

Supplement material

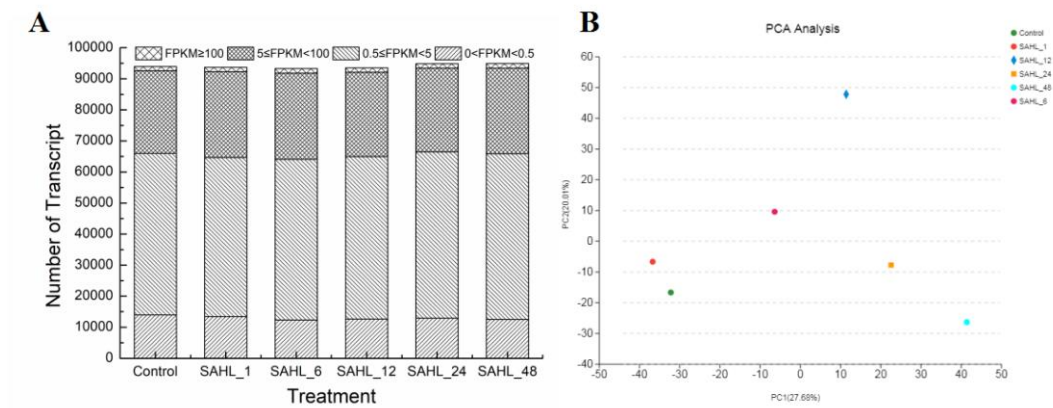


Fig. S1. Global gene expression profiling of *H. pluvialis* cells in different treatment stages. (A) Numbers of detected transcripts in each sample. (B) Principal component analysis of the RNA-Seq data.

Table S1 Changes in significantly enriched functional KEGG Pathways in *H. phuvialis* identified by KEGG pathway classification during treatment stage transitions.

Stage Transition	Change pattern	Description	Cluster Ratio %	P-value	P-adjust
SAHL_1 vs Control	up-regulated	Glyoxylate and dicarboxylate metabolism	5.44	1.79E-12	1.79E-10
		ABC transporters	5.07	6.44E-11	3.22E-09
		Nitrogen metabolism	2.81	4.85E-10	1.62E-08
		Carotenoid biosynthesis	2.63	3.03E-08	7.57E-07
		Alanine, aspartate and glutamate metabolism	3	4.35E-05	8.69 E-04
		Biosynthesis of unsaturated fatty acids	1.69	6.05E-05	1.01 E-03
		Starch and sucrose metabolism	4.32	7.75E-05	1.11 E-03
		Pyruvate metabolism	4.32	9.42E-05	1.18 E-03
		Biosynthesis of terpenoids and steroids	0.56	1.11 E-04	1.23 E-03
		Butanoate metabolism	1.88	2.35 E-04	2.35 E-03
		Arginine biosynthesis	2.06	3.93 E-04	3.57 E-03
		Tyrosine metabolism	1.69	6.04 E-04	4.65 E-03
		Peroxisome	3.38	5.78 E-04	4.82 E-03
		Caffeine metabolism	0.75	8.97 E-04	6.40 E-03
		Ubiquinone and other terpenoid-quinone biosynthesis	1.5	1.06 E-03	7.06 E-03
		Arginine and proline metabolism	2.06	2.87 E-03	0.02
		Glycolysis / Gluconeogenesis	3.19	3.18 E-03	0.02
		Citrate cycle (TCA cycle)	2.06	4.01 E-03	0.02
		Oxidative phosphorylation	3.75	8.04 E-03	0.04
		Fatty acid degradation	1.5	8.03 E-03	0.04
Porphyrin and chlorophyll metabolism	2.44	0.01	0.05		

		Propanoate metabolism	1.88	0.01	0.05
		One carbon pool by folate	1.13	0.01	0.06
		Betalain biosynthesis	0.38	0.04	0.14
		Fatty acid biosynthesis	1.5	0.03	0.15
		Tropane, piperidine and pyridine alkaloid biosynthesis	2.06	2.71E-06	2.38E-04
		Tyrosine metabolism	2.65	1.98E-05	8.72E-04
		Isoquinoline alkaloid biosynthesis	1.77	4.36E-05	1.28 E-03
		Phenylalanine metabolism	2.06	1.26E-04	2.21E-03
		Photosynthesis	3.83	1.06E-04	2.32E-03
	up-regulated	Fatty acid elongation	1.77	2.49E-04	3.66E-03
		Carbon fixation in photosynthetic organisms	2.95	6.46E-03	0.08
		beta-Alanine metabolism	1.47	0.02	0.16
		Cutin, suberine and wax biosynthesis	0.59	0.02	0.17
		AGE-RAGE signaling pathway in diabetic complications	1.47	0.03	0.24
		Vitamin B6 metabolism	0.88	0.03	0.25
		Carotenoid biosynthesis	2.94	4.49E-06	3.95 E-04
		ABC transporters	3.92	1.92 E-04	8.44 E-03
		Caffeine metabolism	0.98	2.08 E-03	0.05
		Arginine and proline metabolism	2.61	2.64 E-03	0.05
	down-regulated	Biosynthesis of terpenoids and steroids	0.65	1.80 E-03	0.05
		Purine metabolism	6.54	0.01	0.18
		Phagosome	2.61	0.02	0.23
		Other types of O-glycan biosynthesis	1.63	0.03	0.32
		Glycolysis / Gluconeogenesis	2.94	0.04	0.43
SAHL_12 vs SAHL_6	up-regulated	Glyoxylate and dicarboxylate metabolism	6.71	5.64E-11	4.85E-09

	Pyruvate metabolism	7.35	1.11E-08	4.78E-07
	Glycolysis / Gluconeogenesis	5.11	2.38E-05	6.82E-04
	Alanine, aspartate and glutamate metabolism	3.83	4.12E-05	8.85E-04
	Carbon fixation in photosynthetic organisms	4.15	7.91E-05	1.36E-03
	Citrate cycle (TCA cycle)	3.19	2.31E-04	3.32E-03
	Purine metabolism	7.35	1.87E-03	0.02
	beta-Alanine metabolism	1.92	2.42E-03	0.03
	Propanoate metabolism	2.56	3.78E-03	0.04
	Pyrimidine metabolism	4.15	0.01	0.12
	Thiamine metabolism	1.28	0.02	0.13
	Biosynthesis of unsaturated fatty acids	1.28	0.02	0.14
	Cysteine and methionine metabolism	2.56	0.02	0.15
	Arginine and proline metabolism	1.92	0.03	0.21
	Fatty acid elongation	0.96	0.05	0.28
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	ABC transporters	6.54	2.89E-10	2.63E-08
	Phenylalanine metabolism	3.27	5.86E-08	2.67E-06
	Tropane, piperidine and pyridine alkaloid biosynthesis	2.29	1.37E-06	4.16E-05
	Isoquinoline alkaloid biosynthesis	1.96	2.45E-05	5.58E-04
	beta-Alanine metabolism	2.29	3.69E-04	6.71E-03
down-regulated	Starch and sucrose metabolism	4.58	1.13E-03	0.02
	Biosynthesis of terpenoids and steroids	0.65	1.80E-03	0.02
	Carotenoid biosynthesis	1.96	1.64E-03	0.02
	Arachidonic acid metabolism	1.96	2.16E-03	0.02
	Tyrosine metabolism	1.96	2.46E-03	0.02
	Photosynthesis	2.94	7.12E-03	0.06
	Linoleic acid metabolism	0.65	0.01	0.08

		Thermogenesis	4.9	0.01	0.08
		Tryptophan metabolism	1.31	0.02	0.10
		Circadian rhythm - plant	0.98	0.02	0.10
		Phenylpropanoid biosynthesis	0.65	0.02	0.12
		Selenocompound metabolism	1.31	0.02	0.13
		Folate biosynthesis	1.63	0.03	0.15
		ABC transporters	5.73	4.39E-10	3.87E-08
		Tropane, piperidine and pyridine alkaloid biosynthesis	2.6	1.39E-09	6.12E-08
		Phenylalanine metabolism	2.86	4.55E-08	1.34E-06
		Biosynthesis of terpenoids and steroids	1.04	2.3E-07	5.07E-06
		Isoquinoline alkaloid biosynthesis	2.08	5.6E-07	9.86E-06
		Carotenoid biosynthesis	2.6	3.75E-06	5.51E-05
		Tyrosine metabolism	2.6	7.84E-06	9.85E-05
		Selenocompound metabolism	2.08	6.86E-05	7.54E-04
	up-regulated	beta-Alanine metabolism	1.82	1.40E-03	0.01
		Starch and sucrose metabolism	4.17	1.37E-03	0.01
		Plant hormone signal transduction	1.82	3.05E-03	0.02
		Photosynthesis - antenna proteins	1.82	2.86E-03	0.02
		Thermogenesis	4.69	9.33E-03	0.06
		Photosynthesis	2.34	0.03	0.16
		Oxidative phosphorylation	3.65	0.03	0.16
		Glycine, serine and threonine metabolism	2.34	0.03	0.17
		Porphyrin and chlorophyll metabolism	2.34	0.04	0.20
		Phenylalanine, tyrosine and tryptophan biosynthesis	1.3	0.04	0.21
	down-regulated	Ribosome biogenesis in eukaryotes	8.1	2.19E-12	1.93E-10
		Nitrogen metabolism	3.43	1.8E-08	7.91E-07

SAHL_24 vs SAHL_12

		Alanine, aspartate and glutamate metabolism	4.98	6.2E-08	1.82E-06
		Glyoxylate and dicarboxylate metabolism	5.3	1.35E-07	2.97E-06
		Pyruvate metabolism	4.05	5.30E-03	0.08
		Citrate cycle (TCA cycle)	2.49	4.59E-03	0.08
		Purine metabolism	6.54	0.01	0.13
		beta-Alanine metabolism	1.56	0.01	0.14
		Carbon fixation in photosynthetic organisms	2.49	0.03	0.34
		Fatty acid elongation	2.25	6.78E-05	5.49E-03
		Fructose and mannose metabolism	3	2.09E-04	8.46E-03
		Cutin, suberine and wax biosynthesis	1.12	3.92E-04	0.01
	up-regulated	Amino sugar and nucleotide sugar metabolism	3	3.65E-03	0.07
		Endocytosis	3.75	6.88E-03	0.11
		Photosynthesis	3	9.84E-03	0.13
		Carbon fixation in photosynthetic organisms	2.62	0.04	0.43
		AGE-RAGE signaling pathway in diabetic complications	1.5	0.05	0.48
SAHL_48 vs SAHL_24		ABC transporters	4.24	8.07E-07	8.07E-05
		Photosynthesis	3.13	4.74E-04	0.02
		Fatty acid elongation	1.34	1.08E-03	0.04
		Cutin, suberine and wax biosynthesis	0.67	1.76E-03	0.04
	down-regulated	Amino sugar and nucleotide sugar metabolism	2.46	3.28E-03	0.07
		Fructose and mannose metabolism	1.79	5.63E-03	0.09
		Carbon fixation in photosynthetic organisms	2.46	0.02	0.23
		AGE-RAGE signaling pathway in diabetic complications	1.34	0.03	0.34
		Oxidative phosphorylation	3.35	0.05	0.53

Table S2 Transcription factor families identified in *H. pluvialis* in this study.

TF family	Gene number	Transcript number
C3H	51	113
MYB	44	80
Nin-like	44	69
MYB_related	35	57
ERF	30	59
bZIP	25	48
GATA	22	42
SBP	21	37
AP2	20	35
bHLH	13	27
CPP	13	23
C2H2	10	15
B3	8	14
HB-other	6	8
WRKY	5	9
HSF	5	7
E2F/DP	5	6
M_type	5	5
NF-X1	3	14
Whirly	3	9
LSD	3	6
CO-like	3	5
DBB	3	5
Dof	3	4
YABBY	3	3

Table S3 Genes involved in astaxanthin and fatty acids biosynthesis pathways and their expression level of FPKM in *H. pluvialis* in this study.

Gene description	Gene_id	Contr ol	SAHL _1	SAHL _6	SAHL_ 12	SAHL_ 24	SAHL_ 48
isopentenyl pyrophosphate isomerase (IPI)	MSTRG.64143	16.9	20.79	20.5	21.62	21.28	19.76
chloroplast geranylgeranyl diphosphate synthase (GGPS)	Ch_GLEAN_10010046	4.29	8.69	5.09	8.37	7.01	4.18
	MSTRG.11757	32.78	34.16	51.19	56.92	55.54	24.34
	MSTRG.61586	33.98	39.09	38.41	33.46	48.02	35.35
	MSTRG.66739	28.92	29.7	26.85	28.66	30.79	28.33
phytoene synthase (PSY)	Ch_GLEAN_10005596	7.82	12.6	8.13	8.45	10.06	5.69
	Ch_GLEAN_10007856	53.99	57.1	67.06	60.48	65.25	60.93
	Ch_GLEAN_10007976	14.97	14.27	11.81	15.08	16.24	15.35
	Ch_GLEAN_10009230	6.39	7.09	4.95	5.16	6.68	3.21
	Ch_GLEAN_10011828	43.59	36.17	43.81	47.88	52.8	49.72
	Ch_GLEAN_10011841	29.28	26.75	30.6	29.59	34.46	29.19
	Ch_GLEAN_10011843	0	0	0.05	0.82	0	0.77
MSTRG.133	0.12	0	0.07	0	0.25	0.26	

	MSTRG.134	4.31	8.27	0	2.95	15.59	0
	MSTRG.54158	8.87	17.28	8.9	6.11	17.65	14.86
	MSTRG.61209	3.78	14.89	12.36	5.74	18.75	10.62
	MSTRG.61210	6.27	21.62	10.72	2.4	17.22	10.25
	MSTRG.61211	5.17	11.55	5.2	3.26	8.93	10.2
phytoene desaturase (PDS)	Ch_GLEAN_10001767	12.3	13.17	12.23	11.4	11.96	10.06
	Ch_GLEAN_10003923	28.77	26.38	28.29	25.71	22.11	30.37
	Ch_GLEAN_10011505	77.76	146.31	92.25	81.79	93.96	81.61
	Ch_GLEAN_10012094	15.41	18.38	16.59	21.58	21.82	24.19
	MSTRG.2769	0.77	2.89	1.81	0.44	1.42	0.21
	MSTRG.8263	53.63	194.76	91.29	56.08	103.13	84.94
	MSTRG.8264	0	0	0	0	0	0.06
chloroplast zeta-carotene desaturase (ZDS)	Ch_GLEAN_10009908	10.68	33.1	16.08	10.27	17.29	12.97
	Ch_GLEAN_10010991	16.48	50.98	22.23	15.76	25.43	17.92
	MSTRG.19044	20.26	61.47	25.01	16.11	27.91	14.47
	MSTRG.20587	0	0	1.07	0	0	1.76
	MSTRG.28397	0	0	3.25	0	0	0
	MSTRG.38225	6.63	20.95	9.9	5.54	10.52	7.48
	MSTRG.38226	18.25	64.15	25.6	17.24	26.44	20.27
lycopene beta cyclase (LCY)	Ch_GLEAN_10007045	18.21	42.14	29.67	16.09	33.94	31.73
	Ch_GLEAN_10007046	0	0	0	0.77	0.13	0.59
	Ch_GLEAN_10010036	13.86	34.24	27.58	11.37	22.41	22.25
	Ch_GLEAN_10010071	86.05	120.53	121.22	97.24	118.98	135.87
beta-carotene hydroxylase (CRTO)	Ch_GLEAN_10006000	8.04	8.18	7.18	7.79	5.18	7.97
	Ch_GLEAN_10011708	4.58	3.72	1.95	2.3	4.6	4.7
	MSTRG.66299	1.38	1.13	0.45	1	2.16	3.92
beta-carotene ketolase (BKT)	Ch_GLEAN_10009207	27.97	23.92	35.26	42.06	37.5	43.72
	Ch_GLEAN_10009310	18.22	22.77	20.87	23.85	24.09	24.2
	MSTRG.24214	0	0	0	0.36	0	0
	MSTRG.24215	0.28	1.78	0.57	1.26	1	1.42
	MSTRG.37469	1.89	10.97	7.74	4.47	9.73	7.48
	MSTRG.37470	1.61	2.85	4.12	2.42	1.68	1.95
	MSTRG.49769	1.17	2.94	2.49	1.28	2.74	2.56
	MSTRG.49770	1.33	5.5	3.01	0.83	3.04	3.06
carotenoid hydroxylase (CRTR-B)	Ch_GLEAN_10000440	0	0	0	0	0	0
	MSTRG.29170	3.45	2.25	3.26	2.5	3.39	2.43
biotin carboxylase (BC)	Ch_GLEAN_10000659	45.9	91.29	71.27	45.17	51.13	39.28
	Ch_GLEAN_10001836	2.87	6.64	8.48	7.07	6.39	8.15
	Ch_GLEAN_10004011	18.69	11.39	21.14	8.92	10.04	10.03
	Ch_GLEAN_10004721	84.8	94.24	86.8	81.01	81.02	67
	Ch_GLEAN_10006331	8.19	3.9	4.82	5.12	5.33	5.69
	Ch_GLEAN_10006501	83.2	85.72	75.98	69.41	66.29	59.38
	Ch_GLEAN_10010198	123.49	82.87	129.89	80.24	80.02	72.84
	MSTRG.10057	0	0	0	0	0	0

MSTRG.11586	35.04	39.6	26.84	36.33	35.04	34.85
MSTRG.1708	0	0.91	0	1.58	0.24	1.21
MSTRG.17869	1.03	0.26	0.94	0	1.08	1.9
MSTRG.17870	54.22	72.56	61.65	62.49	57.71	49.6
MSTRG.23960	8.41	9.63	10.96	6.92	6.76	10.12
MSTRG.25433	23.86	26.47	22.58	22.55	24.24	20.29
MSTRG.35199	10.45	9.8	9.11	9.45	11.23	9.69
MSTRG.41884	0	14.97	0	5.82	6.61	0
MSTRG.45663	51.91	51.89	36.96	45.98	47.69	42.07
MSTRG.45664	22.46	26.95	19.5	27.02	21.45	14.08
MSTRG.50807	54.37	63.22	42.87	53.3	53.2	45
MSTRG.54350	56.95	53.83	46.97	59.11	54.99	45.21
MSTRG.54351	24.7	54.93	58.64	28.09	19.96	40.1
MSTRG.5955	81.34	89.04	95.58	97.19	95.71	82.11
MSTRG.59823	7.46	4.02	7.79	4.46	4.73	3.57
MSTRG.59824	2.96	6.74	0	0	2.2	1.47
MSTRG.7199	4.41	4.08	5.28	4.24	3.18	6.87
MSTRG.7947	2.49	5.19	5.06	4.94	3.11	3.82
MSTRG.7949	0	0	4.06	0	0	0
MSTRG.7950	6.22	8.71	7.5	6.3	6.39	6.87
Ch_GLEAN_10000181	0	0	0	0	0	0
Ch_GLEAN_10000643	0	0	0	0	0	0
Ch_GLEAN_10001844	15.79	20.11	22.39	17.92	23.18	28.05
Ch_GLEAN_10002269	0	0	0	0	0	0
Ch_GLEAN_10002495	12.92	10.96	12.61	11.57	13.87	11.55
Ch_GLEAN_10002614	13.06	7.42	11.19	10.93	13	14.92
Ch_GLEAN_10002742	21.18	13.51	17.41	12.44	18.21	18.17
Ch_GLEAN_10002771	10.83	59.15	40.67	18.08	35.73	29.97
Ch_GLEAN_10002956	18.67	18.85	21.33	19.76	22.64	23.24
Ch_GLEAN_10003108	0	0.83	2.5	0.14	0	1.78
Ch_GLEAN_10003626	44.61	36.02	37.12	33.29	36.59	40.91
Ch_GLEAN_10003639	9.97	15.03	12.85	12.29	15.2	17.82
Ch_GLEAN_10003831	276.31	272.76	268.91	267.09	256.23	303.97
Ch_GLEAN_10003941	16.96	46.52	29.85	28.8	34.13	27.95
Ch_GLEAN_10004007	10.18	53.76	34.99	14.67	33.21	26.57
Ch_GLEAN_10004079	25.93	17.93	19.96	18.18	18.42	14.16
Ch_GLEAN_10004636	52.78	34.82	49.34	64.42	42.87	41.45
Ch_GLEAN_10005332	1.25	7.43	4.42	4.33	6.96	6.27
Ch_GLEAN_10005409	28.4	24.93	24.79	33.73	33.51	28.26
Ch_GLEAN_10005475	19.76	21.81	24.57	31.88	32.11	30.9
Ch_GLEAN_10005522	45.58	73.99	66.78	56.57	66.35	55.3
Ch_GLEAN_10005843	5.57	9.38	17.8	6.58	20.79	22.02
Ch_GLEAN_10005982	30.88	27.18	34.19	33.87	32.87	33.09
Ch_GLEAN_10006059	1.16	0	2.66	6.06	4.05	2.26
Ch_GLEAN_10006151	10.92	9.74	9.95	9.69	10.47	8.43
Ch_GLEAN_10006327	2.17	1.78	2.73	2.92	2.16	4.11

acyl carrier protein (ACP)

Ch_GLEAN_10006380	37.88	36.41	43.88	31.14	43.53	38.51
Ch_GLEAN_10006911	16.56	14.55	13.93	13.99	17.01	18.79
Ch_GLEAN_10006981	11.74	11.05	11.63	11.42	12.29	6.84
Ch_GLEAN_10007431	48.68	68.94	70.32	86.68	75.41	72.07
Ch_GLEAN_10007838	8.71	3.93	8.23	7.74	7.5	7.44
Ch_GLEAN_10008025	3.97	3.16	3.42	4.34	4.41	3.88
Ch_GLEAN_10008565	48.8	20.11	15.79	22.25	15.28	22.17
Ch_GLEAN_10008884	29.03	32.42	24.95	31.12	32.08	22.75
Ch_GLEAN_10009155	3.7	9.06	14.41	19.31	21.13	16.61
Ch_GLEAN_10009434	13.13	8.19	8.06	8.95	16.6	10.83
Ch_GLEAN_10010082	8.23	17.7	28.24	15.18	28.35	53.82
Ch_GLEAN_10010090	26.83	23.56	18.15	24.85	24.44	33.17
Ch_GLEAN_10010364	28.11	32.96	37.73	40.21	35.77	34.2
Ch_GLEAN_10010568	18.05	16.22	17.41	17.42	19.19	19.21
Ch_GLEAN_10010664	17.52	14.41	22.11	19.15	20.88	21.6
Ch_GLEAN_10010676	26.39	21.79	24.74	17.63	21.44	23.07
Ch_GLEAN_10010782	8.86	9.48	11.91	7.91	8.6	9.87
Ch_GLEAN_10010915	37.57	29.34	29.51	26	29.66	28.09
Ch_GLEAN_10011051	33.02	25.6	26.84	31.14	29.98	27.76
Ch_GLEAN_10011171	6.4	4.88	3.93	4.22	4.32	3.35
Ch_GLEAN_10011866	11.56	11.21	13.43	10.26	10.11	10.27
Ch_GLEAN_10012081	21.47	103.03	66.04	37.21	62.08	49.85
Ch_GLEAN_10012091	39.58	37.04	31.36	42.19	41.74	36.29
Ch_GLEAN_10012146	42.08	37.7	39.29	44.32	42.1	40.66
Ch_GLEAN_10012312	2.08	17.65	16.7	6.36	18.43	16.18
Ch_GLEAN_10012421	18.1	55.94	30.21	20.02	28.83	19.99
MSTRG.10492	7.26	8.08	9.28	6.11	11.51	9.51
MSTRG.10767	1.3	1.52	2.67	1.27	1.98	2.6
MSTRG.11053	3.27	8.89	5.56	5.91	8.3	4.83
MSTRG.12646	1.4	1.24	3.28	0.48	3.07	4.26
MSTRG.13187	0	0.05	1.14	0	0.71	1.22
MSTRG.13264	14.17	9.64	11.71	15.05	14.53	13.56
MSTRG.13664	23.81	23.14	34.55	28.68	36.6	30.4
MSTRG.14396	8.27	5.59	4.76	9.16	8.57	9.31
MSTRG.14398	38.05	21.97	30.95	38.74	25.82	26.73
MSTRG.14716	22.7	27.12	17.9	26.69	26.32	20.51
MSTRG.16143	136.17	200.36	129.47	164.84	145.32	115.14
MSTRG.17537	4.12	7.21	5.55	12.43	10.87	10.05
MSTRG.17978	0	0.14	1.2	0	0.61	0
MSTRG.18602	3.03	3.1	3.42	4.71	4.35	3.34
MSTRG.18603	0	0	0	0	0	0
MSTRG.18970	25.09	23.75	25	25.44	21.78	20.33
MSTRG.20674	0.8	0.31	0.57	1.74	0	2.07
MSTRG.2152	4.19	3.55	4.35	5.29	5.21	4.82
MSTRG.21735	0.34	0.32	0.85	0.49	0.3	0.8
MSTRG.21987	12.71	7.9	6.94	6.84	4.76	5.25

MSTRG.23195	12.87	11.98	14.07	12.14	13.14	13.84
MSTRG.24085	11.78	11.99	16.41	11.3	15.22	14.53
MSTRG.24086	16.88	22.57	31.41	18.72	22.66	22.95
MSTRG.24657	0.89	0.92	3.24	2.52	2.47	2.97
MSTRG.25051	97.45	82.93	77.89	66.12	78.49	76.51
MSTRG.25525	7.52	7.09	7.16	10.39	5.86	5.75
MSTRG.25916	1.42	1.66	1.24	1.39	1.56	1.91
MSTRG.26629	71.12	68.61	53.68	68.93	68.77	57.89
MSTRG.26630	0.06	0.06	0.2	0.13	0.19	0.31
MSTRG.29131	0.95	0.38	2.03	0.78	1.76	4.11
MSTRG.29359	10.56	10.83	11.03	13.01	11.43	10.78
MSTRG.29623	2.51	6.92	14.28	2.89	16.15	62.68
MSTRG.3005	2.23	1.66	2.05	2.1	2.38	2
MSTRG.3227	1.83	2.27	2.41	2.31	3.47	2.75
MSTRG.32760	51.92	52.37	43.34	42.07	40.22	42.01
MSTRG.33070	2.03	5.57	9.87	7.19	1.41	2.89
MSTRG.33072	1.88	1.48	1.6	2.72	2.53	3.11
MSTRG.33860	13.2	23.85	25.42	26.21	31.85	30.16
MSTRG.34844	28.77	45.79	43.03	31.88	42.67	31.75
MSTRG.3554	67.7	60.82	63.27	74.74	72.01	75.44
MSTRG.3669	13.12	11.43	12.62	11.23	11.44	8.36
MSTRG.39451	0.46	0.72	1.19	0.63	0.67	1.53
MSTRG.41629	37.6	47.73	39.13	45.17	46.07	37.97
MSTRG.41714	0	0	0	0	0	0
MSTRG.41715	9.92	8	9.93	17.79	13.96	10.42
MSTRG.41716	9.55	8.38	10.82	16.09	12.91	13.42
MSTRG.4221	8.6	8.99	10.04	9.25	9.8	9.97
MSTRG.42581	14.18	4.9	10	12.07	8.66	15.23
MSTRG.42584	0	0	0	0	0	0
MSTRG.43421	22.84	25.39	25	25.68	23.44	21.12
MSTRG.44609	64.42	66.32	60.57	89.29	82.77	58.15
MSTRG.45359	162.7 5	152.79	155.91	172.65	172.9	190.91
MSTRG.45865	1	0.67	1.24	1.16	0.35	2.12
MSTRG.46273	2.15	2.73	3.05	3.08	4.48	4.21
MSTRG.4655	1.11	0.74	0.92	0.85	1.92	2.73
MSTRG.48960	2.79	2.98	1.84	2.63	2.74	2.62
MSTRG.49066	1.1	1.61	0.72	0.82	1.91	1.44
MSTRG.49067	1.01	0.62	0.43	0.94	1.47	0.99
MSTRG.51853	0.5	0.96	2.97	1.17	2.17	8.03
MSTRG.52126	3.56	8.36	17.8	8.36	10.01	14.02
MSTRG.52498	3.29	3.41	2.59	3.97	3.55	3.86
MSTRG.53145	1.31	0.91	2.87	0	0.71	2.68
MSTRG.53148	0.55	0.43	1.72	1.43	1.63	3.15
MSTRG.53161	2.52	4.32	8.45	4.52	4.57	5.17
MSTRG.54141	24.77	36.9	38.06	26.28	40.85	30.32
MSTRG.54142	0	0	0.76	1.55	0	0.85

	MSTRG.55877	13.24	18.1	22.76	12.28	21.9	18.12
	MSTRG.56898	15.69	8.03	20.26	15.44	14.24	16.18
	MSTRG.57409	0.99	2.51	2.17	1.35	1.85	1.17
	MSTRG.57417	2.29	6.23	9.13	4.02	9.5	20.25
	MSTRG.57419	0.47	3.45	2.96	5.72	6.75	9.86
	MSTRG.57422	1.89	1.92	2.45	2.25	1.46	2.8
	MSTRG.57652	0	0	0	0	1.33	1.39
	MSTRG.59403	4.79	4.61	5.51	9.97	5.19	3.31
	MSTRG.61020	5.81	5.9	7.28	5.48	4.65	4.91
	MSTRG.61021	9.65	10.58	11.22	10.88	8.32	7.45
	MSTRG.61233	0	0	0	0	0	0
	MSTRG.61234	285.55	272.27	229.29	273.54	224.93	186.76
	MSTRG.62702	3.82	3.02	3.26	4.2	4.84	4.24
	MSTRG.63223	9.1	9.5	9.88	10.19	9.74	10.46
	MSTRG.63297	3.49	6.27	4.88	5.47	5.84	3.01
	MSTRG.63777	62.47	68.75	68.73	73.81	68.58	64.48
	MSTRG.65882	3.98	8.63	13.83	20.95	15.49	9.99
	MSTRG.66238	11	7.49	7.89	9.36	10.77	6.82
	MSTRG.66239	16.07	6.21	6.41	9.71	17.96	4.12
	MSTRG.66334	0	4.04	5.35	1.51	0.72	5.75
	MSTRG.8549	15.2	13.27	15.09	16.87	15.32	14.02
malonyl-CoA-acyl carrier protein transacylase (MCTK)	Ch_GLEAN_10006327	2.17	1.78	2.73	2.92	2.16	4.11
	Ch_GLEAN_10006911	16.56	14.55	13.93	13.99	17.01	18.79
	MSTRG.16143	136.17	200.36	129.47	164.84	145.32	115.14
	MSTRG.57652	0	0	0	0	1.33	1.39
beta-ketoacyl acyl carrier protein synthase (KAS)	Ch_GLEAN_10008884	29.03	32.42	24.95	31.12	32.08	22.75
	MSTRG.26629	71.12	68.61	53.68	68.93	68.77	57.89
	MSTRG.26630	0.06	0.06	0.2	0.13	0.19	0.31
	MSTRG.61233	0	0	0	0	0	0
	MSTRG.61234	285.55	272.27	229.29	273.54	224.93	186.76
acyl-acyl carrier protein thioesterase (FAFA)	Ch_GLEAN_10006981	11.74	11.05	11.63	11.42	12.29	6.84
	Ch_GLEAN_10012146	42.08	37.7	39.29	44.32	42.1	40.66
	MSTRG.66238	11	7.49	7.89	9.36	10.77	6.82
	MSTRG.66239	16.07	6.21	6.41	9.71	17.96	4.12
fatty acid desaturas3 (FAD)	Ch_GLEAN_10005973	15.59	20.83	11.59	7.44	15.6	13.4
	Ch_GLEAN_10008024	11.86	28.21	14.16	11.21	19.62	14.32
	MSTRG.22936	0.57	1.24	1.59	1.68	3.87	2.61
	MSTRG.22937	0	0	0	0	0	0.84
	MSTRG.35274	0.16	0.46	0.56	1.38	1.54	1.53
	MSTRG.61836	0.82	3.25	1.48	2.11	4.37	4.88
stearoyl-ACP-desaturase (SAD)	Ch_GLEAN_10011482	27.33	33.8	32.53	48.66	40.22	42.74
	MSTRG.33965	120.38	268.86	156.19	139.48	149.92	130.35
	MSTRG.33966	0	0	0.61	0	0.52	0
	MSTRG.33967	24.74	48.06	34.16	26.73	19.77	21.83

MSTRG.47563	4.02	23.52	9.88	44.86	26.77	34.58
MSTRG.5757	50.45	100.18	65.1	60.49	74.33	62.61
MSTRG.59211	50.78	108	67.41	58.19	66.96	55.95
MSTRG.59212	0	0	0	0	0	0
MSTRG.59213	0	0	0	0	0	0
MSTRG.64253	1.15	5.48	5.82	17.45	8.67	13.65

Table S4 Primers for real time RT-PCR in this study

Primer	Primer Sequence (5-3)	References
PSY-F	CGATACCAGACCTTCGACG	[4]
PSY-R	TGCCTTATAGACCACATCCAT	
PDS-F	AAGTTCAGACCCACTCAGCG	This study
PDS-R	AGTCCTCAACAATGGCCTCG	
LYC-F	TGGAGCTGCTGCTGTCCCT	[4]
LYC-R	GAAGAAGAGCGTGATGCCGA	
CRTR-BF	ACACCTCGCACTGGACCCT	[4]
CRTR-BR	GTATAGCGTGATGCCAGCC	
BKT-F	CAATCTTGTCAGCATTCCGC	[4]
BKT-R	CAGGAAGCTCATCACATCAGAT	
IPI-1-F	GCGAGCACGAAATGGACTAC	[4]
IPI-1-R	GCTGCATCATCTGCCGCA	
IPI-2-F	AGTACCTGGCGAAAAGCTG	[4]
IPI-2-R	GTTGGCCCGGATGAATAAGA	
CRTO-F	ACGTACATGCCCCACAAG	[4]
CRTO-R	CAGGTCGAAGTGGTAGCAGGT	
BC-F	CAAGAAGGTGATGATCGCCA	[31]
BC-R	GACGTGCAGCGAGTTCTTGTC	
ACP-F	CAGCTCGGCACTGACCTTG	[31]
ACP-R	CAAGGGTCAGCTCGAACTTCTC	
MCTK-F	GGTGAGGACAAGGCGGTG	[31]
MCTK-R	TCATCCTGGCCTTGAAGCTC	
KAS-F	CACCCCACTCTGAACCAGGA	[31]
KAS-R	GACCTCCAAACCCGAAGGAG	
FATA-F	AGACTCGTTCAGCGAGGAGC	[31]
FAFA-R	CATGCCACAGCATGGTTC	
SAD-F	CCGAGCCCAAGCTTCTAGTG	[31]
SAD-R	TTGCCTCCATGTAATCCCC	
FAD-F	GTAGGTCACCACGTCCAGCC	[31]
FAD-R	CTTGATAGGCATGCTGGGTGT	
Actin-F	ACCTCAGCGTTCAGCCTTGT	[31]

Actin-R TGGTCCACGACACCATCAAC
