

Supplemental data for

Snf1-Independent, Glucose-Resistant Transcription of Adr1-Dependent Genes in a Mediator Mutant of
Saccharomyces cerevisiae

Running title: Snf1-independent transcription in a Mediator mutant

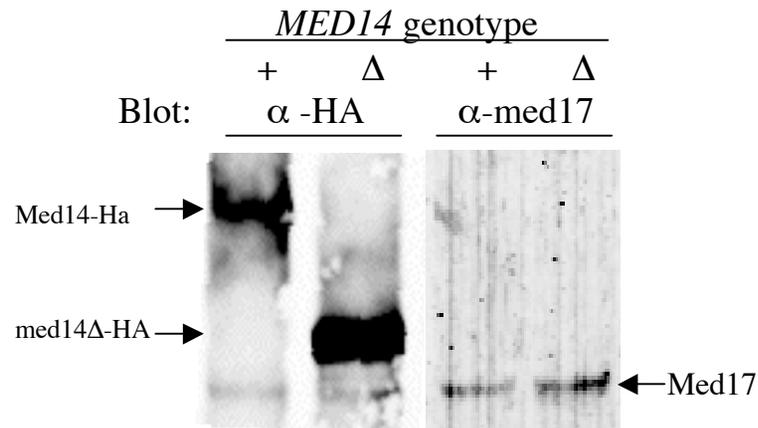
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Supplemental Figure 1S- Stability of Mediator in a *med14Δ* mutant.

Figure 1S part A. Immunoprecipitation for Med14-HA, a middle subunit



Samples IP'd for Med14 and blotted for either Med14 or Med17 in strains TYY544 (*MED14::HA*) and TYY548 (*med14Δ2*).

Figure 1S part A. Samples were immune-precipitated for Med14 in both wildtype and mutant strains, then blotted for Med14-HA (α -HA) and Med17 (α -Med17), a head subunit.

Med17 gives equivalent signals in both strains, suggesting that the *med14Δ* mutation does not affect interaction of the Mediator middle and head regions.

Figure 1S part B. Immunoprecipitation For Med3, a tail subunit.

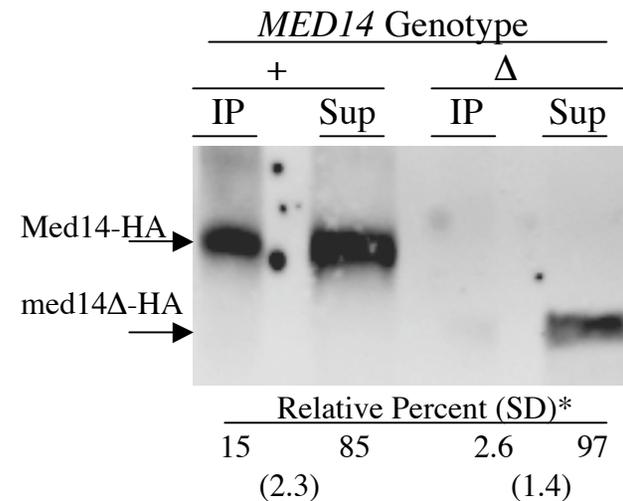


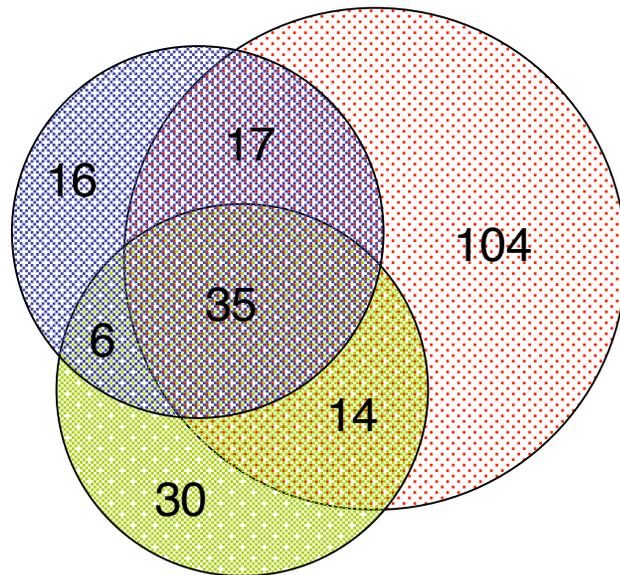
Figure 1S part B. Samples were immune-precipitated for Med3 (α -Med3) and blotted for Med14(α -HA) in strains TYY544 (*MED14::HA*) and TYY548 (*med14Δ::HA*).

IP, immunoprecipitate eluted from protein A sepharose; Sup, supernatant after protein A sepharose elution. *Values are expressed as the percent of total signal for IP plus Sup in each set normalized to the ug of protein loaded on the gel, and are averaged over several sets. (), Standard deviation.

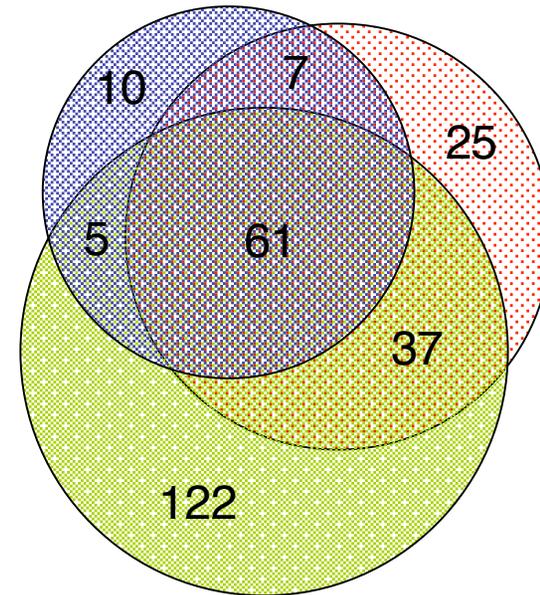
A significant amount of Med14-HA wildtype protein is brought down in the α -Med3 IP. Much less *med14Δ*-HA protein is in the α -Med3 IP, indicating that the middle-tail interaction is weaker in the mutant strain.

Supplemental Figure 2S.- Overlap of altered gene expression in *med14Δ* using three array platforms

Up-regulated



Down-regulated



Total # of genes

	<u>Up</u>	<u>Down</u>
■ – Affymetrix	74	83
■ – Spotted cDNA	85	225
■ – Nimblegen	170	130

Significance criteria

1. Pfp < 0.01
2. Fold-change ≥ 2

Supplemental Table 1S. Snf1-dependence
of gene expression in *MED14* wt and
med14ΔHA strains.

Supplemental Table 1. Snf1 dependence of gene expression in MED14 wt and med14ΔHA strains.								
mRNA relative Amount/ACT1/wt R ¹								
Repressed					Derepressed			
Gene	<i>wt-R</i>	<i>med14Δ</i>	<i>med14Δsnf1Δ</i>	<i>snf1Δ</i>	<i>wt</i>	<i>med14Δ</i>	<i>med14Δsnf1Δ</i>	<i>snf1Δ</i>
<i>ADH2</i>	1.0	128	98	0.64	1100	3100	500	3.8
<i>ADY2</i>	1.0	54	34	0.72	2400	7600	830	3.9
<i>ACS1</i>	1.0	10	9.4	0.95	346	961	185	12
<i>JEN1</i>	1.0	29	23	0.37	1309	2818	152	4.7
<i>ALD4</i>	1.0	22	12	1.10	470	990	140	41.0
<i>CYB2</i>	1.0	18	13	1.1	93	270	35	8
<i>FDH</i>	1.0	2.6	2.3	0.74	29	316	15	2.0
<i>YIL057c</i>	1.0	6.7	5.7	0.46	8313	5453	458	12
<i>CIT3</i>	1.0	4.9	3.9	0.71	242	1138	43	3.8
<i>SPG1</i>	1.0	1.4	11	5.1	682	1597	32	7.6
<i>ATO3</i>	1.0	1.2	1.2	0.57	17	10	3.3	1.3
<i>POX1</i>	1.0	24	28	1.2	90	440	85	11.0
<i>CTA1</i>	1.0	6.7	6.5	1.3	103	811	67	3.9
<i>POT1</i>	1.0	4.2	4.6	1.1	102	1069	60	4.2
<i>SPS19</i>	1.0	52	49	1.2	96	614	147	19
<i>FOX2</i>	1.0	21	22	1.4	154	1407	174	7.3
<i>MLS1</i>	1.0	2.9	3.0	1.2	727	420	5.3	7.9
<i>FBP1</i>	1.0	2.6	0.95	0.60	181	256	3.0	1.9
<i>ICL1</i>	1.0	1.9	3.8	1.1	189	66	8.7	4.5
<i>ADR1</i>	1.0	13	7.4	1.2	8.7	36	19	8.1
<i>CAT8</i>	1.0	1.4	1.7	1.1	45	74	9.1	4.9

¹ The relative amount of each mRNA was determined by quantitative RT-PCR as described in Methods.
described in Methods.

² Repressed growth indicates cultures grown in YP-5% glucose; derepressed growth
indicates growth in YP-0.05% for 6 hr.

Supplemental Table 2S-part A-72
genes significantly up-regulated in
med14Δ in at least two array platforms

TABLE 1S part A-72 genes significantly up-regulated in *med14Δ* in at least two array platforms.

ORF	GENE	Average of three array platforms		WT/med14Δ (log ₂ FC)		
		log ₂ (Mean_FC)	S.D./Variance	Nimblegen	Affymetrix	Spotted cDNA
YCR010C	ADY2	-3.24	0.048	-4.08	-3.29	-2.69
YMR011W	HXT2	-3.05	0.005	-3.10	-2.99	-3.06
YGR142W	BTN2	-2.97	0.016	-2.79	-3.15	-3.00
YKL217W	JEN1	-2.75	0.031	-3.14	-2.59	-2.59
YBR067C	TIP1	-2.45	0.012	-2.52	-2.38	NA
YDR171W	HSP42	-2.44	0.012	-2.35	-2.52	-2.47
YMR303C	ADH2	-2.30	0.040	-2.52	-2.11	-0.38
YOR348C	PUT4	-2.11	0.013	-2.11	-2.04	-2.20
YML058W-A	HUG1	-2.07	0.049	-2.29	-1.87	NA
YER103W	SSA4	-1.95	0.018	-1.95	-2.06	-1.86
YNL202W	SPS19	-1.94	0.052	-2.22	-1.66	-1.99
YLR327C	YLR327C	-1.91	0.060	-2.15	-1.69	NA
YDR343C	HXT6	-1.90	0.085	-2.27	-2.13	-1.45
YER054C	GIP2	-1.88	0.066	-2.27	-1.91	-1.56
YDR342C	HXT7	-1.87	0.084	-2.29	-1.99	-1.45
YGL205W	POX1	-1.85	0.023	-1.83	-1.74	-1.98
YOL155C	YOL155C	-1.74	0.005	-1.76	-1.72	-0.87
YLR216C	CPR6	-1.73	0.049	-1.65	-1.56	-2.02
YNL007C	SIS1	-1.73	0.043	-1.51	-1.87	-1.83
YDR256C	CTA1	-1.69	0.007	-1.67	-1.72	-0.61
YJL144W	YJL144W	-1.67	0.088	-1.99	-1.41	NA
YER159C	BUR6	-1.65	0.043	-1.80	-1.52	-0.90
YKL041W	VPS24	-1.63	0.035	-1.75	-1.53	-0.15
YER030W	YER030W	-1.61	0.004	-1.62	-1.59	-0.50
YPR158W	YPR158W	-1.58	0.013	-0.99	-1.62	-1.54
YKL082C	RRP14	-1.56	0.075	-1.78	-1.23	-1.73
YIL160C	POT1	-1.52	0.100	-1.85	-1.25	-0.95
YHR092C	HXT4	-1.51	0.055	-1.44	-1.79	-1.35
YGR280C	PXR1	-1.50	0.171	-2.10	-1.11	-1.08
YNL091W	NST1	-1.48	0.084	-1.27	-1.33	-1.93
YLR181C	VTA1	-1.47	0.007	-1.49	-1.45	NA
YPR006C	ICL2	-1.41	0.086	-1.83	-1.15	-1.33
YBL075C	SSA3	-1.41	0.034	-1.52	-1.45	-1.27
YKR009C	FOX2	-1.36	0.072	-1.70	-1.18	-1.25
YFL016C	MDJ1	-1.35	0.064	-1.35	-1.62	-1.14
YLR348C	DIC1	-1.34	0.120	-1.94	-1.24	-1.01
YDR258C	HSP78	-1.33	0.027	-0.79	-1.40	-1.26
YIL155C	GUT2	-1.33	0.046	-1.46	-1.15	-1.40
YLR314C	CDC3	-1.33	0.025	-1.25	-1.31	-1.43
YPL240C	HSP82	-1.32	0.064	-0.82	-1.17	-1.50
YMR191W	SPG5	-1.32	0.066	-1.26	-1.13	-1.61
YOR374W	ALD4	-1.31	0.053	-1.43	-1.10	-1.42
YMR186W	HSC82	-1.30	0.064	-1.14	-1.22	-1.59
YIL055C	YIL055C	-1.30	0.109	-0.58	-1.60	-1.05
YNL079C	TPM1	-1.27	0.072	-1.40	-1.46	-1.01
YLL026W	HSP104	-1.26	0.068	-1.09	-1.18	-1.56
YML074C	FPR3	-1.26	0.040	-1.36	-0.94	-1.16
YOR040W	GLO4	-1.25	0.054	-1.39	-1.13	-0.83
YNL308C	KRI1	-1.24	0.038	-1.34	-0.99	-1.15
YKL201C	MNN4	-1.24	0.038	-1.10	-1.33	-1.30
YBR072W	HSP26	-1.23	0.019	-1.16	-1.28	-1.26
YMR252C	YMR252C	-1.23	0.067	-1.40	-1.08	-0.35
YML131W	YML131W	-1.23	0.042	-1.34	-0.76	-1.13
YGL215W	CLG1	-1.23	0.006	-1.21	-1.05	-1.24
YOR027W	STI1	-1.22	0.077	-0.99	-1.05	-1.42
YDR044W	HEM13	-1.21	0.029	-1.14	-0.87	-1.28
YFR016C	YFR016C	-1.21	0.040	-1.08	-1.20	-1.35
YHR146W	CRP1	-1.20	0.088	-1.42	-1.04	-1.01
YNL009W	IDP3	-1.20	0.023	-1.27	-1.21	-1.12
YDL020C	RPN4	-1.19	0.051	-1.05	-1.16	-1.39
YNL012W	SPO1	-1.19	0.095	-1.02	-1.61	-1.02
YLR438W	CAR2	-1.18	0.063	-1.33	-0.84	-1.04
YBR069C	TAT1	-1.18	0.042	-1.05	-1.15	-1.33
YMR039C	SUB1	-1.17	0.008	-1.15	-1.19	0.15
YPR001W	CIT3	-1.17	0.074	-1.34	-0.92	-1.01
YDR200C	VPS64	-1.15	0.052	-1.04	-1.28	-0.45
YDR365C	ESF1	-1.14	0.023	-1.09	-1.06	-1.20
YOR285W	YOR285W	-1.14	0.013	-1.17	-1.11	-0.64
YPR002W	PDH1	-1.13	0.013	-1.10	-0.78	-1.16
YPL106C	SSE1	-1.13	0.027	-0.64	-1.07	-1.19
YNL059C	ARP5	-1.12	0.040	-1.21	-1.00	-1.04
YML071C	COG8	-1.10	0.014	-1.07	-0.79	-1.13

- Expression ratio > 0.5 or/and p-value > 0.01

Supplemental Table 2S-part B-110 genes significantly down-regulated in med14Δ in at least two array platforms

TABLE 1S part B-110 genes significantly down-regulated in med14Δ in at least two array platforms.

Average of three array platforms				WT/med14Δ (log ₂ FC)			Average of three array platforms				WT/med14Δ (log ₂ FC)		
ORF	GENE	log ₂ (Mean_FC)	S.D./Variance	Nimblegen	Affymetrix	Spotted cDNA	ORF	GENE	log ₂ (Mean_FC)	S.D./Variance	Nimblegen	Affymetrix	Spotted cDNA
YML123C	PHO84	4.16	12.69	3.16	15.70	4.75	YIL015W	BAR1	1.67	0.40	1.53	2.97	1.79
YCL064C	CHA1	3.76	7.34	3.06	8.57	4.23	YMR058W	FET3	1.66	0.38	1.53	3.34	1.77
YNL145W	MFA2	3.74	13.91	1.83	4.54	NA	YLR058C	SHM2	1.60	0.18	1.54	2.35	1.66
YHR136C	SPL2	3.24	5.43	2.48	12.78	3.73	YOR107W	RGS2	1.58	0.40	1.44	3.38	1.71
YGR234W	YHB1	3.16	2.37	2.86	5.41	3.41	YNR019W	ARE2	1.57	0.48	1.39	4.60	1.73
YHR143W	DSE2	3.01	3.83	2.41	5.72	3.43	YGR177C	ATF2	1.56	0.14	1.61	3.41	1.51
YPL187W	MF(ALPHA)1	3.00	4.49	2.27	5.17	3.48	YGR044C	RME1	1.56	0.21	1.48	2.95	1.63
YEL071W	DLD3	2.95	4.95	1.81	3.72	2.69	YGR254W	ENO1	1.52	1.09	1.06	2.41	1.86
YDR461W	MFA1	2.72	0.25	1.44	2.69	2.76	YGR260W	TNA1	1.49	0.07	1.46	2.28	1.52
YJR048W	CYC1	2.62	1.04	1.52	2.78	2.43	YIL051C	MMF1	1.48	0.92	1.10	1.96	1.78
YLR286C	CTS1	2.54	1.30	1.46	2.75	2.29	YJL012C	VTC4	1.46	0.48	1.27	2.30	1.62
YDL241W	YDL241W	2.49	2.94	1.63	3.15	2.31	YOR385W	YOR385W	1.46	0.94	1.06	2.08	1.77
YCR018C	SRD1	2.45	4.73	1.09	3.14	NA	YNL134C	YNL134C	1.45	0.01	1.45	2.69	1.46
YLR142W	PUT1	2.45	1.12	2.22	6.38	2.64	YMR272C	SCS7	1.44	0.02	1.43	2.35	1.45
YNL111C	CYB5	2.42	0.43	1.44	2.50	2.33	YOL151W	GRE2	1.43	0.10	1.47	4.10	1.39
YBR296C	PHO89	2.41	1.46	2.10	5.68	2.66	YLR180W	SAM1	1.43	0.27	1.32	2.48	1.53
YLL053C	YLL053C	2.37	3.96	1.09	3.27	1.90	YDR033W	MRH1	1.43	0.77	1.10	2.06	1.69
YGL028C	SCW11	2.36	1.41	2.04	4.07	2.61	YPL019C	VTC3	1.42	0.41	1.25	2.55	1.57
YDR380W	ARO10	2.35	1.13	2.10	4.99	2.56	YNL141W	AAH1	1.41	0.12	1.46	2.71	1.36
YBR158W	AMN1	2.35	2.28	1.68	2.93	2.16	YFL014W	HSP12	1.40	0.21	1.31	2.69	1.48
YFL026W	STE2	2.32	2.89	1.39	3.04	2.04	YOR044W	YOR044W	1.39	0.10	1.35	2.18	1.42
YNR067C	DSE4	2.26	0.39	2.17	5.38	2.34	YNL160W	YGP1	1.38	0.44	1.19	2.59	1.54
YJR104C	SOD1	2.20	1.07	0.86	2.42	1.94	YGR088W	CTT1	1.37	0.11	1.33	2.14	1.41
YMR015C	ERG5	2.17	0.77	1.99	3.09	2.34	YJL213W	YJL213W	1.36	0.59	1.10	2.59	1.58
YMR195W	ICY1	2.17	1.85	1.49	2.69	2.08	YKL216W	URA1	1.35	0.29	1.23	2.10	1.46
YMR316W	DIA1	2.16	2.04	0.88	2.56	1.60	YGL055W	OLE1	1.35	0.47	1.15	1.65	1.53
YGL032C	AGA2	2.16	2.11	0.84	2.58	1.57	YPL274W	SAM3	1.33	0.24	1.23	2.24	1.43
YNL327W	EGT2	2.13	1.07	1.86	3.50	2.36	YMR120C	ADE17	1.31	0.11	1.36	1.97	1.27
YPR194C	OPT2	2.12	2.29	1.44	2.57	0.67	YBR092C	PHO3	1.31	0.01	1.30	1.93	1.31
YNR060W	FRE4	2.10	3.00	1.12	2.68	NA	YNL066W	SUN4	1.30	0.17	1.23	2.30	1.37
YJL078C	PRY3	2.08	1.59	2.42	5.48	1.64	YGR108W	CLB1	1.30	0.45	1.10	2.76	1.47
YDR019C	GCV1	2.04	0.55	1.89	3.69	2.16	YHR140W	YHR140W	1.25	0.39	1.08	2.68	1.41
YPR065W	ROX1	2.02	0.72	1.83	4.20	2.20	YOR273C	TPO4	1.24	0.49	1.02	2.00	1.44
YER091C	MET6	2.02	0.37	2.11	3.05	1.92	YHR215W	PHO12	1.24	0.03	1.23	NA	1.25
YLR411W	CTR3	2.00	2.63	1.11	2.55	0.47	YCR061W	YCR061W	1.23	0.29	1.36	3.35	1.10
YML075C	HMG1	2.00	1.54	1.39	2.50	1.87	YAR071W	PHO11	1.23	0.20	1.14	2.16	1.32
YOL014W	YOL014W	1.94	2.05	1.26	2.40	NA	YHR022C	YHR022C	1.22	0.45	1.41	2.83	1.01
YEL039C	CYC7	1.94	0.91	-0.03	2.16	1.67	YKR061W	KTR2	1.21	0.25	1.10	2.18	1.31
YHR139C	SPS100	1.92	2.21	1.15	2.42	0.83	YBR157C	ICS2	1.21	0.10	1.17	2.56	1.25
YJL048C	UBX6	1.92	1.00	1.62	3.16	2.17	YOL158C	ENB1	1.19	0.11	1.14	2.06	1.24
YOR222W	ODC2	1.92	2.05	0.97	2.39	1.21	YDL179W	PCL9	1.18	0.01	1.19	2.08	1.18
YCR005C	CIT2	1.91	1.95	1.26	2.02	2.36	YBR177C	EHT1	1.18	0.02	1.17	2.15	1.19
YGR248W	SOL4	1.91	1.58	1.26	2.46	1.77	YBR183W	YPC1	1.17	0.17	1.10	2.17	1.25
YDR247W	VHS1	1.90	0.06	1.92	3.15	1.89	YLL012W	YEH1	1.16	0.34	1.00	2.14	1.31
YOR264W	DSE3	1.84	1.82	1.21	2.50	1.47	YDL182W	LYS20	1.15	0.10	1.10	2.54	1.19
YPL061W	ALD6	1.84	1.09	1.49	2.29	2.12	YGL001C	ERG26	1.14	0.11	1.09	1.87	1.19
YLR153C	ACS2	1.83	1.10	1.31	2.22	1.83	YER037W	PHM8	1.14	0.23	1.24	3.09	1.03
YER124C	DSE1	1.81	0.44	1.67	3.35	1.93	YBR093C	PHO5	1.13	0.01	1.14	1.85	1.13
YDR502C	SAM2	1.78	0.31	1.87	3.85	1.69	YHL028W	WSC4	1.12	0.11	1.06	2.74	1.17
YJL088W	ARG3	1.77	0.42	1.89	6.22	1.64	YOR390W	YOR390W	1.11	0.12	1.16	2.36	1.05
YBL043W	ECM13	1.76	1.63	1.07	2.38	1.52	YDL022W	GPD1	1.11	0.02	1.10	2.04	1.11
YBL002W	HTB2	1.73	1.02	1.38	2.14	2.01	YEL024W	RIP1	1.09	0.02	1.10	1.89	1.08
YLL052C	AQY2	1.71	0.64	1.49	3.54	1.90	YMR083W	ADH3	1.08	0.03	1.09	1.64	1.06
YGR060W	ERG25	1.69	1.45	1.14	2.05	2.09	YPL279C	YPL279C	1.07	0.02	1.06	NA	1.08
YGR175C	ERG1	1.67	0.50	1.50	2.02	1.82	YJL101C	GSH1	1.07	0.06	1.10	1.81	1.04

-Data with expression ratio < 2 or/and p-value > 0.01
-Outliers excluded from final ratio values

Supplemental Table 3S. Expression data for miscellaneous ORF's in the *med14Δ* mutant

Up-regulated

PROBE	ORF	GENE	RP	log2_FC	pfp
3744_i_at	YLRWSIGMA3	NA	72.548	-1.755356	4.00E-04
8725_g_at	NA	Hypo_ORF	55.0709	-1.677149	0
4025_i_at	NA	SAGE_ORF	91.5439	-1.599899	8.00E-04
3764_s_at	RDN37-1	NA	57.7999	-1.514985	0
4003_s_at	Q0045	COX1	92.1313	-1.484388	8.00E-04
4001_at	Q0045	COX1	82.6045	-1.471929	3.00E-04
2158_at	NA	NA	84.1757	-1.442222	3.00E-04
3766_s_at	RDN25-1	RDN25-1	89.7035	-1.436354	8.00E-04
4004_at	Q0070	AI5_ALPHA	161.456	-1.372954	0.0037
3137_s_at	YILWTY3-1	TyB Gag-Pol	144.9867	-1.323372	0.002
2894_at	NA	NA	238.8141	-1.319406	0.0121
4005_at	Q0045	COX1	137.3843	-1.298673	0.0021
3954_at	2MIC_REP2	NA	143.4511	-1.296545	0.002
7022_at	NA	SAGE_ORF	236.3444	-1.277884	0.0117
8089_at	NA	SAGE_ORF	149.5607	-1.170069	0.0026
3976_at	Q0130	OLI1	276.4081	-1.081614	0.0184
4586_at	NA	SAGE_ORF	310.7325	-1.056191	0.0248
3996_s_at	Q0045	COX1	238.1517	-1.051399	0.0122
5491_at	NA	SAGE_ORF	278.7255	-1.029146	0.0191

#Probe Sets 19
Unique Seq. 15

Down-regulated

PROBE	ORF	GENE	RP	log2_FC	pfp
9828_at	NA	SAGE_ORF	9326.221	2.935856	1.0004
9830_at	NA	SAGE_ORF	9319.77	2.626603	1.0008
10868_at	NA	SAGE_ORF	9316.551	2.580773	1.0012
9829_at	NA	SAGE_ORF	9320	2.54149	1.0006
4600_at	NA	SAGE_ORF	9296.152	2.208954	1.0021
6963_at	NA	SAGE_ORF	9296.431	2.045548	1.002
6964_s_at	NA	SAGE_ORF	9290.987	1.96857	1.0023
4009_at	NA	SAGE_ORF	9283.411	1.909735	1.0028
4020_at	NA	SAGE_ORF	9258.574	1.78831	1.0038
5476_at	NA	SAGE_ORF	9235.937	1.626065	1.005
4019_at	NA	SAGE_ORF	9224.02	1.547104	1.0056
6965_i_at	NA	SAGE_ORF	9220.15	1.526419	1.0058
8759_at	NA	SAGE_ORF	9215.585	1.514299	1.0061
9236_at	NA	SAGE_ORF	9176.625	1.489286	1.0081
5841_at	NA	SAGE_ORF	9225.507	1.476278	1.0053
8153_at	NA	SAGE_ORF	9217.136	1.468635	1.006
8714_at	SNR66	NA	9213.8	1.446256	1.0063
11244_s_at	NA	SAGE_ORF	9135.934	1.40806	1.0096
3563_s_at	TT(UGU)P	YHR180W-A	8852.214	1.291898	1.0224
4021_at	NA	SAGE_ORF	9137.896	1.276794	1.0095
9847_at	NA	SAGE_ORF	8718.34	1.244704	1.0282
10434_at	NA	SAGE_ORF	9151.197	1.227248	1.0088
3243_at	TL(GAG)G	NA	6632.586	1.212881	1.1305
5804_at	SNR63	NA	8923.291	1.203076	1.0191
7560_at	NA	SAGE_ORF	8700.243	1.201697	1.0288
7490_at	NA	SAGE_ORF	9010.025	1.184725	1.0152
5886_at	NA	SAGE_ORF	9100.897	1.176578	1.0107
5933_at	NA	SAGE_ORF	9086.25	1.169861	1.0114
10782_at	SNR128	NA	8895.886	1.15095	1.0204
5464_i_at	NA	SAGE_ORF	8891.272	1.15017	1.0206
6966_r_at	NA	SAGE_ORF	9087.674	1.145873	1.0113
8044_at	NA	SAGE_ORF	9083.517	1.143393	1.012
7499_at	NA	SAGE_ORF	9070.126	1.136323	1.0128
3545_i_at	YBLWDELTA1	NA	8771.294	1.09842	1.0263
8040_at	NA	SAGE_ORF	8965.16	1.089091	1.0173
7514_at	NA	SAGE_ORF	8975.47	1.061085	1.0168
10396_at	NC_001143	SAGE_ORF	8639.448	1.060601	1.0321
8799_at	NA	SAGE_ORF	9009.327	1.059701	1.0153
6962_at	NA	SAGE_ORF	8753.183	1.037242	1.027
4617_at	NA	SAGE_ORF	8799.548	1.03492	1.0246
5417_at	SNR4	NA	9024.847	1.034145	1.0142
9231_s_at	NA	SAGE_ORF	8967.099	1.031254	1.0172
5413_at	RPR1	NA	7965.556	1.023113	1.0662
4658_at	NA	SAGE_ORF	8952.008	1.006765	1.0179
7052_at	NA	SAGE_ORF	8973.256	1.000433	1.0169

#Probe Sets 45
Unique Seq. 45

Source: Affymetrix YGS98 array data.