

Supplemental Microarray Analysis Materials and Methods

Microarray analysis was performed essentially as described (Angus-Hill et al., 2001; Kristjuhan et al., 2003). Data for individual genes (values) was expressed as the \log_2 of the normalized wild-type/experimental signal ratios or as the fold change of this ratio. For example, values of -1, 0, or +1 correspond to genes that are “down-regulated two-fold”, “unchanged”, or “up-regulated two-fold”, respectively. Each experiment was performed in duplicate or triplicate (a separate sample preparation and labeling/hybridization).

Supplemental References

- Angus-Hill, M.L., Schlichter, A., Roberts, D., Erdjument-Bromage, H., Tempst, P. and Cairns, B.R. (2001) A Rsc3/Rsc30 zinc cluster dimer reveals novel roles for the chromatin remodeler RSC in gene expression and cell cycle control. *Mol Cell*, **7**: 741-751.
- Kristjuhan, A., Wittschieben, B.O., Walker, J., Roberts, D., Cairns, B.R. and Svejstrup, J.Q. (2003) Spreading of Sir3 protein in cells with severe histone H3 hypoacetylation. *Proc Natl Acad Sci U S A*.

Supplemental Table S1. Subset of Genes Affected in *rsc4* BD^{Ts}-

Gene	Function	<i>rsc4-2</i> 37°C		<i>rsc4-7</i> 35°C		<i>rsc4-11</i> 35°C	
		Fold Change	Rank	Fold Change	Rank	Fold Change	Rank
BNA6	Nicotinic Acid Biosynthesis	↓ 2.94	5	↓ 2.56	9	↓ 2.74	22
TNA1	Nicotinic Acid Biosynthesis	↓ 2.20	45	↓ 2.51	10	↓ 2.46	30
SMD3	mRNA Splicing	↓ 2.29	33	↓ 2.29	16	↓ 3.01	9
SMX3	mRNA Splicing	↓ 2.18	48	↓ 2.24	19	↓ 2.78	17
MF(alpha)1	Mating Pathway	↓ 2.95	4	↓ 1.90	55	↓ 4.95	2
MF(alpha)2	Mating Pathway	↓ 1.76	265	↓ 2.33	14	↓ 4.83	3
FUS1	Mating Pathway	↓ 1.07	2471	↓ 2.04	38	↓ 2.99	11
SPR6	Unknown	↓ 2.29	32	↓ 2.72	4	↓ 3.39	6
YKR049C	Unknown	↓ 3.88	1	↓ 3.40	2	↓ 3.89	4
DDR2	Cell Wall/Stress	↑ 4.70	4	↑ 7.69	1	↑ 5.59	1
SED1	Cell Wall/Stress	↑ 3.60	9	↑ 3.81	4	↑ 5.31	2
SNZ1	Cell Wall/Stress	↑ 4.96	2	↑ 6.18	2	↑ 4.83	3
SNO1	Cell Wall/Stress	↑ 2.84	37	↑ 3.60	5	↑ 3.22	9
TIR1	Cell Wall/Stress	↑ 1.15	1914	↑ 2.61	14	↑ 3.82	6
FIT2	Iron Homeostasis	↑ 2.69	61	↑ 2.83	10	↑ 3.85	5
FIT3	Iron Homeostasis	↑ 1.79	325	↑ 1.63	186	↑ 2.95	13
PUT1	Proline Oxidase	↑ 3.20	21	↑ 2.19	33	↑ 2.09	63

Supplemental Table S2. 50 Most Downregulated genes in *rsc4-2* at 37°C

log(2) of ratio of gene expression	ORF	Gene	Description or Biological Process
-1.96	YKR049C		
-1.89	YLR339C		
-1.72	YGL220W		
-1.56	YPL187W	MF(ALPHA)1	Phermone
-1.56	YFR047C	BNA6	Nicotinic acid biosynthesis
-1.54	YBR093C	PHO5	acid phosphatase
-1.48	YLR435W		
-1.45	YOR007C	SGT2	
-1.41	YLR340W	RPP0	
-1.38	YHR053C	CUP1-1	
-1.35	YGR105W	VMA21	Vacuolar acidification
-1.34	YHR089C	GAR1	
-1.34	YGR208W	SER2	Phosphoserine phosphatase
-1.33	YER023W	PRO3	pyrroline 5-carboxylate reductase
-1.31	YML014W		
-1.30	YNL065W	BZR1	
-1.30	YHR055C	CUP1-2	
-1.29	YER117W	RPL23B	Ribosomal protein
-1.29	YOL143C	RIB4	
-1.28	YLR359W	ADE13	Adenylosuccinate lyase
-1.28	YIL133C	RPL16A	Ribosomal protein
-1.27	YML079W		
-1.25	YDL014W	NOP1	Small nuclear ribonucleoprotein
-1.24	YPR051W	MAK3	
-1.24	YLR268W	SEC22	Non-selective vesicle fusion
-1.24	YGR118W	RPS23A	Ribosomal protein
-1.23	YDL130W	RPP1B	Ribosomal protein
-1.22	YIR022W	SEC11	Signal peptidase
-1.21	YBR189W	RPS9B	Ribosomal protein
-1.20	YOR263C		
-1.20	YKL006C-A	SFT1	Intra Golgi transport
-1.19	YER115C	SPR6	
-1.19	YLR147C	SMD3	mRNA splicing
-1.19	YNL178W	RPS3	Ribosomal protein
-1.19	YNL281W	HCH1	Protein folding
-1.18	YKL114C	APN1	DNA (apurinic or apyrimidinic site) lyase
-1.18	YHL001W	RPL14B	Ribosomal protein
-1.18	YBL002W	HTB2	Histone
-1.17	YDR471W	RPL27B	Ribosomal protein
-1.16	YKL081W	TEF4	Translation elongation factor
-1.15	YNL301C	RPL18B	Ribosomal protein
-1.15	YHR010W	RPL27A	Ribosomal protein
-1.15	YBR181C	RPS6B	Ribosomal protein
-1.14	YCR059C	YIH1	Amino acid metabolism regulation
-1.14	YGR260W	TNA1	Nicotinic acid transporter
-1.14	YDL086W		
-1.14	YML063W	RPS1B	Ribosomal protein
-1.13	YPR182W	SMX3	mRNA splicing
-1.13	YFR031C-A	RPL2A	Ribosomal protein
-1.12	YNL112W	DBP2	RNA helicase

Supplemental Table S3. 50 Most Upregulated genes in *rsc4-2* at 37°C

log(2) of ratio of gene expression	ORF	Gene	Description or Biological Process
2.42	YNR066C		
2.31	YMR096W	SNZ1	
2.24	YBR296C	PHO89	phosphate metabolism
2.23	YOL053C-A	DDR2	stress response
2.14	YMR317W		
2.14	YLR267W	BOP2	
2.06	YPL021W	ECM23	
1.86	YBR299W	MAL32	alpha-glucosidase
1.85	YDR077W	SED1	cell wall structural protein
1.83	YJR029W		
1.82	YBR295W	PCA1	hydrogen/potassium-exchanging ATPase
1.80	YPL006W	NCR1	
1.79	YPR184W	GDB1	
1.78	YFR016C		
1.78	YJR027W		
1.76	YNR065C		
1.72	YJR151C	DAN4	
1.71	YGL062W	PYC1	pyruvate carboxylase involved in gluconeogenesis
1.70	YGR032W	GSC2	1,3-beta-glucan synthase
1.68	YJR028W		
1.68	YLR142W	PUT1	Proline oxidase
1.66	YCR100C		
1.66	YDR029W		
1.66	YMR316C-B		
1.64	YML045W	RRN11	RNA polymerase I transcription factor
1.64	YDR250C		
1.63	YHR213W		
1.60	YLR337W	VRP1	actin binding protein
1.58	YBR292C		
1.57	YOL047C		
1.57	YGL177W		
1.54	YML040W	YMD8	
1.52	YMR322C		
1.51	YMR176W	ECM5	
1.51	YMR095C	SNO1	
1.50	YMR050C	ERB1	
1.50	YER067W		
1.50	YGR022C		
1.49	YCR099C		
1.48	YOR178C	GAC1	protein phosphatase type 1 involved in meiosis
1.47	YIL080W		
1.47	YLR338W	KRE21	
1.46	YCL042W		
1.46	YMR046C	IOC4	
1.46	YDR203W		
1.45	YBL005W-A	PDR3	transcription factor involved in transport
1.37	YJL088W	ARG3	ornithine carbamoyltransferase
1.37	YNL285W		
1.38	YGR023W	MTL1	
1.37	YNL285W		

Supplemental Table S4. Genes Upregulated in *rsc4-2* at 35°C

log(2) of ratio of gene expression	ORF	Gene	Description or Biological Process
1.90	YOL053C-A	DDR2	stress response
1.83	YMR096W	SNZ1	
1.72	YDR077W	SED1	cell wall structural protein
1.65	YOR382W	FIT2	Iron homeostasis
1.58	YCL046W		
1.41	YJR029W		
1.41	YMR095C	SNO1	
1.39	YJR027W		
1.22	YPL021W	ECM23	
1.18	YCL018W	LEU2	3-isopropylmalate dehydrogenase
1.14	YCR010C	ADY2	
1.11	YML039W	YMD8	
1.08	YKR013W	PRY2	
1.05	YGR091W	PRP31	mRNA splicing
1.04	YFR024C-A		
1.03	YJL116C	NCA3	
1.02	YML040W	YMD8	
1.01	YJL159W	HSP150	cell wall organization and biogenesis
1.00	YGL206C	CHC1	

Supplemental Table S5. Genes Downregulated in *rsc4-2* at 35°C

log(2) of ratio of gene expression	ORF	Gene	Description or Biological Process
-1.36	YER115C	SPR6	
-1.33	YKR049C		
-1.32	YNL040W		
-1.26	YGR260W	TNA1	Nicotinic acid transporter
-1.22	YGR259C		
-1.19	YPL263C	KEL3	
-1.12	YLR438W	CAR2	
-1.12	YLR446W		
-1.07	YCR059C	YIH1	amino acid metabolism regulation
-1.02	YEL070W		
-1.02	YIL019W		

Supplemental Table S6. 50 Most Downregulated Genes in *rsc4-7* at 35°C

log(2) of ratio of gene expression	ORF	Gene	Description or Biological Process
-2.15	YNL040W		
-1.77	YKR049C		
-1.53	YML079W		
-1.44	YER115C	SPR6	
-1.41	YAL045C		
-1.38	YML094W	GIM5	protein folding
-1.38	YGL220W		
-1.37	YLR268W	SEC22	non-selective vesicle fusion
-1.36	YFR047C	BNA6	
-1.33	YGR260W	TNA1	nicotinamide mononucleotide transport
-1.32	YJL097W		
-1.30	YJR069C	HAM1	
-1.25	YOL143C	RIB4	
-1.22	YGL089C	MF(ALPHA)2	pheromone response
-1.22	YGL221C	NIF3	
-1.20	YLR147C	SMD3	mRNA splicing
-1.19	YML095C-A		
-1.18	YFL044C		
-1.17	YPR182W	SMX3	mRNA splicing
-1.16	YGR105W	VMA21	vacuolar acidification
-1.13	YKL114C	APN1	
-1.13	YDR248C		
-1.13	YGR259C		
-1.13	YOR377W	ATF1	
-1.13	YCR059C	YIH1	amino acid metabolism regulation
-1.12	YLR339C		
-1.11	YML014W		
-1.10	YLR118C		
-1.08	YBR278W	DPB3	nucleotide-excision repair
-1.06	YHR191C	CTF8	
-1.06	YFL046W		
-1.06	YIL013C	PDR11	transport
-1.05	YLR446W		
-1.04	YER023W	PRO3	proline biosynthesis
-1.04	YNL168C		
-1.03	YMR126C		
-1.03	YDL086W		
-1.03	YCL027W	FUS1	conjugation
-1.01	YHR190W	ERG9	ergosterol biosynthesis
-1.00	YPR051W	MAK3	
-0.99	YAR071W	PHO11	acid phosphatase
-0.98	YGL041C		
-0.96	YAL033W	POP5	ribonuclease MRP
-0.96	YBR158W	CST13	
-0.96	YLR303W	MET17	methionine metabolism
-0.96	YHR089C	GAR1	small nuclear ribonucleoprotein
-0.95	YKL214C		
-0.95	YKL091C		
-0.94	YOL126C	MDH2	malic enzyme
-0.94	YKR106W		

Supplemental Table S7. 50 Most Upregulated Genes in *rsc4-7* at 35°C

log(2) of ratio of gene expression	ORF	Gene	Description or Biological Process
2.94	YOL053C-A	DDR2	stress response
2.63	YMR096W	SNZ1	
1.96	YJL116C	NCA3	
1.93	YDR077W	SED1	cell wall organization and biogenesis
1.85	YMR095C	SNO1	
1.76	YGR043C		
1.76	YLR327C		
1.68	YPL021W	ECM23	
1.51	YGR032W	GSC2	cell wall organization and biogenesis
1.50	YOR382W	FIT2	Iron homeostasis
1.46	YLR267W	BOP2	
1.43	YDR218C	SPR28	cell wall organization and biogenesis
1.39	YJL159W	HSP150	cell wall organization and biogenesis
1.38	YER011W	TIR1	cell wall organization and biogenesis
1.38	YMR317W		
1.35	YBR296C	PHO89	phosphate metabolism
1.35	YKR013W	PRY2	
1.34	YGR032W	GSC2	cell wall organization and biogenesis
1.30	YLR121C	YPS3	protein metabolism and modification
1.28	YBL049W		
1.27	YDL215C	GDH2	
1.27	YCR060W		
1.24	YGL117W		
1.24	YKR061W	KTR2	N-linked glycosylation
1.23	YPL197C		
1.21	YGL121C		
1.18	YDR171W	HSP42	stress response
1.18	YDR070C		
1.18	YFL014W	HSP12	oxidative stress response
1.15	YML090W		
1.15	YDR453C		
1.13	YGR142W	BTN2	pH regulation
1.13	YLR142W	PUT1	Proline oxidase
1.12	YKR012C		
1.12	YJR027W		
1.09	YLR194C		
1.09	YHR071W	PCL5	cell cycle
1.08	YML039W	YMD8	
1.07	YJR029W		
1.07	YOR100C	CRC1	fatty acid metabolism
1.07	YBR076W	ECM8	
1.06	YKL163W	PIR3	cell wall organization and biogenesis
1.06	YPL170W		
1.04	YPR197C		
1.03	YGL255W	ZRT1	high-affinity zinc ion transport
1.02	YER185W		
1.02	YMR011W	HXT2	transport
1.01	YDR461W	MFA1	signal transduction of mating signal
1.01	YOL047C		
1.01	YMR309C	NIP1	

Supplemental Table S8. Genes Downregulated in *rsc4-7* at 30°C

log(2) of ratio of gene expression	ORF	Gene	Description or Biological Process
-1.83	YNL040W		
-1.18	YJR078W		
-1.10	YDL021W	GPM2	phosphoglycerate mutase
-1.09	YFL042C		
-1.07	YKR049C		
-1.06	YIL013C	PDR11	transport
-1.03	YGL263W	COS12	

Supplemental Table S9. Genes Upregulated *rsc4-7* at 30°C

log(2) of ratio of gene expression	ORF	Gene	Description or Biological Process
1.80	YOR383C	FIT3	Iron Homeostasis
1.62	YOR382W	FIT2	Iron Homeostasis
1.49	YOL053C-A	DDR2	stress response
1.42	YDR534C	FIT1	Iron Homeostasis
1.25	YOR387C		
1.24	YFL014W	HSP12	heat shock protein
1.22	YJL159W	HSP150	cell wall structural protein
1.18	YPL171C	OYE3	
1.09	YDR218C	SPR28	structural protein of cytoskeleton; cell wall
1.08	YHR054C		

Supplemental Table S10. 50 Most Downregulated Genes in *rsc4-11* at 35°C

log(2) of ratio of gene expression	ORF	Gene	Description or Biological Process
-2.31	YNL040W		
-2.31	YPL187W	MF(ALPHA)1	pheromone
-2.27	YGL089C	MF(ALPHA)2	pheromone
-1.96	YKR049C		
-1.88	YML079W		
-1.76	YER115C	SPR6	
-1.74	YAL018C		
-1.69	YCR059C	YIH1	amino acid metabolism regulation
-1.59	YLR147C	SMD3	mRNA splicing
-1.58	YAL045C		
-1.58	YCL027W	FUS1	conjugation
-1.55	YGR105W	VMA21	vacuolar acidification
-1.55	YML095C-A		
-1.53	YHR191C	CTF8	
-1.53	YML094W	GIM5	protein folding
-1.50	YGL220W		
-1.48	YPR182W	SMX3	mRNA splicing
-1.47	YOR377W	ATF1	alcohol O-acetyltransferase
-1.47	YGL221C	NIF3	
-1.47	YGL041C		
-1.46	YLR118C		
-1.46	YFR047C	BNA6	Nicotinic acid synthesis
-1.45	YDR248C		
-1.42	YIL098C	FMC1	
-1.36	YJL097W		
-1.34	YBL016W	FUS3	MAP kinase
-1.33	YJR069C	HAM1	
-1.31	YML014W		
-1.31	YFL044C		
-1.30	YGR260W	TNA1	Nicotinic acid transporter
-1.28	YDR415C		
-1.28	YKL114C	APN1	
-1.28	YLR452C	SST2	GTPase activator
-1.28	YJR004C	SAG1	cell adhesion receptor
-1.26	YMR222C		
-1.24	YAL009W	SPO7	meiosis
-1.23	YMR126C		
-1.21	YFL046W		
-1.20	YCL076W		
-1.20	YKL091C		
-1.19	YCR076C		
-1.19	YBR158W	CST13	
-1.18	YPR050C		
-1.17	YGL081W		
-1.16	YCL033C		
-1.16	YOL143C	RIB4	
-1.16	YKL177W		
-1.16	YAL033W	POP5	ribonuclease MRP*
-1.16	YHR067W		
-1.15	YGR259C		

Supplemental Table S11. 50 Most Upregulated Genes in *rsc4-11* at 35°C

log(2) of ratio of gene expression	ORF	Gene	Description or Biological Process
2.48	YOL053C-A	DDR2	stress response
2.41	YDR077W	SED1	cell wall structural protein
2.27	YMR096W	SNZ1	
2.04	YPL021W	ECM23	
1.95	YOR382W	FIT2	Iron Homeostasis
1.93	YER011W	TIR1	cell wall structural protein
1.85	YJL116C	NCA3	
1.74	YJL159W	HSP150	cell wall structural protein
1.69	YMR095C	SNO1	
1.68	YJR027W		
1.64	YJR029W		
1.57	YLR267W	BOP2	
1.56	YOR383C	FIT3	Iron Homeostasis
1.56	YCR002C	CDC10	structural protein of cytoskeleton; cell polarity
1.53	YML040W	YMD8	
1.53	YDR218C	SPR28	structural protein of cytoskeleton; cell wall
1.50	YLR121C	YPS3	
1.50	YMR046C	IOC4	
1.49	YGR043C		transaldolase
1.49	YIL011W	TIR3	
1.48	YKL163W	PIR3	cell wall structural protein
1.48	YLR327C		
1.47	YJR026W		
1.44	YGR032W	GSC2	1,3-beta-glucan synthase
1.44	YJR028W		
1.44	YMR051C	ERB1	
1.43	YML045W	RRN11	RNA polymerase I transcription factor
1.42	YBL005W-A	PDR3	transcription factor involved in transport
1.40	YMR317W		
1.36	YPR185W	APG13	
1.33	YIL101C	XBP1	stress response
1.28	YJL079C	PRY1	
1.27	YGR054W		
1.25	YBR012W-A		
1.24	YKR013W	PRY2	
1.23	YBR076W	ECM8	
1.22	YGR161C		
1.21	YIL177C		
1.20	YOR010C	TIR2	cell wall organization and biogenesis
1.19	YIL080W		
1.19	YPL230W	USV1	
1.16	YPL171C	OYE3	NADPH dehydrogenase
1.16	YNR066C		
1.15	YMR181C		
1.14	YML090W		
1.14	YGL117W		
1.13	YER138C		
1.12	YOR228C		
1.12	YLR391W	CCW14	
1.11	YER158C		

Supplemental Table S12. Genes Downregulated in *rsc4-11* at 30°C

log(2) of ratio of gene expression	ORF	Gene	Description or Biological Process
-1.75	YNL040W		
-1.39	YJR004C	SAG1	cell adhesion receptor
-1.25	YGL089C	MF(ALPHA)2	pheromone
-1.22	YCL027W	FUS1	conjugation
-1.12	YKR049C		
-1.09	YJL144W		

Supplemental Table S13. Genes Upregulated in *rsc4-11* at 30°C

log(2) of ratio of gene expression	ORF	Gene	Description or Biological Process
2.66	YOR383C	FIT3	Iron Homeostasis
2.11	YOR387C		
1.66	YOR382W	FIT2	Iron Homeostasis
1.65	YFL014W	HSP12	heat shock protein
1.60	YOL053C-A	DDR2	stress response
1.40	YDR534C	FIT1	Iron homeostasis
1.36	YLR142W	PUT1	Proline oxidase
1.31	YJL159W	HSP150	cell wall structural protein
1.28	YHR054C		
1.24	YMR096W	SNZ1	
1.15	YPL171C	OYE3	NADPH dehydrogenase
1.13	YDR218C	SPR28	structural protein of cytoskeleton; cell wall
