Supplemental Table SI

Primer list.

Primer	Sequence
CTA1fw	TGGTCATACCTATAAATGGTCC
CTA1rv	AATCCTGCTGGCAGTAATCTGG
RDN1fw	CCATGGTTTCAACGGGTAACGG
RDN1rv	GCCTTCCTTGGATGTGGTAGCC
ADH2fw	AGTCGCGCCAATCTTGTGTGCT
ADH2rv	ACTCTGTAACCCATCGCCTTAG

Supplemental Table SII

Comparison of the fold changes of the expression of genes that are upregulated in the post-diauxic phase in WT, Δ*isc1* and petite.

Functinoal Category	ORF	Gene name	Function	Fold change (24 h/4 h)			Change ratio	
				WT	Δ*isc1*	petite	Δ*isc1* / WT	pet/ grande
non-fermentable carbon source utilization	YKL217W	*JEN1*	carboxylic acid transporter protein homolog	1921.41	37.95	42.69	0.02	0.02
non-fermentable carbon source utilization	YOR388C	*FDH1*	protein with similarity to formate dehydrogenases	797.55	15.03	176.36	0.02	0.22
non-fermentable carbon source utilization	YPL276W	*FDH2*	putative formate dehydrogenase/putative pseudogene	685.49	16.41	83.93	0.02	0.12
non-fermentable carbon source utilization	YNL117W	*MLS1*	carbon-catabolite sensitive malate synthase	605.87	81.43	68.75	0.13	0.11
non-fermentable carbon source utilization	YGL205W	*POX1*	fatty-acyl coenzyme A oxidase	566.08	49.62	8.04	0.09	0.01
non-fermentable carbon source utilization	YLR164W		strong similarity to Sdh4p	191.13	20.28	3.99	0.11	0.02
non-fermentable carbon source utilization	YMR303C	*ADH2*	alcohol dehydrogenase II	155.99	17.00	0.54	0.11	0.00
non-fermentable carbon source utilization	YCR010C	*ADY2*	acetate transporter required for normal sporulation	144.57	29.20	7.17	0.20	0.05
non-fermentable carbon source utilization	YDL085W	*NDE2*	mitochondrial external NADH dehydrogenase	124.50	30.37	30.74	0.24	0.25
non-fermentable carbon source utilization	YML042W	*CAT2*	carnitine O-acetyltransferase, peroxisomal and mitochondrial	120.37	21.05	65.55	0.17	0.54
non-fermentable carbon source utilization	YDR256C	*CTA1*	catalase A	114.77	15.30	29.10	0.13	0.25
non-fermentable carbon source utilization	YPR002W	*PDH1*	protein possibly involved in propionate utilization	98.11	18.43	24.74	0.19	0.25
non-fermentable carbon source utilization	YPR001W	*CIT3*	mitochondrial isoform of citrate synthase	88.94	14.26	87.38	0.16	0.98
non-fermentable carbon source utilization	YJL153C	*INO1*	L-myo-inositol-1-phosphate synthase	78.47	13.00	3.39	0.17	0.04
non-fermentable carbon source utilization	YNR002C	*ATO2*	putative transmembrane protein, involved in the export of ammonia	78.42	16.89	73.92	0.22	0.94
non-fermentable carbon source utilization	YNL202W	*SPS19*	peroxisomal 2,4-dienoyl-CoA reductase	75.51	16.47	11.01	0.22	0.15
non-fermentable carbon source utilization	YML054C	*CYB2*	cytochrome b2	52.95	13.31	9.48	0.25	0.18
non-fermentable carbon source utilization	YBR019C	*GAL10*	UDP-glucose 4-epimerase	28.85	2.05	3.21	0.07	0.11
non-fermentable carbon source utilization	YPR006C	*ICL2*	isocitrate lyase 2-methylisocitrate lyase of the mitochondrial matrix	24.85	4.06	0.91	0.16	0.04
non-fermentable carbon source utilization	YPL113C		glyoxylate reductase	20.94	5.30	1.07	0.25	0.05
non-fermentable carbon source utilization	YKL221W		protein with similarity to mammalian monocarboxylate permeases	19.22	2.06	4.05	0.11	0.21
nucleotide/nucleoside processing	YNL014W	*HEF3*	translation elongation factor eEF3 homolog	54.87	13.74	81.98	0.25	1.49
nucleotide/nucleoside processing	YPR193C	*HPA1*	histone and other protein acetyltransferase	16.17	2.06	2.46	0.13	0.15
nucleotide/nucleoside processing	YOR192C	*THI72*	transporter of thiamine or related compound	3.74	0.76	1.52	0.20	0.41
protein catabolism	YGL259W	*YPS1*	GPI-anchored aspartic protease	29.50	2.52	7.78	0.09	0.26
others	YBR045C	*GIP1*	Glc7-interacting protein.	69.03	5.44	10.17	0.08	0.15
others	YDL214C	*PRR2*	protein kinase with a possible role in MAP kinase signaling in the pheromone response pathway	67.19	15.36	50.31	0.23	0.75

others	YLL016W	*SDC25*	Ras guanine nucleotide exchange factor (GEF)	18.91	3.93	47.94	0.21	2.54
others	YGR230W	*BNS1*	molecular function unknown	8.41	2.09	2.03	0.25	0.24
others	YOL091W	*SPO21*	component of the meiotic outer plaque of the spindle pole body	5.44	0.67	0.76	0.12	0.14
others	YKR102W	*FLO10*	lectin-like protein with similarity to Flo1p	3.87	0.96	7.12	0.25	1.84
unknown	YKL107W		molecular function unknown	628.69	55.66	58.85	0.09	0.09
unknown	YIL057C	*RGI2*	molecular function unknown	331.19	44.55	248.70	0.13	0.75
unknown	YBR285W		molecular function unknown	323.83	23.83	1.76	0.07	0.01
unknown	YLR311C		molecular function unknown	266.93	16.72	11.66	0.06	0.04
unknown	YML089C		molecular function unknown	66.59	13.13	1.25	0.20	0.02
unknown	YOL131W		molecular function unknown	52.61	6.76	0.90	0.13	0.02
unknown	YNL335W	*DDI3*	molecular function unknown	44.07	4.95	5.48	0.11	0.12
unknown	YLR053C		molecular function unknown	41.58	9.73	124.07	0.23	2.98
unknown	YJR128W		molecular function unknown	38.56	6.57	19.78	0.17	0.51
unknown	YHR095W		molecular function unknown	34.37	2.31	7.44	0.07	0.22
unknown	YBR046C	*ZTA1*	Zeta-crystallin homolog	27.44	5.98	2.07	0.22	0.08
unknown	YER084W		molecular function unknown	26.28	5.05	5.90	0.19	0.22
unknown	YBR047W	*FMP23*	molecular function unknown	25.87	4.08	1.34	0.16	0.05
unknown	YJR061W		molecular function unknown	24.36	1.75	1.21	0.07	0.05
unknown	YKL187C		molecular function unknown	23.52	4.69	46.05	0.20	1.96
unknown	YPL277C		molecular function unknown	13.01	1.09	2.47	0.08	0.19
unknown	YPL277C		molecular function unknown	9.37	4.20	3.02	0.45	0.32
unknown	YEL008W		molecular function unknown	8.92	1.82	2.34	0.20	0.26
unknown	YPR083W	*MDM36*	molecular function unknown	8.78	1.82	1.35	0.21	0.15
unknown	YGR045C		molecular function unknown	8.17	2.04	1.27	0.25	0.16
unknown	YPL264C		molecular function unknown	8.02	0.87	1.76	0.11	0.22
unknown	YLR280C		molecular function unknown	7.92	1.26	0.68	0.16	0.09
unknown	YML122C		molecular function unknown	7.18	1.45	0.68	0.20	0.09
unknown	YKL037W	*AIM26*	molecular function unknown	6.73	0.82	1.14	0.12	0.17
unknown	YFL063W		molecular function unknown	6.72	1.48	2.95	0.22	0.44
unknown	YOR389W		molecular function unknown	6.10	1.68	3.02	0.28	0.50
unknown	YJL160C		molecular function unknown	5.36	1.25	0.30	0.23	0.06
unknown	YAR053W		molecular function unknown	4.80	1.13	1.14	0.24	0.24
unknown	YIR007W		molecular function unknown	4.58	2.03	1.86	0.44	0.41

unknown	YDR401W	molecular function unknown	3.35	0.76	2.18	0.23	0.65
unknown	YNL034W	molecular function unknown	2.84	0.41	1.89	0.15	0.67
unknown	YKR040C	molecular function unknown	2.20	0.41	0.35	0.19	0.16

Supplemental Table SIII

Comparison of the fold changes of the expression of genes that are similarly upregulated in the post-diauxic phase in WT and Δ*isc1* .

Functional Category	ORF	Gene name	Function	Fold change (24 h/ 4 h Exp. 1)		Δ*isc1* / WT	Average change ratio
				WT	Δ*isc1*	Exp. 1	(Exp. 1 and 2)
nucleotide/nucleoside processing	YJR156C	*THI11*	protein involved in synthesis of the thiamine precursor hydroxymethylpyrimidine	8.92	8.30	0.93	0.61
nucleotide/nucleoside processing	YJL116C	*NCA3*	protein that functions with Nca2p to regulate mitochondrial expression of subunits 6 and 8 of the F_o-F_1 ATP synthase	8.86	8.45	0.95	0.57
nucleotide/nucleoside processing	YMR095C	*SNO1*	protein of unconfirmed function, involved in pyridoxine metabolism	6.07	5.51	0.91	0.67
nucleotide/nucleoside processing	YOR023C	*AHC1*	subunit of the Ada histone acetyltransferase complex	3.54	3.28	0.93	0.78
nucleotide/nucleoside processing	YPL133C	*RDS2*	zinc cluster protein involved in conferring resistance to ketoconazole	3.02	2.95	0.98	0.92
nucleotide/nucleoside processing	YPL164C	*MLH3*	protein involved in DNA mismatch repair	2.97	2.77	0.93	0.88
nucleotide/nucleoside processing	YLR403W	*SFP1*	transcription factor that controls expression of many ribosome biogenesis genes	2.87	3.13	1.09	0.99
nucleotide/nucleoside processing	YDL200C	*MGT1*	DNA repair methyltransferase	2.79	2.86	1.02	0.77
nucleotide/nucleoside processing	YBR150C	*TBS1*	probable Zn-finger protein	2.79	2.80	1.01	1.05
nucleotide/nucleoside processing	YMR201C	*RAD14*	protein that recognizes and binds damaged DNA during nucleotide excision repair	2.78	2.78	1.00	0.92
nucleotide/nucleoside processing	YDR169C	*STB3*	protein that binds Sin3p in a two-hybrid assay	2.77	2.56	0.92	0.92
nucleotide/nucleoside processing	YHL027W	*RIM101*	transcriptional repressor involved in the response to pH	2.74	2.91	1.06	0.93
nucleotide/nucleoside processing	YOR244W	*ESA1*	histone acetyltransferase catalytic subunit of the native multisubunit complex	2.69	2.46	0.91	0.87
nucleotide/nucleoside processing	YKL142W	*MRP8*	putative mitochondrial ribosomal protein	2.68	2.75	1.03	1.05
nucleotide/nucleoside processing	YHL020C	*OPI1*	transcriptional regulator of a variety of genes	2.66	2.75	1.04	1.04
nucleotide/nucleoside processing	YGL037C	*PNC1*	nicotinamidase that converts nicotinamide to nicotinic acid	2.57	2.36	0.92	0.75
nucleotide/nucleoside processing	YJR035W	*RAD26*	protein involved in transcription-coupled repair nucleotide excision repair	2.55	2.41	0.94	0.83
nucleotide/nucleoside processing	YPR023C	*EAF3*	Esa1p-associated factor	2.49	2.40	0.96	0.95
nucleotide/nucleoside processing	YGL181W	*GTS1*	protein containing a zinc-finger in the N-terminus and a long Gln-rich region in the C-terminus	2.40	2.28	0.95	0.94
nucleotide/nucleoside processing	YNL025C	*SSN8*	cyclin-like component of the RNA polymerase II holoenzyme	2.36	2.27	0.96	0.83
nucleotide/nucleoside processing	YDR480W	*DIG1*	regulatory protein of unknown function, pheromone-inducible	2.34	2.16	0.92	0.93
nucleotide/nucleoside processing	YBR119W	*MUD1*	U1 snRNP A protein, homolog of human U1-A	2.30	2.11	0.91	1.02
nucleotide/nucleoside processing	YGL136C	*MRM2*	mitochondrial 21S rRNA methyltransferase	2.28	2.17	0.95	0.67
nucleotide/nucleoside processing	YPL138C	*SPP1*	subunit of COMPASS, a complex which methylates histone H3 on lysine 4	2.25	2.25	1.00	0.95
nucleotide/nucleoside processing	YOR148C	*SPP2*	essential protein that promotes the first step of splicing	2.25	2.08	0.92	0.91
nucleotide/nucleoside processing	YER147C	*SCC4*	subunit of cohesin loading factor (Scc2p-Scc4p)	2.21	2.21	1.00	0.80

nucleotide/nucleoside processing	YGL035C	*MIG1*	transcription factor involved in glucose repression	2.16	2.19	1.01	0.80
nucleotide/nucleoside processing	YAL001C	*TFC3*	largest of six subunits of the RNA polymerase III transcription initiation factor complex	2.16	1.97	0.91	0.88
nucleotide/nucleoside processing	YNL218W	*MGS1*	protein with DNA-dependent ATPase and ssDNA annealing activities	2.15	1.97	0.92	1.00
nucleotide/nucleoside processing	YFR034C	*PHO4*	basic helix-loop-helix transcription factor	2.14	1.96	0.92	0.87
nucleotide/nucleoside processing	YJR052W	*RAD7*	protein that recognizes and binds damaged DNA in an ATP-dependent manner	2.13	1.94	0.91	0.77
nucleotide/nucleoside processing	YLR323C	*CWC24*	component of a complex containing Cef1p	2.11	2.06	0.98	1.10
nucleotide/nucleoside processing	YML007W	*YAP1*	basic leucine zipper (bZIP) transcription factor required for oxidative stress tolerance	2.09	2.23	1.07	0.84
nucleotide/nucleoside processing	YGL127C	*SOH1*	subunit of the RNA polymerase II mediator complex	2.08	1.90	0.91	0.89
nucleotide/nucleoside processing	YNL230C	*ELA1*	Elongin A, F-box protein that forms a heterodimer with Elc1p	2.07	1.89	0.91	0.70
nucleotide/nucleoside processing	YJR060W	*CBF1*	helix-loop-helix protein that binds the motif CACRTG	2.04	1.98	0.97	1.06
nucleotide/nucleoside processing	YGR258C	*RAD2*	single-stranded DNA endonuclease	2.03	2.03	1.00	0.75
protein catabolism	YOR031W	*CRS5*	copper-binding metallothionein	8.89	8.30	0.93	0.64
protein catabolism	YJL048C	*UBX6*	UBX (ubiquitin regulatory X) domain-containing protein that interacts with Cdc48p	3.61	3.66	1.01	0.93
protein catabolism	YCL038C	*ATG22*	protein required for the breakdown of autophagic vesicles in the vacuole	3.25	3.03	0.93	0.80
protein catabolism	YDL216C	*RRI1*	catalytic subunit of the COP9 signalosome complex	3.21	3.13	0.97	0.92
protein catabolism	YDR306C		ubiquitin-ligase complex	3.07	2.99	0.97	0.81
protein catabolism	YBR165W	*UBS1*	ubiquitin-conjugating enzyme suppressor	2.92	2.91	1.00	0.83
protein catabolism	YJR036C	*HUL4*	protein with similarity to hect domain E3 ubiquitin-protein ligases	2.63	2.69	1.02	1.14
protein catabolism	YDL013W	*HEX3*	ring finger protein involved in the DNA damage response with possible recombination role	2.49	2.34	0.94	0.97
protein catabolism	YKL157W	*APE2*	zinc-dependent metallopeptidase yscII	2.13	2.32	1.09	0.96
protein catabolism	YLL042C	*ATG10*	E2-like conjugating enzyme that mediates formation of the Atg12p-Atg5p conjugate	2.01	2.05	1.02	0.98
non-fermentable carbon source utilization	YMR256C	COX7	subunit VII of cytochrome c oxidase	3.54	3.59	1.01	1.00
non-fermentable carbon source utilization	YGR183C	QCR9	subunit 9 of the ubiquinol cytochrome-c reductase complex	2.62	2.77	1.05	0.94
non-fermentable carbon source utilization	YHR051W	COX6	subunit VI of cytochrome c oxidase	2.36	2.44	1.04	1.10
non-fermentable carbon source utilization	YPR191W	QCR2	subunit 2 of the ubiquinol cytochrome-c reductase complex	2.22	2.09	0.94	0.99
non-fermentable carbon source utilization	YGL187C	COX4	subunit IV of cytochrome c oxidase	2.15	2.32	1.08	1.10
non-fermentable carbon source utilization	YLR295C	ATP14	subunit h of the F_0 sector of mitochondrial F_1F_0 ATP synthase	2.14	2.26	1.06	1.01
amino acid metabolism	YMR271C	*URA10*	one of two orotate phosphoribosyltransferase isozymes	14.4	15.0	1.04	0.70
amino acid metabolism	YLR142W	*PUT1*	proline oxidase	10.7	11.5	1.08	0.74
amino acid metabolism	YGL125W	*MET13*	isozyme of methylenetetrahydrofolate reductase	4.36	4.01	0.92	0.84
amino acid metabolism	YDR173C	*ARG82*	protein involved in regulation of arginine-responsive and Mcm1p-dependent genes	2.59	2.62	1.01	1.14
amino acid metabolism	YGR019W	*UGA1*	γ-aminobutyrate transaminase (4-aminobutyrate aminotransferase)	2.53	2.58	1.02	0.83
nutrient uptake	YHR096C	*HXT5*	hexose transporter with moderate affinity for glucose	39.5	37.7	0.96	0.50

nutrient uptake	YDR463W	*STP1*	transcription factor that activates transcription of amino acid permease genes	2.66	2.44	0.92	1.00
nutrient uptake	YDR342C	*HXT7*	high-affinity glucose transporter of the major facilitator superfamily	2.44	2.64	1.08	0.98
nutrient uptake	YGR065C	*VHT1*	high-affinity plasma membrane H$^+$-biotin (vitamin H) symporter	2.15	2.05	0.96	0.74
nutrient uptake	YDR343C	*HXT6*	high-affinity glucose transporter of the major facilitator superfamily	2.10	2.08	0.99	1.02
others	YJR094C	*IME1*	master regulator of meiosis that is active only during meiotic events	9.92	9.77	0.98	0.63
others	YDR277C	*MTH1*	negative regulator of the glucose-sensing signal transduction pathway	7.80	7.95	1.02	0.86
others	YMR169C	*ALD3*	cytoplasmic aldehyde dehydrogenase, involved in β-alanine synthesis	7.43	7.71	1.04	0.67
others	YPR005C	*HAL1*	cytoplasmic protein involved in halotolerance	6.35	5.87	0.92	0.70
others	YPL156C	*PRM4*	pheromone-regulated protein	6.03	5.71	0.95	0.83
others	YOR177C	*MPC54*	component of the meiotic outer plaque	5.09	5.39	1.06	0.72
others	YIR029W	*DAL2*	allantoicase, converts allantoate to urea and ureidoglycolate	4.74	5.06	1.07	0.89
others	YMR068W	*AVO2*	component of a complex containing the Tor2p kinase and other proteins	4.25	4.12	0.97	0.77
others	YPR154W	*PIN3*	protein that induces appearance of *[PIN$^+$]* prion when overproduced	4.05	3.83	0.95	0.84
others	YBR001C	*NTH2*	putative neutral trehalase	3.88	3.74	0.96	0.83
others	YGR023W	*MTL1*	protein with both structural and functional similarity to Mid2p	3.00	2.75	0.92	0.92
others	YDL124W		NADPH-dependent α-keto amide reductase	2.98	2.86	0.96	0.66
others	YDR001C	*NTH1*	neutral trehalase	2.84	2.77	0.97	0.77
others	YLR362W	*STE11*	signal transducing MEK kinase	2.83	3.01	1.06	0.75
others	YJL083W	*TAX4*	protein involved in regulation of phosphatidylinositol 4,5-bisphosphate concentrations	2.71	2.92	1.08	0.84
others	YML004C	*GLO1*	monomeric glyoxalase I	2.62	2.51	0.96	0.80
others	YMR008C	*PLB1*	phospholipase B (lysophospholipase)	2.59	2.39	0.92	0.77
others	YFL053W	*DAK2*	dihydroxyacetone kinase	2.54	2.55	1.00	0.76
others	YNL173C	*MDG1*	plasma membrane protein involved in G-protein mediated pheromone signaling pathway	2.47	2.28	0.93	1.18
others	YBL045C	COR1	core subunit of the ubiquinol-cytochrome c reductase complex	2.46	2.61	1.06	1.34
others	YPL170W	*DAP1*	heme-binding protein involved in regulation of cytochrome P450 protein Erg11p	2.43	2.52	1.03	0.98
others	YIL153W	*RRD1*	peptidyl-prolyl cis-trans isomerase activity	2.42	2.30	0.95	0.72
others	YDR236C	*FMN1*	riboflavin kinase, phosphorylates riboflavin to form riboflavin monophosphate	2.42	2.35	0.97	1.01
others	YHR116W	COX23	mitochondrial intermembrane space protein that functions in mitochondrial copper homeostasis	2.41	2.48	1.03	1.22
others	YOR034C	*AKR2*	ankyrin repeat-containing protein similar to Akr1p	2.40	2.47	1.03	0.78
others	YKL198C	*PTK1*	putative serine/threonine protein kinase that regulates spermine uptake	2.38	2.25	0.94	0.73
others	YLL001W	*DNM1*	dynamin-related GTPase required for mitochondrial fission and the maintenance of mitochondrial morphology	2.37	2.31	0.97	1.03
others	YCL035C	*GRX1*	hydroperoxide and superoxide-radical responsive heat-stable glutathione-dependent disulfide oxidoreductase	2.35	2.43	1.04	0.90
others	YJL053W	*PEP8*	vacuolar protein sorting protein	2.26	2.07	0.91	0.81

others	YML041C	*VPS71*	required for vacuolar protein sorting	2.24	2.32	1.03	1.00
others	YLR396C	*VPS33*	ATP-binding protein that is a subunit of the homotypic vacuole fusion and vacuole protein sorting complex	2.20	2.31	1.05	1.08
others	YKL150W	*MCR1*	mitochondrial NADH-cytochrome b5 reductase	2.18	2.05	0.94	0.87
others	YOR245C	*DGA1*	diacylglycerol acyltransferase	2.17	2.24	1.03	0.87
others	YPL031C	*PHO85*	cyclin-dependent kinase	2.17	2.08	0.96	1.05
others	YLR371W	*ROM2*	GDP/GTP exchange protein for Rho1p and Rho2p	2.14	2.14	1.00	0.99
others	YKL020C	*SPT23*	ER membrane protein involved, with its homolog Mga2p, in regulation of *OLE1* transcription	2.11	2.12	1.01	0.99
others	YCR038C	*BUD5*	GTP/GDP exchange factor for Rsr1p required for both axial and bipolar budding patterns	2.10	1.94	0.92	1.04
others	YLR394W	*CST9*	protein required for synaptonemal complex formation	2.09	1.94	0.93	1.06
others	YPL002C	*SNF8*	component of the ESCRT-II complex	2.08	1.92	0.93	0.91
others	YIL033C	*BCY1*	regulatory subunit of the cyclic AMP-dependent protein kinase	2.05	2.13	1.04	0.82
others	YFR033C	QCR6	subunit 6 of the ubiquinol cytochrome-c reductase complex	2.05	2.06	1.01	1.07
others	YKL161C	*MLP1*	protein kinase implicated in the Slt2p mitogen-activated kinase signaling pathway	2.03	1.87	0.92	0.74
unknown	YFL052W		strong similarity to Mal63p, YPR196w and Mal13p	14.3	15.5	1.09	0.75
unknown	YIL097W	*FYV10*	molecular function unknown	4.63	4.28	0.92	0.71
unknown	YJL057C	*IKS1*	putative serine/threonine kinase	4.02	4.45	1.11	0.91
unknown	YNR073C		molecular function unknown	3.99	3.89	0.97	0.73
unknown	YHR150W	*PEX28*	peroxisomal integral membrane protein	3.56	3.64	1.02	0.82
unknown	YDR358W	*GGA1*	golgi-localized protein with homology to gamma-adaptin	3.21	3.39	1.06	1.06
unknown	YOR054C	*VHS3*	functionally redundant inhibitory subunit of Ppz1p	3.10	2.88	0.93	0.68
unknown	YJL151C	*SNA3*	integral membrane protein localized to vacuolar intralumenal vesicles	2.90	2.74	0.94	0.88
unknown	YKL095W	*YJU2*	essential nuclear protein	2.88	2.70	0.94	0.77
unknown	YHR087W		molecular function unknown	2.79	2.97	1.06	0.77
unknown	YKL201C	*MNN4*	putative positive regulator of mannosylphosphate transferase	2.43	2.47	1.02	0.74
unknown	YJL210W	*PEX2*	peroxisomal membrane protein with a C-terminal zinc-binding RING domain	2.32	2.43	1.05	1.02
unknown	YBR037C	*SCO1*	copper-binding protein of the mitochondrial inner membrane	2.19	2.26	1.03	0.91

Supplemental Table SIV

Comparison of the fold changes of the expression of genes that are downregulated in the post-diauxic phase in WT and Δ*isc1* .

Functional Category	ORF	Gene name	Function	Fold change (24 h/ 4 h Exp. 1)		Δ*isc1* / WT	Average change ratio
				WT	Δ*isc1*	Exp. 1	(Exp. 1 and 2)
nutrient uptake	YML123C	*PHO84*	inorganic phosphate transporter, transmembrane protein	0.05	1.04	18.94	11.31
nutrient uptake	YGR138C	*TPO1*	polyamine transport protein specific for spermine	0.08	0.56	7.37	5.55
nutrient uptake	YDR345C	*HXT3*	low affinity glucose transporter of the major facilitator superfamily	0.10	0.23	2.46	2.32
nutrient uptake	YLR214W	*FRE1*	ferric (and cupric) reductase	0.13	0.50	3.88	2.88
nutrient uptake	YHR094C	*HXT1*	low-affinity glucose transporter of the major facilitator superfamily	0.13	0.32	2.50	2.43
nutrient uptake	YMR011W	*HXT2*	high-affinity glucose transporter of the major facilitator superfamily	0.21	1.41	6.87	5.24
nutrient uptake	YKL120W	*OAC1*	mitochondrial inner membrane transporter, transports oxaloacetate, sulfate, and thiosulfate	0.21	0.51	2.40	1.78
nutrient uptake	YPL019C	*VTC3*	vacuolar membrane protein involved in vacuolar polyphosphate accumulation	0.24	0.56	2.34	2.47
nutrient uptake	YMR319C	*FET4*	low-affinity Fe(II) transport protein	0.29	0.88	3.02	2.05
nutrient uptake	YJL212C	*OPT1*	plasma membrane transporter that transports tetra- and pentapeptides and glutathione	0.37	1.12	3.03	2.43
nutrient uptake	YBR093C	*PHO5*	acid phosphatase, repressible	0.40	2.02	5.06	3.31
nutrient uptake	YDL048C	*STP4*	involved in pre-tRNA splicing and in uptake of branched-chain amino acids	0.44	1.37	3.08	2.30
nutrient uptake	YGL255W	*ZRT1*	high-affinity zinc transporter of the plasma membrane	0.57	2.00	3.51	2.11
amino acid metabolism	YLR180W	*SAM1*	S-adenosylmethionine synthetase	0.10	0.47	4.70	3.90
amino acid metabolism	YAL012W	*CYS3*	cystathionine γ-lyase	0.12	0.66	5.28	4.75
amino acid metabolism	YHR208W	*BAT1*	branched-chain amino acid transaminase	0.16	0.46	2.87	2.25
amino acid metabolism	YGR155W	*CYS4*	cystathionine β-synthase	0.26	0.69	2.66	2.23
amino acid metabolism	YLR303W	*MET17*	O-acetylhomoserine-O-acetylserine sulfhydralase	0.28	1.72	6.04	4.75
amino acid metabolism	YCL018W	*LEU2*	β-isopropylmalate dehydrogenase	0.32	1.44	4.50	2.80
amino acid metabolism	YDR502C	*SAM2*	S-adenosylmethionine synthetase	0.34	1.77	5.28	4.61
amino acid metabolism	YKL001C	*MET14*	adenylylsulfate kinase	0.39	2.67	6.85	4.77
amino acid metabolism	YIL074C	*SER33*	3-phosphoglycerate dehydrogenase	0.39	1.14	2.92	2.52
amino acid metabolism	YPR167C	*MET16*	3-phosphoadenylylsulfate reductase	0.44	1.57	3.61	2.37
nucleotide/nucleoside processing	YDL227C	*HO*	homothallic switching endonuclease	0.06	0.19	3.11	2.52
nucleotide/nucleoside processing	YGR249W	*MGA1*	Mga1p shows similarity to heat shock transcription factor	0.10	1.24	12.72	8.67

nucleotide/nucleoside processing	YLR367W	*RPS22B*	ribosomal protein S22B	0.12	0.39	3.22	2.57
nucleotide/nucleoside processing	YHR170W	*NMD3*	putative Upf1p-interacting protein	0.15	0.40	2.64	2.17
nucleotide/nucleoside processing	YDR432W	*NPL3*	nuclear shuttling protein with an RNA recognition motif	0.25	0.94	3.82	3.09
nucleotide/nucleoside processing	YER130C		similarity to Msn2p and weak similarity to Msn4p	0.44	1.39	3.17	2.28
nucleotide/nucleoside processing	YOR032C	*HMS1*	basic helix-loop-helix protein	0.45	2.58	5.68	4.33
nucleotide/nucleoside processing	YDR337W	*MRPS28*	mitochondrial ribosomal protein MRPS28	0.49	1.11	2.27	1.87
non-fermentable carbon source utilization	YIL070C	*MAM33*	mitochondrial acidic matrix protein	0.43	1.49	3.46	2.59
non-fermentable carbon source utilization	YNL256W	*FOL1*	multifunctional enzyme of the folic acid biosynthesis pathway	0.48	0.56	1.17	1.32
non-fermentable carbon source utilization	Q0280	*COB*	ubiquinol-cytochrome-c reductase subunit (cytochrome B)	0.51	1.11	2.18	1.75
protein catabolism	YLR121C	*YPS3*	GPI-anchored aspartic protease	0.40	0.93	2.35	1.70
others	YGL089C	*MFALPHA2*	α–mating factor	0.02	0.04	2.86	4.06
others	YNL141W	*AAH1*	adenosine deaminase	0.08	0.19	2.26	2.24
others	YDL039C	*PRM7*	pheromone-regulated membrane protein	0.10	0.25	2.59	2.10
others	YBR244W	*GPX2*	phospholipid hydroperoxide glutathione peroxidase	0.14	0.60	4.25	3.27
others	YIL118W	*RHO3*	ras homolog, GTP binding protein	0.31	0.89	2.83	2.38
others	YDR297W	*SUR2*	syringomycin response protein 2	0.35	1.19	3.42	2.31
others	YHR136C	*SPL2*	protein with similarity to cyclin-dependent kinase inhibitors	0.39	1.85	4.73	4.67
others	YOL016C	*CMK2*	Calmodulin-dependent protein kinase	0.42	1.88	4.49	3.80
others	YJL165C	*HAL5*	protein kinase homolog, mutant is salt and pH sensitive	0.43	1.54	3.56	2.53
others	YOR344C	*TYE7*	TYE7, a 33 kDa serine-rich protein, is a potential member of the basic region	0.48	1.17	2.45	1.75
others	YGL143C	*MRF1*	mitochondrial polypeptide chain release factor	0.49	1.48	3.02	2.17
others	YIR035C		similarity to human corticosteroid 11-β-dehydrogenase	0.49	1.16	2.37	1.82
unknown	YDL037C	*BSC1*	strong similarity to glucan 1,4-α-glucosidase	0.06	0.34	5.87	3.39
unknown	YPR157W		strong similarity to YGR141w	0.07	0.28	3.88	2.55
unknown	YDL038C		similarity to mucin proteins	0.08	0.24	3.14	2.10
unknown	YDR222W		strong similarity to hypothetical protein YLR225c	0.10	0.32	3.27	2.62
unknown	YOL019W		similarity to Rim9p and YFR012w	0.21	0.58	2.75	2.20
unknown	YDR281C	*PHM6*	molecular function unknown	0.21	1.05	4.93	4.38
unknown	YDL158C		molecular function unknown	0.30	0.79	2.63	2.07
unknown	YOR385W		strong similarity to hypothetical protein YMR316w	0.30	0.98	3.24	3.93
unknown	YLR194C		molecular function unknown	0.34	2.20	6.57	5.49
unknown	YDL228C		similarity to *A.klebsiana* glutamate dehydrogenase	0.35	0.82	2.34	1.75

unknown	YJL171C	similarity to YBR162c	0.36	1.39	3.85	2.78

Supplemental Table SV

Comparison of the fold changes of the expression of genes involved in retrograde response in the pre-diauxic phase of petite and Δ*isc1* relative to their parental strains.

ORF	Gene name	petite/ grande	Δ *isc1* / WT	Function
YOR136W	*IDH2*	5.0	1.1±0.1	isocitrate dehydrogenase subunit II
YLR304C	*ACO1*	4.0	0.9±0.3	aconitase
YNL037C	*IDH1*	3.6	1.1±0.1	isocitrate dehydrogenase subunit I
YOR153W	*PDR5*	3.0	1.5±0.8	ABC transporter/multidrug resistance
YLR069C	*MEF1*	2.8	0.8±0.1	mitochondrial translation elongation factor G
YKL096W	*CWP1*	2.5	1.2±0.2	cell wall mannoprotein
YLR027C	*AAT2*	2.5	1.3±0.3	aspartate aminotransferase
YML054C	*CYB2*	2.4	1.8±0.2	cytochrome b2
YOR020C	*HSP10*	2.4	0.9±0.0	mitochondrial chaperonin
YIL070C	*MAM33*	2.4	0.6±0.0	required for respiratory growth
YDR316W	*OMS1*	2.4	0.9±0.1	protein integral to the mitochondrial membrane
YAL060W	*BDH1*	2.4	0.9±0.1	NAD-dependent (2R,3R)-2,3-butanediol
YGR132C	*PHB1*	2.3	1.1±0.0	prohibitin
YBR196C	*PGI1*	2.3	0.8±0.0	glucose-6-phosphate isomerase
YMR272C	*SCS7*	2.3	0.8±0.1	ceramide hydrolase
YLR259C	*HSP60*	2.2	0.9±0.0	mitochondrial chaperonin
YPL135W	*ISU1*	2.2	1.1±0.1	ferrous iron binding
YGR035c		2.2	1.5±0.8	molecular function unknown
YFR053C	*HXK1*	2.1	2.2±0.2	hexokinase I
YDR074W	*TPS2*	2.1	0.8±0.2	trehalose-6-phosphate synthase
YDR077W	*SED1*	2.1	1.2±0.1	cell surface glycoprotein
YNL315C	*ATP11*	2.0	0.8±0.1	F_1-ATPase synthase assembly protein
YJR048W	*CYC1*	2.0	0.6±0.0	cytochrome c isoform I
YEL039C	*CYC7*	2.0	1.7±0.1	cytochrome c isoform II
YLR163C	*MAS1*	2.0	0.9±0.0	subunit of mitochondrial processing peptidase
YER053C	*PIC2*	2.0	1.0±0.1	mitochondrial phosphate carrier
YMR145C	*NDE1*	2.0	0.8±0.1	mitochondrial NADH dehydrogenase
YER062C	*HOR2*	2.0	1.6±0.4	DL-glycerol phosphate phosphatase
YOR152c		2.0	1.7±0.3	molecular funtion unknown
YLR258W	*GSY2*	2.0	1.1±0.2	glycogen synthetase isoform 2
YJL159W	*HSP150*	2.0	0.9±0.0	secreted O-glycosylated protein
YDR055W	*PST1*	2.0	1.2±0.3	similar to the Sps2-Ecm33-YCL048 family
YHR030	*MPK1*	2.0	1.3±0.4	serine/threonine protein kinase
YOR354C	*MSC6*	2.0	1.5±0.5	meiotic recombination