Supplementary Information

High throughput gene expression profiling of yeast colonies with microgel-culture Drop-seq

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Supplementary Figure 1. Comparison of ICO-seq data and bulk sequencing data. Bulk sequencing data was collected from W303a yeast cells containing mutations rendering them sensitive to PKA inhibition via the ATP analog 1-NM-PP1. Three samples of exponentially growing cells were collected 40 minutes after adding 3uM 1-NM-PP1 or DMSO and libraries were prepared using the Lexogen Quant-Seq 3' mRNA prep kit (Cat. No. 015.96) at 45 minutes YPD plus and minus 3uM 1-NM-PP1 [B. Heineike, unpublished data]. After filtering the dataset so that only genes analyzed for individual colonies were considered, counts were normalized and multiplied by the same scaling factor as was used for the individual colonies. The same pseudocount as was added to the individual colony data was added to the data prior to taking the log10 value. On the X axis, bulk data from cells without or with 1-NM-PP1 (left, right respectively) was plotted and the log expression averaged over all colonies, or clusters A, B and C were plotted on the Y axis. The Pearson correlation coefficient was calculated and a best fit line is displayed.

Supplementary Figure 2. Comparison of ICO-seq data and bulk sequencing data from cells grown on solid media. This bulk data from yeast colonies on solid media is plotted on the X axis. Average ICO-seq data for all colonies analyzed and grouped by cluster is plotted on the Y axis. Average data for the colonies was calculated by summing counts from all colonies and then normalizing, adding a pseudocount, and taking the log10 of the result. The Pearson correlation coefficient was calculated and a best fit line is displayed.
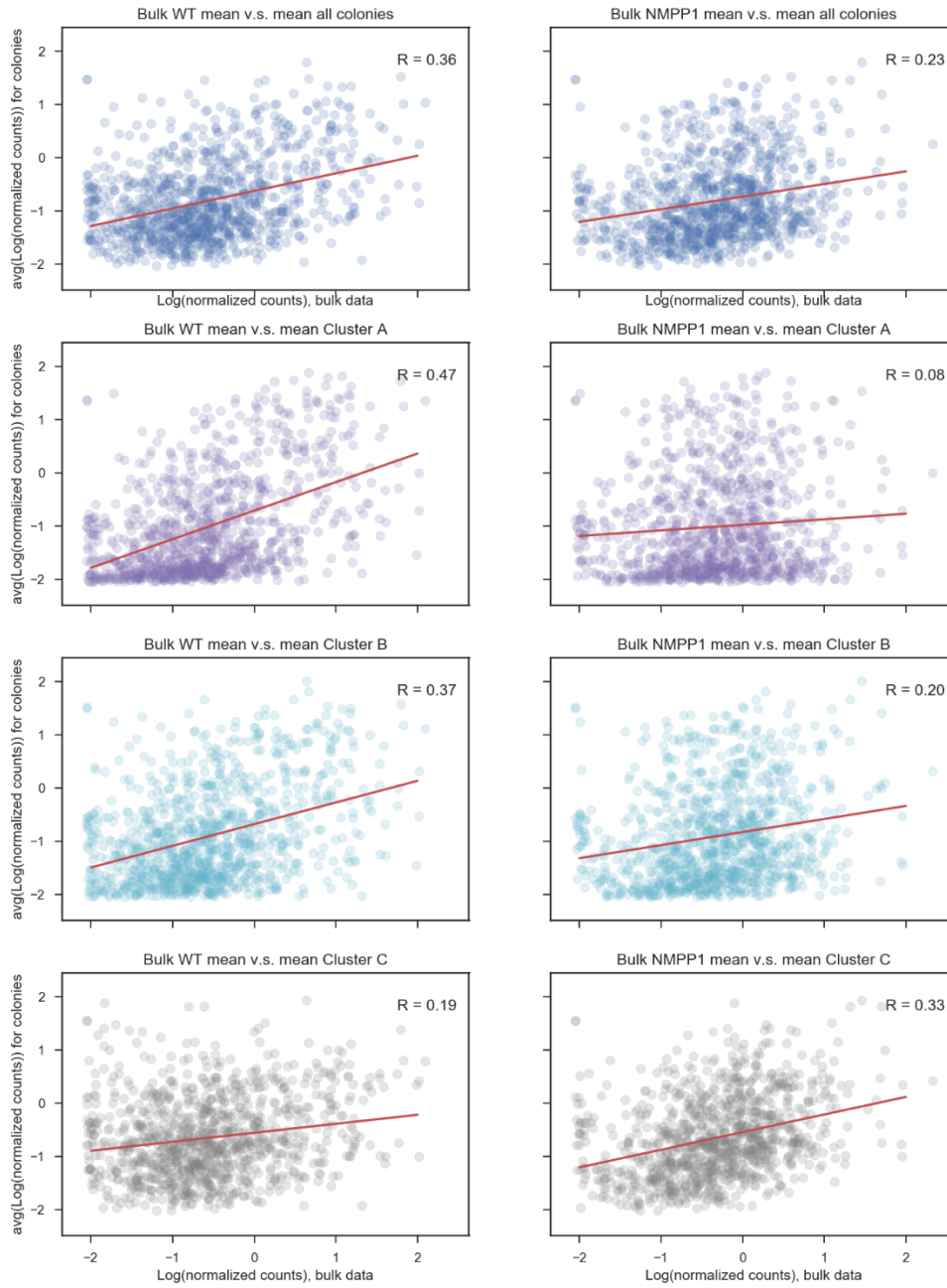
Supplementary Figure 3. A representative bioanalyzer trace of cDNA library generated using ICO-seq. A high sensitivity DNA chip was used to analyze cDNA library generated using ICO-seq with *S. cerevisiae*. The bioanalyzer trace of cDNA library is similar to standard Drop-seq cDNA library.

Supplementary Table 1. Genes that characterize the Principal Components and Vhet and Vsep. Genes of the first three principal components, as well as the vectors Vsep and Vhet with 30 largest magnitude negative and positive coefficients.
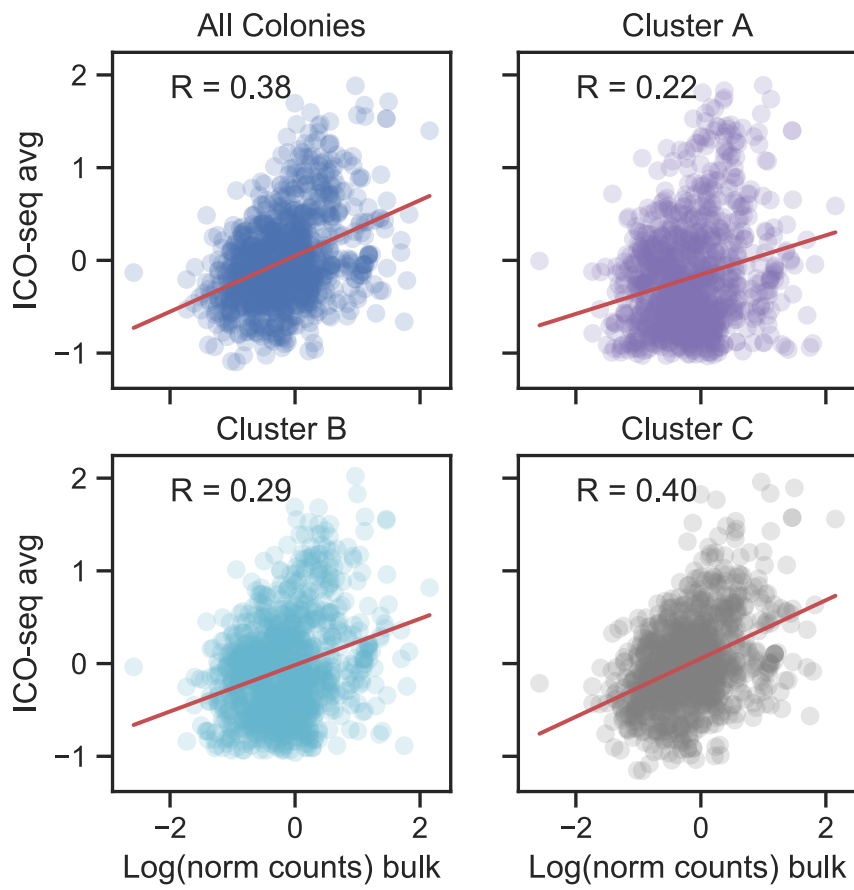
Supplementary Table 2. Top genes differentially expressed between clusters. The log10 normalized counts for each gene in a cluster were averaged and then the values for cluster A was subtracted from cluster C and Cluster B to identify genes that were differentially expressed between clusters. Genes with the 100 largest magnitude negative and positive values are displayed. For the difference between cluster B and A, many of the same genes that separate clusters C and A are present. This is not surprising, as the clusters all separate along the same axis ($\vec{v}_{sep}$). Genes separating clusters B and A which are not present in this table as separating C and A are highlighted in orange or green.

Supplementary Table 3. Go enrichment for genes in Tables 1 and 2. Lists of genes characterizing the principal components, $\vec{v}_{sep}$, and $\vec{v}_{het}$ were submitted for gene list analysis. Genes from the most significant enrichments and their corresponding go terms are listed here.
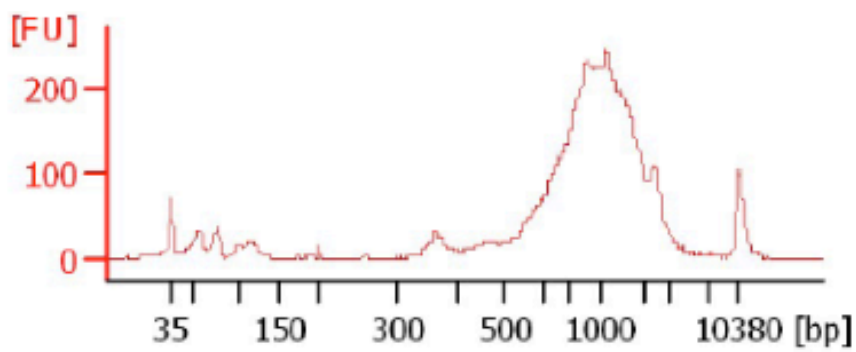
Supplementary Figure 1

Supplementary Figure 2

Supplementary Figure 3

Supplementary Table 1

Rank	PC1 negative genes	PC1 negative values	PC1 positive genes	PC1 positive values
1	RPL33B	-0.043	SPG4	0.083
2	RPS25B	-0.040	SPG1	0.082
3	RPL22B	-0.036	RGI2	0.080
4	NIP7	-0.034	YDR034W-B	0.075
5	RPL21B	-0.031	MRK1	0.075
6	RPS19A	-0.030	YGR035C	0.074
7	TIF11	-0.029	YOR019W	0.074
8	APQ12	-0.028	YDR119W-A	0.070
9	NRK1	-0.027	FMP43	0.069
10	GPX2	-0.027	YKL065W-A	0.067
11	CGR1	-0.026	HXT6	0.066
12	RPB10	-0.025	OM14	0.066
13	RPS27A	-0.025	FMP46	0.064
14	YBL028C	-0.024	YLR312C	0.064
15	URM1	-0.023	OLI1	0.063
16	RPS18B	-0.022	YGR161W-C	0.063
17	RPL34A	-0.022	YGR174W-A	0.063
18	POP8	-0.022	CRS5	0.063
19	YSY6	-0.022	UIP4	0.062
20	RPS22B	-0.021	HXT7	0.062
21	RPL14A	-0.021	GPX1	0.061
22	GLN1	-0.020	YER121W	0.061
23	DTD1	-0.020	DDR2	0.061
24	RPS29A	-0.020	MSC1	0.061
25	RPS17B	-0.019	YPR036W-A	0.061
26	RPL36A	-0.019	TDH1	0.060
27	RPL26A	-0.019	NQM1	0.060
28	RPS30B	-0.018	SCEI	0.060
29	NOP10	-0.018	FOX2	0.060
30	RBL2	-0.018	YBR285W	0.060
Rank	**PC2 negative genes**	**PC2 negative values**	**PC2 positive genes**	**PC2 positive values**
1	RPS25B	-0.089	SPG4	0.081
2	RPL33B	-0.086	SPG1	0.077
3	RPS19A	-0.080	RGI2	0.071
4	GPX2	-0.077	MRK1	0.068
5	RPL21B	-0.077	YDR034W-B	0.066
6	RPL34A	-0.076	FMP43	0.058
7	PHO88	-0.076	YKL065W-A	0.057
8	RPS29A	-0.076	YOR019W	0.056
9	TIF11	-0.075	YDR119W-A	0.055
10	YSY6	-0.075	YER121W	0.051
11	APQ12	-0.075	OLI1	0.050

Rank				
12	RPS22B	-0.074	TMA10	0.048
13	PFD1	-0.074	YPR036W-A	0.048
14	RPL36A	-0.073	CRS5	0.047
15	RPL26A	-0.072	YGR035C	0.046
16	RPB10	-0.071	YNR034W-A	0.043
17	CAF20	-0.071	RGI1	0.042
18	RBL2	-0.071	GPX1	0.040
19	RPS29B	-0.071	HXT6	0.040
20	OST4	-0.070	SCEI	0.038
21	RPL20A	-0.069	CCW12	0.037
22	RPL19A	-0.068	MSC1	0.036
23	RPL14A	-0.068	YGR161W-C	0.036
24	POP8	-0.068	HXT7	0.036
25	RPL40B	-0.068	YOR052C	0.035
26	NTF2	-0.068	UIP4	0.034
27	NIP7	-0.068	YGR174W-A	0.034
28	VMA21	-0.067	SIP18	0.033
29	NOP10	-0.067	YLR257W	0.033
30	YBL028C	-0.067	GLC8	0.032
Rank	PC3 negative genes	PC3 negative values	PC3 positive genes	PC3 positive values
1	YBL028C	-0.133	YLR053C	0.152
2	LRP1	-0.113	YNR034W-A	0.120
3	NIP7	-0.107	SIP18	0.107
4	NOP15	-0.093	RGI1	0.101
5	YML108W	-0.088	HSP104	0.101
6	GPX2	-0.087	SER3	0.095
7	CGR1	-0.085	GLN1	0.090
8	LOC1	-0.076	GPG1	0.089
9	NOP56	-0.075	YMR090W	0.086
10	POP8	-0.072	AFT2	0.086
11	EFB1	-0.068	STF1	0.085
12	CBF5	-0.066	CYC7	0.083
13	ALD6	-0.065	GRX1	0.082
14	EBP2	-0.065	YSA1	0.078
15	RPL2A	-0.065	PHM8	0.075
16	URA1	-0.064	YNK1	0.074
17	MRK1	-0.064	TMA10	0.072
18	RGI2	-0.064	PGM2	0.071
19	RPL43A	-0.063	URA10	0.071
20	15S_rRNA	-0.063	ERG28	0.071
21	SPG1	-0.061	RTC2	0.070
22	NHP2	-0.061	MTD1	0.070
23	RPL37A	-0.061	NRK1	0.070
24	CMS1	-0.060	AYR1	0.069
25	YOR019W	-0.059	ENO1	0.066
26	URM1	-0.058	LYS12	0.065

Rank				
27	RPP2A	-0.057	GLO1	0.065
28	RPL22A	-0.057	GCV1	0.064
29	SPG4	-0.056	HSP12	0.063
30	SNF11	-0.056	ATP16	0.062

Rank	Vsep negative genes	Vsep negative values	Vsep positive genes	Vsep positive values
1	RPL33B	-0.100	SPG4	0.130
2	RPS25B	-0.093	SPG1	0.119
3	TIF11	-0.079	YDR034W-B	0.117
4	RPS18B	-0.076	RGI2	0.108
5	RPS19A	-0.074	TMA10	0.102
6	RPL21B	-0.072	MRK1	0.099
7	NOP10	-0.071	MPC3	0.097
8	RPS29A	-0.070	YER121W	0.095
9	GPX2	-0.070	DPC7	0.091
10	RPL27B	-0.068	COX26	0.090
11	RPS30B	-0.068	SOL1	0.088
12	RPS16A	-0.068	YOR019W	0.088
13	APQ12	-0.067	OLI1	0.084
14	RPS22B	-0.067	CRS5	0.082
15	RPL14A	-0.066	SPO24	0.081
16	RPL36A	-0.066	RGI1	0.080
17	RPS21A	-0.066	YGR035C	0.079
18	YSY6	-0.066	GPX1	0.070
19	RPL26A	-0.065	HXT6	0.069
20	HTA2	-0.065	TMC1	0.066
21	NIP7	-0.064	MSC1	0.065
22	RPL23A	-0.063	YGR161W-C	0.065
23	RPS17B	-0.063	SCEI	0.065
24	RPL34A	-0.063	CCW12	0.065
25	PFD1	-0.063	YGR174W-A	0.065
26	PHO88	-0.063	HXT7	0.065
27	RPS28A	-0.063	YLR257W	0.064
28	RPB10	-0.063	GLC8	0.064
29	RPS23A	-0.062	UIP4	0.063
30	RBL2	-0.060	SIP18	0.063

Rank	Vhet negative genes	Vhet negative values	Vhet positive genes	Vhet positive values
1	MRPL38	-0.050	21S_rRNA	0.006
2	UBC7	-0.050	RPL24A	0.002
3	MRP17	-0.049	CUP1-1	0.001
4	CUE1	-0.049	CUP1-2	0.001
5	MNP1	-0.049	SWE1	0.000
6	YBR230W-A	-0.049	AIM41	0.000
7	MRPS8	-0.047	RPL41A	-0.001
8	TVP18	-0.047	RPL23B	-0.001
9	SRB6	-0.047	RPS31	-0.001

10	MRPL49	-0.047	YBR085C-A		-0.002
11	DAD4	-0.046	MTC6		-0.002
12	MIN7	-0.046	RPL29		-0.002
13	YKL033W-A	-0.045	HMRA1		-0.002
14	RPL2B	-0.045	RPL41B		-0.002
15	TDH2	-0.045	TRX2		-0.003
16	COS4	-0.045	STF2		-0.003
17	VPS60	-0.045	SIP5		-0.003
18	FIS1	-0.045	RPL38		-0.003
19	RPL40B	-0.045	YMC1		-0.003
20	SRP21	-0.044	HOR7		-0.003
21	MIM1	-0.044	PMP3		-0.004
22	RPL18A	-0.044	PRP28		-0.004
23	TVP15	-0.044	BIR1		-0.004
24	ATP20	-0.044	ZEO1		-0.004
25	HUB1	-0.044	URB1		-0.005
26	YBR126W-A	-0.044	RPS30A		-0.005
27	ISD11	-0.044	RPS12		-0.005
28	COX6	-0.044	RPL27A		-0.005
29	SKP1	-0.044	SSS1		-0.005
30	SFT1	-0.044	HHT1		-0.005

Supplementary Table 2

Rank	Cluster C - Cluster A Positive		Cluster C - Cluster A Negative		Cluster B - Cluster A Positive		Cluster B - Cluster A Negative	
	Genes	Values	Genes	Values	Genes	Values	Genes	Values
1	SPG4	3.39	RPL33B	-2.22	YNR034W-A	2.05	GPX2	-1.62
2	YDR034W-B	3.13	RPS25B	-1.96	SIP18	1.79	YBL028C	-1.57
3	SPG1	3.12	TIF11	-1.61	RGI1	1.77	NIP7	-1.50
4	RGI2	2.86	RPS18B	-1.55	GPG1	1.38	POP8	-1.06
5	TMA10	2.85	GPX2	-1.53	YMR090W	1.31	CGR1	-1.05
6	MRK1	2.64	NIP7	-1.51	ENO1	1.29	LRP1	-0.98
7	MPC3	2.63	RPS19A	-1.49	HSP104	1.28	LOC1	-0.95
8	YNR034W-A	2.58	RPL21B	-1.48	TMA10	1.27	URM1	-0.82
9	YER121W	2.57	NOP10	-1.43	GPX1	1.25	RPL37A	-0.81
10	YDR119W-A	2.54	RPS30B	-1.40	YLR053C	1.21	NOP56	-0.78
11	YKL065W-A	2.46	APQ12	-1.37	CRS5	1.19	RPL43A	-0.78
12	YOR019W	2.45	RPS17B	-1.36	CYC7	1.15	RPO26	-0.76
13	CRS5	2.42	RPL27B	-1.36	HSP12	1.15	YDL121C	-0.75
14	RGI1	2.37	RPL22B	-1.34	URA10	1.13	RPL36A	-0.75
15	YGR035C	2.36	RPS23A	-1.32	PGM2	1.10	NOP15	-0.73
16	OLI1	2.23	RPS21A	-1.32	TDH1	1.07	RPS27A	-0.73
17	YPR036W-A	2.22	YBL028C	-1.31	RTC2	1.01	RPL22A	-0.72

#	Gene	Value	Gene	Value	Gene	Value	Gene	Value
18	GPX1	2.13	RPS29A	-1.30	STF1	0.99	RPS29A	-0.71
19	HXT6	2.07	RPS22B	-1.30	PHM8	0.95	NHP2	-0.70
20	TDH1	2.02	YSY6	-1.29	GLO1	0.94	RPL26A	-0.68
21	GPG1	2.01	RPS10A	-1.29	NCE102	0.93	CSN9	-0.68
22	YGR161W-C	1.99	RPB10	-1.27	AFT2	0.93	RPS22B	-0.67
23	YGR174W-A	1.97	POP8	-1.25	GPM1	0.93	RPL31B	-0.67
24	HXT7	1.97	RPL14A	-1.25	MSC1	0.92	NOP10	-0.66
25	SIP18	1.97	RPL36A	-1.24	HSP82	0.90	RPB10	-0.62
26	MSC1	1.96	RPL26A	-1.24	YHR138C	0.90	RPC11	-0.62
27	UIP4	1.94	HTA2	-1.22	GRX1	0.87	CMS1	-0.60
28	FMP46	1.91	RPL34A	-1.20	GPH1	0.86	PFD1	-0.60
29	OM14	1.90	RPS28A	-1.19	HSP78	0.85	RPL40B	-0.60
30	CCW12	1.90	RPS16A	-1.19	YNK1	0.83	YML108W	-0.60
31	YOR052C	1.89	RPL23A	-1.19	GLC3	0.80	YSY6	-0.59
32	DDR2	1.86	RPS18A	-1.17	YOR052C	0.80	FYV7	-0.58
33	FOX2	1.85	PFD1	-1.16	LYS12	0.79	RPS1B	-0.58
34	ATG8	1.84	PHO88	-1.13	UIP4	0.78	RPC10	-0.57
35	GPH1	1.84	NRK1	-1.13	HSP30	0.78	RPL22B	-0.56
36	YLR257W	1.83	RPS7A	-1.12	YSA1	0.77	YIP3	-0.55
37	GLC8	1.81	RBL2	-1.11	ADH1	0.77	RPL37B	-0.55
38	SCEI	1.79	CGR1	-1.11	STF2	0.76	RPL34A	-0.55
39	GRX2	1.79	RPL16A	-1.10	YBR056W	0.76	RPL12A	-0.55
40	HSP82	1.78	RPS17A	-1.10	ERG28	0.76	RPP2A	-0.54
41	YLR312C	1.78	RPS6B	-1.10	COS1	0.75	RPP1A	-0.52
42	URA10	1.76	RPL35B	-1.09	HSC82	0.74	RPL27B	-0.52
43	YHR138C	1.73	URM1	-1.09	ATG8	0.74	RPS15	-0.51
44	RFS1	1.72	RPL21A	-1.09	TDH2	0.71	RPS19A	-0.51
45	VPS21	1.68	RPS27A	-1.08	EMP46	0.70	GIM4	-0.51
46	NHP6B	1.68	RPS22A	-1.07	YKL065W-A	0.70	RPL39	-0.50
47	TMA17	1.67	CAF20	-1.06	AYR1	0.70	RPL13B	-0.49
48	UBI4	1.66	RPL26B	-1.05	PBI2	0.70	RPL21B	-0.49
49	YOR289W	1.64	RPL35A	-1.05	PST2	0.70	PGA2	-0.49
50	SUE1	1.64	OST4	-1.04	GLC8	0.69	RPS29B	-0.47
51	15S_rRNA	1.63	TSC3	-1.03	ARC15	0.69	RPL1A	-0.46
52	GLO1	1.62	RPO26	-1.02	YET1	0.68	URA1	-0.46
53	GLO2	1.62	MFA2	-1.01	YPR098C	0.68	RPL2A	-0.46
54	YGR182C	1.58	RPS30A	-1.01	HSP26	0.68	RPS22A	-0.46
55	MRP8	1.58	YFR032C-B	-0.99	YLR271W	0.67	RPS24B	-0.46
56	YBR285W	1.58	RPS21B	-0.99	DDR2	0.67	EFB1	-0.46
57	HSP12	1.57	RPS8B	-0.98	COS3	0.66	RPL33B	-0.46
58	YMR090W	1.57	GIM4	-0.98	YET2	0.66	RPS16B	-0.46
59	NQM1	1.55	NTF2	-0.98	DCS2	0.66	RPL16A	-0.45
60	MPC1	1.54	RPL43B	-0.96	YDR379C-A	0.65	RPL19A	-0.45
61	UBC8	1.54	SUI1	-0.96	SNA2	0.64	RPS17B	-0.44
62	YBR056W	1.54	RPS6A	-0.95	SER3	0.64	RPL20A	-0.44
63	SNF11	1.52	GLN1	-0.94	RCF1	0.63	HTA1	-0.44

64	YKL091C	1.51	RPS10B	-0.94	YLR227W-B	0.63	YKE2	-0.44
65	FMP16	1.51	ARF1	-0.93	YGR027W-B	0.63	RPS21B	-0.43
66	MIA40	1.50	RPS29B	-0.92	RNY1	0.63	ZEO1	-0.43
67	PST2	1.50	RPS24A	-0.92	YER121W	0.63	RPL19B	-0.42
68	SDH3	1.49	RPS19B	-0.92	YET3	0.62	RPL12B	-0.42
69	PAI3	1.48	RPS9B	-0.89	YDR119W-A	0.62	RPL23A	-0.41
70	GSY2	1.48	RPS8A	-0.89	MBF1	0.62	RPL33A	-0.40
71	GLC3	1.48	RPC11	-0.88	YOR020W-A	0.60	YLR146W-A	-0.39
72	YNL208W	1.48	RPL25	-0.88	BMH1	0.60	RPS25B	-0.39
73	MDG1	1.47	DTD1	-0.88	RFS1	0.60	RPL43B	-0.39
74	PGK1	1.47	RPL31B	-0.88	COX5B	0.60	RPS21A	-0.38
75	YLR346C	1.47	RPC10	-0.87	FIS1	0.59	CBF5	-0.38
76	RRT8	1.46	RPL23B	-0.86	YOR289W	0.59	YDL157C	-0.37
77	ARA1	1.45	NAT5	-0.85	FMP16	0.59	LSM6	-0.37
78	SNC2	1.41	ARL1	-0.85	HXT7	0.58	RPL1B	-0.37
79	RPN8	1.41	RPS27B	-0.85	YKL066W	0.58	RPS11A	-0.36
80	AI1	1.41	YDL121C	-0.83	LIP1	0.58	YEF3	-0.36
81	PDR5	1.40	VMA21	-0.83	ARF2	0.57	RPL38	-0.35
82	YBR201C-A	1.40	RPL43A	-0.83	YBR085C-A	0.57	YBR191W-A	-0.35
83	YJR008W	1.39	RPL20B	-0.83	RRT8	0.57	RPP1B	-0.34
84	NYV1	1.38	RPL11B	-0.83	COS2	0.57	RPL27A	-0.34
85	YBL039W-B	1.38	YNL010W	-0.82	ATP16	0.57	RPS19B	-0.34
86	CYC7	1.37	RPL42A	-0.81	CNL1	0.56	RPS10A	-0.34
87	AI4	1.36	RPL20A	-0.81	YGR174W-A	0.56	RPL16B	-0.34
88	MAG1	1.35	FYV7	-0.80	MRPL36	0.55	DTD1	-0.34
89	YET2	1.35	YEF3	-0.80	PNC1	0.55	ALD6	-0.33
90	GPM1	1.34	RPL39	-0.80	YDC1	0.54	RPS9B	-0.33
91	YLR271W	1.34	LEU1	-0.80	YKL068W-A	0.54	YOL086W-A	-0.33
92	YOR1	1.34	RPL29	-0.80	FMP33	0.54	RPL23B	-0.33
93	YDC1	1.33	YLR146W-A	-0.79	UBC1	0.53	SRB7	-0.33
94	PBI2	1.33	RPS16B	-0.78	MET14	0.53	RPL42A	-0.31
95	FMP33	1.32	RPS26B	-0.77	TVP15	0.53	RPS0B	-0.31
96	ENO1	1.32	YKE2	-0.77	DAP1	0.52	RPS10B	-0.30
97	YGR053C	1.31	YRB1	-0.77	PAI3	0.52	RPS27B	-0.30
98	GRX1	1.31	RPS23B	-0.77	YLR257W	0.51	UPS2	-0.30
99	HYP2	1.31	VMA7	-0.76	ABF2	0.50	APT1	-0.30
100	MCR1	1.30	RPL19A	-0.76	TPI1	0.50	CWP2	-0.30

Supplementary Table 3

Go Term:	ncRNA processing
p-Value:	9.90E-04
Gene List:	30 Genes with largest magnitude positive values in the PC3 vector
Method:	The gene list was submitted to the Saccharomyces Genome Database's Gene List analysis on 08/15/2018.

ORF Name	Gene Name	SGD Identifier	Go Term ID	Go Term Name	Parent Go Term	Parent Go Term Name
YBL018C	POP8	S000000114	GO:0006364	rRNA processing	GO:0034470	ncRNA processing
YBL018C	POP8	S000000114	GO:0008033	tRNA processing	GO:0034470	ncRNA processing
YBL018C	POP8	S000000114	GO:0034965	intronic box C/D snoRNA processing	GO:0034470	ncRNA processing
YDL208W	NHP2	S000002367	GO:0000469	cleavage involved in rRNA processing	GO:0034470	ncRNA processing
YDL208W	NHP2	S000002367	GO:0000470	maturation of LSU-rRNA	GO:0034470	ncRNA processing
YDL208W	NHP2	S000002367	GO:0006364	rRNA processing	GO:0034470	ncRNA processing
YDL208W	NHP2	S000002367	GO:0031118	rRNA pseudouridine synthesis	GO:0034470	ncRNA processing
YFR001W	LOC1	S000001897	GO:0000447	endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	GO:0034470	ncRNA processing
YFR001W	LOC1	S000001897	GO:0000472	endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	GO:0034470	ncRNA processing
YFR001W	LOC1	S000001897	GO:0000480	endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	GO:0034470	ncRNA processing
YGL029W	CGR1	S000002997	GO:0006364	rRNA processing	GO:0034470	ncRNA processing
YHR081W	LRP1	S000001123	GO:0000467	exonucleolytic trimming to generate mature 3'-end of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	GO:0034470	ncRNA processing
YHR081W	LRP1	S000001123	GO:0006364	rRNA processing	GO:0034470	ncRNA processing
YHR081W	LRP1	S000001123	GO:0034475	U4 snRNA 3'-end processing	GO:0034470	ncRNA processing
YHR081W	LRP1	S000001123	GO:0034476	U5 snRNA 3'-end processing	GO:0034470	ncRNA processing
YHR081W	LRP1	S000001123	GO:0071051	polyadenylation-dependent snoRNA 3'-end processing	GO:0034470	ncRNA processing
YIL008W	URM1	S000001270	GO:0002098	tRNA wobble uridine modification	GO:0034470	ncRNA processing
YIL008W	URM1	S000001270	GO:0002143	tRNA wobble position uridine thiolation	GO:0034470	ncRNA processing
YIL008W	URM1	S000001270	GO:0008033	tRNA processing	GO:0034470	ncRNA processing
YIL008W	URM1	S000001270	GO:0034227	tRNA thio-modification	GO:0034470	ncRNA processing
YKL172W	EBP2	S000001655	GO:0006364	rRNA processing	GO:0034470	ncRNA processing
YLR175W	CBF5	S000004165	GO:0000495	box H/ACA snoRNA 3'-end processing	GO:0034470	ncRNA processing
YLR175W	CBF5	S000004165	GO:0006364	rRNA processing	GO:0034470	ncRNA processing
YLR175W	CBF5	S000004165	GO:0031118	rRNA pseudouridine synthesis	GO:0034470	ncRNA processing
YLR185W	RPL37A	S000004175	GO:0000448	cleavage in ITS2 between 5.8S rRNA and LSU-rRNA of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	GO:0034470	ncRNA processing
YLR197W	NOP56	S000004187	GO:0000154	rRNA modification	GO:0034470	ncRNA processing
YLR197W	NOP56	S000004187	GO:0006364	rRNA processing	GO:0034470	ncRNA processing
YNL110C	NOP15	S000005054	GO:0006364	rRNA processing	GO:0034470	ncRNA processing
YPL211W	NIP7	S000006132	GO:0000463	maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	GO:0034470	ncRNA processing

Go Term:	rRNA metabolic process
p-Value:	1.70E-03
Gene List:	30 Genes with largest magnitude positive values in the PC3 vector
Method:	The gene list was submitted to the Saccharomyces Genome Database's Gene List analysis on 08/15/2018.

ORF Name	Gene Name	SGD Identifier	Go Term ID	Go Term Name	Parent Go Term	Parent Go Term Name
YBL018C	POP8	S000000114	GO:0006364	rRNA processing	GO:0016072	rRNA metabolic process
YDL208W	NHP2	S000002367	GO:0000469	cleavage involved in rRNA processing	GO:0016072	rRNA metabolic process
YDL208W	NHP2	S000002367	GO:0000470	maturation of LSU-rRNA	GO:0016072	rRNA metabolic process
YDL208W	NHP2	S000002367	GO:0006364	rRNA processing	GO:0016072	rRNA metabolic process
YDL208W	NHP2	S000002367	GO:0031118	rRNA pseudouridine synthesis	GO:0016072	rRNA metabolic process
YFR001W	LOC1	S000001897	GO:0000447	endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	GO:0016072	rRNA metabolic process
YFR001W	LOC1	S000001897	GO:0000472	endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	GO:0016072	rRNA metabolic process
YFR001W	LOC1	S000001897	GO:0000480	endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	GO:0016072	rRNA metabolic process
YGL029W	CGR1	S000002997	GO:0006364	rRNA processing	GO:0016072	rRNA metabolic process
YHR081W	LRP1	S000001123	GO:0000467	exonucleolytic trimming to generate mature 3'-end of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	GO:0016072	rRNA metabolic process
YHR081W	LRP1	S000001123	GO:0006364	rRNA processing	GO:0016072	rRNA metabolic process
YHR081W	LRP1	S000001123	GO:0071035	nuclear polyadenylation-dependent rRNA catabolic process	GO:0016072	rRNA metabolic process
YKL172W	EBP2	S000001655	GO:0006364	rRNA processing	GO:0016072	rRNA metabolic process
YLR175W	CBF5	S000004165	GO:0006364	rRNA processing	GO:0016072	rRNA metabolic process
YLR175W	CBF5	S000004165	GO:0031118	rRNA pseudouridine synthesis	GO:0016072	rRNA metabolic process
YLR185W	RPL37A	S000004175	GO:0000448	cleavage in ITS2 between 5.8S rRNA and LSU-rRNA of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	GO:0016072	rRNA metabolic process
YLR197W	NOP56	S000004187	GO:0000154	rRNA modification	GO:0016072	rRNA metabolic process
YLR197W	NOP56	S000004187	GO:0006364	rRNA processing	GO:0016072	rRNA metabolic process
YNL110C	NOP15	S000005054	GO:0006364	rRNA processing	GO:0016072	rRNA metabolic process
YPL211W	NIP7	S000006132	GO:0000463	maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	GO:0016072	rRNA metabolic process