

Supplementary Information

Table S1 Gene Ontology (GO) categories altered in *Saccharomyces cerevisiae* under various stress conditions (as predicted by STEM)

Nitrogen Depletion	Heat Shock	H ₂ O ₂	Cumulative	Alias	Function	Complex
YKL148C	YKL148C		YKL148C	SDH1	Succinate dehydrogenase flavoprotein subunit	ETC Complex II
YLL041C	YLL041C	YLL041C	YLL041C	SDH2	Succinate dehydrogenase	
YKL141W	YKL141W		YKL141W	SDH3	Succinate dehydrogenase cytochrome b	
YDR178W	YDR178W		YDR178W	SDH4	Succinate dehydrogenase anchor subunit	
YBL045C	YBL045C	YBL045C	YBL045C	COR1	Peptidase family M16	ETC Complex bc1
YHR001W- A		YHR001W- A	YHR001W- A	QCR10	Ubiquinol-cytochrome c oxidoreductase complex subunit	
YJL166W		YJL166W	YJL166W	QCR8	Ubiquinol--cytochrome-c reductase subunit VIII	
YGR183C		YGR183C	YGR183C	QCR9	Ubiquinol cytochrome-c reductase subunit 9	
	YEL024W		YEL024W	RIP1	Ubiquinol cyt.-c reductase iron- sulfur protein	
YGL191W			YGL191W	COX13		ETC Complex Cyt c oxidase
YJL003W		YJL003W	YJL003W	COX16		
YDR231C	YDR231C		YDR231C	COX20		
YGL187C			YGL187C	COX4		
YNL052W			YNL052W	COX5A		
YHR051W	YHR051W		YHR051W	COX6		
	YBL030C		YBL030C	PET9	ADP/ATP carrier protein	ADP ATP Exchange
	YMR056C		YMR056C	AAC1	ADP/ATP carrier protein	
	YNR001C	YNR001C	YNR001C	CIT1	Citrate synthase	TCA Cycle genes
	YLR304C	YLR304C	YLR304C	ACO1	Aconitate hydratase (aconitase)	
	YOR136W		YOR136W	IDH2	Isocitrate dehydrogenase	
	YIL125W		YIL125W	KGD1	Alpha-ketoglutarate dehydrogenase	
YDR148C	YDR148C	YDR148C	YDR148C	KGD2	2-oxoglutarate dehydrogenase	
YOR142W			YOR142W	LSC1	Succinyl-coa ligase alpha subunit	
	YGR244C	YGR244C	YGR244C	LSC2	Succinyl-coa ligase	
YKL085W	YKL085W	YKL085W	YKL085W	MDH1	Malate dehydrogenase	

Table S2 Gene Ontology (GO) categories altered in response to glucose starvation stress in *Schizosaccharomyces pombe*. The data was sourced from the diploma thesis “Global Transcriptional Responses of Fission Yeast to glucose starvation stress” authored by Michael Sassen, Department of Molecular Genetics and Microbiology, Stony Brook University, New York

Profile No.	GO No.	GO category	p-value	No. of Genes assigned
31	GO:0005739	Mitochondrion	0.001900	27
	GO:0031966	mitochondrial membrane	0.003300	11
	GO:0005740	mitochondrial envelope	0.009200	11
	GO:0005743	mitochondrial inner membrane	0.000570	11
	GO:0006118	electron transport	0.003100	9
	GO:0006811	ion transport	0.240000	5
30	GO:0042221	response to chemical stimulus	0.000014	12
	GO:0006950	response to stress	0.000057	19
29	GO:0005739	mitochondrion	0.060000	12
	GO:0006118	electron transport	0.010000	5
24	GO:0009060	aerobic respiration	0.000043	8
	GO:0005739	mitochondrion	0.120000	20
	GO:0031966	mitochondrial membrane	0.009800	10
	GO:0005740	mitochondrial envelope	0.003300	12
	GO:0005743	mitochondrial inner membrane	0.007100	9
	GO:0006118	electron transport	0.080000	6
17	GO:0005739	mitochondrion	0.004100	18
	GO:0031966	mitochondrial membrane	0.000008	12
	GO:0005743	mitochondrial inner membrane	0.000210	9
	GO:0006118	electron transport	0.040000	5

Table S3: List of genes and the corresponding primers for mitochondrial electron transport chain

Genes	Primer Name	Sequence 5' ----> 3'	Primer length	Primer Tm	Product Length
Complex I					
NDE1	NDE1F	ttttgggtgctaagggatct	20	58.65	163
	NDE1R	ttagcatgggtcattttcca	20	58.97	
NDE2	NDE2F	gaatgggacatgctcaacag	20	59.09	214
	NDE2R	aagcggatttccaaaacaag	20	59.20	
NDI1	NDI1F	gtgaaaggcagcaacaacat	20	58.78	243
	NDI1R	ggatcccagggtatgctaagg	20	58.48	
Complex II					
SDH1	SDH1F	attaacctgtgcctcccaaa	20	59.43	219
	SDH1R	acagttggagggtacggaagg	20	59.06	
SDH2	SDH2F	tcgtactgttggaaccaaga	20	59.13	204
	SDH2R	ttcagcaatagccaaaccag	20	58.92	
SDH3	SDH3F	aatgtggccagtgaatgaa	20	58.98	157
	SDH3R	taagcaccaacgaaatacgg	20	58.70	
SDH4	SDH4F	tatcccaattttgcccgtat	20	59.15	196
	SDH4R	atcagctgcagtggaataacg	20	58.90	
Complex III					
CYC1	CYC1F	ccggttctgctaagaaaggt	20	58.46	180
	CYC1R	cccacaacacgtttttcttg	20	59.07	
CYT1	CYT1F	ttgttgaccgggtatcctga	20	58.97	182
	CYT1R	aagggtgtaacgtcctttgc	20	59.10	
COR1	COR1F	tttatgggggttctctacgg	20	58.90	180
	COR1R	tcattgacgggattaccaga	20	58.92	
QCR2	QCR2F	tttgaagaagggcaaggact	20	58.91	170
	QCR2R	atggcaagttggaacatca	20	58.98	
QCR6	QCR6F	gataaccgttgtgcctgttg	20	59.05	164
	QCR6R	cttctcatcttctgctgca	20	58.96	
QCR7	QCR7F	gtgttcagttgccaatcag	20	59.14	221
	QCR7R	ctctgggctttgatccatt	20	59.13	
QCR8	QCR8F	gtgttccaaagcaaaaaggt	20	59.08	170
	QCR8R	accgttcttcaccagtacc	20	58.92	
QCR9	QCR9F	acgaaacgctgtttttgttg	20	58.87	164
	QCR9R	actcatcatcgtcgtctcca	20	59.21	
QCR10	QCR10F	tgcggtacactcttcatctg	20	57.41	150

	QCR10R	acttaggccatccttctgtga	21	58.80	
RIP1	RIP1F	gtcgggtctatgggtctttt	20	59.06	234
	RIP1R	caaagcggacatatccacac	20	59.00	
Table S3 continued...					
Genes	Primer Name	Sequence 5' ----> 3'	Primer length	Primer Tm	Product Length
Complex IV					
COX4	COX4F	aagccagccacaagaacttt	20	58.98	220
	COX4R	gtttggtgtcgaatacatcg	20	59.02	
COX5A	COX5AF	acgtctgtgtaatggatctg	20	58.90	230
	COX5AR	tagtaggcctgcagcaacac	20	59.10	
COX5B	COX5BF	cagaacgtcaaaagcttcca	20	59.05	172
	COX5BR	ccaaagagcccaaatgagat	20	59.13	
COX6	COX6F	acctggtgttatcatgcaa	20	59.15	206
	COX6R	caataacagcaggagcagga	20	59.02	
COX7	COX7F	cagaaaattctccaatttcca	22	58.30	155
	COX7R	gccttcttggctttgatacc	20	58.79	
COX8	COX8F	tgccaacagatgattagaacg	21	58.78	166
	COX8R	cgaagaacccgaaatgagat	20	59.13	
COX9	COX9F	gtccaattactgggtacgatca	22	59.11	165
	COX9R	ctcttgcttttctctcagc	21	58.47	
COX12	COX12F	atttcccaacaaaacaaa	20	59.15	152
	COX12R	cccatttttcgatccagtct	20	58.98	
COX13	COX13F	ccagataaagtggcagctca	20	59.02	164
	COX13R	tcagcatgctccttttcaac	20	59.00	
Complex V					
ATP1	ATP1F	tgccattaacgttggtttgt	20	58.94	151
	ATP1R	ggaggcatctaaatcggaac	20	58.60	
ATP2	ATP2F	tgtcgccgaagtctttactg	20	59.07	168
	ATP2R	gcggcttaactttcagcttt	20	58.79	
ATP3	ATP3F	taaagatgccccaaacttcc	20	59.02	193
	ATP3R	ctcaaatttgccgaatgatg	20	59.11	
ATP4	ATP4F	ccgatgcaagaatgaagaaa	20	58.84	172
	ATP4R	aaggcttcgcttcaagttc	20	58.72	
ATP5	ATP5F	cgtctgactttggcgtttta	20	58.96	171
	ATP5R	ctggcttaaccacgttttcc	20	59.61	
ATP7	ATP7F	tcgatgcctccaaacaatta	20	59.11	237
	ATP7R	caggtagctcccatttacc	20	59.17	
ATP14	ATP14F	accaccacaaaaaccaa	20	59.05	174
	ATP14R	ctttggtttctcagcatca	20	58.85	
ATP15	ATP15F	gcctggaggaaagctggtat	20	60.60	157
	ATP15R	aagctgcagtgccattttta	20	58.58	
ATP16	ATP16F	ttcccaccgttgaacaatta	20	58.87	219
	ATP16R	ccctggcatcagatgaacta	20	58.67	
ATP17	ATP17F	gcgcattgctaattgtgttc	20	59.33	150
	ATP17R	cctagagcaaaatgccacaa	20	58.92	
TIM11	TIM11F	caggcacagtacgaggagaa	20	59.03	178
	TIM11R	aagcttccttcagggaattca	20	58.86	

Table S4: List of genes involved in the Iron and Copper transport and their corresponding primers

Genes	Primer Name	Sequence 5' ----> 3'	Primer length	Primer Tm	Product Length
Ferrireductase					
FRE1	FRE1F	ctgggtccagtgttgaggac	20	58.11	179
	FRE1R	cccgcagggaataaaaggtaa	20	59.07	
FRE2	FRE2F	caacaggatgagaaggctga	20	58.96	212
	FRE2R	gcggtttcattcctcacttt	20	59.17	
FRE6	FRE6F	atggcgatcaaaaatccttc	20	58.98	183
	FRE6R	gaagcttgtcagttcgggtca	20	59.01	
FRE7	FRE7F	ttggactgggtggaagaca	20	58.98	185
	FRE7R	tcactggcgggtgtctattgt	20	59.17	
High-Affinity Fe Transport					
FET3	FET3F	agcatgccttcattcctacc	20	59.15	204
	FET3R	cctgacgcctcttcattttca	20	59.00	
FTR1	FTR1F	caaccagaaactggacaatg	20	58.98	199
	FTR1R	tcctgggttcaagtgtttca	20	59.11	
Siderophore Fe Transport					
ARN1	ARN1F	catggcgacagttacagctt	20	58.95	157
	ARN1R	tggagattcgtaggcagttg	20	58.87	
ARN2	ARN2F	gacctggctacagcagcata	20	59.05	151
	ARN2R	ggaacatagggcgtgaaaat	20	59.19	
ARN4	ARN4F	cggctctagttagggatgg	20	58.81	188
	ARN4R	cagtaaaagccacgcagaanaa	20	59.11	
FIT1	FIT1F	ctagggatgcccaatctgtt	20	59.01	166
	FIT1R	cccgtgtaattcacgatttg	20	58.89	
SIT1	SIT1F	caagcatccgctaanaactca	20	59.06	169
	SIT1R	ctgtgcagctaagggttga	20	59.07	
Low-Affinity Fe Transport					
FET4	FET4F	ccgaatcgttcaacatgaag	20	59.12	232
	FET4R	caaaccggaagcaatacaaaa	20	58.67	
FET5	FET5F	aggccgatgggtgagagatac	20	59.12	152
	FET5R	acgggtgcctcaataaagac	20	59.06	
High Affinity Cu Transport					
CTR1	CTR1F	aagaggtgggacatccaaag	20	58.99	243
	CTR1R	tcctgagctctgtggcacaat	20	59.26	
CTR3	CTR3F	actcgccagaggagtacgtt	20	58.97	171
	CTR3R	ctggctcgttcaatctcctt	20	59.43	
Low Affinity Cu Transport					
CTR2	CTR2F	atatcaagaccctgcctgga	20	59.51	200
	CTR2R	tgagaatcccacttgcaaac	20	58.70	
Cu Chaperones & Related genes					
ATX1	ATX1F	aatgtcgtcatgacctgctc	20	58.67	174
	ATX1R	aacttccfttccggttttctt	21	58.31	
CCC2	CCC2F	gctcggtcagtgctgttcta	20	59.04	178
	CCC2R	attagtccggcctgtgattc	20	59.01	
COX17	COX17F	gtcgaggacaaacctaaagc	20	59.88	153
	COX17R	ggaacttcgaagccataacc	20	58.65	
CCS1	CCS1F	gtgggaagacctttctgagc	20	58.87	223
	CCS1R	gccaaaggcatcttttctctc	20	59.01	

Table S5 MAPPFinder results for genes in GO categories altered in various experimental conditions. (a) Calorie restriction (b) *Hxk2* deletion (c) Hap4 over-expression (d) Nitrogen depletion (e) H₂O₂ (f) Heat Shock

(a)

Gene Ontology		Number changed	Number measured	Number in GO	% Changed	% Present
GO ID	GO Term					
45333	cellular respiration	28	94	98	29.78723	95.91837
5739	mitochondrion	200	928	967	21.55172	95.96691
5740	mitochondrial envelope	57	195	211	29.23077	92.41706
31966	mitochondrial membrane	51	171	187	29.82456	91.44385
5743	mitochondrial inner membrane	44	143	158	30.76923	90.50633
5746	mitochondrial electron transport chain	11	25	30	44	83.33334
15075	ion transporter activity	46	140	153	32.85714	91.50327
46873	metal ion transporter activity	17	44	44	38.63636	100
16209	antioxidant activity	4	18	18	22.22222	100

(b)

Gene Ontology		Number changed	Number measured	Number in GO	% Changed	% Present
GO ID	GO Term					
45333	cellular respiration	57	94	98	60.6383	95.91837
5739	mitochondrion	362	928	967	39.00862	95.96691
5740	mitochondrial envelope	98	195	211	50.25641	92.41706
31966	mitochondrial membrane	87	171	187	50.87719	91.44385
5743	mitochondrial inner membrane	77	143	158	53.84615	90.50633
5746	mitochondrial electron transport chain	22	25	30	88	83.33334
15075	ion transporter activity	66	140	153	47.14286	91.50327
46873	metal ion transporter activity	20	44	44	45.45454	100
16209	antioxidant activity	7	18	18	38.88889	100

(c)

Gene Ontology		Number changed	Number measured	Number in GO	% Changed	% Present
GO ID	GO Term					
45333	cellular respiration	54	94	98	57.44681	95.91837
5739	mitochondrion	436	924	967	47.18615	95.55326
5740	mitochondrial envelope	104	194	211	53.60825	91.94313
31966	mitochondrial membrane	95	170	187	55.88235	90.90909
5743	mitochondrial inner membrane	81	142	158	57.04226	89.87342
5746	mitochondrial electron transport chain	21	25	30	84	83.33334
15075	ion transporter activity	72	140	153	51.42857	91.50327
46873	metal ion transporter activity	17	44	44	38.63636	100
16209	antioxidant activity	11	18	18	61.11111	100

(d)

Gene Ontology		Number changed	Number measured	Number in GO	% Changed	% Present
GO ID	GO Term					
45333	cellular respiration	61	94	98	64.89362	95.91837
5739	mitochondrion	407	933	967	43.62272	96.48397
5740	mitochondrial envelope	109	196	211	55.61224	92.891
31966	mitochondrial membrane	95	172	187	55.23256	91.97861
5743	mitochondrial inner membrane	83	144	158	57.63889	91.13924
5746	mitochondrial electron transport chain	23	25	30	92	83.33334
15075	ion transporter activity	70	140	153	50	91.50327
46873	metal ion transporter activity	21	44	44	47.72727	100
16209	antioxidant activity	13	18	18	72.22222	100

(e)

Gene Ontology		Number changed	Number measured	Number in GO	% Changed	% Present
GO ID	GO Term					
45333	cellular respiration	47	94	98	50	95.91837
5739	mitochondrion	375	933	967	40.19292	96.48397
5740	mitochondrial envelope	85	196	211	43.36735	92.891
31966	mitochondrial membrane	70	172	187	40.69767	91.97861
5743	mitochondrial inner membrane	61	144	158	42.36111	91.13924
5746	mitochondrial electron transport chain	15	25	30	60	83.33334
15075	ion transporter activity	41	140	153	29.28572	91.50327
46873	metal ion transporter activity	16	44	44	36.36364	100
16209	antioxidant activity	16	18	18	88.88889	100

(f)

Gene Ontology		Number changed	Number measured	Number in GO	% Changed	% Present
GO ID	GO Term					
45333	cellular respiration	44	94	98	46.80851	95.91837
5739	mitochondrion	284	933	967	30.43944	96.48397
5740	mitochondrial envelope	68	196	211	34.69388	92.891
31966	mitochondrial membrane	59	172	187	34.30233	91.97861
5743	mitochondrial inner membrane	49	144	158	34.02778	91.13924
5746	mitochondrial electron transport chain	13	25	30	52	83.33334
15075	ion transporter activity	24	140	153	17.14286	91.50327
46873	metal ion transporter activity	6	44	44	13.63636	100
16209	antioxidant activity	10	18	18	55.55556	100