

Table S7. List of gene accessions

List of genes potentially relevant to acyl sugar chain synthesis for which gene knockdown or real-time/semi-quantitative RT-PCR analyses were performed.

Gene product	EC No.	Alias	Accession ^a		Arabidopsis comparison ^b	
			SGN-Unigene	TIGR TC/GenBank	Top hit	Gene No.
<i>Branched-chain amino acid synthesis</i>						
Acetolactate synthase	2.2.1.6	<i>SuRA</i> ^c	SGN-U213768	TC116383, TC116384	At3g48560	1
Threonine dehydratase/deaminase	4.2.1.16	<i>TD</i>	SGN-U215900	TC125347, TC130656	At3g10050	1
2-isopropylmalate synthase	2.3.3.13	<i>IPMSA</i>	SGN-U213969	AF004165 (<i>S.p.</i>), TC116845	At1g74040	4
		<i>IPMSB</i>	SGN-U232722	AF004166 (<i>S.p.</i>), TC121075	"	4
		<i>IPMSC</i>	-	CN747199 (<i>N.b.</i>), CN747285 (<i>N.b.</i>)	"	4
3-isopropylmalate dehydrogenase	1.1.1.85	<i>IPMD</i>	SGN-U216021	TC172598, TC9040 (<i>N.b.</i>)	At1g80560	5
3-isopropylmalate dehydratase (large subunit)	4.2.1.33	<i>IPDS L</i>	SGN-U217800	TC171246, EB450252 (<i>N.b.</i>)	At4g13430	4
<i>Branched-chain amino acid degradation</i>						
Branched-chain α -keto-acid dehydrogenase	2.7.11.4					
E1 alpha subunit		<i>BCKD E1-αI</i>	-	TC164675, TC166453	At1g21400	4
		<i>BCKD E1-αII</i>	-	BF097511, BE462642	At5g09300	4
		<i>BCKD E1-αII</i>	-	TC163728	At1g21400	4
E1 beta subunit		<i>BCKD E1-β</i>	SGN-U214608	TC154476	At3g13450	2
E2 subunit		<i>BCKD E2</i>	SGN-U221864	TC166484, DV161610 (<i>N.t.</i>)	At3g06850	1
<i>Fatty acid elongation</i>						
Beta-ketoacyl-ACP synthase III	2.3.1.41	<i>KAS III A</i>	SGN-U218414	TC155699	At1g62640	1
		<i>KAS III B</i>	-	AW624974	"	1
Beta-ketoacyl-ACP synthase (mitochondrial)		<i>mt KAS</i>	-	TC159806	At2g04540	1
Beta-ketoacyl-ACP synthase I		<i>KAS I A</i>	-	TC163946, AI490848	At5g46290	1
		<i>KAS I B</i>	-	TC165966, TC163947, AW036186	"	1
		<i>KAS I C</i>	-	TC168565, AW033405	"	1
		<i>KAS II A</i>	-	TC155174	At1g74960	1
Beta-ketoacyl-ACP synthase II		<i>KAS II B</i>	-	TC165868, TC158629	"	1
		<i>KAS II C</i>	-	TC167820	"	1
		<i>KAS II D</i>	-	TC168241	"	1

^aSGN-Unigene numbers correspond to those listed in the TOM2 microarray expression data (Tables S2 and S3). TIGR TC/GenBank gene accessions are from *S. lycopersicum* unless denoted otherwise: *S.p.*, *S. pennellii*; *N.b.*, *N. benthamiana* or *N.t.*, *N. tabacum*. ^bArabidopsis top hit refers to highest scoring Arabidopsis gene in a WuBLAST search using the tomato accession. Gene number refers to the number of genes in Arabidopsis sharing highest homology to a given enzyme primary sequence that was used in the blast search. ^cTOM2 probe is annotated as SuRB (Table I) but corresponds in sequence to the most up to date entry SGN-U313745, annotated as SuRA (Table II).