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Two-dimensional Transcriptome Analysis in Chemostat Cultures

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 (*MATa*) (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 (NH₄)₂SO₄, 3.0 g liter⁻¹ KH₂PO₄, 0.5 g liter⁻¹ MgSO₄·7H₂O, and 25 g liter⁻¹ glucose; for nitrogen-limited cultivation, 0.65 g liter⁻¹ (NH₄)₂SO₄, 5.75 g liter⁻¹ K₂SO₄, 3.0 g liter⁻¹ KH₂PO₄, 0.5 g liter⁻¹

MgSO₄·7H₂O, and 46 g liter⁻¹ glucose; for phosphorus-limited cultivation, 5.0 g liter⁻¹ (NH₄)₂SO₄, 1.9 g liter⁻¹ K₂SO₄, 0.12 g liter⁻¹ KH₂PO₄, 0.5 g liter⁻¹ MgSO₄·7H₂O, and 66 g liter⁻¹ glucose; and for sulfur-limited cultivation, 4.0 g liter⁻¹ NH₄Cl, 0.05 g liter⁻¹ MgSO₄·7H₂O, 3.0 g liter⁻¹ KH₂PO₄, 0.4 g liter⁻¹ MgCl₂, 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 H₂SO₄ 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).

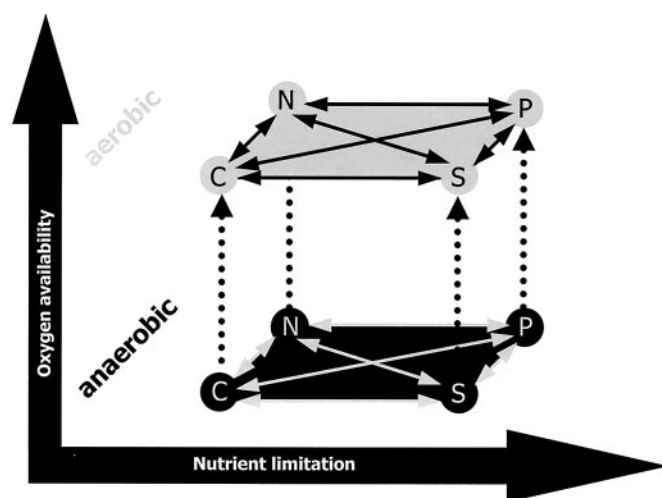


FIG. 1. **Two-dimensional experimental approach.** The experimental design for two-dimensional transcriptome analysis is shown. Each corner of the cube represents a chemostat condition. The upper horizontal surface represents the four aerobic macronutrient limitation regimes (carbon, nitrogen, phosphorus, 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 transcrip-

tome 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 ($\pm$ 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. 3A 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. 3B). 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. 3B 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. 3B and Supplemental Table 5) or anaerobic conditions (set IV, 302 genes) (Fig. 3B 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 $\pm$ S.D. of data from three independent steady-state chemostat cultivations. RQ, respiratory quotient (q_{CO_2}/q_{O_2}); 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-X}^a	q_{Glu}^b	$q_{ethanol}^c$	$q_{O_2}^d$	$q_{CO_2}^e$	RQ	Carbon recovery	
	g/liter	mM	mM	mM							%	
Aerobic												
Carbon	BD	58.2 $\pm$ 1.3	19.8 $\pm$ 0.6	38.6 ^f	0.49 $\pm$ 0.0	1.1 $\pm$ 0.0	0.0 $\pm$ 0.0	2.8 $\pm$ 0.3	2.8 $\pm$ 0.3	1.0 $\pm$ 0.0	98 $\pm$ 3	4
Nitrogen	16.7 $\pm$ 1.0	BD	18.6 $\pm$ 1.0	40.7 $\pm$ 1.0	0.09 $\pm$ 0.0	5.8 $\pm$ 0.1	8.0 $\pm$ 0.1	2.7 $\pm$ 0.1	12.1 $\pm$ 0.2	4.5 $\pm$ 0.2	96 $\pm$ 1	4
Phosphorus	18.1 $\pm$ 1.0	54.3 $\pm$ 0.0	BD	47.5 $\pm$ 1.0	0.09 $\pm$ 0.0	6.1 $\pm$ 0.2	7.8 $\pm$ 0.1	4.0 $\pm$ 0.1	13.5 $\pm$ 0.2	3.4 $\pm$ 0.0	95 $\pm$ 2	4
Sulfur	17.4 $\pm$ 0.6	53.7 $\pm$ 2.4	18.4 $\pm$ 0.2	BD	0.14 $\pm$ 0.0	3.8 $\pm$ 0.1	4.4 $\pm$ 0.1	3.0 $\pm$ 0.0	8.0 $\pm$ 0.8	2.7 $\pm$ 0.2	96 $\pm$ 1	4
Anaerobic												
Carbon	BD ^g	68.6 $\pm$ 2.8 ^g	22.3 $\pm$ 0.6 ^g	42.4 $\pm$ 1.6 ^g	0.09 $\pm$ 0.0	6.0 $\pm$ 0.0	9.6 $\pm$ 0.1	NA	10.3 $\pm$ 0.4	NA	101 $\pm$ 2	
Nitrogen	16.2 $\pm$ 0.6	BD	21.9 $\pm$ 0.4	39.1 $\pm$ 0.8	0.07 $\pm$ 0.0	8.4 $\pm$ 0.0	13.5 $\pm$ 0.6	NA	14.8 $\pm$ 0.3	NA	101 $\pm$ 2	
Phosphorus	19.1 $\pm$ 2.2	60.2 $\pm$ 2.6	BD	50.9 $\pm$ 0.9	0.06 $\pm$ 0.0	8.7 $\pm$ 0.2	13.9 $\pm$ 0.6	NA	15.8 $\pm$ 0.7	NA	101 $\pm$ 2	
Sulfur	21.2 $\pm$ 0.2	61.1 $\pm$ 1.3	21.5 $\pm$ 0.2	BD	0.07 $\pm$ 0.0	7.9 $\pm$ 0.2	11.9 $\pm$ 0.4	NA	13.6 $\pm$ 0.8	NA	98 $\pm$ 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 $\pm$ S.D. of two separate chemostat steady states.

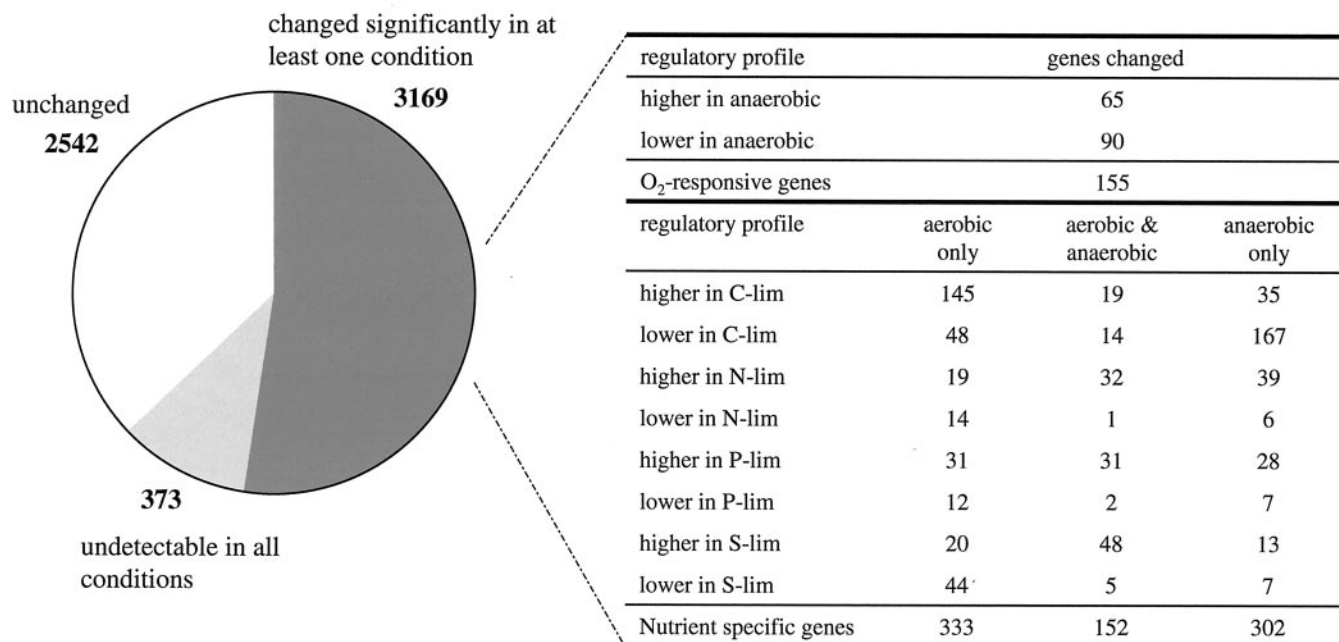


FIG. 2. Global transcriptional responses to growth in aerobic and anaerobic macronutrient-limited chemostats. The genome-wide transcript profiles of *S. cerevisiae* grown under different oxygen availability conditions and limitations (*lim*) for carbon, nitrogen, phosphorus, or sulfur are compared, and 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.

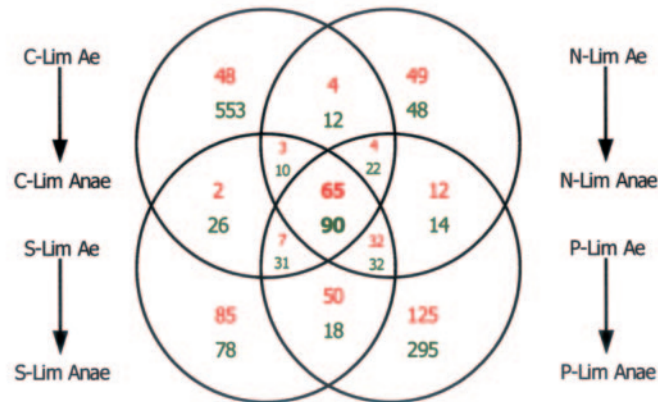
some specific observations on the macronutrient limitation-responsive genes.

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-regu-

lated and 90 down-regulated) (Fig. 3A).

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-

A



B

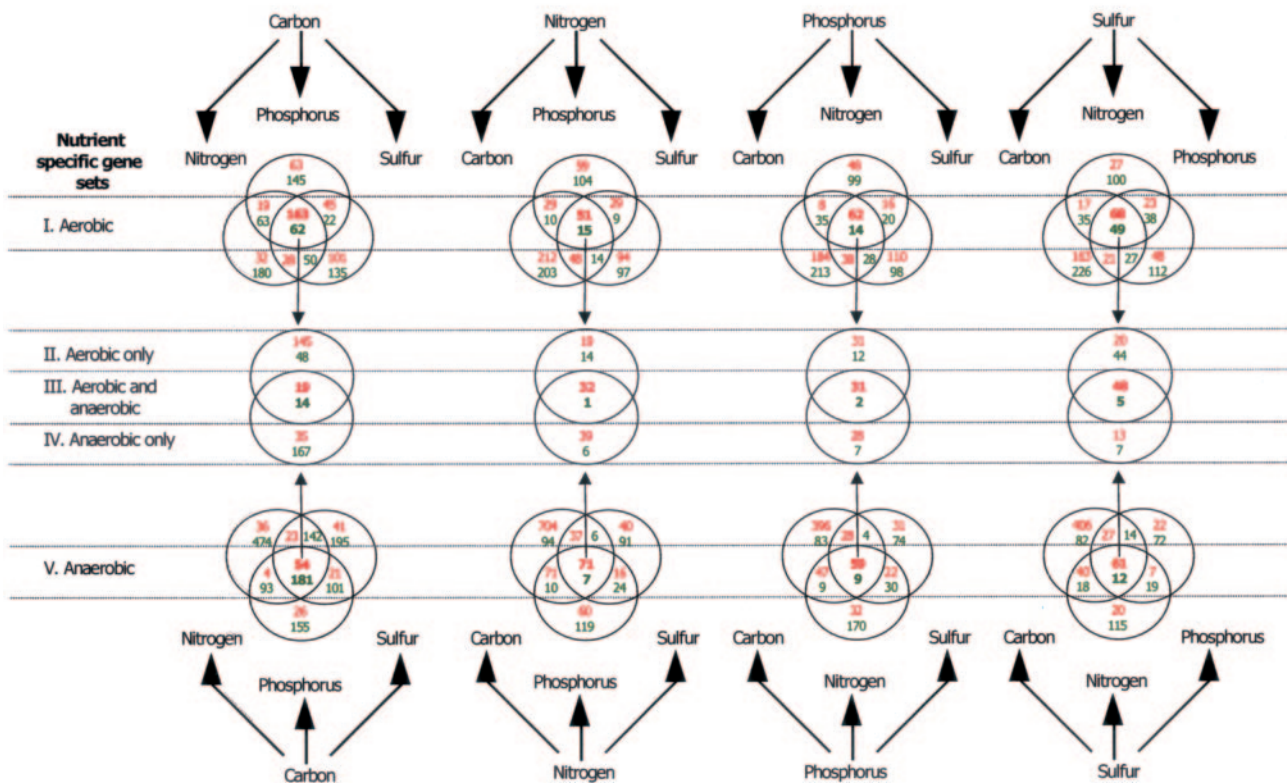


FIG. 3. Data mining strategy: dissection of the transcriptome response with respect to nutrient limitation and oxygen availability. A, Venn diagram of signature anaerobic genes. Red and green represent up-regulation and down-regulation, respectively, under anaerobic conditions. Each of the four circles 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-

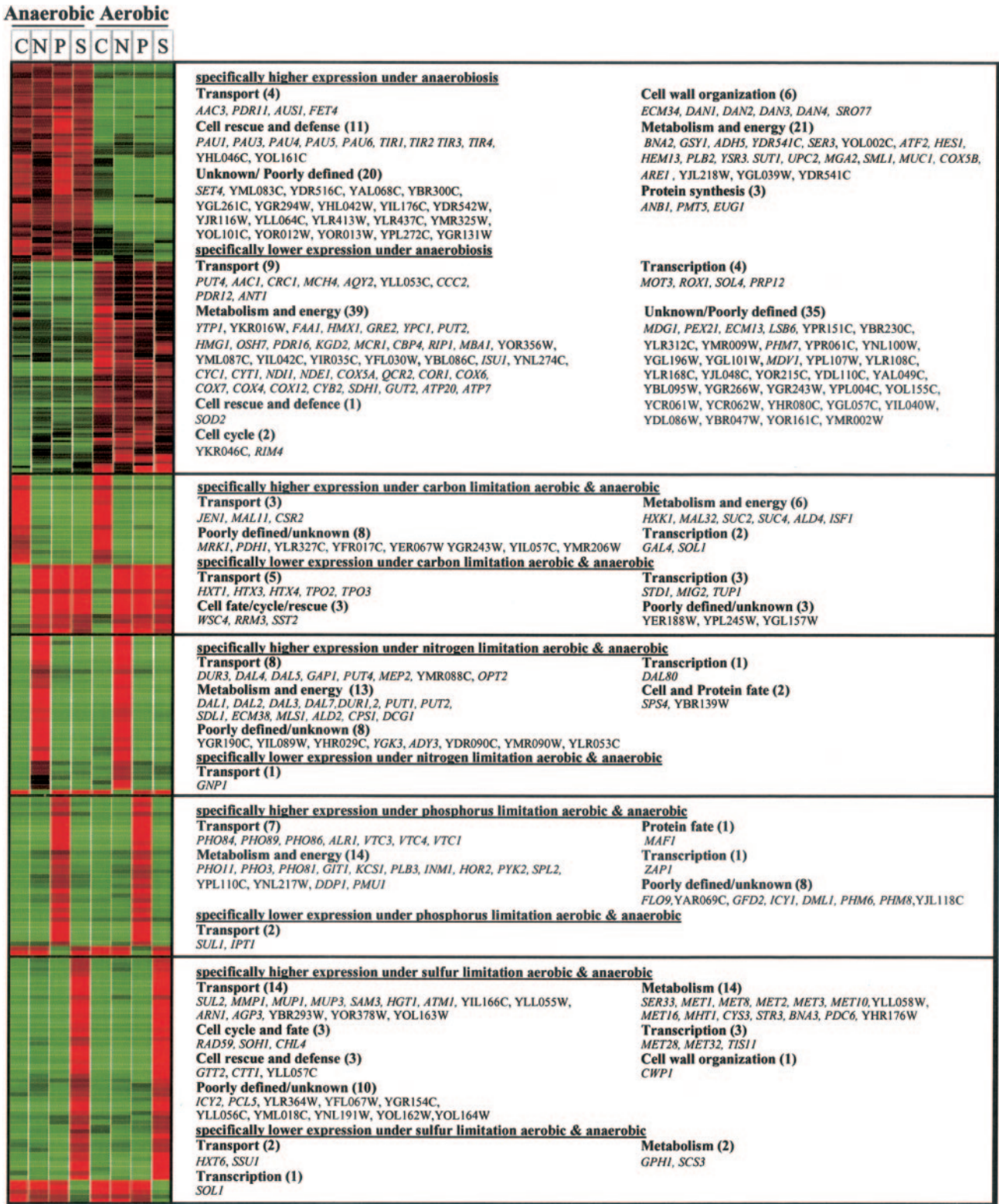


FIG. 4. Signature genes that respond to a single environmental parameter. The three independent transcriptome data sets for each condition were averaged and then compared. Green (relatively low expression) and red (relatively high expression) squares are used to represent the transcription profiles of 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 sphingo-

lipid metabolism, and phospholipase B₂, 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 coproporphyr-

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		%		%		0–3		
				38		8				
	ATTGTTC ^d	GAACAAT	Rox1p	26		12		0–3		
	ddACGAGG ^d	CCTCGThh	Up2p	40		18		0–2		
	TCGTwyAG ^d	CTrwACGA	Up2p	38		7		0–3		
				Set II ^e	Set III ^f	Set IV ^g		Set II	Set III	Set IV
Specifically higher in C limitation	dCCCCdh	dhGGGGh	Mig1p	43	65	25	28	0–5	0–6	0–5
Specifically higher in N limitation	rGATAAs	sTTATCy	Gln3p/Gat1p/Dal80p/Gzf3p	11	61	14	6	0–3	0–5	0–3
Specifically higher in P limitation	CAATGA	TCATTG	Dal82p	11	23	3	13	0–4	0–3	0–2
	mACGTGs	sCACGTk	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. 3B.

^f Set II, containing aerobic and anaerobic nutrient-specific genes, as in Fig. 3B.

^g Set III, containing anaerobic-only nutrient-specific genes, as in Fig. 3B.

nitrogen 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. 3A 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 (TCGTwyAG or CCTCGTwy) was recovered from 34 genes (52%) in the cluster. These sequences are similar to the previously described binding site for Up2p (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 Up2p 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 Up2p-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 sys-

tems 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 to 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 metallo-phosphatase (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

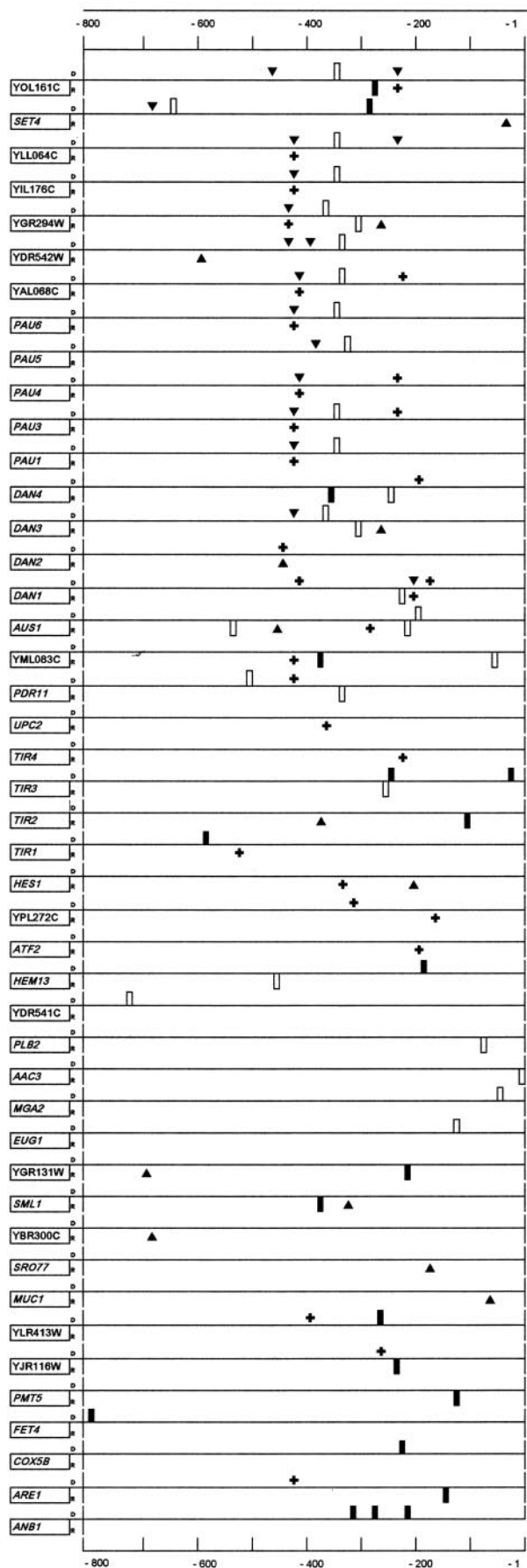


FIG. 5. Localization of the consensus binding site in promoter sequences of up-regulated genes in the absence of oxygen irrespective of nutrient limitation. The promoter regions of genes from

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 *mACGTGs* 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. 3B) 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. 3B), only 33 genes showed a consistent response to carbon limitation irrespective of the availability of oxygen (set III) (Fig. 3B). 193 genes (set II) (Fig. 3B) showed a significant transcriptional response only under aerobic conditions. Of the remaining 202 genes (set IV) (Fig. 3B), 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-

–800 to –1 were based on the sequences obtained from RSA Tools (23). ▲, Upc2p consensus sequence TCGTwyAG; ▼, Upc2p consensus sequence TCGTwyAG found on the Crich stand; +, Upc2p consensus sequence CCTCGThh; ■, 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 Crich 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.

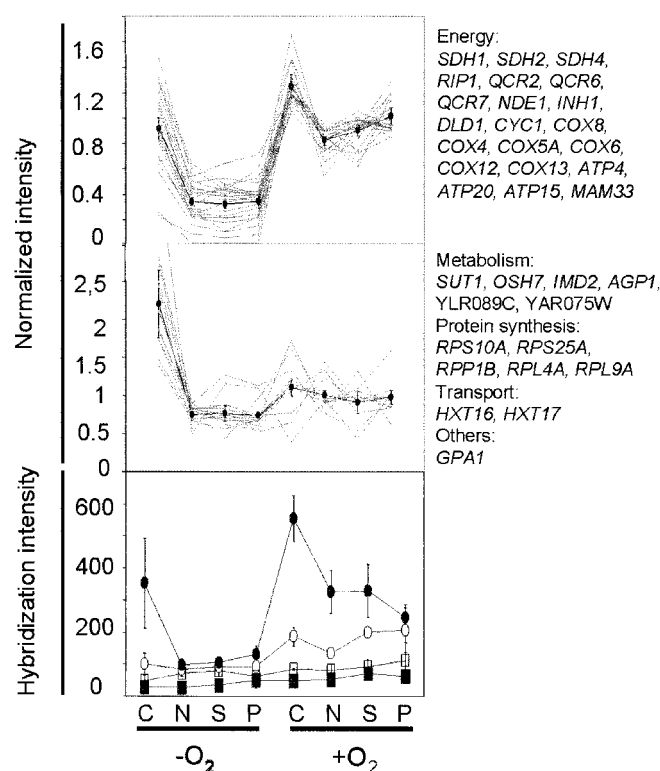


FIG. 6. Hierarchical regulatory control of gene expression. *Upper panel*, normalized transcript profiles of mitochondrial function-related genes that clustered with a set of genes that showed a specific transcriptional up-regulation upon carbon limitation in anaerobic cultures. The transcript level 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 (*RPS10A*, *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 ACCAATnA 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 post-genomic 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.

REFERENCES

- Edgar, R., Domrachev, M., and Lash, A. E. (2002) *Nucleic Acids Res.* **30**, 207–210
- Lelandais, G., Le Crom, S., Devaux, F., Vialette, S., Church, G. M., Jacq, C., and Marc, P. (2004) *Nucleic Acids Res.* **32**, D323–D325
- Wu, L. F., Hughes, T. R., Davierwala, A. P., Robinson, M. D., Stoughton, R., and Altschuler, S. J. (2002) *Nat. Genet.* **31**, 255–265
- Boer, V. M., de Winde, J. H., Pronk, J. T., and Piper, M. D. (2003) *J. Biol. Chem.* **278**, 3265–3274
- Higgins, V. J., Rogers, P. J., and Dawes, I. W. (2003) *Appl. Environ. Microbiol.* **69**, 7535–7540
- Schmidt, U., and Begley, C. G. (2003) *Int. J. Biochem. Cell Biol.* **35**, 119–124
- DeRisi, J. L., Iyer, V. R., and Brown, P. O. (1997) *Science* **278**, 680–686
- Gasch, A. P., Spellman, P. T., Kao, C. M., Carmel-Harel, O., Eisen, M. B., Storz, G., Botstein, D., and Brown, P. O. (2000) *Mol. Biol. Cell* **11**, 4241–4257
- Piper, M. D., Daran-Lapujade, P., Bro, C., Regenber, B., Knudsen, S., Nielsen, J., and Pronk, J. T. (2002) *J. Biol. Chem.* **277**, 37001–37008
- Daran-Lapujade, P., Jansen, M. L., Daran, J.-M., Van Gulik, W., de Winde, J. H., and Pronk, J. T. (2004) *J. Biol. Chem.* **279**, 9125–9138
- Wu, J., Zhang, N., Hayes, A., Panoutsopoulou, K., and Oliver, S. G. (2004) *Proc. Natl. Acad. Sci. U. S. A.* **101**, 3148–3153
- Ter Linde, J. J., Liang, H., Davis, R. W., Steensma, H. Y., van Dijken, J. P., and Pronk, J. T. (1999) *J. Bacteriol.* **181**, 7409–7413
- Koerkamp, M. G., Rep, M., Bussemaker, H. J., Hardy, G. P., Mul, A., Piekarska, K., Szegedy, C. A., De Mattos, J. M., and Tabak, H. F. (2002) *Mol. Biol. Cell* **13**, 2783–2794
- van Dijken, J. P., Bauer, J., Brambilla, L., Duboc, P., Francois, J. M., Gancedo, C., Giuseppe, M. L., Heijnen, J. J., Hoare, M., Lange, H. C., Madden, E. A., Niederberger, P., Nielsen, J., Parrou, J. L., Petit, T., Porro, D., Reuss, M., van Riel, N., Rizzi, M., Steensma, H. Y., Verrips, C. T., Vindelov, J., and Pronk, J. T. (2000) *Enzyme Microb. Technol.* **26**, 706–714
- van den Berg, M. A., Jong-Gubbels, P., Kortland, C. J., van Dijken, J. P., Pronk, J. T., and Steensma, H. Y. (1996) *J. Biol. Chem.* **271**, 28953–28959
- Visser, W., Scheffers, W. A., Batenburg-van der Vegte, W. H., and van Dijken, J. P. (1990) *Appl. Environ. Microbiol.* **56**, 3785–3792
- Ferea, T. L., Botstein, D., Brown, P. O., and Rosenzweig, R. F. (1999) *Proc. Natl. Acad. Sci. U. S. A.* **96**, 9721–9726
- Jansen, M. L., Daran-Lapujade, P., de Winde, J. H., Piper, M. D., and Pronk, J. T. (2004) *Appl. Environ. Microbiol.* **70**, 1956–1963
- Verduyn, C., Postma, E., Scheffers, W. A., and van Dijken, J. P. (1992) *Yeast* **8**, 501–517
- Verduyn, C., Postma, E., Scheffers, W. A., and van Dijken, J. P. (1990) *J. Gen. Microbiol.* **136**, 395–403
- Postma, E., Kuiper, A., Tomasow, W. F., Scheffers, W. A., and van Dijken, J. P. (1989) *Appl. Environ. Microbiol.* **55**, 3214–3220
- Tusher, V. G., Tibshirani, R., and Chu, G. (2001) *Proc. Natl. Acad. Sci. U. S. A.*

- 98, 5116–5121
23. van Helden, J., Andre, B., and Collado-Vides, J. (2000) *Yeast* **16**, 177–187
24. Mewes, H. W., Amid, C., Arnold, R., Frishman, D., Guldener, U., Mannhaupt, G., Munsterkotter, M., Pagel, P., Strack, N., Stumpflen, V., Warfsmann, J., and Ruepp, A. (2004) *Nucleic Acids Res.* **32**, D41–D44
25. Dwight, S. S., Balakrishnan, R., Christie, K. R., Costanzo, M. C., Dolinski, K., Engel, S. R., Feierbach, B., Fisk, D. G., Hirschman, J., Hong, E. L., Issel-Tarver, L., Nash, R. S., Sethuraman, A., Starr, B., Theesfeld, C. L., Andrada, R., Binkley, G., Dong, Q., Lane, C., Schroeder, M., Weng, S., Botstein, D., and Cherry, J. M. (2004) *Brief. Bioinform.* **5**, 9–22
26. Larsson, C., von Stockar, U., Marison, I., and Gustafsson, L. (1993) *J. Bacteriol.* **175**, 4809–4816
27. Rosenfeld, E., and Beauvoit, B. (2003) *Yeast* **20**, 1115–1144
28. Andreassen, A. A., and Stier, T. J. (1953) *J. Cell. Physiol.* **41**, 23–36
29. Andreassen, A. A., and Stier, T. J. (1954) *J. Cell. Physiol.* **43**, 271–281
30. Wilcox, L. J., Balderes, D. A., Wharton, B., Tinkelenberg, A. H., Rao, G., and Sturley, S. L. (2002) *J. Biol. Chem.* **277**, 32466–32472
31. Regnacq, M., Alimardani, P., El Moudni, B., and Berges, T. (2001) *Mol. Microbiol.* **40**, 1085–1096
32. Abramova, N., Sertil, O., Mehta, S., and Lowry, C. V. (2001) *J. Bacteriol.* **183**, 2881–2887
33. Jiang, Y., Vasconcelles, M. J., Wretzel, S., Light, A., Martin, C. E., and Goldberg, M. A. (2001) *Mol. Cell. Biol.* **21**, 6161–6169
34. Jiang, B., Brown, J. L., Sheraton, J., Fortin, N., and Bussey, H. (1994) *Yeast* **10**, 341–353
35. Sandager, L., Dahlqvist, A., Banas, A., Stahl, U., Lenman, M., Gustavsson, M., and Stymne, S. (2000) *Biochem. Soc. Trans.* **28**, 700–702
36. Mao, C., Saba, J. D., and Obeid, L. M. (1999) *Biochem. J.* **342**, 667–675
37. Fyrst, H., Oskouian, B., Kuypers, F. A., and Saba, J. D. (1999) *Biochemistry* **38**, 5864–5871
38. Merkel, O., Fido, M., Mayr, J. A., Pruger, H., Raab, F., Zandonella, G., Kohlwein, S. D., and Paltauf, F. (1999) *J. Biol. Chem.* **274**, 28121–28127
39. Kwast, K. E., Burke, P. V., Staahl, B. T., and Poyton, R. O. (1999) *Proc. Natl. Acad. Sci. U. S. A.* **96**, 5446–5451
40. Cohen, B. D., Sertil, O., Abramova, N. E., Davies, K. J., and Lowry, C. V. (2001) *Nucleic Acids Res.* **29**, 799–808
41. Lowry, C. V., Cerdan, M. E., and Zitomer, R. S. (1990) *Mol. Cell. Biol.* **10**, 5921–5926
42. Persson, B. L., Berhe, A., Fristedt, U., Martinez, P., Pattison, J., Petersson, J., and Weinander, R. (1998) *Biochim. Biophys. Acta* **1365**, 23–30
43. Lau, W.-T. W., Howson, R. W., Malkus, P., Schekman, R., and O'Shea, E. K. (2000) *Proc. Natl. Acad. Sci. U. S. A.* **97**, 1107–1112
44. Almaguer, C., Cheng, W., Nolder, C., and Patton-Vogt, J. (2004) *J. Biol. Chem.* **279**, 31937–31942
45. Ogawa, N., DeRisi, J., and Brown, P. O. (2000) *Mol. Biol. Cell* **11**, 4309–4321
46. Venter, U., and Horz, W. (1989) *Nucleic Acids Res.* **17**, 1353–1369
47. Meyhack, B., Bajwa, W., Rudolph, H., and Hinnen, A. (1982) *EMBO J.* **1**, 675–680
48. Norbeck, J., Pahlman, A. K., Akhtar, N., Blomberg, A., and Adler, L. (1996) *J. Biol. Chem.* **271**, 13875–13881
49. Murray, M., and Greenberg, M. L. (2000) *Mol. Microbiol.* **36**, 651–661
50. Cartwright, J. L., and McLennan, A. G. (1999) *J. Biol. Chem.* **274**, 8604–8610
51. Boles, E., Schulte, F., Miosga, T., Freidel, K., Schluter, E., Zimmermann, F. K., Hollenberg, C. P., and Heinisch, J. J. (1997) *J. Bacteriol.* **179**, 2987–2993
52. Flick, J. S., and Thorner, J. (1998) *Genetics* **148**, 33–48
53. Saiardi, A., Erdjument-Bromage, H., Snowman, A. M., Tempst, P., and Snyder, S. H. (1999) *Curr. Biol.* **9**, 1323–1326
54. Zhao, H., and Eide, D. J. (1997) *Mol. Cell. Biol.* **17**, 5044–5052
55. Upadhya, R., Lee, J., and Willis, I. M. (2002) *Mol. Cell* **10**, 1489–1494
56. Fisher, F., and Goding, C. R. (1992) *EMBO J.* **11**, 4103–4109
57. Lodi, T., Alberti, A., Guiard, B., and Ferrero, I. (1999) *Mol. Gen. Genet.* **262**, 623–632
58. Seytter, T., Lottspeich, F., Neupert, W., and Schwarz, E. (1998) *Yeast* **14**, 303–310
59. Luttik, M. A., Overkamp, K. M., Kotter, P., de Vries, S., van Dijken, J. P., and Pronk, J. T. (1998) *J. Biol. Chem.* **273**, 24529–24534
60. Blom, J., De Mattos, M. J., and Grivell, L. A. (2000) *Appl. Environ. Microbiol.* **66**, 1970–1973
61. Ohlmeier, S., Kastaniotis, A. J., Hiltunen, J. K., and Bergmann, U. (2004) *J. Biol. Chem.* **279**, 3956–3979
62. Forsburg, S. L., and Guarente, L. (1989) *Genes Dev.* **3**, 1166–1178
63. Gancedo, J. M. (1998) *Microbiol. Mol. Biol. Rev.* **62**, 334–361
64. (2004) *Nat. Rev. Genet.* **5**, 229–237
65. Kwast, K. E., Lai, L. C., Menda, N., James, D. T., III, Aref, S., and Burke, P. V. (2002) *J. Bacteriol.* **184**, 250–265
66. Becerra, M., Lombardia-Ferreira, L. J., Hauser, N. C., Hoheisel, J. D., Tizon, B., and Cerdan, M. E. (2002) *Mol. Microbiol.* **43**, 545–555
67. Quackenbush, J. (2003) *Science* **302**, 240–241
68. Homma, T., Iwahashi, H., and Komatsu, Y. (2003) *Cryobiology* **46**, 230–237
69. Kellis, M., Patterson, N., Endrizzi, M., Birren, B., and Lander, E. S. (2003) *Nature* **423**, 241–254

Supplementary data Table 1

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

Up-regulated under anaerobiosis (FC = fold change, ANA = anaerobic, A = aerobic)			cellular function																				
Probe Set	Gene name	systematic name	functional description	C-Lim A Average	C-Lim ANA Sider	N-Lim ANA Average	N-Lim ANA Sider	P-Lim ANA Average	P-Lim ANA Sider	S-Lim ANA Average	S-Lim ANA Sider	C-Lim A Average	C-Lim ANA Sider	N-Lim A Average	N-Lim A Sider	P-Lim A Average	P-Lim A Sider	S-Lim A Average	S-Lim A Sider	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	MG42	YR033W	YR033W may be involved in the remodeling chromatin structure	50.3	56.4	109.7	27.1	102.3	7.6	7.8	29.4	43.7	102.3	7.6	29.4	43.7	23.7	24.5	4.7	4.3	3.7	3.1	
7480_at	SR077	YIL106C	YIL106C yeast homolog of the <i>Drosophila</i> tumor suppressor; lethal giant larvae	244.2	159.3	344.7	61.7	255.5	45.1	258.8	47.7	83.9	19.2	78	13.8	56.9	15.1	37.1	8.9	24.5	4.4	6.9	
11446_at	PAU1	YIL220C	member of the serpinase protein/gene family	443.2	494.1	256.6	60.8	145.1	185.2	209.7	4.6	158.3	129.7	35.3	17	46.3	27	6.4	18.9	4.7	16.4		
4114_at	TR3	YIL011W	YIL011W strongly similar to members of the Srp1p/Tip1p family	389.7	119.9	243.57	592.6	333.7	80.3	330.2	390.3	252.3	93.3	88.8	6	84.2	13.7	174	17.3	15.9	2.6	3.6	
4563_at	PAU5	0 YHL046C	YHL046C strongly similar to members of the Srp1p/Tip1p family	132.71	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_at	TR1	YIL020C	member of the serpinase protein/gene family (see Gene_class PAU)	274.8	274.8	294.2	43.1	356.4	623	188	160.3	109.8	42.8	56	41.6	19.6	67.8	8.4	4.1	6.9	4.6	8.6	
5711_at	YER011W	YER011W Gold shock induced protein of the Srp1p/Tip1p family of serum-alanine-rich	4568.3	3906.3	3953.1	1303.2	4155.5	210.5	4857.4	1028.3	1487	28.1	74.4	11.6	87.4	4.2	137	17.7	53.5	35.2	30.5	35.5	
6786_at	PAU3	YOR010W	YOR010W member of the serpinase protein/gene family (see Gene_class PAU)	361	204.7	216.1	12.2	462.3	42.3	633.5	247.7	139.3	116.5	24.3	65	15.6	45	28.4	6	2.6	8.9	22.3	
8526_at	TR4	YOR009W	YOR009W strongly similar to Tip1p and Trp2p	1466.6	1086.8	2031.6	474	2781.5	146	2998.7	421.9	100.8	44.4	48.7	7.1	42.5	6.1	93.4	29.3	34.2	4.6	6.4	32.1
8527_at	TR2	YOR010C	YOR010C Gold-shock induced protein of the Srp1p/Tip1p family of serum-alanine-rich	1583.1	194.4	599.7	71.5	1052.3	137.5	778.1	58.2	159.4	23.5	129.8	14.9	147.6	20.5	267.7	113.8	10.7	7.7	13.8	23.8
8750_at	TR1	0 YOL181C	YOL181C strongly similar to members of the Srp1p/Tip1p family	460.2	205.1	445.5	74.2	510.8	95.5	801	339.5	59.2	30.4	36.7	13.4	27.8	8.3	45.7	29.9	7.2	12.2	18.4	17.5
8786_at	PAU6	YNR070W	YNR070W member of the serpinase protein/gene family	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
10525_at	YRS3	YKR053C	YKR053C Dsb1 P-1 phosphatase	1218.8	292	825	123.6	1020.1	165.2	2020.3	532.7	214.2	117	114.3	12.7	87.6	6.2	140.6	39.9	5.8	10.7	9.3	13.2
10662_at	BN42	YJR070W	YJR070W similar to mammalian isodioxime 2,3-dioxygenase	317.3	62.8	194.4	28.8	293.8	38.8	332.6	33.8	156.2	42.5	83	2.8	78.4	9.8	54.3	17	2.4	3.7	6.1	3.6
11234_at	ECM34	YHL043W	YHL043W Extracellular Mucant	325	18.8	43.5	14.1	81.7	20.5	76.6	9.5	12	2.9	14.1	3.4	12	27	12	0.6	6.8	6.4	4.6	6.4
4200_at	COO58	YIL111W	YIL111W Cytochrome c-c oxidase chain Vb	149.8	32.6	150.7	15.3	117.9	10.8	169.3	19.9	15.7	0.6	84.5	6.5	31.9	8.1	57.8	18.8	2.3	3.7	2.8	3.8
5357_at	GSY1	YR0105C	YR0105C Glycogen synthase (UDP-glucose-2-UTP glucosyltransferase)	359	60.1	236.9	29	85.5	132	192.7	42.9	92	13.3	68.4	29.9	25.5	34	53.1	6.6	3.9	3.5	3.6	3.9
5696_at	YRS3	YKR053C	YKR053C Dsb1 P-1 phosphatase	852.9	235.7	604.7	60.4	559.8	76.9	1048.4	98.2	43.5	29	56.3	7.5	58	5.8	79.3	21.4	5.8	10.7	9.3	13.2
4876_at	TR4	0 YGR131W	YGR131W strongly similar to Ncdp	214.6	68.9	310.6	58.9	316.2	24.8	508.3	124.8	28.4	5.8	35.3	3.2	18.4	4.4	22.9	8.2	7.6	7.1	10.7	12.8
4565_at	ECM34	YHL043W	YHL043W Extracellular Mucant	325	18.8	43.5	14.1	81.7	20.5	76.6	9.5	12	2.9	14.1	3.4	12	27	12	0.6	6.8	6.4	4.6	6.4
4200_at	COO58	YIL111W	YIL111W Cytochrome c-c oxidase chain Vb	149.8	32.6	150.7	15.3	117.9	10.8	169.3	19.9	15.7	0.6	84.5	6.5	31.9	8.1	57.8	18.8	2.3	3.7	2.8	3.8
5357_at	GSY1	YR0105C	YR0105C Glycogen synthase (UDP-glucose-2-UTP glucosyltransferase)	359	60.1	236.9	29	85.5	132	192.7	42.9	92	13.3	68.4	29.9	25.5	34	53.1	6.6	3.9	3.5	3.6	3.9
10662_at	BN42	YJR070W	YJR070W similar to mammalian isodioxime 2,3-dioxygenase	317.3	62.8	194.4	28.8	293.8	38.8	332.6	33.8	156.2	42.5	83	2.8	78.4	9.8	54.3	17	2.4	3.7	6.1	3.6
11234_at	ECM34	YHL043W	YHL043W Extracellular Mucant	325	18.8	43.5	14.1	81.7	20.5	76.6	9.5	12	2.9	14.1	3.4	12	27	12	0.6	6.8	6.4	4.6	6.4
4200_at	COO58	YIL111W	YIL111W Cytochrome c-c oxidase chain Vb	149.8	32.6	150.7	15.3	117.9	10.8	169.3	19.9	15.7	0.6	84.5	6.5	31.9	8.1	57.8	18.8	2.3	3.7	2.8	3.8
5357_at	GSY1	YR0105C	YR0105C Glycogen synthase (UDP-glucose-2-UTP glucosyltransferase)	359	60.1	236.9	29	85.5	132	192.7	42.9	92	13.3	68.4	29.9	25.5	34	53.1	6.6	3.9	3.5	3.6	3.9
10662_at	BN42	YJR070W	YJR070W similar to mammalian isodioxime 2,3-dioxygenase	317.3	62.8	194.4	28.8	293.8	38.8	332.6	33.8	156.2	42.5	83	2.8	78.4	9.8	54.3	17	2.4	3.7	6.1	3.6
11234_at	ECM34	YHL043W	YHL043W Extracellular Mucant	325	18.8	43.5	14.1	81.7	20.5	76.6	9.5	12	2.9	14.1	3.4	12	27	12	0.6	6.8	6.4	4.6	6.4
4200_at	COO58	YIL111W	YIL111W Cytochrome c-c oxidase chain Vb	149.8	32.6	150.7	15.3	117.9	10.8	169.3	19.9	15.7	0.6	84.5	6.5	31.9	8.1	57.8	18.8	2.3	3.7	2.8	3.8
5357_at	GSY1	YR0105C	YR0105C Glycogen synthase (UDP-glucose-2-UTP glucosyltransferase)	359	60.1	236.9	29	85.5	132	192.7	42.9	92	13.3	68.4	29.9	25.5	34	53.1	6.6	3.9	3.5	3.6	3.9
10662_at	BN42	YJR070W	YJR070W similar to mammalian isodioxime 2,3-dioxygenase	317.3	62.8	194.4	28.8	293.8	38.8	332.6	33.8	156.2	42.5	83	2.8	78.4	9.8	54.3	17	2.4	3.7	6.1	3.6
11234_at	ECM34	YHL043W	YHL043W Extracellular Mucant	325	18.8	43.5	14.1	81.7	20.5	76.6	9.5	12	2.9	14.1	3.4	12	27	12	0.6	6.8	6.4	4.6	6.4
4200_at	COO58	YIL111W	YIL111W Cytochrome c-c oxidase chain Vb	149.8	32.6	150.7	15.3	117.9	10.8	169.3	19.9	15.7	0.6	84.5	6.5	31.9	8.1	57.8	18.8	2.3	3.7	2.8	3.8
5357_at	GSY1	YR0105C	YR0105C Glycogen synthase (UDP-glucose-2-UTP glucosyltransferase)	359	60.1	236.9	29	85.5	132	192.7	42.9	92	13.3	68.4	29.9	25.5	34	53.1	6.6	3.9	3.5	3.6	3.9
10662_at	BN42	YJR070W	YJR070W similar to mammalian isodioxime 2,3-dioxygenase	317.3	62.8	194.4	28.8	293.8	38.8	332.6	33.8	156.2	42.5	83	2.8	78.4	9.8	54.3	17	2.4	3.7	6.1	3.6
11234_at	ECM34	YHL043W	YHL043W Extracellular Mucant	325	18.8	43.5	14.1	81.7	20.5	76.6	9.5	12	2.9	14.1	3.4	12	27	12	0.6	6.8	6.4	4.6	6.4
4200_at	COO58	YIL111W	YIL111W Cytochrome c-c oxidase chain Vb	149.8	32.6	150.7	15.3	117.9	10.8	169.3	19.9	15.7	0.6	84.5	6.5	31.9	8.1	57.8	18.8	2.3	3.7	2.8	3.8
5357_at	GSY1	YR0105C	YR0105C Glycogen synthase (UDP-glucose-2-UTP glucosyltransferase)	359	60.1	236.9	29	85.5	132	192.7	42.9	92	13.3	68.4	29.9	25.5	34	53.1	6.6	3.9	3.5	3.6	3.9
10662_at	BN42	YJR070W	YJR070W similar to mammalian isodioxime 2,3-dioxygenase	317.3	62.8	194.4	28.8	293.8	38.8	332.6	33.8	156.2	42.5	83	2.8	78.4	9.8	54.3	17	2.4	3.7	6.1	3.6
11234_at	ECM34	YHL043W	YHL043W Extracellular Mucant	325	18.8	43.5	14.1	81.7	20.5	76.6	9.5	12	2.9	14.1	3.4	12	27	12	0.6	6.8	6.4	4.6	6.4
4200_at	COO58	YIL111W	YIL111W Cytochrome c-c oxidase chain Vb	149.8	32.6	150.7	15.3	117.9	10.8	169.3	19.9	15.7	0.6	84.5	6.5	31.9	8.1	57.8	18.8	2.3	3.7	2.8	3.8
5357_at	GSY1	YR0105C	YR0105C Glycogen synthase (UDP-glucose-2-UTP glucosyltransferase)	359	60.1	236.9	29	85.5	132	192.7	42.9	92	13.3	68.4	29.9	25.5	34	53.1	6.6	3.9	3.5	3.6	3.9
10662_at	BN42	YJR070W	YJR070W similar to mammalian isodioxime 2,3-dioxygenase	317.3	62.8	194.4	28.8	293.8	38.8	332.6	33.8	156.2	42.5	83	2.8	78.4	9.8	54.3	17	2.4	3.7	6.1	3.6
11234_at	ECM34	YHL043W	YHL043W Extracellular Mucant	325	18.8	43.5	14.1	81.7	20.5	76.6	9.5	12	2.9	14.1	3.4	12	27	12	0.6	6.8	6.4	4.6	6.4
4200_at	COO58	YIL111W	YIL111W Cytochrome c-c oxidase chain Vb	149.8	32.6	150.7	15.3	117.9	10.8	169.3	19.9	15.7	0.6	84.5	6.5	31.9	8.1	57.8	18.8	2.3	3.7	2.8	3.8
5357_at	GSY1	YR0105C	YR0105C Glycogen synthase (UDP-glucose-2-UTP glucosyltransferase)	359	60.1	236.9	29	85.5	132	192.7	42.9	92	13.3	68.4	29.9	25.5	34	53.1	6.6	3.9	3.5	3.6	3.9
10662_at	BN42	YJR070W	YJR070W similar to mammalian isodioxime 2,3-dioxygenase	317.3	62.8	194.4	28.8	293.8	38.8	332.6	33.8	156.2	42.5	83	2.8	78.4	9.8	54.3	17	2.4	3.7	6.1	3.6
11234_at	ECM34	YHL043W	YHL043W Extracellular Mucant	325	18.8	43.5	14.1	81.7	20.5	76.6	9.5	12	2.9	14.1	3.4	12	27	12	0.6	6.8	6.4	4.6	6.4
4200_at	COO58	YIL111W	YIL111W Cytochrome c-c oxidase chain Vb	149.8	32.6	150.7	15.3	117.9	10.8	169.3	19.9	15.7	0.6	84.5	6.5	31.9	8.1	57.8	18.8	2.3	3.7	2.8	3.8
5357_at	GSY1	YR0105C	YR0105C Glycogen synthase (UDP-glucose-2-UTP glucosyltransferase)	359	60.1	236.9	29	85.5	132	192.7	42.9	92	13.3	68.4	29.9	25.5	34	53.1	6.6	3.9	3.5	3.6	3.9
10662_at	BN42	YJR070W	YJR070W similar to mammalian isodioxime 2,3-dioxygenase	317.3	62.8	194.4	28.8	293.8	38.8	332.6	33.8	156.2	42.5	83	2.8	7							

9724_at	HMG1	YML079C	YML079C 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 YLR186C	YLR186C probably involved in intramitochondrial protein sorting	UNKNOWN	49.1	24.4	47.7	7.1	33.3	4.9	38.6	8.3	206.6	71.9	279.4	37.8	316.4	29	252.3	37.7	-5.3	-5.9	-6.5	-6.5
10290_at		COX12	YLR038C subunit VIIa of cytochrome c oxidase	OXIDATIVE PHOSPHORYLATION	1158.6	252.6	386.2	105	364.7	44.8	436	94	2507.4	46.2	1928.2	20.5	2062.8	59.2	1995.4	168.5	-2.1	-6	-5.7	-4.5
4799_at		PQ321	YOR029C 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	-2.9	-10.7	-5.4	-3.3
7943_at		QCR2	YPR191W 45 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	-6	-6.6	-7.2
10591_at		ATV7	YKL016C ATP synthase ε subunit	ATP SYNTHESIS	409.5	104.1	226.3	22.1	82.7	23.4	134.9	6.8	839.5	145.4	902	32.3	555.2	49.3	497.1	47.7	-2	-2.5	-3.4	-3.5
4768_at		SOL4	YOR248W 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	YMR022C integral membrane mitochondrial protein	RNA 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	-3.4	-3.5
9595_at		MOT3	YMR070W 2 Cys-His-His 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	20.8	13.1	25.5	1.6	-2.2	-2.1	-2.5	-2.1
10377_at		AQY2	YLL053C similar 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	2129.6	758.2	-2.2	-15.7	-12.4	-12.4
10376_at		AQY2	YLL053C member of msp 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		CCO2	YOR270W Copper-transporting P-type ATPase with similarity to human Menkes and Wils	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	-3.1
7831_at		PRD12	YPR088C 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		PJT4	YOR048C putative proline-specific permease	TRANSPORT	16.9	6.6	176	26.5	28.1	6.5	21.7	8.9	1262.8	181	2507.3	294	138.5	44.6	616.2	179.5	-74.7	-14.5	-4.9	-23.9
8669_at		MCH4	YOL119C similar to monocarboxylate transporter proteins	UNKNOWN	27.9	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
9596_at		AAC1	YMR050C YMR050C mitochondrial ADP/ATP translocator	TRANSPORT	60.1	1.7	117.5	14.6	102.6	22	72.4	10	528.7	75.7	462.7	67	352.6	26	439.8	223.8	-8.8	-4.1	-3.4	-6.1
10027_at		0 YLR121C	YLR121C 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	154	-6.1	-10.8	-3.3	-10.8
10227_at		0 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	174	112.3	3.8	-4.5	-7.7	-4.9	-7.7
11095_at		LSB6	0 YAL048C YAL048C similarity to hypothetical protein YBR273c	UNKNOWN	103.1	23.2	137.5	14.8	115.6	2.3	143.8	3.2	544.7	56.2	409.6	67.8	473	42	397.5	39.8	-5.3	-3.3	-4.1	-2.8
11102_at		VAL100W	VAL100W 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	-4.2	-12.9
11135_at		MDV1	VAL112W similar to Mcb2p and N. crassa sulfur control-2	UNKNOWN	28.5	17.6	75.2	14.3	58.8	4.9	41.2	3.7	154.1	42.7	210.1	19.7	194.3	34.1	146.7	13.2	-5.8	-2.7	-3.3	-3.6
11359_at		0 YAL049C	YAL049C weak similarity to Legionella small 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 YLD040W	YLD040W 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	51.1	125.1	36.7	-2.4	-2.1	-2.3	-2.4
4462_at		0 YHR080C	YHR080C similarity to hypothetical protein YOR056c, YFL042c and YLR072w	UNKNOWN	23.4	13.8	39.7	5.3	31.9	4.1	25.1	4.2	85.4	21.4	109.8	14.6	75.7	3.9	95	25.5	-4.1	-2.8	-2.4	-3.8
4742_at		0 YGR268W	YGR268W hypothetical protein	UNKNOWN	20.8	5.4	24.2	4.9	21.7	5	21.4	2.6	87.2	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 YOR024W	YOR024W strong similarity to hypothetical protein YHR162w	UNKNOWN	384.2	140.3	68	1.2	59.6	5.9	77	21.3	1789.2	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 YGL186W	YGL186W hypothetical protein	UNKNOWN	24.3	10.6	90.4	25.3	81.6	3.1	51	6.6	148.6	29.2	284.4	37	123.9	7.8	113.6	30.4	-6.1	-3.1	-4.2	-2.2
6555_at		0 YDL086W	YDL086W similarity to hypothetical C. elegans protein C56A3.8	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	-4.8	-2.9	-4.8
6576_at		0 YOL115C	YOL115C hypothetical protein	UNKNOWN	185.7	14.9	150.4	14.4	112.6	38.7	140.1	10.5	695.2	90.4	893.7	43.2	327.1	38.3	441.3	86.6	-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	-1.2	-4.8	-4.9	-6.1
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 YBL059W	YBL059W 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	487.7	77.1	381.6	17	353.3	70.4	-4.9	-7.4	-7.2	-7.7
7594_at		0 YPR161C	YPR161C 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 Synecoccus 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	-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	889.2	55.7	1241.9	65.8	-4.3	-3	-3.2	-3.4
7873_at		0 YPL101W	YPL101W hypothetical protein	UNKNOWN	16.8	8.2	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 YOR218C	YOR218C 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	169.1	39.5	2.5	-5.2	-3.5	-2.5	
8406_at		0 YOR161C	YOR161C similarity to C. elegans cosmid F35C6	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	-2.7	-2.7
8659_at		PHM7	YOL084W YOL084W similarity to A. thaliana hsp1 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	-3.8	-4.5	-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	2198	343.1	-4.3	-2.9	-6.1	-34.2
8977_at		0 YNL100W	YNL100W hypothetical protein	UNKNOWN	37.2	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	-3.8
9024_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

[illegible]

7928_at	UIP4	YPL188C	YPL188C weak similarity to Xenopus protein xlgp7	UNKNOWN	34.9	24.1	86.9	22.7	24.2	4.9	26.2	4.8	318.2	73.7	143.8	13.5	23.2	0.2	47.8	2.7	2.2	13.7	6.7
7957_at		YPL201C	YPL201C hypothetical protein	UNKNOWN	12	2.8	12	2	12	0.4	12	1	501.8	123	12	0.6	12	0.8	12	0.4	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	22	50.8	12.7	3.1	7.4	3.1
8020_at	FDH2	YPL270W	YPL270W formaldehyde dehydrogenase/purative pseudogene	UNKNOWN	12	0.2	12	1	12	1	12	3.3	157.7	7.3	12	0.5	12	1	6.9	12	6.3	86.8	86.8
8142_x_at	FDH1	YOR388C	YOR388C protein with similarity to formalate dehydrogenases	UNKNOWN	12	2.5	12	1	12	1	12	5.3	3028.9	529.5	12	2	12	2.5	15	2.5	169.1	169.1	
8382_at	DCO1	YOR180C	YOR180C Peroxisomal enoyl-CoA hydratase	UNKNOWN	12	2.8	12	1.5	12	1.3	12	0.7	36.1	8.3	12	2	12	2.5	12	3	3	3	3
8412_at	GCY1	YOR120W	YOR120W similar to mammalian adolitoxy 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	9.9	337.7	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
8515_at		YOL085W	YOL085W similarity to YOL026w	UNKNOWN	192.7	30.4	186.2	87	167.8	287	142.1	10.3	587.8	106	181.6	107.12	8.1	147.3	23.8	4.8	5.8	4	4
8542_at		YOL101C	YOL101C similarity to YOL026c and YDR462w	UNKNOWN	421.1	146.3	418.6	43.6	113.5	43.4	454.6	29.8	141.9	30.5	12	3.8	12	3	11.8	12	3.1	11.8	11.8
8563_at	MDH2	YOL128C	YOL128C cytosolic malate dehydrogenase	TCAC CYCLE	69.4	31.3	108	17.5	79.8	5.2	73.5	17	122.4	124.9	150.6	12.9	56.2	47	136.3	18.4	5.3	48	48
8607_at	PEX11	YOL147C	YOL147C Peroxisomal membrane protein	PEROXISOME BIOGENESIS	347.7	53.2	344.6	64.4	364.6	46.8	279.1	5	1018.6	170.4	468.1	44.7	468.9	46.9	379.3	39.9	2.2	2.7	2.7
8615_at	BI05	YNR050C	YNR050C transmembrane regulator of KAPA/DAPA transport	BIOTIN BIOSYNTHESIS	12	2.1	12	1.1	12	1	12	2.4	75.7	21.9	31.5	6.5	22.7	4.8	25.5	7.2	2.4	2.9	2.4
8617_at	BI04	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	1.8	47.8	9.2	2.5	2.4	2.4
8619_at	FRE3	YNR050W	YNR050W 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	3.6	3.6
8650_at	FUN34	YNR020C	YNR020C Putative transmembrane protein	UNKNOWN	145.6	74.5	70.5	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	SP01	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	2.7	2.7	2.7
8886_at	IDP3	YNL009W	YNL009W peroxisomal NADP-dependent isocitrate dehydrogenase	TCAC CYCLE	12.7	7.4	21.6	4.7	21.2	5.1	23.9	7.3	174.6	34.7	25.8	17	23.8	2.5	20.1	4.2	6.8	6.7	6.7
9057_at	SPF19	YNL200W	YNL200W 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	18.5	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	10.7	10.7
9065_at		YNL194C	YNL194C strong similarity to YNL222c and similarity to SurP	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	6.4	6.4
9134_at	ALP1	YNL270C	YNL270C Protein highly homologous to permeases Car1p and Lyp1p for basic amino acid transport	TRANSPORT	12.8	4.6	19.3	4.1	12	1.2	15.8	5.8	43.1	10.2	19.3	1.2	14	13.7	3.4	3.2	3.9	3.2	3.2
9196_x_at		YNL335W	YNL335W similar to M verrucaria cyanamide hydratase. identical to hypothetical protein	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	10.8	12	10.8
9309_at	CAT2	YMR303C	YMR303C alcohol dehydrogenase II	GLYCOLYSIS	28.4	2.7	24.3	5.2	24.1	7.7	20	8.2	3295.2	1249	22.5	4.1	37.3	0.4	52.1	15.4	144.5	67.3	62.4
9320_at	ADH8	YMR280C	YMR280C Zinc-cluster protein involved in activating gluconeogenic genes; related to Gal4	GLUCONEOGENESIS	12.9	9.4	12	1.9	12	4.6	12	11	57.5	11.8	14	4.5	15.6	2.6	17.7	5.6	4.1	3.7	3.7
9416_at		YMR191W	YMR191W hypothetical protein	UNKNOWN	119.1	42.2	100.5	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	2.6
9444_at	PAB3	YMR174C	YMR174C Cytosolic inhibitor of proteinase Pep4p	OSMOTIC STRESS RESPONSE	40	12.6	44.3	13.1	34	9	22.8	4.8	394.1	89.5	63.8	11.2	28.1	3.3	45.8	19.9	5.1	7.4	7.4
9445_at	SP18	YMR175W	YMR175W protein of unknown function	UNKNOWN	27.3	7.8	35.4	19	15.4	3.6	23.5	2.1	954.8	211.1	12	2.4	12	0.8	24	6.2	30.8	30.8	30.8
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	191	17.4	2.4	12	3.7	12	6.2	27.1	27.1	27.1
9535_at	SN01	YMR050C	YMR050C SN2 proximal OFF: stationary phase induced gene	UNKNOWN	16.4	9.5	12.9	3	14.7	3.9	30	5	461.9	74	13.3	13	12.8	3.9	23.1	21.4	3.7	3.3	3.3
9538_at	SM2	YMR050W	YMR050W encodes highly conserved 35 kDa protein that shows increased expression after	UNKNOWN	63.8	16.6	37.5	5.2	52.9	15.9	142.1	30.3	539.1	44.8	27	1.1	44.8	2.7	66.2	8.9	3.2	3.2	3.2
9549_at	FLB2	YMR107W	YMR107W hypothetical protein	UNKNOWN	18.8	15	73.2	10.5	21.7	7.2	19.4	8.5	362.7	320.3	12	1.5	15.9	1.3	12	4.1	218.6	165.3	218.6
9633_at	HXB2	YMR052C	YMR052C strong similarity to Ptp	PHOSPHOLIPID METABOLISM	97.23	171.1	511.8	61.3	555.2	50.2	731.4	6.3	282.7	97.2	81.5	10.8	68.8	1.21	68.2	4.9	8.6	8.6	8.6
9638_at	PLT2	YMR011W	YMR011W affinity hecose transporter-2	TRANSPORT	457.3	288.3	1159.8	50.9	934.1	136.4	1117.7	117.4	1744.9	308.4	42.1	21.5	597.5	69.8	202.6	49.9	1.9	1.9	1.9
9658_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	13.7	13.7
9702_at	CYB2	YML024C	YML024C Cytochrome b2 [β -lactate cytochrome c oxidoreductase]	UNKNOWN	24	23	14.5	26.7	4.1	12	24	23	14.5	26.7	4.1	12	24	23	14.5	26.7	4.1	12	12
9757_at	ADP3	YML128C	YML128C C-terminal part starting with as 292 cause growth inhibition when overexpressed	LACTIC ACID UTILIZATION	61.8	26.7	179.4	5.6	129.1	12.7	115.9	6.1	931.8	230.9	247.3	40.9	121.9	5.6	222.4	46.9	3.8	4.2	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
9802_at	CTP3	YLR141W	YLR141W Protein Transport	TRANSPORT	61.7	22	46.9	22	52.4	5.5	52.9	12	149.3	190.1	429	6.5	54.5	67.3	24.3	26.5	3	3	3
9831_at	FBR1	YLR377C	YLR377C (FBP1) Fructose-1,6-bisphosphatase, gluconeogenic enzyme; activity is inhibited	GLUCONEOGENESIS	12	3.1	12	1.5	12	4.2	12	1.6	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	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	FC C-Lim A vs N-Lim A	FC C-Lim A vs S-Lim A	FC C-Lim A vs P-Lim A
Average	Average	Average	Average	Average	Average	Average	Average	Average	Average	Average	Average	Average	Average	Average	Average	Average	Average	Average	Average	Average	Average	Average	Average
10159_at	YLR179C	YLR179C	strong similarity to Tkp1	UNKNOWN	12	18.1	103.3	83.2	114.12	90.7	11.9	56.7	627.9	123.2	11.16	92.2	92	907.2	92	907.2	-2.2	-3.2	-3.4
10227_at	YLR108C	YLR108C	strong similarity to YDR132c	UNKNOWN	12	29	23.8	3.9	21.5	2.8	23.1	0.7	38	10.6	107.9	12	166	174	112.3	3.8	-2.8	-4.4	-4.4
10358_at	YLR028W	YLR028W	similarity to multidrug resistance proteins	TRANSPORT	204	36.7	322.9	61.5	344.5	45.8	530.6	49.3	197	30.5	465	55.5	394.7	38.5	597.6	89.7	-2.3	-2.3	-2.3
10405_at	PTP2	YKR050W	Peptide transporter	TRANSPORT	60.4	40.1	161.9	47	160.4	7.6	291.9	2	504.9	34	34.9	76.1	122	117	116.7	11.9	-6.5	-6.5	-6.5
10634_at	PHD1	YKL043W	(PHD1) Transcription factor involved in regulation of filamentous growth	SPOROXYTHIAL GROWTH	1042.7	58.8	947.3	225.1	1060.1	257.8	1049.4	35.4	282.7	48.9	1190.3	278.8	606.7	84.2	984	53.4	-4.2	-2.1	-4.2
10634_at	MSN4	YKL062W	(MSN4) Zinc-finger transcriptional activator for genes regulated through Snf1p.	TRANSCRIPTION	60.4	16.9	90.5	13.8	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	-2.6	-2.6
11003_at	STEN	YKL209C	AEC transport of glycoprotein, component of a factor secretion pathway	UNKNOWN	180.3	29.8	265.9	35.2	265.9	35.2	265.9	35.2	265.9	35.2	265.9	35.2	265.9	35.2	265.9	35.2	-2.2	-2.2	-2.2
11004_at	YJR030C	YJR030C	strong 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	-2.5
11259_at	YJL213W	YJL213W	similarity to Methanobacillus ardiakii phosphatase related protein	UNKNOWN	151.5	27.2	119	22.1	159.8	12.5	261.9	45.6	32.7	18.9	364.9	73	356.3	66.6	238	58.8	-11.1	-10.9	-10.9
11260_at	OPT1	YJL212C	strong similarity to S pombe isop1 protein	UNKNOWN	12	13.1	21.6	17.7	17.7	11.9	20.8	11	11.9	42.2	110.5	40.7	47	14.5	80.7	47	14.5	12	12
4200_at	COX5B	YJL111W	YJL111W Cytochrome-c oxidase chain Vb	OXIDATIVE PHOSPHORYLATION	148.8	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	-4.7	-3.7	-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	76.4	22.8	1	61.2	4.5	47.7	1.2	219	89.3	-2.7	-8.6	-8.6
4330_at	OYE2	YHR179W	YHR179W YHR179W dehydrogenase involved in N-glycos																				

6905_at	FUS1	YCL027W	YCL027W series/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	YLO061C	YLO061C 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	2.2
7820_at		YPL150W	YPL150W similarity to sentr/robin protein kinases	UNKNOWN	36.5	8.5	69.8	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	2.3	2.6	2.6
7827_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	3.9	2.9
8505_at	HMS1	YOR032C	YOR032C myc-family transcription factor homolog	PSEUDOPHYLLAL 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	3.3	3.3
8780_at		YMR086C	YMR086C similarity to Bul/p	UNKNOWN	29.3	23.2	146.7	39.6	47.8	3.3	92.8	10.7	61.3	46.8	126.8	20	38.1	0.2	45.2	4.1	2.1	2.8	2.8
8993_at		YML129W	YML129W weak similarity to P. pneumoniae uridine kinase udk	UNKNOWN	59.9	30.6	145.7	24.8	68.2	13.4	103.1	18.1	62.6	24	269.1	12.8	77.3	5.2	42.9	8.2	4.3	6.3	6.3
9284_at	FET4	YMR319C	YMR319C Low-affinity Fet(d) transport protein	TRANSPORT	156.8	41.4	334.3	87.5	315.7	28.2	293.2	16.9	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 Sldew	N-Lim ANA Average	N-Lim ANA Sldew	P-Lim ANA Average	P-Lim ANA Sldew	S-Lim ANA Average	S-Lim ANA Sldew	C-Lim A Average	C-Lim A Sldew	N-Lim A Average	N-Lim A Sldew	P-Lim A Average	P-Lim A Sldew	S-Lim A Average	S-Lim A Sldew	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	17.5	124.4	18.8	348.8	56.7	2716.5	272.8	2125.6	758.2	-3.6	-7.8	-6.1
10378_at	AQZY	YLL052C	YLL052C member of mip family transmembrane channels	TRANSPORT, WATER	23.9	6.8	56.1	7.2	79.3	10	86	18.2	418.7	78.5	130.1	5.7	1356	120.9	1075.8	594.3	-3.2	-10.4	-8.3
11133_at	NCA3	YLL116C	YLL116C With NCA2, regulates proper expression of subunits 6 (Atp6p) and 5 (Atp5p) of ATP SYNTHESIS	ATP SYNTHESIS	27	11.8	44.1	6.8	47.6	5	48.1	15.7	152.3	79.6	13.8	5.7	87.5	11.9	90.3	14.8	-13.9	-6.3	-6.5
4801_at	HIP1	YGR019W	YGR019W histidine permease	TRANSPORT	12.6	18.6	69.3	9.5	133.9	23.4	186.2	17.3	96.8	15.2	37.7	5.7	105.5	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	307.5	126.5	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	YGR021C	YGR021C Heat shock protein located in the plasma membrane with a role in cellular pH homeostasis	STRESS	55.1	24.8	113.9	7.3	88.3	20.4	114.3	13.7	498.8	334.9	62	10.1	246.8	19.9	157.6	77.1	-4.1	-2.5	-4.1
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	STRESS	148.2	41.1	281.1	37.2	352.2	81.9	258.4	31.7	1769.5	371.3	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	190.4	818.6	12	3.1	846.6	181	29.5	3.9	-113.4	-70.9	-113.4
7999_at	ICY2	YPL250C	YPL250C weak similarity to YMR195w	UNKNOWN	185.4	37	163.7	27.8	90.5	138.9	234.3	2.6	304.7	122.5	128.4	33.5	1705.5	181.7	498.7	23.5	-2.4	-13.5	-3.9
8724_at		YPL155C	YPL155C similarity to glucan 1,4-alpha-glucosidase Stalp 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	1627.5	111.2	2196	343.1	-5.3	-8.5	-10.3
9058_at	FET3	YMR058W	YMR058W multicopper oxidase	TRANSPORT	13.8	6	15.2	2.4	45.5	23.1	12	44	126.3	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 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 Sldew	N-Lim ANA Average	N-Lim ANA Sldew	P-Lim ANA Average	P-Lim ANA Sldew	S-Lim ANA Average	S-Lim ANA Sldew	C-Lim A Average	C-Lim A Sldew	N-Lim A Average	N-Lim A Sldew	P-Lim A Average	P-Lim A Sldew	S-Lim A Average	S-Lim A Sldew	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		YLR083W	YLR083W similarity to hypothetical protein YKR019c	UNKNOWN	12	4.8	17.9	4	16.2	6.2	53.6	1.7	16.8	3.4	15.8	1.8	12	1.9	47.3	20.9	2.8	2.8	2.8
3626_at	COS10	YNR075W	YNR075W protein with strong similarity to subdometally-encoded proteins such as Cos10	UNKNOWN	52.9	35	194	64	211.9	37	279.2	33.3	12	1.7	12.2	4.8	12	34	34.5	11	2.5	2.5	2.5
3338_at	AS11	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
4235_at	ICR2	YIL120W	YIL120W similarity to antibiotic resistance proteins	UNKNOWN	21.4	15.8	28.2	3.1	34.9	1.8	49.4	1.7	22.7	7	26.7	1.9	3.1	64.5	1.6	3.1	3.1	4.6	4.6
4232_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	12	219	89.3	9.6	3.6	3.6
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
7815_at		YGR070W	YGR070W hypothetical protein	UNKNOWN	29.1	12.5	41.3	6.7	48.1	5.5	52.3	24.8	41.9	5.5	64.7	9	78.9	19.8	296.1	50.3	7.1	3.8	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	167	688.8	139	4.9	2.6	4.4
5535_at		YER186C	YER186C weak similarity to hypothetical protein YMR319w	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
6930_at	SHE9	YDR039W	YDR039W (identified by a library screen) that causes growth arrest when overexpressed	UNKNOWN	5.8	23.5	21.1	0.8	21.1	0.8	21.1	0.8	21.1	0.8	21.1	0.8	21.1	0.8	21.1	0.8	3.9	3.9	3.9
6577_at		YLO109C	YLO109C strong similarity to thiamine-repressed protein Thp4p	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	BUO23	YCR047C	YCR047C Protein carbonyl 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	4.6	4.6
6894_at	ALT4	YLO083W	YLO083W transmembrane transporter	UNKNOWN	75.3	45.2	158.6	67.3	139.4	56.9	177.6	61.7	13.7	13.7	108.7	20.6	108.7	10.7	16.3	3.9	4.3	4.3	4.3
7361_at	NTH2	YBR001C	YBR001C Neutral trehalase, highly homologous to Nthp1	TRISACCHARIDE 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	7.2	4.4	4.4
7427_at		YLR070C	YLR070C questionable ORF	UNKNOWN	12	2.8	12	2	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	YLR068W	YLR068W ribose-phosphate pyrophosphatase 4	UNKNOWN	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	4	4
7611_at		YPR125W	YPR125W suppressor of msc2-1 mutation	UNKNOWN	149.2	24	139.9	23.8	146.7	21.6	185.5	47.7	185.4	27.7	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	2.9	15.4
8726_at		YOL154W	YOL154W similarity to S. pombe gap FII	UNKNOWN	54	17.7	319.6	3	189.3	31.3	205.9	32.4	161.8	42	159.6	27	129.6	24.2	332.3	64	2.1	2.6	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	2.2	2.2
8896_at		YNL046W	YNL046W hypothetical protein	UNKNOWN	227.2	54.9																	

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	20.8	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		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	83.8	27.8	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	275.6	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	298.6	-3.2	-4	-3.2
4388_at	SPS100	YMR139C	YMR139C sporulation-specific wall maturation protein	SPORELIATION	12.1	5.2	31.7	2.7	26.4	4.8	30.3	2.8	310.8	232	42.1	6.5	18.5	6.2	40	13.3	-16.8	-2.3	-2.6
4732_at	GMD2	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 GOL3	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 (UOP-glucose-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	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	SPH1	YER150W	YER150W strong similarity to putative cell surface glycoprotein SedP	UNKNOWN	170.3	74.3	286.1	21.6	243.4	58.7	291.6	65.7	326.5	55.7	263.1	36.7	117.7	10.3	333.5	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	YEL040W	YEL040W member of the aspiopapsin 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	38.6	2.7	79.5	18.9	-4.5	-2	-2
6128_f_at	HXT7	YDR342C	YDR342C Hexose transporter	TRANSPORT	3224.6	606	1272.9	97.8	649.7	17.8	1460.7	173.8	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	-2.3	-2.3
6171_at	SLR2	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	250.6	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	64.1	10.5	42.9	7.7	42.8	2.1	18	6.2	36	4.7	-2.4	-2	-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	29.3	66.2	5.6	125.7	7.6	26.2	9.2	80.8	12.9	-2.5	-4.8	-3.5
7324_at		YBR058W	YBR058W Homolog to glucan-1,3-glucosidase (EC 3.2.1.5); S. cerevisiae) 2	UNKNOWN	49.9	19.8	128.8	27.6	40.8	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	8.7	67.8	15.7	64.9	5.7	277.3	42.6	358.2	81.8	80.8	8.6	183	20.7	-4.6	-5.9	-3
7631_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	-2.4	-2.1	-2.1
7643_at	SSU1	YPL092W	YPL092W sensitive to sulfite	SULFITE TOLERANCE	217.5	41	238	45.2	84.5	6.3	308.5	30.4	448.7	149.5	287.5	10.9	60.1	4.7	193.8	21.3	-7.5	-3.2	-4.8
7628_at	UPB4	YPL186C	YPL186C weak similarity to Xenopus protein xlgp7	UNKNOWN	34.9	24.1	88.9	22.7	24.2	4.9	28.2	4.6	316.2	73.7	143.8	13.5	23.2	0.2	47.8	4.7	-13.7	-6.2	-2.1
7674_at	USV1	YPL230W	YPL230W Up in Star/Vaion	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
8186_at	TYE7	YOR344C	YOR344C TYE7, a 53 kDa serine-rich protein, is a potential member of the basic region/helix	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	69	18.8	-3.4	-3	-4.9
8192_at	PUT4	YOR348C	YOR348C putative proline-specific peptidase	TRANSPORT	18.9	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	-16.5	-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	65.2	2502.8	1023.5	1288.4	124.2	274.9	17.6	2762.2	750.5	-10.6	-4.7	-10
8663_at	MDH2	YOL129C	YOL129C 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	2.9	27.9	3.1	12.5	1.8	29.6	11.5	-2.5	-2.4	-2.4
8786_at	SOL1	YMR034W	YMR034W hypothetical protein	TRANA SPLICING, PUTATIVE	928.9	166.7	405.9	61.1	144.5	16.2	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
9297_s_at		YMR322C	YMR322C strong similarity to YPL280w, YOR391c and YDR533a	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	-4.6	-4.6	-2.6
9341_at		YMR291W	YMR291W similarity to serifin 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
9380_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 con	TREHALOSE METABOLISM	92.9	13	221.5	2.6	116.5	25.2	147.7	16.8	261.8	25.3	322.8	108.1	115.2	9.7	276.9	15.2	-2.3	-2.4	-2.3
9802_at	CTR3	YLN411W	YLN411W 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)			C-Lim ANA																FC C-Lim ANA vs N-Lim ANA				
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	C-Lim ANA vs S-Lim ANA	FC C-Lim ANA vs P-Lim ANA
10253_at	C0X12	YLR098C	YLR098C 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	SDH2	YLR038C	YLR038C subunit VI 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	20.2	1956.4	168.5	3	3.2	2.7
10320_at	SDH1	YLR148C	YLR148C Succinate dehydrogenase (ubiquinone) iron-sulfur protein subunit	TCA CYCLE, OXIDATIVE PHOSPHORYLATION	1101.3	227	480.5	49.1	523.8	106.6	503.4	21.4	1717.7	48.4	1282.2	37.7	1016.4	20.4	1875.7	268.5	2.3	2.1	2.2
10725_at	SDH4	YLR148C	YLR148C Reovirus protein subunit of succinate dehydrogenase	TCA CYCLE, OXIDATIVE PHOSPHORYLATION	273.8	52.2	117.1	24.1	102.2	22.3	88.7	12.9	108.5	103.9	280.5	35.5	207.4	20.5	312.5	49.8	2.3	2.1	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	1.3	1.5	1.5
11264_s_at	MMAN3	YAR075W	YAR075W strong similarity to IMP dehydrogenases	YAR075W	1465.7	396.1	477.3	70.2	512.7	433.9	162.4	348.5	109.7	556.1	24.7	416.8	55.8	484.9	97.2	3.1	2.9	3.4	
4352_L_at	MD2	YHR218W	YHR218W IMP dehydrogenase; probable PUGS gene	NUCLEOTIDE METABOLISM	1393.9	164.9	379.3	28.1	398.3	62.3	261.7	29	262.2	50.9	586.4	30.9	387.6	15.6	411.4	62	3.7	3.6	3.3
4481_at	C0X6	YHR051W	YHR051W subunit VI of cytochrome c oxidase	OXIDATIVE PHOSPHORYLATION	663.7	42.4	277.4	47.9	292	31.8	290.3	93	1484.6	252.7	1031.6	84.3	1191.2	69.4	1234.6	140.3	2.4	2.3	2.3
4501_at	OSH7	YHR010W	YHR010W 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	60.7	682.9	21.1	765.1	91.3	689.3	114.9	3.2	4	3.3
4520_at	GPA1	YHR035C	YHR035C May act cooperatively with Mds30 in mitochondrial protein import or other related essential	MITOCHONDRIAL PROTEIN TARGETING	853	86	322.2	78.9	400.7	11.9	339.3	30	775.9	63.7	614.8	60.5	626.6	8.7	544.2	55.8	2.1	2.1	2.5
5000_s_at	RPS25A	YGR027C	YGR027C Ribosomal protein S25A (S21A) (Y523)	PROTEIN SYNTHESIS	801.3	25.3	316.9	11	341.5	92.7	312.8	44.3	562.6	87	485.1	12.7	476.4	51.7	412.9	59.8	2.3	2.6	2.6
5142_L_at	RPL1A	YGL147C	YGL147C Ribosomal protein L5A (L8A) (p24) (Y11)	PROTEIN SYNTHESIS	414.8	96.8	188.8	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	2.8	2.2
5173_L_at	SUT1	YGL162W	YGL162W Involved in sterol uptake	TRANSPORT	188.4	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	2.2	2.2	
5188_at	C0X13	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	68.5	798.9	24.8	801.4	17.2	750.7	34.3	743	59.8	3.7	2.3	2.1
5193_at	C0X4	YGL197C	YGL197C 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	688.9	48.7	938.7	40.1	1026.2	78.3	4.1	3.8	3.8
5332_at	QCR8	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	2.4	2.3
5766_at	RPI1	YLR024W	YLR024W Rese iron-sulfur protein of the mitochondrial cytochrome bc1 complex	RESPIRATION	692.1	66.5	201.9	78.4	267.7	3.4	334.3	121	1615	197.5	1136.3	59.8	1323.2	49	1270.6	205.3	3.4	2.4	2.1
5953_at	QCR7	YOR052C	YOR052C ubiquinol-cytochrome c oxidoreductase subunit 7 (14 kDa)	RESPIRATION	1450.8	374.7	609.6	68.7	616.7	84.4	474.8	34.2	184.1	277.6	1475.6	38.9	1030.8	61.2	1555.9	9	2.4	2.8	3.1
6128_L_at	HXT7	YOR342C	Hesxase transporter	TRANSPORT	3229.6	606	1272.9	67.8	649.7	17.8	1460.7	173.6	2254.9	201.2	1340.2	110.7	121.9	131.8	1420.4	88.5	2.5	5	2.2
6279_at	SDH4	YOR178W	YOR178W succinate dehydrogenase membrane anchor subunit	TCA CYCLE, OXIDATIVE PHOSPHORYLATION	1131	91.6	53.1	18.9	387.3	22	532.6	16.9	1688.7	82.2	972.8	110.1	747.1	137.1	1131.7	2.9	2.1	2.9	
6598_at	RFP1B	YOL130W	YOL130W ATPase stabilizing factor	PROTEIN SYNTHESIS	810.6	152.1	430.3	4	364.9	12.6	417	41	1324.5	135.6	595.2	40.3	410.7	18.8	747.3	78.5	4.1	3.1	3.1
6640_at	LDL1	YOL174C	YOL174C mitochondrial enzyme D-lactate ferrioxochrome c oxidoreductase	PROTEIN METABOLISM	608.7	6.4	209.1	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
6854_at	NH1	YOL181W	YOL181W ATPase inhibitor	ATP SYNTHESIS	352.9	102.6	102	17.3	41.1	25	83.2	14.5	798.8	152.7	510.7	90.5	370.6	113.2	706.3	164.1	3.5	4.6	4.2
6907_at	AGP1	YOL025C	YOL025C (AGP1) Broad substrate range amino acid permease with high affinity for asparagine and serine	ATP SYNTHESIS	762.9	56.7	155.9	23.1	363.4	38.5	346.5	31.2	87.2	28.6	206.8	17.3	204.4	116.9	353.1	52.1	2.9	3.2	2.2
7344_L_at	RPL4A	YBR031W	YBR031W Ribosomal protein L4A (L2A) (p2) (Y12)	PROTEIN SYNTHESIS	389.7	8.4	157.9	53.4	109.2	36.8	95.9	207	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	YPR181W	YPR181W 8.5 kDa ubiquinol-cytochrome c oxidoreductase core protein 2	OXIDATIVE PHOSPHORYLATION	121.6	85.5	78.6	1	106.8	58.7	106.8	15.1	188.5	16.1	176.8	6.8	158.4	10.4	158.4	76.8	3.3	3.3	3.3
7727_at	ATP2D	YPR020W	YPR020W hypothetical protein	ATP SYNTHESIS	79.7	15.4	34.1	3.8	26.9	0.5	30	6.1	276.7	11.3	173.3	16	184.6	21.4	187.4	40.4	2.3	3	2.7
7812_at	ATP1A	YPL078C	YPL078C F1 (F0)-ATPase complex delta subunit, mitochondrial	ATP SYNTHESIS	539.2	100.2	240.5	67	252.3	10.3	236.5	28.6	131	813.3	143.5	800.2	28.2	653.3	61.8	551.6	38.2	2.2	2.1
8024_at	ATP1F5	YPL271W	YPL271W nuclear gene for ATP synthase epsilon subunit	ATP SYNTHESIS	381.5	174.4	47.1	79	126.8	59.7	174	162	1206.8	84.3	804.3	43.4	809.7	110.3	829	27.3	2.4	2.3	2.3
8269_s_at	RPS10A	YOR029W	YOR029W Ribosomal protein S10A	PROTEIN SYNTHESIS	1923.9	133.3	912.9	220.7	830.2	187.1	788.3	183.7	1506.8	206.2	1008.3	212.9	1119	154.4	975.5	242.1	2.1	2.3	2.5
8535_at	C0X5A	YOL028W	YOL028W cytochrome c oxidase chain Va	OXIDATIVE PHOSPHORYLATION	55.1	14.6	16.1	1.2	16.1	1.2	16.1	5.1	146	16.2	58.4	5.1	70.2	194.2	150.4	38.7	2.3	2.3	2.3
9500_at	NDE1	YMR145C	YMR145C mitochondrial cytochrome c oxidase chain VII	OXIDATIVE PHOSPHORYLATION	115.7	23.4	45.7	6.1	28.7	4.4	40.9	3.4	1257.3	68.1	833.8	99.7	808.8	62.4	1153.7	124.9	2.5	4	2.8
9630_at	C0X8	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)			C-Lim ANA																FC C-Lim ANA vs N-Lim ANA				
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	C-Lim ANA vs S-Lim ANA	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	-2.2
10021_at	UBC12	YLR336W	YLR336W 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	-3.2	-3.2
10044_at	URF2	YLR246W	YLR246W (URF2) Protein involved in palmitoylation and localization of Ras2p	UNKNOWN	423.4	17.8	212.5	38.1	96.3	13.1	87.8	3.8	83	10.6	17.7	27	103	12.4	97.5	11.5	-4.9	-4.7	-4.9
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	-3.7	-3.7	-3.7
10106_at	FRE1	YLR214W	Fer1-like nuclear ubiquitin protease	IRON HOMEOSTASIS	15.7	8.1	41.7	10.5	38.4	2.4	38.4	1.9	46.4	10.9	43.5	5.4	32.7	2.9	45.2	8.4	-2.4	-2.4	-2.4
10118_at	BUR2	YLR228W	YLR228W hypothetical protein	UNKNOWN	17.8	12.2	38.3	15.8	53.8	8.9	43.7	1.4	34.1	3.9	46	47	62.5	12	57.3	14.8	-2.2	-2.3	-2.5
10119_at	ADY4	YLR227C	YLR227C hypothetical protein	UNKNOWN	21	8.5	78.1	17.8	42.8	7	44.7	22	44.8	47	60.6	7	36.5	5.2	36.6	13.9	-3.7	-2.8	-2.1
10162_at	SRN2	YLR119W	YLR119W suppressor of rna1-1 mutation	RNA EXPORT, PUTATIVE	24.7	12.7	12.7	12.7	12.7	12.7	12.7	12.7	12.7	12.7	12.7	12.7	12.7	12.7					

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	240.1	86	32.9	6.3	62.6	11.4	22.8	3.3	391	62.6	-2.4	-2.4	-20.8
5919_at		YDR540C	YDR540C hypothetical protein	UNKNOWN	22.9	13.2	96.6	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	-2.5	-2.9
5982_at	TLG1	YOR486C	YOR486C ENAGE that affects a Late Golgi compartment	UNKNOWN	37.7	27.8	119.6	30.6	105.8	1.6	87.4	1.6	80.4	11.4	123.8	11.4	119.6	22.8	79.3	18.4	-3.1	-3.1	-2.3
5987_at	PRP3	YDR473C	YDR473C essential splicing factor	MRNA SPLICING	32.9	19.5	85.6	21.6	92	7	79.4	28	70.6	10.6	109.7	7.1	94.6	20.3	87.4	7.5	-2.6	-2.6	-2.4
6018_at		YDR489C	YDR489C weak similarity to YNL226c	UNKNOWN	24.1	11.1	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	-2.7	-2.1
6105_at	CCD40	YDR546C	YDR546C Member of the beta transducin family	CELL CYCLE	29.2	12.2	79.9	69	12.4	18.8	61.1	4.8	56.7	8.6	79.3	20.5	73.1	13.3	83.9	18.1	-2.1	-2.1	-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	-3	-2.4
6233_at		YDR222W	YDR222W strong similarity to hypothetical protein YLR225c	UNKNOWN	12	5.2	36.4	10.6	35.9	34	40	11.7	58.9	16.2	73.2	9	94.6	4.7	52.1	11.2	-3	-3	-3.3
6257_at	VP684	YDR200C	YDR200C hypothetical to hypothetical protein YLR238w	UNKNOWN	27	11.7	57.2	11.9	56.9	42	54.9	10.1	50.1	16.6	96.7	7.2	66	6.6	55.3	5.7	-2.1	-2.1	-2.1
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	3.4	8.3	31.4	11	29.1	6.1	-2.6	-2.6	-6
6346_at		YDR111C	YDR111C strong similarity to alanine transaminase	UNKNOWN	20.8	11.7	94	13.2	196.1	30.7	66.1	7.9	131.1	11.2	69.7	1.8	129.9	13.3	18.2	6.1	-4	-4	-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	-3	-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	4.4	11.2	36.2	9.6	49.6	20.7	-3	-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	-3.4	-3.1
6447_at	MRH1	YDR033W	YDR033W strong similarity to putative heat shock protein YRO2	UNKNOWN	48.6	26.5	1041	224.5	97.1	141.2	1522.8	64.1	657.5	74.8	1939.9	20.7	1196.9	24.8	1986.6	404.1	-2.2	-2.2	-3.3
6483_at	DIA3	YOL040C	YOL040C strong similarity to acid phosphatase	UNKNOWN	18.9	4.9	54	15.7	51.2	1.6	84.1	10.5	42.9	7.7	42.8	2.1	1.8	6.2	36	4.7	-2.7	-2.7	-4.2
6513_at	PKC7	YOL038C	YOL038C 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	-2.9	-2.8
6514_at		YOL038C	YOL038C 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	-4.9	-4.9	-6.2
6762_x_at	KCC4	YOL044W	YOL044W 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	2.8	21.8	6.6	33.5	7.8	-2.5	-2.5	-2.8
6851_at	MAK32	YCR019W	YCR019W Protein required for structural stability of L-A double-stranded RNA- (dsRNA-) containing rRNA PROCESSING/MODIFICATION	UNKNOWN	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	-2.2	-2.3
6870_at	SFG29	YOL010C	YOL010C 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	-3.1	-3.1	-3.7
6905_at	FUS1	YOL027W	YOL027W 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	-2.8	-2.8	-4.6
6922_at	KAR4	YOL055W	YOL055W May assist Site12p in pheromone-dependent expression of KAR4 and CRK1	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	-2.1	-2.6
7127_at	APG12	YBR217W	YBR217W autophagy	UNKNOWN	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	-2.2	-2.5
7286_at		YBR020C	YBR020C Probable phosphatidylethanolamine-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	-2.6	-2.2
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	-2.3	-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	-4.3	-4.3	-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	-2.3	-2.3	-3.5
7463_at	NUPT10	YBL079W	YBL079W Nucleoporin highly similar to Nup157p and to mammalian Nup155p (nup170 mutant can be a NUCLEAR PROTEIN TARGETING	UNKNOWN	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	-3.9	-2.1
7484_at	AUT7	YBL079W	YBL079W Nucleoporin highly similar to Nup157p and to mammalian Nup155p (nup170 mutant can be a NUCLEAR PROTEIN TARGETING	UNKNOWN	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	-3.9	-2.1
7592_at	NCE102	YPR149W	YPR149W involved in secretion of proteins that lack classical secretory signal sequences	SECRETION, NON-CLASSICAL	208.6	24.4	1064.6	276.2	1195.4	121.2	1297.6	125.6	2303.3	593.7	1963	74.5	1771.8	144.4	2020.1	186.5	-2.1	-2.1	-2.6
7595_at		YPR152C	YPR152C hypothetical protein	UNKNOWN	30.4	11	66.7	7.7	76.9	22.7	66.3	18.4	66.1	17.3	44.2	6.3	194.6	14.1	79.6	27.5	-2.2	-2.2	-2.5
7601_at		YPR157W	YPR157W strong similarity to YCR2141w	UNKNOWN	13.5	30.3	6.1	32.1	39	4.3	34	15.4	2.1	3.2	1.8	19.7	3.5	14.8	4.5	-2.3	-2.3	-2.1	
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	14	139.1	5.3	68.7	19.2	-2.6	-2.6	-2.1
7603_at	NTN309	YPR101W	YPR101W splicing factor	MRNA SPLICING	31.1	19.3	32	6.1	89.7	12.1	65.7	15.2	11.8	16.2	15.2	11.8	16.2	15.2	11.8	16.2	-2.5	-2.5	-2.1
7651_at	CLB2	YPR119W	YPR119W G2p2p-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	49	21.3	3.1	-2.3	-2.3	-2.4
7660_at		YPR084W	YPR084W G2p2p-specific B-type cyclin	CELL CYCLE	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	-2.4	-2.1
7686_at	UBA3	YPR068W	YPR068W ubiquitin-like protein activating enzyme	PROTEIN DEGRADATION, RUBP-MEDIATED	13.6	6.6	10.4	13.6	6.6	10.4	13.6	6.6	10.4	13.6	6.6	10.4	13.6	6.6	10.4	13.6	-2.1	-2.1	-2.1
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	-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	-2.2	-2.2	-2.1
7755_at		YPR032C	YPR032C similarity to ubiquitin transposon protein	UNKNOWN	12.3	4.6	42.1	21	29	13.3	34	9.2	27.6	4.6	36.9	5.9	27.1	7.4	32.5	3.6	-3.4	-3.4	-2.1
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	-3.6	-4.3
7915_at		YPL159C	YPL159C weak similarity to YGL144c	UNKNOWN	20.6	12.5	22.1	48.3	12.7	45.7	20.6	12.5	48.3	12.7	45.7	20.6	12.5	48.3	12.7	45.7	-3.1	-3.1	-2.3
7971_at	NSL1	YPL233W	YPL233W hypothetical protein	UNKNOWN	17.2	3.8	35.3	9.9	43.9	8.4	42.4	3.3	25.9	3.4	41.1	17.5	30.2	4.4	48.2	1.8	-2.7	-2.7	-2.1
8145_x_at		YOR030W	YOR030W nearly identical to YNL279c	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	-2.4	-2.5
8218_at	PDR10	YOR032W	YOR032W Putative ABC transporter highly similar to Pdr5p	TRANSPORT	51.2	15.5	195	27.2	17.8	10.7	27.2	17.8	10.7	27.2	17.8	10.7	27.2	17.8	10.7	27.2	-2.1	-2.1	-2.1
8348_x_at		YOR192C	YOR192C strong similarity to Thi3p	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	3.4	-2.1	-2.1	-7.6
8351_at	TOA1	YOR194C	YOR194C Transcription factor IAA, 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	-2.3	-2.3	-2.3
8408_at		YOR161C	YOR161C similarity to C elegans coiled PDS28	UNKNOWN	12	4.7	66.7	6.5	27.2	2.1	57.8	12.6	25.3	67.5	6.6	29.2	3.4	138	29.2	-2.3	-2.3	-2.3	
8421_at	ORT1	YOR130C	YOR130C mitochondrial integral membrane protein	ARGININE METABOLISM	67.6	26.8	150	15.2	154.9	21.8	144	20.3	87.8	18	142.9	10.9	280.2	15.6	83	6.8	-2.2	-2.2	-2.1
8467_at		YOR058C	YOR058C weak similarity to YGL144c	UNKNOWN	153.9	68.7	433.4	67.9	416.8	54.6	342	44.6	21.1	10.9	382.6	88.4	714.6	40.5	293	41.7	-2.6	-2.6	-2.2
8490_at		YOR062C	YOR062C strong similarity to YOR075C	UNKNOWN	28.5	7.8	111.3	16.6	85.4	16.3	27.1	7.7	110.8	16.2	32.2	104.8	17.9	152	82.2	-3.9	-3.9	-2.2	
8524_at		YOR051C	YOR051C weak similarity to myosin heavy chain proteins	UNKNOWN	77.7	14.6	201.3	22.5	198.9	8.6	190.6	24.8	77.2	9.2	163.9	22	134	12	151.3	25.3	-2.7	-2.7	-2.5
8549_at	CN5	YOR026C	YOR026C Protein, can activate transcription from a promoter containing a Yap recognition site	UNKNOWN	20	10.9	136.3	43.1	198.5	16.4	163.4	20.5	129.3	11.3	126.4	10.8	148.4	10.1	160.4	16.4	-2.6	-2.6	-2.1
8627_at		YOL070C	YOL070C hypothetical protein	UNKNOWN	27	16.9</																	

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
4881_at	ROM1	YGR070W	YGR070W GDP-GTP Exchange Protein (GEP) for the Rho p 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	2.4	3.3
5140_at		YOL140C	YOL140C weak similarity to Lactobacillus putative histidine protein kinase SpkK	UNKNOWN	25.1	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	87.1	9.2	4.2	2.7	2.8
5534_at		YER185W	YER185W strong similarity to Rlm1p	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
5604_at	SPB3	YER046W	YER046W hypothetical protein	UNKNOWN	52.7	20.8	107.7	28.4	5.1	5.6	41.9	11.6	79.5	17.2	61.1	8.4	60.4	8.7	37.8	9.8	2	2.1	2.6
5816_at	HPA3	YOL060W	YOL060W Histone and other Protein Acetyltransferase; Has sequence homology to known HATs	CHROMATIN STRUCTURE	447.6	73.6	1550.2	121.2	485.4	87.6	361.4	31.2	522.7	31.3	1048.7	111.3	362.7	12.4	525.3	151.7	3	3	3.1
5844_at		YER052C	YER052C 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
6096_at		YOL391C	YOL391C strong similarity to hypothetical protein YGR013w	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	BR4	YDL231C	YDL231C (BR4) Protein of unknown function, has a putative zinc finger domain	UNKNOWN	69.9	26	264	34	108.3	47	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
7136_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 cotransporter protein	UNKNOWN	45.8	7.9	178.4	29.6	17	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-glucosylase (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	74.4	15.4	13.8	13.1	65.4	7.9	2.6	3.2	2.2
7528_at	UP4	YOL186C	YOL186C weak similarity to Xenopus protein xip7	UNKNOWN	34.9	24.1	86.9	22.7	24.2	4.9	28.2	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 mRNA SPLICING	TRANSPORT	37.2	13.5	138	35.4	57.9	28	56	11.2	29	12.9	148.7	29.3	90.4	4.6	68.1	14.8	2.4	2.5	2.5
8030_at	DPS	YPL265W	YPL265W isobutyryl amino acid permease	TRANSPORT	598.1	48.4	1578.8	319.1	497.3	38.9	332.6	62.2	28.1	9.7	696.8	44.4	445.6	71.1	133.2	2.6	2.8	3.2	4.7
8207_at	THI2	YPL258C	YPL258C similarity to B subtilis transcriptional activator tsaA, and strong similarity to hypothetical protein THIAMINE METABOLISM (PUTATIVE)	UNKNOWN	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	2.1	2.1
8561_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	YOL010W	YOL010W 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 Csp1p	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		YOL234W	YOL234W 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
9386_at	GAD1	YMR250W	YMR250W similarity to glutamate decarboxylase	UNKNOWN	20.3	6	96	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
9462_at	ALD3	YMR188C	YMR188C Aldolase Dehydrogenase (NAD(P)+)	ETHANOL UTILIZATION	63.1	28.6	302.1	50.7	141	31.7	147	22.6	228.7	62.7	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	66.3	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	35.8	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	18.4	4.6	262.7	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	systemic name	functional description	cellular function	C-Lim ANA Average	C-Lim ANA Sides	N-Lim ANA Average	N-Lim ANA Sides	P-Lim ANA Average	P-Lim ANA Sides	S-Lim ANA Average	S-Lim ANA Sides	C-Lim A Average	C-Lim A Sides	N-Lim A Average	N-Lim A Sides	P-Lim A Average	P-Lim A Sides	S-Lim A Average	S-Lim A Sides	FC N-Lim ANA vs C-Lim ANA	FC N-Lim ANA vs S-Lim ANA	FC N-Lim ANA vs P-Lim ANA
10658_at	TEF4	YOL581W	YOL581W Translation elongation factor EF-1gamma	PROTEIN SYNTHESIS	83.3	20	29.5	13.8	112.9	129	150.1	36	97.6	34.6	51.4	21	85.3	7.6	122.3	47.4	-2.8	-4.4	-4.4
2613_at	DL03	YOL071W	YOL071W strong similarity to Ago2	UNKNOWN	521.2	147	257.4	53.7	811.6	334	591.7	21.4	223.7	41	184.7	34.7	735.5	102.1	288.4	34.6	-3.8	-3.2	-2.3
6415_at	BAP3	YOR046C	YOR046C weak similarity to Agrobacterium amino acid permease with high affinity for asparagine and	TRANSPORT	113.1	34.6	12	2.6	357.2	86.9	127.1	9	12	0.6	281	51.2	161	25.2	25.2	25.2	-10.6	-10.6	-10.6
6507_at	AGP1	YOL025C	YOL025C AGP1 Broad substrate range amino acid permease with high affinity for asparagine and	TRANSPORT	762.9	96.7	155.9	23.1	363.4	86.5	346.5	31.2	87.2	28.6	208.6	17.3	240.4	116.9	363.1	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	695.5	57.4	657.9	4.3	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	48.1	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	systemic name	functional description	cellular function	C-Lim ANA Average	C-Lim ANA Sides	N-Lim ANA Average	N-Lim ANA Sides	P-Lim ANA Average	P-Lim ANA Sides	S-Lim ANA Average	S-Lim ANA Sides	C-Lim A Average	C-Lim A Sides	N-Lim A Average	N-Lim A Sides	P-Lim A Average	P-Lim A Sides	S-Lim A Average	S-Lim A Sides	FC P-Lim ANA vs C-Lim ANA	FC P-Lim ANA vs N-Lim ANA	FC P-Lim ANA vs S-Lim ANA
10022_at	CD41	YLR037W	YLR037W Chitin Deacetylase	SPOROULATON	45.1	19.5	49.3	12.8	43	8.3	110.8	2.8	26.6	7.2	3.8	12	0.1	12	4.2	2.2	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	12.3	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	0.4	12	0.4	12	0.4	12	0.4	12	0.4	12	0.4	2.4	2.4	2.4
10443_s_at	FLO10	YMR102W	YMR102W Protein with similarity to floculation 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	19.9	35.3	5.6	23.1	5.8	12.3	12.3
10653_at	DAG1	YJR151C	YJR151C similarity to mucin proteins. YKL224c: Sta1p	UNKNOWN	560.6	298.8	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
10655_at	PGU1	YJR153W	YJR153W putative glucanase	UNKNOWN	12	5.3	19.7	12.8	12	5.3	12	5.3	12	5.3	12	5.3	12	5.3	12	5.3	2.5	2.5	2.5
11186_at		YAL152W	YAL152W 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	3.7	2.5	2.5
11304_s_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	15.3	12	1.7	12	0.4	12	0.7	12	2.2	6.3	6.3	6.3
1386_at	AR09	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	1.7	6.4	6.8
4420_at		YHR128C	YHR128C hypothetical protein	UNKNOWN	25.8	10.7	15.8	4.7	17.3	2.3	54.7	16.7	81.8	65.9	12	0.8	12	0.4	12	2.8	3.5		

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