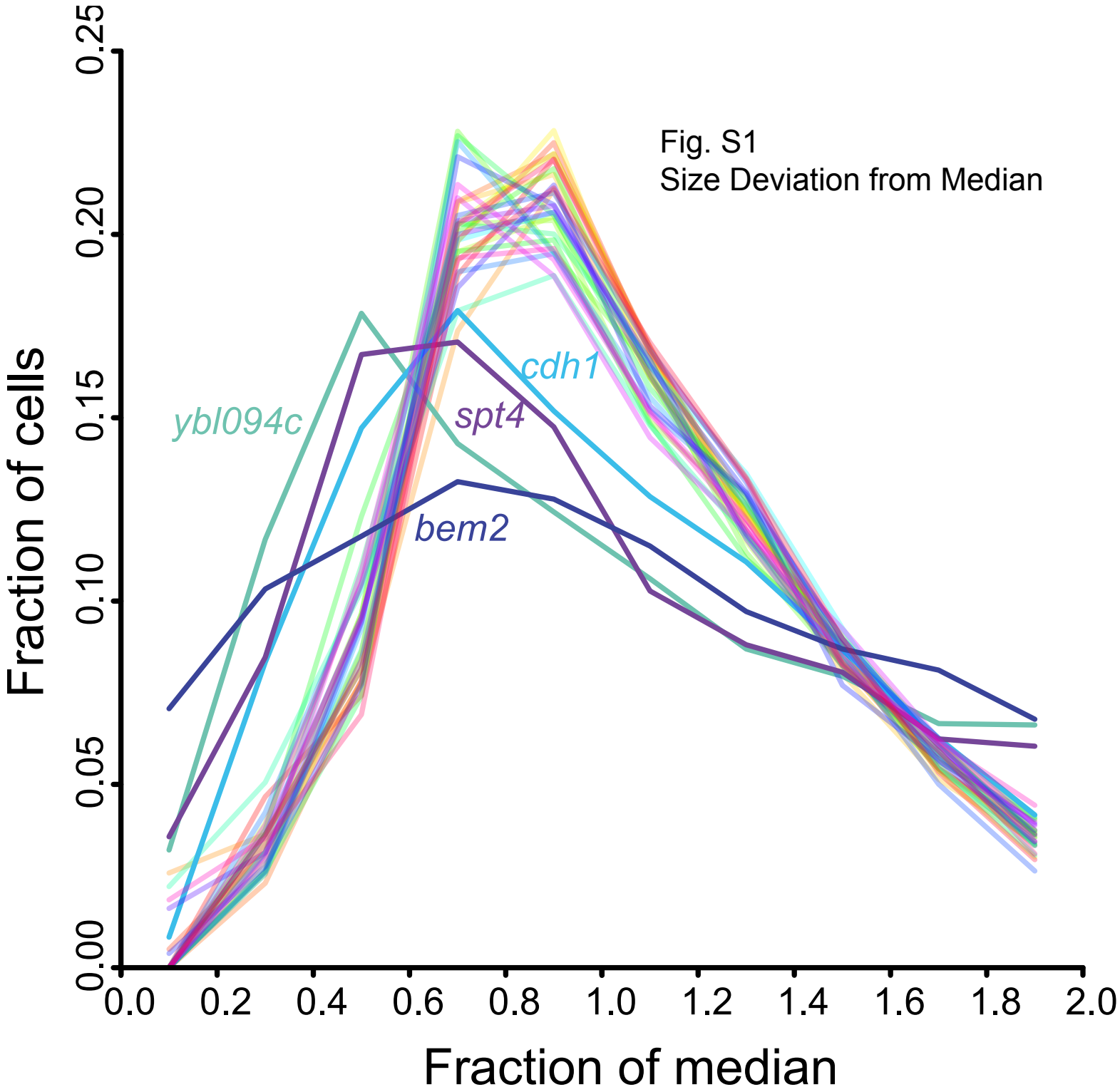
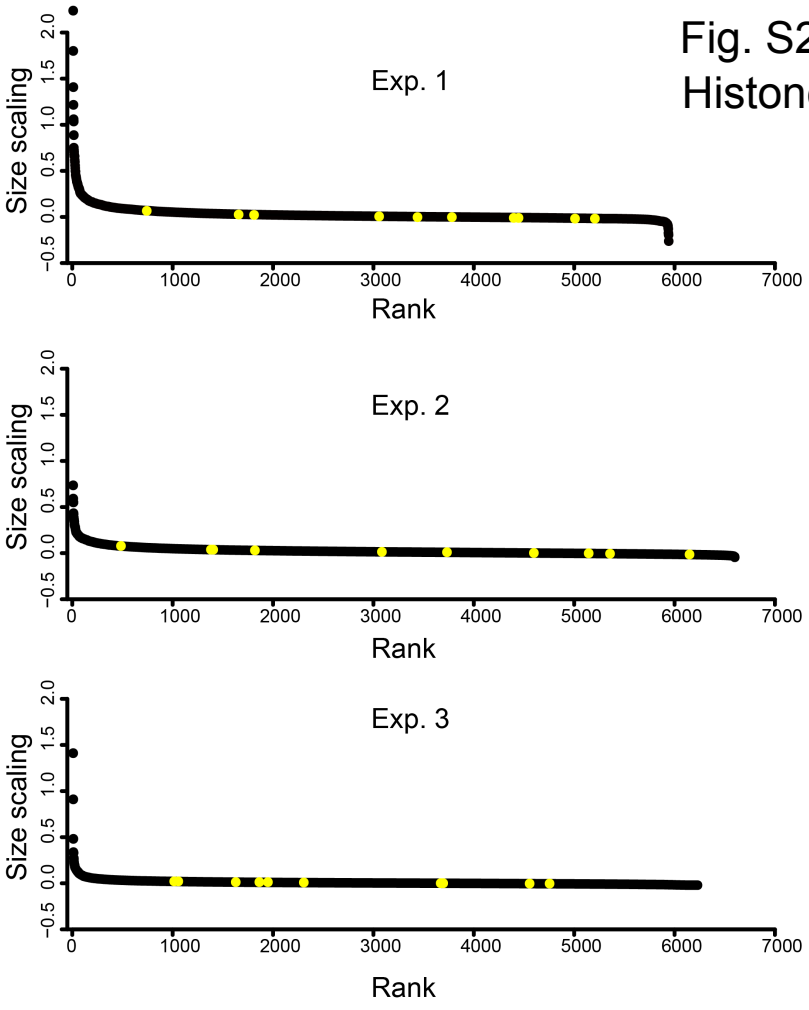


Fig. S1
Size Deviation from Median
Fraction of cells
0.00
0.05
0.10
0.15
0.20
0.25
0.0
0.2
0.4
0.6
0.8
1.0
1.2
1.4
1.6
1.8
2.0
Fraction of median
ybl094c
spt4
cdh1
bem2

Figure S1. Size Deviation from the Median. Cell size distributions of 32 size mutants analyzed by the method of Coudreuse and Nurse (Related to Fig. 1).

The cell size data in Fig. 1E is replotted by the method of Coudreuse and Nurse (2010), but also including mutants *spt4*, *cdh1*, *bem2*, and *ybl094c*. We identified *bem2* and *ybl094c* as mutants with large CVs in genome wide screens.

Fig. S2
Histone Ranks



Column1	Expt. 1	Expt. 2	Expt. 3
HTA2	733	1396	1007
HHF2	1803	1373	1048
HTB2	1649	477	1621
HHO1	3773	1811	1855
HTB1	3431	3725	1941
HHT2	3048	4590	2298
HTA1	5000	3076	3662
HHF1	4389	6141	3687
HHT1	4437	5349	4548
HTZ1	5198	5136	4747

Spearman Correlation Coeffient:

Exp. 1 vs Exp. 2	0.70
Exp. 1 vs Exp. 3	0.90
Exp. 2 vs Exp. 3	0.87

Fig. S2. Histone Ranks. Histone genes have modest but reproducible scaling (Related to Fig. 2).

Top. The ranks of 10 histone genes plotted for each of the three elutriation experiments.

Bottom. The individual ranks are shown, with correlation coefficients between experiments. Even though the histones are mostly in the flat region, nevertheless their ranks are highly repeatable (Spearman correlations from 0.69 to 0.90).

Fig. S3
Ribosome Scaling

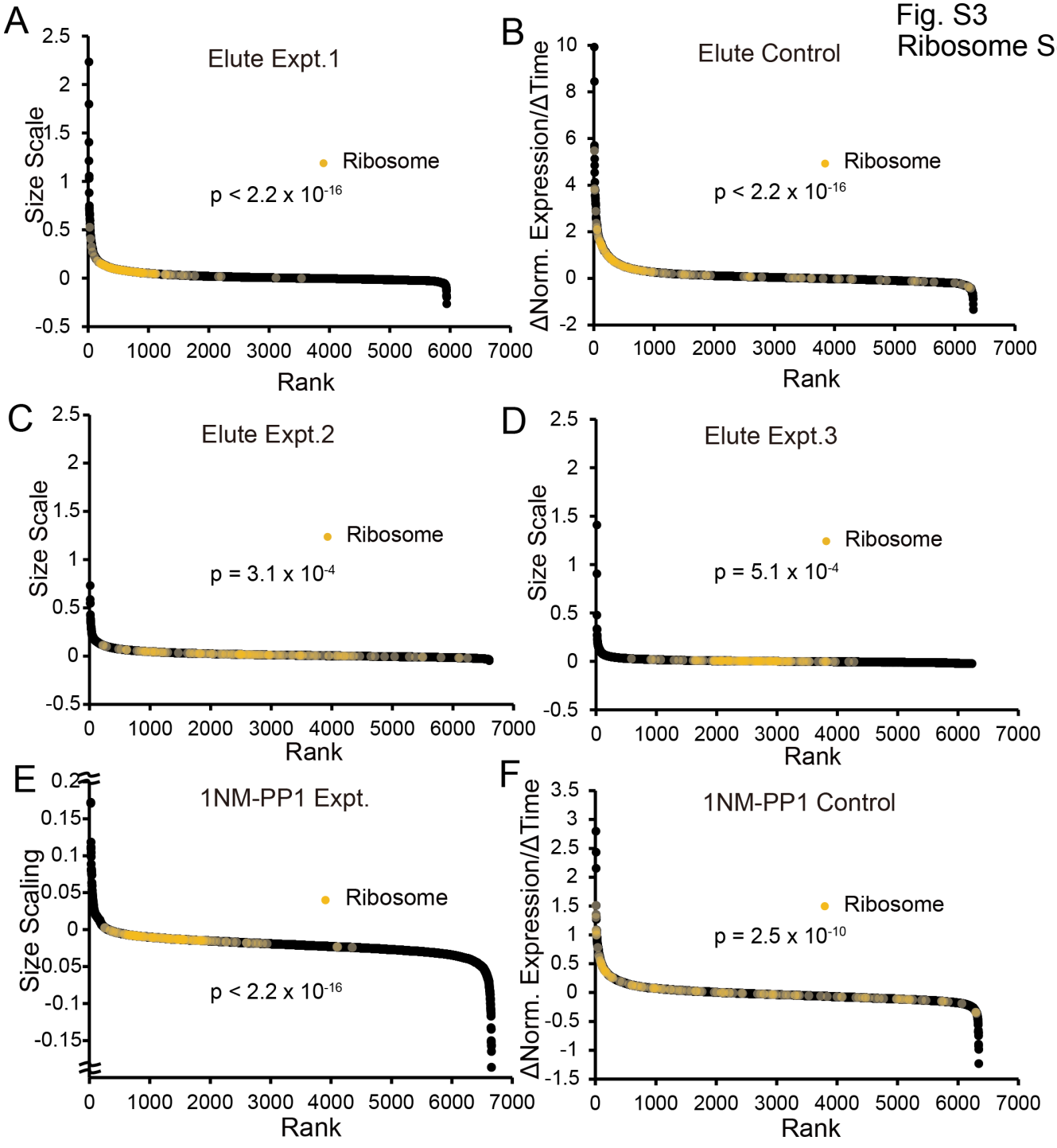


Figure S3. Ribosome Scaling. Size scaling of genes for ribosomal proteins (Related to Fig. 2).

The size-scaling for all ribosomal protein mRNAs is shown. Each ribosomal protein mRNA is marked by a yellow dot. The p-value is for a difference in distribution between the ribosomal protein mRNAs and all other mRNAs. 2.2×10^{-16} was the smallest p-value that could be returned by the software used. Note that super-scaling is present in the control experiments.

Fig. S4 Noise

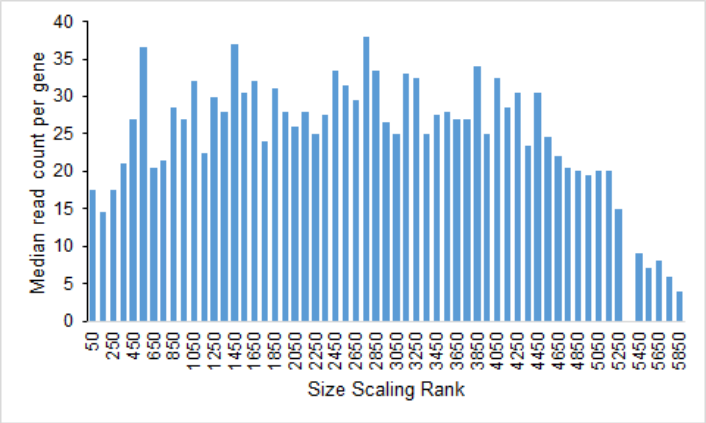

Median read count per gene
0
5
10
15
20
25
30
35
40
50
250
450
650
850
1050
1250
1450
1650
1850
2050
2250
2450
2650
2850
3050
3250
3450
3650
3850
4050
4250
4450
4650
4850
5050
5250
5450
5650
5850
Size Scaling Rank

Figure S4. Contribution of Noise (Related to Fig. 2).

Genes were binned by size-scaling rank. The median number of mRNA reads per gene in each bin was plotted. Genes with very high ranks (i.e., scaling slower-than-size, right end of the distribution) tend to have few reads, and so may have high ranks partly because of noise.

Fig. S5 Protein Scaling

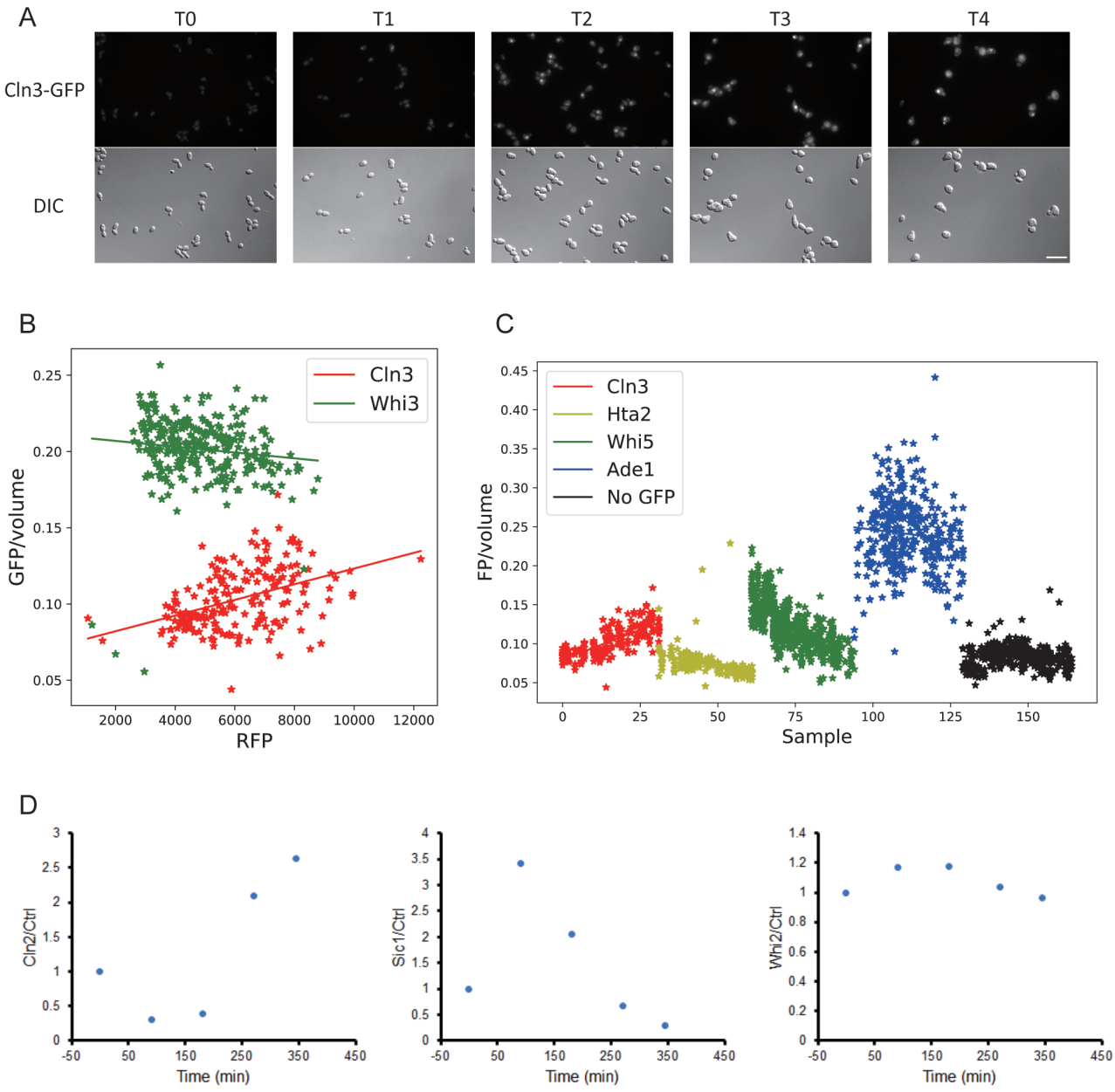


Figure S5A. Images of GFP-Cln3 (Related to Fig. 4).

Cln3 was visualized using the split-GFP system, with 5 copies of GFP beta-strand 11 fused to the N-terminus of Cln3 (Materials and Methods). Cells (*cdc28-as*) were grown to early exponential phase (Materials and Methods). 1NMPP1 was added at 0 time (T0), and a sample taken. Four more samples were taken at 90 minute intervals (T1, T2, T3, T4) (left to right). Cells in each sample were imaged for GFP fluorescence, and for cell morphology using DIC. Unbudded cells were chosen for quantitation (see Fig. 4, Fig. S5B, Fig. S5C). Scalebar = 20 microns.

Figure S5B. Scaling of Cln3 and Whi3 (Related to Fig. 4).

As Fig. 4, but with cell volumes calculated using the sum of intensity of the mCherry proxy, instead of cross-sectional area.

Figure S5C. Scaling of Whi5, Cln3, and controls (Related to Fig. 4).

As Fig. 4, but with the x-axis being sample number (0, 1, 2, 3, 4) rather than volume. Within a sample, points are offset along the x-axis to allow visibility, 6-8 offsets per sample. The "No GFP" sample is a negative control using a strain not containing GFP. The "Ade1" sample is a negative control with the Ade1 gene visualized using the split-GFP system; Ade1 was chosen because its mRNA levels were similar to the mRNA levels of many of the regulators of interest. "Hta2" is a scaling control, which should scale negatively (since the amount of Hta2 should be constant regardless of cell growth). Hta2 was visualized with an mCherry fusion. It was much brighter than any other construct, and was visualized using different settings on the camera and microscope. The y-axis is fluorescent protein per unit volume (i.e., fluorescence intensity per unit volume)

Figure S5D. Quantitation of Western Blots (Related to Fig. 4).

The Western blots of Fig. 4 were quantitated (Materials and Methods). The sample proteins (Cln2, Sic1, Whi2) are compared to both the Arp7 and the Tub1 controls using the exponentiated means of log ratios, normalized to time 0.

Fig. S6 mRNA half-lives

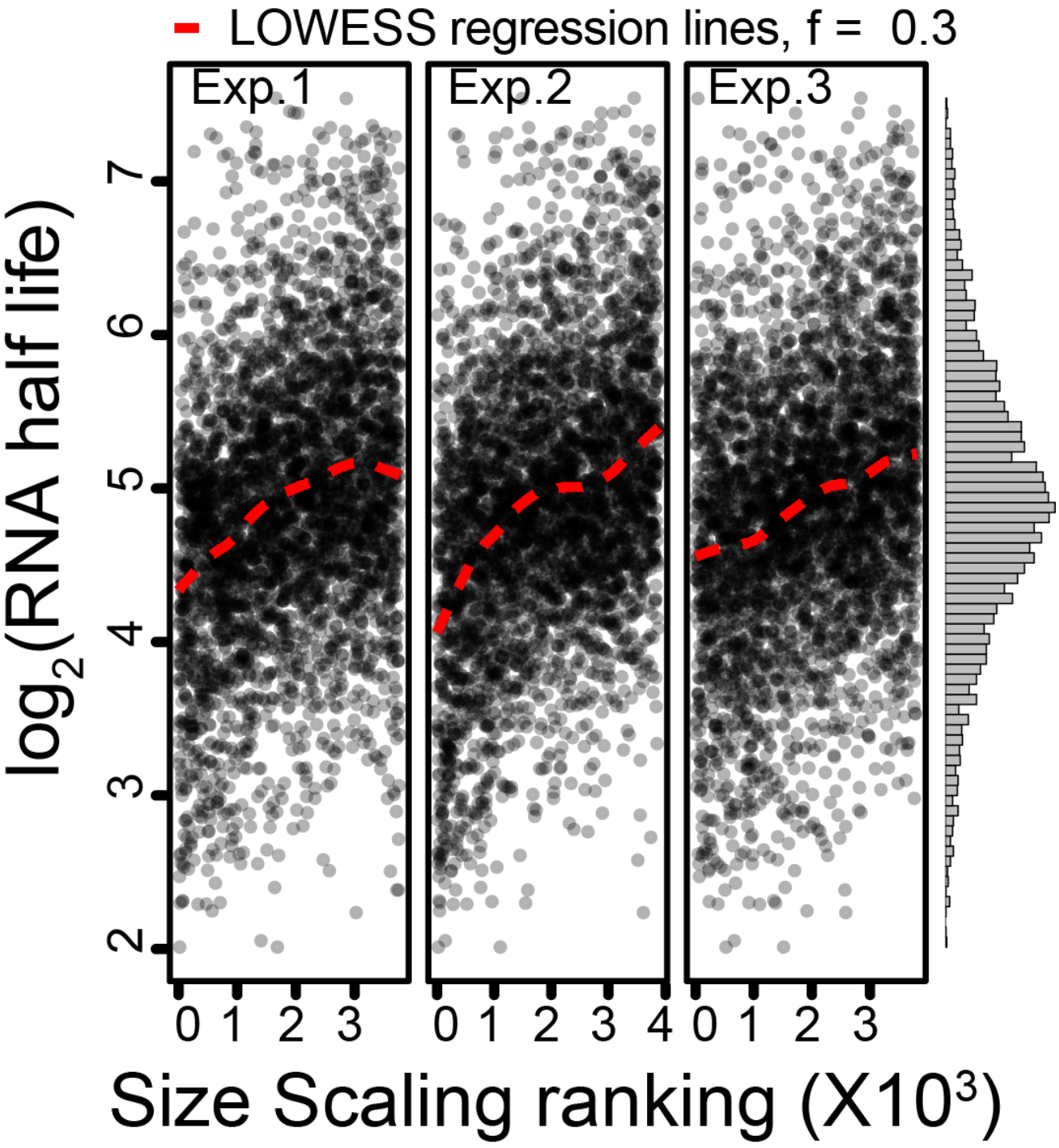


Figure S6. RNA half-lives correlate inversely with size scaling (Related to Fig. 5).

Correlation between log(RNA half-life) (y-axis) and rank of size scaling (x-axis) in the elutriation experiments. RNA half-lives were calculated by combining data from Wang et al. (2001) and Shalem et al. (2008). The average Spearman correlation between half-life and size-scaling over all three experiments is 0.36.

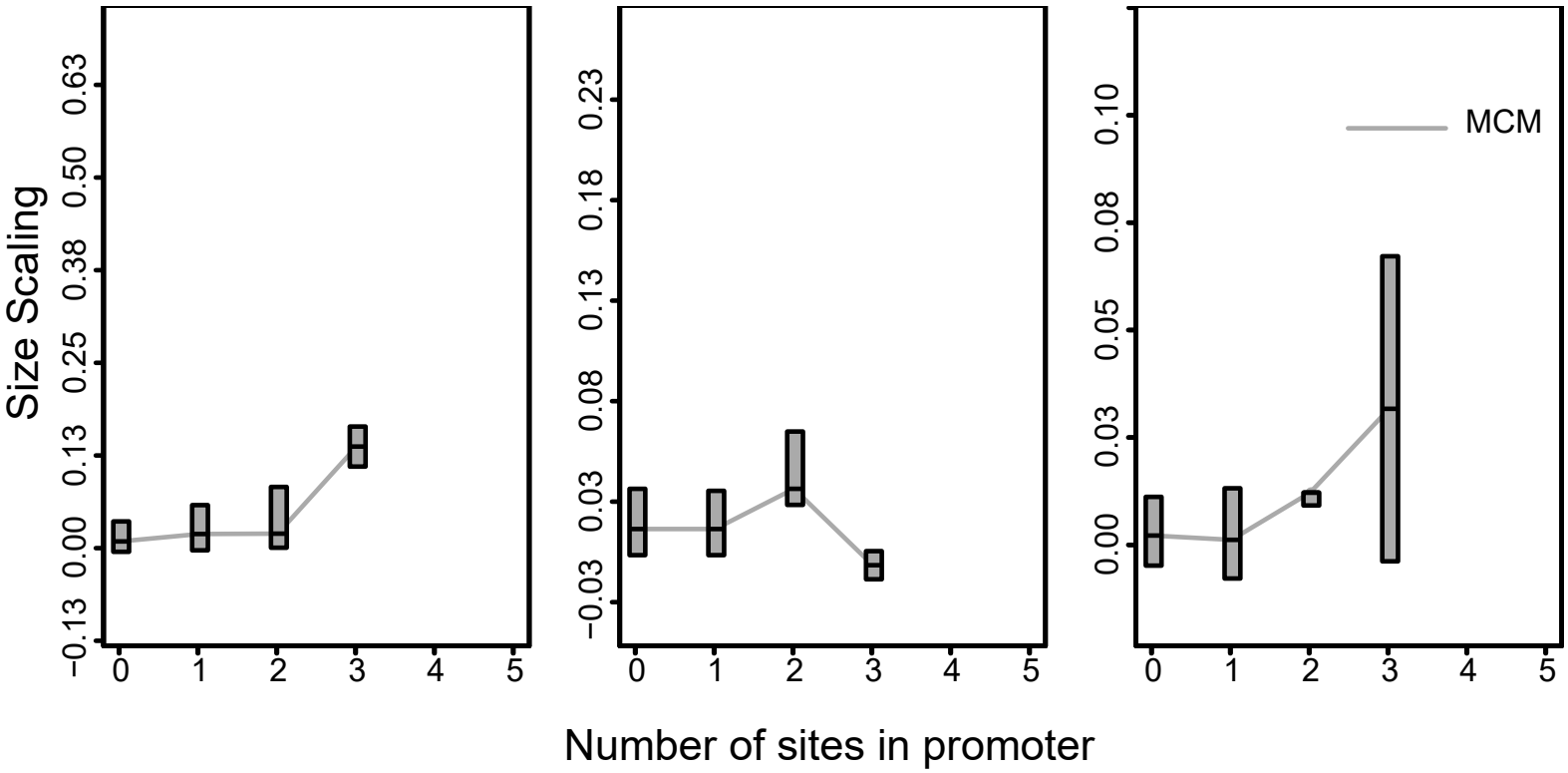


Fig. S7 MCM scaling, Expts 1 to 3

Figure S7. Size-scaling increases with number of binding sites for Mcm1 (Related to Fig. 5).
As Fig. 5, but for the Mcm1 consensus binding site, TTnCCnnnTnnGGnAA.

Table S2. Ranks of cell cycle activators and inhibitors

A

	Gene	CCRS	Rank Exp. 1	Rank Exp. 2	Rank Exp.3
Activators	CLN2	10.9	19	73	62
	CDC28	0.7	91	170	84
	CLB2	10.5	6	50	1302
	CLB5	4.8	880	2714	198
	CLN1	5.4	519	336	1523
	CLN3	2.4	1058	732	3284
	BCK2	0.6	1337	2627	4757
	SWI4	3.2	3497	2338	438
Inhibitors	SRL3	2.4	3347	1971	4908
	SIN3	0.4	4234	4802	4785
	RPD3	0.2	3604	4381	3406
	WHI4	0.4	4158	3814	5292
	WHI3	1.7	3708	4856	5839
	WHI2	0.4	4983	4156	5242
	SIC1	7.4	5646	1858	4227
	WHI5	1.4	6055	5781	6029

B

	Spearman correlations
Expt. 1 vs 2	0.68
Expt. 1 vs 3	0.77
Expt. 2 vs 3	0.75

C

	Wilcoxon p-value rank activator vs inhibitor
Expt.1	6.2×10^{-4}
Expt.2	4.7×10^{-3}
Expt.3	6.2×10^{-4}

Table S2. Ranks of cell cycle activators and inhibitors (Related to Fig. 2).

The ranks of the scaling scores for each of the pre-selected cell cycle activators and inhibitors are given for each of the three elutriation experiments. Also shown are the experiment-to-experiment Spearman correlations for the 16 ranks, and the Wilcoxon p-values for the separations between activators and inhibitors. CCRS is the Cell Cycle Regulation Score from data of Spellman et al. 1998 (see http://genome-www.stanford.edu/cgi-bin/cellcycle/search for actual scores). Higher scores are more strongly cell cycle regulated.