Table S3. A List of Hypoxia-Relocalized Non-mitochondrial Proteins that Recovered their Aerobic Locations in the Absence of Protein Synthesis*

ORF	Protein	Localization in air	Description
YIL034C	CAP2	actin	Beta subunit of the capping protein (CP) heterodimer (Cap1p and Cap2p)
YCR002C	CDC10	bud neck, cell periphery	Component of the septin ring of the mother-bud neck
YER145C	FTR1	cell periphery	High affinity iron permease
YKL051W	SFK1	cell periphery	Plasma membrane protein involved in the generation of phospholipid PI4P
YBR069C	TAT1	cell periphery, bud	Amino acid transport protein
YLL026W	HSP104	cytoplasm	Heat shock protein
YAL005C	SSA1	cytoplasm	Member of heat shock protein 70 (HSP70) family
YCR009C	RVS161	cytoplasm, actin	Amphiphysin-like lipid raft protein
YLL024C	SSA2	cytoplasm, nucleus	Member of heat shock protein 70 (HSP70) family
YPR173C	VPS4	endosome	AAA-ATPase involved in multivesicular body (MVB) protein sorting
YCL025C	AGP1	ER	Low-affinity amino acid permease (Ssy1p-Ptr3p-Ssy5p)
YKL096W-A	CWP2	ER	Covalently linked cell wall mannoprotein
YGR175C	ERG1	ER	Squalene epoxidase
YCR034W	FEN1	ER	Fatty acid elongase
YNL322C	KRE1	ER	Cell wall glycoprotein involved in beta-glucan assembly
YGR260W	TNA1	ER	High affinity nicotinic acid plasma membrane permease
YDL072C	YET3	ER	Protein of unknown function
YLL028W	TPO1	ER, cell periphery, bud	Polyamine transporter
YGR060W	ERG25	ER, vacuole	C-4 methyl sterol oxidase
YCR043C	YCR043C	Golgi	Putative protein of unknown function
YMR089C	YTA12	mitochondrion	Component, with Afg3p, of the mitochondrial inner membrane m-AAA protease
YKR082W	NUP133	nuclear periphery	Subunit of the Nup84p subcomplex of the nuclear pore complex (NPC)
YAR002W	NUP60	nuclear periphery	Subunit of the nuclear pore complex (NPC)
YJL061W	NUP82	nuclear periphery	Nucleoporin, subunit of the nuclear pore complex (NPC)
YDR174W	HMO1	nucleolus	Chromatin associated high mobility group (HMG) family member
YBR236C	ABD1	nucleus	Methyltransferase
YPR180W	AOS1	nucleus	Nuclear protein that activates Smt3p (SUMO)

YNR010W	CSE2	nucleus	Subunit of the RNA polymerase II mediator complex
YIL036W	CST6	nucleus	transcription factor of the ATF/CREB family
YEL018W	EAF5	nucleus	Subunit of the NuA4 acetyltransferase complex
YFL013C	IES1	nucleus	Subunit of the INO80 chromatin remodeling complex
YLR095C	IOC2	nucleus	Member of a complex (Isw1b) with Isw1p and Ioc4p
YDL087C	LUC7	nucleus	Essential protein associated with the U1 snRNP complex
YPR144C	NOC4	nucleus	Nucleolar protein that mediates maturation and nuclear export of 40S ribosomal sub
YOL115W	PAP2	nucleus	Catalytic subunit of TRAMP involved in RNA quality control
YNL282W	POP3	nucleus	Subunit of both RNase MRP and nuclear RNase P
YDR195W	REF2	nucleus	RNA-binding protein
YAR007C	RFA1	nucleus	Subunit of heterotrimeric Replication Protein A (RPA)
YNL290W	RFC3	nucleus	Subunit of heteropentameric Replication factor C (RF-C)
YHR197W	RIX1	nucleus	Essential component of the Rix1 complex (Rix1p, Ipi1p, Ipi3p)
YJL011C	RPC17	nucleus	RNA polymerase III subunit C17
YDR427W	RPN9	nucleus	Non-ATPase regulatory subunit of the 26S proteasome
YDR469W	SDC1	nucleus	Subunit of the COMPASS (Set1C) complex
YCL010C	SGF29	nucleus	Subunit of SAGA histone acetyltransferase complex
YHR206W	SKN7	nucleus	Transcription factor, part of a branched two-component signaling system
YGR074W	SMD1	nucleus	Core Sm protein Sm D1
YPL138C	SPP1	nucleus	Subunit of COMPASS (Set1C)
YBR152W	SPP381	nucleus	mRNA splicing factor
YER161C	SPT2	nucleus	Interacting with both histones and SWI-SNF components
YJL176C	SWI3	nucleus	Subunit of the SWI/SNF chromatin remodeling complex
YGR129W	SYF2	nucleus	Component of the spliceosome complex
YGL112C	TAF6	nucleus	Subunit (60 kDa) of TFIID and SAGA complexes
YDR311W	TFB1	nucleus	Subunit of TFIIH and nucleotide excision repair factor 3 complexes
YPL122C	TFB2	nucleus	Subunit of TFIIH and nucleotide excision repair factor 3 complexes
YDR079C-A	TFB5	nucleus	Component of TFIIH
YNL273W	TOF1	nucleus	Subunit of a replication-pausing checkpoint complex (Tof1p-Mrc1p-Csm3p)
YPL203W	TPK2	nucleus	cAMP-dependent protein kinase catalytic subunit
YDR165W	TRM82	nucleus	Subunit of a tRNA methyltransferase complex

YOR229W	WTM2	nucleus	Transcriptional modulator
YHR090C	YNG2	nucleus	Subunit of the NuA4 histone acetyltransferase complex
YPR107C	YTH1	nucleus	Essential RNA-binding component of cleavage and polyadenylation factor
YGR093W		nucleus	Putative debranching enzyme associated ribonuclease
YPR045C		nucleus	Protein of unknown function
YDL022W	GPD1	peroxisome	NAD-dependent glycerol-3-phosphate dehydrogenase
YGL153W	PEX14	peroxisome	Peroxisomal membrane peroxin
YDR329C	PEX3	peroxisome	Peroxisomal membrane protein (PMP)
YNL084C	END3	punctate composite	EH domain-containing protein
YGR086C	PIL1	punctate composite	Primary component of eisosomes
YDL192W	ARF1	punctate composite, Golgi to ER, Golgi to vacuole	ADP-ribosylation factor, GTPase of the Ras superfamily
YGL225W	VRG4	punctate composite, Golgi, Golgi to ER	Golgi GDP-mannose transporter
YKR083C	DAD2	spindle pole	Essential subunit of the Dam1 complex (aka DASH complex)
YKL042W	SPC42	spindle pole	Central plaque component of spindle pole body (SPB)
YGR055W	MUP1	vacuole	High affinity methionine permease
YMR297W	PRC1	vacuole	Vacuolar carboxypeptidase Y (proteinase C)
YIL117C	PRM5	vacuole	Pheromone-regulated protein

*Hypoxic cells were shifted to aerobic growth conditions in the presence or absence of the protein synthesis inhibitor cycloheximide for 2 hours. Non-mitochondrial proteins that recovered their aerobic locations in the presence of cycloheximide are listed here. Mitochondrial proteins are not listed since all but one recovered their positions in the presence of cycloheximide.