Supplementary information

Rewiring methanol assimilation and reductive glycine pathways in *Saccharomyces cerevisiae* to increase one-carbon recovery

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Whole-genome resequencing and data analysis

The control strain M01 and three evolved strains of M29 were chosen for genome sequencing. The whole genome was sequenced using Illumina HiSeq/Novaseq/MGI2000 at Genewiz Biotech (Suzhou, China). Data analysis was used by fastp (V0.23.0) and annotation for SNV/InDel was performed by Annovar (V21 Apr 2018).

¹³C Metabolite tracer analysis

For ¹³C metabolite tracer analysis, strain M45 was cultivated in YPD overnight and washed twice with PBS (pH=7.2) before being transferred to YNB medium with 0.1% yeast extract and 0.4% ¹³C-methanol (Sigma-Aldrich), initial OD₆₀₀ was around 0.3, then cultured for 144 h. The yeast (about 10⁷ cells) was taken, mixed with 1000 μ L of extraction solution consisting of methanol, acetonitrile, and water in a ratio of 2:2:1 (v/v). The mixture was vortexed for 30 s and then incubated in liquid nitrogen for 1 min. Subsequently, the samples were allowed to thaw at room temperature and vortexed for 30 s. This freeze-thaw cycle was repeated three times. Following that, the samples were sonicated for 10 min in a 4°C water bath and incubated for 1 h at -40°C to precipitate proteins. The samples were centrifuged at 12000 rpm for 15 min at 4°C. The supernatant was collected and evaporated to dryness by a vacuum concentrator. The dried extracts were then reconstituted in 100 μ L of a mixture of acetonitrile and water in a 1:1 ratio (v/v), followed by sonication for 10 min at 50 Hz and 4°C, and centrifugation for 15 min at 16,200 g and 4°C to eliminate insoluble material. The supernatants were transferred to glass vials for subsequent analysis.

For the analysis of polar metabolites, LC-MS/MS was conducted using an UHPLC system (Vanquish, Thermo Fisher Scientific) coupled with a Waters ACQUITY UPLC BEH Amide column (2.1 mm×100 mm, 1.7 μm) and an Orbitrap Exploris 120 mass

spectrometer (Orbitrap MS, Thermo Fisher Scientific). The mobile phase comprised 25 mmol/L of ammonium acetate and 25 mmol/L of ammonia hydroxide in water (pH=9.75) (A) and acetonitrile (B). The auto-sampler temperature was 4°C, and the injection volume was 2 μ L. For the analysis of non-polar metabolites, LC-MS/MS was conducted using an UHPLC system (Vanquish, Thermo Fisher Scientific) coupled with a Phenomenex Kinetex C18 column (2.1 mm×100 mm, 2.6 μ m) and an Orbitrap Exploris 120 mass spectrometer (Orbitrap MS, Thermo Fisher Scientific). The mobile phase consisted of 0.01% acetic acid in water (A) and a mixture of isopropanol and acetonitrile (1:1, v/v) (B). The auto-sampler temperature was 4°C, and the injection volume was 2 μ L. The ESI source conditions were set as follows: sheath gas flow rate at 50 Arb, auxiliary gas flow rate at 15 Arb, capillary temperature at 320°C, full MS resolution at 60,000, MS/MS resolution at 15,000, collision energy set to 20/30/40 eV in NCE mode, and spray voltage at 3.8 kV (positive) or -3.4 kV (negative), respectively.

GC-MS was used for the detection of metabolites in the reductive glycine pathway. Firstly, strain M47 was cultivated in YPD overnight and washed twice with PBS (pH = 7.2) before being transferred to YNB medium with 0.1% yeast extract, 2% methanol, 250 mM sodium formate, 100 mM (NH4)2SO4, and 35 mM NaH¹³CO₃ (Sigma-Aldrich), initial OD₆₀₀ was around 0.2, then cultured for 144 h. The metabolites were subsequently derivatized for GC-MS analysis following a previously published protocol ¹. The cells were ground in liquid nitrogen, re-suspended in 1 mL of cold (-40°C) 50% aqueous methanol, and placed in dry ice for 30 min before thawing the samples on ice. Then, 0.4 mL of chloroform was added, and the mixture was vortexed for 30 s, and centrifuged for 15 min at 14,000 rpm (4°C). The supernatant was then transferred to new 1.5 mL tubes for evaporation and storage at -80°C prior to analysis.

Metabolites were derivatized for GC-MS analysis as follows: First, 70 μ L of O-Isobutylhydroxylamine hydrochloride was added to the dried pellet and incubated for 20 min at 85°C. After cooling, 30 μ L of *N-tert*-butyldimethylsilyl-*N*methyltrifluoroacetamide (MTBSTFA) was added and samples were re-incubated for 60 min at 85°C before centrifugation for 15 min at 12,000 rpm (4°C). The supernatant was transferred to an autosampler vial for GC-MS analysis.

A Shimadzu QP-2020 GC-MS was programmed with an injection temperature of 250°C. The GC column used was a 30 m×0.25 mm×0.25 mm DB-5ms. GC-MS interface temperature was 300°C and ion source temperature was set at 200°C, with 70 V ionization voltage. The mass spectrometer was set to scan m/z range 50-700, with 1 kV detector. GC flow rate with helium carrier gas was 0.92 ml/min. The gradient elution of GC oven temperature was list as follows: 120°C for 3 min, followed by a ramp of 4 °C min⁻¹ to 170°C, 0 min hold; 2°C min⁻¹ to 182°C, 0 min hold; 20°C min⁻¹ to 195°C, 0 min hold; 3°C min⁻¹ to 230°C, 0 min hold; 10°C min⁻¹ to 265°C, 0 min hold; 3°C min⁻¹ to 280°C, 5 min hold, and the injection volume was 5 μL.



Supplementary Fig. S1 Growth in different concentrations of methanol to evaluate their tolerance to methanol. Growth on solid YNB medium with 0.1% yeast extract, and different concentrations of methanol, methanol (MeOH). Images were taken after incubating at 30°C for 6 days.



Supplementary Fig. S2 Fermentation validation of 8 single clones from the evolved strains G2-80 plate. Strains were cultured in YNB medium with 2% methanol, 0.1% yeast extract at 30°C, 220 rpm, and the initial OD₆₀₀ was around 0.15.

Propanoate metabolism	Glyoxylate dicarboxy metaboli	and late sm	Rit met	ooflavin tabolism	s	phing netab	olipid olism
Valine, leucine and isoleucine degradation	Pantothenate and CoA biosynthesis	Amino sugar and nucleotide sugar metabolism		d m	Citrate cycle (TCA cycle)		
	Pyruvate metabolism	Lysir degrada	ne ation ⁽	Glycolysis or Gluconeogenesis			Pyrimidine metabolism
Glutathione metabolism	Cysteine and methionine metabolism	Fructo and manno metabo	ose I ose Iism	Arginine and proline metabolism L Fatty acid biosynthesis Selen metabolism	ysine ynthe noam acid abolis	Alanine aspartal and glutama metabolii Starch sucro metabo	Purine metabolism sm and se lism
0.0 0.5	1.0 1.5 - In <i>P</i> -v	2. /alu	.0 e	2.5		3.0)

Supplementary Fig. S3 Pathway analysis of ¹³C-labelled metabolites in strain M045. The labelled metabolites are mainly involved in glyoxylate metabolism and TCA cycle, suggesting that we have successfully rewired the central carbon metabolism of *S. cerevisiae* through modularization and ALE strategies, engineering it into a methylotrophic yeast.



Supplementary Fig. S4 Comparison of formate consumption in strain M47 in media with and without NaHCO₃. The consumption of formate in the medium with NaHCO₃

was significantly higher than that without NaHCO₃, proving the activity of RGP. Strains were cultured in YNB medium with 0.1% yeast extract, 2% methanol, 250 mM sodium formate, 100 mM (NH₄)₂SO₄, and 100 mM NaHCO₃ at 30°C, 220 rpm.



Supplementary Fig. S5 Biosynthetic pathway of cannabigerolic acid (CBGA) in *S. cerevisiae.* Biosynthetic pathway of CBGA contains heterologous pathway of CBGA (red arrows) and the native pathway of *S. cerevisiae* (black arrows). CsAAE1, acyl activating enzyme from *Cannabis sativa*; ACC1,acetyl-CoA carboxylase; RebktB, β-ketothiolase from *Ralstonia eutropha*; RepaaH1, 3-hydroxybutyryl coenzyme A dehydrogenase from *Ralstonia eutropha*; Cacrt, crotonase from *Clostridium acetobutylicum*; Tdter, trans-2-enoyl-CoA reductase from *Treponema denticola*; CsTKS, polyketide synthase from *C. sativa*; CsOAC, olivetolic acid cyclase from *C. sativa*; CsPT4, geranyl transferase from *C. sativa*; EfmvaE, acetoacetyl-CoA thiolase from *Enterococcus faecalis*; EfmvaS, HMG-CoA synthase from *E. faecalis*; ERG12, mevalonate kinase; ERG8, phosphomevalonate kinase; ERG19, mevalonate pyrophosphate decarboxylase; IDI1, isopentenyl-pyrophosphate delta isomerase; erg20*, farnesyl pyrophosphate; DMAPP, dimethylallyl diphosphate; GPP, geranylgeranyl pyrophosphate, OA, olivetolic acid, CBGA, cannabigerolic acid.

Pathway	Reactions	$\Delta_{\rm r} {\rm G'^m}$
		(kJ/mol)
	Formate+THF+ATP<=>10-formyl-THF+ADP+Orthophosphate	-2.1
RGP	10-formyl-THF<=>5,10-methenyl-THF+H ₂ O	5.4
	5,10-methenyl-THF+NADPH<=>5,10-methylene-THF+NADP+	-6.5
	5,10-methylene-THF+NH ₄ +CO ₂ +NADH<=>Glycine+THF+NAD ⁺	-4.9
Methanol-	Methanol+O ₂ <=>Formaldehyde+H ₂ O ₂	-98.9
RGP	Formaldehyde+THF<=>5,10-methylene-THF+H ₂ O	-5.2
	5,10-methylene-THF+NH ₄ +CO ₂ +NADH<=>Glycine+THF+NAD ⁺	-4.9

Supplementary Table 1 Thermodynamic analysis of different glycine biosynthetic pathways

Supplementary Table 2 Plasmids used in this study

Plasmids	Description	Source
p423-SpSgH	2µ; HIS3; AmpR; pSNR52-BsaI-BsaI-SpSgRNA-tSUP4	2
p426-SpSgH	2µ; URA3; AmpR; pSNR52-BsaI-BsaI-SpSgRNA-tSUP4	3
p423*-ccdB	2µ; HIS3; AmpR; pSNR52-BsaI-ccdB-BsaI-tSUP4	2
p426*-ccdB	2µ; URA3; AmpR; pSNR52-BsaI-ccdB-BsaI-tSUP4	3
p41K-iCas9	2µ; KanMX; AmpR; pTEF1-iCas9-tADH1	4
pESC-URA	2µ; URA3; AmpR; pGAL1-MCS1-tCYC1; pGAL10-MCS2-tADH1	2
pH23	2µ; LEU2; AmpR; tADH1-pGPD1-eGFP-tCYC1-pENO2	2
pH5	2µ; LEU2; AmpR; pTEF1-eGFP-tTEF1	2
pH66	2µ; LEU2; AmpR; tTEF1-pPGK1-eGFP-tHXT7	2
pH5-PFK1	2µ; LEU2; AmpR; pTEF1-PFK1-tTEF1	this study
pH5-PFK2	2µ; LEU2; AmpR; pTEF1-PFK2-tTEF1	this study
pH5-FBA1	2µ; LEU2; AmpR; pTEF1-FBA1-tTEF1	this study
pH7-RPE1	2µ; LEU2; AmpR; pTPI1-RPE1-tTEF1	this study
pH7-Bmplgx	2µ; LEU2; AmpR; pTP11-Bmplgx-tTEF1	this study
pH10-BsMDH	2µ; URA3; AmpR; pGPM1-BsMDH-tTEF1	this study
pH9-ADK1	2µ; LEU2; AmpR; pTEF2-ADK1-tHXT7	this study
pH9-FLS	2µ; LEU2; AmpR; pTEF2-FLS-tTEF1	this study
pH5-HPS	2µ; LEU2; AmpR; pTEF1-HPS-tTEF1	this study
pH5-PHI	2µ; LEU2; AmpR; pTEF1-PHI-tTEF1	this study
pH10-AOX1	2µ; LEU2; AmpR; pGPM1-AOX1-tTEF1	this study
pH10-DAK1	2µ; LEU2; AmpR; pGPM1-DAK1-tTEF1	this study
pH11-DAS2	2µ; LEU2; AmpR; pENO2-DAS2-tTEF1	this study
pH11-CAT1	2µ; LEU2; AmpR; pENO2-CAT1-tTEF1	this study
pH7-TKL1	2µ; LEU2; AmpR; pTPI1-TKL1-tTEF1	this study
pH23-FBP1	2µ; LEU2; AmpR; pGPD1-FBP1-tCYC1	this study
pH23-ZWF1	2µ; LEU2; AmpR; pGPD1-ZWF1-tCYC1	this study
pH12-GCV1	2µ; LEU2; AmpR; pFBA1-GCV1-tTEF1	this study
pH12-GCV2	2µ; LEU2; AmpR; pFBA1-GCV2-tTEF1	this study
pH13-GCV3	2µ; LEU2; AmpR; pPDC1-GCV3-tCYC1	this study
pH13-MIS1	2µ; LEU2; AmpR; pPDC1-MIS1-tCYC1	this study
pH23-SHM2 ^{A194C/S248T}	2µ; LEU2; AmpR; pGPD1-SHM2 ^{A194C/S248T} -tCYC1	this study
		this study

Supplementary Table 3 Strains used in this study

Strains	Description	Source
INVSc1	<i>MATa/MATα his 3Δ1 leu2 trp 1-289 ura3-52</i>	Lian's lab
M01	INVSc1[YPRCδ15c::pPGK1-Tdter-tHXT7; SAP155b::pTEF1-RebktB- tTEF1;1414a::pGAL1-EfmvaS-tCYC1/pGAL10-EfmvaE-tADH1; 1114a::pGAL1-ERG12- tCYC1/pGAL10-IDI-tADH1;SAP155c::pGAL1-RePaaH1-tCYC1/pGAL10-CaCrt- tADH1;1014a::pGAL1-ERG19-tCYC1/pGAL10-ERG8-tADH1; 1622b:: pGAL1-CsOAC- tCYC1/pGAL10-csTKS-tADH1;911b:: pGPD1-CsAAE1-tCYC1; 1021b::pGAL1-tHMG1- tCYC1/pGAL10-erg20*-tADH1; 416d::pGAL1-CsPT4-tCYC1; 308a::pGAL1-CBCAS- tCYC1; X4:: pGAL1-CsOAC-tCYC1/pGAL10-CsTKS-tADH1;XI3:: pGAL1-CsOAC- tCYC1/pGAL10-csTKS-tADH1;XII5:: pGAL1-CsOAC-tCYC1/pGAL10-CsTKS- tADH1;208a:: pGPD1-CsAAE1-tCYC1;106a:: pGPD1-CsAAE1-tCYC1; CAN1y::pGAL1- CsPT4-tCYC1;YOLCd1b::pGAL1-CsPT4-tCYC1; 1021b:: pGAL10-erg20*-tADH1; X11::pTEF1-CHK-tTEF1;XI2::pTEF1-At1PK-tTEF1; XII4::pPGK1-FAA2-tHXT7; X2::pGAL1-IDI1-tCYC1; X3:: pTEF1-ERO1-tTEF1; NS7:: pPGK1-IRE1*-tHXT7; NS8:: pPGK1-PDI1-tHXT7; NS9:: pPGK1-CNE1-tHXT7; NS2:: pTEF1-INO2-tTEF1; NS3::pPGK1-KAR2-tHXT7; NS14:: pPGK1-HAC1s*-tHXT7; YGLCt3:: pTEF1-ERO1- tTEF1; Gal80A]	This study
M02	M01[NS18:: pTEF1-HPS-tTEF1; NS19:: pTEF1-PHI-tTEF1]	This study
M06	M02[NS22:: pTEF1-PFK2-tTEF1; NS23:: pTEF1-FBA1-tTEF1; YORWA22:: pTEF1-PFK1- tTEF1; NS24:: pTPI1-RPE1-tTEF1; NS25:: pTPI1-Bmglpx-tTEF1; NS10:: pGPM1-BsMDH- tTEF1; NS11:: pGPM1-BsMDH-tTEF1]	This study
M07	M06[<i>NS5</i> :: <i>p1EF2-ADK1-t1EF1</i> ; <i>NS6</i> :: <i>p1EF2-FLS-t1EF1</i>]	This study
M09	M06[XI7:: pGPM1-AOX1-tTEF1;XI8:: pGPM1-DAK1-tTEF1;YCRW812:: pENO2-DAS2- tTEF1;YNRC40::pENO2_CAT1_tTEF1]	This study
M14	M09[V1::pGPD1-FBP1-tCYC1;V3::pGPD1-ZWF1-tCYC1; NS17:: pGPD1-TKL1-tCYC1; YGR067C:: tYGR067C]	This study
M15	M14[<i>LPL1</i> Δ; <i>IZH3</i> Δ]	This study
M27	M15-G80-2	This study
M29	M15-G80-2-1	This study
M45	M29[4-OH:: pGPD1-SHM2 ^{A194C/S248T} -tCYC1]	This study
M47	M45[NS20::pFBA1-GCV1-tTEF1;NS21::pFBA1-GCV2-tTEF1; XII3:: pPDC1-GCV3- tCYC1; XI5::pPDC1-MIS1-tCYC1]	This study

primers	sequences (5'-3')
for plasmids const	ruction
IDP2-F	ACACCAGAACTTAGTTTCGACGGATGGATCCATGACAAAGATTAAGGTAGCTAA CC
IDP2-R	GCGTGACATAACTAATTACATGATCTCGAGTTACAATGCAGCTGCCTCGAA
PFK1-F	CTAATCTAAGTTTTAATTACAAAGGATCCATGCAATCTCAAGATTCATGCT
PFK1-R	TATGCAACTAGAAAAGTCTTATCAATCTCCCTCGAGTCATTTGTTTTCAGCGGCTA
PFK2-F	TCTAATCTAAGTTTTAATTACAAAGGATCCATGACTGTTACTACTCCTTTTGTGAA TG
PFK2-R	ACTAGAAAAGTCTTATCAATCTCCCTCGAGTTAATCAACTCTCTTTCTT
FBA1-F	CTAATCTAAGTTTTAATTACAAAGGATCCATGGGTGTTGAACAAATCTTAA
FBA1-R	AGAAAACGTCTTATCAATCTCCCTCGAGTTATAAAGTGTTAGTGGTACGGAAAG
GCV1-F	AACCAAGTAATACATATTCAAAAGGATCCATGTCTATAATCAAAAAAATTGTGTT TAAG
GCV1-R	AGAAAAGTCTTATCAATCTCCCTCGAGTTACTGCTTGTAGTAATGTGTGG
GCV2-F	AACCAAGTAATACATATTCAAAAGGATCCATGCTTAGGACAAGAGTGACT
GCV2-R	AAAGTCTTATCAATCTCCCTCGAGTCATTCAGTTTCGTTCG
GCV3-F	AATCTAAGTTTTAATTACAAAGGATCCATGTTACGCACTACTAGACTATG
GCV3-R	AAAAGTCTTATCAATCTCCCTCGAGTCAGTCATCATGAACCAGTGTCT
MIS1-F	ACACAGTCAAATCAAATCAAAGGATCCATGTTGTCGAGACTATCTTTATTGAGT
MIS1-R	TGACATAACTAATTACATGATCTCGAGTTAAAATAGACCTTCAATTTCACC
for genome integration	
HPS-HOMO-F	GCAAAATAGTATACCATCTTTGGTTCCTGGACCACATTTTCGCGCGTAATACGAC
HPS-HOMO-R	AAAGGGTTCGCTCAATGGCAGATGCTGCCATACGAGGACAATAGCGCCGATCAA AGTAT
PHI-HOMO-F	AACTCCGTCCACAGTACCCGATCAGCTGGCTCATCGTTATGCGCGCGTAATACGA CTCA
PHI-HOMO-R	CTTGCAACGCTAGTAACGCCGTATCCACAGAGAAACCGGGATAGCGCCGATCAA AGTAT
PFK2-HOMO-F	AAGGTTGGCCCGCCAAAATCGTAAGTCTCGGTGCTCTGTTGCGCGCGTAATACGA CTCA
PFK2-HOMO-R	TTACTGGAGTAATGCTTATATTATTCGCGTCCCCCACGCATAGCGCCGATCAAA GTAT
FBA1-HOMO-F	TGTGGTGAATGCACCTGGTGCACGCTGCGAAGGTGACGTAGAGCGCGCGTAATA CGACT
FBA1-HOMO-R	TGGCTTTTAACCTTATTACCCCAAGAGAGTGTCTACAGAAATAGCGCCGATCAAA GTAT
PFK1-HOMO-F	TCTTTTAAATACTTATTAACGTACTCAAACAACTACACTTTGAGCGCGCGTAATA CGAC
PFK1-HOMO-R	GGTCCCTATTCCGATAATCTTAGCAGAGTGAATAGTAATAATAGCGCCGATCAAA GTAT
RPE1-HOMO-F	CATTAGATAGAGAGGGGCAGATGTTCAAGCTATACCCATTCTACTTATTCCCTTC GAGA
RPE1-HOMO-R	ACIGAAAIGAAAAIIICAIAIIIACIIIIIAIIGIIACIGACCAIGAIIACGCCA
Bmglpx-HOMO- F	CCTAATTAGTAGGAAGCGGAAAATAATAATAATAAGAAAGTCTACTTATTCCCTTC GAGA
Bmglpx-HOMO-	TTGCGCGCTCAAGCGGCCCTATACTGCACACCTATTACTTGACCATGATTACGCC
к BsMDH-HOMO- f	AAGC ACTTTTTACCATCCTTTAGCTTTACCTAATATAATGAAATTAGTCGTGCAATGTAT GAC
BsMDH-HOMO- R	TTCGAGAAATAGTTGGTATAAATAACTATAAATAACGTTTATAGCGCCGATCAAA GTAT
BsMDH-HOMO-	AACTAACCTAAGAATTTTGAAATCACAACAAAAATAATTAGTCGTGCAATGTATG

Supplementary Table 4 List of primers used in this study

F	AC
BsMDH-HOMO- R	ACAAAAAAGTAGTAATAAATAGGTCCAAATCTTCTTTATTATAGCGCCGATCAAA GTAT
ADK1-HOMO-F	CATTTGAATTTTAGTAGTAACTAATATAAGATTCCCATCCGGGCGCCATAACCAA GGTA
ADK1-HOMO-R	TCATCTATAAAGACTGTACGCATATTTGGAACTAACTGCTATAGCGCCGATCAAA GTAT
FLS-HOMO-F	ACATTTCAAGTGGTTTCTCAAGGGAGAATCATAGTTTAGCGGGCGCCATAACCAA GGTA
FLS-HOMO-R	CTTCGTATACTTATTACGCAGGTAGGAGTGCAATAGTTGAATAGCGCCGATCAAA GTAT
AOX1-HOMO-F	CTTGACATGTAACGTAAGAAAAAGAAAAAAGAGATGGCAGATAGTCGTGCAATGT ATGAC
AOX1-HOMO-R	AATCATTGCTATCCCCACAAAAAACAGTGCATGTACTTTGATAGCGCCGATCAAA GTAT
DAK1-HOMO-R	TTTTTTGCCATACATTTAGCGCTCCACACTCTAAATAAAGTGTGTCGACGCTGCGG GTAT
DAK1-HOMO-F	TTTATAATATGCAAAAGGCGGTAACGATATGCCGCGCAAAATAGCGCCGATCAA AGTAT
DAS2-HOMO-F	GCCGATGAAATAAAATCCTGATATCATCTATATAGTAGTGTGTCGACGCTGCGGG TAT
DAS2-HOMO-R	TGAAGATATATGAATCTACAAGAGAGAGAGTCAATATTTCTAATAGCGCCGATCAA AGTAT
CAT1-HOMO-F	AGACATTTTTTGGGATTAATTGTTTATAAAAGCTATGAACGTGTCGACGCTGCGG GTAT
CAT1-HOMO-R	GACATAATTGATGGGAAACAGTTATCAAAGTTATTGGATGATAGCGCCGATCAA AGTAT
TKL1-HOMO-R	GATCTGTGAAGGTTTTTGAGAGAATGAGGCGAAAACACAGGCTACTTATTCCCTTC GAGA
TKL1-HOMO-F	AAGCGAGTGATTCATCATGAAAAGAATTTATCACTTCGAAATAGCGCCGATCAA AGTAT
YGR067C- Homo-F	TTTTATTTAAAAACCTTCTCCGGGAGAAGACAATTGTTGAATGGCTGCGGGTCAA
YGR067C-	GCTCTTGCGGATAAGTCTTCTTTATTATAAAATACACTTACGCGGAATCTGCCAA
номо-R	AATA
FBP1-HOMO-F	GTGGAAAATGACCATAATGATAATTATCAATAGATAAAATCCACACCTCTACCG GCATG
FBP1-HOMO-R	CTAAAATGGTAGGCATGAGTGTTCTCCTTCTTGTGTGTCTGCAAATTAAAGCCTTC GAG
ZWF1-HOMO-F	TGAAGACTACTGAACCATGGCAGCTAATACAATCACGCCCCCACACCTCTACCGG CATG
ZWF1-HOMO-R	AAAAAGGCTAGGTACTTTAAAAATTTCCTACAAATATAGAGCAAATTAAAGCCTT CGAG
GCV1-HOMO-F	ATAAGCCCTAGAAACCTTACACCCTAATTTGCACAAGAAATAACAATACTGACA GTACTAA
GCV1-HOMO-R	CATCTGGAATATAATTCCCCCCTCCTGAAGCAAATTTTTCATAGCGCCGATCAAA GTAT
GCV2-HOMO-F	CATCATATAGGGACATACCTCTCAAGTTATTGTCTTGGATAACAATACTGACAGT ACTAAAT
GCV2-HOMO-R	TCCAGGCAGGACGACACGAGAATAGACGGGCTGATCCCGTATAGCGCCGATCAA AGTAT
GCV3-HOMO-F	GACACATCTCTAAGCTGAAAACTGAGAATACTGTTGTAAAACATGCGACTGGGTG AGCAT
GCV3-HOMO-R	AAGTCCATTACCCTTAAGGTTGTTGTCACAACCCACGGAGGCAAATTAAAGCCTT CGAG
MIS1-HOMO-F	AAGCTTCGAAGAATATGTAAATATAGTAGTATGAATCTAACATGCGACTGGGTG AGCAT
MIS1-HOMO-R	GAGTGTCATATATCCCTCCTTTAAATTTTTTTACACTTACGCAAATTAAAGCCTTC GAG
SHM2 ^{A194C/S248T} -	TACATACAACTTTTTAAACTAATATACACATTTTAGCAGACCACACCTCTACCGG
HOMO-F	CATG
SHM2 ^{A194C/S248T} -	ATCCTCATAAGCAGCAATCAATTCTATCTATACTTTAAAAGCAAATTAAAGCCTT
HOMO-R	CGAG
LPL1-UP-F	CCTCAACATTTATCAAATAGTTTAGCAATG
LPL1-UP-R	TCGAATTTACGGCCCAATTACTAGC

LPL1-DOWN-F	${\tt CTAGTAATTGGGCCGTAAATTCGATGAAGCGCTGTATAATATATGGTTG}$
LPL1-DOWN-R	TTGAAGCAAGATATTGGAAAGACAAGGG
IZH3-UP-F	ACTACTGCATGAAATCACTTAAGTTCG
IZH3-UP-R	GGTATGACTGACTACCTTTACTTACAA
IZH3-DOWN-F	TAAGTAAAGGTAGTCAGTCATACCTACTTAATTTGATTGTCTGTTGGGA
IZH3-DOWN-R	CTACGAAATTAGCGTATCCGAAAA

Supplementary Table 5 Mutations in different evolved strains

Protein	M29-1	M29-2	M29-3	Annotation
AAD4	C23F		C23F	Enables aryl-alcohol dehydrogenase (NADP+) activity. Predicted to be involved in cellular aldehyde metabolic process.
AAD10	F33Y		F33Y	Enables aryl-alcohol dehydrogenase (NADP+) activity. Predicted to be involved in cellular aldehyde metabolic process.
DAN4	P216S		P216S	Predicted to be involved in fungal-type cell wall organization.
GDA1	V208I		V208I	Enables GDP phosphatase activity and UDP phosphatase activity. Involved in protein glycosylation.
ADP1	K26I		K26I	Predicted to enable ATPase-coupled transmembrane transporter activity.
RPL30	I92T		I92T	Involved in negative regulation of mRNA splicing, via spliceosome and rRNA processing.
TGL3	A12D		A12D	Involved in cell budding and triglyceride catabolic process.
COS2		R311K	R311K	Predicted to be involved in protein transport to vacuole involved in ubiquitin-dependent protein catabolic process via the multivesicular body sorting pathway.
YHR219W	S251P	S251P		Predicted to be active in cytoplasm.
YMR317W	E323A	E323A		No found.
COS6	V89F			Predicted to be involved in protein transport to vacuole involved in ubiquitin-dependent protein catabolic process via the multivesicular body sorting pathway.
PAU4	I24L			Predicted to be involved in fungal-type cell wall organization.
PFF1		V372F		Predicted to enable metalloexopeptidase activity and zinc ion binding activity. Predicted to be involved in proteolysis.
YPS5		I39T		Predicted to enable aspartic-type endopeptidase activity.
KEX1		A200V		Involved in apoptotic process.
LSG1		G494W		Involved in ribosomal large subunit assembly and ribosomal subunit export from nucleus.

NAM8	A363G	Enables mRNA binding activity. Involved in mRNA splice site recognition and positive regulation of mRNA splicing, via spliceosome. Located in cytoplasm and nucleus.
INA1	D42N	Predicted to be involved in fungal-type cell wall organization.
RAS2	K124T	Involved in several processes, including cytoplasm to vacuole targeting by the Cvt pathway; positive regulation of transcription by galactose; and protein localization to bud neck.

Supplementary Table 6 Integration site used in this study

site	20 bp spacer (5'-3')
NS5	GAGAGAATGACATTGCTCAG
NS6	TAGTTAATATCATCTAGATG
NS10	ΑΤΑΤΑΑΑΑΑΑΑΤΤΟΤΤΑΟΤΑ
NS11	TATTCTTAGGAAAATCAACA
NS17	CTTGCGAAAAGAAAAGGGCA
NS18	AACTGCTCAGGGCGGATAAC
NS22	ATCTTAAATGAAAGACAGAG
NS24	ATTATGAAAGTTTTCAACTA
NS25	CACCATTCAAGTTACCGAGA
YORW $\Delta 22$	CGTTTGGGTAGTTCAGCTAA
YCRWδ12	TTTAATGGAAACGAAATGCA
YNRCΔ9	GCACGGAACTTCGGACCTAG
XI7	GTCAGTAACAGTGATTGCTG
XI8	GATGAAATAGCCTCAGTTAC
V1	CGTTTATAGACGGCACTGTC
V3	GTGCTCTTAAGTCGTAATGA
X1	GTGCCTGCTGCTATGCTCAA
III3	AGACATATGATAATCGAGCA
4-OH	GTTCGTGAAGCATTCTTAGC

Supplementary Table 7 Heterologous genes used in this study

genes	gene sequence (5'-3')
B sMDH	ATGAAAGCTGCTGTTGTTAATGAATTTAAGAAAGCTTTGGAAATTAAAGAAGTTGAAA
	GACCAAAATTGGAAGAAGGTGAAGTTTTGGTTAAAATTGAAGCTTGTGGTGTTTGTCA
	TACTGATTTGCATGCTGCTCATGGTGATTGGCCAATTAAACCAAAATTGCCATTGATTC
	CTGGTCATGAAGGTGTTGGTATTGTTGTTGAAGTTGCTAAAGGTGTTAAATCTATTAAA
	GTTGGTGATAGAGTTGGTATTCCATGGTTGTATTCTGCTTGTGGTGAATGTGAATATTG
	TTTGACTGGTCAAGAAACTTTGTGTCCACATCAATTGAATGGTGGTTATTCTGTTGATG
	GTGGTTATGCTGAATATTGTAAAGCTCCTGCTGATTATGTTGCTAAAATTCCTGATAAT
	TTAGATCCTGTTGAGGTCGCTCCTATTTTGTGTGCTGGTGTTACTACTATAAAGCTTTG
	AAAGTTTCTGGTGCTAGACCTGGTGAATGGGTTGCTATTTATGGTATTGGTGGTTTGGG
	TCATATTGCTTTGCAATATGCTAAAGCTATGGGTTTGAATGTTGTTGCTGTTGATATTTC
	TGATGAAAAATCTAAATTGGCTAAAGATTTGGGTGCTGATATTGCTATTAATGGTTTGA
	AAGAAGATCCTGTTAAAGCTATTCATGATCAAGTTGGTGGTGTTCATGCTGCTATTTCT
	GTTGCTGTTAATAAAAAGGCTTTTGAACAAGCTTATCAATCTGTTAAAAGAGGTGGTA

	CTTTGGTTGTCGTTGGTTTGCCAAATGCTGATTTGCCAATTCCAATTTTTGATACTGTTT
	TGAATGGTGTTTCTGTTAAAGGTTCTATTGTTGGTACTAGAAAAGATATGCAAGAAGCT
	TTGGATTTTGCTGCTAGAGGTAAAGTTAGACCAATTGTTGAAACTGCTGAGTTGGAAG
	AAATTAATGAAGTTTTTGAGAGAATGGAGAAAGGTAAAATTAATGGTAGAATTGTTTT
	GAAATTGAAAGAAGACTAA
BmHPS	ATGGAATTGCAATTGGCTTTGGATTTGGTTAATATTGAAGAAGCAAAACAAGTTGTTG
	CTGAAGTTCAAGAATATGTTGATATTGTTGAAATTGGTACTCCTGTTATTAAAATTTGG
	GGTTTGCAAGCTGTTAAAGGCTGTTAAAGATGCTTTTCCACATTTGCAAGTTTTGGCTGA
	TATGAAAACTATGGATGCTGCAGCTTATGAAGTTGCTAAAGCTGCTGAACATGGTGCT
	GATATTGTTACTATTTTGGCTGCAGCTGAGGACGTTTCTATTAAAGGTGCTGTTGAGGA
	AGCTAAAAAATTGGGTAAAAAAATTTTGGTTGATATGATTGCTGTTAAAAATTTGGAA
	GAAAGAGCAAAGCAAGTTGACGAAATGGGTGTTGATTATATTTGTGTTCATGCTGGTT
	ATGATITACAAGCTGTTGGTAAGAATCCATTGGATGATTTGAAAAAGAATTAAAGCTGT
	TGITAAAAATGCTAAAACTGCTATTGCTGGTGGTATTAAATTGGAAACTTTGCCTGAAG
	TTATTAAAGCIGAACCIGATTIGGITATIGIIGGIGGAGGTATIGCTAATCAAACIGAT
	AAAAAAGCIGCAGCIGAAAAAATTAATAAAATTGGITAAACAAGGITIGTAAACITTAC
	GCCGAGAGGCITTATAGGAAGGACGGTACCATCCCAGTCGACGAGGAAAATAGAATT
	AGAATCGATGACTGGGAACTTGAGGAGGACGTCCAGAAAGCCGTTTCTGCCTTGATGG
	AGAAGGTCACCGGTGAAAATGCCGAGAGTTTGACCGACTTGGCCGGTTACAGACACG
	ACTICITIGGCCAGTAACGGTTTIGACGTTGAGGGAATCAACTACGAGGCCGAAGTTGA
5 5777	
BmPHI	ATGTTGACTACTGAATTTTTGGCTGAAATTGTTAAAGAATTGAATTCTTCTGTTAATCA
	AATTGCTGATGAAGAAGCTGAAGCTTTGGTTAATGGTATTTTGCAATCTAAAAAAGTTT
Rmalnr	
Dingips	TTGCTCAACAACTCACAACAACAACACACTCATCTTTCCATCTTTCCCATCTTTCCCATCTTTCCCATCTTTCCCATCTTCCCATCTTCCCATCTTCCCATCCTTCCATCCTTCCCATCCTTCCCATCCTTCCCCATCCTTCCTCC
	GTTGATAGAGCTGGTACTGAAGCTATGAGAAATAGATTGAATTGATTG
	GTTTGATTGTTATTGGTGAAGGTGAAATGGATGAAGCTCCAATGTTGTATATTGGTGAA
	GAATTGGGTACTGGTAAAAGGTCCACAATTGGATATTGCTGTTGATCCTGTTGATGGTAC
	TGGTTTGATGGCTAAAGGTATGGATAATTCTATTGCTGTTATTGCTGCTTCTACTAGAG
	GTTCTTTGTTGCATGCTCCTGATATGTATATGGAAAAAATTGCTGTTGGTCCAAAAGCT
	AAAGGTTGTGTTAATTTGGATGCTTCTTTGACTGAAAATATGAAATCTGTTGCTAAAGC
	TTTGGGTAAAGATTTGAGAGAATTAACTGTTATGATTCAAGATAGACCAAGACATGAT
	CATTTGATTCAACAAGTTAGAGATGTTGGTGCTAGATTGAAATTGTTTTCTGATGGTGA
	TGTTACTAGAGCTATTGGTACTGCTTTGGAAGAAGTTGATGTTGATATTTTGGTTGG
	CTGGTGGTGCTCCTGAAGGTGTTATCGCTGCTACTGCTTTGAAATGTTTGGGTGGTGAT
	TTTCAAGGTAGATTGGCTCCTCAAAATGAAGAGGAATTTGACAGATGTATCACTATGG
	GTATTACTGACCCTAGAAAAATCTTTACTATTGATGAAAATTGTTAAATCAGATGATTGT
	TTTTTTGTTGCTACTGGTATTACAGATGGTTTGTTGATTAATGGTATTAGAAAAAAAA
	AGACGGTTTGATGCAAACTCATTC
PpAOX	ATGGCTATCCCCGAAGAGTTTGATATCCTAGTTCTAGGTGGTGGATCCAGTGGATCCTG
	TATTGCCGGAAGATTGGCAAACTTGGACCACTCCTTGAAAGTTGGTCTTATCGAAGCA
	GGTGAGAACAACCTCAACAACCCATGGGTCTACCTTCCAGGTATTTACCCAAGAAACA
	TGAAGITGGACTCCAAGACTGCTTCCTTCTACACTTCTAACCCATCTCCTCACTTGAAT
	GGTAGAAGAGCCATTGTTCCATGTGCTAACGTCTTGGGTGGTGGTTCTTCTATCAACTT
	AAAACCAAGGACTTGCTTCCATTGATGAAAAAGACTGAGACCTACCAAAGAGCTTGCA
	GTCACAAGATCTACCGTGCTAGAAACCOTTCCAAGCAAGCCTTGTGTGGTACCAAGAAGCCAA
	CCATTGGTTTTGCAAAGCAAAGCAAATCOTTTGCTGACCAACCAACCAACCAACCAACCAACCAACCAA
	ΤΑΑGCCTTTGGTCAACTTGCCAGGTGTCGGAΔGΔΔΔCTTCCAAGACCACTACTGTTTCT
	TCAGTCCTTACAGAATCAAGCCTCAGTACGAGTCTTTCGATGACTTCGTCCGTGGTGAT
	GCTGAGATTCAAAAGAGAGTCTTTGACCAATGGTACGCCAATGGTACTGGTCCTCTTG
	CCACTAACGGTATCGAAGCTGGTGTCAAGATCAGACCAACACCAGAAGAACTCTCTCA
	AATGGACGAATCCTTCCAGGAGGGTTACAGAGAATACTTCGAAGACAAGCCAGACAA

	GCCAGTTATGCACTACTCCATCATTGCTGGTTTCTTCGGTGACCACACCAAGATTCCTC
	A IGA A TGGA CCA CTTTGCCGGTG A GGTC A CTTCTCA CCA CCCTCTGTTCCCA TA CTCA T
	GAACTEGTCTGGTCTTGCTCACGGTTTCTTGGACTCAACCTTGGAGAAGCCAACTG
	CAATGAGGAGGATGACAAGGCATTGAGACTACATTCGTGAGCACACAGGGAGACCAC
	TGGGGGGGGTGTTTTGGACCACAGATCAACGTTACGGAGTCAAGGGCTGAAGGTTG
	GTGACTGTCTGTCCGGTGGCAGACAATGGTTGGTAGTAGTACACCAACCGCTCTTTG
	ATCGGTGAAAAGACTGCCACTTGGTGGAGAGAGATTAGGATACTCTGGTGAGGCCT
	TAGACATGACTGTTCCTCAGTTCAAGTTGGGCACTTACGAGAAGACCGGTCTTGCTAG
	ATTCTAA
РрСТА	ATGTCTCAACCACCTAAATcGGACAACATCAAATGGTGCTCCTGTCTCCGATGTATTTG
	CTACAGAGAGAGCCACCTTCGACAACGCTAATCACGCTAACAATGCCCCCAAAGTTGG
	GCCTCTGCTGCTACAAGACTTTCAATTGATTGATTCTCTTGCCCATTTCGACAGAGAAC
	GTATTCCAGAGAGAGTTGTGCATGCCAAAGGTGCGGGAGCTTTCGGTGAGTTTGAGGT
	GACTGACGACATATCTGACGTTTGTGCTGCCAAATTCTTGGATACTATTGGGAAGAAA
	ACCCGTATCTTCACTCGATTCTCCACCGTTGGAGGTGAGAAAGGTTCTGCCGACAGTGC
	CCGTGACCCAAGAGGGTTTTCCACCAAGTTTTACACAGAGGAAGGTAACTTGGACCTT
	GTGTACAACAACACTCCCATCTTCTTTATCAGAGATCCATCC
	CCACACCCAAAAGAGGAATCCTGCTACTAACCTGAAGGACGCCAATATGTTCTGGGAT
	TACCTTGTTAACAACCAAGAGTCCATTCATCAGGTGATGTACTTGTTCTCAGATCGTGG
	AACTCCTGCTTCTCTTAGAAAAATGAACGGGTACTCTGGTCACACTTACAAATGGTAC
	AACAAGAAAGGTGAGTGGGTTTACGTACAAGTTCACTTCAAGTCGGACCTGGGTGTCG
	TAAACTTCAACAATGAAGAGGCTGGAAAGCTTGCTGGCGAGGATCCAGACTACCACAC
	CGGIGAICIIIICAACGCCAIIGAGAGAGGCGAGIAICCIICAIGGACIIGIIACAIIC
	AGACCAIGACICAAGAACAAGCIGCCAAGCAACCAIIIICCGIGIIIGACIIGACIAA
	ALACICACCULCALAGALIOGUIGUIAACIALCAGCAGALICULCUCUCAALIGUCAALIG
	GTTACTCCAACTACAAGTCTTCTTTCTGTCCATTCTCTACAGGGCACAGATCCAGA
	AGGTATCCTTGACAGTAAGAGCTACGATTTTGAACAGCCAAGAGCGCTTTGGAAAAGTA
	TTCGGCAAAACTCCTGGTCAGCAACGTAACTTCTGCCACAACGTTGCCGTTCACGTTGC
	GGCTGCCAACCATGAAATTCAAGACAGGGTTTTTGAATACTTCTCCAAGGTTTACCCTG
	AAATTGGTGACCAGATTCGTAAAGAAGTATTGCAGCTATCTCCAAGAGGTGACTCTGC
	AGCAAGATTGTAG
PpDAK	ATGTCTAGTAAACATTGGGATTACAAGAAAGATCTGGTACTCAGCCATCTGGCTGG
	TATGTCAGTCCAACCCCCATGTAAGGCTAATTGAGTCCGAAAGAGTCGTCATCTCCGC
	CGAGAACCAGGAGGACAAGATTACCTTGATCTCTGGTGGAGGTTCAGGACACGAGCCT
	CTACATGCTGGCTTTGTCACCAAGGACGGTCTTTTGGATGCCGCTGTGGCCGGGTTCAT
	CTTTGCCTCGCCATCTACTAAACAGATATTTAGCGCAATCAAAGCCAAACCTTCGAAG
	AAGGGAACTTTGATCATCGTCAAGAACTATACAGGAGACATTCTTCACTTCGGTCTTGC
	CGCCGAAAAGGCCAAGGCCGAAGGTCTCAACGCAGAACTGCTGATTGTTCAGGACGA
	TGTCTCTGTTGGTAAAGCCAAGAATGGCCTGGTAGGGCGTAGAGGTTTGGCTGGAACT
	TCTTTAGTGCACAAGATTTTGGGTGCCAAAGCTTATTTACAAAAGGACAACCTGGAAT
	TGCATCAGCTGGTCACTTTCGGTGAGAAGGTCGTTGCCAACCTGGTTACAATTGGTGCT
	ATGACGAGCACGGCTACGAAGTGCTAAAGCACGATGAATTTGGAAATCGGAATGGGTA
	THURCAAUAATUA IUAAUTUUU TACTUA IUAATAACTIUUUUAAUAACCICAAUAT
	υλυληματική του του μου μου μου κατά μεταλικά τα το κατά του
	ACAATTTATTOTOUCTOUCUAUAAATAUAUUAAUUAAUUAUAUAUTTUTATUTAAUUTATU TGTTGATGCTAAGCTGTATGCTGACCTTCTCCAGTCTCCTCCTCAAAGAACCCCATTTCAA
	ΩΤΤGGCGA ΔΤGGTTCCA ΔΤGCCΔΤΤΤΤΔΔΔΔGGCTCTGGCTGΔΔGGΔΔΑGGTCΔΔΤΟΤΟΔΤΑΑ
	AAAGACGGTGTTAAATCACTGGTGCAAATTACAGACATCGTGGAAAACCITGATGGGTG
	GAACATCTGGAGGTCTGTACTCCATTTTCATCAGCGCTTTAGCAAAGTCTTTGAAAGAG

AddicAdicAl TICATAFICAATACAAGAGACACQITACIGGAGACTEGAAAACT TATTGACGCTTTGGAGACCATTTGAAAGGAATTGCCAAGGCTAGGAAAGTTGGAAACT GCAAACAAAGCTGCCCATGGTGGTGCTGAAGCAACAATTCGAAGGTGAAAGTGAAGGTGGA CTACCTGATCCTGGAGCATTGCCGAGAGAGGTCAAACAATTCGAAGGTGAAGGTGAAGCTGA CTACCTGAACACTATTCTATGCTATTGCTGGTGATGCTTGTTTGCAAAGGGGACCTGG TTTGGAACCACGGTTTGTTGTGGTGGTCCGTCGGTGGACACCTTATTGGTGATGCTG GCTAAGCACCACCATTTCTATGCTATTGTGGTGATGCTTGTTTGCAAGAGGGGACCTGG TTGGAACCCAGGTTTGTTGTGTGGTGTCCGTCGGTGTTAACAACCCGAAGGACACTTT GCTAACCACCAGCATGTGAAGGCCATGGAATGGCCATGGAGAATGGTTGAGGGACACCCTTATGGGTCG GCTAAGGTTAGAACTGAAATGGACAGGATGTCCGTGGAGGATGGAGAGGACCACGCTG GCTCAGCGTTGCAGGACGGCCATGGAAGGCTGATGGGCCAAGCCAGCGTG GATCAACGTTAGAACTGAATTGGACGAGGTGTAGGGCCAAGCCAGCGTG GCCGAGGGTGATCTGGTGAGGAAGGTTCCGGCGAGATGGTGAAGGACCAACCCG GCCGAGGGTGATCTGGTGAGGAAGGTATCGGGAAGGATGGTGAAGCACCCAGGTGT CACGGTTCCACGAGGTGAGGAAGGTATCGGGCAGGGGAGTTAGGGCCAAGTCCCAAGGA GCCGAGGGTGATCACTAGTTGGGAGGAAGTTCTGGGTGACTACCACCAGCGGGTC GCCGAGGAGGTGATCACTAGTTGGGAGGAAGTTTCGAGGGAACTTTCCAAGGA CTGGAAGAATTGTTAGTCCCGGGGAGGACTATTGGAGGGAACTTCCCAAGGA CTGGAAGAAATTGTTAGTCCCGGGGAGGAAACCCACCGGGCCAACTCCCAAGGAGCTCT GCATAGGAAACTTCTGTGGATGGAGGAAATTAAAGGCCCACTCCTGCTGGTGAGAATTATGCGGTTGGG GCTAGGAAAACTTCTATGGAGTGGGTGGGCACAACCCAGGGGCAACTACCAACGAAGGGTA GCTGGTGAAGAACGCCTTAGGTGGGGGGAGAGTTAAGTACTTGCAGCCTG AGCTGGTGAAGAAGGCCATCCACCGCGACGCCAACTGCTGGCGCAACGACGGTCCGTG GCCAAGCACCTCTATGGTGGCTCAGCGCCAATGCCTGGTGCGACTCCCACGG GCCGGTGAAGAAGGCCCAAGCGCCCACGCCATGCCTTGGTGCGACTCCCACGG GCCGACGCCAACGTCCCCCCTGTTCTCTCTGTGTCCAACCACGAGGTTGGCC GTCAAACTGCCTTAGCCCGAAGGCCCAATGCCCTGGCCAACGACGCTCCGTTGGAAGGTTGGCC GTCAAACTGCCGTGGGTGGACCCAACGCCGTGCTGCCAACGACGGTGCGCCAAGGGTGCGCC ACCCCGCGTAAGACGCCGACGCCCCACGCCTATGCTCCGAGGTGCGCCCATGGGAGGATGCC ACCCCCCCGGTAAGACGCCCCCGGGAGGCCAAAGGGAGGTTACGCCCTTGGAGGGGGAAAACC AAGGCCGGCAAACCCTTTGGCTGAGGGGCCAAGGGCGCCAAGGGTGCGCCGGGGGGAAGACCC AAGGCCGGTGAAGACCCCTGGGGGGAAACCCTTGGGTGGG
 IATIGACOCTITIGAAGCCAITIGIAAAGGAATICGCCAAGGAAGCCGAAGCCAAGTT GCAAACAAGCTGCCCAIGATGGTGCGAAGCAAAATTCGAAGCCGAAGCAAGATT GCAAACAAGCCGCATTATGCTTGCGCGATTGGCTGCTTGGCAAGCCAAGCCAAGCGAAGCAAGC
GAAAACAACTTTATITGCCCAAGAAGAGATTCAAACAATTCGAAAGTGAA CTACCTGATCCTGGTGCTATTGGTCGTCGAGAGAGATTCAGAAGATGAAGGTGAA CTTCCAATTCGATCGATGCTATGGTCGTCGCGCTTGGATCACTAGAAGTGAAGGTGAA CTTCAAATTCGGATGCTATGGTGGTGGTGGTGGTGGTGGTGGAAGACCTTATGGTGATGACG TTGGAACCACACTATTCTATGCTATTGTTGGGGATGCTTGGATACCACGGAAGGACCTGG TTGGGAACCACGAGTTTGGTGGTGGTGTGTCGGTGGATGGA
GGAAGAGCATCTTATGTTGGTATTGGTGTGCTGTGGTGATTACGGAATTACTGATGCATA CTTCCAATCTGAAACCAAGTTGTAG <i>PpDAS2</i> ATGGTTGACAACCAAGTTGTTGGTGATGCTTGTTGGCAAGAATGGATGATGATGGATG
 CHACCIGATECIGATECIGATEGITTAGETENTIGETAGECTEGTTGCAAGAGGGACCTGG PpD452 ATGGTTGACAACACTATCTATGGTATTGTTGGTGATGCTTGTTGCAAGAGGGGACCTGG TTGGAACACCACTATCTATGGATGGTTCCGTGGATGGTTGTGCAACTGACCTTATTGTGGATGGTCTAGGG ACAACAACCAGGTTTGTTGTGGATGGTTCCGTGGATGGTCACCTGACACTTATTGTGGATGAGGACACCTC GCTAAGTTTAGAACTGAAATTGGAACGGAATGGCAAGGCAACCCAACCCT GATCAACGTTAGAACTGGAATGGCCACGGAGTGGAAGGCCAACCCACCC
PpDAS2 ATGGTTGACAACACTATTCTATGGTGATGGTTGGTGATGCTTGTTTGCAAGAGGGACCTGG TTTGGAATCGAATTCCTTAGCTGTGTCATTGGTGTGTGACAACCTTATTGTGTATCGAG ACAACAACAGGTTTGTGTGTGTGTGGTGCGTGGGACAACCTTATTGGAGAGACACTTC GCTAAGTTTAGAGCTCGAAACTGGAATGGACAGGATTGGAGAATGAGACCAACTCCT GCTAAGTTGAGAGCTGAAACTAGGACAGGATTCGGGTGGAGAACGAGACCAACTCCT GCTAGGAGGTGAGAACTAGTTCGGGCCAAGGCTGAGAATGAGGACCAACTCCT GCCGAGGTGAGAAACTAGTTCGGTGCCACAGGGAGTTGAGGGCAAGACGCTGAAGAACCGT CACGGAGGTGATCAACTAGTTGCTACGGAAGAACTTTTTGGTGAGAACGCTAAG ACTGCCAGGAGTGATGCAACTAGTTGCACGGAGGACTAACGGTAACGGTCAAGAACCCT GCCGAGGGTGATCAACTAGTTGCACGGGAAGAACACTTTGGAGGAACTTCCAAGA ACTTATCCTCAAGAGGTGAGGGAATTAAAGGCCCGTATTAGAGGTGAAACCCT GCTAGAGAAATTGTTAGATCTCTGGGGAGGAGTTAAGGGGAGAACTTCCAAGA ACTTATCCCGTGTCCATTGTTGCGGGGGGGGACTACCTCCAGGGTAGAGACCTCT GCTAGAGAAATTGTTAGATCTCTGGGGAGGGAGTAAGACACTGCTACCGGAGCACCCG GCTAGAGAACTTCTTGGGATTGGGTGGGGGACTACCTCGGGTGAGATAATTGGAGGTCAGT GCCGAAGGTCCAATCGTAGGCTGACGCCAACGCGACTAGCACCGGCGCATACGACGCCCCTGG GTAGGTGGCGAACCTCTAAGTTGGGCGGGGGACTACCTCGGGAGACCAACCA
7/D352 AIGGITGACAACACIAICIAIGUATIGUATIGUAGIGAIGCITGITIGUAAGAGUAAGUAACUAAGUAGUAACUAACACACGAGUTTGGATAGUAATUGAACUCATATUTGGATGGAACTTATUTGGATGGAACGACTTATUTGGATGGAACGACTTAGGACAGCATTTAGAGTCGAAGGAACTTATUTGGATGAGCAAGCACTTCGGTTAGAACCAGAGAACTTTAGAGCGAGAGGAACGGAACGACACACCCGGACGAAGAACGTTTGGATGAGAGCAAACCAACC
ACAACAACCAGGTITIGTTGTGTGTGTGGGTGGGTGGGAGATACAACACGGAGAGACTTT GCTAAGCTTAGAGCTCAGAACTGGAATGGGCAAGGGCGGGAGAATGGAGACCAACCG GATCAACGTTAGAACTGGAAACTGGAATGGGCAAGGGTGGAGAATGGAAGACCAACGAC GATCAACGTTAGAACTGGAAGGGAAG
ACAACAACCAGGTITIGIGAIGGTICCGICGAGTIGTICAACGAACGAAGACGATIGT GCTAACGTTAGAACTGAAAGCCATCGAATGGTCCGAGAGGGGAGAGAGA
 GCTAAGTTAGACCTAGGAACTGGAATGGCCAAGGCTGGGAAGATGGAGACCAACCCT GATCACCTTGTACCAGGCCTGGAATGGCCAAGGCTAGGAATGGAGACCCACCGCGGC GACCACCTTGCTGCTCGGTAGGAAGGGACCGGAGGTGAAGGCCAAGGCACGGCGGTATGAAGACCACCGCGCGGGGGGATCAACCACCGGGGGGGAAGACCGGTACGAAGACCGCCGGACTGAGGGGGGGAAGATGATGAAGACCTCCCAAGGAGGGGGGGAAGATGCGTTAAGA CCGGAAGGGTGCGATCGACCACGGGCCAAACCACCGGGCCAACGACGGGCCACCGACGGGCGACGA
Internet indicates and the second a
 GATCAACH TAGAACTIGGAAGTATTGGACAGGAATTGAAGGGCCAAGTACGGCTTGG ATGTCGCCTGGGTGTGGGTGGTGCCACAGGAGGTCTATGAAGGGCCAAGTACGGTGAGG GCCGAGGGTGATCAACTAGTTGCTAACTGGAAGAAACTTTTGGATGAAGTACGGTAAGA ACTATCCTCAAGAAGGTGAGGGAGGAATTAAAGGCCCGTATTAGAGGGTGAACTTCCAAAGA CTGGAAGAGTTTGATCCACAGGACAAACCAACCGAGCCAACTGCTACCAGAACCTCT GCTAGAGAAATTGTTGGTGCGGTGGGGCGCAATCGGGGTGACTACCTGGGTACTAGCGGTG GCTAGAGAAATTGTAGATCTGGGGACGAAACCCACCGGGTCATGGTGCGGCAACTTCCAAGAACCTTC GCTAGAGAACACTCTATGTGGGGCGGCACACCTCCGGGTGAATATATTGCGGGTTCGG TGACTTGCCGTGTCCATTCTTGGGGCCAATGCTTGGCTGCATACACAAGGGTG ATCAGAGAACACTCTATGTGGGTGGTGACTACCTGGTAGCAACAACGGGCG GTATGGCGCGCACTTCAGGGTCCAACGCTTTGCTTT
ATGTCGCTAGAAAGTTCTGGTTCCCACAGGAGGTCTTGATTTCTTTGCTGAAAAACC GCCGAGGGTGATCAACTAGTTGCTAACTGGAAGAAACTTTTGGTGGATGAGTAGGTAAGA ACTATCCTCAAGAAGGTGAGGAAATTAAAGGCCGTATTAGAGGTGAACTTCCAAGA CTGGAAGAGTTTCATTCCACAGGACAAACCAACCGAGCCAACTGCTACCAGAACCT GCTAGAGAAATTGTTAGATCTCTGGGAGCAAAACCTTCCTCAGGTTATGCTGGTTCTG TGACTTGTCCGTGTCCATTCTTTGAACTGGGGAGGAGGTTAAGTACTTTCACAGGTTGG TGACTTGCCGTGTTACCCAAGTTGGTGGTGGTGACTACTCTGGTGGCTGCATACAACAAGGGT AGTTACAAAACTTTCTGTGGGATTGGTTGGCTGTTGGCTGCATACAACAAGGGT AGTTACAAAACTTTCTGTGTGGCTATTGCACATGGTAGCACACCGACCTGCCTTGG GTATGGCTGCAAGTTCACGACTTTCTACATGTCTACCGTGTAGCAGCACCTGCCTTGG GTATGGCTGCAAGTTCACAGGTCCAACCAGCCTATGGTTACCACGGCAGCCCGCCC
 ATOTCOC AGGAGATCAACTACTITIC TACAAGGAGOTIC LATOATTITIC TITIC TITICAAGAAAACC GCCGAGGGGGATCAACAACTTIGTGCTAACTGGAAAACTTITTIGAAGAGGGAACTTICAAAGAACTTICCAAGAGAGTTICAATTCCAAGGACAAACCGAGCCAACTGGTAACAGAAACCTIC GCTAGAGAAATTGTTAGATCTCTGGGACAAAACCGAGCCAACTGCTACCAGAACACCTIC GCTAGAGAAATTGTTAGATCTGTGGATGGGGGGACAAAACCTTCCTCAAGGTTATTGCTGGTTCTGA AGTTACAAACTTTCTGTGGATTGGGTGGTGGACTACTCCTGAGGTAAGTACTTCTTCAACGAGAAACTTTCTACAACGATTGCACAACGACCAACGGACATACAACAACGAACCCCACCTGCGT ATCAGAGAAACTCCTATGTGTGGTGCTATTGCCACACTGCTAGGTAGCAACAACAAGGGTA CTTTCTTGCCTATTACCTCAACTTTCTACATTGTCTACCTGTATGCAACACAACAGGGTA CTTTCTTGCCTATTCACAGTTCAACGCACCAGCCTATTGCTTCCTATTATCAAGGACACCTCCACCTGGG AGCTGGTGAAGATGGTCCAACGCACCAGCCTATTGCTTGC
ACTATCCTCAAGAAGGTGAGGAATTAAAGGCCCATATTTAGAGGTGAACTTCCAAAGA CTGGAAGAGTTTCATTCCACAGGACAAACCAACCGAGCGAACTGCTACCAGAACCTG GCTAGAGAAATTGTTAGATCTCTGGGGACGAAACCAACCGAGCGAACTGCTACCAGAACCTG GCTAGAGAAATTGTTAGATCTCTTGGGACAAACCAACCGAGCGAACTGCTACGAGACCTCG GCTAGAGAAACTTTCTGTGGATTGGGGTGGGCGACAACCGAGGTTAGTTGCTGCACCCAACCGACCCAC AGTTACAAACTTTCTGTGGGATTGGGTGGGCGACACCTCCGAGGTAGATAATTGAGGTGG ATCAGAGAACACTCTATGTGTGCTATTGCCAATGGTTTGGCGCATAACAACAGGGGTA CTTTCTTGCCTATTACCTCAACTTTCTACATGTTCTACCTGATGCAGCACCAGCGCCCTGC GTATGGCTGCACTTCAAGGGTGAAAGCAATTCACATTGCTTCACACGACCTCCATCGG AGCTGGTGAAGATGGTCCAACGCACCGCCATTGCCTTTGTCTTCACACGAGCTCCATCGG AGCTGGTGAAGATGGTCCAACGCACCAGCCGATGCTTCCAGCACGAGCTGCAGAGCT GTAGGCTGAAGACTCCGACCAGCCCACTGCTTCTCTCTTGCCAGCACCAGGGTTGAGA GTAGGAGGTAAGACTCGGCTGAGGGAGCCAAAAGAGGTGGTTCCGAATTGGAGTTGAG GTAGGAGGTAAGCCAGACCTCCAACTATAGTGGCGGGTTCCGAATTGGAGTTGCG GTCAAAACTGCTCGTTTGCTAAGACAACAGAAAGGGAGGTGGAAGGTCGAAGTTCGCC GTCAAAACTGCTCGTTTGCTAAGACAACAGAAAGGGATGGAAAGGTCGTGAGAGTTCCC GTCAAAACTGCTCGTTTTGCTAAGACAACAGAAAGGGATGGCAAAGGTTCGTGCCTTAG/ AGAGGAGAGGTTCCAACTGTCGTTGTTGAGGCCTATGTCGCATACGGAGGGAG
CTGGAAGAGTTTCATTCCACAGGACAAACCAACCGAGCCAACTGCTACCAGAACCTCT GCTAGAGAAATTGTTAGATCTCTGGGACAAACCAACCGAGGCAACTGCTACCAGAACCTCT GCTAGAGAAATTGTTAGATCTCTGGGACAACCACCAGGTTAAGTACTACGAGACCCTTA AGTTACAAACTTTCTGTGGATTGGGTGGTGACTACTCTGGTAGATATATTGAGGTTGGT ATCAGAGAACACTCTATGTGTGGTGATTGCCAATGGTTGGCTGCATACAACAAGGGTA CTTTCTTGCCTATTACCTCAACTTTCTACATGTTCTACCTGTATGCAGCACCGACCTCCATCGG GTATGGCTGCACTTCAAGGTTGAAAGCAATTCACATTGCTACACAGGACCCAGCCTCGG GTATGGCTGAGAGATGGTCCAACGCACCAGCCATTGCTTGC
GCTAGAGAAATTGTTGCACAGACGACAAAACCUTACTCAGGTATGCGGGTGGGG GGACTTGTCCGTGTCCATTCTTTGGACTGGGGGGGGGG
 GETAGMANIATIOTICGAACTGGGAGGAGTAAGCATTCACAACAACCAACAACTACTTCTGACCAACAACTAGGGAGTAAGTA
AGTTACAAACTTTCTGTGGATTGGGTGGTGACTACTCTGGTAGATATATTGGGTGGG
ATCAGAGACACTCTATGTGTGCTATTGCCAATGGTTTGGCTGCATACAACAAGGGTA CTTTCTTGCCTATTACCTCAACTTTCTACATGTTTGCTACATGCAGCACCTGCCTG
CTTTCTTGCCTATTACCTCAACTTTCTACATGTTCTACCTGTATGCAGCACCTGCCTTGC GTATGGCTGCACTTCAAGAGTTGAAAGCAATTCACATTGCTACACACGACCCGCTGG AGCTGGTGAAGATGGTCCAACGCCACGCC
GTATGGCTGCACTTCAAGAGTTGAAAGCAATTCACATTGCTACACACGACTCCATCGG AGCTGGTGAAGATGGTCCAACGCACCAGCCATTGCTTTGCTTTCATATTCAGAGCT TGCCCAACTTCACATTAGACCAGCCGATGCTACCGAGGTGCAGCTCGTTTGA/ GTAGCTGTTGAGCTCGAGCACTCCACTTGTTCTCTGTGCCAGACACGAGGTTGAGC/ ATACCCAGGTAAGACTTCGGCTGAGGGAGGCAAAAGAGGTGGTTACGTCGTTGAAGA CTGTGAGGGTAAGCCAGACGTCCAATTAATTGGTGGTGGTGCCGAATTGGAGGTTGGCC GTCAAAACTGCTCGTTTGCTAAGACAACAACAGAAGGGATGGAAGGTCAGAGTTCTGTCAT TCCCATGTCAGAGACTGTTTGACCAACAACAACAGAAGGGATGGAAGGTCAGAGTTCGTCAT AGAGGAGAGG
AGCTGGTGAAGATGGTCCAACGCACCAGCCTATTGCTTGTCTTCATTATTCAGAGCT/ TGCCCAACTTCTACTACATTAGACCAGCCGATGCTACCGAGGTGCAGCTCTGTTGA/ GTAGCTGTTGAGCTCGAGCACTCCACCTTGTTCTCTGTCCAGACCGAGGTGAGC/ ATACCCAGGTAAGACTTCGGCTGAGGGAGCCAAAAGAGGTGGTTACGTCGTGAAGA CTGTGAGGGTAAGCCTTGGGTCGACTAAGAAGAGGGATGGAAGGTCAGAGTTGGCC GTCAAAACTGCTCGTTTGCTAAGACAACAGAAGGGATGGAAGGTCAGAGTTCTGTCAA ACGGCACTGCTCGGTTCCAACTGTCGTTGAGCGCCTATGTCGCATACGGAGGGGAGAGA ACGCCACTGCTGGTTACACCATGAACAATCCCTGGGCATACAGACGTTCGTGCTAG/ AGAGGAGAGGTTCCAACTGTCGTTGAGAGCCTATGTCGCCATACGGGAGGAGA ACGCCACTGCTGGTTACACCATGAACACCTTTGGTAAGTCTCTTCCTGTTGAGGAGAGA ACGCCACTGCTGGTTACACCATGAACACCTTTGGTAGGAGAGGTGCTGCCATACGTCA ACTCTATTAAGGCTAGTCCTCCAACTCCTGAGAAGATTGGTGAGAAGGTTGCTGCATACGTCA ACTCTATTAAGGCTAGTCCTCCAAATCCTTTACGAATTCACCGATTGAAGGCTGGTGGT ACAAATACTTCGGATACACTCCCAAATCCTTTACGAATTCACCGATTGAGAGGGGAAAACC AAAGCACGACAAACTATAA <i>FLS</i> ATGGCTATGATTACCGGTGGTGAATTGGTTGTAGAACCTTTGATAAGGCTGGTGTG/ ACATTTGTTTGGTTTGCACGGGGTATCCACATTGATACCATTTTCCAAGCTTGTTTAGATC, CGATGTTCCAATTATTGATACTAGACACGAAGCCGCTGCTGGTCGGCGCGGGGGGTTCAG CGCTGGGGGCGCTAAGTTAGGTGTGCACTAGCCAGCTGGTGGGGGGGTATTGACA AAGCCTGTTACTCCAATTGCTAAGTAGGAGTGACCACATTTACAAGCTGGTGGTGGTATCAC ACGCTGTGGTGCTTAAGAGAGGATGAAAACTAACACTTTACAAGCTGGTGGTGTCACACGCGGT TACGACAGTGGTGCTAGGTATGCTAAGTGATGAAACTAACACTTTACAAGCTGGTATTGGAACAC AGGTTCGGTGCTTAAGAGAGGATGAAAACTAACACTTTACAAGCTGGTATTGGAACAC ATTCCAAGATTGGTCATGCCAAGGTATACTAGAGCTGCTGGTCCCAAGGGTATTGGAACAC ACTCCAAGATTGGTTTGCCCCCCATGGTGCTCATCCAGACCAGGTTTGGTAAGAACTCCAGGTTTGGTAGTACAA GCCTTGGCACTATTAAGAAAGGCTGAAAGACCAGATTATCGTTTACGTATTGGAAGAACTCCAGG TTTGGTTGGACTATTAAGAAAGGCTGAAAGACCAGATTATCGTGTGCGCACAGGTTTGGAAGAGTT CAAGAACTGCTAGAAAGAACGCGCTATGAAGCCGGTTGGTGCCCAGGTGCTGGTGCACTAGGAAGGTGCAAGGCT TTAGGTCAAAACCTTTACTTTTCTTTCGGTAGGCTCAAGGACTGAGGTGCAGGT TTAGGTAAGAACGCGTTTGCTAGGTTTGGGTGGTGCAATTAGGTAGAAGCACC TTAAGTTAAAACCCTTGCCTGAAGTTGGAAGCCGCTTGGGTCCAAGAAGCCCGCTCCAAGAAGCACCT TCCGCGACTATGAAGAACCGCTTTGCCAGCCTTGGGTGCAAGAGCTTAGGTAGAAGCACCT TTAGGTAAGGTA
 TGCCCAACTTCTACTACATTAGACCAGCCGATGCTACCGAGGTTGCAGCTCTGTTTGA/ GTAGCTGTTGAGCTCGAGCACTCCACCTTGTTCTCTCTGTCCAGACGCGCCAAGACGCGCAAGACGCCAGAAAGAGGTGGTTACGTCGTGTGAGG CTGTGAGGGTAAGCCAGACGTCCAATTAATTGGTGCGGGTCCGAATTGGAGGTTGGTGCC GTCAAAACTGCTCGTTTGCTAAGACAACACAAGAAGGGATGGAAGGTCAGAGTTCTGTCTG
GTAGCTGTTGAGCTCGAGCACTCCACCTTGTTCTCTCTGTCCAGACACGAGGTTGAGC/ ATACCCAGGTAAGACTTCGGCTGAGGGAGCCAAAGAGGGTGGTACGTCGTGTGAAGA CTGTGAGGGTAAGCCAGCGTCCAATTAATTGGTGCTGGTTCCGAATTGGAGGTTGGCG GTCAAAACTGCTCGTTTGCTAAGACAACAGAAGGGATGGAAGGTCGAGAGTTCTGTCTTAG AGAGGAGAGG
ATACCCAGGTAAGACTTCGGCTGAGGGAGCCAAAAGAGGTGGTTACGTCGTTGAAGA CTGTGAGGGTAAGCCAGACGTCCAATTAATTGGTGCTGGTTCCGAATTGGAGTTGCC GTCAAAACTGCTCGTTTGCTAAGACAACAGAAGGGATGGAAGGTCAGAGGTTCTGTCAT TCCCATGTCAGAGACTGTTGACCAACAATCCCTGGCATACAGACGTTCTGTCCTTAG/ AGAGGAGGAGGTTCCAACTGTCGTGTTGTGAGGCCTATGTCGCATACGGAAGGAGAGA ACGCCACTGCTGGTTACACCATGAACACCTTTGGTAAGTCTCTTCCTGTTGAGGAAGAC ACGCCACTGCTGGTTACACCATGAACACCTTTGGTAAGTCTCTTCCTGTTGAGGAAGAC ACGCCACTGCTGGTTACACCATGAACACCTTTGGTAAGTCTCTTCCTGTTGAAGGAAAACC AAAGCACGACAAACTATAA <i>FLS</i> ATGGCTATGATTACCGGTGGTGAATTGGTTGTTAGAACTTTGATTAAGGCTGGTGTTG/ ACATTTGTTTGGTTTGCACGGTGTGAACACGCACATTGATCAAGGCTGGTGTTCA CGATGTTCCAATTATTGATACTAGACACGAAGCCGCTGCTGGTCACGCCGCTGAAGGT TACGCTAGAGCTGGTGCTAAGTTAGGTGTGCACACTTTACAAGCTGGTGTTTCAG CGATGTTCCAATTATTGATACTAGACACGAAGCCGCTGCTGGTCACGCCGCTGAAGGT TACGCTAGAGCTGGTGCTCAAGTTAGGTGTGCAACTACCACTTTACAAGCTGGTGTTTCAG CAGGTTCTGGTGCTTTAAGAGATGATGAAACTAACACTTTACAAGCTGGTGTTTCAG CAAGGTCTTGGTGCTCCAATTACTAAGGTGGTGCCCATAGAGTTATGGCAACTGAACAT ATTCCAAGATTGGTCATGCAAGCTATTAGAGAGCCGCTTGTCTGCTCCCAAGGGGTCCAG TTTGTTGGATTTGGTCATGCAAGCTATTAGAGAGCCCGCTTGTCTGGCTCCAAGGGGTCCAG TTTGTTGGATTTGGTCATGCAAGCTATTAGAGACCAGATTATGGAAGATTCTGTTACA GCCTTGGCACTATTAAGAAAGGCTGAAAGACCAGATTACGTTTTAGGTAAGATCCGTT CAAGAACTGCTAGAAAGACCGCTTTGTCAGCTCCGGCCCATGGAGCTATGAAGAGCCTGT TTGGTGACTATGAAAGACCGCTTTGTCAGCTTCGTGCTGCCCACGGTGTGCAGGTGCCAGT TTTGGTGGACTATTAAGAAAGACCGCTTTGTCAGCTTCGTGCTGCCCACGGTGTGCCCTGT TTCGCTGACTATGAAAGACCGCTTTGTCAGCTTCGTGCTGCCCACTGGTGTCCCGTT TTCGCTGACTATGAAAGACCGCTTTGTCAGCTTCGTGGTGCCACTGGAAGAGCCCG TTTAGTTCAAAACCTTTACGGTTGGAACCAGGTTATGGTTAGGAAGGCCA TGCTTAGGAGCTAGAAAGACCGCTTTGCAGCGCCATAGGATGCCAGCTATGAGAAGGCG TTTAGTTCAAAACCTTTACGGTTGGAACCGGCCATGGGTGCCAGATTGCAAGGCAC TGCTTAAGAACCGTTGCTGCTGCACGGTCATGGAAGGCTTAGGTAGAAGGCCA TGCTTAGGTACAGGTTGCTGCTGAAGGTTGCTGGTCCAAGTAAGCCCG CTCAAGAGCCCTGGTGCGCCAGATAGGTGGTGCCGCTCAAGGATTGCAAGCCT CCAAGACGCTGCTGCTGCTGCTGGTGCCACATAGAAGCCTTAGCTTAGCTCAAGCCC CTCAAGACGCCTGCTGCTGCTGCTGCTGGTGCCCACTAGGTTACCGCCCCCCCC
CTGTGAGGGTAAGCCAGACGTCCAATTAATTGGTGCTGGTTCCGAATTGGAGTTTGCC GTCAAAACTGCTCGTTTGCTAAGACAACAGCAGGGAAGGTCAGAGGTCGTCGCAT TCCCATGTCAGAGACTGTTTGACCAACAATCCCTGGCATACAGACGTTCGTCCTAG AGAGGAGGGTTCCAACTGTCGTGTGTGAGGCCTATGTCGCATACGGAGGGGAGAGA ACGCCACTGCTGGTTACACCATGGAACACCTTTGGTAAGTCTCTTCCTGTTGAGGATGC TACAAATACTTCGGATACACCATGAACACCTTTGGTAAGTCTCTTCCTGTTGAGGATGC ACTCTATTAAGGCTAGTCCTCAAATCCTTTACGAAGTCCCTTCCAGTGCGAACGGC ACTCTATTAAGGCTAGTCCTCAAATCCTTTACGAATTCACCGATTTGAAGGGGGGAAAACC AAAGCACGACAAACTATAA <i>FLS</i> ATGGCTATGATTACCGGTGGTGAATTGGTTGTTAGAACTTTGATTAAGGCTGGTGGTG ACATTTGTTGGGTTGCACGGTGAATTGGTTGTAGAACTTTGATTAAGGCTGGTGGTGC TACGCTAGAGCTGGTGCTAAGTTAGGTGTGCACTGCTGGTGCGCGCGC
GTCAAAACTGCTCGTTTGCTAAGACAACAGAAGGGATGGAAGGTCAGAGTTCTGTCAT TCCCATGTCAGAGACTGTTTGACCAACAATCCCTGGCATACAGACGTTCGTCTTGG/ AGAGGAGAGGTTCCAACTGTCGTTGTGAGGCCTATGTCGCATACGGATGGGAGAGAG ACGCCACTGCTGGTACACCCTGGAGAAGACTCGGTAGAGAAGGTTGCTGCATACGGCA ACTCTATTAAGGCTAGTCCTCAAATCCTTTACGAAAGTTGGCGCACAGGGAAAACC AAAGCACGACAAACTATAA <i>FLS</i> ATGGCTATGATTACCGGTGGTGAAATCGGTGTGAGAAGGTTGCTGGTGTG/ ACATTTGTTTGGTTTGCACGGTGGTGAATTGGTTGTTAGAACGTTGTTAGAAGGGAGAAACC CGATGTTCCAATTATCGGTGGTACACACTGATACCATTTGATTAAGGCTGGTGTG/ ACATTTGTTTGGTTGGCACGGTACCACATTGATACACATTTGATAAGGCTGGTGTTG/ ACATTTGTTTGGTTGGCACGGTATCCACATTGATACCATTTTCCAAGCTTGTTAGATC/ CGATGTTCCAATTATTGATACTAGACACGAAGCCGCTGCGTGCACGCCGCTGAAGGT TACGCTAGAGCTGGTGCTAAGTAGGTGTTGCATTAGTCACTGCTGGTGGTGGTGTTCAA TACGCTGGTGCTTAAGAGATGATGAAACTAACACTTTACAAGCTGGTATTGATCA AGTTGCTATGGCTGCCAATTACTAAGTGGGCCCATAGAGTTATGGCAACTGAACA AGTTGCTATGGCTGCCCAATTACTAAGTGGGCCCATAGAGTTATGGCAACTGAACA ATTCCAAGATTGGTCATGCAAGGCTGATATAGAGCTGCTTGGTGCTCCAAGGGGTCCAG TTTGGTTGGCATGGCA
TCCCATGTCAGAGACTGTTTGACCAACAATCCCTGGCATACAGACGTTCTGTCCTTAG/ AGAGGAGAGGTTCCAACTGTCGTTGTTGAGGCCTATGTCGCATACGGATGGGAGAGA ACGCCACTGCTGGTTACACCATGAACACCTTTGGTAAGTCTCTCCTGTTGAGGATGTC TACAAATACTTCGGATACACTCCTGAGAAGATTGGTGAGAAGGTTGCTGCATACGTCA ACTCTATTAAGGCTAGTCCTCAAATCCTTTACGAAATTCACCGATTTGAGAGGGAGAAACC AAAGCACGACAAACTATAA <i>FLS</i> ATGGCTATGATTACCGGTGGTGAATTGGTTGTTAGAACTTTGATTAAGGCTGGTGTTG CGATGTTCCAATTATTGATACCAGGTATCCACATTGATACCATTTTCCAAGCTGGTGTTCAG CGATGTTCCAATTATTGATACTAGACACGAAGCCGCTGCTGGTCACGCCGCTGAAGGT TACGCTAGAGCTGGTGCTAAGTTAGGTGTTGCATTAGTACCAGTTTGTTT
AGAGGAGAGGTTCCAACTGTCGTTGTTGAGGGCCTATGTCGCATACGGATGGGAGAGA ACGCCACTGCTGGTTACACCATGAACACCTTTGGTAAGTCTCTTCCTGTTGAGGATGTC TACAAATACTTCGGATACACCCCTGAGAAGACTGGTAGAAGGTTGCTGCATACGTCA ACTCTATTAAGGCTAGTCCTCAAATCCTTTACGAATTCACCGATTTGAAGGGAAAACC AAAGCACGACAAACTATAA <i>FLS</i> ATGGCTATGATTACCGGTGGTGAATTGGTTGTTAGAACTTTGATTAAGGCTGGTGTTG/ ACATTTGTTTGGTTTGCACGGTATCCACATTGATACCATTTTCCAAGCTTGTTTAGATC, CGATGTTCCAATTATTGATACTAGACACGAAGCCGCTGCTGGTCACGCCGCTGAAGGT TACGCTAGAGCTGGTGCTAAGTTAGGTGTTGCATTAGTCACTGCTGGTGGTGGTGTTCAA TACGCTGGTGCTTTAAGAGATGATGAACTAACACTTAGCCAGTTTTGTTCTGA CAGGTTCTGGTGCTTTAAGAGAGAGGTGAACTAACACTTAACAGCTGGTATTGATCA AGTTGCTATGGCTGCCCAATTACTAAGTGGGCCCATAGAGCTCAAGCTGAACAT ATTCCAAGATTGGTCATGCAAGCTATTAGAGCTGCCTTGTCTGCTCCAAGGGGTCCAG TTTGTTGGATTTGCCATGGGATATCTTGATGAACCAGATTGATGAAGAGTTCTGTTACA GCCTTGGCACTATTAAGAAAGGCTGAAAGACCAGATTGATGAAGATTCTGTTACA GCCTTGGCACTATTAAGAAAGGCTGAAAGACCAGTTATCGCTGATGGAGGAGCTG TTTGTTGGCATGGAAAGACCGCTTTGCTGCCCAGGTGGTGCTCTGCT CAAGAACTGCTAGAAAGACCGCTTTTGCTGCTCCAGGCGCTGTGTCGCCACGGTGCCTGT TTCGCTGACTATGAAAGACCGCTTTTGCTGCTGCCCCAGGTGTCTGCT CAAGAACTGCTAGAAAGACCGCTTTTGCTGCTGCCCACTGGTGCCCCTGTT TCCGCTGACTATGAAAGACCGGTTTGCTAGGTCCAGGTCCAGTTTGGATGAAGGCTG TTTAGTTCAAACCTTTACTCTTTCGCTAAGGCCGATGCCGCCCCAGATCTAGAGAGGTG TTTAGTTCAAAACCTTTACTCTTTCGCTAAGGCCGATGCCGCCCCAGATCTAGGTGCCACT TCTGCTCAAGATTCGGTTTGAACACCGGTCATGGGTCCAATTAATT
ACGCCACTGCTGGTTACACCATGAACACCTTTGGTAAGTCTCTTCCTGTTGAGGATGTC TACAAATACTTCGGATACACTCCTGAGAAGATTGGTGAGAAGGTTGCTGCATACGTCA ACTCTATTAAGGCTAGTCCTCAAATCCTTTACGAATTCACCGATTTGAAGGGAAAACC AAAGCACGACAAACTATAA <i>FLS</i> ATGGCTATGATTACCGGTGGTGAAATTGGTTGTAGAACTTTGATAAGGCTGGTGGTGGT CGATGTTCGAATTATTGATACTAGACACGAAGCCGCTGCTGGTCACGCCGCTGAAGGT TACGCTAGAGCTGGTGCTAAGTTAGGTGTTGCATAGCACTGCTGGTGGTGGTGTTCAA CGATGTTCCAATTATTGATACTAGACACGAAGCCGCTGCTGGTCACGCCGCTGAAGGT TACGCTAGAGCTGGTGCTAAGTTAGGTGTTGCATTAGTCACTGCTGGTGGTGGTTCAA CAGGTTCTGGTGCTTAAGAAGATGATGAACTAACACTTTACAAGCTGGTGGTGTTCTTGA CAGGTTCTGGTGCTTCAATTGCTAAGTGAGGCCCATAGAGTTATGGCAACTGAACAT AGTTGCTATGGCTGCCCCAATTACTAAGTGGGGCCCATAGAGTTATGGCAACTGAACAT ATTCCAAGATTGGTCATGCAAGCTATTAGAGCTGCCTTGTCTGCTCCAAGGGGTCCAG TTTGTTGGATTTGCCATGGCAAGCTATTAGAGCTGCCTTGTCTGCTCCAAGGGGTCCAG CCCTGGCACTATTAAGAAAGCCCCATGGTGCTCATCCAGACCAGGTTTTGGAACAA GCCTTGGCACTATTAAGAAAGCCGCTTTGTCAGCTCATCCAGACCCAGCTGATTGGAAGAACTA CCCTGGACTATGAAAGACCGCCTTGTCAGCTTTCGTTGCTGCCACTGGTGACCAGT TTCGCTGACTATGAAAGACCGCTTTGTCAGCTTTCGTTGCCCACTGGTGTCCCTGTT CAAGAACTGCTAGAAAGACCGCTTTGTCAGCTTTGGTTGCCCACTGGTGTCCCTGTT TCGCTGACTATGAAAGATTCGTTTGCTAGCCAATGAAGACTAGAAGAGTGCATTGAAGAGTGC TTTAGTTCAAAACCTTTACCTTTCGCTAAGGCCGATGCCGCTCCAGATTGAGAAGAGGCG TTTAGTTCAAAACCTTTACGTTATCGTATCTGGTTGGCCACTGGTAGCAAGGGGG TTTAGTTCAAAACCTTTACGGTTGGAACACCGGTCATGGGTAGATGGAAGGTGCATTGGGTACAAGGCCGATGCCGCTCCAGATTAATTCAAGTTGGTTG
TACAAATACTTCGGATACACTCCTGAGAAGATTGGTGAGAAGGTTGCTGCATACGTCAACTCTATTAAGGCTAGTCCTCAAATCCTTTACGAATTCACCGATTTGAAGGGAAAACCAAAGCACGACAAACTATAAFLSATGGCTATGATTACCGGTGGTGAATTGGTTGTAGAACTTTGATTAAGGCTGGTGTTG/ ACATTTGTTGGTTGCACGGTATCCACACTGATACCATTTTCCAAGCTTGTTAGATC/ CGATGTTCCAATTATTGATACTAGACACGAAGCCGCTGCTGGTCACGCCGCTGAAGGTTACGCTAGAGCTGGTGGTCAAGTTAGGACACGAAGCCGCTGCTGGTCACGCCGCTGAAGGTTACGCTAGAGCTGGTGCTAAGTTAGGTGTTGCATTAGTCACTGCTGGTGGTGGTGTTCAATACGCTAGAGCTGGTGCTAAGTTAGGTGTTGCATTAGTACACGCTGGTGGTGGTGTTCAATACGCTAGAGCTGGTGCTCCAATTGCTAATGCTCGTACTGATAGAACTCCAGTTTGGTCTGACAGGTTCTGGTGCTCCAATTGCTAATGGTGGGCCCATAGAGTTATGGCAACTGAACATAGTTGCTATGGCTGCCCAAGGCTATTAGAGCTGCCCTGTCTGCCCCAAGGGGTCCAG'TTTGTTGGATTGGCCATGGAAACCAAGCTATTAGAGCCGCCTGGTGATTGGAACCAGAGCCTTGGCACTATTAAGAAAGGCTGAAAGACCAGTTATCGTTTAGGTAGG
ACTCTATTAAGGCTAGTCCTCAAATCCTTTACGAATTCACCGATTTGAAGGGAAAACC AAAGCACGACAAACTATAA <i>FLS</i> ATGGCTATGATTACCGGTGGTGAATTGGTTGTTAGAACTTTGATTAAGGCTGGTGTTG/ ACATTTGTTTGGTTTGCACGGTGACCACATTGATACCATTTTCCAAGCTTGTTTAGATC, CGATGTTCCAATTATTGATACTAGACACGAAGCCGCTGCTGGTCACGCCGCTGAAGGT TACGCTAGAGCTGGTGCTAAGTTAGGTGTTGCATTAGTCACTGCTGGTGGTGGTGTTCAC TAACGCTGTTACTCCAATTGCTAATGCTCGTACTGATAGAACTCCAGTTTTGTTCTTGA CAGGTTCTGGGTGCTTTAAGAGAGAGACGACAACACACTTTACAAGCTGGTATTGATCA AGTTGCTATGGCTGGTCCCAATTACTAAGTGGGCCCATAGAGTTATGGCAACTGAACAT ATTCCAAGATTGGTCATGCAAGCTATTAGAGCTGCCTTGTCTGCTCCAAGGGGTCCAG TTTGTTGGATTTGCCATGGGATATCTTGATGAAACCAGATTGATGAAGAACTCATGTTATCA GCCTTGGCATTGGCTTTGCCGCCCATGGTGGCTCATCCAGACCCAGGTGTTGGATCAA GCCTTGGCACTATTAAGAAAGGCTGAAAGACCAGTTATCGTTTTAGGTAGTGAAGATT CAAGAACTGCTAGAAAGACCGCTTTGTCAGCTTTCGTTGCCGCCACTGGTGTCCCTGTT TTCGCTGACTATGAAAGACCGCTTTGTCAGGTTTGCCTGATGCAGGAGGTGCAGT TTTAGTTCAAAACCTTTACTCTTTCGCTAAGGCCGATGCCGCTCCAGATCTAGTTTGG TTTGTGGGTGCTAGATTCGGTTTGAACACCGGTCATGGGTAGAATTAATT
AAAGCACGACAAACTATAA FLS ATGGCTATGATTACCGGTGGTGAATTGGTTGTTAGAACTTTGATTAAGGCTGGTGTTGA ACATTTGTTTGGTTTGCACGGTGTCACACATTGGTACCACTTTGATAAGGCTGGTGTTAGATC, CGATGTTCCAATTATTGATACTAGACACGAAGCCGCTGCTGGTCACGCCGCTGAAGGT TACGCTAGAGCTGGTGCTAAGTAGACCACGAAGCCGCTGGTGGTCACGCCGCTGAAGGT TACGCTGTGTACTCCAATTGCTAATGCTAATGCACTGATAGAACTCCAGTTTTGTTCTGA CAGGTTCTGGTGCTTTAAGAGATGATAAGAACTAACACTTTACAAGCTGGTGTTTGATCA AGTTGCTATGGCTGCCCAATTACTAAGTGGGCCCATAGAGTTATGGCAACTGAACAT ATTCCAAGATTGGTCCAAGCTATAGAGCGGCCATAGAGTTATGGCAACTGAACAT ATTCCAAGATTGGTCCACAGGGATATCTTGATGAACCAGATTGATGAAGATTCTGTTATCA TCCCTGATTTGGCTTTGCCGCCCATGGTGCTCATCCAGACCAGGCTGATTTGGATCAA GCCTTGGCACTATTAAGAAAGGCTGAAAGACCAGTTATCGTTTTAGGTAGG
PLSAIGGCTAIGATTACCGGIGGIGGATTGGITGAGAACTTIGATTAAGGCTGGIGTTG/ ACATTTGTTGGTTTGCACGGTAGTACCACACACACATTGATACCATTTTCCAAGCTTGTTAGATC, CGATGTTCCAATTATTGATACTAGACACGAAGCCGCTGCTGGTCACGCCGCTGAAGGT TACGCTAGAGCTGGTGCTAAGTTAGGTGATGAGACCACGAGCCCGCTGGTGGTGGTGGTTTCAC TAACGCTGTTACTCCAATTGCTAAGTGATGAAACTAACACTTACAAGCTGGTATTGATCA AGTTGCTATGGCTGCTCCAATTACTAAGTGGGCCCATAGAGTTATGGCAACTGAACAT ATTCCAAGATTGGTCATGCAAGCTATTAGAGCTGCCTTGTCTGCTCCAAGGGGTCCAG TTTGTTGGATTTGCCATGGGATATCTTGATGAACCAGATTGATGAAGATTCGTTATCA TCCCTGATTTGGTTTTGTCCGCCCATGGTGCTCATCCAGACCCAGCTGATTGGAACCAG TTTGTTGGCACTATTAAGAAAGCCGCTTTGTCAGCTTCGTTGCTGCCACTGGTGTCCCTGTT CAAGAACTGCTAGAAGACCGCTTTGTCAGCTTTCGTTGCTGCCACTGGTGTCCCTGTT TTCGCTGACTATGAAGAGCTTTACTATGTTATCTGGTTGCCGCCACGAGTGAGAGGTGG TTTAGTTCAAAACCTTTACTTTGATCAAGGCCGATGCCGCTCCAGATCTAGTTTGA TCTGCCTAAGAACCTTTACCTTTCGCTAAGGCCGATGCCGCTCCAGATCTAGTTTGA TCTGCCCAAGTTATCCGTTTGAACACCGGTCATGGTAGCTAGATTGCAAGGCCA TCTGCCCAAGTTATCAGTTATCAGTTGAACACCGGTCATGGGTAGATTGCAAGGCAA TCTGCCCAAGTTATCAATTCCACGTTTGAACACCGGTCATGGAATGGGTAGATTGCAAGGCACCCCCCCAAGACTGCTGCCAAGACTGCAAGCACCCCCCCC
ACATTIGTTIGGTIGGCACGGTATCCACATIGATACCATITICCAAGCTIGTTIAGATC CGATGTTCCAATTATTGATACTAGACACGAAGCCGCTGCTGGTCACGCCGCTGAAGGT TACGCTAGAGCTGGTGCTAAGTTAGGTGTTGCATTAGTCACTGCTGGTGGTGGTTTCAC TAACGCTGTTACTCCAATTGCTAATGCTCGTACTGATAGAACTCCAGTTTTGTTCTTGA CAGGTTCTGGTGGCTCTAAGAGATGATGAAACTAACACTTTACAAGCTGGTATTGATCA AGTTGCTATGGCTGCTCCAATTACTAAGTGGGCCCATAGAGTTATGGCAACTGAACAT ATTCCAAGATTGGTCATGCAAGCTATTAGAGGCTGCCTTGTCTGCTCCAAGGGGTCCAG TTTGTTGGATTTGCCATGGGATATCTTGATGAACCAGATTGATGAAGATTCTGTTATCA TCCCTGATTTGGTTTTGTCCGCCCATGGTGCTCATCCAGACCCAGCTGATTTGGATCAA GCCTTGGCACTATTAAGAAAGGCTGAAAGACCAGTTATCGTTTTAGGTAGTGAAGCTT CAAGAACTGCTAGAAAGACCGCTTTGTCAGCTTTCGTTGCTGCCACTGGTGTCCCTGTT TTCGCTGACTATGAAGGTTTATCTATGTTATCTGGTTTGCCTGATGCTATGAGAGGGTGG TTTAGTTCAAAACCTTTACTCTTTCGCTAAGGCCGATGCCGCTCCAGATCTAGTTTGA TGTTGGGTGCTAGATTCGGTTTGAACACCGGTCATGGTTCTGGTCAATTAATT
TACGCTAGAGCTGGTGCTAAGTTAGAGCGGTGTTGCATTAGTCACGCCGCTGGTGGTGGTTCAG TAACGCTGTTACTCCAATTGCTAATGCTCGTACTGATAGAACTCCAGTTTTGTTCTTGA CAGGTTCTGGTGCTTTAAGAGATGATGATAGAACTAACACTTTACAAGCTGGTATTGATCA AGTTGCTATGGCTGCTCCAATTACTAAGTGGGCCCATAGAGTTATGGCAACTGAACAT ATTCCAAGATTGGTCATGCAAGCTATTAGAGGCGCCCATAGAGTTATGGCAACTGAACAT ATTCCAAGATTGGTCATGCAAGCTATTAGAGGCTGCCTTGTCTGCTCCAAGGGGTCCAG TTTGTTGGATTTGCCATGGGATATCTTGATGAACCAGATTGATGAAGATTCTGTTATCA CCCTGATTTGGTTTTGTCCGCCCATGGTGCTCATCCAGACCCAGCTGATTTGGATCAA GCCTTGGCACTATTAAGAAAGGCTGAAAGACCAGTTATCGTTTTAGGTAGTGAAGCTT CAAGAACTGCTAGAAAGACCGCTTTGTCAGCTTTCGTTGCTGCCACTGGTGTCCCTGTT TTCGCTGACTATGAAGGTTTATCTATGTTATCTGGTTTGCCTGATGCTATGAGAGGTGG TTTAGTTCAAAACCTTTACTCTTTCGCTAAGGCCGATGCCGCTCCAGATCTAGTTTTGA TGTTGGGTGCTAGATTCGGTTTGAACACCGGTCATGGTTCTGGTCAATTAATT
TAACGCTAGTACTCCAATTGCTAATGCTCGTACTGATAGAACTCCAGTTTTGGTTCTGA CAGGTTCTGGTGCTTTAAGAGATGATGATAGAACTAACACTTTACAAGCTGGTATTGATCA AGTTGCTATGGCTGCTCCAATTACTAAGTGGGCCCATAGAGTTATGGCAACTGAACAT ATTCCAAGATTGGTCATGCAAGCTATTAGAGGCTGCCTTGTCTGCTCCAAGGGGTCCAG TTTGTTGGATTTGCCATGGCAAGCTATTAGAGGCTGCCTGGTCGCCCAGGGGTCCAG CCCTGATTTGGTTTTGTCCGCCCATGGTGCTCATCCAGACCCAGCTGATTTGGATTATCA GCCTTGGCACTATTAAGAAAGGCTGAAAGACCAGTTATCGTTTAGGTAGTGAAGACT CAAGAACTGCTAGAAAGACCGCTTTGTCAGCTTTCGTTGCTGCCACTGGTGTCCCTGTT TTCGCTGACTATGAAAGACCGCTTTGTCAGCTTTCGTTGCTGCCACTGGTGTCCCTGTT TTCGCTGACTATGAAGGTTTATCTATGTTATCTGGTTTGCCTGATGCTATGAGAGGTGG TTTAGTTCAAAACCTTTACTCTTTCGCTAAGGCCGATGCCGCTCCAGATCTAGTTTTGA TGTTGGGTGCTAGATTCGGTTTGAACACCGGTCATGGTTCTGGTCAATTAATT
CAGGTTCTGGTGCTTTAAGAGATGATGATGAAACTAACACTTTACAAGCTGGTATTGATCA AGTTGCTATGGCTGCTCCAATTACTAAGTGGGCCCATAGAGTTATGGCAACTGAACAT ATTCCAAGATTGGTCATGCAAGCTATTAGAGGCTGCCTTGTCTGCCCAAGGGGTCCAG TTTGTTGGATTTGCCATGGGATATCTTGATGAACCAGATTGATGAAGATTCTGTTATCA TCCCTGATTTGGTTTTGTCCGCCCATGGTGCTCATCCAGACCCAGCTGATTTGGATCTAA GCCTTGGCACTATTAAGAAAGGCTGAAAGACCAGTTATCGTTTAGGTAGTGAAGCTT CAAGAACTGCTAGAAAGACCGCTTTGTCAGCTTTCGTTGCCGCCACTGGTGTCCCTGTT TTCGCTGACTATGAAAGACCGCTTTGTCAGCTTTCGGTGCCACTGGTGTCCCTGTT TTCGCTGACTATGAAAGGTTAATCTATGTTATCTGGTTTGCCTGATGCTATGAGAGGGTGG TTTAGTTCAAAACCTTTACTCTTTCGCTAAGGCCGATGCCGCTCCAGATCTAGTTTTGA TGTTGGGTGCTAGATTCGGTTTGAACACCGGTCATGGTTCTGGTCAATTAATT
AGTTGCTATGGCTGCTCCAATTACTAAGTGGGCCCATAGAGTTATGGCAACTGAACAT ATTCCAAGATTGGTCATGCAAGCTATTAGAGGCCCATAGAGTTATGGCAACGGAGCCAG TTTGTTGGATTTGCCATGGCAAGCTATTAGAGCTGCCTGTCTGCTCCAAGGGGTCCAG TCCCTGATTTGGTTTTGTCCGCCCATGGTGCTCATCCAGACCCAGCTGATTTGGATCAA GCCTTGGCACTATTAAGAAAGGCTGAAAGACCAGTTATCGTTTAGGTAGTGAAGCTT CAAGAACTGCTAGAAAGACCGCTTGTCAGCTTCGTTGCTGCCACTGGTGTCCCTGTT TTCGCTGACTATGAAAGGCTGCTTGTCAGCTTTGGTGCCACTGGTGTCCCTGTT TTCGCTGACTATGAAGGTTTATCTATGTTATCTGGTTTGCCTGATGCTAGAGGGGGG TTTAGTTCAAAACCTTTACTCTTTCGCTAAGGCCGATGCCGCTCCAGATCTAGTTTTGA TGTTGGGTGCTAGATTCGGTTTGAACACCGGTCATGGTTCGGTCAATTAATT
ATTCCAAGATTGGTCATGCAAGCTATTAGAGCTGCCTTGTCTGCCCAAGGGGTCCAG TTTGTTGGATTTGCCATGGGAAGCTATCTGATGAACCAGATTGATGAAGATTCTGTTATCA TCCCTGATTTGGTTTGTCCGCCCATGGTGCTCATCCAGACCCAGCTGATTTGGATCAA GCCTTGGCACTATTAAGAAAGGCTGAAAGACCAGTTATCGTTTAGGTAGTGAAGGCTG CAAGAACTGCTAGAAAGACCGCTTTGTCAGCTTTCGTTGCTGCCACTGGTGTCCCTGTT TTCGCTGACTATGAAGGTTTATCTATGTTATCTGGTTTGCCTGATGCTATGAGAGGGTGG TTTAGTTCAAAACCTTTACTCTTTCGCTAAGGCCGATGCCGCTCCAGATCTAGTTTTGA TGTTGGGTGCTAGATTCGGTTTGAACACCGGTCATGGTTCTGGTCAATTAATT
TTTGTTGGATTTGCCATGGGATATCTTGATGAACCAGATTGATGAAGATTCTGTTATCA TCCCTGATTTGGTTTGTCCGCCCATGGTGCTCATCCAGACCCAGCTGATTTGGATCAA GCCTTGGCACTATTAAGAAAGGCTGAAAGACCAGTTATCGTTTTAGGTAGTGAAGACTG CAAGAACTGCTAGAAAGACCGCTTTGTCAGCTTTCGTTGCCGCACTGGTGTCCCTGTT TTCGCTGACTATGAAGGTTTATCTATGTTATCTGGTTTGCCTGATGCTATGAGAGGTGG TTTAGTTCAAAACCTTTACTCTTTCGCTAAGGCCGATGCCGCTCCAGATCTAGTTTGA TGTTGGGTGCTAGATTCGGTTTGAACACCGGTCATGGTTCTGGTCAATTAATT
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