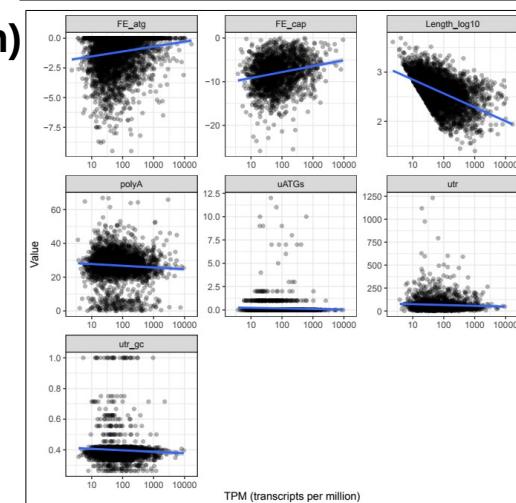
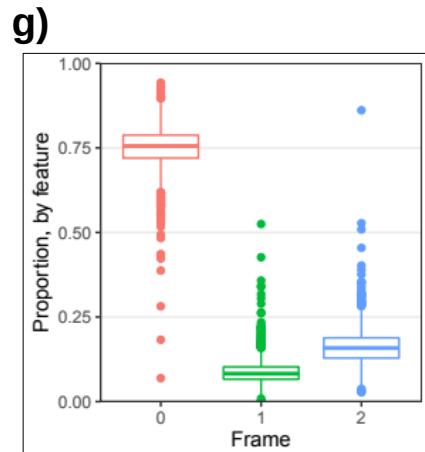
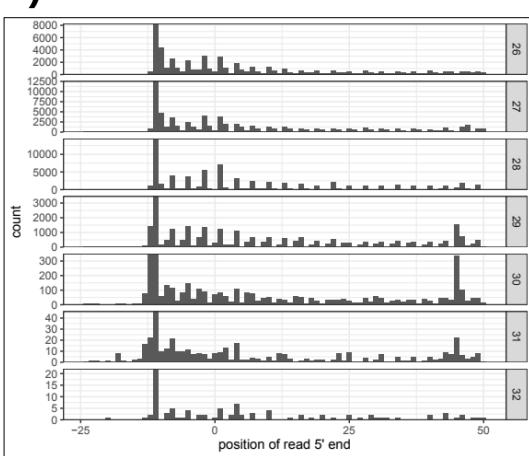
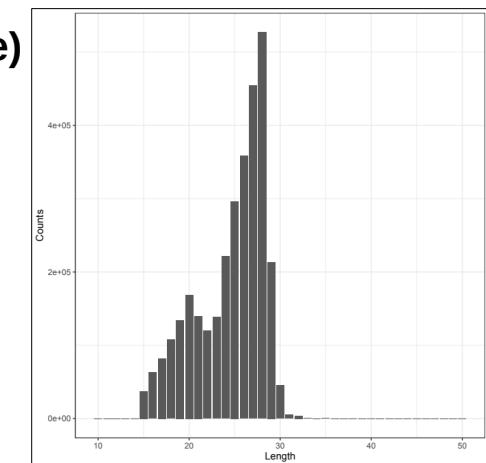
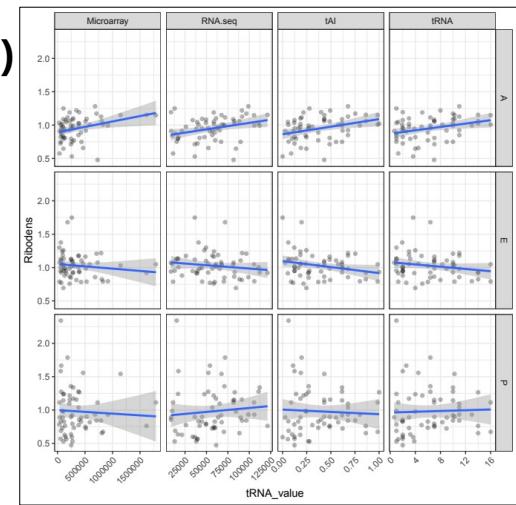
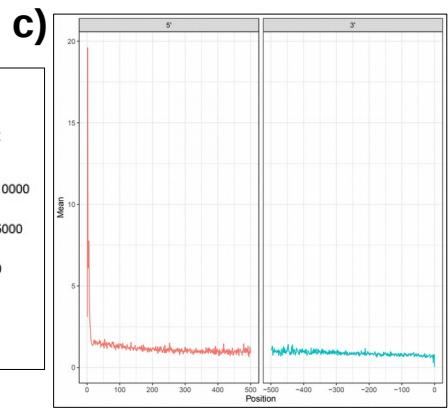
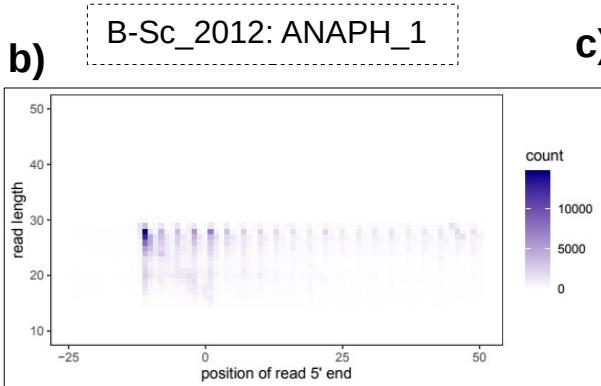
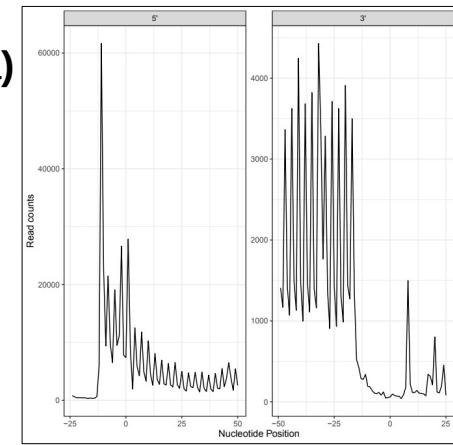


Riboviz Current Outputs

Data abbreviations:

- **B-Sc_2012**: *Saccharomyces cerevisiae* yeast RPF samples at a range of meiotic phases from: High-resolution View of the Yeast Meiotic Program Revealed by Ribosome Profiling, *Brar et al.* 2012
 - Files present: 'all'
- **W-Cn-H99_2020**: *Cryptococcus neoformans* strain H99 yeasts from: Quantitative global studies reveal differential translational control by start codon context across the fungal kingdom. *Wallace et al.* 2020
 - Files *not* present: A-site displacement length, codon positions file, features file, tRNA estimates file
- Yaml config files available at <https://github.com/riboviz/example-datasets>



- a)** 3nt_periodicity.pdf; **b)** startcodon_ribogrid.pdf; **c)** pos_sp_rpf_norm_reads.pdf;
d) codon_ribodens.pdf; **e)** read_lengths.pdf; **f)** 3ntframe_propbygene.pdf; **g)** startcodon_ribogridbar.pdf;
h) features.pdf

a)

Pos	Counts	End
-24	8325'	
-23	5995'	
-22	4575'	
-21	4975'	
-20	4575'	
-19	4625'	
-18	4295'	
-17	3255'	

b)

date 2020-03-04 13:45:40		
	Length	Counts
	10	0
	11	0
	12	0
	13	0
	14	0
	15	37534
	16	62944
	17	82132
	18	107977
	19	134409
	20	168903
	21	139873
	22	120034

e)

AA.Codon	tRNA	tAI	Microarray	RNA.seq	A	P	E
K AAA	7	0.431034	222273	82386	1.05790819002401	1.15291059609784	0.86528716593696
N AAC	10	0.615764	378101	110849	1.0281152292804	1.27708638433922	1.0050442206497
K AAG	14	1	397111	83036	1.0224822832824	1.26675365537118	0.93226129746333
N AAT	6.4	0.27032	241984.64	70943.36	0.99399477267163	1.35673169342604	0.848902424015964
T ACA	4	0.426373	105862	47598	0.819260573895541	1.23679352095319	1.25916809965654
T ACC	7.04	0.487685	244374.4	36396.16	0.71274780107203	0.896873450468225	1.1195384037134
T ACG	1	0.140394	113104	16861	0.797757582450966	1.24033130452294	1.13475360386371
T ACT	11	0.67734	381835	56689	0.849232525038719	1.03763261086384	1.17820012062022
R AGA	11	0.67734	683001	98684	1.28096241976118	0.93292123483255	0.865677205337026
Z AGC	1	0.23153	249498	61334	0.950093444227615	0.47288787628337	1.01587991491282
R AGG	1	0.278325	106890	12911	1.24963311379243	0.52950749627423	0.953871071715205
Z AGT	1.28	0.05464	159966.72	39253.76	1.04600979170965	0.563371259730159	0.914016268811146
I ATA	2	0.123233	54352	39556	0.72403923288364	0.569831032158084	0.951443079270135
I ATC	8.32	0.576355	586391.04	67769.6	1.00775448514063	0.817362847783829	1.04955306675208

f)

gene	Ct_fr0	Ct_fr1	Ct_fr2	pval_fr0vs1	pval_fr0vs2	pval_fr0vsboth
YAL068C	0	0	0	1	1	1
YAL067W-A	0	0	0	1	1	1
YAL067C	8	3	0	0.09154837080959	0.007354384721559	0.003834285390189
YAL065C	1	1	0	0.681324055883031	0.5	0.630558659818236
YAL064W-B	1	0	0	0.5	0.5	0.5
YAL064C-A	0	0	0	1	1	1
YAL064W	0	0	0	1	1	1
YAL063C-A	0	0	0	1	1	1
YAL063C	12	2	8	0.018148283043708	0.091757084963638	0.007742087124372
YAL062W	108	10	15	2.35529750560817E-10	9.00694786412824E-09	2.53109099063683E-17
YAL061W	90	18	24	3.58565108086954E-08	1.6306211759895E-06	6.25221450296923E-13
YAL060W	17	2	3	0.000954008674701	0.002457242914611	1.43343558100775E-05
YAL059W	2	1	0	0.386414996342224	0.17288929307558	0.19193419149591

B-Sc_2012: ANAPH_1**c)**

03-04 13:45:40				
Position	Mean	SD	End	
1	3.09468318483036	0.4618912910735415'		
2	19.5972312330649	0.9235392893943445'		
3	6.619958020074	0.4061772506964855'		
4	6.1029970243865	0.3601949204289585'		
5	6.89248368507423	0.3580052856543145'		
6	7.75982234858604	0.4280735984429265'		
7	4.3147969691262	0.2283302484448355'		
8	3.49490039308476	0.2227345151318555'		
9	2.77353738121589	0.1816180399190935'		
10	2.39400068694424	0.168236938518495'		
11	1.92566213792314	0.1153937526237455'		

d)

Length	Position	Frame	A	C	G	T
10	1	0	0	0	0	0
10	2	0	0	0	0	0
...
30	14	0	0.275	0.196	0.334	0.195
30	15	0	0.167	0.0999	0.159	0.574
30	16	0	0.195	0.549	0.0751	0.181
30	17	0	0.143	0.352	0.207	0.298
30	18	0	0.185	0.324	0.161	0.33
30	19	0	0.2	0.222	0.292	0.286
30	20	0	0.165	0.404	0.106	0.325
30	21	0	0.501	0.2	0.162	0.137
30	22	0	0.181	0.24	0.415	0.164
30	23	0	0.143	0.253	0.227	0.377
30	24	0	0.287	0.0952	0.257	0.36
30	25	0	0.285	0.157	0.394	0.164
30	26	0	0.235	0.249	0.11	0.407
30	27	0	0.177	0.426	0.266	0.13
30	28	0	0.39	0.163	0.289	0.158
30	29	0	0.16	0.174	0.125	0.54
30	30	0	0.192	0.305	0.222	0.282
30	1	1	0.145	0.249	0.0958	0.51

g)

04 13:45:40			
ORF	readcount	rpb	tpm
Q0045	277	0.167675544794189	54.1492075552714
Q0050	5	0.001959247648903	0.632720220010838
Q0275	94	0.109684947491249	35.4217008489988
...
YAL001C	103	0.029178470254958	9.42290686408889
YAL002W	37	0.00955785123967	3.0859407305286
YAL003W	848	1.26946107784431	409.9602686361
YAL005C	10367	5.26465748987854	1694.29308190433
YAL007C	87	0.125178956115108	40.4256328424997
YAL008W	140	0.217391304347826	70.204430484642
YAL009W	33	0.039903264812576	12.886376311592
YAL010C	24	0.0156965333682145	5.06904487053288
YAL011W	37	0.019220779220779	6.20716613551204

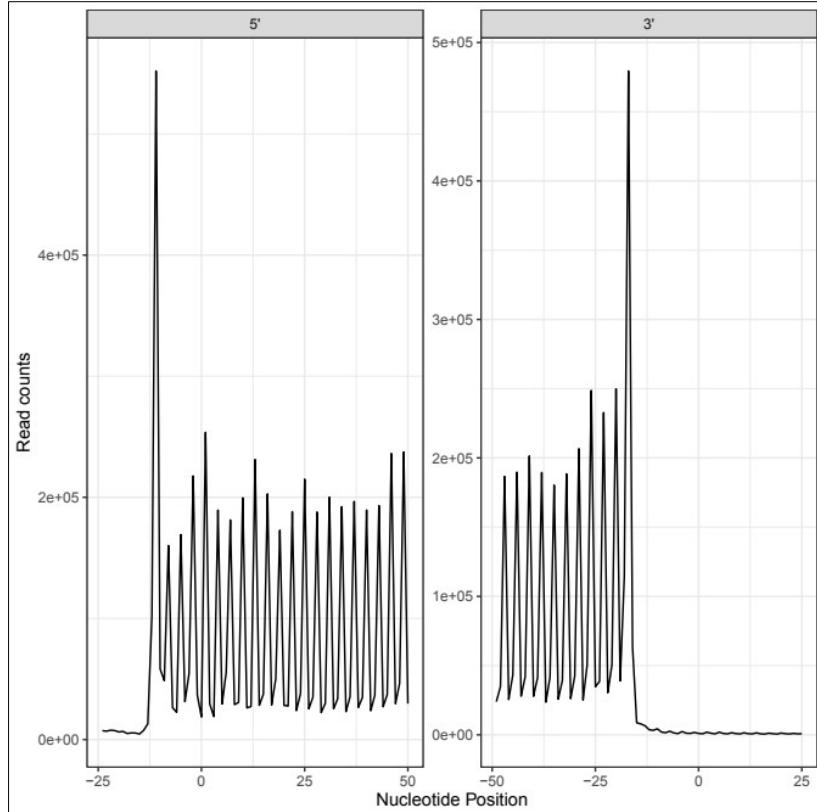
h)*

SampleName	Program	File	NumReads	Description
VEG_1	input	B-Sc_2012/input/SRR38781_GSM843747	21155927	input
VEG_2	input	B-Sc_2012/input/SRR38782_GSM843748	20915375	input
ANAPH_1	input	B-Sc_2012/input/SRR38789_GSM843766	10210064	input
ANAPH_2	input	B-Sc_2012/input/SRR38781_GSM843767	11620421	input
SPORE_1	input	B-Sc_2012/input/SRR38789_GSM843776	11782015	input
SPORE_2	input	B-Sc_2012/input/SRR38789_GSM843775	10793988	input
ANAPH_1	cutadapt	B-Sc_2012/tmp/ANAPH_1/trim.fq	9458608	Reads after removal of sequencing library
ANAPH_1	hisat2	B-Sc_2012/tmp/ANAPH_1/nonrRNA.fq	5999396	rRNA or other contaminating reads removed
ANAPH_1	hisat2	B-Sc_2012/tmp/ANAPH_1/rRNA_map.sam	9458608	Reads with rRNA and other contaminating
ANAPH_1	hisat2	B-Sc_2012/tmp/ANAPH_1/unaligned fq	2919159	Unaligned reads removed by alignment of
ANAPH_1	hisat2	B-Sc_2012/tmp/ANAPH_1/orf.map.sam	3348087	Reads aligned to ORFs index files
ANAPH_1	ribovorts.trim	B-Sc_2012/tmp/ANAPH_1/orf.map.clean.s+	3348087	Reads after trimming of 5' mismatches a
ANAPH_2	cutadapt	B-Sc_2012/tmp/ANAPH_2/trim.fq	11231640	Reads after removal of sequencing library
ANAPH_2	hisat2	B-Sc_2012/tmp/ANAPH_2/nonrRNA.fq	9365904	rRNA or other contaminating reads removed
ANAPH_2	hisat2	B-Sc_2012/tmp/ANAPH_2/rRNA_map.sam	11231649	Reads with rRNA and other contaminating

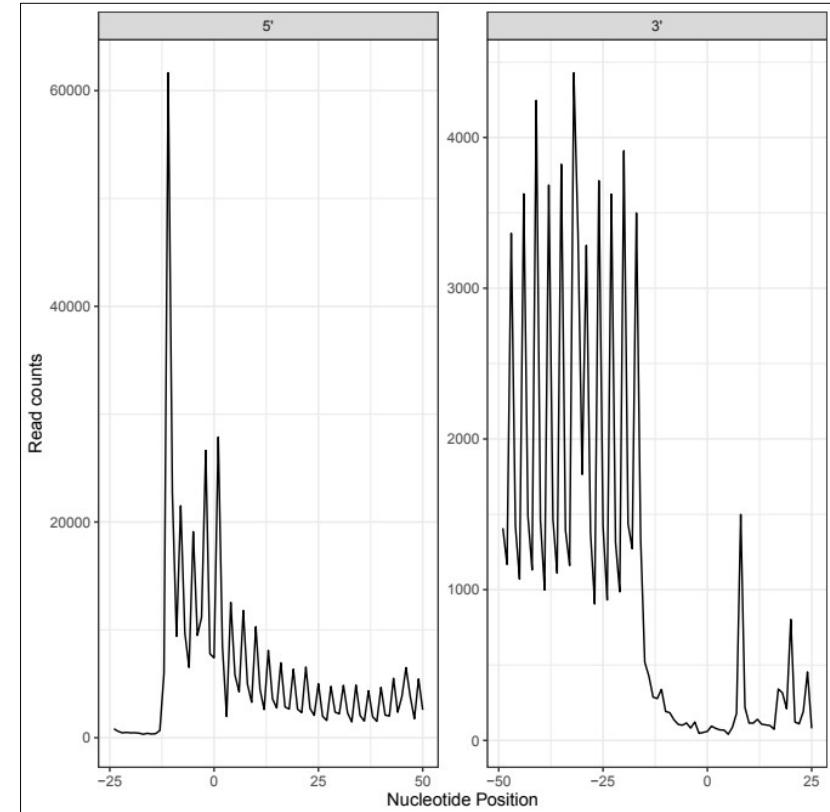
- a) 3nt_periodicity.tsv; b) read_lengths.tsv; c) pos_sp_rpf_norm_reads.tsv;**
d) pos_sp_nt_freq.tsv; e) codon_ribodens.tsv; f) 3ntframe_bygene.tsv; g) tpms.tsv;
h) TPMs_collated.tsv*; i) read_counts.tsv* * collates data from all 6 samples run

3nt_periodicity.pdf

Nucleotide periodicity of mapped reads showing counts, from 5' and 3' ends



W-Cn-H99_2020: H99r1



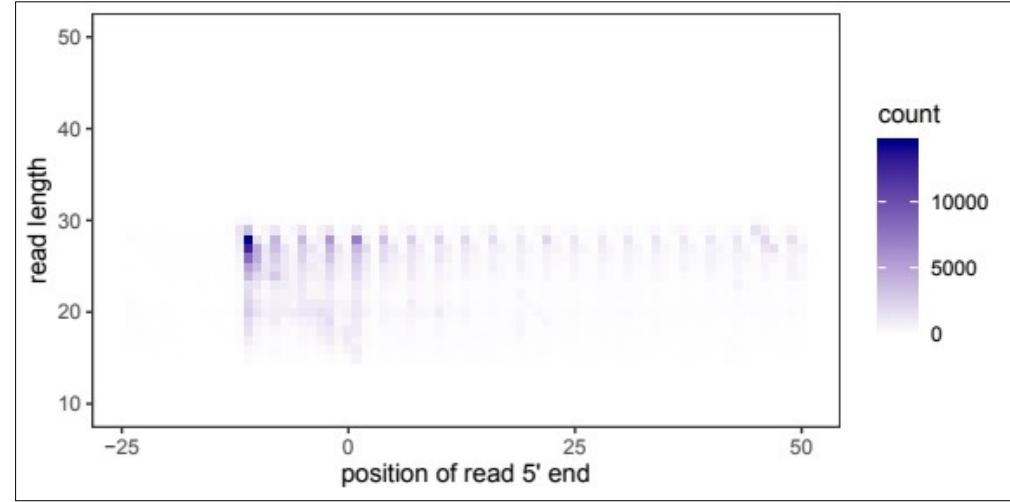
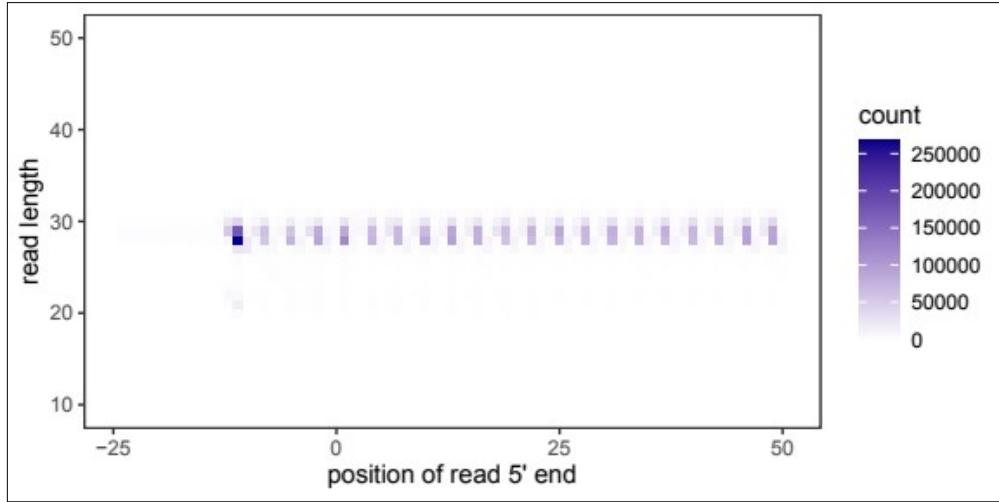
B-Sc_2012: ANAPH_1

Quantitative global studies reveal differential translational control by start codon context across the fungal kingdom. Wallace et al. 2020

High-resolution View of the Yeast Meiotic Program Revealed by Ribosome Profiling, Brar et al. 2012

startcodon_ribogrid.pdf

Counts at different read lengths starting at each nucleotide position



W-Cn-H99_2020: H99r1

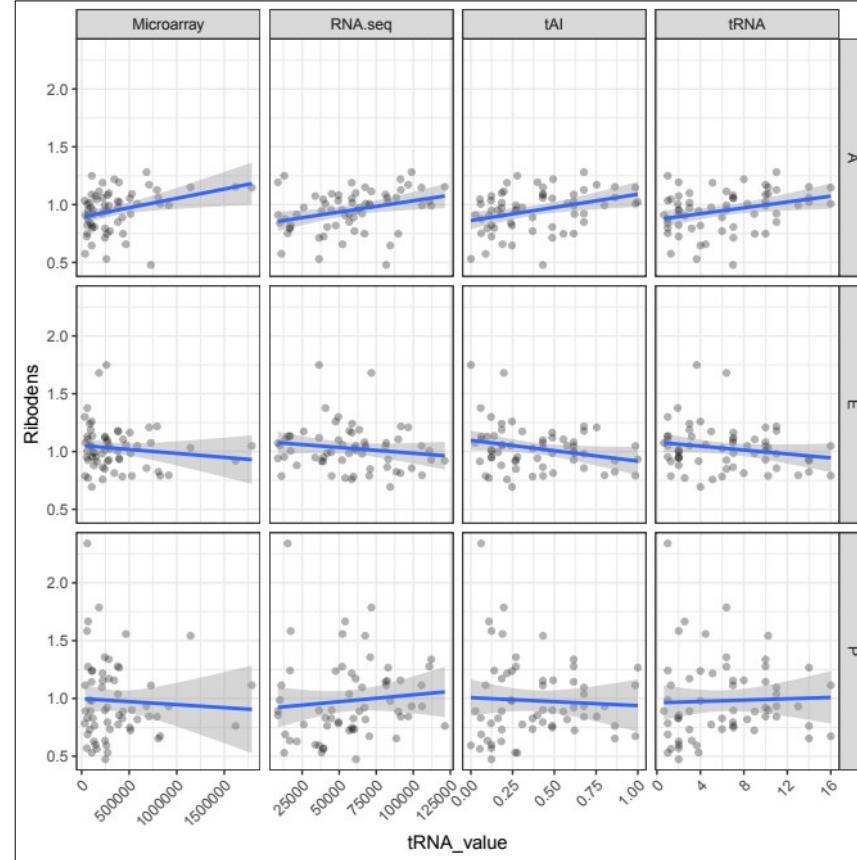
B-Sc_2012: ANAPH_1

Quantitative global studies reveal differential translational control by start codon context across the fungal kingdom. *Wallace et al. 2020*

High-resolution View of the Yeast Meiotic Program Revealed by Ribosome Profiling, *Brar et al. 2012*

codon_ribodens.pdf

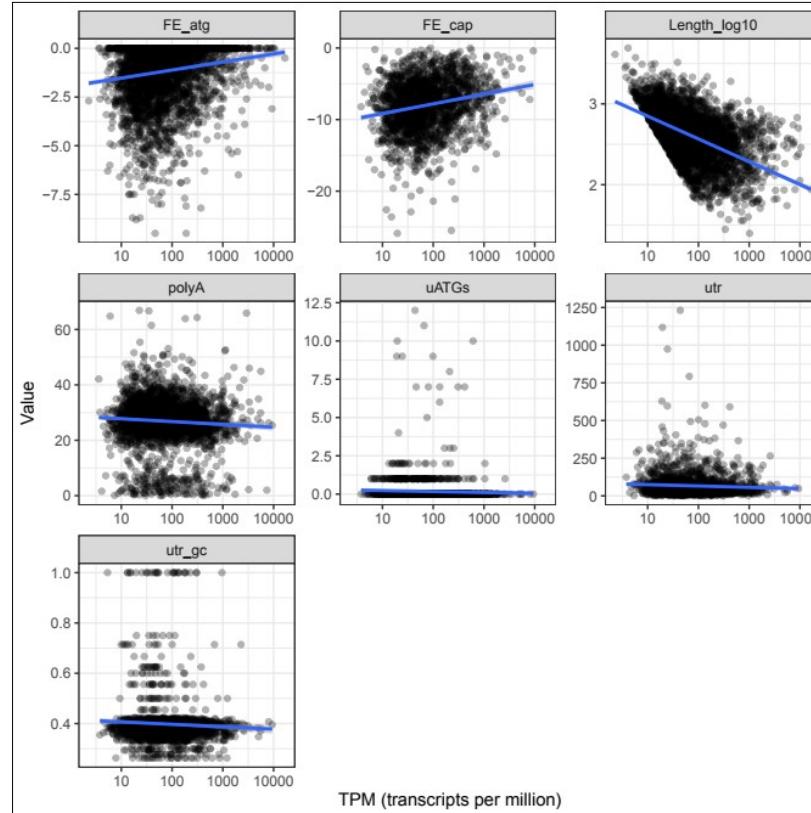
tRNA abundances and ribosome densities



B-Sc_2012: ANAPH_1

features.pdf

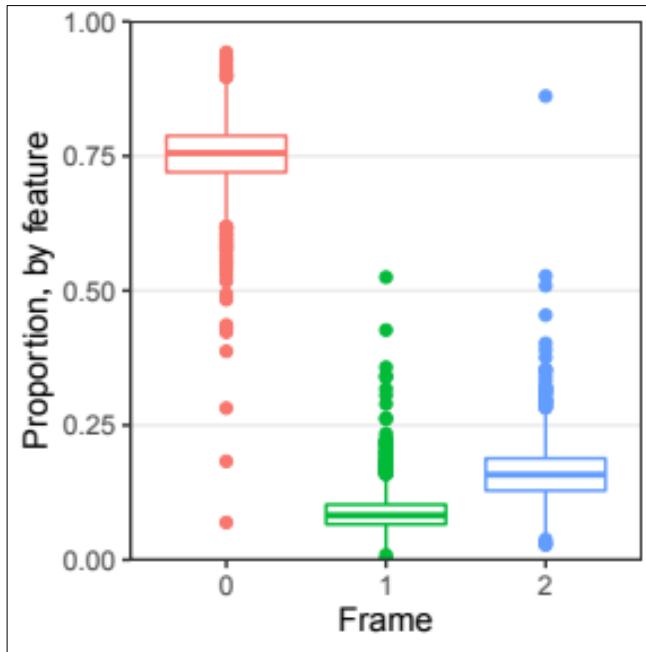
Values of sequence-based features and TPMs



B-Sc_2012: ANAPH_1

3ntframe_propbygene.pdf

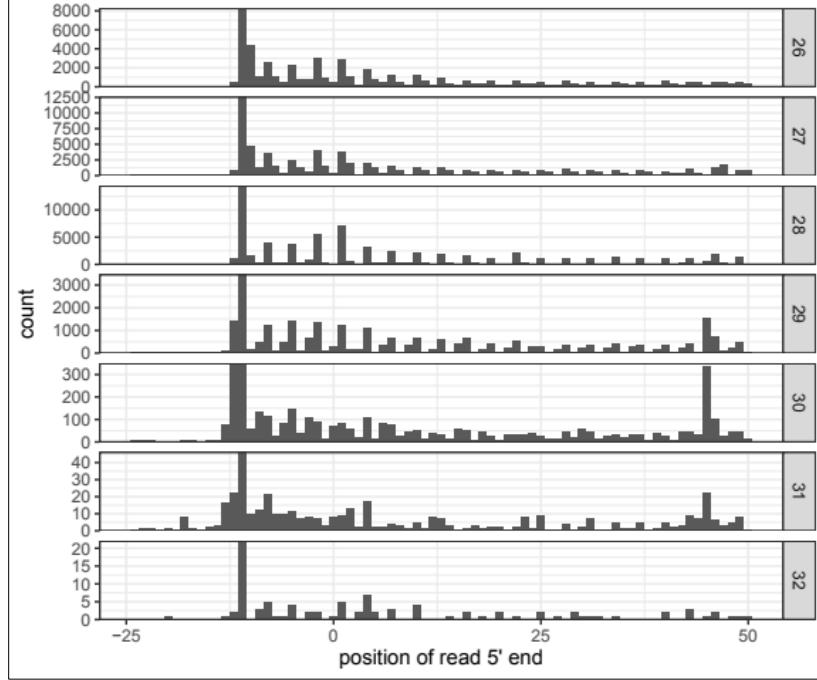
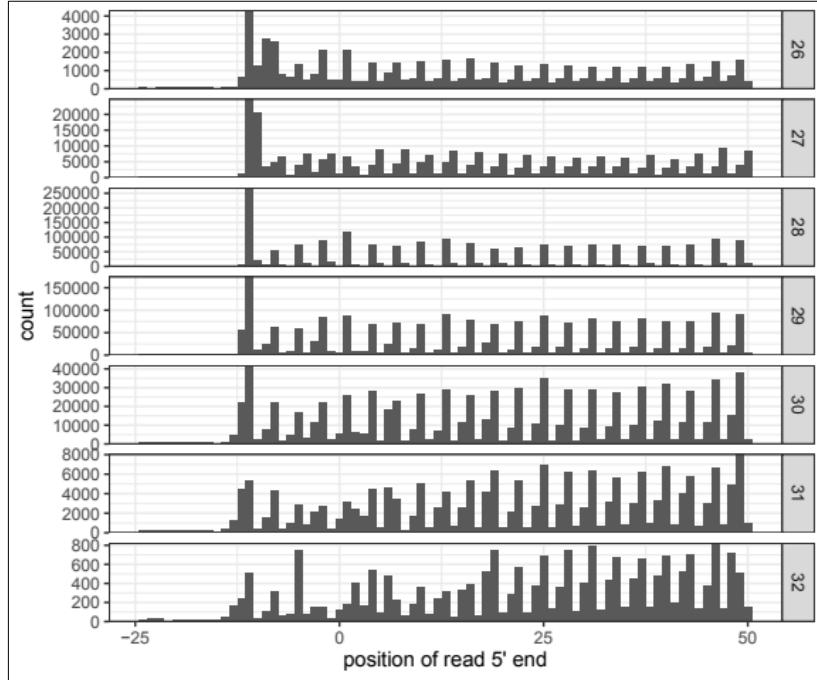
Proportion of reads in each frame



B-Sc_2012: ANAPH_1

startcodon_ribogridbar.pdf

Read counts starting at each nucleotide position, per read length



W-Cn-H99_2020: H99r1

B-Sc_2012: ANAPH_1

Quantitative global studies reveal differential translational control by start codon context across the fungal kingdom. Wallace *et al.* 2020

High-resolution View of the Yeast Meiotic Program Revealed by Ribosome Profiling, Brar *et al.* 2012

3nt_periodicity.tsv

Read counts starting at each nucleotide position, from 5' and 3' ends

	A	B	C	D
1	# Created by: RiboViz			
2	# Date: 2020-07-21 22:50:30			
3	# File: /home/flic/riboviz/rscripts/generate_stats_figs.R			
4	# Version: commit 03a4f13b2d833b8650ebf33bdce81fe2639eb9cf date 2020-07-08 15:42:55			
5		Pos	Counts	End
6		-24	7355	5'
7		-23	6949	5'
8		-22	7728	5'
9		-21	7435	5'
10		-20	6284	5'
11		-19	6731	5'
12		-18	5038	5'
13		-17	5474	5'
14		-16	5424	5'
15		-15	4560	5'
16		-14	7614	5'
17		-13	12959	5'
18		-12	102718	5'

-15,-15,-10		
Pos	Counts	End
-24	832	5'
-23	599	5'
-22	457	5'
-21	497	5'
-20	457	5'
-19	462	5'
-18	429	5'
-17	325	5'

W-Cn-H99_2020: H99r1

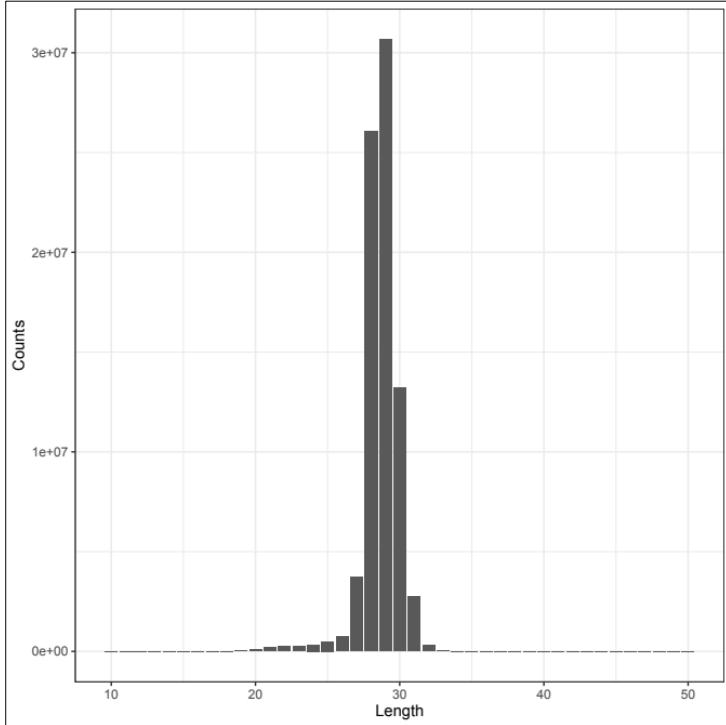
B-Sc_2012: ANAPH_1

Quantitative global studies reveal differential translational control by start codon context across the fungal kingdom. Wallace *et al.* 2020

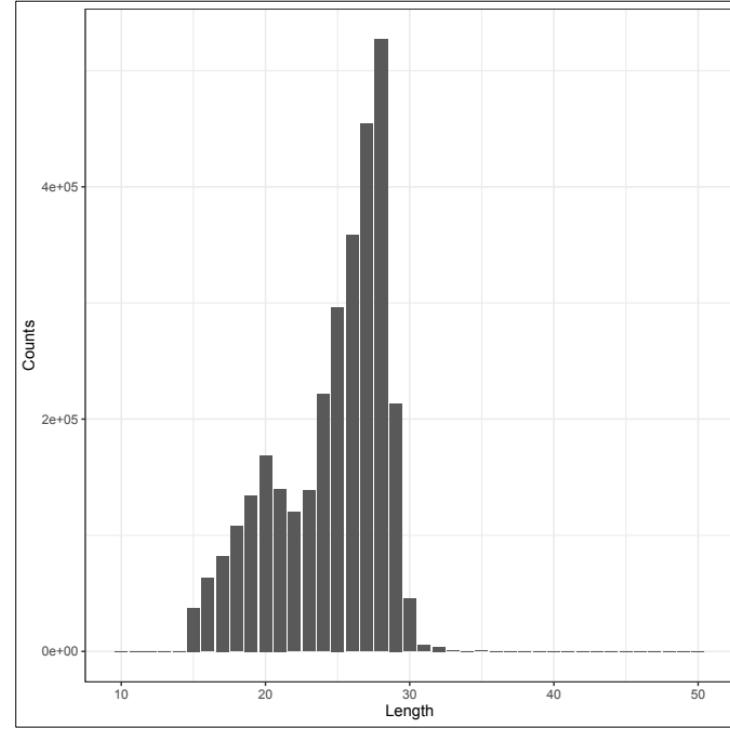
High-resolution View of the Yeast Meiotic Program Revealed by Ribosome Profiling, Brar *et al.* 2012

read_lengths.pdf

Distribution of lengths of reads



W-Cn-H99_2020: H99r1



B-Sc_2012: ANAPH_1

Quantitative global studies reveal differential translational control by start codon context across the fungal kingdom. Wallace *et al.* 2020

High-resolution View of the Yeast Meiotic Program Revealed by Ribosome Profiling, Brar *et al.* 2012

read_lengths.tsv

Counts by read lengths

	A	B	C
1	# Created by: RiboViz		
2	# Date: 2020-07-21 22:50:42		
3	# File: /home/flic/riboviz/rscripts/generate_stats_figs.R		
4	# Version: commit 03a4f13b2d833b8650ebf33bdce81fe2639eb9cf date 2020-07-08 15:42:55		
5			
6		Length	Counts
7		10	0
8		11	0
9		12	0
10		13	0
11		14	0
12		15	970
13		16	2476
14		17	4118
15		18	11192
16		19	28319
17		20	76530
18		21	214894
19		22	266016
20		23	243897
21		24	330478
22		25	489754
23		26	748587
24		27	3718527
25		28	26058264
26		29	30665395
		30	13218447

Date	Length	Counts
2020-03-04 13:45:40	10	0
	11	0
	12	0
	13	0
	14	0
	15	37534
	16	62944
	17	82132
	18	107977
	19	134409
	20	168903
	21	139873
	22	120034

W-Cn-H99_2020: H99r1

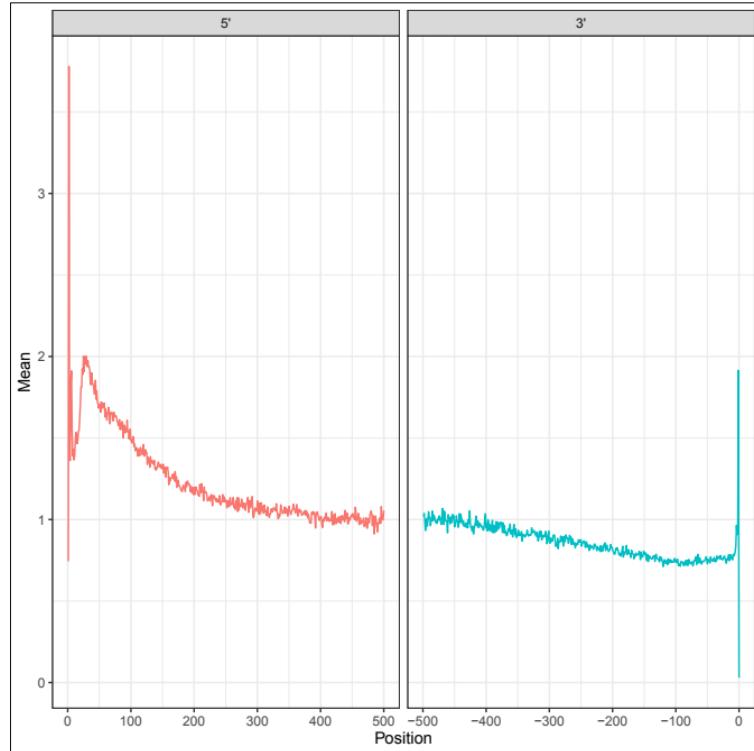
B-Sc_2012: ANAPH_1

Quantitative global studies reveal differential translational control by start codon context across the fungal kingdom. Wallace *et al.* 2020

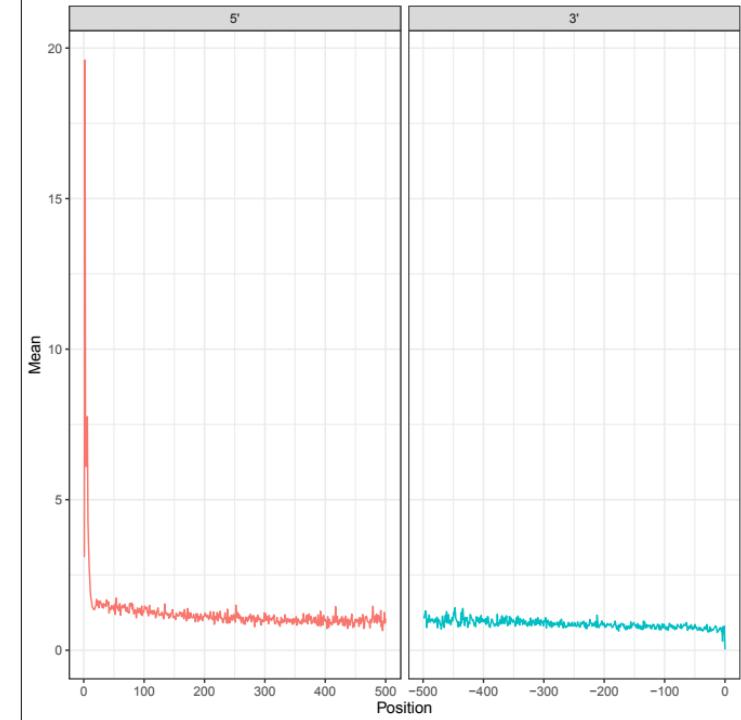
High-resolution View of the Yeast Meiotic Program Revealed by Ribosome Profiling, Brar *et al.* 2012

pos_sp_rpf_norm_reads.pdf

Position specific normalised reads



W-Cn-H99_2020: H99r1



B-Sc_2012: ANAPH_1

Quantitative global studies reveal differential translational control by start codon context across the fungal kingdom. Wallace *et al.* 2020

High-resolution View of the Yeast Meiotic Program Revealed by Ribosome Profiling, Brar *et al.* 2012

pos_sp_rpf_norm_reads.tsv

Position-specific normalised reads

	A	B	C	D	E
1	# Created by: RiboViz				
2	# Date: 2020-07-21 22:50:59				
3	# File: /home/flic/riboviz/rscripts/generate_stats_figs.R				
4	# Version: commit 03a4f13b2d833b8650ebf33bdce81fe2639eb9cf date 2020-07-08 15:42:55				
5		Position	Mean	SD	End
6		1	0.743715220949264	0.031229600187047	5'
7		2	3.77879354687865	0.072439794248305	5'
8		3	1.37367313537526	0.046337619826982	5'
9		4	1.36174888940846	0.043273088613514	5'
10		5	1.83991115267711	0.054171849427169	5'
11		6	1.91145662847791	0.055662380173019	5'
12		7	1.55253682487725	0.045586392331073	5'
13		8	1.39036707972878	0.035570025718962	5'
14		9	1.42971709141922	0.038014496142156	5'
15		10	1.3653261631985	0.035975450081833	5'
16		11	1.39036707972878	0.0390399812953	5'
17		12	1.4786064998831	0.041663315407996	5'
18		13	1.53465045592705	0.04410778583119	5'
19		14	1.51914893617021	0.038586859948562	5'
20		15	1.46548982931962	0.035605798456862	5'
21		16	1.48814589665653	0.035760813654431	5'
22		17	1.54180500350713	0.037191723170447	5'
23		18	1.54538227729717	0.03870610240823	5'
24		19	1.62050502688801	0.0339244779775544	5'
25		20	1.69920505026888	0.037370586859949	5'
26		21	1.81248538695347	0.047363104980126	5'

	Position	Mean	SD	End
03-04 13:45:40	1	3.09468381483036	0.461891291073541	5'
	2	19.5972312330649	0.923539289394344	5'
	3	6.6199958020074	0.406177250696485	5'
	4	6.10299870243865	0.360194920428958	5'
	5	6.89248368507423	0.358005285654314	5'
	6	7.75982234858604	0.428073598442926	5'
	7	4.31479696981262	0.228330248444835	5'
	8	3.49490039308476	0.222734515131855	5'
	9	2.77353738121589	0.181618039919093	5'
	10	2.39400068694424	0.16823693851849	5'
	11	1.92566213792314	0.115393752623745	5'

W-Cn-H99_2020: H99r1

B-Sc_2012: ANAPH_1

Quantitative global studies reveal differential translational control by start codon context across the fungal kingdom. Wallace *et al.* 2020

High-resolution View of the Yeast Meiotic Program Revealed by Ribosome Profiling, Brar *et al.* 2012

pos_sp_nt_freq.tsv

4 13:45:40	Length	Position	Frame	A	C	G	T
	10	1	0	0	0	0	0
	10	2	0	0	0	0	0

	30	14	0	0.275	0.196	0.334	0.195
	30	15	0	0.167	0.0999	0.159	0.574
	30	16	0	0.195	0.549	0.0751	0.181
	30	17	0	0.143	0.352	0.207	0.298
	30	18	0	0.185	0.324	0.161	0.33
	30	19	0	0.2	0.222	0.292	0.286
	30	20	0	0.165	0.404	0.106	0.325
	30	21	0	0.501	0.2	0.162	0.137
	30	22	0	0.181	0.24	0.415	0.164
	30	23	0	0.143	0.253	0.227	0.377
	30	24	0	0.287	0.0952	0.257	0.36
	30	25	0	0.285	0.157	0.394	0.164
	30	26	0	0.235	0.249	0.11	0.407
	30	27	0	0.177	0.426	0.266	0.13
	30	28	0	0.39	0.163	0.289	0.158
	30	29	0	0.16	0.174	0.125	0.54
	30	30	0	0.192	0.305	0.222	0.282
	30	1	1	0.145	0.249	0.0958	0.51

B-Sc_2012: ANAPH_1

3ntframe_bygene.tsv

Calculated read frame per annotated ORF, sum by frame & Wilcoxon

gene	Ct_fr0	Ct_fr1	Ct_fr2	pval_fr0vs1	pval_fr0vs2	pval_fr0vsboth
YAL068C	0	0	0	1	1	1
YAL067W-A	0	0	0	1	1	1
YAL067C	8	3	0	0.09154837080959	0.007354384721559	0.003834285390189
YAL065C	1	1	0	0.681324055883031	0.5	0.630558659818236
YAL064W-B	1	0	0	0.5	0.5	0.5
YAL064C-A	0	0	0	1	1	1
YAL064W	0	0	0	1	1	1
YAL063C-A	0	0	0	1	1	1
YAL063C	12	2	8	0.018148283043708	0.091757084963638	0.007742087124372
YAL062W	108	10	15	2.35529750560817E-10	9.00694786412824E-09	2.53109099063683E-17
YAL061W	90	18	24	3.58565108086954E-08	1.6306211759895E-06	6.25221450296923E-13
YAL060W	17	2	3	0.000954008674701	0.002457242914611	1.43343558100775E-05
YAL059W	2	1	0	0.386414996342224	0.17288929307558	0.191934191495911

B-Sc_2012: ANAPH_1

codon_ribodens.tsv

Values for features

AA	Codon	tRNA	tAI	Microarray	RNA.seq	A	P	E	
K	AAA	7	0.431034	222273	82386	1.05790819002401	1.15291058609784	0.86528716593696	
N	AAC	10	0.615764	378101	110849	1.0281152292804	1.27708638433922	1.0050442206497	
K	AAG	14	1	397111	83036	1.0224822832824	1.26675365537118	0.932261297646333	
N	AAT	6.4	0.27032	241984.64	70943.36	0.99399477627165	1.35673169342604	0.848902424015964	
T	ACA	4	0.246373	105862	47598	0.819260573895541	1.23679352095319	1.25916809965654	
T	ACC	7.04	0.487685	244374.4	36396.16	0.712747801072039	0.896873450468225	1.11953584037134	
T	ACG	1	0.140394	113104	16861	0.797757582450966	1.24033130452294	1.13475360386371	
T	ACT	11	0.67734	381835	56869	0.849232525038719	1.03763261086384	1.17820012062022	
R	AGA	11	0.67734	683001	98864	1.28096241997618	0.932921234833255	0.856577205337026	
Z	AGC	2	0.123153	249948	61334	0.950093444227615	0.47288787628337	1.01587991491282	
R	AGG	1	0.278325	106890	12911	1.24963311379243	0.529507496627423	0.953871071715205	
Z	AGT	1.28	0.054064	159966.72	39253.76	1.04600979170965	0.563371259730159	0.914016268311146	
I	ATA	2	0.123233	54352	39556	0.724039234288364	0.569831032158084	0.951443079270135	
I	ATC	8.32	0.576355	586391.04	67769.6	1.00775448514063	0.817362847783829	1.04955306675208	
I	ATG	10	0.045701	66661	67401	0.710015160014	1.000000000000	1.000000000000	

B-Sc_2012: ANAPH_1

tpms.tsv

TPMs per gene

	A	B	C	D	E
1	# Created by: RiboViz				
2	# Date: 2020-07-21 22:51:47				
3	# File: /home/flic/riboviz/scripts/generate_stats_figs.R				
4	# Version: commit 03a4f13b2d833b8650ebf33bdce81fe2639eb9cf date 2020-07-08 15:42:55				
5					
6		ORF	readcount	rpb	tpm
6 CNAG_00002		3479	6.08216783216783	67.2888954230649	
7 CNAG_00003		33	0.019903498190591	0.220198528757548	
8 CNAG_00004		1471	0.62649063032368	6.9310567395655	
9 CNAG_00005		1390	0.779147798206278	8.61995402475237	
10 CNAG_00006		15122	15.0617529880478	166.632810811397	
11 CNAG_00007		3508	1.9532293986637	21.6091782355655	
12 CNAG_00008		3848	1.008181051447849	11.9684028104778	
13 CNAG_00009		6559	5.72838427947598	63.3748790498934	
14 CNAG_00010		901	0.298641034139874	3.30395771208298	
15 CNAG_00011		1214	1.2019801980198	13.2978770196681	
16 CNAG_00012		7059	5.84354304635762	64.6489159452195	
17 CNAG_00013		4	0.006042296072508	0.066847781869453	
18 CNAG_00014		844	0.446797247220752	4.94305551460502	
19 CNAG_00015		129	0.188046647230321	2.08041795775784	
20 CNAG_00016		8997	29.7913907284768	329.591328380303	
21 CNAG_00017		22	0.009136212624585	0.101076733300115	
22 CNAG_00018		4658	1.91058244462674	21.1373618520833	
23 CNAG_00019		20962	66.1261829652997	731.5743223568	
24 CNAG_00020		4419	1.45314041433739	16.0765398248681	
25 CNAG_00021		10177	7.01378359751895	77.5956474790743	
26 CNAG_00022		8424	9.82963827304551	108.748314754374	
27 CNAG_00023		19	0.016769638128861	0.185527669981018	
28 CNAG_00024		4089	1.85274127775261	20.4974472136045	

	04 13:45:40			
	ORF	readcount	rpb	tpm
Q0045		277	0.167675544794189	54.1492075552714
Q0050		5	0.001959247648903	0.632720220010838
Q0275		94	0.109684947491249	35.4217008489988
...
YAL001C		103	0.029178470254958	9.42290686408889
YAL002W		37	0.009555785123967	3.08594907305286
YAL003W		848	1.26946107784431	409.9602686361
YAL005C		10367	5.24645748987854	1694.29308190438
YAL007C		87	0.125179856115108	40.4256328424997
YAL008W		140	0.217391304347826	70.20443484642
YAL009W		33	0.039903264812576	12.886376311592
YAL010C		24	0.015696533682145	5.06904487053288
YAL011W		37	0.019220779220779	6.20716613551204

W-Cn-H99_2020: H99r1

B-Sc_2012: ANAPH_1

Quantitative global studies reveal differential translational control by start codon context across the fungal kingdom. Wallace *et al.* 2020

High-resolution View of the Yeast Meiotic Program Revealed by Ribosome Profiling, Brar *et al.* 2012

TPMs_collated.tsv

Collated TPMs by genes for all samples run

	A	B	C	D	E	F
1	# Created by: RiboViz					
2	# Date: 2020-07-22 01:08:37					
3	# File: /home/flic/riboviz/rsrcipts/collate_tpms.R					
4	# Version: commit 03a4f13b2d833b8650ebf33bdc81fe2639eb9cf date 2020-07-08 15:42:55					
5		ORF	H99r1	HdGWO1	H99r2	HdAGO1
6	CNAG_00002		67.3	62.2	53	59.9
7	CNAG_00003		0.2	0.1	0.1	0.1
8	CNAG_00004		6.9	6.1	6.4	7
9	CNAG_00005		8.6	7.5	8.6	9.7
10	CNAG_00006		166.6	172.3	184.8	187.5
11	CNAG_00007		21.6	22.6	29.6	29.4
12	CNAG_00008		12	11.3	13.9	14.4
13	CNAG_00009		63.4	58.8	56.1	59.7
14	CNAG_00010		3.3	3.3	3.8	4
15	CNAG_00011		13.3	11.6	11.7	13.4
16	CNAG_00012		64.6	64.4	64.6	68.3
17	CNAG_00013		0.1	0	0.1	0.1
18	CNAG_00014		4.9	4.8	4.9	4.7
19	CNAG_00015		2.1	1.7	2.3	2.1
20	CNAG_00016		329.6	301.9	297.9	292.5
21	CNAG_00017		0.1	0.1	0.1	0.1
22	CNAG_00018		21.1	21.1	21	22.4
23	CNAG_00019		731.6	712.9	726.4	712.2
24	CNAG_00020		16.1	16.8	19.4	20.5
25	CNAG_00021		77.6	79.2	84.9	82.1
26	CNAG_00022		108.7	106.2	107.5	108
27	CNAG_00023		0.2	0.2	0.1	0.1
28	CNAG_00024		20.5	22.2	34.8	38.1
29	CNAG_00025		8.5	9.1	13	13
30	CNAG_00026		213.2	196.3	225.3	243.5
31	CNAG_00027		4.4	3.8	3.9	4.2
32	CNAG_00028		1.1	1.2	1	0.9
33	CNAG_00029		1.4	1.6	1.2	1.4
34	CNAG_00030		4.1	2.8	2.7	3

	-04 13:45:40	ORF	VEG_1	VEG_2	ANAPH_1	ANAPH_2	SPORE_1	SPORE_2
		Q0045	0.5	0.2	54.1	88.4	33.1	44.5
		Q0050	0.7	0.8	0.6	0.9	2	2.6
		Q0055	0.1	0.2	0.4	0.6	0.3	1
		Q0275	0.9	0.7	35.4	58.3	29.1	42.1
	
		YAL001C	3.4	4.7	9.4	10	97.3	46.9
		YAL002W	1.8	2.7	3.1	2.2	2.1	10.9
		YAL003W	4043.5	3676.6	410	300.3	398.7	1623.6
		YAL005C	1345.1	1386.2	1694.3	1327.5	1173.1	637.1
		YAL007C	105.6	87.8	40.4	38.7	11.6	47.6
		YAL008W	11.8	14.7	70.2	84.7	103.6	125.8
		YAL009W	4.2	5.7	12.9	7.4	7.3	4.9
		YAL010C	4.8	5.2	5.1	5.5	1.8	9.2
		YAL011W	4.9	5.7	6.2	7.6	6.9	13.1
		YAL012W	316	353.5	38.3	23.7	31	60.3
		YAL013W	15.1	16.4	35.2	25.5	47.6	85.8
		YAL014C	10.7	12	38.4	32.1	47.8	82.5
		YAL015C	9.6	12.5	21.1	12.0	16.1	20.4

W-Cn-H99_2020: H99r1, HdGWO1, H99r2, HdAGO1

B-Sc_2012: VEG_1, VEG_2, ANAPH_1, ANAPH_2, SPORE_1, SPORE_2

Quantitative global studies reveal differential translational control by start codon context across the fungal kingdom. Wallace et al. 2020

High-resolution View of the Yeast Meiotic Program Revealed by Ribosome Profiling, Brar et al. 2012

read_counts.tsv

Number of reads at each stage of riboviz workflow, for each sample
(Available for both datasets, but only one shown for clarity)

SampleName	Program	File	NumReads	Description
VEG_1	input	B-Sc_2012/input/SRR387871_GSM843747	21155927	input
VEG_2	input	B-Sc_2012/input/SRR387872_GSM843748	20915375	input
ANAPH_1	input	B-Sc_2012/input/SRR387890_GSM843766	10210064	input
ANAPH_2	input	B-Sc_2012/input/SRR387891_GSM843767	11620421	input
SPORE_1	input	B-Sc_2012/input/SRR387898_GSM843774	11782015	input
SPORE_2	input	B-Sc_2012/input/SRR387899_GSM843775	10793988	input
ANAPH_1	cutadapt	B-Sc_2012/tmp/ANAPH_1/trim.fq	9458608	Reads after removal of sequencing library
ANAPH_1	hisat2	B-Sc_2012/tmp/ANAPH_1/nonrRNA.fq	5999936	rRNA or other contaminating reads removed
ANAPH_1	hisat2	B-Sc_2012/tmp/ANAPH_1/rRNA_map.sam	9458608	Reads with rRNA and other contaminating
ANAPH_1	hisat2	B-Sc_2012/tmp/ANAPH_1/unaligned.fq	2919159	Unaligned reads removed by alignment o
ANAPH_1	hisat2	B-Sc_2012/tmp/ANAPH_1/orf_map.sam	3348087	Reads aligned to ORFs index files
ANAPH_1	riboviz.tools.trim	B-Sc_2012/tmp/ANAPH_1/orf_map_clean.sq	3348087	Reads after trimming of 5' mismatches a
ANAPH_2	cutadapt	B-Sc_2012/tmp/ANAPH_2/trim.fq	11231649	Reads after removal of sequencing library
ANAPH_2	hisat2	B-Sc_2012/tmp/ANAPH_2/nonrRNA.fq	9365904	rRNA or other contaminating reads removed
ANAPH_2	hisat2	B-Sc_2012/tmp/ANAPH_2/rRNA_map.sam	11231649	Reads with rRNA and other contaminating

B-Sc_2012: VEG_1, VEG_2, ANAPH_1, ANAPH_2, SPORE_1, SPORE_2

What other diagnostics do we need?