Supporting online material for:
Structural and functional organization of RNA regulons in the yeast posttranscriptional regulatory network

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1 Evaluating transcriptome and translatome clusters with respect to protein complexes

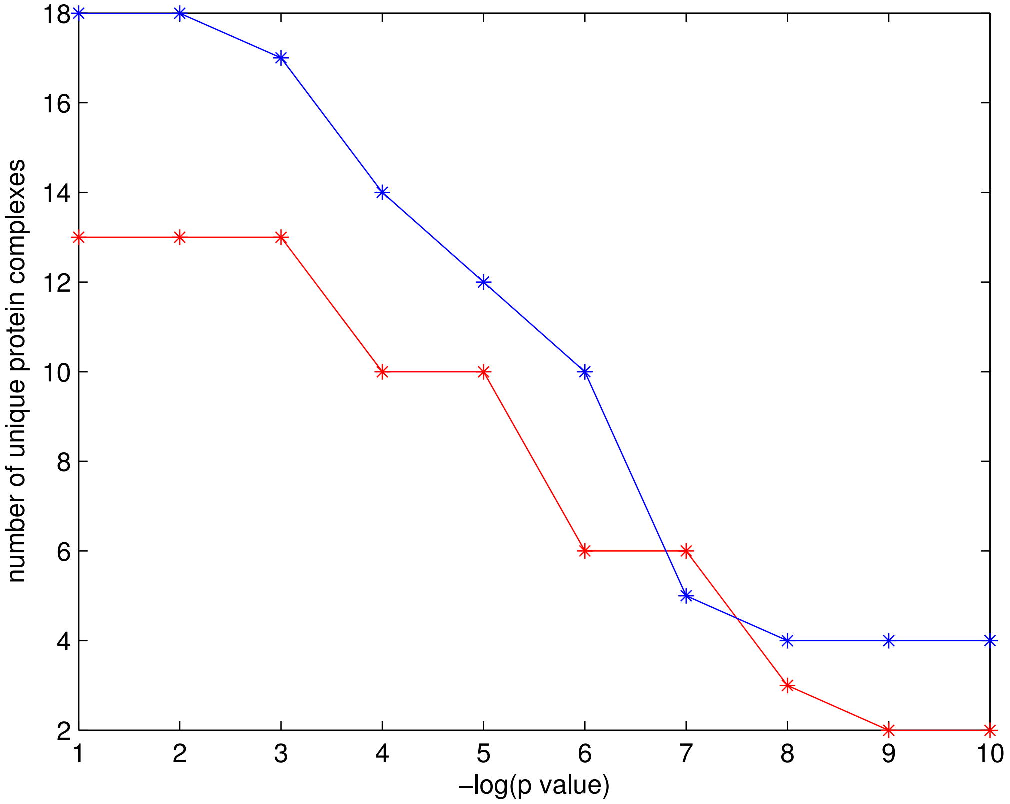


Figure S1: At different P-value cutoffs (x-axis), the total number of protein complexes enriched in transcriptome clusters (red) and translatome clusters (blue), cfr. Figure 1 in the paper.

2 Overrepresented functional categories for translatome clusters ($P < 0.001$)

Class I: Biosynthesis of histidine, biosynthesis of isoleucine, sugar, glucoside, pylyol and carboxylate anabolism and catabolism, metabolism of vitamins, cofactors and prosthetic groups, metabolism of energy reserves, heavy metal binding, sugar transport, cellular import, inorganic chemical agent resistance, detoxification.

Class II: Biosynthesis of histidine, leucine, lysine and argenine, metabolism of porphyrins, urea, aspartate and methionine, catabolism of nitrogenous compounds, sulphate assimilation, alcohol fermentation, rRNA processing, rRNA modification, ribosome biogenesis, ribosomal proteins, translation initiation, translational control, RNA binding, GTP binding, NAD/NADP binding, heat shock response, electron transport, anion transport.

Class III: Metabolism of aspartate, degradation of aspargine, nitrogen, sulphur and selenium metabolism, peptidoglycan anabolism, glycolysis and gluconeogenesis, electron transport and membrane associated energy conservation, DNA topology, aminoacyl tRNA synthetases, N-diercted glucosylation, deglucosylation, RNA binding, electron transport, unfolded protein response, nutrient starvation response, homeostasis of protons.

3 Translatome cluster 24 involved in translational elongation

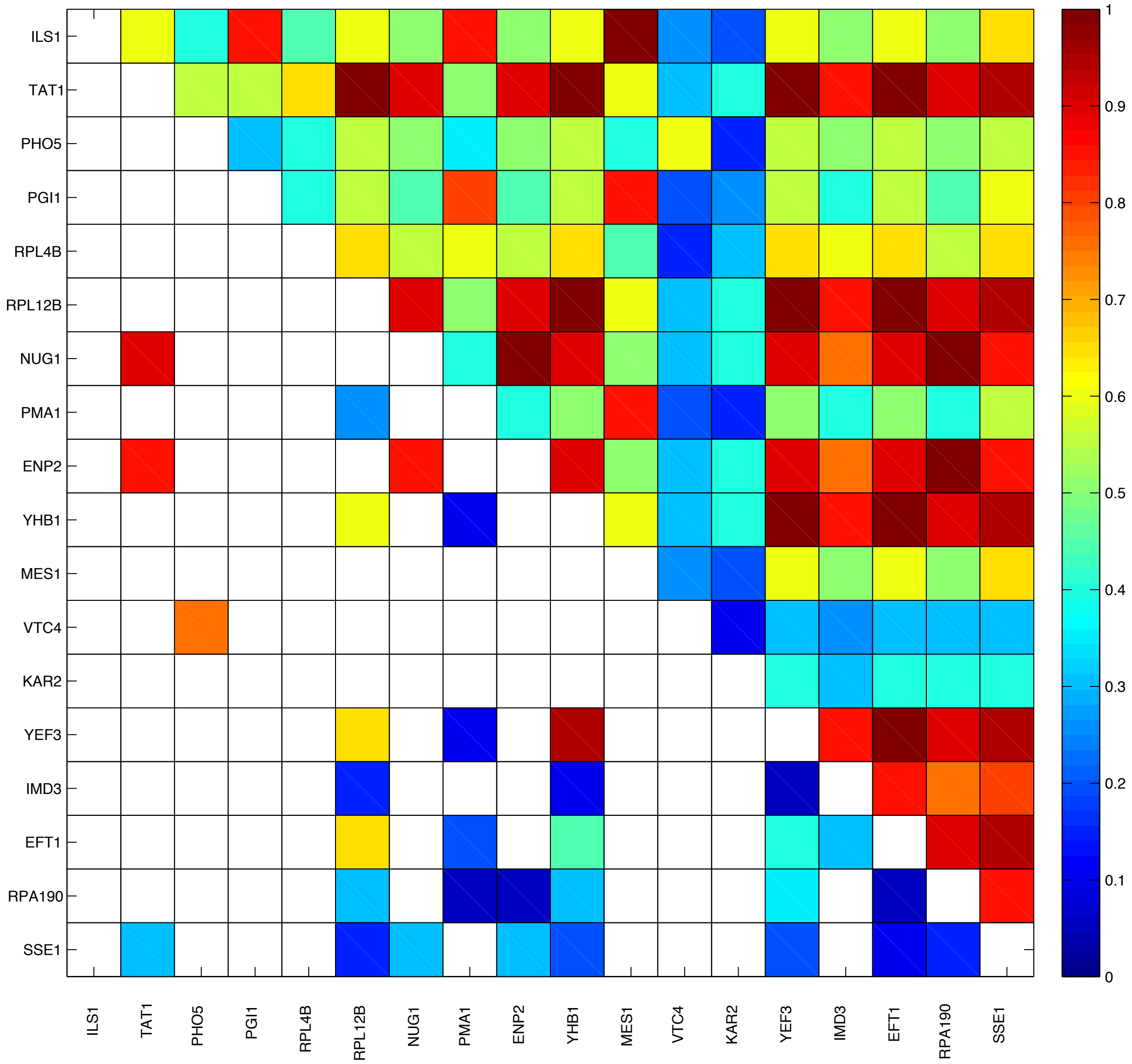


Figure S2: Translatome cluster 24 is a class III cluster involved in translational elongation. The genes in this clusters are coexpressed in translatome data (upper diagonal) but not in transcriptome data (lower diagonal); see also Figure 3 in the paper and the Supplementary Website.

4 FANMOD output

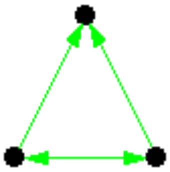
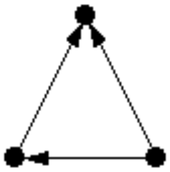
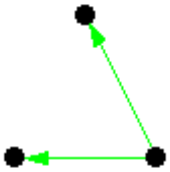
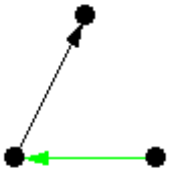
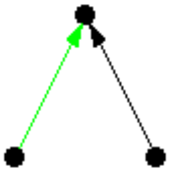
ID	Adj	Frequency [Original]	Mean-Freq [Random]	Standard-Dev [Random]	Z-Score	p-Value
46		0.022948%	0.0099661%	1.1121e-05	11.674	0
38		0.033925%	0.023687%	1.1109e-05	9.2161	0
6		85.726%	85.69%	5.8415e-05	6.1406	0
12		0.33833%	0.33216%	2.363e-05	2.6084	0.002
36		0.33026%	0.32508%	2.4443e-05	2.1212	0.017

Figure S3: FANMOD output showing all network motifs with $P < 0.05$ and occuring at least 100 times in the integrated network of transcriptional (black) and posttranscriptional (green) interactions.

5 Clusters combinatorially regulated at transcriptional and posttranscriptional levels

Table S1: Combinatorially regulated translatome clusters overlapping significantly ($P < 10^{-5}$) with known targets of at least one TF and at least one RBP.

TS cluster	Transcription factors	RNA binding proteins
2	RAP1,FHL1	PAB1
5	GAT3,GCR2,RAP1,FHL1	PAB1
9	SFL1	ACO1
16	RAP1,FHL1	PAB1
19	STB6	SIK1
21	GCN4	HRB1
24	THO2	SCP160,BFR1
31	RAP1,FHL1	PAB1,CBC2
42	HIR2	PAB1,NSR1,PUF2
83	RGM1	SIK1
98	ARO80	YLL032C

6 Median of diverse genomewide properties of gene clusters regulated by each network motif

Table S2: Median value of diverse genomewide properties of gene clusters regulated by each network motif. The bold numbers are significantly higher or lower compared to the other motifs.

	mRNA level	mRNA level	Protein abundance	Protein noise
TF direct	1.60	2.51	4050	17.84
RBP direct	1.83	3.41	5440	17.75
RBP FBL	**2.70**	**7.24**	**9540**	**16.19**
TF FFL	1.72	2.60	5350	16.79
RBP FFL	2.12	4.71	7380	17.44
Mixed bifan	1.94	3.78	6290	17.44

7 Overrepresented functional categories for RBP feedback loops ($P < 0.001$)

Peptidoglycan anabolism, pyruvate dehydrogenase complex, rRNA processing, rRNA modification, ribosomal proteins, translation initiation, aminoacyl tRNA synthetases, N-directed glycosylation, deglycosylation, RNA binding, GTP binding, electron transport, homeostasis of protons.