Electronic Supplementary Information

Biosynthesis of α-bisabolene from low-cost renewable feedstocks by peroxisome engineering and systems metabolic engineering of the yeast *Yarrowia lipolytica*

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Fig. S1 Visualizing the location of peroxisomes.

(A) GFP-ePTS1 is used to indicate the location of peroxisomes in *Y. lipolytica*. Nile red is used to stain intracellular lipids, including those in peroxisomes.

(B) LSCM visualization of peroxisomes using Nile red and GFP-ePTS1. A single focal plane is shown for all micrographs. The scale bar is $5 \,\mu$ m.



Fig. S2 A representative GC-MS profile of solvent overlay-extracted α -bisabolene from a culture of engineered *Y. lipolytica* strains.



Fig. S3 Effects of addition of cerulenin on titers of α-bisabolene.

(A) Effect of 0.5 mg/L cerulenin on α -bisabolene production carried out for Po1g P7, Po1g P8, Po1g P9 and Po1g P10 strains compared to the same strains without supplementation of cerulenin (control).

(B) Effect of 2 mg/L cerulenin on α -bisabolene production carried out for Po1g P7, Po1g P8, Po1g P9 and Po1g P10 strains compared to the same strains without supplementation of cerulenin (control).

YIPex23p Ylr324p Ygr004p Ybr168p Consensus	NSD	31 64 56 31
YIPex23p Ylr324p Ygr004p Ybr168p Consensus	SSIPPTVTKALAOAYPYI LASDKVI GLLTVTEDDOWOSFLLVAVYVTVVVYYEYLVI YCGHI LAV TSIPPTI SKALVKLYPYLI LI DEFLNVVTVTGKNI WSSVLMLCLFI TTVEYFETLVKYFGHLAI I TSIPKTVSRSI VRLYPYLI VVDNFUSI I TWSNDNVSANLLGI FLFTVCVLYFGFI TRYFGHLMI V QI IPPM SSTIFHAYPLLLI FDNALANI WLSDDKCLTFI YLTSI WLTI SFFI PVETEASHFLPF t p I yp d I w h	96 129 121 96
YIPex23p Ylr324p Ygr004p Ybr168p Consensus	$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	145 177 169 161
YIPex23p Ylr324p Ygr004p Ybr168p Consensus	TPRDVT. RLAFTTLFLSPLYNFGAYFFLGPRKFLLTTGVFFLTYHS MAARVTRAVI W . TQDI Q. RLLYTTVI LSPI YVNI TWLLPPRSLMLVVGVFLUTYHSP WSKVARRLLW . AQDVR. RLLFTI AFLSPVYI FLTVFVLSPNYLMLI GGLYVI TYHSKLI RRMRYLW LKLSFDGVNKECSGKRLFCRLFLFGTI FQI VI MRYI SPGTYTRFFI I TGU YNTSSFQATLRLLW r p y w	201 232 224 226
YIPex23p Ylr324p Ygr004p Ybr168p Consensus	KSKAI RLVTI YLTCLDFSNTKRNLGAFGFTQSPLSVQSKDGKPVRFTYVLYENQRR KFKI MRLLVI YVTCLDLGGI NKDQGI FATVQKQVKKLASTENSNGVLSDSKPI RFTYVLYENQRR KFRVVRLLVI FI TCLDLGGPDNNRRLFASVNKKI RSFVWNEVGN. TSNTKKTVLFKVALFENQRR RFTAVRN YYLCI ESFKI SSFLPKHLKMEQI I PLSQ. GRAI TVPLVEVLPKLLRDKKGDDHI H r f g	257 297 288 288
YIPex23p Ylr324p Ygr004p Ybr168p Consensus	WLGI GWTANLLAYERTP WTDEFLNEVTPPSEFKLPDTEGTGNKWOWVDPTWRLDCTN. DGALVI I WLGI GWKPSMLSYERTP WTDEFLNEAPSPENFHLPE. ETNTYVWRWVDKTWRLDMTN. DGAI OVP WLGI GWTSTMLSYERAS WTDEFLNTSPSPEVFTLPE. EQSGNAWE WHDKDWLDLTN. DGI I QLP I QLLLNEQKDNFGNEDLKI LEI EVYENQRRWYQNK. NWSTKLLPYERQNYCI EI KNTDGTLTMR I dg	321 360 351 352
YIPex23p Ylr324p Ygr004p Ybr168p Consensus	GNKALSTP. DPSPSEGW YYDNTWKRPTADDSFSKYTRRRWVRTAELITVTKPTDVVVTVEED. NSKARTSA. DPSPDEGFIYYDNTWKKPSKEDSFSKYTRRRWVRTAELVKTSDFDESVINSNRNS ASAAKTKV. KPGADEGFIYYDNTWNPSATDTYKKYTRRRWIRTATVTTTYDDEPTVEKATPN. SCLPPDGLGEEELPNNWHWINDNWDGTDWIYSDSAWKEIGQYSSLESFTRSRKWKRRLFHL W	384 424 414 413
YIPex23p Ylr324p Ygr004p Ybr168p Consensus	GVTDAAG. DVEI TTETEEK AI EQKVEENSTNGLTAEQELGSNKQEKDNAKKVGEPTTEETKEFAEASNI NEGEFERI SSTDEEV SHALKSEEN. NRVRK. RKV. SFSTAN. EVHI PSSDSSK	403 489 449 413
YIPex23p Ylr324p Ygr004p Ybr168p Consensus	VRRKGI RFEEDS LKSRARDRLAKVLDDTEEKEQSNPTI GRDSKKA LI QI SDVSMSPSL	416 522 462 413

Fig. S4 Sequence alignment of *Y. lipolytica* YIPex23p with the proteins YIr324p, Ygr004p, and Ybr168p encoded by the *S. cerevisiae* genome. Amino acid sequences were aligned with the use of the DNAMAN program. Identical residues in four proteins are shaded black, whereas identical residues in at least three of the proteins are shaded pink, whereas identical residues in two proteins are shaded blue. Similarity rules: G = A = S; A = V; V = I = L = M; I = L = M = F = Y W; K = R = H; D = E = Q = N; and S = T = Q = N.

Strains	Genotype	Reference
Po1g <i>KU70</i> ∆	MATA, xpr2-332, leu2-270, ku70 ⁻ , ura3-302::URA3, Axp- 2	30
Polg-GFP-ePTS1	Polg KU70∆, GFP-ePTSI	This study
Po1g KaBS	Polg $KU70\Delta$, α -Bis	4
Po1g P1	Po1g KU70Δ, Erg10-ePTS1, Erg13-ePTS1, HMGR- ePTS1, Erg12-ePTS1, IDI-ePTS1, Erg8-ePTS1, Erg19- ePTS1, Erg20-ePTS1,α-Bis-ePTS1	This study
Po1g P2	Polg Pl, ABC-Gl	This study
Po1g P3	Polg Pl, ABC-G1-ePTS1	This study
Po1g P4	Polg P1, ABC-G1, HMGR-ePTS1, a-Bis-ePTS1	This study
Polg P5	Polg Pl, ABC-Gl-ePTSl, HMGR-ePTSl, α-Bis-ePTSl	This study
Po1g P6	MATA, xpr2-332, leu2-270, ku70 ⁻ , ura3-302::URA3, Axp- 2, Erg10-ePTS1, Erg13-ePTS1, HMGR-ePTS1, Erg12- ePTS1, IDI-ePTS1, Erg8-ePTS1, Erg19-ePTS1, Erg20- ePTS1,α-Bis-ePTS1, ABC-G1-ePTS1, HMGR-ePTS1,α- Bis-ePTS1, POX2	This study
Po1g P7	MATA, xpr2-332, leu2-270, ku70 ⁻ , ura3-302::URA3, Axp- 2, Erg10-ePTS1, Erg13-ePTS1, HMGR-ePTS1, Erg12- ePTS1, IDI-ePTS1, Erg8-ePTS1, Erg19-ePTS1, Erg20- ePTS1,α-Bis-ePTS1, ABC-G1-ePTS1, HMGR-ePTS1,α- Bis-ePTS1, MFE1	This study
Po1g P8	MATA, xpr2-332, leu2-270, ku70 ⁻ , ura3-302::URA3, Axp- 2, Erg10-ePTS1, Erg13-ePTS1, HMGR-ePTS1, Erg12- ePTS1, IDI-ePTS1, Erg8-ePTS1, Erg19-ePTS1, Erg20- ePTS1,α-Bis-ePTS1, ABC-G1-ePTS1, HMGR-ePTS1,α- Bis-ePTS1, POT1	This study
Po1g P9	MATA, xpr2-332, leu2-270, ku70 ⁻ , ura3-302::URA3, Axp- 2, Erg10-ePTS1, Erg13-ePTS1, HMGR-ePTS1, Erg12- ePTS1, IDI-ePTS1, Erg8-ePTS1, Erg19-ePTS1, Erg20- ePTS1,α-Bis-ePTS1, ABC-G1-ePTS1, HMGR-ePTS1,α- Bis-ePTS1, MFE1,POT1	This study

Table S1 Strains used in this study.

Po1g P10	olg P10 MATA, xpr2-332, leu2-270, ku70 ⁻ , ura3-302::URA3, Axp-		
	2, Erg10-ePTS1, Erg13-ePTS1, HMGR-ePTS1, Erg12-		
	ePTS1, IDI-ePTS1, Erg8-ePTS1, Erg19-ePTS1, Erg20-	This study	
	ePTS1,a-Bis-ePTS1, ABC-G1-ePTS1, HMGR-ePTS1,a-		
	Bis-ePTS1, MFE1,POT1,POX2		
Polg P11	MATA, xpr2-332, leu2-270, ku70 ⁻ , ura3-302::URA3, Axp-		
	2, Erg10-ePTS1, Erg13-ePTS1, HMGR-ePTS1, Erg12-		
	ePTS1, IDI-ePTS1, Erg8-ePTS1, Erg19-ePTS1, Erg20-	This study	
	ePTS1,a-Bis-ePTS1, ABC-G1-ePTS1, HMGR-ePTS1,a-		
	Bis-ePTS1, MFE1,POT1,ANT1		
Polg P12	MATA, xpr2-332, leu2-270, ku70 ⁻ , ura3-302::URA3, Axp-		
	2, Erg10-ePTS1, Erg13-ePTS1, HMGR-ePTS1, Erg12-		
	ePTS1, IDI-ePTS1, Erg8-ePTS1, Erg19-ePTS1, Erg20-	This study	
	ePTS1,a-Bis-ePTS1, ABC-G1-ePTS1, HMGR-ePTS1,a-	This study	
	Bis-ePTS1, MFE1, POT1, ANT1, ΔYlPex23p, GFP-		
	ePTS1		

Plasmids	Features	Reference
pYLEX1(leu2)	Y. lipolytica-integrative plasmid, P_{hp4d} - T_{XPR2} , leu2, Ap^r	This study
pYLEX1-hyg	pYLEX1 variant with the hyg marker	This study
pYLEX1-nat	pYLEX1 variant with the nat marker	This study
pYLEX1-GFP-ePTS1	P_{hp4d} -GFP-ePTS1- T_{XPR2} , leu2, Ap^r	This study
pYLEX1-α-Bis	P_{hp4d} - α -Bis- T_{XPR2} , leu2, Ap^r	This study
pYLEX1-α-Bis- ePTS1	P_{hp4d} - α -Bis-ePTS1- T_{XPR2} , leu2, Ap^r	This study
pYLEX1-Erg10-ePTS1	P_{hp4d} -Erg10-ePTS1- T_{XPR2} , leu2, Ap^r	This study
pYLEX1-Erg13-ePTS1	P_{hp4d} -Erg13-ePTS1- T_{XPR2} , leu2, Ap^r	This study
pYLEX1-HMGR-ePTS1	P _{hp4d} -HMGR-ePTS1-T _{XPR2} , leu2, Ap ^r	This study
pYLEX1-Erg12-ePTS1	P_{hp4d} -Erg12-ePTS1- T_{XPR2} , leu2, Ap^r	This study
pYLEX1-Erg8-ePTS1	P_{hp4d} -Erg8-ePTS1-T _{XPR2} , leu2, leu2, Ap ^r	This study
pYLEX1-Erg19-ePTS1	P_{hp4d} -Erg19-ePTS1- T_{XPR2} , leu2, Ap^r	This study
pYLEX1-IDI-ePTS1	P_{hp4d} -IDI-ePTS1- T_{XPR2} , leu2, Ap^r	This study
pYLEX1-Erg20-ePTS1	P_{hp4d} -Erg20-ePTS1- T_{XPR2} , leu2, Ap^r	This study
pYLEX1-POX2	P_{hp4d} -POX2- T_{XPR2} , leu2, Ap^r	This study
pYLEX1-MFE1	P_{hp4d} -MFE1- T_{XPR2} , leu2, Ap^r	This study
pYLEX1-POT1	P_{hp4d} -POT1- T_{XPR2} , leu2, Ap^r	This study
pYLEX1-ANT1	P_{hp4d} -ANT1- T_{XPR2} , leu2, Ap^r	This study
pYLEX1-Erg10-Erg13- ePTS1	P_{hp4d} -Erg10-ePTS1- T_{XPR2} , P_{hp4d} -Erg13-ePTS1- T_{XPR2} , leu2, Ap^r	This study
pYLEX1-Erg10-Erg13- HMGR-ePTS1	P_{hp4d} - $Erg10$ - $ePTS1$ - T_{XPR2} , P_{hp4d} - $Erg13$ - $ePTS1$ - T_{XPR2} , P_{hp4d} - $HMGR$ - $ePTS1$ - T_{XPR2} , $leu2$, Ap^r	This study
pYLEX1-Erg10-Erg13- HMGR-Erg12-ePTS1	P_{hp4d} - $Erg10$ - $ePTS1$ - T_{XPR2} , P_{hp4d} - $Erg13$ - $ePTS1$ - T_{XPR2} , P_{hp4d} - $HMGR$ - $ePTS1$ - T_{XPR2} , P_{hp4d} - $Erg12$ - $ePTS1$ - T_{XPR2} , $leu2$, Ap^r	This study
pYLEX1-Erg10-Erg13-	P_{hp4d} - $Erg10$ - $ePTS1$ - T_{XPR2} , P_{hp4d} - $Erg13$ - $ePTS1$ - T_{XPR2} , P_{hp4d} - $HMGR$ - $ePTS1$ - T_{XPR2} , P_{hp4d} - $Erg12$ - $ePTS1$ - T_{XPR2} ,	This study

Table S2 Plasmids used in this study.

HMGR-Erg12-Erg8-ePTS1	P_{hp4d} -Erg8-ePTS1- T_{XPR2} , leu2, Ap^r	
pYLEX1-Erg10-Erg13- HMGR-Erg12-Erg8-Erg19- α-Bis-ePTS1	P_{hp4d} - $Erg10$ - $ePTS1$ - T_{XPR2} , P_{hp4d} - $Erg13$ - $ePTS1$ - T_{XPR2} , P_{hp4d} - $HMGR$ - $ePTS1$ - T_{XPR2} , P_{hp4d} - $Erg12$ - $ePTS1$ - T_{XPR2} , P_{hp4d} - $Erg8$ - $ePTS1$ - T_{XPR2} , P_{hp4d} - $Erg19$ - $ePTS1$ - T_{XPR2} , P_{hp4d} - α - Bis - $ePTS1$ - T_{XPR2} , $leu2$, Ap^r	This study
pYLEX1-hyg-IDI-ePTS1	P _{hp4d} -IDI-ePTS1-T _{XPR2} , hyg, Ap ^r	This study
pYLEX1-hyg-IDI-Erg20- ePTS1	P_{hp4d} -IDI-ePTS1- T_{XPR2} , P_{hp4d} -Erg20-ePTS1- T_{XPR2} , hyg, Ap^{r}	This study
pYLEX1-hyg-IDI-Erg20- ePTS1-ABC-G1	P_{hp4d} -IDI-ePTS1- T_{XPR2} , P_{hp4d} - $Erg20$ -ePTS1- T_{XPR2} , $P_{hp}4d$ -ABC-G1-TXPR2, hyg, Ap^r	This study
pYLEX1-hyg-IDI-Erg20- ePTS1-ABC-G1-ePTS1	P_{hp4d} -IDI-ePTS1- T_{XPR2} , P_{hp4d} - $Erg20$ -ePTS1- T_{XPR2} , P_{hp4d} -ABC-G1-ePTS1- T_{XPR2} , hyg, Ap^r	This study
pYLEX1-hyg-IDI-Erg20- HMGR-α-Bis-ePTS1-ABC- G1	P_{hp4d} -IDI-ePTS1- T_{XPR2} , P_{hp4d} - $Erg20$ -ePTS1- T_{XPR2} , P_{hp4d} -HMGR-ePTS1- T_{XPR2} , P_{hp4d} - α -Bis-ePTS1- T_{XPR2} , $P_{hp}4d$ -ABC-G1-TXPR2, hyg, Ap ^r	This study
pYLEX1-hyg-IDI-Erg20- HMGR-α-Bis-ABC-G1- ePTS1	P_{hp4d} -IDI-ePTS1- T_{XPR2} , P_{hp4d} - $Erg20$ -ePTS1- T_{XPR2} , P_{hp4d} -HMGR-ePTS1- T_{XPR2} , P_{hp4d} - α -Bis-ePTS1- T_{XPR2} , P_{hp4d} -ABC-G1-ePTS1- T_{XPR2} , hyg, Ap^r	This study
pYLEX1-nat-POX2	P_{hp4d} -POX2- T_{XPR2} , nat, Ap^r	This study
pYLEX1-nat-MFE1	P_{hp4d} -MFE1- T_{XPR2} , nat, Ap^r	This study
pYLEX1-nat-POT1	P_{hp4d} -POT1- T_{XPR2} , nat, Ap^r	This study
pYLEX1-nat-MFE1-POT1	P_{hp4d} -MFE1- T_{XPR2} , P_{hp4d} -POT1- T_{XPR2} , nat, Ap^r	This study
pYLEX1-nat-MFE1-POT1- POX2	P_{hp4d} -MFE1- T_{XPR2} , P_{hp4d} -POT1- T_{XPR2} , P_{hp4d} -POX2- T_{XPR2} , nat, Ap^r	This study
pYLEX1-nat-MFE1-POT1- ANT1	P_{hp4d} -MFE1-T _{XPR2} , P_{hp4d} -POT1-T _{XPR2} , P_{hp4d} -ANT1- T _{XPR2} , nat, Ap ^r	This study

Applications	Primer	Sequence (5'-3')
Amplify GFP-ePTS1 gene from	Amplify GFP-	CCACACACATCCACaGGTACCaATGCTTTCACTAC
plasmid pYLEX1-GFP-ePTS1,	ePTS1 gene from	GTCAATCTATAAGATTTTTCAAGCCAGCCACAAG
forward primer	plasmid pYLEX1-	AACTTTGTGTAGCTCTAGATATCTGCTTCAGggtacc
	GFP-ePTS1, F	atggtgtctaagcag
Amplify <i>GFP-ePTS1</i> gene from plasmid pYLEX1- <i>GFP-ePTS1</i> , reverse primer	Amplify GFP- ePTS1 gene from plasmid pYLEX1- GFP-ePTS1, R	ttagtttcgggttcccacgtgTTAGTGGTGGTGGTGGTGGTG
Amplify <i>Erg10</i> gene form <i>Y. lipolytica</i> genomic DNA, forward primer	Erg10-ePTS1-F	actttggtctactccggtaccAATGGAGCCCGTCTACATTGTT
Amplify <i>Erg10</i> gene form <i>Y. lipolytica</i> genomic DNA, reverse primer	Erg10-ePTS1-R	GGGACAGGCCATGGAGctacagcttggatcgtcgtcctcggccca gacacttctcaacaatgatag
Amplify <i>HMGR</i> gene form <i>Y</i> . <i>lipolytica</i> genomic DNA, forward primer	HMGR-ePTS1-F	acaaccacacacatccacAATGCTACAAGCAGCTATTGGAA A
Amplify <i>HMGR</i> gene form <i>Y</i> . <i>lipolytica</i> genomic DNA, reverse primer	HMGR-ePTS1-R	TTAGTTTCGGGTTCCCACctacagcttggatcgtcgtcctcggccc agtgaccgtatgcaaatattcg
Amplify <i>Erg13</i> gene form <i>Y. lipolytica</i> genomic DNA, forward primer	Erg13-ePTS1-F	acaaccacacatccacgtgAATGTCGCAACCCCAGAACG
Amplify <i>Erg13</i> gene form <i>Y. lipolytica</i> genomic DNA, reverse primer	Erg13-ePTS1-R	TTAGTTTCGGGTTCCgtgctacagcttggatcgtcgtcctcggccca gctgcttgatctcgtactttc
Amplify <i>Erg12</i> gene form <i>Y. lipolytica</i> genomic DNA, forward primer	Erg12-ePTS1-F	ggaacccgaaactaaggatcAATGGACTACATCATTTCGGC G
Amplify <i>Erg12</i> gene form <i>Y. lipolytica</i> genomic DNA, reverse primer	Erg12-ePTS1-R	ACAAGTTCCGTAGTTGctacagcttggatcgtcgtcctcggcccag atgggtccagggaccgat
Amplify <i>IDI</i> gene form <i>Y. lipolytica</i> genomic DNA, forward primer	IDI-ePTS1-F	actttggtctactccgAATGCTACTTGATCCACCGCC
Amplify <i>IDI</i> gene form <i>Y. lipolytica</i> genomic DNA, reverse primer	IDI-ePTS1-R	GGGACAGGCCATGGAGGTACCTAcagcttggatcgtcgtcc tcggcccagatgacgacgtcttacagc
Amplify α -Bis gene from plasmid	α-bisabolene-F	cgcatagttaagccagtaGGGAGCTGCATGTGTCAGAGG

Table S3 Primers used in PCR.

pYLEX1-α-Bis, forward primer		
Amplify <i>α-Bis</i> gene from plasmid pYLEX1-α-Bis, reverse primer	α-bisabolene-R	tagcgatagcggagtgtaCGCGGCCGCATAGGCCAG
Amplify <i>α-Bis</i> gene from plasmid pYLEX1-α-Bis, forward primer	a-bisabolene- ePTS1-F	acaaccacacacatccacgtgAATGGCCGGTGTCTCTGCC
Amplify <i>α-Bis</i> gene from plasmid pYLEX1-α-Bis, reverse primer	α-bisabolene- ePTS1-R	TTAGTTTCGGGTTCCCACTTAcagcttggatcgtcgtcctcggc ccagGTGGTGATGGTGGTGGTGGAG
Amplify <i>Erg19</i> gene form <i>Y. lipolytica</i> genomic DNA, forward primer	Erg19-ePTS1-F	acaaccacacatccacgtgAATGATCCACCAGGCCTCCA
Amplify <i>Erg19</i> gene form <i>Y. lipolytica</i> genomic DNA, reverse primer	Erg19-ePTS1-R	TTAGTTTCGGGTTCCgtgctacagcttggatcgtcgtcctcggccca gcttgctgttcttcagagaac
Amplify <i>Erg20</i> gene form <i>Y. lipolytica</i> genomic DNA, forward primer	Erg20-ePTS1-F	acaaccacacatccacgtgAATGTCCAAGGCGAAATTCG
Amplify <i>Erg20</i> gene form <i>Y. lipolytica</i> genomic DNA, reverse primer	Erg20-ePTS1-R	TTAGTTTCGGGTTCCgtgctacagcttggatcgtcgtcctcggccca gcttctgtcgcttgtaaatct
Amplify <i>Erg8</i> gene form <i>Y. lipolytica</i> genomic DNA, forward primer	Erg8-ePTS1-F	acaaccacacatccacgtgAATGCTACTTGAACCCCTTCT CG
Amplify <i>Erg8</i> gene form <i>Y. lipolytica</i> genomic DNA, reverse primer	Erg8-ePTS1-R	TTAGTTTCGGGTTCCgtgCTAcagettggategtegteeteggeee agatgaceacetatteggetee
Amplify <i>POX2</i> gene form <i>Y. lipolytica</i> genomic DNA, forward primer	POX2-F	acaaccacacatccacAATGAACCCCAACAACACTGGC
Amplify <i>POX2</i> gene form <i>Y. lipolytica</i> genomic DNA, reverse primer	POX2-R	ttagtttcgggttcccacgtgCTATTCCTCATCAAGCTCGCAA
Amplify <i>MFE1</i> gene form <i>Y. lipolytica</i> genomic DNA, forward primer	MFE1-F	actttggtctactccggtacAATGTCTGGAGAACTAAGATAC GACGG
Amplify <i>MFE1</i> gene form <i>Y. lipolytica</i> genomic DNA, reverse primer	MFE1-R	gggacaggccatggaggtaccTTAGAGCTTAGCATCCTTGGG G
Amplify <i>POT1</i> gene form <i>Y. lipolytica</i> genomic DNA, forward primer	POT1-F	actttggtctactccggtacATGGAGCCCGTCTACATTGTTT
Amplify <i>POT1</i> gene form <i>Y. lipolytica</i> genomic DNA, reverse primer	POT1-R	gggacaggccatggaggtaccCTAACACTTCTCAACAATGAT AGAGGAA
Amplify ANTI gene form Y. lipolytica	ANTI-F	actttggtctactccgAATGGCAGCTATTTCCAAAGACTAT

genomic DNA, forward primer		G
Amplify <i>ANT1</i> gene form <i>Y. lipolytica</i> genomic DNA, reverse primer	ANT1-R	gggacaggccatggaggtacTTATCCCTTGATCAAGGTGGG G
Amplify the gene expression cassette, forward primer	PshAI-F	agtcataagtgcggcgacgaGAGGCCGTTGAGCACCGC
Amplify the gene expression cassette, reverse primer	PshA I-R	gtgggcgcggggcatgactaGATAAGCTGTCAAACATGAGA ATTCG
Amplify the gene expression cassette, forward primer	FspA I-F	gacaggagcacgatcatgcgAGGCCGTTGAGCACCGC
Amplify the gene expression cassette, reverse primer	FspA I-R	gggtcctggccacgggtgcgATAAGCTGTCAAACATGAGAA TTCG
Amplify the gene expression cassette, forward primer	BsaW I-F	atcctgcgatgcagatccggaGAGGCCGTTGAGCACCGC
Amplify the gene expression cassette, reverse primer	BsaW I-R	cctgcaccattatgttccggGATAAGCTGTCAAACATGAGAA TTCG
Amplify the gene expression cassette, forward primer	Nru I-F	ccatccagcctcgcgtcgcgaGAGGCCGTTGAGCACCGC
Amplify the gene expression cassette, reverse primer	Nru I-R	acgtcttgctggcgttcgGATAAGCTGTCAAACATGAGAAT TCG
Amplify the gene expression cassette, forward primer	Sal I-F	ctctcaagggcatcggtcgacGAGGCCGTTGAGCACCGC
Amplify the gene expression cassette, reverse primer	Sal I-R	cgcataagggagagcgtcgaGATAAGCTGTCAAACATGAGA ATTCG
Amplify the gene expression cassette, forward primer	EcoN I-F	ctcccttatgcgactcctgcaGAGGCCGTTGAGCACCGC
Amplify the gene expression cassette, reverse primer	EcoN I-R	actactgggctgcttcctaaGATAAGCTGTCAAACATGAGAA TTCG
Amplify the gene expression cassette, forward primer	BstZ17 I-F	cgcatagttaagccagtaGAGGCCGTTGAGCACCGC
Amplify the gene expression cassette, reverse primer	BstZ17 I-R	tagcgatagcggagtgtaGATAAGCTGTCAAACATGAGAAT TCG

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Amplify the gene expression cassette, forward primer	Spe I-F	cgaggcagcagatccactagGAGGCCGTTGAGCACCGC
Amplify the gene expression cassette, reverse primer	Spe I-R	gcggccgcataggccaGATAAGCTGTCAAACATGAGAAT TCG
Amplify the gene expression cassette, forward primer	Not I-F	cgcatagttaagccagtaGAGGCCGTTGAGCACCGC
Amplify the gene expression cassette, reverse primer	Not I-F	tagcgatagcggagtgtaGATAAGCTGTCAAACATGAGAAT TCG
Amplify the gene expression cassette, forward primer	Aan I-F	taatgaaatgatgatttaGAGGCCGTTGAGCACCGC
Amplify the gene expression cassette, reverse primer	Aan I-R	gggacaggccatggaggtacTTATCCCTTGATCAAGGTGGG G
Amplify the gene expression cassette, forward primer	FspA I-IDI-F	gacaggagcacgatcatgcgAGGCCGTTGAGCACCGC
Amplify the gene expression cassette, reverse primer	FspA I-IDI-R	gggtcctggccacgggtgcgATAAGCTGTCAAACATGAGAA TTCG
Amplify the gene expression cassette, forward primer	Nru I-Erg20-F	ccatccagcctcgcgtcgcgaGAGGCCGTTGAGCACCGC
Amplify the gene expression cassette, reverse primer	Nru I-Erg20-R	acgtcttgctggcgttcgGATAAGCTGTCAAACATGAGAAT TCG
Amplify the gene expression cassette, forward primer	EcoN I-ABC-G1- ePTS1-F	ctcccttatgcgactcctgcaGAGGCCGTTGAGCACCGC
Amplify the gene expression cassette, reverse primer	EcoN I-ABC-G1- ePTS1-R	actactgggctgcttcctaaGATAAGCTGTCAAACATGAGAA TTCG
Amplify the gene expression cassette, forward primer	BstZ17 I-α- bisabolene-ePTS1- F	cgcatagttaagccagtaGAGGCCGTTGAGCACCGC
Amplify the gene expression cassette, reverse primer	BstZ17 I-α- bisabolene-ePTS1- R	tagcgatagcggagtgtaGATAAGCTGTCAAACATGAGAAT TCG
Amplify the gene expression cassette, forward primer	FspA I-MFE1-F	gacaggagcacgatcatgcgAGGCCGTTGAGCACCGC

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Amplify the gene expression cassette,	FspA I-MFE1-R	gggtcctggccacgggtgcgATAAGCTGTCAAACATGAGAA
reverse primer		TTCG
Amplify the gene expression cassette, forward primer	Sal I-POT1-F	ctctcaagggcatcggGAGGCCGTTGAGCACCGC
Amplify the gene expression cassette, reverse primer	Sal I-POT1-R	cgcataagggagagcgtcgaGATAAGCTGTCAAACATGAGA ATTCG