**BZR1-dependent brassinosteroid signaling pathway leads to ectopic activation of quiescent cell division and suppresses columella stem cell differentiation**

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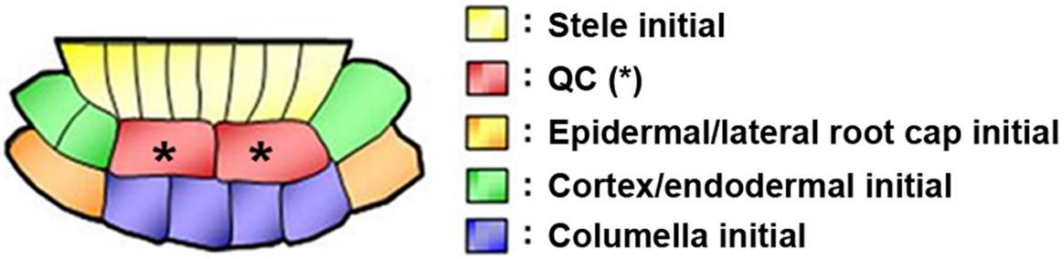
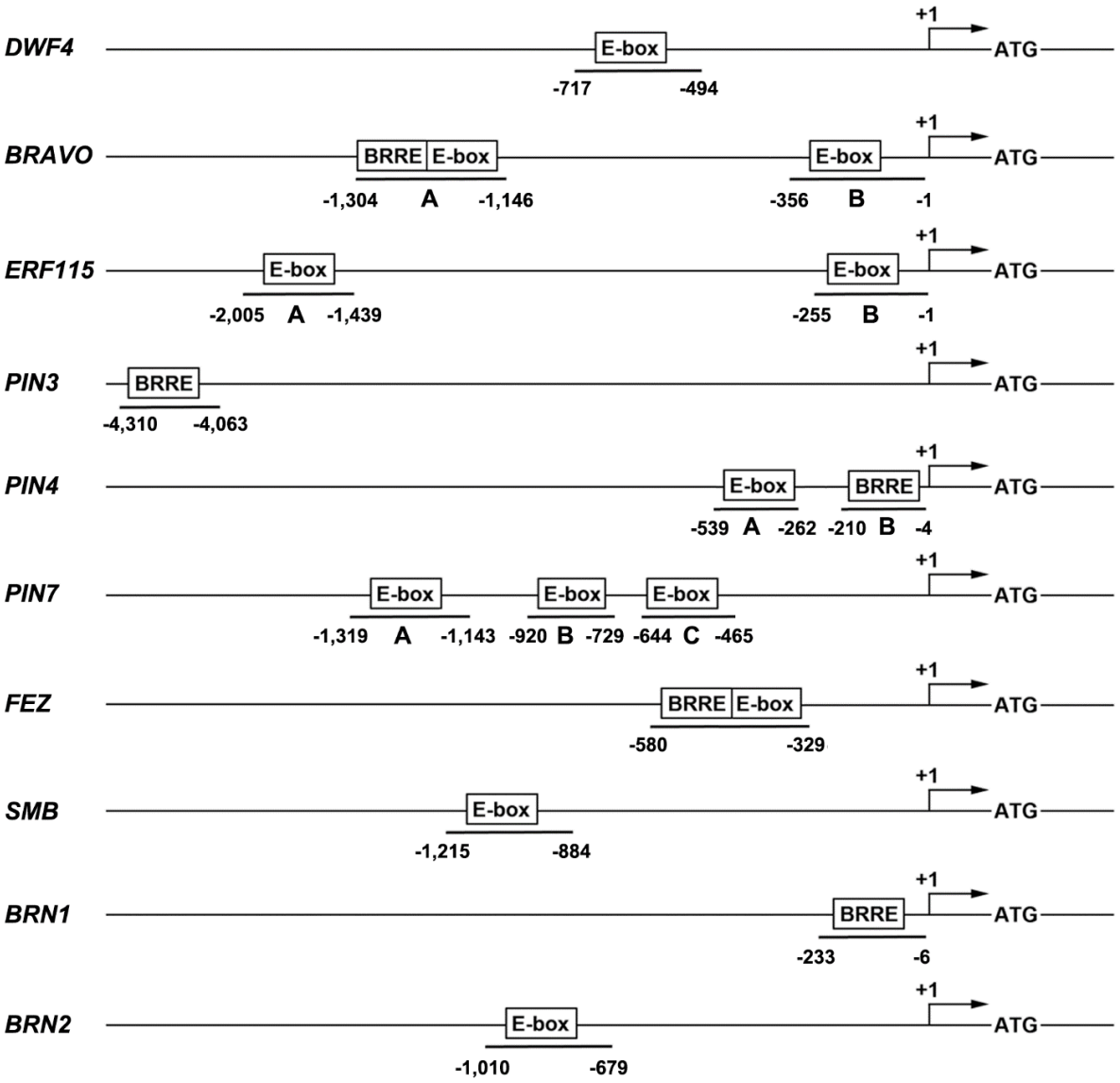
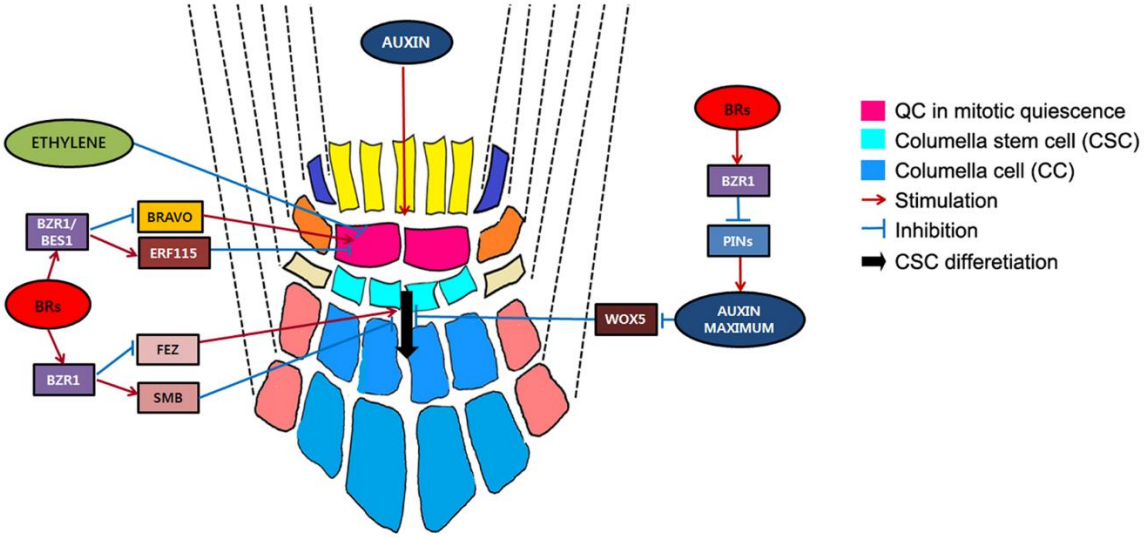



**Supplementary Figure S1.** Schematic diagram of the root SCN area.




**Supplemental Figure S2.** Schematic diagram of potential BZR1- and BES1- binding sites (BRRE and E-box) and the PCR-amplified DNA fragments used for ChIP-qPCR analysis. 5' and 3' position of each fragment is indicated by numbers. +1 represents the transcriptional initiation site of the corresponding gene. Nucleotide positions and fragments lengths are not in scale.




**Supplemental Figure S3.** A schematic model explaining brassinosteroid regulation of the QC maintenance and the columella stem cell (CSC) differentiation. Both BZR1-/BES1-mediated brassinosteroid signaling pathways promote mitotic reactivation of QC cells by inhibiting *BRAVO* (a negative regulator of QC division) and stimulating *ERF115* (a positive regulator of QC division) gene expression. In contrast, BRs regulate CSC differentiaion into columella cells (CCs) in a BZR1-/BES1-dependent manner. BZR1-mediated inhibitory BR action on PINs expression and activities provoke proximal movement of auxin maximum leading to WOX5 -mediated CSC differentiation into CCs. In other hand, BZR1 down-regulates gene expression of FEZ (encoding a protein promoting periclinal root cap-forming cell division), and this may result in another level of suppression for CSC differentiation into CCs. Ethylene pathway and BZR1-mediated BR signaling pathway acts independently on the QC reactivation.

| **Supplemental Table S1. Primers used in quantitative real time RT-PCR analysis** | | |
|---|---|---|
| Gene name | Locus | Primer set (5' to 3') |
| *WOX5* | At3g11260 | TCCAACTCCAAGGTGGACAAAATGA |
| | | ATGGCGGTGGATGTTCCATTTCAG |
| *SCR* | At3g54220 | TTCTCACCCCCTCACTGAGTTTTTG |
| | | GTTGTTGGTCGTGAGATTGCATGG |
| *SHR* | At4g37650 | TGGGAAGAGAGTTTTCCAAGGACGA |
| | | TCATCCGCCACCTCATCACTATACC |
| *BRAVO* | At5g17800 | CGAGGACACTGGAGACCAACAGAAG |
| | | CAG CGT TAT CGG TAC GAC CTG GA |
| *ERF115* | At5g07310 | CAAATCCGCAGACTAATCCGCAAAC |
| | | AGGAGGTGAAGAATCCCCAAAACG |
| *PIN3* | At1g70940 | GGAGCACCTGACAACGATCAAGG |
| | | CTCGGCGTCTTTTGGTCTCTCTG |
| *PIN4* | At2g01420 | ATGTGCATCCCACGATTCTAAGCAC |
| | | CAATCTCCGAGGCTCTCTCAAAAGC |
| *PIN7* | At1g23080 | TTGGGCTCTTGTTGCTTTCAGGT |
| | | CCGCTGGTCCAGTAAAGAATCTCAC |
| *CUL3* | At1g26830 | TCCCGATCATCCGTCTTTCCTCT |
| | | GCAGGACCATGTTGTACGCATTTC |
| *ACS5* | At5g65800 | GCGATGCTTTCCTTTTGCCTACTC |
| | | TTTCTGGGCTTGTTGGTAAGCTTGT |
| *ETO1* | At3g51770 | TGCTGGATGCAGCTGTATGATCGTT |
| | | GCTGCCTTTTGACAATTGAGCCGTA |
| *FEZ* | At1g26870 | TCAGTTTGCAGCACCTTCATGTTTC |
| | | CACCGTGGATGACGACCCTATCT |
| *SMB* | At1g26870 | TCGGAAATGGGAGATAGAAACAACG |
| | | TTGGAAGATCCCAGGGGTCATATTT |
| *BRN1* | At1g33280 | CACGTGCAAGGCAGTAAGTGAATGG |
| | | TCACCGCGCAATGAAAGCAGATTAG |
| *BRN2* | At4g10350 | TCAAGCCAACCCTAGTGAAGATGGA |
| | | TGGACTGTCTCGGTGCATAAAGCTA |
| *CPD* | At5g05690 | GCGGTGTTTTCAGACGTGCAAT |
| | | GAAAGTGCGAGCATCTTTGAAGTGG |

| **Supplemental Table S2. Primers used in ChIP-qPCR analysis** | | |
|---|---|---|
| Gene name | Locus | Primer set (5’ to 3’) |
| *UBC30* | At5g56150 | CAAATCCAAAACCCTAGAAACCGA |
| | | AACGACGAAGATCAAGAACTGGGAA |
| *PP2A* | At1g69960 | AGCAGCACAACCCTCAACAG |
| | | CCAGATGTGCTAAAGACGGAG |
| *DWF4* | At3g50660 | GTGTTTTCTGACTATTGAGGGG |
| | | CGGTACGGTCTCAATCGGTTTA |
| *BRAVO* A | At5g17800 | AAAATTTAAATTTAAACTAGTAGCAAAAAAT |
| | | TTTTACTTATATACTATATTCAGTG |
| *BRAVO* B | At5g17800 | AAAAAAAAAAAAAAATGATAAATAAAA |
| | | GAGAGCACTTGAATGGCTTTTCACTG |
| *ERF115* A | At5g07310 | CGTTCTCGTCAACAAATCTGAAAATAC |
| | | CAATCGAGAAACTGTTGTCTTTTTTT |
| *ERF115* B | At5g07310 | TATGCAAAACTTCTGCTTGACGTTAA |
| | | CTTTGCTAAAATCTTTAAACCTCTTT |
| *PIN3* | At1g70940 | CTCCAATACTCGATCGTGAAGA |
| | | GGATGATAGAGTGTGGATTGG |
| *PIN4* A | At2g01420 | CAAAAACAAAAAACAAAATAT |
| | | AAAGTTGCAAAAGGAACTTTG |
| *PIN4* B | At2g01420 | GCACGACTATTCCATAAAACTGT |
| | | GGATTCGGTGAAGAGGACTA |
| *PIN7* A | At1g23080 | CCAAACCATGAGCAGAATTGT |
| | | CGTTTACACAATTATAATAGCAG |
| *PIN7* B | At1g23080 | CGGTCGCGGAAAGATCTTGA |
| | | CCCAAGAAATCTCACTTTTAAG |
| *PIN7* C | At1g23080 | CGGCGAATATGATCTTGCATT |
| | | GGGCCACTTAACGTATTACTAG |
| *FEZ* | At1g26870 | CGATCGGCCCTTGTATCCTTTTAT |
| | | AAAAATGCACTATCATCATATCGT |
| *SMB* | At1g26870 | TAAGGAGCAAATATGGAACTTTA |
| | | AGGATTAACTATACTAAGCAGTAA |
| *BRN1* | At1g33280 | CTCCGGCGGCGTTGTCACCGGCCG |
| | | GTTAATAAATGATCAATGTTTGTTTG |
| *BRN2* | At4g10350 | TACATTAATATAACACATATTATT |
| | | AGAAACACAAAAAGAAAAACCTTT |

**Supplemental Table S3.** Division of QC in various brassinosteroid mutants

| | Col | *bri1-116* | *bzr1-1D* | *bri1-116* /*bzr1-1D* | En-2 | *bes1-D* |
|---|---|---|---|---|---|---|
| DAG 3 | 0/25 (0)[a] | 0/32 (0) | 0/24 (0) | 0/28 (0) | 0/25 (0) | 0/31 (0) |
| DAG 7 | 2/38 (5) | 0/26 (0) | 14/28 (50) | 10/27 (37) | 0/23 (0) | 21/25 (84) |
| DAG 14 | 5/28 (18) | 2/22 (9) | 24/32 (75) | 20/29 (69) | 2/21 (10) | 33/33 (100) |

[a]: Number of plants with periclinal division of QC / number of plants observed (percentage of plants with the reactivated QC). DAG: Day after germination.