

	Fuc			Rha			Ara			Gal			Glc			Xyl			Man			GalA			GlcA			Cellulose			Acetate		
	AVG	SD	S	AVG	SD	S	AVG	SD	S	AVG	SD	S	AVG	SD	S	AVG	SD	S	AVG	SD	S	AVG	SD	S	AVG	SD	S	AVG	SD	S			
Col-0	1.5 ± 0.2	a	7.6 ± 0.8	a	5.8 ± 1.2	a	10.2 ± 1.2	a	14.0 ± 1.3	a	97.2 ± 5.2	a	9.1 ± 1.1	a	29.0 ± 4.2	a	2.7 ± 0.5	ad	361.1 ± 12.4	ab	45.9 ± 1.5	a											
<i>tbl29</i>	1.5 ± 0.1	a	9.8 ± 0.7	c	9.1 ± 1.1	c	12.0 ± 1.0	a	16.6 ± 1.8	b	102.9 ± 11.7	b	11.1 ± 1.0	b	30.1 ± 1.2	a	3.6 ± 0.7	ac	309.7 ± 33.5	b	27.3 ± 1.5	bd											
<i>tbl29 max4</i>	1.3 ± 0.5	a	7.0 ± 1.7	a	5.7 ± 1.4	a	9.0 ± 2.2	a	15.1 ± 3.5	b	90.7 ± 14.0	a	8.6 ± 1.4	a	29.7 ± 1.0	a	4.7 ± 0.8	bc	364.6 ± 33.2	a	24.2 ± 2.8	b											
<i>irx3</i>	1.7 ± 0.2	a	11.9 ± 0.6	b	19.8 ± 2.2	d	15.4 ± 1.1	b	9.5 ± 1.5	ac	159.5 ± 10.6	c	6.4 ± 0.4	c	38.8 ± 2.5	b	4.3 ± 1.1	c	91.6 ± 15.5	c	72.6 ± 3.7	c											
<i>irx3 max4</i>	1.9 ± 0.2	a	11.7 ± 0.8	b	13.7 ± 2.7	b	14.3 ± 1.4	b	10.5 ± 1.0	c	155.8 ± 12.6	c	7.2 ± 0.4	c	37.1 ± 4.6	b	5.5 ± 0.9	c	120.5 ± 7.6	d	73.7 ± 4.4	c											
<i>parvus</i>	2.5 ± 0.2	b	11.2 ± 0.4	bc	13.1 ± 0.9	b	21.1 ± 1.4	c	21.1 ± 4.2	b	47.7 ± 2.7	d	16.6 ± 1.1	d	35.3 ± 2.6	b	1.0 ± 0.4	d	309.4 ± 14.9	b	31.7 ± 1.5	d											
<i>parvus max4</i>	2.6 ± 0.1	b	11.6 ± 0.3	b	13.7 ± 1.1	b	20.7 ± 1.2	c	20.2 ± 3.7	b	46.2 ± 3.4	d	15.7 ± 1.6	d	35.5 ± 1.7	b	1.4 ± 0.4	d	327.7 ± 9.1	e	31.6 ± 1.9	d											

Supp. Table 1. Effect of *max4* mutation in the cell wall composition of *irx3* and *parvus*. Monosaccharide composition, cellulose and acetate content of stem cell walls. Data are represented as mean (AVG) ± the standard deviation (SD) of biological replicates (n=5). Means with different letters are significantly different (Tukey's HSD, p<0.05) in the significance (S) column.

Fuc=Fucose; Rha=Rhamnose; Ara=Arabinose; Gal=Galactose; Glc=Glucose; Xyl=Xylose; Man=Mannose; GalA=Galacturonic Acid; GlcA=Glucuronic Acid

	Fuc AVG ± SD S	Rha AVG ± SD S	Ara AVG ± SD S	Gal AVG ± SD S	Glc AVG ± SD S	Xyl AVG ± SD S	Man AVG ± SD S	GalA AVG ± SD S	GlcA AVG ± SD S	Cellulose AVG ± SD S	Acetate AVG ± SD S
Col-0	1.3 ± 0.1 a	8.9 ± 0.2 a	7.6 ± 0.5 a	13.7 ± 0.6 a	17.8 ± 1.6 a	92.3 ± 9.9 a	9.1 ± 1.0 ab	39.7 ± 1.9 ab	1.9 ± 1.00 ad	357.9 ± 15.3 ab	38.4 ± 1.5 a
tbl29	1.3 ± 0.1 a	10.1 ± 0.8 b	9.1 ± 0.9 a	14.6 ± 1.2 a	17.5 ± 3.5 a	94.6 ± 9.2 a	9.0 ± 0.7 ab	45.4 ± 4.5 bc	3.9 ± 0.21 abc	310.1 ± 23.4 bd	21.5 ± 0.9 b
max4	1.3 ± 0.1 a	8.7 ± 0.4 ac	7.6 ± 0.6 a	13.7 ± 0.8 a	18.9 ± 2.2 a	100.5 ± 6.2 a	9.6 ± 0.7 ac	37.9 ± 2.9 ab	3.5 ± 0.42 abc	360.1 ± 12.3 a	39.9 ± 0.9 a
tbl29 max4	1.2 ± 0.1 a	8.2 ± 0.7 ac	6.9 ± 0.5 a	12.0 ± 1.0 a	19.6 ± 2.5 a	91.1 ± 9.0 a	8.6 ± 0.8 ac	36.5 ± 3.7 ab	5.0 ± 0.74 bc	362.2 ± 8.9 a	20.3 ± 1.9 b
irx1	1.5 ± 0.0 b	12.7 ± 0.4 de	21.3 ± 2.8 b	23.6 ± 1.5 b	21.9 ± 2.7 a	176.0 ± 5.2 b	12.2 ± 1.0 b	51.2 ± 2.6 cd	5.1 ± 1.91 c	88.0 ± 5.5 c	60.8 ± 1.7 c
irx1 max4	1.5 ± 0.0 ab	11.8 ± 0.5 de	14.6 ± 1.1 c	20.8 ± 0.7 c	18.3 ± 1.6 a	171.8 ± 14.7 b	10.4 ± 0.9 bc	49.6 ± 2.1 cd	5.0 ± 1.10 c	118.3 ± 23.5 d	62.1 ± 2.6 c
irx9	1.6 ± 0.1 b	13.3 ± 0.4 e	14.3 ± 1.0 c	23.6 ± 1.1 b	27.7 ± 2.0 b	55.2 ± 4.4 c	21.4 ± 1.0 d	52.8 ± 2.6 cd	1.0 ± 0.67 d	315.7 ± 15.0 b	34.8 ± 1.9 d
irx9 max4	1.8 ± 0.1 b	13.3 ± 0.4 e	15.5 ± 1.3 c	24.6 ± 0.9 b	32.6 ± 3.6 b	55.7 ± 1.4 c	23.0 ± 1.1 d	52.0 ± 2.2 d	0.8 ± 0.50 d	359.8 ± 26.4 a	34.7 ± 1.6 d

Supp. Table 2. Effect of *max4* mutation in the cell wall composition of *irx1* and *irx9*.

Monosaccharide composition, cellulose and acetate content of stem cell walls. Data are represented as mean (AVG) ± the standard deviation (SD) of biological replicates (n=5). Means with different letters are significantly different (Tukey's HSD, p<0.05) in the significance (S) column.

Fuc=Fucose; Rha=Rhamnose; Ara=Arabinose; Gal=Galactose; Glc=Glucose; Xyl=Xylose; Man=Mannose; GalA=Galacturonic Acid; GlcA=Glucuronic Acid

Mutant	FW	RV	T-DNA
<i>tbl29-1</i>	AATTGCAAGCAAAGCATCAC	TGGGTTTGATAACGAGACG	GCCTTTCAGAAATGGATAAATA
<i>max4-7</i>	GTATGAGAAAACCTTCTTCGAGGA	GCGAGAGAGAGAAAACGTGACATTAT	CCGCAATGAGTTGGCTATTCTC
<i>irx1-5</i>	ACAGGATGCGTGATACGGTAG	ATCCATCCAATCTCAATCCC	ATTTGCCGATTCGGAAC
<i>irx3-5</i>	AGAGAAGCTTAAGGAAACCGC	GAACAAACACAAGAGCAGAGGG	ATTTGCCGATTCGGAAC
<i>irx3-6</i>	TCTTACAATGCATTACTCGCTCAC	TGTGATTTAGTAGCTGGCCATTGT	ATAATAACGCTGCGGACATCTACATTT
<i>irx9-2</i>	GCTGGTAAGGCCTCATTTTC	AACTTACCAACCCACCCATT	ATTTGCCGATTCGGAAC
<i>parvus</i>	GTTGAAGTAGCATGCTTCCG	TATGCACAGACAAACATAGCG	ATTTGCCGATTCGGAAC
<i>irx4-2</i>	CGAAGCTTTACTTCGTCCAC	TTTCACCAATTAAATACCTCATT	ATAATAACGCTGCGGACATCTACATTT
<i>magl3</i>	AAAACACATCAAAACGATGCC	CTCTCCTGAATCAGCGAGTG	ATTTGCCGATTCGGAAC

Supp. Table 3. Primers used to genotype the T-DNA mutants.

FW: Forward gene-specific primer; RV: Reverse gene-specific primer; T-DNA: T-DNA-specific primer

Primer name	Sequence
ixr2-1 Fout	TGCCACTGGGGTTAAAAG
ixr2-1 Rout	TCATAAAAGATTACAGATTGAAA
ixr2-1 Fin	TCTTACACTTCTTGGGTCC
ixr2-1 Rin	CCACAAACGGATTAACCCA
prc1-1 F	GTGGCTCGGGATAAGAAGAA
prc1-1 R	GCGCAGATGCTACAAATAC
max2-1 F	CCCAAAGCTCTCAAAGATGC
max2-1 R	CAATAATCATGCTCGCTCAAGCTCAAGCTCCAATTCCGGTCAAGAAGAATCTTCCCATAAACTCAAAT
max3-9 F	AGGTGTATTTAACATGCCA
max3-9 R	CACAAAATGTGAAGTTGCTT
max1 F	CCTGATGTCTCTCCGTTCTTG
max1 R	GGCTGATAGAGAGATAGGGATGGT
max2-2 F	TCGCTCTCACCAAAAG
max2-2 R	GGCTACACGAACCAAT

Supp. Table 4. Primers used to genotype the EMS mutants.

Mutant	Stock ID
<i>tbl</i> 29-1	sail_856_G11
<i>max</i> 4-7	Ramirez et al., 2018
<i>irx</i> 1-5	SALK_026812C
<i>irx</i> 3-1	N104
<i>irx</i> 3-5	SALK_029940C
<i>irx</i> 3-6	N483791
<i>irx</i> 9-2	SALK_057033
<i>parvus</i>	SALK_045368C
<i>parvus/glz</i> 1	N16279
<i>irx</i> 4-1	N19
<i>irx</i> 4-2	N347577/GK-622C01
<i>magl</i> 3	SALK_023077
<i>max</i> 1	N9564
<i>max</i> 2-1	CS9565
<i>max</i> 2-2	CS9566
<i>max</i> 3-9	CS9567

Supp. Table 5. Stock numbers (ABRC/NASC) of the mutants described.