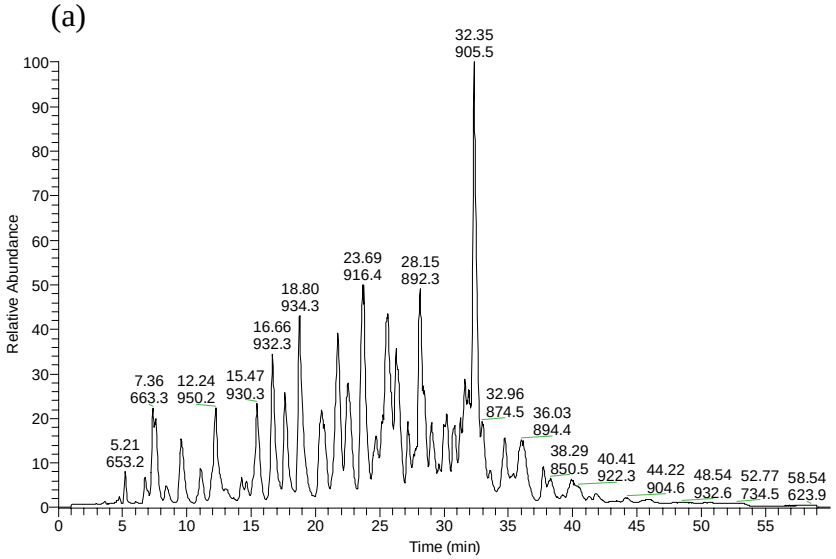
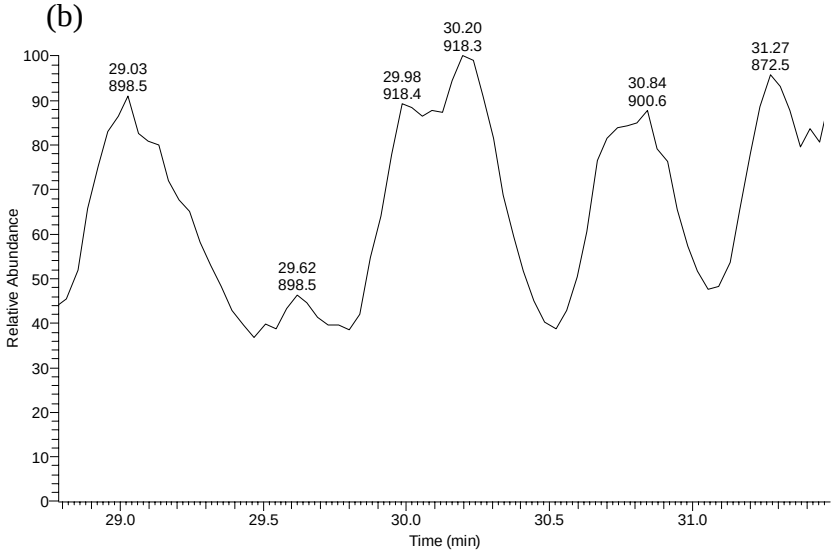
Table S1. Fatty acid compositions of seed samples from four *Arabidopsis* lines. Lines CL7 (parental) and 540 carry only the *FAH12* transgene. Lines 521, 522, 544 and 545 are *FAH12 RcDGAT2* double transgenics.

Transgenic Line	Fatty Acid Composition (percent of total)									
	16:0	**18:0**	**18:1**	**18:2**	**18:3**	**20:1**	**18:1-OH**	**18:2-OH**	**Sum HFA**	**Mean ± s.d.**
CL7	15.8%	6.9%	31.8%	22.0%	5.4%	0.4%	14.7%	3.1%	17.7%	
	15.2%	6.4%	32.2%	22.3%	5.5%	0.4%	15.0%	3.0%	18.0%	
	17.2%	7.3%	28.5%	22.5%	5.5%	0.4%	15.5%	3.0%	18.5%	
	17.8%	7.5%	28.7%	21.8%	5.1%	0.5%	15.3%	3.4%	18.7%	
	16.9%	7.2%	27.5%	23.9%	5.8%	0.4%	15.6%	2.8%	18.4%	
	13.3%	5.9%	34.0%	22.0%	5.9%	0.4%	15.0%	3.4%	18.5%	18.3 ± 0.4
Line 521	11.9%	5.4%	30.2%	23.2%	8.4%	0.4%	16.5%	4.0%	20.5%	
	12.3%	5.8%	26.2%	21.9%	7.1%	0.4%	21.7%	4.6%	26.3%	
	12.8%	6.2%	25.4%	20.9%	6.1%	0.4%	23.8%	4.5%	28.3%	
	12.1%	5.8%	27.7%	20.9%	6.9%	0.4%	21.9%	4.3%	26.2%	
	13.6%	6.2%	21.0%	23.9%	7.3%	0.3%	23.6%	4.0%	27.7%	
	11.7%	5.4%	28.7%	21.0%	6.5%	0.4%	21.9%	4.4%	26.3%	25.9 ± 2.8
Line 522	13.1%	6.5%	23.2%	22.0%	6.6%	0.4%	23.9%	4.4%	28.2%	
	12.3%	5.6%	26.7%	21.0%	6.1%	0.4%	23.6%	4.4%	28.0%	
	13.1%	6.0%	26.1%	20.8%	6.0%	0.4%	23.9%	3.8%	27.7%	
	12.7%	6.0%	25.4%	21.5%	6.5%	0.4%	22.9%	4.6%	27.5%	
	12.0%	5.8%	28.4%	20.5%	6.5%	0.4%	22.0%	4.5%	26.5%	
	12.4%	5.6%	26.3%	20.6%	6.3%	0.4%	23.9%	4.6%	28.5%	27.7 ± 0.7
Line 544	11.6%	5.6%	26.8%	21.3%	7.0%	0.4%	22.8%	4.6%	27.4%	
	12.3%	5.8%	22.4%	21.7%	6.7%	0.4%	26.1%	4.7%	30.8%	
	11.6%	5.4%	26.7%	21.0%	6.6%	0.4%	23.5%	4.9%	28.3%	
	12.9%	6.2%	23.3%	22.7%	7.2%	0.4%	22.9%	4.3%	27.2%	
	11.6%	5.5%	26.1%	21.1%	6.5%	0.4%	24.2%	4.6%	28.8%	
	11.8%	5.8%	25.5%	21.6%	6.5%	0.4%	24.0%	4.4%	28.4%	28.5 ± 1.3
Line 545	12.9%	6.2%	21.9%	23.3%	7.0%	0.4%	24.0%	4.2%	28.3%	
	12.6%	6.0%	23.2%	23.3%	7.0%	0.4%	22.9%	4.5%	27.5%	
	11.8%	5.3%	24.8%	22.6%	7.4%	0.4%	23.1%	4.7%	27.8%	
	12.3%	5.3%	25.2%	23.0%	7.1%	0.4%	22.7%	4.2%	26.8%	
	12.8%	5.9%	21.7%	23.0%	7.1%	0.4%	24.7%	4.5%	29.2%	
	11.5%	5.2%	26.5%	21.8%	7.4%	0.4%	22.3%	4.9%	27.2%	27.8 ± 0.8
Line 540	15.3%	6.7%	31.6%	22.5%	5.6%	0.4%	14.9%	2.9%	17.8%	
	16.4%	7.4%	32.2%	21.1%	5.1%	0.4%	14.6%	2.9%	17.4%	
	16.8%	7.4%	30.3%	22.6%	5.8%	0.4%	14.1%	2.6%	16.7%	
	18.4%	8.0%	29.3%	21.2%	5.1%	2.1%	13.5%	2.5%	16.0%	
	18.6%	8.0%	29.3%	20.7%	4.9%	2.3%	13.6%	2.6%	16.2%	
	19.8%	8.3%	29.1%	19.8%	4.5%	3.5%	12.8%	2.3%	15.1%	16.5 ± 1.0

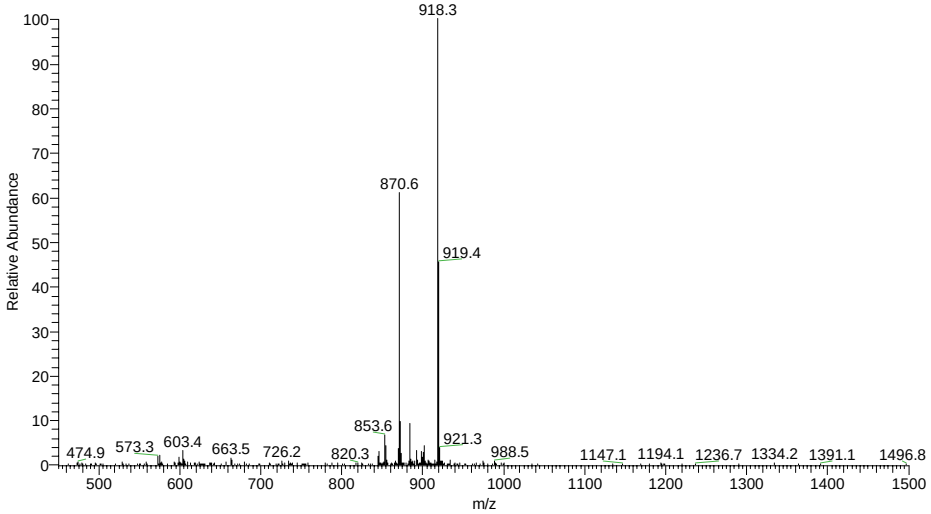
(a)


Relative Abundance
Time (min)
32.35
905.5
23.69
916.4
28.15
892.3
18.80
934.3
16.66
932.3
7.36
663.3
12.24
950.2
15.47
930.3
32.96
874.5
36.03
894.4
5.21
653.2
38.29
850.5
40.41
922.3
44.22
904.6
48.54
932.6
52.77
734.5
58.54
623.9

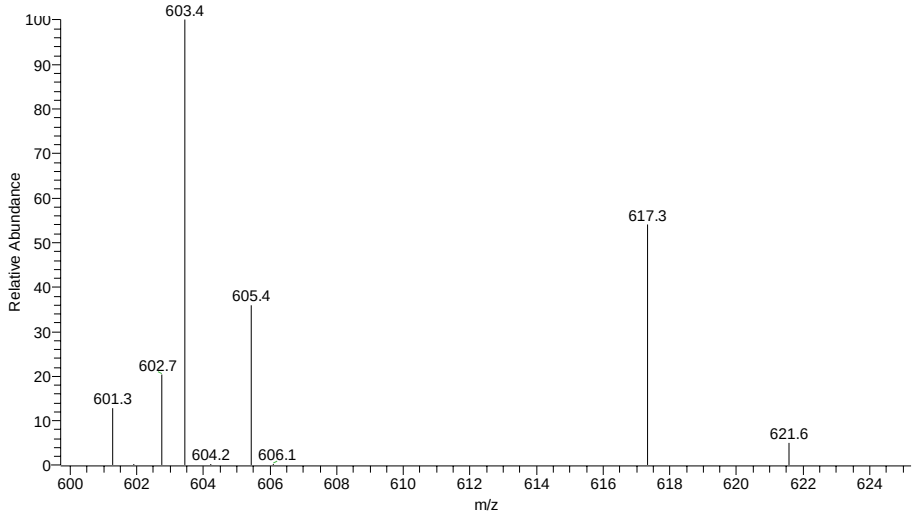
(b)


Relative Abundance
Time (min)
30.20
918.3
31.27
872.5
29.03
898.5
29.98
918.4
30.84
900.6
29.62
898.5

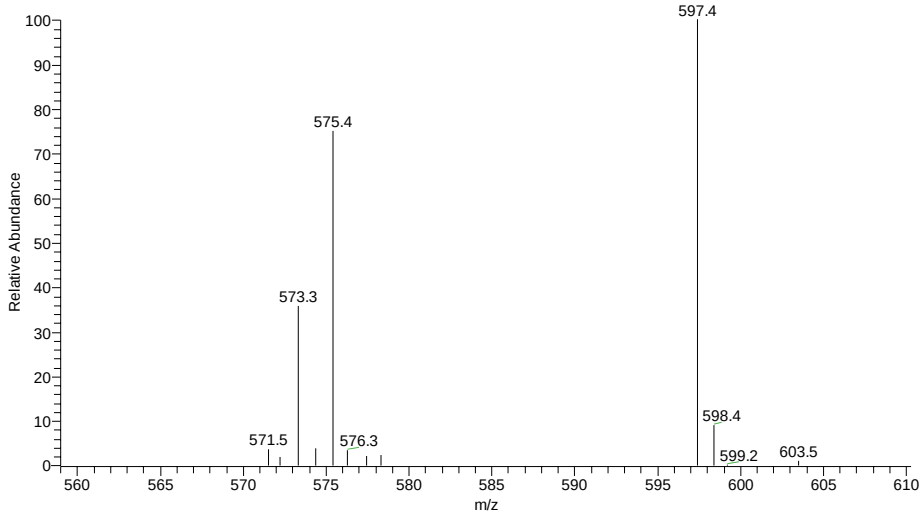
(c)


Relative Abundance
m/z
918.3
870.6
919.4
853.6
921.3
474.9
573.3
603.4
663.5
726.2
820.3
988.5
1147.1
1194.1
1236.7
1334.2
1391.1
1496.8

(d)



(e)



Supplemental Figure S1. LC/MS identification and quantification of triacylglycerols. (a) Total ion chromatogram of TAGs derived from plant line 544. Individual peaks are labeled with the retention time and mass of the corresponding ammoniated molecular ion. The internal standard, ^{13}C-labeled triolein, has a retention time of 32.35 and ammoniated molecular ion mass of 905.5. (b) Expanded region of the total ion chromatogram showing just 2 minutes of separation near the 30 minute mark. Peaks are labeled as in (a). The peak at 30.20 minutes, with a prominent molecular ion at 918.3, is used as an example below for TAG identification. (c) Full ms scan at retention time 30.20, showing the prominent ammoniated molecular ion at 918.3 and a second ammoniated molecular ion at 870.6, representing a minor TAG species co-eluting at the same retention time position. (d) Fragmentation analysis of the molecular ion at 918.3 by collision-induced dissociation and collection of fragments by ms2. Prominent neutral loss ions are observed at 603.4 (loss of ricinoleic acid), 617.3 (loss of stearic acid), and 621.6 (loss of linoleic acid), indicating that the parental molecular ion (mass of 918.3) represents a TAG composed of R, L, and S. While the ms2 fragment of lowest abundance likely represents the loss of a fatty acid from the *sn*-2 position (thereby defining the fatty acid at *sn*-2), no discrimination of sn-2 vs. sn-1 and -3 was made in our analysis due to lack of appropriate molecular standards. (e) Fragmentation analysis of the parental ion at 870.6, showing prominent neutral loss ions at 573.3 (loss of linoleic acid), 575.4 (loss of linolenic acid), and 597.4 (loss of palmitic acid), thereby identifying the TAG as LnLP. Once all molecular ions are identified, the TAGs can be quantified by integrating the respective peak areas in the total ion chromatogram (b) and comparing peak areas to a known amount of internal standard. Ionization efficiencies of different unsaturated TAG species are essentially the same, allowing direct comparison of TAG species to the internal standard (unpublished data).