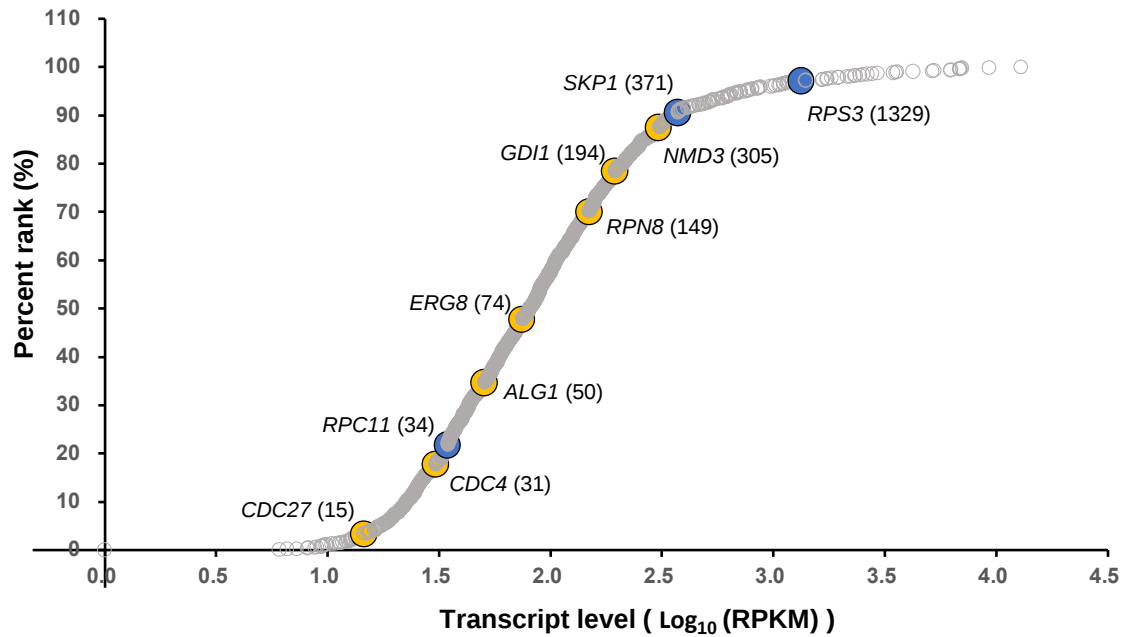
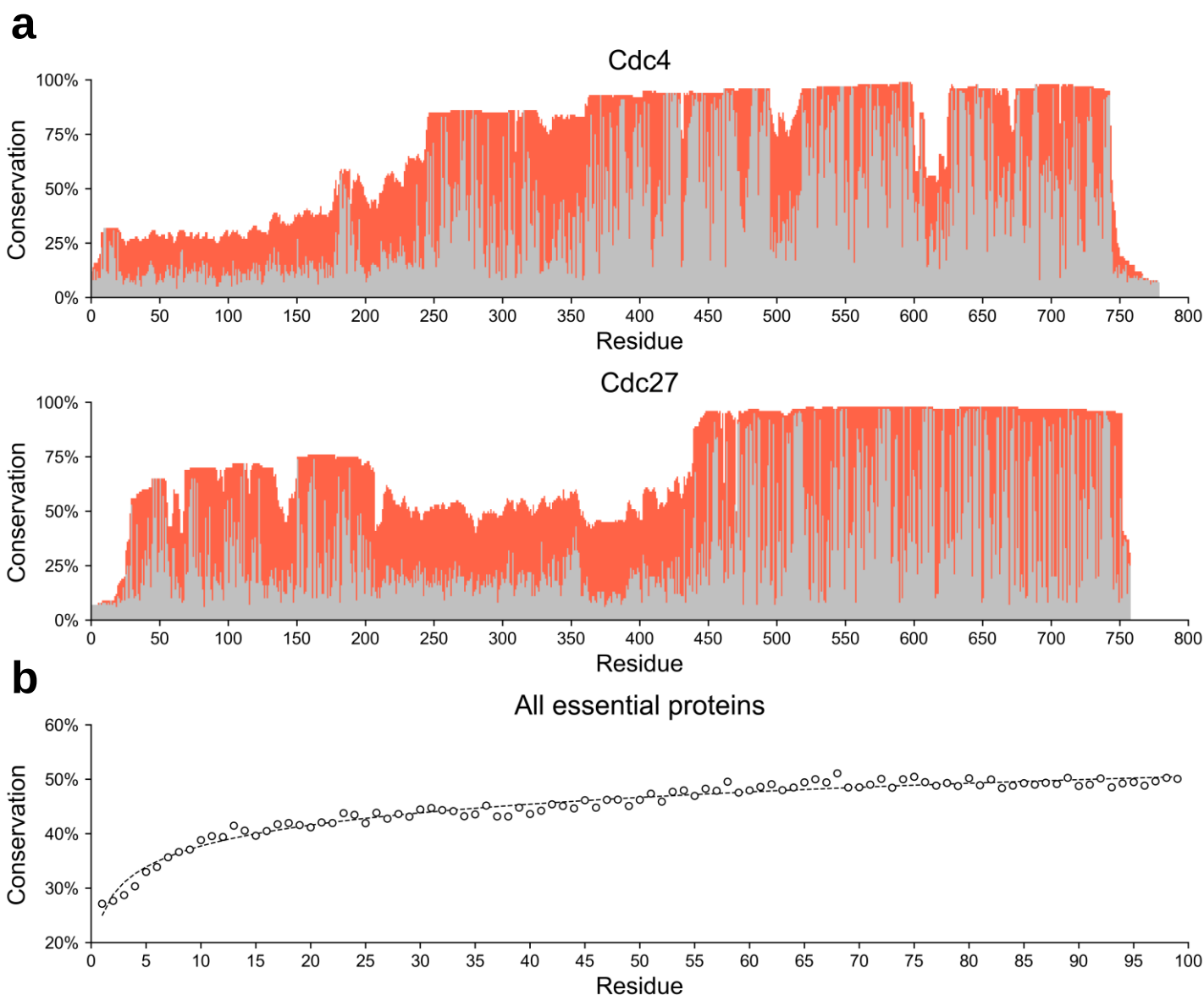
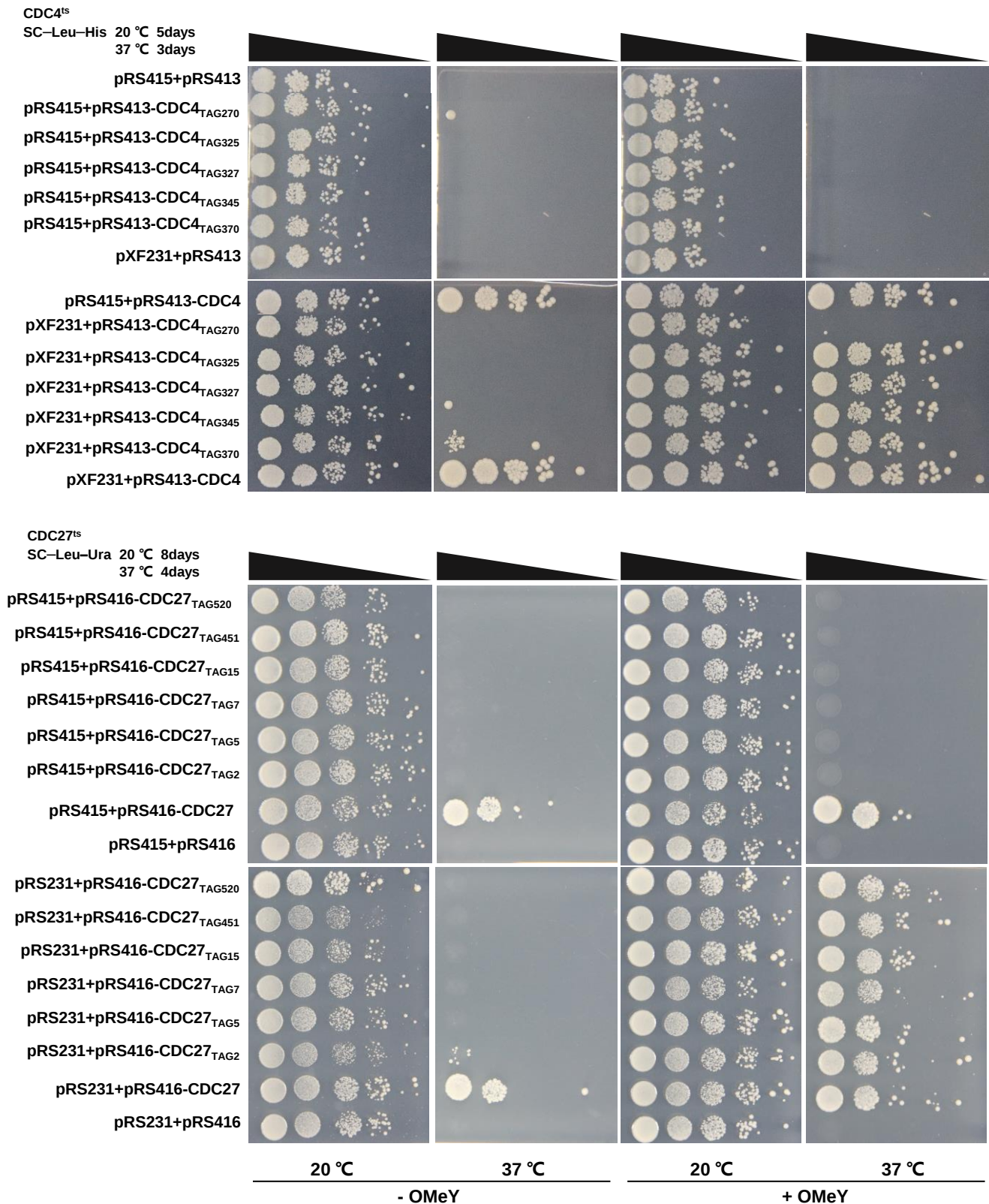




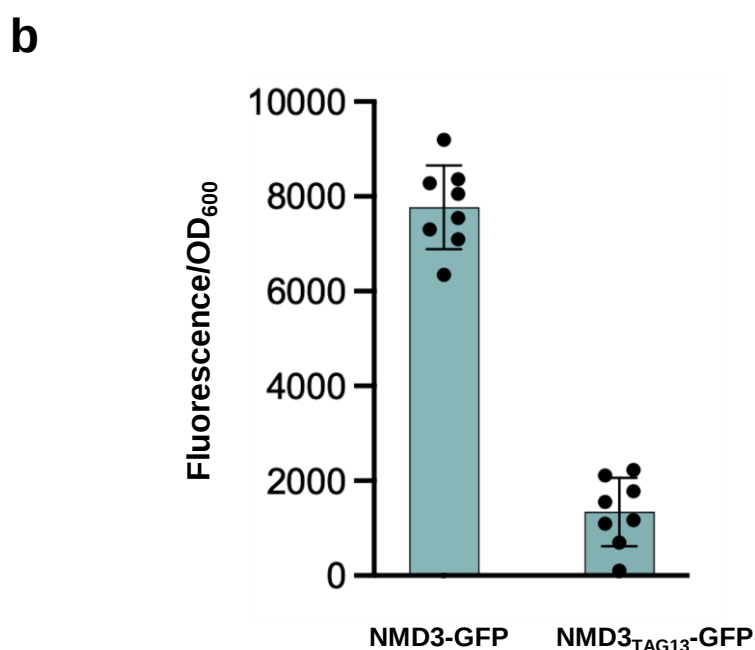
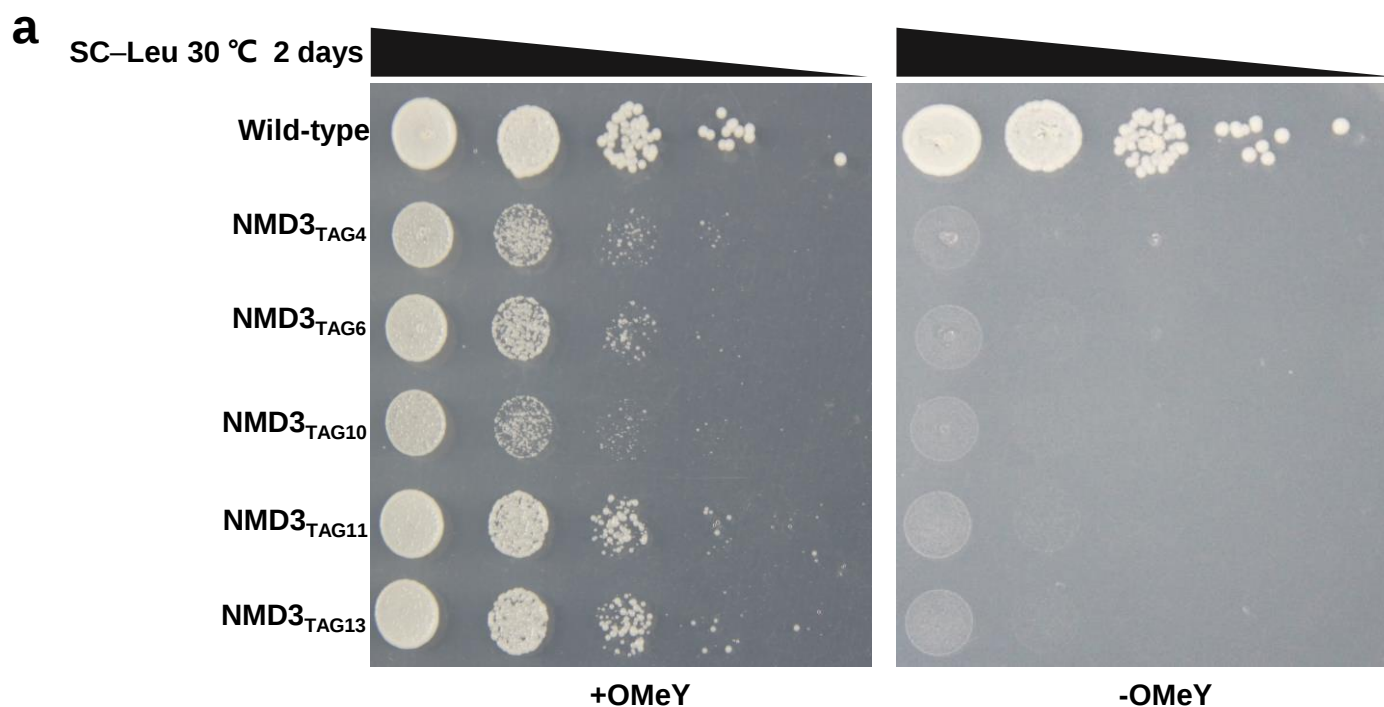
Supplementary Figure 1. Distribution of transcript levels of all essential genes in budding yeast. The percent rank is displayed on the y-axis (the rank of the RPKM value of each essential gene in descending order divided by the total number of essential genes). The transcript level based on $\text{Log}_{10}(\text{RPKM})$ value of essential genes is shown on the x-axis. The gray dot represents different essential genes. The essential genes used for OMeY-dependent and transcriptional-based biocontainment strategies are labeled in yellow and blue respectively. The numbers in parentheses indicate the RPKM value of selected genes. Source data are provided as a Source Data file.



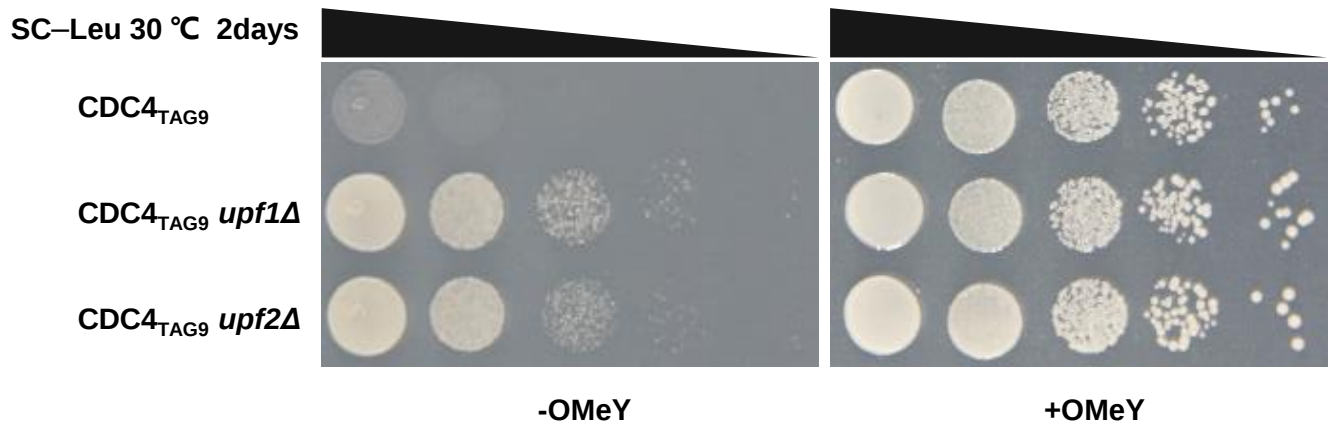
Supplementary Figure 2. Conservation analysis of each residue of essential proteins in budding yeast. **a** Conservation analysis of Cdc4 and Cdc27 proteins. The conservation (y-axis) is represented by the proportion of identical (gray) and substituted (red) amino acids for each residue based on the alignment of protein homologs. The white area denotes the proportion of missing amino acids at the corresponding position among protein homologs. **b** Conservation analysis of the first 100 amino acids for all essential proteins in budding yeast. The y-axis represents the average value of conservation for all essential proteins at the first 100 residues.



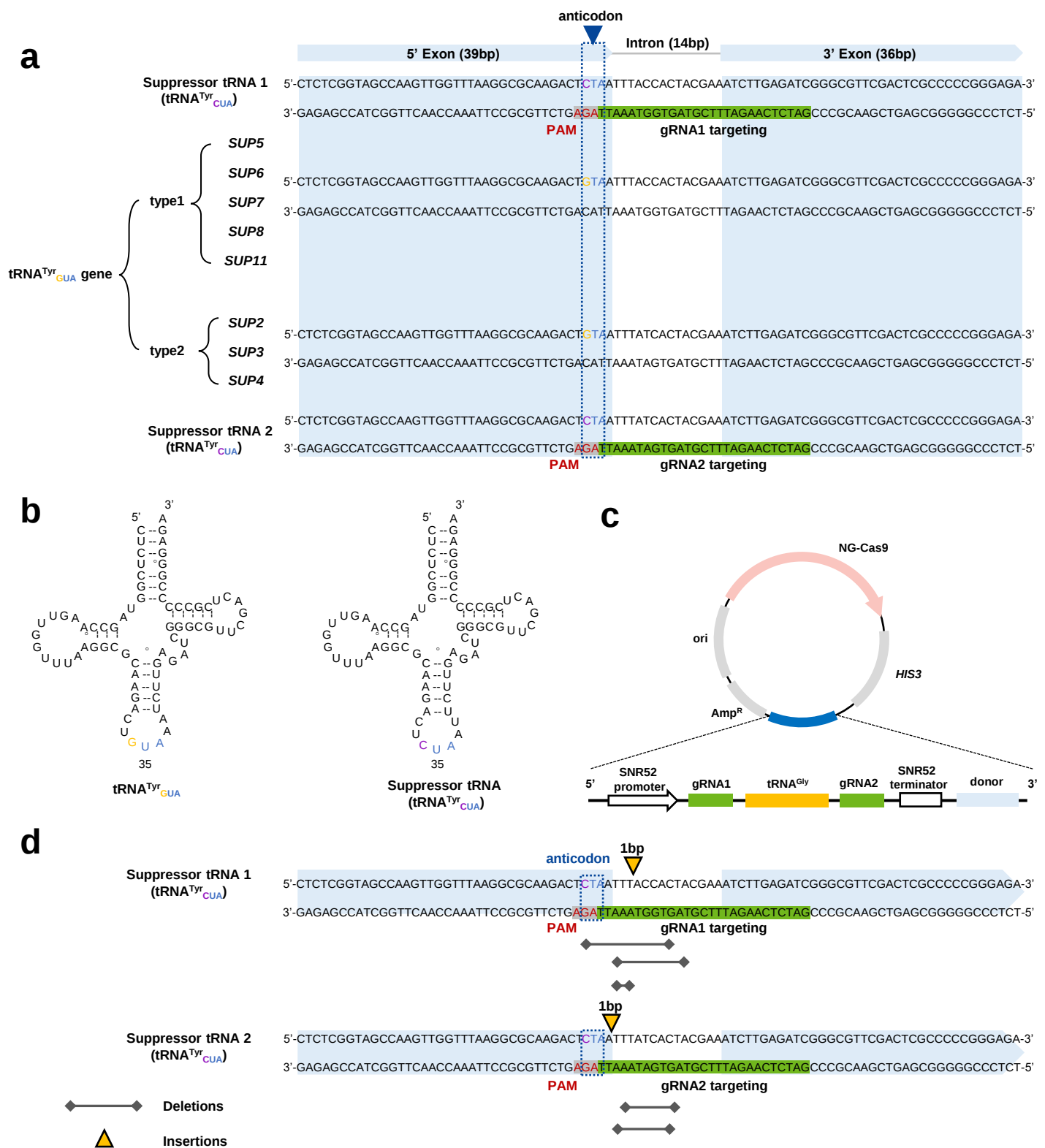
Supplementary Figure 3. Growth measurement to screen permissive sites in Cdc4 and Cdc27 protein for OMeY substitution. The dilution series (by column) of ts mutants co-expressing two plasmids encoding the LeuOmeRS/tRNA_{CUA} pair or empty vector (pRS415) and wild-type *CDC4/27* genes or variants were grown on the corresponding media under different conditions (with and without 1mM OMeY at 20 °C and 37 °C). CDC4^{ts} and CDC27^{ts} mutants were grown on SC–Leu–His and SC–Leu–Ura media plates, respectively. pXF231 is the pRS415 plasmid expressing the LeuOmeRS/tRNA_{CUA} pair.



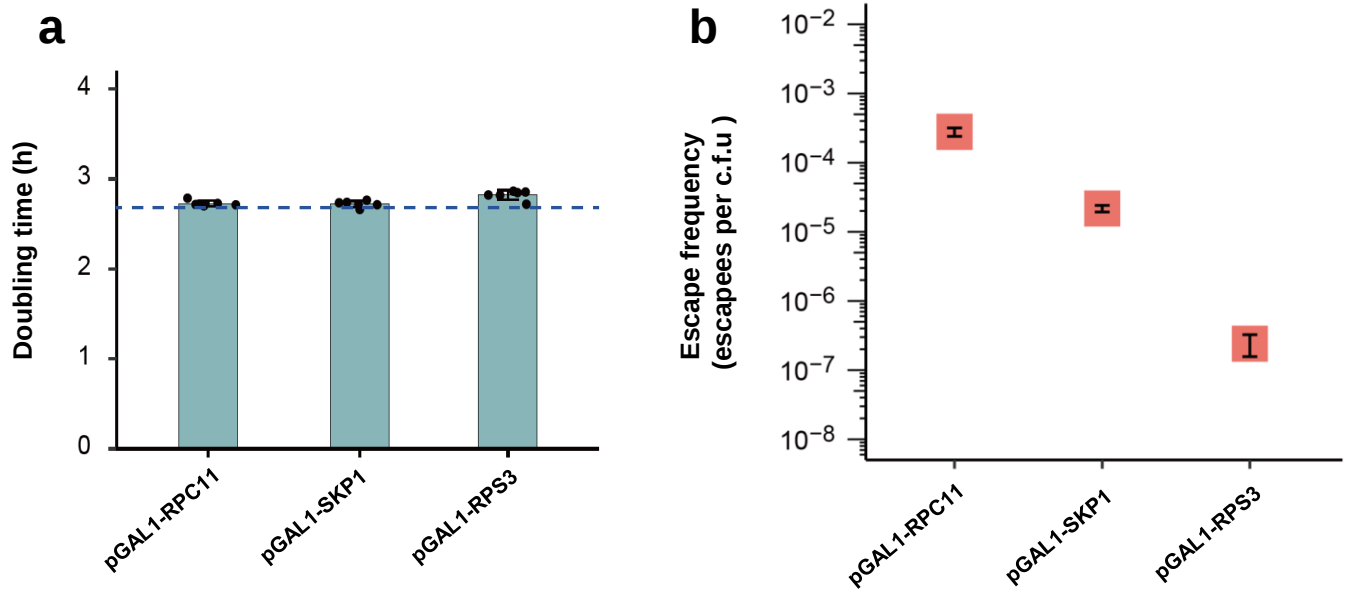
Supplementary Figure 4. Characterization of OMeY autotrophs based on *NMD3* gene. **a** Growth measurement of OMeY-dependent auxotrophs that harbor TAG substitution corresponding to different amino acid residues at the N-terminus of Nmd3 proteins compared with the control strain (BY4741 expressing LeuOmeRS/tRNA_{CUA}). Cells were grown on selective medium plates with and without 1 mM OMeY at 30 °C for 2 days. **b.** Fluorescence measurement of strains encoding Nmd3–GFP fusion proteins (both wild-type and NMD3_{TAG13}) grown in SC–Leu–Ura medium containing 1 mM OMeY to evaluate amber suppression efficiency. All the data are represented as the mean and standard deviation (n=3 for panel b, n=8 for panel c). Source data are provided as a Source Data file.



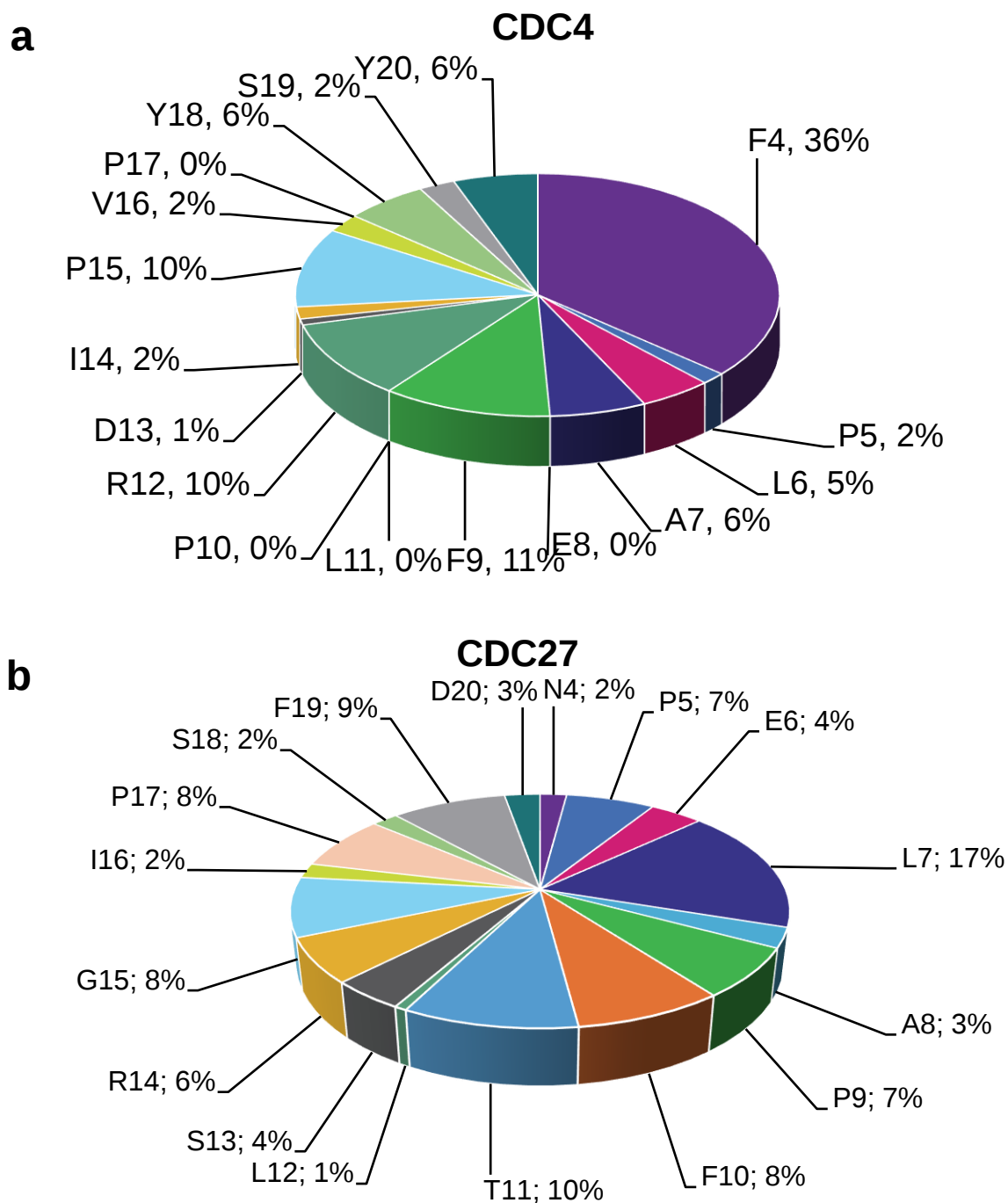
Supplementary Figure 5. Phenotypic assays of mutants with *UPF1* and *UPF2* deletion in comparison with the parental strain (CDC4_{TAG9}). Ten-fold serial dilutions of yeast cells were plated on SC–Leu media plates with and without 1 mM OMeY at 30 °C.



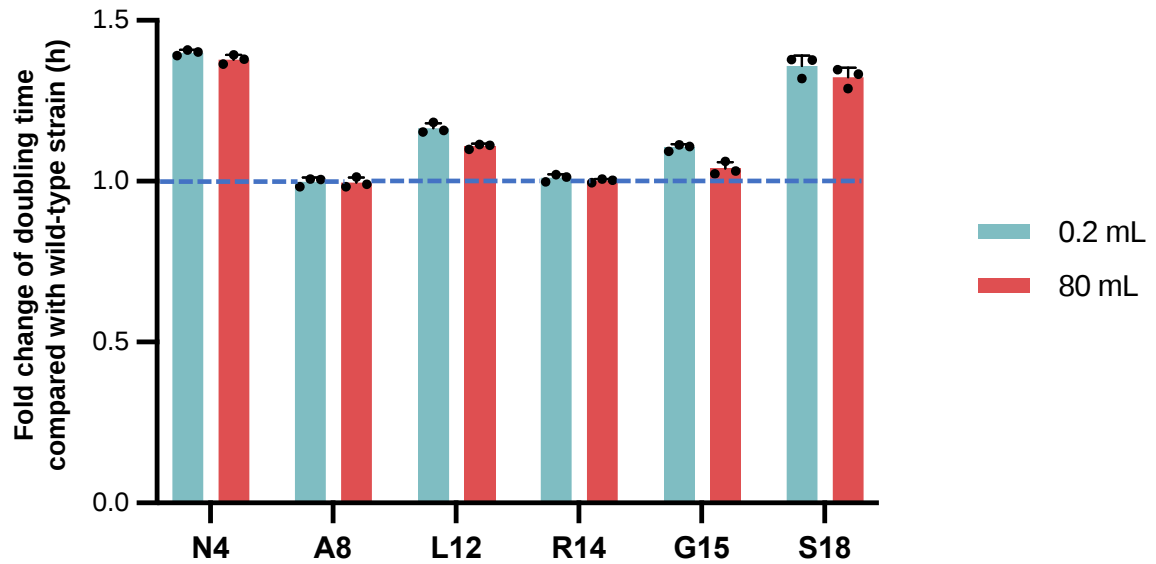
Supplementary Figure 6. Design of CRISPR-Cas9 system for reducing escape frequencies. **a** All tRNA^{Tyr} genes in budding yeast have two types of sequences; the intron sequences differ. SpCas9-NG identified 5'-AGA-3' PAM that is only located at amber suppressor tRNA^{Tyr} . PAM and gRNA target sequences are colored in red and green respectively. The tRNA^{Tyr} exon is shown in the blue region. **b** Cloverleaf structures of yeast wild-type $\text{tRNA}^{\text{Tyr}}_{\text{GUA}}$ and amber suppressor $\text{tRNA}^{\text{Tyr}}_{\text{CUA}}$. The sequences of wild-type and amber suppressor tRNA^{Tyr} differ at nucleotide 34. The colored nucleotides represent anticodons. Open circles denote non-Watson-Crick base pairs and lines denote base pairs. **c** Schematic of CRISPR-Cas9 system components on plasmid. A tRNA^{Gly} (yellow) is introduced between the gRNA1-gRNA2 array (green) to generate functional gRNAs for editing. The tRNA^{Tyr} gene serving as the donor DNA for the homology-directed repair is labeled in light blue. **d** Schematic of the amber suppressor tRNA^{Tyr} targeted for leftover scar interrupts with CRISPR-Cas9 system shown. The yellow triangle indicates corresponding insertion site, and deletions sequence is represented by the location and length of the dark line.



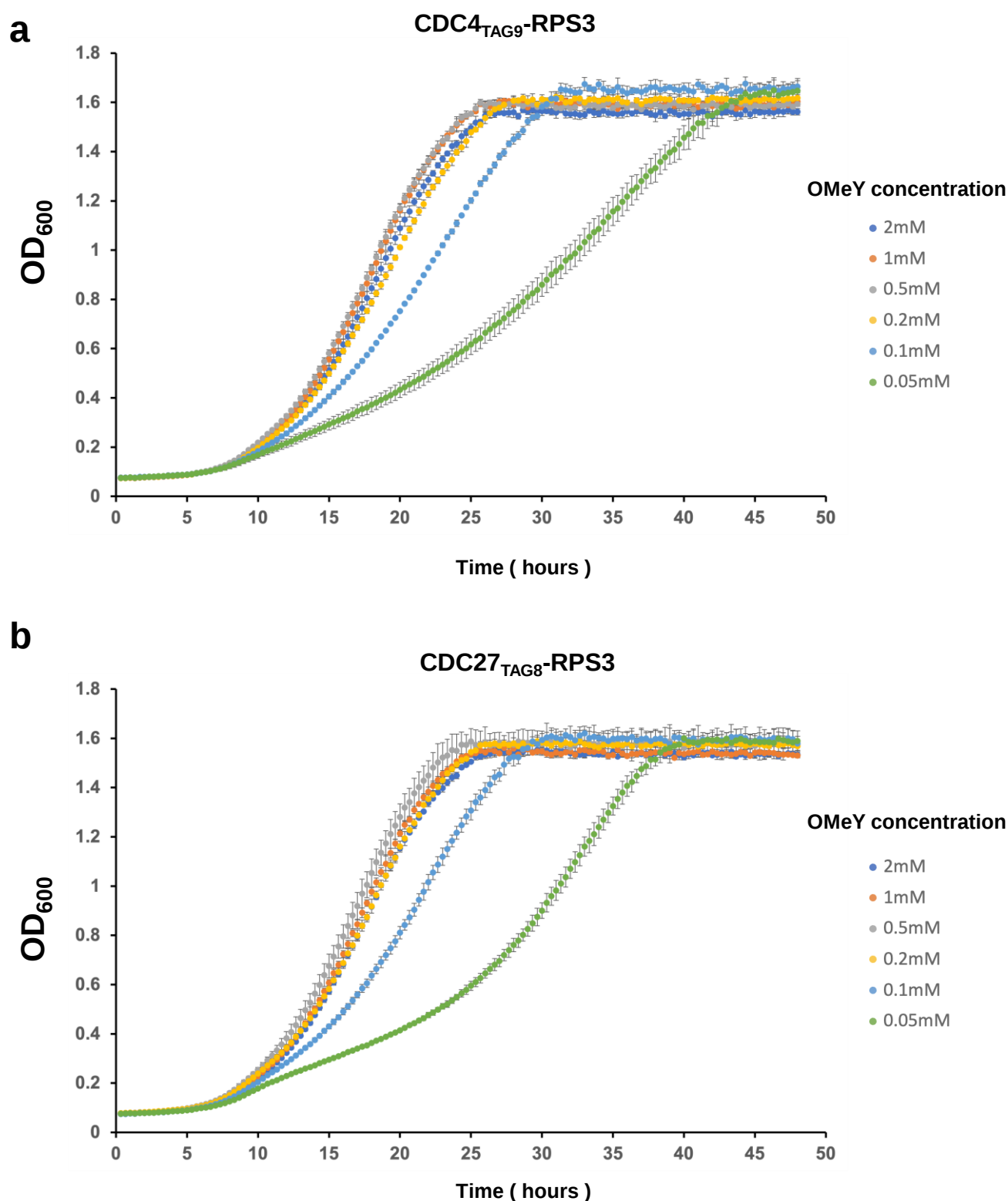
Supplementary Figure 7. Doubling time and escape frequency measurement of the transcriptional-based safeguard strains. **a** Doubling time of all three strains was measured compared with parental strain (BY4741 express LeuOmeRS/tRNA_{CUA}) in SC–Leu medium containing 2% (wt/vol) galactose, and the parental strain doubling times showed by the blue dashed horizontal lines. All the data are represented as the mean $\pm$ SD (standard deviation) from six biological replicates. **b** Escape frequencies of different transcriptional-based safeguard strains on the day 8. All the data are represented as the mean $\pm$ SEM (standard error of the mean) from three biological replicates. Source data are provided as a Source Data file.



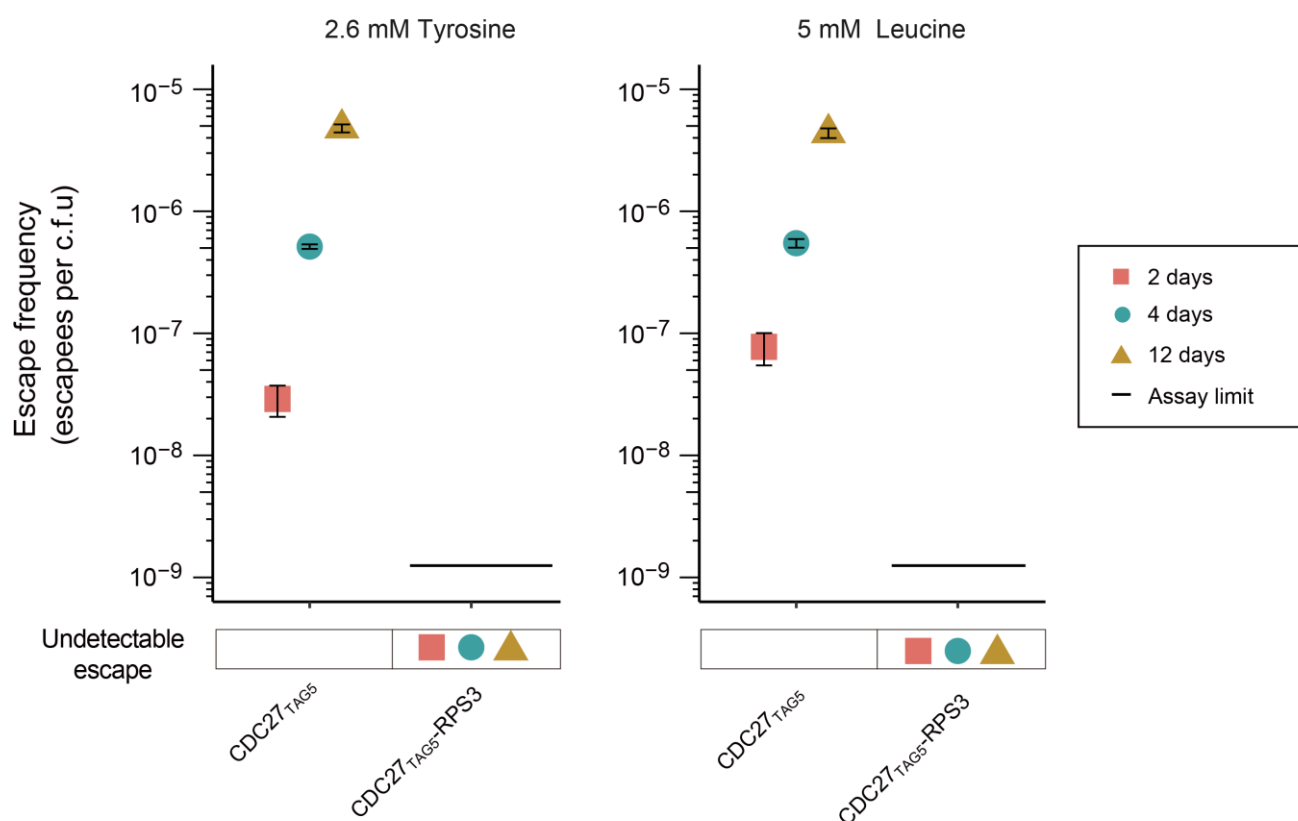
Supplementary Figure 8. Pie charts showing the percentage of TAG substitution corresponding to individual amino acid residues at the N-terminus (from residue 4 to 20) of CDC4 and CDC27. **a.** Total 124 colonies were selected for sanger sequencing of the CDC4 N-terminus. The proportion of TAG codon substitution for each residue is indicated and TAG substitution for residue E8, L11, P10, and P17 was not found. **b.** Total 146 colonies were selected for sanger sequencing of the CDC27 N-terminus. TAG substitution was detected for all tested residues and the proportion of TAG codon substitution for each residue is indicated. Source data are provided as a Source Data file.



Supplementary Figure 9. Doubling time comparison of different Cdc27-based two-layered safeguard strains grown in small and large scale. Strains were grown in 0.2 mL (blue bars) and 80 mL (red bars) SC-Leu medium containing 1 mM OMeY and 2% (wt/vol) galactose respectively. Fold change of doubling time is shown relative to the growth of pGAL1-RPS3 control strain that contain the *URA3* marker integrated upstream of the WT *CDC27* gene (represented by the blue dashed horizontal line). The x-axis shows different residues of Cdc27 that are replaced by OMeY. The error bars show the mean and standard deviation of three biological replicates. Source data are provided as a Source Data file.



Supplementary Figure 10. The growth curve of multiplex safeguard strains (CDC4_{TAG9}-RPS3 and CDC27_{TAG8}-RPS3) growing in SC-Leu medium broth containing 2% (wt/vol) galactose and supplemented with different concentration of OMeY (2, 1, 0.5, 0.2, 0.1 and 0.05 mM). Optical densities (OD₆₀₀) were measured at every 20 minutes. All the data are represented as the mean $\pm$ SD (standard deviation) from three biological replicates. Source data are provided as a Source Data file.



Supplementary Figure 11. Escape frequencies of the OMeY-dependent auxotroph (CDC27_{TAG5}) and the two-layered safeguard strain (CDC27_{TAG5}-RPS3) in the presence of 5 mM leucine or 2.6 mM tyrosine. Escape frequencies were measured at day 2, 4 and 12 indicated as red square, blue circle and yellow triangle respectively. The assay limit is determined by 1/(total CFU plated) with the assay limit of 1.3×10^{-9} escapees per CFU (see source data for details) and the black line represents undetectable growth. Error bars show the mean $\pm$ SEM of six samples including three biological replicates that was conducted in duplicate. Source data are provided as a Source Data file.

Supplementary Tables

Table S1. The reasons of escaper were analyzed by WGS.

Escape mechanisms	OMeY-dependent strain (parental)	Escaper	Gene	Mutation
Mutation of TAG to sense codon	CDC4 _{TAG325}	yXF260	<i>CDC4</i>	OMeY325Q
Occurrence of amber suppressor tRNA	CDC4 _{TAG325}	yXF258	<i>SUP7</i> (tRNA ^{Tyr} _{GUA})	G34>C in anticodon
	CDC4 _{TAG325}	yXF259	tRNA ^{Leu} _{CAA} ^a	A35>U in anticodon
	CDC4 _{TAG325}	yXF261	<i>SUP8</i> (tRNA ^{Tyr} _{GUA})	G34>C in anticodon
	CDC27 _{TAG5}	yXF262	<i>SUP54</i> (tRNA ^{Leu} _{CAA})	A35>U in anticodon
	CDC27 _{TAG5}	yXF263	tRNA ^{Leu} _{CAA} ^b	A35>U in anticodon
	CDC27 _{TAG5}	yXF264	<i>SUP3</i> (tRNA ^{Tyr} _{GUA})	G34>C in anticodon
	CDC27 _{TAG520}	yXF267	<i>SUP7</i> (tRNA ^{Tyr} _{GUA})	G34>C in anticodon
	CDC27 _{TAG520}	yXF268	<i>SUP4</i> (tRNA ^{Tyr} _{GUA})	G34>C in anticodon
	CDC27 _{TAG520}	yXF269	<i>SUP8</i> (tRNA ^{Tyr} _{GUA})	G34>C in anticodon
	CDC27 _{TAG520}	yXF270	<i>SUP3</i> (tRNA ^{Tyr} _{GUA})	G34>C in anticodon
	CDC27 _{TAG520}	yXF271	<i>SUP8</i> (tRNA ^{Tyr} _{GUA})	G34>C in anticodon
	CDC27 _{TAG520}	yXF272	<i>SUP4</i> (tRNA ^{Tyr} _{GUA})	G34>C in anticodon
	CDC27 _{TAG451}	yXF265	tRNA ^{Trp} _{CCA} ^c	C35>U in anticodon
	CDC27 _{TAG451}	yXF266	tRNA ^{Trp} _{CCA} ^d	C35>U in anticodon
Disruption of NMD pathway	CDC4 _{TAG9}	yXF255	<i>NAM7</i>	2670delC (frameshift)
	CDC4 _{TAG9}	yXF256	<i>NMD2</i>	828delC (frameshift)
	CDC4 _{TAG9}	yXF257	<i>NAM7</i>	Y79 (TAA mutation)

tRNA systematic name: ^aYNCL0034W; ^bYNCG0040C; ^cYNCM0022C; ^dYNCG0042C.

Table S2. The leftover scar interrupts analysis based on CRISPR-Cas9 system.

Escaper	OMeY-dependent strain (parental)	Causative interrupts	The leftover scar interrupts location
yXF273	yXF286	<i>SUP5</i> amber suppressor	Insertion of 1-bp T at base pair 43
yXF274	yXF286	<i>SUP3</i> amber suppressor	8-bp deletion between 41 and 48bp
yXF275	yXF286	<i>SUP5</i> amber suppressor	12-bp deletion between 36 and 47bp
yXF276	yXF237	<i>SUP8</i> amber suppressor	10-bp deletion between 40 and 49bp
yXF277	yXF237	<i>SUP4</i> amber suppressor	8-bp deletion between 40 and 47bp
yXF278	yXF237	<i>SUP8</i> amber suppressor	3-bp deletion between 40 and 42bp
yXF279	yXF237	<i>SUP5</i> amber suppressor	Insertion of 1-bp T at base pair 43
yXF280	yXF237	<i>SUP4</i> amber suppressor	Insertion of 1-bp A at base pair 40

Table S3. List of plasmids used in this study.

plasmid	Description	Source or reference
pXF231	<i>LEU2</i> , pRS315 carrying <i>LeuOmeRS/tRNA_{CUA}</i>	1
pXF473	<i>URA3</i> , pRS416 carrying <i>CDC27</i>	This study
pXF474	<i>URA3</i> , pRS416 carrying <i>CDC27_{TAG2}</i>	This study
pXF475	<i>URA3</i> , pRS416 carrying <i>CDC27_{TAG5}</i>	This study
pXF476	<i>URA3</i> , pRS416 carrying <i>CDC27_{TAG7}</i>	This study
pXF478	<i>URA3</i> , pRS416 carrying <i>CDC27_{TAG15}</i>	This study
pXF480	<i>URA3</i> , pRS416 carrying <i>CDC27_{TAG451}</i>	This study
pXF482	<i>URA3</i> , pRS416 carrying <i>CDC27_{TAG520}</i>	This study
pXF484	<i>HIS3</i> , pRS413 carrying <i>CDC4</i>	This study
pXF485	<i>HIS3</i> , pRS413 carrying <i>CDC4_{TAG270}</i>	This study
pXF486	<i>HIS3</i> , pRS413 carrying <i>CDC4_{TAG325}</i>	This study
pXF487	<i>HIS3</i> , pRS413 carrying <i>CDC4_{TAG327}</i>	This study
pXF488	<i>HIS3</i> , pRS413 carrying <i>CDC4_{TAG345}</i>	This study
pXF489	<i>HIS3</i> , pRS413 carrying <i>CDC4_{TAG370}</i>	This study
pXF495	<i>URA3</i> , pRS416 carrying <i>NMD3</i>	This study
pXF496	<i>URA3</i> , pRS416 carrying <i>NMD3_{TAG3}</i>	This study
pXF497	<i>URA3</i> , pRS416 carrying <i>NMD3_{TAG364}</i>	This study
pXF469	<i>HIS3</i> , pRS423 carrying <i>P_{GAL1}-SpCas9-NG-T_{ADH1},P_{SNR52}-gRNA1-SUF17-gRNA2-T_{SNR52}-sup8</i>	This study
pXF500	<i>HIS3</i> , pRS423 carrying <i>P_{GAL1}- SpCas9-NG</i>	This study
pXF509	<i>HIS3</i> , pRS313 carrying <i>LeuOmeRS/tRNA_{CUA}</i>	This study

Table S4. List of primers used in this study.

Primer Pair	Primer Sequence (5'-3') ^a	Description; construct generated
CDC27 ^{ts} -F	5'- CAAGACATGCTATAGAAAAGGCGCTAGCTTGTG	Site-directed mutagenesis G613 of Cdc27 to D; yXF243
CDC27 ^{ts} -R	ATCCTCAGCATTACAATGCATATTACGacttgggt acgagcgctatgaaattaggtc -3'	
CDC27 ^{ts} -KanMX-F	5'- CGTCAAGACTGTCAAGGAGGGTATTCTGGGC CTCCATGTcatcgaggaaccgcagacatgatg -3'	The <i>KanMX</i> cassette with homologous arm amplification primer;yXF243
CDC27 ^{ts} -KanMX-R	5'- gacatggaggccagaataaccctc -3' 5'- AAATAAAAAGTTTACGAATTAATACAATCAAAT TAGACACTGATACTATCAAGAAGTACcagtatagc gaccagcattcacatacgattg -3'	
CDC27-F	5'- gttgtcccatttggtagcttgg -3'	<i>CDC27</i> amplification primer;pXF473 and yXF216
CDC27-R	5'- atcgaggaaccgcagacatg -3'	
CDC4-F	5'- gcacttgaggaggattactttactttgagcc -3'	<i>CDC4</i> amplification primer;pXF484 and yXF217
CDC4-R	5'- ccttctcaactaaaaactgtactttccatatttcaggg -3'	
NMD3-F	5'- gaagtatgtttctatataacgggtgagaaaaatcg -3	<i>NMD3</i> amplification primer;pXF495
NMD3-R	5'- gcggaagttaaaaatcttgcgtaagagctc -3	
CDC27-A2-F	5'- cgaactttcgtgcaggatacataataaaaaatagcatgtaggtaaat cctgagtttagcaccgttcaccctctc -3'	Site-directed mutagenesis A2 of Cdc27 to TAG;pXF474
CDC27-A2-R	5'- gagaggggtgaacgggtgctaactcaggattacctacatgctattttat tatgtatcctgcacgaaaagttc -3'	
CDC27-P5-F	5'- gtgcaggatacataataaaaaatagcatggcggtaaattaggaggtta gcaccgttcaccctctcgagag -3'	Site-directed mutagenesis P5 of Cdc27 to TAG;pXF475 and yXF218
CDC27-P5-R	5'- ctctcgagaggggtgaacgggtgctaactcctaattaccgccatgcta ttttattatgtatcctgcac -3'	
CDC27-L7-F	5'- ggatacataataaaaaatagcatggcggtaaactcctgagtaggcac cgttcaccctctcgag -3'	Site-directed mutagenesis L7 of Cdc27 to TAG;pXF476
CDC27-L7-R	5'- ctcgagaggggtgaacgggtgcctactcaggattaccgccatgctatt tttattatgtatcctgc -3'	
CDC27-G15-F	5'- gagttagcaccgttcaccctctcgagatagatccccagctttgatgat caagctttgagc -3'	Site-directed mutagenesis G15 of Cdc27 to TAG;pXF478 and yXF219
CDC27-G15-R	5'- gctcaaagcttgatcatcaaagctggggatctatctcgagaggggtg aacgggtgctaactc -3'	
CDC27-N451-F	5'- taatttcgctttaatattaaggctgcatcacataactagtcgttcaagg caataagactgttcgag -3'	Site-directed mutagenesis N451 of Cdc27 to TAG;pXF480 and yXF220
CDC27-N451-R	5'- ctagtattgtgatgacgaccttaataataaagcgaaattatacatg - 3'	
CDC27-H520-F	5'- tctactttgctgtggcattttaggacaagggttaaatctcaaatttggc aaatgg -3'	Site-directed mutagenesis H520 of Cdc27 to TAG;pXF482 and yXF221
CDC27-H520-R	5'- aagatttaaccttgcctacaaatgccacagcaaagtagaaaaaat ttccatatc -3'	
CDC27-URA3-F	5'- gagagtgcaccataccacagcttttc -3'	The <i>URA3</i> cassette with homologous arm about <i>CDC27</i> amplification primer;yXF218,yXF219, yXF220 and yXF221
CDC27-URA3-R	5'- AAATAAAAAGTTTACGAATTAATACAATCAAAT	

	TAGACACTGATACTATCAAGAAGTACcggtattttct ccttacgcatctgtgc -3'	
CDC27-BleoR-F	5'- gacatggaggcccagaataaccctc -3'	The <i>BleoR</i> cassette with homologous arm about <i>CDC27</i> amplification primer;yXF230
CDC27-BleoR-R	5'- TAATACAATCAAATTAGACACTGATACTATCAA GAAGTACccggtagaggtgtggtcaataagagc -3'	
CDC4-F9-F	5'- tgag tag ccattacgtgatccctgttccttatagctac	Site-directed mutagenesis F9 of <i>Cdc4</i> to TAG;yXF222
CDC4-F9-R	5'- gtagctataaggaacaggggatcacgtaatgg ct actcagctaa gggaaacgaccccatc -3'	
CDC4-L270-F	5'- actttaatcaaggataa tag aagagggacctaataacgtctttgcct tttg -3'	Site-directed mutagenesis L270 of <i>Cdc4</i> to TAG;pXF485
CDC4-L270-R	5'- acgttattaggtccctct cta attatccttgattaaagtcaccaagtcg gatagttc -3'	
CDC4-F325-F	5'- ctgatatcgga aaatag gtgagccaaagggtttaattctctcaat c -3'	Site-directed mutagenesis F325 of <i>Cdc4</i> to TAG;pXF486 and yXF223
CDC4-F325-R	5'- aataaaacccttgggctcac cta attttccgatcagaagtttttc cacaacgatgtag -3'	
CDC4-S327-F	5'- cttctgatatcgga aaattt gtg tag ccaaagggtttaattctctcaa tctcaaactctcc -3'	Site-directed mutagenesis S327 of <i>Cdc4</i> to TAG;pXF487 and yXF224
CDC4-S327-R	5'- ttgg cta cacaaaattttccgatcagaagttttccacaacg - 3'	
CDC4-L345-F	5'- aatacccaaa tag tcacaacaagatcgcttagattatctttctgg -3'	Site-directed mutagenesis L345 of <i>Cdc4</i> to TAG;pXF488 and yXF225
CDC4-L345-R	5'- gataatctaaggcgatctgtgtg acta ttttgggtattttgggagagt ttgagattgag -3'	
CDC4-F370-F	5'- cattttaaaaaattggtacaatccaag tag gtaccacaaaggacc acgtaagaggc -3'	Site-directed mutagenesis F370 of <i>Cdc4</i> to TAG;pXF489
CDC4-F370-R	5'- ttgtggtac ct acttgggattgtaccaatttttaaatgaatatatttc c -3'	
CDC4-URA3-F	5'- gagagtgaccataccacagctttc -3'	The <i>URA3</i> cassette with homologous arm about <i>CDC4</i> amplification primer;yXF222, yXF223, yXF224 and yXF225
CDC4-URA3-R	5'- CTTTTATATTTTTTAGATCATTTTCAAACTTT CTTAAACcggtattttctcctacgcatctgtgc -3'	
NMD3-F3-F	5'- aatttgacaaaaggatgga tag acacctatagatccgcaccagc -3'	Site-directed mutagenesis F3 of <i>Nmd3</i> to TAG;pXF496
NMD3-F3-R	5'- tgcggtatctataggtgt ct attccatcctttgtcaaatcctcaacg - 3'	
NMD3-F364-F	5'- atctcgggtggtatttg ctag gcaggtgatagtgtatgggtatttcattg c -3'	Site-directed mutagenesis F364 of <i>Nmd3</i> to TAG;pXF497
NMD3-F364-R	5'- cccataacactatcacctgc cta gcaaataccaccgagatgagac ctg -3'	
ALG1-F250-F	5'- tag ataaagaattatattcgcatgattttgatacagaaaaaggc - 3'	Site-directed mutagenesis F250 of <i>Alg</i> to TAG;yXF226
ALG1-F250-R	5'- tttctgtatcaaaatcatcggaatataattcttat ct aggccttggtag ttagggccttttgacg -3'	

ALG1-URA3-F	5'- gagagtgcaccataccacagctttc -3'	The <i>URA3</i> cassette with homologous arm about <i>ALG1</i> amplification primer;yXF226
ALG1-URA3-R	5'- GCGCCATCTTCTAACGCCGGCTATGATAACAT TTTAGGAAcgggtattttctccttacgcatctgtgc -3'	
ERG8-Y401-F	5'- aggagttcttacttgcttaataacctggtgctggtggttaggacgccatt gcagtgattactaagc -3'	Site-directed mutagenesis Y401 of Erg8 to TAG;yXF227
ERG8-Y401-R	5'- ctaaccaccagcaccaggtattaagcaag -3'	
ERG8-URA3-F	5'- gagagtgcaccataccacagctttc -3'	The <i>URA3</i> cassette with homologous arm about <i>ERG8</i> amplification primer;yXF227
ERG8-URA3-R	5'- TAAATGACATAAAGTTATATATCTAGAAAGTTT ATTTATCcggtattttctccttacgcatctgtgc -3'	
RPN8-K7-F	5'- caaattacaatgtctctacaacacgagtagggtaccattgcaccatt agttttgctatc -3'	Site-directed mutagenesis K7 of Rpn8 to TAG;yXF228
RPN8-K7-R	5'- caatggtaaccctactcgtgttagagacattgtaattgattttcc -3'	
RPN8-URA3-F	5'- gagagtgcaccataccacagctttc -3'	The <i>URA3</i> cassette with homologous arm about <i>RPN8</i> amplification primer;yXF228
RPN8-URA3-R	5'- ACGAGAATAGAGGCGATATTATGCATTTATATT TGAAATTcggtattttctccttacgcatctgtgc -3'	
GDI1-T5-F	5'- tagatagacactgactacgacgtgattgtc -3'	Site-directed mutagenesis T5 of Gdi1 to TAG;yXF229
GDI1-T5-R	5'- cggtagcctaagacaatcacgtcgtagtcagtgctctatctattcttgatc cattgtgttatgctatataagtg -3'	
GDI1-URA3-F	5'- gagagtgcaccataccacagctttc -3'	The <i>URA3</i> cassette with homologous arm about <i>GDI1</i> amplification primer;yXF229
GDI1-URA3-R	5'- TTATGAATCAATCAGAATACGCATATAACAAAA AAAAAAcgggtattttctccttacgcatctgtgc -3'	
Pgal1-RPC11-F	5'- Y3GAATGCTGGTCGCTATACTGggatggacgcaaa gaagttaataatcatattac -3'	The <i>P_{gal1}</i> cassette with homologous arm about <i>RPC11</i> amplification primer;yXF239
Pgal1-RPC11-R	5'- TCAGTAGCATATTGTTACACGAAGGACAAAAC GAAAGCATtatagttttctccttgacgttaaagtatagagg -3'	
RPC11-KanMX-F	5'- TTTTGTGTTGCTCATGTCATAGCATTCAACTAC AGATGAAGacatggaggcccagaataccctc -3'	The <i>KanMX</i> cassette with homologous arm about <i>RPC11</i> amplification primer;yXF239
RPC11-KanMX-R	5'- AAACTTCTTTGCGTCCATCCcagtatagcgaccagca ttcacatacgattg -3'	
Pgal1-SKP1-F	5'- GAATGCTGGTCGCTATACTGggatggacgcaaagaa gtttaataatcatattac -3'	The <i>P_{gal1}</i> cassette with homologous arm about <i>SKP1</i> amplification primer;yXF240
Pgal1-SKP1-R	5'- GTGAATCGTTCACCCTCACCCTCACTAGGAC AACATTAGAAGTCACCATtatagttttctccttgacgttaa agtatagagg -3'	
SKP1-KanMX-F	5'- GACATTACCCTGCAGCGATTTAACGGGCGTCT TGGAGAAAAGAAGAGAAAgacatggaggcccagaata ccctc -3'	The <i>KanMX</i> cassette with homologous arm about <i>SKP1</i> amplification primer;yXF240
SKP1-KanMX-R	5'- AAACTTCTTTGCGTCCATCCcagtatagcgaccagca ttcacatacgattg -3'	
Pgal1-RPS3-F	5'- GAATGCTGGTCGCTATACTGggatggacgcaaagaa gtttaataatcatattac -3'	The <i>P_{gal1}</i> cassette with homologous arm about <i>RPS3</i> amplification primer;yXF241
Pgal1-RPS3-R	5'- TTCAGCGTAGAAGACACCGTCAGCGACTAGCT TTCTTTTCTTAGAGATTAAAGCGACCATtatagtttt tctccttgacgttaaagtatagagg -3'	

RPS3-KanMX-F	5'- GTAAATTCTCTTGTCTTTTTTCTTGATTTCAC TCTTTTCATGTTCTTTGGAATAATCgacatggag gcccagaataccctc -3'	The <i>KanMX</i> cassette with homologous arm about <i>RPS3</i> amplification primer;yXF241
RPS3-KanMX-R	5'- AAACTTCTTTGCGTCCATCCcagtatacgaccagca ttcacatacgattg -3'	
P _{CDC27} -URA3-F	5'- CTCGCCAAAAGCCATCTTCGTAC -3'	The <i>URA3</i> cassette with homologous arm about <i>CDC27</i> amplification primer;yXF303~319
P _{CDC27} -URA3-R	5'- CTTGATTTATCGAGAATGGAGCATTGAGC - 3'	The <i>URA3</i> cassette with homologous arm about <i>CDC4</i> amplification primer;yXF290~302
P _{CDC4} -URA3-F	5'- CCACTGAGAGCTGTTCGTAGATAAATC -3'	
P _{CDC4} -URA3-R	5'- CTCTGTCTCAACTGTCTTAGCC -3'	
SpCas9-NG-F	5'- ggattataaagatgacgatgacaaacctcc -3'	<i>SpCas9-NG</i> amplification primer; pXF469 and pXF500
SpCas9-NG-R	5'- gctatacctgagaaagcaacctgacctac -3'	
YPL062W-HIS-F	5'- cacatacgacactgcccctcacgtaagggcCACACCGCAT AGATCCGTCGAGTTTC -3'	Primers amplify the tGeS cassette;yXF281 and yXF282
YPL062W-HoR-R	5'- gggtcagcagtggtcaaatg -3'	
KanMX-F	5'-cggttggtgatgagtg -3'	Primer for specific gene <i>KanMX</i>
KanMX-R	5'-cgattccgactgtccaaca -3'	
P _{NMD3} -URA3-F	5'- AAGAGGGAATCGCTGATGGC -3'	The <i>URA3</i> cassette with homologous arm about <i>NMD3</i> amplification primer;yXF321-325
P _{NMD3} -URA3-R	5'- TCACAGTTTCTGCAAAATGAAATGTTTCG -3'	The <i>GFP</i> cassette with homologous arm about <i>NMD3</i> and <i>KanMX</i> amplification primer;yXF454 and yXF455
NMD3-GFP-F	5'- ATCTCAGCAGggatccgctggctccgctgctggttctggcga agcatccaagggcgaggagc -3'	
GFP-KanMX-R	5'- ATCTCGAGCTATTATTAGTGgtggtggtg -3'	
GFP-KanMX-F	5'- CACTAATAATAGCTCGAGATctcttaacaaactagc atttcagttatc -3'	The <i>KanMX</i> cassette with homologous arm about <i>GFP</i> and <i>NMD3</i> amplification primer; yXF454 and yXF455
KanMX-NMD3-R	5'- TCTTGCGTAAGAGCTCTACAAATGAAAAATCTT GCTTGCTATCTAGTTTgacatggaggccagaatac cc -3'	
pXF231-HIS-F	5'- ggagaaaataccgcatcaggaaattgtaaa -3'	The pXF231 amplification primer via inverse PCR; pXF509
pXF231-HIS-R	5'- agtacaatctgctgatgccgcatagtta -3'	
pXF231-HIS-R	5'- GTTTACAATTTCTGATGCGGTATTTCTCCgc attagtcaggaagtcataacacagtcc -3'	Primer to amplify <i>HIS3</i> cassette with homologous arm on pXF231; pXF509
pXF231-HIS-F	5'- TAACTATGCGGCATCAGAGCAGATTGTACTcac accgcatagatccgtcgagttc -3'	

^a Bolded are the locations for site-directed mutagenesis, while uppercase letters indicate oligonucleotide sequences added to the primers to facilitate cloning.

Table S5. List of strains used in this study.

Strain	Description	Source or reference
Strains:		
<i>S. cerevisiae</i>		
yXF215	<i>MATa ura3Δ0 leu2Δ0 his3Δ1 met15Δ0 [pXF231]</i>	This study
yXF216	<i>yXF215 Δcdc27::CDC27-URA3</i>	This study
yXF218	<i>yXF215 Δcdc27::CDC27_{TAG5}-URA</i>	This study
yXF219	<i>yXF215 Δcdc27::CDC27_{TAG15}-URA</i>	This study
yXF220	<i>yXF215 Δcdc27::CDC27_{TAG451}-URA</i>	This study
yXF221	<i>yXF215 Δcdc27::CDC27_{TAG520}-URA</i>	This study
yXF217	<i>yXF215 Δcdc4::CDC4-URA3</i>	This study
yXF222	<i>yXF215 Δcdc4::CDC4_{TAG9}-URA3</i>	This study
yXF223	<i>yXF215 Δcdc4::CDC4_{TAG325}-URA3</i>	This study
yXF224	<i>yXF215 Δcdc4::CDC4_{TAG327}-URA3</i>	This study
yXF225	<i>yXF215 Δcdc4::CDC4_{TAG345}-URA3</i>	This study
yXF230	<i>yXF215 Δcdc27::CDC27_{TAG520}-BleoR Δcdc4::CDC4_{TAG9}</i>	This study
yXF226	<i>yXF215 Δalg1::ALG1_{TAG250}-URA3</i>	This study
yXF227	<i>yXF215 Δerg8::ERG8_{TAG401}-URA3</i>	This study
yXF228	<i>yXF215 Δrpn8::RPN8_{TAG7}-URA3</i>	This study
yXF229	<i>yXF215 Δgdi1::GDI1_{TAG5}-URA3</i>	This study
yXF237	<i>yXF223 [pXF469]</i>	This study
yXF238	<i>yXF223 [pRS423]</i>	This study
yXF285	<i>yXF223 [pXF500]</i>	This study
yXF286	<i>yXF221 [pXF469]</i>	This study
yXF320	<i>yXF221 [pRS423]</i>	This study
yXF321	<i>yXF221 [pXF500]</i>	This study
yXF239	<i>yXF215 ΔP_{RPC11}-RPC11::KanMX-P_{GAL1}-RPC11</i>	This study
yXF240	<i>yXF215 ΔP_{SKP1}-SKP1::KanMX-P_{GAL1}-SKP1</i>	This study
yXF241	<i>yXF215 ΔP_{RPS3}-RPS3::KanMX-P_{GAL1}-RPS3</i>	This study
yXF251	<i>yXF241 Δcdc4::CDC4_{TAG9}-URA3</i>	This study
yXF252	<i>yXF241 Δcdc4::CDC4_{TAG325}-URA3</i>	This study
yXF253	<i>yXF241 Δcdc27::CDC27_{TAG5}-URA</i>	This study
yXF254	<i>yXF241 Δcdc27::CDC27_{TAG520}-URA</i>	This study
yXF290	<i>yXF241 Δcdc4::URA3-CDC4_{TAG4}</i>	This study
yXF291	<i>yXF241 Δcdc4::URA3-CDC4_{TAG5}</i>	This study
yXF292	<i>yXF241 Δcdc4::URA3-CDC4_{TAG6}</i>	This study
yXF293	<i>yXF241 Δcdc4::URA3-CDC4_{TAG7}</i>	This study
yXF294	<i>yXF241 Δcdc4::URA3-CDC4_{TAG9}</i>	This study
yXF295	<i>yXF241 Δcdc4::URA3-CDC4_{TAG12}</i>	This study
yXF296	<i>yXF241 Δcdc4::URA3-CDC4_{TAG13}</i>	This study
yXF297	<i>yXF241 Δcdc4::URA3-CDC4_{TAG14}</i>	This study
yXF298	<i>yXF241 Δcdc4::URA3-CDC4_{TAG15}</i>	This study
yXF299	<i>yXF241 Δcdc4::URA3-CDC4_{TAG16}</i>	This study
yXF300	<i>yXF241 Δcdc4::URA3-CDC4_{TAG18}</i>	This study

yXF301	yXF241 $\Delta cdc4::URA3-CDC4_{TAG19}$	This study
yXF302	yXF241 $\Delta cdc4::URA3-CDC4_{TAG20}$	This study
yXF303	yXF241 $\Delta cdc27::URA3-CDC27_{TAG4}$	This study
yXF304	yXF241 $\Delta cdc27::URA3-CDC27_{TAG5}$	This study
yXF305	yXF241 $\Delta cdc27::URA3-CDC27_{TAG6}$	This study
yXF306	yXF241 $\Delta cdc27::URA3-CDC27_{TAG7}$	This study
yXF307	yXF241 $\Delta cdc27::URA3-CDC27_{TAG8}$	This study
yXF308	yXF241 $\Delta cdc27::URA3-CDC27_{TAG9}$	This study
yXF309	yXF241 $\Delta cdc27::URA3-CDC27_{TAG10}$	This study
yXF310	yXF241 $\Delta cdc27::URA3-CDC27_{TAG11}$	This study
yXF311	yXF241 $\Delta cdc27::URA3-CDC27_{TAG12}$	This study
yXF312	yXF241 $\Delta cdc27::URA3-CDC27_{TAG13}$	This study
yXF313	yXF241 $\Delta cdc27::URA3-CDC27_{TAG14}$	This study
yXF314	yXF241 $\Delta cdc27::URA3-CDC27_{TAG15}$	This study
yXF315	yXF241 $\Delta cdc27::URA3-CDC27_{TAG16}$	This study
yXF316	yXF241 $\Delta cdc27::URA3-CDC27_{TAG17}$	This study
yXF317	yXF241 $\Delta cdc27::URA3-CDC27_{TAG18}$	This study
yXF318	yXF241 $\Delta cdc27::URA3-CDC27_{TAG19}$	This study
yXF319	yXF241 $\Delta cdc27::URA3-CDC27_{TAG20}$	This study
yXF243	BY4741 $\Delta cdc27::CDC27^{G613D}$ -KanMX	This study
YFL009W ^{ts}	MATa <i>his3Δ1 leu2Δ0 ura3Δ0 LYS2 MET5 can1Δ::LEU2-MFA1pr-HIS3 $\Delta cdc4::CDC4^{ts}$-URA3</i>	Junbiao Dai's lab
yXF289	YFL009W ^{ts} <i>leu2-his3::BleoR</i>	This study
yXF244	BY4741 $\Delta nmd3::NMD3^{ts}$ -KanMX	²
yXF287	yXF222 $\Delta upf1::KanMX$	This study
yXF288	yXF222 $\Delta upf2::KanMX$	This study
yXF281	yXF307 YPL062W::tGeS-HIS3	This study
yXF282	yXF215 YPL062W::tGeS-HIS3	This study
yXF448	yXF215 $\Delta nmd3::URA3-NMD3$	This study
yXF449	yXF215 $\Delta nmd3::URA3-NMD3_{TAG4}$	This study
yXF450	yXF215 $\Delta nmd3::URA3-NMD3_{TAG6}$	This study
yXF451	yXF215 $\Delta nmd3::URA3-NMD3_{TAG10}$	This study
yXF452	yXF215 $\Delta nmd3::URA3-NMD3_{TAG11}$	This study
yXF453	yXF215 $\Delta nmd3::URA3-NMD3_{TAG13}$	This study
yXF454	yXF448 $\Delta nmd3::NMD3$ -GFP-KanMX	This study
yXF455	yXF453 $\Delta nmd3_{TAG13}::NMD3_{TAG13}$ -GFP-KanMX	This study
yXF456	MATa <i>his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 $\Delta cdc27::CDC27_{TAG5}$-URA3 [pXF509]</i>	This study
yXF457	MATa <i>his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 $\Delta cdc27::CDC27_{TAG5}$-URA3 ΔP_{RPC11}-RPC11::KanMX-P_{GAL1}-RPC11 [pXF509]</i>	This study
<i>E. coli</i>		
DH5 α	F ⁻ 80dlacZ M15 (<i>lacZYA-argF</i>) U169 <i>recA1 endA1</i> hsdR17(<i>rk⁻, mk⁺</i>) <i>phoA</i> supE44 <i>-thi-1</i> gyrA96 <i>relA1</i>	Vazyme Cat number: C504-02

Sequence of customized plasmid used in this study

pXF231: **TDH3 promoter**, **LeuOmeRS**, **CYC1 terminator**, **tRNA^{CUA}_{Leu}**, **SNR52 promoter**

Note: The backbone is pRS315.

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pXF509: TDH3 promoter, LeuOmeRS, CYC1 terminator, tRNA^{CUA}^{Leu}, SNR52 promoter

Note: The backbone is pRS313

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aacgcgcga

pXF495-497: NMD3 promoter, NMD3 (TAG codon), NMD3 terminator

Note: The blue corresponding codon were individually replaced with the TAG stop codon via site-directed mutagenesis.

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pXF469/pXF500: GAL1 promoter, SpCas9-NG, ADH1 terminator, SNR52 promoter, gRNA1, SUF17, gRNA2, SNR52 terminator, sub8

15

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