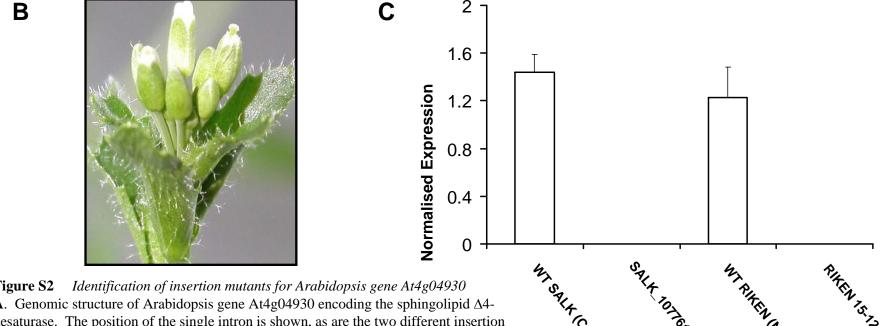
Fig. S1



Structure of Arabidopsis gene At4g04930 encoding the sphingolipid ∆4-desaturase



A. Genomic structure of Arabidopsis gene At4g04930 encoding the sphingolipid Δ4-desaturase. The position of the single intron is shown, as are the two different insertion alleles described in the text. The RIKEN 15-1202-1 mutant is generated by the insertion of modified *Ds*-transposon shortly after the start of the coding sequence. The SALK-107761.42.15.x mutant results from the insertion of a modified T-DNA. Both insertions are predicted to disrupt the ORF of this gene, not least of all with respect to the critical histidine boxes required from desaturase function (indicated by solid stars).

B. Stage of floral development at which RNA was isolated for detection of transcripts derived from At4g04930.

C. Q-PCR was used to detect transcripts from WT (Col-0, No-0) and insertion mutants. Expression was normalised as described in Griffiths et al. (2006).

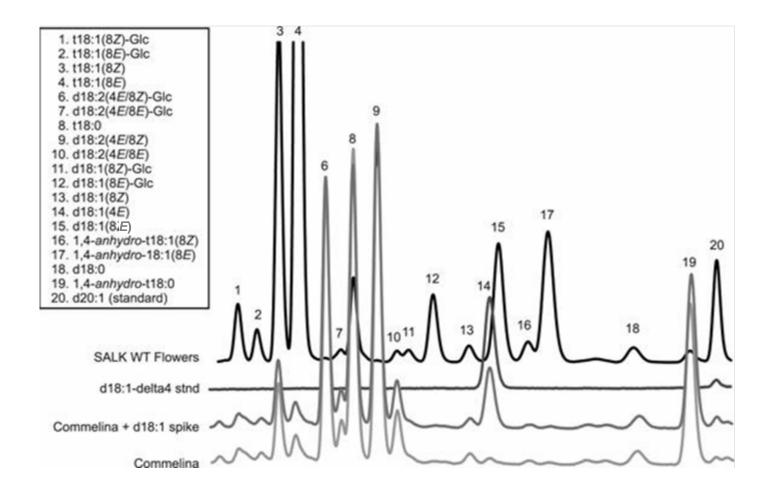
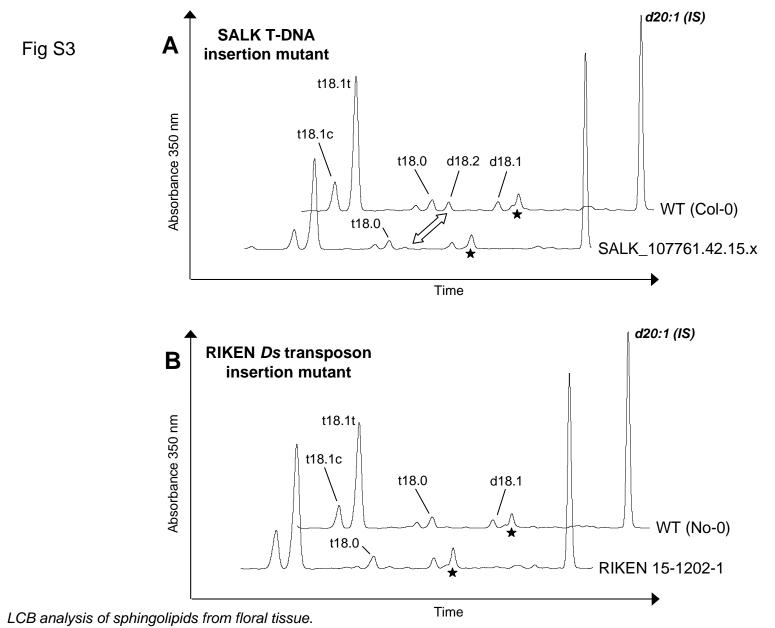


Fig. S2 HPLC separation and identification of plant LCBs.

LCBs were prepared by hydrolysis and o-pthaldialdehyde derivitization as previously described (Markham et al. 2006). Identification of the d18:1(4E) LCB was confirmed in extracts from Commelina by spiking with synthetic d18:1(4E) and comparing retention times with the synthetic standard alone. The Arabidopsis sample contained no detectable amounts of d18:1(4E) and only minor amounts of d18:2(4E/8Z). LCB nomenclature and peak identification labels are described in Markham et al. 2006.



Total LCBs were extracted from developing flowers (Fig 3B) and analysed by highly resolving HPLC). T-DNA insertion mutant SALK_107761.42.15 lacked any detectable $\Delta 4$ -unsaturated LCBs compared with the WT Col-0 (the position of $\Delta 4$ -unsaturated sphinga-4,8-diene is indicated with an open arrow). The No-0 ecotype naturally lacks this LCB (compare WT No-0 with insertion mutant RIKEN 15-1202-1). No d18:1 $\Delta 4$ LCBs were identified in any samples, though low levels of d18:1 $\Delta 8$ are detectable (cf. Table S2). Anhydro-LCBs are indicated with a star (see also Fig S2).

Fig. S4



RIKEN *Ds* transposon mutant



SALK T-DNA insertion mutant

Insertional mutagenesis of sphingolipid $\Delta 4$ -desaturase At4g04930 does not result in any gross phenotypic alteration

Table S1 Microarray-derived tissue-specific expression of At4g04930

Tissue	Expression Level	Standard Deviation		
Dry seed	4.68	3.15		
Imbibed seed, 24 h	3.7	3.18		
1st Node	3.7	1.81		
Flower Stage 12, Stamens	1018.9	23.36		
Cauline Leaf	5.71	1.39		
Cotyledon	7.5	0.42		
Root	4.66	1.05		
Entire Rosette After				
Transition to Flowering	6.36	2		
Flower Stage 9	5.58	1.64		
Flower Stage 10/11	8.68	2.51		
Flower Stage 12	120.35	7.43		
Flower Stage 15	227.5	3.37		
Flower Stage 12, Carpels	6.18	1.36		
Flower Stage 12, Petals	40.38	4.63		
Flower Stage 12, Sepals	26.13	0.94		
Flower Stage 15, Carpels	55.68	8.92		
Flower Stage 15, Petals	55.61	4.78		
Flower Stage 15, Sepals	49.66	4.9		
Flower Stage 15, Stamen	1225.5	34.03		
Flowers Stage 15, Pedicels	9.35	1.61		
Leaf 1 + 2	6.33	1.5		
Leaf 7, Petiole	6.81	4		
Leaf 7, Distal Half	7.4	2.19		
Leaf 7, Proximal Half	8.73	2.48		
Hypocotyl	4.03	0.45		
Root	5.33	1.69		
Rosette Leaf 2	7.06	0.61		
Rosette Leaf 4	6.25	0.56		
Rosette Leaf 6	11.45	1.47		
Rosette Leaf 8	6.65	0.31		
Rosette Leaf 10	9.25	1.24		
Rosette Leaf 12	6.08	1.55		
Senescing Leaf	5.05	1.76		
Shoot Apex, Inflorescence	4.9	1.82		
Shoot Apex, Transition	3.28	0.42		
Shoot Apex, Transition Shoot Apex, Vegetative	3.01	3.45		
Stem, 2nd Internode	7.26	3.24		
Mature Pollen	6802.68	239.51		
Seeds Stage 3 w/ Siliques	256.36	0.51		
Seeds Stage 4 w/ Siliques	25.4	2.02		
Seeds Stage 5 w/ Siliques	24.06	1.65		
Seeds Stage 6 w/o Siliques	9.21	2.21		
Seeds Stage 7 w/o Siliques	10.91	1.88		
Seeds Stage 8 w/o Siliques	11.98	3.03		
	13.73	2		
Seeds Stage 9 w/o Siliques	8.6	2.19		
Seeds Stage 10 w/o Siliques				
Vegetative Rosette	5.01	3.13		

Data extracted from Arabidopsis eFP browser at bar.utoronoto.ca

Table S2

nmol g dw ⁻¹	Col-0 Floral	SALK_107781 Floral	Col-0 Leaf	SALK_107781 Leaf	No-0 Floral	RIKEN 15- 1202-1 Floral	No-0 Leaf	RIKEN 15- 1202-1 Leaf
t18:1(Z)	292	309	204	216	290	283	237	254
t18:1(E)	970	978	601	639	919	888	743	829
t18:0	77	81	121	115	95	88	104	127
d18:2(E/Z)	4	0	0	0	0	0	0	0
d18:2(E/E)	19	0	0	0	0	0	0	0
d18:1(Z)	26	26	18	17	28	22	11	16
d18:1(E)	186	200	111	110	172	159	72	92
d18:0	19	22	31	26	23	21	13	19
TOTAL	1594	1615	1087	1124	1527	1461	1180	1337
mol%								
t18:1(Z)	18	19	19	19	19	19	20	19
t18:1(E)	61	61	55	57	60	61	63	62
t18:0	5	5	11	10	6	6	9	9
d18:2(E/Z)	0	0	0	0	0	0	0	0
d18:2(E/E)	1	0	0	0	0	0	0	0
d18:1(Z)	2	2	2	2	2	2	1	1
d18:1(E)	12	12	10	10	11	11	6	7
d18:0	1	1	3	2	2	1	1	1
TOTAL	100%	100%	100%	100%	100%	100%	100%	100%

Table S2. *LCB analysis of wild-type and sphingolipid ∆4-desaturase mutants.*

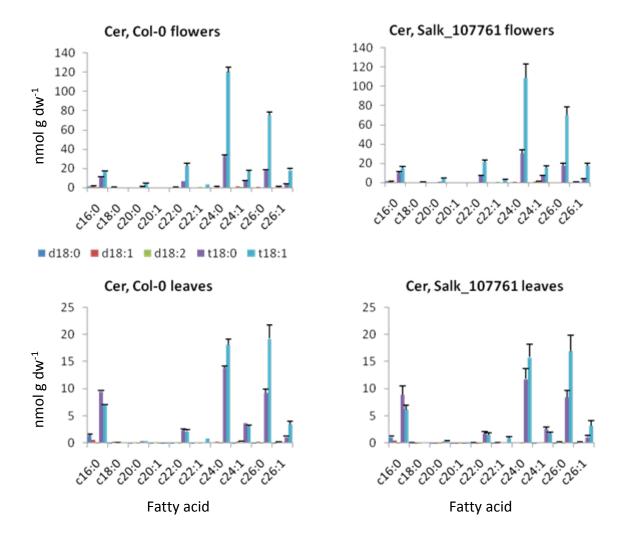
Tissue from each genotype was hydrolyzed in the presence of 1nmol synthetic d20:1 internal standard and the LCB content measured by o-phthaldialdehyde derivatization, HPLC separation and fluorescence detection as previously described (Markham et al. 2006). Δ 4-desaturated LCBs were only detected in Col-0 sample derived from floral tissues, and then only as d18:2 species. No d18:2 was detected in samples from the SALK mutant line and no d18:2 was detectable in leaf tissue or any of the samples in the No-0 backround.

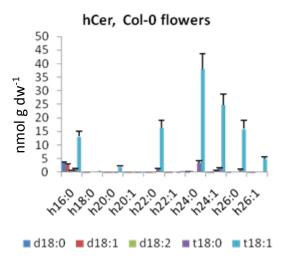
Table S3

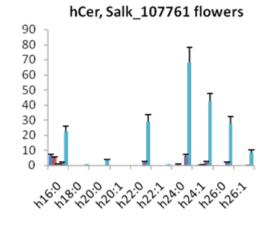
PCR Primers used to generate the P. pastoris sphingolipid $\Delta 4$ -desaturase knockout strain and to express the sphingolipid $\Delta 4$ -desaturase gene of A. thaliana in P. pastoris.

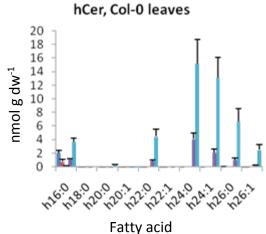
Primer Name	Sequence $(5' \rightarrow 3')$
Delta4-F-EcoRI	G <u>GAATTCC</u> AGTTCAGATCTTAGATACACATG
Delta4-R-HindIII	${\tt CCATGGG} \underline{{\tt AAGCTT}} {\tt GTACACTCTTCACCATACTGCCC}$
Delta4-Test-F	ATCTCCTGCGACGTCTTAATG
Delta4-Test-R	GTCGCCTTTGGTAACCTGAAG
Zeo-F-XbaI	GC <u>TCTAGA</u> CACACACCATAGCTTCAAAATG
Zeo-R-XmnI	<u>GAACAAATTC</u> CCAGCTTGCAAATTAAAGCCTTC
Zeo-int-F	CGGCATAGTATATCGGCAT
Zeo-int-R	ATGCCGATATACTATGCCG
d4At-F	<u>GAATTC</u> ATTATGGGGAAAGGAGGACGTGAG
d4At-R	<u>GCGGCCGC</u> TTAGTCAGACTTTGAGAGCTTCC

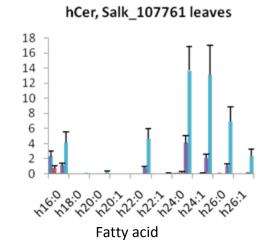
Supplementary Data 1: Sphingolipid analysis

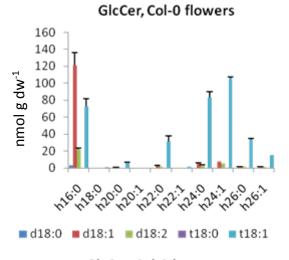


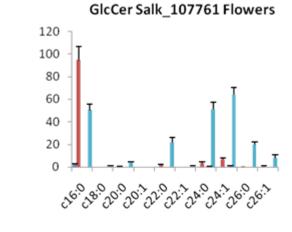


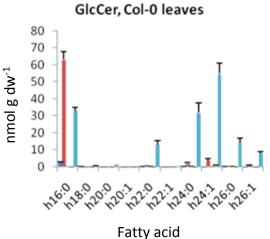


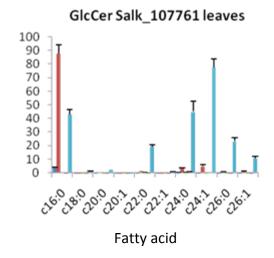


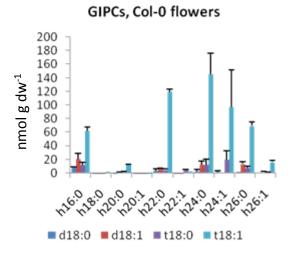


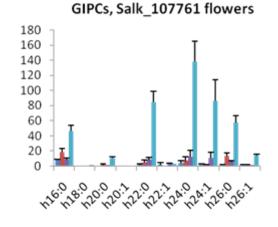


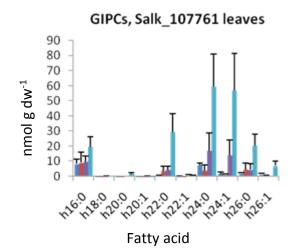


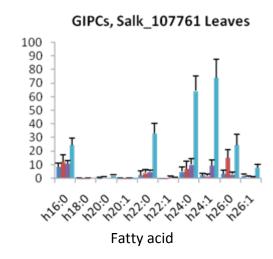


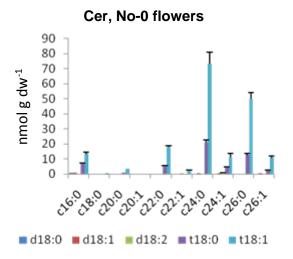


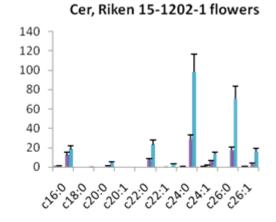


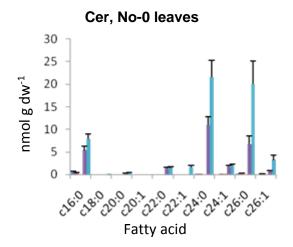


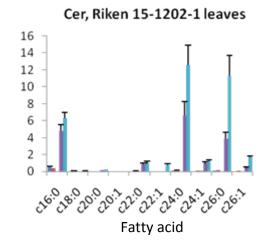


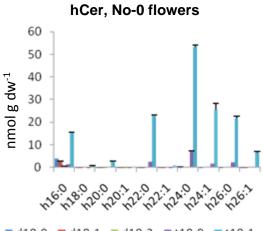


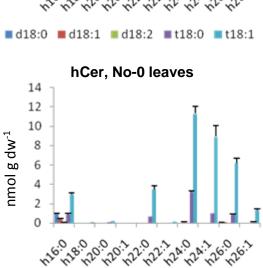












Fatty acid

