

Expanded View Figures

Figure EV1. Comparing FACS and FANS data of CC and QC.

(A) Heatmap of the expression values of published QC- and CC-associated genes in the QC-up and CC-up FANS transcriptome data. Four biological replicates are compared. The hierarchical clustering of the samples is based on Euclidean distance. (B) PCA of published FACS transcriptomes of QC and CCs (Li et al, 2016). Each dot represents one biological replicate. The first two components with the largest contributions are shown. Replicate PET111_3 was considered an outlier and removed for further analysis. (C) Pairwise correlation of QC and CC transcriptomes from this study (FANS) and from published sorted protoplast data (FACS, Li et al, 2016). The red line represents a linear regression. Spearman's rank correlation coefficients (ρ) and P values are shown. Correlation P value between FACS QC and FANS QC is < 2.2e-16. (D) Venn diagrams of FANS DEGs (CC/QC) from this study and FACS DEGs (CC/QC) from (Li et al, 2016). The P values indicate the statistical significances of the overlaps by hypergeometric tests. (E) GO analysis of shared and non-shared DEGs from FANS (this study) and FACS (Li et al, 2016) transcriptomes as shown in (C). The color gradient indicates –log10 (FDR) by Fisher exact test and Yekutieli correction (FDR < 0.05).

Α							
	Columella (5551)	160 n	.S.	4233	P	=4.70e <mark>-360</mark>	1158
	LRC and non hair cells (43)	1 n.s.		34		P= <mark>0.006</mark>	65 8
	Elongation zone (843)	<mark>3</mark> 5 n.	S.	691		P=1.80e- <mark>14</mark>	117
	Mature zone (2726)	126	n.s.	2277		P=3.58e-2 <mark>6</mark>	323
	Mature xylem pole (739)	<mark>2</mark> 8 n.	S.	640		P=0.0010	0 71
	Phloem and companion cells (234)	5 n.s.		208		n.	s.21
	Hair cells (428)	7 n.s.		401		n.	s. <mark>20</mark>
	Non-hair cell (63)	0		61		n	.s. <mark>2</mark>
	Stele (3)	0		3			0
	Phloem pole pericycle (221)	17 n.	s.	200		n	.s. 4
	Protophloem and metaphloem (154)	13 n.	S.	138		n	i.s. <mark>3</mark>
	Mature endodermis (882)	63 P=	0.0072	786		n.	s. 3 <mark>3</mark>
	Developing xylem (604)	63 P	0.00023	530		n.	s. 11
	Mature cortex (199)	23 P	0.0064	168		n	.s. <mark>8</mark>
	Meristematic zone (2017)	235 P	=2.93e-32	1723		n.	s. 5 <mark>9</mark>
	QC (4770)	801 P	=4.41e-240	3764		n.s	20 <mark>5</mark>
	Developing cortex (95)	30 P-	4.25e-16	65			0
	C)%	20%	40%	60%	80%	100%
В	Phloom (42)	0		22		P-5 01o 11	2 20
	Filidem (43)	60 =	0 00034	23		P=0.016-10	144
	Early vessels elements (370) Starch sheath (342)	17 n s		283		P=8 230-0	5 42
	Fibers (134)	11 n.s	· ·	112		n «	s 11
	Enidermis (127)	6 n s		112		n	s 8
	Proximal cambium xylem (54)	3 n.s		48		n	s. 3
	Distal cambium phloem (5)	0	•	5			0
	0	L <u> </u>	20%	40%	60%	80%	100%
С			2070	1070	0070	0070	10070
	Organ primordia (68)	<mark>6 n</mark> .s.		48		P=0.0001	2 14
	Shoot phloem (602)	<mark>35</mark> n.s	3.	452		P=3.0 <mark>2e-25</mark>	115
	Ubiquitous L1 layer (217)	<mark>1</mark> 0 n.s	S.	168		P=1.05 <mark>e-08</mark>	39
	Shoot xylem (426)	<mark>29</mark> n.s	ŝ.	336		P=1.04e- <mark>08</mark>	61
	Meristematic L1 layer (566)	<mark>30</mark> n.s	3.	458		P=5.98e- <mark>10</mark>	78
	Central zone (208)	<mark>16</mark> n.s	S.	170		P=0.020	22
	L3 layer (665)	57 P	=0.00017	516		P=1.40e- <mark>11</mark>	92
	Abaxial organ boundaries (710)	67 P	=2.16e-06	548		P=4.25e- <mark>11</mark>	95
	L2 layer (3295)	327 P	=1.31e-31	2788		n.s	.180
	Adaxial organ boundaries (144)	17 P	=0.0014	117		n.s	s. <mark>10</mark>
	0	%	20%	40%	60%	80%	100%
	Overlap with FANS QC-up DEG	s N	lon-shared	DEGs	Overla	ap with FAN	S CC-u

Figure EV2. Comparison of FANS CC and QC DEGs from this study with published data of different tissues.

(A-C) Comparison of FANS-derived DEGs from this study with tissue-specific DEGs from FACS of root cells (Li et al, 2016) (A), FANS of vascular cells (Shi et al, 2021) (B) and FACS of shoot apical meristem cells regions (Yadav et al, 2014) (C). The numbers of the published tissue-specific DEGs are shown in brackets. The numbers of shared DEGs and non-shared DEGs are indicated. *P* values by hypergeometric test are shown; n.s., not significant.



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	whole root DEGs								
0 WOX5-ad	% 20% ctivated	40% 6 Non-shared	0% 80% 100 ■ WOX5-repre)% ssed					
Stele (3)	0	3	0						
Hair cells (428)	58 P=6.31e-13	366	n.s. 4						
Mature zone (2726)	318 P=9.77e-54	2387	n.s. 21						
Columella (5551)	629 P=1.26e-113	4818	n.s. 104						
Elongation zone (843)	<mark>49</mark> n.s.	763	n.s. 3 <mark>1</mark>						
Non-hair cell (63)	3 n.s.	59	n.s. 1						
Mature endodermis (882)	21 ^{n.s.}	840	n.s. 21						
Mature xylem pole (739)	6 n.s.	702	n.s. <mark>31</mark>						
Phloem pole pericycle (221)	5 n.s.	207	n.s. <mark>9</mark>						
Mature cortex (199)	3 n.s.	186	n.s. <mark>10</mark>						
Phloem and companion cells (234)	4 n.s.	217	n.s. <mark>13</mark>						
LRC and non hair cells (43)	2 n.s.	36	n.s. 5						
Developing cortex (95)	2 n.s.	75	P=4.36e-06 18						
Protophloem and metaphloem (154)	0	116	P=4.40e-15 38						
QC (4770)	102 n.s.	3431	P=1.75e-637 1237						
Meristematic zone (2017)	16 n.s.	1363	P=5.23e-332 638						
Developing xylem (604)	0	375	P=7.48e-130 229						

Figure EV3. Comparison of WOX5 DEGs from sorted nuclei and the whole-root tip.

(A) Venn diagrams of WOX5 DEGs from FANS transcriptomes (this study) and whole-root-tip transcriptome (Padj < 0.05, FC ± 1.5, Clark et al, 2020). P values indicate the statistical significance of the overlaps by hypergeometric tests. (B) Comparison of the WOX5 DEGs derived from whole-root tips (Clark et al, 2020), which are not shared with our FANS data, with FACS-derived DEGs of different root regions from (Li et al, 2016). The numbers of the published tissue-specific DEGs are shown in brackets. The numbers of shared DEGs and non-shared DEGs are indicated. P values by hypergeometric test are shown; n.s., not significant.



Indirectly activated WOX5 DEGs (528)
Indirectly repressed WOX5 DEGs (639)

Figure EV4. Integrated analysis of indirect WOX5 DEGs, dHMs, and dACRs between wox5-1 and WT QC.

(A) Histone modification and chromatin accessibility profiles between 3 kb upstream of TSS and downstream 0.5 kb of TTS of unchanged genes (unchanged expression between *wox5-1* and wild-type QC). (B) Venn diagrams of indirectly regulated WOX5 DEGs and the genes assigned to dHMs and dACRs. *P* values indicate the statistical significance of the overlaps by hypergeometric tests. (C) Comparison of WOX5-increased activating and repressive dHMs reveals no enrichment of bivalent marks in indirect regulated WOX5 DEGs.



Figure EV5. Integrated analysis of QC-up/CC-up DEGs and WOX5 DEGs.

(A) GO analysis of the "paradoxical" gene subset. The color gradient indicates -log10 (FDR) by Fisher exact test and Yekutieli correction (FDR < 0.05). The number of genes in each term is indicated. (B) Venn diagrams of QC-up/CC-up DEGs and indirectly regulated WOX5 DEGs. *P* values indicate the statistical significance of the overlaps by hypergeometric tests.