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COMBINATORIAL EFFECTS OF OXYGEN AVAILABILITY AND MACRONUTRIENT LIMITATION IN *SACCHAROMYCES CEREVISIAE**[S]

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Genome-wide analysis of transcriptional regulation is generally studied by determining sets of "signature transcripts" that are up- or down-regulated relative to a reference situation when a single culture parameter or genetic modification is changed. This approach is especially relevant for defining small subsets of transcripts for use in high throughput, cost-effective diagnostic analyses. However, this approach may overlook the simultaneous control of transcription by more than one environmental parameter. This study represents the first quantitative assessment of the impact of transcriptional cross-regulation by different environmental parameters. As a model, we compared the response of aerobic as well as anaerobic chemostat cultures of the yeast *Saccharomyces cerevisiae* to growth limitation by four different macronutrients (carbon, nitrogen, phosphorus, and sulfur). The identity of the growth-limiting nutrient was shown to have a strong impact on the sets of transcripts that responded to oxygen availability and vice versa. We concluded that identification of reliable signature transcripts for specific environmental parameters can be obtained only by combining transcriptome data sets obtained under several sets of reference conditions. Furthermore, the two-dimensional approach to transcriptome analysis is a valuable new tool to study the interaction of different transcriptional regulation systems.

Recent rapid developments in DNA microarray technology have had a strong impact in research on the yeast *Saccharomyces cerevisiae*, an important industrial microorganism and model eukaryote. With the ability to study genome-wide transcriptome expression in a single microarray, large on-line transcriptome data bases obtained from different mutants and under a wide range of cultivation conditions have become available as research tools (Gene Expression Omnibus (1) and Yeast Microarray Global Viewer (2)).

Transcript profiles contain a wealth of information that may be applied in several ways for fundamental and applied research. When clear correlations are established between cultivation conditions and transcription of subsets of genes, such correlations can be used to guide functional analysis studies of genes with as yet unknown biological functions. Furthermore, correlation of expression data with sequences of upstream regulatory elements can be applied to unravel the intricate networks of transcriptional regulation (3). In industrial biotechnology, one of the key applications of DNA microarrays lies in diagnosing industrial fermentation processes. If transcriptional responses can be directly correlated to important parameters such as nutritional status of industrial microorganisms or to the stresses to which they are exposed in industrial processes, transcriptome analysis can provide invaluable information for process optimization (4, 5). For such diagnostic purposes, it would be preferable to construct small, cost-effective microarrays that contain a limited number of "signature transcripts." Such signature transcripts should respond uniquely to a single chemical or physical parameter that is relevant for the industrial process under study. This approach is analogous to the application of small diagnostic arrays used in clinical research for the rapid typing of tumors (6).

Hitherto, most transcriptome studies with *S. cerevisiae* have been done in shake-flask cultures (7, 8). In such cultures, it is not possible to control a number of important cultivation conditions (dissolved oxygen concentration, metabolite concentrations, pH, etc.). Therefore, shake-flask cultivation by definition involves a continuously changing environment. Consequently, interpretation of transcriptome data from shake-flask cultivation is likely to be complicated by differences in specific growth rate, carbon catabolite repression, nitrogen catabolite repression, product accumulation, acidification, etc.

Chemostat cultivation offers a number of advantages for studies with DNA microarrays because it enables cultivation of microorganisms under tightly defined environmental conditions. In a chemostat, culture broth (including biomass) is continuously replaced by fresh medium at a fixed and accurately determined dilution rate (D, h^{-1}). When the dilution rate is lower than the maximal specific growth rate of the microorganism (μ_{max}, h^{-1}), a steady-state situation will be established in which the specific growth rate equals the dilution rate ($\mu = D$). In such a steady-state chemostat culture, μ is controlled by the (low) residual concentration of a single growth-limiting nutrient. The option to accurately control and manipulate individual culture parameters (including medium composition, nature of the growth-limiting nutrient, pH, temperature, and μ) under steady-state conditions

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[S] The on-line version of this article (available at http://www.jbc.org) contains Supplemental Tables 1–6.

The complete data set has been submitted to the Genome Expression Omnibus Database (available at www.ncbi.nlm.nih.gov/geo/) under series GSE1723.

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makes chemostats excellent tools for studies on genome-wide transcriptional regulation. Indeed, a recent interlaboratory comparison of transcriptome data obtained in chemostat cultures demonstrated that the accuracy and reproducibility of this approach are superior to those obtained in previous studies with shake-flask cultures (9).

Chemostat cultures have recently been applied to study genome-wide transcriptional responses of *S. cerevisiae* to carbon-limited growth on different carbon sources (10); to nutrient limitation for carbon, nitrogen, phosphorus, and sulfur (4); to starvation (11); to the presence and absence of oxygen (9, 12); and to oxidative stress responses (13). In each of these studies, attempts were made to vary a single cultivation parameter while keeping all other parameters constant. This "one-dimensional" approach resulted in sets of signature transcripts that, within the experimental context, responded uniquely to a single cultivation parameter (*e.g.* uniquely up-regulated under nitrogen limitation, uniquely down-regulated during growth on ethanol). There is an important potential pitfall in this approach, as it does not include the possibility that expression of genes is simultaneously controlled by two or more environmental parameters. Such dual or multiple control would complicate the identification of signature transcripts and the interpretation of diagnostic transcriptome analysis.

So far, there have been no dedicated studies to investigate and quantify the way in which different transcriptional regulation responses overlap and interact. The goal of this study was to study this interaction by analyzing genome-wide transcriptional responses to four different nutrient limitation regimes under aerobic and anaerobic conditions in chemostat cultures of *S. cerevisiae*. This "two-dimensional" approach resulted in a new robust set of "anaerobic" and "aerobic" signature transcripts for *S. cerevisiae* as well as the refinement of previous reports on nutrient-responsive genes. Moreover, the identification of genes regulated both by nutrient and oxygen availability provided new insight in cross-regulated network and hierarchy in the control of gene expression. These newly defined sets of signature genes were subjected to *in silico* promoter analysis to identify consensus regulatory elements.

EXPERIMENTAL PROCEDURES

Strain and Growth Conditions—The *S. cerevisiae* prototrophic haploid reference strain CEN.PK113-7D (*MAT***a**) (14) was grown at 30 °C in 2-liter chemostats (Applikon) with a working volume of 1.0 liter as described (15). Cultures were fed with a defined synthetic medium that limited growth by carbon, nitrogen, phosphorus, or sulfur with all other growth requirements in excess and at a constant residual concentration (4). The dilution rate was set at 0.10 h^{-1}. The pH was measured on-line and kept constant at 5.0 by the automatic addition of 2 M KOH using an Applikon ADI 1030 Biocontroller, and the stirrer speed was set at 800 rpm. Anaerobic conditions were maintained by sparging the medium reservoir and the fermentor with pure nitrogen gas (0.5 liter min^{-1}). Furthermore, Norprene tubing and butyl septa were used to minimize oxygen diffusion into the anaerobic cultures (16). The off-gas was cooled by a condenser connected to a cryostat set at 2 °C. Oxygen and carbon dioxide were measured off-line with an NGA 2000 Rosemount gas analyzer. Steady-state samples were taken after ~10–14 volume changes to avoid strain adaptation due to long-term cultivation (17, 18). Biomass dry weight, metabolite, dissolved oxygen, and gas profiles were constant over at least three volume changes prior to sampling for RNA extraction.

Growth Media—The synthetic medium composition was based on that described (19). In all chemostats except for carbon, the residual glucose concentration was targeted to 17 g $liter^{-1}$ to sustain glucose repression at the same level. For anaerobic cultivations, the reservoir medium was supplemented with the anaerobic growth factors Tween 80 and ergosterol as described previously (20). These media contained the following components: for carbon-limited cultivation, 5.0 g $liter^{-1}$ $(NH_4)_2SO_4$, 3.0 g $liter^{-1}$ KH_2PO_4, 0.5 g $liter^{-1}$ $MgSO_4 \cdot 7H_2O$, and 25 g $liter^{-1}$ glucose; for nitrogen-limited cultivation, 0.65 g $liter^{-1}$ $(NH_4)_2SO_4$, 5.75 g $liter^{-1}$ K_2SO_4, 3.0 g $liter^{-1}$ KH_2PO_4, 0.5 g $liter^{-1}$ $MgSO_4 \cdot 7H_2O$, and 46 g $liter^{-1}$ glucose; for phosphorus-limited cultivation, 5.0 g $liter^{-1}$ $(NH_4)_2SO_4$, 1.9 g $liter^{-1}$ K_2SO_4, 0.12 g $liter^{-1}$ KH_2PO_4, 0.5 g $liter^{-1}$ $MgSO_4 \cdot 7H_2O$, and 66 g $liter^{-1}$ glucose; and for sulfur-limited cultivation, 4.0 g $liter^{-1}$ NH_4Cl, 0.05 g $liter^{-1}$ $MgSO_4 \cdot 7H_2O$, 3.0 g $liter^{-1}$ KH_2PO_4, 0.4 g $liter^{-1}$ $MgCl_2$, and 59 g $liter^{-1}$ glucose. The medium composition for the aerobic chemostat cultures was as described previously (4).

Analytical Methods—Culture supernatants were obtained after centrifugation of samples from the chemostats. For the purpose of glucose determination and carbon recovery, culture supernatants and media were analyzed by high performance liquid chromatography on an AMINEX HPX-87H ion exchange column using 5 mM H_2SO_4 as the mobile phase. Residual ammonium, phosphate, and sulfate concentrations were determined using cuvette tests from DRLANGE (Düsseldorf, Germany). Culture dry weights were determined via filtration as described by Postma *et al.* (21).

Microarray Analysis—Sampling of cells from chemostats, probe preparation, and hybridization to Affymetrix Genechip® microarrays were performed as described previously (9). The results for each growth condition were derived from three independently cultured replicates.

Data Acquisition and Analysis—Acquisition and quantification of array images and data filtering were performed using Affymetrix Microarray Suite Version 5.0, MicroDB Version 3.0, and Data Mining Tool Version 3.0. Before comparison, all arrays were globally scaled to a target value of 150 using the average signal from all gene features using Microarray Suite Version 5.0. To eliminate insignificant variations, genes with values below 12 were set to 12 as described (9). From the 9335 transcript features on the YG-S98 arrays, a filter was applied to extract 6383 yeast open reading frames, of which there were 6084 different genes. This discrepancy was due to several genes being represented more than once when suboptimal probe sets were used in the array design. To represent the variation in triplicate measurements, the coefficient of variation (S.D. divided by the mean) was calculated as described previously by Boer *et al.* (4).

For additional statistical analyses, Microsoft Excel running the significance analysis of microarrays (SAM Version 1.12) add-in was used (22) for pairwise comparisons. Genes were considered as being changed in expression if they were called significantly changed using SAM (expected median false discovery rate of 1%) by at least 2-fold from each other condition. Hierarchical clustering of the obtained sets of significantly changed expression levels was subsequently performed using Genespring Version 6.1 (Silicon Genetics).

Promoter analysis was performed using the web-based software Regulatory Sequence Analysis (RSA) Tools (23). The promoters (from −800 to −1) of each set of co-regulated genes were analyzed for over-represented hexanucleotides. When hexanucleotide sequences shared largely common sequences, they were aligned to form longer conserved elements. All of the individual promoter sequences contributing to these elements were then aligned, and the redundant elements were determined by counting the base representation at each position. The relative abundance of these redundant elements was determined from a new enquiry of the co-regulated gene promoters and the entire set of yeast promoters in the genome. The gene annotation was made according to the Comprehensive Yeast Genome Database at the Munich Information Center for Protein Sequence (MIPS; available at mips.gsf.de/genre/proj/yeast/index.jsp) (24), the *Saccharomyces* Genome Database (available at www.yeastgenome.org/) (25) and the Yeast Proteome Database at Incyte (available at www.incyte.com/).

RESULTS

Experimental Design and Physiology of S. cerevisiae in Aerobic and Anaerobic Macronutrient-limited Chemostat Cultures—To investigate the impact of transcriptional cross-regulation on the identification of signature transcripts, we designed a two-dimensional experimental approach (Fig. 1). Four nutrient limitation regimes (carbon, nitrogen, sulfur, and phosphorus) were studied. In one set of experiments, the four nutrient limitation regimes were studied in aerobic chemostat cultures. A second set of experiments was performed under the same nutrient limitation regimes, but in anaerobic chemostat cultures. The resulting set of eight fermentation conditions, each analyzed in three independent replicate cultures, enabled the identification of genes with a specific transcriptional response to one parameter only (*e.g.* induced under anaerobic conditions irrespective of the macronutrient limitation regime).

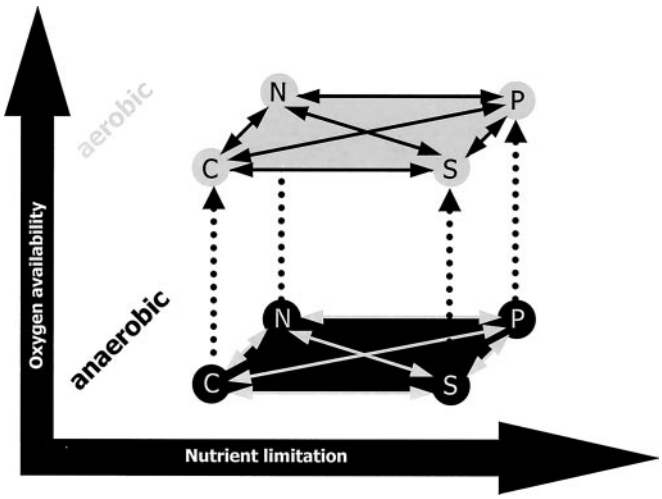


FIG. 1. **Two-dimensional experimental approach.** The experimental design for two-dimensional transcriptome analysis is shown. Each *corner* of the *cube* represents a chemostat condition. The *upper horizontal surface* represents the four aerobic macronutrient limitation regimes (carbon, nitrogen, phosphorus, and sulfur). The *lower horizontal surface* represents the same macronutrient limitation regimes analyzed under anaerobic conditions. The *arrows* indicate the pairwise comparisons included in the present two-dimensional transcriptome analysis.

Furthermore, genes that transcriptionally responded to multiple parameters were identified (*e.g.* induced under anaerobic conditions only when growth was limited by the carbon source).

To minimize experimental "noise," the compositions of the growth media were designed such that residual concentrations of non-growth-limiting nutrients were essentially the same in all chemostat cultures (Table I). Control experiments confirmed that the concentrations of the growth-limiting nutrients were below the detection limit of the respective assay procedures (Table I). The option to control the steady-state concentrations of limiting and excess nutrients concertedly is a unique feature of chemostat cultivations.

The physiological parameters of the eight cultivation conditions are reported in Table I. Under aerobic conditions, only the glucose-limited cultures exhibited a completely respiratory glucose metabolism, without production of ethanol. This resulted in a respiratory quotient close to unity (Table I). Conversely, the aerobic cultures that were not limited by glucose exhibited a respirofermentative glucose metabolism, with simultaneous ethanol production and oxygen consumption (respiratory quotient of >1). In the anaerobic chemostat cultures, alcoholic fermentation was the sole mode of glucose dissimilation, as no oxygen was available for respiration. The ATP yield from alcoholic fermentation is much lower than that from respiratory glucose dissimilation (20), thus explaining the lower biomass yield on glucose of the anaerobic cultivations. The biomass yield on glucose in glucose-limited cultures was higher than in the non-glucose-limited cultures (Table I). Under aerobic conditions, this can be partially explained by the involvement of alcoholic fermentation in the latter cultures. However, a reduction of the biomass yield in non-glucose-limited cultures was also observed under anaerobic conditions (Table I). This may be related to the induction of energy-dependent transport systems during nitrogen-, phosphorus-, and sulfur-limited growth (26).

Microarray Reproducibility, Global Transcriptome Responses, and Data Analysis—To obtain statistically robust, reproducible transcriptome data sets (9), independent triplicate chemostat cultivations and oligonucleotide DNA microarrays were carried out for each of the eight cultivation conditions. The average coefficient of variation for the triplicate transcriptome analyses (4, 9) for each of the eight conditions was <0.21, except for the anaerobic glucose-limited chemostats (coefficient of variation of 0.27). The level of the *ACT1* transcript, a common loading standard for conventional Northern analysis, did vary by <13% over the eight growth conditions (Supplemental Table 1).

The eight different cultivation conditions would, in principle, allow for 56 different pairwise comparisons. In this study, we restricted analysis of the data to pairwise comparisons between cultivation conditions that differed in a single cultivation parameter only. Ultimately, this left 28 pairwise comparisons. Four of these were pairwise comparisons between aerobic and anaerobic cultures grown under the same macronutrient limitation regime (Fig. 1, *vertical arrows*). An additional 24 pairwise comparisons involved all possible combinations of the four macronutrient limitation regimes under either aerobic or anaerobic conditions (Fig. 1, *horizontal surfaces*).

Each pairwise comparison defined a set of genes that were significantly up- or down-regulated (-fold change of >2 with a false discovery rate of 1%; see "Experimental Procedures"). In total, 3169 genes (52% of the genome) exhibited a significantly different transcript level in at least one of the 28 pairwise comparisons. 2542 genes (42%) of the genome did not exhibit a significant difference in transcript level in any of the pairwise comparisons. The remaining 373 transcripts (representing 6% of the *S. cerevisiae* genome) remained below the detection limit under all eight conditions investigated (Fig. 2 and Supplemental Table 2).

Transcripts that showed a consistent difference in the aerobic/anaerobic comparisons under all four macronutrient limitation regimes were identified by combining the four relevant pairwise comparisons (Fig. 1, *vertical arrows*). This set of consistently oxygen-responsive genes contained 155 genes (2.6% of the genome) (Fig. 3*A* and Supplemental Table 3).

To investigate transcriptional responses to macronutrient limitation, we first identified transcripts that responded to a single nutrient limitation regime under either aerobic or anaerobic conditions (sets I and V) (Fig. 3*B*). Combination of sets I and V for each of the four macronutrient limitation regimes yielded a subset of transcripts that showed a consistent response to macronutrient limitation irrespective of oxygen availability (set III, 152 genes) (Fig. 3*B* and Supplemental Table 4). In addition, this comparison yielded two sets of genes that showed a transcriptional response only to one of the four nutrient limitation conditions under either aerobic conditions (set II, 333 genes) (Fig. 3*B* and Supplemental Table 5) or anaerobic conditions (set IV, 302 genes) (Fig. 3*B* and Supplemental Table 6). The data analysis approach described above enabled us to dissect the *S. cerevisiae* genome clusters of genes that showed either a consistent, robust response to oxygen availability or macronutrient limitation or, alternatively, a more complex dual-parameter transcriptional regulation.

Signature Genes with a Consistent Transcriptional Response to Oxygen Availability or Macronutrient Limitation—Ten clusters of genes that were identified showed a specific and consistent response to anaerobiosis, glucose limitation, nitrogen limitation, phosphorus limitation, or sulfur limitation (Fig. 4). In five of these clusters, the transcriptional response was defined as "up-regulated" under the conditions indicated; in the other five clusters, the transcriptional response was defined as "down-regulated." This terminology does not imply any mechanism of regulation. For example, down-regulation under nutrient limitation might, mechanistically, represent up-regulation under conditions of nutrient excess. In our discussion of these "consistent response" genes, we will restrict ourselves to a detailed analysis of the anaerobically up-regulated genes and

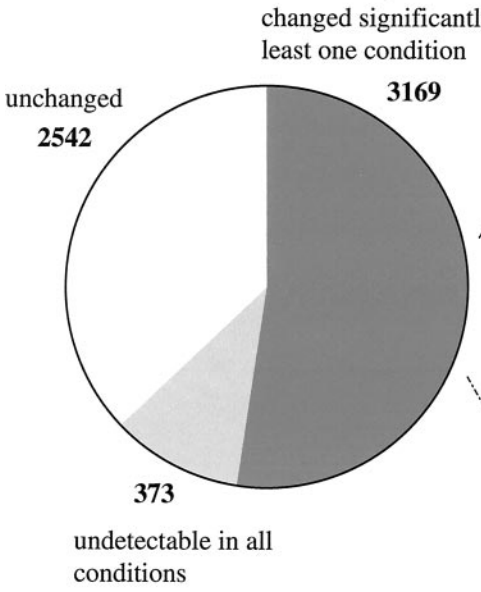
TABLE I

Nutrient concentrations and physiological parameters of chemostat cultures used in this study

Unless indicated otherwise, values represent the mean ± S.D. of data from three independent steady-state chemostat cultivations. RQ, respiratory quotient (q_{CO2}/q_{O2}); BD, below detection limit of assay; NA, not applicable.

Growth-limiting nutrient	Residual nutrient measurements				Physiological parameters							Ref.
	Glc	NH_4^+	PO_4^{3-}	SO_4^{2-}	$Y_{Glc\text{-}X}$ [a]	q_{Glu} [b]	$q_{ethanol}$ [c]	q_{O2} [d]	q_{CO2} [e]	RQ	Carbon recovery	
	g/liter	*mM*	*mM*	*mM*							%	
Aerobic												
Carbon	BD	58.2 ± 1.3	19.8 ± 0.6	38.6[f]	0.49 ± 0.0	1.1 ± 0.0	0.0 ± 0.0	2.8 ± 0.3	2.8 ± 0.3	1.0 ± 0.0	98 ± 3	4
Nitrogen	16.7 ± 1.0	BD	18.6 ± 1.0	40.7 ± 1.0	0.09 ± 0.0	5.8 ± 0.1	8.0 ± 0.1	2.7 ± 0.1	12.1 ± 0.2	4.5 ± 0.2	96 ± 1	4
Phosphorus	18.1 ± 1.0	54.3 ± 0.0	BD	47.5 ± 1.0	0.09 ± 0.0	6.1 ± 0.2	7.8 ± 0.1	4.0 ± 0.1	13.5 ± 0.2	3.4 ± 0.0	95 ± 2	4
Sulfur	17.4 ± 0.6	53.7 ± 2.4	18.4 ± 0.2	BD	0.14 ± 0.0	3.8 ± 0.1	4.4 ± 01	3.0 ± 0.0	8.0 ± 0.8	2.7 ± 0.2	96 ± 1	4
Anaerobic												
Carbon	BD[g]	68.6 ± 2.8[g]	22.3 ± 0.6[g]	42.4 ± 1.6[g]	0.09 ± 0.0	6.0 ± 0.0	9.6 ± 0.1	NA	10.3 ± 0.4	NA	101 ± 2	
Nitrogen	16.2 ± 0.6	BD	21.9 ± 0.4	39.1 ± 0.8	0.07 ± 0.0	8.4 ± 0.0	13.5 ± 0.6	NA	14.8 ± 0.3	NA	101 ± 2	
Phosphorus	19.1 ± 2.2	60.2 ± 2.6	BD	50.9 ± 0.9	0.06 ± 0.0	8.7 ± 0.2	13.9 ± 0.6	NA	15.8 ± 0.7	NA	101 ± 2	
Sulfur	21.2 ± 0.2	61.1 ± 1.3	21.5 ± 0.2	BD	0.07 ± 0.0	7.9 ± 0.2	11.9 ± 0.4	NA	13.6 ± 0.8	NA	98 ± 1	

[a] Biomass yield on glucose (g of biomass/g of glucose consumed).
[b] mmol of glucose consumed per g of biomass/h.
[c] mmol of ethanol produced per g of biomass/h.
[d] mmol of oxygen consumed per g of biomass/h.
[e] mmol of carbon dioxide produced per g of biomass/h.
[f] Single assay measurement.
[g] Mean ± S.D. of two separate chemostat steady states.



regulatory profile	genes changed		
higher in anaerobic	65		
lower in anaerobic	90		
O_2-responsive genes	155		
regulatory profile	aerobic only	aerobic & anaerobic	anaerobic only
higher in C-lim	145	19	35
lower in C-lim	48	14	167
higher in N-lim	19	32	39
lower in N-lim	14	1	6
higher in P-lim	31	31	28
lower in P-lim	12	2	7
higher in S-lim	20	48	13
lower in S-lim	44	5	7
Nutrient specific genes	333	152	302

FIG. 2. **Global transcriptional responses to growth in aerobic and anaerobic macronutrient-limited chemostats.** The genome-wide transcript profiles of *S. cerevisiae* grown under different oxygen availability conditions and limitations (*lim*) for carbon, nitrogen, phosphorus, or sulfur are compared, and the classes of expression profiles are scored. About half of the predicted genome (48%) was either unchanged or not measurable across all eight conditions. The remaining significantly changed genes (3169) were categorized into oxygen-responsive genes (155); genes that responded to macronutrient limitation under solely aerobic conditions (333), solely anaerobic conditions (302), and irrespective of the presence of oxygen (152); and genes with a more complex transcription profile.

some specific observations on the macronutrient limitation-responsive genes.

Anaerobically Up-regulated Genes—Based on a statistically robust, two-laboratory transcriptome analysis of glucose-limited chemostat cultures of *S. cerevisiae*, Piper *et al.* (9) identified 877 transcripts that were differentially expressed in anaerobic and aerobic cultures. These genes were distributed in 133 anaerobically up-regulated and 744 anaerobically down-regulated genes. In our two-dimensional approach, the transcriptional response to oxygen availability of 722 of these genes (82%) depended on the macronutrient limitation regime, and only 155 genes showed a consistent response to anaerobiosis under all four macronutrient limitation regimes (65 up-regulated and 90 down-regulated) (Fig. 3*A*).

Of the 65 anaerobically up-regulated genes, 20 have an as yet poorly defined or unknown biological function. The 45 genes with known function were distributed over the functional categories as follows: metabolism and energy (21 genes), transport (four genes), cell rescue and defense (11 genes), protein synthesis (three genes), and cell wall and organization (six genes) according to the MIPS Database (Fig. 4) (24). A closer inspection reflected the biosynthetic role of molecular oxygen in *S. cerevisiae* (27). Under anaerobic conditions, *S. cerevisiae* is not capable of *de novo* biosynthesis of sterols and unsaturated fatty acids, and therefore, these compounds are required as growth factors under anaerobic conditions (28, 29). Although the an-

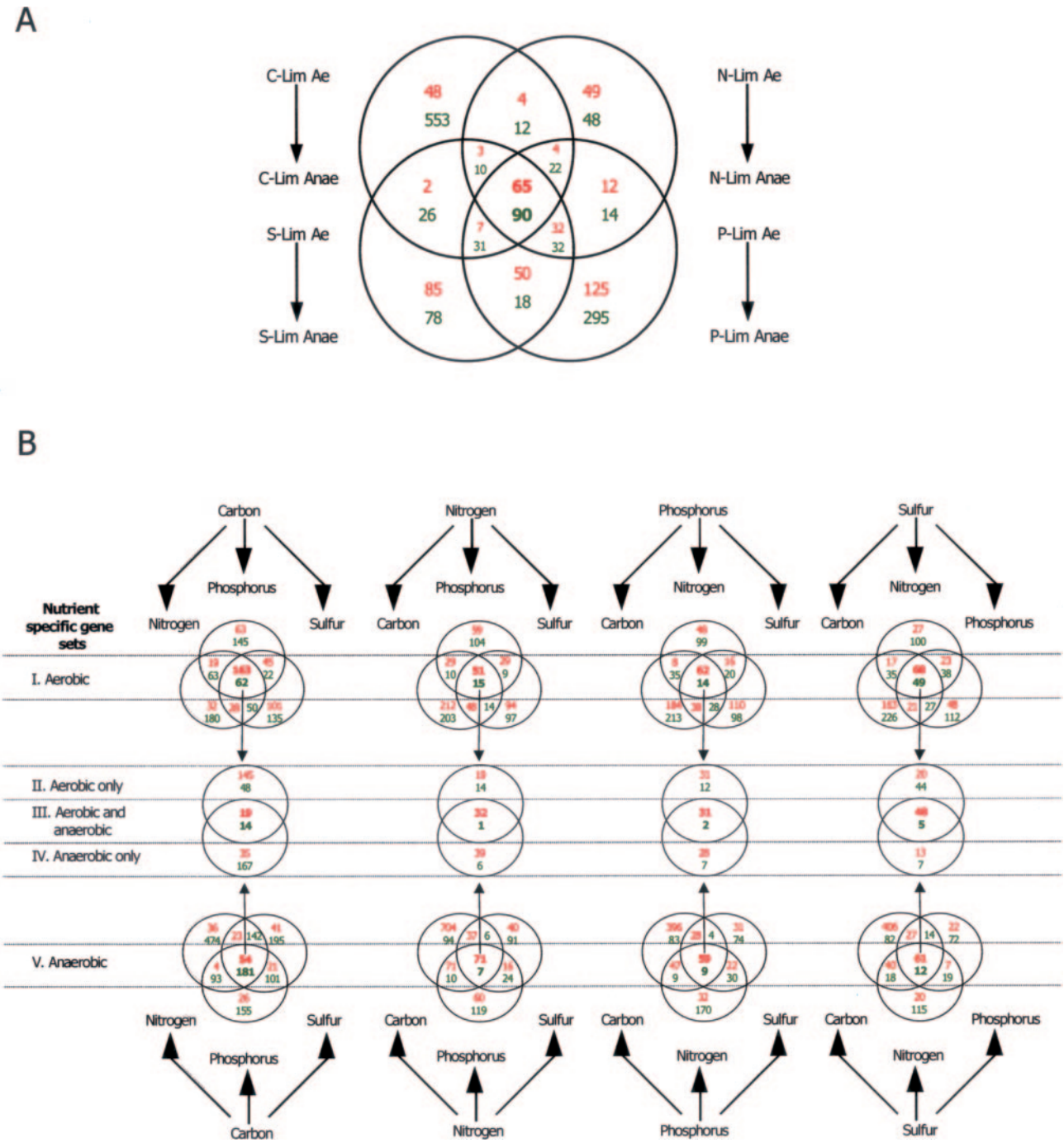


FIG. 3. **Data mining strategy: dissection of the transcriptome response with respect to nutrient limitation and oxygen availability.** *A*, Venn diagram of signature anaerobic genes. *Red* and *green* represent up-regulation and down-regulation, respectively, under anaerobic conditions. Each of the *four circles* corresponds to a cluster of genes that showed a transcriptional response to oxygen availability under one of the four macronutrient limitation regimes. The overlap of the four clusters represents genes that showed a consistent response to oxygen availability irrespective of the nutrient limitation regime. *Lim Ae*, limited aerobic; *Lim Anae*, limited anaerobic. *B*, Venn diagram of macronutrient limitation-responsive genes. The diagram shows pairwise transcriptome comparisons (see Fig. 1) of each macronutrient limitation regime against the other three macronutrient limitation regimes for aerobic and anaerobic cultures. Each *circle* represents the cluster of genes up-regulated (*red*) or down-regulated (*green*) for the reference macronutrient limitation. Sets I and V contain the genes that showed a consistent response to each of the four macronutrient limitation regimes in the three pairwise comparisons under aerobic and anaerobic conditions, respectively. Combination of sets I and V yielded three new subsets of macronutrient limitation-responsive genes. Set III represents signature genes that showed a consistent response to each of the macronutrient limitation regimes under aerobic and anaerobic conditions. Sets II and IV represent genes whose transcriptional response to a single macronutrient limitation regime was specific for aerobic and anaerobic conditions, respectively.

aerobic chemostat cultures were supplied with ergosterol and oleate, 22 of the consistently anaerobically up-regulated genes have been implicated in or associated with sterol or lipid metabolism. Of these genes, *UPC2* and *SUT1* are transcription factors for sterol uptake in yeast, and *PDR11* and *AUS1* (members of the ABC membrane transporter family) have been shown to be involved in sterol uptake for anaerobic growth (30, 31). 13 members of the seripauperin family of possible cell wall mannoproteins (*DAN1*, *DAN2*, *DAN3*, *DAN4*, *TIR1*, *TIR2*, *TIR3*, *TIR4*, *PAU1*, *PAU3*, *PAU4*, *PAU5*, and *PAU6*) that were consistently up-regulated in anaerobic cultures encode mannoproteins. These important determinants of cell wall permeabil-

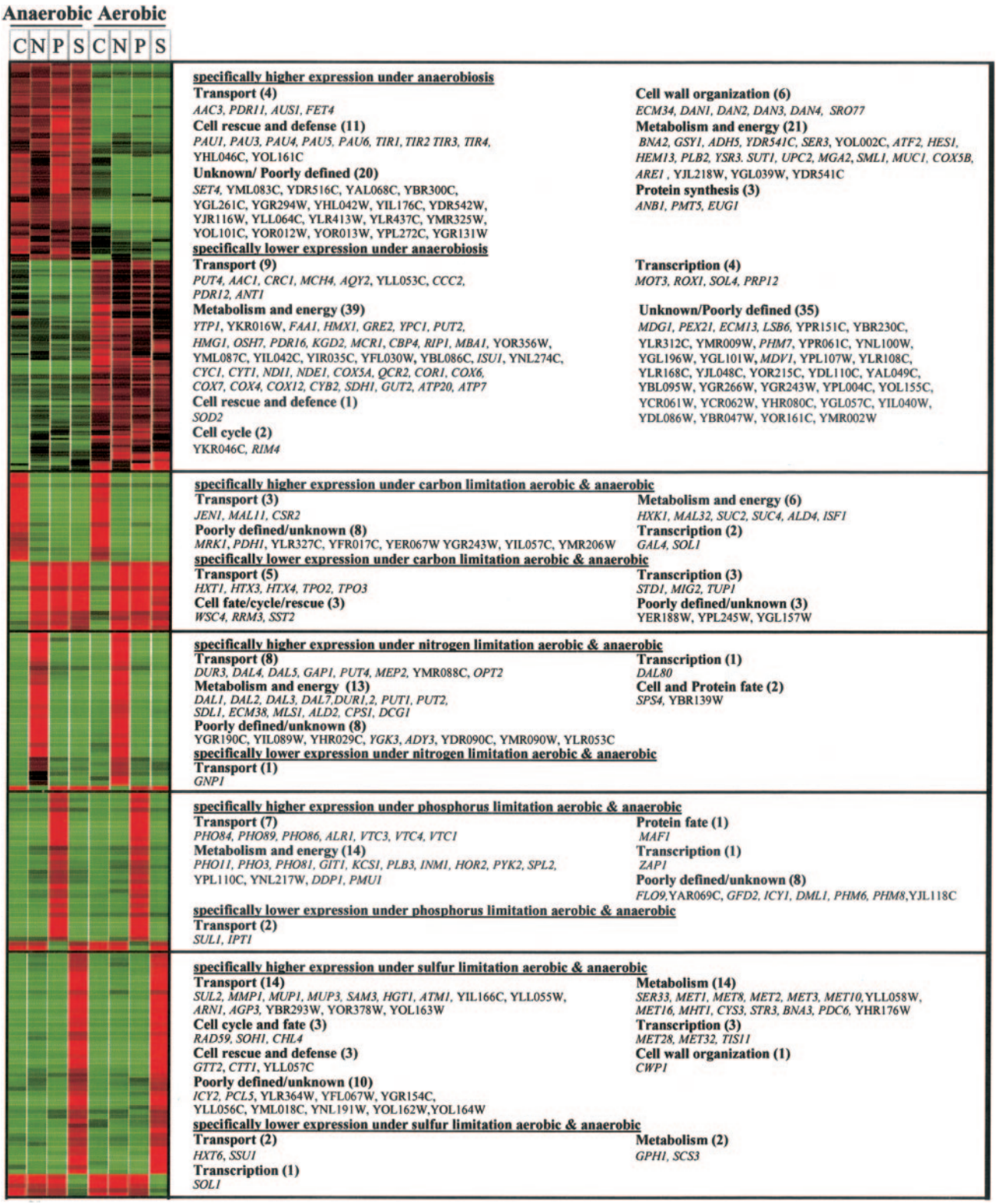


FIG. 4. **Signature genes that respond to a single environmental parameter.** The three independent transcriptome data sets for each condition were averaged and then compared. *Green* (relatively low expression) and *red* (relatively high expression) *squares* are used to represent the transcription profiles of genes deemed specifically changed. The signature genes were sorted by functional categories according to the Comprehensive Yeast Genome Database (24) and the *Saccharomyces* Genome Database (25).

ity during anaerobiosis (32) may be involved in sterol uptake, as recently shown for *DAN1* (30). The *MGA2* gene product regulates the transcription of *OLE1*, which is involved in the biosynthesis of unsaturated fatty acids (33). *HES1*, *ARE1*, *YSR3*, and *PLB2* encode a putative oxysterol-binding protein, an acyl-CoA acetyltransferase, a putative regulator of sphingolipid metabolism, and phospholipase B_2, respectively (34–38). In addition to genes involved in sterol and fatty acid metabolism, *COX5B* and *HEM13* displayed a consistent up-regulation in all anaerobic cultures. *COX5B* encodes the "anoxic subunit" of cytochrome *c* oxidase, which is proposed to be involved in oxygen sensing (39). *HEM13* encodes a cytosolic coproporphy-

TABLE II

Gene coverage of over-represented sequences retrieved from promoters of co-regulated genes

Unless stated otherwise, elements were counted present in a gene promoter only if they occurred at least twice. NS, no significant patterns retrieved by RSA Tools.

Regulatory cluster	Promoter element[a]		Putative-binding protein	Gene coverage			Genome coverage[b]	Range[c]		
	Forward	Reverse								
				%			%			
Specifically higher in anaerobiosis	AAGGCAC[d]	GTGCCTT		38			8	0–3		
	ATTGTTC[d]	GAACAAT	Rox1p	26			12	0–3		
	*dd*ACGAGG[d]	CCTCGT*hh*	Upc2p	40			18	0–2		
	TCGT*wy*AG[d]	CT*rw*ACGA	Upc2p	38			7	0–3		
				Set II[e]	Set III[f]	Set IV[g]		Set II	Set III	Set IV
Specifically higher in C limitation	*d*CCCC*dh*	*dh*GGGG*h*	Mig1p	43	65	25	28	0–5	0–6	0–5
Specifically higher in N limitation	*r*GATAA*s*	*s*TTATC*y*	Gln3p/Gat1p/Dal80p/Gzf3p	11	61	14	6	0–3	0–5	0–3
	CAATGA	TCATTG	Dal82p	11	23	3	13	0–4	0–3	0–2
Specifically higher in P limitation	*m*ACGTG*s*	*s*CACGT*k*	Pho4p	13	58	13	3	0–2	0–6	0–6
Specifically higher in S limitation	GCCACA	TGTGGC	Cbf1p/Met4p/Met28p	5	33	NS	3	0–4	0–5	0–1
	CACGTGA	TCACGTG	Met31p/Met32p	NS	10	NS	2	0–1	0–3	0–1

[a] Redundant nucleotides are as follows: *r* = A or G; *y* = C or T; *s* = G or C; *k* = G or T; *m* = A or C; *w* = A or T; *d* = A, G, or T; and *h* = A, C, or T.
[b] Relative to 6451 open reading frame upstream promoters in the yeast genome according to RSA Tools.
[c] Range of motifs present in each promoter of the specific gene cluster.
[d] Elements counted present in a gene promoter when occurring at least once.
[e] Set I, containing aerobic-only nutrient-specific genes, as in Fig. 3*B*.
[f] Set II, containing aerobic and anaerobic nutrient-specific genes, as in Fig. 3*B*.
[g] Set III, containing anaerobic-only nutrient-specific genes, as in Fig. 3*B*.

rinogen III oxidase and has been described as the first, molecular oxygen-dependent and rate-controlling step of heme biosynthesis (27).

As a further approach to assess the biological significance of the consistent transcriptional responses identified via the two-dimensional approach, we analyzed the enrichment of regulatory motifs in promoter sequences of the oxygen-responsive genes (Figs. 3*A* and 4 and Table II). Four over-represented sequences were recovered from the 65 anaerobically up-regulated gene promoter regions (Table II). At least one of the two overlapping sequences (TCGT*wy*AG or CCTCGT*wy*) was recovered from 34 genes (52%) in the cluster. These sequences are similar to the previously described binding site for Upc2p (CGTTT) (40), a transcription factor whose structural gene itself was consistently up-regulated in the anaerobic cultures. 17 genes (26%) share the element ATTGTTC, which is the known binding site for the anaerobic transcription factor Rox1p (41). We also identified a new motif (AAGGCAC) within this cluster of genes for which no DNA-binding protein has yet been identified. The Upc2p and AAGGCAC motifs showed a remarkable coincidence in the promoters of 12 genes of the cluster (Fig. 5). In the upstream regions of these genes, the Upc2p-binding site is present at −450 to −380, and the AAGGCAC element is present at −360 to −300 (Fig. 5). The conservation of both the distance to the coding region and the distance between the elements strongly suggests biological relevance. 70% of the promoter sequences of the genes that were consistently up-regulated in the anaerobic cultures contain at least one of the three elements discussed above.

Transcriptional Responses to Macronutrient Limitation: Genes Up-regulated upon Phosphate Limitation—The four clusters of genes that were consistently (under aerobic as well as anaerobic conditions) up-regulated in response to growth limitation by a single macronutrient share some conserved features. These involve induction of high affinity uptake systems for the limiting macronutrient, excretion of nutrient-scavenging enzymes to the extracellular medium, induction of systems for mobilization and utilization of intracellular reserves, and induction of systems for transport and assimilation of alternative sources of the limiting nutrient (Fig. 4). This is exemplified by the transcriptional response to phosphorus limitation.

Previous comparison identified 62 up-regulated signature transcripts for aerobic phosphate-limited growth (4). Introducing a second dimension (anaerobic phosphate limitation) resulted in a 50% decrease in the genes composing this cluster. Indeed, 31 genes showed a consistent up-regulation relative to the other macronutrient limitation regimes in aerobic and anaerobic phosphate-limited chemostat cultures. Among these genes, seven are involved in transport, 14 in metabolism, one in protein fate, and one in transcription, and eight have an as yet unknown function according the MIPS Database (24) and the *Saccharomyces* Genome Database (25). 23 of these phosphate limitation-induced genes (74%) could be directly related to phosphorus metabolism. All seven genes classified in the transport category were associated with phosphate transport (*PHO84*, high affinity inorganic phosphate/proton symporter; *PHO89*, high affinity sodium-dependent phosphate transporter (42); *PHO86*, protein associated with the phosphate transport complex (43); *GIT1*, glycerophosphoinositol transporter belonging to the major facilitator superfamily (44); and *VTC1*, *VTC3*, and *VTC4*, subunits of the vacuolar membrane polyphosphate transporter complex (45)). Of the remaining genes in this cluster, several are involved in phosphate mobilization: *PHO11* and *PHO3* encode phosphatases; *HOR2* encodes a glycerol-3-phosphate phosphatase (46, 47); *INM1* encodes an inositol monophosphatase (48); YNL217W encodes a putative metallophosphatase (49); YPL110C encodes a putative glycerophosphoryl-diester phosphodiesterase; *DDP1* encodes a diadenosine-hexaphosphate hydrolase (50); *PLB3* encodes phospholipase B (38); and *PYK2* encodes a glucose-repressed pyruvate kinase (51). The proteins encoded by *PHM6* and *PHM8* are likely to encode proteins involved in phosphate metabolism (45) as well, and their promoter regions exhibit a Pho4p-binding

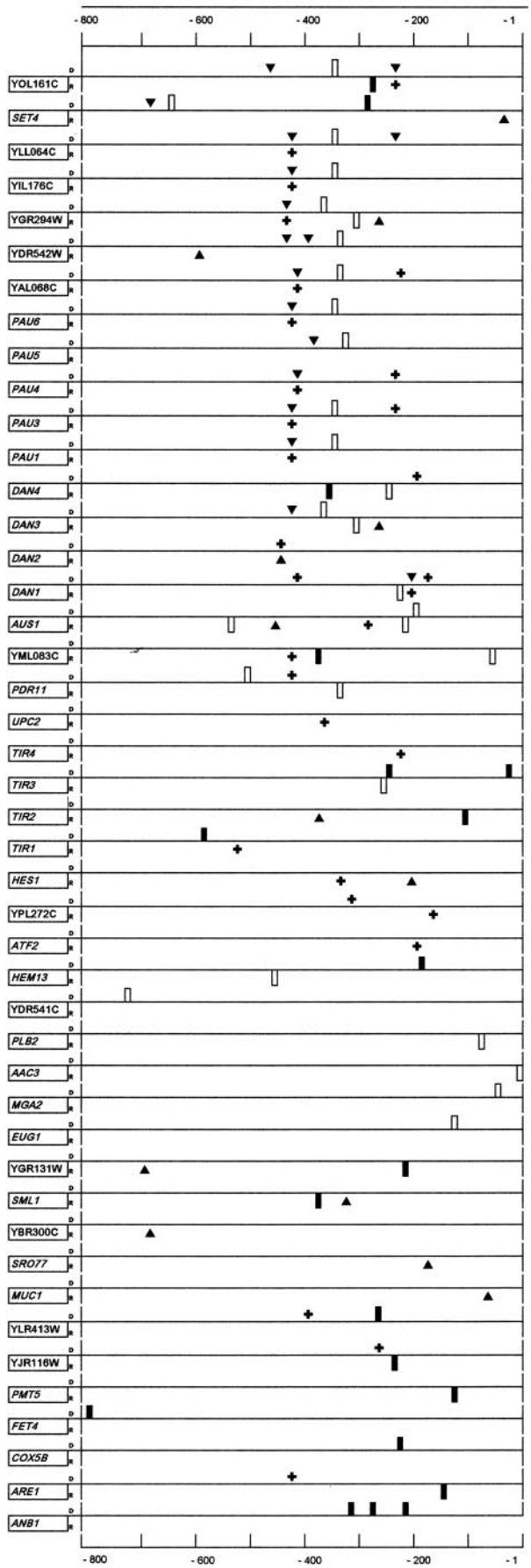


FIG. 5. **Localization of the consensus binding site in promoter sequences of up-regulated genes in the absence of oxygen irrespective of nutrient limitation.** The promoter regions of genes from −800 to −1 were based on the sequences obtained from RSA Tools (23). ▲, Upc2p consensus sequence TCGT*wy*AG; ▼, Upc2p consensus sequence TCGTwyAG found on the Crich stand; +, Upc2p consensus sequence CCTCGT*hh*; ■, Rox1p consensus sequence (ATTGTTC); □, AAGGCAC consensus sequence. Consensus sequences on both strands are indicated. The open reading frames on the Watson strand and on the Crick strand are indicated by *D* and *R*, respectively. [a] Redundant nucleotides are as follows: *r* = A or G; *y* = C or T; *s* = G or C; *k* = G or T; *m* = A or C; *w* = A or T; *d* = A, G, or T; and *h* = A, C, or T.

site. *PHO81* and *SPL2* are presumed inhibitors of the Pho80p-Pho85p cyclin-dependent protein-kinase complex and positive regulators of phosphate-related genes (52). Furthermore, *KCS1*, an inositol-1,2,3,4,5,6-hexaphosphate kinase involved in inositol metabolism (53), was up-regulated. The remaining eight genes in the cluster (25%) could not be directly associated with phosphate metabolism. Interestingly, two of these genes are involved in transcriptional regulation: *ZAP1* encodes a zinc-responsive transcriptional activator (54), and *MAF1* encodes a putative repressor of RNA polymerase III transcription and a common component of multiple signaling pathways in *S. cerevisiae* that sense changes in the cellular environment (55).

In silico promoter analysis of the genes that were consistently up-regulated upon phosphate limitation revealed an over-represented *m*ACGTG*s* motif (present in 58% of the genes in the cluster as opposed to 3% in the *S. cerevisiae* genome). This sequence shows strong similarity to the CACGTG consensus sequence for the binding site of Pho4p (56), the main transcription factor required for expression of the phosphate-related genes (Table II).

Transcriptional Cross-regulation Identified by Two-dimensional Transcriptome Analysis—By combining the transcriptional responses to (an)aerobiosis in cultures subjected to four different macronutrient limitation regimes, it was possible to identify gene clusters that were subjected to transcriptional regulation by two environmental parameters. Identification of such clusters is not possible in conventional one-dimensional pairwise comparisons between cultivation conditions. Eight such clusters (sets II and IV) (Fig. 3*B*) could be assigned. To explore the biological significance of defining these clusters, we will discuss one of these clusters in more detail.

Of the 428 genes that showed a transcriptional response to carbon limitation in our analysis (sets II–IV) (Fig. 3*B*), only 33 genes showed a consistent response to carbon limitation irrespective of the availability of oxygen (set III) (Fig. 3*B*). 193 genes (set II) (Fig. 3*B*) showed a significant transcriptional response only under aerobic conditions. Of the remaining 202 genes (set IV) (Fig. 3*B*), which responded only to carbon limitation in the anaerobic cultures, 167 genes were down-regulated in anaerobic carbon-limited cultures, and 35 genes were up-regulated.

Of the 35 genes that were uniquely up-regulated in anaerobic carbon-limited chemostat cultures at the level of transcription, 21 genes are related to mitochondrial function (Fig. 6, *upper panel*), even though glucose dissimilation in these cultures was completely fermentative. 15 of these mitochondrial function-related genes are involved in oxidative phosphorylation and respiration: *QCR2*, *QCR6*, *QCR7*, and *RIP1* as core subunits of ubiquinol-cytochrome *c* reductase (complex III); *COX4*, *COX5A*, *COX6*, *COX8*, *COX12*, and *COX13* as core subunits of cytochrome *c* oxidase (complex IV); *ATP4*, *ATP15*, and *ATP20* as core subunits of the F_0 subunit of the mitochondrial ATP synthase; *INH1* as the inhibitory subunit of the mitochondrial ATP synthase; and finally, *CYC1* as the predominant aerobic isoform of cytochrome *c*. In addition, three of the four subunits of succinate dehydrogenase (*SDH1*, *SDH2*, and *SDH4*) were significantly up-regulated in the anaerobic carbon-limited cul-

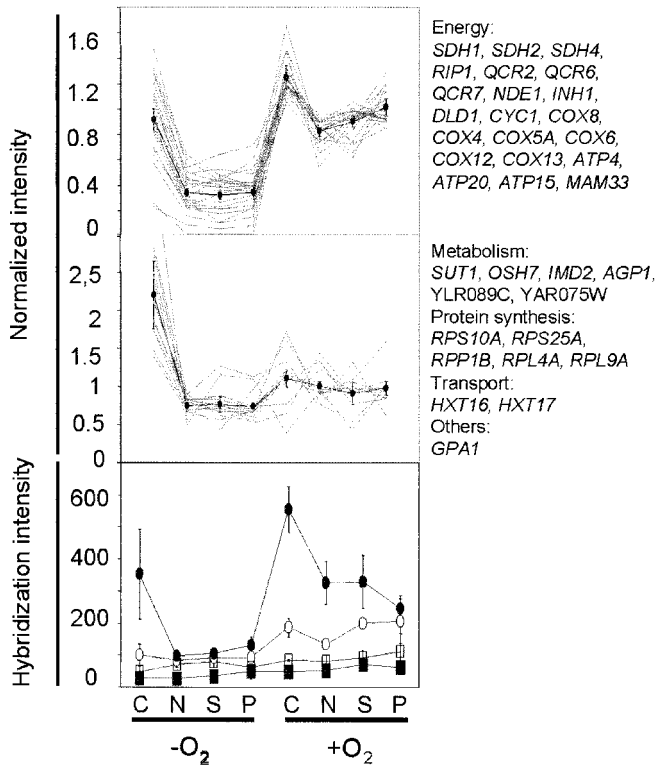


FIG. 6. **Hierarchical regulatory control of gene expression.** *Upper panel*, normalized transcript profiles of mitochondrial function-related genes that clustered with a set of genes that showed a specific transcriptional up-regulation upon carbon limitation in anaerobic cultures. The transcript level across the four conditions for each gene was normalized relative to mean and variance. The data represent the normalized abundance of all transcripts for each cultivation condition, as well as the normalized average abundance of all transcripts of the cluster (*thick black line*). *Error bars* represent S.D. *Middle panel*, normalized transcript profiles of genes belonging to the cluster described for *A* that do not have a (known) relation to mitochondrial function. The data are presented as described for the *upper panel*. *Lower panel*, transcript profiles of the structural genes for the components of the Hap2/3/4/5p complex. *Error bars* represent S.D. ■, *HAP2*; ○, *HAP3*; ●, *HAP4*; □, *HAP5*.

tures. *DLD1* encodes mitochondrial D-lactate-ferricytochrome *c* oxidoreductase (57); *MAM33* encodes a mitochondrial protein required for normal respiratory growth (58); and *NDE1* encodes a mitochondrial, cytosolically directed NADH dehydrogenase (59). The remaining 14 genes of the 35 genes of the discussed cluster were composed of two hexose transporter genes (*HXT16* and *HXT17*), five genes encoding ribosomal proteins (*RSP10A*, *RPS25A*, *RPP1B*, *RPL4A*, and *RPL9A*), and seven genes belonging to different metabolic routes (*SUT1*, *OSH7*, *AGP1*, *IMD2*, YLR089C, YAR075W, and *GPA1*) (Fig. 6, *middle panel*).

The low mRNA levels of these genes in anaerobic chemostat cultures that were limited by nitrogen, phosphorus, or sulfur and thus had a high residual glucose concentration strongly suggest that glucose catabolite plays an important role in their transcriptional regulation. Conversely, under aerobic conditions, the identity of the growth-limiting nutrient did not significantly affect transcription. In fact, closer inspection indicated that, in the aerobic cultures, high transcript levels were observed in all four macronutrient limitation regimes (Fig. 6, *upper panel*). Furthermore, also in the aerobic cultures, the combined expression patterns of these genes suggest a moderate induction under glucose-limited conditions (Fig. 6, *upper panel*). However, the statistical criteria used for the definition of the cluster did not identify this induction as significant.

A simple verbal model to explain these observations is that, for this particular subset of *S. cerevisiae* genes, induction by oxygen supersedes glucose catabolite repression. It is beyond the scope of this work to analyze the molecular basis for this apparent hierarchy in transcriptional regulation. However, several genes of this cluster such as *DLD1*, *QCR2*, *QCR7*, and *CYC1* are known targets of the Hap2/3/4/5p complex (Fig. 6, *upper panel*) (57, 60–62). *In silico* promoter analysis of the 35 genes of this subset revealed a significant over-representation (3-fold) of the ACCAAT*n*A sequence, which overlaps the CCAAT core of the Hap2/3/4/5p-binding site. Furthermore, the transcript level of *HAP4*, known as the regulatory subunit of the Hap2/3/4/5p complex, correlated with the expression pattern within this subset of genes (Fig. 6, *lower panel*). Interestingly, *HAP4* expression is reported to be glucose-repressible, being up-regulated after the diauxic shift and during growth on respiratory carbon sources (63). Further research is required to investigate which factors, in addition to regulation by the Hap2/3/4/5p complex, are involved in oxygen regulation of these genes and which factors determine the relative impact of glucose repression and oxygen induction.

DISCUSSION

DNA Microarrays as a Diagnostic Tool for Biotechnology—A detailed understanding of the environmental stimuli to which microorganisms are exposed in industrial fermentation processes is invaluable for rational design and optimization of such processes. DNA microarrays provide an interface that allows, in principle, the use of the microorganisms themselves as the ultimate "biosensor." An unequivocal coupling between relevant environmental parameters and transcriptional responses is essential for this application of DNA microarrays. An important concept in this context is that of the signature transcript, a transcript whose levels specifically increase (or decrease) in response to a single environmental stimulus.

This study indicates that, in general, robust signature transcripts cannot be identified by varying the process parameter of interest against a single constant experimental background (one-dimensional transcriptome analysis). Instead, identification of robust signature transcripts requires that transcriptional responses to an environmental parameter be analyzed against multiple experimental backgrounds. For example, the sets of signature transcripts for (an)aerobiosis and growth limitation by four macronutrients that were previously established in one-dimensional transcriptome comparisons (4, 9, 11, 12) were considerably reduced in size by the two-dimensional approach followed in this study. Chemostat cultivation is an indispensable tool for this combinatorial approach, as, in contrast to batch cultivation, it allows the manipulation of individual culture parameters while other relevant parameters, including the specific growth rate, are kept constant (4, 9, 11, 13).

Although this study covers only a minute fraction of the staggering diversity of environmental conditions to which *S. cerevisiae* may be exposed in nature and in industry, it clearly demonstrates the complexity of transcriptional regulation. In real life, transcriptional responses of cells are influenced by hundreds of extracellular signals. The interplay of these signals results in a multidimensional space in which each possible combination of signals results in a unique transcriptome. It is therefore to be anticipated that the number of robust signature transcripts will decrease further when, in addition to nutrient limitation and oxygen availability, other chemical or physical process parameters are included.

The significance of the combinatorial nature of the regulation of gene expression extends beyond *S. cerevisiae* and industrial biotechnology. For example, in the medical field, it is to be ex-

pected that the transcriptional profiles coupled to a disease or pharmacological efficacy will be equally sensitive to other stimuli and variance received by the cells. Although, in a statistical sense, such effects may be averaged out when the identification of disease-correlated signature transcripts is based on large numbers of healthy and ill individuals (64), this does not exclude a strong impact of transcriptional "cross-talk" in individual patients that have been exposed to special circumstances.

Unraveling Transcriptional Regulation—Despite the combinatorial nature of transcriptional regulation, identification of unequivocal signature transcripts should be possible when mechanisms of transcriptional regulation are fully understood. Ideally, signature transcripts should be encoded by genes that respond to a single transcriptional regulator protein whose expression and activity are uniquely dependent on a single environmental stimulus. Identification of such genes and regulators requires detailed knowledge of the regulons and recognition sequences of all relevant transcriptional regulators. Such knowledge is also essential for rational and predictable reprogramming of transcriptional regulation to improve the performance of industrial microorganisms.

Even for well studied organisms like *S. cerevisiae*, the physiological roles of many transcriptional regulators, as well as the sequence motifs they recognize, remain to be identified. The two-dimensional chemostat-based approach proposed in this study provides a powerful new tool for unraveling transcriptional regulation networks. This is exemplified by the enrichment of regulatory motifs in the consistently anaerobically induced transcripts (Table II). Clearly, regulation by known transcriptional regulators (relief of *ROX1* repression and transcriptional activation by *UPC2*) (30, 65, 66) is not sufficient to account for the transcriptional response of all 65 genes that were consistently up-regulated under anaerobic conditions. Indeed, our study strongly suggests that at least a third factor, which recognizes an AAGGCAC motif, is involved in transcriptional regulation by oxygen availability. This motif had gone unnoticed in a previous one-dimensional aerobic/anaerobic comparison (12). In general, a combinatorial analysis of the transcriptional responses to environmental stimuli is likely to increase enrichment of relevant regulatory elements and facilitate their identification.

The approach used in this study also allows statements on the hierarchy of transcriptional regulation. This is exemplified by a subset of genes related to mitochondrial function. Under anaerobic conditions, these genes were regulated primarily by glucose repression/derepression. However, under aerobic conditions, a high transcript level was observed even under excess glucose conditions. Together, these data indicate that, in the aerobic cultures, oxygen regulation supersedes glucose repression (Fig. 6). By expanding data sets and combining them with an *in silico* analysis of promoter structure, combinatorial analysis of transcriptomes can accelerate the unraveling of transcriptional regulation networks.

Functional Analysis—Assigning physiological functions to "unknown function" genes still poses a major challenge in the postgenomic era. By identifying groups of genes that appear to be coexpressed (67), DNA microarrays can guide functional analysis. Indeed, many studies have correlated mRNA levels to cultivation conditions. However, even when chemostat cultivation is used to change only a single environmental parameter, pairwise comparisons characteristically lead to large numbers of target genes, complicating functional analysis (4, 9, 10, 12). Moreover, in a recent study on the genome-wide transcriptional responses to low temperature (68), a very poor correlation was observed between transcriptional responses of genes and the phenotype of the corresponding null mutants at low temperature.

Compared with previous one-dimensional studies, the combinatorial approach followed in this study led to a clear enrichment in our "robust response sets" of (i) genes with known function related to the environmental status under study (Fig. 4) and/or (ii) genes with relevant regulatory elements (Table II). By implication, also the unknown function genes found in the corresponding data sets are more likely to have a direct functional relationship to the corresponding nutritional/environmental status. We are currently testing this hypothesis for the subset of genes that showed a consistent up-regulation under anaerobic conditions.

Among the robust response signature genes identified in this study, 38% do not have a clearly established biological function (Fig. 4). It is noteworthy that some of these (YJL118C, YAR069C, and YGR190C) belong to a group of open reading frames for which it has recently been proposed that they should be discarded from the yeast genome directory based on genomic comparison of *S. cerevisiae*, *Saccharomyces bayanus*, *Saccharomyces mikatae*, and *Saccharomyces paradoxus* (69). The observation that three of these genes showed a consistent response to phosphate limitation (YJL118C and YAR069C) or nitrogen limitation (YGR190C) strongly suggests they are *bona fide*, biologically relevant genes.

Provided that yeast strains and cultivation procedures are standardized, DNA microarray analysis of chemostat cultures is well reproducible in different laboratories (9). We propose that a multi-laboratory effort to build an extensive, chemostat-based, "multidimensional" gene expression data base is an invaluable research tool for functional analysis of the *S. cerevisiae* genome and for yeast system biology. Obviously, such a data base should not necessarily be confined to transcriptome data, but could also cover other levels of information.

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Culture limiting nutrient	Oxygen availability	Average coefficient of variation	ACT1
Carbon	Aerobic	0.18	2489 ± 81
Nitrogen	Aerobic	0.14	2265 ± 106
Phosphorus	Aerobic	0.21	2314 ± 266
Sulfur	Aerobic	0.13	2172 ± 249
Carbon	Anaerobic	0.27	3118 ± 319
Nitrogen	Anaerobic	0.19	2287 ± 363
Phosphorus	Anaerobic	0.17	2517 ± 101
Sulfur	Anaerobic	0.15	2346 ± 249

Genes below detection limits

Probe Set	Gene name	systematic name	functional description	cellular function	C-Lim Anaerobic 1	C-Lim Anaerobic 2	C-Lim Anaerobic 3	N-Lim Anaerobic 1
					Signal	Signal	Signal	Signal
6657_at		YDL163W	YDL163W questionable ORF	UNKNOWN	0.6	0.1	0.6	0.3
8356_at		YOR199W	YOR199W questionable ORF	UNKNOWN	0.6	0	0.5	0.2
4495_at	A ECM12	YHR021W	YHR021W ExtraCellular Mutant	CELL WALL MAINTENANCE	0.3	1.6	0.2	0.3
11116_at		YJL086C	YJL086C questionable ORF	UNKNOWN	0.4	0.2	0.4	0.3
6960_at		YCL065W	YCL065W questionable ORF	UNKNOWN	0.4	1.6	0.7	0.1
5655_n_at	ERG28	YER044C	YER044C Required for full sporulation, Dispensable for axial cores but requin	UNKNOWN	1.2	1.5	0.1	1
5248_at	EDC1	YGL222C	YGL222C hypothetical protein	UNKNOWN	0.4	0.3	0.8	0.3
10308_at		YLR012C	YLR012C hypothetical protein	UNKNOWN	0.3	0.1	0.4	0.3
9470_at		YMR158W	YMR158W questionable ORF	UNKNOWN	0.6	0.2	0.6	0.7
8878_s_at		YNL017C	YNL017C hypothetical protein	UNKNOWN	0.4	0.1	0.3	0.2
3936_at	SUC4	SUC4	SUC4 invertase (sucrose hydrolyzing enzyme)	SUCROSE UTILIZATION	0.2	0	0.3	0.2
9965_at	SPO77	YLR341W	YLR341W hypothetical protein	UNKNOWN	0.7	0.1	0.2	1.1
4906_at		YGR115C	YGR115C questionable ORF	UNKNOWN	0.6	0.2	0.8	0.4
5421_i_at		YFL067W	YFL067W similarity to mouse period clock protein	UNKNOWN	1.1	0.2	0.3	0.1
9674_at	AMD1	YML035C	YML035C questionable ORF	UNKNOWN	0.4	0.7	0.3	0.5
6658_at		YDL162C	YDL162C hypothetical protein	UNKNOWN	0.5	0.3	1.2	1.6
7859_at	MEI5	YPL121C	YPL121C Meiotic protein required for synapsis and meiotic recombination	MEIOSIS, SYNAPSIS AND RECOMBINATION	2.4	0.1	1.3	0.6
10578_at		YKR015C	YKR015C similarity to hypothetical protein YJL043w	UNKNOWN	2.1	1.6	2.1	0.2
11383_at		YAL064C	YAL064C putative pseudogene	UNKNOWN	0.5	0.4	1.8	0.2
5311_at		YFR057W	YFR057W weak similarity to Cha4p	UNKNOWN	0.8	0.2	0.5	0.3
5628_at		YER097W	YER097W weak similarity to ribosomal S3 proteins	UNKNOWN	0.2	2.8	0.7	1.1
5808_i_at	C	YEL076W-C	YEL076W-C questionable ORF	UNKNOWN	3	0.1	0.5	0.1
3934_at	RTM1	RTM1	RTM1 Protein that confers resistance to molasses	UNKNOWN	0.2	0.2	0.2	0.2
6954_at	LSR1	LSR1	LSR1 snRNA	MRNA SPLICING	0.4	0.1	0.3	0.2
8195_at	MEK1	YOR351C	YOR351C mRNA is induced in meiosis, encodes a meiosis-specific serine\/th	MEIOSIS	0.9	0.2	2.3	1.3
10309_at	GAT3	YLR013W	YLR013W weak similarity to nitrogen regulatory proteins	UNKNOWN	3.1	0.1	0.6	0.4
3957_r_at	Q0220	Q0220	F1F0-ATPase complex, F0 subunit 8 Found forward in NC_001224 between :	ATP SYNTHESIS	0.6	0	1.8	1
4332_at		YHR131W	YHR131W questionable ORF	UNKNOWN	3.2	0.2	0.5	0.2
5374_at		YFL013W	YFL013W questionable ORF	UNKNOWN	2.9	0.8	0.6	0.6
8141_at		YOR387C	YOR387C strong similarity to YGL258w	UNKNOWN	0.8	0.1	2.9	2.2
4325_at		YHL046W	YHL046W questionable ORF	UNKNOWN	1.5	0.2	0.2	1.7
5205_at	SAE2	YGL175C	YGL175C involved in meiotic recombination and chromosome metabolism	MEIOSIS, RECOMBINATION	3.2	0.3	0.2	0.5
6931_at		YCL046W	YCL046W questionable ORF	UNKNOWN	1	0.3	0.2	1.7
4208_at		YIL102C	YIL102C strong similarity to YIL014c-a	UNKNOWN	0.3	0.1	0.4	0.7
4741_at		YGR265W	YGR265W questionable ORF	UNKNOWN	0.7	0.5	2.9	2.2
8301_at	SNR17A	YOR235W	YOR235W encodes snRNA U3, SNR17B also encodes snRNA U3	UNKNOWN	3.4	0.3	0.4	1.2
8525_at	SLG1	YOR008C	YOR008C Killed In Mutagen, reduced growth in diepoxybutane and\/or mitom	SIGNALING, STRESS RESPONSE AND CELL WAL	0.4	0.2	3.5	0.4
9991_at	VPS65	YLR322W	YLR322W questionable ORF	UNKNOWN	0.2	0.2	0.5	0.5
9053_at		YNL205C	YNL205C questionable ORF	UNKNOWN	0.2	0.1	0.7	0.4
9960_at		YLR379W	YLR379W questionable ORF	UNKNOWN	2.1	0.3	0.4	0.7
6164_at		YDR290W	YDR290W questionable ORF	UNKNOWN	0.6	0.1	0.5	0.2
6455_s_at	ENA2	YDR039C	YDR039C plasma membrane protein\; putative Na+ pump\; P-type ATPase	TRANSPORT	0.1	1.2	0.2	0.6
5197_at	MND1	YGL183C	YGL183C hypothetical protein	UNKNOWN	0.2	0.1	0.1	1.3
6453_at	ENA5	YDR038C	YDR038C P-type ATPase involved in Na+ efflux	TRANSPORT	0.3	1.5	0.6	0.2
5530_at		YER181C	YER181C questionable ORF	UNKNOWN	0.5	0.3	3.9	1.6
8606_at		YOL046C	YOL046C questionable ORF	UNKNOWN	0.3	0.1	3.4	0.2
4557_at		YHL005C	YHL005C hypothetical protein	UNKNOWN	0.2	1.1	0.9	1.3
8715_at		YOL166C	YOL166C hypothetical protein	UNKNOWN	1.2	2.4	0.7	0.4
5233_at		YGL235W	YGL235W questionable ORF	UNKNOWN	1.5	0.4	0.7	0.4
8385_at	FYV12	YOR183W	YOR183W hypothetical protein	UNKNOWN	2.7	1.4	0.7	0.3
6800_at	RDS1	YCR106W	YCR106W Transcription regulator	UNKNOWN	0.6	0.2	2.9	0.3
6130_at		YDR344C	YDR344C hypothetical protein	UNKNOWN	0.6	0.8	1.1	4.2
10371_at	SDC25	YLL017W	YLL017W maybe part of SCD25	UNKNOWN	2.4	0.2	4.3	0.3
9093_at	MER1	YNL210W	YNL210W encodes protein with RNA-binding motifs required for MRE2-deper	MEIOSIS, MER2 MRNA SPLICING	2.4	0.1	0.3	0.6
4460_i_at	IRE1	YHR079C	YHR079C Ire1p is a transmembrane protein that has both serine-threonine ki	PROTEIN FOLDING	4.3	1.3	1.6	0.7
8034_at		YPL261C	YPL261C questionable ORF	UNKNOWN	1.7	0.3	2.2	3.2
6101_at		YDR360W	YDR360W questionable ORF	UNKNOWN	0.5	0.2	1.5	0.8
6037_at		YDR431W	YDR431W questionable ORF	UNKNOWN	0.7	1.7	0.5	2.1
5949_at	API2	YDR525W	YDR525W hypothetical protein		0.7	3.8	4.4	0.1
10074_at		YLR269C	YLR269C questionable ORF	UNKNOWN	4.5	2.1	0.7	0.9
9340_at		YMR290W	YMR290W questionable ORF	UNKNOWN	1.1	1.8	0.5	2.7
7554_at	ARR3	YPR201W	YPR201W Arsenic-resistance protein, member of the arsenical resistance-3 (	STRESS	4.2	1.2	0.5	1.5
8853_at		YNR005C	YNR005C questionable ORF	UNKNOWN	3.8	0.1	2.4	2
10616_at		YKL036C	YKL036C questionable ORF	UNKNOWN	0.4	0.2	0.5	3.3
8333_at	MCT1	YOR221C	YOR221C malonyl-CoA:ACP transferase	FATTY ACID METABOLISM	2.2	0.1	0.6	2.4
6755_i_at	SRD1	YCR018C	YCR018C hypothetical protein	RRNA PROCESSING	0.4	1.8	0.2	1.3
10876_at		YJR128W	YJR128W questionable ORF	UNKNOWN	0.7	1	0.6	1.1
5501_at		YER068C	YER068C questionable ORF	UNKNOWN	1.2	3	4.6	1.1
11300_at		YAR047C	YAR047C predicted nuclear targeting signal	UNKNOWN	0.3	0.2	0.6	1.1
7816_at		YPL073C	YPL073C questionable ORF	UNKNOWN	3.2	0.5	0.3	0.6
7443_at	BRN1	YBL097W	YBL097W Subunit of condensin protein complex required for proper chromos	CHROMATIN STRUCTURE	1.6	0.9	0.8	0.8
4146_at		YIL025C	YIL025C weak similarity to E,gracilis RNA polymerase subunit	UNKNOWN	0.6	0.2	0.5	3
6417_at		YDR048C	YDR048C questionable ORF	UNKNOWN	3.9	0.1	3	1.2
6360_at	ECM18	YDR125C	YDR125C ExtraCellular Mutant	CELL WALL MAINTENANCE	3.7	0.4	0.4	1.3
6382_at		YDR102C	YDR102C hypothetical protein	UNKNOWN	0.4	0.1	0.4	2.2
6014_at		YDR455C	YDR455C questionable ORF	UNKNOWN	3.8	0.3	0.2	0.4
10682_at		YKL102C	YKL102C hypothetical protein	UNKNOWN	1.6	0.2	4.8	1.5
3956_i_at	Q0220	Q0220	F1F0-ATPase complex, F0 subunit 8 Found forward in NC_001224 between :	ATP SYNTHESIS	3.5	1.1	4.8	0.1
5264_at	ZIP2	YGL249W	YGL249W Required for 'ZIPpering' up meiotic chromosomes during chromos	MEIOSIS, SYNAPSIS	2.7	2.1	2.7	0.2
7274_at	PHO5	YBR093C	YBR093C Acid phosphatase, repressible	PHOSPHATE METABOLISM	0.7	1.4	1.3	1.5
4329_at		YHR056W	YHR056W questionable ORF	UNKNOWN	1.5	0.4	1.3	4.7
6252_at	BUD26	YDR241W	YDR241W questionable ORF	UNKNOWN	0.5	0.1	0.6	0.3
5309_at		YFR056C	YFR056C questionable ORF	UNKNOWN	0.8	0.2	3	0.1
8972_at		YNL105W	YNL105W questionable ORF	UNKNOWN	4.9	0.6	4.7	1.9
5185_at	HOS2	YGL194C	YGL194C Protein with similarity to Hda1p, Rpd3p, Hos1p, and Hos3p	CHROMATIN STRUCTURE	1	0.1	0.5	1
11381_at		YAL065C	YAL065C putative pseudogene	UNKNOWN	3.6	1.4	0.5	0.5
5736_at		YEL010W	YEL010W hypothetical protein	UNKNOWN	0.3	3.2	1.3	4.1
4041_at		YIR020C	YIR020C hypothetical protein	UNKNOWN	1	3.8	0.4	0.3
6326_at	VPS61	YDR136C	YDR136C questionable ORF	UNKNOWN	0.8	0.3	2.5	0.4
11215_at		YJL211C	YJL211C questionable ORF	UNKNOWN	0.3	0.6	0.6	1.2
5604_at		YER119C	YER119C questionable ORF	UNKNOWN	3.5	0.4	0.8	0.5
6878_at	RER1	YCL001W	YCL001W similarity to Dom34p	UNKNOWN	0.5	0.2	0.6	1
11231_at		YJL195C	YJL195C questionable ORF	UNKNOWN	1.3	0.9	0.7	2.4
6518_at		YDL034W	YDL034W questionable ORF	UNKNOWN	0.6	1.7	0.3	0.7
10004_at		YLR334C	YLR334C questionable ORF	UNKNOWN	0.5	0.5	0.2	1.1
4389_at	SPS100	YHR139C	YHR139C hypothetical protein	UNKNOWN	5	1.8	0.5	1.1
9945_at		YLR366W	YLR366W hypothetical protein	UNKNOWN	0.4	0.3	5.1	0.6
5078_at		YGL074C	YGL074C questionable ORF	UNKNOWN	0.8	1.9	0.4	0.5
3959_at	Q0230	Q0230	F1F0-ATPase complex, FO A subunit Found forward in NC_001224 between	ATP SYNTHESIS	0.7	1.6	0.5	3.6
7225_at		YBR134W	YBR134W questionable ORF	UNKNOWN	0.4	0.1	0.4	3.2
8782_at	PDR18	YNR070W	YNR070W strong similarity to Snq2p	UNKNOWN	0.4	1.4	0.2	0.4
9715_at		YML084W	YML084W hypothetical protein	UNKNOWN	0.8	0.1	5.5	0.5
3935_at	STRP	STRP	STRP Tropomyosin-related protein with transmembrane domain and basic C-	UNKNOWN	0.3	3	5.5	0.3
3854_f_at		YKL225W	YKL225W strong similarity to Gin11p, YKL225w and other subtelomeric enco	UNKNOWN	4.4	4.4	2.6	0.7
10109_at		YLR217W	YLR217W questionable ORF	UNKNOWN	2.8	0.1	5.1	0.3
7720_at	SMK1	YPR054W	YPR054W MAP kinase	SPORULATION	0.4	0.4	3	2.3
6928_at		YCL048W	YCL048W strong similarity to sporulation-specific protein Sps2p	UNKNOWN	4.4	0.4	4.4	5.6
10356_at		YLL030C	YLL030C hypothetical protein	UNKNOWN	5.2	0.6	5.6	0.9
4977_at		YGR051C	YGR051C questionable ORF	UNKNOWN	2.1	0.6	1.4	3.5
6750_i_at		YCL075W	YCL075W TY5-1	UNKNOWN	0.3	3	4	1
7777_at	ECM23	YPL021W	YPL021W ExtraCellular Mutant\; similar to SRD1	CELL WALL MAINTENANCE	5.7	2.4	0.3	0.4
8783_at		YNR071C	YNR071C strong similarity to UDP-glucose 4-epimerase Gal10p	UNKNOWN	5.6	0	2.8	0.2
5354_at		YFR012W	YFR012W similarity to hypothetical protein YOL019w	UNKNOWN	0.3	0.4	1.8	0.9
10549_at		YKR032W	YKR032W hypothetical protein	UNKNOWN	1.8	0.8	0.9	1
4950_at		YGR069W	YGR069W questionable ORF	UNKNOWN	1.7	1.1	4.4	0.7
5399_at		YFL032W	YFL032W questionable ORF	UNKNOWN	2	0.1	1.7	0.8
4749_at		YGR273C	YGR273C similarity to hypothetical protein YMR295c	UNKNOWN	1.1	0.6	3.2	2.6
7648_at		YPR116W	YPR116W hypothetical protein	UNKNOWN	1.3	2.8	5.1	3.6
3544_at		YBL108W	YBL108W strong similarity to subtelomeric encoded proteins	UNKNOWN	0.2	0.2	5.8	1
11252_s_at		YJL220W	YJL220W questionable ORF	UNKNOWN	2.6	3.3	0.3	3.7
4552_at		YHL010C	YHL010C similarity to C,elegans hypothetical protein	UNKNOWN	2.9	0.2	1.6	2.2
8502_at		YOR029W	YOR029W hypothetical protein	UNKNOWN	1.2	0.6	1.3	0.7
7187_at	PCH2	YBR186W	YBR186W Putative ATPase	MEIOSIS, CHECKPOINT	3.1	1.4	3	3
6198_at		YDR278C	YDR278C hypothetical protein	UNKNOWN	5.1	0.3	2.6	3.6
4034_at		YIR020W	YIR020W hypothetical protein	UNKNOWN	1	0.4	5.2	3.1
11140_at		YJL107C	YJL107C similarity to hypothetical S, pombe protein	UNKNOWN	5.4	0.2	2.7	3.2
6096_at		YDR355C	YDR355C questionable ORF	UNKNOWN	0.7	0.4	1	3.8
11375_at		YAL035C	YAL035C questionable ORF	UNKNOWN	0.4	1.3	0.3	0.5
6476_at		YDR015C	YDR015C hypothetical protein	UNKNOWN	5.8	0.7	1.5	1.6
11323_at	TFC3	YAL001C	YAL001C transcription factor tau (TFIIIC) subunit 138	TRANSCRIPTION	0.2	0.1	0.1	5.9
9920_at		YLR385C	YLR385C hypothetical protein	UNKNOWN	2.7	0.2	4.5	0.6
5156_at		YGL132W	YGL132W questionable ORF	UNKNOWN	2.2	3.6	1.3	3.1
5693_at	KRE29	YER038C	YER038C hypothetical protein	UNKNOWN	2.6	2.3	0.9	3.8
10486_s_at		YKR105C	YKR105C strong similarity to Sge1p and hypothetical protein YCL069w	UNKNOWN	3.9	2.1	4.2	1.2
4533_at	SPO13	YHR014W	YHR014W Encodes a 33,4 kDa basic protein that localizes to the nucleus, Th	MEIOSIS	5.4	3.3	4.1	4.5
6126_at		YDR340W	YDR340W questionable ORF	UNKNOWN	3.4	0.8	0.5	0.1
9944_at		YLR365W	YLR365W weak similarity to Udf2p	UNKNOWN	3.6	1.6	3.8	2.2
4039_at		YIL066W	YIL066W questionable ORF	DNA REPAIR	3.9	0.6	1.1	6.2
7198_at	SPP381	YBR152W	YBR152W U4\/U6,U5-associated snRNP protein\; contains a PEST proteolys	MRNA PROCESSING (PUTATIVE)	0.4	0.1	0.6	3.9
7346_at		YBR032W	YBR032W hypothetical protein	UNKNOWN	6.2	3.6	5.4	0.2
9741_at		YML102C	YML102C questionable ORF	UNKNOWN	1.9	1.5	2.1	1
8570_at		YOL037C	YOL037C questionable ORF	UNKNOWN	4.4	0.1	0.7	1.1
5505_at	BRR2	YER172C	YER172C hypothetical protein	MRNA SPLICING	0.6	0.4	4	0.7
5229_at		YGL239C	YGL239C questionable ORF	UNKNOWN	0.3	0.6	6.3	2.2
4257_at	TID3	YIL144W	YIL144W Dmc1p interacting protein	CYTOSKELETON	2.2	0.8	0.9	2.2
11045_at		YJL022W	YJL022W questionable ORF	UNKNOWN	0.6	0.2	0.4	2.6
6796_at		YCR101C	YCR101C strong similarity to Pep1p	UNKNOWN	0.2	0.2	0.2	0.1
5151_at		YGL138C	YGL138C hypothetical protein	UNKNOWN	0.1	0	0.5	0.4
6829_at		YCR041W	YCR041W questionable ORF	UNKNOWN	6.4	1.2	0.2	2.5
3983_at	Q0085	Q0085	Q0085 cytochrome-c oxidase subunit II	RESPIRATION	5	2.1	0.7	1.3
8778_at		YNR066C	YNR066C strong similarity to Pep1p	UNKNOWN	1.2	2.6	0.5	5.3
11198_at		YJL182C	YJL182C questionable ORF	UNKNOWN	1.8	0.2	6.5	1
8258_at		YOR282W	YOR282W questionable ORF	UNKNOWN	1.2	0.5	1.3	2.3
5207_at		YGL218W	YGL218W questionable ORF	UNKNOWN	0.7	0	0.8	1.4
8785_at		YNR074C	YNR074C weak similarity to B,subtilis nitrite reductase (nirB)	UNKNOWN	5.3	0.8	4.5	0.4
11380_at		YAL066W	YAL066W hypothetical protein	UNKNOWN	3.2	2.1	4.2	0.6
4550_at		YHL012W	YHL012W UDP Glucose pyrophosphorylase	UNKNOWN	1	0.1	1	0.4
11014_at		YJL007C	YJL007C hypothetical protein	UNKNOWN	6.2	0.5	6.6	4.4
9620_at		YML003W	YML003W hypothetical protein	UNKNOWN	4.9	0.5	4.5	2.9
9652_at		YML013C	YML013C questionable ORF	UNKNOWN	4.5	0.6	1.5	5.5
6181_r_at	HNT2	YDR305C	YDR305C Yeast member of the Histidine Triad protein family (HIT)	UNKNOWN	4.4	1.3	4.8	2.3
3855_s_at		YKL223W	YKL223W strong similarity to subtelomeric encoded proteins	UNKNOWN	5.1	2.7	6.6	0.4
4142_at		YIL029C	YIL029C strong similarity to hypothetical protein YPR071w	UNKNOWN	1.2	2	4.7	2.7
5177_at	RCK1	YGL158W	YGL158W Serine\/threonine protein kinase	UNKNOWN	1	0.2	0.4	2.2
4819_at		YGR164W	YGR164W questionable ORF	UNKNOWN	0.7	1.2	0.1	0.3
11382_at		YAL064W	YAL064W putative pseudogene	UNKNOWN	3.7	1.6	2.5	2
4904_at		YGR114C	YGR114C questionable ORF	UNKNOWN	4.6	2.3	4.8	1.7
5946_at	SPS2	YDR522C	YDR522C Middle\/late gene of meiosis	MEIOSIS	0.6	0.5	0.6	0.8
6955_s_at		YCL076W	YCL076W putative pseudo-TY5	UNKNOWN	1.6	0.6	0.6	1.6
5028_at		YGL034C	YGL034C questionable ORF	UNKNOWN	2.5	0.7	6.8	0.7
8189_at		YOR345C	YOR345C questionable ORF	UNKNOWN	0.9	0.4	1.1	0.6
4461_r_at	IRE1	YHR079C	YHR079C Ire1p is a transmembrane protein that has both serine-threonine ki	PROTEIN FOLDING	5.1	1.3	0.7	5.6
6592_at		YDL094C	YDL094C questionable ORF	UNKNOWN	0.3	1.2	0.3	1
4885_at		YGR139W	YGR139W questionable ORF	UNKNOWN	4.4	1.8	0.8	2.2
5239_at		YGL230C	YGL230C hypothetical protein	UNKNOWN	5.2	0.9	5.7	2.3
8639_at	NDJ1	YOL104C	YOL104C Involved in meiotic chromosome segregation\; may stabilize homol	MEIOSIS, CHROMOSOME SEGREGATION	0.4	0.8	0.5	1.4
5700_at	ERG28	YER044C	YER044C Required for full sporulation, Dispensable for axial cores but requin	UNKNOWN	3.7	1.5	1.1	3.3
4792_at		YGR226C	YGR226C hypothetical protein	UNKNOWN	1.5	0.1	0.4	1.6
11160_at		YJL135W	YJL135W questionable ORF	UNKNOWN	4.3	3	2.8	4.5
11208_at		YJL175W	YJL175W questionable ORF	UNKNOWN	6.1	0.9	1.5	1.9
3933_s_at	MEL1	MEL1	MEL1 Required for the catabolism of melibiose and regulated by several GAL	MELIBIOSE UTILIZATION	2.6	0.4	0.4	0.4
9077_at		YNL226W	YNL226W questionable ORF	UNKNOWN	1.2	1	1.2	3.6
5613_at		YER085C	YER085C weak similarity to myosins	UNKNOWN	6.9	3.3	3.6	3.4
9314_at		YMR306C	YMR306C questionable ORF	UNKNOWN	1.8	2.3	1.7	4.3
10293_at		YLR041W	YLR041W questionable ORF	UNKNOWN	1.2	0.3	3.8	3.5
8018_i_at		YPL277C	YPL277C strong similarity to hypothetical protein YOR389w/putative pseudog	UNKNOWN	2.5	0.3	6.3	3.9
6836_at		YCR049C	YCR049C questionable ORF	UNKNOWN	0.9	0.4	1.8	7.2
7424_at		YBL073W	YBL073W questionable ORF	UNKNOWN	2.1	0.6	0.9	3.8
6032_at		YDR426C	YDR426C questionable ORF	UNKNOWN	3.4	3	3.9	2.1

Probe Set	N-Lim Anaerobic 2	N-Lim Anaerobic 3	P-Lim Anaerobic 1	P-Lim Anaerobic 2	P-Lim Anaerobic 3	S-Lim Anaerobic 1	S-Lim Anaerobic 2	S-Lim Anaerobic 3	C-Lim aerobic 1	C-Lim aerobic 2	C-Lim aerobic 3	N-Lim aerobic 1	N-Lim aerobic 2	N-Lim aerobic 3	P-Lim aerobic 1	P-Lim aerobic 2	P-Lim aerobic 3	S-Lim aerobic 1	S-Lim aerobic 2	S-Lim aerobic 3
	Signal	Signal	Signal	Signal	Signal	Signal	Signal	Signal	Signal	Signal	Signal	Signal	Signal	Signal	Signal	Signal	Signal	Signal	Signal	Signal
6657_at	0.2	0.2	0.4	0.4	1.1	0.2	0.4	0.2	0.2	0.2	0.3	0.2	0.2	0.3	1	0.3	0.4	0.2	0.2	0.3
8356_at	0.1	0.2	0.3	0.3	0.9	0.2	0.2	0.4	0.4	0.5	0.5	0.3	0.1	0.3	1.1	0.2	0.2	0.4	1.1	0.4
4495_at	0.2	0.2	0.3	0.5	1.1	0.3	0.4	0.3	0.2	0.2	0.4	0.2	0.2	0.2	1.4	0.2	0.5	0.2	0.2	0.2
11116_at	0.1	0.1	0.3	0.2	1.2	0.3	0.2	0.2	0.2	0.3	0.2	0.4	0.3	0.7	1.6	0.3	0.3	0.2	0.2	0.2
6960_at	0.3	0.2	0.2	0.2	0.5	0.1	0.2	0.1	1	0.2	0.2	0.2	0.1	0.1	0.4	1.3	0.4	0.2	0.1	0.7
5655_n_at	0	0.1	0.2	0.2	0.8	1.8	1.5	0.2	0.1	0.5	0.1	1.2	0.4	0.1	0.8	0.3	0.3	0.3	0.1	0.2
5248_at	0.3	0.3	0.5	0.4	1.9	0.5	0.6	0.3	0.5	0.4	0.4	0.4	0.3	0.3	1.6	0.4	0.4	0.5	0.3	0.5
10308_at	0.2	0.3	0.5	0.4	1	0.3	0.3	0.3	0.8	1.9	0.3	0.3	0.2	0.2	1.1	0.4	0.6	0.3	0.3	0.2
9470_at	0.8	0.4	1.2	0.5	1.9	0.9	0.7	1.3	0.8	0.5	0.7	0.4	0.4	0.3	1.4	0.7	0.6	0.6	0.7	0.5
8878_s_at	0.5	0.3	0.3	0.2	2	0.3	0.4	0.3	0.3	0.9	0.7	0.8	2	0.8	1.7	0.5	0.3	0.2	0.3	0.3
3936_at	0.1	0.1	0.2	0.1	1.6	0.1	2.2	0.1	0.1	0.2	0.1	0.1	0.1	0.3	1.2	0.1	0.1	0.1	0.2	0.2
9965_at	0.2	0.4	0.9	0.4	2.2	2.2	0.4	0.5	0.6	0.7	0.6	0.2	0.9	0.3	1.2	2.2	0.3	0.2	1.2	0.5
4906_at	0.4	0.3	0.5	1	2.2	0.5	1.1	1.6	0.4	0.6	0.9	0.8	0.3	0.4	1	0.4	0.6	1	0.7	0.7
5421_i_at	0.3	0.3	1	1	1.5	0.9	2.2	1.4	0.3	0.1	0.3	1.6	0.2	1.5	1.6	0.2	0.3	1.3	2.2	0.1
9674_at	0.6	0.4	0.3	0.4	2.2	0.9	0.5	0.3	0.4	0.7	0.4	0.6	2.2	0.2	1.5	0.8	0.9	0.9	2.3	0.7
6658_at	0.4	0.6	0.7	0.4	2.3	0.5	1.9	0.6	0.4	0.7	0.5	0.4	0.4	0.5	1.8	0.9	1.2	0.6	0.5	0.5
7859_at	0.2	0.3	0.3	0.3	0.7	0.1	0.7	0.1	0.6	1.5	0.3	0.3	0.1	0.7	0.9	0.3	1.7	0.3	2.4	1.8
10578_at	0.2	0.2	0.4	2.1	1.6	0.5	0.4	0.2	1.6	2.2	1.6	0.5	2.5	0.4	1	0.7	1.6	2.4	1.7	0.3
11383_at	0.1	0.2	0.2	0.1	2.6	0.4	0.2	0.1	2.2	0.4	0.9	0.3	0.4	0.3	2.5	0.4	0.4	0.2	0.4	0.6
5311_at	0.3	0.1	0.6	0.2	1.4	0.1	0.1	0.1	0.2	0.3	0.3	0.5	0.2	0.8	0.6	2.9	0.2	0.3	0.3	0.2
5628_at	0.4	0.3	1	2.9	1.9	1	1.1	1.2	1.7	0.2	1.7	0.4	1.1	0.6	0.8	0.4	1.2	1.7	1.9	1.8
5808_i_at	0.1	0.2	0.2	0.2	0.8	0.2	0.2	0.1	0.1	0.3	0.3	0.2	0.2	0.2	1.4	0.3	0.3	0.2	0.2	0.2
3934_at	0.2	0.1	0.4	0.3	3	0.2	0.2	0.1	0.1	0.4	0.7	0.2	0.1	0.1	1.4	0.2	0.2	0.2	0.1	0.1
6954_at	1	0.2	0.3	0.2	1.2	1.5	0.2	0.2	0.4	2.2	3	0.3	1.1	1.1	0.6	1.3	0.2	0.1	1.4	0.4
8195_at	2.5	2.1	1.8	0.9	1.5	1.1	3	0.2	0.5	0.3	0.7	2.9	0.2	1.4	0.8	0.6	0.5	0.6	0.2	0.3
10309_at	0.6	0.2	0.3	0.3	1.9	0.2	0.4	0.2	1.4	1.1	1.2	0.3	0.1	0.7	1.9	0.4	2.6	0.3	0.2	0.3
3957_r_at	0.1	0.3	3	1.3	0	1.4	1	3.1	0.4	2.6	2.7	2.1	2.6	0.1	0	0.1	0.2	1.8	0.2	1.9
4332_at	0.3	0.2	0.5	0.4	2.8	0.4	0.2	0.3	0.2	0.3	0.2	0.3	0.2	1.4	1	0.4	0.3	1.7	0.4	0.2
5374_at	0.9	0.4	0.7	0.8	3.2	0.4	1.3	0.5	0.5	2.7	2.7	0.4	0.4	0.4	1.5	0.4	0.3	2.9	0.9	0.3
8141_at	2.7	1.4	3.2	0.3	1	0.1	1	1.2	1.2	2.3	2.3	1.5	0.1	0.4	0.7	0.3	2.2	0.2	0.5	0.8
4325_at	0.8	2.9	1.7	0.3	2.2	0.2	0.7	2.3	3.2	1.6	2.5	0.5	0.2	0.3	1.5	0.6	0.4	3	0.3	1.3
5205_at	0.4	0.3	0.5	0.9	3.3	0.5	0.3	2.3	0.2	0.9	0.9	2.6	0.2	2.5	0.8	0.5	0.5	0.4	0.2	0.4
6931_at	2.3	0.4	1.9	1.2	3.3	0.5	0.7	0.2	0.5	2.6	0.8	1.8	2.9	1.7	1.6	3	0.9	0.4	0.6	1.7
4208_at	1.5	0.2	0.3	1.9	3.4	2.3	0.6	1.5	0.4	1	0.5	3	1.2	0.4	2.9	2.3	0.4	0.8	0.5	0.1
4741_at	0.9	0.2	1.8	2.8	2	1.3	0.8	3.3	0.4	0.7	1	2.7	1.5	0.5	2.1	0.3	0.2	1.6	0.9	3.4
8301_at	1.2	1.5	0.8	0.3	2	0.3	2.6	1.2	0.3	2.7	0.5	2.3	2.6	2	1.2	0.2	1	0.2	0.3	1
8525_at	0.7	1.8	0.5	1.5	0.9	0.1	0.4	1.5	0.7	1.7	0.4	2.4	0.1	0.1	0.7	0.9	0.5	0.6	0.1	0.3
9991_at	0.5	0.6	0.5	0.2	1.1	1	0.4	2.6	0.6	0.7	0.9	3.5	1.1	0.2	1.2	0.7	1	0.5	1	0.9
9053_at	1.2	0.5	0.4	0.7	3.4	3.5	0.4	3.3	0.6	0.4	0.8	0.3	3.5	0.5	1.5	0.4	0.5	1.9	2.2	0.4
9960_at	0.3	0.3	0.7	1.1	2.1	0.6	0.4	0.5	0.8	1	0.6	0.8	0.9	0.4	2.2	1.7	0.7	1.2	1	3.6
6164_at	0.4	0.1	0.3	0.2	2.8	0.2	0.4	2	0.8	3	3.6	0.1	0.3	0.4	1.7	1.7	1	2.1	0.5	0.2
6455_s_at	0.1	0.4	0.6	0.1	1.4	0.1	0.4	0.1	0.2	3.8	1	0.3	0.2	1.3	3.7	1	0.2	0.5	1.6	0.4
5197_at	0.1	1.7	0.7	0.1	1.2	0.2	1.3	1.4	2.2	1.7	0.5	0.9	0.9	0.3	0.8	0.4	2.6	3.8	1	2
6453_at	0.9	0.2	0.3	0	1.1	0.6	0.3	0.2	2	0.6	2.5	0.3	1.6	0.6	1.9	3.8	1.7	0.4	0.4	0.3
5530_at	1.5	1.7	2.1	0.7	2	2.3	0.5	0.3	0.3	0.6	2.1	0.5	0.8	0.5	0.9	0.1	0.3	2.2	1	1.2
8606_at	2.1	2.2	0.5	0.4	2.4	1.3	0.3	0.4	0.4	0.6	0.6	0.4	1.4	0.1	3	0.7	3.9	0.9	0.2	0.5
4557_at	1.1	0.2	0.9	0.6	2.8	0.2	0.6	0.2	0.7	3.9	3.3	1.6	2.4	0.4	1.7	2.1	0.9	0.4	1.7	0.2
8715_at	2.2	4	2.4	2.9	2.2	0.5	0.6	0.5	2.8	3.4	1.7	1.6	0.1	0.4	1.2	0.3	0.6	0.9	2.1	0.2
5233_at	1	0.3	0.8	0.4	4.2	1	0.7	0.6	1.1	0.9	0.8	0.5	0.4	0.3	2.1	1.3	0.5	0.7	2.8	1
8385_at	0.3	1.2	2.5	0.8	4.2	0.4	0.6	0.4	0.2	0.5	4	0.6	3.8	2.9	1.7	2.9	0.5	0.7	2.5	3.4
6800_at	1	0.3	1.8	3.3	1.8	1.2	3.7	1.6	4.2	1.8	3.3	1.9	1.6	3.2	3.8	0.5	0.5	2.8	0.3	1.8
6130_at	0.7	1.5	0.9	3.1	2.6	0.6	0.6	1.1	0.2	1.7	0.6	4.3	0.8	0.6	2.2	1.1	1.5	0.6	1	0.5
10371_at	1.3	1.2	1	0.5	3.7	0.2	0.6	0.2	0.8	3.1	2.5	4.3	1.2	1.1	1.6	1.4	4.2	0.5	0.6	0.3
9093_at	0.4	2.8	3.1	2	2.4	1	3.5	1.3	1.5	3.5	2.4	1.1	0.3	0.3	4.3	0.6	0.6	1.8	0.7	1.7
4460_i_at	0.1	0.2	4.1	3.6	0.7	0.9	0.3	1.8	0.1	2.4	0.1	0.3	1.7	1.7	3.4	0.1	0.2	0.2	0.1	0.3
8034_at	3.7	2.6	3	3.6	0.7	1.8	3.1	0.7	0.8	4.3	0.5	0.9	2	2.9	2.9	2	2.3	1.2	0.5	1.6
6101_at	1	0.6	3.3	0.3	3	0.6	1.5	2.2	3.9	1	2.4	2	0.2	3.1	3.4	1.9	4.3	0.7	3.4	2.8
6037_at	1.2	3.5	3.9	3.1	4.3	1.5	0.9	1.6	0.5	1.8	0.6	0.5	0.3	0.2	3.5	4.3	2.6	0.2	0.3	0.2
5949_at	0.2	4	0.5	2.9	3.4	0.9	0.5	0.3	2.5	1.5	2.8	0.7	0.4	1.8	1.9	0.7	1.6	0.4	0.6	1
10074_at	0.6	0.6	0.9	0.7	2	0.8	1.2	1.2	0.4	2.7	3.1	1	0.8	0.3	3.5	2.3	1.8	1.6	0.4	0.3
9340_at	0.8	0.4	1.2	4	3.4	0.4	0.4	2.5	3.7	0.4	2.8	0.5	2.4	1.2	4.5	1.2	2	2.6	2.4	2.2
7554_at	2.6	1.5	2.1	2.7	4.5	2.8	1.9	3.3	3	0.3	2	4	3.7	0.6	0.7	0.5	0.4	2.4	3.3	1.6
8853_at	1.7	1.2	4	3.1	2	3.1	3.4	3.2	1.7	0.3	4.5	3.2	0.4	2.2	1.3	1.3	2.1	1.7	1.8	0.5
10616_at	0.3	0.6	2.3	4.5	1.8	3.6	1.7	4	0.3	0.7	0.6	3.4	0.4	2.6	1.4	0.8	3.9	2.1	3.7	4.1
8333_at	0.3	2.3	1.6	0.2	1.1	3.1	2.2	0.9	0.6	2.8	0.4	0.8	0.9	0.7	4.6	0.4	0.3	0.6	2	0.2
6755_i_at	0.4	0	0.6	0.8	0.3	0.1	0.1	1.6	3.4	0.1	3.4	0.9	0.4	1.3	4.6	1.5	0.3	0.1	3.9	0.2
10876_at	4.6	0.6	4.4	0.5	3	1.4	3.7	1.4	0.7	3.7	0.9	0.9	2.5	1.3	1.5	0.7	1	2.5	0.6	0.7
5501_at	1.3	1.9	0.3	0.4	2.1	0.6	0.2	2.8	3.4	2.8	1.6	1.2	1.6	1.7	1.6	1.4	0.2	2.1	3	0.2
11300_at	1.5	1.8	0.1	0.4	0.8	0.3	2.4	0.2	3.3	1.2	1.2	3.3	2.8	1.5	1.1	4.6	3.5	1.2	1	2
7816_at	0.6	0.3	0.5	0.4	2.4	0.5	3.3	1.8	4.6	0.7	4.4	0.4	0.2	0.6	2.1	0.9	1.2	0.5	0.8	0.9
7443_at	1.4	1.1	0.5	1.2	4.4	1.5	0.6	0.1	3.1	4.6	2.1	0.2	2.5	0.2	1.5	2.8	1.9	0.3	0.3	0.4
4146_at	0.9	0.2	0.3	0.6	1.5	0.2	0.5	0.3	4.7	0.7	0.5	0.5	0.2	0.4	0.9	0.8	0.2	0.1	0.2	0.4
6417_at	0.6	1.9	4.7	1.5	1.4	0.3	1.9	2.8	0.9	0.5	3.5	0.2	1.6	0.6	1	0.7	1.8	0	1.7	2.1
6360_at	0.7	0.9	3.1	2.5	2.2	3.4	1.4	2.7	0.7	4.7	1	0.9	4.7	0.5	1.3	0.7	0.4	0.9	0.8	0.3
6382_at	0.4	0.2	0.2	3.6	3.1	2.3	2.8	0.4	2.5	2.4	4.7	2	2	0.5	1.4	3.7	2.1	1.6	2.6	4.2
6014_at	1.4	0.2	0.3	0.2	1.9	0.3	4.6	0.3	4.8	0.7	0.5	0.5	0.2	0.2	1.6	0.8	0.4	0.7	1.1	0.5
10682_at	0.5	0.7	0.9	0.4	2	0.2	0.9	0.4	1.1	0.7	0.8	0.4	0.5	0.4	1.2	1.3	1.4	1.5	0.9	0.4
3956_i_at	1.5	0.2	0.1	3.9	0	1	2.7	2.5	2	3.4	0.2	0.8	1.4	0	0.2	0.1	4.1	3.7	3.1	2.8
5264_at	1.5	3.3	3.9	3.6	2.8	2.1	1.9	0.3	0.2	1.2	4.8	2.7	2.4	1.7	4.8	3.9	2.6	0.8	1.7	1.3
7274_at	0.6	0.7	4.8	2.4	4.5	0.2	0.3	0.4	1.2	0.3	2.1	0.4	0.2	1.1	2.8	1	1.3	0.6	0.3	1.7
4329_at	0.6	0.5	1.1	2.4	4.9	0.8	0.7	1	4.5	1.1	1.1	0.6	1	0.8	3.2	1.8	1.7	0.9	1.6	0.8
6252_at	1.4	1.2	0.2	0.1	0.6	0.2	0.1	0.1	1.7	0.2	0.3	0.3	1.4	1.6	0.5	0.1	2	4.9	1.7	2.1
5309_at	2	0.4	0.5	2.6	0.9	0.5	0.3	1.6	3.5	4.9	0.9	1.8	3.1	0.6	1	0.2	0.7	0.4	0.2	0.2
8972_at	0.5	0.2	0.3	0.3	0.9	2.3	0.6	1	4.2	0.2	2.7	1.7	2	1.8	3.6	1.6	2.1	0.2	1.6	1.3
5185_at	0.2	0.3	3.7	3.4	3.3	2.5	1	2.5	4.9	2.2	1.7	4.2	2.7	3	2.3	0.6	1.6	0.7	1.9	2.3
11381_at	2.8	0.8	0.8	0.5	5	0.6	1	0.7	0.4	0.4	1.1	0.5	0.7	2.2	3.3	1.2	1.7	1.5	4.7	0.5
5736_at	2.7	3.4	5	3.4	3.2	2.4	3.2	0.8	0.8	1.1	0.6	2.7	3.7	3.2	4.6	0.9	1.9	0.6	1.2	0.4
4041_at	0.3	1.6	0.7	2	2.4	5	0.7	0.7	0.4	0.4	0.7	0.7	0.5	1	1.1	1.1	1.4	1.2	0.7	5.1
6326_at	1.4	0.5	0.4	2	3.2	0.2	4.2	0.2	5.1	2.3	0.8	0.3	0.5	0.3	1.4	0.2	0.6	0.6	0.2	0.2
11215_at	0.2	0.5	0.4	2.4	3.9	2.9	1.2	1.2	2.7	5.1	3.1	1.1	0.8	0.5	1.6	1.1	0.9	2	1.8	0.2
5604_at	1.8	0.4	0.3	0.4	1.2	2.4	0.8	0.1	0.6	0.4	4.4	2.7	2.6	0.8	2.2	0.8	5.2	1.1	0.5	0.3
6878_at	0.4	0.8	1.5	0.2	1	2.3	5.2	1	0.3	1	1.7	2.4	3	0.4	1.9	0.4	1.2	0.1	2.6	3.6
11231_at	3.6	1.1	2	2.5	5.2	0.8	4.3	3.2	0.9	0.9	0.6	1.4	4.4	0.8	3.4	0.6	1.8	1.9	0.6	0.9
6518_at	0.1	2.2	2.7	1.4	1.8	0.2	1.7	0.2	3.1	2.8	0.8	3.1	0.8	1.1	2.8	2.6	5.2	4.4	3.2	0.7
10004_at	0.6	3.8	0.4	0.5	1	0.6	0.5	0.3	0.6	2.2	3.4	0.6	0.9	1.7	0.5	1.9	2.5	5.3	0.5	0.2
4389_at	0.3	2.4	2.7	2.3	1.5	0.4	5	0.2	0.6	1.4	0.9	1.1	2	1.1	1.2	2.6	5.3	0.8	3.1	0.5
9945_at	4	2.1	5.1	1.9	1.2	1.5	3.2	3.2	4.3	3.8	2.8	2.1	2.2	0.7	5.3	4.2	4.7	0.3	2	0.7
5078_at	0.2	0.6	0.3	0.5	5.4	0.5	0.5	0.5	1.4	0.7	0.4	1.3	0.3	1.4	1.3	0.4	0.6	4.1	0.4	0.4
3959_at	0.3	0.1	0.8	0.2	5.4	1.8	0.2	3.1	0.1	1.5	0.3	0.7	0.3	0.9	2	0.4	0.8	0.5	0.3	1.5
7225_at	2.5	2.6	2.9	1	5.4	3.1	3.1	1.3	0.6	1.4	3	2.5	0.2	2.5	1.9	3.2	2.9	5.2	1.5	1.8
8782_at	2.1	0.1	3.1	0.9	1.8	0.5	0.5	1.1	1.2	0.4	4.5	0.4	0.7	0.6	5.4	2.5	4.2	0.6	1.8	0.8
9715_at	0.2	0.3	0.3	0.5	1.6	0.6	0.3	0.5	0.5	0.8	1.2	0.2	0.5	0.1	1.1	0.3	0.2	0.3	0.3	0.3
3935_at	0.3	0.4	0.2	0.4	2.4	0.2	0.1	0.5	3.6	2.8	4.9	0.1	0.5	0.2	1.7	0.4	0.6	2.2	0.3	0.1
3854_f_at	4.5	2	4.5	1.8	3.4	0.9	5.5	0.8	0.3	2.2	3.5	2.2	3.4	1.8	4.6	5.5	0.4	3.4	0.5	0.4
10109_at	1.9	0.2	0.4	2.4	4.2	1.6	2.1	4.5	4.9	5.4	3.5	1.3	0.2	0.3	1.9	0.8	1.7	5.5	1.2	2.4
7720_at	3.2	3	5.6	1.9	1.9	0.6	1.9	1.9	0.5	1	1.1	4.1	2.4	0.5	2.5	1	1.8	0.6	0.2	1.3
6928_at	2.3	1	3.6	2.1	1.3	3.5	3.4	3.4	3.6	3.3	2.1	2	3	1.4	1.8	4	0.7	0.4	0.6	0.4
10356_at	0.2	0.9	1.3	0.6	1.5	2.9	0.6	2.2	4	0.8	1	2.8	1.7	1.3	4.2	0.6	4.6	4.7	2.2	3.1
4977_at	3	1.1	2.6	0.9	3.7	1.3	5.2	4.6	1.3	1.4	0.9	1.3	0.2	0.3	5.6	5	3.2	1.8	0.4	0.4
6750_i_at	2.4	0.5	0.4	0.3	1.5	0.8	2.5	1.8	0.4	1.5	5.7	0.3	0.3	1	2.1	0.4	2.3	1.8	0.4	0.5
7777_at	0.8	2.7	1.7	0.5	2	3.7	2.2	0.3	0.4	2.9	0.7	0.9	0.2	0.1	1.3	4.6	0.4	0.7	0.3	0.4
8783_at	1.2	0.4	2.3	1.8	2.3	2	1.5	3.8	0.7	3	3.1	5.7	0.2	0.4	0.8	1.4	4.6	2.6	1.2	3.8
5354_at	1.5	0.7	1.4	4.1	5	3.5	5.7	2.2	0.2	0.3	0.7	1.3	1.7	0.4	4.6	3.2	1.5	0.3	0.5	0.3
10549_at	1.3	1.2	1.4	0.9	3.1	0.8	1.5	0.7	0.7	0.6	1.1	0.7	2.1	0.6	5.8	1	1.5	0.8	4.7	0.7
4950_at	0.6	3.1	1.2	0.6	1.8	0.2	1.1	0.1	2	3.8	5.8	1.7	1.6	2.2	1.7	0.7	1.8	3.2	2.3	0.5
5399_at	0.2	1.2	0.4	0.4	3.1	0.1	0.6	0.7	0.7	5.6	2.9	1.6	2.4	2	1.8	5.8	4.1	0.9	2.2	0.4
4749_at	1.1	0.6	2.8	3.8	5.8	0.6	4.7	0.5	1.1	5.3	0.8	0.5	1.5	3.6	1.9	0.5	0.8	0.9	0.9	0.6
7648_at	1.1	3.6	5.8	3.1	4.9	4.8	2	5.3	1	1.9	1.1	3	1.6	0.5	2.1	0.5	0.8	2.4	0.7	1.2
3544_at	3.4	2.3	4.9	3.9	2.5	5.2	5.4	5.8	3.3	0.6	3.9	3.9	4.3	2	5.5	0.5	0.4	4.9	3.5	2.6
11252_s_at	0.5	3.7	2.7	0.8	2.6	2.4	0.3	0.2	5.9	1.8	3.2	0.5	0.3	1.5	2.3	1.5	0.4	3.7	1.6	2.8
4552_at	5.5	0.3	0.4	0.4	1.5	0.2	0.6	0.3	2.2	4.1	5.9	5.2	2.1	5.6	5.4	4.3	3.3	0.8	0.4	0.2
8502_at	2.3	0.3	1.2	1.2	4.6	3.3	0.9	0.4	1.3	1.8	6	1.1	1.2	0.7	3.3	1.1	1.6	0.8	0.3	4.8
7187_at	1.8	1.5	0.8	1.1	1.1	1.2	1.8	1.3	4.6	0.2	6	0.4	1.2	1	1.3	1.3	3.9	0.1	2.1	0.2
6198_at	3.9	0.3	0.4	3.7	3.4	0.4	0.9	0.5	2.4	3.2	6	1.7	1.4	2.4	3.8	3.5	1.1	2.2	2.5	1.9
4034_at	0.5	0.3	1	6	5.3	3.9	0.2	4.2	0.4	0.8	1.4	0.3	0.5	2.1	3.4	1.5	3	3.7	2.2	0.5
11140_at	2	2.6	3.2	3	6	2.9	2	4.7	4.5	3.6	4.3	0.3	1.8	1.8	0.9	3	3.4	3.8	4.8	4.5
6096_at	0.8	0.5	4.5	5.9	5.3	2.4	3.1	6	3.1	4.4	5.1	1	1.6	4.2	2.4	2.7	0.5	1.9	0.6	1.1
11375_at	0.7	0.3	2	0.3	6.1	1.4	3	0.5	0.3	3.1	1.3	0.5	2.5	0.4	3.5	0.7	4.4	4.5	2.4	0.7
6476_at	3.5	3.8	2.6	0.4	2.9	2.1	2.9	2.4	0.2	1.5	6.1	1.4	0.3	3	2	3.1	2.9	3.5	1.8	1.5
11323_at	2.8	1.5	3.1	0.3	1.3	2.1	3.5	2.9	0.3	0.2	0.2	0.8	3.1	3.9	1.9	0.7	6.1	0.2	2.4	0.5
9920_at	0.5	2.7	0.5	0.2	1.3	0.9	3.3	1.4	2.7	1.2	2	0.6	0.5	0.4	6.1	1.2	3.1	3.1	0.3	2.5
5156_at	3	2.2	2.4	0.3	2.6	1.3	4.5	2.3	2.8	1.6	3.4	4.8	1.3	1.4	1.6	4.7	0.5	3.6	6.1	1.6
5693_at	3.2	2.8	5.1	2.7	2	3.2	1.2	2.1	3.4	0.3	2.6	5.3	2.4	2.9	4	6.1	2	2.8	0.4	4.5
10486_s_at	2.8	3.5	0.8	4.7	2.6	4.7	6.1	1.6	2.2	0.8	4.9	3.6	3.6	0.4	2.2	5.9	2	4.6	0.3	2.3
4533_at	6.1	2.3	2.6	0.4	6.1	3.4	4	3	6	2.8	2	1.7	3.3	3.7	3.9	3.9	0.1	1.4	2.9	1.1
6126_at	0.1	0.1	0.5	0.6	5.8	0.3	0.7	0.5	0.5	2.1	6.2	0.7	0.4	0.1	0.9	2.2	0.7	0.2	0.4	3.2
9944_at	4	3.5	0.4	3.7	1.1	3.4	0.5	2.2	3.8	2	5.3	3.3	4.6	2.7	3.8	1.5	6.2	4.7	4.8	2.6
4039_at	3.5	3	0.5	3.5	2.3	3.4	0.6	5.1	1.3	0.6	2.1	0.7	0.7	0.9	1.6	0.9	0.4	1.3	3.2	1.7
7198_at	4.1	1.2	1.8	6.2	5	4	2	4.4	0.6	2.7	4	3.9	2.1	2.7	6.1	2.2	4.2	4.8	5.8	2.9
7346_at	1.4	3.3	1.8	3.6	2.7	0.7	4.2	2.3	2.7	3.1	5.4	1.5	0.4	2.4	2	4.8	2.7	4	0.6	2.5
9741_at	1.5	1.6	1.8	4.2	6.3	1.9	6	1.4	1.7	1	2.4	1.2	1.1	1.4	2.5	1.5	1	1.3	2	2.5
8570_at	2.7	0.7	3.5	3.3	6.2	4.9	1.6	1.3	1	1.6	3.7	0.7	0.2	2.1	2.9	0.3	6.3	0.6	1.6	1.5
5505_at	4	1.9	5.1	3.9	4.4	0.6	0.7	2	0.4	0.8	2.2	1.2	1.3	0.6	6.3	1	3.2	2.1	2	0.4
5229_at	3.6	2.2	4.9	5.1	2.8	5.1	3.8	5.1	4.1	5.8	2.1	2.3	0.7	1.1	5.6	4.1	4.8	3.5	4.5	3.8
4257_at	3.7	0.6	0.2	4.8	1.4	3.4	6.3	1.7	0.3	2.6	3.3	4.7	6	1.8	3.7	3	2.1	4.7	4.8	5.1
11045_at	0.3	0.2	0.3	0.9	3.3	0.2	0.3	0.9	6.3	3.4	5.1	0.2	2.9	2.8	2.8	1.1	3.3	0.3	0.4	0.3
6796_at	2.2	0.3	0.3	1.9	6.4	1.8	0.5	2.2	0.1	0.4	3.2	2.2	0.2	2.1	1	1.2	0.3	0.4	1.1	0.3
5151_at	1.2	0.8	1.9	1.1	6.4	0.2	4.6	0.2	0.2	0.2	4.2	0.3	0.6	0.3	4	0.2	0.3	1.3	0.3	0.3
6829_at	1.4	3.3	2.8	1.8	5.6	2.5	5.5	1.7	1.8	3.9	2.4	2.6	1.6	3	1.9	0.1	0.4	3.2	2.9	2.8
3983_at	2	2.1	1	1.8	5.2	1.7	6.4	3.1	1.3	0.8	2.7	3.5	2.5	2.2	3.9	0.8	4.3	0.7	2.9	1.9
8778_at	3.2	0.9	2.7	5.1	4.3	3.1	6.4	3	0.8	4.5	2	3.8	1.4	4.4	2.8	4.9	1.3	1.4	0.4	4.2
11198_at	0.6	0.3	0.5	0.3	4.3	0.7	0.4	0.5	0.3	0.7	3.5	1.1	1.7	0.8	1.6	0.3	1	0.4	1.3	0.3
8258_at	4	3.2	0.8	5.2	3.9	3.1	1.8	3.2	0.4	3.3	6.5	4.9	2	0.3	1.9	6.1	0.7	3.4	1.2	2.5
5207_at	0.3	1.2	0.6	3.7	6.5	2.8	2.9	0.7	0.4	0.7	1.3	0.6	0.8	2.9	1.5	0.5	1.9	2.5	3.7	0.7
8785_at	0.4	2.4	0.8	0.7	6.3	0.5	0.6	0.2	3.3	3.9	3.8	0.5	0.1	0.4	5.6	6.5	0.4	0.3	0.5	0.2
11380_at	1.9	1.3	0.2	1.2	1.2	0.4	4.2	1	4.9	2.5	4.6	0.6	1.5	1.7	4.4	6.5	1.9	1.1	0.6	1.2
4550_at	2.3	0.3	3.8	3.5	1	0.2	0.8	2.1	0.2	2.5	0.6	0.4	0.3	0.2	5.3	6.6	1.2	0.4	0.3	1
11014_at	1.5	0.9	2.7	0.6	1.6	2.3	4.2	6.2	1.2	0.5	3.1	2.9	0.6	0.4	1.8	2.4	0.7	2.9	3	0.5
9620_at	0.4	3	5.6	5.5	2.7	3.1	5.8	4.2	3.3	2.3	1	5	3.6	0.3	1.5	2.3	3.3	2.7	0.3	6.6
9652_at	0.6	3	2.4	3.7	5.1	6.1	4.2	3.5	6.6	5.2	1.2	3.5	1	0.6	1.4	1.1	0.8	2.5	0.7	4.8
6181_r_at	3.7	2.6	2.6	2.1	0.3	1.5	0.1	3	3.5	4	6.4	2.4	3.7	1.2	2	1	3	6.6	5.1	1
3855_s_at	0.2	0.6	0.2	0.9	1.2	0.4	0.5	0.5	0.1	0.3	3.5	0.2	0.1	1	0.7	2	2	0.2	0.2	0.6
4142_at	2.7	3.1	5.4	4.4	4.8	6.4	3.8	2.1	2.9	2.9	3.8	2.6	3.3	1.6	1.7	6.6	4.5	3.7	3.3	4.8
5177_at	2.9	0.5	0.5	2.3	4.3	6.6	6.1	3.4	0.3	4	0.4	1.8	0.8	0.9	1.7	0.6	0.3	0.7	3	0.4
4819_at	0.3	2.6	0.5	0.1	1.5	0.3	0.4	0.3	2.3	0.2	2.3	0.7	2.4	2.6	6.7	1.7	0.1	2.7	1.8	3.3
11382_at	0.7	2.6	0.8	1.7	5.1	2.8	4.5	1.2	4.5	1.6	5.2	1.1	0.7	0.5	6.7	0.4	1.5	0.8	0.5	0.3
4904_at	2	0.7	0.3	1.5	6.7	1.2	5.9	0.2	4	0.9	1.1	0.4	1.8	3.3	2.6	0.6	0.4	2.2	0.4	2.8
5946_at	0.7	0.4	6.7	1.5	5.7	0.9	0.4	0.9	0.7	1	0.7	0.4	0.6	0.3	2.3	0.4	1.8	0.6	0.5	0.7
6955_s_at	1.8	0.4	0.3	0.1	2.2	0.9	4.3	1.4	2	3.2	1.3	1	0.3	0.2	6.8	0.8	1.3	6.4	0.6	0.3
5028_at	0.7	0.7	1.3	1.6	4.8	0.9	2.8	2.4	0.8	5.4	1.4	0.8	1.3	1.4	2.4	1.6	1.1	0.8	1.1	0.9
8189_at	1.4	0.9	0.4	1.1	1.6	0.7	1.5	0.8	1.3	0.9	3.8	6.8	0.6	4.8	4.9	1.6	6.1	1.1	1.5	0.8
4461_r_at	2.3	1.7	3.5	6.8	2.4	1.5	0.7	1.9	4.7	3.7	2.1	2.6	4.1	0.2	1.1	2.4	2.2	4.1	1.3	0.5
6592_at	3.1	1.9	1	0.3	6.8	0.4	3.8	0.4	0.9	3.4	3.4	4.5	4.7	4	5.6	2.4	1.4	4.9	5	1.3
4885_at	2.4	0.7	3.5	5.1	2.8	3.2	5.2	1.1	3.6	0.7	5.4	2.5	1.7	2.6	6.8	3.3	4.5	4.4	1.4	2.2
5239_at	3	3.5	3.6	4.4	5.9	4.1	2.6	3	6.2	6.8	3.8	2.4	2.5	1.2	2	0.5	3.5	1.5	2.2	1.5
8639_at	0.8	1	0.2	0.2	6.9	0.2	0.4	0.2	3.2	2.9	0.6	0.7	3.1	0.8	1	0.8	0.5	0.5	1.2	0.6
5700_at	2	0.2	3.3	5.2	6.9	3.8	2	2.3	0.5	3.8	6.2	2	0.3	1.5	5	0.5	2.2	0.8	2.8	4.3
4792_at	2.3	0.3	0.7	1.6	7	0.8	0.8	0.2	0.6	0.9	3.8	2	1.5	0.8	0.9	0.9	1.4	0.7	0.8	0.5
11160_at	3.4	4.5	2.9	4.6	5.1	2.1	4.7	4.2	6	2.6	7	3	2.6	2.4	1.8	2.6	6	4.5	2.8	0.7
11208_at	2.1	1.3	6.4	3.6	6.4	5.2	2.7	5.3	6.5	7	2.7	2	5	1.1	6.9	2.4	3.3	1.6	2.2	1.5
3933_s_at	0.6	0.3	0.5	0.4	6.7	0.3	0.3	0.3	2.1	1.3	0.4	0.6	0.4	0.2	7.1	1.6	0.6	0.3	0.6	0.4
9077_at	2	0.9	2.4	1.2	3.8	3.4	1.9	1	3.8	7.1	1.8	3.2	0.5	1.2	4.2	1.6	1.6	4.4	3.7	1.4
5613_at	3	4.2	4.8	5.4	3.5	2.2	6.8	4.1	4.9	2.4	0.8	4.2	2.6	4.2	7.1	2.8	4.4	2.7	1.4	0.5
9314_at	4	5	3.2	5.5	2.4	3.6	3	5.4	3.7	5.1	6	4	2.6	5	7.1	4.7	2.1	1.7	2	1.1
10293_at	2.7	2.2	2.3	3.6	2.5	4.7	5.9	0.6	7.1	4.5	4.6	4	2.3	1.8	1.1	2.4	2	0.4	2.9	2.7
8018_i_at	0.6	3.1	0.4	1.8	5.7	1.7	0.1	1.9	2.8	3.5	1.3	3.7	5.6	0.9	4.4	5.4	7.1	0.2	4.6	0.2
6836_at	3.4	0.4	1.4	1	3.6	2.4	3.4	1.5	0.5	1.6	0.6	0.8	2.1	0.8	1.5	1.3	0.6	3.1	0.7	1.2
7424_at	2.4	1	2.3	4.9	2.5	3.7	7.2	0.4	0.7	2.1	2.5	4.8	0.6	3.5	6.1	0.5	0.9	3.3	1.9	2.4
6032_at	0.2	0.4	3.5	0.6	1.8	3.2	7.2	1.5	1.1	2.6	4.9	6.4	4.4	0.2	1.1	1.9	4.8	4.4	3.8	2.6

Probe Set	C-Lim ANA	C-Lim ANA	N-Lim ANA	N-Lim ANA	P-Lim ANA	P-Lim ANA	S-Lim ANA	S-Lim ANA	C-Lim A	C-Lim A	N-Lim A	N-Lim A	P-Lim A	P-Lim A	S-Lim A	S-Lim A
	Average	Stdev	Average	Stdev	Average	Stdev	Average	Stdev	Average	Stdev	Average	Stdev	Average	Stdev	Average	Stdev
6657_at	0.43	0.29	0.23	0.06	0.63	0.4	0.27	0.12	0.23	0.06	0.23	0.06	0.57	0.38	0.23	0.06
8356_at	0.37	0.32	0.17	0.06	0.5	0.35	0.27	0.12	0.47	0.06	0.23	0.12	0.5	0.52	0.63	0.4
4495_at	0.7	0.78	0.23	0.06	0.63	0.42	0.33	0.06	0.27	0.12	0.2	0	0.7	0.62	0.2	0
11116_at	0.33	0.12	0.17	0.12	0.57	0.55	0.23	0.06	0.23	0.06	0.47	0.21	0.73	0.75	0.2	0
6960_at	0.9	0.62	0.2	0.1	0.3	0.17	0.13	0.06	0.47	0.46	0.13	0.06	0.7	0.52	0.33	0.32
5655_n_at	0.93	0.74	0.37	0.55	0.4	0.35	1.17	0.85	0.23	0.23	0.57	0.57	0.47	0.29	0.2	0.1
5248_at	0.5	0.26	0.3	0	0.93	0.84	0.47	0.15	0.43	0.06	0.33	0.06	0.8	0.69	0.43	0.12
10308_at	0.27	0.15	0.27	0.06	0.63	0.32	0.3	0	1	0.82	0.23	0.06	0.7	0.36	0.27	0.06
9470_at	0.47	0.23	0.63	0.21	1.2	0.7	0.97	0.31	0.67	0.15	0.37	0.06	0.9	0.44	0.6	0.1
8878_s_at	0.27	0.15	0.33	0.15	0.83	1.01	0.33	0.06	0.63	0.31	1.2	0.69	0.83	0.76	0.27	0.06
3936_at	0.17	0.15	0.13	0.06	0.63	0.84	0.8	1.21	0.13	0.06	0.17	0.12	0.47	0.64	0.17	0.06
9965_at	0.33	0.32	0.57	0.47	1.17	0.93	1.03	1.01	0.63	0.06	0.47	0.38	1.23	0.95	0.63	0.51
4906_at	0.53	0.31	0.37	0.06	1.23	0.87	1.07	0.55	0.63	0.25	0.5	0.26	0.67	0.31	0.8	0.17
5421_i_at	0.53	0.49	0.23	0.12	1.17	0.29	1.5	0.66	0.23	0.12	1.1	0.78	0.7	0.78	1.2	1.05
9674_at	0.47	0.21	0.5	0.1	0.97	1.07	0.57	0.31	0.5	0.17	1	1.06	1.07	0.38	1.3	0.87
6658_at	0.67	0.47	0.87	0.64	1.13	1.02	1	0.78	0.53	0.15	0.43	0.06	1.3	0.46	0.53	0.06
7859_at	1.27	1.15	0.37	0.21	0.43	0.23	0.3	0.35	0.8	0.62	0.37	0.31	0.97	0.7	1.5	1.08
10578_at	1.93	0.29	0.2	0	1.37	0.87	0.37	0.15	1.8	0.35	1.13	1.18	1.1	0.46	1.47	1.07
11383_at	0.9	0.78	0.17	0.06	0.97	1.42	0.23	0.15	1.17	0.93	0.33	0.06	1.1	1.21	0.4	0.2
5311_at	0.5	0.3	0.23	0.12	0.73	0.61	0.1	0	0.27	0.06	0.5	0.3	1.23	1.46	0.27	0.06
5628_at	1.23	1.38	0.6	0.44	1.93	0.95	1.1	0.1	1.2	0.87	0.7	0.36	0.8	0.4	1.8	0.1
5808_i_at	1.2	1.57	0.13	0.06	0.4	0.35	0.17	0.06	0.23	0.12	0.2	0	0.67	0.64	0.2	0
3934_at	0.2	0	0.17	0.06	1.23	1.53	0.17	0.06	0.4	0.3	0.13	0.06	0.6	0.69	0.13	0.06
6954_at	0.27	0.15	0.47	0.46	0.57	0.55	0.63	0.75	1.87	1.33	0.83	0.46	0.7	0.56	0.63	0.68
8195_at	1.13	1.07	1.97	0.61	1.4	0.46	1.43	1.43	0.5	0.2	1.5	1.35	0.63	0.15	0.37	0.21
10309_at	1.27	1.61	0.4	0.2	0.83	0.92	0.27	0.12	1.23	0.15	0.37	0.31	1.63	1.12	0.27	0.06
3957_r_at	0.8	0.92	0.47	0.47	1.43	1.5	1.83	1.12	1.9	1.3	1.6	1.32	0.1	0.1	1.3	0.95
4332_at	1.3	1.65	0.23	0.06	1.23	1.36	0.3	0.1	0.23	0.06	0.63	0.67	0.57	0.38	0.77	0.81
5374_at	1.43	1.27	0.63	0.25	1.57	1.42	0.73	0.49	1.97	1.27	0.4	0	0.73	0.67	1.37	1.36
8141_at	1.27	1.46	2.1	0.66	1.5	1.51	0.77	0.59	1.93	0.64	0.67	0.74	1.07	1	0.5	0.3
4325_at	0.63	0.75	1.8	1.05	1.4	0.98	1.07	1.1	2.43	0.8	0.33	0.15	0.83	0.59	1.53	1.37
5205_at	1.23	1.7	0.4	0.1	1.57	1.51	1.03	1.1	0.67	0.4	1.77	1.36	0.6	0.17	0.33	0.12
6931_at	0.5	0.44	1.47	0.97	2.13	1.07	0.47	0.25	1.3	1.14	2.13	0.67	1.83	1.07	0.9	0.7
4208_at	0.27	0.15	0.8	0.66	1.87	1.55	1.47	0.85	0.63	0.32	1.53	1.33	1.87	1.31	0.47	0.35
4741_at	1.37	1.33	1.1	1.01	2.2	0.53	1.8	1.32	0.7	0.3	1.57	1.1	0.87	1.07	1.97	1.29
8301_at	1.37	1.76	1.3	0.17	1.03	0.87	1.37	1.16	1.17	1.33	2.3	0.3	0.8	0.53	0.5	0.44
8525_at	1.37	1.85	0.97	0.74	0.97	0.5	0.67	0.74	0.93	0.68	0.87	1.33	0.7	0.2	0.33	0.25
9991_at	0.3	0.17	0.53	0.06	0.6	0.46	1.33	1.14	0.73	0.15	1.6	1.71	0.97	0.25	0.8	0.26
9053_at	0.33	0.32	0.7	0.44	1.5	1.65	2.4	1.73	0.6	0.2	1.43	1.79	0.8	0.61	1.5	0.96
9960_at	0.93	1.01	0.43	0.23	1.3	0.72	0.5	0.1	0.8	0.2	0.7	0.26	1.53	0.76	1.93	1.45
6164_at	0.4	0.26	0.23	0.15	1.1	1.47	0.87	0.99	2.47	1.47	0.27	0.15	1.47	0.4	0.93	1.02
6455_s_at	0.5	0.61	0.37	0.25	0.7	0.66	0.2	0.17	1.67	1.89	0.6	0.61	1.63	1.83	0.83	0.67
5197_at	0.13	0.06	1.03	0.83	0.67	0.55	0.97	0.67	1.47	0.87	0.7	0.35	1.27	1.17	2.27	1.42
6453_at	0.8	0.62	0.43	0.4	0.47	0.57	0.37	0.21	1.7	0.98	0.83	0.68	2.47	1.16	0.37	0.06
5530_at	1.57	2.02	1.6	0.1	1.6	0.78	1.03	1.1	1	0.96	0.6	0.17	0.43	0.42	1.47	0.64
8606_at	1.27	1.85	1.5	1.13	1.1	1.13	0.67	0.55	0.53	0.12	0.63	0.68	2.53	1.65	0.53	0.35
4557_at	0.73	0.47	0.87	0.59	1.43	1.19	0.33	0.23	2.63	1.7	1.47	1.01	1.57	0.61	0.77	0.81
8715_at	1.43	0.87	2.2	1.8	2.5	0.36	0.53	0.06	2.63	0.86	0.7	0.79	0.7	0.46	1.07	0.96
5233_at	0.87	0.57	0.57	0.38	1.8	2.09	0.77	0.21	0.93	0.15	0.4	0.1	1.3	0.8	1.5	1.14
8385_at	1.6	1.01	0.6	0.52	2.5	1.7	0.47	0.12	1.57	2.11	2.43	1.65	1.7	1.2	2.2	1.37
6800_at	1.23	1.46	0.53	0.4	2.3	0.87	2.17	1.34	3.1	1.21	2.23	0.85	1.6	1.91	1.63	1.26
6130_at	0.83	0.25	2.13	1.83	2.2	1.15	0.77	0.29	0.83	0.78	1.9	2.08	1.6	0.56	0.7	0.26
10371_at	2.3	2.05	0.93	0.55	1.73	1.72	0.33	0.23	2.13	1.19	2.2	1.82	2.4	1.56	0.47	0.15
9093_at	0.93	1.27	1.27	1.33	2.5	0.56	1.93	1.37	2.47	1	0.57	0.46	1.83	2.14	1.4	0.61
4460_i_at	2.4	1.65	0.33	0.32	2.8	1.84	1	0.75	0.87	1.33	1.23	0.81	1.23	1.88	0.2	0.1
8034_at	1.4	0.98	3.17	0.55	2.43	1.53	1.87	1.2	1.87	2.11	1.93	1	2.4	0.46	1.1	0.56
6101_at	0.73	0.68	0.8	0.2	2.2	1.65	1.43	0.8	2.43	1.45	1.77	1.46	3.2	1.21	2.3	1.42
6037_at	0.97	0.64	2.27	1.16	3.77	0.61	1.33	0.38	0.97	0.72	0.33	0.15	3.47	0.85	0.23	0.06
5949_at	2.97	1.99	1.43	2.22	2.27	1.55	0.57	0.31	2.27	0.68	0.97	0.74	1.4	0.62	0.67	0.31
10074_at	2.43	1.92	0.7	0.17	1.2	0.7	1.07	0.23	2.07	1.46	0.7	0.36	2.53	0.87	0.77	0.72
9340_at	1.13	0.65	1.3	1.23	2.87	1.47	1.1	1.21	2.3	1.71	1.37	0.96	2.57	1.72	2.4	0.2
7554_at	1.97	1.97	1.87	0.64	3.1	1.25	2.67	0.71	1.77	1.37	2.77	1.88	0.53	0.15	2.43	0.85
8853_at	2.1	1.87	1.63	0.4	3.03	1	3.23	0.15	2.17	2.14	1.93	1.42	1.57	0.46	1.33	0.72
10616_at	0.37	0.15	1.4	1.65	2.87	1.44	3.1	1.23	0.53	0.21	2.13	1.55	2.03	1.64	3.3	1.06
8333_at	0.97	1.1	1.67	1.18	0.97	0.71	2.07	1.11	1.27	1.33	0.8	0.1	1.77	2.45	0.93	0.95
6755_i_at	0.8	0.87	0.57	0.67	0.57	0.25	0.6	0.87	2.3	1.91	0.87	0.45	2.13	2.22	1.4	2.17
10876_at	0.77	0.21	2.1	2.18	2.63	1.98	2.17	1.33	1.77	1.68	1.57	0.83	1.07	0.4	1.27	1.07
5501_at	2.93	1.7	1.43	0.42	0.93	1.01	1.2	1.4	2.6	0.92	1.5	0.26	1.07	0.76	1.77	1.43
11300_at	0.37	0.21	1.47	0.35	0.43	0.35	0.97	1.24	1.9	1.21	2.53	0.93	3.07	1.79	1.4	0.53
7816_at	1.33	1.62	0.5	0.17	1.1	1.13	1.87	1.4	3.23	2.2	0.4	0.2	1.4	0.62	0.73	0.21
7443_at	1.1	0.44	1.1	0.3	2.03	2.08	0.73	0.71	3.27	1.26	0.97	1.33	2.07	0.67	0.33	0.06
4146_at	0.43	0.21	1.37	1.46	0.8	0.62	0.33	0.15	1.97	2.37	0.37	0.15	0.63	0.38	0.23	0.15
6417_at	2.33	1.99	1.23	0.65	2.53	1.88	1.67	1.27	1.63	1.63	0.8	0.72	1.17	0.57	1.27	1.12
6360_at	1.5	1.91	0.97	0.31	2.6	0.46	2.5	1.01	2.13	2.23	2.03	2.32	0.8	0.46	0.67	0.32
6382_at	0.3	0.17	0.93	1.1	2.3	1.84	1.83	1.27	3.2	1.3	1.5	0.87	2.4	1.18	2.8	1.31
6014_at	1.43	2.05	0.67	0.64	0.8	0.95	1.73	2.48	2	2.43	0.3	0.17	0.93	0.61	0.77	0.31
10682_at	2.2	2.36	0.9	0.53	1.1	0.82	0.5	0.36	0.87	0.21	0.43	0.06	1.3	0.1	0.93	0.55
3956_i_at	3.13	1.88	0.6	0.78	1.33	2.22	2.07	0.93	1.87	1.6	0.73	0.7	1.47	2.28	3.2	0.46
5264_at	2.5	0.35	1.67	1.56	3.43	0.57	1.43	0.99	2.07	2.42	2.27	0.51	3.77	1.11	1.27	0.45
7274_at	1.13	0.38	0.93	0.49	3.9	1.31	0.3	0.1	1.2	0.9	0.57	0.47	1.7	0.96	0.87	0.74
4329_at	1.07	0.59	1.93	2.4	2.8	1.93	0.83	0.15	2.23	1.96	0.8	0.2	2.23	0.84	1.1	0.44
6252_at	0.4	0.26	0.97	0.59	0.3	0.26	0.13	0.06	0.73	0.84	1.1	0.7	0.87	1	2.9	1.74
5309_at	1.33	1.47	0.83	1.02	1.33	1.12	0.8	0.7	3.1	2.03	1.83	1.25	0.63	0.4	0.27	0.12
8972_at	3.4	2.43	0.87	0.91	0.5	0.35	1.3	0.89	2.37	2.02	1.83	0.15	2.43	1.04	1.03	0.74
5185_at	0.53	0.45	0.5	0.44	3.47	0.21	2	0.87	2.93	1.72	3.3	0.79	1.5	0.85	1.63	0.83
11381_at	1.83	1.59	1.37	1.25	2.1	2.52	0.77	0.21	0.63	0.4	1.13	0.93	2.07	1.1	2.23	2.19
5736_at	1.6	1.47	3.4	0.7	3.87	0.99	2.13	1.22	0.83	0.25	3.2	0.5	2.47	1.91	0.73	0.42
4041_at	1.73	1.81	0.73	0.75	1.7	0.89	2.13	2.48	0.5	0.17	0.73	0.25	1.2	0.17	2.33	2.41
6326_at	1.2	1.15	0.77	0.55	1.87	1.4	1.53	2.31	2.73	2.18	0.37	0.12	0.73	0.61	0.33	0.23
11215_at	0.5	0.17	0.63	0.51	2.23	1.76	1.77	0.98	3.63	1.29	0.8	0.3	1.2	0.36	1.33	0.99
5604_at	1.57	1.69	0.9	0.78	0.63	0.49	1.1	1.18	1.8	2.25	2.03	1.07	2.73	2.25	0.63	0.42
6878_at	0.43	0.21	0.73	0.31	0.9	0.66	2.83	2.15	1	0.7	1.93	1.36	1.17	0.75	2.1	1.8
11231_at	0.97	0.31	2.37	1.25	3.23	1.72	2.77	1.79	0.8	0.17	2.2	1.93	1.93	1.4	1.13	0.68
6518_at	0.87	0.74	1	1.08	1.97	0.67	0.7	0.87	2.23	1.25	1.67	1.25	3.53	1.45	2.77	1.89
10004_at	0.4	0.17	1.83	1.72	0.63	0.32	0.47	0.15	2.07	1.4	1.07	0.57	1.63	1.03	2	2.86
4389_at	2.43	2.32	1.27	1.06	2.17	0.61	1.87	2.72	0.97	0.4	1.4	0.52	3.03	2.08	1.47	1.42
9945_at	1.93	2.74	2.23	1.7	2.73	2.08	2.63	0.98	3.63	0.76	1.67	0.84	4.73	0.55	1	0.89
5078_at	1.03	0.78	0.43	0.21	2.07	2.89	0.5	0	0.83	0.51	1	0.61	0.77	0.47	1.63	2.14
3959_at	0.93	0.59	1.33	1.97	2.13	2.84	1.7	1.45	0.63	0.76	0.63	0.31	1.07	0.83	0.77	0.64
7225_at	0.3	0.17	2.77	0.38	3.1	2.21	2.5	1.04	1.67	1.22	1.73	1.33	2.67	0.68	2.83	2.06
8782_at	0.67	0.64	0.87	1.08	1.93	1.11	0.7	0.35	2.03	2.17	0.57	0.15	4.03	1.46	1.07	0.64
9715_at	2.13	2.94	0.33	0.15	0.8	0.7	0.47	0.15	0.83	0.35	0.27	0.21	0.53	0.49	0.3	0
3935_at	2.93	2.6	0.33	0.06	1	1.22	0.27	0.21	3.77	1.06	0.27	0.21	0.9	0.7	0.87	1.16
3854_f_at	3.8	1.04	2.4	1.93	3.23	1.36	2.4	2.69	2	1.61	2.47	0.83	3.5	2.72	1.43	1.7
10109_at	2.67	2.5	0.8	0.95	2.33	1.9	2.73	1.55	4.6	0.98	0.6	0.61	1.47	0.59	3.03	2.22
7720_at	1.27	1.5	2.83	0.47	3.13	2.14	1.47	0.75	0.87	0.32	2.33	1.8	1.77	0.75	0.7	0.56
6928_at	3.07	2.31	2.97	2.37	2.33	1.17	3.43	0.06	3	0.79	2.13	0.81	2.17	1.68	0.47	0.12
10356_at	3.8	2.78	0.67	0.4	1.13	0.47	1.9	1.18	1.93	1.79	1.93	0.78	3.13	2.2	3.33	1.27
4977_at	1.37	0.75	2.53	1.27	2.4	1.41	3.7	2.1	1.2	0.26	0.6	0.61	4.6	1.25	0.87	0.81
6750_i_at	2.43	1.91	1.3	0.98	0.73	0.67	1.7	0.85	2.53	2.8	0.53	0.4	1.6	1.04	0.9	0.78
7777_at	2.8	2.72	1.3	1.23	1.4	0.79	2.07	1.7	1.33	1.37	0.4	0.44	2.1	2.21	0.47	0.21
8783_at	2.8	2.8	0.6	0.53	2.13	0.29	2.43	1.21	2.27	1.36	2.1	3.12	2.27	2.04	2.53	1.3
5354_at	0.83	0.84	1.03	0.42	3.5	1.87	3.8	1.77	0.4	0.26	1.13	0.67	3.1	1.55	0.37	0.12
10549_at	1.17	0.55	1.17	0.15	1.8	1.15	1	0.44	0.8	0.26	1.13	0.84	2.77	2.64	2.07	2.28
4950_at	2.4	1.76	1.47	1.42	1.2	0.6	0.47	0.55	3.87	1.9	1.83	0.32	1.4	0.61	2	1.37
5399_at	1.27	1.02	0.73	0.5	1.3	1.56	0.47	0.32	3.07	2.45	2	0.4	3.9	2.01	1.17	0.93
4749_at	1.63	1.38	1.43	1.04	4.13	1.53	1.93	2.4	2.4	2.52	1.87	1.58	1.07	0.74	0.8	0.17
7648_at	3.07	1.91	2.77	1.44	4.6	1.37	4.03	1.78	1.33	0.49	1.7	1.25	1.13	0.85	1.43	0.87
3544_at	2.07	3.23	2.23	1.2	3.77	1.21	5.47	0.31	2.6	1.76	3.4	1.23	2.13	2.92	3.67	1.16
11252_s_at	2.07	1.57	2.63	1.85	2.03	1.07	0.97	1.24	3.63	2.08	0.77	0.64	1.4	0.95	2.7	1.05
4552_at	1.57	1.35	2.67	2.63	0.77	0.64	0.37	0.21	4.07	1.85	4.3	1.92	4.33	1.05	0.47	0.31
8502_at	1.03	0.38	1.1	1.06	2.33	1.96	1.53	1.55	3.03	2.58	1	0.26	2	1.15	1.97	2.47
7187_at	2.5	0.95	2.1	0.79	1	0.17	1.43	0.32	3.6	3.03	0.87	0.42	2.17	1.5	0.8	1.13
6198_at	2.67	2.4	2.6	2	2.5	1.82	0.6	0.26	3.87	1.89	1.83	0.51	2.8	1.48	2.2	0.3
4034_at	2.2	2.62	1.3	1.56	4.1	2.71	2.77	2.23	0.87	0.5	0.97	0.99	2.63	1	2.13	1.6
11140_at	2.77	2.6	2.6	0.6	4.07	1.68	3.2	1.37	4.13	0.47	1.3	0.87	2.43	1.34	4.37	0.51
6096_at	0.7	0.3	1.7	1.82	5.23	0.7	3.83	1.91	4.2	1.01	2.27	1.7	1.87	1.19	1.2	0.66
11375_at	0.67	0.55	0.5	0.2	2.8	2.98	1.63	1.27	1.57	1.42	1.13	1.18	2.87	1.93	2.53	1.9
6476_at	2.67	2.74	2.97	1.19	1.97	1.37	2.47	0.4	2.6	3.1	1.57	1.36	2.67	0.59	2.27	1.08
11323_at	0.13	0.06	3.4	2.26	1.57	1.42	2.83	0.7	0.23	0.06	2.6	1.61	2.9	2.84	1.03	1.19
9920_at	2.47	2.16	1.27	1.24	0.67	0.57	1.87	1.27	1.97	0.75	0.5	0.1	3.47	2.47	1.97	1.47
5156_at	2.37	1.16	2.77	0.49	1.77	1.27	2.7	1.64	2.6	0.92	2.5	1.99	2.27	2.18	3.77	2.25
5693_at	1.93	0.91	3.27	0.5	3.27	1.63	2.17	1	2.1	1.61	3.53	1.55	4.03	2.05	2.57	2.06
10486_s_at	3.4	1.14	2.5	1.18	2.7	1.95	4.13	2.3	2.63	2.08	2.53	1.85	3.37	2.2	2.4	2.15
4533_at	4.27	1.06	4.3	1.91	3.03	2.87	3.47	0.5	3.6	2.12	2.9	1.06	2.63	2.19	1.8	0.96
6126_at	1.57	1.59	0.1	0	2.3	3.03	0.5	0.2	2.93	2.94	0.4	0.3	1.27	0.81	1.27	1.68
9944_at	3	1.22	3.23	0.93	1.73	1.74	2.03	1.46	3.7	1.65	3.53	0.97	3.83	2.35	4.03	1.24
4039_at	1.87	1.78	4.23	1.72	2.1	1.51	3.03	2.27	1.33	0.75	0.77	0.12	0.97	0.6	2.07	1
7198_at	0.37	0.25	3.07	1.62	4.33	2.27	3.47	1.29	2.43	1.72	2.9	0.92	4.17	1.95	4.5	1.47
7346_at	5.07	1.33	1.63	1.56	2.7	0.9	2.4	1.75	3.73	1.46	1.43	1	3.17	1.46	2.37	1.7
9741_at	1.83	0.31	1.37	0.32	4.1	2.25	3.1	2.52	1.7	0.7	1.23	0.15	1.67	0.76	1.93	0.6
8570_at	1.73	2.33	1.5	1.06	4.33	1.62	2.6	2	2.1	1.42	1	0.98	3.17	3.01	1.23	0.55
5505_at	1.67	2.02	2.2	1.67	4.47	0.6	1.1	0.78	1.13	0.95	1.03	0.38	3.5	2.66	1.5	0.95
5229_at	2.4	3.38	2.67	0.81	4.27	1.27	4.67	0.75	4	1.85	1.37	0.83	4.83	0.75	3.93	0.51
4257_at	1.3	0.78	2.17	1.55	2.13	2.39	3.8	2.33	2.07	1.57	4.17	2.15	2.93	0.8	4.87	0.21
11045_at	0.4	0.2	1.03	1.36	1.5	1.59	0.47	0.38	4.93	1.46	1.97	1.53	2.4	1.15	0.33	0.06
6796_at	0.2	0	0.87	1.16	2.87	3.16	1.5	0.89	1.23	1.71	1.5	1.13	0.83	0.47	0.6	0.44
5151_at	0.2	0.26	0.8	0.4	3.13	2.86	1.67	2.54	1.53	2.31	0.4	0.17	1.5	2.17	0.63	0.58
6829_at	2.6	3.33	2.4	0.95	3.4	1.97	3.23	2	2.7	1.08	2.4	0.72	0.8	0.96	2.97	0.21
3983_at	2.6	2.19	1.8	0.44	2.67	2.23	3.73	2.41	1.6	0.98	2.73	0.68	3	1.92	1.83	1.1
8778_at	1.43	1.07	3.13	2.2	4.03	1.22	4.17	1.93	2.43	1.89	3.2	1.59	3	1.81	2	1.97
11198_at	2.83	3.27	0.63	0.35	1.7	2.25	0.53	0.15	1.5	1.74	1.2	0.46	0.97	0.65	0.67	0.55
8258_at	1	0.44	3.17	0.85	3.3	2.26	2.7	0.78	3.4	3.05	2.4	2.33	2.9	2.84	2.37	1.11
5207_at	0.5	0.44	0.97	0.59	3.6	2.95	2.13	1.24	0.8	0.46	1.43	1.27	1.3	0.72	2.3	1.51
8785_at	3.53	2.4	1.07	1.15	2.6	3.2	0.43	0.21	3.67	0.32	0.33	0.21	4.17	3.29	0.33	0.15
11380_at	3.17	1.05	1.27	0.65	0.87	0.58	1.87	2.04	4	1.31	1.27	0.59	4.27	2.3	0.97	0.32
4550_at	0.7	0.52	1	1.13	2.77	1.54	1.03	0.97	1.1	1.23	0.3	0.1	4.37	2.82	0.57	0.38
11014_at	4.43	3.41	2.27	1.87	1.63	1.05	4.23	1.95	1.6	1.35	1.3	1.39	1.63	0.86	2.13	1.42
9620_at	3.3	2.43	2.1	1.47	4.6	1.65	4.37	1.36	2.2	1.15	2.97	2.41	2.37	0.9	3.2	3.18
9652_at	2.2	2.04	3.03	2.45	3.73	1.35	4.6	1.35	4.33	2.8	1.7	1.57	1.1	0.3	2.67	2.06
6181_r_at	3.5	1.92	2.87	0.74	1.67	1.21	1.53	1.45	4.63	1.55	2.43	1.25	2	1	4.23	2.9
3855_s_at	4.8	1.97	0.4	0.2	0.77	0.51	0.47	0.06	1.3	1.91	0.43	0.49	1.57	0.75	0.33	0.23
4142_at	2.63	1.83	2.83	0.23	4.87	0.5	4.1	2.17	3.2	0.52	2.5	0.85	4.27	2.46	3.93	0.78
5177_at	0.53	0.42	1.87	1.23	2.37	1.9	5.37	1.72	1.57	2.11	1.17	0.55	0.87	0.74	1.37	1.42
4819_at	0.67	0.55	1.07	1.33	0.7	0.72	0.33	0.06	1.6	1.21	1.9	1.04	2.83	3.44	2.6	0.75
11382_at	2.6	1.05	1.77	0.97	2.53	2.27	2.83	1.65	3.77	1.91	0.77	0.31	2.87	3.37	0.53	0.25
4904_at	3.9	1.39	1.47	0.68	2.83	3.4	2.43	3.04	2	1.73	1.83	1.45	1.2	1.22	1.8	1.25
5946_at	0.57	0.06	0.63	0.21	4.63	2.76	0.73	0.29	0.8	0.17	0.43	0.15	1.5	0.98	0.6	0.1
6955_s_at	0.93	0.58	1.27	0.76	0.87	1.16	2.2	1.84	2.17	0.96	0.5	0.44	2.97	3.33	2.43	3.44
5028_at	3.33	3.13	0.7	0	2.57	1.94	2.03	1	2.53	2.5	1.17	0.32	1.7	0.66	0.93	0.15
8189_at	0.8	0.36	0.97	0.4	1.03	0.6	1	0.44	2	1.57	4.07	3.16	4.2	2.33	1.13	0.35
4461_r_at	2.37	2.39	3.2	2.1	4.23	2.29	1.37	0.61	3.5	1.31	2.3	1.97	1.9	0.7	1.97	1.89
6592_at	0.6	0.52	2	1.05	2.7	3.57	1.53	1.96	2.57	1.44	4.4	0.36	3.13	2.19	3.73	2.11
4885_at	2.33	1.86	1.77	0.93	3.8	1.18	3.17	2.05	3.23	2.37	2.27	0.49	4.87	1.78	2.67	1.55
5239_at	3.93	2.64	2.93	0.6	4.63	1.17	3.23	0.78	5.6	1.59	2.03	0.72	2	1.5	1.73	0.4
8639_at	0.57	0.21	1.07	0.31	2.43	3.87	0.27	0.12	2.23	1.42	1.53	1.36	0.77	0.25	0.77	0.38
5700_at	2.1	1.4	1.83	1.56	5.13	1.8	2.7	0.96	3.5	2.86	1.27	0.87	2.57	2.27	2.63	1.76
4792_at	0.67	0.74	1.4	1.01	3.1	3.41	0.6	0.35	1.77	1.77	1.43	0.6	1.07	0.29	0.67	0.15
11160_at	3.37	0.81	4.13	0.64	4.2	1.15	3.67	1.38	5.2	2.31	2.67	0.31	3.47	2.23	2.67	1.9
11208_at	2.83	2.84	1.77	0.42	5.47	1.62	4.4	1.47	5.4	2.35	2.7	2.04	4.2	2.38	1.77	0.38
3933_s_at	1.13	1.27	0.43	0.15	2.53	3.61	0.3	0	1.27	0.85	0.4	0.2	3.1	3.5	0.43	0.15
9077_at	1.13	0.12	2.17	1.36	2.47	1.3	2.1	1.21	4.23	2.68	1.63	1.4	2.47	1.5	3.17	1.57
5613_at	4.6	2	3.53	0.61	4.57	0.97	4.37	2.31	2.7	2.07	3.67	0.92	4.77	2.17	1.53	1.11
9314_at	1.93	0.32	4.43	0.51	3.7	1.61	4	1.25	4.93	1.16	3.87	1.21	4.63	2.5	1.6	0.46
10293_at	1.77	1.82	2.8	0.66	2.8	0.7	3.73	2.78	5.4	1.47	2.7	1.15	1.83	0.67	2	1.39
8018_i_at	3.03	3.04	2.53	1.72	2.63	2.75	1.23	0.99	2.53	1.12	3.4	2.36	5.63	1.37	1.67	2.54
6836_at	1.03	0.71	3.67	3.41	2	1.4	2.43	0.95	0.9	0.61	1.23	0.75	1.13	0.47	1.67	1.27
7424_at	1.2	0.79	2.4	1.4	3.23	1.45	3.77	3.4	1.77	0.95	2.97	2.15	2.5	3.12	2.53	0.71
6032_at	3.43	0.45	0.9	1.04	1.97	1.46	3.97	2.93	2.87	1.91	3.67	3.16	2.6	1.95	3.6	0.92

4331_at		YHR070C	YHR070C questionable ORF	UNKNOWN
9143_at	KRE25	YNL296W	YNL296W questionable ORF	UNKNOWN
9471_at	APG16	YMR159C	YMR159C Protein homologous to human Sin3 complex component SAP18, p	UNKNOWN
9894_at		YLR445W	YLR445W hypothetical protein	UNKNOWN
7040_g_at		YBR266C	YBR266C probable membrane protein	UNKNOWN
5916_at		YDR537C	YDR537C questionable ORF	UNKNOWN
7721_at		YPR014C	YPR014C hypothetical protein	UNKNOWN
4473_i_at	DOG1	YHR044C	YHR044C 2-deoxyglucose-6-phosphate phosphatase	NUTRITIONAL ANALOGUE RESISTANCE
9206_at		YNL324W	YNL324W hypothetical protein	UNKNOWN
7039_at		YBR266C	YBR266C probable membrane protein	UNKNOWN
9862_at		YLR458W	YLR458W questionable ORF	UNKNOWN
6956_s_at		YCL074W	YCL074W Reverse transcriptase	UNKNOWN
10000_at	JIP3	YLR331C	YLR331C questionable ORF	UNKNOWN
8284_at		YOR263C	YOR263C questionable ORF	UNKNOWN
5411_at		YFL019C	YFL019C hypothetical protein	UNKNOWN
6833_at		YCR045C	YCR045C Protease	UNKNOWN
6879_at		YCR001W	YCR001W hypothetical protein	UNKNOWN
9486_at	REC114	YMR133W	YMR133W mRNA is induced early in sporulation	MEIOSIS, RECOMBINATION
3628_f_at	COS10	YNR075W	YNR075W Protein with strong similarity to subtelomerically-encoded proteins	UNKNOWN
6711_at		YDL242W	YDL242W strong similarity to hypothetical protein YPR079w	UNKNOWN
10330_at	PUF3	YLL013C	YLL013C similarity to Drosophila pumilio protein	UNKNOWN
7215_at		YBR124W	YBR124W questionable ORF	UNKNOWN
5254_i_at		YGL258W	YGL258W strong similarity to hypothetical protein YOR387c	UNKNOWN
6953_at	LSR1	LSR1	LSR1 snRNA	MRNA SPLICING
9002_at		YNL120C	YNL120C questionable ORF	UNKNOWN
7575_at		YPR177C	YPR177C questionable ORF	UNKNOWN
4998_at		YGR025W	YGR025W questionable ORF	UNKNOWN
9063_at	SLZ1	YNL196C	YNL196C sporulation-specific protein with a leucine zipper motif, regulated by	MEIOSIS
8164_at		YOR365C	YOR365C strong similarity to YAL053w	UNKNOWN
5187_at	IME4	YGL192W	YGL192W IME4 appears to activate IME1 in response to cell-type and nutritic	MEIOSIS
4327_at		YHL006W	YHL006W questionable ORF	UNKNOWN
5945_at		YDR521W	YDR521W questionable ORF	UNKNOWN
10913_at		YJR120W	YJR120W hypothetical protein	UNKNOWN
3975_at	Q0280	Q0280	ubiquinol--cytochrome-c reductase subunit (cytochrome B) Found forward in I	RESPIRATION
4762_at		YGR242W	YGR242W questionable ORF	UNKNOWN
9906_at		YLR415C	YLR415C questionable ORF	UNKNOWN
5202_at		YGL177W	YGL177W questionable ORF	UNKNOWN
7165_at		YBR209W	YBR209W hypothetical protein	UNKNOWN
7599_i_at	TPO3	YPR156C	YPR156C similarity to multidrug resistance proteins	UNKNOWN
10383_at		YLL047W	YLL047W questionable ORF	UNKNOWN
5391_at		YFL040W	YFL040W similarity to yeast glucose transport proteins	UNKNOWN
9609_at		YMR031W	YMR031W questionable ORF	UNKNOWN
8250_at		YOR314W	YOR314W hypothetical protein	UNKNOWN
11379_at	SEO1	YAL067C	YAL067C Suppressor of Sulfoxyde Ethionine resistance	DRUG RESISTANCE
9506_at	YIM2	YMR151W	YMR151W hypothetical protein	UNKNOWN
5002_at		YGL015C	YGL015C hypothetical protein	UNKNOWN
9289_at		YMR324C	YMR324C strong similarity to YBL108w, YCR103c and YKL223w	UNKNOWN
9076_at		YNL228W	YNL228W questionable ORF	UNKNOWN
9867_s_at		YLR465C	YLR465C questionable ORF	UNKNOWN
6959_s_at	HMLALPHA1	YCL066W	YCL066W transcripton factor involved in the regulation of the alpha-specific g	TRANSCRIPTION
10083_g_at		YLR235C	YLR235C questionable ORF	UNKNOWN
7287_at		YBR064W	YBR064W questionable ORF	UNKNOWN
10920_at		YJR079W	YJR079W questionable ORF	UNKNOWN
4791_at	AMA1	YGR225W	YGR225W weak similarity to human p55CDC and Cdc20p	SPORULATION
7271_at		YBR090C	YBR090C questionable ORF	UNKNOWN
7319_at		YBR051W	YBR051W questionable ORF	UNKNOWN
7437_at		YBL059W	YBL059W weak similarity to hypothetical protein YER093c-a	UNKNOWN
8939_at	YPT53	YNL093W	YNL093W rab5-like GTPase involved in vacuolar protein sorting and endocyt	ENDOCYTOSIS
7394_at	FMT1	YBL013W	YBL013W Probable met-tRNA formyltransferase, mitochondrial	UNKNOWN
11173_at	HAL5	YJL165C	YJL165C Protein kinase homolog, mutant is salt and pH sensitive	SALT TOLERANCE
11378_at	ALD1	ALD1	ALD1 Aldehyde dehydrogenase 1, mitochondrial	ETHANOL UTILIZATION
9514_at	SPC24	YMR117C	YMR117C component of spindle pole	CYTOSKELETON
7550_at		YPR197C	YPR197C questionable ORF	UNKNOWN
5540_at	MET6	YER091C	YER091C hypothetical protein identified by SAGE	METHIONINE BIOSYNTHESIS
7158_at		YBR203W	YBR203W hypothetical protein	UNKNOWN
5198_at		YGL182C	YGL182C questionable ORF	UNKNOWN
9166_at	HXT14	YNL318C	YNL318C hexose transport protein	TRANSPORT
6799_at		YCR105W	YCR105W Alcohol dehydrogenase	UNKNOWN
7395_at		YBL012C	YBL012C questionable ORF	UNKNOWN
8913_at		YNL028W	YNL028W questionable ORF	UNKNOWN
4567_at		YHL041W	YHL041W weak similarity to Drosophila hypothetical protein 6	UNKNOWN
10711_at		YKL118W	YKL118W questionable ORF	UNKNOWN
4745_at		YGR269W	YGR269W questionable ORF	UNKNOWN
7710_at		YPR045C	YPR045C similarity to C,elegans hypothetical protein	UNKNOWN
10165_at		YLR184W	YLR184W weak similarity to ribulose-bisphosphate carboxylase	UNKNOWN
8852_at		YNR004W	YNR004W weak similarity to bovine interferon gamma precursor	UNKNOWN
9061_at		YNL198C	YNL198C questionable ORF	UNKNOWN
10299_at		YLR047C	YLR047C similarity to hypothetical protein YGL160w	UNKNOWN
4562_at	ARN2	YHL047C	YHL047C similarity to C,carbonum toxin pump	UNKNOWN
9417_at		YMR192W	YMR192W similarity to mouse Tbc1 protein	UNKNOWN
5140_at		YGL149W	YGL149W questionable ORF	UNKNOWN
6443_at		YDR029W	YDR029W hypothetical protein	UNKNOWN
5738_at		YEL008W	YEL008W hypothetical protein	UNKNOWN
7182_at	DTR1	YBR180W	YBR180W Probable resistance protein	UNKNOWN
4871_at		YGR126W	YGR126W weak similarity to hypothetical protein YPR156c	UNKNOWN
4345_at	PFS1	YHR185C	YHR185C hypothetical protein	MEIOSIS (PUTATIVE)
5499_at	SPO73	YER046W	YER046W questionable ORF	UNKNOWN
6359_at		YDR124W	YDR124W hypothetical protein	UNKNOWN
9570_at		YMR084W	YMR084W putative pseudogene	UNKNOWN
9389_at		YMR251W	YMR251W strong similarity to YKR076w and YGR154c	UNKNOWN
10966_at		YJR037W	YJR037W questionable ORF	UNKNOWN
7372_at		YBR013C	YBR013C hypothetical protein	UNKNOWN
5029_at	HOP2	YGL033W	YGL033W Meiosis-specific gene required for the pairing of homologous chror	MEIOSIS, CHROMOSOME PAIRING (PUTATIVE)
9733_at	SMA2	YML066C	YML066C hypothetical protein	UNKNOWN
10513_at		YKR041W	YKR041W hypothetical protein	UNKNOWN
4540_at	SPO11	YHL022C	YHL022C Encodes one of the earliest meiosis-specific recombination functior	MEIOSIS, RECOMBINATION
6667_at		YDL196W	YDL196W hypothetical protein	UNKNOWN
8483_at		YOR055W	YOR055W questionable ORF	UNKNOWN
3988_at	Q0115	Q0115	Q0115 cytochrome-c oxidase chain III	RESPIRATION
8148_at		YOL013W	YOL013W hypothetical protein identified by SAGE	UNKNOWN
7773_at		YPL025C	YPL025C questionable ORF	UNKNOWN
5978_at		YDR509W	YDR509W questionable ORF	UNKNOWN
7889_at		YPL136W	YPL136W questionable ORF	UNKNOWN
7180_at		YBR178W	YBR178W questionable ORF	UNKNOWN
6520_at		YDL032W	YDL032W questionable ORF	UNKNOWN
5594_at	FLO8	YER109C	YER109C putative transcriptional activator of FLO1	FLOCCULATION
4163_at	FYV2	YIL054W	YIL054W weak similarity to fruit fly NADH dehydrogenase	UNKNOWN
4831_at		YGR176W	YGR176W questionable ORF	UNKNOWN
11093_at		YJL064W	YJL064W hypothetical protein	UNKNOWN
11360_at		YAL048C	YAL048C weak similarity to GTP-binding proteins	SECRETION (PUTATIVE)
6686_at		YDL221W	YDL221W questionable ORF	UNKNOWN
6260_at		YDR203W	YDR203W questionable ORF	UNKNOWN
7696_at		YPR076W	YPR076W questionable ORF	UNKNOWN
7176_at		YBR174C	YBR174C questionable ORF	UNKNOWN
5167_at		YGL168W	YGL168W questionable ORF	UNKNOWN
8877_r_at		YNL017C	YNL017C hypothetical protein	UNKNOWN
6581_at	QRI2	YDL105W	YDL105W protein of unknown function	UNKNOWN
6623_at		YDL152W	YDL152W questionable ORF	UNKNOWN
9671_at		YML037C	YML037C hypothetical protein	UNKNOWN
6855_at		YCR022C	YCR022C hypothetical protein	UNKNOWN
4147_at	HOP1	YIL072W	YIL072W Meiosis-specific protein involved in homologous chromosome synap	MEIOSIS, SYNAPSIS
8619_at		YOL079W	YOL079W similarity to NADH dehydrogenases	UNKNOWN
10955_at		YJR071W	YJR071W questionable ORF	UNKNOWN
7734_at		YPR027C	YPR027C similarity to YNL019c and YNL033w	UNKNOWN
4094_at	GAT4	YIR013C	YIR013C strong similarity to YLR013w, similarity to YMR136w	UNKNOWN
7408_at		YBL044W	YBL044W hypothetical protein	UNKNOWN
8628_at	NUF2	YOL069W	YOL069W 53-kDa coiled-coil protein	CYTOSKELETON
7988_at		YPL216W	YPL216W similarity to YGL133w	UNKNOWN
5133_at		YGL109W	YGL109W questionable ORF	UNKNOWN
6295_at		YDR193W	YDR193W questionable ORF	UNKNOWN
9419_at		YMR193C	YMR193C questionable ORF	UNKNOWN
9543_at	SRT1	YMR101C	YMR101C similarity to YBR002c	PROTEIN GLYCOSYLATION
5165_at	SPO74	YGL170C	YGL170C hypothetical protein	UNKNOWN
11053_at		YJL015C	YJL015C questionable ORF	UNKNOWN
5984_at	UGO1	YDR470C	YDR470C similarity to chromosome segregation protein Cse1p	UNKNOWN
5262_at	HFM1	YGL251C	YGL251C C4 zinc finger DNA-binding protein of low sequence specificity in v	UNKNOWN
6758_at		YCR102W	YCR102W hypothetical protein identified by SAGE	UNKNOWN
4721_at		YGR291C	YGR291C hypothetical protein	UNKNOWN
7672_at		YPR096C	YPR096C hypothetical protein	UNKNOWN
6116_at		YDR374C	YDR374C similarity to hypothetical A, thaliana protein BAC F21M12	UNKNOWN
4035_at	UBP7	YIL156W	YIL156W questionable ORF	PROTEIN DEGRADATION, UBIQUITIN-MEDIATED
6303_at		YDR157W	YDR157W questionable ORF	UNKNOWN
6873_at		YCL006C	YCL006C questionable ORF	UNKNOWN
5726_at	MMS21	YEL019C	YEL019C Protein involved in DNA repair	DNA REPAIR
8822_at		YNR063W	YNR063W weak similarity to CYC1/CYP3 transcription activator	UNKNOWN
7665_at		YPR089W	YPR089W questionable ORF	UNKNOWN
7249_at		YBR113W	YBR113W questionable ORF	UNKNOWN
5124_at		YGL118C	YGL118C questionable ORF	UNKNOWN
8325_at		YOR214C	YOR214C hypothetical protein	UNKNOWN
7142_at		YBR232C	YBR232C questionable ORF	UNKNOWN
11292_at		YAR030C	YAR030C hypothetical protein	UNKNOWN
5809_i_at		YEL074W	YEL074W similarity to subtelomeric encoded proteins	UNKNOWN
5498_at		YER038W	YER038W questionable ORF	UNKNOWN
6439_at	FYV1	YDR024W	YDR024W hypothetical protein	UNKNOWN
9935_at		YLR400W	YLR400W hypothetical protein	UNKNOWN
6491_at		YDL016C	YDL016C questionable ORF	UNKNOWN
8152_f_at	CDC21	YOR074C	YOR074C Thymidylate synthase	DNA REPLICATION
6934_at		YCL041C	YCL041C questionable ORF	UNKNOWN
8496_at		YOR068C	YOR068C hypothetical protein	UNKNOWN
6007_at	ECM11	YDR446W	YDR446W ExtraCellular Mutant	CELL WALL MAINTENANCE
9596_at	SOV1	YMR066W	YMR066W Synthesis Of Var	RESPIRATION (PUTATIVE)
4349_at		YHR189W	YHR189W similarity to peptidyl-tRNA hydrolases	PROTEIN SYNTHESIS
3974_at	Q0280	Q0280	ubiquinol--cytochrome-c reductase subunit (cytochrome B) Found forward in I	RESPIRATION
5273_at	DOC1	YGL240W	YGL240W Doc1p and Cdc26p are associated with the anaphase-promoting c	CELL CYCLE
5255_s_at		YGL258W	YGL258W strong similarity to hypothetical protein YOR387c	UNKNOWN
5108_at	MF(ALPHA)2	YGL089C	YGL089C alpha mating factor	MATING
10972_at	POL32	YJR043C	YJR043C third (55 kDa) subunit of DNA polymerase delta	DNA REPLICATION
4897_at		YGR107W	YGR107W questionable ORF	UNKNOWN
6003_at		YDR442W	YDR442W questionable ORF	UNKNOWN
8700_at		YOL134C	YOL134C questionable ORF	UNKNOWN
6804_at		YCR064C	YCR064C questionable ORF	UNKNOWN
10687_at		YKL097C	YKL097C hypothetical protein	UNKNOWN
6613_at		YDL118W	YDL118W questionable ORF	UNKNOWN
7703_at		YPR039W	YPR039W questionable ORF	UNKNOWN
6224_at	YAP6	YDR259C	YDR259C bZIP protein	SALT TOLERANCE
7679_at		YPR059C	YPR059C questionable ORF	UNKNOWN
9362_at	PRP24	YMR268C	YMR268C U4/U6 snRNA-associated splicing factor	MRNA SPLICING
7624_at	FYV15	YPR136C	YPR136C questionable ORF	UNKNOWN
9866_i_at		YLR465C	YLR465C questionable ORF	UNKNOWN
11188_at		YJL150W	YJL150W questionable ORF	UNKNOWN
5950_at		YDR526C	YDR526C questionable ORF	UNKNOWN
6908_at		YCL023C	YCL023C questionable ORF	UNKNOWN
9709_at	GSF2	YML048W	YML048W questionable ORF	UNKNOWN
8146_at		YOR392W	YOR392W hypothetical protein	UNKNOWN

Up-regulated under anaerobiosis (FC = fold change, ANA = anaerobic, A = aerobic)

Probe Set	Gene name	systematic name	functional description	cellular function	C-Lim ANA Average	C-Lim ANA Stdev	N-Lim ANA Average	N-Lim ANA Stdev	P-Lim ANA Average	P-Lim ANA Stdev	S-Lim ANA Average	S-Lim ANA Stdev	C-Lim A Average	C-Lim A Stdev	N-Lim A Average	N-Lim A Stdev	P-Lim A Average	P-Lim A Stdev	S-Lim A Average	S-Lim A Stdev	FC C-Lim ANA vs C-Lim A	FC N-Lim ANA vs N-Lim A	FC S-Lim ANA vs S-Lim A	FC P-Lim ANA vs P-Lim A
4069_at	MGA2	YIR033W	YIR033W may be involved in the remodeling chromatin structure	TRANSCRIPTION	103.3	56.4	109.7	27.1	102.3	7.6	77.2	8.9	45.7	7.9	29.6	4.4	23.7	5	24.5	4.7	2.3	3.7	4.3	3.1
7480_at	SRO77	YBL106C	YBL106C yeast homolog of the Drosphila tumor suppressor. lethal giant larvae	SECRETION (PUTATIVE)	244.2	159.3	345.7	61.7	255.5	45.1	255.8	47.7	83.9	19.2	78	13.8	56.9	15.1	37.1	8.9	2.9	4.4	4.5	6.9
11249_f_at	PAU1	YJL223C	YJL223C strong similarity to members of the Srp1p/Tip1p family	UNKNOWN	1482.5	494.1	1064.6	60.6	1454.1	196.2	2809.7	662.2	336	168.3	126.9	17.3	77	10.5	171.2	64	4.4	8.4	18.9	16.4
4114_at	TIR3	YIL011W	YIL011W strong similarity to members of the Srp1p/Tip1p family	UNKNOWN	3937.6	1175.9	2435.7	592.6	3335.7	80.3	3306.2	390.3	252.3	93.3	88.8	6	84.2	13.7	174	17.3	15.6	27.4	39.6	19
4563_f_at	0	YHL046C	YHL046C strong similarity to members of the Srp1p/Tip1p family	UNKNOWN	1321.7	414.8	737.2	120.6	1128.7	78.3	2915.5	867	153.2	61.1	88.3	7.5	74.2	10	137.1	20.1	8.6	8.3	15.2	21.3
5410_f_at	PAU5	YFL020C	YFL020C member of the seripauperin protein\/gene family (see Gene_class PAU)	UNKNOWN	649.2	274.8	294.2	43.1	356.4	43.8	623	188	160.3	109.8	42.8	5.6	41.6	19.6	67.9	9.4	4.1	6.9	8.6	9.2
5711_at	TIR1	YER011W	YER011W Cold-shock induced protein of the Srp1p\/Tip1p family of serine-alanine-rich pr	STRESS RESPONSE (PUTATIVE)	4568.3	3906.3	3953.1	1303.2	4155.5	210.5	4857.4	1028.3	149.7	28.1	74.4	11.6	87.4	4.2	137	17.7	30.5	53.2	47.5	35.5
6798_f_at	PAU3	YCR104W	YCR104W member of the seripauperin protein\/gene family (see Gene_class PAU)	UNKNOWN	361	204.7	216.1	12.2	462.3	42.3	633.6	247.7	139.3	116.5	24.3	6.5	15.6	4.5	28.4	6	2.6	8.9	29.6	22.3
8526_at	TIR4	YOR009W	YOR009W similarity to Tir1p and Tir2p	UNKNOWN	3446.6	1086.8	2031.6	474	2781.5	145	2998.7	421.9	100.8	44.4	48.7	7.1	42.5	6.1	93.4	29.3	34.2	41.7	65.4	32.1
8527_at	TIR2	YOR010C	YOR010C Cold-shock induced protein of the Srp1p\/Tip1p family of serine-alanine-rich pr	UNKNOWN	1563.1	194.4	599.7	71.5	1052.3	137.3	778.1	58.2	159.4	23.5	129.8	14.9	147.6	20.5	267.7	113.8	9.8	4.6	7.1	2.9
8720_f_at	0	YOL161C	YOL161C strong similarity to members of the Srp1p/Tip1p family	UNKNOWN	460.2	206.1	448.5	74.2	510.8	55.5	801	339.5	59.2	30.4	36.7	13.4	27.8	8.3	45.7	29.9	7.8	12.2	18.4	17.5
8786_f_at	PAU6	YNR076W	YNR076W member of the seripauperin protein\/gene family	UNKNOWN	554.4	175	435.7	65.4	483.5	31.1	1011.8	389.7	64.2	22	61.4	4.9	45	5.6	73.3	14.7	8.6	7.1	10.7	13.8
9865_f_at	PAU4	YLR461W	YLR461W member of the seripauperin protein\/gene family (see Gene_class PAU)	UNKNOWN	1218.8	292	825	123.6	1020.1	165.2	2029.3	532.7	214.2	117	114.3	12.7	86.7	6.2	140.6	30.9	5.7	7.2	11.8	14.4
4876_at	0	YGR131W	YGR131W strong similarity to Nce2p	UNKNOWN	214.6	88.9	310.6	58.9	316.2	24.9	508.3	124.8	28.4	5.8	35.3	3.2	18.4	4.4	22.9	8.2	7.6	8.8	17.2	22.2
4565_at	ECM34	YHL043W	YHL043W ExtraCellular Mutant	CELL WALL MAINTENANCE	32.5	18.8	43.5	14.1	81.7	20.5	76.6	9.5	12	2.9	14.1	3.4	12	2.7	12	0.6	2.7	3.1	6.8	6.4
4200_at	COX5B	YIL111W	YIL111W Cytochrome-c oxidase chain Vb	OXIDATIVE PHOSPHORYLATION	149.8	32.6	190.7	15.3	117.9	10.8	169.3	19.9	15.7	0.6	84.5	6.5	31.9	8.1	57.8	19.8	9.5	2.3	3.7	2.9
5357_at	GSY1	YFR015C	YFR015C Glycogen synthase (UDP-gluocse--starch glucosyltransferase)	GLYCOGEN METABOLISM	358	60.1	236.9	29	98.5	13.2	192.7	42.9	92	13.3	68.4	29.9	25.5	3.4	53.1	6.6	3.9	3.5	3.9	3.6
10525_at	YSR3	YKR053C	YKR053C DHS-1-P phosphatase	SPHINGOLIPID METABOLISM	852.8	235.7	604.7	60.4	539.8	76.9	1048.4	98.2	43.5	19	56.3	7.5	58	5.8	79.3	21.4	19.6	10.7	9.3	13.2
10962_at	BNA2	YJR078W	YJR078W similarity to mammalian indoleamine 2.3-dioxygenase	UNKNOWN	371.3	62.8	194.4	28.8	293.9	38.8	332.6	33.6	156.2	42.5	83	2.8	78.4	9.8	54.3	17	2.4	2.3	3.7	6.1
11254_at	0	YJL218W	YJL218W strong similarity to E.coli galactoside O-acetyltransferase	UNKNOWN	113.5	34.8	76.3	23	106.4	15.8	123.1	15.3	36.3	7.6	21.8	4.1	17.6	2	41.6	12.5	3.1	3.5	6	3
4100_at	MUC1	YIR019C	YIR019C cell surface flocculin with structure similar to serine\/threonine-rich GPI-anchorec	FLOCCULATION	760.4	209.2	1190.4	109.6	1289.9	82.9	2355.4	119	30.7	6.9	56.5	5.1	74.3	26.1	84.8	8.6	24.7	21.1	17.4	27.8
4832_at	ATF2	YGR177C	YGR177C Sterol O-acetyltransferase. acetylates certain toxic steroids such as pregnenolc	OTHER METABOLISM	384.6	16.4	467.8	50.9	415.5	22.4	368.2	105.4	79.8	43.5	34.1	4.5	31	1.8	46.1	23.5	4.8	13.7	13.4	8
5068_at	0	YGL039W	YGL039W similarity to V. vinifera dihydroflavonol reductase	UNKNOWN	291.1	47.4	291.5	33.7	398.7	55.8	414.9	12.2	103.7	19.1	59	7.3	122.8	11.1	78.4	11.9	2.8	4.9	3.2	5.3
5173_at	SUT1	YGL162W	YGL162W Involved in sterol uptake	TRANSPORT	168.4	14.5	53	7.3	75.6	19.2	67.4	9.4	37.5	8.7	20.6	3.8	37.3	1.2	17.3	2.4	4.5	2.6	2	3.9
5654_at	SER3	YER081W	YER081W strong similarity to phosphoglycerate dehydrogenases	UNKNOWN	123.1	24.3	73.4	13.6	58.1	26.7	136.7	32.8	33.5	5.9	31.8	1.4	22.4	0.4	36.1	4	3.7	2.3	2.6	3.8
5920_at	0	YDR541C	YDR541C similarity to dihydroflavonol-4-reductases	UNKNOWN	95	7.3	120.9	20.7	183.4	12.5	168	13.6	31.3	13	16.5	3.9	62.9	6.4	35.5	6	3	7.3	2.9	4.7
5940_at	0	YDR516C	YDR516C strong similarity to glucokinase	UNKNOWN	896.9	178.9	528	42.1	369.1	14.1	603.4	64.3	305.5	43.6	220.7	43.1	118.7	1.3	192.8	27	2.9	2.4	3.1	3.1
6270_at	UPC2	YDR213W	YDR213W regulatory protein involved in control of sterol uptake	UNKNOWN	34.3	26.5	49.9	21.9	66.2	15.4	90.3	15.7	13.2	5.7	12	3.3	12	1	12	5.4	2.6	4.2	5.5	7.5
6413_at	HEM13	YDR044W	YDR044W Coproporphyrinogen III oxidase	HEME BIOSYNTHESIS	836.7	385.8	659	23.1	703.4	165.5	918.4	176.4	54	10.3	49.7	4.6	45.9	12.1	35.7	1.9	15.5	13.3	15.3	25.7
6837_at	ARE1	YCR048W	YCR048W Acyl-CoA cholesterol acyltransferase (sterol-ester synthetase)	STEROL METABOLISM	385.8	17.2	412.2	13.2	576.3	38.2	555.8	71.3	74.5	28.6	77.8	6.1	101.9	56.8	138.9	79.6	5.2	5.3	5.7	4
7236_at	ADH5	YBR145W	YBR145W alcohol dehydrogenase isoenzyme V	GLYCOLYSIS	945.7	94.6	307.3	59.1	342.6	71.9	882.4	70.4	164.2	2.8	123	9.3	85.1	9.5	128.3	25.3	5.8	2.5	4	6.9
7263_at	AAC3	YBR085W	YBR085W mitochondrial ADP\/ATP translocator	TRANSPORT	354.5	147.5	310.8	70.8	386.9	105	588	23.3	12	1.5	20.2	2.5	21.6	6.5	21.1	3.6	29.5	15.4	17.9	27.8
8303_at	HES1	YOR237W	YOR237W homology to human oxysterol binding protein	STEROL METABOLISM	137.1	79.4	198.5	8	208.2	20.9	221.7	57.9	16.6	11	12	1.4	12	0.9	12	1.6	8.3	16.5	17.4	18.5
8560_at	0	YOL002C	YOL002C strong similarity to YDR492w and S.pombe hypothetical protein	UNKNOWN	685.5	182.4	1056.9	25.1	1073.7	138.1	1180.4	87.3	245.5	22.1	395.9	53.8	245.8	32.2	334.3	35	2.8	2.7	4.4	3.5
9293_at	SML1	YML058W	YML058W identified by SAGE	DNA REPLICATION	766.2	144.1	486.1	56.3	682.1	89.4	647.7	71	15.7	3.7	12	1.7	12	2	19.1	4.6	48.8	40.5	56.8	34
9628_at	PLB2	YMR006C	YMR006C strong similarity to Plb1p	PHOSPHOLIPID METABOLISM	972.3	171.1	511.8	61.3	563.2	90.2	731.4	68.9	352.9	97.2	81.5	10.8	68.2	12.1	69.2	16.1	2.8	6.3	8.3	10.6
5942_at	EUG1	YDR518W	YDR518W Protein disulfide isomerase homolog	PROTEIN FOLDING	194.4	60.4	192.5	36.2	170.7	15.1	186.3	28.9	32.3	12.9	40.3	2.5	32	4.2	31.3	8.1	6	4.8	5.3	6
6593_at	PMT5	YDL093W	YDL093W dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase	PROTEIN GLYCOSYLATION	102.2	46.3	113.3	6	132.4	9.9	114	19.9	37.9	2.4	40.2	3.2	37.4	4.6	41.3	10.8	2.7	2.8	3.5	2.8
10976_at	ANB1	YJR047C	YJR047C anaerobically expressed form of translation initiation factor eIF-5A	PROTEIN SYNTHESIS	3319.8	456.6	2392.3	253.5	2966.9	298.7	3193.4	443.9	24.7	5.9	16.1	2.7	18.3	3.3	25.2	3.8	134.2	148.6	161.9	126.9
9284_at	FET4	YMR319C	YMR319C Low-affinity Fe(II) transport protein	TRANSPORT	156.8	41.4	334.3	87.5	315.7	28.2	293.2	18.9	12	1.9	122.9	30.2	17.4	2.8	55.1	5.4	13.1	2.7	18.2	5.3
4112_at	PDR11	YIL013C	YIL013C Putative member of the ABC family of membrane transporters	TRANSPORT	114.3	22.7	123.2	6.9	148.2	18.3	118.9	18	27.3	3.9	32.3	5.4	42.7	2	27.4	5.1	4.2	3.8	3.5	4.3
8528_at	AUS1	YOR011W	YOR011W strong similarity to ATP-dependent permeases	UNKNOWN	801.5	181.8	772.9	56.4	865.9	98.1	896.3	72.8	35	10.5	55.2	12.4	45.3	9.5	33	10.3	22.9	14	19.1	27.2
10412_f_at	0	YLL064C	YLL064C strong similarity to members of the Srp1/Tip1p family	UNKNOWN	639.1	205.5	483.6	77	603.1	85.3	1408.3	553.1	84.3	25.7	70.8	11.6	52.9	1.5	81.9	27.4	7.6	6.8	11.4	17.2
10909_at	0	YJR116W	YJR116W similarity to hypothetical protein YPR114w	UNKNOWN	549.9	82.1	471.5	40.6	450.6	92.9	573.4	31.1	121.8	28.1	76.7	10.4	79.2	4.9	93.1	25.6	4.5	6.1	5.7	6.2
11142_at	SET4	YJL105W	YJL105W similarity to hypothetical protein YKR029c	UNKNOWN	89.8	41.1	80.1	24.3	70.2	5.8	79.1	9	13.4	9.3	12	1.8	12	2.9	12	3.3	6.7	6.7	5.9	6.6
3403_f_at	0	YDR542W	YDR542W strong similarity to subtelomeric encoded proteins	UNKNOWN	907.3	421.6	516	96	705.8	71.1	1645.2	498.3	188.3	119.3	79.1	6.9	50.1	4.4	93.6	17	4.8	6.5	14.1	17.6
3907_f_at	0	YAL068C	YAL068C strong similarity to subtelomeric encoded proteins	UNKNOWN	1067.4	182.5	580	39.9	740.6	1.7	1315.8	570.8	195.9	94.2	106.4	11.8	74.5	4.5	138.2	7.1	5.4	5.4	9.9	9.5
4280_f_at	0	YIL176C	YIL176C strong similarity to members of the Srp1p/Tip1p family	UNKNOWN	1487	558.6	944.9	94.7	1230.9	76.5	2595.5	503.2	285.2	156.4	124.5	6	72.8	11.3	194.4	33.3	5.2	7.6	16.9	13.4
4566_at	0	YHL042W	YHL042W similarity to subtelomeric encoded proteins	UNKNOWN	136.2	46.7	221.4	19.4	297.4	30.1	257.6	19.4	12	1.9	41.6	7.3	16.5	4.7	26	1.6	11.4	5.3	18.1	9.9
4723_f_at	0	YGR294W	YGR294W strong similarity to members of the Srp1p/Tip1p family	UNKNOWN	992.8	73.1	492.3	56.4	582.8	38.2	1609.8	576.7	206.5	126.7	74.7	11.9	48.9	15	106.9	28.8	4.8	6.6	11.9	15.1
5251_f_at	0	YGL261C	YGL261C strong similarity to members of the Srp1/Tip1 family	UNKNOWN	772	95.4	530.3	24.7	670.6	39.3	1517.9	462.3	161.3	93.4	84.5	13.1	70.7	6.1	94	22.2	4.8	6.3	9.5	16.1
6712_at	0	YDL241W	YDL241W hypothetical protein	UNKNOWN	60.8	10.5	48.6	19.9	59.8	10.5	62.9	16.8	12	6	12.3	3.3	12	1.6	12	6.1	5.1	4	5	5.2
7073_at	0	YBR300C	YBR300C strong similarity to hypothetical protein YGR293c	UNKNOWN	33.4	8.8	26.8	4	39.5	5.3	44.2	17	12	2.8	12	2.3	12	2.3	12	4.8	2.8	2.2	3.3	3.7
8023_at	0	YPL272C	YPL272C hypothetical protein	UNKNOWN	71.9	27	80.1	8.1	69.4	8.1	54.4	11.2	14.1	5.4	12	1	12	1.3	12	3.9	5.1	6.7	5.8	4.5
8530_g_at	0	YOR012W	YOR012W similarity to YDR391c	UNKNOWN	188.6	62.7	151.6	5	275.1	67.9	275.2	17.1	22.7	8	62.4	12.1	45.5	4.5	39.7	2.8	8.3	2.4	6	6.9
8531_at	0	YOR013W	YOR013W strong similarity to YDR391c	UNKNOWN	413.5	77.2	296.6	44.9	369.5	47.9	383	14.5	61.3	5.1	109.7	20.5	76.3	12.9	82.9	13.9	6.7	2.7	4.8	4.6
8642_at	0	YOL101C	YOL101C similarity to YOL002c and YDR492w	UNKNOWN	421.1	146.3	418.6	43.6	513.5	43.4	454.6	29.8	141.9	39.5	12	3.8	12	2	12	3.1	3	34.9	42.8	37.9
9290_f_at	0	YMR325W	YMR325W strong similarity to members of the Srp1p/Tip1p family	UNKNOWN	451.4	181.9	261.9	22.1	509.4	58.6	721.2	326.5	157	127.4	29.4	6.9	19.2	1.7	36.9	7.4	2.9	8.9	26.6	19.5
9716_at	0	YML083C	YML083C hypothetical protein	UNKNOWN	82	28.8	60.5	6.8	89.1	4.3	82.5	3.4	12	1.7	12	0	12	0.1	12	0.8	6.8	5	7.4	6.9
9884_at	0	YLR437C	YLR437C hypothetical protein	UNKNOWN	437.8	133.9	483.5	89.9	600	137.2	518.3	45.1	184.9	66.6	134.5	24.5	165.5	21.1	155.6	56.5	2.4	3.6	3.6	3.3
9904_at	0	YLR413W	YLR413W strong similarity to YKL187c	UNKNOWN	187.6	36.3	320.3	18.9	272	10.7	307.3	42.3	12.6	0.9	14	1.3	24.4	5.5	21.9	3.3	14.9	22.9	11.1	14
10289_f_at	DAN2	YLR037C	YLR037C strong similarity to members of the Srp1p/Tip1p family	UNKNOWN	940.4	193.2	410.8	27.6	410.4	67.2	1343.9	809.6	192.2	71.4	90.4	20.7	65.9	11.2	96.2	28.9	4.9	4.5	6.2	14
10852_at	DAN1	YJR150C	YJR150C Protein induced during anaerobic growth	UNKNOWN	3902.3	1578.5	2756.1	468.8	3169.2	138	4020.2	439.8	18.4	11.5	12	1.6	12	1.2	12	3	212.4	229.7	264.1	335
10853_at	DAN4	YJR151C	YJR151C similarity to mucin proteins. YKL224c. Sta1p	UNKNOWN	560.6	259.8	701.2	22.9	618.5	55.3	1551.8	341.6	111.6	29.8	115.2	27.7	96.3	6.4	132.6	58.3	5	6.1	6.4	11.7
7074_f_at	DAN3	YBR301W	YBR301W YKL224 c homolog	UNKNOWN	764.2	68.3	262.1	33	365.7	42.1	858.9	381.2	120.4	60.3	44.6	7	36.5	2.4	64.8	13.3	6.3	5.9	10	13.3

Down-regulated under anaerobiosis (FC = fold change, ANA = anaerobic, A = aerobic)

Probe Set	Gene name	systematic name	functional description	cellular function	C-Lim ANA Average	C-Lim ANA Stdev	N-Lim ANA Average	N-Lim ANA Stdev	P-Lim ANA Average	P-Lim ANA Stdev	S-Lim ANA Average	S-Lim ANA Stdev	C-Lim A Average	C-Lim A Stdev	N-Lim A Average	N-Lim A Stdev	P-Lim A Average	P-Lim A Stdev	S-Lim A Average	S-Lim A Stdev	FC C-Lim ANA vs C-Lim A	FC N-Lim ANA vs N-Lim A	FC S-Lim ANA vs S-Lim A	FC P-Lim ANA vs P-Lim A
10518_at	0	YKR046C	YKR046C hypothetical protein	UNKNOWN	181.2	32.5	254.5	6.7	240.2	34.9	241.7	31.2	1523	219.2	1617.4	122.1	1977.8	172.2	1658.6	565.6	-8.4	-6.4	-8.2	-6.9
4584_at	RIM4	YHL024W	YHL024W RNA binding domain (N-term) with asparagine rich region?	SPORULATION (PUTATIVE)	13.8	8.9	29.9	2	15.7	1.4	14.8	6.4	211.9	11.2	126.5	14.4	101	17.7	64.7	15.3	-15.4	-4.2	-6.4	-4.4
4526_at	SOD2	YHR008C	YHR008C Manganese-containing superoxide dismutase	OXIDATIVE STRESS RESPONSE	177.2	85.2	97.7	6.4	88.5	21.3	87.3	14.3	1124.6	140	666.1	132.7	604.4	90.3	1121	364.3	-6.3	-6.8	-6.8	-12.8
9040_at	MDG1	YNL173C	YNL173C multicopy suppressor of bem1 mutation. may be involved in G-protein mediated	SIGNALING. PHEROMONE PATHWAY	29.1	16.9	31.3	6.4	16.8	4.2	17.9	3	144.7	7.8	161.7	24	63.3	8.4	109.6	33.5	-5	-5.2	-3.8	-6.1
7614_at	ANT1	YPR128C	YPR128C similarity to carrier protein FLX1	UNKNOWN	49.5	15	75.7	8.2	75.9	7.6	58.2	10.9	190.5	32.5	170.6	18.4	165	7.5	143.1	34.7	-3.9	-2.3	-2.2	-2.5
8437_at	CRC1	YOR100C	YOR100C mitochondrial carnitine carrier	TRANSPORT	12	4.8	16.1	0.5	12	2.3	12	6.2	245.8	33	41.6	5.5	24.5	7	31.2	2.1	-20.5	-2.6	-2	-2.6
6803_at	0	YCR062W	YCR062W similarity to Ytp1p protein	UNKNOWN	12	0.8	12	2.2	12	2.6	17.6	8.8	48.7	8.1	36.3	3.1	34.8	10.6	58.6	4.6	-4.1	-3	-2.9	-3.3
7409_at	ECM13	YBL043W	YBL043W ExtraCellular Mutant	CELL WALL MAINTENANCE	26.3	15.1	22.6	4.3	16.5	0.6	26.6	7.2	601.6	188.7	242.9	31.3	172.8	73.9	321.9	127.1	-22.9	-10.7	-10.5	-12.1
10533_at	0	YKR016W	YKR016W weak similarity to mysoin heavy chain proteins	UNKNOWN	46.5	25.1	55.1	12.5	44.7	7.9	37	5.9	125.4	29.3	127.3	25.9	121.3	11.5	95.5	12.8	-2.7	-2.3	-2.7	-2.6
10723_at	MCR1	YKL150W	YKL150W NADH-cytochrome b5 reductase	ENERGY METABOLISM	320.7	88.9	234.6	19.9	176.7	30.6	170.5	19.8	770.3	91.7	518.2	54.3	523.6	26.3	539	54.4	-2.4	-2.2	-3	-3.2
10977_at	CYC1	YJR048W	YJR048W iso-1-cytochrome c	OXIDATIVE PHOSPHORYLATION	179.6	82.8	12	2.5	12	1.2	12	5.6	1608.9	226.9	940.9	93.8	1248.6	74.7	1611.3	155	-9	-78.4	-104.1	-134.3
4481_at	COX6	YHR051W	YHR051W subunit VI of cytochrome c oxidase	OXIDATIVE PHOSPHORYLATION	663.7	42.4	277.4	47.9	292	31.8	290.3	93	1494.6	252.7	1031.6	84.3	1191.2	69.4	1234.6	140.3	-2.3	-3.7	-4.1	-4.3
4829_at	CBP4	YGR174C	YGR174C Essential for the expression and activity of ubiquinol-cytochrome c reductase	RESPIRATION	80.9	18	73.1	16.4	37.6	3.2	35	10.5	230.4	50.5	177.7	8.6	95.9	6.5	94.1	20	-2.8	-2.4	-2.6	-2.7
5193_at	COX4	YGL187C	YGL187C subunit IV of cytochrome c oxidase	OXIDATIVE PHOSPHORYLATION	568.5	44.6	142.4	16.2	138.7	9.9	151.3	41.2	1225.6	116.1	888.9	48.7	938.7	49.1	1026.2	78.3	-2.2	-6.2	-6.8	-6.8
5766_at	RIP1	YEL024W	YEL024W Rieske iron-sulfur protein of the mitochondrial cytochrome bc1 complex	RESPIRATION	692.1	66.5	201.9	78.4	287.7	3.4	334.3	12.1	1615	197.5	1136.3	59.8	1323.2	69	1270.6	205.3	-2.3	-5.6	-4.6	-3.8
6339_at	KGD2	YDR148C	YDR148C dihydrolipoyl transsuccinylase component of alpha-ketoglutarate dehydrogenas	TCA CYCLE	268.1	28.4	123.9	30.4	118.1	15.2	156.5	20.7	594.1	55.5	337.8	48	255.9	89.5	390.2	90.8	-2.2	-2.7	-2.2	-2.5
7186_at	MBA1	YBR185C	YBR185C respiratory chain assembly protein	RESPIRATION	84.2	40.8	79.2	19.3	75.6	17.6	84.3	8.7	260.4	29	174.1	33	156.5	26.5	185.4	17.1	-3.1	-2.2	-2.1	-2.2
7407_at	COR1	YBL045C	YBL045C 44 kDa core protein of yeast coenzyme QH2 cytochrome c reductase	OXIDATIVE PHOSPHORYLATION	253.6	32.7	78.6	32.6	98	54.2	142.4	17.7	622.9	237.2	288.6	32.1	424.7	109.2	537.9	138	-2.5	-3.7	-4.3	-3.8
7727_at	ATP20	YPR020W	YPR020W hypothetical protein	ATP SYNTHESIS	79.7	15.4	34.1	3.8	26.9	0.5	30	6.1	276	71.3	173.3	16	194.6	21.4	187.4	40.4	-3.5	-5.1	-7.2	-6.2
8200_at	0	YOR356W	YOR356W strong similarity to human electron transfer flavoprotein-ubiquinone oxidoreduc	UNKNOWN	107	38.6	86.2	11	48.4	1.8	70.8	6	452.5	39.7	252.3	25.5	250.4	27.7	239.1	17.8	-4.2	-2.9	-5.2	-3.4
8493_at	CYT1	YOR065W	YOR065W Cytochrome c1	OXIDATIVE PHOSPHORYLATION	163.7	63.5	55.5	13.3	62.3	2.4	65	9.8	762.5	191.6	663	144.2	704.9	81.2	800.4	276.2	-4.7	-11.9	-11.3	-12.3
8935_at	COX5A	YNL052W	YNL052W Cytochrome-c oxidase chain Va	OXIDATIVE PHOSPHORYLATION	321.3	14.6	88.3	11.6	58.4	8.7	85.1	9.6	1167.2	265.6	800.7	70.2	940.2	113.8	1004.3	38.9	-3.6	-9.1	-16.1	-11.8
9111_at	YTP1	YNL237W	YNL237W Yeast putative Transmembrane Protein	UNKNOWN	12	1.3	12	0.5	12	2.3	12	1.3	108	2.5	80.2	17.6	63	4	93.8	14.2	-9	-6.7	-5.2	-7.8
9350_at	COX7	YMR256C	YMR256C subunit VII of cytochrome c oxidase	OXIDATIVE PHOSPHORYLATION	861.5	336.1	492.8	108.2	387.6	17.8	503.1	32.1	1901.5	184.3	1432.4	99.5	1519.5	39.2	1510.6	160.9	-2.2	-2.9	-3.9	-3
9500_at	NDE1	YMR145C	YMR145C mitochondrial cytosolically directed NADH dehydrogenase	UNKNOWN	115.7	23.4	45.7	6.1	28.7	4.4	40.9	3.4	1257.3	68.1	633.8	99.7	808.8	62.4	1153.7	124.9	-10.9	-13.9	-28.2	-28.2
9712_at	0	YML087C	YML087C strong similarity to YML125c. similarity to cytochrome-b5- and nitrate reductase	UNKNOWN	24.5	11.1	18.8	6	13.4	3.6	18.1	8.7	59.3	15.5	52.2	3.1	33	5.7	39.5	17.5	-2.4	-2.8	-2.5	-2.2
9765_at	NDI1	YML120C	YML120C mitochondrial NADH ubiquinone 6 oxidoreductase	OXIDATIVE PHOSPHORYLATION	179.9	63.6	71	17.5	72.6	11.4	84.4	4.9	799.8	229.4	445.9	26.5	468.8	31.1	701.7	241.7	-4.4	-6.3	-6.5	-8.3
10143_at	HMX1	YLR205C	YLR205C hypothetical protein	UNKNOWN	18.9	9.3	21.4	6.4	28.5	3.3	25.8	7.9	478.4	91.3	230.1	82.9	321.9	27.1	351.4	33.8	-25.3	-10.8	-11.3	-13.6
10725_at	SDH1	YKL148C	YKL148C flavoprotein subunit of succinate dehydrogenase	TCA CYCLE. OXIDATIVE PHOSPHORYLATION	273.8	52.2	117.1	24.7	100.2	22.3	88.7	12.9	608.5	103.9	280.5	35.5	267.4	20.5	312.5	49.8	-2.2	-2.4	-2.7	-3.5
4071_at	0	YIR035C	YIR035C similarity to human corticosteroid 11-beta-dehydrogenase	UNKNOWN	59.7	15.1	120.7	11.2	71.2	12.2	118.3	3	167.4	39.3	270.7	27.5	168.5	8.1	491.6	142.8	-2.8	-2.2	-2.4	-4.2
4129_at	0	YIL042C	YIL042C similarity to rat branched-chain alpha-ketoacid dehydrogenase kinase	UNKNOWN	58.7	16.2	97.9	29.3	97.9	19.9	69.2	20.1	193.5	9.9	243.8	55.4	205.5	34	321.1	82.9	-3.3	-2.5	-2.1	-4.6
4246_at	GUT2	YIL155C	YIL155C glycerol-3-phosphate dehydrogenase. mitochondrial	GLYCEROL METABOLISM	99.9	45.9	72.1	18.1	60.5	16.5	32.6	5.3	1154.6	248.4	398.9	91.7	285.5	42.3	260	19.8	-11.6	-5.5	-4.7	-8
4511_at	PUT2	YHR037W	YHR037W delta-1-pyrroline-5-carboxylate dehydrogenase	PROLINE METABOLISM	110.9	33.3	317.2	31.6	114.9	5.3	151.2	9	271.1	22	770.1	72.3	317	13.1	344.5	67.4	-2.4	-2.4	-2.8	-2.3
4518_at	OSH7	YHR001W	YHR001W 8.5 kDa subunit of the ubiquinol-cytochrome c oxidoreductase complex	OXIDATIVE PHOSPHORYLATION	305.6	52.1	94.6	23.4	77.3	5.1	93	9.4	799	66.7	662.9	21.1	766.1	91.3	689.3	114.9	-2.6	-7	-9.9	-7.4
5400_at	0	YFL030W	YFL030W similarity to several transaminases	UNKNOWN	132.5	34.5	134.5	20.4	66.1	8.1	47.5	3	2110.8	142.1	744.8	63.2	586.6	15.8	782.7	60.4	-15.9	-5.5	-8.9	-16.5
7184_at	YPC1	YBR183W	YBR183W strong similarity to hypothetical protein YPL087w	UNKNOWN	18.7	14.6	62.9	25.3	19	5.9	42.7	12.2	129.3	29.2	223.1	26.7	122.2	11.8	188.1	20.6	-6.9	-3.5	-6.4	-4.4
7455_at	0	YBL086C	YBL086C involved in sugar metabolism	UNKNOWN	12.1	7.8	15.7	4.5	19.5	2	20.5	7.6	48	16.4	65.7	21.1	51.8	6.7	57	24.2	-4	-4.2	-2.7	-2.8
7685_at	ROX1	YPR065W	YPR065W site-specific DNA binding protein. repressor	TRANSCRIPTION. OXYGEN-DEPENDENT	18.4	10.3	12.7	4.3	17.9	1.1	16.5	3.2	83	31.4	52.9	4.9	71.2	12.9	49.8	10.7	-4.5	-4.2	-4	-3
7890_at	ISU1	YPL135W	YPL135W NifU-like protein A	UNKNOWN	179	44.1	207	40	207.1	37.1	235.6	23.8	819.9	171.3	607.3	44.9	642.1	67.3	843.1	276.4	-4.6	-2.9	-3.1	-3.6
8207_at	FAA1	YOR317W	YOR317W long chain fatty acyl:CoA synthetase	FATTY ACID METABOLISM	25.6	17.5	86.6	39.5	19	1	22.6	3.6	370.9	64.3	516.9	93.3	308.7	47.1	311	45	-14.5	-6	-16.2	-13.8
8683_at	GRE2	YOL151W	YOL151W induced by osmotic stress\; similar to dihydroflavonol 4-reductase from plants	UNKNOWN	18.4	11	95.7	3.7	119.8	20.9	63	4.8	200	55.2	284	21.9	359.1	47.3	307.4	37.2	-10.9	-3	-3	-4.9
9117_at	PDR16	YNL231C	YNL231C weak similarity to Sec14p	DRUG RESISTANCE	57.9	30.9	147.5	33	126.3	10.5	210.2	36.4	223.9	39.1	484.2	60.7	359.2	35.9	447.8	53.3	-3.9	-3.3	-2.8	-2.1
9120_at	0	YNL274C	YNL274C similarity to glycerate- and formate-dehydrogenases	UNKNOWN	57.1	22.7	77.5	18.3	68	11.5	76.1	27.5	302.5	26.6	191.2	32.4	140.6	11.9	155.5	12	-5.3	-2.5	-2.1	-2
9702_at	CYB2	YML054C	YML054C Cytochrome b2 [L--lactate cytochrome-c oxidoreductase]	LACTATE UTILIZATION	21.3	9.7	26.7	4.1	12	2.4	23	14.5	2375.4	191.9	669	126.4	552	42	1150.9	86.5	-111.4	-25	-46	-50

9724_at	HMG1	YML075C	YML075C 3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA) reductase isozyme	STEROL METABOLISM	258.7	56.8	346.4	36.9	221.3	53.2	240.2	24.7	1301.6	135.2	850.1	55.2	995.8	75.1	901	247.2	-5	-2.5	-4.5	-3.8
10148_at		0 YLR168C	YLR168C probably involved in intramitochondrial protein sorting	UNKNOWN	49.1	24.4	47.7	7.1	33.3	4.9	38.6	8.3	260.6	71.9	279.4	37.6	316.4	29	252.3	37.7	-5.3	-5.9	-9.5	-6.5
10290_at	COX12	YLR038C	YLR038C subunit Vlb of cytochrome c oxidase	OXIDATIVE PHOSPHORYLATION	1168.6	252.6	386.2	105	364.7	44.8	436	54	2507.4	46.2	1928.2	20.5	2092.8	59.2	1956.4	168.5	-2.1	-5	-5.7	-4.5
4759_at	PEX21	YGR239C	YGR239C weak similarity to hypothetical protein YHR160c	PEROXISOME BIOGENESIS (PUTATIVE)	34.4	10.4	43.8	8.2	42	3.5	32.4	11.5	193.4	7.3	128.7	20.7	226.4	25.1	105.7	32.4	-5.6	-2.9	-5.4	-3.3
7543_at	QCR2	YPR191W	YPR191W 40 kDa ubiquinol cytochrome-c reductase core protein 2	OXIDATIVE PHOSPHORYLATION	321.6	78.6	113.4	10.7	106.9	16.1	137.6	3.8	808	99.5	571.6	97.7	709.4	31.9	986.2	22.7	-2.5	-5	-6.6	-7.2
10591_at	ATP7	YKL016C	YKL016C ATP synthase d subunit	ATP SYNTHESIS	409.5	104.1	226.3	22.1	162.7	23.4	134.9	6.8	838.5	145.4	562	32.3	555.2	49.3	467.1	47.7	-2	-2.5	-3.4	-3.5
4768_at	SOL4	YGR248W	YGR248W similar to SOL3	UNKNOWN	47.9	27.2	87.1	8	48.3	18.5	61.2	18.6	568.3	184.4	363.7	153	110.6	4.9	528.4	75	-11.9	4.2	-2.3	-8.6
9308_at	PRP12	YMR302C	YMR302C Integral membrane mitochondrial protein	RRNA PROCESSING	40.5	12.1	66.5	13.4	55.9	4.1	42.4	3.2	150.2	19.6	178.5	6.7	198.2	21.3	145.8	28.9	-3.7	-2.7	-3.5	-3.4
9555_at	MOT3	YMR070W	YMR070W 2 Cys2-His2 zinc fingers at c-terminus. glutamine and asparagine rich	MATING	12	3.8	12	3	12	2.2	12	5.4	25.9	4.6	25.3	7	29.8	13.1	25.5	1.6	-2.2	-2.1	-2.5	-2.1
10377_at	AQY2	YLL053C	YLL053C similarity to water channel proteins	UNKNOWN	75	23.3	157.4	12.9	172.9	33.2	171.5	47.5	1248.4	136.8	348.8	56.7	2716.5	272.8	2125.6	758.2	-16.6	-2.2	-15.7	-12.4
10378_at	AQY2	YLL052C	YLL052C member of mip family transmembrane channels	TRANSPORT, WATER	23.9	6.8	56.1	7.2	77.3	10	86	18.2	418.7	78.5	130.1	5.7	1355	120.9	1075.8	594.3	-17.5	-2.3	-17.5	-12.5
6190_at	CCC2	YDR270W	YDR270W Copper-transporting P-type ATPase with similarity to human Menkes and Wilso	OXIDATIVE PHOSPHORYLATION	29.4	8.6	32	2.5	39.8	8.6	41.7	8.5	135.7	10	100	13.4	165.6	40.5	137.3	12.3	-4.6	-3.1	-4.2	-3.3
7831_at	PDR12	YPL058C	YPL058C multidrug resistance transporter	DRUG RESISTANCE	70.4	31.6	114.3	19.8	61.7	6.9	65.9	22.6	637.9	155.7	523.1	92.3	217.5	15.3	467.6	55.3	-9.1	-4.6	-3.5	-7.1
8192_at	PUT4	YOR348C	YOR348C putative proline-specific permease	TRANSPORT	16.9	6.6	176	26.5	28.1	6.5	21.7	8.9	1262.8	181	2557.3	204	138.5	44.6	518.2	179.5	-74.7	-14.5	-4.9	-23.9
8669_at	MCH4	YOL119C	YOL119C similarity to monocarboxylate transporter proteins	UNKNOWN	27.8	7.5	56.8	20.5	42.6	3.4	50	4.4	73.3	8.3	272.8	50.5	243.1	37.5	111.9	48.3	-2.6	-4.8	-5.7	-2.2
9586_at	AAC1	YMR056C	YMR056C mitochondrial ADP\/ATP translocator	TRANSPORT	60.1	1.7	117.5	14.6	102.6	22	72.4	10	528.7	75.7	482.7	67	352.6	26	439.8	233.8	-8.8	-4.1	-3.4	-6.1
10027_at		0 YLR312C	YLR312C hypothetical protein	UNKNOWN	27.3	21.2	81.1	32.5	37.4	11.8	32	6.7	289.2	10.8	173.3	27.2	124.6	6.1	66.5	15.4	-10.6	-2.1	-3.3	-2.1
10227_at		0 YLR108C	YLR108C strong similarity to YOR132c	UNKNOWN	12	2.9	23.8	3.9	21.5	2.8	23.1	0.7	38	10.6	107.9	12	166	17.4	112.3	3.8	-3.2	-4.5	-7.7	-4.9
11065_at		0 YJL048C	YJL048C similarity to hypothetical protein YBR273c	UNKNOWN	103.1	23.2	137.5	14.8	115.6	2.2	143.8	3.2	544.7	56.2	459.6	67.8	473	42	397.5	39.8	-5.3	-3.3	-4.1	-2.8
11102_at	LSB6	YJL100W	YJL100W similarity to hypothetical C. elegans protein C56A3.8	UNKNOWN	19.1	8.7	19.8	1.3	32.2	2.8	15	2.3	279.3	127.1	170	51.4	265.6	14.8	192.8	8.7	-14.6	-8.6	-8.2	-12.9
11135_at	MDV1	YJL112W	YJL112W similarity to Met30p and N.crassa sulfur controller-2	UNKNOWN	28.5	17.6	79.2	14.3	58.8	4.9	41.2	3.7	164.1	42.7	210.1	19.7	194.3	34.1	148.7	13.2	-5.8	-2.7	-3.3	-3.6
11359_at		0 YAL049C	YAL049C weak similarity to Legionella small basic protein sbpA	UNKNOWN	124.6	21.4	302.3	10.2	169.2	38.1	218.4	19.2	620.9	45.1	731.6	57.4	610.5	81.3	642.9	242.4	-5	-2.4	-3.6	-2.9
4131_at		0 YIL040W	YIL040W weak similarity to T.brucei NADH dehydrogenase	UNKNOWN	51	23.9	58.7	3.8	54.8	1.9	52.8	15.2	123.7	10.3	125.9	20	126.5	14.1	125.1	36.7	-2.4	-2.1	-2.3	-2.4
4462_at		0 YHR080C	YHR080C similarity to hypothetical protein YDR326c. YFL042c and YLR072w	UNKNOWN	23.4	13.8	39.7	5.3	31.9	4.1	25.1	4.2	95.4	21.4	109.8	14.6	75.7	3.9	95	25.5	-4.1	-2.8	-2.4	-3.8
4742_at		0 YGR286W	YGR286W hypothetical protein	UNKNOWN	20.8	5.4	24.2	4.9	21.7	5	21.4	2.6	97.2	9.6	76.5	7.3	125.7	21.1	57.1	11.5	-4.7	-3.2	-5.8	-2.7
4763_at		0 YGR243W	YGR243W strong similarity to hypothetical protein YHR162w	UNKNOWN	384.2	140.3	68	1.2	59.6	5.8	77	21.3	1769.2	97.7	155.6	9.6	178.2	41.4	203.3	45.6	-4.6	-2.3	-3	-2.6
5050_at		0 YGL057C	YGL057C hypothetical protein	UNKNOWN	26.5	8.2	33.3	10.5	37	6.5	31.1	7.2	70.4	8.8	70.2	5	81.8	7.6	71.2	21.2	-2.7	-2.1	-2.2	-2.3
5096_at		0 YGL101W	YGL101W strong similarity to hypothetical protein YBR242w	UNKNOWN	12.7	6.4	25.7	7.1	21	5.3	24.2	3.5	77.8	7.6	122.9	23.1	127.6	6.2	85.7	8.1	-6.1	-4.8	-6.1	-3.5
5183_at		0 YGL196W	YGL196W hypothetical protein	UNKNOWN	24.3	10.6	90.4	25.3	51.6	3.1	51	6.6	148.6	29.2	284.4	37	123.9	7.8	113.6	20.4	-6.1	-3.1	-2.4	-2.2
6555_at		0 YDL086W	YDL086W similarity to hypothetical Synechocystis protein	UNKNOWN	461.6	183	327.9	75	333.5	95.2	265.5	22.9	1051.6	137.6	903	156	963.8	74.1	1006.1	221.7	-2.3	-2.8	-2.9	-3.8
6576_at		0 YDL110C	YDL110C hypothetical protein	UNKNOWN	186.7	14.9	150.4	14.4	112.6	38.7	140.1	10.5	956.2	90.4	593.7	43.2	327.1	38.3	441.3	96.6	-5.1	-3.9	-2.9	-3.2
6846_at		0 YCR061W	YCR061W hypothetical protein	UNKNOWN	12	1.5	12	2.3	12	2	22.7	4.6	61.4	13.3	49	10	50.2	5.1	129.5	90.4	-5.1	-4.1	-4.2	-5.7
7140_at		0 YBR230C	YBR230C hypothetical protein	UNKNOWN	136.7	24.5	76.1	17.8	53.4	1.2	50	3.1	1635.1	197.6	364.2	56.9	262.7	25.7	353.5	38.4	-12	-4.8	-4.9	-7.1
7315_at		0 YBR047W	YBR047W hypothetical protein	UNKNOWN	12	4.1	14.7	3.6	19.8	1.4	15.5	4.1	121.4	54.3	41.7	2.4	68.5	8.7	39.4	2.9	-10.1	-2.8	-3.5	-2.5
7445_at		0 YBL095W	YBL095W similarity to C.albicans hypothetical protein	UNKNOWN	29	14.7	62	6.7	52.8	8.6	46.2	4.7	141.8	57.5	457.7	77.1	381.6	17	353.3	70.4	-4.9	-7.4	-7.2	-7.7
7594_at		0 YPR151C	YPR151C weak similarity to YPL159c	UNKNOWN	12	2.7	12	0.7	12	1.6	12	2.1	721.4	197.9	385.8	102.5	334.9	25	322.3	22.5	-60.1	-32.2	-27.9	-26.9
7681_at		0 YPR061C	YPR061C weak similarity to Synechococcus sp. DnaJ protein	UNKNOWN	12	4.1	12	0.9	12	0.6	12	3.7	48.2	2.9	44.7	5.6	44.3	1.5	35.4	8.2	-4	-3.7	-3.7	-3
7749_at		0 YPL004C	YPL004C strong similarity to YGR086c	UNKNOWN	403.2	123.3	454.1	69.3	375	74.2	369.7	63.8	1734.4	299.2	1344.8	173.2	868.2	55.7	1241.9	65.8	-4.3	-3	-2.3	-3.4
7873_at		0 YPL107W	YPL107W hypothetical protein	UNKNOWN	16.8	9.2	36.3	3.6	30.1	1.6	26.3	8.3	95	3.5	108.3	11.9	107.8	3.9	106.4	7.5	-5.6	-3	-3.6	-4
8326_at		0 YOR215C	YOR215C similarity to M.xanthus hypothetical protein	UNKNOWN	62.2	22.7	69.9	5.6	62.7	16.3	48.8	7.8	322.5	40.6	226.4	6	157.1	23.5	169.1	39.5	-5.2	-3.2	-2.5	-3.5
8408_at		0 YOR161C	YOR161C similarity to C.elegans cosmid F35G8	UNKNOWN	12	4.7	66.7	6.5	27.2	2.1	51.8	10.6	125.6	57.5	164	34.3	59	7	138	29.2	-10.5	-2.5	-2.2	-2.7
8659_at	PHM7	YOL084W	YOL084W similarity to A.thaliana hyp1 protein	UNKNOWN	12	5.5	13.1	3	12	0.8	12	3.6	53.6	13.7	47	23.3	39.1	4	33.8	0.7	-4.5	-3.6	-3.3	-2.8
8724_at		0 YOL155C	YOL155C similarity to glucan 1,4-alpha-glucosidase Sta1p and YAR066w	UNKNOWN	264.4	136.8	73	40.6	300.2	29.4	64.3	28.6	1133.3	588.4	214	144.1	1827.5	111.2	2196	343.1	-4.3	-2.9	-6.1	-34.2
8977_at		0 YNL100W	YNL100W hypothetical protein	UNKNOWN	97.2	41.8	91.6	24.6	93.9	14.4	87	7.6	604.8	101.2	348.8	40.3	325.4	6.2	253.7	18	-6.2	-3.8	-3.5	-2.9
9624_at		0 YMR002W	YMR002W similarity to hypothetical S.pombe and C.elegans proteins	UNKNOWN	327.2	48.4	244.1	42.7	269.3	46.1	219.7	46.2	2217.2	364.2	1192.4	59.3	1940.1	222.8	2047.2	805.9	-6.8	-4.9	-7.2	-9.3
9631_at		0 YMR009W	YMR009W weak similarity to P.aeruginosa regulatory protein mmsR	UNKNOWN	73.5	29.4	117.3	33.1	298	71.6	73.8	18.4	776.5	105.3	357.3	45.4	1442.4	54.3	291.5	39.1	-10.6	-3	-4.8	-3.9

Up-regulated under C-Lim under aerobic and anaerobic conditions (FC = fold change, ANA = anaerobic, A = aerobic)

Probe Set	Gene name	systematic name	functional description	cellular function	C-Lim ANA Average	C-Lim ANA Stdev	N-Lim ANA Average	N-Lim ANA Stdev	P-Lim ANA Average	P-Lim ANA Stdev	S-Lim ANA Average	S-Lim ANA Stdev	C-Lim A Average	C-Lim A Stdev	N-Lim A Average	N-Lim A Stdev	P-Lim A Average	P-Lim A Stdev	S-Lim A Average	S-Lim A Stdev	FC C-Lim ANA vs N-Lim ANA	FC C-Lim ANA vs S-Lim ANA	FC C-Lim ANA vs P-Lim ANA	FC C-Lim AE vs N-Lim AE	FC C-Lim AE vs S-Lim AE	FC C-Lim AE vs P-Lim AE
6563_at	MRK1	YDL079C	YDL079C MDS1 related protein kinase	UNKNOWN	301.3	95.8	27.7	3.9	29.7	4.8	27.6	6.5	97.4	9.3	26.5	5.3	17.5	3.5	21.1	3.7	10.9	10.1	10.9	3.7	5.6	4.6
7072_s_at	MAL32	YBR299W	YBR299W Maltase (EC 3.2.1.20)	MALTOSE METABOLISM	1512.7	617.9	119.1	17.7	39.1	10.5	30.3	5.6	505.4	245.7	81.1	23.3	18.3	2.8	15	1.1	12.7	38.7	49.9	6.2	27.6	33.8
8173_at	ALD4	YOR374W	YOR374W aldehyde dehydrogenase (E.C. 1.2.1.5) (sold by SIGMA under the catalogue	ETHANOL UTILIZATION	1177.8	296	430.4	23.6	339.3	13	223.8	44.1	2516.6	297.5	682.3	146.8	506.3	13.6	480.8	28.8	2.7	3.5	5.3	3.7	5	5.2
10795_at	JEN1	YKL217W	YKL217W carboxylic acid transporter protein homolog	TRANSPORT	68.4	20.6	27.7	8.4	12.6	3.4	16	8.9	1943.4	142.8	39.5	4.3	18.2	8.3	42	12.8	2.5	5.4	4.3	49.2	106.8	46.3
4043_s_at	SUC2	YIL162W	YIL162W invertase (sucrose hydrolyzing enzyme)	SUCROSE UTILIZATION	1671.8	188.3	113.9	4.7	112.9	17.9	117.3	24.4	532.3	99.5	91.6	4.7	63.6	16	49.6	15.7	14.7	14.8	14.3	5.8	8.4	10.7
4719_at	MAL11	YGR289C	YGR289C alpha-glucoside transporter	TRANSPORT	1099.9	284.4	176.6	29.3	72.8	4.2	74	7.6	494.3	86.5	104.6	9.3	53.4	4.2	66.9	11.6	6.2	15.1	14.9	4.7	9.3	7.4
5307_at	HXK1	YFR053C	YFR053C Hexokinase I (PI) (also called Hexokinase A)	GLYCOLYSIS	3699.5	1319.4	739.8	65.8	381.9	62.8	869	72.8	1723.1	298.4	542.9	230	69.6	4.1	492.8	65.3	5	9.7	4.3	3.2	24.8	3.5
8002_at	GAL4	YPL248C	YPL248C zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain ty	GALACTOSE METABOLISM	31.8	7	12	1.9	12	1.6	12	1.3	26.7	4.9	12	0.2	12	0.8	12	4.9	2.7	2.7	2.7	2.2	2.2	2.2
9567_at	ISF1	YMR081C	YMR081C May regulate NAM7 function. possibly at level of mRNA turnover	RNA SPLICING. MITOCHONDRIAL	512.6	143.4	133.9	22.5	25.9	2.8	64.3	14.4	483.6	74.7	118	17.5	17.1	4.5	31.5	3.7	3.8	19.8	8	4.1	28.2	15.4
9996_at	0	YLR327C	YLR327C strong similarity to Stf2p	UNKNOWN	1537.8	284.6	466	42.1	389.2	31.1	253.3	28.5	1969.8	169.5	312.7	71.3	363.7	34.7	85.5	9.5	3.3	4	6.1	6.3	5.4	23
8788_at	SOL1	YNR034W	YNR034W hypothetical protein	TRNA SPLICING. PUTATIVE	929.9	166.7	405.9	61.1	144.5	18.2	362.3	76.4	835.7	234.4	233.8	20.4	42.3	3.1	92.4	6.7	2.3	6.4	2.6	3.6	19.8	9
4160_at	0	YIL057C	YIL057C strong similarity to YER067w	UNKNOWN	648	87.5	14.1	1.5	12	1.5	12	3.6	1984	149.9	12	1.6	12	1.3	12	2	46	54	54	165.3	165.3	165.3
4763_at	0	YGR243W	YGR243W strong similarity to hypothetical protein YHR162w	UNKNOWN	384.2	140.3	68	1.2	59.6	5.8	77	21.3	1769.2	97.7	155.6	9.6	178.2	41.4	203.3	45.6	5.7	6.4	5	11.4	9.9	8.7
5359_at	0	YFR017C	YFR017C hypothetical protein	UNKNOWN	214.6	80.3	94.1	16.5	45.3	7.3	49.6	9.1	198.9	48.4	58.7	26.2	33.4	9.9	83.1	22.4	2.3	4.7	4.3	3.4	6	2.4
5640_at	0	YER067W	YER067W strong similarity to hypothetical protein YIL057c	UNKNOWN	621.8	171.9	189.1	26.6	104.4	15.2	224.3	52.5	323.4	69.9	122.7	29.4	51.8	13	76	14.8	3.3	6	2.8	2.6	6.2	4.3
7738_at	CSR2	YPR030W	YPR030W similarity to YBL101c	UNKNOWN	54.4	19.1	12.5	3.1	12	1.3	12	5.2	78.3	6.9	16.9	2.5	13.1	1.9	12	6.8	4.3	4.5	4.5	4.6	6	6.5
9433_at	0	YMR206W	YMR206W weak similarity to hypothetical protein YNR014w	UNKNOWN	183	62.9	60.3	6.5	12.4	6.7	27.6	3.3	349.8	48.7	29.1	9.2	12	0.2	15	3	3	14.7	6.6	12	29.1	23.3
3937_g_at	SUC4	SUC4	SUC4 invertase (sucrose hydrolyzing enzyme)	SUCROSE UTILIZATION	1763.4	422.2	138.3	25	85.2	11.5	116.8	17.5	467.2	78	90.6	4.3	72.6	8.3	46.3	11	12.7	20.7	15.1	5.2	6.4	10.1
7754_at	PDH1	YPR002W	YPR002W similarity to B.subtilis mmgE protein	UNKNOWN	86.1	34.5	21.4	5.3	15.9	4.8	18.2	9.3	644	92.2	28.6	5.7	213.7	35.9	38.3	4	4	5.4	4.7	22.5	3	16.8

Down-regulated under C-Lim under aerobic and anaerobic conditions (FC = fold change, ANA = anaerobic, A = aerobic)

Probe Set	Gene name	systematic name	functional description	cellular function	C-Lim ANA Average	C-Lim ANA Stdev	N-Lim ANA Average	N-Lim ANA Stdev	P-Lim ANA Average	P-Lim ANA Stdev	S-Lim ANA Average	S-Lim ANA Stdev	C-Lim A Average	C-Lim A Stdev	N-Lim A Average	N-Lim A Stdev	P-Lim A Average	P-Lim A Stdev	S-Lim A Average	S-Lim A Stdev	FC C-Lim ANA vs N-Lim ANA	FC C-Lim ANA vs S-Lim ANA	FC C-Lim ANA vs P-Lim ANA	FC C-Lim AE vs N-Lim AE	FC C-Lim AE vs S-Lim AE	FC C-Lim AE vs P-Lim AE
4505_at	RRM3	YHR031C	YHR031C Pif1p. mitochondrial DNA repair and recombination protein	TRANSPOSITION	17.1	8.9	64.2	22	38.2	2.4	57.8	7.6	30	3.7	68.5	4.6	67.2	9.2	96	20	-3.8	-2.2	-3.4	-2.3	-2.2	-3.2
9856_at	SST2	YLR452C	YLR452C (SST2) Regulator of G-protein signaling family member that negatively regula	MATING	70.7	26.6	191.2	49.4	172.4	22.4	191.4	35	33.7	9.1	155.9	2	143.6	5.8	116.4	12.1	-2.7	-2.4	-2.7	-4.6	-4.3	-3.5
4580_at	WSC4	YHL028W	YHL028W Putative integral membrane protein containing novel cysteine motif. Similarity	CELL WALL MAINTENANCE	31.3	13.7	259.9	7.2	189.3	44.9	246.4	5	24.3	4.5	410.7	37.2	83	6.4	390	25.5	-8.3	-6	-7.9	-16.9	-3.4	-16
4884_i_at	TPO2	YGR138C	YGR138C similarity to multidrug resistance proteins	UNKNOWN	14.4	9.6	141	28.9	230.1	46.3	214.5	20.7	32.3	6.5	181	49.2	304.6	14.6	388.3	96.9	-9.8	-15.9	-14.9	-5.6	-9.4	-12
4428_at	HXT4	YHR092C	YHR092C low to moderate-affinity glucose transporter	TRANSPORT	13.1	6.2	828.3	90.2	650.9	116.2	937.3	136.7	69.7	13.8	469.6	26.4	315.5	34.9	577.7	103.8	-63.4	-49.8	-71.7	-6.7	-4.5	-8.3
4430_at	HXT1	YHR094C	YHR094C low-affinity hexose (glucose) transporter	TRANSPORT	12	2.7	150.2	4.9	286.9	71.3	54.1	7.4	14.1	2.8	313.1	10.8	432.9	28	532.6	157.1	-12.5	-23.9	-4.5	-22.2	-30.7	-37.8
5178_at	0	YGL157W	YGL157W similarity to V.vinifera dihydroflavonol 4-reductase	UNKNOWN	15.5	7.3	116.5	8.6	95.7	3	78.3	27.7	14.4	4.3	112.4	7.1	75.9	8.5	104.8	41.3	-7.5	-6.2	-5	-7.8	-5.3	-7.3
6131_at	HXT3	YDR345C	YDR345C low-affinity glucose transporter	TRANSPORT	62.2	29.6	2426.4	374.2	1941.6	83.4	1604.7	406.1	83.9	20.5	2359.7	143.3	1488.4	78.8	1931	96.8	-39	-31.2	-25.8	-28.1	-17.7	-23
5216_at	MIG2	YGL209W	YGL209W (MIG2) Zinc-finger protein involved in glucose repression of SUC2. contains	GLUCOSE REPRESSION	12	5.7	87.9	21.1	75.6	31.7	74.7	24.8	18.2	1.6	111	28.6	49.8	8.9	195.9	47.1	-7.3	-6.3	-6.2	-6.1	-2.7	-10.8
6823_at	TUP1	YCR084C	YCR084C glucose repression regulatory protein. exhibits similarity to beta subunits of G	TRANSCRIPTION	88.5	39.8	202.5	51.4	228.3	49.4	193.6	14.4	91.7	8.1	207.6	48.5	218	19.8	213	37	-2.3	-2.6	-2.2	-2.3	-2.4	-2.3
8520_at	STD1	YOR047C	YOR047C Dosage-dependent modulator of glucose repression. increased dosage resto	CARBOHYDRATE METABOLISM	19.8	5.2	163.1	7	175.9	19.8	167.4	18.8	29.9	4.6	185.8	13	131.7	16	168.2	28.4	-8.2	-8.9	-8.5	-6.2	-4.4	-5.6
7600_s_at	TPO3	YPR156C	YPR156C similarity to multidrug resistance proteins	UNKNOWN	236.8	55.7	580.5	81.5	817.3	92.2	840.7	116.9	278.8	29.1	657.4	54.1	801.3	8.5	1215.3	63.9	-2.5	-3.5	-3.6	-2.4	-2.9	-4.4
5537_at	0	YER188W	YER188W hypothetical protein	UNKNOWN	101.8	30.2	448	24.7	212	28.7	956	71.3	16.2	6.6	472	12.8	43.8	6.2	334.4	113.5	-4.4	-2.1	-9.4	-29.1	-2.7	-20.6
8005_at	0	YPL245W	YPL245W weak similarity to human mutL protein homolog	UNKNOWN	37.8	14.8	121.2	23.9	85.9	8.7	93.9	7.2	65.8	4.7	197.5	29.8	150.1	5.1	132.6	14	-3.2	-2.3	-2.5	-3	-2.3	-2

Up-regulated under N-Lim anaerobic and aerobic conditions (FC = fold change, ANA = anaerobic, A = aerobic)

Probe Set	Gene name	systematic name	functional description	cellular function	C-Lim ANA Average	C-Lim ANA Stdev	N-Lim ANA Average	N-Lim ANA Stdev	P-Lim ANA Average	P-Lim ANA Stdev	S-Lim ANA Average	S-Lim ANA Stdev	C-Lim A Average	C-Lim A Stdev	N-Lim A Average	N-Lim A Stdev	P-Lim A Average	P-Lim A Stdev	S-Lim A Average	S-Lim A Stdev	FC N-Lim ANA vs C-Lim ANA	FC N-lim ANA vs S-ANA	FC N-lim ANA vs P-lim ANA	FC N-Lim AE vs C-Lim AE	FC N-lim AE vs S-AE	FC N-lim AE vs P-lim AE
8249_at	SPS4	YOR313C	YOR313C sporulation-specific protein	SPORULATION	25.2	11.7	103.5	17.8	32	6.8	50.8	2.8	12	4.3	109.8	6.4	18.3	3.7	23.9	5.9	4.1	3.2	2	9.2	6	4.6
9483_at	ALD2	YMR170C	YMR170C aldehyde dehydrogenase. (NAD(P)+). likely cytosolic	ETHANOL UTILIZATION	15.9	5.9	125.9	44.7	23.5	4.9	25.1	7.7	35.2	4.5	100.2	19.1	22	3.8	24.5	4.3	7.9	5.4	5	2.8	4.5	4.1
10014_at	ECM38	YLR299W	YLR299W gamma-glutamyltransferase homolog	GLUTATHIONE METABOLISM	66.8	10.3	276.1	13.6	100.2	21.8	83.5	10.7	153.6	25.9	417.3	108.1	196.5	13.1	169.8	64.2	4.1	2.8	3.3	2.7	2.1	2.5
10172_at	PUT1	YLR142W	YLR142W (PUT1) Proline oxidase (proline dehydrogenase). first step in synthesis of glu	PROLINE UTILIZATION	12	3.3	491.5	104	23.2	4.3	30.1	6.8	146.9	34.2	663.4	58.4	27.8	8.4	40.7	13.7	41	21.2	16.3	4.5	23.9	16.3
10511_at	GAP1	YKR039W	YKR039W (GAP1) General amino acid permease. proton symport transporter for all nat	TRANSPORT	136.6	37.8	3029.1	649.8	179.4	42.2	224.7	49	522	82.9	2898.3	203.9	276.9	24.8	426.8	92	22.2	16.9	13.5	5.6	10.5	6.8
10551_at	DAL80	YKR034W	YKR034W negative regulator of multiple nitrogen catabolic genes	NITROGEN CATABOLISM	16.1	4.7	604.8	46.9	20.2	5.7	63.9	9.4	12.7	3	829.6	180.2	12	2.7	44.4	6.8	37.6	29.9	9.5	65.5	69.1	18.7
11211_at	CPS1	YJL172W	YJL172W carboxypeptidase yscS	PROTEIN DEGRADATION	19.2	5.9	249.4	169.1	26.5	5.5	38.9	15.5	32.4	14.5	333.4	150	23.1	5.2	25.3	8.1	13	9.4	6.4	10.3	14.5	13.2
4063_at	DAL1	YIR027C	YIR027C allantoinase	ALLANTOIN UTILIZATION	16.8	7.1	201.9	24.8	26.2	10.5	53.5	9.9	14.8	3.5	222.7	56.3	12	1	24.2	7.6	12	7.7	3.8	15.1	18.6	9.2
4065_at	DAL2	YIR029W	YIR029W (DAL2) Allantoicase. carries out the second step in the degradation of allantoi	ALLANTOIN UTILIZATION	18.2	6.8	141.3	22.1	17	0.5	12	5.5	39.9	10.7	199.2	51.9	19.4	5.5	18.3	8.7	7.8	8.3	11.8	5	10.3	10.9
4066_at	DCG1	YIR030C	YIR030C involved in nitrogen-catabolite metabolism	UNKNOWN	12	6.7	67	16.3	17.5	5.8	18.8	5.7	17.7	2.1	98.5	5.6	12.7	1.9	18.1	4.5	5.6	3.8	3.6	5.6	7.7	5.5
4067_at	DAL7	YIR031C	YIR031C Malate synthase 2	ALLANTOIN UTILIZATION	15.6	6.6	179.3	15.4	29.2	5.4	25.2	7.4	16.1	5.4	219	23.8	33.3	7	30.2	11.2	11.5	6.1	7.1	13.6	6.6	7.3
4068_at	DAL3	YIR032C	YIR032C ureidoglycolate hydrolase	PURINE METABOLISM	74.6	19	630	48.8	104.6	27.7	137.2	33.2	328.9	63.8	766	120	255.6	37.9	183.7	36.6	8.4	6	4.6	2.3	3	4.2
4284_at	SDL1	YIL167W	YIL167W (SDL1) Serine dehydratase. converts serine to pyruvate and ammonia for gluc	GLUCONEOGENESIS	13.4	8.8	115	28.3	26.7	1.9	22.5	2.9	18.8	3.7	88.6	7.1	30.3	2.7	14.4	0.3	8.6	4.3	5.1	4.7	2.9	6.1
4511_at	PUT2	YHR037W	YHR037W delta-1-pyrroline-5-carboxylate dehydrogenase	PROLINE METABOLISM	110.9	33.3	317.2	31.6	114.9	5.3	151.2	9	271.1	22	770.1	72.3	317	13.1	344.5	67.4	2.9	2.8	2.1	2.8	2.4	2.2
7164_at	DUR1.2	YBR208C	YBR208C (DUR1.2) Urea amidolyase. contains urea carboxylase and allophanate hydr	NITROGEN. AMINO ACID. NUCLEOTIDE METAI	27.3	14.4	341.9	21.1	36.8	3.2	30.3	2.5	99.5	27.1	458.9	62.3	54.5	1.2	67.2	19.6	12.5	9.3	11.3	4.6	8.4	6.8
8959_at	MLS1	YNL117W	YNL117W (MLS1) Malate synthase 1. functions in glyoxylate cycle. has near identity to	GLYOXYLATE CYCLE	12	1.3	295.9	25.2	12	0.7	12	2.5	381.2	139.5	997.6	73	23.2	5.8	45.4	13	24.7	24.7	24.7	2.6	43.1	22
7230_at	0	YBR139W	YBR139W Probable serine-type carboxypeptidase (EC 3.4.16.1)	UNKNOWN	77.2	23.7	254.3	30	122.9	17.3	117.1	3.7	138.6	32.9	399.7	58.6	145.1	6.3	189.4	28.5	3.3	2.1	2.2	2.9	2.8	2.1
4546_at	DUR3	YHL016C	YHL016C Urea transporter	TRANSPORT	20.3	6.9	164.2	33.8	32.1	0.9	68.9	31.9	61.9	23.1	455.5	49.6	43.6	5.5	101	38.6	8.1	5.1	2.4	7.4	10.4	4.5
10854_at	DAL5	YJR152W	YJR152W allantoate permease	ALLANTOIN UTILIZATION	88.9	26	2031.3	393.2	110.5	15.9	117.9	4.6	90.8	18	2436.8	167.9	105.5	7.3	102.3	14.6	22.8	18.4	17.2	26.8	23.1	23.8
4064_at	DAL4	YIR028W	YIR028W allantoin permease	ALLANTOIN UTILIZATION	16.7	7.3	64.8	20.3	19.8	1.1	22.2	14.1	20.5	2.3	238.4	21.2	12	1.6	23.6	8.7	3.9	3.3	2.9	11.6	19.9	10.1
7546_at	OPT2	YPR194C	YPR194C similarity to S.pombe isp4 protein	UNKNOWN	81.3	28.8	1697.2	265.4	12	0.4	214.4	27.2	12	1.2	1426.6	114.1	12	4	91.4	28.8	20.9	141.4	7.9	118.9	118.9	15.6
8192_at	PUT4	YOR348C	YOR348C putative proline-specific permease	TRANSPORT	16.9	6.6	176	26.5	28.1	6.5	21.7	8.9	1262.8	181	2557.3	204	138.5	44.6	518.2	179.5	10.4	6.3	8.1	2	18.5	4.9
9026_at	MEP2	YNL142W	YNL142W (MEP2) Ammonia permease of low capacity and high affinity. involved gener	TRANSPORT	91.6	41.6	1635.1	489.6	88.7	27.9	159.4	23.4	421.2	219.4	2025	85.5	209.5	33.5	242.9	65.2	17.9	18.4	10.3	4.8	9.7	8.3
9530_at	0	YMR088C	YMR088C similarity to multidrug resistance proteins	UNKNOWN	120.4	31.2	1200.9	185	115	7	111.2	12.3	102.6	22.6	1280.1	28.5	95.1	6	81.6	11.9	10	10.4	10.8	12.5	13.5	15.7
10262_at	0	YLR053C	YLR053C hypothetical protein	UNKNOWN	12	6.9	73.2	8.2	12	3.7	26.3	11.1	81.8	23.4	335.2	21.8	28	3	104.1	37.9	6.1	6.1	2.8	4.1	12	3.2
4177_at	0	YIL089W	YIL089W similarity to hypothetical protein YLR036c	UNKNOWN	12	5.1	56.1	17.2	23.4	3	20.6	6.2	25.8	6.5	94.2	9.3	46.2	7.2	37.5	6	4.7	2.4	2.7	3.7	2	2.5
4503_at	0	YHR029C	YHR029C Thymidylate synthase (putative\; weak)	UNKNOWN	103.3	14.2	487.5	51.7	100.2	9.7	112.5	18.1	113.5	26.2	477	61.9	157	8.6	71.7	16.7	4.7	4.9	4.3	4.2	3	6.7
4800_at	0	YGR190C	YGR190C questionable ORF	UNKNOWN	12	1.2	63.7	19.3	12	0.4	12	2.4	12	1	51	9.5	12	2.1	12	2.1	5.3	5.3	5.3	4.3	4.3	4.3
6369_at	0	YDR090C	YDR090C weak similarity to YRO2 protein	UNKNOWN	171.1	34.6	795.1	83	215.2	32.7	217.5	15.4	177.5	20.2	703.2	112.4	199.4	17.1	192.6	5.9	4.6	3.7	3.7	4	3.5	3.7
6714_at	ADY3	YDL239C	YDL239C hypothetical protein	UNKNOWN	23.2	9.3	84.6	28.9	26	7.6	32.1	6.4	29.6	9.7	141.9	13.7	36.2	5.6	48.4	18.9	3.6	3.3	2.6	4.8	3.9	2.9
8661_at	YGK3	YOL128C	YOL128C strong similarity to protein kinase Mck1p	UNKNOWN	21.9	11.6	117.3	27.8	32.6	1.3	35.9	1.8	40.2	8.2	182.4	37.7	49.1	6.8	38.2	9	5.4	3.6	3.3	4.5	3.7	4.8
9532_at	0	YMR090W	YMR090W strong similarity to B. subtilis conserved hypothetical protein yhfK	UNKNOWN	36.6	10.8	163.3	18.5	69.3	11.3	77.1	8.8	90.4	36.6	338.2	33.6	124.5	8.1	166.7	11.6	4.5	2.4	2.1	3.7	2.7	2

Down-regulated under N-Lim anaerobic and aerobic conditions (FC = fold change, ANA = anaerobic, A = aerobic)

Probe Set	Gene name	systematic name	functional description	cellular function	C-Lim ANA Average	C-Lim ANA Stdev	N-Lim ANA Average	N-Lim ANA Stdev	P-Lim ANA Average	P-Lim ANA Stdev	S-Lim ANA Average	S-Lim ANA Stdev	C-Lim A Average	C-Lim A Stdev	N-Lim A Average	N-Lim A Stdev	P-Lim A Average	P-Lim A Stdev	S-Lim A Average	S-Lim A Stdev	FC N-Lim ANA vs C-Lim ANA	FC N-lim ANA vs S-ANA	FC N-lim ANA vs P-lim ANA	FC N-Lim AE vs C-Lim AE	FC N-lim AE vs S-AE	FC N-lim AE vs P-lim AE
5977_at	GNP1	YDR508C	YDR508C high-affinity glutamine permease	TRANSPORT	253.5	119.3	30.9	10.1	359.5	106.1	154.3	12.1	78.5	9.9	16.7	2.6	273.1	33.7	64.2	16.2	-8.2	-11.6	-5	-4.7	-16.4	-3.8

Up-regulated under P-Lim anaerpbic and aerobic only (FC = fold change, ANA = anaerobic, A = aerobic)

Probe Set	Gene name	systematic name	functional description	cellular function	C-Lim ANA Average	C-Lim ANA Stdev	N-Lim ANA Average	N-Lim ANA Stdev	P-Lim ANA Average	P-Lim ANA Stdev	S-Lim ANA Average	S-Lim ANA Stdev	C-Lim A Average	C-Lim A Stdev	N-Lim A Average	N-Lim A Stdev	P-Lim A Average	P-Lim A Stdev	S-Lim A Average	S-Lim A Stdev	FC P-Lim ANA vs C-Lim ANA	FC P-lim ANA vs N-lim ANA	FC P-lim ANA vs S-Lim ANA	FC P-Lim AE vs C-Lim AE	FC P-lim AE vs N-lim AE	FC P-lim AE vs S-Lim AE
5645_at	VTC1	YER072W	YER072W Homolog of S. pombe Nrf1 (97\% identical in predicted amino acid sequence	SIGNALING. POLARIZED GROWTH (PUTATIVE	321.8	15	424.8	60.7	336.8	3.4	1959.8	28.6	348.8	141.5	671.9	34.3	551.6	35.4	2381.2	74.7	6.1	4.6	5.8	6.8	3.5	4.3
8410_at	DDP1	YOR163W	YOR163W strong similarity to S.pombe SPAC13G6.14 protein	UNKNOWN	48.6	18.1	83	10.3	66.1	5.8	175.5	17	84.9	0.7	110.5	19.7	106.4	6.8	251.1	50.1	3.6	2.1	2.7	3	2.3	2.4
7779_at	VTC3	YPL019C	YPL019C strong similarity to YFL004w. similarity to YJL012c	UNKNOWN	39.5	13.5	101.9	36.2	69.8	12.7	747.2	160.7	72.7	31.3	108.3	12.1	200.3	22.7	1013.6	50.8	18.9	7.3	10.7	13.9	9.4	5.1
8704_at	ALR1	YOL130W	YOL130W ALuminium Resistance 1	METAL RESISTANCE	144.6	34.7	243.9	28.5	210.9	13.4	489.7	23.3	163.4	23.3	207.5	16.2	184.1	4.1	562.9	127.6	3.4	2	2.3	3.4	2.7	3.1
4385_at	SPL2	YHR136C	YHR136C 17 kDa protein	CELL CYCLE	12	3.1	13.8	1.8	12	2.1	1117.4	195.7	60.8	85.4	12	0.6	12	1	1267.3	83.9	93.1	80.8	93.1	20.9	105.6	105.6
10700_at	PMU1	YKL128C	YKL128C Phospo-mutase homolog	UNKNOWN	256.5	55.5	284.5	33.5	323	45.1	670.5	23.6	235.5	64.7	274	6	319	49.3	768.8	298.6	2.6	2.4	2.1	3.3	2.8	2.4
11262_s_at	PHO11	YAR071W	YAR071W Acid phosphatase. secreted	PHOSPHATE METABOLISM	43.9	20.4	112.4	17.9	84.9	9.8	3368.6	262.6	55.2	37.1	68.2	12.1	44.7	4.2	2357.2	114	76.8	30	39.7	42.7	34.6	52.7
4475_at	INM1	YHR046C	YHR046C Inositol monophosphatase	UNKNOWN	44.2	18.4	72.5	19.7	84.3	4	251.7	54.1	43	6.3	81.6	3.9	77.7	5.8	188.7	56.4	5.7	3.5	3	4.4	2.3	2.4
4753_at	PHO81	YGR233C	YGR233C Positive regulatory protein of phosphate pathway	CELL CYCLE	188.9	29.1	343	21.5	190.5	20.6	832.6	72.5	207.9	78.5	381	20.3	285.6	12.6	968.8	122	4.4	2.4	4.4	4.7	2.5	3.4
5633_at	HOR2	YER062C	YER062C DL-glycerol-3-phosphatase	GLYCEROL METABOLISM	54.9	14.8	50.6	4.5	66.5	2.5	320.7	6.2	66.5	1.2	66.4	10.8	83	14.4	419.9	122.8	5.8	6.3	4.8	6.3	6.3	5.1
6793_at	GIT1	YCR098C	YCR098C permease involved in the uptake of glycerophosphoinositol (GroPIns)	UNKNOWN	12	6.5	12.3	5.1	12.9	2.1	800.1	61.4	13.3	7.9	12.7	4.1	12	3.5	983.3	117.8	66.7	65.2	62.2	74.1	77.2	81.9
7273_at	PHO3	YBR092C	YBR092C Acid phosphatase. constitutive	THIAMINE UPTAKE	173.2	54.5	157.1	65.6	71	10.8	2233.6	357.8	279.8	334	210.9	33.8	64.6	2	2012.5	165.6	12.9	14.2	31.4	7.2	9.5	31.2
8191_at	PYK2	YOR347C	YOR347C Pyruvate kinase. glucose-repressed isoform	GLYCOLYSIS	74.8	14.5	76.7	7	71.7	13	195.1	44.5	57.9	6.7	60.2	12.2	51.8	1.9	226.4	73.8	2.6	2.5	2.7	3.9	3.8	4.4
8551_at	PLB3	YOL011W	YOL011W strong similarity to phospholipases	PHOSPHOLIPID METABOLISM	90.1	36.3	155.7	12.5	139.4	6	374.6	36.5	142.6	16.9	132.2	32.5	96.6	4.4	396.7	40.5	4.2	2.4	2.7	2.8	3	4.1
9762_at	PHO84	YML123C	YML123C inorganic phosphate transporter. transmembrane protein	TRANSPORT	14.6	4.5	31.1	2.8	18.2	6.2	3221.6	496.5	332.4	512.3	19.7	5	16.4	6.2	3244.6	353.9	220.2	103.6	177.3	9.8	165	198.2
6466_at	MAF1	YDR005C	YDR005C required for sorting of Mod5p	PROTEIN TARGETING (PUTATIVE)	57.5	21	103.5	29.3	100.3	10	238.7	45.1	99.8	9.4	127.5	9	99.4	7	411.8	52.7	4.2	2.3	2.4	4.1	3.2	4.1
9086_at		YNL217W	YNL217W weak similarity to E.coli bis(5'-nucleosyl)-tetraphosphatase	UNKNOWN	154	51.5	246.8	38.1	252.9	23.4	699.1	25.5	126.8	32.8	305.9	27.6	207.8	8	724.7	34.3	4.5	2.8	2.8	5.7	2.4	3.5
11132_at	PHO86	YJL117W	YJL117W Putative inorganic phosphate transporter	TRANSPORT	235.9	48.1	304.8	58.8	355	21.2	992.7	92.2	367.1	64.3	364.5	34.4	422.9	37.5	867.7	73.2	4.2	3.3	2.8	2.4	2.4	2.1
7069_at	PHO89	YBR296C	YBR296C Homolog to phosphate-repressible phosphate permease	PHOSPHATE METABOLISM	18.7	6.3	35.7	9	29.6	5.4	899.3	104.1	112.5	94.8	25.3	2.9	150.9	122.9	1088.1	42.5	48.1	25.2	30.4	9.7	43	7.2
11101_at	ZAP1	YJL056C	YJL056C Metalloregulatory protein involved in zinc-responsive transcriptional regulation	TRANSPORT (ZN)	12	6.4	24	7.1	25.1	2.5	58.8	7.6	19.9	1.7	27.9	1	22.9	2.9	69	15.1	4.9	2.4	2.3	3.5	2.5	3
6478_at	KCS1	YDR017C	YDR017C Shows homology to basic leucine zipper family of transcription factors	CELL WALL MAINTENANCE	86.5	46.4	174.2	48.6	138.5	20.1	440.9	23.7	125.3	17.3	259.1	22.3	124.5	67.8	578	43.7	5.1	2.5	3.2	4.6	2.2	4.6
11056_at	VTC4	YJL012C	YJL012C weak similarity to regulatory protein PHO81	UNKNOWN	171.2	22.9	243	10	269.5	47.6	1848.6	333.4	324.6	163	368.8	31.1	396.8	72	1852.8	175.3	10.8	7.6	6.9	5.7	5	4.7
11130_at		YJL119C	YJL119C questionable ORF	UNKNOWN	12.4	4.7	14.7	6.2	12	4.3	77.4	7.1	17.5	4.5	12	3	16.5	2.2	88.6	15.4	6.3	5.3	6.5	5.1	7.4	5.4
11309_at		YAR069C	YAR069C Potential membrane protein	UNKNOWN	28.4	9.5	31.2	8.1	21.5	7.4	158.1	17.3	12	2.1	12	1.7	12	3.7	97.6	30.4	5.6	5.1	7.4	8.1	8.1	8.1
5692_at	PHM8	YER037W	YER037W strong similarity to hypothetical protein YGL224c	UNKNOWN	12	1.8	35	3.7	29.2	3	249.1	86	32.9	6.3	62.6	11.4	22.8	3.3	391	62.6	20.8	7.1	8.5	11.9	6.2	17.1
6201_at	PHM6	YDR281C	YDR281C hypothetical protein	UNKNOWN	28.9	14.1	50.4	12.8	24.8	1.5	960.9	64.8	28.2	25.7	49.8	11.8	22.4	5.6	960.1	89.7	33.3	19.1	38.7	34.1	19.3	42.9
6896_at	GFD2	YCL036W	YCL036W similarity to hypothetical protein YDR514c	UNKNOWN	40.1	12	50.4	13	29	7.7	225.2	24.9	61.4	19.9	58.7	31.3	37.9	4.9	451.7	121.7	5.6	4.5	7.8	7.4	7.7	11.9
7870_at		YPL110C	YPL110C similarity to C.elegans hypothetical protein. weak similarity to Pho81p	UNKNOWN	84.5	16.3	94.7	10.2	96.3	12	362.7	7.2	113.5	24.3	104.1	2.6	104.9	16.9	799.4	46	4.3	3.8	3.8	7	7.7	7.6
9422_at	ICY1	YMR195W	YMR195W similarity to YPL250c	UNKNOWN	612.9	105.8	655.5	21.8	163.2	25.1	1353.2	99.1	140.2	31.5	766.5	113.4	168.9	23	1842.4	137.6	2.2	2.1	8.3	13.1	2.4	10.9
9438_at	DML1	YMR211W	YMR211W weak similarity to beta tubulins	UNKNOWN	25	13.4	33.6	7.4	34.9	5	116.4	35.9	37.2	7.2	35.6	2.5	37.9	3.6	115.5	29	4.6	3.5	3.3	3.1	3.2	3
11385_s_at	FLO9	YAL063C	YAL063C putative Flo1p homolog	FLOCCULATION	37.9	9.4	149.8	23.3	74.3	14.3	581.3	76.5	68.5	10.1	92.1	4.1	73.5	8.8	421	91.1	15.3	3.9	7.8	6.1	4.6	5.7

Down-regulated under P-Lim anaerpbic and aerobic only (FC = fold change, ANA = anaerobic, A = aerobic)

Probe Set	Gene name	systematic name	functional description	cellular function	C-Lim ANA Average	C-Lim ANA Stdev	N-Lim ANA Average	N-Lim ANA Stdev	P-Lim ANA Average	P-Lim ANA Stdev	S-Lim ANA Average	S-Lim ANA Stdev	C-Lim A Average	C-Lim A Stdev	N-Lim A Average	N-Lim A Stdev	P-Lim A Average	P-Lim A Stdev	S-Lim A Average	S-Lim A Stdev	FC P-Lim ANA vs C-Lim ANA	FC P-lim ANA vs N-lim ANA	FC P-lim ANA vs S-Lim ANA	FC P-Lim AE vs C-Lim AE	FC P-lim AE vs N-lim AE	FC P-lim AE vs S-Lim AE
6396_at	IPT1	YDR072C	YDR072C inositolphosphotransferase 1	SPHINGOLIPID BIOSYNTHESIS	75.3	14.7	73.9	6.4	60.9	8.1	26.8	3.8	136.4	17.8	109.1	16	84.7	10.6	32.1	10.3	-2.8	-2.8	-2.3	-4.3	-3.4	-2.6
7067_at	SUL1	YBR294W	YBR294W Probable sulfate transport protein	TRANSPORT	703.3	134.8	407.8	75.5	1450.4	319.9	12	2.3	1035.2	67.4	487.2	30.5	1885.4	396.9	42	8.1	-58.6	-34	-120.9	-24.6	-11.6	-44.9

Up-regulated under S-Lim anaerobic and aerobic conditions (FC = fold change, ANA = anaerobic, A = aerobic)

Probe Set	Gene name	systematic name	functional description	cellular function	C-Lim ANA Average	C-Lim ANA Stdev	N-Lim ANA Average	N-Lim ANA Stdev	P-Lim ANA Average	P-Lim ANA Stdev	S-Lim ANA Average	S-Lim ANA Stdev	C-Lim A Average	C-Lim A Stdev	N-Lim A Average	N-Lim A Stdev	P-Lim A Average	P-Lim A Stdev	S-Lim A Average	S-Lim A Stdev	FC S-Lim ANA vs C-Lim ANA	FC S-lim ANA vs N-ANA	FC S-lim ANA vs P-Lim ANA	FC S-Lim AE vs C-Lim AE	FC S-lim AE vs N-AE	FC S-lim AE vs P-Lim AE
5115_at	SOH1	YGL127C	YGL127C SOH1 encodes a novel 14-kD protein with limited sequence similarity to RNA	UNKNOWN	116	18.8	153.6	26.1	641	116.2	126.6	22	120.6	12.1	130.3	25.8	688.9	116.6	150.9	25.5	5.5	4.2	5.1	5.7	5.3	4.6
6219_at	CHL4	YDR254W	YDR254W Protein necessary for stability of ARS-CEN plasmids\; suggested to be requi	MITOSIS. CHROMOSOME SEGREGATION	30.5	14.8	34.1	11.5	79.1	27.1	33.9	6.8	46.1	13.2	63.3	26.5	155	20.3	30.8	5.7	2.6	2.3	2.3	3.4	2.4	5
6539_at	RAD59	YDL059C	YDL059C A mutation in this gene results in RADiation sensitivity and recombination def	DNA REPAIR	137.4	78.1	247.4	36.8	723.8	56.2	91.5	5.9	179.8	14	415	65.5	1059.4	244.4	267.7	19.5	5.3	2.9	7.9	5.9	2.6	4
11260_at	OPT1	YJL212C	YJL212C strong similarity to S.pombe isp4 protein	UNKNOWN	24.6	10.1	175.7	37.1	717.7	119	20.8	11	12	1.7	366.8	48.2	1109.6	80.7	47.5	14.6	29.2	4.1	34.5	92.5	3	23.4
10373_at	0	YLL057C	YLL057C similarity to E.coli dioxygenase	UNKNOWN	12	2.2	14.5	0.9	1580.5	330.3	12	5	12	4.3	12	2.1	2232.7	354.1	12	4.1	131.7	108.8	131.7	186.1	186.1	186.1
10416_at	GTT2	YLL060C	YLL060C Glutathione transferase	GLUTATHIONE METABOLISM	115.3	39.7	148.7	13.6	607.8	120	87.2	9.8	98.3	16.1	98.5	9.3	906.2	88.8	90.5	36.7	5.3	4.1	7	9.2	9.2	10
4924_at	CTT1	YGR088W	YGR088W cytoplasmic catalase T	OXIDATIVE STRESS RESPONSE	12	1.6	15.7	5.2	45.2	12.2	12	3.3	37.3	17.1	21.7	6.3	74.9	10.6	28.9	10	3.8	2.9	3.8	2	3.4	2.6
4452_at	PCL5	YHR071W	YHR071W G1\/S cyclin (weak)	CELL CYCLE	219.6	16.3	206.2	33.8	561.5	78.6	267.5	7.6	215.5	130.3	244.2	47	497.7	37.5	165.9	15.5	2.6	2.7	2.1	2.3	2	3
8717_at	0	YOL164W	YOL164W similarity to Pseudomonas alkyl sulfatase	UNKNOWN	19.8	13.1	71.5	9.4	1284.5	153.9	71.3	17.7	25.9	12.4	40.8	8.3	1738.9	192.8	41.6	11.9	64.9	18	18	67.1	42.6	41.8
10418_at	0	YLL058W	YLL058W similarity to N.crassa O-succinylhomoserine (thiol)-lyase	UNKNOWN	26.9	12.5	44.7	4.7	702.1	76.4	44	12.9	25	2	25.6	3.3	596	9	26.8	4.2	26.1	15.7	16	23.8	23.3	22.2

10494_at	MET1	YKR069W	YKR069W siroheme synthase	METHIONINE BIOSYNTHESIS	477.4	63.2	476.5	72.1	1861.9	151.2	328.5	36.4	548.4	111.1	526.8	70.1	2159.3	32.1	889.9	384.9	3.9	3.9	5.7	3.9	4.1	2.4
11032_at	MET3	YJR010W	YJR010W ATP sulfurylase	METHIONINE BIOSYNTHESIS	922.1	103.5	793.1	54.8	2051.2	191.6	318.2	54.9	784.5	112.8	924.8	62.7	2175.3	165.3	699.8	6.6	2.2	2.6	6.4	2.8	2.4	3.1
11097_at	BNA3	YJL060W	YJL060W similarity to kynurenine aminotransferase and glutamine-phenylpyruvate trans	UNKNOWN	153.6	20.2	255.4	48.3	635	54.9	134.4	20.7	188.7	17.1	380.2	82.2	867	115	202.1	15.9	4.1	2.5	4.7	4.6	2.3	4.3
11355_at	CYS3	YAL012W	YAL012W cystathionine gamma-lyase	METHIONINE BIOSYNTHESIS	1004.9	264.7	649.7	148.9	3240.4	512.4	614.2	84.5	658.9	151.3	800.6	214.4	2928.7	361.1	1378.1	644.4	3.2	5	5.3	4.5	3.7	2.1
4098_at	MET28	YIR017C	YIR017C Transcriptional activator of sulfur amino acid metabolism	SULFUR AMINO ACID METBOLISM	275.8	28.6	252.3	10.9	1010.4	97.9	181.3	34.7	289.9	28.3	271.7	39.3	1141.1	85.9	251.5	14.3	3.7	4	5.6	3.9	4.2	4.5
4190_at	SER33	YIL074C	YIL074C strong similarity to E.coli phosphoglycerate dehydrogenase	UNKNOWN	369.2	11.7	306.5	35.4	754	22.1	182.4	46.6	181.4	21.8	218.6	11.8	712.5	104.8	258.9	58.4	2	2.5	4.1	3.9	3.3	2.8
4336_at		0 YHR176W	YHR176W Dimethylaniline monooxygenase	UNKNOWN	33.7	10.6	66.1	9.5	559.8	65.7	33.2	6.6	42.3	6.3	119.8	20.9	700.8	39.4	83.2	25.8	16.6	8.5	16.9	16.6	5.9	8.4
4572_at	MUP3	YHL036W	YHL036W (MUP3) very low affinity methionine permease	TRANSPORT	62.2	18.9	144.8	31.6	432.6	66.4	53.9	14	65.3	9.2	206.3	38.6	628.3	87.2	116.3	10.5	7	3	8	9.6	3	5.4
4923_at	PDC6	YGR087C	YGR087C Third. minor isozyme of pyruvate decarboxylase	GLYCOLYSIS	18.5	8.6	73.5	18.2	1160.3	254.5	24	9.1	66	43.9	161.1	30.3	1874.3	235.7	37.4	7.3	62.8	15.8	48.4	28.4	11.6	50.1
4936_at	MUP1	YGR055W	YGR055W high affinity methionine permease	TRANSPORT	41.7	20.3	48.1	5.1	896.7	113.3	29.5	8.5	104.8	33.9	151.8	26.3	1544.3	221.3	237.4	30.6	21.5	18.7	30.4	14.7	10.2	6.5
5196_at	STR3	YGL184C	YGL184C strong similarity to Emericella nidulans cystathionine beta-lyase	UNKNOWN	50	15.8	98.7	14.3	545.8	13.9	48.7	7.4	248.2	73.9	180.6	16.9	939	88.1	184.5	6.6	10.9	5.5	11.2	3.8	5.2	5.1
5327_at	MET10	YPR030W	YPR030W subunit of assimilatory sulfite reductase	SULFATE ASSIMILATION	358.2	53.1	441.9	32.2	941.6	176.2	142.6	5.4	329.2	35.8	391.9	24.9	1038.3	109.9	336.4	89.6	2.6	2.1	6.6	3.2	2.6	3.1
6218_at	MET32	YDR253C	YDR253C zinc finger DNA binding factor. transcriptional regulator of sulfur amino acid m	METHIONINE METABOLISM	100.9	28.1	104.9	46.9	443	76.1	29.5	8.4	217.2	47	142.6	13.6	836.4	97.7	86.9	13.6	4.4	4.2	15	3.9	5.9	9.6
7169_at	MET8	YBR213W	YBR213W Effector in the expression of PAPS reductase and sulfite reductase	SULFATE ASSIMILATION	30.8	2.4	29.5	10.9	402	73.7	23.8	3.2	42.7	17.8	51.3	12.2	663	99.4	120.1	58.5	13.1	13.6	16.9	15.5	12.9	5.5
7565_at	MET16	YPR167C	YPR167C 3'phosphoadenylylsulfate reductase	SULFATE ASSIMILATION	247.7	44	364.9	31.9	917.1	238.7	175.6	10	242.4	39.7	386.6	43.1	1072.4	136.6	328.5	78.4	3.7	2.5	5.2	4.4	2.8	3.3
8021_at	SAM3	YPL274W	YPL274W strong similarity to amino-acid transport proteins	TRANSPORT. AMINO ACID	52.1	8.4	74	11.9	158.4	28.1	50.4	17.8	58.9	5	81	19.5	238.1	54.6	118.7	17.7	3	2.1	3.1	4	2.9	2
9162_at	MET2	YNL277W	YNL277W homoserine O-trans-acetylase	METHIONINE BIOSYNTHESIS	501.2	41.5	640.7	107.1	1466.7	158.2	363	42.3	389.5	42	614.2	81.5	1592.7	52.3	709.3	199.5	2.9	2.3	4	4.1	2.6	2.2
10256_at	SUL2	YLR092W	YLR092W high affinity sulfate permease	TRANSPORT	536.6	95	408.8	62.1	1396.3	89.8	91.1	22.2	340.9	43.8	433.3	30.5	1193.7	102	344.7	26	2.6	3.4	15.3	3.5	2.8	3.5
10210_at	TIS11	YLR136C	YLR136C zinc finger containing homolog of mammalian TIS11. glucose repressible gen	UNKNOWN	12	3.4	15.2	6.2	53.6	18	12	1.9	16.2	5.7	12	3.3	35.2	12.2	14.4	3.9	4.5	3.5	4.5	2.2	2.9	2.4
10375_at		0 YLL059W	YLL059W similarity to DalSp	UNKNOWN	93.9	18.6	321.3	23.6	1992.5	245.1	75.2	8.2	174.2	69.1	454	22.4	2023.7	187.4	146.8	35.1	21.2	6.2	26.5	11.6	4.5	13.8
10415_at	MMP1	YLL061W	YLL061W (MMP1) High affinity S-methylmethionine permease. has similarity to Gap1p	TRANSPORT. AMINO ACID	110.2	50.6	153.5	48.7	794.4	102.3	28.5	6.6	324.9	16.2	23.8	2.3	827.9	54.4	17.6	4.9	7.2	5.2	27.8	2.5	34.8	47
4285_at		0 YIL166C	YIL166C similarity to allantoate permease DalSp	UNKNOWN	12	6.3	20.6	5.7	324.5	141.1	25.3	3.4	22.3	2.9	21.7	2.2	1650.4	271.2	24.3	4.4	27	15.8	12.8	73.9	75.9	68
4568_at	ARN1	YHL040C	YHL040C Protein involved in the transport of ferrichromes. member of the yeast-specifi	UNKNOWN	23.1	10.9	70.3	5.1	175.4	21.8	42.2	11.9	57	16.4	43.4	5.7	325.9	68.8	53.6	13.5	7.6	2.5	4.2	5.7	7.5	6.1
5425_at	AGP3	YFL055W	YFL055W Amino acid permease	TRANSPORT	12	1.9	12.1	2.7	420.2	54.5	12	4.6	31.6	4.8	12	0.2	773.8	111.3	12	2.3	35	34.7	35	24.5	64.5	64.5
7066_at		0 YBR293W	YBR293W Probable multidrug resistance protein	UNKNOWN	99.8	14.3	126.3	18.3	546.7	105.4	137.1	11.7	113.4	14.2	121.1	20.5	997.1	84.8	110.9	3	5.5	4.3	4	8.8	8.2	9
8177_at		0 YOR378W	YOR378W strong similarity to aminotriazole resistance protein	UNKNOWN	12	3.9	12	2	53.1	15.2	12.3	4.8	12	1.6	12	1.8	62.9	1.6	12	1.5	4.4	4.3	5.2	5.2	5.2	5.2
8718_at		0 YOL163W	YOL163W similarity to P.putida phthalate transporter	UNKNOWN	12	5	55.9	16	440.5	94.6	22.1	1.7	12	2.8	21.9	3.6	638	19.6	12	1.7	36.7	7.9	19.9	53.2	29.1	53.2
9307_at	ATM1	YMR301C	YMR301C mitochondrial ABC transporter protein	TRANSPORT	55.8	15.7	91.9	13.3	243.2	49.3	66.6	7.5	72.5	17.6	95.9	13.3	329.8	57.6	100.3	15.4	4.4	2.6	3.7	4.5	3.4	3.3
10374_at		0 YLL056C	YLL056C weak similarity to Y.pseudotuberculosis CDP-3,6-dideoxy-D-glycero-L-glycero	UNKNOWN	25.1	10.4	52.8	7.6	206.8	50.7	41.3	9.7	45.5	9.3	40.1	7.4	588.3	26.5	53.7	10.9	8.2	3.9	5	12.9	14.7	11
10414_at	MHT1	YLL062C	YLL062C weak similarity to M.leprae metH2 protein	UNKNOWN	77.4	21.6	55.6	14.9	595.6	160.2	19.5	2.7	100.3	17.5	19.5	4.3	663.8	17.9	12	4.4	7.7	10.7	30.6	6.6	34.1	55.3
4855_at		0 YGR154C	YGR154C strong similarity to hypothetical proteins YKR076w and YMR251w	UNKNOWN	16.6	7.6	49.2	13.1	122	12.3	15.4	6.8	45.6	18.4	73	6.9	304.5	35.1	30	7.8	7.3	2.5	7.9	6.7	4.2	10.1
5422_s_at		0 YFL067W	YFL067W similarity to mouse period clock protein	UNKNOWN	14.7	10.7	12	4.9	42.4	3	19.8	6.5	12	2.1	18.5	7.6	42.7	10.5	17.4	6.8	2.9	3.5	2.1	3.6	2.3	2.5
7999_at	ICY2	YPL250C	YPL250C weak similarity to YMR195w	UNKNOWN	185.4	37	163.7	27.8	905.5	138.9	234.3	2.6	304.7	122.5	126.4	33.5	1705.5	181.7	498.7	23.5	4.9	5.5	3.9	5.6	13.5	3.4
8719_at		0 YOL162W	YOL162W strong similarity to hypothetical protein YIL168c	UNKNOWN	15.5	4.4	50.4	8.6	277.7	42.2	18.8	3	13.8	3.5	32.4	3.1	614.7	39.1	13.2	6.2	18	5.5	14.8	44.4	19	46.7
9068_at		0 YNL191W	YNL191W similarity to Synechocystis hypothetical protein	UNKNOWN	48.4	10	88.2	17.4	509.5	69.1	53	2.1	66.5	2.8	100.4	11.1	662.2	116.8	63.9	11.2	10.5	5.8	9.6	10	6.6	10.4
9646_at		0 YML018C	YML018C similarity to YDR438w	UNKNOWN	404.3	46.6	582.2	28.9	1480.2	177	428.6	87.5	258.9	11.6	540.1	66.4	1243.8	27.5	354	50.2	3.7	2.5	3.5	4.8	2.3	3.5
9943_at		0 YLR364W	YLR364W hypothetical protein	UNKNOWN	61.3	22	70.8	15.9	441.2	60.3	29.7	3.7	100.7	21	124.7	7.5	714	64.5	108.1	26.8	7.2	6.2	14.8	7.1	5.7	6.6
10689_at	CWP1	YKL096W	YKL096W cell wall mannoprotein	CELL WALL MAINTENANCE	195.6	54.7	98.4	8.9	421.8	110.6	116.7	35.2	262.3	99.3	100.8	17.5	1222	68.6	69.5	24.3	2.2	4.3	3.6	4.7	12.1	17.6

Down-regulated under S-Lim anaerobic and aerobic conditions (FC = fold change, ANA = anaerobic, A = aerobic)

Probe Set	Gene name	systematic name	functional description	cellular function	C-Lim ANA Average	C-Lim ANA Stdev	N-Lim ANA Average	N-Lim ANA Stdev	P-Lim ANA Average	P-Lim ANA Stdev	S-Lim ANA Average	S-Lim ANA Stdev	C-Lim A Average	C-Lim A Stdev	N-Lim A Average	N-Lim A Stdev	P-Lim A Average	P-Lim A Stdev	S-Lim A Average	S-Lim A Stdev	FC S-Lim ANA vs C-Lim ANA	FC S-lim ANA vs N-ANA	FC S-lim ANA vs P-Lim ANA	FC S-Lim AE vs C-Lim AE	FC S-lim AE vs N-AE	FC S-lim AE vs P-Lim AE
7843_at	SSU1	YPL092W	YPL092W sensitive to sulfite	SULFITE TOLERANCE	217.5	41	238	45.2	84.5	6.3	308.5	30.4	449.7	149.5	287.5	10.9	60.1	4.7	193.8	21.3	-2.6	-2.8	-3.7	-7.5	-4.8	-3.2
5116_at	SCS3	YOL126W	YOL126W required for inositol prototrophy	PHOSPHOLIPID METABOLISM	419.3	47.3	471	117.8	33.5	15.3	665.8	186.9	369.3	289.8	438.9	206.2	12	3.7	602.7	251.5	-12.5	-14.1	-19.9	-30.8	-36.6	-50.2
6129_f_at	HXT6	YDR343C	YDR343C Hexose transporter	TRANSPORT	3297.3	1034.2	1591.8	124.5	784.4	38.3	1839.1	138	2086.8	527.7	1770.1	131.9	816.6	88.8	1844.5	251.5	-4.2	-2	-2.3	-2.6	-2.2	-2.3
7604_at	GPH1	YPR160W	YPR160W Glycogen phosphorylase	GLYCOGEN METABOLISM	450.9	71.7	441.3	43.3	77.1	9.8	267.1	44.9	303.6	44.3	431.6	100.6	35	2.4	393.6	33.3	-5.8	-5.7	-3.5	-8.7	-12.3	-11.2
8788_at	SOL1	YNR034W	YNR034W hypothetical protein	TRNA SPLICING. PUTATIVE	929.9	166.7	405.9	61.1	144.5	18.2	362.3	76.4	835.7	234.4	233.8	20.4	42.3	3.1	92.4	6.7	-6.4	-2.8	-2.5	-19.8	-5.5	-2.2

Up-regulated under C-Lim Aerobic only (FC = fold change, ANA = anaerobic, A = aerobic)

Probe Set	Gene name	systematic name	functional description	cellular function	C-Lim ANA Average	C-Lim ANA Stdev	N-Lim ANA Average	N-Lim ANA Stdev	P-Lim ANA Average	P-Lim ANA Stdev	S-Lim ANA Average	S-Lim ANA Stdev	C-Lim A Average	C-Lim A Stdev	N-Lim A Average	N-Lim A Stdev	P-Lim A Average	P-Lim A Stdev	S-Lim A Average	S-Lim A Stdev	FC C-Lim AE vs N-Lim AE	FC C-Lim AE vs S-Lim AE	FC C-Lim AE vs P-Lim AE
10022_at	CDA1	YLR307W	YLR307W Chitin Deacetylase	SPORULATION	45.1	19.5	49.3	12.8	43	8.3	110.6	2.8	26.6	7.2	12	3.6	12	0.1	12	4.2	2.2	2.2	2.2
10043_at	ECI1	YLR284C	YLR284C Peroxisomal enoyl-CoA hydratase	UNKNOWN	36.6	18.3	71.2	7.9	64.4	12.6	64.8	13.4	394.1	39.8	92.7	12.7	48.4	2.5	54.8	13.1	4.3	8.1	7.2
10129_at		YLR194C	YLR194C hypothetical protein	UNKNOWN	301.9	42.3	216.4	17.8	236.2	43.1	259.1	28	458.6	114.3	88.9	6.3	168.8	6.5	149.2	35.5	5.2	2.7	3.1
10154_at	IDP2	YLR174W	YLR174W Cytosolic form of NADP-dependent isocitrate dehydrogenase	TCA CYCLE	12	2.6	39.2	2.7	21.5	3.7	19.8	7.4	669	86.9	51.8	9.5	41	5.4	34.3	14.7	12.9	16.3	19.5
10470_at	SRL3	YKR091W	YKR091W Suppressor of rad53 lethality	UNKNOWN	107.8	32.2	104.2	7.4	121.9	22.5	153.1	17.4	89.8	8	34.5	5.4	29.8	1.6	27.7	10.4	2.6	3	3.2
10492_at	GPT2	YKR067W	YKR067W strong similarity to Sct1p	UNKNOWN	174.2	27.2	179.8	36	173	54.5	148.2	42	543.6	59.4	237	62	171.6	32.9	180.7	65.7	2.3	3.2	3
10500_at		YKR075C	YKR075C weak similarity to negative regulator Reg1p	UNKNOWN	38.6	13.8	64	12.1	39.5	1.1	31.1	5	186.9	26.6	65.5	3.4	51.7	5	37.5	6.4	2.9	3.6	5
10501_at	ECM4	YKR076W	YKR076W ExtraCellular Mutant	CELL WALL MAINTENANCE	46.1	14.2	63.9	22.2	44.7	7.3	23	3.6	213.1	46.8	83.9	14.2	72.2	11.5	51.9	5.8	2.5	3	4.1
10521_at		YKR049C	YKR049C hypothetical protein	UNKNOWN	377.2	86.2	344.9	47.3	243.1	67.2	258	9.7	1064.8	301.7	362.1	21.6	201.4	19.6	452.9	147.4	2.9	5.3	2.4
10572_at	FOX2	YKR009C	YKR009C peroxisomal multifunctional beta-oxidation protein	FATTY ACID METABOLISM	30.7	3.4	102.4	8.7	63.3	8.6	54.7	14.4	894.6	254.8	104.8	24.4	75.5	17.4	67.6	12.1	8.5	11.8	13.2
10581_at	GPX1	YKL026C	YKL026C strong similarity to glutathione peroxidase	UNKNOWN	92.9	53.8	96.6	23.2	48.5	14.2	56.8	6.3	763.5	181.7	134.5	23.8	59	5.9	70.9	4.9	5.7	12.9	10.8
10646_at	MBR1	YKL093W	YKL093W MBR1 protein precursor	MITOCHONDRIAL BIOGENESIS	19.2	7.7	16	6.2	17.3	2.5	12	1.6	302	76.6	21.5	1.3	52.6	3.2	16.7	4.5	14	5.7	18.1
10677_at		YKL107W	YKL107W weak similarity to S.antibioticus probable oxidoreductase	UNKNOWN	12	2.6	12	0.2	12	1.8	12	0.9	46.9	12	12	3.7	12	2.1	12	1	3.9	3.9	3.9
10735_at	MRPL31	YKL138C	YKL138C 15.5 kDa mitochondrial ribosomal protein YmL31	PROTEIN SYNTHESIS	110.2	31.3	72.7	17.5	60.7	6.3	59.8	5.9	189.5	41.4	90.2	21.1	85.4	1.9	79.5	14.7	2.1	2.2	2.4
10748_at		YKL171W	YKL171W probable serine\/threonine-specific protein kinase (EC 2.7.1.-)	UNKNOWN	98.9	20.8	88.9	23.6	79.1	1	87.5	12	205.2	29.3	86.4	4.4	60.1	5.1	52	2.8	2.4	3.4	3.9
10776_at		YKL187C	YKL187C strong similarity to hypothetical protein YLR413w	UNKNOWN	19.8	9.8	22.3	1.5	21	5.4	22.8	9.2	175.3	64.2	15.4	4.2	19	1.9	17.4	2.2	11.4	9.2	10.1
10858_s_at	THI11	YJR156C	YJR156C Thiamine biosynthetic enzyme	PYRIMIDINE BIOSYNTHESIS	90.6	25	92	10.6	85.4	17.8	83.1	5.2	160.5	3.9	50.5	10.3	25	4.9	22.3	9.4	3.2	6.4	7.2
10902_at	CPA2	YJR109C	YJR109C carbamyl phosphate synthetase	GLUTAMATE METABOLISM	333.7	44.9	308.8	69.7	196.9	18.5	427.7	60	441.3	83	217.4	13.6	167.2	17.1	167.4	39.8	2	2.6	2.6
10932_at	IME1	YJR094C	YJR094C meiotic gene expression\; meiosis inducing protein	MEIOSIS	19.7	10.4	20.2	6.2	48.7	22.8	36.4	5.3	51.4	3.3	16.1	3.4	15.5	0.1	23.1	10.4	3.2	3.3	2.2
10934_at	SFC1	YJR095W	YJR095W protein related to mitochondrial carriers	TRANSPORT	12	2.4	12	1.7	12	2.1	12	4	507.1	30.2	12	1.6	12	0.6	12	2.5	42.3	42.3	42.3
10935_at		YJR096W	YJR096W similarity to Corynebacterium 2.5-diketo-D-gluconic acid reductase and aldehyde	UNKNOWN	109.4	42.8	144.6	31.9	144.3	42.1	106.3	16.3	455.8	144.6	222.1	13.7	138.9	9.3	104.3	11.1	2.1	3.3	4.4
10996_at	TES1	YJR019C	YJR019C peroxisomal acyl-CoA thioesterase	FATTY ACID METABOLISM	225.9	87.3	188.3	42.4	188.4	67.5	123.5	12.7	1423.8	191.5	359.8	84.5	289.2	32.7	321.6	159.2	4	4.9	4.4
11068_at		YJL045W	YJL045W strong similarity to succinate dehydrogenase flavoprotein	UNKNOWN	22	6.6	39.7	4.2	29.8	3.7	46.1	5.6	119.6	46.1	27.5	6.4	12	2	22.5	8.6	4.3	10	5.3
11075_at		YJL037W	YJL037W strong similarity to hypothetical protein YJL038c	UNKNOWN	229.3	95	170.5	22.3	123.5	23.7	99.1	13.6	177.1	20.6	34.5	0.7	18.3	3.6	23.5	6.8	5.1	9.7	7.5
11113_at	SIP4	YJL089W	YJL089W (SIP4) Transcriptional activator of gluconeogenic genes through CSRE elements	GLUCOSE DEREPRESSION	12	1.9	12	5.8	25.4	1.4	16.9	4.2	58.2	12.5	12	2.8	12	1.9	12	3.9	4.9	4.9	4.9
11149_at		YJL144W	YJL144W hypothetical protein	UNKNOWN	52.6	21.1	139.2	32	115.4	48.7	71.2	12.1	247.5	71.4	73.1	31.2	72.6	8.9	74.9	38.5	3.4	3.4	3.3
11157_at	GLG2	YJL137C	YJL137C self-glucosylating initiator of glycogen synthesis\; similar to mammalian glycogeni	GLYCOGEN METABOLISM	21.5	7.1	25.6	4.9	24.9	4.4	20.9	5.9	70.3	16	24.8	6.8	26.9	4.5	31.6	10.2	2.8	2.6	2.2
11177_at		YJL161W	YJL161W hypothetical protein	UNKNOWN	21.4	8.7	17.7	4.6	16.9	4.5	12	3.1	57.1	19.4	22.8	5.1	12	0.4	13.3	2	2.5	4.8	4.3
11185_at	INO1	YJL153C	YJL153C L-myo-inositol-1-phosphate synthase	INOSITOL METABOLISM	92.9	24.8	135.2	27.8	35.3	7.5	66	9.8	684.2	147.2	249.6	29.2	32.3	5.9	30.2	4.6	2.7	21.2	22.6
11195_at		YJL185C	YJL185C hypothetical protein	UNKNOWN	35.7	11.7	45.5	3.9	50.3	7.6	40.8	1.9	116.9	26.2	42.7	9.4	49.2	5.7	43.1	4.7	2.7	2.4	2.7
11235_at	RPS14B	YJL191W	YJL191W Ribosomal protein S14B (rp59B)	PROTEIN SYNTHESIS	872.7	229.2	729.5	84.9	784.9	102.5	398.6	58.2	1068.7	134.5	426.6	46.9	468.4	50.2	406	188.9	2.5	2.3	2.6
11255_at		YJL217W	YJL217W hypothetical protein	UNKNOWN	676.7	122.5	160.9	24.6	201.9	43.1	411.2	27.3	903.7	26.4	286	18.2	229.2	9.2	409.7	39.2	3.2	3.9	2.2
11256_at		YJL216C	YJL216C strong similarity to Mal62p	UNKNOWN	12	2.4	12	0.8	12	1.4	12	0.5	35.8	6.6	12	1.2	12	0.1	12	3.1	3	3	3
11308_s_at		YAR068W	YAR068W Potential membrane protein	UNKNOWN	74.8	38.9	140.2	40.6	142.4	21.8	108.5	47	355.7	14.6	41.9	6.5	168.8	14.7	23.8	11.3	8.5	2.1	14.9
11356_at	ACS1	YAL054C	YAL054C inducible acetyl-coenzyme A synthetase	CARBOHYDRATE METABOLISM	107.5	19.8	107.6	6.5	92.8	14.1	101.4	3.6	1950.6	357.3	92	8.6	88.3	7.7	76.8	14.2	21.2	22.1	25.4
4074_at	GTT1	YIR038C	YIR038C Glutathione transferase	GLUTATHIONE METABOLISM	278.2	33.6	398.1	40.4	301	50	165.9	11.7	968.6	269.8	375	16.7	358.8	16.9	304.2	53.2	2.6	2.7	3.2
4097_at		YIR016W	YIR016W weak similarity to YOL036w	UNKNOWN	854	104.9	501.4	79.9	294	54.5	341.6	22.7	1403.2	382.6	321.2	30.1	231.1	9.7	259.8	45.6	4.4	6.1	5.4
4194_at	PRM5	YIL117C	YIL117C hydrophobic transmembrane domain	UNKNOWN	257	35.6	155.2	9.2	249.9	12.7	278	75.8	254.1	40.5	47.3	3.2	121.3	17.4	38.2	10.6	5.4	2.1	6.7
4204_at	PFK26	YIL107C	YIL107C 6-Phosphofructose-2-kinase	CARBOHYDRATE METABOLISM	172.7	34.3	144.9	12.7	300.8	74.1	165.4	12.8	288.5	1.8	110	28.2	111.6	18.8	98	10.9	2.6	2.6	2.9
4220_at	OM45	YIL136W	YIL136W 45-kDa mitochondrial outer membrane protein	MITOCHONDRIAL ORGANIZATION	88.6	33.5	88.8	11.5	55	4.6	36.4	2.1	723.6	206.1	156.2	35.1	68.6	7.8	119.4	27	4.6	10.5	6.1
4241_at	POT1	YIL160C	YIL160C peroxisomal 3-oxoacyl CoA thiolase	FATTY ACID METABOLISM	72	13.4	44.8	10.4	41.9	13.8	31.6	1.7	1083.7	365.4	65.3	5.3	34.4	5.9	75.3	13.6	16.6	31.5	14.4
4246_at	GUT2	YIL155C	YIL155C glycerol-3-phosphate dehydrogenase. mitochondrial	GLYCEROL METABOLISM	99.9	45.9	72.1	18.1	60.5	16.5	32.6	5.3	1154.6	248.4	398.9	91.7	285.5	42.3	260	19.8	2.9	4	4.4
4287_s_at		YHR209W	YHR209W similarity to hypothetical protein YER175c	UNKNOWN	13	6.2	22.2	7.3	19.9	4.5	12.7	5	41	2.3	18.2	1.5	17.3	5.6	15.1	1.7	2.3	2.4	2.7
4432_at	HXT5	YHR096C	YHR096C hexose transporter	TRANSPORT	32.8	13.4	39.4	6.3	26.6	5.1	19.7	9.5	1207.9	342.2	39.1	6.2	67.3	16.9	25.5	4.1	30.9	17.9	47.4
4534_at	MIP6	YHR015W	YHR015W PolyA-binding protein	MRNA EXPORT. PUTATIVE	85.9	12.9	56.4	9.4	98	10	95.7	20.4	64.1	3.5	20.6	2.4	12	1.3	12	3.4	3.1	5.3	5.3
4576_at	GUT1	YHL032C	YHL032C glyerol kinase (converts glycerol to glycerol-3-phosphate	GLYCEROL METABOLISM	79.3	35.2	89.8	24.7	48.6	8.8	44.8	6.6	446.7	37.9	54	9.8	34.8	1.2	72.5	17.5	8.3	12.8	6.2
4732_at	GND2	YGR256W	YGR256W 6-phosphogluconate dehydrogenase	PENTOSE PHOSPHATE CYCLE	21.1	10.5	40.2	2.9	24.5	5.4	40.9	7.3	316.4	69.2	26.9	5.7	12	3.1	78.8	10.7	11.8	26.4	4
4756_at	SPG1	YGR236C	YGR236C questionable ORF	UNKNOWN	12	2.5	12	0.6	12	1.2	12	2	351.5	160.9	12	2.7	12	0.9	12	0.8	29.3	29.3	29.3
4770_at		YGR250C	YGR250C weak similarity to human cleavage stimulation factor 64K chain	UNKNOWN	98.5	33.7	117.3	13.4	66.8	4.4	66.7	4.5	404.8	106.5	153	13.8	109.1	17.9	196	53.9	2.6	3.7	2.1
4796_at	BNS1	YGR230W	YGR230W questionable ORF	UNKNOWN	19.6	8.9	58.2	16.1	35.9	4.6	34.2	3.8	211.4	47.9	57.4	11.8	61	2.7	60.5	11.7	3.7	3.5	3.5
4811_at		YGR201C	YGR201C strong similarity to translation elongation factor eEF1 alpha chain Cam1p	UNKNOWN	73.3	14	149	21.8	76.5	0.3	100.1	14.7	198.4	65.7	55.9	6.7	56	2.9	87.1	14.8	3.6	3.5	2.3
4948_at		YGR067C	YGR067C weak similarity to transcription factors	UNKNOWN	12	2.5	20.5	2.2	30.1	9.1	17.5	2.1	221.6	16.4	30.1	2.5	35.1	2.6	22	3	7.4	6.3	10.1
4969_at		YGR043C	YGR043C strong similarity to transaldolase	UNKNOWN	28.7	11	39.1	6.9	33	3.2	23.6	7.3	310.8	136.1	19.6	0.4	14.8	1.6	12.2	1.7	15.9	21	25.4
5071_at		YGL080W	YGL080W strong similarity to C.elegans R07E5.13 protein	UNKNOWN	137.3	39.6	136.3	9.2	148.8	15.2	137.7	35.1	411.1	97.6	196.5	36.6	181.2	21.6	153.4	17.6	2.1	2.3	2.7
5125_at		YGL117W	YGL117W hypothetical protein	UNKNOWN	74.6	20	39.9	1.2	40.5	11.2	85.4	15.7	105	34.4	44.1	3	45.7	10.5	49.1	11.3	2.4	2.3	2.1
5217_at	SIP2	YGL208W	YGL208W Member of a family of proteins. including Sip1p and Gal83p. that interact with Sr	TRANSCRIPTION	36.1	14.8	28.3	5.9	23.6	6.5	26.8	5.2	134.2	51.1	32.5	1.7	23.2	1.7	62.2	7.6	4.1	5.8	2.2
5220_at	POX1	YGL205W	YGL205W fatty-acyl coenzyme A oxidase	FATTY ACID METABOLISM	14.8	6.9	12	1.8	12	0.5	12	6.3	246.7	27	13.6	2.5	12.4	2.2	15.6	5	18.1	19.8	15.8
5376_at	HXT10	YFL011W	YFL011W High-affinity hexose transporter	TRANSPORT	12	2.2	12	1.1	12	1.2	12	1	29.7	7.5	12	1.4	12	0.5	12	0.8	2.5	2.5	2.5
5400_at		YFL030W	YFL030W similarity to several transaminases	UNKNOWN	132.5	34.5	134.5	20.4	66.1	8.1	47.5	3	2110.8	142.1	744.8	63.2	586.6	15.8	782.7	60.4	2.8	3.6	2.7
5588_at	SSA4	YER103W	YER103W member of 70 kDa heat shock protein family	PROTEIN TRANSLOCATION	71.4	18.2	174.8	37.3	146.1	34.4	130.5	31.9	405.7	55.8	113.4	16.7	166.3	102.5	125.2	41	3.6	2.4	3.2
5606_at		YER121W	YER121W hypothetical protein	UNKNOWN	63.5	17.9	97.1	12.4	55.7	5	63.6	18.5	763.7	289.1	106.4	5.3	47	2.7	61.1	13.7	7.2	16.2	12.5
5636_at	ICL1	YER065C	YER065C isocitrate lyase	GLYOXYLATE CYCLE	97.5	11.1	193.1	29.7	119	5.6	105.9	4.9	740.9	46.5	131.9	13.3	96.3	2.2	99.6	13.5	5.6	7.7	7.4
5679_at	YAT2	YER024W	YER024W (YAT2) Protein with carnitine acetyltransferase function. may function in the cytc	UNKNOWN	52.3	19.8	78.7	4.6	63.8	3.9	67.9	14.1	713.8	172.2	53.9	10.9	70.6	6.8	54.7	12.1	13.2	10.1	13.1
5715_at	FAA2	YER015W	YER015W Acyl-CoA synthetase (fatty acid activator 2)	FATTY ACID METABOLISM	19.3	7.7	15.1	2.8	12	0.8	12	4.4	152.2	34.1	18	1.5	13.6	1.6	16.2	7.1	8.5	11.2	9.4
5749_at		YEL041W	YEL041W strong similarity to Utr1p	UNKNOWN	29.6	10.7	60.4	28.1	69.2	3.5	44.7	3.8	266.4	12.9	87.7	23.2	61.5	6	42.6	10.2	3	4.3	6.3
5778_at		YEL057C	YEL057C hypothetical protein	UNKNOWN	12	5.3	12	0.3	12	0.9	12	0.8	43.7	2.1	12	2.2	12	0.8	12	0.9	3.6	3.6	3.6
5915_at	STL1	YDR536W	YDR536W sugar transporter-like protein	TRANSPORT	12	4.1	12	1.4	12	1.2	12	4.4	71.3	12.9	12	1.9	12	0.9	12	3.7	5.9	5.9	5.9
6012_at	TSA2	YDR453C	YDR453C strong similarity to thiol-specific antioxidant proteins	UNKNOWN	204.6	42.4	190.9	20.7	130.3	18.3	171.7	39.9	127.2	68.7	38.9	3	28.5	1.4	32	3.9	3.3	4.5	4
6077_at	ARO10	YDR380W	YDR380W similarity to Pdc6p. Thi3p and to pyruvate decarboxylases	UNKNOWN	12	3	12	1.4	12	1.7	12	3	67.2	3.9	12	2.9	12	0.9	14.4	1.3	5.6	5.6	4.7
6082_at		YDR384C	YDR384C strong similarity to Y.lipolytica GPR1 gene	UNKNOWN	150.7	23.4	79.8	9.6	82.7	9.2	66.7	13.7	1543.4	62.1	35.5	6.9	23.2	2.9	51.4	4.4	43.5	66.5	30
6221_at	CTA1	YDR256C	YDR256C catalase A	OXIDATIVE STRESS RESPONSE	12	4.3	12	2.4	12	1.4	12	3.5	1239.3	241.1	12	1	12	0.4	12	2.4	103.3	103.3	103.3
6273_at	ADR1	YDR216W	YDR216W positive transcriptional regulator of ADH2 and peroxisomal protein genes	TRANSCRIPTION	12	4	12	2.4	12.8	1.8	12	2.4	52.3	3.4	14.5	7	22.7	4	13.9	2.4	3.6	2.3	3.8
6394_at		YDR070C	YDR070C hypothetical protein	UNKNOWN	45.5	36.7	39.4	0.8	24.7	9.1	23.7	4	1056	188.3	112.5	30.2	16.3	3.1	73.1	4.4	9.4	64.8	14.4
6401_at	SED1	YDR077W	YDR077W putative cell surface glycoprotein	UNKNOWN	935.1	77.1	682.6	61.2	988.7	142.7	1155	124.6	1846.1	405.8	753.2	76.1	533.6	74.4	844.1	219.8	2.5	3.5	2.2
6449_at		YDR034W	YDR034W identified by SAGE expression analysis	UNKNOWN	101.2	41.6	94	6.2	88.3	6.8	52.7	14.7	282.8	65.7	51.7	9.9	61.5	6.8	89.5	23.3	5.5	4.6	3.2
6479_at		YDR018C	YDR018C strong similarity to hypothetical protein YBR042c	UNKNOWN	24.5	11	32.7	5.5	15.2	2.1	17.2	1.6	59.4	15	28.2	0.6	12	2.5	12	4	2.1	4.9	4.9
6498_at		YDL009C	YDL009C questionable ORF	UNKNOWN	91.7	29.7	69.6	7.4	81.6	12.7	69	7.9	155.5	25.2	68	33.8	68.5	5.2	56.3	42.2	2.3	2.3	2.8
6549_at	KNH1	YDL049C	YDL049C KRE9 homolog	CELL WALL MAINTENANCE	42.8	12.4	22.5	0.9	25.5	1.3	31.8	8.2	142.9	22	45.6	3.8	27.5	1.4	33.3	7	3.1	5.2	4.3
6556_at	NDE2	YDL085W	YDL085W Mitochondrial NADH dehydrogenase that catalyzes the oxidation of cytosolic NA	RESPIRATION	12	3.9	23	3.1	12	1.2	12	1.8	307.1	90.2	22.8	3	12	3.4	18.5	5	13.5	25.6	16.6
6694_at	PRR2	YDL214C	YDL214C strong similarity to putative protein kinase NPR1	UNKNOWN	12	6.6	12.3	5.3	12	3.6	12	3	150.5	27.7	28.9	5.6	12	0.2	12	0.8	5.2	12.5	12.5
6704_at		YDL204W	YDL204W similarity to hypothetical protein YDR233c	UNKNOWN	12	4	12	1.9	12	1.6	12	1.4	83.9	31	17.3	3.8	12	2.6	16.4	1.1	4.8	7	5.1
6729_at	HBT1	YDL223C	YDL223C weak similarity to mucin	UNKNOWN	28	11.6	39.5	8.3	38.3	0.7	39.2	9.6	247.4	106.7	38.2	5.9	35.7	1.2	64.4	17.4	6.5	6.9	3.8
6850_at	SRD1	YCR018C	YCR018C Transcription regulator	RRNA PROCESSING	230	63	254.2	34.8	214.4	26.8	306.1	17.2	285.9	38.5	128.3	17.3	83.9	41.4	86.7	18.7	2.2	3.4	3.3
6887_at	ADY2	YCR010C	YCR010C strong similarity to Y.lipolytica GPR1 protein and Fun34p	UNKNOWN	12	2.4	14.2	1.9	12	2.6	12	4	1032	149.1	12	0.9	12	2.5	12	3	86	86	86
7068_at	PCA1	YBR295W	YBR295W Putative P-type Cu(2+)-transporting ATPase	TRANSPORT	32	9.6	73.3	19.3	33.6	1.7	49.1	7.5	252.8	41.4	49.3	3.7	62.8	6	61.1	10.8	5.1	4	4.1
7140_at		YBR230C	YBR230C hypothetical protein	UNKNOWN	136.7	24.5	76.1	17.8	53.4	1.2	50	3.1	1635.1	197.6	364.2	56.9	262.7	25.7	353.5	38.4	4.5	6.2	4.6
7196_at	TBS1	YBR150C	YBR150C Probable Zn-finger protein	UNKNOWN	62	38.1	85.4	16.6	87.8	37.1	58.4	14.3	151.5	40.6	67.8	7.4	70.7	20.6	46.9	8.3	2.2	2.1	3.2
7203_at	ICS2	YBR157C	YBR157C hypothetical protein	UNKNOWN	26.9	9.3	36.9	11	40	3.8	56.6	3.6	221.8	56.3	37.1	2	37.5	3.3	88.3	24.2	6	5.9	2.5
7252_at		YBR116C	YBR116C questionable ORF	UNKNOWN	12.6	11.7	31.3	8.2	18.6	3.1	27.4	12.2	160	69	12	2.1	13.9	3.3	21.3	8.8	13.3	11.5	7.5
7254_at	TKL2	YBR117C	YBR117C transketolase. homologous to tkl1	PENTOSE PHOSPHATE CYCLE	12	2.6	12	0.9	12	2.3	12	1.2	138.5	66.6	12	3.1	12	1.1	12	4.7	11.5	11.5	11.5
7291_at	BAP2	YBR068C	YBR068C probable amino acid permease for leucine. valine. and isoleucine	TRANSPORT	102	9.4	26.7	4.8	99.4	9.7	45.1	9.4	336.3	77.4	20.3	3.8	119.3	14.3	44.2	5	16.6	2.8	7.6
7295_at	HSP26	YBR072W	YBR072W Heat shock protein of 26 kDa. expressed during entry to stationary phase and in	STRESS	148.2	41.1	281.1	37.2	352.2	81.9	258.4	31.7	1769.5	317.3	222.6	27.3	519	74.1	734.3	121.1	7.9	3.4	2.4
7314_at	ZTA1	YBR046C	YBR046C Homolog to quinone oxidoreductase (E. coli)	UNKNOWN	38.4	18	33.2	6.1	63.5	2	33.1	4.5	263.8	64.2	91.2	22.3	102.1	18	114	18.1	2.9	2.6	2.3
7339_at	MRF1'	YBR026C	YBR026C Nuclear protein that binds to T-rich strand of core consensus sequence of autonc	MITOCHONDRIAL RESPIRATION	15	6.1	19.9	3.4	12	2.5	13.4	9	121.2	39.3	51.3	8	17.4	9.1	28.8	4.6	2.4	7	4.2
7580_at	SMX3	YPR182W	YPR182W Sm or Sm-like snRNP protein	MRNA SPLICING	245.4	54.4	221.4	68.8	215.1	42.2	173.1	32.6	645.4	127.3	224.4	47.5	263	31.7	229.5	60.3	2.9	2.5	2.8
7733_at	ATH1	YPR026W	YPR026W null mutant is viable\; increased tolerance to dehydration. freezing. and toxic leve	TREHALOSE METABOLISM	40.5	13.7	55	11.4	44.4	5.7	42.8	4.5	205	26.2	73.9	26.8	48.4	4.4	56.3	6.8	2.8	4.2	3.6
7753_at	CIT3	YPR001W	YPR001W Mitochondrial isoform of citrate synthase	TCA CYCLE	16.6	9.6	12	1.4	12	3.2	12	3.4	376.3	66	12	0.5	12	0.9	12	3.9	31.4	31.4	31.4
7754_at	PDH1	YPR002W	YPR002W similarity to B.subtilis mmgE protein	UNKNOWN	86.1	34.5	21.4	5.3	15.9	4.8	18.2	9.3	644	92.2	28.6	5.7	213.7	35.9	38.3	4	22.5	3	16.8
7758_at	ICL2	YPR006C	YPR006C 2-methylisocitrate lyase	CARBOHYDRATE METABOLISM	75.4	14.5	138.6	20	88.3	9.1	111.1	5.7	536.2	55.3	98.5	5.1	95.2	7.2	91.6	3.1	5.4	5.6	5.9
7807_at	PMA2	YPL036W	YPL036W plasma membrane ATPase	SMALL MOLECULE TRANSPORT	23.1	13.6	38.1	11.5	44.7	11.7	33.6	9.4	322.9	183.1	37.2	3.3	42.1	5.9	51.5	15.1	8.7	7.7	6.3
7867_at		YPL113C	YPL113C similarity to glycerate dehydrogenases	UNKNOWN	54.9	14.1	25.4	4.9	31.6	1.1	25.9	4.5	269.3	24.1	16.3	4	39.2	1.6	16.1	6.9	16.5	6.9	16.8
7871_at		YPL109C	YPL109C similarity to aminoglycoside acetyltransferase regulator from P. stuartii	UNKNOWN	22.2	6	32.8	6.3	31.5	7.6	20.8	1.5	121.6	14.1	54.6	1.2	55	2.1	54.2	11.9	2.2	2.2	2.2
7891_at	ODC1	YPL134C	YPL134C 2-oxodicarboxylate transporter. has specificity for 2-oxoadipate and 2-oxoglutarat	TRANSPORT	299	45.6	168.4	37.3	112.5	4.1	88.8	8	569.2	112	233.4	6.4	148.7	7.9	165	36.8	2.4	3.8	3.4
7914_at	PRM4	YPL156C	YPL156C weak similarity to YDL010w	UNKNOWN	295.9	25.2	198	23.3	229.9	15.5	249.7	56.5	789	173.5	51.6	1.3	82.3	5.8	66.9	10.9	15.3	9.6	11.8
7923_at	PXA1	YPL147W	YPL147W Pxa1p and Pxa2p appear to be subunits of a peroxisomal ATP-binding cassette	TRANSPORT	12	6.6	14.8	6	13.6	1.8	15.6	4.4	177.7	7.6	24.7	0.9	21.2	1.7	21.1	1.1	7.2	8.4	8.4

7928_at	UIP4	YPL186C	YPL186C weak similarity to Xenopus protein xlgv7	UNKNOWN	34.9	24.1	86.9	22.7	24.2	4.9	26.2	4.6	318.2	73.7	143.8	13.5	23.2	0.2	47.8	4.7	2.2	13.7	6.7
7957_at		YPL201C	YPL201C hypothetical protein	UNKNOWN	12	2.6	12	2	12	0.4	12	1	501.8	123	12	0.6	12	0.8	12	0.4	41.8	41.8	41.8
7974_at	USV1	YPL230W	YPL230W Up in StarVation	UNKNOWN	51.9	33.8	43.9	8.1	23.9	5	13	2.4	157.5	30.4	53.1	21.8	21.2	2.2	50.8	12.7	3	7.4	3.1
8020_s_at	FDH2	YPL276W	YPL276W putative formate dehydrogenase/putative pseudogene	UNKNOWN	12	0.2	12	1	12	1.4	12	3.3	1041.7	307.3	12	0.9	12	1	12	6.3	86.8	86.8	86.8
8142_s_at	FDH1	YOR388C	YOR388C Protein with similarity to formate dehydrogenases	UNKNOWN	12	2.5	12	1.7	12	1	12	5.3	2028.9	529.5	12	2	12	2.5	15	2.5	169.1	169.1	135.5
8382_at	DCI1	YOR180C	YOR180C Peroxisomal enoyl-CoA hydratase	FATTY ACID METABOLISM	12	2.8	12	1.5	12	1.3	12	0.7	36.1	8.3	12	2	12	2.2	12	3	3	3	3
8412_at	GCY1	YOR120W	YOR120W Similar to mammalian aldo\/keto reductases	UNKNOWN	130.1	62.4	179.9	24.2	94.3	19.6	122.2	14.8	826.8	98.4	273.9	27.2	166.4	9	337.2	67.9	3	5	2.5
8437_at	CRC1	YOR100C	YOR100C mitochondrial carnitine carrier	TRANSPORT	12	4.8	16.1	0.5	12	2.3	12	6.2	245.8	33	41.6	5.5	24.5	7	31.2	2.1	5.9	10	7.9
8615_at		YOL083W	YOL083W similarity to YOL082w	UNKNOWN	192.7	30.4	186.2	8.7	167.8	28.7	142.1	10.3	587.8	106	181.6	10.7	101.2	8.1	147.3	23.8	3.2	5.8	4
8642_at		YOL101C	YOL101C similarity to YOL002c and YDR492w	UNKNOWN	421.1	146.3	418.6	43.6	513.5	43.4	454.6	29.8	141.9	39.5	12	3.8	12	2	12	3.1	11.8	11.8	11.8
8663_at	MDH2	YOL126C	YOL126C cytosolic malate dehydrogenase	TCA CYCLE	69.4	31.3	108	17.5	79.8	5.2	73.5	17	722.4	124.9	150.6	12.9	56.2	4.7	136.3	18.4	4.8	12.9	5.3
8687_at	PEX11	YOL147C	YOL147C Peroxisomal membrane protein	PEROXISOME BIOGENESIS	347.7	53.2	344.6	64.4	364.6	46.6	279.1	5	1018.6	170.4	468.1	44.7	469.9	46.9	379.3	39	2.2	2.2	2.7
8815_at	BIO5	YNR056C	YNR056C transmembrane regulator of KAPA\/DAPA transport	BIOTIN BIOSYNTHESIS	12	2.1	21.6	9.3	19	1.1	17	2.4	75.7	33.9	31.5	8.5	22.7	4.8	25.9	7.2	2.4	3.3	2.9
8817_at	BIO3	YNR058W	YNR058W 7.8-diamino-pelargonic acid aminotransferase (DAPA) aminotransferase	BIOTIN BIOSYNTHESIS	30.2	13.8	63.6	8.6	53.2	10.9	59.5	14.3	112.5	34	44.8	7.2	46.3	1.6	47.8	9.2	2.5	2.4	2.4
8819_at	FRE4	YNR060W	YNR060W similar to FRE2	UNKNOWN	15.8	9.5	15.2	3	13	2.2	16.5	5.2	59.1	11.4	12	2.4	12	1.5	16.5	6.4	4.9	4.9	3.6
8850_at	FUN34	YNR002C	YNR002C Putative transmembrane protein	UNKNOWN	145.6	74.5	79.5	0.9	45.3	8.2	40.1	5.8	1617.8	147.9	42.9	13.8	77.2	8.7	87.2	6.1	37.7	21	18.6
8883_at	SPO1	YNL012W	YNL012W encodes a protein with high similarity to phospholipase B	MEIOSIS (SPOR.)	12	2.4	14	3.7	12	3	12	4.5	32.5	8.2	12.4	2.9	12	0.7	12	2.6	2.6	2.7	2.7
8886_at	IDP3	YNL009W	YNL009W peroxisomal NADP-dependent isocitrate dehydrogenase	TCA CYCLE	12.7	7.4	21.6	4.7	21.2	5.1	23.9	7.3	174.6	34.7	25.8	1.7	23.8	2.5	20.1	4.2	6.8	7.3	8.7
9057_at	SPS19	YNL202W	YNL202W peroxisomal 2.4-dienoyl-CoA reductase	FATTY ACID METABOLISM	78	24.7	82.2	18.7	65.2	13.4	50.1	13	1050.2	126.9	134	8.2	55.9	5	56.9	9.5	7.8	18.8	18.5
9064_at		YNL195C	YNL195C hypothetical protein	UNKNOWN	17.7	6.3	33.1	9.3	15.6	2.7	22.5	10.6	381.7	133.8	35.4	12.9	21.9	2.7	35.7	9.9	10.8	17.4	10.7
9065_at		YNL194C	YNL194C strong similarity to YDL222c and similarity to Sur7p	UNKNOWN	12	1.6	18.1	5.6	12	2.4	12	0.6	202.9	86.9	47.6	16.1	12	1.1	31.6	12.6	4.3	16.9	6.4
9124_at	ALP1	YNL270C	YNL270C Protein highly homologous to permeases Can1p and Lyp1p for basic amino acids	TRANSPORT	12.8	4.6	19.3	4.1	12	1.2	15.8	5.8	43.1	10.2	19.3	1.2	12	1.4	13.7	3.4	2.2	3.6	3.2
9196_s_at		YNL335W	YNL335W similarity to M.verrucaria cyanamide hydratase. identical to hypothetical protein Y	UNKNOWN	12	2.6	17.6	6.9	12	2.4	12	2.6	158.1	20.7	28.1	3.5	14.9	2.5	13.2	1.3	5.6	10.6	12
9309_at	ADH2	YMR303C	YMR303C alcohol dehydrogenase II	GLYCOLYSIS	26.4	2.7	24.3	5.2	24.1	7.7	20	8.2	3255.2	1249	22.5	4.1	37.3	0.4	52.1	15.4	144.5	87.3	62.4
9329_at	CAT8	YMR280C	YMR280C Zinc-cluster protein involved in activating gluconeogenic genes\; related to Gal4p	GLUCONEOGENESIS	12.9	9.4	12	1.9	12	4.6	12	1.1	57.5	11.8	14	4.5	15.6	4	17.7	5.6	4.1	3.7	3.3
9416_at		YMR191W	YMR191W hypothetical protein	UNKNOWN	119.1	42.2	160.5	14	146.4	18.8	109.5	6.5	439.4	47.5	140.4	15.6	172.2	2.9	147.2	12.3	3.1	2.6	3
9444_at	PAI3	YMR174C	YMR174C Cytoplasmic inhibitor of proteinase Pep4p	OSMOTIC STRESS RESPONSE	40	12.6	44.3	13.1	34	9	22.8	4.8	340.1	89.5	63.8	11.2	29.1	3.3	45.8	9.9	5.3	11.7	7.4
9445_at	SIP18	YMR175W	YMR175W protein of unknown function	UNKNOWN	27.3	7.8	35.4	1.9	15.4	3.6	23.5	2.1	954.8	211.1	12	2.4	12	0.8	24	6.2	79.6	79.6	39.8
9515_at		YMR118C	YMR118C strong similarity to succinate dehydrogenase	UNKNOWN	16.5	11.2	56.3	12.4	23.9	3.5	22.7	4.7	325.4	181	17.4	2.4	12	3.7	12	6.2	18.7	27.1	27.1
9537_at	SNO1	YMR095C	YMR095C SNZ1 proximal ORF. stationary phase induced gene	UNKNOWN	16.4	9.5	12.9	3	14.7	3.9	30	5.8	49.9	7.4	13.3	1.3	12.9	3.9	23.1	2.1	3.7	3.9	2.2
9538_at	SNZ1	YMR096W	YMR096W encodes highly conserved 35 kDa protein that shows increased expression afte	UNKNOWN	63.5	26.3	57.5	18.6	37.5	5.2	70	15.9	142.1	30.3	53.9	5.1	44.8	4.7	66.2	9.8	2.6	3.2	2.1
9549_at		YMR107W	YMR107W hypothetical protein	UNKNOWN	18.8	15	73.2	10.5	21.7	7.2	19.4	4.5	2622.7	320.3	12	1.5	15.9	1.3	12	4.1	218.6	165.3	218.6
9628_at	PLB2	YMR006C	YMR006C strong similarity to Plb1p	PHOSPHOLIPID METABOLISM	972.3	171.1	511.8	61.3	563.2	90.2	731.4	68.9	352.9	97.2	81.5	10.8	68.2	12.1	69.2	16.1	4.3	5.2	5.1
9633_at	HXT2	YMR011W	YMR011W high affinity hexose transporter-2	TRANSPORT	457.3	283.3	1169.8	50.9	934.1	136.4	1117.7	117.4	1744.9	308.4	92.1	21.5	597.5	69.5	202.6	49.9	19	2.9	8.6
9668_at	CAT2	YML042W	YML042W Carnitine O-acetyltransferase. peroxisomal and mitochondrial	FATTY ACID METABOLISM	54.6	19.3	55.7	16.4	35.1	8.3	32	11.9	554.2	92	86.6	34.1	33.5	5.8	40.5	18.9	6.4	16.6	13.7
9702_at	CYB2	YML054C	YML054C Cytochrome b2 [L--lactate cytochrome-c oxidoreductase]	LACTATE UTILIZATION	21.3	9.7	26.7	4.1	12	2.4	23	14.5	2375.4	191.9	669	126.4	552	42	1150.9	86.5	3.6	4.3	2.1
9757_at	MSC1	YML128C	YML128C C-terminal part starting with aa 262 cause growth inhibition when overexpressed	UNKNOWN	81.8	29.8	179.4	5.6	129.1	12.7	115.9	6.1	931.8	290.9	247.3	40.9	121.9	5.6	222.4	46.9	3.8	7.6	4.2
9763_at		YML122C	YML122C hypothetical protein	UNKNOWN	12	2.8	12	1.1	12	1	12	0.8	41.1	5.4	12	0.5	12	3.2	12	3.1	3.4	3.4	3.4
9902_at	CTR3	YLR411W	YLR411W Copper Transporter	TRANSPORT	61.7	22	40.9	9.2	23.4	5.5	34.9	12	1039.9	139.1	439	29.3	26.6	5.5	345.3	57.2	2.4	39.1	3
9958_at	FBP1	YLR377C	YLR377C (FBP1) Fructose-1.6-bisphosphatase. gluconeogenic enzyme. activity is inhibitec	GLUCONEOGENESIS	12	3.1	12	1.5	12	4.2	12	4.6	214.4	30	12	0.9	12	2	12	4.5	17.9	17.9	17.9

Down-regulated under C-Lim Aerobic only (FC = fold change, ANA = anaerobic, A = aerobic)

Probe Set	Gene name	systematic name	functional description	cellular function	C-Lim ANA Average	C-Lim ANA Stdev	N-Lim ANA Average	N-Lim ANA Stdev	P-Lim ANA Average	P-Lim ANA Stdev	S-Lim ANA Average	S-Lim ANA Stdev	C-Lim A Average	C-Lim A Stdev	N-Lim A Average	N-Lim A Stdev	P-Lim A Average	P-Lim A Stdev	S-Lim A Average	S-Lim A Stdev	FC C-Lim AE vs N-Lim AE	FC C-Lim AE vs S-Lim AE	FC C-Lim AE vs P-Lim AE
10159_at		YLR179C	YLR179C similarity to Tfs1p	UNKNOWN	1237.2	181.8	1035.3	83.2	1141.9	90.7	1116	35.4	279.5	56.5	627.9	123.2	902.5	92	957.2	158.9	-2.2	-3.2	-3.4
10227_at		YLR108C	YLR108C strong similarity to YDR132c	UNKNOWN	12	2.9	23.8	3.9	21.5	2.8	23.1	0.7	38	10.6	107.9	12	166	17.4	112.3	3.8	-2.8	-4.4	-3
10358_at	TPO1	YLL028W	YLL028W similarity to multidrug resistance proteins	TRANSPORT	204	36.7	322.9	65.6	314.5	45.8	530.6	49.3	197	30.5	455	55.5	394.7	38.5	597.6	89.7	-2.3	-2	-3
10472_at	PTR2	YKR093W	YKR093W Peptide transporter	TRANSPORT	89.4	40.1	141.9	47	90.3	21.4	79.8	7.6	26.6	2	504.6	34.9	867.4	76.1	172.7	11.8	-19	-32.6	-6.5
10609_at	PHD1	YKL043W	YKL043W (PHD1) Transcription factor involved in regulation of filamentous growth	PSEUDOHYPHAL GROWTH	1042.7	59.8	947.3	225.1	1060.1	257.8	1049.4	33.4	282.7	48.9	1190.3	278.8	606.7	84.2	984	53.4	-4.2	-2.1	-3.5
10634_at	MSN4	YKL062W	YKL062W (MSN4) Zinc-finger transcriptional activator for genes regulated through Snf1p. h	TRANSCRIPTION	60.4	18.9	90.5	13.6	136.8	24.7	78.2	8.5	47.8	2.1	151.5	27.3	150.5	8.2	123.8	20.8	-3.2	-3.1	-2.6
10803_at	STE6	YKL209C	YKL209C ABC transporter. glycoprotein. component of a-factor secretory pathway	MATING	110.7	35.2	262.9	33.6	232.8	42.7	202.9	20.3	85.7	17.3	299.3	30.4	180.3	9.3	187.3	20.3	-3.5	-2.1	-2.2
11004_at		YJR030C	YJR030C similarity to hypothetical protein YJL181w	UNKNOWN	35.6	12.4	67.7	26.4	63.3	27.7	40	12.2	55.9	25.3	140.4	17.3	137	34	112.2	27.5	-2.5	-2.5	-2
11259_at		YJL213W	YJL213W similarity to Methanobacterium aryldialkylphosphatase related protein	UNKNOWN	151.5	27.2	119	22.1	156.8	12.5	261.9	45.6	32.7	18.9	364.9	73	356.3	66.6	238	58.8	-11.1	-10.9	-7.3
11260_at	OPT1	YJL212C	YJL212C strong similarity to S.pombe isp4 protein	UNKNOWN	24.6	10.1	175.7	37.1	717.7	119	20.8	11	12	1.7	366.8	48.2	1109.6	80.7	47.5	14.6	-30.6	-92.5	-4
4200_at	COX5B	YIL111W	YIL111W Cytochrome-c oxidase chain Vb	OXIDATIVE PHOSPHORYLATION	149.8	32.6	190.7	15.3	117.9	10.8	169.3	19.9	15.7	0.6	84.5	6.5	31.9	8.1	57.8	19.8	-5.4	-2	-3.7
4322_at		YHR210C	YHR210C UDP-glucose-4-epimerase (GAL10. galE)	UNKNOWN	300.3	77.5	109.1	13.1	75	4	338.3	78.4	22.8	1	61.2	4.5	47.7	1.2	219	89.3	-2.7	-2.1	-9.6
4339_at	OYE2	YHR179W	YHR179W NAPDH dehydrogenase (old yellow enzyme). isoform 2	UNKNOWN	1358.9	218.4	775.2	55	940.4	90	941.3	295.4	342	62.9	779.5	56.8	1114.5	92.6	1080.9	195.2	-2.3	-3.3	-3.2
4477_at		YHR048W	YHR048W similarity to multidrug resistance proteins	UNKNOWN	46.1	13.4	79.8	19.1	82.9	7.2	66.1	13.8	12	0.8	32	10.4	62.5	3.8	39.2	2.3	-2.7	-5.2	-3.3
4478_at	FSH1	YHR049W	YHR049W similarity to S.pombe dihydrofolate reductase and YOR280c	UNKNOWN	489	118.9	731.2	160.9	746.7	180.2	814.3	253.6	147.6	57.5	967.6	126.3	558	63.8	807.4	70	-6.6	-3.8	-5.5
4802_i_at	TDH3	YGR192C	YGR192C Glyceraldehyde-3-phosphate dehydrogenase 3	GLYCOLYSIS	4423.6	3862.1	3800.4	1228.9	4024.2	207.6	4907	933.7	1430	2149	3612	169.6	3684	225.9	3924.4	163.2	-2.5	-2.6	-2.7
4870_at		YGR125W	YGR125W similarity to S.pombe hypothetical protein SPAC24H6.11c	UNKNOWN	106.6	17.9	606.8	109.5	178.9	24.3	140.8	17.6	112.9	10.2	724.6	96.1	415.8	69.5	236.1	46.9	-6.4	-3.7	-2.1
4967_at	BUD9	YGR041W	YGR041W Among a group of genes whose products are necessary for bud-site selection\;	BUD SITE SELECTION	39.9	12.1	65	18.9	84.7	25.6	35.6	3.1	24.6	1.8	82.6	12.9	79.7	3.2	60.9	12.4	-3.4	-3.2	-2.5
5087_at	ALG2	YGL065C	YGL065C (ALG2) Mannosyltransferase involved in N-glycosylation. converts Man[2]GlcNA	PROTEIN GLYCOSYLATION	36.4	18.4	61.3	9.7	73.7	15.1	67.2	4.2	38.9	6.5	83	10.2	89.9	11.4	96	13	-2.1	-2.3	-2.5
5404_at	STE2	YFL026W	YFL026W (STE2) Pheromone alpha-factor G protein-coupled receptor (GPCR). member of	MATING	315.6	53.9	578.3	74.3	418.4	43.3	360.8	72	119.7	16.9	672	10.3	331.2	73.8	396.5	96.8	-5.6	-2.8	-3.3
5405_at	BST1	YFL025C	YFL025C (BST1) Protein that negatively regulates COPII vesicle formation. required for prc	SECRETION	59	21.1	111	10.5	98.9	28.6	78.1	1.5	67.1	17.6	188.8	21.3	145.3	11.8	143.2	34.4	-2.8	-2.2	-2.1
5609_at	DSE1	YER124C	YER124C weak similarity to Dictyostelium WD40 repeat protein 2	UNKNOWN	48.5	48.2	63.7	22.7	51.1	7	54	9.6	28.5	2.6	131.4	25.9	63	8.7	81.8	32.5	-4.6	-2.2	-2.9
5665_at		YER053C	YER053C strong similarity to mitochondrial phosphate carrier protein	UNKNOWN	98.7	38.3	224.1	39.6	174.3	16.3	251.9	67.5	135.5	14.7	746.1	127.2	494.5	51.8	674.5	122.7	-5.5	-3.6	-5
5683_at		YER028C	YER028C similarity to Mig1p	UNKNOWN	12	2	32.9	7.8	28.4	7.3	12	4.4	12	2.6	29.6	6.5	24.7	4.6	24.5	5.3	-2.5	-2.1	-2
5731_at		YEL016C	YEL016C similarity to human nucleotide pyrophosphatase	UNKNOWN	25.7	13.2	59.7	13.3	60.5	3	50.6	15.6	23.7	5.9	80.2	3.8	55.3	3.9	63.6	8.4	-3.4	-2.3	-2.7
5746_at	MNN1	YER001W	YER001W (MNN1) Alpha-1.3-mannosyltransferase. required for complex glycosylation of b	PROTEIN GLYCOSYLATION	133.4	50.4	240.8	16.1	174.6	42.1	306.9	36.8	84.8	12.4	451	62.9	395.4	64.6	471.3	83.4	-5.3	-4.7	-5.6
5957_at		YDR533C	YDR533C strong similarity to hypothetical proteins YPL280w. YOR391c and YMR322c	UNKNOWN	582.9	28	823.5	76.2	757	231.6	662.4	185.1	401.5	46.1	961.4	129.5	1047.5	209.3	1495.3	113.9	-2.4	-2.6	-3.7
6138_at		YDR352W	YDR352W weak similarity to hypothetical proteins YOL092w. YBR147w and YMR010w	UNKNOWN	30.5	8.9	83.5	7.9	53.1	2.4	63.8	15.2	49.6	6.2	144.7	13.2	109.2	28.2	109.5	17.6	-2.9	-2.2	-2.2
6186_at	GIC2	YDR309C	YDR309C (GIC2) Putative effector of Cdc42p. important for bud emergence	BUD EMERGENCE	375.9	58.2	407.9	19.3	561.7	68.1	503.8	108.9	204.8	51.7	590.3	98.3	679.2	193	493.8	81.3	-2.9	-3.3	-2.4
6797_at		YCR102C	YCR102C Alcohol dehydrogenase	UNKNOWN	261.6	47.9	238.3	25.2	401	46.8	244.3	67.6	20.7	14.4	72.6	3.6	159.4	19.3	133.4	20	-3.5	-7.7	-6.4
6831_at		YCR043C	YCR043C hypothetical protein	UNKNOWN	31.6	20.1	58.8	13.2	33.6	5.3	27.8	2.5	27	2.7	83.8	8	54.5	12.3	55.5	5.8	-3.1	-2	-2.1
6907_at	AGP1	YCL025C	YCL025C (AGP1) Broad substrate range amino acid permease with high affinity for asparaç	TRANSPORT	762.9	56.7	155.9	23.1	363.4	68.5	346.5	31.2	87.2	28.6	208.6	17.3	240.4	116.9	353.1	52.1	-2.4	-2.8	-4
7207_at		YBR161W	YBR161W Homolog to suppressor of reduced viability of starvation (SUR1. S. cerevisiae)	UNKNOWN	101.9	31.7	169.6	15.6	167.3	22.3	215.8	33.4	37.5	5.3	187.1	13.2	78.5	8.3	128.4	7.5	-5	-2.1	-3.4
7376_at		YBL029W	YBL029W hypothetical protein	UNKNOWN	120.1	30.3	235.3	7.6	140.7	18.8	159.6	28.5	17.1	3.8	353.6	19.8	52.8	6.7	233.6	79.8	-20.7	-3.1	-13.7
7445_at		YBL095W	YBL095W similarity to C.albicans hypothetical protein	UNKNOWN	29	14.7	62	6.7	52.8	8.6	46.2	4.7	141.8	57.5	457.7	77.1	381.6	17	353.3	70.4	-3.2	-2.7	-2.5
7626_at	MEP3	YPR138C	YPR138C (MEP3) Ammonia permease of high capacity and low affinity	TRANSPORT	105.3	40.6	85.7	34.5	70.4	29.8	61.1	4.6	32.1	9.3	152.7	5.1	73.9	3.7	111.2	6.5	-4.8	-2.3	-3.5
7637_at	ISR1	YPR106W	YPR106W protein kinase	STAUROSPORINE RESISTANCE	23.8	5.7	56.2	1.1	45.2	7.7	45.5	6	34	10.5	100.6	22.3	77.2	9.8	84.4	17.5	-3	-2.3	-2.5
7765_at		YPR013C	YPR013C similarity to transcription factors	UNKNOWN	46.5	12	77.7	7.7	77.4	9.9	75.7	25	24.7	12.1	63.9	11.9	56.4	10.3	77.8	36.3	-2.6	-2.3	-3.1
7840_at		YPL095C	YPL095C strong similarity to YBR177c	UNKNOWN	501.2	56.9	457.7	40.2	306.4	58.3	328.7	63.1	57	5.7	1032.3	51.9	172.4	30.4	682.7	79.7	-18.1	-3	-12
8373_at	LCB4	YOR171C	YOR171C sphingoid long chain base (LCB) kinase	SPHINGOLIPID METABOLISM	12	4.9	21.5	4	18.1	1.8	17.4	4.2	26.7	5.6	59.8	6.1	59.7	0.8	66.7	17.6	-2.2	-2.2	-2.5
8698_at	PFK27	YOL136C	YOL136C (PFK27) 6-Phosphofructose-2-kinase. isozyme 2	CARBOHYDRATE METABOLISM	25.5	13.8	30.8	4.8	26.9	4.8	44.5	12.9	15.4	4	46.4	14.9	38.1	4.4	45.7	16.4	-3	-2.5	-3
8787_at		YNR032C	YNR032C hypothetical protein identified by SAGE	SIGNALING. HIGH OSMOLARITY PATHWAY	77.7	24	242	49.6	180.9	5.5	116	21.8	87	10.8	185.4	48.4	233.2	14.7	189.9	60	-2.1	-2.7	-2.2
8922_at	SUN4	YNL066W	YNL066W Protein involved in the aging process	AGING	433.5	182.9	649.6	98.7	665.6	5.2	725.1	76	227.2	30.2	706.2	43.7	613.6	49.1	879.7	192.5	-3.1	-2.7	-3.9
8988_at		YNL134C	YNL134C similarity to C.carbonum toxD gene	UNKNOWN	378.7	128.8	501.7	39.6	539.2	52.1	530.1	45.8	167.8	43.8	464.9	42.7	576.2	42.4	594	53.5	-2.8	-3.4	-3.5
9334_at	NGL2	YMR285C	YMR285C similarity to Ccr4p	UNKNOWN	54.3	17	119.7	5.9	129.7	27.2	99.4	9.9	46.7	6.1	160.1	17.1	132.9	9.7	142.3	17.3	-3.4	-2.8	-3
9363_at		YMR269W	YMR269W weak similarity to C.elegans hypothetical protein CELT23B3	UNKNOWN	15.4	10.4	21.5	2.2	23.2	4.4	21.1	3.5	12.6	3.4	28.6	4	31.5	2.3	31.3	4.1	-2.3	-2.5	-2.5
9587_at		YMR057C	YMR057C hypothetical protein	UNKNOWN	34.7	12.4	97.2	12.8	71.1	8.6	34.7	6.9	19.5	12.2	61.6	6.8	63.3	15.5	49.5	16.6	-3.2	-3.3	-2.5
9864_at		YLR460C	YLR460C similarity to C.carbonum toxD protein	UNKNOWN	122.4	63.9	294.5	65.8	282.3	25.8	174.5	24.6	17.6	8.2	110.3	13.2	195.7	32.5	116.7	23.6	-6.3	-11.1	-6.6

Up-regulated under N-Lim aerobic only (FC = fold change, ANA = anaerobic, A = aerobic)

Probe Set	Gene name	systematic name	functional description	cellular function	C-Lim ANA Average	C-Lim ANA Stdev	N-Lim ANA Average	N-Lim ANA Stdev	P-Lim ANA Average	P-Lim ANA Stdev	S-Lim ANA Average	S-Lim ANA Stdev	C-Lim A Average	C-Lim A Stdev	N-Lim A Average	N-Lim A Stdev	P-Lim A Average	P-Lim A Stdev	S-Lim A Average	S-Lim A Stdev	FC N-Lim AE vs C-Lim AE	FC N-lim AE vs S-AE	FC N-lim AE vs P-lim AE
10208_at	PDC5	YLR134W	YLR134W pyruvate decarboxylase	GLYCOLYSIS	84.9	27.4	225.3	19.7	103.9	9.4	130.2	5.1	95.3	4.6	1708.3	86.5	168.6	36.4	835.6	33.4	17.9	10.1	2
10346_at		YLR004C	YLR004C similarity to allantoate transport protein	UNKNOWN	22	10	83.4	32.2	43.6	2.8	64.8	24.5	39.1	6.9	112	19.9	19.6	6.6	21	6.1	2.9	5.7	5.3
10681_at	LAP4	YKL103C	YKL103C vacuolar aminopeptidase ysc1	PROTEIN DEGRADATION	625.7	189.7	1191.8	18.8	580.8	166.4	617.2	35.7	284.2	14	888.5	179.3	426.8	35.5	411.2	11.1	3.1	2.1	2.2
4109_at	BAR1	YIL015W	YIL015W (BAR1) Secreted pepsin-like protease that degrades alpha-factor	MATING	374.9	26.6	717.1	80	464.1	45.3	715.6	88.9	187.5	107.1	642	129	317.1	7.1	313.9	78.7	3.4	2	2
4134_at	PRM2	YIL037C	YIL037C hypothetical protein	UNKNOWN	77.5	18.8	122.4	25	95.2	19.6	103	45.9	59.8	16.1	126.2	16.1	43.7	5.9	14.2	9.3	2.1	2.9	8.9
4158_at		YIL059C	YIL059C hypothetical protein	UNKNOWN	20.1	4.4	96.7	20.4	18.7	4.3	56	10.7	27.6	3.3	236.2	24.9	25.3	5.6	57.6	4.4	8.6	9.3	4.1
4340_at		YHR180W	YHR180W hypothetical protein	UNKNOWN	35.8	15.2	75.5	6.6	43.8	3.3	42.3	12.8	46.2	4	158.1	11.8	39.4	7.3	67.2	20.8	3.4	4	2.4
4961_at		YGR035C	YGR035C hypothetical protein	UNKNOWN	14.1	5.5	18.5	3.1	12	2.1	18.7	4.5	12	1.7	89	15	24.6	2	39.1	4.2	7.4	3.6	2.3
5310_at		YFR055W	YFR055W strong similarity to beta-cystathionases	UNKNOWN	25.6	12.1	100.2	46.5	34.1	6.6	66.5	7	12	5.8	92	12.9	22.1	2.2	37.1	13	7.7	4.2	2.5
6253_at	AMD2	YDR242W	YDR242W putative amidase	UNKNOWN	24.2	13.8	120.2	30.8	43.3	7.9	67.5	4.1	34.7	5.6	130.5	4	30.5	11.1	33.8	4.5	3.8	4.3	3.9
6562_at	THI3	YDL080C	YDL080C positive regulatory factor with thiamin pyrophosphate-binding motif for thiamin me	THIAMINE METABOLISM	76.1	17.6	155.5	24.3	147.2	6.8	128.9	21.3	91.7	9.3	248.7	33.9	104.8	15.8	120.3	26.9	2.7	2.4	2.1

6905_at	FUS1	YCL027W	YCL027W serine/threonine-rich membrane protein	MATING; CELL FUSION	25.6	10.2	74.8	9.5	72.7	3.7	117.1	19.4	23.9	8.1	75	19.2	37.5	7.4	33.6	3.3	3.1	2	2.2
6917_at	MRC1	YCL061C	YCL061C similarity to myosin heavy chain form b from Chicken and Xenopus	UNKNOWN	20.8	9.3	37.9	4.4	34.6	15.3	32.7	5.2	23	5.7	50.6	13.4	23.8	10.9	24.7	8.6	2.2	2.1	2
7920_at		YPL150W	YPL150W similarity to ser/thr protein kinases	UNKNOWN	36.5	8.5	66.8	22.6	52.4	8.3	41.1	6.5	48.9	22.1	140.3	32.6	60.7	3	53.7	11.3	2.9	2.3	2.6
7927_at	MF(ALPHA)1	YPL187W	YPL187W mating factor alpha	MATING	49.8	15.3	79.3	29.6	26.1	8.2	82.1	14.6	104.6	110.3	305.5	45.4	14	0.9	77.5	19.7	2.9	21.9	3.9
8505_at	HMS1	YOR032C	YOR032C myc-family transcription factor homolog	PSEUDOHYPHAL GROWTH	53.5	26.6	72.2	0.9	19.9	1.8	67	8	12	2.5	63.5	13.9	12	0.1	31.3	3.2	5.3	5.3	2
8780_at		YNR068C	YNR068C similarity to Bul1p	UNKNOWN	29.3	23.2	146.7	39.6	47.9	3.3	92.8	10.7	61.3	4.8	126.8	20	38.1	0.2	45.2	4.1	2.1	3.3	2.8
8993_at		YNL129W	YNL129W weak similarity to M.pneumoniae uridine kinase udk	UNKNOWN	58.9	30.6	145.7	24.8	98.2	13.4	103.1	18.1	62.6	2.4	269.1	12.8	77.3	5.2	42.9	8.2	4.3	3.5	6.3
9284_at	FET4	YMR319C	YMR319C Low-affinity Fe(II) transport protein	TRANSPORT	156.8	41.4	334.3	87.5	315.7	28.2	293.2	18.9	12	1.9	122.9	30.2	17.4	2.8	55.1	5.4	10.2	7.1	2.2

Down-regulated under N-Lim aerobic only (FC = fold change, ANA = anaerobic, A = aerobic)

Probe Set	Gene name	systematic name	functional description	cellular function	C-Lim ANA Average	C-Lim ANA Stdev	N-Lim ANA Average	N-Lim ANA Stdev	P-Lim ANA Average	P-Lim ANA Stdev	S-Lim ANA Average	S-Lim ANA Stdev	C-Lim A Average	C-Lim A Stdev	N-Lim A Average	N-Lim A Stdev	P-Lim A Average	P-Lim A Stdev	S-Lim A Average	S-Lim A Stdev	FC N-Lim AE vs C-Lim AE	FC N-lim AE vs S-AE	FC N-lim AE vs P-lim AE
10377_at		YLL053C	YLL053C similarity to water channel proteins	UNKNOWN	75	23.3	157.4	12.9	172.9	33.2	171.5	47.5	1248.4	136.8	348.8	56.7	2716.5	272.8	2125.6	758.2	-3.6	-7.8	-6.1
10378_at	AQY2	YLL052C	YLL052C member of mip family transmembrane channels	TRANSPORT, WATER	23.9	6.8	56.1	7.2	77.3	10	86	18.2	418.7	78.5	130.1	5.7	1355	120.9	1075.8	594.3	-3.2	-10.4	-8.3
11133_at	NCA3	YJL116C	YJL116C With NCA2. regulates proper expression of subunits 6 (Atp6p) and 8 (Atp8p) of t	ATP SYNTHESIS	27	11.8	44.1	6.8	47.6	5	49.1	15.7	192.3	79.6	13.8	5.7	87.5	11.9	90.3	14.8	-13.9	-6.3	-6.5
4801_at	HIP1	YGR191W	YGR191W histidine permease	TRANSPORT	123.6	18.6	69.3	9.5	133.9	23.4	186.2	17.3	96.8	15.2	37.7	5.7	109.5	3.6	185.1	6.8	-2.6	-2.9	-4.9
4846_at		YGR146C	YGR146C hypothetical protein	UNKNOWN	78.3	25.5	74.7	14.4	165.8	26.1	168.9	82.7	148	36.3	13.8	2.8	53.7	11	137.4	28.3	-10.7	-3.9	-9.9
4860_at	NSR1	YGR159C	YGR159C nuclear localization sequence binding protein	NUCLEAR PROTEIN TARGETING	394.4	54.1	224.9	44.7	307.9	126.6	412.6	65.9	518.4	127.2	137.3	76.4	367.8	238	408.4	111	-3.8	-2.7	-3
6854_at	HSP30	YCR021C	YCR021C Heat shock protein located in the plasma membrane with a role in cellular pH ho	STRESS	55.1	24.8	113.9	7.3	98.3	20.4	114.3	13.7	499.8	334.9	62	10.1	246.8	19.9	157.6	77.1	-8.1	-4	-2.5
7291_at	BAP2	YBR068C	YBR068C probable amino acid permease for leucine. valine. and isoleucine	TRANSPORT	102	9.4	26.7	4.8	99.4	9.7	45.1	9.4	336.3	77.4	20.3	3.8	119.3	14.3	44.2	5	-16.6	-5.9	-2.2
7295_at	HSP26	YBR072W	YBR072W Heat shock protein of 26 kDa. expressed during entry to stationary phase and in	STRESS	148.2	41.1	281.1	37.2	352.2	81.9	258.4	31.7	1769.5	317.3	222.6	27.3	519	74.1	734.3	121.1	-7.9	-2.3	-3.3
7981_at	GRE1	YPL223C	YPL223C Induced by osmotic stress	UNKNOWN	13.3	4.4	24.9	1.5	47.3	12.6	20.1	7.4	1360.4	918.6	12	3.1	846.6	181	29.5	3.9	-113.4	-70.6	-2.5
7999_at	ICY2	YPL250C	YPL250C weak similarity to YMR195w	UNKNOWN	185.4	37	163.7	27.8	905.5	138.9	234.3	2.6	304.7	122.5	126.4	33.5	1705.5	181.7	498.7	23.5	-2.4	-13.5	-3.9
8724_at		YOL155C	YOL155C similarity to glucan 1.4-alpha-glucosidase Sta1p and YAR066w	UNKNOWN	264.4	136.8	73	40.6	300.2	29.4	64.3	28.6	1133.3	588.4	214	144.1	1827.5	111.2	2196	343.1	-5.3	-8.5	-10.3
9588_at	FET3	YMR058W	YMR058W multicopper oxidase	TRANSPORT	13.8	6	15.2	2.8	45.5	23.1	12	4.4	128.3	43.3	28.9	2.8	109.5	35.8	136.2	18.8	-4.4	-3.8	-4.7
9633_at	HXT2	YMR011W	YMR011W high affinity hexose transporter-2	TRANSPORT	457.3	283.3	1169.8	50.9	934.1	136.4	1117.7	117.4	1744.9	308.4	92.1	21.5	597.5	69.5	202.6	49.9	-19	-6.5	-2.2

Up-regulated under P-Lim aerobic only (FC = fold change, ANA = anaerobic, A = aerobic)

Probe Set	Gene name	systematic name	functional description	cellular function	C-Lim ANA Average	C-Lim ANA Stdev	N-Lim ANA Average	N-Lim ANA Stdev	P-Lim ANA Average	P-Lim ANA Stdev	S-Lim ANA Average	S-Lim ANA Stdev	C-Lim A Average	C-Lim A Stdev	N-Lim A Average	N-Lim A Stdev	P-Lim A Average	P-Lim A Stdev	S-Lim A Average	S-Lim A Stdev	FC P-Lim AE vs C-Lim AE	FC P-lim AE vs N-lim AE	FC P-lim AE vs S-Lim AE
10310_at	PPR1	YLR014C	YLR014C zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type	PYRIMIDINE BIOSYNTHESIS	40.2	19.5	85.8	12.2	68.1	9	161.6	19.2	39.4	13	63.8	5.3	65.7	7.8	186.3	7.7	4.7	2.9	2.8
10522_at	TRK2	YKR050W	YKR050W membrane protein\; low affinity potassium transport	TRANSPORT	15.4	11.1	68.5	9.1	46.1	8.3	63.7	10.2	44.4	3.9	48	8.6	46.6	5.5	116.5	6.1	2.6	2.4	2.5
11119_at		YJL083W	YJL083W similarity to hypothetical protein YKR019c	UNKNOWN	12	4.8	17.9	4	16.2	6.2	23.6	1.7	18.8	3.4	15.8	1.6	12	1.9	47.3	20.6	2.5	3	3.9
3626_i_at	COS10	YNR075W	YNR075W Protein with strong similarity to subtelomerically-encoded proteins such as Cos5	UNKNOWN	52.9	35	124	64	211.9	37	278.2	33.3	12	1.7	12.2	4.8	12	3.4	34.5	11	2.9	3.7	2.9
3938_at	AST1	YBL069W	YBL069W Protein involved in targeting of plasma membrane [H+]ATPase	PLASMA MEMBRANE PROTEIN TARGETING	12	3.3	23.7	3	18.8	3.9	35.1	6.2	16.7	1.9	19	0.9	22.1	2.3	71.2	19.7	4.3	3.7	3.2
4236_at	QDR1	YIL120W	YIL120W similarity to antibiotic resistance proteins	UNKNOWN	24.6	5.3	28.2	3.1	34.9	4	49.4	11.9	21.7	7	20.7	4.7	13.5	3.4	64.6	17.5	3	3.1	4.8
4322_at		YHR210C	YHR210C UDP-glucose-4-epimerase (GAL10. galE)	UNKNOWN	300.3	77.5	109.1	13.1	75	4	338.3	78.4	22.8	1	61.2	4.5	47.7	1.2	219	89.3	9.6	3.6	4.6
4506_at		YHR032W	YHR032W ethionine resistance protein	UNKNOWN	27	5.1	53.1	12.9	37.8	4.5	93.5	4.1	33.9	16.2	35.2	5.1	34.8	19.2	138.5	79.8	4.1	3.9	4
4915_at		YGR079W	YGR079W hypothetical protein	UNKNOWN	29.1	12.5	41.3	6.7	48.1	5.5	82.3	24.8	41.9	5.5	64.7	9	78.8	19.8	298.1	50.3	7.1	4.6	3.8
5246_at	SDT1	YGL224C	YGL224C strong similarity to hypothetical protein YER037w	UNKNOWN	66.8	24.3	257.7	46	148.4	28.8	476.9	117	140.7	28.2	269.9	21	155.6	16.7	688.8	139	4.9	2.6	4.4
5535_at		YER186C	YER186C weak similarity to hypothetical protein YMR316w	UNKNOWN	121.9	58	251.9	15.6	216.8	59.5	391.6	63.4	135	29.8	184.3	70.2	169.3	21.9	743.2	111.5	5.5	4	4.4
6090_at	SHE9	YDR393W	YDR393W mRNA (identified by a library screen) that causes growth arrest when overexpre	UNKNOWN	23.5	5.6	21.1	0.8	21.8	1	34.4	5.3	22.6	2.6	31.3	1.6	23.4	3.9	78.6	25.2	3.5	2.5	3.4
6577_at		YDL109C	YDL109C strong similarity to thiamine-repressed protein Thi4p	UNKNOWN	12	2.3	14.6	2	12	2.7	21.3	15.2	13.3	1.6	12	1.4	12	3.2	31	15.2	2.3	2.6	2.6
6835_at	BUD23	YCR047C	YCR047C Protein carboxyl methylase	UNKNOWN	74.6	4	228.3	14.9	109.2	13.6	193.5	11.8	85.8	57.2	87.3	41.1	56.3	8.7	258.9	120	3	3	4.6
6894_at	AUT4	YCL038C	YCL038C Membrane transporter	UNKNOWN	75.3	45.2	158.6	67.3	119.4	35.9	309.8	17.6	61.7	13.1	108.7	20.3	72.1	10.7	265.6	44.7	4.3	2.4	3.7
7361_at	NTH2	YBR001C	YBR001C Neutral trehalase. highly homologous to Nth1p	TREHALOSE METABOLISM	55.6	12.5	122.7	36.6	71.6	2.8	103.7	9.3	126.5	15.3	146.5	9.6	75.2	4.3	328	60.9	2.6	2.2	4.4
7427_at		YBL070C	YBL070C questionable protein	UNKNOWN	12	2.8	12	1	12	3.4	12	3.1	12	0.9	12	1.1	12	1.3	68.4	9	5.7	5.7	5.7
7428_at	PRS4	YBL068W	YBL068W ribose-phosphate pyrophosphokinase 4	PENTOSE PHOSPHATE CYCLE	131.8	33.9	195.9	41.4	147.3	18.3	348.2	18.5	164	25.2	180.3	20	175.9	17.4	700.3	86.5	4.3	3.9	4
7611_at		YPR125W	YPR125W suppressor of mrs2-1 mutation	UNKNOWN	149.2	2.4	139.9	23.8	146.7	21.6	185.5	47.7	185.4	27.3	188.3	16	193.5	9.4	443.2	133.7	2.4	2.4	2.3
8187_at		YOR343C	YOR343C hypothetical protein	UNKNOWN	74.4	29	49.1	15.2	57.8	3.9	146.9	21.1	74.1	13.7	29.6	6.9	13.8	9.2	212.5	111.4	2.9	7.2	15.4
8726_at		YOL154W	YOL154W similarity to S.cerevisiae Asp Fll	UNKNOWN	54	17.7	319.6	3	189.3	31.3	206.9	32.4	161.8	42	159.6	27	129.6	24.2	332.3	64	2.1	2.1	2.6
8862_at		YNR014W	YNR014W weak similarity to hypothetical protein YMR206w	UNKNOWN	87.3	26.5	52.9	4.8	34.7	7.6	47.1	14.4	14	3	19.3	3.5	18	2.9	40.3	16.7	2.9	2.1	2.2
8896_at		YNL046W	YNL046W hypothetical protein	UNKNOWN	227.2	54.9	338.7	42.1	218.7	44	269	24.1	188.1	19.8	228.3	50.6	195.8	12.2	474.2	184.9	2.5	2.1	2.4
9079_at		YNL224C	YNL224C hypothetical protein	UNKNOWN	13.2	7.2	15.5	1.7	18	4.7	28.7	8.1	12.6	0.4	17	2.1	18	1.7	37.5	0.7	3	2.2	2.1
9107_at	APG2	YNL242W	YNL242W similarity to human hypothetical protein KIAA0404	UNKNOWN	14.5	7	27.4	3.2	18.4	4.5	19.5	5.1	40.7	8	37.7	17	39.3	2.8	135	45	3.3	3.6	3.4
9292_at		YMR194C	YMR194C hypothetical protein identified by SAGE	UNKNOWN	12	4.1	12.1	0.6	13.4	3.7	26	7.7	12	0.6	12	1.8	13.5	2.3	27.4	10.6	2.3	2.3	2
9328_at		YMR279C	YMR279C strong similarity to aminotriazole resistance protein	UNKNOWN	31.4	14.6	32.3	7.1	45.2	6.1	55.3	15.7	12	5.5	12	3.5	12.7	3.2	30.4	10.2	2.5	2.5	2.4
9700_at	IMD4	YML056C	YML056C strong similarity to IMP dehydrogenases	UNKNOWN	63.3	29.1	56.5	28.5	131	32.1	183.1	25	40.8	7.5	30	5.3	60.2	6	121	57.3	3	4	2
9711_at	UFO1	YML088W	YML088W hypothetical protein	UNKNOWN	32.7	15.6	47.6	12.1	60.3	8.5	97.5	31.4	37.1	3.4	46.2	3.6	51.9	3.8	122.7	19.8	3.3	2.7	2.4
9901_at	VIP1	YLR410W	YLR410W Homologous to S. pombe asp1+	UNKNOWN	51	22.6	112.1	9.7	122.8	21.1	214.3	39.1	76.1	13.5	104.7	21.6	129.7	4.2	387.7	101.4	5.1	3.7	3
9970_at		YLR346C	YLR346C weak similarity to YGR035c	UNKNOWN	20.4	8.5	86.6	25	32.2	7.6	72.1	21.5	86.8	13.5	96	4.5	69.5	5.6	229.1	19	2.6	2.4	3.3

Down-regulated under P-Lim aerobic only (FC = fold change, ANA = anaerobic, A = aerobic)

Probe Set	Gene name	systematic name	functional description	cellular function	C-Lim ANA Average	C-Lim ANA Stdev	N-Lim ANA Average	N-Lim ANA Stdev	P-Lim ANA Average	P-Lim ANA Stdev	S-Lim ANA Average	S-Lim ANA Stdev	C-Lim A Average	C-Lim A Stdev	N-Lim A Average	N-Lim A Stdev	P-Lim A Average	P-Lim A Stdev	S-Lim A Average	S-Lim A Stdev	FC P-Lim AE vs C-Lim AE	FC P-lim AE vs N-lim AE	FC P-lim AE vs S-Lim AE
10601_at		YKL051W	YKL051W hypothetical protein	UNKNOWN	14.5	8.5	20.5	5.4	19.5	3.4	12	2.7	81.6	26.4	115.5	11.7	56.3	10.1	13.4	1.9	-6.1	-8.6	-4.2
3949_i_at	YIP3	YNL044W	YNL044W protein of unknown function	UNKNOWN	138.2	43	131.2	18.2	129.2	34.2	113.8	28.4	287.2	116.8	195.5	47.2	196.8	13.7	85.1	51.3	-3.4	-2.3	-2.3
4134_at	PRM2	YIL037C	YIL037C hypothetical protein	UNKNOWN	77.5	18.8	122.4	25	95.2	19.6	103	45.9	59.8	16.1	126.2	16.1	43.7	5.9	14.2	9.3	-4.2	-8.9	-3.1
5769_at	SIT1	YEL065W	YEL065W probably multidrug resistance protein	TRANSPORT	32.8	15.9	168.7	32.2	267.2	106.3	48.8	5.1	87.6	21	185.3	5.9	100.2	19	34.9	9	-2.5	-5.3	-2.9
6346_at		YDR111C	YDR111C strong similarity to alanine transaminase	UNKNOWN	20.8	11.1	84	13.2	199.1	32.7	69.1	7.9	131.1	11.2	49.7	1.8	129.9	13.3	18.2	0.1	-7.2	-2.7	-7.1
7280_at		YBR099C	YBR099C weak similarity to T.brucei mitochondrion hypothetical protein 6	UNKNOWN	23.8	9.6	66.2	12.3	83.3	2.1	46.5	9.2	109.2	37.3	91.9	6.2	100	9.8	43.8	4.1	-2.5	-2.1	-2.3
7403_at		YBL049W	YBL049W hypothetical protein	UNKNOWN	148.9	58.6	200.6	56.5	222.2	32.6	245.5	38	392	16.1	330.3	75.1	300.5	55.1	138.1	33.1	-2.8	-2.4	-2.2
7960_i_at	RPL7B	YPL198W	YPL198W Ribosomal protein L7B (L6B) (rp11) (YL8)	PROTEIN SYNTHESIS	335	160.3	149	95.6	464.9	89.5	227.9	91.5	529.9	154.9	171.7	53.8	337.6	76.9	72.5	10	-7.3	-2.4	-4.7
8030_at	DIP5	YPL265W	YPL265W dicarboxylic amino acid permease	TRANSPORT	559.1	48.4	1576.8	319.1	497.3	38.9	332.6	82.2	28.1	9.7	696.8	44.4	445.6	71.1	13.2	2.6	-2.1	-52.7	-33.7
9869_at		YLR264C	YLR264C identified by SAGE	UNKNOWN	166.3	88.7	115.4	50.2	142.4	9.8	144.9	22.5	190.8	96.9	119.8	25.3	115.5	6	49.9	24.5	-3.8	-2.4	-2.3
9946_at	RPS22B	YLR367W	YLR367W Ribosomal protein S22B (S24B) (rp50) (YS22)	PROTEIN SYNTHESIS	303.9	69.7	407.5	75.9	568.5	65.5	435.2	53.2	520.1	92.1	517.4	93.4	519	92	234.8	15.3	-2.2	-2.2	-2.2
9996_at		YLR327C	YLR327C strong similarity to Stf2p	UNKNOWN	1537.8	284.6	466	42.1	389.2	31.1	253.3	28.5	1969.8	169.5	312.7	71.3	363.7	34.7	85.5	9.5	-23	-3.7	-4.3

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Probe Set	Gene name	systematic name	functional description	cellular function	C-Lim ANA Average	C-Lim ANA Stdev	N-Lim ANA Average	N-Lim ANA Stdev	P-Lim ANA Average	P-Lim ANA Stdev	S-Lim ANA Average	S-Lim ANA Stdev	C-Lim A Average	C-Lim A Stdev	N-Lim A Average	N-Lim A Stdev	P-Lim A Average	P-Lim A Stdev	S-Lim A Average	S-Lim A Stdev	FC S-Lim AE vs C-Lim AE	FC S-lim AE vs N-AE	FC S-lim AE vs P-Lim AE
10625_at		YKL071W	YKL071W weak similarity to A.parasiticus nor-1 protein	UNKNOWN	12	5.4	34.7	12.8	19	4.9	25.5	4.3	19.1	4.1	30.2	4.5	102.6	29.9	47.8	2.1	5.4	3.4	2.1
11217_at	CBP1	YJL209W	YJL209W Protein required for COB mRNA stability or 5' processing	MRNA STABILITY. COB MRNA	18.9	7.1	22.2	2.3	43.9	19.4	34.4	13.1	22.1	8.1	21.9	2.2	66.1	2.7	24.6	5.1	3	3	2.7
4077_at		YIR042C	YIR042C weak similarity to B.lichenifORm hypothetical protein P20	UNKNOWN	20.2	10.1	99.7	19.5	124.4	6.6	41.3	13.1	22.8	2.7	134.8	23.4	353.1	21.8	35	4.2	15.5	2.6	10.1
4224_at	CSM2	YIL132C	YIL132C hypothetical protein	UNKNOWN	12	6	18.6	2.3	33.7	5.3	16.8	1.7	12	7.8	16.9	1.1	40.9	1.4	18	4.6	3.4	2.4	2.3
4440_at	KIC1	YHR102W	YHR102W Ser/Thr protein kinase	MITOSIS (PUTATIVE)	52.4	15.8	90.1	29.4	83.2	25.2	38.7	12.5	49.5	16.8	85.6	10.8	323.7	16.8	53.4	10.3	6.5	3.8	6.1
5423_s_at		YFL057C	YFL057C strong similarity to aryl-alcohol dehydrogenases	UNKNOWN	468.3	125.5	526.8	32.7	693.9	104.7	306.7	34.2	286.8	38	320.4	83.9	1207.4	49.4	405.8	73.5	4.2	3.8	3
5812_at		YEL072W	YEL072W hypothetical protein	UNKNOWN	26.4	13.3	66.1	13	110.9	10.1	26.9	4.3	18.2	4.6	64.5	6.6	134.8	18.8	35	9	7.4	2.1	3.8
5813_at	DLD3	YEL071W	YEL071W strong similarity to Aip2p	UNKNOWN	921.2	147.8	257.4	53.7	811.6	33.4	591.7	21.4	223.7	41.6	184.7	34.7	735.5	102.1	289.4	56.7	3.3	4	2.5
5977_at	GNP1	YDR508C	YDR508C high-affinity glutamine permease	TRANSPORT	253.5	119.3	30.9	10.1	359.5	106.1	154.3	12.1	78.5	9.9	16.7	2.6	273.1	33.7	64.2	16.2	3.5	16.4	4.3
7065_at		YBR292C	YBR292C hypothetical protein	UNKNOWN	13	3.3	17.9	4.8	31.6	6.2	12	2.7	18	0.9	17	2.3	98.3	7.5	13.7	3.4	5.5	5.8	7.2
7099_at		YBR281C	YBR281C Probable G-protein. -transducin type	UNKNOWN	25.2	21.1	49.3	9.2	74.8	3.8	31.9	3.6	55.3	13.1	54.9	10.3	170.3	21.3	46.3	15.2	3.1	3.1	3.7
7367_at	FLR1	YBR008C	YBR008C Member of the multidrug-resistance 12-spanner (DHA12) family of the major faci	SMALL MOLECULE TRANSPORT	72.6	7.6	171.7	38.1	153.5	18.3	107.8	8.1	100.8	18.8	135.8	20.5	484	13.9	178.6	47.8	4.8	3.6	2.7
7791_at		YPL052W	YPL052W hypothetical protein	UNKNOWN	100.4	29.6	161.3	38.1	238.5	34	121.8	19.9	135.7	12.6	133.9	29	493.3	16.1	94.4	16.4	3.6	3.7	5.2
7944_at	OYE3	YPL171C	YPL171C NAD(P)H dehydrogenase	UNKNOWN	146.2	51.9	84.8	18.2	171.6	15.8	44.1	4.1	198.6	36.9	177.8	13.1	1202.5	121.1	284	128.9	6.1	6.8	4.2
8206_at	COT1	YOR316C	YOR316C Protein involved in cobalt accumulation\; dosage dependent suppressor of cobal	SMALL MOLECULE TRANSPORT	331.4	29.8	295.6	25.3	454.9	55.8	221.4	30.5	288.4	57.4	294.7	33.2	597.6	50.1	271.4	26.4	2.1	2	2.2
8236_at		YOR302W	YOR302W CPA1 leader peptide	UNKNOWN	266.5	49.9	274.7	199.3	827.4	77.9	700.2	127.8	399.7	136.5	438.8	38.3	1051.2	168.5	395.6	302.2	2.6	2.4	2.7
8241_at	MCH5	YOR306C	YOR306C similarity to human X-linked PEST-containing transporter	UNKNOWN	106	47	176.5	33.2	439.8	36.8	312.6	56.3	67.4	25.7	73.8	2.7	181.1	5.4	86.6	19.1	2.7	2.5	2.1
8486_at	ASE1	YOR058C	YOR058C(ASE1) Microtubule-associated protein localized to the spindle midzone. required	MITOSIS	29.9	17.6	60.3	12.6	89.8	20.8	51.8	11.3	43.4	11.6	104.1	3.1	266.2	16.9	66.3	23.1	6.1	2.6	4
8633_at	MET22	YOL064C	YOL064C 3'(2')5'-bisphosphate nucleotidase	METHIONINE BIOSYNTHESIS	732.4	95.4	752.5	35	1465.7	111.4	840.5	63.4	402.9	39.6	557.2	48.5	1173.4	103.3	532.1	14.4	2.9	2.1	2.2
8937_at		YNL095C	YNL095C strong similarity to YOR092w	UNKNOWN	24.8	12.1	44.4	8.2	96.5	7.2	57.2	6.8	38	3.2	39	1.4	104.1	12.4	38.1	3.4	2.7	2.7	2.7

Down-regulated under S-Lim aerobic only (FC = fold change, ANA = anaerobic, A = aerobic)

Probe Set	Gene name	systematic name	functional description	cellular function	C-Lim ANA Average	C-Lim ANA Stdev	N-Lim ANA Average	N-Lim ANA Stdev	P-Lim ANA Average	P-Lim ANA Stdev	S-Lim ANA Average	S-Lim ANA Stdev	C-Lim A Average	C-Lim A Stdev	N-Lim A Average	N-Lim A Stdev	P-Lim A Average	P-Lim A Stdev	S-Lim A Average	S-Lim A Stdev	FC S-Lim AE vs C-Lim AE	FC S-lim AE vs N-AE	FC S-lim AE vs P-Lim AE
10060_at	GSY2	YLR258W	YLR258W Glycogen synthase (UDP-gluocse--starch glucosyltransferase)	GLYCOGEN METABOLISM	165.1	32.2	216.3	19.8	134	34.7	209.4	52	234.8	28.5	207.3	8.9	92.1	9.8	202.5	8.9	-2.5	-2.3	-2.2
10158_at	TFS1	YLR178C	YLR178C suppressor of cdc25	CELL CYCLE	431.3	63.6	723.5	118.5	327.8	44.5	326.4	5.7	913.3	146.8	484.4	124.2	219.3	13.9	482.5	154.4	-4.2	-2.2	-2.2

10262_at		YLR053C	YLR053C hypothetical protein	UNKNOWN	12	6.9	73.2	8.2	12	3.7	26.3	11.1	81.8	23.4	335.2	21.8	28	3	104.1	37.9	-2.9	-12	-3.7
10795_at	JEN1	YKL217W	YKL217W carboxylic acid transporter protein homolog	TRANSPORT	68.4	20.6	27.7	8.4	12.6	3.4	16	8.9	1943.4	142.8	39.5	4.3	18.2	8.3	42	12.8	-106.8	-2.2	-2.3
10865_at	BNA1	YJR025C	YJR025C C-terminal part of YJR030c	NICOTINIC ACID BIOSYNTHESIS	224.1	26	218.8	47	148.4	37.9	414.5	29	114.9	6.1	63.4	2.6	21.5	3.4	53.1	19.8	-5.4	-3	-2.5
10908_at		YJR115W	YJR115W similarity to hypothetical protein YBL043w	UNKNOWN	83.5	48.6	122.3	8.9	35.4	1.5	93.8	27.6	237.7	91.2	57.2	27.4	20.7	5.6	117.5	54.4	-11.5	-2.8	-5.7
11052_at		YJL016W	YJL016W weak similarity to hypothetical protein YNL278w and YLR187w	UNKNOWN	194.2	41.9	483.8	65.6	268.6	34.4	378.9	64.7	233.7	82.4	305.3	2.3	103.1	14.7	273.6	41.4	-2.3	-3	-2.7
11060_at	TDH1	YJL052W	YJL052W Glyceraldehyde-3-phosphate dehydrogenase 1	GLYCOLYSIS	2717.7	728	1568.6	297.6	1001.5	80.7	2508.8	272.9	1453	285.8	1417.2	82.6	447.6	23.3	1798.3	298.8	-3.2	-3.2	-4
4388_at	SPS100	YHR139C	YHR139C sporulation-specific wall maturation protein	SPORULATION	12.1	5.2	31.7	2.7	26.4	4.8	30.3	2.8	310.8	232	42.1	8.5	18.5	6.2	49	13.3	-16.8	-2.3	-2.6
4732_at	GND2	YGR256W	YGR256W 6-phosphogluconate dehydrogenase	PENTOSE PHOSPHATE CYCLE	21.1	10.5	40.2	2.9	24.5	5.4	40.9	7.3	316.4	69.2	26.9	5.7	12	3.1	78.8	10.7	-26.4	-2.2	-6.6
4768_at	SOL4	YGR248W	YGR248W similar to SOL3	UNKNOWN	47.9	27.2	87.1	8	48.3	18.5	61.2	18.6	568.3	184.4	363.7	153	110.6	4.9	528.4	75	-5.1	-3.3	-4.8
5121_at		YGL121C	YGL121C hypothetical protein	UNKNOWN	345.8	6.6	337.5	34	180.9	10.4	195.5	82.5	884.9	113.3	473.1	37.8	125	17.9	330.2	77.3	-7.1	-3.8	-2.6
5357_at	GSY1	YFR015C	YFR015C Glycogen synthase (UDP-gluocse--starch glucosyltransferase)	GLYCOGEN METABOLISM	358	60.1	236.9	29	98.5	13.2	192.7	42.9	92	13.3	68.4	29.9	25.5	3.4	53.1	6.6	-3.6	-2.7	-2.1
5372_at	HSP12	YFL014W	YFL014W Heat shock protein of 12 kDa. induced by heat. osmotic stress. oxidative stress a	STRESS	681.6	335	1316.4	95.4	708.3	209.7	855.5	208.1	3088.1	342	2276.7	194.2	926.4	100.3	2357.1	345.4	-3.3	-2.5	-2.5
5544_at	SPI1	YER150W	YER150W strong similarity to putative cell surface glycoprotein Sed1p	UNKNOWN	170.3	74.3	286.1	21.8	243.4	58.7	291.6	65.7	326.9	55.7	283.1	39.7	117.7	10.3	333.9	30.4	-2.8	-2.4	-2.8
5690_at	EDC2	YER035W	YER035W hypothetical protein	UNKNOWN	48.4	23.2	145.3	12.4	59.2	8.1	74.4	20.8	121.2	33.6	140.1	9.4	60	5.4	140.7	58.8	-2	-2.3	-2.3
5735_at	GLC3	YEL011W	YEL011W 1,4-glucan-6-(1,4-glucano)-transferase	CELL WALL MAINTENANCE	415.2	91.9	317.1	36.8	241.7	14	200.5	56.9	323.1	48.7	351.6	144.2	108.7	44.5	329.3	100.1	-3	-3.2	-3
5786_f_at	PAU2	YEL049W	YEL049W member of the seripauperin protein/gene family (see Gene_class PAU)	UNKNOWN	614.1	107.1	276.6	42.1	305.5	8.7	1577.5	588.1	329.7	231.6	80.5	12.9	38.8	2.7	78.9	18.9	-8.5	-2.1	-2
6128_f_at	HXT7	YDR342C	YDR342C Hexose transporter	TRANSPORT	3229.6	606	1272.9	97.8	649.7	17.8	1460.7	173.6	2254.9	201.2	1340.2	110.7	621.9	131.8	1420.4	88.5	-3.6	-2.2	-2.3
6129_f_at	HXT6	YDR343C	YDR343C Hexose transporter	TRANSPORT	3297.3	1034.2	1591.8	124.5	784.4	38.3	1839.1	138	2086.8	527.7	1770.1	131.9	816.6	88.8	1844.5	251.5	-2.6	-2.2	-2.3
6171_at	SUR2	YDR297W	YDR297W Syringomycin response protein 2	SPHINGOLIPID METABOLISM	439.8	56.6	302.1	59.8	311.2	47.4	428.6	34.5	176.4	51.1	259.6	30.2	83	4	172.5	50.2	-2.1	-3.1	-2.1
6394_at		YDR070C	YDR070C hypothetical protein	UNKNOWN	45.5	36.7	39.4	0.8	24.7	9.1	23.7	4	1056	188.3	112.5	30.2	16.3	3.1	73.1	4.4	-64.8	-6.9	-4.5
6483_at	DIA3	YDL024C	YDL024C strong similarity to acid phosphatase	UNKNOWN	19.9	4.9	54	15.7	51.2	1.6	84.1	10.5	42.9	7.7	42.8	2.1	18	6.2	36	4.7	-2.4	-2.4	-2
6486_at	GPM2	YDL021W	YDL021W Similar to GPM1 (phosphoglycerate mutase)	GLYCOLYSIS	174.6	60.6	203.3	30.7	103.5	11.1	269.8	28.3	66.2	5.6	125.7	7.6	26.2	9.2	90.8	12.9	-2.5	-4.8	-3.5
7324_at		YBR056W	YBR056W Homolog to glucan-1,3--glucosidase (EC 3.2.1.5\; S. cerevisiae) 2	UNKNOWN	49.9	19.8	128.8	27.6	40.6	10.5	57.4	2.6	68.2	12	74	15.4	31.8	13.1	65.4	7.9	-2.1	-2.3	-2.1
7604_at	GPH1	YPR160W	YPR160W Glycogen phosphorylase	GLYCOGEN METABOLISM	450.9	71.7	441.3	43.3	77.1	9.8	267.1	44.9	303.6	44.3	431.6	100.6	35	2.4	393.6	33.3	-8.7	-12.3	-11.2
7610_at	CTR1	YPR124W	YPR124W High affinity copper transporter into the cell. probable integral membrane protein	TRANSPORT	114.2	26.1	76.1	9.7	57.8	15.7	64.9	5.7	277.3	42.6	358.2	81.8	60.8	8.6	183	20.7	-4.6	-5.9	-3
7831_at	PDR12	YPL058C	YPL058C multidrug resistance transporter	DRUG RESISTANCE	70.4	31.6	114.3	19.8	61.7	6.9	65.9	22.6	637.9	155.7	523.1	92.3	217.5	15.3	467.6	55.3	-2.9	-2.4	-2.1
7843_at	SSU1	YPL092W	YPL092W sensitive to sulfite	SULFITE TOLERANCE	217.5	41	238	45.2	84.5	6.3	308.5	30.4	449.7	149.5	287.5	10.9	60.1	4.7	193.8	21.3	-7.5	-4.8	-3.2
7928_at	UIP4	YPL186C	YPL186C weak similarity to Xenopus protein xlgv7	UNKNOWN	34.9	24.1	86.9	22.7	24.2	4.9	26.2	4.6	318.2	73.7	143.8	13.5	23.2	0.2	47.8	4.7	-13.7	-6.2	-2.1
7974_at	USV1	YPL230W	YPL230W Up in StarVation	UNKNOWN	51.9	33.8	43.9	8.1	23.9	5	13	2.4	157.5	30.4	53.1	21.8	21.2	2.2	50.8	12.7	-7.4	-2.5	-2.4
8188_at	TYE7	YOR344C	YOR344C TYE7. a 33 kDa serine-rich protein. is a potential member of the basic region/he	GLYCOLYSIS	33.5	14.9	38.6	14.9	35.4	7.7	93.9	26.2	41.2	2	36.4	5	12	1.8	59	18.8	-3.4	-3	-4.9
8192_at	PUT4	YOR348C	YOR348C putative proline-specific permease	TRANSPORT	16.9	6.6	176	26.5	28.1	6.5	21.7	8.9	1262.8	181	2557.3	204	138.5	44.6	518.2	179.5	-9.1	-18.5	-3.7
8375_at		YOR173W	YOR173W strong similarity to YLR270w	UNKNOWN	148.7	33.2	183	22.9	123.7	24.5	114	16.1	452.6	55.2	280.8	48.9	107	9.3	226	29.3	-4.2	-2.6	-2.1
8599_at		YOL053C	YOL053C DNA Damage Responsive	UNKNOWN	678.1	212.9	817.1	71.6	352	51.2	419	85.2	2902.8	1023.5	1288.4	124.2	274.9	17.6	2762.2	730.5	-10.6	-4.7	-10
8663_at	MDH2	YOL126C	YOL126C cytosolic malate dehydrogenase	TCA CYCLE	69.4	31.3	108	17.5	79.8	5.2	73.5	17	722.4	124.9	150.6	12.9	56.2	4.7	136.3	18.4	-12.9	-2.7	-2.4
8727_at		YOL153C	YOL153C strong similarity to Cps1p	UNKNOWN	12	2.2	26.4	4.9	12	2.3	12	1.7	31.9	2.8	27.9	3.1	12.5	1.8	29.6	11.5	-2.5	-2.2	-2.4
8788_at	SOL1	YNR034W	YNR034W hypothetical protein	TRNA SPLICING. PUTATIVE	929.9	166.7	405.9	61.1	144.5	18.2	362.3	76.4	835.7	234.4	233.8	20.4	42.3	3.1	92.4	6.7	-19.8	-5.5	-2.2
9287_s_at		YMR322C	YMR322C strong similarity to YPL280w. YOR391c and YDR533c	UNKNOWN	32.5	18	59.6	5.5	46.5	3.4	70.5	13.1	135.3	14	83	5.7	18.1	2.4	51.5	9.3	-7.5	-4.6	-2.8
9341_at		YMR291W	YMR291W similarity to ser/thr protein kinase	UNKNOWN	112.9	38.5	62.1	5.6	44.3	0.7	106.2	22.9	104.2	33.6	42.5	14.8	13.7	1	89.2	13.5	-7.6	-3.1	-6.5
9388_at	GAD1	YMR250W	YMR250W similarity to glutamate decarboxylases	UNKNOWN	20.3	6	56	14	22.5	3.2	28	4.9	47.8	16.7	64.5	18.3	13.4	1.5	105.7	9.3	-3.6	-4.8	-7.9
9547_at	PGM2	YMR105C	YMR105C Phosphoglucomutase	GLYCOLYSIS	326.4	156.4	237.1	42	120.5	17.4	197.9	57.9	325.8	4.9	214.1	84	47.5	6	221	28.4	-6.9	-4.5	-4.7
9743_at	TSL1	YML100W	YML100W 123 kD regulatory subunit of trehalose-6-phosphate synthase\/phosphatase com	TREHALOSE METABOLISM	92.9	13	221.5	2.6	116.5	25.2	147.7	18.8	261.8	25.3	322.8	108.1	115.2	9.7	276.9	15.2	-2.3	-2.8	-2.4
9902_at	CTR3	YLR411W	YLR411W Copper Transporter	TRANSPORT	61.7	22	40.9	9.2	23.4	5.5	34.9	12	1039.9	139.1	439	29.3	26.6	5.5	345.3	57.2	-39.1	-16.5	-13

Up-regulated under C-Lim Anaerobic only (FC = fold change, ANA = anaerobic, A = aerobic)

Probe Set	Gene name	systematic name	functional description	cellular function	C-Lim ANA Average	C-Lim ANA Stdev	N-Lim ANA Average	N-Lim ANA Stdev	P-Lim ANA Average	P-Lim ANA Stdev	S-Lim ANA Average	S-Lim ANA Stdev	C-Lim A Average	C-Lim A Stdev	N-Lim A Average	N-Lim A Stdev	P-Lim A Average	P-Lim A Stdev	S-Lim A Average	S-Lim A Stdev	FC C-Lim ANA vs N-Lim ANA	FC C-Lim ANA vs S-Lim AN	FC C-Lim ANA vs P-Lim ANA
10253_at		YLR089C	YLR089C strong similarity to alanine transaminases	UNKNOWN	1255.2	256.5	534.6	33.3	448.5	77	442.6	62.8	805.2	11.4	1008.2	67.2	582.6	50.5	633.7	59.1	2.3	2.8	2.8
10290_at	COX12	YLR038C	YLR038C subunit VIb of cytochrome c oxidase	OXIDATIVE PHOSPHORYLATION	1168.6	252.6	386.2	105	364.7	44.8	436	54	2507.4	46.2	1928.2	20.5	2092.8	59.2	1956.4	168.5	3	3.2	2.7
10390_at	SDH2	YLL041C	YLL041C Succinate dehydrogenase (ubiquinone) iron-sulfur protein subunit	TCA CYCLE. OXIDATIVE PHOSPHORYLATION	1101.3	22.7	480.5	49.1	523.8	106.6	503.4	21.4	2171.7	68.4	1282.2	37.7	1616.4	208.4	1875.7	290.6	2.3	2.1	2.2
10725_at	SDH1	YKL148C	YKL148C flavoprotein subunit of succinate dehydrogenase	TCA CYCLE. OXIDATIVE PHOSPHORYLATION	273.8	52.2	117.1	24.7	100.2	22.3	88.7	12.9	608.5	103.9	280.5	35.5	267.4	20.5	312.5	49.8	2.3	2.7	3.1
10860_s_at	HXT16	YJR158W	YJR158W hexose transporter	TRANSPORT	84.2	38.3	12	2.3	12	6.8	12	2	13.5	6.1	12	3.1	12	3.6	15.7	3.5	7	7	7
10977_at	CYC1	YJR048W	YJR048W iso-1-cytochrome c	OXIDATIVE PHOSPHORYLATION	179.6	82.8	12	2.5	12	1.2	12	5.6	1608.9	226.9	940.9	93.8	1248.6	74.7	1611.3	155	15	15	15
11264_f_at		YAR075W	YAR075W strong similarity to IMP dehydrogenases	UNKNOWN	1465.7	396.1	477.3	70.2	512.7	59.1	433.9	152.4	348.5	109.7	556.1	24.7	416.8	55.8	484.9	97.2	3.1	2.9	3.4
4149_at	MAM33	YIL070C	YIL070C mitochondrial acidic matrix protein	RESPIRATION	523.1	5.9	192.6	6.2	230.1	42	254.2	85	488.7	3.9	385.9	61	304.8	17.4	468.1	59.8	2.7	2.3	2.1
4323_f_at	IMD2	YHR216W	YHR216W IMP dehydrogenase\; probable PUR5 gene	NUCLEOTIDE METABOLISM	1390.9	164.9	379.3	28.1	398.3	82.3	261.7	26	262.2	50.9	586.4	30.9	367.6	15.6	411.4	62	3.7	3.5	5.3
4481_at	COX6	YHR051W	YHR051W subunit VI of cytochrome c oxidase	OXIDATIVE PHOSPHORYLATION	663.7	42.4	277.4	47.9	292	31.8	290.3	93	1494.6	252.7	1031.6	84.3	1191.2	69.4	1234.6	140.3	2.4	2.3	2.3
4518_at	OSH7	YHR001W	YHR001W 8.5 kDa subunit of the ubiqunol-cytochrome c oxidoreductase complex	OXIDATIVE PHOSPHORYLATION	305.6	52.1	94.6	23.4	77.3	5.1	93	9.4	799	66.7	662.9	21.1	766.1	91.3	689.3	114.9	3.2	4	3.3
4523_at	GPA1	YHR005C	YHR005C May act cooperatively with Mrs5p in mitochondrial protein import or other related essential	MITOCHONDRIAL PROTEIN TARGETING	833	86	392.2	78.9	400.7	11.9	338.3	30	775.9	93.7	614.8	80.5	629.6	9.7	544.2	55.8	2.1	2.1	2.5
5000_i_at	RPS25A	YGR027C	YGR027C Ribosomal protein S25A (S31A) (rp45) (YS23)	PROTEIN SYNTHESIS	801.3	25.3	316.9	11	341.5	92.7	312.8	44.3	562.6	97	485.1	12.7	476.4	51.7	412.9	99.6	2.5	2.3	2.6
5142_i_at	RPL9A	YGL147C	YGL147C Ribosomal protein L9A (L8A) (rp24) (YL11)	PROTEIN SYNTHESIS	414.6	96.8	186.8	39.4	186.3	47.2	162.4	29.4	234.1	42.5	194.4	44.8	223.6	59.8	197.3	64.6	2.2	2.2	2.6
5173_at	SUT1	YGL162W	YGL162W Involved in sterol uptake	TRANSPORT	168.4	14.5	53	7.3	75.6	19.2	67.4	9.4	37.5	8.7	20.6	3.8	37.3	1.2	17.3	2.4	3.2	2.2	2.5
5188_at	COX13	YGL191W	YGL191W subunit VIa of cytochrome c oxidase. may specifically interact with ATP	OXIDATIVE PHOSPHORYLATION	644.9	127	172.2	23.3	280.1	41.3	309.5	66.5	945.9	85.6	786.9	24.8	801.4	17.2	750.7	34.3	3.7	2.3	2.1
5193_at	COX4	YGL187C	YGL187C subunit IV of cytochrome c oxidase	OXIDATIVE PHOSPHORYLATION	568.5	44.6	142.4	16.2	138.7	9.9	151.3	41.2	1225.6	116.1	888.9	48.7	938.7	49.1	1026.2	78.3	4	4.1	3.8
5332_at	QCR6	YFR033C	YFR033C ubiquinol-cytochrome c oxidoreductase subunit 6 (17 kDa)	OXIDATIVE PHOSPHORYLATION	885.8	87.6	314.8	46.9	386.9	13.9	307.5	53.4	1371.8	40.7	1101.7	137.6	1113.9	41.6	1271	89.6	2.8	2.3	2.9
5766_at	RIP1	YEL024W	YEL024W Rieske iron-sulfur protein of the mitochondrial cytochrome bc1 complex	RESPIRATION	692.1	66.5	201.9	78.4	287.7	3.4	334.3	12.1	1615	197.5	1136.3	59.8	1323.2	69	1270.6	205.3	3.4	2.4	2.1
5953_at	QCR7	YDR529C	YDR529C ubiquinol-cytochrome c oxidoreductase subunit 7 (14 kDa)	RESPIRATION	1450.8	374.7	609.6	68.7	516.7	94.4	474.8	34.2	1984.1	277.6	1475.6	38.9	1630.8	61.2	1505.9	9	2.4	2.8	3.1
6128_f_at	HXT7	YDR342C	YDR342C Hexose transporter	TRANSPORT	3229.6	606	1272.9	97.8	649.7	17.8	1460.7	173.6	2254.9	201.2	1340.2	110.7	621.9	131.8	1420.4	88.5	2.5	5	2.2
6279_at	SDH4	YDR178W	YDR178W succinate dehydrogenase membrane anchor subunit	TCA CYCLE. OXIDATIVE PHOSPHORYLATION	1131	91.6	534.1	18.9	387.3	22	532.6	16.9	1668.7	82.2	972.8	110.1	747.1	137.1	1131.7	2.9	2.1	2.9	2.1
6598_at	RPP1B	YDL130W	YDL130W ATPase stabilizing factor	PROTEIN SYNTHESIS	910.6	152.1	436.3	43	364.9	12.6	441.7	41	1324.5	135.6	595.2	49.3	410.7	18.8	747.3	78.5	2.1	2.5	2.1
6646_at	DLD1	YDL174C	YDL174C mitochondrial enzyme D-lactate ferricytochrome c oxidoreductase	PYRUVATE METABOLISM	608.7	64	209.1	8.8	188.9	35.8	198.2	13.2	921	117.8	345.6	24.8	583.3	78.7	682.4	116.1	2.9	3.2	3.1
6684_at	INH1	YDL181W	YDL181W ATPase inhibitor	ATP SYNTHESIS	352.9	102.6	102	17.3	41.1	2.5	83.2	14.5	798.8	152.7	516.7	90.5	370.6	113.2	706.3	164.1	3.5	8.6	4.2
6907_at	AGP1	YCL025C	YCL025C (AGP1) Broad substrate range amino acid permease with high affinity for asparagine and g	TRANSPORT	762.9	56.7	155.9	23.1	363.4	68.5	346.5	31.2	87.2	28.6	208.6	17.3	240.4	116.9	353.1	52.1	4.9	2.1	2.2
7344_i_at	RPL4A	YBR031W	YBR031W Ribosomal protein L4A (L2A) (rp2) (YL2)	PROTEIN SYNTHESIS	369.7	84.4	157.9	53.4	109.2	36.8	95.9	20.7	196.9	61.3	164.2	15.6	155.8	35.3	159.8	51.5	2.3	3.4	3.9
7543_at	QCR2	YPR191W	YPR191W 40 kDa ubiquinol cytochrome-c reductase core protein 2	OXIDATIVE PHOSPHORYLATION	321.6	78.6	113.4	10.7	106.9	16.1	137.6	3.8	808	99.5	571.6	97.7	709.4	31.9	986.2	22.7	2.8	3	2.3
7727_at	ATP20	YPR020W	YPR020W hypothetical protein	ATP SYNTHESIS	79.7	15.4	34.1	3.8	26.9	0.5	30	6.1	276	71.3	173.3	16	194.6	21.4	187.4	40.4	2.3	3	2.7
7812_at	ATP4	YPL078C	YPL078C F(1)F(0)-ATPase complex delta subunit. mitochondrial	ATP SYNTHESIS	539.2	100.2	240.5	6.7	252.3	15.3	236	13.1	813.3	143.5	580.2	28.6	653.3	61.6	551.6	38.2	2.2	2.1	2.3
8024_at	ATP15	YPL271W	YPL271W nuclear gene for ATP synthase epsilon subunit	ATP SYNTHESIS	981.5	174.4	477.1	79	356.8	59.7	291.9	16.2	1209.8	84.3	804.3	43.4	909.7	110.3	926	27.3	2.1	2.8	3.4
8269_f_at	RPS10A	YOR293W	YOR293W Ribosomal protein S10A	PROTEIN SYNTHESIS	1923.9	133.3	912.9	220.7	830.2	187.1	783.5	183.7	1366	206.2	1008.3	212.9	1119	154.4	975.5	242.1	2.1	2.3	2.5
8935_at	COX5A	YNL052W	YNL052W Cytochrome-c oxidase chain Va	OXIDATIVE PHOSPHORYLATION	321.3	14.6	88.3	11.6	58.4	8.7	85.1	9.6	1167.2	265.6	800.7	70.2	940.2	113.8	1004.3	38.9	3.6	5.5	3.8
9500_at	NDE1	YMR145C	YMR145C mitochondrial cytosolically directed NADH dehydrogenase	UNKNOWN	115.7	23.4	45.7	6.1	28.7	4.4	40.9	3.4	1257.3	68.1	633.8	99.7	808.8	62.4	1153.7	124.9	2.5	4	2.8
9930_at	COX8	YLR395C	YLR395C Cytochrome-c oxidase chain VIII	OXIDATIVE PHOSPHORYLATION	1223.3	130.2	517.3	59.9	475	56.4	494.2	65.7	2121	160.1	1631.7	19.3	1785	71.4	1665	112.4	2.4	2.6	2.5

Down-regulated under C-Lim Anaerobic only (FC = fold change, ANA = anaerobic, A = aerobic)

Probe Set	Gene name	systematic name	functional description	cellular function	C-Lim ANA Average	C-Lim ANA Stdev	N-Lim ANA Average	N-Lim ANA Stdev	P-Lim ANA Average	P-Lim ANA Stdev	S-Lim ANA Average	S-Lim ANA Stdev	C-Lim A Average	C-Lim A Stdev	N-Lim A Average	N-Lim A Stdev	P-Lim A Average	P-Lim A Stdev	S-Lim A Average	S-Lim A Stdev	FC C-Lim ANA vs N-Lim ANA	FC C-Lim ANA vs S-Lim AN	FC C-Lim ANA vs P-Lim ANA
10012_at		YLR297W	YLR297W weak similarity to Vibrio vulnificus VvpC protein	UNKNOWN	53.1	27.2	143.9	15	115.5	8.5	161	50.1	119.8	43.3	83.1	11	75.2	7.3	107.5	17.9	-2.7	-2.2	-3
10021_at	UBC12	YLR306W	YLR306W Ubiquitin-conjugating enzyme	PROTEIN DEGRADATION. UBIQUITIN-MEDIATED	25.3	13	75.7	20.8	54.8	2.9	80	7.3	35	4	71.3	17	44.9	5.9	62.2	9	-3	-2.2	-3.2
10094_at	ERF2	YLR246W	YLR246W (ERF2) Protein involved in palmitoylation and localization of Ras2p	UNKNOWN	43.4	17.8	212.5	38.1	96.3	13.1	87.8	7	53	10.6	177	27	103	12.4	97.5	11.5	-4.9	-2.2	-2
10103_at		YLR211C	YLR211C hypothetical protein	UNKNOWN	30.2	12.5	73.5	12.8	112.4	19.1	95.8	24.9	68.8	5.3	68.5	16.2	69.2	7.5	52.4	3.3	-2.4	-3.7	-3.2
10106_at	FRE1	YLR214W	YLR214W Ferric (and cupric) reductase	IRON HOMEOSTASIS	15.7	8.1	41.7	10.5	38.4	2.4	36.4	1.9	46.4	10.9	43.5	5.4	32.7	2.9	45.2	8.4	-2.7	-2.5	-2.3
10118_at	BUR2	YLR226W	YLR226W hypothetical protein	UNKNOWN	17.8	12.2	38.3	15.8	53.8	8.9	43.7	1.4	34.1	3.9	46	4.7	62.5	12	57.3	14.8	-2.2	-3	-2.5
10119_at	ADY4	YLR227C	YLR227C hypothetical protein	UNKNOWN	21	8.5	78.1	17.8	42.8	7	44.7	2.2	44.8	4.7	60.6	7.7	36.5	5.2	36.6	13.9	-3.7	-2	-2.1
10192_at	SRN2	YLR119W	YLR119W suppressor of rna1-1 mutation	RNA EXPORT. PUTATIVE	24.7	12.7	68.4	15.1	67.6	10.4	51.2	8.9	43.1	3.2	68.4	25.7	53	3.4	42.9	5.5	-2.8	-2.7	-2.1
10217_at	CHA4	YLR098C	YLR098C DNA-binding transcriptional activator or CHA1	SER/THR METABOLISM	17.5	7.5	49.6	19.1	44.3	4.4	36.8	2	26.6	3	44.5	19.7	38	4.7	35	2.9	-2.8	-2.5	-2.1
10260_at		YLR051C	YLR051C similarity to human acidic 82 kDa protein	UNKNOWN	51.1	32.7	104.7	44	133.9	14.6	121.4	13.3	102.5	25	157.8	36.8	179	34.6	125.9	24	-2.1	-2.6	-2.4
10318_at		YLR022C	YLR022C similarity to C.elegans and M.jannaschii hypothetical proteins	UNKNOWN	40.7	19	114.5	5.1	116.5	28.4	97.6	17.6	40.7	2.4	79	19.3	89	8.7	70.1	19.7	-2.8	-2.9	-2.4
10377_at		YLL053C	YLL053C similarity to water channel proteins	UNKNOWN	75	23.3	157.4	12.9	172.9	33.2	171.5	47.5	1248.4	136.8	348.8	56.7	2716.5	272.8	2125.6	758.2	-2.1	-2.3	-2.3
10378_at	AQY2	YLL052C	YLL052C member of mip family transmembrane channels	TRANSPORT. WATER	23.9	6.8	56.1	7.2	77.3	10	86	18.2	418.7	78.5	130.1	5.7	1355	120.9	1075.8	594.3	-2.3	-3.2	-3.6
10444_at		YKR035C	YKR035C hypothetical protein	UNKNOWN	22.1	10.9	46.2	7.8	52.5	13.4	63	26.4	50.1	16.9	34.1	3.1	32.1	2.9	30.7	9.7	-2.1	-2.4	-2.8
10445_s_at	MNN4	YKL201C	YKL201C regulates the mannosylphosphorylation	PROTEIN GLYCOSYLATION	40.1	21	190.2	53.2	161.6	4.5	313.7	45.3	106.7	37.4	284.8	89.8	176.2	10.3	168	47.6	-4.7	-4	-7.8
10465_at	PRP16	YKR086W	YKR086W putative ATP-binding protein	MRNA SPLICING	25.2	13.3	64	12.1	55.4	11.3	56.8	7.9	56	15.5	67.2	12.5	34.9	3.6	49.5	7.6	-2.5	-2.2	-2.3
10485_at		YKR104W	YKR104W similarity to multidrug resistance proteins	UNKNOWN	12	6.1	42	8.9	32.1	8.4	31.4	2.4	21.4	5.6	47.1	9.1	24	5.2	45.6	6.3	-3.5	-2.7	-2.6
10488_at	LAS1	YKR063C	YKR063C May regulate expression of genes involved in bud formation and morphogenesis	MORPHOGENESIS. CYTOSKELETAL ASSEMBLY.	38.7	14.3	82	17.3	115.5	20.2	89.5	17.7	57.7	5	101.6	4.6	111.7	4.7	76.6	5.1	-2.1	-3	-2.3
10522_at	TRK2	YKR050W	YKR050W membrane protein\; low affinity potassium transport	TRANSPORT	15.4	11.1	68.5	9.1	46.1	8.3	63.7	10.2	44.4	3.9	48	8.6	46.6	5.5	116.5	6.1	-4.4	-3	-4.1
10531_at		YKR060W	YKR060W hypothetical protein	UNKNOWN	24.3	12.6	93	22.2	57.7	11.1	55.2	9.4	54.4	2.8	100.5	10.8	78.7	8.6	94.3	36.1	-3.8	-2.4	-2.3
10540_at		YKR023W	YKR023W similarity to S.pombe hypothetical protein SPAC23C4	UNKNOWN	14.9	6.7	32.3	7.8	37	5.4	30.6	2.7	23	4.4	46.6	11.2	37.1	1	33	4	-2.2	-2.5	-2.1
10545_at	SAP190	YKR028W	YKR028W Type 2A-related protein phosphatase	CELL CYCLE	100	27.7	243.9	36.1	214.6	46.8	211.7	52.7	118.3	14.2	236.1	46.7	228.5	17.9	196.9	51.4	-2.4	-2.1	-2.1
10586_at	MAK11	YKL021C	YKL021C contains four beta-transducin repeats	RNA PROCESSING/MODIFICATION	22.8	8.8	51.7	11.2	51.1	2.6	48.9	5.9	48.6	8.9	58.6	4.1	81.6	11.5	65.5	7.4	-2.3	-2.2	-2.1
10621_at		YKL031W	YKL031W hypothetical protein	UNKNOWN	18.5	8.6	52.4	13.1	50.3	4.7	77.4	7.5	12	8	33.4	2.9	18.6	6.3	34.4	16.2	-2.8	-2.7	-4.2
10664_at		YKL076C	YKL076C questionable ORF	UNKNOWN	45.1	19.6	174.1	15	144.4	19.1	111	10	73.6	15.7	172.2	25.3	159.7	35.4	104.8	18.6	-3.9	-3.2	-2.5
10666_at		YKL075C	YKL075C hypothetical protein	UNKNOWN	35.8	19.3	84.8	24.1	110.9	25.3	90.8	1.9	64.9	18.4	114.4	11.1	138.2	23.5	94.5	12	-2.4	-3.1	-2.5
10670_at	APN1	YKL114C	YKL114C major apurinic\/apyrimidinic endonuclease\/3'-repair diesterase	DNA REPAIR	75	39.6	172.6	44.3	171	15.5	211.8	2.6	147.1	13.5	162.5	6.5	202.1	29.6	168.8	14	-2.3	-2.3	-2.8
10673_at		YKL111C	YKL111C questionable ORF	UNKNOWN	12.4	4.1	31.3	6.4	40.4	7.1	45	4.8	25.8	12	18.5	4.7	21.6	2.5	16	6.4	-2.5	-3.3	-3.6
10696_at	RMA1	YKL132C	YKL132C probable folyl-polyglutamate synthetase	UNKNOWN	14.6	6.6	63.4	14.8	37.3	5.8	42.6	6.6	18.4	3.3	51.8	8.6	25.9	5.3	41.9	2.4	-4.3	-2.6	-2.9
10713_at	PRR1	YKL116C	YKL116C probable serine\/threonine-specific protein kinase (EC 2.7.1.-)	UNKNOWN	21.8	9.7	52.6	6	55.5	18.8	55.5	16.3	39.6	3.2	58.6	5	53.8	1.8	39.3	3.7	-2.4	-2.5	-2.6
10746_at	SNU114	YKL173W	YKL173W U5 snRNP-specific protein related to EF-2	MRNA SPLICING	20.7	10.2	54.1	11.3	42.6	5.6	43	10.3	46.4	10.7	79.8	7.9	51.5	6.4	60.6	15.4	-2.6	-2.1	-2.1
10857_at	AAD10	YJR155W	YJR155W Hypothetical aryl-alcohol dehydrogenase (AAD)	UNKNOWN	74.7	40.3	197.6	34.4	164.7	28.8	157.9	14.3	121.1	6	110.2	16.1	86.3	3.8	88.3	15.8	-2.6	-2.2	-2.1
10975_at	TAH11	YJR046W	YJR046W weak similarity to Xenopus vimentin 4	UNKNOWN	34	12	76.8	2.5	129.1	16.4	101.1	5.1	66.6	19.4	81.8	25.9	139.4	15	62.7	15.8	-2.3	-3.8	-3
10983_at		YJR054W	YJR054W similarity to hypothetical protein YML047c	UNKNOWN	41.9	12.8	86	16.3	92.2	6.5	85.1	11.8	41.7	6.3	66.6	10.3	69.1	6.6	44.8	5.6	-2.1	-2.2	-2
11000_at	LSM8	YJR022W	YJR022W Sm-like protein	MRNA SPLICING	43	9.3	90.4	13.1	93.9	26.7	106	27.9	84.5	9.8	125.3	24.9	96.2	21.8	68.4	16.7	-2.1	-2.2	-2.5
11033_at	A SPC1	YJR010C	YJR010C Homologue of the SPC12 subunit of mammalian signal peptidase complex. Protein is impc	SECRETION	16.4	5.6	42.3	20.1	36.6	7.7	36.2	1.1	22.3	10.4	22.6	10.1	19.5	2.7	17.3	7	-2.6	-2.2	-2.2
11043_at	APS3	YJL024C	YJL024C similar to Aps1p and mammalian small subunit (sigma-2 adaptin) of plasma membrane-ass	VACUOLAR PROTEIN TARGETING	18.2	4.9	41.5	11.7	42.1	4.6	37.1	6.1	27.4	4.3	40.8	7.1	45	12.4	34.8	4	-2.3	-2.3	-2
11051_at		YJL017W	YJL017W hypothetical protein	UNKNOWN	20	11.3	89.2	38.6	61.1	6.4	86.3	16.1	34.4	10.6	52	6.1	21.8	2.5	41.5	10.1	-4.5	-3.1	-4.3
11064_at		YJL049W	YJL049W hypothetical protein	UNKNOWN	50.5	28.7	122.4	37.1	136.1	12.2	131.1	1.9	113.6	14.6	159.6	19.6	170.1	28.4	129.9	17.3	-2.4	-2.7	-2.6
11108_at	KHA1	YJL094C	YJL094C similarity to E.hirae NaH-antiporter NapA	UNKNOWN	75.6	31.7	263.2	65.2	275.3	28.7	206.1	15.3	143.8	23.5	211.1	2.8	154.6	56.5	117.2	21.4	-3.5	-3.6	-2.7
11111_at		YJL091C	YJL091C weak similarity to human G protein-coupled receptor	UNKNOWN	143.9	49.5	347.4	83	317.8	50.9	390.1	20.1	167.3	34.2	306.5	34.2	246.2	39	219	25.4	-2.4	-2.2	-2.7
11169_at	NIT2	YJL126W	YJL126W Nit2 nitrilase	UNKNOWN	36.5	13.6	80	10.5	82.4	14	90.7	5.9	66.8	8.4	71.6	6.2	71.7	5.8	66.8	7.9	-2.2	-2.3	-2.5
11182_at	SSY5	YJL156C	YJL156C sensitive to sulfonylurea herbicides on complex media (YPD)	TRANSPORT. AMINO ACID (PUTATIVE)	38.6	12.7	91.7	21.6	110.8	23.1	106.5	6.3	85.4	5	148	1.7	116.3	12.5	116.2	10.1	-2.4	-2.9	-2.8
11191_at		YJL147C	YJL147C weak similarity to C.elegans hypothetical protein C43G2.4	UNKNOWN	19.6	2.9	44.1	4.3	46	14.2	42.3	6.7	62.6	8.3	79	13.6	82.2	10.1	64.3	19.7	-2.3	-2.4	-2.2
11295_r_at		YAR033W	YAR033W membrane protein	UNKNOWN	12	6.8	28.2	17.7	50.2	14.6	39.7	0.7	12	2.6	19.7	6.1	17.6	6.3	22	1.7	-2.4	-4.2	-3.3
11326_at	SWD1	YAR003W	YAR003W beta transducin domain	UNKNOWN	55.3	31.2	154.2	61.1	138.3	21.1	185.3	13.5	59.9	19.9	105.1	27.5	95.1	12.1	106.6	10.1	-2.8	-2.5	-3.3
11328_at	SEN34	YAR008W	YAR008W 34kDa subunit of the tetrameric tRNA splicing endonuclease	TRNA SPLICING	28.3	10.6	80	11.5	73.2	11.7	64.2	4.9	45.8	13.1	74.1	14.1	81.7	4.4	58.9	3.2	-2.8	-2.6	-2.3
11340_at		YAL027W	YAL027W hypothetical protein	UNKNOWN	16.4	11.6	48.7	10.9	44.3	12.1	51.4	8.9	87.1	2.5	58.6	2.9	61.4	5.2	45.8	4.3	-3	-2.7	-3.1
11343_at	LTE1	YAL024C	YAL024C putative GTP-exchange protein	CELL CYCLE	12.5	8.6	43.7	17.1	35.3	3.3	32.5	8.6	26.6	2.7	36.5	5.1	21.8	2.5	27	2.9	-3.5	-2.8	-2.6
11390_at	CNE1	YAL058W	YAL058W Calnexin and calreticulin homolog	SECRETION	15.5	1.4	40.3	4.8	38.2	8.6	40.9	14.3	29	11.5	30.4	5	25.6	6.3	31.8	6.7	-2.6	-2.5	-2.6
3625_at	COS10	YNR075W	YNR075W Protein with strong similarity to subtelomerically-encoded proteins such as Cos5p. Ybr302	UNKNOWN	12	4.8	28.6	18.1	44.5	7.4	67.4	7.7	12	2.6	12	3.4	12	1.1	12	4.5	-2.4	-3.7	-5.6
3789_s_at		YLL067C	YLL067C strong similarity to subtelomeric encoded proteins	UNKNOWN	12.9	5.7	186.7	194.1	55.3	4.5	117.9	10.4	31.6	40	30.2	19.4	16.9	2.9	205.2	185.4	-14.5	-4.3	-9.1
4056_at		YIR020C	YIR020C hypothetical protein	UNKNOWN	13.9	7.6	40.2	6.3	28.8	4.4	33	8.5	14.2	2.4	15.5	3.5	12	2	17	6.9	-2.9	-2.1	-2.4
4081_at		YIL001W	YIL001W similarity to S.pombe hypothetical protein. weak similarity to human ankyrin	UNKNOWN	19.8	10.2	43.5	10.9	42.6	11.2	40.9	8.7	42.3	4.1	55.1	8.3	50.5	9.4	37.9	11.6	-2.2	-2.1	-2.1
4192_at	RPI1	YIL119C	YIL119C inhibitor of ras	SIGNALING. RAS PATHWAY	19.3	7.4	76.4	27.7	91.3	9	79	13.3	80.9	18.9	232.3	42.3	114.1	9.9	129.2	49.6	-4	-4.7	-4.1
4221_at		YIL135C	YIL135C similarity to Ymk1p	UNKNOWN	78.5	4.7	261.7	26.2	220.9	77.3	275.3	57.9	73.7	6.5	197.1	11.5	126.7	24.9	170.9	43.2	-3.3	-2.8	-3.5
4363_at	KEL1	YHR158C	YHR158C protein containing kelch repeats. similar to YGR238c	UNKNOWN	28.6	12.4	59.3	20.4	71.9	18.2	58.3	5.5	27.3	14.1	92.8	10.8	73.5	14.3	52.2	9.1	-2.1	-2.5	-2
4377_at	SPC97	YHR172W	YHR172W spindle pole body component. associates in a complex with Spc98p and Tub4p perhaps a	CYTOSKELETON	31.1	10.1	90.9	43.1	89	20.3	72.4	7.3	37.4	8	78.6	6.3	57	17.1	62.3	12.7	-2.9	-2.9	-2.3
4388_at	SPS100	YHR139C	YHR139C sporulation-specific wall maturation protein	SPORULATION	12.1	5.2	31.7	2.7	26.4	4.8	30.3	2.8	310.8	232	42.1	8.5	18.5	6.2	49	13.3	-2.6	-2.2	-2.5
4448_at		YHR067W	YHR067W hypothetical protein	UNKNOWN	35	12.2	103.5	24.4	71.4	4.2	77.8	6.5	80.5	19.3	127.9	11.4	75.3	4.7	57.7	8	-3	-2	-2.2
4898_at	CLB1	YGR108W	YGR108W G(sub)2-specific B-type cyclin	CELL CYCLE	16.3	7.9	44.1	7.5	60.8	11.8	37.3	9.4	48.7	5.2	73.3	6	47.1	1.8	122.8	30	-2.7	-3.7	-2.3
5063_at	RNA15	YGL044C	YGL044C component of the cleavage and polyadenylation factor CF I involved in pre-mRNA 3'-end p	MRNA 3'-END PROCESSING	27.4	13	56.3	7.8	69.1	13.2	63.9	20.4	35.8	3	46.3	8	47	1.2	76.6	33.3	-2.1	-2.5	-2.3
5171_at		YGL164C	YGL164C similarity to S.pombe hypothetical protein SPAC31A2.10	UNKNOWN	32.1	11.5	129.2	71.4	197.6	66.2	157.7	60.7	60	18.8	147	90.6	97.6	8.5	104.6	38.7	-4	-6.2	-4.9
5183_at		YGL196W	YGL196W hypothetical protein	UNKNOWN	24.3	10.6	90.4	25.3	51.6	3.1	51	6.6	148.6	29.2	284.4	37	123.9	7.8	113.6	20.4	-3.7	-2.1	-2.1
5246_at	SDT1	YGL224C	YGL224C strong similarity to hypothetical protein YER037w	UNKNOWN	66.8	24.3	257.7	46	148.4	28.8	476.9	117	140.7	28.2	269.9	21	155.6	16.7	688.8	139	-3.9	-2.2	-7.1
5323_at		YFR026C	YFR026C hypothetical protein	UNKNOWN	16.1	7.5	54	23.2	36.6	8.9	56.8	26	19.7	3	28.1	4.9	28.9	4.7	33.7	9.7	-3.3	-2.3	-3.5
5324_at	ECO1	YFR027W	YFR027W hypothetical protein	MITOSIS. SISTER CHROMATID COHESION (PUT	27.4	9.8	89.9	9.1	72.6	12.4	63.8	12.7	50.5	14.9	75.2	11.3	96.4	17.6	61.1	19.5	-3.3	-2.6	-2.3
5381_at	BLM3	YFL007W	YFL007W weak similarity to Mms19p	DRUG RESISTANCE	33.9	20.7	125.4	77.4	118.7	3.4	153.4	21.6	97.9	12.4	62	20.2	77.7	5.8	97.6	57.3	-3.7	-3.5	-4.5
5543_at	PEA2	YER149C	YER149C Protein with coiled-coil domain	MATING	34.2	4.9	77.5	10.1	123.9	57.1	73.8	5.1	55.2	15.4	71.8	11.5	109	4.9	58.4	8.8	-2.3	-3.6	-2.2
5572_at	PMD1	YER132C	YER132C Paralog of MDS3	MEIOSIS	48.1	13.4	118.1	12.2	120.4	3.7	105.5	10.5	73.5	14.3	144.5	7.8	84.2	4.5	122.4	10.8	-2.5	-2.5	-2.2

5656_at	ACA1	YER045C	YER045C weak similarity to transcription factor Sko1p	UNKNOWN	14.9	2.7	38.4	4.8	40.5	3.1	34.4	6.2	25.6	4.1	35	3.1	38.3	3	26.7	7.7	-2.6	-2.7	-2.3
5692_at	PHM8	YER037W	YER037W strong similarity to hypothetical protein YGL224c	UNKNOWN	12	1.8	35	3.7	29.2	3	249.1	86	32.9	6.3	62.6	11.4	22.8	3.3	391	62.6	-2.9	-2.4	-20.8
5919_at		YDR540C	YDR540C hypothetical protein	UNKNOWN	22.9	13.2	56.6	15.2	46.5	2.6	67.5	8	12	0.5	30.2	3.4	13.7	1.7	22	8.2	-2.5	-2	-2.9
5982_at	TLG1	YDR468C	YDR468C tSNARE that affects a Late Golgi compartment	ENDOCYTOSIS	37.7	27.8	115	30.6	105.5	16.4	85.4	1.6	80.6	5.4	123.8	11	119.5	22.8	79.3	19.4	-3.1	-2.8	-2.3
5987_at	PRP3	YDR473C	YDR473C essential splicing factor	MRNA SPLICING	32.9	19.5	85.6	21.6	92	7	79.4	2.8	70.6	10.6	109.7	7.1	94.6	20.3	87.4	7.5	-2.6	-2.8	-2.4
6018_at		YDR459C	YDR459C weak similarity to YNL326c	UNKNOWN	24.1	11	66	14.5	51.3	6	49.3	12.9	32.7	5.7	62.7	7.7	47.8	12.4	59	6.4	-2.7	-2.1	-2
6106_at	CDC40	YDR364C	YDR364C Member of the beta transducin family	CELL CYCLE	29.2	12.9	69	12.4	72	18.8	61.1	4.8	56.7	8.6	79.3	20.5	73.1	13.3	83.9	18.1	-2.4	-2.5	-2.1
6112_at		YDR370C	YDR370C hypothetical protein	UNKNOWN	27.3	16.8	81.8	28.1	57.1	14.9	65.7	10.5	42.7	9	73.5	16.2	54.1	15	58.4	14.2	-3	-2.1	-2.4
6233_at		YDR222W	YDR222W strong similarity to hypothetical protein YLR225c	UNKNOWN	12	5.2	36.4	10.6	35.9	3.4	40	11.7	58.9	16.2	52	9	94.6	4.7	52.1	11.2	-3	-3	-3.3
6257_at	VPS64	YDR200C	YDR200C similarity to hypothetical protein YLR238w	UNKNOWN	27	11.7	57.2	11.9	56.9	4.2	54.9	10.1	50.1	16.6	96.7	7.2	66	6.6	55.3	5.7	-2.1	-2.1	-2
6266_at		YDR209C	YDR209C questionable ORF	UNKNOWN	27.4	17	71	17.4	87.5	25.2	137.3	12.7	16.3	2.5	34	8.3	31.4	11	29.1	6.1	-2.6	-3.2	-5
6346_at		YDR111C	YDR111C strong similarity to alanine transaminase	UNKNOWN	20.8	11.1	84	13.2	199.1	32.7	69.1	7.9	131.1	11.2	49.7	1.8	129.9	13.3	18.2	0.1	-4	-9.6	-3.3
6353_at	APC4	YDR118W	YDR118W subunit of the anaphase promoting complex (APC)	CELL CYCLE	22.6	8.8	68.6	17.7	46.7	2.3	50	12	61.9	26.4	60.9	11.8	51.6	4.4	49.4	16.6	-3	-2.1	-2.2
6358_at	INO2	YDR123C	YDR123C helix-loop-helix protein	PHOSPHOLIPID BIOSYNTHESIS	19.1	7.7	58.2	10.7	44.8	2.4	47.8	3.1	40.5	12.7	44	11.2	36.2	9.6	49.6	20.7	-3	-2.3	-2.5
6444_at	RAD28	YDR030C	YDR030C Protein involved in the same pathway as Rad26p. has beta-transducin (WD-40) repeats	DNA REPAIR	16.5	5.2	55.9	5	51.6	12	38.6	12.9	53.6	4.5	102.7	2.2	71.9	10.9	83.7	8.9	-3.4	-3.1	-2.3
6447_at	MRH1	YDR033W	YDR033W strong similarity to putative heat shock protein YRO2	UNKNOWN	464.6	26.5	1041	224.5	971	141.2	1522.8	64.1	657.5	74.8	1639.9	20.7	1196.9	24.8	1986.6	404.1	-2.2	-2.1	-3.3
6483_at	DIA3	YDL024C	YDL024C strong similarity to acid phosphatase	UNKNOWN	19.9	4.9	54	15.7	51.2	1.6	84.1	10.5	42.9	7.7	42.8	2.1	18	6.2	36	4.7	-2.7	-2.6	-4.2
6513_at	PRM7	YDL039C	YDL039C questionable ORF	UNKNOWN	67.3	7.2	198.4	36.1	187.9	19.7	189.1	20.5	38	7.2	93.9	30.2	47.1	3.6	103.4	13.8	-2.9	-2.8	-2.8
6514_at		YDL038C	YDL038C similarity to mucin proteins	UNKNOWN	18.3	7	73.7	14.5	108.4	3.4	114.4	33.2	20.5	4.8	36	1.1	20.2	4	39.3	17.6	-4	-5.9	-6.2
6762_s_at	KCC4	YCL024W	YCL024W Ser\/Thr protein kinase	UNKNOWN	12	7.7	29.8	7.4	30.7	3.6	33.9	6.4	21.4	4.8	31.9	2.6	21.8	6.6	33.5	7.8	-2.5	-2.6	-2.8
6851_at	MAK32	YCR019W	YCR019W Protein required for structural stability of L-A double-stranded RNA- (dsRNA-) containing	RNA PROCESSING/MODIFICATION	20.6	5.9	45.9	10.5	54	4.6	46.5	6.4	42.1	8.2	71.3	3.9	50.6	27.6	52	3	-2.2	-2.6	-2.3
6870_at	SGF29	YCL010C	YCL010C strong similarity to Saccharomyces pastorianus hypothetical protein LgYCL010c	UNKNOWN	25.3	10.6	53.1	31.1	59.4	17.7	92.5	9.5	27.2	11.9	36.1	13.1	49.7	23.5	61.7	66.6	-2.1	-2.3	-3.7
6905_at	FUS1	YCL027W	YCL027W serine\/threonine-rich membrane protein	MATING; CELL FUSION	25.6	10.2	74.8	9.5	72.7	3.7	117.1	19.4	23.9	8.1	75	19.2	37.5	7.4	33.6	3.3	-2.9	-2.8	-4.6
6922_at	KAR4	YCL055W	YCL055W May assist Ste12p in pheromone-dependent expression of KAR3 and CIK1	MATING RESPONSE	37	19.2	78	11.4	84.4	14	74.1	9.9	61.6	17.4	99	16.3	96.9	22.5	55.8	10.6	-2.1	-2.3	-2
7127_at	APG12	YBR217W	YBR217W autophagy	AUTOPHAGY	22.6	12.5	50.5	14.9	58	9.4	56.7	2.7	41.4	1.4	53.6	2.9	57.5	8	33.2	1.5	-2.2	-2.6	-2.5
7286_at		YBR063C	YBR063C Probable phosphopantethein-binding protein	UNKNOWN	29.9	11.3	78	14.3	66.9	5.5	67.4	5.9	31.8	3.9	67.1	6.3	65.3	3.7	50.1	10	-2.6	-2.2	-2.3
7382_at	RRN10	YBL025W	YBL025W Upstream activation factor subunit	TRANSCRIPTION	23.3	16	53.5	21.2	51.9	8.3	54.1	6	36.7	6.8	57.9	5.5	64.6	6.7	60.2	17.8	-2.3	-2.2	-2.3
7422_at	SSA3	YBL075C	YBL075C heat-inducible cytosolic member of the 70 kDa heat shock protein family	PROTEIN TRANSLOCATION	25.2	13.7	99.7	7.4	57.1	12.2	52.6	8.9	559.8	483.5	47.6	8.1	41.9	19.2	51.4	31.9	-4	-2.3	-2.1
7436_at		YBL060W	YBL060W hypothetical protein	UNKNOWN	15.6	5.7	74.4	20.7	35	3.4	55.1	8.2	28.4	7.2	42.8	1.9	47.2	5	61.9	25.3	-4.8	-2.2	-3.5
7463_at	NUP170	YBL079W	YBL079W Nucleoporin highly similar to Nup157p and to mammalian Nup155p (nup170 mutant can b	NUCLEAR PROTEIN TARGETING	24.3	19.4	94.6	37.8	49.9	25	54	5.1	45.9	5.4	77.6	13.3	53.8	20.6	68.5	19.4	-3.9	-2.1	-2.2
7464_at	AUT7	YBL078C	YBL078C Form a protein complex with Aut2p. to mediate attachment of autophagosomes to microtut	AUTOPHAGY	206.8	53.5	437.4	112.5	481.6	147.3	430.8	60.6	521.9	61.1	721.9	89.8	575.9	116.3	440.6	42.8	-2.1	-2.3	-2.1
7592_at	NCE102	YPR149W	YPR149W involved in secretion of proteins that lack classical secretory signal sequences	SECRETION. NON-CLASSICAL	508.6	247.4	1064.6	276.2	1195.4	121.2	1297.6	125.6	2303.3	593.7	1953	74.5	1771.8	144.4	2020.1	186.5	-2.1	-2.4	-2.6
7595_at		YPR152C	YPR152C hypothetical protein	UNKNOWN	30.4	11	66.7	7.7	76.9	22.7	66.3	16.4	66.1	17.3	44.2	6.3	194.6	147.1	79.6	27.5	-2.2	-2.5	-2.2
7601_at		YPR157W	YPR157W strong similarity to YGR141w	UNKNOWN	13.5	7.3	30.3	6.1	32.9	3.5	44.3	3.4	15.4	2.1	12	1.8	19.7	3.5	14.8	4.5	-2.3	-2.4	-3.3
7602_at		YPR158W	YPR158W similarity to YGR142w	UNKNOWN	33.9	17.6	90	11.3	87.7	6.7	71.6	7.9	74.7	11.8	98	1.4	139.1	5.3	68.7	19.2	-2.7	-2.6	-2.1
7631_at	SNT309	YPR101W	YPR101W splicing factor	MRNA SPLICING	31.1	19.3	76.1	32.1	66	18.6	75.7	5.7	52	11.8	91.3	11.2	93.7	18.1	59.5	15	-2.5	-2.1	-2.4
7651_at	CLB2	YPR119W	YPR119W G(sub)2-specific B-type cyclin	CELL CYCLE	12	4.4	27.9	4	31.4	1.5	29.2	3.3	12	2.7	24.6	2.5	25	4.9	21.3	3.1	-2.3	-2.6	-2.4
7660_at		YPR084W	YPR084W hypothetical protein	UNKNOWN	23.4	7.4	55.4	19.6	51.3	11.4	48.8	6.2	46.7	6.9	49.1	10.7	37	4.7	54.8	9.9	-2.4	-2.2	-2.1
7686_at	UBA3	YPR066W	YPR066W ubiquitin-like protein activating enzyme	PROTEIN DEGRADATION. RUB1P-MEDIATED	13.6	2.4	40.2	10.3	31.4	7.3	39.9	7.4	24.6	2	38.7	6.4	44.9	2.5	47	15	-3	-2.3	-2.9
7711_at	MCM16	YPR046W	YPR046W Required for chromosome segregation	MITOSIS.CHROMOSOME SEGREGATION	31.2	9.5	68.3	8.3	63.9	6.6	64	16	67.9	13.3	97.1	25.1	124.8	19.4	79.4	9.6	-2.2	-2	-2.1
7719_at		YPR053C	YPR053C questionable ORF	UNKNOWN	19.2	11.8	50.3	6.6	42.5	2.5	40.5	5.4	35.7	11.6	41.9	3.6	38.7	2.4	57.6	3.1	-2.6	-2.2	-2.1
7755_at		YPR003C	YPR003C similarity to sulphate transporter proteins	UNKNOWN	12.3	4.6	42.1	21	28	13.3	35.4	9.2	27.6	4.6	36.9	5.9	27.1	7.4	32.5	3.6	-3.4	-2.3	-2.9
7908_at		YPL162C	YPL162C hypothetical protein	UNKNOWN	12	8.5	43.1	10.3	33.9	8.4	52.1	4.5	39.3	9.6	41.5	12	36.3	5.3	52.7	23.1	-3.6	-2.8	-4.3
7911_at		YPL159C	YPL159C weak similarity to YPR151c	UNKNOWN	20.6	4	63.5	22.1	48.2	12.7	45.7	3.2	63.9	15.4	61.7	1.8	69	9.5	81	27.5	-3.1	-2.3	-2.2
7971_at	NSL1	YPL233W	YPL233W hypothetical protein	UNKNOWN	17.2	3.8	35.3	9.9	40.4	6	46.7	3.3	25.9	3.4	41.1	17.5	30.2	0.4	48.2	1.8	-2.1	-2.4	-2.7
8145_s_at		YOR390W	YOR390W nearly identical to YPL279c	UNKNOWN	12	8.1	28.2	9.9	26.1	6.3	30.5	4.2	15.9	8.1	36.9	9.5	32.4	1.2	47.6	17.3	-2.4	-2.2	-2.5
8218_at	PDR10	YOR328W	YOR328W Putative ABC transporter highly similar to Pdr5p	TRANSPORT	51.2	15.5	220.2	24.9	177.1	30.2	171	27	205.2	78.4	138.3	29	305.1	72.4	112.7	19.8	-4.3	-3.5	-3.3
8348_i_at		YOR192C	YOR192C strong similarity to Thi10p	UNKNOWN	41.5	14.6	86.8	37.8	92.1	18.9	315.8	38.4	57.2	18	44.2	6.3	24.6	4.2	52.2	34	-2.1	-2.2	-7.6
8351_at	TOA1	YOR194C	YOR194C Transcription factor IIA. large chain	TRANSCRIPTION	38.1	21.3	92.9	6.1	83.4	7.3	87.1	6.3	64.8	2.2	94.1	4.7	96.4	7.4	98.7	14.2	-2.4	-2.2	-2.3
8408_at		YOR161C	YOR161C similarity to C.elegans cosmid F35C8	UNKNOWN	12	4.7	66.7	6.5	27.2	2.1	51.8	10.6	125.6	57.5	164	34.3	59	7	138	29.2	-5.6	-2.3	-4.3
8422_at	ORT1	YOR130C	YOR130C mitochondrial integral membrane protein	ARGININE METABOLISM	67.6	26.8	150	15.2	154.9	21.8	144	20.3	87.7	18	142.9	10.9	280.2	15.6	83	6.8	-2.2	-2.3	-2.1
8487_at		YOR059C	YOR059C weak similarity to YGL144c	UNKNOWN	153.9	68.7	435.4	67.9	416.8	54.6	342	44.6	211	10.9	382.6	88.4	714.6	40.5	293	41.7	-2.8	-2.7	-2.2
8490_at		YOR062C	YOR062C strong similarity to YKR075c	UNKNOWN	28.5	7.8	111.3	16.6	85.4	16.3	57.1	7.7	110.6	7	158.2	32.2	104.8	17.9	152	55.2	-3.9	-3	-2
8524_at		YOR051C	YOR051C weak similarity to myosin heavy chain proteins	UNKNOWN	77.7	14.6	201.3	22.5	168.9	8.6	190.6	24.8	77.2	9.2	163.9	22	134	12	151.3	25.3	-2.6	-2.2	-2.5
8546_at	CIN5	YOR028C	YOR028C bZIP protein. can activate transcription from a promoter containing a Yap recognition site	SALT TOLERANCE	20	10.9	136.9	43.6	128.5	14.8	183.5	20.5	53.4	11.3	122.1	16.3	58.4	7.3	100.1	10.6	-6.9	-6.4	-9.2
8627_at		YOL070C	YOL070C hypothetical protein	UNKNOWN	27	16.9	59	6.2	65	7.3	56	6.1	67.2	13.8	73.3	12	91.1	3.1	47.4	1	-2.2	-2.4	-2.1
8638_at	WSC3	YOL105C	YOL105C Putative integral membrane protein containing novel cysteine motif. Similarity to SLG1 (W	SIGNALING	35.1	20.7	95.6	10	71.8	12.9	79.2	10.1	60.9	9.3	73.5	1.8	48.9	5.9	43	1.8	-2.7	-2	-2.3
8683_at	GRE2	YOL151W	YOL151W induced by osmotic stress\; similar to dihydroflavonol 4-reductase from plants	UNKNOWN	18.4	11	95.7	3.7	119.8	20.9	63	4.8	200	55.2	284	21.9	359.1	47.3	307.4	37.2	-5.2	-6.5	-3.4
8697_at		YOL137W	YOL137W weak similarity to tetracycline resistance proteins	UNKNOWN	17.6	10.2	61.4	15	41.1	9.7	46.7	2.5	29.3	9.1	50.6	2.6	36.5	1	55.8	19.5	-3.5	-2.3	-2.7
8717_at		YOL164W	YOL164W similarity to Pseudomonas alkyl sulfatase	UNKNOWN	19.8	13.1	71.5	9.4	1284.5	153.9	71.3	17.7	25.9	12.4	40.8	8.3	1738.9	192.8	41.6	11.9	-3.6	-64.9	-3.6
8726_at		YOL154W	YOL154W similarity to S.fumigata Asp FII	UNKNOWN	54	17.7	319.6	3	189.3	31.3	206.9	32.4	161.8	42	159.6	27	129.6	24.2	332.3	64	-5.9	-3.5	-3.8
8802_at	AGA1	YNR044W	YNR044W anchorage subunit of a-agglutinin	MATING	43.2	13.5	195.1	7.1	191.7	46.8	258	29.3	84.6	39.5	239	46.4	106.6	16.2	129	22.8	-4.5	-4.4	-6
8809_at	BRE5	YNR051C	YNR051C weak similarity to chicken nucleolin	UNKNOWN	31.9	14.6	78.3	39.9	167.4	31.4	114.8	20.6	46.1	13.4	59.5	5	75.1	10.9	58.9	1.7	-2.5	-5.2	-3.6
8816_at	BIO4	YNR057C	YNR057C dethiobiotin synthetase	BIOTIN BIOSYNTHESIS	45.7	10.5	128.3	26.5	91.8	15.8	97.4	2.7	141.9	25.3	75.4	13.4	116.9	16.6	127.7	32.9	-2.8	-2	-2.1
8842_at	ZRG17	YNR039C	YNR039C weak similarity to Anopheles mitochondrial NADH dehydrogenase subunit 2	UNKNOWN	51.1	18.1	118.3	24.3	117	25.4	120	26.4	109.2	10.1	141.5	25.7	150.2	24.6	106.8	7.7	-2.3	-2.3	-2.3
8892_at		YNL050C	YNL050C hypothetical protein	UNKNOWN	41.5	19	85.6	10.8	112.8	18.4	84.8	10	68.9	12.8	111.4	17.5	122.3	14.3	109.8	9	-2.1	-2.7	-2
8899_at	BOP3	YNL042W	YNL042W Bypass of PAM1	UNKNOWN	12	4.7	41	4.7	28.2	2.3	29.6	2.7	12.2	2.1	51.3	10.2	24	3.1	63.7	9.2	-3.4	-2.4	-2.5
8969_at		YNL108C	YNL108C strong similarity to YOR110w	UNKNOWN	24.3	8.7	52.5	12.5	54.9	12.9	66.4	22.9	22.4	2.3	40.4	6.4	51.8	2.6	52.5	19.8	-2.2	-2.3	-2.7
9010_at		YNL158W	YNL158W hypothetical protein	UNKNOWN	42	16.2	90.4	15.2	96.3	12.4	97.3	13.8	67.7	6	69.2	15.3	72	4	77.9	32.7	-2.2	-2.3	-2.3
9085_at	MGS1	YNL218W	YNL218W similarity to E.coli hypothetical protein in serS 5'region	UNKNOWN	12	3.4	48.1	5	35.6	9.3	46.5	3.6	15.2	4.1	39.6	7.1	29.5	9.5	45.2	22	-4	-3	-3.9
9110_at	KEX2	YNL238W	YNL238W Ca2+-dependent serine protease	SECRETION	52.6	23.8	140.4	14.4	145.4	24.3	144.9	7.8	72.1	2.2	113.7	4.6	126.4	3.8	149.8	14.3	-2.7	-2.8	-2.8
9117_at	PDR16	YNL231C	YNL231C weak similarity to Sec14p	DRUG RESISTANCE	57.9	30.9	147.5	33	126.3	10.5	210.2	36.4	223.9	39.1	484.2	60.7	359.2	35.9	447.8	53.3	-2.5	-2.2	-3.6
9157_at	POP3	YNL282W	YNL282W involved in processsing of tRNAs and rRNAs	RRNA AND TRNA PROCESSING	19	5.7	48.2	13.1	57	14.5	60.7	6.6	20.6	6.7	35.8	1.1	51.4	1	82.8	63.8	-2.5	-3	-3.2
9160_at	PRM1	YNL279W	YNL279W hypothetical protein	UNKNOWN	82.8	37.8	168	4.1	207.7	59.4	359.4	57.8	39.7	12.7	78.3	4.6	92.3	6.4	44.7	6.2	-2	-2.5	-4.3
9285_at		YMR320W	YMR320W hypothetical protein	UNKNOWN	22.3	15.8	85.2	30.4	44.9	3.5	82.4	5	14.8	1.6	23.8	2.1	21.4	2.6	25	1.8	-3.8	-2	-3.7
9313_at	FKS3	YMR306W	YMR306W Protein with similarity to Gls1p and Gls2p (GB:Z49212)	UNKNOWN	17.3	10.5	55.3	16.7	49.4	8.5	36.7	7.8	35.7	17.7	41.5	11	40.1	11.3	32.1	5.9	-3.2	-2.9	-2.1
9337_at	HSH155	YMR288W	YMR288W strong similarity to hypothetical S.pombe and C.elegans proteins	UNKNOWN	22.3	7.8	58.3	12.8	49.9	9.9	45.4	8.1	44.7	8.4	63.3	8.5	59.4	8.6	58.7	8	-2.6	-2.2	-2
9349_at	GFD1	YMR255W	YMR255W hypothetical protein	RNA PROCESSING (PUTATIVE)	35.6	24	86.1	10.9	77.3	4.2	127.9	23.4	80	5.1	115.2	16.6	147.4	27.3	192.9	17.7	-2.4	-2.2	-3.6
9356_at		YMR262W	YMR262W similarity to S.pombe scn1 protein	UNKNOWN	41	17	167.6	24.5	104.7	17.4	98.6	26.9	83.6	16.9	131.9	22.7	138.4	13	206.8	64.7	-4.1	-2.6	-2.4
9405_at	UBP8	YMR223W	YMR223W encodes putative deubiquitinating enzyme	PROTEIN DEGRADATION. UBIQUITIN-MEDIATED	16.8	10	39.3	11.2	39.7	8.7	38.5	4.8	32.3	2.4	33.8	1.5	30.6	2	31.5	4.1	-2.3	-2.4	-2.3
9482_g_at	ALD3	YMR169C	YMR169C Aldehyde Dehydrogenase (NAD(P)+)	ETHANOL UTILIZATION	63.1	28.6	352.1	50.7	141	31.7	147	22.6	228.7	82.7	307.4	27.1	127.7	17.4	145.6	3.8	-5.6	-2.2	-2.3
9563_at	VPS20	YMR077C	YMR077C similarity to SNF7 protein	UNKNOWN	40.4	25.4	113.1	35.7	104.9	3.3	96.9	3.9	93.8	8.8	156.6	9	110.2	2.7	77	5.6	-2.8	-2.6	-2.4
9566_at	NAM7	YMR080C	YMR080C putative helicase	MRNA DECAY	27.1	17.7	69.5	21.5	60.3	22.5	56.1	5.9	37.1	4.7	67.7	17.1	67.8	5.1	61.3	3.4	-2.6	-2.2	-2.1
9578_at	NUP116	YMR047C	YMR047C Nuclear pore complex protein that is member of GLFG repeat-containing family of nucleop	NUCLEAR PROTEIN TARGETING	130.3	70.3	289.7	14.3	291.4	33.6	282	24.8	142.5	23.6	229.9	20.2	226.5	14.2	229.8	27.4	-2.2	-2.2	-2.2
9598_at	MAC1	YMR021C	YMR021C metal-binding transcriptional activator	METAL-DEPENDENT GENE REGULATION	46.7	19.7	113.1	17.8	104.6	18.4	116.7	23	66.4	27.8	217.8	37.7	127.4	14.3	114.6	16.6	-2.4	-2.2	-2.5
9633_at	HXT2	YMR011W	YMR011W high affinity hexose transporter-2	TRANSPORT	457.3	283.3	1169.8	50.9	934.1	136.4	1117.7	117.4	1744.9	308.4	92.1	21.5	597.5	69.5	202.6	49.9	-2.6	-2	-2.4
9636_at	BUD22	YMR014W	YMR014W weak similarity to S.pombe hypothetical protein SPAC4F10	UNKNOWN	30	12.9	71.2	12.2	103.7	14	105.3	11.8	68	17.3	76.7	26.7	62.9	9	74.2	25.5	-2.4	-3.5	-3.5
9675_at	SRC1	YML034W	YML034W similarity to YDR458c	UNKNOWN	18.2	9.3	52	12.1	71.3	1.5	48.2	9.5	34.9	10.7	38.5	1.5	75.4	7.6	37.9	13.4	-2.9	-3.9	-2.7
9901_at	VIP1	YLR410W	YLR410W Homologous to S. pombe asp1+	UNKNOWN	51	22.6	112.1	9.7	122.8	21.1	214.3	39.1	76.1	13.5	104.7	21.6	129.7	4.2	387.7	101.4	-2.2	-2.4	-4.2
9915_at		YLR424W	YLR424W weak similarity to Stu1p	UNKNOWN	12	8	39.1	7.3	27.3	2.8	29.7	6.6	27.4	4.4	39.3	6.7	24.3	7.3	25.9	4.9	-3.3	-2.3	-2.5
9938_at	SFP1	YLR403W	YLR403W split zinc finger protein	UNKNOWN	36.8	18.3	94.6	13.4	75.8	9.7	74.2	11.4	45.8	13.1	86.7	13	89.5	6.7	73.8	13.2	-2.6	-2.1	-2
9939_at		YLR404W	YLR404W hypothetical protein	UNKNOWN	20.4	2.1	55.5	9.5	46.5	7.1	44.9	8.4	53.6	10.7	79.7	14.9	52.7	9.8	39.5	8.5	-2.7	-2.3	-2.2
9957_at		YLR376C	YLR376C hypothetical protein	UNKNOWN	19.1	8.1	69.3	20.2	56.3	25.1	50.7	7.6	34.3	2.7	48.5	0.7	42.3	7.2	44.6	3.6	-3.6	-2.9	-2.7
9985_at	DCR2	YLR361C	YLR361C similarity to YOR3329c	UNKNOWN	23.5	10.1	73.5	27.8	48.5	5.3	48.6	4.4	54.7	4.9	64.7	6.7	57.2	2.8	52.6	4.7	-3.1	-2.1	-2.1
9988_at	BUD6	YLR319C	YLR319C Actin Interacting Protein	BUD SITE SELECTION	28.9	18.1	92	34	70.9	14.1	75.4	7.4	58.1	8.2	82.5	16.9	67.9	10.8	91.1	33.7	-3.2	-2.4	-2.6
9992_at	CWC24	YLR323C	YLR323C weak similarity to N.crassa uvs2 protein	UNKNOWN	25.1	8.2	63.1	12.1	73.4	22.7	53	1.5	45.5	6.7	76.5	5.4	78.7	3.4	61.8	4.2	-2.5	-2.9	-2.1
AFFX-YEL021	URA3	YEL021W	YEL021W orotidine-5'-phosphate decarboxylase	PYRIMIDINE BIOSYNTHESIS	82.8	39.9	181.8	34.9	195	4	172.8	10.1	131.8	28.4	164.7	30.2	239.5	19.8	162.7	41.1	-2.2	-2.4	-2.1

Up-regulated under N-Lim anaerobic only (FC = fold change, ANA = anaerobic, A = aerobic)

Probe Set	Gene name	systematic name	functional description	cellular function	C-Lim ANA Average	C-Lim ANA Stdev	N-Lim ANA Average	N-Lim ANA Stdev	P-Lim ANA Average	P-Lim ANA Stdev	S-Lim ANA Average	S-Lim ANA Stdev	C-Lim A Average	C-Lim A Stdev	N-Lim A Average	N-Lim A Stdev	P-Lim A Average	P-Lim A Stdev	S-Lim A Average	S-Lim A Stdev	FC N-Lim ANA vs C-Lim ANA	FC N-lim ANA vs S-ANA	FC N-lim ANA vs P-lim ANA
10027_at		YLR312C	YLR312C hypothetical protein	UNKNOWN	27.3	21.2	81.1	32.5	37.4	11.8	32	6.7	289.2	10.8	173.3	27.2	124.6	6.1	66.5	15.4	3	2.2	2.5
10059_at		YLR257W	YLR257W hypothetical protein	UNKNOWN	361.3	92.6	1160.1	137.7	410.6	63.6	482.3	51.8	365.3	76.6	654.7	61.2	241.8	15.8	503.3	162.2	3.2	2.8	2.4
10067_at	RED1	YLR263W	YLR263W Meiosis-specific protein involved in homologous chromosome synapsis and chiasmata for	MEIOSIS. SYNAPSIS	12	5.5	40.8	6.8	16.5	3.5	18.8	5.4	15.9	0.9	28.1	3.5	15.6	0.4	17.6	5.7	3.4	2.5	2.2
10094_at	ERF2	YLR246W	YLR246W (ERF2) Protein involved in palmitoylation and localization of Ras2p	UNKNOWN	43.4	17.8	212.5	38.1	96.3	13.1	87.8	7	53	10.6	177	27	103	12.4	97.5	11.5	4.9	2.2	2.4
10140_r_at		YLR202C	YLR202C questionable ORF	UNKNOWN	221.9	85.4	576.9	97.5	268.3	100.2	181.4	70	233.4	26.1	378.1	29.5	168.7	54.7	262.6	97.1	2.6	2.2	3.2
10186_s_at		YLR156W	YLR156W identical to hypothetical proteins YLR161w and YLR159w	UNKNOWN	13.4	3.2	105.4	19.1	24.4	6.3	33.6	6.5	35.7	13.5	26.5	3.9	13.9	3.3	30.6	13.2	7.9	4.3	3.1
11175_at		YJL163C	YJL163C hypothetical protein	UNKNOWN	22.9	9.6	111.6	20.8	51.3	19.8	42.9	16.2	89.1	15.7	73.5	3	37.8	8.1	36.7	5.6	4.9	2.2	2.6
11387_at		YAL061W	YAL061W similarity to alcohol/sorbitol dehydrogenase	UNKNOWN	12	7.7	89.5	14.1	30.9	7.1	35.3	17.8	126.7	64.9	156.7	36.4	105.5	13.5	177.6	68.5	7.5	2.9	2.5
4178_at		YIL088C	YIL088C weak similarity to A.thaliana aminoacid permease AAP4	UNKNOWN	191.7	89.5	397.6	59.6	151.5	28.2	121	40	125.8	14	404.9	60.4	279.2	21.6	175.1	75.3	2.1	2.6	3.3
4283_at	SDL1	YIL168W	YIL168W (SDL1) Serine dehydratase. converts serine to pyruvate and ammonia for gluconeogenesis	GLUCONEOGENESIS	12	3.7	34.1	13.3	12	2.4	12.8	6.4	12	3.1	24	3.5	14.6	3.2	12	1.7	2.8	2.8	2.7
4767_at	CPD1	YGR247W	YGR247W hypothetical protein	UNKNOWN	16	5.9	43.4	7.7	17.1	2	12.8	4	21.4	12.8	25.4	17.2	22.1	0.9	27.6	3.2	2.7	2.5	3.4

4866_at	MEP1	YGR121C	YGR121C ammonia permease	TRANSPORT	204.5	19.2	508.7	16.8	91	37.9	153.4	23.9	308.3	59.2	236	14.7	153.5	6.5	238.2	29.1	2.5	5.6	3.3
4870_at		YGR125W	YGR125W similarity to S.pombe hypothetical protein SPAC24H6.11c	UNKNOWN	106.6	17.9	606.8	109.5	178.9	24.3	140.8	17.6	112.9	10.2	724.6	96.1	415.8	69.5	236.1	46.9	5.7	3.4	4.3
4951_at	ROM1	YGR070W	YGR070W GDP-GTP Exchange Protein (GEP) for the Rho1p Small GTP-binding Protein	SIGNALING	84.2	38.7	225	89.3	79.3	12.8	72.9	20.5	93.1	15.4	99	12.2	51.7	1.9	74.5	22	2.7	2.8	3.1
5149_at		YGL140C	YGL140C weak similarity to Lactobacillus putative histidine protein kinase SppK	UNKNOWN	25.6	10.1	108.6	20.4	40.1	10.7	39.2	4.3	39.5	2	127.9	17.8	94.7	2.6	67.1	9.2	4.2	2.7	2.8
5534_at		YER185W	YER185W strong similarity to Rtm1p	UNKNOWN	12	3.2	35.7	1.8	17.4	1.5	14.8	5.2	22.1	2.6	19.9	7.7	20.6	2.1	17	8.6	3	2.1	2.4
5657_at	SPO73	YER046W	YER046W hypothetical protein	UNKNOWN	52.7	20.8	107.7	28.4	51	5.6	41.9	11.6	75	17.2	61.1	8.4	60.4	9.7	37.8	9.6	2	2.1	2.6
5816_at	HPA3	YEL066W	YEL066W Histone and other Protein Acetyltransferase\; Has sequence homology to known HATs an	CHROMATIN STRUCTURE	447.6	73.6	1350.2	121.2	485.4	87.6	361.4	31.2	522.7	31.3	1048.7	111.3	382.7	12.4	525.3	151.7	3	2.8	3.7
5944_at		YDR520C	YDR520C weak similarity to transcription factors of the zinc finger class	UNKNOWN	37.7	16.2	165.8	39.7	74.6	14.2	73.6	15.4	53.3	10.6	189.2	22.3	79.7	11.7	101.8	19.3	4.4	2.2	2.3
6088_at		YDR391C	YDR391C strong similarity to hypothetical protein YOR013w	UNKNOWN	47.7	11.1	139	14.5	65.9	7.5	51.2	7.1	52.6	3.5	114.4	19.4	47.1	13.6	81.7	20.9	2.9	2.1	2.7
6722_at	BRE4	YDL231C	YDL231C (BRE4) Protein of unknown function. has a putative zinc finger domain	UNKNOWN	69.9	26	264	3.4	108.3	4.7	101.6	15.4	103.1	14.5	264.4	19	165.1	10.5	153.3	7.9	3.8	2.4	2.6
7138_at	SLX1	YBR228W	YBR228W similarity to hypothetical A.thaliana protein	UNKNOWN	17.9	6.2	38.4	12.2	18.6	2.6	15	4.8	21.3	1.9	41.9	4.6	38.1	5.4	30.3	9.8	2.1	2.1	2.6
7145_at		YBR235W	YBR235W similarity to bumetanide-sensitive Na-K-Cl cotransport protein	UNKNOWN	45.8	7.9	178.4	29.6	71.7	3.9	55.7	11.7	71	4.3	191.1	6	98.8	17.2	91.6	17.5	3.9	2.5	3.2
7219_at	APG14	YBR128C	YBR128C required for autophagy	AUTOPHAGY	12	5.8	31.4	4.5	15.6	2.1	13.2	3.3	21.9	0.9	36.9	1.7	19.2	2.2	24.5	1.7	2.6	2	2.4
7324_at		YBR056W	YBR056W Homolog to glucan-1.3--glucosidase (EC 3.2.1.5\; S. cerevisiae) 2	UNKNOWN	49.9	19.8	128.8	27.6	40.6	10.5	57.4	2.6	68.2	12	74	15.4	31.8	13.1	65.4	7.9	2.6	3.2	2.2
7928_at	UIP4	YPL186C	YPL186C weak similarity to Xenopus protein xlgv7	UNKNOWN	34.9	24.1	86.9	22.7	24.2	4.9	26.2	4.6	318.2	73.7	143.8	13.5	23.2	0.2	47.8	4.7	2.5	3.6	3.3
7991_at	LEA1	YPL213W	YPL213W (LEA1) Component of the U2 snRNP complex similar to human U2A' protein. involved in tl	MRNA SPLICING	37.2	13.5	138	35.4	57.9	2.8	56	11.2	39	12.9	148.7	29.3	90.4	4.6	68.1	14.8	3.7	2.4	2.5
8030_at	DIP5	YPL265W	YPL265W dicarboxylic amino acid permease	TRANSPORT	559.1	48.4	1576.8	319.1	497.3	38.9	332.6	82.2	28.1	9.7	696.8	44.4	445.6	71.1	13.2	2.6	2.8	3.2	4.7
8037_at	THI21	YPL258C	YPL258C similarity to B.subtilis transcriptional activator tenA. and strong similarity to hypothetical prc	THIAMINE METABOLISM (PUTATIVE)	40.1	16.9	177.9	26.4	48.7	6.2	84.7	10.1	45.1	5.9	77.7	6.2	44.3	4.7	58.2	16.8	4.4	3.7	2.1
8207_at	FAA1	YOR317W	YOR317W long chain fatty acyl:CoA synthetase	FATTY ACID METABOLISM	25.6	17.5	86.6	39.5	19	1	22.6	3.6	370.9	64.3	516.9	93.3	308.7	47.1	311	45	3.4	4.6	3.8
8561_at	PHO80	YOL001W	YOL001W negative transcriptional regulator	CELL CYCLE	42.2	15.7	113.1	24.8	51.6	5.6	54.9	6.6	51.8	3.5	79.9	10.4	54.2	2.1	110.8	33	2.7	2.2	2.1
8727_at		YOL153C	YOL153C strong similarity to Cps1p	UNKNOWN	12	2.2	26.4	4.9	12	2.3	12	1.7	31.9	2.9	27.9	3.1	12.5	1.8	29.6	11.5	2.2	2.2	2.2
9114_at		YNL234W	YNL234W weak similarity to mouse hemoglobin zeta chain	UNKNOWN	12	2	26	5.6	12	4.1	12	2.4	12	1.2	52.7	6.8	20.3	1.6	40.5	1.6	2.2	2.2	2.2
9388_at	GAD1	YMR250W	YMR250W similarity to glutamate decarboxylases	UNKNOWN	20.3	6	56	14	22.5	3.2	28	4.9	47.8	16.7	64.5	18.3	13.4	1.5	105.7	9.3	2.8	2.5	2
9466_at		YMR155W	YMR155W weak similarity to E.coli hypothetical protein f402	UNKNOWN	18.2	9.3	74.7	13.2	33.4	5	27.4	3.6	45.6	2.6	95.6	1.5	54.4	4.9	32.1	9.9	4.1	2.2	2.7
9482_g_at	ALD3	YMR169C	YMR169C Aldehyde Dehydrogenase (NAD(P)+)	ETHANOL UTILIZATION	63.1	28.6	352.1	50.7	141	31.7	147	22.6	228.7	82.7	307.4	27.1	127.7	17.4	145.6	3.8	5.6	2.5	2.4
9515_at		YMR118C	YMR118C strong similarity to succinate dehydrogenase	UNKNOWN	16.5	11.2	56.3	12.4	23.9	3.5	22.7	4.7	325.4	181	17.4	2.4	12	3.7	12	6.2	3.4	2.4	2.5
9518_at	ASI1	YMR119W	YMR119W questionable ORF	UNKNOWN	34.9	10.1	71.9	19.4	34.3	2.2	28.2	3.4	55.3	9.3	66	9.3	38.8	2.3	39.1	8.7	2.1	2.1	2.5
9549_at		YMR107W	YMR107W hypothetical protein	UNKNOWN	18.8	15	73.2	10.5	21.7	7.2	19.4	4.5	2622.7	320.3	12	1.5	15.9	1.3	12	4.1	3.9	3.4	3.8

Down-regulated under N-Lim anaerobic only (FC = fold change, ANA = anaerobic, A = aerobic)

Probe Set	Gene name	systematic name	functional description	cellular function	C-Lim ANA Average	C-Lim ANA Stdev	N-Lim ANA Average	N-Lim ANA Stdev	P-Lim ANA Average	P-Lim ANA Stdev	S-Lim ANA Average	S-Lim ANA Stdev	C-Lim A Average	C-Lim A Stdev	N-Lim A Average	N-Lim A Stdev	P-Lim A Average	P-Lim A Stdev	S-Lim A Average	S-Lim A Stdev	FC N-Lim ANA vs C-Lim ANA	FC N-lim ANA vs S-ANA	FC N-lim ANA vs P-lim ANA
10658_at	TEF4	YKL081W	YKL081W Translation elongation factor EF-1gamma	PROTEIN SYNTHESIS	83.3	30	29.5	13.8	112.9	12.9	190.1	36	97.6	34.6	51.4	21	85.3	7.6	122.3	47.4	-2.8	-3.8	-6.4
5813_at	DLD3	YEL071W	YEL071W strong similarity to Aip2p	UNKNOWN	921.2	147.8	257.4	53.7	811.6	33.4	591.7	21.4	223.7	41.6	184.7	34.7	735.5	102.1	289.4	56.7	-3.6	-3.2	-2.3
6415_at	BAP3	YDR046C	YDR046C Valine transporter	TRANSPORT	113.1	34.6	12	2.6	357.2	86.6	127.1	3.9	12	2	12	0.6	281	51.2	161	25.2	-9.4	-29.8	-10.6
6907_at	AGP1	YCL025C	YCL025C (AGP1) Broad substrate range amino acid permease with high affinity for asparagine and g	TRANSPORT	762.9	56.7	155.9	23.1	363.4	68.5	346.5	31.2	87.2	28.6	208.6	17.3	240.4	116.9	353.1	52.1	-4.9	-2.3	-2.2
7945_at		YPL170W	YPL170W similarity to C.elegans LIM homeobox protein	UNKNOWN	714.7	106.1	322.3	105.8	659.5	57.4	657.9	44.3	539	112	200.4	24.7	294	16.9	340.6	30.2	-2.2	-2	-2
8587_at	TAT2	YOL020W	YOL020W Tryptophan permease. high affinity	TRANSPORT	68.7	30.4	12	1.2	77.2	6.7	84.8	7.3	46.1	5.5	36.3	2.3	76.2	10.5	105.6	21.3	-5.7	-6.4	-7.1

Up-regulated under P-Lim anaerobic only (FC = fold change, ANA = anaerobic, A = aerobic)

Probe Set	Gene name	systematic name	functional description	cellular function	C-Lim ANA Average	C-Lim ANA Stdev	N-Lim ANA Average	N-Lim ANA Stdev	P-Lim ANA Average	P-Lim ANA Stdev	S-Lim ANA Average	S-Lim ANA Stdev	C-Lim A Average	C-Lim A Stdev	N-Lim A Average	N-Lim A Stdev	P-Lim A Average	P-Lim A Stdev	S-Lim A Average	S-Lim A Stdev	FC P-Lim ANA vs C-Lim ANA	C P-lim ANA vs N-lim AN	FC P-lim ANA vs S-Lim ANA
10022_at	CDA1	YLR307W	YLR307W Chitin Deacetylase	SPORULATION	45.1	19.5	49.3	12.8	43	8.3	110.6	2.8	26.6	7.2	12	3.6	12	0.1	12	4.2	2.5	2.2	2.6
10294_at		YLR042C	YLR042C hypothetical protein	UNKNOWN	27	6.1	29.6	2.4	23.2	4.5	65.1	7.6	30.9	11.3	16	3.4	12.2	3.1	12	1.7	2.4	2.2	2.8
10442_s_at		YKL200C	YKL200C regulates the mannosylphosphorylation	PROTEIN GLYCOSYLATION	12	0.4	12	3.8	12	0.5	28.5	5.9	12	3.2	12	5.8	12	2.1	12	7.1	2.4	2.4	2.4
10483_at	FLO10	YKR102W	YKR102W Protein with similarity to flocculation protein Flo1p	UNKNOWN	16.5	9.4	65.4	6.1	30.8	5.9	380	43.7	25.9	6.8	37.2	6.9	29.3	1.9	35.3	5.6	23.1	5.8	12.3
10853_at	DAN4	YJR151C	YJR151C similarity to mucin proteins. YKL224c. Sta1p	UNKNOWN	560.6	259.8	701.2	22.9	618.5	55.3	1551.8	341.6	111.6	29.8	115.2	27.7	96.3	6.4	132.6	58.3	2.8	2.2	2.5
10855_at	PGU1	YJR153W	YJR153W Endo-polygalacturonase	UNKNOWN	12	5.3	19.7	3.6	12	1.4	67.5	21.9	12	1.4	12	3.1	12	2	12	1.5	5.6	3.4	5.6
11186_at		YJL152W	YJL152W questionable ORF	UNKNOWN	23.2	5.3	25.5	6.6	38.8	6.1	95.2	18	17.9	6	15.5	1.8	24.1	4.3	18.2	8.4	4.1	3.7	2.5
11304_at		YAR061W	YAR061W putative pseudogene	UNKNOWN	12	4.5	13	2.2	12	3.2	38.8	11.9	12	2	12	5.7	12	0.8	12	4.7	3.2	3	3.2
11305_s_at		YAR062W	YAR062W putative pseudogene	UNKNOWN	12	0.9	14	6.9	12	1.3	76.1	19.3	12	1.7	12	0.4	12	0.7	12	2.2	6.3	5.4	6.3
4386_at	ARO9	YHR137W	YHR137W aromatic amino acid aminotransferase II	AROMATIC AMINO ACID METABOLISM	13.8	6.7	23.2	2.8	21.5	5.7	147.2	17	314.6	21	19.6	6	12	3.9	172.6	36.2	10.7	6.4	6.8
4420_at		YHR126C	YHR126C hypothetical protein	UNKNOWN	25.8	10.7	15.8	4.7	17.3	2.3	54.7	16.7	87.8	65.9	12	0.8	12	0.4	12	2.8	2.1	3.5	3.2
4563_f_at		YHL046C	YHL046C strong similarity to members of the Srp1p/Tip1p family	UNKNOWN	1321.7	414.8	737.2	120.6	1128.7	78.3	2915.5	867	153.2	61.1	88.3	7.5	74.2	10	137.1	20.1	2.2	4	2.6
5537_at		YER188W	YER188W hypothetical protein	UNKNOWN	101.8	30.2	448	24.7	212	28.7	956	71.3	16.2	6.6	472	12.8	43.8	6.2	334.4	113.5	9.4	2.1	4.5
5786_f_at	PAU2	YEL049W	YEL049W member of the seripauperin protein\/gene family (see Gene_class PAU)	UNKNOWN	614.1	107.1	276.6	42.1	305.5	8.7	1577.5	588.1	329.7	231.6	80.5	12.9	38.8	2.7	78.9	18.9	2.6	5.7	5.2
6051_at	URH1	YDR400W	YDR400W similarity to C. fasciculata inosine-uridine preferring nucleoside hydrolase (EC 3.2.2.1)	UNKNOWN	65.7	37.2	61.1	20.1	61.3	12.7	160.7	15.7	48.7	9.8	54	3.9	66.3	12.6	120.3	8.8	2.4	2.6	2.6
6617_at		YDL114W	YDL114W weak similarity to Rhizobium nodulation protein nodG	UNKNOWN	12	4.7	12	5.6	12	0.3	35	1.7	12	0.3	12	0.4	12	0.1	12	1.5	2.9	2.9	2.9
6906_at		YCL026C	YCL026C Protein involved in the integration of lipid signaling pathways with cellular homeostatis	UNKNOWN	16.8	8.6	16.6	5.1	19.8	4.6	51.8	9.9	12	3.9	12	1	25.4	6.6	13.7	3.7	3.1	3.1	2.6
7308_at	FIG1	YBR040W	YBR040W integral membrane protein	MATING	20.6	7.2	27.7	11.1	28.6	7.2	75.7	3.7	12	3	14.3	0.7	12	1.2	12	2	3.7	2.7	2.6
7547_at		YPR195C	YPR195C hypothetical protein	UNKNOWN	12	3.3	19	7	12	1.9	46.9	5.7	12	1.2	12	2.1	12	2.7	26.2	16.1	3.9	2.5	3.9
7697_i_at		YPR077C	YPR077C questionable ORF	UNKNOWN	12	7.9	12	1.4	12	1.9	29	5.7	12	4.8	12	1.6	12	0.4	13.6	6.6	2.4	2.4	2.4
7780_at	CTF19	YPL018W	YPL018W Important for chromosome segregation	MITOSIS. CHROMOSOME SEGREGATION	12	1.5	12	0.7	12	0.7	33.5	12.9	12	1.1	12	1.7	12	1.3	65.4	48.6	2.8	2.8	2.8
7810_at		YPL033C	YPL033C weak similarity to YLR426w	UNKNOWN	12	4.4	12	1.5	12	1.7	31.3	8.5	12	1.1	12	1	12	0.1	12	2.1	2.6	2.6	2.6
8188_at	TYE7	YOR344C	YOR344C TYE7. a 33 kDa serine-rich protein. is a potential member of the basic region\/helix-loop-h	GLYCOLYSIS	33.5	14.9	38.6	14.9	35.4	7.7	93.9	26.2	41.2	2	36.4	5	12	1.8	59	18.8	2.8	2.4	2.7
8348_i_at		YOR192C	YOR192C strong similarity to Thi10p	UNKNOWN	41.5	14.6	86.8	37.8	92.1	18.9	315.8	38.4	57.2	18	44.2	6.3	24.6	4.2	52.2	34	7.6	3.6	3.4
8498_at		YOR071C	YOR071C strong similarity to Thi10p	TRANSPORT	24.5	9.7	22	3.5	20.5	2.4	55.3	8.2	12	2.6	16.1	0.7	12	0.9	15.5	3	2.3	2.5	2.7
8871_at		YNL024C	YNL024C weak similarity to YBR271w and YJR129c	UNKNOWN	13.1	4.9	21.2	1.1	22.4	5.1	54	15.2	12	1.6	12	1.6	12	1.6	12.9	1.4	4.1	2.5	2.4
9282_at		YMR317W	YMR317W similarity to mucins. glucan 1.4-alpha-glucosidase and exo-alpha-sialidase	UNKNOWN	12	8.7	17.7	6	14.4	1.7	100.1	52.3	12	2.5	12	2.6	12	1	12	1.1	8.3	5.7	7
9973_at		YLR349W	YLR349W questionable ORF	UNKNOWN	19.6	8.2	22	1	21.5	6.3	45.7	12.3	28.7	14.9	19.8	3.2	19.9	4.2	25.3	12.5	2.3	2.1	2.1

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Probe Set	Gene name	systematic name	functional description	cellular function	C-Lim ANA Average	C-Lim ANA Stdev	N-Lim ANA Average	N-Lim ANA Stdev	P-Lim ANA Average	P-Lim ANA Stdev	S-Lim ANA Average	S-Lim ANA Stdev	C-Lim A Average	C-Lim A Stdev	N-Lim A Average	N-Lim A Stdev	P-Lim A Average	P-Lim A Stdev	S-Lim A Average	S-Lim A Stdev	FC P-Lim ANA vs C-Lim ANA	C P-lim ANA vs N-lim AN	FC P-lim ANA vs S-Lim ANA
10256_at	SUL2	YLR092W	YLR092W high affinity sulfate permease	TRANSPORT	536.6	95	408.8	62.1	1396.3	89.8	91.1	22.2	340.9	43.8	433.3	30.5	1193.7	102	344.7	26	-5.9	-4.5	-15.3
10414_at	MHT1	YLL062C	YLL062C weak similarity to M.leprae metH2 protein	UNKNOWN	77.4	21.6	55.6	14.9	595.6	160.2	19.5	2.7	100.3	17.5	19.5	4.3	663.8	17.9	12	4.4	-4	-2.9	-30.6
11032_at	MET3	YJR010W	YJR010W ATP sulfurylase	METHIONINE BIOSYNTHESIS	922.1	103.5	793.1	54.8	2051.2	191.6	318.2	54.9	784.5	112.8	924.8	62.7	2175.3	165.3	699.8	6.6	-2.9	-2.5	-6.4
5327_at	MET10	YFR030W	YFR030W subunit of assimilatory sulfite reductase	SULFATE ASSIMILATION	358.2	53.1	441.9	32.2	941.6	176.2	142.6	5.4	329.2	35.8	391.9	24.9	1038.3	109.9	336.4	89.6	-2.5	-3.1	-6.6
5697_at	MXR1	YER042W	YER042W responsible for the reduction of methionine sulfoxide	OXIDATIVE STRESS RESPONSE	144.7	16.6	176.4	36.7	179.3	40.2	68.4	15	278.9	43.5	288.4	29.4	495.2	70.2	159.9	27.5	-2.1	-2.6	-2.6
6218_at	MET32	YDR253C	YDR253C zinc finger DNA binding factor. transcriptional regulator of sulfur amino acid metabolism. h	METHIONINE METABOLISM	100.9	28.1	104.9	46.9	443	76.1	29.5	8.4	217.2	47	142.6	13.6	836.4	97.7	86.9	13.6	-3.4	-3.6	-15
6607_at		YDL124W	YDL124W similarity to aldose reductases	UNKNOWN	304.8	27.6	306.1	21.9	561.3	37.2	148.1	8.2	353.9	55.2	254.2	54.6	675.8	86.4	201.3	69	-2.1	-2.1	-3.8

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Probe Set	Gene name	systematic name	functional description	cellular function	C-Lim ANA Average	C-Lim ANA Stdev	N-Lim ANA Average	N-Lim ANA Stdev	P-Lim ANA Average	P-Lim ANA Stdev	S-Lim ANA Average	S-Lim ANA Stdev	C-Lim A Average	C-Lim A Stdev	N-Lim A Average	N-Lim A Stdev	P-Lim A Average	P-Lim A Stdev	S-Lim A Average	S-Lim A Stdev	FC S-Lim ANA vs C-Lim ANA	FC S-lim ANA vs N-ANA	FC S-lim ANA vs P-Lim ANA
11146_at	GSH1	YJL101C	YJL101C gamma-glutamylcysteine synthetase	GLUTATHIONE METABOLISM	80.8	16.4	104.7	21.8	299	12.1	52.3	5.2	102.5	4.3	150.3	37.2	330.5	39.4	195.9	22.6	3.701869506	2.855778415	5.717017208
4040_at		YIR017W	YIR017W questionable ORF	UNKNOWN	12	5.5	15	2.6	65.7	12.1	21.6	11.4	17.3	11.1	12	1	30.9	7.5	12	4.2	5.4775	4.373253493	3.0472879
4856_at	CYS4	YGR155W	YGR155W Cystathionine beta-synthase	METHIONINE BIOSYNTHESIS	589	89.5	576.4	32.8	1195	53.1	404.8	75.8	504.6	26.2	786.1	114.5	1518.1	251.4	629.1	73.5	2.028913413	2.073373007	2.952368011
6234_at		YDR223W	YDR223W similarity to Ifh1p	UNKNOWN	12	3.1	12.7	2	66.4	22.9	14.7	3.5	110.2	45.4	12	1.5	184.3	21.9	12	1.5	5.535833333	5.218381775	4.519047619
6346_at		YDR111C	YDR111C strong similarity to alanine transaminase	UNKNOWN	20.8	11.1	84	13.2	199.1	32.7	69.1	7.9	131.1	11.2	49.7	1.8	129.9	13.3	18.2	0.1	9.570673077	2.369880952	2.882148545
6415_at	BAP3	YDR046C	YDR046C Valine transporter	TRANSPORT	113.1	34.6	12	2.6	357.2	86.6	127.1	3.9	12	2	12	0.6	281	51.2	161	25.2	3.158001768	29.76416667	2.809486353
7067_at	SUL1	YBR294W	YBR294W Probable sulfate transport protein	TRANSPORT	703.3	134.8	407.8	75.5	1450.4	319.9	12	2.3	1035.2	67.4	487.2	30.5	1885.4	396.9	42	8.1	2.062147214	3.556571849	120.8641667
8181_at	FIT2	YOR382W	YOR382W hypothetical protein	UNKNOWN	75.7	32.1	54.7	3.6	219.9	97	39.3	8.6	128	40.5	25.2	2.6	210.9	67.9	33.2	2.6	2.905642923	4.017357939	5.598930481
8182_at	FIT3	YOR383C	YOR383C weak similarity to L.mexicana secreted acid phosphatase 2	UNKNOWN	170.9	59.8	222.2	11.5	1088.5	371.1	167.8	31	739.9	208.8	168	42.9	821.7	196.7	239.2	82.8	6.369046226	4.89860486	6.486710369
8723_at	ENB1	YOL158C	YOL158C similarity to subtelomeric encoded proteins	UNKNOWN	199.1	36.2	353.6	25.6	824.6	215.3	346.8	29	208.2	44.4	189.5	23	587.1	123.1	312.9	112.8	4.141013408	2.332013575	2.377533662
9118_at		YNL276C	YNL276C questionable ORF	UNKNOWN	12	4.3	12.5	1.6	43.6	2	12	5.6	13.9	1.4	12	4.3	25.1	3.8	12	4	3.635833333	3.498797113	3.635833333
9588_at	FET3	YMR058W	YMR058W multicopper oxidase	TRANSPORT	13.8	6	15.2	2.8	45.5	23.1	12	4.4	128.3	43.3	28.9	2.8	109.5	35.8	136.2	18.8	3.292118583	2.995394737	3.794166667
9631_at		YMR009W	YMR009W weak similarity to P.aeruginosa regulatory protein mmsR	UNKNOWN	73.5	29.4	117.3	33.1	298	71.6	73.8	18.4	776.5	105.3	357.3	45.4	1442.4	54.3	291.5	39.1	4.055668981	2.540238704	4.037533875

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Probe Set	Gene name	systematic name	functional description	cellular function	C-Lim ANA Average	C-Lim ANA Stdev	N-Lim ANA Average	N-Lim ANA Stdev	P-Lim ANA Average	P-Lim ANA Stdev	S-Lim ANA Average	S-Lim ANA Stdev	C-Lim A Average	C-Lim A Stdev	N-Lim A Average	N-Lim A Stdev	P-Lim A Average	P-Lim A Stdev	S-Lim A Average	S-Lim A Stdev	FC S-Lim ANA vs C-Lim ANA	FC S-lim ANA vs N-ANA	FC S-lim ANA vs P-Lim ANA
11388_at	BDH1	YAL060W	YAL060W similarity to alcohol/sorbitol dehydrogenase	UNKNOWN	757.4	172.4	654.9	57.1	244.6	21.9	629.6	29.1	792.8	145.4	249.9	81.6	401.8	27	151.8	53.5	-3.096226955	-2.676981564	-2.573805339
6684_at	INH1	YDL181W	YDL181W ATPase inhibitor	ATP SYNTHESIS	352.9	102.6	102	17.3	41.1	2.5	83.2	14.5	798.8	152.7	516.7	90.5	370.6	113.2	706.3	164.1	-8.586374696	-2.481021898	-2.0243309
7273_at	PHO3	YBR092C	YBR092C Acid phosphatase. constitutive	THIAMINE UPTAKE	173.2	54.5	157.1	65.6	71	10.8	2233.6	357.8	279.8	334	210.9	33.8	64.6	2	2012.5	165.6	-2.438828664	-2.211741518	-31.44586794
7546_at	OPT2	YPR194C	YPR194C similarity to S.pombe isp4 protein	UNKNOWN	81.3	28.8	1697.2	265.4	12	0.4	214.4	27.2	12	1.2	1426.6	114.1	12	4	91.4	28.8	-6.7725	-141.4308333	-17.86666667
9422_at	ICY1	YMR195W	YMR195W similarity to YPL250c	UNKNOWN	612.9	105.8	655.5	21.8	163.2	25.1	1353.2	99.1	140.2	31.5	766.5	113.4	168.9	23	1842.4	137.6	-3.756021327	-4.017098731	-8.29319115
9433_at		YMR206W	YMR206W weak similarity to hypothetical protein YNR014w	UNKNOWN	183	62.9	60.3	6.5	12.4	6.7	27.6	3.3	349.8	48.7	29.1	9.2	12	0.2	15	3	-14.7224457	-4.853580048	-2.220434433
9567_at	ISF1	YMR081C	YMR081C May regulate NAM7 function. possibly at level of mRNA turnover	RNA SPLICING. MITOCHONDRIAL	512.6	143.4	133.9	22.5	25.9	2.8	64.3	14.4	483.6	74.7	118	17.5	17.1	4.5	31.5	3.7	-19.81561654	-5.175879397	-2.484344801

Two-dimensional Transcriptome Analysis in Chemostat Cultures: COMBINATORIAL EFFECTS OF OXYGEN AVAILABILITY AND MACRONUTRIENT LIMITATION IN SACCHAROMYCES CEREVISIAE

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