

1. Supplemental Tables

Table S1. Primers used in this study

Primer name	Restriction enzyme	Oligo nucleotide sequence(5'-3') ^a	Function
Fad-F	<i>EcoRI</i>	<u>CCGGAATTC</u> ATGGCTTCGTCCACCGTTG	FADS15 amplification for expression in <i>S. cerevisiae</i>
Fad-R	<i>XhoI</i>	CCG <u>CTCGAGT</u> TAGTTAGCCTTGGTCTTGGCAG	
Rid-F	<i>EcoRI</i>	<u>CCGGAATTC</u> ATGTCGCCCTTGGAGC	oRiFADS17 amplification for expression in <i>S. cerevisiae</i>
Rid-R	<i>XhoI</i>	CCG <u>CTCGAGT</u> TACTGGTTCTTCTCCTTCTGG	
T7	-	TAATACGACTCACTATAGGG	Target genes detection for yeast transformants
pYES2.R	-	TCGGTTAGAGCGGATGTG	
FA	-	AAGTCCCTCCAGTACGTCGTC <u>CAAGGATCTGG</u>	
FB	-	AAGTCGATCCTGCATGTCCTGTGGGACCTC	
FC	-	CACGACTGCGGCCACGGAGCGTTCTCGGAC	
FD	-	CACGAGTGCGGCCATGGTTCGTTCTCCCG	
FE	-	CACCGCCACCACCACA <u>AAGGGCACTGGATCC</u>	
FF	-	CATTCCAAGCACCACA <u>AAGAACACCGGAAACATCG</u>	
FG	-	GTTCTGAAGAACCGTCGCAAGAACATTTTC	
FH	-	GTATGAGCCTCACCAGCTCGGTGCCATCATCTCG	Overlap extension PCR for 12 fusion genes
FI	-	GCTCGTGGCTGGTCATC <u>ATCACCTATCTCCAGC</u>	
FJ	-	GCTTGGATCGTCTGC <u>ACCACCTTCCTCCACC</u>	
RA	-	<u>CCAGATCCTTGACGACG</u> TACTGGAGGGACT T	
RB	-	<u>GAGGTCCCACAGGACATGC</u> AGGATCGACTT	
RC	-	<u>GTCCGAGAACGCTCC</u> GTGGCCGCAGTCGTG	
RD	-	<u>CGGGAGAACGAACCAT</u> GGCCGCACTCGTG	
RE	-	<u>GGATCCAGTGCCCTT</u> GTGGTGGTGGCGGTG	

RF	-	<u>CGATGTTCCGGTGTCTT</u> GTGGTGCTTGAATG	
RG	-	GAAAATGTTCTTGCGACGGTTCTTCAGGAAC	
RH	-	<u>CGAGATGATGGCACCGAGCT</u> GGTGAGGCTCATA	
RI	-	<u>GCTGGAGATAGGTGAT</u> GATGACCAGCCACGAGC	
RJ	-	<u>GGTGGAGGAAGGTGGT</u> GCAGACGATCCAAGC	
W129T		CACCATCTTTGGA <u>ACGGT</u> CCTTCACTCTGC	Targetgeted mutagenesis for constructing FADS15 mutants
V137T		CACTCTGCTCTTTTG <u>ACG</u> CCCTACCAGGCTTG	
Y139F		GCTCTTTTGGTGCCCT <u>TC</u> CAGGCTTGGGCC	
S145T		GGCTTGGGCCATG <u>ACGC</u> ATTCCAAGCACCAC	
T144W		CGACATCATCGGCT <u>IGG</u> TTGCTGCACACCTTC	Targetgeted mutagenesis for constructing oRiFADS17 mutants
V152T		CACCTTCATCTTG <u>ACCC</u> CTACACCACCTGG	
Y154F		CATCTTGGTCCCT <u>TC</u> ACCACCTGGAAGCTG	
S160T		CCACCTGGAAGCTG <u>ACCC</u> ACCGCCACCACCAC	

^aUnderlined sequences indicate the additional restriction sites, fragments in FADS15 sequence or the mutant sites.

Table S2. Literature summary of catalytic efficiency of ω -3 desaturases from various species with LA, GLA, DGLA and AA substrates.

Rank ^a	Preference Index ^b	Strain name	The catalytic efficiency of ω 3Des on LA (%) ^{c,d}	The catalytic efficiency of ω 3Des on GLA (%)	The catalytic efficiency of ω 3Des on DGLA (%)	The catalytic efficiency of ω 3Des on AA (%)	Locus	Reference or source
+9	>>56	<i>Pythium aphanidermatum</i>	-	5.97	28.85	56.46	FW362186.1	15
+8	>>49	<i>Phytophthora sojae</i>	-	6.18	35.45	48.79	FW362213.1	15
+7	>>37	<i>Phytophthora ramorum</i>	-	4.70	31.02	37.12	FW362214.1	15
+6	>>31	<i>Phytophthora infestans</i>	-	-	-	30.94	CAJ30870.1	14
+5	>>26	<i>Saprolegnia diclina</i>	-	-	4.98	25.9	AY373823	13
+4	5	<i>Phytophthora parasitica</i>	7.11	5.63	25.34	49.70	KT372001	16
+3	5.1	<i>Octopus bimaculoides</i>	4.4	4.3	23.5	22.6	MH028785	Our lab
+2	5.1	<i>Caenorhabditis elegans</i>	11	-	0	≈ 56	CELE_Y67H2A.8	34
+1	1.7	<i>Rhizophagus irregularis</i>	34.2	41.8	61.8	58.5	MH028784	This study
0	1	<i>Pichia pastoris</i>	36.5	33.8	35.1	35.3	EF116884	33
-1	-1.7	<i>Mortierella alpina</i> 1S-4	11.50	8.90	3.60	6.70	AB182163	11
-2	-2.6	<i>Mortierella alpina</i> ATCC32222	62.37	63.99	41.82	23.67	AGZ84120.1	This study
-3	-4	<i>Magnaporthe grisea</i>	18.6	3.40	4.6	4.7	XP 362963	9
-4	-5	<i>Fusarium moniliforme</i>	49.30	15.70	17.50	9.80	DQ272516	9
-5	-6.2	<i>Fusarium graminearum</i>	17.40	3.10	5.80	2.80	EAA75859	9
-6	-13.8	<i>Saccharomyces kluyveri</i>	22.0	10.0	3.9	1.60	AB118663	7,8
-7	<<-10.6	<i>Perilla frutescens</i>	10.6	-	-	-	KX880389	12
-8	<<-16.9	<i>Salvia hispanica</i>	16.9	-	-	-	KX610653	12

^a The “Rank” numbers represent the substrate preference level of corresponding ω 3Des. E.g.: “+9” represents the strongest AA substrate preference; “-8” represents the strongest LA substrate preference; “0” represents no substrate preference.

^b Preference indexes = [Catalytic efficiency EPA / Catalytic efficiency LA] or - [Catalytic efficiency LA / Catalytic efficiency EPA].

^c These data indicated catalytic efficiency of LA, GLA, DGLA and AA, respectively.

^d The “-” represents catalytic efficiency not mentioned in corresponding reference, but its preference is known.

2. Supplemental Figures

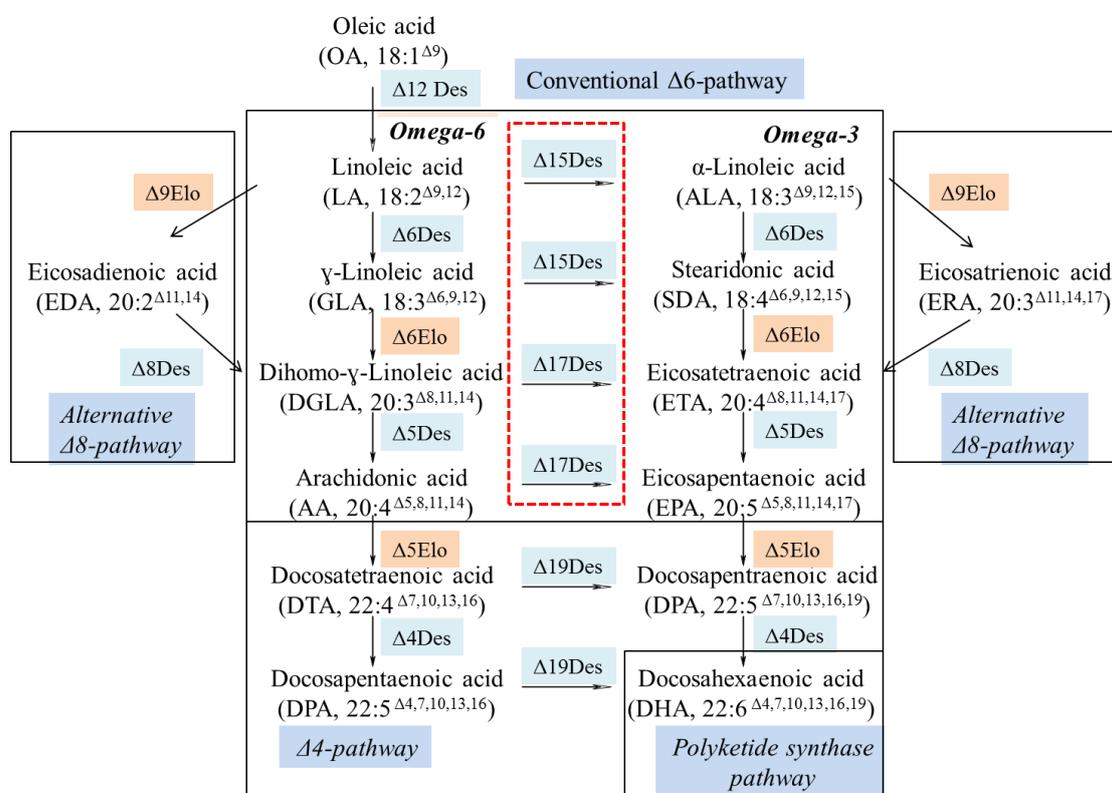


Figure S1. Schematic diagram of the fatty acid pathways for EPA and DHA synthesis.