

The *Acer truncatum* genome provides insights into the nervonic acid biosynthesis

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Table S1. K-mer statistics of *A. truncatum*.

K-mer	K-mer number	K-mer Depth	Genome Size (Mbp)	Revised Genome Size (Mbp)	Heterozygous Ratio (%)	Repeat (%)
17	50,317,377,088	76	662.08	653.44	1.12	61.70

Table S2. Sequencing data of *A. truncatum*.

Paired-end libraries	Insert size	Total data (G)	Sequence coverage (X)*
Illumina reads	350 bp	117.93	180.48
PacBio long reads	20kb	75.7	115.85
10X Genomics	-	81.54	124.79
Hi-C reads	-	72.21	110.51
Total	-	347.38	531.63

* 653.44M genome size estimated by survey.

Table S3. Summary of *A. truncatum* pseudomolecules.

Chromosome	Length(bp)	Gene number	Gap base (N)
chr1	70,314,080	2,754	463,938
chr2	67,888,635	2,427	647,076
chr3	67,579,682	2,985	442,334
chr4	49,301,835	2,029	375,130
chr5	48,765,855	2,619	250,582
chr6	46,359,076	2,521	369,439
chr7	43,170,434	1,920	268,073
chr8	41,982,645	1,871	160,723
chr9	40,653,649	1,864	248,943
chr10	40,269,369	1,570	423,772
chr11	39,201,709	1,954	280,111
chr12	37,356,478	1,851	263,834
chr13	36,914,844	1,925	244,204
Total	629,758,291 (99.44%)	28,290 (99.48%)	4,448,159

The rest of scaffolds unanchored to chromosome are not listed.

Table S4. The Hi-c assemble results of *A.truncatum*.

	length		number	
	Contig** (bp)	Scaffold (bp)	Contig**	Scaffold
Total	628,843,326	633,281,485	1,453	34
Max	4,570,384	70,314,080	—	—
Number > = 2000	—	—	1,453	34
N50	773,169	46,359,076	239	6
N60	605,964	43,170,434	330	7
N70	455,890	40,653,649	450	9
N80	321,326	40,269,369	614	10
N90	196,874	37,356,478	859	12

**Contig after scaffolding

Table S5. Coverage statistics of the *A. truncatum* genome.

-	Percentage
Mapping rate (%)	97.24
Coverage (%)	99.47
Coverage at least 4X (%)	99.34
Coverage at least 10X (%)	99.25
Coverage at least 20X (%)	99.11

Average sequence depth: The average depth of each base in the genome that is covered by the reads. Coverage: The proportion of the genome covered by the reads.

Table S6. CEGMA evaluation results.

Complete		Complete + partial	
# Prots	% Completeness	# Prots	% Completeness
232	93.55	239	96.37

Complete: core genes that were completely assembled with identity greater than 0.7.

Partial: core genes that were assembled but not complete.

Prots: the number of core genes.

% Completeness: percentage of assembled core genes to core genes.

Table S7. BUSCO notation assessment of *A. truncatum* genome and annotation.

BUSCO	Genome		Proteins	
	Count	Ratio(%)	Count	Ratio(%)
Complete BUSCOs	1342	93.2	1395	96.9
Complete BUSCOs	sigle-copy 1275	88.5	1240	86.1
Complete BUSCOs	duplicated 68	4.7	155	10.8
Fragmented BUSCOs	18	1.3	30	2.1
Missing BUSCOs	79	5.5	15	1
Total BUSCO serached	group 1440		1440	

Table S8. Assessing the gene region assembly by mapping RNA assembly to *A. truncatum* genome.

Dataset	Number	Total (bp)	Sequences with >90% sequence in with >50% sequence in				
			length covered by one scaffold assembly (%)	Number	Percent	Number	Percent
>500bp	106,055	178,432,686	95.97	94,327	88.94	100,924	95.16
>1000bp	67,579	151,355,839	99.40	62,942	93.14	66,919	99.02
>2000bp	31,334	98,869,172	99.77	29,229	93.28	31,133	99.36
>5000bp	2,133	13,361,783	99.86	1,911	89.59	2,107	98.78

Table S9. Statistical results of gene functional annotations.

	Number	Percent (%)
Total	28,438	-
Swiss-Prot	21,289	74.86
NR	27,202	95.65
KEGG	21,276	74.81
IterPro	27,826	97.84
GO	25,432	89.43
Pfam	21,579	75.87
Annotated	28,023	98.54
Un-annotated	415	0.01

Table S10. Statistical results of non-coding RNAs.

Type	Copy	Average length (bp)	Total length (bp)	(%) of genome	
miRNA	1,345	132.48	178,186	0.028137	
tRNA	744	75.11	55,883	0.008824	
rRNA	rRNA	368	169.31	62,307	0.009839
	18S	54	497.61	26,871	0.004243
	28S	42	125.14	5,256	0.00083
	5.8S	15	123.46	1,852	0.000292
	5S	257	110.23	28,328	0.004473
snRNA	snRNA	868	113	98,086	0.015489
	CD-box	655	102.54	67,164	0.010606
	HACA-box	51	139/82	7,131	0.001126
	Splicing	160	147.04	23,526	0.003715

Table S11. Classification of repetitive elements in the *A. truncatum* genome.

Type	Length (bp)	Percentage of genome (%)
DNA	48,529,125	7.66
LINE	33,244,458	5.24
SINE	281,678	0.04
LTR	287,494,231	45.4
LTR/Copia	163,812,683	25.87
LTR/Gypsy	99,823,924	15.76
Tandem repeats	29,043,401	4.59
Satellite	1,088,584	0.17
Simple repeats	4,660,170	0.74
Unknown	20,698,204	3.27
Total	391,045,082	61.75

The total length of all repetitive elements is the result of removing redundancy

Table S12. The LTR subfamilies in *A. truncatum* and other published genomes.

superfamily	family	number in <i>A. truncatum</i>	number <i>A.yangbiense</i>	in number <i>C. sinensis</i>	in number <i>M. oleifera</i>
Ty3/Gypsy	reina	260	210	161	57
Ty3/Gypsy	tat	1,789	1,831	271	1,162
Ty3/Gypsy	athila	1,094	676	751	2,045
Ty3/Gypsy	crm	506	463	118	544
Ty3/Gypsy	galadriel	36	23	48	928
Ty3/Gypsy	del	13	10	62	10,005
Ty1/Copia	sire	1,727	6,624	321	8,373
Ty1/Copia	tork	2,200	1,772	668	2,379
Ty1/Copia	retrofit	1,269	924	425	1,838
Ty1/Copia	oryco	262	212	103	498
Caulimoviridae	caulimovirus	43	96	181	94
Caulimoviridae	badnavirus	8	11	27	8
Caulimoviridae	soymovirus	2	1	6	1
Caulimoviridae	cavemovirus	0	2	5	8
Unclassified		835	661	47	125
Total		10,044	13,516	3,194	28,065

Table S13. The seed sequences of **putative centromeric regions of *A. truncatum* and *A. yangbiense* chromosomes.**

Species	Monomer sequence	Length	GC(%)
<i>A. truncatum</i>	GAAGTAAGGAACCAGGTACCCCGATGAGGCATCCCGATCTTA CTGTAAGTCTGTCCTGGTAGGCAACTAAGGCCACTTTAGCACC AGGCTTCTTGAGGAGGGTATTCCCCGACCAAGGCAGCAGGA GCGCCATAAGGCTATTTCCCTGGTCTTGAAATGGC	161	53
<i>A. yangbiense</i>	CTTTTTGGAATGCAAACCTTCTTTTTGGCATGCGGGCATGCTTT TTTGAATGCGAGAGTGGTTTTTAGCTCTCGAGCGTGCTTTTTA GTTTCCAAACGTTCTTTTTGGCTTTCGGGCGTTCTTTTTTGCAA GCAAACCTTCTTTTTGGCTTTTGGGCGTT	160	41.25

Table S14. Details of the chloroplast genome sequences used for the phylogenetic analysis.

No.	Taxon	Family	Order	GenBank Accession number
1	<i>Acer yangbiense</i>	Aceraceae	Sapindales	MK479229
2	<i>Acer wilsonii</i>	Aceraceae	Sapindales	NC_040988
3	<i>Acer triflorum</i>	Aceraceae	Sapindales	NC_047296
4	<i>Acer takesimense</i>	Aceraceae	Sapindales	NC_046488
5	<i>Acer sino-oblongum</i>	Aceraceae	Sapindales	NC_040106
6	<i>Acer pseudosieboldianum</i>	Aceraceae	Sapindales	NC_046487
7	<i>Acer laevigatum</i>	Aceraceae	Sapindales	NC_042443
8	<i>Acer fenzelianum</i>	Aceraceae	Sapindales	NC_045527
9	<i>Acer catalpifolium</i>	Aceraceae	Sapindales	MK479218
10	<i>Dipteronia dyeriana</i>	Sapindaceae	Sapindales	NC_031899
11	<i>Dipteronia sinensis</i>	Sapindaceae	Sapindales	NC_029338
12	<i>Acer buergerianum</i>	Aceraceae	Sapindales	NC_034744
13	<i>Acer davidii</i>	Aceraceae	Sapindales	NC_030331
14	<i>Acer griseum</i>	Aceraceae	Sapindales	NC_034346
15	<i>Acer miaotaiense</i>	Aceraceae	Sapindales	NC_030343
16	<i>Acer morrisonense</i>	Aceraceae	Sapindales	KT970611
17	<i>Acer truncatum</i>	Aceraceae	Sapindales	MH638284
18	<i>Dimocarpus longan</i>	Sapindaceae	Sapindales	NC_037447

Table S15. Go enrichment results for expanded genes in *A. truncatum*.

GO_ID	GO_Term	GO_Class	Pvalue	AdjustedPv	Gene_Number
GO:0005515	protein binding	MF	0.001959647	0.040608303	299
	oxidoreductase activity, acting on				
GO:0016705	paired donors, with incorporation or	MF	0.001401486	0.032359948	61
	reduction of molecular oxygen				
GO:0043531	ADP binding	MF	3.38831E-66	6.10235E-63	56
GO:0016746	transferase activity, transferring acyl	MF	9.09257E-11	4.09393E-08	48
	groups				
GO:0030246	carbohydrate binding	MF	6.41451E-37	5.77627E-34	46
GO:0016747	transferase activity, transferring acyl	MF	1.80621E-14	1.08433E-11	42
	groups other than amino-acyl groups				
GO:0044283	small molecule biosynthetic process	BP	0.000187938	0.007051585	37
GO:0046394	carboxylic acid biosynthetic process	BP	3.0831E-05	0.001914714	36
GO:0046983	protein dimerization activity	MF	0.001604763	0.03628026	31
GO:0005618	cell wall	CC	2.47237E-07	4.94748E-05	22
GO:0006631	fatty acid metabolic process	BP	7.6302E-06	0.000654381	22
GO:0006633	fatty acid biosynthetic process	BP	9.51125E-07	0.000171298	21
GO:0005976	polysaccharide metabolic process	BP	0.001631705	0.03628026	21
GO:0044264	cellular polysaccharide metabolic	BP	0.000204111	0.00750212	20
	process				
GO:0006073	cellular glucan metabolic process	BP	4.57111E-05	0.002007944	19
GO:0004983	neuropeptide Y receptor activity	MF	0.00161711	0.03628026	14
GO:0016903	oxidoreductase activity, acting on	MF	3.44434E-06	0.000345239	13
	the aldehyde or oxo group of donors				
GO:0000160	phosphorelay signal transduction	BP	3.84716E-05	0.002007944	13
	system				
GO:0044703	multi-organism reproductive process	BP	0.000406762	0.011099665	12
GO:0016762	xyloglucan:xyloglucosyl transferase	MF	9.98602E-09	2.2481E-06	11
	activity				
GO:0048046	apoplast	CC	9.98602E-09	2.2481E-06	11
GO:0004176	ATP-dependent peptidase activity	MF	3.40201E-09	1.02117E-06	10
GO:0008408	3'-5' exonuclease activity	MF	8.64985E-06	0.000688866	9
GO:0010333	terpene synthase activity	MF	0.000173781	0.006659156	9
GO:0009067	aspartate family amino acid	BP	0.000173781	0.006659156	9
	biosynthetic process				
GO:0016570	histone modification	BP	0.000214961	0.007591075	9
GO:0048544	recognition of pollen	BP	0.000263928	0.00833919	9
GO:0043624	cellular protein complex	BP	0.001961645	0.040608303	9
	disassembly				
GO:0080019	fatty-acyl-CoA reductase	MF	7.13271E-10	2.5692E-07	8
	(alcohol-forming) activity				
GO:0030042	actin filament depolymerization	BP	2.21586E-06	0.000249422	8

GO:0003871	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity	MF	3.64216E-06	0.000345239	8
GO:0009086	methionine biosynthetic process	BP	5.77669E-06	0.000520191	8
GO:0009678	hydrogen-translocating pyrophosphatase activity	MF	1.94249E-06	0.000249422	7
GO:0004523	RNA-DNA hybrid ribonuclease activity	MF	1.94249E-06	0.000249422	7
GO:0003950	NAD ⁺ ADP-ribosyltransferase activity	MF	1.11834E-05	0.000805655	7
GO:0004427	inorganic diphosphatase activity	MF	4.25544E-05	0.002007944	7
GO:0030321	transepithelial chloride transport	BP	0.002199364	0.043053925	7
GO:0008113	peptide-methionine (S)-S-oxidoreductase activity	MF	2.01358E-06	0.000249422	6
GO:0031625	ubiquitin protein ligase binding	MF	3.39559E-05	0.001972728	6
GO:0031461	cullin-RING ubiquitin ligase complex	CC	0.000403295	0.011099665	6
GO:0016624	oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor	MF	0.000288205	0.008509136	5
GO:0005730	nucleolus	CC	0.001787014	0.03924893	5
GO:0003852	2-isopropylmalate synthase activity	MF	9.17978E-06	0.000688866	4
GO:0009098	leucine biosynthetic process	BP	4.38813E-05	0.002007944	4
GO:0031429	box H/ACA snoRNP complex	CC	4.38813E-05	0.002007944	4
GO:0006850	mitochondrial pyruvate transport	BP	0.000280832	0.008429636	4
GO:0004602	glutathione peroxidase activity	MF	0.000924636	0.023128731	4
GO:0000148	1,3-beta-D-glucan synthase complex	CC	0.002215603	0.043053925	4
GO:0006075	(1->3)-beta-D-glucan biosynthetic process	BP	0.002215603	0.043053925	4
GO:0008241	peptidyl-dipeptidase activity	MF	0.000166951	0.006659156	3

Table S16. Go enrichment results for contracted genes in *A. truncatum*.

GO_ID	GO_Term	GO_Class	Pvalue	Adjusted Pvalue	Gene_Number
GO:0005488	binding	MF	0.001224735	0.015433824	459
GO:0003824	catalytic activity	MF	0.000767117	0.012004113	375
GO:0043167	ion binding	MF	6.05711E-05	0.001627419	268
GO:0046872	metal ion binding	MF	0.000187665	0.004049007	141
GO:0055114	oxidation-reduction process	BP	1.52291E-10	2.16863E-08	129
GO:0016491	oxidoreductase activity	MF	4.52941E-08	3.22494E-06	128
GO:0046914	transition metal ion binding	MF	2.36744E-05	0.000749162	96
GO:0016705	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	MF	3.54928E-19	2.52709E-16	66
GO:0005506	iron ion binding	MF	5.1146E-14	1.45664E-11	59
GO:0020037	heme binding	MF	6.53946E-11	1.33031E-08	57
GO:0009055	electron carrier activity	MF	7.87919E-13	1.86999E-10	50
GO:0043531	ADP binding	MF	3.04669E-25	4.33848E-22	39
GO:0004497	monooxygenase activity	MF	2.34938E-05	0.000749162	29
GO:0016829	lyase activity	MF	9.46905E-11	1.49821E-08	28
GO:0016757	transferase activity, transferring glycosyl groups	MF	0.003123367	0.035021064	28
GO:0016758	transferase activity, transferring hexosyl groups	MF	9.03521E-05	0.002297524	26
GO:0016835	carbon-oxygen lyase activity	MF	1.66335E-09	2.15328E-07	21
GO:0010333	terpene synthase activity	MF	1.50937E-17	7.1645E-15	18
GO:0000287	magnesium ion binding	MF	6.72147E-06	0.000258686	17
GO:0005507	copper ion binding	MF	2.72163E-05	0.000824596	16
GO:0006457	protein folding	BP	0.000136332	0.003081532	16
GO:0003755	peptidyl-prolyl cis-trans isomerase activity	MF	1.87739E-08	1.59168E-06	15
GO:0016712	oxidoreductase activity, acting on paired donors	MF	4.067E-05	0.001206545	13
GO:0007156	homophilic cell adhesion	BP	0.001142326	0.014523858	13
GO:0051213	dioxygenase activity	MF	0.004505467	0.048975453	12
GO:0004650	polygalacturonase activity	MF	1.4332E-06	6.37775E-05	11
GO:0016706	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	MF	0.001304524	0.016186741	11
GO:0022414	reproductive process	BP	0.001458979	0.017606667	10
GO:0044703	multi-organism reproductive process	BP	0.001609227	0.019096158	8

GO:0008146	sulfotransferase activity	MF	3.38632E-09	4.01843E-07	7
GO:0048544	recognition of pollen	BP	0.000230028	0.004549442	7
GO:0008171	O-methyltransferase activity	MF	0.000724779	0.011467612	6
GO:0010181	FMN binding	MF	0.003544788	0.038829068	5
GO:0004144	diacylglycerol O-acyltransferase activity	MF	0.000109881	0.002565081	4
GO:0019064	fusion of virus membrane with host plasma membrane	BP	0.001022891	0.013241788	4
GO:0046789	host cell surface receptor binding	MF	0.001022891	0.013241788	4
GO:0003968	RNA-directed polymerase activity	RNA MF	0.00132995	0.016186741	4
GO:0004970	ionotropic glutamate receptor activity	MF	0.00132995	0.016186741	4
GO:0019031	viral envelope	CC	0.002126459	0.024820311	4
GO:0005234	extracellular-glutamate-gated ion channel activity	MF	0.003202222	0.035624716	4
GO:0004351	glutamate activity	decarboxylase MF	0.000997672	0.013241788	2

Table S17. GO enrichment results for the genes in *A. truncatum*-specific gene families.

GO_ID	GO_Term	GO_Class	Pvalue	AdjustedPv	Gene number
GO:0008194	UDP-glycosyltransferase activity	MF	0.000307838	0.034714635	9
GO:0035251	UDP-glycosyltransferase activity	MF	4.19407E-05	0.006148512	8
GO:0003843	1,3-beta-D-glucan synthase activity	MF	6.14017E-09	3.469E-06	7
GO:0051274	beta-glucan biosynthetic process	BP	7.27861E-05	0.009700403	7
GO:0000148	1,3-beta-D-glucan synthase complex	CC	9.46522E-09	3.469E-06	6
GO:0006075	(1->3)-beta-D-glucan biosynthetic process	BP	9.46522E-09	3.469E-06	6
GO:0005730	nucleolus	CC	2.32706E-07	6.82294E-05	6
GO:0004650	polygalacturonase activity	MF	0.000386561	0.037779935	6
GO:0031429	box H/ACA snoRNP complex	CC	3.91238E-07	8.19363E-05	4

Table S18. KEGG enrichment results for expanded genes in *A.truncatum*.

MapID	MapTitle	Pvalue	AdjustedPv	Gene_Number
map04626	Plant-pathogen interaction	7.01167E-05	0.000893988	58
map04014	Ras signaling pathway	1.29733E-27	2.64655E-25	56
map00940	Phenylpropanoid biosynthesis	5.46096E-10	2.22807E-08	43
map00941	Flavonoid biosynthesis	1.20338E-25	1.22744E-23	37
map00062	Fatty acid elongation	5.72091E-14	3.89022E-12	23
map00910	Nitrogen metabolism	3.72291E-10	1.89868E-08	21
map00073	Cutin, suberine and wax biosynthesis	9.48272E-08	1.75861E-06	19
map00945	Stilbenoid, diarylheptanoid and gingerol biosynthesis	2.91522E-08	6.60783E-07	18
map00460	Cyanoamino acid metabolism	0.00321129	0.019267738	17
map00750	Vitamin B6 metabolism	3.52365E-09	1.02689E-07	16
map00350	Tyrosine metabolism	0.009863451	0.049076685	13
map00909	Sesquiterpenoid and triterpenoid biosynthesis	0.005271027	0.028297091	9
map00591	Linoleic acid metabolism	0.000720599	0.005880088	8
map00450	Selenocompound metabolism	0.001991129	0.012308799	8
map00643	Styrene degradation	0.000354078	0.003283269	5

Table S19. Go enrichment results for expanded genes in *A. yangbiense*.

GO_ID	GO_Term	GO_Class	Pvalue	AdjustedPv	Gene_Number
GO:0046914	transition metal ion binding	MF	2.37E-71	6.58E-68	932
GO:0004803	transposase activity	MF	2.16E-62	2E-59	126
GO:0006313	transposition, DNA-mediated	BP	1.23E-60	6.82E-58	131
GO:0008270	zinc ion binding	MF	5.84E-58	2.7E-55	683
GO:0043531	ADP binding	MF	1.4E-54	5.53E-52	201
GO:0015074	DNA integration	BP	7.7E-53	2.67E-50	111
GO:0048544	recognition of pollen	BP	1.19E-50	2.74E-48	122
GO:0044703	multi-organism reproductive process	BP	3.22E-40	4.7E-38	138
GO:0046872	metal ion binding	MF	2.99E-38	4.15E-36	1087
GO:0043169	cation binding	MF	4.27E-37	5.64E-35	1088
GO:0022414	reproductive process	BP	1.48E-36	1.87E-34	139
GO:0005488	binding	MF	3.28E-33	3.5E-31	3392
GO:0006310	DNA recombination	BP	1.05E-28	9.42E-27	176
GO:0046906	tetrapyrrole binding	MF	1.5E-26	1.19E-24	252
GO:0020037	heme binding	MF	9.92E-24	6.72E-22	241
GO:0003676	nucleic acid binding	MF	5.97E-22	3.95E-20	1182
GO:0016705	oxidoreductase activity, acting on paired donors	MF	4.89E-20	2.77E-18	224
GO:0032501	multicellular organismal process	BP	2.31E-19	1.21E-17	196
GO:0045735	nutrient reservoir activity	MF	4.14E-19	2.13E-17	63
GO:0044707	single-multicellular organism process	BP	4.23E-19	2.13E-17	180
GO:0006259	DNA metabolic process	BP	6.64E-19	3.29E-17	412
GO:0097159	organic cyclic compound binding	MF	5.39E-18	2.45E-16	1935
GO:1901363	heterocyclic compound binding	MF	1.32E-17	5.63E-16	1931
GO:0005506	iron ion binding	MF	3.96E-16	1.64E-14	203
GO:0016758	transferase activity, transferring hexosyl groups	MF	8.39E-16	3.38E-14	205
GO:0004970	ionotropic glutamate receptor activity	MF	1.54E-15	6.03E-14	38
GO:0015276	ligand-gated ion channel activity	MF	1.53E-14	5.59E-13	44
GO:0005515	protein binding	MF	1.3E-13	4.53E-12	1518
GO:0008234	cysteine-type peptidase activity	MF	1.6E-12	4.88E-11	97
GO:0043167	ion binding	MF	2.12E-11	5.45E-10	1663

GO:0009733	response to auxin	BP	4.31E-11	1.08E-09	53
GO:0010309	acireductone dioxygenase [iron(II)-requiring] activity	MF	5.75E-09	0.000000122	23
GO:0022836	gated channel activity	MF	1.55E-08	0.000000307	53
GO:0004523	RNA-DNA hybrid ribonuclease activity	MF	2.52E-08	0.000000483	21
GO:0016757	transferase activity, transferring glycosyl groups	MF	2.95E-08	0.000000557	223
GO:0000413	protein peptidyl-prolyl isomerization	BP	3.16E-08	0.000000581	56
GO:0003755	peptidyl-prolyl cis-trans isomerase activity	MF	3.16E-08	0.000000581	56
GO:0034062	RNA polymerase activity	MF	3.59E-08	0.000000656	115
GO:0005216	ion channel activity	MF	0.000000343	0.00000561	76
GO:0004888	transmembrane signaling receptor activity	MF	0.000000351	0.0000057	56
GO:0051704	multi-organism process	BP	0.000000598	0.00000922	295
GO:0003899	DNA-directed RNA polymerase activity	MF	0.0000015	0.0000217	87
GO:0016702	oxidoreductase activity	MF	0.00000195	0.0000279	37
GO:0008146	sulfotransferase activity	MF	0.00000217	0.0000308	15
GO:0016725	oxidoreductase activity, acting on CH or CH2 groups	MF	0.00000217	0.0000308	15
GO:0004650	polygalacturonase activity	MF	0.00000281	0.0000392	36
GO:0007283	spermatogenesis	BP	0.00000298	0.0000408	15
GO:0016717	oxidoreductase activity	MF	0.00000304	0.0000412	13
GO:0009725	response to hormone	BP	0.00000544	0.0000712	57
GO:0016168	chlorophyll binding	MF	0.00000681	0.000086	10
GO:0018193	peptidyl-amino acid modification	BP	0.00000726	0.0000904	58
GO:0016701	oxidoreductase activity	MF	0.00000742	0.0000915	45
GO:0055114	oxidation-reduction process	BP	0.00000889	0.000108223	614
GO:0004748	ribonucleoside-diphosphate reductase activity	MF	0.00000999	0.000119522	13
GO:0015105	arsenite transmembrane transporter activity	MF	0.0000132	0.000155028	8
GO:0015700	arsenite transport	BP	0.0000132	0.000155028	8
GO:0000723	telomere maintenance	BP	0.0000232	0.000258538	23
GO:0045300	acyl-[acyl-carrier-protein] desaturase activity	MF	0.0000253	0.000277704	9
GO:0006784	heme a biosynthetic process	BP	0.0000332	0.000357347	11
GO:0010033	response to organic	BP	0.0000634	0.000609258	59

	substance					
GO:0019013	viral nucleocapsid	CC	0.000075	0.000710877	27	
GO:0051213	dioxygenase activity	MF	0.000082	0.000771205	39	
GO:0016491	oxidoreductase activity	MF	0.0000934	0.000867116	619	
GO:0009289	pilus	CC	0.0000967	0.000888965	11	
GO:0003677	DNA binding	MF	0.000101952	0.000930985	668	
	sequence-specific DNA					
GO:0000981	binding RNA polymerase II	MF	0.000197423	0.001686293	13	
	transcription factor activity					
GO:0005173	stem cell factor receptor	MF	0.000338845	0.002766568	9	
	binding					
GO:0030639	polyketide biosynthetic	BP	0.000364424	0.002915395	8	
	process					
GO:0009318	exodeoxyribonuclease VII	CC	0.000364424	0.002915395	8	
	complex					
GO:0038023	signaling receptor activity	MF	0.000425649	0.003361409	68	
GO:0047134	protein-disulfide reductase	MF	0.000427441	0.003361409	21	
	activity					
GO:0009767	photosynthetic electron	BP	0.000529747	0.004073623	11	
	transport chain					
GO:0004872	receptor activity	MF	0.000842189	0.006217866	74	
GO:0016984	ribulose-bisphosphate	MF	0.000894494	0.00656909	5	
	carboxylase activity					
GO:0004867	serine-type endopeptidase	MF	0.000989441	0.007190285	20	
	inhibitor activity					
GO:0007131	reciprocal meiotic	BP	0.001046767	0.007528048	8	
	recombination					
GO:0006308	DNA catabolic process	BP	0.00188296	0.013067743	9	
GO:0010277	chlorophyllide a oxygenase	MF	0.002462613	0.016714457	8	
	[overall] activity					
GO:0009611	response to wounding	BP	0.002931785	0.019527739	30	
GO:0009507	chloroplast	CC	0.00339389	0.022220376	11	
GO:0042627	chylomicron	CC	0.003642443	0.02308544	4	
GO:0015485	cholesterol binding	MF	0.003642443	0.02308544	4	
	hydroxymethylglutaryl-Co					
GO:0004420	A reductase (NADPH)	MF	0.003642443	0.02308544	4	
	activity					
GO:0015385	sodium:proton antiporter	MF	0.004268802	0.026451328	5	
	activity					
GO:0010333	terpene synthase activity	MF	0.004479536	0.02739029	26	
GO:0007127	meiosis I	BP	0.006595219	0.03895389	9	
GO:0007276	gamete generation	BP	0.006701728	0.039323766	16	
GO:0005246	calcium channel regulator	MF	0.006813664	0.039323766	7	

	activity				
GO:0004026	alcohol O-acetyltransferase activity	MF	0.006813664	0.039323766	7
GO:0007016	cytoskeletal anchoring at plasma membrane	BP	0.006813664	0.039323766	7
GO:0004656	procollagen-proline 4-dioxygenase activity	MF	0.006813664	0.039323766	7
GO:0098519	nucleotide phosphatase activity	MF	0.008192751	0.046796452	34

Table S20. Go enrichment results for contracted genes in *A. yangbiense*.

GO_ID	GO_Term	GO_Class	Pvalue	AdjustedPv	Gene_Number
GO:0043531	ADP binding	MF	8.09E-73	1.31E-69	48
GO:0030246	carbohydrate binding	MF	2.16E-53	1.75E-50	44
GO:0016747	transferase activity	MF	2.26E-27	1.23E-24	43
GO:0004713	protein tyrosine kinase activity	MF	7.41E-19	3.01E-16	77
GO:0016746	transferase activity, transferring acyl groups	MF	1.4E-16	4.55E-14	44
GO:0006633	fatty acid biosynthetic process	BP	9.38E-15	2.31E-12	23
GO:0004672	protein kinase activity	MF	9.93E-15	2.31E-12	92
GO:0006631	fatty acid metabolic process	BP	3.97E-13	7.17E-11	24
GO:0048544	recognition of pollen	BP	8.22E-12	1.03E-09	15
GO:0006468	protein phosphorylation	BP	1.13E-11	1.31E-09	88
GO:0016762	xyloglucan:xyloglucosyl transferase activity	MF	2.18E-10	2.08E-08	11
GO:0048046	apoplast	CC	2.18E-10	2.08E-08	11
GO:0016740	transferase activity	MF	2.27E-09	0.000000205	195
GO:0030554	adenyl nucleotide binding	MF	2.45E-09	0.00000021	179
GO:0016310	phosphorylation	BP	3.31E-09	0.000000269	92
GO:0004523	RNA-DNA hybrid ribonuclease activity	MF	4.88E-09	0.000000378	8
GO:0032559	adenyl ribonucleotide binding	MF	7.19E-09	0.000000532	175
GO:0046394	carboxylic acid biosynthetic process	BP	1.22E-08	0.0000008	33
GO:0017076	purine nucleotide binding	MF	1.23E-08	0.0000008	205
GO:0032555	purine ribonucleotide	MF	1.64E-08	0.000000981	201

	binding					
GO:0032550	purine ribonucleoside binding	MF	1.69E-08	0.000000981	200	
GO:0016773	phosphotransferase activity, alcohol group as acceptor	MF	0.000000038	0.00000193	95	
GO:0016301	kinase activity	MF	6.35E-08	0.00000304	101	
GO:0043412	macromolecule modification	BP	7.38E-08	0.00000343	100	
GO:0006464	cellular protein modification process	BP	9.88E-08	0.00000423	95	
GO:0030042	actin filament depolymerization	BP	0.00000014	0.00000568	8	
GO:0009678	hydrogen-translocating pyrophosphatase activity	MF	0.000000166	0.00000638	7	
GO:0000166	nucleotide binding	MF	0.000000169	0.00000638	213	
GO:0005488	binding	MF	0.000000636	0.000023	577	
GO:0030036	actin cytoskeleton organization	BP	0.00000242	0.0000839	16	
GO:0004427	inorganic diphosphatase activity	MF	0.00000398	0.000124336	7	
GO:0003871	5-methyltetrahydropteroyltryglutamate-homocysteine S-methyltransferase activity	MF	0.00000398	0.000124336	7	
GO:0006073	cellular glucan metabolic process	BP	0.00000553	0.000166566	16	
GO:0043168	anion binding	MF	0.00000564	0.000166628	208	
GO:0009086	methionine biosynthetic process	BP	0.00000592	0.000171751	7	
GO:0005618	cell wall	CC	0.00000647	0.00018468	16	
GO:0031429	box H/ACA snoRNP complex	CC	0.0000104	0.000271884	4	
GO:0005856	cytoskeleton	CC	0.0000118	0.000304912	53	
GO:0005515	protein binding	MF	0.0000137	0.000347269	229	
GO:0044264	cellular polysaccharide metabolic process	BP	0.0000181	0.000446959	17	
GO:0000160	phosphorelay signal transduction system	BP	0.0000284	0.00067969	11	
GO:0006796	phosphate-containing compound metabolic process	BP	0.0000776	0.001752006	115	
GO:0009067	aspartate family amino	BP	0.000079	0.001759818	8	

	acid biosynthetic process					
	Ttransferring					
GO:0016772	phosphorus-containing groups	MF	0.0000973	0.002080798	112	
GO:0005452	inorganic anion exchanger activity	MF	0.000134525	0.002804331	16	
GO:0043624	cellular protein complex disassembly	BP	0.000142659	0.002828816	9	
GO:0004602	glutathione peroxidase activity	MF	0.000230886	0.004416721	4	
GO:0015405	P-P-bond-hydrolysis-driven transmembrane transporter activity	MF	0.000242776	0.004537392	23	
GO:0005730	nucleolus	CC	0.000343401	0.006345118	5	
GO:0000148	1,3-beta-D-glucan synthase complex	CC	0.000568618	0.010049703	4	
GO:0006075	(1->3)-beta-D-glucan biosynthetic process	BP	0.000568618	0.010049703	4	
GO:0043167	ion binding	MF	0.000834611	0.013939755	310	
GO:0044255	cellular lipid metabolic process	BP	0.001073147	0.017625625	26	
GO:0032787	monocarboxylic acid metabolic process	BP	0.001247597	0.020085075	28	
GO:0006026	aminoglycan catabolic process	BP	0.001417589	0.022598034	6	
GO:0007010	cytoskeleton organization	BP	0.001505952	0.023414636	25	
GO:0008154	actin polymerization or depolymerization	BP	0.001512015	0.023414636	9	
GO:1901363	heterocyclic compound binding	MF	0.001590837	0.024402834	350	
GO:0008171	O-methyltransferase activity	MF	0.001946788	0.028920648	6	
GO:0004553	hydrolase activity, hydrolyzing O-glycosyl compounds	MF	0.001956501	0.028920648	36	
GO:0035556	intracellular signal transduction	BP	0.002306731	0.033790497	27	
GO:0097159	organic cyclic compound binding	MF	0.002375685	0.03418463	350	
GO:0003682	chromatin binding	MF	0.002764538	0.039431048	21	
GO:0016712	oxidoreductase activity,	MF	0.003091261	0.043113172	11	
GO:0016798	hydrolase activity, acting	MF	0.003127957	0.043113172	37	

	on glycosyl bonds				
GO:0004568	chitinase activity	MF	0.003261328	0.043113172	5
GO:0006032	chitin catabolic process	BP	0.003261328	0.043113172	5
GO:0003843	1,3-beta-D-glucan synthase activity	MF	0.003413191	0.044756844	4

Table S21. KEGG enrichment results for expanded genes in *A. yangbiense*.

MapID	MapTitle	Pvalue	AdjustedPv	Gene_Number
map04110	Cell cycle	1.25E-75	4.54E-74	344
map04626	Plant-pathogen interaction	9.59E-58	2.79E-56	449
map00903	Limonene and pinene degradation	5.44E-35	1.32E-33	103
map00460	Cyanoamino acid metabolism	1.16E-28	2.6E-27	146
map00624	Polycyclic aromatic hydrocarbon degradation	3.69E-24	7.66E-23	72
map00363	Bisphenol degradation	1.23E-23	2.38E-22	67
map00627	Aminobenzoate degradation	1.68E-20	2.88E-19	78
map03020	RNA polymerase	2.75E-19	4.45E-18	97
map00943	Isoflavonoid biosynthesis	2.32E-14	3.22E-13	39
map00945	Stilbenoid, diarylheptanoid and gingerol biosynthesis	2.1E-12	2.28E-11	76
map00950	Isoquinoline alkaloid biosynthesis	7.04E-11	6.4E-10	69
map00942	Anthocyanin biosynthesis	9.15E-11	8.06E-10	27
map03018	RNA degradation	1.23E-10	1.05E-09	154
map00140	Steroid hormone biosynthesis	1.91E-10	1.59E-09	76
map00940	Phenylpropanoid biosynthesis	5.3E-10	4.28E-09	172
map00966	Glucosinolate biosynthesis	2.3E-09	1.72E-08	20
map02010	ABC transporters	2.59E-08	0.000000171	107
map00380	Tryptophan metabolism	0.000000104	0.000000605	55
map00944	Flavone and flavonol biosynthesis	0.000000979	0.00000459	21
map00350	Tyrosine metabolism	0.000002	0.00000925	69
map00625	Chloroalkane and chloroalkene degradation	0.00000248	0.0000113	42
map00340	Histidine metabolism	0.000003	0.0000132	36
map00410	beta-Alanine metabolism	0.00000908	0.0000367	69
map02020	Two-component system	0.0000119	0.0000469	29
map00190	Oxidative phosphorylation	0.0000246	0.0000944	92
map00071	Fatty acid degradation	0.0000464	0.000160842	42
map00040	Pentose and glucuronate interconversions	0.0000534	0.000180588	125
map03320	PPAR signaling pathway	0.000234972	0.000697724	32

map03008	Ribosome biogenesis in eukaryotes	0.000333736	0.000957837	80
map00908	Zeatin biosynthesis	0.000711345	0.001916678	22
map00053	Ascorbate and aldarate metabolism	0.000979026	0.002543719	50
map00960	Tropane, piperidine and pyridine alkaloid biosynthesis	0.001214326	0.003020246	46
map00901	Indole alkaloid biosynthesis	0.001561423	0.003786451	10
map00480	Glutathione metabolism	0.001683074	0.004047722	64
map00330	Arginine and proline metabolism	0.002505086	0.005564732	47
map00240	Pyrimidine metabolism	0.003086864	0.006805132	104
map00310	Lysine degradation	0.005026666	0.010374183	36
map00591	Linoleic acid metabolism	0.010101875	0.019597637	16
map00643	Styrene degradation	0.010512425	0.020125761	11
map00730	Thiamine metabolism	0.01658878	0.029798363	26
map00280	Valine, leucine and isoleucine degradation	0.024037992	0.040906758	43
map00980	Metabolism of xenobiotics by cytochrome P450	0.028726579	0.047228444	36

Table S22. A summary of Drought-tolerant genes identified in *A. truncatum* and other published genomes.

Genes	<i>A.truncatum</i>	<i>A.yangbiense</i>	<i>A. thaliana</i>	<i>C. sinensis</i>	<i>M. oleifera</i>	<i>S. indicum</i>
APX	16	16	20	18	13	22
DHA	4	1	6	4	3	5
GCL	4	8	3	2	2	4
GLO	24	23	18	16	11	11
GR	12	12	16	16	12	28
GSH-Px	5	4	8	5	5	6
MDHAR	3	3	5	3	2	3
MSR	8	3	4	2	1	3
POD	57	78	73	72	54	84
AQP1	13	9	9	8	8	11
LEA	82	68	50	72	55	74
LEW	12	9	10	9	10	9
NLM	7	10	9	8	6	8
OSM	6	10	2	3	4	12
PIP	7	10	19	11	8	14
SIP	3	2	3	2	2	3

SOS1	1	1	2	1	0	1
TIP	14	9	11	9	9	12
ACP	3	4	4	3	1	4
ALAT	2	2	4	2	2	5
AST	7	7	5	6	5	4
CHI	2	2	3	1	2	2
GOGAT	1	1	2	1	0	1
MDH	6	5	5	5	3	5
MS	5	2	3	3	2	2
NAD-ME	2	2	2	2	1	2
NIR	1	1	1	1	1	2
NR	1	0	2	1	0	1
PCK	2	2	2	2	2	2
PEPC1	6	4	3	3	4	4
PPDK	1	1	1	1	1	1
SAH	1	1	2	1	1	3
SAMS	1	5	4	4	4	4
AFL1	0	0	1	0	0	0
COMT	9	14	2	28	2	3
GRP	14	9	31	11	12	17
LOX	5	12	6	10	8	15
MDA1	1	1	1	1	1	1
PAE	10	12	14	9	7	11
PAL	2	8	4	4	5	8
PGIP	0	0	3	1	0	0
PLD	3	3	3	2	3	5
RGP	3	3	5	5	7	8
XI	4	5	10	5	2	8
XTH	25	10	33	31	30	36
BADH	1	1	2	1	0	2
COD1	0	0	1	0	0	0
DMT	4	2	5	2	2	2
P5CDH	1	1	1	1	0	1
P5CR	2	2	1	1	1	1
P5CS	1	1	2	2	2	2
PEAMT	1	1	1	1	0	2
ProDH	1	1	2	1	1	2
SPS	5	4	6	5	2	5
SUS	12	6	9	7	7	7
TPS	10	8	10	8	11	10

Table S23. A summary of drought-tolerant transcription factors identified in *A. truncatum* and other published genomes.

Genes	<i>A. truncatum</i>	<i>A.yangbiense</i>	<i>A. thaliana</i>	<i>C. sinensis</i>	<i>M. oleifera</i>	<i>S. indicum</i>
ADH	6	5	7	9	10	8
AREB	0	1	5	2	4	1
COR	0	0	2	0	0	0
DREB	6	9	9	6	3	7
EIL1	4	3	3	4	2	5
HARDY	5	5	5	9	1	4
KIN	43	33	47	37	31	38
MYB	19	16	28	19	15	19
NAC3	15	3	27	24	3	18
NAC6	30	7	50	34	7	42
RD22	1	1	1	1	1	1
RD29B	0	0	1	0	0	0
WRKY	2	2	11	5	7	2
bZIP23	1	1	3	2	2	2

Table S24. The gene copy number of VLCFA biosynthesis in 12 plants.

GeneID	<i>A.truncatum</i>	<i>A.yangbiense</i>	<i>A.thaliana</i>	<i>C.sinensis</i>	<i>G.max</i>	<i>G.raimondii</i>	<i>H.annuus</i>	<i>M.oleifera</i>	<i>O.europae</i>	<i>S.indicum</i>	<i>S.lycopersicum</i>	<i>X.sorbifolium</i>
ACC	1	1	2	0	2	2	2	0	1	1	1	1
a-CT	1	2	1	1	3	2	3	0	3	3	1	0
BCCP	2	2	2	2	5	4	2	2	4	1	2	0
BC	1	1	1	1	2	2	2	0	1	1	1	1
b-CT	0	1	1	0	0	0	0	0	0	0	1	0
ECR	3	2	1	1	2	2	3	1	2	1	1	1
ER	3	3	2	2	5	4	5	4	4	4	5	2
FATA	2	1	2	1	1	3	1	0	2	1	1	1
FATB	1	1	1	1	4	4	3	1	1	1	1	2
HAD	3	3	3	1	7	3	3	2	2	2	3	2
HCD	2	2	2	2	3	2	3	1	3	3	2	2
KAR	3	3	7	4	6	4	9	2	4	8	7	2
KASIII	1	1	1	0	3	2	3	0	2	2	2	0
KASII	1	1	2	5	7	8	9	3	8	6	5	0
KASI	2	2	2	3	8	7	9	2	8	6	5	1
KCR	1	4	2	2	3	3	4	2	4	3	2	2
KCS	28	22	21	15	31	26	33	19	28	21	17	13
LACS	9	7	9	7	20	12	13	5	11	9	9	2
MCMT	1	1	1	1	2	1	2	1	0	1	1	1
SAD	3	10	7	6	5	8	2	6	5	7	7	4

Table S25. Expression levels significantly up-regulated between 85 DAF and 100DAF in the fatty acid elongation stage of the VLCFA biosynthesis pathway.

GENE_ID	readcount_100DAF	readcount_85DAF	log2FoldChange	p-value
Atru.chr4.2307	117.7472816	4.410290476	4.7387	3.15E-16
Atru.chr4.2308	8356.115812	439.3283629	4.2495	1.12E-87
Atru.chr4.2311	4979.706479	512.3433797	3.2809	3.32E-10

Table S26. The transcription factors (TF)/transcription regulatory factors (TR) in black module of WGCNA analysis.

Module	TF/TR	Family	Gene ID
black	TF	MYB-related	Atru.chr1.3799, Atru.chr8.1841, Atru.chr3.3572
	TF	Alfin-like	Atru.chr1.3876
	TF	Trihelix	Atru.chr11.2229.1
	TF	WRKY	Atru.chr12.201, Atru.chr12.202, Atru.chr9.2017, Atru.chr4.3047
	TF	C3H	Atru.chr13.328
	TF	LOB	Atru.chr3.3711
	TF	B3	Atru.chr5.2849.2
	TF	NAC	Atru.chr5.3491
	TF	bZIP	Atru.chr5.613
	TF	ERF	Atru.chr5.683
	TR	MBF1	Atru.chr7.1330
	TF	ERF	Atru.chr7.2513

Table S27. List of *KCS* gene-specific primer (5' - 3') used for real-time RT-PCR.

gene name	Forward primer	Reverse primer
Atru.chr4.2308	TTGGGCAAATGACTTACGGG	AATCATTGCCGATAAAGACG
Atru.chr4.2307	TCCAAACTTCTTCCTCTCTG	AGACAAAGGCAACAGAGCAT
Atru.chr4.2311	TTCATCCCAACTACTATGCG	TCGGTTGGAGAGGAGGATGG
Atru.chr4.2309	GTTGATGCAGGTCCTCATA	CTAGGCTTCACTCCAGTTTT
Atru.chr4.2822	TGGATGCGAGAAAGGAGACA	CTGATAAAGACGGCGTTGGA
Actin	ATCATGTTTGAGACCTTCAACAC	GATCTTCATGAGGTAGTCAGTCAGGT

Table S28. List of *LEA* gene-specific primer (5' - 3') used for real-time RT-PCR.

Gene name	Forward primer	Reverse primer
LEA1-Atru.chr6.1738	AAGCAGCAGCGAGGACAGAG	GGTCACCGCCAGATGGGATT
LEA2-Atru.chr3.1961	GATTACGAGGTTTGGCTGTC	TTGTTCTTCTTGAGGCGAGT
LEA2-Atru.chr10.2344	CATGCCCTTTCCTTCCCTAA	TCATCGTGCTTGACTTCCTG
LEA2-Atru.chr1.3277	ATCATCACAGTCATCATCCTCCTC	CGTGTCTAGCTTCTCCTCCT
LEA3-Atru.chr12.2033	CTCCTCCTACGGCTCAACTC	CAGGCTTTCTCCTCCAACAC
LEA4-Atru.chr6.2817	AACAGCAAGGTCGTCCACAG	CAGTTCACGACCAAGTTTA
LEA5-Atru.chr12.68	ATGTTAGTGTTACGGAGGTTTGA	CCTAGCCTTGGTGTCGAGTT
SMP-Atru.chr5.1467	TCTCACCGACATCACCAGAG	AGTTGCCACATTAGGCTTTG
Dehydrin-Atru.chr5.3081	GGATGATGGGCAAGGTGGAA	AGGCAACGGTTGTGGTCTGT
Dehydrin-Atru.chr3.677	TGGGATACGGAAGAAGAAGG	GACAGGAGTAGTGGTGGTTGC