Upregulated High-Ribo		BY4741		EY0690	
Systematic Name	Name	mRNA	Ribo	mRNA	Ribo
YER067W	RGI1	6.7	0.6	4.6	-0.3
YLR327C	TMA10	5.9	2.9	6.0	0.9
YCR021C	HSP30	5.9	2.5	6.9	0.8
YDR277C	MTH1	5.1	1.3	3.6	-0.7
YGR142W	BTN2	5.0	2.0	5.2	0.6
YHR087W	RTC3	5.0	0.8	4.4	0.7
YKR075C		4.6	1.3	4.4	-0.4
YGR008C	STF2	4.5	1.9	2.9	0.2
YER150W	SPI1	4.2	0.9	4.6	0.2
YOL052C-A	DDR2	4.1	1.1	4.5	-0.1
YBR072W	HSP26	3.9	1.1	4.9	0.3
YLL026W	HSP104	3.8	0.7	3.1	0.3
YHL021C		3.7	1.3	3.7	-0.1
YGR243W	FMP43	3.7	2.2	3.0	0.7
YDR258C	HSP78	3.5	0.3	2.6	-0.2
YJL144W		3.5	3.2	5.2	-0.4
YGL255W	ZRT1	3.3	0.1	-0.9	0.0
YGL037C	PNC1	3.3	0.8	1.7	0.4
YMR120C	ADE17	3.3	0.1	-0.9	-0.1
YMR105C	PGM2	3.2	2.2	3.2	-0.9
YKL086W	SRX1	3.1	2.3	5.3	0.5
YML128C	MSC1	3.1	0.4	3.2	-0.2
YFL014W	HSP12	3.1	0.8	2.6	0.9
YKL109W	HAP4	3.1	0.7	1.8	-1.0
YOR173W	DCS2	3.0	0.6	3.3	-1.6
YMR104C	YPK2	2.9	0.3	2.6	-1.0
YLR177W		2.8	0.7	2.9	-1.5
YER103W	SSA4	2.8	1.1	4.9	-0.3
YPL240C	HSP82	2.8	0.1	2.2	0.1
YBL078C	ATG8	2.8	0.8	2.2	1.1
YHR097C		2.7	0.4	2.9	-0.1
YNR014W		2.7	1.3	2.4	0.1
YMR280C	CAT8	2.6	3.2	3.5	-0.2

Upregulated Low-Ribo		BY4741		EY0690	
Systematic Name	Name	mRNA	Ribo	mRNA	Ribo
YKL217W	JEN1	6.0	-1.6	5.6	-1.5
YFR015C	GSY1	6.0	-1.7	3.7	-2.6
YDR171W	HSP42	5.8	-2.0	4.7	-1.5
YFR053C	HXK1	5.5	-1.9	3.5	-1.3
YEL011W	GLC3	5.5	-1.8	5.0	-2.7
YGR249W	MGA1	5.1	-1.8	5.4	-2.2
YDR342C	HXT6	4.2	-1.4	3.2	-0.1
YPR160W	GPH1	4.2	-1.8	3.6	-2.0
YGL205W	POX1	4.1	-1.3	2.8	-1.8
YGR088W	CTT1	3.9	-1.0	4.4	-1.2
YLR258W	GSY2	3.3	-1.1	1.4	-1.1
YMR303C	ADH2	3.0	-1.1	0.3	0.7
YJL052W	TDH1	2.9	-1.5	2.7	-1.3
YDL021W	GPM2	2.9	-1.6	2.2	0.7
YDR453C	TSA2	2.8	-1.9	2.9	0.3
YOL032W	OPI10	2.8	-1.5	2.7	-2.4
YHR092C	HXT4	2.7	-1.5	1.9	-0.2
YCR091W	KIN82	2.6	-2.1	2.9	-1.9
YBR147W	RTC2	2.5	-2.9	3.0	-2.6

Upregulated		BY4741		EY0690	
Systematic Name	Name	mRNA	Ribo	mRNA	Ribo
YLR149C		3.8	-0.8	3.5	-1.2
YDR516C	EMI2	3.6	-0.3	2.7	0.1
YGR043C	NQM1	3.6	-0.5		
YDL048C	STP4	3.6	-0.4	1.8	-1.5
YLR142W	PUT1	3.5	-0.4	3.2	0.1
YCL042W	Vnx1	3.2	-0.9	2.4	-1.2
YNL077W	APJ1	3.1	-0.4	3.2	-0.7
YBR214W	SDS24	3.1	0.1	2.4	-1.0
YAL054C	ACS1	3.0	-0.1	1.7	1.2
YML100W	TSL1	2.9	0.0	2.2	-1.1
YCL040W	GLK1	2.9	-0.3	2.1	-1.1
YOR019W		2.9	-0.7	3.0	-0.2
YBR169C	Rrp43	2.9	-0.9	3.1	-1.5
YMR011W	HXT2	2.7	0.0	3.9	0.2
YMR250W	Tdp1	2.7	-0.9	2.2	-2.5
YNL009W	IDP3	2.6	-0.5		
YPL123C	RNY1	2.6	-0.5	1.6	0.5
YPL186C	UIP4	2.6	-0.3		
YIL101C	XBP1	2.5	-0.4	2.2	-0.5

SupplementaryTable 1 | mRNAs upregulated during glucose starvation have differences in ribosome occupancy. Fold-change in mRNA levels and in ribosome occupancy after 15 minutes of glucose starvation from one measurement of BY4741 and one measurement of EY0690 on total non-polyA selected mRNA. mRNA upregulated, higher ribosome occupancy genes (mRNA>2.5, Ribo>0.09, pink), mRNA upregulated, lower ribosome occupancy genes (mRNA>2.5, Ribo<-1.0, blue), mRNA upregulated (mRNA>2.5, -1.0<Ribo<-0.09, white). mRNA upregulated, higher ribosome occupancy EY0690 (mRNA>2.5, Ribo>-0.5, pink), mRNA upregulated, lower ribosome occupancy EY0690 (mRNA>2.5, Ribo < -1.0, blue), mRNA upregulated (mRNA>2.5, -1<Ribo<-0.5, white) and not upregulated (T<2.5, grey). The cutoff for higher ribosome occupancy was set by the median ribosome occupancy of all genes (BY4741 = 0.09, EY0690 = -0.5). mRNA = log2 mRNA fold change for glucose starvation vs. log-phase glucose-rich. Ribo = log2 ribosome occupancy fold change for glucose starvation vs. log-phase glucose-rich.

Strain Number	Genotype
EY2536	BY4741
EY0690	W303
EY2888	W303, P_{MYO2}*-MS2-CP-GFP(3x)::HIS3, DCP2-mRFP1.3::KanMX6*
EY2889	EY2888, *PUTR*$_{PGK1(-600-0)}$*PGK1-MS2-ADH1_3'UTR::LEU2*
EY2890	EY2888, *PUTR*$_{PDC1(-898-0)}$*PDC1-MS2-ADH1_3'UTR::LEU2*
EY2891	EY2888, *PUTR*$_{GLC3(-396-0)}$*GLC3-MS2-ADH1_3'UTR::LEU2*
EY2892	EY2888, *PUTR*$_{HXK1(-940-0)}$*HXK1-MS2-ADH1_3'UTR::LEU2*
EY2893	EY2888, *PUTR*$_{HSP26(-604-0)}$*HSP26-MS2-ADH1_3'UTR::LEU2*
EY2894	EY2888, *PUTR*$_{HSP30(-1010-0)}$*HSP30-MS2-ADH1_3'UTR::LEU2*
EY2895	EY2888, *PUTR*$_{PGK1(-600-0)}$*PGK1-MS2-ADH1_3'UTR::LEU2, PAB1-CFP::URA3*
EY2896	EY2888, *PUTR*$_{GLC3(-396-0)}$*GLC3-MS2-ADH1_3'UTR::LEU2, PAB1-CFP::URA3*
EY2897	EY2888, P_{TetO7}*-lacZ-MS2-ADH1_3'UTR::LEU2*, P_{ERV14}*-rtTA(S2)::URA3*
EY2898	EY2888, *PUTR*$_{HSP30(-1010-0)}$*CFP-MS2-ADH1_3'UTR::LEU2*
EY2899	EY2888, *PUTR*$_{HSP26(-604-0)}$*CFP-MS2-ADH1_3'UTR::LEU2*
EY2900	EY2888, *PUTR*$_{GLC3(-396-0)}$*CFP-MS2-ADH1_3'UTR::LEU2*
EY2901	EY2888, *PUTR*$_{HXK1(-940-0)}$*CFP-MS2-ADH1_3'UTR::LEU2*
EY2902	EY2888, $P_{HSP26(-604--39)}$*UTR*$_{GLC3(-32-0)}$*CFP-MS2-ADH1_3'UTR::LEU2*
EY2903	EY2888, $P_{GLC3(-396--32)}$*UTR*$_{HSP26(-39-0)}$*CFP-MS2-ADH1_3'UTR::LEU2*
EY2904	EY2888, $P_{HXK1(-940--105)}$*UTR*$_{HSP26(-39-0)}$*CFP-MS2-ADH1_3'UTR::LEU2*
EY2905	EY2888, Chim1*PUTR*$_{HSP26(-694--448)}$*)*$_{\mathrm{GLC3(-263-0)}}$*CFP-MS2-ADH1_3'UTR::LEU2*
EY2906	EY2888, Chim2*PUTR*$_{HSP26(-694--317)}$*)*$_{\mathrm{GLC3(-202-0)}}$*CFP-MS2-ADH1_3'UTR::LEU2*
EY2907	EY2888, Chim3*PUTR*$_{GLC3(-397--245)}$*)*$_{\mathrm{HSP26(-407-0)}}$*CFP-MS2-ADH1_3'UTR::LEU2*
EY2908	EY2888, Chim4*PUTR*$_{GLC3(-397--202)}$*)*$_{\mathrm{HSP26(-316-0)}}$*CFP-MS2-ADH1_3'UTR::LEU2*
EY2909	EY2888, P_{STRE}*CFP-MS2-ADH1_3'UTR::LEU2*
EY2910	EY2888, $P_{STRE+HSE}$*CFP-MS2-ADH1_3'UTR::LEU2*
Open Biosystems	BY4741, *HSP30::TAP::HIS3*
Open Biosystems	BY4741, *HSP26::TAP::HIS3*
Open Biosystems	BY4741, *GLC3::TAP::HIS3*
Open Biosystems	BY4741, *GSY1::TAP::HIS3*
Open Biosystems	BY4741, *RPB3::TAP::HIS3*

Supplementary Table 2 | Yeast strains used in this study

Primer	Sequence
*ACT1*_F	CTGCCGGTATTGACCAAACT
*ACT1*_R	CGGTGATTTCCTTTTGCATT
*PGK1*_F	GGACAAGCGTGTCTTCATCA
*PGK1*_R	CGTTTCTTTCACCGTTTGGT
*PDC1*_F	GGCAATACCGTTCAAAGCAG
*PDC1*_R	CTTACGCCGCTGATGGTTAC
*CDC19*_F	CACCACCGATGACAAGTACG
*CDC19*_R	CTTGTCGTCAACGACTTCCA
*PGI1*_F	ACAACCACTTCACCCAAACC
*PGI1*_R	TTGCAAGTAGGCTGGGAATC
*HSP30*_F	CAATCCGGAAACCAAAGAAA
*HSP30*_R	CGAAATCGCCGTTAGGTAAA
*HSP26*_F	AAGGCGGCTTAAGAGGCTAC
*HSP26*_R	ATCATAAAGAGCGCCAGCAT
*HSP104*_F	CGACGCTGCTAACATCTTGA
*HSP104*_R	CACTTGGTTCAGCGACTTCA
*HSP12*_F	CGAAAAAGGCAAGGATAACG
*HSP12*_R	TTGGTTGGGTCTTCTTCACC
*GLC3*_F	CAATCCGGAAACCAAAGAAA
*GLC3*_R	CGAAATCGCCGTTAGGTAAA
*GSY1*_F	GCCGCTGGTGATGTAGATTT
*GSY1*_R	GCAGTGATTTGCGACACAGT
*HXK1*_F	GTACCCAGCTTCCCAAAACA
*HXK1*_R	TTTGTAGCAATGGGACGACA
*GPH1*_F	TTCCCCAAGAAATCAAGTCAA
*GPH1*_R	TCATAAGCAGCCATGTCATCA
Telomeric_F	CCCAGGTACGAAACGCTAAG
Telomeric_R	ATAAGGTTGTCGACGGTTGC
*CFP*_F	GGTCACAAGTTCTCTGTTTCTG
*CFP*_R	CCAAGTCAAAGTAGTAACCAAAG
oTi225	pGATCGTCGGACTGTAGAACTCTGAACCTGTCGGTGGTCGCCGTATCATT/Sp18/CACTCA/Sp18/CAAGCAGAAGACGGCATACGATTTTTTTTTTTTTTTTTTTVN
oTi9pA	pAGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTAGATCTCGGTGGTCGC/Sp18/CACTCA/Sp18/TTCAGACGTGTGCTCTTCCGATCTTTTTTTTTTTTTTTTTTTVN

Supplementary Table 3 | List of primers used for RT-qPCR, CHIP-qPCR and Ribosome profiling. ‘p’ designates 5’ phosphorylation, ‘Sp18’ designates a hexa-ethyleneglycol spacer, and ‘V’ ,’N’ indicate degenerate nucleotides.