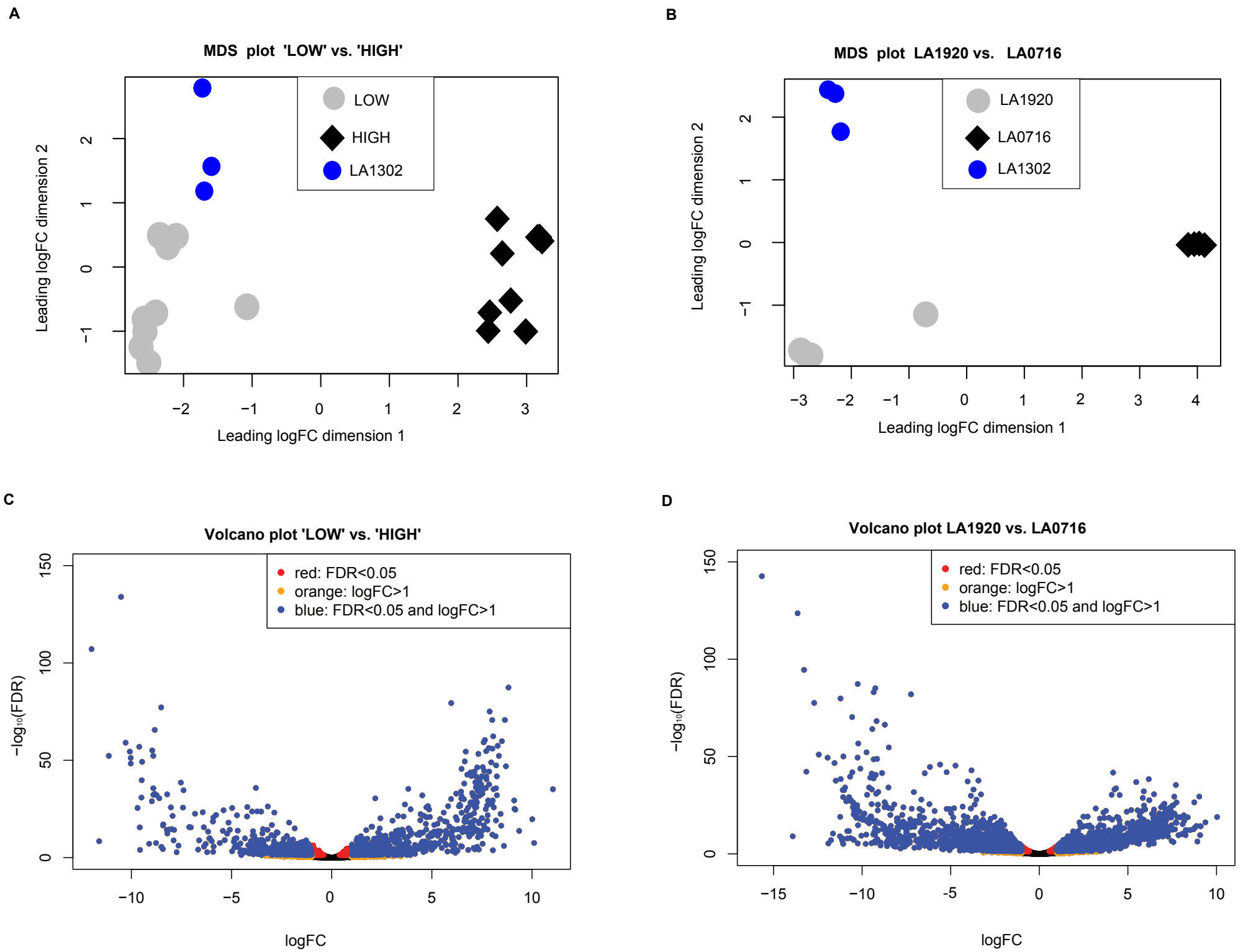


Supplemental Figure 1. Distribution of gene ontology (GO) terms associated with the 1087 common DEGs. Only top-20 most abundant categories are shown here. Abbreviations: BP= biological process; MF= molecular function; CC= cellular component.

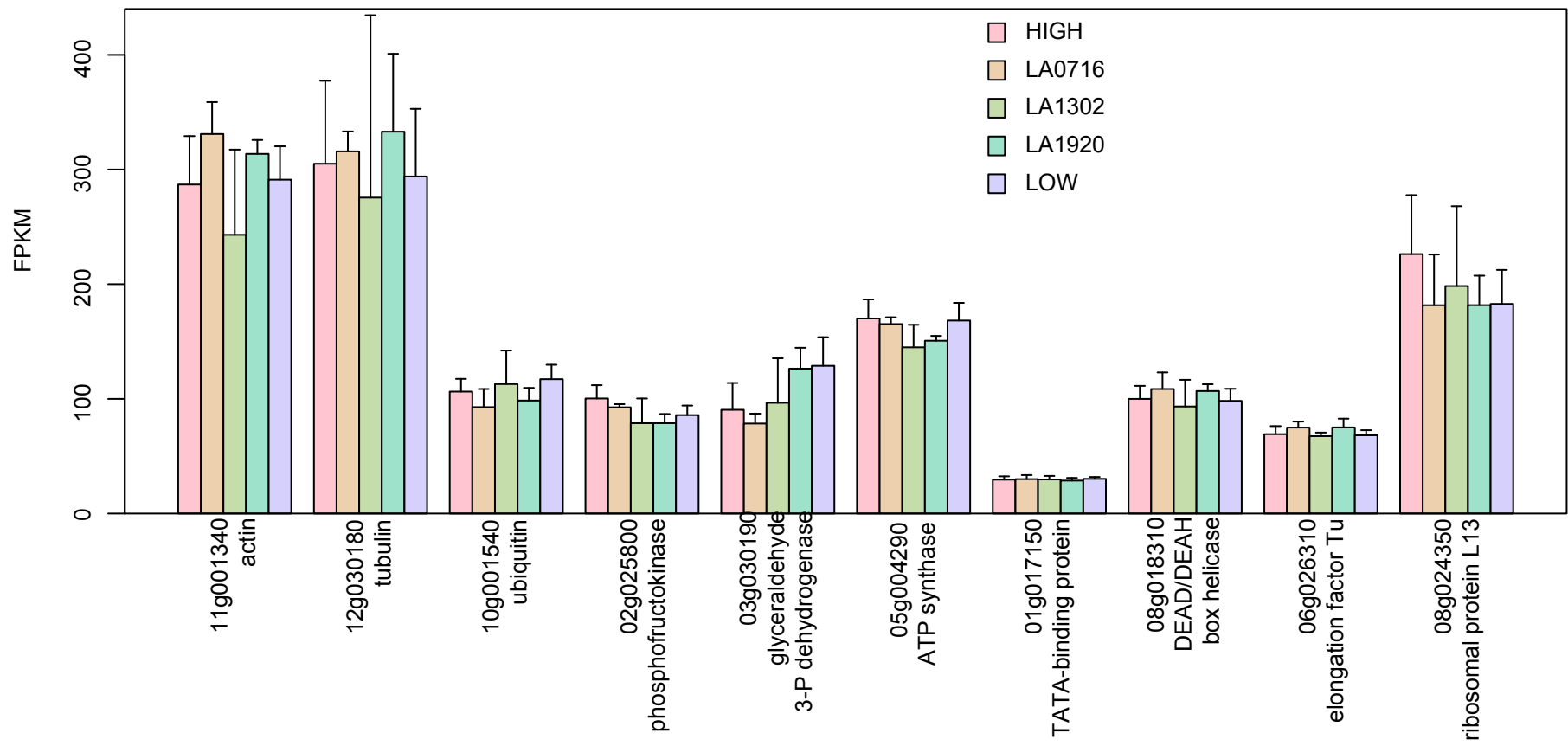


Supplemental Figure 2. Differential gene expression analyses between low- and high-acylsugar-producing accessions.

(A) and (B) Multi-dimensional scaling (MDS) plots showing 'LOW' vs. 'HIGH' comparison and LA1920 vs. LA0716 comparison, respectively. Three biological replicates of LA1302 were also included to show their gene expression profiles relative to low- and high-acylsugar-producing accessions. Distances were determined by edgeR (Robinson et al., 2010) based on expression profiles of top-500 genes differing in fold changes.

(C) and (D) Volcano plots showing 'LOW' vs. 'HIGH' comparison and LA1920 vs. LA0716 comparison, respectively. Positive logFC values indicate higher expression levels in high-acylsugar-producing accessions.

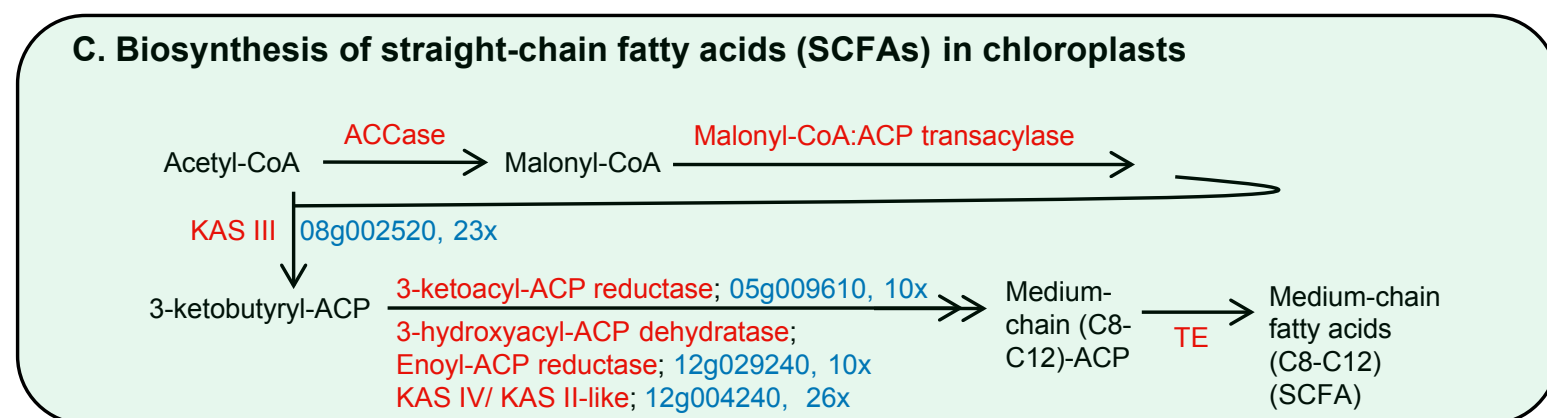
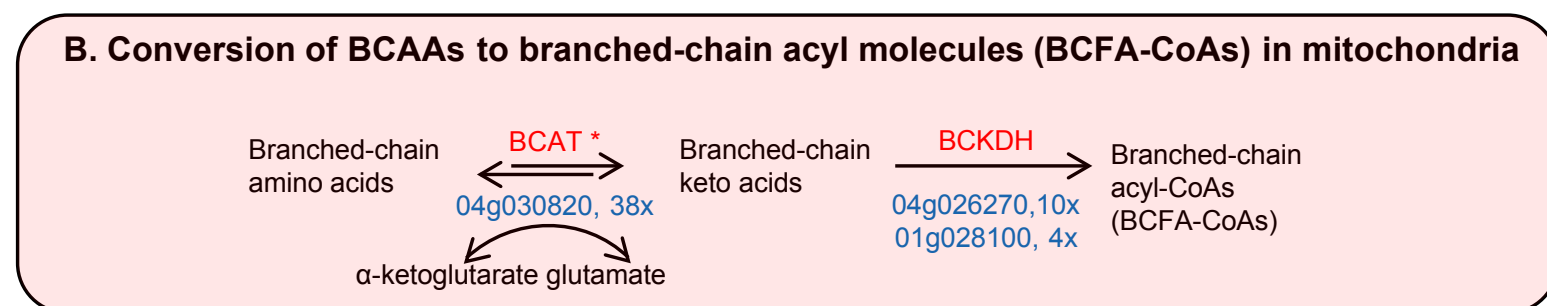
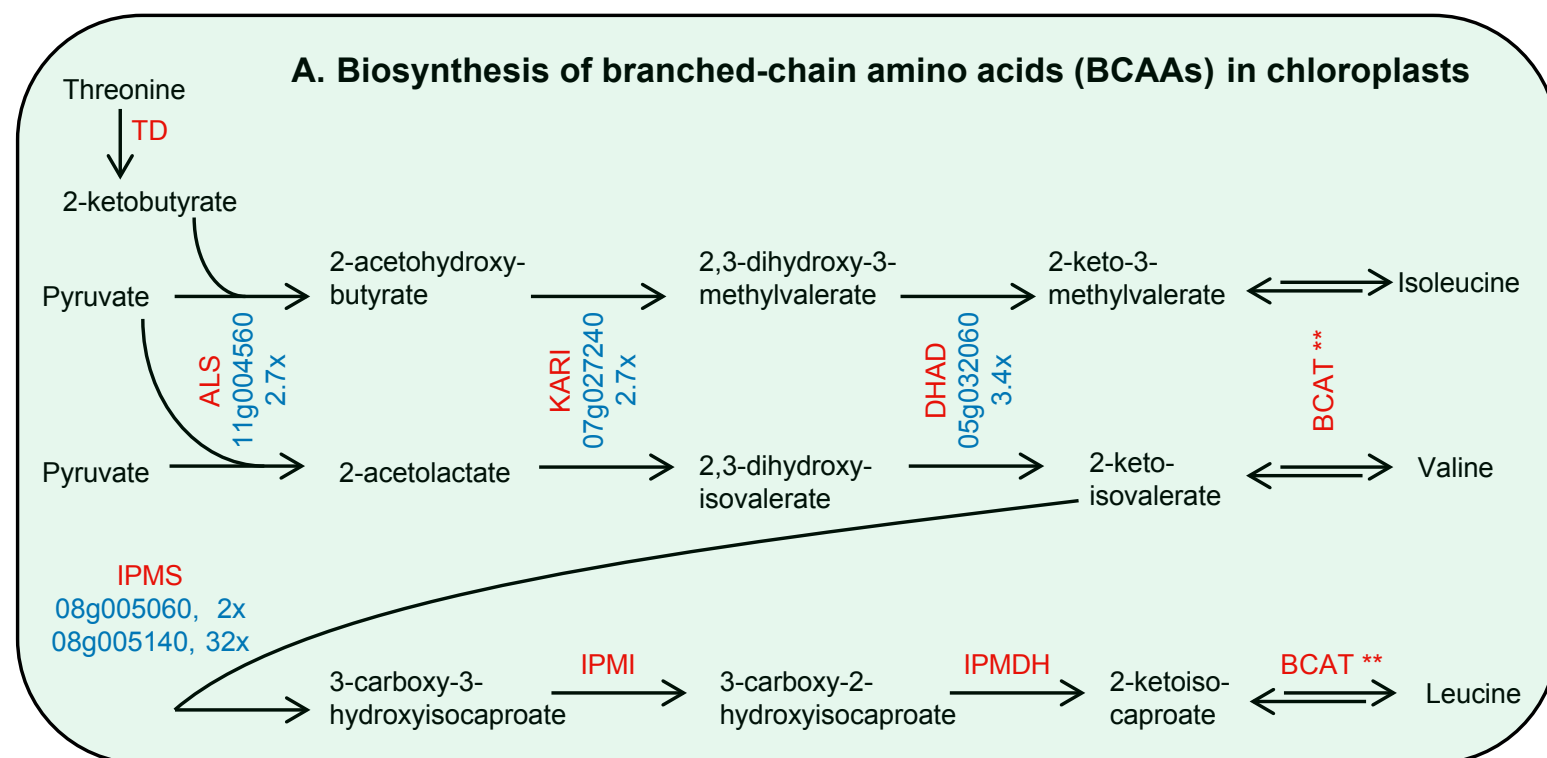
Abbreviations: FDR= false discovery rate; logFC= log₂(fold-change).



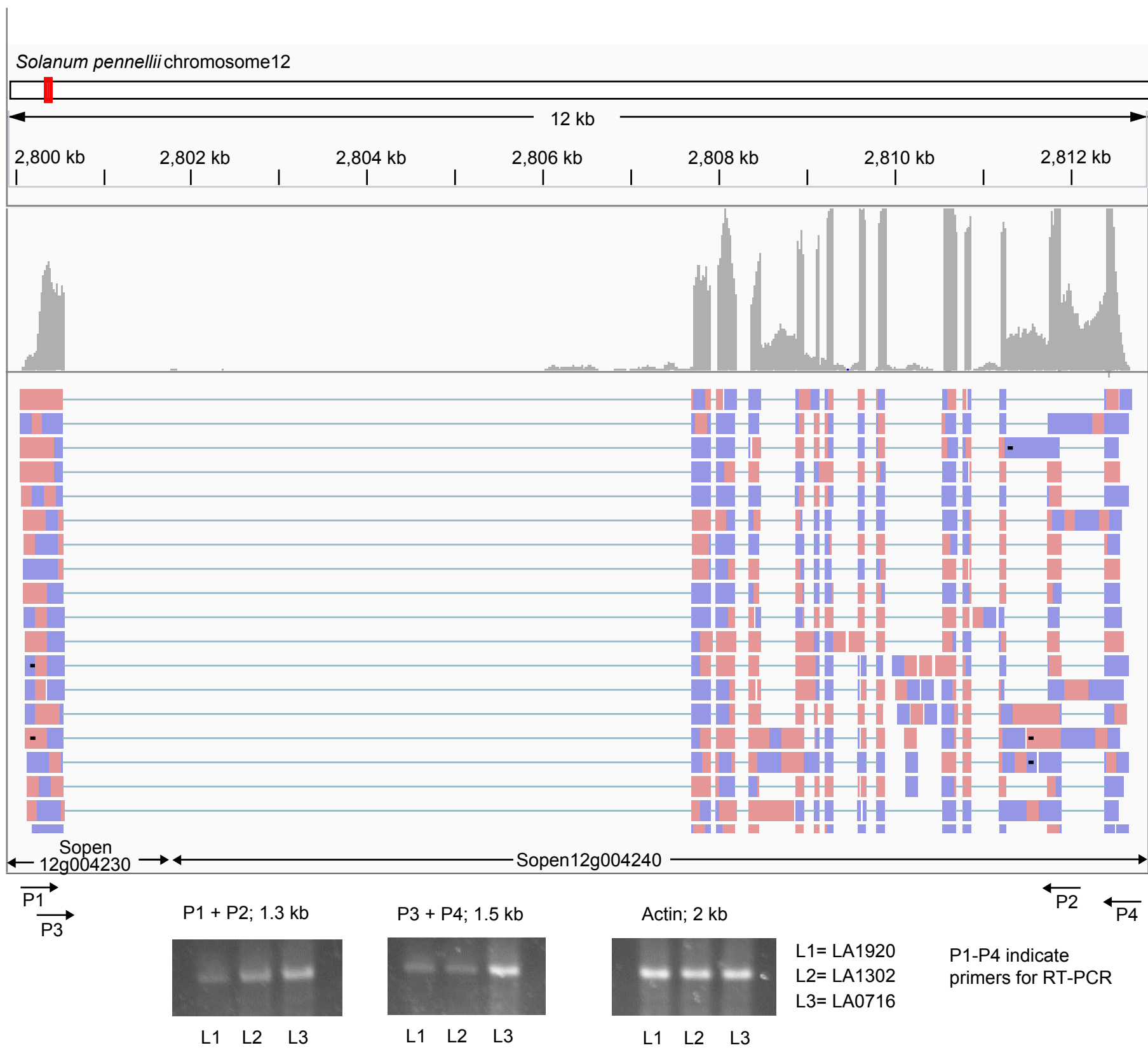
Supplemental Figure 3. Expression levels of ten selected ‘housekeeping genes’ in different biological groups.

Genes are designated by their gene identifier numbers (Sopen IDs). Error bars represent 95% confidence interval (only upper limits are shown).

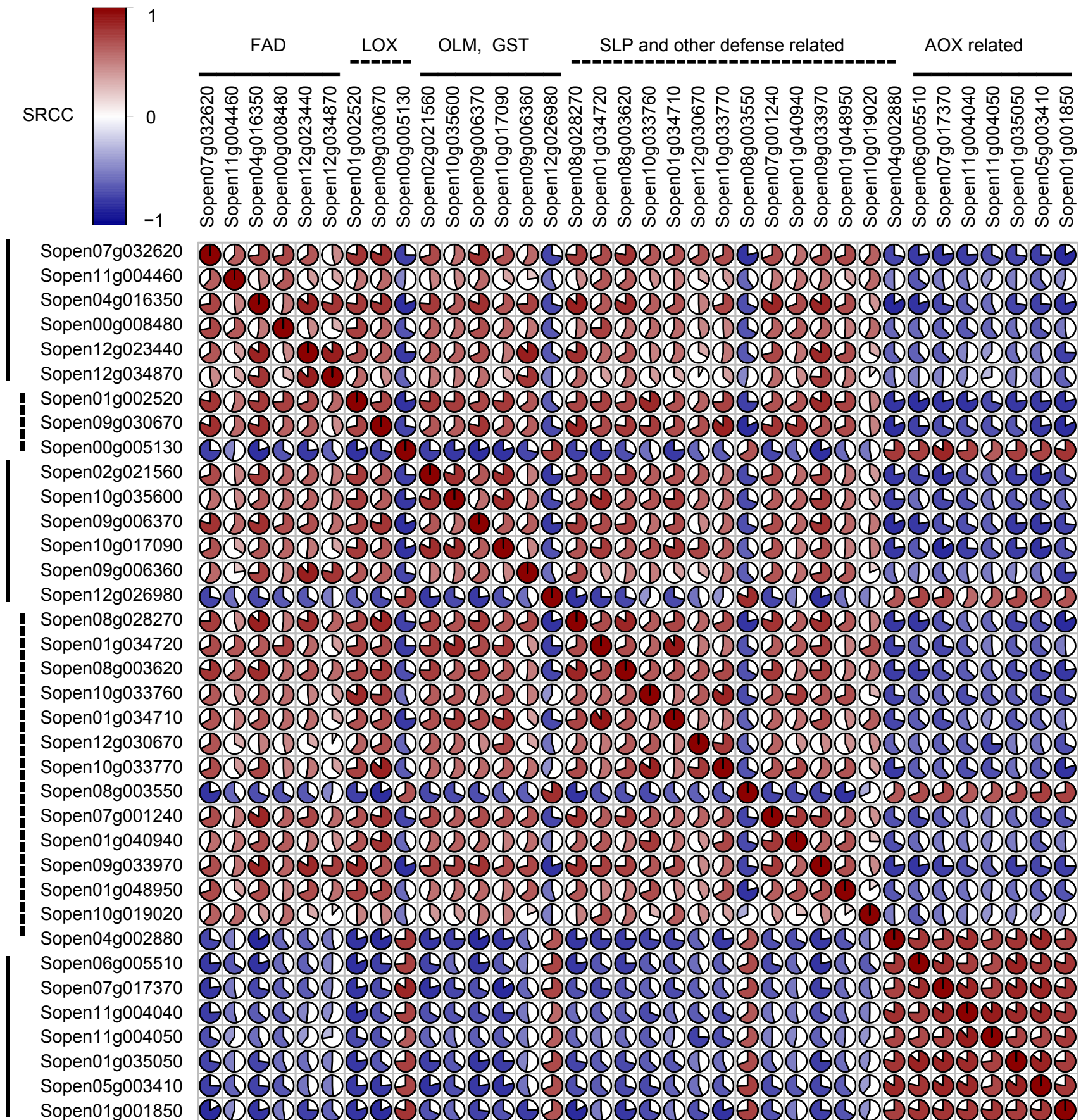
Abbreviation: FPKM= fragments per kilobase of transcript per million mapped reads.



Supplemental Figure 4. Biosynthesis of branched-chain (A and B) and straight-chain (C) acyl molecules. Enzymes are highlighted in red. Gene identifiers of differentially expressed genes (DEGs) and their fold-changes are highlighted in blue. 10x indicates 10-fold higher expression in the 'HIGH' group relative to the 'LOW' group. Significance levels associated with fold-changes of DEGs are given in Table 1. Conversion of BCAAs to branched-chain acyl molecules is initiated by a transamination reaction, which is reversibly catalyzed by branched-chain aminotransferase (BCAT; marked with an asterisk) enzymes in mitochondria. On the other hand, chloroplast BCATs (marked with double asterisk) catalyze the last step in the biosynthesis of all three BCAAs (Binder, 2010). Subcellular localization studies using GFP and complementation studies with *Escherichia coli* auxotrophic cells showed that mitochondrial BCAT-1 and BCAT-2 are involved primarily in the conversion of BCAAs to BCFA-CoAs, whereas chloroplast BCAT-3 and BCAT-4 function primarily in BCAA biosynthesis in *Solanum lycopersicum* (Maloney et al., 2010). *Sopen04g030820* was annotated as BCAT isoform-2, suggesting its role in BCFA production in mitochondria, rather than in BCAA biosynthesis in chloroplasts. Abbreviations: TD= threonine dehydratase; ALS= acetolactate synthase; KARI= ketol-acid reductoisomerase; DHAD= dihydroxy-acid dehydratase; IPMS= isopropylmalate synthase; IPMI= isopropylmalate isomerase; IPMDH= isopropylmalate dehydrogenase; BCAT= branched-chain aminotransferase; BCKDH= branched-chain keto acid dehydrogenase; ACCase= acetyl-CoA carboxylase; KAS= beta-ketoacyl-ACP synthase; TE= thioesterase; ACP= acyl carrier protein.

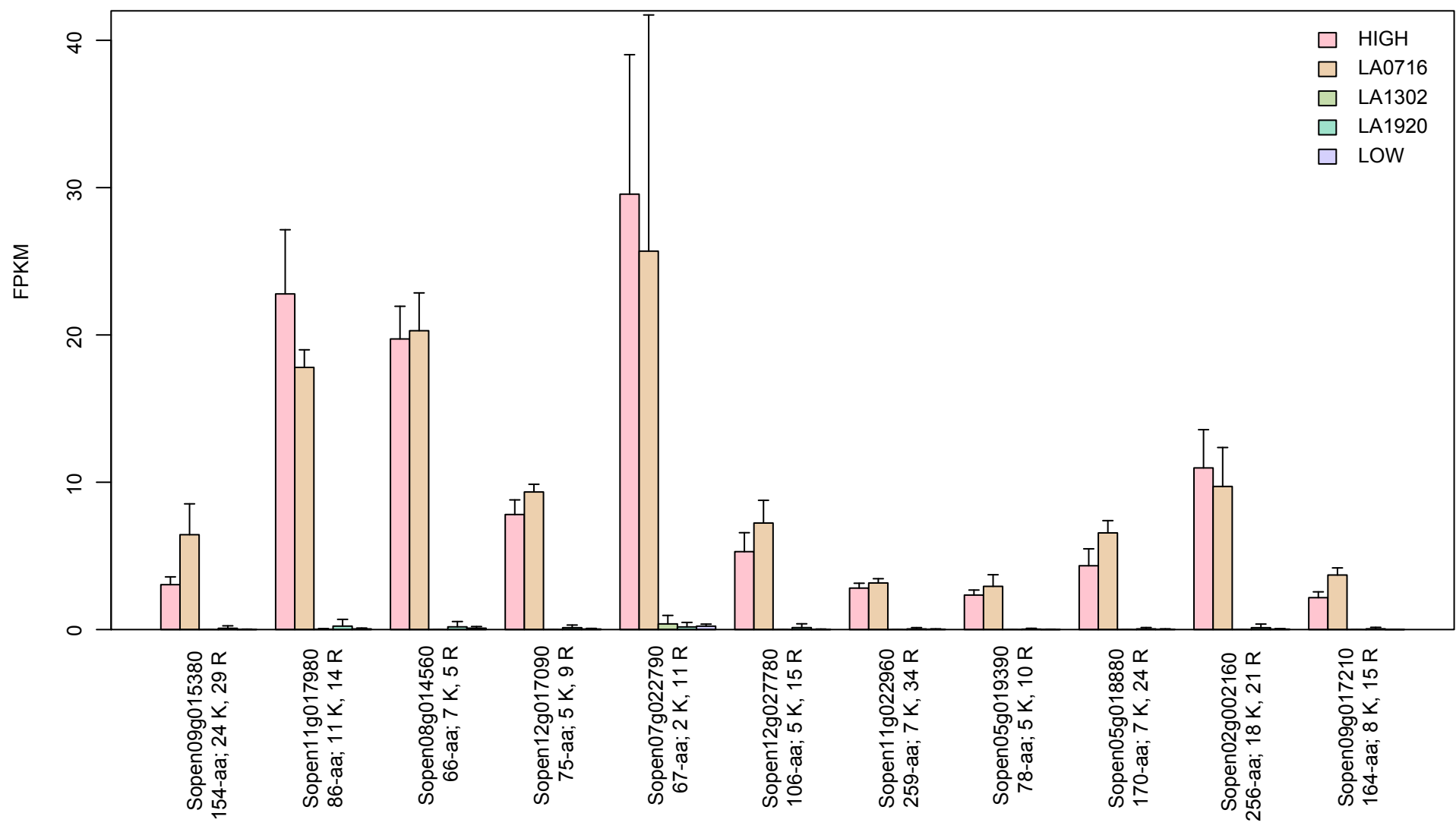


Supplemental Figure 5. Single transcript produced by the locus containing Sopen12g004230-Sopen12g004240. Integrated Genome Viewer (Thorvaldsdottir et al., 2013) was used to visualize RNA-Seq reads mapped to *S. pennellii* chromosome 12 locus containing *Sopen12g004230-Sopen12g004240*. Arrows labeled P1-P4 indicate primers for RT-PCR.

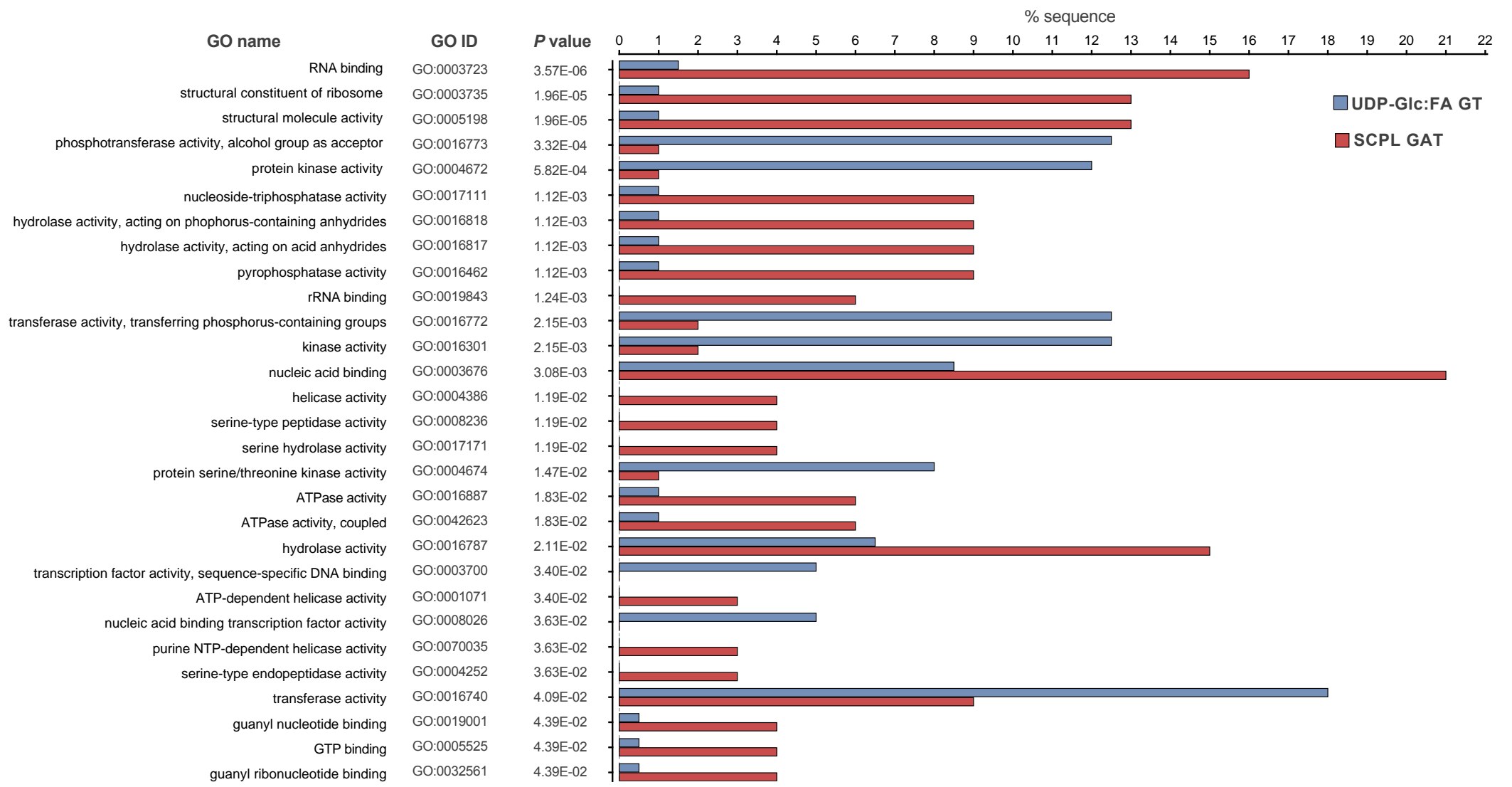


Supplemental Figure 6. Correlation among expression profiles of putative defense genes. Expression profiles (FPKM values) for each of 36 genes (from Table 4) in our 29 samples were used to determine pairwise Spearman's rank correlation coefficient (SRCC).

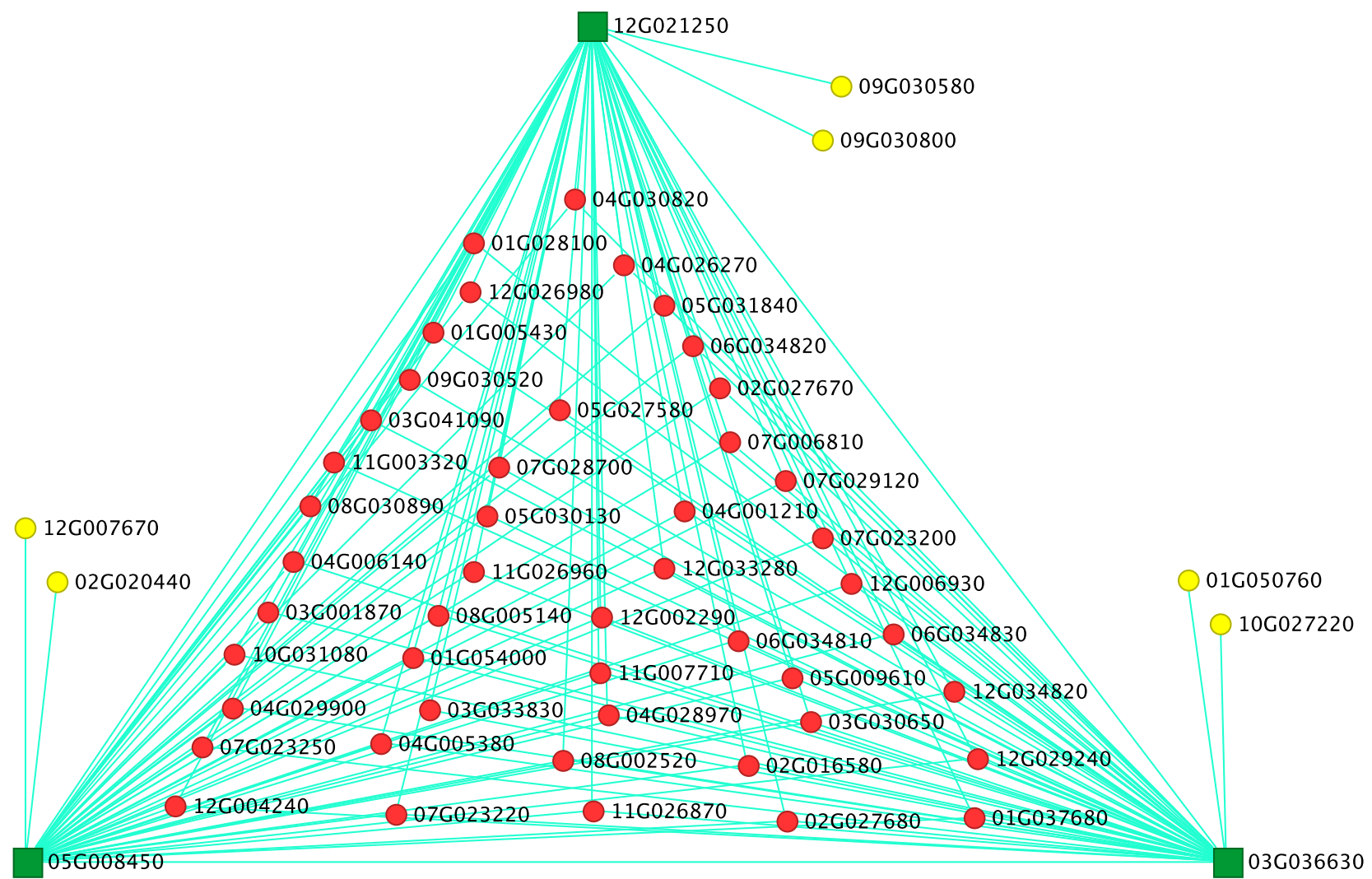
Abbreviations: FAD= fatty acid desaturase; LOX= lipoxygenase; OLM= oxylipin metabolism; GST= glutathione S-transferase; SLP= subtilisin-like protease; AOX= amine oxidase.



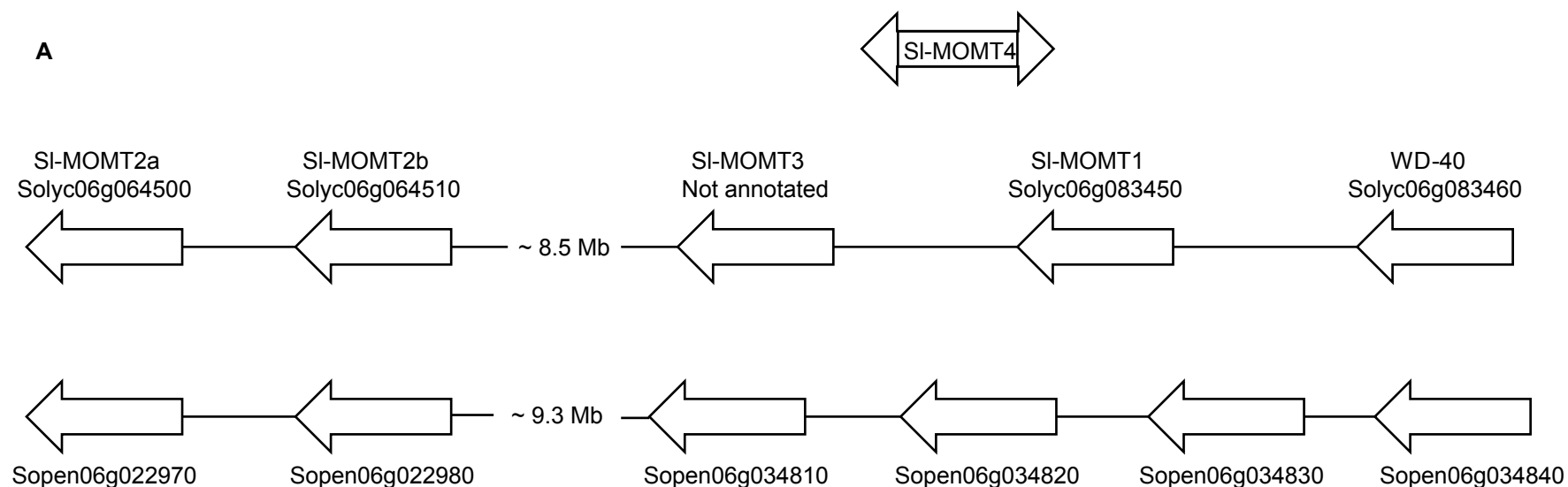
Supplemental Figure 7. Lys and Arg content of selected proteins encoded by genes co-expressed with *Sopen11g004040* (FLOWERING LOCUS D; amine oxidase domain). Gene expression levels are represented as fragments per kilobase of transcript per million mapped reads (FPKM).



Supplemental Figure 8. Full list of enriched gene ontology (GO) terms associated with genes strongly correlated with the UDP-Glc:FA GT and the SCPL GAT.



Supplemental Figure 9. Top-50 most strongly connected genes for each of the three AP2-family transcription factor genes. Intramodular connectivity strengths were determined by weighted gene correlation network analysis (WGCNA). Green squares represent AP2-family transcription factor genes. Red circles represent genes connected to all three AP2-family transcription factor genes. Yellow circles represent genes connected to only one of three AP2-family transcription factor genes.



B

Gene	'LOW' vs. 'HIGH'		LA1920 vs. LA0716		Imazapyr 0.1 mM		Imazapyr 1 mM		Annotation
	Log ₂ FC	FDR	Log ₂ FC	FDR	Log ₂ FC	FDR	Log ₂ FC	FDR	
Sopen06g022970	1.10	1.20E-01	-1.63	1.20E-02	-0.57	4.82E-01	-2.70	6.63E-05	O-methyltransferase
Sopen06g022980	Low expression levels				-1.61	9.31E-02	-2.80	6.87E-04	O-methyltransferase
Sopen06g034810	7.02	5.70E-18	5.14	7.79E-15	-1.61	1.27E-02	-5.32	1.59E-14	O-methyltransferase
Sopen06g034820	6.06	1.23E-09	5.04	6.55E-09	-1.72	5.07E-03	-6.29	3.80E-18	O-methyltransferase
Sopen06g034830	5.71	1.91E-12	4.43	1.55E-05	-2.58	4.54E-04	-8.38	1.36E-15	O-methyltransferase
Sopen06g034840	0.33	1.47E-01	0.45	1.77E-01	-0.25	4.73E-01	0.54	3.57E-02	WD domain repeat

Supplemental Figure 10. Selected O-methyltransferase genes on chromosome 6 involved in flavonoid metabolism in *S. pennellii* and *S. lycopersicum*.

(A) Homologous regions in *S. lycopersicum* and *S. pennellii* containing MOMT (myricetin O-methyltransferase) genes. SI-MOMT4 is not present in *S. lycopersicum* Heinz 1706 reference genome; in M82 cultivar, SI-MOMT4 is located near SI-MOMT1, but not directly adjacent to SI-MOMT1 (Kim et al., 2014).

(B) Differential expression of O-methyltransferase genes in low- and high-acylsugar-producing accessions. Effect of imazapyr treatment on expression levels of these genes in accession LA0716 is also shown.

Abbreviations: FDR= false discovery rate; logFC= log₂(fold-change).

Accession	% LDW	Std. Dev.
LA1911	0.45	0.09
LA1912	0.69	0.13
LA1920	0.55	0.23
LA1926	0.65	0.17
LA1302	5.62	0.96
LA1941	12.21	0.63
LA1946	12.57	0.35
LA0716	13.92	0.43

Supplemental Table 1. Amount of total acylsugars produced by different accessions of *Solanum pennellii*. Amounts are represented as mean percentage of leaf dry weight (% LDW) from 10-week-old plants (n=8).

Biological group	Accession_replicate	Input reads (paired-end)	Left reads mapped	% Left reads mapped	Right reads mapped	% Right reads mapped	Aligned pairs	Multiple alignments	% Multiple alignments
LOW	LA1911_1	28076632 x2	25670656	91.43	25460139	90.68	24479209	1402216	5.73
LOW	LA1911_2	25897024 x2	23979058	92.59	23833753	92.03	22916745	1357221	5.92
LOW	LA1911_3	23381377 x2	21606735	92.41	21468199	91.82	20477277	1280584	6.25
LOW	LA1912_1	26513055 x2	24446188	92.20	24223469	91.36	23238773	1384616	5.96
LOW	LA1912_2	27459168 x2	25464977	92.74	25350740	92.32	24300336	1532525	6.31
LOW	LA1912_3	27197768 x2	25230181	92.77	25091449	92.26	24040708	1411414	5.87
LOW	LA1926_1	24579536 x2	22652595	92.16	22408034	91.17	21458492	1302270	6.07
LOW	LA1926_2	25068349 x2	23131746	92.27	22993018	91.72	22011845	1398082	6.35
LOW	LA1926_3	24724627 x2	22833110	92.35	22734307	91.95	21738682	1205420	5.55
HIGH	LA1941_1	12288246 x2	11502460	93.61	11432671	93.04	11179476	540316	4.83
HIGH	LA1941_2	26080846 x2	24793307	95.06	24642137	94.48	23941692	1517300	6.34
HIGH	LA1941_3	26040582 x2	24769968	95.12	24691874	94.82	23981049	1525979	6.36
HIGH	LA1946_1	24173944 x2	22771758	94.20	22569746	93.36	21959695	1286378	5.86
HIGH	LA1946_2	31780978 x2	30153635	94.88	29916301	94.13	29036842	2017167	6.95
HIGH	LA1946_3	29730066 x2	28193764	94.83	28075357	94.43	27248926	1671475	6.13
HIGH	LA0716_1	30522535 x2	29677629	97.23	29484523	96.60	29001962	1728181	5.96
HIGH	LA0716_2	33592217 x2	32412058	96.49	32213141	95.89	31522686	2192129	6.95
HIGH	LA0716_3	28833828 x2	28017182	97.17	27920559	96.83	27454445	1630720	5.94
MEDIUM	LA1302_1	22253612 x2	20010595	89.92	19866310	89.27	19017544	1106004	5.82
MEDIUM	LA1302_2	26994304 x2	24817574	91.94	24703973	91.52	23593535	1699083	7.20
MEDIUM	LA1302_3	26601942 x2	24436183	91.86	24316523	91.41	23197918	1482818	6.39
LA1920	LA1920_1	25852990 x2	23916352	92.51	23823834	92.15	22843819	2579519	11.29
LA1920	LA1920_2	27558000 x2	25525014	92.62	25367999	92.05	24316564	1595845	6.56
LA1920	LA1920_3	41277779 x2	38095756	92.29	38002335	92.06	36328058	2266688	6.24
LA1920	LA1920_4	52957983 x2	48942356	92.42	48714958	91.99	46652941	2998256	6.43
LA0716	LA0716_1	28097123 x2	27323686	97.25	27106013	96.47	26656972	1530910	5.74
LA0716	LA0716_2	26072342 x2	24860684	95.35	24722176	94.82	24324913	1749564	7.19
LA0716	LA0716_3	48846961 x2	47425319	97.09	47182276	96.59	46348049	2595647	5.60
LA0716	LA0716_4	54976879 x2	53381600	97.10	53172897	96.72	52208391	3057741	5.86

Supplemental Table 2. Read-mapping (TopHat2 alignment) results with different accessions of *S. pennellii*. TopHat2 was used for mapping reads to *S. pennellii* genome. Input reads indicate paired-end reads (x2) that passed quality-filtering process.

			Sopen12g001230				Sopen12g001240			
GenBank accession	Cuphea species	Enzyme (length)	% Coverage	% Identity	% Similarity	E-value	% Coverage	% Identity	% Similarity	E-value
AF060518	<i>C. pulcherrima</i>	KAS IV (545-aa)	12	24	43	1.0	82	83	92	0.0
AF060519	<i>C. hookeriana</i>	KAS IV (533-aa)	3	50	80	0.3	90	77	87	0.0
U67317	<i>C. wrightii</i>	KAS II (540-aa)	13	47	58	4.1	86	82	90	0.0
U67316	<i>C. wrightii</i>	KAS II (517-aa)	11	22	43	3.0	85	82	90	0.0
AJ344250	<i>C. lanceolata</i>	KAS IV (538-aa)	7	36	54	4.7	83	81	89	0.0

Supplemental Table 3. Sequence similarity between *Cuphea* KAS IV/ KAS II-like enzymes and Sopen12g004230-Sopen12g004240. Amino acid sequences of KAV IV/KAS II-like enzymes from five *Cuphea* species were obtained, and BLASTp was used for determining sequence similarity.

Gene	Annotation / domain	Module	GS_FLD	P_GS_FLD
Sopen11g004040	Flowering locus D (flavin containing amine oxidoreductase)	turquoise	1.000	8.38E-209
Sopen11g004050	Flowering locus D (flavin containing amine oxidoreductase)	turquoise	0.881	2.93E-10
Sopen05g003400	F-box associated	turquoise	0.930	2.89E-13
Sopen01g020690	Leucine rich repeat	turquoise	0.908	1.12E-11
Sopen02g027300	PDZ domain	turquoise	0.898	3.87E-11
Sopen12g009260	Exostosin family	turquoise	0.895	5.90E-11
Sopen05g008030	Protein tyrosine kinase	turquoise	0.890	1.03E-10
Sopen08g003240	Myb-like DNA-binding domain	turquoise	0.877	4.49E-10
Sopen11g004020	F-box domain	turquoise	0.868	1.04E-09
Sopen09g023850	hAT family C-terminal dimerization region	turquoise	0.866	1.33E-09
Sopen11g019590	BED zinc finger	turquoise	0.863	1.67E-09
Sopen08g014860	NB-ARC domain	turquoise	0.849	5.99E-09
Sopen07g017370	Copper amine oxidase, enzyme domain	turquoise	0.849	6.10E-09
Sopen01g037050	WD domain, G-beta repeat	turquoise	0.841	1.15E-08
Sopen05g003410	Extensin-like	turquoise	0.838	1.36E-08
Sopen08g003250	Exostosin family	turquoise	0.830	2.50E-08
Sopen01g035050	Molybdopterin-binding domain of aldehyde dehydrogenase	turquoise	0.828	2.91E-08
Sopen03g012060	Protein of unknown function (DUF3754)	turquoise	0.825	3.79E-08
Sopen03g021480	Ras family	turquoise	0.823	4.29E-08

Supplemental Table 4. Selected genes strongly correlated with *Sopen11g004040* (FLOWERING LOCUS D; amine oxidase domain). GS_FLD indicates gene significance (GS) of a gene with expression profile of *Sopen11g004040*. P_GS_FLD indicates *P* value associated with GS_FLD.

Gene	Annotation / domain	Module color	GS	P value
Signal recognition particles				
Sopen01g037350	SRP54-type protein, GTPase domain	green	0.761	1.64E-06
Sopen09g004690	SRP54-type protein, GTPase domain	green	0.757	1.99E-06
RNA binding domain				
Sopen11g003080	RNA recognition motif	green	0.757	1.99E-06
Sopen09g005950	RNA recognition motif	green	0.755	2.20E-06
Sopen09g002690	RNA recognition motif	green	0.737	5.02E-06
Ribosomal proteins				
Sopen01g023660	Ribosomal protein S6	green	0.832	2.22E-08
Sopen02g022830	Ribosomal protein S5, C-terminal domain	green	0.802	1.64E-07
Sopen04g033370	Ribosomal protein S9/S16	green	0.802	1.69E-07
Sopen02g017200	Ribosomal protein S21	green	0.739	4.70E-06
Sopen07g030180	Ribosomal protein L4/L1 family	green	0.755	2.25E-06
Sopen01g025250	Ribosomal protein L34	green	0.744	3.75E-06
Sopen06g017110	Ribosomal protein L3	green	0.753	2.41E-06
Sopen08g026520	Ribosomal protein L19	green	0.772	9.16E-07
Sopen05g005170	Ribosomal protein L18e/L15	green	0.746	3.43E-06
Sopen06g034110	Ribosomal protein L17	green	0.733	6.12E-06
Sopen09g033320	Ribosomal L28 family	green	0.73	7.11E-06
Translation process related				
Sopen12g033130	Translation initiation factor 1A / IF-1	green	0.778	6.85E-07
Sopen06g028080	Elongation factor Tu GTP binding domain	green	0.814	7.95E-08
Sopen07g007510	Elongation factor TS	green	0.741	4.30E-06
Sopen02g022200	50S ribosome-binding GTPase	green	0.755	2.20E-06
Sopen05g033080	tRNA synthetases class I (M)	green	0.764	1.45E-06
Sopen08g006220	Putative tRNA binding domain	green	0.843	9.65E-09
Sopen01g035990	Glycyl-tRNA synthetase beta subunit	green	0.751	2.72E-06

Supplemental Table 5. Selected genes in WGCNA 'green' module showing strong correlation with the SCPL GAT. GS indicates gene significance.

Gene	Annotation / domain	Module color	GS	P val
Ten selected housekeeping genes				
Sopen11g001340	Actin	yellow	-0.251	0.1895
Sopen12g030180	Tubulin/FtsZ family, GTPase domain	greenyellow	0.036	0.8531
Sopen10g001540	Ubiquitin family	green	0.471	0.0098
Sopen02g025800	Phosphofructokinase	cyan	0.321	0.0899
Sopen03g030190	Glyceraldehyde 3-phosphate dehydrogenase	purple	-0.129	0.5046
Sopen05g004290	ATP synthase alpha/beta family	cyan	0.369	0.0489
Sopen01g017150	TATA-binding protein, TBP (TFIID)	grey	-0.06	0.7587
Sopen08g018310	DEAD/DEAH box helicase	yellow	-0.104	0.5916
Sopen06g026310	Elongation factor Tu GTP binding domain	brown	-0.047	0.8095
Sopen08g024350	Ribosomal protein L13e	cyan	0.312	0.0991
Signal recognition particles				
Sopen06g018440	Signal recognition particle 14kD protein	pink	0.223	0.2446
Sopen12g034450	Signal recognition particle 9 kDa protein	pink	0.203	0.291
Sopen03g031530	Signal recognition particle receptor beta subunit	brown	-0.053	0.786
Sopen11g019580	Signal recognition particle receptor beta subunit	pink	-0.061	0.7529
Sopen12g004860	Signal recognition particle, alpha subunit	brown	-0.466	0.0108
Sopen08g030970	SRP19 protein	pink	0.326	0.0848
Sopen07g004220	SRP40, C-terminal domain	pink	0.412	0.0264
Sopen03g035740	SRP54-type protein, GTPase domain	black	-0.003	0.9858
Sopen12g021920	SRP54-type protein, GTPase domain	brown	-0.461	0.0118
Sopen11g024250	SRP72 RNA-binding domain	turquoise	0.097	0.6165
Translation initiation factors and elongation actors				
Sopen05g028630	Translation initiation factor 1A / IF-1	grey	0.47	0.0101
Sopen05g030710	Translation initiation factor 1A / IF-1	pink	0.185	0.3361
Sopen03g025590	Translation initiation factor 1A / IF-1	turquoise	-0.014	0.9434
Sopen12g034140	Elongation factor Tu GTP binding domain	cyan	-0.074	0.7033
Sopen03g015600	Elongation factor Tu GTP binding domain	blue	-0.062	0.7491
Sopen01g028310	Elongation factor Tu GTP binding domain	turquoise	0.044	0.8213
Sopen06g001040	Elongation factor Tu GTP binding domain	cyan	-0.015	0.9373
Sopen12g006600	Elongation factor TS	pink	0.22	0.2511
Ribosomal protein S6 family				
Sopen08g030910	Ribosomal protein S6	green	0.647	0.0001
Sopen05g033450	Ribosomal protein S6	cyan	0.39	0.0364
Sopen02g029090	Ribosomal protein S6	turquoise	-0.073	0.707
Sopen08g022890	Ribosomal protein S6e	cyan	0.497	0.0061
Sopen12g032160	Ribosomal protein S6e	cyan	0.298	0.1164
Ribosomal protein S5 family				
Sopen11g004490	Ribosomal protein S5, C-terminal domain	blue	0.316	0.095
Sopen04g029430	Ribosomal protein S5, N-terminal domain	cyan	0.421	0.023

Sopen04g026210	Ribosomal protein S5, N-terminal domain	cyan	0.258	0.177
Ribosomal protein S9/S16 family				
Sopen01g030490	Ribosomal protein S9/S16	cyan	0.349	0.064
Sopen04g014030	Ribosomal protein S9/S16	cyan	0.325	0.086
Sopen05g001690	Ribosomal protein S9/S16	cyan	0.209	0.276
Sopen10g030770	Ribosomal protein S9/S16	magenta	0.183	0.341

Supplemental Table 6. Selected housekeeping genes and translation-related genes showing correlations in gene expression profiles (GS) with the SCPL GAT. GS indicates gene significance.

Gene	Imazapyr 0.1 mM		Imazapyr 1 mM		Annotation / domain
	Log ₂ FC	FDR	Log ₂ FC	FDR	
Sopen02g020400	1.078	0.006991	4.217	4.38E-33	ABC transporter B family
Sopen03g003490	1.151	0.00018	1.901	7.16E-12	ABC transporter C family member 10-like
Sopen06g025860	1.024	0.002743	1.656	3.81E-08	ABC transporter I family
Sopen08g031080	0.421	0.226405	1.459	7.11E-08	ABC transporter F family
Sopen04g024980	0.245	0.506156	1.346	1.79E-07	ABC transporter D family
Sopen01g044530	1.200	0.185844	3.320	1.88E-07	pleiotropic drug resistance protein
Sopen06g017680	-0.301	0.383764	1.259	4.36E-07	putative ABC1 protein At2g40090
Sopen09g017780	0.470	0.126481	1.226	6.28E-07	ABC transporter B family
Sopen01g043640	0.459	0.137201	1.189	1.33E-06	ABC transporter F family
Sopen06g012460	-0.476	0.187344	1.182	1.69E-05	ABC transporter C family
Sopen06g031340	-0.063	0.89446	1.079	5.21E-05	ABC transporter F family
Sopen11g027810	0.279	0.520061	1.222	6.96E-05	ABC transporter F family
Sopen08g023990	0.260	0.656472	1.267	0.001124	ABC transporter E family
Sopen11g026980	0.007	1	1.900	0.002469	ABC transporter B family
Sopen01g047950	0.390	0.551545	1.265	0.006381	ABC transporter G family
DEGs with higher expression levels in low-acylsugar-producing accessions					
Sopen04g023150	-0.014	0.987791	-0.243	0.511372	ABC transporter F family
Sopen01g047950	0.390	0.551545	1.265	0.006381	ABC transporter G family

Supplemental Table 7. Effect of imazapyr treatment on expression levels of ABC transporter genes in LA0716. FC and FDR indicate fold-change and false discovery rate, respectively. DEGs= differentially expressed genes.

Gene	Annotation / domain	Imazapyr 0.1 mM		Imazapyr 1 mM	
		Log ₂ F _C	FDR	Log ₂ F _C	FDR
Sopen11g004040	Flowering locus D (favin containing amine oxidoreductase)	-0.256	0.647	0.235	0.581
Sopen11g004050	Flowering locus D (favin containing amine oxidoreductase)	-0.309	0.566	0.365	0.365
Sopen05g003400	F-box associated	0.726	0.134	0.582	0.159
Sopen01g020690	Leucine rich repeat	0.587	0.269	0.637	0.139
Sopen02g027300	PDZ domain	0.088	0.859	0.979	5.62E-05
Sopen12g009260	Exostosin family	-1.288	0.035	0.136	0.824
Sopen05g008030	Protein tyrosine kinase	0.199	0.665	1.390	3.12E-06
Sopen08g003240	Myb-like DNA-binding domain	-0.538	0.164	-0.352	0.292
Sopen11g004020	F-box domain	-0.039	0.956	-0.228	0.538
Sopen09g023850	hAT family C-terminal dimerisation region	0.034	0.976	-0.270	0.539
Sopen11g019590	BED zinc finger	0.604	0.295	-0.315	0.535
Sopen08g014860	NB-ARC domain	-0.117	0.873	0.149	0.758
Sopen07g017370	Copper amine oxidase, enzyme domain	0.314	0.405	1.204	1.01E-05
Sopen01g037050	WD domain, G-beta repeat	0.376	0.253	0.491	0.063
Sopen05g003410	Extensin-like	0.543	0.072	0.220	0.426
Sopen08g003250	Exostosin family	0.642	0.032	0.803	0.002
Sopen01g035050	Molybdopterin-binding domain of aldehyde dehydrogenase	-0.197	0.671	-0.041	0.917
Sopen03g012060	Protein of unknown function (DUF3754)	-0.018	0.981	0.724	0.016
Sopen03g021480	Ras family	0.202	0.656	-0.029	0.942

Supplemental Table 8. Effect of imazapyr treatment on expression levels of selected genes strongly correlated with FLOWERING LOCUS D gene *Sopen11g004040* (Supplemental Table 4 genes). FC and FDR indicate fold-change and false discovery rate, respectively.