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1 **Physiological and transcriptomic response of *Saccharomyces pastorianus* to cold storage**

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9 **Abstract**

10 Removal of yeast biomass at the end of fermentation, followed by a period of storage before re-inoculation into

11 a subsequent fermentation, is common in the brewing industry. Storage is typically conducted at cold

12 temperatures to preserve yeast quality, a practice which has unfavourable cost and environmental implications.

13 To determine the potential for alleviating these effects, the transcriptomic and physiological response of

14 *Saccharomyces pastorianus* strain W34/70 to standard (4°C) and elevated (10°C) storage temperatures was

15 explored. Higher temperatures resulted in increased expression of genes associated with the production and

16 mobilisation of intracellular glycogen, trehalose, glycerol and fatty acids, although these observations were

17 limited to early stages of storage. Intracellular trehalose and glycerol concentrations were higher at 4°C than at

18 10°C, as a consequence of the cellular response to cold stress. However, significant changes in glycogen

19 degradation or cellular fatty acid composition did not occur between the two sets of populations, ensuring that

20 cell viability remained consistent. It is anticipated that this data may lead to changes in standard practice for

21 handling yeast cultures, without compromising yeast quality. This work has significance not only for the

22 brewing industry, but also for food and biofuel sectors requiring short term storage of liquid yeast.

23

24 **Keywords** – Brewing, cold shock, lager yeast, membrane fluidity, repitching, yeast stress

25

26

27 **Introduction**

28 The practice of serial repitching, whereby yeast biomass is recovered from a fermentation (cropped) and used to
29 inoculate a subsequent fermentation (repitched) is common practise in the brewing industry. This cycle is
30 typically repeated 5-10 times, although in some instances extended repitching can be performed with some
31 cultures used indefinitely. The extent to which a yeast culture is repitched depends largely on company policy as
32 well as the health and fermentation potential of the yeast culture (McCaig and Bendiak 1985b). However, in
33 recent years the trend has been to reduce the number of repitchings, predominantly due to a drive for quality in
34 conjunction with intensification of the fermentation process.

35 Cropped yeast is often required to be stored between successive fermentations, providing operational flexibility.
36 Brewing yeast biomass is typically stored cold, either in the form of a slurry comprising a suspension of yeast in
37 beer taken directly from the fermenter, or as a 'pressed cake' (Quain and Tubb 1982; Boulton and Quain 2001).
38 Storage in cake form is usually associated with breweries employing traditional top-cropped fermentations and,
39 despite economic benefits, has been suggested to exert an adverse effect upon yeast quality as a consequence of
40 increased contamination risks due primarily to exposure to atmospheric air. Difficulty in controlling temperature
41 and variation in population heterogeneity due to desiccation or localised metabolic activity within the cake are
42 additional risks (Boulton and Quain, 2001). As a result the most accepted practice is to store cropped yeast in
43 the form of a slurry in an enclosed vessel for a defined period of time (normally for less than 48 hr). Yeast slurry
44 is typically held at between 0-4°C in anaerobic conditions under pressure. Periodic agitation is also applied to
45 homogenise the culture and assure an even temperature across the population prior to repitching (Briggs *et al.*
46 2004).

47 One of the primary aims of storage is to maintain strain integrity while preventing contamination or
48 deterioration of the physiological state of the cropped yeast (McCaig and Bendiak 1985a; Lodolo *et al.* 2008).
49 This is particularly important since changes to yeast physiology during serial repitching constitute a major
50 source of variation to fermentation performance (Sall *et al.* 1988). Brewing yeast quality during storage is
51 influenced by a number of factors including duration, rate of agitation, presence of air, nutrient availability, and
52 temperature (McCaig and Bendiak 1985a; McCaig and Bendiak 1985b). Of these, temperature arguably plays
53 the most important role since it has a direct influence on the metabolic activity of the yeast (Murray 1984;

54 McCaig and Bendiak 1985a). Current standard practice is to store yeast within the recommended range of 0-4°C
55 to reduce metabolic activity and preserve viability and vitality. Higher storage temperatures are believed to be
56 detrimental as, under such conditions, intracellular carbohydrate reserves (primarily glycogen) are broken down,
57 forcing the yeast population to degrade vital cellular components potentially resulting in autolysis and cell death
58 (Quain and Tubb 1982). Conversely, application of near-freezing storage temperatures can lead to considerable
59 cold stress thereby compromising transcriptional efficiency, impairing the microorganism's translational
60 capacity and perhaps more importantly reducing the plasma membrane's fluidity (Al-Fageeh and Smales 2006;
61 Aguilera *et al*. 2007; Gibson *et al*. 2007). The latter can adversely affect the functioning of membrane bound
62 enzymes, reduce diffusion rates and hinder the cross-membrane transport of proteins and metabolites (Ruis and
63 Schuller 1995; Al-Fageeh and Smales 2006). Indeed, thermal downshift has been shown to elicit considerable
64 regulation in *S. cerevisiae*'s global gene expression along with crucial adaptations at the level of cellular
65 physiology which mainly involves accumulation of trehalose, glycerol and changes in fatty acid distribution
66 (Lashkari *et al*. 1997; Sahara *et al*. 2002; Schade *et al*. 2004; Al-Fageeh and Smales 2006; Murata *et al*. 2006;
67 Aguilera *et al*. 2007).
68 Although it has previously been reported that storage of propagated brewing yeast slurry at 4 and 10°C does not
69 appear to elicit notable differences in cellular physiology (Garcia-Rios *et al*. 2017), the impact of storage at
70 these temperatures on subsequent fermentation performance is not well understood (Gibson *et al*. 2009).
71 Brewing yeast transcriptional changes occurring as a consequence of storage temperature have also not
72 previously been investigated. Transcriptomic analyses demonstrated by haploid model laboratory and industrial
73 yeast strains to different degrees of thermal downshift suggested time-dependent upregulation of genes
74 associated with biosynthesis of reserve cellular carbohydrates (glycogen and trehalose), rRNA and ribosomal
75 machinery, glycerol, intracellular fatty acids and cold shock proteins (Lashkari *et al*. 1997; Sahara *et al*. 2002;
76 Schade *et al*. 2004; Murata *et al*. 2006; Panadero *et al*. 2006; Garcia-Rios *et al*. 2017). Whilst these studies have
77 undoubtedly provided considerable insight into yeast behaviour at low temperatures, their direct relevance to
78 cold storage of lager brewing yeast *Saccharomyces pastorianus* is limited. This is due partly to the allopolyploid
79 lager genome, which comprises significant contribution from the cryotolerant *Saccharomyces eubayanus*
80 (Libkind *et al*. 2011; Peris *et al*. 2014). In addition, selective pressures imposed by low temperature

fermentations over many years (Dunn and Sherlock 2008; Gallone *et al*. 2016) and the concomitant presence of additional environmental stresses such as nutrient limitation, anaerobiosis and plausible ethanol stress are also likely to have resulted in physiological differences to previously studied strains (Gibson *et al*. 2007). In this study we investigate transcriptomic changes within yeast populations in association with key physiological characteristics during storage of serially repitched lager yeast slurries.

Materials and methods

Yeast strain and wort composition

Saccharomyces pastorianus (W34/70) received from Hefebank Weihenstephan GmbH (Germany) was utilized for all experiments. Wort (hopped, sterile) was obtained from a commercial brewery by sampling from the paraflow (plate heat exchanger) into a sterile transfer vessel immediately following boiling. Wort exhibited a total extract content of 14.5°P (1056 g/cm^3), comprising fermentable sugars [fructose – 2.7 g/L, glucose – 19 g/L, maltose - 99 g/L, maltotriose - 23 g/L] and free amino nitrogen (FAN) (217 mg/L).

Yeast propagation & pre-storage fermentation

Representative W34/70 colonies from YPD agar (1% yeast extract, 2% neutralized bacteriological peptone, 2% dextrose and 2% agar; all in w/v) slopes were cultivated under aerobic conditions using incremental volumes of sterile wort (20 mL, 100 mL, 250 mL, and 1 L) at 25°C for 24, 24, 24 and 48 hr respectively. Harvested cells were inoculated into sterile, air-saturated wort (14°Plato) in triplicate bioreactors (Techfors-S, Infors HT, Switzerland) at a rate of 1.8 x 10^7 cells / mL to represent pre-storage fermentations. Fermentations were conducted at 10°C in the initial phases followed by a controlled rise to 13°C until attenuation was achieved. No significant difference between cellular characteristics, such as cell density (1.36 x 10^8 cells/ml; $CV < 5\%$), cell viability (98%; $CV < 1\%$) and cellular budding index, or wort characteristics, including final wort gravity (2°Plato; $CV < 1\%$), ethanol (6% alcohol by volume; $CV < 5\%$) and pH (4.1; $CV < 5\%$), could be observed between triplicate fermentations indicating homogeneity between cultures used for subsequent storage. Pre-storage fermentation profiles have been shown within supplementary data (Fig. S1).

Brewing yeast ‘cropping’ and storage

As round-bottomed Infors bioreactors were used to conduct fermentations, cone cropping was not permissible (since no cone was present in the vessels). As a result, an in-house method was developed to promote yeast

108 sedimentation and slurry collection. Spent wort (including yeast) was collected by opening the valve at the
109 bottom of the fermenter into sterile externally-graduated reaction vessels (capacity 2.5 L). Following transfer,
110 vessels were stored in cooled incubators (Sanyo, Osaka, Japan) and maintained at 10°C for a further 24hr,
111 without stirring, to facilitate yeast sedimentation. The bulk of the supernatant was then removed under nitrogen
112 pressure leaving behind approximately 30% (w/v) of 'cropped' brewing yeast slurry. Cropped yeast slurries
113 from 3 bioreactors were aseptically pooled to maintain homogeneity, and equal aliquots (200 mL) were
114 transferred into Duran vessels using nitrogen top-pressure.
115 Cropped yeast was stored in Duran vessels (500 mL; Infors, HT, Switzerland) sealed with 2-port stainless steel
116 plates (Infors, HT, Switzerland) to maintain anaerobiosis. One of the ports was fitted with a sterile gas filter and
117 served as a gas inlet whilst the other served as a gas outlet and sampling port. Both ports were sealed during
118 storage to prevent air (oxygen) ingress into the vessel. Two sets of triplicate storage vessels were maintained in
119 static incubators at either 4°C or 10°C. Sampling of stored yeast slurry was performed aseptically whilst
120 flushing the headspace with nitrogen via the gas inlet port, using sterile, stainless steel syringe needles (10 inch,
121 18 gauge) (Sigma Aldrich, UK). Samples were taken at key time points as indicated in the relevant results
122 sections, selected to represent the different stages of yeast storage and considering 48 hr to be the typical
123 maximum storage time. Yeast slurry was washed once with sterile saline (0.8 % NaCl), flash frozen (using
124 liquid nitrogen) and stored at -20°C until required for analysis.
125 **Cell viability, concentration and budding index**
126 Cell concentration was determined using a haemocytometer. Methylene violet (0.01% in 2% w/v sodium citrate)
127 (3RAX, Sigma-Aldrich, UK) was utilized to determine cell viability according to the method of Smart *et al.*
128 (1999). A minimum of 400 cells were scored for each sample. Viability and budding index (representing the
129 fraction of budding cells in the population) were determined using a haemocytometer and expressed as a
130 percentage of the total population based on triplicate analyses.
131 **Microarray data acquisition and analysis**
132 RNA was extracted from yeast pellets using a RiboPure-Yeast Kit (Ambion, Applied biosystems, UK). Sample
133 preparation, hybridization to a yeast genome 2.0 array and scanning was performed according to the
134 manufacturer's instructions (GeneChip Expression Analysis, Affymetrix). Following scanning, the GeneChip

135 command console (AGCC, Affymetrix Inc., USA) was used to generate non-scaled RNA (.cel) files which were
136 analysed using GeneSpring GX 11 (Agilent Technologies, USA) software and pre-normalized as a single
137 experimental group using the Robust Multichip Average (RMA) algorithm, as described previously (Gibson *et*
138 *al*. 2008; Gibson *et al*. 2009). Probe selection was performed using the Xspecies (cross species) hybridization
139 approach through probe masking files generated using a parser script written in Perl (Gibson *et al*. 2008; Gibson
140 *et al*. 2009). Differential expression was deemed to have occurred when, compared to the start of cold storage,
141 the transcript levels changed by more than 1.3 fold at significance of $p < 0.05$ (assessed by one way ANOVA
142 with Benjamini-Hochberg (BH) false discovery rate (FDR) correction).

143 **Intracellular glycogen, trehalose & glycerol**

144 Intracellular glycogen and trehalose in recovered yeast cells were determined using a method based on that
145 described by Parrou and Francois (1997), as detailed previously (Garcia-Rios *et al*. 2017). Yeast slurry was
146 diluted to 1×10^9 cells/mL and glycogen and trehalose were quantified separately based on specific enzymatic
147 digestion to glucose using a D-glucose assay kit (GOPOD, Megazyme). Analysis was conducted in triplicate
148 and results expressed as mg glucose / g slurry dry weight (SDW).

149 Intracellular glycerol determination was conducted as reported previously (Wojda *et al*. 2003). Final glycerol
150 content was estimated using a commercial kit (Megazyme, Ireland) following the manufacturer's instructions.
151 Results were presented as µg glycerol / mg SDW over triplicate analyses.

152 **Intracellular fatty acids**

153 Intracellular fatty acid (FA) distribution was assessed in cell pellets containing 1×10^9 cells using GC-MS as
154 described previously (Garcia-Rios *et al*. 2017). Besides the major long-chain FAs (C14:0, C16:0, C18:0, C16:1
155 and C18:1), the profile of relatively less prevalent medium-chain FAs (C10:0 and C12:0) were also determined.
156 The membrane unsaturation index (UI) and percentage Medium Chain Fatty Acid (MCFA) distribution were
157 calculated as follows - UI $= \sum(C14{:}0 + C16{:}0 + C18{:}0) \, / \sum(C16{:}1 + C18{:}1)$

158 $MCFA = \sum(C10{:}0 + C12{:}0)$

159 **Statistical analysis**

160 Probability (*p*) values were generated following pairwise comparisons between means using unpaired Student's
161 T test (SPSS 16.0.0). $p < 0.05$ was deemed to be significant in each instance. Normal distribution for the

162 variables was established using the One-Sample Kolmogorov-Smirnov Test whilst group variance on the
163 dependent variable was tested using Levene's Test of Homogeneity of Variance.

164 **Results**

165 In order to investigate the relationship between storage temperature, yeast physiology and the cellular
166 transcriptome, yeast slurries were stored at standard (4°C) and elevated (10°C) temperatures for 72 hours. The
167 10°C upper limit was applied since this matched the lowest temperature encountered in fermentations conducted
168 prior to storage. Analysis over 72h was performed since this exceeds the 48h maximum storage time widely
169 regarded as exceeding that recommended for good brewing practise (Boulton and Quain 2001; Briggs *et al.*
170 2004). Besides the cellular transcriptome, expression of key genes were monitored through storage to provide an
171 indication of the relative response of yeast to temperature at the molecular level. In addition, yeast populations
172 were analysed for viability, budding index, carbohydrate reserves, glycerol and aspects of membrane fluidity.

173 **Cell viability and budding index**

174 During storage, cropped brewing yeast cell viability remained consistently above 95% irrespective of
175 temperature (Fig. 1). Budding index was also consistent through storage and remained lower than 3% for yeast
176 stored at 4°C (1.7 ± 0.13 to 2.3 ± 0.64 percent) and at 10°C (1.9 ± 0.33 to 2.3 ± 0.63 percent). This data
177 indicates a lack of active cell division during slurry storage, most likely due to a combination of thermal
178 downshift combined with oxygen and nutrient limitation. However, it also provides reassurance that yeast
179 populations were representative of brewery-stored cultures, with typically high viability accompanied by a
180 reduced divisional rate.

181 **Impact of higher storage temperature on cropped yeast global transcriptome**

182 For transcriptome comparison as a function of temperature, fermented slurry samples harvested after 0, 6, 24
183 and 48 hr of incubation at 4°C and 10°C were compared. The 6 hr time point was chosen to encompass any
184 immediate and rapid alterations in global gene expression following stressful environmental exposure, as
185 proposed by Gasch and co-workers (Gasch *et al.* 2000), whilst the latter sampling points represent the typical
186 storage durations adopted within the brewing industry. Transcript abundance in slurry stored at 10°C was
187 compared with that at 4°C treating them as distinct experiments.

188 None of the ORFs were differentially expressed at the 0 hr sampling point between the two populations
189 suggesting similar transcriptional status at the beginning of differential storage. 506 genes (8.8 % of the total
190 genome) were found to be differentially expressed after 6 hr, with increased transcript abundance in 174 entities
191 (3% of total) and reduced transcript numbers in 332 entities (5.8% of total). Only 3 entities were differentially
192 expressed between W34/70 populations after 24 hr, whilst no difference in global transcription was evident after
193 48 hr.
194 Genes demonstrating significant changes in transcript abundance after 6 hr of cold storage were annotated using
195 the MIPS FunCat scheme (Ruepp *et al*. 2004). Amongst the genes with higher transcript abundance, functions
196 associated with cellular metabolism, particularly vitamin biosynthesis and secondary metabolism, were
197 significantly over-represented (Table 1) suggesting higher energy requirement for yeast survival in the initial
198 stages of storage at 10°C. Almost 12% of ORFs with increased transcript abundance after 6 hr of incubation at
199 10°C were involved in stress responses, particularly cellular detoxification (see Table 1). Further MIPS analysis
200 of genes within the "cell rescue, defence and virulence" category revealed the presence of genes associated with
201 oxidative stress (*GRX1, PST2, FMP46*) and osmotic/salt stress (*MYO3, GCY1, RRD2*). Storage at the higher
202 temperature also seemed to cause induction of genes associated with protein modification, auto-proteolysis and
203 reorganisation of the mitochondrion (Table 1). Together these observations indicate the prevalence of increased
204 stress during the initial phases of slurry storage at 10°C.
205 ORFs which were repressed when the storage temperature was increased from 4 to 10°C comprised 41.5% of
206 the total, and included genes associated with cellular transcription, particularly the rRNA machineries
207 (processing, modification and synthesis) (Table 1). A large fraction of ORFs (15.9% of total) encoding proteins
208 known to bind to nucleic acids were also present in this group. This suggests reduced cellular efforts to overhaul
209 its transcriptional apparatus when stored at the higher temperature, an observation complemented by lower
210 transcript abundance of genes involved in nucleotide/nucleoside/nucleobase metabolism along with nucleo-
211 cytoplasmic transport of proteins and RNA (Table 1). Genes involved in the biogenesis of various cellular
212 compartments, including cytoskeletal proteins and nuclear membrane were also repressed following an increase
213 in storage temperature (Table 1).

214 Amongst the 3 differentially expressed genes after 24 hr of cold storage, *STE14* was induced following an
215 increment in the storage temperature whilst *YJL144W* and *HSP10* were repressed. Both *YJL144W* and *HSP10*
216 are stress-responsive genes; *YJL144W* is induced during osmotic stress and starvation (Gasch *et al*. 2000) whilst
217 *HSP10* encodes for a mitochondrial chaperonin involved in protein folding and sorting (Laroche *et al*. 2001).
218 None of the microarray entities demonstrated significant change in expression after 48 hr. As a result, no
219 conclusions could be drawn except that the transcriptional status of *S. pastorianus* W34/70 is seemingly
220 unaffected by an increase in storage temperature after 48 hr of anaerobic maintenance, at least under the
221 laboratory-scale conditions used in current study.

222 **Monitoring gene expression during cold storage of cropped lager brewing yeast slurry**

223 Genes known to be involved in the metabolism of glycogen, trehalose, glycerol and intracellular fatty acids (GO
224 classification obtained from *Saccharomyces* Genome Database, (Gallone *et al*. 2016)) were investigated after 0,
225 6, 24 and 48 hr of incubation at 4°C and 10°C.

226 **Expression of genes associated with reserve carbohydrate metabolism during storage at 4°C**

227 Of the 18 genes involved in the biosynthesis (GO:0005978) and catabolism (GO:0005980) of glycogen in *S.*
228 *cerevisiae*, 10 demonstrated a significant difference in transcript levels during 4°C-storage (Fig. 2a and 2b).
229 *GSY1* and *GSY2*, which encode glycogen synthases responsible for glycogen chain elongation, along with
230 *GLC3*, whose protein product catalyzes glycogen branching, were induced after 24 hr (Fig. 2a). Progressive
231 repression of *GLG2*, whose protein product (along with GLG1p) initiates glycogen formation, was observed
232 throughout 48 hr of cropped slurry storage at 4°C (Fig. 2a). *GLC8* encodes the regulatory subunit of type 1
233 serine/threonine protein phosphatase (PP1) whilst PIG1p tethers PP1 to the glycogen synthase GSY2p thereby
234 aiding the latter's activation for glycogen accumulation. Transcript levels for both *GLC8* and *PIG1* were lower
235 during the initial stages of 4°C-storage (Fig. 2b). Products of *PGM2* and *UGP1* catalyze the sequential
236 conversion of glucose-6-phosphate to glucose-1-phosphate and glucose-1-phosphate to UDP-glucose
237 respectively, thereby providing the necessary substrates for glycogen (and trehalose) synthesis (Daran *et al.*
238 1997). After initial down-regulation, *PGM2* was induced in a sustained manner until 48 hr whilst transcription
239 of *UGP1* remained largely unchanged after 24hr (Fig. 2b). Amongst genes associated with glycogen catabolism,

240 glycogen phosphorylase encoding *GPH1* demonstrated initial repression followed by sustained induction to
241 yield peak levels after 48 hr of 4°C-storage (Fig. 2b).
242 Amongst the 11 genes involved in trehalose biosynthesis (GO:0005992), catabolism (GO:0005993) and
243 transport (GO:0015771), expression of 8 genes (including *PGM1* and *UGP1* mentioned earlier) were
244 significantly altered during storage at 4°C. Similar to glycogen metabolism, most of the genes involved in
245 trehalose metabolism were suppressed during the first 6 hr of storage (Fig. 2c). Of the genes associated with
246 trehalose biosynthesis, *TPS1*, which encodes the synthase subunit of trehalose-6-phosphate/synthase complex,
247 was induced after 24 hr (Fig. 2c). Final *TPS1* transcript levels were 1.9 fold higher than those preceding storage.
248 Following initial down regulation, transcription of genes encoding the phosphatase (*TPS2*) and one of the two
249 structural subunits (*TSL1*) of the trehalose-6-phosphate synthase complex returned to levels comparable to the
250 start of cold storage (Fig. 2c). Cytosolic neutral trehalase encoding *NTH1* and *NTH2* were significantly induced
251 following 24 hr of W34/70 incubation at 4°C whilst transcript abundance of the vacuolar acid trehalase-encoded
252 by *ATH1* remained largely stable until 48 hr (Fig. 2c).
253 **Expression of genes associated with glycerol metabolism during storage at 4°C**
254 Transcript abundance of 8 (out of 12) genes involved in glycerol biosynthesis (GO:0006114), catabolism
255 (GO:0019563) and transport (GO:0015793) were significantly regulated during 4°C-storage. Amongst the genes
256 associated with glycerol biosynthesis, glycerol-3-phosphatase encoding *GPP1 and GPP2* demonstrated marked
257 induction after 48 hr (Fig. 2d), whilst *YIG1*, whose protein product facilitates glycerol metabolism under
258 anaerobic conditions, was gradually repressed (Fig. 2d). Amongst the glycerol transporter genes, *STL1* was
259 heavily repressed whilst *FPS1*, associated with glycerol efflux, was marginally induced (Fig. 2d). All of the
260 differentially expressed genes associated with glycerol catabolism, namely *DAK1, GUT1* and *GUT2*, were
261 repressed during cropped W34/70 storage at 4°C (Fig. 2e).
262 **Expression of genes associated with yeast fatty acid biosynthesis and transport during storage at 4°C**
263 Five of the 8 genes associated with yeast MCFA biosynthesis (GO:0051792), UFA biosynthesis (GO:0006636),
264 UFA elongation (GO:0019368) and FA transport (GO:0015908 and GO:1902001) were significantly expressed.
265 The two genes, *EEB1* and *YMR210W*, part of a cohort of three genes involved in MCFA biosynthesis,
266 demonstrated sustained induction until 24 hr followed by a stabilization in expression (Fig. 2f). *ELO1*, which is

267 involved with the elongation of synthesized unsaturated fatty acid precursors, demonstrated peak expression in
268 the initial storage stages followed by repression (Fig. 2f). Amongst the FA transport genes, *PXA1*, which
269 encodes a subunit of the ABC transport complex for importing FAs into the peroxisomes for beta-oxidation,
270 showed maximal transcript abundance after 24 hr of 4°C-storage (Fig. 2f). *RSB1*, whose product is a putative
271 membrane transporter transferring long chain bases from the cytoplasm into the extracytoplasmic space showed
272 initial repression followed by increased transcript levels after 24 hr (Fig. 2f). Notably the Δ9-desaturase
273 encoding *OLE1,* responsible for UFA biosynthesis, did not show any significant change in expression during
274 storage.

275 **Changes in gene expression when cropped lager yeast storage temperature was increased from 4°C to**
276 **10°C**

277 In addition to monitoring gene expression at the traditionally practiced temperature of 4°C, evaluation of the
278 activity of genes involved in yeast glycogen, trehalose, glycerol and fatty acid machinery was also conducted
279 during storage at 10°C. Specifically, transcript abundance at 10°C was compared to that at 4°C at each of the
280 four sampling points (0, 6, 24 and 48 hr). This comparison revealed that changes in transcript abundance were
281 confined to the initial stages of storage (6 hr), after which time no changes were observed (Table 2). Amongst
282 glycogen biosynthesis genes, *GLG2* and *GAC1,* which functions to regulate protein phosphatase I, were induced
283 during the first 6 hr (Table 2). None of the glycogen catabolism genes were influenced by the storage
284 temperature applied. This suggests partial remodelling of the W34/70 transcriptome to facilitate de-
285 phosphorylation of glycogen synthase (GSY2p) and hence glycogen accumulation (Francois and Parrou 2001;
286 Wu *et al*. 2001). Furthermore, increased storage temperature did not influence trehalose biosynthesis, catabolism
287 or transport genes. However, considerable repression of genes responsible for glycerol biosynthesis (*GPP1* and
288 *GPP2*) was observed, along with concomitant induction of ORFs associated with glycerol dissimilation (*GCY1*
289 and *GUT1*) (Table 2). Interestingly, the use of a higher storage temperature also resulted in lower transcript
290 abundance of the glycerol transporter-encoding *FPS1*. Increasing the storage temperature did not affect the
291 expression of the majority of the genes involved in FA metabolism with only *ELO1* demonstrating differential
292 expression (Table 2).

293 **Storage temperature-dependent changes in lager yeast physiology**

294 **Intracellular carbohydrate reserves**

295 To support the transcriptome analysis, brewing yeast slurries were analysed for cellular glycogen content over
296 72 hr of anaerobic storage at 10 and 4°C (Fig. 3a). Glycogen levels in yeast slurry stored at 4°C remained
297 statistically constant and was relatively higher when compared to yeast stored at 10°C. Irrespective of the
298 temperature deployed, glycogen breakdown occurred as a function of the duration of storage.
299 Intracellular levels of the disaccharide trehalose were largely independent of both time and temperature of
300 storage over the first 24 hr of cold incubation (Fig. 3b). After 36 hr, increased trehalose levels ($p < 0.05$) were
301 observed in brewing yeast stored at 4°C but not for that stored at 10°C. Following 72 hr, yeast obtained from
302 4°C storage had significantly ($p < 0.05$) higher trehalose compared to 10°C; final levels indicating a 14%
303 increase in trehalose content under traditional slurry storage regime as opposed to a 9% drop at the higher
304 storage temperature.

305 **Intracellular glycerol**

306 The glycerol content within W34/70 cell populations stored at 4°C remained constant until 48 hr of storage (Fig.
307 3c). After 72 hr these were higher when compared to samples taken at 0 hr (1.5 ± 0.1 compared to 2.1 ± 0.2 µg /
308 mg SDW), corresponding to the transcriptome data reported above. An increase in storage temperature to 10°C
309 resulted in higher intracellular glycerol after 12 hours of incubation followed by gradual dissimilation and return
310 to basal levels after 36 hr with no change thereafter. Intracellular glycerol content was slightly elevated after 72
311 hours of slurry storage at 4°C in comparison to W34/70 maintenance at 10°C.

312 **Storage temperature-dependent changes in membrane fluidity**

313 To obtain a holistic view of variations in individual long-chain (LCFA) and medium-chain (MCFA) fatty acids
314 and corresponding impact over plasma membrane fluidity, the yeast membrane unsaturation index (UI) and
315 percent MCFA content were calculated (Fig. 4). UI was largely unaffected by the storage temperature and a
316 slight decrease (albeit not significant) was observed throughout storage (Fig. 4a). Although the MCFA content
317 in 10°C stored slurry was lower than 4°C-stored populations after 24 hr of storage (Fig. 4b), no significant
318 difference could be observed between the two sets of yeast populations.

319 **Discussion**

320 Maintenance of yeast physiological condition between successive fermentations is important in dictating both
321 the consistency of subsequent fermentations and final beer quality. In this study, the impact of storage
322 temperature on gene expression and key performance indicators for yeast condition were assessed.
323 Brewing yeast cell viability, the most widely utilized indicator of yeast quality in the brewing industry, was
324 observed to be consistent independent of storage temperature. These observations partially support those of
325 McCaig and Bendiak (1985b) who reported cell viability maintenance following 2 days of yeast storage at 1, 4
326 and 10°C. However, these authors suggested that prolonged storage at 10°C yielded poor cell viability, a
327 hypothesis not supported in the current study where longer term yeast slurry storage (3 days) at 10°C did not
328 result in any decline in cell viability. The low budding index (< 2%) during cold incubation of cropped yeast
329 was comparable to earlier values reported by Miller *et al.* (2012).
330 More than 99% of the temperature-dependent changes in cropped yeast gene expression occurred in the early
331 phase of storage suggesting that major transcriptome events are limited to this stage. Induction of genes
332 associated with cellular energy was observed in cells stored at 10°C compared to those at 4°C. This is probably
333 due to the ability of lager brewing yeast to conserve metabolic function between 8 -12°C on account of its
334 hybrid nature, and likely a result of the *S. eubayanus* contribution to the genome (Sato *et al*. 2002; Dunn and
335 Sherlock 2008; Nakao *et al*. 2009; Libkind *et al*. 2011; Gallone *et al*. 2016). Analysis of ORFs related to
336 oxidative and osmotic stress indicated that increasing the storage temperature from 4 to 10°C resulted in an
337 enhanced yeast stress response during early storage. This is in contrast to previous reports linking an induction
338 of antioxidant and oxidative stress gene activity following temperature downshift to low temperatures (Huang *et*
339 *al*. 1998), and in near-freezing conditions (Aguilera *et al*. 2007). The reason for this phenomenon is not yet
340 known and warrants further investigation, but may also be inherent to the strains employed and the robust nature
341 of brewing strains at relatively cold temperatures. Alternatively, it is worth considering that the capacity of lager
342 strain W34/70 to survive at 10°C without adverse effects may be dependent on gene activity associated with
343 alleviating stress factors. It should be noted that extensive remodelling of yeast transcriptional and translational
344 machinery at near-freezing temperatures has been widely reported (Sahara *et al*. 2002; Schade *et al*. 2004;
345 Murata *et al*. 2006; Isasa *et al*. 2016; Garcia-Rios *et al*. 2017) and is predominantly driven by widespread
346 inactivation of cellular ribosomes, protein synthesis and increased stabilization of mRNA secondary structures

347 (Al-Fageeh and Smales 2006; Aguilera *et al*. 2007). Storage of yeast slurry at higher temperature could perhaps
348 reduce such requirements as evident by a reduction in cellular efforts towards refurbishing
349 transcriptional/translational apparatus at the higher temperature applied here.

350 A high glycogen content in cropped yeast is vital for maintaining cell viability during cold storage since it fuels
351 yeast basal metabolism in the absence of assimilable nutrients (Quain and Tubb 1982). Elevated storage
352 temperatures have been linked to an accelerating metabolism rate and cellular energy demand, resulting in
353 increased degradation of yeast glycogen (McCaig and Bendiak 1985a). However, under the conditions
354 employed in the current study, slurries stored at 10°C did not significantly exhibit an altered glycogen
355 mobilization rate. Furthermore, higher storage temperatures prompted an initial transcriptional response towards
356 glycogen accumulation, although this was not sustained during the later stages of storage. The expression of
357 glycogen-associated genes was largely supported by the physiological data obtained. Simultaneous induction of
358 genes associated with both glycogen accumulation and mobilization observed during cropped W34/70 slurry
359 storage at 4°C mimics the response of *S. cerevisiae* to cold shock (Sahara *et al*. 2002; Schade *et al*. 2004;
360 Murata *et al*. 2006), heat shock and oxidative stress (Parrou *et al*. 1997). In contrast to the proposed recycling of
361 glycogen in response to heat and oxidative stresses (Parrou *et al*. 1997), Schade *et al.* (2004) reported
362 accumulation of this carbohydrate following thermal downshift. This was not observed in the current study,
363 albeit conducted using a different yeast species, gaseous environment and nutritional availability. It is therefore
364 proposed that under brewery storage conditions, glycogen accumulation may not be an absolute prerequisite for
365 cold shock adaptation. In support of this hypothesis, an absence of glycogen accumulation in *S. cerevisiae*
366 cultures maintained in a chemostat at low temperatures and under nutrient limiting conditions has been
367 previously observed. (Tai *et al*. 2007).
368 Trehalose is a well-recognised cellular protectant which is known to accumulate in response to numerous yeast
369 stress factors (Odumeru *et al*. 1993; Majara *et al*. 1996; Parrou and Francois 1997; Hounsa *et al*. 1998).
370 Significantly higher levels of this disaccharide were observed in W34/70 populations stored at near-freezing
371 temperatures, presumably due its requirement for maintaining and stabilising cellular membrane structures
372 (Kandror *et al*. 2002; Kandror *et al*. 2004). In contrast, the presence of this sugar did not appear to be imperative
373 for yeast survival at 10°C. In the absence of an exogenous carbon source and extracellular uptake (due to non-

374 significant regulation of transporter *MAL11* in current study) (Plourde-Owobi *et al*. 2000), trehalose
375 accumulation could have occurred at the expense of internal cellular carbon reserves (Jorgensen *et al*. 2002),
376 including glycogen. A difference in yeast trehalose synthesis as a function of temperature was not observed at
377 the level of transcriptome regulation. Such disparity between gene expression and cell physiology could partly
378 be explained by the sensitive post-translational control exerted upon most enzymes involved in trehalose (and
379 glycogen) metabolism (Hwang *et al*. 1989; Huang *et al*. 1998; Parrou *et al*. 1999; Gasch *et al*. 2000). Similar to
380 glycogen, simultaneous activation of both trehalose accumulation and mobilization genes appeared to occur
381 under both storage conditions presumably for rapid and sensitive regulation of its internal reserves (Gasch *et al*.
382 2000).
383 The observation that low levels of intracellular glycerol were accumulated during the later stages of storage at
384 4°C was supported by the genetic response; simultaneous activation and repression of key glycerol biosynthesis
385 and catabolism genes was noted. Since *S. cerevisiae* has a general propensity to curtail glycerol production
386 under nutrient limiting conditions (O'Connor and Wyrick 2007), glycerol accumulation in brewing yeast cells
387 may be a protective mechanism against freeze injury and, like trehalose, has been suggested to be a vital factor
388 in maintaining cellular viability (Panadero *et al.* 2006; Zhao *et al*. 2015). During the early stages of slurry
389 storage at 10°C, a transient increase in intracellular glycerol concentration was observed. This was surprising
390 given that previous reports have indicated that higher glycerol accumulation occurs in *S. cerevisiae* following a
391 temperature drop to 4°C than to 12°C (Panadero *et al.* 2006). One reason for such a discrepancy could lie in the
392 pivotal role played by the glycerol export channel FPS1p (encoded by *FPS1*) in glycerol accumulation. Cold-
393 induced accumulation of glycerol has been attributed to lower activity levels of FPS1p (Tamas *et al*. 1999;
394 Panadero *et al*. 2006) whereas *FPS1* deletion in *S. cerevisiae* was shown to enhance intracellular glycerol and
395 impart freeze tolerance (Tumu *et al*. 2012). However in the current study, significantly lower transcription of
396 *FPS1* was observed in the early stages of lager yeast storage at 10°C when compared to the traditional storage
397 regime. Decreased *FPS1* activation could thus lead to reduced glycerol efflux eventually resulting in a net
398 intracellular accumulation of this solute.
399 The 'homeoviscous' adaptive response (Sinensky 1974) in yeast aims to compensate for cold stress-induced
400 reduction in membrane fluidity primarily through an increase in the membrane's unsaturation levels or the

401 shortening of its mean fatty acid chain length via increments in MCFA proportions (Redon *et al*. 2011). The
402 absence of any obvious difference in UI between W34/70 populations at 10 and 4°C suggests no obvious change
403 in membrane unsaturation. Despite induction of genes associated with MCFA biosynthesis, the MCFA content
404 in 4°C-stored yeast populations was observed to be relatively constant over time. Other possible mechanisms for
405 membrane fluidity maintenance include alterations to the membrane's triacylglycerol and phospholipid
406 distribution (Redon *et al*. 2011) or increased disorder in the distribution of membrane fatty acids by the action of
407 glycerol (Boggs and Rangaraj 1985; Beranova *et al*. 2008). Nevertheless, changing the storage temperature from
408 4 to 10°C did not elicit any obvious physiological adaptation in FA distribution.

409 Maintenance of pitching yeast quality following cropping is vital for the performance and consistency of
410 subsequent fermentations. Although this study was completed using a single lager brewing yeast strain and did
411 not investigate the impact of increased storage temperature on subsequent fermentation performance, the data
412 presented here suggests that when yeast is cropped and stored, cell physiology is not significantly affected by a
413 shift in storage temperature conditions (4°C to 10°C for a maximum of 72 hr). Lack of significant changes in
414 cell viability, intracellular glycogen or cellular fatty acid and confinement of temperature dependent changes in
415 yeast transcriptome to early stages of storage, followed by attainment of a steady transcriptional state, indicates
416 that marked differences in subsequent fermentation characteristics are unlikely. However, further assessment is
417 required to discern the impact of increased yeast storage temperature over multiple pitching cycles. Due to the
418 expense associated with maintaining yeast at low temperatures, this study offers the brewer the opportunity to
419 explore alterations to yeast storage regime and enhancing cost efficiency without impacting on the quality of the
420 yeast culture.

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545

Legends

Table 1. MIPS Functional classification of the differentially transcribed genes after 6 hrs of increasing the cropped yeast storage temperature from 4°C to 10°C. A total 506 genes were divided into groups of induced (174) and repressed (332) genes before functional annotation. Differential expression was defined as a fold change of >1.3 with $p < 0.05$. The cut off for the enrichment magnitude for the functional categories was $p < 0.05$. "Grp occ" - number of genes in the cluster belonging to the specified functional category. "Genome occ" – number of genes in the genome belonging to the specified functional category.

Table 2. Fold-change in expression level of genes associated with glycogen, trehalose, glycerol and fatty acid production after 6h, 24h and 48 hrs of storage at 10°C and 4°C. Data points represent the mean of three per-gene normalized transcription values. All genes presented show a statistically significant change in expression (corrected $p < 0.05$; Benjamini-Hochberg FDR) and a fold change cut off ≥ 1.3. Descriptions for gene functions were obtained following those of the *Saccharomyces* Genome Database (SGD) (Cherry et al., 2012)

Fig 1. Cell viability during anaerobic W34/70 slurry storage at 10°C and 4°C for 72 hours in the absence of agitation. Values represent the mean of three independent replicates and the error bars represent the standard deviation from the mean

Fig 2. Transcription profiles of genes associated with the regulation of yeast glycogen (a and b), trehalose (c), glycerol (d and e) and fatty acids (f) during yeast storage at 4°C. All presented genes show a statistically significant change in expression of $p < 0.05$ (one-way ANOVA with BH-FDR correction) and fold change of > 1.3. Data points represent the mean of three per-gene normalized transcription values.

Fig 3. Intracellular glycogen (a), trehalose (b), and glycerol (c) during yeast storage at 10°C and 4°C for 72 hr. For glycogen and trehalose final values are expressed as mg glucose released per gram of slurry dry weight (SDW). Values represent the mean of three independent replicates and the error bars represent the standard deviation around the mean.

Fig 4. Alterations in unsaturation index (UI; a) and medium chain fatty acids (MCFA; b) in yeast populations maintained at 10°C and 4°C for 72 hours. Values represent the mean of three independent replicates. Error bars represent the standard deviation around mean. UI = Σ(C16:1 + C 18:1) / (C14:0 + C16:0 + C18:0); MCFA = Σ(C10:0 + C12:0).

Table 1.

MIPS Functional Category - 10°C vs 4°C - 6 Hr (continued later)	Up-regulated			Down-regulated		
	Grp Occ	Genome Occ	P - Value	Grp Occ	Genome Occ	P - Value
01 METABOLISM						
01.01.09.07.01 biosynthesis of histidine				0.91	0.24	4.24E-02
01.03 nucleotide/nucleoside/nucleobase metabolism				6.42	3.65	7.99E-03
01.03.01 purin nucleotide/nucleoside/nucleobase metabolism				2.14	0.99	4.24E-02
01.06.06.11 tetracyclic and pentacyclic triterpenes metabolism				1.52	0.58	4.06E-02
01.07 metabolism of vitamins, cofactors, and prosthetic groups	7.59	2.67	1.01E-03			
01.07.01 biosynthesis of vitamins, cofactors, and prosthetic groups	6.96	1.79	1.11E-04			
01.20 secondary metabolism	3.79	1.27	1.49E-02			
01.20.27 metabolism of secondary products derived from aspartic acid and threonine	0.63	0.01	2.58E-02			
02 ENERGY	10.1	5.98	2.64E-02			
02.08 pyruvate dehydrogenase complex	1.89	0.08	1.62E-04			
02.13.03 aerobic respiration	3.79	1.25	1.40E-02			
02.16.09 mixed acid and butanediol fermentation	0.63	0.01	2.58E-02			
10 CELL CYCLE AND DNA PROCESSING						
10.01.03.03 ori recognition and priming complex formation				1.22	0.4	4.14E-02
10.03.03 cytokinesis (cell division) /septum formation and hydrolysis				2.44	1.15	3.42E-02
11 TRANSCRIPTION				41.5	17.5	7.29E-26
11.02.01 rRNA synthesis				3.97	1.35	3.97E-04
11.04 RNA processing				28.1	7.11	1.70E-33
11.04.01 rRNA processing				23.2	3.34	2.77E-46
11.06 RNA modification				7.03	1.04	4.92E-14
11.06.01 rRNA modification				2.75	0.29	9.95E-08
11.06.02 tRNA modification				3.97	0.7	1.91E-07
12 PROTEIN SYNTHESIS				18.3	7.83	1.57E-10
12.01 ribosome biogenesis				13.4	5.05	1.18E-09
12.10 aminoacyl-tRNA-synthetases				2.44	0.63	8.65E-04
14 PROTEIN FATE (folding, modification, destination)						
14.04 protein targeting, sorting and translocation	8.22	4.56	2.80E-02			
14.07.03 modification by phosphorylation, dephosphorylation, autophosphorylation				4.89	3.03	3.91E-02
14.07.11 protein processing (proteolytic)	4.43	1.45	7.77E-03			
14.07.11.01 autoproteolytic processing	1.89	0.42	2.83E-02			
16 PROTEIN WITH BINDING FUNCTION OR COFACTOR REQUIREMENT				32.4	17.1	2.66E-12
16.03 nucleic acid binding				15.9	5.56	1.72E-12
16.03.03 RNA binding				12.5	3.09	3.51E-15
16.07 structural protein binding				2.1	0.91	2.82E-02
16.13 C-compound binding	1.3	0.14	2.11E-02			
16.13.03 fatty acid binding (e.g. acyl-carrier protein)	0.6	0.01	2.58E-02			
16.19 nucleotide/nucleoside/nucleobase binding				6.7	3.67	4.07E-03
16.19.03 ATP binding				6.1	3.11	2.77E-03
20 CELLULAR TRANSPORT, TRANSPORT FACILITIES AND ROUTES						
20.01.10 protein transport				4.3	2.28	1.67E-02
20.01.21 RNA transport				4.3	1.4	1.57E-04
20.09.01 nuclear transport				5.5	1.38	3.51E-07
32 CELL RESCUE, DEFENSE AND VIRULENCE	15.8	9.03	3.77E-03			
32.01 stress response	12.0	7.34	2.18E-02			
32.07 detoxification	4.4	1.9	3.09E-02			
32.07.07.03 glutathione conjugation reaction	1.3	0.08	6.27E-03			
34 INTERACTION WITH THE ENVIRONMENT						
34.07 cell adhesion	1.3	0.21	4.27E-02			
34.07.01 cell-cell adhesion	1.3	0.16	2.59E-02			
40 CELL FATE				7.0	4.45	1.90E-02
40.01 cell growth / morphogenesis				6.7	3.88	7.89E-03
42 BIOGENESIS OF CELLULAR COMPONENTS						
42.04 cytoskeleton/structural proteins				6.4	4.11	2.71E-02
42.10 nucleus				4.6	2.43	1.28E-02
42.10.05 nuclear membrane				1.8	0.48	4.40E-03
42.16 mitochondrion	7.6	2.78	1.45E-03			
43 CELL TYPE DIFFERENTIATION	12.0	7.37	2.27E-02			
43.01 fungal/microorganismic cell type differentiation	12.0	7.37	2.27E-02			
43.01.03 fungal and other eukaryotic cell type differentiation	12.0	7.37	2.27E-02			
43.01.03.09 development of asco- basidio- or zygospore	7.0	2.72	3.73E-03			
11 TRANSCRIPTION				41.5	17.5	7.29E-26
11.02.01 rRNA synthesis				3.97	1.35	3.97E-04
11.04 RNA processing				28.1	7.11	1.70E-33
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14.07.11 protein processing (proteolytic)	4.43	1.45	7.77E-03			
14.07.11.01 autoproteolytic processing	1.89	0.42	2.83E-02			

Table 2.

Genes	10°C Vs 4°C					
	6h		24h		48h	
	Reg	FC	Reg	FC	Reg	FC
Glycogen						
GIP2	up	1.7	-	-	-	-
GLG2	up	1.7	-	-	-	-
GAC1	up	1.3	-	-	-	-
Trehalose						
None						
Glycerol						
GPP1	down	2.5	-	-	-	-
GPP2	down	2.1	-	-	-	-
GCY1	up	2.2	-	-	-	-
GUT1	up	1.3	-	-	-	-
FPS1	down	1.5	-	-	-	-
Fatty Acid						
ELO1	down	1.5	-	-	-	-

Reg – Regulation; FC – Fold Change

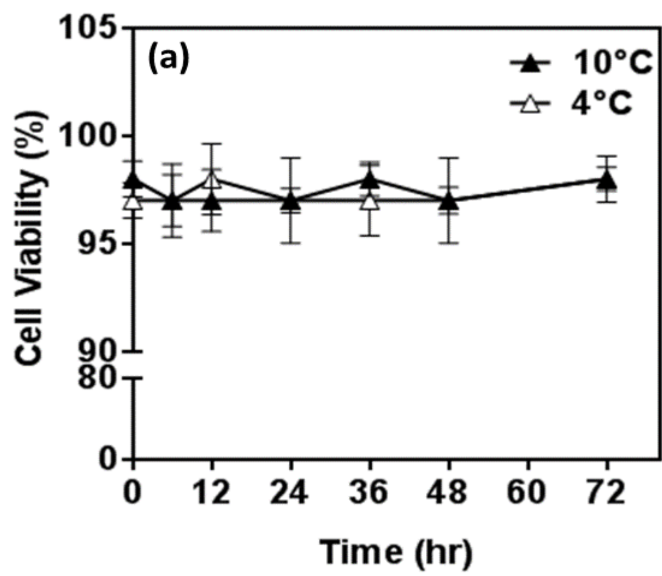


Fig. 1

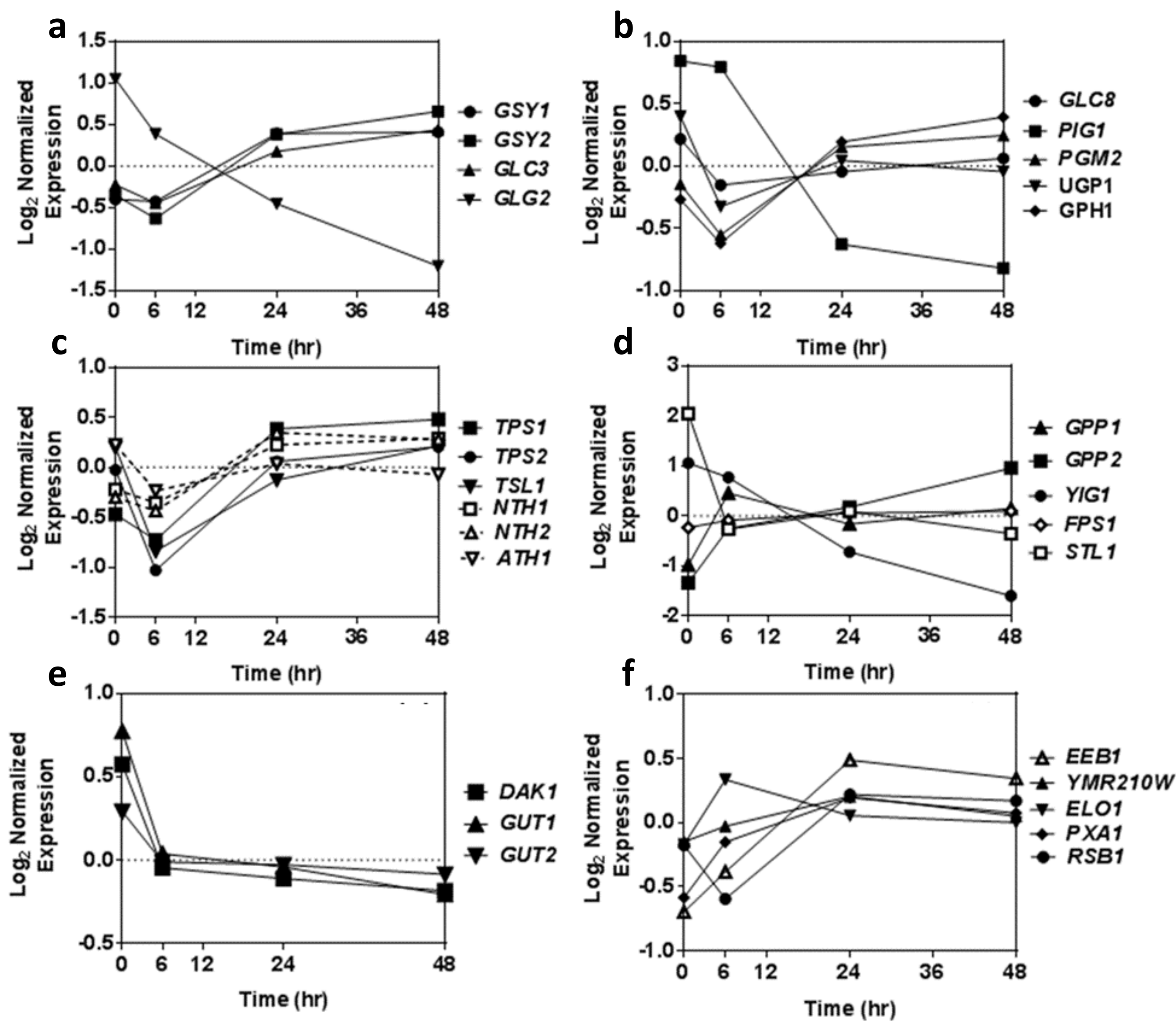


Fig. 2

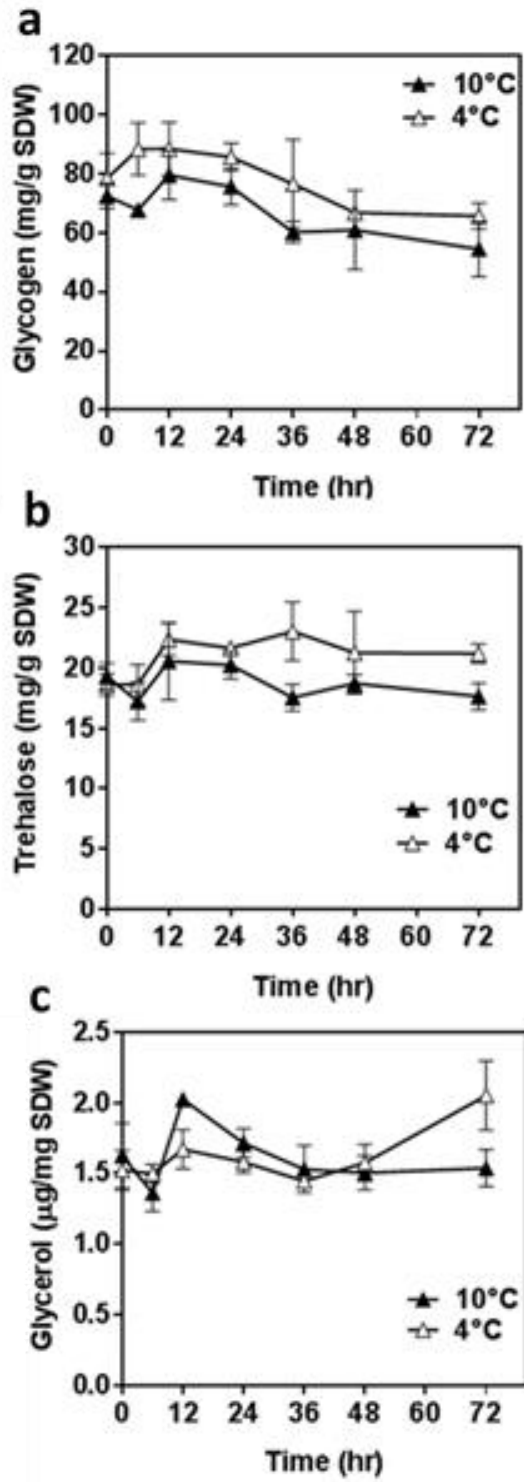


Fig. 3

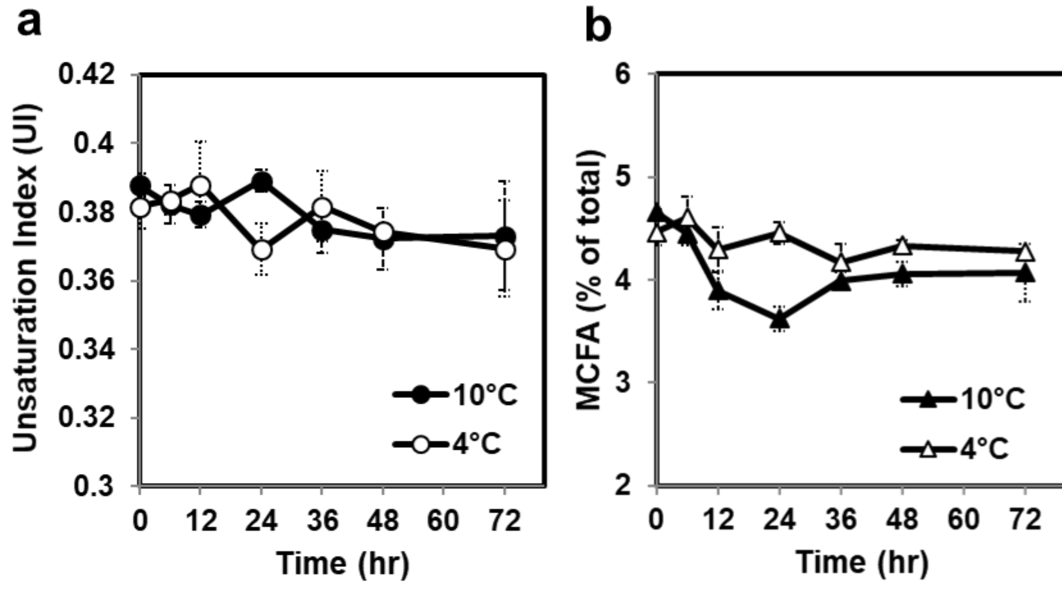
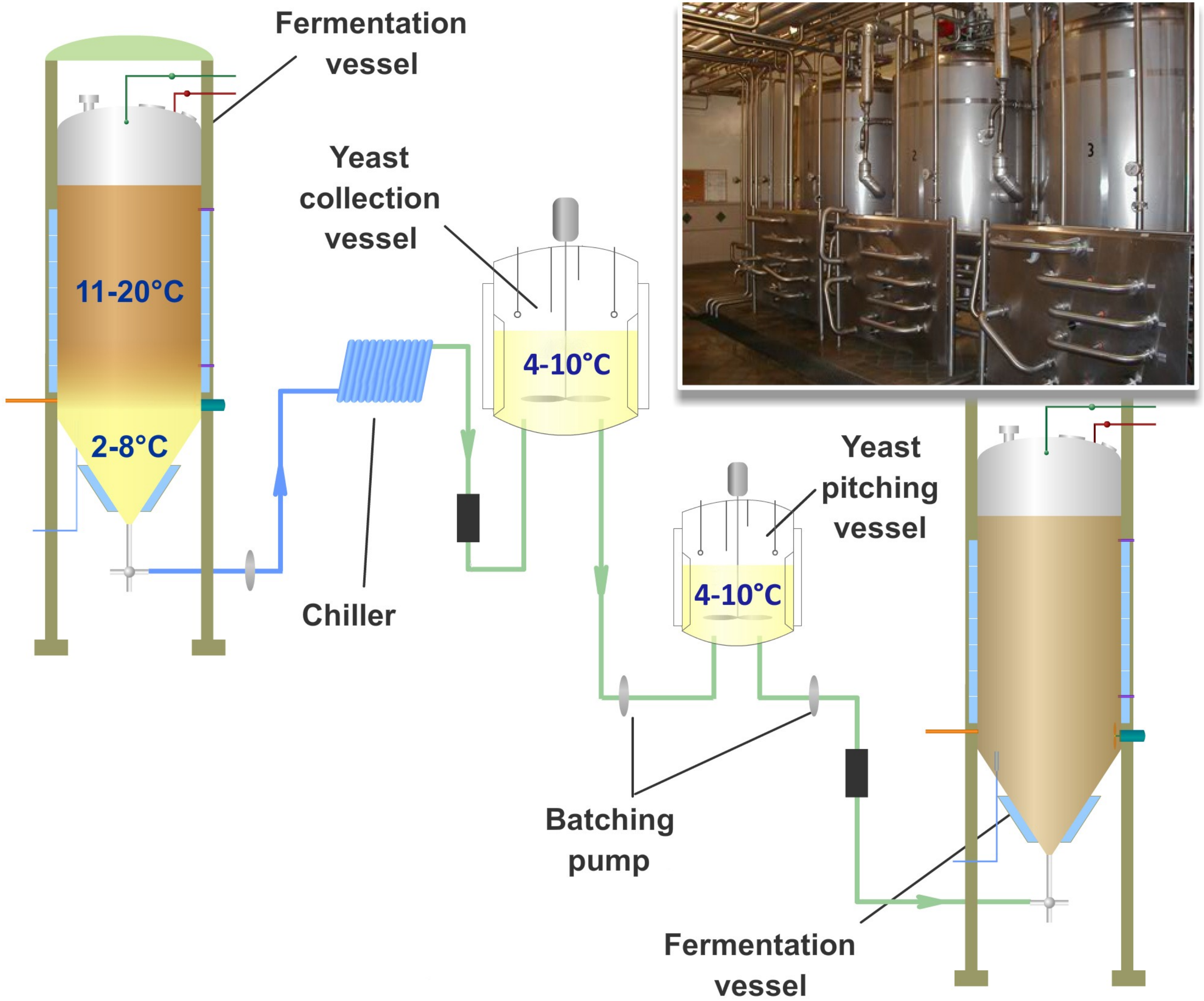


Fig. 4


Fermentation vessel
Yeast collection vessel
11-20°C
2-8°C
4-10°C
Chiller
Yeast pitching vessel
4-10°C
Batching pump
Fermentation vessel
1
2
3

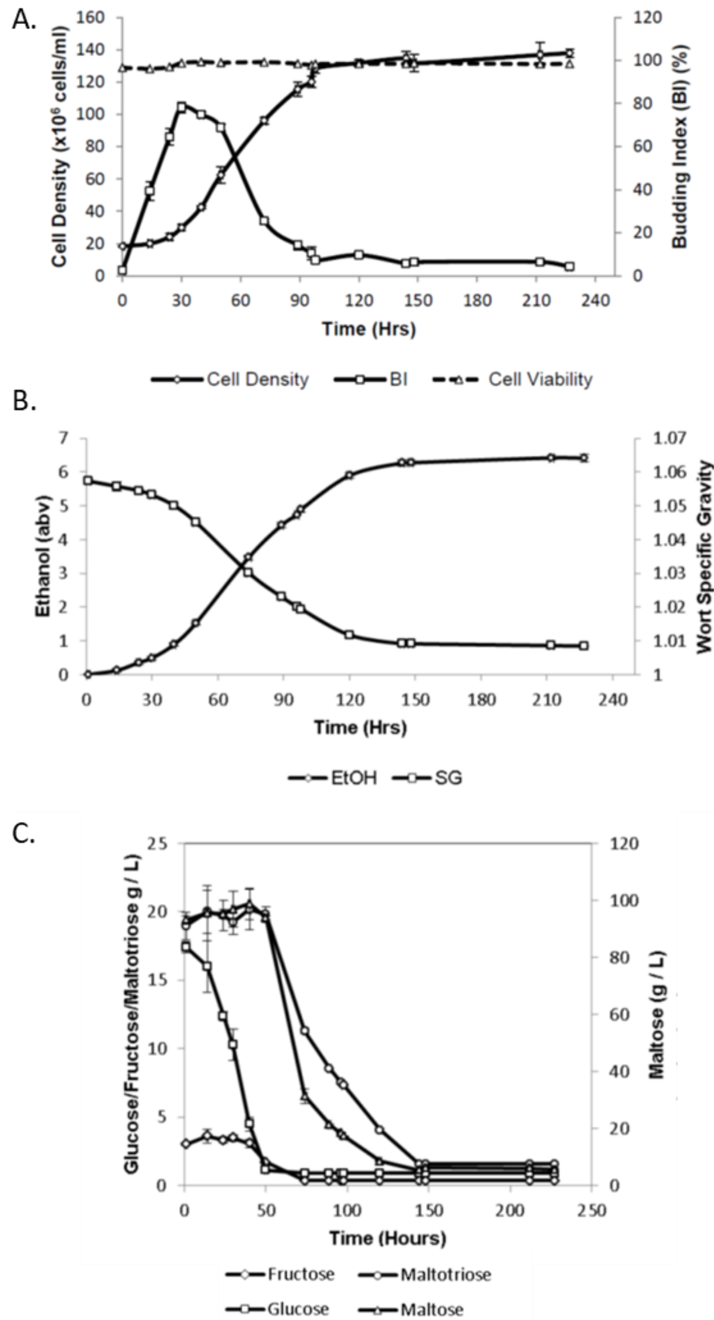


Figure S1 – Fermentation profile of *Saccharomyces pastorianus* W34/70 prior to storage. (A) Yeast cell viability, density and budding index along with wort characteristics including (B) specific gravity, ethanol and (C) major fermentable sugars were assessed. Values represent the mean of three independent replicates and the error bars represent the standard deviation from the mean.

Probe Set ID	Corrected p-value	p-value	FCAbsolute	regulation	Gene Symbol	Target Description	Species Scientific Name
1779813_at	0.02	1.07E-04	4.3	down	RPA49	S. cerevisiae YNL248C /GEN=RPA49 /DB_XREF=GI:6324081 /SEG=NC_001146:-181360,182607 /DEF=RNA polymerase I subunit A49 /NOTE=Rpa49p; go_component: DNA-directed RNA polymerase I complex [goid GO:0005736] [evidence TAS] [pmid 8246845]; go_function: DNA-directed RNA polymerase activity [goid GO:0	Saccharomyces cerevisiae
1775052_at	0.01	4.52E-06	4.1	down	UTP8	S. cerevisiae YGR128C /GEN=UTP8 /DB_XREF=GI:6321567 /SEG=NC_001139:-747953,750094 /DEF=Nucleolar protein required for export of tRNAs from the nucleus; also copurifies with the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA /NOTE=Utp8p; go_compo	Saccharomyces cerevisiae
1779136_at	0.02	1.60E-04	3.6	down	RSA4	S. cerevisiae YCR072C /GEN=IMG2 /DB_XREF=GI:10383804 /SEG=NC_001135:-240800,242347 /DEF=Protein required for cell viability /NOTE=Ycr072cp; go_component: cellular_component unknown [goid GO:0008372] [evidence ND]; go_function: molecular_function unknown [goid GO:0005554] [evidence ND]; go_proce	Saccharomyces cerevisiae
1773258_at	0.02	2.54E-04	3.3	down	MAK21	S. cerevisiae YDR060W /GEN=MAK21 /DB_XREF=GI:6320265 /SEG=NC_001136:+570644,573721 /DEF=essential for 60s ribosome biogenesis; involved in nuclear export of pre-ribosomes /NOTE=Mak21p; go_component: nucleolus [goid GO:0005730] [evidence IDA] [pmid 11371346]; go_component: nucleus [goid GO:0005	Saccharomyces cerevisiae
1779491_at	0.02	3.74E-04	3.3	down	NEW1	S. cerevisiae YPL226W /GEN=NEW1 /DB_XREF=GI:6325030 /SEG=NC_001148:+121767,125357 /DEF=This gene encodes a protein with an Q/N-rich amino terminal domain that acts as a prion, termed [NU]+. /NOTE=New1p; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 14562095]; go_function: ATP-b	Saccharomyces cerevisiae
1776118_at	0.01	3.84E-05	3.3	down	UTP21	S. cerevisiae YLR409C /GEN=UTP21 /DB_XREF=GI:6323441 /SEG=NC_001144:-934411,937230 /DEF=Possible U3 snoRNP protein involved in maturation of pre-18S rRNA, based on computational analysis of large-scale protein-protein interaction data /NOTE=Utp21p; go_component: nucleus [goid GO:0005634] [evidence ID	Saccharomyces cerevisiae
1778980_at	0.02	2.26E-04	3.2	down	UTP4	S. cerevisiae YDR324C /GEN=UTP4 /DB_XREF=GI:6320531 /SEG=NC_001136:-1114426,1116756 /DEF=Nucleolar protein, component of the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA /NOTE=Utp4p; go_component: small nucleolar ribonucleoprotein complex [	Saccharomyces cerevisiae
1770485_at	0.03	4.25E-04	3.2	down	RPA34	S. cerevisiae YJL148W /GEN=RPA34 /DB_XREF=GI:6322313 /SEG=NC_001142:+140355,141056 /DEF=RNA polymerase I subunit A34.5 /NOTE=Rpa34p; go_component: DNA-directed RNA polymerase I complex [goid GO:0005736] [evidence TAS] [pmid 8246845]; go_component: nucleolus [goid GO:0005730] [evidence IDA]	Saccharomyces cerevisiae
1774186_at	0.02	1.39E-04	3.1	down	SSF1	S. cerevisiae YHR066W /GEN=SSF1 /DB_XREF=GI:6321857 /SEG=NC_001140:+229336,230697 /DEF=putative involvement in mating /NOTE=Ssf1p; go_component: nucleolus [goid GO:0005730] [evidence IDA] [pmid 9611192]; go_function: rRNA binding [goid GO:0019843] [evidence IPI] [pmid 11864606]; go_process: conju	Saccharomyces cerevisiae
1776091_at	0.04	0.002111994	3.1	down	RPA43	S. cerevisiae YOR340C /GEN=RPA43 /DB_XREF=GI:6324916 /SEG=NC_001147:-959197,960177 /DEF=RNA polymerase I subunit A43 /NOTE=Rpa43p; go_component: DNA-directed RNA polymerase I complex [goid GO:0005736] [evidence TAS] [pmid 8246845]; go_function: DNA-directed RNA polymerase activity [goid GO:0	Saccharomyces cerevisiae
1779152_at	0.01	4.32E-05	3.1	down	SDA1	S. cerevisiae YGR245C /GEN=SDA1 /DB_XREF=GI:6321684 /SEG=NC_001139:-979769,982072 /DEF=Severe Depolymerization of Actin /NOTE=Sda1p; go_component: nucleus [goid GO:0005634] [evidence IDA] [pmid 10704371]; go_function: molecular_function unknown [goid GO:0005554] [evidence ND]; go_process: actin	Saccharomyces cerevisiae
1775352_at	0.02	1.42E-04	3.1	down	PRP43	S. cerevisiae YGL120C /GEN=PRP43 /DB_XREF=GI:6321318 /SEG=NC_001139:-281638,283941 /DEF=RNA helicase in the DEAH-box family, involved in release of the lariat-intron from the spliceosome /NOTE=Prp43p; go_component: spliceosome complex [goid GO:0005681] [evidence TAS] [pmid 9476892]; go_function: A	Saccharomyces cerevisiae
1778275_at	0.01	5.42E-05	3.0	down	UTP9	S. cerevisiae YHR196W /GEN=UTP9 /DB_XREF=GI:6321990 /SEG=NC_001140:+491929,493656 /DEF=Nucleolar protein, component of the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA /NOTE=Utp9p; go_component: nucleolus [goid GO:0005730] [evidence IDA]	Saccharomyces cerevisiae
1775006_at	0.04	0.001528688	3.0	down	HXT4	S. cerevisiae YHR092C /GEN=HXT4 /DB_XREF=GI:6321884 /SEG=NC_001140:-287131,288813 /DEF=High-affinity glucose transporter of the major facilitator superfamily, expression is induced by low levels of glucose and repressed by high levels of glucose /NOTE=Hxt4p; go_component: plasma membrane [goid GO:00058	Saccharomyces cerevisiae
1778508_at	0.03	5.58E-04	3.0	down	DBP7	S. cerevisiae YKR024C /GEN=DBP7 /DB_XREF=GI:6322876 /SEG=NC_001143:-484787,487015 /DEF=Dead-box protein /NOTE=Dbp7p; go_component: nucleolus [goid GO:0005730] [evidence IDA] [pmid 9582098]; go_function: ATP-dependent RNA helicase activity [goid GO:0004004] [evidence TAS] [pmid 10690410]; go_pr	Saccharomyces cerevisiae
1769709_at	0.02	1.41E-04	3.0	down	SPB1	S. cerevisiae YCL054W /GEN=SPB1 /DB_XREF=GI:6319796 /SEG=NC_001135:+31449,33974 /DEF=Suppressor of PaB1 mutant; encodes a S-adenosylmethionine-dependent methyltransferase; involved in 60S ribosomal subunit biogenesis and rRNA processing /NOTE=Spb1p; go_component: nucleolus [goid GO:0005730] [e	Saccharomyces cerevisiae
1778594_at	0.04	0.001559727	3.0	down	PDE2	S. cerevisiae YOR360C /GEN=PDE2 /DB_XREF=GI:6324936 /SEG=NC_001147:-1013237,1014817 /DEF=low-Km (high-affinity) cAMP phosphodiesterase /NOTE=Pde2p; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 14562095]; go_component: nucleus [goid GO:0005634] [evidence IDA] [pmid 14562095	Saccharomyces cerevisiae
1778685_at	0.03	8.10E-04	2.9	down	UTP6	S. cerevisiae YDR449C /GEN=UTP6 /DB_XREF=GI:6320657 /SEG=NC_001136:-1357568,1358890 /DEF=Nucleolar protein, component of the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA /NOTE=Utp6p; go_component: small nucleolar ribonucleoprotein complex [	Saccharomyces cerevisiae
1779238_at	0.02	2.89E-04	2.9	down	KRS1	S. cerevisiae YDR037W /GEN=KRS1 /DB_XREF=GI:6320242 /SEG=NC_001136:+525435,527210 /DEF=lysyl-tRNA synthetase /NOTE=Krs1p; go_component: cytoplasm [goid GO:0005737] [evidence TAS] [pmid 2668951]; go_function: lysine-tRNA ligase activity [goid GO:0004824] [evidence IDA] [pmid 2903861]; go_process: ly	Saccharomyces cerevisiae
1771304_at	0.04	0.002058213	2.9	down	UTP13	S. cerevisiae YLR222C /GEN=UTP13 /DB_XREF=GI:6323251 /SEG=NC_001144:-579320,581773 /DEF=Nucleolar protein, component of the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA /NOTE=Utp13p; go_component: small nucleolar ribonucleoprotein complex [	Saccharomyces cerevisiae
1774092_at	0.02	8.04E-05	2.9	down	RRN11	S. cerevisiae YML043C /GEN=RRN11 /DB_XREF=GI:6323598 /SEG=NC_001145:-190244,191767 /DEF=rDNA transcription factor CF component, which also contains Rrn6p and Rrn7p, which is required for rDNA transcription by RNA polymerase I /NOTE=Rrn11p; go_component: RNA polymerase I transcription factor comple	Saccharomyces cerevisiae
1775528_at	0.03	9.49E-04	2.9	down	GRC3	S. cerevisiae YLL035W /GEN=GRC3 /DB_XREF=GI:6322993 /SEG=NC_001144:+68579,70477 /DEF=Protein of unknown function, required for cell growth and possibly involved in rRNA processing; mRNA is cell cycle regulated /NOTE=Grc3p; go_component: cellular_component unknown [goid GO:0008372] [evidence ND]; g	Saccharomyces cerevisiae
1775626_at	0.03	9.54E-04	2.8	down	URA7	S. cerevisiae YBL039C /GEN=URA7 /DB_XREF=GI:6319432 /SEG=NC_001134:-143954,145693 /DEF=Catalyzes the ATP-dependent transfer of amide nitrogen from glutamine to UTP to form CTP in last step of pyrimidine biosynthesis, very similar to URA8p but appears to be responsible for the majority of CTP synthesis /NO	Saccharomyces cerevisiae
1776558_at	0.02	2.47E-04	2.8	down	HXT2	S. cerevisiae YMR011W /GEN=HXT2 /DB_XREF=GI:6323653 /SEG=NC_001145:+288078,289703 /DEF=High-affinity glucose transporter of the major facilitator superfamily, expression is induced by low levels of glucose and repressed by high levels of glucose /NOTE=Hxt2p; go_component: plasma membrane [goid GO:0005	Saccharomyces cerevisiae
1774335_at	0.01	9.64E-06	2.8	down	NOP58	S. cerevisiae YOR310C /GEN=NOP58 /DB_XREF=GI:6324886 /SEG=NC_001147:-896820,898355 /DEF=Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA /NOTE=Nop58p; go_componen	Saccharomyces cerevisiae
1779808_at	0.01	5.00E-04	2.8	down	NAN1	S. cerevisiae YPL126W /GEN=NAN1 /DB_XREF=GI:6325131 /SEG=NC_001148:+310209,312899 /DEF=part of small (ribosomal) subunit (SSU) processosome (contains U3 snoRNA); Net1-Associated Nucleolar protein 1 /NOTE=Nan1p; go_component: small nucleolar ribonucleoprotein complex [goid GO:0005732] [evidence IF	Saccharomyces cerevisiae
1778811_at	0.05	0.002642765	2.8	down	TRM11	S. cerevisiae YOL124C /GEN=MDH2 /DB_XREF=GI:6324448 /SEG=NC_001147:-85455,86756 /DEF=Putative S-adenosylmethionine-dependent methyltransferase of the seven beta-strand family /NOTE=Yol124cp; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 14562095]; go_function: S-adenosylmethio	Saccharomyces cerevisiae
1779073_at	0.01	1.81E-06	2.8	down	UTP18	S. cerevisiae YJL069C /GEN=UTP18 /DB_XREF=GI:6322392 /SEG=NC_001142:-310838,312622 /DEF=Possible U3 snoRNP protein involved in maturation of pre-18S rRNA, based on computational analysis of large-scale protein-protein interaction data /NOTE=Utp18p; go_component: nucleolus [goid GO:0005730] [evidence	Saccharomyces cerevisiae
1777632_at	0.02	2.59E-04	2.7	down	DIP2	S. cerevisiae YLR129W /GEN=DIP2 /DB_XREF=GI:6323158 /SEG=NC_001144:+399658,402489 /DEF=Nucleolar protein, specifically associated with the U3 snoRNA, part of the large ribonucleoprotein complex known as the small subunit (SSU) processome, required for 18S rRNA biogenesis, part of the active pre-rRNA proce	Saccharomyces cerevisiae
1779514_at	0.02	2.33E-04	2.7	down	ALB1	S. cerevisiae YJL122W /GEN=LSM1 /DB_XREF=GI:6322339 /SEG=NC_001142:+189636,190163 /DEF=Hypothetical ORF /NOTE=Yjl122wp; go_component: nucleolus [goid GO:0005634] [evidence IDA] [pmid 14562095]; go_function: molecular_function unknown [goid GO:0005554] [evidence ND]; go_process: biological_proce	Saccharomyces cerevisiae
1773490_at	0.03	5.00E-04	2.7	down	REX4	S. cerevisiae YOL080C /GEN=REX4 /DB_XREF=GI:6324493 /SEG=NC_001147:-180557,181426 /DEF=RNA EXonuclease; member of 3'->5' exonuclease family. See Moser et al. 1997 Nucleic acids Res. 25:5110-5118 /NOTE=Rex4p; go_component: nucleolus [goid GO:0005730] [evidence IDA] [pmid 14562095]; go_component:	Saccharomyces cerevisiae
1779904_at	0.02	1.92E-04	2.7	down	YHK8	S. cerevisiae YHR048W /GEN=AAP1' /DB_XREF=GI:6321838 /SEG=NC_001140:+204599,206143 /DEF=Hypothetical ORF /NOTE=Yhr048wp; go_component: integral to membrane [goid GO:0016021] [evidence ISS] [pmid 12697649]; go_function: drug transporter activity [goid GO:0015238] [evidence	Saccharomyces cerevisiae
1777153_at	0.02	1.15E-04	2.7	down	MRD1	S. cerevisiae YPR112C /GEN=MRD1 /DB_XREF=GI:6325369 /SEG=NC_001148:-749252,751915 /DEF=Essential conserved protein that associates with 35S precursor rRNA and is required for its initial processing at the A(0)-A(2) cleavage sites, shows partial nucleolar localization, contains five consensus RNA-binding domains	Saccharomyces cerevisiae
1773340_at	0.01	1.38E-05	2.6	down	NOP12	S. cerevisiae YOL041C /GEN=NOP12 /DB_XREF=GI:6324532 /SEG=NC_001147:-251265,252644 /DEF=Nucleolar protein, required for pre-25S rRNA processing; contains an RNA recognition motif (RRM) and has similarity to Nop13p, Nsr1p, and putative orthologs in Drosophila and S. pombe /NOTE=Nop12p; go_component	Saccharomyces cerevisiae
1779097_at	0.05	0.002444166	2.6	down	RKI1	S. cerevisiae YOR095C /GEN=RKI1 /DB_XREF=GI:6324669 /SEG=NC_001147:-503552,504328 /DEF=Ribose-5-phosphate ketol-isomerase /NOTE=Rki1p; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 14562095]; go_component: nucleus [goid GO:0005634] [evidence IDA] [pmid 14562095]; go_function:	Saccharomyces cerevisiae
1777927_at	0.01	6.11E-06	2.6	down	DHR2	S. cerevisiae YKL078W /GEN=DHR2 /DB_XREF=GI:6322772 /SEG=NC_001143:+288490,290697 /DEF=Predominantly nucleolar DEAH-box RNA helicase, required for 18S rRNA synthesis /NOTE=Dhr2p; go_component: nucleolus [goid GO:0005730] [evidence IDA] [pmid 10982841]; go_function: RNA helicase activity [goid GO	Saccharomyces cerevisiae
1772817_at	0.03	4.15E-04	2.6	down	NSR1	S. cerevisiae YGR159C /GEN=NSR1 /DB_XREF=GI:6321599 /SEG=NC_001139:-806415,807659 /DEF=Nucleolar protein that binds nuclear localization sequences, required for pre-rRNA processing and ribosome biogenesis /NOTE=Nsr1p; go_component: nucleolus [goid GO:0005730] [evidence TAS] [pmid 10690410]; go_com	Saccharomyces cerevisiae
1773300_at	0.04	0.002004511	2.6	down	SNU13	S. cerevisiae YEL026W /GEN=SNU13 /DB_XREF=GI:6320809 /SEG=NC_001137:+101943,102323 /DEF=part of small (ribosomal) subunit (SSU) processosome (contains U3 snoRNA); RNA binding protein (putative), similar to Nhp2p /NOTE=Snu13p; go_component: nucleolus [goid GO:0005730] [evidence IDA] [pmid 1068424	Saccharomyces cerevisiae
1770943_at	0.04	0.001487741	2.6	down	RNT1	S. cerevisiae YMR239C /GEN=RNT1 /DB_XREF=GI:6323895 /SEG=NC_001145:-748261,749676 /DEF=RNAase III; cleaves a stem-loop structure at the 3' end of U2 snRNA to ensure formation of the correct U2 3' end /NOTE=Rnt1p; go_component: nucleolus [goid GO:0005730] [evidence TAS] [pmid 10690410]; go_function:	Saccharomyces cerevisiae
1769550_at	0.04	0.001837745	2.6	down	RIX1	S. cerevisiae YHR197W /GEN=RIX1 /DB_XREF=GI:6321991 /SEG=NC_001140:+493894,496185 /DEF=RIbosome eXport /NOTE=Rix1p; go_component: nucleoplasm [goid GO:0005654] [evidence IDA] [pmid 12374754]; go_component: nucleus [goid GO:0005634] [evidence IDA] [pmid 14690591]; go_function: molecular_func	Saccharomyces cerevisiae
1777706_at	0.01	3.97E-05	2.6	down	EMG1	S. cerevisiae YLR186W /GEN=EMG1 /DB_XREF=GI:6323215 /SEG=NC_001144:+523634,524392 /DEF=Essential for Mitotic Growth /NOTE=Emg1p; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 11914276]; go_component: nucleus [goid GO:0005634] [evidence IDA] [pmid 11935223]; go_function: snoR	Saccharomyces cerevisiae
1772209_at	0.01	2.82E-05	2.6	down	SHQ1	S. cerevisiae YIL104C /GEN=SHQ1 /DB_XREF=GI:6322087 /SEG=NC_001141:-169979,171502 /DEF=Essential nuclear protein, required for accumulation of box H/ACA snoRNAs and for rRNA processing; interacts with Naf1p /NOTE=Shq1p; go_component: nucleoplasm [goid GO:0005654] [evidence IDA] [pmid 12228251]; go	Saccharomyces cerevisiae
1776014_at	0.01	4.32E-05	2.6	down	RRP1	S. cerevisiae YDR087C /GEN=RRP1 /DB_XREF=GI:6320292 /SEG=NC_001136:-617464,618300 /DEF=involved in processing rRNA precursor species to mature rRNAs /NOTE=Rrp1p; go_component: nucleolus [goid GO:0005730] [evidence IDA] [pmid 14562095]; go_component: nucleus [goid GO:0005634] [evidence IDA] [pm	Saccharomyces cerevisiae
1779169_at	0.01	9.23E-06	2.6	down	MAK16	S. cerevisiae YAL025C /GEN=MAK16 /DB_XREF=GI:6319294 /SEG=NC_001133:-100228,101148 /DEF=putative nuclear protein /NOTE=Mak16p; go_component: nucleolus [goid GO:0005730] [evidence IDA] [pmid 10838225]; go_function: molecular_function unknown [goid GO:0005554] [evidence ND]; go_process: host-pat	Saccharomyces cerevisiae
1774980_at	0.02	2.12E-04	2.5	down	SOF1	S. cerevisiae YLL011W /GEN=SOF1 /DB_XREF=GI:6323018 /SEG=NC_001144:+127522,128991 /DEF=part of small (ribosomal) subunit (SSU) processosome (contains U3 snoRNA); 56 kDa nucleolar snRNP protein that shows homology to beta subunits of G-proteins and the splicing factor Prp4 /NOTE=Sof1p; go_component:	Saccharomyces cerevisiae
1776498_at	0.01	3.20E-05	2.5	down	UTP15	S. cerevisiae YMR093W /GEN=UTP15 /DB_XREF=GI:6323740 /SEG=NC_001145:+454014,455555 /DEF=Nucleolar protein, component of the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA /NOTE=Utp15p; go_component: small nucleolar ribonucleoprotein comple	Saccharomyces cerevisiae
1770043_at	0.01	4.07E-05	2.5	down	NMD3	S. cerevisiae YHR170W /GEN=NMD3 /DB_XREF=GI:6321964 /SEG=NC_001140:+443827,445383 /DEF=putative Upf1p-interacting protein /NOTE=Nmd3p; go_component: cytosol [goid GO:0005829] [evidence IDA] [pmid 10022925]; go_component: cytosolic large ribosomal subunit (sensu Eukarya) [goid GO:0005842] [evid	Saccharomyces cerevisiae
1769597_at	0.01	5.13E-05	2.5	down	ERB1	S. cerevisiae YMR049C /GEN=ERB1 /DB_XREF=GI:6323693 /SEG=NC_001145:-368093,370516 /DEF=Protein required for maturation of the 25S and 5.8S ribosomal RNAs; homologous to mammalian Bop1 /NOTE=Erb1p; go_component: nucleolus [goid GO:0005730] [evidence IDA] [pmid 14562095]; go_component: nucleu	Saccharomyces cerevisiae
1769852_at	0.02	8.95E-05	2.5	down	MAK5	S. cerevisiae YBR142W /GEN=MAK5 /DB_XREF=GI:6319618 /SEG=NC_001134:+528273,530594 /DEF=Necessary for maintenance of dsRNA killer plasmids. Is predicted to encode an DEAD-box RNA helicase /NOTE=Mak5p; go_component: nucleolus [goid GO:0005730] [evidence IDA] [pmid 13680366]; go_function: ATP-de	Saccharomyces cerevisiae
1778503_at	0.02	3.13E-04	2.4	down	TKL1	S. cerevisiae YPR074C /GEN=TKL1 /DB_XREF=GI:6325331 /SEG=NC_001148:-692791,694833 /DEF=Transketolase 1 /NOTE=Tkl1p; go_component: cytoplasm [goid GO:0005737] [evidence ISS] [pmid 2843500]; go_function: transketolase activity [goid GO:0004802] [evidence IMP,ISS] [pmid 8226984]; go_process: pentose-pl	Saccharomyces cerevisiae
1769890_at	0.02	3.91E-04	2.4	down	RRB1	S. cerevisiae YMR131C /GEN=RRB1 /DB_XREF=GI:6323779 /SEG=NC_001145:-533162,534697 /DEF=RiboSome Assembly 2 /NOTE=Rrb1p; go_component: nucleolus [goid GO:0005730] [evidence IDA] [pmid 10684247]; go_function: molecular_function unknown [goid GO:0005554] [evidence ND]; go_process: ribosome bio	Saccharomyces cerevisiae
1771557_at	0.03	6.70E-04	2.4	down	DAL7	S. cerevisiae YIR031C /GEN=DAL7 /DB_XREF=GI:6322222 /SEG=NC_001141:-413012,414676 /DEF=Malate synthase, role in allantoin degradation unknown; expression sensitive to nitrogen catabolite repression and induced by allophanate, an intermediate in allantoin degradation /NOTE=Dal7p; go_component: cytoplasm	Saccharomyces cerevisiae
1778063_at	0.01	5.60E-05	2.4	down	NOG1	S. cerevisiae YPL093W /GEN=NOG1 /DB_XREF=GI:6325164 /SEG=NC_001148:+370973,372916 /DEF=Putative GTPase that associates with free 60S ribosomal subunits in the nucleolus and is required for 60S ribosomal subunit biogenesis; member of the ODN family of nucleolar G-proteins /NOTE=Nog1p; go_component: r	Saccharomyces cerevisiae
1771819_at	0.03	6.73E-04	2.4	down	PWP2	S. cerevisiae YCR057C /GEN=PWP2 /DB_XREF=GI:6319903 /SEG=NC_001135:-220452,223223 /DEF=part of small (ribosomal) subunit (SSU) processosome (contains U3 snoRNA); Eight WD-repeats with homology with G protein beta subunits flanked by nonhomologous N-terminal and C-terminal extensions /NOTE=Pwp2p;	Saccharomyces cerevisiae
1777602_at	0.02	2.97E-04	2.4	down	UTP7	S. cerevisiae YER082C /GEN=UTP7 /DB_XREF=GI:6320926 /SEG=NC_001137:-324268,325932 /DEF=Nucleolar protein, component of the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA /NOTE=Utp7p; go_component: small nucleolar ribonucleoprotein complex [go	Saccharomyces cerevisiae
1774694_at	0.03	6.30E-04	2.4	down	YDL063C	S. cerevisiae YDL063C /GEN=UBC9 /DB_XREF=GI:6320141 /SEG=NC_001136:-338272,340134 /DEF=Hypothetical ORF /NOTE=Ydl063cp; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 14562095]; go_component: nucleus [goid GO:0005634] [evidence IDA] [pmid 14562095]; go_function: molecular_fun	Saccharomyces cerevisiae
1773397_at	0.03	9.77E-04	2.4	down	UTP5	S. cerevisiae YDR398W /GEN=UTP5 /DB_XREF=GI:6320606 /SEG=NC_001136:+1267459,1269390 /DEF=Nucleolar protein, component of the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA /NOTE=Utp5p; go_component: small nucleolar ribonucleoprotein complex	Saccharomyces cerevisiae
1779029_at	0.04	0.001736367	2.4	down	BUD20	S. cerevisiae YLR074C /GEN=BUD20 /DB_XREF=GI:6323103 /SEG=NC_001144:-281957,282457 /DEF=Protein involved in bud-site selection; diploid mutants display a random budding pattern instead of the wild-type bipolar pattern /NOTE=Bud20p; go_component: nucleus [goid GO:0005634] [evidence IDA] [pmid 1145201	Saccharomyces cerevisiae
1769431_at	0.02	2.93E-04	2.4	down	NRP1	S. cerevisiae YDL167C /GEN=NRP1 /DB_XREF=GI:6320034 /SEG=NC_001136:-160996,163155 /DEF=Protein of unknown function, rich in asparagine residues /NOTE=Nrp1p; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 14562095]; go_function: molecular_function unknown [goid GO:0005554] [evide	Saccharomyces cerevisiae
1774349_at	0.05	0.002591062	2.4	down	MRT4	S. cerevisiae YKL009W /GEN=MRT4 /DB_XREF=GI:6322843 /SEG=NC_001143:+425885,426595 /DEF=Protein involved in mRNA turnover and ribosome assembly, localizes to the nucleolus /NOTE=Mrt4p; go_component: nucleolus [goid GO:0005730] [evidence IDA] [pmid 14562095]; go_component: nucleus [goid GO:0005	Saccharomyces cerevisiae
1772349_at	0.02	1.40E-04	2.4	down	IPI3	S. cerevisiae YNL182C /GEN=IPI3 /DB_XREF=GI:6324147 /SEG=NC_001146:-295960,297627 /DEF=Protein required for cell viability; computational analysis of large-scale protein-protein interaction data suggests a possible role in assembly of the ribosomal large subunit /NOTE=Ipi3p; go_component: nucleus [goid GO:0005	Saccharomyces cerevisiae
1770205_at	0.04	0.001423734	2.3	down	YVH1	S. cerevisiae YIR026C /GEN=YVH1 /DB_XREF=GI:6322217 /SEG=NC_001141:-404870,405964 /DEF=nitrogen starvation-induced protein phosphatase /NOTE=Yvh1p; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 14562095]; go_function: protein tyrosine phosphatase activity [goid GO:0004725] [eviden	Saccharomyces cerevisiae
1774035_at	0.03	6.24E-04	2.3	down	NOC3	S. cerevisiae YLR002C /GEN=NOC3 /DB_XREF=GI:6323030 /SEG=NC_001144:-154342,156333 /DEF=Protein that forms a nuclear complex with Noc2p that binds to 66S ribosomal precursors to mediate their intranuclear transport; also binds to chromatin to promote the association of DNA replication factors and replicatio	Saccharomyces cerevisiae
1777242_at	0.02	9.90E-05	2.3	down	FRS1	S. cerevisiae YLR060W /GEN=FRS1 /DB_XREF=GI:6323089 /SEG=NC_001144:+260980,262767 /DEF=Alpha (large) subunit of cytoplasmic phenylalanyl-tRNA synthetase /NOTE=Frs1p; go_component: phenylalanine-tRNA ligase complex [goid GO:0009328] [evidence TAS] [pmid 3049607]; go_function: phenylalanine-tRNA lig	Saccharomyces cerevisiae
1778686_at	0.02	2.15E-04	2.3	down	TPO4	S. cerevisiae YOR273C /GEN=TPO4 /DB_XREF=GI:6324847 /SEG=NC_001147:-834449,836428 /DEF=Polyamine transport protein /NOTE=Tpo4p; go_component: plasma membrane [goid GO:0005886] [evidence IDA] [pmid 12562762]; go_component: vacuolar membrane [goid GO:0005774] [evidence IMP] [pmid 11171066	Saccharomyces cerevisiae
1773669_at	0.02	3.02E-04	2.3	down	UTP23	S. cerevisiae YOR004W /GEN=YSP3 /DB_XREF=GI:6324577 /SEG=NC_001147:+333592,334356 /DEF=Protein required for cell viability /NOTE=Yor004wp; go_component: mitochondrion [goid GO:0005739] [evidence IDA] [pmid 14562095]; go_component: nucleolus [goid GO:0005730] [evidence IDA] [pmid 14690591]; go_f	Saccharomyces cerevisiae
1771973_at	0.03	4.57E-04	2.3	down	SQT1	S. cerevisiae YIR012W /GEN=SQT1 /DB_XREF=GI:6322202 /SEG=NC_001141:+378483,379778 /DEF=Involved in a late step of 60S ribosomal subunit assembly or modification; contains multiple WD repeats; interacts with Qsr1p /NOTE=Sqt1p; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 11914276];	Saccharomyces cerevisiae
1773154_at	0.05	0.002406022	2.3	down	RCL1	S. cerevisiae YOL010W /GEN=RCL1 /DB_XREF=GI:6324564 /SEG=NC_001147:+307938,309041 /DEF=RNA terminal phosphate cyclase-like protein involved in rRNA processing at sites A0, A1, and A2; does not possess detectable RNA cyclase activity /NOTE=Rcl1p; go_component: nucleolus [goid GO:0005730] [evidence IDA]	Saccharomyces cerevisiae
1769388_at	0.04	0.001782712	2.3	down	DUS3	S. cerevisiae YLR401C /GEN=DUS3 /DB_XREF=GI:6323433 /SEG=NC_001144:-922618,924447 /DEF=Dihydrouridine synthase, member of a widespread family of conserved proteins including Smm1p, Dus1p, and Dus4p; contains a consensus oleate response element (ORE) in its promoter region /NOTE=Dus3p; go_compone	Saccharomyces cerevisiae
1770106_at	0.03	5.25E-04	2.3	down	SLX9	S. cerevisiae YGR081C /GEN=SLX9 /DB_XREF=GI:6321518 /SEG=NC_001139:-643150,643782 /DEF=Protein of unknown function; deletion mutant has synthetic fitness defect with an sgs1 deletion mutant /NOTE=Slx9p; go_component: nucleolus [goid GO:0005730] [evidence IDA] [pmid 14562095]; go_component: nucleus	Saccharomyces cerevisiae
1771133_at	0.03	4.79E-04	2.3	down	DBP10	S. cerevisiae YDL031W /GEN=DBP10 /DB_XREF=GI:6320173 /SEG=NC_001136:+394214,397201 /DEF=Dead box protein 10 /NOTE=Dbp10p; go_component: nucleolus [goid GO:0005730] [evidence IDA] [pmid 10871363]; go_function: ATP-dependent RNA helicase activity [goid GO:0004004] [evidence TAS] [pmid 10690410	Saccharomyces cerevisiae
1779544_at	0.04	0.002040307	2.3	down	LCP5	S. cerevisiae YER127W /GEN=LCP5 /DB_XREF=GI:6320974 /SEG=NC_001137:+414477,415550 /DEF=Lethal with conditional pap1 allele /NOTE=Lcp5p; go_component: small nuclear ribonucleoprotein complex [goid GO:0030532] [evidence TAS] [pmid 10690410]; go_component: small nucleolar ribonucleoprotein complex	Saccharomyces cerevisiae
1774438_at	0.02	1.40E-04	2.3	down	FCP1	S. cerevisiae YMR277W /GEN=FCP1 /DB_XREF=GI:6323933 /SEG=NC_001145:+820255,822453 /DEF=Carboxy-terminal domain (CTD) phosphatase, essential for dephosphorylation of the repeated C-terminal domain of the RNA polymerase II large subunit (Rpo21p) /NOTE=Fcp1p; go_component: nucleus [goid GO:000563	Saccharomyces cerevisiae
1773459_at	0.02	2.99E-04	2.3	down	ARX1	S. cerevisiae YDR101C /GEN=ARX1 /DB_XREF=GI:6320306 /SEG=NC_001136:-655680,657461 /DEF=Arx1p /NOTE=go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 12374754]; go_component: nucleoplasm [goid GO:0005654] [evidence IDA] [pmid 12374754]; go_function: molecular_function unknown [g	Saccharomyces cerevisiae
1775669_at	0.01	2.79E-05	2.2	down	RIO2	S. cerevisiae YNL207W /GEN=RIO2 /DB_XREF=GI:6324122 /SEG=NC_001146:+255352,256629 /DEF=Protein required for cell viability /NOTE=Rio2p; go_component: cytosol [goid GO:0005829] [evidence IDA] [pmid 12612080]; go_component: nucleus [goid GO:0005634] [evidence IDA] [pmid 12612080]; go_function: nucle	Saccharomyces cerevisiae
1779114_at	0.02	1.76E-04	2.2	down	RSR1	S. cerevisiae YGR152C /GEN=RSR1 /DB_XREF=GI:6321591 /SEG=NC_001139:-794677,795495 /DEF=Gtp-binding protein of the ras superfamily involved in bud site selection /NOTE=Rsr1p; go_component: bud [goid GO:0005933] [evidence TAS] [pmid 9759491]; go_component: plasma membrane [goid GO:0005886] [evider	Saccharomyces cerevisiae
1774541_at	0.03	6.35E-04	2.2	down	PWP1	S. cerevisiae YLR196W /GEN=PWP1 /DB_XREF=GI:6323225 /SEG=NC_001144:+543970,545700 /DEF=periodic tryptophan proteinProtein with periodic trytophan residues that resembles members of beta-transducin superfamily because of presence of WD-40 repeats /NOTE=Pwp1p; go_component: cytoplasm [goid GO:00	Saccharomyces cerevisiae
1771444_at	0.02	3.79E-04	2.2	down	RPG1	S. cerevisiae YBR079C /GEN=RPG1 /DB_XREF=GI:6319553 /SEG=NC_001134:-395340,398234 /DEF=Subunit of the core complex of translation initiation factor 3(eIF3), essential for translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that stimulates binding of mRNA and tRNA(i)Met to ribosomes /NOTE=Rpg1p; go_comp	Saccharomyces cerevisiae
1776524_at	0.04	0.001546767	2.2	down	YBL028C	S. cerevisiae YBL028C /GEN=PET9 /DB_XREF=GI:6319443 /SEG=NC_001134:-167483,167803 /DEF=Hypothetical ORF /NOTE=Ybl028cp; go_component: nucleolus [goid GO:0005730] [evidence IDA] [pmid 14562095]; go_component: nucleus [goid GO:0005634] [evidence IDA] [pmid 14562095]; go_function: molecular_funct	Saccharomyces cerevisiae
1779772_at	0.05	0.002231696	2.2	down	YEH1	S. cerevisiae YLL012W /GEN=PUF3 /DB_XREF=GI:6323017 /SEG=NC_001144:+125533,127254 /DEF=Hypothetical ORF /NOTE=Yll012wp; go_component: lipid particle [goid GO:0005811] [evidence IDA] [pmid 14562095]; go_function: molecular_function unknown [goid GO:0005554] [evidence ND]; go_process: biological_p	Saccharomyces cerevisiae
1770147_at	0.02	2.25E-04	2.2	down	DBP8	S. cerevisiae YHR169W /GEN=DBP8 /DB_XREF=GI:6321963 /SEG=NC_001140:+442180,443475 /DEF=Dead-Box Protein 8, ATP-dependent helicase involved in rRNA processing /NOTE=Dbp8p; go_component: nucleolus [goid GO:0005730] [evidence TAS] [pmid 10690410]; go_component: nucleolus [goid GO:0005730] [evid	Saccharomyces cerevisiae
1776348_at	0.01	6.39E-06	2.2	down	FAL1	S. cerevisiae YDR021W /GEN=FAL1 /DB_XREF=GI:6320224 /SEG=NC_001136:+486800,487999 /DEF=Nucleolar protein required for maturation of 18S rRNA, member of the eIF4A subfamily of DEAD-box ATP-dependent RNA helicases /NOTE=Fal1p; go_component: nucleolus [goid GO:0005730] [evidence TAS] [pmid 10690	Saccharomyces cerevisiae
1775762_at	0.01	4.15E-05	2.2	down	NOP56	S. cerevisiae YLR197W /GEN=SIK1 /DB_XREF=GI:6323226 /SEG=NC_001144:+546099,547613 /DEF=part of small (ribosomal) subunit (SSU) processosome (contains U3 snoRNA); similar to microtubule binding proteins and to X90565_5.cds /NOTE=Sik1p; go_component: nucleolus [goid GO:0005730] [evidence IDA] [pmid 1	Saccharomyces cerevisiae
1780244_at	0.01	5.49E-05	2.2	down	RBG2	S. cerevisiae YGR173W /GEN=YIP1 /DB_XREF=GI:6321612 /SEG=NC_001139:+843857,844963 /DEF=GTPase, interacts with ribosomes /NOTE=Ygr173wp	Saccharomyces cerevisiae
1773118_at	0.02	1.88E-04	2.2	down	DUS1	S. cerevisiae YML080W /GEN=DUS1 /DB_XREF=GI:6323560 /SEG=NC_001145:+108806,110077 /DEF=Dihydrouridine synthase, member of a widespread family of conserved proteins including Smm1p, Dus3p, and Dus4p; modifies pre-tRNA(Phe) at U17 /NOTE=Dus1p; go_component: nucleus [goid GO:0005634] [evidence I	Saccharomyces cerevisiae
1778653_at	0.04	0.001395534	2.1	down	RIX7	S. cerevisiae YLL034C /GEN=RIX7 /DB_XREF=GI:6322994 /SEG=NC_001144:-70632,73145 /DEF=Putative ATPase of the AAA family, required for export of pre-ribosomal large subunits from the nucleus; distributed between the nucleolus, nucleoplasm, and nuclear periphery depending on growth conditions /NOTE=Rix7p;	Saccharomyces cerevisiae
1772442_at	0.04	0.00118517	2.1	down	CBF5	S. cerevisiae YLR175W /GEN=CBF5 /DB_XREF=GI:6323204 /SEG=NC_001144:+506136,507587 /DEF=major low affinity 55 kDa Centromere/microtubule binding protein /NOTE=Cbf5p; go_component: small nucleolar ribonucleoprotein complex [goid GO:0005732] [evidence IPI] [pmid 9472021]; go_function: pseudouridylat	Saccharomyces cerevisiae
1774976_at	0.04	0.00126992	2.1	down	NOC4	S. cerevisiae YPR144C /GEN=NOC4 /DB_XREF=GI:6325402 /SEG=NC_001148:-819759,821417 /DEF=Nucleolar protein, forms a complex with Nop14p that mediates maturation and nuclear export of 40S ribosomal subunits /NOTE=Noc4p; go_component: nucleus [goid GO:0005634] [evidence IDA] [pmid 10684247]; go_fun	Saccharomyces cerevisiae

1772101_at	0.02	1.97E-04	2.1	down	OGG1	S. cerevisiae YML060W /GEN=OGG1 /DB_XREF=GI:6323580 /SEG=NC_001145:+151871,153001 /DEF=Mitochondrial glycosylase/lyase that specifically excises 7,8-dihydro-8-oxoguanine residues located opposite cytosine or thymine residues in DNA, repairs oxidative damage to mitochondrial DNA /NOTE=Ogg1p; go_comp	Saccharomyces cerevisiae
1770297_at	0.04	0.001848524	2.1	down	UTP14	S. cerevisiae YML093W /GEN=UTP14 /DB_XREF=GI:6323546 /SEG=NC_001145:+83090,85789 /DEF=Nucleolar protein, component of the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA /NOTE=Utp14p; go_component: small nucleolar ribonucleoprotein complex [	Saccharomyces cerevisiae
1770200_at	0.03	8.45E-04	2.1	down	YTM1	S. cerevisiae YOR272W /GEN=YTM1 /DB_XREF=GI:6324846 /SEG=NC_001147:+832810,834192 /DEF=microtubule-associated protein /NOTE=Ytm1p; go_component: nucleolus [goid GO:0005730] [evidence IDA] [pmid 11583614]; go_component: nucleus [goid GO:0005634] [evidence IDA] [pmid 11914276]; go_function: m	Saccharomyces cerevisiae
1772336_at	0.04	0.001539358	2.1	down	ERG3	S. cerevisiae YLR056W /GEN=ERG3 /DB_XREF=GI:6323085 /SEG=NC_001144:+253862,254959 /DEF=C-5 sterol desaturase, catalyzes the introduction of a C-5(6) double bond into episterol, a precursor in ergosterol biosynthesis; mutants are viable, but cannot grow on non-fermentable carbon sources /NOTE=Erg3p; go_co	Saccharomyces cerevisiae
1771706_at	0.04	0.001676864	2.1	down	RPB5	S. cerevisiae YBR154C /GEN=RPB5 /DB_XREF=GI:6319630 /SEG=NC_001134:-548318,548965 /DEF=RNA polymerase subunit, found in RNA polymerase complexes I, II, and III /NOTE=Rpb5p; go_component: DNA-directed RNA polymerase I complex [goid GO:0005736] [evidence TAS] [pmid 9774381]; go_component: DNA-d	Saccharomyces cerevisiae
1779256_at	0.01	2.50E-05	2.1	down	FUI1	S. cerevisiae YBL042C /GEN=FUI1 /DB_XREF=GI:6319429 /SEG=NC_001134:-138306,140225 /DEF=High affinity uridine permease, localized to the plasma membrane; not involved in uracil transport /NOTE=Fui1p; go_component: plasma membrane [goid GO:0005886] [evidence IGI,IMP] [pmid 10827169]; go_function: urid	Saccharomyces cerevisiae
1776711_at	0.05	0.002494093	2.1	down	SMI1	S. cerevisiae YGR229C /GEN=SMI1 /DB_XREF=GI:6321668 /SEG=NC_001139:-949382,950899 /DEF=Protein involved in (1,3)-beta-glucan synthesis, possibly through regulation of cell wall glucan and chitin synthesis; chromatin binding protein /NOTE=Smi1p; go_component: bud tip [goid GO:0005934] [evidence TAS] [pmid	Saccharomyces cerevisiae
1772032_at	0.02	1.90E-04	2.1	down	DSN1	S. cerevisiae YIR010W /GEN=DSN1 /DB_XREF=GI:6322200 /SEG=NC_001141:+375428,377158 /DEF=Essential component of the MIND kinetochore complex (Mtw1p Including Nnf1p-Nsl1p-Dsn1p) which joins kinetochore subunits contacting DNA to those contacting microtubules; important for chromosome segregation /N	Saccharomyces cerevisiae
1779287_at	0.05	0.002341642	2.1	down	NOG2	S. cerevisiae YNR053C /GEN=NOG2 /DB_XREF=GI:6324381 /SEG=NC_001146:-721119,723110 /DEF=Putative GTPase that associates with pre-60S ribosomal subunits in the nucleolus and is required for their nuclear export and maturation /NOTE=Nog2p; go_component: nucleolus [goid GO:0005730] [evidence IDA] [pmid	Saccharomyces cerevisiae
1777206_at	0.01	1.12E-05	2.1	down	NOP9	S. cerevisiae YJL010C /GEN=RPC17 /DB_XREF=GI:6322450 /SEG=NC_001142:-417477,419477 /DEF=Protein required for cell viability /NOTE=Yjl010cp; go_component: nucleolus [goid GO:0005730] [evidence IDA] [pmid 14690591]; go_component: nucleus [goid GO:0005634] [evidence IDA] [pmid 14690591]; go_function: R	Saccharomyces cerevisiae
1778563_at	0.04	0.001143889	2.1	down	ALT2	S. cerevisiae YDR111C /GEN=FOB1 /DB_XREF=GI:6320317 /SEG=NC_001136:-678235,679758 /DEF=putative alanine transaminase (glutamyc pyruvic transaminase) /NOTE=Ydr111cp	Saccharomyces cerevisiae
1773158_at	0.02	1.56E-04	2.1	down	VTS1	S. cerevisiae YOR359W /GEN=VTS1 /DB_XREF=GI:6324935 /SEG=NC_001147:+1011185,1012756 /DEF=Vts1p /NOTE=go_component: cytosol [goid GO:0005829] [evidence IDA] [pmid 11445562]; go_function: RNA binding [goid GO:0003723] [evidence IDA] [pmid 12858164]; go_function: intracellular transporter activity [g	Saccharomyces cerevisiae
1771626_at	0.03	7.94E-04	2.1	down	RPF2	S. cerevisiae YKR081C /GEN=RPF2 /DB_XREF=GI:6322934 /SEG=NC_001143:-591148,592182 /DEF=Rpf2p /NOTE=go_component: nucleolus [goid GO:0005730] [evidence IDA] [pmid 11864606]; go_component: nucleolus [goid GO:0005730] [evidence IPI] [pmid 11864607]; go_function: 5S rRNA binding [goid GO:0008097] [	Saccharomyces cerevisiae
1779249_at	0.04	0.001282022	2.0	down	ECM1	S. cerevisiae YAL059W /GEN=ECM1 /DB_XREF=GI:6319259 /SEG=NC_001133:+36510,37148 /DEF=Protein of unknown function, localized in the nucleoplasm and the nucleolus, genetically interacts with MTR2 in 60S ribosomal protein subunit export /NOTE=Ecm1p; go_component: nucleolus [goid GO:0005730] [evidence	Saccharomyces cerevisiae
1771396_at	0.02	3.83E-04	2.0	down	BRX1	S. cerevisiae YOL077C /GEN=BRX1 /DB_XREF=GI:6324496 /SEG=NC_001147:-185847,186722 /DEF=Essential nucleolar protein required for biogenesis of the 60S ribosomal subunit /NOTE=Brx1p; go_component: nucleolus [goid GO:0005730] [evidence IPI] [pmid 11864607]; go_function: 5S rRNA binding [goid GO:0008097	Saccharomyces cerevisiae
1771126_at	0.05	0.002406951	2.0	down	PUF6	S. cerevisiae YDR496C /GEN=PUF6 /DB_XREF=GI:6320704 /SEG=NC_001136:-1441421,1443391 /DEF=member of the PUF protein family /NOTE=Puf6p; go_component: nucleolus [goid GO:0005730] [evidence IDA] [pmid 14562095]; go_component: nucleus [goid GO:0005634] [evidence IDA] [pmid 14562095]; go_function	Saccharomyces cerevisiae
1779404_at	0.03	8.18E-04	2.0	down	NUP82	S. cerevisiae YJL061W /GEN=NUP82 /DB_XREF=GI:6322400 /SEG=NC_001142:+319932,322073 /DEF=Subunit of the nuclear pore complex (NPC), forms a subcomplex with Nup159p and Nsp1p, interacts with Nup116p and is required for proper localization of Nup116p in the NPC /NOTE=Nup82p; go_component: nuclear p	Saccharomyces cerevisiae
1777639_at	0.02	1.30E-04	2.0	down	PPT1	S. cerevisiae YGR123C /GEN=PPT1 /DB_XREF=GI:6321562 /SEG=NC_001139:-736665,738206 /DEF=Protein serine/threonine phosphatase with similarity to human phosphatase PP5; present in both the nucleus and cytoplasm; expressed during logarithmic growth /NOTE=Ppt1p; go_component: cytoplasm [goid GO:00057	Saccharomyces cerevisiae
1770705_at	0.02	3.21E-04	2.0	down	SYF1	S. cerevisiae YDR416W /GEN=SYF1 /DB_XREF=GI:6320624 /SEG=NC_001136:+1298420,1300999 /DEF=SYnthetic lethal with cdcForty /NOTE=Syf1p; go_component: spliceosome complex [goid GO:0005681] [evidence IDA] [pmid 12088152]; go_function: molecular_function unknown [goid GO:0005554] [evidence ND]; go_	Saccharomyces cerevisiae
1777786_at	0.05	0.002745991	2.0	down	TPA1	S. cerevisiae YER049W /GEN=CAJ1 /DB_XREF=GI:6320890 /SEG=NC_001137:+251727,253661 /DEF=Hypothetical ORF /NOTE=Yer049wp; go_component: nucleus [goid GO:0005634] [evidence IDA] [pmid 14562095]; go_function: molecular_function unknown [goid GO:0005554] [evidence ND]; go_process: biological_proc	Saccharomyces cerevisiae
1771367_at	0.02	1.81E-04	2.0	down	RPP1	S. cerevisiae YHR062C /GEN=RPP1 /DB_XREF=GI:6321853 /SEG=NC_001140:-222878,223759 /DEF=Subunit of both RNase MRP, which cleaves pre-rRNA, and nuclear RNase P, which cleaves tRNA precursors to generate mature 5' ends /NOTE=Rpp1p; go_component: nucleolar ribonuclease P complex [goid GO:0005655] [e	Saccharomyces cerevisiae
1772239_at	0.05	0.002572373	2.0	down	RLP7	S. cerevisiae YNL002C /GEN=RLP7 /DB_XREF=GI:6324326 /SEG=NC_001146:-626173,627141 /DEF=Significant sequence similarity to RPL7B, but neither can functionally replace the other. Does not correspond to any ribosomal component identified so far, based on its biochemical features /NOTE=Rlp7p; go_component: n	Saccharomyces cerevisiae
1774719_at	0.04	0.001487051	2.0	down	CGR1	S. cerevisiae YGL029W /GEN=CGR1 /DB_XREF=GI:6321409 /SEG=NC_001139:+440066,440428 /DEF=Coiled-coil growth-regulated. May contribute to compartmentalization of nucleolar constituents. /NOTE=Cgr1p; go_component: nucleolus [goid GO:0005730] [evidence IDA] [pmid 11116400]; go_function: molecular_func	Saccharomyces cerevisiae
1778323_at	0.03	5.72E-04	2.0	down	RRP9	S. cerevisiae YPR137W /GEN=RRP9 /DB_XREF=GI:6325394 /SEG=NC_001148:+802353,804074 /DEF=part of small (ribosomal) subunit (SSU) processosome (contains U3 snoRNA); Rrp9p is an ortholog of the human U3-55k protein; the human cDNA partially complements a yeast rrp9 null mutant. (Pluk et al. (1998) Mol. Cel	Saccharomyces cerevisiae
1774503_at	0.04	0.001478156	2.0	down	UTP11	S. cerevisiae YKL099C /GEN=UTP11 /DB_XREF=GI:6322750 /SEG=NC_001143:-255347,256117 /DEF=Nucleolar protein, component of the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA /NOTE=Utp11p; go_component: small nucleolar ribonucleoprotein complex [	Saccharomyces cerevisiae
1778921_at	0.04	0.00202999	2.0	down	ESF1	S. cerevisiae YDR365C /GEN=ESF1 /DB_XREF=GI:6320573 /SEG=NC_001136:-1204485,1206371 /DEF=Nucleolar protein involved in pre-rRNA processing; depletion causes severely decreased 18S rRNA levels /NOTE=Esf1p; go_component: nucleolus [goid GO:0005730] [evidence IDA] [pmid 14562095]; go_component: nucle	Saccharomyces cerevisiae
1771183_at	0.02	3.57E-04	2.0	down	ERG2	S. cerevisiae YMR202W /GEN=ERG2 /DB_XREF=GI:6323858 /SEG=NC_001145:+667536,668204 /DEF=C-8 sterol isomerase, catalyzes the isomerization of the delta-8 double bond to the delta-7 position at an intermediate step in ergosterol biosynthesis /NOTE=Erg2p; go_component: endoplasmic reticulum [goid GO:00057	Saccharomyces cerevisiae
1777853_at	0.02	1.52E-04	2.0	down	FTR1	S. cerevisiae YER145C /GEN=FTR1 /DB_XREF=GI:6320993 /SEG=NC_001137:-460521,461735 /DEF=High affinity iron permease involved in the transport of iron across the plasma membrane; forms complex with Fet3p; expression is regulated by iron /NOTE=Ftr1p; go_component: plasma membrane [goid GO:0005886] [ev	Saccharomyces cerevisiae
1770624_at	0.03	4.14E-04	2.0	down	PAC10	S. cerevisiae YGR078C /GEN=PAC10 /DB_XREF=GI:6321515 /SEG=NC_001139:-639774,640373 /DEF=Polypeptide 3 of a Yeast Non-native Actin Binding Complex, homolog of a component of the bovine NABC complex /NOTE=Pac10p; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 9463374]; go_compo	Saccharomyces cerevisiae
1774770_at	0.02	1.25E-04	1.9	down	ENT5	S. cerevisiae YDR153C /GEN=ENT5 /DB_XREF=GI:6320357 /SEG=NC_001136:-766730,767965 /DEF=Protein containing an N-terminal epsin-like domain involved in clathrin recruitment and traffic between the Golgi and endosomes; associates with the clathrin adaptor Gga2p, clathrin adaptor complex AP-1, and clathrin /N	Saccharomyces cerevisiae
1771835_at	0.01	4.56E-05	1.9	down	YIL091C	S. cerevisiae YIL091C /GEN=RSM25 /DB_XREF=GI:6322100 /SEG=NC_001141:-191027,193192 /DEF=Protein required for cell viability /NOTE=Yil091cp; go_component: nucleolus [goid GO:0005730] [evidence IDA] [pmid 14690591]; go_component: nucleus [goid GO:0005634] [evidence IDA] [pmid 14690591]; go_function:	Saccharomyces cerevisiae
1773994_at	0.02	2.13E-04	1.9	down	ENP2	S. cerevisiae YGR145W /GEN=THI4 /DB_XREF=GI:6321584 /SEG=NC_001139:+781770,783893 /DEF=Essential protein of unknown function /NOTE=Ygr145wp	Saccharomyces cerevisiae
1772225_at	0.02	3.75E-04	1.9	down	PUS1	S. cerevisiae YPL212C /GEN=PUS1 /DB_XREF=GI:6325044 /SEG=NC_001148:-151514,153148 /DEF=Involved in tRNA biogenesis /NOTE=Pus1p; go_component: nucleus [goid GO:0005634] [evidence IPI] [pmid 8641292]; go_function: pseudouridylate synthase activity [goid GO:0004730] [evidence IDA] [pmid 10356324]; go	Saccharomyces cerevisiae
1769511_at	0.04	0.001794818	1.9	down	DBP6	S. cerevisiae YNR038W /GEN=DBP6 /DB_XREF=GI:6324366 /SEG=NC_001146:+695594,697483 /DEF=Dead Box Protein 6 /NOTE=Dbp6p; go_component: nucleolar preribosome, large subunit precursor [goid GO:0030687] [evidence IDA] [pmid 15126390]; go_component: nucleolus [goid GO:0005730] [evidence IDA] [pmid	Saccharomyces cerevisiae
1771012_at	0.02	1.90E-04	1.9	down	TSR1	S. cerevisiae YDL060W /GEN=TSR1 /DB_XREF=GI:6320143 /SEG=NC_001136:+341619,343985 /DEF=Twenty S rRNA accumulation /NOTE=Tsr1p; go_component: nucleolus [goid GO:0005730] [evidence IDA] [pmid 11565749]; go_function: molecular_function unknown [goid GO:0005554] [evidence ND]; go_process: rRNA p	Saccharomyces cerevisiae
1772723_at	0.03	5.91E-04	1.9	down	GCD10	S. cerevisiae YNL062C /GEN=GCD10 /DB_XREF=GI:6324267 /SEG=NC_001146:-508774,510210 /DEF=Subunit of tRNA (1-methyladenosine) methyltransferase with Gcd14p, required for the modification of the adenine at position 58 in tRNAs, especially tRNAi-Met; first identified as a negative regulator of GCN4 expression	Saccharomyces cerevisiae
1770257_at	0.03	7.22E-04	1.9	down	YNL313C	S. cerevisiae YNL313C /GEN=DAL82 /DB_XREF=GI:6324016 /SEG=NC_001146:-45307,48021 /DEF=Protein required for cell viability /NOTE=Ynl313cp; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 14690591]; go_component: nucleus [goid GO:0005634] [evidence IDA] [pmid 14690591]; go_function: n	Saccharomyces cerevisiae
1772832_at	0.03	3.93E-04	1.9	down	GCN20	S. cerevisiae YFR009W /GEN=GCN20 /DB_XREF=GI:14318531 /SEG=NC_001138:+162482,164740 /DEF=Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn1p; proposed to stimulate Gcn2p activation by an uncharged tRNA /NOTE=Gcn20p; go_component: cytosol [goid GO:0005829] [evidence IPI] [pm	Saccharomyces cerevisiae
1772744_at	0.02	1.56E-04	1.9	down	EMC1	S. cerevisiae YCL045C /GEN=APA1 /DB_XREF=GI:6319804 /SEG=NC_001135:-44623,46905 /DEF=Hypothetical ORF /NOTE=Ycl045cp; go_component: endoplasmic reticulum [goid GO:0005783] [evidence IDA] [pmid 14562095]; go_function: molecular_function unknown [goid GO:0005554] [evidence ND]; go_process: biolo	Saccharomyces cerevisiae
1770820_at	0.03	7.84E-04	1.9	down	WRS1	S. cerevisiae YOL097C /GEN=WRS1 /DB_XREF=GI:6324475 /SEG=NC_001147:-136526,137824 /DEF=W = IUPAC for tryptophan, RS = convention for aminoacyl-tRNA synthetases /NOTE=Wrs1p; go_component: cytoplasm [goid GO:0005737] [evidence TAS] [pmid 10950302]; go_function: tryptophan-tRNA ligase activity [goi	Saccharomyces cerevisiae
1778235_at	0.04	0.00124524	1.9	down	EDC3	S. cerevisiae YEL015W /GEN=EDC3 /DB_XREF=GI:6320822 /SEG=NC_001137:+126629,128284 /DEF=Non-essential conserved protein of unknown function, plays a role in mRNA decapping by specifically affecting the function of the decapping enzyme Dcp1p; localizes to cytoplasmic mRNA processing bodies /NOTE=Edc3p;	Saccharomyces cerevisiae
1775468_at	0.02	1.80E-04	1.9	down	NHP2	S. cerevisiae YDL208W /GEN=NHP2 /DB_XREF=GI:6319993 /SEG=NC_001136:+87462,87983 /DEF=HMG-like nuclear protein /NOTE=Nhp2p; go_component: small nuclear ribonucleoprotein complex [goid GO:0030532] [evidence TAS] [pmid 10690410]; go_function: RNA binding [goid GO:0003723] [evidence IDA] [pmid 11	Saccharomyces cerevisiae
1772950_at	0.02	7.82E-05	1.9	down	NOP6	S. cerevisiae YDL213C /GEN=NOP6 /DB_XREF=GI:6319988 /SEG=NC_001136:-77290,77967 /DEF=Protein with similarity to hydrophilins, which are involved in the adaptive response to hyperosmotic conditions; computational analysis of large-scale protein-protein interaction data suggests a possible role in rRNA processin	Saccharomyces cerevisiae
1776269_at	0.03	6.87E-04	1.9	down	UBP3	S. cerevisiae YER151C /GEN=UBP3 /DB_XREF=GI:6320999 /SEG=NC_001137:-469681,472419 /DEF=Ubiquitin-specific protease that interacts with Bre5p to co-regulate anterograde and retrograde transport between endoplasmic reticulum and Golgi compartments; inhibitor of gene sillencing; cleaves ubiquitin fusions but	Saccharomyces cerevisiae
1773099_at	0.03	7.12E-04	1.9	down	KRE33	S. cerevisiae YNL132W /GEN=KRE33 /DB_XREF=GI:6324197 /SEG=NC_001146:+375321,378491 /DEF=Killer toxin REsistant /NOTE=Kre33p; go_component: nucleolus [goid GO:0005730] [evidence IDA] [pmid 14562095]; go_function: molecular_function unknown [goid GO:0005554] [evidence ND]; go_process: biological_p	Saccharomyces cerevisiae
1775130_at	0.03	5.39E-04	1.9	down	CNS1	S. cerevisiae YBR155W /GEN=CNS1 /DB_XREF=GI:6319631 /SEG=NC_001134:+549727,550884 /DEF=cyclophilin seven suppressor /NOTE=Cns1p; go_component: cytoplasm [goid GO:0005737] [evidence IPI] [pmid 9819421]; go_function: chaperone activity [goid GO:0003754] [evidence IPI] [pmid 9819421]; go_process: pro	Saccharomyces cerevisiae
1779635_at	0.05	0.00243132	1.9	down	MCX1	S. cerevisiae YBR227C /GEN=MCX1 /DB_XREF=GI:6319704 /SEG=NC_001134:-673529,675091 /DEF=Mitochondrial ATP-binding protein, similar to ClpX /NOTE=Mcx1p; go_component: mitochondrial matrix [goid GO:0005759] [evidence IDA] [pmid 9827555]; go_function: ATP binding [goid GO:0005524] [evidence ISS] [pmi	Saccharomyces cerevisiae
1773288_at	0.04	0.001815617	1.9	down	RPC40	S. cerevisiae YPR110C /GEN=RPC40 /DB_XREF=GI:6325367 /SEG=NC_001148:-745824,746831 /DEF=RNA polymerase subunit, common to RNA polymerase I and III /NOTE=Rpc40p; go_component: DNA-directed RNA polymerase I complex [goid GO:0005736] [evidence TAS] [pmid 8246845]; go_component: DNA-directed	Saccharomyces cerevisiae
1776619_at	0.02	1.60E-04	1.9	down	URB2	S. cerevisiae YJR041C /GEN=GEF1 /DB_XREF=GI:6322501 /SEG=NC_001142:-510153,513677 /DEF=Protein required for cell viability /NOTE=Yjr041cp	Saccharomyces cerevisiae
1771658_at	0.02	2.09E-04	1.8	down	NIP1	S. cerevisiae YMR309C /GEN=NIP1 /DB_XREF=GI:6323969 /SEG=NC_001145:-892987,895425 /DEF=Protein required for nuclear import with some similarity to Nsr1p, another protein involved in nuclear transport /NOTE=Nip1p; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 11914276]; go_componer	Saccharomyces cerevisiae
1770861_at	0.03	0.001046029	1.8	down	UTP10	S. cerevisiae YJL109C /GEN=UTP10 /DB_XREF=GI:6322352 /SEG=NC_001142:-211917,217226 /DEF=Nucleolar protein, component of the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA /NOTE=Utp10p; go_component: small nucleolar ribonucleoprotein complex [g	Saccharomyces cerevisiae
1769331_at	0.03	7.87E-04	1.8	down	STE20	S. cerevisiae YHL007C /GEN=STE20 /DB_XREF=GI:6321780 /SEG=NC_001140:-95113,97932 /DEF=Involved in pheromone response and pseudohyphal growth pathways /NOTE=Ste20p; go_component: incipient bud site [goid GO:0000131] [evidence IDA] [pmid 9003780]; go_component: shmoo tip [goid GO:0005937] [evid	Saccharomyces cerevisiae
1774914_at	0.03	4.08E-04	1.8	down	YCR016W	S. cerevisiae YCR016W /GEN=POL4 /DB_XREF=GI:10383784 /SEG=NC_001135:+143631,144503 /DEF=Hypothetical ORF /NOTE=Ycr016wp; go_component: nucleolus [goid GO:0005730] [evidence IDA] [pmid 14562095]; go_component: nucleus [goid GO:0005634] [evidence IDA] [pmid 14562095]; go_function: molecular_fu	Saccharomyces cerevisiae
1773261_at	0.03	8.77E-04	1.8	down	AIR1	S. cerevisiae YIL079C /GEN=AIR1 /DB_XREF=GI:6322111 /SEG=NC_001141:-210920,212002 /DEF=arginine methyltransferase-interacting RING finger protein /NOTE=Air1p; go_component: nucleolus [goid GO:0005730] [evidence IDA] [pmid 11489916]; go_component: nucleus [goid GO:0005634] [evidence IPI] [pmid 10896	Saccharomyces cerevisiae
1770824_at	0.03	9.94E-04	1.8	down	RPA190	S. cerevisiae YOR341W /GEN=RPA190 /DB_XREF=GI:6324917 /SEG=NC_001147:+960982,965976 /DEF=RNA polymerase I subunit alpha; largest subunit of RNA polymerase I /NOTE=Rpa190p; go_component: DNA-directed RNA polymerase I complex [goid GO:0005736] [evidence TAS] [pmid 8246845]; go_function: DNA-di	Saccharomyces cerevisiae
1773706_at	0.05	0.00231814	1.8	down	PNO1	S. cerevisiae YOR145C /GEN=PNO1 /DB_XREF=GI:6324720 /SEG=NC_001147:-605347,606171 /DEF=Partner of Nob1 /NOTE=Pno1p; go_component: nucleolus [goid GO:0005730] [evidence IDA] [pmid 10923024]; go_component: nucleus [goid GO:0005634] [evidence IDA] [pmid 12502737]; go_function: chaperone activity	Saccharomyces cerevisiae
1777616_at	0.01	3.35E-05	1.8	down	YML018C	S. cerevisiae YML018C /GEN=OST6 /DB_XREF=GI:6323623 /SEG=NC_001145:-234771,235952 /DEF=Hypothetical ORF /NOTE=Yml018cp; go_component: vacuolar membrane (sensu Fungi) [goid GO:0000329] [evidence IDA] [pmid 14562095]; go_function: molecular_function unknown [goid GO:0005554] [evidence ND]; go_	Saccharomyces cerevisiae
1770628_at	0.02	7.77E-05	1.8	down	POM34	S. cerevisiae YLR018C /GEN=POM34 /DB_XREF=GI:6323046 /SEG=NC_001144:-178706,179605 /DEF=nuclear pore integral membrane protein /NOTE=Pom34p; go_component: nuclear pore [goid GO:0005643] [evidence IDA] [pmid 10684247]; go_component: nuclear pore [goid GO:0005643] [evidence TAS] [pmid 113439	Saccharomyces cerevisiae
1773722_at	0.02	3.45E-04	1.8	down	UBP10	S. cerevisiae YNL186W /GEN=UBP10 /DB_XREF=GI:6324143 /SEG=NC_001146:+289498,291876 /DEF=Ubiquitin-specific protease that deubiquitinates ubiquitin-protein moeties; may regulate silencing by acting on Sir4p; involved in posttranscriptionally regulating Gap1p and possibly other transporters; primarily located i	Saccharomyces cerevisiae
1770963_at	0.04	0.00147677	1.8	down	TRM5	S. cerevisiae YHR070W /GEN=TRM5 /DB_XREF=GI:6321861 /SEG=NC_001140:+234882,236381 /DEF=tRNA modification enzyme /NOTE=Trm5p; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 14562095]; go_component: nucleus [goid GO:0005634] [evidence IDA] [pmid 14562095]; go_function: tRNA	Saccharomyces cerevisiae
1772892_at	0.05	0.002590552	1.8	down	NCL1	S. cerevisiae YBL024W /GEN=NCL1 /DB_XREF=GI:6319447 /SEG=NC_001134:+172499,174553 /DEF=Nuclear protein 1, similar to NOP2 and human proliferation associated nucleolar protein p120 /NOTE=Ncl1p; go_component: nucleus [goid GO:0005634] [evidence IDA] [pmid 9767141]; go_function: tRNA (cytosine-5-)-me	Saccharomyces cerevisiae
1774721_at	0.04	0.002073079	1.8	down	ENP1	S. cerevisiae YBR247C /GEN=ENP1 /DB_XREF=GI:6319724 /SEG=NC_001134:-712961,714412 /DEF=Protein associated with U3 and U14 snoRNAs, required for pre-rRNA processing and 40S ribosomal subunit synthesis; localized in the nucleus and concentrated in the nucleolus /NOTE=Enp1p; go_component: nucleolus [go	Saccharomyces cerevisiae
1776003_at	0.05	0.002496757	1.8	down	SEC63	S. cerevisiae YOR254C /GEN=SEC63 /DB_XREF=GI:6324828 /SEG=NC_001147:-805031,807022 /DEF=Protein involved in protein import into ER /NOTE=Sec63p; go_component: endoplasmic reticulum membrane [goid GO:0005789] [evidence TAS] [pmid 10564637]; go_function: protein transporter activity [goid GO:00085	Saccharomyces cerevisiae
1773231_at	0.02	3.27E-04	1.8	down	HCA4	S. cerevisiae YJL033W /GEN=HCA4 /DB_XREF=GI:6322427 /SEG=NC_001142:+383753,386065 /DEF=Putative nucleolar DEAD box RNA helicase; high-copy number suppression of a U14 snoRNA processing mutant suggests an involvement in 18S rRNA synthesis /NOTE=Hca4p; go_component: nucleolus [goid GO:0005730] [	Saccharomyces cerevisiae
1778308_at	0.02	1.58E-04	1.8	down	NUP84	S. cerevisiae YDL116W /GEN=NUP84 /DB_XREF=GI:6320087 /SEG=NC_001136:+251566,253746 /DEF=Subunit of the nuclear pore complex (NPC), forms a subcomplex with Nup85p, Nup120p, Nup145p-C, Sec13p, and Seh1p that plays a role in nuclear mRNA export and NPC biogenesis /NOTE=Nup84p; go_component: nu	Saccharomyces cerevisiae
1773426_at	0.04	0.002032635	1.8	down	CLA4	S. cerevisiae YNL298W /GEN=CLA4 /DB_XREF=GI:6324031 /SEG=NC_001146:+68913,71441 /DEF=Involved in localizing cell growth with respect to the septin ring /NOTE=Cla4p; go_component: actin cap (sensu Fungi) [goid GO:0030478] [evidence IDA] [pmid 10652251]; go_function: protein serine/threonine kinase activity	Saccharomyces cerevisiae
1773719_at	0.03	9.34E-04	1.8	down	NOC2	S. cerevisiae YOR206W /GEN=NOC2 /DB_XREF=GI:6324780 /SEG=NC_001147:+727512,729644 /DEF=Protein that forms a nucleolar complex with Mak21p that binds to 90S and 66S pre-ribosomes, as well as a nuclear complex with Noc3p that binds to 66S pre-ribosomes; both complexes mediate intranuclear transport of	Saccharomyces cerevisiae
1770063_at	0.04	0.001517095	1.8	down	DIS3	S. cerevisiae YOL021C /GEN=DIS3 /DB_XREF=GI:6324552 /SEG=NC_001147:-282421,285426 /DEF=Nucleolar exosome component, involved in rRNA processing and RNA degradation, binds Gsp1p/Ran and enhances the GEF activity of Srm1p, implicated in mitotic control, homologous to the E. coli RNase R of the RNase II f	Saccharomyces cerevisiae
1772352_at	0.03	4.75E-04	1.8	down	GCN3	S. cerevisiae YKR026C /GEN=GCN3 /DB_XREF=GI:6322878 /SEG=NC_001143:-488381,489298 /DEF=Alpha subunit of the translation initiation factor eIF2B, the guanine-nucleotide exchange factor for eIF2; activity subsequently regulated by phosphorylated eIF2; first identified as a positive regulator of GCN4 expression /N	Saccharomyces cerevisiae
1775150_at	0.05	0.002576534	1.8	down	NIP7	S. cerevisiae YPL211W /GEN=NIP7 /DB_XREF=GI:6325045 /SEG=NC_001148:+153494,154039 /DEF=Nip7p is required for 60S ribosome subunit biogenesis /NOTE=Nip7p; go_component: cytosolic large ribosomal subunit (sensu Eukarya) [goid GO:0005842] [evidence TAS] [pmid 9891085]; go_component: nucleolus [goid G	Saccharomyces cerevisiae
1772847_at	0.02	2.68E-04	1.8	down	EBP2	S. cerevisiae YKL172W /GEN=EBP2 /DB_XREF=GI:6322676 /SEG=NC_001143:+125764,127047 /DEF=Essential protein required for the maturation of 25S rRNA and 60S ribosomal subunit assembly, localizes to the nucleolus /NOTE=Ebp2p; go_component: nucleolus [goid GO:0005730] [evidence IDA] [pmid 10849420]; go_f	Saccharomyces cerevisiae
1777217_at	0.04	0.001917316	1.8	down	SDO1	S. cerevisiae YLR022C /GEN=PSR2 /DB_XREF=GI:6323050 /SEG=NC_001144:-184173,184925 /DEF=Protein required for cell viability /NOTE=Ylr022cp; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 14690591]; go_component: nucleus [goid GO:0005634] [evidence IDA] [pmid 14562095]; go_function: r	Saccharomyces cerevisiae
1774223_at	0.04	0.001531282	1.8	down	HAS1	S. cerevisiae YMR290C /GEN=HAS1 /DB_XREF=GI:6323947 /SEG=NC_001145:-850073,851590 /DEF=Putative ATP-dependent RNA helicase; localizes to both the nuclear periphery and nucleolus; highly enriched in nuclear pore complex fractions /NOTE=Has1p; go_component: nuclear membrane [goid GO:0005635] [evide	Saccharomyces cerevisiae
1769863_at	0.03	0.001052993	1.7	down	RRN7	S. cerevisiae YJL025W /GEN=RRN7 /DB_XREF=GI:6322435 /SEG=NC_001142:+393883,395427 /DEF=involved in the transcription of 35S rRNA genes by RNA polymerase I /NOTE=Rrn7p; go_component: RNA polymerase I transcription factor complex [goid GO:0000120] [evidence TAS] [pmid 9932458]; go_function: RNA pol	Saccharomyces cerevisiae
1773627_at	0.04	0.00172487	1.7	down	TRM44	S. cerevisiae YPL030W /GEN=PHO85 /DB_XREF=GI:6325227 /SEG=NC_001148:+493539,495242 /DEF=Hypothetical ORF /NOTE=Ypl030wp; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 14562095]; go_function: molecular_function unknown [goid GO:0005554] [evidence ND]; go_process: biological_p	Saccharomyces cerevisiae
1780093_at	0.03	7.85E-04	1.7	down	YML082W	S. cerevisiae YML082W /GEN=TUB1 /DB_XREF=GI:6323557 /SEG=NC_001145:+101862,103811 /DEF=Hypothetical ORF /NOTE=Yml082wp; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 14562095]; go_component: nucleus [goid GO:0005634] [evidence IDA] [pmid 14562095]; go_function: carbon-sulf	Saccharomyces cerevisiae
1775962_at	0.05	0.002586662	1.7	down	NOP53	S. cerevisiae YPL146C /GEN=PXA1 /DB_XREF=GI:6325111 /SEG=NC_001148:-276161,277528 /DEF=Protein required for cell viability /NOTE=Ypl146cp; go_component: nucleolus [goid GO:0005730] [evidence IDA] [pmid 10684247]; go_component: nucleus [goid GO:0005634] [evidence IDA] [pmid 11914276]; go_function: r	Saccharomyces cerevisiae
1772805_at	0.04	0.001136424	1.7	down	UTP22	S. cerevisiae YGR090W /GEN=UTP22 /DB_XREF=GI:6321527 /SEG=NC_001139:+662360,666073 /DEF=Possible U3 snoRNP protein involved in maturation of pre-18S rRNA, based on computational analysis of large-scale protein-protein interaction data /NOTE=Utp22p; go_component: nucleolus [goid GO:0005730] [eviden	Saccharomyces cerevisiae
1778190_at	0.05	0.002406203	1.7	down	LSG1	S. cerevisiae YGL099W /GEN=LSG1 /DB_XREF=GI:6321339 /SEG=NC_001139:+314632,316554 /DEF=Killer toxin REsistant /NOTE=Lsg1p; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 12773575]; go_function: GTPase activity [goid GO:0003924] [evidence ISS] [pmid 12773575]; go_process: conjugation	Saccharomyces cerevisiae
1774049_at	0.03	5.35E-04	1.7	down	RSC2	S. cerevisiae YLR357W /GEN=RSC2 /DB_XREF=GI:6323389 /SEG=NC_001144:+841330,843999 /DEF=RSC2 is a member of RSC complex, which Remodels the Structure of Chromatin. Also essential for the 2-micron plasmid to overcome maternal inheritance bias. /NOTE=Rsc2p; go_component: nucleosome remodeling comp	Saccharomyces cerevisiae
1780031_at	0.04	0.001115681	1.7	down	DFG5	S. cerevisiae YMR238W /GEN=DFG5 /DB_XREF=GI:6323894 /SEG=NC_001145:+746352,747728 /DEF=Mannosidase, essential glycosylphosphatidylinositol (GPI)-anchored membrane protein required for cell wall biogenesis, involved in filamentous growth, homologous to Dcw1p /NOTE=Dfg5p; go_component: extrinsic to	Saccharomyces cerevisiae
1776748_at	0.04	0.00149538	1.7	down	FPR4	S. cerevisiae YLR449W /GEN=FPR4 /DB_XREF=GI:6323482 /SEG=NC_001144:+1030829,1032007 /DEF=Nuclear protein, putative peptidyl-prolyl cis-trans isomerase (PPIase) with similarity to Fpr3p; overproduction suppresses the growth defect resulting from the absence of E3 ubiquitin-protein ligase Tom1p /NOTE=Fpr4p;	Saccharomyces cerevisiae
1769434_at	0.02	1.07E-04	1.7	down	RMT2	S. cerevisiae YDR465C /GEN=RMT2 /DB_XREF=GI:6320673 /SEG=NC_001136:-1393324,1394562 /DEF=Arginine methyltransferase; ribosomal protein L12 is a substrate /NOTE=Rmt2p; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 14562095]; go_component: nucleus [goid GO:0005634] [evidence IDA	Saccharomyces cerevisiae
1771574_at	0.04	0.002047594	1.7	down	UPC2	S. cerevisiae YDR213W /GEN=UPC2 /DB_XREF=GI:6320419 /SEG=NC_001136:+889744,892485 /DEF=involved in sterol uptake /NOTE=Upc2p; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 11914276]; go_component: nucleus [goid GO:0005634] [evidence IPI] [pmid 11533229]; go_function: RNA poly	Saccharomyces cerevisiae
1777531_at	0.02	3.33E-04	1.7	down	YIL067C	S. cerevisiae YIL067C /GEN=SEC6 /DB_XREF=GI:6322122 /SEG=NC_001141:-235721,237757 /DEF=Hypothetical ORF /NOTE=Yil067cp; go_component: vacuole (sensu Fungi) [goid GO:0000324] [evidence IDA] [pmid 14562095]; go_function: molecular_function unknown [goid GO:0005554] [evidence ND]; go_process: biolog	Saccharomyces cerevisiae
1770556_at	0.04	0.001409366	1.7	down	ENT4	S. cerevisiae YLL038C /GEN=ENT4 /DB_XREF=GI:6322990 /SEG=NC_001144:-65774,66517 /DEF=Protein of unknown function, contains an N-terminal epsin-like domain /NOTE=Ent4p; go_component: actin cortical patch (sensu Fungi) [goid GO:0030479] [evidence IPI] [pmid 10652251]; go_function: clathrin binding [goid G	Saccharomyces cerevisiae
1778073_at	0.05	0.002551197	1.7	down	TRM10	S. cerevisiae YOL093W /GEN=TRM10 /DB_XREF=GI:6324479 /SEG=NC_001147:+142814,143695 /DEF=responsible for most, if not all, m(1)G(9) modification of tRNAs. /NOTE=Trm10p; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 14562095]; go_component: nucleus [goid GO:0005634] [evidence IDA	Saccharomyces cerevisiae
1772827_at	0.03	6.19E-04	1.7	down	TRM8	S. cerevisiae YDL201W /GEN=TRM8 /DB_XREF=GI:6320000 /SEG=NC_001136:+99562,100422 /DEF=Transfer RNA methyltransferase /NOTE=Trm8p; go_component: nucleus [goid GO:0005634] [evidence IDA] [pmid 14562095]; go_function: protein binding [goid GO:0005515] [evidence IPI] [pmid 12403464]; go_function: t	Saccharomyces cerevisiae
1779402_at	0.03	9.00E-04	1.7	down	ALG5	S. cerevisiae YPL227C /GEN=ALG5 /DB_XREF=GI:6325029 /SEG=NC_001148:-120163,121167 /DEF=UDP-glucose:dolichyl-phosphate glucosyltransferase, involved in asparagine-linked glycosylation in the endoplasmic reticulum /NOTE=Alg5p; go_component: endoplasmic reticulum membrane [goid GO:0005789] [evidence	Saccharomyces cerevisiae
1770016_at	0.03	8.11E-04	1.7	down	RIA1	S. cerevisiae YNL163C /GEN=RIA1 /DB_XREF=GI:6324166 /SEG=NC_001146:-326741,330073 /DEF=RIbosome Assembly; Elongation Factor Like /NOTE=Ria1p; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 11779510]; go_function: translation elongation factor activity [goid GO:0003746] [evidence ISS]	Saccharomyces cerevisiae

1778756_at	0.03	9.89E-04	1.7	down	STU2	S. cerevisiae YLR045C /GEN=STU2 /DB_XREF=GI:6323074 /SEG=NC_001144:-235038,237704 /DEF=Control of microtubule dynamics by Stu2p is essential for spindle orientation and metaphase chromosome alignment. /NOTE=Stu2p; go_component: spindle pole body [goid GO:0005816] [evidence IDA] [pmid 9606209]; go_	Saccharomyces cerevisiae
1776027_at	0.03	6.57E-04	1.7	down	CDC60	S. cerevisiae YPL160W /GEN=CDC60 /DB_XREF=GI:6325097 /SEG=NC_001148:+246989,250261 /DEF=Cytosolic leucyl tRNA synthetase, ligates leucine to the appropriate tRNA /NOTE=Cdc60p; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 9742237]; go_function: leucine-tRNA ligase activity [goid GO:0	Saccharomyces cerevisiae
1770589_at	0.05	0.002651819	1.7	down	TMA16	S. cerevisiae YOR252W /GEN=CLP1 /DB_XREF=GI:6324826 /SEG=NC_001147:+803777,804202 /DEF=Hypothetical ORF /NOTE=Yor252wp; go_component: nucleus [goid GO:0005634] [evidence IDA] [pmid 14562095]; go_function: molecular_function unknown [goid GO:0005554] [evidence ND]; go_process: biological_proc	Saccharomyces cerevisiae
1770404_at	0.05	0.002763915	1.7	down	RRT2	S. cerevisiae YBR246W /GEN=ISW1 /DB_XREF=GI:6319723 /SEG=NC_001134:+711548,712711 /DEF=Hypothetical ORF /NOTE=Ybr246wp; go_component: cellular_component unknown [goid GO:0008372] [evidence ND]; go_function: molecular_function unknown [goid GO:0005554] [evidence ND]; go_process: biological_	Saccharomyces cerevisiae
1774990_at	0.04	0.001665022	1.7	down	SME1	S. cerevisiae YOR159C /GEN=SME1 /DB_XREF=GI:6324733 /SEG=NC_001147:-633282,633566 /DEF=Required for pre-mRNA splicing, cap modification and U1, U2, U4 and U5 snRNA stability /NOTE=Sme1p; go_component: small nuclear ribonucleoprotein complex [goid GO:0030532] [evidence IDA] [pmid 10377396]; go_fu	Saccharomyces cerevisiae
1778092_at	0.03	0.001049008	1.7	down	ELP2	S. cerevisiae YGR200C /GEN=ELP2 /DB_XREF=GI:6321639 /SEG=NC_001139:-899907,902273 /DEF=Elongator protein, part of the six-subunit RNA polymerase II Elongator histone acetyltransferase complex; target of Kluyveromyces lactis zymocin /NOTE=Elp2p; go_component: transcription elongation factor complex [goid	Saccharomyces cerevisiae
1773982_at	0.02	1.67E-04	1.7	down	SRP72	S. cerevisiae YPL210C /GEN=SRP72 /DB_XREF=GI:37362700 /SEG=NC_001148:-154289,156211 /DEF=part of the signal recognition particle (SRP) ribonucleoprotein (RNP) complex that functions in protein targeting to the endoplasmic reticulum (ER) membrane /NOTE=Srp72p; go_component: signal recognition particle [go	Saccharomyces cerevisiae
1776171_at	0.03	6.05E-04	1.7	down	ALA1	S. cerevisiae YOR335C /GEN=ALA1 /DB_XREF=GI:6324911 /SEG=NC_001147:-946228,949104 /DEF=Cytoplasmic alanyl-tRNA synthetase, required for protein synthesis; point mutation (cdc64-1 allele) causes cell cycle arrest at G1; lethality of null mutation is functionally complemented by human homolog /NOTE=Ala1p; go	Saccharomyces cerevisiae
1772793_at	0.04	0.001690331	1.7	down	HCM1	S. cerevisiae YCR065W /GEN=HCM1 /DB_XREF=GI:10383801 /SEG=NC_001135:+229305,230999 /DEF=Forkhead transcription factor involved in cell cycle specific transcription of SPC110, encoding a spindle pole body (SPB) calmodulin binding protein; dosage-dependent suppressor of calmodulin mutants with specific defe	Saccharomyces cerevisiae
1771534_at	0.04	0.001254085	1.7	down	RSA1	S. cerevisiae YPL193W /GEN=RSA1 /DB_XREF=GI:6325063 /SEG=NC_001148:+181402,182547 /DEF=RiboSome Assembly /NOTE=Rsa1p; go_component: nucleoplasm [goid GO:0005654] [evidence IDA] [pmid 10567587]; go_function: molecular_function unknown [goid GO:0005554] [evidence ND]; go_process: ribosomal la	Saccharomyces cerevisiae
1771209_at	0.04	0.001934497	1.7	down	SRP21	S. cerevisiae YKL122C /GEN=SRP21 /DB_XREF=GI:6322727 /SEG=NC_001143:-212141,212644 /DEF=part of the signal recognition particle (SRP) ribonucleoprotein (RNP) complex that functions in protein targeting to the endoplasmic reticulum (ER) membrane /NOTE=Srp21p; go_component: nucleus [goid GO:0005634] [ev	Saccharomyces cerevisiae
1772317_at	0.02	8.45E-05	1.7	down	MES1	S. cerevisiae YGR264C /GEN=MES1 /DB_XREF=GI:6321704 /SEG=NC_001139:-1019603,1021858 /DEF=Methionyl-tRNA synthetase, forms a complex with glutamyl-tRNA synthetase (Ygl245wp) and Arc1p, which increases the catalytic efficiency of both tRNA synthetases; also has a role in nuclear export of tRNAs /NOTE=Me	Saccharomyces cerevisiae
1774710_at	0.03	5.13E-04	1.7	down	YMC2	S. cerevisiae YBR104W /GEN=YMC2 /DB_XREF=GI:6319580 /SEG=NC_001134:+449624,450613 /DEF=Putative mitochondrial inner membrane transporter, member of the mitochondrial carrier (MCF) family /NOTE=Ymc2p; go_component: mitochondrial inner membrane [goid GO:0005743] [evidence ISS] [pmid 10930523];	Saccharomyces cerevisiae
1776009_at	0.03	4.37E-04	1.7	down	PRT1	S. cerevisiae YOR361C /GEN=PRT1 /DB_XREF=GI:6324937 /SEG=NC_001147:-1015357,1017648 /DEF=Subunit of the core complex of translation initiation factor 3(eIF3), essential for translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that stimulates binding of mRNA and tRNA(i)Met to ribosomes /NOTE=Prt1p; go_com	Saccharomyces cerevisiae
1775775_at	0.03	5.01E-04	1.7	down	DPH1	S. cerevisiae YIL103W /GEN=SHQ1 /DB_XREF=GI:6322088 /SEG=NC_001141:+171748,173025 /DEF=Hypothetical ORF /NOTE=Yil103wp; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 14562095]; go_function: molecular_function unknown [goid GO:0005554] [evidence ND]; go_process: biological_pro	Saccharomyces cerevisiae
1770092_at	0.02	1.94E-04	1.7	down	YDR266C	S. cerevisiae YDR266C /GEN=PEX10 /DB_XREF=GI:6320472 /SEG=NC_001136:-1000096,1002015 /DEF=Hypothetical ORF /NOTE=Ydr266cp; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 14562095]; go_function: molecular_function unknown [goid GO:0005554] [evidence ND]; go_process: biological_	Saccharomyces cerevisiae
1769871_at	0.04	0.002038372	1.7	down	ECM16	S. cerevisiae YMR128W /GEN=ECM16 /DB_XREF=GI:6323776 /SEG=NC_001145:+523695,527498 /DEF=Essential DEAH-box ATP-dependent RNA helicase specific to the U3 snoRNP, predominantly nucleolar in distribution, required for 18S rRNA synthesis /NOTE=Ecm16p; go_component: nucleolus [goid GO:0005730] [evid	Saccharomyces cerevisiae
1771490_at	0.03	8.03E-04	1.6	down	NSA2	S. cerevisiae YER126C /GEN=NSA2 /DB_XREF=GI:6320973 /SEG=NC_001137:-413390,414175 /DEF=Constituent of 66S pre-ribosomal particles, involved in 60S ribosomal subunit biogenesis /NOTE=Nsa2p; go_component: nucleus [goid GO:0005634] [evidence IDA] [pmid 10684247]; go_function: molecular_function unkno	Saccharomyces cerevisiae
1779493_at	0.05	0.00265802	1.6	down	REV1	S. cerevisiae YOR346W /GEN=REV1 /DB_XREF=GI:6324921 /SEG=NC_001147:+981823,984780 /DEF=Protein required for mutagenesis by physical and chemical agents /NOTE=Rev1p; go_component: nucleus [goid GO:0005634] [evidence IC] [pmid 11850424]; go_function: DNA-directed DNA polymerase activity [goid GO:	Saccharomyces cerevisiae
1772347_at	0.05	0.00213238	1.6	down	CCC2	S. cerevisiae YDR270W /GEN=CCC2 /DB_XREF=GI:6320475 /SEG=NC_001136:+1005667,1008681 /DEF=copper-transporting P-type ATPase with similarity to human Menkes and Wilsons genes /NOTE=Ccc2p; go_component: Golgi trans face [goid GO:0005802] [evidence IDA] [pmid 9325307]; go_function: copper-exporting	Saccharomyces cerevisiae
1776357_at	0.02	6.44E-05	1.6	down	SRP68	S. cerevisiae YPL243W /GEN=SRP68 /DB_XREF=GI:6325013 /SEG=NC_001148:+88517,90316 /DEF=part of the signal recognition particle (SRP) ribonucleoprotein (RNP) complex that functions in protein targeting to the endoplasmic reticulum (ER) membrane /NOTE=Srp68p; go_component: signal recognition particle [goid	Saccharomyces cerevisiae
1775611_at	0.03	9.10E-04	1.6	down	NMD5	S. cerevisiae YJR132W /GEN=NMD5 /DB_XREF=GI:6322592 /SEG=NC_001142:+669437,672583 /DEF=Involved in nuclear import /NOTE=Nmd5p; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 9852143]; go_component: nucleus [goid GO:0005634] [evidence IDA] [pmid 9852143]; go_function: protein	Saccharomyces cerevisiae
1775694_at	0.02	2.07E-04	1.6	down	PSE1	S. cerevisiae YMR308C /GEN=PSE1 /DB_XREF=GI:6323968 /SEG=NC_001145:-888951,892220 /DEF=Functions in nuclear transport of proteins /NOTE=Pse1p; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 9238021]; go_component: nucleus [goid GO:0005634] [evidence IDA] [pmid 9238021]; go_funct	Saccharomyces cerevisiae
1771302_at	0.02	1.66E-04	1.6	down	YOR246C	S. cerevisiae YOR246C /GEN=DGA1 /DB_XREF=GI:6324820 /SEG=NC_001147:-795801,796793 /DEF=Hypothetical ORF /NOTE=Yor246cp; go_component: lipid particle [goid GO:0005811] [evidence IDA] [pmid 14562095]; go_function: oxidoreductase activity [goid GO:0016491] [evidence ISS] [pmid 8972580]; go_process: bi	Saccharomyces cerevisiae
1778347_at	0.03	9.79E-04	1.6	down	NOP15	S. cerevisiae YNL110C /GEN=NOP15 /DB_XREF=GI:6324219 /SEG=NC_001146:-417826,418488 /DEF=Constituent of 66S pre-ribosomal particles, involved in 60S ribosomal subunit biogenesis; localizes to both nucleolus and cytoplasm /NOTE=Nop15p; go_component: nucleolus [goid GO:0005730] [evidence IDA] [pmid 115	Saccharomyces cerevisiae
1770407_at	0.05	0.002796428	1.6	down	TRM2	S. cerevisiae YKR056W /GEN=TRM2 /DB_XREF=GI:42759862 /SEG=NC_001143:+549090,551009 /DEF=tRNA methyltransferase /NOTE=Trm2p; go_component: cellular_component unknown [goid GO:0008372] [evidence ND]; go_function: tRNA methyltransferase activity [goid GO:0008175] [evidence IDA] [pmid 10864043]	Saccharomyces cerevisiae
1773771_at	0.02	2.61E-04	1.6	down	OCA5	S. cerevisiae YHL029C /GEN=ECM29 /DB_XREF=GI:6321758 /SEG=NC_001140:-45927,47966 /DEF=Hypothetical ORF /NOTE=Yhl029cp; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 14562095]; go_function: molecular_function unknown [goid GO:0005554] [evidence ND]; go_process: metabolism [goi	Saccharomyces cerevisiae
1773600_at	0.02	1.06E-04	1.6	down	SER33	S. cerevisiae YIL074C /GEN=SER33 /DB_XREF=GI:6322116 /SEG=NC_001141:-221078,222487 /DEF=3-phosphoglycerate dehydrogenase, catalyzes the first step in serine and glycine biosynthesis; isozyme of Ser3p /NOTE=Ser33p; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 14562095]; go_function:	Saccharomyces cerevisiae
1777048_at	0.04	0.002101089	1.6	down	OYE2	S. cerevisiae YHR179W /GEN=OYE2 /DB_XREF=GI:6321973 /SEG=NC_001140:+462500,463702 /DEF=Widely conserved NADPH oxidoreductase containing flavin mononucleotide (FMN), homologous to Oye3p with slight differences in ligand binding and catalytic properties; may be involved in sterol metabolism /NOTE=Oy	Saccharomyces cerevisiae
1777367_at	0.04	0.001629718	1.6	down	SLI15	S. cerevisiae YBR156C /GEN=SLI15 /DB_XREF=GI:6319632 /SEG=NC_001134:-551060,553156 /DEF=Mitotic spindle protein involved in chromosome segregation. /NOTE=Sli15p; go_component: kinetochore microtubule [goid GO:0005828] [evidence IDA] [pmid 11724818]; go_component: spindle microtubule [goid GO:000	Saccharomyces cerevisiae
1777703_at	0.04	0.001244063	1.6	down	MDJ2	S. cerevisiae YNL328C /GEN=MDJ2 /DB_XREF=GI:6324001 /SEG=NC_001146:-22834,23274 /DEF=Protein of the mitochondrial inner membrane with similarity to E. coli DnaJ and other DnaJ-like proteins, function partially overlaps that of Mdj1p /NOTE=Mdj2p; go_component: mitochondrial inner membrane [goid GO:000	Saccharomyces cerevisiae
1775023_at	0.03	6.80E-04	1.6	down	YJR003C	S. cerevisiae YJR003C /GEN=MPP10 /DB_XREF=GI:6322462 /SEG=NC_001142:-440908,442527 /DEF=Hypothetical ORF /NOTE=Yjr003cp; go_component: mitochondrion [goid GO:0005739] [evidence IDA] [pmid 14562095]; go_function: molecular_function unknown [goid GO:0005554] [evidence ND]; go_process: biological	Saccharomyces cerevisiae
1772810_at	0.03	8.11E-04	1.6	down	PXL1	S. cerevisiae YKR090W /GEN=PXL1 /DB_XREF=GI:6322943 /SEG=NC_001143:+608587,610707 /DEF=LIM domain-containing protein that localizes to sites of polarized growth, required for selection and/or maintenance of polarized growth sites, may modulate signaling by the GTPases Cdc42p and Rho1p; has similarity to m	Saccharomyces cerevisiae
1778120_at	0.04	0.001340523	1.6	down	MEU1	S. cerevisiae YLR017W /GEN=MEU1 /DB_XREF=GI:6323045 /SEG=NC_001144:+177607,178620 /DEF=Protein that regulates ADH2 gene expression /NOTE=Meu1p; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 8807288]; go_function: molecular_function unknown [goid GO:0005554] [evidence ND]; g	Saccharomyces cerevisiae
1775054_at	0.04	0.002094728	1.6	down	RRP46	S. cerevisiae YGR095C /GEN=RRP46 /DB_XREF=GI:37362654 /SEG=NC_001139:-675673,676344 /DEF=Ribosomal RNA Processing /NOTE=Rrp46p; go_component: cytoplasmic exosome (RNase complex) [goid GO:0000177] [evidence IDA] [pmid 10465791]; go_component: nuclear exosome (RNase complex) [goid GO:00001	Saccharomyces cerevisiae
1775233_at	0.05	0.002178735	1.6	down	DIM1	S. cerevisiae YPL266W /GEN=DIM1 /DB_XREF=GI:6324989 /SEG=NC_001148:+39121,40077 /DEF=Essential 18S rRNA dimethylase, responsible for conserved m6(2)Am6(2)A dimethylation in 3'-terminal loop of 18 S rRNA, part of 90S and 40S pre-particles in nucleolus, involved in pre-ribosomal RNA processing /NOTE=Dim1	Saccharomyces cerevisiae
1776298_at	0.03	4.67E-04	1.6	down	YHR192W	S. cerevisiae YHR192W /GEN=CTF8 /DB_XREF=GI:6321986 /SEG=NC_001140:+486824,487660 /DEF=Hypothetical ORF /NOTE=Yhr192wp; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 14562095]; go_function: molecular_function unknown [goid GO:0005554] [evidence ND]; go_process: biological_pr	Saccharomyces cerevisiae
1779508_at	0.03	6.71E-04	1.6	down	NMA111	S. cerevisiae YNL123W /GEN=NAF1 /DB_XREF=GI:6324206 /SEG=NC_001146:+394685,397678 /DEF=shows protein sequence similarity to the mammalian Omi/HtrA2 family of serine proteases /NOTE=Ynl123wp; go_component: nucleus [goid GO:0005634] [evidence IDA] [pmid 14562095]; go_function: serine-type peptida	Saccharomyces cerevisiae
1772205_at	0.03	7.64E-04	1.6	down	BUD6	S. cerevisiae YLR319C /GEN=BUD6 /DB_XREF=GI:6323351 /SEG=NC_001144:-769318,771684 /DEF=Actin- and formin-interacting protein, involved in actin cable nucleation and polarized cell growth; isolated as bipolar budding mutant; potential Cdc28p substrate /NOTE=Bud6p; go_component: actin cap (sensu Fungi) [goi	Saccharomyces cerevisiae
1779360_at	0.04	0.001563804	1.6	down	FOL1	S. cerevisiae YNL256W /GEN=FOL1 /DB_XREF=GI:37362687 /SEG=NC_001146:+164622,167096 /DEF=Multifunctional enzyme of the folic acid biosynthesis pathway, has dihydropteroate synthetase, dihydro-6-hydroxymethylpterin pyrophosphokinase, and dihydroneopterin aldolase activities /NOTE=Fol1p; go_component	Saccharomyces cerevisiae
1779927_at	0.05	0.002179788	1.6	down	YDR049W	S. cerevisiae YDR049W /GEN=HEM12 /DB_XREF=GI:6320253 /SEG=NC_001136:+553250,555148 /DEF=Hypothetical ORF /NOTE=Ydr049wp; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 14562095]; go_function: molecular_function unknown [goid GO:0005554] [evidence ND]; go_process: biological_	Saccharomyces cerevisiae
1773602_at	0.04	0.001783116	1.6	down	DBP5	S. cerevisiae YOR046C /GEN=DBP5 /DB_XREF=GI:6324620 /SEG=NC_001147:-414459,415907 /DEF=Cytoplasmic DExD/H-box protein essential for poly(A)+ RNA export /NOTE=Dbp5p; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 9564048]; go_component: nuclear pore [goid GO:0005643] [evidence	Saccharomyces cerevisiae
1771544_at	0.04	0.001242432	1.6	down	SXM1	S. cerevisiae YDR395W /GEN=SXM1 /DB_XREF=GI:6320603 /SEG=NC_001136:+1263312,1266146 /DEF=Suppressor of mRNA export mutant; Importin-beta like gene /NOTE=Sxm1p; go_component: nucleus [goid GO:0005634] [evidence IDA] [pmid 9238021]; go_function: protein carrier activity [goid GO:0008320] [evidenc	Saccharomyces cerevisiae
1776254_at	0.05	0.002383488	1.6	down	PRP24	S. cerevisiae YMR268C /GEN=PRP24 /DB_XREF=GI:6323924 /SEG=NC_001145:-802887,804221 /DEF=Splicing factor that reanneals U4 and U6 snRNPs during spliceosome recycling /NOTE=Prp24p; go_component: spliceosome complex [goid GO:0005681] [evidence TAS] [pmid 9476892]; go_function: pre-mRNA splicing fac	Saccharomyces cerevisiae
1777921_at	0.05	0.002539371	1.6	down	YGR251W	S. cerevisiae YGR251W /GEN=MGA1 /DB_XREF=GI:6321690 /SEG=NC_001139:+995643,996233 /DEF=Protein required for cell viability /NOTE=Ygr251wp; go_component: nucleolus [goid GO:0005730] [evidence IDA] [pmid 14690591]; go_component: nucleus [goid GO:0005634] [evidence IDA] [pmid 14690591]; go_functio	Saccharomyces cerevisiae
1769606_at	0.01	2.58E-05	1.6	down	IPT1	S. cerevisiae YDR072C /GEN=IPT1 /DB_XREF=GI:6320277 /SEG=NC_001136:-589757,591340 /DEF=Inositolphosphotransferase 1, involved in synthesis of mannose-(inositol-P)2-ceramide (M(IP)2C), which is the most abundant sphingolipid in cells, mutation confers resistance to the antifungals syringomycin E and DmAMP1	Saccharomyces cerevisiae
1779200_at	0.03	7.78E-04	1.6	down	SKT5	S. cerevisiae YBL061C /GEN=SKT5 /DB_XREF=GI:6319410 /SEG=NC_001134:-105280,107370 /DEF=Activator of Chs3p (chitin synthase III), recruits Chs3p to the bud neck via interaction with Bni4p; has similarity to Shc1p, which activates Chs3p during sporulation /NOTE=Skt5p; go_component: contractile ring (sensu Saccha	Saccharomyces cerevisiae
1772749_at	0.04	0.002023505	1.6	down	YPR084W	S. cerevisiae YPR084W /GEN=MDM36 /DB_XREF=GI:6325341 /SEG=NC_001148:+706968,708338 /DEF=Hypothetical ORF /NOTE=Ypr084wp; go_component: cellular_component unknown [goid GO:0008372] [evidence ND]; go_function: molecular_function unknown [goid GO:0005554] [evidence ND]; go_process: biologic	Saccharomyces cerevisiae
1774175_at	0.05	0.002765912	1.6	down	ESF2	S. cerevisiae YNR054C /GEN=NOG2 /DB_XREF=GI:6324382 /SEG=NC_001146:-723354,724304 /DEF=Protein required for cell viability /NOTE=Ynr054cp; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 14562095]; go_component: nucleolus [goid GO:0005730] [evidence IDA] [pmid 14562095]; go_functio	Saccharomyces cerevisiae
1778627_at	0.02	1.18E-04	1.6	down	RPB3	S. cerevisiae YIL021W /GEN=RPB3 /DB_XREF=GI:6322168 /SEG=NC_001141:+312903,313859 /DEF=RNA polymerase II core subunit /NOTE=Rpb3p; go_component: DNA-directed RNA polymerase II, core complex [goid GO:0005665] [evidence TAS] [pmid 9774381]; go_function: DNA-directed RNA polymerase activity [goid	Saccharomyces cerevisiae
1772105_at	0.05	0.002419307	1.6	down	BNI5	S. cerevisiae YNL166C /GEN=BNI5 /DB_XREF=GI:6324163 /SEG=NC_001146:-322219,323565 /DEF=Protein involved in organization of septins at the mother-bud neck, may interact directly with the Cdc11p septin, localizes to bud neck in a septin-dependent manner /NOTE=Bni5p; go_component: bud neck [goid GO:00059	Saccharomyces cerevisiae
1770967_at	0.05	0.002384645	1.6	down	YIL096C	S. cerevisiae YIL096C /GEN=FYV10 /DB_XREF=GI:6322095 /SEG=NC_001141:-182114,183124 /DEF=Hypothetical ORF /NOTE=Yil096cp; go_component: nucleolus [goid GO:0005730] [evidence IDA] [pmid 14562095]; go_component: nucleus [goid GO:0005634] [evidence IDA] [pmid 14562095]; go_function: molecular_funct	Saccharomyces cerevisiae
1777399_at	0.02	1.97E-04	1.5	down	ARD1	S. cerevisiae YHR013C /GEN=ARD1 /DB_XREF=GI:6321801 /SEG=NC_001140:-130723,131439 /DEF=subunit of the major N alpha-acetyltransferase; complexes with Nat1p /NOTE=Ard1p; go_component: cytoplasm [goid GO:0005737] [evidence IC] [pmid 1600941]; go_function: peptide alpha-N-acetyltransferase activity [go	Saccharomyces cerevisiae
1775199_at	0.05	0.002148674	1.5	down	HIS7	S. cerevisiae YBR248C /GEN=HIS7 /DB_XREF=GI:6319725 /SEG=NC_001134:-714764,716422 /DEF=Imidazole glycerol phosphate synthase (glutamine amidotransferase:cyclase), catalyzes the fifth and sixth steps of histidine biosynthesis and also produces 5-aminoimidazole-4-carboxamide ribotide (AICAR), a purine precurs	Saccharomyces cerevisiae
1776097_at	0.05	0.002737233	1.5	down	PRS3	S. cerevisiae YHL011C /GEN=PRS3 /DB_XREF=GI:6321776 /SEG=NC_001140:-80649,81611 /DEF=5-phospho-ribosyl-1(alpha)-pyrophosphate synthetase, involved in nucleotide, histidine, and tryptophan biosynthesis; one of a five related enzymes, which are active as heteromultimeric complexes /NOTE=Prs3p; go_compone	Saccharomyces cerevisiae
1778381_at	0.03	4.85E-04	1.5	down	DUS4	S. cerevisiae YLR405W /GEN=DUS4 /DB_XREF=GI:6323437 /SEG=NC_001144:+929787,930890 /DEF=Dihydrouridine synthase, member of a widespread family of conserved proteins including Smm1p, Dus1p, and Dus3p /NOTE=Dus4p; go_component: cellular_component unknown [goid GO:0008372] [evidence ND]; go_fu	Saccharomyces cerevisiae
1772448_at	0.04	0.001741202	1.5	down	FLC1	S. cerevisiae YPL221W /GEN=GRE1 /DB_XREF=GI:6325035 /SEG=NC_001148:+133042,135423 /DEF=Protein of unknown function, overproduction suppresses a pam1 slv3 double null mutation /NOTE=Ypl221wp	Saccharomyces cerevisiae
1771525_at	0.03	6.93E-04	1.5	down	CBK1	S. cerevisiae YNL161W /GEN=CBK1 /DB_XREF=GI:6324168 /SEG=NC_001146:+332597,334867 /DEF=Cell wall biosynthesis kinase; required for efficient apical growth, proper mating projection morphology, bipolar bud site selection in diploid cells, and cell separation. /NOTE=Cbk1p; go_component: bud [goid GO:0005933	Saccharomyces cerevisiae
1770170_at	0.04	0.001384537	1.5	down	RAD2	S. cerevisiae YGR258C /GEN=RAD2 /DB_XREF=GI:6321697 /SEG=NC_001139:-1007676,1010771 /DEF=Single-stranded DNA endonuclease, cleaves single-stranded DNA during nucleotide excision repair to excise damaged DNA; subunit of Nucleotide Excision Repair Factor 3 (NEF3); homolog of human XPG protein /NOTE=I	Saccharomyces cerevisiae
1775172_at	0.03	7.41E-04	1.5	down	FCF2	S. cerevisiae YLR051C /GEN=RPS0B /DB_XREF=GI:6323080 /SEG=NC_001144:-246325,246978 /DEF=Protein required for cell viability /NOTE=Ylr051cp; go_component: nucleolus [goid GO:0005730] [evidence IDA] [pmid 14690591]; go_component: nucleus [goid GO:0005634] [evidence IDA] [pmid 14690591]; go_function:	Saccharomyces cerevisiae
1776603_at	0.02	3.60E-04	1.5	down	ILV1	S. cerevisiae YER086W /GEN=ILV1 /DB_XREF=GI:6320930 /SEG=NC_001137:+328473,330203 /DEF=Threonine deaminase, catalyzes the first step in isoleucine biosynthesis; expression is under general amino acid control; ILV1 locus exhibits highly positioned nucleosomes whose organization is independent of known ILV1	Saccharomyces cerevisiae
1778202_at	0.02	1.43E-04	1.5	down	RRP6	S. cerevisiae YOR001W /GEN=RRP6 /DB_XREF=GI:6324574 /SEG=NC_001147:+326832,329033 /DEF=Exonuclease component of the nuclear exosome; contributes to the quality-control system that retains and degrades aberrant mRNAs in the nucleus /NOTE=Rrp6p; go_component: nuclear exosome (RNase complex) [goi	Saccharomyces cerevisiae
1769756_at	0.02	6.92E-05	1.5	down	KAP104	S. cerevisiae YBR017C /GEN=KAP104 /DB_XREF=GI:6319491 /SEG=NC_001134:-270909,273665 /DEF=Transportin, cytosolic karyopherin beta 2 involved in delivery of heterogeneous nuclear ribonucleoproteins to the nucleoplasm, binds rg-nuclear localization signals on Nab2p and Hrp1p, plays a role in cell-cycle progressi	Saccharomyces cerevisiae
1779538_at	0.03	5.23E-04	1.5	down	NUP100	S. cerevisiae YKL068W /GEN=NUP100 /DB_XREF=GI:6322782 /SEG=NC_001143:+309844,312723 /DEF=Subunit of the nuclear pore complex (NPC) that is localized to both sides of the pore; contains a repetitive GLFG motif that interacts with mRNA export factor Mex67p and with karyopherin Kap95p; homologous to Nup1	Saccharomyces cerevisiae
1773122_at	0.03	4.66E-04	1.5	down	FPS1	S. cerevisiae YLL043W /GEN=FPS1 /DB_XREF=GI:6322985 /SEG=NC_001144:+49937,51946 /DEF=Plasma membrane glycerol channel, member of the major intrinsic protein (MIP) family of channel proteins; involved in efflux of glycerol and in uptake of the trivalent metalloids arsenite and antimonite /NOTE=Fps1p; go_co	Saccharomyces cerevisiae
1779815_at	0.04	0.001899966	1.5	down	TEL2	S. cerevisiae YGR099W /GEN=TEL2 /DB_XREF=GI:6321536 /SEG=NC_001139:+687901,689967 /DEF=Essential DNA-binding protein specific to single-stranded yeast telomeric DNA repeats, required for telomere length regulation and telomere position effect /NOTE=Tel2p; go_component: nuclear telomere cap complex [g	Saccharomyces cerevisiae
1769885_at	0.05	0.002358279	1.5	down	ELO1	S. cerevisiae YJL196C /GEN=ELO1 /DB_XREF=GI:6322265 /SEG=NC_001142:-67849,68781 /DEF=Elongase I, medium-chain acyl elongase, catalyzes carboxy-terminal elongation of unsaturated C12-C16 fatty acyl-CoAs to C16-C18 fatty acids /NOTE=Elo1p; go_component: membrane [goid GO:0016020] [evidence ISS] [pmid 8	Saccharomyces cerevisiae
1770699_at	0.04	0.001445936	1.5	down	NUP42	S. cerevisiae YDR192C /GEN=NUP42 /DB_XREF=GI:6320399 /SEG=NC_001136:-843562,844854 /DEF=Subunit of the nuclear pore complex (NPC) that localizes exclusively to the cytoplasmic side; involved in RNA export, most likely at a terminal step; interacts with Gle1p /NOTE=Nup42p; go_component: nuclear pore [goid	Saccharomyces cerevisiae
1771687_at	0.01	5.16E-05	1.5	down	ADE3	S. cerevisiae YGR204W /GEN=ADE3 /DB_XREF=GI:6321643 /SEG=NC_001139:+905937,908777 /DEF=Cytoplasmic trifunctional enzyme C1-tetrahydrofolate synthase, involved in single carbon metabolism and required for biosynthesis of purines, thymidylate, methionine, and histidine /NOTE=Ade3p; go_component: cytop	Saccharomyces cerevisiae
1773210_at	0.04	0.001708207	1.5	down	POP2	S. cerevisiae YNR052C /GEN=POP2 /DB_XREF=GI:6324380 /SEG=NC_001146:-719345,720646 /DEF=RNase of the DEDD superfamily, subunit of the Ccr4-Not complex that mediates 3' to 5' mRNA deadenylation /NOTE=Pop2p; go_component: CCR4-NOT core complex [goid GO:0030015] [evidence IPI] [pmid 10490603]; go_	Saccharomyces cerevisiae
1769961_at	0.02	2.24E-04	1.5	down	PHO13	S. cerevisiae YDL236W /GEN=PHO13 /DB_XREF=GI:6319965 /SEG=NC_001136:+32296,33234 /DEF=Alkaline phosphatase specific for p-nitrophenyl phosphate, involved in dephosphorylation of histone II-A and casein /NOTE=Pho13p; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 14562095]; go_com	Saccharomyces cerevisiae
1775295_at	0.02	3.66E-04	1.5	down	ASP1	S. cerevisiae YDR321W /GEN=ASP1 /DB_XREF=GI:6320527 /SEG=NC_001136:+1108695,1109840 /DEF=Cytosolic L-asparaginase, involved in asparagine catabolism /NOTE=Asp1p; go_component: cytosol [goid GO:0005829] [evidence TAS]; go_component: intracellular [goid GO:0005622] [evidence IDA] [pmid 8026756]; go_	Saccharomyces cerevisiae
1769710_at	0.03	7.73E-04	1.5	down	SOK1	S. cerevisiae YDR006C /GEN=SOK1 /DB_XREF=GI:6320209 /SEG=NC_001136:-458539,461244 /DEF=gene dosage suppressors of the conditional growth defect of several temperature-sensitive A kinase mutants /NOTE=Sok1p; go_component: nucleus [goid GO:0005634] [evidence IDA] [pmid 8065298]; go_function: molecu	Saccharomyces cerevisiae
1769587_at	0.03	4.16E-04	1.5	down	ERG8	S. cerevisiae YMR220W /GEN=ERG8 /DB_XREF=GI:6323876 /SEG=NC_001145:+712315,713670 /DEF=Phosphomevalonate kinase, an essential cytosolic enzyme that acts in the biosynthesis of isoprenoids and sterols, including ergosterol, from mevalonate /NOTE=Erg8p; go_component: cytosol [goid GO:0005829] [evidenc	Saccharomyces cerevisiae
1774583_at	0.05	0.002261826	1.5	down	DUG2	S. cerevisiae YBR281C /GEN=PAF1 /DB_XREF=GI:6319758 /SEG=NC_001134:-764928,767564 /DEF=Hypothetical ORF /NOTE=Ybr281cp; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 14562095]; go_component: nucleus [goid GO:0005634] [evidence IDA] [pmid 14562095]; go_function: molecular_fun	Saccharomyces cerevisiae
1776854_at	0.03	0.001072635	1.5	down	YMR124W	S. cerevisiae YMR124W /GEN=PKR1 /DB_XREF=GI:6323772 /SEG=NC_001145:+514455,517286 /DEF=Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery, cytoplasm, bud, and bud neck /NOTE=Ymr124wp; go_component: cytoplasm [goid GO:0005737] [evidence IDA]	Saccharomyces cerevisiae
1776745_at	0.03	0.001018663	1.5	down	CDC7	S. cerevisiae YDL017W /GEN=CDC7 /DB_XREF=GI:6320187 /SEG=NC_001136:+424206,425729 /DEF=DDK (Dbf4-dependent kinase) catalytic subunit required for firing origins and replication fork progression in mitosis through phosphorylation of Mcm2-7p complexes and Cdc45p; kinase activity correlates with cyclical DBF4	Saccharomyces cerevisiae
1769887_at	0.04	0.001300862	1.5	down	NSG1	S. cerevisiae YHR133C /GEN=ECM14 /DB_XREF=GI:6321925 /SEG=NC_001140:-370723,371598 /DEF=Protein of unknown function, potential homolog of mammalian Insig 1; green fluorescent protein (GFP)-fusion protein localizes to the nuclear periphery /NOTE=Yhr133cp	Saccharomyces cerevisiae
1777689_at	0.05	0.002586632	1.5	down	SLY41	S. cerevisiae YOR307C /GEN=SLY41 /DB_XREF=GI:6324883 /SEG=NC_001147:-892726,894087 /DEF=multicopy suppressor of ypt1 deletion /NOTE=Sly41p; go_component: endoplasmic reticulum [goid GO:0005783] [evidence IDA] [pmid 14562095]; go_function: molecular_function unknown [goid GO:0005554] [evidence N	Saccharomyces cerevisiae
1774768_at	0.04	0.001959482	1.5	down	TYS1	S. cerevisiae YGR185C /GEN=TYS1 /DB_XREF=GI:6321624 /SEG=NC_001139:-866339,867523 /DEF=tyrosyl-tRNA synthetase, cytoplasmic /NOTE=Tys1p; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 11359929]; go_component: nucleus [goid GO:0005634] [evidence IDA,IMP,ISS] [pmid 11359929]; go_f	Saccharomyces cerevisiae
1770129_at	0.01	2.80E-06	1.5	down	SIW14	S. cerevisiae YNL032W /GEN=SIW14 /DB_XREF=GI:6324296 /SEG=NC_001146:+574504,575349 /DEF=Synthetic interaction with Whi2 /NOTE=Siw14p; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 14562095]; go_function: protein tyrosine phosphatase activity [goid GO:0004725] [evidence ISS] [pmid	Saccharomyces cerevisiae
1776926_at	0.04	0.001328676	1.5	down	YGL176C	S. cerevisiae YGL176C /GEN=MPT5 /DB_XREF=GI:6321262 /SEG=NC_001139:-171419,173083 /DEF=Hypothetical ORF /NOTE=Ygl176cp; go_component: cellular_component unknown [goid GO:0008372] [evidence ND]; go_function: molecular_function unknown [goid GO:0005554] [evidence ND]; go_process: biological_pr	Saccharomyces cerevisiae
1778813_at	0.05	0.00214259	1.5	down	EAF5	S. cerevisiae YEL018W /GEN=EAF5 /DB_XREF=GI:6320818 /SEG=NC_001137:+121471,122310 /DEF=Esa1p-associated factor, subunit of the NuA4 acetyltransferase complex /NOTE=Eaf5p; go_component: nucleus [goid GO:0005634] [evidence IDA] [pmid 14562095]; go_function: molecular_function unknown [goid GO:000	Saccharomyces cerevisiae
1769614_at	0.01	2.11E-05	1.5	down	MID1	S. cerevisiae YNL291C /GEN=MID1 /DB_XREF=GI:6324038 /SEG=NC_001146:-84167,85813 /DEF=N-glycosylated integral plasma membrane protein /NOTE=Mid1p; go_component: plasma membrane [goid GO:0005886] [evidence IDA] [pmid 10958666]; go_function: calcium channel activity [goid GO:0005262] [evidence ID	Saccharomyces cerevisiae
1770622_at	0.05	0.002671168	1.5	down	BUD14	S. cerevisiae YAR014C /GEN=BUD14 /DB_XREF=GI:41629669 /SEG=NC_001133:-166745,168868 /DEF=Protein involved in bud-site selection; diploid mutants display a random budding pattern instead of the wild-type bipolar pattern /NOTE=Bud14p; go_component: bud neck [goid GO:0005935] [evidence IDA] [pmid 1145	Saccharomyces cerevisiae
1769823_at	0.04	0.001640983	1.5	down	BCK2	S. cerevisiae YER167W /GEN=BCK2 /DB_XREF=GI:6321015 /SEG=NC_001137:+518211,520766 /DEF=Rich in serine/threonine residues and functions in the protein kinase C mediated pathway /NOTE=Bck2p; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 14562095]; go_component: nucleus [goid GO:0	Saccharomyces cerevisiae
1769741_at	0.03	4.96E-04	1.5	down	VBA4	S. cerevisiae YDR119W /GEN=APC4 /DB_XREF=GI:6320324 /SEG=NC_001136:+688221,690527 /DEF=Hypothetical ORF /NOTE=Ydr119wp; go_component: vacuolar membrane (sensu Fungi) [goid GO:0000329] [evidence IDA] [pmid 14562095]; go_function: molecular_function unknown [goid GO:0005554] [evidence ND]; g	Saccharomyces cerevisiae
1779139_at	0.03	6.25E-04	1.5	down	ILS1	S. cerevisiae YBL076C /GEN=ILS1 /DB_XREF=GI:6319395 /SEG=NC_001134:-81041,84259 /DEF=Cytoplasmic isoleucine-tRNA synthetase, target of the G1-specific inhibitor reveromycin A /NOTE=Ils1p; go_component: cytosol [goid GO:0005829] [evidence IDA] [pmid 7619074]; go_function: isoleucine-tRNA ligase activity [g	Saccharomyces cerevisiae
1776127_at	0.05	0.002602468	1.5	down	YMR102C	S. cerevisiae YMR102C /GEN=SRT1 /DB_XREF=GI:6323749 /SEG=NC_001145:-469847,472351 /DEF=Protein of unknown function, transcription is activated by paralogous transcription factors Yrm1p and Yrr1p along with genes involved in multidrug resistance /NOTE=Ymr102cp; go_component: cellular_component unkno	Saccharomyces cerevisiae
1773102_at	0.03	5.14E-04	1.5	down	SHE2	S. cerevisiae YKL130C /GEN=SHE2 /DB_XREF=GI:6322719 /SEG=NC_001143:-195289,196029 /DEF=RNA-binding protein that binds specific mRNAs and interacts with She3p; part of the mRNA localization machinery that restricts accumulation of certain proteins to the bud /NOTE=She2p; go_component: cytoplasm [goid G	Saccharomyces cerevisiae

1771598_at	0.05	0.002449372	1.5	down	CKA2	S. cerevisiae YOR061W /GEN=CKA2 /DB_XREF=GI:6324635 /SEG=NC_001147:+441535,442554 /DEF=may have a role in regulation and/or execution of the eukaryotic cell cycle /NOTE=Cka2p; go_component: protein kinase CK2 complex [goid GO:0005956] [evidence IDA] [pmid 9427841]; go_function: protein kinase CK2 a	Saccharomyces cerevisiae
1772052_at	0.05	0.002338857	1.5	down	SFH1	S. cerevisiae YLR321C /GEN=SFH1 /DB_XREF=GI:6323354 /SEG=NC_001144:-776584,777864 /DEF=Involved in chromatin modeling, cell cycle progression /NOTE=Sfh1p; go_component: nucleosome remodeling complex [goid GO:0005679] [evidence IPI] [pmid 10025404]; go_function: protein binding [goid GO:0005515] [e	Saccharomyces cerevisiae
1779055_at	0.04	0.001689331	1.4	down	RVB1	S. cerevisiae YDR190C /GEN=RVB1 /DB_XREF=GI:6320396 /SEG=NC_001136:-840597,841988 /DEF=RUVB-like protein, TIP49a Homologue /NOTE=Rvb1p; go_component: SWR1 complex [goid GO:0000812] [evidence IPI] [pmid 14690608]; go_component: chromatin remodeling complex [goid GO:0016585] [evidence IDA] [	Saccharomyces cerevisiae
1775234_at	0.03	9.34E-04	1.4	down	BEM1	S. cerevisiae YBR200W /GEN=BEM1 /DB_XREF=GI:6319677 /SEG=NC_001134:+620829,622484 /DEF=SH3-domain protein that binds Cdc24p, Ste5p and Ste20p, and the Rsr1p/Bud2p/Bup5p GTPase /NOTE=Bem1p; go_component: bud neck [goid GO:0005935] [evidence IDA] [pmid 11927541]; go_component: bud tip [goi	Saccharomyces cerevisiae
1771836_at	0.04	0.001686233	1.4	down	LSM5	S. cerevisiae YER146W /GEN=LSM5 /DB_XREF=GI:6320994 /SEG=NC_001137:+462580,462861 /DEF=Like Sm-E protein /NOTE=Lsm5p; go_component: small nuclear ribonucleoprotein complex [goid GO:0030532] [evidence IDA] [pmid 10377396]; go_function: pre-mRNA splicing factor activity [goid GO:0008248] [evidence	Saccharomyces cerevisiae
1777604_at	0.02	3.11E-04	1.4	down	NTC20	S. cerevisiae YBR188C /GEN=NTC20 /DB_XREF=GI:6319665 /SEG=NC_001134:-603642,604064 /DEF=Member of a complex, including Prp19p, that binds to the spliceosome; required for pre-mRNA splicing /NOTE=Ntc20p; go_component: spliceosome complex [goid GO:0005681] [evidence IDA,IGI] [pmid 11018040]; go_fu	Saccharomyces cerevisiae
1779734_at	0.02	2.26E-04	1.4	down	GUA1	S. cerevisiae YMR217W /GEN=GUA1 /DB_XREF=GI:6323873 /SEG=NC_001145:+701789,703366 /DEF=GMP synthase, an enzyme that catalyzes the second step in the biosynthesis of GMP from inosine 5'-phosphate (IMP); transcription is not subject to regulation by guanine but is negatively regulated by nutrient starvation	Saccharomyces cerevisiae
1776987_at	0.05	0.002612397	1.4	down	SEC18	S. cerevisiae YBR080C /GEN=SEC18 /DB_XREF=GI:6319554 /SEG=NC_001134:-398571,400847 /DEF=cytoplasmic protein involved in protein transport between ER and Golgi; ATPase /NOTE=Sec18p; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 9624182]; go_component: extrinsic to plasma membrar	Saccharomyces cerevisiae
1777405_at	0.03	4.68E-04	1.4	down	RPF1	S. cerevisiae YHR088W /GEN=RPF1 /DB_XREF=GI:6321880 /SEG=NC_001140:+281496,282383 /DEF=Nucleolar protein involved in the assembly of the large ribosomal subunit; contains a sigma(70)-like motif, which is thought to bind RNA /NOTE=Rpf1p; go_component: nucleolus [goid GO:0005730] [evidence IDA] [pmid 1	Saccharomyces cerevisiae
1779144_at	0.04	0.001371495	1.4	down	RPS27A	S. cerevisiae YKL156W /GEN=RPS27A /DB_XREF=GI:6322693 /SEG=NC_001143:+158619,159217 /DEF=Protein component of the small (40S) ribosomal subunit; nearly identical to Rps27Bp and has similarity to rat S27 ribosomal protein /NOTE=Rps27ap; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 1	Saccharomyces cerevisiae
1770941_at	0.02	2.55E-04	1.4	down	ELM1	S. cerevisiae YKL048C /GEN=ELM1 /DB_XREF=GI:6322803 /SEG=NC_001143:-346859,348781 /DEF=Serine/threonine protein kinase that regulates cellular morphogenesis, septin behavior, and cytokinesis; required for the regulation of other kinases; forms part of the bud neck ring /NOTE=Elm1p; go_component: contracti	Saccharomyces cerevisiae
1772682_at	0.04	0.001568826	1.4	down	CDC4	S. cerevisiae YFL009W /GEN=CDC4 /DB_XREF=GI:14318513 /SEG=NC_001138:+116139,118478 /DEF=F-box protein which associates with and directs SCF complexes (ubiquitin-protein ligases) to substrates /NOTE=Cdc4p; go_component: nucleus [goid GO:0005634] [evidence IDA] [pmid 11080155]; go_component: ubiquit	Saccharomyces cerevisiae
1778840_at	0.03	0.001001532	1.4	down	SET2	S. cerevisiae YJL168C /GEN=SET2 /DB_XREF=GI:6322293 /SEG=NC_001142:-102220,104421 /DEF=Histone methyltransferase with a role in transcriptional elongation, methylates a lysine residue of histone H3; associates with the C-terminal domain of Rpo21p; histone methylation activity is regulated by phosphorylation st	Saccharomyces cerevisiae
1777121_at	0.03	0.001084561	1.4	down	RPA14	S. cerevisiae YDR156W /GEN=RPA14 /DB_XREF=GI:6320360 /SEG=NC_001136:+769519,769932 /DEF=RNA polymerase I subunit A14 /NOTE=Rpa14p; go_component: DNA-directed RNA polymerase I complex [goid GO:0005736] [evidence IDA] [pmid 7768955]; go_function: DNA-directed RNA polymerase activity [goid GO:	Saccharomyces cerevisiae
1769650_at	0.04	0.00115283	1.4	down	PKH3	S. cerevisiae YDR466W /GEN=PKH3 /DB_XREF=GI:6320674 /SEG=NC_001136:+1395109,1397805 /DEF=Protein kinase with similarity to mammalian phosphoinositide-dependent kinase 1 (PDK1) and yeast Pkh1p and Pkh2p, two redundant upsteam activators of Pkc1p; identified as a multicopy suppressor of a pkh1/pkh2 d	Saccharomyces cerevisiae
1771426_at	0.05	0.002600418	1.4	down	SFB2	S. cerevisiae YNL049C /GEN=SFB2 /DB_XREF=GI:6324279 /SEG=NC_001146:-535279,537909 /DEF=Probable component of COPII coated vesicles that binds to Sec23p; similar to and functionally redundant with Sec24p, but expressed at low levels; involved in ER to Golgi transport and in autophagy /NOTE=Sfb2p; go_comp	Saccharomyces cerevisiae
1773434_at	0.03	8.57E-04	1.4	down	SSE1	S. cerevisiae YPL106C /GEN=SSE1 /DB_XREF=GI:6325151 /SEG=NC_001148:-350189,352270 /DEF=HSP70 family member, highly homologous to Ssa1p and Sse2p /NOTE=Sse1p; go_component: cytoplasm [goid GO:0005737] [evidence IC] [pmid 10480867]; go_function: co-chaperone activity [goid GO:0003767] [evidence IN	Saccharomyces cerevisiae
1779689_at	0.02	1.18E-04	1.4	down	GIS4	S. cerevisiae YML006C /GEN=GIS4 /DB_XREF=GI:6323637 /SEG=NC_001145:-256092,258416 /DEF=GIG3 suppressor /NOTE=Gis4p; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 14562095]; go_function: molecular_function unknown [goid GO:0005554] [evidence ISS] [pmid 10628841]; go_process: int	Saccharomyces cerevisiae
1772095_at	0.05	0.002201448	1.4	down	MNI1	S. cerevisiae YIL110W /GEN=COX5B /DB_XREF=GI:6322081 /SEG=NC_001141:+156042,157175 /DEF=Putative S-adenosylmethionine-dependent methyltransferase of the seven beta-strand family /NOTE=Yil110wp; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 14562095]; go_component: nucleus [go	Saccharomyces cerevisiae
1774218_at	0.04	0.001376081	1.4	down	NUP133	S. cerevisiae YKR082W /GEN=NUP133 /DB_XREF=GI:6322935 /SEG=NC_001143:+592467,595940 /DEF=Subunit of the Nup84p subcomplex of the nuclear pore complex (NPC), localizes to both sides of the NPC, required to establish a normal nucleocytoplasmic concentration gradient of the GTPase Gsp1p /NOTE=Nup133p	Saccharomyces cerevisiae
1775166_at	0.01	2.05E-06	1.4	down	SBE2	S. cerevisiae YDR351W /GEN=SBE2 /DB_XREF=GI:6320558 /SEG=NC_001136:+1178655,1181249 /DEF=Required for bud growth /NOTE=Sbe2p; go_component: Golgi apparatus [goid GO:0005794] [evidence IDA] [pmid 10679005]; go_function: molecular_function unknown [goid GO:0005554] [evidence ND]; go_process: c	Saccharomyces cerevisiae
1769591_at	0.03	8.79E-04	1.4	down	NUP60	S. cerevisiae YAR002W /GEN=NUP60 /DB_XREF=GI:6319318 /SEG=NC_001133:+152261,153880 /DEF=Subunit of the nuclear pore complex (NPC), functions to anchor Nup2p to the NPC in a dynamic process that is controlled by the nucleoplasmic concentration of Gsp1p-GTP; potential Cdc28p substrate /NOTE=Nup60p; g	Saccharomyces cerevisiae
1773333_at	0.02	1.43E-04	1.4	down	NET1	S. cerevisiae YJL076W /GEN=NET1 /DB_XREF=GI:6322385 /SEG=NC_001142:+295161,298730 /DEF=Nucleolar protein involved in exit from mitosis /NOTE=Net1p; go_component: nucleolus [goid GO:0005730] [evidence TAS] [pmid 10690410]; go_function: ribosomal DNA (rDNA) binding [goid GO:0000182] [evidence IDA]	Saccharomyces cerevisiae
1780102_at	0.03	8.23E-04	1.4	down	YHR032W	S. cerevisiae YHR032W /GEN=RRM3 /DB_XREF=GI:6321821 /SEG=NC_001140:+173336,175081 /DEF=Hypothetical ORF /NOTE=Yhr032wp; go_component: cellular_component unknown [goid GO:0008372] [evidence ND]; go_function: molecular_function unknown [goid GO:0005554] [evidence ND]; go_process: biological_	Saccharomyces cerevisiae
1769557_at	0.02	1.98E-04	1.4	down	SKY1	S. cerevisiae YMR216C /GEN=SKY1 /DB_XREF=GI:6323872 /SEG=NC_001145:-698810,701038 /DEF=SRPK1-like Kinase in Yeast (SRPK1 is a human serine kinase that specifically phosphoryates arginine-serine rich domains found in the SR family of splicing factors.) /NOTE=Sky1p; go_component: cytoplasm [goid GO:0005737	Saccharomyces cerevisiae
1769720_at	0.05	0.002744289	1.4	down	RGD2	S. cerevisiae YFL047W /GEN=RGD2 /DB_XREF=GI:16198342 /SEG=NC_001138:+40421,42565 /DEF=specific GTPase activating protein (RhoGAP) /NOTE=Rgd2p; go_component: bud neck [goid GO:0005935] [evidence IDA] [pmid 14562095]; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 14562095]; go_	Saccharomyces cerevisiae
1773695_at	0.02	3.08E-04	1.4	down	HIS1	S. cerevisiae YER055C /GEN=HIS1 /DB_XREF=GI:6320896 /SEG=NC_001137:-264891,265784 /DEF=ATP phosphoribosyltransferase, a hexameric enzyme, catalyzes the first step in histidine biosynthesis; mutations cause histidine auxotrophy and sensitivity to Cu, Co, and Ni salts; transcription is regulated by general amino a	Saccharomyces cerevisiae
1772710_at	0.04	0.001821105	1.4	down	THP2	S. cerevisiae YHR167W /GEN=THP2 /DB_XREF=GI:6321961 /SEG=NC_001140:+439342,440127 /DEF=affects transcription elongation /NOTE=Thp2p; go_component: THO complex [goid GO:0000347] [evidence IMP,IPI] [pmid 11060033]; go_function: nucleic acid binding [goid GO:0003676] [evidence IDA] [pmid 12093753];	Saccharomyces cerevisiae
1770571_at	0.05	0.002607887	1.4	down	MVD1	S. cerevisiae YNR043W /GEN=MVD1 /DB_XREF=GI:6324371 /SEG=NC_001146:+701894,703084 /DEF=involved in the polyisoprene biosynthesis pathway /NOTE=Mvd1p; go_component: cytosol [goid GO:0005829] [evidence TAS]; go_function: diphosphomevalonate decarboxylase activity [goid GO:0004163] [evidence TAS]	Saccharomyces cerevisiae
1769570_at	0.04	0.001448342	1.4	down	MNN10	S. cerevisiae YDR245W /GEN=MNN10 /DB_XREF=GI:6320451 /SEG=NC_001136:+952792,953973 /DEF=Required for mannan synthesis and for polarized growth and bud emergence /NOTE=Mnn10p; go_component: mannosyltransferase complex [goid GO:0000136] [evidence IDA] [pmid 10037752]; go_function: alpha-1,6-	Saccharomyces cerevisiae
1776015_at	0.05	0.002293742	1.4	down	KAP123	S. cerevisiae YER110C /GEN=KAP123 /DB_XREF=GI:6320956 /SEG=NC_001137:-378758,382099 /DEF=Karyopherin beta, mediates nuclear import of ribosomal proteins prior to assembly into ribosomes and import of histones H3 and H4; localizes to the nuclear pore, nucleus, and cytoplasm; exhibits genetic interactions wi	Saccharomyces cerevisiae
1773015_at	0.03	7.50E-04	1.4	down	FLO8	S. cerevisiae YER109C /GEN=FLO8 /DB_XREF=GI:6320955 /SEG=NC_001137:-375211,377610 /DEF=Transcription factor required for flocculation, diploid filamentous growth, and haploid invasive growth; genome reference strain S288C and most laboratory strains have a mutation in this gene /NOTE=Flo8p; go_component	Saccharomyces cerevisiae
1777111_at	0.04	0.00157342	1.4	down	HRB1	S. cerevisiae YNL004W /GEN=HRB1 /DB_XREF=GI:6324324 /SEG=NC_001146:+623331,624620 /DEF=Poly(A+) RNA-binding protein, involved in the export of mRNAs from the nucleus to the cytoplasm; similar to Gbp2p and Npl3p /NOTE=Hrb1p; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 9499403]	Saccharomyces cerevisiae
1774040_at	0.04	0.001559848	1.4	down	LYP1	S. cerevisiae YNL268W /GEN=LYP1 /DB_XREF=GI:6324061 /SEG=NC_001146:+138549,140384 /DEF=lysine permease /NOTE=Lyp1p; go_component: plasma membrane [goid GO:0005886] [evidence ISS] [pmid 10654085]; go_function: basic amino acid transporter activity [goid GO:0015174] [evidence IDA] [pmid 10654085]	Saccharomyces cerevisiae
1774513_at	0.03	7.02E-04	1.4	down	MNN11	S. cerevisiae YJL183W /GEN=MNN11 /DB_XREF=GI:6322278 /SEG=NC_001142:+84066,85334 /DEF=member of a cis Golgi complex that is involved in mannan synthesis, other complex members include Mnn10p, Hoc1p, Anp1p, Mnn9p /NOTE=Mnn11p; go_component: mannosyltransferase complex [goid GO:0000136] [ev	Saccharomyces cerevisiae
1777986_at	0.02	2.18E-04	1.4	down	YMR130W	S. cerevisiae YMR130W /GEN=POM152 /DB_XREF=GI:6323778 /SEG=NC_001145:+532118,533026 /DEF=Hypothetical ORF /NOTE=Ymr130wp; go_component: cellular_component unknown [goid GO:0008372] [evidence ND]; go_function: molecular_function unknown [goid GO:0005554] [evidence ND]; go_process: biolog	Saccharomyces cerevisiae
1770419_at	0.02	6.93E-05	1.4	down	PRP22	S. cerevisiae YER013W /GEN=PRP22 /DB_XREF=GI:6320850 /SEG=NC_001137:+178840,182277 /DEF=RNA-dependent ATPase/ATP-dependent RNA helicase in the DEAH-box family, associates with the lariat intermediate before the second catalytic step of splicing /NOTE=Prp22p; go_component: spliceosome complex [goi	Saccharomyces cerevisiae
1777807_at	0.04	0.001211729	1.4	down	MAD3	S. cerevisiae YJL013C /GEN=MAD3 /DB_XREF=GI:6322447 /SEG=NC_001142:-409408,410955 /DEF=checkpoint protein required for cell cycle arrest in response to loss of microtubule function /NOTE=Mad3p; go_component: nucleus [goid GO:0005634] [evidence IDA] [pmid 10704439]; go_function: molecular_function unl	Saccharomyces cerevisiae
1771334_at	0.04	0.002053954	1.4	down	KRE11	S. cerevisiae YGR166W /GEN=KRE11 /DB_XREF=GI:6321605 /SEG=NC_001139:+830518,832200 /DEF=Involved in biosynthetic pathway for cell wall beta-glucans /NOTE=Kre11p; go_component: TRAPP [goid GO:0030008] [evidence IDA] [pmid 10727015]; go_function: molecular_function unknown [goid GO:0005554] [evid	Saccharomyces cerevisiae
1770837_at	0.04	0.001950314	1.4	down	YGR266W	S. cerevisiae YGR266W /GEN=MES1 /DB_XREF=GI:6321705 /SEG=NC_001139:+1022661,1024766 /DEF=probably contains a single transmembrane span /NOTE=Ygr266wp; go_component: plasma membrane [goid GO:0005886] [evidence IDA] [pmid 12469340]; go_function: molecular_function unknown [goid GO:0005554	Saccharomyces cerevisiae
1776876_at	0.01	3.36E-05	1.4	down	HAA1	S. cerevisiae YPR008W /GEN=HAA1 /DB_XREF=GI:6325265 /SEG=NC_001148:+573013,575097 /DEF=Transcriptional activator involved in the transcription of TPO2, HSP30 and other genes encoding membrane stress proteins; despite sequence similarity with the transcription factor Ace1p, it is not subject to metalloregula	Saccharomyces cerevisiae
1777112_at	0.04	0.001348638	1.4	down	DPL1	S. cerevisiae YDR294C /GEN=DPL1 /DB_XREF=GI:6320500 /SEG=NC_001136:-1050451,1052220 /DEF=Dihydrosphingosine phosphate lyase, regulates intracellular levels of sphingolipid long-chain base phosphates (LCBPs), degrades phosphorylated long chain bases, prefers C16 dihydrosphingosine-l-phosphate as a substra	Saccharomyces cerevisiae
1776843_at	0.02	1.19E-04	1.4	down	MCM2	S. cerevisiae YBL023C /GEN=MCM2 /DB_XREF=GI:6319448 /SEG=NC_001134:-174885,177491 /DEF=Member of complex that acts at ARS's to initiate replication /NOTE=Mcm2p; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 10704410]; go_component: cytoplasm [goid GO:0005737] [evidence TAS] [p	Saccharomyces cerevisiae
1776707_at	0.03	4.64E-04	1.4	down	MCM6	S. cerevisiae YGL201C /GEN=MCM6 /DB_XREF=GI:41629691 /SEG=NC_001139:-117856,120909 /DEF=Member of the MCM/P1 family of proteins involved in DNA replication /NOTE=Mcm6p; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 10704410]; go_component: cytoplasm [goid GO:0005737] [evid	Saccharomyces cerevisiae
1778912_at	0.05	0.00249697	1.4	down	NOP2	S. cerevisiae YNL061W /GEN=NOP2 /DB_XREF=GI:6324268 /SEG=NC_001146:+510538,512394 /DEF=Probable RNA m(5)C methyltransferase, essential for processing and maturation of 27S pre-rRNA and large ribosomal subunit biogenesis; localized to the nucleolus /NOTE=Nop2p; go_component: nucleolus [goid GO:0005	Saccharomyces cerevisiae
1776541_at	0.03	6.19E-04	1.3	down	RSC9	S. cerevisiae YML127W /GEN=RSC9 /DB_XREF=GI:6323508 /SEG=NC_001145:+17065,18810 /DEF=Remodels the Structure of Chromatin /NOTE=Rsc9p; go_component: chromatin remodeling complex [goid GO:0016585] [evidence IDA] [pmid 11931764]; go_function: chromatin binding [goid GO:0003682] [evidence IPI] [pr	Saccharomyces cerevisiae
1772201_at	0.02	1.92E-04	1.3	down	NUP1	S. cerevisiae YOR098C /GEN=NUP1 /DB_XREF=GI:6324672 /SEG=NC_001147:-507948,511178 /DEF=Nuclear pore complex (NPC) subunit, involved in protein import/export and in export of RNAs, possible karyopherin release factor that accelerates release of karyopherin-cargo complexes after transport across NPC; poten	Saccharomyces cerevisiae
1779197_at	0.03	5.43E-04	1.3	down	KRE27	S. cerevisiae YIL027C /GEN=KRE27 /DB_XREF=GI:6322162 /SEG=NC_001141:-303677,304102 /DEF=Killer toxin REsistant /NOTE=Kre27p; go_component: endoplasmic reticulum [goid GO:0005783] [evidence IDA] [pmid 14562095]; go_function: molecular_function unknown [goid GO:0005554] [evidence ND]; go_process: b	Saccharomyces cerevisiae
1769366_at	0.03	8.70E-04	1.3	down	DAS2	S. cerevisiae YDR020C /GEN=GCV1 /DB_XREF=GI:6320223 /SEG=NC_001136:-485742,486440 /DEF=Hypothetical ORF /NOTE=Ydr020cp; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 14562095]; go_component: nucleus [goid GO:0005634] [evidence IDA] [pmid 14562095]; go_function: molecular_fun	Saccharomyces cerevisiae
1773179_at	0.03	8.20E-04	1.3	down	PRP6	S. cerevisiae YBR055C /GEN=PRP6 /DB_XREF=GI:6319529 /SEG=NC_001134:-344562,347261 /DEF=Splicing factor, component of the U4/U6-U5 snRNP complex /NOTE=Prp6p; go_component: U4/U6 x U5 tri-snRNP complex [goid GO:0046540] [evidence TAS] [pmid 10377396]; go_function: pre-mRNA splicing factor activity	Saccharomyces cerevisiae
1776781_at	0.05	0.002469445	1.3	down	DAD1	S. cerevisiae YDR016C /GEN=DAD1 /DB_XREF=GI:6320219 /SEG=NC_001136:-478470,478754 /DEF=Essential protein, component of the DASH complex, involved in spindle integrity and kinetochore function; interacts with Duo1p and Dam1p; localizes to intranuclear spindles and kintechore /NOTE=Dad1p; go_component	Saccharomyces cerevisiae
1771429_at	0.04	0.001927649	1.3	down	SEC13	S. cerevisiae YLR208W /GEN=SEC13 /DB_XREF=GI:6323237 /SEG=NC_001144:+559553,560446 /DEF=cytoplasmic protein involved in release of transport vesicles from the ER /NOTE=Sec13p; go_component: COPII vesicle coat [goid GO:0030127] [evidence TAS] [pmid 11252894]; go_component: cytoplasm [goid GO:00057	Saccharomyces cerevisiae
1778723_at	0.04	0.001730759	1.3	down	LAS17	S. cerevisiae YOR181W /GEN=LAS17 /DB_XREF=GI:6324755 /SEG=NC_001147:+675939,677840 /DEF=Homolog of human WASP, proline-rich protein /NOTE=Las17p; go_component: actin cortical patch (sensu Fungi) [goid GO:0030479] [evidence IDA] [pmid 10512884]; go_component: cytoplasm [goid GO:0005737] [evider	Saccharomyces cerevisiae
1772985_at	0.04	0.001309481	1.3	down	ERT1	S. cerevisiae YBR239C /GEN=PRP5 /DB_XREF=GI:6319716 /SEG=NC_001134:-698311,699900 /DEF=Hypothetical ORF /NOTE=Ybr239cp; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 14562095]; go_component: nucleus [goid GO:0005634] [evidence IDA] [pmid 14562095]; go_function: molecular_fun	Saccharomyces cerevisiae
1771766_at	0.03	4.21E-04	1.3	down	MAP1	S. cerevisiae YLR244C /GEN=MAP1 /DB_XREF=GI:6323273 /SEG=NC_001144:-625170,626333 /DEF=methionine aminopeptidase /NOTE=Map1p; go_component: cytosolic ribosome (sensu Eukarya) [goid GO:0005830] [evidence IDA] [pmid 11968008]; go_function: methionyl aminopeptidase activity [goid GO:0004239] [evi	Saccharomyces cerevisiae
1770862_at	0.05	0.002227322	1.3	down	HRR25	S. cerevisiae YPL204W /GEN=HRR25 /DB_XREF=GI:6325052 /SEG=NC_001148:+164275,165759 /DEF=Similar to YCK1 and YCK2, two other casein kinase I isoforms; found primarily in nucleus; may be involved in DNA-damage repair /NOTE=Hrr25p; go_component: nucleus [goid GO:0005634] [evidence TAS] [pmid 1409656	Saccharomyces cerevisiae
1775889_at	0.01	7.95E-06	1.3	down	SNF5	S. cerevisiae YBR289W /GEN=SNF5 /DB_XREF=GI:6319766 /SEG=NC_001134:+779625,782342 /DEF=Involved in global regulation of transcription /NOTE=Snf5p; go_component: SWI/SNF complex [goid GO:0016514] [evidence TAS] [pmid 9726966]; go_component: nucleosome remodeling complex [goid GO:0005679] [evid	Saccharomyces cerevisiae
1776858_at	0.05	0.002199316	1.3	down	UFO1	S. cerevisiae YML088W /GEN=UFO1 /DB_XREF=GI:6323551 /SEG=NC_001145:+92235,94241 /DEF=F-box receptor protein, subunit of the Skp1-Cdc53-F-box receptor (SCF) E3 ubiquitin ligase complex; binds to phosphorylated Ho endonuclease, allowing its ubiquitylation by SCF and subsequent degradation /NOTE=Ufo1p;	Saccharomyces cerevisiae
1771042_at	0.04	0.001893926	1.3	down	UNG1	S. cerevisiae YML021C /GEN=UNG1 /DB_XREF=GI:6323620 /SEG=NC_001145:-229734,230813 /DEF=uracil DNA glycosylase /NOTE=Ung1p; go_component: mitochondrion [goid GO:0005739] [evidence IDA] [pmid 11812822]; go_component: nucleus [goid GO:0005634] [evidence IDA] [pmid 11812822]; go_function: uracil D	Saccharomyces cerevisiae
1774200_at	0.03	9.78E-04	1.3	down	GIP3	S. cerevisiae YPL137C /GEN=SPP1 /DB_XREF=GI:6325121 /SEG=NC_001148:-292816,296646 /DEF=Hypothetical ORF /NOTE=Ypl137cp; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 14562095]; go_component: endoplasmic reticulum [goid GO:0005783] [evidence IDA] [pmid 14562095]; go_function:	Saccharomyces cerevisiae
1777629_at	0.04	0.001352314	1.3	down	LEU3	S. cerevisiae YLR451W /GEN=LEU3 /DB_XREF=GI:6323484 /SEG=NC_001144:+1036089,1038749 /DEF=Regulates genes involved in branched chain amino acid biosynthesis and in ammonia assimilation. Positively regulated by alpha-isopropylmalate, an intermediate in leucine biosynthesis. /NOTE=Leu3p; go_component: n	Saccharomyces cerevisiae
1771523_at	0.02	2.20E-04	1.3	down	YDL160C	S. cerevisiae YDL160C-A /GEN=ENT1 /DB_XREF=GI:33438778 /SEG=NC_001136:-169367,169609 /DEF=Identified by homology to Ashbya gossypii /NOTE=Ydl160c-ap; go_component: cellular_component unknown [goid GO:0008372] [evidence ND]; go_function: molecular_function unknown [goid GO:0005554] [evidence N	Saccharomyces cerevisiae
1773276_at	0.02	2.08E-04	1.3	down	TAF5	S. cerevisiae YBR198C /GEN=TAF5 /DB_XREF=GI:6319675 /SEG=NC_001134:-616084,618480 /DEF=Subunit (90 kDa) of TFIID and SAGA complexes, involved in RNA polymerase II transcription initiation and in chromatin modification /NOTE=Taf5p; go_component: SAGA complex [goid GO:0000124] [evidence IDA] [pmid 96	Saccharomyces cerevisiae
1772166_at	0.02	3.07E-04	1.3	down	PEP7	S. cerevisiae YDR323C /GEN=PEP7 /DB_XREF=GI:6320530 /SEG=NC_001136:-1112473,1114020 /DEF=vacuolar segregation protein required for vacuole inheritance and vacuole protein sorting /NOTE=Pep7p; go_component: cytoplasm [goid GO:0005737] [evidence IDA] [pmid 9168472]; go_component: external side of en	Saccharomyces cerevisiae