

1 **Supporting information for**

2
3 **Recombination machinery engineering facilitates metabolic**
4 **engineering of the industrial yeast *Pichia pastoris***

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6 Peng Cai^{1,5,#}, Xingpeng Duan^{1,3,#}, Xiaoyan Wu^{1,3,4}, Linhui Gao^{1,3,4}, Min Ye^{1,3,4}, Yongjin J.
7 Zhou^{1,2,3,6}

8
9 ¹ Division of Biotechnology, Dalian Institute of Chemical Physics, Chinese Academy of
10 Sciences, Dalian 116023, China

11 ² CAS Key Laboratory of Separation Science for Analytical Chemistry, Dalian Institute of
12 Chemical Physics, Chinese Academy of Sciences, Dalian 116023, China

13 ³Dalian Key Laboratory of Energy Biotechnology, Dalian Institute of Chemical Physics,
14 Chinese Academy of Sciences, Dalian 116023, China

15 ⁴University of Chinese Academy of Sciences, Beijing 100049, China

16 ⁵School of Bioengineering, Dalian University of Technology,

17 ⁶ www.synbc.dicp.ac.cn

18 #These authors contribute equally to this work

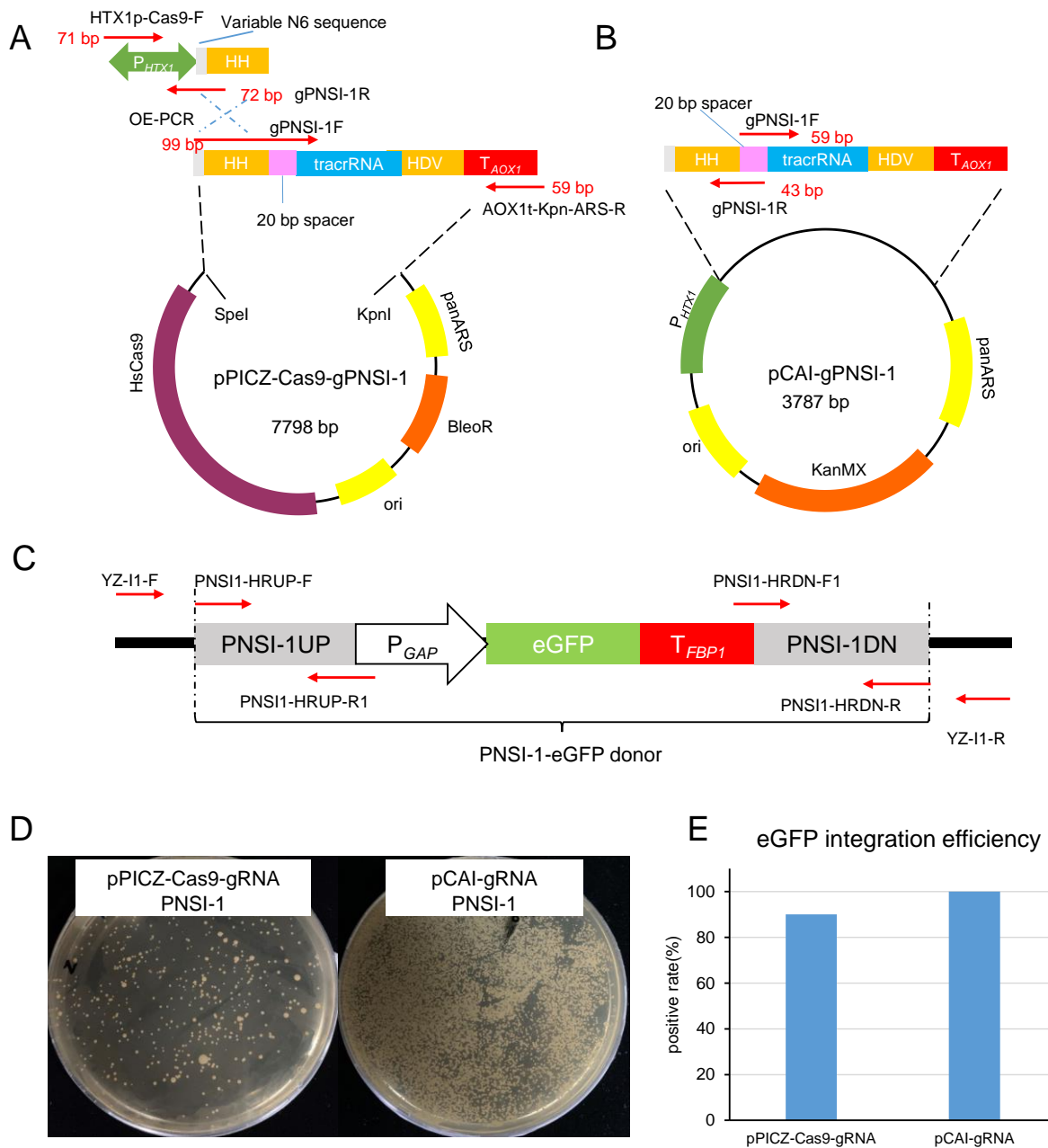
19 *Correspondence to: Yongjin J. Zhou.

20 E-mail: zhouyongjin@dicp.ac.cn

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25 **This PDF file includes:**

26 Figures S1 to S12

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34 **Supplementary Fig S1. Establishing and optimizing CRISPR-Cas9 systems for *P. pastoris*.** The

35 PNSI-1 site was used as an example to introduce the CRISPR-Cas9 system, which can be applied

36 to any neutral site. (A) The first version of Cas9-gRNA plasmid was constructed according to a

37 previous report (11, 14). The gRNA is flanked by 5' and 3' self-processing RNA elements to

38 obtain correctly processed gRNAs. HH part is the 5' ribozyme cleaving sequence. This strategy

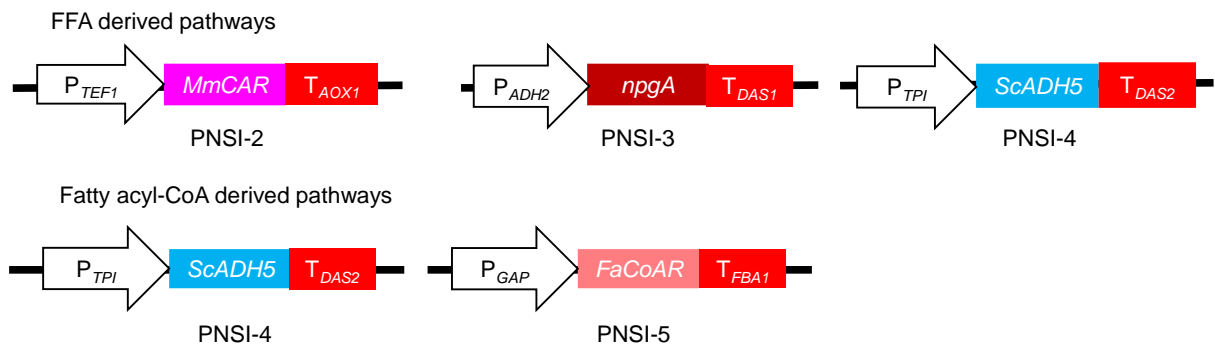
39 required the alteration of a short 6 bp sequence of the 5' cleaving HH ribozyme reverse

40 complement to the first 6 bps of gRNA (N6 variable sequences). In detail, primers HTX1p-Cas9-

41 F/ gPNSI-1R, gPNSI-1F/ AOX1t-Kpn-ARS-R were used to amplify the P_{HTX1} and sgRNA parts.

42 Then, the two parts were fused by overlap extension PCR and cloned into the plasmid

43 backbone by the Gibson Assembly cloning method. Primers of 301 bp (about \$73) were used
44 to construct the Cas9-gRNA plasmid. (B) Simplified gRNA plasmid construction (right). Primer
45 pair pCAI-gPNSI-1F/pCAI-gPNSI-1R was used to mutate the 20 bp target sequence directly in
46 plasmid with 15 cycles of PCR. Primers of 102 bp (about \$15) were used in the construction of
47 the simplified gRNA plasmid. In addition, there was no need for overlap extension PCR or gel
48 extraction procedures. (C) An eGFP expression cassette was used as an integration donor at
49 the PNSI-1 site. Primer pairs PNSI-HRUP-F/PNSI-HRUP-R1 and PNSI-HRDN-R1/PNSI-HRDN-R
50 were used to amplify the upstream and downstream homologous arms. YZ-I1-F/YZ-I1-R were
51 used for colony PCR. (D) The transformants on plates. (E) For pPICZ-Cas9-gPNSI-1 plasmid, the
52 positive rate was about 90% (9/10), and the positive rate of pCAI-gPNSI-1 was 100% (10/10).
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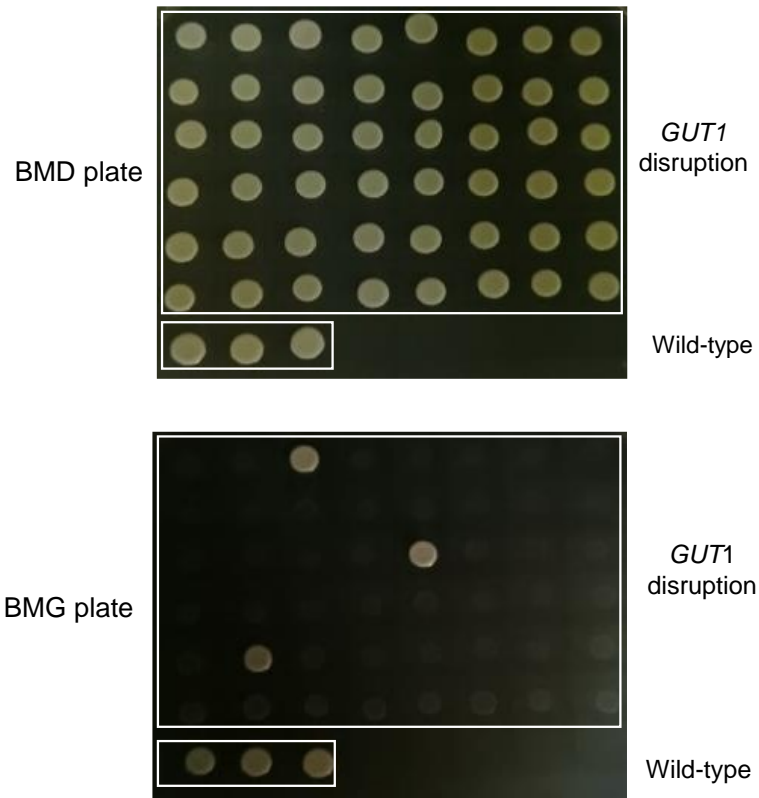
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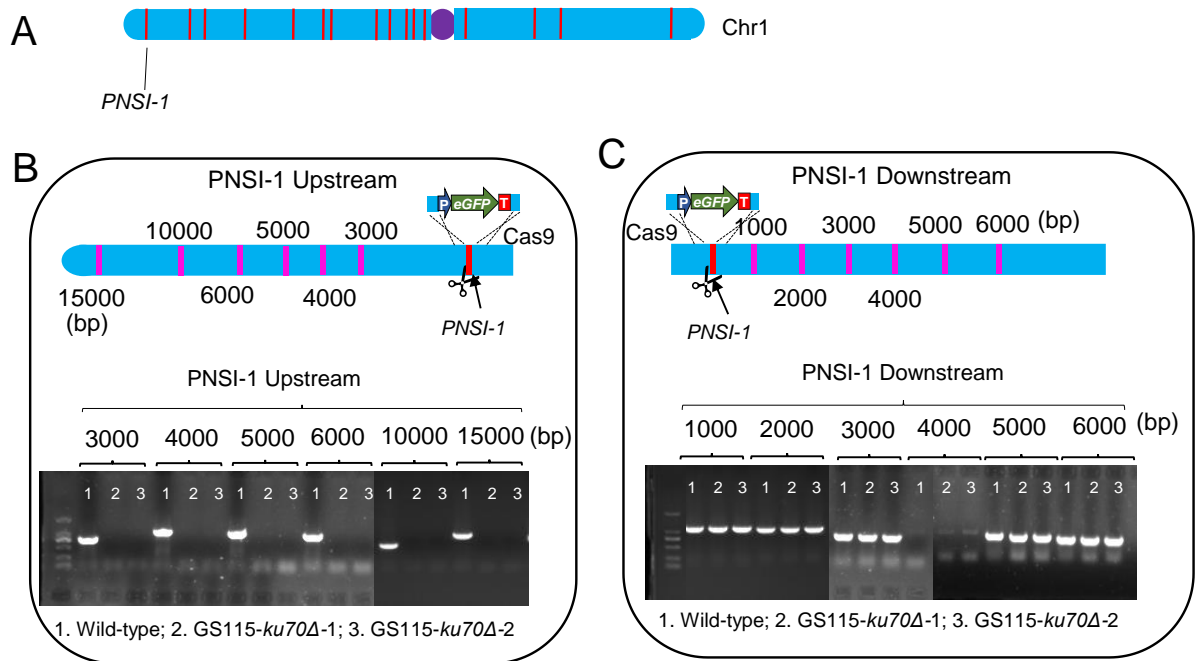
Supplementary Fig S2. Fatty alcohol biosynthetic pathway construction. The scheme of DNA organization of FFA derived pathway and fatty acyl-CoA derived pathways in separate neutral sites. Each gene with 1 kb HA was integrated into one neutral site.



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59 **Supplementary Fig S3. Phenotypic statistics were used to characterize the targeting**
60 **efficiency of *GUT1*-gRNA without donor.** 48 random transformants were transferred to
61 minimal media agar plates with either glucose (BMD) or glycerol (BMG) as carbon source. It
62 has been reported that *GUT1* disruption cutting by Cas9 result a growth defect on BMG plate
63 (Weninger et al., J. Biotechnol., 2016, 235,139–149, doi: 10.1016/j.jbiotec.2016.03.027).
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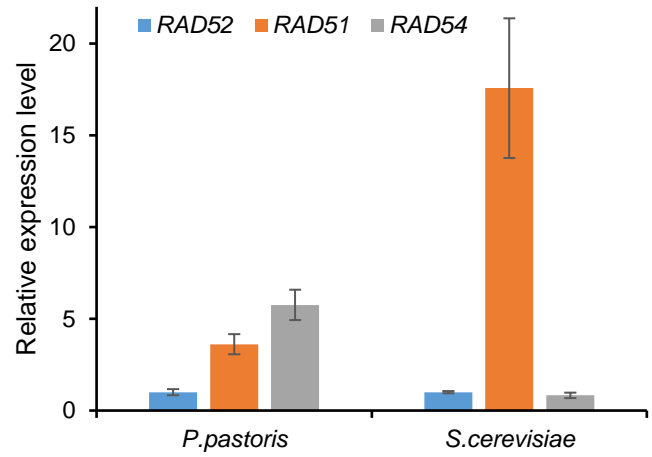
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67 **Supplementary Fig S4. The *KU70* deletion caused the loss of a large chromosomal fragment**
68 **after genome integration of an eGFP cassette.**

69 (A) The localization of the PNSI-1 site in the genome of *P. pastoris*, which was used for genome
70 integration of an eGFP cassette with the aid of Cas9/gRNA system. 1 kb homologous arm was
71 used to construct the eGFP expression cassette. (B) PCR analysis of fragments located
72 upstream of PNSI-1 site after the genome cutting by Cas9. The top is the scheme of the
73 location of primer binding sites and PNSI-1, and the bottom is electrophoretic analysis of PCR
74 products upstream of PNSI-1 site after CRISPR/Cas9 editing. (C) PCR analysis of fragments
75 located downstream of PNSI-1 site after the genome cutting by Cas9. The top is the scheme
76 of the location of primer binding sites and PNSI-1, and the bottom is electrophoretic analysis
77 of PCR products downstream of PNSI site after CRISPR/Cas9 editing. The failure to detect
78 corresponding fragments in *KU70* deletion strains (electrophoretic band 2 and 3) suggested
79 the loss of a large chromosomal fragment in the left-hand side of chromosome 1.

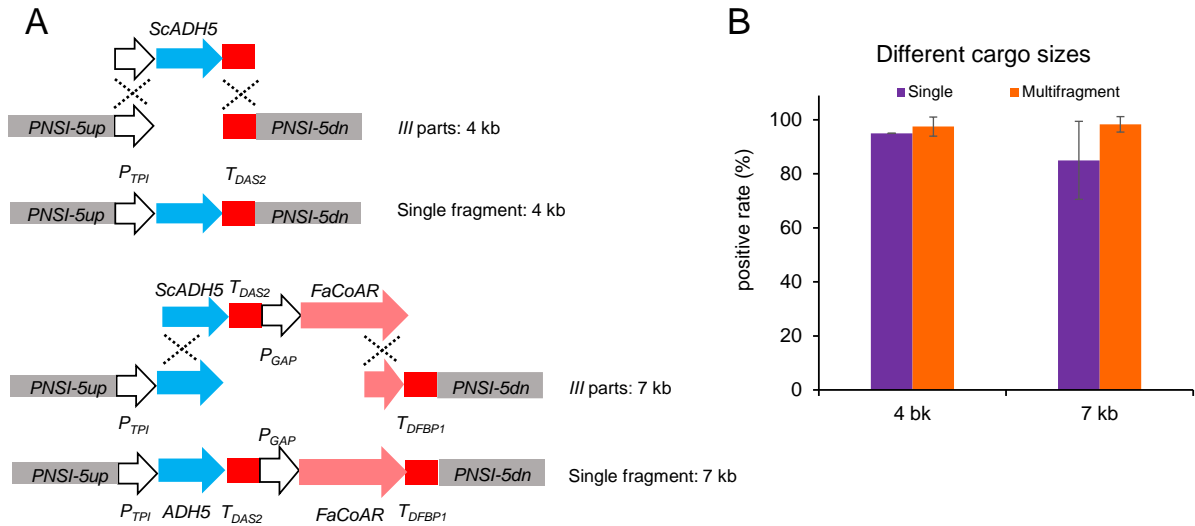
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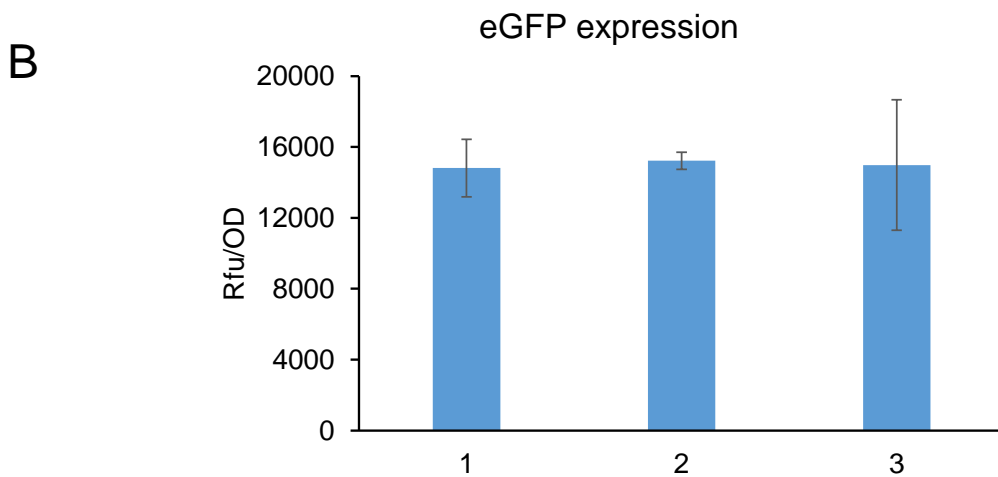
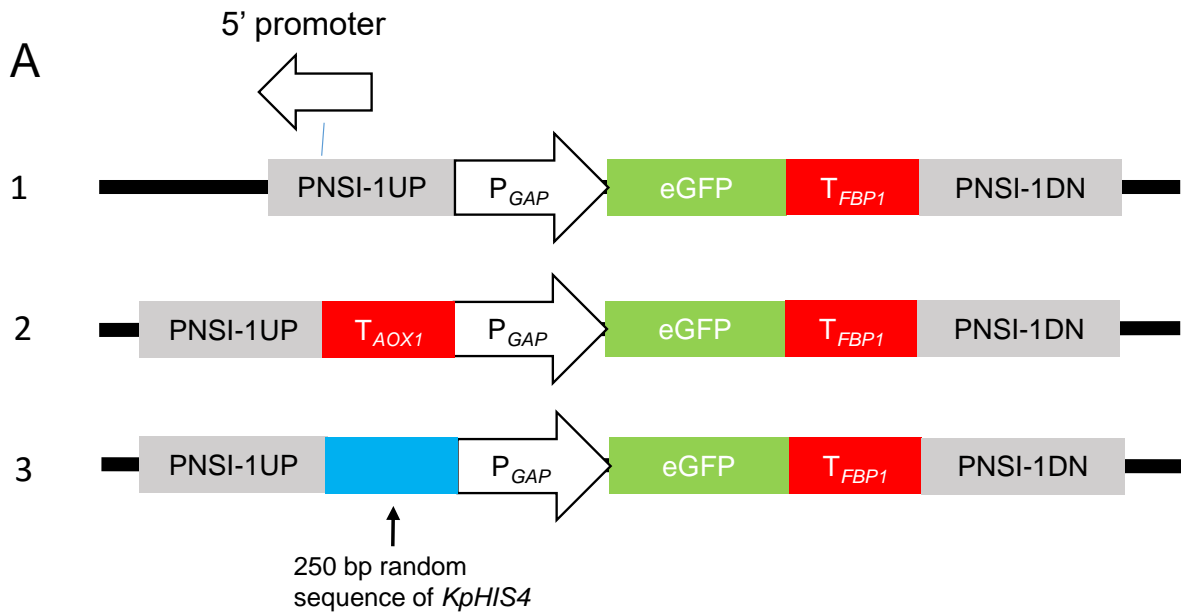
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Supplementary Fig S5. Relative expression level of RAD family genes in *P. pastoris* and *S. cerevisiae*. Actin gene was chosen as the endogenous reference gene, and the data analysis was conducted by the method of $2^{-\Delta\Delta C_T}$. Relative expression level of these genes was calculated by normalized the expression level of RAD52 in the respective strains.

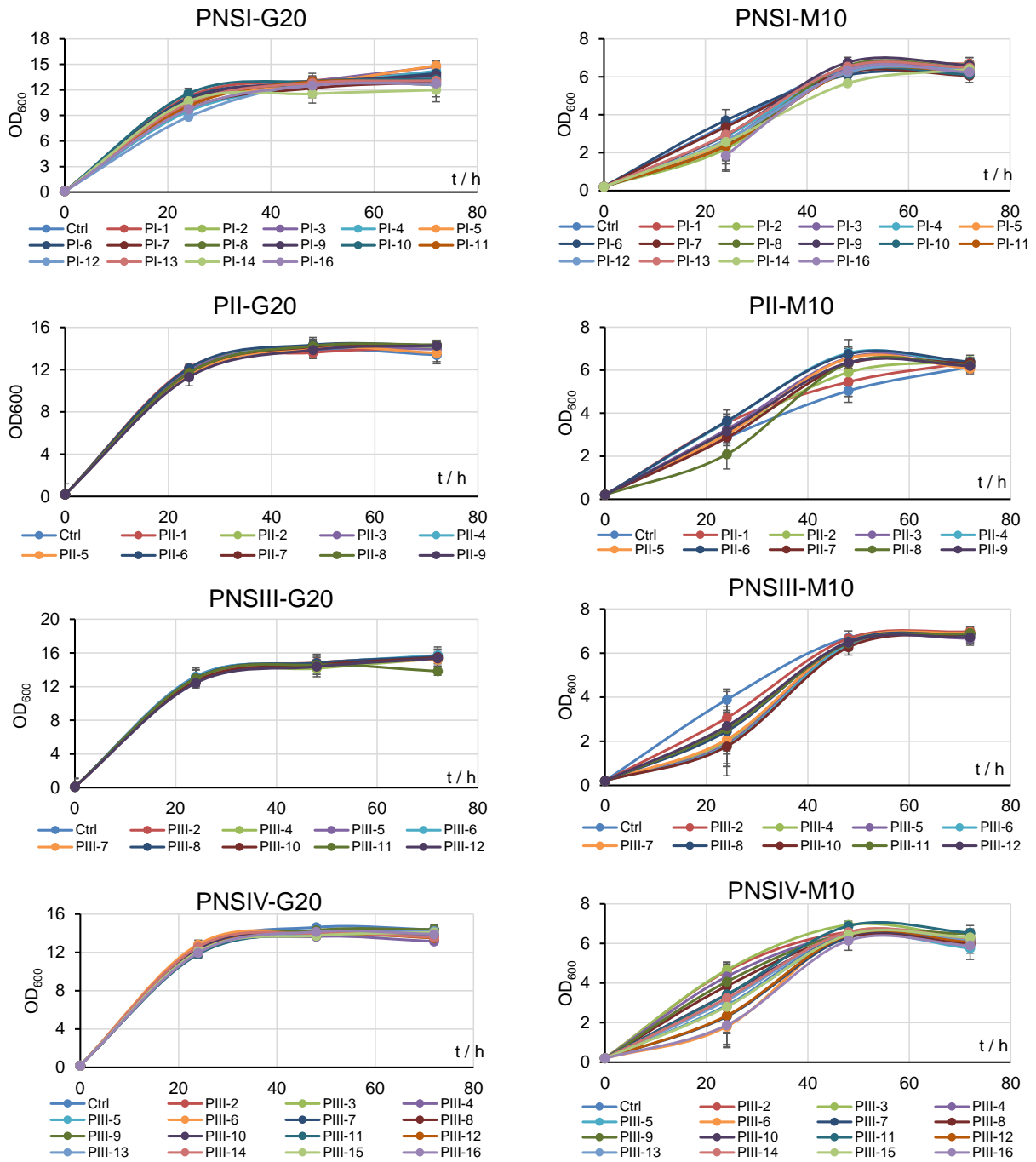


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Supplementary Fig S6. Comparison of a single fragment with that of multiple fragments for different cargo sizes at a single site. (A) The scheme of integration with different donor size and repair mode. Single fragment and three fragments integration with 1 kb HA were compared at PNSI-5 site. (B) Positive rates in integrating various cargo sizes of expression cassettes via different repair mode.



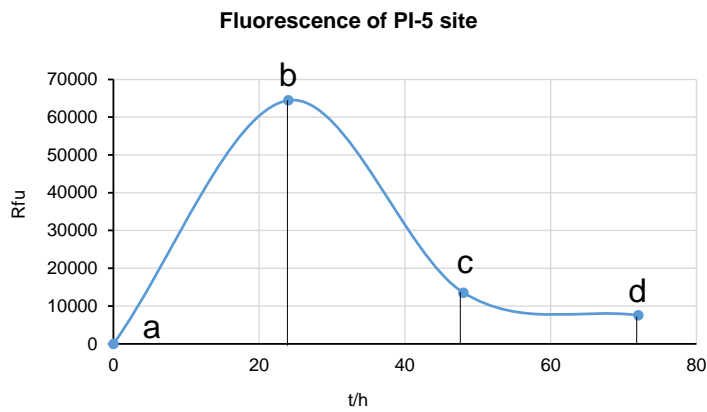
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98 **Supplementary Fig S7.** Influence of 5' upstream sequence on gene expression at neutral site.
99 (A) The scheme of 5' sequences localization to the upstream of P_{GAP} . (B) The fluorescence
100 intensity was the same for all integrations, which suggested that the small upstream fragment
101 did not affect promoter strength. All data represent the mean \pm s.d. of three yeast clones
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106 **Supplementary Fig S8. Cell growth of eGFP integrated strains at different neutral sites. G20**
 107 means Deft-His-20 g/L glucose medium. M10 means Deft-His-10 g/L MeOH medium. In G20
 108 medium, cell growth was the same for control strain PC110 or PC111 during the entire phase.
 109 In M10 medium, OD600 varied at logarithmic growth period due to the weaker methanol
 110 utilization capacity. Biomass reached the same level at 48h when cell growth entered a
 111 plateau phase. All data represent the mean±s.d. of three yeast clones

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$$S = F(X) = \int_{t_0}^t f(x) * dt \approx \frac{(a + b)}{2} * 24 + \frac{(b + c)}{2} * 24 + \frac{(c + d)}{2} * 24$$

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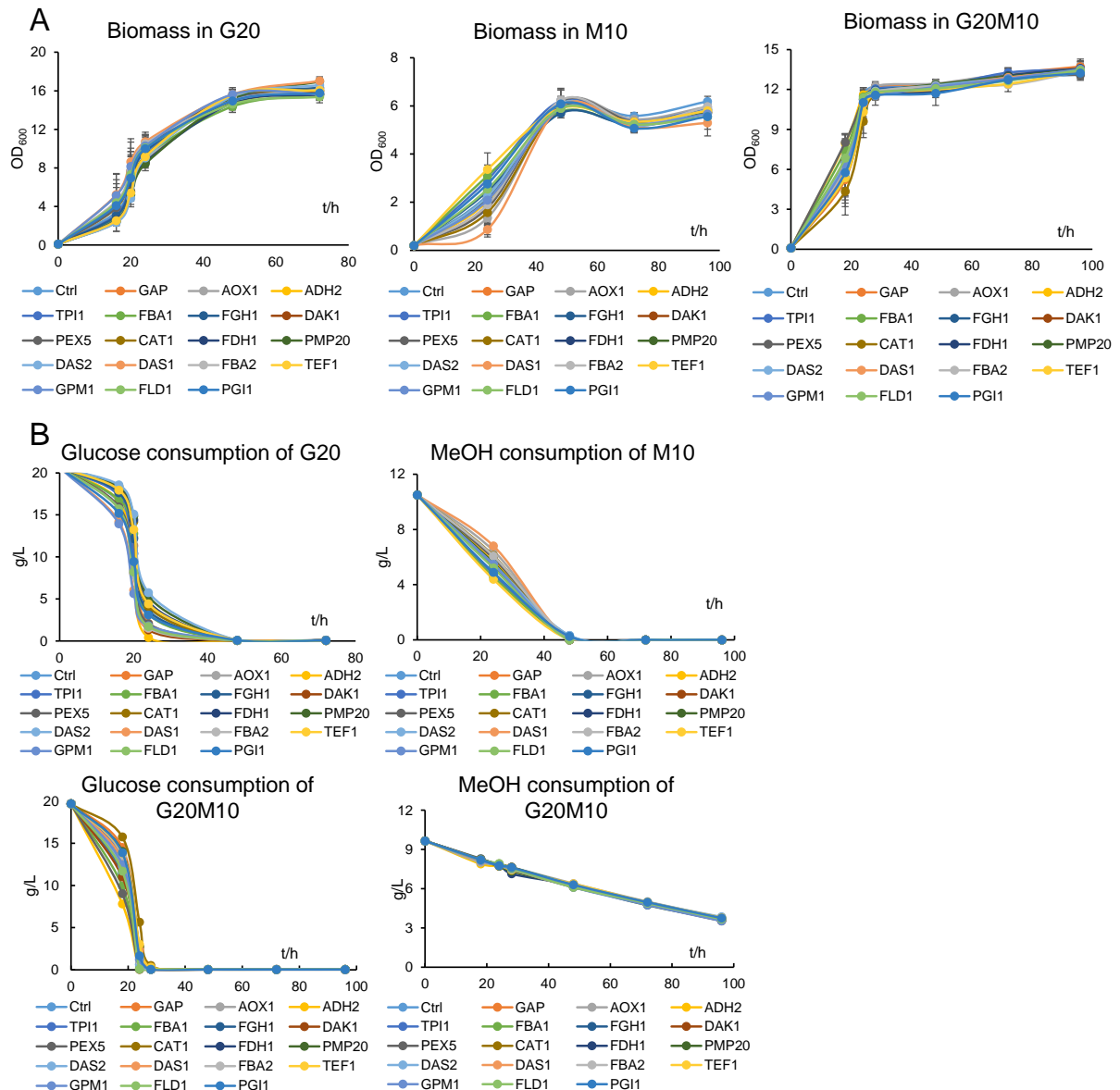
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Supplementary Fig S9. Total fluorescence intensity was calculated by the integral of fluorescence intensity with time. The total fatty alcohols were accumulated by enzymatic (FacoAR) biosynthesis of fatty alcohols, in other word, it was positive correlated with the integral of FacoAR activity. We thus investigated the possible correlation of fluorescence intensity integral with the fatty alcohol titers. Total fluorescence intensity can be roughly calculated by the bottom equation that based on the fluorescence intensity measured at 24h, 48 h and 72 h. The half-life of eGFP protein was about 7-12 h which means the area of the integral is approximately equal to total fluorescence intensity.

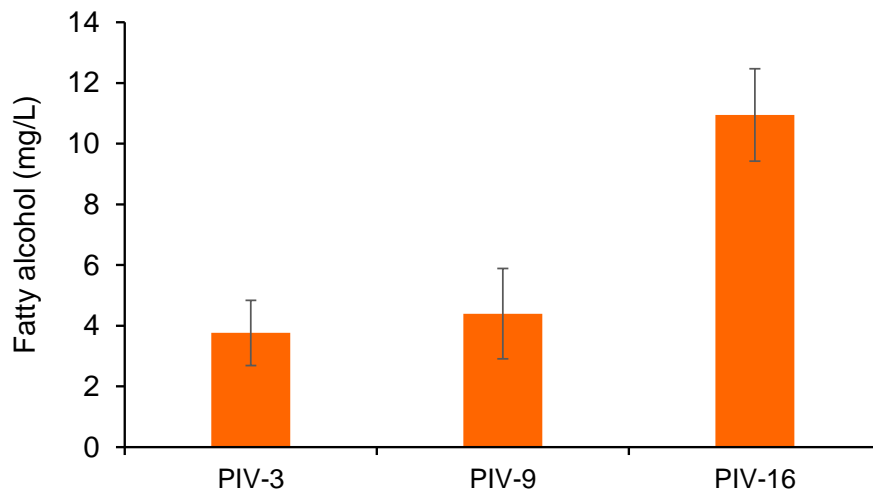


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126 **Supplementary Fig S10. The cell growth and consumption of carbon sources of various**
 127 **strains harboring integrating eGFP expression cassettes driven by different promoters.**

128 (A) The cell growth curves. Recombinant strains were cultured in minimal medium with
 129 different carbon source. Yeast cell growth into plateau stage after 24 hours when glucose was
 130 used as carbon source, and the stationary phase was extended to 48 h when MeOH as the
 131 carbon source. (B) Glucose was depleted after about 24 hours' cultivation both in G20 or
 132 G20M10 medium. It took 48 hours for methanol to be fully consumed when it was used as
 133 unique carbon source. Since the metabolism of methanol is severely inhibited by glucose,
 134 there were still 4 g/L methanol in medium till the end of cultivation in G20M10 media. All data
 135 represent the mean \pm s.d. of three yeast clones

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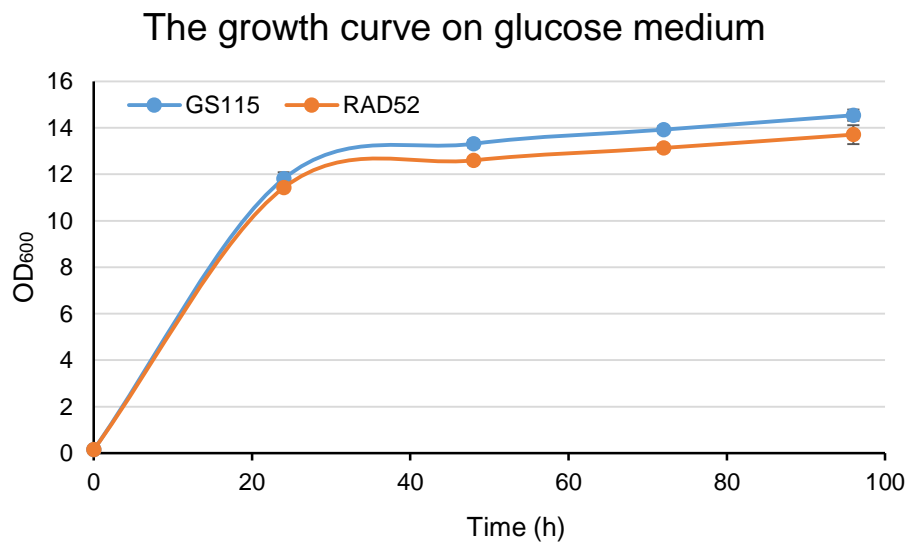
138 **Supplementary Fig S11. Fatty alcohol production by using methanol as a sole carbon source.**

139 The fatty alcohol producing strains were cultivated in Delft media with 10 g/L methanol as a

140 sole carbon source. All data represent the mean \pm s.d. of three yeast clones.

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Supplementary Fig S12. The growth curve of wild type and *RAD52* overexpressed strains on Deft-medium with 20 g/L glucose. The initial inoculation of OD₆₀₀ was 0.15, and the cell growth was analyzed by sampling every 24 hours.

148 **Supplementary Table S1 Strains list**

Strain name	Genotype	Resource or Reference
GS115	Mut+, <i>his4</i> -, <i>AOX1</i> , <i>AOX2</i>	From Pro Cai
PC110	GS115, <i>HIS4</i> :: <i>P_{GAP}-PpRAD52-T_{AOX1}</i>	This study
PC111	PC110, <i>PNSI-2</i> :: <i>P_{GAP}-hCas9-T_{DAS1}</i>	This study
PC139	PC110, <i>hfd1Δ</i> , <i>faa1Δ</i> , <i>PNSI-2</i> :: <i>P_{TEF1}-MmCAR-PpOptR1-T_{AOX1}</i> , <i>PNSI-3</i> :: <i>P_{ADH2}-npgA-PpOptR1-T_{DAS1}</i> , <i>PNSI-4</i> :: <i>P_{TP11}-ScADH5-T_{DAS2}</i>	This study
PC204	PC110, <i>hfd1Δ</i> , <i>PNSI-4</i> :: <i>P_{TP11}-ScADH5-T_{DAS2}</i> , <i>PNSI-5</i> :: <i>P_{GAP}-FaCoAR-PpOptR1-T_{FBP1}</i>	This study
XPD02	GS115, <i>HIS4</i> :: <i>P_{ADH2}-PpRAD52-T_{AOX1}</i>	This study
XPD03	GS115, <i>HIS4</i> :: <i>P_{GAP}-ScRAD51-T_{AOX1}</i>	This study
XPD04	GS115, <i>HIS4</i> :: <i>P_{GAP}-ScRAD52-T_{AOX1}</i>	This study
XPD05	GS115, <i>HIS4</i> :: <i>P_{GAP}-ScRAD54-T_{AOX1}</i>	This study
XPD06	GS115, <i>HIS4</i> :: <i>P_{GAP}-ScSAE2-T_{AOX1}</i>	This study
XPD07	GS115, <i>HIS4</i> :: <i>P_{GAP}-PpRAD51-T_{AOX1}</i>	This study
XPD08	GS115, <i>HIS4</i> :: <i>P_{GAP}-PpRAD54-T_{AOX1}</i>	This study
XPD11	PC110, <i>mph1Δ</i>	This study
XPD12	PC110, <i>sgs1Δ</i>	This study
XPD13	PC110, <i>top3Δ</i>	This study
XPD14	PC110, <i>rmi1Δ</i>	This study
XPD15	PC110, <i>PNSI-1</i> :: <i>P_{GAP}-PpMUS81-T_{FBP1}+T_{ADH2}-PpMMS4-P_{TEF1}</i>	This study
XPD16	PC110, <i>PNSI-1</i> :: <i>P_{GAP}-PpSLX1-T_{FBP1}+T_{ADH2}-PpSLX4-P_{TEF1}</i>	This study
XPD17	PC110, <i>PNSI-1</i> :: <i>P_{GAP}-PpYEN1-T_{FBP1}</i>	This study
XPD18	XPD11, <i>sgs1Δ</i>	This study
XPD19	XPD11, <i>top3Δ</i>	This study
XPD20	XPD11, <i>rmi1Δ</i>	This study
XPD21	XPD11, <i>PNSI-1</i> :: <i>P_{GAP}-PpMUS81-T_{FBP1}+T_{ADH2}-PpMMS4-P_{TEF1}</i>	This study
XPD22	XPD11, <i>PNSI-1</i> :: <i>P_{GAP}-PpSLX1-T_{FBP1}+T_{ADH2}-PpSLX4-P_{TEF1}</i>	This study
XPD23	XPD11, <i>PNSI-1</i> :: <i>P_{GAP}-PpSLX1-T_{FBP1}</i>	This study

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Supplementary Table S2. Primer list

No	Primer name	Sequence 5'-3'
P1	Cas9-F	cgaaacgATGGACAAGAAGTACTCCATTGGG
P2	Cas9-R	TTAAACTTTTCTTTCTTCTTTGG
P3	panARS-F	CGggatccGCAACATCTTTGGATAATATCAGAATGAGAAAAG
P4	panARS-R	GccttagaTAGTGCTGATTATGATTTGACGTTTATATACATG
P5	HTX1-F	GTTTCGTCCTCACGGACTCATCAGTGCAAT TTTGATTTGTTTAGGTAACCTGAACTG
P6	HTX1-R	AATGGAGTACTTCTTGCCATCGTTTTCG TGTTGTAGTTTTAATATAGTTTGAGTATGAG
P7	H-F	ATTGCACTGATGAGTCCGTGAGGAC
P8	H-R	GTCCCATTCGCCATGCCGAAG
P9	M1	TTTTCAAGTTGATAACGGACTAGCCTTATTTAACTTGCTATTTCTAGCTCTAAAACGCCTGGCTGAGGAAATTGCAGACGAGCTTACTCGTTTCGTCC TCACGGACTCATCAGTGCAAT
P10	M2	ATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGCCGGCATGGTCCCAGCCTCCTCGCTGGCGCCGGCTGGGCAACA TGCTTCGGCATGGCGAATGGGAC
P11	T _{AOX1} -F	AACGTCAAATCATAATCAGCACTAGCACAAACGAAGGTCTCACTTAATC
P12	T _{AOX1} -R	GGCAACATGCTTCGGCATGGCGAATGGGACTCAAGAGGATGTCAGAATGCCATTTG
P13	T _{DAS1} -F	GCTGACCCCAAGAAGAAGAGGAAGGTGTGAACGGGAAGTCTTTACAGTTTTAGTTAG
P14	T _{DAS1} -R	TCTCAGCTCGGTGGAGACAGCAGGGCTGACCCA GTTAAGGGATTTTGGTCATGAGATCAGATCTGACCCTTGTGACTGACACTTTGG
P15	RAD52-F	ATGTCTTTCGATGACGCTGAGC
P16	RAD52-R	GccttagaTTAATTCGAAGCTGGAGAGTTTTTC
P17	P _{GAP} -F	GTTAAGGGATTTTGGTCATGAGATCAGATCTTTTTTGTAGAAATGTCTTGGTGTCC
P18	P _{GAP} -R	TGCGTTTGAGCTCAGCGTCATCGAAAGACATTGTGTTTTGATAGTTGTTCAATTGATTG
P19	P _{ADH2} -F	TCCCCGCGGCGCAGCGTTTTCTGACGGTACTAGA
P20	P _{ADH2} -R	CTCAGCGTCATCGAAAGACATTTTCGTAAGTAAATAAGATAAAAGCTAGTAGCTGATG
P21	P _{GAP-ScRAD51} -R	CTGATATATGTTGTTCTTGAACCTTGAGACATTGTGTTTTGATAGTTGTTCAATTGATTG
P22	P _{GAP-ScRAD52} -R	TCTTCTCATCCATATCCATAATTCATTCAATTGTGTTTTGATAGTTGTTCAATTGATTG

P23	<i>ScRAD51-F</i>	ATGTCTCAAGTTCAAGAACAACATATATC
P24	<i>ScRAD51-R</i>	GCTCTAGACTACTCGTCTTCTTCTGCGGGTC
P25	<i>ScRAD52-F</i>	ATGAATGAAATTATGGATATGGATGAG
P26	<i>ScRAD52-R</i>	GCTCTAGATCAAGTAGGCTTGCCTGCATG
P27	<i>PpRAD51-F</i>	TCAATTGAACAACATCAAAACACAATGTGCAACCATGAAGTCATAGAG
P28	<i>PpRAD51-R</i>	CAAATGGCATTCTGACATCCTCTTGATTAGTCATCATCCTCTCTAGGGTCC
P29	<i>PpRAD54-F</i>	TCAATTGAACAACATCAAAACACAATGGCAAAGAACTTCATAAACC
P30	<i>PpRAD54-R</i>	CAAATGGCATTCTGACATCCTCTTGACTAATGTGATATATATTGGAAACAGTAGCTG
P31	<i>pPICZA-T_{Aox1}-F</i>	TCAAGAGGATGTCAGAATGCC
P32	<i>pPICZA-P_{GAP}-R</i>	TGTGTTTTGATAGTTGTTCAATTGATTG
P33	<i>5GUT1_fw</i>	AAATCTAGGTCATCCTACAGCAAACACC
P34	<i>5GUT1_rv</i>	GACCTAACATGATAATATAATTACAGCTGCTCGTAGAAGAAGAGTCTTTTTCAGTCCTTG
P35	<i>3GUT1_fw</i>	CAAGGACTGAAAAAGACTCTTCTTCTACGAGCAGCTGTAATTATATTATCATGTTAGGTC
P36	<i>3GUT1_rv</i>	AAATATAAGAGGAAACAACGTTTCGTATCGTGATC
P37	<i>5GUT1-fw(500)</i>	GGGTTGCGGAGCGTCAAAAG
P38	<i>3GUT1-rv(500)</i>	CGCTGCCAGAGCTGTACATAC
P39	<i>5GUT1-fw(200)</i>	CTCCGTGCTCCGATAATAACAGTG
P40	<i>3GUT1-rv(200)</i>	CAGCCCTCTGTCAATAGTGATGG
P41	<i>FAA1up-F</i>	AGGTATCAAAGCTGATTTTTATTGCTATTGTTGATTTAC
P42	<i>FAA1up-R</i>	CAATCGGCTGCTCGCTTCTTGAAGTTTTCTTTGTACGCGTGTGTTG
P43	<i>FAA1dn-F</i>	TTCCTTGTTGCCTTCTGAGGGAGACTAAGATGTAGTTTTTAGACTTGA
P44	<i>FAA1dn-R</i>	CATCCTCTCTGATGCAAGTCTCTTTG
P45	<i>FAA2up-F</i>	ACACCCAGTTTGAATAATAAAGCAGAGCTAC
P46	<i>FAA2up-R</i>	CTTAGTCTCCCTCAGGAAGGCAACAAGGAAACGAGAATGGTA
P47	<i>FAA2dn-F</i>	TTCCTTGTTGCCTTCTGAGGGAGACTAAGATGTAGTTTTTAGACTTGA
P48	<i>FAA2dn-R</i>	CATCCTCTCTGATGCAAGTCTCTTTG
P49	<i>KU70up-F</i>	TCTCACGGGTGATTACTTGTGTTAC
P50	<i>KU70up-R</i>	CCCGTTTCTCTATAAGTACTAAAGCC

P51	KU70dn-F	TTGTATAGGCTTTAGTACTTATAGAGGAAACGGGTTCTGTTCCTTACTTTTTCTCGC
P52	KU70dn-R	GGATTCCGAGAGACTAGTTACGTT
P53	MPH1up-F	GTAAACTTGTGATGATTGGACCC
P54	MPH1up-R	GGGATTATTAAGGGATAGTAAGTTACTTTGTTCCATCTAAGGGTTAACGGGTTTCCAAAG
P55	MPH1dn-F	AGATGGAACAAAGTAACTTACTATCCCTTAATAATCCC
P56	MPH1dn-R	CCTTCCTATAGTGGCTATCGAGG
P57	SGS1up-F	GACTTGTCAAAGTTGAGAAAGTTGGG
P58	SGS1up-R	AGAGTGGGAGTTGCGGAGAAAAG
P59	SGS1dn-F	TTAATCAACCTTTTCTCCGCACTCCCACTCTCATCTACTTCAAGGAAAGCTTCAGTTC
P60	SGS1dn-R	ATCTGAACTTTATTCGTGCAATCTTCACTG
P61	TOP3up-F	GTTGCTCACTGATTGACGTCTGTC
P62	TOP3up-R	CTAGCGATGTGATACATACACGTC
P63	TOP3dn-F	GAATCTTATTGACGTGTATGTATCACATCGCTAGAATTACATAGTTACCTGTGGGCCAG
P64	TOP3dn-R	TCCCCAGATAAATATCCGCCATTTG
P65	RMI1up-F	GTTGTTGTCGTTTCTTTTCTTCC
P66	RMI1up-R	AGACGGTGACCATTAACAGATTAGAG
P67	RMI1dn-F	AAGAACCTCTAATCTGTTAATGGTCACCGTCTGGTTCAATGCATGTCATTAAGGACAAC
P68	RMI1dn-R	CATGGTGAGGTCAATGGGTATC
P69	19P-94	TATGGTTGCTTAAGATGATAGGAGAATCAAACC
P70	19P-95	GTCATATGACAAGTTGGGTAGGTTGC
P71	19P-96	TGTAGAAATGTCTTGGTGTCTCG
P72	19P-97	TGTGTTTTGATAGTTGTTCAATTGATTG
P73	19P-98	CCCTATTTCAATCAATTGAACAACATCAAAACACAATGTGTATGCCTGAGGATCAAGG
P74	19P-99	ACCCCATGTCTGGAATATTTTTTCG
P75	19P-100	TGCGTTCGATTGGCACTGTTTC
P76	19P-101	TCTTCCAGATCTAGCGACTCTGGCAGATAAGACGCGAACCTTACTTTTCTATTATCCC
P77	19P-102	CATCATAGGGATAATAGAAAAGTAAGGTTCCGCTTATCTGCCAGAGTCGCTAGATC
P78	19P-103	GCCGAATAGTTTGTATACGTCTTATGTAATG
P79	19P-104	CATTACATAAGACGTATACAACTATTCCGGCTTAATTTATCAACTCGTTTGGGTTGTCACACG

P80	19P-105	ATTCTACTACATACATTTTAGTTATTCGCCAACATGAGTCTCAATTGTGGTGATTCTG
P81	19P-106	GTTGGCGAATAACTAAAATGTATGTAGTGAG
P82	19P-107	CCTTTTTATGTCAAGTCCGCGTCCCAACTTGCTTATAACTGTCGCCTCTTTTATCTGCC
P83	19P-49	AAACACGCGTACAAAAGAAAACCTCAAGAAACGCAGCGTTTTCTGACGGTAC
P84	19P-02	GCTTGATGTGTCTTGACCATTTTCGTAAAGTAAATAAGATAAAAAGCTAGTAGCTGATG
P85	19P-03	ACTAGCTTTTATCTTATTTACTTTACGAAAATGGTGCAAGACACATCAAGCG
P86	19P-04	CTCCTAACTAAAACGTAAAGACTTCCCGTTTAGGATAGGCAATTACACACCCC
P87	19P-05	ACGGGAAGTCTTTACAGTTTTAGTTAGG
P88	19P-06	CTTGTGACTGACACTTTGG
P89	19P-07	GGGTCTCTACTTAATCTTCTGTACTCTGAAGAGG
P90	19P-08	GTTGTAATCAAGAGGATGTCAGAATGCC
P91	19P-09	CAGGCAAATGGCATTCTGACATCCTCTTGATTACAACAAACCAACAATCTCAA
P92	19P-10	TCACTACATACATTTTAGTTATTCGCCAACATGTACCTATCACCAGAGAAGAAAG
P93	19P-11	GACATGTTGGCGAATAACTAAAATGTATGTAG
P94	19P-12	GAATAACTGTCGCCTCTTTTATCTGCC
P95	19P-13	AGTGCGGCAGATAAAAGAGGCGACAGTTATTCAACGAGACACTCTCCGTCAG
P96	19P-14	TGTGTTTGTGATAGATCTTGATATCAATG
P97	19P-15	CATTGATATACAAGATCTATCACAACACAATGCCTTCGCAAGTCATTCC
P98	19P-16	TTAGAAGTCTCAACAACATATCTAC
P99	19P-17	GTAGATTTGGCCACTAACGGGTTAG
P100	19P-18	CAGACACCAGGTCATTGAACTAACGACAAGGACGGGGTTCGTAAACTGGTTC
P101	19P-53	GTCCGTAGAAAACCTCAATCGGCTGCTCGCGACGGGGTTCGTAAACTGGTTC
P102	19P-47	AGGTATCAAAGCTGATTTTTATTTGCTATTGTTGATTTAC
P103	19P-48	TTTCTTGAAGTTTTCTTTGTACGCGTGTGG
P104	19P-51	GCATGGTTATGGTGCCGGTTTGG
P105	19P-52	GCGAGCAGCCGATTGAAGTTTTCTA
P106	19P-74	AATGGAGTACTTCTGTCCATCGTTTCGCCGCGGTGTTGTAGTTTTAATATAGTTTGAGTATGAG
P107	19P-75	AACGTCAAATCATAATCAGCACTATCTAGAGCACAAACGAAGGTCTCACTTAATC
P108	19P-76	TCGTTTCGTCTCACGGACTCATCAGTCTCATTTTGATTTGTTTAGGTAACCTGAACTG

P109	19P-77	ATGAGACTGATGAGTCCGTGAGGACGAAACGAGTAAGCTCGTCTCTCATGTAGACGACGACTGGTTTTAGAGCTAGAAAATAGCAAGTTAAAATAAG
P110	19P-78	TCGTTTCGTCTCACGGACTCATCAGCAAGCGTTTGATTTGTTTAGGTAACCTGAACTG
P111	19P-79	CGTTTGCTGATGAGTCCGTGAGGACGAAACGAGTAAGCTCGTCCAAGCGGAATCTCCTCAATGGTTTTAGAGCTAGAAAATAGCAAGTTAAAATAAG
P112	19P-80	TCGTTTCGTCTCACGGACTCATCAGGGTTTGTTTGATTTGTTTAGGTAACCTGAACTG
P113	19P-81	CAAACCCTGATGAGTCCGTGAGGACGAAACGAGTAAGCTCGTCGGTTTGATACTGTGACGTCGGTTTTAGAGCTAGAAAATAGCAAGTTAAAATAAG
P114	19P-160	TCGTTTCGTCTCACGGACTCATCAGGCATGCTTTGATTTGTTTAGGTAACCTGAACTG
P115	19P-161	GCATGCCTGATGAGTCCGTGAGGACGAAACGAGTAAGCTCGTCGCATGCCTGAGCTTTGAGGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAATAAG
P116	FAA1UP-YZ-F	CATGGCCCAACTGGTTACGAAGA
P117	FAA1DN-YZ-R	AGACCGTTTACAGCTAGACAAAATTTCAACA
P118	HTX1-Cas9-F	GGAGTACTTCTTGTCCATCGTTTCGACTAGTTGTTGTAGTTTTAATATAGTTTGAGTATGAGATGGAACCTC
P119	AOX1t-Kpn-ARS-R	AAACGTCAAATCATAATCAGCACTAGGTACCGCACAAACGAACGTCTCACTTAATCTTC
P120	gPNSI-1R	GTTTCGTCCTCACGGACTCATCAGGCTATCTTTGATTTGTTTAGGTAACCTGAACTGGATGTATTAGTTTGG
P121	gPNSI-1F	GATAGCCTGATGAGTCCGTGAGGACGAAACGAGTAAGCTCGTCGCTATCGCCAACATCCAAGTGTTTTAGAGCTAGAAAATAGCAAGTTAAAATAAGG CT
P122	gPNSI-2R	GTTTCGTCCTCACGGACTCATCAGGGTTGGTTTGATTTGTTTAGGTAACCTGAACTGGATGTATTAGTTTGG
P123	gPNSI-2F	CCAACCCTGATGAGTCCGTGAGGACGAAACGAGTAAGCTCGTCGGTTGGTACTATGTCCAACAGTTTTAGAGCTAGAAAATAGCAAGTTAAAATAAGG CT
P124	gPNSI-3R	GTTTCGTCCTCACGGACTCATCAGTGTGTCTTTGATTTGTTTAGGTAACCTGAACTGGATGTATTAGTTTGG
P125	gPNSI-3F	GACACACTGATGAGTCCGTGAGGACGAAACGAGTAAGCTCGTCTGTGTCTTTGAAGCACACAGGTTTTAGAGCTAGAAAATAGCAAGTTAAAATAAGG CT
P126	gPNSI-4R	GTTTCGTCCTCACGGACTCATCAGTTGTGGTTTGATTTGTTTAGGTAACCTGAACTGGATGTATTAGTTTGG
P127	gPNSI-4F	CCACAACCTGATGAGTCCGTGAGGACGAAACGAGTAAGCTCGTCTTGTGGCTATGGCTTGAATGGTTTTAGAGCTAGAAAATAGCAAGTTAAAATAAGG CT
P128	gPNSI-5R	GTTTCGTCCTCACGGACTCATCAGCACGAGTTTGATTTGTTTAGGTAACCTGAACTGGATGTATTAGTTTGG
P129	gPNSI-5F	CTCGTGCTGATGAGTCCGTGAGGACGAAACGAGTAAGCTCGTCCAGGAGCCGAGTAATAACCGTTTTAGAGCTAGAAAATAGCAAGTTAAAATAAG GCT
P130	pCAI-gPNSI-1F	GCTATCGCCAACATCCAAGTGTTTTAGAGCTAGAAAATAGCAAGTTAAAATAAGGCTAGT
P131	pCAI-gPNSI-1R	ACTTGGATGTTGGCGATAGCGACGAGCTTACTCGTTTCGTCCT
P132	pCAI-gPNSI-2F	GGTTGGTACTATGTCCAACAGTTTTAGAGCTAGAAAATAGCAAGTTAAAATAAGGCTAGT

P133	pCAI-gPNSI-2R	TGTTGGACATAGTACCAACCGACGAGCTTACTCGTTTCGTCCT
P134	pCAI-gPNSI-3F	TGTGTCTTTGAAGCACACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGT
P135	pCAI-gPNSI-3R	CTGTGTGCTTCAAAGACACAGACGAGCTTACTCGTTTCGTCCT
P136	pCAI-gPNSI-4F	TTGTGGCTATGGCTTGAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGT
P137	pCAI-gPNSI-4R	CATTCAAGCCATAGCCACAAGACGAGCTTACTCGTTTCGTCCT
P138	pCAI-gPNSI-5F	CACGAGCCGAGTAATAACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGT
P139	pCAI-gPNSI-5R	CGGTTTACTCGGCTCGTGGACGAGCTTACTCGTTTCGTCCT
P140	FAA1-HRUP-F	AGGTATCAAAAGCTGATTTTTATTGCTATTGTTGATTAC
P141	FAA1-HRUP-R	CAATCGGCTGCTCGCTTTCTTGAAGTTTTCTTTGTACGCGTGTGTTG
P142	FAA1-HRDN-F	GAAAACCTCAAGAAAGCGAGCAGCCGATTGAAGTTTTCTA
P143	FAA1-HRDN-R	GCATGGTTATGGTGCCGTTTGG
P144	PNSI-1UP-F	TATGGTTGCTTAAGATGATAGGAGAATCAAACC
P145	PNSI-1UP-R1	GACGAGGACACCAAGACATTTCTACAAAAAGTCATATGACAAGTTGGGTAGGTTGC
P146	PNSI-1DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGAAGCAAGTTGGGACGCGGAC
P147	PNSI-1DN-R	ATCCAGTTGCTCCACCCCCC
P148	PNSI-2UP-F	CCATATAAGTGATGTCTTAACAGTTACCATAGTCAAA
P149	PNSI-2UP-R1	GACGAGGACACCAAGACATTTCTACAAAAAAGTAACAAAAAATGAAAAAATTAAGTTTGACACGGAC
P150	PNSI-2DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGTCTACGTTTTAAGATCAATCAAATCACTTTAGCTACAT
P151	PNSI-2DN-R	GAATTCTTTGACTATTTGGATAGCAAAGGAGG
P152	PNSI-3UP-F	AATAAAAAATTCTCAGTCAGTGGCATGTGAAAG
P153	PNSI-3UP-R1	GACGAGGACACCAAGACATTTCTACAAAAAAGGGGCAAAGACTGGCATAAGTA
P154	PNSI-3DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGGAATACAATGTGTAAAGTGCAAGTCTTTCT
P155	PNSI-3DN-R	TTAAGGATTGATAACCAGATCGTTAAGCCAAATA
P156	PNSI-4UP-F	TGTGAATCAGTCACTTTGCTATGGC
P157	PNSI-4UP-R1	GACGAGGACACCAAGACATTTCTACAAAAACTCCTAGAACACCTAACATTGTATCACAA
P158	PNSI-4DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGCAGGACGAGATATCAAATAAAGGGCT
P159	PNSI-4DN-R	TCTCTAAGAACGGTCCATGGCTCTC
P160	PNSI-5UP-F	AGTGCCTCACAAAAAACGGGT
P161	PNSI-5UP-R1	GACGAGGACACCAAGACATTTCTACAAAAAGCAACATGAAGTAAATAACCGAAACTCAA

P162	PNSI-5DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGGGTAGGGCTGGTGACTAGCATG
P163	PNSI-5DN-R	AGTCGTGATCAGGCTTCACCGA
P164	gPNSI-6F	GGGGTCCTGATGAGTCCGTGAGGACGAAACGAGTAAGCTCGTACCCCGTAATAATCGACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG GCT
P165	gPNSI-6R	GTTTCGTCCTCACGGACTCATCAGGACCCCTTTGATTTGTTTAGGTAACCTGAACTGGATGTATTAGTTTGG
P166	gPNSI-7F	TTGCCACTGATGAGTCCGTGAGGACGAAACGAGTAAGCTCGTCTGGCAATAGGTAATTCAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CT
P167	gPNSI-7R	GTTTCGTCCTCACGGACTCATCAGTGGCAATTTGATTTGTTTAGGTAACCTGAACTGGATGTATTAGTTTGG
P168	gPNSI-8F	GGTCCCCTGATGAGTCCGTGAGGACGAAACGAGTAAGCTCGTCCGGACCGAGTAACAACCTCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG GCT
P169	gPNSI-8R	GTTTCGTCCTCACGGACTCATCAGGGGACCTTTGATTTGTTTAGGTAACCTGAACTGGATGTATTAGTTTGG
P170	gPNSI-9F	CCAATTCTGATGAGTCCGTGAGGACGAAACGAGTAAGCTCGTCAATTGGTTATGTTAGCAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CT
P171	gPNSI-9R	GTTTCGTCCTCACGGACTCATCAGAATTGGTTTGATTTGTTTAGGTAACCTGAACTGGATGTATTAGTTTGG
P172	gPNSI-10F	CAGAACCTGATGAGTCCGTGAGGACGAAACGAGTAAGCTCGTCTGTGACATAGTACCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CT
P173	gPNSI-10R	GTTTCGTCCTCACGGACTCATCAGGTTCTGTTTGATTTGTTTAGGTAACCTGAACTGGATGTATTAGTTTGG
P174	gPNSI-11F	GGGTTTCTGATGAGTCCGTGAGGACGAAACGAGTAAGCTCGTCAAACCCGAGAGGATGTACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG GCT
P175	gPNSI-11R	GTTTCGTCCTCACGGACTCATCAGAAACCCTTTGATTTGTTTAGGTAACCTGAACTGGATGTATTAGTTTGG
P176	gPNSI-12F	ATTTACCTGATGAGTCCGTGAGGACGAAACGAGTAAGCTCGTCTGTAATCTTCGGATATAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG CT
P177	gPNSI-12R	GTTTCGTCCTCACGGACTCATCAGGTAATTTTGATTTGTTTAGGTAACCTGAACTGGATGTATTAGTTTGG
P178	gPNSI-13F	TGGTTGCTGATGAGTCCGTGAGGACGAAACGAGTAAGCTCGTCCAACCGATAAAGACAGACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG GCT
P179	gPNSI-13R	GTTTCGTCCTCACGGACTCATCAGCAACCATTTGATTTGTTTAGGTAACCTGAACTGGATGTATTAGTTTGG
P180	gPNSI-14F	GCACACCTGATGAGTCCGTGAGGACGAAACGAGTAAGCTCGTCTGTGCTTTTGGTAAAGAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG GCT
P181	gPNSI-14R	GTTTCGTCCTCACGGACTCATCAGGTGTGCTTTGATTTGTTTAGGTAACCTGAACTGGATGTATTAGTTTGG

P182	gPNSI-15F	TAAGATCTGATGAGTCCGTGAGGACGAAACGAGTAAGCTCGTCATCTTACCAACAGAAACAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG GCT
P183	gPNSI-15R	GTTTCGTCCTCACGGACTCATCAGATCTTATTTGATTTGTTTAGGTAACCTGAACTGGATGTATTAGTTTGG
P184	gPNSI-16F	GCTACTCTGATGAGTCCGTGAGGACGAAACGAGTAAGCTCGTCAGTAGCTTGAGAAGTGACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG GCT
P185	gPNSI-16R	GTTTCGTCCTCACGGACTCATCAGAGTAGCTTTGATTTGTTTAGGTAACCTGAACTGGATGTATTAGTTTGG
P186	PNSI-6UP-F	GTCAGGAGGGACGGTAGGTG
P187	PNSI-6UP-R1	GACGAGGACACCAAGACATTTCTACAAAAAAGTAGTCAACCTTGAGCTATTATTTCTT
P188	PNSI-6DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGAATTTCAAAGTTCAACTTCCGCACC
P189	PNSI-6DN-R	TTGTCAATCATGCTCTCAAGGACTACCA
P190	PNSI-7UP-F	TAACTCATGGTAGTCCTTGAGAGCAT
P191	PNSI-7UP-R1	GACGAGGACACCAAGACATTTCTACAAAAAATGGCTTCACTATCTAATTACGGCATG
P192	PNSI-7DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGATGCCGGAGATTCTCATTCTCAATG
P193	PNSI-7DN-R	AGAAGAAGTGAAGACAAAGGAAAGGGAAA
P194	PNSI-8UP-F	TCCGCGATACAAGACGCCAAG
P195	PNSI-8UP-R1	GACGAGGACACCAAGACATTTCTACAAAAATTTTACAGCCAGCGACCAAAATATGCTA
P196	PNSI-8DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGTCAATGTTTTAATTTTTTTTTTTTCTTTCAATGCTC
P197	PNSI-8DN-R	TAGCGGTTAAATACGAAGTTCAAGTACCAATT
P198	PNSI-9UP-F	GTAATCTATTCAGGTCCGAAAGTTGAGAGC
P199	PNSI-9UP-R1	GACGAGGACACCAAGACATTTCTACAAAAATAGCGTATATTGTGGTGAGAAACCTGGG
P200	PNSI-9DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGTACTGAGCAGAGTACTATGAGTATGCTT
P201	PNSI-9DN-R	AGATTAATCGAAGGCCAATACTGCAAG
P202	PNSI-10UP-F	ATGATAGTATGTGCTCATAAGATCCAACCTACG
P203	PNSI-10UP-R1	GACGAGGACACCAAGACATTTCTACAAAAATAGGGGTTACAGTCCGAGTCGG
P204	PNSI-10DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGTGTTCGAGATTTCTTCGGACTTTTGC
P205	PNSI-10DN-R	CTATCCCTGAGTTTTTGAAGCAATAAACGAC
P206	PNSI-11UP-F	AGTCGAAAACCTTTCTGCATTCTACTTGAT
P207	PNSI-11UP-R1	GACGAGGACACCAAGACATTTCTACAAAAAGTCTCTGAATTTACAATTATACGATCGAG
P208	PNSI-11DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGCGTGGGTAGAGTTGTATGGCACAT

P209	PNSI-11DN-R	GGAGATCCTCCCTAGCCTCTTGG
P210	PNSI-12UP-F	AGTAGTAATACCTCCTTAAGATTGTTTTCAATCTGA
P211	PNSI-12UP-R1	GACGAGGACACCAAGACATTTCTACAAAACTGTATTTGTCTTAACAGTGAGTAGGTTT
P212	PNSI-12DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGACGCCAACTTAAGATCTGGTCTACC
P213	PNSI-12DN-R	ACTGAGCGTTACCTAGTCTTTCCAAG
P214	PNSI-13UP-F	ATAAACACTCAGATTGAAAACAATCTTAAGGAGGT
P215	PNSI-13UP-R1	GACGAGGACACCAAGACATTTCTACAAAAATCGCGAATTCGAATTTACCGATAAAAAGA
P216	PNSI-13DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGGAAGGATGTAAGATGGGGATTCACTCACT
P217	PNSI-13DN-R	TTCAACGTCCATAAGTAACATTTTCATACCC
P218	PNSI-14UP-F	GTGAGCGTTTCGCTTGATGCAG
P219	PNSI-14UP-R1	GACGAGGACACCAAGACATTTCTACAAAAAAGATACGGGCAATCTTATTAAGAGCAAA
P220	PNSI-14DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGACATTTCCAGAATGGTCACCACT
P221	PNSI-14DN-R	TCGTCAATGTCAATAGAGGCGTTAAA
P222	PNSI-15UP-F	CCAGAGTTTTGTAAATGTTGGGAATCTTG
P223	PNSI-15UP-R1	GACGAGGACACCAAGACATTTCTACAAAAATCTGTTGATCTTGGAGAAGTTCAGAGCT
P224	PNSI-15DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGCTCCAAGCTCTCAAGAAGGAGG
P225	PNSI-15DN-R	GAGCTCTGAAGTTGATAAAATGGTCATAC
P226	PNSI-16UP-F	ACCTCCTCCAGTGGTAAAAAGGT
P227	PNSI-16UP-R1	GACGAGGACACCAAGACATTTCTACAAAAATGTCAAATCATTCAATGGATTAGCCTCAC
P228	PNSI-16DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGAAAGGATGGCAAAGAAATGTATGCTGAG
P229	PNSI-16DN-R	CCACTTTTGGTAACCCAATACTTGATGC
P230	YZ-I1-F	TAACGACTGGACAATCACTTGTGAATGA
P231	YZ-I1-R	TGGCCTTACGAGTCTGATCAATGTAA
P232	YZ-I2-F	ACATTGTAACAGGTTTGGCATCGT
P233	YZ-I2-R	GTCACGATTGCTTGAGGATACTGAT
P234	YZ-I3-F	GGATACTGTGACAGATGGTGAACAG
P235	YZ-I3-R	GTTCTGAAAGTCGGAGGAAGAATAG
P236	YZ-I4-F	CGTAATCGGACGGTAACGAACAT
P237	YZ-I4-R	CCAGTCCAATCAAGAACTAAGAGAACTAA

P238	YZ-I5-F	CGATGCTGAAGATCCGAAACCA
P239	YZ-I5-R	GTGATGAACGTAATGCTGAGGGTG
P240	YZ-I6-F	GAACCAGTCAATCCCAGTTTAGAGAT
P241	YZ-I6-R	AGGCACCAGTTGGACTCACC
P242	YZ-I7-F	CAATAAAAAGGGATCGTCAATGGTGT
P243	YZ-I7-R	GTGATCTTCTCGTTGTTAGTCGTCG
P244	YZ-I8-F	AATGCCAATTTCTTGAAGTCCATTCAA
P245	YZ-I8-R	CGGTGGCGATCTAATTGTATTATAAATCG
P246	YZ-I9-F	CGTATCCCAACCTTGGTATGCCA
P247	YZ-I9-R	GTTCTGGTGTGTTCCGAAAGC
P248	YZ-I10-F	CAAGTTATCGAACCTGTATGTTGCAGT
P249	YZ-I10-R	GAACAACGGGTCCTCCAAAGAT
P250	YZ-I11-F	GCCAGAAGCGTTTTCAACTCATGT
P251	YZ-I11-R	TGCCTCGAATACACCTTCAACAC
P252	YZ-I12-F	TGGCTGTATACTGTCTGGATTCCAT
P253	YZ-I12-R	CGTAGTCATTATCGTTACGAATTGTGG
P254	YZ-I13-F	CGGATTGTTTTGCCCTATTAGTTGC
P255	YZ-I13-R	AGAGCTAAGATGAACAAGGAACTAAGAG
P256	YZ-I14-F	CGTGTACCGTATGATTATCCGAACG
P257	YZ-I14-R	CTCTTCTGGTGTGTTGAGCTCTCA
P258	YZ-I15-F	CACAGCTAGTCTGGTAGTCAGGAG
P259	YZ-I15-R	ACCTTGTCTTTGCAAGAACTGGG
P260	YZ-I16-F	ATGACTATTAAGGCGGTGTACAGAAACC
P261	YZ-I16-R	GACTACCTAGTTTCAATATCGTTAGCTGG
P262	pCAI-gPNSII-1F	TAAAGTAACAGAGCATCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGT
P263	pCAI-gPNSII-1R	CAGGATGCTCTGTTACTTTAGACGAGCTTACTCGTTTCGTCCT
P264	pCAI-gPNSII-2F	TCATTGCTACTACTGAATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGT
P265	pCAI-gPNSII-2R	CCATTGCTAGTAGCAATGAGACGAGCTTACTCGTTTCGTCCT
P266	pCAI-gPNSII-3F	TATAAGGCTCTGTAGATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGT

P267	pCAI-gPNSII-3R	CCATCTACAAGAGCCTTATAGACGAGCTTACTCGTTTCGTCCT
P268	pCAI-gPNSII-4F	CCTAAATACTACCTAAACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGT
P269	pCAI-gPNSII-4R	CTGTTTAGGTAGTATTTAGGGACGAGCTTACTCGTTTCGTCCT
P270	pCAI-gPNSII-5F	AACTTTGAAACAAAAGAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGT
P271	pCAI-gPNSII-5R	CCTTCTTTTGTTCAAAGTTGACGAGCTTACTCGTTTCGTCCT
P272	pCAI-gPNSII-6F	CCAATATAGGATTGAACTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGT
P273	pCAI-gPNSII-6R	CGAGTTCAATCCTATATTGGGACGAGCTTACTCGTTTCGTCCT
P274	pCAI-gPNSII-7F	AAGTCAATCATAACTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGT
P275	pCAI-gPNSII-7R	CGTAGTATTATGATTGACTTGACGAGCTTACTCGTTTCGTCCT
P276	pCAI-gPNSII-8F	GTTACTGGATTAGAACGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGT
P277	pCAI-gPNSII-8R	CGTCGTTCTAATCCAGTAACGACGAGCTTACTCGTTTCGTCCT
P278	pCAI-gPNSII-9F	GAACAATAACATGACCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGT
P279	pCAI-gPNSII-9R	TGTGGTCATGTTTATTGTTTCGACGAGCTTACTCGTTTCGTCCT
P280	PNSII-1UP-F	GTGAAGCTTTGAACTTGTCGATTCCACC
P281	PNSII-1UP-R1	GACGAGGACACCAAGACATTTCTACAAAAACTATTATGGCTAGTGTATTTTGTATTTTGAAGCT
P282	PNSII-1DN-F1	CATAGGGATAATAGAAAAGTAAGGTTCCGCGTCAAACGGGAGCCCGATGGTG
P283	PNSII-1DN-R	GGCCGTGGAACAAAATTATATGGATTATACAAAT
P284	PNSII-2UP-F	AGTCGATAAAACCAAAAACGATCTGATCAATAACT
P285	PNSII-2UP-R1	GACGAGGACACCAAGACATTTCTACAAAAAGCAAGGTCGGAGATTGCTTTTAAGC
P286	PNSII-2DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGTGCTGGTGGTTATATTACAAGCTTGGTAG
P287	PNSII-2DN-R	CAATCGGTATTTAATTCATAGATATTC AATAACCAATTCTCCAC
P288	PNSII-3UP-F	TTTCAATTCCTTGAAAGCTTTAAAGTTGTTCTAATTTG
P289	PNSII-3UP-R1	GACGAGGACACCAAGACATTTCTACAAAAATCGACAAGCAGAACACTAAGATCTAGAGA
P290	PNSII-3DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGAATGCTAGCCTAGTTGTCAGAGCTT
P291	PNSII-3DN-R	AATGCAGATTCTGAGACTACACAGATACTC
P292	PNSII-4UP-F	GTGTTGCGGAGAACGAGATCTTTC
P293	PNSII-4UP-R1	GACGAGGACACCAAGACATTTCTACAAAAATCGTGTGCGCGACAACACAGT
P294	PNSII-4DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGAATAGTAAGGACCGGGTTCAGTTGACT
P295	PNSII-4DN-R	AATCTTCCGCACTCATTAGTTTTTATCTTTCTTCTT

P296	PNSII-5UP-F	AGGCCAGACCTATAACCATCATGAAAAC
P297	PNSII-5UP-R1	GACGAGGACACCAAGACATTTCTACAAAAAGCATGGACCTGCTTATCTCATCT
P298	PNSII-5DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGAAGTAGTCATCTAATTTAATCATAAAAAGGGAAATCGAT
P299	PNSII-5DN-R	TTGGTAAAAATTTGATATTGGTACTGGCTGTG
P300	PNSII-6UP-F	AACTGACCATCTTCATCTATCAGCATACTT
P301	PNSII-6UP-R1	GACGAGGACACCAAGACATTTCTACAAAAAAGTATTCCATAAACAGAAATTTTAAATAAAACAGTACACT
P302	PNSII-6DN-F1	TAGGGATAATAGAAAAGTAAGGTTCCGCGTGAAGCTTTACATGGTAAAGCATAGTGTAG
P303	PNSII-6DN-R	GTTTCGTATTTGAAATGCTGACCCAGC
P304	PNSII-7UP-F	ATCAATCGCTTTAAAATCACTTTTCATCTCTTGAAC
P305	PNSII-7UP-R1	GACGAGGACACCAAGACATTTCTACAAAAACAAGGGTGTGATTTAACGGACTAAAAG
P306	PNSII-7DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGTTCTCCGGTGAAGAAGTGTGTAC
P307	PNSII-7DN-R	ATCAACTATTTAACCTTCTATCTGTTTCTATTATTTTCTACAT
P308	PNSII-8UP-F	CATGCATATAGTGTAGCCGAGACGAC
P309	PNSII-8UP-R1	GACGAGGACACCAAGACATTTCTACAAAAAATTCGCAAGTTTCAGATTGCTTGC
P310	PNSII-8DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGATCACGGATGTTGATTCCCCTAACATAG
P311	PNSII-8DN-R	CGGATTAACGGGGTTGTATATATAGAGTTAAAAGATC
P312	PNSII-9UP-F	GAACATCTCTGTGCCGACATTAACG
P313	PNSII-9UP-R1	GACGAGGACACCAAGACATTTCTACAAAAATCGATTTAACCAAACCGTCTTGTCTG
P314	PNSII-9DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGACTTCATATCCAAATAAACTTTTGCGATTATCAATT
P315	PNSII-9DN-R	CCGTAACACGGGATATATATTGTGTACAATTGAC
P316	PNSII-YZ-1F	CAAAGCTCCCCTTGTTGCTAATCC
P317	PNSII-YZ-1R	CTCGTCTTTCAAGACACCCGAAATTAG
P318	PNSII-YZ-2F	CTACTATGCCGTATTGGAAAGGCGA
P319	PNSII-YZ-2R	GAGTCATATTACGGTTTCAATTTCTGCTGT
P320	PNSII-YZ-3F	CGTCTTGGACAACCTCATCAGAATCTTG
P321	PNSII-YZ-3R	GCGTCACTGTAACATTATCAGTGTGG
P322	PNSII-YZ-4F	GGGTCAAGTAGGGTGCAAACAAAG
P323	PNSII-YZ-4R	GTGACATGAACTGACAAAGTAGGAAAGTG
P324	PNSII-YZ-5F	CCAACAAAGATGGCTGTGGTCAC

P325	PNSII-YZ-5R	GTGCCTCGATGGTCAATTGTTTCTC
P326	PNSII-YZ-6F	CAACTCTGAGCCACTCAAAGAATGCA
P327	PNSII-YZ-6R	GGATCGTGTTCTCGCTGTTTTATTATCTAC
P328	PNSII-YZ-7F	GCTCCAACGGCATTGCAACA
P329	PNSII-YZ-7R	GCACTGGATCAATTACCGTTGTTCC
P330	PNSII-YZ-8F	CGGTTATCAAGAGAGGTTTGCAATTAG
P331	PNSII-YZ-8R	GGATTTGTTCTGTGGAATCTGGATACAG
P332	PNSII-YZ-9F	ACGTGTGCTATGTGGCAATTATC
P333	PNSII-YZ-9R	GGAGTGTCTCTCCTTATTGTTCTCGGA
P334	gPNSIII-1-F	GGTCGATAGGATGATCACTTGTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGT
P335	gPNSIII-1-R	AAGTGATCATCCTATCGACCGACGAGCTTACTCGTTTCGTCCT
P336	gPNSIII-2-F	GCATTTTAAGAAAAACCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGT
P337	gPNSIII-2-R	CAGGTTTTTCTTAAAATGCGACGAGCTTACTCGTTTCGTCCT
P338	gPNSIII-3-F	TGCTCGGATAGGGTCAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGT
P339	gPNSIII-3-R	CTTTGGACCCTATCCGAGCAGACGAGCTTACTCGTTTCGTCCT
P340	gPNSIII-4-F	GTATTTATTCCAGAACAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGT
P341	gPNSIII-4-R	CCTTGTCTGGAATAAATACGACGAGCTTACTCGTTTCGTCCT
P342	gPNSIII-5-F	ATACTAGTTAACAACTGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGT
P343	gPNSIII-5-R	CCCAGTTTGTTAACTAGTATGACGAGCTTACTCGTTTCGTCCT
P344	gPNSIII-6-F	CGGAGTTTAATAAAGCATGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGT
P345	gPNSIII-6-R	ACATGCTTTATTAACTCCGGACGAGCTTACTCGTTTCGTCCT
P346	gPNSIII-7-F	TTGTGATCGATAATAAACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGT
P347	gPNSIII-7-R	CCGTTTATTATCGATCACAAGACGAGCTTACTCGTTTCGTCCT
P348	gPNSIII-8-F	AGTTAGGAGATATAGTAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGT
P349	gPNSIII-8-R	CGTACTATATCTCCTAACTGACGAGCTTACTCGTTTCGTCCT
P350	gPNSIII-9-F	GTTTGTACGCATGAGCTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGT
P351	gPNSIII-9-R	CACAGCTCATGCGTACAAACGACGAGCTTACTCGTTTCGTCCT
P352	gPNSIII-10-F	CGGCGAAAATTGGTAAACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGT
P353	gPNSIII-10-R	CTGTTTACCAATTTTCGCCGACGAGCTTACTCGTTTCGTCCT

P354	gPNSIII-11-F	AGCTCTGAAGATACTACCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGT
P355	gPNSIII-11-R	TCGGTAGTATCTTCAGAGCTGACGAGCTTACTCGTTTCGTCCT
P356	gPNSIII-12-F	GGAACGAGGAGATAAATACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGT
P357	gPNSIII-12-R	CGTATTTATCTCCTCGTTCGACGAGCTTACTCGTTTCGTCCT
P358	gPNSIV-1-F	AATATGCACGAAATCAAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGT
P359	gPNSIV-1-R	CAC TTGATTTCTGTCATATTGACGAGCTTACTCGTTTCGTCCT
P360	gPNSIV-2-F	GTACAATCACTCGATACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGT
P361	gPNSIV-2-R	ACGTATCGAGTGAATTGTACGACGAGCTTACTCGTTTCGTCCT
P362	gPNSIV-3-F	TTCCCTTCGGATACTACACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGT
P363	gPNSIV-3-R	AGTGTAGTATCCGAAGGGAAGACGAGCTTACTCGTTTCGTCCT
P364	gPNSIV-4-F	TGTCAAATGAAAAAGATACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGT
P365	gPNSIV-4-R	CGTATCTTTTTCATTTGACAGACGAGCTTACTCGTTTCGTCCT
P366	gPNSIV-5-F	CGTATGTTCTAAGATTACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGT
P367	gPNSIV-5-R	TCGTAATCTTAGAACATACGGACGAGCTTACTCGTTTCGTCCT
P368	gPNSIV-6-F	TGGTTGTATCAGTGAAATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGT
P369	gPNSIV-6-R	CCATTTCACTGATACAACCAGACGAGCTTACTCGTTTCGTCCT
P370	gPNSIV-7-F	TCTCGATGGACGGATAACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGT
P371	gPNSIV-7-R	CTGTTATCCGTCCATCGAGAGACGAGCTTACTCGTTTCGTCCT
P372	gPNSIV-8-F	CTCGAGTGCAAAATTAACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGT
P373	gPNSIV-8-R	AGGTTAATTTTGCCTCGAGGACGAGCTTACTCGTTTCGTCCT
P374	gPNSIV-9-F	ATTATCGTTTGGGATACGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGT
P375	gPNSIV-9-R	CTCGTATCCCAAACGATAATGACGAGCTTACTCGTTTCGTCCT
P376	gPNSIV-10-F	TACCAAGTTAATCAGCAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGT
P377	gPNSIV-10-R	CGCTGCTGATTAACCTGGTAGACGAGCTTACTCGTTTCGTCCT
P378	gPNSIV-11-F	TATAAGTTGATCAAAACCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGT
P379	gPNSIV-11-R	CAGGTTTTGATCAACTTATAGACGAGCTTACTCGTTTCGTCCT
P380	gPNSIV-12-F	ACCATTAAGGATAACCAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGT
P381	gPNSIV-12-R	CCCTGGTTATCCTTAATGGTGACGAGCTTACTCGTTTCGTCCT
P382	gPNSIV-13-F	TACTCTGAACAACAGCCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGT

P383	gPNSIV-13-R	CCTGGCTGTTGTTTCAGAGTAGACGAGCTTACTCGTTTCGTCCT
P384	gPNSIV-14-F	GCCAGAGAGTACCCAGCATGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGCTAGT
P385	gPNSIV-14-R	CATGCTGGGTACTCTCTGGCGACGAGCTTACTCGTTTCGTCCT
P386	gPNSIV-15-F	TATGAAAATCTATATCTAGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGCTAGT
P387	gPNSIV-15-R	CCTAGATATAGATTTTCATAGACGAGCTTACTCGTTTCGTCCT
P388	gPNSIV-16-F	AGTATACGGTGAGTATTCGGGTTTTAGAGCTAGAAAATAGCAAGTTAAAAAAGGCTAGT
P389	gPNSIV-16-R	CCGAATACTCACCGTATACTGACGAGCTTACTCGTTTCGTCCT
P390	PNSIII-1UP-F	TGCAAGGCCAGACCTGATG
P391	PNSIII-1UP-R1	GACGAGGACACCAAGACATTTCTACAAAAACTACCCTTTGTTGAGTAACTTCAACACTG
P392	PNSIII-1DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGCAATTTAAATAGCCTTCATTTTGATACAGTGTCTGC
P393	PNSIII-1DN-R	CCACTCTTGACGATACGCATTCTACA
P394	PNSIII-2UP-F	AGAGAACAAGAGGCAATAAGAGATCACTAAATG
P395	PNSIII-2UP-R1	GACGAGGACACCAAGACATTTCTACAAAAACTATCGAACTACTTTGCGGACACTG
P396	PNSIII-2DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGCACTGGTTGCTCAAAAAGGGCTGA
P397	PNSIII-2DN-R	GCTGCTTTGAAATGGAATCAAAGTAAACTCAA
P398	PNSIII-3UP-F	CAAACAAGGCGTCAATTTTGAAAATAAATATTTTTG
P399	PNSIII-3UP-R1	GACGAGGACACCAAGACATTTCTACAAAAAGCGTTAAGCTCAGGTACGTCCAAA
P400	PNSIII-3DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGCTGTTGTTATTTGTGGAATAGTTTCATCAGCT
P401	PNSIII-3DN-R	AAACAATCAGGGGTGACAGTTCAATCAA
P402	PNSIII-4UP-F	TCTACAATCCAAAGAAATGTGGATTCCGTAGA
P403	PNSIII-4UP-R1	GACGAGGACACCAAGACATTTCTACAAAAACAGTTCAAAGGAGACATCGTCCAATACAA
P404	PNSIII-4DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGCATCAGCAGCAACCAGCAAGT
P405	PNSIII-4DN-R	TAACGTTCTCTCAGTTGAATCGAAATACTGA
P406	PNSIII-5UP-F	GCGCTTGTAACGCTTTTCTTGATC
P407	PNSIII-5UP-R1	GACGAGGACACCAAGACATTTCTACAAAAACTCTCAACCAGCAAATGATACTAGTAGTG
P408	PNSIII-5DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGATTAATAGAAATTAGATCTCGATAGGACGCGATC
P409	PNSIII-5DN-R	TACAATTTGAGCGGATCATTGTTTCAGCTA
P410	PNSIII-6UP-F	TTTTAAAAAAGTCGAAAGATAGGTTCTTTTTAACCACATCT
P411	PNSIII-6UP-R1	GACGAGGACACCAAGACATTTCTACAAAAATGAACTCAAAGACTATCACAAACAGTGTG

P412	PNSIII-6DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGAAAAAATTGTTCTGATGTGCAACACAAAC
P413	PNSIII-6DN-R	ACTTGAGCTGTTCAAGCTCCCAG
P414	PNSIII-7UP-F	TAGGTCATGACTCAGAGACACAAGCG
P415	PNSIII-7UP-R1	ACGAGGACACCAAGACATTTCTACAAAAAGGTTTAGAGTCTGAATCTGAATATGAAGG
P416	PNSIII-7DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGTAACTAGTGGTTATTGTTTCTGATATAATTAGTTTGACGTG
P417	PNSIII-7DN-R	GCAGGACCAGAGAATTTGGCTGT
P418	PNSIII-8UP-F	AGTTTACATTTTGAECTATATCTCTATCTGATTTGCTGAA
P419	PNSIII-8UP-R1	GACGAGGACACCAAGACATTTCTACAAAAAGCAGTAGAGTAATAAATTTTTGCGAACCCAG
P420	PNSIII-8DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGCGTTGGTTAGTATTGATGTGACCCATACT
P421	PNSIII-8DN-R	AACTGCAACAATAATAAGCGTTTACCT
P422	PNSIII-9UP-F	TTTTGTAAGCACTGACTTCTGTCTATTGGG
P423	PNSIII-9UP-R1	GACGAGGACACCAAGACATTTCTACAAAAAATAGTATTGCATCTCAAGTCTCACGAAC
P424	PNSIII-9DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGAGAATGGAGACAGAGTCTGCGATGTAC
P425	PNSIII-9DN-R	TAAAAGATGAGCAGGAACTCTTTCTTTTTTCCC
P426	PNSIII-10UP-F	GCGAGGTTTATGTAACCACCACCC
P427	PNSIII-10UP-R1	GACGAGGACACCAAGACATTTCTACAAAAACAGATGAGTCGGAATGTACCACGAC
P428	PNSIII-10DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGTCTAATGGAGCGCCTTGGTTAAGTG
P429	PNSIII-10DN-R	CTACTTTGTTGAGCTTCTTTGTATAGTTTGATTACCT
P430	PNSIII-11UP-F	CTTTTTCTTCGACAATGGATTGTACTTTTTTTCATC
P431	PNSIII-11UP-R1	GACGAGGACACCAAGACATTTCTACAAAAATTTTTGTCAGTTATATTAGGTACCTTATAGGTGGCC
P432	PNSIII-11DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGCTCAACAAGAATGAGAAAATTATTTTAAATGGTTACGTC
P433	PNSIII-11DN-R	TTTATCGAACATTGCCGAAGCTATGCC
P434	PNSIII-12UP-F	GACGGTAGGTATCAGACCGACGA
P435	PNSIII-12UP-R1	GACGAGGACACCAAGACATTTCTACAAAAATTCATTTGCATCAACAAAAAACGTATTGATGC
P436	PNSIII-12DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGCCTACTATAATAAGAGAGTTTGGTTCTGGTTTTACTAGT
P437	PNSIII-12DN-R	CTACGAGAAAACACTTCGAGATCCCTC
P438	YZ-PNSIII-1F	CTCATCTACGCTTAATCCACATTCTGG
P439	YZ-PNSIII-1R	GTCACTGTGAAGACAACAAGCATTAGTG
P440	YZ-PNSIII-2F	AGCAGTCATCAAAAGAAGTCTTCTTGC

P441	YZ-PNSIII-2R	GGATGGCACAATCAAATGATTCAGATG
P442	YZ-PNSIII-3F	GCCTGAGCATACGATAGAGTTAAATTCG
P443	YZ-PNSIII-3R	GAAGAGAAGCAAAGTCAGTACTCTACGG
P444	YZ-PNSIII-4F	GGAGTCTTCTTGCCCGCTTGAATTAC
P445	YZ-PNSIII-4R	TGTGAAAGACTGGTAGTTCGAAGTACTTAC
P446	YZ-PNSIII-5F	CGTTCTTGCAAGCGCTGTTCTGA
P447	YZ-PNSIII-5R	CAAACAGGCTAGCTTTTTGCACTAGTAG
P448	YZ-PNSIII-6F	TTGACCACAACAGTAAATTGGCAAGGA
P449	YZ-PNSIII-6R	GAAAGAGTCAGAAATCCAAAAGAACACATAATTGAA
P450	YZ-PNSIII-7F	GATTGGGGTACATTCTTCCCTGC
P451	YZ-PNSIII-7R	CTGTTTGCCATGACTGTGCAGAAA
P452	YZ-PNSIII-8F	GCTGACAATAGAACAGCAATGTACTTTGTC
P453	YZ-PNSIII-8R	GCGAACAATAAGCTGTGAAAGTAAAAGCAA
P454	YZ-PNSIII-9F	GAGCTCGTCTGTTGACGAAAATGAG
P455	YZ-PNSIII-9R	GACTTCATCAACAGATCGCACCAATACATA
P456	YZ-PNSIII-10F	CCATATTGGAGCACTTCCACAATTCC
P457	YZ-PNSIII-10R	GGAATAGATGCTTGGATGAAATGTTCAATTGG
P458	YZ-PNSIII-11F	CAACAGGAGAAATACTCGTTGTTTAGCAGA
P459	YZ-PNSIII-11R	GCTCCATGCTTTTGAGTTGTTGTACAAC
P460	YZ-PNSIII-12F	GGTTCTGCACTCCATGAGCTAAATCA
P461	YZ-PNSIII-12R	CCGCAACAGTAGAGAAACCAAATGG
P462	PNSIV-1UP-F	TATAGCTGAGCAAATCACAACGAGCG
P463	PNSIV-1UP-R1	GACGAGGACACCAAGACATTTCTACAAAAAACTAAGAATTATTTATGGTACTATCCTGTTTAGTCTATTCC
P464	PNSIV-1DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGTTAAAACCAAATGTATGACCATCCTGCCA
P465	PNSIV-1DN-R	ACAGTTCTTTCCGGTTCCTATTGAAAGC
P466	YZ-PNSIV1-F	CTCATCGTTCAGAGCAGCAATGTG
P467	YZ-PNSIV1-R	GAAAGTGTGCTACTGCTATTGTTGGC
P468	PNSIV-2UP-F	AACAGACATTATTATCTCCATGAATCAGTATTCTTCG
P469	PNSIV-2UP-R1	GACGAGGACACCAAGACATTTCTACAAAAACTATTGAGCAATTGAGTTGAAAAAATGAAAATTGC

P470	PNSIV-2DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGTGCGGATGGGACAAACCTTCTTATG
P471	PNSIV-2DN-R	TATCACTGCTATTTTCTGTTGTGTCGGGT
P472	YZ-PNSIV2-F	CTCTTACTACATCATAAGCCTTTGCGAGC
P473	YZ-PNSIV2-R	GCCTTCTCATCCAAATGATAAGCCAGG
P474	PNSIV-3UP-F	GGTTGCATGCACCCACCGAA
P475	PNSIV-3UP-R1	GACGAGGACACCAAGACATTTCTACAAAAAACAATAATCGTGTGGCCTGCA
P476	PNSIV-3DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGGAGAGTTTTGTTGATGCAACTGTCCTG
P477	PNSIV-3DN-R	TTTACTGCCTGGGTTGTGTTGC
P478	YZ-PNSIV3-F	AGAAGGTGCGCGATAAAAAGCAA
P479	YZ-PNSIV3-R	GAGTGTTATTAGTGGTTGCGCATTG
P480	PNSIV-4UP-F	TAATCTCCTCAAAAAGTGAAGGGAATGATTTAAATATTTGG
P481	PNSIV-4UP-R1	GACGAGGACACCAAGACATTTCTACAAAAACAGAGGATGAGACAAACAAAGACAAAGAC
P482	PNSIV-4DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGACGTCTATAACAGTTAGTTTTCAAAACATTCAAAAATATTT
P483	PNSIV-4DN-R	AGCAAGCTGATTGAACTCCGC
P484	YZ-PNSIV4-F	GAAGACGTTACCCAGGTGTCTATG
P485	YZ-PNSIV4-R	GCCTAAGTTGCACAAGAAGTGACGTATA
P486	PNSIV-5UP-F	CTTATTATTGCAATCTGAAAGTTAAGCCTAAGTC
P487	PNSIV-5UP-R1	GACGAGGACACCAAGACATTTCTACAAAAAGGAGAGGGCAGGAGCAAAAA
P488	PNSIV-5DN-F1	TAGGGATAATAGAAAAGTAAGGTTCCGCGCTTTACTGGTAAACGATCTTCAAGTTGTCT
P489	PNSIV-5DN-R	GATCGCCCTTGATGGAAAATTGAG
P490	YZ-PNSIV5-F	CCTCCACCAACCACTGAGAAGC
P491	YZ-PNSIV5-R	GATGAATTGCAACGATAATCCGAGCAGTTTA
P492	PNSIV-6UP-F	CTTAGAATCGGTGCCGTTTCATTTGG
P493	PNSIV-6UP-R1	GACGAGGACACCAAGACATTTCTACAAAAACAGAAAATGGATTCTGCCAGAGACAATA
P494	PNSIV-6DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGTTTTGAAAAGAAACCTCCACGCGCA
P495	PNSIV-6DN-R	ATACCACCTTGATCGCCTAAGAACACTA
P496	YZ-PNSIV6-F	CCCATGTTGGTGATACATTCAGTGC
P497	YZ-PNSIV6-R	CGGATATATGAGGGGACAAGCGA
P498	PNSIV-7UP-F	TAGAGCCATTGCACCAGGGTCA

P499	PNSIV-7UP-R1	GACGAGGACACCAAGACATTTCTACAAAAATTTAGCATTTTATTGCGACTGAAAGCTTATTTTGT
P500	PNSIV-7DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGTGGATTTTTATCAGATTGATCAATCAAAAACGATAATATCAGTTAC
P501	PNSIV-7DN-R	TAGCGATCGCTGATGTAGAGAGGC
P502	YZ-PNSIV7-F	CAAAGTAATCTTGAGTCAAGTTGAAAAGTGAAC
P503	YZ-PNSIV7-R	GTTGTATGGAGCGCCTTCCAGC
P504	PNSIV-8UP-F	TGTCAGTGGGGAATTTGCAGGTAGTAG
P505	PNSIV-8UP-R1	GACGAGGACACCAAGACATTTCTACAAAAACCTTCACTTCATGTAACATTTAGTCAAATTGAGG
P506	PNSIV-8DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGTTTATCCCAAAGTGTTTTGGTTGCAT
P507	PNSIV-8DN-R	TCAACAGAAAGGCTCCAGTTGG
P508	YZ-PNSIV8-F	ACCAGTCTTTGCTGGAGAATGGA
P509	YZ-PNSIV8-R	GTGCTCCTGGTTGGAAAATACAGGTAC
P510	PNSIV-9UP-F	TAAGAGCTCCACAATCGCCAAGC
P511	PNSIV-9UP-R1	GACGAGGACACCAAGACATTTCTACAAAAATTTTCAAGTTCTAGCGGAACTCTCTC
P512	PNSIV-9DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGGCTCAAACAGGTTTATTCCATGGACC
P513	PNSIV-9DN-R	TACTAACTTATAGTGGATTGTGGTAGATACGTTACTATCT
P514	YZ-PNSIV9-F	TCGTATCATAATGAAAACCTTATGTACCAAG
P515	YZ-PNSIV9-R	AACACAGAACCATTTCATTCGCAAGATAGAA
P516	PNSIV-10UP-F	GCCAGTGAGGCTCATACTTGGT
P517	PNSIV-10UP-R1	GACGAGGACACCAAGACATTTCTACAAAAAGCGGGTTTAAAAGACATAATAGGGT
P518	PNSIV-10DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGATCAACTCACTATTTTATTTCATGTCAACAGC
P519	PNSIV-10DN-R	ATCATTAAAAACTCAATTAAGTATTTTTCCCCACC
P520	YZ-PNSIV10-F	GTCACCAACCATAGTTGGTTTAAATTTGAATACAAA
P521	YZ-PNSIV10-R	CATTGAAACCGTTCGAACATACCTCG
P522	PNSIV-11UP-F	AGGCTTGCATCATCATTCTCGTAATC
P523	PNSIV-11UP-R1	GACGAGGACACCAAGACATTTCTACAAAAATCAGTAGGACTGTGCGTGTGTAGC
P524	PNSIV-11DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGTTGCTAAAACATAAATGTTGTAGCCGTATATGATAAAACAG
P525	PNSIV-11DN-R	GAAATTCGCAGCTATTTATTTCTACGGGG
P526	YZ-PNSIV11-F	GAATTGACCTAAACGATCCAGAATTCAACG
P527	YZ-PNSIV11-R	GAATTCAGTGCTCTTCAATCTTGATCTTG

P528	PNSIV-12UP-F	TATGATATTGAACGTCTTGAACGTACAGATGAG
P529	PNSIV-12UP-R1	GACGAGGACACCAAGACATTTCTACAAAAATCCATATATTAATTATACATACTGTGCCCTTAAAATTA CTCTCG
P530	PNSIV-12DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGTCTGTATTGTCCAAACATTGTTACTATCGTTTTTCTC
P531	PNSIV-12DN-R	GATGAATGCTCATGGCTTGGTACC
P532	YZ-PNSIV12-F	GGGTCATATAATTGCCCGAAACAAGTC
P533	YZ-PNSIV12-R	CTTTCAGTTAAAGTTGAAGTTTGATCGGTGATAT
P534	PNSIV-13UP-F	GGGGAAAAACAACACTACTATTAATGCAACT
P535	PNSIV-13UP-R1	GACGAGGACACCAAGACATTTCTACAAAAAAGTAGGTGAAACTTTGTAGCTGCG
P536	PNSIV-13DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGCCGAGCGTTGAAATTTGGAGTGG
P537	PNSIV-13DN-R	ATGCTCCTCATTCTAAGTTTCCGATGG
P538	YZ-PNSIV13-F	CGGGTGTGAGAAAGCAAAGTATTCTG
P539	YZ-PNSIV13-R	GCAAGAGTGACCGAGTCTACCC
P540	PNSIV-14UP-F	GGTAATCGGAATATTAAGATTCAACATAAAAGAAAGAACTAC
P541	PNSIV-14UP-R1	GACGAGGACACCAAGACATTTCTACAAAAA CTACAATGAAGTTGGGAGTTTCATGACT
P542	PNSIV-14DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGTTTAAAAACAGCTCTTTTGCAAGAGCCA
P543	PNSIV-14DN-R	GTGACTAATCTGTACTACCTCTGTATGTGTGG
P544	YZ-PNSIV14-F	CTGAGACCATACCTGCATCAACTA
P545	YZ-PNSIV14-R	CGTCAGACTAATCAAGATAGGTCTTGCAAT
P546	PNSIV-15UP-F	TAGGCTGACAACTCTTCTTTGAATATAAAATATTTTCCTAGT
P547	PNSIV-15UP-R1	GACGAGGACACCAAGACATTTCTACAAAAATCTTGTTAGAAAAATTCAAACGATAGGATGAGGGA
P548	PNSIV-15DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGGCATAAAAAATTGTTGGTCTCTTATCAGATGACTC
P549	PNSIV-15DN-R	CGGCTAAGACCATCCATCACCATAC
P550	YZ-PNSIV15-F	GCGTTTTCCAGCTCTGTATTCAAGTA
P551	YZ-PNSIV15-R	GCCAGTAGCTTCCAATCTAGTCCAAATTAT
P552	PNSIV-16UP-F	AAATATTTTATATTTCAAAGAAGAGTTTGTCAGCCTACGAT
P553	PNSIV-16UP-R1	GACGAGGACACCAAGACATTTCTACAAAAAGAGCTTGGGTCATGGGTAGATTA ACTC
P554	PNSIV-16DN-F1	ATAGGGATAATAGAAAAGTAAGGTTCCGCGCGCGCAAGTAGTTTCCTTCATTCC
P555	PNSIV-16DN-R	CAATGGACTCAATTAGGTATGTGCTATTCTAGC
P556	YZ-PNSIV16-F	GCACGGATAAGTGGTTACATAAATTTTGG

P557 YZ-PNSIV16A-R GCATCCAGCATTAAAACTAAGTAAGTTCTGTTG

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Supplementary Table S3 Details of neutral sites and integration efficiency

No.	Neutral sites	sgRNA sequence (20 bp+NGG)	Plasmid	Host strain	Integration efficiency	Chromosome
1	PNSI-1	GCTATCGCCAACATCCAAGTGGG	pPICZ-Cas9-gPNSI-1 or pCAI-gPNSI-1	PC110 or PC111	8/10 = 80% or 10/10 = 100%	chr1
2	PNSI-2	GGTTGGTACTATGTCCAACACGG	pPICZ-Cas9-gPNSI-2	PC110	8/10 = 80%	chr1
3	PNSI-3	TGTGTCTTTGAAGCACACAGAGG	pPICZ-Cas9-gPNSI-3 or pCAI-gPNSI-3	PC110 or PC111	7/10 = 70% or 9/10 = 90%	chr1
4	PNSI-4	TTGTGGCTATGGCTTGAATGAGG	pPICZ-Cas9-gPNSI-4 or pCAI-gPNSI-4	PC110 or PC111	9/10 = 90% or 10/10 = 100%	chr1
5	PNSI-5	CACGAGCCGAGTAATAACCGTGG	pPICZ-Cas9-gPNSI-5 or pCAI-gPNSI-5	PC110 or PC111	9/10 = 90% or 10/10 = 100%	chr1
6	PNSI-6	GACCCGTAATAATCGACGTCGG	pPICZ-Cas9-gPNSI-6	PC110	10/10 = 100%	chr1
7	PNSI-7	TGGCAATAGGTAATTCAACGAGG	pPICZ-Cas9-gPNSI-7	PC110	10/10 = 100%	chr1
8	PNSI-8	GGGACCGAGTAACAACCTCAAGGG	pPICZ-Cas9-gPNSI-8	PC110	10/10 = 100%	chr1
9	PNSI-9	AATTGGTTATGTTAGCAAAGTGG	pPICZ-Cas9-gPNSI-9	PC110	9/10 = 90%	chr1
10	PNSI-10	GTTCTGTGACATAGTACCAGGGG	pPICZ-Cas9-gPNSI-10	PC110	10/10 = 100%	chr1
11	PNSI-11	AAACCCGAGAGGATGTACGGCGG	pPICZ-Cas9-gPNSI-11	PC110	10/10 = 100%	chr1
12	PNSI-12	GTAAATCTTCGGATATAGGGGGG	pPICZ-Cas9-gPNSI-12	PC110	10/10 = 100%	chr1
13	PNSI-13	CAACCAGTAAAGACAGACGACGG	pPICZ-Cas9-gPNSI-13	PC110	9/10 = 90%	chr1
14	PNSI-14	GTGTGCTTTTGGTAAAGAGGTGG	pPICZ-Cas9-gPNSI-14	PC110	9/10 = 90%	chr1
15	PNSI-15	ATCTTACCAACAGAAAACAGGAGG	pPICZ-Cas9-gPNSI-15	PC110	0/10 = 0%	chr1
16	PNSI-16	AGTAGCTTGAGAAGTGACGGTGG	pPICZ-Cas9-gPNSI-16	PC110	8/10 = 80%	chr1
17	PNSII-1	TAAAGTAACAGAGCATCCTGAGG	pCAI-gPNSII-1	PC111	8/10 = 80%	chr2
18	PNSII-2	TCATTGCTACTACTGAATGGAGG	pCAI-gPNSII-2	PC111	4/10 = 40%	chr2
19	PNSII-3	TATAAGGCTCTTGTAGATGGAGG	pCAI-gPNSII-3	PC111	10/10 = 100%	chr2

20	PNSII-4	CCTAAATACTACCTAAACAGGGG	pCAI-gPNSII-4	PC111	10/10 = 90%	chr2
21	PNSII-5	AACTTTGAAACAAAAGAAGGAGG	pCAI-gPNSII-5	PC111	8/10 = 80%	chr2
22	PNSII-6	CCAATATAGGATTGAACTCGAGG	pCAI-gPNSII-6	PC111	9/10 = 90%	chr2
23	PNSII-7	AAGTCAATCATAACTACTCGGGG	pCAI-gPNSII-7	PC111	10/10 = 100%	chr2
24	PNSII-8	GTTACTGGATTAGAACGACGAGG	pCAI-gPNSII-8	PC111	10/10 = 100%	chr2
25	PNSII-9	GAACAATAAACATGACCACAGGG	pCAI-gPNSII-9	PC111	9/10 = 90%	chr2
26	PNSIII-1	GGTCGATAGGATGATCACTTCGG	pCAI-gPNSIII-1	PC111	0/8 = 0%	chr3
27	PNSIII-2	GCATTTTAAGAAAAACCTGCGG	pCAI-gPNSIII-2	PC111	2/8 = 25%	chr3
28	PNSIII-3	TGCTCGGATAGGGTCCAAAGGGG	pCAI-gPNSIII-3	PC111	/	chr3
29	PNSIII-4	GTATTTATCCAGAACAAGGCGG	pCAI-gPNSIII-4	PC111	7/8 = 87.5%	chr3
30	PNSIII-5	ATACTAGTTAACAACTGGGCGG	pCAI-gPNSIII-5	PC111	7/8 = 87.5%	chr3
31	PNSIII-6	CGGAGTTAATAAAGCATGTTCGG	pCAI-gPNSIII-6	PC111	8/8 = 100%	chr3
32	PNSIII-7	TTGTGATCGATAATAAACGGTGG	pCAI-gPNSIII-7	PC111	8/8 = 100%	chr3
33	PNSIII-8	AGTTAGGAGATATAGTAACGAGG	pCAI-gPNSIII-8	PC111	8/8 = 100%	chr3
34	PNSIII-9	GTTTGACGCATGAGCTGTTCGG	pCAI-gPNSIII-9	PC111	/	chr3
35	PNSIII-10	CGGCGAAAATTGGTAAACAGTGG	pCAI-gPNSIII-10	PC111	6/8 = 75%	chr3
36	PNSIII-11	AGCTCTGAAGATACTACCGAAGG	pCAI-gPNSIII-11	PC111	8/8 = 100%	chr3
37	PNSIII-12	GGAACGAGGAGATAAATACGTGG	pCAI-gPNSIII-12	PC111	7/8 = 87.5%	chr3
38	PNSIV-1	AATATGCACGAAATCAAGTGGGG	pCAI-gPNSIV-1	PC111	0/8 = 0%	chr4
39	PNSIV-2	GTACAATTCACTCGATACGTGGG	pCAI-gPNSIV-2	PC111	8/8 = 100%	chr4
40	PNSIV-3	TTCCCTTCGGATACTACACTAGG	pCAI-gPNSIV-3	PC111	6/8 = 75%	chr4
41	PNSIV-4	TGTCAAATGAAAAAGATACGGGG	pCAI-gPNSIV-4	PC111	8/8 = 100%	chr4
42	PNSIV-5	CGTATGTTCTAAGATTACGAGGG	pCAI-gPNSIV-5	PC111	8/8 = 100%	chr4
43	PNSIV-6	TGGTTGTATCAGTAAAATGGCGG	pCAI-gPNSIV-6	PC111	8/8 = 100%	chr4
44	PNSIV-7	TCTCGATGGACGGATAACAGAGG	pCAI-gPNSIV-7	PC111	8/8 = 100%	chr4
45	PNSIV-8	CTCGAGTGCAAAATTAACCTAGG	pCAI-gPNSIV-8	PC111	8/8 = 100%	chr4
46	PNSIV-9	ATTATCGTTTGGGATACGAGGGG	pCAI-gPNSIV-9	PC111	8/8 = 100%	chr4

47	PNSIV-10	TACCAAGTTAATCAGCAGCGGGG	pCAI-gPNSIV-10	PC111	8/8 = 100%	chr4
48	PNSIV-11	TATAAGTTGATCAAAACCTGCGG	pCAI-gPNSIV-11	PC111	8/8 = 100%	chr4
49	PNSIV-12	ACCATTAAGGATAACCAGGGGGG	pCAI-gPNSIV-12	PC111	8/8 = 100%	chr4
50	PNSIV-13	TACTCTGAACAACAGCCAGGAGG	pCAI-gPNSIV-13	PC111	8/8 = 100%	chr4
51	PNSIV-14	GCCAGAGAGTACCCAGCATGCGG	pCAI-gPNSIV-14	PC111	7/8 = 87.5%	chr4
52	PNSIV-15	TATGAAAATCTATATCTAGGAGG	pCAI-gPNSIV-15	PC111	8/8 = 100%	chr4
53	PNSIV-16	AGTATACGGTGAGTATTCGGGGG	pCAI-gPNSIV-16	PC111	7/8 = 87.5%	chr4

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156 **Supplementary Table S4 Production of fatty alcohol in Non-oleaginous yeast.**

Host strain	Gene	Genetic manipulation	Shake flask titer (mg/L)	Reference
<i>S. cerevisiae</i>	<i>TaFAR1</i>	<i>dga1::HIS3</i> , pYES2- <i>P_{GAL1}-TaFAR1</i> ,	73	62
<i>S. cerevisiae</i>	<i>MmFAR1</i>	<i>acc1::P_{TEF1}-ACC1</i> , <i>fas1::P_{TEF1}-FAS1</i> , <i>fas2::P_{TEF1}-FAS2</i> , pESC- <i>P_{GAL1}-mFAR1/P_{GAL10}-MaME</i>	98	63
<i>S. cerevisiae</i>	<i>MalFAR</i>	4x <i>MalFAR</i> , <i>pex10Δ</i> , <i>hfd1Δ</i>	105	64
<i>S. cerevisiae</i>	<i>MmCAR</i> & <i>FaCoAR</i>	<i>hfd1Δ</i> , <i>pox1Δ</i> , <i>faa1Δ</i> , <i>faa4Δ</i> , <i>adh6Δ</i> , pYX212-(<i>P_{TPI1}-npgA-T_{FBA1}</i>)+(P _{TDH3} - <i>MmCAR-T_{ADH1}</i>)+(P _{TEF1} - <i>FaCoAR-T_{pYX212}</i>)	115	14
<i>S. cerevisiae</i>	<i>MmCAR</i>	<i>pox1Δ</i> , <i>tpo1Δ</i> , <i>hfd1Δ</i> , <i>XI-3::P_{TEF1}-eCAS9-T_{ADH1}</i> <i>XI2::P_{GAL1}-AnACLα-T_{CYC1}/P_{GAL10}-AnACLB-T_{ADH1}</i> , <i>gal80Δ::P_{TDH3}-RPS25Ai-FAS2(ACP-AcTesA, KS*)-T_{FBA1}</i> , <i>FAS1pΔ::P_{eTDH3}-RPS25Ai</i> , <i>hfd1Δ::(P_{TPI1}-MmACL-T_{FBA1})+(P_{TDH3}-RtME-T_{CYC1})+(P_{tHXT7}-MDH3-T_{TDH2})+(P_{PGK1}-CTP1-T_{ADH1})</i> , pZW01-(P _{TDH3} - <i>MmCAR*-T_{ADH1}</i>)+(P _{TPI1} - <i>NpgA-T_{FBA1}</i>)	252	65
<i>S. cerevisiae</i>	<i>TaFAR1</i>	<i>rpmΔ</i> , pRS425-(P _{TEF1} - <i>TaFAR-T_{TEF1}</i>)-(P _{PGK1} - <i>ACC1-T_{HXT7}</i>), pRS423-(P _{TPI1} - <i>YIACL1-T_{TPI1}</i>)-(P _{TEF1} - <i>YIACL2-T_{TEF1}</i>)	330.2	66
<i>S. cerevisiae</i>	<i>MmFAR1</i>	1622b::P _{GAL1} - <i>MmFAR1-T_{TDH1}</i> , 208a::P _{TEF1} - <i>MmFAR1-T_{CYC1}</i> , <i>YPRCd15c::P_{GAL1}-ACC1**-T_{ENO2}</i> , <i>hfd1Δ</i> , <i>adh6Δ</i> , <i>gdh1Δ</i> , <i>dga1Δ</i> , 1014a::P _{TEF2} - <i>OLE1-T_{ADH1}</i> , <i>gal801::P_{TDH3}-GAL4</i>	1200	67
<i>Pichia pastoris</i>	<i>FaCoAR</i>	<i>hfd1Δ</i> , <i>HIS4::P_{GAP}-PpRAD52-T_{AOX1}</i> , <i>PNSI-2::P_{GAP}-hCas9-T_{DAS1}</i> , <i>PNSI-4::P_{TPI1}-SCADH5-T_{DAS2}</i> , <i>PNSI-5::P_{GAP}-FaCoAR-T_{FBP1}</i>	380	This study

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