Table S1. Yeast RAN translation screen hits.

Table S1: Summary of Ribosomal mutant poly(GP) and GFP expression			
	poly(GP)	**GFP**	***C9 intron 1* RNA**
	Log_2 Fold-change compared to WT		***Fold-change compared to WT***
WT	-2.3279	-5.7347	0
WT C9 2R	-1.9209	N/A	N/A
WT C9 40R	-0.0111	N/A	1.0834
WT GFP	N/A	0.3101	N/A
rpl41AΔ	-1.7816	-1.3378	2.1206
rpp1BΔ	-1.6908	-0.7982	0.9201
rpl15BΔ	-1.5628	-1.2188	0.8173
rpl2BΔ	-1.2698	-0.2953	0.3316
rps25AΔ	-1.1326	-0.1500	1.1137
rps12*	-1.1033	-0.0822	0.2990
rpl42AΔ	-0.8627	-0.8697	1.0284
rps11AΔ	-0.7606	-0.1734	0.7185
rpl21AΔ	-0.6812	0.3603	0.5386
rps18AΔ	-0.6804	-3.5692	1.7100
rps15*	-0.6252	-0.1242	0.3331
rpl8BΔ	-0.6213	0.8560	0.5573
rps28BΔ	-0.5867	-0.8043	0.5404
rps17BΔ	-0.5755	-0.1397	1.1212
rps24BΔ	-0.5229	-1.4129	0.9248
rpl16BΔ	-0.5021	0.0433	0.7738
rpl31AΔ	-0.5008	1.3977	0.6704
rps6AΔ	-0.3368	-0.4489	0.9135
rps0AΔ	-0.2900	0.0541	0.5250
rpl32*	-0.2834	0.6834	1.2538
rpl41BΔ	-0.2443	-0.7782	0.6305
rps4BΔ	-0.2055	-0.9040	1.4418
rpl31BΔ	-0.2005	-0.7524	2.2669
rps6BΔ	-0.1576	-0.4807	0.5953
rps21BΔ	-0.1445	-3.2626	1.1192
rpl4AΔ	-0.1381	0.3529	0.9896
rpl29Δ	-0.0792	-0.2170	1.3798
rpl42B*	-0.0726	-1.0861	0.2082
rpl30*	-0.0437	-0.3303	N/A
rpp1AΔ	-0.0357	-0.4251	0.9590
rps16AΔ	0.0063	-0.6581	0.3659
rpl6BΔ	0.0141	-0.8005	0.3940
rpl27BΔ	0.0169	-0.7078	0.1861
rpl20AΔ	0.0247	-0.5626	0.6332
rpl35BΔ	0.0772	-0.1235	1.6190

rpl26AΔ	0.1339	-0.8351	0.5633
rps25BΔ	0.1510	-0.7915	1.0583
rpl40AΔ	0.2169	-0.7335	0.2053
rpl39Δ	0.2743	0.5273	0.8619
rpl37BΔ	0.3013	-0.8326	0.4006
rps9AΔ	0.3055	-0.3970	0.9117
rpl1AΔ	0.3095	-0.7042	0.6824
rpl9BΔ	0.3381	0.2370	0.9838
rpl36AΔ	0.3779	-0.1246	0.4771
rps14BΔ	0.3893	-0.7360	0.5110
rpl23AΔ	0.4028	-0.1124	0.8918
rps10BΔ	0.4061	-0.6305	N/A
rps12Δ	0.4539	-3.2970	0.3861
rpl43BΔ	0.4885	-0.7157	0.5648
rpl34AΔ	0.4966	-1.0446	0.3268
rps21A*	0.5027	0.6620	N/A
rpl7AΔ	0.5364	-0.5748	0.4599
rpl43AΔ	0.5469	-0.1751	0.6321
rps30BΔ	0.5639	-0.3612	1.2307
rps10AΔ	0.5931	0.1941	1.4429
rps11BΔ	0.6437	-4.2429	0.8987
rps7BΔ	0.6710	-0.3615	0.5845
rpp2AΔ	0.7022	-0.3153	0.4686
rpl8AΔ	0.7186	0.1017	0.5323
rps4AΔ	0.7411	-0.8356	0.6145
rpl20BΔ	0.7422	-0.3908	0.5308
rpl2AΔ	0.7929	0.2506	1.5188
rpl40BΔ	0.7952	0.4184	1.4828
rps22AΔ	0.7976	-1.0015	0.9639
rps23BΔ	0.8030	-0.6988	0.5605
rpl18BΔ	0.8472	-0.9011	0.7172
rps22BΔ	0.8556	-0.5677	0.6358
rps27BΔ	0.8625	-0.7607	0.4473
rpl16AΔ	0.9157	-0.5072	0.5418
rpl22BΔ	0.9238	-0.7162	0.9439
rps7AΔ	0.9514	-1.2944	0.5447
rpl11BΔ	0.9520	0.0451	0.4193
rpl27AΔ	1.0042	0.7242	0.6693
rps28AΔ	1.0044	-0.2632	0.7361
rps8AΔ	1.0121	-2.1198	0.3737
rpl37AΔ	1.0375	-0.5218	0.7382
rps16BΔ	1.0545	-1.4544	0.5306
rps19AΔ	1.0707	-0.5146	0.6991
rps19BΔ	1.0870	0.9776	0.6075
rpl17BΔ	1.0978	0.2613	0.9007
rpl7BΔ	1.1164	0.7857	0.4578
rpl19AΔ	1.1483	0.7821	1.1590
rps24AΔ	1.1518	-0.7943	0.7135

rps29BΔ	1.1564	0.1296	1.8416
rps9BΔ	1.1700	0.4536	0.7013
rpl34BΔ	1.1717	0.1153	0.4220
rpl19BΔ	1.1804	-0.5372	1.4921
rpl24AΔ	1.2407	0.0357	0.5255
rps1AΔ	1.2448	-0.2217	0.4843
rps18BΔ	1.2473	-0.1781	0.6264
rpl14AΔ	1.2553	0.1901	0.5445
rpl33BΔ	1.2649	-3.2181	0.8675
rps14AΔ	1.2662	-1.0332	0.0988
rps23AΔ	1.3306	-0.7730	0.2552
rps27AΔ	1.3340	-0.3125	0.3357
rps29AΔ	1.4873	-0.5714	0.3903
rpl24BΔ	1.4877	-1.5035	0.9346
rps1BΔ	1.5712	-0.0879	0.7604
rpl26BΔ	1.5817	-0.5430	0.5708
rpl21BΔ	1.7052	0.5740	1.2292
rpl35AΔ	1.7136	0.4387	0.4784
rpl22AΔ	1.7765	1.0847	0.4434
rpl38Δ	1.8226	0.0898	0.2705
rpl12BΔ	1.8751	-0.0816	0.5250
rps17AΔ	1.9710	0.0812	0.6362
rps21AΔ	2.1486	-0.0301	0.3452
rpl2AΔ	2.8269	-0.0351	1.3058
rpl12AΔ	3.2192	0.0810	0.3321
rpl13AΔ	3.2581	0.5301	1.2735

Yeast lysates were immunoassayed for poly(GP) and ATG-eGFP. Average Log_2 fold-change of biological triplicates of mutant poly(GP) and GFP (for ribosomal mutants) compared to wildtype were calculated and listed for mutants which increased or decreased poly(GP) levels. Yeast mutants with differential poly(GP) expression and not similarly changed GFP expression are indicated in blue (decreased poly(GP)) and red (increased poly(GP)). Negative values indicate lower expression compared to wildtype (WT, BY4741) yeast levels and positive values indicate an increase in expression. Values approaching 0 indicate less differential expression compared to WT expression. Average fold-change in *C9 intron 1* RNA levels yeast mutants compared to wildtype are listed where values approaching 1 indicate similar expression to WT C9 40R yeast. Additionally, 6 non-ribosomal mutants which all increase poly(GP) levels and do not similarly affect GFP levels: *mdm38Δ, asc1Δ, rex3Δ, ngl2Δ, pbp1Δ, ltv1Δ.*

* indicates mutants from the DAmP collection.

Table S2. HTT plasmid information from Coriell.

pcDNA3.1 HTT with variable CAG lengths		
Length	**Plasmid Name**	**Coriell Plamsid ID**
CAG10	Htt-Q10-pcDNA3.1	CH01660
CAG22	HTT-Q22, CAG, 1-90, HUMAN (in pcDNA3.1)	CH00027
CAG39	HTT-Q39-PCDNA3.1, 1-90, S13A S16A (IRBM)	CH01685
CAG82	HTT-Q82-PCDNA3.1, PURE, 1-586 (K6R)	CH01352

Original, unmodified constructs in pcDNA3.1 vector were used in this study.

Table S3. Information regarding patient-derived iPSCs used in this study.

iPSC Experiments							
ID	**Sample name**	**Group**	**Disease duration**	**Onset site**	**Age at DOD**	**Gender**	**Source**
2242-1	control 1	N/A	N/A	N/A	4	M	Dr. Sergiu Pasca
8858-1	control 2	N/A	N/A	N/A	22	M	
33	patient 1	C9ORF72	>9 yrs	spinal	70	M	Dr. Jeff Rothstein
92	patient 2	C9ORF72	>4 yrs	bulbar	53	M	
ND50000	patient 3	C9ORF72	N/A	N/A	64	F	Target ALS

iMN Experiments								
NINDS/ Coriell Code	**Sample name**	**Mutation**	**Disease**	**Age of Onset**	**Age at sampling**	**Gender**	**iPSC karyotype**	**Source**
ND03231	control 3	control	N/A	N/A	56	M	normal	Dr. Justin Ichida
ND05280	control 4	control	N/A	N/A	72	F	normal	
ND03719	control 5	control	N/A	N/A	33	M	normal	
ND06769	patient 4	C9ORF72	ALS/FTD	45	46	F	normal	
ND10689	patient 5	C9ORF72	ALS/FTD	49	51	F	normal	
ND12099	patient 6	C9ORF72	ALS/FTD	48	49	M	normal	