

Figure S1. Expression profiles of *AtWR1* in Arabidopsis root. Data are obtained from the Arabidopsis eFP browser (<http://bar.utoronto.ca/efp/cgi-bin/efpWeb.cgi>).

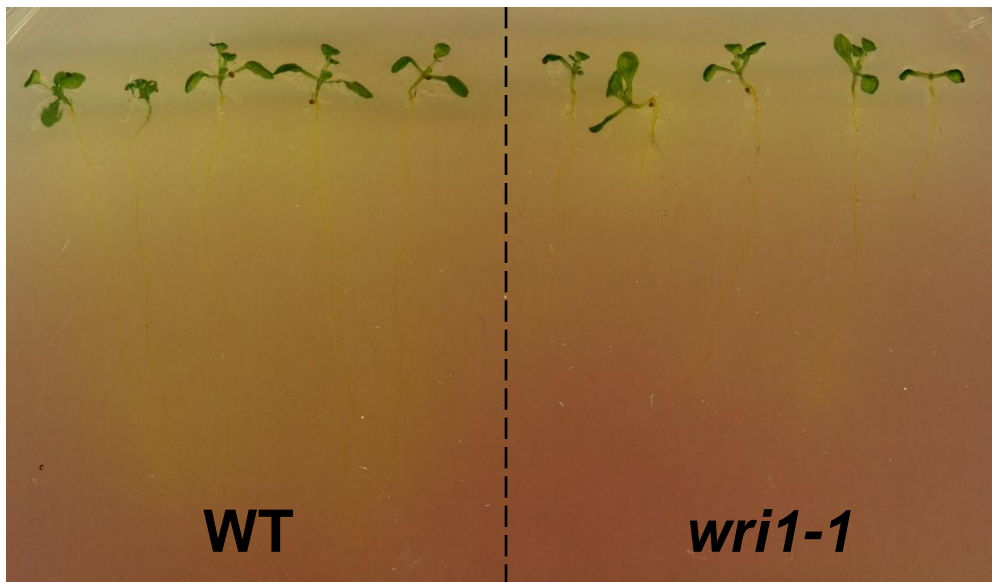
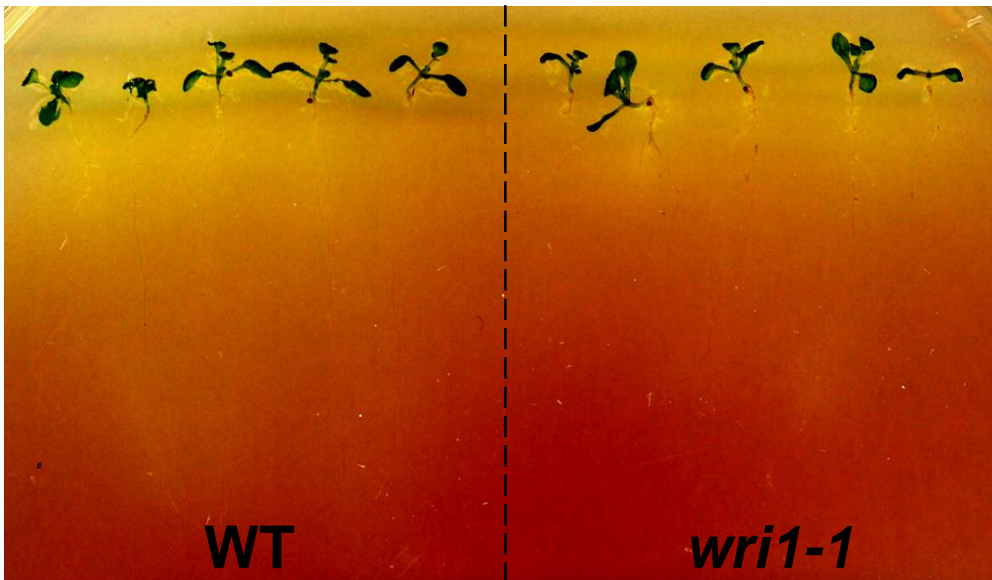
A**B**

Figure S2. Growth phenotype of WT and *wri1-1* on pH indicator plates. **A)** Original picture of WT and *wri1-1* seedlings grown on pH indicator plates. **B)** Same picture as shown in **A)** with the contrast increased.

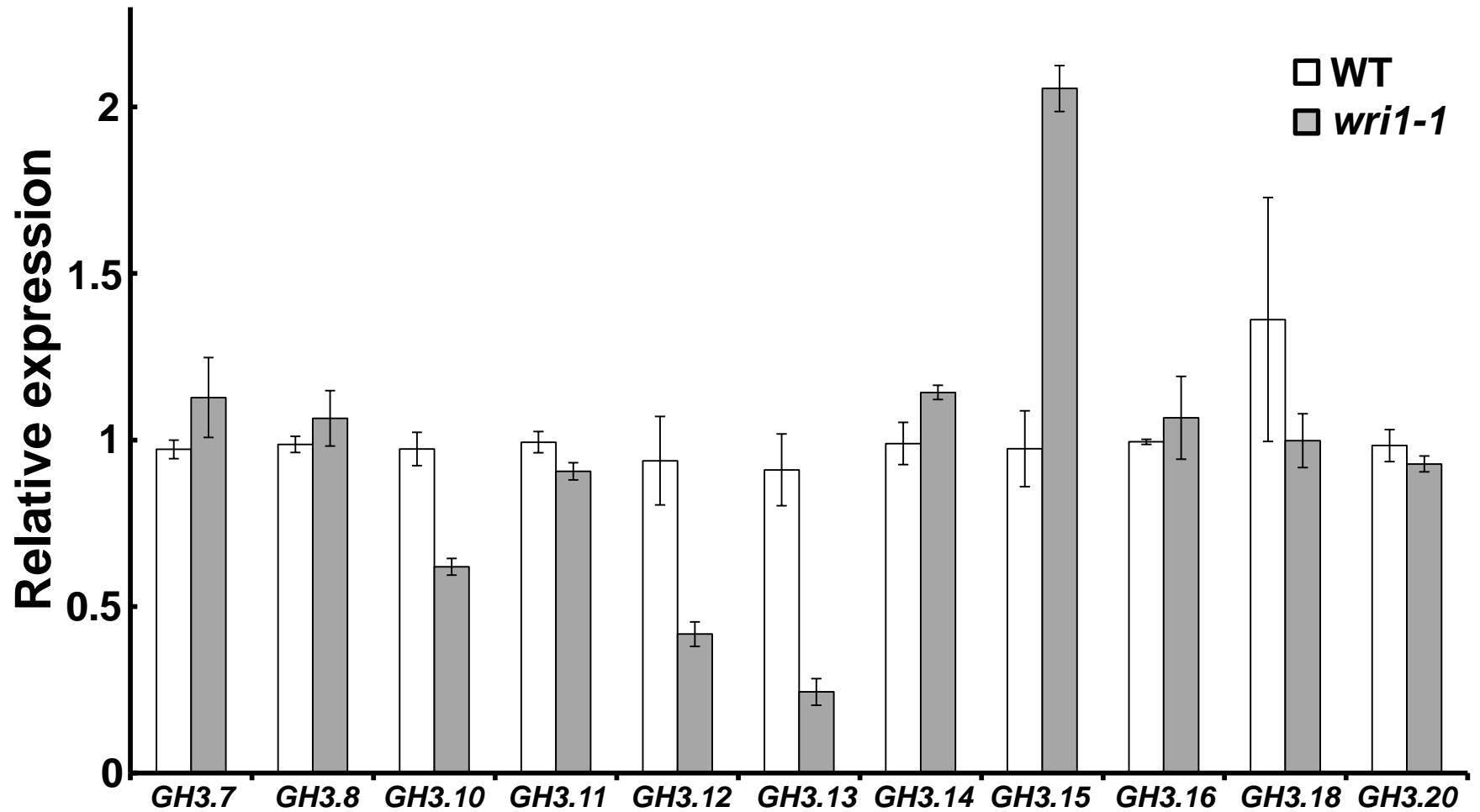


Figure S3. Gene expression of *GH3* genes of unknown function. *GH3* transcripts of WT and *wri1-1* plants were measured by quantitative real-time PCR. Results are shown as mean \pm SE ($n = 3$).

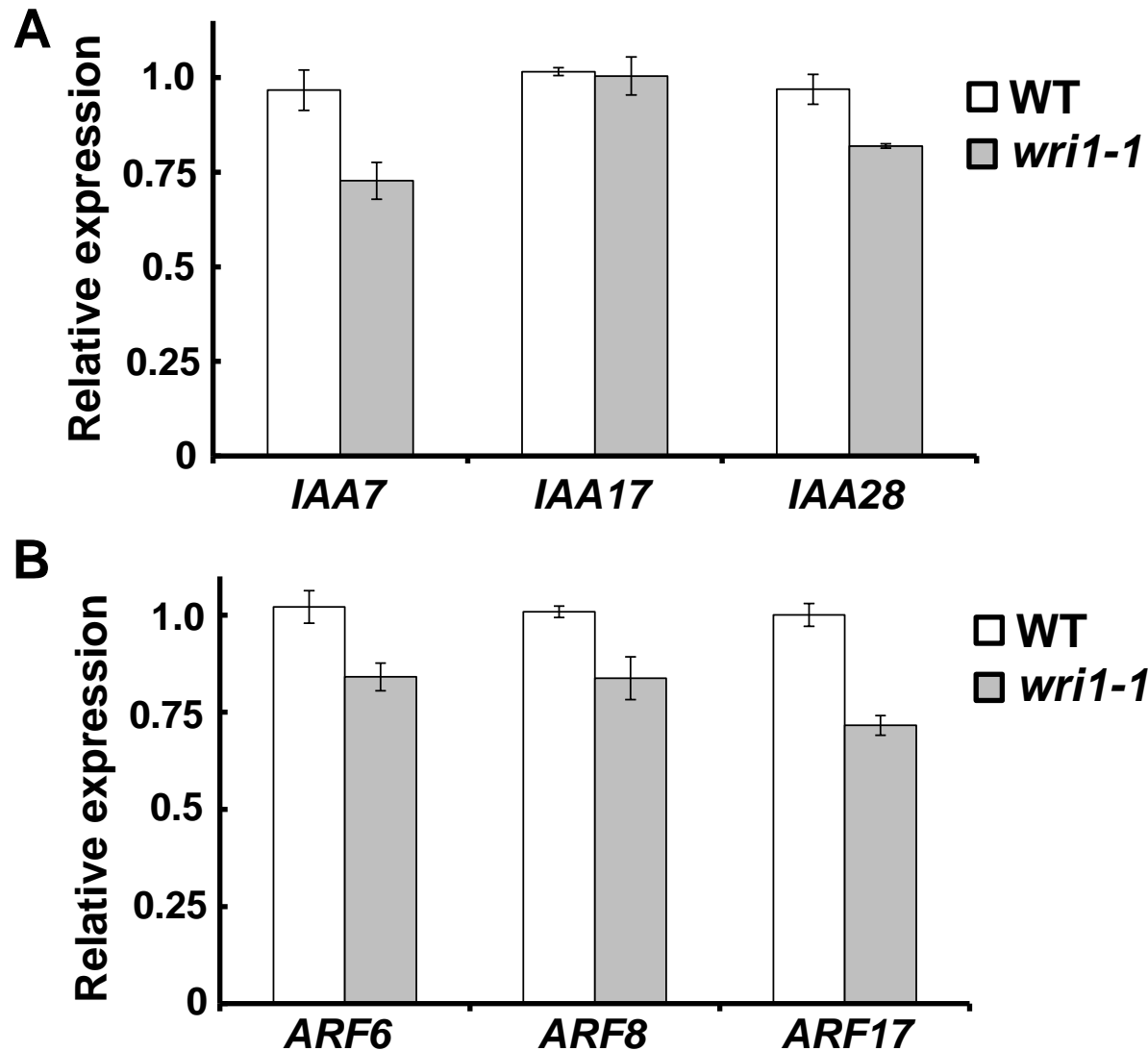


Figure S4. Gene expression of *IAA* and *ARF* auxin-responsive genes. **A)** *IAAs* and **B)** *ARFs* transcripts of WT and *wri1-1* plants were quantified by quantitative real-time PCR. Results are shown as mean \pm SE ($n = 3$).

A

GH3.3 Pro1 GATTAAAATGGTATTTGTAAGTGATAATATTAGACTTTGTGTTTGATGAT
GH3.3 Pro2 AATATTAGACTTTGTGTTTGATGATGAGGAGATATTGAAACTCGACGAGT
GH3.3 Pro3 GAGGAGATATTGAAACTCGACGAGTATGGGGTTGTATTTATAGTGGCAAG
GH3.3 Pro4 ATGGGGTTGTATTTATAGTGGCAAGAAGGAGAAAACCAACGTCAGCCAAA
GH3.3 Pro5 AGCCAAATTCCACGTCGACATAAAAAGTGGGCTCGGTTTGTTATCGTTAGA
GH3.3 Pro6 TGGGCTCGGTTTGTTATCGTTAGACCGAGACAGGGGACAAGAGGGACCGC
GH3.3 Pro7 CCGAGACAGGGGACAAGAGGGACCGCGGTCACGTAATCTTTGGCTAGTTT
GH3.3 Pro8 AGGGACCGCGGTCACGTAATCTTTGGCTAGTTTTGGGCAGACATGTGGGACTGA
GH3.3 Pro9 TGGGCAGACATGTGGGACTGATATGTCTGCGCCACGTTGGCATGTTACTT

B

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Pro1      gattaaaatggtatTTTgtaagtgataatattagactTTTgtgTTTgatgat-----  
Pro8      -----agggaccgCGGTCACGTAATCTTTggctagTTTTgggcagacatgtgggactga  
          ** *                **** * * * *      * * * **
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Figure S5. Probes for the promoter of *GH3.3* used in EMSA. **A)** The DNA sequences of probes used for the EMSA are shown. **B)** Alignment of the sequences of pro1 and pro8 by CLUSTAL O program (<http://www.ebi.ac.uk/Tools/msa/clustalo/>).

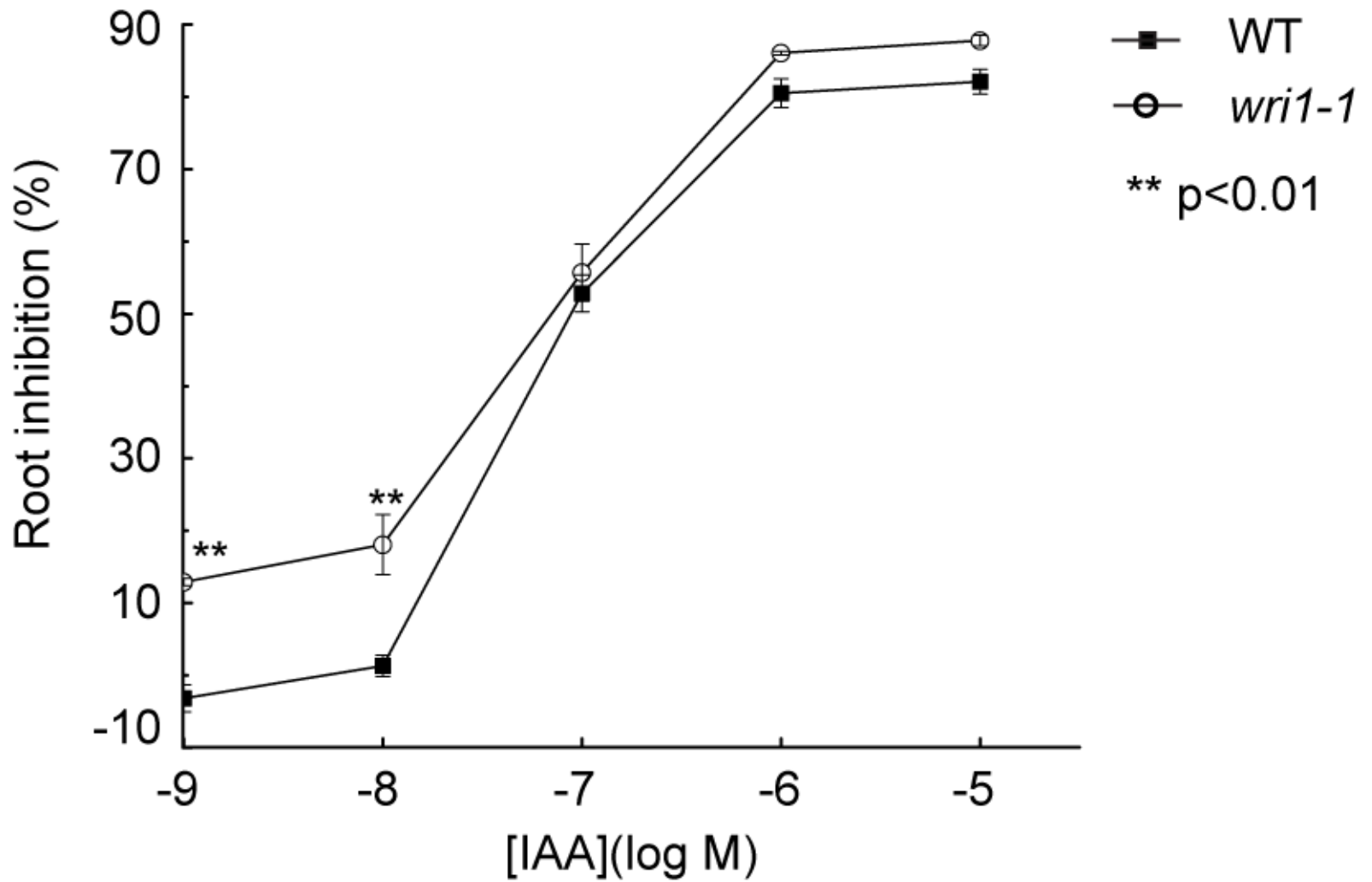


Figure S6. Primary root growth inhibition in response to different concentrations of IAA. 4-day-old seedlings of WT and *wri1-1* were transferred to growth media with various concentrations of IAA and continued growing for 6 days. In each experiment, 13 seedlings were measured. Results shown are based on three independent experiments as mean \pm SE (n=3). “**” indicate significant difference (P<0.01, t-test) to WT.

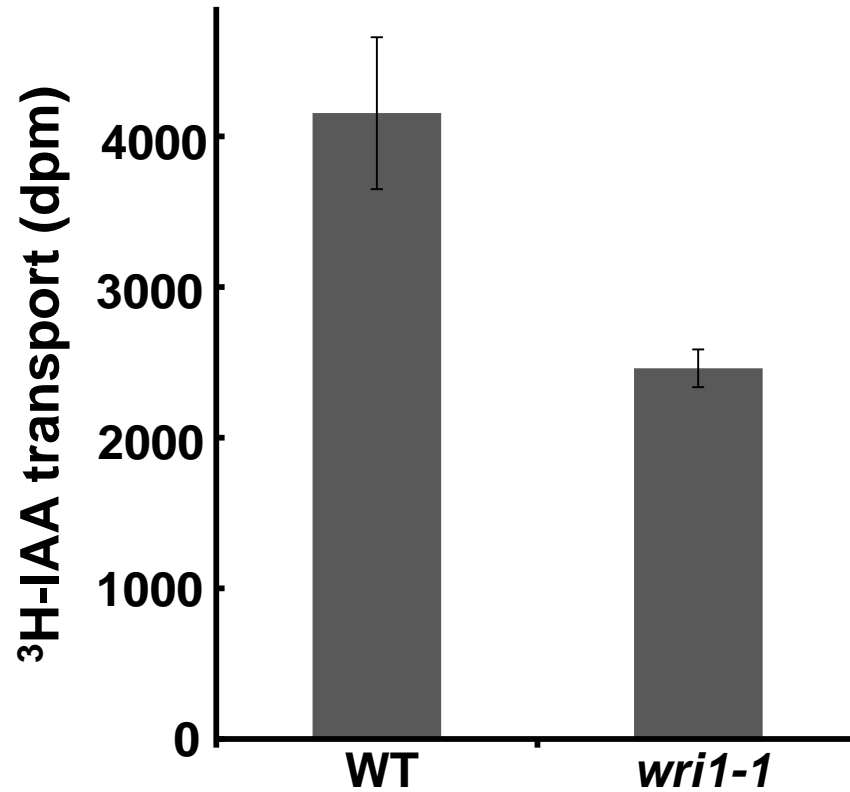


Figure S7. Auxin transport in roots of WT and *wri1-1*. Values are means \pm SE (n=3).

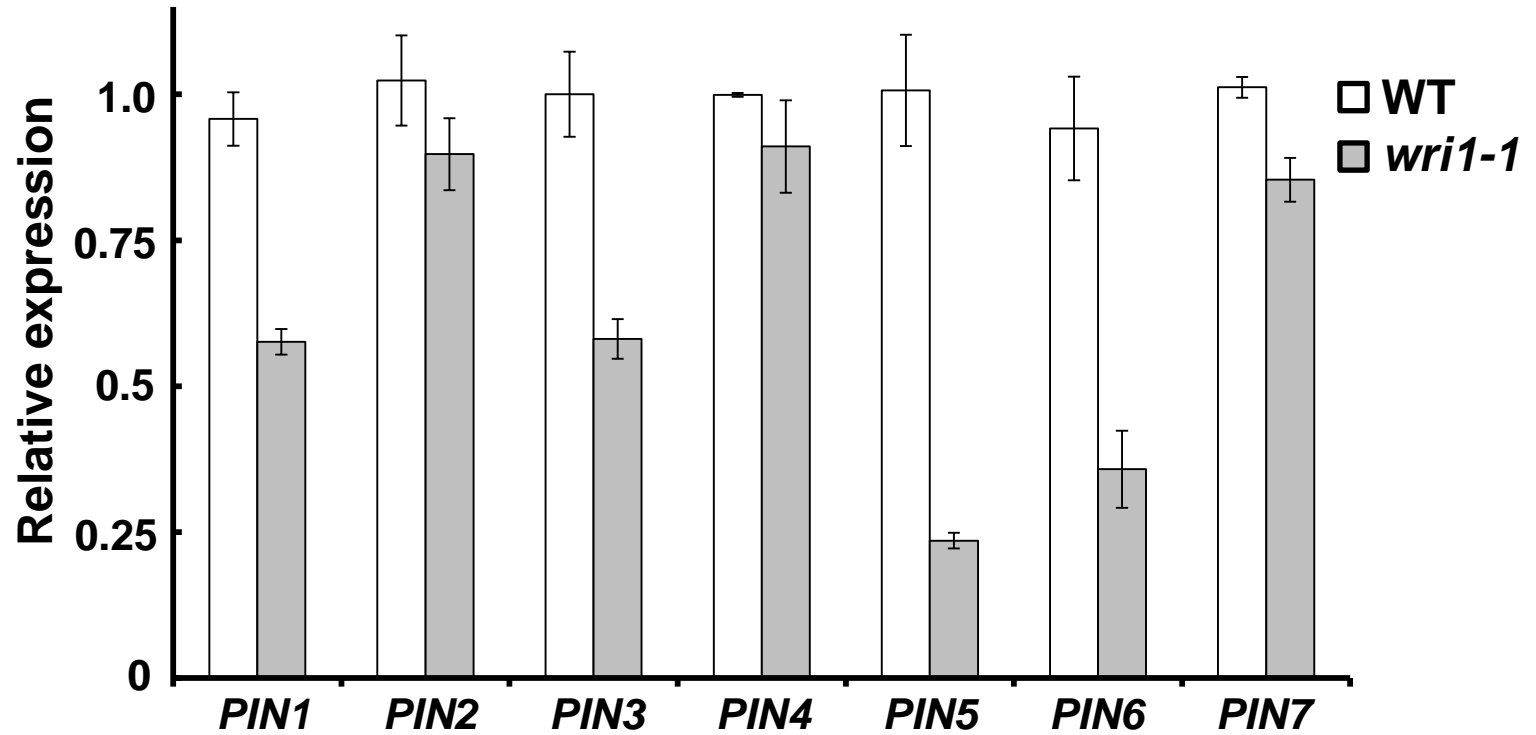


Figure S8. Expression of *PIN* genes. *PINs* transcripts of WT and *wri1-1* plants were quantified by quantitative real-time PCR. Results are shown as mean \pm SE (n = 3-4).

| Primer Name | Sequence 5' to 3' |
|--------------------|--------------------------|
| GH3.1-FW | GTCCTCCTCAGCATCGACTC |
| GH3.1-RV | ATCGTGCTTGTGTCTGCGTA |
| GH3.2-FW | GCTGTTTGGAGATGGAGGAA |
| GH3.2-RV | CCGATCGATTTATCAGCGAC |
| GH3.3-FW | ATCAGTACAAGGTGCCGAGG |
| GH3.3-RV | AAAGCTGGGCTGAAGTGTGT |
| GH3.4-FW | TGGAGGAATCGCTGAACGCGG |
| GH3.4-RV | TGCCGTTCTGCACCACACGTA |
| GH3.5-FW | TACTTCAGCCCCAAGTGTCC |
| GH3.5-RV | TCTTCACGTTCCACATTCCA |
| GH3.6-FW | CTTGAGAAACATTGGCCTGAG |
| GH3.6-RV | CAGATTCGACGAAATCAGCA |
| GH3.7-FW | TGATCTGTTTAAGGCGGTGA |
| GH3.7-RV | TAGTGTCCCGGGATAGTGA |
| GH3.8-FW | GACCTTTTAAACGCGGTCAC |
| GH3.8-RV | GTCGTTGCGGTATTTTGCTT |
| GH3.9-FW | GCAGGACGAAAGAGAGATCG |
| GH3.9-RV | AACGACCCTCCTTGGCTTAT |
| GH3.10-FW | GGGAAATCAGAGGAGAAGCA |
| GH3.10-RV | AACGTTCCCTCGTTCCACAAC |
| GH3.11-FW | GTTTCATCGGCTGGACAGTTT |
| GH3.11-RV | TCAAACGCTGTGCTGAAGT |
| GH3.12-FW | AGGGAGAGGAGAAGGAGACG |
| GH3.12-RV | ATCGATCCGTCTTTGAATCG |
| GH3.13-FW | GTGTGGATTTCGTCCTCGTTT |
| GH3.13-RV | TCAACGGTGAAGCAACATTC |
| GH3.14-FW | CACTAGCCGTGTGGATTCCCT |
| GH3.14-RV | GCAGCATTCCCTCCAAAACAT |
| GH3.15-FW | CCGCGATGTTATGGAAGAAT |
| GH3.15-RV | CGCCAGGCTTAACAACCTTA |
| GH3.16-FW | GTTAAACCTGGCGCTTTTGA |
| GH3.16-RV | AGGCTTCTTCATGCGTCACT |

| | |
|-----------|---------------------------|
| GH3.17-FW | TCGTCTCTGCTCAGCCCATCACA |
| GH3.17-RV | GCTGTAGAAGGCATCAACTTCGGCT |
| GH3.18-FW | ATCTCCCAAGGAGGTTTCGAT |
| GH3.18-RV | TTTCGCTAAAGAATCGAGCAA |
| GH3.19-FW | TGGTTCGGTTGCTCAATACA |
| GH3.19-RV | GAGGAGGAGATTTTTGGCTGT |
| GH3.20-FW | TTGGGGAAGGAAAAGTGATG |
| GH3.20-RV | GATGGCCGGTTCTTGAAATA |
| IAA7-FW | GCCAAGCTACGAGGACAAAG |
| IAA7-RV | CTCTCGGAGCAAGTCCAAC |
| IAA17-FW | AAGACGGTGATTGGATGCTC |
| IAA17-RV | TCTGCTCTTGCACTTCTCCA |
| IAA28-FW | ATGCCGTTGACCAACTCTTC |
| IAA28-RV | CATCCCCGACCAGAACTTTA |
| ARF6-FW | AATGGGAAAAAGAGGCCTTG |
| ARF6-RV | ATGCGATACCGTTACCGAGA |
| ARF8-FW | GACCCATGGGAGTCATTTGT |
| ARF8-RV | TAGAGATGGGTCGGGTTTTG |
| ARF17-FW | GGAAATGACCTGGTTGGAAA |
| ARF17-RV | GACTCTTTGCTGCCATCCTC |
| PP2A-FW | TAACGTGGCCAAAATGATGC |
| PP2A-RV | GTTCTCCACAACCGCTTGGT |
| PIN1-FW | GGCATGGCTATGTTTCAGTCTTGGG |
| PIN1-RV | ACGGCAGGTCCAACGACAAATC |
| PIN2-FW | TCACGACAACCTCGCTACTAAAGC |
| PIN2-RV | TGCCCATGTAAGGTGACTTTCCC |
| PIN3-FW | AAGGCGGAAGATCTGACCAAGG |
| PIN3-RV | TGCTGGATGAGCTACAGCTTTG |
| PIN4-FW | ACAACGTGGCAACGGAACAATC |
| PIN4-RV | GCCGATATCATCACCACCACTC |
| PIN5-FW | CCATCGGCTCTATTGTCCTTG |
| PIN5-RV | GCGACGAGCACAGGTAGAGA |
| PIN6-FW | TGGGCCGTTTTCTTCAAAGC |
| PIN6-RV | GATTGATCCGGCTGCTTGAC |

| | |
|---------|--------------------------|
| PIN7-FW | CGTGTGGCCATTGTTCAAGCTG |
| PIN7-RV | CCCTGTAICTAAGATTGCGGGATG |

Table S1. Quantitative real-time PCR primers used in this study.

| Probe ID | AGI | fold change (WT/ <i>wri1-1</i>) | P.Value | Annotation |
|-------------|-----------|-------------------------------------|----------|--|
| 256940_at | At3g30720 | 0.02 | 6.15E-12 | QQS__qua-quine starch |
| 265560_at | At2g05520 | 0.29 | 2.23E-06 | ATGRP-3_ATGRP3_GRP-3_GRP3_glycine-rich protein 3 |
| 260522_x_at | At2g41730 | 0.34 | 4.34E-06 | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G24640.1) |
| 252347_at | At3g48130 | 0.37 | 2.73E-06 | Ribosomal protein L13 homolog |
| 254150_at | At4g24350 | 0.40 | 4.69E-06 | Phosphorylase superfamily protein |
| 245076_at | At2g23170 | 0.47 | 1.22E-05 | GH3.3__Auxin-responsive GH3 family protein |
| 267262_at | At2g22990 | 0.49 | 5.37E-06 | SCPL8_SNG1__sinapoylglucose 1 |
| 265817_at | At2g18050 | 0.49 | 1.73E-05 | HIS1-3__histone H1-3 |
| 251799_at | At3g55520 | 0.49 | 1.20E-06 | FKBP-like peptidyl-prolyl cis-trans isomerase family protein |
| 258727_at | At3g11930 | 0.50 | 4.23E-06 | Adenine nucleotide alpha hydrolases-like superfamily protein |
| 263948_at | At2g35980 | 0.52 | 1.06E-05 | ATNHL10_NHL10_YLS9 |
| 263909_at | At2g36490 | 0.53 | 1.59E-05 | DML1_ROS1__demeter-like 1 |
| 263515_at | At2g21640 | 0.59 | 1.16E-05 | Encodes a protein of unknown function that is a marker for oxidative stress response. |
| 263491_at | At2g42600 | 0.62 | 3.40E-05 | ATPPC2_PPC2__phosphoenolpyruvate carboxylase 2 |
| 256502_at | At1g36730 | 0.67 | 3.97E-05 | Translation initiation factor IF2/IF5 |
| 260392_at | At1g74030 | 1.54 | 2.80E-05 | ENO1__enolase 1 |
| 257895_at | At3g16950 | 1.57 | 3.83E-05 | LPD1_ptlpd1__lipoamide dehydrogenase 1 |
| 245220_at | At1g59171 | 1.58 | 2.84E-05 | Inositol-pentakisphosphate 2-kinase family protein |
| 249384_at | At5g39890 | 1.61 | 1.00E-05 | Plant cysteine oxidase 2 |
| 254845_at | At4g11820 | 1.61 | 2.45E-05 | HMGS_MVA1__hydroxymethylglutaryl-CoA synthase / HMG-CoA synthase / 3-hydroxy-3-methylglutaryl coenzyme A synthase |
| 259969_at | At1g76550 | 1.62 | 2.47E-05 | Phosphofructokinase family protein |
| 262157_at | At1g52670 | 1.65 | 7.88E-06 | BCCP-like protein1, BLP1 |
| 255558_at | At4g01900 | 1.65 | 4.00E-05 | GLB1_PII__GLNB1 homolog |
| 256160_at | At1g30120 | 1.69 | 7.58E-06 | PDH-E1 BETA__pyruvate dehydrogenase E1 beta |
| 259095_at | At3g05020 | 1.70 | 1.68E-05 | ACP_ACP1__acyl carrier protein 1 |
| 266426_x_at | At2g07140 | 1.71 | 5.92E-06 | F-box and associated interaction domains-containing protein |
| 266426_x_at | At3g44120 | 1.71 | 5.92E-06 | Phosphoenolpyruvate/phosphate translocator |

| | | | | |
|-------------|--|------|----------|--|
| 249366_at | At5g40610 | 1.72 | 2.42E-06 | NAD-dependent glycerol-3-phosphate dehydrogenase family protein |
| 258086_at | At3g25860 | 1.73 | 6.88E-06 | LTA2_PLE2__2-oxoacid dehydrogenases acyltransferase family protein |
| 258485_at | At3g02630 | 1.80 | 1.02E-05 | Plant stearoyl-acyl-carrier-protein desaturase family protein |
| 264419_s_at | At1g43310 | 1.80 | 1.42E-05 | Nucleotide-sugar transporter family protein |
| 264419_s_at | At5g33320 | 1.80 | 1.42E-05 | Phosphoenolpyruvate/phosphate translocator |
| 247345_at | At5g63760 | 1.88 | 1.51E-06 | ARI15_ATARI15__RING/U-box superfamily protein |
| 248903_at | At5g46290 | 1.89 | 1.54E-05 | KAS I_KAS1__3-ketoacyl-acyl carrier protein synthase I |
| 248690_at | At5g48230 | 1.90 | 2.65E-05 | ACAT2_EMB1276__acetoacetyl-CoA thiolase 2 |
| 266035_at | At2g05990 | 1.93 | 2.14E-06 | ENR1_MOD1__enoyl-ACP reductase |
| 246565_at | At5g15530 | 1.95 | 4.07E-06 | BCCP2_CAC1-B__biotin carboxyl carrier protein 2 |
| 249490_s_at | At5g39110 At5g39120 At5g39150 At5g39180 | 2.06 | 2.16E-05 | RmlC-like cupins superfamily protein |
| 260982_at | At1g53520 | 2.08 | 1.62E-06 | Fatty acid binding protein |
| 265843_at | At2g35690 | 2.11 | 9.09E-07 | ACX5__acyl-CoA oxidase 5 |
| 252863_at | At4g39800 | 2.11 | 1.17E-06 | ATIPS1_ATMIPS1_MI-1-P SYNTHASE_MIPS1__myo-inositol-1-phosphate synthase 1 |
| 253660_at | At4g30140 | 2.17 | 2.09E-05 | CDEF1__GDSL-like Lipase/Acylhydrolase superfamily protein |
| 249474_s_at | At5g39130 At5g39160 At5g39190 | 2.19 | 1.97E-05 | RmlC-like cupins superfamily protein |
| 251378_at | At3g60660 | 2.42 | 1.12E-07 | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1395 (InterPro:IPR009829) |
| 250472_at | At5g10210 | 2.43 | 1.99E-05 | CONTAINS InterPro DOMAIN/s: C2 calcium-dependent membrane targeting (InterPro:IPR000008); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G65030.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). |
| 261335_at | At1g44800 | 2.43 | 3.45E-05 | nodulin MtN21 /EamA-like transporter family protein |

| | | | | |
|-----------|-----------|------|----------|---|
| 259813_at | At1g49860 | 2.44 | 1.65E-05 | ATGSTF14_GSTF14__glutathione S-transferase (class phi) 14 |
| 260475_at | At1g11080 | 2.47 | 3.50E-05 | scpl31__serine carboxypeptidase-like 31 |
| 264014_at | At2g21210 | 2.65 | 2.43E-05 | SAUR-like auxin-responsive protein family |
| 249675_at | At5g35940 | 2.88 | 5.49E-07 | Mannose-binding lectin superfamily protein |
| 267626_at | At2g42250 | 3.27 | 5.72E-06 | CYP712A1__cytochrome P450, family 712, subfamily A, polypeptide 1 |
| 245571_at | At4g14695 | 3.47 | 7.79E-07 | Uncharacterised protein family (UPF0041) |

Table S2. Genes expressed differently in roots of *wri1-1* compared to WT plants in microarray analysis.