

Table 1. Origin and Nature of Lines.

Line	Origin/Nature
PIN1::gPIN1:YFP	(Xu et al., 2006)
PIN1::nYFP	Transcriptional fusion of <i>PIN1</i> (AT1G73590; -4,171 to -1; primers: “PIN1 transc 4171 forw” and “PIN1 transc rev”) to HTA6:EYFP (Zhang et al., 2005)
PIN1::gPIN1:CFP	(Gordon et al., 2007)
<i>pin1-051</i>	NASC; GK-051A10-012139 (Kleinboelting et al., 2012); contains a T-DNA insertion after +2234 of <i>PIN1</i>
PIN1::gPIN1:GFP	Xu et al. 2006
ATML1::cPIN1:GFP	Transcriptional fusion of <i>ATML1</i> (AT4G21750; -5,016 to -1,597; primers “XhoI ATML1 p F” and “BamHI ATML1p R”) to translational fusion of <i>PIN1</i> cDNA (GenBank accession no. AY093960; ABRC clone no. U12338; primers “BamHI PIN1 cDNA F” and “KpnI PIN1 cDNA R”) to EGFP (Clontech; insertion after +651 of <i>PIN1</i> ; primers “XhoI GFP no ATG Fwd” and “XhoI GFP no* Rev”)
PIN1::cPIN1:GFP	Transcriptional fusion of <i>PIN1</i> (-4,168 to -14; primers “XhoI full length PIN1p F” and “BamHI PIN1p rev”) to translational fusion of <i>PIN1</i> cDNA (GenBank accession no. AY093960; ABRC clone no. U12338; primers “BamHI PIN1 cDNA F” and “KpnI PIN1 cDNA R”) to EGFP (Clontech; insertion after +651 of <i>PIN1</i> ; primers “XhoI GFP no ATG Fwd” and “XhoI GFP no* Rev”)

SHR::cPIN1:GFP	Transcriptional fusion of <i>SHR</i> (AT4G37650; -2505 to -16; primers “SHR prom SalI Forw2” and “SHR prom BamHI Rev”) to translational fusion of <i>PIN1</i> cDNA (GenBank accession no. AY093960; ABRC clone no. U12338; primers “BamHI PIN1 cDNA F” and “KpnI PIN1 cDNA R”) to EGFP (Clontech; insertion after +651 of <i>PIN1</i> ; primers “XhoI GFP no ATG Fwd” and “XhoI GFP no* Rev”)
SCL32::cPIN1:GFP	Transcriptional fusion of <i>SCL32</i> (AT3G49950; -2888 to -2; primers “SCL32 Translational FWD” and “SCL32 prom BamHI Rev”) to translational fusion of <i>PIN1</i> cDNA (GenBank accession no. AY093960; ABRC clone no. U12338; primers “BamHI PIN1 cDNA F” and “KpnI PIN1 cDNA R”) to EGFP (Clontech; insertion after +651 of <i>PIN1</i> ; primers “XhoI GFP no ATG Fwd” and “XhoI GFP no* Rev”)
PIN3::gPIN3:YFP	ABRC; (Zhou et al., 2011)
PIN4::gPIN4:YFP	ABRC; (Zhou et al., 2011)
PIN7::gPIN7:YFP	ABRC; (Zhou et al., 2011)
<i>pin1-1</i>	ABRC; WT at the <i>TTG1</i> (AT5G24520) locus (Galweiler et al., 1998; Goto N, 1987; Sawchuk et al., 2013)
<i>pin3-3</i>	(Friml et al., 2002b)
<i>pin4-2</i>	(Friml et al., 2002a)
<i>pin7^{En}</i>	(Blilou et al., 2005)

Blilou, I., Xu, J., Wildwater, M., Willemsen, V., Paponov, I., Friml, J., Heidstra, R., Aida, M., Palme, K., Scheres, B., 2005. The PIN auxin efflux

- facilitator network controls growth and patterning in Arabidopsis roots. *Nature* 433, 39-44.
- Friml, J., Benkova, E., Blilou, I., Wisniewska, J., Hamann, T., Ljung, K., Woody, S., Sandberg, G., Scheres, B., Jurgens, G., Palme, K., 2002a. AtPIN4 mediates sink-driven auxin gradients and root patterning in Arabidopsis. *Cell* 108, 661-673.
- Friml, J., Wisniewska, J., Benkova, E., Mendgen, K., Palme, K., 2002b. Lateral relocation of auxin efflux regulator PIN3 mediates tropism in Arabidopsis. *Nature* 415, 806-809.
- Galweiler, L., Guan, C., Muller, A., Wisman, E., Mendgen, K., Yephremov, A., Palme, K., 1998. Regulation of polar auxin transport by AtPIN1 in Arabidopsis vascular tissue. *Science* 282, 2226-2230.
- Gordon, S.P., Heisler, M.G., Reddy, G.V., Ohno, C., Das, P., Meyerowitz, E.M., 2007. Pattern formation during de novo assembly of the Arabidopsis shoot meristem. *Development* 134, 3539-3548.
- Goto N, S.M., Kranz AR, 1987. Effect of gibberellins on flower development of the pin-formed mutant of Arabidopsis thaliana. *Arabidopsis Information Service* 23, 66-71.
- Kleinboelting, N., Huep, G., Kloetgen, A., Viehoever, P., Weisshaar, B., 2012. GABI-Kat SimpleSearch: new features of the Arabidopsis thaliana T-DNA mutant database. *Nucleic Acids Res* 40, D1211-5.
- Sawchuk, M.G., Edgar, A., Scarpella, E., 2013. Patterning of leaf vein networks by convergent auxin transport pathways. *PLoS Genet* 9, e1003294.
- Xu, J., Hofhuis, H., Heidstra, R., Sauer, M., Friml, J., Scheres, B., 2006. A molecular framework for plant regeneration. *Science* 311, 385-388.
- Zhang, C., Gong, F.C., Lambert, G.M., Galbraith, D.W., 2005. Cell type-specific characterization of nuclear DNA contents within complex tissues and organs. *Plant Methods* 1, 7.
- Zhou, R., Benavente, L.M., Stepanova, A.N., Alonso, J.M., 2011. A recombineering-based gene tagging system for Arabidopsis. *Plant J* 66, 712-723.