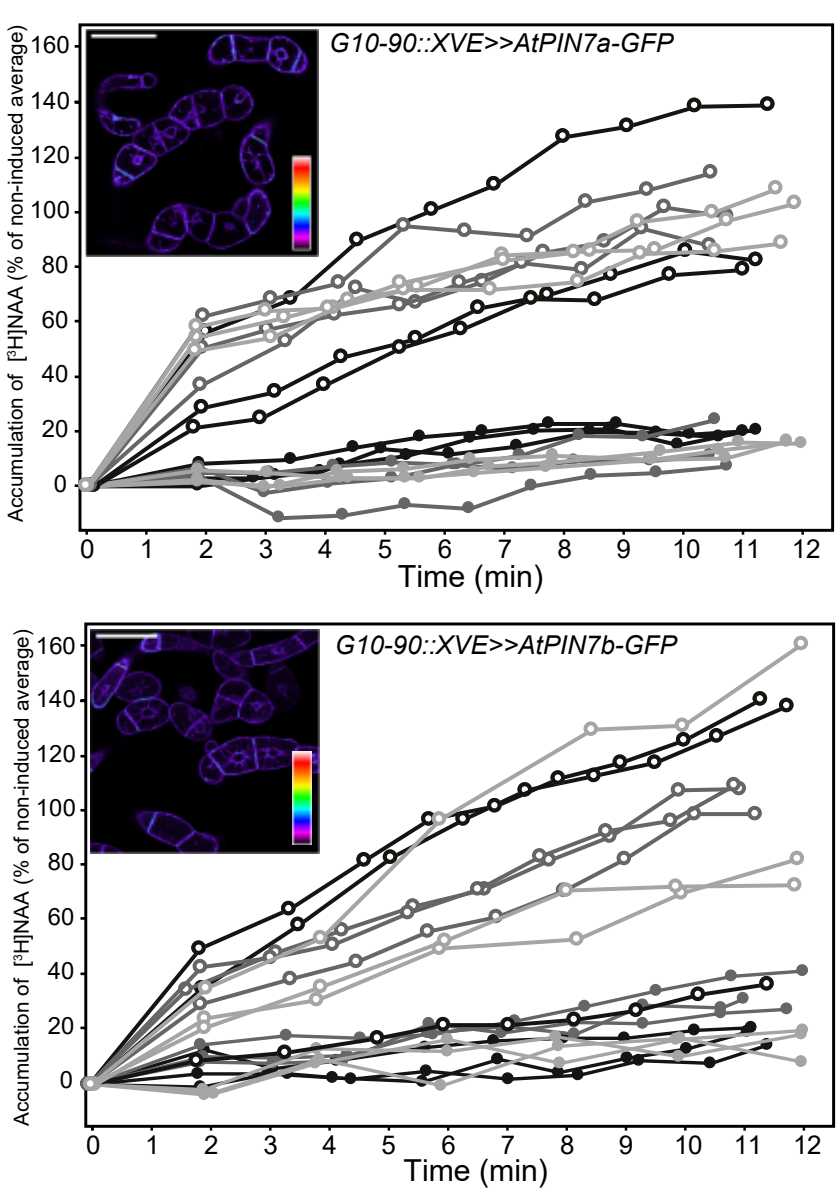
A

| Part | *PIN4a* | *PIN4b* | *PIN4c* | *PIN4a* | *PIN4b* | *PIN4c* | References |
|---|---|---|---|---|---|---|---|
| Aerial | 299 | 314 | 27 | 49.14% | 46.64% | 4.22% | (Cheng et al., 2017) |
| Dark grown seedling | 437 | 333 | 28 | 54.76% | 41.73% | 3.51% | (Cheng et al., 2017) |
| Leaf | 1274 | 1197 | 79 | 49.96% | 46.94% | 3.10% | (Cheng et al., 2017) |
| Light grown seedling | 1463 | 1341 | 52 | 51.23% | 46.95% | 1.82% | (Cheng et al., 2017) |
| Root | 101 | 50 | 4 | 65.16% | 32.26% | 2.58% | (Cheng et al., 2017) |
| Root tip | 167 | 120 | 6 | 57.00% | 40.95% | 2.05% | (Ruzicka et al., 2017) |
| Root apical meristem | 51 | 53 | 19 | 41.46% | 43.49% | 15.45% | (Cheng et al., 2017) |
| Seedling hypocotyl | 41 | 30 | 6 | 53.54% | 31.15% | 7.79% | (Klepikova et al., 2016) |

B




**Supplemental Figure 1. Determination of the relative presence of PIN4 transcripts in selected tissues and organs and [3H]NAA accumulation kinetics of PIN7a and PIN7b. Related to Figure 1.**

(A) Quantification of the RNA-seq reads spanning the exon1-exon2 junction corresponding to the detected PIN4 transcripts in selected Arabidopsis thaliana tissue sources, their ratio was calculated as a percentage total reads mapped to this area, as assessed from the genome browser graphic interface.

(B) [3H]NAA accumulation kinetics in tobacco BY-2 cells following 2-day induction of either G10-90::XVE>>AtPIN7a-GFP (upper plot) or G10-90::XVE>>AtPIN7b-GFP (lower plot) constructs with 1 μM β-estradiol. Inset: representative images of GFP fluorescence of the respective protein on the plasma membrane in the β-estradiol treated cells. Obtained values were normalized to the average maximum [3H]NAA accumulation rates in the non-induced lines. Closed symbols: β-estradiol-induced lines, open symbols: solvent control. Different shades of gray denote corresponding biological replicates done at the same time for PIN7a, PIN7b and their respective non-induced controls. Bars, 50 μm.