

Additional File 11: List of differentially-expressed genes in the *cti6Δ (ypl18lwΔ)* mutant.

Differentially-expressed genes in one experiment are shown with expression levels in logarithmic scale with base of two. The GO biological process from FunSpec was used to categorize genes according to their cellular functions.

UP-REGULATED GENES

Gene ID	Gene Name	Average expression	Function/ Activity
<i>Carbohydrate metabolism and energy metabolism (12)</i>			
YAL038W	CDC19	1.45	Pyruvate kinase
YBL082C	RHK1	0.62	Mannosyltransferase involved in N-glycosylation
YCR012W	PGK1	1.36	Phosphoglycerate kinase
YDL066W	IDP1	0.76	Isocitrate dehydrogenase
YGR192C	TDH3	1.36	Glyceraldehyde-3-phosphate dehydrogenase 3
YGR240C	PFK1	1.48	Phosphofructokinase alpha subunit
YGR254W	ENO1	1.30	Enolase 1
YJL137C	GLG2	0.62	Self-glucosylating initiator of glycogen synthesis
YKL085W	MDH1	0.84	Malate dehydrogenase, mitochondrial
YLR304C	ACO1	0.75	Aconitase
YML110C	COQ5	0.71	Mitochondrial C-methyltransferase
YOL059W	GPD2	1.04	Glycerol-3-phosphate dehydrogenase
<i>Metal homeostasis (4)</i>			
YBR295W	PCA1	0.88	P-type copper-transporting ATPase
YGL166W	ACE1	2.14	Copper-dependent transcription factor
YLR136C	TIS11	1.48	Protein of the inducible CCCH zinc finger family
YMR319C	FET4	0.78	Low-affinity Fe(II) transport protein
<i>Nucleotide metabolism (14)</i>			
YBL002W	HTB2	1.30	Histone H2B
YBL088C	TEL1	1.08	Phosphatidylinositol 3-kinase
YBR010W	HHT1	1.24	Histone H3
YBR253W	SRB6	0.62	Component of the RNA polymerase II holoenzyme
YDL160C	DHH1	0.84	Putative RNA helicase
YDR224C	HTB1	1.40	Histone H2B
YDR225W	HTA1	1.22	Histone H2A
YGL073W	HSF1	1.03	Heat shock transcription factor
YHL027W	RIM101	1.03	Transcription factor for sporulation related genes
YIL066C	RNR3	0.87	Ribonucleotide reductase
YLR398C	SKI2	0.72	Antiviral protein and probable helicase
YMR283C	RIT1	2.29	Initiator tRNA phosphoribosyl-transferase
YPL089C	RLM1	1.62	Transcription factor of the MADS box family
YPR018W	RLF2	0.64	Chromatin assembly complex subunit 1
<i>Others (4)</i>			
YAL002W	VPS8	1.22	Protein involved in vacuolar sorting
YBR222C	PCS60	0.78	Peroxisomal AMP-binding protein
YGL205W	POX1	1.28	Acyl-CoA oxidase

Gene ID	Gene Name	Average expression	Function/ Activity
<i>Others</i>			
<i>YOR370C</i>	<i>MRS6</i>	0.70	Rab geranylgeranyltransferase regulatory component and rab guanine nucleotide dissociation inhibitor
<i>Protein metabolism (25)</i>			
<i>YBR118W</i>	<i>TEF2</i>	1.46	Translation elongation factor EF-1alpha
<i>YBR181C</i>	<i>RPS6B</i>	1.20	Ribosomal protein S6
<i>YBR189W</i>	<i>RPS9B</i>	1.39	Ribosomal protein S9
<i>YBR191W</i>	<i>RPL21A</i>	1.38	Ribosomal protein L21
<i>YDL075W</i>	<i>RPL31A</i>	1.31	Ribosomal protein L31
<i>YDL130W</i>	<i>RPP1B</i>	1.30	Acidic ribosomal protein P1B
<i>YGL031C</i>	<i>RPL24A</i>	1.39	Ribosomal protein L24A
<i>YGL135W</i>	<i>RPL1B</i>	1.51	Large subunit ribosomal protein L1
<i>YGL189C</i>	<i>RPS26A</i>	1.10	Ribosomal protein S26
<i>YGR085C</i>	<i>RPL11B</i>	1.50	Ribosomal protein L11
<i>YGR148C</i>	<i>RPL24B</i>	1.43	Ribosomal protein L24B
<i>YHL033C</i>	<i>RPL8A</i>	1.46	Ribosomal protein L8
<i>YJL138C</i>	<i>TIF2</i>	1.37	Translation initiation factor 4A
<i>YJR123W</i>	<i>RPS5</i>	1.04	Ribosomal protein Rps5p
<i>YJR145C</i>	<i>RPS4A</i>	1.29	Ribosomal protein S4
<i>YKL006W</i>	<i>RPL14A</i>	1.10	Ribosomal protein L14
<i>YKR059W</i>	<i>TIF1</i>	1.44	Translation initiation factor 4A
<i>YLR075W</i>	<i>RPL10</i>	1.42	Ribosomal protein L10
<i>YLR264W</i>	<i>RPS28B</i>	1.19	Ribosomal protein S28
<i>YLR303W</i>	<i>MET17</i>	4.51	O-Acetylhomoserine sulfhydrylase
<i>YLR333C</i>	<i>RPS25B</i>	1.25	Ribosomal protein S25B
<i>YNL178W</i>	<i>RPS3</i>	1.31	Ribosomal protein S3
<i>YNL244C</i>	<i>SUI1</i>	1.23	Translation initiation factor eIF3
<i>YPL037C</i>	<i>EGD1</i>	1.45	Beta subunit of the nascent polypeptide-associated complex
<i>YPR132W</i>	<i>RPS23B</i>	1.35	Ribosomal protein S23
<i>Transporters (4)</i>			
<i>YDR011W</i>	<i>SNQ2</i>	0.78	Drug-efflux pump involved in resistance to multiple drugs
<i>YDR039C</i>	<i>ENA2</i>	0.59	Member of the Na ⁺ -transporting P-type ATPases family
<i>YNL070W</i>	<i>TOM7</i>	1.24	Subunit of the translocase involved in mitochondrial protein import
<i>YOR153W</i>	<i>PDR5</i>	0.60	Drug-efflux pump
<i>Functionally unknown genes (3)</i>			
<i>YDR077W</i>	<i>SED1</i>	1.02	Abundant cell surface glycoprotein
<i>YKL095W</i>	<i>YJU2</i>	0.66	Protein possibly involved in pre-mRNA splicing
<i>YOR135C</i>	<i>YOR135C</i>	1.03	Protein possibly required for full induction of IME1 during early meiosis

DOWN-REGULATED GENES

Gene ID	Gene Name	Average expression	Function/ Activity
<i>Carbohydrate metabolism (12)</i>			
YBL015W	ACH1	-0.73	Acetyl-CoA hydrolase
YBR019C	GAL10	-0.95	UDP-glucose 4-epimerase
YBR297W	MAL33	-1.11	Maltose fermentation regulatory protein
YDL021W	GPM2	-1.60	Phosphoglycerate mutase
YER178W	PDA1	-0.82	Pyruvate dehydrogenase complex
YFL018C	LPD1	-0.79	Dihydrolipoamide dehydrogenase
YFR015C	GSY1	-0.83	Glycogen synthetase isoform 1
YGR143W	SKN1	-1.14	Glucan synthase
YHR044C	DOG1	-1.08	2-Deoxyglucose-6-phosphate phosphatase
YJR158W	HXT16	-1.02	Member of the hexose transporter family of the major facilitator superfamily (MFS)
YJR159W	SOR1	-2.63	Sorbitol dehydrogenase
YLR273C	PIG1	-1.01	Involved in glycogen synthesis
<i>Cell growth and maintenance (23)</i>			
YBL016W	FUS3	-1.90	Serine/threonine protein kinase
YBR073W	RDH54	-1.67	Required for mitotic diploid-specific recombination and repair and for meiosis
YDL240W	LRG1	-0.68	GTPase-activating protein of the rho/rac family
YFL003C	MSH4	-1.24	Meiosis-specific protein
YFL026W	STE2	-3.70	Pheromone alpha-factor G protein-coupled receptor
YGL032C	AGA2	-4.74	Binding subunit of a-agglutinin
YGL086W	MAD1	-1.32	Involved in spindle-assembly checkpoint
YGR044C	RME1	-2.82	Transcription factor that represses meiosis in non-a/alpha cells
YHR084W	STE12	-0.77	Transcription factor that binds to pheromone response element
YHR086W	NAM8	-1.04	U1 snRNA-associated protein
YIL015W	BAR1	-5.85	Secreted pepsin-like protease that degrades alpha-factor
YIL140W	AXL2	-0.80	Glycoprotein localized at site of bud emergence
YJR086W	STE18	-1.30	Mediates signal transduction by pheromones during mating
YKL178C	STE3	-1.46	Pheromone a-factor G protein-coupled receptor
YKL209C	STE6	-1.26	Membrane transporter responsible for export of a factor mating pheromone
YLR452C	SST2	-4.07	Negatively regulates the mating pheromone response pathway
YMR055C	BUB2	-1.28	Checkpoint protein required for cell cycle arrest
YNL145W	MFA2	-6.66	a-Factor mating pheromone precursor
YNL289W	PCL1	-0.82	G1/S-specific cyclin
YNR044W	AGA1	-1.22	Anchor subunit of a-agglutinin
YOR212W	STE4	-3.79	Mediates signal transduction by pheromones
YPL121C	MEI5	-0.80	Meiotic protein required for synapsis and meiotic recombination
YPL256C	CLN2	-0.95	G1/S-specific cyclin
<i>Nucleotide metabolism (13)</i>			
YBR083W	TEC1	-2.31	Transcriptional activator
YCR097WB	HMRA1	-0.85	Homeodomain regulatory protein
YER172C	BRR2	-1.26	RNA helicase-related protein
YGL248W	PDE1	-0.69	3',5'-Cyclic-nucleotide phosphodiesterase
YGR091W	PRP31	-0.62	Required for pre-mRNA splicing

Gene ID	Gene Name	Average expression	Function/ Activity
<i>Nucleotide metabolism</i>			
<i>YIR017C</i>	<i>MET28</i>	-0.96	Transcriptional activator regulating sulfur amino acid metabolism
<i>YJL130C</i>	<i>URA2</i>	-1.44	Multifunctional protein of pyrimidine biosynthesis pathway
<i>YKL062W</i>	<i>MSN4</i>	-0.92	Transcriptional activator for genes regulated through Snf1p,
<i>YLR256W</i>	<i>HAP1</i>	-1.17	Transcription factor with heme-dependent DNA-binding activity
<i>YML061C</i>	<i>PIF1</i>	-1.72	DNA-dependent ATPase and 5'-3' DNA helicase
<i>YNL261W</i>	<i>ORC5</i>	-0.67	Origin recognition complex
<i>YOL004W</i>	<i>SIN3</i>	-1.05	Component of histone deacetylase B
<i>YPR047W</i>	<i>MSF1</i>	-0.62	Phenylalanyl-tRNA synthetase
<i>Others (31)</i>			
<i>YDR058C</i>	<i>TGL2</i>	-1.09	Triglyceride lipase
<i>YDR127W</i>	<i>ARO1</i>	-1.24	Arom pentafunctional enzyme
<i>YDR212W</i>	<i>TCP1</i>	-1.13	Component of chaperonin-containing T-complex
<i>YDR538W</i>	<i>PAD1</i>	-0.98	Phenylacrylic acid decarboxylase
<i>YER120W</i>	<i>SCS2</i>	-0.80	Suppressor of choline synthesis
<i>YER155C</i>	<i>BEM2</i>	-1.08	GTPase-activating (GAP) protein involved in cell organization
<i>YFL058W</i>	<i>THI5</i>	-1.97	Involved in the production of thiamine precursor
<i>YGL252C</i>	<i>RTG2</i>	-0.67	Involved in inter-organelle communication
<i>YGR144W</i>	<i>THI4</i>	-0.92	Thiamine-repressed protein
<i>YGR286C</i>	<i>BIO2</i>	-0.67	Biotin synthetase
<i>YHL003C</i>	<i>LAG1</i>	-0.60	Required for ceramide synthesis and ER-to-Golgi transport of GPI-anchored proteins
<i>YHR215W</i>	<i>PHO12</i>	-1.36	Acid phosphatase
<i>YIL114C</i>	<i>POR2</i>	-0.86	Outer mitochondrial membrane porin
<i>YIR028W</i>	<i>DAL4</i>	-2.15	Allantoin permease
<i>YJL165C</i>	<i>HAL5</i>	-0.71	Serine/threonine protein kinase involved in salt and pH tolerance
<i>YJR121W</i>	<i>ATP2</i>	-1.30	Beta subunit of the F1 subunit of ATP synthase
<i>YLL001W</i>	<i>DNM1</i>	-1.08	Dynamin-related protein
<i>YLR078C</i>	<i>BOS1</i>	-0.74	Synaptobrevin homolog
<i>YLR113W</i>	<i>HOG1</i>	-0.67	MAP kinase
<i>YLR248W</i>	<i>RCK2</i>	-0.70	Calcium/calmodulin-dependent serine/threonine protein kinase
<i>YLR292C</i>	<i>SEC72</i>	-0.61	Component of ER protein-translocation subcomplex
<i>YLR393W</i>	<i>ATP10</i>	-1.05	Protein required for F1-F0 ATP synthase assembly
<i>YMR008C</i>	<i>PLB1</i>	-1.03	Phospholipase B
<i>YMR056C</i>	<i>AAC1</i>	-0.73	ADP/ATP carrier protein of the mitochondrial carrier family (MCF) of membrane transporters
<i>YMR169C</i>	<i>ALD3</i>	-1.12	Stress inducible aldehyde dehydrogenase
<i>YNL093W</i>	<i>YPT53</i>	-0.87	Involved in endocytosis and transport of proteins to the vacuole
<i>YNL329C</i>	<i>PEX6</i>	-0.70	Peroxisomal biogenesis protein
<i>YNR015W</i>	<i>SMM1</i>	-0.76	Member of conserved dihydrouridine synthase family
<i>YNR033W</i>	<i>ABZ1</i>	-0.92	Para-aminobenzoate synthase
<i>YPL057C</i>	<i>SUR1</i>	-0.80	Required for the synthesis of mannosylated sphingolipids
<i>YPL177C</i>	<i>CUP9</i>	-0.80	Involved in copper homeostasis
<i>Protein metabolism (3)</i>			
<i>YDR158W</i>	<i>HOM2</i>	-1.39	Aspartate-semialdehyde dehydrogenase
<i>YHR010W</i>	<i>RPL27A</i>	-0.76	Ribosomal protein L27

Gene ID	Gene Name	Average expression	Function/ Activity
<i>Protein metabolism (cont'd)</i>			
<i>YKL210W</i>	<i>UBA1</i>	-1.04	Ubiquitin-activating (E1) enzyme
<i>Functionally unknown genes (10)</i>			
<i>YAL067C</i>	<i>SEO1</i>	-0.78	Member of the allantoate permease family of the major facilitator superfamily (MFS)
<i>YCR097WA</i>	<i>YCR097WA</i>	-0.72	Unknown
<i>YDL048C</i>	<i>STP4</i>	-0.59	Protein with strong similarity to Stp1p
<i>YEL049W</i>	<i>PAU2</i>	-0.95	Protein with strong similarity to <i>S. cerevisiae</i> Yal068p
<i>YER101C</i>	<i>AST2</i>	-0.66	Protein involved in sorting of membrane proteins
<i>YFL020C</i>	<i>PAU5</i>	-0.79	Member of the seripauperin (PAU) family
<i>YIR030C</i>	<i>DCG1</i>	-2.70	Protein possibly involved in cell wall structure or biosynthesis
<i>YLL019C</i>	<i>KNS1</i>	-0.77	Serine/threonine protein kinase with unknown role
<i>YOR156C</i>	<i>NFII</i>	-0.71	Chromatin protein
<i>YPL058C</i>	<i>PDR12</i>	-0.78	Member of the ATP-binding cassette (ABC) superfamily of membrane transporters