Key to deletion results

ORF ORF name
Name Gene name

Annotation Gene annotation (from SGD)
Ess sim Essential (YPD) simulation
Ess call Essential call (FP/TN)
Slow sim Slow growth simulation

Slow exp Slow growth experimental [Giaever02]

Slow call Slow growth call (FP/TN)

MMD sim Glucose minimal media simulation

MMD experimental (1=normal growth, 0=retarded growth)

MMD average of experimental scores

MMD call (FP/FN/TP/TN)
YPGal sim YP galactose simulation

YPGal exp YPGal experimental (1=normal growth, 0=retarded growth)

YPGal average of experimental scores

YPGal call (FP/FN/TP/TN)

YPD sim YPD simulation
YPD exp YPD experimental
YPD call YPD call (FP/FN/TP/TN)
YPDGE sim YPDGE experimental
YPDGE call YPDGE call (FP/FN/TP/TN)

YPG sim YPG simulation
YPG exp YPG experimental
YPG call (FP/FN/TP/TN)

YPE sim YPE simulation
YPE exp YPE experimental
YPE call (FP/FN/TP/TN)

YPL sim YPL simulation
YPL exp YPL experimental
YPL call (FP/FN/TP/TN)

Class Primary source for false prediction(s)

Explanation Detailed explanation for false prediction(s)

Forster et al Result in Forster et al. study - only false predictions are listed

Abbreviations for sources for false predictions

Acc Accumulation of a toxic intermediate

Bio Problems with in silico biomass constitution

Den Dead end in the in silico model
Dis Discrepancy in experimental data

Iso Problems with in silico gene-protein-reaction associations

Med Problems with in silico media composition
Mod Problems with in silico model structure

Oth Involvement of the gene in non-metabolic processes

Reg Missing transcriptional regulation
Unk Unknown source for false prediction

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ORF	ame		ss sim	ss call	ow sim	ow exp	ow ca	MD sim	MD ex	AIMD ave	MD call	Gal sim	Gal exp	PGal ave	PGal cal	/PD sim	PD exp	PD call	PDGE sim	PDGE exp	PDGE	/PG sim	PG exp	G call	/PE sim	/PE exp	PE call	/PL sim	PL exp	L call	Class	Explanation Explanation
		Annotation ADP/ATP translocator	NA.	ES	NA	NA	Š	2	Ξ	_	Ē TP	<u>}</u>	_	.06	⋝	_	_	<u> </u>				_	.03	_	1.12	1.03	TP 1		⊭ 1.03	,	NA	
TWKUSOC	AACT	Adenine aminohydrolase (adenine	INA	INA	INA	INA	INA		<u> </u>	0.04	IF	-	1 -0	1.06	IF I	.06	1.02 1	P	1.1	1.02	IF I	.11	.03	IF.	1.12	1.03	IF	.11	1.03	IF	INA	INA INA
YNL141W	AAH1	deaminase)	NA	NA	NA	NA	NA	1	1 -	0.01	TP	1	1 -0	.07	TP 1	.08	1 T	ΓP 1			TP 1				1.12		TP 1		1		NA	NA NA
YKL106W	AAT1	Aspartate aminotransferase	NA	NA	NA	NA	NA	1	1 -	0.04	TP	1	1 -(.05	TP 1	.08	D.98 T	ΓP 1	1.1	0.97	ΓP 1	.09 0).87	TP 1	1.11	0.82	TP	1.1 (0.84	TP	NA	NA NA
YLR027C	AAT2	Aspartate aminotransferase	NA	NA	NA	NA	NA	1	1	0.96	TP	1	1	0 -	TP 1	.08 0	0.93 T	ГР 1	1.1	0.83	-P 1	.08 0	0.74	FP 1	1.11	0.65	FP	1.1	0.87	TP	Unk	The model correctly predicts that the effect of the deletion is larger on non-fermentable carbon sources, but the predicted change in growth rate is too small for the slow growth criterion. The model does not predict higher growth of lactate than on other non-fermentable carbon sources though.
		Aminodeoxychorismate synthase			NA					0.04										1.01												
YGR037C	ACB1	Acyl-CoA-binding protein (ACBP)/diazepam binding inhibitor (DBI)/endozepine (EP)			NA		NA	0	1 (0.23	FN	0	1 -(1.04 F	₹N	0 0	0.93 F	FN.	0	0.97 F	-N	0 0).94 [FN	0	0.95	FN	0 (0.94	FN	Unk	Product of ACB1 is part of FAS complex; involved in termination of fatty acid synthesis and transport of newly synthesized acyl-CoA esters from the fatty acid synthetase to acyl-CoA-consuming processes, may also transport mediumand long-chain acyl CoA esters [MIPS]; since enzymatic mechanism is unknown and transport function is not well defined, may want to remove from FAS complex.
YNR016C		Acetyl CoA carboxylase	0		NA	NA	NA	NA	NA	NA	NA	NA I						A N		NA I			NA I			NA		NA	NA	NA	NA	NA NA
YBL015W	ACH1	Acetyl CoA hydrolase	NA	NA	NA	NA	NA	1	1 -	0.01	TP (0.99	1 -0	.05	TP 1	.08 1	1.03 T	ΓP 1	1.1	1.05	TP 1	1.1 1	.04	TP (0.96	1.06	TP 1	.11	1.06	TP	NA	NA NA
YLR304C	ACO1	Aconitase	NA	NA	1	3.6	FP	1	1 .	0.02	TP	1	1 (TD 4	00 0	2 06 5	D 1		0.75 F	-D 4	11 0	. 50	ED 4	1 12	0.50	ED.	11	0.6	FP	Iso	YJL200C codes for an isozyme for Aco1p, but Aco1p is probably the major isoform. NA
TLK304C	ACOT	Aconitase	INA	INA		3.0	FF		- '	0.02	IF	-	1 -0	1.04	IF I	.06 (J.00 F	P	1.1	0.75	FI	.11 ().59	r P	1.12	0.52	FF	. 1 1	0.6	FF	150	Acp1p used in synthesis of fatty-acyl ACPs, which are not
YKL192C		Acyl carrier protein	1	FP	NA	NA	NA	NA	NA	NA	NA	NA I	NA I	A A	1 AV	NA I	NA N	A N	NA	NA I	1 A	NA I	NA I	NA	NA	NA	NA	NA	NA	NA	Bio	required in the model. NA
		Acetyl CoA synthetase	_	_	NA	NA	NA	1	_		TP	1		.03	_					1.02											NA	NA NA
YLR153C	ACS2	Acetyl CoA synthetase Phosphoribosyl amino	0	IN	NA	NA	NA	NA	NA	NA	NA	NA I	NA I	1 AV	1 AV	NA I	NA N	1 AI	VA	NA I	NA I	VA I	NA I	NA	NA	NA	NA	NA	NA	NA	NA	NA FP
		imidazolesuccinocarbozamide																														Should be an adenine auxotroph [SGD] - should not grow
YAR015W	ADE1	synthetase	NA	NA	NA	NA	NA	0	1 (0.02	FN	1	1	0	TP 1	.08	0.97 T	ΓP 1	1.1	0.93	TP 1	.11 0	0.99	TP 1	1.12	0.97	TP 1	.11	0.95	TP	Med	normally on minimal media. NA
YNL220W	ADE12	Adenylosuccinate synthetase	NA	NA	1	4.5	FP	0	1 -	0.01	TN	1	1	0 -	TP 1	NA I	NA N	1 AI	NA	NA I	1 AV	NA I	NA I	NA	NA	NA	NA	NA	NA	NA	Med	
VI DOEOW	ADE40	A depute que cipate luga e	,		NIA	NIA	NIA	NIA		NIA		NIA .				NIA .				NIA N					NIA	NIA	NIA	NIA	NI A		Mad	Null mutant is an adenine auxotroph [MIPS]. The deletion is
		Adenylosuccinate lyase 5-aminoimidazole-4-carboxamide ribonucleotide (AICAR) transformylase/IMP cyclohydrolase	NA NA		NA NA	NA NA		NA 1		0.01		NA I		0.01						NA N						NA 1.05					Med NA	
		5-aminoimidazole-4-carboxamide ribonucleotide (AICAR)																														
YMR120C	ADE17	transformylase/IMP cyclohydrolase	NA	NA	NA	NA	NA	1	1 -	0.02	TP	1	1 -0	.02	TP 1	.08 1	1.01 T	rP 1	1.1	1.01	TP 1	.11 1	.01	TP 1	1.12	1.02	TP 1	.11	1.02	ТР	NA	NA NA
		C1-tetrahydrofolate synthase	NA	_	NA	NA		0		2.08										0.99							TP 1		1		NA	Weak false negative FN
VMDOOOO	ADE 4	Phosphoribosylpyrophosphate						_	_	4.0						00	, ,			4.04	-						TD				NIA	NA NA
YMR300C	ADE4	amidotransferase Aminoimidazole ribotide	NA	NA	NA	NA	NA	0	0	4.2	TN	1	1 -(0.06	IP 1	.08	1 1	IP 1	1.1	1.01	IP 1	.11 1	1.02	IP 1	1.12	1	TP 1	.11	1	IP	NA	
YGL234W	ADE5,	synthetase glycinamide ribotide synthetase 5'-phosphoribosylformyl	NA	NA	NA	NA	NA	0	1 (0.95	FN	1	1 -0	.03	TP 1	.08	D.99 T	гР 1	1.1	0.99	ГР 1	.11	1	TP 1	1.12	1	TP 1	.11 (0.99	TP	Med	Should be an adenine auxotroph [SGD] - should not grow normally on minimal media.
YGR061C	ADE6	glycinamidine synthetase	NA	NA	NA	NA	NA	0	0	5.08	TN	1	1 -0	.02	TP 1	.08 1	1.03 T	гР 1	1.1	1.03	ГР 1	.11 1	.03	TP 1	1.12	1.04	TP 1	.11	1.03	TP	NA	NA NA
YDR408C	ADE8	Glycinamide ribotide transformylase	NA	NA	NA	NA	NA	0	1	1.1	TN	1	1	0 -	TP 1	.08	1 T	ΓP 1	1.1	1.01	ΓP 1	.11 1	1.02	TP 1	1.12	1.02	TP 1	.11	1.02	TP	NA	
																																Most likely a regulatory effect as this may be the only isozyme (out of five) active under severely glucose repressed
		Alcohol dehydrogenase				10.1				0	TP	1	1	0	TP 1	.08	0.76 F	P 1	1.1	0.87	ΓP 1	.11 1	1.12	TP 1	1.12	1.09	TP 1	.11	1.15	TP	Reg	conditions. NA
YMR303C	ADH2	Alcohol dehydrogenase II Alcohol dehydrogenase isoenzyme	NA	NA	NA	NA	NA	1	1 (0.13	12	1	1 -(.04	IP 1	.08	1 1	1	1.1	1	1 1	.11 1	.01	12 1	1.12	0.98	17 1	.11 (J.99	11	NA	NA NA
YMR083W	ADH3	III	NA	NA	NA	NA	NA	1	1	1.2	TP	1	1 -0	.01	TP 1	.08	D.98 T	TP 1	1.1	0.97	TP 1	.11	0.97	TP 1	1.12	0.93	TP 1	.11	0.95	TP	NA	NA NA
YGL256W	ADH4		NA	NA	NA	NA	NA	1	1 -	0.03	TP	1	1 -0	0.07	TP 1	.08 1	1.02 T	ΓP 1	1.1	1.02	ΓP 1	.11 1	1.01	TP 1	1.12	1.03	TP 1	1.11	1.02	TP	NA	NA NA
VDD4.45\41	4 D. 15	Alcohol dehydrogenase isoenzyme	l ,,.		ļ ,	,				0.00	[, [[4.00						4.60					NI A	NA
	ADH5 ADK1	Adenylate kinase	NA NA				NA TN	0	1 -	0.03		0		0.04						1.02 T												
		Adenylate kinase mitochondrial																														
YER170W	ADK2	GTP:AMP phosphotransferase	NA	NA	NA	NA	NA	1	1 (0.04	TP	1	1 0	.02	TP 1	.08 1	1.01 T	TP 1	1.1	1.02	TP 1	.11 1	.02	TP 1	1.12	1.03	TP 1	.11	1.02	TP	NA	NA NA

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ų,	me		ssim	ss call	Slow sim	w exp	w call	MMD sim	MD exp	имр аve	IMD call	/PGal sim	PGal exp	'PGal ave	PGal call	'PD sim	/PD exp	PD call	PDGE sim	PDGE exp	PDGE cal	PG sim	PG exp	PG call	'PE sim	PE exp	PE call	PL sim	dxe 7	L call	Class	Explanation Explanation
O. P.	Na	Annotation	Es	Ess	Slo	Sio	Sio	Σ	2	Σ	Σ	Ă.	γÞ	Ă.	ΥP	ΥP	γP	ΥP	ΥP	ΥP	ΥP	Ϋ́	γP	ΥP	∠	ΥP	Υ	∠	YPL	YPL	ਠੱ	Explanation There is an alternative pathway involving Pnp1p that can
																																substitute for the function of this adenosine kinase. This
YJR105W	ΔDO1	Adenosine kinase	ΝΔ	ΝΔ	NA	NA	NΔ	. 1	1	0.73	TP	1	1	0	TD	1 08	0.70	FD	11	0.8	FD	1 11	0 04	тр	1 12	0.00) TE	1.11	١١٥٥	и тр	Unl	activity of Pnp1p does not seem to have been established conclusively in the literature.
YCL025C		Amino acid permease			NA					-0.04		1	1	0		1.08																NA NA NA
		The acronym may be misleading. AGP3 has not been shown to be a																														
		general amino acid permease with																														
YFL055W	AGP3	broad substrate specificity Cytoplasmic alanyl-tRNA	NA	NA	NA	NA	NA	1	1	0.12	TP	1	1	-0.02	TP	1.08	1.03	TP	1.1	1.03	TP	1.11	0.99	TP	1.12	1.03	3 TF	1.11	1.0	1 TP	NA	NA NA
YOR335C	ALA1	synthetase gene	1	FP	NA	NA	NA	NA	NA	NA		NA																NA		NA	Oth	Protein synthesis not required in the model. NA
YMR170C YMR169C		Aldeyhde dehydrogenase Aldehyde dehydrogenase	NA NA		NA NA		_	1	1	0.08	TP TP	1	1	-0.04 0	TP TP	1.08	_	TP										1.11				NA NA NA
		Aldehyde dehydrogenase			NA		_	1	1	0.02	TP	1	1	-0.08	TP	1.08	1.01	TP		1.02		1.11						1.11				NA NA
YER073W	ALD5	Aldehyde dehydrogenase	NA	NA	NA	NA	NA	1	1	0.02	TP	1	1	-0.03	TP	1.08	1.01	TP	1.1	1.03	TP	1.11	1.07	TP	1.12	1.07	7 TF	1.11	1.0	6 TP	NA	NA NA The model uses a mitochondrial acetaldehyde
																																dehydrogenase in the deletion strain. In vivo this activity
YPL061W		Aldehyde dehydrogenase Basic amino acid permease	NA NA	_	NA			1	1	0.1	TP	1		-0.04	TP TP					0.91								1.11				c cannot fully compensate for the cytoplasmic activity. NA NA NA
YNL270C YML035C		AMP deaminase			NA NA			1	1	-0.01 -0.01	TP TP	1	1	-0.07 -0.01	TP	1.08	1.02	TP TP		0.99								1.11			NA NA	NA NA
		Amidase (putative)			NA			1	1	-0.02	TP	1	1	0	TP	1.08		TP		1.01			1					1.11			NA	NA NA
YPR128C	ANTT	Adenine nucleotide transporter Diadenosine 5',5"'-P1,P4-	NA	NA	NA	NA	NA	1	1	0.02	TP	1	1	-0.04	TP	1.08	1.01	IP	1.1	0.99	IP	1.11	0.99	IP	1.12	1	11-	1.11	1.0	1 11	INA	NA NA
YCL050C	APA1	tetraphosphate phosphorylase I	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1	-0.07	TP	1.08	1.01	TP	1.1	1.04	TP	1.11	1.06	TP	1.12	1.07	7 TF	1.11	1.0	6 TP	NA	NA NA
YDR530C	APA2	5',5"'-P-1,P-4-tetraphosphate phosphorylase II	NA	NA	NA	NA	NA	. 1	1	-0.04	TP	1	1	-0.06	TP	1.08	1.02	TP	1.1	1.04	TP	1.11	1.03	TP	1.12	1.06	S TF	1.11	1.0	4 TP	NA	NA NA
\/ \ 41, 000\\	4 DT4	A		İ			Ī																									
YML022W	AP11	Adenine phosphoribosyltransferase	NA	NA	NA	NA	NA	1	1	1.41	TP	1	1	0	TP	1.08	0.96	TP	1.1	0.95	TP	1.11	0.96	TP	1.12	0.96	S TF	1.11	0.9	6 TP	NA	NA NA
		Similar to adenine																														
YDR441C	APT2	phosphoribosyltransferase; appears to be a nonfunctional pseudogene	NA	NA	NA	NA	NA	. 1	1	0.11	TP	1	1	-0.02	TP	1.08	0.99	TP	1.1	1	TP	1.11	0.97	TP	1.12	1.01	I TF	1.11	1.0	1 TP	NA	NA NA
YBR149W	ARA1	D-arabinose dehydrogenase	NA	NA	NA	NA	NA		1	0.01	TP	1	1	-0.03	TP	1.08	0.99	TP	1.1		TP	1.11	1	TP	1.12	0.98	3 TF	1.11	0.9	8 TP	NA	NA NA
YOL058W YJL071W		Arginosuccinate synthetase Acetylglutamate synthase	_	NA NA	NA NA	_	-	0	_	5.51 3.27	TN TP	1	1	-0.07 -0.06	TP TP	1.08	1.01		1.1	_	_	1.11						1.11			NA NA	
YJL088W	ARG3	Ornithine carbamoyltransferase	NA	NA	NA	NA	NA		1	2.1	TN	1	1	-0.01	ΤP	1.08	1.02	TP	1.1	1.03	TP	1.11	1.05	TP	1.12	1.04	1 TF	1.1	1.0	4 TP	NA	Weak false negative NA
YHR018C	ARG4	Argininosuccinate lyase N-acetyl-gamma-glutamyl-	NA	NA	NA	NA	NA	0	1	6.58	TN	1	1	0	TP	1.08	1.01	TP	1.1	1.02	TP	1.11	1.03	TP	1.12	1.04	1 TF	1.1	1.0	3 TP	NA	Weak false negative NA
		phosphate reductase and																														
YER069W	ARG5	acetylglutamate kinase 3-dehydroquinate dehydratase (3-	NA	NA	NA	NA	NA	. 0	1	2.36	TN	1	1	-0.06	TP	1.08	1	TP	1.1	1.02	TP	1.11	1.02	TP	1.12	1.01	I TF	1.11	1.0	1 TP	NA	Weak false negative NA
		dehydroquinase) 3-dehydroquinate																														
		synthase epsp synthase pentafunctional arom																														
		polypeptide shikimate 5-																														FP for rich media - TN for MMD. There appears to be an
	ARO1	dehydrogenase shikimate kinase		NΑ	1 NA	10.5 NA		0	1	-0.03 -0.05		1		-0.03 -0.02		1.08		TP				1.11						1.11				d extra component in the in silico rich medium. NA NA NA
YGL148W		Chorismate synthase			NA		_	0	1	5.13		1	_	-0.02	_			TP		1.03		1.11						1.11				
		DAHP synthase; a.k.a. phospho-2-dehydro-3-deoxyheptonate																														
		aldolase, phenylalanine-inhibited;																														
		phospho-2-keto-3-deoxyheptonate aldolase; 2-dehydro-3-																														
		deoxyphosphoheptonate aldolase; 3																														
VDB03EW	A D O 2	deoxy-D-arabine-heptulosonate-7-	NIA.		NIA	NIA		,		0.00	TD	,	4	0.05	TD	4.00	4 04	TD	4.4	4.00			4.00	TD	4 40	4.00	. _		1 4 0		NIA	NA NA
1 DK035W	ARU3	phosphate synthase 3-deoxy-D-arabino-heptulosonate 7-	NA	INA	NA	NA	INA	Т	1	-0.03	12			-0.05	1P	1.08	1.01	112	1.1	1.03	IP.	1.11	1.03	۱P	1.12	1.06) 16	1.11	1.0	o IP	NA	NA NA
VPP240C	ABO4	phosphate (DAHP) synthase	NI A	N/A	NI A	NIA.	NIA			0.04			1	0.04	TD	1.00	1.00	TD	1.4	1.00	TD	1 11	1.00	ТЪ	1 40	1.0	J.,	1 4 4	4.0	4 T.	NIA.	NA NA
YBR249C YPR060C		isoenzyme Chorismate mutase			NA NA			0		0.04 3.64		1		-0.02																		NA NA NA
VGI 202/M		Aromatic amino acid aminotransferase	NIA	NIA	NA	NIA	NIA	1		0.05		1		-0.01														1.11				
YGL202W	ANU8	aniinullansierase	NA	INA	NA	NA	NA		H	0.05	117		_	-0.01	112	1.08	1.01	117	1.1	1	IP.	1.11	0.99	117	1.12	1.02	11	1.11	1 1	IP	NA	ARO8 should be able to complement ARO9 deletion on
VUD40714	ABOC	Aromatic amino acid		N. A	N.O.		N. C	_		0.40				0.00		4.00			4.4	4.00	TO		4.00	_	4.40	4.0					,	minimal media, but the gpr association might be wrong
YHK13/W	AKU9	aminotransferase II	NΑ	NΑ	NA	NA	NA	0	1	0.18	FΝ	1	1	-0.02	IΡ	1.08	1	ΠP	1.1	1.02	IΡ	1.11	1.03	IΡ	1.12	1.0	I I F	1.11	1.0	ijΙΡ	ISO	[Urrestarazu98]. NA

																													<u> </u>
			ء	_	sim	dxə	=	sim	Ω×	e Ve	call	Sin I	dxa	a c	E	9		'PDGE sim	(PDGE exp	E E	: .	call	Ε	9	=	۽ ا ۽	. -		i e i
	ORF	ıme	s sim	s call	Slow si)w e	Slow C	MMD s	MMD exp	MMD ave	MMD c	YPGal sim	r r Gal exp		YPD sim	YPD exp	YPD call	DGE	PDGE exp	YPG sim	YPG exp	PG	YPE sim	YPE exp	'PE call	(PL sim	dyo I I		Explanation
	ō :	Annotation Provides low levels of resistance	e to	Es	š	Š	š	Ē	Ē	Ē	Ξ	<u>}</u>	5	5		Ϋ́	7	Υ.	7 5		: }	7	7	7	¥	<u>}</u>	: }	: 0	Explanation $\underline{\mathcal{C}}$
YDL100	ARR	R4 arsenicals	NA NA	N.A	NA NA	A NA	NA	1	1	0.4	TP	1	1 -0.	.01 T	P 1.08				0.96 T								92 T	P N	
YPR145		N1 Asparagine synthetase			N/			1	1	0.05	TP	1			P 1.08				1.02 T	_									A NA NA
YGR124	W ASN	N2 Asparagine synthetase	NA	N.F	NA NA	A NA	NA	1	1	0.07	TP	1	1 0.	03 T	P 1.08	1.01	TP	1.1	1 T	P 1.1	11 1	TP	1.12	0.99	TP 1	.11 0.	99 T	P N	A NA NA
YDR321		P1 Asparaginase I intracellular isoz		N/				1	1		TP	1			P 1.08				0.99 T										
YPR026		H1 Acid trehalase P1 F1F0-ATPase alpha subunit			NA 0.9		NA TN				TP (1			P 0.98				1.01 T							.11 1.			
YBL099\	VAIP	P1 F1F0-A1Fase alpha suburili	NA	N/	4 0.9	11 4	IN	0.91	1	0	IP	J.82	1 -0.	.03 1	0.98	0.91	IP	0.24	0.81 1	N 0.1	14 0.5	6 IN	0.16	0.49	IN	0.05 0.	04 11	N N	Mitochondrial maintenance not required in the model in
YLR2950	C ATP	P14 ATP synthase subunit h	NA	N/	0.9	1 4.7	TN	0.91	1	0	TP (0.82	1 -0.	.01 T	P 0.98	0.73	FP (0.24	0.59 T	N 0.1	14 0.5	6 TN	0.16	0.52	TN (0.05 0	5 TI	N Ot	h primarily fermentative conditions. NA
YPL271\	,	ATP synthase epsilon P15 subunit nuclear encoded	NA.	NIA.	0.9	1 9.5	TN	0.91	4	-0.03	TD.	200		.03 T	P 0.98	0.72	ED (0.24	0.69 T	N O		0 TN	0.46	0.54	TNI (0.05	 T	N O1	Mitochondrial maintenance not required in the model in h primarily fermentative conditions.
YDL004		P16 ATP synthase delta subunit	0.9		NA NA			NA	NA		NA			IA N			NA			IA N			NA		NA			A N	
																													Mitochondrial maintenance not required in the model in
YDR377	W ATP	P17 ATP synthase subunit f	NA	N/	A 0.9	1 3.3	TN	0.91	1	-0.03	TP (0.82	1 -0.	.04 T	P 0.98	0.83	FP (0.24	0.78 T	N 0.1	14 0.6	6 TN	0.16	0.66	TN (0.05 0.	59 T	N Of	h primarily fermentative conditions. NA
																													This is probably due to excessive respiration under the
																													simulation conditions - glucose vs oxygen limitation, may
YML081	CA ATP	P18 ATP synthase associated protein F(1)F(0)-ATPase complex beta	n NA	N/	A NA	A NA	NA	0.91	1	-0.02	TP (0.82	1 0.	15 T	P 0.98	1.03	TP (0.24	0.96 F	N 0.1	14 0.6	5 TN	0.16	0.63	TN (0.05 0.	35 T	N Me	d consider increasing maximum glc uptake in YPDGE medium. NA This is close enough to count as a correct prediction. With
YJR121\		P2 subunit	NA	N.A	NA NA	A NA	NA	0.91	1	0	TP (0.82	1 -0.	.02 T	P 0.98	0.86	FP (0.24	0.82 T	N 0.1	14 0.5	1 TN	0.16	0.55	TN (0.05 0.	53 TI	N Me	ed small changes in uptake rates this would be true negative. NA
YPR020	W ATP	P20 ATP synthase subunit g homolo	g NA	N.A	N/	A NA	NA	1	1	-0.04	TP	1	1 -0.	.02 T	P 1.08	1	TP	1.1	0.98 T	P 1.1	11 0.9	4 TP	1.12	0.95	TP 1	.11 0.	94 T	P N	
YPL0780	ATP	P4 F(1)F(0)-ATPase complex subu	nit b NA	N/	A 0.9	1 4.1	TN	0.91	1	0.19	TP	0.82	1 0.	15 T	P 0.98	0.83	FP (0.24	0.77 T	N 0.1	14 0.5	2 TN	0.16	0.51	TN	0.05 0.	54 T	N Ot	Mitochondrial maintenance not required in the model in h primarily fermentative conditions.
		() ()																											
VDDOOG	_ _	ATP synthase subunit 5 oligomy						0.04		0.00		2.00		00 -	D 0 00	0.75		0.04	0.00				0.40						Mitochondrial maintenance not required in the model in
YDR298	CAIP	P5 sensitivity-conferring protein	NA	N/	1 0.9	1 7.7	IIN	0.91	1	-0.03	IP	J.82	1 -0.	.02 1	0.98	0.75	FP	0.24	0.66 T	N U.	14 0.5	3 IIN	0.16	0.53	IIN	1.05 0.	0/ 11	N OI	h primarily fermentative conditions. NA Mitochondrial maintenance not required in the model in
YKL0160		P7 ATP synthase d subunit	N/	_		1 3.7			1	-0.03	_								0.64 T										h primarily fermentative conditions. NA
YKL004\	V AUR	R1 Involved in phospolipid metaboli	ism 1	FF	N/	A NA	NA	NA	NA	NA	NA	NA N	IA N	IA N	A NA	NA	NA	NA	NA N	IA N	A NA	NA.	NA	NA	NA	NA N	A N	A Bi	o Sphingolipid synthesis not required in the model FP
YOR011	w AUS	S1 ATP-binding cassette (ABC) fan	nily NA	N.A	A NA	A NA	NA	1	1	-0.03	TP	1	1 (о Т	P 1.08	1.02	TP	1.1	1.02 T	P 1.1	11 1.0	з ТР	1.12	1.02	TP 1	.11 1.	03 T	P N	A NA NA
		Amino acid permease for leucing	-																										
YBR068 YDR046		P2 valine, and isoleucine (putative) P3 Valine transporter			A NA				_	-0.05	TP	1			P 1.08				1.03 T										
101040	C DAI	Valine transporter	INA	1 11/	1 14/-	1 11/4	INA	<u>'</u>		-0.03	15	-	1 -0.	.04 1	1.00	1.02	IF	1.1	1.04 1	- 1.	11 1.0	4 11	1.12	1.00	IF	.11 1.	00 1	r IV	BAT2 single deletion should not be lethal as there is a
																													mitochondrial isozyme (BAT1) - double deletion should be
		Branched-chain amino acid																											lethal. Bat1p currently does not catalyze valine transamination so this functionality should probably be added
YJR148\	V BAT	T2 transaminase	NA	N/	NA NA	A NA	NA	0	1	-0.04	FN	1	1 -0.	.01 T	P 0.69	1.03	FN	1.1	1.04 T	P 1.1	11 1.0	4 TP	1.12	1.06	TP 1	.11 1.	05 T	P Is	
VDD476		Geranylgeranyltransferase type T2 beta subunit	II	-	, NA	, I NIA	NIA.	NIA.	NI A	NIA		NIA	1A N		A NIA	NIA	NI A	NIA	NIA N	IA N		. NIA	NIA	NIA.	NIA	NIA N	, ,,	, D:	Quinone biosynthesis is not required in the model.
YPR176	DEI	Geranylgeranyltransferase type	II I	FF	NA	A NA	NA	NA	NA	NA	INA	NA N	IA N	IA IN	A NA	INA	INA	INA	NA N	IA N	A INA	NA	INA	INA	INA	NA IN	A IN	А БІ	O Quinone biosynthesis is not required in the model. FP
		alpha subunit (PGGTase-II, alph																											
YJL0310 YGR282		T4 subunit) L2 Cell wall endo-beta-1,3-glucana	1 se NA		NA NA				NA 1		NA TP	NA N			A NA P 1.08	NA 1.03	NA	NA 1 1	NA N	A N	A N/	NA 2 TD	1.12	NA 1 02	NA TD 4	NA N	A N	A Bi	O Quinone biosynthesis is not required in the model. NA NA NA NA
YGR286				_	A NA	_		1	1		TP	1			P 1.08				0.99 T										
		7,8-diamino-pelargonic acid																											
YNR058	w BIO:	aminotransferase (DAPA) aminotransferase	NA	N/	A NA	A NA	NA	1	1	-0.03	ТР	1	1 -0	02 T	P 1 08	1 04	TP	11	1.04 T	P 1 1	11 1 0	2 TP	1 12	1 06	TP 4	11 1	14 T	P N	A NA NA
		Dethiobiotin synthetase		_	_	A NA	_		-		_	1			_	-	_		1.03 T		_			_	_		_		
VNDOCC	O BIO	Transmembrane regulator of								0.00			1 2	00	D 4.00	1 00			4.00				4.40	4.05		,,[,		D	A NA
YNR056	C BIO	D5 KAPA/DAPA transport 3-hydroxyanthranilic acid	NA	N.F	N/	A NA	INA	1	1	-0.02	112	1	1 0.	US T	1.08	1.03	1P	1.1	1.03 T	P 1.1	1.0	∠ IP	1.12	1.05	IP 1	.11 1.	J4 [r N	A NA NA
YJR0250		A1 dioxygenase			NA NA					-0.06		1	1 -0	.01 T	P 1.08	1.01	TP	1.1	1.02 T	P 1.1	11 1.0	2 TP	1.12	1.02	TP 1	.11 1.)2 T	P N	A NA NA
YJR078\ YBL098\		A2 Tryptophan 2,3-dioxygenase A4 Kynurenine 3-mono oxygenase			A NA					-0.03 0.05									1.05 T										
YLR2310		A5 Kynureninase			A NA					0.05		1							1.01 T										
		Quinolinate phosphoribosyl																											
YFR0470		A6 transferase H1 Beige protein homologue 1			A NA	A NA				-0.03 -0.01		1							1 T										A NA NA NA NA
YEL0630		N1 Arginine permease			A NA		NA		-	0.1		1	1 -0.	.03 T	P 1.08	0.99	TP	1.1	1.01 T	P 1.1	11 1.0	1 TP	1.12	0.99	TP 1	.11	Т	P N	A NA NA
YPL111\		R1 Arginase				NA NA				0.03			1 -0.	.06 T	P 1.08	1.01	TP	1.1	1.02 T	P 0.9	99 1	TP	1.11	0.98	TP 1	.03 0.	97 T		A NA NA
YLR438\ YML042		R2 Ornithine aminotransferase T2 Carnitine O-acetyltransferase				A NA				-0.03	TP								1.03 T										
YLR307		A1 Chitin deacetylase		NA NA						-0.04		1																	A NA NA

	Φ.		sim	call	sim	dxe.	call	sim	MD exp	MMD ave	call	Galsim	r F Gal exp	r Gal ave	YPD sim	YPD exp	PD call	PDGE sim	/PDGE exp	PDGE call	YPG sim	d exb	PG call	YPEsim	/PE exp	PEcall	SIM	dxe	call	υ	Explanation Explanation
OR.	lam	Annotation	SS	SS (Nois	Nois	No lo	AIMD		₩	Q W	P. I	5 0	Ď	9	PD	PD	PD	PD	PD	PG	PG	PG	PE	PE	J E	2	ا ل	١	Class	Explanation
		Chitin deacetylase	NA	NA	NA	NA	NA	1		0.05	TP	1	1 0.	_	P 1.0	_	2 TP	1.1	1	TP	1.11	1	_	_	_	TP 1	.11				NA NA
YAL038W	CDC19	Pyruvate kinase	1	FP	NA	NA	NA	NA N	NA	NA I	NA I	NA N	IA N	A N	A NA	N.A	NA.	NA	NA	NA	NA	NA	NA	NA	NA	NA N	1 A	1 AV	NΑ	Reg	Model has Pyk2p as an isozyme. Pyk2p may only be expressed under conditions of very low glycolytic flux [MIPS] FP Essential for nuclear and mitochondrial biosynthesis, which
YOR074C	CDC2	Thymidylate synthase	1	FP	NA	NA	NA	NA N	NΑ	NA I	NA	NA N	IA N	A N	A NA	NA	NA NA	NA	NA	NA	NA	NA	NA	NA	NA	NA N	1 A	A N	NΑ	Oth	
		Protein geranylgeranyltransferase																													
		type 1 polypeptide subunit LeucinetRNA ligase			NA NA		NΑ	NA N					IA N		A NA				NA NA												Quinone biosynthesis is not required in the model. NA Protein synthesis not required in the model NA
11 210011	0000	Louding INTO III	<u> </u>	Ë	14/1	107	14/	14/	-				.,, .,	, ,	74 147	147	100	14/1	10/1		14/1	10/1	10/	14/	14/1					Our	Essential for DNA synthesis, which is not required in our
		Thymidylate kinase			NA		NA	NA N					IA N		A NA				NA									1 AV			
YBR029C	CDS1	Phosphatidate cytidylyltransferase	0	IN	NA	NA	NA	NA N	NA	NA I	VA	NA N	IA N	A N	A NA	N.P	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA 1	NA I	1 AV	NΑ	NA	NA
																															related to fatty acids, which is essential for mitochondrial
YER061C	CEM1	Beta-keto-acyl synthase homolog	NA	NA	NA	NA	NA	1	1 ().55	TP	1	1 0.	05 T	P 1.0	8 0.8	1 FP	1.1	0.77	FP	1.11	0.57	FP ′	1.12	0.54	FP 1	.11 0	.54 F	Р	Oth	function. NA
YCL064C	CHA1	Catabolic serine (threonine) dehydratase	NA	NA	NA	NA	NA	1	1 -	0.03	TP	1	1 -0.	05 T	P 1.0	8 1.0	2 TP	1.1	1.02	TP	1.11	1.04	TP	1.12	1.05	TP 1	.11 1	.04	ГР	NA	NA NA
		Phosphatidyl-ethanolamine N-methyltransferase			NA			0		0.03		0	1 -0.				1 FN									FN					Catalyzes 1st step in pathway from PE to PC. Opi3p can also catalyze this step, but it is very inefficient; mutant cells are viable and not auxotrophic for choline or other phospholipid intermediates; membranes of mutants contain 10% PC and 40-50% PE (WT is 40-45% PC and 15-20% PE); this deletion is lethal in silico since we require fixed amounts of these specific phospholipids in our biomass (in vivo there is flexibility as to which phospholipids are used).
		Chitin synthase 1			NA					0.02		1		03 T			NA					NA				NA N					NA NA
		Chitin synthase 2	1	FP	NA	NA	NA	1	1	0	ТР	1	1 -0.	03 T	P NA	N/A	NA NA	NA	NA	NA	NA	NA	NA	NA	NA	NA N	1 AL	1 AV	NA.	Dis	Gene is listed as essential, but there is data for MMD and YPGal. In any case chitin synthesis is not required in the
YBR023C	CHS3	Chitin synthase 3		NA	NA	NA	NA	1	1 -	0.03	TP	1		03 T	P 1.0	8 1.0	1 TP	1.1	1	TP	1.11	1.01	TP ′	1.12	0.99	TP 1	.11 1	.01	ГΡ	NA	NA NA
		Citrate synthase			NA		NA	1	_		TP	1	_	02 T	P 1.0		9 TP		_							TP 1		.81		NA	NA NA
	CIT2 CIT3	Citrate synthase Citrate synthase	NA NA	_	NA NA	NA NA	NΑ	1	_		TP TP	1		07 T	P 1.0		2 TP	1.1	1.03	_			TP '			TP 1		.03		NA	NA NA NA
		Choline kinase			NA		NA	1	_	_	TP	1	_		P 1.0		9 TP														NA NA
YBR003W	COQ1	Hexaprenyl pyrophosphate synthetase Para hydroxybenzoate: polyprenyl	NA	NA	NA	NA	NA	1	1 (0.04	ТР	1	1 0.	09 T	P 1.0	8 0.9	5 TP	1.1	0.83	FP	1.11	0.48	FP '	1.12	0.45	FP 1	.11 0	.58 F	ъ	Bio	Quinone biosynthesis is not required in the model. NA
YNR041C	COQ2	transferase	NA	NA	NA	NA	NA	1	1 (0.01	TP	1	1 0.	11 T	P 1.0	8 0.9	5 TP	1.1	0.91	TP	1.11	0.56	FP	1.12	0.54	FP 1	.11 0	.52 F	ъ	Bio	Quinone biosynthesis is not required in the model. NA
VOI 0000	0000	3,4-dihydroxy-5- hexaprenylbenzoate			1	4.0		4					4	00 T	D 4.0				0.70		4.44	0.54	ED.	1.10	0.40	FD 4	44 0		-	D:-	O disease bissenth sale is not seen in the model.
		methyltransferase C-methyltransferase (putative)	NA NA		1	4.3		1		0.21	TP	1							0.78												Quinone biosynthesis is not required in the model. NA Quinone biosynthesis is not required in the model NA
		Monooxygenase	_	_	NA	_		1	_	_	TP	1	1 0.		P 1.0				0.8											Bio	
		Coenzyme QH2 cytochrome c reductase 44 kDa core protein subunit Farnesyl transferase (putative)			0.9	4 NA	TN	0.89		0.03		1.82			P 0.9				0.77												Mitochondrial maintenance not required in the model in primarily fermentative conditions. NA Quinone biosynthesis is not required in the model NA
YLR038C								0.89																							This is probably due to excessive respiration under the simulation conditions - glucose vs oxygen limitation, may consider increasing maximum glc uptake in YPDGE medium. NA
YNL052W	COYE	Cytochrome c oxidase chain Va	NIA	NIA	NIA	NA	NΙΛ	1	1	0.03	тр	1	1 0	17 7	D 10	8 1 0	2 TD	1.1	0.94	тр	1 11	0.65	ED.	1 12	0.61	ED 4	11 0	69 1	ь	leo	COX5A is the dominant isoform - COX5B cannot fully compensate [SGD].
		Cytochrome c oxidase chain Vb				NA		1		0.03		1			P 1.0				1.01												
																		0.5	0.7-			0.00			0.01		0.5				Higher oxygen uptake rate or lower glucose uptake rate will
		Cytochrome c oxidase subunit			NA			0.89																							Mitochondrial maintenance not required in the model in
		Cytochrome c oxidase subunit VII Cytochrome c oxidase chain VIII						0.89											0.74												Null mutant is viable, but should be deficient in cellular respiration and cytochrome C oxidase activity [SGD] so there should be a growth defect on non-fermentable carbon
		,																													Higher oxygen uptake rate or lower glucose uptake rate will
YDL067C	COX9	Cytochrome c oxidase subunit VIIa Arginine specific carbamoyl	NA	NA	NA	NA	NA	0.89	1 ().14	TP C	.82	1 0.	05 T	P 0.9	8.0	2 FP	0.24	0.75	TN	0.14	0.53	TN (80.0	0.5	TN 0	.05 0	.52	ΓN	Med	make this deleterious in the model. NA
YOR303W	CPA1	phosphate synthetase	NA	NA	NA	NA	NA	0	1 (5.82	TN	1	1 -0	.1 T	P 1.0	8 1.0	2 TP	1.1	0.98	TP	1.11	0.98	TP	1.12	0.98	TP 1	.1 0	.98	ГР	NA	Weak false negative NA

			_		Ε	٩	=	Ε	9	Ð	=	Ē	dx	Ne	=	اء	ا ۵	_ -	sim	PDGE exp	ا ا		l_	_		1_	_				eta
ш	me		sim	call	w sim	e e	w ca	D sim	MD exp	MMD ave	MD call	/PGal sin	Gale	Gal ave	PGal cal	(PD sim	PD exp	PD call	PDGE sin	PDGE exp	(P.G. sim	dxe	3 call	/PE sim	(PE exp	call	/PL sim	dxə -	- call	Class	Explanation
ORF	Naı	Annotation	Ess	Ess	Slo	Slo	Slo	DIMIN	Z	Σ	M	Ϋ́	γP(Ϋ́	YP(YPI	ΥPI	4 2	YPI	YPI	ΛÞ	YPG	YPG	YPI	YPI	YPE	YPI	IЫ	YPI		
YJR109C		Carbamyl phosphate synthetase	NA	NA	NA	NA	NA	0	1	8.21	TN	1	1	0.07	TP	1.08	1.02	ΓP 1	1.1	1.03 T	P 1.1	11 1.03	3 TP	1.12	2 1.04	1 TP	1.1	1.04	TP	NA	Weak false negative NA
YNL130C		Sn-1,2-diacylglycerol cholinephosphotransferase	NA	ΝΔ	NA	NA	NΔ	1	1	0.03	TP	1	1	-0.04	тр	1.08	1 7	ΓP 1	1.1	1 T	P 1 .	11 0.99	ТР	1 12) n q	I TP	1 11	n 99	ТР	NA	NA NA
		Carnitine transporter			NA		NA	1	1	-0.03	TP	1	1	-0.06				ΓP 1		1.02 T							1.11	1.01		NA	NA NA
YDL142C	CRD1	Cardiolipin synthase	NA	NA	NA	NA	NA	1	1	0.01	TP	1	1	-0.02	TP	1.08	0.98	ΓP 1	1.1	0.99 T	P 1.1	11 0.93	3 TP	1.12	0.85	TP	1.11	0.93	TP	NA	
YBR036C	CSG2	Required for mannosylation of inositolphosphorylceramide (IPC)	NΙΛ	NIA	NA	NA	NA	1	1	-0.02	TP	1	1	-0.05	тр	1 00	1 02 7	TD 1		1 01 T	D 1 .	11 0.98	ть	1 12	0 00		1 11	1 01	тр	NΙΛ	NA NA
		Catalase A			NA				1	0.28		1	1	0.05			1.02					11 0.99					1.11	1.01		NA	
																															Lower oxygen uptake rate would correct this false negative
		Citrate tranporter		_	NA		_		1	-0.05		1	1	0.21								11 0.96									
YGR088W	CITT	Catalase I	NA	NA	NA	NA	NA	1	1	-0.02	IP	1	1	-0.07	IP	1.08	1 7	1 1	1.1	1.01 1	P 1.	11 1.01	I IP	1.12	2 1.02	2 112	1.11	1.01	IP	INA	INA NA
		17 kDa VO sector subunit dicyclohexylcarbodiimide																													
		binding subunit proteolipid vacuolar ATP synthase proteolipid C vacuolar ATPase V0 domain																													The cup5 null mutant is viable but lacks vacuolar (H)- ATPase activity, and is defective in vacuolar acidification, vacuole biogenesis, vacuolar protein targeting, and
YEL027W		subunit c (dicyclohexylcarbodiimide binding subunit) (17 kDa)	NA	NA	1	17.9	FP	1	1	-0.01	TP	1	1	0	TP	1.08	0.72 F	P 1	1.1	0.62 F	P 1.1	11 0.53	3 FP	1.12	2 0.58	3 FP	1.11	0.58	FP	Oth	endocytosis [SGD]. The slow growth phenotype could be due to problems in pH balancing.
VMI 0540	CVB3	L-lactate cytochrome c	NIA	NIA.	NI A	NIA.	NI A	_		0.04	TD	,	1	0	TD	1.00	1 04 3	rp .		1 04 -		11 4 04		1.40	1 00	, , , ,	0.04	1.07	EVI	N/1~-	Lower oxygen uptake rate would correct this false negative prediction.
YML054C	CYBZ	oxidoreductase cytochrome b2	NA	NA	NA	NA	NA	1	1	0.01	IP	1	1	0	IP	1.08	1.01	PT	1.1	1.04 1	71.	11 1.06) IP	1.12	2 1.08	3 IP	0.64	1.07	FN	ivied	prediction. NA cAMP synthesis not required in model as its primarily used as
YJL005W	CYR1	Adenylate cyclase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA N	NA N	AV	NA N	A N.	A NA	NA	NA	NA	NA	NA	NA	NA	Oth	a signaling molecule. FP This reaction is not used in complete media, because
YAL012W	CYS3	Cystathionine gamma-lyase	NA	NA	NA	NA	NA	1	1	0.29	TP	1	1	0.63	тр	1 08	0 94 7	TP 1	1	0.9 T	P 1 ·	11 0 67	7 FP	1 12	0.77	7 FP	1 11	0.88	ТР	Med	cysteine is available. Should only be a cysteine auxotroph [SGD].
171201211	0100	System of miss gamma tydes	147.	14/	147.	10/1			Ė	0.20				0.00		1.00	0.04			0.0 1	Ë	11 0.07	Ť	1.12	0.77	Ë		0.00	Ħ	Wied	
																															CYS4 null mutant is deficient in vacuolar ATPase activity and vacuolar acidification [MIPS]. The false positives could be
YGR155W	CYS4	Cystathionine beta-synthase	NA	NA	1	3.7	FP	1	1	0.11	TP	1	1	0.17	TP	1.08	0.91	ΓP 1	1.1	0.9 T	P 1.1	11 0.71	1 FP	1.12	0.72	2 FP	1.11	0.83	TP	Oth	due to pH balancing, which is not accounted for in the model. NA
																															This is now below the second in the second s
																															This is probably due to excessive respiration under the simulation conditions - glucose vs oxygen limitation, may
YOR065W	CYT1	Cytochrome c1	NA	NA	NA	NA	NA	0.89	1	0.02	TP	0.82	1	0.23	TP	0.98	0.96	ΓP 0.	.24	0.92 F	N 0.	14 0.62	2 TN	0.08	0.57	7 TN	0.17	0.61	TN	Med	consider increasing maximum glc uptake in YPDGE medium. NA
		Dihydroxyacetone kinase (putative) Dihydroxyacetone kinase			NA NA		NA NA	1	1	0.03	TP	1	1	0 -0.06								11 1.02 11 1.01									
		Allantoinase		_	NA		_	1	1	0.05	TP	1	1	-0.06	_	_	1.02	_	_		_	11 0.98	_	_			1.11	1.02	TP	NA	INA INA
	DAL2	Allantoicase		_	NA		_	1	1	0	TP	1	1	-0.05	_	_		ΓP 1	_	1.04 T	_	_	_	_	2 1.07			1.05	TP	NA	NA NA
		Ureidoglycolate hydrolase		_	NA		_	1	1	0.02	TP	1	1	0	TP			_	_		_	11 0.98	_	_		_		0.99	TP	NA	
		Allantoin permease Allantoate permease			NA NA			1	1	0.03	TP	1	1	-0.01	TP		1.02 T		1.1		P 1.1			1.12		I TP		1	TP	NA NA	NA NA NA
		Malate synthase 2			NA		_	1	1	-0.02 0	TP	1	1	-0.01	_							11 1.0 ² 11 0.98									INA INA INA
		Asparaginyl-tRNA synthetase	1	_	NA		_	NA	NA	NA	-	NA	NA		_		NA N			NA N				NA			NA	NA	_	Oth	
		Similar to rRNA methyltransferase																													
		(Caenorhabditis elegans) and hypothetical 28K protein (alkaline																													
		endoglucanase gene 5' region)																													
YFL001W	DEG1	from Bacillus sp.	NA	NA	1	3.5	FP	1	1	-0.02	TP	1	1	-0.02	TP	1.08	0.86 F	P 1	1.1	0.79 F	P 1.1	11 0.8	TP	1.12	0.8	TP	1.11	0.81	TP	Oth	Pseudouridine biosynthesis not required in the model. NA
VOD000M	DED4	Dibdasfalata as divetas				1	l		l																1	l			ll		Folate biosynthesis is not required in rich media. Lethality
1 UR 236W	DFR1	Dihydrofolate reductase Protein similar to bacterial seryl-	1	FP	NA	NA	NΑ	NA	NA	NA	NΑ	NA	NΑ	NΑ	IVA	AVI	NA N	NA N	NΑ	NA N	A N.	A NA	NA	NA	NA	NA	NA	NA	NΑ	ACC	may be due to toxicity of DHP [Bayly02]. FP
YHR011W		tRNA synthases	NA			6.5			1	-0.04			1	0.19	TP	1.08	0.74 F	P 1	1.1	0.65 F	P 1.1	11 0.54	4 FP	1.12	0.44	FP	1.11	0.49	FP	Oth	Protein synthesis not included in the model. NA
		Dicarboxylate transport protein			NA		_			-0.02												11 1.03									NA NA
		Dimethyladenosine transferase			NA		_		_																						Quinone biosynthesis is not required in the model FP
YPL265W	DIP5	Dicarboxylic amino acid permease D-lactate ferricytochrome c	NA	NA	NA	NA	NA	1	1	0	TP	1	1	0.03	TP	1.08	0.99	ΓP 1	1.1	0.96 T	P 1.1	11 0.87	7 TP	1.12	0.81	I TP	1.11	0.88	TP	NA	NA NA
YDL174C	DLD1	oxidoreductase	NA	NA	NA	NA	NA	1	1	0.01	TP	1	1									11 1.02									
YLR172C	DPH5	Diphthamide biosynthesis	NA	NA	NA	NA	NA	1	1	-0.02	TP	1	1									11 1									
		Dihydrosphingosine phosphate lyase (also known as sphingosine																													
YDR294C	DPL1	phosphate lyase)	NA	NA	NA	NA	NA	1	1	0.06	TP	1	1	-0.03	TP	1.08	1.01	TP 1	1.1	1.02 T	P 1.1	11 1.02	2 TP	1.12	2 1.04	1 TP	1.11	1.03	TP	NA	NA NA
		Dolichol phosphate mannose																													
YPR183W	DPM1	synthase Diacylglycerol pyrophosphate	0	TN	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA N	NA N	NΑ	NA N	A N.	A NA	NA	NA	NA	NA	NA	NA	NA	NA	NA NA
YDR284C	DPP1	phosphatase	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	-0.03	TP .	1.08	1.01	TP 1	1.1	0.99 T	P 1.1	11 0.98	з тр	1.12	0.98	ТР	1.11	0.99	TP	NA	NA FN
																							-								

			_		sim	dxə	=	sim	<u>.</u>	e :	call	<u>د</u> ا	ave	l =	u	Q.	_	'PDGE sim	/PDGE exp	. E	ء ا :	. =	۽	۵	l_	_	۵	_		Explanation Explanation
щ.	me		s sim	s call	is vi	(e) %	W C	MMD si	M exp	MMD ave	MMD	rPGal sim	YP Gal ave	/PGal cal	YPD sim	ҮРD ехр	/PD call		PDGE exp	YPG sim	YPG exp	PG call	YPE sim	(PE exp	PE call	/PL sim	L exp	L call	Class	st
ORF	Z	Annotation	Es	Es	Slo	Slo	Slo	Σ :			_					•	_	_		- /	_	_	_	_	-	-		YPL		
YLL018C	DPS1	Aspartyl-tRNA synthetase Urea amidolyase (contains urea	1	FP	NA	NA	NA	NA N	1 AI	1 AV	1 A	N AI	A NA	NA	NA	NA	NA	NA	NA N	IA N.	A N	A NA	NA	. NA	NA	NA	NA	NA	Oth	Protein synthesis not required in the model NA
		carboxylase and allophanate																												
		hydrolase)			NA								0.02						0.98 T											
YHL016C	DUR3	Urea active transport protein	NA	NA	NA	NA	NA	1	1 0	.04	ГР	1 1	-0.0	TP	1.08	1.01	TP	1.1	1.02 T	P 1.0	07 1.0	3 TF	1.11	1 1.04	1 TP	1.07	1.02	TP	NA	
																														Converts dUTP to dUMP preventing uracil incorporation into DNA [MIPS]. Since we do not include DNA replication in our
YBR252W	DUT1	DUTP pyrophosphatase	1	FP	NA	NA	NA	NA N	I AI	A A	1 AI	N A	A NA	NA	NA	NA	NA	NA	NA N	IA N	A N	A NA	NA	. NA	NA	NA	NA	NA	Oth	model, this function is unnecessary.
.																														Dys1p catalyzes first two steps in hypusine biosynthesis.
		Deoxyhypusine synthase Sulfite reductase (putative)	1 NA		NA NA	NA NA		NA N		NA N .28		NA N	A NA		NA 1.08				NA N											Hypusine is required in our model. FP NA NA
		ExtraCellular Mutant			NA		_	1	_	_	ГР	1 1	0.00	TP					1.04 T											
		Gamma-glutamyltransferase																												
		homolog			NA NA			0			TP N	1 1							0.99 T											NA NA Weak false negative NA
		Acetylornithine acetyltransferase Ethanolamine kinase	NA		NA		_	1	_	_	ΓP	1 1	-0.0	TP	1.08	1.03				P 1.				2 0.98			1.01		NA	NA NA
YGR254W						NA		1			ГР	1 1		7 TP	1.08				1.02 T								1.02			
VHD123\\\/	EDT1	Sn-1,2-diacylglycerol ethanolamine- and cholinephosphotranferase	NIA	NIA	NΙΛ	NA	NΙΛ	1	, ,	.05	гр	1 1	0.0		1 00	1.01	тр	1 1	1.02 T	D 4 .	11 1 0	12 TE	1 11	1 03	ТБ	1 11	1.02	тр	NΙΛ	NA NA
		Squalene monooxygenase	0					NA N				IA N			NA				NA N			A NA					NA			
YPL028W		Acetoacetyl CoA thiolase	0	TN			_	NA N				N AI			NA	NA			NA N			A NA							NA	NA FP
\/\ \D0070	ED04	Cytochrome P450 lanosterol 14a-	_			l	l		. II.					l							.			l	l				.	NA NA
		demethylase Mevalonate kinase	0		NA NA		_	NA N				N AI	A NA A NA		NA NA				NA N			A NA		NA NA			NA NA			NA NA NA
TWITTEGOTT	LIKOTZ	3-hydroxy-3-methylglutaryl	Ů		1471	147		14/	<u>" </u>				147	1.47.	14/1	1471		1471	10/	14.	/\ \\\		147.	147	1471	14/1	14/1		14/1	Deletion of ERG13 is lethal [Daum98]. Discrepancy between
YML126C	ERG13	coenzyme A synthase	0	TN	NA	NA	NA	NA N	1 AI	1 A	1 AI	N A	A NA	NA	0	0.96	FN	0	0.91 F	N C	0.9	2 FN	0	0.9	FN	0	0.9	FN	Dis	the two experimental studies.
																														Ergosterol can be synthesized by the model from zymosterol, which bypasses the reaction catalyzed by the ERG2 gene
YMR202W	ERG2	C-8 sterol isomerase	NA	NA	1	3.2	FP	1	1 0	.54	гР	1 1	0.16	l _{TP}	1.08	0.92	TP	1.1	0.76 F	P 1.1	11 0.8	6 TF	1.12	0.75	5 FP	1.11	0.73	FP	Mod	product. This bypass is probably incorrect.
		Farnesyl diphosphate synthetase												T		0.02			-											
		(FPP synthetase)	0		NA		_					N AI		NA					NA N			_		. NA			NA			
		Sterol C-14 reductase C-4 sterol methyl oxidase	NA 0		0 NA		TΝ	0 NA N				0 1 NA N	0 A NA	TN NA		0.79 NA	NA		0.62 T	N C			0 NA		TN NA		0.68 NA			
		C-3 sterol dehydrogenase	0	_	NA		_	NA N		_		VA N					NA	_		A N	_	_	NA		NA				NA	NA NA
YLR100W	ERG27	3-keto sterol reductase	0	TN	NA	NA	NA	NA N	1 Al	A A	1 A	N AI	A NA	NA	NA	NA	NA	NA	NA N	IA N	A N	A NA	NA	. NA	NA	NA	NA	NA	NA	NA NA
																														Ergosterol can be synthesized by the model from zymosterol, which bypasses the reaction catalyzed by the ERG3 gene
YLR056W	ERG3	C-5 sterol desaturase	NA	NA	1	5.5	FP	1	1 0	.06	гР	1 1	-0.0	↓ ITP	1.08	0.92	TP	1.1	0.9 T	P 1.	11 0.8	2 TF	1.12	0.84	1 TP	1.11	0.92	ТР	Mod	product. This bypass is probably incorrect.
																														Erg4p catalyzes the last step in the synthesis of ergosterol.
																														when it is deleted, the precursor accounts for 90% of the
																														cell's sterol composition, suggesting that Erg4p is the only enzyme that can catalyze this reaction; ergosterol is
																														completely replaced by its precursor in the plasma
																														membrane of erg4 mutants; the mutant is viable, but there
																														are distinct defects relating to drug sensitivity [Zweytick00]; thus, this FN is a result of our biomass function, which
YGL012W	ERG4	Sterol C-24 reductase	NA	NA	NA	NA	NA	0	1 0	.03 F	N	0 1	0	FN	0	0.96	FN	0	0.96 F	N C	0.9	3 FN	0	1.01	I FN	0	0.95	FN	Bio	requires ergosterol.
		Cytochrome P450 involved in C-22				1			Ť					Ť				_	-				Ť	1						
		denaturation of the ergosterol side-							. .																					L.
YMR015C	ERG5	cnain	NA	NA	NA	NA	NA	1	1 0	.14	P	1 1	-0.1	TP	1.08	1	TP	1.1	1.03 T	P 1.1	11 1.0	04 TF	1.12	2 1.03	3 TP	1.11	1.04	TP	NA	NA FN Ergosterol can be synthesized by the model from zymosterol,
																														which bypasses the reaction catalyzed by the ERG6 gene
YML008C	ERG6	Ergosterol synthesis	NA	NA	1	3.2	FP	1	1 0	.36	ГР	1 1	0.02	TP	1.08	0.84	FP	1.1	0.81 F	P 1.	11 0.8	2 TF	1.12	0.78	TP.	1.11	0.72	FP	Mod	
YHR072W	EDO-	2,3-oxidosqualene-lanosterol	_			N. A	N. A	NIA.							N/A	NI A	NIC	NIA	NIA .						N. A	NIA	NI A	NIC	NIA	NA NA
		48 kDa phosphomevalonate kinase	0		NA NA			NA N					A NA			NA NA	NA	NA NA	NA N	A N	A N	A NA	NA NA	NA NA	NA	NA NA	NA	NA	NA	NA NA NA
YHR190W		Squalene synthetase	0		NA			NA N											NA N											NA NA
		Exo-1,3-beta-glucanase			NA			1		.05		1 1	0						1.01 T											NA NA
YDR261C	EXG2	Exo-1,3-beta-glucanase Long chain fatty acyl:CoA	NA	NA	NA	NA	NA	1	1 0	.03	Р	1 1	-0.0	2 TP	1.08	1	TP	1.1	1 T	P 1.1	11 1	TP	1.12	2 1	TP	1.11	1	TP	NA	NA NA
YOR317W	FAA1	synthetase	NA	NA	NA	NA	NA	1	1 -0	.04	ГР	1 1	0	TP	1.08	1.01	TP	1.1	1.01 T	P 1.1	11 1.0	1 TF	1.12	2 1.01	ТР	1.11	1.01	ТР	NA	NA NA
		Acyl-CoA synthase			NA			1		0.01		1 1	-0.0						1.01 T											
		Long chain fatty acyl:CoA																												
YMR246W	FAA4	synthetase long-chain fatty acid:CoA ligase	NA	NΑ	NΑ	NA	NΑ	1	1 0	.03	гР	1 1	-0.0	ТР	1.08	1.01	ТР	1.1	1.02 T	P 1	11 1 0)4 TF	1 13	2 1 03	ТР	1.11	1.02	ТР	NA	NA NA
1011				, \	, \		. 47 (. 50			0.0		00								2	7.02					, .	TVA

	0		sim	call	sim	dxə	call	sim	exp	лмD ave	call	PGal sim	l exp	l ave	PGal call	mis	dxe	all	PDGE sim	PDGE exp	PDGE call	sim	dxe	call	im	dx	all	m.	dxə	call		er et al
ORF	ame	Annotation	S SS	SS C	Slow sim	No	low	MMD sim	IMD exp	MD	IMD	PGa	PGal	PGal	PGa	'PD sim	PD exp	PD call	PDG	PDG	PDG	PG sim	PG exp	PG	'PE sim	PE exp	PE call	'PL sim	YPL e	YPLo	Class	Explanation
YFR019W	FAB1	1-phosphatidylinositol-3-phosphate 5-kinase FAD synthetase				8.3 NA		1	1 NA	0	TP	1 NA I	1 -	_		1.08	0.63	FP	1.1	0.73 NA		1.11	<u> </u>		1.12	0.5	FP	1.11	0.54	FP		Mutation causes pleiotropic effects on nuclear migration and orientation, and separation of mitotic chromosomes (forms aploid and binucleate cells).Mutant has defects in vacuolar function and morphology [SGD]. Riboflavin biosynthesis is not required in the model FP
TDE043C	IADI	I AD Synthetase	<u> </u>	1 -	INA	INA	INA	INA	INA	INA	INA	INA	N/A	INA	INA	INA	INA	INA	INA	INA	INA	INA	INA	INA	INA	INA	INA	INA	INA	INA	Otti	INDUIAVIT DIOSYTUTESIS IS TIOL TEQUITED IT THE THOUGH
YKL182W	FAS1	Acetyl transferase dehydratase enoyl reductase malonyl/palmityl transferase pentafunctional enzyme	0	TN	NA	NA	NA	NA	NA	NA	NA	NA I	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA NA
YPL231W	FAS2	Fatty acid synthase alpha subuni	0	TN	NA	NA	NA	NA	NA	NA	NA	NA I	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NΑ	NA	NA	NA	NA		NA	NA	NA NA
YBR041W	FAT1	Fatty acid transporter 5,10-methenyltetrahydrofolate	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1 -	0.01	TP	1.08	1.01	TP	1.1	1	TP	1.11	0.99	TP	1.12	0.99	TP	1.11	1	TP	NA	NA NA
YER183C	FAU1	synthetase	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1 -	0.02	TP	1.08	1.01	TP	1.1	1.02	TP	1.11	1.02	TP	1.12	1.03	ТР	1.11	1.02	TP	NA	NA NA
YKL060C	FBA1	Aldolase	0.19	TN	NA	NA	NA	NA	NA	NA	NA	NA I	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	In silico slow growth.
YLR377C	FBP1	Fructose-1,6-bisphosphatase	NA	NA	NA	NA	NA	1	1	-0.02	TP	1	1	0	TP	1.08	1	TP	1.1	1	TP	1.11	0.85	TP	0.41	0.84	FN	0.89	0.88	TP	Med	Lower oxygen uptake rate would correct this false negative prediction.
YJL155C	FBP26	Fructose-2,6-bisphosphatase	NA	NA	NA	NA	NA	1	1	0.01	TP	1		0.05	_	1.08	1.01	TP	1.1	1.03	TP	1.11	0.96	TP	1.12	0.91	TP	1.11		TP	NA	NA NA
		Cytosine deaminase Purine-cytosine permease	NA NA		NA NA	NA NA	NA	1	_	-0.03 -0.02	TP TP	1		0.07	_	1.08	1.02 0.97	_	1.1	1.02	_	1.11	1.02	_	1.12	1.04	_	1.11	1.03		NA NA	NA NA NA
		Purine-cytosine permease	_	_	NA	NA	_	1	_		TP	1	_	0.04	_	1.08	1.02			1.02						1.02			1.03	_		NA NA
YER060WA	FCY22	Purine-cytosine permease	NA	NA	NA	NA	NA	1	1	-0.04	TP	1	1 (0.01	TP	1.08	1.01	TP	1.1	1.03	TP	1.11	1.04	TP	1.12	1.04	TP	1.11	1.04	TP	NA	NA NA
YCR034W	EEN1	1,3-beta-glucan synthase subunit (putative) ELO1 homolog	NA	NIA	NIA	NA	NIA	•	1	0.26	ENI	0	1	0.05	ENI	0	0.03	EN	0	0.04	EN	0	0.02	EN	0	0.91	EN	0	0.04	EN	Pio	Involved in synthesis of 1,3-beta-glucan, probable beta-1,3-glucan synthase subunit - unknown whether it is a catalytic subunit or GTP-binding subunit. Membranes of mutant cells have 90% less beta-1,3-glucan synthase activity - could an alternate subunit exist? This is lethal in silico because beta-1,3-glucan is required in biomass.
1 CRU34VV	FENI	Plasma Membrane H+-	INA	INA	NA	NA	INA	0	1	0.36	FIN	0	1 -	0.05	FIN	0	0.93	FIN	U	0.94	FIN	U	0.92	FIN	U	0.81	FIN	U	0.94	FIN	DIO	Pantothenate is necessary for CoA biosynthesis, which is not
YCR028C	FEN2	Pantothenate Symporter	NA	NA	1	3.1	FP	1	1	0.11	TP	1	1	0	TP	1.08	0.8	FP	1.1	0.8	FP	1.11	0.83	TP	1.12	0.77	FP	1.11	0.72	FP	Oth	required by the model. NA
YLR342W	FKS1	1,3-beta-D-glucan synthase	NA	NA	1	4.5	FP	1	1	-0.01	TP	1	1	0	TP	1.08	0.62	FP	1.1	0.74	FP	1.11	0.84	TP	1.12	0.84	TP	1.11	0.87	TP	Iso	There are three alternate isozymes in the model, but FKS1 deletion experimentally disrupts the enzymatic function significantly.
YMR306W	FKS3	Protein with similarity to Gls1p and Gls2p (GB:Z49212)	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1 -	0.05	TP	1.08	1.01	TP	1.1	1.02	TP	1.11	1.03	TP	1.12	1.01	TP	1.11	1.02	TP	NA	NA NA
YIL134W	FLX1	FAD carrier protein	NA	NA	1	3.4	FP	1	1	-0.02	TP	1		0.01						1.03											Dis	There is no evidence of significant deleterious phenotype. Experimentally flx1 strain has low FMN/FAD ratio [MIPS]. The two studies also show conflicting results. NA
		Riboflavin kinase	1		NA			NA	NA 1	NA		NA I				NA	NA			NA			NA			NA			NA	NA	Bio	Riboflavin biosynthesis is not required in the model FP NA NA
		Methionyl-tRNA transformylase Dihydro-6-hydroxymethylpterin pyrophosphokinase dihydroneopteri n aldolase dihydropteroate synthetase			NA NA	NA NA		NA		0.42 NA		NA I								1.04 NA												Folate biosynthesis is not required in rich media. Lethality may be due to toxicity of DHP [Bayly02].
VCD267C	FOL 2	CTD systemydrates I			NIA	NIA		NIA	NIA	NIA	NI A	NIA I		NIA	NIA	NIA	N. A.	NI A	NIA	NIA	NIA	N14	NIA	NI A		NIA	NI A	NIA.	NIA	NIA	٨٥٥	Folate biosynthesis is not required in rich media. Lethality
YGR267C	I-OLZ	GTP-cyclohydrolase I		FP	NA	NA	NA	NA	NA	NA	INA	INA	NA	NA	INA	INA	INA	INA	AVI	NA	INA	INA	IVA	INA	INA	NA	ΝA	INA	NA	INA	ACC	may be due to toxicity of DHP [Bayly02]. FP Folate biosynthesis is not required in rich media. Lethality
YMR113W	FOL3	Dihydrofolate synthetase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA I	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Acc	may be due to toxicity of DHP [Bayly02].
YKR009C	FOX2	Multifunctional beta-oxidation protein	NA	NA	NA	NA	NA	1	1	0	TP	1	1 -	0.07	ТР	1.08	1.03	TP	1.1	1.05	TP	1.11	1,04	TP	1,12	1.07	TP	1,11	1.06	ТР	NA	NA NA
YLL043W	FPS1	Glycerol channel proteir	NA	NA	NA	NA	NA	1	-	-0.02	TP	1	1 -	0.04	TP	1.08	0.99	TP	1.08	1.02	TP	0.9	1.05	TP	1.12	1.03	TP	1.11	1.03	TP	NA	NA NA
YLR060W YFL022C		Phenylalanine-tRNA ligase subuni Phenylalanine-tRNA ligase subuni	_	_	NA NA	_	_	NA NA	NA					NA NA						NA NA												Protein synthesis not required in the model NA Protein synthesis not required in the model NA
	FUI1	Uridine permease			NA		_	NA 1		0.03		1 1								0.89												
		Fumarase (fumarate hydralase) Glutamate decarboxylase	NA NA		NA NA		NΑ	1	1		TP TP	1	1 (0.96												The model predicts a reduced growth rate, but the drop is not that large. NA NA NA
		Galactokinase				NA		1		-0.01	TP			2.08	TN	1.08	0.99	TP	1.1	0.97	TP	1.11	0.99	TP	1.12	0.98	TP	1.11	0.99	TP	NA	NA NA
YBR019C	GAL10	UDP-glucose 4-epimerase	NA	NA	NA	NA	NA	1	1	-0.01	TP	0.18	0 ;	3.14	TN	1.08	1.01	TP	1.1	1.01	TP	1.11	1.01	TP	1.12	0.99	TP	1.11	0.99	TP	NA	
YLR081W	GAL2	Galactose permease	NA	NA	NA	NA	NA	1	1	-0.04	TP	1	0	1.52	FP	1.08	1.01	TP	1.1	1.03	TP	1.11	1.03	TP	1.12	1.05	TP	1.11	1.04	TP	Iso	Gal2p is the high-affinity galactose transporter, which is known to be a major player in gal transport. Deletion of GAL2 drastically reduces growth on galactose [Douglas64]. Model includes other isozymes (HXT genes) that are not nearly as efficient for gal transport so disabling their gal transport ability should result correct prediction.

					_		_		0		E 9	/e	=			E 5	axp Sall										et al
ORF	ame		Ess sim	es call	Slow sim	Slow exp	MMD sim	MMD exp	ММD аve	MMD cal	PGal sım	YP Gal ave	YPGal cal	YPD exp	/PD call	rPDGE sim	PDGE cal	YPG sim	YPG exp	YPE sim	YPEexp	(PE call	YPL sim	YPL exp	rPL call		Forster
ō	ž	Annotation	ű	Ш	S	<u>0</u>	ñΞ	Σ	Σ	Σ	<u> </u>	¥	F F	<u> </u>	⊁ :	÷ 5	=	¥	× 5	= =	×	۲	⊁	₹	7 5	Explanation	Ĕ
YBR018C	GAL 7	Galactose-1-phosphate uridyl transferase	NA	NA	NA	NA N	IA 1	1	-0.02	TP 0	18 0	5 37	TN 1 (1.01	TP 1	1 1	01 TE	1 11	1 T	P 1.12	1 0	1 TP	1 11	1 01	re N	A NA	NA
YKR039W		General amino acid permease		NA	_				0.02					8 1.01												A NA	NA
		Glycine decarboxylase complex T																									
YDR019C	GCV1	subunit	NA	NA	NA	NA N	IA 1	1	-0.03	TP 0	.99 1	-0.03	TP 1.0	1.03	TP 1	.09 1.	05 TF	1.03	1.05 T	P 0.87	7 1.0	8 TP	1.04	1.06	TP N	A NA	NA
		Glycine cleavage system P subunit glycine decarboxylase																									
YMR189W		complex P subunit glycine synthase P subunit		NA	NA	NA N	IA 1	1	0.02	TP 0	.99 1	-0.04	TP 1.0	0.99	TP 1	.09 1.0	01 TF	1.03	1.03 T	P 0.87	7 1.0	2 TP	1.04	1.02	TP N	A NA	NA
																										Should not be deleterious except when glycine is the only	
VAL044C		Glycine cleavage system H-protein subunit	NIA.	NIA	NIA	NA N	1 1	1	0	TD	00 1	0.01	TD 4	7 0 76	ED 1	00 0	77 55	1.02	06 5	D 0 0	7 0 5	o ED	1.04	0.55	-D D	nitrogen source [Nagarajan97]. Could also be due to complicated gene-protein-reaction associations.	NA
YAL044C	GCV3	Guanosine diphosphatase of Golgi	NA	INA	NA	NA N	IA I	+	U	TP 0	.99 1	-0.01	IP I.	0.76	FP I	.09 0.	// FF	1.03	0.6 F	P 0.87	0.5	8 FP	1.04	0.55 1	-P D	is complicated gene-protein-reaction associations.	INA
YEL042W	GDA1	membrane	NA	NA	NA	NA N	IA 1	1	-0.01	TP	1 1	-0.06	TP 1.0	0.97	TP 1	.1 0.	97 TF	1.11	1.02 T	P 1.12	0.9	9 TP	1.11	0.98	TP N	A NA	NA
YOR375C	CDH1	NADP-specific glutamate dehydrogenase	NA	NA	NA	NA N	IA 1	1	0.39	тр	1 1	0.03	TP 1.0	10 1	TD 1	.1 1.	01 TE	1 11	1 T	P 1.12	2 1	TP	1 11	1 -	TP N	A NA	NA
101(3/30	GDITI	NAD-dependent glutamate	INA	INA	INA	INA IN	1	+	0.55	IF	<u> </u>	-0.02	11 1.0	70 1	IF I	.1 1.	01 11	1.11	<u> </u>	F 1.12		IF	1.11	-	I		INA
YDL215C	GDH2	dehydrogenase	NA	NA	NA	NA N	IA 1	1	-0.06	TP	1 1	-0.05	TP 1.0	1.01	TP 1	.1 1.0	02 TF	1.11	1.03 T	P 1.12	2 1.0	5 TP	1.11	1.04	TP N	A NA	NA
		NADP-linked glutamate																									
YAL062W	GDH3	dehydrogenase	NA	NA	NA	NA N	IA 1	1	-0.03	TP	1 1	-0.02	TP 1.0	1.01	TP 1	1.1	04 TF	1.11	1.05 T	P 1.12	2 1.0	6 TP	1.11	1.05	TP N	A INA	NA
		Glucoseamine-6-phosphate synthase glutamine_fructose-6-																								Essential for synthesis of cell wall precursors (leading to	
YKL104C		phosphate amidotransferase	1	FP	NA	NA N	IA NA	NA	NA	NA I	IA NA	NA NA	NA N	A NA	NA N	N AIN	IA NA	NA	NA N	IA NA	. NA	NA NA	NA	1 AN	IA B	io chitin biosynthesis), which are not required in the model.	FP
		Permease involved in the uptake of																									
YCR098C	GIT1	glycerophosphoinositol (GroPIns)	NA	NA	NA	NA N	IA 1	1	0.03	TP	1 1	-0.02	TP 1.0	0.97	TP 1	.1 0.	94 TF	1.11	0.97 T	P 1.12	2 0.9	4 TP	1.11	0.97	TP N	A NA	NA
YEL011W	GLC3	1,4-glucan-6-(1,4-glucano)- transferase	NA	NA	NA	NA N	IA 1	1	-0.02	TP	1 1	0	TP 1.0	08 1	TD 1	1 1	01 TE	1 11	1.03 T	D 1 11	1 0	2 TD	1 11	1 01	re N	A NA	NA
YCL040W		Glucokinase		NA					0.02			-0.03							1.03 T							A NA	NA
																										Null mutants are glutamine auxotrophs [MIPS]. The deletion	
		Glutamine synthetase	1				IA NA					NA.	NA N			N AI			NA N							ed is lethal if glutamine is removed from the media.	NA
YOR168W	GLN4	Glutamine-tRNA ligase	1	FP	NA	NA N	IA NA	NA	NA	NA I	IA NA	NA NA	NA 1.0	1.03	TP 1	.1 1.	04 TF	1.11	1.04 T	P 1.12	2 1.0	6 TP	1.11	1.03	TP O	th Protein synthesis not required in the model	NA
YML004C	GLO1	Lactoylglutathione lyase (glyoxalase	NA	NA	NA	NA N	IA 1	1	0.01	TP	1 1	0	TP 1.0	08 1 03	TP 1	1 1	06 TE	1 11	1.07 T	P 1 12	1 0	7 TP	1 11	1 07	re N	A NA	NA
YDR272W		Glyoxylase-II		NA				_	0.07		1 1	_	TP 1.0						1.01 T					1.03		A NA	NA
YOR040W	GLO4	Glyoxylase-II	NA	NA	NA	NA N	IA 1	1	-0.03	TP	1 1	-0.07	TP 1.0)8 1	TP 1	.1 1.	02 TF	1.11	1.02 T	P 1.12	2 1.0	1 TP	1.11	1.01	TP N	A NA	NA
VDI 00 4144	0.54	Glutathione oxidoreductase EC																									
YPL091W YDL171C		1.6.4.2 Glutamate synthase (NADH)	_	NA NA	_				-0.03 0.29				TP 1.0	08 1 08 1.02		.1 1.				P 1.12			1.11			A NA A NA	NA NA
IBLITIO	OLIT	Gidamate synthase (IVADIT)	IVA	INA	INA	IVA	1/1	+	0.23		' '	-0.07	11 1.0	1.02			01 11	1.11	<u> </u>	1 1.12	0.3	3 11	1.11	-		Should be a glycine auxotroph when grown on glucose so	IVA
																										that the deletion strain should grow normally in complex	
YEL046C	GLY1	Threonine aldolase	NA	NA	1	5.5 F	P 1	1	0.03	TP	1 1	0	TP 1.0	0.71	FP 1	.1 0	.7 FF	1.11	0.83 T	P 1.12	2 0.7	7 FP	1.11	0.85	TP D	is media [Monschau97].	NA
VEL0470	CNIA 1	Glucosamine-phosphate N-	١,	FP	NIA	NIA N	IA NIA	. NA	NIA	NIA .		NIA.	NIA NI	A NIA	NIA N			NIA	NIA NI		NI A	. INIA	NIA	NIA N	, D	is N. Acetylgluggeamine synthesis is not required in the model	NA
YFL017C		acetyltransferase 6-phosphogluconate	1	FP	NA	NA N	IA NA	NA	NA	NA I	IA NA	NA NA	NA N	A NA	NA I	N AI	IA NA	NA	NA N	IA NA	. INA	NA	NA	NA I	NA B	io N-Acetylglucosamine synthesis is not required in the model.	INA
		dehydrogenase, decarboxylating;																									
		converts 6-phosphogluconate +																									
		NADP to ribulose-5-phosphate +																									
YHR183W		NADPH + CO2 6-phosphogluconate	NA	NA	. 1	5 F	P 1	1	-0.01	TP	1 1	-0.04	TP 1.0	0.65	FP 1	.1 0.	82 FF	1.11	0.83 T	P 1.12	2 0.9	9 TP	1.11	0.95	TP Is	This is the major isozyme (80% of activity) [MIPS].	NA
YGR256W		dehydrogenase	NA	NA	NA	NA N	JA 1	1	-0.03	TP	1 1	0.03	TP 1 (1.02	TP 1	1 .	1 TE	1 11	0 99 T	P 1 12	1	ТР	1 11	1 .	re N	A NA	NA
		High affinity glutamine permease				NA N			0					1.03													NA
		Glycerol-3-phosphate																									
YDL022W	GPD1	dehydrogenase	NA	NA	NA	NA N	IA 1	1	-0.04	TP	1 1	-0.05	TP 1.0	1.03	TP 1	.1 1.0	06 TF	1.11	1.05 T	P 1.12	2 1.0	8 TP	1.11	1.06	TP N	A NA	NA
YOL059W	CDD2	Glycerol-3-phosphate dehydrogenase (NAD+)	NIA	NA	NA	NA N	1 1	1	0.24	тр	, ,	0	TD 1	1.01	TD 1	1 1	02 TE	1 11	1 02 T	D 1 11	1 0	4 TD	1 11	1 01	ro N	A NA	NA
		Glycogen phosphorylase			NA		IA 1	1	-0.02		1 1		TP 1.0	8 1.03	TP 1	1.1	1 TF	1.11	1 T							A NA	NA
		, 0. 1		<u> </u>																							
				FP	NA	NA N	IA NA	NA	NA	NA I	IA NA	NA NA	NA N	A NA	NA N	N AI	IA NA	NA	NA N	IA NA	. NA	NA NA	NA	1 AN	NA O	th Essential for sporulation, which is not required in our model.	FP
YKL152C		Phosphoglycerate mutase	1	гг							_																
		Similar to GPM1 (phosphoglycerate	1	FF																							۱ ا
		Similar to GPM1 (phosphoglycerate mutase); converts 3-	1	FF																							
YKL152C		Similar to GPM1 (phosphoglycerate			NA.		IA 1	1	0.03	TP	1 1	-0.05	TP 1.0	08 1.02	TP 1	1.1 1.0	04 TF	1.11	1.06 T	P 1.12	2 1.0	7 TP	1.11	1.07	TP N	A NA	NA
YKL152C YDL021W YOL056W	GPM2 GPM3	Similar to GPM1 (phosphoglycerate mutase); converts 3- phosphoglycerate to 2- phosphoglycerate in glycolysis Phosphoglycerate mutase	NA NA	NA NA	NA NA	NA N	IA 1	1	-0.01	TP	1 1	-0.03	TP 1.0	08 1.02 08 1	TP 1	.1 1.	01 TF	1.11	1.02 T	P 1.12	2 1.0	2 TP	1.11	1.02	TP N	A NA	NA
YKL152C YDL021W YOL056W YKL026C	GPM2 GPM3 GPX1	Similar to GPM1 (phosphoglycerate mutase); converts 3- phosphoglycerate to 2- phosphoglycerate in glycolysis	NA NA NA	NA NA NA	NA NA	NA N	IA 1 IA 1	1	-0.01	TP TP	1 1 1 1	-0.03	TP 1.0	08 1.02 08 1 08 1.01 08 0.98	TP 1	i.1 1.0	01 TF 02 TF	1.11	1.02 T 0.99 T	P 1.12	2 1.0 2 1.0	2 TP 1 TP	1.11 1.11	1.02	TP N	A NA	

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			sim	all	sim	dxe	call	sim	MD exp	ave	call	l sim	ave	call	Ë	dxe	i all	'PDGE sim	PDGE exp	Ë	dxə	call	Ë	dxe	call	exp	all	"	Explanation Explanation
ORF	Vam.	Annotation	s ss	ss c	Nols	Nols	Nols	MIMD	/IMD	ммр аve	MM M	/PGal sim	(PGal ave	/PGal cal	YPD sim	YPD exp	/PD call	PDG	(PDGE	/PG sim	PG	/PG	/PE sim	/PE exp	PE (PLe	P.	Class	Explanation
YHR104W		Aldose reductase			NA		_	1		0.05	TP	1 .	1 -0.0)1 TP	1.08	0.99	TP 1	1.1	1 TF	1.11		_	1.12	0.99	TP 1.	_		NA	NA NA
YBR121C	GRS1	Glycine-tRNA ligase 1,3-beta-D-glucan synthase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA N	A NA	A NA	NA	NA I	1 AV	NA	NA NA	NA.	NA	NA	NA	NA	NA N	A NA	NA	Oth	Protein synthesis not required in the model NA
YGR032W	GSC2	catalytic component	NA	NA	NA	NA	NA	1	1 -	0.02	TP	1 .	-0.0)5 TP	1.08	1.02	TP 1	1.1 1	1.03 TF	1.11	1.02	TP	1.12	1.05	TP 1.	11 1.0	4 TP	NA	NA NA
YJL101C	GSH1	Gamma-glutamylcysteine synthetase	NA	NA	NA	NA	NA	1	1 -	0.02	ТР	1 .	0.2	2 TP	1.08	0.99	TP 1	1.1	1 TE	1.11	0.93	TP	1.12	0.94	TP 1.	11 0.9	4 TP	NA	NA NA
YOL049W		Glutathione synthetase			NA		NA	1			TP	1 '			1.08				1.02 TF										
YFR015C	GSY1	Glycogen synthase (UDP-glucose- starch glucosyltransferase)	NA	NA	NA	NA	NA	1	1 -	0.05	TP	1	-0.0)2 TP	1.08	1.03	TP 1	1.1 1	1.04 TF	1.11	1.03	TP	1.12	1.07	TP 1.	11 1.0	4 TP	NA	NA NA
YLR258W	GSY2	Glycogen synthase (UDP-glucose- starch glucosyltransferase)	NΔ	NΔ	NA	NA	NΑ	1	1 -	0.04	TP	1 .	1 -0 ()7 TP	1.08	1.03	TP 1	1 1 1	1.03 TF	1 11	1 03	TP	1 12	1.05	TP 1	11 1 0	5 TP	NΑ	NA NA
YDR454C		Guanylate kinase			NA		NA	NA				NA N			NA				NA NA						NA N			NA	
YHL032C	GUT1	Converts glycerol to glycerol-3- phosphate glyerol kinase	NΔ	NΔ	NA	NA	NA	1	1 -	0.01	TP	1 .	1 -0 (18 TP	1.08	1	TP 1	08 1	1.02 TF	0.9	0.98	TP	1 12	1	TP 1	11 1 0	1 TP	NΑ	NA NA
		Glycerol-3-phosphate					IVA	_	H																				
YIL155C YDR232W		dehydrogenase 5-aminolevulinate synthase			NA NA		NA	1	1		TP	1 NA N			1.08 NA				0.99 TF NA NA						TP 1. NA N				NA NA Heme biosynthesis not required in the model FP
		Uroporphyrinogen decarboxylase			NA			NA				NA N			NA				NA NA						NA N			Bio	
YDR044W		Coproporphyrinogen III oxidase	1		NA		_	NA		NA		NA N					1 AV			NA	NA	NA			NA N			Bio	
YFR014W	HEM14	Protoporphyrinogen oxidase	NΔ	NΔ	NA	NA	NA	NA	NΑ	NA	NΑ	NA N	Δ ΝΑ	ΔNA	1.08	0.82	FP 1	1 1 ().84 FF	1 11	0.85	TP	1 12	0.68	FP 1	11 0 7	4 FP	Acc	Heme is not required in the model. May also result in heme precursor accumulation in vivo [SGD].
		The second secon			1.0.	10.				10.					1.00	0.02			,,,,,,,	ļ	0.00	1		0.00	<u> </u>		Ť	7100	Only deemed to be essential in one study [Giaever02]. The
\(OD470\\\		Ferrochelatase (protoheme																									. _	D: .	other study [Steinmetz02] shows normal growth on all
YOR176W	HEM1	Delta-aminolevulinate dehydratase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA N	A NA	A NA	1.08	1.04	IP 1	1.1 1	1.04 TF	1.11	1.04	IP	1.12	1.03	IP 1.	11 1.0	4 IP	DIS	substrates. FP
YGL040C	HEM2	(porphobilinogen synthase)	1	FP	NA	NA	NA	NA	NA	NA	NA	NA N	A NA	NA NA	NA	NA	NA N	NA	NA NA	NA.	NA	NA	NA	NA	NA N	A NA	NA	Bio	Heme biosynthesis not required in the model.
		Phorphobilinogen deaminase																											Only deemed to be essential in one study [Giaever02]. The other study [Steinmetz02] shows normal growth on all
YDL205C	НЕМ3	(uroporphyrinogen synthase)	1	FP	NA	NA	NA	NA	NA	NA	NA	NA N	A NA	NA NA	1.08				1.04 TF										substrates. FP
YOR278W	HEM4	Uroporphyrinogen III synthase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA N	A NA	A NA	NA	NA	1 AV	NA	NA NA	NA.	NA	NA	NA	NA	NA N	A NA	NA	Bio	
																													Used as a histidine transporter in our model, but there are isozymes for this function. Lethality may be due to the role of
YGR191W	HIP1	Histidine permease	1	FP	NA	NA	NA	NA	NA	NA	NA	NA N	A NA	NA NA	NA	NA	NA N	NA	NA NA	NA	NA	NA	NA	NA	NA N	A NA	NA	Oth	Hip1p in Mg2+ transport.
YER055C		ATP phosphoribosyltransferase			NA			1			TP	1 1	-0.0	_	1.08				1.01 TF									NA	
YFR025C	HIS2	Histidinolphosphatase Imidazoleglycerol-phosphate	NA	NA	NA	NA	NA	1	1 -	0.04	TP	1 1	0.0	2 TP	1.08	1	TP 1	1.1).99 TF	1.11	1	TP	1.12	1.01	TP 1.	1 1	TP	NA	NA NA
YOR202W	HIS3	dehydratase	NA	NA	NA	NA	NA	1	1 -	0.01	TP	1 -	-0.0)8 TP	1.08	1.01	TP 1	1.1 1	1.02 TF	1.11	1.03	TP	1.12	1.03	TP 1.	11 1.0	2 TP	NA	NA NA
YCL030C	HIS4	Histidinol dehydrogenase	NA	NA	NA	NA	NA	1	1	0	TP	1 1	0		1.08				1.02 TF										
YIL116W	HIS5	Histidinol-phosphate aminotransferase	NIA	NIA	NA	NA	NA	1	1 -	0.01	тр	1 .)6 TD	1.08	1 01	TD 1	1 1 1	1.02 TF	1 11	1.04	тр	1 12	1.02	TD 1	11 1 0	л Д ТБ	NΙΛ	NA NA
TILITOVV	ПІЗЗ	Phosphoribosyl-5-amino-1-	INA	INA	INA	INA	INA	_	H	0.01	IF	_	-0.0	JO 1 F	1.06	1.01	IF I	1.1	1.02 16	1.11	1.04	IF	1.12	1.02	IF I.	11 1.0	4 11	INA	IVA IVA
		phosphoribosyl-4-																									_		l
YIL020C	HIS6	imidazolecarboxiamide isomerase Glutamine	NA	NA	NA	NA	NA	1	1	0.09	TP	1 '	1 -0.0)6 TP	1.08	1.01	TP 1	1.1 1	1.01 TF	1.11	1.03	TP	1.12	1.03	TP 1.	11 1.0	3 TP	NA	NA NA
		amidotransferase:cyclase imidazole																											
		glycerol phosphate synthase																											
YBR248C	HIS7	(synonym) 3-hydroxy-3-methylglutaryl-	NA	NA	NA	NA	NA	1	1 -	0.01	TP	1 1	0.1	3 TP	1.08	1	TP 1	1.1	1 TF	1.11	1.01	TP	1.12	0.98	TP 1.	11 0.9	9 TP	NA	NA NA
		coenzyme A (HMG-CoA) reductase																											
YML075C	HMG1	isozyme	NA	NA	NA	NA	NA	1	1	0.06	TP	1 1	-0.0)2 TP	1.08	1.01	TP 1	1.1 1	1.01 TF	1.11	0.99	TP	1.12	1.01	TP 1.	1 1.0	1 TP	NA	NA NA
		3-hydroxy-3-methylglutaryl- coenzyme A (HMG-CoA) reductase																											
YLR450W	HMG2	isozyme	NA	NA	NA	NA	NA	1	1	0.04	TP	1	0	TP	1.08	0.99	TP 1	1.1).99 TF	1.11	0.98	TP	1.12	0.98	TP 1.	1 0.9	в ТР	NA	NA NA
		Arginine methyltransferase mono-																											
YBR034C	HMT1	and asymmetrically dimethylating enzyme	NΙΔ	ΝΔ	NΔ	NA	ΝΔ	1	1	0.06	тр	1		и Тр	1.08	1	TD 1	1 1 1	1.01 TF	1 11	1 02	тр	1 12	1 04	TD 1	11 1 0	2 TD	ΝΔ	NA NA
1010040	. mvi i i	Transporter (permease) for choline	14/4	1474	14/4	INA	14/4	-		0.00			0.0	7 15	1.00				1.01 11	1.11	1.02		1.12	7.04	1.	1.0	J 11 ²	1474	IVA
VOI 0770	LININA	and nitrogen mustard; share	N. A		NIA.	NIA.	NI A	,	1	0.04	_{TC}				4.00	4.04	TD				0.00	т.	4.40	4.04	TD .			NIA.	NA NA
YGL077C	minivi1	homology with UGA4 Fhit homolog, member of the	NA	NA	NA	NA	NA	1	1	0.31	12	1 '	-0.0	io IP	1.08	1.01	12 1	1.1 1	1.01 TF	1.11	0.99	IP	1.12	1.01	IP 1.	1.0	I IP	IVA	NA NA
		histidine triad superfamily of																											
YDR305C	HNT2	nucleotide binding-proteins	NA	NA	NA	NA	NA	1	1	0.03	TP	1 '	-0.0)3 TP	1.08	1.01	TP 1	1.1).99 TF	1.11	0.98	TP	1.12	0.97	TP 1.	11 0.9	8 TP	NA	
																													Homocysteine can be produced in the model using CYSTL
																													(Cys1p) and AHCi (Sah1p) reactions in addition to this
\\\ 5		Aspartic beta semi-aldehyde dehydrogenase				NA	NA		0 1	10.74			0	TP	1.08				1.03 TF										pathway, but neither of these reactions can be removed from

												۔	a	е	_				Ē	dx	all											et al
ORF	ame		ss sim	ss call	Slow sim	ом ехр	ow call	MMD sim	имD ехр	MMD ave	MMD call	YPGal sim	Gal exp	rPGal ave	/PGal cal	YPD sim	YPD exp	rPD call	YPDGE sim	/PDGE exp	PDGE cal	YPG sim	YPG exp	PG call	YPE sim	YPE exp	'PE call	YPL sim		YPL call	Class	ster
0	Z	Annotation	ш	Ш	S	<u>w</u>	S	Σ	Σ	Σ	Σ	⋝	>	>	-	>	> 3	× -	⋝	>	X	-	>	⋝	>	¥	⋝	-	>	⋝	O	Explanation Homocysteine can be produced in the model using CYSTL (Cys1p) and AHCi (Sah1p) reactions in addition to this
YER052C	НОМЗ	Aspartate kinase (L-aspartate 4-P-transferase) (EC 2.7.2.4)	NA	NA	NA	NA	NA	1	0	4.46	FP	1	1 (0.04	TP 1	.08	1 1	ΓP 1	1.1	1.02	ΓP 1	.11	1.03	TP ·	1.12	1.02	TP 1	.11	.05	TP	Unk	pathway, but neither of these reactions can be removed from the model.
		L-homoserine:NADP																														Homocysteine can be produced in the model using CYSTL (Cys1p) and AHCi (Sah1p) reactions in addition to this
YJR139C	НОМ6	oxidoreductase homoserine dehydrogenase	NA	NA	NA	NA	NA	1	0	9.11	FP	1	1 -	0.03	TP 1	.08	0.98 7	ГР 1	1.1	0.98	ΓP 1	.11	0.96	TP ·	1.12	0.91	TP 1	.11	0.97	TP	Unk	pathway, but neither of these reactions can be removed from the model.
YER062C		DL-glycerol-3-phosphatase	NA				NA	1		0.02	TP	1					1.01 1								1.12							
YDR399W	HPT1	Hypoxanthine guanine phosphoribosyltransferase	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	0	TP 1	.08	0.99 1	ГР 1	1.1	0.99	TP 1	.11	1.01	TP ·	1.12	1.01	TP 1	.11	.01	TP	NA	NA NA
YPR033C		Histidine-tRNA ligase		_	NA		NA	NA	NA		_	NA I			_			_	_	NA I	_	_	_	_	_	_	_	_	_	_		Protein synthesis not required in the model FP
YFR053C	HXK1	Hexokinase I (PI) (also called hexokinase A)	NA	NA	NA	NA	NA	1	1	-0.04	TP	1	1 -	0.05	TP 1	1.08	1.03 1	ΓP 1	1.1	1.04	TP 1	.11	1.03	TP	1.12	1.05	TP 1	.11	.04	TP	NA	NA NA
YGL253W	HXK2	Hexokinase II (PII) (also called hexokinase B)	NA	NA	NA	NA	NA	1	1	0.05	TP	1	1	0	TP 1	.08 (0.95 1	ΓP 1	1.1	1.02	ΓP 1	.11	1.07	TP ·	1.12	1.07	TP 1	.11	.07	TP	NA	NA NA
		Hexose transporter		_	NA		NA	1	-	0.03	TP	1			_		1.01 1	_	_		ΓP 1	_	_	_	1.12	_	_	_	_	_		
		High affinity hexose transporter Hexose transporter	NA NA		NA NA		NΑ	1	1	-0.05 0.1	TP	1		0.03	TP 1	.08 1	1.02 1	TP 1	_	0.97 ⁻	ΓΡ 1 ΓΡ 1	_	_	_	_	0.97 1.01	TP 1	.11 (0.97	_	NA NA	NA NA NA
		Hexose transporter		_	NA		NA	1	1	0.08	TP	1		0.04	TP 1	.08 1	1.02 7	ΓP 1	_	1.02	_	_	_	_	_	_	TP 1	.11 ′	.01		NA	NA NA
		High affinity hexose transporter-2	NA	_	_		NA	1	1	-0.01	TP	1	_	0.05	TP 1			ГР 1	_	1.06	_	_	1.07	_	_	1.07	_	.11 1	.07	_	NA	NA NA
		Low affinity glucose transporter High affinity glucose transporter	NA NA	_	NA NA		NA	1	1	-0.06 -0.01	TP TP	1		0.03	TP 1		1.01 T	TP 1	1.1	1.02	_	_	1.04 1.06		1.12	_	TP 1	_	.06		NA NA	NA NA NA
		Hexose transporter			NA		NA	1	1	0.85	TP	1	_	0.03	TP 1		1.01 1		1.1	1.04	_	_			1.12				.03	_	NA	
YJL214W		Hexose permease		_	NA		NA	1	1	0	TP	1		0.03	_			ΓP 1	_			.11	_	_	1.12	_	TP 1	_	_	_	NA	NA NA
YIR037W	HYR1	Glutathione-peroxidase (putative)	NA	NA	NA	NA	NA	1	1	0.03	TP	1	1	0 .	TP 1	.08	1 1	ΓP 1	1.1	0.97	ΓP 1	.11 (0.98	TP ·	1.12	0.96	TP 1	.11 ().97	TP	NA	NA NA
YER065C	ICL1	Isocitrate lyase	NA	NA	NA	NA	NA	1	1	-0.02	TP	1		0.04			1 1	ΓP 1	1.1	1	ΓP 1	.11	1.02	TP (0.79	0.99	FN 1	.08	1	TP	Med	
YPR006C	ICL2	2-methylisocitrate lyase	NA	NA	NA	NA	NA	1	1	0.03	TP	1	1 -	0.02	TP 1	.08 1	1.02 1	ΓP 1	1.1	1.02	ΓP 1	.11	1.02	TP ·	1.12	1.03	TP 1	.11 ′	.03	TP	NA	NA NA
YNL037C	IDH1	Isocitrate dehydrogenase 1 alpha-4- beta-4 subunit	NA	NA	1	4.7	FP	1	1	-0.06	TP	1	1 (0.02	TP I	NA	NA N	1 AV	NA	NA I	1 AV	NA	NA	NA	NA	NA	NA I	NA	NA I	NA	Unk	The model does not utilize this part of the TCA cycle.
VOD400W	IDIIIO	NAD-dependent isocitrate									-															. =-						The model does not use the corresponding reaction when grown on glycerol or lactate. In vivo there is a NAD/NADH
YOR136W	IDH2	dehydrogenase Isopentenyl	NA	NA	NA	NA	NA	1	1	0.96	IP	1	1 ().17	IP 1	.08 ().99 1	IP 1	1.1	0.88	IP 1	.11 (0.68	FP '	1.12	0.78	IP 1	.11	0.6	FP	Unk	balancing issue. NA
		diphosphate:dimethylallyl																														
YPL117C	IDI1	diphosphate isomerase (IPP isomerase)	0	TN	NA	NA	NA	NA	NA	NA	NA	NA I	NΑ	1 AN	NA I	NA	NA N	1 AV	NA	NA I	1 AV	NA	NA	NA	NA	NA	NA I	NA	NA I	NA	NA	NA NA
YDL066W	IDP1	NADP-dependent isocitrate dehydrogenase	NA	NA	NA	NA	NA	1	1	0.12	TP	1	1 (0.03	TP 1	1.08	1.01 T	ΓP 1	1.1	1.02	ΓP 1	.11	1.07	TP ·	1.12	1.05	TP 1	.11	.09	TP	NA	NA NA
YLR174W	IDP2	NADP-dependent isocitrate dehydrogenase	NA	NA	NA	NA	NA	1	1	0.04	TP	1	1	0	TP 1	.08	1 1	ΓP 1	1.1	1.01	ΓP 1	.11 (0.99	TP ·	1.12	1	TP 1	.11 (0.98	TP	NA	NA NA
YNL009W	IDP3	NADP-dependent isocitrate dehydrogenase	NA	NA	NA	NA	NA	1	1	0.03	TP	1	1 -	0.02	TP 1	1.08 1	1.04 T	ГР 1	1 1	1 -	ΓP 1	11	1.01	TP ·	1.12						NA	NA NA
YBL076C	ILS1	Isoleucine-tRNA synthetase		_	NA		NA	NA	NA	NA		NA I						A A	NA	NA I			NA				NA I					Protein synthesis not required in the model NA
YER086W	ILV1	Threonine deaminase	NA	_	_		NA	0	0	10.66	TN	1			_			_	_	0.98	_	_	_	_	1.12	_	_	_	_	_	NA	NA NA
YJR016C	ILV3	Dihydroxyacid dehydratase Acetohydroxyacid	0.64	TN	NA	NA	NA	NA	NA	NA	NA	NA I	NA	1 AN	NA I	NA	NA N	1 AV	NA	NA I	1 A	NA	NA	NA	NA	NA	1 AN	NA	NA I	NA	NA	In silico slow growth.
YLR355C	ILV5	reductoisomerase	0.64	TN	NA	NA	NA	NA	NA	NA	NA	NA I	NA	NA I	NA I	NA	NA N	1 A	NA	NA I	1 A	NA	NA	NA	NA	NA	NA I	NA	NA I	NA	NA	In silico slow growth.
		Acetolactate synthase regulatory																														Ilv6p is the regulatory subunit of phenylalanine transaminase [SGD]. Null mutant has defective retroinhibition by valine [Cullin96], but apparently this subunit is otherwise non-
	ILV6	subunit				NA		0		-0.01		1				0.69	1.01 F	-N 1	1.1	1.02	ΓP 1	.11	1.01	TP	1.12	1	TP 1	.11				essential for the enzymatic function.
YLR432W YML056C	IMD3 IMD4	IMP dehydrogenase homolog IMP dehydrogenase homolog			NA NA			1		0.02		1			TP 1	.08 1	1.01 T	TP 1	1.1	1.04	TP 1	.11			1.12						NΑ	
	INM1	Inositol monophosphatase			NA NA		NA	0	1	-0.06 0	FN	0		0.07						1.04 1.04 F												VDR287W may code for an isozyme for Inm1p. May not be lethal if inositol is in media.
		L-myo-inositol-1-phosphate							İ																							Null mutant is viable, but an inositol auxotroph [SGD]. This is consistent with in silico results. Thus, experiments may have
	INO1	synthase				NA			1	0.11																						some inositol in media.
	IPP1 IPT1	Inorganic pyrophosphatase Inositolphosphotransferase 1			NA NA		-	NA 1	NA 1	NA -0.05		NA I		NA 1			NA N			NA N			NA n ga				NA I				NA NA	
	ISM1	Isoleucine-tRNA ligase	NA					1		-0.03		1	1 -	0.03	TP 1	.08).69 F	P 1	1.1	0.66 F	P 1	.11 (0.48	FP '	1.12	0.45	FP 1	.11 ().56	FP	Oth	Protein synthesis not required in the model NA
	ITR1	Myo-inositol transporter			NA			1		0.09		1								1.03												NA NA
YOL103W	ITR2	Myo-inositol transporter	NA	NA	NA	NA	NA	1	1	0.03	TP	1	1 -	0.05	TP 1	.08 1	1.03	TP 1	1.1	1.02	TP 1	.11	1.01	TP	1.12	1.03	TP 1	.11 ′	.01	TP	NA	NA NA

			E	_	im	exp	sim	dx	ıve	all	sim	Gal ave	100	<u> </u>	dx	all	E S I	Eexp	in call	dx	all I	E	e =	₹ E	9	=			er et al
ORF	lame	Annotation	Ess sim	ss call	Slow sim	Slow exp	MMD	иМD ехр	MMD ave	MMD	/PGal sim	YPGal ave	/PGal cal	YPD sim	YPD exp	/PD call	PDGE SIM	(PDGE exp	YPG sim	YPG exp	YPG call	YPE SIM	YPE exp	YPL sim	YPL exp	YPL call	Class	Explanation	Forster
YKL217W		Carboxylic acid transporter protein		NA	NA	0, 0,			-0.02							T				0.99								Lower oxygen uptake rate would correct this false negative prediction.	NA
TRLZITVV	JEINT	Homolog	INA	INA	INA	INA IN	A 1	<u> </u>	-0.02	IF	-	1 -0.0	05 1	1.00	1.03	IF I	.1 1.	.01 1	1.11	0.99	IF I.	.12	- '	0.04	1.01	FIN	ivieu	Should definitely have a growth defect on non-fermentable	
YIL125W	KGD1	Alpha-ketoglutarate dehydrogenase	NA	NA	NA	NA N	A 1	1	0.02	TP	1	1 0.0)3 T	P 1.08	0.96	TP 1	.1 0.	.92 T	P 1.09	0.6	FP 1.	.11 0).66 F	P 1.1	0.66	FP	Unk	carbon sources. The model just adjusts the flux distribution to utilize more amino acids and dumps acetate.	o NA
		Alpha-ketoglutarate dehydrogenase complex dihydrolipoyl	:																									Should definitely have a growth defect on non-fermentable carbon sources. The model just adjusts the flux distribution to	
YDR148C		transsuccinylase component	NA	NA	NA	NA N	A 1	1	0.01	TP	1	1 0.0)6 T	P 1.08	1	TP 1	.1 0	.95 T	P 1.09	0.64	FP 1.	.11 0).71 F	P 1.1	0.6	FP	Unk	1 .	NA
YDR483W		Alpha-1,2-mannosyltransferase	_	NA		NA N			-0.03			1 0		P 1.08						1.04									NA
		Lysine-tRNA ligase Type II transmembrane protein	1 NA	FP NA	NA NA	NA N	_	_	NA 0	NA TP		IA N		A NA					NA NA	NA 1 1.04	NA N			A NA				Protein synthesis not required in the model NA	FP NA
101(09944	KIIKI	Type ii transmembrane protein	INA	INA	INA	INA IN		+-	- 0	IF	-+	1 -0.0	03 1	1.00	1.03	1 -	. 1	.05 1	1.11	1.04	IF I.	. 12 1	1.00 1	1.11	1.05	IF	INA	IVA	INA
YKR061W	KTR2	Mannosyltransferase (putative) type 2 membrane protein		NA	NA	NA N	A 1	1	0.05	ТР	1	1 -0.0	06 T	P 1.08	1.02	TP 1	.1 1.	.03 T	P 1.11	1.03	TP 1.	.12 1	1.05 T	P 1.11	1.04	TP	NA	NA	NA
YBR205W	KTR3	Alpha-1,2-mannosyltransferase (putative)	NΔ	NΔ	NA	NA N	Δ 1	1	0.13	тр	1	1 -0.0	мт	P 1.08	1.02	TD 1	1 1	01 T	D 1 11	1	TP 1.	12	1 T	P 1.11	1	тр	ΝΔ	NA	N/
		Alpha-1,2-mannosyltransferase																											
YBR199W	KTR4	(putative)	NA	NA	NA	NA N	A 1	1	-0.05	TP	1	1 0.0)6 T	1.08	1.01	IP 1	.1 1.	.02 T	P 1.11	1.02	TP 1.	.12 1	T 80.1	P 1.11	1.03	ſΡ	NA	NA Affects cell wall composition, but should not necessarily have	N/
YNL029C	KTR5	Mannosyltransferase (putative)	NA	NA	1	4.2 FI	P 1	1	-0.02	TP	1	1 0	, Іт	P NA	NA I	VA N	IA N	NA N	IA NA	NA	NA N	I AL	NA IN	IA NA	NA	NA	Oth	a slow growth phenotype [MIPS].	NA
YPL053C		Mannosylphosphate transferase			NA		A 1	1	0.02											1.02							NA		NA
		Pyruvate dehydrogenase complex dihydrolipoamide acetyltransferase																											
YNL071W	LAT1	component (E2)	NA	NA	NA	NA N	A 1	1	0.01	TP	1	1 -0.0	03 T	P 1.08	1.02	TP 1	.1 0.	.99 T	P 1.11	0.78	FP 1.	.12 0).89 T	P 1.11	0.89	TP	Unk	The model can bypass the PDH complex if necessary.	N/
YMR296C	LCB1	Serine palmitoyltransferase component	1	FP	NA	NA N	A NA	NA	NA	NA	NA N	IA N	A N	A NA	NA I	NA N	IA N	NA N	IA NA	NA	NA N	JA I	NA N	IA NA	NA	NA	Bio	Sphingolipid synthesis not required in the model.	FF
YDR062W	LCB2	Serine palmitoyltransferase	1	FP	NA	NA N	ΔΝΔ	NΔ	ΝΔ	NΔ	NA N	IA N	ΔΝ	A NA	ΝΔΙ	NA N	ΙΔ Ν	MA N	ΙΔ ΝΙΔ	NΔ	NA N	. ΔΙ	NIA N	ΙΔ ΝΙΔ	NΔ	NΔ	Rio	Sphingolipid synthesis not required in the model.	FF
		Dihydrosphingosine-1-phosphate		Ħ																									
YJL134W	LCB3	phophatase Sphingoid long chain base (LCB)	NA	NA	NA	NA N	A 1	1	-0.02	TP	1	1 0) T	P 1.08	1.01	TP 1	.1 1.	.05 T	P 1.11	1.06	TP 1.	.12 1	1.07 T	P 1.11	1.06	TP	NA	NA .	N/
YOR171C	LCB4	kinase Sphingoid long chain base (LCB)	NA	NA	NA	NA N	A 1	1	0.23	TP	1	1 -0.0	07 T	P 1.08	1.01	TP 1	.1 1.	.01 T	P 1.11	1.02	TP 1.	.12	1 T	P 1.11	1	TP	NA	NA	N.
YLR260W YGL009C		kinase	_	NA NA	1 NA	4.2 FI			-0.02 -0.01					P 1.08						0.55								Sphingolipid synthesis not required in the model. NA	N.
1 GL009C	LEUI	Isopropylmalate isomerase Alpha-isopropylmalate synthase (2-	INA	INA	INA	INA IN	A 1	-	-0.01	IF	_	1 -0.0	03 1	1.00	1.03	IF I	.1 1.	.04 1	F 1.11	1.04	IF I.	. 12 1	1.07	F 1.11	1.05	IF	INA	IVA	IN.
YNL104C	LEU4	isopropylmalate synthase) Alpha-isopropylmalate synthase (2-	NA	NA	NA	NA N	A 1	1	-0.01	TP	1	1 -0.0	03 T	P 1.08	1.01	TP 1	.1 1.	.03 T	P 1.11	1.03	TP 1.	.12 1	1.04 T	P 1.11	1.04	TP	NA	NA	N.
YOR108W	LEU9	isopropylmalate synthase)	NA	NA	NA	NA N	A 1	1	-0.02	TP	1	1 -0.0	03 T	P 1.08	1.02	TP 1	.1 1.	.02 T	P 1.11	1.03	TP 1.	.12 1	1.04 T	P 1.11	1.03	TP	NA	NA	N.
		Dihydrolipoamide dehydrogenase precursor (mature protein is the E3																										Should definitely have a growth defect on non-fermentable	
VEL 0400		component of alpha-ketoacid	l	l																			_					carbon sources. The model just adjusts the flux distribution to	
YFL018C YDR503C		dehydrogenase complexes) Lipid phosphate phosphatase		NA	NA	3.7 FI		_	-0.03											1.03									N.
TDN303C	LITI	Alpha subunit of succinyl-CoA	INA	INA	INA	IN/A IN		-	-0.03	15	-	1 0	<u>'</u>	1.00	1.02	1 - 1	. 1 1.	.04 1	1.11	1.03	IF I.	. 12 1	1.07	1.11	1.03	IF	INA	IVA	111/
		ligase (synthetase; ATP-forming), a																											
VOD4 40W		mitochondrial enzyme of the TCA	l	l		l l		١.										. _					. _				.	NA	1,,
YOR142W	LSC1	cycle Beta subunit of succinyl-CoA ligase	NA	NA	NA	NA N	A 1	1	0.08	TP	1	1 -0.0	02 T	P 1.08	1	TP 1	.1	1 T	P 1.09	0.96	TP 1.	.11	1 1	P 1.1	0.98	TP	NA	NA .	N.
		(synthetase; ATP-forming), a mitochondrial enzyme of the TCA																											
YGR244C	LSC2		NA	NA	NA	NA N	A 1	1	0.38	TP	1	1 0	, Т	P 1.08	1,02	TP 1	.1 1	.03 т	P 1.09	0.98	TP 1	11 1	I.05 T	P 11	1.01	TP	NA	NA	N
YNL268W		Lysine permease						_	-0.01					P 1.08						1.01								NA	N/
YIR034C	LYS1	Saccharopine dehydrogenase	_	NA				_	2.88	TN	1									0.98								NA	N/
YIL094C		Homo-isocitrate dehydrogenase YDL131W (LYS21)	NA	NA	NA	NA N	A 0	0	5.15		1									1.03								NA	N/
YDL182W	LYS20	homolog homocitrate synthase	NA	NA	NA	NA N	A 1	1	0.3	TP	1	1 -0.0	04 T	P 1.08	1	TP 1	.1 1.	.01 T	P 1.11	1	TP 1.	.12 0).99 T	P 1.11	0.99	TP	NA	NA	N/
YDL131W	LYS21	YDL182W (LYS20) homolog homocitrate synthase	NA	NA	NA	NA N	A 1	1	-0.03	TP	1	1 -0 (03 T	P 1.08	1.02	TP 1	.1 1	.02 Т	P 1.11	1.04	TP 1	12 1	1.05 T	P 1.11	1.04	TP	NA	NA	N/
		Homoaconitase			NA				1.55											1.02									N/
YGL154C	LYS5	Alpha aminoadipate reductase phosphopantetheinyl transferase	NA	NA	NA	NA N	A 0	0	8.33	TN	1	1 0.0)1 T	P 1.08	1.02	TP 1	.1 1	.03 T	P 1.11	1.03	TP 1.	.12 1	1.05 T	P 1.11	1.03	TP	NA	NA	N/
		Seventh step in lysine biosynthesis																											
		pathway Malic enzyme		NA NA	NA NA	NA N			1.27 -0.01			1 -0.0 1 0	02 T	P 1.08	1.01	TP 1	.1 0.	.97 T	P 1.11	0.97	TP 1.	.12 1 .12 1	1.03 T	P 1.11	1.03	TP		INA INA	NA NA
																													_

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L.	me		s sim	s call	w sim	w exp	w call	MMD sim	MMD exp	ммр аve	MMD call	/PGal sim	Gal exp	YPGal ave	YPGal call	ا د	YPD call	YPDGE sim	/PDGF exp	PDGE cal	YPG sim	YPG exp	PG call	YPE sim	YPEexp	PEcall	YPL sim	YPL exp	L call				Forster e
ORF	Z	Annotation	Es	Es	Slow	Slo	Slo	2	Σ	Σ	Σ	Ϋ́P	Ϋ́	Y Y	۲ م ۲	<u> </u>	} }	Ϋ́	<u>م</u> ۷	Ϋ́	ΥP	ΥP	ΥP	Ϋ́	ΥP	Α.	. Y	Ϋ́	YPL	ċ	Explanation	n	<u>د</u>
		Alpha-glucoside transporter hexose																															
		transporter maltose permease		NA			NA	1			TP	1		.03 1			.01 TF)2 TF					2 1.0						NA NA		N/
		Maltase		_	NA	_	NA	1			TP	1			TP 1.0		.03 TF														NA NA		N/
		Maltose permease Maltase	NA		NA NA		NΑ	1		0.14	TP	1	_	.16 7	_		.97 TF														A NA A NA		NA NA
		Malonyl-CoA:ACP transferase			NA			1			TP	1			ΓP 1.0		1.8 FF														Component of phopholipids does not according to the contract of the contract o	of the mitochondrial FAS that supplies s to the mitochondrial membrane. The moc count for the formation of the mitochondrial	lel
		Malate dehydrogenase			NA	NA	_	1		0.01	TP	1		.03 1	ΓP 1.0		.01 TF					1 0.8									NA NA		N/
		Malate dehydrogenase			NA	NA	NA	1	1 -	0.03	TP	1	1 -0	.07 1	TP 1.0	08 1	.04 TF	1.1	1.0)6 TF	1.1	1 1.0	3 TF	1.12	2 1.0	6 TI	P 1.1	1 1.0	6 TP	N			N/
		Malate dehydrogenase		_	NA	_	NA	1		0.01	TP	1	_	0 1	ΓP 1.0		.02 TF	_				1 1.0				_	_		3 TP	N			N/
		Ammonia permease			NA		NA	1	_	0.25	TP	1			_		.01 TF)1 TF				1.12			P 1.1		TP		NA NA		N/
		Ammonia transport protein NH4+ transporter	NA NA	_	NA NA	NA NA	NA	1		0.01	TP	1	_	.03 1	TP 1.0	_	.03 TF	_				1 1.0 1 0.9							2 TP	N			NA NA
		Methionine-tRNA ligase			NA		NA	NA			NA	I NA I			IA N	_		1.1 A NA		A NA					2 0.9 NA							thesis not required in the model	N/
		Methionine metabolism			NA		_			1.55		1	_		TP 1.0																NA NA		N/
		Assimilatory sulfite reductase subunit				NA		1		0.29		1																			A NA		N/
		Methylenetetrahydrofolate																															
YPL023C	MET12	reductase (mthfr) (putative)	NA	NA	NA	NA	NA	1	1	0.33	TP	1	1 -0	.05 1	TP 1.0	08 1	.01 TF	1.1	1.0)2 TF	1.1	1 1.0	3 TF	1.12	2 1.0	3 TI	P 1.1	1 1.0	3 TP	N			N/
YGL125W	MET13	Methylenetetrahydrofolate reductase (mthfr) (putative)	NA	NA	NA	NA	NA	1	0	3.97	FP	1	1 -0	.01 7	TP 1.0	08	1 TE	1.1	0.9	99 TF	1.1	1 1	TF	1.12	2 1.0	2 TI	P 1.1	1 1.0	2 TP	ls		ne dominant isozyme, but the model contain sozyme (Met12p).	ns an N <i>A</i>
																																grow as sulfate as only sulfur source [Thon	
V((() 0040		A London Marco Discour		l															۱.,		١											mal media in experimental study has some	
YKL001C	ME I 14	Adenylylsulfate kinase	NA	NA	NA	NA	NA	0	1	0.18	ͰN	1	1 -0	1 80.0	IP 1.0	08 1.	.03 11	J 1.1	1.0)2 11-	1.1	1 1.0	2 11	1.12	2 1.0	2 11	P 1.1	1 1.0	12 TP	, IVI	d sulfur source	es. grow as sulfate as only sulfur source [Thon	NA
																																mal media in experimental study has some	
YPR167C	MET16	3'phosphoadenylylsulfate reductase	NA	NA	NA	NA	NA	0	1	0.64	FN	1	1 -0	.04 7	TP 1.0	08 1	.03 TF	1.1	1 1.0)2 TF	1.1	1 1	TE	1.12	2 1.0	зТ	P 1.1	1 1.0	3 TP	M	d sulfur source		N/
																																ine can be produced in the model using CY	
																															(Cys1p) and	d AHCi (Sah1p) reactions in addition to this	
																																ut neither of these reactions can be remove	
YLR303W	MET17	O-acetylhomoserine (thiol)-lyase	NA	NA	NA	NA	NA	1	0	2.78	FP	1	1	0 1	TP 1.0	08 1	.01 TF	2 1.1	1.0)1 TF	1.1	1 0.9	9 TF	1.12	2 1.0	1 TI	P 1.1	1 1.0	1 TP) Ui	k the model.		N/
YOL064C	METO	3'(2')5'-bisphosphate nucleotidase	NA	NIA	NA	NA	NΙΛ	0.99	1	1.33	тр	1	1	0 1	TD 1 /	م ا م	.84 FF	1 1	ا ا) E	1 1	1 0 0	4 TC	1 11	0 0	, 1 TI	0 1 1	1 0 0	E TD	Λ,		pably accumulates phosphoadenylyl sulfate ich is toxic [Thomas90].	N/
		ATP sulfurylase				NA				0.96		1																			NA NA	ichis toxic [momasso].	N/
131(01000	WILTS	Vitamin B12-(cobalamin)- independent isozyme of methionine	INA	INA	IVA	INA	IVA		Ť	0.30	"		1 -0	1.00	1	00 1	.01 11		1.0	/	1.1	+	T"	1.12	0.3	3 11	T	1 0.3	70 11		100		14/
YER091C	MET6	synthase (also called N5- methyltetrahydrofolate homocysteine methyltransferase or 5-methyltetrahydropteroyl triglutamate homocysteine methyltransferase)	NA	NA	NA	NA	NA	0	0	3.2	TN	0	1	0 F	-N (0	1 FN	N 0	1	FN	1 0	1.0	1 FN	0	1	FI	N O	1	FN	I Ui	homocysteine biosynthesis. at least not in k off excess ho		o drain FN
																																ad end in the model, but it should be part o	
VOR241W	METZ	Folylpolyalutamata synthetase	NΛ	NA	1	7.1	ED	1	1	0.01	тр	1	1 (102 7	FD 11	00 0	74 50	0 11		72 55	11	1.05	0 55	1 1 1	2 0 4	0 51	D 11	1 0 5	:1 ED	D .	present in bo causes a peti f-Met-tRNA (metabolic conversions. Also the gene product cytoplam and mitochondia and its deleteitie phenotype as the production of mitoch (necessary for mitochondrial translation) is	tion ondrial
10K241W	IVIE I /	Folylpolyglutamate synthetase S-Methylmethionine Homocysteine	INA	IVA		7.1	FP	-	-	0.01	12	-	1 -0	.02 1	F 1.0	00 0	74 F	1.1	0.7	3 FF	1.1	1 0.5	o FF	1.12	2 0.4	o FI	1.1	1 0.5	I FP	D	n disrupted [De	coouzavoj.	N/
YLL062C	MHT1	methylTransferase	NA	NA	NA	NA	NA	1	1 -	0.02	TP	1	1 -0	.03 1	ΓP 1.0	08 1	.01 TF	1.1	1.0)2 TF	1.1	1 1.0	3 TF	1.12	2 1.0	2 TI	P 1.1	1 1.0	2 TP	N	NA NA	licated in blocking mitochondrial protein imp	N/
																																s mitochondrial function [MIPS]. Model has	
YJR077C	MIR1	Product of gene unknown	NA	NA	NA	NA	NA	0.96	1	0.24	TP	0.96	1 ().1	TP 1	05 0	.98 TF	0.9	1 0.9	2 TF	0.9	2 0.6	4 FF	0.94	1 0.6	1 F	0.9	3 0.6	6 FP	0		resport phosphate into mitochondria.	NA NA
		C1-tetrahydrofolate synthase			NA			1		0.02		1					.01 TF															, , , , , , , , , , , , , , , , , , , ,	N/
		Carbon-catabolite sensitive malate					NA	1		0.05		1					.01 TF														A NA		NA
		synthase High affinity S-methylmethionine			NA										ΓP 1.0																		
		permease			NA		NA	1		0.03		1					1 TF														NA Drotoin overth	thesis not required in the second	N/
		Aspartyl-tRNA synthetase Glutamine-tRNA ligase	NA NA		NA 1	NA 6.3	_	1		0.02		1																				thesis not required in the model thesis not required in the model	NA NA
1000000	WIGET	Phenylalanyl-tRNA synthetase	IVA	IVA	_	0.3		-	-	0.03	11	+	1 -0	.02 1	- 1.0	00 0	7 1 5		0.0	,, ,,	1.1	1 0.5	J FF	1.14	0.5	9 [7]	1.1	1 0.5	,5		i i rotolii syritii	noolo not required in the model	INF
YPR047W	MSF1	alpha subunit	NA	NA	1	3.7	FP	1	1	0.01	TP	1	1 -0	.01 7	TP 1.0	0 80	79 FF	1.1	0.6	69 FF	1.1	1 0.4	9 FF	1.12	0.4	5 FI	P 1.1	1 0.5	3 FP	0	h Protein synth	thesis not required in the model.	N/
YNL073W	MSK1	Lysine-tRNA ligase	NA	NA	1	4.9	FP	1	1	0	TP	1	1 -0	.01 1	TP 1.0	08 80	74 FF	1.1	0.	7 FF	1.1	1 0.5	1 FF	1.12	2 0.5	2 Fi	P 1.1	1 0.5	8 FP	0	h Protein synth	thesis not required in the model	N/

Phosphatidylinositol 4-phosphate 1 FP NA NA NA NA NA NA NA NA NA NA NA NA NA	required in the model d by this reaction leads to a dead end -trisphosphate = IP3). This metabolite or processes such as signaling. required in the model required in the model
YCR208W MS4 Rinase YDR208W MS5 Rinase YDR208	required in the model d by this reaction leads to a dead end -trisphosphate = IP3). This metabolite tr processes such as signaling. required in the model required in the model
VPRO98W MSS Almase	required in the model d by this reaction leads to a dead end -trisphosphate = IP3). This metabolite tr processes such as signaling. required in the model required in the model
Phosphalighi produce (10-my-lenois) 1,4, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,	d by this reaction leads to a dead end -trisphosphate = IP3). This metabolite or processes such as signaling. required in the model required in the model
VR288W MSVI Typophan-IRNA ligase Na Na Na Na Na Na Na Na Na Na Na Na Na	i-trisphosphate = IP3). This metabolite in processes such as signaling. required in the model required in the model
VEROSOW MSV1 Tyrosine-RNA ligase	required in the model
NAD-dependent 5.10- methylenetetralydrafolate NA NA NA NA NA NA NA NA NA NA NA NA NA N	
VRR080W MUD1 High affinity methionine permesse	
VERY REPORT NOT MUCH 1 September 1	
YERJOSW MUP1 High affinity methionine permease NA NA NA NA NA NA NA NA NA NA NA NA NA N	
\text{YHL036W} MUP3 permease	
Yelloge Murpa Nurpa Nu	
Choline phosphate cytidylyltransferase (also called phosphoethanolamine cytidylyltransferase or phosphoethanolamine cytidylyltransferase) YGR007W MUC1 Cytidylyltransferase) NA NA NA NA NA NA NA NA NA NA NA NA NA N	
Cyticylyltransferase (also called phosphoethanolamine cytidylyltransferase or phosphoethanolamine cytidylyltransferase or phosphoethanolamine cytidylyltransferase or phosphoethanolamine cytidylyltransferase or phosphoethanolamine cytidylyltransferase or phosphoethanolamine cytidylyltransferase or phosphoetholine Na Na Na Na Na Na Na Na Na Na Na Na Na	
YNR043W MVD1 decarboxylase	
YRA32C NAM2 Leucine-tRNA ligase NA NA 1 11.2 FP 1 1 1 0.01 TP 1 1 0.02 TP 1.08 0.69 FP 1.1 0.68 FP 1.1 0.51 FP 1.12 0.56 FP 0.th Protein synthesis not YDL040C NAT1 N-terminal acetyltransferase NA NA 1 3.8 FP 1 1 1 0.04 TP 1 1 0.02 TP 1.08 0.89 TP 1.1 0.87 TP 1.1 0.88 TP 1.12 0.8 TP 1.11 0.89 TP 0.th Protein synthesis not Only deemed to be either study [Steinmet YGR147C NAT2 Nalpha-acetyltransferase NA NA NA NA NA NA NA NA NA NA NA NA NA	
YDL040C NAT1 N-terminal acetyltransferase NA NA 1 3.8 FP 1 1 -0.04 TP 1 1 -0.02 TP 1.08 0.89 TP 1.1 0.87 TP 1.11 0.88 TP 1.12 0.8 TP 1.11 0.89 TP 0th Protein N-terminal accomply deemed to be a construction of the study [Steinment Study] (Steinment Study) (Steinmen	required in the model
YGR147C NAT2 Nalpha-acetyltransferase 1 FP NA NA NA NA NA NA NA NA NA NA NA NA NA	
YGR147C NAT2 N alpha-acetyltransferase 1 FP NA NA NA NA NA NA NA NA NA NA NA NA NA	
YDL085W NDE2 Hypothetical ORF NA	202] shows normal growth on all
YML120C NDI1 NADH dehydrogenase (ubiquinone) NA NA NA NA NA NA NA NA NA NA NA NA NA	
YML120C NDI1 NADH dehydrogenase (ubiquinone) NA	
YLR138W NHA1 Putative Na+/H+ antiporter NA NA NA NA NA NA NA NA NA NA NA NA NA	t glycerol or lactate in a ndi1 strain, but
YJL126W NIT2 Nit protein, nitrilase superfamily member NA <	wer than the wha type strain yield.
YLR328W NMA1 mononucleotide adenylyltransferase NA NA NA NA NA NA NA NA NA NA NA NA NA	
YLR351C NIT3 Nit protein, nitrilase superfamily member NA NA NA NA NA NA NA NA NA NA NA NA NA	
YLR351C NIT3 member	
YLR328W NMA1 Nicotinamide/nicotinic acid Mononucleotide adenylyltransferase NA NA NA NA NA NA NA NA NA NA NA NA NA	
Nicotina mida/nicotinic acid	
YGR010W NMA2 mononucleotide adenylyltransferase NA NA NA NA NA NA NA 1 1 1 0.38 TP 1 1 -0.03 TP 1.08 1.03 TP 1.1 1.01 TP 1.11 1.01 TP 1.12 1.03 TP 1.11 1.02 TP NA NA	
	by this reaction is a dead-end (N-
YLR195C NMT1 N-myristoyl transferase 1 FP Na Na Na Na Na Na Na Na Na Na Na Na Na	
	ed in cromatin silencing through
YOR209C NPT1 phosphoribosyltransferase NA NA 1 4.8 FP 1 1 0 TP 1 1 0.06 TP 1.08 0.89 TP 1.1 0.9 TP 1.11 0.97 TP 1.12 0.92 TP 1.11 0.95 TP Oth adjusting the NAD/N/	DH balance.
YGL067W NPY1 NADH pyrophosphatase 1 NA NA NA NA NA NA 1 1 1 0.04 TP 1 1 1-0.04 TP 1.08 1.01 TP 1.1 1.02 TP 1.11 1.01 TP 1.12 1.01 TP 1.12 1.01 TP 1.11 1.01 TP NA NA	
YDR001C NTH1 Neutral trehalase NA NA NA NA NA NA NA 1 1 1 0.02 TP 1 1 -0.04 TP 1.08 1.01 TP 1.11 1.01 TP 1.11 1.01 TP 1.12 1.04 TP 1.11 1.04 TP NA NA	
YBR001C NTH2 Neutral trehalase NA NA NA NA NA NA NA NA NA NA NA NA NA	
YKL120W OAC1 Oxaloacetate transport protein NA NA NA NA NA NA NA N	
acid synthase is to pr mitochondrial inner m	that the role of the mitochondrial fatty
Mitochondrial 2-oxodicarboxylate	ovide phospholipids for the embrane and that the disruption of uding OAR1) would lead into inability to e inner membrane (Schneider97).
YPL134C ODC1 transport protein NA NA NA NA NA NA NA NA NA NA NA 1 1 - 0.01 TP 1 1 0.05 TP 1.08 1.01 TP 1.1 1.01 TP 1.1 1.01 TP 1.12 1 TP 1.11 1.01 TP 1.12 1 TP 1.11 1.01 TP NA NA	embrane and that the disruption of uding OAR1) would lead into inability to
Mitochondrial 2-oxodicarboxylate	embrane and that the disruption of uding OAR1) would lead into inability to
YOR222W ODC2 transport protein NA NA NA NA NA NA NA N	embrane and that the disruption of uding OAR1) would lead into inability to e inner membrane [Schneider97].
YGL055W OLE1 Delta-9-fatty acid desaturase 0 TN NA NA NA NA NA NA NA NA NA NA NA NA NA	embrane and that the disruption of uding OAR1) would lead into inability to e inner membrane [Schneider97].

Name Ess sim Ess sim MMD call NPG a low YPD a low	YPL exp	YPL call	Explanation 4
YJR073C OPI3 Unsaturated phospholipid N- NA NA NA NA NA NA O 1 1.04 TN 0 1 0.16 FN 0 1.01 FN 0 0.97 FN 0 1.03 FN 0	1.03 F		The activities catalyzed by this gene are totally lost when it is disrupted, but mutants are viable. The cells accumulate mmPE and membrane is devoid of PC [MIPS]. Surpsingly, mutant were not strict choline auxotrophs (choline req'd for ar alternate route to produce PC). Reason why cells are viable is unknown; it has been speculated that a mutation in CHO2 may alter its substrate specificity (CHO2 catalyzes 1st of 3 steps in pathway from PE to PC, OPI3 primarily catalyzes 2nd and 3rd steps, can also catalyze 1st step but is very inefficient).
Mitochondrial integral membrane YOR130C ORT1 protein, ornithine transporter NA NA NA NA NA NA O 1 4.31 TN 1 1 -0.04 TP 1.08 1.01 TP 1.1 1.03 TP 1.11 1.02 TP 1.12 1.02 TP 1.12	1 1.02 T	TP NA	Weak false negative NA
YJR051W OSM1 Osmotic growth protein NA NA NA NA NA NA NA 1 1 1 0.27 TP 1 1 1 -0.03 TP 1.08 1.02 TP 1.1 1.03 TP 1.11 1.03 TP 1.12 1.04 TP 1.17	1 1.04 T	TP NA	NA NA
YDR538W PAD1 Phenylacrylic acid decarboxylase NA NA NA NA NA NA NA NA NA NA NA NA NA		TP NA	
Phosphoenolpyruvate		11 19/3	Lower oxygen uptake rate would correct this false negative
YKR097W PCK1 carboxylkinase NA NA NA NA NA NA NA NA NA NA NA NA NA	3 1.04 T	TP Med	d prediction. NA
	NA N	NA Bio	N-Acetylglucosamine synthesis is not required in the model. FP
Cholinephosphate Cytidylyltransferase phosphorylcholi NA NA NA NA NA NA NA NA NA NA NA NA NA	1 0.99 T	TP NA	
Pyruvate dehydrogenase alpha YER178W PDA1 subunit (E1 alpha) NA NA NA NA NA NA NA 1 1 0.35 TP 1 1 0.28 TP 1.08 1 TP 1.1 0.96 TP 1.11 0.78 FP 1.12 0.79 TP 1.11	1 0.9 T	TP Unl	Pyruvate dehydrogenase (coded by PDA1 & PDB1) is not used by the model when grown on glycerol.
Pyruvate dehydrogenase beta YBR221C PDB1 subunit (E1 beta) NA NA NA NA NA NA NA 1 1 0.09 TP 1 1 0 0.71 1.08 0.93 TP 1.1 0.91 TP 1.11 0.66 FP 1.12 0.71 FP 1.11			Pyruvate dehydrogenase (coded by PDA1 & PDB1) is not
15/12/20 1551 declarate 1 50:00 11 11 0 0 11 11 11 0 0 11 11 12 0 11 11 11 0 0 11 11 12 0 11 11 11	1 0.0 1	11 0111	There are three alternate isozymes in the model , but PDC1 deletion alone is sufficient to reduce PDC activity significantly
YLR044C PDC1 Pyruvate decarboxylase NA NA 1 3.8 FP 1 1 -0.03 TP 1 1 -0.03 TP 1.08 1 TP 1.1 1 TP 1.1 1 TP 1.11 1 TP 1.12 0.97 TP 1.12	1 0.99 T	TP Iso	enough to result in a slow growth phenotype. NA
YLR134W PDC5 Pyruvate decarboxylase NA NA NA NA NA NA NA NA 1 1 0.04 TP 1 1 0 TP 1.08 1 TP 1.1 1 TP 1.11 1 TP 1.12 1 TP 1.12 1 TP 1.15			
YGR087C PDC6 Pyruvate decarboxylase isozyme	1 1.02 T	TP NA	NA NA
YGL248W PDE1 phosphodiesterase, low affinity NA NA NA NA NA NA NA 1 1 2.85 TP 1 1 2.85 TP 1.08 0.99 TP 1.1 0.99 TP 1.11 0.99 TP 1.11 0.98 TP 1.12 0.97 TP 1.12	1 0.98 T	TP NA	NA NA
YOR360C PDE2 phosphodiesterase	1 0.99 T	TP NA	NA NA
YBR035C PDX3 phosphate oxidase NA NA NA NA NA NA 1 1 1 0.71 TP 1 1 1 -0.05 TP 1.08 0.86 FP 1.1 0.85 FP 1.11 0.74 FP 1.12 0.55 FP 1.11	1 0.61 F	FP Der	
YBL030C PET9 ADP/ATP translocator 1 FP NA NA NA NA NA NA NA NA NA NA NA NA NA	1 1.03 T	TP Dis	Only deemed to be essential in one study [Giaever02]. The other study [Steinmetz02] shows normal growth on all substrates.
YGR240C PFK1 Phosphofructokinase alpha subunit NA NA 0.19 4.8 TN 0.18 1 -0.01 TN 0.19 1 0 TN 0.2 0.89 FN 1.06 0.95 TP 1.1 1.05 TP 1.12 1.08 TP 1.17	1 1.05 T	TP Dis	
YMR205C PFK2 Phosphofructokinase beta subunit NA NA 0.19 16.7 TN 0.18 1 -0.01 TN 0.19 1 -0.03 TN 0.2 0.7 TN 1.06 0.76 FP 1.1 0.95 TP 1.12 1.01 TP 1.11	1 0.97 T	TP Med	In YPDGE media the max glc uptake in the simulation is too do low to cause pfk2 to have a growth defect.
YIL107C PFK26 6-phosphofructose-2-kinase NA NA NA NA NA NA NA NA NA NA NA NA NA			
YOL136C PFK27 6-phosphofructo-2-kinase		TP NA	
YCR012W PGK1 3-phosphoglycerate kinase 0.1 TN NA NA NA NA NA NA NA NA NA NA NA NA NA		NA NA	
Phosphoglucomutase minor YKL127W PGM1 isoform NA NA NA NA NA NA NA NA NA NA NA NA NA	1 1.04 T	TP NA	NA NA
			Pgm2p is major isomform of phosphoglucomutase. Maybe the minor isoform (Pgm1p) can't fully compensate for loss of
YMR105C PGM2 Phosphoglucomutase	1 1 T	TP Iso	
YCL004W PGS1 synthase 1 FP NA NA NA NA NA NA NA NA NA NA NA NA NA			Should not be absolutely essential [SGD]. Disrupts mitochondrial function somewhat.
YNL316C PHA2 Prephenate dehydratase NA NA NA NA NA NA NA NA NA NA NA NA NA			
YDR481C PHO8 Repressible alkaline phosphatase NA NA NA NA NA NA NA 1 1 0.19 TP 1 1 0 TP 1.08 1.03 TP 1.1 1.01 TP 1.11 1.01 TP 1.12 1.02 TP 1.12			
YML123C PHO84 Inorganic phosphate transporter NA NA NA NA NA 1 1 1 -0.03 TP 1 1 1 -0.02 TP 1.08 0.96 TP 1.1 0.83 FP 1.11 0.85 TP 1.12 0.82 TP 1.12			There are multiple alternative isozymes for the phosphate transporters, but Pho84p may be the dominant one under some conditions.
YCR037C PHO87 Phosphate permease NA NA NA NA NA NA NA 1 1 1 0.02 TP 1 1 0 TP 1.08 1 TP 1.1 1 TP 1.11 1.01 TP 1.12 1 TP 1.12 1 TP 1.15	1 1.01 T	TP NA	NA NA
YBR296C PHO8 Na+/Pi symporter (putative) NA NA NA NA NA NA NA NA NA NA NA NA NA			
YJL198W PHO9(Low-affinity phosphate transporter NA NA NA NA NA NA NA NA NA NA NA NA NA			

																			-	۵ =											<u> </u>
	0		sim	=	sim	exp	call	Sign	dxə	ave	call	l sim	PGal exp	/PGal ave	8	<u>ڇ</u>	d z	PDGFsim		PDGE exp	E	d X	la:	<u>۽</u>	Q.	call	<u>.</u> <u>E</u>	dxə	call		ster et
ORF	lame	Annotation	SS S	ss call	Nol	Nol	NO.	MMD sim	IMD exp	имр аve	IMD call	PGal sim	PGa	PGa	PGa	'PD sim	PD exp		3		/PG sim	PG exp	PG call	/PE sim	/PE exp	PE	/PL sim	PLe	/PL c	Class	Explanation Explanation
		Amotation	Ш	Ш	S	S	S	2	2		2	<u> </u>	_	> ;	_	>	> >	>		> >		· >		<u> </u>	<u> </u>		<u> </u>	-	>	0	Phospholipid produced by this reaction leads to a dead-end
VAII 007\A	DUZA	Dheanhatidulinaaital 4 kinaaa	١.															١,,												D	(1D-myo-Inositol 1,4,5-trisphosphate). Also Stt4p is an
	PIK1 PIS1	Phosphatidylinositol 4-kinase Phosphatidylinositol synthase	0	TN	NA NA			NA NA	_	NA NA		NA I		NA N	1 Al			A N		NA N		A NA		NA NA			NA			NA	isozyme. FP
		Phosphoinositide-specific																													
YPL268W	PLC1	phospholipase C	NA	NA	1	14.8	3 FP	1	1	-0.02	TP	1	1 -(0.01 7	TP 1	.08 0).72 F	P 1.	.1 (0.7 FI	1.1	11 0.88	B TP	1.12	2 0.8	1 TP	1.11	0.89	TP	Oth	Also involved in kinetochore function. NA This is the major isoform of the cytosolic ATPase, but in the
																															model a minor isoform can compensate for the function.
		Diameter ATD																													Deletion of the minor isoform (which contains Pma2p instead
YGL008C YPL036W		Plasma membrane H+-ATPase Plasma membrane ATPase	NA		NA NA			NA 1		-0.04		NA I	NA I 1 -(NA N 0.01 T	NA N	.08 1	NA N	A N P 1.	A N	.03 TI	1.1	A NA	NA 3 TP	1.12	NA 2 1.0	NA 3 TP	1.11	1.03	TP	ISO NA	of Pma1p) is not lethal experimentally. FP NA NA
YER003C		Mannose-6-phosphate isomerase	0		NA		NΑ			NA		NA I		NA N			NA N			NA N				NA			NA			NA	NA NA
VCD024CA	DMD4	Proteolipid associated with plasma	NIA.	NI A	NIA	NIA	N 1 A	0.05		0.04	TD	0.00	4	04	NI O			D 4	00.4	00 T	1.0	7 4 0	_ TD	4.00		4	4.04	_	1	Mad	If oxygen uptake rate on YPGal is increased the pmp1 growth rate increases to that of the wild type. NA
YCR024CA	PIMPT	membrane H(+)-ATPase (Pma1p) Proteolipid associated with plasma	NA	NA	NA	. NA	IN/	0.85	1	0.04	IP	0.23	1 0	1.01 F	N U	1.99	1.03 1	P 1.0	03 1	.03 11	1.0	1.02	2 112	1.03	3 1	IP	1.04	1	IP	Med	rate increases to that of the wild type. NA If oxygen uptake rate on YPGal is increased the pmp2 growth
YEL017CA	PMP2	membrane H(+)-ATPase (Pma1p)	NA	NA	NA	NA	NΑ	0.85	1	0.33	TP	0.23	1	0 F	N 0	.99 1	1.02 T	P 1.0	03 1	.03 TI	1.0	7 1.0	з ТР	1.03	3 1.0	4 TP	1.04	1.03	TP	Med	
		Dolichyl phosphate-D- mannose:protein O-D-																													
YDL095W	PMT1	•	NA	NA	NA	. NA	NΑ	1	1	-0.02	TP	1	1 -0	0.04	TP 1	.08).99 T	P 1.	.1 1	.02 TI	1.1	11 0.98	в ТР	1.12	2 1.04	4 TP	1.11	1.03	TP	NA	NA NA
		Dolichyl phosphate-D-																													
YAL023C	PMT2	mannose:protein O-D- mannosyltransferase	NΔ	NA	. 1	63	FP	1	1	-0.01	тр	1	1 -0	ו מים	гр	08 0	04 T	D 1	1 0	ω/ TI	1 1	11 0 0	и тр	1 12	0 0	e TE	1 11	0.06	тр	Oth	Mannosyntransferase activity not required in the model. NA
TALOZOO	1 10112	Dolichyl phosphate-D-	IVA	INA	<u> </u>	0.5	+	<u> </u>	H	-0.01	"	_	1 -0	7.02	<u> </u>	.00 0	7.54 1		.1 0	.54 11	1	0.3	· · ·	1.12	0.3	0 11	1.11	0.30	1	Otti	manifolymanistrates activity not required in the model.
		mannose:protein O-D-																													l
YOR321W	PMT3	mannosyltransferase Dolichyl phosphate-D-	NA	NA	NA	. NA	NA	1	1	-0.05	TP	1	1 -(0.05 1	TP 1	.08 1	1.01 T	P 1.	.1 1	.02 TI	1.1	1.02	2 TP	1.12	2 1.0	2 TP	1.11	1.03	TP	NA	NA NA
		mannose:protein O-D-																													
YDL093W	PMT5	mannosyltransferase	NA	NA	NA	. NA	NA	1	1	-0.06	TP	1	1 -(0.06	TP 1	.08 1	1.02 T	P 1.	.1 1	.04 TI	1.1	11 1.04	4 TP	1.12	2 1.0	6 TP	1.11	1.03	TP	NA	NA NA
		Dolichyl phosphate-D- mannose:protein O-D-																													
		mannosyltransferase				. NA			1			1										11 0.99									NA NA
YGL037C YLR209C		Nicotinamidase pyrazinamidase Purine nucleoside phosphorylase			NA NA				1	0.01	TP TP	1		0.05 1	TP 1					.06 TI		11 1.0								NA NA	
TENZUSC	FINE	Turrie riudieoside priosprioryiase	INA	INA	INA	INA	INA		Ė	- 0	IF	_	1 0	.04	IFI	.00	- 1	F 1.	.1 1	.02 11	1.0	JS 1	IF	1.1	1.0.	2 115	1.07	1.01	IF	INA	Does not grow well under aerobic conditions, because Pos5p
																															is the primary source of NADPH in mitochondria [Outten03].
YPL188W	POS5	Involved in oxidative stress	NA	NA	1	8.3	FP	1	1	0.01	TP	1	1 -0	0 02 1	rel 1	08	07 F	P 1	1 0	82 FI	1 1	11 0.58	R FP	1 12	0.5	4 FP	1 11	0.6	FP	Mod	May need to change the model so that only Pos5p can provide NADPH in mitochondria.
YIL160C	POT1	3-oxoacyl CoA thiolase	NA	NA	NA	. NA	NΑ	1	1	0.69	TP	1	1 -0	0.03	ΓP 1	.08 1	1.02 T	P 1.	.1	1 TI	1.1	11 1.0	1 TP	1.12	0.9	5 TP	1.11	0.98	TP	NA	NA NA
YGL205W	POX1	Fatty-acyl coenzyme A oxidase Proteolipid vacuolar ATPase V0	NA	NA	NA	. NA	NA	1	1	0.05	TP	1	1 -(0.01	TP 1	.08 1	1.01 T	P 1.	.1	1 TI	1.1	11 0.9	7 TP	1.12	2 1	TP	1.11	0.99	TP	NA	NA NA
YHR026W	PPA1	domain subunit c"	NA	NA	1	5.6	FP	1	1	0.03	TP	1	1 0	.01 7	TP 1	.08	0.8 F	P 1.	.1 0	.65 FI	1.1	11 0.6	1 FP	1.12	0.6	FP	1.11	0.68	FP	Oth	See other vacuolar ATPase components. NA
																															PPA2 deletion strain has lost mitochondrial DNA apparently because pyrophosphate produced during replication cannot
																															be converted into phosphate [Lundin91]. The model does not
\/MD007\\/	DD 4.0	Ingrania nyranhaanhataa								0.04	TD					00 0					١.,			4.40				0.54		N 4 = =	run any of the reactions producing ppi[m] in the ppa2 and
YMR267W	PPA2	Inorganic pyrophosphatase Phosphopantetheine:protein	NA	NA	. 1	3.4	FP	1	1	-0.04	IP	1	1 -().02 1	IP 1	.08 ().74 F	P 1.	.1 0	.67 FI	1.1	11 0.54	4 FP	1.12	2 0.4	9 FP	1.11	0.54	FP	IVIOG	utilizes the cytoplasmic forms of the reactions instead. NA
YPL148C	PPT2	transferase (PPTase)	NA	NA	1	7	FP	1	1	0.04	TP	1	1 -0	0.03	TP 1	.08).64 F	P 1.	.1 0	.65 FI	1.1	11 0.52	2 FP	1.12	0.5	3 FP	1.11	0.51	FP	Oth	CoA biosynthesis not required in the model.
																															Should be a proline auxotroph, but should grow fine on rich
YDR300C	PRO1	Gamma-glutamyl kinase	NA	NA	1	12.6	S FP	1	1	-0.01	TP	1	1	0 1	TP 1	.08).64 F	P 1.	.1 0	.69 FI	1.1	11 0.9	5 TP	1.12	0.9	7 TP	1.11	1.06	TP	Unk	ornithine as an intermediate.
\(\(\text{O}\) = 0.000		Gamma-glutamyl phosphate																													Should be a proline auxotroph. Model synthesizes proline
YOR323C	PRO2	reductase	NA	NA	NA	. NA	NA	1	0	5.16	FP	1	1 -(0.03	TP 1	.08	1 T	P 1.	.1	1 TI	1.1	11 1.02	2 TP	1.12	2 1.0	2 TP	1.11	1.01	TP	Unk	from glutamate using ornithine as an intermediate. NA Only deemed to be essential in one study [Giaever02]. The
		Delta 1-pyrroline-5-carboxylate																													other study [Steinmetz02] shows normal growth on all
YER023W	PRO3	reductase	1	FP	NA	. NA	NΑ	NA	NA	NA	NA	NA I	NA I	NA N	NA 1	.08 1	1.06 T	P 1.	.1 1	.05 TI	1.0	1.04	4 TP	1.11	1.1	1 TP	1.05	1.06	TP	Dis	substrates. FP
		Ribose-phosphate																													Prs3p has an unknown role in controlling cell growth. Its deletion causes a wide variety of phenotypes including small
YHL011C	PRS3	pyrophosphokinase	NA	NA	1	7.6	FP	1	1	-0.02	TP	1	1	0 1	TP 1	.08	0.66 F	P 1.	.1 0	.73 FI	1.1	1 1	TP	1.12	0.9	1 TP	1.11	0.92	TP	Oth	cell size.
YBL068W	DRS4	Ribose-phosphate pyrophosphokinase	NIA	NIA	NA	. NA	NA	1	4	-0.03	тр	1	1	0 1	TD 4	08 4	1 01 -	D 1	1 1	03 7	1 1	11 1.03	3 TD	1.10	1 0	5 TD	1 11	1.04	ТБ	NIA	NA NA
IDLUGGW	1 134	Phosphoribosylpyrophosphate	INA	INA	INA	INA	INA		H	-0.03	16	-	+	J		.00 1	1.01 1	1.	1 1	.00 11	1.1	1.0	J 1P	1.12	1.0	JIP	1.11	1.04	12	INA	INA INA
VOI 65 !!!	DD Or	synthetase (ribose-phosphate								0.5-																					NIA
YOL061W	PRS5	pyrophosphokinase)	NA	NA	NA	. NA	NΑ	1	1	0.05	TP	1	1 -(0.02	P 1	.08).99 T	입 1.	.1 1	.01 TI	1.1	11 1.03	3 TP	1.12	2 1.0	3 TP	1.11	1.02	ΤP	NA	NA NA

The control of the																															
Column C				_		Ε	9	=	Ε	9	e e	=	mis ax	ave .	=	ے	۵	_	sim	exp	3 2	_ <u>_</u>	_	u	۵	l_I	اء	_ ا	.		
Column C	ш	ae L		sin	cal	.s	e ×	W C2	D Si	De	D a	٥	Sal s	3al 8	3al c	Sir	ex	Ca	g	9 9	1 1	S S	3 ca	sir	ex	ca	is.	e E	5	SS	ste
Proceedings Process	OR	Na		Ess	Ess	Slo	Slo	Slo	Σ	Σ	Σ	Σ	Y P(ΥP	ΥP(ΥPI	ΥPI	ΥPI	ΥPI	YPI	- A	Y P	ΥP(УP	ΥP	ΥPI	Y P	7 PI	;	S C	Explanation [한
Part Description plant pla																															
Part Part	YDI 055C	PSA1		0	TNI	NΔ	NΑ	NΔ	NΔ	NΔ	NΑ	NΔ	NA NA	NA	NΔ	NΔ	NΔ	NΔ	NΔ	NA N	ΔN	ΔΝΔ	NΔ	NΑ	NΔ	NA N	JA I	NA N	٨٨	NA	NA NA
PROCESSON PROC					_		_	_	1			_	1 1																		
Fig. 12 Fig. 13 Fig. 14 Fig.				_	_		_	_	1	_		TP	1 1		_	1.08	1.03	TP	1.1	1.02 T	P 1.	11 1.01	_	_			.11 1	.01 T	_		NA NA
Fig. Fig. Procedure designation St. St				_	_			_	1	1		TP	1 1	_	_					1 T	_	_	_	_			.11 1	.03 T	_	_	NA NA
PRINCIPLY PRIN									1	1		_	1 1																		NA NA
Fig. Public provides Pub							_	_	1	_		TP	1 1	_	_		_		_		_						.11 1	.02 T			NA NA
Miles Mile	YLR142W	PUT1		NA	NA	NA	NA	NA	1	1 -	-0.05	TP	1 1	-0.0	4 TP	1.08	1.01	TP 1	1.09	1 T	P 0.9	91 1	TP	1.1	1	TP 0	.99 1	.01 T	PΝ	NA	NA NA
Vicinity Vicinity	VHD027W	DUITO		NIA.	NIA.	NIA.	NIA.	NI A	4	,	0.00	TD				4.00	4.04	TD		4 00 T	D 4	44 4 04	TD	4 40	0.07	TD 4	44	04		NIA	NA NA
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VEX. Psychological and provided and prov								NA	1	_		_	1 1	_														.05 T			
YREZES CR. Private intrinsprises N. N. W. M. M. W. M								_	1	_		TP	1 1																		
VPR327C PVR2 glotters				_	_		_	_	1	_		TP	1 1	_	_		_	_													
Ubiquind cytochrome c ubiquind cytochrome c ubiquind cytochrome c complex 8.5 kDa NA	15112100			10,		10.0	1.0.		·	Ť	0.10	Ï		0	+ -	1100					Ϋ́		Ė					.0.	Ť	*	
Part Part	YOR347C	PYK2	isoform	NA	NA	NA	NA	NA	1	1 -	-0.04	TP	1 1	-0.0	6 TP	1.08	1.01	TP	1.1	1.03 T	P 1.	11 1.04	TP	1.12	1.04	TP 1	.11 1	.02 T	PΝ	NA	
Ubiquinol-cytochrome C oxidereductase complex & S. Na. Na. Na. Na. Na. Na. Na. Na. Na. Na																															Deletion of QCR10 does not impair growth on non-
Ubiquario-lypochrome c doubleway we have modeled the complex. This subunit should be made a non-assertal part of the MA NA																															
94R091WA QCR1 (aubumit			Ubiqunol-cytochrome c																												
40 kDa ubiquinol cytochrome-c YPR191W QCR2 reductase core protein 2 NA NA 09 44 TN 080 1 -0.01 TP 082 1 -0.05 TP 080 102 TP 0.24 0.87 FN 0.14 0.49 TN 0.08 0.39 TN 0.17 0.5 TN Med consider increasing maximum glu uptake in YPQE medium. NA Ubiquinol cytochrome C Ubiquinol cyto																															
9R191W QCR2 reductase core protein 2	YHR001WA	QCR1	subunit	NA	NA	NA	NA	NA	0.89	1 -	-0.03	TP ().82 1	0	TP	0.98	1.01	TP (0.24	1.02 F	N 0.	14 1.02	FN.	0.08	1.01	FN 0	.17 1	.03 FI	N I	SO	complex since it only plays structural role. NA
9R191W QCR2 eductase core protein 2																															This is probably due to excessive respiration under the
Deletion of QCR8 does not have significant effect on the formation or stability of cytochrome C Ubiquinol cytochrome C GUBiquinol Cytochrome C GuBiqui			40 kDa ubiquinol cytochrome-c																												
Ubiquind cytochrome C Ubiq	YPR191W	QCR2	reductase core protein 2	NA	NA	0.9	4.4	TN	0.89	1 -	-0.01	TP ().82 1	-0.0	5 TP	0.98	0.92	TP (0.24	0.87 F	N 0.	14 0.49	TN	0.08	0.39	TN 0	.17	0.6 TI	N N	/led	consider increasing maximum glc uptake in YPDGE medium. NA
Ubiquind cytochrome C Ubiq																															Deleties of OCDC deep and house simplificant offers as the
Ubiquinol cytochrome C CR7 Code of addreductases subunit 6 (17 kBa) NA NA NA NA NA NA NA NA NA NA NA NA NA																															
YER032C CCR6 oxdooreductase subunit 6 (17 kDa) Na Na Na Na Na Na Na			Ubiquinol cytochrome C																												
YR1539C QCR7 oxidoreductase subunit 7 (14 kDa)	YFR033C	QCR6	oxidoreductase subunit 6 (17 kDa)	NA	NA	NA	NA	NA	0.89	1 -	-0.02	TP ().82 1	0.1	TP	0.98	1.02	TP (0.24	0.98 F	N 0.	14 0.87	FN.	0.08	0.82	FN 0	.17 0	.92 FI	N I		indicated by the gene-protein-reaction associations currently. NA
Ubiquinol cytochrome C reductase YJL166W OCR8 subunit 8	VDDEGGG	0007		١	l																										
Value Valu	YDR529C	QCR7	oxidoreductase subunit 7 (14 kDa)	NA	NA	0.9	5.3	IN	0.89	1 .	-0.02	IP ().82 1	-0.0	2 12	0.98	0.67	FP (J.24	0.65 1	N 0.	14 0.53	IIN	0.08	0.51	IN 0	.17 0	1.59 11	N C	Jtn	primarily termentative conditions.
Value Valu																															This is probably due to excessive respiration under the
Ublquinol cytochrome c oxidoreductase complex 7.3 kDa subunit 9																															simulation conditions - glucose vs oxygen limitation, may
VRR183C QCR9 subunit 9 NA NA NA NA NA NA NA NA NA NA NA NA NA	YJL166W	QCR8		NA	NA	0.9	6.3	TN	0.89	1	0.05	TP ().82 1	0.1	5 TP	0.98	0.93	TP (0.24	0.86 F	N 0.	14 0.6	TN	0.08	0.52	TN 0	.17 0	.54 TI	N N	/led	consider increasing maximum glc uptake in YPDGE medium. NA
YER183C QCR9 subunit 9 NA NA NA NA NA NA NA NA NA NA NA NA NA N																															
FP FP FP FP FP FP FP FP	YGR183C	QCR9	-	NA	NA	NA	NA	NA	0.89	1	0.13	TP ().82 1	0.2	1 TP	0.98	0.96	TP (0.24	0.85 T	N 0.	14 0.6	TN	0.08	0.58	TN 0	.17 0	.63 TI	N N	NA	NA NA
UDP-N-acetylglucosamine			Glutamine-dependent NAD																												
\(\) \\ \(\) \\ \(\) \\ \(\) \\ \(\) \\ \(\) \\ \(\) \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\	YHR074W	QNS1		1	FP	NA	NA	NA	NA	NA	NA	NA	NA N	NA	NA.	NA	NA	NA	NA	NA N	A N	A NA	NA	NA	NA	1 AN	NA I	NA N	A E	3io	
\(\begin{array}{c c c c c c c c c c c c c c c c c c c	YDI 103C	ORI1	, ,	1	FP	NΔ	NΑ	NΔ	NΔ	NΔ	NΑ	NΔ	NA NA	NA	NΔ	NΔ	NΔ	NΔ	NΔ	NA N	ΔN	ΔΝΔ	NΔ	NΑ	NΔ	NA N	JA I	NA N	ΔLF	Rio	
CAAX farnesyltransferase alpha YKL019W RAM2 Subunit 1 FP NA NA NA NA NA NA NA N				NA		1	7		_				1 1																		
YCR036W RBK1 Ribokinase NA			CAAX farnesyltransferase alpha																												·
YBR002C RER2 Cis-prenyltransferase 1 FP NA NA <t< td=""><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td>Quinone biosynthesis is not required in the model. NA</td></t<>																															Quinone biosynthesis is not required in the model. NA
YIL053W RHR2 DL-glycerol-3-phosphatase NA																															NA NA Outpone biosynthesis is not required in the model ED
YBL033C RIB1 GTP cyclohydrolase II NA NA 1 10.3 FP 1 1 -0.04 TP 1 1 -0.01 TP 1.1 0.67 FP 1.11 0.67 FP 1.11 0.67 FP Bio FAD biosynthesis not required in the model NA YOL143C RIB4 synthase (DMRL synthase) NA NA 1 4.5 FP 1 1 -0.01 TP NA								_																							NA NA
YOL143C RIB4 synthase) NA NA 1 4.5 FP 1 1 -0.01 TP NA NA NA NA NA NA NA NA NA NA NA NA NA																															
YBR256C RIB5 Riboflavin biosynthesis 1 FP NA NA NA NA NA NA NA NA NA NA NA NA NA		515																													
Protein involved in the biosynthesis of riboflavin, second step in the riboflavin biosynthesis pathway YBR153W RIB7 riboflavin biosynthesis pathway 1 FP NA NA NA NA NA NA NA NA NA NA NA NA NA													1 1	-0.0	1 TP	NA	NA NA	NA	NA	NA N	A N	A NA	NA	NA	NA	NA I	I AV	NA N	A E	310 3ic	
YBR153W RIB7 riboflavin biosynthesis pathway 1 FP NA NA NA NA NA NA NA NA NA NA NA NA NA	1 BKZ30C	KIDS	Tribonaviii biosyntilesis	_	FP	INA	INA	INA	INA	INA	AVI	INA	INA IN	1 INA	INA	INA	NA	INA	INA	INA IN	A N	AINA	INA	INA	INA	IVA I	vA I	VA IV.	^ E	טוכ	Tribonaviii biosynthesis is not required in the model
YBR153W RIB7 riboflavin biosynthesis pathway 1 FP NA NA NA NA NA NA NA NA NA NA NA NA NA			Protein involved in the biosynthesis																												
Rieske iron-sulfur protein of the mitochondrial cytochrome bc1																															
mitochondrial cytochrome bc1	YBR153W	RIB7		1	FP	NA	NA	NA	NA	NA	NA	NA	NA N	NA	NA	NA	NA	NA	NA	NA N	A N	A NA	NA	NA	NA	NA I	NA I	NA N	A E	3io	Riboflavin biosynthesis is not required in the model. NA
YEL024W RIP1 complex NA NA NA NA NA NA NA NA NA NA NA NA NA			·																												
	YEL024W	RIP1		NA	NA	NA	NA	NA	0.89	1	0.36	TP (0.82 1	0.46	6 TP	0.98	0.9	TP (0.24	0.82 T	N 0.	14 0.54	TN	0.08	0.42	TN 0	.17 0	.55 TI	N N	NA	NA NA

75	ıme		s sim	Ess call	Slow sim	Slow exp	ow call	MMD sim	имр ехр	MMD ave	MMD call	/PGal sim	Gal exp	YPGal ave	'PGal call	YPD sim	YPD exp	/PD call	YPDGE sim	YPDGE exp	DGE Call	/PG sim	YPG exp	/PG call	TPE SIM	Tre exp	L sim		L call	Class		rster et al
ORF	Na	Annotation Ribose-5-phosphate ketol-	Es	Es	Sic	SIC	Š	ź	٤	ź	ź	<u>}</u>	۲.	Ϋ́	∠	Ϋ́	7	Ă.	7	<u>}</u> }	-	}	7	<u>}</u>	- 5	- >	<u> </u>	YPL	YPL	Ö	Explanation	<u>6</u>
YOR095C	RKI1	isomerase	0.81	TN	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA I	NA	NA	NA N	A A	NA	NA I	NA N	IA N	A N	A NA	NA	NA	NA	In silico slow growth.	NA
VED070W	DND4	Ribonucleotide reductase, large				00.0		,		0.04	TD			0.04																Oth	DNIA sundhasia and an united in the madel	NIA
YER070W	KNK1	(R1) subunit Ribonucleotide reductase	NA	NA	1	22.3	FP	1	1	-0.04	IP	1	1	-0.04	IP	NA	NA I	VA	NA	NA N	IA I	NA	NA I	NA N	IA N	A N	A NA	NA	NA	Oth	DNA synthesis not required in the model.	NA
		subunit ribonucleotide reductase,																														
YJL026W	RNR2	small (R2) subunit Ribonucleotide reductase, large	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA I	NA	NA	NA N	1 Al	NA	NA I	NA N	IA N	A N	A NA	NA	NA	Oth	DNA synthesis not required in the model.	NA
YIL066C	RNR3	(R1) subunit	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1	-0.05	TP	1.08	1	TP	1.1	1.02 T	P 1	.11 1	.03	TP 1.	12 1.	03 T	P 1.11	1.03	ТР	NA	NA	NA
VOD4000	DND 4	Ribonucleotide reductase, small																												0:1	DNA - d - i - i - i - i - i - i - i - i - i	
YGR180C		(R2) subunit D-ribulose-5-Phosphate 3-	NA	NA	1	8.5	FP	1	1	-0.03	IP	1	1	-0.02	IP '	1.08	0.81	FP	1.1	0.69 F	P 1	.11 ().59	-P 1.	12 0.	62 F	1.11	0.6	FP	Oth	DNA synthesis not required in the model. The PPP is only used at a low level on glycerol. The effect of	NA
YJL121C		epimerase .	NA	NA	NA	NA	NA	0.97	1	0.67	TP	1	1	0.22	TP	1.08	0.92	TP	1.1	0.84 F	P 1	.06).78	FP 1.	11 0.	78 T	P 1.08	0.92	TP	Unk		NA
YER043C	C \ L 1	S-adenosyl-L-homocysteine	0	TNI	NIA	NIA	NIA	NIA	NIA	NIA	NIA	NΙΛ	NIA	NIA	NIA	NIA	NA.	NIA.	NIA	NIA NI	١,	NIA	NIA	JA N		ı A	A NIA	NIA	NIA	NΙΛ	NA.	NA
		hydrolase (putative) S-adenosylmethionine synthetase		_	NA	_		NA 1		-0.02							0.98			NA N 0.96 T												NA
		Methionine biosynthesis regulation			NA					-0.03										1.02 T												NA
YPL274W	SVM3	High affinity S-adenosylmethionine permease	NΙΔ	ΝΔ	ΝΔ	NA	NΔ	1	1	0	TP	1	1	0	тр	1 08	1 02	тр	1 1	1.05 T	D 1	11 1	05	TD 1	12 1	07 T	D 1 11	1 06	ТР	ΝΔ	NA	NA
11 LZ/400	SAIVIS	AdoMet-homocysteine	INA	INA	INA	INA	INA	-	-+	0	1F		-	U	IF	1.00	1.02	IF	1.1	1.03 1	F		.03	IF 1.	12 1.	07 1	1.11	1.00) IF	INA	INA	INA
		methyltransferase	NA	_	_	_	_	1	1	0	TP	1	1				1.01		1.1	1.04 T			.05	ΓP 1.		05 T				NA		NA
YMR272C		Desaturase hydroxylase Succinate dehydrogenase	NA	NA	NA	NA	NA	1	1	2.17	TP	1	1	0	TP	1.08	0.99	ĪΡ	1.1	1.01 T	P 1	.11 1	.01	ΓP 1.	12 0.	99 T	P 1.11	0.98	TP	NA	Sdh1p is not considered to be an essential part of the	NA
YKL148C		flavoprotein subunit	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1	0.06	TP	1.08	1	TP	1.1	0.97 T	P 1	.11 (0.69	FP 1.	12 0.	79 T	P 1.11	0.61	FP	Iso	succinate dehydrogenase complex.	NA
		Succinate dehydrogenase																													With a lower locate untake rate the model shows alow	
YLL041C	SDH2	(ubiquinone) iron-sulfur protein subunit	NA	NA	NA	NA	NA	1	1	0.01	TP	1	1	0.07	тР	1.08	0.97	TP 1	1.01	0.97 T	P (0.8	0.67	ΓN 0.	58 0.	75 T	0.93	0.59	FP	Med	With a lower lactate uptake rate the model shows slow growth on lactate.	NA
									Ť												Ť										The model has an isozyme that includes an alternate subunit	
VIZI 4.44\A/		Succinate dehydrogenase cytochrome b	,	ED	NIA	NIA	NIA	NIA		NI A	NIA	NIA	NI A	NIA	NIA	NIA	NIA .		NI A	NIA NI		NIA		JA N				NIA	NIA.	Link	with high imilarity to Sdh3p, but even if this is removed the	NA
YKL141W	SDH3	Succinate dehydrogenase	-	FF	INA	INA	INA	INA	INA	INA	INA	INA	INA	INA	INA	INA	INA	VA	INA	INA IN	A	NA	INA I	NA IV	IA IN	A IN	A INA	INA	INA	UIIK	mutation is non-lethal. Sdh4p is not considered to be an essential part of the	INA
		membrane anchor subunit				NA				-0.07		1					1.02						_	_							succinate dehydrogenase complex.	NA
YIL168W YFL045C	_	NA Phosphomannomutase	_	NA TN	NA NA			1 NA	_	-0.03 NA		1 NA			TP NA		1.02 NA I			1.03 T NA N			_	TP 1.			P 1.11 A NA			NA NA	NA NA	NA NA
11 20450	OLOGO	Membrane protein required for core		111	INA	INA	IVA	INA	IVA	IVA	INA	INA	INA	IVA	IVA	INA	INA	VA.	INA	INA IN	Α Ι	VA.	IVA II	NA IN	1A IN	A	IVA	INA	IVA	14/3		IVA
YMR013C	SEC59	glycosylation	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA I	NΑ	NA	NA N	1 AI	NA	NA I	N AV	IA N	A N	A NA	NA	NA	Den	Substrate in this reaction is a dead-end (dolichol).	FP
YOR184W	SER1	Phosphoserine transaminase	NA	NA	NA	NA	NA	1	0	28.8	FP	0.99	1	-0.02	TP	1.07	1.03	TP 1	1.09	1.02 T	·P 1	1.1 1	1.02	ΓP 1.	12 0.	99 T	P 1.11	1.04	TP.	Unk	Removing AGT reaction (catalyzed by Agx1p) would fix this false positive. Agx1p is annotated as a alanine-glyoxylate aminotransferase and there is evidence that this enzymatic function is indeed found in yeast [Monschau97], but the pathway is only active on a non-fermentative carbon source.	NA
YGR208W	SER2	Phosphoserine phosphatase	NA	NA	NA	NA	NA	1	0	5.08	FP	0.99	1	0.03	TP	1.07	1.02	TP 1	1.09	0.99 T	·P 1	1.1 ().98 ·	TP 1.	12 0.	95 T	P 1.11	1	TP	Unk	Removing AGT reaction (catalyzed by Agx1p) would fix this false positive. Agx1p is annotated as a alanine-glyoxylate aminotransferase and there is evidence that this enzymatic function is indeed found in yeast [Monschau97], but the pathway is only active on a non-fermentative carbon source.	NA
																															N/A	NI.
YER081W	SER3	3-phosphoglycerate dehydrogenase	NA	NA	NA	NA	NA	1	1	0.33	TP	1	1	-0.08	TP	1.08	1.01	ĪΡ	1.1	1.01 T	P 1	.11 1	.01	ΓP 1.	12 0.	98 T	P 1.11	0.99	TP	NA	INA I	NA
		3-phosphoglycerate dehydrogenase				NA				-0.02		1	1	-0.02	TP	1.08	1.02	TP	1.1	1.04 T	P 1	.11 1	.04	TP 1.	12 1.	05 T	P 1.11	1.05	TP	NA	NA	NA
YDR023W		Serine-tRNA ligase Glutathione-dependent	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA I	NΑ	NA	NA N	1 Al	NA	NA I	NA N	IA N	A N	A NA	NA	NA	Oth	Protein synthesis not required in the model	NA
		formaldehyde dehydrogenase long-																														
YDL168W	SFA1	chain alcohol dehydrogenase	NA	NA	NA	NA	NA	1	1	-0.02	TP	1	1	-0.02	TP	1.08	1.02	TP	1.1	1.03 T	P 1	.11 1	.02	TP 1.	12 1.	03 T	P 1.11	1.03	TP	NA	NA	NA
YJR095W		Succinate-fumarate transport protein	NA	NΑ	NA	NA	NA	1	1	-0.03	TP	1	1	0.01	TP.	1.08	1.02	TP	1.1	1.04 T	P 1	.11 1	.04	TP 1	12 1	08 T	P 1 11	1.06	ТР	NA	NA .	NA
		Serine hydroxymethyltransferase,								5.50																						
YBR263W	SHM1	mitochondrial	NA	NA	NA	NA	NA	1	1	0	TP	1	1	0.06	TP	1.08	1.03	TP	1.1	1.03 T	P 1	.11 1	.02	TP 1.	12 1.	04 T	P 1.11	1.02	TP	NA	INA	NA
YLR058C	SHM2	Serine hydroxymethyltransferase	NA	NA	NA	NA	NA	1	0	4.29	FP	1	1	0	TP	1.08	1	TP	1.1	1.01 T	P 1	.11 1	1.01	TP 1.	12	1 T	P 1.11	1.01	TP	Unk	Shm2p should not be required for growth in minimal media as even a shm1/shm2 double mutant is a glycine prototroph.	NA

	o.		Ë	all	sim	dxə	sim	exp	ave	call	/PGal sim	dxə		sim	dxe	call	PDGE sim	PDGE exp	PDGE call	sim	exp	Ë	dxe	call	mi	exp	all	"		ter et al
ORF	Vame	Annotation	Ess sim	es cal	Nols	Molic	MMD sim	MMD exp	MMD ave	AIMD	PGa	PGal	PGal	PD sim	(PD exp	PD	(PDG	/PDG	/PDG	/PG sim	/PG call	/PE sim	/PE exp	PE	YPL sim	YPL e	YPL call	Slass	Explanation	Forster
	_	1-acyl-sn-gylcerol-3-phosphate acyl			U,	0, 0			_																				Two distinct enzymes are necessary for PA synthesis in lipid particles: the second step, acylation of lysophosphatidic acid is catalyzed by Slc1p; a specific point mutant allows cells to grow without making sphingolipids; this deletion is lethal	
		transferase (putative)		NA			A 0		0.1	FN	0	1 0.		N 0		FN			FN		0.99 FI			4 FN		1	FN	Bio		NA
		Multicopy Suppressor Of los1	_	NA		NA N		_	-0.05	TP	1			P 1.0		TP			TP 1			1.12			1.11		TP	NA		NA
YCRU73VVA	SULZ	Multicopy suppressor of los1-1 Weak multicopy suppressor of los1-	NA	NA	NA	NA N	A 1	1	0.12	TP	1	1 -0.	.01 1	P 1.0	8 1	TP	1.1	1.01	IP.	1.11	1.01 TI	7 1.12	2 1	IP	1.11	1	TP	NA	INA I	NA
YHR163W	SOL3	1	NA	NA	NA	NA N	A 1	1	0.31	TP	1	1 (0 1	P 1.0	8 1	TP	1.1	1.02	TP ·	1.11	1 TI	1.12	2 1	TP	1.11	1.01	TP	NA	NA	NA
YGR248W	SOL4	6-phosphogluconolactonase	NA	NA	NA	NA N	A 1	1	-0.01	TP	1	1 -0.	.06 1	P 1.0	8 1.02	TP	1.1	1.03	TP 1	1.11	1.03 TI	1.12	2 1.0	6 TP	1.11	1.05	TP	NA		NA
YKL184W	SPE1	Ornithine decarboxylase	NA	NA	NA	NA N	A 1	1	-0.01	TP	1	1 -0.	.05 1	P 1.0	8 1.01	TP	1.1	1.04	TP 1	1.11	1.03 TI	1.12	2 1.0	7 TP	1.11	1.05	TP	NA	NA	NA
VOI 0500	CDEO	S-adenosylmethionine							_				,					4 00			4.05 7		1 0			4.07		NIA	NA.	l NIA
YOL052C	SPEZ	decarboxylase	NA	NA	NA	NA N	A 1	1	0	TP	1	1 (0 1	P 1.0	8 1.03	I I P	1.1	1.06	IP	1.11	1.05 TI	7 1.12	2 1.0	8 11	1.11	1.07	IP	NA	INA .	NA
		Putrescine aminopropyltransferase																												
YPR069C		(spermidine synthase)	NA	NA	NA	NA N	A 1	1	0.01	TP	1	1 -0.	.08	P 1.0	8 1.01	TP	1.1	1.02	TP [•]	1.11	1.02 TI	1.12	2 1.0	3 ТР	1.11	1.02	TP	NA		NA
YLR146C	SPE4	Spermine synthase	NA	NA	NA	NA N	A 1	1	0	TP	1	1 -0.	.04 1	P 1.0	8 1.02	TP	1.1	1.03	TP 1	1.11	1.04 TI	1.12	2 1.0	4 TP	1.11	1.03	TP	NA	NA	NA
VOD400W	0004	Exo-1,3-beta-glucanase,	l	l																				_ _					NIA.	
		sporulation-specific Cis-prenyltransferase	NΑ	NA NA	NA NA	NA N	A 1		-0.01		1										1.04 TI						TP	NA NA		NA NA
TWINTOTO	OICTT	Pyridoxal-5'phosphate-dependent	IVA	INA	INA	IN/A IN	1	+	-0.01	 	-	1 -0.	.01 1	1 1.0	1.0	1	1.1	1.01		1.11	1.01 11	1.12	2 1.0	' ' '	1.11	1.01		14/3	IVA	INA
		enzyme homologous to mouse glial																												
YKL218C		serine racemase	NA		NA	NA N	A 1	1	0	TP		1 -0.		P 1.0							1.03 TI									NA
YDR536W		Sugar transporter-like protein	NA		NA		A 1	_	-0.03		1	_	_	P 1.0	_			1.02	_			1.12	_	_	1.11		_			NA
YJR130C	STR2	Cystathionine gamma-synthase	NA	NA	NA	NA N	A 1	1	0.07	TP	1	1 0.	.01 1	P 1.0	8 1.01	TP	1.1	1.04	IP '	1.11	1.03 TI	1.12	2 1.0	5 IP	1.11	1.03	IP	NA	Phospholipid produced by this reaction leads to a dead-end	NA
YLR305C	STT4	Phosphatidylinositol-4-kinase similar to VPC34	1	FP	NA	NA N	A NA	A NA	NA	NA	NA N	NA N	IA N	IA NA	. NA	NA	NA	NA	NA	NA	NA N	A NA	. NA	NA NA	. NA	NA	NA	Den	(1D-myo-Inositol 1,4,5-trisphosphate). Also Pik1p is an	FP
YMR054W	STV1	110 kDa subunit; not in vacuole membrane vacuolar H-ATPase	NA	NA	NA	NA N	IA 1	1	-0.06	TP	1	1 -0.	.05 1	P 1.0	8 0.97	TP	1.1	0.97	TP ·	1.11	0.83 TI	2 1.12	2 0.8	6 TP	1.11	0.97	TP	NA	NA	NA
	01100	Invertase (sucrose hydrolyzing		l																										l
YIL162W	SUC2	enzyme) Sulfate uptake is mediated by	NA	NA	NA	NA N	A 1	1	0.02	TP	1	1 -0.	.02 1	P 1.0	8 1.02	2 TP	1.1	1	TP '	1.11	0.98 TI	1.12	2 0.9	6 TP	1.11	0.97	TP	NA	INA	NA
VDD004M		specific sulfate transporters SUL1 and SUL2, which control the concentration of endogenous																											NA.	
YBR294W YLR092W		activated sulfate intermediates. High affinity sulfate permease	NA	NA	NA NA	NA N	A 1	1	0.08	TP	1			P 1.0		TP		1.02			1.02 TI	1.12			1.11		TP	NA NA		NA NA
TEIX092VV	JULZ	Integral membrane protein similar	INA	INA	INA	IN/A IN		+	0.1	15	- +	1 0.	.02 1	1.0	1.0	IF	1.1	1.01	IF	1.11	1.01 11	1.12		117	1.11	1.01	IF	INA	IVA	INA
YPL057C	SUR1	to YBR161w, Hoc1p, and Och1p	NA	NA	NA	NA N	A 1	1	-0.03	TP	1	1 -0.	.02 1	P 1.0	8 1.01	TP	1.1	1.01	TP ·	1.11	1 TI	1.12	2 0.9	7 TP	1.11	0.99	TP	NA	NA	NA
YDR297W	SUR2	Sphingosine hydroxylase	NA	NA	NA	NA N	A 1	1	0.29	TP	1	1 (0 1	P 1.0	8 1	TP	1.1	0.99	TP 1	1.11	0.99 TI	1.12	2 0.9	9 TP	1.11	1	TP	NA		NA
YLR372W	SUR4	Elongase	NA	NA	1	3.4 F	P 1	1	-0.01	TP	1	1 -0.	.02 1	P 1.0	8 0.75	FP	1.1	0.79	FP ·	1.11	0.89 TI	2 1.12	2 0.9	1 TP	1.11	0.92	TP	Bio	Involved in sphingolipid biosynthesis. These lipids are not currently required for growth by the model.	NA
YLR354C	TAL 1	Transaldolase, enzyme in the	NA	NA	NA	NA N	A 1	4	0	TP	1	1 -0.	02 7	D 1 0	0 00	тр	1 1	1.02	TD.	1 11	0.92 TI	1 1	2 4 0		1 11	0.05	тр	NA	NA.	NA
TLN354C	TAL1	pentose phosphate pathway Amino acid transport protein for	INA	INA	INA	INA IN	A	+	U	IF	-	1 -0.	.02 1	1.00	0.98	, IF	1.1	1.02	IF	1.11	0.92 11	1.12	2 1.0	9 15	1.11	0.95	IF	INA	INA	INA
		valine, leucine, isoleucine, and																											There are multiple alternative isozymes for amino acid	
YBR069C	TAT1	tyrosine	NA	NA	NA	NA N	A 1	1	0.7	TP	1	1 (о Т	P 1.0	8 0.87	FP.	1.1	0.98	TP ·	1.11	1.01 TI	1.12	2 1	TP	1.11	1.01	TP	Iso	transporters.	NA
YOL020W	TAT2	Tryptophan permease, high affinity	NA	NA	NA	NA N	A 1	1	0.05	TP	1	1 -0.	.08 1	P 1.0	8 1	TP	1.1	1	TP 1	1.11	1.01 Ti	1.12	2 1.0	2 TP	1.11	1.01	TP	NA	NA	NA
YJL052W	TDH1	Glyceraldehyde-3-phosphate dehydrogenase 1	NA	NA	NA	NA N	A 1	1	-0.01	ТР	1	1 (0 1	P 1.0	8 0.99	TP	1.1	1.02	TP ·	1.11	1.05 TI	1.12	2 1.0	5 TP	1.11	1.03	TP	NA	NA	NA
YJR009C	TDH2	Glyceraldehyde 3-phosphate dehydrogenase	NA	NA	NA	NA N	A 1	1	-0.03	TP	1	1 -0.	02 7	P 1.0	8 1	ТР	1.1	1	TP .	1 11	1.02 TI	0 1 1	2 0 0	Q TD	1 11	1	ТР	NA	NA	NA
10110090	10112	Glyceraldehyde-3-phosphate	INA	INA	14/1	INA IN	1	+	-0.03	1.0		, -0.	.02 1	1.0	1	1F	1.1			1.11	1.02 11	1.12	_ 0.9	J 11 ²	1.11			14/1		14/
YGR192C	TDH3	dehydrogenase 3	NA	NA	NA	NA N	A 1	1	0.01	TP	1	1 -0	.01 7	P 1.0	8 0.97	TP	1.1	0.94	TP	1.11	0.98 TI	1.12	2 0.9	5 TP	1.11	0.98	TP	NA	NA	NA

щ	me		Ess sim	Ess call	low sim	low exp	ow call	IMD sim	IMD exp		MD call	/PGal sim	PGal exp	YPGal ave	PGal call	/PD sim	YPD exp	PD call	PDGE sim	YPDGE exp	PDGE call	/PG sim	/PG exp	PG call	YPE sim	YPE exp	YPE call	YPL sim	L exp	YPL call	Class	Explanation
ORF	Sa	Annotation	Es	Es	Slo	Slo	Sic	2	Σ	Ξ	Σ	ΥP	Ϋ́	ΥP	ΥP	\	ΥP	ΥP	ΥP	ΥP	ΥP	\	Ϋ́	Ϋ́	ΥP	ΥP	Ϋ́	ΥP	YPL	Ϋ́	ວັ	Explanation
YDL185W		Site-specific endonuclease VDE (PI Scel) vacuolar ATPase V1 domain subunit A (69 kDa) protein with three regions (ABC) that are spliced to yield the extein AC and the intein B; AC is a 69K vacuolar (H+)-ATPase, and B is a 50K site-specific endonuclease named VDE (PI-Scel) that is homologous to HO. Cleavage is meiosis-specific and induces ge		NA	1	12.2	: FP	1	1 .	-0.03	TP	1	1	-0.02	TP	1.08	0.7	FP	1.1	0.66	FP	1.11	0.49) FP	1.12	2 0.5	7 FP	1.11	0.5	9 FP	Oth	The tfp1 null mutant is viable but is calcium-sensitive, lacks vacuolar (H)-ATPase activity, and is defective in vacuolar acidification and assembly of the remaining V1 subunits [SGD]. pH balancing problem.
		Vacuolar ATPase V0 domain																														71 01
YPL234C	TED2	subunit c' (17 kDa) vacuolar H(+) ATPase 17 kDa subunit C	NIA	NA	1	71	ED	1	1	0.02	тр	1	,	0.04	TD	1 00	0.70	ED	11	0.66	ED	1 11	0.61	ED	1 10	١	ا	1 11	0.6	, ED	Oth	See other vacuolar ATPase components.
		THI for thiamine metabolism. Transcribed in the presence of low level of thiamine (10-8M) and turned off in the presence of high level (10-6M) of thiamine. Under the positive control of THI2 and THI3.			NA																										NA NA	
YPL258C		THI for thiamine metabolism. Transcribed in the presence of low level of thiamine (10-8M) and turned off in the presence of high level (10-6M) of thiamine. Under the positive control of THI2 and THI3.		NA	NA	NA	NA	1	1	-0.04	TP	1	1	-0.1	TP	1.08	1.01	TP	1.1	1.03	s TP	1.11	1.04	4 TP	1.12	2 1.0	4 TP	1.11	1.0	3 TP	NA	NA
		THI for thiamine metabolism. Transcribed in the presence of low level of thiamine (10-8M) and turned off in the presence of high level (10-6M) of thiamine. Under the																														
YPR121W	THI22	positive control of THI2 and THI3.	NA	NA	NA	NA	NA	1	1	0.02	TP	1	1	-0.02	TP	1.08	1.02	TP	1.1	0.99	TP	1.11	1	TP	1.12	1.0	1 TP	1.11	1.0	1 TP	NA	NA
		pyrophosphorylase hydroxyethylthia																														
		zole kinase	NA		NA			1		0.07		1																			NA	
YLR237W YOR143C	THI7	Thiamine transporter Thiamin pyrophosphokinase	NA 1	NA FP	NA NA		NΑ	1 NA		0.01 NA	TP NA	1 NA		0.01 NA		1.08 NA			1.1 NA			1.11 NA	1.07 NA		1.12 NA			1.11 NA		_		NA Thiamin biosynthesis not required in the model
		Homoserine kinase	NA	Ħ	NA		NA			6.34		1																				This should only be a threonine auxotroph [SGD]. May play some other uncharacterized role. Threonine can be synthesized by the model from glycine
VCDOESW	TUDA	Thropping gypthage	N. A	N: A	N: A	NIA	N: A	4		7.67		1	1	0.00	TO	1.00	1.04	TC	1.4	1.00	TE	1 1 1	4	TC	1.40			1 4 4	14.0) TC	Lini	using Gly1p. If CYSTL (Cys1p) and AHCi (Sah1p) reactions are removed the false positive prediction is corrected and both of these have putative assignments, but neither can be removed from the model.
YIL078W		Threonine synthase Threonine-tRNA ligase	1 1	FP	NA NA			NA		NA		NA				1.08			1.1						1.12			1.11				removed from the model. Protein synthesis not required in the model
	TKL1	Transketolase 1	NA	NA	NA		NA				_	1		0.1		1.08			1.1						1.12			1.11		_		NA .
YJR066W	TOR1	Phosphatidylinositol kinase	NA	NΔ	NΔ	NΑ	NΙΔ	1		-0.01	тр	1	1	-0.04	TP	1 09	1.01	ТР	1 1	1.03	ТР	1 11	1.01	R TD	1 12	1 0	3 TE	1 11	1 1 0	тп	NA	NA
		Putative protein/phosphatidylinositol kinase involved in signaling activation of translation initiation, distribution of the actin cytoskeleton, and meiosis	I		NA					-0.01																						Phospholipid produced by this reaction leads to a dead end (phosphatidyl-10-myo-inositol 3,4-bisphosphate).
		Triosephosphate isomerase			NA			NA																								Mutant is unable to grow on glucose as sole carbon source. If ethanol or acetate is added to media containing glucose or galactose, cells are viable. Impaired growth probably due to NADH/energy shortage on glucose [Compagno01]. In one study this gene is found to be essential [Giaever02], wheras in the other one it has no phenotype [Steinmetz02].

																	L L	۵	 											t al
	ē		sin	call	Slow sim	Slow exp	MMD sim	MMD exp	ММD ave	MMD call	YPGal sim	Galexp	YPGal ave	YPGal call	YPD exp	call	/PDGE sim	(PDGE exp	/PDGE cal	YPG sim	YPG exp	YPE sim		YPE call	sim	dxe	call	Ω		ster et
ORF	Nam	Annotation	Ess sim	Ess call	Slow	Slow		MM	MMD	MMD	YPĞ	YPĞ	ΥΡĞ	YPG	YPD	YPD call	YPD	YPD	YPD	YPG	YPG	Y 3	. 9	YPE call	YPL sim	YPL exp	YPL call	Class	Explanation	Forster
VPD4000	TDC4	Trehalose-6-phosphate synthase/phosphatase complex 56				0.0			0.00	T11		4 0		TD 4.0							0.04		10.0	00 7			-	Made	Essential for growth on glucose and fructose [MIPS]. Deletion of TPS1 totally abolishes trehalose-6-phosphate synthase activity and measurable trehalose-production, but YP media	
YBR126C	TPS1	kDa synthase subunit Trehalose-6-phosphate	NA	NA	1	6.8 F	P 0) 1	-0.06	IN	1	1 -0).02	TP 1.0	8 0.8	I FP	1.1	0.83	FP	1.11	0.91 1	P 1.1	12 0.	86 11	1.11	0.89) IP	ivied	contains trehalose so TPS1 should not be required.	NA
YDR074W	TPS2	phosphatase	NA	NA	1	18 F	P 0) 1	0	TN	1	1 -0	0.05	TP 1.0	8 0.96	3 TP	1.1	0.95	TP	1.11	1.06 T	P 1.1	12 1.	03 TF	1.11	1.02	TP	Med	See TPS1.	NA
YMR261C	TPS3	Trehalose-6-phosphate synthase/phosphatase complex 115 kDa regulatory subunit		NA	NA	NA N	A 1	1	0.1	TP	1	1	0	TP 1.0	8 0.99	Э ТР	1.1	0.98	TP	1.11	0.99 T	P 1.1	12 0.	96 TI	1.11	0.97	TP	NA	NA	NA
YDR007W	TRP1	N-(5'-phosphoribosyl)-anthranilate isomerase	NA	NA	NA	NA N	A C	0	5.83	TN	1	1 0	.02	TP 1.0	8 1	ТР	1.1	1.02	ТР	1.11	1.03 T	P 1.1	12 1.0	05 TE	1.11	1.03	ТР	NA	NA	NA
YER090W		Anthranilate synthase component		NA		NA N	A 1	1	2.88		1	1 -0		TP 1.0			1.1												NA	NA
YKL211C	TRP3	Anthranilate synthase component II indole-3-phosphate	NA	NA	NA	NA N	A C	0	7.77	TN	1	1 -0	0.07	TP 1.0	8 1.02	2 TP	1.1	1.03	TP	1.11	1.03 T	P 1.1	12 1.0	06 TF	1.11	1.04	I TP	NA	NA NA	NA
		Anthranilate phosphoribosyl																												
YDR354W YGL026C		Tryptophan synthetase	_	NA NA	_	NA N		_	2.64 1.4		1			TP 1.0							1.01 T 0.95 T						TP		Weak false negative Weak false negative	NA NA
YDR353W	TRR1	Thioredoxin reductase EC 1.6.4.5	0	TN	NA	NA N	A N		NA	NA	NA I	1 AN	NA I	NA NA	NA	NA	NA	NA	NA	NA	NA N	A N	A N	A N	A NA	NA		NA	NA	NA
YHR106W YBR265W		Thioredoxin reductase 3-ketosphinganine reductase	NA 1	_	NA NA	NA N	A 1	1	-0.05 NA		1 NA			TP 1.0			1.1	1.01 NA	TP		1.01 T		_		1.11 A NA	_	TP	_	NA Sphingolipid synthesis not required in the model	NA FP
YML100W		Similar to TPS3 gene product trehalose-6-phosphate synthase/phosphatase complex 123 kDa regulatory subunit	3		NA																1.04 T									NA
		Prephenate dehydrogenase			INA			T.																					Should be a tyrosine auxotroph, but the media contains tyrosine. Also, the model has an alternative reaction with no	
YBR166C YGR185C		(NADP+) Tyrosine-tRNA ligase	NA 1	NA FP	1 NA	3.5 F NA N	P 1 A N	1 A NA	0 NA	TP NA	1 NA			TP NA			NA NA	NA NA			NA N				A NA				gene association. Protein synthesis not required in the model	NA NA
		Gamma-aminobutyrate (GABA) transaminase (4-aminobutyrate aminotransferase)	NA		NA				-0.04												1.01 T									NA
		Succinate semialdehyde																												
YBR006W YDL210W		dehydrogenase GABA-specific transport protein	NA NA	NA NA	NA NA	NA N	A 1	_	-0.02 0.11		1	1 -0		TP 1.0			1.1	1 02			0.99 T 1.02 T								NA NA	NA NA
		Uridinephosphoglucose																											Reaction produces UDPglc, which is not required in our	
YKL035W YKL216W		pyrophosphorylase Dihydroorotate dehydrogenase	1 NA	FP NA	NA NA		A N		-0.02			NA 1 1 -0		NA NA				NA 0.98			NA N 0.98 T				NA NA		TP		model. NA	FP NA
		Orotate phosphoribosyltransferase																												
YMR271C		2 Aspartate transcarbamylase carbamoyl	NA	NA	NA	NA N	A 1	1	-0.01	TP	1	1 -0	0.07	TP 1.0	8 1.0	1 TP	1.1	1.03	TP	1.11	1.02 T	P 1.1	12	1 TF	1.11	1	TP	NA	NA .	NA
YJL130C		phosphate synthetase glutamine amidotransferase	NΔ	NA	NA	NA N	A 1	1	-0.06	тр	1	1	0	TP 1 0	8 1 0	1 TD	11	1 03	тр	1 11	1.03 T	D 1 1	12 1	02 T	1 11	1 1 03	ТР	ΝΔ	NA NA	NA
YLR420W		Dihydrooratase	NA	_		NA N		_	0	TP	1			TP 1.0		2 TP		1.03	TP		1.03 T						TP		NA NA	NA
YML106W	URA5	Orotate phosphoribosyltransferase 1 Uridine-monophosphate kinase	NA	NA	NA	NA N	A 1	1	0.03	TP	1	1 0	.01	TP 1.0	8 1	TP	1.1	1.01	TP	1.11	1.02 T	P 1.1	12 1.	03 TF	1.11	1.01	TP	NA	NA .	NA
YKL024C		(uridylate kinase)	1	_		NA N					_	NA N		NA NA				NA											RNA and protein synthesis not required in the model.	FP
YBL039C		CTP synthase CTP synthase	_	NΑ		3.2 F NA N	_	_	-0.03				-	_	_		_	_	_			_	_			_	_		Model does not require ctp to grow on complex media.	NA NA
131/10344	UNAO	Uridine nucleosidase (uridine	INA	INA	INA	INA IN	A 1	+	0.01	IF	-	1 -0).07	11.0	6 1.0	III	1.1		IF	1.11	1.01 1	F 1.1	12	' ''	1.11	-	IF	INA	IVA	INA
		ribohydrolase); EC 3.2.2.3		NA		NA N		1	-0.02		1		0.01	TP 1.0	8 1.0	1 TP	1.1	1	TP	1.11	0.99 T	P 1.1	12 0.	99 TF	1.11	1 1		NA	NA NA	NA
		Uridine kinase Associated with ferric reductase			NA NA			_	0.06		1										0.99 T 0.98 T								NA NA	NA NA
		Valine-tRNA ligase	1	_	_						NA I										NA N								Protein synthesis not required in the model	NA
YGR065C	VHT1	H+-biotin symporter	1	FP	NA	NA N	A N	A NA	NA	NA	NA I	NA N	NA I	NA NA	A NA	NA	NA	NA	NA	NA	NA N	IA N	A N	IA N	A NA	NA	NA	Bio	Biotin not required in our model, but bakers' yeast is auxotrophic for biotin (vitamin H) and depends on the efficien uptake of this compound from the environment [Stolz99].	NA
		Vacuolar H(+) ATPase V1 sector																												
		54 kDa subunit Vacuolar ATPase V1 domain	NA		1	5.9 F		1	-0.04		1																		See other vacuolar ATPase components.	NA
YBR127C	VMA2	subunit B (60 kDa) E subunit of V1 sector vacuolar	NA	NA	1	10.6 F	P 1	1	-0.03	TP	1	1 -0	0.02	TP 1.0	8 0.86	6 FP	1.1	0.7	FP	1.11	0.75 F	P 1.1	12 0	.7 FF	1.11	0.73	FP	Oth	See other vacuolar ATPase components.	NA
YOR332W	VMA4	H(+) ATPase 27 kDa subunit	NA	NA	1	5.2 F	P 1	1	0.02	TP	1	1 -0	0.03	TP 1.0	8 0.9	TP	1.1	0.87	TP	1.11	0.65 F	P 1.1	12 0.	61 FF	1.11	0.66	FP	Oth	See other vacuolar ATPase components.	NA

					Ε	9	=	Ε	сb)e	=	mis	dxe	ave	, ,	=	۵ =	sim		call	L L	۵	_	ء	a						et a
ORF	ame		ss sim	ss call	Slow sim	ow exp	ow ca	MMD sim	IMD exp	MMD ave	IMD call	PGal sim	Call Call		Poal call		PD call	PDGE sim	3000	PDGE call	PG sim	PG exp	PG call	'PE sim	PE exp	PEcall	PL sim	/PL exp	/PL call	Class	Explanation 2
		Annotation V1 sector hydrophilic subunit C vacuolar ATPase V1 domain subunit C (42 kDa) vacuolar H-	Ш	E	S	Ĭ,	S	Σ	Σ	Σ	Σ	<u> </u>	 	5	5		<u> </u>	<u> </u>	5	.	Ϋ́	>	Ϋ́	<u></u>	¥	>	=	,	Ϋ́	<u></u>	Explanation
YKL080W	VMA5	ATPase Vacuolar ATPase V0 domain	NA	NA	1	6.1	FP	1	1 -(0.02	ΓP	1	1 -0.	.02 T	P 1.	08 0.	.66 FI	P 1.1	1 0.	62 FF	1.1	1 0.5	7 FP	1.12	2 0.5	1 FI	P 1.1	0.5	7 FP	Oth	See other vacuolar ATPase components. NA
YLR447C	VMA6	subunit d (36 kDa) vacuolar H(+) ATPase 36 kDa subunit (D subunit of VO sector)	NA	NA	1	10.9	FP	1	1 -(0.03	ΤР	1	1 -0.	.02 T	P 1.	08 0.	.65 FI	P 1.1	1 0.	59 FF	1.1	1 0.58	8 FP	1.1	2 0.5	7 FI	P 1.1	0.6	5 FP	Oth	The vma6 null mutant is viable but shows a growth defect at neutral pH and is sensitive to calcium. pH balancing problem. NA
YGR020C	VMA7	Vacuolar ATPase V1 domain subunit F (14 kDa)	NA	NA	1	9.9	FP	1	1 -(0.01	ΓР	1	1 () Т	P 1.	08 0.	.72 FI	P 1.1	1 0.	62 FF	1.1	1 0.63	3 FP	1.12	2 0.6	4 FI	P 1.1	0.6	6 FP	Oth	See other vacuolar ATPase components. NA
YEL051W		V1 catalytic sector D subunit vacuolar H-ATPase	NA	NA	1	14.4	FP	1	1 -(0.02	ТР	1	1 -0.	.01 T	P 1.	08 0.	.75 FI	P 1.1	1 0.	65 FF	1.1	1 0.5	7 FP	1.1:	2 0.5	8 FI	P 1.1	0.6	3 FP	Oth	The vma8 null mutant is viable but lacks vacuolar (H)- ATPase activity, cannot grow at neutral pH or on nonfermentable carbon sources, and fails to accumulate quinacrine in the vacuole [SGD]. The slow growth phenotype is probably because of problems with pH balancing.
V0D2700	V/DLI4	V0 sector subunit essential for vacuolar acidification and vacuolar H-ATPase activity vacuolar ATPase V0 domain subunit a (100	NIA	NIA	4	2.4	ָב	4	4	04	TD.	4	4 0	00. T	TD 4.	00.0	00 7	D 4.	1 0	70 55		4 0 0			0.07	0 7			1 10	Oth	See other vacualar ATDage companyers
		kDa) vacuolar H-ATPase		NA		3.4				0.01																					See other vacuolar ATPase components. NA PI3 kinase activity involved in signaling processes - in the
		Phosphatidylinositol 3-kinase Tryptophan-tRNA ligase	NA 1		1 NA	18.9 NA	_	1 NA		0.01 NA I			1 -0. IA N		P 1.					56 FF		1 0.6									model this leads to a dead end. NA Protein synthesis not required in the model NA
YGR194C	XKS1	Xylulokinase Xanthine phosphoribosyl	NA	NA	NA	NA	NA	1	1 -0	0.03	ΤР	1	1 0.	14 T	P 1.	08 1.	.01 TI	P 1.1	1 1.	01 TF	1.1	1 1	TP	1.12	2 1.0	1 TI	P 1.1	1.0	2 TP	NA	
		transferase			NA		NA	1			ΤР	1										1 1.04									
		Xylitol Dehydrogenase Carnitine acetyltransferase			NA NA		_	1	_	0.03	TP	1			P 1.			P 1.1				1 1.04 1 1.04							TP	NA NA	
		Hypothetical ORF	_	_	NA		_	1	_	_	TP	1	_		_	_		P 1.				1 0.9							3 TP		
		Hypothetical ORF	_	_	NA		NA	1	_	_	TP	1	_		_							1 1.04							_		NA NA
		Hypothetical ORF Hypothetical ORF			1 NA	5.2 NA		1 0.95			TP 0	1					73 FI					1 0.6								Oth	
		Protein required for cell viability				NA		NA I		0.02 T				.01 T								1 1.04 A NA									Protein synthesis not required in the model FP
		Pantothenate kinase (ATP:D- pantothenate 4'- phosphotransferase, EC 2.7.1.33) catalyzes the first committed step in the universal biosynthetic pathway leading to CoA.	1																												CoA biosynthesis not required in the model.
		Hypothetical ORF	NA			NA		1					1 -0.									1 1.00									NA NA
YEL047C	YEL04	Fumurate ReDuctase Soluble	NA	NA	NA	NA	NA	1	1 (0.01	ΤP	1	1 -0.	.03 T	P 1.	08 1.	.02 TI	P 1.	1 1.	03 TF	1.1	1 1.03	3 TP	1.12	2 1.0	3 TI	P 1.1	1.0	1 TP	NA	NA NA
	YER05	Sequence similarity to mitochondrial phosphate transporters	NA		NA).22				.06 T	P 1.	08 1.	.01 TI	P 1.1	1 1.	03 TF	1.1	1 1.0	3 TP	1.1	2 1.0	1 TI	P 1.1	1.0	2 TP	NA	NA NA
YER087W	YER08	Hypothetical ORF	NA	NA	1	7.5	FP	1	1 -(0.02	ſΡ	1	1 () T	P 1.	08 0.	.97 TI	P 1.1	1 0.	89 TF	1.1	1 0.78	8 FP	1.12	2 0.7	2 FI	P 1.1	0.7	3 FP	Oth	Protein synthesis not required in the model NA Lower oxygen uptake rate would correct this false negative
YFL030W	YFL03	NA	NA	NA	NA	NA	NA	1	1 0	0.08	ТР	1	1 -0.	.06 T	P 1.																prediction. NA
		Hypothetical ORF	_	_	NA		_			0.01		1		.07 T		08 1.	.03 TI	P 1.	1 1.	02 TF	1.1	1 1.0	1 TP	1.13	2 1.0	3 TI	P 1.1	1.0	2 TP	NA	NA NA
		Protein required for cell viability Hypothetical ORF			NA NA		NA NA	NA I	NA 1		NA I	NA N										1 0.98									Protein synthesis not required in the model FP Model can't make cysteine without the rxn catalyzed by this gene. Might be able to bypass this by making cys from pyr using CYS1 [KEGG]. NA
YGR043C	YGR04	Hypothetical ORF	NA	NA	NA	NA	NA			0.02	TP	1	1 -0.	.01 T	P 1.	08 1.	.01 TI	P 1.1	1 1.	01 TF	1.1	1 1	TP	1.12	2 1.0	4 TI	P 1.1	1.0	3 TP	NA	NA NA
		Hypothetical ORF			NA			1			TP	1								02 TF					2 1.0						NA NA
		Hypothetical ORF Hypothetical ORF			NA NA					0.05	ΓP	1			P 1.		.03 TI					1 1.0° 1 0.90									
		Protein required for cell viability			NA							NA N	IA N	IA N	IA N	A N	IA N	A NA	A N	A NA	N.A	A NA	NA	NA	NA NA	N,	A NA	NA	NA	Oth	Protein synthesis not required in the model NA
YJL045W		Similar to SDH1			NA							1				08 1.	.01 TI	P 1.1	1 1.	03 TF	1.1	1 1.0	4 TP	1.12	2 1.0	3 TI	P 1.1	1.0	3 TP	NA	NA NA
		Hypothetical ORF Hypothetical ORF			NΑ	NA NA				0.04		1										1 1.0									
																															Aco1p acts as an isozyme for this reaction. For some reason
		Hypothetical ORF Hypothetical ORF				NA NA				i.69 i.01		1	1 -0.	.04 T	P 1.	08 1.	.02 TI	P 1.	1 1.	01 TF	1.1	1 1.02	9 TP	1.12	2 1.0	1 TI	1.1°	1.0	2 TP	NA	YJL200C gene product is only required on minimal media. NA NA NA

ORF	Name	Annotation	Ess sim	Ess call	Slow sim	Slow exp	Slow call	MMD sim	ММD ехр	MMD ave	MMD call	r PGal SIM	d sall exp	YPGal ave	YPGal call		YPD exp	Y PD call	YPDGE sim	YPDGE exp	YPDGE call	YPG sim	YPG exp	YPG call	YPE sim	YPEexp	YPE call	YPLsim	YPL exp	YPL call	Class	Explanation	Forster et al
YKL132C		Probable folyl-polyglutamate				N10		,	,		9	,			,					4 04	1		4.04	TD	4 40	4.00	7		4.00	TD	NIA	NA	NIA
YLR089C		synthetase				NA NA				.26					ΓΡ 1.																NA NA		NA NA
1LKU09C		Hypothetical ORF	NA	INA	IVA	INA	NA	1	1 1	.20	TP	_	1 -0	0.05	IP 1.	08	1 1	PI	1.1	1.03	IP	1.11	0.94	IP	1.12	0.99	IP	1.11	1.01	IP	INA	IVA	INA
YLR164W		YLR164Wp is homologous to	ΝΔ	ΝΔ	NA	NA	ΝΔ	1	1 0	.09	тр	1	۱ ۱	0.03	TD 1	ng l	, ,	TD 1	1 1	n aa	тр	1 11	n aa	тр	1 12	n aa	тр	1 11	n aa	тр	NA	NΔ	NA
		Hypothetical ORF					_	1	-		TP																				NA		NA
		Hypothetical ORF					_	1	-	0.03																					NA		NA
		Hypothetical ORF	_	_			_	1	_	_	TP	1 .																			NA		NA
		Hypothetical ORF						1	1 -0			1 .																			NA		NA
		Hypothetical ORF	_	_			_	1			TP																				NA		NA
TWICTIOO		Protein similar to bacterial glutamyl-		INA	IVA	INA	IVA	_	-	0		•	1 -0	7.02	1.	00 1	.02			1.02		1.11	1.02		1.12	1.02		1.11	1.02		14/-1	IVA	14/3
YMR293C		tRNA amidotransferases	NA	NA	1	3.1	FP	1	1 -0	0.04	TP	1	ı I-0	0.01	TP 1.	08 0).74 F	P 1	1.1	0.7	FP	1.11	0.63	FP	1.12	0.59	FP	1.11	0.63	FP	Den	This reaction is a dead end.	NA
																																Null mutant retains 10% of nucleoside diphosphate kinase activity. Sources of remaining enzyme activity are unknown, but possibilities are discussed in [Fukuchi93]. Reaction w/o gene associations could be added to the model to represent	
		Nucleoside diphosphate kinase	NA	NA																												these unidentified enzymes.	FN
		Protein required for cell viability																														Protein synthesis not required in the model	NA
YOR071C	YOR07	Hypothetical ORF	NA	NA	NA	NA	NA	1	1 0	.04	TP	1	1 -0	0.07	ΓP 1.	08 1	I.01 T	ΓP 1	1.1	1.02	TP 1	1.11	1.01	TP	1.12	1.01	TP	1.11	1.01	TP	NA	NA	NA
YOR192C	YOR19	Hypothetical ORF	NA	NA	NA	NA	NA	1			TP	1																			NA		NA
YKR053C		DHS-1-P phosphatase	NA	NA	NA	NA	NA	1		0.03		1	1 -0																		NA		NA
YJL139C	YUR1	Mannosyltransferase	NA	NΑ	NA	NA	NA	1	1 0	.13	TP	1	1	0	ΓP 1.	08 0).97]	TP 1	1.1	0.99	TP 1	1.11	0.95	TP	1.12	0.98	TP	1.11	0.99	TP	NA	NA	NA