SUPPORTING INFORMATION

Multiplexed Sequence-Specific Capture of Chromatin and Mass Spectrometric Discovery of Associated Proteins

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SI Table S-1. Capture Oligonucleotide Sequences. The 5' ends are biotinylated. Red indicates toehold sequences that do not hybridize with targets.

Gene target	Capture Oligonucleotides Sequence (5'-3')
25S rDNA	GTTTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA
ARX1	CCCAGGTTAAATATTCTACAGGAATCGGTCTTGAACAA
	CCCAGGTTTCTGGTGGATGGTGCCCCGAAATAGATGAT
	CCCAGGTTCTGGCAGGCCAAAACGAAGGTATTGTTGCC
	CCCAGGTTTAGTAACTTTAGAAACCGTTGACTCTTACA
	CCCAGGTTGCTCGTGAATGTAATACCATCGTATTATGT
CTT1	AGTGTCACGACCAGACGGCCCTATCTTACTGCAAGACT
	AGTGTCACGGGTCTTCAACAATACTCCCGTCTTCTTCC
	AGTGTCACCCTTTGAGAAAATTTGGTACCATCACCCTA
	AGTGTCACGGCCCAATGAGTTACTACAATTTCGGTCCT
	AGTGTCACTTATTCATAATTATTCGTAATTATATCTCC
RPL30	TAACCAGGCGGAGTGTTTAAGAACCTACAGCTTATTCA
	TAACCAGGGATTAGCAAGAAGGCTTGGAATACAAACAT
	TAACCAGGAGAATCTATCAACCAAAAGTTGGCTTTGGT
	TAACCAGGTTGATCATCATTGCCGCTAACACTCCAGTT
	TAACCAGGACAACGAATTGGGTACTGCTGTCGGTAAGT

SI Table S-2. Release Oligonucleotide Sequences. Green indicates toehold sequences complementary to their capture toehold counterparts.

Gene target	Release Oligonucleotides Sequence (5'-3')
25S rDNA	TCCTCCGCTTATTGATATGCTTAAGTTCAGCGGGTAAAC
ARX1	TTGTTCAAGACCGATTCCTGTAGAATATTTAACCTGGG
	ATCATCTATTTCGGGGCACCATCCACCAGAAACCTGGG
	GGCAACAATACCTTCGTTTTGGCCTGCCAGAACCTGGG
	TGTAAGAGTCAACGGTTTCTAAAGTTACTAAACCTGGG
	ACATAATACGATGGTATTACATTCACGAGCAACCTGGG
CTT1	AGTCTTGCAGTAAGATAGGGCCGTCTGGTCGTGACACT
	AGGAAGAAGACGGGAGTATTGTTGAAGACCCGTGACACT
	TAGGGTGATGGTACCAAATTTTCTCAAAGGGTGACACT
	AGGACCGAAATTGTAGTAACTCATTGGGCCGTGACACT
	GGAGATATAATTACGAATAATTATGAATAAGTGACACT
RPL30	TGAATAAGCTGTAGGTTCTTAAACACTCCGCCTGGTTA
	ATGTTTGTATTCCAAGCCTTCTTGCTAATCCCTGGTTA
	ACCAAAGCCAACTTTTGGTTGATAGATTCTCCTGGTTA
	AACTGGAGTGTTAGCGGCAATGATGATCAACCTGGTTA
	ACTTACCGACAGCAGTACCCAATTCGTTGTCCTGGTTA

SI Table S-3. Primer and Probe Design of the 4 qPCR Assays.

qPCR Assays	Position	Sequence (5’-3’)
25S rDNA	Forward	TTAGTAACGGCGAGTGAAGC
	Reverse	CAAAGTTGCCCTCTCCAAAT
	Probe	TCTGGTACCTTCGGTGCCCGA
ARX1	Forward	TGCCGAAAGGGAATATAAGG
	Reverse	CCACTGTTAAATCCTTGGCA
	Probe	TTGGACAGAGTCCCATCAAGAAGCA
CTT1	Forward	CCATCACCCTAACGGAGAAT
	Reverse	TGGCTTGTAGAACGGAATCA
	Probe	TGAACAAGTTGCATTCAGTCCAACGA
RPL30	Forward	TTCCTGCTCTTGTGTTTGAGA
	Reverse	GCCTGTTGAAATGTAAACGATAA
	Probe	CCGTTCAAAGGATGCTTCTCCATGA

SUPPLEMENTARY EXPERIMENTAL METHODS.

A video tutorial of the main HyCCAPP procedure, from cell lysis to target release, is available on the YouTube platform (https://youtu.be/vN_jHLInSlk), or search "HyCCAPP Tutorial".

TCA Precipitation.

A volume of 320 µL 100% trichloroacetic acid (TCA) was added to one of each of the four released samples and the uncaptured lysate control. The samples were gently mixed, incubated on ice for 10 min, and centrifuged at 20,000 g at 4 ˚C for 20 min. The resulting supernatants were decanted from the pellets. During centrifugation, the second tubes of each samples and lysate were TCA precipitated as previously described and added to the pellet in the first tubes. This serial addition of each TCA precipitated release sample was repeated for all four tubes of each sample. TCA pellets were washed twice with 750 µL chilled acetone and centrifuged at 20,000 g at 4 ˚C for 5 min. Pellets were heated at 95 ˚C for 2 min to remove the residual acetone.

eFASP Procedure.

Filter units and eFASP (*J. Proteome Res.* 2014, *13*, 1885-1895) collection tubes were passivated by soaking in 5% Tween 20 overnight. Filter units and collection tubes were rinsed at least three times using nanopure water. Each pellet was resuspended in 810 µL eFASP exchange buffer (8 M Urea, 0.10% deoxycholic acid). 90 µL DNaseI reaction buffer and 1 µL DNaseI was added, and the samples were incubated at 37 ˚C for 10 min to degrade the remaining release oligonucleotides. A volume of 450 µL of each DNaseI treated samples was each transferred to a passivated filter unit, which was then inserted into an unpassivated tube, and centrifuged at 14,000 g at 15 ˚C for 10 min. The flowthrough was discarded and the rest of the sample was added into its respective filter unit and the centrifugation was repeated. A volume of 200 µL of exchange buffer was added in each filter unit, and the samples were centrifuged at 14,000 g at 15 ˚C for 10 min. The flowthrough was discarded. This washing step was repeated three times. Then 200 µL eFASP reducing buffer (8 M Urea, 20 mM dithiothreitol (DTT)) was added to each filter unit, and the samples were incubated at room temperature for 30 min. The samples were then centrifuged at 14,000 g at 15 ˚C for 10 min. Flowthrough was discarded again. A volume of 200 µL eFASP alkylation buffer (8 M urea, 50 mM iodoacetamide, 50mM ammonium bicarbonate) was added to each filter unit, and the samples were incubated at room temperature in the dark for 30 min. 15 µL DTT was added to each sample and incubated for 10 min. The samples were centrifuged again at 14,000 g at 15 ˚C for 10 min, and the flowthrough was discarded. 200 µL eFASP digestion buffer (1 M urea, 50mM ammonium bicarbonate, 0.1% deoxycholic acid) was added in each filter unit, and the samples were centrifuged at 14,000 g at 15 ˚C for 10 min. The flowthrough was discarded. This washing step was repeated three times. The filters were transferred to passivated collection tubes. A volume of 100 µL digestion buffer was added to each filter unit. Trypsin (0.4 µg) was added to capture samples, whereas 1 µg trypsin was added to lysate control. Tubes and filter units were wrapped in Parafilm®, and incubated at 37 ˚C overnight with no rotation. Following digestion, the Parafilm® was removed and the tubes were centrifuged at 14,000 g at 15 ˚C for 10 min. A volume of 50 µL of 50mM Ammonium Bicarbonate was added in each filter unit and centrifuged at 14,000 g at 15 ˚C for 10 min. This step was repeated twice. The flowthrough was transferred to new 1.7 mL low-retention tubes. A volume of 200 µL ethyl acetate and 200 µL 1% trifluoroacetic acid (TFA) was added to the samples, and were shaken for 1 min. Samples were centrifuged at 15,800 g at 15 ˚C for 2 min. The top layer was removed and discarded from each tube, and another 200 µL ethyl acetate were added, and shaken for 1 min. The samples were centrifuged again at 15,800 g at 15 ˚C for 2 min, and the top layer was removed. Samples were dried in a Savant SpeedVac™ Concentrator to dryness for about 150 min. Dry tube contents were dissolved in 180 µL 0.1% TFA and vortexed to mix.

C18 Solid-Phase Extraction.

Extraction pipette tips (Agilent Technologies, A57003100K, OMIX C18 tips) were activated by pipetting 180 µL 70% acetonitrile (ACN) up and down three times, and were washed in 0.1 TFA three times by pipetting and discarding 180 µL of 0.1% TFA. Each sample was pipetted up and down 3 times using the washed tip. Extraction tips were than washed in 0.1% TFA as previously described. Peptides were eluted from the tip by repeated (5×) aspiration of a 150 µL volume of 70% ACN with 0.1% TFA in a 600 µL low retention tube. Eluted samples were evaporated to dryness in the SpeedVac™ for about 50 min. Tube contents were reconstituted in 95:5 H_2O:ACN and 0.1% formic acid solution, 200 µL for lysate control, and 18 µL for capture samples. On the mass spectrometer, one technical replicate injection consisted of either 9 µL of each sample or 2 µL of control. Two technical replicates were performed for each sample.

MaxQuant.

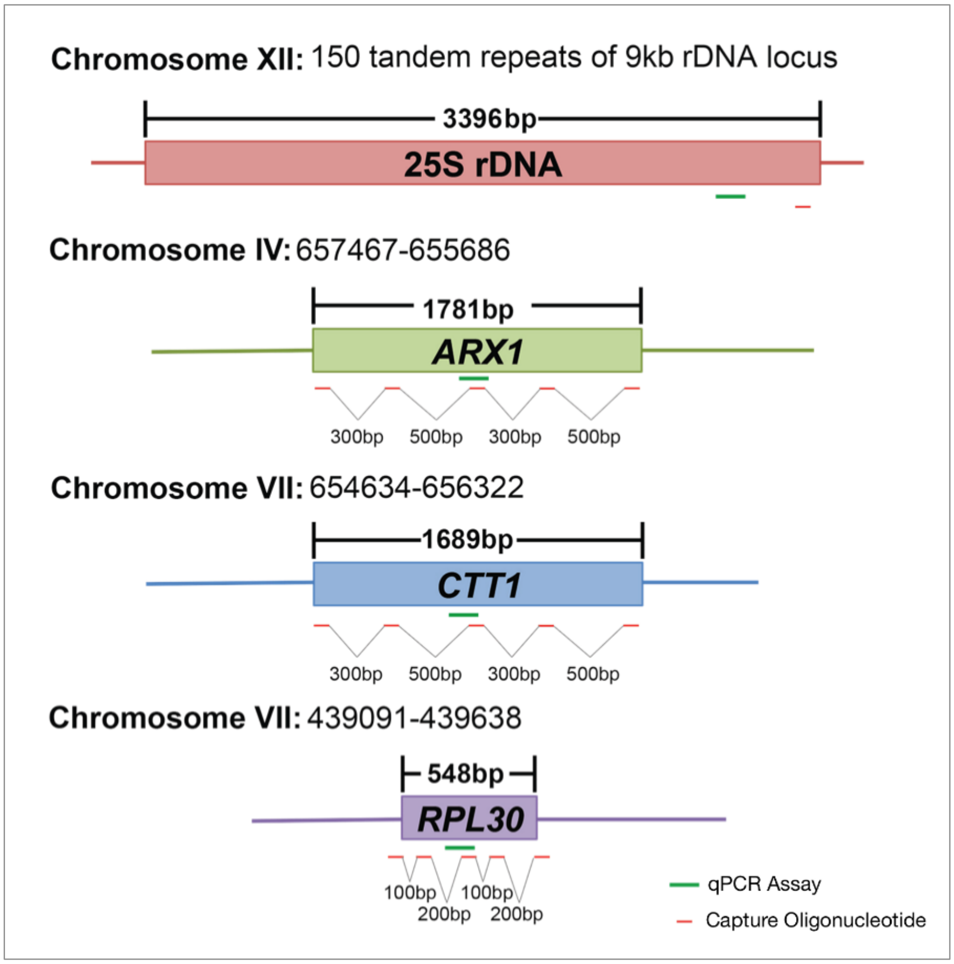
The 60 data files (in .raw) were loaded in MaxQuant (version 1.5.5.1). The two technical replicates were grouped into one experiment, resulting in 30 experiments. Spectra were searched against the *Saccharomyces cerevisiae* canonical protein database from UniProt, and a list of potential contaminants. Carbamidomethylation of cysteine was set as a fixed modification, and oxidation of methionine was set as a variable modification. First search peptide tolerance was set to 20 ppm. Main search was set to 4.5 ppm. Trypsin enzyme with 2 maximal missed cleavages was elected for the digestion mode. Match between runs function were enabled. A false discovery rate (FDR) of 1% was allowed for both peptides and proteins. The Label-Free Quantification (LFQ) algorithm was employed to assess relative quantification. Unique and razor peptides were used for quantification.

Perseus.

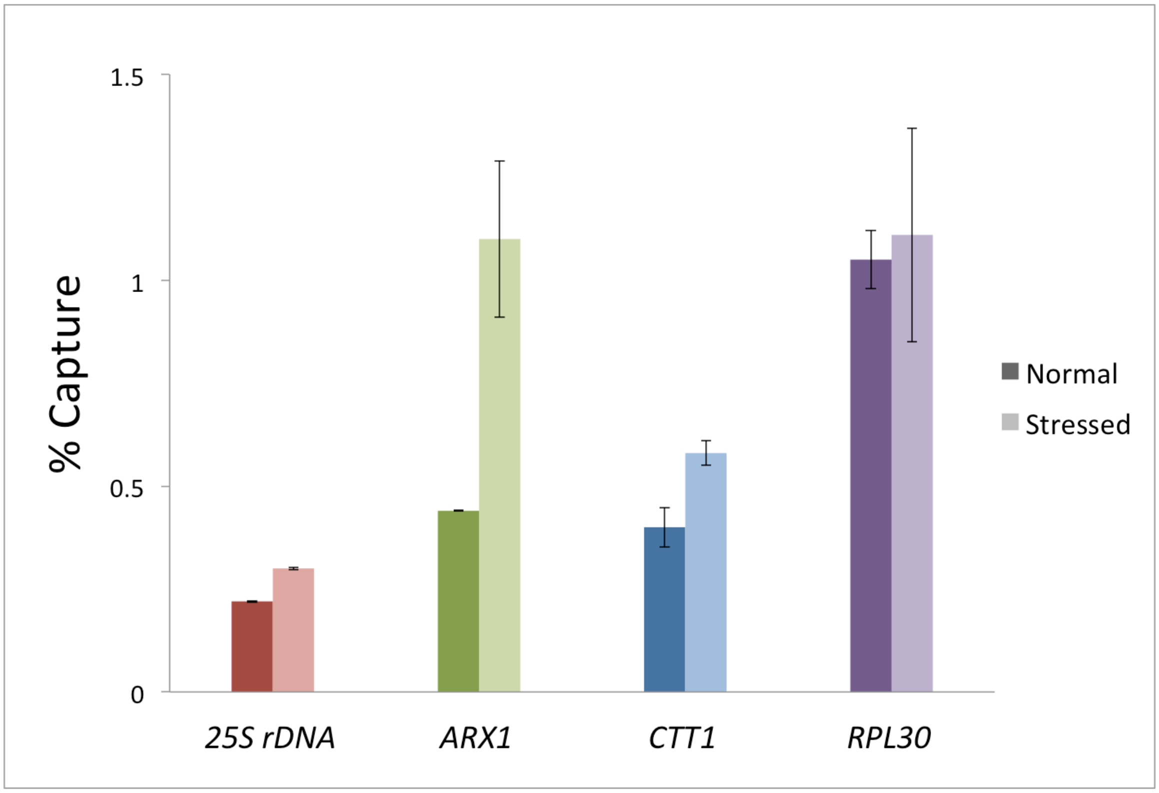
The output matrix file from MaxQuant was imported into Perseus (version 1.5.6.0). Proteins from the reverse database, proteins only identified by site, as well as contaminants were filtered out. LFQ intensity values were $\log_2(x)$ transformed. Experiments were grouped into categories of each gene capture or lysate. Protein lists were filtered to retain only the proteins with three observations in at least one group. Missing values were imputed from normal distribution (width = 0.3 standard deviations, downshift = 1.8 standard deviations) Two-sided Student's *t*-tests were performed to compare normal capture and lysate control. A permutation-based 1% FDR cutoff (s0 = 2) was used to select proteins with significant abundance difference. Perseus was used to prepare the protein heat map. Proteins filtered from the delta-percentile-rank analysis and their normalized average LFQ intensity for each sample and condition were made into a matrix and imported into Perseus. Values were $\log_2(x)$ transformed and the missing values were imputed from normal distribution (width = 0.15 standard deviations, downshift = 2.5 standard deviations). Hierarchical clustering was performed on the proteins (column) with Euclidean distance. A rainbow color gradient was used to show relative abundance. Column order was arranged in two different ways to show condition difference and also locus difference (Figure 2 and SI Figure S-5).

RAW DATA FILES.

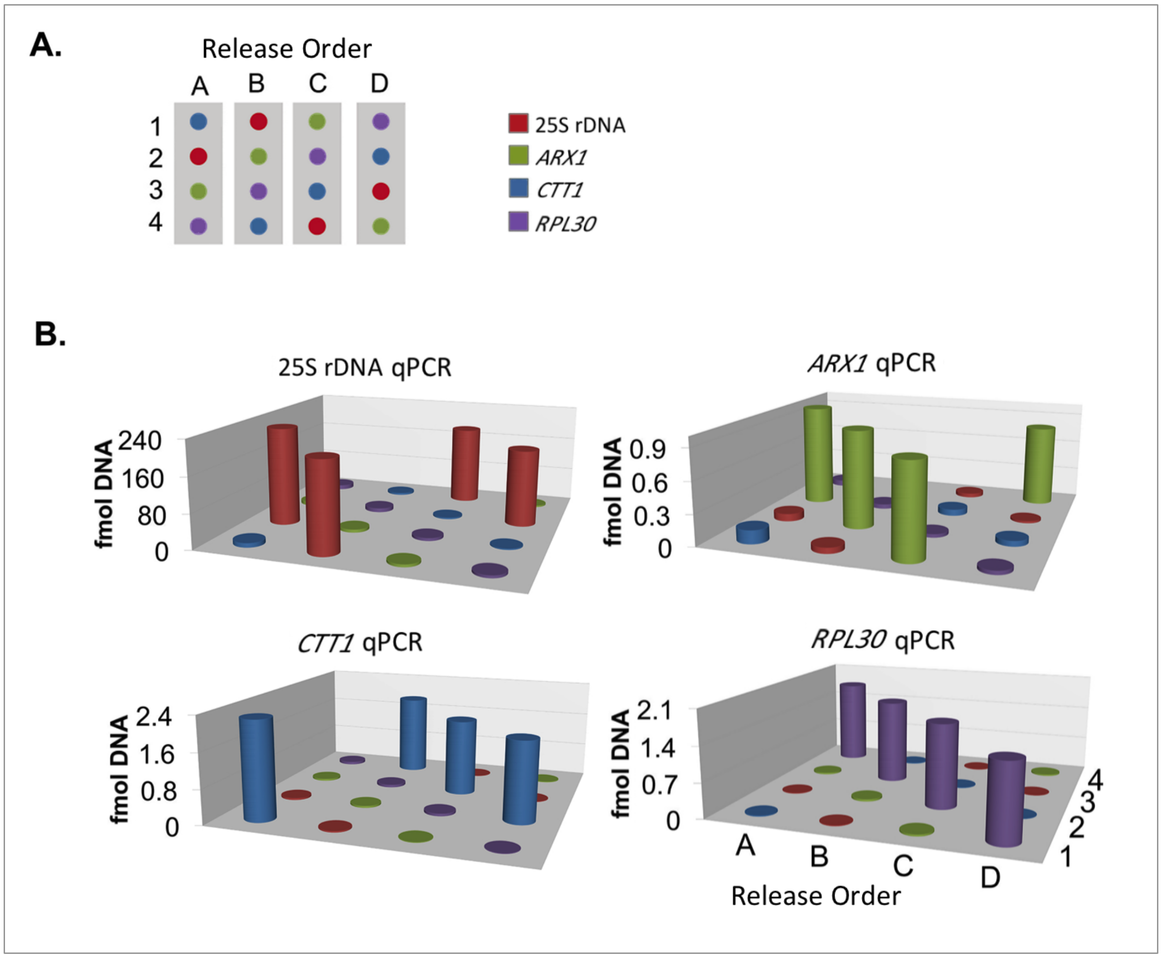
All 60 spectra files (in .raw format) from bottom-up proteomics (4 samples + 1 control, 2 growth conditions, 3 biological replicates with 2 technical replicates each) are available on the MassIVE platform (MSV000081066, ftp://massive.ucsd.edu/MSV000081066).



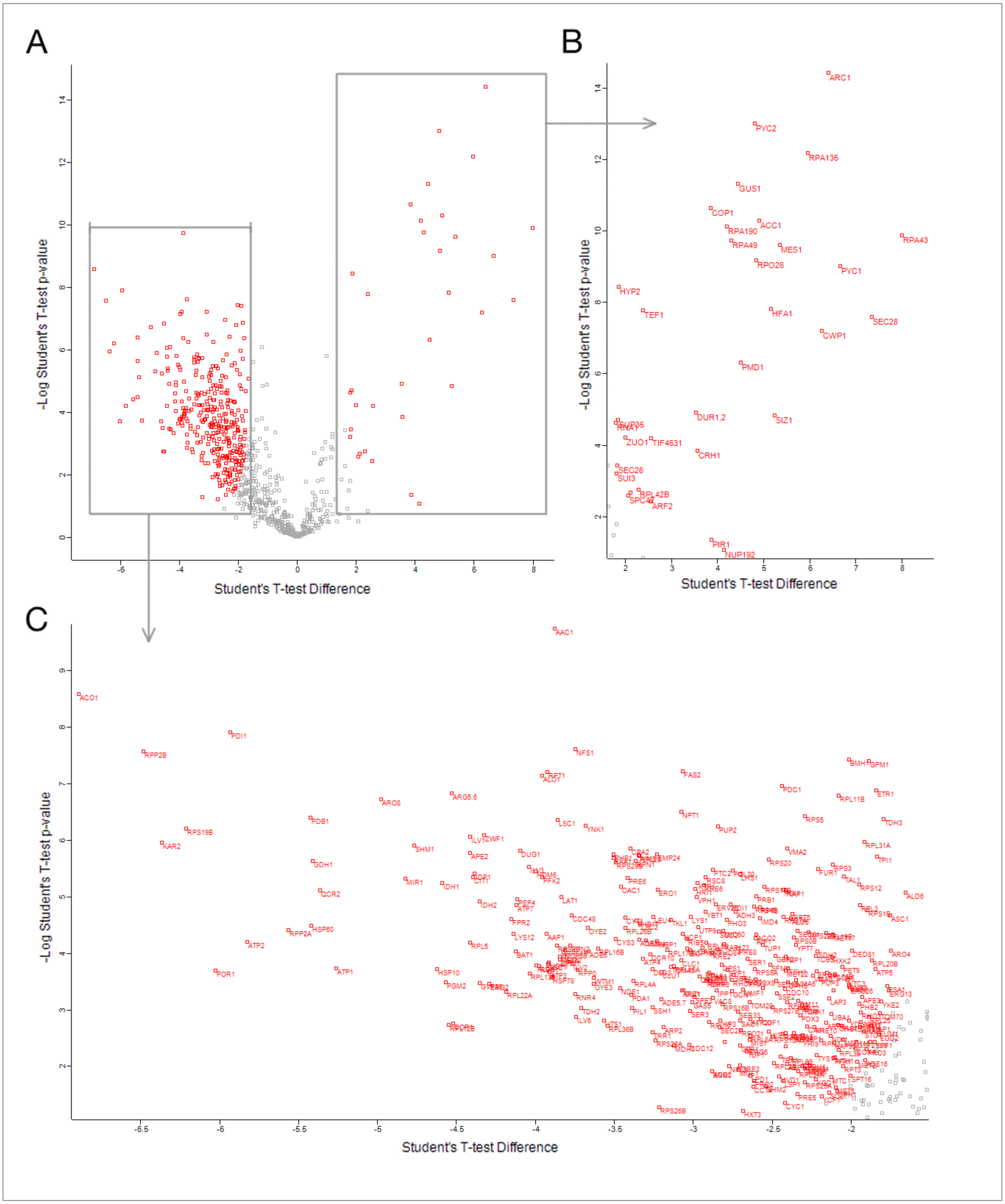
SI Figure S-1. Genomic sites for the capture oligonucleotides and qPCR assay in the 4 investigated loci.



SI Figure S-2. Capture efficiency of the 4 targeted sequences under normal and stressed conditions, calculated from qPCR results. The error bars represent standard deviations calculated from two qPCR measurements.



SI Figure S-3. Captured target and off-target sequence abundance from qPCR assays. Each set of toehold release oligonucleotides specifically releases its target at each step. Specificity was consistent regardless of adding release oligonucleotides in different orders.



SI Figure S-4. A. A volcano plot showing proteins enriched in pooled capture data under normal conditions, and proteins that are more abundant in uncaptured lysate, as revealed with a Student's *t*-test. B. Proteins enriched at normal condition captures. C. Proteins that are more abundant in uncaptured lysate.

SI Table S-4. Quantitative Data of the 161 Enriched Proteins. These were identified as enriched at one or more of the four loci. The values before "\|" are the corresponding relative abundances (percentile ranks). The values after are the log$_2$(x) transformed and normalized LFQs, which were used to generate heat maps (Figure 2, and Figure S-5). The proteins with "100 \| - -" were not found at the corresponding locus or condition, thus having the highest percentile rank "100", and a missing transformed LFQ value. The missing values were imputed from normal distribution (width = 0.15, downshift = 2.5) when making the heat maps in Perseus.

	Normal					Stressed				
Gene Names	25S	ARX1	CTT1	RPL30	Lysate	25S	ARX1	CTT1	RPL30	Lysate
ADE4	90.16 | 13.59	70.06 | 15.13	85.38 | 13.73	100 | - -	87.49 | 17.01	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -
ADE8	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	94.16 | 14.34	100 | - -	100 | - -
APA1	55.31 | 16.13	53.95 | 16.28	44.03 | 17.01	36.1 | 17.72	57.14 | 19.89	71.04 | 15.24	71.86 | 15.28	57.06 | 16.75	53.73 | 16.99	24.87 | 20.92
ARC1	0.31 | 25.96	0.3 | 26	0.31 | 25.89	0.46 | 25.85	17.54 | 23.12	0.39 | 25.27	0.3 | 25.35	0.75 | 25	0.78 | 25.04	18.02 | 22.05
ARC40	100 | - -	86.32 | 13.71	100 | - -	88.94 | 13.44	100 | - -	55.98 | 18.07	57.93 | 17.7	30.13 | 18.97	60.39 | 17.66	42.49 | 19
ARF2	44.53 | 16.94	45.14 | 16.83	36.64 | 17.64	42.24 | 17.04	100 | - -	100 | - -	67.37 | 15.6	100 | - -	100 | - -	65.56 | 17.58
ARG3	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	92.28 | 14.5	100 | - -	100 | - -
ARI1	59.69 | 15.77	43.16 | 16.96	37.42 | 17.52	50.08 | 16.55	60.99 | 19.66	50.19 | 16.67	45.66 | 17.07	77.21 | 15.83	100 | - -	36.04 | 19.88
ARL1	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	80.2 | 16.16	100 | - -
ATM1	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	89.41 | 14.71	100 | - -
ATP6	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	65.06 | 17.12	100 | - -	100 | - -	100 | - -	100 | - -
AUS1	100 | - -	100 | - -	83.81 | 13.96	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -
BDH1	100 | - -	100 | - -	100 | - -	81.72 | 14.29	100 | - -	100 | - -	100 | - -	93.22 | 13.5	91.76 | 13.77	100 | - -
BGL2	22.19 | 18.84	30.09 | 18.29	22.33 | 18.82	29.65 | 18.13	25.71 | 22.16	8.88 | 21.97	7.78 | 21.77	5.84 | 22.05	12.94 | 21.43	13.7 | 22.23
CCW14	49.38 | 16.53	53.19 | 16.32	98.74 | 11.98	68.97 | 15.09	96.26 | 15.68	26.83 | 19.14	15.42 | 20.49	15.44 | 20.21	21.37 | 20.31	100 | - -
CDC28	50.16 | 16.58	59.12 | 15.79	49.53 | 16.57	49.62 | 16.61	65.71 | 19.29	69.31 | 16.72	65.87 | 16.81	83.99 | 14.29	67.25 | 15.96	39.76 | 19.35
CDC33	37.19 | 17.7	34.95 | 17.73	36.48 | 17.63	36.41 | 17.65	34.09 | 21.4	34.56 | 18.03	23.5 | 19.79	44.26 | 17.68	51.57 | 17.3	33.44 | 20.16
CFT1	100 | - -	6.23 | 21.08	19.34 | 19.15	26.11 | 18.34	100 | - -	20.46 | 19.59	100 | - -	100 | - -	100 | - -	100 | - -
CIS3	43.75 | 16.81	54.71 | 16.2	48.27 | 16.6	56.99 | 15.96	100 | - -	100 | - -	45.81 | 17.37	100 | - -	41.76 | 18.33	100 | - -
CIT2	42.97 | 16.96	39.36 | 17.31	55.35 | 16.14	42.86 | 17.05	50.64 | 20.27	100 | - -	61.68 | 17.26	100 | - -	100 | - -	33.05 | 19.73
COP1	5.63 | 21.65	5.17 | 21.52	4.72 | 21.58	4.92 | 21.55	35.37 | 21.3	11.39 | 21.34	10.48 | 21.23	7.53 | 21.57	10.59 | 21.47	20.81 | 21.39
COX2	100 | - -	87.69 | 13.55	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -
CRH1	24.06 | 18.74	41.64 | 17.03	40.88 | 17.23	33.64 | 17.84	100 | - -	29.54 | 18.78	25.6 | 19.49	17.33 | 20.03	37.06 | 18.92	60.24 | 18.2
CWP1	6.41 | 21.18	11.09 | 20.07	7.55 | 20.67	8.76 | 20.41	100 | - -	2.51 | 23.34	2.99 | 22.81	2.45 | 23.37	4.9 | 22.6	53.32 | 18.73
DAP1	72.19 | 15.11	100 | - -	75.31 | 14.84	64.21 | 15.7	77.04 | 18.29	78.19 | 14.86	76.5 | 14.94	100 | - -	100 | - -	52.26 | 18.79
DBP3	61.88 | 15.68	72.34 | 14.97	55.19 | 16.23	63.59 | 15.62	61.67 | 19.66	19.5 | 21.51	48.2 | 18.5	88.51 | 13.94	36.08 | 19.42	60.84 | 18.14
DCP2	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	91.17 | 13.57	100 | - -	100 | - -	100 | - -
DEF1	100 | - -	76.29 | 14.67	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -
DUR1,2	25.31 | 18.69	34.5 | 17.82	27.67 | 18.39	28.88 | 18.32	74.78 | 18.45	55.41 | 16.37	58.83 | 15.84	61.77 | 16.52	67.84 | 16.1	57.98 | 17.85
ECM33	70.94 | 14.92	59.42 | 15.76	50.16 | 16.55	48.39 | 16.67	52.02 | 20.25	42.28 | 17.58	38.92 | 18.58	23.92 | 19.48	46.47 | 18.37	50.13 | 19.01
EMW1	86.09 | 13.92	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	68.48 | 16.19
END3	65.78 | 15.39	89.36 | 13.45	56.45 | 16.22	79.11 | 14.51	78.62 | 18.06	100 | - -	100 | - -	83.43 | 15.24	88.04 | 14.89	56.65 | 18
ENT3	72.81 | 15.09	16.26 | 19.58	74.37 | 14.92	31.03 | 18.16	83.74 | 17.63	46.14 | 18.49	47.46 | 18.37	81.73 | 14.53	85.69 | 14.33	18.62 | 20.99
ERG3	86.88 | 14.08	100 | - -	100 | - -	77.11 | 14.69	100 | - -	100 | - -	88.02 | 13.96	100 | - -	100 | - -	76.46 | 16.58
ERV29	62.81 | 15.72	100 | - -	69.18 | 15.36	75.73 | 14.8	78.72 | 18.11	100 | - -	62.72 | 17.39	52.73 | 17.12	100 | - -	42.29 | 18.93
ETT1	100 | - -	77.96 | 14.53	96.86 | 12.46	100 | - -	98.13 | 14.73	100 | - -	98.8 | 12.04	98.31 | 13.25	100 | - -	31.65 | 19.45
FCY1	62.5 | 15.58	85.87 | 13.74	63.52 | 15.62	75.42 | 14.75	75.86 | 18.35	100 | - -	85.78 | 14.16	100 | - -	100 | - -	59.84 | 17.5
FOL2	84.06 | 14.28	100 | - -	92.3 | 13.35	90.48 | 13.61	100 | - -	100 | - -	89.07 | 13.79	100 | - -	100 | - -	100 | - -
FPR4	43.91 | 16.84	47.26 | 16.69	40.09 | 17.18	50.54 | 16.52	68.87 | 19.12	100 | - -	100 | - -	100 | - -	100 | - -	57.25 | 18.42
FRD1	65.31 | 15.38	92.1 | 13.09	82.23 | 14.28	60.52 | 15.87	71.53 | 18.76	80.69 | 14.65	82.19 | 14.43	68.17 | 16.34	75.88 | 15.94	26.93 | 20.18
FRS2	49.53 | 16.62	48.18 | 16.64	47.33 | 16.79	46.08 | 16.86	57.93 | 19.83	76.25 | 15	50.15 | 18	83.05 | 15.24	82.16 | 15.39	26.86 | 20.39
GAS3	36.72 | 17.68	56.84 | 15.96	51.73 | 16.35	58.99 | 15.98	62.76 | 19.57	59.46 | 16.43	43.56 | 18.32	34.46 | 18.46	62.35 | 16.61	43.42 | 19.09
GCS1	41.56 | 17.14	45.59 | 16.82	42.61 | 17.06	44.39 | 16.99	53.89 | 20.07	75.68 | 15.03	69.31 | 14.65	66.85 | 15.97	82.35 | 14.64	47.61 | 18.63
GFA1	24.69 | 18.73	28.57 | 18.43	23.74 | 18.81	22.73 | 18.87	35.07 | 21.32	32.24 | 19.24	22.46 | 20.48	35.03 | 18.38	28.43 | 19.46	11.77 | 22.46
GLN1	20.78 | 19.02	22.49 | 18.92	21.86 | 18.93	19.66 | 19.13	33.89 | 21.42	43.05 | 17.47	24.25 | 20.14	36.53 | 18.48	39.41 | 18.29	23.01 | 20.95
GLO3	58.28 | 16.01	67.63 | 15.32	77.52 | 14.5	65.44 | 15.56	91.43 | 16.54	100 | - -	100 | - -	100 | - -	100 | - -	87.57 | 15.59
GPD2	59.84 | 15.82	61.55 | 15.72	63.36 | 15.63	51.15 | 16.6	67.29 | 19.19	58.88 | 16.48	55.24 | 16.57	78.72 | 14.81	80.39 | 14.79	34.18 | 20.29
GPM2	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	86.98 | 15.39	100 | - -	100 | - -	100 | - -
GSP1; GSP2	8.44 | 20.79	10.03 | 20.29	7.86 | 20.63	7.22 | 20.78	18.42 | 22.98	22.78 | 19.41	15.12 | 20.77	18.83 | 19.96	19.22 | 20.05	11.7 | 22.82
HAS1	100 | - -	66.11 | 15.48	34.91 | 17.7	100 | - -	100 | - -	21.24 | 21.31	100 | - -	100 | - -	100 | - -	100 | - -
HCH1	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	93.53 | 14.24	100 | - -
HCR1	35.94 | 17.79	42.55 | 16.98	34.59 | 17.81	33.03 | 17.99	61.18 | 19.67	62.16 | 16.08	45.21 | 18.05	49.15 | 17.45	39.22 | 18.04	32.65 | 20.07
HEF3	100 | - -	100 | - -	88.52 | 13.54	100 | - -	100 | - -	53.47 | 16.82	74.1 | 15.14	62.9 | 16.75	83.53 | 15.21	100 | - -
HFA1	16.72 | 19.61	20.82 | 19.06	14.94 | 19.56	13.67 | 19.75	100 | - -	45.37 | 16.94	42.22 | 17.17	30.89 | 18.32	34.51 | 18.23	92.95 | 13.66
HHT1	19.22 | 19.18	34.35 | 17.85	26.73 | 18.5	23.81 | 18.71	32.51 | 21.52	41.89 | 17.52	26.2 | 19.89	44.82 | 17.49	46.86 | 17.47	31.98 | 20.13
HIS5	100 | - -	100 | - -	100 | - -	81.26 | 14.35	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	69.22 | 16.11
HMX1	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	86.38 | 15.44	100 | - -	100 | - -	100 | - -
HOG1	100 | - -	86.17 | 13.71	89.62 | 13.4	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	74.53 | 16.8
HOM3	42.34 | 17.11	40.58 | 17.1	36.16 | 17.71	33.95 | 17.92	56.85 | 19.89	63.51 | 15.93	50 | 17.83	51.98 | 17.08	59.8 | 16.72	28.86 | 20.44
HRR25	80.31 | 14.52	78.88 | 14.47	77.2 | 14.45	94.78 | 13.03	91.03 | 16.63	93.24 | 13.66	91.32 | 13.56	100 | - -	100 | - -	40.29 | 18.93
HSP150	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	13.14 | 21.13	100 | - -
HSP26	33.13 | 17.95	17.02 | 19.44	28.14 | 18.36	23.5 | 18.76	32.91 | 21.48	34.17 | 19.06	34.13 | 19.03	38.79 | 18.22	36.27 | 18.62	15.82 | 22.2
HSP30	100 | - -	58.36 | 15.82	100 | - -	100 | - -	100 | - -	47.68 | 18.75	39.07 | 19.33	38.04 | 18.3	43.14 | 18.82	37.63 | 19.34
HTA2; HTA1	12.5 | 20.02	16.57 | 19.5	15.72 | 19.51	18.59 | 19.24	20.2 | 22.8	9.85 | 22.35	18.56 | 20.31	22.03 | 19.57	23.53 | 20.3	17.22 | 22.09

IMD2	93.44 | 13.2	55.47 | 16.12	88.68 | 13.51	82.49 | 13.91	80.89 | 17.91	100 | - -	100 | - -	100 | - -	100 | - -	47.54 | 18.89
LOC1	100 | - -	100 | - -	88.05 | 13.85	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -
LSG1	100 | - -	100 | - -	89.78 | 13.39	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -
MBF1	45.63 | 16.81	72.19 | 15.01	62.11 | 15.81	55.3 | 16.27	56.95 | 19.89	57.14 | 16.36	44.01 | 17.11	79.47 | 14.76	63.73 | 16.45	44.88 | 19.09
MDY2	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	90.77 | 14.64	100 | - -	100 | - -
MES1	1.72 | 23.49	1.52 | 23.75	1.57 | 23.78	1.54 | 23.74	28.08 | 21.92	2.7 | 23.02	1.5 | 23.35	2.26 | 23.4	2.75 | 23.22	15.76 | 21.75
MET12	89.53 | 13.88	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -
MXR1	55.78 | 16.07	54.1 | 16.26	66.98 | 15.29	51 | 16.51	62.07 | 19.61	100 | - -	100 | - -	100 | - -	100 | - -	60.04 | 18.21
MYO2	100 | - -	85.11 | 13.87	86.79 | 13.94	76.19 | 14.65	92.51 | 16.4	100 | - -	74.85 | 16.46	100 | - -	100 | - -	47.41 | 18.48
MYO5; MYO3	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	94.76 | 13.13	100 | - -	100 | - -	100 | - -
NEW1	31.56 | 18.14	31 | 18.21	29.4 | 18.26	24.12 | 18.68	35.76 | 21.26	63.32 | 15.97	35.03 | 18.92	41.24 | 17.98	45.88 | 17.57	18.75 | 21.2
NIP7	87.81 | 13.77	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -
NOG1	57.19 | 15.96	100 | - -	75.94 | 14.47	67.28 | 15.2	78.13 | 18.17	96.14 | 13.23	100 | - -	100 | - -	100 | - -	74.6 | 16.8
NOP12	100 | - -	100 | - -	100 | - -	100 | - -	68.97 | 19.09	100 | - -	80.09 | 15.91	100 | - -	100 | - -	100 | - -
NOP6	100 | - -	100 | - -	100 | - -	78.65 | 14.26	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -
NUM1	100 | - -	56.23 | 16.05	100 | - -	100 | - -	75.37 | 18.39	63.9 | 15.86	70.51 | 15.39	82.49 | 15.3	100 | - -	70.55 | 17.15
NUP192	18.75 | 19.29	19.45 | 19.17	10.85 | 20.06	5.99 | 21.15	100 | - -	100 | - -	26.8 | 19.04	100 | - -	100 | - -	100 | - -
OLE1	37.97 | 17.61	36.32 | 17.62	37.89 | 17.56	45.78 | 16.8	46.4 | 20.54	39.77 | 17.58	33.23 | 19.01	55.18 | 17.1	40.39 | 17.94	36.3 | 19.99
PAN1	85.31 | 14.24	100 | - -	83.49 | 13.87	80.95 | 14.38	100 | - -	100 | - -	83.23 | 14.34	100 | - -	100 | - -	100 | - -
PAN5	57.5 | 16.01	100 | - -	74.53 | 14.78	86.02 | 13.94	65.22 | 19.32	100 | - -	100 | - -	91.34 | 13.68	90 | 13.93	100 | - -
PBI2	36.56 | 17.71	38.15 | 17.42	39.62 | 17.33	39.78 | 17.39	65.91 | 19.28	100 | - -	57.19 | 17.64	85.12 | 14.2	95.88 | 13.67	45.21 | 18.65
PHO88	52.81 | 16.31	77.05 | 14.61	66.19 | 15.39	65.9 | 15.42	68.18 | 19.17	81.08 | 14.63	79.79 | 14.58	100 | - -	100 | - -	51.53 | 18.87
PIC2	61.72 | 15.54	100 | - -	74.06 | 14.77	48.08 | 16.66	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	66.69 | 16.34
PIR1	15.31 | 19.66	19.91 | 19.13	19.5 | 19.12	24.42 | 18.61	100 | - -	6.37 | 21.69	4.04 | 22.05	3.77 | 23.07	7.65 | 21.64	70.08 | 17.19
PIS1	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	63.92 | 17.25	56.31 | 16.84	65.88 | 17.24	75.13 | 15.6
PMD1	15.16 | 19.69	21.43 | 19.02	21.7 | 18.93	18.43 | 19.25	100 | - -	76.83 | 14.99	100 | - -	100 | - -	100 | - -	100 | - -
POL5	49.06 | 16.76	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	54.26 | 17.47
PPT1	100 | - -	100 | - -	100 | - -	78.8 | 14.26	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	63.63 | 16.67
PRS5	100 | - -	100 | - -	100 | - -	100 | - -	76.85 | 18.21	100 | - -	85.18 | 14.21	100 | - -	100 | - -	100 | - -
PYC1	9.38 | 20.48	5.47 | 21.18	6.13 | 21.06	5.22 | 21.5	81.58 | 17.88	5.98 | 21.77	5.84 | 21.16	7.72 | 21.34	10.78 | 21.03	56.98 | 17.82
PYC2	1.41 | 24.1	1.37 | 24.02	1.42 | 24.01	1.23 | 24.3	19.61 | 22.87	1.93 | 23.65	1.35 | 23.95	2.07 | 23.69	2.16 | 23.87	8.44 | 23.19
RAD16	100 | - -	100 | - -	100 | - -	78.96 | 14.25	100 | - -	100 | - -	100 | - -	67.61 | 15.5	100 | - -	100 | - -
RCK2	88.91 | 13.91	100 | - -	100 | - -	91.71 | 13.5	68.37 | 19.15	100 | - -	94.46 | 13.16	100 | - -	100 | - -	100 | - -
RET3	43.13 | 16.95	100 | - -	65.72 | 15.31	46.7 | 16.78	57.24 | 19.88	100 | - -	73.5 | 15.17	62.52 | 16.19	81.96 | 15.42	100 | - -
RIM1	100 | - -	100 | - -	100 | - -	100 | - -	44.24 | 20.72	53.86 | 18.19	30.99 | 19.96	10.17 | 21.11	20 | 21.08	43.88 | 19.37
RIO1	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	82.34 | 13.61	100 | - -	100 | - -	100 | - -
RLP7	78.44 | 14.53	100 | - -	100 | - -	77.57 | 14.66	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	58.98 | 17.13
RNA1	45.16 | 16.81	47.42 | 16.67	45.75 | 16.88	51.77 | 16.46	74.68 | 18.48	77.61 | 14.91	57.78 | 17.21	82.67 | 15.3	64.12 | 16.2	27.79 | 20.11
RNR1; RNR3	56.88 | 16.11	100 | - -	68.71 | 15.31	67.43 | 15.35	100 | - -	84.17 | 14.42	85.93 | 14.15	81.54 | 15.45	100 | - -	100 | - -
RPA12	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	69.41 | 15.66	100 | - -
RPA135	4.84 | 21.87	3.95 | 21.89	4.25 | 21.97	4.3 | 21.75	63.25 | 19.48	7.53 | 21.09	4.79 | 21.19	7.16 | 21.27	7.25 | 21.45	39.36 | 19.41
RPA190	3.13 | 22.7	3.34 | 22.32	3.3 | 22.44	3.38 | 22.31	28.97 | 21.85	8.3 | 21.07	4.49 | 21.5	6.03 | 21.74	6.08 | 21.69	35.24 | 20.04
RPA34	55.47 | 16.09	51.06 | 16.44	55.5 | 16.23	50.84 | 16.55	100 | - -	100 | - -	72.01 | 14.47	76.08 | 15.01	76.86 | 15.14	100 | - -
RPA43	2.97 | 22.83	2.89 | 22.73	2.2 | 23.25	2.61 | 22.93	74.88 | 18.46	5.41 | 21.62	4.34 | 21.47	4.71 | 21.96	4.12 | 22.4	62.43 | 17.94
RPA49	11.25 | 20.27	9.88 | 20.29	8.81 | 20.44	9.06 | 20.45	58.52 | 19.83	24.32 | 19.55	19.76 | 19.48	25.24 | 19.11	25.49 | 19.04	32.58 | 19.71
RPB10	84.53 | 14.11	49.39 | 16.54	75.47 | 14.63	74.65 | 14.88	91.13 | 16.63	100 | - -	76.35 | 16.34	82.3 | 15.34	100 | - -	53.66 | 17.79
RPB2	58.91 | 15.86	48.94 | 16.6	47.17 | 16.8	46.85 | 16.78	59.21 | 19.78	100 | - -	69.01 | 15.04	90.4 | 14.72	100 | - -	35.84 | 19.43
RPB5	59.22 | 15.78	54.41 | 16.21	54.4 | 16.24	56.68 | 16.14	100 | - -	100 | - -	100 | - -	80.41 | 14.65	81.57 | 14.71	100 | - -
RPC25	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	61.37 | 16.17	100 | - -
RPL33A	8.91 | 20.65	28.27 | 18.43	17.92 | 19.32	21.51 | 18.93	21.87 | 22.58	100 | - -	51.65 | 16.53	65.35 | 16.57	45.69 | 17.56	18.42 | 22.08
RPL42B;	26.56 | 18.64	30.4 | 18.24	33.81 | 17.96	36.87 | 17.65	66.9 | 19.23	39.38 | 19.38	77.1 | 14.08	47.65 | 17.29	100 | - -	77.39 | 16.53
RPL43B;	19.06 | 19.3	20.21 | 19.11	16.35 | 19.5	26.73 | 18.49	32.02 | 21.56	58.3 | 16.09	37.87 | 18.89	61.02 | 16.58	48.43 | 18.15	55.39 | 18.55
RPO26	18.28 | 19.33	27.36 | 18.5	20.28 | 19.1	18.74 | 19.24	96.65 | 15.59	35.33 | 17.94	40.27 | 17.33	39.55 | 17.92	38.04 | 18.04	76.13 | 16.25
RPS29A	58.44 | 15.83	53.65 | 16.3	56.13 | 16.2	55.76 | 16.27	30.84 | 21.67	100 | - -	9.58 | 22.29	83.62 | 14.31	100 | - -	15.56 | 22.11
RPS30B;	100 | - -	100 | - -	85.85 | 13.8	85.71 | 13.68	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	35.9 | 20.2
RTT10	100 | - -	100 | - -	100 | - -	86.48 | 13.91	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -
SAC6	56.09 | 16.13	47.72 | 16.67	38.84 | 17.45	34.25 | 17.88	44.93 | 20.65	56.95 | 16.2	49.1 | 18.07	56.12 | 16.93	63.14 | 16.5	14.16 | 21.89
SAM1	17.97 | 19.45	17.33 | 19.41	34.43 | 17.98	33.33 | 18.05	27.88 | 21.92	19.11 | 19.89	28.89 | 18.88	23.35 | 19.82	10.2 | 20.92	23.34 | 21.42
SCW4	56.56 | 15.94	79.64 | 14.39	81.6 | 14.03	100 | - -	85.71 | 17.31	49.42 | 17.26	52.69 | 17.48	37.66 | 18.38	59.41 | 16.96	79.72 | 16.36
SEC26	15.63 | 19.68	12.92 | 19.83	13.84 | 19.71	16.44 | 19.47	33.2 | 21.5	50.39 | 17.14	33.83 | 17.99	39.17 | 18.28	39.8 | 18.24	26.4 | 20.78
SEC27	23.13 | 18.87	22.95 | 18.89	24.84 | 18.66	20.43 | 19.05	31.63 | 21.58	55.79 | 16.69	47.16 | 17.21	39.74 | 18.31	45.1 | 17.79	24.27 | 21.21
SEC28	3.59 | 22.41	2.74 | 23.01	2.52 | 22.91	2.92 | 22.56	72.12 | 18.72	2.12 | 24.81	2.84 | 23.74	0.94 | 25	1.76 | 25.18	52.66 | 18.41
SEC4	38.28 | 17.5	31.61 | 18.13	35.53 | 17.74	13.82 | 19.77	31.53 | 21.58	35.71 | 19.72	32.04 | 19.63	32.2 | 18.73	28.04 | 19.8	18.48 | 21.64
SEC53	7.03 | 21.05	6.53 | 21.03	7.08 | 21.02	6.45 | 21.01	19.41 | 22.9	13.13 | 21.18	6.14 | 22.11	11.11 | 20.82	12.55 | 21.14	11.37 | 22.61
SFA1	44.84 | 16.85	44.38 | 16.89	47.01 | 16.74	41.78 | 17.19	67 | 19.21	100 | - -	49.55 | 17.96	55.93 | 16.82	89.61 | 13.95	45.15 | 18.92
SIN3	100 | - -	100 | - -	100 | - -	85.87 | 13.94	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -
SIZ1	18.59 | 19.25	29.18 | 18.36	14.31 | 19.68	16.74 | 19.4	100 | - -	60.62 | 16.33	25 | 20.52	54.8 | 16.59	77.25 | 15.82	100 | - -
SLA2	80.47 | 14.61	100 | - -	88.21 | 13.84	86.18 | 13.93	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	74.27 | 15.66
SPC110	88.59 | 13.7	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -
SPC42	68.44 | 15.11	69.3 | 15.18	69.97 | 15	72.04 | 14.94	100 | - -	93.63 | 13.58	93.71 | 13.25	100 | - -	100 | - -	100 | - -
SRP54	100 | - -	100 | - -	100 | - -	87.71 | 13.53	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -
SSA4	25.94 | 18.56	66.87 | 15.4	31.6 | 17.98	41.17 | 17.24	44.53 | 20.67	100 | - -	54.49 | 18.04	100 | - -	100 | - -	48.01 | 19.14
SUI1	76.25 | 14.92	43.77 | 16.93	69.03 | 15.07	100 | - -	54.88 | 20.03	100 | - -	63.32 | 15.96	66.1 | 16.53	100 | - -	100 | - -
SUI3	50 | 16.64	44.83 | 16.83	46.38 | 16.86	47.47 | 16.74	74.38 | 18.51	91.89 | 13.79	81.74 | 14.45	78.53 | 15.23	77.06 | 15.43	50.93 | 18.27
SUP35	19.84 | 19.13	24.01 | 18.76	20.91 | 19.05	20.58 | 19.07	43.55 | 20.72	27.99 | 19.99	31.74 | 18.78	38.98 | 18.28	40.78 | 18.18	40.36 | 19.4
TIF4631	30.31 | 18.22	32.83 | 18.03	34.12 | 17.84	28.11 | 18.31	67.59 | 19.18	44.59 | 18.43	41.62 | 18.07	43.13 | 17.98	47.45 | 18.11	29.32 | 19.93
TMA20	79.53 | 14.68	66.57 | 15.41	59.75 | 15.82	63.9 | 15.62	75.96 | 18.33	57.34 | 17.97	100 | - -	100 | - -	100 | - -	38.36 | 19.36
TMA22	100 | - -	100 | - -	100 | - -	65.75 | 15.53	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -
TMA46	92.34 | 13.37	69.45 | 15.14	72.96 | 14.8	89.09 | 13.42	81.87 | 17.83	85.52 | 14.27	90.42 | 13.61	76.46 | 15.51	100 | - -	55.19 | 18.24

TOP1	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	46.91 | 16.75	100 | - -	100 | - -	100 | - -	100 | - -
TPM1	46.09 | 16.79	52.58 | 16.36	48.9 | 16.69	40.4 | 17.29	57.83 | 19.85	59.07 | 16.48	67.81 | 15.59	49.53 | 17.39	61.76 | 16.59	32.11 | 20.16
TPM2	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	94.12 | 14.03	100 | - -
TRL1	48.44 | 16.59	63.37 | 15.52	63.68 | 15.43	50.38 | 16.53	94.78 | 15.94	100 | - -	100 | - -	100 | - -	68.63 | 15.7	100 | - -
TRM732	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	78.57 | 14.86	100 | - -	100 | - -	100 | - -	100 | - -
TUB1	100 | - -	91.03 | 13.25	100 | - -	80.03 | 14.29	100 | - -	96.91 | 13.15	100 | - -	100 | - -	100 | - -	100 | - -
TUS1	32.03 | 18.01	43.01 | 16.94	31.29 | 17.99	27.96 | 18.41	100 | - -	51.93 | 18.36	100 | - -	100 | - -	100 | - -	100 | - -
TY1	27.81 | 18.51	24.77 | 18.72	20.44 | 19.07	30.11 | 18.17	35.67 | 21.28	20.27 | 21.14	10.18 | 22	14.5 | 20.43	20.39 | 20.82	3.32 | 23.98
URA6	50.31 | 16.57	47.87 | 16.65	49.37 | 16.61	50.69 | 16.53	58.23 | 19.83	84.36 | 14.42	77.69 | 14.81	71.56 | 16.22	79.8 | 14.85	36.37 | 19.84
URA7	28.91 | 18.41	36.02 | 17.63	25.63 | 18.57	25.04 | 18.64	52.22 | 20.21	48.26 | 17.09	33.53 | 18.99	47.46 | 17.57	52.55 | 17.11	28.19 | 20.35
VPS30	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	35.88 | 19.49	100 | - -
YAR1	69.22 | 15.17	100 | - -	86.64 | 13.95	82.95 | 14.16	71.23 | 18.82	100 | - -	83.98 | 14.31	100 | - -	100 | - -	100 | - -
YDJ1	14.38 | 19.82	12.16 | 19.86	11.32 | 20.16	9.98 | 20.24	23.15 | 22.43	23.17 | 20.11	16.77 | 20.51	19.21 | 19.96	25.29 | 19.61	14.43 | 22.11
YPT1	100 | - -	100 | - -	100 | - -	63.75 | 15.47	100 | - -	100 | - -	77.99 | 14.78	85.88 | 15.07	70.39 | 15.55	33.38 | 20.15
YRB1	32.66 | 18.01	32.98 | 18.02	36.32 | 17.66	32.1 | 18.02	42.36 | 20.79	41.12 | 17.64	39.97 | 17.53	46.14 | 17.71	43.73 | 17.96	34.04 | 20.23
ZPR1	36.41 | 17.74	45.74 | 16.82	53.62 | 16.38	36.71 | 17.65	55.37 | 19.98	66.8 | 15.6	63.77 | 15.89	58.38 | 16.61	55.49 | 16.91	29.99 | 20.08
ZRT1	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	100 | - -	86.25 | 14.64	100 | - -	100 | - -
ZUO1	15.47 | 19.73	15.65 | 19.59	15.25 | 19.58	11.52 | 20.01	33.99 | 21.41	31.85 | 18.44	19.01 | 20.26	25.42 | 19.26	22.75 | 19.87	21.34 | 21.13

SI Table S-5. List of Enriched Proteins and the Corresponding Delta-Percentile-Rank. This list shows 34-88 proteins enriched at each locus under either condition (normal or stressed). The first delta-percentile-rank was from the analysis against the uncaptured lysate. The second delta-percentile-rank was calculated against other off-target capture (e.g. 25S rDNA v. the average of the other three). Proteins whose delta-percentile-rank were greater than 10% (normal conditions) or 5% (stressed conditions) were considered to be enriched.

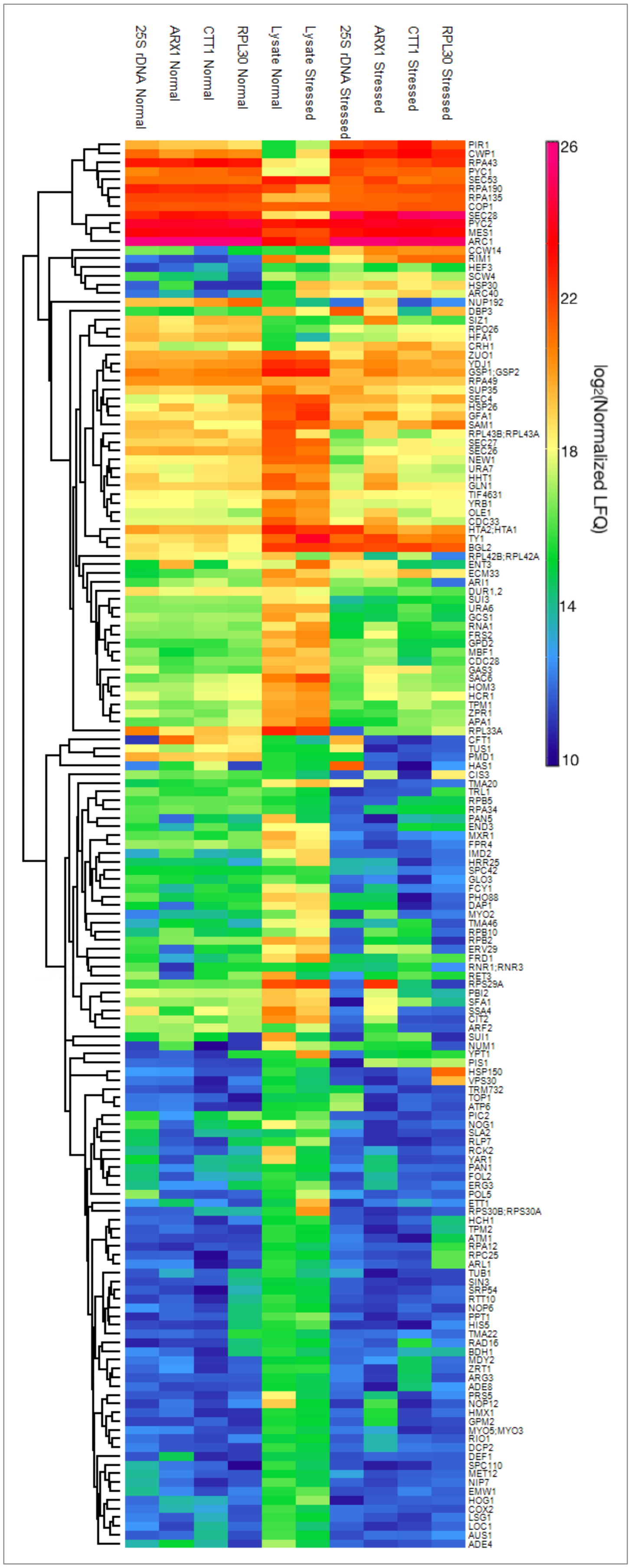
Normal 25S rDNA			**Normal *ARX1***		
Gene Name	**ΔPercentile Rank (Lysate, Other Loci)**		**Gene Name**	**ΔPercentile Rank (Lysate, Other Loci)**	
POL5	50.94	50.94	NUM1	19.14	43.77
SCW4	29.15	30.52	ENT3	67.48	43.14
RET3	14.12	27.68	CFT1	93.77	42.25
CCW14	46.88	24.26	HSP30	41.64	41.64
NOG1	20.94	23.89	SUI1	11.11	37.99
RNR1; RNR3	43.13	21.84	IMD2	25.42	32.73
SSA4	18.59	20.61	RPB10	41.74	28.83
GAS3	26.04	19.13	DEF1	23.71	23.71
ERV29	15.91	18.82	ADE4	17.43	21.78
MBF1	11.32	17.57	ETT1	20.16	20.99
PHO88	15.36	16.90	CCW14	43.06	19.17
CRH1	75.94	14.66	TMA46	12.42	15.34
RLP7	21.56	14.09	COX2	12.31	12.31
EMW1	13.91	13.91	HAS1	33.89	12.19
RPL33A	12.97	13.66	SAM1	10.56	11.25
FCY1	13.36	12.44	HSP26	15.89	11.24
PIC2	38.28	12.33	HOG1	13.83	10.37
NIP7	12.19	12.19	CWP1	88.91	
GLO3	33.15	11.91	NUP192	80.55	
SPC110	11.41	11.41	PIR1	80.09	
SLA2	19.53	10.99	HFA1	79.18	
TRL1	46.34	10.71	PMD1	78.57	
MET12	10.47	10.47	PYC1	76.11	
FOL2	15.94	10.19	RPA43	71.99	
CWP1	93.59		SIZ1	70.82	
PMD1	84.84		SEC28	69.38	
PIR1	84.69		RPO26	69.29	
HFA1	83.28		RPA135	59.30	
SIZ1	81.41		CRH1	58.36	
NUP192	81.25		TUS1	56.99	
RPO26	78.37		ARF2	54.86	
PYC1	72.20		RPA34	48.94	
RPA43	71.91		RPA49	48.64	
SEC28	68.52		RPB5	45.59	
TUS1	67.97		CIS3	45.29	
RPA135	58.41		DUR1, 2	40.28	
CIS3	56.25		RPL42B; RPL42A	36.50	
ARF2	55.47		TIF4631	34.76	
DUR1,2	49.47		TRL1	31.40	
RPA49	47.27		SPC42	30.70	
RPA34	44.53		COP1	30.20	
RPB5	40.78		SUI3	29.55	
RPL42B; RPL42A	40.33		PBI2	27.77	
TIF4631	37.27		RNA1	27.26	
SPC42	31.56		MES1	26.56	
COP1	29.74		RPA190	25.62	
RNA1	29.52		GLO3	23.80	

PBI2	29.35		SFA1	22.62	
MES1	26.36		FPR4	21.60	
RPA190	25.84		SEC26	20.28	
HCR1	25.24		SUP35	19.53	
FPR4	24.96		HCR1	18.63	
SUI3	24.38		ZUO1	18.34	
SUP35	23.70		PYC2	18.24	
URA7	23.31		ARI1	17.82	
SFA1	22.15		ARC1	17.23	
ZPR1	18.96		HOM3	16.27	
ZUO1	18.52		URA7	16.20	
PYC2	18.20		ARC40	13.68	
SEC26	17.58		SEC53	12.87	
ARC1	17.22		HRR25	12.16	
CDC28	15.56		RPL43B; RPL43A	11.81	
PAN1	14.69		GLN1	11.40	
HOM3	14.50		CIT2	11.28	
HHT1	13.29		YDJ1	10.99	
ERG3	13.13		TY1	10.89	
GLN1	13.11		URA6	10.35	
RPL43B; RPL43A	12.96		RPB2	10.28	
END3	12.84		OLE1	10.08	
SEC53	12.38				
GCS1	12.33				
TPM1	11.74				
ENT3	10.93				
HRR25	10.72				
GFA1	10.39				
Normal *CTT1*			**Normal *RPL30***		
Gene Name	**ΔPercentile Rank (Lysate, Other Loci)**		**Gene Name**	**ΔPercentile Rank (Lysate, Other Loci)**	
HAS1	65.09	53.80	YPT1	36.25	36.25
CFT1	80.66	24.78	TMA22	34.25	34.25
END3	22.17	21.64	PIC2	51.92	30.51
AUS1	16.19	16.19	ENT3	52.71	23.45
ARI1	23.56	13.55	RET3	10.54	22.92
SSA4	12.93	13.05	NOP6	21.35	21.35
LOC1	11.95	11.95	SEC4	17.70	21.32
HEF3	11.48	11.48	PPT1	21.20	21.20
FCY1	12.34	11.07	RAD16	21.04	21.04
TMA20	16.21	10.25	FRD1	11.00	19.36
LSG1	10.22	10.22	HIS5	18.74	18.74
CWP1	92.45		ERG3	22.89	18.51
NUP192	89.15		DAP1	12.84	18.29
SIZ1	85.69		BDH1	18.28	18.28
HFA1	85.06		TUB1	19.97	16.98
PIR1	80.50		CFT1	73.89	15.74
PMD1	78.30		RLP7	22.43	15.24
RPO26	76.37		APA1	21.04	15.00
PYC1	75.44		MYO2	16.32	14.44
RPA43	72.68		SIN3	14.13	14.13
SEC28	69.60		RTT10	13.52	13.52
TUS1	68.71		SAC6	10.67	13.30
ARF2	63.36		SRP54	12.29	12.29
CRH1	59.12		GPD2	16.14	10.43
RPA135	59.01		NOG1	10.85	10.43
CIS3	51.73		NUP192	94.01	10.36

RPA49	49.72		CWP1	91.24	
DUR1, 2	47.11		HFA1	86.33	
RPB5	45.60		SIZ1	83.26	
RPA34	44.50		PMD1	81.57	
TIF4631	33.47		RPO26	77.91	
RPL42B; RPL42A	33.09		PYC1	76.35	
RNR1; RNR3	31.29		PIR1	75.58	
TRL1	31.10		RPA43	72.27	
COP1	30.65		TUS1	72.04	
SPC42	30.03		SEC28	69.20	
RNA1	28.93		CRH1	66.36	
FPR4	28.77		RPA135	58.95	
SUI3	28.00		ARF2	57.76	
HCR1	26.59		RPA49	49.46	
URA7	26.59		RPA34	49.16	
MES1	26.51		DUR1, 2	45.90	
PBI2	26.29		TRL1	44.39	
PIC2	25.94		RPB5	43.32	
RPA190	25.66		CIS3	43.01	
SUP35	22.63		TIF4631	39.48	
HOM3	20.68		RNR1; RNR3	32.57	
SFA1	19.98		COP1	30.45	
SEC26	19.37		RPL42B; RPL42A	30.03	
ZUO1	18.74		HCR1	28.16	
PYC2	18.19		SPC42	27.96	
ARC1	17.22		CCW14	27.29	
PAN1	16.51		URA7	27.18	
CDC28	16.19		SUI3	26.92	
RPL43B; RPL43A	15.67		MES1	26.54	
RPB10	15.66		PBI2	26.13	
TY1	15.22		GLO3	25.99	
RPS30B; RPS30A	14.15		RPA190	25.59	
GLO3	13.91		SFA1	25.21	
HRR25	13.83		SUP35	22.96	
APA1	13.12		RNA1	22.91	
SEC53	12.33		HOM3	22.90	
RPB2	12.04		ZUO1	22.47	
GLN1	12.04		PAN1	19.05	
YDJ1	11.83		ZPR1	18.66	
SLA2	11.79		PYC2	18.38	
GFA1	11.33		FPR4	18.33	
GCS1	11.28		TPM1	17.43	
GAS3	11.03		ARC1	17.08	
FRS2	10.60		SEC26	16.77	
GSP1; GSP2	10.56		RPB10	16.48	
HOG1	10.38		CDC28	16.10	
			RPS30B; RPS30A	14.29	
			GLN1	14.23	
			SLA2	13.82	
			YDJ1	13.17	
			SEC53	12.96	
			RPB2	12.36	
			GFA1	12.34	
			TMA20	12.06	
			FRS2	11.85	
			NEW1	11.65	

			GSP1; GSP2	11.20	
			SEC27	11.20	
			MXR1	11.07	
			ARC40	11.06	
			ARI1	10.91	
			YRB1	10.26	
Stressed 25S rDNA			**Stressed *ARX1***		
Gene Name	**ΔPercentile Rank (Lysate, Other Loci)**		**Gene Name**	**ΔPercentile Rank (Lysate, Other Loci)**	
CFT1	79.54	79.54	RPS29A	5.98	84.96
HAS1	78.76	78.76	NUP192	73.20	73.20
TOP1	53.09	53.09	SIZ1	75.00	39.22
TUS1	48.07	48.07	CIS3	54.19	34.78
DBP3	41.34	38.10	SUI1	36.68	25.38
RPL42B; RPL42A	38.01	35.53	CDC33	9.94	19.96
ATP6	34.94	34.94	NOP12	19.91	19.91
PMD1	23.17	23.17	HHT1	5.78	18.33
TRM732	21.43	21.43	RPL43B; RPL43A	17.51	18.04
NUM1	6.65	20.43	RIO1	17.66	17.66
HEF3	46.53	20.04	PAN1	16.77	16.77
HTA2; HTA1	7.38	11.53	YAR1	16.02	16.02
SUP35	12.37	9.18	PRS5	14.82	14.82
CCW14	73.17		HMX1	13.62	13.62
PIR1	63.71		GPM2	13.02	13.02
RPA43	57.03		RPA34	27.99	12.31
PYC1	51.00		FOL2	10.93	10.93
CWP1	50.81		PIS1	11.21	10.14
SEC28	50.54		DCP2	8.83	8.83
HFA1	47.59		RET3	26.50	7.99
RPO26	40.80		SEC53	5.23	6.12
SIZ1	39.38		CCW14	84.58	5.80
RPA135	31.83		RCK2	5.54	5.54
CRH1	30.70		RPA49	12.82	5.26
SCW4	30.30		MYO5; MYO3	5.24	5.24
RPA190	26.94		PIR1	66.04	
ARC1	17.63		RPA43	58.09	
RNR1; RNR3	15.83		PYC1	51.14	
MES1	13.06		HFA1	50.74	
COP1	9.42		CWP1	50.33	
RPA49	8.26		SEC28	49.82	
ECM33	7.85		RPO26	35.86	
PYC2	6.51		CRH1	34.64	
SPC42	6.37		RPA135	34.57	
			RPA190	30.75	
			SCW4	27.03	
			HEF3	25.90	
			ARC1	17.72	
			MES1	14.26	
			RNR1; RNR3	14.07	
			RIM1	12.89	
			DBP3	12.63	
			ECM33	11.21	
			COP1	10.33	
			SUP35	8.62	
			PYC2	7.10	
			SPC42	6.29	
			BGL2	5.91	

Stressed *CTT1*			**Stressed *RPL30***		
Gene Name	**ΔPercentile Rank (Lysate, Other Loci)**		**Gene Name**	**ΔPercentile Rank (Lysate, Other Loci)**	
RAD16	32.39	32.39	HSP150	86.86	86.86
ARC40	12.35	27.97	VPS30	64.12	64.12
RIM1	33.71	24.78	CIS3	58.24	40.17
RPL42B; RPL42A	29.75	24.51	RPC25	38.63	38.63
RET3	37.48	22.63	TRL1	31.37	31.37
SUI1	33.90	21.67	RPA12	30.59	30.59
GAS3	8.95	20.66	ARL1	19.80	19.80
PIS1	18.82	20.29	DBP3	24.76	15.99
ECM33	26.22	18.64	SAM1	13.14	13.59
SCW4	42.06	16.18	RPB5	18.43	11.90
ZRT1	13.75	13.75	RIM1	23.88	11.67
RPB5	19.59	13.44	ATM1	10.59	10.59
CRH1	42.91	13.41	PIS1	9.25	7.53
HFA1	62.07	9.81	PAN5	10.00	7.11
MDY2	9.23	9.23	HCH1	6.47	6.47
RNR1; RNR3	18.46	8.49	BDH1	8.24	5.98
ARG3	7.72	7.72	TPM2	5.88	5.88
HEF3	37.10	7.47	RPA34	23.14	5.83
RPA34	23.92	6.87	CCW14	78.63	
ADE8	5.84	5.84	PIR1	62.43	
CCW14	84.56	5.77	HFA1	58.44	
PAN5	8.66	5.33	RPA43	58.32	
PIR1	66.31		SEC28	50.89	
RPA43	57.73		CWP1	48.42	
SEC28	51.72		PYC1	46.20	
CWP1	50.88		RPO26	38.09	
PYC1	49.26		RPA135	32.11	
SIZ1	45.20		RPA190	29.16	
RPO26	36.58		CRH1	23.18	
RPA135	32.21		SIZ1	22.75	
RPA190	29.21		SCW4	20.31	
ARC1	17.27		RET3	18.04	
MES1	13.50		ARC1	17.23	
COP1	13.28		HEF3	16.47	
BGL2	7.86		MES1	13.01	
RPA49	7.34		COP1	10.22	
BDH1	6.78		RPA49	7.09	
PYC2	6.37		RPL43B; RPL43A	6.95	
			PYC2	6.29	



SI Figure S-5. Heat map of the 161 enriched proteins. This is the figure rearranged from Figure 2 with four capture and lysate control aligned in two conditions to show locus difference. Although many lysate proteins have higher LFQ values, their percentile ranks were lower in the list (SI Table S-4, 5).