

Table S1 Genetic characteristics of the paralogs considered for deletion

Genes that were deleted in this study are marked in red. Protein similarity was based on global alignment using BLOSUM62 of the translated genes of the *S. cerevisiae* CEN.PK113-7D genome sequence (Salazar *et al.* 2017). WGD pairs are indicated (Byrne and Wolfe 2005).

Pathway	Gene	% Protein Similarity	Type of duplication
Pentose phosphate pathway	<i>GND1</i> (YHR183W) / <i>GND2</i> (YGR256W)	87%	WGD
	<i>TKL1</i> (YPR074C) / <i>TKL2</i> (YBR117C)	71%	WGD
	<i>SOL3</i> (YHR163W) / <i>SOL4</i> (YGR248W)	47%	WGD
	<i>TAL1</i> (YLR354C) / <i>NQM1</i> (YGR043C)	68%	WGD
TCA cycle + anaplerotic reactions	<i>PYC1</i> (YGL062W) / <i>PYC2</i> (YBR218C)	92%	WGD
	<i>SDH1</i> (YKL148C) / <i>SDH1b</i> (YJL045W)	84%	WGD
	<i>SDH3</i> (YKL141W) / <i>SHH3</i> (YMR118C)	42%	WGD
	<i>SDH4</i> (YDR178W) / <i>SHH4</i> (YLR164W)	47%	WGD
	<i>CIT1</i> (YNR001C) / <i>CIT2</i> (YCR005C) / <i>CIT3</i> (YPR001W)	<i>CIT1/CIT2</i> =75% <b><i>CIT1/CIT3</i>=42%</b>	<i>CIT1/CIT2</i> =WGD
Mitochondrial transporters	<i>AAC1</i> (YMR056C) / <i>AAC2</i> (YBL030C) / <i>AAC3</i> (YBR085W)	<i>AAC2/AAC1</i> =73% <i>AAC2/AAC3</i> =87%	<i>AAC2/AAC3</i> =WGD
	<i>SAL1</i> (YNL083W)		
	<i>MPC1</i> (YGL080W) / <i>MPC2</i> (YHR162W) / <i>MPC3</i> (YGR243W)	<b><i>MPC2/MPC3</i>=65%</b> <i>MPC2/MPC1</i> =25%	<i>MPC2/MPC3</i> =WGD
	<i>CTP1</i> (YBR291C)		
	<i>ODC1</i> (YPL134C) / <i>ODC2</i> (YOR222W)	61%	WGD
	<i>NDT1</i> (YIL006W) / <i>NDT2</i> (YEL006W)	51%	WGD
	<i>OSM1</i> (YJR051W) / <i>FRDS1</i> (YEL047C)	59%	WGD
Glyoxylate and TCA cycle	<i>IDP1</i> (YDL066W) / <i>IDP2</i> (YLR174W) / <i>IDP3</i> (YNL009W)	<i>IDP1/IDP3</i> =65% <i>IDP2/IDP3</i> =73%	<i>IDP2/IDP3</i> =WGD

<b>acetyl-CoA synthesis</b>	<i>ALD2</i> (YMR170C) / <i>ALD3</i> (YMR169C)	91%	
<b>Glycerol synthesis</b>	<i>GPD1</i> (YDL022W) / <i>GPD2</i> (YOL059W)	72%	WGD
	<i>GPP1</i> (YIL053W) / <i>GPP2</i> (YER062C)	92%	WGD

Salazar AN, Gorter de Vries AR, van den Broek M et al. Nanopore sequencing enables near-complete *de novo* assembly of *Saccharomyces cerevisiae* reference strain CEN.PK113-7D. FEMS Yeast Res 2017;17.

Byrne KP, Wolfe KH. The Yeast Gene Order Browser: combining curated homology and syntenic context reveals gene fate in polyploid species. Genome Res 2005;15: 1456-61.