of the GPS1 sensor.

We have now added a short description of GA signalling.

Line 47: A reference to the enhanced dimerization variant of cerulean, to Aphrodite and to

the nls used would be helpful.

[We have now included more references](#)

In the protocol:

Line 84: Are these seeds surface sterilized? If they are, the protocol should be added.

[We have now added the sterilization method.](#)

Line 84: "Microspore paper tape", Micropore tape?

[We have corrected it](#)

Line 98: In this section, I think a non-specialist reader will find it hard to picture the setup. Perhaps add a picture/diagram?

Line 129: Similarly, for the section on chemical exchange, a diagram or picture might help understand the setup

[We thank the reviewer for the suggestion. We have now included a new Figure \(Figure 1\) with schematic presentation of the different sample mountings](#)

Line 151: adding the approximate total volume of GA4 that flows through over the 10 minutes would help researchers know if they were reproducing the required exchange.

[We have added the approximate volume of GA to use during the exchange.](#)

For the section on image J processing (line 201-), it would help immensely to have notes explaining what each step is accomplishing. For example, Line 206: What is the rolling ball local background subtraction designed to do? What are the 3 images being processed in this step? Line 216: Why is the Gaussian blur being applied? Without the explanation of this step it sounds like this will change pixel values prior to ratio calculation. Some annotations for the processing steps might help clear up these kinds of questions.

[We thank for the suggestion, we have now included more details.](#)

Line 276: It would be helpful here to provide references to examples of the other techniques being compared to in order for the reader to be able to see the kinds of resolutions made by these alternative methods.

[We have added more references](#)

Line 290: Some references showing environmental sensitivity of GA levels would be helpful here for the interested reader to get an idea of how variable the GA levels are likely to be.

[We have added more references](#)

Line 293: Providing some examples of what kinds of things will make a tissue not amenable to ratiometric imaging would be very helpful to those planning these kinds of experiments.

[Thank you for the suggestion, a clarifying example was provided.](#)

Line 306: Could the GA affinities be listed to help the reader make the comparison?

[We added more information on affinities.](#)

Figure 1. Are the yellow images in each pair presented the YFP Aphrodite signal? If so, it would be good to label the panels, especially as the order of the images is different in A-D vs E and F. Presenting an example of quantitative data extracted from these images would also be very useful.

[We have corrected it and add the quantitative analysis.](#)

Figure 2. These look like tiled images of the cotyledons and the hypocotyl section below. It would be useful to describe this in the legend.

[We have included a short description in the figure legend. The images were acquired as two stage position and we did not make the stitching.](#)

Line 325: GA is noted as 1uM here but 0.1 uM in line 261.

[We have corrected it](#)

Last page comments and description: There is an orphan sentence fragment "dissolve in EtH70 % , and keep at -20°C"

We have corrected it