Figure S1

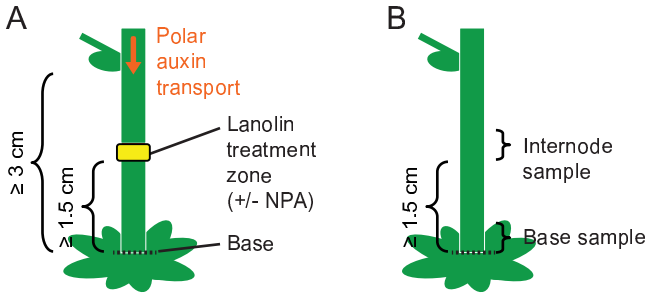

Figure S1. Schematic representation of the regions along the inflorescence stem analyzed in this study. **(A)** Habitus of plants indicating the lanolin treatment zone and the position of the stem designated as the 'base'. **(B)** Samples taken from wild type and *wox4-1* plants for genome-wide transcriptional profilings.

Figure S2

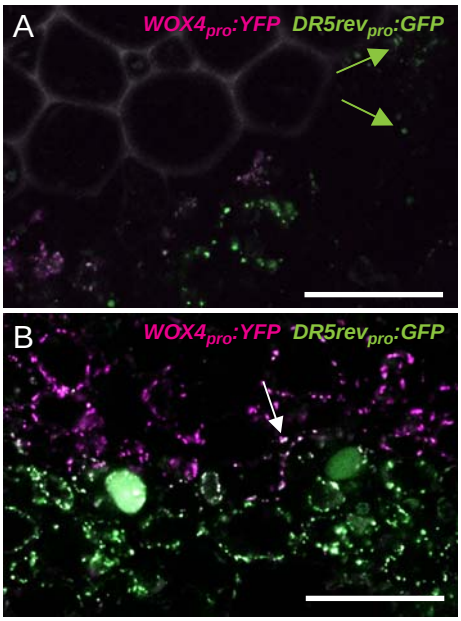

Figure S2. Two-channel overlays of the *WOX4$_{pro}$:YFP* (magenta) and *DR5rev$_{pro}$:GFP* (green) images shown in Figure 1G and 1J. **(A)** Cross section taken from 10 mm above the base. **(B)** Cross section taken from the base. Co-localization of both signals is marked by a white arrow. Green arrows point towards interfascicular *DR5rev$_{pro}$:GFP* signals. Scale bar: 25 µm.

Figure S3

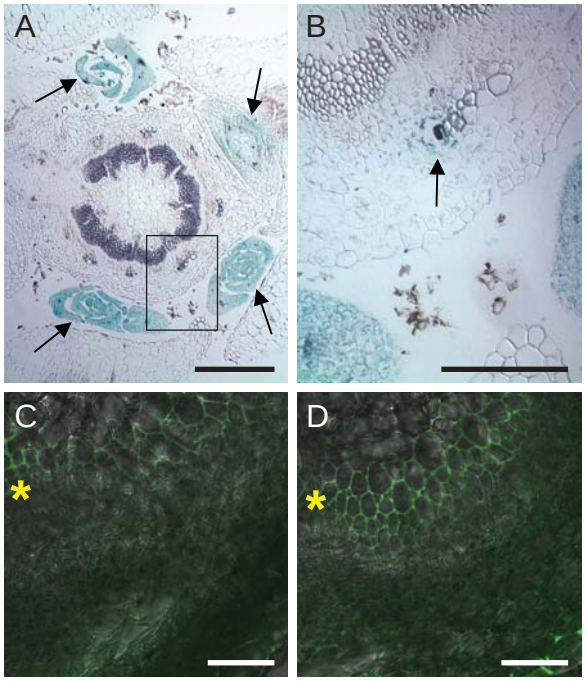

Figure S3. *AtGH3.3$_{pro}$:GUS* activity in stems and autofluorescence detected in the GFP and YFP-specific channels used for analysis of *DR5* and *WOX4* promoter activities. **(A, B)** Cross section from the base of the inflorescence stem of a 15 cm tall plant. *AtGH3.3$_{pro}$:GUS* activity is detected in young tissues of side shoots originating from the base of *Arabidopsis* stems (A, arrows), as well as in phloem-related tissues in the main stem (B, arrow). **(C, D)** Autofluorescence at the base of wild type stems, using the GFP (C) and YFP (D) specific channels. Stars indicate the position of primary vascular bundles. Scale bars: 0.5 mm (A), 0.2 mm (B) and 50 μm (C, D).

Figure S4

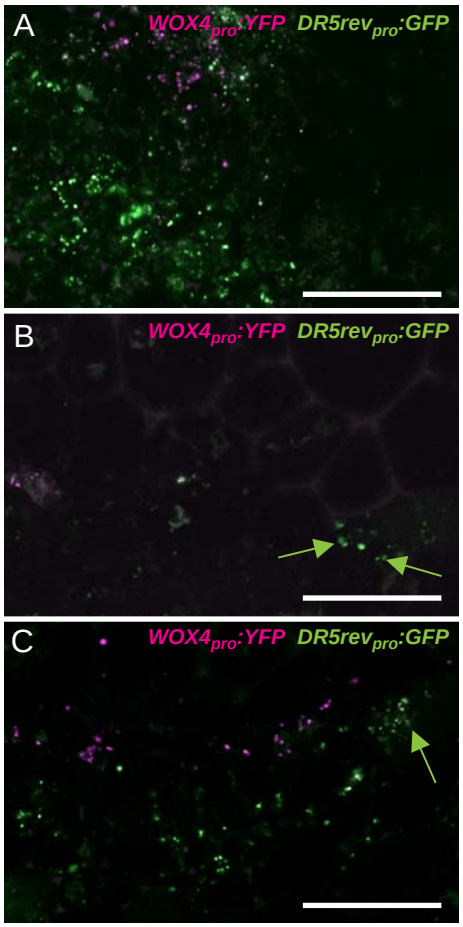

Figure S4. Two-channel overlays of the *WOX4$_{pro}$:YFP* (magenta) and *DR5rev$_{pro}$:GFP* (green) images shown in Figure 2C, 2F and 2I. Cross sections taken from 5 mm above the base of 5 cm (A), 15 cm (B) and 30 cm (C) tall plants. Green arrows point towards interfascicular *DR5rev$_{pro}$:GFP* signals. Scale bar: 25 µm.

Figure S5

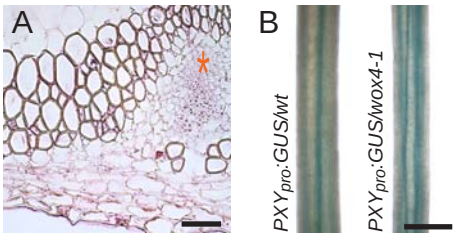

Figure S5. Sense control for *in situ* hybridizations, and PXY_{pro}*:GUS* expression in *wox4-1*. **(A)** Hybridization of a stem section with the *PXY*-specific sense probe. (B) PXY_{pro}*:GUS* activity in stems of wild type and *wox4-1*. Scale bars: 50 µm (A), 0.5mm (B).

Figure S6

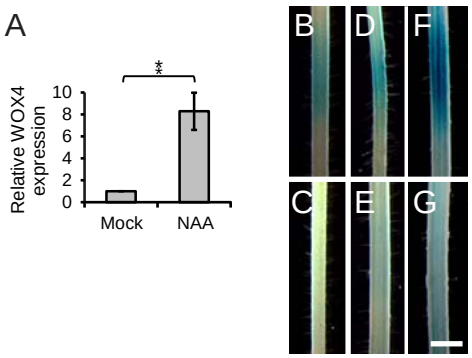

Figure S6. (A) qRT-PCR analysis of *WOX4* transcript accumulation in NAA-treated stems. Two biological replicates with three technical replicates each were included. Asterisks indicate a significance lavel of $P < 0.01$. **(B-G)** $DR5_{pro}$*:GUS* (B, C) and $WOX4_{pro}$*:GUS* (D, E) are both locally induced by NPA treatment (B, D) but not by mock treatment (C, E). $DR5_{pro}$*:GUS* induction upon NPA treatment in the *wox4-1* mutant background (F) is the same as in wild type (B) but likewise not observed in the mock-treated control (G). Scale bar: 2 mm.

Figure S7

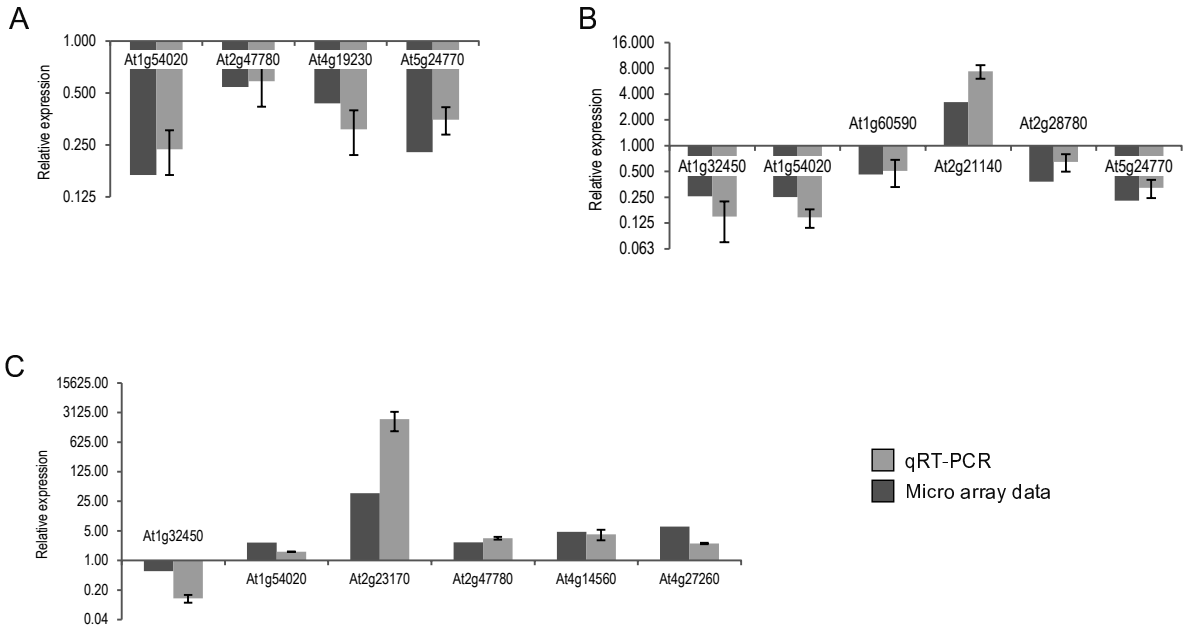

Figure S7. Micro array data validation. Selected genes that were found to be differentially expressed in *wox4-1* primary stem fragments compared to wild type primary stems (A), at the base of *wox4-1* stems compared to the base of the wild type stems (B) and in NPA-treated compared to mock-treated stems (C). Three technical replicates per sample were included in the analysis and normalized to the control (*UBC28*, *At1g64320*). The respective reference sample (wild type internode in A, wild type base in B and mock-treated in C) was set to 1. All data are shown in comparison to relative expression changes determined by respective micro array experiments.

Table S1 (A) Cloning primers

Primer	Sequence 5'-3'
ATHB8for5	TCACTCTTCTTGTGAACTCCTCTC
ATHB8rev5	TACCGGAGATAAGGCCTTGA
At5g57130for1	ATGGCAAAGCTAGAGAGAGG
At5g57130rev1	GCTTTTATGTTCAGGTCGAGG
H4_for	TTCACATCTTTCTCACCCAAATCTACT
H4_rev	TTTCAACCGAAACTGCTGAAGC
PXYfor7	TTTCCCTCGACCTCTCTCAC
PXYrev7	CCGTTCTCTTTGTTTTTTCCCC
WOX4for2	GGTAGGATCCATGCTAGCGAAGTCATGAAGGTGAGGCAGAAA
WOX4for4	CGAGAAAGGCATGCATAGCATT
WOX4for8	ACTAGGTACCTTTGGTTCATTTGGTTTTGGGAGC
WOX4rev2	ACTAGAGCTCTTGAAAAGATTCTTCTTGTTATCATCTCAT
WOX4rev4	TCATGACTTCATCTCCCTTCAGGA
WOX4rev8	GCATGGATCCTACCATGGCTATATGTTAAAACTAGCAAATGC

Table S1 (B) Primers used for (q)RT –PCR

Primer	Sequence 5'-3'
At1g32450_for	TTCTCAGCGATTCGTATTGG
At1g32450_rev	TTCTTTAGGATGCTCCTCATC
At1g60590_for	TCGAGGCCTCAACGATGATC
At1g60590_rev	GCCTCTTCCATCAATAACACC
At2g21140_for	GTCATTGGCTACTCAGAAATC
At2g21140_rev	TCGATAGAAACACGATCTTGG
At2g23170_for	GTTGATTCAGCTCTGCGATC
At2g23170_rev	TCATCAATGGTTGGCATCAAC
At2g28780_for	ATGATAGCATGTCAGCAACG
At2g28780_rev	ACACGTTCTTGTATATTCTTG
At3g01500_for	AACCGAAGCATACGACGAG
At3g01500_rev	CACACACGTGAGTCTGAAC
At4g14560_for	TCCGTTAAAGTATAGTGAGAG
At4g14560_rev	ATATGGAGCTCCGTCCATAC
At4g27260_for	GATATTGAGCCTGAGATCAAC
At4g27260_rev	TCCTGGAGTCTTGGATTCG
At5g14740_for	GATGATCTGAAGGATGTAGC
At5g14740_rev	CAAGACAGCGTATTCAATGG
At5g24770_for	CTATGTTGAAGACTACTTGATC
At5g24770_rev	CTGAGTATGATGGGTTCAATC
At5g54020_for	AGCTTTCGTTACTTCTGTCAC
At5g54020_rev	ATAACTTCGAGTGCACGTTAG
At3g12590_for	CTACTCTTGCGTCAAGACAG
At3g12590_rev	GAAGCTGTAATTGCTCTCAAG
PIN1for7	TGTTACTGTTCGTCGTTCTAATGC
PIN1rev7	ACCACCAGAAGCCATCATCG
TUB_for3	TTCGTTCCTCGTGCAGTGCTCA
TUB_rev3	CCCTCACCTGTGTACCAATGCAAGA
UBC28q_for	TCCAGAAGGATCCTCCAACTTCCTGCAGT
UBC28q_rev	ATGGTTACGAGAAAGACACCGCCTGAATA
WOX4_for17	CTTAGCCTAAGCTGCAAAC
WOX4_rev14	CAGTGGTCGTGAAGCTGC