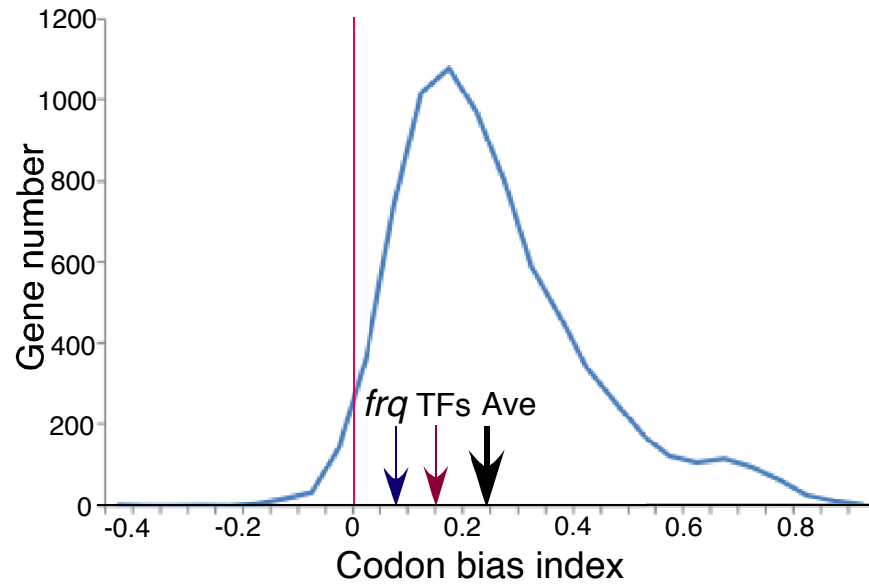


a



b

	All genes	Top100	<i>frq</i>	<i>frh</i>
GC	56%	59%	56%	54%
GC 3 rd	64%	76%	58%	69%
Fop	52%	78%	43%	64%
CBI	0.24	0.64	0.08	0.42
ENC	53	34	57	44

Figure s1: (a) Distribution of *Neurospora* genes based on their CBI values. Numbers of genes within each 0.05 unit of CBI were counted. The red line indicates CBI value of 0, meaning that codon usage is random. The CBI values of average *Neurospora* genes, *frq*, and the average *Neurospora* transcription factors are indicated. (b) A table summarizing the GC content, GC content at the 3rd position of codons, Fop, CBI and ENC for all predicted *Neurospora* protein-encoding genes, genes encoding the top 100 proteins, *frq* and *frh*.

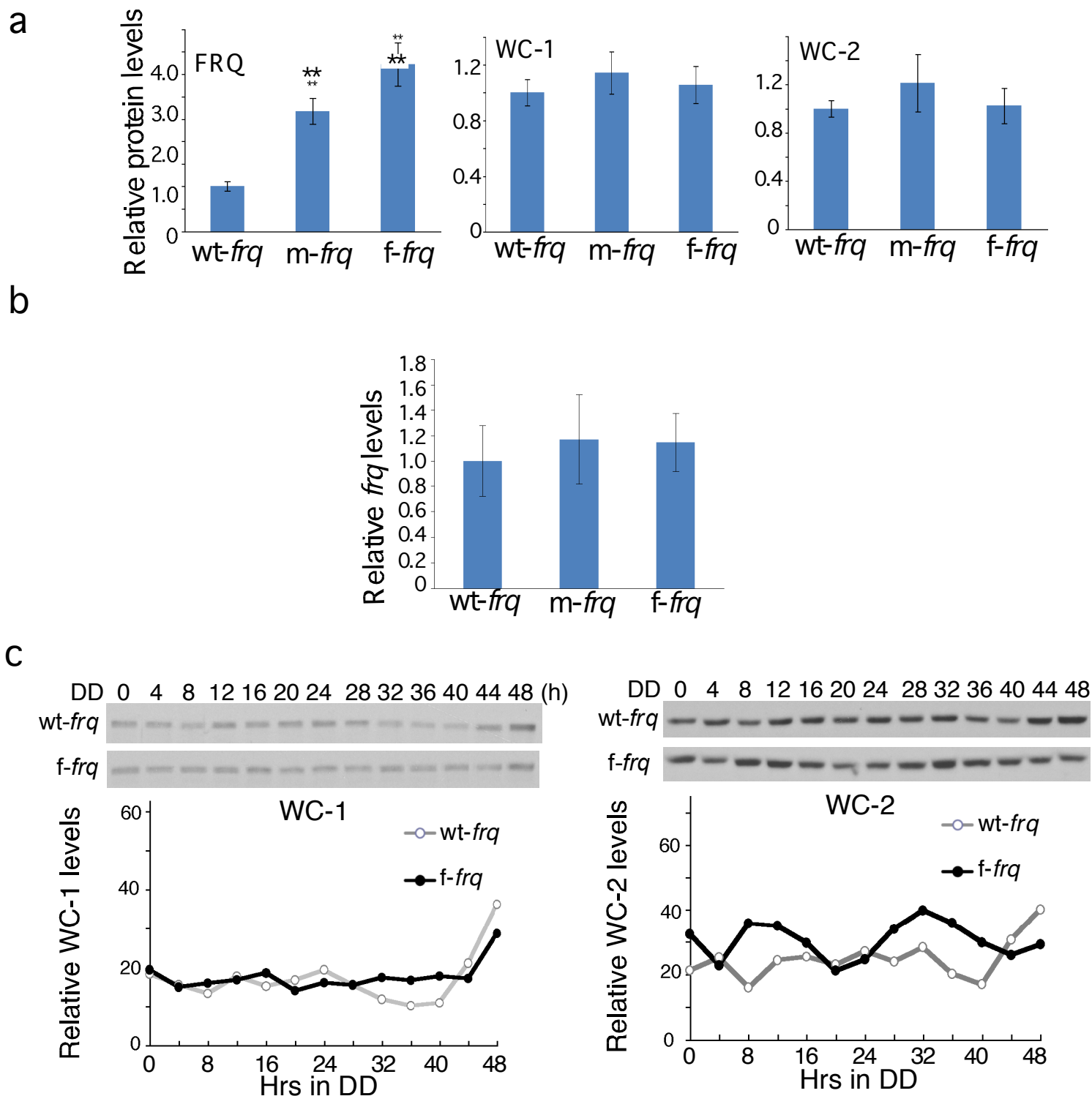


Figure s2: (a) Densitometric analysis of the results shown in Figure 1b. The error bars are standard deviations. n=3. The asterisks indicate p value < 0.01. (b) Quantitative RT-PCR results showing that the levels of *frq* mRNA in LL. Error bars are standard deviation. n=3. (c) Western blot analyses results showing the levels of WC-1 (left panels) and WC-2 (right panels) in the wt-*frq* and f-*frq* strains. *Neurospora* cultures were harvested in DD at the indicated time points.

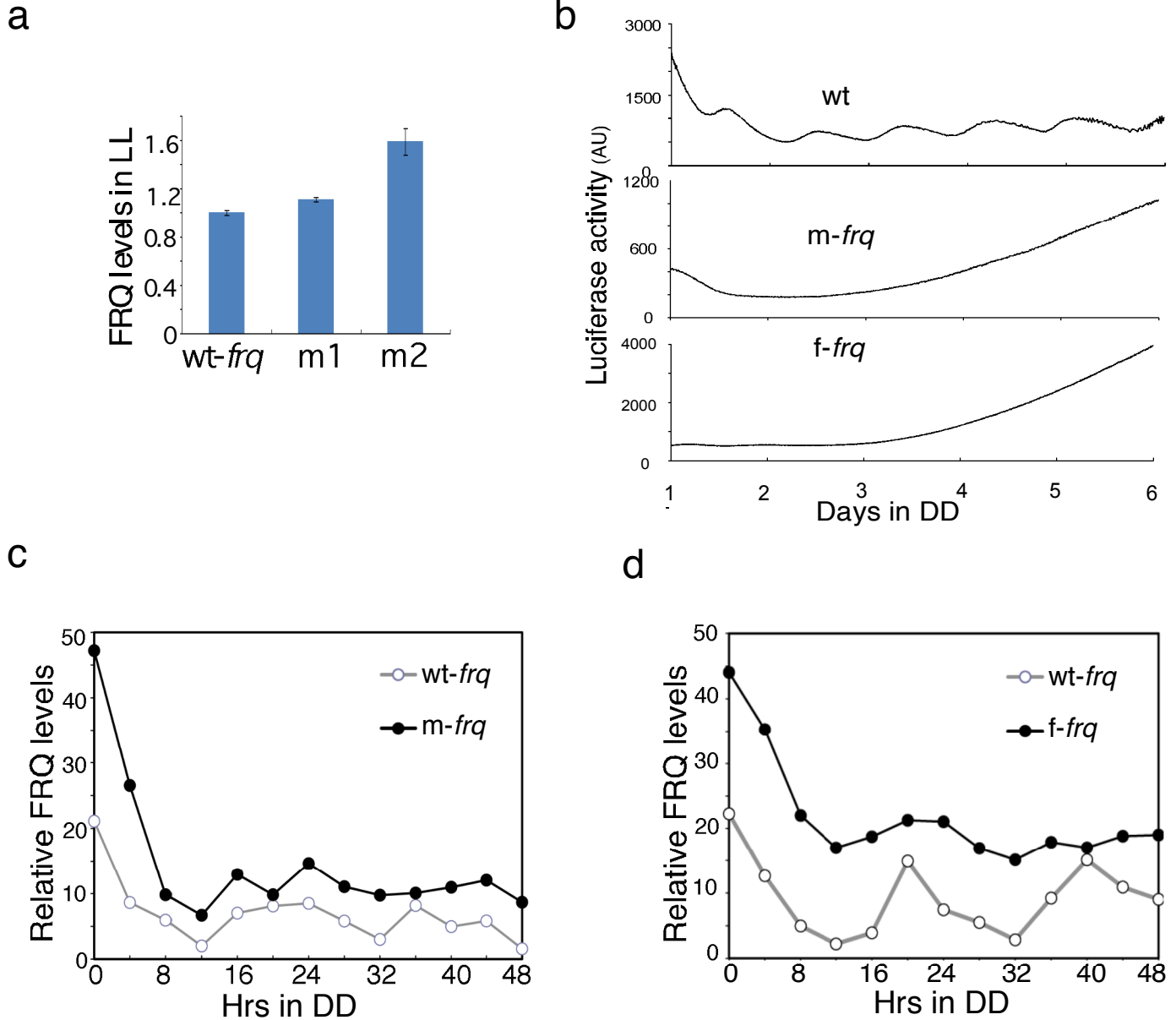
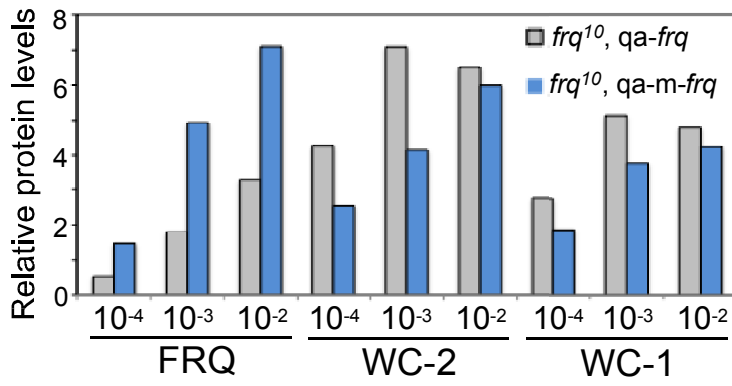


Figure s3: (a) Quantification of western blot results showing the levels of FRQ in the wt-*frq*, m1-*frq* and m2-*frq* strains. Error bars are standard deviation. n=3. (b) Luciferase reporter assay showing the *frq* promoter activity in the *frq10*, wt-*frq*; *frq10*, m-*frq* and *frq10*, f-*frq* strains after one day in DD. The un-normalized raw luciferase activity of the experiments in Figure 2b was shown. (c) Quantification of Western blot analyses results showing in Figure 1e. (d) Quantification of Western blot analyses results showing in Figure 1f.

a



b

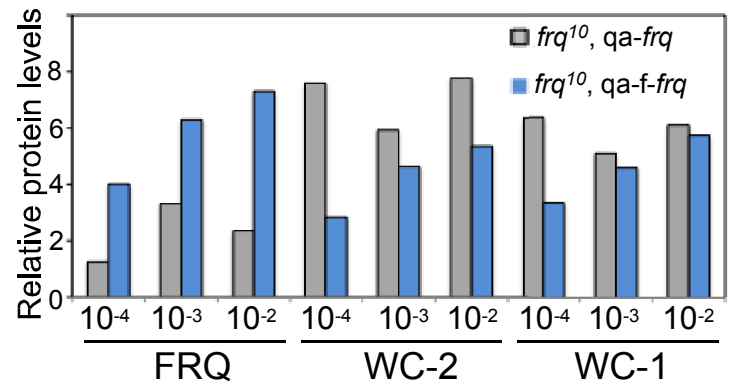
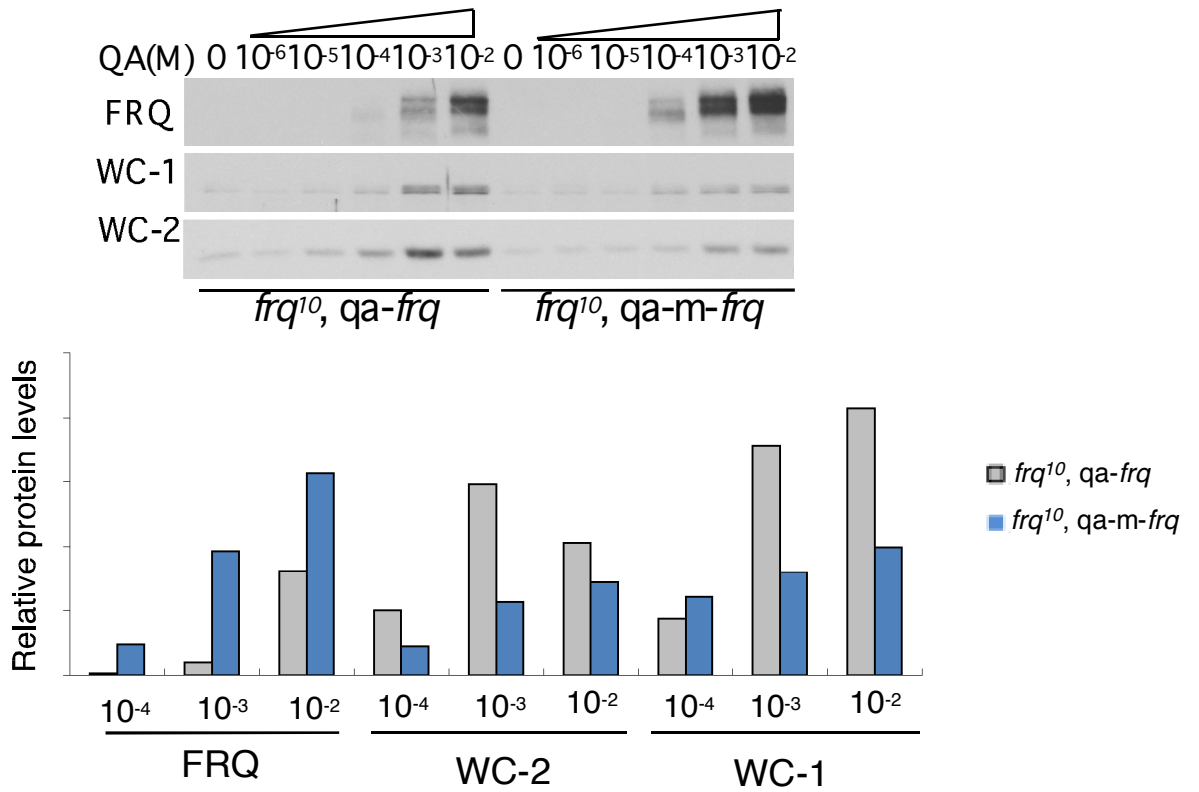


Figure s4: (a) and (b) Densitometric analyses of the results of the Western blot results shown in Figure 2b and 2c, respectively.

a



b

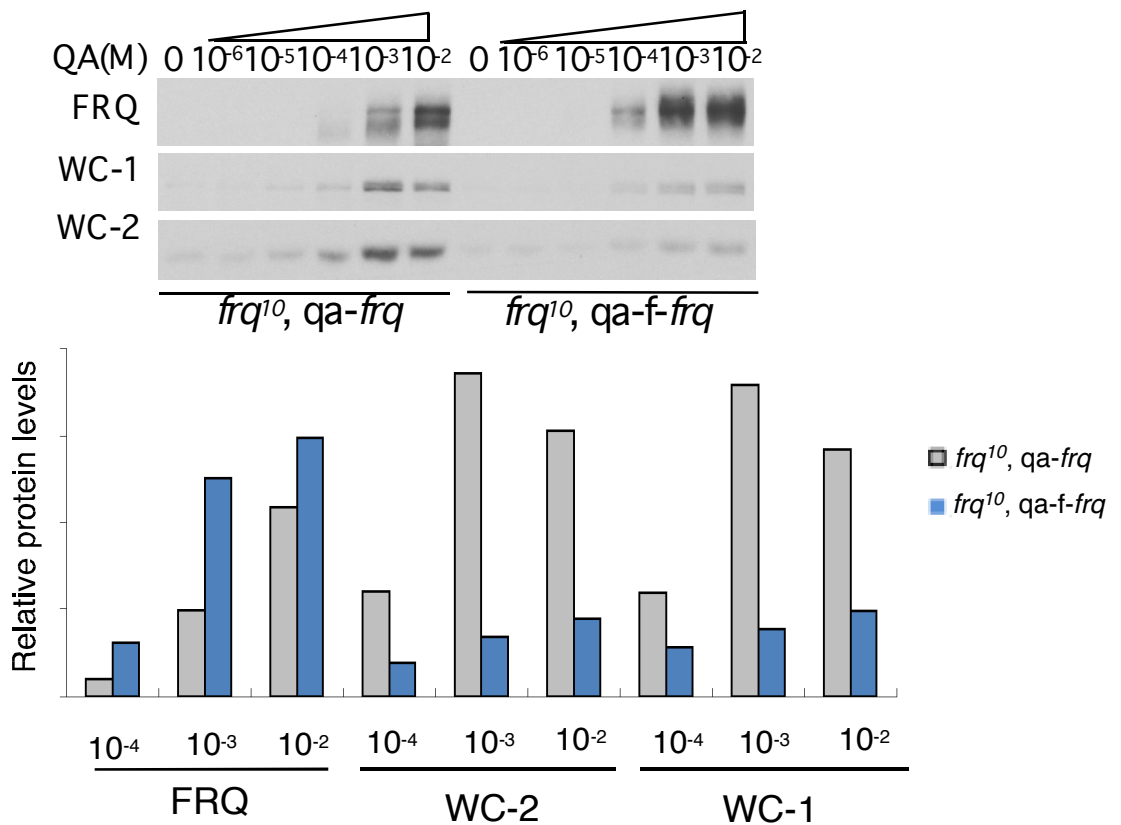


Figure s5: Western blot analysis results of independent experiments as in Figure 2b & 2c showing the levels of WC-1, WC-2, and FRQ in the indicated strains at different concentrations of QA in LL. The lower panels show the densitometric analyses of the Western blot results

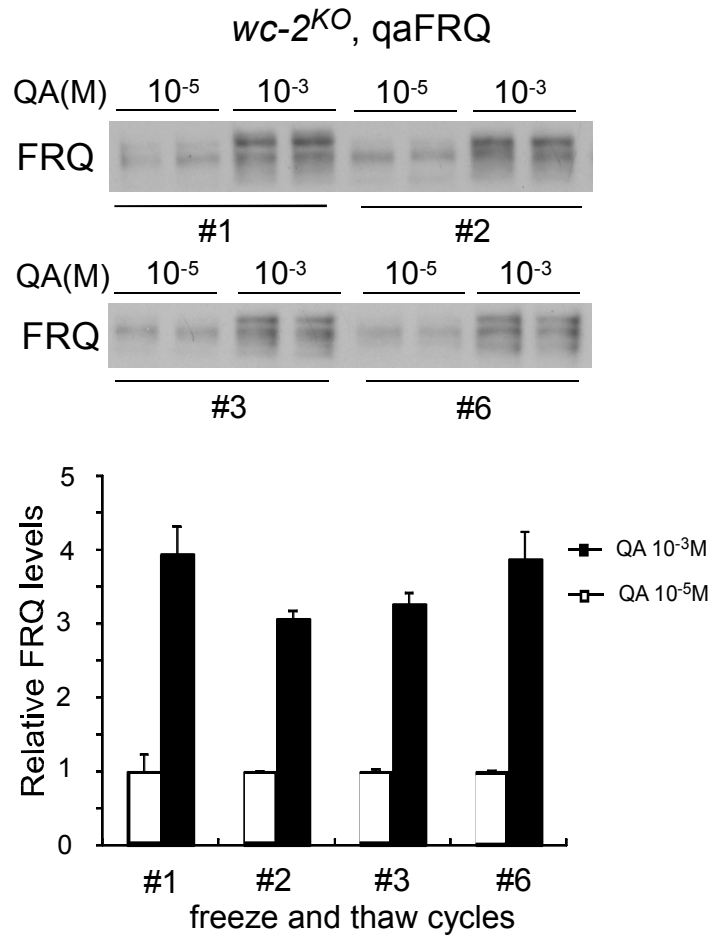
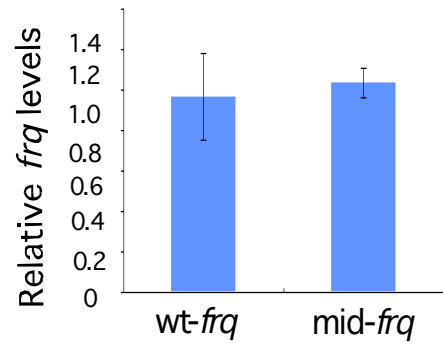


Figure s6: Overexpression of wild-type *frq* in a *wc-2^{KO}* strain does not affect the freeze-thaw sensitivity of FRQ. *frq* expression was induced in the *wc-2^{KO}*, qa-*frq* strain by culturing at 10⁻⁵M and 10⁻³M, so that FRQ levels are comparable to that of the wild-type and f-*frq* strain, respectively. Western blot analysis of FRQ was performed after the indicated number of freeze-thaw cycles. The densitometric analysis of the results was shown below.

a



b

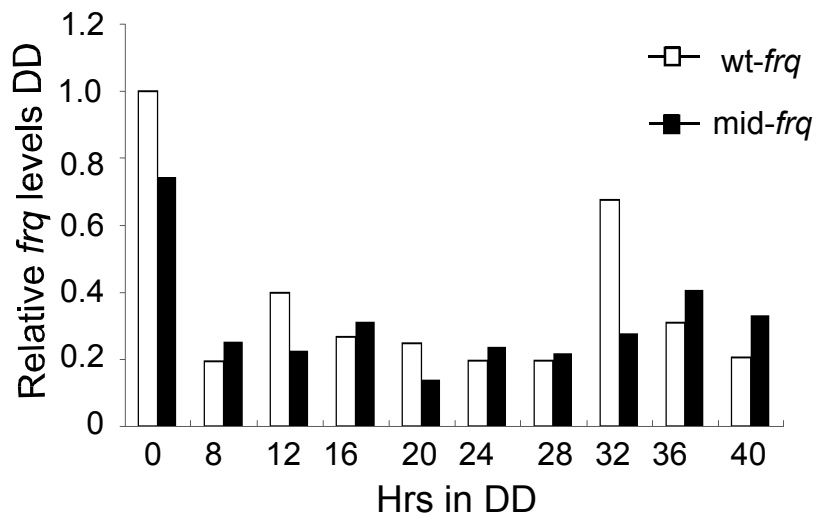


Figure s7: qRT-PCR results showing *frq* mRNA levels in LL (a) and DD (b).

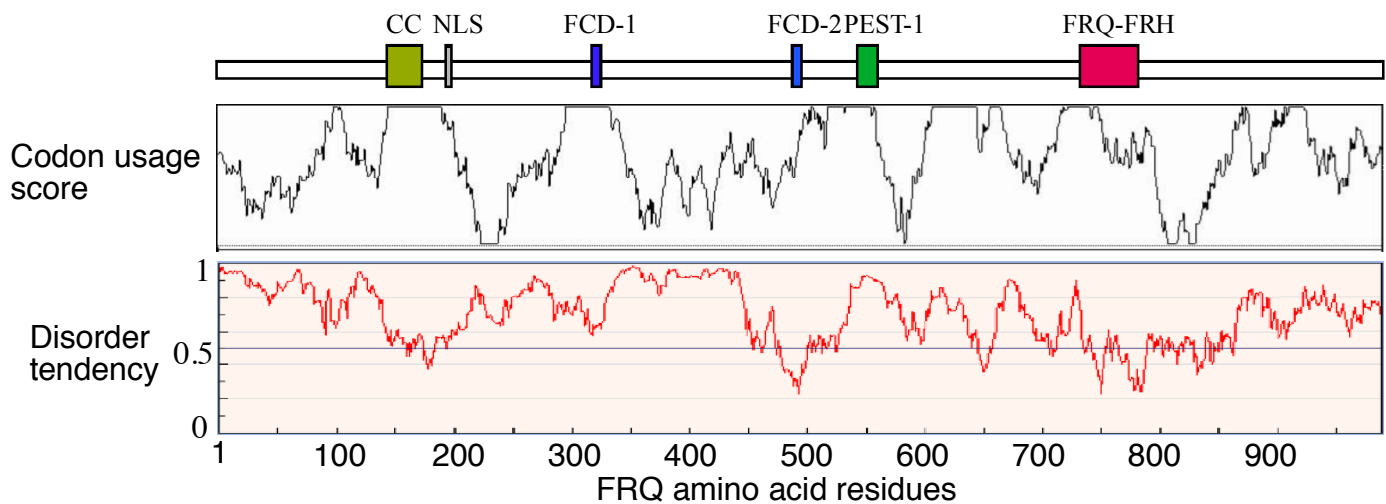


Figure s8: Plots shows the location of the previously identified FRQ domains, the *frq* codon usage score and the predicted disorder tendency of FRQ protein. Codon usage score plot was obtained using Codon Usage 3.5 (window size 35nt, and logarithmic range 3). The codon usage score is highest when codons contain the highest frequency of preferentially used codons in the genome. Protein disorder tendency was determined by IUPred (<http://iupred.enzim.hu/>). Residues with a score above 0.5 can be regarded as disordered.

SphI

wt ATGGCGGATAGTGGGGATAAATCCCAGGGCATGCGCCACCACCCTTTGACAGCCGTGGTCACCCTCTTCCC 72
 m-frq ATGGCGGATAGTGGGGATAAATCCCAGGGCATGCGCCCCCCGCCCTTCGACAGCCGCGGCCACCCCTCCCCC
 f-frq ATGGCCGACTCCGGCGACAAGTCCCAGGGCATGCGCCCCCCCCCCTTCGACTCCCGCGGCCACCCCTCCCCC

wt CGACGTGCTTCCCCAGACAAATCAATAACACTTAAAAATCACCGCCTTGCCGGAGATACTAGCAGCAGAGT 143
 m-frq CGCCGCGCTTCCCCCGACAAGTCCATCACCCTCGAGAACCACCGCCTCGCCCGCGATACCAGCAGCAGAGT
 f-frq CGCCGCGCTTCCCCCGACAAGTCCATCACCCTCGAAAATCACCGCCTTGCCGGAGATACTAGCAGCAGAGT

wt TACTTCATCTTCCGCACTGGGAGTGACCGAATCCCAACCCCAACTCAAGAGCTCGCCACCCGAAGGAATT 214
 m-frq CACCTCGTCCTCCGCCTGGGCGTGACCGAGTCCCAGCCCCAGCTCAAGAGCTCGCCACCCGCGAGGAACT
 f-frq CACCTCCTCCTCCGCCTCGGCGTCACCGAGTCCCAGCCCCAGCTCAAGTCCTCCCCCACCCGCCGCAACT

wt CGTCTGGAGAGAGCGAGCCCACGAATTGGTTTTAATCAATCCAATCGTAACCCTGCCGCGGCCTTTCATGAC 285
 m-frq CGTCCGGAGAGAGCGAGCCCACGAACTGGTTTTACCAGTCCAACCGCAACCCTGCCGCTGCCTTCCACGAC
 f-frq CCTCCGGCGAGTCCGAGCCCACCAACTGGTTCAACCAGTCCAACCGCAACCCGCCGCGCCTTCCACGAC

wt GAGAGCCATATCATGGAAGTCGATCCTCCTTTTTATCAAAGGAGACTGACTCCTCCAACGAGGAATCCAG 356
 m-frq GAGAGCCACATCATGGAGGTCGATCCTCCCTTCTACCGAAGGAGACCGACTCCTCCAACGAGGAGTCCCG
 f-frq GAGTCCCACATCATGGAGGTCGACCCCCTTCTACCGAAGGAGACCGACTCCTCCAACGAGGAGTCCCG

wt GTATCCGCCTGGACGAAACCCTGTACATCCGCCCGGTGGTGTCCAGTTACCCGGGTTCGCCCCGGTTGCTG 427
 m-frq CTACCCCCCTGGACGCAACCCTGTCCACCCGCCCGGTGGCGTCCAGCTCCCGGCTTCCGCCCGGTCGCCG
 f-frq CTACCCCCCCGGCGCAACCCCGTCCACCCCCCCGGCGGCGTCCAGCTCCCGGCTTCCGCCCGTCGCCG

AflII

wt CTCACAGCAGCGCCGCGATGACTACCGCAGTGTTCATGACGACTTGACTGTGAAAACAAGCGGCCTTAAG 498
 m-frq CTCACAGCAGCGCCGCGATGACTACCGCAGCGTTCATCGACGACTTGACTCGTGCAGAAACAAGCGCCTTAAG
 f-frq CCACTCTCCGCCGCGACGACTACCGTCCGTTCATCGACGACTCACCGTGCAGAAACAAGCGCCTTAAG

Figure s9: N-terminal nucleotide sequence comparison of the *frq* gene in the wild-type, *m-frq* and *f-frq* strains.

vt-*frq* TTGTTTGAGATCAAGGTACATGGCTTACCTAGAAGAAAGAAACGTGAGTTGGAGGCAACGCTCCGCGACTTTG 62:
 iid-*frq* **CTCTT**CGAGATCAAGGT**CCACGGCT****CCCCCGCCG**CAAGAAG**CGCGAGCT**CGAGGCC**ACCCT**CCGCGACT**TCG**

vt-*frq* CTGCCAGTCTCGGGGACTCGAGCGAATCGACATCGCAGAGGAGAAAGACTGGCAGACATGGAACGGCCGTTCA 69:
 iid-*frq* **CCGCTCCCT**CGG**CGACTCT**CCGAG**TCCACCTCC**AG**CGCCG**CAAGAC**CGGCCGCC**AC**CGGCAC**CGCCGT**CCA**

vt-*frq* CTCGTCTGGGGTTTCGTTGTCGAAACACGATTTCGTTCGTTCATCGTTCGCGCAGTTCGTCTGTTCGATTCTGCATAC 77:
 iid-*frq* **CTCTCCGGCGTCTCCCTCT**CAAGCACGACT**CTCTCTCTCT**CCG**CTCCCG**CCCGT**CGACTCCGC**TAC

vt-*frq* AACTCTATGTCGACGGGCCGTAGCTCTCATGCGCCCCACTCTTCCGGTCCGTTCGCTCGGACGACCTTCGCTGA 84:
 iid-*frq* AACT**CCATGTCCAC**CGGCC**CTCTCTCC**AC**CGCCCC**CACT**CTCCGGCCC**CT**CTCTCGG**CGCC**CTCCCT**CA

vt-*frq* CCAGGGCAAATCCGTTCGGGACCCAAAAGGTAGAAAATCTGCGCGACACGCCCGATGGCCTGCTTCCTCA 91:
 iid-*frq* **CCCGCGCAAGT**CCGTTCGG**CACCCAG**AAGGT**CGAGAACT**CT**CCGCGACAC**CCCG**ACGGCCTCT**CCCCA

vt-*frq* CCATATTGTCATGACCGACAAGGAGAAGAAGAAGCTGGTTGTCCGACGCTTGGAGCAACTGTTACCCGGAAAG 99:
 iid-*frq* **CCACAT**CGTCATGACCGACAAGGAGAAGAAGAAGCT**CGT**CGTCCG**CCGCT**CGAG**CACTCT**TACCCGG**CAAG**

vt-*frq* ATCAGTGGACGAAACATGCAGCGCAACCAGTTCGATGCCGAGCATGGATGCACCACTCGCGCCGGAAGGAACCA 106:
 iid-*frq* AT**CTCCGGCCG**CAACATGCAGCGCAACCAGT**CCATGCC**CT**CCATGGAC**CGCC**CCCTCGC**CCCGAGGG**CCACCA**

vt-*frq* ACATGGCCCCCCCCTCGCCCCCTCCGGAAGGATTGCGCGAAGCTTGCATCCAACCTACAGGATGGAGACAACCC 113:
 iid-*frq* ACATGGCCCCCCCC**CCGCCCCC**CCCGAGGG**CTCCGCGAGGC**CTGCAT**CCAGCTCC**AGGAC**CGCGACA**ACCC

vt-*frq* GCGAAAGAACCCTCCTCCAAGACAATGGTTCTGCATCCAACCTCGGGTGGCGATCAAACCGAACTTGGCGGA 120:
 iid-*frq* **CCGCAAGA**ACC**CTCCTCCA**AGGACA**ACGGCTCCGC**CTCCAAC**CTCCGG**CGCGAC**CCAG**ACCGAG**CTCGGCGGC**

vt-*frq* ACTGGGACTGGAAGCGGAGATGGAAGTGAAGCGGCGGTTCGCACTGGTAACAACACCTCGCCCCCGGGAGCTA 128:
 iid-*frq* **ACCGGCAC**CGG**CTCCGGCG**ACGG**CTCCGGCT**CCGGCGG**CCGCAC**CGG**CAACAAC**ACCT**CCCCCC**CGG**CGCCA**

vt-*frq* TTGCGCCGGACCAACGACCAACCAGGCCTCGCGATTTGGACCCGGACCGCGTCCAGATACCATCCGAGAATAT 135:
 iid-*frq* **TCGCCCCG**ACCAG**CGCCCC**ACC**CGCCCC**CGCG**ACTCG**ACCC**CGACCG**CGTCCAGAT**CCCCT**CCGAGAA**CAT**

vt-*frq* GGACTACATCCGTTCATCTGGGCCTTGTATCTCCCGAATTCCTTGCAGGGAAGCCGGACCAGCTATCAAGATGTT 142:
 iid-*frq* GGACTACATCCG**CCACCT**CGGCCT**CGTCT**CCCCGAG**TCTCC**AGGG**CTCCCG**CAC**CTCCT**ACCAGGAC**CTC**

vt-*frq* GCTCCGGATGCGGAAGGCTGGGTGTATCTCAATCTGCTTTGTAACTGGCCCAGCTGCACATGGTTAACGTAA 150:
 iid-*frq* **GCCCCG**AC**CGCCGAG**GGCTGGGT**CTACCT**CA**ACTCTCT**G**CAACT**CGCCCAG**CTCC**ACATGGT**CAACGTCA**

vt-*frq* CGCCGAGTTTTATTCCGCAAGCTGTCTCCGAAAAGAGCACAAAGTTCAGCTGTCTGCTGATGGTTCGGAAAAT 157:
 iid-*frq* **CCCCCT**CTT**CATCCG**CA**GGCGTCT**CCGAG**AAGTCC**AC**CAAGTTC**AGCT**CTCC**GG**CGACGG**CCG**CAAGAT**

vt-*frq* CCGCTGGCGTGGCGGA 1590
 iid-*frq* CCGCTGGCG**CGCGGC**

Figure s10: Nucleotide sequence comparison of the *frq* gene in the wild-type and mid-*frq* strains.

Table s1: The top 100 most abundant *Neurospora* proteins identified by mass spectrometry analysis.

Gene	protein_description	prot_hit	score	mass	matches	coverage	prot_emPAI
NCU07826T0	40S ribosomal protein S19 (150 aa)	73	1963	16660	84	49.0	27.96
NCU02744T0	60S ribosomal protein L9 (194 aa)	52	2279	21739	61	58.5	22.42
NCU07830T0	cytoplasmic ribosomal protein-2 (151 aa)	47	2574	15987	62	68.7	21.89
NCU04120T0	calmodulin A (150 aa)	141	1105	16986	29	69.1	21.85
NCU03148T0	nascent polypeptide-associated complex beta subunit (153 aa)	98	1552	16556	34	54.6	19.71
NCU01808T0	cytochrome c (109 aa)	199	773	11806	36	42.6	18.10
NCU00979T0	60S acidic ribosomal protein P2 (111 aa)	39	2960	11096	51	81.8	16.37
NCU11745T0	hypothetical protein (72 aa)	371	360	7914	14	80.3	16.17
NCU09345T0	no message in thiamine-1 (343 aa)	6	10479	38174	315	62.6	15.09
NCU07914T0	phosphoglycerate kinase (419 aa)	14	6049	45029	168	62.9	11.14
NCU04140T0	FK506 resistant-2 (176 aa)	65	2069	19217	55	44.6	10.86
NCU07182T0	40S ribosomal protein S24 (137 aa)	115	1377	15553	39	50.0	10.69
NCU09995T0	hypothetical protein (96 aa)	131	1187	10742	25	49.5	10.06
NCU06431T0	40S ribosomal protein S22 (131 aa)	113	1392	14811	36	61.5	9.84
NCU10042T0	enolase (439 aa)	1	27348	47565	542	61.9	9.64
NCU01528T0	glyceraldehyde-3-phosphate dehydrogenase-1 (339 aa)	5	12266	36270	303	56.2	9.33
NCU06512T0	methionine synthase (770 aa)	3	14407	86259	391	62.9	9.09
NCU06661T0	60S ribosomal protein L22 (127 aa)	137	1133	14201	36	54.8	8.63
NCU04779T0	60S ribosomal protein L8 (263 aa)	103	1505	29349	45	45.8	8.59
NCU00726T0	cyclosporin-resistant-1 (224 aa)	17	4816	24049	102	62.8	8.37
NCU00294T0	60S ribosomal protein L10a (218 aa)	87	1765	24111	37	37.8	8.37
NCU00634T0	ribosomal protein L14 (143 aa)	156	973	15844	35	52.8	8.25
NCU02136T0	transaldolase (301 aa)	28	3913	32752	100	59.3	8.15
NCU06550T0	pyridoxine 1 (309 aa)	57	2209	32334	64	52.9	7.58
NCU05804T0	60S ribosomal protein L19 (193 aa)	125	1249	22334	40	48.4	7.51

NCU03565T0	ribosomal protein L26 (137 aa)	169	903	15322	26	50.7	7.24
NCU09602T0	heat shock protein 70-1 (647 aa)	25	4251	70510	122	53.1	7.04
NCU04334T0	chaperonin (105 aa)	434	282	11127	10	51.9	6.97
NCU01949T0	40S ribosomal protein S9 (191 aa)	123	1266	21793	53	51.1	6.82
NCU07700T0	colonial temperature-sensitive-3 (845 aa)	7	9462	93203	285	56.0	6.70
NCU00489T0	cytoplasmic ribosomal protein-10 (263 aa)	132	1169	28649	33	59.2	6.36
NCU08340T0	ADP-ribosylation factor 1 (186 aa)	211	739	20966	25	63.8	6.30
NCU06110T0	thiazole biosynthetic enzyme (345 aa)	2	15382	36841	320	54.7	6.19
NCU02274T0	serine hydroxymethyltransferase (481 aa)	38	2966	52944	90	54.2	6.08
NCU00464T0	60S ribosomal protein L32 (132 aa)	164	921	14955	27	40.5	6.08
NCU05498T0	hypothetical protein (181 aa)	215	722	19738	28	58.9	6.07
NCU07287T0	hypothetical protein (227 aa)	99	1550	24509	36	76.1	6.05
NCU02181T0	40S ribosomal protein S4 (262 aa)	97	1610	29578	50	52.9	5.95
NCU04202T0	nucleoside diphosphate kinase-1 (153 aa)	74	1955	16890	56	52.0	5.85
NCU06226T0	60S ribosomal protein L25 (157 aa)	108	1445	17109	39	45.5	5.69
NCU01204T0	tropomyosin (162 aa)	129	1207	18771	26	52.8	5.67
NCU04173T0	actin (376 aa)	51	2282	41581	76	54.7	5.66
NCU08620T0	40S ribosomal protein S16 (143 aa)	174	881	15714	37	52.1	5.46
NCU01452T0	40S ribosomal protein S1 (257 aa)	116	1359	29051	36	42.2	5.45
NCU02133T0	superoxide dismutase (155 aa)	70	1989	15875	47	55.8	5.38
NCU06075T0	pyruvate kinase (528 aa)	20	4547	57834	119	53.7	5.35
NCU02629T0	bifunctional purine biosynthesis protein (595 aa)	36	3094	64646	79	65.7	5.33
NCU00475T0	40S ribosomal protein S18 (157 aa)	111	1426	17758	54	51.9	5.25
NCU02252T0	phosphoglycerate mutase (520 aa)	37	3091	56782	79	47.2	5.21
NCU06346T0	hypothetical protein (102 aa)	196	782	11057	18	64.4	5.15
NCU05599T0	40S ribosomal protein S28 (69 aa)	204	762	7716	20	36.8	5.05
NCU08627T0	cytoplasmic ribosomal protein-7 (88 aa)	197	781	9655	19	48.3	4.88

NCU03302T0	60S ribosomal protein L36 (105 aa)	444	275	11549	20	43.3	4.76
NCU02806T0	14-3-3 family protein 7 (263 aa)	157	971	29311	29	50.0	4.74
NCU07922T0	elongation factor 3 (1057 aa)	15	5419	117036	166	59.1	4.67
NCU08963T0	60S ribosomal protein L30 (110 aa)	146	1064	11695	25	22.0	4.67
NCU01195T0	amination-deficient (455 aa)	10	7945	48823	166	59.9	4.38
NCU01827T0	60S ribosomal protein L27 (136 aa)	228	631	15713	28	41.5	4.36
NCU06031T0	mitochondrial peroxiredoxin PRX1 (226 aa)	109	1438	25097	35	51.1	4.33
NCU04826T0	hypothetical protein (1423 aa)	30	3643	152765	109	56.0	4.12
NCU06783T0	ATP citrate lyase (488 aa)	84	1792	52937	63	60.6	4.02
NCU08389T0	60S ribosomal protein L20 (175 aa)	92	1690	20330	41	40.2	4.01
NCU07807T0	fructose bisphosphate aldolase (363 aa)	11	7494	39864	133	53.9	3.95
NCU02003T0	translation elongation factor-1 (461 aa)	4	13798	49641	382	36.3	3.93
NCU02765T0	RNA binding protein (116 aa)	298	478	12973	10	55.7	3.80
NCU03608T0	ketol-acid reductoisomerase (403 aa)	61	2130	44596	53	49.5	3.79
NCU03757T0	60S ribosomal protein L4-A (362 aa)	53	2249	38790	59	44.9	3.78
NCU07014T0	cytoplasmic ribosomal protein-3 (147 aa)	133	1156	16932	28	51.4	3.78
NCU00147T0	ARD/ARD family protein (179 aa)	331	421	20960	14	64.6	3.77
NCU05290T0	orotate phosphoribosyltransferase (234 aa)	210	740	25131	16	57.5	3.73
NCU00413T0	60S ribosomal protein L2 (255 aa)	152	987	27340	41	50.0	3.67
NCU07027T0	glycogen phosphorylase (888 aa)	50	2304	100731	71	49.0	3.60
NCU09475T0	40s ribosomal protein s5 (214 aa)	168	905	23665	30	34.7	3.56
NCU08287T0	pyrABCN (1833 aa)	9	8580	202548	271	43.7	3.51
NCU05554T0	60S ribosomal protein L13 (215 aa)	58	2185	23862	47	45.3	3.50
NCU07307T0	fatty acid synthase beta subunit dehydratase (2093 aa)	8	9211	232306	260	51.3	3.49
NCU05238T0	sulfite reductase beta subunit (1539 aa)	21	4495	168954	135	48.3	3.46

NCU07281T0	glucose-6-phosphate isomerase (562 aa)	78	1901	61360	52	48.8	3.45
NCU09269T0	ran-like (216 aa)	330	421	24260	17	44.7	3.38
NCU02797T0	UTP-glucose-1-phosphate uridylyltransferase (522 aa)	79	1866	58154	55	54.5	3.35
NCU06047T0	40S ribosomal protein S2 (266 aa)	34	3242	28739	68	47.2	3.33
NCU03100T0	6-phosphogluconate dehydrogenase (493 aa)	80	1835	54191	53	43.3	3.32
NCU06397T0	profilin (134 aa)	140	1108	13954	27	66.9	3.32
NCU09285T0	zinc-containing alcohol dehydrogenase (347 aa)	119	1320	37272	42	54.0	3.31
NCU04142T0	heat shock protein 80 (706 aa)	44	2663	80139	77	40.6	3.28
NCU07267T0	blue light-induced-3 (210 aa)	279	511	22674	14	49.3	3.27
NCU03988T0	60S ribosomal protein L18 (184 aa)	134	1155	20590	34	39.3	3.26
NCU03102T0	40S ribosomal protein S11 (162 aa)	192	791	18417	22	34.2	3.25
NCU02505T0	succinate (1193 aa)	19	4655	130901	133	45.1	3.20
NCU03806T0	ribosomal protein L27a.e (150 aa)	147	1059	16587	32	47.0	3.16
NCU02193T0	cellular filament polypeptide (571 aa)	13	6127	62223	171	45.6	3.15
NCU04331T0	cytoplasmic ribosomal protein-4 (302 aa)	95	1658	34391	40	46.2	3.08
NCU06464T0	hypothetical protein (171 aa)	304	472	19015	19	42.4	3.08
NCU07308T0	fatty acid synthase alpha subunit reductase (1865 aa)	12	7225	204804	223	42.8	3.06
NCU02905T0	60S ribosomal protein L23 (140 aa)	96	1612	14690	25	25.2	3.06
NCU03826T0	elongation factor 1-gamma (409 aa)	104	1504	45712	54	47.8	3.04
NCU05488T0	RNA-binding protein Vip1 (284 aa)	193	789	30304	23	64.3	3.03
NCU02595T0	hypothetical protein (136 aa)	284	504	14767	12	48.1	3.02
NCU02948T0	non-anchored cell wall protein-4 (206 aa)	249	586	21537	14	68.3	2.99
NCU11181T0	Ras superfamily GTPase (190 aa)	413	310	21569	10	44.4	2.99

Table s2: *Neurospora* codon usage frequencies and the predicted translation elongation rate based on tRNA copy numbers and anticodon-codon interaction.

		Observed codon frequency	Elongation rate (au)			Observed codon frequency	Elongation rate (au)
aa	codon	<i>N.crassa</i>		aa	codon	<i>N.crassa</i>	
Phe	UUU	0.348	0.333	Glu	GAA	0.344	0.222
	UUC	0.652	1		GAG	0.656	0.852
Leu	UUA	0.033	0.065	Ser	UCU	0.146	0.172
	UUG	0.180	0.183		UCC	0.245	0.517
	CUU	0.171	0.172		UCA	0.113	0.299
	CUC	0.323	0.516		UCG	0.177	0.184
	CUA	0.072	0.269		AGU	0.106	0.069
	CUG	0.221	0.194		AGC	0.213	0.207
Ile	AUU	0.314	0.3		Pro	CCU	0.234
	AUC	0.594	0.9	CCC		0.347	0.579
	AUA	0.092	0.383	CCA		0.192	0.404
Met	AUG	1	1	CCG		0.226	0.281
	Val	GUU	0.232	0.244	Thr	ACU	0.186
GUC		0.417	0.731	ACC		0.411	0.619
GUA		0.091	0.359	ACA		0.178	0.381
GUG		0.261	0.192	ACG		0.225	0.254
Tyr	UAU	0.327	0.333	Ala	GCU	0.243	0.226
	UAC	0.673	1		GCC	0.414	0.679
Stop	UAA	0.316			GCA	0.145	0.405
	UAG	0.263			GCG	0.199	0.202
	UGA	0.421		Cys	UGU	0.306	0.333
Trp	UGG	1	1		UGC	0.694	1
	His	CAU	0.391	0.333	Arg	CGU	0.144
CAC		0.609	1	CGC		0.285	0.629
Gln	CAA	0.395	0.267	CGA		0.115	0.267
	CAG	0.605	0.822	CGG		0.138	0.105
Asn	AAU	0.276	0.333	AGA		0.128	0.171
	AAC	0.724	1	AGG		0.191	0.114
Lys	AAA	0.225	0.111	Gly	GGU	0.255	0.241
	AAG	0.775	0.926		GGC	0.404	0.722
Asp	GAU	0.425	0.333		GGA	0.189	0.139
	GAC	0.575	1	GGG	0.152	0.185	

Table s3: Predicted free energy values (ΔG (kcal/mol)) of *frq* mRNA using mfold.

	<i>wt-frq</i>	<i>m-frq</i>	<i>f-frq</i>	<i>m1-frq</i>	<i>m2-frq</i>	<i>mid-frq</i>
1-30 nt	-7.10	-7.10	-8.20	-7.10	-7.10	-7.10
1-800 nt	-274.90	-292.50	-272.80	-285.30	-275.80	-264.70
553-1590 nt	-374.60					-339.60
full length	-1135.40	-1160.10	-1148.00	-1136.30	-1142.10	-1130.00