

SUPPLEMENTARY INFORMATION

1. Information on weather conditions and soil physicochemical parameters during the course of growth of plants (Supplementary Table 1).
2. Fatty acid methyl ester (FAME) profiles of total lipids, PC, DAG and TAG components at 34, 37 and 40 DAA (Supplementary Table 2).
3. Data for molecular mass of DAG molecules adducted with sodium ions (Supplementary Table 3).
4. Data for molecular mass of ammoniated TAG molecules (Supplementary Table 4).
5. Individual chromatograms of FAME separations of PC, DAG and TAG at 34, 37 and 40 DAA (Supplementary Figure S1 A-J).
6. Individual chromatograms depicting separation of molecular species of DAG and TAG at 34, 37 469 and 40 DAA (Supplementary Figure S2 A-C).
7. Chromatograms depicting fatty acid composition at sn-1 and sn-2 positions of DAG from 34, 37 and 40 DAA (Supplementary Figure S3 A-F).

Supplementary Table 1. Annual weather data recorded during the course of growth of *Jatropha curcas* trees and selected soil characteristics of the study site. The weather data is presented as a measured range (lowest value - highest value) while the soil data is presented as the average of the measurements.

Climatic conditions	Growth Months		
	November - February	March - June	July - October
Mean max. temperature (°C)	27.9 – 31.8	35.4 – 44.8	30.7 – 34.8
Mean min. temperature (°C)	10.2 – 22.2	22.4 – 29.4	24.7 – 25.8
Relative humidity (%)	49 - 58	39 - 60	63 - 74
Mean rainfall (mm)	8 - 24	10 - 108	95 - 165
Atmospheric CO ₂ concentration (μmol m ⁻² s ⁻¹)	380 - 395	380 - 395	380 - 395
Wind velocity (km h ⁻¹)	3	2	4 - 12
Mean photosynthetic flux (μmol m ⁻² s ⁻¹)	1000 - 1200	1200 - 1500	1000 - 1200
Soil characteristics (at 0–30 cm soil depth)			
Texture	Sandy loam	Sandy loam	Sandy loam
pH	7.2	7.2	7.2
Organic carbon (%)	0.8	0.8	0.8
Available N (kg ha ⁻¹)	105	105	105
Available P (kg ha ⁻¹)	1.3	1.3	1.3
Available K(kg ha ⁻¹)	113	113	113

Supplementary Table 2. Fatty acid methyl ester (FAME) profiles of total lipids (TL), PC, DAG and TAG components at 34, 37 and 40 DAA stages of seed development. Samples were analyzed in triplicates and values presented as mean \pm SD. Different letters indicate that the values are significant at P<0.05.

Supplementary Table 3. Molecular mass of DAG molecules adducted with sodium ions have been calculated and shown. DAG molecules containing unsaturated fatty acids at the *sn*-2 position have been selected for analysis.

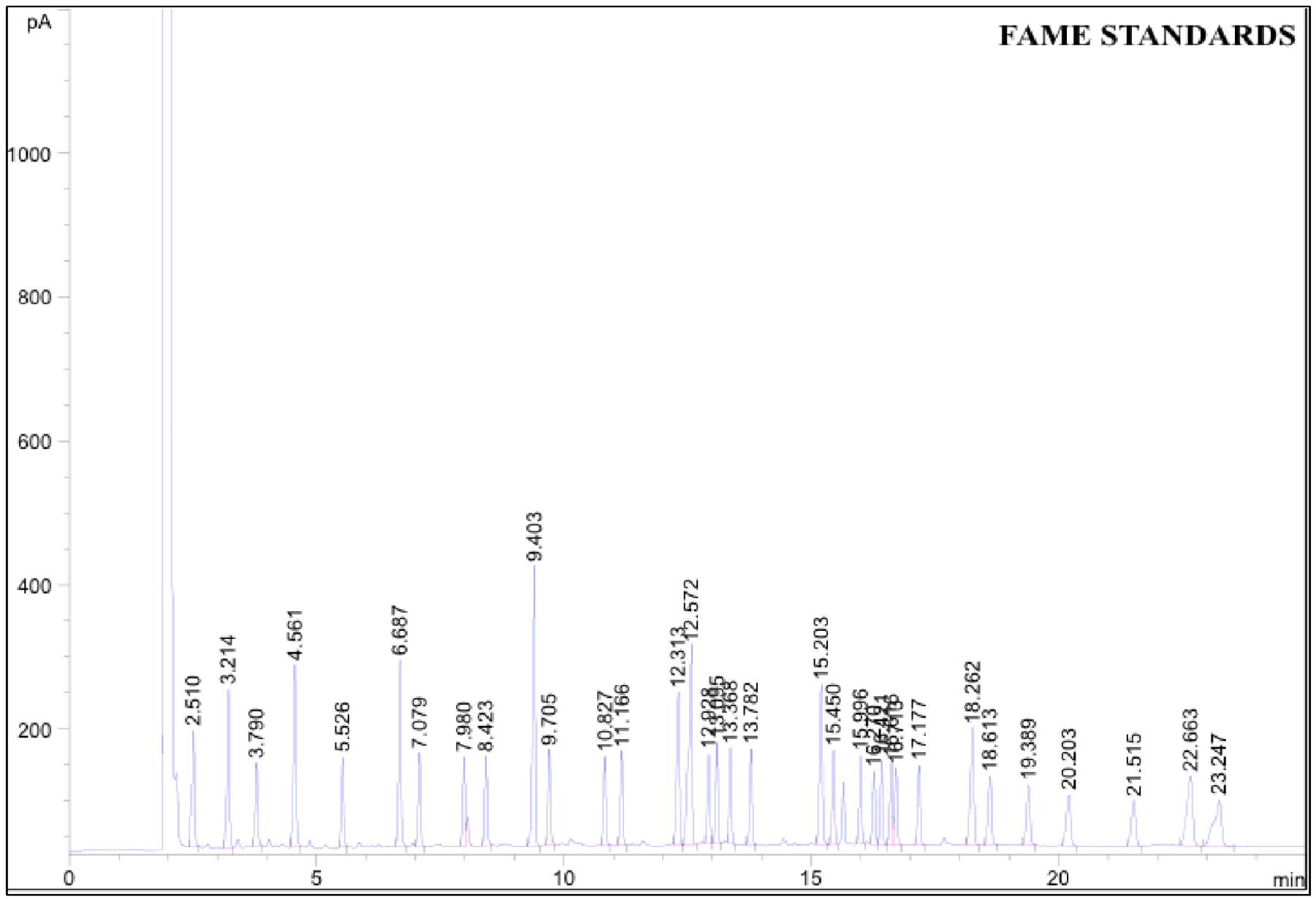
Molecular Species	Molecular weight	Na ⁺ adduct (MW+23)
16:0;18:2	594	617
16:0;18:1	596	619
18:1;18:1	622	645
18:1;18:2	620	643
18:2;18:2	618	641
18:0;18:1	624	647
18:0;18:2	622	645

Supplementary Table 4. Molecular mass of ammoniated TAG molecules have been calculated and shown. TAG molecules containing unsaturated fatty acids at the *sn*-2 position have been selected for analysis.

Molecular Species	Molecular weight	NH ₄ ⁺ adduct (MW+18)
16:0;16:0;16:0	809	827
16:0;18:2;16:0	833	851
16:0;18:1;16:0	835	853
16:0;18:1;18:1	861	879
16:0;18:1;18:2	859	877
16:0;18:2;18:2	857	875
18:2;18:2;18:2	881	899
18:1;18:2;18:1	885	903
18:1;18:1;18:1	887	905
18:0;18:2;18:1	887	905
18:0;18:2;16:0	861	879
18:0;18:1;16:0	863	881
18:0;18:1;18:1	889	907
18:0;18:2;18:0	889	907
18:0;18:1;18:0	891	909
18:0;18:0;18:0	893	911

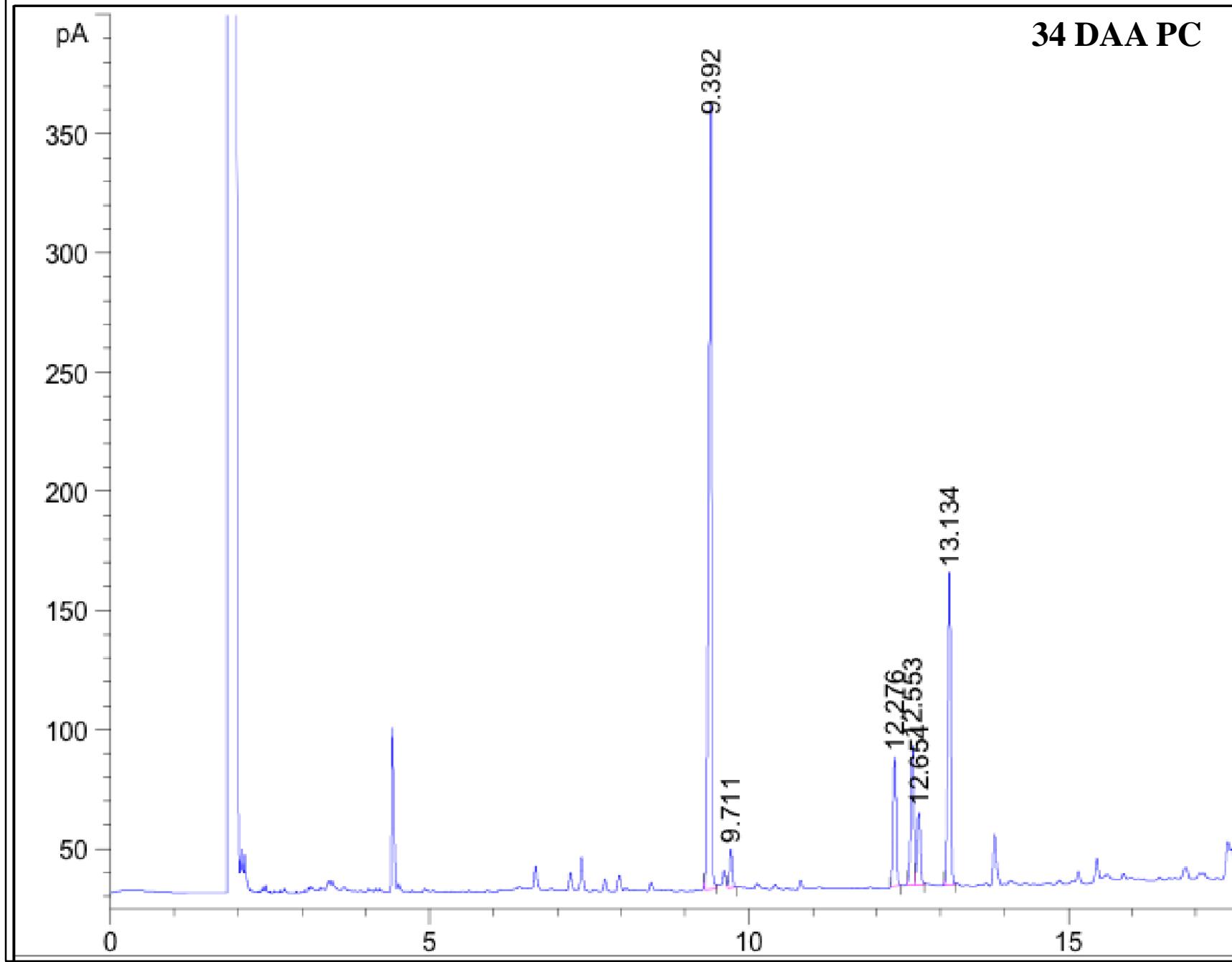
Supplementary Figure S1

FAME STANDARDS



(A) Chromatogram showing FAME standards. The retention times of major fatty acids are as follows follows; palmitic acid – 9.3xx minutes, stearic acid – 12.2xx minutes, oleic acid – 12.6xx minutes and linoleic acid – 13.1xx minutes.

34 DAA PC



(B) Individual chromatogram of FAME separations of PC at 34 DAA

34 DAA DAG

pA

350

300

250

200

150

100

50

0

5

10

15

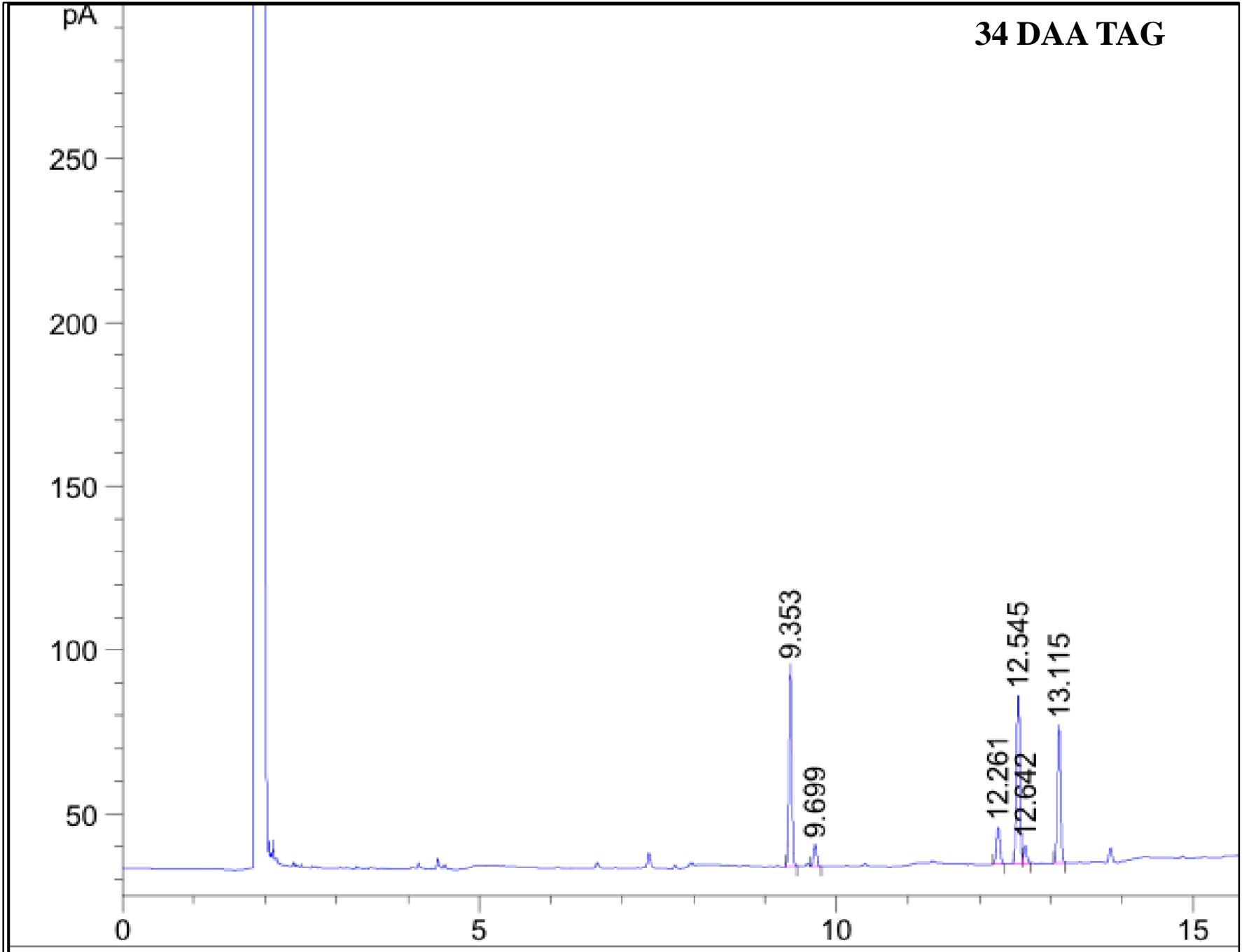
9.356
9.697

12.268
12.646
12.564

13.123

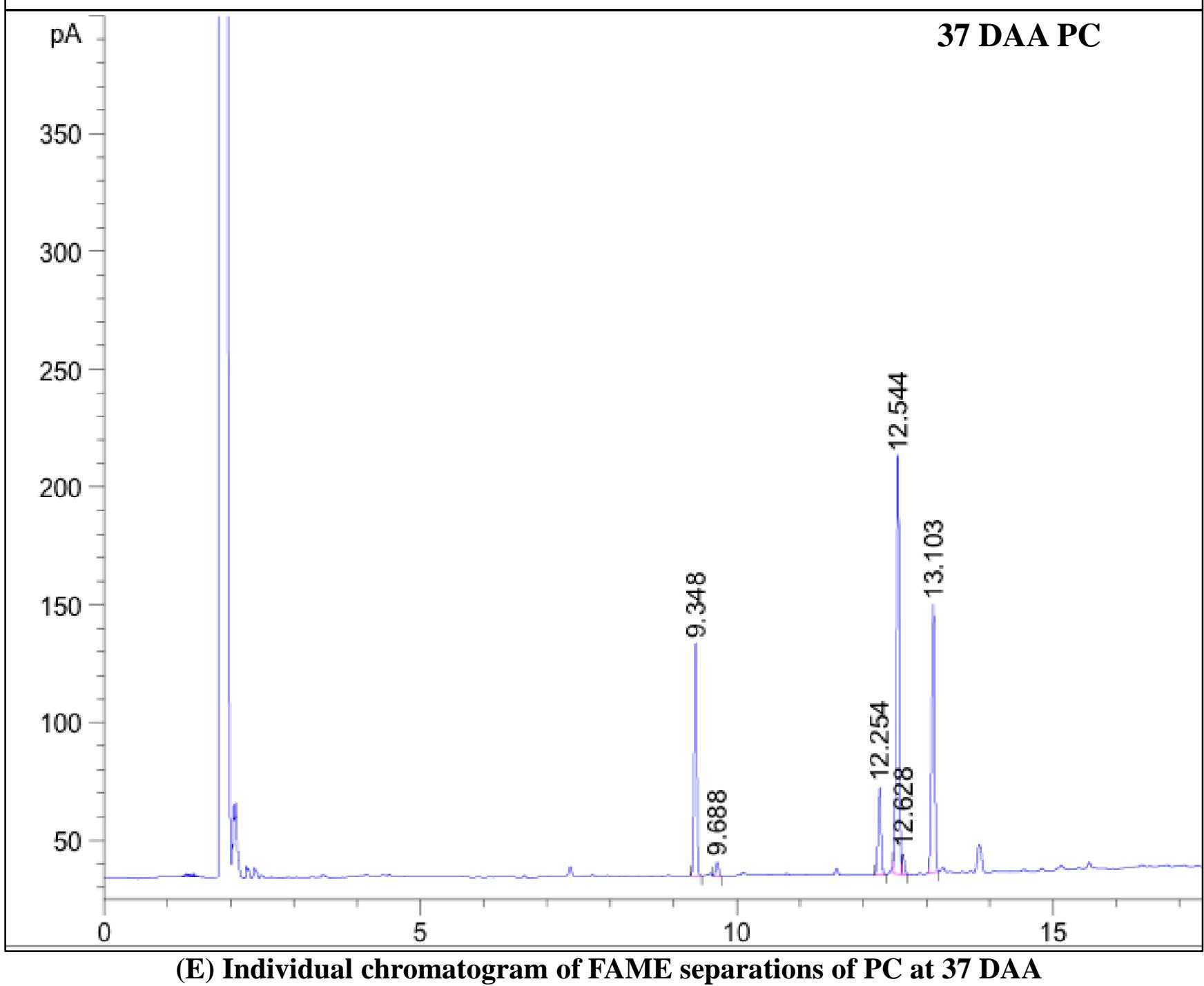
(C) Individual chromatogram of FAME separations of DAG at 34 DAA

34 DAA TAG

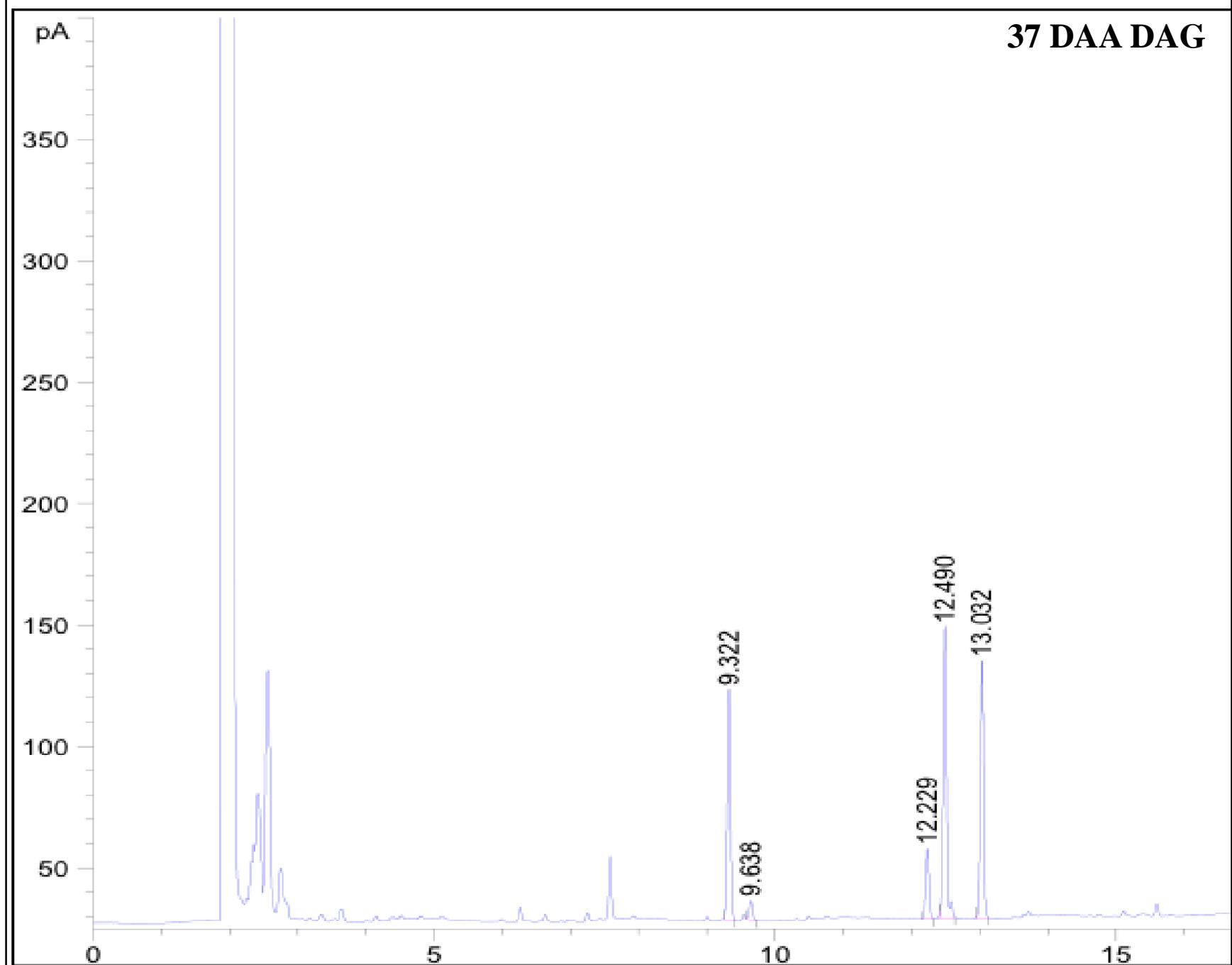


(D) Individual chromatogram of FAME separations of TAG at 34 DAA

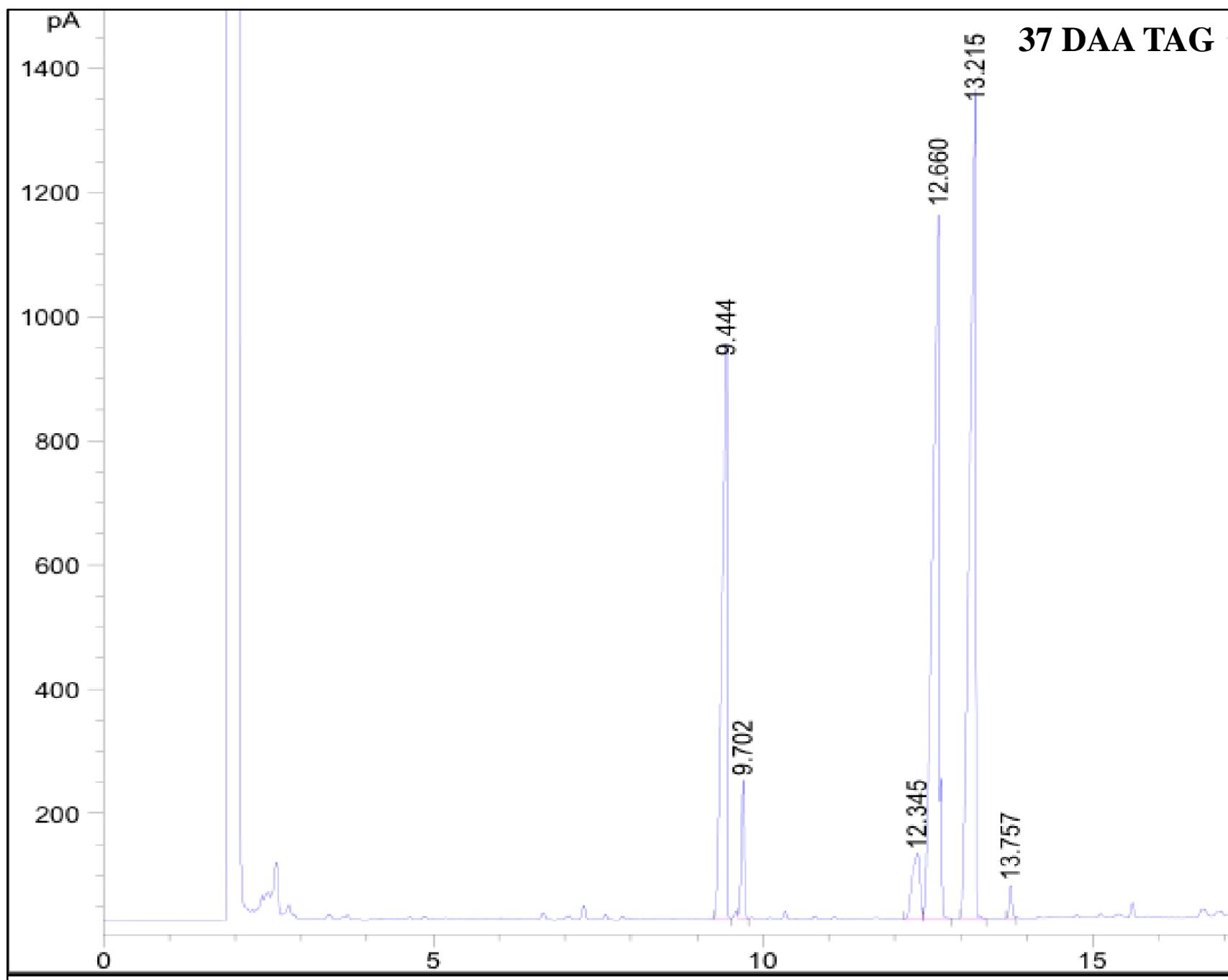
37 DAA PC



37 DAA DAG



(F) Individual chromatogram of FAME separations of DAG at 37 DAA



pA

40 DAA PC

350

300

250

200

150

100

50

0

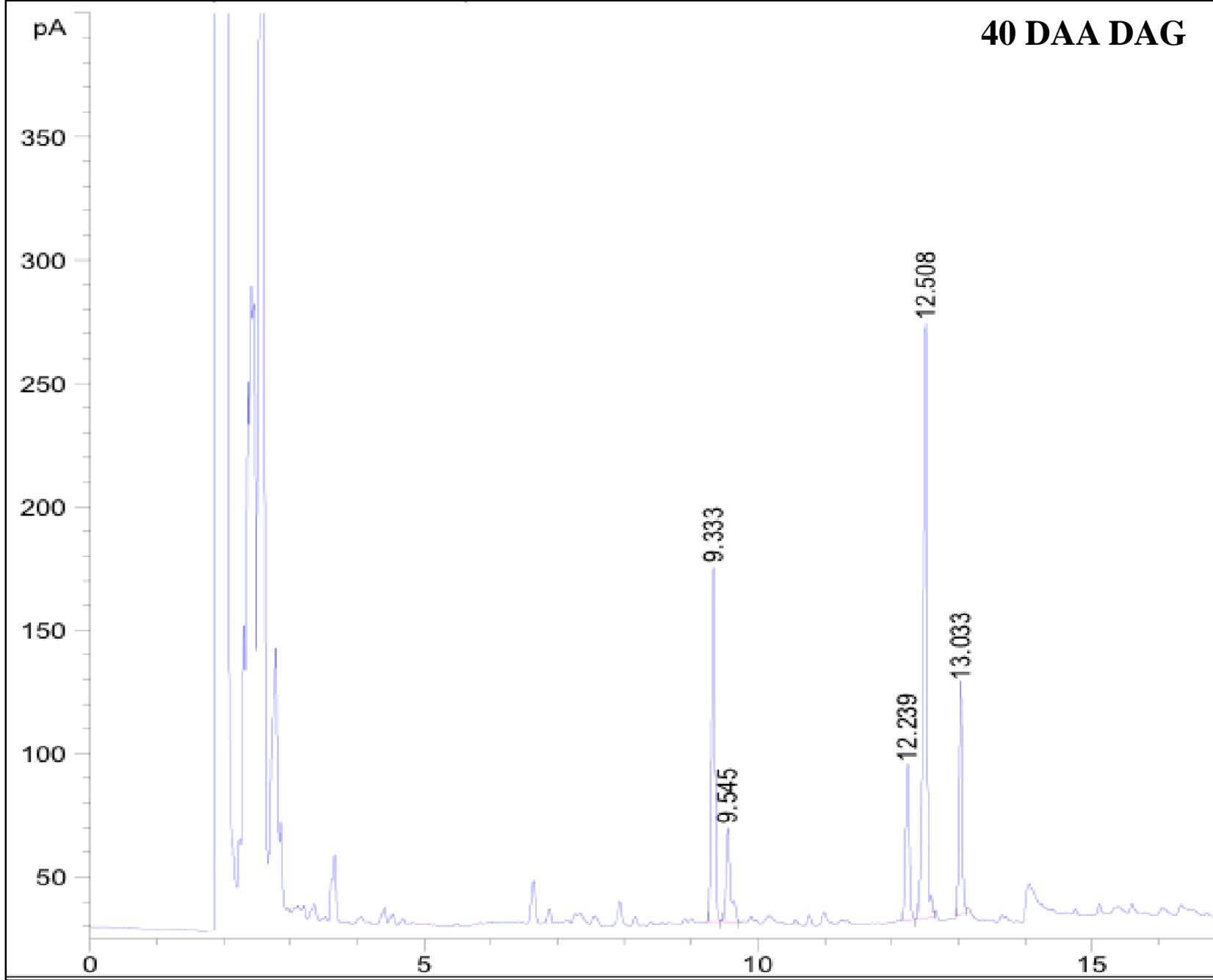
9.351
9.701

12.262
12.543

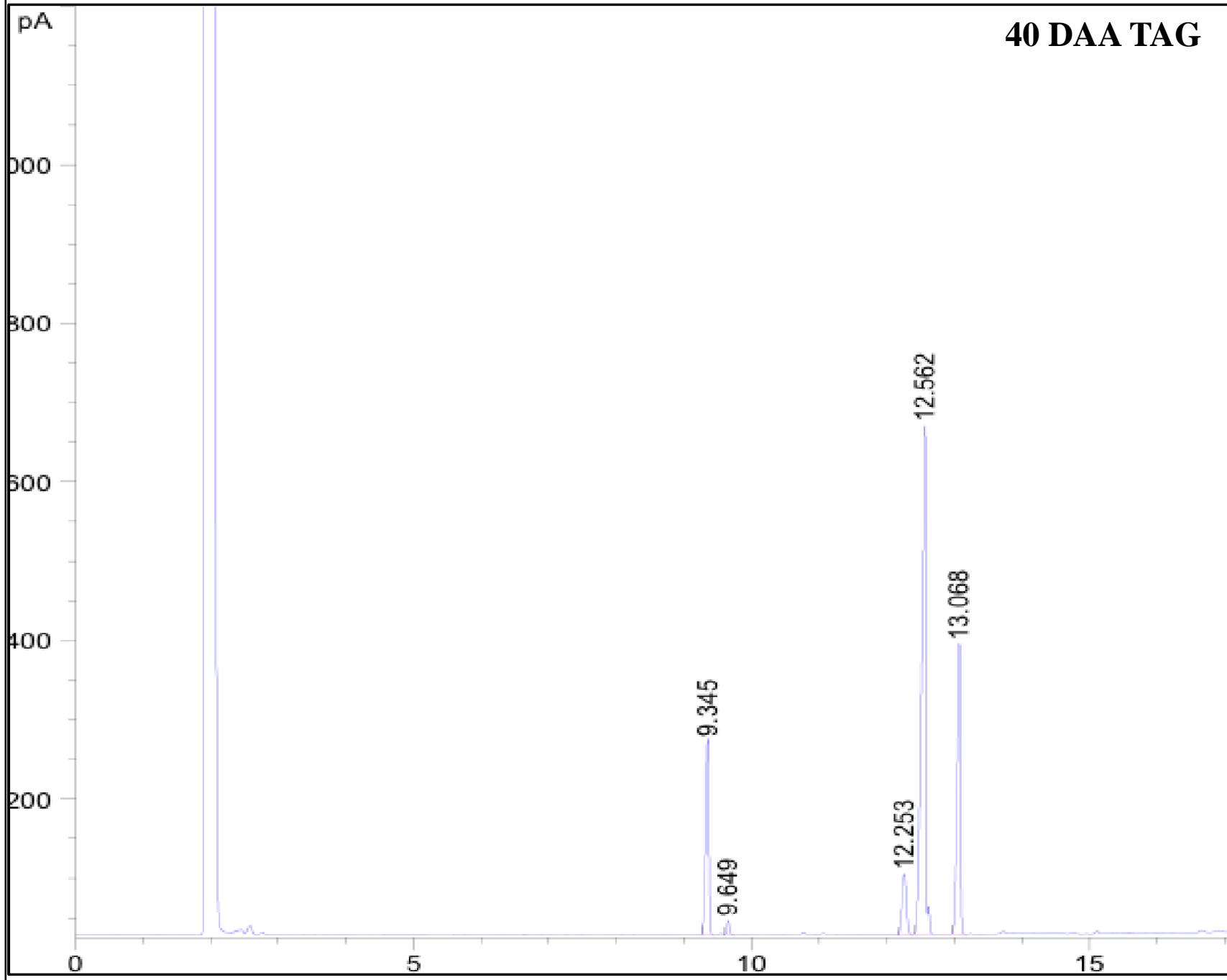
13.113

(H) Individual chromatogram of FAME separations of PC at 40 DAA

40 DAA DAG

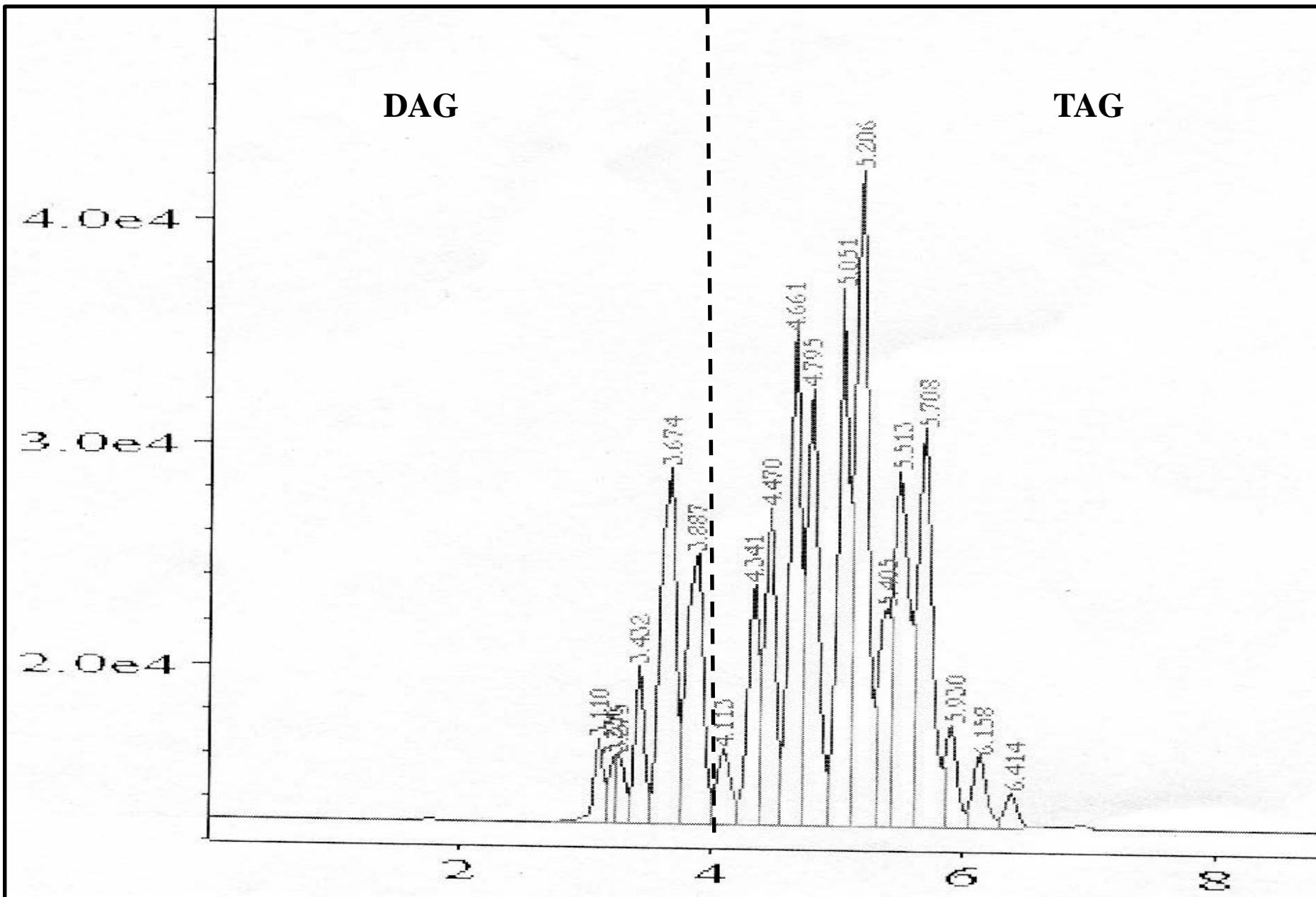


(I) Individual chromatogram of FAME separations of DAG at 40 DAA

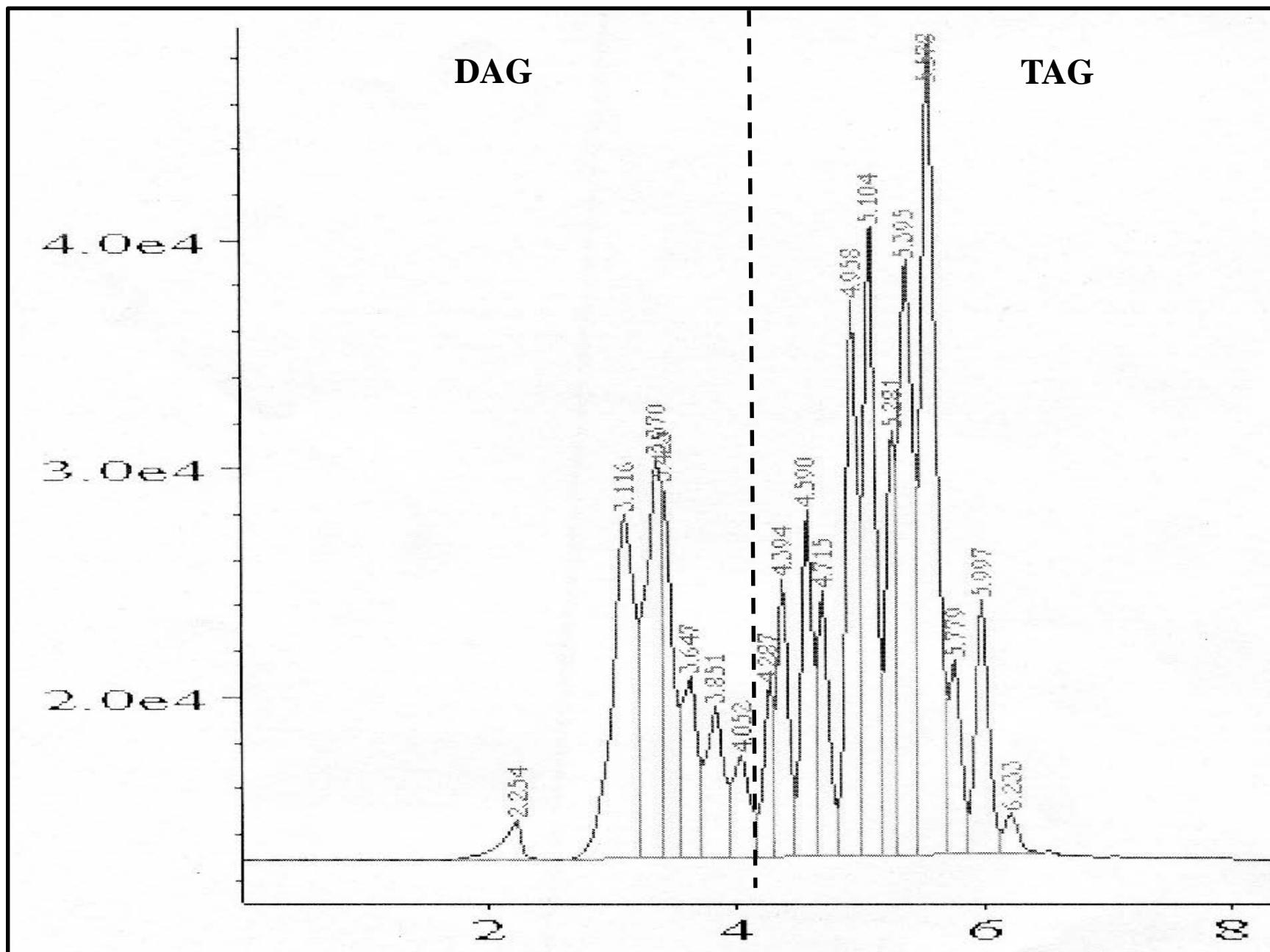


(J) Individual chromatogram of FAME separations of TAG at 40 DAA

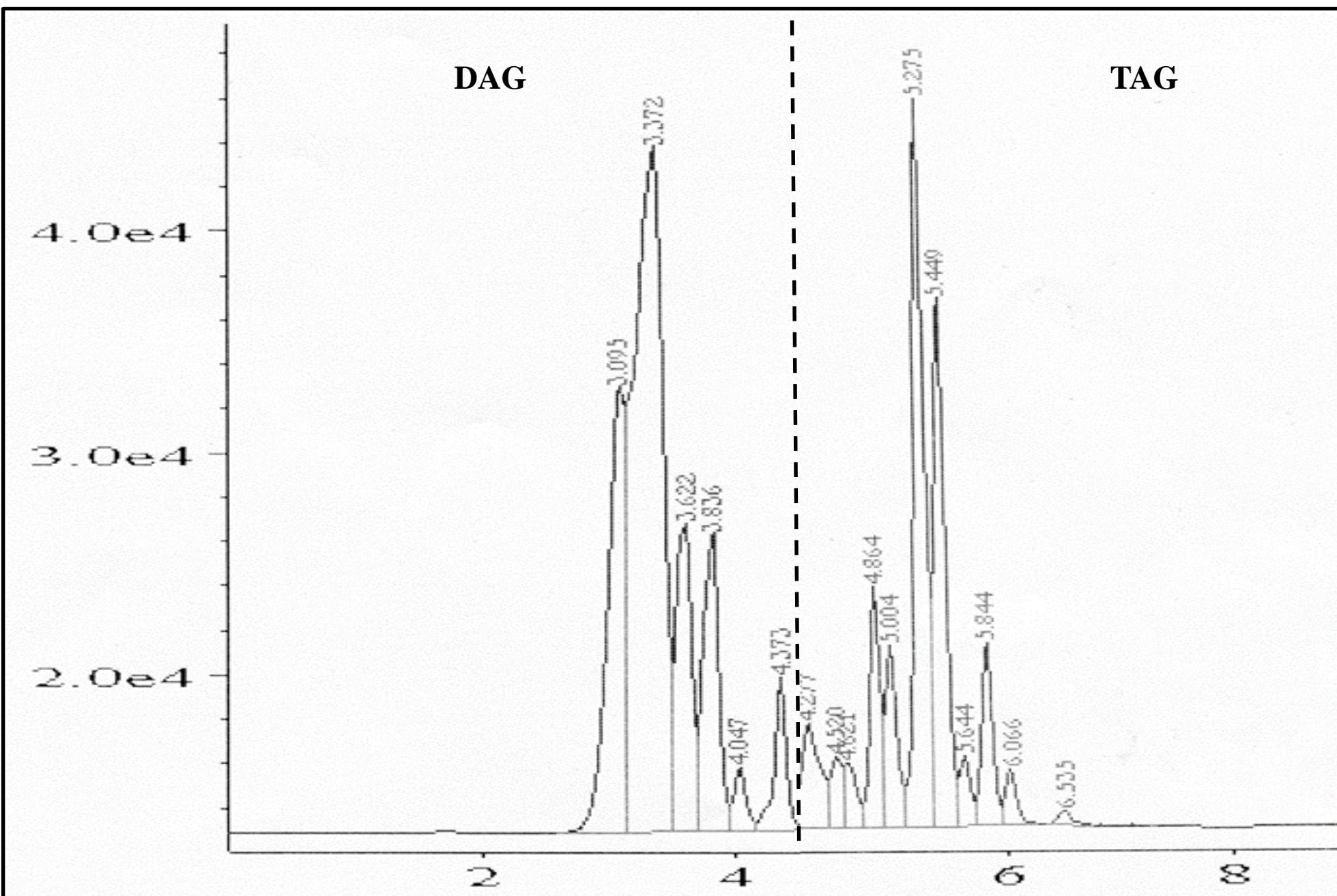
Supplementary Figure S2



(A) Individual chromatogram depicting separation of molecular species of DAG and TAG at 34 DAA during seed development. The dotted line differentiates DAG and TAG molecules.



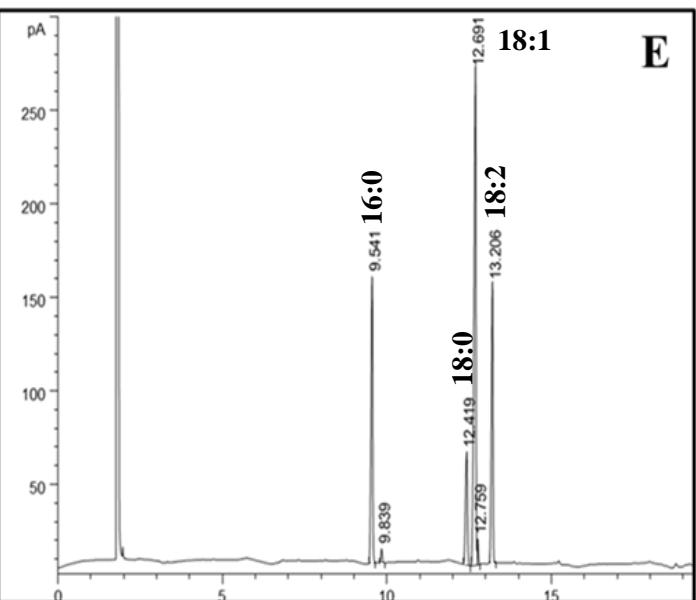
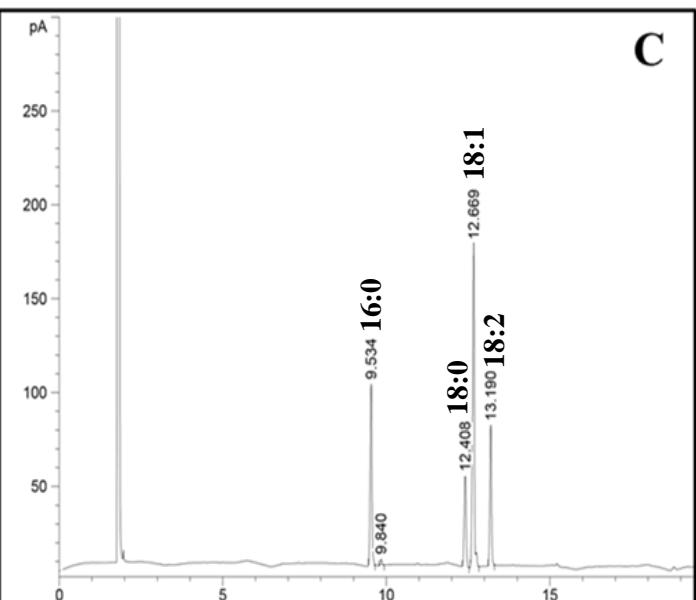
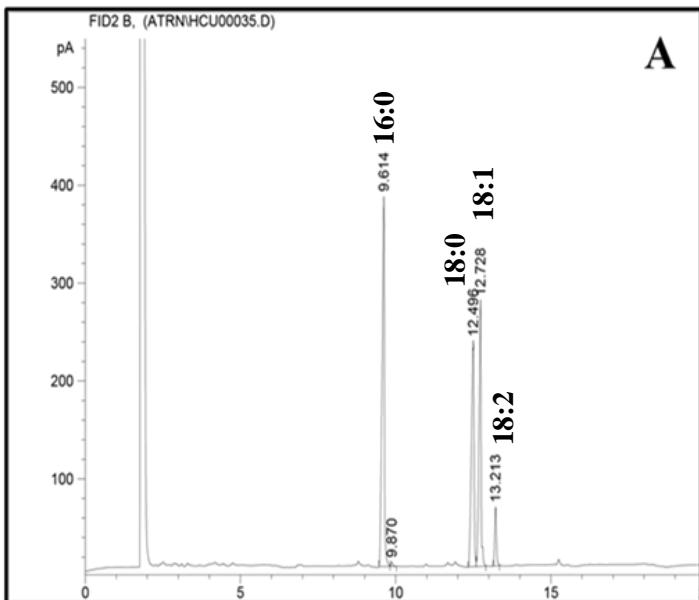
(B) Individual chromatogram depicting separation of molecular species of DAG and TAG at 37 DAA during seed development. The dotted line differentiates DAG and TAG molecules.



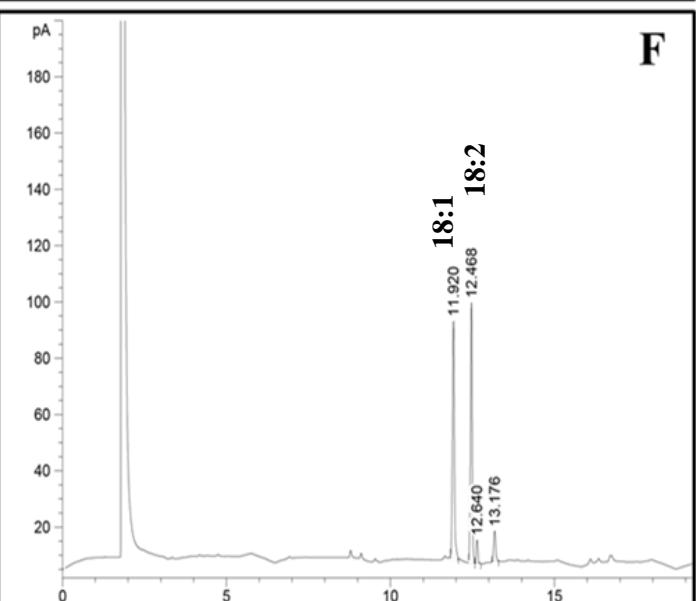
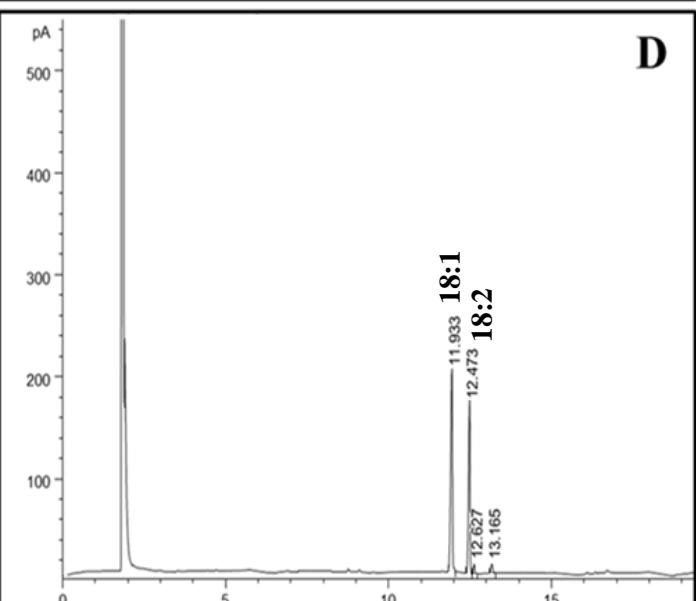
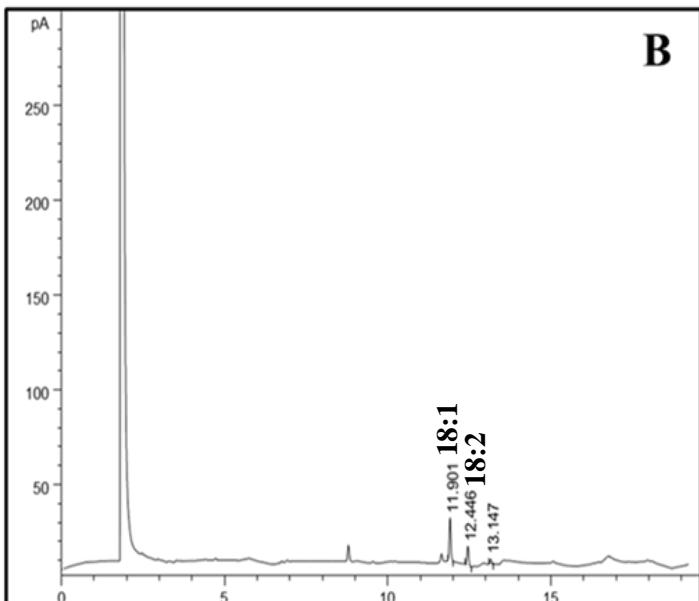
(C) Individual chromatogram depicting separation of molecular species of DAG and TAG at 40 DAA during seed development. The dotted line differentiates DAG and TAG molecules.

Supplementary Figure S3

Fatty acids at
sn-1 position of
DAG



Fatty acids at
sn-2 position of
DAG



34 DAA

37 DAA

40 DAA

Chromatograms depicting fatty acid composition at sn-1 and sn-2 positions of DAG from 34 (A, B), 37 (C, D) and 40 DAA (E, F) endosperm during seed development