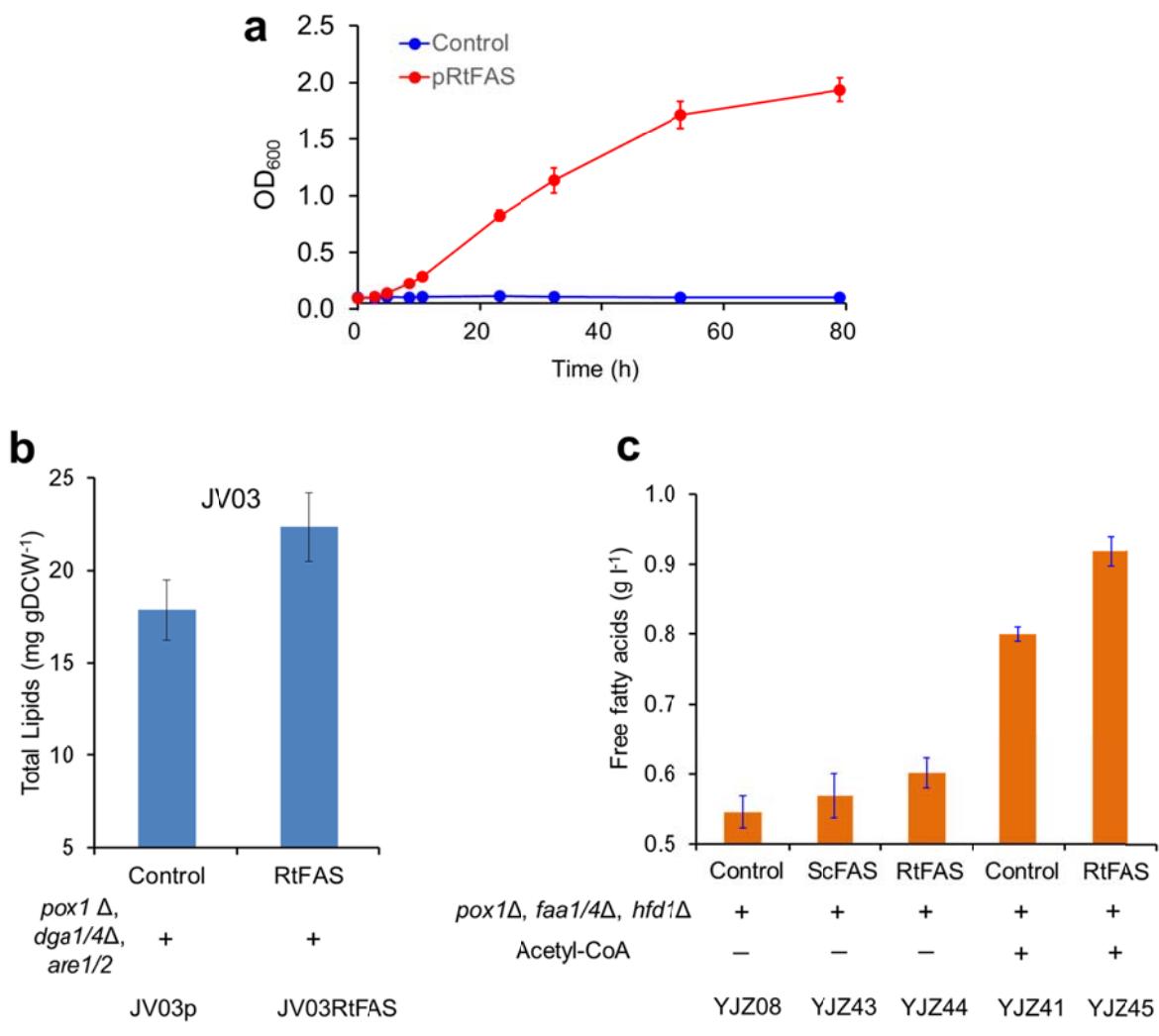


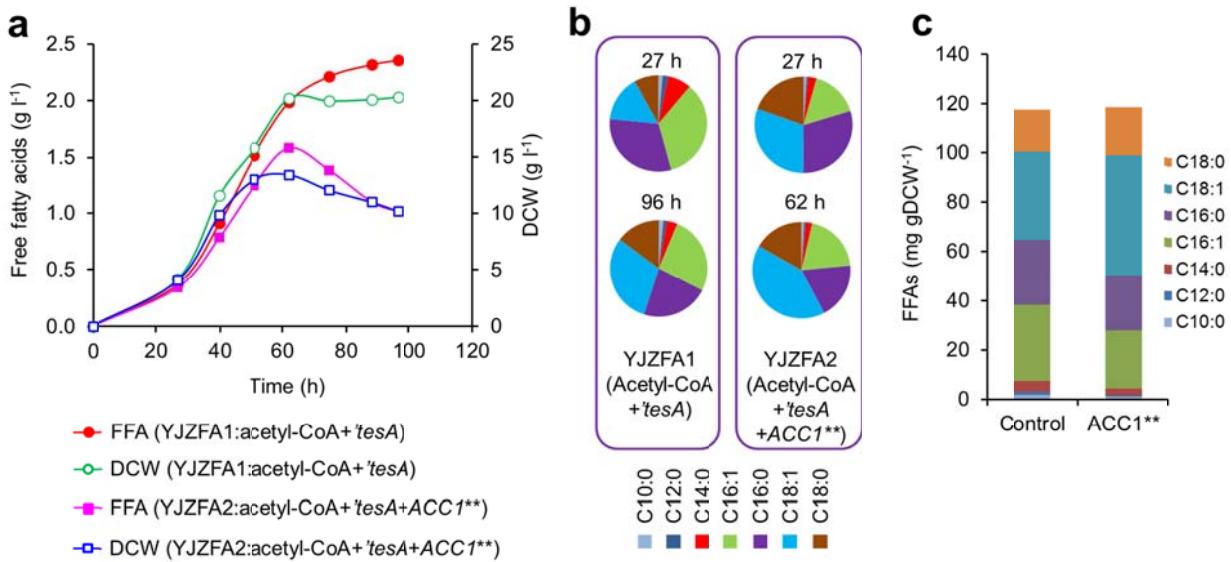
1

2 Supplementary Fig. 1. Genome integrated acetyl-CoA pathway had higher biomass and FFA titer
3 compare to plasmid pathway. The plasmid pCoA4 transformed to YJZ08 and the same pathway
4 was integrated to the YJZ08 genome. All data represent the mean \pm s.d. of biological triplicates.

5

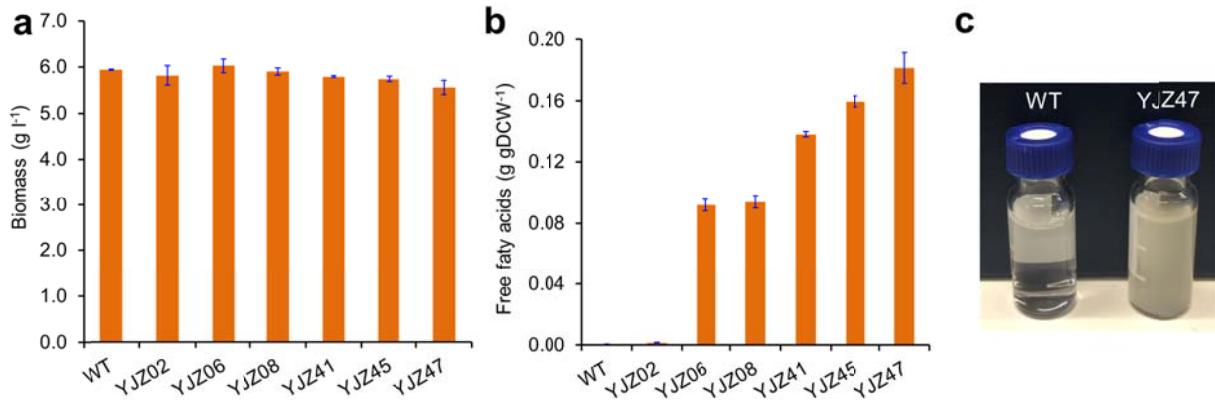


6
 7 Supplementary Fig. 2. Expression of *R. toruloides* fatty acid synthase (RtFAS) increased the total lipid and
 8 FFA production. (A) RtFAS complemented the endogenous FAS deletion in *S. cerevisiae* PWY12
 9 ($\Delta fas1::LEU2$, $\Delta fas2::HIS3$). (B) Expression of RtFAS increased the total lipid content in a JV03
 10 background. (C) Expression of RtFAS was more efficient than overexpression of endogenous ScFAS in
 11 terms of increasing FFA production. All data represent the mean \pm s.d. of biological triplicates.

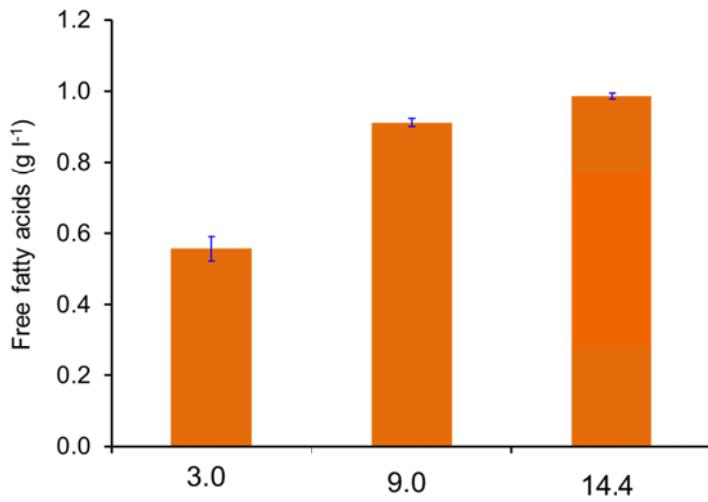


13
14 Supplementary Fig. 3. Effect of acetyl-CoA carboxylase mutant ($\text{Acc1}^{\text{S1157A,S659A}}$, Acc1^{**}) on FFA
15 production. (a) Fed batch fermentation of strains YJZFA1 and YJZFA2. Time courses of FFA titers (filled
16 symbols) and cell mass (open symbols) are shown. YJZFA1 is a prototrophic strain harboring the ACL
17 based pathway in plasmid pFab1 and YJZFA2 additionally expresseses ACC1^{**} . Here, 300 g l⁻¹ glucose
18 was fed and 2 M KOH was used for pH control other than described in Methods. (b) FFA profiles of the
19 strain YJZFA1 and YJZFA2 at the time point where feeding was initiated and at the highest titer. (C) The
20 maximal biomass specific free fatty acid titer.

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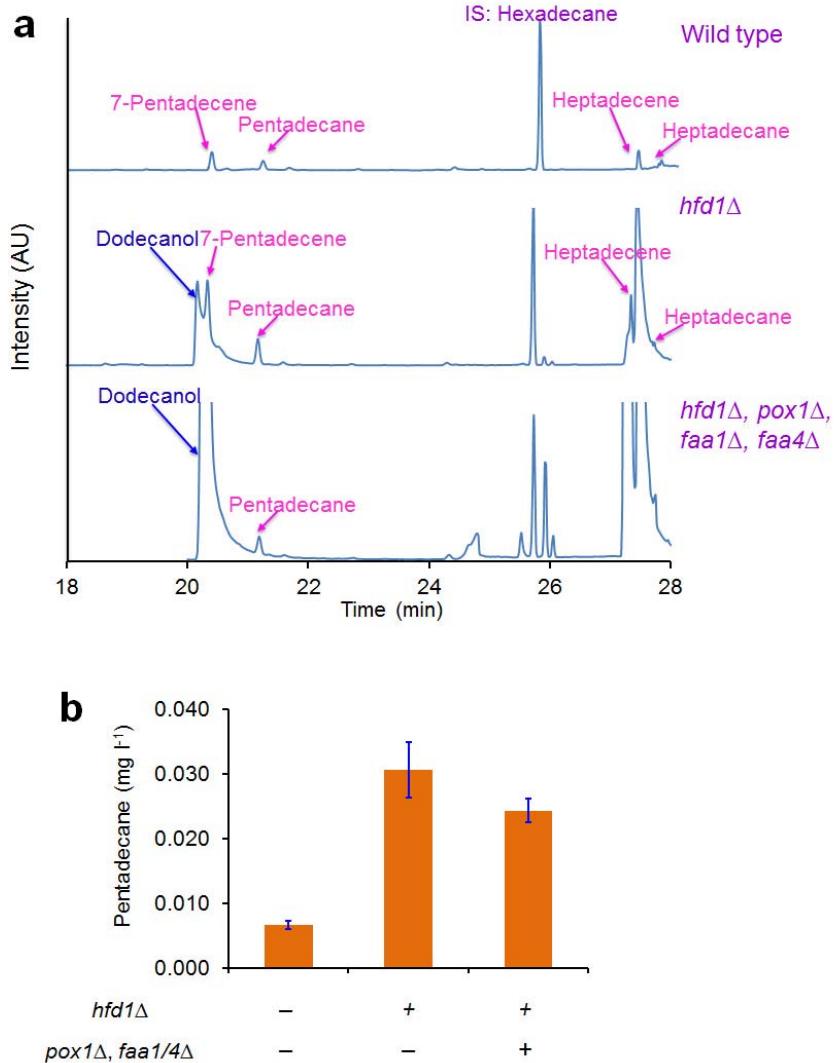
22
23 Supplementary Fig. 4 Comparison the biomass titers and specific FFA titers among recombinant *S.*
24 *cerevisiae* variants. (a) The final biomass titers. (b) The specific FFA titers. (c) Comparison of cell culture
25 between wild-type strain and final strain YJZ47. The cell cultures were centrifuged and the cell pellets
26 were removed. The engineered strains were cultivated in shake flasks containing 15 mL optimized
27 minimal media for 72 h at 200 rpm, 30 °C. All data represent the mean \pm s.d. of biological triplicates.
28



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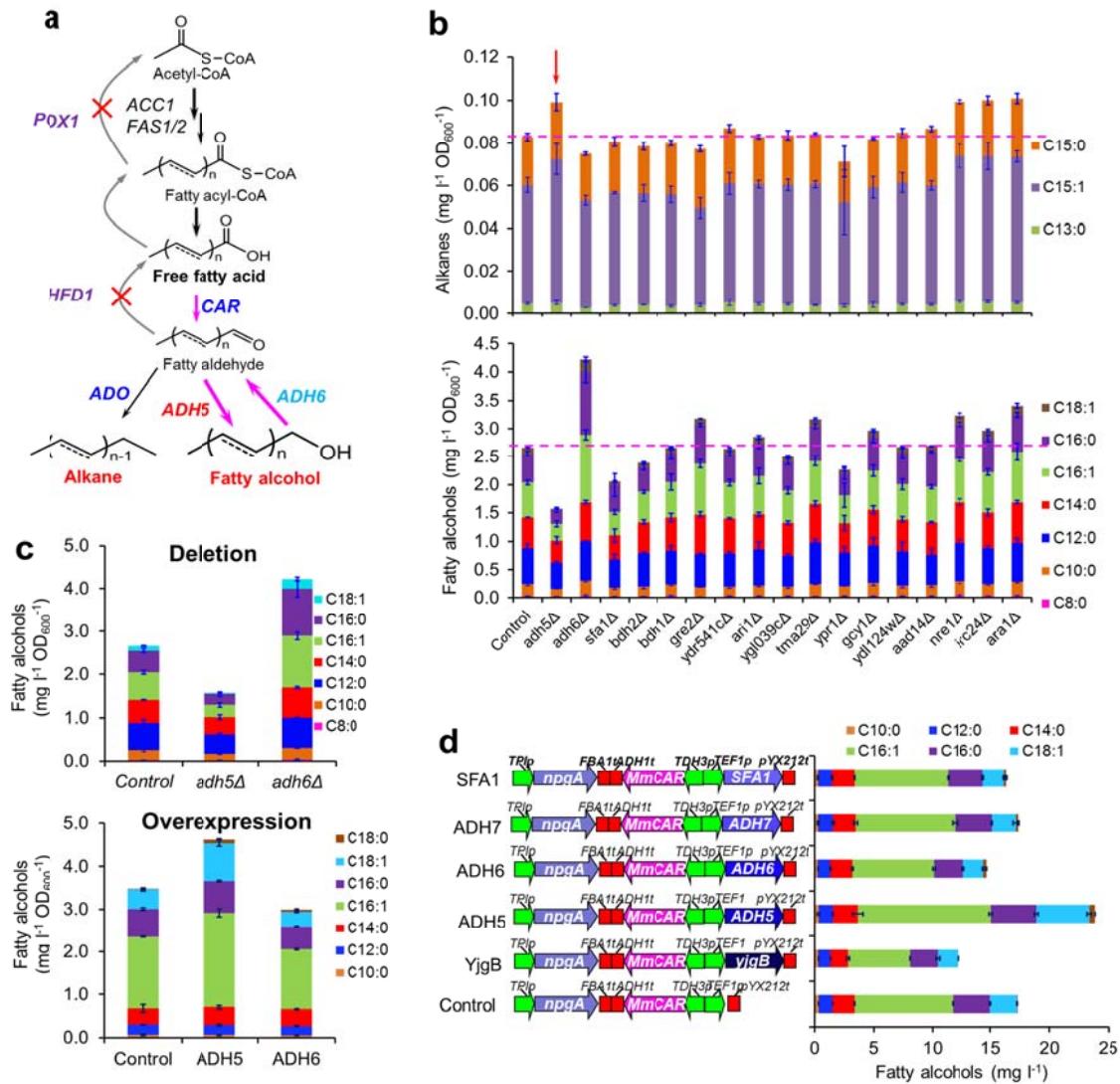
30 Supplementary Fig. 5 the effect of KH₂PO₄ level on FFA production. The other media components were 5
31 g l⁻¹ (NH₄)₂SO₄, 0.5 g l⁻¹ MgSO₄•7H₂O, 30 g l⁻¹ glucose, trace metal and vitamin solutions¹ supplemented
32 with 40 mg l⁻¹ histidine and/or 60 mg l⁻¹ uracil. The engineered strain YJZ47 were cultivated in shake flasks
33 containing 15 mL media for 72 h at 200 rpm, 30 °C. All data represent the mean±s.d. of biological
34 triplicates.

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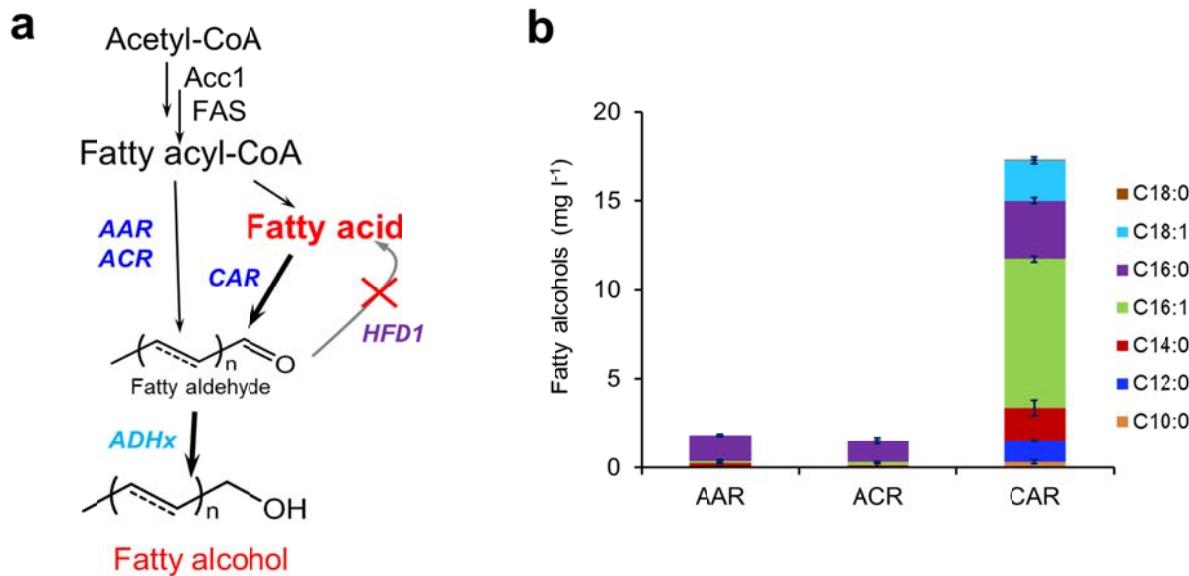
37 Supplementary Fig. 6. The ADO catalyzed step is rate limiting for alkane production, precursors are in
 38 sufficient supply. (a) GC chromatograms of extracted metabolites from different background strains
 39 harboring pAlkane16. *HFD1* deletion (middle chromatogram) increased the production of alkanes and
 40 fatty alcohols compared with the wild-type background (top chromatogram), which might be attributed
 41 to the blockage of fatty aldehyde dehydrogenation to fatty acids. Further increasing fatty acid supply
 42 (*hfd1 Δ pox1 Δ faa1 Δ faa4 Δ*) increased the amount of fatty alcohols, whose peaks covered the alkane
 43 peaks (bottom chromatogram). (b) Pentadecane production in the corresponding strains. The data
 44 represent the mean \pm s.d. of biological triplicates. As the peaks of 7-pentadecene and 8-heptadecene
 45 were covered by the fatty alcohols in the fatty acid overproducing strain, it became impossible to reliably
 46 quantify the alkanes. We thus compared the pentadecane titers, which indicated that a higher fatty acid
 47 supply did not increase the alkane but fatty alcohol production instead. These results indicated that the
 48 ADO is a limiting step and fatty acids might inhibit ADO activity, as the ADO has been shown to have fatty
 49 acid binding activity².



51 Supplementary Fig. 7 Engineering expression of alcohol dehydrogenase/aldehyde reductase genes for
52 production of alkanes or fatty alcohols. (a) Schematic illustration of the engineered metabolic pathways
53 of fatty alcohol biosynthesis. (b) The effect of single gene deletions on production of alkanes (top) and
54 fatty alcohols (bottom). The targeted genes, encoding an alcohol dehydrogenase or aldehyde reductase,
55 were selected based on the catalytic efficiency toward aldehyde reduction (Supplementary Table 1). And
56 they were deleted in the YJZ03 background, and plasmid pAlkane16 was introduced for alkane
57 production. Here, *ADH5* deletion showed increased alkane production and decreased fatty alcohol
58 accumulation, and was considered as the first target for improving alkane production. (c) Opposite roles
59 of alcohol dehydrogenases *Adh5* and *Adh6* in fatty alcohol biosynthesis. The effect of *ADH5* or *ADH6*
60 deletion on fatty alcohol accumulation in strain YJZ03 (*hfd1Δ* and *pox1Δ*) harboring the plasmid
61 pAlkane16 (top panel). The effect of *ADH5* or *ADH6* overexpression on fatty alcohol production in strain
62 YJZ01 (*hfd1Δ*) harboring PAOHO (bottom panel). (d) The amount of fatty alcohol produced with
63 overexpression of genes encoding different alcohol dehydrogenase or aldehyde reductase in YJZ01. The
64 data represent the mean \pm s.d. of three independent clones.

65

66



67

68 Supplementary Fig. 8 Comparison of fatty alcohol production with the expression of fatty acyl-CoA
 69 reductase ACR from *Acinetobacter baylyi*, fatty acyl-ACP/CoA reductase AAR from *Synechococcus*
 70 *elongatus* or carboxylic acid reductase CAR from *Mycobacterium marinum* (with its cofactor encoding
 71 gene *npgA* from *Aspergillus nidulans*). (a) Schematic illustration of the engineered metabolic pathways
 72 for fatty alcohol production. (b) CAR overexpression resulted in a much higher fatty alcohol level
 73 compared with overexpression of AAR and ACR. All data are presented as the mean \pm s.d. of biological
 74 triplicates.

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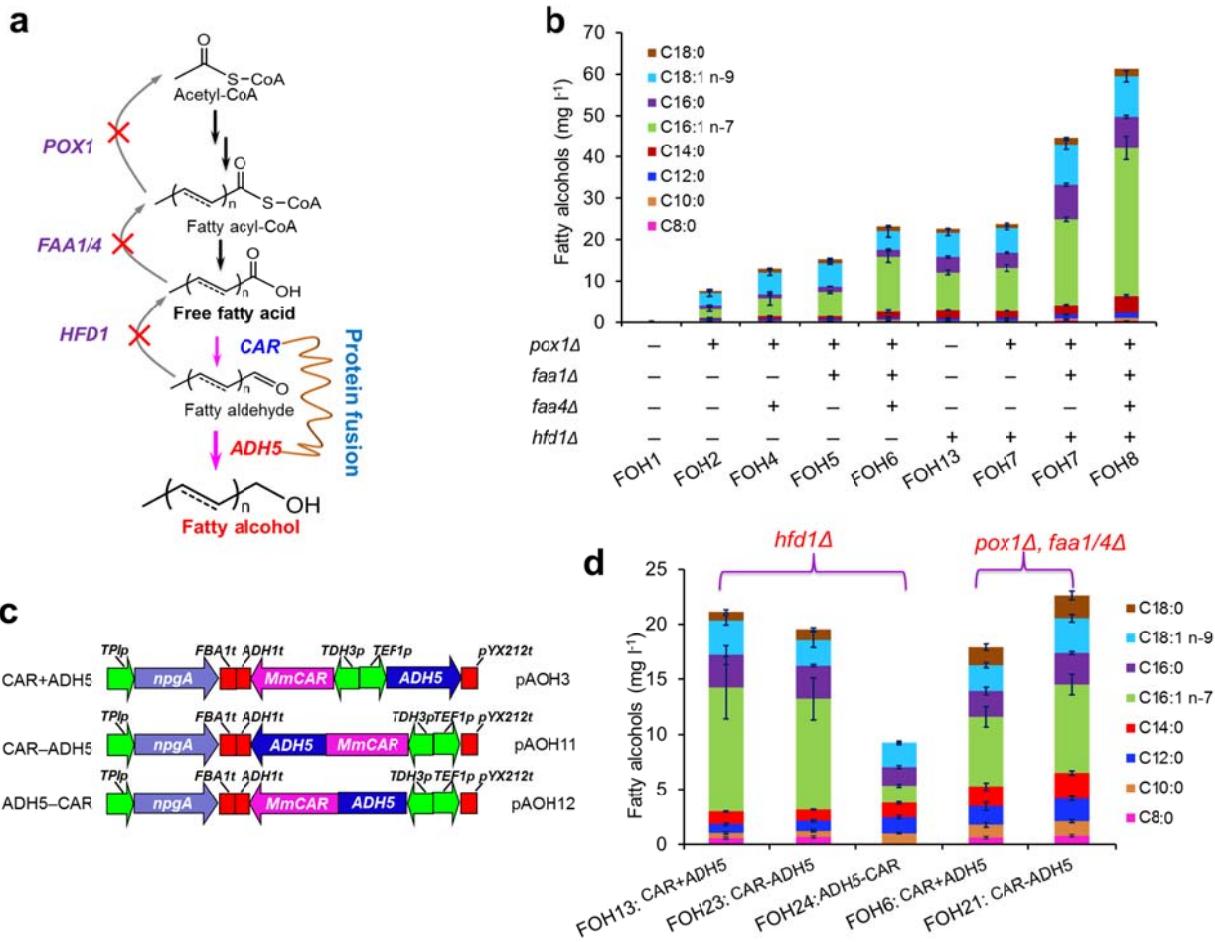
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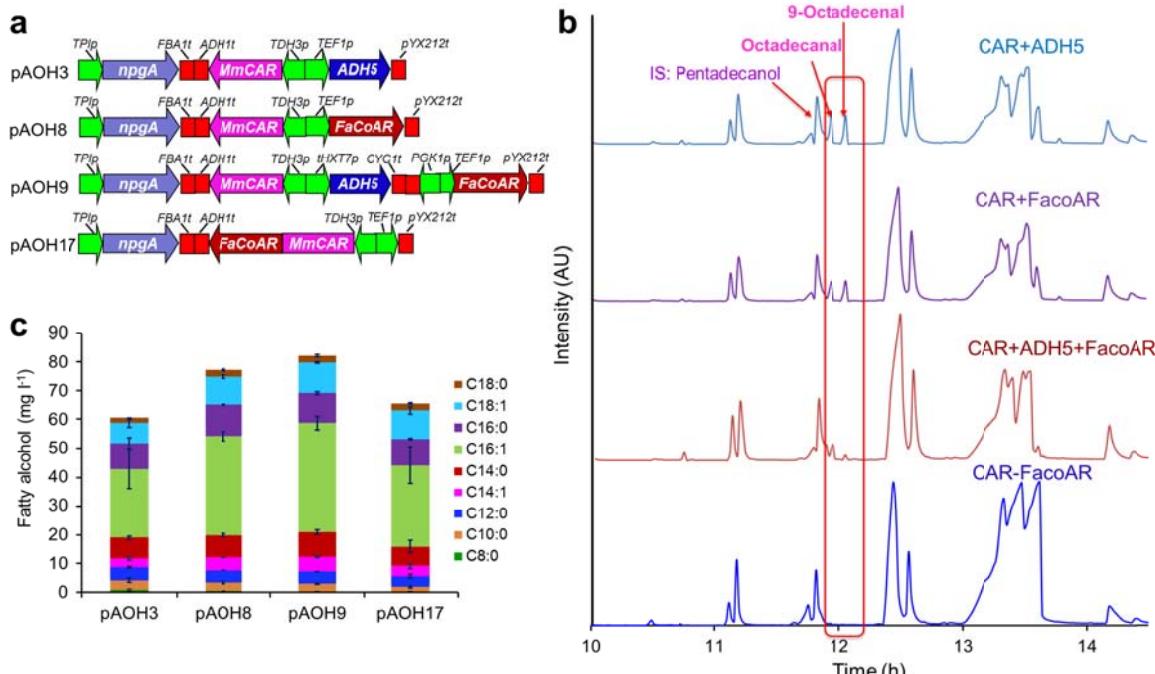
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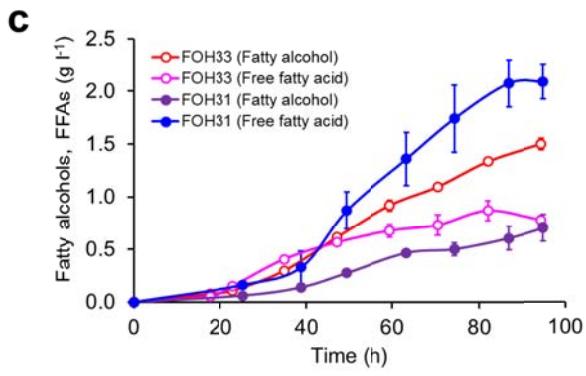
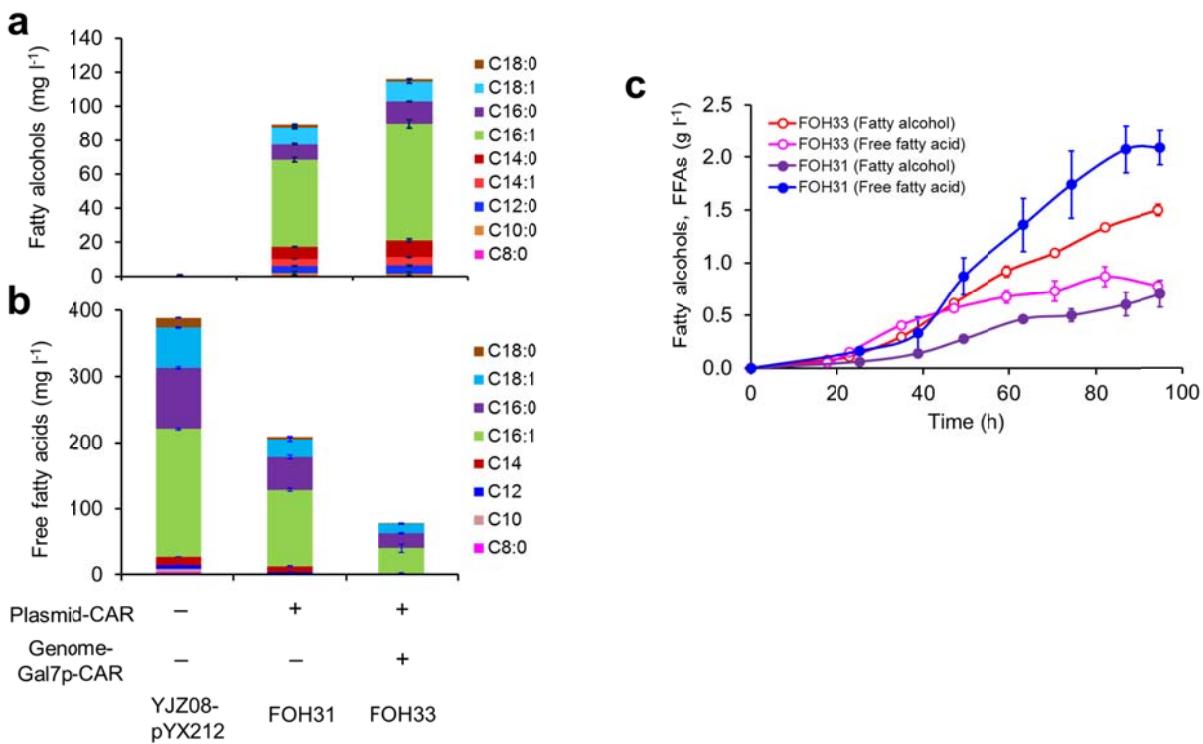
86 Supplementary Fig. 9 Engineered fatty alcohol production by blocking the reverse reactions and enzyme
87 fusion. (a) Schematic representation of the engineered fatty alcohol biosynthetic pathways. (b) Fatty
88 alcohol production from the engineered strains with deletion of *Pox1*, *Faa1*, *Faa4* and *Hfd1*. (c)
89 Schematic representation of gene fusion constructs for fatty alcohol biosynthesis, CAR+ADH5 represents
90 non-fusion expression of CAR and ADH5 (plasmid pAOH3); CAR-ADH5 represents the fusion expression of
91 CAR-ADH5 with the CAR at N-terminus (plasmid pAOH11), and ADH5-CAR represents the fusion
92 expression of ADH5-CAR with the Adh5 at the N-terminus (plasmid pAOH12). The fusion enzymes
93 encoding genes were constructed by inserting a widely used GGGS linker encoding sequence “GGT
94 GGT GGT TCT” between the two corresponding genes. (d) The amount of fatty alcohol produced by the
95 fatty acid overproducing strain (YJZ06, Δ pox1; Δ faa1; Δ faa4) and *Hfd1* deletion strain (YJZ01) harboring
96 different plasmids represented in c. The strain variants were cultivated in shake flasks for 72 h, at
97 30°C, 200 rpm. The data represent the mean \pm s. d. of three independent clones.



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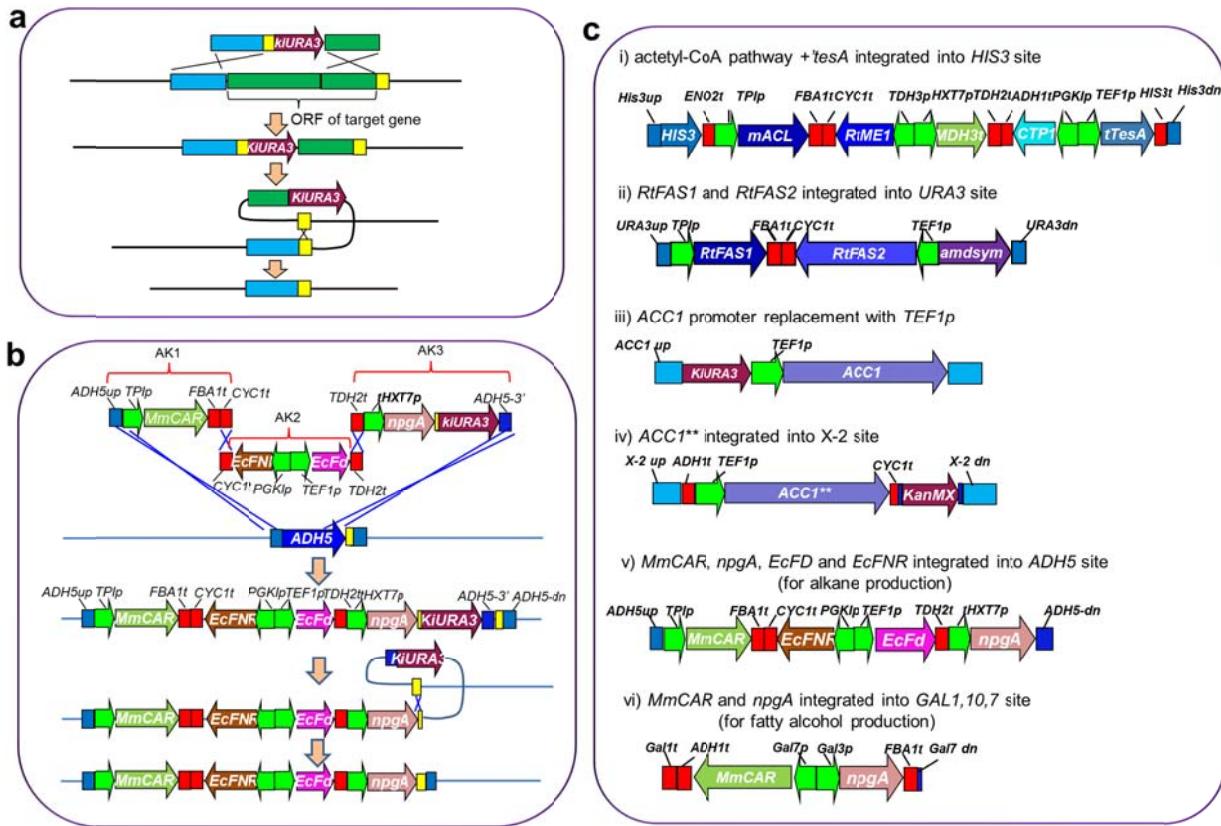
100 Supplementary Fig. 10 Overexpression of *FaCoAR* and *ADH5* increased long chain fatty alcohol
101 production and decreased C18 fatty aldehyde accumulation. (a) Schematic representation of gene
102 arrangement of the metabolic pathway for fatty alcohol biosynthesis. All these pathways were
103 assembled on a pYX212 vector and then transformed into YJZ08 (*hfd1Δ* *pox1Δ* *faa1Δ* *faa4Δ*). (b) GC
104 chromatograms of the extracts from the strains containing the corresponding pathways as shown in a.
105 *FacoAR* expression decreased the accumulation of C18 fatty aldehyde octadecanal and 9-octadecenal.
106 The fusion of CAR and FaCoAR avoided accumulation of octadecanal and 9-octadecenal completely,
107 though the total fatty alcohol titer decreased by 15.2% as shown in c. (c) Titer of fatty alcohols from the
108 strains harboring the corresponding plasmids. The data represent the mean \pm s.d. of three independent
109 clones.

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111

112 Supplementary Fig. 11. Enhancing fatty acid reduction for fatty alcohol production. **(a)** Fatty alcohol titer
 113 in shake flasks. **(b)** FFA titer from the strains harboring the corresponding pathways in shake flasks. The
 114 strain variants were cultivated in minimal media for 72 h, at 30°C, 200 rpm. The data represent the mean
 115 \pm s.d. of three independent clones. **(c)** The accumulation of fatty alcohols and FFAs from FOH11 and
 116 FOH33 in fed-batch fermentation.



117

118 Supplementary Fig. 12 Schematic illustration of genome engineering strategy. (a) The seamless gene
 119 deletion strategy. (b) Modular pathway integration strategy. (c) The genetic arrangement of genome-
 120 integrated pathways.

121

Supplementary Table 1. *S. cerevisiae* (putative) alcohol dehydrogenases and aldehyde reductases^a

| Enzyme | Descriptions | Localization |
|---|---|----------------------------|
| Medium to long-chain alcohol dehydrogenase (alcohol formation) | | |
| ADH3 (YMR083W) | Involved in shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production ⁴ . | Mitochondria |
| ADH4 (YGL256W) | Adh4 is seemingly not expressed in laboratory <i>S. cerevisiae</i> strains. | Cytoplasm |
| ADH5 (YBR145W) | Overexpression of <i>ADH5</i> increased isobutanol production in <i>S. cerevisiae</i> ⁵ . | Cytoplasm |
| ADH6 (YMR318C) | NADPH-dependent aldehyde reductase. k_{cat}/K_m is $1-3 \times 10^5 \text{ mM}^{-1} \text{ min}^{-1}$ (Ref. 6); <i>ADH6</i> deletion decreased the reduction of vanillin to vanillyl alcohol ⁷ . | Cytoplasm |
| ADH7 (YCR105W) | Involved in fusel alcohol synthesis or in aldehyde tolerance ⁸ . Absent in CEN.PK strains. | Cytoplasm |
| SFA1 (YDL168W) | Reduction of long chain and complex aldehydes to corresponding alcohols ⁹ . | Cytoplasm/ Mitochondria |
| XYL2 (YLR070C) | Xylitol dehydrogenase that converts xylitol to D-xylulose ¹⁰ . | Unknown |
| BDH1 (YAL061w) | NAD-dependent butanediol dehydrogenase, catalyzes reduction of acetoin to 2,3-butanediol ^{11,12} . | Cytoplasm |
| BDH2 (Yal060w) | Homolog of <i>BDH1</i> | Cytoplasm |
| GRE2 (YOL151W) | Reduction activity toward complex aldehydes and ketones ¹³ . | Cytoplasm |
| ARI1 (YGL157w) | Reduction activity toward furan aldehydes ¹⁴ and high activity ($k_{cat}/K_m=550 \text{ min}^{-1} \text{ mM}^{-1}$) toward phenylacetaldehyde ¹⁵ . | Cytoplasm/ Nucleus |
| YGL039w | Reduction activity toward phenylacetaldehyde ¹⁵ , short chain fatty aldehydes with a NADH preference ¹⁶ . | Cytoplasm |
| YDR541c | Reduction activity toward fatty aldehydes (up to C8) and benzyl aldehydes with a NADPH preference ¹⁶ . | Unknown |
| YBR159w | 3-ketoreductase of the microsomal fatty acid elongase ¹⁷ . | Endoplasmic reticulum |
| TMA29 (YMR226c) | Reduction activity toward aromatic α -ketoesters and aliphatic ketones ¹⁸ . | Cytoplasm/ Nucleus |
| NRE1 (YIR035c) | Short chain alcohol dehydrogenase ¹⁹ . | Cytosol |
| IRC24 (YIR036c) | Reduction activity toward benzyl ($k_{cat}/K_m=44 \text{ min}^{-1} \text{ mM}^{-1}$) and 1-phenyl-1,2- | Cytoplasm |

| | | |
|---|--|----------------------------|
| | propanedione ($k_{cat}/K_m = 3\ 000\ min^{-1}\ mM^{-1}$) ²⁰ . | |
| AYR1 (YIL124w) | 1-Acyldihydroxyacetone-phosphate reductase ²¹ | Lipid particles |
| YKL107w | Putative short-chain dehydrogenase/reductase, proposed to be a palmitoylated membrane protein | Unknown |
| AAD14 (YNL331c) | Aryl alcohol dehydrogenase ²² , combination of Aad3, 4, 10, 14-16 may be involved in biosynthesis of long-chain and complex alcohols ⁹ | Unknown |
| AAD3 (YCR107w) | Homolog of <i>AAD14</i> | Unknown |
| AAD4 (YDL243c) | Homolog of <i>AAD14</i> | Unknown |
| AAD10 (YJR155w) | Homolog of <i>AAD14</i> | Unknown |
| AAD16 (YFL057c) | Homolog of <i>AAD14</i> | Unknown |
| AAD15 (YOL165c) | Homolog of <i>AAD14</i> | Unknown |
| Aldose reductase family | | |
| YPR1 (YDR368w) | Reduction activity toward diacetyl and ethyl acetoacetate ¹⁹ | Cytoplasm/ Nucleus |
| GCY1 (YOR120w) | High activity toward dl-glyceraldehyde ($k_{cat}/K_m = 556\ min^{-1}\ mM^{-1}$) and nitrobenzaldehyde ($k_{cat}/K_m = 546\ min^{-1}\ mM^{-1}$) ^{23,24} | Cytoplasm/ Nucleus |
| YDL124w | Reduction activity toward dl-Glyceraldehyde ($k_{cat}/K_m = 17\ min^{-1}\ mM^{-1}$) and nitrobenzaldehyde ($k_{cat}/K_m = 110\ min^{-1}\ mM^{-1}$) but lower than Gcy1 ²³ | Cytoplasm/ Nucleus |
| YJR096w | Much lower reduction activity than Gcy1 and YDL124Wp ²³ | Cytoplasm/ Nucleus |
| ARA1 (YBR149w) | Showed reduction activity toward diacetyl ²⁵ and acetoin ¹² | Cytoplasm |
| GRE3 (YHR104w) | Involved in reduction of aldoses such as d-xylose ^{10,26} . | Cytoplasm/ Nucleus |
| D-Hydroxyacid dehydrogenase family | | |
| GOR1 (YNL274c) | Glyoxylate reductase, showed activity toward glyoxylate and hydroxypyruvate ²⁷ | Cytoplasm/ Mitochondria |
| YPL113c | Glyoxylate reductase, showed activity toward glyoxylate and hydroxypyruvate, but much lower compared with Gcor1 ²⁷ | Unknown |
| YGL185c | Glyoxylate reductase, showed activity toward glyoxylate and hydroxypyruvate, but much lower compared with Gcor1 ²⁷ | Cytoplasm |

| | | |
|----------------|---|-----------|
| FDH1 (YOR388c) | NAD ⁺ -dependent formate dehydrogenase ²⁸ | Cytoplasm |
| FDH2 (YPL275w) | NAD ⁺ -dependent formate dehydrogenase ²⁸ | Cytoplasm |

123

124 a, Genes selected for deletion are indicated in bold

Supplementary Table 2. Plasmids used in this study^a

| Plasmids | Genotype or characteristic | Resource |
|----------|---|-------------|
| pYX212 | 2 μm, AmpR, <i>URA3</i> , TPIp, pYX212t | R&D systems |
| pCoA1 | pYX212-(<i>TPIp-RtACL-FBA1t</i>)+(TDH3p- <i>RtME-CYC1t</i>) | This study |
| pCoA2 | pYX212-(<i>TPIp-RtACL-FBA1t</i>)+(TDH3p- <i>LsME-CYC1t</i>) | This study |
| pCoA3 | pYX212-(<i>TPIp-RtACL-FBA1t</i>)+(TDH3p- <i>RtME-CYC1t</i>)+(tHXT7p-' MDH3 -pYX212t) | This study |
| pCoA4 | pYX212-(<i>TPIp-RtACL-FBA1t</i>)+(TDH3p- <i>RtME-CYC1t</i>)+(tHXT7p-' MDH3 -TDH2t)+(PGK1p- CTP1 -ADH1t) | This study |
| pFab1 | pYX212-(<i>TPIp-RtACL-FBA1t</i>)+(TDH3p- <i>RtME-CYC1t</i>)+(tHXT7p-' MDH3 -TDH2t)+(PGK1p- CTP1 -ADH1t)+(TEF1p-' tesA -pYX212t) | This study |
| pFab3 | pYX212-(<i>TPIp-RtACL-FBA1t</i>)+(TDH3p- <i>RtME-CYC1t</i>)+(tHXT7p-' MDH3 -TDH2t)+(PGK1p- CTP1 -ADH1t)+(TEF1p- fadM -pYX212t) | This study |
| pRtFAS | pYX212-(<i>TPIp-RtFAS1-FBA1t</i>)+(TEF1p- <i>RtFAS2-CYC1t</i>) | This study |
| pAOH0 | pYX212-(<i>TPIp-npgA-FBA1t</i>)+(TDH3p- <i>MmCAR</i> -ADH1t) | This study |
| pAOH1 | pYX212-(<i>TPIp-npgA-FBA1t</i>)+(TDH3p- <i>MmCAR</i> -ADH1t)+(TEF1p- <i>yjbB</i> -pYX212t) | This study |
| pAOH3 | pYX212-(<i>TPIp-npgA-FBA1t</i>)+(TDH3p- <i>MmCAR</i> -ADH1t)+(TEF1p- ADH5 -pYX212t) | This study |
| pAOH4 | pYX212-(<i>TPIp-npgA-FBA1t</i>)+(TDH3p- <i>MmCAR</i> -ADH1t)+(TEF1p- ADH6 -pYX212t) | This study |
| pAOH5 | pYX212-(<i>TPIp-npgA-FBA1t</i>)+(TDH3p- <i>MmCAR</i> -ADH1t)+(TEF1p- ADH7 -pYX212t) | This study |
| pAOH6 | pYX212-(<i>TPIp-npgA-FBA1t</i>)+(TDH3p- <i>MmCAR</i> -ADH1t)+(TEF1p- SFA1 -pYX212t) | This study |
| pAOH8 | pYX212-(<i>TPIp-npgA-FBA1t</i>)+(TDH3p- <i>MmCAR</i> -ADH1t)+(TEF1p- FacoAR -pYX212t) | This study |
| pAOH9 | pYX212-(<i>TPIp-npgA-FBA1t</i>)+(TDH3p- <i>MmCAR</i> -ADH1t)+(tHXT7p- ADH5 -CYC1t)+(TEF1p- FacoAR -pYX212t) | This study |
| pAOH11 | pYX212-(<i>TPIp-npgA-FBA1t</i>)+(TDH3p- <i>MmCAR</i> -ADH5-ADH1t) | This study |
| pAOH12 | pYX212-(<i>TPIp-npgA-FBA1t</i>)+(TDH3p- ADH5-MmCAR -ADH1t) | This study |
| pAOH17 | pYX212-(<i>TPIp-npgA-FBA1t</i>)+(TDH3p- <i>MmCAR</i> - FacoAR -ADH1t) | This study |

| | | |
|-----------|--|------------|
| pAlkane7 | pYX212-(<i>TPIp-SeAAR-FBA1t</i>)+(PGK1p- <i>EcFNR-CYC1t</i>)+(TEF1p- <i>EcFD-TDH2t</i>)+(TDH3p- <i>SeADO</i> -ADH1t) | 29 |
| pAlkane16 | pYX212-(<i>TPIp-MmCAR-FBA1t</i>)+(PGK1p- <i>EcFNR-CYC1t</i>)+(TEF1p- <i>EcFD-TDH2t</i>)+(TDH3p- <i>SeADO</i> -ADH1t)+(tHXT7p- <i>npgA-pYX212t</i>) | This study |
| pAlkane65 | pYX212-(<i>UAS-TDH3p-SeADO-pYX212t</i>) | This study |
| pAlkane67 | pYX212-(<i>UAS-TDH3p-SeADO-pYX212t</i>) | This study |
| pAlkane68 | pYX212-(<i>GAL7p-NpADO-CYC1t</i>)+(UAS-TDH3p- <i>SeADO</i> -pYX212t) | This study |

126 a, Expressed genes are indicated in bold

127 b, per1 means the peroxisome targeting peptide 1 encoding sequence:

128 GGTGGTGGTTCTTCTAACTA and per2 means peroxisome targeting peptide 1 encoding

129 sequence: GGTGGTGGTTCTGCCGCTGTAAAATATCGCAGGCAAAATCTAACTA

Supplementary Table 3 *S. cerevisiae* strains used in this study.

| Strain | Genotype or characteristic | Resource |
|--|---|--|
| Background strains/fatty acid producing strains | | |
| CEN.PK 113-11C | MAT α MAL2-8c SUC2 his3Δ1 ura3-52 | Kötter, University of Frankfurt, Germany |
| EY1673 | MAT α his3Δ1 leu2Δ0 lys2Δ0 ura3Δ0 PEX3-mRFP+kanMX6 | ³ |
| YJZ01 | MAT α MAL2-8c SUC2 his3Δ1 ura3-52 hfd1Δ | ²⁹ |
| YJZ02 | MAT α MAL2-8c SUC2 his3Δ1 ura3-52 pox1Δ | This study |
| YJZ03 | MAT α MAL2-8c SUC2 his3Δ1 ura3-52 hfd1Δ pox1Δ | This study |
| YJZ04 | MAT α MAL2-8c SUC2 his3Δ1 ura3-52 pox1Δ faa4Δ | This study |
| YJZ05 | MAT α MAL2-8c SUC2 his3Δ1 ura3-52 pox1Δ faa1Δ | This study |
| YJZ06 | MAT α MAL2-8c SUC2 his3Δ1 ura3-52 pox1Δ faa1Δ faa4Δ | This study |
| YJZ07 | MAT α MAL2-8c SUC2 his3Δ1 ura3-52 hfd1Δ pox1Δ faa1Δ | This study |
| YJZ08 | MAT α MAL2-8c SUC2 his3Δ1 ura3-52 hfd1Δ pox1Δ faa1Δ faa4Δ | This study |
| JV03 | MAT α MAL2-8c SUC2 ura3-52 HIS3 are1Δ dga1Δ are2Δ lro1Δ pox1Δ | ³⁰ |
| JV03RtFAS | MAT α MAL2-8c SUC2 ura3-52 HIS3 are1Δ dga1Δ are2Δ lro1Δ pox1Δ pRtFAS | This study |
| RWB837 | MAT α pdc1Δ(-6,-2)::loxP pdc5Δ(-6,-2)::loxP pdc6Δ(-6,-2)::loxP ura3-52 | ³¹ |
| IMI076 | MAT α pdc1Δ(-6,-2)::loxP pdc5Δ(-6,-2)::loxP pdc6Δ(-6,-2)::loxP ura3-52 MTH1-ΔT | ³¹ |
| FA0 | MAT α MAL2-8c SUC2 his3Δ1 ura3-52 hfd1Δ pox1Δ faa1Δ faa4Δ pYX212 | This study |
| FA1 | MAT α MAL2-8c SUC2 his3Δ1 ura3-52 hfd1Δ pox1Δ faa1Δ faa4Δ pCoA1 | This study |
| FA2 | MAT α MAL2-8c SUC2 his3Δ1 ura3-52 hfd1Δ pox1Δ faa1Δ faa4Δ pCoA2 | This study |
| FA3 | MAT α MAL2-8c SUC2 his3Δ1 ura3-52 hfd1Δ pox1Δ faa1Δ faa4Δ pCoA3 | This study |
| FA4 | MAT α MAL2-8c SUC2 his3Δ1 ura3-52 hfd1Δ pox1Δ faa1Δ faa4Δ pCoA4 | This study |
| YJZFA1 | MAT α MAL2-8c SUC2 his3Δ1 ura3-52 hfd1Δ pox1Δ faa1Δ faa4Δ pFab1, p413::HIS3 | This study |
| YJZFA2 | MAT α MAL2-8c SUC2 his3Δ1 ura3-52 hfd1Δ pox1Δ faa1Δ faa4Δ X2::(TEF1p- ACC1**-CYC1t) pFab1 p413::HIS3 | This study |
| YJZ13 | MAT α MAL2-8c SUC2 ura3-52 hfd1Δ pox1Δ faa1Δ faa4Δ his3Δ::HIS3+(TEF1p-'tesA-HIS3t) | This study |
| YJZ39 | MAT α MAL2-8c SUC2 ura3-52 hfd1Δ pox1Δ faa1Δ faa4Δ his3Δ::HIS3+(TPIp-RtACL-FBA1t)+(TDH3p-RtME-CYC1t)+(tHXT7p-'MDH3-TDH2t)+(PGK1p-CTP1-ADH1t)+(TEF1p-'tesA-HIS3t) | This study |

| | | |
|--------|---|------------|
| YJZ41 | <i>MATA; MAL2-8c SUC2 ura3-52 hfd1Δ pox1Δ faa1Δ faa4Δ his3Δ::HIS3+(TPIp-MmACL-FBA1t)+(TDH3p-RtME-CYC1t)+(tHXT7p-'MDH3-TDH2t)+(PGK1p-CTP1-ADH1t)+(TEF1p-'tesA-HIS3t)</i> | This study |
| YJZ42 | <i>MATA MAL2-8c SUC2 ura3-52 hfd1Δ pox1Δ faa1Δ faa4Δ his3Δ::HIS3+(TPIp-HsACL-FBA1t)+(TDH3p-RtME-CYC1t)+(tHXT7p-'MDH3-TDH2t)+(PGK1p-CTP1-ADH1t)+(TEF1p-'tesA-HIS3t)</i> | This study |
| YJZ43 | <i>MATA MAL2-8c SUC2 his3Δ1 ura3-52 hfd1Δ pox1Δ faa1Δ faa4Δ ura3Δ::(TPIp-ScFAS1-FBA1t)+(TEF1p-ScFAS2-CYC1t)+amdSym</i> | This study |
| YJZ44 | <i>MATA MAL2-8c SUC2 his3Δ1 ura3-52 hfd1Δ pox1Δ faa1Δ faa4Δ ura3Δ::(TPIp-RtFAS1-FBA1t)+(TEF1p-RtFAS2-CYC1t)+amdSym</i> | This study |
| YJZ45 | <i>MATA MAL2-8c SUC2 ura3-52 hfd1Δ pox1Δ faa1Δ faa4Δ his3Δ::HIS3+(TPIp-MmACL-FBA1t)+(TDH3p-RtME-CYC1t)+(tHXT7p-'MDH3-TDH2t)+(PGK1p-CTP1-ADH1t)+(TEF1p-'tesA-HIS3t) ura3Δ::(TPIp-RtFAS1-FBA1t)+(TEF1p-RtFAS2-CYC1t)+amdSym</i> | This study |
| YJZ45U | <i>MATA MAL2-8c SUC2 ura3-52 hfd1Δ pox1Δ faa1Δ faa4Δ his3Δ::HIS3+(TPIp-MmACL-FBA1t)+(TDH3p-RtME-CYC1t)+(tHXT7p-'MDH3-TDH2t)+(PGK1p-CTP1-ADH1t)+(TEF1p-'tesA-HIS3t) ura3Δ::(TPIp-RtFAS1-FBA1t)+(TEF1p-RtFAS2-CYC1t)+amdSym p416::URA3</i> | This study |
| YJZ47 | <i>MATA MAL2-8c SUC2 hfd1Δ pox1Δ faa1Δ faa4Δ his3Δ::HIS3+(TPIp-MmACL-FBA1t)+(TDH3p-RtME-CYC1t)+(tHXT7p-'MDH3-TDH2t)+(PGK1p-CTP1-ADH1t)+(TEF1p-'tesA-HIS3t) ura3Δ::(TPIp-RtFAS1-FBA1t)+(TEF1p-RtFAS2-CYC1t)+amdSym acc1::KIURA3+TEF1p+ACC1</i> | This study |

Fatty alcohol producing strains

| | | |
|-------|---|------------|
| FOH1 | CEN.PK 113-11C, pAOH3 | This study |
| FOH2 | <i>MATA MAL2-8cSUC2 his3Δ1 ura3-52 pox1Δ pAOH3</i> | This study |
| FOH3 | <i>MATA MAL2-8c SUC2 his3Δ1 ura3-52 hfd1Δ pox1Δ pAOH3</i> | This study |
| FOH4 | <i>MATA MAL2-8c SUC2 his3Δ1 ura3-52 pox1Δ faa4Δ pAOH3</i> | This study |
| FOH5 | <i>MATA MAL2-8c SUC2 his3Δ1 ura3-52 pox1Δ faa1Δ pAOH3</i> | This study |
| FOH6 | <i>MATA MAL2-8c SUC2 his3Δ1 ura3-52 pox1Δ faa4Δ pAOH3</i> | This study |
| FOH7 | <i>MATA MAL2-8c SUC2 his3Δ1 ura3-52 hfd1Δ pox1Δ faa1Δ pAOH3</i> | This study |
| FOH8 | <i>MATA MAL2-8c SUC2 his3Δ1 ura3-52 hfd1Δ pox1Δ faa1Δ faa4Δ pAOH3</i> | This study |
| FOH10 | <i>MATA MAL2-8c SUC2 his3Δ1 ura3-52 hfd1Δ pAOH0</i> | This study |
| FOH11 | <i>MATA MAL2-8c SUC2 his3Δ1 ura3-52 hfd1Δ pAOH1</i> | This study |
| FOH13 | <i>MATA MAL2-8c SUC2 his3Δ1 ura3-52 hfd1Δ pAOH3</i> | This study |

| | | |
|-------|--|------------|
| FOH14 | <i>MATa MAL2-8c SUC2 his3Δ1 ura3-52 hfd1Δ pAOH4</i> | This study |
| FOH15 | <i>MATa MAL2-8c SUC2 his3Δ1 ura3-52 hfd1Δ pAOH5</i> | This study |
| FOH16 | <i>MATa MAL2-8c SUC2 his3Δ1 ura3-52 hfd1Δ pAOH6</i> | This study |
| FOH21 | <i>MATa MAL2-8c SUC2 his3Δ1 ura3-52 pox1Δ faa1Δ faa4Δ pAOH11</i> | This study |
| FOH23 | <i>MATa MAL2-8c SUC2 his3Δ1 ura3-52 hfd1Δ pAOH11</i> | This study |
| FOH24 | <i>MATa MAL2-8c SUC2 his3Δ1 ura3-52 hfd1Δ pAOH12</i> | This study |
| FOH28 | <i>MATa MAL2-8c SUC2 his3Δ1 ura3-52 hfd1Δ pox1Δ faa1Δ faa4Δ pAOH8</i> | This study |
| FOH29 | <i>MATa MAL2-8c SUC2 his3Δ1 ura3-52 hfd1Δ pox1Δ faa1Δ faa4Δ pAOH9</i> | This study |
| FOH30 | <i>MATa MAL2-8c SUC2 his3Δ1 ura3-52 hfd1Δ pox1Δ faa1Δ faa4Δ pAOH17</i> | This study |
| FOH31 | <i>MATa MAL2-8c SUC2 ura3-52 hfd1Δ pox1Δ faa1Δ faa4Δ adh6Δ::kanMX, pAOH9</i> | This study |
| FOH33 | <i>MATa MAL2-8c SUC2 ura3-52 hfd1Δ pox1Δ faa1Δ faa4Δ, adh6Δ::kanMX, gal80Δ, gal1/10/7Δ::(GAL7p-MmCAR-ADH1t)+(GAL3p-npgA-FBA1t) pAOH9</i> | This study |

Alkane producing strains

| | | |
|-------|---|---------------|
| ZW31 | <i>MATa MAL2-8c SUC2 his3Δ1 ura3-52 hfd1Δ pox1Δ adh5Δ</i> | This study |
| YJZ60 | <i>MATa MAL2-8c SUC2 his3Δ1 ura3-52 hfd1Δ pox1Δ Gal80Δ:: SeFNR+SeFd adh5Δ:: (TPIp-MmCAR-FBA1t)+(PGK1p-EcFNR-CYC1t)+(TEF1p-EcFD-TDH2t)+(tHXT7p-npgA-ADH5t)</i> | This study |
| A0 | <i>MATa MAL2-8c SUC2 his3Δ1 ura3-52 hfd1Δ pAlkane7 (previously named as KB19)</i> | ²⁹ |
| A1 | <i>MATa MAL2-8c SUC2 his3Δ1 ura3-52 hfd1Δ pAlkane06</i> | This study |
| A2 | <i>MATa MAL2-8c SUC2 his3Δ1 ura3-52 hfd1Δ pox1Δ pAlkane06</i> | This study |
| A3 | <i>MATa MAL2-8c SUC2 his3Δ1 ura3-52 hfd1Δ pox1Δ adh5Δ pAlkane06</i> | This study |
| A5 | <i>MATa MAL2-8c SUC2 his3Δ1 ura3-52 hfd1Δ pox1Δ Gal80Δ:: SeFNR+SeFd adh5Δ:: (TPIp-MmCAR-FBA1t)+(PGK1p-EcFNR-CYC1t)+(TEF1p-EcFD-TDH2t)+(tHXT7p-npgA-ADH5t) pAlkane67</i> | This study |
| A6 | <i>MATa MAL2-8c SUC2 his3Δ1 ura3-52 hfd1Δ pox1Δ Gal80Δ:: SeFNR+SeFd adh5Δ:: (TPIp-MmCAR-FBA1t)+(PGK1p-EcFNR-CYC1t)+(TEF1p-EcFD-TDH2t)+(tHXT7p-npgA-ADH5t) pAlkane68</i> | This study |

Supplementary Table 4. Primers used in this study

| Primer No. | Name | Sequence (5'-3') |
|---|------------|--|
| Primers for seamless gene deletion of <i>POX1</i>, <i>FAA1</i> and <i>FAA4</i> | | |
| p1 | POX1(up)-F | GATTCCTTCAGTTCCACTTTTGC |
| p2 | POX1(up)-R | GAATTGAAACAAAGTCGAAAACAGAGGGTCAAGGAAAACAGGAAACCTCTACTC ACATATCGCAATACTAATTATTAT |
| p3 | KIURA3-F1 | CTTCGAACCCCTCTGTTTGCACCTTGTTCAATTCAACTAGTGTGCCAGTTAACG TGATTCTGGTAGAAGATCG |
| p4 | KIURA3-R2 | GAGCCAATAGTTGGCTGCACAACCTTAGAGAGATCCATCGATAAGCTTGATATCG |
| p5 | POX1(dw)-F | GATCTCTAAAGTTGTGCAGCCAC |
| p6 | POX1(dw)-R | CGCATTAGCTGCACCACCTAAC |
| p7 | FAA1(up)-F | CACCCACCCATCGCATATCAGG |
| p8 | FAA1(up)-R | CTGAAAAAGTCTTAGTATGATGAGGCTTCATCATGAAATGTTGATCCATTACA TATTGTTGTCTTTTGTC |
| p9 | KIURA3-F2 | GATAGGAAAGCCTCATCATACTAAAGCACTTTCAGTTTGCTTAGAACTGCTACC GTGATTCTGGTAGAAGATCG |
| p10 | KIURA3-R2 | CAACATATTGTTAGATCTGTAACGGACTCTAATTCCATCGATAAGCTTGATATCG |
| p11 | FAA1(dw)-F | GAAATTAGAGTCCGTTACAGATC |
| p12 | FAA1(dw)-R | GTCAAAGAACACTATGCCTGCTAG |
| p13 | FAA4(up)-F | GTCCCCATCAATTAAAGAACCCCTC |
| p14 | FAA4(up)-R | GAAAATGAAACGTAGTGTATGAAGGGCAGGGGGAAAGTAAAAACTATGTTCC TTTACATTTGATGCGTACTTCTAG |
| p15 | KIURA3-F3 | CTTCCCCCTGCCCTCATAACACTACGTTCTATTCTAAGAGCATCAATTGCGTGA TTCTGGTAGAAGATCG |
| p16 | KIURA3-R4 | GATATCACCGGTACGGAACCAAGCCATCATCGTAAAGGCATCGATAAGCTTGATATCG |
| p17 | FAA4(dw)-F | CCTTACCGATGATGGCTGGTTC |
| p18 | FAA4(dw)-R | GATGTAACAAGACCGTTCTGGAG |
| Primers for episomal plasmid construction for fatty acid production | | |
| p19 | TPIp-F | GTTTAAAGATTACGGATATTAACCTACTTAGAATAATG |
| p20 | TPIp-R | CATTTTAGTTATGTATGTTTTGTAG |
| p21 | PGK1p-F | CGCACAGATATTATAACATCTGCACAATAGG |
| p22 | PGK1p-R | CATTTGTTATATTGTTAAAAAGTAGATAATTAC |
| p23 | TEF1p-F | ATAGCTCAAAATGTTCTACTCCTTTTACTC |
| p24 | TEF1p-R | CATTTGTAATTAAAACCTAGATTAGATTGCTATGC |
| p25 | TDH3p-F | CTCGAGTTATCATTATCAACTTGCCATTTC |
| p26 | TDH3p-R | GTTTGTATGTGTGTTATCGAAACTAAGTCTTGGTG |
| p27 | tHXT7p-F | GTATTCTTGAATGGCAGTATTGATAATGATAAAACTCGAGCTCGTAGGAACAATTG |
| p28 | tHXT7p-R | CATTTTGATTAAAATAAAAAACTTTTGTGTTTG |
| p29 | FBA1t-F | GTAAATTCAAATTGATATAGTTTTAATGAG |
| p30 | FBA1t-R | AGTAAGCTACTATGAAAGACTTACAAAGAAC |
| p31 | CYC1t-F | GATACCGTCGACCTCGAGTCATGTAATTAGTTATGTC |

| | | |
|-----|-----------|---|
| p32 | CYC1t-R | GGGTACCGGCCGCAAATTAAAGCCTCGAGCGTCC |
| p33 | TDH2t-F | ATTTAACTCCTTAAGTTACTTTAATGATTAGTTTTA |
| p34 | TDH2t-R | GCGAAAAGCCAATTAGTGTGATAC |
| p35 | ADH1t-F | GCGAATTCTTATGATTATGATTTTATTATAAAG |
| p36 | ADH1t-R | GCATATCTACAATTGGGTGAAATGGGGAGCGATTG |
| p37 | pYX212t-F | TAGGGCCCACAAGCTTACCGCTGACCCGGGTATCC |
| p38 | pYX212t-R | GCGTAAACCACAAATCGGAACCCCTAAAGG |
| p39 | RtACL-F1 | CTATAACTACAAAAAACACATACATAAACTAAAAATGTCCGCAAAGCCTATCAGAG |
| p40 | RtACL-R1 | CTCATTTAAACTATATCAATTAATTGAATTAACTTATTGTCTTGACTAAAATT C |
| p41 | RtME1-F1 | CAAGAACTTAGTTCGAATAAACACACACATAAACAAACAAATGCCTGCTCATTTGCC |
| p42 | RtME1-R1 | GACATAACTAATTACATGACTCGAGGTCGACGGTATCTCATACTTTCTCAATGGTC |
| p43 | LsME1-F1 | CAAGAACTTAGTTCGAATAAACACACACATAAACAAACAAATGGCCCTAAATCCTCCA |
| p44 | LSME1-R1 | GTGACATAACTAATTACATGACTCGAGGTCGACGGTATCTCATACTTTCTCAATGGTC |
| p45 | MDH3t-F1 | GTTTTTTAATTAAATCAAAAAATGGTCAAAGTCGAATTCTTG |
| p46 | MDH3t-R1 | GGATACCCGGGTCGACCGTAAGCTTGTGGCCCTATCAAGAGTCTAGGATGAAACTC |
| p47 | MDH3t-R2 | AAAAAAACTAAATCATTAAAGTAACTTAAGGAGTTAAATTCAAGAGTCTAGGATGAAAC |
| p48 | CTP1-R | CTTATTTAATAATAAAATCATAAATCATAAGAAATTGCTCAGGCTAGCATAACTAAG |
| P49 | CTP1-F | GAAGTAATTATCTACTTTACAACAAATATAACAAATGTCCAGTAAAGCTACCAAAA G |
| P50 | tTesA-F: | GCATAGCAATCTAATCTAAGTTTAATTACAAAATGGCGACTTTGTTAATT |
| P51 | tTesA-R | GGATACCCGGGTCGACCGTAAGCTTGTGGCCCTATCAAGAATCGTATTGACTAAT G |
| P52 | PGK1p-R2 | CTTATTTAATAATAAAATCATAAATCATAAGAAATTGCTTGTATATTGTTAAA AAG |
| P53 | fadM-F | GCATAGCAATCTAATCTAAGTTTAATTACAAAATGCAAACCCAAATTAGGTTAG |
| P54 | fadM-R | GGATACCCGGGTCGACCGTAAGCTTGTGGCCCTATTATTTACCATTGTTCTAAC |

Primers for constructing pathways for alkane production

| | | |
|-----|---------------------|--|
| p55 | CAR-F2 | CTATAACTACAAAAAACACATACATAAACTAAAAATGTCACCTATCACCAAGAGAAG |
| p56 | CAR-R2 | CTCATTAAAAAACTATATCAATTAATTGAATTAACTCACAACAAACCAACAATCTC |
| p57 | npgA-F4 | CACAAAAACAAAAGTTTTAATTAAATCAAAAAATGGTCAAGACACATCAAG |
| p58 | npgA-R4 | GGATACCCGGGTCGACCGTAAGCTTGTGGCCCTATTAGGATAGGCAATTACACACC |
| p59 | ADH5up-F | AAAAATGACTGATGTCTACAGGAC |
| p60 | ADH5up-R | CATTATTCTAAGTAAAGTTAAATATCCGAATCTTAAACCATGATGCTTGATTGTAG ATATG |
| p61 | ADH5dn-F | CGCCCTTGCTATGGGTTACAG |
| p62 | ADH5dn-R | ACCTCTGGCGAAGAAATCTAAAGC |
| p63 | TDH2t(tHxt 7p)-R | GAAGAACACGCAGGGGCCGAAATTGTCCTACGAGCGAAAAGCCAATTAGTGTGATA C |
| p64 | npgA-R5 | GCTTATATAAAAAGTAAAATATTCAAAATTGTTACAAAGATTAGGATAGGCA ATTACACACC |
| p65 | KIURA3-F6 | CGAATTGATGAATATTTTACTTTATATAAGCTATTGTAGATATTGACGTGATT CTGGGTAGAAGATCG |

p66 KIURA3-R6 CGATACCAATGACCTGTAAACCCATAGCAAGGGCGATCGATAAGCTTGATATCG

Primers for constructing pathways for fatty alcohol production

| | | |
|-----|------------|--|
| p67 | CAR-F1 | CAAGAACCTAGTTCGAATAAACACACATAAAACAAACAAAATGTCACCTATCACCAGAG AAG |
| p68 | CAR-R1 | CTTATTAAATAATAAAAAATCATAAATCATAAGAAATTGCGTTACAACAAACCCAACAATC TC |
| p69 | npgA-F3 | GCTTAAATCTATAACTACAAAAACACATACATAAACTAAAAATGGTGCAAGACACATC AAG |
| p70 | npgA-R3 | CTCATTAAAAACTATATCAATTAATTGAATTAACTTAGGATAGGCATTACACAC |
| p71 | YjgB-F | GAAAGCATAGCAATCTAATCTAAGTTTAATTACAAAATGTCATGATAAAAAGTTAC |
| p72 | YjgB-R | GGATACCCGGTCGACCGTAAGCTTGTGGCCCTATTAGTGTGGTATGGTGGTGGTGGTGG TAATC |
| p73 | ADH5-F | GAAAGCATAGCAATCTAATCTAAGTTTAATTACAAAATGCCTCGCAAGTCATTCTGA AAAAC |
| p74 | ADH5-R | GGATACCCGGTCGACCGTAAGCTTGTGGCCCTATCATTAGAAGTCTCAACAAACAT ATC |
| p75 | ADH6-F | GAAAGCATAGCAATCTAATCTAAGTTTAATTACAAAATGTCTTACCTGAGAAATTGA AG |
| p76 | ADH6-R | GGATACCCGGTCGACCGTAAGCTTGTGGCCCTATTAGTCTGAAAATTCTTGTG AGC |
| p77 | ADH7-F | GAAAGCATAGCAATCTAATCTAAGTTTAATTACAAAATGCTTACCCAGAAAAATTCA GG |
| p78 | ADH7-R | GGATACCCGGTCGACCGTAAGCTTGTGGCCCTATTATTATGGAATTCTTATCAT AATC |
| p79 | SFA1-F | GAAAGCATAGCAATCTAATCTAAGTTTAATTACAAAATGTCGCCGCTACTGTTGGTA AAC |
| p80 | SFA1-R | GGATACCCGGTCGACCGTAAGCTTGTGGCCCTACTATTATTATTCATCAGACTCA AGACG |
| p81 | CAR-R3: | CCACCCAACAAACCAACAATCTCAAATC |
| p82 | ADH5-F2 | GTATCAGATTGAGATTGTTGGTTGTTGGTGGTGGTCTGGTGGTGGTTATGCC TTCGCAAGTCATTCTG |
| p83 | ADH5-R2 | CTTATTAAATAATAAAAATCATAAATCATAAGAAATTGCGTTATTAGAAGTCTCAACAA CATATC |
| p84 | ADH5-F3 | CAAGAACCTAGTTCGAATAAACACACATAAAACAAACAAAATGCCTCGCAAGTCATT CTG |
| p85 | ADH5-R3 | CTAATCTTCTCTGGTGATAGGTGACATAGAACCAACCACAGAACCCACACCTTAG AAGTCTCAACAAACATATC |
| p86 | CAR-F3 | GTGGTTCTATGTCACCTATCACCAGAGAAG |
| p87 | ADH5-F4 | CACAAAAACAAAAGTTTTAATTAAATCAAAAAATGCCTCGCAAGTCATTCTGA AAAAC |
| p88 | ADH5-R4 | GACATAACTAATTACATGACTCGAGGTGACGGTATCTCATTAGAAGTCTCAACAAACA TATC |
| p89 | FaCoAR-F1 | GCATAGCAATCTAATCTAAGTTTAATTACAAAATGAATTATTCTTGACAGGTG |
| p90 | FaCoAR-R1 | GGATACCCGGTCGACCGTAAGCTTGTGGCCCTATTACCAATAGATACCTCTCA |
| p91 | FaCoAR -F2 | GTATCAGATTGAGATTGTTGGTTGTTGGTGGTGGTCTGGTGGTGGTTATGAA TTATTCTTGACAGG |
| p92 | FaCoAR -R2 | CTTATTAAATAATAAAAATCATAAATCATAAGAAATTGCGTTACCAATAGATACCTCTCA TAATG |

| | | |
|------|-------------------|---|
| P93 | Gal10t-F2 | CTGGGCTGCAGGAATTGATATCAAGCTTATCGATGGGAGACACTATTGAGGGTACGG AG |
| P94 | Gal10t-R | GTTTCACCGTTTCAAGGTTACAC |
| P95 | MmCAR-F6 | CATGATAAAAAAAACAGTTGAATATTCCCTAAAAATGTACCTATCACAGAGAAGA AAG |
| P96 | npgA-F6 | GAGAAAATAAAAGTAAAAGGTAGGGCAACACATAGTATGGTCAAGACACATCAAG |
| P97 | Gal7p-F | TTTGCCAGCTTACTATCCTTCTG |
| P98 | Gal7p-R | CATTTTGAGGGAATTCACAG |
| P99 | Gal3p-F | GTGCATATTCAGAAGGATAGTAAGCTGGCAAATTGCTAGCCTTCGGTCTGC |
| P100 | Gal3p-R | ACTATGTGTTGCCCTACCTTTAC |
| P101 | FBA1t- URA3-R1 | CATTCATATCATATTTTCTATTAACTGCCTGGTTCTTAAATTTTTATTGGTTGTCG CATCGATAAGCTTGTATCG |
| P102 | URA3(Gal7) -F | CGAGGTCCCTCCTCACCATGGTAAATTGGCTGTGATTCTGGTAGAACATCG |
| P103 | Gal7(dn)-F | AGCCAATTAAACCAATGGTGAAG |
| P104 | Gal7(dn)-R | CAGTCTTGTAGATAATGAATCTG |

Primers for genomic integration for free fatty acid production

| | | |
|------|--------------------|---|
| P105 | His3(up)-F | CTCTTGGCCTCCTCTAGTACACTC |
| P106 | His-R3 | GCAGAAAAGACTAATAATTCTAGTTAAAGCACTCTACATAAGAACACCTTGGTGG |
| P107 | ENO2t-F | AGTGCTTTAACTAAGAATTATTAGTC |
| P108 | ENO2t-R | AGGTATCATCTCCATCTCCATATGCATATCA |
| P109 | ENO2t- TPIp-F | CCACAGTGATATGCATATGGGAGATGGAGATGATACTGATCTACGTATGGTCATTCT C |
| P110 | 'TesA-R2 | CGTATGCTGCAGCTTAAATAATCGGTGTCATCAAGAACATCGTATTGACTAATG |
| P111 | His3t-F | GACACCGATTATTTAAAGCTGCAG |
| P112 | His3t-R | CTGTTATTCTGGCACTTCTTGG |
| P114 | MmACL-F | CTATAACTACAAAAACACATACATAAAACTAAAAATGTCCGCTAAAGCTATTCC |
| P115 | MmACL-R | GGATACCCGGGTCACCGTAAGCTGTGGGCCCTATTACATACTCATGTGTCAGG |
| P116 | HsACL-F | CTATAACTACAAAAACACATACATAAAACTAAAAATGTCCGCAAAGCATTCC |
| P117 | HsACL-R | GGATACCCGGGTCACCGTAAGCTGTGGGCCCTATTACATACTCATGTGTCAGG |
| P118 | URA3(up)-F | AAACGACGTTGAAATTGAGGCTACTGCG |
| P119 | URA3(up)-R | GAAGAAGAACATGACCACATCGTAGATCCCCATTGGACTAGGATGAGTAGCACGTT CC |
| P120 | RtFAS1-F | CTATAACTACAAAAACACATACATAAAACTAAAAATGAACGGCCGAGCGACGCCAG |
| P121 | RtFAS1-R | CTCATTAACCAATTATCAATTAAATTGAATTAACTCAGAGCCGCCAACGCTGA G |
| P122 | RtFAS2-F | GAAAGCATAGCAATCTAATCTAAGTTAATTACAAAATGGTCGCGGCCAGGACTTGC |
| P123 | RtFAS2-R | GACATAACTAATTACATGACTCGAGGTCGACGGTATCCTACTTCTGGCGATGACGACG |
| P124 | TEF1p(URA 3)-F: | GTTTGCTGGCCGCATCTCTCAAATATGCTTCCCAGCCATAGCTCAAAATGTTCTACT CC |
| P125 | Amdsym-F | GAGTAAAAAGGAGTAGAACATTGAGCTATAAGCTCGTACGCTGCAGGTG |
| P126 | Amdsym-R | CTGGCCGCATCTCTCAAATATGCTTCCCAGCCACTACTAGGGAGACCG |
| P127 | URA3(dn)-F | GGGAAGCATATTGAGAACATGCGGC |

| | | |
|------|-------------------|--|
| P128 | URA3(dn)-R | GGAAACGCTGCCCTACACGTTCGC |
| P129 | ACC1(up)-F | CGTTACGCCCTCCAGAGTCACC |
| P130 | ACC1(up)-R | CTGGGCTGCAGGAATTGATATCAAGCTTATCGATGCTAGGCTATACTGTGCCAGAATA CG |
| P131 | TEF1p(ACC1)-F | CATCCAATGCAGACCGATCTCTACCCAGAACATCACATAGCTTCAAAATGTTCTACTCC |
| P132 | TEF1p(ACC1)-R | CTGTGGAGAAGACTCGAATAAGCTTCTCGCTATTTGTAATTAAAAGCTTAGATTAG |
| P133 | ACC1-F | ATGAGCGAAGAAAGCTTATTG |
| P134 | ACC1(In)-R | GTACCACCTGGCACTTCAATG |

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Supplementary Table 5. Codon optimized genes used in this study.

| Synthesized genes | Sequence (5'-3') |
|-------------------|--|
| RtACL | ATGTCGCAAAGCTATCAGAGAACGACGCCAATTGTTAGCCTATCACTTAGCAAG AGCCCCTACCGCAGGTTCAAAGCAGTGCAGAGATGGTTCAATCTCCAGAAAGTAAAA GTTGCCAAGTCTCATGGGACCCTGAAACCAATCAAGTAACCTCCAGATGCTGCATTGCCCA TTGGGTTTCACTGAAAATTGGTTGTCAAGCCAGATCAATTGATTAAAAGACGTGGTAAAG CAGGTTGTTAGCCTAAACAAAACCTGGGCTGAAGGTAACAATGGATAGCCGAAAGAGC TGGTAAACAAGTCCAAGTAGAAAAGACTACAGGTACATTGAACAACCTCATCGTTGAACCAT TCTGTCCACATCCTCCGATGCTGAATACTACATTGCATCAACAGTGTAGAGAAGGTGAC GTAATTGTTACTCAGGAAGGTGGTGTGAATTGCCCTCAGAGATGAAATCAGAAAGTCAATTGTA TTGTTAGTACCGAGTTGGTGTGAATTGCCCTCAGAGATGAAATCAGAAAGTCAATTGTA AGCATGTTACAGGTGCAGAAAGACAAGAAGCCTTAATAGACTACATCATCAGATTGACTCC GTCTACGTAGATTGCACTTGCTTACTTAGAAATCAATCCATTGGTGCAGTCGAAAACCT TCTACTGGTAAAACAGATATTCTATTGGATATGCCGCTAAGTTGGACCAAACGCTGA ATACGTAGTTGGTCCAAAATGGGCAATAGCCAGAGATCCTCAATCATTAATCCAGCAGCCG CTCCTATGTCTAACGGTAAAATCTAGCTGATAAGGGTCCACCTATGTTTGGCACCTCCAT TCGGTAGAGACTTAACTAAGGAAGAAGCATATATTGCCAAGTTGGATGGTCTACAGGTGC CTCATTGAAATTGACCGTATTAAATGCTGAAGGTAGAAATATGGACAATGGTTGCTGGTGT GGTGCATCCGTCGTATATAGTGATGCTATCGCAGCTCATGGTTTGGCACGAAATTGGCTAA TTATGGTGAATACTCTGGTCACCAACTCAAACACAAACCTATGAATACGCCAAAACATT GGATTGATGACCAAGAGGTACTCCAAACCTCAGGTAAATTGTTTATTGGTGTGGTGT TTGCAAATTACTAACGTTGCTGCAACATTCAAAGGTATCATCACAGCTTGAAGGAATACC AACATAGATTGCAAGAACACAAAGTTAGAAATCTCGTCAGAAGAGGTGGTCAAATTACCA AGAAGGTTAAAGGCTATGAGATTGTTAGGTAAACTTGGGTGTAGAAATCCAAGTTTC GGTCCAGAAACACATATTACCTCTATAGTCCATTGGTTAGGTTGATTAATCAGTTGAT GACGCCCTAAAGGTCCCAGGTGCTAGAGCTGCTGATGCAACTGGTACATTAACCCAGT TCCTGGTCCCCAAAAGTAGAGCCGCTCAATTGCCCTACAGGTGCATCTACCCCATCAAGAC AACAAACCTCAAGATAACATAGTATCCTTAGTGATAAAGTTCATGCTCCAGACTCTGGT CCTGGTATAGACCTTCGATGAAACCACTAGAAGTATAGTTACGGTTACAACCTAGAGC TATCCAAGGCATGTTGGATTTGACTCGCATGTTGAGAAACACCATCTGTCGAGCTA TGGTTATCCTTGGTCATCACGTTAAAAATTCTACTGGGTACTAAGGAACATTGT TGCCAGTTTACTTCATGAAGGAAGCTGTCGCAAAGTGCCTGATGCCGACGTTGCGTA AACTCGCTTCAAGATCAGTTACCAATCTACTTGGAAAGCATTGAAATTCCACAAATC AAAGCCATTGCTTGATAGCTGAAGGTGTTCTGAAAGACATGCAAGAGAAATTACACTT GGCCAAAAGAAAGAAGTAATTATCATCGGCCAGCTACTGTTGGTGTATTAACCGAGT TGTTTCAAATCGTAACACAGGTGGTATGAACGAAACATCTGTCAGTAAATTGTATAG AGCTGGTCTGAGGTTACGTTCTAAGTCAGGTGGCATGTCATAAGAATTAAACACATAT TATCATTGACAACCGACGGTGCTTATGAAGGTATGCAATTGGTGTGACAGATAACCCAGG TACTACTTTATTGACCATTGTTGAGATACGAAGCAGATCCTAAGTGAAGATGTTGGTTT GTTGGGTGAAGTCGGTGTAGAAGAATACAGAGTTATTGAAGGCTGTCAAATCTGGTCAA ATTAAGAAACCAATCGTCGATGGCCATAGGTACTTGCCTGCAAAGATGTTGCCACAGACG TACAATTGGTCACGCTGGTTATGGCTAATTGTCATTGGAAACAGCTGAAGCTAAAC AACGCAATGAGAGCTGGTTTATTGTTCTCCAACCTCGAAGAATTGCCACAAGTTTG GCTGAAACATACCAAAAATTGGTCGGTACGGTACTATTCAACCAAAGCCTGAAGTCC ACCTCAAATACCAATGGATTACAATTGGGCAAAACATTGGGTATGGTCAGAAAACCTGCC GCTTTATCTCCACCATTAGTGACGAAAGAGGTCAAGAATTGTTATGCTGGTATGCCAAT TTCTAAGGTTTCAAGAAGATAGGTATCGGTGGTGTCTATTGTTGGTCAAGA |

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| | <p>GAAGATTACCAGCCTACGCTACTAAGTCTGGAAATGGTTGATGTTGACTGCTGATCAT GGTCTGCCGCTCTGGTCTATGACCACTGTAATTACAACCAGAGCCGGTAAAGATTGGT ATCTTCATTAGTTGCTGGTTGTTAATCTAGGTGACAGATTGGTGGTGCTTAGACGGTG CAGCCCAAGAGTTACTAGAGCTTCGAAGCAGGTTGACTCCAAGAGAATTGTTGATTCT ATGAGAAAGGCAAATAAGTTAACCAAGGTATCGGTATAAGGTCAAATCAAAGGCTAATC CTGATAAAAGAGTTGAATTGGTCAAAAACACTACGTTAACACTCCCATCCGCAAAGTTG TTAGAATACGCATTAGCCGTAGAAGATGTTACCAAGTGTCAAGAAAGACACTTGTCTGAA CGTTGATGGTGTATTGCAGTCCTTGATGTTGAAAAATTCTGGTGCCTCACCGC TGAAGAAGCTGCTGAATACATGAAGATCGGTACTTGAACGGTTGTTGTTGGTAGAT CAATCGGTTCATAGCACATCACTGGTCAAAAGAGATTGAAGCAACCATTACAGACAT CCTGCTGACGACATTTCATCCAACCATTCAACACTGACAGAATTAGTCCAACAAAGACAA TAA</p> |
| <i>MmACL</i> | <p>ATGTCCGCTAAAGCTATTCCGAACAAACTGGTAAAGAATTATTACAGTACATTGCAC CACCTCAGCCATACAAACAGATTCAAGTATGCAAGAGTTACCCAGATACCGACTGGGCC ATTTGTTACAAGATCACCTGGTTATCTCAATCATTGGTGTCAAACCTGACCAATTGA TTAAAAGACGTGGTAAATTGGGTTAGTCGGTGTAAACTGAGTTAGATGGTGTAAAGTCT TGGTTGAAGCCAAGATTAGGTATGAAGCTACAGTTGGTAAAGCAAAGGGTTCTTGAAGAA ATTTCTTGATCGAACCATCGTACCTCACTCACAAGCTGAAGAATTACGTTGTATCTATG CAACTAGAGAAGGTGACTATGTTCTCATCACGAAGGTGGTGTGACGTCGGTACGTT GACGCCAAAGCTCAAAAGTTGTTAGTAGGTGTGATGAAAAGTTAAACACAGAAGACATCA AGAGACATTGTTGGTACACGCCAGAAGATAAAAAGGAAGTTGGCTTCTTATAAGT GGTTGTTAATTCTACGAAGATTGACTTCACCTACTGGAAATTAAACCTTAGTAGTTA CTAAGGATGGTGTCTATATATTGGACTTAGCTGCAAAAGTAGATGCAACTGCCGACTACATC TGTAAGGTTAAGTGGGTGACATTGAATTCCACCTCATTGGTAGAGAAGCATATCCAGA AGAACCTACATTGCTATTGGACGCAAAATCTGGCCTCATTGAAGTTAACATTGTTGA ACCCTAAGGGTAAATGGACTATGGTGTGCAAGTGTCTATATTCTGA TACAATCTGCACTGGGTGGTGTAAACGAATTAGCTAACTACGGTGAATACTCAGGTGCAC CATCCGAACAAACAAACTTATGATTACGCTAAAGACCATCTTGAGTTAATGACTAGAGAAAAG CATCCTGAAGGTAAAATTGATCATCGTGGTTCTATAGCAAACCTCACTAACGTTGCCGCT ACATTCAAGGGTATAGTCAGAGCTATCAGAGATTCAAGGTCCATTGAAGGAACACGAAG TTACAATATTCTGTCAGAAGAGGTGGCTAACTACCAAGAAGGTTAAGAGTAATGGGTGA AGTTGGAAAACACAGGTATCCCATTGTTAGCTGAAAGTGTCTGCAAGGAACTGGCC TCGTTGGTATGGCTTAGGTATGACCAATTCTAATCAACCTCCAACAGCAGGCCACACC GCCAATTCTGTTAACGCTCCGGTAGTACCTCTACTCCAGCACCATTCAAGAAGTGCCTCA TTCTCCGAAAGTAGAGCTGATGAAGGTTGCTCCAGCTAAAGAAAGCAAACAGCCATGCCTC AAGACTCCGTTCAAGTCTAGATCATTGCAAGGTAATCAGCAACATTATTCTCAGACAT ACCAAAGCCATTGTATGGGTATGCAAACAAAGAGCTGTTCAAGGCATGTTGGATTGACT ATGTTGTTAGAGATGAACCATCTGCGCTGCAATGGTATATCCTTACCGGTGACCAT AAACAAAAGTTCTACTGGGTACAAGGAAATTAAATCCCAGTTAAAACATGGCG TGCTATGAAAAGCATCCTGAAGGTTGATGTATTGATTAACCTCGCTTCAATTAGATCCGCTT TGATTCTACTATGGAAACAATGAACACTACGCAAAATTAGAACCATAGCTATCATTGCAAG GTATACCAGAAGCATTGACTAGAAAGTTAATCAAAAAGGCCGATCAAAAGGTGTCACTAT AATCGGTCCAGCTACAGTAGGTGGTATAAAACCTGGTGTAAAGATCGGTAAACTGGTG GCATGTTGGATAACATATTGGCATCAAAATTGTTAGACCAAGGTTCCGTAGCTTACGTTCA AGAAGCGGTGGTATGAGTAACGAATTGAACACATAATTCAAGAACCACGTGATGGTGT ATGAAGGTGTCGCTATTGGTGGTACAGATACCCAGGTTCACTTTATGGATCATGTTTG AGATATCAAGACACACCTGGTCAAAATGATCGTCTAGGTGAAATAGGTGGTACTG AAGAATACAAAATTGCAAGAGGTATAAAGGAAGGTAGATTGACAAAACCAGTAGTTGTTG</p> |

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| | <p>GTGCATTGGTACTTGTGCAACTATGTTCTTCAGAACGTTCAATTGGCATGCAGGTGCCTG CGCTAATCAAGCATCTGAAACAGCAGTGCCAAAACCAAGCCTAAAGGAAGCTGGTGT TTTGTCCTAGATCATTGATGAATTGGGTGAAATCATTCAATCCGTATATGAAGACTTAGTT GCCAAGGGTGTATTGTCAGCTAAGAACGTTACCTCACACTGTTCTATGGATTACTCA TGGGCAAGAGAATTGGGTTGATCAGAAAGCCAGCTAGTTTATGACCTCTATGTGATGA AAGAGGTCAAGAACATTGATCTATGCTGGTATGCCTATCACTGAAGTCTCAAGGAAGAACAT GGTATCGGTGGTGTATTGGGTTGTTGTTCAAAGAACGATTACCAAAGTACTCATGTCA ATTATAGAAATGTGCTTAATGGTTACAGCTGATCATGGTCCAGCTGTTCTGGTCCCACA ACACCATAATCTGCGCTAGAGCAGGTAAAGATTGGTTCTTCTTGACCTCTGGTTGTTAA CTATTGGTACAGATTGGTGGTGCATTGGACGCCGCTGCAAAAATGTTCAAAGGCTTTC GATTCCGGTATAATCCAATGGAATTGTTAATAAGATGAAAAAGGAGGGTAAATTATCAT GGGTATCGGTATCGTGTAAAGTCAATTAAACCTGATATGAGAGTCAAATATTGAAGG ACTTCGTAAGCAACACTCCCAGCAACACCTTGTAGATTACGCCCTAGAAGTTGAAAG ATTACAACCTCTAAAAGCCAATTGATCTTGAACGTTGATGGTTTATAGGTGTCGCTTTC GTAGACATGTTAAGAAACTGTGGTCTTTACTAGAGAAGAACCGATGAATATGTTGACAT TGGTGTCTTAGGTATATTGCTTAGGTAGATCAATGGGTTTATTGGTCATTACTTGG TCAAAAGAGATTAAAGCAAGGTTGTATAGACACCCTGGGACGATATTCTACGTTTGC CTGAACACATGAGTATGTA</p> |
| HsACL | <p>ATGTCGCAAAAGCCATTCCGAACAAACTGGTAAAGAACATTATTACAGTTCATCTGCAC AACCTCAGCCATACAAACAGATTCAAGTATGCAAGAGTTACTCCAGATACAGACTGGCC AGATTGTTACAAGATCATCCTGGTTGTTACAAAACCTGGTTGTCAGCCTGACCAATTG ATTTAAAGACGTGGTAAATTGGGTTAGTAGGTGTTAATTGACATTAGATGGTGTAAAGTC CTGGTTGAAGCCAAGATTAGGTCAAGAACGCAACCGTCGGTAAGCCACTGGTTCTGAAA AATTCTTGTATCGAACCTTCGTAACCTCATTCTCAAGCTGAAGAACATTACGTTGTTATATAC GCAACTAGAGAACGGTGAATATGCTTGTTCATCAGAACGGTGGTTGATGTAGGTGACG TAGACGCCAAAGCTCAAAGTTGTTAGTTGGTGTGATGAAAAATTGAACCCAGAACAGACAT TAAAAAGCATTGTTGGTCACGCCCTGAAGATAAAAAGGAAATTGGCTCTTTATCTC AGGTTGTTAATTCTACGAAGATTGACTTCACTTACTGGAAATTACCCATTGGTAGT TACAAAGGATGGTGTATACGTTGGACTTAGCTGCAAAGGTCGATGCAACAGCCGACTAC ATTTGTAAGTAAAGTGGGTGACATAGAATTCCACCTCATTGGTAGAGAACATATCC AGAAGAACGCTACATTGCTGATTGGACGCCAAATCCGGTGTAGTTGAAGTTAACCTGT TGAACCTAAAGGTAGAATCTGGACTATGGTGCAGGGGGTGCCTCAGTCGTATATTCC GATACTATTGCGACTGGGTGGTTAACGAATTAGCTAACTACGGTGAATACAGTGGTGC ACCATCTGAACAACAAACCTATGATTACGCTAACAGACTATCTGAGTTAATGACAAGAGAAA AGCATCCTGATGGAAAATTGATCATCGTGGTTCTATCGCTAACCTCACAAACGTGCC GCTACCTCAAAGGTATAGTAAGAGCAATCAGAGATTACCAAGGTCATTGAAGGAACACG AAGTAACCATTGGTAAAGAGGGTGGCTTAACCTACCAAGAACGGTTAACAGTCATGGG TGAAGTAGGTAAAACACAGGTATCCAATTGATCTTGTAGTTGACTGAAACTCACATGACTG CTATTGTTGGTATGGCATTAGGTATAGACCAACCTAACCAACCTCCACTGCTGCTACA CAGCTAACCTCTGTTAACGCTGTTCAACATCCACCCCCAGCCCCATCAAGAACAGCTA GTTTCTGTAATCAAGAGCTGATGAAGTTGCTCCAGCTAACAGAACGGTTAACAGTC CAAGACTCTGTCATCACCTAGATCCTGCAAGGTAAAAGTACCAACTTGTGTTCAAGACAT ACAAAAGCAATTGTTGGGTATGCAAACAGAGCCGTCACGGCATGTTGGATTTCGACT ATGTTGTTCAAGAGATGAACCATCCGTTGCTGCAATGGTCTATCCTTTACTGGTAGCCATA AACAAAAGTTCACTGGGGTACAAGGAAATTAAATCCAGTTTAAAACATGGCCGAT GCTATGAGAACGATCCGTAAGTTGATGTATTGATTAACCTCGCAAGTTAACAGTC TGATTCAACTATGGAAACTATGAACTACGCTAACATCAGAACACTATTGCTATCATTGCAAG GTATCCCAGAACGATTGACAAGAAAATTAAATTTAAAAGGCAGATCAAAAGGGTGTAAACCAT AATCGGTCCAGCAACTGTTGGTGGTACCAACCTGGTTGTTAAGATTGGTAATACAGGTG</p> |

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| | GCATGTTGGATAACATATTGGCTCAAAATTGTATAGACCAGGTTCCGTCGCATACTGATCC AGAAGTGGTGGTATGAGTAACGAATTAAACAACATAATTCAAGAACAAACCGATGGTGTAT ATGAAGGTGGTCTATTGGTGGTACAGATACCCAGGTTACTTTATGGATCATGTTTG AGATATCAAGACACCCCTGGTGTCAAATGATCGTTCTTAGGTGAAATAGGTGGTACAG AAGAATACAAAATTGTAGAGGTATTAAGGAAGGTAGATTGACCAAACCAATTGTTGTTG GTGCATAGGTACATGTGCTACCAGTCTTCAGAAGTTCAATTGGTCACCGCAGGTGCC GCGCTAATCAAGCATCTGAAACAGCAGTGCACAAACCAAGCATTGAAGGAAGCAGGTGT TTTGTCCCTAGATCATTGATGAATTGGTGAATATTCAATCCGTATGAAGACTTAGT AGCCAATGGTGTATTGTCAGCTCAAGAAGTCCCTCACCTACTGTCCTATGGATTACTC TTGGGCTAGAGAATTGGGTTAACAGAAAACCAGCTTCTTTATGACTTCCATTGTGATGA AAGAGGTCAAGAATTGATCTATGCTGGTATGCCTATCACAGAAGTTCAAGGAAGAAATG GGTATAGGTGGTCTTGGGTTGGTGGTCAAAAGAGATTGCCAAGTACTCATGTCA ATTCAATTGAAATGTGCTTAATGGTACCGCTGATCATGGTCCTGCCGTATCCGGTGT ACACTATAATCTGCGTAGAGCAGGTAAGAGTTGGTTCTTCTTGACTTCAGGTTGTTAA CAATTGGTACAGATTGGTGGTCTTGGACGCCGCTGCAAAGATGTTAGTAAGGCATT GATTCTGGTATAATCCAATGGAATTGTTAACAGATGAAAAAGGAGGGTAAATTACAT GGGTATCGGTATCGTGTAAAGTCTATAAATAACCCCTGATATGAGAGTACAAATCTGAAGG ACTATGTTAGACAACACTTCCAGCAACACCTTGTAGATTACGCCCTAGAAGTTGAAAAG ATTACTACATCTAACGAAACCAATTGATCTGAACGTTGATGGTTGATCGGTGTTGCTTT GTTGATATGTTAACGAAACTGTGGTAGTTCACTAGAGAAGGCCATGAATATATTGACAT CGGTGCTTGAACGGTATCTCGTTGGTAGATCAATGGGTTTATTGGTCATTACTTGG TCAAAAGAGATTAAAGCAAGGTTGTATAGACACCCCTGGGATGATATTCCACGTTG CTGAACACATGAGTATGAA |
| RtME | ATGCCTGCTCATTTGCCCTTCACAACCATTACAAGGTGGTCATCCCTCACATTGGGT CCTAAAGAATTATTGATAGAAAGAGCATTGACAAGAGATTGAGATCAATCCAAACGATTGG AAAAATATACCTTTGCCGGTTAACAGAGGTAGAAATCCTGATGTCCTACGGTTAGTA GGTGGTAACATGAAGGAATGTTGCCAATTATCTACTCCTGTTAGGTTAGCTTGTC AAATTGGCCTTGTATCCACCTCCACCTGAAAGTGTATCCAACAATTGACGCATTGATT GTCTTACTCAGATTGCCAAACTTACCTCAATTGATCGGTGGTTGAAGACTAGATTGCC CGATCAAATGCAAATCTCGTTGTACAGACGGTAGTAGAGTATTGGGTTGGGTACTTG GGTGGTGGTGGTATGGGTATATCTCAGGGTAAATTGTCTTACGTTGCTGCTGGTGGT CAATCCAAGGCCACTTACCTATCGTATTGATTTGGTACTGACAACGAAACTTGTAGC TGATCCATTGATCGTTGGTCAAAGAATTAGAAGATTACTCAAGAAAAGTGGTTGGAGTT TGGAAAGTTTCATGAGATGCATGAAACCTCCAAATATGGTTATTCAACACGAAGAC TGGCAAACCTCATTGGCTTCCCTTGTGCTACAGAAGAGATTGTACCCCTTGTCAAC GATGACATTCAAGGTACTGGTCAGTAGTTAGCAGGTGCCATAAGAGCTTCACTTAA CGGTGTTGATTGAAGGATCAAAGATTGGTTGGTCTCAGGTGGT TCGCTGAAACAATATGCAAGTACTCGAATTGCAAGGCATGCTGAAGACGAAGCCAATC AAAGTTCTGGTGGTAGATTCAAAGGGTTGGTCTACAGGTTGACACATTACCAT CTCACAAAAAGTATTGGCAAGATCAGAACCCAGATGCCCTAAATTGAGAACCTTGAAGGA AGTCGTAGAACATGTTCAACCAACTGCTTGTAGGTTATCTACAGTCGGTGGTACTTTAC AAAGGAAATCTGGAGCTATGGCAACTACAATAAGAGACCAATTGTCCTTGCTTATCAA ACCCGTAGCCAAGCTGAATGTACCTCGAAGAACGCTGTTGAAGGTTACTGACGGTAGAGT CTTGTACGCATCCGGTAGTCCATTGATCCTGTTGAATACAAGGGTAAAGATACGAACCA GTCAAGGTAAACATGTATCTCCCTGGTTAGGTATTGGTCTATATTGGCAAGAGTC TCCAAAATTCCAGAAGAATTAGTACATGCATCCGCCAAGGTTAGCAGACAGTTGACACC AGAAGAAACGCCAGACACTGTTGACCGCTGATATCGAAAGAATTAGAGAAGTTCTATAA AAATCGCTGAAACAGTTATACAAGCCGCTAAAGTTAGGTGATAGAAACGAAGAATT GCGTGGTAAATCCAGTGCAGAAATTGACGCCATTGTCAGAAAGGTATGTATCACCCATT |

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| | TAGAAGCAGAACACAAGCACAATGA |
| <i>LsME</i> | ATGGCCCTAAATCCTCCACCAGAGTTCCATTATCGTCAAAGGTCCAATAGACTGC CCTTATGAAGGTAAAGAAATGTTAAACTTACCTCAATTCAATAGAGGTACAGCCTTC ACCGCTGAAGAAAGAGATTGTTAATTGGTCGGAATTGCCAGCTGCATTACAA ACTTGCAAAATCAAGTAGACAGAGCCTATGATCAATACTCTCAATTCTACAGCTT TGGTAAAAACACCTTTAATGTCATTGAAGGTCCAAAACGAAGTATTGACTTCA AATTGTTACAAGATCATTGAAGGAAATGTTCAATCATCTATACTCCAACAGAAC TGAAGCTATCGAACATTATTCAAGATTGTTAGAAGACCAGAAGGTTGTTCTGAA CATCAACCACCCAGAATACATCGAAAGATCCTAGCCGCTGGGTACAGAAGAAG ATATTGACTACATCATTGTTAGTGACGGTAAGAAATTGGGTAGAGTGACCAA GGTGTGGTGTAGGTATCTCAGTGCAAAAGCGTATTAAATGACCTGTGTGCA GGTGTTCATCCATCAAGATGCATTCCAGTTGCCTAGACGTCGGTACTGATAACGAA CAATTGTTAGAAGATGAATTATTTGGTAACAGACACAAACAGAGTTAGAGGTTG TAGATACGATAAATTGTCGATGACTCGTTCAATGTCAGGTTATCAGAAGATTGTTAGATAC TTACAGACCAAGATTGGCTGTTAATGATGACGTCCAAGGTACTGGTGAGTAAC TTTAGCAGCCTGTCTCAGCTGTCAGAGTAGCAGGTATCGATTAGAGACTTGAG AACAGTTATTCGGTGCAGGTACTGCCGTACAGGTATAGCTGACCAATTAAAGAG ATTCTGAATACCAAGGTATCTAAACAAACAAGTTATCGACCATATTGGTTGGT CGATAAGCCTGGTTGTTATTGAAATCCATGCACGATAAGTGACTAGTGACAAAG ACCATACGCTGCATCTGATGACAGATGGAAGGAAATAGATAACAAAGTCCTAAGTG AAATCGTTAGAAAGTTAAGCCTCACGTTGATTGGTTGTTACTAAACCAAAAGG CCTCAACGAAGCTGTTAAGAGAAATGGCTAACGATGTAGAAAGACCAATCGTT TCCCTTGTCAAACCCAACTAGATTGACAGCTACACCAGCTGAAATTAAATA CACCGATGGTAAAGCATTGGTAGCTACTGGTCCCCATTGATCCTGTTGACGGTAA AGAAATCGCTAAAACAACAACTGCTCGTTACCCAGGTATCGGTATGGTTCTAT TTTGTCAAGAGCAGATAGAGTACCGAAACTATGATAGCCGCTGTTGTCAGAAATT AGCATTGGCCCTAGTGAAGAAAGATCCAACAGGTGCATTATTGCTGATGTTGC CGACATAAGAGATATCTGCTAAATTGCTACAGCAGTAGTTGCAAGCATTGGA AGAAGGTAUTGCAAGAGTCGAAGAAATAGAAGGTATTAAAGTCCAAGAGATAGA GACCATTGTTGGAATGGTAAAAGAACAAATGTGGCAACCTGAATACAGACCATT GAGAAAAGTATGA |
| 'tesA | ATGGCCGATACTTGTAAATTGGGTGACTCTTATCAGCCGGTTAGAATGTC GCTAGTGTGATGCCAGCATTGTTAACGATAATGGCAATCTAAGACTCAGTT GTCAATGCATCTATATCAGGTGACACATCACAACAAGGTTGCCAGATTACAGCT TTGTTAAAACAACATCAACCTAGATGGGCTTGGTAGAATTAGGTGGTAACGATGG TTTGGAGAGGTTTCAACCTAACAAACCGAACAAACTTGGAGACAAATCTACAAGA TGTAAAGGCCGCTAATGCAGAACATTGTTAATGCAAATTAGATTACCTGCCAACTA TGGTAGAAGATAACATGAAGCATTCTGCAATCTATCCAAAATTGGCAAAGGAATT TGATGTACCATGTTGCCATTTCATGGAGAAGTTACTAAAACCTCAATGGAT GCAAGATGACGGTATTCCAAACAGAGATGCTAACCTTATAGCAGACTGGAT GGCCAAACAATTGCAACCATTAGTCATCACGATTCTGA |
| AAR | ATGTCGGTTAATAGGTCACTAACAGTTAGAACAAAGCCAGAGATGTCAGTAG AAGAATGGGTTACGATGAATACGCAGACCAAGGTTAGAATTGGTCTTCAGCCC CACCTCAAATCGTAGATGAAATTACAGTTACCTCTGCTACTGGTAAAGTCATTGATG |

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| | <p>GTAGATACATCGAACATGTTCTGCCAGAAATGTTGGCTGCAAGAAGATTCAAAA CTGCAACAAGAAAGGTTGAATGCAATGCCATGCCAAAAGCACGGTATCGAT ATTCCGCATTGGGTGTTACAAGTATAATCTCGAAAACCTCGATTGGCTAGTT TGAGACAAGTTAGAGACACTACATTGAAATTGAAAGATTACCACTGGTAACACC CACACTGCTTACGTCATTGTAGACAAGTAGAAGCCGCTGCAAAAACCTGGGTATA GATATCACACAAGCCACCGTTGCTGTCGGTGCTACTGGTACATCGGTTCCGCA GTATGCAGATGGTGGATTGAAATTGGGTGTTGGTACTTAATCTGACAGCTAG AAACCAAGAAAGATTGGATAACTGCAAGCAGAATTAGGTAGAGGTAACATCTGC CATTGGAAGCCGCTTGCCTGAAGCCGATTTATCGTTGGTCGCTTATGCCAC AAGGTGTAGTTATTGATCCAGCTACCTAAAACAACCTGCGTTGATAGACGGTG GTTATCCTAAAATTGGTTCTAAGGTTCAAGGTGAAGGTATCTATGTTGAACG GTGGTGTCTAGAACATTGTTGATATAGACTGGCAAATCATGTCAGCAGCCGAA ATGGCAAGACCTGAAAGACAAATGTTGCCTGCTGCTGAAGCAATGTTGTTAGA ATTTGAAGGTTGGCACACTAATTCTCTGGGTAGAAACCAAATTACAATAGAAAA GATGGAAGCCATCGGTGAAGCCTCTGTTAGACACGGTTCCAACCTTAGCCTAGC AATCTGA</p> |
| ACR1 | <p>ATGAATAAGAAGTTAGAACGCATTGTTAGAGAAAATGTCAGGGTAAAGTCGCTT AACACTGGTGCCTCCTCAGGTATCGGTTAACTATCGCAAAAAGAATTGCTGCAAGC CGGTGCCATGTTGTTAGTCGCTAGAACTCAAGAACATTGGAAGAAGTTAAGG CTGCAATCGAACACAACAGGTGGTCAAGCATCTATATTCCATGTGATTGACAGACA TGAATGCAATAGATCAATTATCCAACAAATCATGGCCAGTGTAGATCATGTTGACT TTTGATTAATAACGCAGGTAGATCTATAAGAAGAGCCGTTCATGAATCATTTGATA GATTCCACGACTTCGAAAGAACAAATGCAATTAAACTACTTCGGTGCTGTCAGATTGG TATTGAACTTGTGCCTCACATGATCAAGAGAAAGAATGGTCAAATTATAACATCT CTTCAATCGGTGATTGCCAACGCTACCAAGATTCTGCTTATGTTGATCAAAG CCGCTTAGATGCTTTCCAGATGCTGAGTGCAGAAGTTGAAGCATAAGATCT CTATAACTCAATCTATGCCATTGGTCAGAACACCAATGATGCACTACCAAAAT CTATAAGTACGTTCAACATTGTCCTGAAGAACAGCCGATTGATAGTTATGCT TATCGTCAAGAGACCTACAGAACATTGCCACTCACTGGTAGATTAGCTTCCATTAC CTACGCAATAGCCCCAGACATAAACACATCTGATGTCTATTGGTTAATTGTT CCTCCAGTACTGCTGCATTAGGTGAACAAGAAAAATTGAACATTACAAAGAGCC TACGCAAGATTATCCCTGGTGAACATTGGTGA</p> |
| CAR | <p>ATGTCACCTATCACCAAGAGAACAGAAAGATTAGAACAGAACATACAAGACTTACGC CAACGATCCTCAATTGCCCGCTGCCAGCCAGCAACAGCCATACCGCTGCAATTGA AAGACCAGGTTGCCATTGCCTCAAATCATGAAACTGTTATGACAGGTTATGCTGA TAGACCTGCTTGGCACAAAGATCAGTAGAATTGTTACAGATGCAGGTACTGGTC ATACTACATTGAGATTGTTACACACTTCGAAACTATCTTACGGTGAATTATGGG ACAGAACATTCTGCCATTGGCTGATGTTTATCAACCGAACAAACTGTTAACCTGGTG ACAGAGTCTGTTGGTTAATTCTGTTGACTACGCAACTATAGATATGACATT GGCCAGATTAGGTGCAGTAGCCGTTCCATTGCAAACCTCTGCCGCTATTACTCAATT ACAACCAATAGTCGCTGAAACACAAACCTACCATGATAGCAGCCTCTGAGATGCTT GGCAGACGCCACTGAATTGGTTATCAGGTCAAACGTCAACAAAGAGTCTTAGTATT CGACCATCACAGACAAGTTGATGCCCATAGAGCTGCTGTTGAATCCGCTAGAGAAA GATTGGCAGGTAGTGCCGTTGCAAACCTTAGCTGAAGCAATAGCTAGAGGTGAC GTTCCAAGAGGTGCTCTGCTGGTCTGCTCCGGTACAGACGTCTCCGATGACAGT</p> |

TTGGCATTGTTAATCTACCTGGTCAACTGGGCCAAAAGGTGCTATGTAC
CCTAGAAGAAATGTTGCTACATTTGGAGAAAGAGAACCTGGTCAGGGTGTAA
CGAACCATCTACACTTGAACTTCATGCCTATGTCACATGTTATGGTAGACAAATC
TTGTATGGTACTTTATGCAACGGTGGTACAGCATACTTGCCAAAGTCTGACTTG
TCAACATTATCGAAGATTGGCTTAGTCAGACCAACTGAATTAACATTGTCCTCA
GAGTATGGATATGGTTTGACGAATTCAATCAGAAGTCGATAGAAGATTGGA
GATGGTGTGACAGAGTAGCTTAGAAGCACAAGTTAAGGCAGAAATAAGAAACG
ATGTTTGGGTGGTAGATATACATCTGCCTAACCGGTTCTGCTCCAATATCAGACG
AAATGAAGGCTGGTAGAAGAATTGTTAGATATGCATTGGTGAAGGTTACGGT
TCAACTGAAGCTGGTATGATATTAATCGACGGTCAATTAGAAGACCAGCCGTTT
GGATTATAAATTGGTTGATGTCCTGACTTGGTTACTTTAACTGATAGACCACA
CCCTAGAGGTGAATTGTTGGTAAGACAGATTCTTGTCCCAGGTTATTACCAAAG
AGCTGAAGTTACAGCAGATGCTTGATGCTGACGGTTCTATAGAACCGGTGACAT
TATGGCAGAAGTCGGCCTGAACAATTGTTACTTAGATAGAAGAAACAACGTTT
GAAATTGTCAGGGTGAATTGTTAAAGACAGATTCTTGTCCCAGGTTATTACCAAAG
CTCTCATTAGTTAGACAAATATATACGGTAATTGCCAGAGCTTATTGTTA
GCAGTCATAGTACCAACACAAGAAGCCTGGATGCTGTCGAAAGAATTGAA
AGCCAGATTGGGTGACTCCTGCAAGAAGTTGCAAAGGCCGCTGGTTGCAAAGTT
ACGAAATCCAAGAGATTTCATCATGAAACCACTCCTGGACCTAGAAAACGGTT
TGTAACTGGTATCAGAAAATTGGCTAGACCACAATTGAAAAAGCATTACGGTGA
TTGTTAGAACAAATATACTGACTTGGCCCACGGTCAAGCTGATGAATTGAGATCC
TTAAGACAAAGTGGTGCAGATGCCAGTATTAGTTACAGTCTGTAGAGCAGCCGC
TGCATTGTTAGGTGGTCCGCTAGTGTGATGTTCAACCTGACGCACATTACCGATT
GGGTGGTGAECTTTGTCAGCTTACAAATTGTCACGAAATCTCGAT
ATAGAAGTACCAAGTGGTGTATTGATCACCTGCTAACGATTGCAAGCATTGGCA
GATTATGTTGAAGCCGCTAGAAAACCAGGTTCTCAAGACCTACTTTGCTCTGTT
ATGGTGCATCAAATGGTCAAGTTACAGAAGTCCACGCTGGTACTGTCCTGGATA
AGTCATTGATGCAGCCACTTGGCGAAGCTCCAAGATTACCTGCTGCAAACACTC
AAGTAAGAACAGTTGTTAACCGGTGCTACTGGTTCTGGTAGATATTGGCAT
TAGAATGGTTAGAAGAATGGATTGGTGCAGGTAATTGATTGCTTAGTCAGA
GCAAAGTCCGACACTGAAGCAAGAGCCAGATTGGATAAAACATTGATAGTGGT
ACCCAGAATTGTTAGCACATTACAGAGCTTAGCAGGTGACCACTTGGAAAGTTAG
CCGGTACAAGGGTGAAGCTGACTTGGTTAGATAGACAAACATGGCAAAGATT
GGCTGATACCGTAGACTTAATGTTGATCCAGCCGCTTAGTCACCATGTATTGCC
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TTGTTAAGAGAACGCCATGATTGTTGAGCTGCTGTCTTAGATGCGA
CATGATTGGCAGATACAACCTGGCCGGTCAATTGAAACGTTCCAGATATGTCAC
AAGAATGATCTGTCCTAGCAGCCACCGGTAGTCCTGGTAGTTCTATGAATT
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TTGCCGAAGCTATCTCCACCTAGGTGCTCAAAGTCAAGATGGTTCCATACTTATCA
CGTAATGAATCCATACGATGACGGTATTGGTTGGACGAATTGTTGATTGGTAAA
CGAATCTGGTGTCTATTCAAAGAATAGCTGATTGGTACTGGTACAAAGATT

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| | CGAAACTGCTTGAGAGCATTACCAAGATAGACAAAGACATTCCAGTTGTTACCTT GTTACACAATTACAGACAACCAGAAAGACCTGTCAAGAGGTTCTATTGCTCTACAGA TAGATTCAAGAGGCCGTGTACAAGAAGCAAAAATAGGTCCAGATAAGGACATCCCTC ATGTTGGTGCTCTATTATCGTAAAGTATGTATCAGATTGAGATTGTTGGGTTGTT GTAA |
| <i>npgA</i> | ATGGTGCAAGACACATCAAGCGCAAGCACTCGCCAATTAAACAAGATGGTACAT CGACACCCGCCCTCAACCGCCTCAACAGCAGCCCTCCTCCTGAAACCCCTCCAG CCCGCTGATCAAATCTCCGTCAAAAATACTACCATCTGAAGGATAAACACATGTCT CTCGCCTCTAATCTGCTCAAATACCTCTCGTCCACCGAAACTGTCGCATCCCCTGGT CTTCATCGTGTACTCTCGAACCCCCAGATCCGCACAGACGACCATGCTATATTCCACC CTCAGGCTCACAGGAAGACAGCTCAAAGACGGATACCGGCATCAACGTTGAGT TCAACGTCAGCCACCAAGCCTCAATGGTCGCGATCGCGGGAACAGCTTTACTCCCA ATAGTGGTGGGGACAGCAAACCTCAAACCCGAAGTCGAATTGATATTACGTGCGTA AACGAGCGGCAGGGACGGAACGGGGAGAGCGGAGCCTGGAATCGCTACGTCAA TATATTGATATATTCTCGGAAGTGTGTTCCACTGCAGAGATGGCCAATATAAGGAGG TTAGATGGAGTCTCATCATCCTCACTGTCTGCTGATCGTCTTGACTACGGGTAC AGACTCTTCTACACTTACTGGCGCTCAAAGAGGGCTATATAAAATGACTGGGA GGCCCTTCTAGCACCGTGGTTACGGGAACCTGGAATTCACTGATGTCGCCCCGG CCGCTGTTGCGGAGAGTGGGATTGGCTGGGATTCGGCTGGGAGCCGTACCGGG TGTCAAGGACGACTTTATATAAAATCTCGTTGAGGATGTGAGGATTGAAGTTGCTG CTCTGGCGGTGATTACCTATTGCAACGGCTGCGAGGGGTGGTGGATTGGAGCT AGTTCTAGACCAGGAGGTGGTCCAGACGGAAGTGGCATCCGAAGCCAGGATCCCT GGAGGCCCTTCAAGAAGTTAGATATAGAGCGAGATATCCAGCCGTGCGACTGGG GTGTGAATTGCTATCCTAA |
| <i>SeADO</i> | ATGCCACAATTAGAACCTCTAGAATTAGACTTCAATCAGAATCATATAAAGAT GCTTACAGTAGAAATCAACGCAATCGTCATTGAAGGTGAACAAGAAGCATTGATAA CTACAACAGATTGGCAGAAATGTTACCAAGATCAAAGAGACGAATTGCATAAATTGG CCAAGATGGAACAAAGACACATGAAAGGTTCATGGCTGTGGAAAAAATTGTC GTTACTCCTGATATGGTTTCGCACAAAGTTTCGAAAGATTGCATGAAAACCTC AAAGCTGCAGCCGCTGAGGGTAAAGTTGCACATGTTGTTGATCCAATCTTGATA ATCGAATGCTTGCTATCGCAGCCTATAATATCTACATTCCAGTCGCTGATGCATTG CCAGAAAGATTACCGAAGGTGTAGTTAGAGACGAATATTGCACAGAAACTTCGGT GAAGAATGGTTGAAGGCAAACCTCGATGCTTAAGGCAGAAATTGGAAGAAGCTA ATAGACAAAACCTGCCTTAGTCTGGTTGATGTTAAATGAAGTAGCCGATGACGCTA GAGAATTGGGTATGAAAGAGAAATCATTAGTTGAAGACTTCATGATCGCATACGGT GAAGCCTTAGAAAACATCGGTTTACTACCAGAGAAATAATGAGAATGTCCGCATA CGGTTGGCAGCAGTCTAA |
| <i>NpADO</i> | ATGCAACAATTACAGACCAATCAAAGGAATTAGACTCAAATCAGAAACTTACAA GATGCCTACTCCAGAATCAACGCAATCGTCATTGAAGGTGAACAAGAAGCACATGA AAACTACATCACCTGGCCAATTATTACCAAGATCCCATGATGAATTGATCAGATT GTCTAAGATGGAATCAAGACACAAAAAGGGTTTGAAGCCTGTGGTAGAAATTGG CTGTTACTCCTGACTTACAATTGCCAAAGAATTCTCTGGTTGCACCAAAACTT CCAAACTGCTGCAGCCGAGGGTAAAGTTGTCACATGTTGTTGATCCAATCATTAA AATCGAATGCTTGCTATCGCTGCATATAATCTACATTCCAGTTGCCGATGACTTC GCTAGAAAATTACAGAAGGTGTAGTTAGGAAGAATATTCCATTGAAACTTTGG |

TGAAGTCTGGTTAAAAGAACACTTCGAGAGAGTAAGGCCATTGAAATTAGCAA
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CGGTTGATAGGTGCTTGA

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