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Supplementary Data

Transcriptome-wide identification of genes related to fatty acid biosynthesis in the medicinal plant *Salvia miltiorrhiza*

Jianhui Zhang*, Haimei Chen*, Kai Wu, Chang Liu†

Supplementary Tables

Table S1. Genes related to fatty acid biosynthesis in *S. miltiorrhiza* were scanned against the Pfam database to determine the Pfam Hidden Markov Models they match significantly (E-value <= 1e-5).

Gene Name	Alignment start	Alignment end	HMM acc	HMM name	E-value	At. ortholog gene name	HMM acc	E-value
SmPDHa1	66	361	PF00676.15	E1_dh	1.00E-118	AtPDHa	PF00676.15	7.10E-98
SmPDHb1	79	249	PF02779.19	Transket_pyr	1.80E-46	AtPDHb1	PF02779.19	7.80E-49
SmPDHb1	265	383	PF02780.15	Transketolase_C	3.30E-34	AtPDHb1	PF02780.15	3.30E-35
SmPDHb2	86	256	PF02779.19	Transket_pyr	4.10E-49	AtPDHb2	PF02779.19	7.80E-49
SmPDHb2	272	390	PF02780.15	Transketolase_C	1.90E-34	AtPDHb2	PF02780.15	6.50E-35
SmDHLAT1	42	113	PF00364.17	Biotin_lipoyl	7.20E-17	AtDHLAT1	PF00364.17	2.40E-16
SmDHLAT1	185	222	PF02817.12	E3_binding	8.00E-15	AtDHLAT1	PF02817.12	6.70E-13
SmDHLAT1	251	469	PF00198.18	2-oxoacid_dh	9.90E-67	AtDHLAT1	PF00198.18	1.00E-68
SmDHLAT2	40	110	PF00364.17	Biotin_lipoyl	9.70E-16	AtDHLAT2	PF00364.17	1.40E-15
SmDHLAT2	166	204	PF02817.12	E3_binding	1.20E-13	AtDHLAT2	PF02817.12	5.70E-14
SmDHLAT2	242	462	PF00198.18	2-oxoacid_dh	1.00E-67	AtDHLAT2	PF00198.18	1.90E-66
SmLPD1	82	403	PF07992.9	Pyr_redox_2	3.20E-33	AtLPD1pt	PF07992.9	6.60E-36
SmLPD1	255	330	PF00070.22	Pyr_redox	1.10E-15	AtLPD1pt	PF00070.22	2.70E-15
SmLPD1	435	547	PF02852.17	Pyr_redox_dim	3.30E-31	AtLPD1pt	PF02852.17	1.20E-31
SmLPD2	45	357	PF07992.9	Pyr_redox_2	1.30E-45	AtLPD2pt	PF07992.9	2.60E-34
SmLPD2	216	291	PF00070.22	Pyr_redox	1.80E-18	AtLPD2pt	PF00070.22	4.70E-16

SmLPD2	388	497	PF02852.17	Pyr_redox_dim	3.40E-40	AtLPD2pt	PF02852.17	1.90E-30
SmLPD3	4	192	PF07992.9	Pyr_redox_2	1.00E-16	AtLPD1mt	Pyr_redox_2	1.90E-42
SmLPD3	51	126	PF00070.22	Pyr_redox	1.60E-16	AtLPD1mt	Pyr_redox	2.80E-20
SmLPD3	223	330	PF02852.17	Pyr_redox_dim	1.10E-33	AtLPD1mt	Pyr_redox_dim	1.50E-40
SmLPD4	85	406	PF07992.9	Pyr_redox_2	1.00E-33	AtLPD2mt	Pyr_redox_2	3.30E-44
SmLPD4	258	334	PF00070.22	Pyr_redox	5.60E-15	AtLPD2mt	Pyr_redox	6.00E-20
SmLPD4	438	549	PF02852.17	Pyr_redox_dim	2.30E-31	AtLPD2mt	Pyr_redox_dim	8.00E-40
SmCTa1	98	241	PF03255.9	ACCA	6.80E-62	AtCTa	PF03255.9	2.00E-63
SmCTa2	100	243	PF03255.9	ACCA	1.20E-60			
SmCTb1	284	453	PF01039.17	Carboxyl_trans	4.70E-21	AtCTb	PF01039.17	7.80E-19
SmBC1	70	177	PF00289.17	CPSase_L_chain	4.20E-38	AtBC	PF00289.17	3.10E-38
SmBC1	182	389	PF02786.12	CPSase_L_D2	6.90E-82	AtBC	PF02786.12	1.80E-81
SmBC1	403	508	PF02785.14	Biotin_carb_C	2.70E-37	AtBC	PF02785.14	1.70E-37
SmBCCP1	179	251	PF00364.17	Biotin_lipoyl	6.20E-26	AtBCCP1	PF00364.17	9.50E-26
SmBCCP2	211	283	PF00364.17	Biotin_lipoyl	1.70E-25	AtBCCP2	PF00364.17	6.20E-25
SmACC1	48	167	PF00289.17	CPSase_L_chain	8.70E-27	AtACC1	PF00289.17	4.10E-26
SmACC1	214	397	PF02786.12	CPSase_L_D2	3.00E-47	AtACC1	PF02786.12	3.70E-46
SmACC1	444	550	PF02785.14	Biotin_carb_C	9.70E-21	AtACC1	PF02785.14	2.50E-21
SmACC1	693	754	PF00364.17	Biotin_lipoyl	1.50E-10	AtACC1	PF00364.17	2.80E-08
SmACC1	755	1490	PF08326.7	ACC_central	2.20E-213	AtACC1	PF08326.7	8.00E-229
SmACC1	1591	2142	PF01039.17	Carboxyl_trans	1.80E-166	AtACC1	PF01039.17	1.20E-170
						AtACC2	PF00289.17	1.20E-26
						AtACC2	PF02786.12	8.10E-46
						AtACC2	PF02785.14	1.20E-21
						AtACC2	PF00364.17	1.20E-08
						AtACC2	PF08326.7	3.80E-216
						AtACC2	PF01039.17	1.20E-167
SmHACPS1	148	275	PF01648.15	ACPS	2.40E-16	AtHACPS1	PF01648.15	3.00E-14
						AtHACPS2	PF01648.15	1.30E-16
SmACP1	55	117	PF00550.20	PP-binding	6.70E-13	AtACP1	PF00550.20	9.10E-10
SmACP2	56	101	PF00550.20	PP-binding	1.80E-09	AtACP2	PF00550.20	1.70E-11
SmACP3	52	113	PF00550.20	PP-binding	2.40E-10	AtACP3	PF00550.20	1.70E-11
SmACP4	46	100	PF00550.20	PP-binding	2.00E-11	AtACP4	PF00550.20	2.70E-12
SmACP5	54	120	PF00550.20	PP-binding	1.20E-09	AtACP5	PF00550.20	2.40E-11

SmACP6	61	127	PF00550.20	PP-binding	6.50E-10	AtACP6	PF00550.20	5.80E-11
SmACP7	61	128	PF00550.20	PP-binding	8.30E-14	AtACP7	PF00550.20	2.30E-10
SmACP8	61	127	PF00550.20	PP-binding	2.80E-09	AtACP8	PF00550.20	1.30E-08
SmMCMT1	106	386	PF00698.16	Acyl_transf_1	2.00E-30	AtMCMT	PF00698.16	2.40E-27
SmKASIII1	170	249	PF08545.5	ACP_syn_III	2.90E-26	AtKASIII	PF08545.5	8.70E-28
SmKASIII1	310	399	PF08541.5	ACP_syn_III_C	1.40E-38	AtKASIII	PF08541.5	6.90E-38
SmKASIII2	80	159	PF08545.5	ACP_syn_III	4.40E-28			
SmKASIII2	221	310	PF08541.5	ACP_syn_III_C	1.90E-37			
SmKAR1	77	243	PF00106.20	adh_short	4.50E-44	AtKAR1	PF00106.20	4.20E-43
SmKAR2	1	161	PF00106.20	adh_short	1.30E-35	AtKAR2	PF00106.20	1.80E-28
SmKAR3	2	115	PF00106.20	adh_short	1.20E-22	AtKAR3	PF00106.20	3.30E-29
SmKAR4	1	131	PF00106.20	adh_short	4.40E-32	AtKAR4	PF00106.20	3.00E-28
						AtKAR5	PF00106.20	4.70E-30
						AtKAR6	PF00106.20	5.00E-29
SmHAD1	91	216	PF07977.8	FabA	2.00E-38	AtHAD1	PF07977.8	2.00E-37
						AtHAD2	PF07977.8	1.30E-37
						AtHAD3	PF13238.1	2.30E-21
SmENR1	100	371	PF13561.1	adh_short_C2	3.70E-102	AtENR1	PF13561.1	2.20E-101
SmENR2	100	371	PF13561.1	adh_short_C2	2.80E-104			
SmENR3	75	137	PF08240.7	ADH_N	8.80E-10	AtENR2	PF08240.7	1.30E-09
SmENR3	200	335	PF00107.21	ADH_zinc_N	7.10E-16	AtENR2	PF00107.21	1.00E-18
SmKASI1	61	307	PF00109.21	ketoacyl-synt	1.50E-58	AtKASI	PF00109.21	1.20E-57
SmKASI1	316	427	PF02801.17	Ketoacyl-synt_C	1.30E-32	AtKASI	PF02801.17	1.00E-33
SmKASI2	77	323	PF00109.21	ketoacyl-synt	8.90E-50			
SmKASI2	333	445	PF02801.17	Ketoacyl-synt_C	3.70E-33			
SmLS1	144	306	PF04055.16	Radical_SAM	4.60E-13	AtLS1	PF04055.16	6.90E-13
SmLS2	117	277	PF04055.16	Radical_SAM	2.90E-15	AtLS2	PF04055.16	2.50E-16
SmLT1	78	184	PF03099.14	BPL_LplA_LipB	1.40E-12	AtLT1	PF03099.14	6.50E-13
SmLT2	112	208	PF03099.14	BPL_LplA_LipB	7.50E-15	AtLT2	PF03099.14	3.80E-16
SmFATa1	81	365	PF01643.12	Acyl-ACP_TE	2.90E-120	AtFATa1	PF01643.12	1.40E-116
						AtFATa2	PF01643.12	4.30E-119
SmFATb1	1	129	PF12590.3	Acyl-thio_N	1.40E-50	AtFATb	PF12590.3	5.60E-52
SmFATb1	140	405	PF01643.12	Acyl-ACP_TE	9.20E-115	AtFATb	PF01643.12	9.20E-114
SmKASII1	123	368	PF00109.21	ketoacyl-synt	1.00E-58	AtKASII	PF00109.21	2.10E-56

SmKASII1	376	490	PF02801.17	Ketoacyl-synt_C	1.10E-34	AtKASII	PF02801.17	8.40E-35
SmKASII2	35	300	PF00109.21	ketoacyl-synt	8.30E-56			
SmKASII2	367	448	PF02801.17	Ketoacyl-synt_C	3.70E-25			
SmKASII3	2	106	PF00109.21	ketoacyl-synt	2.30E-29			
SmKASII3	124	183	PF02801.17	Ketoacyl-synt_C	9.40E-12			
SmSAD1	66	394	PF03405.9	FA_desaturase_2	4.40E-188	AtSAD	PF03405.9	2.70E-183
SmSAD2	1	227	PF03405.9	FA_desaturase_2	4.50E-131			
SmSAD3	38	341	PF03405.9	FA_desaturase_2	3.40E-175			
SmLACS1	108	549	PF00501.23	AMP-binding	1.00E-98	AtLACS1	PF00501.23	4.20E-97
SmLACS2	98	565	PF00501.23	AMP-binding	8.90E-94	AtLACS2	PF00501.23	3.20E-94
SmLACS3	95	535	PF00501.23	AMP-binding	5.30E-95	AtLACS3	PF00501.23	8.00E-96
SmLACS4	56	525	PF00501.23	AMP-binding	2.00E-95	AtLACS4	PF00501.23	2.70E-99
SmLACS5	54	524	PF00501.23	AMP-binding	1.80E-94	AtLACS5	PF00501.23	2.70E-98
SmLACS6	69	523	PF00501.23	AMP-binding	2.00E-93	AtLACS6	PF00501.23	1.70E-98
SmLACS7	50	521	PF00501.23	AMP-binding	1.80E-90	AtLACS7	PF00501.23	1.10E-93
SmLACS8	119	585	PF00501.23	AMP-binding	3.40E-95	AtLACS8	PF00501.23	3.20E-97
						AtLACS9	PF00501.23	7.00E-99
SmABCAT1	83	361	PF06472.10	ABC_membrane_2	9.00E-84	AtABCAT1	PF06472.10	4.80E-88
SmABCAT1	465	610	PF00005.22	ABC_tran	1.10E-19	AtABCAT1	PF00005.22	1.20E-18
SmABCAT1	741	1010	PF06472.10	ABC_membrane_2	5.10E-80	AtABCAT1	PF06472.10	6.10E-78
SmABCAT1	1119	1279	PF00005.22	ABC_tran	5.10E-13	AtABCAT1	PF00005.22	9.20E-12
SmABCAT2	97	370	PF06472.10	ABC_membrane_2	5.10E-58	AtABCAT2	PF06472.10	1.10E-60
SmABCAT2	478	679	PF00005.22	ABC_tran	4.40E-19	AtABCAT2	PF00005.22	8.10E-18
SmAAS1	86	594	PF00501.23	AMP-binding	9.40E-95	AtAAS	PF00501.23	7.30E-98
SmAAS2	5	236	PF00501.23	AMP-binding	1.20E-55			
SmAAS2	245	319	PF13193.1	AMP-binding_C	2.90E-15			
SmTGD1	58	271	PF02405.11	Permease	1.50E-68	AtTGD1	PF02405.11	5.40E-71
SmGLB1	77	179	PF00543.17	P-II	3.10E-32	AtGLB1	PF00543.17	1.70E-34
SmWRI1	58	117	PF00847.15	AP2	3.60E-13	AtWRI1	PF00847.15	1.10E-12
SmWRI1	160	211	PF00847.15	AP2	5.10E-14	AtWRI1	PF00847.15	3.10E-14
SmWRI2	35	94	PF00847.15	AP2	4.70E-13			
SmWRI2	137	188	PF00847.15	AP2	7.50E-14			
SmWRI3	82	141	PF00847.15	AP2	9.40E-12			
SmWRI4	141	190	PF00847.15	AP2	1.00E-14			

SmWRI4	233	283	PF00847.15	AP2	6.50E-11
SmWRI5	46	104	PF00847.15	AP2	3.10E-12
SmWRI5	147	199	PF00847.15	AP2	3.10E-14
SmWRI6	215	274	PF00847.15	AP2	5.90E-14
SmWRI6	317	368	PF00847.15	AP2	2.10E-12
SmWRI7	36	88	PF00847.15	AP2	2.10E-13
SmWRI8	92	151	PF00847.15	AP2	1.50E-12
SmWRI8	194	228	PF00847.15	AP2	4.50E-06
SmWRI9	63	122	PF00847.15	AP2	1.20E-14
SmWRI10	158	207	PF00847.15	AP2	1.80E-14
SmWRI10	250	297	PF00847.15	AP2	4.50E-10
SmWRI11	111	160	PF00847.15	AP2	2.70E-15
SmWRI12	258	317	PF00847.15	AP2	4.50E-13
SmWRI12	360	411	PF00847.15	AP2	2.70E-12

Table S2. The expression levels of the 76 genes involved in fatty acid biosynthesis. The numbers are fragments per kilobase per million fragments (FPKM).

Gene Name	Flower	Leaf	Root
SmPDHa1	117.98	118.03	100.62
SmPDHb1	50.13	31.24	12.49
SmPDHb2	24.62	93.5	6.99
SmDHLAT1	40.19	62.73	9.41
SmDHLAT2	24.7	32.68	12.73
SmLPD1	11.51	20.73	4.87
SmLPD2	100.04	195.2	58.84
SmLPD3	0.07	0	3.55
SmLPD4	37.38	20.08	12.16
SmCTa1	212.28	90.78	136.19
SmCTa2	34	70.42	15.22
SmCTb1	2.56	1.81	1.33
SmBC1	89.62	47.87	36.3
SmBCCP1	28.54	26.41	8.51
SmBCCP2	9.09	62.58	8.36
SmACC1	46.19	82.66	14.4
SmHACPS1	22.28	15.11	14.04
SmACP1	7.02	16.37	3.93
SmACP2	15.75	19.88	5.39
SmACP3	6.04	6.5	7.09
SmACP4	74.72	95.14	87.37
SmACP5	9.74	18.47	6.71
SmACP6	73.76	31.45	70.68
SmACP7	58.17	184.55	3.46
SmACP8	116.24	26.52	18.55
SmMCMT1	35.05	32.21	14.86
SmKASIII1	56.62	183.31	66.24

SmKASIII2	15.5	29.85	4.2
SmKAR1	58.05	100.55	12.19
SmKAR2	0.06	0	0.72
SmKAR3	0	0	0.65
SmKAR4	29.51	10.73	18.02
SmHAD1	87.92	92.03	30.51
SmENR1	74.71	30.75	17.24
SmENR2	7.75	49.74	0.6
SmENR3	20.39	18.36	4.31
SmKASI1	60.47	99.97	25.58
SmKASI2	15.84	1.68	0.41
SmLS1	17.68	98.67	9.54
SmLS2	10.52	15.15	6.59
SmLT1	54.44	53.74	57.88
SmLT2	16.35	26.09	6.75
SmFATa1	33.84	111.52	13.36
SmFATb1	101.7	83.11	38.86
SmKASII1	34.37	95.84	22.66
SmKASII2	4.25	5.78	3.48
SmKASII3	0.38	0.08	1.83
SmSAD1	15.62	134.39	6.99
SmSAD2	43.32	39.74	55.96
SmSAD3	32.58	17.75	15.15
SmLACS1	18.67	17.77	20.98
SmLACS2	18.84	74.24	15.97
SmLACS3	47.49	24.61	39.43
SmLACS4	142.08	2.51	6.48
SmLACS5	91.05	111.07	44.37
SmLACS6	82.91	17.42	5.95
SmLACS7	63.06	48.21	0.03
SmLACS8	7.98	4.35	11.38
SmABCAT1	19.73	26.25	23.38

SmABCAT2	6.47	51.5	2.14
SmLAAS1	249.92	280.02	79.6
SmLAAS2	0.1	0	1.78
SmTGD1	10.68	23.67	7.55
SmGLB1	69.85	30.67	25.29
SmWRI1	3.5	0.95	3.52
SmWRI10	43.59	38.65	32.6
SmWRI11	1.63	14.06	74.19
SmWRI12	102.25	11.88	117.26
SmWRI2	13.34	0.99	15.08
SmWRI3	0.9	0.93	5.9
SmWRI4	7.31	4.23	3.27
SmWRI5	5.02	3.7	0.07
SmWRI6	11.08	2.08	6.01
SmWRI7	3.92	1.19	0.17
SmWRI8	5.48	0.6	2.11
SmWRI9	4.43	4.09	3.76

Table S3. List of primers used in qRT-PCR experiments.

Gene Name	Primers
SmPDHa1	F:TCTGATCCTGGAAGCACATATC
	R:CGGTATCCTTCAGTTCCTTCTC
SmPDHb1	F:AGAGAAGGACTGGAGGAAGAA
	R:ACCCTTGCTGACCTTGTATG
SmPDHb2	F:ATGAGAACGGGTGGAATTGG
	R:CACGTCCTGAGATGACAAACA
SmDHLAT1	F:CAGCTCCAGCCTCAAGAATATAA
	R:AGTTCCCGGTGGCAATATG
SmLPD1	F:CAGTCGCTGACCATGCTAATA
	R:CCACTATGGTGCCAAATCCT
SmLPD3	F:TGACAGAGCAAGAAGCAGAAG
	R:AGCAAGAGCACGACCATTAG
SmCTa1	F:CATGGTGATCGAGCTGGATATG
	R:TTTCGTGTTCCTTCCCTTCTG
SmCTa2	F:GGGCTTGGTTTGAAGATTGATG
	R:CACTTCCCTTATCTCTGCTTCC
SmCTb1	F:AGAAGGGAGTTTGAGCCTAATG
	R:CCCACCAGTAGTAGGAGATGTA
SmBC1	F:ACCCGGACCAGGTAGAATAA
	R:CGTTGGAGCCCAGACAATAA
SmBCCP1	F:GTCGGAGATAAGGTCCAGAAAG
	R:TTCCCATCATCCGCAAGTATC
SmBCCP2	F:CGCTTCTCGTCCAAGAGTTT
	R:CTCTGATTGGGAAGAAGTGGAG
SmACC1	F:CGAGAAGTCTCTCGGAGTTAGA
	R:GCTTCCATCCGTTCGTTTATTG
SmHACPS1	F:ACTGAGAAGCACTCTGCATTAG
	R:GCATCTGTTCCAGAGACGTATT
SmACP1	F:CCATAACGATCTTGGTCTGGATAG
	R:GTCTGCTTCGTTGTCTGGAA
SmACP7	F:CTCCCTTGACACTGTGGAAATA

	R:AGCTTCTTGGATGCAGGTTAT
SmACP8	F:AGCCCGAGACAGTCAATAAAG
	R:CAAGAGAGTCAGCACCAAGT
SmMCMT1	F:CTAAGCCAGCCAGCTATCTATG
	R:ATGCAAGGGCTGTGTATTCT
SmKASIII1	F:GCTTCCTATTGGGCCTAGTTT
	R:CGGTCAACATAACGCGATAGA
SmKASIII2	F:GCTTCCTATTGGGCCTAGTTT
	R:CGGTCAACATAACGCGATAGA
SmKAR1	F:GCGGAGATGTTTCCAAAGAAG
	R:CAACAAACCATCCCTCGTAATG
SmHAD1	F:GCTGGAGTGGACAAAGTAAGAT
	R:TTCCCTTCCATCTTTGCTATCC
SmENR1	F:CCACAACAACGCTTCTAAACC
	R:ATGCCCTCTTCCCTCTTAAATC
SmENR2	F:TCAACCGTACCTTCACATCTTC
	R:CATCAGCAACACCAGCAATAAA
SmENR3	F:CCAGAACCCGCATTAGGATTTA
	R:GATCCTGTGGAGACGGTTATTG
SmKASI1	F:CTGGAGTCTTGGTTATGGAAAGT
	R:CCTGGGATCAGTCATGTGATAAG
SmKASI2	F:GAAGGTGCTGGTGTGTTGATA
	R:CCTCCCAAATACTCGGCATAAA
SmLS1	F:GCTTTACGCTCTCTCGATTCA
	R:TCGAGGGTATGTGGGTAGTT
SmLT1	F:GGAAGATGGGAGCTGTGAATTA
	R:AATGTGGGTGGATGCTGTAG
SmFATa1	F:CGAAGACGGCTTGTCGTATAA
	R:TCCTGCAAGAGATTGGCTATG
SmFATb1	F:ATGGTATGCGTCGAGATTGG
	R:AACCTCCGCGTCTCTTTATTC
SmKASII1	F:GAAACCTCCAACCAAGCAAAG
	R:CTGGCTCCTTCAAGCAGATTA
SmSAD1	F:AGAGACTACGCCGACATTCTA

	R:AGGCAATCCACAGACGTATTC
SmLACS1	F:CTGTGTGCCGAGTACCTTAAA
	R:GGAGGGTAGAGATGGTAGATGT
SmLACS2	R:ACACCAGAAGGTCCCATAGA
	F:TGGTGGACTCCCAAAGAAAC
SmLACS4	R:CTTGTACCCTCTGCTCATGTTAT
	F:ACACAGGTTTGGTGGAGAAG
SmLACS6	R:CCATTAGGCATCATCTCTCCTATG
	F:GTCTCCATTTGCCGGGTATTA
SmLACS7	F:GTGCCTGAGATGGGATATGATG
	R:CGTTTATGGTAGCCGGAGAATAA
SmABCAT1	F:AGAAGGCGGATGGGATACTA
	R:ACTGAGGCTTGTGGAAGAAC
SmABCAT2	F:GGAAGAGGTCAGGAGTTGTTAG
	R:TAGGCCCTGAAATCAGAAGATG
SmLAAS1	F:CCGCAAGTGATGAAGGGTTA
	R:GAGGACAGATCCAGCCAATATC
SmTGD1	F:TGTGAGGGAATTCACCAGATTAG
	R:ATACGCCCAGCAACAACA
SmGLB1	F:CCTGTGGCCGACATAATAAGAG
	R:GAGGATCCAACGGAGAACATATC
SmWRI1	F:GTAGAGGGCTACACCAAAGATG
	R:CCTTGCTACACCGCGATATT
SmWRI2	F:CTCACCCAGACAACCCAAATA
	R:GTGGTCGAGTTCACCTAATTCT
SmWRI5	F:GGGCAGTCAAAGGAAGAATACA
	R:CTTGCTACGCCTCGGTATTT
SmWRI7	F:CGCTTCCATATACAGAGGAGTG
	R:GCTTCTTCTTGGGTGCTAAATG
SmWRI8	F:CAGAGGTGTTACAAGGCATCA
	R:TGCAAATGTTCCGAGGTAGAG
SmWRI12	F:GCAGACTGTTCATCGCAAATC
	R:TCCCACAAGTGAGCTTCATAC
SmbActin	F:TGTCAGCAACTGGGATGATATG

R:CGATTGGCCTTGGGATTAAGA

Table S4 Correlation analyses of tissue expression profiles obtained from RNA-Seq and qRT-PCR experiments.

Gene Name	RNA-seq			qRT-PCR						Pearson correlation coefficients
	Log(Expression level)#			Average of Normalized Expression levels*			STDEV of Normalized Expression Levels			
	Flower	Leaf	Root	Flower	Leaf	Root	Flower	Leaf	Root	
SmPDHa1	1.945	-0.869	-1.076	0.227	-0.179	-0.048	0.231	0.085	0.057	0.928
SmPDHb1	2.774	-1.466	-1.308	1.047	-0.042	-1.004	0.128	0.282	0.084	0.868
SmPDHb2	-0.589	0.170	0.419	-0.067	1.816	-1.748	0.024	0.015	0.177	-0.205
SmDHLAT1	2.397	-0.718	-1.679	0.635	0.870	-1.506	0.019	0.053	0.313	0.614
SmLPD1	-0.016	0.828	-0.812	0.098	0.895	-0.993	0.215	0.068	0.245	0.994
SmLPD3	-1.720	1.078	0.642	-0.664	-0.761	1.425	0.245	0.036	0.102	0.332
SmCTa2	-0.014	1.612	-1.598	0.027	1.056	-1.083	0.098	0.010	0.317	1.000
SmCTa1	0.573	-0.427	-0.146	0.773	-0.860	0.086	0.096	0.491	0.019	0.943
SmCTb1	0.622	0.325	-0.947	0.633	-0.274	-0.358	0.017	0.017	0.079	0.703
SmBC1	2.158	-0.898	-1.261	0.887	-0.424	-0.463	0.106	0.021	0.407	0.997
SmBCCP1	2.111	-1.084	-1.027	0.770	0.251	-1.022	0.071	0.086	0.045	0.713
SmBCCP2	0.305	0.288	-0.593	-0.849	1.807	-0.957	0.027	0.025	0.074	0.515
SmACC1	1.624	-1.461	-0.163	0.432	0.864	-1.296	0.012	0.408	0.029	-0.099
SmHACPS1	1.532	-0.526	-1.006	0.560	-0.407	-0.153	0.054	0.047	0.155	0.906
SmACP7	1.099	2.835	-3.933	0.694	2.342	-3.036	0.081	0.029	0.224	0.999
SmACP8	2.661	-1.387	-1.273	1.558	-0.533	-1.026	0.034	0.023	0.031	0.979
SmACP1	1.625	-0.542	-1.083	0.023	0.837	-0.860	0.040	0.057	0.073	0.211
SmMCMT1	2.159	-1.290	-0.869	0.604	0.075	-0.680	0.089	0.217	0.071	0.740
SmKASIII2	0.595	-0.835	0.240	0.254	1.157	-1.412	0.020	0.024	0.068	-0.594
SmKASIII1	0.877	-1.862	0.985	-0.489	0.799	-0.309	0.030	0.266	0.040	-0.987
SmKAR1	2.382	-1.092	-1.290	0.637	1.023	-1.660	0.028	0.018	0.024	0.424
SmHAD1	2.328	-0.699	-1.630	0.638	0.297	-0.935	0.038	0.021	0.010	0.818
SmENR2	0.673	2.626	-3.299	-0.028	2.508	-2.479	0.143	0.104	0.010	0.979
SmENR3	1.136	0.214	-1.350	0.718	0.574	-1.292	0.326	0.120	0.094	0.952
SmENR1	2.809	-1.818	-0.991	1.283	-0.405	-0.879	0.329	0.586	0.114	0.929
SmKASI2	3.603	-0.099	-3.504	2.077	-0.575	-1.502	0.100	0.013	0.052	0.970
SmKASI1	1.836	-0.964	-0.872	0.323	0.641	-0.964	0.015	0.032	0.023	0.302

SmLS1	1.558	-0.579	-0.979	-0.379	1.694	-1.315	0.065	0.138	0.177	-0.067
SmLT1	1.017	-0.772	-0.245	0.128	-0.298	0.170	0.589	0.250	0.208	0.669
SmFATa1	1.177	0.421	-1.598	0.025	1.338	-1.363	0.293	0.417	0.569	0.715
SmFATb1	2.295	-1.290	-1.006	0.711	0.013	-0.723	0.093	0.095	0.130	0.820
SmKASII1	1.367	-0.904	-0.462	-0.142	0.931	-0.789	0.198	0.094	0.219	-0.321
SmSAD1	-0.023	1.435	-1.411	-0.497	2.201	-1.704	0.061	0.044	0.083	0.980
SmLACS6	2.493	-0.265	-2.229	1.927	-0.260	-1.667	0.209	0.118	0.313	1.000
SmLACS7	4.022	1.344	-5.366	2.113	1.733	-3.846	0.154	0.090	0.098	0.975
SmLACS2	-0.084	0.748	-0.664	-0.566	1.357	-0.791	0.236	0.116	0.311	0.948
SmLACS1	3.653	-5.852	2.199	0.119	-0.360	0.241	0.157	0.092	0.195	0.944
SmLACS4	2.231	-0.473	-1.758	3.202	-2.147	-1.055	0.180	0.214	0.415	0.870
SmABCAT2	0.418	2.121	-2.539	-0.521	2.292	-1.771	0.136	0.133	0.198	0.931
SmABCAT1	1.538	-0.658	-0.880	-0.068	-0.063	0.131	0.077	0.277	0.044	-0.588
SmLAAS1	1.649	-0.757	-0.892	0.647	0.404	-1.050	0.102	0.186	0.083	0.647
SmTGD1	0.609	0.237	-0.845	-0.065	0.676	-0.611	0.066	0.227	0.285	0.653
SmGLB1	2.323	-1.093	-1.231	1.035	-0.559	-0.476	0.071	0.053	0.113	0.997
SmWRI2	0.516	-1.286	0.769	0.895	-1.955	1.060	0.320	0.643	0.129	0.998
SmWRI5	3.433	1.024	-4.457	0.950	0.593	-1.542	0.125	0.125	0.044	0.986
SmWRI7	1.645	-0.473	-1.172	1.080	-0.088	-0.992	0.353	0.158	0.080	0.978
SmWRI8	1.716	-2.277	0.561	1.026	-0.992	-0.033	0.396	0.258	0.317	0.964
SmWRI1	1.531	-1.880	0.348	0.775	-1.513	0.737	0.285	0.385	0.190	0.945
SmWRI12	-0.199	-1.535	1.735	0.936	-2.067	1.132	0.068	0.064	0.099	0.840

#Expression level is expressed as FPKM. The log transformation uses 2 as the base.

*Normalized expression level is calculated as Ct[ACT]-Ct[X]. Here 'Ct' stands for cycle number; 'ACT' stands for Actin gene; 'X' stands for fatty acid biosynthesis genes tested in this study.