

Supplemental Table S1. Primer sequences used in the study.

Gene	Sequence	Use
<i>CrWUL</i>	F-cacc*cactcgccaatctcaagcat	Insert for RNAi region 1
	R-ctaaccggttctgtgcgataaagg	
	F-cacc*tcagctgaaccgtgatgtag	Insert for RNAi region 2
	R-cttgagattggcgagtgtttg	
	F-atgagagaatatgtgcggggatc	RT-qPCR
	R-attgtagccgtacagagaccac	
	F-cactcgccaatctcaagcat	<i>In situ</i> probes anti-sense
	R-taatacgactcactataggg*ctaaccggttctgtgcgataaagg	
	F-taatacgactcactataggg*atgagagaatatgtgcggggatc	<i>In situ</i> probes sense
	R-attgtagccgtacagagaccac	
	F-cacc*atgagagaatatgtgcggggatc	Whole mount <i>in situ</i> probes anti-sense
	R-taatacgactcactataggg*attgtagccgtacagagaccac	
	F-taatacgactcactataggg*cgaaggagaacatggtaatg	Whole mount <i>in situ</i> probes sense
	R-cttgagattggcgagtgtttg	
	F-cacc*atgagagaatatgtgcggggatc	Full-length for <i>atwox4</i> rescue
R-aggagaacgctaactttcagttc		

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<i>AtWOX4</i>	F-cacc*cgagaaaggcatgcatagcatt	<i>In situ</i> probes anti-sense
	R-taatacgactcactataggg*tcatgacttcatctcccttcagga	
	F-taatacgactcactataggg*cgagaaaggcatgcatagcatt	<i>In situ</i> probes sense
	R-tcatgacttcatctcccttcagga	
	F-nnnaagctt*ggcaagttagtgaggagg	Promoter cloning for <i>atwox4</i> rescue
	R-nnnttaattaa*tgctatatgttaaactagcaaagtctatg	
<i>CrUBQ</i>	F-gatggccgtactcttcagac	Expression analysis RT-qPCR
	R-ggagacgaagcagagatga	
<i>CrHistone4</i>	F-taatacgactcactataggg*atgtctggaaggggaaaaggag	<i>In situ</i> probes
	R-taatacgactcactataggg*tcagccgccgaagccatagag	
Hygromycin	F-aggtctacccccctttcaacg	Genotyping
	R-aatgtgtgggttcagttggag	
Gabi-Kat	F-aggtctacccccctttcaacg	Genotyping <i>atwox4</i> null mutants (Primer Set 1)
	R-aatgtgtgggttcagttggag	
	F-gcaatgagtatgatggccaatg	Left border of pAC161 (Primer Set 2)
	R-gggctacactgaattgtagctc	
	F-atattgaccatcatactcattgc	

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	R-aatgtgtgggttcagttggag	o8409 and Set 1 R (primer set 3)
<i>SkWOX11c</i>	F-taatacgactcactataggg*atggaggcgccaggcac	<i>In situ</i> probes
	R-taatacgactcactataggg*tcaggctgcactcccgc	
<i>SkWOX11b</i>	F-taatacgactcactataggg*atgctgccgtgccaagaaagtc	<i>In situ</i> probes
	R-taatacgactcactataggg*ttactgctgcagctgctgctg	

Sequences left of * are added for directional cloning or T7 promoter sequence. All sequences are 5' to 3'

Table S2: Statistics for gametophyte cell counts

Dunnett's multiple comparisons test	Predicted (LS) mean diff.	95.00% CI of diff.	Below threshold?	Summary	Adjusted P Value
7					
RN3 vs. crwul1	-22.69	-107.6 to 62.22	No	ns	0.8719
RN3 vs. crwul3	-118.9	-215.7 to -22.06	Yes	*	0.011
RN3 vs. crwul2	-21.22	-118.0 to 75.59	No	ns	0.9233
10					
RN3 vs. crwul1	-96.31	-204.1 to 11.50	No	ns	0.091
RN3 vs. crwul3	-275.4	-376.2 to -174.7	Yes	****	<0.0001
RN3 vs. crwul2	-163.2	-268.6 to -57.77	Yes	***	0.0009
14					
RN3 vs. crwul1	-343.3	-436.1 to -250.4	Yes	****	<0.0001
RN3 vs. crwul3	-266.1	-362.5 to -169.6	Yes	****	<0.0001
RN3 vs. crwul2	-46.01	-134.3 to 42.29	No	ns	0.4749