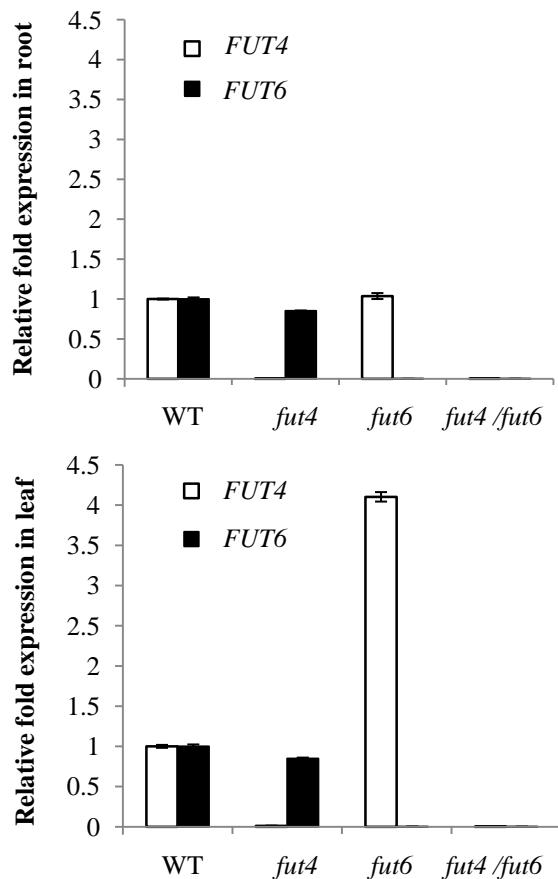
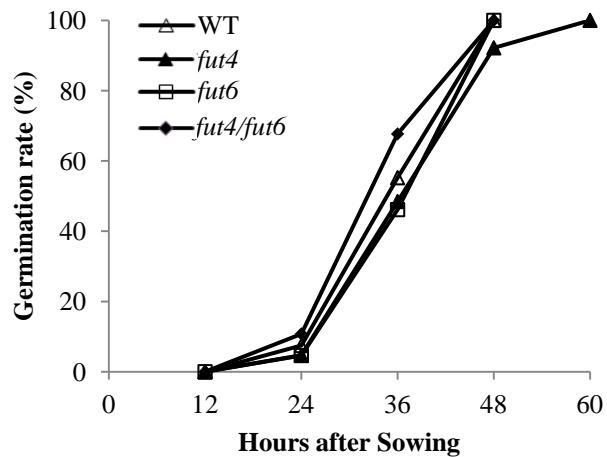


# Figure S1



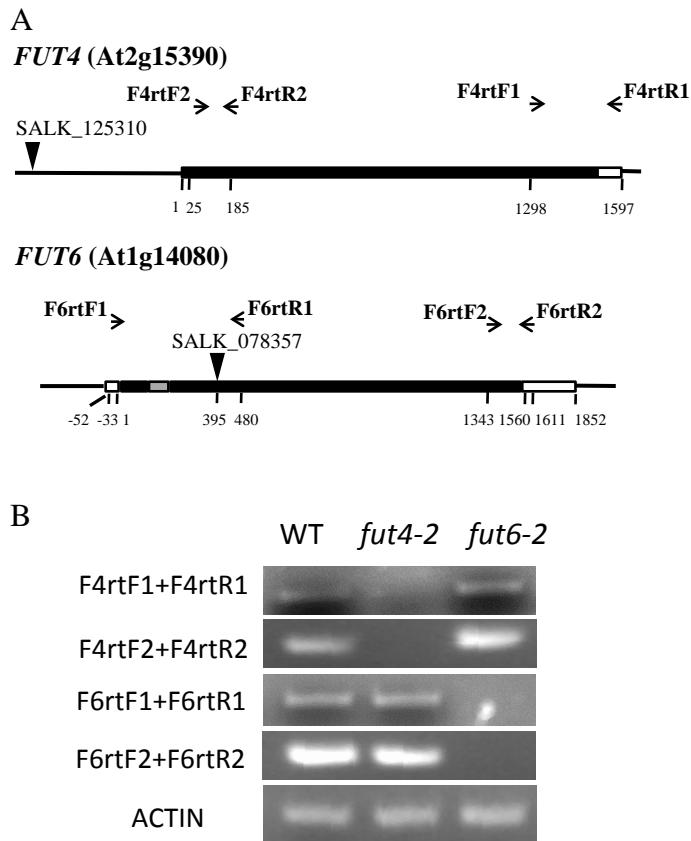
**Figure S1.** RT-qPCR analysis of *FUT4* and *FUT6* mRNA level in root and leaf tissues of Arabidopsis wild type and *fut4*, *fut6* and *fut4/fut6* double mutant plants.

## Figure S2



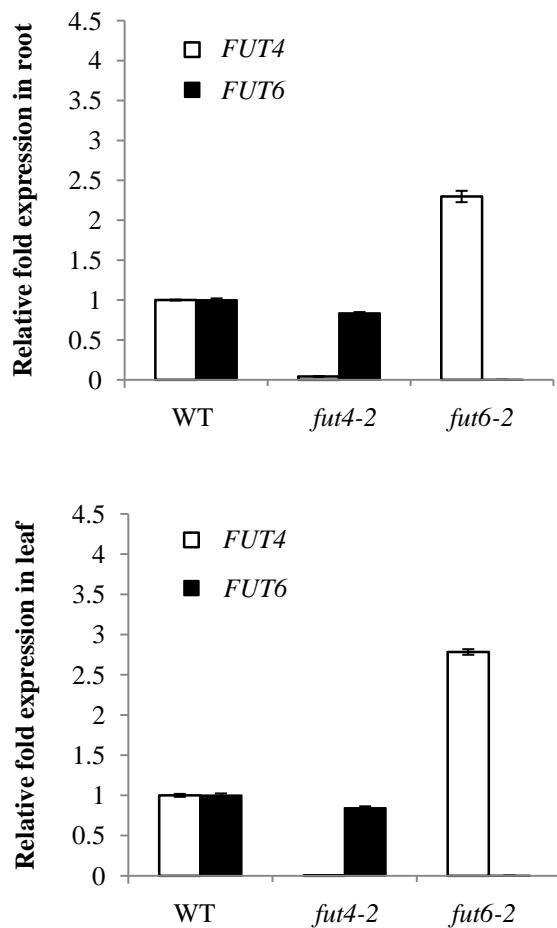
**Figure S2.** Germination rate of *Arabidopsis fut4*, *fut6* and *fut4/fut6* double mutant and wild type plants. Plant seeds were sown on MS plates containing 0.5% sucrose. Over 50 seeds were analyzed for each line.

# Figure S3



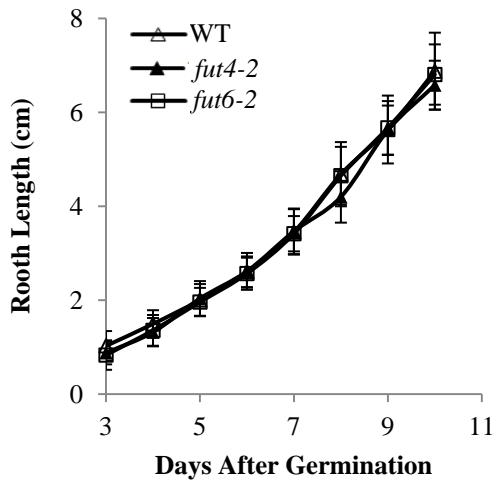
**Figure S3.** RNA transcript levels of *FUT4* and *FUT6* genes in homozygous *fut4-2*, *fut6-2* mutant and wild type seedlings. A, Schematic diagrams of mutant *FUT4* and *FUT6* genes with T-DNA insertions. Black box, grey box and white box represent exons, introns and untranslated regions, respectively. B, RT-PCR of total RNAs isolated from *Arabidopsis* seedlings 15 DAG. Positions of the RT-PCR primers are shown in A with arrows. *ACTIN* was used as a control for loading.

## Figure S4



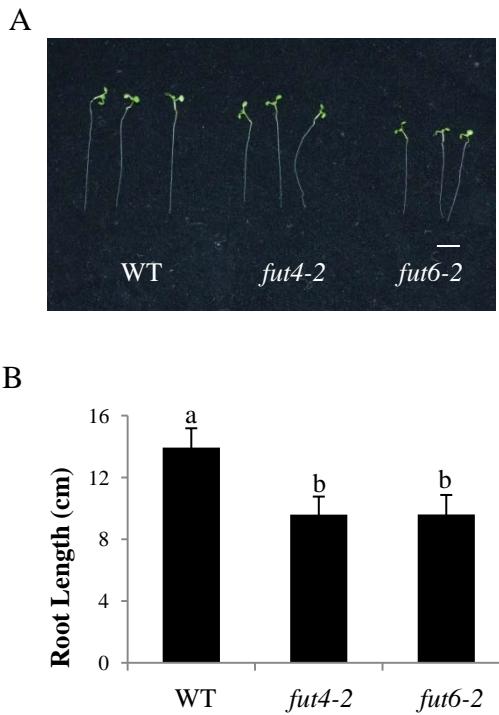
**Figure S4.** RT-qPCR analysis of *FUT4* and *FUT6* mRNA level in root and leaf tissues of Arabidopsis wild type and *fut4-2* and *fut6-2* mutant plants.

Figure S5



**Figure S5.** Root growth of *Arabidopsis* wild type, *fut4-2*, *fut6-2* mutant plants. Plants were grown on MS plates containing 0.5% sucrose. Root length was measured daily as a function of time from 3-10 DAG. Values shown were averages of data from over 24 individual plants per line, with standard errors shown as error bars.

## Figure S6



**Figure S6.** Root length measurement of *Arabidopsis* *fut4-2*, *fut6-2* and wild type plants grown under salt stress. *Arabidopsis* seeds were germinated on NaCl-free MS plates and then transferred to MS plates containing 150 mM NaCl on the 3 DAG. A, Seedling images of wild type, *fut4-2* and *fut6-2* mutant plants on the 10<sup>th</sup> day after transfer. Three representative seedlings of each plant line were photographed. Scale bar, 3 cm. B, Measurement of primary root length on the 10<sup>th</sup> day after transfer. Data and error bars represent mean  $\pm$  SD ( $n = 31$ ). Values annotated with different letters are significantly different ( $P < 0.01$ ; Tukey honestly significant difference test).

# Table S1

**Table S1.** Sequence and annealing temperatures of the primers used in this work

Purpose	Name	Primer Sequences (5'→3')	Annealing
Absence of insertion of <i>FUT4</i>	F4LP	CCATGTAGTTACATTCCAACCG	54° C
	F4RP	CCACGTCGATGGAGCCTGTTT	
Presence of insertion 1 in SAIL_284_B05	LB3	TAGCATCTGAATTCATAACCAATCTCGATACAC	49° C
	F4RP	GAACATGTTTCAGAGCGAGC	
Presence of insertion 2 in SAIL_284_B05	LB3	TAGCATCTGAATTCATAACCAATCTCGATACAC	54° C
	F4LP	CCATGTAGTTACATTCCAACCG	
Absence of insertion of <i>FUT6</i>	F6LP	CACATCTTCAGATCTCCAGCG	55° C
	F6RP	CTTCTTGTAAGCATCCGTGC	
Presence of insertion 1 in SALK_099500	LBa1	TGGTTCACGTAGTGGGCCATCG	54° C
	F6RP	CTTCTTGTAAGCATCCGTGC	
Presence of insertion 2 in SALK_099500	LBa1	TGGTTCACGTAGTGGGCCATCG	54° C
	F6LP	TGTTTGCTAGCAACGAAAGC	
RT -PCR for <i>FUT4</i> 3' end primers	F4rtF1	TGGAGGATTAAAGCCATGGTTAC	52° C
	F4rtR1	AATGAAAAAGGAAGATATATAACA	
RT -PCR for <i>FUT6</i> 5' end primers	F6rtF1	TCCAGCGAAGTTTCAGAGC	52° C
	F6rtR1	CGCAACCCACACAATGTATC	
RT -PCR for <i>FUT4</i> 5' end primers	F4rtF2	GCGAAGTTATCAAGGGTTGGG	58° C
	F4rtR2	CTTGTATCGCAAGCCTTCACC	
RT -PCR for <i>FUT6</i> 3' end primers	F6rtF2	TGGAGGATTAAAGCCATGGTTAC	58° C
	F6rtR2	GGATTGTGAGTTATTGAAACAGAGA	
RT -PCR for <i>ACTIN</i>	Actin F	GTCGTACTACCGGTATTGTGCTCG	58° C
	Actin R	CGGCGATTCCAGGAAACATTGTGG	
Ubiquitin 10 for RT- qPCR	Ubi F	GTCGACCCTTCACTTGGTGT	58° C
	Ubi R	ATCCTCAAGCTGCTTCCAG	

# Table S2

**Table S2.** Statistic analysis for comparisons of root length measurements among wild type and *fut4*, *fut4-2*, *fut6*, *fut6-2*, *fut4/fut6* mutant plants grown under salt stress.

<i>P</i> <sup>a</sup>	WT	<i>fut4</i>	<i>fut4-2</i>	<i>fut6</i>	<i>fut6-2</i>	<i>fut4/fut6</i>
WT	-	<10 <sup>-4</sup>				
<i>fut4</i>	<10 <sup>-4</sup>	-	0.9462	0.9909	0.9382	0.0013
<i>fut4-2</i>	<10 <sup>-4</sup>	0.9462	-	0.9997	1.0000	<10 <sup>-4</sup>
<i>fut6</i>	<10 <sup>-4</sup>	0.9909	0.9997	-	0.9995	<10 <sup>-4</sup>
<i>fut6-2</i>	<10 <sup>-4</sup>	0.9382	1.0000	0.9995	-	<10 <sup>-4</sup>
<i>fut4/fut6</i>	<10 <sup>-4</sup>	0.0013	<10 <sup>-4</sup>	<10 <sup>-4</sup>	<10 <sup>-4</sup>	-

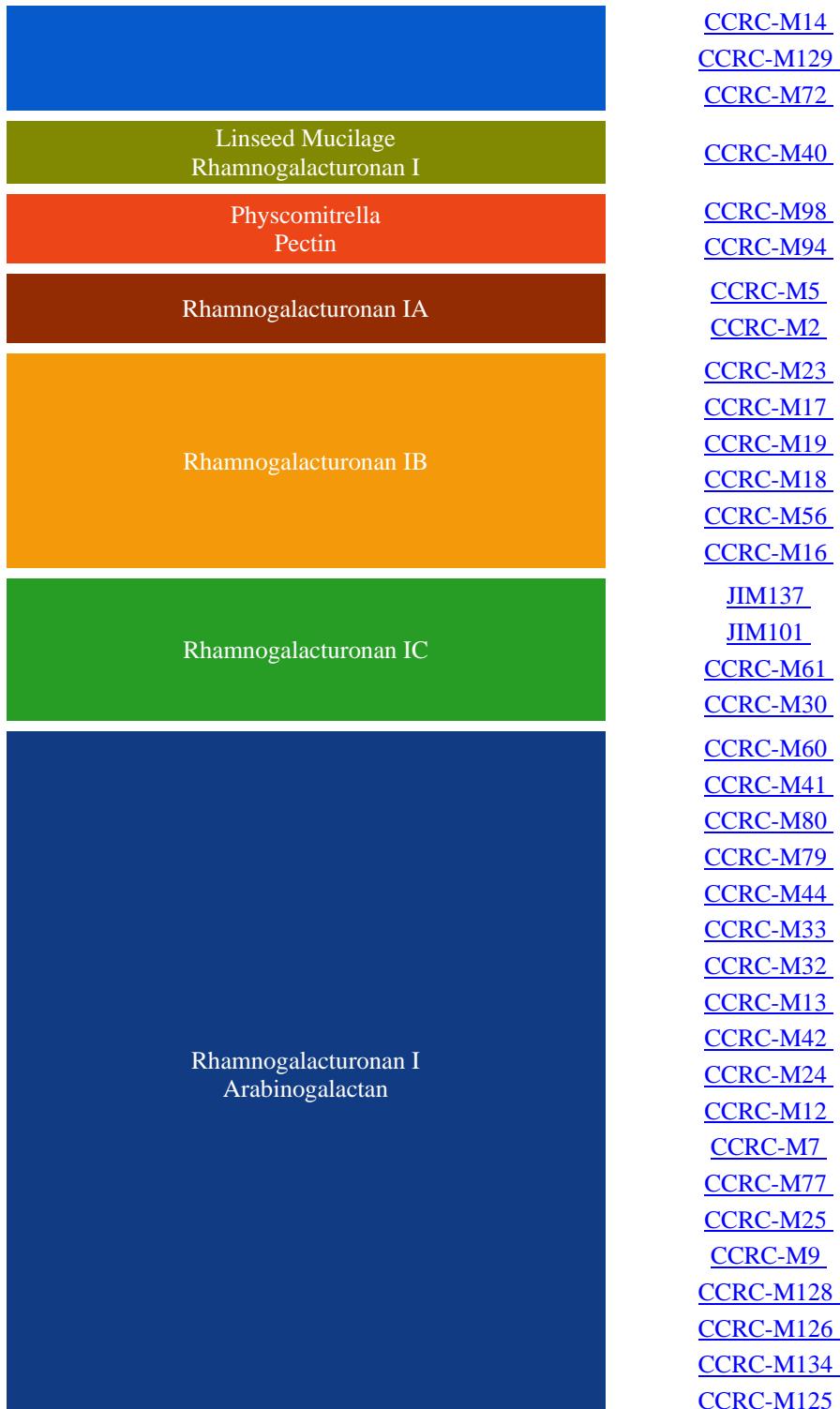
<sup>a</sup>One-way ANOVA was performed using JMP software and showed significant difference (*P*<0.0001) in root lengths among wild type and mutant lines grown under salt stress (150 mM NaCl). Significant levels of differences in root lengths were subsequently analyzed by Tukey honestly significant difference test as presented in this table. For root measurement data and plant growth conditions see Fig. 5 and Fig. S6.

## Table S3

**Table S3.** Expanded list of all plant cell wall glycan-directed monoclonal antibodies (mAbs) used in this study for glycome profiling (Fig. 7 and Fig. 8).

Glycan Group Recognized	mAb Name <sup>a</sup>
Non-Fucosylated Xyloglucan	<a href="#">CCRC-M54</a> <a href="#">CCRC-M48</a> <a href="#">CCRC-M49</a> <a href="#">CCRC-M96</a> <a href="#">CCRC-M50</a> <a href="#">CCRC-M51</a> <a href="#">CCRC-M53</a> <a href="#">CCRC-M100</a> <a href="#">CCRC-M103</a> <a href="#">CCRC-M58</a> <a href="#">CCRC-M86</a> <a href="#">CCRC-M55</a> <a href="#">CCRC-M52</a> <a href="#">CCRC-M99</a> <a href="#">CCRC-M95</a> <a href="#">CCRC-M101</a> <a href="#">CCRC-M104</a> <a href="#">CCRC-M89</a> <a href="#">CCRC-M93</a> <a href="#">CCRC-M87</a> <a href="#">CCRC-M88</a> <a href="#">CCRC-M57</a> <a href="#">CCRC-M90</a>
Fucosylated Xyloglucan	<a href="#">CCRC-M102</a> <a href="#">CCRC-M39</a> <a href="#">CCRC-M106</a> <a href="#">CCRC-M84</a> <a href="#">CCRC-M1</a>
Xylan 1/XG	<a href="#">CCRC-M111</a> <a href="#">CCRC-M108</a> <a href="#">CCRC-M109</a>

	<a href="#"><u>CCRC-M119</u></a>
	<a href="#"><u>CCRC-M115</u></a>
	<a href="#"><u>CCRC-M110</u></a>
	<a href="#"><u>CCRC-M105</u></a>
	<a href="#"><u>CCRC-M117</u></a>
	<a href="#"><u>CCRC-M113</u></a>
	<a href="#"><u>CCRC-M120</u></a>
	<a href="#"><u>CCRC-M118</u></a>
	<a href="#"><u>CCRC-M116</u></a>
	<a href="#"><u>CCRC-M114</u></a>
Xylan 2	CCRC-M154
	CCRC-M150
	<a href="#"><u>CCRC-M160</u></a>
	<a href="#"><u>CCRC-M137</u></a>
Xylan 3	CCRC-M152
	CCRC-M149
	CCRC-M144
	CCRC-M146
	CCRC-M145
	CCRC-M155
Xylan 4	CCRC-M153
	CCRC-M151
	CCRC-M148
	<a href="#"><u>CCRC-M140</u></a>
	<a href="#"><u>CCRC-M139</u></a>
	<a href="#"><u>CCRC-M138</u></a>
Seed Galactomannan	<a href="#"><u>CCRC-M75</u></a>
	<a href="#"><u>CCRC-M70</u></a>
	<a href="#"><u>CCRC-M74</u></a>
	<a href="#"><u>CCRC-M131</u></a>
	<a href="#"><u>CCRC-M38</u></a>
Homogalacturonan Backbone	<u>JIM5</u>
	<u>JIM136</u>
	<u>JIM7</u>
	<a href="#"><u>CCRC-M34</u></a>
Rhamnogalacturonan I Backbone	<a href="#"><u>CCRC-M69</u></a>
	<a href="#"><u>CCRC-M35</u></a>
	<a href="#"><u>CCRC-M36</u></a>





Unidentified

[CCRC-M78](#)

[MAC265](#)

[CCRC-M97](#)

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<sup>a</sup>The majority of listings link to the WallMabDB plant cell wall monoclonal antibody database (<http://www.wallmabdb.net>) that provides detailed descriptions of each mAb, including immunogen, antibody isotype, epitope structure (to the extent known), supplier information, and related literature citations.

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