

Additional Files

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LuPDCT1          -----MS-AAPTTTVAATAIPLKRKKTDA-----
LuPDCT2          -----MS-ATPTAAVAATAIPLKRKKTDA-----
AtROD1           -----MS-----AAAETDVSLRRRSNSLNGNHTNGVA----- IDGTLDNRRRVDG
RcROD1           -----MKSTVPPTTTTTTTTTLYKRKKDINLTSVNDVS-----DMVS-----NKN-----
Brassica         -----MSTNTVVPLRRRS---NGYHTNGVA-----FNG-----
Brachypodium     -----MPPPSLAAAQDQVAANAA--G-----NGIDARRRAGK GK-----KVHP
Gossypium        -----MKTAEATAATTTVLSRQYKRSPKS-----NG-----KVNGT
Glycin           -----MNGGA-----EASV-----NHRRRHQ
Hordeum          -----MPPASLTAADRASAANG--L-----AGPETRRRAGK GK-----KVHP
Medicago        -----MNGGA-----ASSSGDATVLKRRTHT
Oryza            -----MPPPPPSLTANTASSMGNAE--AVVVLPAANGARRRADKVV-----HPAP
Picea            -----MSCRRRSSEDNGGETDMIYVDRRTKQCLGNLFCICSQEIQ
Populus          -----ME-----NKN-----
Sorghum          -----MPPPSLTAATAATTT-----TRRRKD-----HP
Helianthus       MTVEKLHHRTPVPTTTT-----ILQPPNNIS-----
Zea              -----MPPPSLTAAGTTTT-----TTRRRNDRAA-----KVHQ
  
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LuPDCT1          -AA-KTQKNNQG-----NEDEQEAI VESVAPFTKWRRRDAMNAVREHWLPVILGGALLF
LuPDCT2          -AA-KTQKNNQG-----NEDEQEAI VESVAPFTKWRRRDAMNAVREHWLPVILGGALLF
AtROD1           TNTHMDSAKKTD-NGYANGVGGGG-WRSKASFTTWTARDIVVYVRYHWI PCMFAAGLLF
RcROD1           -F--ANGNVNGG-----GGYTA FNRFDP SFMKWTT HDVVNVVK FHWLP CVFGLGLLF
Brassica         ----MDNIVKKTDCY TNGNGNGGVERSKASFLT WTRDAVYVARYHWI PCFFAVGVLF
Brachypodium     LPDAG---TTMGD-GVGMGG---GESRKGRPEWM--TPAGAAGVLRHPLP VVVFACGLLL
Gossypium        AA--KKTGVNHG-----NGGDISNGKASF MKWTLDDVVYVAKYHRLPCFFAAWFLF
Glycin           AA--SANGVKIAN-GAM---AKPSS TLCYDASF MKWTVADAVHVATHHWMPCLFALGLLF
Hordeum          LPPDG---AAMGD-GGERLA---GG--RRPADWL--SPSGVAGILRRHPLPALFACGLLL
Medicago        TN--QTNHNSQKN-PMPKNSSSLSCLSYSSASFLKWTISDVVHVATHHWMPCLFACGLLF
Oryza            MPDRAAGGAMERE-GGGVGGGGEVGGW--RRPEWC--SAAGVAGVLRRH PAAA AFGCGLLL
Picea            RKLRDLMGANGNVVHQEKSPFLGDTAVYPSFMGWSMTYLI GTARFHPLPVLLVGCGLLF
Populus          -K--QTNGITTD-----GAANGFYGDPSFLKWTLRD VVNVAKHHLWPCFLGFGLLF
Sorghum          APG---GGAGAKE-MGAAA--SAAEGWARRPEWC--SAAGVAGVLRRH PAPA LFGCGLLL
Helianthus       ----INKINLKNTHNHETTTTFSHRWSF DAFCLRW MVADV FGLLYHPVPCFFGVSLLF
Zea              VLG---EGAGTEE-MGAV-----ADGWT-RPEWC--SAAGVAGVLRRH PAPA LFGCGLLL
  
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LuPDCT1          FMWVEYTLRMVPTSSQPFDLGFVATRALHRL LSSSPELNSVLAALNTV FVGMQTSY I LW T
LuPDCT2          FMWVEYTLRMVPTSSQPFDLGFVATRALHRL LSSSPELNSVLAALNTV FVGMQTSY I LW T
AtROD1           FMGVEYTLQMI PARSEPF DLGFVVTRSLNRV LASSPDLNTVLAALNTV FVGMQTT Y I VWT
RcROD1           FMAVEYTLRMVPASSPFDLGFVTRHLHL LSSWPALNTLLAFLNTV FVLMQ TAY I LW T
Brassica         FMGVEYTLQMPAKSEPF D IGFVATRSLNRV LASSPDLNTLLAALNTV FVAMQTT Y I VWT
Brachypodium     FMGVEYTI PMVPHAAPPLD LGF LATAAMHDG IAARPWLN SLLAALNTV FVAMQ TAY I LW A
Gossypium        FIYVEYTLRMVPDSSPFDLGFVVT RSLHRALASWPELNSLLAALNTV FVAMQ SVY I IGT
Glycin           FMAVEYTLMLVPPSSPFDLGF IAT RSLHALLESSPNLNTL FAGLNTV FVGMQTSY I LW T
Hordeum          FMGVEYTI PMIPAAAPPLD LGFHATAAMHAG IAARPWLN SLLAALNTV FVAMQ AAY I LW A
Medicago        FMAVEYTLFMVSSSPFDLGFVTRSLHRVLESSPQLNNVLAALNTV FVLMQ TSY I LW T
Oryza            FMAVEYTI PMVPPAAPVDLGF AATAALHAG IAARPWLN SLLAALNTV FVAMQ AAY I LW A
Picea            FMAVEYTLVMVPAGSQPYDVGFVWTQSL HDLL LERPALNTVLAAMNTV FVGMQTF Y I LW T
Populus          FMAVEYTLRMVPSSSPFDLGFVTRRLHGL LSSWPELNTSLAGLNTV FVGMQ TAY I LW T
Sorghum          FMAVEYTI PMVRPDSPPDLGF IATRNMHAAVAATP WLN SLLAALNTV I VAMQ AAY I LW A
Helianthus       FMGVEYTLWMVPSSSPFDI G FVATAWLHRVLAASPVLNTVLAGLNTV FVGMQTT Y I LW T
Zea              FMAVEYTI PMVKPDAPPLD LGF LATAAGMHA A I ARPWLN SLLAALNTV FVAMQ AAY I LW A
  
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LuPDCT1          FVVEGRGRPTISALFMFTCRGILGYSTQLPLPEGYLGSGVDFPVGNVSFFLFFSGHVAGS
LuPDCT2          FVVEGRGRPTISALFMFTCRGILGYSTQLPLPEGYLGSGVDFPVGNVSFFLFFSGHVAGS
AtROD1           WLVEGRARATIAALFMFTCRGILGYSTQLPLPQDFLGSVDFPVGNVSFFLFFSGHVAGS
RcROD1           WLI EGRPRATISALFMFTCRGILGYSTQLPLPEGFLGSVDFPVGNVSFFLFFSGHVAGS
Brassica         WLM EGRPRATISACFMFTCRGILGYSTQLPLPQDFLGSVDFPVGNVSFFLFFSGHVAGS
Brachypodium     ILAEQRPRAAIATLMMFTCRGLLGCSTQLPLPAEFLSGMDFPVGNVSFFLFFSGHVAGA
Gossypium        WVVEGRPRATISALFMFTCRGILGYSTQLPLPQEFVSGMDFPVGNVSFFLFFSGHVAGS
  
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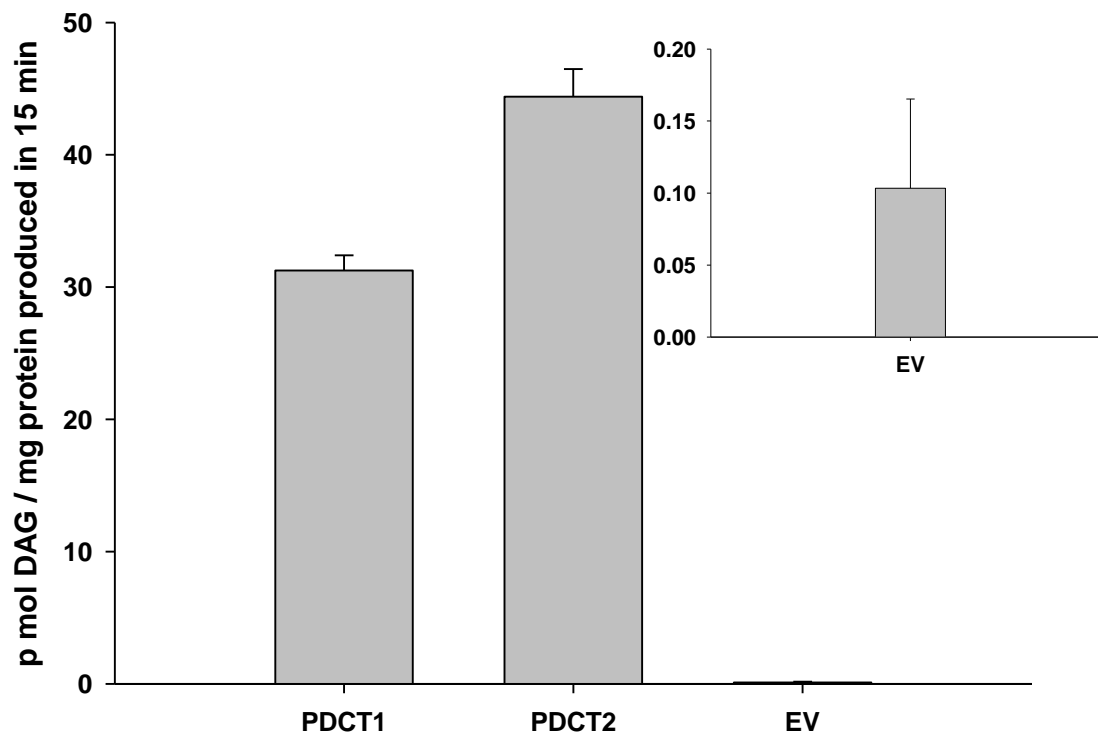



Figure S2: Production of radio-labeled diacylglycerol (DAG) catalyzed by LuPDCT1 or LuPDCT2 after 15 min incubation. Data shown represent means \pm SE, with sample numbers of $n=3$

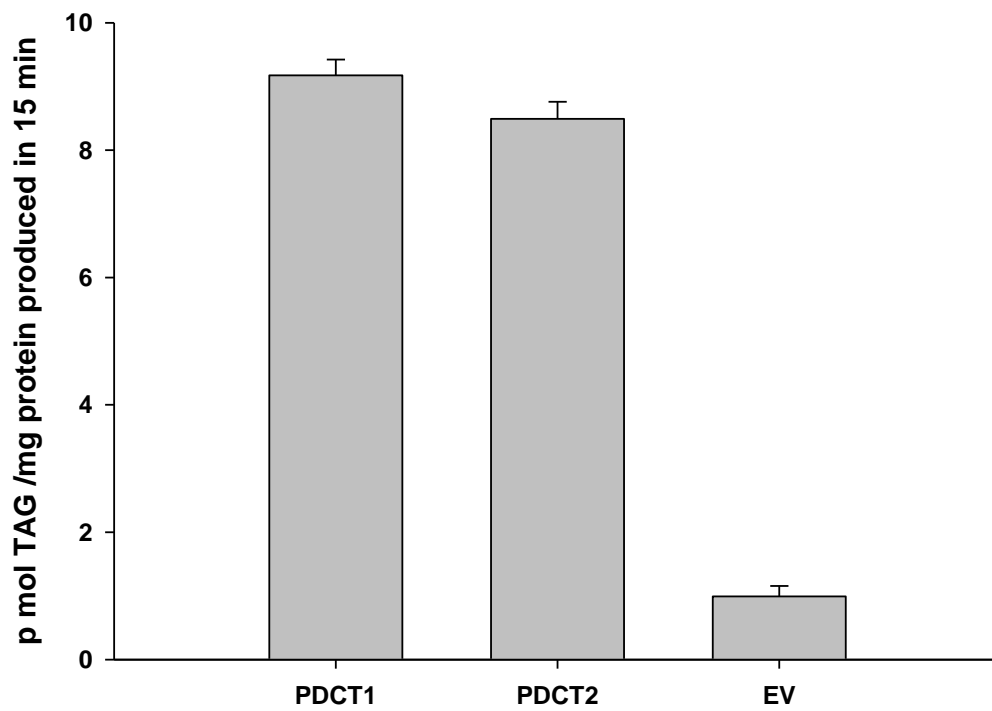


Figure S3: Production of radio-labeled triacylglycerol (TAG) during the assay of PDCT in the direction of radio-labeled diacylglycerol (DAG) formation. The incubation time was 15 min. Data shown represent means \pm SE, with sample numbers of $n=3$

S Table 1: Proportions of C18:1, C18:2 and C18:3 in non-transformed wild-type (WT) and *rod1* mutant Arabidopsis seeds, as well as T₂ *rod1* seeds bearing empty vector, *LuPDCT1* (P1) or *LuPDCT2* expression cassettes. Results represent the average (\pm SE) of triplicate measurements of 10 independent transgenic lines for *PDCT* genes and five independent transgenic lines for empty vector (EV) transformed lines. For WT and *rod1* mutant lines, n=3.

Line	Fatty acid composition (mol %)		
	C18:1	C18:2	C18:3
WT	16.48 \pm 0.66	28.11 \pm 0.33	16.33 \pm 0.11
<i>rod1</i>	32.87 \pm 0.65	14.81 \pm 0.47	13.99 \pm 0.48
<i>rod1</i> +EV	37.74 \pm 0.32 (36.75-38.53) ^a	13.21 \pm 0.31 (12.26-13.45)	12.36 \pm 0.49 (10.67-13.37)
<i>rod1</i> +PDCT1	20.62 \pm 1.00 (15.40-24.29)	25.79 \pm 0.28 (24.55-27.44)	15.29 \pm 0.75 (12.86-19.03)
<i>rod1</i> +PDCT2	21.38 \pm 0.52 (18.20-22.77)	26.04 \pm 0.46 (23.62-28.02)	15.00 \pm 0.60 (12.76-17.80)

^a Percent molar range among independent transformants.

S Table 2: Fatty acid composition of transgenic *A. thaliana* T₂ seeds expressing *LuPDCT1* and *LuPDCT2*. Results represent the average (\pm SE) of triplicate measurements of 10 independent transgenic lines for *PDCT* genes and five independent transgenic lines for empty vector (EV) transformed lines. For wild type (WT) lines n=5.

Construct	Fatty acid composition (mol %)									
	C16:0	C18:0	C18:1	C18:2	C18:3	C20:0	C20:1	C20:2	C22:1	18:2+18:3
PDCT1	9.77 \pm 0.13 (9.14-10.27) ^a	3.77 \pm 0.05 (3.50-3.92)	12.08 \pm 0.28 (9.99-12.99)	29.28 \pm 0.12 (28.66-29.95)	20.87 \pm 0.36 (19.52-22.83)	1.76 \pm 0.02 (1.67-1.90)	18.03 \pm 0.23 (17.21-19.44)	2.83 \pm 0.04 (2.67-3.12)	1.61 \pm 0.05 (1.40-1.93)	50.15 \pm 0.27 (49.08-51.49)
PDCT2	9.61 \pm 0.18 (8.82-10.55)	3.57 \pm 0.10 (3.10-4.24)	12.04 \pm 0.30 (9.73-13.28)	29.11 \pm 0.34 (27.78-31.64)	22.47 \pm 0.40 (20.09-24.24)	1.68 \pm 0.09 (1.24-2.35)	17.18 \pm 0.53 (13.51-19.35)	2.81 \pm 0.10 (2.30-3.20)	1.52 \pm 0.12 (1.02-2.29)	51.59 \pm 0.61 (49.35-55.84)
EV	8.71 \pm 0.15 (8.44-9.28)	4.71 \pm 0.27 (4.00-5.68)	17.90 \pm 0.21 (17.17-18.39)	26.43 \pm 0.36 (25.82-27.81)	16.67 \pm 0.28 (15.67-17.36)	2.75 \pm 0.18 (2.28-3.16)	18.83 \pm 0.45 (17.29-19.04)	2.36 \pm 0.06 (2.31-2.57)	1.82 \pm 0.03 (1.74-1.92)	43.10 \pm 0.57 (41.76-43.10)
WT	8.94 \pm 0.13 (8.54-9.16)	4.24 \pm 0.18 (3.76-4.65)	18.77 \pm 0.19 (18.26-19.31)	26.90 \pm 0.36 (25.69-27.79)	16.31 \pm 0.21 (15.86-16.98)	2.25 \pm 0.13 (1.81-2.60)	18.35 \pm 0.09 (18.09-18.64)	2.34 \pm 0.09 (2.09-2.54)	1.78 \pm 0.17 (1.46-2.38)	43.21 \pm 0.53 (41.56-43.62)

^a Percent molar range among independent transformants.

S Table 3: Primers and probes used for qRT-PCR assay.

Gene	Forward primer	Reverse primer	Probe
<i>PDCT1</i>	TGCGATGAATGCGGTTAGG	CAACAGGGCACCTCCCAATA	AGCATTGGTTGCCTGTC
<i>PDCT2</i>	ACACCATTGATTTGGCCGCC	GGCGGTCTTGGTTTGGAGG	CTGCTCTTTGACTCACTTG
<i>GAPDH</i>	GACATCGTCTCCAACGCTAGCT	CATTGATAACCTTGGCCAAAG	ACCACTAACTGCCTTGC
<i>Ubi2</i>	CGGACACCATCGACAATGT	TCCGGCGGGATTCCTT	AAGGCCAAGATCCAG