

**Supplementary Table 1: List of cloning primers**

cloning system	gene ID	alias	primer name	orientation	sequence
GreenGate	<b>Promoter modules</b>				
	AT3G11260	pWOX5	RD_GreenGate pWOX5 F	F	AAAGGTCTCAACCTAAAGACTTTTATCTACCA ACTTCAAAAAG
			RD_GreenGate pWOX5 R	R	AAAGGTCTCATGTTTCGTTTCAGATGTAAAG
			RD_GG pWOX5 BsaI a v2 F	F	AGAGACCAAATTATTTTGGTTATATGGTAG
			RD_GG pWOX5 BsaI a v2 R	R	CTACCATATAACCAAATAATTTGGTCTCT
			RD_GreenGate pWOX5 BsaI b F	F	ATTACGATGTGAGAGCGCCTTCAACTTT
			RD_GreenGate pWOX5 BsaI b R	R	AAAGTTGAAGGCGCTCTCACATCGTAAT
	AT5G10510	pPLT3	RD_GG pPLT3 F V2	F	AAAGGTCTCAACCTAATTTAACGTATTCTTTC
			RD_GG pPLT3 R V2	R	AAAGGTCTCATGTTAACTTTCTTATAAAAAC AATT
	<b>CDS modules</b>				
	AT3G11260	WOX5	RD_GreenGate WOX5 F	F	AAAGGTCTCAGGCTTAATGTCTTTCTCCGTG
			RD_GreenGate WOX5 Mitte R	R	GACGTCGTGGTGGTTTCTCGAATATATT
			RD_GreenGate WOX5 Mitte F	F	AATATATTCGAGAAACCACCACGACGTC
			RD_GreenGate WOX5 R	R	AAAGGTCTCACTGAAAAGAAAGCTTAATCG
	AT5G10510	PLT3	RD_GreenGate PLT3 F	F	AAAGGTCTCAGGCTTAATGGAGATGTTGAG
			RD_GreenGate PLT3 R	R	AAAGGTCTCACTGAGTAAGACTGATTAGGC
		PLT3ΔPrD	RD_GreenGate PLT3 F	F	AAAGGTCTCAGGCTTAATGGAGATGTTGAG
			RD_PLT3ΔPrD1 CDS1 R	R	CCAGCTGCAACACCAAGTGACAAAG
			RD_PLT3ΔPrD1 linker F	F	CTTGGTGTTCAGCTGGTGCTG
			RD_PLT3ΔPrD1 linker R	R	GTCTTCTCTGCTCCTGCGGCAG
RD_PLT3ΔPrD1 CDS2 F			F	CGCAGGAGCAGAGAAGACAGATTCTG	
RD_GG PLT3ΔPrDs R			R	AAAGGTCTCACTGAGTGAAGTTGATGATGAC	
Gateway	AT3G11260	WOX5	YS_WOX5 F CACC	F	CACCATGTCTTTCTCCGTGAAAGGTCGAAGCTT ACG
			YS_WOX5 R -stop	R	AAGAAAGCTTAATCGAAGATCTAATGGC
	AT3G20840	PLT1	YS_PLT1 F CACC	F	CACCATGAATTCTAACAACCTGGCTTGGCT
			YS_PLT1 r -stop	R	CTCATTCCACATAGTGAAAACACCACCAGGG
	AT1G51190	PLT2	YS_PLT2 F CACC	F	CACCATGAATTCTAACAACCTGGCTCGCGTTCCC TCT
			YS_PLT2 R -stop	R	TTCATTCCACATCGTGAAAACACCTCCT
	AT5G10510	PLT3	YS_PLT3 F CACC	F	CACCATGGAGATGTTGAGGTCATCTGATCAGT CTCA
			YS_PLT3 R -stop	R	GTAAGACTGATTAGGCCAGAGGAAG
		PLT3ΔQ	YS_PLT3 F CACC	F	CACCATGGAGATGTTGAGGTCATCTGATCAGT CTCA
			RD_PLT3 Seg1 R	R	GAGATGAGAAATGGTGAAGTTGATGATGAC
			RD_PLT3 Seg2 F	F	CTTCACCATTTCTCATCTCCTAATCACAGTAGC
			RD_PLT3 Seg2 R	R	GAAGAAGTTGTGGTGGTAAAGAGCAG
			RD_PLT3 Seg3 F	F	CACCACCACAACCTTCTCCAGCATTTTCC
			YS_PLT3 R -stop	R	GTAAGACTGATTAGGCCAGAGGAAG

**Supplementary Table 2: List of genotyping primers**

gene ID	alias	primer name	orientation	sequence
AT3G11260	<i>wox5-1</i>	GK_WOX5 F	F	AAACAGTTGAGGACTTTACATCTGA
		WOX5 R	R	CGGATAATATGTCATAATTCAAAT
AT5G10510	<i>plt3-1</i>	GK_PLT3L	F	TTGTGATTGCCATTGACTAAAGGT
		GK_PLT3R	R	GAAAACAGTCCAATGGTCTCACATC
AT1G51190	<i>plt2</i>	RD_plt2 SALK128164 neu L	F	GCTTAAATAGATATATGGTCATGCTTATATC
		RD_plt2 SALK128164 neu R	R	CAAGAAGACTCCAGCCGATC
		SALK LBB1V2		AAACCAGCGTGGACCGCTTGCTGCAACTCT

**Supplementary Table 3: List of expression vectors used in this study**

cloning system	constructs	promoter	N-tag	CDS	C-tag	terminator	plant sel. marker	destination Vector	bacterial sel. marker	plasmid ID	
		module A	module B	module C	module D	module E	module F	module Z			
GreenGate	<b>pWOX5::mVenus-NLS</b>	WOX5 promoter	Ω-element (pGGB002)	mVenus	linker-NLS (pGGD007)	tUBQ10 (pGGE009)	BASTA (pGGF002)	pGGZ001	Spec	pVS10	
	<b>pWOX5::WOX5-mV</b>	WOX5 promoter	Ω-element (pGGB002)	WOX5	mVenus	tUBQ10 (pGGE009)	Hyg (pGGF005)	pGGZ001	Spec	pRD48	
	<b>pPLT3::PLT3-mV</b>	PLT3 promoter	Ω-element (pGGB002)	PLT3	mVenus	tUBQ10 (pGGE009)	Hyg (pGGF005)	pGGZ001	Spec	pRD73	
	<b>pPLT3::PLT3-mCh</b>	PLT3 promoter	Ω-element (pGGB002)	PLT3	mCherry	tUBQ10 (pGGE009)	-	pGGM000	Kan	pRD83	
	<b>pWOX5::WOX5-mV</b>	WOX5 promoter	Ω-element (pGGB002)	WOX5	mVenus	tUBQ10 (pGGE009)	Hyg (pGGF005)	pGGN000	Kan	pRD84	
	<b>pPLT3::PLT3-mCh</b> <b>pWOX5::WOX5-mV</b>	pRD83 + pRD84							pGGZ001	Spec	pRD89
	<b>pPLT3::PLT3ΔPrD-mV</b>	PLT3 promoter	Ω-element (pGGB002)	PLT3 ΔPrD	mVenus	tUBQ10 (pGGE009)	Hyg (pGGF005)	pGGZ001	Spec	pRD125	
	<b>inducible PLT3ΔPrD-mV</b>	Ubi-XVE oLexA-35S	Ω-element (pGGB002)	PLT3 ΔPrD	mVenus	tUBQ10 (pGGE009)	Hyg (pGGF005)	pGGZ001	Spec	pRD106	
	<b>inducible PLT3ΔPrD-mCh</b>	Ubi-XVE oLexA-35S	Ω-element (pGGB002)	PLT3 ΔPrD	mCherry	tUBQ10 (pGGE009)	Hyg (pGGF005)	pGGZ001	Spec	pRD138	
Gateway	<b>inducible WOX5-mV</b>	Ubi-XVE oLexA-35S	-	WOX5	mVenus	T3A	Hyg	pRD04	Spec	pRD26	
	<b>inducible WOX5-mCh</b>	Ubi-XVE oLexA-35S	-	WOX5	mCherry	T3A	Hyg	pABind mCherry	Spec	pFB02	
	<b>inducible PLT1-mCh</b>	Ubi-XVE oLexA-35S	-	PLT1	mCherry	T3A	Hyg	pABind mCherry	Spec	pRD144	
	<b>inducible PLT2-mCh</b>	Ubi-XVE oLexA-35S	-	PLT2	mCherry	T3A	Hyg	pABind mCherry	Spec	pRD147	
	<b>inducible PLT3-mV</b>	Ubi-XVE oLexA-35S	-	PLT3	mVenus	T3A	Hyg	pRD04	Spec	pRD25	
	<b>inducible PLT3-mCh</b>	Ubi-XVE oLexA-35S	-	PLT3	mCherry	T3A	Hyg	pABind mCherry	Spec	pFB06	
	<b>inducible PLT3ΔQ-mV</b>	Ubi-XVE oLexA-35S	-	PLT3 ΔQ	mVenus	T3A	Hyg	pRD04	Spec	pRD57	
	<b>inducible PLT3ΔQ-mCh</b>	Ubi-XVE oLexA-35S	-	PLT3 ΔQ	mCherry	T3A	Hyg	pABind mCherry	Spec	pRD81	
	<b>inducible free mCherry</b>	Ubi-XVE oLexA-35S	-	mCherry	-	T3A	Hyg	pMDC7	Spec	-	

**Supplementary Table 4: *Arabidopsis* mutants and transgenic lines**

<b>gene ID</b>	<b>alias</b>	<b>reference</b>
AT3G11260	<i>wox5-1</i>	SALK038262 (ABRC)
AT5G10510	<i>plt3-1</i>	Galinha <i>et al.</i> (2007)
AT1G51190	<i>plt2</i>	SALK_128164 (ABRC)
AT1G51190, AT5G10510	<i>plt2, plt3</i>	this study, crossing of <i>plt2</i> and <i>plt3-1</i>
AT3G11260, AT5G10510	<i>wox5, plt3</i>	this study, crossing of <i>wox5-1</i> and <i>plt3-1</i>
AT3G11260, AT1G51190, AT5G10510	<i>wox5, plt2, plt3</i>	this study, crossing of <i>plt2, plt3</i> and <i>wox5, plt3</i>
AT5G10510	pPLT3::erCFP ( <i>Col-0</i> )	Galinha <i>et al.</i> (2007)
AT5G10510	pPLT3::erCFP ( <i>wox5-1</i> )	this study, crossing of pPLT3::erCFP ( <i>Col-0</i> ) and <i>wox5-1</i>
AT5G10510	pPLT3::PLT3-YFP ( <i>Col-0</i> )	Galinha <i>et al.</i> (2007)
AT5G10510	pPLT3:: PLT3-YFP ( <i>wox5-1</i> )	this study, crossing of pPLT3::PLT3-YFP ( <i>Col-0</i> ) and <i>wox5-1</i>
AT5G10510	pPLT3::PLT3-mVenus ( <i>plt2, plt3</i> )	this study
AT5G10510	pPLT3::PLT3ΔPrD-mVenus ( <i>plt2, plt3</i> )	this study
AT3G11260	pWOX5::mVenus-NLS ( <i>Col-0</i> )	this study
AT3G11260	pWOX5::mVenus-NLS ( <i>plt2</i> )	this study
AT3G11260	pWOX5::mVenus-NLS ( <i>plt3-1</i> )	this study
AT3G11260	pWOX5::mVenus-NLS ( <i>plt2, plt3</i> )	this study

**Supplementary Table 5: Intensity values of transcriptional and translational FP tagged PLT3 expression experiments in *Col-0* and *wox5* related to Fig. 1.**

root #	pPLT3::erCFP fluorescence intensity [%]		pPLT3::PLT3-YFP fluorescence intensity [%]	
	<i>Col-0</i>	<i>wox5</i>	<i>Col-0</i>	<i>wox5</i>
<b>1</b>	84	65	96	69
<b>2</b>	108	67	121	31
<b>3</b>	81	78	73	72
<b>4</b>	93	48	68	64
<b>5</b>	101	46	68	38
<b>6</b>	95	65	95	109
<b>7</b>	113	52	109	75
<b>8</b>	128	53	72	39
<b>9</b>	82	58	78	79
<b>10</b>	71		127	30
<b>11</b>	105		164	63
<b>12</b>	139		84	39
<b>13</b>			145	66
<b>14</b>				55
<b>15</b>				56
<b>16</b>				99
<b>mean</b>	<b>100</b>	<b>59</b>	<b>100</b>	<b>62</b>
<b>st. dev.</b>	<b>20.10</b>	<b>10.39</b>	<b>31.13</b>	<b>23.01</b>

**Supplementary Table 6: Quantification of transcriptional mVenus tagged WOX5 expression in the QC region of *Col* and *plt2*, *plt3* related to Fig. 2.**

root #	number of cells with WOX5 expression		lateral area of WOX5 expression in the root tip [ $\mu\text{m}^2$ ]	
	<i>Col</i>	<i>plt2</i> , <i>plt3</i>	<i>Col</i>	<i>plt2</i> , <i>plt3</i>
<b>1</b>	7	14	432.03	719.28
<b>2</b>	4	9	345.88	886.24
<b>3</b>	7	13	393.67	861.28
<b>4</b>	7	13	400.62	882.48
<b>5</b>	8	12	346.86	548.73
<b>6</b>	6	11	430.11	736.44
<b>7</b>	8	14	467.05	793.77
<b>8</b>	6	12	512.33	693.18
<b>9</b>	7	13	444.99	948.22
<b>10</b>	9	14	474.60	747.27
<b>mean</b>	<b>6.90</b>	<b>12.50</b>	<b>424.81</b>	<b>781.69</b>
<b>st. dev.</b>	<b>1.30</b>	<b>1.50</b>	<b>51.26</b>	<b>111.59</b>

**Supplementary Table 7: Average QC and CSC phenotypes related to Fig. 3.**

<b>Genotype</b>	<b>average QC cell-divisions per root (<math>\pm</math> st. dev.)</b>	<b>average CSC layers per root (<math>\pm</math> st. dev.)</b>	<b>number of analyzed roots</b>
<i>Col</i>	$0.34 \pm 0.59$	$0.99 \pm 0.59$	146
<i>plt2</i>	$0.53 \pm 0.64$	$0.82 \pm 0.72$	77
<i>plt3</i>	$0.61 \pm 0.64$	$0.85 \pm 0.69$	121
<i>plt2, plt3</i>	$0.81 \pm 0.88$	$0.84 \pm 0.82$	105
<i>wox5</i>	$1.87 \pm 0.98$	$0.23 \pm 0.44$	118
<i>wox5, plt3</i>	$2.11 \pm 0.98$	$0.31 \pm 0.51$	87
<i>wox5, plt2, plt3</i>	$2.83 \pm 1.05$	$0.24 \pm 0.46$	98

**Supplementary Table 8: Percentage of periclinal cell divisions in the QC shown in Supplementary Fig. 2.**

<b>Genotype</b>	<b>periclinal QC cell divisions [%]</b>	<b>number of analyzed roots</b>
<i>Col</i>	3	146
<i>plt2</i>	21	77
<i>plt3</i>	21	121
<i>plt2, plt3</i>	53	105
<i>wox5</i>	41	118
<i>wox5, plt3</i>	43	87
<i>wox5, plt2, plt3</i>	53	98



**Supplementary Table 9: Average QC and CSC phenotypes of rescue experiments**

<b>Genotype</b>	<b>average QC cell-divisions per root (<math>\pm</math> SD)</b>	<b>average CSC layers per root (<math>\pm</math> SD)</b>	<b>number of analyzed roots</b>
rescue experiment of <i>wox5</i> mutant			
<i>Col</i>	0.33 $\pm$ 0.61	0.83 $\pm$ 0.59	30
<i>wox5</i>	1.77 $\pm$ 1.14	0.33 $\pm$ 0.55	30
<i>wox5</i> <i>pWOX5::WOX5-mV</i>	0.43 $\pm$ 0.67	0.88 $\pm$ 0.65	51
rescue experiment of <i>plt3</i> mutant			
<i>Col</i>	0.46 $\pm$ 0.65	1.00 $\pm$ 0.40	26
<i>plt3</i>	1.60 $\pm$ 1.14	0.85 $\pm$ 0.59	20
<i>plt3</i> <i>pPLT3::PLT3-mV</i>	0.81 $\pm$ 0.87	0.87 $\pm$ 0.43	31

**Supplementary Table 10: FLIM results of subnuclear data analysis in WOX5-mV and PLT3-mCh co-expressing *N. benthamiana* epidermal cells related to Fig. 5.**

date	measurement #	WOX5-mVenus fluorescence lifetime [ns]	
		bodies-only	nucleoplasm
2019-06-11	WOX5-mV PLT3-mCh_7	2.24	2.76
	WOX5-mV PLT3-mCh_15	2.19	2.85
2019-06-10	WOX5-mV PLT3-mCh_23	2.60	2.92
	WOX5-mV PLT3-mCh_25	2.55	2.88
2018-06-29	WOX5-mV PLT3-mCh_4	2.56	2.89
2018-06-28	WOX5-mV PLT3-mCh_1	2.50	2.84
	WOX5-mV PLT3-mCh_9	2.50	2.69
<b>mean</b>		<b>2.45</b>	<b>2.83</b>
<b>st. dev.</b>		<b>0.15</b>	<b>0.07</b>