

Supplementary Table 2: 50 proteins identified in the control preparation

All proteins are sorted by codon bias. For column information, please see comments by positioning pointer over column headings.

ORF name	Gene Name	#UpEP	Other names	Codon Bias	Function	MolEnv	SGD process	SGD function	Genbank annotation	Comment
YGR192C	IDH3	18	IDH3/IGLD1/SSS2/IGPD3/HS	0.988	met	sol	glycolysis	glyceralddehyde 3-phosphate de	Glyceralddehyde-3-phosphate de	abundant
YJR099C	IDH2	1	IDH2/IGLD2/IGPD2/YJ1433/YJ1	0.982	met	sol	glycolysis	glyceralddehyde 3-phosphate de	glyceratehyde 3-phosphate de	abundant
YAL038W	CDC19	19	PYK1/CDC19/YAL038W	0.965	met	sol	glycolysis	pyruvate kinase	Required for START A in the c	abundant
YLR044C	PDG1	6	PDG1/21.04/YLR044C	0.963	met	met		alpha-1,3-mannosyl-glycoprote	pyruvate decarboxylase	abundant
YKL060C	FBA1	15	FBA1/YKL320/YKL060C	0.936	met	sol	glycolysis	fructose-bisphosphate aldolase	aldolase	abundant
YBR118W	TEF2	27	TEF2/YBR0913/YBR118W	0.933	tm, str	act, psf	protein synthesis elongation	translational elongation factor E	translational elongation factor E	abundant
YPR080W	TEF1	1	TEF1/EF1A/PR913.7/YPR080W	0.929	tm, str	act, psf, rib	protein synthesis elongation	translational elongation factor E	translational elongation factor E	abundant
YOL066C	ADH1	6	ADH1/ADG1/ADE1/Y0094/7/Y	0.913	met	sol		acetylglutone-phosphate reduct	Alcohol dehydrogenase	abundant
YOR064W	RPS13	2	RPS13/Y315/YD9609.18/D42	0.893	tm	psf	protein biosynthesis	structural protein of ribosome	Homology to rat S13	abundant
YOR063W	EFT1	1	EFT1/O3317/YOR3317/YOR13	0.89	tm	psf	protein synthesis elongation	translational elongation factor	translational elongation factor 2 (	abundant
YOR385W	EFT2	32	EFT2/D9609.5/D9481.22/YDR1	0.888	tm	psf	protein synthesis elongation	translational elongation factor	translational elongation factor 2 (	abundant
YBL092W	RPL32	2	RPL32/YBL0838/YBL092W	0.874	tm	rib	protein biosynthesis	structural protein of ribosome	Homology to rat L32 and mam	abundant
YGL076C	RPL7A	6	RPL7A/Y1.8A/G3216/YGL076C	0.866	tm	rib	protein biosynthesis	structural protein of ribosome	Homology to rat L7 and E. coli	abundant
YLR249W	YEF3	24	YEF3/TEF3/TEF3/Y19672.5/	0.865	tm	psf	protein synthesis elongation	translational elongation factor	contains two ABC cassettes, a	abundant
YFL039C	ACT1	25	ACT1/END7/ABY1/SLC1/YFL	0.825	ma, tp, str, dn	act	establishment of cell polarity (s	structural protein of cytoskeleton	Involved in cell polarization, en	abundant
YPL198W	RPL7B	1	RPL7B/Y1.8B/P1890/YPL198W	0.821	tm	rib	protein biosynthesis	structural protein of ribosome	Homolog of mammalian riboso	abundant
YBR196C	PGI1	29	PGI1/CDC30/YBR1407/YBR19	0.793	met	sol	glycolysis	glucose-6-phosphate isomerase	Phosphoglucosomerase	abundant
YGL103W	RPL28	9	RPL28/CYH2/G3101/YGL103W	0.792	tm, ma	rib	protein biosynthesis	structural protein of ribosome	Homology to rat, mouse L27a	His-rich
YHR183W	GND1	14	GND1/YHR183W	0.766	met	sol		phosphoglucuronate dehydrogen	6-phosphoglucuronate dehydrog	abundant
YMR186W	HSC82	25	HSC82/YMR8010.16/YMR186W	0.696	tm, r, sp		stress response	chaperone	constitutively expressed heat s	abundant
YPL240C	HSP82	6	HSP82/HSP83/HSP90/P1045/	0.658	tm, r, sp		stress response	heat shock protein	82 kDa heat shock protein; hor	abundant
YJL026W	RNR2	15	RNR2/CRT6/1271/YJL026W	0.641	met		DNA replication	ribonucleoside-diphosphate red	involved in glycerol production	abundant
YJL167W	ERG20	1	ERG20/FDST1/PP1/YB013/Y0J5	0.516	met		ergosterol biosynthesis	dimethylallyltransferase	May be rate-limiting step in ste	abundant
YLR438W	CAR2	11	CAR2/CARGB1/9763.2/YLR43	0.495	met	sol		ornithine-coo-acid aminotrans	ornithine aminotransferase	abundant
YHL034C	SBP1	1	SBP1/SSBR1/SSB1/YHL034	0.495	ma	ma	RNA processing	(acyl-carrier protein) S-acylyl	single stranded nucleic acid b	abundant
YKL182W	FAS1	51	FAS1/YKL182W	0.48	met, r, sp		biological	fatty acid biosynthesis	nicotinamide	abundant
YGL037C	PNC1	6	YGL037C/53629	0.4	met, r, sp		biological	process unknown		abundant
YCL037C	SRO9	15	SRO9/SVS2/YCL037C	0.38	tm, tp	rib				abundant
YJL130C	URA2	7	URA2/0686/YJL130C	0.362	met	sol		aspartate carboxyltransferas		abundant
YOL059W	GPD2	6	GPD2/GPD3/O1222/YOL059W	0.293	met	sol		UDP-N-acetylmuramate dehyd	involved in glycerol production	abundant
YOR317W	FAA1	17	FAA1/O6136/YOR317W	0.266	met		biological	long-chain-fatty-acid-CoA-ligas	cellular lipid metabolism and p	His-rich
YBR238C	YBR238C	9	YBR238C/YBR1608	0.243	unk		biological	process unknown		His-rich
YGR087C	PCO6	5	PCO6/G4624/YGR087C	0.24	met	sol		alpha-1,3-mannosyl-glycoprote		His-rich
YER088C	DOT6	3	YER088C	0.235	met	ma			Third, minor isozyme of pyruva	His-rich
YOR267C	YOR267C	26	YOR267C/O5420	0.171	tp	ma	biological	process unknown		His-rich
YDR417W	SNF1	33	SNF1/CA17/CCR1/PAS14/HAI	0.158	met, ma, r, sp		biological	protein phosphorylation	SNF1A/AMP-activated protein	His-rich
YDL223C	YDL223C	46	YDL223C/D0843	0.152	unk		biological	process unknown	Required for release from gluc	His-rich
YML050W	YML050W	1	YML050W/YM9827.02	0.109	unk		biological	process unknown	molecular function unknown	His-rich
YDL025C	YDL025C	28	YDL025C/D2810	0.099	unk		biological	process unknown		His-rich
YML150W	NLM1	15	NLM1/PAC12/RVS27/ZV/D835	0.099	cdc, str	act, lub			May function in nuclear mitrai	His-rich
YHL038C	CBP2	1	CBP2/YHL038C	0.097	ma	ma			Protein required for splitting of	His-rich
YLR371W	ROM2	11	ROM2/L8039.3/YLR371W	0.094	rsp, str		establishment of cell polarity (s	signal transducer	Gdp-GTP Exchange Protein (G	His-rich
YMR004W	NUP1	1	NUP1/YMR8270.06/YMR004W	0.091	tp	per			Protein required for sorting prot	His-rich
YMR037C	MSN2	1	MSN2/YM9532.02/YMR037C	0.066	ma, r, sp	ma	stress response		multicopy suppressor of snf1 m	His-rich
YDL0123C	INO2	2	INO2/SCS1/DIE1/YD9727.18	0.061	met, cdc, ma	ma	phospholipid biosynthesis	transcription factor	Transcription factor required to	His-rich
YJL056C	ZAP1	5	ZAP1/J1145/YJL056C	0.03	ma	ma	transcription regulation from P	specific RNA polymerase II tra	Zinc-regulated DNA binding pr	His-rich
YMR070W	MOT3	19	HMS1/YM9916.09/YMR070W	0.016	ma, dna, r, sp	dna	mating (sensu Saccharomyces	RNA polymerase III transcripti	High Copy Suppressor of MOT	His-rich
YPR186C	PZF1	3	TFG2/PZF1/TFIIA/P9677.9/YH	-0.002	ma	dna	transcription initiation from Pol		Transcription factor IIfa (TFIIA	His-rich
YBR255W	YBR255W	1	YBR255W/YBR1723	-0.009	unk		biological	process unknown	molecular function unknown	His-rich