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Functional Plant Biology

Supplementary Material

***Glycine max* acyl–acyl carrier protein thioesterase B gene overexpression alters lipid content and fatty acid profile of *Arabidopsis* seeds**

Shihui Zhao^A, Fan Yan^A, Yajing Liu^A, Monan Sun^A, Ying Wang^A, Jingwen Li^A, Xinsheng Zhang^A, Xuguang Yang^{A,*}, and Qingyu Wang^{A,*}

^ACollege of Plant Science, Jilin University, Changchun, China.

*Correspondence to: Xuguang Yang College of Plant Science, Jilin University, Changchun, China Email: xgyang@jlu.edu.cn Qingyu Wang College of Plant Science, Jilin University, Changchun, China Email: qywang@jlu.edu.cn

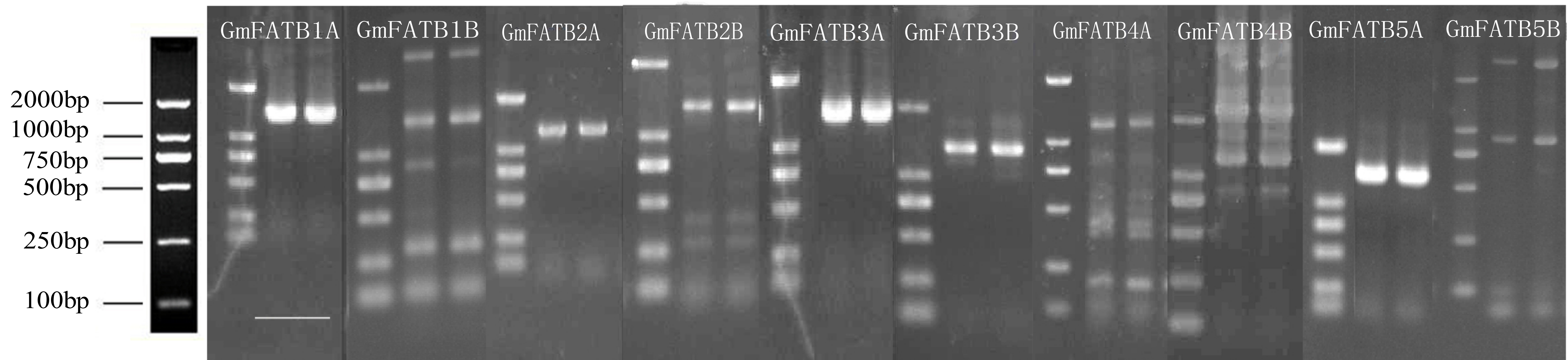


Figure S1. PCR amplification of the full-length GmFATB gene family CDS.
M, DNA marker DL2000; 1, GmFATB gene family CDS PCR product from cDNA

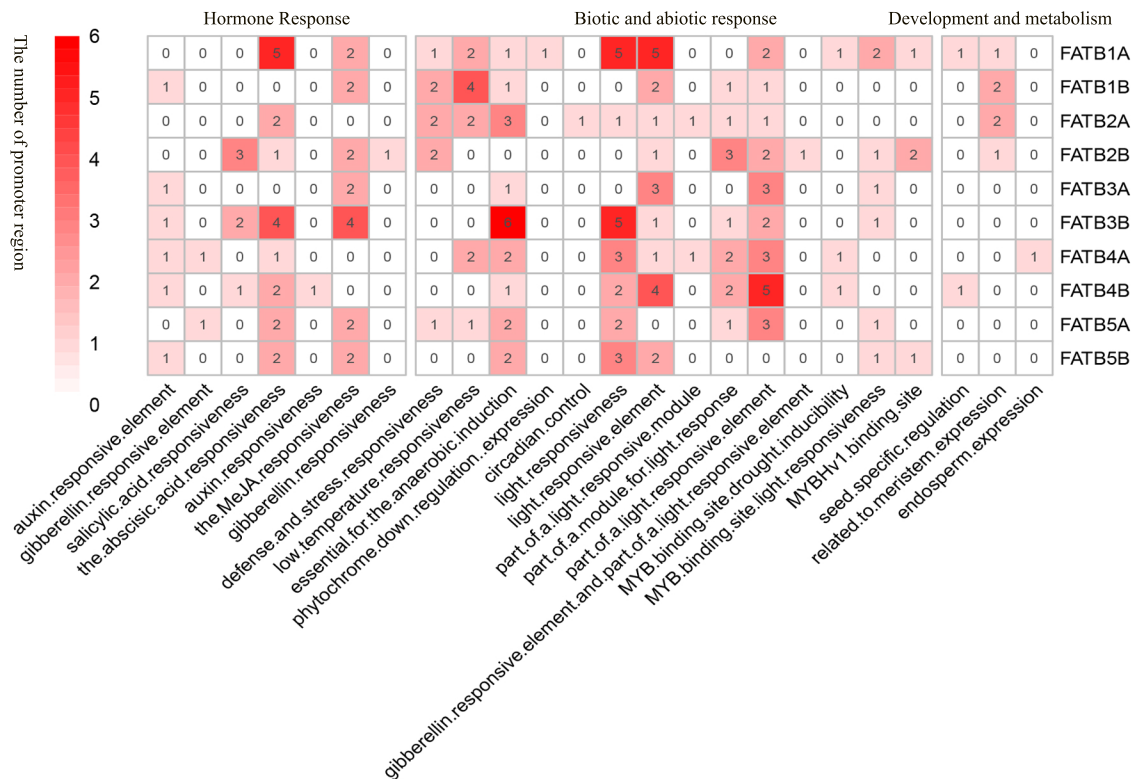


Figure S2. Promoter cis-element analysis of GmFATB genes. Numbers indicate the sum of the responses of different cis-acting elements to similar stimuli.

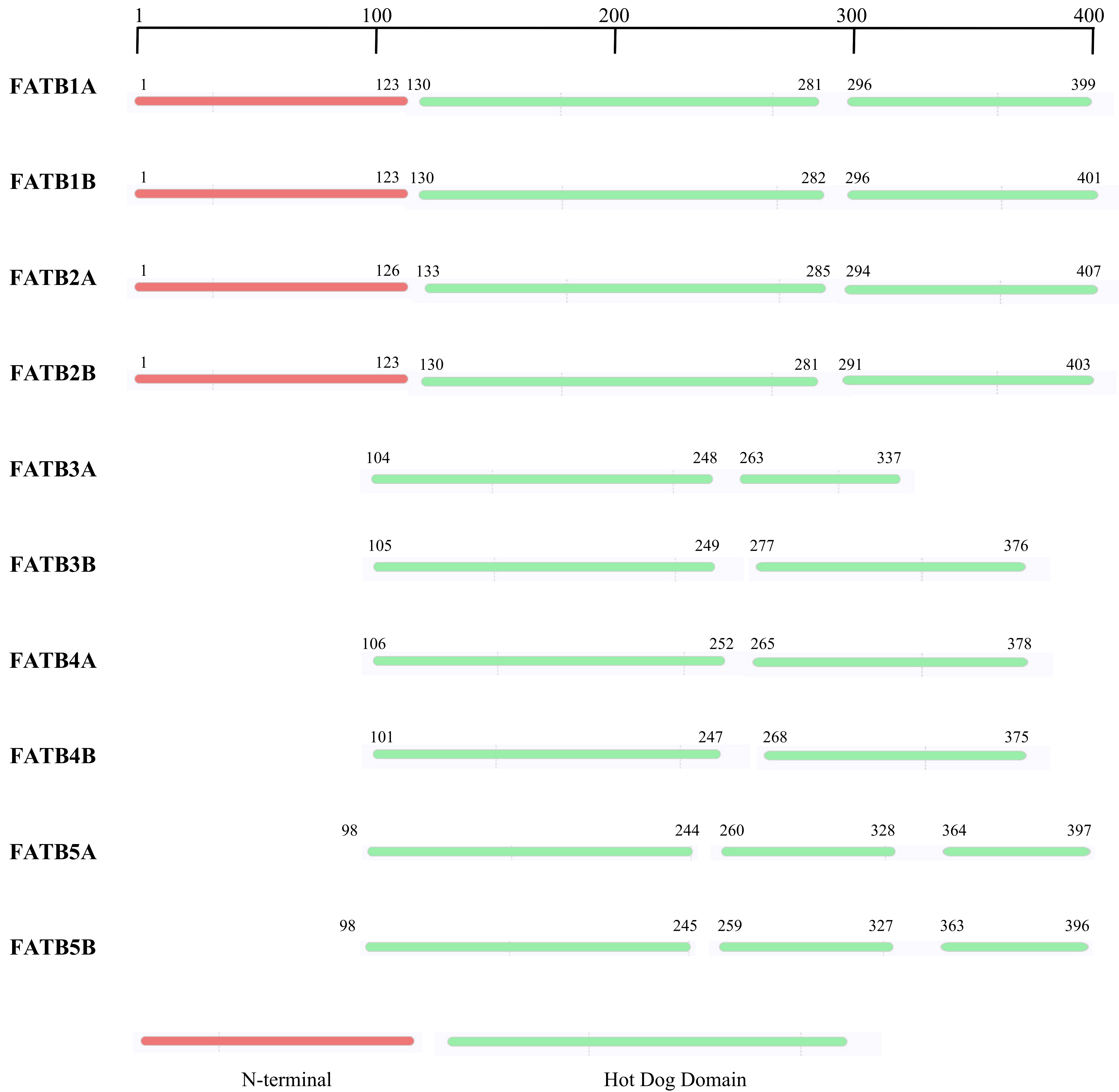












Figure S3. GmFatBs Protein Domain

Motif	Symbol	Motif Consensus
1.		GLSPRWNDLDVNVNKHVYIGWILESVPEILESHELSSMTLEYRRECG
2.		GATPEMCKKNLIWVVTRMQVVVDYPTWGDVVZVDTWVDASGKNGMRRDW
3.		ZDGLVFRQNFVIRSYEIGADKTATIE TJMNFLQETALNHVKSAGLLGDGF
4.		RDHKTGEIJTRATSTWMMNRETRRLSKIPEEVROEJSPYFVD
5.		PRTFINQLPDWSMLLAAITTFILAAEKQWMLDVKPRRPDMLIDPFGIGK
6.		GAEIVRGRTEWRPKP
7.		DSSSVISGSBVGSLARKPDLZYTHLLRLQ
8.		PIEEDNEKJTKLDDETAEI I
9.		MVATAATSSFFPGNLPDANKGGPKLKLGG
10.		PRFSYPASTYFVRFVLSVRENHDDVPRKMDSSNRVNGNGRSP

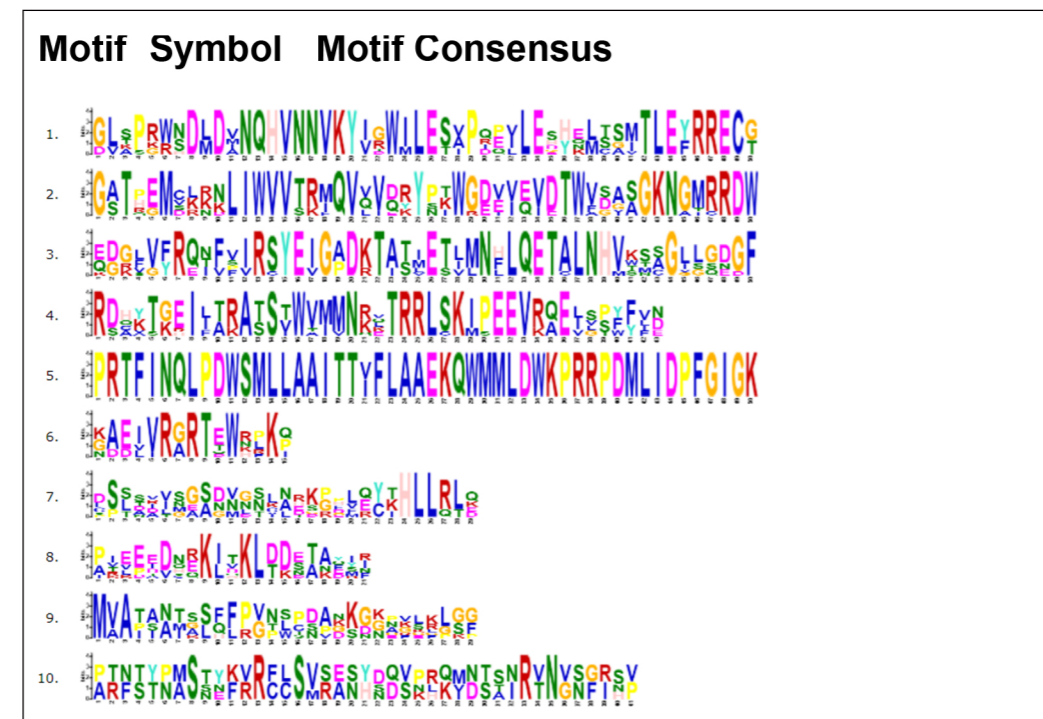


Figure S4. *GmFATBs* Motif Consensus

Appendix A. Supplementary data

Table S1 Sequences of primers and sizes of PCR-amplified products.

<i>Rename</i>	Gene	Primer (5'-3')	TM (°C)	Location	CDS length (bp)
<i>GmFATB1A</i>	Glyma.05G012300	F:TCTACCGGAGAAGCGACCTT R:CTCTCCCCAGGGACCAGAAT	58	Flower	1158
<i>GmFATB1B</i>	Glyma.17G120400	F:TACGTACGTGTCCGAAACT R:AGCTTGCATAAATACACGCTGG	64	Root	1251
<i>GmFATB2A</i>	Glyma.04G151600	F:GCTCTGGTTCAGTAAGGCGA R:TATGCCACTCCTCCTCCAGT	60	Root	1140
<i>GmFATB2B</i>	Glyma.06G211300	F:CTGGTTCGGTAAGGCGTAGG R:GCAAAGCTCTCCAATCTGCAA	64	Root	1152
<i>GmFATB3A</i>	Glyma.04G197400	F:TCCCACTTGCCGAATTCCT R:AAGGGTACAGGGTCCACAGA	58	Root	1260
<i>GmFATB3B</i>	Glyma.06G168100	F:ACTAGCAATTGCATCGGTCA R:AGCAATCTACAATTCTCCTCACAGA	58	Root	1260
<i>GmFATB4A</i>	Glyma.04G197500				1251
<i>GmFATB4B</i>	Glyma.06G168000	F:ATGGTGGCACCCATCAACAT R:TTCACCTGCCCATCCAAAG	65	Flower	1200
<i>GmFATB5A</i>	Glyma.10G268200	F:CTCAGACTTCCAAGTCCTGCTT R:GGGTACACACCATGACCAGA	62	Leaf	1125
<i>GmFATB5B</i>	Glyma.20G122900	F:TCCTTGCAGCCACAACACAAG R:TTTGTTCCTTCCCAGTCCACAT	64	Leaf	1128

TM: Annealing Temperature; CDS: Sequence coding for amino acids in protein.

Table S2 Primers used for RT-qPCR.

Gene	Forward primer (5'-3')	Reverse primer (5'-3')
<i>Actin</i>	GTCCTTTCAGGAGGTACAACC	CCACATCTGCTGGAAGGTGC
<i>FATB1A</i>	AGGGAAACAACAAGGACGCA	TGCAGAAAAAGCGGGTTTGG
<i>FATB1B</i>	TGCACCTCCACTCTCCACTC	CGGCGAGGGTGAAGTAACAG
<i>FATB2A</i>	GCCCAAACCTTTAAGCAGCA	CTCCTCCAGTGATGCCAATC
<i>FATB2B</i>	CCACTACTTTCCTACTGCTCC	GAGGCCTTTCCTGCAAGCTA
<i>FATB3A</i>	CCCACTTGCCGAATTCATAT	AGTAGTGTGCGTGGAGAACA
<i>FATB3B</i>	TGTGGACCCTGTACCCTTCT	AGCAATCTACAATTCTCCTCACAGA
<i>FATB4A</i>	ACTAAAGCCGAGTTGGTCCG	TGGTTGGGTCCACATATGCC
<i>FATB4B</i>	AGAAAACCCGCTGCAATA	GATTTACCTGCCCATCCA
<i>FATB5A</i>	ACAACCAAGAAGCGTTTGGAG	GGGTATAAACCTGCATTCACACG
<i>FATB5B</i>	AAATTGTATCTATGGGGGCAAACT	TCATGTGGGTTGCTCTCA

Table S3 Characteristics of FATBs in soybean.

Names	Amino acids (aa)	Genomics position
<i>FATB1A</i>	416	Gm05:1130754-1134962
<i>FATB1B</i>	416	Gm17:9565137-9565308
<i>FATB2A</i>	422	Gm04:32542473-32542754
<i>FATB2B</i>	419	Gm06:20899407-20904594
<i>FATB3A</i>	382	Gm04:45772582-45772830
<i>FATB3B</i>	383	Gm06:13994569-13998084
<i>FATB4A</i>	385	Gm04:45777553-45777804
<i>FATB4B</i>	379	Gm06:13984425-13988460
<i>FATB5A</i>	400	Gm10:49148981-49152327
<i>FATB5B</i>	399	Gm20:36564032-36567770

Table S4 Fatty acid profiles of seeds of each Arabidopsis line.

Type	LINE	C _{16:0}	C _{18:0}	C _{18:1}	C _{18:2}	C _{18:3}
WT	Line-4	7.09±0.64	4.32±0.69	12.77±1.43	30.98±1.35	18.23±1.54
	Line-6	7.34±0.77	4.65±0.89	12.31±0.98	30.1±0.86	18.67±1.63
	Line-10	7.14±1.02	4.53±0.74	12.42±0.87	31.02±0.97	18.6±1.24
fatb-ko	Line-2	3.22±0.62	2.31±0.39	11.26±0.76	34.93±1.04	14.97±1.22
	Line-4	3.66±0.99	2.2±0.82	11.59±0.88	34.25±1.32	16.32±1.34
	Line-7	3.32±1.28	2.09±1.11	11.05±0.54	36.12±0.78	15.21±0.42
OE-FATB1A	Line-3	9.87±0.95	4.69±1.25	11.79±1.45	27.17±1.14	16.45±0.98
	Line-4	9.45±0.85	4.85±1.34	11.87±0.77	29.42±0.65	16.53±0.98
	Line-9	11.28±0.67	5.16±1.62	12.04±1.87	29.33±0.86	18.22±1.98
OE-FATB1B	Line-1	10.19±0.44	5.25±1.32	10.35±0.99	28.17±1.42	16.07±1.33
	Line-2	10.28±0.54	5.23±0.46	10.67±0.77	27.63±1.01	16.19±0.69
	Line-3	10.73±0.77	5.27±1.41	10.48±0.05	26.43±0.34	18.34±0.88
OE-FATB2A	Line-3	9.74±0.81	5.42±0.43	10.31±1.53	27.45±0.89	16.21±0.71
	Line-5	10.65±0.97	5.13±0.81	10.36±0.63	28.38±1.19	16.27±0.87
	Line-6	9.91±1.86	5.05±0.33	10.44±0.85	29.13±0.43	16.18±0.19
OE-FATB2B	Line-1	10.12±0.21	5.27±0.22	10.19±0.92	28.67±0.77	17.35±0.34
	Line-11	9.83±1.13	5.22±1.26	10.43±0.81	28.77±0.94	17.36±0.23
	Line-13	9.75±0.65	5.41±1.06	10.13±1.42	28.63±1.03	17.19±0.46

Fatty acid content is expressed as percentage of total fatty acids. Each value is the mean±SE of six biological replicates.

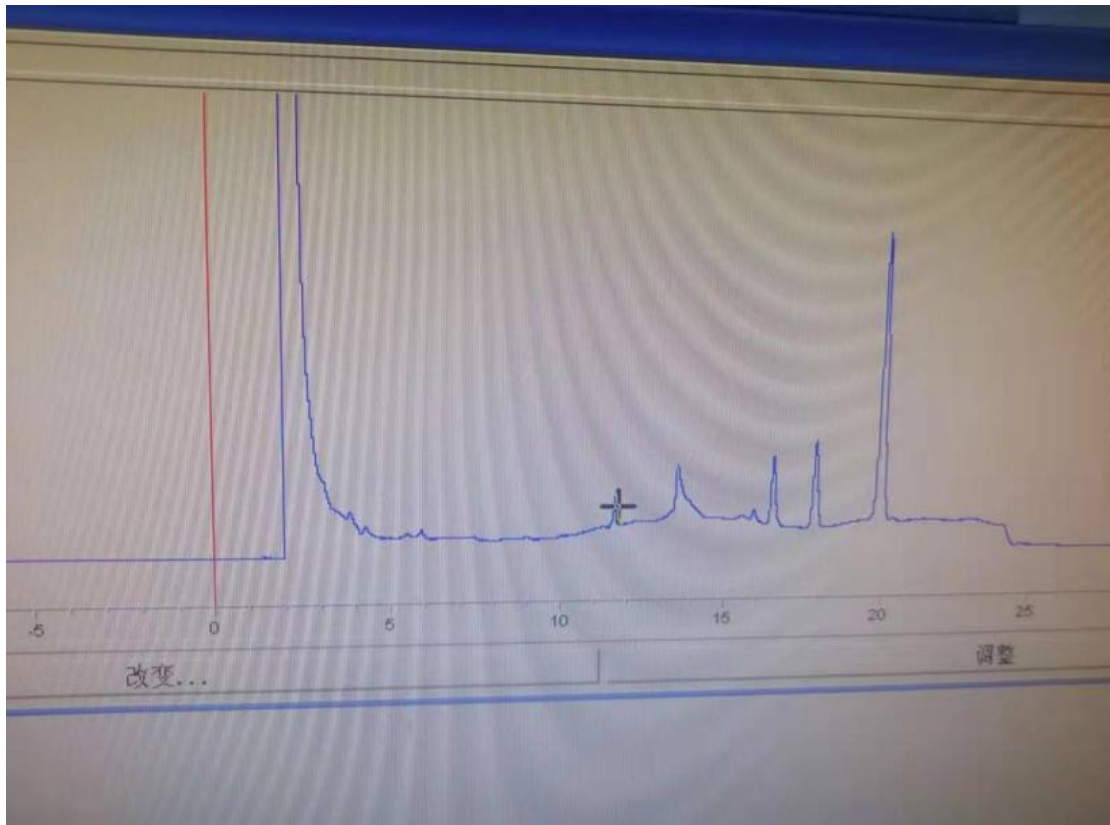
Table S4 Total FA content of seeds of each Arabidopsis line.

Type	WT				fatb-ko	
LINE	Line-4	Line-6	Line-10	Line-2	Line-4	Line-7
Total FA content	19.98±0.22	20.06±0.49	19.56±0.72	17.58±0.38	18.23±0.42	18.02±0.83
Type	OE-FATB1A			OE-FATB1B		
LINE	Line-3	Line-4	Line-9	Line-1	Line-2	Line-3

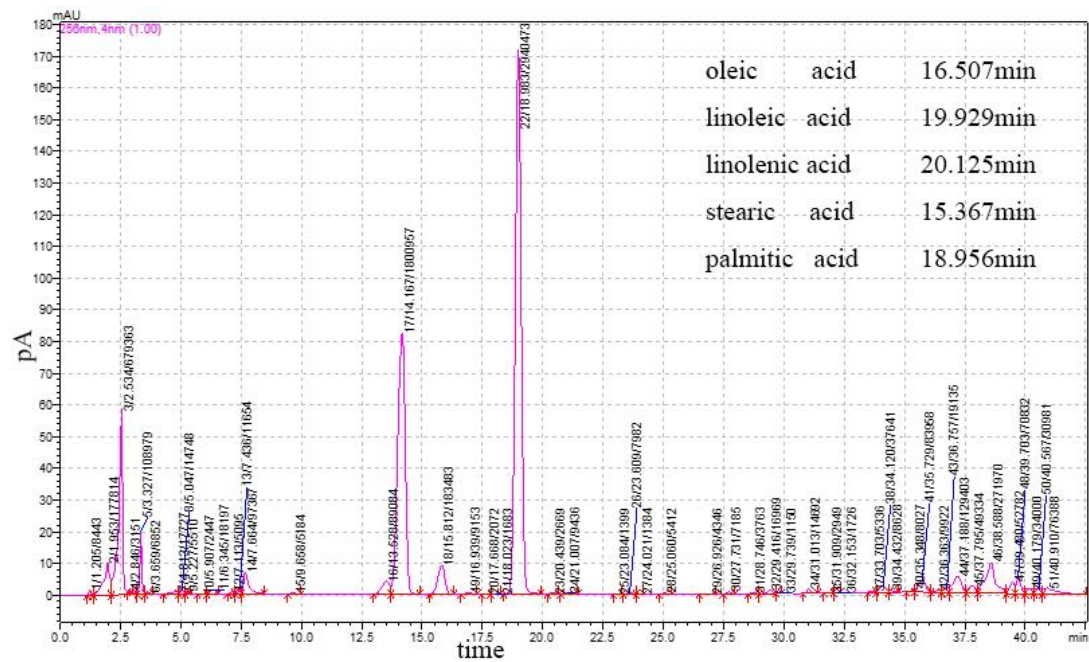
Total FA content	21.76±0.64	21.80±0.06	22.02±0.37	21.08±0.44	20.98±0.46	21.32±0.28
Type	OE-FATB2A			OE-FATB2B		
LINE	Line-3	Line-5	Line-6	Line-1	Line-11	Line-13
Total FA content	21.44±0.81	21.45±0.62	21.78±1.03	22.01±0.97	21.97±0.29	21.75±0.94

Total FA content of WT and T0 transgenic plants. Each value is the mean±SE of three biological replicates.

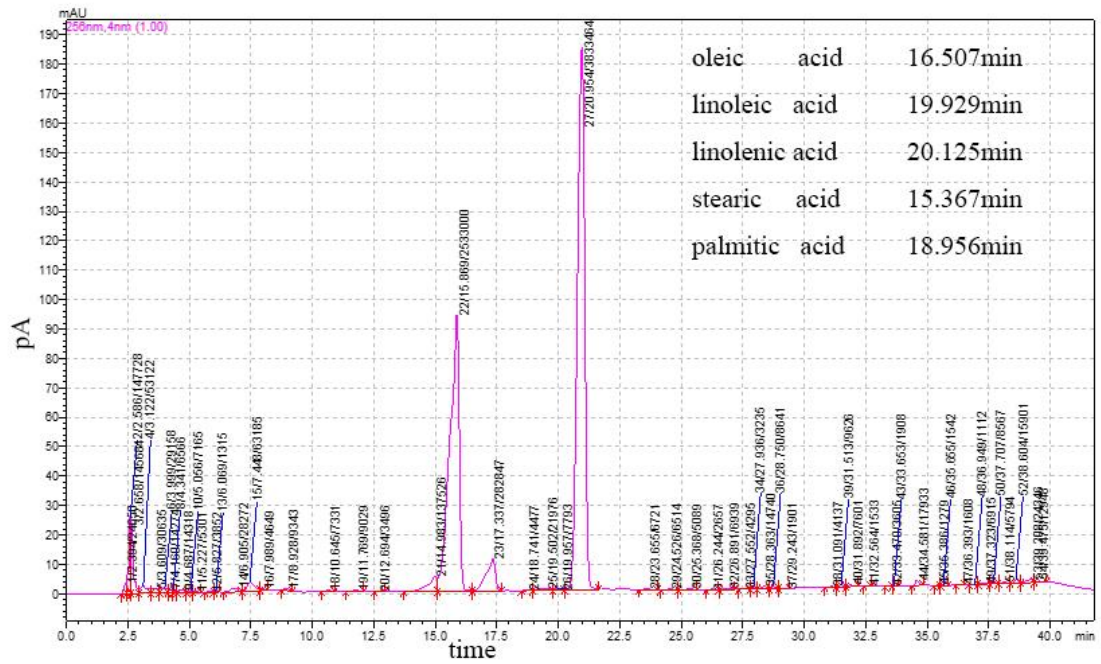
1. Chromatogram of standard mixture



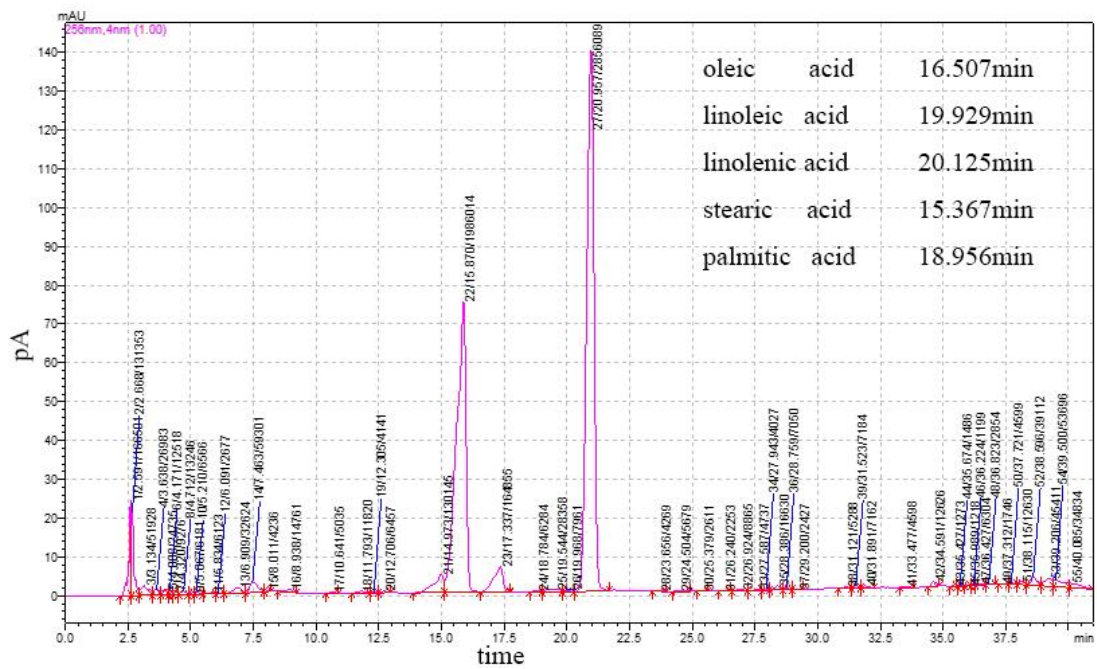
2. GC-FID chromatogram of seed oil from a GmFATB overexpression of WT



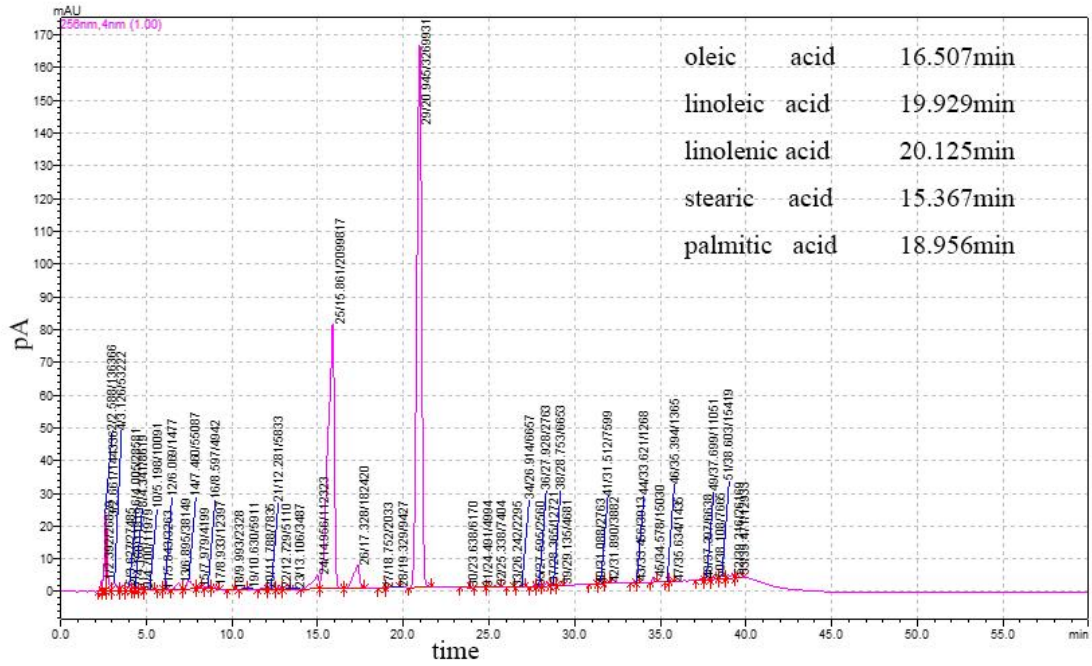
3. GC-FID chromatogram of seed oil from a GmFATB overexpression of Fatb-ko



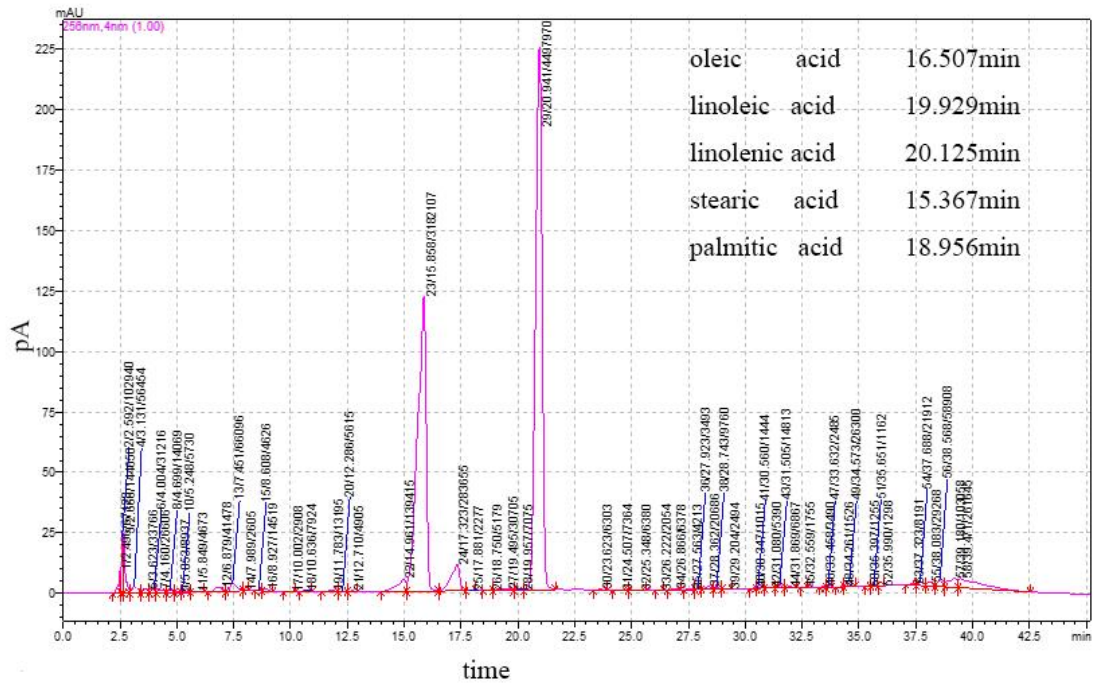
4. GC-FID chromatogram of seed oil from a GmFATB overexpression of OE-Fat1A line-9



5. GC-FID chromatogram of seed oil from a GmFATB overexpression of OE-Fat1B line-2



6. GC-FID chromatogram of seed oil from a GmFATB overexpression of OE-Fat2A line-5



7. GC-FID chromatogram of seed oil from a GmFATB overexpression of OE-Fat2B line-11

