

Supplementary material

Table S1. Summary of label free quantification and significance analyses for transcription factors, and proteins involved in retrograde response and ergosterol or heme biosynthesis for *S. cerevisiae* CEN.PK113-7D and UFMG-CM-Y259 cultivated in aerobic batch bioreactors with either sucrose or glucose as sole carbon source.

Accession	Gene code	Log2_(Suc/Glu)	Significance	Function
Transcription factor				
CEN.PK113-7D				
Q12363	WTM1	0.7312	27.22	Transcriptional modulator WTM1
P11938	RAP1	0.6229	20.47	DNA-binding protein RAP1
P14922	CYC8	1.1570	37.27	General transcriptional corepressor CYC8
P32485	HOG1	-0.4540	33.07	Mitogen-activated protein kinase HOG1
UFMG-CM-Y259				
P32608	RGT2	0.5059	14.01	Retrograde regulation protein 2
P14922	CYC8	-0.8890	18.61	General transcriptional corepressor CYC8
Q03973	HMO1	-0.4344	22.78	High mobility group protein 1
Q12363	WTM1	-0.6439	25.40	Transcriptional modulator WTM1
Retrograde target				
CEN.PK113-7D				
P41939	IDP2	-0.4941	14.57	Isocitrate dehydrogenase [NADP] cytoplasmic
P28834	IDH1	0.5059	44.72	Isocitrate dehydrogenase [NAD] subunit 1 mitochondrial
P28241	IDH2	0.3561	17.86	Isocitrate dehydrogenase [NAD] subunit 2 mitochondrial
UFMG-CM-Y259				
P08679	CIT2	-0.8890	24.20	Citrate synthase peroxisomal
P19414	ACO1	-0.4540	24.11	Aconitate hydratase mitochondrial
P41939	IDP2	-0.4540	28.86	Isocitrate dehydrogenase [NADP] cytoplasmic
P28834	IDH1	-0.4739	17.81	Isocitrate dehydrogenase [NAD] subunit 1 mitochondrial

Accession	Gene code	Log2_(Suc/Glu)	Significance	Function
P28241	IDH2	-0.6666	52.80	Isocitrate dehydrogenase [NAD] subunit 2 mitochondrial
Ergosterol or heme biosynthesis				
CEN.PK113-7D				
P54839	ERG13	0.7991	40.05	Hydroxymethylglutaryl-CoA synthase
P07143	CYT1	0.5656	25.95	Cytochrome c1 heme protein mitochondrial
P11353	HEM13	0.6229	21.05	Oxygen-dependent coproporphyrinogen- III oxidase
P21147	OLE1	1.2690	21.52	Acyl-CoA desaturase 1
UFMG-CM-Y259				
P32476	ERG1	0.4436	17.94	Squalene monooxygenase
P54781	ERG5	0.5460	28.03	Cytochrome P450 61
P10614	ERG11	0.2750	24.54	Lanosterol 14-alpha demethylase
P07277	ERG12	1.3951	19.63	Mevalonate kinase
P54839	ERG13	0.5850	18.04	Hydroxymethylglutaryl-CoA synthase
P53199	ERG26	0.7137	27.93	Sterol-4-alpha-carboxylate 3- dehydrogenase decarboxylating
P32352	ERG2	-0.2863	17.05	C-8 sterol isomerase
P32353	ERG3	-0.2863	15.41	Delta(7)-sterol 5(6)-desaturase
P53045	ERG25	-2.0000	16.54	Methylsterol monooxygenase
P09950	HEM1	0.4647	19.40	5-aminolevulinic acid synthase mitochondrial
P05373	HEM2	0.7398	17.85	Delta-aminolevulinic acid dehydratase
P28789	HEM3	1.0072	26.17	Porphobilinogen deaminase
P40075	SCS2	0.9411	21.38	Vesicle-associated membrane protein- associated protein

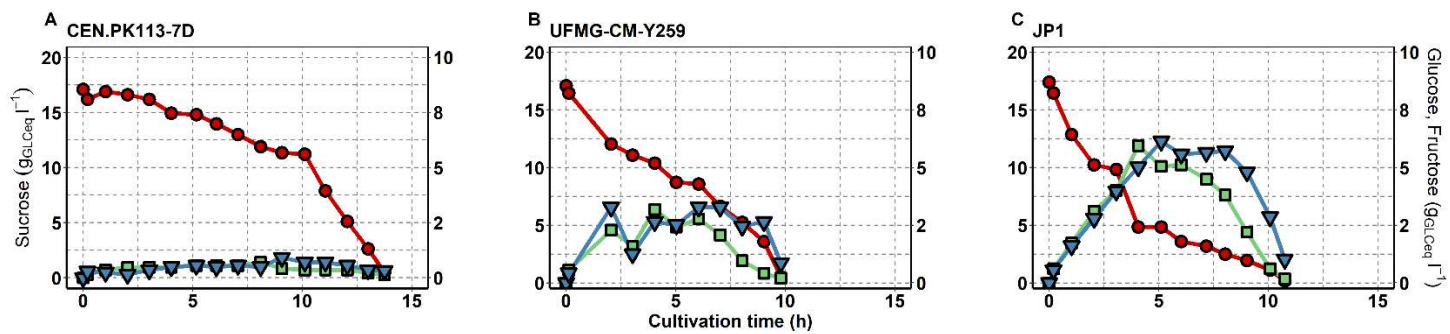


Figure S1. Sugar concentration during aerobic batch cultivations of *S. cerevisiae* CEN.PK113-7D, UFMG-CM-Y259, and JP1 in synthetic medium supplemented with sucrose as sole carbon and energy source.