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Supplementary Material

Role of *Glycine max* *ABSCISIC ACID INSENSITIVE 3* (*GmABI3*) in lipid biosynthesis and stress tolerance in soybean

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MKSLHVAANAGDLAEDCGILGGDADDTVLMDGIDEVGREIWLDHGGDNNHVHGHQDDDLIV
HHDPSIFYGDLPTLPDFPCMSSSSSSSTSPAPVNAIVSSASSSSAASSSTSSAASWAILRSDGEDPTPN
QNQYASGNCDDSSGALQSTASMEIPLDSSQGFGCGEGGGDCIDMMETFGYMDLLDSNEFFDTSAI
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NKETVSAEDLRKVKIKKATIESAARRLGGGKEAMKQLLKLILEWVQTNHLQRRRTTTTTNLSYQQS
FQQDPFQNPNNNNLIPPSDQTCFSPSTWVPPPQQQAFVSDPGFGYMPAPNYPPQPEFLPLE
SPPSWPPPQSGMPHQQFMPPTSQYNQFGDPTGFNGYNMNPYQYPYVPAGQMRDQRLRL
CSSATKEARKKRMARQRRFLSHHRHNNNNNNNNNNQNNQNTQIGETCAAVAPQLNPVATTATG
GTWMYWPNVPAVPPQLPPVMETQLPTMDRAGSASAMPRQQVVPDRRQGWKPEKNLRFLLQK
VLKQSDVGNLGRIVLPKKEAETHLPELEARDGISLAMEDIGTSRVWNMRYRFWPNNKSRMYLLEN
TGDFVKTNGLQEGDFIVIYSDVKCGKYLIRGVKVRQPSGQKPEAPPSSAATKRQNKSRNINNNSPS
ANVVVASPTSQTVK

Fig. S1. Protein sequence of AtABI3. *Arabidopsis* ABI3 sequence form TAIR is used as template to search GmABI3 in phytozome database (www.phytozome.net).

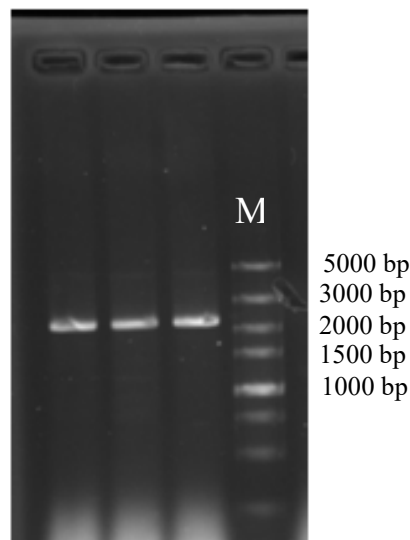


Fig. S2. PCR amplification of *GmABI3*.

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TTTGGCGTTGCTGAGAGAGAGATGTGGCTGAACAGTGACCAAGACGAGTTCCTAGGTGTCATGATGCCTCCATGTTCTACGCTGATTTCCCTCCTC
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TTCCTCTTCTTCTTGGGCCATGTTGAAGTCAGATGCTGAGGAAGATGCAGAGAAAAACATTGCAACCGATACATGCATGACCAACTTGATGCAAC
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TGAGTTCTCAAACCTTTGCAACAGATCAGGCTCCTCTCATGGTGCCTCCACAGCAATTTCCACAACCCATGGTTGGTATGTGGGTGACCCCTACACTAG
TGGTGTGCTTCAAATAACATATCAGCCACTATAACCATAACAACAGCAACCCTTATCAACCTGTGTCAGAACAAATACCACATGTTGGAGTCAGCACAT
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AGAAAACCCAGCATGGGACAGGGACTAATGCATCAAGTACAGCTGGTACTGCTGTAATAATGGCACGTCATCGTACCAGAAAACCAATCTGAAAA
AGTAGTAAATTAATATA

Fig. S3. Gene sequence of cloned *GmABI3*.

GmABI3 Glyma.08G357600.1	ATGGAGTGTGAAGTTGAATTACAAGGGGGAGATCTGCATGCAGGGGAGGTAAGTACCCAAACCCATTGGTTTTGGCAAATGGAAAACGAACACAC ATGGAGTGTGAAGTTGAATTACAAGGGGGAGATCTGCATGCAGGGGAGGTAAGTACCCAAACCCATTGGTTTTGGCAAATGGAAAACGAACACAC *****
GmABI3 Glyma.08G357600.1	AACCCCTATTGGTTTTTGGCAA-ATGGAAAACGAACACACTTTGGCGGTTGCTGAGAGAGAG AACCCCTATTGGTTTTTGGCAACATGGAAGATGAACACACTTTGGCGGTTGCTGAGAGAGAG ***** * *****
GmABI3 Glyma.08G357600.1	ATGTGGCTGAACAGTGACCAAGACGAGTTCCTAGGTGTCATGATGCCTCCATGTTCTAC ATGTGGCTGAACAGTGACCAAGACGAGTTCCTAGGTGTCATGATGCCTCCATGTTCTAC *****
GmABI3 Glyma.08G357600.1	GCTGATTTCCCTCCTCTCCCTGATTTCCCTTGATGTCATCATCATCTTCATCTTCA GCTGATTTCCCTCCTCTCCCTGATTTCCCTTGATGTCATCATCATCTTCATCTTCA *****
GmABI3 Glyma.08G357600.1	GCAACACCCTTCCCGTGAAGACCATGACATGTTCCACCACCACCACCCTTCCCTCTTCT GCAACACCCTTCCCGTGAAGACCATGACATGTTCCACCACCACCACCCTTCCCTCTTCT *****
GmABI3 Glyma.08G357600.1	TCCTCTTCCCTCTTCTTGGGCCATGTTGAAGTCAGATGCTGAGGAAGATGCAGAGAAAAAC TCCTCTTCCCTCTTCTTGGGCCATGTTGAAGTCAGATGCTGAGGAAGATGCAGAGAAAAAC *****
GmABI3 Glyma.08G357600.1	CATTGCAACCGATACATGCATGACCAACTTGATGCAACTTTGTCTTCCACCCTTCCATG CATTGCAACCGATACATGCATGACCAACTTGATGCAACTTTGTCTTCCACCCTTCCATG *****
GmABI3 Glyma.08G357600.1	GAGATTTCTCAACAGCAAAACCCCTGATCCTG-CCTTGGTGGCACTGTTGGAGAGTGCATG GAGATTTCTCAACAGCAAAACCCCTGATCCTGGCCTTGGTGGCACTGTTGGAGAGTGCATG *****

GmABI3
Glyma.08G357600.1
GATGATGTTATGGACACTTTTGGTTACATGGAGCTTTTGGAGGCCAATGATTTCTTTGAC
GATGATGTTATGGACACTTTTGGTTACATGGAGCTTTTGGAGGCCAATGATTTCTTTGAC

GmABI3
Glyma.08G357600.1
CCTGCCTCTATCTTTCAGAACGAGGGTAACGAAAACCTTTAGAGGAGTTTGGCACACTG
CCTGCCTCTATCTTTCAGAACGAGGGTAACGAAAACCTTTAGAGGAGTTTGGCACACTG

GmABI3
Glyma.08G357600.1
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GAGGAGCATGTGCCGTTTCATGAAGAGCAACATGCAATGGTGCATCATCAGCAAGGGCAA

GmABI3
Glyma.08G357600.1
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GCAGAAGAGGAAGATCATCAGGTTCCCTTTTTGTGAAGAGATCCAAGGAGGTGAAGAAGGT

GmABI3
Glyma.08G357600.1
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GmABI3
Glyma.08G357600.1
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GmABI3
Glyma.08G357600.1
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GAAAGCGCGCGAGGCGGCTAGGGGGAGGAAAAGAAGCCATGAAGCAGTTGCTGAAGCTG

GmABI3
Glyma.08G357600.1
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ATTCTTGAGTGGGTTCAAACCAGCCATCTTCAATAAGCGCCGAAAGGAGAATAATGGT

GmABI3
Glyma.08G357600.1
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AGTAGTATTAGCAGTGTACTTCAGGCACAGTTTCAGGATCCTAGTGGCCAGAACAACAAC

GmABI3
Glyma.08G357600.1
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CAGAATACACAAAGTGGTTCATTTGCACCTGAATCAAACACTTGTTTCAACAACCAAACA

GmABI3
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GmABI3
Glyma.08G357600.1
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GmABI3
Glyma.08G357600.1
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GmABI3
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GmABI3
Glyma.08G357600.1
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AACTATAGTCAGTCTTTTGGGACAATAATGGTCTTAACCCACATGGGGTTTCGGTGGT

GmABI3
Glyma.08G357600.1
GGAGGCTATGGCAATAACCAGTACCCTTATCAGTTTTTTTCA-GGCCCTGG-GATAGGT-G
GGAGGCTATGGCAATAACCAGTACCCTTATCAGTTTTTTTCAATGGCCCTGGTATAGGTTG

```

GmABI3          ATGAGGT-GGGGCCCTCCGCGACGAAGGAAGCGAGGAAGAAGAGAATGGCAAGGCAAAGA
Glyma.08G357600.1 ATGAGGTTGGGGCCCTCCGCGACGAAGGAAGCGAGGAAGAAGAGAATGGCAAGGCAAAGA
*****

GmABI3          AGGTTTCTGTCTCATCACAGGCATCATAGTGGTAATCACCAGAATCAAGGGTCTGACCCT
Glyma.08G357600.1 AGGTTTCTGTCTCATCACAGGCATCATAGTGGTAATCACCAGAATCAAGGGTCTGACCCT
*****

GmABI3          CATGCAAGAATGGGGGGTGATAATTGCAACACTGCTTTGGCTGCACCTCATCACGCAAAT
Glyma.08G357600.1 CATGCAAGAATGGGGGGTGATAATTGCAACACTGCTTTGGCTGCACCTCATCACGCAAAT
*****

GmABI3          CCTTCAGCCAATTGGATGTACTGGCAGGCTATGATTGGCGGCGCGGCAGGTCCTTTGGCT
Glyma.08G357600.1 CCTTCAGCCAATTGGATGTACTGGCAGGCTATGATTGGCGGCGCGGCAGGTCCTTTGGCT
*****

GmABI3          CCGGTGATTCCGGCCGAGCCGCCGGTGGTGCAACCGGTCGTGGGCCGGTCCGCCATGGAG
Glyma.08G357600.1 CCGGTGATTCCGGCCGAGCCGCCGGTGGTACACCGGTCGTGGACCGGTCGGCCATGCAG
*****

GmABI3          ACACAGAATTGTCATCAGAATCGAGTTGCATTAGATAGGGGACAGGGTTGGAAGCCTGAG
Glyma.08G357600.1 ACACAGAATTGTCATCAGAATCGAGTTGCATTAGATAGGGGACAGGGTTGGAAGCCTGAG
*****

GmABI3          AAGAACTTGAGGTTCCCTTCTGCAGAAGGTGTTGAAACAAAGCGATGTTGGAAGTTGGGG
Glyma.08G357600.1 AAGAACTTGAGGTTCCCTTCTGCAGAAGGTGTTGAAACAAAGCGATGTTGGAAGTTGGGG
*****

GmABI3          AGAATAGTTTTGCCAAAAAAGAGGCAGAAACCCATTTGCCAGAGCTGGAGGCAAGAGAT
Glyma.08G357600.1 AGAATAGTTTTGCCAAAAAAGAGGCAGAAACCCATTTGCCAGAGCTGGAGGCAAGAGAT
*****

GmABI3          GGAATTTCAATAACAATGGAAGACATTGGAACTTCACGTGTTTGAACATGCGCTATAGA
Glyma.08G357600.1 GGAATTTCCATAACAATGGAAGACATTGGAACTTCACGTGTTTGAACATGCGCTATAGA
*****

GmABI3          TACTGGCCGAACAACAAAAGCAGAATGTATTTGCTCGAGAACACTGGTGACTTTGTGAGA
Glyma.08G357600.1 TACTGGCCGAACAACAAAAGCAGAATGTATTTGCTCGAGAACACTGGTGACTTTGTGAGA
*****

GmABI3          GCCAATGGACTCTAAGAAGGAGATTTTCATAGTGATATACTCAGATGTGAAGTGTGGCAA
Glyma.08G357600.1 GCCAATGGACTCCAAGAGGGAGATTTTCATAGTGATATACTCAGATGTGAAGTGTGGCAA
*****

GmABI3          TATATGATGAGAGGAGTGAAAGTGAGGCAACAAGGTGTGAAACCAGAGACCAAGAAAGCA
Glyma.08G357600.1 TATATGATAAGAGGAGTGAAAGTGAGGCAACAAGGTGTGAAACCAGAGACCAAGAAAGCA
*****

GmABI3          GGAAAATCGCAGAAAAACCAGCATGGGACAGGGACTAATGCATCAAGTACAGCTGGTACT
Glyma.08G357600.1 GGAAAATCGCAGAAAAACCAGCATGGGACAGGGACTAATGCATCAAGTACAGCTGGTACT
*****

GmABI3          GCTGCTAATAATGGCACGTTCATCGTCACCGAAAACCAATCTGAAAAAAGTAGTAAATTA
Glyma.08G357600.1 GCTGCTAATAATGGCACGTTCATCGTCACCGAAAACCAATCTGAAAAAAGTAGTAAATTA
*****

GmABI3          ATATAA
Glyma.08G357600.1 ATATAA
*****



```

Fig. S4. Sequence alignment of cloned *GmABI3* and *Glyma.08G357600.1*.

Glyma.08G357600 Nine Tissue Gene-level Expression ✕

FPKM Coefficient of variance: 2.831

(across samples below)

pod	: 6.848	
root_hairs	: 0.061	
leaves	: 0.013	
root	: 0.067	
nodules	: 0.000	
seed	: 131.349	
sam	: 0.000	
stem	: 0.000	
flower	: 0.084	

Glyma.18G176100 Gene-level FPKM values

Coefficient of variance: 2.81526306947976

(across samples below)



Pod	: 4.187	
Root Hairs	: 0.125	
Leaves	: 0.000	
Root	: 0.212	
Nodules	: 0.018	
Seed	: 80.075	
Sam	: 0.047	
Stem	: 0.000	
Flower	: 0.145	

Fig. S5. Expression of *GmABI3*. The expression of *GmABI3* in different tissues of soybean plant according to phytozome database.

Table S1. List of primers used in this study

Gene name	Primer sequence
ABI3 F	5'-ATGGAGTGTGAAGTTGAATTAC-3'
ABI3R	5'-CCGCGGTTATATTAATTTACTACTT-3'
pDON-ABI3 F	5'-ggggacaagttgtacaaaaagcaggcttc ATGGAGTGTGAAGTTGAATTAC-3'
pDON-ABI3 R	5'-ggggaccactttgtacaagaaagct GGGTATTATATTAATTTACTACTT-3'
GmABI3-qRT F	5'-GGGGGGTGGTGATAATTGCACC-3'
GmABI3-qRT R	5'-AAGGCAGACCGGTCCACAGCTG-3'
GmActin-qRTF	5'-CTTCCCTCAGCACCTTCCAA-3'
GmActin-qRTR	5'-GGTCCAGCTTTCACACTCCAT-3'
18s univ F	5'-CTATCAACTTTCGATGGTAGG-3'
18s univ R	5'-CCGTGTCAGG ATTGGGTAATTT-3'

Table S2. GC analysis of fatty acid composition and TAG content of representative control and transgenic lines

Wildtype (Col-0)

col-1				
C16:0	3.729926	256.0265	0.353948	11.72012
C17:0	4.190384	144.6691		
C18:0	4.691985	89.93452	0.124331	4.116932
C18:1	4.857539	350.7519	0.484902	16.05636
C18:2	5.15564	909.9279	1.257944	41.65376
C18:3	5.53924	551.1545	0.761952	25.23019
C20:1	6.065645	509.4117	0.704244	23.31933
Total			0.005098	122.0967

col-2				
C16:0	3.730928	268.3187	0.356992	11.6664
C17:0	4.191438	150.322		
C18:0	4.694817	95.27427	0.12676	4.142491
C18:1	4.858122	369.9016	0.492146	16.08319
C18:2	5.155443	962.9914	1.281238	41.87052
C18:3	5.538991	584.3076	0.777408	25.40548
C20:1	6.067271	549.1747	0.730664	23.87792
Total			0.00501	123.046

Overexpressed Line-1

ABI3-OE1-1				
C16:0	3.730939	356.4675	0.488314	15.85435
C17:0 (internal)	4.190689	145.9993		
C18:0	4.694743	113.1791	0.155041	5.033785
C18:1	4.857838	499.5392	0.684304	22.21765
C18:2	5.15952	1284.214	1.759206	57.11709
C18:3	5.540662	828.0688	1.134346	36.82943
C20:1	6.07127	851.588	1.166565	37.87548
Total			5.387776	174.9278

ABI3-OE1-2				
C16:0	3.729203	355.1688	0.51933	17.08322
C17:0 (internal)	4.189781	136.7797		

C18:0	4.692978	111.7449	0.163394	5.374801
C18:1	4.859547	488.9516	0.714948	23.51802
C18:2	5.158347	1283.767	1.877132	61.74775
C18:3	5.540314	821.0491	1.200543	39.49153
C20:1	6.071881	815.5323	1.192476	39.22618
Total			0.008288	186.4415

Overexpressed Line-2

ABI3-OE2-1				
C16:0	3.730248	359.0098	0.511418	17.45454
C17:0 (internal)	4.189869	140.3978		
C18:0	4.692319	131.8752	0.187859	6.411581
C18:1	4.861873	720.4401	1.026284	35.02675
C18:2	5.159677	1314.424	1.872428	63.90541
C18:3	5.541126	779.7766	1.11081	37.9116
C20:1	6.072602	859.8202	1.224834	41.80321
Total			0.008453	202.5131

ABI3-OE2-2				
C16:0	3.729489	344.7368	0.489207	16.09232
C17:0 (internal)	4.191567	140.9371		
C18:0	4.695023	124.8942	0.177234	5.830062
C18:1	4.86055	681.4619	0.967044	31.81066
C18:2	5.159592	1253.06	1.778182	58.49284
C18:3	5.541005	739.5233	1.049437	34.52096
C20:1	6.07237	810.8545	1.150661	37.8507
Total			0.007964	184.5975

Overexpressed Line-3

ABI3-OE3-1				
C16:0	3.729423	351.1942	0.483641	16.0146
C17:0 (internal)	4.188519	145.2293		
C18:0	4.693868	123.7845	0.170468	5.644623
C18:1	4.860641	564.875	0.777908	25.75853
C18:2	5.158916	1212.91	1.670338	55.30919
C18:3	5.540014	680.3681	0.936957	31.02507
C20:1	6.069331	794.8569	1.094623	36.2458
Total			0.00707	169.9978

ABI3-OE3-1				
C16:0	3.729423	351.1942	0.483641	16.0146
C17:0 (internal)	4.188519	145.2293		
C18:0	4.693868	123.7845	0.170468	5.644623
C18:1	4.860641	564.875	0.777908	25.75853
C18:2	5.158916	1212.91	1.670338	55.30919
C18:3	5.540014	680.3681	0.936957	31.02507
C20:1	6.069331	794.8569	1.094623	36.2458
Total			0.00707	169.9978

Overexpressed Line-4

ABI3-OE4-1				
C16:0	3.729978	354.9616	0.51254	16.80457
C17:0 (internal)	4.189946	138.5109		
C18:0	4.692486	133.7504	0.193126	6.332004
C18:1	4.861097	667.9615	0.964489	31.6226
C18:2	5.158675	1298.338	1.874708	61.46583
C18:3	5.541719	759.0956	1.096081	35.93707
C20:1	6.070668	835.1408	1.205885	39.5372
Total			0.008442	191.6993

ABI3-OE4-2				
C16:0	3.730402	333.6177	0.464837	15.44308
C17:0 (internal)	4.189912	143.5419		
C18:0	4.694196	119.4497	0.166432	5.529297
C18:1	4.86154	609.1751	0.848777	28.19856
C18:2	5.160505	1190.525	1.658784	55.10911
C18:3	5.54167	690.3605	0.961894	31.95661
C20:1	6.071069	744.4763	1.037295	34.46162
Total			0.007159	170.6983

Overexpressed Line-5

ABI3-OE5-1				
C16:0	3.729633	361.9738	0.505339	15.9413
C17:0 (internal)	4.188658	143.2597		
C18:0	4.692126	125.1754	0.174753	5.512717
C18:1	4.860711	606.2527	0.846369	26.69933
C18:2	5.159414	1296.345	1.809783	57.09096
C18:3	5.540834	728.9492	1.017661	32.10288
C20:1	6.070663	834.2244	1.164632	36.73919
Total			0.007704	174.0864

ABI3-OE5-2				
C16:0	3.731128	405.5934	0.547276	18.24253
C17:0 (internal)	4.189716	148.2227		
C18:0	4.694137	148.8259	0.200814	6.693799
C18:1	4.861565	720.5735	0.972285	32.40951
C18:2	5.162516	1513.8	2.042603	68.08676
C18:3	5.542351	850.555	1.147672	38.25573
C20:1	6.071166	976.2495	1.317274	43.90914
Total			0.008403	207.5975

Complementary line-1

GmABI3/atabi3-1-1					
C16:0	3.256	10.7	0.008483	0.279049	0.340277
C17:0 (internal)	3.459	378.4			
C18:0	3.9	117.6	0.093235	3.06693	3.739863
C18:1	4.551	434.8	0.344715	11.3393	13.82732
C18:2	4.811	1134.3	0.899286	29.58179	36.07251
C18:3	5.151	807.4	0.640116	21.05646	25.67658
C20:1	5.693	639.7	0.507162	16.68295	20.34346
Total			2.492997	82.00647	

GmABI3/atabi3-1-2					
C16:0	3.255	9.9	0.008581	0.285094	0.353989
C17:0 (internal)	3.463	346.1			
C18:0	3.917	109.4	0.094828	3.150435	3.911753
C18:1	4.543	419.1	0.363277	12.06899	14.98552
C18:2	4.816	1023.7	0.887345	29.47989	36.60385
C18:3	5.148	635.2	0.550592	18.2921	22.71248
C20:1	5.68	599.4	0.519561	17.26116	21.4324
Total			2.424184	80.53767	

Complementary line-2

GmABI3/atabi3-2-1					
C16:0	3.253	10.8	0.008938	0.312515	0.329409
C17:0 (internal)	3.457	362.5			
C18:0	3.907	96.7	0.080028	2.798167	2.94943
C18:1	4.53	562	0.465103	16.26236	17.14146
C18:2	4.816	1167.2	0.965959	33.77478	35.60056
C18:3	5.15	774	0.640552	22.39691	23.60764
C20:1	5.735	667.9	0.552745	19.32674	20.3715
Total			2.713324	94.87147	

GmABI3/atabi3-2-2					
C16:0	3.255	12	0.009293	0.320439	0.343299
C17:0 (internal)	3.465	387.4			
C18:0	3.904	92.2	0.071399	2.462037	2.637677
C18:1	4.541	658.7	0.510093	17.58941	18.84423
C18:2	4.816	1270.9	0.984177	33.93712	36.35817
C18:3	5.145	788.9	0.610919	21.06617	22.56902
C20:1	5.695	672.8	0.521012	17.96593	19.2476
Total			2.706892	93.34111	

Complementary line-3

GmABI3/atabi3-3-1					
C16:0	3.265	58.2	0.022835	0.722641	3.265
C17:0 (internal)	3.475	764.6			3.475
C18:0	3.912	246.5	0.096717	3.060672	3.912
C18:1	4.568	841.8	0.33029	10.45223	4.568
C18:2	4.825	2270.5	0.890858	28.19171	4.825
C18:3	5.164	1023.1	0.401426	12.70334	5.164
C20:1	5.711	990.2	0.388517	12.29484	5.711
Total			2.130643	67.42543	

GmABI3/atabi3-3-2					
C16:0	3.252	14.9	0.022542	0.805057	0.888385
C17:0 (internal)	3.458	198.3			
C18:0	3.897	89.6	0.135552	4.84115	5.342237
C18:1	4.532	386.9	0.585325	20.90447	23.06821
C18:2	4.804	670.5	1.014372	36.22758	39.97734
C18:3	5.14	293.6	0.444175	15.86341	17.50537
C20:1	5.691	221.7	0.335401	11.9786	13.21846
Total			2.537368	90.62027	

Mutant

Atabi3 Mutant					
C16:0	3.252	13.1	0.017552	0.626874	0.729439
C17:0 (internal)	3.456	223.9			
C18:0	3.902	94.2	0.126217	4.507752	5.245281
C18:1	4.545	270.1	0.361903	12.92509	15.03981
C18:2	4.807	654.6	0.877088	31.32457	36.44969
C18:3	5.134	405.1	0.542787	19.38525	22.55694
C20:1	5.699	358.8	0.48075	17.16965	19.97884
Total			2.406297	85.93919	

Atabi3 Mutant					
C16:0	3.252	13.1	0.017552	0.626874	0.729439
C17:0 (internal)	3.456	223.9			
C18:0	3.902	94.2	0.126217	4.507752	5.245281

C18:1	4.545	270.1	0.361903	12.92509	15.03981
C18:2	4.807	654.6	0.877088	31.32457	36.44969
C18:3	5.134	405.1	0.542787	19.38525	22.55694
C20:1	5.699	358.8	0.48075	17.16965	19.97884
Total			2.406297	85.93919	

Wildtype (Ler-0)

Ler-0-1					
C16:0	3.254	8.9	0.007789	0.268579	0.318688
C17:0 (internal)	3.456	286			
C18:0	3.903	108.5	0.113811	3.768582	3.578024
C18:1	4.537	484.7	0.508427	16.83532	15.98404
C18:2	4.805	937.6	0.983497	32.56611	30.9194
C18:3	5.147	771.3	0.809056	26.78993	25.4353
C20:1	5.693	730.3	0.766049	25.36586	24.08323
Total			3.180839	105.3258	

Ler-0-2					
C16:0	3.254	9.5	0.007602	0.249247	0.308662
C17:0 (internal)	3.46	285.8			
C18:0	3.901	106.6	0.111896	3.717489	3.388753
C18:1	4.542	530.4	0.556753	18.49678	16.86111
C18:2	4.817	984.3	1.033205	34.32575	31.29033
C18:3	5.144	733	0.769419	25.5621	23.30165
C20:1	5.685	791.4	0.830721	27.5987	25.15815
Total			3.301994	109.7008	