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**Supplementary information**

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**Specification of leaf dorsiventrality via a  
prepatterened binary readout of a uniform  
auxin input**

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## **Specification of leaf dorsiventrality via a pre-patterned binary readout of a uniform auxin input**

Agata Burian<sup>1#</sup>, Gael Paszkiewicz<sup>2#</sup>, Khoa Thi Nguyen<sup>2,3</sup>, Shreyas Meda<sup>2</sup>, Magdalena Raczyńska-Szajgin<sup>1</sup>, and Marja C. P. Timmermans<sup>2,\*</sup>

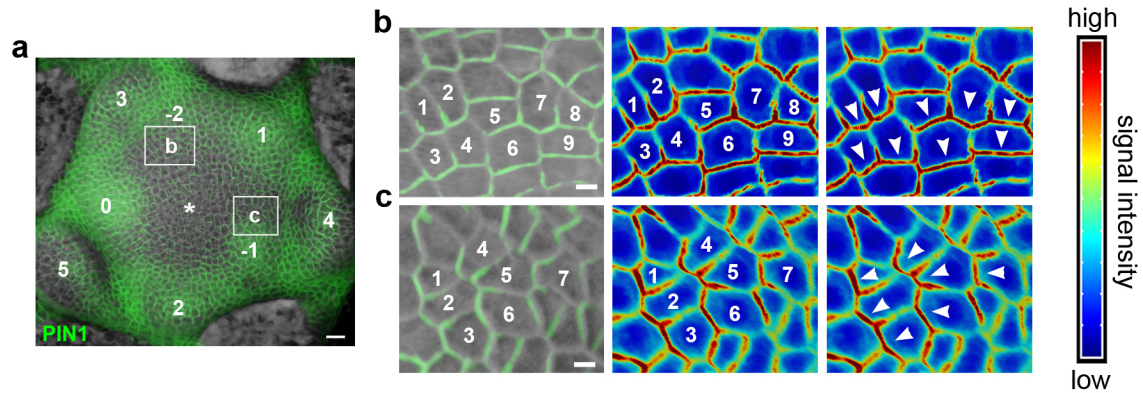
<sup>1</sup> Institute of Biology, Biotechnology and Environmental Protection, University of Silesia in Katowice, Jagiellońska 28, 40-032 Katowice, Poland

<sup>2</sup> Center for Plant Molecular Biology, University of Tübingen, Auf der Morgenstelle 32, 72076 Tübingen, Germany

<sup>3</sup> NTT Hi-Tech Institute, Nguyen Tat Thanh University, 298-300A Nguyen Tat Thanh Street, District 4, Ho Chi Minh City, Vietnam

#These authors contributed equally

\*Corresponding author: Marja C. P. Timmermans  
email: marja.timmermans@zmbp.uni-tuebingen.de  
tel: +49 7071 29 78099



**Supplemental Data Fig 1. Quantification of PIN1 expression and identification of PIN1 polarity.**

**a**, Representative expression of *pPIN1:PIN1-GFP* at the shoot apex (Fig. 3a). Regions framed and shown in magnification in **(b)** and **(c)** illustrate PIN1-GFP polarization is oriented towards the meristem centre at p-2 **(b)** and towards the adaxial side of the primordium at p-1 **(c)**. **b-c**, The representative PIN1-GFP signal from original confocal z-stacks (left) at a depth of 1-6  $\mu\text{m}$  below the surface corresponding to the L1 cell layer was projected onto the apex surface (middle). The signal intensity is shown in a qualitative colour scale. The PIN1-GFP polarity (arrowheads) was manually recognized in each cell based on locally higher signal forming an arc around cell junctions (right). Arrowheads, PIN1-GFP polarity; asterisks, meristem centre. Cell walls were stained by PI. **(a-c)** Scale bar =20  $\mu\text{m}$  **(a)**; 5  $\mu\text{m}$  **(b-c)**.  $n = 6$  independent apices **(a-c)**.

**Supplemental Table 1: Cloning primers used in this study**

| Purpose                     | Gene                            | Primer name | Primer sequence                                    |
|-----------------------------|---------------------------------|-------------|----------------------------------------------------|
| Confocal imaging            | <i>AS2</i><br><i>AT1G65620</i>  | AS2p_F      | GTGTGGATCCtcatacttgaatgaggaacccta                  |
|                             |                                 | AS2p_R      | GTGTCCTAGGtttaatgacttgaaaatggagtttttc              |
|                             | <i>KAN1</i><br><i>At5g16560</i> | KAN1p_F     | AACAGGTCTCAACCTgtcatattggatctcactcaccgac           |
|                             |                                 | KAN1p_R     | AACAGGTCTCATGTTtctatcaatataatataaattattttacggctaga |
|                             |                                 | KAN1g_F     | AACAGGTCTCAAACAtgggtttacttggtgaaaggtgaaaaag        |
|                             |                                 | KAN1g_R     | AACAGGTCTCAAGCCtttctcgtgccaatctggtctgc             |
|                             |                                 | KAN13U_F    | AACAGGTCTCACTGctatgactttcttgatcaatttgattttat       |
|                             |                                 | KAN13U_R    | AACAGGTCTCAtagtcatatccatatgaaatctcaactcag          |
|                             | <i>ARF3</i><br><i>At2g33860</i> | ARF3p_F     | AACAGGTCTCAACCTttaatgagcaatcctatacggagttc          |
|                             |                                 | ARF3p_R     | AACAGGTCTCATGTTtaaagagagagaaacagagataaaga          |
|                             |                                 | ARF3g_F     | AACAGGTCTCAAACAatgggtggtttaatcgatctgaacgtg         |
|                             |                                 | ARF3g_R     | AACAGGTCTCAAGCCgagagcaatgtctagcaacatgtc            |
|                             |                                 | ARF33U_F    | AACAGGTCTCACTGctatagaagggttcttggtttctgtg           |
|                             |                                 | ARF33U_R    | AACAGGTCTCAtagttggattacgttttctttagtggtgc           |
| ChiP                        | KAN1-YFP                        | KAN1_F      | CACC ATGTCTATGGAAGGTGTTTTTC                        |
|                             |                                 | KAN1_R      | GTGT GCGCGGCC CTATGCATGCATGCCGAGAG                 |
| Transient Luciferase assays | <i>AS2</i><br><i>AT1G65620</i>  | AS2_Fcfs    | GAG TGA CTGCAGatggcatcttcttcaacaaac                |
|                             |                                 | AS2_Rcfs    | GACATG GAATTCtcaagacggatcaacagtacggc               |
|                             |                                 | pAS2_F      | GTGT GGATCC tcatacttgaatgaggaacccta                |
|                             |                                 | pAS2_R      | GTGT CCTAGG tttaatgacttgaaaatggagtttttc            |
|                             | <i>KAN1</i><br><i>At5g16560</i> | KAN1_Fcfs   | GAGTGACTGCAGatgtctatggaaggtgtttt                   |
|                             |                                 | KAN1_Rcfs   | GACATG GAATTC tcatttctcgtgccaatctg                 |
|                             |                                 | pKAN1_F     | GTGT GGATCC cacttcaaactctatttaactgaaac             |
|                             |                                 | pKAN1_R     | GTGT ACTAGT aattaaagaaacctttcttctgtattg            |
|                             | <i>ARF3</i><br><i>At2g33860</i> | pARF3_F     | GTGT GGATCC gaagcattgaatgaaagtggg                  |
|                             |                                 | pARF3_R     | GTGT CCTAGG taaagagagagaaacagagataaag              |

**Supplemental Table 2: ChIP-qPCR primers used in this study.**

| Purpose       | Promotor fragment | Forward primer              | Reverse primer             |
|---------------|-------------------|-----------------------------|----------------------------|
| AS2-YFP ChIP  | KAN1-a            | CACAGAATCCGATCAAACGTC       | AACAGTAGTACAGAAGTAGTAGT    |
|               | KAN1-b            | AGTGAAGTGAGAAGCGAAGAG       | GAGAGAGTGCTTTGATTTTGGT     |
|               | KAN1-c            | TCGAGGAACAACATCTCACACA      | CATGCTCAAAGTAAGACGCAG      |
|               | KAN1-d            | CCTAAGCAAAACCCTCAGGAG       | GAAAAACACCTTCCATAGACAT     |
|               | ARF3-a            | GCAATGGGAAGAGCGTGAGG        | CGCGAGACAGTGTAGATGTAG      |
|               | ARF3-b            | GGTATAAGAATATCACTTAGCAGAGAC | CGGCATCAAAGTAAACGAGAGATTTG |
|               | ARF3-c            | ATTTGTTTCTCTCAATATGCCCTACCA | CATGAACCTGTTATCAACGGCGA    |
|               | ARF3-d            | ACGGTAGTCCAAATCTTCGCCACA    | CGTCTCTGTTGTCTCTTTGTCTTTG  |
| KAN1-YFP ChIP | AS2-a             | TTTGACCGAAGAACTTTGAGGAC     | CTGATGGATCTTGGGATGAAG      |
|               | ARF3-a            | GTTCTACTGCAAAGAGAGTGAG      | CCGACATCTGTTTCCTATCTTC     |
|               | ARF3-b            | GCTACATTGTGCTTGTTGTTGAG     | CAAACCACAATTTGAATATCTTCTC  |
|               | ARF3-c            | GGTATAAGAATATCACTTAGCAGAGAC | CGGCATCAAAGTAAACGAGAGATTTG |
|               | ARF3-d            | ATTTGTTTCTCTCAATATGCCCTACCA | CATGAACCTGTTATCAACGGCGA    |
|               | ARF3-e            | GTGAGGAAGAAACAATGTGGTC      | TACGACCTATTCATCATCGCCT     |
|               | ARF3-f            | CACTGATTATTTATCACAAAGGTG    | TGTGGCGAAGATTTGGACTAC      |
|               | ARF3-g            | ACGGTAGTCCAAATCTTCGCCACA    | CGTCTCTGTTGTCTCTTTGTCTTTG  |

**Supplemental Table 3: p-values for ChIP analyses**

| <b>TF binding</b> | <b>Promotor site</b> | <b>Biological rep.1</b> | <b>Biological rep.2</b> | <b>Biological rep.3</b> | <b>Average</b> | <b>STDEV</b> | <b>p-value</b> |
|-------------------|----------------------|-------------------------|-------------------------|-------------------------|----------------|--------------|----------------|
| KAN1              | <i>pAS2-a</i>        | 2.826                   | 4.036                   | 3.317                   | 3.393          | 0.351        | 0.021          |
|                   | <i>pARF3-a</i>       | 4.075                   | 3.473                   | 2.843                   | 3.464          | 0.355        | 0.020          |
|                   | <i>pARF3-b</i>       | 2.141                   | 1.039                   | 1.509                   | 1.563          | 0.319        | 0.220          |
|                   | <i>pARF3-c</i>       | 1.970                   | 0.852                   | 1.197                   | 1.340          | 0.330        | 0.412          |
|                   | <i>pARF3-d</i>       | 2.852                   | 2.188                   | 2.786                   | 2.608          | 0.211        | 0.017          |
|                   | <i>pARF3-e</i>       | 1.539                   | 0.899                   | 1.405                   | 1.281          | 0.195        | 0.286          |
|                   | <i>pARF3-f</i>       | 0.968                   | 0.546                   | 0.810                   | 0.775          | 0.123        | 0.208          |
|                   | <i>pARF3-g</i>       | 0.795                   | 0.632                   | 0.823                   | 0.750          | 0.060        | 0.053          |
| AS2               | <i>pKAN1-a</i>       | 0.689                   | 0.705                   | 0.748                   | 0.714          | 0.018        | 0.004          |
|                   | <i>pKAN1-b</i>       | 5.175                   | 4.692                   | 5.101                   | 4.989          | 0.150        | 0.001          |
|                   | <i>pKAN1-c</i>       | 3.522                   | 3.065                   | 3.369                   | 3.319          | 0.134        | 0.003          |
|                   | <i>pKAN1-d</i>       | 2.151                   | 1.786                   | 1.838                   | 1.925          | 0.114        | 0.015          |
|                   | <i>pARF3-a</i>       | 2.682                   | 2.306                   | 3.409                   | 2.799          | 0.324        | 0.031          |
|                   | <i>pARF3-b</i>       | 1.389                   | 0.906                   | 1.568                   | 1.288          | 0.198        | 0.283          |
|                   | <i>pARF3-c</i>       | 1.371                   | 0.847                   | 1.110                   | 1.109          | 0.151        | 0.546          |
|                   | <i>pARF3-d</i>       | 1.622                   | 1.057                   | 1.410                   | 1.363          | 0.165        | 0.158          |