

Additional File 12: List of differentially-expressed genes in the *dap1Δ* mutant. Genes that were up- or down-regulated in at least three out of four independent experiments are listed and categorized according to their cellular functions using the GO biological process from Funspec. The average expression level is shown in logarithmic scale with base of two.

UP-REGULATED GENES

Gene ID	Gene Name	Average expression	Function / Activity
<i>Cell growth and maintenance (3)</i>			
<i>YIL131C</i>	<i>FKH1</i>	0.30	Homolog of Drosophila forkhead protein, involved in transcriptional silencing, cell morphology and cell cycle
<i>YIL146C</i>	<i>ECM37</i>	2.61	Protein possibly involved in cell wall structure or biosynthesis
<i>YLR390W</i>	<i>ECM19</i>	1.49	Protein possibly involved in cell wall structure or biosynthesis
<i>Others (8)</i>			
<i>YAL002W</i>	<i>VPS8</i>	1.07	Protein involved in vacuolar sorting
<i>YAL038W</i>	<i>CDC19</i>	1.05	Pyruvate kinase, catalyzes final step in glycolysis
<i>YBR093C</i>	<i>PHO5</i>	0.92	Acid phosphatase
<i>YBR182C</i>	<i>SMP1</i>	1.25	Transcription factor and target of the Hog1p (MAPK) high osmolarity signal transduction pathway
<i>YCR012W</i>	<i>PGK1</i>	1.05	Phosphoglycerate kinase in glycolysis
<i>YGL055W</i>	<i>OLE1</i>	1.11	Stearoyl-CoA desaturase, required for synthesis of unsaturated fatty acids
<i>YLR386W</i>	<i>VAC14</i>	1.31	Protein involved in Fab1p-dependent phosphatidylinositol(3,5) bisphosphate synthesis, vacuolar size and acidity, and transport of Ppn5p to the multivesicular body
<i>YNL070W</i>	<i>TOM7</i>	1.11	Small subunit of the translocase involved in mitochondrial protein import
<i>Protein metabolism (6)</i>			
<i>YBR118W</i>	<i>TEF2</i>	1.06	Translation elongation factor EF-1alpha
<i>YDR012W</i>	<i>RPL4B</i>	1.07	Ribosomal protein L4
<i>YGR085C</i>	<i>RPL11B</i>	1.11	Ribosomal protein L11
<i>YJL138C</i>	<i>TIF2</i>	1.12	Translation initiation factor 4A
<i>YLR303W</i>	<i>MET17</i>	3.88	O-Acetylhomoserine sulfhydrylase
<i>YPR102C</i>	<i>RPL11A</i>	1.08	Ribosomal protein L11
<i>Functionally unknown genes (13)</i>			
<i>YAR068W</i>	<i>YAR068W</i>	2.25	Unknown
<i>YCR013C</i>	<i>YCR013C</i>	1.13	Unknown
<i>YDL228C</i>	<i>YDL228C</i>	1.42	Unknown

Gene ID	Gene Name	Average expression	Function / Activity
<i>Functionally unknown genes (cont'd)</i>			
<i>YDR077W</i>	<i>SED1</i>	0.86	Abundant cell surface glycoprotein that may contribute to cell wall integrity and stress resistance
<i>YER067W</i>	<i>YER067W</i>	0.70	Unknown
<i>YGR139W</i>	<i>YGR139W</i>	0.84	Unknown
<i>YHR214W</i>	<i>YHR214W</i>	1.83	Unknown
<i>YHR214W-A</i>	<i>YHR214W-A</i>	2.12	Unknown
<i>YIR042C</i>	<i>YIR042C</i>	1.26	Member of the acetyltransferase (GNAT) family
<i>YJL078C</i>	<i>PRY3</i>	0.71	Protein with similarity to plant pathogenesis-related proteins
<i>YOL098C</i>	<i>YOL098C</i>	0.95	Member of the insulinase (peptidase M16) family
<i>YOL155C</i>	<i>YOL155C</i>	1.57	Protein with similarity to <i>S. cerevisiae</i> glucan 1,4-alpha-glucosidase
<i>YOR366W</i>	<i>YOR366W</i>	1.04	Unknown

DOWN-REGULATED GENES

Gene ID	Gene Name	Average expression	Function / Activity
<i>Cell growth and maintenance (17)</i>			
<i>YDR309C</i>	<i>GIC2</i>	-0.80	Putative effector of Cdc42p, important for bud emergence
<i>YFL026W</i>	<i>STE2</i>	-4.29	Pheromone alpha-factor G protein-coupled receptor
<i>YGL032C</i>	<i>AGA2</i>	-2.63	Binding subunit of a-agglutinin
<i>YGL086W</i>	<i>MAD1</i>	-1.16	Protein involved in spindle-assembly checkpoint, required for cell cycle delay in response to impaired kinetochore function
<i>YGR143W</i>	<i>SKN1</i>	-1.51	Glucan synthase subunit involved in synthesis of beta-1,6-glucan
<i>YHR056C</i>	<i>RSC30</i>	-0.81	Component of the abundant RSC chromatin remodeling complex
<i>YHR185C</i>	<i>PFS1</i>	-0.93	Protein required for prospore membrane formation during sporulation
<i>YIL015W</i>	<i>BAR1</i>	-2.89	Secreted pepsin-like protease that degrades alpha-factor
<i>YJR086W</i>	<i>STE18</i>	-1.48	Gamma subunit of the guanine nucleotide-binding protein that mediates signal transduction by pheromones during mating
<i>YKL178C</i>	<i>STE3</i>	-0.94	Pheromone a-factor G protein-coupled receptor
<i>YLR265C</i>	<i>NEJ1</i>	-1.92	Protein involved in nonhomologous end-joining (NHEJ) pathway for repair of DNA double-strand breaks
<i>YMR055C</i>	<i>BUB2</i>	-1.01	Checkpoint protein required for cell cycle arrest in response to loss of microtubule function
<i>YNL127W</i>	<i>FAR11</i>	-0.70	Component of a high-molecular-weight complex containing Far3p
<i>YNL145W</i>	<i>MFA2</i>	-3.74	Mating pheromone a-factor
<i>YOR212W</i>	<i>STE4</i>	-2.76	Beta subunit of the trimeric G protein that mediates signal transduction by pheromones
<i>YPL256C</i>	<i>CLN2</i>	-0.70	G1/S-specific cyclin
<i>YPR122W</i>	<i>AXL1</i>	-1.46	Protease involved in second proteolytic step of a-factor N-terminal processing
<i>Iron metabolism (7)</i>			
<i>YEL065W</i>	<i>ARN3</i>	-0.77	Siderophore iron permease
<i>YLR136C</i>	<i>TIS11</i>	-1.46	Zinc finger containing protein that belongs to iron regulon
<i>YMR058W</i>	<i>FET3</i>	-0.83	Cell surface ferroxidase, required for high-affinity ferrous iron uptake
<i>YOL158C</i>	<i>ARN4</i>	-1.29	Protein involved in iron uptake via a siderophore enterobactin
<i>YOR382W</i>	<i>FIT2</i>	-2.33	Cell wall mannoprotein of iron transport facilitator
<i>YOR383C</i>	<i>FIT3</i>	-1.41	Cell wall mannoprotein of iron transport facilitator
<i>YOR384W</i>	<i>FRE5</i>	-0.81	Protein with similarity to Fre2p, ferric reductase
<i>Nucleotide metabolism (9)</i>			
<i>YBR083W</i>	<i>TEC1</i>	-1.16	Transcriptional activator, involved with Ste12p in pseudohyphal formation

Gene ID	Gene Name	Average expression	Function / Activity
<i>Nucleotide metabolism (cont'd)</i>			
<i>YBR158W</i>	<i>AMN1</i>	-1.02	Protein involved in the AMEN pathway (Antagonist of Mitotic Exit Network) in daughter cells required for exit from mitotic exit and cell cycle reset
<i>YGL073W</i>	<i>HSF1</i>	-1.89	Heat shock transcription factor that binds to the heat shock DNA element at both normal and elevated temperatures
<i>YGL248W</i>	<i>PDE1</i>	-0.87	3',5'-Cyclic-nucleotide phosphodiesterase
<i>YHL027W</i>	<i>RIM101</i>	-1.13	Transcription factor involved in induction of IME1, IME2, DIT1, and DIT2 transcription, has three C2H2-type zinc fingers
<i>YJL130C</i>	<i>URA2</i>	-0.16	Multifunctional protein of pyrimidine biosynthesis pathway
<i>YLR256W</i>	<i>HAP1</i>	-0.97	Transcription factor with heme-dependent DNA-binding activity, responsible for heme-dependent activation of many genes
<i>YML061C</i>	<i>PIF1</i>	-1.63	Single-stranded DNA-dependent ATPase and 5'-3' DNA helicase required for maintenance and repair of mitochondrial DNA, also functions in nucleus to regulate telomere length
<i>YMR287C</i>	<i>MSU1</i>	-0.70	Component of a mitochondrial 3'-5' exonuclease complex that is essential for mitochondrial biogenesis
<i>Others (15)</i>			
<i>YBR208C</i>	<i>DUR1,2</i>	-1.04	Urea amidolyase, contains urea carboxylase and allophanate hydrolase activities fused together in a single polypeptide
<i>YCL040W</i>	<i>GLK1</i>	-1.02	Glucokinase
<i>YDR158W</i>	<i>HOM2</i>	-1.04	Aspartate-semialdehyde dehydrogenase, in common pathway for methionine and threonine biosynthesis
<i>YFL059W</i>	<i>SNZ3</i>	-1.65	Putative pyridoxine (vitamin B6) biosynthetic enzyme
<i>YJR025C</i>	<i>BNAI</i>	-0.71	3-hydroxyanthranilate 3,4-dioxygenase, in biosynthesis of nicotinic acid
<i>YJR159W</i>	<i>SOR1</i>	-1.06	Sorbitol dehydrogenase
<i>YKL142W</i>	<i>MRP8</i>	-0.99	Mitochondrial ribosomal protein of the small subunit
<i>YMR173W</i>	<i>DDR4ϵ</i>	-1.08	Stress protein induced by heat shock, DNA damage, or osmotic stress
<i>YNL160W</i>	<i>YGP1</i>	-1.09	Secreted glycoprotein produced in response to nutrient limitation
<i>YNL333W</i>	<i>SNZ2</i>	-1.47	Putative pyridoxine (vitamin B6) biosynthetic enzyme
<i>YNL334C</i>	<i>SNO2</i>	-1.60	Putative pyridoxine (vitamin B6) biosynthetic enzyme with similarity to glutamine aminotransferases
<i>YOR136W</i>	<i>IDH2</i>	-0.74	Isocitrate dehydrogenase, in the tricarboxylic acid cycle
<i>YPL057C</i>	<i>SUR1</i>	-1.00	Protein required for the synthesis of mannosylated sphingolipids
<i>YPL058C</i>	<i>PDR12</i>	-1.03	Protein required for weak organic acid resistance, member of the ATP-binding cassette (ABC) superfamily of membrane transporters

Gene ID	Gene Name	Average expression	Function / Activity
<i>Others (cont'd)</i>			
<i>YPL170W</i>	<i>DAPI</i>	-3.05	Protein involved in ergosterol biosynthesis, response to UV, mitochondrial genome maintenance, and telomere maintenance, member of the membrane-associated progesterone receptor family
<i>Functionally unknown genes (39)</i>			
<i>YBL005W-B</i>	<i>YBL005W-B</i>	-0.87	Unknown
<i>YBL034C</i>	<i>STU1</i>	-0.80	Suppressor of beta-tubulin mutation that is required for assembly of the mitotic spindle
<i>YBL101W-A</i>	<i>YBL101W-A</i>	-0.79	Unknown
<i>YBL101W-B</i>	<i>YBL101W-B</i>	-0.97	Unknown
<i>YBR012C</i>	<i>YBR012C</i>	-0.88	Unknown
<i>YBR073W</i>	<i>RDH54</i>	-1.26	Protein required for mitotic diploid-specific recombination and repair and for meiosis
<i>YBR157C</i>	<i>ICS2</i>	-1.41	Protein required for normal resistance to copper
<i>YBR293W</i>	<i>YBR293W</i>	-1.02	Unknown
<i>YBR296C</i>	<i>PHO89</i>	-0.80	Na ⁺ /Pi symporter (putative)
<i>YCL019W</i>	<i>YCL019W</i>	-1.08	Unknown
<i>YCL020W</i>	<i>YCL020W</i>	-0.95	Unknown
<i>YDR024W</i>	<i>FYV1</i>	-1.53	Unknown
<i>YDR128W</i>	<i>YDR128W</i>	-0.82	Unknown
<i>YDR340W</i>	<i>YDR340W</i>	-0.92	Unknown
<i>YER138C</i>	<i>YER138C</i>	-1.31	Unknown
<i>YER160C</i>	<i>YER160C</i>	-1.19	Unknown
<i>YER189W</i>	<i>YER189W</i>	-0.80	Unknown
<i>YFL027C</i>	<i>GYP8</i>	-0.94	Possible GTPase activating protein
<i>YFL061W</i>	<i>YFL061W</i>	-0.85	Unknown
<i>YFL064C</i>	<i>YFL064C</i>	-0.85	Unknown
<i>YGL193C</i>	<i>YGL193C</i>	-1.02	Unknown
<i>YHR214C-B</i>	<i>YHR214C-B</i>	-1.22	Unknown
<i>YJR027W</i>	<i>YJR027W</i>	-1.17	Unknown
<i>YJR029W</i>	<i>YJR029W</i>	-0.95	Unknown
<i>YLR343W</i>	<i>YLR343W</i>	-1.38	Unknown
<i>YLR346C</i>	<i>YLR346C</i>	-0.98	Unknown
<i>YML039W</i>	<i>YML039W</i>	-0.91	Unknown
<i>YML040W</i>	<i>YML040W</i>	-1.28	Unknown
<i>YML045W</i>	<i>YML045W</i>	-1.45	Unknown
<i>YMR045C</i>	<i>YMR045C</i>	-1.29	Unknown
<i>YMR173W-A</i>	<i>YMR173W-A</i>	-1.11	Unknown
<i>YNL078W</i>	<i>NIS1</i>	-0.77	Protein that interacts with septins and interacts with Gin4p, Kcc4p, and Nap1p, suggesting a possible role in the mitotic signaling network
<i>YNL155W</i>	<i>YNL155W</i>	-0.82	Unknown
<i>YOR072W</i>	<i>YOR072W</i>	-0.68	Unknown

Gene ID	Gene Name	Average expression	Function / Activity
<i>Functionally unknown genes (cont'd)</i>			
<i>YOR135C</i>	<i>YOR135C</i>	-0.64	Unknown
<i>YOR284W</i>	<i>HUA2</i>	-0.71	Protein that may have a role in assembly of cortical actin patches
<i>YOR289W</i>	<i>YOR289W</i>	-0.81	Unknown
<i>YPL107W</i>	<i>YPL107W</i>	-1.00	Unknown
<i>YPR027C</i>	<i>YPR027C</i>	-1.09	Unknown