

**Supplementary information for**  
**Cascaded de novo biosynthesis of lacto-proteins from CO<sub>2</sub> by engineered *Pichia***  
***pastoris***

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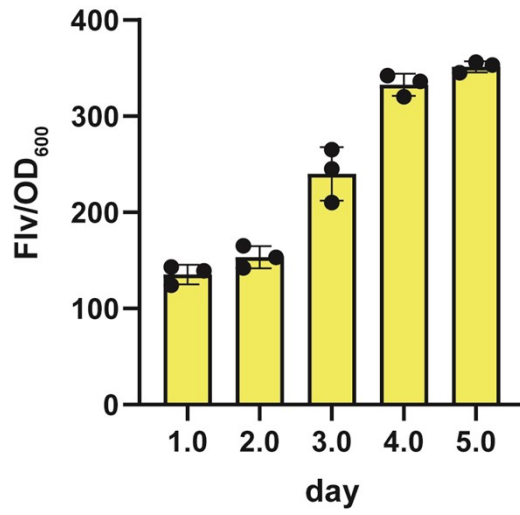
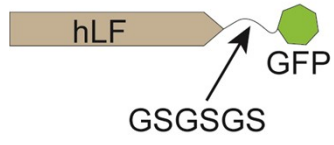
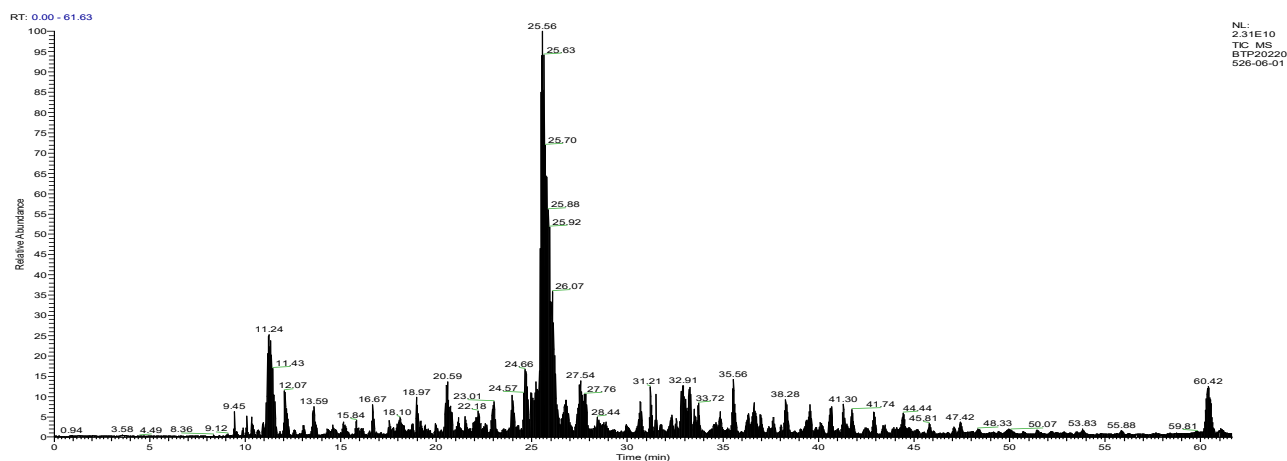


Fig. S1 The fluorescence in the supernatant of the fermentation broth.



Protein ID	Peptides	Sequence coverage [%]	Mol. weight [kDa]	Sequence length	Score	Intensity
HLF	57	65.1	76.164	691	323.31	5470000000
A0A1B2JHD1	45	45.5	74.126	677	323.31	3222700000
A0A1B2J5W9	32	42.7	70.741	656	263.37	4013800000
A0A1B2JGS7	24	34.6	69.65	645	165.9	923040000
A0A1B2JII2	16	22.3	73.911	663	138.3	625050000

Protein ID: protein number in the Uniprot database; Peptides: the number of all peptides of the protein identified;

Sequence coverage [%]: the coverage of all peptides identified by the protein; Mol. weight [kDa]: the molecular weight of the corresponding protein; Sequence length: The total number of protein theoretical amino acids; Score: Protein scoring;

Intensity: Protein abundance.

Fig. S2 The protein mass spectrometry of protein synthesized by shake flask fermentation. The table shows only 5 proteins in the sample.

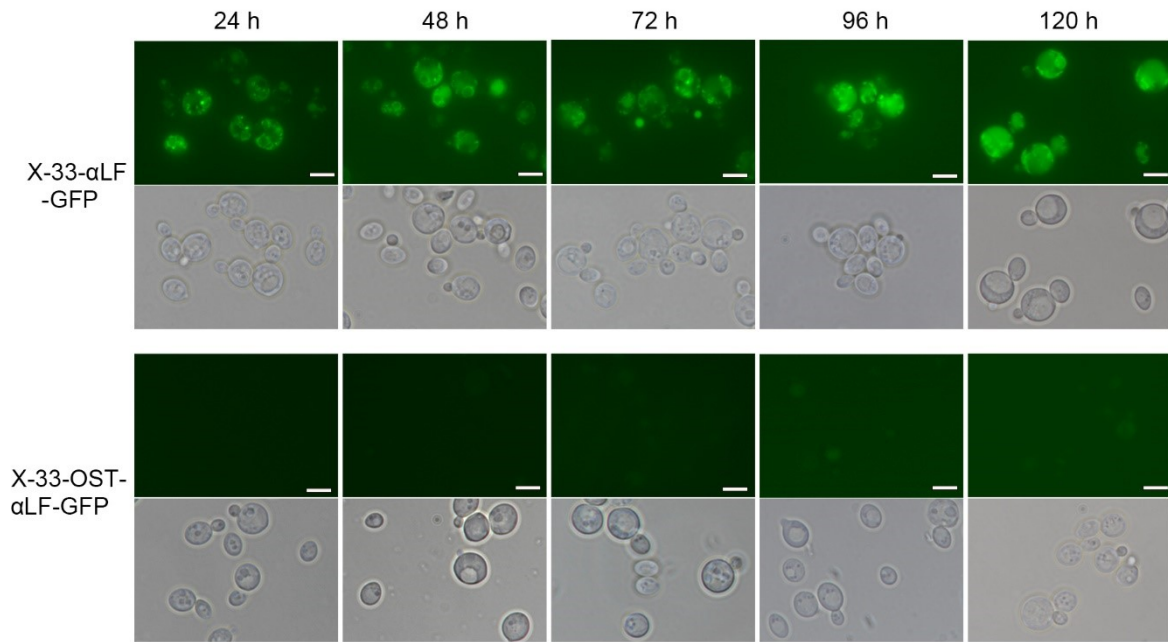
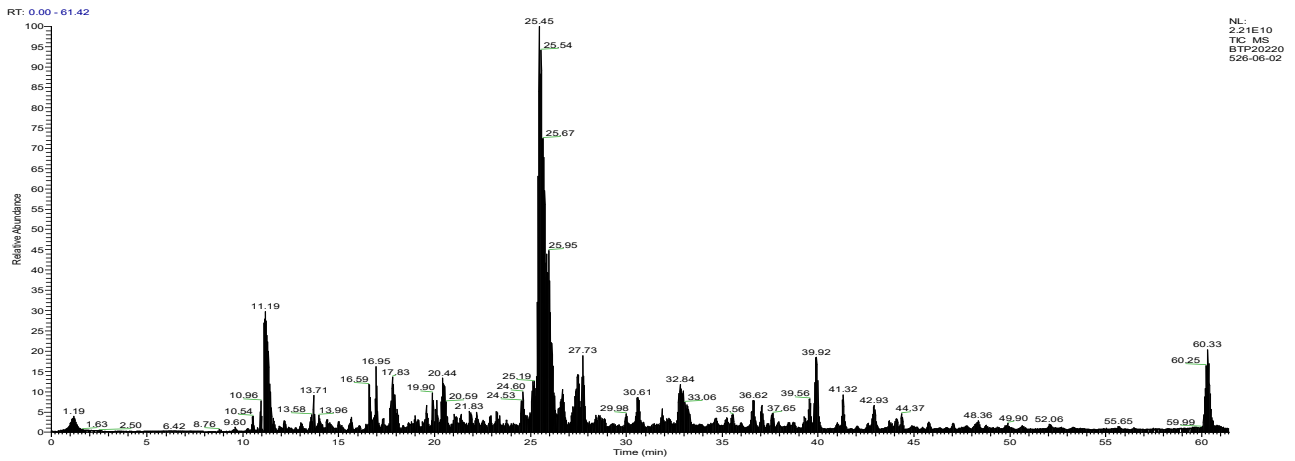


Fig. S3 The fluorescence distribution of hLF-GFP in different *P. pichia* strains. Bars = 5 μm.



Protein ID	Peptides	Sequence coverage [%]	Mol. weight [kDa]	Sequence length	Score	Intensity
HLF	19	25.6	76.164	691	312.46	1295400000
A0A1B2JII2	2	18.4	73.911	663	184.98	583410000
A0A1B2J5W9	7	23.3	70.741	656	138.61	388380000
A0A1B2JGF9	5	19.2	78.934	707	108.72	573630000

A0A1B2JFF8	11	24.4	55.352	496	82.512	374650000
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Protein ID: protein number in the Uniprot database; Peptides: the number of all peptides of the protein identified;

Sequence coverage [%]: the coverage of all peptides identified by the protein; Mol. weight [kDa]: the molecular weight of the corresponding protein; Sequence length: The total number of protein theoretical amino acids; Score: Protein scoring;

Intensity: Protein abundance.

Fig. S4 The protein mass spectrometry of protein synthesized by 3-L bioreactor. The table shows only 5 proteins in the sample.

Table S1 Molecular chaperones used in the study

Name	Sequence ID	Promoter
BIP	NP_012500.3	pGAP
PDI	NP_009887.1	pGAP
ERO1	NP_013576.1	pGAP
SEC12	NP_014423.1	pGAP
CUP5	NP_010887.3	pGAP
ScERV29	NP_011800.3	pGAP
PsERV29	ANZ77560	pGAP
CPR5	NP_010590.3	pGAP

Table S2 Solubilization tags used in the study

Name	Protein Sequence	Promoter
TF	MQVSVETTQGLGRRVTITIAADSIETAVKSELVNVAKKVRIDGFRKGKVP MNIVAQRYGASVRQDVLGDLMSRNFID AIIKEKINPAGAPTYVPG EYKLGEDFTYSVEFEVYPEVELQGLEAIEVEKPIVEVTDADVDGMLD LTRKQQATWKEK DGAVEAEDRVTIDFTGSVDGEEFEGGKASDFVLAMGQGRMIPGFEDGIKGHKAGEEFTIDVTFPEEYHAENLKGK AAKFAINLKKVEERELPELTAEFIKRFGVEDGSVEGLRAEVRKNMERELKSAIRNRVKSQAIEGLVKANDIDVPAALI DSEIDVLRQAAQRFGGNEKQALELPRELFEEQAKRRVVVGLLLGEVIRTNELKADEERVKGLIEEMASAYEDPKE VIEFYSKNELMDNMRNVALEEQAVEAVLAKAKVTEKETTFNELMNQQA MKIEEGKLV I WINGDKGYNGLAEVGKKFEKDTGIKVTVEHPDKLEEKFPQVAATGDGPD IIFWAHDRFGGYAQSGL LAEITPDKAFQDKLYPFTWDAVRYNGKLIAYPIAVEALSLIYNKDLLPNPPKTWEEIPALDKELKAKGKSALMFNLQE	pGAP
MBP	PYFTWPLIAADGGYAFKYENK YDIKDVGV DNAGAKAGLTFLVDLIK NKMADTDYSIAEAAFNKGETAMTINGP WAWSNIDTSKVNYGVTLP TFKGQSPKPFVGLSAGINAASPNKELAKEFLENYLLTDEGLEAVNKDKPLGAVALK SYEEELVKDPRI AATMENAQKGEIMP NIPQMSAFWYAVRTAVINAASGRQTVDEALKDAQT	pGAP
TrxA	MSDKIIHLTDDSFDTDVLKADGAILVDFWAEWCGPCKMIAPILDEIADEYQGKLTVAKLNIDQNP GTAPKYGIRGIPT LLL FKNGEVAATKVGALSKGQLKEFLDANLA MNKEILAVVEAVSNEKALPREKIFEAL ESALATATKKKYEQEIDVRVQIDRKSGDFDTFRRWL VVDEVTQPTKEITLE AARYEDES LNLGDYVEDQIESVTFDRITTQAKQVIVQKVREAERAMVVDQFREHEGEIITGVVKKVNRDNISLDLG NNAEAVILREDMLPRENFRPGDRVRGVLVSVRPEARQAQLFVTRSKPEMLIELFRIEVPEIGEEVIEIKAAARDPGS	pGAP
NusA	RAKIAVKTNDKRIDPVGACVGMRGARVQAVSTELGGERIDIVLWDDNPAQFVINAMAPADVASIVVDEDKHTMDIA VEAGNLAQAIGRNQNVRLASQLSGWELNVMTVDDLQAKHQAEAHAAIDTFTKYLDIDEDFATV LVEEGFSTLEEL AYVPMKELLEIEGLDEPTVEALRERAKNALATIAQAQEE SLGDNKPADDLLNLEGVDRDLAFKLAARGVCTLEDLAE QGIDDLADIEGLTDEKAGALIMAARNICWFGDEA	pGAP
GST	MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEFPNLPYYIDGDVKLTQSM AIIRYIADK HNMLGGCPKERA EISMLEGAVLDIRYGVSR IAYSKDFETLKVDFLSKLP EMLKMFEDRLCHKTYLNGDHVTHPDFM LYDALDVVLYMDPMCLDAFPKLVCFKKRIEAI PQIDKYLKSSKYIAWPLQGWQATFGGGDHPPK	pGAP
SUMO	DSEVNQEAKPEVKPEVKPETHINLKVSDGSSEIFFKIKKTTPLRRLMEAF AKRQGGKEMDSL RFLYDGIRIQADQAPE DLDMEDNDIIEAHREQIG	pGAP

Table S3 Signal peptides used in the study

Name	Gene Sequence	Promoter
OST	ATGAGGCAGGTTTGGTTCTCTTGGATTGTGGGATTGTTCTATGTTTTTCAACGTGTCTTCTGCT	pAOX1
INU	ATGAAGTTAGCATACTCCCTCTTGCTTCCATTGGCAGGAGTCAGTGCTTCAGTTATCAATTACAAGAGA	pAOX1
MEL	ATGAGAGCTTTCTTGTTTCTCACCGCATGCATCAGTTGCCAGGCGTTTTTGGGGTGAACGAGACT	pAOX1
PHO	ATGTTGAAGTCAGCCGTTTATTCAATTTAGCCGTTCTTTGGTTAATGCA	pAOX1
SUC	ATGCTTTTGCAAGCTTTCCTTTTCCTTTTGGCTGGTTTTGCAGCCAAAATATCTGCA	pAOX1



Table S4 Catalytic performance of CuZnAlC catalyst for CO<sub>2</sub> hydrogenation to methanol

Time on Stream	CO <sub>2</sub> conversion (%)	Methanol Selectivity (%)	Space time yield (gMeOH gcat <sup>-1</sup> h <sup>-1</sup> )
0-24 h	8.5	79	0.038
48-72 h	8.0	75	0.034

Reaction conditions: 2 g of catalyst, H<sub>2</sub>/CO<sub>2</sub>/N<sub>2</sub> at 72/24/4, 6000 mL gcat<sup>-1</sup> hour<sup>-1</sup>, 3 MPa, 200 °C.

Table S5 Molecular formula and Molecular mass and Sequence of lacto-proteins

Name	Uniprot ID	Molecular Formula	Molecular mass	Moles of Carbon atoms	production	yield
hLF	P02788	C <sub>3338</sub> H <sub>5233</sub> N <sub>957</sub> O <sub>1013</sub> S <sub>37</sub>	76165	3338	56 mg/L	1.12 mg/g <sub>TC-methanol</sub>
OPN	P10451	C <sub>1260</sub> H <sub>1916</sub> N <sub>360</sub> O <sub>477</sub> S <sub>4</sub>	29836	1260	78 µg/L	
LA	P00709	C <sub>623</sub> H <sub>978</sub> N <sub>156</sub> O <sub>194</sub> S <sub>10</sub>	11288	623	3.2 mg/L	0.064 mg/g <sub>TC-methanol</sub>

Sequence of Lactoferrin:

MKLVFLVLLFLGALGLCLAGRRRSVQWCAVSQPEATKCFQWQRNMRKVRGPPVSCIKRDSPIQCIQAIENRADAVTLDDGGFIYEAGLAPYKLRPVAEEVYGTERQPRT  
 HYYAVAVVKKGGSFQLNELQGLKSCHTGLRRTAGWNVPIGTLRPFLNWTGPPEPIEAAVARFFSASCVPGADKGQFPNLCRLCAGTGENKCAFSSQEPYFSYSGAFK  
 CLRDGAGDVAFIRESTVFEDLSDEAERDEYELLCPDNTRKPVDFKDKCHLARVPSHAVVARSVNGKEDAIWNLLRQAQEKFGDKSPKFQLFGSPSGQKDLLFKDSAI  
 GFSRVPPRIDSGLYLGSYFTAQNLKSEEEVAARRARVWCAVGEQELRKCQWSGLSEGSVTCSSASTTEDCIALVLKGEADAMSLDGGYVYTAGKCGLVPVLAE  
 NYKSQQSSDPDPCVDRPVEGYLAVAVVRRSDTSLTWNVSVKGGKKSCHTAVDRTAGWNIPMGLLFNQGTGCKFDEYFSQSCAPGSDPRSNLALCALCIGDEQGENKCV  
 NSNERYYGYTGAFRCLAENAGDVAFVKDVTVLQNTDGNNEAWAKDLKLADDFALLCLDGKRKPVTEARSCHLAMAPNHAVVSRMDKVERLKQVLLHQQAKFGRNGS  
 DCPDKFCLFQSETKNLLFNDNTECLARLHGKTTYEKYLGQYVAGITNLKCKCSTSPILLEACEFLRK

Sequence of Osteopontin:

MRIAVICFLLGITCAIPVKQADSGSSEEKQLYNKYPDAVATWLNPDPSQKQNLAPQNAVSSSEETNDFKQETLPSKSNESHDMDDMDEDDDDHVDSQDSIDSNDS  
 DDVDDTDDSHQSDSHHSDESDELVTDFPTDLPATEVFTPVPTVDTYDGRGDSVVYGLRSKSKKFRPDIQYPDATDEDITSHMESEELNGAYKAIPVAQDLNAPSD  
 WDSRGKDSYETSQLDDQSAETHSHKQSRLYKRKANDESNEHSDVIDSQELSKVSREFHSHEFHSHEDMLVDPKSKEEDKHLKFRISHELDSASSEVN

Sequence of Lactalbumin:

MRFFVPLFLVGILFPAILAKQFTKCELSQLLKDIDGYGGIALPELICTMFHTSGYDTQAIVENNESTEYGLFQISNKLWCKSSQVPQSRNICDISCDKFLDDDDITDDIMCAKKI  
 LDIKGIDYWLAHKALCTEKLEQWLCEKL

The yellow mark is the signal peptide, not included in the Molecular mass

Table S6 Comparative of human lacto-proteins yields in different host

Host	lactoferrin origen	Vector	Expression level	Reference
<i>Pichia pastoris</i>	HLF	pPIC9K	1200 mg/L	1
	HLF	pPIC3.5K	115 mg/L	2
<i>Aspergillus nidulans</i>	HLF	pAL3hLFT	5 mg/l	3
<i>Aspergillus oryzae</i>	HLF	pAhLFG	25 mg/l	4
<i>Aspergillus awamori</i>	HLF	pPLF-19	2 g/l	5
<i>Pichia pastoris</i>	HALA	pPICZa	56.3 mg/L	6

Table S7 The strains used in this study

Name of Strain	Genotype of the Strain
X-33	Wild type
X-33-ahLF	pAOX1-ahLF::pAOX1
X-33-PGAP-ahLF	pGAP-ahLF::pGAP
X-33-LF-GFP	pAOX1-ahLF-GFP::pAOX1
X-33-LF-GFP-sec12	pAOX1-ahLF-GFP::pAOX1; pGAP-sec12::pGAP
X-33-LF-GFP-odhl	pAOX1-ahLF-GFP::pAOX1; pGAP-odhl::pGAP
X-33-ahLF-BIP	pAOX1-ahLF::pAOX1; pGAP-BIP::pGAP
X-33-ahLF-PDI	pAOX1-ahLF::pAOX1; pGAP-PDI::pGAP
X-33-ahLF-EROI	pAOX1-ahLF::pAOX1; pGAP-EROI::pGAP
X-33-ahLF-SEC12	pAOX1-ahLF::pAOX1; pGAP-SEC12::pGAP
X-33-ahLF-CUP5	pAOX1-ahLF::pAOX1; pGAP-CUP5::pGAP
X-33-ahLF-ScERV29	pAOX1-ahLF::pAOX1; pGAP-ScERV29::pGAP
X-33-ahLF- PsERV29	pAOX1-ahLF::pAOX1; pGAP-PsERV29::pGAP
X-33-ahLF- CPR5	pAOX1-ahLF::pAOX1; pGAP-CPR5::pGAP
X-33- $\alpha$ -TFhLF	pAOX1- $\alpha$ -TFhLF::pAOX1; pGAP-CPR5::pGAP
X-33- $\alpha$ -MBPhLF	pAOX1- $\alpha$ -MBPhLF::pAOX1; pGAP-CPR5::pGAP
X-33- $\alpha$ -TrxAhLF	pAOX1- $\alpha$ -TrxAhLF::pAOX1; pGAP-CPR5::pGAP
X-33- $\alpha$ -NusAhLF	pAOX1- $\alpha$ -NusAhLF::pAOX1; pGAP-CPR5::pGAP
X-33- $\alpha$ -GSThLF	pAOX1- $\alpha$ -GSThLF::pAOX1; pGAP-CPR5::pGAP
X-33- $\alpha$ -SUMOhLF	pAOX1- $\alpha$ -SUMOhLF::PAOX1; pGAP-CPR5::pGAP
X-33-OST-hLF	pAOX1-OSThLF::pAOX1; pGAP-CPR5::pGAP
X-33-INU-hLF	pAOX1-INUhLF::pAOX1; pGAP-CPR5::pGAP
X-33-MEL-hLF	pAOX1-MELhLF::pAOX1; pGAP-CPR5::pGAP
X-33-PHO-hLF	pAOX1-PHOhLF::pAOX1; pGAP-CPR5::pGAP
X-33-SUC-hLF	pAOX1-SUCChLF::pAOX1; pGAP-CPR5::pGAP
X-33- OST-ahLF	pAOX1-OST-ahLF::pAOX1; pGAP-CPR5::pGAP
X-33- INU-ahLF	pAOX1- INU-ahLF::pAOX1; pGAP-CPR5::pGAP
X-33- SUC-ahLF	pAOX1- SUC-ahLF::pAOX1; pGAP-CPR5::pGAP
X-33- OST-ahLF-Bcy1	pAOX1-OST-ahLF::pAOX1; pGAP-CPR5::pGAP; pGAP-Bcy1::Bcy1
X-33- OST-ahLF-Rlii	pAOX1-OST-ahLF::pAOX1; pGAP-CPR5::pGAP; pGAP- Rlii:: Rlii
X-33- OST-ahLF-Pab1	pAOX1-OST-ahLF::pAOX1; pGAP-CPR5::pGAP; pGAP- Pab1:: Pab1
X-33- OST-ahLF-4A	pAOX1-OST-ahLF::pAOX1; pGAP-CPR5::pGAP; pGAP- eIF4A:: eIF4A

X-33- OST-ahLF- 4E	pAOX1-OST-ahLF::pAOX1; pGAP-CPR5::pGAP; pGAP- eIF4E:: eIF4E
X-33- OST-ahLF- 4G	PAOX1-OST-ahLF::pAOX1; pGAP-CPR5::pGAP; pGAP- eIF4G:: eIF4G
X-33-OST-αLF-4E-AFT1	pAOX1-OST-ahLF::pAOX1; pGAP-CPR5::pGAP; pGAP- eIF4E:: eIF4E; pGAP- AFT1::HIS4
X-33-OST-αLF-4E-HAC1	pAOX1-OST-ahLF::pAOX1; pGAP-CPR5::pGAP; pGAP- eIF4E:: eIF4E; pGAP- HAC1:: HIS4
X-33-OST-αLF-4E-Mxr1	pAOX1-OST-ahLF::pAOX1; pGAP-CPR5::pGAP; pGAP- eIF4E:: eIF4E; pGAP- Mxr1:: HIS4
X-33-OST-αLF-4E-FHL1P	pAOX1-OST-ahLF::pAOX1; pGAP-CPR5::pGAP; pGAP- eIF4E:: eIF4E; pGAP- FHL1P:: HIS4

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Table S8 The primers used in this study

Name of primer	Sequence of primer
AOX-LINE.FOR	AAACGCTGTCTTGGAACCTAATATGAC
AOX-LINE.REV	AAACTGTCAGTTTTGGGCCATTTGG
HLF-ZA.FOR	AGAAAAGAGAGGCTGAAGCTGGTAGAAGGAGAAGGTCTGTTCAATGGTG
HLF-ZA.REV	GATGATGATGATGATGTTTTCTCAAAAATTCACAAGCTTCCAACAATG
ZA-YZ.FOR	TCGCAGCATCCTCCGCATT
ZA-YZ.REV	TCCAACCAGCAGTCCTATCAACA
ZA-HLF.FOR	GAATTTTTGAGAAAACATCATCATCATCATTGAGTTTGTAGCC
ZA-HLF.REV	AACAGACCTTCTCCTTCTACCAGCTTCAGCCTCTCTTTTCTCGAG
HLF-PLS.FOR	TTTCAATCAATTGAACAACACTATATGAGATTTCTTCAATTTTTACTGCTGTTTTA
HLF-PLS.REV	ACACCAAGACATTTCTACAAAAATGATCTCATGACCAAAATCCCTTAACGTG
PGAP.FOR	GTTAAGGGATTTTGGTCATGAGATCATTTTTGTAGAAATGTCTTGGTGTCTCG
PGAP.REV	CAGTAAAAATTGAAGGAAATCTCATATAGTTGTTCAATTGATTGAAATAGGGAC AA
GFP.FOR	GAGAAAAGGTAGCGGCAGCGGCAGCATGGGTAAGGGAGAAGAAGCTTTTCAC
GFP.REV	CTGGGCCACGTGAATTCTTATTTGTACAGTTCATCCATGCCATGTGTAAT
HLF-GFP.FOR	GGCATGGATGAACTGTACAAATAAGAATTCACGTGGCCCAGCC
HLF-GFP.REV	CCCTTACCCATGCTGCCGCTGCCGCTACCTTTTCTCAAAAATTCACAAGCTTCC AAC
MCHERRY-SEC12.REV	GATGGTCGACGGCGCTATTCTTGTACAGCTCGTCCATGCC
SEC12-MCHERRY.FOR	AAAGTACAATAGGGGGGCCAAAGAACAAAAACTCATCTCAGAAGAGGATCT
SEC12P.FOR	TTGAACAACACTATTTTCAAACGATGGACAATATAACTGACAGACTACCATC
SEC12P.REV	CTTCTGAGATGAGTTTTTGTCTTTGGCCCCCTATTGTACTTTGC
VSEC12.FOR	ACGAGCTGTACAAGAATAGCGCCGTCGACCATCATC
VSEC12P.REV	AGTCTGTCAGTTATATTGTCCATCGTTTTCGAAATAGTTGTTCAATTGATTGA AAGGACGAACAAAAACTCATCTCAGAAGAGGATCTGATGGCCATCATCAAGGA
MCHERRY-ODH1.FOR	GTTCA
MCHERRY-ODH1.REV	AGTCATGTCTAAGGCTAAACTCACTTGTACAGCTCGTCCATGCC
ODH1.FOR	AATTGAACAACACTATTTTCAAACGATGGCGAAGGCAGATGGCAG
ODH1.REV	GCCATCAGATCCTCTTCTGAGATGAGTTTTTGTTCGTCCTTCCAACCTTCTTCA AATGTATG
VODH1.FOR	GGACGAGCTGTACAAGTGAGTTTTAGCCTTAGACATGACTGTTCC
VODH1.REV	AACTGCCATCTGCCTTCGCCATCGTTTTCGAAATAGTTGTTCAATTGATTGA
BIP.FOR	CAATTGAACAACACTATTTTCAAACGATGTTTTTCAACAGACTAAGCGCTGG
BIP.REV	ATGATGATGATGGTCTACAATTCGTCGTGTTTCAAATAATCAC
VBIP.FOR	CGAACACGACGAATTGTAGGACCATCATCATCATCATTGAGTT
VBIP.REV	TAGTCTGTTGAAAAACATCGTTTTCGAAATAGTTGTTCAATTGATTGAAAT
PDI.FOR	TTCAATCAATTGAACAACACTATTTTCAAACGATGAAGTTTTCTGCTGGTGCCG
PDI.REV	AATGATGATGATGATGATGGTCTTACAATTCATCGTGAATGGCATCTTC
VPDI.FOR	AATGATGATGATGATGATGGTCTTACAATTCATCGTGAATGGCATCTTC

VPDI.REV	CGGCACCAGCAGAAAACCTTCATCGTTTCGAAATAGTTGTTCAATTGATTGAAA
EROI.FOR	CGGCACCAGCAGAAAACCTTCATCGTTTCGAAATAGTTGTTCAATTGATTGAAA
EROI.REV	TCAATGATGATGATGATGATGGTCTTATTGTATATCTAGCTTATAGGAAATAAGC TCTCG
VERO1.FOR	TCAATGATGATGATGATGATGGTCTTATTGTATATCTAGCTTATAGGAAATAAGC TCTCG
VERO1.REV	GCAATGGCGGTTCTTAATCTCATCGTTTCGAAATAGTTGTTCAATTGATTGAAAT
SEC12.FOR	AATCAATTGAACAACCTATTTTCGAAACGATGAAGTTCGTGACAGCTAGTTATAAC
SEC12.REV	ACTCAATGATGATGATGATGATGGTCTCAAGCATCATCTATTTCTCGAAAAGTT GC
VSEC12.FOR	GAGAAATAGATGATGCTTGAGACCATCATCATCATCATTGAGTTTTA
VSEC12.REV	AACTAGCTGTCACGAACTTCATCGTTTCGAAATAGTTGTTCAATTGATTGAAATA G
CUP5.FOR	CAATTGAACAACCTATTTTCGAAACGATGACTGAATTGTGTCCTGTCTACG
CUP5.FOR	CTCAAGATGTTGTCTGTTAAGACCATCATCATCATCATTGAGTTTTA
CUP5.REV	ATGATGATGATGATGGTCTTAACAGACAACATCTTGAGTAGCCC
VCUP5.REV	AGACAGGACACAATTCAGTCATCGTTTCGAAATAGTTGTTCAATTGATTGAAAT AG
SCERV29.FOR	AATCAATTGAACAACCTATTTTCGAAACGATGTCTTACAGAGGACCTATTGAAAT
SCERV29.REV	ATGATGATGATGATGGTCTTAGTAAATCTTCTTTCTTTTCATCAACGGATAATTCA C
VSCERV29.FOR	AAAAGAAGAAGATTTACTAGGACCATCATCATCATCATTGAGTTTTA
VSCERV29.REV	CAATAGGTCCTCTGTAAGACATCGTTTCGAAATAGTTGTTCAATTGATTGAAATA G
VPSERV29.FOR	AAAAGAAAAAGATCTACTAAGACCATCATCATCATCATTGAGTTTTA
VPSERV29.REV	GAAACTGAGGGCGATAAGACATCGTTTCGAAATAGTTGTTCAATTGATTGAAAT AG
PSERV29.FOR	AATTGAACAACCTATTTTCGAAACGATGTCTTATCGCCCTCAGTTTCAAC
PSERV29.REV	ATGATGATGATGATGGTCTTAGTAGATCTTTTTCTTTTCATCAAAAACCTCAAC
CPR5.FOR	AATTGAACAACCTATTTTCGAAACGATGAAGCTTCAATTTTTTTCTTTATTACCT
CPR5.REV	TCAATGATGATGATGATGATGGTTCGATGCAGTTTAGAGTTCATCGTGGG
VCPR5.FOR	GATGAACCTCTAAACTGCATCGACCATCATCATCATCATTGAGTTTTA
VCPR5.REV	AGGAAAAAATTGAAGCTTCATCGTTTCGAAATAGTTGTTCAATTGATTGAAATA GGGAC
GST.FOR	TCGAGAAAAGAGAGGCTGAAGCTATGTCCCCTATACTAGGTTATTGGAAA
GST.REV	TGAACAGATCTCCTTCTACCTTTTGGAGGATGGTCGCCAC
MBP.FOR	CTCGAGAAAAGAGAGGCTGAAGCTATGAAAATCGAAGAAGGTAAACTGGTAA
MBP.REV	TGCACACCATTGAACAGATCTCCTTCTACCAGTCTGCGCGTCTTTTCAGGG
NUSA.FOR	CTCGAGAAAAGAGAGGCTGAAGCTATGAACAAAGAAATTTTGGCTGTAGTTG
NUSA.REV	CATTGAACAGATCTCCTTCTACCCGCTTCGTCACCGAACCCAG
SUMO.FOR	TCTCGAGAAAAGAGAGGCTGAAGCTATGGACTCAGAAGTCAATCAAGAAGCTA

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AGC

SUMO.REV	ACACCATTGAACAGATCTCCTTCTACCTCTAGACTGCAGGTCGACAAGCT
TF.FOR	TCTCGAGAAAAGAGAGGCTGAAGCTATGCAAGTTTCAGTTGAAACCACTCAA
TF.REV	ACACCATTGAACAGATCTCCTTCTACCCGCCTGCTGGTTCATCAGC
TRXA.FOR	TCTCGAGAAAAGAGAGGCTGAAGCTATGAGCGATAAAATTATTCACCTGACTG
TRXA.REV	ACCATTGAACAGATCTCCTTCTACCGGCCAGGTTAGCGTCGAGGAA
INU.FOR	CCTCTTGCTTCCATTGGCAGGAGTCAGTGCTTCAGTTATCAATTACAAGAGAGG TAGAAGGAGATCTGTTCAATGGTG
INU.REV	AAGCACTGACTCCTGCCAATGGAAGCAAGAGGGAGTATGCTAACTTCATCGTT TCGAATAATTAGTTGTTTTTTGATCT
MEL1.FOR	CCGCATGCATCAGTTTGCCAGGCGTTTTTGGGGTGAACGAGACTGGTAGAAG GAGATCTGTTCAATGGTG
MEL1.REV	GGCAAACCTGATGCATGCGGTGAGAAACAAGAAAGCTCTCATCGTTTCGAATAA TTAGTTGTTTTTTGATCTTC
OST.FOR	CTTGGATTGTGGGATTGTTCCCTATGTTTTTTCAACGTGTCTTCTGCTGGTAGAA GGAGATCTGTTCAATGGTG
OST.REV	GAAAAACATAGGAACAATCCCACAATCCAAGAGAACCAAACCTGCCTCATCG TTTCGAATAATTAGTTGTTTTTTGATC
PHO11.FOR	TATTCAATTTTAGCCGCTTCTTTGGTTAATGCAGGTAGAAGGAGATCTGTTCAA TGGTG
PHO11.REV	AAGCGGCTAAAATTGAATAAACGGCTGACTTCAACATCGTTTCGAATAATTAGT TGTTTTTTGATCTTC
SUC.FOR	CCTTTTCCTTTTGGCTGGTTTTTGCAGCCAAAATATCTGCAGGTAGAAGGAGATC TGTTCAATGGTG
SUC.REV	AAAACCAGCCAAAAGGAAAAGGAAAGCTTGCAAAGCATCGTTTCGAATAATTA GTTGTTTTTTGATCTTC
INU-AFACTOR.FOR	CCTCTTGCTTCCATTGGCAGGAGTCAGTGCTTCAGTTATCAATTACAAGAGAGC TCCAGTCAACACTACAACAGAAGAT
INU-AFACTOR.REV	AAGCACTGACTCCTGCCAATGGAAGCAAGAGGGAGTATGCTAACTTCATCGTT TCGAATAATTAGTTGTTTTTTGATCT
MEL1-AFACTOR.FOR	CCGCATGCATCAGTTTGCCAGGCGTTTTTGGGGTGAACGAGACTGCTCCAGTC AACACTACAACAGAAG
MEL1-AFACTOR.REV	GGCAAACCTGATGCATGCGGTGAGAAACAAGAAAGCTCTCATCGTTTCGAATAA TTAGTTGTTTTTTGATCTTC
OST-AFACTOR.FOR	CTTGGATTGTGGGATTGTTCCCTATGTTTTTTCAACGTGTCTTCTGCTGCTCCAG TCAACACTACAACAGAAG
OST-AFACTOR.REV	GAAAAACATAGGAACAATCCCACAATCCAAGAGAACCAAACCTGCCTCATCG TTTCGAATAATTAGTTGTTTTTTGATC
PHO11-AFACTOR.FOR	TATTCAATTTTAGCCGCTTCTTTGGTTAATGCAGCTCCAGTCAACACTACAACA GAAGAT
PHO11-AFACTOR.REV	AAGCGGCTAAAATTGAATAAACGGCTGACTTCAACATCGTTTCGAATAATTAGT

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	TGTTTTTGGATCTTC
SUC-AFACTOR.FOR	CCTTTTCCTTTTGGCTGGTTTTGCAGCCAAAATATCTGCAGCTCCAGTCAACAC TACAACAGAAG
SUC-AFACTOR.REV	AAAACCAGCCAAAAGGAAAAGGAAAAGCTTGCAAAGCATCGTTTTGAATAATTA GTTGTTTTTGGATCTTC
GAP-Bcy1-F	ACTATTTTCGAAACGATGACAGCATAACACGGACG
GAP-Bcy1-R	GGCTAAAACCTAGATCTTGGTGGGATCTTGCAG
GAP-Bcy1-out-F	CAAGATCTAGGTTTTAGCCTTAGACATGACTGTTCC
GAP-Bcy1-out-R	CTGTCATCGTTTCGAAATAGTTGTTCAATTGATTGAA
GAP-eIF4A-F	ATTGAACAACCTATATGTCTGAAGGTATTATTGAAATCGACACTAACT
GAP-eIF4A-R	GGCTAAAACCTAAGACTCATTAACTTCTCAGTCTCAAACAA
GAP-eIF4A-out-F	AATGAGTCTTAGGTTTTAGCCTTAGACATGACTGTTCC
GAP-eIF4A-out-R	CAGACATATAGTTGTTCAATTGATTGAAATAGGGACAAATA
GAP-eIF4E-F	TTGAACAACCTATATGCTACCAACACCTTTGACCAAAGA
GAP-eIF4E-R	GCTAAAACCTACCTTCGAATAAACCTCCAAACAGTCAAC
GAP-eIF4E-out-F	ATTCGAAGGTAGGTTTTAGCCTTAGACATGACTGTTCC
GAP-eIF4E-out-R	GGTAGCATATAGTTGTTCAATTGATTGAAATAGGGACAAATA
GAP-eIF4G-F	AATTGAACAACCTATATGGAGTGTAATAAAGTCAAAGATCGCC
GAP-eIF4G-R	GGCTAAAACCTAAAGTCCGTTTTTCGCCTCTCTCAG
GAP-eIF4G-out-F	AACGGACTTTAGGTTTTAGCCTTAGACATGACTGTTCC
GAP-eIF4G-out-R	ACTCCATATAGTTGTTCAATTGATTGAAATAGGGACAAATA
GAP-Pab1-F	AATTGAACAACCTATATGTCCCAAATCAAGAACGCCC
GAP-Pab1-R	GGCTAAAACCTCACCTCAGGTCCTTGTATCACTTCT
GAP-Pab1-out-F	ACCTGAGGTGAGTTTTAGCCTTAGACATGACTGTTCC
GAP-Pab1-out-R	GGGACATATAGTTGTTCAATTGATTGAAATAGGGACAAATA
GAP-Rli1-F	TTGAACAACCTATATGAGTGAGAAAAACACACGTATTGCC
GAP-Rli1-R	AAGGCTAAAACCTATAACTCAGTGTTCTCAAGGAAGAAGTAATTACC
GAP-RLI1-OUT-F	ACTGAGTTATAAGTTTTAGCCTTAGACATGACTGTTCC
GAP-RLI1-OUT-R	CTCACTCATATAGTTGTTCAATTGATTGAAATAGGGACAAATA
GAP-AFT1-F	ATTTTCGAAACGATGAACTCCGTTAGTCCCTCCTAAC
GAP-AFT1-R	AGGCTAAAACCTAGCTTTTCCTCTCTCCCAAACCT
GAP-AFT1-OUT-F	GGAAAAGCTAGGTTTTAGCCTTAGACATGACTGTTCC
GAP-AFT1-OUT-R	GAGTTCATCGTTTCGAAATAGTTGTTCAATTGATTGAA
GAP-HAC1-F	TATTTTCGAAACGATGCCCGTAGATTCTTCTCATAAGA
GAP-HAC1-R	AAGGCTAAAACCTCACCTGATCGCTATGCATGT
GAP-HAC1-OUT-F	TCAGGTGAGTTTTAGCCTTAGACATGACTGTTCC
GAP-HAC1-OUT-R	GGGCATCGTTTCGAAATAGTTGTTCAATTGATTGAA
GAP-FHL1P-F	GTCCCTATTTCAATCAATTGAACAACCTATATGGATGGGGAAATGGCAATAATAG
	A
GAP- FHL1P -R	GATGATGATGATGATGTTAAAGTTTTTCTCAAGGATAACATTTACTTC
GAP- FHL1P -OUT-F	ATCCCTTGAGGAAAACCTTTAACATCATCATCATCATCATTGAGTTTTGTAG

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GAP- FHL1P -OUT-R	TTATTGCCATTTCCCCATCCATATAGTTGTTCAATTGATTGAAATAGGGACAAAT AAATTAAATT
GAP-MXR1-F	CCCTATTTCAATCAATTGAACAACCTATATGTCTCAAGGAACCCCTTTTCATTAC
GAP- MXR1 -R	ATGATGATGATGATGATGCTATTTCAAACCTTACCATCAGCAATCTC
GAP- MXR1 -OUT-F	CTGATGGTAAGGTTTTGAAATAGCATCATCATCATCATTGAGTTTGTA
GAP- MXR1 -OUT-R	TGAAAAGGGTTCCTTGAGACATATAGTTGTTCAATTGATTGAAATAGGGACAAA TAAATTAAATTT

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