Global Metabolic Regulation via Mig1 as a Transcriptional Regulator in Thermotolerant Yeast *Kluyveromyces marxianus* DMKU3-1042

PhD Thesis

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CONTENTS

CONTENTS
(Continued)

CONTENTS
(Continued)

LIST OF TABLES

Tables **Pages**

CHAPTER 2

CHAPTER 3

APPENDIX

LIST OF FIGURES

Figures **Pages**

CHAPTER 2

CHAPTER 3

LIST OF FIGURES
(Continued)

APPENDIX

CHAPTER 1

General Introduction

Alternative sources of energy for fuels have become necessary due to the increasing worlwide human population, global warming and increasing petroleum prices. Unlike fossil fuels, bioethanol is classified as a renewable and environmentally friendly fuel since it is derived from organic matter and thus has little emission of carbon dioxide. Bioethanol is produced worldwide. The production of bioethanol is performed by microorganisms through fermentation processes, mostly from carbohydrates such as sugarcane juice, molasses and starch hydrolysates. According to Naik *et al*. (2010), bioethanol can be produced from sugar-rich biomass or starch-rich biomass. The former generally refers to grass crops such as sugar cane and root crops such as sugar beet, and the latter mainly consists of cereal grains or crops such as maize, wheat, barley, rye and rice and tuber crops such as cassava, sweet potato and potato. Lignocellulosic biomass can also be used as an alternative feedstock for bioethanol production. This biomass mainly refers to non-food biomass containing cellulose, hemicellulose and lignin, which are major components of the plant cell wall (Horn *et al*. 2012).

Some microorganisms including *Saccharomyces cerevisiae* and *Zymomonas mobilis* are able to produce ethanol as a primary metabolite, which provides NAD^+ to the glycolysis pathway under the condition that the ratio of NADH/ NAD^+ increases. *Kluyveromyces marxianus* and *S. cerevisiae*, which are closely related species of budding yeast, have many advantageous potentials for application to the production of food biomass, hydrolytic enzymes and ethanol. Both species exhibit rapid growth rates and their generation times are therefore relatively short. Both species are generally recognized as being safe (GRAS). *K. marxianus* and *Kluyveromyces lactis* can utilize lactose as a carbon source, but this capability is absent in *S. cerevisiae*. *K. marxianus* produces several useful enzymes including inulinase, β-galactosidase, β-glucosidase, and polygalacturonase (Fonseca *et al*. 2008; Kango and Jain, 2011; Lertwattanasakul *et al*. 2011; Zhou *et al*. 2013; Zhou *et al*. 2014). Unlike *S. cerevisiae*, which has less ability to utilize pentose sugars, *K. marxianus* has attractive characteristics including the ability to utilize various sugars including not only hexose sugars but also pentose sugars such as xylose and arabinose (Rodrussamee *et al.* 2011; Lertwattanasakul *et al.* 2013). *K. marxianus* DMKU3-1042, which was isolated in Thailand, can be classified as a thermotolerant and ethanologenic yeast due to its growth ability at high temperatures up to 45 °C at which it can produce ethanol from various carbon sources (Limtong *et al.* 2007; Nonklang *et al.* 2008; Rodrussamee *et al.* 2011). These excellent characteristics of the yeast have the potential for application in the ethanol industry, especially in tropical countries.

In most organisms, the utilization of other sugars is delayed in the presence of glucose, a phenomenon that is known as glucose repression. Similarly, yeast cells down-regulate the metabolism of alternative sugars when glucose coexists. According to Ahuatzi *et al.* (2004), a high glucose concentration is a signal for repression of the Glc7/Reg1 protein phosphatase in *S. cerevisiae*. This enzyme interacts with phosphorylated Mig1 (repressor) to remove the phosphate group in order to make Mig1 an active repressor, and the active Mig1 moves from the cytoplasm to nucleus. Moreover, in the presence of a high glucose concentration, Hxk2 (hexokinase) also moves to the nucleus and make a complex with Mig1, Cyc8 and Tup1 (the latter two being co-repressors), and the complex binds to histone and RNA-PII for repressing Mig1 target genes including *GAL83*, *SUC2, MAL62, LAC4,* and *LAC12* (Gancedo and Gancedo, 1986; Nehlin and Ronne, 1990; Sun *et al.* 2012; Lin *et al.* 2014; Zou *et al.* 2015). On the other hand, for the nuclear export of Mig1, phosphorylation of its serine 311 by Snf1 kinase is required. Hxk2 prevents the phosphorylation of Mig1 by interacting both with Mig1 and Snf1, resulting in the maintenance of repressive conditions for several glucose-regulated genes (Ahuatzi *et al.* 2007).

On the other hand, in the presence of a low concentration of glucose or absence of glucose, Hxk2 and Mig1 remain in the cytoplasm, where neither Mig1 nor Hxk2 can repress Mig1-regulated genes (Ahuatzi *et al.* 2004). According to Ahuatzi *et al.* (2007), during a period in which there is a low concentration of glucose, Hxk2 does not interact with Mig1 but still interacts with Snf1. Inhibition of the interaction between Hxk2 and Mig1 facilitates the phosphorylation of Mig1 at serine 311 by Snf1. Snf1 itself is regulated by phosphorylation by Sak1, and phosphorylated Snf1 forms a complex with Snf4 and Gal8 to become an active state. The Snf1 complex inhibits the formation of a Mig1-Hxk2-Cyc8-Tup1 complex, in which Mig1 is phosphorylated or in an inactive state and is absent in the nucleus, resulting in derepression of Mig1-regulated genes.

Molecular level analysis of regulators involved in glucose repression in *S. cerevisiae* has been extensively performed. However, the corresponding regulators in *K. marxianus* have not been investigated in detail. Mig1 and Rag5 of *K. marxianus* are orthologues of Mig1 and Hxk2 of *S. cerevisiae*, respectively. Only a few studies have been performed to elucidate the functions of Mig1 and Rag5 in *K. lactis* (Cassart *et al*. 1995; Prior *et al*. 1993) and *K. marxianus* (Zhou *et al*. 2013; Zhou *et al*. 2014; Zhang *et al*. 2017). The present study focused on the molecular functions of Mig1 and Rag5, especially as expressional regulators, in the thermotolerant yeast *K. marxianus* DMKU3-1042.

There were two main objectives of this study. The first objective was analysis of Mig1 and Rag5 as expressional regulators in *K. marxianus* DMKU3-1042. *kan*MX4-inserted mutants of *Kmmig1* and *Kmrag5* were constructed by site-specific homologous recombination, and their phenotypes and metabolic profiles were compared with those of corresponding mutant strains in *S. cerevisiae* under conditions with different types of sugars. Enzyme assays of gluco-hexokinase, hexokinase and inulinase activities and gene expression levels of *INU1* for inulinase, *GLK1* for glucokinase and *RAG1* for a low affinity glucose transporter were also examined. Notably, when the growth abilities of mutants were examined in low-glucose and high-glucose minimum media, a histidine-auxotrophic phenotype of *Kmmig1* was found. The second objective was thus analysis of Mig1 as a positive regulator for the histidine biosynthetic pathway and as a global regulator in *K. marxianus.* Genome-wide expression analysis that was carried out to search for candidate genes for the histidine-auxotrophic phenotype of *Kmmig1* led to the discovery of global regulation by Mig1. The genome-wide expression analysis was performed by RNA-Seq with RNAs from *Kmmig1* and its parent, and their profiles were compared. Differentially expressed genes (DEGs) were further subjected to Gene Ontology (GO) enrichment analysis and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway mapping.

CHAPTER 2

Functional analysis of Mig1 and Rag5 as expressional regulators in thermotolerant yeast *Kluyveromyces marxianus*

2.1 Abstract

To analyze the glucose repression mechanism in the thermotolerant yeast *Kluyveromyces marxianus*, disrupted mutants of genes for Mig1 and Rag5 as orthologs of Mig1 and Hxk2, respectively, in *Saccharomyces cerevisiae* were constructed, and their characteristics were compared with those of the corresponding mutants of *S. cerevisiae*. *MIG1* mutants of both yeasts exhibited more resistance than the corresponding parental strains to 2-deoxyglucose (2-DOG). Histidine was found to be essential for the growth of *Kmmig1*, but not that of *Kmrag5*, suggesting that *MIG1* is required for histidine biosynthesis in *K. marxianus*. Moreover, *Kmrag5* and *Schxk2* were more resistant than the corresponding *MIG1* mutant to 2-DOG, and only the latter increased the utilization speed of sucrose in the presence of glucose. *Kmrag5* exhibited very low activities for gluco-hexokinase and hexokinase and, unlike *Schxk2,* showed very slow growth and a low level of ethanol production in a glucose medium. Furthermore, *Kmrag5*, but not *Kmmig1*, exhibited high inulinase activity in a glucose medium and exhibited greatly delayed utilization of accumulated fructose in the medium containing both glucose and sucrose. Transcription analysis revealed that the expression levels of *INU1* for inulinase and *GLK1* for glucokinase in *Kmrag5* were higher than those in the parental strain; the expression level of *INU1* in *Kmmig1* was higher, but the expression levels of *RAG1* for a low-affinity glucose transporter in *Kmmig1* and *Kmrag5* were lower. These findings suggest that except for regulation of histidine biosynthesis, Mig1 and Rag5 of *K. marxianus* play similar roles in the regulation of gene expression and share some functions with Mig1 and Hxk2, respectively, in *S. cerevisiae*.

2.2 Introduction

Kluyveromyces marxianus is a budding yeast that has a prominent potential for production of bioethanol, hydrolytic enzymes, food biomass and food additives (Limtong *et al.* 2007; Fonseca *et al.* 2008; Gethins *et al.* 2014). This yeast can also produce volatile compounds and flavor metabolites (Gethins *et al.* 2014), enzymes such as β-galactosidase (Fonseca *et al.* 2008; Zhou *et al.* 2013), β-glucosidase and polygalacturonase (Fonseca *et al.* 2008), and inulinase (Fonseca *et al.* 2008; Kango and Jain 2011; Lertwattanasakul *et al.* 2011; Zhou *et al.* 2014) in addition to ethanol from various primary biomasses (Limtong *et al.* 2007; Fonseca *et al.* 2008; Goshima *et al.* 2013) including cellulosic biomass (Matsuzaki *et al.* 2012; Goshima *et al.* 2013). *K. marxianus* DMKU3-1042 which was isolated in Thailand, is one of the most thermotolerant yeast strains that can efficiently produce ethanol at a high temperature (Limtong *et al.* 2007) and can utilize various sugars such as glucose, galactose, sucrose, arabinose and xylose (Rodrussamee *et al.* 2011; Lertwattanasakul *et al.* 2013; Lertwattanasakul *et al.* 2015). However, like other microbes, *K. marxianus* has an intrinsic system of glucose repression, which prevents utilization of other sugars.

Unlike *S. cerevisiae,* which exhibits a strong glucose repression on sucrose utilization, *K. marxianus* DMKU3-1042 utilizes sucrose resistantly to glucose repression (Lertwattanasakul *et al.* 2011). In *S. cerevisiae,* Mig1 and Hxk2 play key roles as a regulator complex in glucose repression (Ahuatzi *et al.* 2004), and Mig1 represses the expression of several genes, including *GAL83*, *SUC2, MAL62, LAC4* and *LAC12,* when glucose is present (Gancedo and Gancedo 1986; Nehlin and Ronne 1990; Sun *et al.* 2012; Lin *et al.* 2014; Zou *et al.* 2015). *K. marxianus* with *MIG1* mutation exhibited increased inulinase production (Zhou *et al.* 2014) and increased lactose hydrolysis (Zhou *et al.* 2013). The hexokinase protein Hxk2 in *S. cerevisiae,* which is an ortholog of Rag5 in *K. lactis* (Prior *et al.* 1993) and *K. marxianus,* is a hexokinase in the glycolytic pathway and also a transcriptional regulator as a complex with Mig1 and other proteins (Ahuatzi *et al.* 2004; Ahuatzi *et al.* 2007). Hxk2 is thus a bi-functional protein that is localized in both the cytoplasm and the nucleus (Pelaez *et al.* 2010; Bergdahl *et al.* 2013). Recently, Zhang *et al.* (2017) reported that *HXK1*-disrupted mutant in *K. marxianus* exhibited enhancements of inulin hydrolysis and fructose production.

The intracellular location of Hxk2 in *S. cerevisiae* is changed by the concentration of glucose available. In the presence of a high concentration of glucose, Hxk2 in the cytoplasm moves to the nucleus and forms a complex with dephosphorylated Mig1 and a general co-repressor complex of Cyc8-Tup1 (Ahuatzi *et al.* 2004). This complex then binds to the upstream regions of promoters of glucose-repressible genes including respiratory and gluconeogenic genes. However, in the presence of a low concentration or absence of glucose, Hxk2 and Mig1 remain in the cytoplasm, where neither Mig1 nor Hxk2 can repress Mig1-regulated genes (Ahuatzi *et al.* 2004).

Functional analysis of regulators involved in glucose repression in *S. cerevisiae* have been extensively performed, but the corresponding regulators of *K. marxianus* has not been investigated well. In particular, no comparison between *MIG1* null mutant and *RAG5* null mutant has been reported. In this study, to elucidate the roles of *MIG1* and *RAG5* in glucose repression in *K. marxianus*, we constructed disrupted mutants of both genes and compared their effects on growth or sugar metabolism with those of disrupted mutants of the corresponding genes, *MIG1* and *HXK2*, respectively, in *S. cerevisiae.* The first extensive study on the two regulators in *K. marxianus* suggests that the negative regulation by Mig1 and Rag5 is shared with that by Mig1 and Hxk2 in *S. cerevisiae.* Positive regulation by Mig1 and Rag5 were discovered, the corresponding one of which has not been reported in *S. cerevisiae.* Our results also suggest that Mig1 is essential, probably as a positive regulator, for the His biosynthesis pathway in *K. marxianus*.

2.3 Materials and methods

2.3.1 Materials

Oligonucleotide primers were synthesized by Greiner Bio-One (Japan). DNA purification kits (PCR purification kit and gel extraction kit) were purchased from QIAgen (Japan). A DNA sequencing kit was purchased from Beckman Coulter (Germany). *Eco*RV and *Xho*I restriction enzymes were purchased from Biolabs (Japan) and Takara (Japan), respectively. *Ex Taq* and primeSTAR DNA polymerases were purchased from Takara (Japan). A One-step RNA PCR kit (AMV) and a DNase treatment kit were purchased from Takara (Japan). Zymolyase, 2-deoxy-glucose and yeast extract were purchased from Nacalai

Tesque (Japan). Peptone was purchased from Kyokuto (Japan). Glucose 6-phosphate dehydrogenase, ATP and β-NADP$^+$ were purchased from Oriental Yeast (Japan). G418 (geneticin) sulfate was purchased from Calbiochem (Japan). Yeast marker carrier DNA was purchased from Clontech (Japan). RNase A, D-glucose, D-sucrose and 3,5-dinitrosalicylic acid were purchased from SIGMA (Japan). D-xylose and D-galactose were purchased from Wako (Japan). Yeast Nitrogen Base without amino acids was purchased from DIFCO (USA). Other chemicals used in this study were of analytical grade.

2.3.2 Strains, media, and growth conditions

The yeast strains used in this study are listed in Table 1. *S cerevisiae* strains used were isogenic to BY4741 (Brachmann *et al.* 1998) and thermotolerant *K. marxianus* strains were isogenic to DMKU3-1042 (Limtong *et al.* 2007). YP contains 1% (w/v) yeast extract and 2% (w/v) peptone. To examine growth characteristics of yeast strains on agar plates, YP was supplemented with 1.5% (w/v) agar and one of the carbon sources YPD (2% (w/v) glucose), YPG (2% (w/v) galactose), YPS (2% (w/v) sucrose), and YPX (2% (w/v) xylose) with or wihout the addition of 2-DOG. To distinguish the amino acid requirement for the growth of yeast strains on a minimal medium, YNB (0.67% (w/v) yeast nitrogen base without amino acids) was supplemented with 2% (w/v) glucose and 0.01% (w/v) amino acids including histidine (Sambrook and Russell 2001).

Cells were pre-cultured in 5 ml of YPG medium at 30°C under a shaking condition at 160 rpm overnight. To observe growth characteristics of yeast strains on agar plates, cells were streaked on YP or YNB plates containing glucose and supplemented with different types of amino acids and incubated at 30°C for 48 h. To observe growth and metabolic profiles of yeast strains in liquid media, cells were transferred to 100 ml of YP medium containing a single sugar (YPD or YPX) or mixed sugars (YPDS, containing 2% (w/v) glucose and 2% (w/v) sucrose; and YPDX, containing 2% (w/v) glucose and 2% (w/v) xylose) with adjustment of the initial optical density at 660 nm (OD_{660}) to 0.1, followed by incubation at 30°C under a shaking condition at 160 rpm for 96 h. For a spotting test, after preculture in YPG medium, the initial OD_{660} was adjusted to 1 with a fresh medium. One mililiter of the adjusted preculture was subjected to low speed centrifugation, and the pellet of cells was washed with deionized water, suspended in deionized water at approximately 1x10^7 cells ml^{-1}, 10-fold sequentially diluted, and spotted onto plates of YPD and YPS with or without 0.01, 0.05 or 0.1% (w/v) 2-DOG. The plates were incubated at 30°C for 48 h.

Table 2.1 Strains and plasmid used in this study

Name	Relevant genotype	Reference
Plasmid		
pUG6	LoxP-*kan*MX-LoxP	Guldener *et al*. (1996)
pSH65	*Cre*-recombinase; *ble*	Guldener *et al*. (2002)
Yeast strains		
Kluyveromyces marxianus		
DMKU3-1042	Isolated from Thailand	Limtong *et al*. (2007)
Kmmig1	*MIG1*-*kan*MX-*MIG1*	This study
Kmrag5	*RAG5*-*kan*MX-*RAG5*	This study
Saccharomyces cerevisiae		
BY4741	*MAT*a his3Δ1 leu2Δ0 met15Δ0 ura3Δ0	Brachmann *et al*. (1998)
YGL035C	BY4741; *mig1* disruption	*MAT*a library
YGL253W	BY4741; *hxk2* disruption	*MAT*a library

2.3.3 Analytical methods

Cell density was measured turbidimetrically at 660 nm on a spectrophotometer (U-2000A, Hitachi, Japan). Cultures were subjected to low speed centrifugation at 5,000 rpm. The supernatant was kept at -20°C until use. Quantitative analysis of metabolic profiles (sugars, ethanol, glycerol and xylitol) was performed by high-performance liquid chromatography (HPLC) (Hitachi Model D-2000 Elite HPLC System Manager, Japan) as described previously (Rodrussamee *et al*. 2011; Suprayogi *et al*. 2015). A GL-C610-S gel pack column (Hitachi, Japan) was used together with a refractive index detector (Model L-2490) at 60°C with 0.5 ml min^{-1} eluent of deionized water.

2.3.4 Construction of *kan*MX4-inserted disrupted mutants of *Kmmig1* and *Kmrag5* by site-specific homologous recombination

MIG1 and *RAG5* DNA fragments were amplified by PCR using the genomic DNA of *K. marxianus* DMKU3-1042 as a template with a corresponding set of primers as shown in Table 2. Genomic DNA was prepared as described previously (Sambrook and Russell 2001). PCR amplification was performed using primeSTAR DNA polymerase. Preparation of all fragments is shown in Appendix Fig. S1. The 1.4-kb upstream and 1.2-kb downstream DNA fragments of *MIG1* were amplified with primers of MIG1-5’-F and MIG1-5’-R and primers of MIG1-3’-F and MIG1-3’-R, respectively. This design allowed to construct *MIG1* (4.2 kb) in the final construct of a *kan*MX4-inserted mutant, *Kmmig1*. The 1.2-kb upstream and 1.2-kb downstream DNA fragments of *RAG5* were amplified with primers of RAG5-5’-F and RAG5-5’-R and primers of RAG5-3’-F and RAG5-3’-R, respectively. This design allowed to construct *RAG5* (3.9 kb) in the final construct of a *kan*MX4-inserted mutant, *Kmrag5*. The 1.1-kb upstream and 1.1-kb downstream DNA fragments of *kan*MX4 were amplified with pUG6 plasmid DNA as a template and primers of KmMIG1-5’-F and KmMIG1-5’-R and primers of KmMIG1-3’-F and KmMIG1-3’-R, respectively. The two DNA fragments of *kan*MX4 have a 600 bp overlapping sequence, which was expected to facilitate homologous recombination. Without the overlapping sequence, almost no homologous recombinants were obtained. Instead, most of the recombinants were found to be non-homologous ones. These amplified DNA fragments were separated by agarose gel electrophoresis and purified by using a QIAquick PCR purification kit (QIAgen). The purified upstream DNA fragment of *MIG1* was fused with the purified upstream DNA fragment of *kan*MX4 by using the fusion PCR method (Chai-am *et al.* 2009). The fusion PCR amplification was divided into two steps. In the first step, amplification was performed without the addition of primers as follows: one cycle of 1 min denaturation at 98°C, 5 cycles of 10 s denaturation at 98°C, 5 s annealing at 50-53°C, 2 min extension at 72°C and 1 cycle of 5 min extension at 72°C. In the second step, amplification with the addition of primers was performed as follows: one cycle of 1 min denaturation at 98°C, 25 cycles of 10 s denaturation at 98°C, 5 s annealing at 53°C, 2 min extension at 72°C and 1 cycle of 5 min extension at 72°C. Similarly, fusion PCRs were performed for preparation of the downstream DNA fragment of *MIG1* and the downstream DNA fragment of *kan*MX4, the upstream DNA fragment of *RAG5* and the upstream DNA fragment of *kan*MX4, and the downstream DNA fragment of *RAG5* and the downstream DNA fragment of *kan*MX4.

The fusion PCR fragments were separated by electrophoresis on 0.7% (w/v) agarose gel and purified by using a QIAquick gel extraction kit. The purified fragments were adjusted to 100 ng, followed by transformation using the lithium acetate method (Gietz and Schiestl 2007; Abdel-Banat *et al*. 2010) with a slight modification. Transformation solutions used in this study were PEG/LiAc/Tris/EDTA with single stranded carrier DNA (ssDNA). After the transformation process with competent cells, the cells were incubated in YPD at 30°C with 160 rpm for 3 h before plating on plates. Screening of homologous recombinants was performed on YPX plates that each contained 150 μg ml^{-1} G418 with incubation at 30°C for 2-4 days. Disruption of *MIG1* and *RAG5* was confirmed by PCR followed by restriction enzyme analysis. PCR was performed as follows: one cycle of 1 min denaturation at 98°C, 25 cycles of 10 s denaturation at 98°C, 5 s annealing at 53°C, 4 min extension at 72°C and 1 cycle of 5 min extension at 72°C. The PCR products were digested at 37°C for 1 h with *Xho*I or *Eco*RV, respectively, which were able to cleave the inside of *kan*MX4. The insertion site of *kan*MX4 into *MIG1* or *RAG5* on the genome of *K. marxianus* was also confirmed by a direct sequencing method. Fourteen colonies of *MIG1* and 5 colonies of *RAG5* candidate mutants were grown on YPX plates containing G418 sulfate (150 μg ml^{-1}). To confirm positive colonies, PCR amplification and restriction enzyme digestion were carried out. Three of the 14 *MIG1* colonies (21.4%) and one of the 5 *RAG5* colonies (20%) showed expected results and they were named *Kmmig1* and *Kmrag5* mutants, respectively.

Table 2.2 Primers list for construction of *Kmmig1* and *Kmrag5* disrupted mutants, RT-PCR analysis of *ACT1, RAG1, GLK1* and *INU1* and complementation of *Kmmig1*

No	Primer Name	Nucleotide Sequences
1.	MIG1-5'-F	5'-TTCCTCATTTCTGATTGTGC-3'
2.	MIG1-5'-R	5'CGAAGCTTCAGCTGGAATGAACTTAAAGGATGGG
3.	KmMIG1-5'-F	5'-TCCTTTAAGTTCATTCCAGCTGAAGCTTCGTACGC-3'
4.	KmMIG1-5'-R	5'-CACCGAGGCAGTTCCATAGG-3'
5.	KmMIG1-3'-F	5'-CTCACGTTTCGAGGCCGCG-3'
6.	KmMIG1-3'-R	5'-TAGTGGTGGTCTATCCGCATAGGCCACTAGTGGAT-3'
7.	MIG1-3'-F	5'-CTAGTGGCCTATGCGGATAGACCACCACTAACG-3'
8.	MIG1-3'-R	5'-CTCTTGTCTCTTTCACCG-3'
9.	RAG5-5'-F	5'-CAGTTGCCAGCCGTCTGTTGC-3'
10.	RAG5-5'-R	5'-CGAGGCAAGCTAAACGGTGGTATCGTTGATCAAGGC-3'
11.	KmRAG5-5'-F	5'-ATCAACGATACCACCGTTTAGCTTGCCTCGTCCCC-3'
12.	KmRAG5-5'-R	5'- CACCGAGGCAGTTCCATAGG-3'
13.	KmRAG5-3'-F	5'-CTCACGTTTCGAGGCCGCG-3'
14.	KmRAG5-3'-R	5'-AGCAACCAAGGTACCCGCATAGGCCACTAGTGGAT-3'
15.	RAG5-3'-F	5'-CTAGTGGCCTATGCGGGTACCTTGGTTGCTTCTCT-3'
16.	RAG5-3'-R	5'-GCGTCAGAGCGCTTTGGAAG-3'
17.	RT-ACT1-5'-F	5'-ACGTTGTTCCAATCTACGCC-3'
18.	RT-ACT1-3'-R	5'-AGAAGATGGAGCCAAAGCAG-3'
19.	RT-RAG1-5'-F	5'-CCATGGCAAGACACCTTCAGC-3'
20.	RT-RAG1-3'-R	5'-CGGTCGTCGTAACTGTTTGC-3'
21.	RT-GLK1-5'-F	5'-GTGACAGACAAGCCTACTGGAC-3'
22.	RT-GLK1-3'-R	5'-GCACCCGATAACAGGCTCACT-3'
23.	RT-INU1-5'-F	5'-GTACAACCCAGCAGCCA-3'
24.	RT-INU1-3'-R	5'-GCTTGGAGTCGGAGGAG-3'
25.	C-mig1-5'-F	5'-TCCGTTTGTCTGCTGGGCCGT-3'
26.	C-mig1-3'-R	5'-CATCGACCACATCTGCCTGC-3'
27.	C-ble-5'-F	5'-CAGATGTGGTCGATGTCGATGACCTCCCATTGATA-3'
28.	C-ble-3'-R	5'-CGGTACCCGGGGATCTCCGTCGAGTGGGTGGTGAG-3'

Underline indicated additional hanging 15 nucleotides for fusion PCR

2.3.5 Preparation of cell extracts

Kmmig1 and *Kmrag5* and the parental strains were pre-cultured in 5 ml of YPG at 30°C under a shaking condition at 160 rpm for 18 h. The preculture was inoculated into a 300-ml flask containing 100 ml of YPD medium at an initial OD of 0.1. Cultivation was performed at 30°C under a shaking condition at 160 rpm for 7 h (KmWT and *Kmmig1*), for 18 h (mutant No 23), and for 66 h (*Kmrag5*). Those incubation times were sufficient for each yeast strains to consume about 50% of the glucose in the medium. Cells were harvested by centrifugation at 5,000 rpm for 10 min at 4°C. The cells were washed with 0.85% saline followed by pipetting. Then the cells were transferred to a steriled falcon tube and centrifuged at 5,000 rpm for 10 min at 4°C. The cells were re-suspended by pipetting in 10 ml of 10 mM potassium phosphate buffer (pH 7.0) containing

$MgCl_2$. The cell suspension was disrupted by a French pressure cell press (Aminico, USA) at 1,000 psi twice and centrifuged at 9,000 rpm for 10 min at 4°C to remove cell debris. The supernatant was subjected to ultracentrifugation at 44,000 rpm for 1 h at 4°C (Himac CS 100GXL, Hitachi, Japan). The interphase was used as cell extracts for measurement of gluco-hexokinase and hexokinase activities.

2.3.6 Enzyme assay

Hexokinase and gluco-hexokinase activities were determined by measuring the formation of NADPH by coupling the phosphorylation of glucose to the reduction of NADP$^+$ by glucose 6-phosphate dehydrogenase (G6PDH) (Caceres *et al.* 2003) at 340 nm and 25°C on a spectrophotometer (U-2000A, Hitachi, Japan). The assay was performed according to the procedure described previously (Suprayogi *et al.* 2015) in a 1-ml cuvette containing 0.24 M triethanolamine (pH 7.5), 5 mM $MgCl_2$, 5.3 mM ATP (pH 7.0), 4 mM D-glucose or D-fructose, 0.72 mM β-NADP$^+$ (pH 7.0), 2 U/ml G6PDH, and crude enzymes from cell extracts of *K. marxianus* strains. One unit of hexokinase or gluco-hexokinase activity was defined as the amount of enzyme that phosphorylates 1 μmol of D-glucose or D-fructose per min at pH 7.0 at room temperature. Specific activities of the enzymes were calculated per milligram of protein. Protein concentration was quantitatively determined by using the Lowry method (Lowry *et al.* 1951). Bovine serum albumin was used as a standard. Inulinase activity was performed at 50°C as described previously (Rouwenhorst *et al.* 1988; Lertwattanasakul *et al.* 2011) with a slight modification. The amount of reducing sugar released was determined by the colorimetric 3,5-dinitrosalicylic acid method (Miller 1959). Cells were grown in 100 ml of YPD at 30°C under a shaking condition at 160 rpm until the consumption of about 50% of the glucose in the medium. The cells were harvested by centrifugation at 5,000 rpm for 10 min at 4°C. The supernatant was used for measurement of inulinase activity. Cells as a pellet were used for determination of cell dry weight. One unit of inulinase activity was defined as 1 μmol of fructose per min at pH 4.5 and 50°C. Specific activity of the enzyme was calculated per milligram of cell dry weight.

2.3.7 Complementation of *mig1* in *K. marxianus*

For complementation of *mig1,* disrupted mutation of *MIG1* was performed by introducing amplified DNA fragments of the corresponding target gene (*MIG1*) and a drug-resistance gene (*ble,* which encodes a zeomycin resistance protein). The *MIG1* fragment was amplified by PCR using genomic DNA of the parental strain as a template and primers C-mig1-5’-F and C-mig1-3’-R (Table 2). The primers were designed to amplify the fragment encompassing the region from 1,783-bp upstream and 583-bp downstream of the coding region of *MIG1*. The *ble* gene was amplified by PCR from pSH65 plasmid DNA as a template with primers C-ble-5’-F and C-ble-3’-R (Guldener *et al*. 2002). The amplified fragments were purified by using a QIAquick gel extraction kit. The *MIG1* fragment was connected to *ble* fragments by the fusion PCR method. This procedure allowed construction of an *MIG1-ble* fragment (4,657 bp). The fragment was directly introduced into *Kmmig1* by the lithium acetate method (Gietz and Schiestl 2007; Abdel-Banat *et al*. 2010). Transformants were obtained on YPD plates containing zeomycin (100 μg ml^{-1}) and confirmed by PCR to check the existence of the *MIG1* gene, generating *Kmmig1-MIG1-ble*. A complementation test was carried out on YNB plates containing 2% (w/v) glucose or galactose and in the absence or presence of 0.01% (w/v) histidine.

2.3.8 RT-PCR analysis

Cells were pre-cultured in 5 ml of YPG medium at 30°C under a shaking condition at 160 rpm for 18 h. The preculture was inoculated into a 300-ml flask containing 100 ml of YPD with adjustment of the initial OD_{660} to 0.1, followed by incubation at 30°C under a shaking condition at 160 rpm for 7 h (in the case of KmWT and *Kmmig1*), for 18 h (in the case of mutant No 23), and for 66 h (in the case of *Kmrag5*). Total RNAs were then isolated by the hot phenol method (Aiba *et al*. 1981; Lertwattanasakul *et al*. 2007) followed by DNase treatment using a DNase kit (Takara, Japan). RT-PCR analysis was performed as described previously (Lertwattanasakul *et al*. 2007; Sootsuwan *et al*. 2007). Primers used for *KmINU1*, *KmGLK1*, *KmRAG1* and *KmACT1* are shown in Table 2. Relative band intensities were quantitatively determined using scanned images and IMAGE-J software.

Under applied conditions, RT-PCR was able to detect mRNA specifically because no band was observed when the reverse transcriptase enzyme was absent.

2.3.9 Statistical analysis

All the data obtained by enzyme assay and transcriptomic analysis were used to conduct an *F*-test together with Turkey's honestly significant difference (HSD) test. All statistical analyses were performed using SPSS statistics software version 19.0 (IBM, New York, USA).

2.4. Results

2.4.1 Growth comparison of *K. marxianus* and *S. cerevisiae* mutants and their parental strains on YP plates containing sucrose and 2-DOG

Mig1 and Rag5 in *K. marxianus* are orthologs of Mig1 and Hxk2, respectively, involved in glucose repression in *S. cerevisiae* (Nehlin and Ronne 1990; Ahuatzi *et al*. 2004; Bergdahl *et al*. 2013). To examine the effect of 2-DOG as a glucose analog on sucrose utilization, *Kmmig1*, *Kmrag5*, *Scmig1*, *Schxk2* and their parents (KmWT and ScWT) were grown at 30°C on YP agar plates containing sucrose and 2-DOG at different concentrations (Fig. 2.1). *S. cerevisiae* strains grew slowly on tested plates. When grown on YPD and YPS plates, *Kmrag5* and *Schxk2* exhibited significantly and slightly slow growth, respectively, compared to that of the coresponding parental strain, but the growth of *Kmmig1* and *Scmig1* was similar to that of each parental strain. On YP plates containing sucrose and 2-DOG, they exhibited different growth phenotypes. *Kmmig1* and *Scmig1* showed slightly better growth than that of each parental strain, and *Kmrag5* and *Schxk2* showed much more better growth. Notably, growth differences were observed in the presence of 0.1% 2-DOG between *Kmrag5* and *Kmmig1* at 24 h and between *Schxk2* and *Scmig1* at 24 h and 48 h. The results suggested that the glucose analog inhibits cell growth via a mechanism that involves *MIG1* and *RAG5* or *HXK2* in both yeasts.

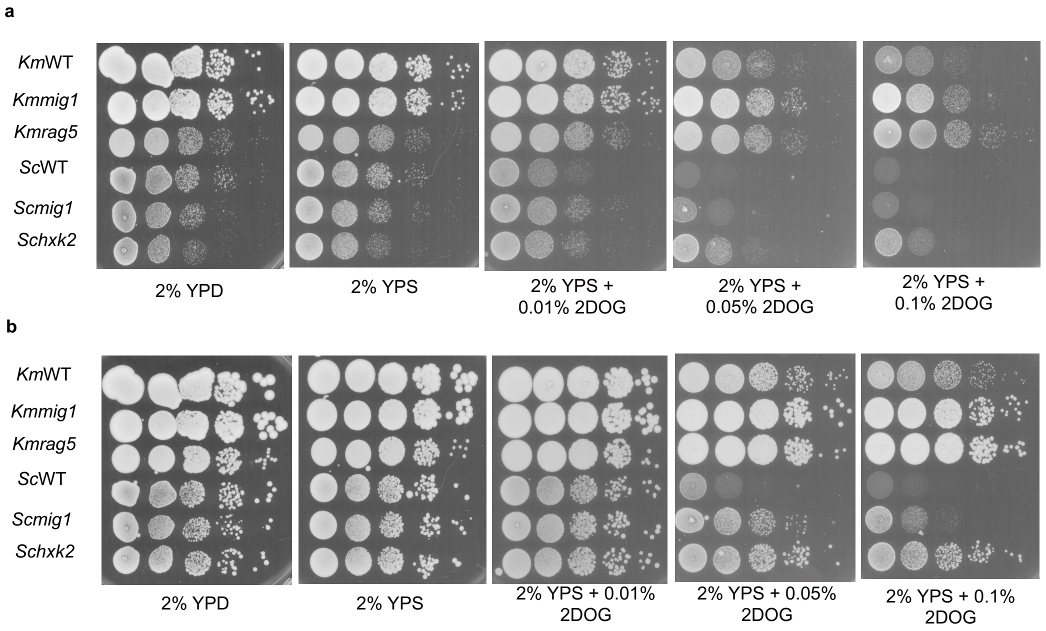


Fig. 2.1 Growth comparison of *K. marxianus* and *S. cerevisiae* on YP plates containing glucose or sucrose and 2-DOG. Cells were grown in 5 ml of YPG at 30°C under a shaking condition at 160 rpm for 15-18 h. The initial OD_{660} was adjusted to 1 or 10^0 and diluted to 10^{-1} 10^{-2} 10^{-3} and 10^{-4}. About 5 µl of each serial dilution was spotted on YPD, YPS and YPS containing 0.01, 0.05, and 0.1% (w/v) 2-DOG. The plates were incubated at 30°C and the growth was observed at 24 h (a) and 48 h (b).

2.4.2 Growth and metabolic profiles of *K. marxianus* and *S. cerevisiae* mutants and their parental strains in YP medium containing a single sugar or mixed sugars

To examine the effects of disruption of *MIG1* and *RAG5* or *HXK2* on sugar utilization ability, the mutant and parental strains were grown at 30°C in YP liquid medium containing a single sugar (YPD or YPX) or mixed sugars (YPDS or YPDX). Only *K. marxianus* strains were tested in YPX and YPDX media because *S. cerevisiae* is unable to assimilate xylose (Figs. 2.2-2.5). Metabolic profiles that were analyzed in this study represent accumulation of fructose, ethanol, glycerol and xylitol in the medium.

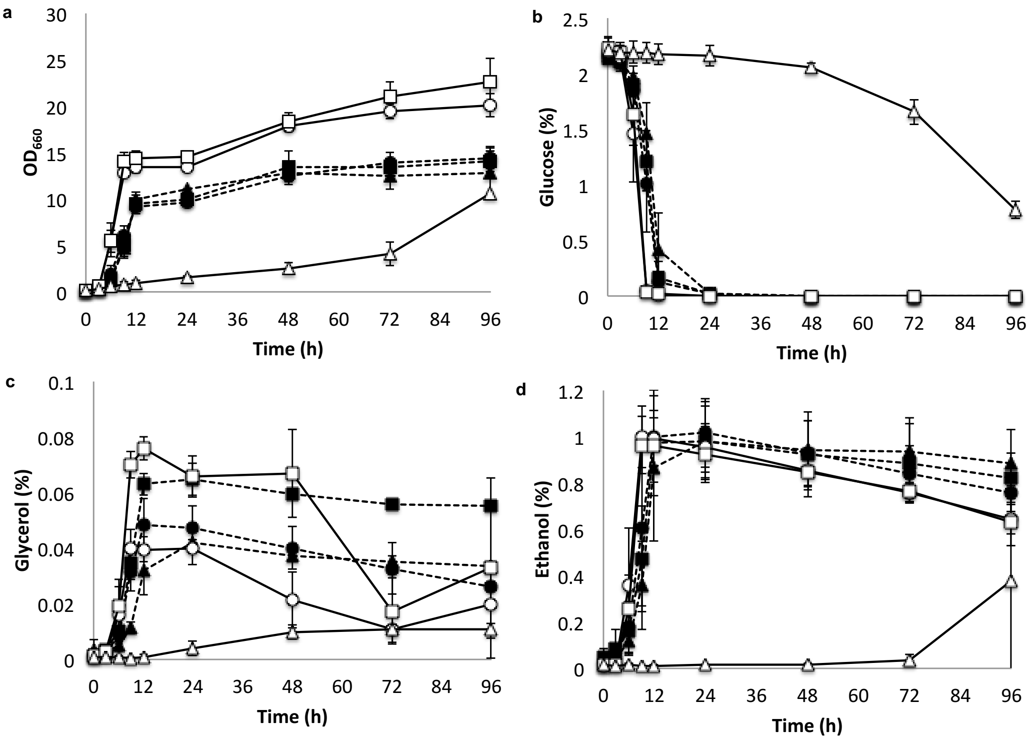


Fig. 2.2 Comparison of growth, sugar utilization and metabolite production of *K. marxianus* and *S. cerevisiae* in liquid YPD. Cells were pre-cultured in 5 ml of YPG at 30°C under a shaking condition at 160 rpm for 15-18 h. The initial OD$_{660}$ was adjusted to 0.1 and the cells were cultivated in 100 ml of YPD at 30°C under a shaking condition at 160 rpm for 96 h. The parental strain of *K. marxianus* DMKU3-1042 (straight line and open circles), *Kmmig1* (straight line and open squares), *Kmrag5* (straight line and open triangles), the parental strain of *S. cerevisiae* BY4741 (dotted line and filled circles), *Scmig1* (dotted line and filled squares) and *Schxk2* (dotted line and filled triangles) were compared by measuring OD$_{660}$ (a) and the concentrations of glucose (b), glycerol (c) and ethanol (d) in the medium. Data presented are averages of triplicate experiments, and error bars indicate standard deviations.

In YPD medium (Fig. 2.2), *Kmmig1* showed slightly higher OD$_{660}$ and about 1.5-3.0-times higher glycerol yield than those of the parental strain. The ethanol yield of *Kmmig1* at 12 h was 0.43 g/g, which was similar to that of the parental strain (0.45 g/g). *Scmig1* showed metabolic profiles similar to those of *Kmmig1,* including relatively high accumulation of glycerol compared to that of the parental strain and *Schxk2*. On the other hand, *Kmrag5* Showed greatly reduced growth and glucose utilization and produced small amounts of glycerol and ethanol. *Schxk2* showed almost no effect on utilization of glucose or production of glycerol and ethanol, which were different from those of *Kmrag5*.

The large defect of glucose utilization in *Kmrag5* may be due to the reduction in expression of *RAG1* for a low affinity glucose transporter (Prior *et al*. 1993; Betina *et al*. 2001). In YPDS medium (Fig. 2.3), *Kmmig1* grew slightly better and showed a slightly higher OD_{600} than did the parental strain until 48 h. However, as in the case of YPD medium (Fig. 2.2), *Kmrag5* grew very slowly and showed very low levels of glucose utilization and ethanol production but extremely high accumulation of fructose (0.54-0.76 g/g). Interestingly, the consumption of sucrose in *S. cerevisie* was enhanced by *Scmig1* and *Schxk2* (Fig. 2.3C), probably due to cancellation of glucose repression by these mutations. On the other hand, no such difference was observed between *Kmmig1* or *Kmrag5* and the parental strain. These findings suggest that *S. cerevisiae* is more sensitive to glucose repression in a sucrose medium, being consistent with results in a previous report (Lertwattanasakul *et al*. 2011). Moreover, *Scmig1* and *Schxk2* showed slow consumption of fructose compared to that of the parental strain, probably due to overhydrolysis of sucrose. *Kmmig1* and *Scmig1* accumulated relatively large amounts of glycerol (0.05 and 0.03 g/g, respectively) compared to those of the corresponding parental strains at 48 h.

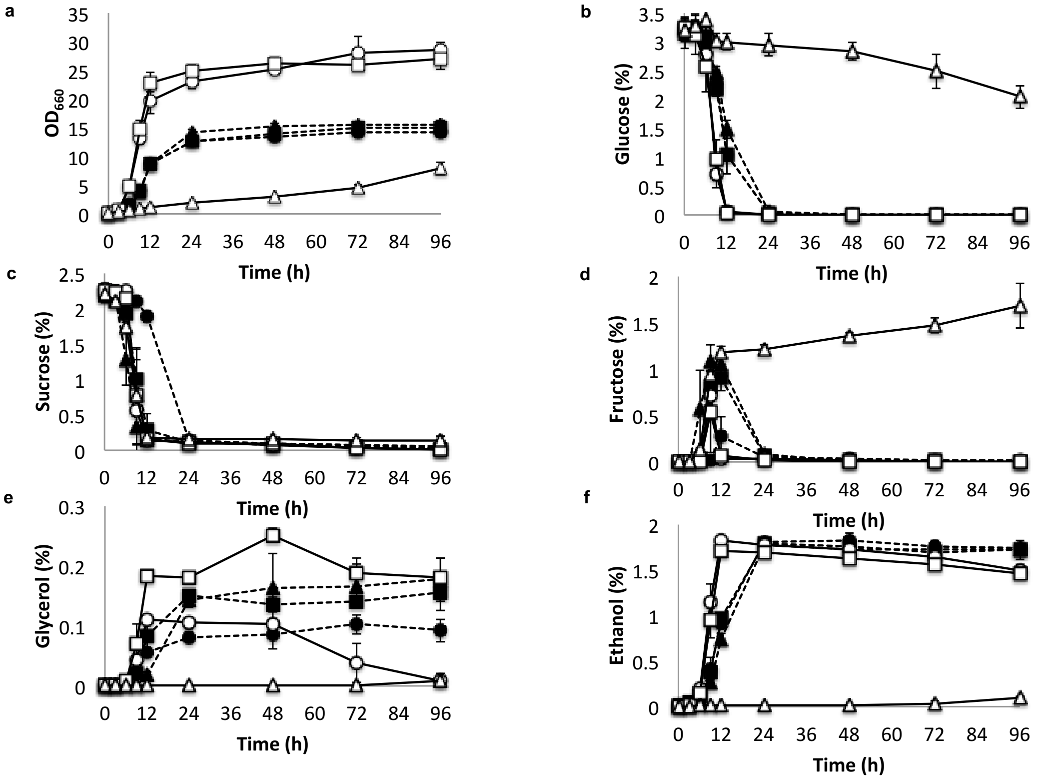


Fig. 2.3 Comparison of growth, sugar utilization and metabolite production of *K. marxianus* and *S. cerevisiae* in liquid YPDS. Cells were pre-cultured in 5 ml of YPG at 30°C under a shaking condition at 160 rpm for 15-18 h. The initial OD_{660} was adjusted to 0.1 and the cells were cultivated in 100 ml of YPDS at 30°C under a shaking condition at 160 rpm for 96 h. The parental strain of *K. marxianus* DMKU3-1042 (straight line and open circles), *Kmmig1* (straight line and open squares), *Kmrag5* (straight line and open triangles), the parental strain of *S. cerevisiae* BY4741 (dotted line and filled circles), *Scmig1* (dotted line and filled squares) and *Schxk2* (dotted line and filled triangles) were compared by measuring OD_{660} (a) and the concentrations of glucose (b), sucrose (c), fructose (d), glycerol (e) and ethanol (f) in the medium. Data presented are averages of triplicate experiments, and error bars indicate standard deviations.

In YPX medium (Fig. 2.4), *Kmmig1* showed slightly better growth, slighlty higher turbidity, slightly faster xylose utilization at 24 h and larger ethanol accumulation at 48 h than those of the parental strain and *Kmrag5*. *Kmmig1* showed increased accumulation of xylitol and glycerol at 24 h and 48 h, respectively. These findings suggest that Mig1 represses the utilization of xylose even in the absence of glucose and that increased utilization of xylose in *Kmmig1* causes limitation of NAD^+, which leads to the accumulation of xylitol and glycerol as reported previously (Suprayogi *et al.* 2015; Suprayogi *et al.* 2016). In YPDX medium (Fig. 2.5), *Kmmig1* showed slightly better growth than that of the parental strain at 24 h and utilized glucose slightly faster but accumulated more glycerol. This mutant started to utilize xylose after depletion of glucose around 12 h. Its consumption of xylose was fast at 48-72 h and it accumulated more xylitol and glycerol than did the parent. On the other hand, the ethanol production of *Kmmig1* was similar to that of the parental strain. *Kmrag5* grew slowly and reached the same growth level as that of the parental strain after 48 h. Consistently, glucose utilization in the mutant was slow and glucose was depleted after 96 h. Xylose utilization was also slow in *Kmrag5*, but the utilization started after 48 h when glucose still remained. Concomitantly, glycerol was dramatically increased, but xylitol was not accumulated. Ethanol in *Kmrag5* was accumulated slowly, but after 48 h, it seemed to be produced from not only glucose but also xylose. The growth and metabolic profiles of *S. cerevisiae* strains in YPDX medium were also examined, but they could not utilize xylose (data not shown).

Enhanced accumulation of metabolites such as glycerol and xylitol was observed in some liquid media in *Kmmig1* and *Kmrag5* mutants (Figs. 2.3 and 2.5). However, their accumulated amounts are very small compared to those in other microorganisms reported (Pagliaro *et al.* 2007; Nolleau *et al.* 1993). On the other hand, *Kmrag5* was shown to accumulate fairly high levels of fructose in YPDS liquid medium (Fig. 2.3). This ability of *Kmrag5* might be useful for bioconversion of sucrose-containing agricultural products to sweeter foods as in the case of an *HXK1* null mutant in *K. marxianus* NBRC 1777 (Zhang *et al.* 2017).

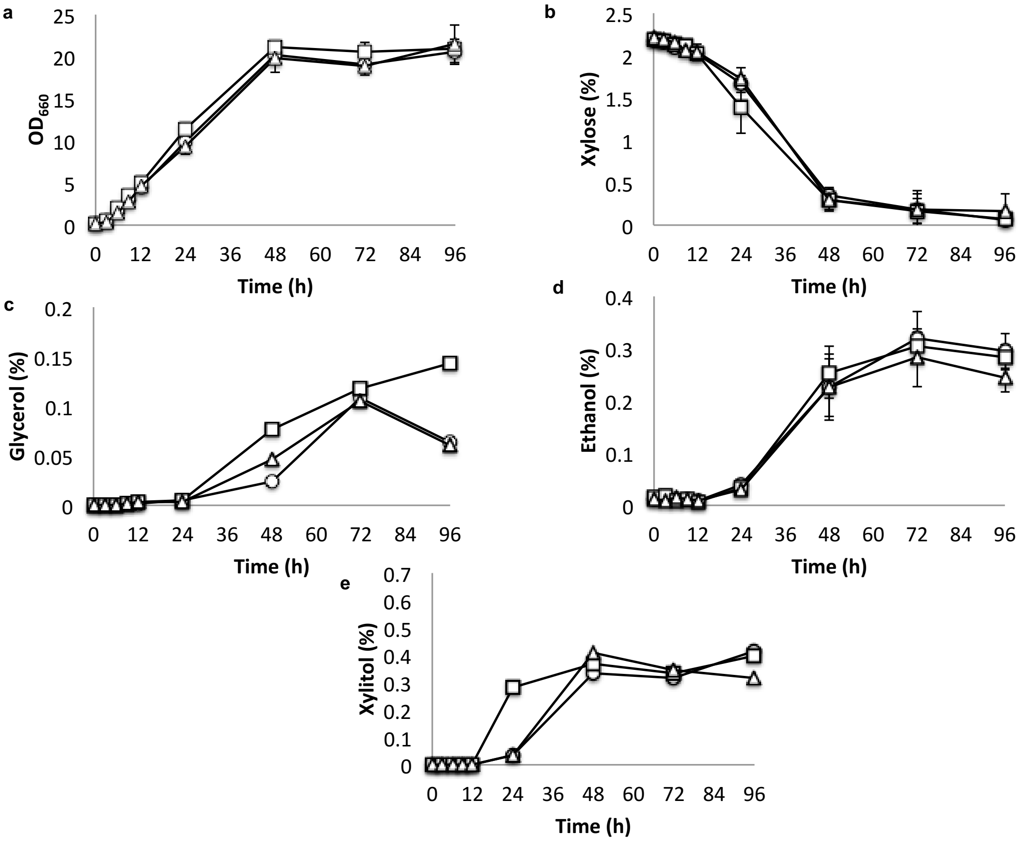


Fig. 2.4 Growth, sugar utilization and metabolite production of *K. marxianus* DMKU3-1042 and its disrupted mutants in liquid YPX. Cells were pre-cultured in 5 ml of YPG at 30°C under a shaking condition at 160 rpm for 15-18 h. The initial OD_{660} was adjusted to 0.1 and the cells were cultivated in 100 ml of YPX at 30°C under a shaking condition at 160 rpm for 96 h. The parental strain of *K. marxianus* DMKU3-1042 (straight line and open circles), *Kmmig1* (straight line and open squares) and *Kmrag5* (straight line and open triangles) were compared by measuring OD_{660} (a) and the concentrations of xylose (b), glycerol (c) ethanol (d), and xylitol (e) in the medium. Data presented are averages of triplicate experiments, and error bars indicate standard deviations.

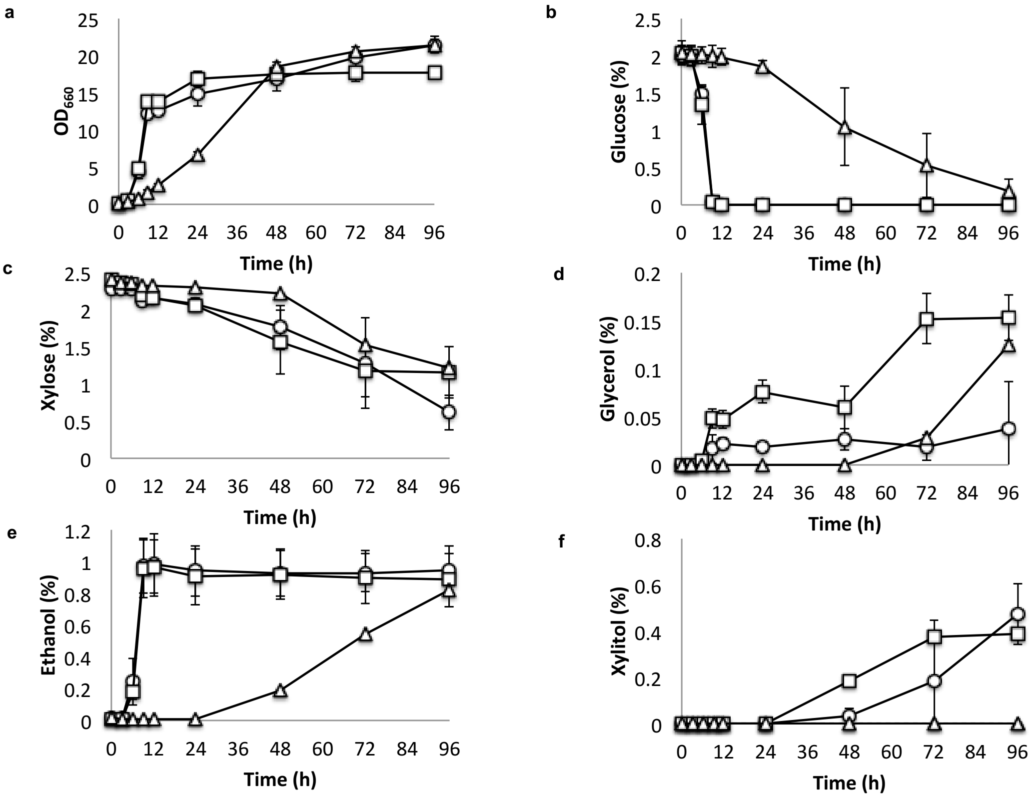


Fig. 2.5 Growth, sugar utilization and metabolite production of *K. marxianus* DMKU3-1042 and its disrupted mutants in liquid YPDX. Cells were pre-cultured in 5 ml of YPG at 30°C under a shaking condition at 160 rpm for 15-18 h. The initial OD_{660} was adjusted to 0.1 and the cells were cultivated in 100 ml of YPDX at 30°C under a shaking condition at 160 rpm for 96 h. The parental strain of *K. marxianus* DMKU3-1042 (straight line and open circles), *Kmmig1* (straight line and open squares) and *Kmrag5* (straight line and open triangles) were compared by measuring OD_{660} (a) and the concentrations of glucose (b), xylose (c) glycerol (d), ethanol (e), and xylitol (f) in the medium. Data presented are averages of triplicate experiments, and error bars indicated standard deviations.

2.4.3 Effects of *MIG1*- and *RAG5*-disrupted mutations on hexokinase and gluco-hexokinase activities

Since *Kmrag5* and *Kmmig1* grew much more slowly and sliglthty faster, respectively, than the parental strain in YPD and YPDS media (Figs. 2.2 and 2.3) and since *RAG5* encodes hexokinase, the effects of *MIG1*- and *RAG5*-disrupted mutations on hexokinase and gluco-hexokinase activities were determined (Fig. 2.6A). *Kmmig1* exhibited specific activities of hexokinase and gluco-hexokinase that were 1.1- and 1.3-times higher, respectively, than those of the parental strain. Surprisingly, *Kmrag5* showed almost no activity of either enzyme, indicating no activity of glucokinase, which is encoded by *GLK1*. Therefore, it is likely that Rag5 is involved in the expression of not only *RAG1* but also *GLK1*. Interestingly, a mutant, called No 23, having a *RAG1* mutation of G270S by a single nucleotide substitution seems to retain glucokinase activity but to have almost no hexokinase activity (Suprayogi *et al*., 2015). The mutation of No 23 thus affects glucokinase activity but not *GLK1* expression regulation activity of Rag5. On the other hand, the small influence of the disrupted mutation of *Kmmig1* on both activities suggests that Mig1 has a weak negative effect on the expression of either *RAG1* or *GLK1*.

2.4.4 Effects of *MIG1*- and *RAG5*-disrupted mutations on inulinase activity

To further examine the regulatory functions of Rag5 and Mig1, the effects of *MIG1*- and *RAG5*-disrupted mutations on inulinase activity were determined (Fig. 2.6) since *INU1* encoding inulinase has been proposed to be under the control of Mig1 (Lertwattanasakul *et al.* 2011). *Kmrag5* showed about 80-times higher inulinase activity than the parental strain. This finding suggests that Rag5 is a negative regulator for *INU1* as well as *RAG1* and *GLK1*. The mutation of *Kmmig1*, however, had almost no effect on inulinase activity. Notably, the mutation of No 23 increased inulinase activity, though the activity was about half of that in *Kmrag5*, suggesting that the mutation of No 23 causes reduction of *INU1* expression regulation activity of Rag5 (Fig. 2.6B). These results including results of experiments on hexokinase and gluco-hexokinase activities indicate that *MIG1* and *RAG5* in *K. marxianus* play different roles in gene expression regulation.

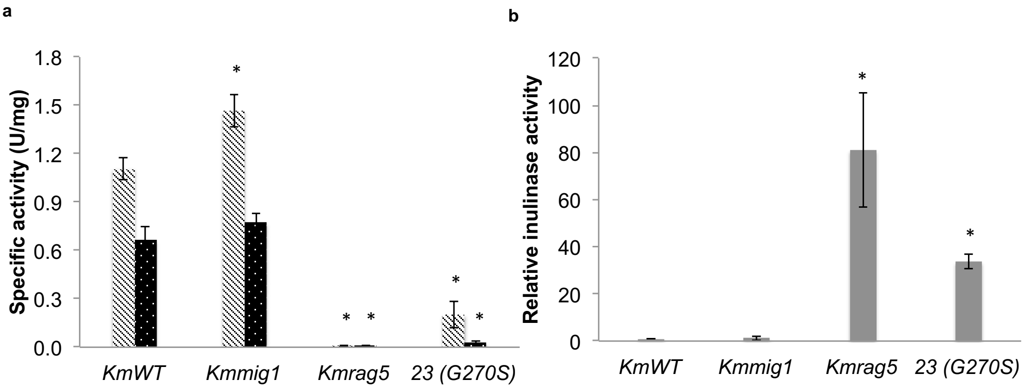


Fig. 2.6 Hexokinase, gluco-hexokinase and inulinase activities of *K. marxianus* DMKU3-1042 and its disrupted mutants. Cells were pre-cultured in 5 ml of YPG at 30°C under a shaking condition at 160 rpm for 15-18 h. Hexokinase (dot and black bar) and gluco-hexokinase (backslash and gray bar) activities (a). The initial OD_{660} was adjusted to 0.1 and the cells were cultivated in 100 ml of YPD at 30°C under a shaking condition at 160 rpm until 50% of the glucose remained. Bars represent ±SD of values from experiments performed in triplicate. Inulinase activity (gray bar) (b). The initial OD_{660} was adjusted to 0.1 and the cells were cultivated in 100 ml of YPD at 30°C under shaking condition at 160 rpm until 50% of the glucose remained. Supernatants were collected by centrifugation at 5,000 rpm for 10 min and then used for examination of inulinase activity by using the DNS method. Bars represent ±SD of values from experiments performed in triplicate. Each single asterisk indicates significantly higher or lower enzyme activity than that of the parental strain ($P<0.05$).

2.4.5 Effects of *MIG1*- and *RAG5*-disrupted mutations on expression of *INU1*, *GLK1*, and *RAG1*

To further examine the regulatory functions of *MIG1* and *RAG5* at the transcription level on the expression of *INU1*, *GLK1* and *RAG1*, RT-PCR was carried out (Fig. 2.7). The expression of *INU1* has been shown to be enhanced by *MIG1* and *RAG5*. *RAG5* disruption caused a dramatic increase in *INU1* expression, being consistent with its effect on inulinase activity, while *MIG1* disruption caused a slight increase in *INU1* expression, though its effect on inulinase activity was negligible (Figs. 2.6B and 2.7B). The expression levels of *INU1* and *GLK1* in *Kmrag5* were 22-times and 11-times higher, respectively, than those of the parental strain. However, *RAG1* expression levels in *Kmmig1* and *Kmrag5* was about 2.5-times and 18-times lower, respectively, than that of the parental strain. Disruption of *MIG1* had almost no effect on *GLK1* expression but increased *INU1* expression to a level about 8-times higher than that of the parental strain. Therefore, these results suggest that *RAG5* is a negative regulator for *INU1* and *GLK1* and a positive regulator for *RAG1* and that *MIG1* might be involved as a minor factor in the negative regulation of *INU1* and the positive regulation of *RAG1*.

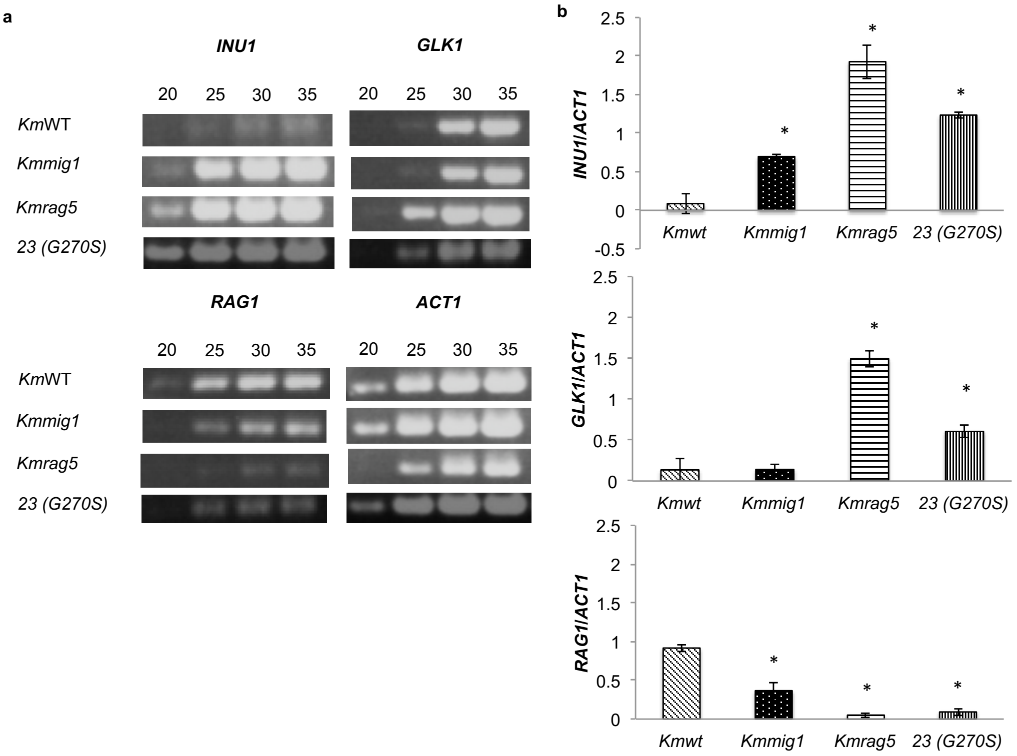


Fig. 2.7 Expression of *KmINU1*, *KmGLK1* and *KmRAG1* in YPD under a shaking condition. Cells grown in YPG medium for 18 h were cultivated in YPD at 30°C under a shaking condition at 160 rpm for 7 h (KmWT and *Kmmig1*), for 18 h (Mutant No 23) and for 66 h (*Kmrag5*). Total RNA was then isolated and subjected to RT-PCR with primers specific to corresponding genes that amplify an approximately 500-bp DNA fragment. (a) After reverse transcriptase reaction, PCR products of 20, 25, 30 and 35 cycles were subjected to 1.2% agarose gel electrophoresis and stained with ethidium bromide. (b) Relative band intensities were determined using scanned images and IMAGE-J software. Each single asterisk indicates significantly higher or lower gene expression level than that of the parental strain ($P<0.05$).

2.4.6 Effects of *MIG1*- and *RAG5*-disrupted mutations on growth in a minimal medium containing glucose or galactose and amino acids

To further examine the effects of mutations of *MIG1* and *RAG5* on hexose sugar utilization, growth rates in a minimal medium containing glucose or galactose were compared (Fig. 2.8). As expected, *Kmrag5* grew much more slowly than the parental strain in glucose, being consistent with data shown in Fig. 2.1. Surprisingly, *Kmmig1* exhibited almost no growth in a glucose or galactose medium. We thus examined the requirement of nutrients for *Kmmig1* and found that histidine is essential for the mutant (Fig. 2.8). Since this is the first indication of involvement of Mig1 in histidine biosynthesis, complementation experiments were performed by introduction of *MIG1* from the parental strain. It was found that the *MIG1*-complemented strain grew in glucose minimal medium without histidine. Therefore, these findings suggest that Mig1 is involved in the expression of some genes related to histidine biosynthesis in *K. marxianus*. On the other hand, the reqirement of Mig1 in *S. cerevisiae* is not clear because the strain used in this study has genotypes of *his*, *met*, *leu* and *ura*.

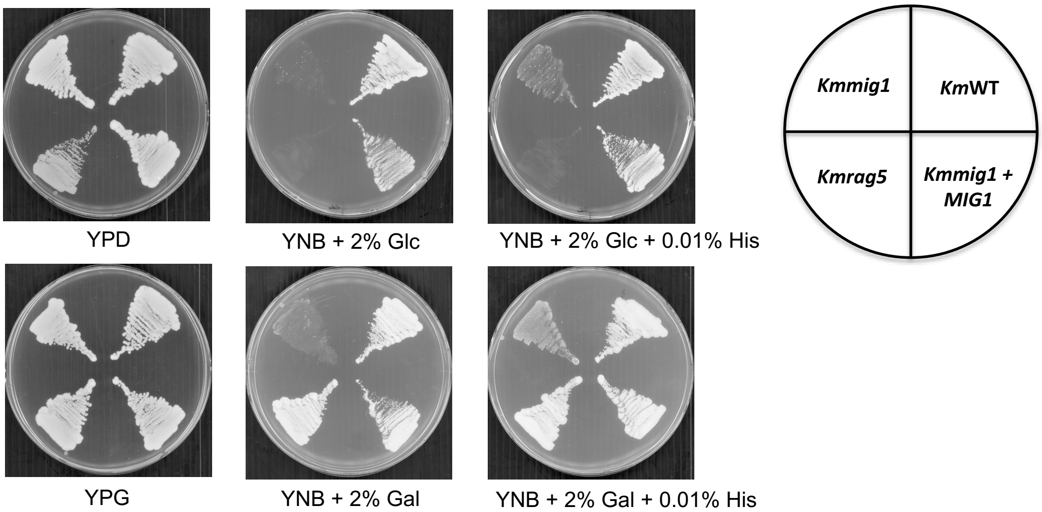


Fig. 2.8 Effect of histidine on the growth of *K. marxianus* DMKU3-1042 and its disrupted mutants on YNB agar containing glucose or galactose. Cells were pre-cultured in 5 ml of YPG at 30°C under a shaking condition at 160 rpm for 15-18 h. The cells were streaked on YPD and YPG as a control and on a Yeast Nitrogen Base (YNB) plate containing 2% (w/v) glucose or 2% (w/v) galactose or 2% (w/v) glycerol and supplemented with 0.01% (w/v) histidine. The plates were incubated at 30^{o}C and observed at 48 h.

2.5 Discussion

In order to understand the physiological functions of Mig1 and Rag5 including their contribution to glucose repression in *K. marxianus* DMKU3-1042, we constructed two *kan*MX4-inserted mutants, *Kmmig1* and *Kmrag5*, and examined the effects of the mutations on sucrose utilization in the presence of glucose (YPDS) since extensive studies have been performed with corresponding mutations under such conditions in *S. cerevisiae*. *K. marxianus* and *S. cerevisiae* are able to assimilate sucrose via inulinase-dependent hydrolysis and invertase-dependent hydrolysis, respectively, and can grow well in YPDS medium. The latter, but not the former, shows glucose-sensitive sucrose assimilation (Lertwattanasakul *et al*. 2011). When 2-DOG was used instead of glucose, *MIG1* mutations caused both yeasts to become resistant to 2-DOG to some extent compared to the corresponding parent (Fig. 2.1), indicating the possibility that Mig1 is involved in the repressive effect of glucose on sucrose utilization in *K. marxianus*. On the other hand, *RAG5* and *HXK2* mutations caused more resistance to 2-DOG (0.1% 2-DOG in the case of *K. marxianus*) than that of the corresponding *MIG1* mutant. This stronger phenotype may be due to mutations of the genes for hexokinase that converts 2-DOG to 2-DOG-6-phosphate, which blocks glycolysis as an inhibitor of phospho-hexose isomerase (Sols and Crane 1954; Wick *et al*. 1957; Chen and Guéron 1992).

Scmig1 and *Schxk2* similarly exhibited increased utilization speed of sucrose compared to that of the parental strain in YPDS medium (Fig. 2.3C), being consistent with the fact that the Mig1 and Hxk2 complex functions as a negative regulator in *S. cerevisiae* (Ahuatzi *et al*., 2004) and the findings that invertase activities of *Δhxk2* and *Δmig1* are significantly higher than that of the parental strain under the condition with glucose (Vega *et al*. 2016). On the other hand, *Kmmig1* and *Kmrag5* showed no significant difference from that of the parental strain in the same medium (Fig. 2.3C). Inconsistent with this, *MIG1* and *RAG5* mutations significantly increased the transcription level of *INU1,* and the latter mutation also increased inulinase activity in YPD medium (Figs. 2.6B and 2.7). The inconsistency might be due to the existence of inulinase activity more than the rate-limiting in the parental strain as discussed previously (Lertwattanasakul *et al*. 2011). Notably, *MIG1* and *INU1* transcription levels are higher and lower, respectively, in YPDS than in YPS (Lertwattanasakul *et al*. 2011). The present and previous transcription analyses suggest that *INU1* is down-regulated by *MIG1* and *RAG5*. We have no idea about the negligible increase in inulinase activity in *Kmmig1*, but there might be post-transcriptional regulation for *INU1* expression.

In *K. lactis*, the transcriptional regulation of *RAG1* requires the hexokinase gene (Betina *et al*. 2001), and similarly *HXK2* is needed for the expression of *HXT1-2* in *S. cerevisiae* (Ozcan and Johnston, 1995). We also noticed the requirement of Rag5 for *RAG1* transcription in *K. marxianus*. *Kmrag5*, but not *Schxk2*, showed very slow utilization of glucose and accumulation of a large amount of fructose (Fig. 2.3B and D). Interestingly, both *Kmrag5* and *Kmmig1* reduced the transcription level of *RAG1* (Fig. 2.7). The reduction of *RAG1* expression may be responsible for the slowdown of glucose consumption because it encodes a low-affinity glucose transporter. *Kmmig1*, however, exhibited glucose utilization and fructose accumulation equivalent to those of the parental strain. Surprisingly, *Kmrag5* greatly increased *GLK1* transcription but had almost no effect on glucokinase activity (Figs. 2.6A and 2.7). There might be some regulation for the synthesis of glucokinase or formation of its active form after transcription. Eventually, *Kmrag5* has almost no kinase activity for glucose because *RAG5* is only one gene for hexose kinase in the genome of *K. marxianus* DMKU3-1042 (Lertwattanasakul *et al*. 2015). These findings suggest that the knockout of *RAG5* caused elimination of kinase activity for glucose and fructose, a decrease in Rag1 as a glucose transporter and an increase in inulinase activity, which in turn gave rise to reduction of glucose utilization and accumulation of fructose. Since the effect of the *MIG1* mutation on *GLK1* transcription was insignificant (Fig. 2.7), only Rag5 (Rag5 complex except for Mig1 if it forms a complex with other proteins) may perform negative regulation of *GLK1*

Kmmig1 showed a very slightly higher OD until 96 h in YPD and until 48 h in YPDS than that of the parental strain (Figs. 2.2 and 2.3), which may be consistent with slightly higher hexokinase and glucokinase activities (Fig. 2.6A). Moreover, disruption of *MIG1* also affected the accumulation of glycerol (Figs. 2.2 and 2.3). The amount of accumulated glycerol was quite small, but the amount was increased when the total sugar amount in the medium was doubled (Figs. 2.2 and 2.3). Similar accumulation of glycerol and increase of its accumulation in *Kmmig1* were observed in YPX and YPDX (Figs. 2.4 and 2.5). The glycerol production pathway might be induced to supply NAD^+, which promotes glycolysis to import and catabolize glucose (Suprayogi *et al*. 2015), eventually increasing cell growth. Therefore, it is thought that Mig1 weakly down-regulates glycolysis or its downstream even in the absence of glucose. At least under the condition with glucose, glycerol accumulation was detected in *Scmig1* and *Schxk2*, possibly due to derepression of negative regulation for glycolysis or its downstream by the Mig1-Hxk2 complex as reported previously (Rose *et al*. 1991; Entian and Barnett 1992; Ahuatzi *et al*. 2004).

Since *K. marxianus,* but not *S. cerevisiae,* possesses xylose assimilation activity, we investigated the involvement of Mig1 and Rag5 in the activity. *Kmmig1* accumulated more xylitol than that of the parental strain in YPX at 24 h (Fig. 2.4E) and in YPDX at 48 h (Fig. 2.5F) in addition to accumulation of glycerol as mentioned above. On the other hand, *Kmrag5* showed slower growth and remarkable retardation in consumption of not only glucose but also xylose in YPDX like that of glucose in YPD or YPDX, suggesting that hexose transporters including Rag1 are responsible for the xylose import in *K. marxianus* as suggested previously (Hamacher *et al*. 2002; Suprayogi *et al*. 2015). In a comparison of results obtained in YPX and in YPDX, retardation of xylose consumption was also noticed in *Kmmig1.* Since the extent of retardation was similar to that of the parental strain, it is possible that Mig1 is not involved in glucose repression on xylose assimilation or it is possible that Mig1 is involved in the repression but that glucose is preferably imported by glucose repression-insensitive hexose transporters to leave xylose behind. The mechanism of glucose repression on genes related to xylose metabolism in yeast has not been clarified except for *KmXYL1* which is repressed in the presence of glucose (Rodrussamee *et al*. 2011). Rodrussamee *et al*. (2011) found that the coexsistence of glucose causes delayed utilization of galactose, xylose and arabinose in *K. marxianus*, suggesting that symporters for the latter three sugars are sensitive to glucose repression.

Interestingly, *Kmmig1* was found to have a defect of growth in a minimal medium and the defect was suppressed when histidine was added. It is thus likely that Mig1 is essential for histidine biosynthesis in *K. marxianus*. It might be an activator of some genes for histidine biosynthesis. Unfortunately, *Scmig1* could not be tested for this phenotype due to *his3Δ1* mutation in the background (Brachmann *et al*. 1998). *Kmrag5*, however, seems not to be involved in histidine biosynthesis. *Kmrag5* showed relatively slow growth not because of the involvement of histidine biosynthesis but because of its weak glucose uptake. Indeed, there is no known reason why Mig1 is only necessary for histidine biosynthesis but not necessary for other amino acid biosyntheses. Since PRPP (5-phosphoribosyl 1-diphosphate) such as purine and pyrimidine nucleotide biosyntheses is used for histidine biosynthesis, enhancement of histidine biosynthesis by Mig1 may reduce the amount of purine and pyrimidine nucleotides and may inhibit cell proliferation. Perhaps if histidine is low, Mig1 may somehow notice low levels of histidine, actively enhance histidine biosynthesis and attenuate the production of DNA precursors. If this is true, Mig1-mediated regulation may provide a mechanism by which protein synthesis has precedence over DNA synthesis.

In *S. cerevisiae*, Mig1 and Hxk2 are the two main mediators for glucose repression and have a strong interaction with each other in a high-glucose medium (Ahuatzi *et al*. 2007) to form a complex with co-repressor proteins Cyc8-Tup1 (Ahuatzi *et al*. 2004). This study has provided evidence indicating some physiological functions of Mig1 and Rag5 in *K. marxianus* DMKU3-1042. This study also suggests that Mig1 and Rag5 in *K. marxianus* share some functions with Mig1 and Hxk2, respectively, in *S. cerevisiae*, especially in the negative regulation of *INU1* and *SUC2* in the presence of glucose and the positive regulation of *RAG1* and *HXT1-2* by *RAG5* and *HXK2*, respectively. Considering the possible shared functions and more than 75% similarity in primary structures, Mig1 and Rag5 in *K. marxianus* may form a complex similar to that consisting of Mig1 and Hxk2 in *S. cerevisiae.* Further studies including genome-wide gene expression analysis of *MIG1* or *RAG5* mutants and analysis of protein-protein interaction of Mig1 and Rag5 are required.

2.6 Conclusion

We constructed disrupted mutants of *MIG1* and *RAG5* in the non-conventional yeast *K. marxianus* and investigated their effects on the utilization of xylose and sucrose in the presence of glucose and on expression of several genes including *INU1* for inulinase and *RAG1* for a low-affinity glucose transporter.

These results suggest that both Mig1 and Rag5 are involved not only in negative regulation but also in positive regulation of gene expression. In the negative regulation, Mig1 and Rag5 of *K. marxianus* seem to share some functions with Mig1 and Hxk2, respectively, in *S. cerevisiae*. Moreover, the *MIG1* mutant, but not the *RAG5* mutant, required histidine, suggesting that *MIG1* is involved in histidine biosynthesis in *K. marxianus*. A genome-wide expression analysis of Mig1 regulation is underway, which makes it possible to find genes regulated by Mig1 for histidine biosynthesis.

CHAPTER 3

MIG1 as a positive regulator for the histidine biosynthesis pathway and as a global regulator in thermotolerant yeast *Kluyveromyces marxianus*

3.1 Abstract

Kmmig1 as a disrupted mutant of *MIG1* encoding a regulator for glucose repression in *Kluyveromyces marxianus* exhibits a histidine-auxotrophic phenotype. Genome-wide expression analysis revealed that only *HIS4* in seven *HIS* genes for histidine biosynthesis was down-regulated in *Kmmig1*. Consistently, introduction of *HIS4* into *Kmmig1* suppressed the requirement of histidine. Considering the fact that His4 catalyzes four of ten steps in histidine biosynthesis, *K. marxianus* has evolved a novel and effective regulation mechanism via Mig1 for the control of histidine biosynthesis. Moreover, RNA-Seq analysis revealed that there were more than 1,000 differentially expressed genes in *Kmmig1*, suggesting that Mig1 is directly or indirectly involved in the regulation of their expression as a global regulator.

3.2 Introduction

Kluyveromyces marxianus, a nonconventional yeast, has attractive characteristics including good thermotolerance, high ethanol productivity (Limtong *et al*. 2007), a broad spectrum in sugar assimilation (Rodrussamee *et al*. 2011; Lertwattanasakul *et al*. 2013) and weak glucose repression on sucrose assimilation (Lertwattanasakul *et al*. 2011). There have been several studies on sugar utilization and ethanol production by *K. marxianus* at high temperatures (Limtong *et al*. 2007; Rodrussamee *et al*. 2011; Lertwattanasakul *et al*. 2011; Madeira-Jr and Gombert, 2018) that were carried out with the aim of establishing high-temperature fermentation, which has advantages including reduction of cooling costs, prevention of contamination and reduction of enzymatic hydrolysis cost (Murata *et al*. 2015; Kosaka *et al*. 2018; Madeira-Jr and Gombert, 2018). The regulation of some genes related to glucose repression in *K. marxianus* has also been investigated (Lertwattanasakul *et al*. 2011; Nurcholis *et al*. 2019), and such studies may provide crucial information for utilization of mixed sugars such as mixed sugars in general biomass.

One of the most important factors in the regulation of glucose repression in *K. marxianus* and its sister yeast species, *Saccharomyces cerevisiae*, is Mig1. ScMig1 has been shown to function as a regulator complex including ScHxk2 in glucose repression (Ahuatzi *et al.* 2004; Ahuatzi *et al.* 2007) and to be involved in negative regulation of the expression of several genes including *GAL83*, *SUC2*, *MAL62*, *LAC4* and *LAC12* when glucose co-exists (Gancedo and Gancedo 1986; Nehlin and Ronne 1990; Sun *et al.* 2012; Lin *et al.* 2014; Zou *et al.* 2015). In *K. marxianus*, *MIG1* mutants have been shown to exhibit increased activities of β-galactosidase and inulinase (Zhou *et al.* 2013; Zhou *et al.* 2014). KmMig1 with KmRag5, a orthologue of ScHxk2, is involved in negative regulation of the expression of *INU1* encoding inulinase and positive regulation of the expression of *RAG1* for a low-affinity glucose transporter, and, notably a *MIG1*-disrupted mutant (*Kmmig1*), but not a *RAG5* mutant, exhibited a histidine-auxotrophic phenotype (Nurcholis *et al.* 2019).

The histidine biosynthesis pathway has been studied in detail in prokaryotes and lower eukaryotes (Alifano *et al.* 1996; Brenner and Ames 1971). The pathways in *Escherichia coli* and *Salmonella typhimurium* consist of 8 histidine genes (Carlomagno *et al.* 1988), , whereas the pathway in *S. cerevisiae* has 7 genes including *HIS1*, *HIS2*, *HIS3*, *HIS4*, *HIS5*, *HIS6* and *HIS7* (Hinnebusch *et al.* 1983; Malone *et al.* 1994; Struhl 1985; Donahue *et al.* 1982; Nishiwaki *et al.* 1987; Kuenzler *et al.* 1993). *K. marxianus* DMKU3-1042 also has seven *HIS* genes, the products of which are involved in ten steps of the histidine biosynthesis pathway (Lertwattanasakul *et al.* 2015).

On the basis of a histidine-auxotrophic phenotype of *Kmmig1* in *K. marxianus* (Nurcholis *et al.* 2019), in order to understand the role of Mig1 for histidine biosynthesis, we performed a genome-wide expression analysis with *Kmmig1* and complementation experiments with a candidate gene regulated by Mig1. The results suggested a novel regulation by Mig1, that is, *HIS4*, which encodes an enzyme catalyzing 4 steps of histidine biosynthesis, is positively regulated by Mig1. Additionally, the genome-wide expression analysis revealed that a defect of *MIG1* significantly affected the expression of 1,150 genes, in which 689 and 461 were up- and down-regulated, respectively. The results thus suggest that Mig1 is involved in the positive regulation and negative regulation of the expression of many genes in *K. marxianus*.

3.3 Materials and methods

3.3.1 Materials

Oligonucleotide primers were purchased from Greiner Bio-one (Tokyo, Japan). A PCR purification kit, gel extraction kit and RNeasy plus mini kit were from QIAGEN (Hilden, Germany). *Ex Taq* and primeSTAR DNA polymerases, In-fusion HD cloning kit, DNase treatment kit, and Yeastmaker^{TM} carrier DNA-Clontech were from Takara Bio (Shiga, Japan). A DNA sequencing kit was from Beckman Coulter (Deutschland, Germany). Zeomycin (Zeocin^{TM}) was from Invitrogen-Thermo Fisher Scientific (Brookfield, USA). Yeast extract and zymolyase were from Nacalai Tesque (Kyoto, Japan). Peptone was from Kyokuto (Tokyo, Japan). D-glucose and RNase A were from SIGMA-ALDRICH (Tokyo, Japan). D-galactose was from Wako (Osaka, Japan). Yeast nitrogen base without amino acids was from DIFCO (Houston, USA). Other chemicals used in this study were of analytical grade.

3.3.2 Strains, media and growth conditions

The yeast strains used in this study were *K. marxianus* DMKU3-1042 (Limtong *et al*. 2007), *Kmmig1*, *Kmmig1 KmMIG1* (Nurcholis *et al*. 2019) and *Kmmig1 TDH3-HIS4-ble* (in this study), and *S. cerevisiae* BY4741 (*MAT*a *his3Δ1 leu2Δ0 met15Δ0 ura3Δ0*) (Brachmann *et al*. 1998). YP consists of 1% (*w/v*) yeast extract and 2% (*w/v*) peptone. The medium used to examine growth characteristics of yeast strains on agar plates was YP supplemented with 1.5% (*w/v*) agar and a carbon source, YPG (2% (*w/v*) galactose). The medium used to observe growth characteristics of yeast strains on minimal medium agar plates was 0.67% (*w/v*) yeast nitrogen base (YNB) without amino acids supplemented with 1.5% (*w/v*) agar and a carbon source, YNBD (2% (*w/v*) glucose) or YNBG (2% (*w/v*) galactose). If necessary, 0.01% (*w/v*) histidine was added. *E. coli DH5α* and SOC medium (Toyobo, Japan) were used for the In-fusion cloning method. LB (1% (*w/v*) tryptone (Nacalai Tesque, Japan), 0.5% (*w/v*) yeast extract (Nacalai Tesque, Japan), and 1% (*w/v*) NaCl (SIGMA-ALDRICH, Japan)) was used as a general medium for *E. coli*. If necessary, ampicillin (25 μg ml^{-1}) (Wako, Japan), X-Gal (40 μg ml^{-1}) (Nacalai Tesque, Japan), or IPTG (40 μg ml^{-1}) (Nacalai Tesque, Japan) was added.

Cells were pre-cultured in 5 ml of YPG medium at 30 °C under a shaking condition at 160 rpm for 18 h. The pre-culture was inoculated into a 300-ml flask containing 100 ml of YNBG and 0.01% (*w/v*) histidine to adjust the initial optical density at 660 nm (OD_{660}) to 0.1, followed by incubation at 30 °C for 24 h under a shaking condition at 160 rpm. Cell density was measured turbidimetrically at 660 nm on a spectrophotometer (U-2000A, Hitachi, Japan). To observe growth characteristics of yeast strains on agar plates, cells were streaked on YPG or YNBG and 0.01% (*w/v*) histidine and incubated at 30 °C for 24 h and 48 h.

3.3.3 RNA preparation for RNA-Seq

Cells were pre-cultured in 5 ml of YPG at 30 °C under a shaking condition at 160 rpm for 18 h. The pre-culture was inoculated into a 300-ml flask containing 100 ml of YNBG and 0.01% (*w/v*) histidine at 30 °C under a shaking condition at 160 rpm for 12 h (in the case of wild type) and for 18 h (in the case of *Kmmig1*). At the mid-log phase, cells were harvested by centrifugation at 5,000 rpm for 5 min at 4 °C. The different pre-culture times were due to the fact that the growth of the latter was slower than that of the former. The cells were washed with YNBG and transferred to 100 ml of YNBG, followed by incubation at 30 °C for 1 h. The cells were harvested by centrifugation at 5,000 rpm for 5 min at 4 °C and subjected to an RNA preparation process. RNA was prepared by a modified procedure on the basis of the procedure reported previously (Lertwattanasakul *et al.* 2015). The RNA samples then were subjected to RNase-free DNase treatment. All RNA samples were purified by using an RNeasy plus mini kit (QIAGEN) according to the protocol provided by supplier.

3.3.4 RNA-Seq-based transcriptomic analysis

The purified RNA samples were analysed on an Illumina MiniSeq at the Research Center of Yamaguchi University. The detailed procedure for RNA-Seq has been described previously (Kim *et al.* 2013). All these data were deposited under accession number DRA008595 in the DDBJ Sequence Read Archive (https://www.ddbj.nig.ac.jp/dra/index-e.html). The sequencing results were analysed using CLC genomic workbench version 10.1.1. All mapped reads at exons were counted, and the numbers were converted to unique exon reads. The unique exon reads from three biological replicates of *Kmmig1* were compared to those of the parental strain.

Gene expression profiles of *Kmmig1* and the parental strain were compared to find differentially expressed genes (DEGs) based on unique exon read values from CLC genomic workbench outputs using DESeq2 R package (Anders and Huber 2010). The resulting *P*-values were adjusted using the Benjamin-Hochberg's method for controlling the false discovery rate. Genes with adjusted *P* values less than 0.01 ($P_{adj}<0.01$) and $\log_2$ (fold change) values greater than 1 or lower than -1 were assigned as significant DEGs. Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway mapping with these significant DEGs was performed by KEGG web tools (http://www.genome.jp/keg/tool/map_pathway1.html). Gene ontology (GO) enrichment analysis of significant DEGs was performed using topGO R package (Alexa and Rahnenfuher 2018). GO terms with *P* values less than 0.01 were considered significantly enriched.

3.3.5 Increased expression of *HIS4* in *Kmmig1*

For increased expression of *HIS4* in *Kmmig1,* a *TDH3-HIS4-ble* DNA fragment was constructed as follows. The *TDH3* promoter fragment was amplified by PCR using genomic DNA of *S. cerevisiae* BY4741 as a template and primers prTDH3-5'-F and prTDH3-3'-R (Table 3.1). The primers were designed to amplify the fragment corresponding to the region from the *TDH3* start codon to 993-bp upstream of the start codon. The *HIS4* fragment was amplified by PCR using genomic DNA of *K. marxianus* DMKU 3-1042 as a template and primers

HIS4TD-5’-F and HIS4BL-3’-R. The primers were designed to amplify the fragment corresponding to the region from the start codon of *HIS4* (2,409 bp). The *ble* gene (zeomycin resistance gene) was amplified by PCR from pSH65 plasmid DNA as a template with primers BLE-5’-F and BLE-3’-R (Guldener *et al*. 2002). Linear pUC19 DNA (Takara Bio, Japan) was prepared by PCR amplification with primers pUC19-5’-F and pUC19-3’-R (Table 1). The four amplified fragments were purified using a QIAquick gel extraction kit, connected by the In-fusion cloning method (Takara Bio, Japan), introduced into *E. coli DH5α* by using the heat shock method (Sambrook and Russell, 2001), and screened on LB plates containing ampicillin, IPTG and X-Gal. Transformants harboring pUC19 containing a *TDH3-HIS4-ble* fragment (3,905 bp) were confirmed by colony PCR. The *TDH3-HIS4-ble* fragment was amplified by PCR and directly introduced into *Kmmig1* by the lithium acetate method (Gietz and Schiestl, 2007; Abdel-Banat *et al*. 2010). Transformants were obtained on YPD plates containing zeomycin (100 µg ml^{-1}), and recombinants were then examined by PCR to check the existence of the *TDH3-HIS4-b1e* fragment, generating *Kmmig1 TDH3-HIS4-ble*. Physiological confirmation tests were carried out on YNBD or YNBG plates in the absence or presence of 0.01% (*w/v*) histidine.

Table 3.1. Primers used in this study

No.	Primer name	Nucleotide sequences
1	pUC19-5’-F	5’-GATCCTCTAGAGTCGACCTG-3’
2	pUC19-3’-R	5’-GATCCCCGGGTACCGAGCTC-3’
3	prTDH3-5’-F	5’-CGACTCTAGAGGATCCGAGGACCTTGTCACCTTGAG-3’
4	prTDH3-3’-R	5’-TTTGTTTGTTTATGTGTGTT-3’
5	HIS4TD-5’-F	5’-ACATAAACAAACAAAATGTTACCTCTTGTGCCCTTA-3’
6	HIS4BL-3’-R	5’-TCGCCCTTAGATTAGTTATTCAAAATTAGGTGGTA-3’
7	BLE-5’-F	5’-CTAATCTAAGGGCGAGCTCG-3’
8	BLE-3’-R	5’-CGGTACCCGGGGATCTCCGTCGAGTGGGTGGTGA-3’

Underline indicates additional hanging 15 nucleotides for in-fusion cloning

3.4 Results

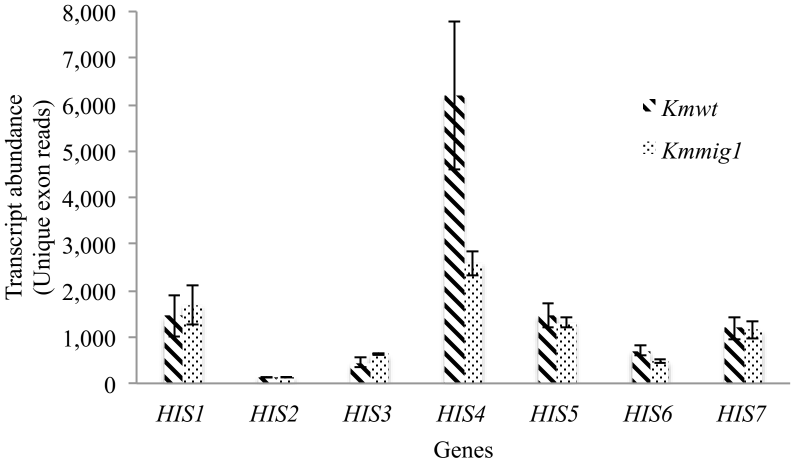
3.4.1 Effect of *MIG1*-disrupted mutation on expression of genes for histidine biosynthesis

K. marxianus became histidine-auxotrophic when *MIG1* was disrupted (Nurcholis *et al.* 2019), but the possibility that *MIG1* is not directly involved in the regulation of histidine biosynthesis but that other genes are directly involved could not be excluded. We thus decided not to examine only genes for histidine biosynthesis but to perform genome-wide expression analysis by RNA-Seq. RNA-Seq analysis was performed with RNAs prepared from *Kmmig1* and parental cells that had been incubated for 1 h after shifting from a minimal medium in the presence of histidine to that in the absence of histidine. After sequencing and removing the adaptors and the low quality reads, more than 0.8 Gb clean data qualified for follow-up analysis were acquired from each sample, being equivalent to more than 75-fold genome coverage. Unique exon reads of each gene were determined as transcript abundance. The difference in expression of each gene in *Kmmig1* from that in the parental strain was shown as the ratio of unique exon reads in *Kmmig1* to that in the parental strain. To further explore the transcriptional changes in *Kmmig1* compared to those in the parental strain, we conducted analysis of DEGs based on the ratio of unique exon reads. Significant DEGs showed changes in the transcription level with $\log_2$ (fold change) >1 and $\log_2$ (fold change) <-1 and ($P_{\mathrm{adj}}<0.01$). *Kmmig1* was found to have 1,150 DEGs including 689 up-regulated and 461 down-regulated genes (Appendix Fig. S2 and Table S3).

In order to explore the gene(s) responsible for a histidine-auxotrophic phenotype in *Kmmig1,* the unique exon reads of seven *HIS* genes for histidine biosynthesis were compared in *Kmmig1* and the parental strain (Fig. 3.1a). Analysis of DEGs indicated that the expression level of *HIS4* in *Kmmig1* was 2.4-times lower than that in the parental strain (Fig. 3.2). There was almost no difference between the expression levels of other *HIS* genes. Therefore, these findings indicated the possibility that the histidine-auxotrophic phenotype of *Kmmig1* was due to reduction in the expression of *HIS4.*

To confirm the significance of down-regulation of *HIS4*, the consistency of the RNA-Seq data and previous RT-PCR data for *INU1*, *RAG1* and *GLK1* was examined. A comparison of the RT-PCR data for *Kmmig1* and the parental strain (Nurcholis *et al*. 2019) revealed that the *MIG1*-disrupted mutation increased *INU1* expression by 3 fold, decreased *RAG1* expression by more than 2 fold and had almost no effect on *GLK1* expression. Consistently, the unique exon reads of *INU1* and *RAG1* in *Kmmig1* were 2.2-times higher and 5.3-times lower, respectively, than those in the parental strain, and the unique exon reads of *GLK1* in *Kmmig1* were not different from those in the parental strain (Fig. 3.1b). Therefore, the RNA-Seq data confirmed the previous conclusion that Mig1 is involved in the negative regulation of *INU1* and in the positive regulation of *RAG1* (Nurcholis *et al*. 2019) and suggested positive regulation of *HIS4* by Mig1. Notably, although the RNA samples were prepared from cells grown under different medium conditions, YPD for RT-PCR analysis and histidine-free YNBG for RNA-Seq analysis, data obtained from the different medium conditions showed good consistency in expression of the three genes. These facts may indicate that incubation in histidine-free YNBG for 1 h has almost no effect on cell metabolism and that the data therefore reflect only the effects of *MIG1*-disrupted mutation on the expression of genomic genes and that the influence of histidine-free YNBG is limited and is specific to some pathways, for example, histidine biosynthesis.

(a)



(b)

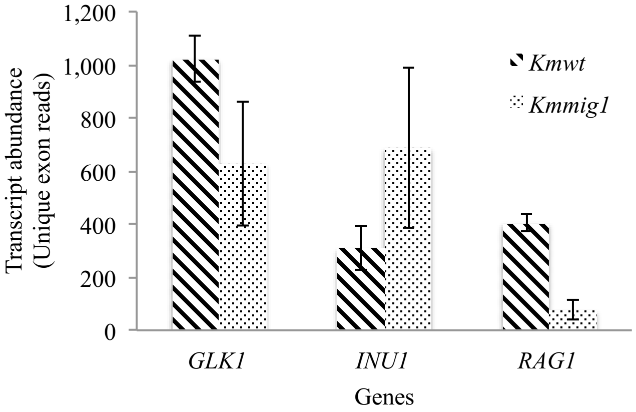


Fig. 3.1 Effects of *MIG1*-disrupted mutation on transcription of several genes for histidine biosynthesis and of *GLK1*, *INU1* and *RAG1* in *K. marxianus* RNA-Seq analysis was performed as described in Materials and methods. Transcript abundance in the form of unique exon reads of *Km*WT and *Kmmig1* was estimated for several genes for histidine biosynthesis (**a**) and *GLK1* for glucokinase, *INU1* for inulinase and *RAG1* for glucose transporter (**b**) in *K. marxianus*. Data presented are averages of triplicate independent experiments, and error bars indicated standard deviations.

3.4.2 Increased expression of *HIS4* in *Kmmig1*

RNA-Seq analysis indicated the possibility that the down-regulation of the expression of *HIS4* was responsible for the histidine-auxotrophic phenotype in *Kmmig1*. Interestingly, His4 is involved in the 4 catalytic steps of the histidine biosynthesis pathway (Fig. 3.2) and thus down-regulation (58% reduction) at each step thus led to a large effect (97% reduction) on the entire histidine biosynthesis. Increased expression of *HIS4* in *Kmmig1* was thus tested (Fig. 3.3). A DNA fragment of *TDH3-HIS4-ble*, in which *HIS4* was under the control of the promoter of *TDH3* as one of the strong promoters from *S. cerevisiae*, was constructed and introduced into the genome of *Kmmig1*. The growth of the recombinant on YNBG without histidine was compared with that of *Kmmig1* (Fig. 3.3a). *Kmmig1* exhibited almost no growth as expected, but the recombinant grew well like the wild type. Similarly, the recombinant showed growth equivalent to that of the wild type in the liquid minimal medium, but *Kmmig1* showed greatly retarded growth even with the addition of 0.01% (*w/v*) histidine to the medium (Fig. 3.3b). These results and the down-regulation of *HIS4* in *Kmmig1* (*MIG1*-disruption mutation) suggest that the down-regulation of *HIS4* in *Kmmig1* caused the defect of growth in the minimal medium and that Mig1 positively regulates *HIS4* expression. However, we cannot exclude the possibility that Mig1 regulates the *His4* expression via another regulator(s).

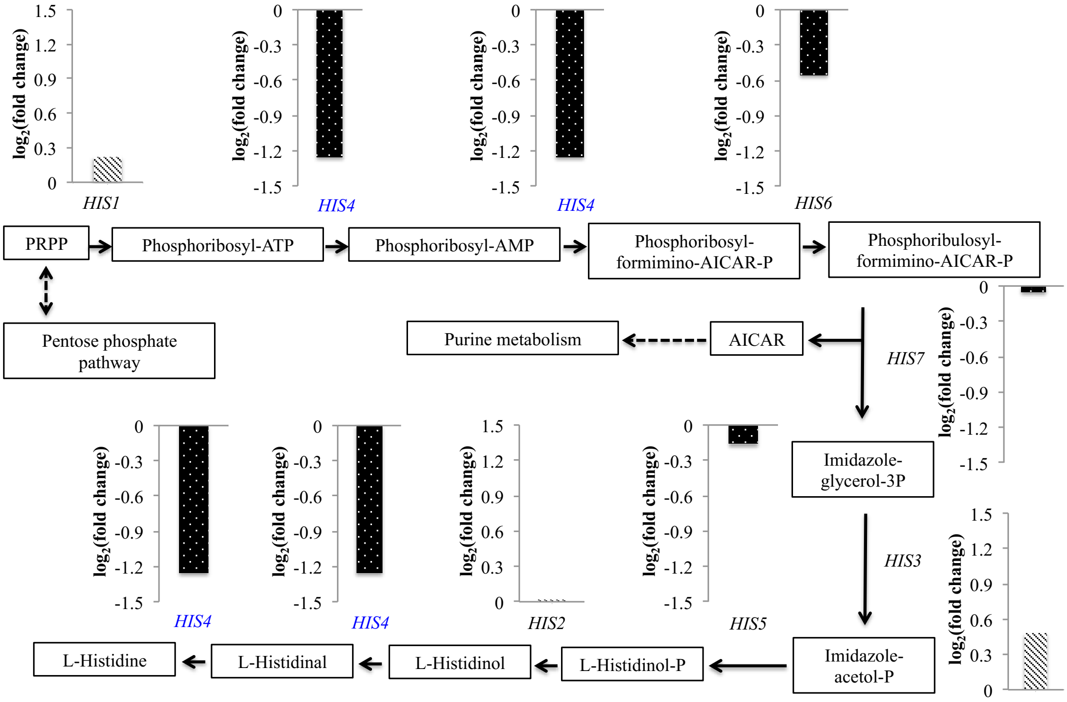


Fig. 3.2 Schematic representation of *MIG1*-disruption effects on the expression of *HIS* genes for histidine biosynthesis in *K. marxianus*. The ratio of transcriptional level of each gene in *Kmmig1* to that in the parental strain is presented by $\log_2$(fold change). The $\log_2$(fold change) values of the up-regulation are represented as backslash columns, while the down-regulation are as dotted columns. Further details are given in Supplementary Information File S4 (available online at https://doi.org/10.1038/s41598-019-46411-5).

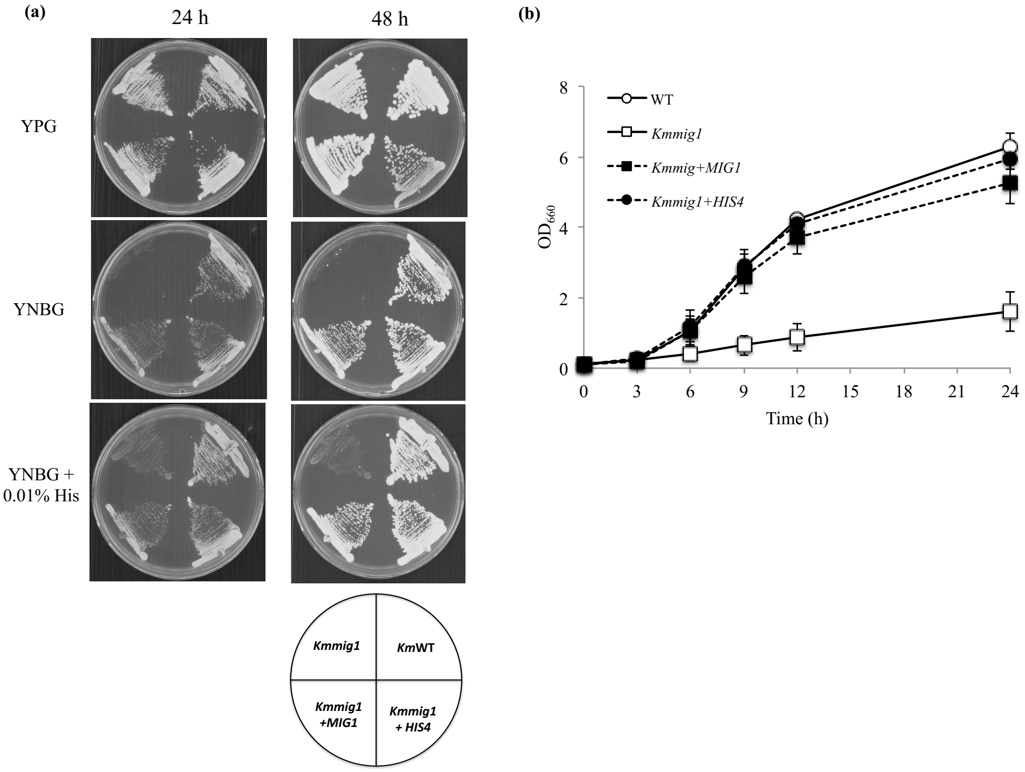


Fig. 3.3 Complementation experiments by increased expression of *HIS4* under the *S. cerevisiae TDH3* promoter in *Kmmig1*. Cells were pre-cultured in 5 ml of YPG at 30 °C under a shaking condition at 160 rpm for 15-18 h. (**a**) The cells were streaked on plates of YNBG, YNBG supplemented with 0.01% (*w/v*) histidine and YPG as a control. The plates were incubated at 30 ^{o}C and their photos were taken at 24 h and 48 h. (**b**) The pre-cultured cells were inoculated in 100 ml of YNBG and 0.01% (*w/v*) histidine at the final OD_{660} of 0.1 and cultivated at 30 °C under a shaking condition at 160 rpm for 24 h.

3.4.3 Effects of *MIG1*-disrupted mutation on expression of genomic genes

Since there were many significant DEGs caused by the *MIG1*-disrupted mutation, suggesting its global influence on the genomic genes in *K. marxianus*, these DEGs were subjected to a GO term enrichment test (Appendix Table S4). In the 689 up-regulated DEGs, the enriched GO terms for biological processes were related to the lipid catabolic process, cellular lipid catabolic process, fatty acid catabolic process, fatty acid oxidation, lipid oxidation, fatty acid beta-oxidation, fatty acid metabolic process, organic acid catabolic process, carboxylic acid catabolic process, small molecule catabolic process, monocarboxylic acid catabolic process, lipid modification, antibiotic metabolic process, glutamate metabolic process, and other processes. The enriched GO terms for cellular components included an integral component of the membrane, intrinsic component of the membrane, membrane part, peroxisome organelle, integral component of the peroxisome, peroxisomal matrix and intrinsic component of the peroxisome, cell wall, and other cellular components. The GO terms for molecular functions included oxidoreductase activity, catalytic activity, transmembrane transporter activity, hydrolase activity, transporter activity, coenzyme binding, and other molecular functions (Appendix Table S4).

On the other hand, in the 461 down-regulated DEGs, the enriched GO terms for biological processes included ribosome biogenesis, rRNA processing, ribonucleoprotein complex biogenesis, rRNA metabolic process, ncRNA processing, ncRNA metabolic process, glycolytic process, ATP generation from ADP, pyruvate biosynthetic process, nucleoside diphosphate metabolic process, purine nucleoside diphosphate metabolic process, purine ribonucleoside diphosphate metabolic process, and pyridine nucleotide biosynthetic process. The enriched GO terms for cellular components included the preribosome, nucleolus, small-subunit processome, ribonucleoprotein complex, nucleolar part, 90S preribosome, preribosome, large subunit precursor, nuclear lumen, cytosolic ribosome, cytosolic large ribosomal subunit, nucleolus, and nucleus. The enriched GO terms for molecular functions included snoRNA binding, RNA binding, rRNA binding, oxidoreductase acitivity, oxidoreductase activity, organic cyclic compound binding, heterocyclic compound binding, iron ion binding, coenzyme binding, and nucleic acid binding (Appendix Table S4).

The up-regulated and down-regulated DEGs were also mapped to the terms in the KEGG database (Appendix Table S5). The mapping analysis revealed that pathways related to the 689 up-regulated DEGs included metabolic pathways, biosynthesis of secondary metabolites, biosynthesis of antibiotics, carbon metabolism, autophagy, MAPK signaling pathway, biosynthesis of amino acids, meiosis, peroxisome, glyoxylate and dicarboxylate metabolism, spliceosome, fatty acid degradation, glycolysis/gluconeogenesis, glycerolipid metabolism, endocytosis, arginine and proline metabolism, citrate cycle (TCA cycle), glycine, serine, and threonine metabolism, tyrosine metabolism, phenylalanine metabolism, autophagy, pyruvate metabolism, purine metabolism, and pyrimidine metabolism. Pathways related to the 461 down-regulated DEGs included metabolic pathways, biosynthesis of secondary metabolites, biosynthesis of antibiotics, ribosome biogenesis in eukaryotes, biosynthesis of amino acids, carbon metabolism, glycolysis/gluconeogenesis, ribosome, purine metabolism, RNA transport, methane metabolism, starch and sucrose metabolism, cysteine and methionine metabolism, MAPK signaling pathway, galactose metabolism, RNA polymerase, cell cycle, glycine, serine and threonine metabolism, steroid biosynthesis, amino sugar and nucleotide sugar metabolism, pentose phosphate pathway, pyruvate metabolism, fatty acid metabolism, and pyrimidine metabolism.

To further understand the possible downstream relationship from Mig1, we explored significant DEGs for transcription factors (TFs) and TF-associated proteins (TF-APs) that are orthologues to those of *S. cerevisiae*, from the lists in Appendix Table S3 (Wu and Chen, 2007; Marion *et al.* 2004; Ozcan *et al.* 1996; Kim *et al.* 2003; Lafuente *et al.* 2000; Lakshmanan *et al.* 2003; Moriya and Johnston, 2004; Kurihara *et al.* 1996; Denis and Young, 1983; van Bakel *et al.* 2008; Lesage *et al.* 1996; Vincent and Carlson, 1998). As a result, three down-regulated genes corresponding to *SFP1*, *RGT1*, and *MTH1* in *S. cerevisiae* and four up-regulated genes corresponding to *KAR4*, *ADR1, GSM1,* and *SIP4* in *S. cerevisiae* were found, and they were subjected to GO and KEGG analyses but no item in KEGG pathway was found for all TFs (Appendix Table S1). Based on the physiological functions of these TFs in *S. cerevisiae* (Appendix Table S2), it is assumed that KLMA_60316 (Rgt1) and KLMA_30237 (Mth1) function under a glucose-rich condition, whereas KLMA_60316 (Rgt1), KLMA_20117 (Adr1), KLMA_20140 (Gsm1), and KLMA_30166 (Sip4) function under a glucose-starved condition. Such glucose level-specific manners might indicate the link with Mig1. The remaining two, KLMA_40457 (Sfp1) and KLMA_10029 (Kar4), presumably regulate cognate genes under a condition unrelated to glucose level. These putative TFs could be involved in expression regulation of the expression of genes included in terms of GO (Appendix Table S1). Notably, in *S. cerevisiae*, Sip4 expression is negatively regulated by Mig1 via Cat8 (Turcotte *et al.* 2010), Sip4 activates the expression of many genes for gluconeogenesis (Roth *et al.*

2004), and the expression of 108 genes is significantly decreased in the absence of Adr1 (Young *et al*. 2003). Taken together, the results indicate the possibility that Mig1 regulates many genes directly or indirectly via various TFs including the seven putative TFs described above.

3.4.4 Effects of *MIG1*-disrupted mutation on central carbon metabolism

Since Mig1 is known to be a regulator of glucose repression in *K. marxianus* (Nurcholis *et al*. 2019; Schabort *et al*. 2018) as well as *S. cerevisiae* (Kayikci and Nielsen 2015; Cai *et al*. 2018), the effects of *MIG1*-disrupted mutation on central carbon metabolism were focused on. The mutation caused changes in the transcriptional levels of most of the genes involved in central carbon metabolism (Fig. 3.4 and Appendix Table S3). Most of the genes for the glycolytic pathway including *RAG5* for hexokinase, *RAG2* for glucose-6-phosphate isomerase, *PFK1* and *PFK2* for phosphofructokinase, *FBA1* for fructose-bisphosphate aldolase, *GAP1* for glyceraldehyde-3-phosphate dehydrogenase 1, *GAP3* for glyceraldehyde-3-phosphate dehydrogenase 3, *PGK* for phosphoglycerate kinase, *GPM1* for phosphoglycerate mutase 1, *GPM3* for phosphoglycerate mutase 3, *ENO* for enolase and *PYK1* for pyruvate kinase were significantly down-regulated in *Kmmig1*. In addition, *PDC1* for pyruvate decarboxylase, *ADH1* for alcohol dehydrogenase 1 and *ADH2* for alcohol dehydrogenase 2, which are related to ethanol production (Lertwattanasakul *et al*. 2007; Lertwattanasakul *et al*. 2009), and *GPD1* for glycerol-3-phosphate dehydrogenase and *RHR2* for glycerol-3-phosphatase 1, which are related to glycerol production (Petelenz-Kurdziel *et al*. 2013; Gao *et al*. 2015), were down-regulated. On the other hand, *FBP1* for fructose-1,6-bisphosphatase, which is involved in gluconeogenesis, was significantly up-regulated. Many genes for ethanol degradation, TCA cycle and fatty acid degradation, including *ADH3*, *ADH6*, *ACS1*, *CIT1*, *CIT3*, *ACO2b*, *IDP1*, *MDH2*, *MDH3*, *POX1*, *ACAD11* and *POT1* encoding alcohol dehydrogenase 3, alcohol dehydrogenase 6, acetyl-coenzyme A synthetase 1, citrate synthase 1, citrate synthase 3, aconitate hydratase, isocitrate dehydrogenase, malate dehydrogenase 2, malate dehydrogenase 3, acyl-coenzyme A oxidase, acyl-CoA dehydrogenase family member 11 and 3-ketoacyl-CoA thiolase, respectively, were also significantly up-regulated (Fig. 3.4 and Appendix Table S3).

3.5 Discussion

Physiological analysis of the effect of *MIG1*-disrupted mutation indicated the possibility that Mig1 is required for histidine biosynthesis (Nurcholis *et al.* 2019). In this study, in order to understand the role of Mig1 in histidine biosynthesis, genome-wide expression analysis was performed. Among seven *HIS* genes for enzymes related to the histidine biosynthesis pathway, only the expression level of *HIS4* in the *MIG1*-disrupted mutant was significantly down-regulated compared to that in the parental strain. The level of reduction of *HIS4* expression was only 58%, but it is assumed that such an intermediate level of the effect becomes very strong in total to cause the defect of growth in a minimal medium because His4 catalyzes 4 steps in the histidine biosynthesis pathway. This assumption was examined by increased expression of *HIS4* in *Kmmig1*, resulting in the recovery of growth in the minimal medium without the addition of histidine (Fig. 3). Consequently, it is thought that Mig1 is a positive regulator for *HIS4* and thus for histidine biosynthesis. It is noteworthy that the regulation of histidine biosynthesis in *K. marxianus* by Mig1 creates a novel and effective mechanism targeting one gene, *HIS4*, of which the product is involved in 4 catalytic steps of histidine biosynthesis. Interestingly, *S. cerevisiae* has three His4-involved steps in the histidine biosynthesis pathway (Donahue *et al.* 1982), though its regulation by Mig1 remains to be investigated. On the other hand, Hua *et al.* reported that *Kmmig1* was isolated on a minimal medium (SD medium) (Hua *et al.* 2019). It is possible that they took slowly formed colonies when *Kmmig1* was screened because we noticed that *Kmmig1* is able to grow on a minimal medium, though very slowly (Nurcholis *et al.* 2019 and Fig 3.3). Alternatively, their *Kmmig1* might have an additional suppressor mutation that allowed it to grow on the SD medium or the histidine-auxotrophoc phenotype of *Kmmig1* might be strain-specific.

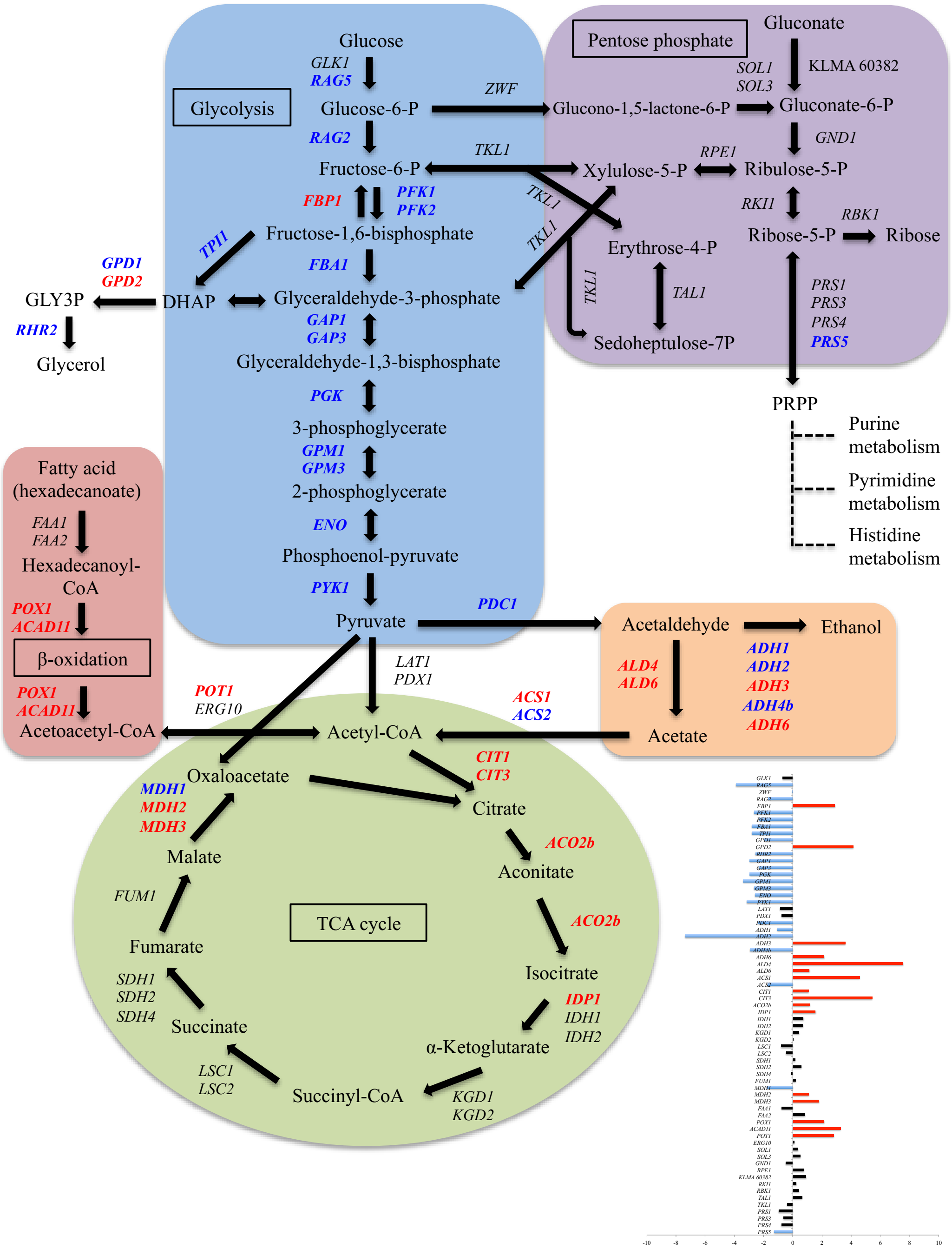


Fig. 3.4 Expressional change of genes for the central carbon metabolic network in *Kmmig1*. The ratio of transcriptional level of each gene in *Kmmig1* to that in the parental strain that is presented by $\log_2$(fold change) is shown at the right bottom side. Red coloured bars: significantly up-regulated genes in *Kmmig1*; blue coloured bars: significantly down-regulated genes; black coloured bars: not significantly changed genes. In the central carbon metabolic network, significantly up-regulated and down-regulated genes in *Kmmig1* are represented in red and blue, respectively, and genes that were not significantly changed in *Kmmig1* are represented in black. Further details are given in Supplementary Information File S4 (available online at https://doi.org/10.1038/s41598-019-46411-5).

In *S. cerevisiae*, Mig1 has been extensively analysed and shown to be a key regulator as a complex with other proteins including Hxk2 for glucose repression (Ahuatzi *et al*. 2004; Ahuatzi *et al*. 2007). Surprisingly, the present study indicated the possibility that Mig1 is a global regulator for genomic genes in *K. marxianus*. Transcriptome analysis of the *MIG1*-disrupted mutant and its parental strain was performed with RNAs prepared from cells that were cultivated in a minimal medium containing galactose as a sole carbon source (under a condition with no glucose repression). The analysis suggests that Mig1 acts as a positive regulator for most genes (except *GLK1* and *FBP1*) in glycolysis and as a negative regulator for many genes in the TCA cycle and fatty acid degradation (Fig. 3.4). In anabolic pathways, Mig1 may activate the expression of genes for biosynthesis of secondary metabolites, antibiotics and amino acids, ribosome biogenesis, rRNA processing, and purine and pyrimidine metabolism and inhibit the expression of genes for biosynthesis of secondary metabolites, antibiotics and amino acids, and for gluconeogenesis. Considering that the medium still contained a sufficient amount of galactose under the condition in which RNA was prepared for RNA-Seq and considering that Mig1 seems to activate genes for the ethanol synthesis pathway in addition to genes for glycolysis and to inhibit genes for the TCA cycle, it is likely that Mig1 is a crucial regulation factor to enhance ethanol production in *K. marxianus*.

In addition, as shown in KEGG analysis, the down-regulation of genes for ribosome biogenesis, biosynthesis of amino acids, carbon metabolism, ribosome, RNA transport, RNA polymerase and purine and pyrimidine metabolism in *Kmmig1* suggests that Mig1 promotes cell proliferation. There are some pathways that seem to be subjected to both positive regulation and negative regulation by Mig1; for example, biosynthesis of secondary metabolites, antibiotics, amino acids, purine and pyrimidine. It is assumed that such a dual regulation by Mig1 contributes to the fine tuning of these pathways or balanced metabolism in cells. Further analysis of the regulation of individual gene expression in these pathways may lead to an understanding of the physiological importance of Mig1-directed regulation in each pathway.

3.6 Conclusion

We conducted genome wide expression analysis of disrupted mutants of *MIG1* (*Kmmig1*) and its parental strain *K. marxianus.* Our investigation showed that *HIS4* in seven *HIS* genes for histidine biosynthesis was significantly down-regulated in *Kmmig1*. Consistently, introduction of *HIS4* into *Kmmig1* suppresed the requirement of histidine. Moreover, our result also showed that Mig1 is a global regulator which directly or indirectly involved in the expression of more than 1,000 DEGs.

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LIST OF PUBLICATIONS

1. **Functional analysis of Mig1 and Rag5 as expressional regulators in thermotolerant yeast *Kluyveromyces marxianus***

   Mochamad Nurcholis, Sukanya Nitiyon, Suprayogi, Nadchanok Rodrussamee, Noppon Lertwattanasakul, Savitree Limtong, Tomoyuki Kosaka, Mamoru Yamada

   Applied Microbiology and Biotechnology, 2019, 103:395-410, DOI: 10.1007/s00253-018-9462-y

2. ***MIG1* as a positive regulator for histidine biosynthetic pathway and as a global regulator in thermotolerant yeast *Kluyveromyces marxianus***

   Mochamad Nurcholis, Masayuki Murata, Savitree Limtong, Tomoyuki Kosaka, Mamoru Yamada

   Scientific Reports, 2019, 9:9926, DOI: 10.1038/s41598-019-46411-5

APPENDIX

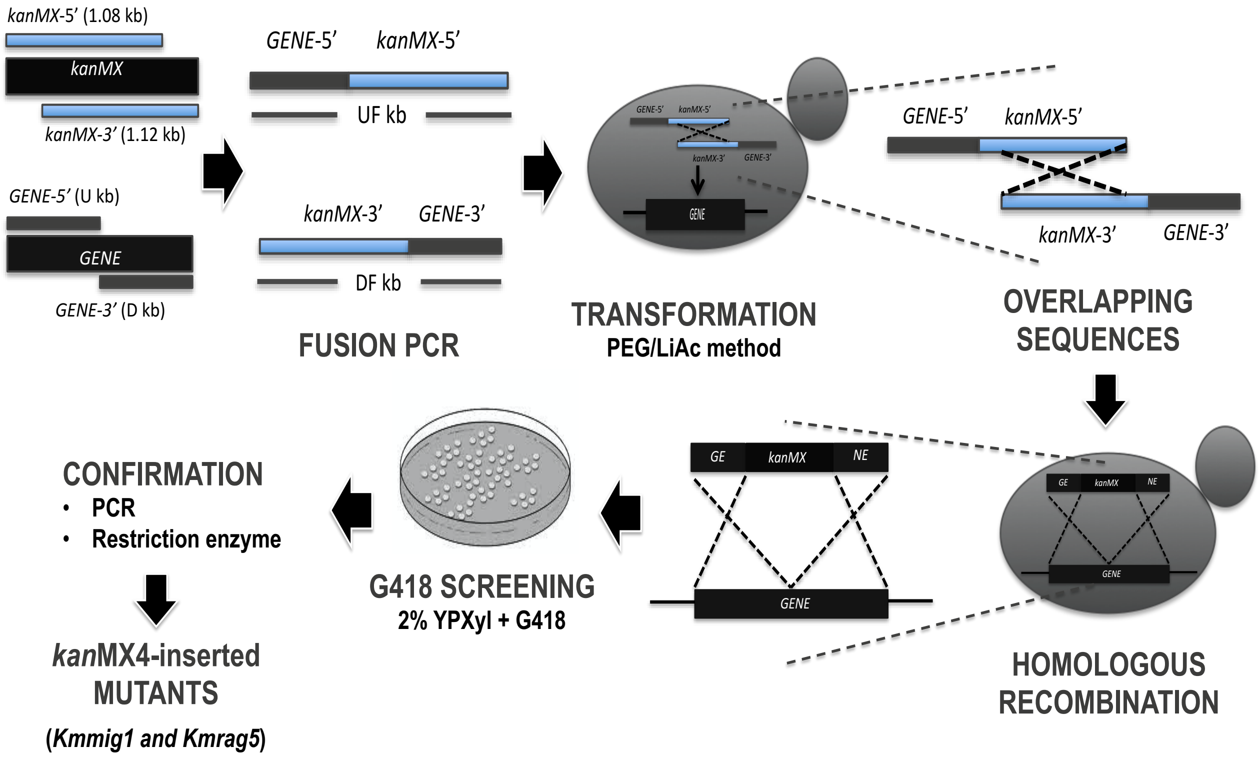

Fig. S1 Procedure of construction of disrupted mutants of *Kmmig1* and *Kmrag5*

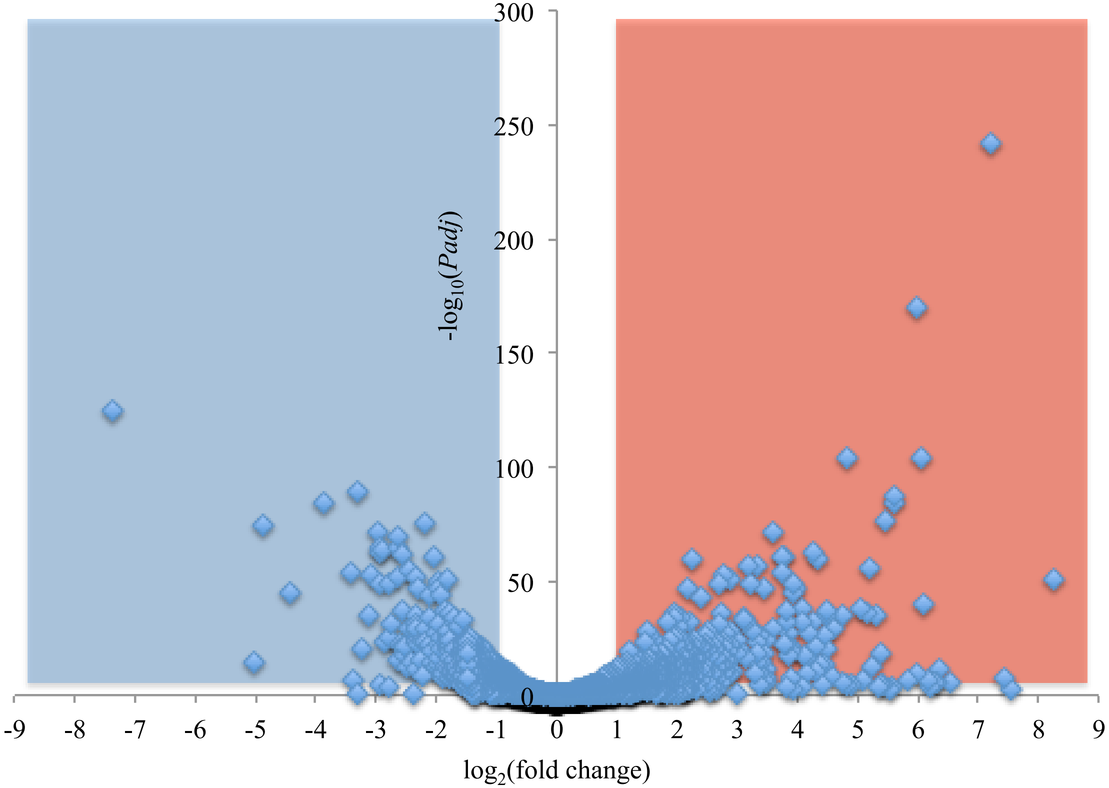

Fig. S2 Diagram plots of differentially expressed genes (DEGs) for *Kmmig1* and the parental strain of *K. marxianus*. Genes with adjusted *P* values (*Padj*) less than 0.01 and log$_2$(fold change) values greater than 1 were assigned as differentially expressed. Red coloured bar: significantly up-regulated genes in *Kmmig1*; blue coloured bar: significantly down-regulated genes in *Kmmig1*.

Table S1. Transcription factors (TFs) that are assumed to be under the control of *MIG1* in *K. marxianus*

TFs		Query coverage [a] (%)	Identity [a] (%)	Analyses [b]	
S.cerevisiae	*K. marxianus*			DEGs [c]	GO terms
Sfp1	KLMA_40457 (Sfp1)	75	45	D	Organic cyclic compound binding, nucleic acid binding
Rgt1	KLMA_60316 (Rgt1)	56	33	D	Organic substance metabolic process, metabolic process, small molecule metabolic process, primary metabolic process, hexose metabolic process, monosaccharide metabolic process, carbohydrate metabolic process, glucose metabolic process, nucleus, organic cyclic compound binding, heterocyclic compound binding, nucleic acid binding, transition metal ion binding
Mth1	KLMA_30237 (Mth1)	99	50	D	-
Kar4	KLMA_10029 (Kar4)	89	70	U	Reproductive process, multi organism process, response to pheromone
Adr1	KLMA_20117 (Adr1)	70	32	U	-
Gsm1	KLMA_20140 (Gsm1)	99	37	U	Drug metabolic process, transition metal ion binding, zinc ion binding
Sip4	KLMA_30166 (Sip4)	80	31	U	Transition metal ion binding, zinc ion binding

[a] Query coverage and identity when TF in *S. cerevisiae* was compared with the corresponding ortholog (https://blast.ncbi.nlm.nih.gov/Blast.cgi) in *K. marxianus*.

[b] These data are from Appendix Table S3 and S4

[c] D, significantly down-regulated by *MIG1* disruption; U, significantly up-regulated by *MIG1* disruption in *K. marxianus*.

"-" mean that the transcription-related factors were not included any items in GO terms.

Table S2. **Transcription factors (TFs) of *S. cerevisiae*, of which orthologs in *K. marxianus* are presumably located downstream of Mig1**

TFs [a]	Description/Function	Reference
Sfp1	A stress- and nutrient-sensitive regulator of ribosomal protein (RP) gene expression and biogenesis genes; Novel heat shock TFs and regulates RP gene expression in response to heat shock.	Wu and Chen, 2007; Marion *et al*. 2004
Rgt1	Glucose-responsive transcription factor; regulates expression of several glucose transporter (HXT) genes in response to glucose; bind to promoters and acts both as a transcriptional activator and repressor	Ozcan *et al*. 1996; Kim *et al*. 2003
Mth1	Negative regulator of the glucose-sensing signal transduction pathway; required for repression of transcription by Rgt1; interacts with Rgt1 and the Snf3 and Rgt2 glucose sensors.	Lafuente *et al*. 2000; Lakshmanan *et al*. 2003; Moriya and Johnston, 2004
Kar4	Acting at a subset of Ste12-inducible genes in the pheromone-dependent expression; a karyogamy-specific component; required for the induction of *KAR3* and *CIK1*.	Kurihara *et al*. 1996
Adr1	A carbon source-responsive zinc-finger transcription factor; required for transcription of the glucose-repressed genes for ethanol, glycerol and fatty acid utilization.	Young *et al*. 2003; Denis and Young, 1983
Gsm1	Putative zinc cluster protein of unknown function; proposed to be involved in the regulation of energy metabolism based on pattern of expression.	van Bakel *et al*. 2008
Sip4	C_6 zinc cluster transcriptional activator; binds to the carbon source-responsive element (CSRE) of gluconeogenic genes; involved in the positive regulation of gluconeogenesis; regulated by Snf1 protein kinase.	Roth *et al*. 2004; Lesage *et al*. 1996; Vincent and Carlson, 1998

[a] These TFs are shown in Table S1.

Table S3. Differentially expressed genes (DEGs) based on unique exon reads for *Kmmig1* and the parental strain of *K. marxianus*

Down-regulated DEGs

	UniProt _gene	Product	baseMean	log$_2$FoldChange	lfcSE	stat	pvalue	padj
KLMA_10031	SPB1	adoMet-dependent rRNA methyltransferase SPB1	894.1376186	-1.041340272	0.151229212	-6.885840745	5.74E-12	5.45E-11
KLMA_10035	APA2	5',5'''-P-1,P-4-tetraphosphate phosphorylase 2	2494.817491	-1.781132181	0.202374251	-8.801179868	1.35E-18	2.63E-17
KLMA_10050	GRH1	GRASP65 homolog protein 1	503.3257319	-1.190414472	0.171256722	-6.951052532	3.63E-12	3.53E-11
KLMA_10054	SRO9	RNA-binding protein SRO9	611.7488969	-1.114073206	0.21231716	-5.247212269	1.54E-07	7.80E-07
KLMA_10065	HIS4	histidine biosynthesis trifunctional protein	4388.328621	-1.255591334	0.218378988	-5.749597737	8.95E-09	5.49E-08
KLMA_10068		SH3 super family	262.6397174	-1.074486655	0.196817564	-5.459302696	4.78E-08	2.62E-07
KLMA_10078	LPP1	lipid phosphate phosphatase 1	129.9127625	-1.197386511	0.260387051	-4.598487158	4.26E-06	1.70E-05
KLMA_10079	SAM2	S-adenosylmethionine synthetase 2	11798.21897	-1.760611861	0.279709217	-6.294436356	3.09E-10	2.30E-09
KLMA_10083	RpL37a	ribosomal_L37e super family	2271.817758	-1.089999768	0.226536375	-4.811588288	1.50E-06	6.51E-06
KLMA_10100	CCN1	G1/S-specific cyclin CLN1	1269.053296	-1.427923225	0.168394807	-8.479615547	2.26E-17	3.90E-16
KLMA_10106	CAN1	arginine permease	5708.034862	-1.807486782	0.253320546	-7.135176405	9.67E-13	1.01E-11
KLMA_10107	LYP1	lysine-specific permease	5983.841715	-1.514040177	0.173318901	-8.735574526	2.42E-18	4.61E-17
KLMA_10113		uncharacterized membrane protein YGL140C	1808.983135	-1.291808264	0.163264792	-7.912350527	2.53E-15	3.53E-14
KLMA_10134	RPA49	DNA-directed RNA polymerase I subunit RPA49	1455.520381	-1.12743058	0.150066316	-7.512882392	5.78E-14	6.91E-13
KLMA_10146		Zn2/Cys6 DNA-binding domain	1023.450608	-1.203074301	0.21121543	-5.69595839	1.23E-08	7.35E-08
KLMA_10153	ACO2	probable aconitate hydratase 2	1449.860785	-1.0319743	0.255734799	-4.035329977	5.45E-05	0.000172253
KLMA_10176	PRS5	ribose-phosphate pyrophosphokinase 5	1254.392765	-1.260334383	0.140589109	-8.964665833	3.11E-19	6.39E-18

	UniProt _gene	Product	baseMean	$\log_2$FoldChange	lfcSE	stat	pvalue	padj
KLMA_10179	GPD1	glycerol-3-phosphate dehydrogenase [NAD+] 1	12492.90635	-1.949083761	0.192187305	-10.14158434	3.61E-24	1.14E-22
KLMA_10182	GPM3	phosphoglycerate mutase 3	1336.33172	-2.640043092	0.169630591	-15.56348464	1.29E-54	1.75E-52
KLMA_10199	NOP1	rRNA 2'-O-methyltransferase fibrillarin	3741.071188	-1.370254553	0.287188493	-4.77127247	1.83E-06	7.84E-06
KLMA_10225	GSP1	GTP-binding nuclear protein GSP1/Ran	2556.470636	-1.164741274	0.187860029	-6.200048414	5.64E-10	4.12E-09
KLMA_10238		hypothetical protein	1688.529958	-2.064856886	0.216897084	-9.519984526	1.73E-21	4.17E-20
KLMA_10244	OLE1	acyl-CoA desaturase 1	35818.34597	-1.217264125	0.2834003	-4.29521114	1.75E-05	6.16E-05
KLMA_10245	SDS23	protein SDS23	967.0167794	-1.149009072	0.150233322	-7.648163922	2.04E-14	2.53E-13
KLMA_10255	SOH1	mediator of RNA polymerase II transcription subunit 31	47.88991982	-1.116590043	0.33823059	-3.301268652	0.000962487	0.002289715
KLMA_10278	DSS1	exoribonuclease II	632.2214344	-1.171570409	0.155075124	-7.554857164	4.19E-14	5.09E-13
KLMA_10282	PNO1	pre-rRNA-processing protein PNO1	648.2827106	-1.00970132	0.153042454	-6.597524355	4.18E-11	3.54E-10
KLMA_10293	UTP5	U3 small nucleolar RNA-associated protein 5	804.9826495	-1.131332665	0.178744246	-6.329337522	2.46E-10	1.87E-09
KLMA_10294	HPT1	hypoxanthine-guanine phosphoribosyltransferase	1563.401708	-1.345243433	0.164324672	-8.186496998	2.69E-16	4.14E-15
KLMA_10305		probable phosphoglycerate mutase YOR283W	612.253329	-1.270593148	0.173451212	-7.325363331	2.38E-13	2.66E-12
KLMA_10317	GUA1	GMP synthase	7461.181859	-1.429034677	0.240991103	-5.929823373	3.03E-09	2.00E-08
KLMA_10320	GAS3	probable 1,3-beta-glucanosyltransferase GAS3	4180.83398	-1.082675114	0.175674372	-6.162965613	7.14E-10	5.17E-09
KLMA_10334	SDA1	protein SDA1	947.443798	-1.249471405	0.148609505	-8.407748891	4.18E-17	7.09E-16
KLMA_10341	PFK1	6-phosphofructokinase subunit alpha	15263.93002	-2.640809857	0.146797317	-17.9894968	2.35E-72	7.19E-70
KLMA_10348	TIF1	ATP-dependent RNA helicase eIF4A	13443.44369	-1.063102703	0.19713128	-5.392866628	6.93E-08	3.70E-07
KLMA_10356	BIO2	biotin synthase	1051.91972	-1.968773362	0.228226209	-8.626412243	6.33E-18	1.16E-16
KLMA_10376	RPL17B	ribosomal_L22	9005.104751	-1.091349165	0.215241096	-5.070356853	3.97E-07	1.87E-06

	UniProt _gene	Product	baseMean	log$_2$FoldChange	lfcSE	stat	pvalue	padj
KLMA_10388	EBP2	rRNA-processing protein EBP2	707.6693472	-1.001755274	0.15198119	-6.591310915	4.36E-11	3.68E-10
KLMA_10404	ATX2	zinc/iron permease	451.0110051	-1.411507447	0.196855834	-7.170259682	7.49E-13	7.88E-12
KLMA_10418	RPF2	ribosome biogenesis protein RPF2	789.5340646	-1.194914251	0.167115114	-7.150246442	8.66E-13	9.06E-12
KLMA_10425	RSE1	pre-mRNA-splicing factor RSE1	839.5689713	-1.039923533	0.153244909	-6.786023366	1.15E-11	1.06E-10
KLMA_10427	GAL80	galactose/lactose metabolism regulatory protein GAL80	7563.520855	-2.203361321	0.116997722	-18.83251466	4.09E-79	1.66E-76
KLMA_10458	KYE1	enoate reductase 1	11211.97802	-3.089059005	0.196356545	-15.73188717	9.14E-56	1.31E-53
KLMA_10462	ENO	enolase	197772.0979	-2.567456121	0.260257513	-9.865060527	5.90E-23	1.63E-21
KLMA_10475	TNA1	high-affinity nicotinic acid transporter	7522.923924	-2.212869687	0.365482442	-6.054653876	1.41E-09	9.72E-09
KLMA_10483	MES1	methionyl-tRNA synthetase	3012.908779	-1.187524774	0.219172921	-5.418209361	6.02E-08	3.26E-07
KLMA_10484	HAS1	ATP-dependent RNA helicase HAS1	1447.493641	-1.560360676	0.150763737	-10.34970814	4.20E-25	1.44E-23
KLMA_10487	TDA1	probable serine/threonine-protein kinase YMR291W	1275.696206	-2.527690544	0.251804151	-10.0383196	1.03E-23	3.08E-22
KLMA_10491	YTA7	TAT-binding homolog 7	2061.769883	-1.200762067	0.155863504	-7.703933508	1.32E-14	1.69E-13
KLMA_10500	LIP1	ceramide synthase subunit LIP1	319.1530522	-1.063545974	0.201249428	-5.2847155	1.26E-07	6.44E-07
KLMA_10513	FAU1	5-formyltetrahydrofolate cyclo-ligase	607.5176754	-1.11488885	0.356432484	-3.127910335	0.001760539	0.003961061
KLMA_10517		uncharacterized protein conserved in bacteria	341.3432005	-1.039624013	0.204117391	-5.093265246	3.52E-07	1.67E-06
KLMA_10532	TAT2	tryptophan permease	2532.393485	-1.641427223	0.245264041	-6.692490338	2.19E-11	1.93E-10
KLMA_10540	PGK	phosphoglycerate kinase	70718.63609	-2.93840867	0.19365807	-15.1731796	5.32E-52	6.19E-50
KLMA_10548	CWH43	protein CWH43	2190.992292	-1.535375958	0.198234778	-7.745240115	9.54E-15	1.26E-13
KLMA_10577	SCS7	inositolphosphorylceramide-B C-26 hydroxylase	3204.286643	-1.246707238	0.257166296	-4.847864038	1.25E-06	5.48E-06
KLMA_10578		uncharacterized protein YML108W	64.10315166	-1.474618504	0.3451787	-4.272043744	1.94E-05	6.79E-05
KLMA_10612	PRY2	protein PRY1	530.6555327	-1.362221242	0.23093505	-5.898720198	3.66E-09	2.41E-08
KLMA_10654	FUR4	uracil permease	773.4095232	-1.425127077	0.201635513	-7.067837669	1.57E-12	1.58E-11

	UniProt _gene	Product	baseMean	log_2FoldChange	lfcSE	stat	pvalue	padj
KLMA_10660	SCO1	SCO	1108.363623	-1.497905229	0.187879282	-7.972700419	1.55E-15	2.24E-14
KLMA_10671	OCA5	uncharacterized protein YHL029C	1838.009208	-2.334900529	0.192646091	-12.12015526	8.26E-34	4.58E-32
KLMA_10677	MET17	protein MET17	14501.85954	-1.556866639	0.284175473	-5.478539793	4.29E-08	2.37E-07
KLMA_10692	MSW1	tryptophanyl-tRNA synthetase	341.7188264	-1.374654685	0.235742252	-5.831176524	5.50E-09	3.50E-08
KLMA_10704	bioA	uncharacterized aminotransferase C1771.03c	370.0329324	-1.333477257	0.275883841	-4.833473586	1.34E-06	5.85E-06
KLMA_10711	TAH11	hypothetical protein	277.7064567	-1.340055436	0.211288249	-6.342309354	2.26E-10	1.73E-09
KLMA_10735	FUR1	uracil phosphoribosyltransferase	1014.279239	-1.684360617	0.2655921	-6.34190783	2.27E-10	1.73E-09
KLMA_10747	AAH1	adenosine deaminase	752.6387687	-1.529148165	0.169350465	-9.029489	1.72E-19	3.63E-18
KLMA_10758	GCR1	glycolytic genes transcriptional activator GCR1	2710.667128	-2.895389133	0.16785961	-17.24887324	1.14E-66	2.93E-64
KLMA_10763	RAG2	glucose-6-phosphate isomerase	29864.27498	-1.669829927	0.240537597	-6.942074536	3.86E-12	3.75E-11
KLMA_10768	RIM2	mitochondrial carrier protein RIM2	567.3929963	-1.090510705	0.161955789	-6.73338514	1.66E-11	1.49E-10
KLMA_10770		hypothetical protein	10549.00849	-1.036111586	0.257178933	-4.028757613	5.61E-05	0.000176341
KLMA_10791	NOG1	nucleolar GTP-binding protein 1	2408.612156	-1.242491891	0.125973229	-9.863142387	6.01E-23	1.65E-21
KLMA_10832	URA1	dihydroorotate dehydrogenase	2949.733803	-2.939976881	0.168742333	-17.42287682	5.53E-68	1.59E-65
KLMA_20023	TPS2	trehalose-phosphatase	8094.628903	-1.071475723	0.161166816	-6.648240316	2.97E-11	2.56E-10
KLMA_20052		uncharacterized membrane protein YGR149W	538.5182779	-1.336557248	0.307551506	-4.345799717	1.39E-05	4.99E-05
KLMA_20054	RPL24	60S ribosomal protein L24	7955.338496	-1.102117706	0.213931268	-5.151737357	2.58E-07	1.25E-06
KLMA_20074	TSL1	trehalose synthase complex regulatory subunit TPS3	3506.881249	-1.504207374	0.153457654	-9.802100662	1.10E-22	2.96E-21
KLMA_20090		ras-related protein rapC	242.6519106	-1.06919232	0.190190731	-5.62168468	1.89E-08	1.10E-07
KLMA_20098	GPM1	phosphoglycerate mutase 1	34135.68355	-3.402956455	0.214844014	-15.83919601	1.67E-56	2.55E-54
KLMA_20107		jmjC super family	669.2382984	-1.270327818	0.159901055	-7.944461769	1.95E-15	2.75E-14
KLMA_20126	UTP13	U3 small nucleolar RNA-associated protein 13	822.633694	-1.174086402	0.18342692	-6.40084019	1.55E-10	1.21E-09

	UniProt _gene	Product	baseMean	log_2FoldChange	lfcSE	stat	pvalue	padj
KLMA_20138	RPC37	DNA-directed RNA polymerase III subunit rpc5	354.7554812	-1.090769118	0.178978361	-6.094418958	1.10E-09	7.73E-09
KLMA_20139	DBP7	ATP-dependent RNA helicase DBP7	535.6351908	-1.317599917	0.157425612	-8.369666804	5.78E-17	9.53E-16
KLMA_20147	UTP15	U3 small nucleolar RNA-associated protein 15	844.0264385	-1.2804268	0.17974385	-7.123619543	1.05E-12	1.08E-11
KLMA_20157	HSL1	probable serine/threonine-protein kinase HSL1	1173.692509	-1.001189911	0.166301853	-6.020317239	1.74E-09	1.18E-08
KLMA_20158	ADH4	alcohol dehydrogenase 4	2997.662752	-2.936023481	0.63087214	-4.653912092	3.26E-06	1.33E-05
KLMA_20159	UTP11	U3 small nucleolar RNA-associated protein 11	198.2393025	-1.07633911	0.203154343	-5.298134871	1.17E-07	6.02E-07
KLMA_20165	ADK1	adenylate kinase 1	2572.406413	-1.308084245	0.193339052	-6.765752861	1.33E-11	1.20E-10
KLMA_20173	ARX1	probable metalloprotease ARX1	822.220041	-1.823384132	0.170328951	-10.70507464	9.64E-27	3.89E-25
KLMA_20186		conserved hypothetical protein	846.7099628	-1.515573244	0.340859546	-4.446327707	8.74E-06	3.26E-05
KLMA_20192	NOP53	ribosome biogenesis protein NOP53	716.284206	-1.001363292	0.209191493	-4.786826077	1.69E-06	7.30E-06
KLMA_20239	RMD9	protein RMD9	7714.160346	-1.822888312	0.118354418	-15.40194562	1.59E-53	1.99E-51
KLMA_20268	RPS2	40S ribosomal protein S2	17354.0792	-1.106138147	0.271643009	-4.072028766	4.66E-05	0.000149652
KLMA_20276	MET13	methylenetetrahydrofolate reductase 2	1161.753648	-1.848996539	0.242017053	-7.639943198	2.17E-14	2.69E-13
KLMA_20288	CYS4	cystathionine beta-synthase	3781.141055	-1.059017729	0.217273349	-4.874126239	1.09E-06	4.83E-06
KLMA_20305	SHM2	serine hydroxymethyltransferase	12779.74086	-1.40802017	0.318385505	-4.422375229	9.76E-06	3.62E-05
KLMA_20308	ERG3	c-5 sterol desaturase	3994.822075	-2.350025826	0.184404233	-12.74388218	3.37E-37	2.32E-35
KLMA_20320	NOP58	nucleolar protein 58	4632.938909	-1.112204874	0.189728491	-5.862086747	4.57E-09	2.94E-08
KLMA_20323	SLY41	uncharacterized transporter SLY41	504.3726713	-1.045702615	0.144484308	-7.237482274	4.57E-13	4.96E-12
KLMA_20326	MCH5	riboflavin transporter MCH5	766.2728748	-1.126854228	0.244961468	-4.600128491	4.22E-06	1.68E-05
KLMA_20331	GAL7	galactose-1-phosphate uridylyltransferase	18497.94383	-1.80911301	0.157175713	-11.51013077	1.17E-30	5.85E-29
KLMA_20332	GAL10	bifunctional protein GAL10	41677.65387	-2.64693837	0.1526667	-17.33802047	2.43E-67	6.59E-65

	UniProt _gene	Product	baseMean	$\log_2$FoldChange	lfcSE	stat	pvalue	padj
KLMA_20333	GAL1	galactokinase	58630.29623	-1.767183527	0.167155082	-10.57211967	4.01E-26	1.56E-24
KLMA_20341	FHL1	pre-rRNA-processing protein FHL1	642.671196	-1.08550499	0.142091016	-7.639504733	2.18E-14	2.70E-13
KLMA_20354	CYS3	cystathionine gamma-lyase	3530.015886	-1.702415507	0.225747458	-7.541238878	4.66E-14	5.64E-13
KLMA_20355		60S acidic ribosomal protein P2-alpha	3098.008596	-1.018838116	0.267552291	-3.807996238	0.000140097	0.000406557
KLMA_20359	NOP12	nucleolar protein 12	726.4948091	-1.152400867	0.15440536	-7.463477098	8.43E-14	9.85E-13
KLMA_20374	CCC2	copper-transporting ATPase	1570.859465	-1.127814871	0.146436487	-7.701733992	1.34E-14	1.71E-13
KLMA_20375		SERF-like protein YDL085C-A	42.39041633	-1.176082281	0.32142361	-3.658979127	0.000253222	0.000689374
KLMA_20392		delta(12) fatty acid desaturase	1779.345069	-1.299013656	0.200102479	-6.491741941	8.48E-11	6.87E-10
KLMA_20411	ENP1	essential nuclear protein 1	788.440287	-1.550890202	0.1612715	-9.616641523	6.80E-22	1.69E-20
KLMA_20417	CLN2	G1/S-specific cyclin CLN2	2318.131598	-1.561326802	0.162464822	-9.610245379	7.24E-22	1.79E-20
KLMA_20429	UBP3	ubiquitin carboxyl-terminal hydrolase 3	983.2670094	-1.051630983	0.136759878	-7.689616271	1.48E-14	1.87E-13
KLMA_20478	CBF5	centromere/microtubule-binding protein CBF5	2484.101399	-1.442347896	0.170367375	-8.466103879	2.54E-17	4.36E-16
KLMA_20481		RFX-like DNA-binding protein RFX1	382.6192262	-1.550990371	0.178886251	-8.670260362	4.31E-18	8.10E-17
KLMA_20482	RLP7	ribosome biogenesis protein RLP7	960.2710059	-1.169461129	0.161215197	-7.254037763	4.05E-13	4.43E-12
KLMA_20495	RPL22A	60S ribosomal protein L22-A	5880.589439	-1.008483955	0.272518312	-3.700609875	0.000215082	0.000596852
KLMA_20508	UTP8	U3 small nucleolar RNA-associated protein 8	881.1440257	-1.15158208	0.170010562	-6.773591405	1.26E-11	1.14E-10
KLMA_20514	TPA1	PKHD-type hydroxylase TPA1	1664.224497	-1.840706513	0.14015262	-13.13358617	2.11E-39	1.67E-37
KLMA_20527	ERG28	ergosterol biosynthetic protein 28	817.0077082	-1.076349804	0.228112853	-4.718496967	2.38E-06	9.90E-06
KLMA_20551	CYP707A7	lanosterol 14-alpha demethylase	4390.081646	-2.248096093	0.26870506	-8.366407731	5.94E-17	9.77E-16
KLMA_20555	TDA3	UPF0673 membrane protein YHR009C	1691.317538	-1.234722031	0.156230636	-7.90320045	2.72E-15	3.76E-14
KLMA_20591	ORT1	mitochondrial ornithine carrier	383.6747024	-1.064601725	0.195270051	-5.451945755	4.98E-08	2.73E-07

	UniProt_gene	Product	baseMean	$\log_2$FoldChange	lfcSE	stat	pvalue	padj
		protein						
KLMA_20598	ADE2	phosphoribosylaminoimidazole carboxylase	2437.790869	-1.011415122	0.192585145	-5.251781615	1.51E-07	7.62E-07
KLMA_20619	YPR1	putative reductase 1	6119.972547	-1.424835339	0.157836111	-9.027308985	1.76E-19	3.69E-18
KLMA_20640	PET494	COX3 mRNA-specific translational activator PET494	298.0614566	-1.346240916	0.193345258	-6.962885607	3.33E-12	3.26E-11
KLMA_20682	MPP10	U3 small nucleolar RNA-associated protein MPP10	732.8990518	-1.175456754	0.200541231	-5.861421862	4.59E-09	2.95E-08
KLMA_20704	GAC1	CBM_21 super family	2229.471895	-1.089697847	0.16035681	-6.795457231	1.08E-11	9.93E-11
KLMA_20722	ERG9	squalene synthetase	1524.730457	-1.073329592	0.164012743	-6.544184145	5.98E-11	4.95E-10
KLMA_20724		non-structural maintenance of chromosome element 3	289.6123453	-1.033096314	0.196951131	-5.245444942	1.56E-07	7.87E-07
KLMA_20726	DTD1	D-tyrosyl-tRNA(Tyr) deacylase	248.7927933	-1.620871315	0.234780532	-6.903772225	5.06E-12	4.86E-11
KLMA_20739	IPI3	pre-rRNA-processing protein IPI3	543.5442432	-1.230722159	0.187826538	-6.552440204	5.66E-11	4.70E-10
KLMA_20742	RPS3	40S ribosomal protein S3	18707.71784	-1.209348225	0.213389013	-5.66734064	1.45E-08	8.58E-08
KLMA_20800	RPL5	60S ribosomal protein L5	16607.49874	-1.143255863	0.203990231	-5.6044638	2.09E-08	1.20E-07
KLMA_20810	NAN1	NET1-associated nuclear protein 1	1125.590175	-1.0791989	0.14019185	-7.698014528	1.38E-14	1.76E-13
KLMA_20829	PHO3	repressible acid phosphatase	212.4177213	-2.072868964	0.251559797	-8.240064528	1.72E-16	2.71E-15
KLMA_20830	LAC12	lactose permease	2951.356361	-1.068546837	0.295515535	-3.61587365	0.000299336	0.000799885
KLMA_30010	LAC12	lactose permease	87973.73377	-1.531320189	0.215348717	-7.110886058	1.15E-12	1.18E-11
KLMA_30041	LIA1	deoxyhypusine hydroxylase	1686.151989	-1.791583841	0.13694094	-13.08289432	4.12E-39	3.15E-37
KLMA_30042	HAM1	protein HAM1	117.4065179	-1.218970438	0.235257202	-5.181437289	2.20E-07	1.08E-06
KLMA_30060	MRT4	mRNA turnover protein 4	1076.365305	-1.276581439	0.200050155	-6.381306934	1.76E-10	1.37E-09
KLMA_30073	MUP1	high-affinity methionine permease	4850.640315	-1.48926886	0.284808485	-5.229018591	1.70E-07	8.53E-07
KLMA_30074	RSC2	chromatin structure-remodeling complex subunit RSC2	946.7547179	-1.079305519	0.206935367	-5.215664844	1.83E-07	9.11E-07
KLMA_30083	RRS1	regulator of ribosome biosynthesis	545.3308817	-1.082068847	0.200740114	-5.39039671	7.03E-08	3.74E-07

	UniProt _gene	Product	baseMean	log_2FoldChange	lfcSE	stat	pvalue	padj
KLMA_30099	PGM2	phosphoglucomutase-2	5880.12941	-2.578455332	0.151530137	-17.01612218	6.24E-65	1.38E-62
KLMA_30102	PMU1	uncharacterized protein YKL128C	200.0704808	-1.266567857	0.252099191	-5.024085378	5.06E-07	2.34E-06
KLMA_30119	CMC1	COX assembly mitochondrial protein	84.42747653	-1.047180325	0.337827607	-3.099747632	0.001936856	0.004311579
KLMA_30153	TEF3	elongation factor 3	47110.32692	-1.427915699	0.243184485	-5.871738474	4.31E-09	2.79E-08
KLMA_30154	GSH1	glutamate--cysteine ligase	1874.157265	-1.166272134	0.201179629	-5.797168134	6.74E-09	4.24E-08
KLMA_30158	PHS1	protein PHS1	401.8401563	-1.000033591	0.190843164	-5.240080749	1.61E-07	8.08E-07
KLMA_30190	IPI1	pre-rRNA-processing protein IPI1	144.5546233	-1.748560311	0.260685159	-6.707556039	1.98E-11	1.76E-10
KLMA_30199	RNR2	ribonucleoside-diphosphate reductase small chain 1	4227.229987	-1.641727582	0.137570151	-11.93374849	7.89E-33	4.24E-31
KLMA_30203	ATF1	alcohol O-acetyltransferase 1	756.5288467	-1.178988769	0.2055632	-5.735407738	9.73E-09	5.92E-08
KLMA_30204	ERG1	squalene monooxygenase	2894.071572	-2.532186591	0.277529151	-9.12403825	7.24E-20	1.57E-18
KLMA_30222	DCAF13	protein SOF1	483.3480997	-1.135962316	0.15170933	-7.487755131	7.01E-14	8.27E-13
KLMA_30225	MEU1	multicopy enhancer of UAS2	1514.957488	-1.005165319	0.200683553	-5.008707998	5.48E-07	2.53E-06
KLMA_30226		cytochrome c oxidase copper chaperone	99.2770965	-1.186117924	0.259083721	-4.578126016	4.69E-06	1.86E-05
KLMA_30229	DRS1	ATP-dependent RNA helicase DRS1	741.640094	-1.074469018	0.176084271	-6.102015869	1.05E-09	7.46E-09
KLMA_30237	MTH1	protein MTH1	3687.119688	-1.413858274	0.174415588	-8.10626099	5.22E-16	7.84E-15
KLMA_30249	ETT1	uncharacterized protein YOR051C	1211.130745	-2.199689104	0.209591232	-10.49513897	9.09E-26	3.27E-24
KLMA_30254	VHS3	protein VHS3	716.6044525	-1.024628019	0.148972753	-6.877955859	6.07E-12	5.74E-11
KLMA_30255	NOB1	20S-pre-rRNA D-site endonuclease NOB1	318.8515328	-1.370526364	0.181965009	-7.531812696	5.00E-14	6.02E-13
KLMA_30263		uncharacterized protein YKR075C	3946.516419	-1.949886075	0.131494533	-14.82864751	9.56E-50	9.94E-48
KLMA_30264	RPL3	60S ribosomal protein L3	29512.4949	-1.259745403	0.206617585	-6.096990267	1.08E-09	7.63E-09
KLMA_30274		fumarate reductase	4706.01433	-2.017987336	0.177751432	-11.35286122	7.18E-30	3.34E-28
KLMA_30299	PAB1	polyadenylate-binding protein	4014.179959	-1.037142845	0.188373632	-5.505775056	3.68E-08	2.05E-07
KLMA_30301	RLI1	translation initiation factor RLI1	3815.999557	-1.087977997	0.30089278	-3.615832851	0.000299384	0.000799885

	UniProt _gene	Product	baseMean	$\log_2$FoldChange	lfcSE	stat	pvalue	padj
KLMA_30308	MRPL15	54S ribosomal protein L15	753.7958276	-1.027668205	0.23353062	-4.400571568	1.08E-05	3.96E-05
KLMA_30317		hypothetical protein	194.7154789	-1.658654357	0.223164978	-7.432413344	1.07E-13	1.23E-12
KLMA_30320		glyco_transf_15 super family protein	1474.659223	-1.102956907	0.125386699	-8.796442615	1.41E-18	2.74E-17
KLMA_30326	PIB2	phosphatidylinositol-3-phosphate-binding protein 2	1450.37963	-1.000146419	0.151777524	-6.589555496	4.41E-11	3.71E-10
KLMA_30370	GSY2	glycogen [starch] synthase isoform 2	5494.268558	-1.800426946	0.15724387	-11.44990228	2.35E-30	1.15E-28
KLMA_30372	PDC2	protein PDC2	785.4351139	-1.452556056	0.133037834	-10.91836823	9.42E-28	4.03E-26
KLMA_30380	ALK2	serine/threonine-protein kinase Haspin homolog	645.3653109	-1.052260483	0.261393842	-4.025574881	5.68E-05	0.000178544
KLMA_30382	NSR1	nuclear localization sequence-binding protein	1943.958007	-1.937465975	0.135152663	-14.33538882	1.32E-46	1.19E-44
KLMA_30430	SUR2	sphingolipid C4-hydroxylase SUR2	3712.363003	-1.673043223	0.241755816	-6.920384592	4.50E-12	4.34E-11
KLMA_30432	BFR2	protein BFR2	552.761611	-1.336631053	0.148867766	-8.978646565	2.74E-19	5.67E-18
KLMA_30457	MEX67	mRNA export factor MEX67	841.0828889	-1.109745678	0.150322272	-7.382443477	1.55E-13	1.78E-12
KLMA_30477	SER3	D-3-phosphoglycerate dehydrogenase 1	5482.837952	-1.375391904	0.242944798	-5.661335055	1.50E-08	8.86E-08
KLMA_30493	PWP2	periodic tryptophan protein 2	1021.304607	-1.122810265	0.180940961	-6.205395713	5.46E-10	4.00E-09
KLMA_30495	YIH1	protein IMPACT homolog	283.4447524	-1.162596855	0.184354306	-6.306317861	2.86E-10	2.14E-09
KLMA_30509	HNM1	choline transport protein	3011.90997	-1.390899115	0.299624103	-4.642146941	3.45E-06	1.40E-05
KLMA_30511	DBP3	ATP-dependent RNA helicase DBP3	986.7386386	-1.299219512	0.176568378	-7.358166414	1.86E-13	2.11E-12
KLMA_30545	PAN5	2-dehydropantoate 2-reductase	506.4747077	-1.217637594	0.172228261	-7.069905882	1.55E-12	1.56E-11
KLMA_30548	RRP3	ATP-dependent rRNA helicase RRP3	551.0694452	-1.138539395	0.1881501	-6.051229295	1.44E-09	9.89E-09
KLMA_30549	SSF1	ribosome biogenesis protein SSF2	703.3910784	-1.031816114	0.188258313	-5.480852864	4.23E-08	2.34E-07
KLMA_30552	TIF32	eukaryotic translation initiation factor 3 subunit A	3923.256932	-1.354467046	0.185030317	-7.320243901	2.48E-13	2.75E-12
KLMA_30576	HAL9	halotolerance protein 9	2141.53969	-1.117462847	0.148886846	-7.505450475	6.12E-14	7.27E-13
KLMA_30587	VTS1	protein VTS1	1266.428536	-1.115326268	0.191641488	-5.819858092	5.89E-09	3.74E-08

	UniProt_gene	Product	baseMean	log$_2$FoldChange	lfcSE	stat	pvalue	padj
KLMA_30608	SCW4	probable family 17 glucosidase SCW10	841.0897549	-1.177969609	0.198809601	-5.9251143	3.12E-09	2.06E-08
KLMA_30614		hypothetical protein	2705.394871	-2.309608643	0.155990082	-14.80612493	1.34E-49	1.36E-47
KLMA_30615	RAD54	DNA repair and recombination protein RAD54	523.3188553	-1.113129404	0.158668099	-7.015458139	2.29E-12	2.26E-11
KLMA_30639	KSS1	mitogen-activated protein kinase KSS1	397.3341351	-1.265497808	0.164756414	-7.681023028	1.58E-14	1.99E-13
KLMA_30667	HKR1	herpes_gp2	1129.019862	-1.250665898	0.149171219	-8.384096525	5.11E-17	8.49E-16
KLMA_30671	ERG6	sterol 24-C-methyltransferase	1180.449648	-1.567822167	0.199873847	-7.844058604	4.36E-15	5.93E-14
KLMA_30687	SAH1	adenosylhomocysteinase	21362.46627	-1.085736862	0.307765516	-3.527805446	0.00041902	0.001078237
KLMA_30695	DUG1	cys-Gly metallodipeptidase DUG1	2219.749609	-1.428077942	0.158080635	-9.033857552	1.66E-19	3.52E-18
KLMA_30697	ADE5,7	bifunctional purine biosynthetic protein ADE5	8831.68422	-1.084240679	0.217316477	-4.989224434	6.06E-07	2.77E-06
KLMA_30698	MTO1	mitochondrial translation optimization protein 1	510.6959817	-1.010649563	0.151902426	-6.653281263	2.87E-11	2.48E-10
KLMA_30709	GUS1	glutamyl-tRNA synthetase	5844.806784	-1.222477478	0.166475288	-7.343296979	2.08E-13	2.34E-12
KLMA_30715		LCB5	1670.946983	-1.38565146	0.293371501	-4.723197235	2.32E-06	9.69E-06
KLMA_30717		uncharacterized protein YKR096W	3633.943524	-1.556861589	0.124530727	-12.50182687	7.30E-36	4.57E-34
KLMA_40014	BRE5	UBP3-associated protein BRE5	1660.215085	-1.22800495	0.157859186	-7.779116186	7.30E-15	9.69E-14
KLMA_40019	YCT1	uncharacterized transporter YLL055W	776.352917	-1.099552374	0.369693879	-2.974223907	0.002937307	0.006314175
KLMA_40064	RRB1	ribosome assembly protein RRB1	1126.08915	-1.389375542	0.18353406	-7.570123727	3.73E-14	4.55E-13
KLMA_40072	ECM16	probable ATP-dependent RNA helicase DHR1	465.1122678	-1.035697279	0.17073282	-6.06618739	1.31E-09	9.09E-09
KLMA_40080	RPL15B	60S ribosomal protein L15-B	7543.379505	-1.358425085	0.211284816	-6.429354987	1.28E-10	1.01E-09
KLMA_40102	ADH1	alcohol dehydrogenase 1	81946.03565	-1.065723927	0.20492703	-5.200504436	1.99E-07	9.81E-07
KLMA_40111	dsd1	dihydroceramide delta(4)-desaturase	790.6514724	-1.543497167	0.248915257	-6.20089417	5.61E-10	4.10E-09
KLMA_40115	HEM13	coproporphyrinogen-III oxidase	1507.255044	-1.976950314	0.248634657	-7.951225845	1.85E-15	2.62E-14

	UniProt _gene	Product	baseMean	log$_2$FoldChange	lfcSE	stat	pvalue	padj
KLMA_40123	BAP3	valine amino-acid permease	3547.357009	-2.478077914	0.321375815	-7.710841316	1.25E-14	1.61E-13
KLMA_40125	TPI1	triosephosphate isomerase	20614.28544	-2.799656701	0.185124719	-15.12308414	1.14E-51	1.27E-49
KLMA_40132		transcription activator	931.4865252	-1.507910508	0.143332191	-10.52038974	6.96E-26	2.59E-24
KLMA_40147	SUL2	sulfate permease 2	9165.907466	-1.096250976	0.221883932	-4.940650583	7.79E-07	3.53E-06
KLMA_40149		hypothetical protein	4127.869111	-1.548204097	0.159455575	-9.70931307	2.75E-22	7.07E-21
KLMA_40153	fmo1	thiol-specific monooxygenase	742.0892315	-1.560386616	0.172554643	-9.042855006	1.53E-19	3.26E-18
KLMA_40168	MDN1	midasin	2167.566691	-1.498092464	0.191989395	-7.802995899	6.05E-15	8.13E-14
KLMA_40194	LCB5	sphingoid long chain base kinase 5	1645.028382	-1.103232002	0.156505506	-7.049157738	1.80E-12	1.80E-11
KLMA_40209	GCR2	hypothetical protein	375.8710421	-1.578624279	0.176020271	-8.968423205	3.01E-19	6.20E-18
KLMA_40218	GAP1	glyceraldehyde-3-phosphate dehydrogenase 1	79994.31241	-2.957491564	0.162016095	-18.25430721	1.91E-74	6.23E-72
KLMA_40220	ADH2	alcohol dehydrogenase 2	50497.17099	-7.380279973	0.306526555	-24.07713081	4.34E-128	5.30E-125
KLMA_40225	RIB7	5-amino-6-(5-phosphoribosylamino)uracil reductase	6676.337237	-1.695942535	0.202613213	-8.370345185	5.74E-17	9.51E-16
KLMA_40226	SPP381	pre-mRNA-splicing factor SPP381	558.9371746	-1.974767274	0.16240069	-12.15984536	5.09E-34	2.85E-32
KLMA_40228	UTP10	U3 small nucleolar RNA-associated protein 10	2047.662215	-1.46033005	0.172942777	-8.444007199	3.07E-17	5.22E-16
KLMA_40240	GAR1	H/ACA ribonucleoprotein complex subunit 1	1296.711556	-1.169132179	0.259083889	-4.512562265	6.40E-06	2.47E-05
KLMA_40251	CIC1	proteasome-interacting protein CIC1	939.4831471	-1.05964129	0.195805476	-5.411704062	6.24E-08	3.37E-07
KLMA_40254		calcipressin-like protein	87.82736266	-1.124491215	0.238781582	-4.709287897	2.49E-06	1.04E-05
KLMA_40263	SFB3	SED5-binding protein 3	771.5881702	-1.309488478	0.208425109	-6.282776984	3.33E-10	2.46E-09
KLMA_40297	HAP1	hap1 transcriptional regulatory prottein	2425.739774	-2.470003276	0.15466934	-15.96957269	2.08E-57	3.28E-55
KLMA_40302	ERB1	ribosome biogenesis protein ERB1	1005.189181	-1.297714851	0.156867073	-8.27270392	1.31E-16	2.09E-15
KLMA_40304		hypothetical protein	55.99621093	-1.605992477	0.35214786	-4.560562928	5.10E-06	2.00E-05

	UniProt _gene	Product	baseMean	$\log_2$FoldChange	lfcSE	stat	pvalue	padj
KLMA_40305	NUP116	nucleoporin NUP116/NSP116	2618.183003	-1.089746463	0.145582404	-7.485427025	7.13E-14	8.39E-13
KLMA_40307	MCM1	pheromone receptor transcription factor	609.8824689	-1.294360272	0.151048126	-8.569191182	1.04E-17	1.85E-16
KLMA_40308		hypothetical protein	6525.206016	-1.456327909	0.255131432	-5.708147742	1.14E-08	6.90E-08
KLMA_40318	IMP2	mitochondrial inner membrane protease subunit 2	71.46757159	-1.163903123	0.276977287	-4.202160892	2.64E-05	8.99E-05
KLMA_40328	RRP12	ribosomal RNA-processing protein 12	1719.035853	-1.354612164	0.129336573	-10.47354302	1.14E-25	4.07E-24
KLMA_40374	MKS1	negative regulator of RAS-cAMP pathway	887.6796643	-1.129273505	0.175375797	-6.439163907	1.20E-10	9.54E-10
KLMA_40375	IMP4	U3 small nucleolar ribonucleoprotein protein IMP4	216.8980256	-1.446357648	0.189742827	-7.622726353	2.48E-14	3.06E-13
KLMA_40378	FMS1	polyamine oxidase FMS1	431.6987648	-1.39488125	0.175379094	-7.953520667	1.81E-15	2.59E-14
KLMA_40388	FBA1	fructose-bisphosphate aldolase	91591.73868	-2.802818706	0.25675687	-10.91623645	9.64E-28	4.09E-26
KLMA_40390	TRM13	tRNA guanosine-2'-O-methyltransferase TRM13	328.0503889	-1.029068786	0.1754717	-5.864585492	4.50E-09	2.91E-08
KLMA_40404	ALD5	aldehyde dehydrogenase 5	1284.147401	-3.40219444	0.639350295	-5.321330834	1.03E-07	5.35E-07
KLMA_40407	MAM33	mitochondrial acidic protein MAM33	787.0926995	-1.165864507	0.174149862	-6.694604838	2.16E-11	1.91E-10
KLMA_40415	HRK1	serine/threonine-protein kinase HRK1	2406.995409	-1.598756978	0.16666065	-9.592888194	8.57E-22	2.09E-20
KLMA_40422	YTM1	ribosome biogenesis protein YTM1	1000.37013	-1.19423701	0.187499102	-6.369294546	1.90E-10	1.47E-09
KLMA_40431	NOP19	uncharacterized protein YGR251W	98.80625074	-1.008840348	0.265631942	-3.797887942	0.000145934	0.000421741
KLMA_40432	NMD3	60S ribosomal export protein NMD3	1146.606766	-1.298663145	0.13760862	-9.437367669	3.82E-21	8.93E-20
KLMA_40444	FPR3	FK506-binding protein 3	2211.456146	-1.0648629	0.169979345	-6.264660561	3.74E-10	2.76E-09
KLMA_40445	HMG1	3-hydroxy-3-methylglutaryl-coenzyme A reductase 1	4589.558944	-1.605187442	0.265961455	-6.035413819	1.59E-09	1.08E-08
KLMA_40457	SFP1	zinc finger protein SFP1	1234.045656	-1.980675465	0.12936137	-15.31118188	6.44E-53	7.67E-51
KLMA_40458	DUS3	tRNA-dihydrouridine synthase 3	374.9667423	-1.092107384	0.166199847	-6.57104927	5.00E-11	4.17E-10

	UniProt _gene	Product	baseMean	$\log_2$FoldChange	lfcSE	stat	pvalue	padj
KLMA_40471	DPM1	dolichol-phosphate mannosyltransferase	1709.667323	-1.022302422	0.184582757	-5.538450278	3.05E-08	1.73E-07
KLMA_40478	RPC82	DNA-directed RNA polymerase III subunit RPC3	722.192777	-1.455972716	0.176939092	-8.228666169	1.89E-16	2.97E-15
KLMA_40494	MET5	sulfite reductase [NADPH] subunit beta	10826.06949	-1.102703765	0.221612022	-4.97583007	6.50E-07	2.97E-06
KLMA_40500	RIX1	pre-rRNA-processing protein RIX1	1080.23942	-1.022740821	0.130866394	-7.815152442	5.49E-15	7.41E-14
KLMA_40501	SGM1	protein SGM1	756.9239091	-1.051266257	0.17477664	-6.01491285	1.80E-09	1.22E-08
KLMA_40502	XPT1	xanthine phosphoribosyltransferase 1	1025.066076	-1.407011214	0.171430505	-8.207472826	2.26E-16	3.50E-15
KLMA_40522	UTP21	U3 small nucleolar RNA-associated protein 21	1111.446385	-1.333177648	0.151422641	-8.804348118	1.32E-18	2.57E-17
KLMA_40526	FAS1	fatty acid synthase subunit beta	19115.91845	-1.249140895	0.254181053	-4.914374537	8.91E-07	3.99E-06
KLMA_40530	MTR2	mRNA transport regulator MTR2	132.0623085	-1.019663229	0.211585791	-4.819147946	1.44E-06	6.27E-06
KLMA_40531		uncharacterized protein YKL187C	16272.32995	-1.152051786	0.145633588	-7.9106187	2.56E-15	3.57E-14
KLMA_40547	PUS1	tRNA pseudouridine synthase 1	622.409884	-1.043241684	0.144150949	-7.237147519	4.58E-13	4.96E-12
KLMA_40555	BMS1	ribosome biogenesis protein BMS1	1421.406084	-1.40248081	0.135534876	-10.34774849	4.28E-25	1.46E-23
KLMA_40558	RPL10A	60S ribosomal protein L10a	13500.34226	-1.040946855	0.241317147	-4.31360502	1.61E-05	5.71E-05
KLMA_40571	GUK1	guanylate kinase	706.2789182	-1.338869942	0.188059144	-7.11940889	1.08E-12	1.11E-11
KLMA_40579	UTP6	U3 small nucleolar RNA-associated protein 6	515.6879526	-1.025770094	0.15013078	-6.832510261	8.34E-12	7.76E-11
KLMA_40582		hypothetical protein	162.991639	-1.887893409	0.334415959	-5.645344844	1.65E-08	9.64E-08
KLMA_40583	DLD1	D-lactate dehydrogenase [cytochrome] 1	6837.124499	-4.866943488	0.261004985	-18.64693691	1.34E-77	5.02E-75
KLMA_40593		uncharacterized vacuolar membrane protein YML018C	1590.804891	-1.267526563	0.192406124	-6.587766216	4.46E-11	3.75E-10
KLMA_40619	PRP43	pre-mRNA-splicing factor ATP-dependent RNA helicase PRP43	1466.469287	-1.149542136	0.148608974	-7.735348019	1.03E-14	1.35E-13
KLMA_40626		flocculation protein FLO9	477.624138	-1.352354868	0.25208115	-5.364759987	8.11E-08	4.28E-07

	UniProt _gene	Product	baseMean	$\log_2$FoldChange	lfcSE	stat	pvalue	padj
KLMA_50044	MEI5	meiosis protein 5	23.51674743	-1.383361484	0.410668126	-3.368563067	0.000755611	0.001842439
KLMA_50045	NOC2	nucleolar complex protein 2	1229.578738	-1.283276784	0.160400617	-8.000447947	1.24E-15	1.81E-14
KLMA_50046	GEP3	mitochondrial protein FMP38	402.3799288	-1.021662346	0.168101626	-6.077647007	1.22E-09	8.50E-09
KLMA_50050	SHM1	serine hydroxymethyltransferase	2104.251634	-1.357562564	0.142648204	-9.516857016	1.78E-21	4.27E-20
KLMA_50057	MTR4	ATP-dependent RNA helicase DOB1	1306.473971	-1.120418857	0.130495244	-8.585898001	9.01E-18	1.63E-16
KLMA_50085	UTP18	U3 small nucleolar RNA-associated protein 18	599.6877603	-1.064039481	0.163698249	-6.500005251	8.03E-11	6.54E-10
KLMA_50101		SWIRM domain-containing protein YOR338W	3371.929078	-1.296985686	0.231354495	-5.60605355	2.07E-08	1.19E-07
KLMA_50120	LTE1	guanine nucleotide exchange factor LTE1	1115.212092	-1.013011182	0.140607653	-7.204523782	5.82E-13	6.21E-12
KLMA_50125	UPC2	sterol regulatory element-binding protein ECM22	1352.986883	-2.439527324	0.209409852	-11.64953466	2.31E-31	1.19E-29
KLMA_50140	ENP2	ribosome biogenesis protein ENP2	871.4643968	-1.075700895	0.137040935	-7.849485941	4.18E-15	5.70E-14
KLMA_50142	TIF4632	eukaryotic initiation factor 4F subunit p150	2382.853542	-1.19253123	0.154306705	-7.728317638	1.09E-14	1.42E-13
KLMA_50154	LEU1	3-isopropylmalate dehydratase	3740.246868	-1.322640396	0.231612543	-5.710573256	1.13E-08	6.81E-08
KLMA_50183	IMD4	inosine-5'-monophosphate dehydrogenase	15103.02929	-1.912303401	0.177359213	-10.78209226	4.18E-27	1.73E-25
KLMA_50206	ERV1	mitochondrial FAD-linked sulfhydryl oxidase ERV1	285.0978943	-2.358489781	0.224372847	-10.51147592	7.65E-26	2.81E-24
KLMA_50214	RPA135	DNA-directed RNA polymerase I subunit RPA2	3413.501695	-1.420041402	0.153389408	-9.25775398	2.09E-20	4.70E-19
KLMA_50215	CWP1	cell wall protein CWP1	16353.96716	-1.253562573	0.216738359	-5.783759636	7.30E-09	4.56E-08
KLMA_50217	YJU3	serine hydrolase YJU3	1305.069786	-1.248466944	0.30519521	-4.090716048	4.30E-05	0.000139019
KLMA_50218		protein MBR1	2283.272964	-1.54705675	0.152495333	-10.14494492	3.49E-24	1.11E-22
KLMA_50222	PTK2	serine/threonine-protein kinase PTK2	2246.401425	-1.263268263	0.182986901	-6.90359942	5.07E-12	4.86E-11
KLMA_50241	PDX3	pyridoxamine 5'-phosphate oxidase	902.9108208	-1.34913441	0.248342749	-5.432550042	5.56E-08	3.03E-07

	UniProt _gene	Product	baseMean	log_2FoldChange	lfcSE	stat	pvalue	padj
KLMA_50255	PIR3	cell wall mannoprotein HSP150	3724.245338	-1.002485454	0.260915605	-3.842182816	0.000121945	0.000359867
KLMA_50260	CCP1	cytochrome c peroxidase	5877.969183	-2.322097237	0.149542603	-15.52799802	2.24E-54	2.96E-52
KLMA_50264	RPS14	40S ribosomal protein S14	9285.488798	-1.106511556	0.245162498	-4.513380161	6.38E-06	2.46E-05
KLMA_50271	SUR4	elongation of fatty acids protein 3	2077.042137	-1.085853726	0.255355386	-4.252323572	2.12E-05	7.35E-05
KLMA_50278	VHT1	vitamin H transporter	2154.221029	-1.325611467	0.275038602	-4.819728794	1.44E-06	6.26E-06
KLMA_50283	ADE6	phosphoribosylformylglycinamidine synthase	5738.764521	-1.090986549	0.246549645	-4.425017728	9.64E-06	3.58E-05
KLMA_50284	ERG25	c-4 methylsterol oxidase	3103.621139	-1.742888257	0.241870073	-7.205886338	5.77E-13	6.16E-12
KLMA_50291	RRP5	rRNA biogenesis protein RRP5	2499.509234	-1.398351869	0.145531776	-9.608567347	7.36E-22	1.81E-20
KLMA_50309	PWP1	periodic tryptophan protein 1	872.7385649	-1.071654215	0.163806617	-6.542191246	6.06E-11	5.01E-10
KLMA_50311	NOP56	nucleolar protein 56	3558.350424	-1.262897163	0.176574901	-7.152189541	8.54E-13	8.95E-12
KLMA_50319	MSS51	protein MSS51	1359.558942	-1.70765213	0.134688962	-12.67848608	7.78E-37	5.21E-35
KLMA_50330	LAC9	lactose regulatory protein LAC9	2043.665205	-1.097489961	0.180037175	-6.095907465	1.09E-09	7.67E-09
KLMA_50332	SEO1	probable transporter SEO1	2417.144937	-1.498720882	0.260676022	-5.74936225	8.96E-09	5.49E-08
KLMA_50338		uncharacterized protein YPL245W	172.7661419	-2.10588339	0.20782874	-10.13278235	3.95E-24	1.22E-22
KLMA_50349	APE2	aminopeptidase 2	1360.596304	-1.133952433	0.299499218	-3.786161586	0.000152992	0.000439538
KLMA_50356	UTP4	U3 small nucleolar RNA-associated protein 4	1060.326827	-1.411058996	0.168786129	-8.36004121	6.27E-17	1.02E-15
KLMA_50360	KHT2	hexose transporter 2	10182.55276	-3.220038628	0.331270678	-9.720264542	2.47E-22	6.39E-21
KLMA_50361	KHT2	hexose transporter 2	15464.67737	-2.796062059	0.760807846	-3.675122536	0.000237735	0.000652303
KLMA_50362	KHT2	hexose transporter	24030.04473	-5.022981045	0.608670376	-8.25238297	1.55E-16	2.45E-15
KLMA_50363	RAG1	low-affinity glucose transporter	240.6783052	-2.40408063	0.298403574	-8.056473974	7.85E-16	1.17E-14
KLMA_50378	NUG1	nuclear GTP-binding protein NUG1	642.4116782	-1.074590926	0.140082322	-7.671138721	1.70E-14	2.14E-13
KLMA_50397		gti1_Pac2 super family conserved domain	253.3403098	-1.722175672	0.231122354	-7.451359184	9.24E-14	1.07E-12
KLMA_50409	MUC1	flo11 super family	19168.46235	-4.430898567	0.305647358	-14.49676711	1.27E-47	1.17E-45

	UniProt _gene	Product	baseMean	$\log_2$FoldChange	lfcSE	stat	pvalue	padj
KLMA_50410		bZIP_1 super family conserved domain	125.1631431	-1.020489717	0.253564021	-4.02458406	5.71E-05	0.000179151
KLMA_50422	NNF2	protein NNF2	519.3261046	-1.068445224	0.158247602	-6.751730911	1.46E-11	1.32E-10
KLMA_50426	RPC40	DNA-directed RNA polymerases I and III subunit RPAC1	829.0243151	-1.544520579	0.254754552	-6.062779124	1.34E-09	9.27E-09
KLMA_50431	VAS1	valyl-tRNA synthetase	1963.149986	-1.449744141	0.206296823	-7.027467114	2.10E-12	2.08E-11
KLMA_50445	NOP7	pescadillo homolog	1649.95709	-1.384501287	0.146559399	-9.446690508	3.50E-21	8.21E-20
KLMA_50471	MET10	sulfite reductase [NADPH] flavoprotein component	7792.702245	-1.318452071	0.252144002	-5.228964641	1.70E-07	8.53E-07
KLMA_50473	RPL2	60S ribosomal protein L2	29029.77255	-1.045299017	0.248634797	-4.204154168	2.62E-05	8.93E-05
KLMA_50487	DIP2	U3 small nucleolar RNA-associated protein 12	1228.939622	-1.184270796	0.179443891	-6.599671837	4.12E-11	3.50E-10
KLMA_50502		DNA-directed RNA polymerase I subunit RPA14	484.9145812	-1.531957261	0.198758128	-7.707645849	1.28E-14	1.65E-13
KLMA_50506	NHA1	Na(+)/H(+) antiporter	2136.545811	-1.109078781	0.1266027	-8.760309093	1.95E-18	3.74E-17
KLMA_50531		uncharacterized transporter YLR152C	2677.814568	-1.550404412	0.147561122	-10.50686243	8.03E-26	2.93E-24
KLMA_50533	ACS2	acetyl-coenzyme A synthetase 2	7877.173596	-1.702106598	0.175345773	-9.707143624	2.81E-22	7.19E-21
KLMA_50566	MAP1	methionine aminopeptidase 1	1135.031558	-1.060938252	0.132152609	-8.028129471	9.90E-16	1.46E-14
KLMA_50596	BRE4	protein BRE4	2037.68916	-1.49747656	0.15199393	-9.852212925	6.71E-23	1.83E-21
KLMA_60007		flocculation protein FLO9	2449.368093	-2.76462293	0.228847343	-12.08064249	1.34E-33	7.25E-32
KLMA_60018	UTH1	protein UTH1	1050.848115	-1.345407366	0.287814096	-4.674570798	2.95E-06	1.21E-05
KLMA_60019	SHB17	uncharacterized protein YKR043C	440.2982211	-1.320130907	0.224204477	-5.88806667	3.91E-09	2.55E-08
KLMA_60025	ALB1	ribosome biogenesis protein ALB1	365.8017339	-1.061805093	0.153000678	-6.939871796	3.92E-12	3.80E-11
KLMA_60037	URA2	protein URA1	11253.01147	-1.548349037	0.284604292	-5.440357294	5.32E-08	2.90E-07
KLMA_60042	PEX21	peroxisomal membrane protein PEX21	513.2626469	-1.239972572	0.251640497	-4.927555722	8.33E-07	3.75E-06
KLMA_60062	IMP3	U3 small nucleolar ribonucleoprotein	193.8961987	-1.046636306	0.189691696	-5.517565218	3.44E-08	1.93E-07

	UniProt _gene	Product	baseMean	$\log_2$FoldChange	lfcSE	stat	pvalue	padj
		protein IMP3						
KLMA_60069		40S ribosomal protein S0	13481.65401	-1.116406235	0.276069861	-4.043926521	5.26E-05	0.000166701
KLMA_60075	PDC1	pyruvate decarboxylase	70134.64616	-2.354794995	0.22350894	-10.53557408	5.92E-26	2.24E-24
KLMA_60087	ADE3	c-1-tetrahydrofolate synthase	5190.121043	-1.560267173	0.203917101	-7.651477804	1.99E-14	2.48E-13
KLMA_60096	EXO1	exodeoxyribonuclease 1	284.8749108	-1.261528833	0.223919734	-5.633843934	1.76E-08	1.02E-07
KLMA_60097	HMS1	probable transcription factor HMS1	3721.520346	-1.375055343	0.138811884	-9.905890649	3.92E-23	1.10E-21
KLMA_60131	IPP1	inorganic pyrophosphatase	8932.030189	-1.387254156	0.176170095	-7.874515562	3.42E-15	4.71E-14
KLMA_60135	MDM20	N-terminal acetyltransferase B complex subunit MDM20	1102.137603	-1.488116959	0.161470405	-9.216035364	3.08E-20	6.91E-19
KLMA_60136	BRX1	ribosome biogenesis protein BRX1	607.6967641	-1.021315733	0.155473642	-6.569060339	5.06E-11	4.22E-10
KLMA_60153	URB1	nucleolar pre-ribosomal-associated protein 1	1057.301024	-1.067148704	0.141556763	-7.538662807	4.75E-14	5.74E-13
KLMA_60167	MDH1	malate dehydrogenase	6488.853334	-1.789701489	0.187723564	-9.533707198	1.52E-21	3.67E-20
KLMA_60173	TEF4	eukaryotic elongation factor 1Bgamma	3798.2559	-1.059360534	0.234518496	-4.517172644	6.27E-06	2.42E-05
KLMA_60179	DHR2	probable ATP-dependent RNA helicase DHR2	178.843765	-1.205987767	0.219068156	-5.505080201	3.69E-08	2.06E-07
KLMA_60187	FET3	iron transport multicopper oxidase FET3	12971.78769	-1.775864714	0.312558562	-5.681702352	1.33E-08	7.95E-08
KLMA_60209	RPA190	DNA-directed RNA polymerase I subunit RPA1	2986.544354	-1.495281641	0.141908828	-10.53691771	5.84E-26	2.23E-24
KLMA_60210	FUN12	eukaryotic translation initiation factor 5B	3047.897413	-1.067840469	0.162071885	-6.588684192	4.44E-11	3.73E-10
KLMA_60214		uncharacterized protein YOR342C	1558.912478	-3.325300092	0.163135959	-20.38361199	2.34E-92	1.63E-89
KLMA_60217	TYE7	hypothetical protein	1268.312248	-2.100294884	0.14733166	-14.25555705	4.14E-46	3.68E-44
KLMA_60218	REV1	DNA repair protein REV1	880.1147264	-1.791842912	0.178874779	-10.01730329	1.28E-23	3.76E-22
KLMA_60219	PYK1	pyruvate kinase	62631.949	-3.138032503	0.244289871	-12.8455285	9.11E-38	6.45E-36
KLMA_60226	LEU4	2-isopropylmalate synthase	2923.937904	-1.325423031	0.210411806	-6.299185672	2.99E-10	2.24E-09

	UniProt_gene	**Product**	**baseMean**	**log$_2$FoldChange**	**lfcSE**	**stat**	**pvalue**	**padj**
KLMA_60229	YAF9	protein AF-9 homolog	599.9116869	-1.296188292	0.154457093	-8.391898788	4.78E-17	7.97E-16
KLMA_60230	TFC7	transcription factor tau 55 kDa subunit	2953.072485	-2.127709408	0.168702323	-12.61221172	1.81E-36	1.16E-34
KLMA_60232	NOP15	ribosome biogenesis protein 15	561.2658671	-1.221348812	0.152733374	-7.996607298	1.28E-15	1.86E-14
KLMA_60233	CYB5	cytochrome b5	1758.768459	-1.253166482	0.264133266	-4.744447758	2.09E-06	8.86E-06
KLMA_60234	CEX1	uncharacterized protein YOR112W	581.2447081	-1.188779034	0.22013767	-5.400161795	6.66E-08	3.57E-07
KLMA_60237	AZF1	zf-C2H2 super family protein	1995.055303	-1.147186684	0.135714041	-8.452969786	2.84E-17	4.85E-16
KLMA_60265	KRE33	UPF0202 protein YNL132W	1184.74556	-1.368539653	0.138089501	-9.910526432	3.75E-23	1.06E-21
KLMA_60297	EPL1	enhancer of polycomb-like protein 1	1240.953437	-1.211387797	0.156890419	-7.721235018	1.15E-14	1.49E-13
KLMA_60303	FCF2	rRNA-processing protein FCF2	217.8000483	-1.021466876	0.222529223	-4.590259479	4.43E-06	1.76E-05
KLMA_60313		40S ribosomal protein S20	9926.39281	-1.255292212	0.235871493	-5.321932698	1.03E-07	5.34E-07
KLMA_60316	RGT1	uncharacterized transcriptional regulatory protein YKL038W	2884.430991	-1.384508985	0.14614266	-9.473681321	2.70E-21	6.40E-20
KLMA_60317	UGP1	UTP--glucose-1-phosphate uridylyltransferase	4721.539652	-1.827546577	0.16367633	-11.16561314	6.01E-29	2.69E-27
KLMA_60380	TRS23	transport protein particle 23 kDa subunit	212.5084734	-2.647890935	0.310241053	-8.534946975	1.40E-17	2.47E-16
KLMA_60381	SKS1	serine/threonine-protein kinase SKS1	5467.705939	-2.947323726	0.172485033	-17.08741724	1.84E-65	4.28E-63
KLMA_60396	NOP4	nucleolar protein 4	822.2946629	-1.098765106	0.194684367	-5.643828132	1.66E-08	9.72E-08
KLMA_60402	PDAT9	pisatin demethylase	499.3968993	-1.013227487	0.29857722	-3.393519066	0.000690008	0.001698587
KLMA_60412	RAG5	hexokinase	21510.28912	-3.871007849	0.194914453	-19.86003499	9.02E-88	4.41E-85
KLMA_60417	cyp524A1	cytochrome P450 61	5650.434244	-1.885231252	0.28385234	-6.641591366	3.10E-11	2.65E-10
KLMA_60433	JHD2	histone demethylase JHD2	796.5880846	-1.08935628	0.201196357	-5.414393675	6.15E-08	3.32E-07
KLMA_60441	LEU3	regulatory protein LEU3	829.867322	-1.78583097	0.175320008	-10.18612191	2.29E-24	7.35E-23
KLMA_60445	ERG13	hydroxymethylglutaryl-CoA synthase	2605.020566	-1.352999692	0.213144031	-6.347818823	2.18E-10	1.67E-09
KLMA_60461	PFK2	6-phosphofructokinase subunit beta	24633.73479	-2.319491955	0.228912093	-10.13267549	3.96E-24	1.22E-22

	UniProt _gene	Product	baseMean	log$_2$FoldChange	lfcSE	stat	pvalue	padj
KLMA_60468	SMM1	tRNA-dihydrouridine synthase 2	424.1595733	-1.270160688	0.190108596	-6.681237522	2.37E-11	2.07E-10
KLMA_60512	RPB1	DNA-directed RNA polymerase II subunit RPB1	5712.972867	-1.092447659	0.168620536	-6.478734341	9.25E-11	7.44E-10
KLMA_70017	CDC60	leucyl-tRNA synthetase	5293.152312	-1.498952376	0.161738376	-9.267759529	1.90E-20	4.30E-19
KLMA_70048	PET309	pentatricopeptide repeat-containing protein PET309	904.8465916	-1.122732748	0.149002264	-7.535004632	4.88E-14	5.89E-13
KLMA_70066		conserved hypothetical membrane protein	93.99167192	-1.340977055	0.289685297	-4.629082214	3.67E-06	1.48E-05
KLMA_70073	IKI3	elongator complex protein 1	1116.034609	-1.009606656	0.175516982	-5.75218787	8.81E-09	5.42E-08
KLMA_70080		conserved hypothetical protein	1856.110577	-1.235649067	0.126529585	-9.765692889	1.58E-22	4.19E-21
KLMA_70083	FUI1	uridine permease	2053.661711	-2.235681048	0.212683193	-10.51178994	7.62E-26	2.81E-24
KLMA_70086	URA7	CTP synthase	2850.452886	-1.470130299	0.157501266	-9.334085607	1.02E-20	2.35E-19
KLMA_70105	CFL1	probable ferric reductase transmembrane component	1751.481023	-1.424830545	0.34276557	-4.156866007	3.23E-05	0.000107197
KLMA_70126	AIM24	uncharacterized protein YJR080C	833.1502164	-1.452409783	0.146943486	-9.884138627	4.88E-23	1.36E-21
KLMA_70148	ROX3	mediator of RNA polymerase II transcription subunit 19	784.8277553	-1.164196514	0.1329762	-8.75492389	2.04E-18	3.91E-17
KLMA_70170	RNR1	ribonucleoside-diphosphate reductase large chain 1	5553.962551	-1.612426074	0.18063386	-8.926488506	4.40E-19	8.95E-18
KLMA_70180	VHR1	transcription factor VHR1	600.9472937	-1.241325941	0.146246789	-8.487885115	2.10E-17	3.66E-16
KLMA_70183	RHR2	(DL)-glycerol-3-phosphatase 1	5769.616889	-2.547286043	0.193234519	-13.1823551	1.11E-39	8.88E-38
KLMA_70186	FCY2	purine-cytosine permease FCY2	7677.443189	-1.919161867	0.198095773	-9.688050549	3.39E-22	8.62E-21
KLMA_70187	PCL6	PHO85 cyclin-6	725.327599	-1.181389348	0.142806945	-8.272632321	1.31E-16	2.09E-15
KLMA_70197	RSA4	WD repeat-containing protein YCR072C	799.3583154	-1.101900468	0.187073642	-5.890196276	3.86E-09	2.52E-08
KLMA_70212	HSL7	protein arginine N-methyltransferase HSL7	366.0373977	-1.037150693	0.214077875	-4.844735555	1.27E-06	5.56E-06
KLMA_70219	FAS2	fatty acid synthase subunit alpha	9564.457747	-1.658129108	0.222476486	-7.453053312	9.12E-14	1.06E-12

	UniProt _gene	Product	baseMean	$\log_2$FoldChange	lfcSE	stat	pvalue	padj
KLMA_70224	SPT21	protein SPT21	263.023691	-1.059003272	0.208708323	-5.074082616	3.89E-07	1.84E-06
KLMA_70225	NEW1	[NU+] prion formation protein 1	2530.509267	-1.436821452	0.141013473	-10.18924946	2.21E-24	7.16E-23
KLMA_70235	NOP14	probable nucleolar complex protein 14	707.45551	-1.031132503	0.199493562	-5.168750772	2.36E-07	1.15E-06
KLMA_70265	TIF3	eukaryotic translation initiation factor 4B	1134.665915	-1.239831221	0.221292559	-5.602679222	2.11E-08	1.22E-07
KLMA_70271	MET16	phosphoadenosine phosphosulfate reductase	1515.467045	-1.3545099	0.252232349	-5.370087962	7.87E-08	4.16E-07
KLMA_70282	NOC4	nucleolar complex protein 4	844.4202511	-1.185759154	0.16629791	-7.130331061	1.00E-12	1.04E-11
KLMA_70290	RRP9	ribosomal RNA-processing protein 9	541.9616374	-1.09490812	0.193459884	-5.659613226	1.52E-08	8.93E-08
KLMA_70313	HEM14	protoporphyrinogen oxidase	593.7442584	-1.240942356	0.143509253	-8.647124371	5.28E-18	9.85E-17
KLMA_70323		uncharacterized protein YOL036W	691.7469606	-1.030914922	0.142697488	-7.224478417	5.03E-13	5.40E-12
KLMA_70324		transcriptional activator of sulfur metabolism	513.970424	-1.043973004	0.188037746	-5.551933209	2.83E-08	1.61E-07
KLMA_70355		uncharacterized protein YBL029C-A	98.82020058	-1.009875706	0.272568832	-3.705030028	0.000211366	0.000587541
KLMA_70357		UPF0642 protein YBL028C	186.8878598	-1.143676388	0.191551729	-5.970587651	2.36E-09	1.58E-08
KLMA_70358	RPL19B	60S ribosomal protein L19	13982.16313	-1.038751897	0.22369752	-4.643555714	3.42E-06	1.39E-05
KLMA_70359	MIS1	c-1-tetrahydrofolate synthase	1031.851812	-1.48139576	0.148738451	-9.959736349	2.29E-23	6.57E-22
KLMA_70362	MAK21	ribosome biogenesis protein MAK21	902.7957044	-1.714055527	0.138910411	-12.33928775	5.56E-35	3.36E-33
KLMA_70371	DYS1	deoxyhypusine synthase	2722.953291	-1.300248704	0.226284634	-5.746076008	9.13E-09	5.58E-08
KLMA_70383	PTR2	peptide transporter PTR2	1709.39415	-1.666507139	0.272724318	-6.110592388	9.93E-10	7.08E-09
KLMA_70384	UGA4	GABA-specific permease	270.1909531	-2.01402386	0.263151793	-7.653468119	1.96E-14	2.44E-13
KLMA_70390	SRP40	suppressor protein SRP40	388.0140383	-1.821845364	0.18864566	-9.657499482	4.57E-22	1.14E-20
KLMA_70395	PUS4	tRNA pseudouridine synthase 4	243.652581	-1.35986326	0.181970259	-7.472997314	7.84E-14	9.20E-13
KLMA_70398	PCL1	PHO85 cyclin-1	1595.193433	-1.295032437	0.161539038	-8.016838856	1.09E-15	1.59E-14
KLMA_70408		zinc finger protein YPR022C	941.9306644	-1.536368889	0.16795165	-9.147685591	5.82E-20	1.27E-18

	UniProt _gene	Product	baseMean	log$_2$FoldChange	lfcSE	stat	pvalue	padj
KLMA_70417	NOP9	pumilio domain-containing protein YJL010C	587.96101	-1.430665994	0.165696653	-8.634247984	5.91E-18	1.09E-16
KLMA_70419	LTV1	protein LTV1	339.6707018	-1.43615168	0.173725322	-8.266795344	1.38E-16	2.19E-15
KLMA_80006	UGA4	GABA-specific permease	161.138846	-1.037856143	0.210017367	-4.941763417	7.74E-07	3.51E-06
KLMA_80054	HIP1	histidine permease	1933.134107	-2.610815928	0.258543	-10.09818842	5.63E-24	1.72E-22
KLMA_80059	GAP3	glyceraldehyde-3-phosphate dehydrogenase 3	138843.9088	-2.331840323	0.316649401	-7.364107802	1.78E-13	2.03E-12
KLMA_80061	MET3	sulfate adenylyltransferase	3317.219457	-1.312126246	0.310330001	-4.228164351	2.36E-05	8.11E-05
KLMA_80063	MNN1	alpha-1,3-mannosyltransferase	596.1594134	-2.334800007	0.200668723	-11.63509674	2.73E-31	1.39E-29
KLMA_80064	MNN1	alpha-1,3-mannosyltransferase	1075.060207	-1.349491429	0.244505871	-5.519259824	3.40E-08	1.92E-07
KLMA_80081	RLP24	ribosome biogenesis protein RLP24	635.50128	-1.113803903	0.154622704	-7.203365818	5.87E-13	6.25E-12
KLMA_80090		uncharacterized protein YGL146C	467.4310244	-1.74275345	0.25615296	-6.803565546	1.02E-11	9.41E-11
KLMA_80091	RRP42	exosome complex component RRP42	578.2467804	-1.051281935	0.175537976	-5.988914512	2.11E-09	1.42E-08
KLMA_80112	PUB1	nuclear and cytoplasmic polyadenylated RNA-binding protein PUB1	1395.676942	-1.010988452	0.200510657	-5.04206842	4.61E-07	2.15E-06
KLMA_80126	UTP25	uncharacterized protein YIL091C	363.4660159	-1.044077679	0.184223464	-5.667452204	1.45E-08	8.58E-08
KLMA_80132	HDA1	histone deacetylase HDA1	759.5866174	-1.389904704	0.197192327	-7.048472555	1.81E-12	1.81E-11
KLMA_80170	NOP2	putative ribosomal RNA methyltransferase Nop2	1039.47978	-1.417909647	0.152719314	-9.284416038	1.63E-20	3.73E-19
KLMA_80171	TRM6	tRNA (adenine-N(1)-)-methyltransferase non-catalytic subunit TRM6	386.4151926	-1.02017771	0.190312651	-5.360535431	8.30E-08	4.37E-07
KLMA_80174	AQR1	probable transporter AQR1	2248.496291	-2.84732638	0.274459081	-10.37432017	3.25E-25	1.12E-23
KLMA_80175	QDR2	quinidine resistance protein 2	544.0663972	-1.237421581	0.210716577	-5.872445339	4.29E-09	2.79E-08
KLMA_80180		uncharacterized sulfatase PB10D8.02c	199.7677152	-1.046163433	0.276193718	-3.787788661	0.000151994	0.000436927
KLMA_80185	BGL2	glucan 1	6309.316048	-1.282940334	0.210319662	-6.099954333	1.06E-09	7.52E-09

	UniProt _gene	Product	baseMean	log_2FoldChange	lfcSE	stat	pvalue	padj
KLMA_80186	NIP1	eukaryotic translation initiation factor 3 subunit C	3594.360517	-1.031404603	0.15870516	-6.498872528	8.09E-11	6.58E-10
KLMA_80217	ECM3	protein ECM3	931.5051079	-1.215600152	0.141386167	-8.597730441	8.13E-18	1.48E-16
KLMA_80224		nucleoporin NUP1	289.1798116	-1.004799843	0.244654761	-4.107011201	4.01E-05	0.000130679
KLMA_80236	MET4	transcriptional activator of sulfur metabolism MET4	269.3081775	-1.0170114	0.184707124	-5.506075669	3.67E-08	2.05E-07
KLMA_80241		jmjC domain-containing protein 4	1245.630376	-2.203965783	0.189479986	-11.63165477	2.85E-31	1.43E-29
KLMA_80242	GDS1	protein GDS1	1633.21274	-1.486329301	0.146631942	-10.1364633	3.81E-24	1.19E-22
KLMA_80243	CIR2	probable electron transfer flavoprotein-ubiquinone oxidoreductase	2210.66694	-1.198496774	0.205194108	-5.840795273	5.20E-09	3.30E-08
KLMA_80249		UPF0364 protein YMR027W	1706.248388	-1.142551435	0.162514295	-7.03046728	2.06E-12	2.04E-11
KLMA_80256		translationally-controlled tumor protein homolog	8876.546859	-1.090842128	0.192361113	-5.670803795	1.42E-08	8.43E-08
KLMA_80257	DEF1	uncharacterized protein YKL054C	2549.726423	-1.014921935	0.192856909	-5.262564559	1.42E-07	7.22E-07
KLMA_80272	PUF6	pumilio homology domain family member 6	1207.777655	-1.228052281	0.157647133	-7.789880189	6.71E-15	8.97E-14
KLMA_80284	VID24	vacuolar import and degradation protein 24	1267.386433	-2.336073336	0.20479501	-11.40688604	3.86E-30	1.85E-28
KLMA_80303		protein OPY2	1000.155967	-1.048726058	0.142195328	-7.37524978	1.64E-13	1.87E-12
KLMA_80317	TPS1	trehalose-6-phosphate synthase	3741.522418	-2.057364518	0.122274923	-16.82572732	1.58E-63	3.09E-61
KLMA_80325	ROY1	uncharacterized protein YMR258C	909.1595721	-1.71413587	0.175609716	-9.761053696	1.65E-22	4.37E-21
KLMA_80338	PIN4	RNA-binding protein PIN4	1158.607375	-1.041707966	0.189843733	-5.487186475	4.08E-08	2.26E-07
KLMA_80341	DOT6	transcriptional regulatory protein DOT6	1669.285155	-1.004530395	0.128391707	-7.823950768	5.12E-15	6.93E-14
KLMA_80345	PTH2	peptidyl-tRNA hydrolase 2	547.9289814	-1.197349682	0.192759312	-6.211630824	5.24E-10	3.85E-09
KLMA_80348	MET6	5-methyltetrahydropteroyltriglutamate homocysteine methyltransferase	34841.92933	-1.509066135	0.292086419	-5.166505656	2.39E-07	1.16E-06

	UniProt _gene	Product	baseMean	log_2FoldChange	lfcSE	stat	pvalue	padj
KLMA_80369	ILS1	isoleucyl-tRNA synthetase	3563.051555	-1.114724036	0.21800376	-5.113324822	3.17E-07	1.51E-06
KLMA_80380	KAP123	importin subunit beta-4	5121.453418	-1.062836044	0.204361068	-5.200775529	1.98E-07	9.81E-07
KLMA_80413	RPL8B	60S ribosomal protein L8-B	11122.54698	-1.181748106	0.234807504	-5.032837901	4.83E-07	2.25E-06

Up-regulated DEGs

Locus_tag	UniProt_gene	Product	baseMean	log$_2$FoldChange	lfcSE	stat	pvalue	padj
KLMA_10001	TY2B-GR2	RVT_2 super family	135.1219604	1.179543128	0.258634609	4.560654643	5.10E-06	2.00E-05
KLMA_10010	ARN2	siderophore iron transporter ARN2	587.9678966	1.111944794	0.330792751	3.361454539	0.000775331	0.001883747
KLMA_10012		uncharacterized protein C11D3.14c	145.674767	2.128284189	0.374716489	5.679718533	1.35E-08	8.04E-08
KLMA_10013		hypothetical protein	4.949355681	5.523381439	1.574300017	3.508468132	0.000450695	0.001149112
KLMA_10014	MATALPHA1	mating-type protein ALPHA1	116.0169163	6.191096258	1.626356452	3.806727763	0.000140818	0.000408405
KLMA_10015	HMLALPHA2	mating-type protein ALPHA2	134.8495506	5.388038136	1.243557331	4.332762151	1.47E-05	5.26E-05
KLMA_10016	HMLALPHA3	mating-type protein ALPHA3	415.2763966	6.173309106	1.117379849	5.52480798	3.30E-08	1.86E-07
KLMA_10018	CHA1	catabolic L-serine/threonine dehydratase	83.70306925	1.442253488	0.40139345	3.593116654	0.000326746	0.000865886
KLMA_10026		hypothetical protein	185.0524112	1.68621591	0.248756718	6.778574352	1.21E-11	1.11E-10
KLMA_10029	KAR4	karyogamy protein KAR4	120.2627024	2.128584442	0.24838394	8.569734599	1.04E-17	1.85E-16
KLMA_10039		protein SNA2	997.3173102	3.867979941	0.342455669	11.29483402	1.39E-29	6.35E-28
KLMA_10044	SPS22	cell wall mannoprotein PST1	92.09984338	1.447410885	0.466614995	3.101938218	0.001922581	0.004287619
KLMA_10059	LSB5	LAS seventeen-binding protein 5	861.851194	1.115876078	0.156403044	7.134618687	9.71E-13	1.01E-11
KLMA_10060	MXR2	selR super family	149.5119675	1.504101865	0.237692647	6.327927626	2.48E-10	1.88E-09
KLMA_10080	VTA1	vacuolar protein sorting-associated protein VTA1	222.6843313	1.314448744	0.212865871	6.175009341	6.62E-10	4.82E-09
KLMA_10086	PRM1	plasma membrane fusion protein PRM1	36.33378322	2.182975613	0.528222078	4.132685292	3.59E-05	0.000118435
KLMA_10091	ATG26	sterol 3-beta-glucosyltransferase	1212.936963	1.811120583	0.248943263	7.275234374	3.46E-13	3.81E-12
KLMA_10110	IST1	vacuolar protein sorting-associated protein IST1	627.9422748	1.501591362	0.178786774	8.398783252	4.51E-17	7.57E-16
KLMA_10115	CWC23	pre-mRNA-splicing factor CWC23	171.7796805	1.029573538	0.216453868	4.756549505	1.97E-06	8.39E-06

Locus_tag	UniProt _gene	Product	baseMean	$\log_2$FoldChange	lfcSE	stat	pvalue	padj
KLMA_10120		uncharacterized ORAOV1 family protein YNL260C	123.7490443	1.354627863	0.322326744	4.202654254	2.64E-05	8.98E-05
KLMA_10151	ECM25	protein ECM25	400.2907156	1.06109618	0.188412382	5.631775206	1.78E-08	1.04E-07
KLMA_10162	VPS60	vacuolar protein-sorting-associated protein 60	303.9554338	1.072019023	0.226314329	4.736858813	2.17E-06	9.17E-06
KLMA_10170		SMC_prok_B	196.0533717	1.543934255	0.345281487	4.471523421	7.77E-06	2.93E-05
KLMA_10174		hypothetical protein	528.664432	1.847224552	0.270153881	6.837675415	8.05E-12	7.50E-11
KLMA_10186	YAT1	putative mitochondrial carnitine O-acetyltransferase	492.3689816	2.752429932	0.175682851	15.66703818	2.54E-55	3.55E-53
KLMA_10188	KIN3	serine/threonine-protein kinase KIN3	331.7400086	1.981242852	0.201610496	9.82708187	8.61E-23	2.34E-21
KLMA_10195	CDC7	cell division control protein 7	212.2628273	1.053476602	0.216226363	4.872100639	1.10E-06	4.88E-06
KLMA_10214	ECI1	3,2-trans-enoyl-CoA isomerase	109.2528317	1.678788977	0.265000039	6.335051813	2.37E-10	1.80E-09
KLMA_10228	YHC1	U1 small nuclear ribonucleoprotein C homolog	185.8747004	1.274923664	0.220177866	5.790426116	7.02E-09	4.40E-08
KLMA_10231	ECM38	gamma-glutamyltransferase	303.8355855	1.582756848	0.230479855	6.867224231	6.55E-12	6.16E-11
KLMA_10235		WW domain-containing protein YFL010C	647.2211903	1.329966871	0.18097695	7.348819124	2.00E-13	2.25E-12
KLMA_10239		hypothetical protein	49.66799514	5.971300472	0.898703751	6.644347999	3.05E-11	2.62E-10
KLMA_10246		hypothetical protein	100.8296517	1.316999695	0.337374208	3.903676282	9.47E-05	0.000285631
KLMA_10251	ATG12	autophagy-related protein 12	38.80800482	1.448289815	0.418133401	3.463702764	0.000532795	0.001337189
KLMA_10257	HRD1	ERAD-associated E3 ubiquitin-protein ligase HRD1	872.4707991	1.290794688	0.202351877	6.378960792	1.78E-10	1.39E-09
KLMA_10258		OPA3-like protein	128.285885	1.701710664	0.235436446	7.227898198	4.91E-13	5.30E-12
KLMA_10260	PLB	lysophospholipase	5998.562713	1.380244887	0.18340058	7.525848007	5.24E-14	6.29E-13
KLMA_10268	MIC17	mitochondrial intermembrane space cysteine motif-containing protein MIC17	427.0223318	1.349774379	0.173444885	7.782151527	7.13E-15	9.49E-14
KLMA_10277		hypothetical protein	281.2374108	1.26914199	0.196677904	6.452895646	1.10E-10	8.77E-10

Locus_tag	UniProt_gene	Product	baseMean	log$_2$FoldChange	lfcSE	stat	pvalue	padj
KLMA_10295	MCH2	probable transporter MCH2	786.9181775	2.978593796	0.277132731	10.74789609	6.06E-27	2.49E-25
KLMA_10297	URH1	uridine nucleosidase	656.917421	1.480318839	0.251461152	5.886868914	3.94E-09	2.57E-08
KLMA_10298	DIT2	cytochrome P450-DIT2	360.3743391	1.289716554	0.245006793	5.264003244	1.41E-07	7.18E-07
KLMA_10316	HEM4	uroporphyrinogen-III synthase	91.95607237	1.63730494	0.277027482	5.91026179	3.42E-09	2.25E-08
KLMA_10338	FMP43	UPF0041 protein FMP43	173.6415599	1.013212147	0.229238052	4.419912572	9.87E-06	3.65E-05
KLMA_10375	ATG27	autophagy-related protein 27	928.9080772	1.078773778	0.216291951	4.987581698	6.11E-07	2.80E-06
KLMA_10382	STE3	pheromone a factor receptor	297.2023461	2.03338532	0.276960867	7.341778422	2.11E-13	2.36E-12
KLMA_10393		lrgB super family	834.0380258	1.899629918	0.283629622	6.697572372	2.12E-11	1.87E-10
KLMA_10426	AIM32	hypothetical protein	76.03933196	1.616661449	0.275814685	5.861404547	4.59E-09	2.95E-08
KLMA_10430	PES4	RRM	285.8610061	3.032585753	0.311089532	9.748273221	1.88E-22	4.90E-21
KLMA_10432	YSD83	NADB_Rossmann super family	720.5700545	1.068118931	0.219332545	4.86986065	1.12E-06	4.93E-06
KLMA_10443		hypothetical protein	157.4447019	2.585267916	0.386869669	6.682529351	2.35E-11	2.06E-10
KLMA_10454	PMC1	calcium-transporting ATPase 2	4405.746308	1.992111481	0.234202121	8.505949797	1.80E-17	3.14E-16
KLMA_10457	PMA1	plasma membrane ATPase	70784.90236	1.842842517	0.150150534	12.27329979	1.26E-34	7.16E-33
KLMA_10469	SSP1	hypothetical protein	83.82636602	1.504676045	0.309397196	4.863250419	1.15E-06	5.09E-06
KLMA_10486		uncharacterized protein YGR266W	210.1218754	2.010652469	0.261540365	7.687732891	1.50E-14	1.89E-13
KLMA_10516	PGU1	polygalacturonase	205.0538828	1.400742471	0.400143773	3.500597952	0.000464216	0.001181464
KLMA_10518	INU1	inulinase	498.0170365	1.159534575	0.312901722	3.705746867	0.000210769	0.000586216
KLMA_10520		uncharacterized protein AN0679	144.5749667	2.660041101	0.327121135	8.131669933	4.23E-16	6.42E-15
KLMA_10522	ZTA1	probable quinone oxidoreductase	777.0712947	1.081415922	0.214734283	5.03606554	4.75E-07	2.21E-06
KLMA_10523		hypothetical protein	116.3779047	1.342579443	0.287649986	4.667406593	3.05E-06	1.25E-05
KLMA_10525		atg31 super family	74.51048502	1.07057498	0.295694609	3.620542772	0.000293986	0.000788915
KLMA_10545	HGT1	high-affinity glucose transporter	776.7843966	3.158288303	0.356832457	8.850899751	8.68E-19	1.71E-17
KLMA_10551		N-terminal acetyltransferase C complex subunit MAK31	32.47682521	1.698254159	0.43555709	3.899039181	9.66E-05	0.000290977

Locus_tag	UniProt _gene	Product	baseMean	$\log_2$FoldChange	lfcSE	stat	pvalue	padj
KLMA_10552	MAK32	protein MAK32	330.3431807	1.084176792	0.181358648	5.978081584	2.26E-09	1.51E-08
KLMA_10560		glutathione transferase 3	1008.148504	1.877496112	0.175141274	10.71989523	8.21E-27	3.34E-25
KLMA_10567		hypothetical protein	257.0683753	1.787810243	0.25906729	6.900949338	5.17E-12	4.94E-11
KLMA_10570		SF3b10 super family	35.03736657	1.275003238	0.452027374	2.820632798	0.004792903	0.00988119
KLMA_10583	CTK3	CTD kinase subunit gamma	404.0603607	1.431641132	0.290393379	4.930006107	8.22E-07	3.70E-06
KLMA_10592	KYE1	enoate reductase 1	797.2244774	1.441860974	0.270696547	5.326484538	1.00E-07	5.22E-07
KLMA_10596		hemocyanin	26.14010686	3.365500226	0.798002867	4.217403679	2.47E-05	8.46E-05
KLMA_10598	RRT8	DUF540	41.23520499	2.197402915	0.430248217	5.107291156	3.27E-07	1.56E-06
KLMA_10603	IRS4	increased rDNA silencing protein 4	159.1381163	1.010216354	0.291763131	3.462453771	0.000535274	0.00134189
KLMA_10605		RING finger protein YKR017C	482.8750539	1.197825987	0.184344535	6.497756951	8.15E-11	6.61E-10
KLMA_10613		uncharacterized protein KLLA0D02464g	119.7056861	2.27231658	0.308530816	7.364958244	1.77E-13	2.02E-12
KLMA_10622	YKT6	synaptobrevin homolog YKT6	589.5436992	1.2435548	0.14807427	8.398182891	4.53E-17	7.58E-16
KLMA_10624	SPP382	pre-mRNA-splicing factor SPP382	230.5146956	1.68681779	0.292463769	5.767612841	8.04E-09	5.00E-08
KLMA_10625	ATG17	autophagy-related protein 17	220.6734963	2.208982693	0.270339019	8.17115748	3.05E-16	4.69E-15
KLMA_10635	DAL5	allantoate permease	390.941102	1.178567761	0.239984168	4.911022966	9.06E-07	4.05E-06
KLMA_10637		hypothetical protein	59.95557766	3.378472744	0.512588571	6.591002873	4.37E-11	3.69E-10
KLMA_10647		hypothetical protein	461.6861575	2.068812412	0.163987503	12.61567112	1.73E-36	1.13E-34
KLMA_10667	SMD1	small nuclear ribonucleoprotein Sm D1	208.3527117	1.531700683	0.198195418	7.728234592	1.09E-14	1.42E-13
KLMA_10674	ENT4	epsin-4	201.9343045	1.843066552	0.208226755	8.851247527	8.65E-19	1.71E-17
KLMA_10679	RAN1	putative copper-transporting ATPase 3	4137.270928	2.308352284	0.263712029	8.753306762	2.07E-18	3.95E-17
KLMA_10688	BIG1	protein BIG1	149.5932511	1.102308622	0.230628244	4.779590744	1.76E-06	7.55E-06
KLMA_10689	PEP12	syntaxin PEP12	373.8036757	1.491701995	0.241931223	6.165810182	7.01E-10	5.10E-09
KLMA_10715	SOU2	sorbose reductase homolog SOU2	1924.10284	5.188854139	0.321982759	16.11531674	1.99E-58	3.24E-56

Locus_tag	UniProt _gene	Product	baseMean	$\log_2$FoldChange	lfcSE	stat	pvalue	padj
KLMA_10722	HUL4	probable E3 ubiquitin-protein ligase HUL4	246.0094938	1.502928629	0.423982412	3.544790031	0.000392926	0.001018713
KLMA_10725	RAD26	DNA repair and recombination protein RAD26	676.4161987	2.46493218	0.36120844	6.824126748	8.85E-12	8.18E-11
KLMA_10743	COS111	F-box protein COS111	1130.008392	1.073788052	0.296753333	3.618453219	0.000296369	0.000794002
KLMA_10749		uncharacterized protein YPL067C	358.451379	1.146700463	0.169925682	6.748246958	1.50E-11	1.35E-10
KLMA_10754		uncharacterized protein YPL071C	75.31638723	2.001911485	0.31910017	6.273614596	3.53E-10	2.61E-09
KLMA_10756	UBP16	hypothetical protein	597.0030858	1.402961032	0.222323437	6.310450444	2.78E-10	2.09E-09
KLMA_10757	YTA6	probable 26S protease subunit YTA6	234.6443378	2.106431212	0.266740931	7.896917819	2.86E-15	3.94E-14
KLMA_10774	GDT1	UPF0016 membrane protein YBR187W	1194.496652	1.752261765	0.191514689	9.149490191	5.72E-20	1.25E-18
KLMA_10775	PCH2	pachytene checkpoint protein 2	168.4662498	1.844415501	0.23436171	7.869952386	3.55E-15	4.87E-14
KLMA_10781	GLY1	low specificity L-threonine aldolase	241.8618811	1.604501933	0.21659914	7.407702217	1.29E-13	1.48E-12
KLMA_10782	YDC1	alkaline ceramidase YDC1	1933.886018	2.179408546	0.358579907	6.077888092	1.22E-09	8.50E-09
KLMA_10783	SOU1	sorbose reductase SOU1	1972.091823	3.954532465	0.267438334	14.78670765	1.78E-49	1.78E-47
KLMA_10796	PNG1	peptide-N(4)-(N-acetyl-beta-glucosaminyl)asparagine amidase	249.5895478	1.153575148	0.220300057	5.236381534	1.64E-07	8.21E-07
KLMA_10804	ECM31	3-methyl-2-oxobutanoate hydroxymethyltransferase	192.5479121	1.017617337	0.22276683	4.56808285	4.92E-06	1.94E-05
KLMA_10805		uncharacterized abhydrolase domain-containing protein YGR015C	435.4059795	4.273516875	0.347010356	12.31524304	7.50E-35	4.41E-33
KLMA_10806		hypothetical protein	28.69197955	1.851504958	0.453668379	4.081185829	4.48E-05	0.00014435
KLMA_10814		oxidored-like super family	238.2390819	1.168555631	0.227909947	5.127269112	2.94E-07	1.41E-06
KLMA_10818	DAL3	ureidoglycolate hydrolase	115.7907542	1.769524885	0.278750649	6.348056548	2.18E-10	1.67E-09
KLMA_10830	Nqo2	ribosyldihydronicotinamide dehydrogenase [quinone]	1432.562977	1.379877548	0.18597687	7.41961917	1.17E-13	1.35E-12
KLMA_10836	FCY2	purine-cytosine permease FCY2	80.82266089	4.372459182	0.561315867	7.789658972	6.72E-15	8.97E-14
KLMA_20003		conserved hypothetical membrane	19.30093819	2.179065617	0.540139657	4.034263343	5.48E-05	0.000172925

Locus_tag	UniProt _gene	Product	baseMean	$\log_2$FoldChange	lfcSE	stat	pvalue	padj
		protein						
KLMA_20007	yxeK	putative monooxygenase yxeK	140.776473	1.045818822	0.280242584	3.731834059	0.000190091	0.000534486
KLMA_20008	FRE4	ferric reductase transmembrane component 4	510.0486481	1.377534857	0.39435097	3.493169697	0.000477323	0.001211037
KLMA_20009	ADY2	hypothetical protein	973.5749856	5.055265245	0.380980512	13.26909143	3.50E-40	2.90E-38
KLMA_20010		protein crtK	62.45035844	1.713544307	0.32835637	5.218550531	1.80E-07	8.98E-07
KLMA_20012	yciC	ras_like_GTPase super family	521.8543153	2.613848432	0.72399871	3.610294321	0.00030585	0.000815377
KLMA_20014		hypothetical protein	269.2869929	1.37867165	0.190817214	7.225090538	5.01E-13	5.39E-12
KLMA_20015	YUH1	ubiquitin carboxyl-terminal hydrolase YUH1	226.2714781	1.549550879	0.224184938	6.911931268	4.78E-12	4.60E-11
KLMA_20018	AIM25	altered inheritance rate of mitochondria protein 25	401.3976183	1.088491573	0.193644121	5.621092789	1.90E-08	1.10E-07
KLMA_20020		protein PEA2	505.9184859	1.07080115	0.252548676	4.239979266	2.24E-05	7.73E-05
KLMA_20027		hypothetical protein	93.34323512	4.891834387	1.041833132	4.695410652	2.66E-06	1.10E-05
KLMA_20032	MAG1	DNA-3-methyladenine glycosylase	148.9368	1.382079055	0.292230242	4.729418301	2.25E-06	9.45E-06
KLMA_20037	RFT1	oligosaccharide translocation protein RFT1	764.2834556	1.137040961	0.162842311	6.982466394	2.90E-12	2.85E-11
KLMA_20041	FUS3	mitogen-activated protein kinase FUS3	126.7124933	4.311361955	0.436855033	9.869090731	5.67E-23	1.57E-21
KLMA_20050	MIOX5	inositol oxygenase 1	118.160789	1.082384394	0.237066183	4.56574777	4.98E-06	1.96E-05
KLMA_20057		uricase	52.79982582	1.188525291	0.350502452	3.390918617	0.000696588	0.001712197
KLMA_20064		hypothetical conserved protein	68.54658907	1.818088635	0.32126928	5.659080238	1.52E-08	8.94E-08
KLMA_20069	SAP30	transcriptional regulatory protein SAP30	368.2727	1.776556652	0.309776863	5.734955908	9.75E-09	5.93E-08
KLMA_20070		metallo-dependent_hydrolases	108.8756023	2.41877036	0.304845157	7.934422781	2.11E-15	2.97E-14
KLMA_20072		hypothetical conserved protein	366.5317699	1.374159213	0.273644455	5.021695804	5.12E-07	2.37E-06
KLMA_20076	NIPA2	magnesium transporter NIPA2	195.00354	1.770913051	0.21186976	8.358498413	6.35E-17	1.03E-15

Locus_tag	UniProt _gene	Product	baseMean	log$_2$FoldChange	lfcSE	stat	pvalue	padj
KLMA_20101		sterol-sensing super family	1654.865426	1.332116775	0.306562856	4.345330002	1.39E-05	4.99E-05
KLMA_20105	CIT1	citrate synthase	12244.51674	1.089419556	0.157908457	6.8990577	5.23E-12	4.98E-11
KLMA_20111	RTT109	histone acetyltransferase RTT109	212.9501928	1.207433	0.20516639	5.885140361	3.98E-09	2.59E-08
KLMA_20117	ADR1	regulatory protein ADR1	971.8228571	3.750399573	0.222783414	16.83428538	1.37E-63	2.78E-61
KLMA_20130	ECM4	glutathione S-transferase omega-like 2	2419.741019	3.936429688	0.271365832	14.50598868	1.11E-47	1.04E-45
KLMA_20131		Golgi apparatus membrane protein TVP15	1853.089021	1.828624647	0.267415201	6.838147731	8.02E-12	7.49E-11
KLMA_20140	GSM1	glucose starvation modulator protein 1	204.8465582	1.65318214	0.29705993	5.565146873	2.62E-08	1.50E-07
KLMA_20164		hypothetical protein	120.7863109	1.475328268	0.286122395	5.156283794	2.52E-07	1.22E-06
KLMA_20174	DMC1	meiotic recombination protein DMC1	75.33177002	1.085756422	0.313309963	3.465438545	0.000529367	0.001329954
KLMA_20176		actin superfamily	94.10225983	1.075760407	0.244095988	4.40712039	1.05E-05	3.86E-05
KLMA_20193	PXA1	peroxisomal long-chain fatty acid import protein 2	181.7155576	3.331772079	0.319473883	10.42893414	1.83E-25	6.47E-24
KLMA_20194		UPF0613 protein PB24D3.06c	523.9225658	1.720381433	0.279536958	6.154397068	7.54E-10	5.44E-09
KLMA_20195	ppr1	acetyltransferases	241.7148361	1.579388938	0.180258368	8.761806466	1.92E-18	3.71E-17
KLMA_20200		SGT1 super family	112.9460357	1.092397368	0.325260254	3.358533222	0.000783573	0.001902073
KLMA_20203	SSP2	sporulation-specific protein 2	64.21992969	6.339799428	0.874986954	7.24559309	4.31E-13	4.70E-12
KLMA_20212	HST2	NAD-dependent deacetylase HST2	90.66735386	1.005913607	0.30051939	3.347250263	0.000816175	0.001974343
KLMA_20220	POT1	3-ketoacyl-CoA thiolase	153.0895362	2.814214995	0.32807027	8.578086013	9.65E-18	1.74E-16
KLMA_20221	THI72	thiamine transporter	218.7279271	1.641600696	0.228770882	7.175741443	7.19E-13	7.60E-12
KLMA_20223	DSD1	D-serine dehydratase	491.7746084	1.129170303	0.166516716	6.781122837	1.19E-11	1.09E-10
KLMA_20241	ERT1	uncharacterized transcriptional regulatory protein YBR239C	476.9056834	1.328156524	0.318142744	4.174718887	2.98E-05	0.000100149
KLMA_20248	CSM1	monopolin complex subunit CSM1	100.5858473	1.191211376	0.226744938	5.253530177	1.49E-07	7.56E-07
KLMA_20258	JEN1	putative sialic acid transporter	234.3247852	2.895917741	0.251954227	11.49382481	1.42E-30	6.99E-29

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KLMA_20261		hypothetical protein	50.6852782	1.54724904	0.369654621	4.185661297	2.84E-05	9.60E-05
KLMA_20263	POX1	acyl-coenzyme A oxidase	362.2944928	2.145403376	0.213884326	10.03067131	1.12E-23	3.31E-22
KLMA_20269		mitochondrial outer membrane protein OM14	1462.791683	3.471927784	0.582639608	5.958962859	2.54E-09	1.69E-08
KLMA_20273	SLX1	structure-specific endonuclease subunit SLX1	306.5188488	3.154955458	0.256608459	12.29482253	9.66E-35	5.61E-33
KLMA_20292		uncharacterized protein YEL137C	160.2186623	1.638812129	0.250574846	6.540210065	6.14E-11	5.07E-10
KLMA_20296	GPD2	glyceraldehyde-3-phosphate dehydrogenase 2	65.64796201	4.149256117	0.477471807	8.690054695	3.62E-18	6.86E-17
KLMA_20298	IME4	N6-adenosine-methyltransferase IME4	166.972017	2.786545368	0.43196793	6.45081538	1.11E-10	8.88E-10
KLMA_20301	RIM15	serine/threonine-protein kinase RIM15	1634.850192	1.327082225	0.222815957	5.955956839	2.59E-09	1.72E-08
KLMA_20303		basic-leucine zipper (bZIP) transcription factor	22658.11645	1.082331172	0.220443586	4.909787547	9.12E-07	4.07E-06
KLMA_20304	AGX1	alanine--glyoxylate aminotransferase 1	912.5706414	3.210109506	0.212513887	15.10541056	1.49E-51	1.62E-49
KLMA_20317	SPS4	sporulation-specific protein 4	95.92074163	1.489349374	0.365766948	4.071853355	4.66E-05	0.000149666
KLMA_20324	YHM2	mitochondrial DNA replication protein YHM2	1661.947786	1.070450563	0.214468119	4.991187355	6.00E-07	2.75E-06
KLMA_20327	RRG7	uncharacterized protein YOR305W	70.83302543	1.027191166	0.294609263	3.486622092	0.000489162	0.0012385
KLMA_20329	CUS1	protein CUS1	238.4940638	1.218919974	0.188452918	6.468034503	9.93E-11	7.98E-10
KLMA_20334		hypothetical protein	37.78137545	1.635866505	0.436171249	3.750514294	0.000176472	0.000500517
KLMA_20345		protein FUN14	850.9703904	2.757756831	0.275607051	10.00611856	1.43E-23	4.19E-22
KLMA_20368		uncharacterized membrane protein YAL018C	6.305924971	3.922408551	1.291702348	3.036619509	0.002392472	0.005246895
KLMA_20380		hypothetical protein	103.7894433	3.825251332	0.935482225	4.089068963	4.33E-05	0.000139808
KLMA_20381	OSW5	hypothetical protein	16.74067895	5.400034187	1.160385291	4.653656184	3.26E-06	1.33E-05
KLMA_20383	IMP1	mitochondrial inner membrane	54.8515523	1.089772379	0.298158982	3.655004358	0.000257178	0.000697825

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		protease subunit 1						
KLMA_20384		hypothetical protein	13.7410609	4.056579205	0.988679439	4.103027779	4.08E-05	0.000132331
KLMA_20389	RAM1	protein farnesyltransferase subunit beta	184.2868112	1.199898397	0.208150868	5.764561102	8.19E-09	5.07E-08
KLMA_20426	RAD55	p-loop NTPase super family	453.7824541	1.316187607	0.243328708	5.409092989	6.33E-08	3.41E-07
KLMA_20427		hypothetical protein	17930.03697	2.195052392	0.717247062	3.060385339	0.002210524	0.004869733
KLMA_20428	MUC1	flocculation protein FLO11	448.5524221	1.166211339	0.201340917	5.792222256	6.95E-09	4.35E-08
KLMA_20431		uncharacterized protein YER152C	328.0191474	1.308065739	0.236349969	5.534444292	3.12E-08	1.76E-07
KLMA_20435		KH domain-containing protein YLL032C	586.2676888	1.244845826	0.146201518	8.514588953	1.67E-17	2.93E-16
KLMA_20442	UBI4	ubiquitin	7738.090765	1.355329856	0.233802235	5.796907188	6.75E-09	4.24E-08
KLMA_20457	POM33	UPF0121 membrane protein YLL023C	1400.186072	1.163419105	0.190383188	6.110934044	9.90E-10	7.07E-09
KLMA_20462	uapC	purine permease	681.5739341	2.205409339	0.179664619	12.27514552	1.23E-34	7.08E-33
KLMA_20473	FAB1	1-phosphatidylinositol-3-phosphate 5-kinase FAB1	1906.983516	1.526975133	0.155420718	9.824784962	8.81E-23	2.38E-21
KLMA_20499	AOS1	DNA damage tolerance protein RHC31	262.1606128	1.117087136	0.177401517	6.296942394	3.04E-10	2.27E-09
KLMA_20504		NAP1-binding protein	173.0073955	1.079716344	0.223213064	4.837155687	1.32E-06	5.75E-06
KLMA_20509	SYF2	pre-mRNA-splicing factor SYF2	112.5429639	1.049783567	0.238430459	4.402892027	1.07E-05	3.93E-05
KLMA_20523		hypothetical protein	95.99023749	1.51795182	0.286980966	5.289381522	1.23E-07	6.29E-07
KLMA_20536		yjgF_YER057c_UK114_family	387.1525869	1.401620152	0.219854043	6.375230268	1.83E-10	1.42E-09
KLMA_20542	PIN3	[PSI+] inducibility protein 3	957.744179	2.164736897	0.224999424	9.621077503	6.51E-22	1.62E-20
KLMA_20546	VPS62	vacuolar protein sorting-associated protein 62	830.8364889	1.956692314	0.180381051	10.84754916	2.05E-27	8.62E-26
KLMA_20547		protein BTN2	197.1536396	1.513752723	0.246707136	6.135828677	8.47E-10	6.09E-09
KLMA_20581	MUS81	crossover junction endonuclease MUS81	201.0318506	1.141245875	0.252626187	4.517528014	6.26E-06	2.42E-05

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KLMA_20586	ATO2	hypothetical protein	3811.784197	1.079339657	0.346425782	3.115644711	0.001835433	0.00411393
KLMA_20597	ARO10	transaminated amino acid decarboxylase	480.4351197	1.29959802	0.221894883	5.856818348	4.72E-09	3.02E-08
KLMA_20604	IAH1	isoamyl acetate-hydrolyzing esterase	274.305299	4.479833965	0.350547827	12.77952284	2.13E-37	1.49E-35
KLMA_20607		YTH super family	188.6633963	5.299209629	0.411196102	12.88730512	5.31E-38	3.81E-36
KLMA_20609	FRQ1	calcium-binding protein NCS-1	534.0676391	1.049123213	0.196517785	5.338566253	9.37E-08	4.90E-07
KLMA_20612	CTS2	sporulation-specific chitinase 2	246.3059911	2.303690181	0.803697092	2.866366201	0.004152136	0.008666254
KLMA_20621	SNG1	nitrosoguanidine resistance protein SNG1	489.3150796	1.277859768	0.18447985	6.926825699	4.30E-12	4.16E-11
KLMA_20634	PEX11	peroxisomal membrane protein PMP27	188.0454326	1.357801523	0.298429424	4.549824558	5.37E-06	2.10E-05
KLMA_20654	SNU23	U4/U6.U5 small nuclear ribonucleoprotein component	95.64155853	1.44225754	0.279411555	5.161767702	2.45E-07	1.19E-06
KLMA_20658		uncharacterized membrane protein YMR155W	626.8152388	1.967314099	0.192918925	10.19762111	2.03E-24	6.62E-23
KLMA_20659	MSC1	meiotic sister chromatid recombination protein 1	2177.629594	3.888270744	0.662325109	5.870637684	4.34E-09	2.81E-08
KLMA_20660		UPF0549 protein C1D4.09c	224.0987323	1.628075524	0.313780604	5.188579232	2.12E-07	1.04E-06
KLMA_20673	ALD2	aldehyde dehydrogenase [NAD(P)+] 1	506.3715929	1.304185113	0.255589301	5.102659254	3.35E-07	1.60E-06
KLMA_20675	MLH1	DNA mismatch repair protein MLH1	172.9476537	1.098051164	0.196329624	5.592895987	2.23E-08	1.28E-07
KLMA_20685		uncharacterized protein YJR003C	307.5585631	1.13674584	0.209429537	5.427820042	5.70E-08	3.10E-07
KLMA_20689	FYV8	protein FYV8	328.621875	1.398007356	0.18250535	7.660089722	1.86E-14	2.33E-13
KLMA_20709	ATG14	autophagy-related protein 14	211.146902	2.870562391	0.445993505	6.436332271	1.22E-10	9.70E-10
KLMA_20730		hypothetical protein	147.6403959	1.914567815	0.332597541	5.756410019	8.59E-09	5.31E-08
KLMA_20734	GDH2	NAD-specific glutamate dehydrogenase	2593.153872	2.402657443	0.169407389	14.18271933	1.17E-45	1.02E-43
KLMA_20757		uncharacterized protein YNL165W	709.9704412	1.312705284	0.218164413	6.017045884	1.78E-09	1.20E-08

Locus_tag	UniProt _gene	Product	baseMean	log$_2$FoldChange	lfcSE	stat	pvalue	padj
KLMA_20766	MEP2	ammonium transporter MEP2	389.3130207	2.735485493	0.209486073	13.05807803	5.72E-39	4.29E-37
KLMA_20771	HSP12	12 kDa heat shock protein	1483.443403	6.269192017	1.241956183	5.047836713	4.47E-07	2.09E-06
KLMA_20780		chaperone_DMP super family	50.98069963	1.14883461	0.314633906	3.651337599	0.000260878	0.000706671
KLMA_20781	YUC8	trkA	489.3694883	4.092210698	0.305733578	13.38489125	7.41E-41	6.24E-39
KLMA_20791	ISU1	iron sulfur cluster assembly protein 1	850.7194042	1.09772464	0.169888415	6.46144493	1.04E-10	8.32E-10
KLMA_20793		MTP18 super family	869.8342261	1.484777154	0.171244482	8.670510919	4.30E-18	8.10E-17
KLMA_20795	ODC2	mitochondrial 2-oxodicarboxylate carrier 2	3416.066541	1.020746788	0.327171072	3.119917606	0.001809016	0.004064046
KLMA_20797	RDS2	regulator of drug sensitivity 2	347.8440585	1.012360121	0.193617346	5.228664393	1.71E-07	8.54E-07
KLMA_20806	STE4	guanine nucleotide-binding protein subunit beta	620.2074151	1.446588743	0.201240699	7.188350819	6.56E-13	6.95E-12
KLMA_20813	PTP2	tyrosine-protein phosphatase 2	810.851954	1.642629411	0.315245708	5.210632119	1.88E-07	9.34E-07
KLMA_20815	RNY1	ribonuclease T2-like	323.2263949	2.552075718	0.287043914	8.890889475	6.06E-19	1.21E-17
KLMA_20816	RNY1	ribonuclease T2-like	356.6415712	2.645372773	0.306389243	8.634026275	5.92E-18	1.09E-16
KLMA_20819		hypothetical protein	229.6539206	5.169572214	0.396161623	13.04914942	6.43E-39	4.76E-37
KLMA_20823		uncharacterized transporter YBR287W	2292.590749	1.431853914	0.320081325	4.473406612	7.70E-06	2.91E-05
KLMA_20825	KHA1	K(+)/H(+) antiporter 1	1792.297338	1.06021564	0.178103661	5.952800936	2.64E-09	1.75E-08
KLMA_20826	FEN2	pantothenate transporter FEN2	253.6651656	1.909576131	0.221896431	8.605709091	7.58E-18	1.38E-16
KLMA_20834	amdS	acetamidase	54.44747654	2.326278401	0.513181129	4.533055231	5.81E-06	2.26E-05
KLMA_20837		FMN_red super family	223.0102796	1.466085771	0.387789949	3.780618283	0.000156439	0.000446813
KLMA_30011		beta-glucosidase	4366.573528	1.429097352	0.209343352	6.826571463	8.70E-12	8.06E-11
KLMA_30013	CYB2	cytochrome b2	83.88934111	1.566667939	0.353981382	4.42584842	9.61E-06	3.57E-05
KLMA_30014		conserved hypothetical transmembrane protein	169.9859108	1.394524632	0.309363451	4.507722646	6.55E-06	2.52E-05
KLMA_30015	bioA	uncharacterized aminotransferase C1771.03c	279.3998338	2.490550055	0.254524114	9.785124154	1.30E-22	3.48E-21

Locus_tag	UniProt_gene	Product	baseMean	log_2FoldChange	lfcSE	stat	pvalue	padj
KLMA_30016	YPR1	putative reductase 1	931.5779752	2.880781785	0.186857999	15.41695727	1.26E-53	1.62E-51
KLMA_30017	PUT4	probable proline-specific permease put4	536.1977841	3.317044136	0.36083073	9.192798352	3.83E-20	8.50E-19
KLMA_30018	ARI1	putative uncharacterized oxidoreductase YGL157W	167.3680953	1.370515385	0.367280719	3.731520098	0.000190328	0.000534845
KLMA_30019	fmo1	thiol-specific monooxygenase	292.8724967	2.094024224	0.331073037	6.324961527	2.53E-10	1.92E-09
KLMA_30037	mug157	meiotically up-regulated gene 157 protein	527.1059178	1.809902359	0.23464809	7.713262694	1.23E-14	1.58E-13
KLMA_30056		ubiquitin-binding protein CUE2	30.53808261	1.132426481	0.375153179	3.018570931	0.002539699	0.005537452
KLMA_30079		centromere DNA-binding protein complex CBF3 subunit	145.6581766	1.349292022	0.314908225	4.284715082	1.83E-05	6.43E-05
KLMA_30082	FUS2	nuclear fusion protein FUS2	15.20699002	1.937596595	0.583085428	3.323006378	0.000890529	0.00213832
KLMA_30086	mug14	meiotically up-regulated gene 14 protein	285.680689	2.159344378	0.258418748	8.355989632	6.49E-17	1.05E-15
KLMA_30087	RNH1	ribonuclease H	34.44237925	1.756384919	0.473219896	3.711561861	0.000205984	0.000574217
KLMA_30095		signal recognition particle subunit SRP21	314.6930668	1.502261583	0.19822891	7.57841823	3.50E-14	4.28E-13
KLMA_30100	YKU80	ATP-dependent DNA helicase II subunit 2	194.0653444	1.47926363	0.261751859	5.651396848	1.59E-08	9.32E-08
KLMA_30101	SPG4	uncharacterized protein YMR107W	635.3724629	5.596596728	0.27721779	20.18844722	1.24E-90	7.55E-88
KLMA_30112		uncharacterized protein YMR114C	246.6882976	2.123774099	0.299800446	7.083959114	1.40E-12	1.42E-11
KLMA_30124		succinate dehydrogenase [ubiquinone] cytochrome b subunit	4043.444797	1.018807738	0.177078683	5.753418322	8.75E-09	5.39E-08
KLMA_30129		hypothetical protein	831.6314501	2.839148636	0.331218008	8.571842615	1.02E-17	1.83E-16
KLMA_30133	RRG1	uncharacterized protein YDR065W	268.8951464	1.307507759	0.264838508	4.937000178	7.93E-07	3.58E-06
KLMA_30134	RTR1	RNA polymerase II-associated protein 2 homolog	182.3174693	1.802671723	0.247675275	7.278367717	3.38E-13	3.73E-12
KLMA_30137	mlo2	protein mlo2	639.3390379	2.124470387	0.228906884	9.280937088	1.68E-20	3.83E-19
KLMA_30151	SSP120	protein SSP120	281.6091493	1.336332366	0.209813404	6.369146776	1.90E-10	1.47E-09

Locus_tag	UniProt _gene	Product	baseMean	log$_2$FoldChange	lfcSE	stat	pvalue	padj
KLMA_30152	SPO1	putative meiotic phospholipase SPO1	61.83229519	2.80575277	0.41311635	6.791676901	1.11E-11	1.02E-10
KLMA_30161	TOK1	outward-rectifier potassium channel TOK1	376.9623613	1.648552304	0.246697572	6.682482889	2.35E-11	2.06E-10
KLMA_30163	SRS2	ATP-dependent DNA helicase SRS2	257.8171535	1.003477998	0.211526039	4.743992766	2.10E-06	8.88E-06
KLMA_30166	SIP4	protein SIP4	703.8982253	2.441905476	0.336352615	7.259956868	3.87E-13	4.25E-12
KLMA_30183	RTG1	retrograde regulation protein 1	50.6167148	1.15260692	0.370976478	3.106954185	0.001890257	0.004221314
KLMA_30191	NAM8	protein NAM8	1063.204489	1.003817872	0.329571085	3.045831133	0.002320381	0.005100244
KLMA_30192		protein PET130	197.4121661	1.63836736	0.197677835	8.288068096	1.15E-16	1.86E-15
KLMA_30200	OKP1	central kinetochore subunit OKP1	207.8774319	1.019181795	0.200401786	5.085692177	3.66E-07	1.74E-06
KLMA_30231	MMM1	maintenance of mitochondrial morphology protein 1	158.0517389	1.033397238	0.225435604	4.584001902	4.56E-06	1.81E-05
KLMA_30242	CUE5	ubiquitin-binding protein CUE5	653.4153458	1.057930296	0.231338959	4.573074509	4.81E-06	1.90E-05
KLMA_30243	GLO4	hydroxyacylglutathione hydrolase	969.1779845	2.471063738	0.222588608	11.10148341	1.23E-28	5.48E-27
KLMA_30244		WD40 super family protein	360.4243561	2.089180221	0.281316012	7.426453284	1.12E-13	1.29E-12
KLMA_30245		protein midA homolog	184.8125607	1.965205734	0.239154287	8.217313427	2.08E-16	3.25E-15
KLMA_30258	ASE1	anaphase spindle elongation protein	393.0480176	1.15982633	0.182981521	6.338488838	2.32E-10	1.77E-09
KLMA_30260		putative lipase YOR059C	553.2972238	1.068072956	0.155287916	6.87801721	6.07E-12	5.74E-11
KLMA_30272		DUF676 super family[cl10636]	279.9073774	1.295487051	0.208915716	6.201003338	5.61E-10	4.10E-09
KLMA_30282		NAD(+) kinase	449.294741	1.149948719	0.168419273	6.827892658	8.62E-12	8.00E-11
KLMA_30312	ACO2	aconitate hydratase	19972.30461	1.149186381	0.265759499	4.324159196	1.53E-05	5.45E-05
KLMA_30316	UBC12	NEDD8-conjugating enzyme UBC12	49.93655073	1.246106908	0.334469455	3.725622438	0.000194834	0.000546251
KLMA_30321	ATG1	serine/threonine-protein kinase ATG1	1303.272335	1.071755996	0.173963958	6.16079335	7.24E-10	5.24E-09
KLMA_30322	MND1	meiotic nuclear division protein 1	13.17406897	4.426757143	0.982687388	4.504746062	6.65E-06	2.55E-05
KLMA_30323		zinc finger protein YER130C	2118.329391	2.115381103	0.308660091	6.853432504	7.21E-12	6.76E-11
KLMA_30331		hypothetical protein	79.61131714	2.275559764	0.370272163	6.145640938	7.96E-10	5.74E-09

Locus_tag	**UniProt _gene**	**Product**	**baseMean**	**log$_2$FoldChange**	**lfcSE**	**stat**	**pvalue**	**padj**
KLMA_30332		sporulation protein 23	839.546106	3.322236212	0.204709713	16.22901111	3.14E-59	5.30E-57
KLMA_30336	VTI1	t-SNARE VTI1	786.5702055	1.024489762	0.15295909	6.697802393	2.12E-11	1.87E-10
KLMA_30343		central kinetochore subunit MCM21	357.1900685	1.866346689	0.205472265	9.083204921	1.05E-19	2.26E-18
KLMA_30344		protein HIM1	1362.741455	3.438406864	0.232776498	14.77128013	2.24E-49	2.19E-47
KLMA_30354	LEE1	YTH1[COG5084]	900.8554218	2.084734728	0.194776293	10.70322621	9.83E-27	3.94E-25
KLMA_30363	PDR12	ATP-dependent permease PDR12	1941.947745	2.067693351	0.196899053	10.50128641	8.52E-26	3.08E-24
KLMA_30364	EXO5	defects in morphology protein 1	176.8825277	1.378469987	0.254198622	5.422806686	5.87E-08	3.18E-07
KLMA_30365		putative pyridoxal reductase	959.6556111	2.700993618	0.179150085	15.07670853	2.30E-51	2.45E-49
KLMA_30369		hypothetical protein	2243.343337	1.087041042	0.235353364	4.618761429	3.86E-06	1.55E-05
KLMA_30371	CMK2	calcium/calmodulin-dependent protein kinase II	920.5136217	1.381843962	0.235863805	5.858652051	4.67E-09	2.99E-08
KLMA_30395		ZZ_NBR1_like protein	606.2873295	1.074766149	0.236148248	4.551234901	5.33E-06	2.08E-05
KLMA_30396	PHM7	phosphate metabolism protein 7	1874.616193	3.463461277	0.325384845	10.64419972	1.86E-26	7.31E-25
KLMA_30399		conserved hypothetical membrane protein	26.03912406	2.171532311	0.624074307	3.479605371	0.000502153	0.001266795
KLMA_30405	TAD2	tRNA-specific adenosine deaminase subunit TAD2	79.85094363	1.317839346	0.282387676	4.666773579	3.06E-06	1.25E-05
KLMA_30406	SNX4	sorting nexin-4	366.371942	1.321689994	0.239991791	5.507230021	3.65E-08	2.05E-07
KLMA_30410	ZIP1	synaptonemal complex protein ZIP1	222.5970575	1.634635673	0.2292642	7.129921183	1.00E-12	1.04E-11
KLMA_30411	YIM1	uncharacterized protein YMR152W	2843.871327	1.197699314	0.126037771	9.502701457	2.05E-21	4.87E-20
KLMA_30412	DPP1	diacylglycerol pyrophosphate phosphatase 1	1858.495359	1.332091607	0.239361009	5.565198835	2.62E-08	1.50E-07
KLMA_30426	DPL1	sphingosine-1-phosphate lyase	1957.856656	2.324473844	0.255325832	9.10395094	8.71E-20	1.88E-18
KLMA_30428		uncharacterized protein YHR035W	432.3789557	1.446246576	0.177190272	8.162110489	3.29E-16	5.02E-15
KLMA_30434	PIH1	protein interacting with Hsp90 1	186.0959243	1.118812726	0.192427925	5.814191074	6.09E-09	3.85E-08
KLMA_30444		vacuolar membrane protein YPL162C	240.5935458	1.388137003	0.221870683	6.256513852	3.94E-10	2.90E-09

Locus_tag	UniProt _gene	Product	baseMean	$\log_2$FoldChange	lfcSE	stat	pvalue	padj
KLMA_30446	MLH3	DNA mismatch repair protein MLH3	317.0666202	1.215233056	0.263562318	4.610799703	4.01E-06	1.61E-05
KLMA_30452	REV3	DNA polymerase zeta catalytic subunit	246.3242622	1.244289164	0.261512053	4.758056664	1.95E-06	8.33E-06
KLMA_30462	NIP100	protein NIP100	253.1540416	1.058374242	0.195532663	5.412774663	6.21E-08	3.35E-07
KLMA_30482		glyoxalase super family protein	1614.900021	2.164268537	0.146554061	14.76771458	2.37E-49	2.27E-47
KLMA_30518		uncharacterized protein YDR239C	274.7289725	1.402745645	0.265945646	5.274557664	1.33E-07	6.79E-07
KLMA_30524		putative cation exchanger YDL206W	512.7289997	1.455403676	0.231589764	6.284404159	3.29E-10	2.44E-09
KLMA_30533		4,5-DOPA dioxygenase extradiol-like protein	377.2173351	1.804269972	0.213185297	8.463388414	2.60E-17	4.45E-16
KLMA_30538		hypothetical protein	205.3992384	2.050587867	0.362509247	5.656649815	1.54E-08	9.06E-08
KLMA_30550	PIB1	E3 ubiquitin-protein ligase PIB1	255.1185711	1.314251402	0.212606573	6.181612286	6.35E-10	4.63E-09
KLMA_30555		conserved hypothetical transmembrane protein	484.7814036	5.067269813	0.931051577	5.442523202	5.25E-08	2.87E-07
KLMA_30556	GAD1	glutamate decarboxylase	3467.503444	1.175980069	0.16629716	7.071558358	1.53E-12	1.55E-11
KLMA_30563	PRR1	probable serine/threonine-protein kinase YKL116C	652.3221481	2.021677923	0.250764124	8.062070003	7.50E-16	1.12E-14
KLMA_30564	APN1	DNA-(apurinic or apyrimidinic site) lyase 1	188.4454669	1.103067627	0.220305956	5.006980498	5.53E-07	2.55E-06
KLMA_30572	IME2	meiosis induction protein kinase IME2/SME1	140.7087514	1.206086633	0.282422662	4.270502313	1.95E-05	6.83E-05
KLMA_30573		conserved hypothetical transmembrane protein	2857.23106	2.759254336	0.265625961	10.38774344	2.82E-25	9.84E-24
KLMA_30577	ARA1	D-arabinose dehydrogenase [NAD(P)+] heavy chain	323.1826635	2.14100021	0.206053076	10.39052777	2.74E-25	9.62E-24
KLMA_30597	OAF1	peroxisome proliferation transcriptional regulator	528.1383281	1.092309874	0.164946585	6.622203622	3.54E-11	3.01E-10
KLMA_30598	OAF1	oleate-activated transcription factor 1	257.252577	1.38600887	0.208667443	6.642190308	3.09E-11	2.65E-10
KLMA_30601		probable metabolite transport protein C1271.09	166.6553464	1.143196387	0.284610554	4.016704124	5.90E-05	0.000184534

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KLMA_30602	ACS1	acetyl-coenzyme A synthetase 1	2646.297416	4.58474723	0.389158693	11.78117645	4.88E-32	2.56E-30
KLMA_30604		probable 2-nitropropane dioxygenase	332.504821	1.793399591	0.213396797	8.404060472	4.31E-17	7.26E-16
KLMA_30607	STL1	sugar transporter STL1	1427.785343	2.632552507	0.269993543	9.750427658	1.84E-22	4.82E-21
KLMA_30619	REC8	meiotic recombination protein REC8	135.8765806	1.082080091	0.238550109	4.53607042	5.73E-06	2.23E-05
KLMA_30623	mug70	meiotically up-regulated gene 70 protein	308.9018338	1.012850683	0.249370352	4.061632332	4.87E-05	0.000155862
KLMA_30624		conserved hypothetical transmembrane protein	87.77147143	1.738614013	0.371861046	4.675440006	2.93E-06	1.20E-05
KLMA_30629	FMP48	calcium/calmodulin-dependent protein kinase type 1D	4358.048289	1.679145066	0.248120728	6.767451795	1.31E-11	1.19E-10
KLMA_30633	RME1	conserved hypothetical membrane protein	672.5736643	1.82987836	0.218880998	8.360151753	6.26E-17	1.02E-15
KLMA_30642		conserved hypothetical transmembrane protein	189.9347656	1.180887384	0.329318579	3.585851086	0.000335981	0.000887949
KLMA_30644	PNS1	protein PNS1	1163.083967	2.204111764	0.232771177	9.469006389	2.83E-21	6.67E-20
KLMA_30654	CAT2	carnitine O-acetyltransferase	429.0585324	2.651457374	0.35295648	7.512136833	5.82E-14	6.93E-13
KLMA_30672		probable metabolite transport protein C1271.09	1311.023465	3.820914106	0.288294348	13.25351721	4.31E-40	3.50E-38
KLMA_30673		vacuolar morphogenesis protein 7	317.7691255	1.344458339	0.179553908	7.487769855	7.01E-14	8.27E-13
KLMA_30679	SDT1	protein SSM1	457.0114827	2.615785959	0.270425752	9.672843413	3.93E-22	9.95E-21
KLMA_30710	ATG32	protein ECM37	654.0120583	1.215597329	0.198280845	6.130684622	8.75E-10	6.27E-09
KLMA_30728	LAC12	lactose permease	406.3984377	2.43779149	0.372284034	6.548203157	5.82E-11	4.83E-10
KLMA_40003		probable acid phosphatase	599.7285525	8.262336911	0.537324639	15.37680632	2.34E-53	2.86E-51
KLMA_40004	THI13	pyrimidine precursor biosynthesis enzyme THI13	20.86457075	3.442345456	0.630349347	5.461012174	4.73E-08	2.60E-07
KLMA_40005		UPF0317 protein C5H10.01	59.90718468	1.537630517	0.400335175	3.840857894	0.000122605	0.000361378
KLMA_40006		uncharacterized transporter C1683.12	207.1629797	1.458628205	0.187117392	7.795257223	6.43E-15	8.62E-14
KLMA_40007	OXP1	uncharacterized protein YKL215C	215.789259	1.708172226	0.210149532	8.128365593	4.35E-16	6.58E-15

Locus_tag	**UniProt_gene**	**Product**	**baseMean**	**log$_2$FoldChange**	**lfcSE**	**stat**	**pvalue**	**padj**
KLMA_40010		uncharacterized protein YMR315W	1535.021268	1.292530154	0.203937318	6.337879536	2.33E-10	1.77E-09
KLMA_40011	ESF2	pre-rRNA-processing protein ESF2	359.802767	1.374868012	0.209756543	6.554589395	5.58E-11	4.64E-10
KLMA_40016	LYS9	saccharopine dehydrogenase [NADP+	5841.631212	1.082113109	0.273248299	3.960182422	7.49E-05	0.000230773
KLMA_40031	EST2	telomerase reverse transcriptase	422.1515767	1.072248537	0.202536877	5.294090406	1.20E-07	6.14E-07
KLMA_40040	TFG2	transcription initiation factor IIF subunit beta	814.3767172	1.018240331	0.201835607	5.044899384	4.54E-07	2.12E-06
KLMA_40041		pre-mRNA-splicing factor 18	64.21661998	1.220433615	0.304970974	4.001802524	6.29E-05	0.000196052
KLMA_40042		uncharacterized membrane protein YLR326W	134.2907549	1.387221318	0.277412249	5.000577026	5.72E-07	2.63E-06
KLMA_40049	MSB2	hansenula MRAKII killer toxin-resistant protein	2803.634644	1.49956631	0.131628308	11.39243021	4.56E-30	2.14E-28
KLMA_40050		uncharacterized abhydrolase domain-containing protein YGR015C	566.9396959	2.029491367	0.188166571	10.78561063	4.03E-27	1.68E-25
KLMA_40052		meiotic recombination protein REC102	196.4816087	1.238175687	0.211128893	5.86454877	4.50E-09	2.91E-08
KLMA_40055	MDH3	malate dehydrogenase	950.8141094	1.797938294	0.207638841	8.658969045	4.76E-18	8.91E-17
KLMA_40057	PSO2	interstrand crosslink repair protein	498.0169871	1.439145414	0.220481417	6.52728668	6.70E-11	5.50E-10
KLMA_40058	GAT2	hypothetical protein	393.6871854	1.091593666	0.19743768	5.528801108	3.22E-08	1.82E-07
KLMA_40059	GID8	glucose-induced degradation protein 8	243.566174	1.315262973	0.206798632	6.360114464	2.02E-10	1.55E-09
KLMA_40061		cell wall protein YLR040C	171.9520924	4.729713681	0.371315208	12.73773222	3.65E-37	2.47E-35
KLMA_40062		meiotic recombination protein	10.2993785	2.495706727	0.801337812	3.114425265	0.001843036	0.004129078
KLMA_40068		DNA mismatch repair protein MLH2	132.2281772	3.877969746	0.411790174	9.417344043	4.63E-21	1.08E-19
KLMA_40098	ISA1	iron sulfur assembly-related protein	646.5715374	1.428260353	0.234557923	6.089158417	1.14E-09	7.96E-09
KLMA_40105		uncharacterized glycosyl hydrolase YBR056W	446.8236855	2.169050036	0.242695862	8.937317753	3.99E-19	8.15E-18
KLMA_40106		uncharacterized protein YDR210W	75.80536615	1.52424988	0.299824743	5.083802834	3.70E-07	1.75E-06

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KLMA_40117	NRG1	transcriptional regulator NRG1	231.9858597	1.225904739	0.218336629	5.614746104	1.97E-08	1.14E-07
KLMA_40128	HSP26	heat shock protein 26	756.1213352	2.462879127	0.238715523	10.31721396	5.89E-25	2.00E-23
KLMA_40133		uncharacterized sugar kinase YDR109C	1982.729631	1.698564063	0.309282504	5.491950055	3.98E-08	2.21E-07
KLMA_40145	TMA64	translation machinery-associated protein 64	652.314623	1.291149855	0.215715392	5.985432201	2.16E-09	1.45E-08
KLMA_40148		putative aryl-alcohol dehydrogenase YPL088W	493.7320749	1.631912874	0.238333103	6.847193504	7.53E-12	7.05E-11
KLMA_40152	NYV1	vacuolar v-SNARE NYV1	364.2452045	1.161709886	0.182851347	6.353302308	2.11E-10	1.62E-09
KLMA_40172		uncharacterized protein YDR132C	683.9139554	1.555578497	0.141642854	10.98240014	4.64E-28	2.01E-26
KLMA_40173	AHP1	peroxiredoxin type-2	5236.618332	1.973801893	0.276630237	7.135163222	9.67E-13	1.01E-11
KLMA_40181		hypothetical protein	165.1462997	1.043176228	0.24210782	4.308725871	1.64E-05	5.83E-05
KLMA_40198	UGA1	4-aminobutyrate aminotransferase	1650.097234	3.360683204	0.303137097	11.08634753	1.46E-28	6.43E-27
KLMA_40202	ENA5	sodium transport ATPase 5	495.6445977	2.627482203	0.264196974	9.945163895	2.65E-23	7.56E-22
KLMA_40212		solute carrier family 2	206.597566	4.169176996	0.368172114	11.32398906	9.98E-30	4.60E-28
KLMA_40213		MOG interacting and ectopic P-granules protein	475.7809636	2.767336426	0.356306792	7.766723748	8.05E-15	1.06E-13
KLMA_40215	CDC13	cell division control protein 13	443.3896016	1.092553108	0.232332838	4.702534173	2.57E-06	1.07E-05
KLMA_40216		uncharacterized protein YNL193W	455.2188191	3.006078706	0.32195122	9.337062623	9.90E-21	2.29E-19
KLMA_40217	CHS1	chitin synthase 1	1824.862783	1.258720888	0.237514217	5.299560186	1.16E-07	5.99E-07
KLMA_40230		hypothetical protein	75.65480635	1.778679779	0.345816444	5.143421628	2.70E-07	1.30E-06
KLMA_40231	SPO14	phospholipase D1	182.3936214	1.063473061	0.293069885	3.628735386	0.000284813	0.000765562
KLMA_40244	PDR5	ATP-dependent permease PDR15	543.784625	2.719842044	0.299017971	9.095915	9.38E-20	2.02E-18
KLMA_40246		hypothetical protein	264.9013118	1.649409962	0.208536673	7.90944796	2.59E-15	3.60E-14
KLMA_40247	RTC3	SDO1-like protein YHR087W	243.0724462	4.474415421	0.341240261	13.11221429	2.80E-39	2.17E-37
KLMA_40260		hypothetical protein	5.08612249	5.562896157	1.50597452	3.693884646	0.000220854	0.000610788

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KLMA_40262	YPS7	aspartic proteinase yapsin-7	722.4430116	1.641552597	0.195326179	8.40416071	4.31E-17	7.26E-16
KLMA_40271		zinc finger protein	18.6647369	7.438410921	1.284882895	5.789174213	7.07E-09	4.42E-08
KLMA_40272		v-type proton ATPase catalytic subunit A	258.3423796	1.881732123	0.319477095	5.890037671	3.86E-09	2.52E-08
KLMA_40276	SAE2	hypothetical protein	106.0539711	1.041876181	0.273921184	3.803561905	0.00014263	0.000413171
KLMA_40282		uncharacterized protein YJL016W/YJL017W	1535.108056	2.260015952	0.134839622	16.76077042	4.72E-63	8.88E-61
KLMA_40288		hypothetical protein	66.63328198	2.075879628	0.322693699	6.432972305	1.25E-10	9.89E-10
KLMA_40293		leucine-rich repeat-containing protein 6	54.59444021	2.147048336	0.476508975	4.505787823	6.61E-06	2.54E-05
KLMA_40316	ELM1	probable myosin light chain kinase DDB_G0271550	67.3873092	1.551324397	0.270857295	5.727460279	1.02E-08	6.19E-08
KLMA_40333		uncharacterized protein YCR075W-A	43.51401298	1.845896508	0.398187062	4.635752096	3.56E-06	1.44E-05
KLMA_40335		pyruvate dehydrogenase kinase	237.4506302	1.671600334	0.235743683	7.090753456	1.33E-12	1.36E-11
KLMA_40351		hypothetical protein	433.4302173	3.572341831	0.305324366	11.70015313	1.27E-31	6.61E-30
KLMA_40358		protein ASI2	156.3056201	1.08017323	0.208906554	5.1706048	2.33E-07	1.14E-06
KLMA_40359		putative agmatinase 2	513.5803992	2.317251418	0.228077512	10.15992937	2.99E-24	9.55E-23
KLMA_40368	LYS1	saccharopine dehydrogenase [NAD+	1851.503167	1.062769419	0.215206958	4.938359936	7.88E-07	3.56E-06
KLMA_40373	OM45	hypothetical protein	714.8877424	2.296844832	0.37709656	6.09086657	1.12E-09	7.89E-09
KLMA_40383	BLI1	hypothetical protein	46.52111069	1.035645481	0.320445671	3.231891007	0.00122974	0.002853745
KLMA_40391	MDH2	malate dehydrogenase	6581.989059	1.100173757	0.181744712	6.053401743	1.42E-09	9.78E-09
KLMA_40399	GAS4	glycolipid-anchored surface protein 4 precursor	149.4225897	1.070703329	0.2321707	4.611707375	3.99E-06	1.60E-05
KLMA_40403	VTC1	vacuolar transporter chaperone 1	928.1374545	1.291254267	0.273168757	4.72694712	2.28E-06	9.55E-06
KLMA_40411	HOP1	meiosis-specific protein HOP1	99.17097402	1.864071956	0.370899478	5.025814445	5.01E-07	2.33E-06
KLMA_40446		conserved hypothetical membrane protein	21.48334092	2.668329267	0.752174755	3.547485805	0.000388927	0.001011017

Locus_tag	UniProt _gene	Product	baseMean	$\log_2$FoldChange	lfcSE	stat	pvalue	padj
KLMA_40459	YET3	endoplasmic reticulum transmembrane protein 3	417.1839625	1.119791133	0.240483195	4.656421554	3.22E-06	1.31E-05
KLMA_40469	CST9	hypothetical protein	140.4759977	2.203221042	0.309097212	7.127922728	1.02E-12	1.05E-11
KLMA_40470	IDP1	isocitrate dehydrogenase [NADP]	2360.886824	1.55482984	0.19658828	7.909066803	2.59E-15	3.60E-14
KLMA_40476		myosin light chain 2	225.1314067	1.139873821	0.198291258	5.748482481	9.00E-09	5.51E-08
KLMA_40484		hypothetical protein	36.13765357	4.1312402	0.637518197	6.480191808	9.16E-11	7.38E-10
KLMA_40532	PUN1	cell membrane protein YLR414C	1299.611205	3.879160965	0.38582347	10.05423793	8.80E-24	2.65E-22
KLMA_40533	PXA2	peroxisomal long-chain fatty acid import protein 1	241.9771316	3.102700729	0.249518897	12.43473248	1.69E-35	1.05E-33
KLMA_40536	NPY1	NADH pyrophosphatase	181.2651603	1.168302147	0.25619928	4.560130486	5.11E-06	2.00E-05
KLMA_40551	LEA1	U2 small nuclear ribonucleoprotein A'	123.2363397	1.043979738	0.259841524	4.017755599	5.88E-05	0.000183831
KLMA_40564		hypothetical protein	27.4342946	4.746767048	0.971509407	4.885971267	1.03E-06	4.56E-06
KLMA_40565	FMP40	UPF0061 protein FMP40	486.3474155	1.081867456	0.23912021	4.524366449	6.06E-06	2.35E-05
KLMA_40605	RAD33	DNA repair protein RAD33	205.2599083	1.182108692	0.201943545	5.853659213	4.81E-09	3.07E-08
KLMA_40621		hypothetical protein	38.24699185	2.577190303	0.626651942	4.112634353	3.91E-05	0.00012822
KLMA_40624	adh	alcohol dehydrogenase	4239.399453	2.035434392	0.171579959	11.86289124	1.84E-32	9.79E-31
KLMA_40625	THI4	thiazole biosynthetic enzyme	302.2836399	1.100776108	0.179822098	6.121472933	9.27E-10	6.63E-09
KLMA_40627	GEX1	siderophore iron transporter ARN1	1064.804808	1.989158546	0.610972407	3.255725664	0.00113103	0.002641774
KLMA_40628		NADPH-dependent methylglyoxal reductase GRE2	89.44986712	1.306193005	0.342883916	3.809432124	0.000139286	0.000404444
KLMA_40629		transposon Ty1-H Gag-Pol polyprotein	55.32656103	1.141518298	0.321970077	3.545417357	0.000391992	0.001017803
KLMA_40630	TY2B-GR2	transposon Ty2-F/Ty2-GR2 Gag-Pol polyprotein	14.86226405	2.126483954	0.692060172	3.072686511	0.002121412	0.004690347
KLMA_50012	ALD4	potassium-activated aldehyde dehydrogenase	9788.172554	7.554556679	0.178401552	42.34580132	0	0
KLMA_50017	BDH2	(2R,3R)-2,3-butanediol	2434.139407	1.902884193	0.239289995	7.952209599	1.83E-15	2.61E-14

Locus_tag	UniProt _gene	Product	baseMean	log$_2$FoldChange	lfcSE	stat	pvalue	padj
		dehydrogenase						
KLMA_50021		zinc-type alcohol dehydrogenase-like protein C2E1P3.01	347.4903697	1.027613732	0.26761223	3.839935607	0.000123067	0.000362519
KLMA_50022	GDE1	glycerophosphodiester phosphodiesterase GDE1	780.0108984	1.272822896	0.202359878	6.289897529	3.18E-10	2.37E-09
KLMA_50023		hypothetical protein	671.7423865	4.808087417	0.217980577	22.05741209	8.11E-108	6.70E-105
KLMA_50024	CAR1	arginase	254.2661282	2.199468257	0.239379831	9.188193693	3.99E-20	8.83E-19
KLMA_50025	PEX25	peroxisomal membrane protein PEX25	436.5878513	1.207940161	0.169656324	7.119924171	1.08E-12	1.11E-11
KLMA_50032	HGT1	high-affinity glucose transporter	3772.842969	5.61229215	0.282575735	19.86119633	8.82E-88	4.41E-85
KLMA_50049	THI72	thiamine transporter THI72	204.0180411	1.001974515	0.252002405	3.976051398	7.01E-05	0.000216456
KLMA_50051	VPS21	vacuolar protein sorting-associated protein 21	294.0847304	1.035630429	0.221522161	4.675064666	2.94E-06	1.21E-05
KLMA_50065	BTN1	protein BTN1	314.6710397	1.226978745	0.168868157	7.265897638	3.71E-13	4.08E-12
KLMA_50078	DPB3	DNA polymerase epsilon subunit C	80.70589921	1.591975524	0.422238988	3.770318631	0.000163039	0.000463765
KLMA_50091		COG5647 (Cullin	373.2377103	1.750745319	0.248495102	7.045391647	1.85E-12	1.84E-11
KLMA_50092		hypothetical protein	336.4860254	1.224694937	0.243333808	5.032983075	4.83E-07	2.25E-06
KLMA_50093		COMPASS component SHG1	89.50588294	1.054288209	0.319285436	3.30202411	0.000959898	0.002285841
KLMA_50094	POP4	RNases MRP/P 32.9 kDa subunit	317.4171388	1.338870498	0.252115764	5.310538604	1.09E-07	5.65E-07
KLMA_50106	PRP45	pre-mRNA-processing protein 45	258.544702	1.028869299	0.210285817	4.892718457	9.95E-07	4.41E-06
KLMA_50115	SAW1	single-strand annealing weakened protein 1	144.3701192	1.203154484	0.226584943	5.309948973	1.10E-07	5.67E-07
KLMA_50123		uncharacterized CDP-alcohol phosphatidyltransferase class-I family protein with HAD_like super family	2106.284556	4.343235633	0.259166977	16.7584454	4.91E-63	8.89E-61
KLMA_50149	KAP122	pleiotropic drug resistance regulatory protein 6	332.4917937	1.187527674	0.175125486	6.781010007	1.19E-11	1.09E-10
KLMA_50151	ARO8	aromatic amino acid	372.6393015	1.701952998	0.261746853	6.502286392	7.91E-11	6.45E-10

Locus_tag	UniProt _gene	Product	baseMean	$\log_2$FoldChange	lfcSE	stat	pvalue	padj
		aminotransferase 1						
KLMA_50156		uncharacterized endoplasmic reticulum membrane protein YGL010W	517.6336347	1.342068666	0.33368273	4.021990182	5.77E-05	0.00018102
KLMA_50160		BAR super family and SH3	49.72899554	2.493574299	0.503014194	4.957264284	7.15E-07	3.25E-06
KLMA_50161	DAK1	dihydroxyacetone kinase 1	3528.330863	2.676425951	0.221491072	12.08367421	1.29E-33	7.07E-32
KLMA_50163	ITT1	translation termination inhibitor protein ITT1	426.1004133	1.107891075	0.237998904	4.655025952	3.24E-06	1.32E-05
KLMA_50164		putative transcriptional activator YLR445W	21.80824309	1.710938516	0.483531319	3.538423367	0.000402524	0.001041275
KLMA_50178	CAR2	ornithine aminotransferase	250.8427874	2.847704436	0.297614526	9.568432276	1.09E-21	2.64E-20
KLMA_50198		nested antisense gene NAG1	293.5288316	1.435482613	0.318413337	4.508236454	6.54E-06	2.51E-05
KLMA_50199		hypothetical protein	57.32926229	1.875169479	0.469858819	3.990921106	6.58E-05	0.000204226
KLMA_50202		DUF3445 super family conserved domain	282.2504522	1.458105253	0.177705845	8.20516204	2.30E-16	3.56E-15
KLMA_50225	APS2	AP-2 complex subunit sigma	141.8474223	2.108822829	0.246736494	8.546862256	1.26E-17	2.24E-16
KLMA_50228	ECO1	N-acetyltransferase ECO1	89.39262822	1.23612298	0.323712521	3.818582538	0.000134221	0.000391597
KLMA_50233	QDR3	uncharacterized transporter YBR043C	325.8077077	1.334712093	0.200175708	6.667702618	2.60E-11	2.27E-10
KLMA_50236	FIG1	factor-induced gene 1 protein	107.2377919	6.546218147	1.332449648	4.912919717	8.97E-07	4.01E-06
KLMA_50249		uncharacterized membrane protein YJL163C	1738.094332	1.940451327	0.154079236	12.59385354	2.28E-36	1.45E-34
KLMA_50251		J protein JJJ2	350.0782455	1.93711026	0.39545541	4.898429031	9.66E-07	4.30E-06
KLMA_50252		mitochondrial membrane protein FMP33	70.92057303	2.151082178	0.286663048	7.503869776	6.20E-14	7.35E-13
KLMA_50253	PIR1	cell wall mannoprotein HSP150	12771.61535	1.166779585	0.156257254	7.467042702	8.20E-14	9.61E-13
KLMA_50265	SOP4	protein SOP4	348.2121304	1.098179227	0.169408898	6.482417619	9.03E-11	7.29E-10
KLMA_50268		hypothetical protein	63.0170567	4.832888141	1.093756323	4.418615043	9.93E-06	3.67E-05

Locus_tag	UniProt _gene	Product	baseMean	$\log_2$FoldChange	lfcSE	stat	pvalue	padj
KLMA_50296	sdh	uncharacterized oxidoreductase YMR226C	652.1200418	1.62073309	0.182083591	8.901038715	5.53E-19	1.11E-17
KLMA_50300		hypothetical protein	877.9531853	3.779046086	0.366690239	10.3058268	6.63E-25	2.23E-23
KLMA_50304	GLT1	glutamate synthase [NADH]	5801.108729	1.231919778	0.257931009	4.776160046	1.79E-06	7.66E-06
KLMA_50310		protein UGX2	640.0783637	1.24072677	0.259591564	4.779534252	1.76E-06	7.55E-06
KLMA_50315	SFA1	S-(hydroxymethyl)glutathione dehydrogenase	3388.669075	1.50229903	0.166356396	9.030605787	1.71E-19	3.61E-18
KLMA_50327		uncharacterized MFS-type transporter C1271.10c	122.5164798	1.902528233	0.328645453	5.788999107	7.08E-09	4.42E-08
KLMA_50329		GAL4-like Zn2Cys6 binuclear cluster DNA-binding conserved domain	216.9238898	2.624964544	0.248598133	10.55906782	4.61E-26	1.77E-24
KLMA_50339	HUT1	UDP-galactose transporter homolog 1	316.6059337	1.156151755	0.191118616	6.049393725	1.45E-09	9.99E-09
KLMA_50343		tubulin-specific chaperone C	69.38482064	1.872758556	0.306979572	6.100596672	1.06E-09	7.51E-09
KLMA_50364	RAG1	low-affinity glucose transporter	314.49797	2.216356265	0.413944575	5.354234355	8.59E-08	4.52E-07
KLMA_50369	IST3	U2 snRNP component IST3	67.16242001	1.375959295	0.311302074	4.420013266	9.87E-06	3.65E-05
KLMA_50379	HAK1	high affinity potassium transporter	29992.82726	7.19044832	0.214562838	33.51208619	3.21E-246	7.85E-243
KLMA_50383		dynactin subunit 5	37.02605452	1.188864053	0.345629707	3.439704487	0.00058235	0.001451861
KLMA_50392	VAB2	protein VAB2	398.3474666	1.025151806	0.21672753	4.730141143	2.24E-06	9.43E-06
KLMA_50415	AIM17	uncharacterized oxidoreductase YHL021C	229.8689876	2.637971494	0.26453869	9.971968524	2.02E-23	5.84E-22
KLMA_50419	CTT1	catalase T	1035.374366	3.240695668	0.284181026	11.4036314	4.01E-30	1.90E-28
KLMA_50437		NADH-dependent flavin oxidoreductase (predicted); FlaRed super family conserved domain	74.94469985	1.251256084	0.358048353	3.494656723	0.000474672	0.001206109
KLMA_50440	TEL2	telomere length regulation protein TEL2	264.9920132	1.1937198	0.266805078	4.474126984	7.67E-06	2.90E-05
KLMA_50450	OPT2	oligopeptide transporter 2	516.4656471	1.328124258	0.184616736	7.193953739	6.29E-13	6.68E-12
KLMA_50451		acyl-coenzyme A:6-	28.77476762	4.577056334	0.74237968	6.165384721	7.03E-10	5.10E-09

Locus_tag	UniProt _gene	Product	baseMean	$\log_2$FoldChange	lfcSE	stat	pvalue	padj
		aminopenicillanic-acid-acyltransferase 40 kDa form						
KLMA_50456		hypothetical protein	32.60904014	2.641333269	0.465072639	5.679399405	1.35E-08	8.04E-08
KLMA_50457	AXL1	putative protease AXL1	108.3155563	1.482023049	0.293075156	5.056802054	4.26E-07	2.00E-06
KLMA_50458		uncharacterized protein YGR111W	215.1139374	2.410730669	0.270843892	8.900812394	5.54E-19	1.11E-17
KLMA_50462	TRS20	transport protein particle 20 kDa subunit	55.16275582	1.144324703	0.310709429	3.682941673	0.000230558	0.000634034
KLMA_50463	MTC4	conserved hypothetical membrane protein	275.883025	1.171550891	0.206445569	5.674865766	1.39E-08	8.25E-08
KLMA_50468	BAR1	aspartic proteinase yapsin-3	171.6170954	1.073743985	0.272089089	3.946295643	7.94E-05	0.000242579
KLMA_50482	NCE102	non-classical export protein 2	1206.299814	1.7729939	0.234621676	7.556820542	4.13E-14	5.03E-13
KLMA_50484	APC2	anaphase-promoting complex subunit 2	195.818692	1.221540984	0.21823426	5.597384144	2.18E-08	1.25E-07
KLMA_50485	DCN1	defective in cullin neddylation protein 1	129.215156	1.318495682	0.29564009	4.45980003	8.20E-06	3.08E-05
KLMA_50488	INO1	inositol-3-phosphate synthase	6465.302614	2.748356613	0.341886286	8.038803317	9.07E-16	1.34E-14
KLMA_50496	VPS70	vacuolar protein sorting-associated protein 70	1318.249977	1.243147106	0.18700253	6.647755535	2.98E-11	2.56E-10
KLMA_50504	RKM5	uncharacterized protein YLR137W	67.37089533	1.214251612	0.324238726	3.744930861	0.000180443	0.000511187
KLMA_50513	PUT1	proline dehydrogenase	1015.919942	1.305923027	0.185652012	7.034251936	2.00E-12	1.99E-11
KLMA_50528	STB3	protein STB3	392.2216966	1.027731172	0.211386837	4.861850362	1.16E-06	5.12E-06
KLMA_50530	PCD1	peroxisomal coenzyme A diphosphatase 1	158.4496338	1.050517494	0.199772682	5.25856429	1.45E-07	7.37E-07
KLMA_50535	URC1	putative GTP cyclohydrolase URC1	155.7634185	2.174740114	0.273116007	7.96269737	1.68E-15	2.42E-14
KLMA_50587	SPS19	peroxisomal 2	258.7293391	3.822914719	0.309434081	12.35453675	4.60E-35	2.81E-33
KLMA_50589	dpp1	probable diacylglycerol pyrophosphate phosphatase 1	88.84598235	1.744975321	0.357369519	4.882831999	1.05E-06	4.63E-06
KLMA_50601		peroxisomal membrane protein PEX17	346.2726392	1.693435607	0.21979755	7.704524499	1.31E-14	1.68E-13

Locus_tag	UniProt _gene	Product	baseMean	$\log_2$FoldChange	lfcSE	stat	pvalue	padj
KLMA_50613	GUD1	probable guanine deaminase	553.4344942	2.44760069	0.318584872	7.682727278	1.56E-14	1.97E-13
KLMA_50615	ATG4	probable cysteine protease ATG4	687.0642127	1.425817318	0.183571721	7.76708584	8.03E-15	1.06E-13
KLMA_60003	yxeK	putative monooxygenase yxeK	417.7077066	1.657819701	0.24126915	6.871246079	6.36E-12	6.00E-11
KLMA_60005		UNC93-like protein	121.27343	1.272696868	0.315677685	4.031633931	5.54E-05	0.000174517
KLMA_60012	KIN28	serine/threonine-protein kinase KIN28	485.9200049	1.667733578	0.209884289	7.945966719	1.93E-15	2.72E-14
KLMA_60013	MRF1	peptide chain release factor 1	315.3250006	1.708863702	0.218125013	7.834331695	4.71E-15	6.39E-14
KLMA_60027	FMP46	putative redox protein FMP46	214.5492087	1.680018447	0.205652849	8.16919606	3.10E-16	4.75E-15
KLMA_60029	ACAD11	acyl-CoA dehydrogenase family member 11	135.5400385	3.276766101	0.490411186	6.681670804	2.36E-11	2.07E-10
KLMA_60030		hypothetical protein	775.9766048	1.343532911	0.251028442	5.352114296	8.69E-08	4.57E-07
KLMA_60032	NIT2	probable hydrolase NIT2	542.2568403	1.181284278	0.203198764	5.813442248	6.12E-09	3.86E-08
KLMA_60039		uncharacterized protein YJL132W	644.8477331	2.091646364	0.203375823	10.28463629	8.27E-25	2.76E-23
KLMA_60049		hypothetical protein	4.371601739	5.345064621	1.455719053	3.671769364	0.000240877	0.000659072
KLMA_60051		probable 26S proteasome regulatory subunit p28	225.3193884	1.227941565	0.253589261	4.842245922	1.28E-06	5.62E-06
KLMA_60053		spo12 super family protein	37.35116111	1.095293271	0.37216678	2.943017297	0.003250303	0.006929061
KLMA_60059	HSV2	SVP1-like protein 2	193.3066412	1.448713671	0.217724577	6.653882135	2.85E-11	2.48E-10
KLMA_60074	DIP5	dicarboxylic amino acid permease	278.2154943	1.507510051	0.320595983	4.702211295	2.57E-06	1.07E-05
KLMA_60085	TDA10	uncharacterized kinase YGR205W	183.4732898	1.326212999	0.251980587	5.263155453	1.42E-07	7.20E-07
KLMA_60086	TES1	peroxisomal acyl-coenzyme A thioester hydrolase 1	368.8381457	1.485259169	0.214549587	6.922684807	4.43E-12	4.28E-11
KLMA_60089	YCH1	uncharacterized protein YGR203W	379.3907602	2.513930609	0.220168107	11.41823239	3.39E-30	1.64E-28
KLMA_60101	HSP78	heat shock protein 78	1053.795514	1.192030543	0.257118672	4.636110367	3.55E-06	1.44E-05
KLMA_60105		hypothetical protein	50.72216832	1.746449979	0.407722319	4.28342992	1.84E-05	6.47E-05
KLMA_60120	RMD1	sporulation protein RMD1	311.4973524	1.157805288	0.179647366	6.444877605	1.16E-10	9.20E-10

Locus_tag	UniProt _gene	Product	baseMean	log_2FoldChange	lfcSE	stat	pvalue	padj
KLMA_60123		RCR super family protein	436.4946765	1.454959082	0.281652675	5.165791815	2.39E-07	1.17E-06
KLMA_60124		RCR super family protein	121.6783051	3.40304502	0.419955404	8.103348565	5.35E-16	8.01E-15
KLMA_60125	gabD	succinate-semialdehyde dehydrogenase [NADP+]	675.995075	3.829405806	0.374475037	10.2260643	1.52E-24	4.97E-23
KLMA_60132	APC11	anaphase-promoting complex subunit 11	58.51862821	1.48631785	0.299833504	4.957143988	7.15E-07	3.25E-06
KLMA_60161		hypothetical protein	8.639724054	6.326817224	1.323881905	4.778989123	1.76E-06	7.56E-06
KLMA_60165	GPA1	guanine nucleotide-binding protein alpha-1 subunit	44.13910922	4.432487995	0.563811587	7.861647572	3.79E-15	5.19E-14
KLMA_60176	JLP1	alpha-ketoglutarate-dependent sulfonate dioxygenase	208.2326175	2.189417631	0.302346163	7.241426876	4.44E-13	4.83E-12
KLMA_60180	STL1	sugar transporter STL1	286.9688094	2.121138078	0.683142482	3.104971707	0.001902972	0.004245828
KLMA_60195		tRNA_bindingDomain super family protein	38.90658186	1.220033254	0.400375806	3.047220224	0.002309684	0.005081305
KLMA_60206		probable 5-hydroxyisourate hydrolase	120.7368482	1.273366018	0.247207104	5.151008995	2.59E-07	1.26E-06
KLMA_60208	VCX1	vacuolar calcium ion transporter	183.8798491	2.613761462	0.392721736	6.655504967	2.82E-11	2.45E-10
KLMA_60221	PUT4	proline-specific permease	1072.829003	2.105423976	0.256300872	8.214657887	2.13E-16	3.31E-15
KLMA_60241		uncharacterized vacuolar membrane protein SCY_4679	1004.375441	1.314770738	0.198504225	6.623389197	3.51E-11	2.99E-10
KLMA_60268		uncharacterized protein YNL134C	2752.893253	2.574786951	0.25173117	10.22831998	1.48E-24	4.89E-23
KLMA_60271	ETR1	probable trans-2-enoyl-CoA reductase	1255.102962	1.471637644	0.255342345	5.763390497	8.24E-09	5.10E-08
KLMA_60273		hypothetical protein	36.25356841	1.207720042	0.389524171	3.100500893	0.001931936	0.004302589
KLMA_60293		LPLAT super family protein	58.38953679	1.79748793	0.390299445	4.605407344	4.12E-06	1.65E-05
KLMA_60312	URC4	uracil catabolism protein 4	458.6027232	1.015176904	0.22545624	4.502766941	6.71E-06	2.57E-05
KLMA_60321	ETP1	RING finger protein ETP1	336.0676858	1.229684567	0.236739486	5.19425207	2.06E-07	1.01E-06
KLMA_60323		uncharacterized transporter YHL008C	293.9063765	1.363798439	0.237464613	5.743164933	9.29E-09	5.67E-08

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KLMA_60327	AO-I	copper amine oxidase 1	324.7303144	1.655080786	0.226131951	7.319093029	2.50E-13	2.77E-12
KLMA_60355		ULP1-interacting protein 4	697.6293447	1.985307945	0.26395219	7.521467986	5.42E-14	6.48E-13
KLMA_60356	MF(ALPHA)1	mating factor alpha-1	101.6657033	4.494196437	0.465231494	9.660129413	4.45E-22	1.12E-20
KLMA_60362	SCY1	protein kinase-like protein SCY1	605.2154789	1.470472919	0.347361058	4.233269344	2.30E-05	7.95E-05
KLMA_60366		uncharacterized protein YGL082W	1264.40348	1.014133305	0.216121825	4.692415048	2.70E-06	1.11E-05
KLMA_60367		hypothetical membrane protein	964.3397269	2.087140684	0.245918203	8.487133776	2.12E-17	3.67E-16
KLMA_60368		hypothetical protein	115.0938994	2.407593664	0.445447833	5.404883544	6.49E-08	3.48E-07
KLMA_60369	RSA1	ribosome assembly 1 protein	148.3034138	1.209481498	0.33234139	3.639274353	0.000273407	0.000738155
KLMA_60370	FMP37	UPF0041 protein FMP37	499.8417217	1.094302115	0.186269943	5.874818554	4.23E-09	2.75E-08
KLMA_60377	RAD1	DNA repair protein RAD1	278.7579774	1.181492012	0.247922972	4.765560862	1.88E-06	8.05E-06
KLMA_60387	PHO85	negative regulator of the PHO system	971.3791286	1.31400472	0.148649076	8.839642715	9.60E-19	1.88E-17
KLMA_60404		hypothetical protein	261.0644312	1.1949176	0.202133548	5.911525378	3.39E-09	2.23E-08
KLMA_60405		37S ribosomal protein YMR-31	278.5154782	1.113255162	0.200377516	5.555788813	2.76E-08	1.57E-07
KLMA_60406	PDE1	low-affinity cyclic AMP phosphodiesterase	380.7269714	2.423339706	0.240678036	10.06880289	7.59E-24	2.30E-22
KLMA_60409	ZIP2	protein ZIP2	308.5841076	6.088535001	0.447486278	13.60608203	3.68E-42	3.16E-40
KLMA_60413		uncharacterized esterase/lipase C417.12	314.0601026	1.679557012	0.19722602	8.51589974	1.65E-17	2.90E-16
KLMA_60414	DAL5	allantoate permease	344.8058134	5.220350291	0.686902408	7.599842758	2.96E-14	3.65E-13
KLMA_60415		uncharacterized esterase/lipase C417.12	222.9096169	1.682090941	0.217575905	7.731053406	1.07E-14	1.39E-13
KLMA_60423	ARO9	aromatic amino acid aminotransferase 2	429.8102448	1.483246193	0.203518526	7.288015597	3.15E-13	3.48E-12
KLMA_60425	GRE2	NADPH-dependent methylglyoxal reductase GRE2	1669.566386	1.170883988	0.141718276	8.262053594	1.43E-16	2.27E-15
KLMA_60426		putative lipase YJR107W	10.71199019	2.160730976	0.711329299	3.037595918	0.002384735	0.005232276

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KLMA_60443	SST2	protein SST2	610.2201999	2.082805595	0.209881184	9.923736656	3.28E-23	9.32E-22
KLMA_60450		platinum sensitivity protein 3	242.1795528	1.413432638	0.265566488	5.322330572	1.02E-07	5.33E-07
KLMA_60452	FBP1	fructose-1,6-bisphosphatas	265.6374308	2.87567171	0.284688061	10.10113211	5.46E-24	1.68E-22
KLMA_60454	ATG3	autophagy-related protein 3	486.8621491	1.932224469	0.233322469	8.281347614	1.22E-16	1.96E-15
KLMA_60460	INP1	inheritance of peroxisomes protein 1	350.0937195	1.136382351	0.211177195	5.3811793	7.40E-08	3.93E-07
KLMA_60475		uncharacterized protein YIL077C	330.0619501	1.191658337	0.233411644	5.105393711	3.30E-07	1.58E-06
KLMA_60487	VCX1	vacuolar calcium ion transporter	2714.56491	1.636416311	0.204489603	8.00244259	1.22E-15	1.78E-14
KLMA_60495	SRF1	hypothetical membrane protein	313.1370028	1.34323083	0.238973494	5.620836047	1.90E-08	1.10E-07
KLMA_60496		uncharacterized protein YDL183C	440.0985563	1.686570853	0.212124837	7.950841027	1.85E-15	2.62E-14
KLMA_60498		uncharacterized protein YDL186W	124.9888369	3.490084252	0.483325666	7.220978519	5.16E-13	5.53E-12
KLMA_60500		probable allantoinase 1	164.768399	2.040174428	0.253064518	8.061874682	7.51E-16	1.12E-14
KLMA_60522	CRR1	probable glycosidase CRR1	254.3207073	1.879668907	0.333338567	5.63891819	1.71E-08	9.97E-08
KLMA_60551		uncharacterized protein YBR053C	843.6709614	1.059337812	0.212882695	4.976157467	6.49E-07	2.96E-06
KLMA_60552	ERC1	uncharacterized transporter C4B3.13	585.6484161	1.289057844	0.143122824	9.006654648	2.12E-19	4.42E-18
KLMA_60558		aminotriazole resistance protein	398.4774814	1.806939594	0.244162326	7.400566758	1.36E-13	1.55E-12
KLMA_70001		aminotriazole resistance protein	206.5461504	1.279673078	0.292802327	4.370433429	1.24E-05	4.50E-05
KLMA_70002		arylsulfatase	217.3405221	1.412618752	0.365498945	3.864905137	0.000111132	0.000331358
KLMA_70003	HXT15	hexose transporter HXT9	227.694327	2.930841636	0.4214497	6.954190829	3.55E-12	3.46E-11
KLMA_70004		conserved hypothetical protein	501.4625286	1.825976019	0.367910262	4.96310162	6.94E-07	3.16E-06
KLMA_70011		uncharacterized protein YJL171C	3252.703975	1.160358568	0.225312677	5.149992378	2.60E-07	1.26E-06
KLMA_70012		1-aminocyclopropane-1-carboxylate oxidase	514.7806564	1.817668084	0.220912509	8.227999833	1.90E-16	2.98E-15
KLMA_70023	PRM4	pheromone-regulated membrane protein 4	644.968071	1.665463495	0.246672451	6.751720718	1.46E-11	1.32E-10
KLMA_70024	KIP2	kinesin-like protein KIP2	541.5999095	1.799076975	0.223814739	8.038241733	9.11E-16	1.34E-14

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KLMA_70030		protein SIC1	261.0828951	1.031165618	0.203964497	5.055613282	4.29E-07	2.01E-06
KLMA_70033	FMP32	protein FMP32	142.9045615	1.130672012	0.246247109	4.591615374	4.40E-06	1.75E-05
KLMA_70040	OTU1	ubiquitin thioesterase OTU1	168.0898734	1.406537274	0.236914532	5.936897423	2.90E-09	1.92E-08
KLMA_70044	SOR1	sorbitol dehydrogenase 1	8515.325102	3.766594126	0.223676663	16.83945959	1.25E-63	2.66E-61
KLMA_70053		transmembrane protein 208 homolog	484.5961906	1.585578829	0.183547635	8.638514062	5.69E-18	1.06E-16
KLMA_70055	PER33	UPF0121 membrane protein YLR064W	768.9335377	1.094808302	0.179465611	6.100379325	1.06E-09	7.51E-09
KLMA_70089		conserved hypothetical membrane protein	17.99417167	2.149715938	0.611703103	3.514312628	0.000440894	0.001126805
KLMA_70094		hypothetical protein	234.9838094	2.78774122	0.248472468	11.21951757	3.27E-29	1.48E-27
KLMA_70102	YMR1	phosphoinositide 3-phosphatase	550.515876	1.032150855	0.194729803	5.300425708	1.16E-07	5.96E-07
KLMA_70103	MOH1	protein yippee-like MOH1	746.907493	1.993272001	0.346512803	5.752376194	8.80E-09	5.42E-08
KLMA_70107		hypothetical protein	419.0820662	2.295677149	0.282029231	8.139855371	3.96E-16	6.02E-15
KLMA_70117	ERV2	FAD-linked sulfhydryl oxidase ERV2	343.5785608	1.181034637	0.240221659	4.916436929	8.81E-07	3.95E-06
KLMA_70118		guanine nucleotide-binding protein subunit gamma	40.29053379	4.301905414	0.623768761	6.896634916	5.32E-12	5.06E-11
KLMA_70132	NTO1	nuA3 HAT complex component NTO1	535.5766334	1.085127445	0.201018493	5.398147342	6.73E-08	3.61E-07
KLMA_70139	ATH1	vacuolar acid trehalase	801.1242488	1.123472682	0.292160846	3.845390976	0.00012036	0.000356051
KLMA_70145	ywtG	conserved hypothetical membrane protein	317.3002229	3.48861536	0.678883034	5.138757616	2.77E-07	1.33E-06
KLMA_70146		uncharacterized protein YBL095W	337.8929403	1.06612706	0.195098947	5.464545447	4.64E-08	2.55E-07
KLMA_70154	TEL1	serine/threonine-protein kinase TEL1	680.809854	1.11592769	0.248126283	4.497418324	6.88E-06	2.62E-05
KLMA_70156		conserved hypothetical protein	84.43110807	1.295534615	0.411408153	3.149025135	0.001638161	0.003704064
KLMA_70172	SEE1	uncharacterized methyltransferase YIL064W	277.9121662	1.015450116	0.183199167	5.542875172	2.98E-08	1.69E-07
KLMA_70179	ICL1	isocitrate lyase	88.97440535	2.107149473	0.53932291	3.907027562	9.34E-05	0.000282572

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KLMA_70189	MMF1	protein MMF1	632.7361859	1.107964765	0.173485082	6.386513197	1.70E-10	1.33E-09
KLMA_70199	ALG12	dolichyl-P-Man:Man(7)GlcNAc(2)-PP-dolichyl-alpha-1	2032.947333	1.011477228	0.133254103	7.590589744	3.18E-14	3.91E-13
KLMA_70200		uncharacterized protein YNR029C	387.2829207	1.183821813	0.185006292	6.398819186	1.57E-10	1.23E-09
KLMA_70209		uncharacterized PH domain-containing protein YPR091C	377.800751	2.080719786	0.233503802	8.910860403	5.06E-19	1.02E-17
KLMA_70214	AGP2	general amino acid permease AGP2	1209.00893	1.543164826	0.180069226	8.569842035	1.04E-17	1.85E-16
KLMA_70220	USV1	conserved hypothetical protein	371.6169436	1.001610528	0.244085198	4.103528345	4.07E-05	0.000132133
KLMA_70230		hypothetical protein	3782.328386	6.052276523	0.274395532	22.05676046	8.23E-108	6.70E-105
KLMA_70233		uncharacterized protein YLR211C	283.3690025	1.100470956	0.193381462	5.690674506	1.27E-08	7.57E-08
KLMA_70236	ATG9	autophagy-related protein 9	409.8842218	1.185435278	0.228938929	5.177954145	2.24E-07	1.10E-06
KLMA_70242		conserved hypothetical protein	139.5148873	2.059344879	0.341182138	6.03591059	1.58E-09	1.08E-08
KLMA_70258	PHO84	inorganic phosphate transporter	9008.079883	5.362272787	0.584561722	9.173150723	4.59E-20	1.01E-18
KLMA_70266	FMP27	protein FMP27	1238.005922	1.152922887	0.261708006	4.405378754	1.06E-05	3.89E-05
KLMA_70270		uncharacterized protein C1F7.10	107.5800892	1.361781078	0.246318847	5.528529767	3.23E-08	1.82E-07
KLMA_70301	ANT1	peroxisomal adenine nucleotide transporter 1	586.7903661	2.276035432	0.213160054	10.67758893	1.30E-26	5.15E-25
KLMA_70303		probable 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase	219.2793861	1.782376479	0.24601875	7.24488063	4.33E-13	4.72E-12
KLMA_70317		uncharacterized glycosyl hydrolase YIR007W	437.1371806	1.927131806	0.261818144	7.360573921	1.83E-13	2.08E-12
KLMA_70348		uncharacterized protein YBR085C-A	149.2835605	1.854302643	0.275521873	6.730146779	1.69E-11	1.51E-10
KLMA_70361	TEC1	conserved hypothetical protein	139.0558023	2.268054227	0.263110139	8.620170387	6.69E-18	1.22E-16
KLMA_70381	PTR2	peptide transporter PTR2	150.2193158	2.402237504	0.337087056	7.126460243	1.03E-12	1.06E-11
KLMA_70392	LPX1	peroxisomal membrane protein LPX1	369.7485438	2.260965875	0.219916498	10.2810198	8.58E-25	2.85E-23
KLMA_70404	FAD1	FAD synthetase	507.0035503	1.439664337	0.26169608	5.501283535	3.77E-08	2.10E-07
KLMA_70416	VFA1	uncharacterized protein YER128W	76.36547475	1.143705371	0.287594244	3.976802018	6.98E-05	0.000215911

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KLMA_70426	FOX2	peroxisomal hydratase-dehydrogenase-epimerase	314.3608921	2.10326663	0.210764689	9.979217309	1.88E-23	5.46E-22
KLMA_70428		conserved hypothetical protein	134.4534576	1.357128777	0.315893381	4.296160861	1.74E-05	6.14E-05
KLMA_70429	ICL2	mitochondrial 2-methylisocitrate lyase	732.3865228	4.072975856	0.330538073	12.32225932	6.87E-35	4.09E-33
KLMA_70430		hypothetical protein	254.4437536	1.602538121	0.341454827	4.693265385	2.69E-06	1.11E-05
KLMA_70431		hypothetical protein	1133.53665	2.230347415	0.288349985	7.734862262	1.04E-14	1.36E-13
KLMA_70434		uncharacterized protein YDL144C	31.26571882	1.586119695	0.435406444	3.642848467	0.000269638	0.000729186
KLMA_70439	SAD1	pre-mRNA-splicing factor SAD1	214.3339286	1.221739236	0.223331442	5.470520526	4.49E-08	2.47E-07
KLMA_70443	PDH1	probable 2-methylcitrate dehydratase	1056.555518	3.726465537	0.235455433	15.82662792	2.04E-56	3.02E-54
KLMA_70444	CIT3	citrate synthase 3	423.7431707	5.440632367	0.287025591	18.95521705	4.00E-80	1.78E-77
KLMA_70447	SNF8	vacuolar-sorting protein SNF8	221.8084295	1.985389089	0.248957413	7.974814111	1.53E-15	2.21E-14
KLMA_70450	ULA1	NEDD8-activating enzyme E1 regulatory subunit	382.0463406	1.097309175	0.190110996	5.771939553	7.84E-09	4.88E-08
KLMA_70455	ADY2	hypothetical protein	830.7702585	1.735978417	0.188642594	9.202473214	3.50E-20	7.80E-19
KLMA_70458	ywnB	uncharacterized protein ywnB	591.0143929	1.808064319	0.185850449	9.728598071	2.28E-22	5.92E-21
KLMA_70459	MCH2	probable transporter MCH2	213.6977078	1.13267586	0.256449688	4.416756632	1.00E-05	3.70E-05
KLMA_70462	FCY2	purine-cytosine permease FCY2	130.4332947	4.09305162	0.458804126	8.921130795	4.62E-19	9.35E-18
KLMA_80004		putative uncharacterized oxidoreductase YGL039W	227.4544403	1.228026269	0.252759834	4.858470777	1.18E-06	5.20E-06
KLMA_80005	LAC12	high-affinity glucose transporter	171.8440177	2.281399818	0.392031486	5.819430074	5.90E-09	3.74E-08
KLMA_80008		conserved hypothetical protein	495.7343798	3.170532668	0.194978329	16.26094901	1.87E-59	3.26E-57
KLMA_80011	PHR1	deoxyribodipyrimidine photo-lyase	225.912537	1.476838484	0.212405416	6.952922921	3.58E-12	3.49E-11
KLMA_80014	hyuA	conserved hypothetical protein	344.5582131	1.1545994	0.19017659	6.071196251	1.27E-09	8.82E-09
KLMA_80038	Pir	pirin-like protein	685.1033002	1.723723593	0.24981258	6.900067205	5.20E-12	4.96E-11
KLMA_80053		DNA-directed RNA polymerase II subunit RPB1	64.1981807	3.320013064	0.408610636	8.125126402	4.47E-16	6.74E-15

Locus_tag	UniProt _gene	Product	baseMean	log_2FoldChange	lfcSE	stat	pvalue	padj
KLMA_80056	tsc2	conserved hypothetical protein	214.1774324	1.207556917	0.232591465	5.191750777	2.08E-07	1.02E-06
KLMA_80058		UPF0103 protein YJR008W	440.164588	2.068987597	0.32453104	6.375314969	1.83E-10	1.42E-09
KLMA_80068	mcfL	mitochondrial substrate carrier family protein L	264.3277	1.721908833	0.255872965	6.729545771	1.70E-11	1.52E-10
KLMA_80078	SSK1	conserved hypothetical protein	209.8403369	1.180611881	0.204766674	5.765644677	8.13E-09	5.04E-08
KLMA_80089	TMA17	translation machinery-associated protein 17	199.253766	1.421147315	0.215518756	6.594077192	4.28E-11	3.62E-10
KLMA_80093	ATG20	autophagy-related protein 20	648.0735943	1.359609938	0.270242327	5.031076929	4.88E-07	2.27E-06
KLMA_80094		uncharacterized oxidoreductase SSP0419	45.36253108	2.714918435	0.54061313	5.021924706	5.12E-07	2.37E-06
KLMA_80101	ywtG	conserved hypothetical protein containing the Major Facilitator Superfamily (MFS) domain	1164.256818	5.984991118	0.212643608	28.14564313	2.71E-174	4.41E-171
KLMA_80105	LYS5	L-aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	74.65588446	1.357342675	0.298811933	4.54246476	5.56E-06	2.17E-05
KLMA_80108		protease B inhibitors 2 and 1	883.3465306	3.443229404	0.371352354	9.272135661	1.82E-20	4.14E-19
KLMA_80110		uncharacterized protein YDL121C	172.2274437	1.235879065	0.291190617	4.244226954	2.19E-05	7.60E-05
KLMA_80117	KTR5	probable mannosyltransferase KTR5	148.6874522	1.519451105	0.251090314	6.051412664	1.44E-09	9.89E-09
KLMA_80120	AIM19	loss of respiratory capacity protein 2	173.0965387	2.204543091	0.265592876	8.300460173	1.04E-16	1.68E-15
KLMA_80121	SIW14	tyrosine-protein phosphatase SIW14	371.4547031	1.508816772	0.284993689	5.294211168	1.20E-07	6.14E-07
KLMA_80122	AVT7	vacuolar amino acid transporter 7	1144.089024	1.35634636	0.226719067	5.982497969	2.20E-09	1.47E-08
KLMA_80123	lag1	sphingosine N-acyltransferase lac1	338.3760087	2.065296391	0.229301219	9.006914128	2.12E-19	4.42E-18
KLMA_80136		conserved hypothetical protein containing PIG-H super family	25.00748895	1.261124623	0.444568965	2.836735628	0.004557733	0.009428196
KLMA_80141	SGA1	glucoamylase	447.1482702	2.382864387	0.237301127	10.04152157	1.00E-23	3.00E-22
KLMA_80142	NCE103	carbonic anhydrase	1866.057042	3.109567932	0.24615317	12.63265443	1.39E-36	9.21E-35
KLMA_80161	MSG5	tyrosine-protein phosphatase MSG5	1614.669065	1.070417415	0.231677092	4.620298911	3.83E-06	1.54E-05

Locus_tag	UniProt _gene	Product	baseMean	$\log_2$FoldChange	lfcSE	stat	pvalue	padj
KLMA_80176		uncharacterized oxidoreductase YJR096W	339.2055372	4.251626582	0.247589744	17.17206262	4.30E-66	1.05E-63
KLMA_80177	SFC1	succinate/fumarate mitochondrial transporter	1284.809239	1.25828326	0.254753983	4.939209363	7.84E-07	3.55E-06
KLMA_80191	mug70	meiotically up-regulated gene 70 protein	74.10500993	1.250904525	0.284372987	4.398816283	1.09E-05	3.99E-05
KLMA_80192		conserved hypothetical membrane brotien	44.30851123	1.509277758	0.366944239	4.113098391	3.90E-05	0.000128091
KLMA_80226	CRC1	mitochondrial carnitine carrier	206.6167149	4.453528584	0.405038302	10.99532701	4.02E-28	1.75E-26
KLMA_80231		[PSI+] induction protein 2	1824.733822	1.465339124	0.139118125	10.53305686	6.08E-26	2.29E-24
KLMA_80235	VAM3	syntaxin VAM3	147.3544295	1.173435614	0.211624891	5.544884656	2.94E-08	1.67E-07
KLMA_80260	SFK1	protein SFK1	320.2569617	1.346099146	0.1927887	6.982251257	2.90E-12	2.85E-11
KLMA_80262	HOF1	cytokinesis protein 2	432.5166044	1.152338542	0.177697824	6.4848208	8.88E-11	7.18E-10
KLMA_80286	UBA3	NEDD8-activating enzyme E1 catalytic subunit	43.86081784	1.808737015	0.34540807	5.236522173	1.64E-07	8.21E-07
KLMA_80288		hypothetical protein	246.6154645	1.724921704	0.245333958	7.030912962	2.05E-12	2.04E-11
KLMA_80306	ADH3	alcohol dehydrogenase 3	4011.530088	3.596547636	0.196704685	18.28399584	1.11E-74	3.87E-72
KLMA_80318	amdS	putative amidase C550.07	346.4716158	1.081295707	0.189655759	5.701359739	1.19E-08	7.15E-08
KLMA_80332	ARO7	chorismate mutase	449.8324325	1.609601175	0.152180912	10.57689268	3.81E-26	1.49E-24
KLMA_80339	ADH6	NADP-dependent alcohol dehydrogenase 6	903.6790303	2.148704847	0.329852454	6.514139346	7.31E-11	5.99E-10
KLMA_80340	SAS3	histone acetyltransferase SAS3	185.9394351	1.065665172	0.203386514	5.23960588	1.61E-07	8.09E-07
KLMA_80372	ATG8	autophagy-related protein 8	284.305815	2.238524109	0.280273483	7.986927922	1.38E-15	2.00E-14
KLMA_80374		conserved hypothetical protein	22.63143625	5.828412445	1.111367839	5.244359465	1.57E-07	7.90E-07
KLMA_80389	HXT14	hexose transporter HXT14	1359.565003	3.917602092	0.258313977	15.1660477	5.93E-52	6.74E-50
KLMA_80412	GUT1	glycerol kinase	806.7726206	1.963952768	0.151386704	12.97308626	1.74E-38	1.27E-36
KLMA_80427	FCY2	purine-cytosine permease FCY2	406.5200701	3.838064583	0.432191112	8.880480131	6.66E-19	1.32E-17

Table S4. GO enrichment of differentially expressed genes for *Kmmig1* and the parental strain of *K. marxianus*

GO terms enriched in significantly down-regulated genes (biological process)

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0042254	ribosome biogenesis	256	94	25.76	< 1e-30	SPB1,UTP5,SDA1,EBP2,RPF2,HAS1,NOG1,UTP13,DBP7,UTP15,UTP11,ARX1,NOP53,RPS2,NOP58,NOP12,ENP1,CBF5,RLP7,UTP8,MPP10,IPI3,RPS3,RPL5,NAN1,MRT4,RRS1,IPI1,DCAF13,DRS1,NOB1,RPL3,RLI1,BFR2,MEX67,PWP2,DBP3,RRP3,RRB1,ECM16,MDN1,UTP10,GAR1,CIC1,ERB1,RRP12,IMP4,YTM1,NOP19,NMD3,RIX1,UTP21,MTR2,BMS1,UTP6,PRP43,NOC2,GEP3,MTR4,UTP18,ENP2,RRP5,PWP1,NOP56,UTP4,NUG1,NOP7,DIP2,ALB1,IMP3,KLMA_60069,BRX1,URB1,DHR2,FUN12,NOP15,KRE33,FCF2,KLMA_60313,NOP4,RSA4,NEW1,NOP14,NOC4,RRP9,MAK21,NOP9,LTV1,RLP24,RRP42,UTP25,NOP2,PUF6,RPL8B
GO:0006364	rRNA processing	183	74	18.41	1.40E-29	SPB1,UTP5,EBP2,RPF2,HAS1,NOG1,UTP13,DBP7,UTP15,UTP11,NOP53,NOP58,NOP12,ENP1,CBF5,RLP7,UTP8,MPP10,IPI3,NAN1,MRT4,RRS1,IPI1,DCAF13,DRS1,NOB1,RPL3,BFR2,PWP2,DBP3,RRP3,ECM16,MDN1,UTP10,GAR1,CIC1,ERB1,RRP12,IMP4,YTM1,NOP19,RIX1,UTP21,BMS1,UTP6,PRP43,GEP3,MTR4,UTP18,ENP2,RRP5,PWP1,NOP56,UTP4,NUG1,NOP7,DIP2,IMP3,BRX1,URB1,DHR2,FUN12,NOP15,KRE33,FCF2,KLMA_60313,NOP4,NOP14,NOC4,RRP9,NOP9,RRP42,UTP25,NOP2
GO:0022613	ribonucleoprotein complex biogenesis	319	99	32.1	7.40E-29	SPB1,UTP5,SDA1,EBP2,RPF2,RSE1,HAS1,NOG1,UTP13,DBP7,UTP15,UTP11,ARX1,NOP53,RPS2,NOP58,NOP12,ENP1,CBF5,RLP7,UTP8,MPP10,IPI3,RPS3,RPL5,NAN1,MRT4,RRS1,IPI1,DCAF13,DRS1,NOB1,RPL3,RLI1,BFR2,MEX67,PWP2,DBP3,RRP3,TIF32,RRB1,ECM16,MDN1,UTP10,GAR1,CIC1,ERB1,RRP12,IMP4,YTM1,NOP19,NMD3,RIX1,UTP21,MTR2,BMS1,UTP6,PRP43,NOC2,GEP3,MTR4,UTP18,ENP2,RRP5,PWP1,NOP56,UTP4,NUG1,NOP7,DIP2,ALB1,IMP3,KLMA_60069,BRX1,URB1,DHR2,FUN12,NOP15,KRE33,FCF2,KLMA_60313,NOP4,RSA4,NEW1,NOP14,TIF3,

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
						NOC4,RRP9,MAK21,NOP9,LTV1,RLP24,RRP42,PUB1,UTP25,NOP2,NIP1,PUF6,RPL8B
GO:0016072	rRNA metabolic process	207	77	20.83	6.50E-28	SPB1,RPA49,UTP5,EBP2,RPF2,HAS1,NOG1,UTP13,DBP7,UTP15,UTP11,NOP53,NOP58,NOP12,ENP1,CBF5,RLP7,UTP8,MPP10,IPI3,NAN1,MRT4,RRS1,IPI1,DCAF13,DRS1,NOB1,RPL3,BFR2,PWP2,DBP3,RRP3,ECM16,MDN1,UTP10,GAR1,CIC1,ERB1,RRP12,IMP4,YTM1,NOP19,RIX1,UTP21,BMS1,UTP6,PRP43,GEP3,MTR4,UTP18,ENP2,RPA135,RRP5,PWP1,NOP56,UTP4,NUG1,NOP7,DIP2,IMP3,BRX1,URB1,DHR2,RPA190,FUN12,NOP15,KRE33,FCF2,KLMA_60313,NOP4,NOP14,NOC4,RRP9,NOP9,RRP42,UTP25,NOP2
GO:0034470	ncRNA processing	254	78	25.56	5.10E-22	SPB1,NOP1,UTP5,EBP2,RPF2,HAS1,NOG1,UTP13,DBP7,UTP15,UTP11,NOP53,NOP58,NOP12,ENP1,CBF5,RLP7,UTP8,MPP10,IPI3,NAN1,MRT4,RRS1,IPI1,DCAF13,DRS1,NOB1,RPL3,BFR2,PWP2,DBP3,RRP3,MTO1,ECM16,MDN1,UTP10,GAR1,CIC1,ERB1,RRP12,IMP4,YTM1,NOP19,RIX1,UTP21,PUS1,BMS1,UTP6,PRP43,GEP3,MTR4,UTP18,ENP2,RRP5,PWP1,NOP56,UTP4,NUG1,NOP7,DIP2,IMP3,BRX1,URB1,DHR2,FUN12,NOP15,KRE33,FCF2,KLMA_60313,NOP4,IKI3,NOP14,NOC4,RRP9,NOP9,RRP42,UTP25,NOP2
GO:0034660	ncRNA metabolic process	339	91	34.11	3.30E-21	SPB1,RPA49,NOP1,UTP5,EBP2,RPF2,MES1,HAS1,MSW1,NOG1,UTP13,RPC37,DBP7,UTP15,UTP11,NOP53,NOP58,NOP12,ENP1,CBF5,RLP7,UTP8,MPP10,IPI3,NAN1,MRT4,RRS1,IPI1,DCAF13,DRS1,NOB1,RPL3,BFR2,PWP2,DBP3,RRP3,MTO1,GUS1,ECM16,MDN1,UTP10,GAR1,CIC1,ERB1,RRP12,IMP4,YTM1,NOP19,RPC82,RIX1,UTP21,PUS1,BMS1,UTP6,PRP43,GEP3,MTR4,UTP18,ENP2,RPA135,RRP5,PWP1,NOP56,UTP4,NUG1,RPC40,VAS1,NOP7,DIP2,IMP3,BRX1,URB1,DHR2,RPA190,FUN12,NOP15,KRE33,FCF2,KLMA_60313,NOP4,JHD2,CDC60,IKI3,NOP14,NOC4,RRP9,NOP9,RRP42,UTP25,NOP2,ILS1

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0042274	ribosomal small subunit biogenesis	94	44	9.46	1.20E-20	UTP5,HAS1,UTP13,UTP15,UTP11,NOP58,ENP1,UTP8,MPP10,NAN1,RRS1,DCAF13,NOB1,BFR2,PWP2,RRP3,ECM16,UTP10,RRP12,IMP4,NOP19,BMS1,UTP6,PRP43,GEP3,UTP18,ENP2,RRP5,UTP4,NOP7,DIP2,IMP3,KLMA_60069,DHR2,FUN12,KRE33,FCF2,KLMA_60313,NEW1,NOP14,NOC4,NOP9,LTV1,UTP25
GO:0000462	maturation of SSU-rRNA from tricistronic...	72	37	7.24	3.20E-19	UTP5,HAS1,UTP13,UTP15,UTP11,NOP58,ENP1,UTP8,MPP10,NAN1,RRS1,DCAF13,NOB1,BFR2,PWP2,RRP3,ECM16,UTP10,RRP12,NOP19,BMS1,UTP6,PRP43,UTP18,ENP2,RRP5,UTP4,NOP7,DIP2,DHR2,FUN12,FCF2,KLMA_60313,NOP14,NOC4,NOP9,UTP25
GO:0042273	ribosomal large subunit biogenesis	76	38	7.65	3.50E-19	SPB1,SDA1,RPF2,HAS1,NOG1,DBP7,NOP53,NOP12,RLP7,IPI3,RPL5,MRT4,RRS1,IPI1,DRS1,RPL3,RLI1,DBP3,MDN1,CIC1,ERB1,YTM1,RIX1,PRP43,NOC2,RRP5,NUG1,NOP7,ALB1,BRX1,URB1,NOP15,NOP4,RSA4,MAK21,RLP24,NOP2,PUF6
GO:0030490	maturation of SSU-rRNA	80	38	8.05	3.40E-18	UTP5,HAS1,UTP13,UTP15,UTP11,NOP58,ENP1,UTP8,MPP10,NAN1,RRS1,DCAF13,NOB1,BFR2,PWP2,RRP3,ECM16,UTP10,RRP12,NOP19,BMS1,UTP6,PRP43,GEP3,UTP18,ENP2,RRP5,UTP4,NOP7,DIP2,DHR2,FUN12,FCF2,KLMA_60313,NOP14,NOC4,NOP9,UTP25
GO:0006396	RNA processing	366	81	36.82	2.20E-13	SPB1,NOP1,UTP5,EBP2,RPF2,RSE1,HAS1,NOG1,UTP13,DBP7,UTP15,UTP11,NOP53,NOP58,NOP12,ENP1,CBF5,RLP7,UTP8,MPP10,IPI3,NAN1,MRT4,RRS1,IPI1,DCAF13,DRS1,NOB1,RPL3,MRPL15,BFR2,PWP2,DBP3,RRP3,MTO1,ECM16,MDN1,UTP10,GAR1,CIC1,ERB1,RRP12,IMP4,YTM1,NOP19,RIX1,UTP21,PUS1,BMS1,UTP6,PRP43,GEP3,MTR4,UTP18,ENP2,RRP5,PWP1,NOP56,UTP4,NUG1,NOP7,DIP2,IMP3,BRX1,URB1,DHR2,FUN12,NOP15,KRE33,FCF2,KLMA_60313,NOP4,IKI3,NOP14,NOC4,RRP9,PUS4,NOP9,RRP42,UTP25,NOP2
GO:0000463	maturation of LSU-rRNA from	35	21	3.52	3.90E-13	SPB1,RPF2,HAS1,DBP7,NOP53,NOP12,RLP7,IPI1,DBP3,CIC1,ERB1,YTM1,PRP43,RRP5,NUG1,NOP7,BRX1,URB1,NOP15,NOP4,NOP2

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
	tricistronic...					
GO:0000460	maturation of 5.8S rRNA	73	30	7.34	1.70E-12	SPB1,RPF2,UTP13,UTP11,NOP58,ENP1,RLP7,MPP10,RRS1,PWP2,DBP3,UTP10,CIC1,ERB1,YTM1,NOP19,UTP6,PRP43,MTR4,UTP18,RRP5,NOP7,DIP2,BRX1,URB1,FCF2,NOP14,NOC4,NOP9,RRP42
GO:0000466	maturation of 5.8S rRNA from tricistroni...	73	30	7.34	1.70E-12	SPB1,RPF2,UTP13,UTP11,NOP58,ENP1,RLP7,MPP10,RRS1,PWP2,DBP3,UTP10,CIC1,ERB1,YTM1,NOP19,UTP6,PRP43,MTR4,UTP18,RRP5,NOP7,DIP2,BRX1,URB1,FCF2,NOP14,NOC4,NOP9,RRP42
GO:0000470	maturation of LSU-rRNA	37	21	3.72	1.80E-12	SPB1,RPF2,HAS1,DBP7,NOP53,NOP12,RLP7,IPI1,DBP3,CIC1,ERB1,YTM1,PRP43,RRP5,NUG1,NOP7,BRX1,URB1,NOP15,NOP4,NOP2
GO:0009185	ribonucleoside diphosphate metabolic pro...	23	16	2.31	1.00E-11	GPM3,ENO,PGK,RAG2,GPM1,ADK1,RNR2,PDC2,TPI1,GAP1,FBA1,GUK1,PYK1,RAG5,RNR1,GAP3
GO:0000967	rRNA 5'-end processing	31	18	3.12	4.40E-11	UTP13,UTP11,NOP58,RLP7,MPP10,PWP2,UTP10,NOP19,BMS1,UTP6,UTP18,RRP5,DIP2,BRX1,FCF2,NOP14,NOC4,NOP9
GO:0009132	nucleoside diphosphate metabolic process	25	16	2.52	6.90E-11	GPM3,ENO,PGK,RAG2,GPM1,ADK1,RNR2,PDC2,TPI1,GAP1,FBA1,GUK1,PYK1,RAG5,RNR1,GAP3
GO:0044283	small molecule biosynthetic process	254	58	25.56	3.30E-10	HIS4,GPM3,OLE1,HPT1,GUA1,BIO2,ENO,FAU1,PGK,SCS7,RAG2,URA1,GPM1,ADH4,MET13,CYS4,SHM2,ERG3,ERG28,CYP707A7,ORT1,ERG9,HAM1,PHS1,ERG1,MEU1,PDC2,SER3,PAN5,ERG6,dsd1,TPI1,GAP1,RIB7,FMS1,FBA1,ALD5,MET5,FAS1,GUK1,SHM1,LEU1,PDX3,SUR4,ERG25,PDC1,PYK1,LEU4,RAG5,cyp524A1,LEU3,ERG13,URA7,FAS2,GAP3,MET3,VID24,MET6
GO:0000966	RNA 5'-end processing	34	18	3.42	3.50E-10	UTP13,UTP11,NOP58,RLP7,MPP10,PWP2,UTP10,NOP19,BMS1,UTP6,UTP18,RRP5,DIP2,BRX1,FCF2,NOP14,NOC4,NOP9

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0034471	ncRNA 5'-end processing	34	18	3.42	3.50E-10	UTP13,UTP11,NOP58,RLP7,MPP10,PWP2,UTP10,NOP19,BMS1,UTP6,UTP18,RRP5,DIP2,BRX1,FCF2,NOP14,NOC4,NOP9
GO:0000478	endonucleolytic cleavage involved in rRN...	42	20	4.23	4.20E-10	UTP13,UTP11,NOP58,ENP1,MPP10,RRS1,PWP2,DBP3,UTP10,NOP19,BMS1,UTP6,UTP18,RRP5,DIP2,BRX1,FCF2,NOP14,NOC4,NOP9
GO:0000479	endonucleolytic cleavage of tricistronic...	42	20	4.23	4.20E-10	UTP13,UTP11,NOP58,ENP1,MPP10,RRS1,PWP2,DBP3,UTP10,NOP19,BMS1,UTP6,UTP18,RRP5,DIP2,BRX1,FCF2,NOP14,NOC4,NOP9
GO:0090502	RNA phosphodiester bond hydrolysis, endo...	42	20	4.23	4.20E-10	UTP13,UTP11,NOP58,ENP1,MPP10,RRS1,PWP2,DBP3,UTP10,NOP19,BMS1,UTP6,UTP18,RRP5,DIP2,BRX1,FCF2,NOP14,NOC4,NOP9
GO:0009135	purine nucleoside diphosphate metabolic ...	21	14	2.11	5.10E-10	GPM3,ENO,PGK,RAG2,GPM1,ADK1,PDC2,TPI1,GAP1,FBA1,GUK1,PYK1,RAG5,GAP3
GO:0009179	purine ribonucleoside diphosphate metabo...	21	14	2.11	5.10E-10	GPM3,ENO,PGK,RAG2,GPM1,ADK1,PDC2,TPI1,GAP1,FBA1,GUK1,PYK1,RAG5,GAP3
GO:0000469	cleavage involved in rRNA processing	61	24	6.14	9.50E-10	UTP13,UTP11,NOP58,ENP1,RLP7,MPP10,RRS1,NOB1,PWP2,DBP3,UTP10,NOP19,BMS1,UTP6,MTR4,UTP18,RRP5,DIP2,BRX1,FCF2,NOP14,NOC4,NOP9,RRP42
GO:0034404	nucleobase-containing small molecule bio...	36	18	3.62	1.20E-09	GPM3,HPT1,GUA1,ENO,PGK,RAG2,URA1,GPM1,HAM1,MEU1,TPI1,GAP1,FBA1,GUK1,PYK1,RAG5,URA7,GAP3

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0000472	endonucleolytic cleavage to generate mat...	29	16	2.92	1.60E-09	UTP13,UTP11,NOP58,MPP10,PWP2,UTP10,NOP19,BMS1,UTP6,UTP18,RRP5,DIP2,FCF2,NOP14,NOC4,NOP9
GO:0000480	endonucleolytic cleavage in 5'-ETS of tr...	30	16	3.02	3.00E-09	UTP13,UTP11,NOP58,MPP10,PWP2,UTP10,NOP19,BMS1,UTP6,UTP18,RRP5,DIP2,FCF2,NOP14,NOC4,NOP9
GO:0046031	ADP metabolic process	20	13	2.01	3.50E-09	GPM3,ENO,PGK,RAG2,GPM1,ADK1,PDC2,TPI1,GAP1,FBA1,PYK1,RAG5,GAP3
GO:0034641	cellular nitrogen compound metabolic pro...	1503	201	151.22	4.60E-09	SPB1,APA2,HIS4,RpL37a,RPA49,PRS5,GPM3,NOP1,SOH1,DSS1,UTP5,HPT1,GUA1,BIO2,RPL17B,EBP2,RPF2,RSE1,GAL80,ENO,MES1,HAS1,YTA7,LIP1,FAU1,PGK,MSW1,FUR1,AAH1,RAG2,NOG1,URA1,GPM1,UTP13,RPC37,DBP7,UTP15,ADH4,UTP11,ADK1,NOP53,RPS2,MET13,SHM2,NOP58,FHL1,KLMA_20355,NOP12,ENP1,CBF5,KLMA_20481,RLP7,RPL22A,UTP8,TPA1,ADE2,MPP10,IPI3,RPS3,RPL5,NAN1,HAM1,MRT4,RRS1,GSH1,IPI1,RNR2,DCAF13,MEU1,DRS1,ETT1,NOB1,RPL3,PAB1,RLI1,MRPL15,PDC2,BFR2,PWP2,YIH1,DBP3,PAN5,RRP3,TIF32,HAL9,VTS1,RAD54,KSS1,SAH1,DUG1,ADE5,7,MTO1,GUS1,ECM16,RPL15B,dsd1,HEM13,TPI1,MDN1,GAP1,RIB7,UTP10,GAR1,CIC1,HAP1,ERB1,MCM1,IMP2,RRP12,IMP4,FMS1,FBA1,MAM33,YTM1,NOP19,HMG1,RPC82,RIX1,XPT1,UTP21,PUS1,BMS1,RPL10A,GUK1,UTP6,PRP43,GEP3,SHM1,MTR4,UTP18,ENP2,RPA135,PDX3,RPS14,ADE6,RRP5,PWP1,NOP56,MSS51,LAC9,UTP4,NUG1,RPC40,VAS1,NOP7,RPL2,DIP2,ACS2,URA2,IMP3,KLMA_60069,PDC1,EXO1,BRX1,URB1,DHR2,RPA190,FUN12,REV1,PYK1,YAF9,NOP15,KRE33,EPL1,FCF2,KLMA_60313,UGP1,NOP4,RAG5,JHD2,LEU3,ERG13,RPB1,CDC60,PET309,IKI3,URA7,ROX3,RNR1,SPT21,NOP14,TIF3,MET16,NOC4,RRP9,HEM14,RPL19B,PUS4,KLMA_70408,NOP9,GAP3,RRP42,PUB1,UTP25,HDA1,NOP2,NIP1,KLMA_80256,DEF1,MET6,ILS1

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0000447	endonucleolytic cleavage in ITS1 to sepa...	35	17	3.52	6.20E-09	UTP13,UTP11,NOP58,ENP1,MPP10,RRS1,PWP2,UTP10,NOP19,UTP6,UTP18,RRP5,DIP2,FCF2,NOP14,NOC4,NOP9
GO:0000027	ribosomal large subunit assembly	24	14	2.41	6.40E-09	RPF2,NOP53,IPI3,RPL5,MRT4,IPI1,DRS1,RPL3,MDN1,RIX1,RRP5,BRX1,RSA4,MAK21
GO:0071704	organic substance metabolic process	2233	267	224.67	2.60E-08	SPB1,APA2,HIS4,LPP1,SAM2,RpL37a,RPA49,ACO2,PRS5,GPD1,GPM3,NOP1,OLE1,SOH1,DSS1,UTP5,HPT1,GUA1,PFK1,BIO2,RPL17B,EBP2,RPF2,RSE1,GAL80,ENO,MES1,HAS1,TDA1,YTA7,LIP1,FAU1,PGK,CWH43,SCS7,MSW1,FUR1,AAH1,RAG2,NOG1,URA1,TPS2,KLMA_20052,TSL1,GPM1,UTP13,RPC37,DBP7,UTP15,HSL1,ADH4,UTP11,ADK1,NOP53,RPS2,MET13,CYS4,SHM2,ERG3,NOP58,GAL7,GAL10,GAL1,FHL1,KLMA_20355,NOP12,KLMA_20392,ENP1,CLN2,UBP3,CBF5,KLMA_20481,RLP7,RPL22A,UTP8,TPA1,ERG28,CYP707A7,ORT1,ADE2,MPP10,ERG9,DTD1,IPI3,RPS3,RPL5,NAN1,LIA1,HAM1,MRT4,RRS1,PGM2,GSH1,PHS1,IPI1,RNR2,ERG1,DCAF13,MEU1,DRS1,ETT1,NOB1,RPL3,PAB1,RLI1,MRPL15,KLMA_30320,GSY2,PDC2,SUR2,BFR2,MEX67,SER3,PWP2,YIH1,DBP3,PAN5,RRP3,TIF32,HAL9,VTS1,SCW4,RAD54,KSS1,ERG6,SAH1,DUG1,ADE5,7,MTO1,GUS1,ECM16,RPL15B,dsd1,HEM13,TPI1,MDN1,GAP1,RIB7,UTP10,GAR1,CIC1,HAP1,ERB1,MCM1,IMP2,RRP12,IMP4,FMS1,FBA1,ALD5,MAM33,YTM1,NOP19,HMG1,DPM1,RPC82,MET5,RIX1,XPT1,UTP21,FAS1,MTR2,PUS1,BMS1,RPL10A,GUK1,UTP6,PRP43,GEP3,SHM1,MTR4,UTP18,ENP2,LEU1,RPA135,YJU3,PDX3,RPS14,SUR4,ADE6,ERG25,RRP5,PWP1,NOP56,MSS51,LAC9,UTP4,NUG1,RPC40,VAS1,NOP7,RPL2,DIP2,ACS2,MAP1,SHB17,URA2,IMP3,KLMA_60069,PDC1,EXO1,MDM20,BRX1,URB1,MDH1,DHR2,RPA190,FUN12,REV1,PYK1,LEU4,YAF9,NOP15,KRE33,EPL1,FCF2,KLMA_60313,RGT1,UGP1,NOP4,RAG5,cyp524A1,JHD2,LEU3,ERG13,PFK2,RPB1,CDC60,PET309,IKI3,URA7,ROX3,RNR1,PCL6,HSL7,FAS2,SPT21,NEW1,NOP14,TIF3,MET16,NOC4,RRP9,H

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
						EM14,RPL19B,DYS1,PUS4,KLMA_70408,NOP9,GAP3,MET3,MNN1,RRP42,PUB1,UTP25,HDA1,NOP2,BGL2,NIP1,KLMA_80256,DEF1,VID24,TPS1,PTH2,MET6,ILS1
GO:1901360	organic cyclic compound metabolic proces...	1310	178	131.8	4.00E-08	SPB1,APA2,HIS4,RPA49,PRS5,GPM3,NOP1,SOH1,DSS1,UTP5,HPT1,GUA1,BIO2,EBP2,RPF2,RSE1,GAL80,ENO,MES1,HAS1,YTA7,FAU1,PGK,MSW1,FUR1,AAH1,RAG2,NOG1,URA1,GPM1,UTP13,RPC37,DBP7,UTP15,ADH4,UTP11,ADK1,NOP53,MET13,SHM2,ERG3,NOP58,FHL1,NOP12,ENP1,CBF5,KLMA_20481,RLP7,UTP8,TPA1,ERG28,CYP707A7,ADE2,MPP10,ERG9,DTD1,IPI3,NAN1,HAM1,MRT4,RRS1,IPI1,RNR2,ERG1,DCAF13,MEU1,DRS1,NOB1,RPL3,PAB1,MRPL15,PDC2,BFR2,PWP2,DBP3,RRP3,HAL9,VTS1,RAD54,KSS1,ERG6,SAH1,ADE5,7,MTO1,GUS1,ECM16,HEM13,TPI1,MDN1,GAP1,RIB7,UTP10,GAR1,CIC1,HAP1,ERB1,MCM1,RRP12,IMP4,FBA1,YTM1,NOP19,HMG1,RPC82,RIX1,XPT1,UTP21,PUS1,BMS1,GUK1,UTP6,PRP43,GEP3,SHM1,MTR4,UTP18,ENP2,RPA135,PDX3,ADE6,ERG25,RRP5,PWP1,NOP56,LAC9,UTP4,NUG1,RPC40,VAS1,NOP7,DIP2,ACS2,URA2,IMP3,PDC1,EXO1,BRX1,URB1,DHR2,RPA190,FUN12,REV1,PYK1,YAF9,NOP15,KRE33,EPL1,FCF2,KLMA_60313,UGP1,NOP4,RAG5,cyp524A1,JHD2,ERG13,RPB1,CDC60,IKI3,URA7,ROX3,RNR1,SPT21,NOP14,NOC4,RRP9,HEM14,PUS4,KLMA_70408,NOP9,GAP3,RRP42,PUB1,UTP25,HDA1,NOP2,DEF1,MET6,ILS1
GO:0046390	ribose phosphate biosynthetic process	72	24	7.24	4.50E-08	PRS5,GPM3,HPT1,GUA1,ENO,PGK,RAG2,URA1,GPM1,ADK1,ADE2,ADE5,7,TPI1,GAP1,FBA1,XPT1,GUK1,ADE6,ACS2,SHB17,PYK1,RAG5,URA7,GAP3
GO:0006096	glycolytic process	17	11	1.71	6.50E-08	GPM3,ENO,PGK,RAG2,GPM1,TPI1,GAP1,FBA1,PYK1,RAG5,GAP3

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0006757	ATP generation from ADP	17	11	1.71	6.50E-08	GPM3,ENO,PGK,RAG2,GPM1,TPI1,GAP1,FBA1,PYK1,RAG5,GAP3
GO:0042866	pyruvate biosynthetic process	17	11	1.71	6.50E-08	GPM3,ENO,PGK,RAG2,GPM1,TPI1,GAP1,FBA1,PYK1,RAG5,GAP3
GO:0042255	ribosome assembly	36	16	3.62	8.70E-08	RPF2,NOP53,IPI3,RPL5,MRT4,IPI1,DRS1,RPL3,MDN1,RIX1,RRP5,KLMA_60069,BRX1,FUN12,RSA4,MAK21
GO:0009156	ribonucleoside monophosphate biosyntheti...	59	21	5.94	8.90E-08	PRS5,GPM3,HPT1,GUA1,ENO,PGK,AAH1,RAG2,URA1,GPM1,ADK1,ADE2,ADE5,7,TPI1,GAP1,FBA1,XPT1,ADE6,PYK1,RAG5,GAP3
GO:0072330	monocarboxylic acid biosynthetic process	59	21	5.94	8.90E-08	GPM3,OLE1,BIO2,ENO,PGK,SCS7,RAG2,GPM1,PHS1,PAN5,TPI1,GAP1,FMS1,FBA1,ALD5,FAS1,SUR4,PYK1,RAG5,FAS2,GAP3
GO:0009127	purine nucleoside monophosphate biosynth...	50	19	5.03	1.10E-07	GPM3,HPT1,GUA1,ENO,PGK,AAH1,RAG2,GPM1,ADK1,ADE2,ADE5,7,TPI1,GAP1,FBA1,XPT1,ADE6,PYK1,RAG5,GAP3
GO:0009168	purine ribonucleoside monophosphate bios...	50	19	5.03	1.10E-07	GPM3,HPT1,GUA1,ENO,PGK,AAH1,RAG2,GPM1,ADK1,ADE2,ADE5,7,TPI1,GAP1,FBA1,XPT1,ADE6,PYK1,RAG5,GAP3
GO:0006165	nucleoside diphosphate phosphorylation	18	11	1.81	1.50E-07	GPM3,ENO,PGK,RAG2,GPM1,TPI1,GAP1,FBA1,PYK1,RAG5,GAP3
GO:0046939	nucleotide phosphorylation	18	11	1.81	1.50E-07	GPM3,ENO,PGK,RAG2,GPM1,TPI1,GAP1,FBA1,PYK1,RAG5,GAP3

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0009124	nucleoside monophosphate biosynthetic pr...	61	21	6.14	1.70E-07	PRS5,GPM3,HPT1,GUA1,ENO,PGK,AAH1,RAG2,URA1,GPM1,ADK1,ADE2,ADE5,7,TPI1,GAP1,FBA1,XPT1,ADE6,PYK1,RAG5,GAP3
GO:0008152	metabolic process	2320	272	233.42	1.80E-07	SPB1,APA2,HIS4,LPP1,SAM2,RpL37a,RPA49,ACO2,PRS5,GPD1,GPM3,NOP1,OLE1,SOH1,DSS1,UTP5,HPT1,GUA1,PFK1,BIO2,RPL17B,EBP2,RPF2,RSE1,GAL80,ENO,MES1,HAS1,TDA1,YTA7,LIP1,FAU1,PGK,CWH43,SCS7,MSW1,FUR1,AAH1,RAG2,NOG1,URA1,TPS2,KLMA_20052,TSL1,GPM1,UTP13,RPC37,DBP7,UTP15,HSL1,ADH4,UTP11,ADK1,NOP53,RPS2,MET13,CYS4,SHM2,ERG3,NOP58,GAL7,GAL10,GAL1,FHL1,KLMA_20355,NOP12,KLMA_20392,ENP1,CLN2,UBP3,CBF5,KLMA_20481,RLP7,RPL22A,UTP8,TPA1,ERG28,CYP707A7,ORT1,ADE2,MPP10,ERG9,DTD1,IPI3,RPS3,RPL5,NAN1,LIA1,HAM1,MRT4,RRS1,PGM2,GSH1,PHS1,IPI1,RNR2,ERG1,DCAF13,MEU1,DRS1,ETT1,NOB1,RPL3,PAB1,RLI1,MRPL15,KLMA_30320,GSY2,PDC2,SUR2,BFR2,MEX67,SER3,PWP2,YIH1,DBP3,PAN5,RRP3,TIF32,HAL9,VTS1,SCW4,RAD54,KSS1,ERG6,SAH1,DUG1,ADE5,7,MTO1,GUS1,ECM16,RPL15B,dsd1,HEM13,TPI1,MDN1,GAP1,RIB7,UTP10,GAR1,CIC1,HAP1,ERB1,MCM1,IMP2,RRP12,IMP4,FMS1,FBA1,ALD5,MAM33,YTM1,NOP19,HMG1,DPM1,RPC82,MET5,RIX1,XPT1,UTP21,FAS1,MTR2,PUS1,BMS1,RPL10A,GUK1,UTP6,PRP43,GEP3,SHM1,MTR4,UTP18,ENP2,LEU1,RPA135,YJU3,PDX3,RPS14,SUR4,ADE6,ERG25,RRP5,PWP1,NOP56,MSS51,LAC9,UTP4,NUG1,RPC40,VAS1,NOP7,MET10,RPL2,DIP2,ACS2,MAP1,UTH1,SHB17,URA2,IMP3,KLMA_60069,PDC1,EXO1,IPP1,MDM20,BRX1,URB1,MDH1,DHR2,RPA190,FUN12,REV1,PYK1,LEU4,YAF9,NOP15,KRE33,EPL1,FCF2,KLMA_60313,RGT1,UGP1,NOP4,RAG5,cyp524A1,JHD2,LEU3,ERG13,PFK2,RPB1,CDC60,PET309,IKI3,URA7,ROX3,RNR1,PCL6,HSL7,FAS2,SPT21,NEW1,NOP14,TIF3,MET16,NOC4,RRP9,HEM14,RPL19B,DYS1,PUS4,PCL1,KLMA_70408,NOP9,GAP3,MET3,MNN1,RRP42,PUB1,UTP25,HDA1,NOP2,BG

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
						L2,NIP1,GDS1,KLMA_80256,DEF1,VID24,TPS1,PTH2,MET6,ILS1
GO:0044281	small molecule metabolic process	540	89	54.33	2.20E-07	APA2,HIS4,SAM2,ACO2,PRS5,GPM3,OLE1,HPT1,GUA1,BIO2,GAL80,ENO,MES1,FAU1,PGK,SCS7,MSW1,FUR1,AAH1,RAG2,URA1,GPM1,ADH4,ADK1,MET13,CYS4,SHM2,ERG3,GAL7,GAL10,GAL1,ERG28,CYP707A7,ORT1,ADE2,ERG9,DTD1,HAM1,PHS1,RNR2,ERG1,MEU1,PDC2,SER3,PAN5,ERG6,SAH1,ADE5,7,GUS1,dsd1,TPI1,GAP1,RIB7,FMS1,FBA1,ALD5,HMG1,MET5,XPT1,FAS1,GUK1,SHM1,LEU1,PDX3,SUR4,ADE6,ERG25,VAS1,ACS2,URA2,PDC1,MDH1,PYK1,LEU4,RGT1,UGP1,RAG5,cyp524A1,LEU3,ERG13,CDC60,URA7,RNR1,FAS2,GAP3,MET3,VID24,MET6,ILS1
GO:1901292	nucleoside phosphate catabolic process	22	12	2.21	2.30E-07	GPM3,ENO,PGK,RAG2,GPM1,HAM1,TPI1,GAP1,FBA1,PYK1,RAG5,GAP3
GO:0072522	purine-containing compound biosynthetic ...	73	23	7.34	2.80E-07	GPM3,HPT1,GUA1,ENO,PGK,AAH1,RAG2,GPM1,ADK1,ADE2,MEU1,ADE5,7,TPI1,GAP1,FBA1,XPT1,GUK1,ADE6,ACS2,PYK1,RAG5,GAP3,MET6
GO:0009260	ribonucleotide biosynthetic process	68	22	6.84	3.00E-07	GPM3,HPT1,GUA1,ENO,PGK,RAG2,URA1,GPM1,ADK1,ADE2,ADE5,7,TPI1,GAP1,FBA1,XPT1,GUK1,ADE6,ACS2,PYK1,RAG5,URA7,GAP3
GO:0090501	RNA phosphodiester bond hydrolysis	79	24	7.95	3.30E-07	UTP13,UTP11,NOP58,ENP1,RLP7,MPP10,RRS1,NOB1,PWP2,DBP3,UTP10,NOP19,BMS1,UTP6,MTR4,UTP18,RRP5,DIP2,BRX1,FCF2,NOP14,NOC4,NOP9,RRP42

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0016053	organic acid biosynthetic process	151	36	15.19	3.50E-07	HIS4,GPM3,OLE1,BIO2,ENO,FAU1,PGK,SCS7,RAG2,GPM1,MET13,CYS4,SHM2,ORT1,PHS1,MEU1,SER3,PAN5,TPI1,GAP1,FMS1,FBA1,ALD5,MET5,FAS1,SHM1,LEU1,SUR4,PYK1,LEU4,RAG5,LEU3,FAS2,GAP3,MET3,MET6
GO:0046394	carboxylic acid biosynthetic process	151	36	15.19	3.50E-07	HIS4,GPM3,OLE1,BIO2,ENO,FAU1,PGK,SCS7,RAG2,GPM1,MET13,CYS4,SHM2,ORT1,PHS1,MEU1,SER3,PAN5,TPI1,GAP1,FMS1,FBA1,ALD5,MET5,FAS1,SHM1,LEU1,SUR4,PYK1,LEU4,RAG5,LEU3,FAS2,GAP3,MET3,MET6
GO:0006725	cellular aromatic compound metabolic pro...	1260	168	126.77	7.70E-07	SPB1,APA2,HIS4,RPA49,PRS5,GPM3,NOP1,SOH1,DSS1,UTP5,HPT1,GUA1,EBP2,RPF2,RSE1,GAL80,ENO,MES1,HAS1,YTA7,FAU1,PGK,MSW1,FUR1,AAH1,RAG2,NOG1,URA1,GPM1,UTP13,RPC37,DBP7,UTP15,ADH4,UTP11,ADK1,NOP53,MET13,SHM2,NOP58,FHL1,NOP12,ENP1,CBF5,KLMA_20481,RLP7,UTP8,TPA1,ADE2,MPP10,DTD1,IPI3,NAN1,HAM1,MRT4,RRS1,IPI1,RNR2,DCAF13,MEU1,DRS1,NOB1,RPL3,PAB1,MRPL15,PDC2,BFR2,PWP2,DBP3,RRP3,HAL9,VTS1,RAD54,KSS1,SAH1,ADE5,7,MTO1,GUS1,ECM16,HEM13,TPI1,MDN1,GAP1,UTP10,GAR1,CIC1,HAP1,ERB1,MCM1,RRP12,IMP4,FBA1,YTM1,NOP19,HMG1,RPC82,RIX1,XPT1,UTP21,PUS1,BMS1,GUK1,UTP6,PRP43,GEP3,SHM1,MTR4,UTP18,ENP2,RPA135,PDX3,ADE6,RRP5,PWP1,NOP56,LAC9,UTP4,NUG1,RPC40,VAS1,NOP7,DIP2,ACS2,URA2,IMP3,PDC1,EXO1,BRX1,URB1,DHR2,RPA190,FUN12,REV1,PYK1,YAF9,NOP15,KRE33,EPL1,FCF2,KLMA_60313,UGP1,NOP4,RAG5,JHD2,ERG13,RPB1,CDC60,IKI3,URA7,ROX3,RNR1,SPT21,NOP14,NOC4,RRP9,HEM14,PUS4,KLMA_70408,NOP9,GAP3,RRP42,PUB1,UTP25,HDA1,NOP2,DEF1,MET6,ILS1

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0046483	heterocycle metabolic process	1270	169	127.78	7.90E-07	SPB1,APA2,HIS4,RPA49,PRS5,GPM3,NOP1,SOH1,DSS1,UTP5,HPT1,GUA1,BIO2,EBP2,RPF2,RSE1,GAL80,ENO,MES1,HAS1,YTA7,FAU1,PGK,MSW1,FUR1,AAH1,RAG2,NOG1,URA1,GPM1,UTP13,RPC37,DBP7,UTP15,ADH4,UTP11,ADK1,NOP53,MET13,SHM2,NOP58,FHL1,NOP12,ENP1,CBF5,KLMA_20481,RLP7,UTP8,TPA1,ADE2,MPP10,IPI3,NAN1,HAM1,MRT4,RRS1,IPI1,RNR2,DCAF13,MEU1,DRS1,NOB1,RPL3,PAB1,MRPL15,PDC2,BFR2,PWP2,DBP3,RRP3,HAL9,VTS1,RAD54,KSS1,SAH1,ADE5,7,MTO1,GUS1,ECM16,HEM13,TPI1,MDN1,GAP1,RIB7,UTP10,GAR1,CIC1,HAP1,ERB1,MCM1,RRP12,IMP4,FBA1,YTM1,NOP19,HMG1,RPC82,RIX1,XPT1,UTP21,PUS1,BMS1,GUK1,UTP6,PRP43,GEP3,SHM1,MTR4,UTP18,ENP2,RPA135,PDX3,ADE6,RRP5,PWP1,NOP56,LAC9,UTP4,NUG1,RPC40,VAS1,NOP7,DIP2,ACS2,URA2,IMP3,PDC1,EXO1,BRX1,URB1,DHR2,RPA190,FUN12,REV1,PYK1,YAF9,NOP15,KRE33,EPL1,FCF2,KLMA_60313,UGP1,NOP4,RAG5,JHD2,ERG13,RPB1,CDC60,IKI3,URA7,ROX3,RNR1,SPT21,NOP14,NOC4,RRP9,HEM14,PUS4,KLMA_70408,NOP9,GAP3,RRP42,PUB1,UTP25,HDA1,NOP2,DEF1,MET6,ILS1
GO:1901293	nucleoside phosphate biosynthetic proces...	94	26	9.46	8.20E-07	PRS5,GPM3,HPT1,GUA1,ENO,PGK,AAH1,RAG2,URA1,GPM1,ADK1,ADE2,RNR2,ADE5,7,TPI1,GAP1,FBA1,XPT1,GUK1,ADE6,ACS2,PYK1,RAG5,URA7,RNR1,GAP3
GO:1901566	organonitrogen compound biosynthetic pro...	639	99	64.29	8.40E-07	HIS4,RpL37a,GPM3,HPT1,GUA1,BIO2,RPL17B,ENO,MES1,LIP1,FAU1,PGK,CWH43,MSW1,FUR1,AAH1,RAG2,URA1,KLMA_20052,GPM1,UTP11,ADK1,RPS2,MET13,CYS4,SHM2,KLMA_20355,RPL22A,TPA1,ORT1,ADE2,RPS3,RPL5,GSH1,PHS1,RNR2,MEU1,ETT1,RPL3,PAB1,RLI1,KLMA_30320,PDC2,SUR2,SER3,YIH1,PAN5,TIF32,SAH1,ADE5,7,GUS1,RPL15B,dsd1,HEM13,TPI1,GAP1,RIB7,FMS1,FBA1,MAM33,DPM1,MET5,XPT1,RPL10A,GUK1,SHM1,LEU1,PDX3,RPS14,ADE6,MSS51,VAS1,RPL2,ACS2,URA2,KLMA_60069,FUN12,PYK1,LEU4,KLMA_60313,RAG5,LEU3,CDC60,PET309,IKI3,URA7,RNR1,TIF3,MET16,HEM14,RPL1

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
						9B,GAP3,MET3,MNN1,NIP1,KLMA_80256,MET6,ILS1
GO:0006164	purine nucleotide biosynthetic process	62	20	6.24	1.10E-06	GPM3,HPT1,GUA1,ENO,PGK,RAG2,GPM1,ADK1,ADE2,ADE5,7,TPI1,GAP1,FBA1,XPT1,GUK1,ADE6,ACS2,PYK1,RAG5,GAP3
GO:0009152	purine ribonucleotide biosynthetic proce...	62	20	6.24	1.10E-06	GPM3,HPT1,GUA1,ENO,PGK,RAG2,GPM1,ADK1,ADE2,ADE5,7,TPI1,GAP1,FBA1,XPT1,GUK1,ADE6,ACS2,PYK1,RAG5,GAP3
GO:0009166	nucleotide catabolic process	21	11	2.11	1.30E-06	GPM3,ENO,PGK,RAG2,GPM1,TPI1,GAP1,FBA1,PYK1,RAG5,GAP3
GO:0046434	organophosphate catabolic process	29	13	2.92	1.30E-06	GPD1,GPM3,ENO,PGK,RAG2,GPM1,HAM1,TPI1,GAP1,FBA1,PYK1,RAG5,GAP3
GO:0006090	pyruvate metabolic process	25	12	2.52	1.40E-06	GPM3,ENO,PGK,RAG2,GPM1,PDC2,TPI1,GAP1,FBA1,PYK1,RAG5,GAP3
GO:0019752	carboxylic acid metabolic process	294	55	29.58	1.60E-06	HIS4,SAM2,ACO2,GPM3,OLE1,GUA1,BIO2,ENO,MES1,FAU1,PGK,SCS7,MSW1,RAG2,GPM1,ADH4,MET13,CYS4,SHM2,ORT1,DTD1,PHS1,MEU1,PDC2,SER3,PAN5,SAH1,GUS1,TPI1,GAP1,FMS1,FBA1,ALD5,MET5,FAS1,SHM1,LEU1,SUR4,ADE6,VAS1,ACS2,URA2,PDC1,MDH1,PYK1,LEU4,RAG5,LEU3,CDC60,URA7,FAS2,GAP3,MET3,MET6,ILS1
GO:0044237	cellular metabolic process	2232	261	224.57	1.80E-06	SPB1,APA2,HIS4,LPP1,SAM2,RpL37a,RPA49,ACO2,PRS5,GPD1,GPM3,NOP1,OLE1,SOH1,DSS1,UTP5,HPT1,GUA1,PFK1,BIO2,RPL17B,EBP2,RPF2,RSE1,GAL80,ENO,MES1,HAS1,TDA1,YTA7,LIP1,FAU1,PGK,CWH43,SCS7,MSW1,FUR1,AAH1,RAG2,NOG1,URA1,TPS2,KLMA_20052,TSL1,GPM1,UTP13,RPC37,DBP7,UTP15,HSL1,ADH4,UTP11,ADK1,NOP53,RPS2,MET13,CYS4,SHM2,ERG3,NOP58,FHL1,KLMA_20355,NOP12,ENP1,CLN2,UBP3,CB

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
						F5,KLMA_20481,RLP7,RPL22A,UTP8,TPA1,ERG28,CYP707A7,ORT1,ADE2,MPP10,ERG9,DTD1,IPI3,RPS3,RPL5,NAN1,LIA1,HAM1,MRT4,RRS1,GSH1,PHS1,IPI1,RNR2,ERG1,DCAF13,MEU1,DRS1,ETT1,NOB1,RPL3,PAB1,RLI1,MRPL15,KLMA_30320,GSY2,PDC2,SUR2,BFR2,SER3,PWP2,YIH1,DBP3,PAN5,RRP3,TIF32,HAL9,VTS1,RAD54,KSS1,ERG6,SAH1,DUG1,ADE5,7,MTO1,GUS1,ECM16,RPL15B,dsd1,HEM13,TPI1,MDN1,GAP1,RIB7,UTP10,GAR1,CIC1,HAP1,ERB1,MCM1,IMP2,RRP12,IMP4,FMS1,FBA1,ALD5,MAM33,YTM1,NOP19,HMG1,DPM1,RPC82,MET5,RIX1,XPT1,UTP21,FAS1,PUS1,BMS1,RPL10A,GUK1,UTP6,PRP43,GEP3,SHM1,MTR4,UTP18,ENP2,LEU1,RPA135,YJU3,PDX3,RPS14,SUR4,ADE6,ERG25,RRP5,PWP1,NOP56,MSS51,LAC9,UTP4,NUG1,RPC40,VAS1,NOP7,MET10,RPL2,DIP2,ACS2,MAP1,UTH1,SHB17,URA2,IMP3,KLMA_60069,PDC1,EXO1,IPP1,MDM20,BRX1,URB1,MDH1,DHR2,RPA190,FUN12,REV1,PYK1,LEU4,YAF9,NOP15,KRE33,EPL1,FCF2,KLMA_60313,UGP1,NOP4,RAG5,cyp524A1,JHD2,LEU3,ERG13,PFK2,RPB1,CDC60,PET309,IKI3,URA7,ROX3,RNR1,PCL6,HSL7,FAS2,SPT21,NOP14,TIF3,MET16,NOC4,RRP9,HEM14,RPL19B,DYS1,PUS4,PCL1,KLMA_70408,NOP9,GAP3,MET3,MNN1,RRP42,PUB1,UTP25,HDA1,NOP2,NIP1,GDS1,KLMA_80256,DEF1,VID24,TPS1,PTH2,MET6,ILS1
GO:0009165	nucleotide biosynthetic process	92	25	9.26	1.90E-06	PRS5,GPM3,HPT1,GUA1,ENO,PGK,RAG2,URA1,GPM1,ADK1,ADE2,RNR2,ADE5,7,TPI1,GAP1,FBA1,XPT1,GUK1,ADE6,ACS2,PYK1,RAG5,URA7,RNR1,GAP3
GO:0019693	ribose phosphate metabolic process	117	29	11.77	2.30E-06	PRS5,GPM3,HPT1,GUA1,ENO,PGK,RAG2,URA1,GPM1,ADK1,ADE2,RNR2,PDC2,ADE5,7,TPI1,GAP1,FBA1,HMG1,XPT1,GUK1,ADE6,ACS2,SHB17,PYK1,RAG5,ERG13,URA7,RNR1,GAP3
GO:0009259	ribonucleotide metabolic process	105	27	10.56	2.40E-06	GPM3,HPT1,GUA1,ENO,PGK,RAG2,URA1,GPM1,ADK1,ADE2,RNR2,PDC2,ADE5,7,TPI1,GAP1,FBA1,HMG1,XPT1,GUK1,ADE6,ACS2,PYK1,RAG5,ERG13,URA7,RNR1,GAP3

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0044238	primary metabolic process	2108	249	212.09	2.90E-06	SPB1,APA2,HIS4,LPP1,SAM2,RpL37a,RPA49,ACO2,PRS5,GPD1,GPM3,NOP1,OLE1,SOH1,DSS1,UTP5,HPT1,GUA1,RPL17B,EBP2,RPF2,RSE1,GAL80,ENO,MES1,HAS1,TDA1,YTA7,LIP1,PGK,CWH43,SCS7,MSW1,FUR1,AAH1,RAG2,NOG1,URA1,TPS2,KLMA_20052,TSL1,GPM1,UTP13,RPC37,DBP7,UTP15,HSL1,ADH4,UTP11,ADK1,NOP53,RPS2,MET13,CYS4,SHM2,ERG3,NOP58,GAL7,GAL10,GAL1,FHL1,KLMA_20355,NOP12,KLMA_20392,ENP1,CLN2,UBP3,CBF5,KLMA_20481,RLP7,RPL22A,UTP8,TPA1,ERG28,CYP707A7,ORT1,ADE2,MPP10,ERG9,DTD1,IPI3,RPS3,RPL5,NAN1,LIA1,HAM1,MRT4,RRS1,PGM2,PHS1,IPI1,RNR2,ERG1,DCAF13,MEU1,DRS1,ETT1,NOB1,RPL3,PAB1,RLI1,MRPL15,KLMA_30320,GSY2,PDC2,SUR2,BFR2,SER3,PWP2,YIH1,DBP3,RRP3,TIF32,HAL9,VTS1,SCW4,RAD54,KSS1,ERG6,SAH1,ADE5,7,MTO1,GUS1,ECM16,RPL15B,dsd1,TPI1,MDN1,GAP1,UTP10,GAR1,CIC1,HAP1,ERB1,MCM1,IMP2,RRP12,IMP4,FBA1,MAM33,YTM1,NOP19,HMG1,DPM1,RPC82,MET5,RIX1,XPT1,UTP21,FAS1,PUS1,BMS1,RPL10A,GUK1,UTP6,PRP43,GEP3,SHM1,MTR4,UTP18,ENP2,LEU1,RPA135,YJU3,RPS14,SUR4,ADE6,ERG25,RRP5,PWP1,NOP56,MSS51,LAC9,UTP4,NUG1,RPC40,VAS1,NOP7,RPL2,DIP2,ACS2,MAP1,URA2,IMP3,KLMA_60069,PDC1,EXO1,MDM20,BRX1,URB1,MDH1,DHR2,RPA190,FUN12,REV1,PYK1,LEU4,YAF9,NOP15,KRE33,EPL1,FCF2,KLMA_60313,RGT1,UGP1,NOP4,RAG5,cyp524A1,JHD2,LEU3,ERG13,RPB1,CDC60,PET309,IKI3,URA7,ROX3,RNR1,PCL6,HSL7,FAS2,SPT21,NOP14,TIF3,NOC4,RRP9,RPL19B,DYS1,PUS4,KLMA_70408,NOP9,GAP3,MET3,MNN1,RRP42,PUB1,UTP25,HDA1,NOP2,BGL2,NIP1,KLMA_80256,DEF1,VID24,TPS1,PTH2,MET6,ILS1

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0044085	cellular component biogenesis	746	109	75.06	4.00E-06	SPB1,UTP5,SDA1,EBP2,RPF2,RSE1,HAS1,SCO1,NOG1,UTP13,DBP7,UTP15,UTP11,ARX1,NOP53,RPS2,NOP58,NOP12,ENP1,CBF5,RLP7,UTP8,MPP10,IPI3,RPS3,RPL5,NAN1,MRT4,RRS1,IPI1,DCAF13,DRS1,NOB1,RPL3,RLI1,BFR2,MEX67,PWP2,YIH1,DBP3,RRP3,TIF32,KSS1,RRB1,ECM16,MDN1,UTP10,GAR1,CIC1,SFB3,ERB1,RRP12,IMP4,YTM1,NOP19,NMD3,RIX1,UTP21,MTR2,BMS1,UTP6,PRP43,NOC2,GEP3,MTR4,UTP18,ENP2,CWP1,RRP5,PWP1,NOP56,MSS51,UTP4,NUG1,NOP7,DIP2,UTH1,ALB1,IMP3,KLMA_60069,BRX1,URB1,DHR2,FUN12,NOP15,KRE33,FCF2,KLMA_60313,NOP4,PFK2,PET309,RSA4,NEW1,NOP14,TIF3,NOC4,RRP9,MAK21,NOP9,LTV1,RLP24,RRP42,PUB1,UTP25,HDA1,NOP2,NIP1,PUF6,RPL8B
GO:0043436	oxoacid metabolic process	303	55	30.49	4.20E-06	HIS4,SAM2,ACO2,GPM3,OLE1,GUA1,BIO2,ENO,MES1,FAU1,PGK,SCS7,MSW1,RAG2,GPM1,ADH4,MET13,CYS4,SHM2,ORT1,DTD1,PHS1,MEU1,PDC2,SER3,PAN5,SAH1,GUS1,TPI1,GAP1,FMS1,FBA1,ALD5,MET5,FAS1,SHM1,LEU1,SUR4,ADE6,VAS1,ACS2,URA2,PDC1,MDH1,PYK1,LEU4,RAG5,LEU3,CDC60,URA7,FAS2,GAP3,MET3,MET6,ILS1
GO:0055086	nucleobase-containing small molecule met...	180	38	18.11	4.20E-06	APA2,PRS5,GPM3,HPT1,GUA1,ENO,PGK,FUR1,AAH1,RAG2,URA1,GPM1,ADH4,ADK1,ADE2,HAM1,RNR2,MEU1,PDC2,SAH1,ADE5,7,TPI1,GAP1,FBA1,HMG1,XPT1,GUK1,ADE6,ACS2,URA2,PYK1,UGP1,RAG5,ERG13,URA7,RNR1,GAP3,MET6
GO:0010467	gene expression	1083	146	108.96	4.70E-06	SPB1,RpL37a,RPA49,NOP1,SOH1,UTP5,RPL17B,EBP2,RPF2,RSE1,GAL80,MES1,HAS1,YTA7,MSW1,NOG1,UTP13,RPC37,DBP7,UTP15,UTP11,NOP53,RPS2,NOP58,FHL1,KLMA_20355,NOP12,ENP1,CBF5,KLMA_20481,RLP7,RPL22A,UTP8,TPA1,MPP10,IPI3,RPS3,RPL5,NAN1,LIA1,MRT4,RRS1,IPI1,DCAF13,DRS1,ETT1,NOB1,RPL3,PAB1,RLI1,MRPL15,PDC2,BFR2,MEX67,PWP2,YIH1,DBP3,RRP3,TIF32,HAL9,VTS1,KSS1,MTO1,GUS1,ECM16,RPL15B,MDN1,UTP10,GAR1,CIC1,HAP1,ERB1,MCM1,IMP2,RRP12,

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
						IMP4,MAM33,YTM1,NOP19,RPC82,RIX1,UTP21,MTR2,PUS1,BMS1,RPL10A,UTP6,PRP43,GEP3,MTR4,UTP18,ENP2,RPA135,RPS14,RRP5,PWP1,NOP56,MSS51,LAC9,UTP4,NUG1,RPC40,VAS1,NOP7,RPL2,DIP2,MAP1,IMP3,KLMA_60069,MDM20,BRX1,URB1,DHR2,RPA190,FUN12,YAF9,NOP15,KRE33,EPL1,FCF2,KLMA_60313,NOP4,JHD2,CDC60,PET309,IKI3,ROX3,SPT21,NEW1,NOP14,TIF3,NOC4,RRP9,RPL19B,DYS1,PUS4,KLMA_70408,NOP9,RRP42,PUB1,UTP25,HDA1,NOP2,NIP1,KLMA_80256,ILS1
GO:0006139	nucleobase-containing compound metabolic...	1196	158	120.33	4.80E-06	SPB1,APA2,RPA49,PRS5,GPM3,NOP1,SOH1,DSS1,UTP5,HPT1,GUA1,EBP2,RPF2,RSE1,GAL80,ENO,MES1,HAS1,YTA7,PGK,MSW1,FUR1,AAH1,RAG2,NOG1,URA1,GPM1,UTP13,RPC37,DBP7,UTP15,ADH4,UTP11,ADK1,NOP53,NOP58,FHL1,NOP12,ENP1,CBF5,KLMA_20481,RLP7,UTP8,TPA1,ADE2,MPP10,IPI3,NAN1,HAM1,MRT4,RRS1,IPI1,RNR2,DCAF13,MEU1,DRS1,NOB1,RPL3,PAB1,MRPL15,PDC2,BFR2,PWP2,DBP3,RRP3,HAL9,VTS1,RAD54,KSS1,SAH1,ADE5,7,MTO1,GUS1,ECM16,TPI1,MDN1,GAP1,UTP10,GAR1,CIC1,HAP1,ERB1,MCM1,RRP12,IMP4,FBA1,YTM1,NOP19,HMG1,RPC82,RIX1,XPT1,UTP21,PUS1,BMS1,GUK1,UTP6,PRP43,GEP3,MTR4,UTP18,ENP2,RPA135,ADE6,RRP5,PWP1,NOP56,LAC9,UTP4,NUG1,RPC40,VAS1,NOP7,DIP2,ACS2,URA2,IMP3,EXO1,BRX1,URB1,DHR2,RPA190,FUN12,REV1,PYK1,YAF9,NOP15,KRE33,EPL1,FCF2,KLMA_60313,UGP1,NOP4,RAG5,JHD2,ERG13,RPB1,CDC60,IKI3,URA7,ROX3,RNR1,SPT21,NOP14,NOC4,RRP9,PUS4,KLMA_70408,NOP9,GAP3,RRP42,PUB1,UTP25,HDA1,NOP2,DEF1,MET6,ILS1
GO:0006082	organic acid metabolic process	305	55	30.69	5.20E-06	HIS4,SAM2,ACO2,GPM3,OLE1,GUA1,BIO2,ENO,MES1,FAU1,PGK,SCS7,MSW1,RAG2,GPM1,ADH4,MET13,CYS4,SHM2,ORT1,DTD1,PHS1,MEU1,PDC2,SER3,PAN5,SAH1,GUS1,TPI1,GAP1,FMS1,FBA1,ALD5,MET5,FAS1,SHM1,LEU1,SUR4,ADE6,VAS1,ACS2,URA2,PDC1,MDH1,PYK1,LEU4,RAG5,LEU3,CDC60,URA7,FAS2,GAP3,MET3,MET6,ILS1

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0016052	carbohydrate catabolic process	38	14	3.82	8.50E-06	GPM3,ENO,PGK,RAG2,GPM1,GAL7,GAL10,PDC2,TPI1,GAP1,FBA1,PYK1,RAG5,GAP3
GO:0019318	hexose metabolic process	43	15	4.33	8.80E-06	GAL80,PGK,RAG2,GPM1,GAL7,GAL10,GAL1,PDC2,TPI1,GAP1,FBA1,PYK1,RGT1,GAP3,VID24
GO:0019359	nicotinamide nucleotide biosynthetic pro...	25	11	2.52	1.10E-05	GPM3,ENO,PGK,RAG2,GPM1,TPI1,GAP1,FBA1,PYK1,RAG5,GAP3
GO:0019363	pyridine nucleotide biosynthetic process	25	11	2.52	1.10E-05	GPM3,ENO,PGK,RAG2,GPM1,TPI1,GAP1,FBA1,PYK1,RAG5,GAP3
GO:0009161	ribonucleoside monophosphate metabolic p...	84	22	8.45	1.60E-05	PRS5,GPM3,HPT1,GUA1,ENO,PGK,AAH1,RAG2,URA1,GPM1,ADK1,ADE2,PDC2,ADE5,7,TPI1,GAP1,FBA1,XPT1,ADE6,PYK1,RAG5,GAP3
GO:0071428	rRNA-containing ribonucleoprotein comple...	45	15	4.53	1.70E-05	SDA1,NOG1,ARX1,NOP53,RPS2,RPS3,RRS1,RLI1,MEX67,NMD3,RIX1,MTR2,NUG1,NOP9,LTV1
GO:0072521	purine-containing compound metabolic pro...	116	27	11.67	1.80E-05	GPM3,HPT1,GUA1,ENO,PGK,AAH1,RAG2,GPM1,ADK1,ADE2,MEU1,PDC2,SAH1,ADE5,7,TPI1,GAP1,FBA1,HMG1,XPT1,GUK1,ADE6,ACS2,PYK1,RAG5,ERG13,GAP3,MET6
GO:0009123	nucleoside monophosphate metabolic proce...	86	22	8.65	2.30E-05	PRS5,GPM3,HPT1,GUA1,ENO,PGK,AAH1,RAG2,URA1,GPM1,ADK1,ADE2,PDC2,ADE5,7,TPI1,GAP1,FBA1,XPT1,ADE6,PYK1,RAG5,GAP3

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0000054	ribosomal subunit export from nucleus	41	14	4.13	2.30E-05	SDA1,NOG1,ARX1,NOP53,RPS3,RRS1,RLI1,MEX67,NMD3,RIX1,MTR2,NUG1,NOP9,LTV1
GO:0033750	ribosome localization	41	14	4.13	2.30E-05	SDA1,NOG1,ARX1,NOP53,RPS3,RRS1,RLI1,MEX67,NMD3,RIX1,MTR2,NUG1,NOP9,LTV1
GO:0009117	nucleotide metabolic process	152	32	15.29	2.70E-05	APA2,PRS5,GPM3,HPT1,GUA1,ENO,PGK,AAH1,RAG2,URA1,GPM1,ADH4,ADK1,ADE2,HAM1,RNR2,PDC2,ADE5,7,TPI1,GAP1,FBA1,HMG1,XPT1,GUK1,ADE6,ACS2,PYK1,RAG5,ERG13,URA7,RNR1,GAP3
GO:0009126	purine nucleoside monophosphate metaboli...	75	20	7.55	2.90E-05	GPM3,HPT1,GUA1,ENO,PGK,AAH1,RAG2,GPM1,ADK1,ADE2,PDC2,ADE5,7,TPI1,GAP1,FBA1,XPT1,ADE6,PYK1,RAG5,GAP3
GO:0009167	purine ribonucleoside monophosphate meta...	75	20	7.55	2.90E-05	GPM3,HPT1,GUA1,ENO,PGK,AAH1,RAG2,GPM1,ADK1,ADE2,PDC2,ADE5,7,TPI1,GAP1,FBA1,XPT1,ADE6,PYK1,RAG5,GAP3
GO:0005996	monosaccharide metabolic process	47	15	4.73	3.00E-05	GAL80,PGK,RAG2,GPM1,GAL7,GAL10,GAL1,PDC2,TPI1,GAP1,FBA1,PYK1,RGT1,GAP3,VID24
GO:0072525	pyridine-containing compound biosyntheti...	32	12	3.22	3.10E-05	GPM3,ENO,PGK,RAG2,GPM1,TPI1,GAP1,FBA1,PDX3,PYK1,RAG5,GAP3
GO:0090305	nucleic acid phosphodiester bond hydroly...	100	24	10.06	3.10E-05	UTP13,UTP11,NOP58,ENP1,RLP7,MPP10,RRS1,NOB1,PWP2,DBP3,UTP10,NOP19,BMS1,UTP6,MTR4,UTP18,RRP5,DIP2,BRX1,FCF2,NOP14,NOC4,NOP9,RRP42

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0006753	nucleoside phosphate metabolic process	153	32	15.39	3.10E-05	APA2,PRS5,GPM3,HPT1,GUA1,ENO,PGK,AAH1,RAG2,URA1,GPM1,ADH4,ADK1,ADE2,HAM1,RNR2,PDC2,ADE5,7,TPI1,GAP1,FBA1,HMG1,XPT1,GUK1,ADE6,ACS2,PYK1,RAG5,ERG13,URA7,RNR1,GAP3
GO:0016070	RNA metabolic process	843	116	84.82	3.60E-05	SPB1,RPA49,NOP1,SOH1,DSS1,UTP5,EBP2,RPF2,RSE1,GAL80,MES1,HAS1,YTA7,MSW1,NOG1,UTP13,RPC37,DBP7,UTP15,UTP11,NOP53,NOP58,FHL1,NOP12,ENP1,CBF5,KLMA_20481,RLP7,UTP8,TPA1,MPP10,IPI3,NAN1,MRT4,RRS1,IPI1,DCAF13,DRS1,NOB1,RPL3,PAB1,MRPL15,PDC2,BFR2,PWP2,DBP3,RRP3,HAL9,VTS1,KSS1,MTO1,GUS1,ECM16,MDN1,UTP10,GAR1,CIC1,HAP1,ERB1,MCM1,RRP12,IMP4,YTM1,NOP19,RPC82,RIX1,UTP21,PUS1,BMS1,UTP6,PRP43,GEP3,MTR4,UTP18,ENP2,RPA135,RRP5,PWP1,NOP56,LAC9,UTP4,NUG1,RPC40,VAS1,NOP7,DIP2,IMP3,BRX1,URB1,DHR2,RPA190,FUN12,YAF9,NOP15,KRE33,EPL1,FCF2,KLMA_60313,NOP4,JHD2,CDC60,IKI3,ROX3,SPT21,NOP14,NOC4,RRP9,PUS4,KLMA_70408,NOP9,RRP42,PUB1,UTP25,HDA1,NOP2,ILS1
GO:0009058	biosynthetic process	1301	165	130.9	3.80E-05	HIS4,SAM2,RpL37a,RPA49,PRS5,GPM3,NOP1,OLE1,SOH1,UTP5,HPT1,GUA1,BIO2,RPL17B,GAL80,ENO,MES1,YTA7,LIP1,FAU1,PGK,CWH43,SCS7,MSW1,FUR1,AAH1,RAG2,URA1,TPS2,KLMA_20052,TSL1,GPM1,RPC37,UTP15,ADH4,UTP11,ADK1,RPS2,MET13,CYS4,SHM2,ERG3,FHL1,KLMA_20355,KLMA_20481,RPL22A,UTP8,TPA1,ERG28,CYP707A7,ORT1,ADE2,ERG9,IPI3,RPS3,RPL5,NAN1,LIA1,HAM1,GSH1,PHS1,IPI1,RNR2,ERG1,MEU1,ETT1,RPL3,PAB1,RLI1,KLMA_30320,GSY2,PDC2,SUR2,SER3,YIH1,PAN5,TIF32,HAL9,KSS1,ERG6,SAH1,ADE5,7,GUS1,RPL15B,dsd1,HEM13,TPI1,GAP1,RIB7,UTP10,HAP1,MCM1,FMS1,FBA1,ALD5,MAM33,HMG1,DPM1,RPC82,MET5,RIX1,XPT1,FAS1,RPL10A,GUK1,SHM1,LEU1,RPA135,PDX3,RPS14,SUR4,ADE6,ERG25,MSS51,LAC9,UTP4,RPC40,VAS1,NOP7,RPL2,ACS2,SHB17,URA2,KLMA_60069,PDC1,RPA190,FUN12,REV1,PYK1,LEU4,YAF9,EPL1,KLMA_60313,UGP1,RAG5,cyp524A1,JHD2,LEU3,E

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
						RG13,RPB1,CDC60,PET309,IKI3,URA7,ROX3,RNR1,FAS2,SPT21,TIF3,MET16,HEM14,RPL19B,DYS1,KLMA_70408,GAP3,MET3,MNN1,HDA1,NIP1,KLMA_80256,VID24,TPS1,MET6,ILS1
GO:0071826	ribonucleoprotein complex subunit organi...	115	26	11.57	4.50E-05	RPF2,RSE1,NOG1,NOP53,IPI3,RPL5,MRT4,IPI1,DRS1,RPL3,RLI1,TIF32,MDN1,RIX1,PRP43,RRP5,KLMA_60069,BRX1,FUN12,RSA4,TIF3,MAK21,RLP24,PUB1,NOP2,NIP1
GO:1901576	organic substance biosynthetic process	1289	163	129.69	5.50E-05	HIS4,SAM2,RpL37a,RPA49,PRS5,GPM3,NOP1,OLE1,SOH1,UTP5,HPT1,GUA1,BIO2,RPL17B,GAL80,ENO,MES1,YTA7,LIP1,FAU1,PGK,CWH43,SCS7,MSW1,FUR1,AAH1,RAG2,URA1,TPS2,KLMA_20052,TSL1,GPM1,RPC37,UTP15,ADH4,UTP11,ADK1,RPS2,MET13,CYS4,SHM2,ERG3,FHL1,KLMA_20355,KLMA_20481,RPL22A,UTP8,TPA1,ERG28,CYP707A7,ORT1,ADE2,ERG9,IPI3,RPS3,RPL5,NAN1,HAM1,GSH1,PHS1,IPI1,RNR2,ERG1,MEU1,ETT1,RPL3,PAB1,RLI1,KLMA_30320,GSY2,PDC2,SUR2,SER3,YIH1,PAN5,TIF32,HAL9,KSS1,ERG6,SAH1,ADE5,7,GUS1,RPL15B,dsd1,HEM13,TPI1,GAP1,RIB7,UTP10,HAP1,MCM1,FMS1,FBA1,ALD5,MAM33,HMG1,DPM1,RPC82,MET5,RIX1,XPT1,FAS1,RPL10A,GUK1,SHM1,LEU1,RPA135,PDX3,RPS14,SUR4,ADE6,ERG25,MSS51,LAC9,UTP4,RPC40,VAS1,NOP7,RPL2,ACS2,SHB17,URA2,KLMA_60069,PDC1,RPA190,FUN12,REV1,PYK1,LEU4,YAF9,EPL1,KLMA_60313,UGP1,RAG5,cyp524A1,JHD2,LEU3,ERG13,RPB1,CDC60,PET309,IKI3,URA7,ROX3,RNR1,FAS2,SPT21,TIF3,MET16,HEM14,RPL19B,KLMA_70408,GAP3,MET3,MNN1,HDA1,NIP1,KLMA_80256,VID24,TPS1,MET6,ILS1
GO:0009150	purine ribonucleotide metabolic process	97	23	9.76	5.70E-05	GPM3,HPT1,GUA1,ENO,PGK,RAG2,GPM1,ADK1,ADE2,PDC2,ADE5,7,TPI1,GAP1,FBA1,HMG1,XPT1,GUK1,ADE6,ACS2,PYK1,RAG5,ERG13,GAP3

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0009116	nucleoside metabolic process	34	12	3.42	6.30E-05	PRS5,HPT1,GUA1,FUR1,URA1,RNR2,MEU1,SAH1,XPT1,GUK1,URA7,RNR1
GO:0006163	purine nucleotide metabolic process	98	23	9.86	6.70E-05	GPM3,HPT1,GUA1,ENO,PGK,RAG2,GPM1,ADK1,ADE2,PDC2,ADE5,7,TPI1,GAP1,FBA1,HMG1,XPT1,GUK1,ADE6,ACS2,PYK1,RAG5,ERG13,GAP3
GO:0009142	nucleoside triphosphate biosynthetic pro...	40	13	4.02	8.30E-05	GPM3,ENO,PGK,RAG2,GPM1,TPI1,GAP1,FBA1,PYK1,RAG5,URA7,RNR1,GAP3
GO:1901657	glycosyl compound metabolic process	35	12	3.52	8.70E-05	PRS5,HPT1,GUA1,FUR1,URA1,RNR2,MEU1,SAH1,XPT1,GUK1,URA7,RNR1
GO:0005992	trehalose biosynthetic process	4	4	0.4	0.0001	TPS2,TSL1,UGP1,TPS1
GO:0009312	oligosaccharide biosynthetic process	4	4	0.4	0.0001	TPS2,TSL1,UGP1,TPS1
GO:0046351	disaccharide biosynthetic process	4	4	0.4	0.0001	TPS2,TSL1,UGP1,TPS1
GO:0044249	cellular biosynthetic process	1278	160	128.58	0.00013	HIS4,SAM2,RpL37a,RPA49,PRS5,GPM3,NOP1,OLE1,SOH1,UTP5,HPT1,GUA1,BIO2,RPL17B,GAL80,ENO,MES1,YTA7,LIP1,FAU1,PGK,CWH43,SCS7,MSW1,FUR1,AAH1,RAG2,URA1,TPS2,KLMA_20052,TSL1,GPM1,RPC37,UTP15,UTP11,ADK1,RPS2,MET13,CYS4,SHM2,ERG3,FHL1,KLMA_20355,KLMA_20481,RPL22A,UTP8,TPA1,ERG28,CYP707A7,ORT1,ADE2,ERG9,IPI3,RPS3,RPL5,NAN1,HAM1,GSH1,PHS1,IPI1,RNR2,ERG1,MEU1,ETT1,RPL

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
						3,PAB1,RLI1,KLMA_30320,GSY2,PDC2,SUR2,SER3,YIH1,PAN5,TIF32,HAL9,KSS1,ERG6,SAH1,ADE5,7,GUS1,RPL15B,dsd1,HEM13,TPI1,GAP1,RIB7,UTP10,HAP1,MCM1,FMS1,FBA1,ALD5,MAM33,HMG1,DPM1,RPC82,MET5,RIX1,XPT1,FAS1,RPL10A,GUK1,SHM1,LEU1,RPA135,PDX3,RPS14,SUR4,ADE6,ERG25,MSS51,LAC9,UTP4,RPC40,VAS1,NOP7,RPL2,ACS2,URA2,KLMA_60069,RPA190,FUN12,REV1,PYK1,LEU4,YAF9,EPL1,KLMA_60313,UGP1,RAG5,cyp524A1,JHD2,LEU3,ERG13,RPB1,CDC60,PET309,IKI3,URA7,ROX3,RNR1,FAS2,SPT21,TIF3,MET16,HEM14,RPL19B,KLMA_70408,GAP3,MET3,MNN1,HDA1,NIP1,KLMA_80256,VID24,TPS1,MET6,ILS1
GO:0006807	nitrogen compound metabolic process	1991	231	200.32	0.00013	SPB1,APA2,HIS4,SAM2,RpL37a,RPA49,PRS5,GPM3,NOP1,SOH1,DSS1,UTP5,HPT1,GUA1,BIO2,RPL17B,EBP2,RPF2,RSE1,GAL80,ENO,MES1,HAS1,TDA1,YTA7,LIP1,FAU1,PGK,CWH43,SCS7,MSW1,FUR1,AAH1,RAG2,NOG1,URA1,KLMA_20052,GPM1,UTP13,RPC37,DBP7,UTP15,HSL1,ADH4,UTP11,ADK1,NOP53,RPS2,MET13,CYS4,SHM2,NOP58,FHL1,KLMA_20355,NOP12,ENP1,CLN2,UBP3,CBF5,KLMA_20481,RLP7,RPL22A,UTP8,TPA1,ORT1,ADE2,MPP10,DTD1,IPI3,RPS3,RPL5,NAN1,LIA1,HAM1,MRT4,RRS1,GSH1,PHS1,IPI1,RNR2,DCAF13,MEU1,DRS1,ETT1,NOB1,RPL3,PAB1,RLI1,MRPL15,KLMA_30320,PDC2,SUR2,BFR2,SER3,PWP2,YIH1,DBP3,PAN5,RRP3,TIF32,HAL9,VTS1,RAD54,KSS1,SAH1,DUG1,ADE5,7,MTO1,GUS1,ECM16,RPL15B,dsd1,HEM13,TPI1,MDN1,GAP1,RIB7,UTP10,GAR1,CIC1,HAP1,ERB1,MCM1,IMP2,RRP12,IMP4,FMS1,FBA1,MAM33,YTM1,NOP19,HMG1,DPM1,RPC82,MET5,RIX1,XPT1,UTP21,PUS1,BMS1,RPL10A,GUK1,UTP6,PRP43,GEP3,SHM1,MTR4,UTP18,ENP2,LEU1,RPA135,PDX3,RPS14,ADE6,RRP5,PWP1,NOP56,MSS51,LAC9,UTP4,NUG1,RPC40,VAS1,NOP7,RPL2,DIP2,ACS2,MAP1,URA2,IMP3,KLMA_60069,PDC1,EXO1,MDM20,BRX1,URB1,DHR2,RPA190,FUN12,REV1,PYK1,LEU4,YAF9,NOP15,KRE33,EPL1,FCF2,KLMA_60313,UGP1,NOP4,RAG5,JHD2,LEU3,ERG13,RPB1,CDC60,PET3

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
						09,IKI3,URA7,ROX3,RNR1,PCL6,HSL7,SPT21,NOP14,TIF3,MET16,NOC4,RRP9,HEM14,RPL19B,DYS1,PUS4,KLMA_70408,NOP9,GAP3,MET3,MNN1,RRP42,PUB1,UTP25,HDA1,NOP2,NIP1,KLMA_80256,DEF1,VID24,PTH2,MET6,ILS1
GO:0022618	ribonucleoprotein complex assembly	109	24	10.97	0.00014	RPF2,RSE1,NOG1,NOP53,IPI3,RPL5,MRT4,IPI1,DRS1,RPL3,TIF32,MDN1,RIX1,RRP5,KLMA_60069,BRX1,FUN12,RSA4,TIF3,MAK21,RLP24,PUB1,NOP2,NIP1
GO:0005975	carbohydrate metabolic process	137	28	13.78	0.00015	GPD1,GPM3,GAL80,ENO,PGK,RAG2,TPS2,TSL1,GPM1,GAL7,GAL10,GAL1,PGM2,GSY2,PDC2,SCW4,TPI1,GAP1,FBA1,MDH1,PYK1,RGT1,UGP1,RAG5,GAP3,BGL2,VID24,TPS1
GO:0009201	ribonucleoside triphosphate biosynthetic...	37	12	3.72	0.00016	GPM3,ENO,PGK,RAG2,GPM1,TPI1,GAP1,FBA1,PYK1,RAG5,URA7,GAP3
GO:0071166	ribonucleoprotein complex localization	84	20	8.45	0.00016	SDA1,NOG1,ARX1,NOP53,RPS2,ENP1,UTP8,RPS3,RRS1,RLI1,MEX67,NMD3,RIX1,MTR2,MTR4,NUG1,CEX1,NEW1,NOP9,LTV1
GO:0071426	ribonucleoprotein complex export from nu...	84	20	8.45	0.00016	SDA1,NOG1,ARX1,NOP53,RPS2,ENP1,UTP8,RPS3,RRS1,RLI1,MEX67,NMD3,RIX1,MTR2,MTR4,NUG1,CEX1,NEW1,NOP9,LTV1
GO:0006006	glucose metabolic process	32	11	3.22	0.00017	PGK,RAG2,GPM1,PDC2,TPI1,GAP1,FBA1,PYK1,RGT1,GAP3,VID24

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0019362	pyridine nucleotide metabolic process	43	13	4.33	0.00019	GPM3,ENO,PGK,RAG2,GPM1,ADH4,PDC2,TPI1,GAP1,FBA1,PYK1,RAG5,GAP3
GO:0046496	nicotinamide nucleotide metabolic proces...	43	13	4.33	0.00019	GPM3,ENO,PGK,RAG2,GPM1,ADH4,PDC2,TPI1,GAP1,FBA1,PYK1,RAG5,GAP3
GO:0006405	RNA export from nucleus	85	20	8.55	0.00019	SDA1,NOG1,ARX1,NOP53,RPS2,ENP1,UTP8,RPS3,RRS1,RLI1,MEX67,NMD3,RIX1,MTR2,MTR4,NUG1,CEX1,NEW1,NOP9,LTV1
GO:0032787	monocarboxylic acid metabolic process	105	23	10.56	0.00021	GPM3,OLE1,BIO2,ENO,PGK,SCS7,RAG2,GPM1,PHS1,PDC2,PAN5,TPI1,GAP1,FMS1,FBA1,ALD5,FAS1,SUR4,ACS2,PYK1,RAG5,FAS2,GAP3
GO:0072524	pyridine-containing compound metabolic p...	49	14	4.93	0.00021	GPM3,ENO,PGK,RAG2,GPM1,ADH4,PDC2,TPI1,GAP1,FBA1,PDX3,PYK1,RAG5,GAP3
GO:0009119	ribonucleoside metabolic process	23	9	2.31	0.00022	HPT1,GUA1,URA1,RNR2,MEU1,SAH1,GUK1,URA7,RNR1
GO:0046165	alcohol biosynthetic process	39	12	3.92	0.00028	ADH4,ERG3,ERG28,CYP707A7,ERG9,ERG1,ERG6,dsd1,ERG25,PDC1,cyp524A1,ERG13
GO:0090407	organophosphate biosynthetic process	178	33	17.91	0.00028	PRS5,GPM3,HPT1,GUA1,ENO,PGK,CWH43,AAH1,RAG2,URA1,KLMA_20052,GPM1,ADK1,ADE2,RNR2,SAH1,ADE5,7,TPI1,GAP1,FBA1,HMG1,DPM1,XPT1,GUK1,ADE6,ACS2,SHB17,PYK1,RAG5,ERG13,URA7,RNR1,GAP3

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0006732	coenzyme metabolic process	114	24	11.47	0.00029	SAM2,GPM3,BIO2,ENO,FAU1,PGK,RAG2,GPM1,ADH4,MET13,SHM2,PDC2,PAN5,TPI1,GAP1,FMS1,FBA1,HMG1,SHM1,ACS2,PYK1,RAG5,ERG13,GAP3
GO:0006754	ATP biosynthetic process	34	11	3.42	0.00031	GPM3,ENO,PGK,RAG2,GPM1,TPI1,GAP1,FBA1,PYK1,RAG5,GAP3
GO:0051188	cofactor biosynthetic process	101	22	10.16	0.00031	SAM2,GPM3,BIO2,ENO,FAU1,PGK,RAG2,GPM1,GSH1,PAN5,HEM13,TPI1,GAP1,FMS1,FBA1,PDX3,ACS2,PYK1,RAG5,MET16,HEM14,GAP3
GO:0006696	ergosterol biosynthetic process	24	9	2.41	0.00031	ERG3,ERG28,CYP707A7,ERG9,ERG1,ERG6,ERG25,cyp524A1,ERG13
GO:0008204	ergosterol metabolic process	24	9	2.41	0.00031	ERG3,ERG28,CYP707A7,ERG9,ERG1,ERG6,ERG25,cyp524A1,ERG13
GO:0016128	phytosteroid metabolic process	24	9	2.41	0.00031	ERG3,ERG28,CYP707A7,ERG9,ERG1,ERG6,ERG25,cyp524A1,ERG13
GO:0016129	phytosteroid biosynthetic process	24	9	2.41	0.00031	ERG3,ERG28,CYP707A7,ERG9,ERG1,ERG6,ERG25,cyp524A1,ERG13
GO:0044108	cellular alcohol biosynthetic process	24	9	2.41	0.00031	ERG3,ERG28,CYP707A7,ERG9,ERG1,ERG6,ERG25,cyp524A1,ERG13
GO:0097384	cellular lipid biosynthetic process	24	9	2.41	0.00031	ERG3,ERG28,CYP707A7,ERG9,ERG1,ERG6,ERG25,cyp524A1,ERG13

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0006611	protein export from nucleus	89	20	8.95	0.00038	SDA1,NOG1,ARX1,NOP53,RPS2,ENP1,UTP8,RPS3,RRS1,RLI1,MEX67,NMD3,RIX1,MTR2,MTR4,NUG1,CEX1,NEW1,NOP9,LTV1
GO:0009145	purine nucleoside triphosphate biosynthe...	35	11	3.52	0.00041	GPM3,ENO,PGK,RAG2,GPM1,TPI1,GAP1,FBA1,PYK1,RAG5,GAP3
GO:0009206	purine ribonucleoside triphosphate biosy...	35	11	3.52	0.00041	GPM3,ENO,PGK,RAG2,GPM1,TPI1,GAP1,FBA1,PYK1,RAG5,GAP3
GO:0051168	nuclear export	90	20	9.06	0.00044	SDA1,NOG1,ARX1,NOP53,RPS2,ENP1,UTP8,RPS3,RRS1,RLI1,MEX67,NMD3,RIX1,MTR2,MTR4,NUG1,CEX1,NEW1,NOP9,LTV1
GO:1902652	secondary alcohol metabolic process	25	9	2.52	0.00045	ERG3,ERG28,CYP707A7,ERG9,ERG1,ERG6,ERG25,cyp524A1,ERG13
GO:1902653	secondary alcohol biosynthetic process	25	9	2.52	0.00045	ERG3,ERG28,CYP707A7,ERG9,ERG1,ERG6,ERG25,cyp524A1,ERG13
GO:0006012	galactose metabolic process	5	4	0.5	0.00046	GAL80,GAL7,GAL10,GAL1
GO:0051186	cofactor metabolic process	169	31	17	0.00053	SAM2,GPM3,BIO2,ENO,FAU1,PGK,RAG2,GPM1,ADH4,MET13,SHM2,GSH1,PDC2,PAN5,SAH1,DUG1,HEM13,TPI1,GAP1,FMS1,FBA1,HMG1,SHM1,PDX3,ACS2,PYK1,RAG5,ERG13,MET16,HEM14,GAP3

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:1901137	carbohydrate derivative biosynthetic pro...	177	32	17.81	0.00056	PRS5,GPM3,HPT1,GUA1,ENO,PGK,CWH43,RAG2,URA1,GPM1,ADK1,ADE2,RNR2,MEU1,KLMA_30320,ADE5,7,TPI1,GAP1,FBA1,DPM1,XPT1,GUK1,ADE6,ACS2,SHB17,PYK1,RAG5,URA7,RNR1,GAP3,MNN1
GO:0044107	cellular alcohol metabolic process	26	9	2.62	0.00063	ERG3,ERG28,CYP707A7,ERG9,ERG1,ERG6,ERG25,cyp524A1,ERG13
GO:0050657	nucleic acid transport	94	20	9.46	0.0008	SDA1,NOG1,ARX1,NOP53,RPS2,ENP1,UTP8,RPS3,RRS1,RLI1,MEX67,NMD3,RIX1,MTR2,MTR4,NUG1,CEX1,NEW1,NOP9,LTV1
GO:0050658	RNA transport	94	20	9.46	0.0008	SDA1,NOG1,ARX1,NOP53,RPS2,ENP1,UTP8,RPS3,RRS1,RLI1,MEX67,NMD3,RIX1,MTR2,MTR4,NUG1,CEX1,NEW1,NOP9,LTV1
GO:0051236	establishment of RNA localization	94	20	9.46	0.0008	SDA1,NOG1,ARX1,NOP53,RPS2,ENP1,UTP8,RPS3,RRS1,RLI1,MEX67,NMD3,RIX1,MTR2,MTR4,NUG1,CEX1,NEW1,NOP9,LTV1
GO:1901135	carbohydrate derivative metabolic proces...	260	42	26.16	0.00094	PRS5,GPD1,GPM3,HPT1,GUA1,PFK1,ENO,PGK,CWH43,FUR1,RAG2,URA1,GPM1,ADK1,ADE2,RNR2,MEU1,KLMA_30320,PDC2,SUR2,SAH1,ADE5,7,TPI1,GAP1,FBA1,HMG1,DPM1,XPT1,GUK1,ADE6,ACS2,SHB17,PYK1,UGP1,RAG5,ERG13,PFK2,URA7,RNR1,GAP3,MNN1
GO:1901617	organic hydroxy compound biosynthetic pr...	50	13	5.03	0.00096	ADH4,ERG3,ERG28,CYP707A7,ERG9,ERG1,ERG6,dsd1,PDX3,ERG25,PDC1,cyp524A1,ERG13
GO:0009141	nucleoside triphosphate metabolic proces...	69	16	6.94	0.00101	GPM3,ENO,PGK,RAG2,GPM1,ADK1,HAM1,PDC2,TPI1,GAP1,FBA1,PYK1,RAG5,URA7,RNR1,GAP3

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0000464	endonucleolytic cleavage in ITS1 upstrea...	3	3	0.3	0.00101	DBP3,RRP5,BRX1
GO:0019637	organophosphate metabolic process	270	43	27.17	0.0011	APA2,LPP1,PRS5,GPD1,GPM3,HPT1,GUA1,PFK1,ENO,PGK,CWH43,SCS7,AAH1,RAG2,URA1,KLMA_20052,GPM1,ADH4,ADK1,ADE2,HAM1,RNR2,PDC2,SUR2,SAH1,ADE5,7,TPI1,GAP1,FBA1,HMG1,DPM1,XPT1,GUK1,ADE6,ACS2,SHB17,PYK1,RAG5,ERG13,PFK2,URA7,RNR1,GAP3
GO:0009133	nucleoside diphosphate biosynthetic proc...	6	4	0.6	0.00128	ADK1,RNR2,GUK1,RNR1
GO:0006066	alcohol metabolic process	52	13	5.23	0.00143	ADH4,ERG3,ERG28,CYP707A7,ERG9,ERG1,PDC2,ERG6,dsd1,ERG25,PDC1,cyp524A1,ERG13
GO:0009163	nucleoside biosynthetic process	14	6	1.41	0.00148	HPT1,GUA1,URA1,MEU1,GUK1,URA7
GO:0042455	ribonucleoside biosynthetic process	14	6	1.41	0.00148	HPT1,GUA1,URA1,MEU1,GUK1,URA7
GO:1901659	glycosyl compound biosynthetic process	14	6	1.41	0.00148	HPT1,GUA1,URA1,MEU1,GUK1,URA7
GO:0006694	steroid biosynthetic process	29	9	2.92	0.00153	ERG3,ERG28,CYP707A7,ERG9,ERG1,ERG6,ERG25,cyp524A1,ERG13
GO:0016126	sterol biosynthetic process	29	9	2.92	0.00153	ERG3,ERG28,CYP707A7,ERG9,ERG1,ERG6,ERG25,cyp524A1,ERG13

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0000055	ribosomal large subunit export from nucl...	24	8	2.41	0.00167	SDA1,ARX1,NOP53,RRS1,MEX67,NMD3,MTR2,NUG1
GO:0044272	sulfur compound biosynthetic process	47	12	4.73	0.00178	SAM2,BIO2,MET13,CYS4,GSH1,MEU1,PDC2,MET5,ACS2,MET16,MET3,MET6
GO:0019439	aromatic compound catabolic process	136	25	13.68	0.00178	GPM3,DSS1,ENO,PGK,AAH1,RAG2,GPM1,TPA1,DTD1,HAM1,MRT4,PAB1,VTS1,SAH1,TPI1,GAP1,FBA1,MTR4,PDC1,PYK1,RAG5,JHD2,GAP3,RRP42,PUB1
GO:0009108	coenzyme biosynthetic process	81	17	8.15	0.00229	SAM2,GPM3,BIO2,ENO,FAU1,PGK,RAG2,GPM1,PAN5,TPI1,GAP1,FMS1,FBA1,ACS2,PYK1,RAG5,GAP3
GO:0043603	cellular amide metabolic process	347	51	34.91	0.00243	RpL37a,BIO2,RPL17B,MES1,LIP1,FAU1,MSW1,UTP11,RPS2,MET13,SHM2,KLMA_20355,RPL22A,TPA1,RPS3,RPL5,GSH1,ETT1,RPL3,PAB1,RLI1,YIH1,PAN5,TIF32,DUG1,GUS1,RPL15B,IMP2,FMS1,MAM33,HMG1,RPL10A,SHM1,RPS14,MSS51,VAS1,RPL2,ACS2,KLMA_60069,FUN12,KLMA_60313,ERG13,CDC60,PET309,IKI3,TIF3,MET16,RPL19B,NIP1,KLMA_80256,ILS1
GO:0016125	sterol metabolic process	31	9	3.12	0.00257	ERG3,ERG28,CYP707A7,ERG9,ERG1,ERG6,ERG25,cyp524A1,ERG13
GO:1902626	assembly of large subunit precursor of p...	7	4	0.7	0.00275	RPF2,NOG1,RLP24,NOP2
GO:0031503	protein-containing complex localization	104	20	10.46	0.00294	SDA1,NOG1,ARX1,NOP53,RPS2,ENP1,UTP8,RPS3,RRS1,RLI1,MEX67,NMD3,RIX1,MTR2,MTR4,NUG1,CEX1,NEW1,NOP9,LTV1

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0009112	nucleobase metabolic process	26	8	2.62	0.00297	AAH1,URA1,ADE2,ADE5,7,XPT1,URA2,URA7,MET6
GO:0017144	drug metabolic process	180	30	18.11	0.00318	SAM2,ACO2,GPM3,BIO2,ENO,PGK,RAG2,GPM1,ADK1,CYS4,SHM2,MEU1,PDC2,TPI1,GAP1,RIB7,FMS1,FBA1,ALD5,MET5,SHM1,PDX3,ACS2,PDC1,MDH1,PYK1,RAG5,GAP3,MET3,MET6
GO:0008202	steroid metabolic process	32	9	3.22	0.00326	ERG3,ERG28,CYP707A7,ERG9,ERG1,ERG6,ERG25,cyp524A1,ERG13
GO:0006520	cellular amino acid metabolic process	173	29	17.41	0.00341	HIS4,SAM2,GUA1,MES1,MSW1,ADH4,MET13,CYS4,SHM2,ORT1,DTD1,MEU1,SER3,SAH1,GUS1,MET5,SHM1,LEU1,ADE6,VAS1,URA2,PDC1,LEU4,LEU3,CDC60,URA7,MET3,MET6,ILS1
GO:0006733	oxidoreduction coenzyme metabolic proces...	57	13	5.73	0.00346	GPM3,ENO,PGK,RAG2,GPM1,ADH4,PDC2,TPI1,GAP1,FBA1,PYK1,RAG5,GAP3
GO:1901605	alpha-amino acid metabolic process	113	21	11.37	0.00358	HIS4,SAM2,GUA1,MET13,CYS4,SHM2,ORT1,DTD1,MEU1,SER3,SAH1,SHM1,LEU1,ADE6,URA2,PDC1,LEU4,LEU3,URA7,MET3,MET6
GO:1901361	organic cyclic compound catabolic proces...	143	25	14.39	0.00364	GPM3,DSS1,ENO,PGK,AAH1,RAG2,GPM1,TPA1,DTD1,HAM1,MRT4,PAB1,VTS1,SAH1,TPI1,GAP1,FBA1,MTR4,PDC1,PYK1,RAG5,JHD2,GAP3,RRP42,PUB1
GO:0009199	ribonucleoside triphosphate metabolic pr...	64	14	6.44	0.00368	GPM3,ENO,PGK,RAG2,GPM1,ADK1,PDC2,TPI1,GAP1,FBA1,PYK1,RAG5,URA7,GAP3
GO:0009403	toxin biosynthetic process	4	3	0.4	0.00374	CYS4,MET5,MET3
GO:0009404	toxin metabolic process	4	3	0.4	0.00374	CYS4,MET5,MET3

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0019320	hexose catabolic process	4	3	0.4	0.00374	GAL7,GAL10,PYK1
GO:0035999	tetrahydrofolate interconversion	4	3	0.4	0.00374	MET13,SHM2,SHM1
GO:0070813	hydrogen sulfide metabolic process	4	3	0.4	0.00374	CYS4,MET5,MET3
GO:0070814	hydrogen sulfide biosynthetic process	4	3	0.4	0.00374	CYS4,MET5,MET3
GO:1901070	guanosine-containing compound biosynthet...	4	3	0.4	0.00374	HPT1,GUA1,GUK1
GO:0000056	ribosomal small subunit export from nucl...	12	5	1.21	0.00436	RPS3,MEX67,MTR2,NOP9,LTV1
GO:0006730	one-carbon metabolic process	12	5	1.21	0.00436	SAM2,MET13,SHM2,SAH1,SHM1
GO:0008610	lipid biosynthetic process	138	24	13.88	0.00467	OLE1,LIP1,CWH43,SCS7,KLMA_20052,ERG3,ERG28,CYP707A7,ERG9,PHS1,ERG1,SUR2,ERG6,SAH1,dsd1,HMG1,DPM1,FAS1,SUR4,ERG25,cyp524A1,ERG13,URA7,FAS2
GO:0000103	sulfate assimilation	8	4	0.8	0.00507	MET5,MET10,MET16,MET3
GO:0005991	trehalose metabolic process	8	4	0.8	0.00507	TPS2,TSL1,UGP1,TPS1
GO:0006551	leucine metabolic	8	4	0.8	0.00507	DTD1,LEU1,LEU4,LEU3

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
	process					
GO:0009218	pyrimidine ribonucleotide metabolic proc...	8	4	0.8	0.00507	URA1,RNR2,URA7,RNR1
GO:0019748	secondary metabolic process	8	4	0.8	0.00507	CYS4,GSH1,MET5,MET3
GO:0044550	secondary metabolite biosynthetic proces...	8	4	0.8	0.00507	CYS4,GSH1,MET5,MET3
GO:0044270	cellular nitrogen compound catabolic pro...	139	24	13.99	0.00513	GPM3,DSS1,ENO,PGK,AAH1,RAG2,GPM1,TPA1,HAM1,MRT4,PAB1,VTS1,SAH1,TPI1,GAP1,FBA1,MTR4,PDC1,PYK1,RAG5,JHD2,GAP3,RRP42,PUB1
GO:0046700	heterocycle catabolic process	139	24	13.99	0.00513	GPM3,DSS1,ENO,PGK,AAH1,RAG2,GPM1,TPA1,HAM1,MRT4,PAB1,VTS1,SAH1,TPI1,GAP1,FBA1,MTR4,PDC1,PYK1,RAG5,JHD2,GAP3,RRP42,PUB1
GO:0006403	RNA localization	109	20	10.97	0.00515	SDA1,NOG1,ARX1,NOP53,RPS2,ENP1,UTP8,RPS3,RRS1,RLI1,MEX67,NMD3,RIX1,MTR2,MTR4,NUG1,CEX1,NEW1,NOP9,LTV1
GO:0044271	cellular nitrogen compound biosynthetic ...	910	112	91.56	0.00541	RpL37a,RPA49,PRS5,GPM3,NOP1,SOH1,UTP5,HPT1,GUA1,BIO2,RPL17B,GAL80,ENO,MES1,YTA7,LIP1,FAU1,PGK,MSW1,FUR1,AAH1,RAG2,URA1,GPM1,RPC37,UTP15,UTP11,ADK1,RPS2,FHL1,KLMA_20355,KLMA_20481,RPL22A,UTP8,TPA1,ADE2,RPS3,RPL5,NAN1,HAM1,GSH1,RNR2,MEU1,ETT1,RPL3,PAB1,RLI1,PDC2,YIH1,PAN5,TIF32,HAL9,KSS1,ADE5,7,GUS1,RPL15B,dsd1,HEM13,TPI1,GAP1,RIB7,UTP10,HAP1,MCM1,FMS1,FBA1,MAM33,RPC82,XPT1,RPL10A,GUK1,RPA135,PDX3,RPS14,ADE6,MSS51,LAC9,UTP4,RPC40,VAS1,RPL2,ACS2,URA2,KLMA_60

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
						069,RPA190,FUN12,REV1,PYK1,YAF9,EPL1,KLMA_60313,RAG5,JHD2,RPB1,CDC60,PET309,IKI3,URA7,ROX3,RNR1,SPT21,TIF3,MET16,HEM14,RPL19B,KLMA_70408,GAP3,HDA1,NIP1,KLMA_80256,MET6,ILS1
GO:0046034	ATP metabolic process	60	13	6.04	0.00553	GPM3,ENO,PGK,RAG2,GPM1,ADK1,PDC2,TPI1,GAP1,FBA1,PYK1,RAG5,GAP3
GO:0043604	amide biosynthetic process	302	44	30.38	0.00577	RpL37a,BIO2,RPL17B,MES1,LIP1,FAU1,MSW1,UTP11,RPS2,KLMA_20355,RPL22A,TPA1,RPS3,RPL5,GSH1,ETT1,RPL3,PAB1,RLI1,YIH1,PAN5,TIF32,GUS1,RPL15B,FMS1,MAM33,RPL10A,RPS14,MSS51,VAS1,RPL2,ACS2,KLMA_60069,FUN12,KLMA_60313,CDC60,PET309,IKI3,TIF3,MET16,RPL19B,NIP1,KLMA_80256,ILS1
GO:0000096	sulfur amino acid metabolic process	23	7	2.31	0.00578	SAM2,MET13,CYS4,MEU1,MET5,MET3,MET6
GO:0006091	generation of precursor metabolites and ...	103	19	10.36	0.00597	ACO2,GPM3,ENO,PGK,RAG2,GPM1,GSY2,PDC2,TPI1,GAP1,HAP1,FBA1,MAM33,MDH1,PYK1,UGP1,RAG5,GAP3,GDS1
GO:0006575	cellular modified amino acid metabolic p...	41	10	4.13	0.00604	FAU1,MET13,SHM2,GSH1,PAN5,SAH1,DUG1,FMS1,SHM1,MET16
GO:0070925	organelle assembly	89	17	8.95	0.00637	RPF2,NOP53,IPI3,RPL5,MRT4,IPI1,DRS1,RPL3,MDN1,RIX1,RRP5,KLMA_60069,BRX1,FUN12,RSA4,MAK21,PUB1
GO:0006913	nucleocytoplasmic transport	127	22	12.78	0.00698	GSP1,SDA1,NOG1,ARX1,NOP53,RPS2,ENP1,UTP8,RPS3,RRS1,RLI1,MEX67,NMD3,RIX1,MTR2,MTR4,NUG1,CEX1,NEW1,NOP9,LTV1,KAP123

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0034655	nucleobase-containing compound catabolic...	127	22	12.78	0.00698	GPM3,DSS1,ENO,PGK,RAG2,GPM1,TPA1,HAM1,MRT4,PAB1,VTS1,SAH1,TPI1,GAP1,FBA1,MTR4,PYK1,RAG5,JHD2,GAP3,RRP42,PUB1
GO:0051169	nuclear transport	127	22	12.78	0.00698	GSP1,SDA1,NOG1,ARX1,NOP53,RPS2,ENP1,UTP8,RPS3,RRS1,RLI1,MEX67,NMD3,RIX1,MTR2,MTR4,NUG1,CEX1,NEW1,NOP9,LTV1,KAP123
GO:0009205	purine ribonucleoside triphosphate metab...	62	13	6.24	0.00739	GPM3,ENO,PGK,RAG2,GPM1,ADK1,PDC2,TPI1,GAP1,FBA1,PYK1,RAG5,GAP3
GO:0090304	nucleic acid metabolic process	1024	123	103.03	0.00789	SPB1,RPA49,NOP1,SOH1,DSS1,UTP5,EBP2,RPF2,RSE1,GAL80,MES1,HAS1,YTA7,MSW1,NOG1,UTP13,RPC37,DBP7,UTP15,UTP11,ADK1,NOP53,NOP58,FHL1,NOP12,ENP1,CBF5,KLMA_20481,RLP7,UTP8,TPA1,MPP10,IPI3,NAN1,MRT4,RRS1,IPI1,DCAF13,DRS1,NOB1,RPL3,PAB1,MRPL15,PDC2,BFR2,PWP2,DBP3,RRP3,HAL9,VTS1,RAD54,KSS1,MTO1,GUS1,ECM16,MDN1,UTP10,GAR1,CIC1,HAP1,ERB1,MCM1,RRP12,IMP4,YTM1,NOP19,RPC82,RIX1,UTP21,PUS1,BMS1,UTP6,PRP43,GEP3,MTR4,UTP18,ENP2,RPA135,RRP5,PWP1,NOP56,LAC9,UTP4,NUG1,RPC40,VAS1,NOP7,DIP2,IMP3,EXO1,BRX1,URB1,DHR2,RPA190,FUN12,REV1,YAF9,NOP15,KRE33,EPL1,FCF2,KLMA_60313,NOP4,JHD2,RPB1,CDC60,IKI3,ROX3,RNR1,SPT21,NOP14,NOC4,RRP9,PUS4,KLMA_70408,NOP9,RRP42,PUB1,UTP25,HDA1,NOP2,DEF1,ILS1
GO:0006760	folic acid-containing compound metabolic...	9	4	0.91	0.00841	FAU1,MET13,SHM2,SHM1
GO:0042451	purine nucleoside biosynthetic	9	4	0.91	0.00841	HPT1,GUA1,MEU1,GUK1

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
	process					
GO:0043101	purine-containing compound salvage	9	4	0.91	0.00841	HPT1,AAH1,MEU1,XPT1
GO:0046129	purine ribonucleoside biosynthetic proce...	9	4	0.91	0.00841	HPT1,GUA1,MEU1,GUK1
GO:0009144	purine nucleoside triphosphate metabolic...	63	13	6.34	0.00848	GPM3,ENO,PGK,RAG2,GPM1,ADK1,PDC2,TPI1,GAP1,FBA1,PYK1,RAG5,GAP3
GO:1901615	organic hydroxy compound metabolic proce...	70	14	7.04	0.00852	ADH4,ERG3,ERG28,CYP707A7,ERG9,ERG1,PDC2,ERG6,dsd1,PDX3,ERG25,PDC1,cyp524A1,ERG13
GO:0000097	sulfur amino acid biosynthetic process	19	6	1.91	0.00864	MET13,CYS4,MEU1,MET5,MET3,MET6
GO:0006633	fatty acid biosynthetic process	19	6	1.91	0.00864	OLE1,SCS7,PHS1,FAS1,SUR4,FAS2
GO:0046112	nucleobase biosynthetic process	19	6	1.91	0.00864	AAH1,URA1,ADE5,7,URA2,URA7,MET6
GO:0009098	leucine biosynthetic process	5	3	0.5	0.00865	LEU1,LEU4,LEU3
GO:0031120	snRNA	5	3	0.5	0.00865	CBF5,GAR1,PUS1

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
	pseudouridine synthesis					
GO:0040031	snRNA modification	5	3	0.5	0.00865	CBF5,GAR1,PUS1
GO:0016051	carbohydrate biosynthetic process	50	11	5.03	0.00924	PGK,RAG2,TPS2,TSL1,GPM1,GSY2,TPI1,FBA1,UGP1,VID24,TPS1
GO:0042278	purine nucleoside metabolic process	14	5	1.41	0.00931	HPT1,GUA1,MEU1,SAH1,GUK1
GO:0046128	purine ribonucleoside metabolic process	14	5	1.41	0.00931	HPT1,GUA1,MEU1,SAH1,GUK1
GO:0006790	sulfur compound metabolic process	93	17	9.36	0.00997	SAM2,BIO2,MET13,CYS4,GSH1,MEU1,PDC2,SAH1,DUG1,HMG1,MET5,MET10,ACS2,ERG13,MET16,MET3,MET6

GO terms enriched in significantly up-regulated genes (biological process)

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0016042	lipid catabolic process	31	19	3.08	2.50E-12	PLB,PXA1,POT1,POX1,SPO1,MDH3,SPO14,PXA2,GDE1,KLMA_50156,SPS19,TES1,ANT1,KLMA_70317,LPX1,FOX2,ICL2,PDH1,CIT3
GO:0044242	cellular lipid catabolic process	26	17	2.58	8.30E-12	PLB,PXA1,POT1,POX1,SPO1,MDH3,PXA2,GDE1,KLMA_50156,SPS19,TES1,ANT1,LPX1,FOX2,ICL2,PDH1,CIT3
GO:0009062	fatty acid catabolic process	13	12	1.29	9.10E-12	PXA1,POT1,POX1,MDH3,PXA2,SPS19,TES1,ANT1,FOX2,ICL2,PDH1,CIT3
GO:0016054	organic acid catabolic process	47	21	4.67	5.30E-10	CHA1,PXA1,POT1,POX1,ARO10,GDH2,GAD1,MDH3,UGA1,PXA2,CAR1,CAR2,PUT1,SPS19,TES1,gabD,ANT1,FOX2,ICL2,PDH1,CIT3
GO:0046395	carboxylic acid catabolic process	47	21	4.67	5.30E-10	CHA1,PXA1,POT1,POX1,ARO10,GDH2,GAD1,MDH3,UGA1,PXA2,CAR1,CAR2,PUT1,SPS19,TES1,gabD,ANT1,FOX2,ICL2,PDH1,CIT3
GO:0044282	small molecule catabolic process	68	25	6.76	1.70E-09	CHA1,URH1,MIOX5,KLMA_20057,PXA1,POT1,POX1,ARO10,GDH2,GAD1,MDH3,UGA1,PXA2,CAR1,CAR2,PUT1,SPS19,TES1,gabD,ANT1,FOX2,ICL2,PDH1,CIT3,KLMA_80176
GO:0072329	monocarboxylic acid catabolic process	24	14	2.39	5.50E-09	PXA1,POT1,POX1,MDH3,UGA1,PXA2,SPS19,TES1,gabD,ANT1,FOX2,ICL2,PDH1,CIT3
GO:0019395	fatty acid oxidation	10	9	0.99	7.80E-09	PXA1,POT1,POX1,PEX11,MDH3,PXA2,TES1,ANT1,FOX2
GO:0034440	lipid oxidation	10	9	0.99	7.80E-09	PXA1,POT1,POX1,PEX11,MDH3,PXA2,TES1,ANT1,FOX2
GO:0006635	fatty acid beta-oxidation	9	8	0.89	7.20E-08	PXA1,POT1,POX1,MDH3,PXA2,TES1,ANT1,FOX2
GO:0030258	lipid modification	20	11	1.99	5.90E-07	ATG26,PXA1,POT1,POX1,PEX11,MDH3,PXA2,TES1,YMR1,ANT1,FOX2

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0006631	fatty acid metabolic process	38	15	3.78	1.20E-06	PXA1,POT1,POX1,PEX11,MDH3,PXA2,SPS19,TES1,ETR1,ANT1,FOX2,ICL2,PDH1,CIT3,CRC1
GO:0016999	antibiotic metabolic process	40	15	3.98	2.60E-06	CIT1,IAH1,KLMA_30124,ACO2,ACS1,MDH3,MDH2,IDP1,ALD4,SFA1,CTT1,KLMA_60405,ICL2,PDH1,CIT3
GO:0006536	glutamate metabolic process	9	6	0.89	6.00E-05	GDH2,GAD1,IDP1,GLT1,PUT1,gabD
GO:0009065	glutamine family amino acid catabolic pr...	9	6	0.89	6.00E-05	GDH2,GAD1,CAR1,CAR2,PUT1,gabD
GO:0055114	oxidation-reduction process	106	24	10.54	7.10E-05	MIC17,CIT1,PXA1,POT1,POX1,PEX11,KLMA_30124,ACO2,ACS1,KLMA_40010,MDH3,MDH2,IDP1,PXA2,ALD4,SFA1,TES1,ETR1,PHO85,KLMA_60405,ANT1,FOX2,CIT3,SGA1
GO:0022414	reproductive process	232	41	23.06	0.00012	MATALPHA1,KAR4,PRM1,ATG26,CDC7,DIT2,STE3,FUS3,DMC1,CSM1,IME4,RIM15,SPS4,KLMA_20368,UBI4,MUS81,MSC1,MLH1,STE4,MND1,MLH3,PRR1,KLMA_40061,KLMA_40062,CHS1,SPO14,ELM1,GAS4,HOP1,ECO1,QDR3,FIG1,AXL1,SPS19,GPA1,MF(ALPHA)1,RAD1,SST2,CRR1,KLMA_70118,SNF8
GO:0005975	carbohydrate metabolic process	137	28	13.62	0.00012	ATG26,PGU1,INU1,BIG1,MIOX5,ERT1,GPD2,CTS2,RDS2,KLMA_30011,ARA1,MDH3,GID8,KLMA_40105,KLMA_40133,CHS1,MDH2,DAK1,INO1,PHO85,FBP1,CRR1,ATH1,KLMA_70303,KLMA_70317,SGA1,KLMA_80176,GUT1
GO:0032787	monocarboxylic acid metabolic process	105	23	10.44	0.00017	ECM31,PXA1,POT1,POX1,GPD2,IAH1,PEX11,ACS1,MDH3,ISA1,UGA1,PXA2,ALD4,SPS19,TES1,gabD,ETR1,ANT1,FOX2,ICL2,PDH1,CIT3,CRC1
GO:0043648	dicarboxylic acid metabolic process	23	9	2.29	0.0002	GDH2,GAD1,MDH3,IDP1,GLT1,PUT1,gabD,KLMA_60405,ARO7

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0019953	sexual reproduction	113	24	11.23	0.00021	KAR4,PRM1,ATG26,DIT2,STE3,FUS3,SPS4,KLMA_20368,STE4,PRR1,KLMA_40061,CHS1,SPO14,GAS4,QDR3,FIG1,AXL1,SPS19,GPA1,MF(ALPHA)1,SST2,CRR1,KLMA_70118,SNF8
GO:0044703	multi-organism reproductive process	113	24	11.23	0.00021	KAR4,PRM1,ATG26,DIT2,STE3,FUS3,SPS4,KLMA_20368,STE4,PRR1,KLMA_40061,CHS1,SPO14,GAS4,QDR3,FIG1,AXL1,SPS19,GPA1,MF(ALPHA)1,SST2,CRR1,KLMA_70118,SNF8
GO:0000003	reproduction	240	41	23.85	0.00025	MATALPHA1,KAR4,PRM1,ATG26,CDC7,DIT2,STE3,FUS3,DMC1,CSM1,IME4,RIM15,SPS4,KLMA_20368,UBI4,MUS81,MSC1,MLH1,STE4,MND1,MLH3,PRR1,KLMA_40061,KLMA_40062,CHS1,SPO14,ELM1,GAS4,HOP1,ECO1,QDR3,FIG1,AXL1,SPS19,GPA1,MF(ALPHA)1,RAD1,SST2,CRR1,KLMA_70118,SNF8
GO:0008643	carbohydrate transport	11	6	1.09	0.00028	HGT1,STL1,RAG1,LAC12
GO:0006082	organic acid metabolic process	305	49	30.31	0.00029	CHA1,GLY1,ECM31,KLMA_20057,CIT1,PXA1,POT1,DSD1,POX1,GPD2,AGX1,ARO10,IAH1,PEX11,GDH2,KLMA_30124,ACO2,DPL1,GAD1,ACS1,LYS9,MDH3,ISA1,UGA1,LYS1,MDH2,VTC1,IDP1,PXA2,ALD4,CAR1,CAR2,GLT1,PUT1,SPS19,TES1,gabD,ETR1,KLMA_60405,ARO9,ICL1,PHO84,ANT1,FOX2,ICL2,PDH1,CIT3,CRC1,ARO7
GO:0045116	protein neddylation	5	4	0.5	0.00044	UBC12,DCN1,ULA1,UBA3
GO:0043436	oxoacid metabolic process	303	48	30.11	0.00047	CHA1,GLY1,ECM31,CIT1,PXA1,POT1,DSD1,POX1,GPD2,AGX1,ARO10,IAH1,PEX11,GDH2,KLMA_30124,ACO2,DPL1,GAD1,ACS1,LYS9,MDH3,ISA1,UGA1,LYS1,MDH2,VTC1,IDP1,PXA2,ALD4,CAR1,CAR2,GLT1,PUT1,SPS19,TES1,gabD,ETR1,KLMA_60405,ARO9,ICL1,PHO84,ANT1,FOX2,ICL2,PDH1,CIT3,CRC1,ARO7
GO:0051704	multi-organism process	127	25	12.62	0.00053	KAR4,PRM1,ATG26,DIT2,STE3,MAK32,FUS3,SPS4,KLMA_20368,STE4,PRR1,KLMA_40061,CHS1,SPO14,GAS4,QDR3,FIG1,AXL1,SPS19,GPA1,MF(ALPHA)1,SST2,CRR1,KLMA_70118,SNF8

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:1901606	alpha-amino acid catabolic process	21	8	2.09	0.00056	CHA1,ARO10,GDH2,GAD1,CAR1,CAR2,PUT1,gabD
GO:0006099	tricarboxylic acid cycle	22	8	2.19	0.0008	CIT1,KLMA_30124,ACO2,MDH3,MDH2,IDP1,KLMA_60405,CIT3
GO:0006101	citrate metabolic process	22	8	2.19	0.0008	CIT1,KLMA_30124,ACO2,MDH3,MDH2,IDP1,KLMA_60405,CIT3
GO:0072350	tricarboxylic acid metabolic process	22	8	2.19	0.0008	CIT1,KLMA_30124,ACO2,MDH3,MDH2,IDP1,KLMA_60405,CIT3
GO:0019752	carboxylic acid metabolic process	294	46	29.22	0.00083	CHA1,GLY1,ECM31,CIT1,PXA1,POT1,DSD1,POX1,GPD2,AGX1,ARO10,IAH1,PEX11,GDH2,KLMA_30124,ACO2,DPL1,GAD1,ACS1,LYS9,MDH3,ISA1,UGA1,LYS1,MDH2,IDP1,PXA2,ALD4,CAR1,CAR2,GLT1,PUT1,SPS19,TES1,gabD,ETR1,KLMA_60405,ARO9,ICL1,ANT1,FOX2,ICL2,PDH1,CIT3,CRC1,ARO7
GO:0006538	glutamate catabolic process	3	3	0.3	0.00097	GDH2,GAD1,gabD
GO:0019541	propionate metabolic process	3	3	0.3	0.00097	ICL2,PDH1,CIT3
GO:0019543	propionate catabolic process	3	3	0.3	0.00097	ICL2,PDH1,CIT3
GO:0019626	short-chain fatty acid catabolic process	3	3	0.3	0.00097	ICL2,PDH1,CIT3
GO:0019629	propionate catabolic process, 2-methylci...	3	3	0.3	0.00097	ICL2,PDH1,CIT3
GO:0043649	dicarboxylic acid catabolic process	3	3	0.3	0.00097	GDH2,GAD1,gabD
GO:0017144	drug metabolic process	180	31	17.89	0.0013	PGU1,DAL3,CIT1,GSM1,DSD1,GPD2,AGX1,ARO10,IAH1,KLMA_30124,ACO2,ACS1,THI13,MDH3,ISA1,CHS1,MDH2,IDP1,THI4,ALD4,CAR2,SFA1,CTT1,URC1,gabD,KLMA_60405,ARO9,ICL2,PDH1,CIT3,ARO7

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0051321	meiotic cell cycle	150	27	14.91	0.00136	KAR4,ATG26,CDC7,DIT2,FUS3,DMC1,CSM1,IME4,RIM15,SPS4,KLMA_20368,UBI4,MUS81,MSC1,MLH1,MND1,MLH3,KLMA_40062,CHS1,SPO14,GAS4,HOP1,ECO1,QDR3,SPS19,RAD1,CRR1
GO:0009063	cellular amino acid catabolic process	29	9	2.88	0.0014	CHA1,ARO10,GDH2,GAD1,UGA1,CAR1,CAR2,PUT1,gabD
GO:0015718	monocarboxylic acid transport	10	5	0.99	0.00156	FMP43,PXA1,PXA2,PUT4,FMP37
GO:0042737	drug catabolic process	19	7	1.89	0.00157	PGU1,DAL3,ARO10,CTT1,ICL2,PDH1,CIT3
GO:0000746	conjugation	67	15	6.66	0.00186	KAR4,PRM1,STE3,FUS3,STE4,PRR1,KLMA_40061,SPO14,FIG1,AXL1,GPA1,MF(ALPHA)1,SST2,KLMA_70118,SNF8
GO:0000747	conjugation with cellular fusion	67	15	6.66	0.00186	KAR4,PRM1,STE3,FUS3,STE4,PRR1,KLMA_40061,SPO14,FIG1,AXL1,GPA1,MF(ALPHA)1,SST2,KLMA_70118,SNF8
GO:0140253	cell-cell fusion	67	15	6.66	0.00186	KAR4,PRM1,STE3,FUS3,STE4,PRR1,KLMA_40061,SPO14,FIG1,AXL1,GPA1,MF(ALPHA)1,SST2,KLMA_70118,SNF8
GO:0030435	sporulation resulting in formation of a ...	56	13	5.57	0.00262	ATG26,DIT2,FUS3,SPS4,KLMA_20368,OSW5,CTS2,CHS1,SPO14,GAS4,QDR3,SPS19,CRR1
GO:0017001	antibiotic catabolic process	7	4	0.7	0.00263	CTT1,ICL2,PDH1,CIT3
GO:0009056	catabolic process	484	66	48.1	0.00282	CHA1,ECM38,HRD1,PLB,URH1,ATG27,PGU1,KLMA_10605,PEP12,UBP16,PNG1,DAL3,YUH1,AIM25,MIOX5,KLMA_20057,PXA1,POT1,POX1,GPD2,RIM15,ARO10,GDH2,KLMA_30011,RNH1,SPO1,CUE5,VTI1,SNX4,GAD1,MDH3,GID8,UGA1,SPO14,VTC1,PXA2,GDE1,CAR1,POP4,KLMA_50156,CAR2,CTT1,PUT1,SPS19,GUD1,TES1,gabD,APC11,JLP1,PHO85,PDE1,OTU1,ATH1,KLMA_70233,ANT1,KLMA_70317,LPX1,FOX2,ICL2,PDH1,CIT3,SNF8,ATG20,SGA1,KLMA_80176,VAM3

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0044764	multi-organism cellular process	70	15	6.96	0.00294	KAR4,PRM1,STE3,FUS3,STE4,PRR1,KLMA_40061,SPO14,FIG1,AXL1,GPA1,MF(ALPHA)1,SST2,KLMA_70118,SNF8
GO:0044281	small molecule metabolic process	540	72	53.67	0.00323	CHA1,URH1,GLY1,ECM31,MIOX5,KLMA_20057,CIT1,GSM1,PXA1,POT1,DSD1,ERT1,POX1,GPD2,AGX1,ARO10,IAH1,PEX11,GDH2,RDS2,KLMA_30124,KLMA_30282,ACO2,DPL1,GAD1,ACS1,THI13,KLMA_40010,LYS9,MDH3,GID8,ISA1,KLMA_40133,UGA1,LYS1,MDH2,VTC1,IDP1,PXA2,THI4,ALD4,CAR1,DAK1,CAR2,GLT1,SFA1,INO1,PUT1,URC1,SPS19,GUD1,TES1,gabD,KLMA_60206,ETR1,PHO85,KLMA_60405,PDE1,ARO9,FBP1,ICL1,PHO84,ANT1,KLMA_70303,FAD1,FOX2,ICL2,PDH1,CIT3,KLMA_80176,CRC1,ARO7
GO:0022413	reproductive process in single-celled or...	71	15	7.06	0.0034	PRM1,ATG26,DIT2,STE3,FUS3,SPS4,KLMA_20368,CHS1,SPO14,GAS4,QDR3,FIG1,AXL1,SPS19,CRR1
GO:0046459	short-chain fatty acid metabolic process	4	3	0.4	0.00361	ICL2,PDH1,CIT3
GO:0043934	sporulation	58	13	5.76	0.00365	ATG26,DIT2,FUS3,SPS4,KLMA_20368,OSW5,CTS2,CHS1,SPO14,GAS4,QDR3,SPS19,CRR1
GO:0019236	response to pheromone	39	10	3.88	0.00376	KAR4,STE3,FUS3,STE4,PRR1,KLMA_40061,GPA1,MF(ALPHA)1,SST2,KLMA_70118
GO:0071444	cellular response to pheromone	39	10	3.88	0.00376	KAR4,STE3,FUS3,STE4,PRR1,KLMA_40061,GPA1,MF(ALPHA)1,SST2,KLMA_70118
GO:0044248	cellular catabolic process	464	63	46.12	0.00397	CHA1,ECM38,HRD1,PLB,URH1,ATG27,PGU1,KLMA_10605,PEP12,UBP16,PNG1,DAL3,YUH1,AIM25,MIOX5,KLMA_20057,PXA1,POT1,POX1,GPD2,RIM15,ARO10,GDH2,KLMA_30011,RNH1,SPO1,CUE5,VTI1,SNX4,GAD1,MDH3,GID8,UGA1,VTC1,PXA2,GDE1,CAR1,POP4,KLMA_50156,CAR2,CTT1,PUT1,SPS19,GUD1,TES1,gabD,APC11,JLP1,PHO85,PDE1,OTU1,ATH1,KLMA_70233,ANT1,LPX1,FOX2,ICL2,PDH1,CIT3,SNF8,ATG20,SGA1,VAM3
GO:0048646	anatomical structure formation involved ...	59	13	5.86	0.00427	ATG26,DIT2,FUS3,SPS4,KLMA_20368,OSW5,CTS2,CHS1,SPO14,GAS4,QDR3,SPS19,CRR1

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:1903046	meiotic cell cycle process	133	23	13.22	0.00515	ATG26,CDC7,DIT2,FUS3,DMC1,CSM1,SPS4,KLMA_20368,MUS81,MSC1,MLH1,MND1,MLH3,KLMA_40062,CHS1,SPO14,GAS4,HOP1,ECO1,QDR3,SPS19,RAD1,CRR1
GO:0000750	pheromone-dependent signal transduction ...	18	6	1.79	0.00607	STE3,FUS3,STE4,GPA1,MF(ALPHA)1,KLMA_70118
GO:0032005	signal transduction involved in positive...	18	6	1.79	0.00607	STE3,FUS3,STE4,GPA1,MF(ALPHA)1,KLMA_70118
GO:0009653	anatomical structure morphogenesis	83	16	8.25	0.00652	ATG26,DIT2,FUS3,SPS4,KLMA_20368,OSW5,CTS2,CHS1,SPO14,ELM1,GAS4,QDR3,FIG1,KLMA_50343,SPS19,CRR1
GO:0048856	anatomical structure development	83	16	8.25	0.00652	ATG26,DIT2,FUS3,SPS4,KLMA_20368,OSW5,CTS2,CHS1,SPO14,ELM1,GAS4,QDR3,FIG1,KLMA_50343,SPS19,CRR1
GO:0030154	cell differentiation	69	14	6.86	0.00671	MATALPHA1,ATG26,DIT2,FUS3,SPS4,KLMA_20368,OSW5,CTS2,CHS1,SPO14,GAS4,QDR3,SPS19,CRR1
GO:0031137	regulation of conjugation with cellular ...	43	10	4.27	0.00791	STE3,FUS3,STE4,PRR1,KLMA_40061,AXL1,GPA1,MF(ALPHA)1,SST2,KLMA_70118
GO:0046999	regulation of conjugation	43	10	4.27	0.00791	STE3,FUS3,STE4,PRR1,KLMA_40061,AXL1,GPA1,MF(ALPHA)1,SST2,KLMA_70118
GO:0048869	cellular developmental process	130	22	12.92	0.008	MATALPHA1,ATG26,DIT2,AIM25,FUS3,HST2,RIM15,SPS4,KLMA_20368,OSW5,CTS2,EST2,CHS1,SPO14,ELM1,GAS4,QDR3,FIG1,KLMA_50343,SPS19,CRR1,PHO84
GO:0000755	cytogamy	9	4	0.89	0.00805	PRM1,STE3,FIG1,AXL1
GO:0006874	cellular calcium ion homeostasis	9	4	0.89	0.00805	PMC1,GDT1,FRQ1,VCX1
GO:0042149	cellular response to glucose starvation	9	4	0.89	0.00805	RIM15,ENA5,ELM1,FBP1
GO:0030437	ascospore formation	50	11	4.97	0.00844	ATG26,DIT2,FUS3,SPS4,KLMA_20368,CHS1,SPO14,GAS4,QDR3,SPS19,CRR1

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0048468	cell development	50	11	4.97	0.00844	ATG26,DIT2,FUS3,SPS4,KLMA_20368,CHS1,SPO14,GAS4,QDR3,SPS19,CRR1
GO:0034293	sexual sporulation	51	11	5.07	0.00984	ATG26,DIT2,FUS3,SPS4,KLMA_20368,CHS1,SPO14,GAS4,QDR3,SPS19,CRR1
GO:0043935	sexual sporulation resulting in formatio...	51	11	5.07	0.00984	ATG26,DIT2,FUS3,SPS4,KLMA_20368,CHS1,SPO14,GAS4,QDR3,SPS19,CRR1
GO:0000437	carbon catabolite repression of transcri...	2	2	0.2	0.00985	ERT1,RDS2
GO:0006527	arginine catabolic process	2	2	0.2	0.00985	CAR1,CAR2
GO:0006850	mitochondrial pyruvate transmembrane tra...	2	2	0.2	0.00985	FMP43,FMP37
GO:0032220	plasma membrane fusion involved in cytog...	2	2	0.2	0.00985	PRM1,FIG1
GO:0042758	long-chain fatty acid catabolic process	2	2	0.2	0.00985	PXA1,PXA2
GO:0044375	regulation of peroxisome size	2	2	0.2	0.00985	PEX11,PEX25
GO:0045026	plasma membrane fusion	2	2	0.2	0.00985	PRM1,FIG1
GO:0061415	negative regulation of transcription fro...	2	2	0.2	0.00985	ERT1,RDS2
GO:0071466	cellular response to xenobiotic stimulus	2	2	0.2	0.00985	ECM38,RDS2
GO:0009123	nucleoside monophosphate metabolic proce...	86	22	8.65	2.30E-05	PRS5,GPM3,HPT1,GUA1,ENO,PGK,AAH1,RAG2,URA1,GPM1,ADK1,ADE2,PDC2,ADE5,7,TPI1,GAP1,FBA1,XPT1,ADE6,PYK1,RAG5,GAP3

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0000054	ribosomal subunit export from nucleus	41	14	4.13	2.30E-05	SDA1,NOG1,ARX1,NOP53,RPS3,RRS1,RLI1,MEX67,NMD3,RIX1,MTR2,NUG1,NOP9,LTV1
GO:0033750	ribosome localization	41	14	4.13	2.30E-05	SDA1,NOG1,ARX1,NOP53,RPS3,RRS1,RLI1,MEX67,NMD3,RIX1,MTR2,NUG1,NOP9,LTV1
GO:0009117	nucleotide metabolic process	152	32	15.29	2.70E-05	APA2,PRS5,GPM3,HPT1,GUA1,ENO,PGK,AAH1,RAG2,URA1,GPM1,ADH4,ADK1,ADE2,HAM1,RNR2,PDC2,ADE5,7,TPI1,GAP1,FBA1,HMG1,XPT1,GUK1,ADE6,ACS2,PYK1,RAG5,ERG13,URA7,RNR1,GAP3
GO:0009126	purine nucleoside monophosphate metaboli...	75	20	7.55	2.90E-05	GPM3,HPT1,GUA1,ENO,PGK,AAH1,RAG2,GPM1,ADK1,ADE2,PDC2,ADE5,7,TPI1,GAP1,FBA1,XPT1,ADE6,PYK1,RAG5,GAP3
GO:0009167	purine ribonucleoside monophosphate meta...	75	20	7.55	2.90E-05	GPM3,HPT1,GUA1,ENO,PGK,AAH1,RAG2,GPM1,ADK1,ADE2,PDC2,ADE5,7,TPI1,GAP1,FBA1,XPT1,ADE6,PYK1,RAG5,GAP3
GO:0005996	monosaccharide metabolic process	47	15	4.73	3.00E-05	GAL80,PGK,RAG2,GPM1,GAL7,GAL10,GAL1,PDC2,TPI1,GAP1,FBA1,PYK1,RGT1,GAP3,VID24
GO:0072525	pyridine-containing compound biosyntheti...	32	12	3.22	3.10E-05	GPM3,ENO,PGK,RAG2,GPM1,TPI1,GAP1,FBA1,PDX3,PYK1,RAG5,GAP3
GO:0090305	nucleic acid phosphodiester bond hydroly...	100	24	10.06	3.10E-05	UTP13,UTP11,NOP58,ENP1,RLP7,MPP10,RRS1,NOB1,PWP2,DBP3,UTP10,NOP19,BMS1,UTP6,MTR4,UTP18,RRP5,DIP2,BRX1,FCF2,NOP14,NOC4,NOP9,RRP42
GO:0006753	nucleoside phosphate metabolic process	153	32	15.39	3.10E-05	APA2,PRS5,GPM3,HPT1,GUA1,ENO,PGK,AAH1,RAG2,URA1,GPM1,ADH4,ADK1,ADE2,HAM1,RNR2,PDC2,ADE5,7,TPI1,GAP1,FBA1,HMG1,XPT1,GUK1,ADE6,ACS2,PYK1,RAG5,ERG13,URA7,RNR1,GAP3
GO:0016070	RNA metabolic process	843	116	84.82	3.60E-05	SPB1,RPA49,NOP1,SOH1,DSS1,UTP5,EBP2,RPF2,RSE1,GAL80,MES1,HAS1,YTA7,MSW1,NOG1,UTP13,RPC37,DBP7,UTP15,UTP11,NOP53,NOP58,FHL1,NOP12,ENP1,CBF5,KLMA_20481,RLP7,UTP8,TPA1,MPP10,IPI3,NAN1,MRT4,RRS1,IPI1,DCAF13,DRS1,NOB1,RPL3,PAB1,MRPL15,PDC2,BFR2,PWP2,DBP3,RR

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
						P3,HAL9,VTS1,KSS1,MTO1,GUS1,ECM16,MDN1,UTP10,GAR1,CIC1,HAP1,ERB1,MCM1,RRP12,IMP4,YTM1,NOP19,RPC82,RIX1,UTP21,PUS1,BMS1,UTP6,PRP43,GEP3,MTR4,UTP18,ENP2,RPA135,RRP5,PWP1,NOP56,LAC9,UTP4,NUG1,RPC40,VAS1,NOP7,DIP2,IMP3,BRX1,URB1,DHR2,RPA190,FUN12,YAF9,NOP15,KRE33,EPL1,FCF2,KLMA_60313,NOP4,JHD2,CDC60,IKI3,ROX3,SPT21,NOP14,NOC4,RRP9,PUS4,KLMA_70408,NOP9,RRP42,PUB1,UTP25,HDA1,NOP2,ILS1
GO:0009058	biosynthetic process	1301	165	130.9	3.80E-05	HIS4,SAM2,RpL37a,RPA49,PRS5,GPM3,NOP1,OLE1,SOH1,UTP5,HPT1,GUA1,BIO2,RPL17B,GAL80,ENO,MES1,YTA7,LIP1,FAU1,PGK,CWH43,SCS7,MSW1,FUR1,AAH1,RAG2,URA1,TPS2,KLMA_20052,TSL1,GPM1,RPC37,UTP15,ADH4,UTP11,ADK1,RPS2,MET13,CYS4,SHM2,ERG3,FHL1,KLMA_20355,KLMA_20481,RPL22A,UTP8,TPA1,ERG28,CYP707A7,ORT1,ADE2,ERG9,IPI3,RPS3,RPL5,NAN1,LIA1,HAM1,GSH1,PHS1,IPI1,RNR2,ERG1,MEU1,ETT1,RPL3,PAB1,RLI1,KLMA_30320,GSY2,PDC2,SUR2,SER3,YIH1,PAN5,TIF32,HAL9,KSS1,ERG6,SAH1,ADE5,7,GUS1,RPL15B,dsd1,HEM13,TPI1,GAP1,RIB7,UTP10,HAP1,MCM1,FMS1,FBA1,ALD5,MAM33,HMG1,DPM1,RPC82,MET5,RIX1,XPT1,FAS1,RPL10A,GUK1,SHM1,LEU1,RPA135,PDX3,RPS14,SUR4,ADE6,ERG25,MSS51,LAC9,UTP4,RPC40,VAS1,NOP7,RPL2,ACS2,SHB17,URA2,KLMA_60069,PDC1,RPA190,FUN12,REV1,PYK1,LEU4,YAF9,EPL1,KLMA_60313,UGP1,RAG5,cyp524A1,JHD2,LEU3,ERG13,RPB1,CDC60,PET309,IKI3,URA7,ROX3,RNR1,FAS2,SPT21,TIF3,MET16,HEM14,RPL19B,DYS1,KLMA_70408,GAP3,MET3,MNN1,HDA1,NIP1,KLMA_80256,VID24,TPS1,MET6,ILS1
GO:0071826	ribonucleoprotein complex subunit organi...	115	26	11.57	4.50E-05	RPF2,RSE1,NOG1,NOP53,IPI3,RPL5,MRT4,IPI1,DRS1,RPL3,RLI1,TIF32,MDN1,RIX1,PRP43,RRP5,KLMA_60069,BRX1,FUN12,RSA4,TIF3,MAK21,RLP24,PUB1,NOP2,NIP1

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:1901576	organic substance biosynthetic process	1289	163	129.69	5.50E-05	HIS4,SAM2,RpL37a,RPA49,PRS5,GPM3,NOP1,OLE1,SOH1,UTP5,HPT1,GUA1,BIO2,RPL17B,GAL80,ENO,MES1,YTA7,LIP1,FAU1,PGK,CWH43,SCS7,MSW1,FUR1,AAH1,RAG2,URA1,TPS2,KLMA_20052,TSL1,GPM1,RPC37,UTP15,ADH4,UTP11,ADK1,RPS2,MET13,CYS4,SHM2,ERG3,FHL1,KLMA_20355,KLMA_20481,RPL22A,UTP8,TPA1,ERG28,CYP707A7,ORT1,ADE2,ERG9,IPI3,RPS3,RPL5,NAN1,HAM1,GSH1,PHS1,IPI1,RNR2,ERG1,MEU1,ETT1,RPL3,PAB1,RLI1,KLMA_30320,GSY2,PDC2,SUR2,SER3,YIH1,PAN5,TIF32,HAL9,KSS1,ERG6,SAH1,ADE5,7,GUS1,RPL15B,dsd1,HEM13,TPI1,GAP1,RIB7,UTP10,HAP1,MCM1,FMS1,FBA1,ALD5,MAM33,HMG1,DPM1,RPC82,MET5,RIX1,XPT1,FAS1,RPL10A,GUK1,SHM1,LEU1,RPA135,PDX3,RPS14,SUR4,ADE6,ERG25,MSS51,LAC9,UTP4,RPC40,VAS1,NOP7,RPL2,ACS2,SHB17,URA2,KLMA_60069,PDC1,RPA190,FUN12,REV1,PYK1,LEU4,YAF9,EPL1,KLMA_60313,UGP1,RAG5,cyp524A1,JHD2,LEU3,ERG13,RPB1,CDC60,PET309,IKI3,URA7,ROX3,RNR1,FAS2,SPT21,TIF3,MET16,HEM14,RPL19B,KLMA_70408,GAP3,MET3,MNN1,HDA1,NIP1,KLMA_80256,VID24,TPS1,MET6,ILS1
GO:0009150	purine ribonucleotide metabolic process	97	23	9.76	5.70E-05	GPM3,HPT1,GUA1,ENO,PGK,RAG2,GPM1,ADK1,ADE2,PDC2,ADE5,7,TPI1,GAP1,FBA1,HMG1,XPT1,GUK1,ADE6,ACS2,PYK1,RAG5,ERG13,GAP3
GO:0009116	nucleoside metabolic process	34	12	3.42	6.30E-05	PRS5,HPT1,GUA1,FUR1,URA1,RNR2,MEU1,SAH1,XPT1,GUK1,URA7,RNR1
GO:0006163	purine nucleotide metabolic process	98	23	9.86	6.70E-05	GPM3,HPT1,GUA1,ENO,PGK,RAG2,GPM1,ADK1,ADE2,PDC2,ADE5,7,TPI1,GAP1,FBA1,HMG1,XPT1,GUK1,ADE6,ACS2,PYK1,RAG5,ERG13,GAP3
GO:0009142	nucleoside triphosphate biosynthetic pro...	40	13	4.02	8.30E-05	GPM3,ENO,PGK,RAG2,GPM1,TPI1,GAP1,FBA1,PYK1,RAG5,URA7,RNR1,GAP3
GO:1901657	glycosyl compound metabolic process	35	12	3.52	8.70E-05	PRS5,HPT1,GUA1,FUR1,URA1,RNR2,MEU1,SAH1,XPT1,GUK1,URA7,RNR1

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0005992	trehalose biosynthetic process	4	4	0.4	0.0001	TPS2,TSL1,UGP1,TPS1
GO:0009312	oligosaccharide biosynthetic process	4	4	0.4	0.0001	TPS2,TSL1,UGP1,TPS1
GO:0046351	disaccharide biosynthetic process	4	4	0.4	0.0001	TPS2,TSL1,UGP1,TPS1
GO:0044249	cellular biosynthetic process	1278	160	128.58	0.00013	HIS4,SAM2,RpL37a,RPA49,PRS5,GPM3,NOP1,OLE1,SOH1,UTP5,HPT1,GUA1,BIO2,RPL17B,GAL80,ENO,MES1,YTA7,LIP1,FAU1,PGK,CWH43,SCS7,MSW1,FUR1,AAH1,RAG2,URA1,TPS2,KLMA_20052,TSL1,GPM1,RPC37,UTP15,UTP11,ADK1,RPS2,MET13,CYS4,SHM2,ERG3,FHL1,KLMA_20355,KLMA_20481,RPL22A,UTP8,TPA1,ERG28,CYP707A7,ORT1,ADE2,ERG9,IPI3,RPS3,RPL5,NAN1,HAM1,GSH1,PHS1,IPI1,RNR2,ERG1,MEU1,ETT1,RPL3,PAB1,RLI1,KLMA_30320,GSY2,PDC2,SUR2,SER3,YIH1,PAN5,TIF32,HAL9,KSS1,ERG6,SAH1,ADE5,7,GUS1,RPL15B,dsd1,HEM13,TPI1,GAP1,RIB7,UTP10,HAP1,MCM1,FMS1,FBA1,ALD5,MAM33,HMG1,DPM1,RPC82,MET5,RIX1,XPT1,FAS1,RPL10A,GUK1,SHM1,LEU1,RPA135,PDX3,RPS14,SUR4,ADE6,ERG25,MSS51,LAC9,UTP4,RPC40,VAS1,NOP7,RPL2,ACS2,URA2,KLMA_60069,RPA190,FUN12,REV1,PYK1,LEU4,YAF9,EPL1,KLMA_60313,UGP1,RAG5,cyp524A1,JHD2,LEU3,ERG13,RPB1,CDC60,PET309,IKI3,URA7,ROX3,RNR1,FAS2,SPT21,TIF3,MET16,HEM14,RPL19B,KLMA_70408,GAP3,MET3,MNN1,HDA1,NIP1,KLMA_80256,VID24,TPS1,MET6,ILS1
GO:0006807	nitrogen compound metabolic process	1991	231	200.32	0.00013	SPB1,APA2,HIS4,SAM2,RpL37a,RPA49,PRS5,GPM3,NOP1,SOH1,DSS1,UTP5,HPT1,GUA1,BIO2,RPL17B,EBP2,RPF2,RSE1,GAL80,ENO,MES1,HAS1,TDA1,YTA7,LIP1,FAU1,PGK,CWH43,SCS7,MSW1,FUR1,AAH1,RAG2,NOG1,URA1,KLMA_20052,GPM1,UTP13,RPC37,DBP7,UTP15,HSL1,ADH4,UTP11,ADK1,NOP53,RPS2,MET13,CYS4,SHM2,NOP58,FHL1,KLMA_20355,NOP12,ENP1,CLN2,UBP3,CBF5,KLMA_20481,RLP7,RPL22A,UTP8,TPA1,ORT1,ADE2,MPP10,DTD1,IPI3,RPS3,RPL5,NAN1,LIA

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
						1,HAM1,MRT4,RRS1,GSH1,PHS1,IPI1,RNR2,DCAF13,MEU1,DRS1,ETT1,NOB1,RPL3,PAB1,RLI1,MRPL15,KLMA_30320,PDC2,SUR2,BFR2,SER3,PWP2,YIH1,DBP3,PAN5,RRP3,TIF32,HAL9,VTS1,RAD54,KSS1,SAH1,DUG1,ADE5,7,MTO1,GUS1,ECM16,RPL15B,dsd1,HEM13,TPI1,MDN1,GAP1,RIB7,UTP10,GAR1,CIC1,HAP1,ERB1,MCM1,IMP2,RRP12,IMP4,FMS1,FBA1,MAM33,YTM1,NOP19,HMG1,DPM1,RPC82,MET5,RIX1,XPT1,UTP21,PUS1,BMS1,RPL10A,GUK1,UTP6,PRP43,GEP3,SHM1,MTR4,UTP18,ENP2,LEU1,RPA135,PDX3,RPS14,ADE6,RRP5,PWP1,NOP56,MSS51,LAC9,UTP4,NUG1,RPC40,VAS1,NOP7,RPL2,DIP2,ACS2,MAP1,URA2,IMP3,KLMA_60069,PDC1,EXO1,MDM20,BRX1,URB1,DHR2,RPA190,FUN12,REV1,PYK1,LEU4,YAF9,NOP15,KRE33,EPL1,FCF2,KLMA_60313,UGP1,NOP4,RAG5,JHD2,LEU3,ERG13,RPB1,CDC60,PET309,IKI3,URA7,ROX3,RNR1,PCL6,HSL7,SPT21,NOP14,TIF3,MET16,NOC4,RRP9,HEM14,RPL19B,DYS1,PUS4,KLMA_70408,NOP9,GAP3,MET3,MNN1,RRP42,PUB1,UTP25,HDA1,NOP2,NIP1,KLMA_80256,DEF1,VID24,PTH2,MET6,ILS1
GO:0022618	ribonucleoprotein complex assembly	109	24	10.97	0.00014	RPF2,RSE1,NOG1,NOP53,IPI3,RPL5,MRT4,IPI1,DRS1,RPL3,TIF32,MDN1,RIX1,RRP5,KLMA_60069,BRX1,FUN12,RSA4,TIF3,MAK21,RLP24,PUB1,NOP2,NIP1
GO:0005975	carbohydrate metabolic process	137	28	13.78	0.00015	GPD1,GPM3,GAL80,ENO,PGK,RAG2,TPS2,TSL1,GPM1,GAL7,GAL10,GAL1,PGM2,GSY2,PDC2,SCW4,TPI1,GAP1,FBA1,MDH1,PYK1,RGT1,UGP1,RAG5,GAP3,BGL2,VID24,TPS1
GO:0009201	ribonucleoside triphosphate biosynthetic...	37	12	3.72	0.00016	GPM3,ENO,PGK,RAG2,GPM1,TPI1,GAP1,FBA1,PYK1,RAG5,URA7,GAP3
GO:0071166	ribonucleoprotein complex localization	84	20	8.45	0.00016	SDA1,NOG1,ARX1,NOP53,RPS2,ENP1,UTP8,RPS3,RRS1,RLI1,MEX67,NMD3,RIX1,MTR2,MTR4,NUG1,CEX1,NEW1,NOP9,LTV1

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0071426	ribonucleoprotein complex export from nu...	84	20	8.45	0.00016	SDA1,NOG1,ARX1,NOP53,RPS2,ENP1,UTP8,RPS3,RRS1,RLI1,MEX67,NMD3,RIX1,MTR2,MTR4,NUG1,CEX1,NEW1,NOP9,LTV1
GO:0006006	glucose metabolic process	32	11	3.22	0.00017	PGK,RAG2,GPM1,PDC2,TPI1,GAP1,FBA1,PYK1,RGT1,GAP3,VID24
GO:0019362	pyridine nucleotide metabolic process	43	13	4.33	0.00019	GPM3,ENO,PGK,RAG2,GPM1,ADH4,PDC2,TPI1,GAP1,FBA1,PYK1,RAG5,GAP3
GO:0046496	nicotinamide nucleotide metabolic proces...	43	13	4.33	0.00019	GPM3,ENO,PGK,RAG2,GPM1,ADH4,PDC2,TPI1,GAP1,FBA1,PYK1,RAG5,GAP3
GO:0006405	RNA export from nucleus	85	20	8.55	0.00019	SDA1,NOG1,ARX1,NOP53,RPS2,ENP1,UTP8,RPS3,RRS1,RLI1,MEX67,NMD3,RIX1,MTR2,MTR4,NUG1,CEX1,NEW1,NOP9,LTV1
GO:0032787	monocarboxylic acid metabolic process	105	23	10.56	0.00021	GPM3,OLE1,BIO2,ENO,PGK,SCS7,RAG2,GPM1,PHS1,PDC2,PAN5,TPI1,GAP1,FMS1,FBA1,ALD5,FAS1,SUR4,ACS2,PYK1,RAG5,FAS2,GAP3
GO:0072524	pyridine-containing compound metabolic p...	49	14	4.93	0.00021	GPM3,ENO,PGK,RAG2,GPM1,ADH4,PDC2,TPI1,GAP1,FBA1,PDX3,PYK1,RAG5,GAP3
GO:0009119	ribonucleoside metabolic process	23	9	2.31	0.00022	HPT1,GUA1,URA1,RNR2,MEU1,SAH1,GUK1,URA7,RNR1
GO:0046165	alcohol biosynthetic process	39	12	3.92	0.00028	ADH4,ERG3,ERG28,CYP707A7,ERG9,ERG1,ERG6,dsd1,ERG25,PDC1,cyp524A1,ERG13
GO:0090407	organophosphate biosynthetic process	178	33	17.91	0.00028	PRS5,GPM3,HPT1,GUA1,ENO,PGK,CWH43,AAH1,RAG2,URA1,KLMA_20052,GPM1,ADK1,ADE2,RNR2,SAH1,ADE5,7,TPI1,GAP1,FBA1,HMG1,DPM1,XPT1,GUK1,ADE6,ACS2,SHB17,PYK1,RAG5,ERG13,URA7,RNR1,GAP3
GO:0006732	coenzyme metabolic process	114	24	11.47	0.00029	SAM2,GPM3,BIO2,ENO,FAU1,PGK,RAG2,GPM1,ADH4,MET13,SHM2,PDC2,PAN5,TPI1,GAP1,FMS1,FBA1,HMG1,SHM1,ACS2,PYK1,RAG5,ERG13,GAP3
GO:0006754	ATP biosynthetic process	34	11	3.42	0.00031	GPM3,ENO,PGK,RAG2,GPM1,TPI1,GAP1,FBA1,PYK1,RAG5,GAP3

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0051188	cofactor biosynthetic process	101	22	10.16	0.00031	SAM2,GPM3,BIO2,ENO,FAU1,PGK,RAG2,GPM1,GSH1,PAN5,HEM13,TPI1,GAP1,FMS1,FBA1,PDX3,ACS2,PYK1,RAG5,MET16,HEM14,GAP3
GO:0006696	ergosterol biosynthetic process	24	9	2.41	0.00031	ERG3,ERG28,CYP707A7,ERG9,ERG1,ERG6,ERG25,cyp524A1,ERG13
GO:0008204	ergosterol metabolic process	24	9	2.41	0.00031	ERG3,ERG28,CYP707A7,ERG9,ERG1,ERG6,ERG25,cyp524A1,ERG13
GO:0016128	phytosteroid metabolic process	24	9	2.41	0.00031	ERG3,ERG28,CYP707A7,ERG9,ERG1,ERG6,ERG25,cyp524A1,ERG13
GO:0016129	phytosteroid biosynthetic process	24	9	2.41	0.00031	ERG3,ERG28,CYP707A7,ERG9,ERG1,ERG6,ERG25,cyp524A1,ERG13
GO:0044108	cellular alcohol biosynthetic process	24	9	2.41	0.00031	ERG3,ERG28,CYP707A7,ERG9,ERG1,ERG6,ERG25,cyp524A1,ERG13
GO:0097384	cellular lipid biosynthetic process	24	9	2.41	0.00031	ERG3,ERG28,CYP707A7,ERG9,ERG1,ERG6,ERG25,cyp524A1,ERG13
GO:0006611	protein export from nucleus	89	20	8.95	0.00038	SDA1,NOG1,ARX1,NOP53,RPS2,ENP1,UTP8,RPS3,RRS1,RLI1,MEX67,NMD3,RIX1,MTR2,MTR4,NUG1,CEX1,NEW1,NOP9,LTV1
GO:0009145	purine nucleoside triphosphate biosynthe...	35	11	3.52	0.00041	GPM3,ENO,PGK,RAG2,GPM1,TPI1,GAP1,FBA1,PYK1,RAG5,GAP3
GO:0009206	purine ribonucleoside triphosphate biosy...	35	11	3.52	0.00041	GPM3,ENO,PGK,RAG2,GPM1,TPI1,GAP1,FBA1,PYK1,RAG5,GAP3
GO:0051168	nuclear export	90	20	9.06	0.00044	SDA1,NOG1,ARX1,NOP53,RPS2,ENP1,UTP8,RPS3,RRS1,RLI1,MEX67,NMD3,RIX1,MTR2,MTR4,NUG1,CEX1,NEW1,NOP9,LTV1
GO:1902652	secondary alcohol metabolic process	25	9	2.52	0.00045	ERG3,ERG28,CYP707A7,ERG9,ERG1,ERG6,ERG25,cyp524A1,ERG13
GO:1902653	secondary alcohol biosynthetic process	25	9	2.52	0.00045	ERG3,ERG28,CYP707A7,ERG9,ERG1,ERG6,ERG25,cyp524A1,ERG13

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0006012	galactose metabolic process	5	4	0.5	0.00046	GAL80,GAL7,GAL10,GAL1
GO:0051186	cofactor metabolic process	169	31	17	0.00053	SAM2,GPM3,BIO2,ENO,FAU1,PGK,RAG2,GPM1,ADH4,MET13,SHM2,GSH1,PDC2,PAN5,SAH1,DUG1,HEM13,TPI1,GAP1,FMS1,FBA1,HMG1,SHM1,PDX3,ACS2,PYK1,RAG5,ERG13,MET16,HEM14,GAP3
GO:1901137	carbohydrate derivative biosynthetic pro...	177	32	17.81	0.00056	PRS5,GPM3,HPT1,GUA1,ENO,PGK,CWH43,RAG2,URA1,GPM1,ADK1,ADE2,RNR2,MEU1,KLMA_30320,ADE5,7,TPI1,GAP1,FBA1,DPM1,XPT1,GUK1,ADE6,ACS2,SHB17,PYK1,RAG5,URA7,RNR1,GAP3,MNN1
GO:0044107	cellular alcohol metabolic process	26	9	2.62	0.00063	ERG3,ERG28,CYP707A7,ERG9,ERG1,ERG6,ERG25,cyp524A1,ERG13
GO:0050657	nucleic acid transport	94	20	9.46	0.0008	SDA1,NOG1,ARX1,NOP53,RPS2,ENP1,UTP8,RPS3,RRS1,RLI1,MEX67,NMD3,RIX1,MTR2,MTR4,NUG1,CEX1,NEW1,NOP9,LTV1
GO:0050658	RNA transport	94	20	9.46	0.0008	SDA1,NOG1,ARX1,NOP53,RPS2,ENP1,UTP8,RPS3,RRS1,RLI1,MEX67,NMD3,RIX1,MTR2,MTR4,NUG1,CEX1,NEW1,NOP9,LTV1
GO:0051236	establishment of RNA localization	94	20	9.46	0.0008	SDA1,NOG1,ARX1,NOP53,RPS2,ENP1,UTP8,RPS3,RRS1,RLI1,MEX67,NMD3,RIX1,MTR2,MTR4,NUG1,CEX1,NEW1,NOP9,LTV1
GO:1901135	carbohydrate derivative metabolic proces...	260	42	26.16	0.00094	PRS5,GPD1,GPM3,HPT1,GUA1,PFK1,ENO,PGK,CWH43,FUR1,RAG2,URA1,GPM1,ADK1,ADE2,RNR2,MEU1,KLMA_30320,PDC2,SUR2,SAH1,ADE5,7,TPI1,GAP1,FBA1,HMG1,DPM1,XPT1,GUK1,ADE6,ACS2,SHB17,PYK1,UGP1,RAG5,ERG13,PFK2,URA7,RNR1,GAP3,MNN1
GO:1901617	organic hydroxy compound biosynthetic pr...	50	13	5.03	0.00096	ADH4,ERG3,ERG28,CYP707A7,ERG9,ERG1,ERG6,dsd1,PDX3,ERG25,PDC1,cyp524A1,ERG13

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0009141	nucleoside triphosphate metabolic proces...	69	16	6.94	0.00101	GPM3,ENO,PGK,RAG2,GPM1,ADK1,HAM1,PDC2,TPI1,GAP1,FBA1,PYK1,RAG5,URA7,RNR1,GAP3
GO:0000464	endonucleolytic cleavage in ITS1 upstrea...	3	3	0.3	0.00101	DBP3,RRP5,BRX1
GO:0019637	organophosphate metabolic process	270	43	27.17	0.0011	APA2,LPP1,PRS5,GPD1,GPM3,HPT1,GUA1,PFK1,ENO,PGK,CWH43,SCS7,AAH1,RAG2,URA1,KLMA_20052,GPM1,ADH4,ADK1,ADE2,HAM1,RNR2,PDC2,SUR2,SAH1,ADE5,7,TPI1,GAP1,FBA1,HMG1,DPM1,XPT1,GUK1,ADE6,ACS2,SHB17,PYK1,RAG5,ERG13,PFK2,URA7,RNR1,GAP3
GO:0009133	nucleoside diphosphate biosynthetic proc...	6	4	0.6	0.00128	ADK1,RNR2,GUK1,RNR1
GO:0006066	alcohol metabolic process	52	13	5.23	0.00143	ADH4,ERG3,ERG28,CYP707A7,ERG9,ERG1,PDC2,ERG6,dsd1,ERG25,PDC1,cyp524A1,ERG13
GO:0009163	nucleoside biosynthetic process	14	6	1.41	0.00148	HPT1,GUA1,URA1,MEU1,GUK1,URA7
GO:0042455	ribonucleoside biosynthetic process	14	6	1.41	0.00148	HPT1,GUA1,URA1,MEU1,GUK1,URA7
GO:1901659	glycosyl compound biosynthetic process	14	6	1.41	0.00148	HPT1,GUA1,URA1,MEU1,GUK1,URA7
GO:0006694	steroid biosynthetic process	29	9	2.92	0.00153	ERG3,ERG28,CYP707A7,ERG9,ERG1,ERG6,ERG25,cyp524A1,ERG13
GO:0016126	sterol biosynthetic process	29	9	2.92	0.00153	ERG3,ERG28,CYP707A7,ERG9,ERG1,ERG6,ERG25,cyp524A1,ERG13
GO:0000055	ribosomal large subunit export from nucl...	24	8	2.41	0.00167	SDA1,ARX1,NOP53,RRS1,MEX67,NMD3,MTR2,NUG1
GO:0044272	sulfur compound biosynthetic process	47	12	4.73	0.00178	SAM2,BIO2,MET13,CYS4,GSH1,MEU1,PDC2,MET5,ACS2,MET16,MET3,MET6

GO.ID	**Term**	**Annotated gene**	**Significant**	**Expected**	**P-value**	**Genes**
GO:0019439	aromatic compound catabolic process	136	25	13.68	0.00178	GPM3,DSS1,ENO,PGK,AAH1,RAG2,GPM1,TPA1,DTD1,HAM1,MRT4,PAB1,VTS1,SAH1,TPI1,GAP1,FBA1,MTR4,PDC1,PYK1,RAG5,JHD2,GAP3,RRP42,PUB1
GO:0009108	coenzyme biosynthetic process	81	17	8.15	0.00229	SAM2,GPM3,BIO2,ENO,FAU1,PGK,RAG2,GPM1,PAN5,TPI1,GAP1,FMS1,FBA1,ACS2,PYK1,RAG5,GAP3
GO:0043603	cellular amide metabolic process	347	51	34.91	0.00243	RpL37a,BIO2,RPL17B,MES1,LIP1,FAU1,MSW1,UTP11,RPS2,MET13,SHM2,KLMA_20355,RPL22A,TPA1,RPS3,RPL5,GSH1,ETT1,RPL3,PAB1,RLI1,YIH1,PAN5,TIF32,DUG1,GUS1,RPL15B,IMP2,FMS1,MAM33,HMG1,RPL10A,SHM1,RPS14,MSS51,VAS1,RPL2,ACS2,KLMA_60069,FUN12,KLMA_60313,ERG13,CDC60,PET309,IKI3,TIF3,MET16,RPL19B,NIP1,KLMA_80256,ILS1
GO:0016125	sterol metabolic process	31	9	3.12	0.00257	ERG3,ERG28,CYP707A7,ERG9,ERG1,ERG6,ERG25,cyp524A1,ERG13
GO:1902626	assembly of large subunit precursor of p...	7	4	0.7	0.00275	RPF2,NOG1,RLP24,NOP2
GO:0031503	protein-containing complex localization	104	20	10.46	0.00294	SDA1,NOG1,ARX1,NOP53,RPS2,ENP1,UTP8,RPS3,RRS1,RLI1,MEX67,NMD3,RIX1,MTR2,MTR4,NUG1,CEX1,NEW1,NOP9,LTV1
GO:0009112	nucleobase metabolic process	26	8	2.62	0.00297	AAH1,URA1,ADE2,ADE5,7,XPT1,URA2,URA7,MET6
GO:0017144	drug metabolic process	180	30	18.11	0.00318	SAM2,ACO2,GPM3,BIO2,ENO,PGK,RAG2,GPM1,ADK1,CYS4,SHM2,MEU1,PDC2,TPI1,GAP1,RIB7,FMS1,FBA1,ALD5,MET5,SHM1,PDX3,ACS2,PDC1,MDH1,PYK1,RAG5,GAP3,MET3,MET6
GO:0008202	steroid metabolic process	32	9	3.22	0.00326	ERG3,ERG28,CYP707A7,ERG9,ERG1,ERG6,ERG25,cyp524A1,ERG13
GO:0006520	cellular amino acid metabolic process	173	29	17.41	0.00341	HIS4,SAM2,GUA1,MES1,MSW1,ADH4,MET13,CYS4,SHM2,ORT1,DTD1,MEU1,SER3,SAH1,GUS1,MET5,SHM1,LEU1,ADE6,VAS1,URA2,PDC1,LEU4,LEU3,CDC60,URA7,MET3,MET6,ILS1

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0006733	oxidoreduction coenzyme metabolic proces...	57	13	5.73	0.00346	GPM3,ENO,PGK,RAG2,GPM1,ADH4,PDC2,TPI1,GAP1,FBA1,PYK1,RAG5,GAP3
GO:1901605	alpha-amino acid metabolic process	113	21	11.37	0.00358	HIS4,SAM2,GUA1,MET13,CYS4,SHM2,ORT1,DTD1,MEU1,SER3,SAH1,SHM1,LEU1,ADE6,URA2,PDC1,LEU4,LEU3,URA7,MET3,MET6
GO:1901361	organic cyclic compound catabolic proces...	143	25	14.39	0.00364	GPM3,DSS1,ENO,PGK,AAH1,RAG2,GPM1,TPA1,DTD1,HAM1,MRT4,PAB1,VTS1,SAH1,TPI1,GAP1,FBA1,MTR4,PDC1,PYK1,RAG5,JHD2,GAP3,RRP42,PUB1
GO:0009199	ribonucleoside triphosphate metabolic pr...	64	14	6.44	0.00368	GPM3,ENO,PGK,RAG2,GPM1,ADK1,PDC2,TPI1,GAP1,FBA1,PYK1,RAG5,URA7,GAP3
GO:0009403	toxin biosynthetic process	4	3	0.4	0.00374	CYS4,MET5,MET3
GO:0009404	toxin metabolic process	4	3	0.4	0.00374	CYS4,MET5,MET3
GO:0019320	hexose catabolic process	4	3	0.4	0.00374	GAL7,GAL10,PYK1
GO:0035999	tetrahydrofolate interconversion	4	3	0.4	0.00374	MET13,SHM2,SHM1
GO:0070813	hydrogen sulfide metabolic process	4	3	0.4	0.00374	CYS4,MET5,MET3
GO:0070814	hydrogen sulfide biosynthetic process	4	3	0.4	0.00374	CYS4,MET5,MET3
GO:1901070	guanosine-containing compound biosynthet...	4	3	0.4	0.00374	HPT1,GUA1,GUK1
GO:0000056	ribosomal small subunit export from nucl...	12	5	1.21	0.00436	RPS3,MEX67,MTR2,NOP9,LTV1

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0006730	one-carbon metabolic process	12	5	1.21	0.00436	SAM2,MET13,SHM2,SAH1,SHM1
GO:0008610	lipid biosynthetic process	138	24	13.88	0.00467	OLE1,LIP1,CWH43,SCS7,KLMA_20052,ERG3,ERG28,CYP707A7,ERG9,PHS1,ERG1,SUR2,ERG6,SAH1,dsd1,HMG1,DPM1,FAS1,SUR4,ERG25,cyp524A1,ERG13,URA7,FAS2
GO:0000103	sulfate assimilation	8	4	0.8	0.00507	MET5,MET10,MET16,MET3
GO:0005991	trehalose metabolic process	8	4	0.8	0.00507	TPS2,TSL1,UGP1,TPS1
GO:0006551	leucine metabolic process	8	4	0.8	0.00507	DTD1,LEU1,LEU4,LEU3
GO:0009218	pyrimidine ribonucleotide metabolic proc...	8	4	0.8	0.00507	URA1,RNR2,URA7,RNR1
GO:0019748	secondary metabolic process	8	4	0.8	0.00507	CYS4,GSH1,MET5,MET3
GO:0044550	secondary metabolite biosynthetic proces...	8	4	0.8	0.00507	CYS4,GSH1,MET5,MET3
GO:0044270	cellular nitrogen compound catabolic pro...	139	24	13.99	0.00513	GPM3,DSS1,ENO,PGK,AAH1,RAG2,GPM1,TPA1,HAM1,MRT4,PAB1,VTS1,SAH1,TPI1,GAP1,FBA1,MTR4,PDC1,PYK1,RAG5,JHD2,GAP3,RRP42,PUB1
GO:0046700	heterocycle catabolic process	139	24	13.99	0.00513	GPM3,DSS1,ENO,PGK,AAH1,RAG2,GPM1,TPA1,HAM1,MRT4,PAB1,VTS1,SAH1,TPI1,GAP1,FBA1,MTR4,PDC1,PYK1,RAG5,JHD2,GAP3,RRP42,PUB1
GO:0006403	RNA localization	109	20	10.97	0.00515	SDA1,NOG1,ARX1,NOP53,RPS2,ENP1,UTP8,RPS3,RRS1,RLI1,MEX67,NMD3,RIX1,MTR2,MTR4,NUG1,CEX1,NEW1,NOP9,LTV1

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0044271	cellular nitrogen compound biosynthetic ...	910	112	91.56	0.00541	RpL37a,RPA49,PRS5,GPM3,NOP1,SOH1,UTP5,HPT1,GUA1,BIO2,RPL17B,GAL80,ENO,MES1,YTA7,LIP1,FAU1,PGK,MSW1,FUR1,AAH1,RAG2,URA1,GPM1,RPC37,UTP15,UTP11,ADK1,RPS2,FHL1,KLMA_20355,KLMA_20481,RPL22A,UTP8,TPA1,ADE2,RPS3,RPL5,NAN1,HAM1,GSH1,RNR2,MEU1,ETT1,RPL3,PAB1,RLI1,PDC2,YIH1,PAN5,TIF32,HAL9,KSS1,ADE5,7,GUS1,RPL15B,dsd1,HEM13,TPI1,GAP1,RIB7,UTP10,HAP1,MCM1,FMS1,FBA1,MAM33,RPC82,XPT1,RPL10A,GUK1,RPA135,PDX3,RPS14,ADE6,MSS51,LAC9,UTP4,RPC40,VAS1,RPL2,ACS2,URA2,KLMA_60069,RPA190,FUN12,REV1,PYK1,YAF9,EPL1,KLMA_60313,RAG5,JHD2,RPB1,CDC60,PET309,IKI3,URA7,ROX3,RNR1,SPT21,TIF3,MET16,HEM14,RPL19B,KLMA_70408,GAP3,HDA1,NIP1,KLMA_80256,MET6,ILS1
GO:0046034	ATP metabolic process	60	13	6.04	0.00553	GPM3,ENO,PGK,RAG2,GPM1,ADK1,PDC2,TPI1,GAP1,FBA1,PYK1,RAG5,GAP3
GO:0043604	amide biosynthetic process	302	44	30.38	0.00577	RpL37a,BIO2,RPL17B,MES1,LIP1,FAU1,MSW1,UTP11,RPS2,KLMA_20355,RPL22A,TPA1,RPS3,RPL5,GSH1,ETT1,RPL3,PAB1,RLI1,YIH1,PAN5,TIF32,GUS1,RPL15B,FMS1,MAM33,RPL10A,RPS14,MSS51,VAS1,RPL2,ACS2,KLMA_60069,FUN12,KLMA_60313,CDC60,PET309,IKI3,TIF3,MET16,RPL19B,NIP1,KLMA_80256,ILS1
GO:0000096	sulfur amino acid metabolic process	23	7	2.31	0.00578	SAM2,MET13,CYS4,MEU1,MET5,MET3,MET6
GO:0006091	generation of precursor metabolites and ...	103	19	10.36	0.00597	ACO2,GPM3,ENO,PGK,RAG2,GPM1,GSY2,PDC2,TPI1,GAP1,HAP1,FBA1,MAM33,MDH1,PYK1,UGP1,RAG5,GAP3,GDS1
GO:0006575	cellular modified amino acid metabolic p...	41	10	4.13	0.00604	FAU1,MET13,SHM2,GSH1,PAN5,SAH1,DUG1,FMS1,SHM1,MET16
GO:0070925	organelle assembly	89	17	8.95	0.00637	RPF2,NOP53,IPI3,RPL5,MRT4,IPI1,DRS1,RPL3,MDN1,RIX1,RRP5,KLMA_60069,BRX1,FUN12,RSA4,MAK21,PUB1

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0006913	nucleocytoplasmic transport	127	22	12.78	0.00698	GSP1,SDA1,NOG1,ARX1,NOP53,RPS2,ENP1,UTP8,RPS3,RRS1,RLI1,MEX67,NMD3,RIX1,MTR2,MTR4,NUG1,CEX1,NEW1,NOP9,LTV1,KAP123
GO:0034655	nucleobase-containing compound catabolic...	127	22	12.78	0.00698	GPM3,DSS1,ENO,PGK,RAG2,GPM1,TPA1,HAM1,MRT4,PAB1,VTS1,SAH1,TPI1,GAP1,FBA1,MTR4,PYK1,RAG5,JHD2,GAP3,RRP42,PUB1
GO:0051169	nuclear transport	127	22	12.78	0.00698	GSP1,SDA1,NOG1,ARX1,NOP53,RPS2,ENP1,UTP8,RPS3,RRS1,RLI1,MEX67,NMD3,RIX1,MTR2,MTR4,NUG1,CEX1,NEW1,NOP9,LTV1,KAP123
GO:0009205	purine ribonucleoside triphosphate metab...	62	13	6.24	0.00739	GPM3,ENO,PGK,RAG2,GPM1,ADK1,PDC2,TPI1,GAP1,FBA1,PYK1,RAG5,GAP3
GO:0090304	nucleic acid metabolic process	1024	123	103.03	0.00789	SPB1,RPA49,NOP1,SOH1,DSS1,UTP5,EBP2,RPF2,RSE1,GAL80,MES1,HAS1,YTA7,MSW1,NOG1,UTP13,RPC37,DBP7,UTP15,UTP11,ADK1,NOP53,NOP58,FHL1,NOP12,ENP1,CBF5,KLMA_20481,RLP7,UTP8,TPA1,MPP10,IPI3,NAN1,MRT4,RRS1,IPI1,DCAF13,DRS1,NOB1,RPL3,PAB1,MRPL15,PDC2,BFR2,PWP2,DBP3,RRP3,HAL9,VTS1,RAD54,KSS1,MTO1,GUS1,ECM16,MDN1,UTP10,GAR1,CIC1,HAP1,ERB1,MCM1,RRP12,IMP4,YTM1,NOP19,RPC82,RIX1,UTP21,PUS1,BMS1,UTP6,PRP43,GEP3,MTR4,UTP18,ENP2,RPA135,RRP5,PWP1,NOP56,LAC9,UTP4,NUG1,RPC40,VAS1,NOP7,DIP2,IMP3,EXO1,BRX1,URB1,DHR2,RPA190,FUN12,REV1,YAF9,NOP15,KRE33,EPL1,FCF2,KLMA_60313,NOP4,JHD2,RPB1,CDC60,IKI3,ROX3,RNR1,SPT21,NOP14,NOC4,RRP9,PUS4,KLMA_70408,NOP9,RRP42,PUB1,UTP25,HDA1,NOP2,DEF1,ILS1
GO:0006760	folic acid-containing compound metabolic...	9	4	0.91	0.00841	FAU1,MET13,SHM2,SHM1
GO:0042451	purine nucleoside biosynthetic process	9	4	0.91	0.00841	HPT1,GUA1,MEU1,GUK1
GO:0043101	purine-containing	9	4	0.91	0.00841	HPT1,AAH1,MEU1,XPT1

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
	compound salvage					
GO:0046129	purine ribonucleoside biosynthetic proce...	9	4	0.91	0.00841	HPT1,GUA1,MEU1,GUK1
GO:0009144	purine nucleoside triphosphate metabolic...	63	13	6.34	0.00848	GPM3,ENO,PGK,RAG2,GPM1,ADK1,PDC2,TPI1,GAP1,FBA1,PYK1,RAG5,GAP3
GO:1901615	organic hydroxy compound metabolic proce...	70	14	7.04	0.00852	ADH4,ERG3,ERG28,CYP707A7,ERG9,ERG1,PDC2,ERG6,dsd1,PDX3,ERG25,PDC1,cyp524A1,ERG13
GO:0000097	sulfur amino acid biosynthetic process	19	6	1.91	0.00864	MET13,CYS4,MEU1,MET5,MET3,MET6
GO:0006633	fatty acid biosynthetic process	19	6	1.91	0.00864	OLE1,SCS7,PHS1,FAS1,SUR4,FAS2
GO:0046112	nucleobase biosynthetic process	19	6	1.91	0.00864	AAH1,URA1,ADE5,7,URA2,URA7,MET6
GO:0009098	leucine biosynthetic process	5	3	0.5	0.00865	LEU1,LEU4,LEU3
GO:0031120	snRNA pseudouridine synthesis	5	3	0.5	0.00865	CBF5,GAR1,PUS1
GO:0040031	snRNA modification	5	3	0.5	0.00865	CBF5,GAR1,PUS1
GO:0016051	carbohydrate biosynthetic process	50	11	5.03	0.00924	PGK,RAG2,TPS2,TSL1,GPM1,GSY2,TPI1,FBA1,UGP1,VID24,TPS1
GO:0042278	purine nucleoside metabolic process	14	5	1.41	0.00931	HPT1,GUA1,MEU1,SAH1,GUK1
GO:0046128	purine ribonucleoside metabolic process	14	5	1.41	0.00931	HPT1,GUA1,MEU1,SAH1,GUK1
GO:0006790	sulfur compound metabolic process	93	17	9.36	0.00997	SAM2,BIO2,MET13,CYS4,GSH1,MEU1,PDC2,SAH1,DUG1,HMG1,MET5,MET10,ACS2,ERG13,MET16,MET3,MET6

GO terms enriched in significantly down-regulated genes (cellular components)

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0030684	preribosome	116	61	11.18	< 1e-30	SPB1,NOP1,UTP5,EBP2,HAS1,NOG1,UTP13,UTP15,UTP11,ARX1,RPS2,NOP58,NOP12,ENP1,RLP7,UTP8,MPP10,RPS3,NAN1,MRT4,RRS1,DCAF13,DRS1,NOB1,BFR2,PWP2,DBP3,ECM16,UTP10,CIC1,ERB1,RRP12,IMP4,YTM1,NOP19,UTP21,BMS1,UTP6,NOC2,UTP18,ENP2,RRP5,NOP56,UTP4,NUG1,NOP7,DIP2,IMP3,BRX1,NOP15,KRE33,NOP14,NOC4,RRP9,MAK21,NOP9,LTV1,RLP24,UTP25,NOP2,PUF6
GO:0005730	nucleolus	197	72	18.99	1.20E-26	SPB1,RPA49,NOP1,UTP5,EBP2,RPF2,HAS1,NOG1,UTP13,DBP7,UTP15,UTP11,ARX1,NOP53,NOP58,FHL1,NOP12,ENP1,CBF5,RLP7,UTP8,MPP10,NAN1,MRT4,RRS1,DCAF13,NOB1,BFR2,PWP2,DBP3,RRB1,ECM16,UTP10,GAR1,CIC1,ERB1,IMP4,YTM1,NOP19,UTP21,BMS1,UTP6,MTR4,UTP18,ENP2,RPA135,RRP5,PWP1,NOP56,UTP4,NUG1,RPC40,NOP7,DIP2,ACS2,IMP3,BRX1,URB1,DHR2,RPA190,NOP15,KRE33,RSA4,NOP14,NOC4,RRP9,SRP40,NOP9,RLP24,UTP25,HDA1,NOP2
GO:0032040	small-subunit processome	41	29	3.95	2.90E-21	NOP1,UTP5,UTP13,UTP15,UTP11,RPS2,NOP58,UTP8,MPP10,NAN1,DCAF13,BFR2,PWP2,ECM16,UTP10,IMP4,UTP21,UTP6,UTP18,ENP2,RRP5,NOP56,UTP4,DIP2,IMP3,NOP14,NOC4,RRP9,UTP25
GO:1990904	ribonucleoprotein complex	470	102	45.3	7.50E-18	SPB1,RpL37a,NOP1,UTP5,RPL17B,EBP2,RSE1,HAS1,NOG1,RPL24,UTP13,UTP15,UTP11,ARX1,RPS2,CYS4,NOP58,KLMA_20355,NOP12,ENP1,CBF5,RLP7,RPL22A,UTP8,MPP10,RPS3,RPL5,NAN1,MRT4,RRS1,DCAF13,DRS1,NOB1,RPL3,PAB1,RLI1,MRPL15,BFR2,PWP2,YIH1,DBP3,TIF32,VTS1,GUS1,ECM16,RPL15B,UTP10,GAR1,CIC1,ERB1,RRP12,IMP4,YTM1,NOP19,NMD3,MET5,UTP21,BMS1,RPL10A,UTP6,PRP43,NOC2,UTP18,ENP2,LEU1,RPS14,RRP5,NOP56,UTP4,NUG1,NOP7,RPL2,DIP2,MAP1,IMP3,KLMA_60069,BRX1,TEF4,FUN12,NOP15,KRE33,KLMA_60313,UGP1,RPB1,NEW1,NOP14,TIF3,NOC4,RRP9,RPL19B,MAK21,NO

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
						P9,LTV1,RLP24,PUB1,UTP25,NOP2,NIP1,KLMA_80256,PUF6,KAP123,RPL8B
GO:0044452	nucleolar part	67	30	6.46	3.40E-14	RPA49,NOP1,UTP5,HAS1,UTP13,UTP15,NOP58,CBF5,UTP8,MPP10,NAN1,PWP2,UTP10,GAR1,ERB1,IMP4,YTM1,UTP21,UTP6,UTP18,RPA135,NOP56,UTP4,RPC40,NOP7,DIP2,IMP3,RPA190,RRP9,HDA1
GO:0030686	90S preribosome	40	22	3.86	5.10E-13	UTP13,ENP1,MPP10,PWP2,UTP10,ERB1,IMP4,YTM1,NOP19,UTP21,BMS1,UTP6,NOC2,UTP18,UTP4,NOP7,DIP2,IMP3,NOP14,NOC4,MAK21,NOP9
GO:0030687	preribosome, large subunit precursor	46	22	4.43	2.10E-11	SPB1,EBP2,HAS1,NOG1,ARX1,RLP7,MRT4,RRS1,DRS1,DBP3,CIC1,ERB1,YTM1,NOC2,NUG1,NOP7,BRX1,NOP15,MAK21,RLP24,NOP2,PUF6
GO:0031981	nuclear lumen	560	87	53.97	7.00E-07	SPB1,RPA49,NOP1,SOH1,UTP5,EBP2,RPF2,HAS1,NOG1,UTP13,DBP7,UTP15,UTP11,ARX1,NOP53,NOP58,FHL1,NOP12,ENP1,CBF5,RLP7,UTP8,MPP10,IPI3,NAN1,MRT4,RSC2,RRS1,IPI1,DCAF13,NOB1,BFR2,MEX67,PWP2,DBP3,RRB1,ECM16,MDN1,UTP10,GAR1,CIC1,ERB1,IMP4,YTM1,NOP19,DUS3,RIX1,UTP21,MTR2,BMS1,UTP6,MTR4,UTP18,ENP2,RPA135,RRP5,PWP1,NOP56,UTP4,NUG1,RPC40,NOP7,DIP2,ACS2,IMP3,BRX1,URB1,DHR2,RPA190,REV1,YAF9,NOP15,KRE33,EPL1,RPB1,ROX3,RSA4,NOP14,NOC4,RRP9,SRP40,NOP9,RLP24,RRP42,UTP25,HDA1,NOP2
GO:0034388	Pwp2p-containing subcomplex of 90S preri...	6	6	0.58	7.70E-07	UTP13,PWP2,UTP21,UTP6,UTP18,DIP2
GO:0043228	non-membrane-bounded organelle	883	121	85.11	2.60E-06	SPB1,RpL37a,RPA49,NOP1,UTP5,RPL17B,EBP2,RPF2,HAS1,NOG1,RPL24,UTP13,DBP7,UTP15,HSL1,UTP11,ARX1,NOP53,RPS2,CYS4,NOP58,FHL1,KLMA_20355,NOP12,ENP1,CBF5,RLP7,RPL22A,UTP8,MPP10,RPS3,RPL5,NAN1,MRT4,RSC2,RRS1,ERG1,DCAF13,NOB1,RPL3,PAB1,RLI1,MRPL15,BFR2,PWP2,YIH1,DBP3,TIF32,VTS1,ERG6,GUS1,RRB1,ECM16,RPL15B,UTP10,GAR1,CIC1,ERB1,IMP4,YTM1,NOP19,NMD3,MET5,UTP21,FAS1,BMS

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
						1,RPL10A,UTP6,MTR4,UTP18,ENP2,LEU1,RPA135,YJU3,RPS14,RRP5,PWP1,NOP56,UTP4,NUG1,RPC40,NOP7,RPL2,DIP2,ACS2,MAP1,IMP3,KLMA_60069,BRX1,URB1,TEF4,DHR2,RPA190,FUN12,REV1,YAF9,NOP15,KRE33,KLMA_60313,UGP1,RPB1,RSA4,HSL7,SPT21,NOP14,TIF3,NOC4,RRP9,RPL19B,SRP40,NOP9,RLP24,PUB1,UTP25,HDA1,NOP2,NIP1,KLMA_80256,PUF6,KAP123,RPL8B
GO:0043232	intracellular non-membrane-bounded organ...	883	121	85.11	2.60E-06	SPB1,RpL37a,RPA49,NOP1,UTP5,RPL17B,EBP2,RPF2,HAS1,NOG1,RPL24,UTP13,DBP7,UTP15,HSL1,UTP11,ARX1,NOP53,RPS2,CYS4,NOP58,FHL1,KLMA_20355,NOP12,ENP1,CBF5,RLP7,RPL22A,UTP8,MPP10,RPS3,RPL5,NAN1,MRT4,RSC2,RRS1,ERG1,DCAF13,NOB1,RPL3,PAB1,RLI1,MRPL15,BFR2,PWP2,YIH1,DBP3,TIF32,VTS1,ERG6,GUS1,RRB1,ECM16,RPL15B,UTP10,GAR1,CIC1,ERB1,IMP4,YTM1,NOP19,NMD3,MET5,UTP21,FAS1,BMS1,RPL10A,UTP6,MTR4,UTP18,ENP2,LEU1,RPA135,YJU3,RPS14,RRP5,PWP1,NOP56,UTP4,NUG1,RPC40,NOP7,RPL2,DIP2,ACS2,MAP1,IMP3,KLMA_60069,BRX1,URB1,TEF4,DHR2,RPA190,FUN12,REV1,YAF9,NOP15,KRE33,KLMA_60313,UGP1,RPB1,RSA4,HSL7,SPT21,NOP14,TIF3,NOC4,RRP9,RPL19B,SRP40,NOP9,RLP24,PUB1,UTP25,HDA1,NOP2,NIP1,KLMA_80256,PUF6,KAP123,RPL8B
GO:0034455	t-UTP complex	7	6	0.67	4.90E-06	UTP5,UTP15,UTP8,NAN1,UTP10,UTP4
GO:0030688	preribosome, small subunit precursor	21	10	2.02	8.10E-06	ENP1,RPS3,NOB1,UTP10,RRP12,KRE33,NOP14,NOC4,NOP9,LTV1
GO:0031428	box C/D snoRNP complex	6	5	0.58	4.50E-05	NOP1,HAS1,NOP58,NOP56,RRP9

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0044445	cytosolic part	97	22	9.35	8.80E-05	PFK1,ENO,ARX1,RPS2,KLMA_20355,RPL22A,RPS3,RPL5,RNR2,RPL3,RLI1,NMD3,FAS1,LEU1,MAP1,KLMA_60069,FUN12,KLMA_60313,PFK2,RNR1,FAS2,RPL19B
GO:0022626	cytosolic ribosome	48	14	4.63	0.0001	ARX1,RPS2,KLMA_20355,RPL22A,RPS3,RPL5,RPL3,RLI1,NMD3,MAP1,KLMA_60069,FUN12,KLMA_60313,RPL19B
GO:0010494	cytoplasmic stress granule	60	16	5.78	0.00011	CYS4,PAB1,TIF32,GUS1,MET5,LEU1,MAP1,TEF4,FUN12,UGP1,RPB1,TIF3,PUB1,NIP1,KLMA_80256,KAP123
GO:0044428	nuclear part	739	98	71.23	0.00016	SPB1,RPA49,NOP1,SOH1,UTP5,EBP2,RPF2,RSE1,HAS1,NOG1,UTP13,RPC37,DBP7,UTP15,UTP11,ARX1,NOP53,NOP58,FHL1,NOP12,ENP1,CBF5,RLP7,UTP8,MPP10,IPI3,NAN1,MRT4,RSC2,RRS1,IPI1,DCAF13,NOB1,NSR1,BFR2,MEX67,PWP2,DBP3,RRB1,ECM16,MDN1,UTP10,GAR1,CIC1,ERB1,NUP116,IMP4,YTM1,NOP19,HMG1,DUS3,RPC82,RIX1,UTP21,MTR2,BMS1,UTP6,PRP43,NOC2,MTR4,UTP18,ENP2,RPA135,RRP5,PWP1,NOP56,UTP4,NUG1,RPC40,NOP7,DIP2,ACS2,IMP3,BRX1,URB1,DHR2,RPA190,REV1,YAF9,NOP15,CEX1,KRE33,EPL1,RPB1,ROX3,RSA4,NOP14,NOC4,RRP9,MAK21,SRP40,NOP9,RLP24,RRP42,UTP25,HDA1,NOP2,KAP123

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0005634	nucleus	1128	138	108.72	0.00023	SPB1,CCN1,RPA49,KLMA_10146,NOP1,GSP1,SOH1,UTP5,SDA1,EBP2,RPF2,RSE1,GAL80,HAS1,TDA1,YTA7,AAH1,NOG1,UTP13,RPC37,DBP7,UTP15,UTP11,ARX1,NOP53,NOP58,FHL1,NOP12,ENP1,CBF5,RLP7,UTP8,TPA1,MPP10,IPI3,NAN1,LIA1,HAM1,MRT4,RSC2,RRS1,IPI1,RNR2,DCAF13,MEU1,ETT1,NOB1,PAB1,RLI1,NSR1,BFR2,MEX67,PWP2,DBP3,HAL9,VTS1,KLMA_30614,RAD54,KSS1,RRB1,ECM16,MDN1,UTP10,GAR1,CIC1,HAP1,ERB1,NUP116,MCM1,RRP12,IMP4,YTM1,NOP19,NMD3,HMG1,DUS3,RPC82,RIX1,UTP21,MTR2,PUS1,BMS1,UTP6,PRP43,NOC2,MTR4,UTP18,UPC2,ENP2,RPA135,RRP5,PWP1,NOP56,LAC9,UTP4,NUG1,RPC40,NOP7,DIP2,ACS2,ALB1,IMP3,EXO1,BRX1,URB1,DHR2,RPA190,REV1,YAF9,NOP15,CEX1,KRE33,EPL1,RGT1,JHD2,LEU3,RPB1,IKI3,ROX3,RSA4,NOP14,NOC4,RRP9,MAK21,SRP40,PCL1,KLMA_70408,NOP9,LTV1,RLP24,RRP42,PUB1,UTP25,HDA1,NOP2,TRM6,DEF1,KAP123
GO:0033553	rDNA heterochromatin	11	6	1.06	0.00023	UTP5,UTP15,UTP8,NAN1,UTP10,HDA1
GO:0030689	Noc complex	5	4	0.48	0.00039	NOC2,NOP14,NOC4,MAK21
GO:0035770	ribonucleoprotein granule	76	17	7.33	0.00067	CYS4,PAB1,TIF32,VTS1,GUS1,MET5,LEU1,MAP1,TEF4,FUN12,UGP1,RPB1,TIF3,PUB1,NIP1,KLMA_80256,KAP123
GO:0036464	cytoplasmic ribonucleoprotein granule	76	17	7.33	0.00067	CYS4,PAB1,TIF32,VTS1,GUS1,MET5,LEU1,MAP1,TEF4,FUN12,UGP1,RPB1,TIF3,PUB1,NIP1,KLMA_80256,KAP123
GO:0034457	Mpp10 complex	3	3	0.29	0.00089	MPP10,IMP4,IMP3
GO:0070545	PeBoW complex	3	3	0.29	0.00089	ERB1,YTM1,NOP7
GO:0097344	Rix1 complex	3	3	0.29	0.00089	IPI3,IPI1,RIX1

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0031974	membrane-enclosed lumen	790	97	76.14	0.00302	SPB1,RPA49,NOP1,SOH1,UTP5,EBP2,RPF2,HAS1,NOG1,GPM1,UTP13,DBP7,UTP15,ADH4,UTP11,ADK1,ARX1,NOP53,ERG3,NOP58,FHL1,NOP12,ENP1,CBF5,RLP7,UTP8,MPP10,IPI3,NAN1,MRT4,RSC2,RRS1,IPI1,DCAF13,KLMA_30226,NOB1,MRPL15,BFR2,MEX67,PWP2,DBP3,RRB1,ECM16,MDN1,UTP10,GAR1,CIC1,ERB1,IMP4,MAM33,YTM1,NOP19,DUS3,RIX1,UTP21,MTR2,BMS1,UTP6,MTR4,UTP18,ENP2,ERV1,RPA135,PDX3,CCP1,RRP5,PWP1,NOP56,UTP4,NUG1,RPC40,NOP7,DIP2,ACS2,IMP3,BRX1,URB1,DHR2,RPA190,REV1,YAF9,NOP15,KRE33,EPL1,RPB1,ROX3,RSA4,NOP14,NOC4,RRP9,SRP40,NOP9,RLP24,RRP42,UTP25,HDA1,NOP2
GO:0043233	organelle lumen	790	97	76.14	0.00302	SPB1,RPA49,NOP1,SOH1,UTP5,EBP2,RPF2,HAS1,NOG1,GPM1,UTP13,DBP7,UTP15,ADH4,UTP11,ADK1,ARX1,NOP53,ERG3,NOP58,FHL1,NOP12,ENP1,CBF5,RLP7,UTP8,MPP10,IPI3,NAN1,MRT4,RSC2,RRS1,IPI1,DCAF13,KLMA_30226,NOB1,MRPL15,BFR2,MEX67,PWP2,DBP3,RRB1,ECM16,MDN1,UTP10,GAR1,CIC1,ERB1,IMP4,MAM33,YTM1,NOP19,DUS3,RIX1,UTP21,MTR2,BMS1,UTP6,MTR4,UTP18,ENP2,ERV1,RPA135,PDX3,CCP1,RRP5,PWP1,NOP56,UTP4,NUG1,RPC40,NOP7,DIP2,ACS2,IMP3,BRX1,URB1,DHR2,RPA190,REV1,YAF9,NOP15,KRE33,EPL1,RPB1,ROX3,RSA4,NOP14,NOC4,RRP9,SRP40,NOP9,RLP24,RRP42,UTP25,HDA1,NOP2

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0070013	intracellular organelle lumen	790	97	76.14	0.00302	SPB1,RPA49,NOP1,SOH1,UTP5,EBP2,RPF2,HAS1,NOG1,GPM1,UTP13,DBP7,UTP15,ADH4,UTP11,ADK1,ARX1,NOP53,ERG3,NOP58,FHL1,NOP12,ENP1,CBF5,RLP7,UTP8,MPP10,IPI3,NAN1,MRT4,RSC2,RRS1,IPI1,DCAF13,KLMA_30226,NOB1,MRPL15,BFR2,MEX67,PWP2,DBP3,RRB1,ECM16,MDN1,UTP10,GAR1,CIC1,ERB1,IMP4,MAM33,YTM1,NOP19,DUS3,RIX1,UTP21,MTR2,BMS1,UTP6,MTR4,UTP18,ENP2,ERV1,RPA135,PDX3,CCP1,RRP5,PWP1,NOP56,UTP4,NUG1,RPC40,NOP7,DIP2,ACS2,IMP3,BRX1,URB1,DHR2,RPA190,REV1,YAF9,NOP15,KRE33,EPL1,RPB1,ROX3,RSA4,NOP14,NOC4,RRP9,SRP40,NOP9,RLP24,RRP42,UTP25,HDA1,NOP2
GO:0005732	small nucleolar ribonucleoprotein comple...	28	8	2.7	0.00378	NOP1,HAS1,NOP58,CBF5,MPP10,GAR1,NOP56,RRP9
GO:0022625	cytosolic large ribosomal subunit	24	7	2.31	0.00591	ARX1,KLMA_20355,RPL22A,RPL5,RPL3,NMD3,RPL19B
GO:0000792	heterochromatin	19	6	1.83	0.00701	UTP5,UTP15,UTP8,NAN1,UTP10,HDA1
GO:0031429	box H/ACA snoRNP complex	5	3	0.48	0.00765	HAS1,CBF5,GAR1
GO:0072588	box H/ACA RNP complex	5	3	0.48	0.00765	HAS1,CBF5,GAR1
GO:0005835	fatty acid synthase complex	2	2	0.19	0.00926	FAS1,FAS2
GO:0005945	6-phosphofructoki	2	2	0.19	0.00926	PFK1,PFK2

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
	nase complex					
GO:0005946	alpha,alpha-trehalose-phosphate synthase...	2	2	0.19	0.00926	TPS2,TPS1
GO:0005971	ribonucleoside-diphosphate reductase com...	2	2	0.19	0.00926	RNR2,RNR1
GO:0009337	sulfite reductase complex (NADPH)	2	2	0.19	0.00926	MET5,MET10
GO:0030690	Noc1p-Noc2p complex	2	2	0.19	0.00926	NOC2,MAK21
GO:0030692	Noc4p-Nop14p complex	2	2	0.19	0.00926	NOP14,NOC4
GO:0042272	nuclear RNA export factor complex	2	2	0.19	0.00926	MEX67,MTR2

GO terms enriched in significantly up-regulated genes (cellular components)

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0016021	integral component of membrane	973	176	99.84	6.10E-20	ARN2,KLMA_10026,KLMA_10039,PRM1,KLMA_10174,KLMA_10246,HRD1,MCH2,DIT2,ATG27,STE3,KLMA_10393,PMC1,PMA1,HGT1,KLMA_10560,RRT8,YKT6,DAL5,RAN1,BIG1,PEP12,UBP16,GDT1,YDC1,FCY2,KLMA_20003,FRE4,ADY2,KLMA_20010,RFT1,KLMA_20072,NIPA2,KLMA_20101,KLMA_20131,PXA1,THI72,JEN1,KLMA_20269,YHM2,KLMA_20345,KLMA_20368,OSW5,POM33,uapC,ATO2,CTS2,SNG1,PEX11,KLMA_20658,KLMA_20730,MEP2,ODC2,KLMA_20823,KHA1,FEN2,KLMA_30014,PUT4,mug157,KLMA_30124,TOK1,MMM1,KLMA_30260,KLMA_30272,VTI1,PDR12,PHM7,KLMA_30399,DPP1,KLMA_30444,KLMA_30524,KLMA_30555,KLMA_30573,KLMA_30601,STL1,mug70,KLMA_30624,KLMA_30642,PNS1,KLMA_30672,ATG32,LAC12,KLMA_40006,KLMA_40042,MSB2,NYV1,ENA5,KLMA_40213,CHS1,PDR5,KLMA_40260,KLMA_40272,KLMA_40358,GAS4,VTC1,KLMA_40446,YET3,KLMA_40484,PUN1,PXA2,GEX1,PEX25,BTN1,KLMA_50156,QDR3,FIG1,KLMA_50249,KLMA_50252,SOP4,KLMA_50327,HUT1,RAG1,HAK1,OPT2,MTC4,NCE102,VPS70,dpp1,KLMA_50601,KLMA_60005,DIP5,RMD1,KLMA_60123,KLMA_60124,VCX1,KLMA_60241,KLMA_60293,KLMA_60323,KLMA_60367,FMP37,KLMA_60426,KLMA_60475,SRF1,KLMA_60496,ERC1,KLMA_60558,KLMA_70001,HXT15,KLMA_70004,FMP32,KLMA_70053,PER33,KLMA_70089,ERV2,ywtG,ALG12,KLMA_70209,AGP2,PHO84,FMP27,ANT1,PTR2,mcfL,KLMA_80110,KTR5,AVT7,lag1,SGA1,SFC1,CRC1,KLMA_80231,VAM3,SFK1,HXT14
GO:0031224	intrinsic component of membrane	978	176	100.35	1.10E-19	ARN2,KLMA_10026,KLMA_10039,PRM1,KLMA_10174,KLMA_10246,HRD1,MCH2,DIT2,ATG27,STE3,KLMA_10393,PMC1,PMA1,HGT1,KLMA_10560,RRT8,YKT6,DAL5,RAN1,BIG1,PEP12,UBP16,GDT1,YDC1,FCY2,KLMA_20003,FRE4,ADY2,KLMA_20010,RFT1,KLMA_20072,NIPA2,KLMA_20101,KLMA_20131,PXA1,THI72,JEN1,KLMA_20269,YHM2,KLMA_20345,KLMA_20368,OSW5,PO

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
						M33,uapC,ATO2,CTS2,SNG1,PEX11,KLMA_20658,KLMA_20730,MEP2,ODC2,KLMA_20823,KHA1,FEN2,KLMA_30014,PUT4,mug157,KLMA_30124,TOK1,MMM1,KLMA_30260,KLMA_30272,VTI1,PDR12,PHM7,KLMA_30399,DPP1,KLMA_30444,KLMA_30524,KLMA_30555,KLMA_30573,KLMA_30601,STL1,mug70,KLMA_30624,KLMA_30642,PNS1,KLMA_30672,ATG32,LAC12,KLMA_40006,KLMA_40042,MSB2,NYV1,ENA5,KLMA_40213,CHS1,PDR5,KLMA_40260,KLMA_40272,KLMA_40358,GAS4,VTC1,KLMA_40446,YET3,KLMA_40484,PUN1,PXA2,GEX1,PEX25,BTN1,KLMA_50156,QDR3,FIG1,KLMA_50249,KLMA_50252,SOP4,KLMA_50327,HUT1,RAG1,HAK1,OPT2,MTC4,NCE102,VPS70,dpp1,KLMA_50601,KLMA_60005,DIP5,RMD1,KLMA_60123,KLMA_60124,VCX1,KLMA_60241,KLMA_60293,KLMA_60323,KLMA_60367,FMP37,KLMA_60426,KLMA_60475,SRF1,KLMA_60496,ERC1,KLMA_60558,KLMA_70001,HXT15,KLMA_70004,FMP32,KLMA_70053,PER33,KLMA_70089,ERV2,ywtG,ALG12,KLMA_70209,AGP2,PHO84,FMP27,ANT1,PTR2,mcfL,KLMA_80110,KTR5,AVT7,lag1,SGA1,SFC1,CRC1,KLMA_80231,VAM3,SFK1,HXT14
GO:0044425	membrane part	1193	189	122.41	8.70E-15	ARN2,KLMA_10026,KLMA_10039,PRM1,KLMA_10174,KLMA_10246,HRD1,MCH2,DIT2,ATG27,STE3,KLMA_10393,PMC1,PMA1,HGT1,KLMA_10560,RRT8,YKT6,DAL5,RAN1,BIG1,PEP12,UBP16,GDT1,YDC1,FCY2,KLMA_20003,FRE4,ADY2,KLMA_20010,RFT1,KLMA_20072,NIPA2,KLMA_20101,KLMA_20131,PXA1,THI72,JEN1,KLMA_20269,YHM2,KLMA_20345,KLMA_20368,OSW5,IMP1,POM33,uapC,FAB1,ATO2,CTS2,SNG1,PEX11,KLMA_20658,KLMA_20730,MEP2,ODC2,STE4,KLMA_20823,KHA1,FEN2,KLMA_30014,PUT4,mug157,KLMA_30124,TOK1,MMM1,KLMA_30260,KLMA_30272,VTI1,PDR12,PHM7,KLMA_30399,SNX4,DPP1,KLMA_30428,KLMA_30444,KLMA_30524,KLMA_30555,KLMA_30573,KLMA_30601,STL1,mug70,KLMA_30624,KLMA_30642,PNS1,KLMA_30672,ATG32,LAC12,KLMA_40006,KLMA_40042,MSB2,NYV1,ENA5,KLMA_40213,CHS1,PDR5,KLMA_40260,KLMA_40272,

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
						KLMA_40333,KLMA_40358,GAS4,VTC1,KLMA_40446,YET3,KLMA_40484,PUN1,PXA2,GEX1,PEX25,BTN1,KLMA_50156,APS2,QDR3,FIG1,KLMA_50249,KLMA_50252,SOP4,KLMA_50327,HUT1,RAG1,HAK1,OPT2,MTC4,NCE102,VPS70,dpp1,KLMA_50601,KLMA_60005,DIP5,RMD1,KLMA_60123,KLMA_60124,GPA1,VCX1,KLMA_60241,KLMA_60293,KLMA_60323,KLMA_60367,FMP37,KLMA_60426,INP1,KLMA_60475,SRF1,KLMA_60496,ERC1,KLMA_60558,KLMA_70001,HXT15,KLMA_70004,FMP32,KLMA_70053,PER33,KLMA_70089,ERV2,KLMA_70118,ywtG,ALG12,KLMA_70209,AGP2,KLMA_70233,PHO84,FMP27,ANT1,PTR2,SNF8,mcfL,ATG20,KLMA_80110,KTR5,AVT7,lag1,SGA1,SFC1,CRC1,KLMA_80231,VAM3,SFK1,HXT14
GO:0016020	membrane	1335	201	136.98	1.70E-13	ARN2,KLMA_10026,KLMA_10039,PRM1,ATG26,VPS60,KLMA_10174,KLMA_10246,HRD1,PLB,MCH2,DIT2,FMP43,ATG27,STE3,KLMA_10393,PMC1,PMA1,KLMA_10486,HGT1,KLMA_10560,RRT8,YKT6,DAL5,RAN1,BIG1,PEP12,UBP16,GDT1,YDC1,FCY2,KLMA_20003,FRE4,ADY2,KLMA_20010,RFT1,KLMA_20072,NIPA2,KLMA_20101,KLMA_20131,PXA1,THI72,JEN1,KLMA_20269,YHM2,KLMA_20345,KLMA_20368,OSW5,IMP1,POM33,uapC,FAB1,ATO2,FRQ1,CTS2,SNG1,PEX11,KLMA_20658,KLMA_20730,MEP2,HSP12,ODC2,STE4,KLMA_20823,KHA1,FEN2,KLMA_30014,PUT4,mug157,KLMA_30124,TOK1,MMM1,KLMA_30260,KLMA_30272,VTI1,PDR12,PHM7,KLMA_30399,SNX4,DPP1,KLMA_30428,KLMA_30444,KLMA_30524,PIB1,KLMA_30555,KLMA_30573,KLMA_30601,STL1,mug70,KLMA_30624,KLMA_30642,PNS1,KLMA_30672,ATG32,LAC12,KLMA_40006,KLMA_40042,MSB2,NYV1,ENA5,KLMA_40213,CHS1,SPO14,PDR5,KLMA_40260,KLMA_40272,KLMA_40333,KLMA_40358,GAS4,VTC1,KLMA_40446,YET3,KLMA_40484,PUN1,PXA2,GEX1,PEX25,BTN1,KLMA_50156,APS2,QDR3,FIG1,KLMA_50249,KLMA_50252,SOP4,KLMA_50327,HUT1,RAG1,HAK1,OPT2,MTC4,NCE102,VPS70,dpp1,KLMA_50601,KLMA_60005,MRF1,DIP5,RMD1,KLMA_60123,KLMA_60124,GP

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
						A1,VCX1,KLMA_60241,KLMA_60293,KLMA_60323,KLMA_60367,FMP37,KLMA_60426,SST2,INP1,KLMA_60475,SRF1,KLMA_60496,ERC1,KLMA_60558,KLMA_70001,HXT15,KLMA_70004,FMP32,KLMA_70053,PER33,KLMA_70089,ERV2,KLMA_70118,ywtG,KLMA_70146,ALG12,KLMA_70209,AGP2,KLMA_70233,PHO84,FMP27,ANT1,PTR2,SNF8,mcfL,ATG20,KLMA_80110,KTR5,AVT7,lag1,SGA1,SFC1,CRC1,KLMA_80231,VAM3,SFK1,HXT14
GO:0044438	microbody part	30	12	3.08	1.80E-05	KLMA_10026,PXA1,POT1,POX1,PEX11,MDH3,PXA2,PEX25,SPS19,INP1,ANT1,LPX1
GO:0044439	peroxisomal part	30	12	3.08	1.80E-05	KLMA_10026,PXA1,POT1,POX1,PEX11,MDH3,PXA2,PEX25,SPS19,INP1,ANT1,LPX1
GO:0005777	peroxisome	52	16	5.34	3.50E-05	KLMA_10026,KLMA_20057,PXA1,POT1,POX1,PEX11,CAT2,MDH3,PXA2,PEX25,PCD1,SPS19,TES1,INP1,ANT1,LPX1
GO:0042579	microbody	52	16	5.34	3.50E-05	KLMA_10026,KLMA_20057,PXA1,POT1,POX1,PEX11,CAT2,MDH3,PXA2,PEX25,PCD1,SPS19,TES1,INP1,ANT1,LPX1
GO:0005782	peroxisomal matrix	9	5	0.92	0.00098	POT1,POX1,MDH3,SPS19,LPX1
GO:0031907	microbody lumen	9	5	0.92	0.00098	POT1,POX1,MDH3,SPS19,LPX1
GO:0005779	integral component of peroxisomal membra...	13	6	1.33	0.00103	KLMA_10026,PXA1,PEX11,PXA2,PEX25,ANT1
GO:0031231	intrinsic component of peroxisomal membr...	13	6	1.33	0.00103	KLMA_10026,PXA1,PEX11,PXA2,PEX25,ANT1
GO:1990429	peroxisomal importomer complex	13	6	1.33	0.00103	PXA1,UBI4,PEX11,CAT2,MDH3,PEX25
GO:0005834	heterotrimeric G-protein	3	3	0.31	0.00107	STE4,GPA1,KLMA_70118

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
	complex					
GO:0042597	periplasmic space	3	3	0.31	0.00107	PLB,FBP1,ATH1
GO:1905360	GTPase complex	3	3	0.31	0.00107	STE4,GPA1,KLMA_70118
GO:1990415	Pex17p-Pex14p docking complex	14	6	1.44	0.00164	PXA1,UBI4,PEX11,CAT2,MDH3,PEX25
GO:0071944	cell periphery	258	41	26.47	0.00225	LSB5,PLB,STE3,PMA1,KLMA_10486,YTA6,KLMA_20368,PIN3,FRQ1,MEP2,HSP12,STE4,TOK1,DPL1,MSB2,KLMA_40061,ENA5,KLMA_40213,PDR5,ELM1,GAS4,KLMA_40476,PUN1,APS2,QDR3,FIG1,PIR1,GPA1,STL1,SST2,CRR1,KLMA_70011,KIP2,KLMA_70118,ATH1,AGP2,PHO84,KLMA_80053,AVT7,SFK1,HOF1
GO:0005778	peroxisomal membrane	21	7	2.15	0.00367	KLMA_10026,PXA1,PEX11,PXA2,PEX25,INP1,ANT1
GO:0031903	microbody membrane	21	7	2.15	0.00367	KLMA_10026,PXA1,PEX11,PXA2,PEX25,INP1,ANT1
GO:0005886	plasma membrane	145	25	14.88	0.00573	PLB,STE3,PMA1,KLMA_10486,FRQ1,MEP2,HSP12,STE4,TOK1,MSB2,ENA5,KLMA_40213,PDR5,GAS4,PUN1,APS2,QDR3,GPA1,STL1,SST2,KLMA_70118,AGP2,PHO84,AVT7,SFK1
GO:0005618	cell wall	34	9	3.49	0.00581	KLMA_20368,KLMA_40061,GAS4,FIG1,PIR1,CRR1,KLMA_70011,ATH1,KLMA_80053
GO:0030312	external encapsulating structure	34	9	3.49	0.00581	KLMA_20368,KLMA_40061,GAS4,FIG1,PIR1,CRR1,KLMA_70011,ATH1,KLMA_80053
GO:0031234	extrinsic component of cytoplasmic side ...	5	3	0.51	0.00915	STE4,GPA1,KLMA_70118

GO terms enriched in significantly down-regulated genes (molecular functions)

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0030515	snoRNA binding	24	17	2.53	3.10E-12	UTP13,UTP15,ENP1,UTP8,NAN1,PWP2,UTP10,GAR1,IMP4,BMS1,UTP6,RRP5,DIP2,IMP3,NOP14,RRP9,UTP25
GO:0003723	RNA binding	365	71	38.55	5.10E-08	SRO9,NOP1,PNO1,RPF2,RSE1,HAS1,UTP13,DBP7,UTP15,NOP53,RPS2,NOP58,NOP12,ENP1,UBP3,CBF5,UTP8,TPA1,DTD1,RPS3,RPL5,NAN1,TEF3,MEU1,NOB1,PAB1,RLI1,NSR1,MEX67,PWP2,TIF32,VTS1,BRE5,UTP10,GAR1,CIC1,ERB1,IMP4,PUS1,BMS1,RPL10A,UTP6,MTR4,TIF4632,RRP5,NUG1,NOP7,DIP2,MAP1,IMP3,BRX1,TEF4,FUN12,NOP15,CEX1,NOP4,PFK2,PET309,IKI3,NOP14,TIF3,RRP9,PUS4,NOP9,PUB1,UTP25,NOP2,NIP1,PUF6,PIN4,ILS1
GO:0019843	rRNA binding	36	16	3.8	1.70E-07	RPF2,NOP53,RPS2,NOP12,RPL5,NOB1,CIC1,ERB1,IMP4,RRP5,NOP7,IMP3,BRX1,NOP15,NOP4,UTP25
GO:0016705	oxidoreductase activity, acting on paire...	27	13	2.85	8.30E-07	OLE1,ERG3,TPA1,CYP707A7,LIA1,ERG1,SUR2,dsd1,fmo1,ERG25,PDAT9,cyp524A1,JHD2
GO:0016491	oxidoreductase activity	293	56	30.95	3.10E-06	HIS4,GPD1,OLE1,GAL80,KYE1,SCS7,URA1,ADH4,MET13,ERG3,TPA1,CYP707A7,TDA3,YPR1,LIA1,RNR2,ERG1,KLMA_30274,SUR2,SER3,PAN5,ADH1,dsd1,HEM13,fmo1,GAP1,ADH2,RIB7,FMS1,ALD5,HMG1,DUS3,MET5,FAS1,DLD1,MTR4,IMD4,ERV1,PDX3,CCP1,ERG25,MET10,ADE3,MDH1,FET3,PDAT9,cyp524A1,JHD2,SMM1,CFL1,RNR1,FAS2,MET16,HEM14,MIS1,GAP3

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0097159	organic cyclic compound binding	1315	174	138.89	4.00E-05	APA2,SRO9,HIS4,SAM2,RPA49,KLMA_10146,GPD1,NOP1,GSP1,OLE1,PNO1,GUA1,PFK1,TIF1,RPF2,RSE1,KYE1,MES1,HAS1,TDA1,YTA7,FAU1,PGK,SCS7,PRY2,MET17,MSW1,bioA,NOG1,KLMA_20090,UTP13,DBP7,UTP15,HSL1,ADK1,KLMA_20186,NOP53,RPS2,SHM2,NOP58,GAL1,FHL1,CYS3,NOP12,CCC2,ENP1,UBP3,CBF5,KLMA_20481,UTP8,TPA1,CYP707A7,ADE2,DTD1,RPS3,RPL5,NAN1,HAM1,TEF3,ERG1,MEU1,DRS1,NOB1,PAB1,RLI1,PDC2,ALK2,NSR1,MEX67,SER3,PWP2,DBP3,RRP3,TIF32,HAL9,VTS1,RAD54,KSS1,SAH1,ADE5,7,MTO1,GUS1,BRE5,ECM16,fmo1,MDN1,GAP1,RIB7,UTP10,GAR1,CIC1,HAP1,ERB1,MCM1,IMP4,MAM33,HRK1,HMG1,SFP1,DUS3,RPC82,MET5,PUS1,BMS1,RPL10A,UTP6,DLD1,PRP43,GEP3,SHM1,MTR4,KLMA_50101,TIF4632,RPA135,PTK2,PDX3,CCP1,RRP5,LAC9,NUG1,RPC40,VAS1,NOP7,DIP2,ACS2,MAP1,URA2,IMP3,PDC1,ADE3,EXO1,BRX1,TEF4,DHR2,RPA190,FUN12,REV1,NOP15,CYB5,CEX1,AZF1,KRE33,RGT1,SKS1,NOP4,PDAT9,RAG5,cyp524A1,PFK2,SMM1,RPB1,CDC60,PET309,IKI3,URA7,RNR1,NEW1,NOP14,TIF3,RRP9,MIS1,PUS4,KLMA_70408,NOP9,GAP3,MET3,PUB1,UTP25,NOP2,NIP1,PUF6,PIN4,DOT6,ILS1
GO:1901363	heterocyclic compound binding	1314	173	138.79	6.10E-05	APA2,SRO9,HIS4,SAM2,RPA49,KLMA_10146,GPD1,NOP1,GSP1,OLE1,PNO1,GUA1,PFK1,TIF1,RPF2,RSE1,KYE1,MES1,HAS1,TDA1,YTA7,FAU1,PGK,SCS7,MET17,MSW1,bioA,NOG1,KLMA_20090,UTP13,DBP7,UTP15,HSL1,ADK1,KLMA_20186,NOP53,RPS2,SHM2,NOP58,GAL1,FHL1,CYS3,NOP12,CCC2,ENP1,UBP3,CBF5,KLMA_20481,UTP8,TPA1,CYP707A7,ADE2,DTD1,RPS3,RPL5,NAN1,HAM1,TEF3,ERG1,MEU1,DRS1,NOB1,PAB1,RLI1,PDC2,ALK2,NSR1,MEX67,SER3,PWP2,DBP3,RRP3,TIF32,HAL9,VTS1,RAD54,KSS1,SAH1,ADE5,7,MTO1,GUS1,BRE5,ECM16,fmo1,MDN1,GAP1,RIB7,UTP10,GAR1,CIC1,HAP1,ERB1,MCM1,IMP4,MAM33,HRK1,HMG1,SFP1,DUS3,RPC82,MET5,PUS1,BMS1,RPL10A,UTP6,DLD1,PRP43,GEP3,SHM1,MTR4,

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
						KLMA_50101,TIF4632,RPA135,PTK2,PDX3,CCP1,RRP5,LAC9,NUG1,RPC40,VAS1,NOP7,DIP2,ACS2,MAP1,URA2,IMP3,PDC1,ADE3,EXO1,BRX1,TEF4,DHR2,RPA190,FUN12,REV1,NOP15,CYB5,CEX1,AZF1,KRE33,RGT1,SKS1,NOP4,PDAT9,RAG5,cyp524A1,PFK2,SMM1,RPB1,CDC60,PET309,IKI3,URA7,RNR1,NEW1,NOP14,TIF3,RRP9,MIS1,PUS4,KLMA_70408,NOP9,GAP3,MET3,PUB1,UTP25,NOP2,NIP1,PUF6,PIN4,DOT6,ILS1
GO:0005506	iron ion binding	25	10	2.64	0.00012	SCS7,ERG3,TPA1,CYP707A7,RNR2,RLI1,SUR2,ERG25,PDAT9,cyp524A1
GO:0048037	cofactor binding	181	35	19.12	0.00021	HIS4,ACO2,GPD1,OLE1,BIO2,KYE1,SCS7,MET17,bioA,SHM2,GAL10,CYS3,TPA1,CYP707A7,ERG1,SER3,SAH1,MTO1,fmo1,GAP1,RIB7,HMG1,DUS3,MET5,DLD1,SHM1,LEU1,PDX3,CCP1,PDC1,CYB5,PDAT9,cyp524A1,SMM1,GAP3
GO:0034511	U3 snoRNA binding	7	5	0.74	0.00022	NAN1,BMS1,RRP5,RRP9,UTP25
GO:0050662	coenzyme binding	120	25	12.67	0.00055	HIS4,GPD1,KYE1,MET17,bioA,SHM2,GAL10,CYS3,TPA1,ERG1,SER3,SAH1,MTO1,fmo1,GAP1,RIB7,HMG1,DUS3,MET5,DLD1,SHM1,PDX3,PDC1,SMM1,GAP3
GO:0070180	large ribosomal subunit rRNA binding	5	4	0.53	0.00056	CIC1,ERB1,NOP7,NOP4
GO:0004497	monooxygenase activity	17	7	1.8	0.00105	CYP707A7,LIA1,ERG1,fmo1,ERG25,PDAT9,cyp524A1
GO:0020037	heme binding	24	8	2.53	0.0023	OLE1,SCS7,CYP707A7,MET5,CCP1,CYB5,PDAT9,cyp524A1
GO:0046906	tetrapyrrole binding	24	8	2.53	0.0023	OLE1,SCS7,CYP707A7,MET5,CCP1,CYB5,PDAT9,cyp524A1

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0140098	catalytic activity, acting on RNA	194	33	20.49	0.00319	SPB1,RPA49,NOP1,DSS1,MES1,HAS1,MSW1,RPC37,DTD1,NOB1,MRPL15,DBP3,RRP3,GUS1,ECM16,TRM13,DUS3,RPC82,PRP43,MTR4,RPA135,RPC40,VAS1,KLMA_50502,DHR2,RPA190,SMM1,RPB1,CDC60,NOP2,TRM6,PTH2,ILS1
GO:0016879	ligase activity, forming carbon-nitrogen...	37	10	3.91	0.00388	GUA1,FAU1,GSH1,ADE5,7,ADE6,ACS2,URA2,ADE3,URA7,MIS1
GO:0008097	5S rRNA binding	4	3	0.42	0.00431	RPF2,RPL5,BRX1
GO:0016717	oxidoreductase activity, acting on paire...	4	3	0.42	0.00431	OLE1,ERG3,cyp524A1
GO:0032451	demethylase activity	4	3	0.42	0.00431	TPA1,CYP707A7,JHD2
GO:0003724	RNA helicase activity	21	7	2.22	0.00432	HAS1,DBP3,RRP3,ECM16,PRP43,MTR4,DHR2
GO:0016866	intramolecular transferase activity	17	6	1.8	0.00598	GPM3,GPM1,CBF5,PGM2,PUS1,PUS4
GO:0002161	aminoacyl-tRNA editing activity	8	4	0.84	0.00606	DTD1,VAS1,CDC60,ILS1
GO:0046914	transition metal ion binding	210	34	22.18	0.00625	HIS4,KLMA_10146,SCS7,SCO1,AAH1,ADH4,ERG3,GAL7,CCC2,TPA1,CYP707A7,RNR2,KLMA_30226,RLI1,SUR2,HAL9,KLMA_30614,ADH1,ADH2,SFB3,HAP1,FBA1,UPC2,ERG25,LAC9,APE2,FET3,RPA190,RGT1,PDAT9,cyp524A1,LEU3,KLMA_70408,MET6

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0003676	nucleic acid binding	786	102	83.02	0.008	SRO9,RPA49,KLMA_10146,NOP1,PNO1,TIF1,RPF2,RSE1,HAS1,UTP13,DBP7,UTP15,KLMA_20186,NOP53,RPS2,NOP58,FHL1,NOP12,ENP1,UBP3,CBF5,KLMA_20481,UTP8,TPA1,DTD1,RPS3,RPL5,NAN1,TEF3,MEU1,DRS1,NOB1,PAB1,RLI1,PDC2,NSR1,MEX67,PWP2,DBP3,RRP3,TIF32,HAL9,VTS1,BRE5,ECM16,UTP10,GAR1,CIC1,HAP1,ERB1,MCM1,IMP4,MAM33,SFP1,RPC82,PUS1,BMS1,RPL10A,UTP6,PRP43,MTR4,KLMA_50101,TIF4632,RPA135,RRP5,LAC9,NUG1,RPC40,NOP7,DIP2,MAP1,IMP3,EXO1,BRX1,TEF4,DHR2,RPA190,FUN12,REV1,NOP15,CEX1,AZF1,RGT1,NOP4,PFK2,RPB1,PET309,IKI3,NOP14,TIF3,RRP9,PUS4,KLMA_70408,NOP9,PUB1,UTP25,NOP2,NIP1,PUF6,PIN4,DOT6,ILS1
GO:0048029	monosaccharide binding	5	3	0.53	0.00993	GAL1,TPA1,RAG5

GO terms enriched in significantly up-regulated genes (molecular functions)

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0016491	oxidoreductase activity	293	58	34.09	1.50E-05	MXR2,DIT2,ZTA1,KYE1,SOU2,SOU1,yxeK,FRE4,MIOX5,KLMA_20057,POX1,GPD2,ALD2,GDH2,YUC8,CYB2,YPR1,fmo1,KLMA_30124,YIM1,KLMA_30533,ARA1,KLMA_30604,KLMA_40010,LYS9,MDH3,AHP1,LYS1,MDH2,IDP1,adh,ALD4,BDH2,KLMA_50021,sdh,GLT1,SFA1,AIM17,CTT1,PUT1,SPS19,FMP46,ACAD11,gabD,JLP1,KLMA_60268,ETR1,AO-I,KLMA_60405,KLMA_70012,SOR1,ERV2,FOX2,KLMA_70434,KLMA_80176,ADH3,ADH6
GO:0003824	catalytic activity	1905	254	221.62	0.00024	KLMA_10012,CHA1,MXR2,ATG26,YAT1,KIN3,CDC7,ECI1,ECM38,HRD1,PLB,URH1,DIT2,HEM4,PMC1,PMA1,PGU1,INU1,ZTA1,KLMA_10551,KLMA_10560,CTK3,KYE1,KLMA_10605,YKT6,RAN1,SOU2,HUL4,RAD26,UBP16,YTA6,GLY1,YDC1,SOU1,PNG1,ECM31,KLMA_10805,DAL3,yxeK,FRE4,YUH1,MAG1,FUS3,MIOX5,KLMA_20057,SAP30,KLMA_20070,CIT1,RTT109,ECM4,DMC1,PXA1,ppr1,HST2,POT1,DSD1,POX1,SLX1,GPD2,IME4,RIM15,AGX1,IMP1,RAM1,RAD55,KLMA_20431,FAB1,AOS1,MUS81,ARO10,IAH1,CTS2,ALD2,MLH1,GDH2,YUC8,PTP2,RNY1,amdS,KLMA_30011,CYB2,bioA,YPR1,ARI1,fmo1,mug157,RNH1,YKU80,KLMA_30124,SPO1,SRS2,GLO4,KLMA_30245,KLMA_30260,KLMA_30282,ACO2,UBC12,PDR12,EXO5,CMK2,TAD2,YIM1,DPP1,DPL1,MLH3,REV3,KLMA_30533,PIB1,GAD1,PRR1,APN1,IME2,ARA1,ACS1,KLMA_30604,FMP48,CAT2,SDT1,KLMA_40003,OXP1,KLMA_40010,LYS9,EST2,KLMA_40050,MDH3,KLMA_40068,KLMA_40105,KLMA_40133,AHP1,UGA1,ENA5,CHS1,SPO14,PDR5,YPS7,ELM1,KLMA_40335,KLMA_40359,LYS1,MDH2,GAS4,IDP1,PXA2,NPY1,adh,KLMA_40628,ALD4,BDH2,KLMA_50021,GDE1,CAR1,VPS21,KLMA_50093,POP4,KLMA_50123,ARO8,DAK1,ITT1,CAR2,ECO1,sdh,GLT1,SFA1,IST3,AIM17,CTT1,KLMA_50451,AXL1,BAR1,INO1,RKM5,PUT1,PCD1,URC1,SPS19,GUD1,KIN28,FMP46,ACAD1

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
						1,NIT2,TDA10,TES1,YCH1,HSP78,gabD,APC11,GPA1,JLP1,KLMA_60206,KLMA_60268,ETR1,KLMA_60293,AO-I,SCY1,KLMA_60366,RAD1,PHO85,KLMA_60405,PDE1,KLMA_60413,KLMA_60415,ARO9,GRE2,KLMA_60426,FBP1,CRR1,KLMA_70002,KLMA_70012,KIP2,OTU1,SOR1,YMR1,ERV2,ATH1,TEL1,KLMA_70156,SEE1,ICL1,ALG12,KLMA_70270,KLMA_70303,KLMA_70317,LPX1,FAD1,FOX2,ICL2,KLMA_70434,SAD1,PDH1,CIT3,ULA1,KLMA_80004,PHR1,hyuA,KLMA_80053,LYS5,KLMA_80108,KTR5,SIW14,lag1,KLMA_80136,SGA1,NCE103,MSG5,KLMA_80176,UBA3,ADH3,ARO7,ADH6,SAS3,GUT1
GO:0022857	transmembrane transporter activity	267	48	31.06	0.00096	PMC1,PMA1,HGT1,RAN1,GDT1,FCY2,NIPA2,PXA1,THI72,YHM2,uapC,MEP2,ODC2,KHA1,PUT4,TOK1,PDR12,KLMA_30601,STL1,KLMA_30672,LAC12,ENA5,PDR5,PXA2,QDR3,RAG1,HAK1,DIP5,KLMA_60323,VCX1,ERC1,HXT15,ywtG,AGP2,PHO84,ANT1,PTR2,SFC1,CRC1,HXT14
GO:0016810	hydrolase activity, acting on carbon-nit...	54	14	6.28	0.00266	YDC1,PNG1,DAL3,SAP30,HST2,amdS,TAD2,OXP1,KLMA_40359,CAR1,URC1,GUD1,KLMA_60206
GO:0015079	potassium ion transmembrane transporter ...	10	5	1.16	0.00318	KHA1,TOK1,ENA5,HAK1,VCX1
GO:0016798	hydrolase activity, acting on glycosyl b...	39	11	4.54	0.00372	URH1,PGU1,INU1,MAG1,CTS2,KLMA_30011,KLMA_40105,CRR1,ATH1,KLMA_70317,SGA1
GO:0005215	transporter activity	314	52	36.53	0.00391	PMC1,PMA1,HGT1,RAN1,GDT1,FCY2,RFT1,NIPA2,PXA1,THI72,YHM2,uapC,MEP2,ODC2,KHA1,PUT4,TOK1,MMM1,PDR12,KLMA_30601,STL1,KLMA_30672,LAC12,ENA5,PDR5,PXA2,KAP122,APS2,QDR3,RAG1,HAK1,DIP5,KLMA_60323,VCX1,ERC1,HXT15,ywtG,AGP2,PHO84,ANT1,PTR2,SFC1,CRC1,HXT14

GO.ID	Term	Annotated gene	Significant	Expected	P-value	Genes
GO:0050662	coenzyme binding	120	24	13.96	0.00478	CHA1,KYE1,HST2,POX1,GPD2,KLMA_20431,ARO10,YUC8,bioA,ARI1,fmo1,DPL1,GAD1,UGA1,IDP1,KLMA_40628,ARO8,CAR2,GLT1,KLMA_50437,ACAD11,ARO9,GRE2,KLMA_80004
GO:0048037	cofactor binding	181	33	21.06	0.00484	CHA1,DIT2,KLMA_10520,KYE1,HST2,POX1,GPD2,KLMA_20431,ARO10,YUC8,ISU1,bioA,ARI1,fmo1,ACO2,DPL1,REV3,GAD1,ISA1,UGA1,IDP1,KLMA_40628,ARO8,CAR2,GLT1,CTT1,KLMA_50437,ACAD11,AO-I,ARO9,GRE2,PDH1,KLMA_80004
GO:0046914	transition metal ion binding	210	37	24.43	0.00527	YHC1,DIT2,ZTA1,MIOX5,GSM1,HST2,ERT1,KLMA_20292,ISU1,RDS2,mlo2,SIP4,KLMA_30395,TAD2,KLMA_30428,KLMA_30533,APN1,OAF1,GAT2,ISA1,adh,THI4,BDH2,CAR1,GLT1,SFA1,KLMA_50329,GUD1,ETP1,AO-I,SOR1,KLMA_70242,SAD1,KLMA_80008,NCE103,ADH3,ADH6
GO:0004622	lysophospholipase activity	4	3	0.47	0.00571	PLB,SPO1,KLMA_30260
GO:0016701	oxidoreductase activity, acting on singl...	4	3	0.47	0.00571	MIOX5,KLMA_30533,KLMA_30604
GO:0016829	lyase activity	73	16	8.49	0.00821	CHA1,HEM4,GLY1,DAL3,DSD1,ARO10,ACO2,DPL1,GAD1,APN1,ICL1,FOX2,ICL2,PDH1,PHR1,NCE103
GO:0004553	hydrolase activity, hydrolyzing O-glycos...	32	9	3.72	0.00863	PGU1,INU1,CTS2,KLMA_30011,KLMA_40105,CRR1,ATH1,KLMA_70317,SGA1
GO:0008270	zinc ion binding	168	30	19.54	0.00958	YHC1,ZTA1,GSM1,HST2,ERT1,KLMA_20292,RDS2,mlo2,SIP4,KLMA_30395,TAD2,KLMA_30428,KLMA_30533,APN1,OAF1,GAT2,adh,BDH2,CAR1,SFA1,KLMA_50329,GUD1,ETP1,SOR1,KLMA_70242,SAD1,KLMA_80008,NCE103,ADH3,ADH6
GO:0004497	monooxygenase activity	17	6	1.98	0.00962	DIT2,yxeK,YUC8,fmo1,KLMA_30604

Table S5. KEGG mapper analysis of differentially expressed genes for *Kmmig1* and the parental strain of *K. marxianus*

KEGG Mapper analysis of down-regulated DEGs

No	Code	Pathway	Genes number	Gene name
1	kmx01100	Metabolic pathways	100	APA2, HIS4, SAM2, ACO2A, PRS5, GPM3, HPT1, GUA1, PFK1, BIO2, ENO, FAU1, PGK, MET17, FUR1, AAH1, RAG2, URA1, TPS2, TSL1, GPM1, ADH4b, ADK1, MET13, CYS4, SHM2, ERG3, GAL7, GAL10, GAL1, CYS3, CYP707A7, ADE2, YPR1, ERG9, PHO3, HAM1, PGM2, GSH1, PHS1, RNR2, ERG1, MEU1, KLMA_30226, GSY2, SUR2, SER3, PAN5, ERG6, SAH1, DUG1, ADE5, GUS1, ADH1, dsd1, HEM13, TPI1, LCB5, GAP1, ADH2, RIB7, FBA1, ALD5, HMG1, DPM1, MET5, FAS1, GUK1, SHM1, LEU1, IMD4, YJU3, PDX3, SUR4, ADE6, ERG25, MET10, ACS2, URA2, PDC1, ADE3, MDH1, PYK1, LEU4, UGP1, RAG5, cyp524A1, ERG13, PFK2, URA7, RNR1, RHR2, FAS2, MET16, HEM14, MIS1, GAP3, MET3, TPS1, MET6
2	kmx01110	Biosynthesis of secondary metabolites	52	HIS4, LPP1, SAM2, PRS5, GPD1, GPM3, HPT1, PFK1, ENO, PGK, MET17, RAG2, GPM1, ADH4b, ADK1, SHM2, ERG3, GAL10, CYP707A7, ADE2, ERG9, PGM2, PHS1, ERG1, PAN5, ERG6, ADE5, GUS1, ADH1, HEM13, TPI1, GAP1, ADH2, FBA1, ALD5, HMG1, SHM1, LEU1, IMD4, SUR4, ADE6, ACS2, PDC1, MDH1, PYK1, LEU4, RAG5, ERG13, PFK2, HEM14, GAP3, MET6
3	kmx01130	Biosynthesis of antibiotics	43	ACO2a, PRS5, GPM3, PFK1, ENO, PGK, MET17, RAG2, GPM1, ADH4b, ADK1, CYS4, SHM2, ERG3, GAL10, CYS3, CYP707A7, ERG9, PGM2, ERG1, SER3, ERG6, ADE5, ADH1, TPI1, GAP1, ADH2, FBA1, ALD5, HMG1, SHM1, ADE6, ERG25, ACS2, MDH1, PYK1, UGP1, RAG5, cyp524A1, ERG13, PFK2, GAP3, MET3
4	kmx03008	Ribosome biogenesis in eukaryotes	31	NOP1, GSP1, UTP5, NOG1, UTP13, UTP15, NOP58, CBF5, UTP8, MPP10, NAN1, NOB1, MEX67, PWP2, MDN1, UTP10, GAR1, IMP4, NMD3, UTP21, MTR2, BMS1, UTP6, UTP18, NOP56, UTP4, NUG1, DIP2, IMP3, KRE33, NOP4
5	kmx01230	Biosynthesis of amino acids	24	HIS4, SAM2, ACO2a, PRS5, GPM3, PFK1, ENO, PGK, MET17, GPM1, CYS4, SHM2, CYS3, SER3, TPI1, GAP1, FBA1, SHM1, LEU1, PYK1, LEU4, PFK2, GAP3, MET6
6	kmx01200	Carbon metabolism	21	PRS5, GPM3, PFK1, ENO, PGK, MET17, RAG2, GPM1, MET13, SHM2, SER3, TPI1, GAP1, FBA1, SHM1, ACS2, MDH1, PYK1, RAG5,PFK2, GAP3
7	kmx00010	Glycolysis / Gluconeogenesis	21	GPM3, PFK1, ENO, PGK, RAG2, GPM1, ADH4, GAL10, PGM2, ADH1, TPI1, GAP1, ADH2, FBA1, ALD5, ACS2, PDC1, PYK1, RAG5, PFK2, GAP3

No	Code	Pathway	Genes number	Gene name
8	kmx03010	Ribosome	19	RPL37a, RPL17B, RPL24, RPS2, KLMA_20355, RLP7, RPL22A, RPS3, RPL5, RPL3, RPL15B, RPL10A, RPS14, RPL2, KLMA_60069, KLMA_60313, RPL19B, RLP24, RPL8B
9	kmx00230	Purine metabolism	17	APA2, PRS5, HPT1, GUA1, AAH1, ADK1, ADE2, HAM1, PGM2, RNR2, ADE5, GUK1, IMD4, ADE6, PYK1, RNR1, MET3
10	kmx03013	RNA transport	13	GSP1, TIF1, PAB1, MEX67, TIF32, NUP116, NMD3, MTR2, TIF4632, FUN12, HSL7, TIF3, NIP1
11	kmx00680	Methane metabolism	10	GPM3, PFK1, ENO, GPM1, SHM2, SER3, FBA1, SHM1, ACS2, PFK2
12	kmx00500	Starch and sucrose metabolism	9	RAG2, TPS2, TSL1, PGM2, GSY2, UGP1, RAG5, BGL2, TPS1
13	kmx00270	Cysteine and methionine metabolism	9	SAM2, MET17, CYS4, CYS3, GSH1, MEU1, SAH1, MDH1, MET6
14	kmx04011	MAPK signaling pathway	8	SH3, GPD1, HSL1, CLN2, KSS1, MCM1, HSL7, KLMA_80303
15	kmx00052	Galactose metabolism	8	PFK1, GAL7, GAL10, GAL1, PGM2, UGP1, RAG5, PFK2
16	kmx03020	RNA polymerase	8	RPA49, RPC37, RPC82, RPA135, RPC40, KLMA_50426, KLMA_50502, RPA190, RPB1
17	kmx04111	Cell cycle	8	TAH11, HSL1, CLN2, KLMA_20481, MCM1, LTE1, HSL7, PCL1
18	kmx00260	Glycine, serine and threonine metabolism	7	GPM3, GPM1, CYS4, SHM2, CYS3, SER3, SHM1
19	kmx00100	Steroid biosynthesis	7	ERG3, CYP707A7, ERG9, ERG1, ERG6, ERG25, CYP524A1
20	kmx00520	Amino sugar and nucleotide sugar metabolism	7	RAG2, GAL7, GAL10, GAL1, PGM2, UGP1, RAG5
21	kmx00030	Pentose phosphate pathway	6	PRS5, PFK1, RAG2, PGM2, FBA1, PFK2
22	kmx00670	One carbon pool by folate	6	FAU1, MET13, SHM2, SHM1 ADE3, MIS1
23	kmx00920	Sulfur metabolism	6	APA2, MET17, MET5, MET10, MET16, MET3
24	kmx00970	Aminoacyl-tRNA biosynthesis	6	MES1, MSW1, GUS1, VAS1, CDC60, ILS1
25	kmx00620	Pyruvate metabolism	6	ALD5, DLD1, ACS2, MDH1, PYK1, LEU4
26	kmx01212	Fatty acid metabolism	6	OLE1, KLMA_20392, PHS1, FAS1, SUR4, FAS2
27	kmx00240	Pyrimidine metabolism	6	FUR1, URA1, RNR2, URA2, URA7, RNR1

No	Code	Pathway	Genes number	Gene name
28	kmx03018	RNA degradation	6	PFK1, ENO, PAB1, MTR4, PFK2, RRP42
29	kmx00561	Glycerolipid metabolism	5	LPP1, YPR1, ALD5, YJU3, RHR2
30	kmx00051	Fructose and mannose metabolism	5	PFK1, PFK2, RAG5, TPI1, FBA1
31	kmx00450	Selenocompound metabolism	4	MES1, CYS3, MET3, MET6
32	kmx00480	Glutathione metabolism	4	GSH1, RNR2, DUG1, RNR1
33	kmx00071	Fatty acid degradation	4	ADH4b, ADH1, ADH2, ALD5
34	kmx04113	Meiosis	4	TAH11, CLN2, KHT2, RAG1
35	kmx00630	Glyoxylate and dicarboxylate metabolism	4	SHM1, SHM2, ACS2, MDH1
36	kmx00600	Sphingolipid metabolism	4	SUR2, dsd1, LCB5, KLMA_80180
37	kmx01040	Biosynthesis of unsaturated fatty acids	4	OLE1, KLMA_20392, PHS1, SUR4
38	kmx00860	Porphyrin and chlorophyll metabolism	3	GUS1, HEM13, HEM14
39	kmx01210	2-Oxocarboxylic acid metabolism	3	ACO2a, LEU1, LEU4
40	kmx00350	Tyrosine metabolism	3	ADH1, ADH2, ADH4b
41	kmx03015	mRNA surveillance pathway	3	PAB1, MEX67, MTR2
42	kmx00190	Oxidative phosphorylation	2	KLMA_30226, IPP1
43	kmx00740	Riboflavin metabolism	2	PHO3, RIB7
44	kmx00340	Histidine metabolism	2	HIS4, ALD5
45	kmx00564	Glycerophospholipid metabolism	2	LPP1, GPD1
46	kmx00290	Valine, leucine and isoleucine biosynthesis	2	LEU1, LEU4
47	kmx00280	Valine, leucine and isoleucine degradation	2	ALD5, ERG13
48	kmx03040	Spliceosome	2	RSE1, PRP43
49	kmx00730	Thiamine metabolism	2	ADK1, PHO3
50	kmx00062	Fatty acid elongation	2	PHS1, SUR4

No	Code	Pathway	Genes number	Gene name
51	kmx00061	Fatty acid biosynthesis	2	FAS1, FAS2
52	kmx00900	Terpenoid backbone biosynthesis	2	HMG1, ERG13
53	kmx00410	beta-Alanine metabolism	2	FMS1, ALD5
54	kmx00909	Sesquiterpenoid and triterpenoid biosynthesis	2	ERG9, ERG1
55	kmx00330	Arginine and proline metabolism	2	FMS1, ALD5
56	kmx00460	Cyanoamino acid metabolism	2	SHM1, SHM2
57	kmx04139	Mitophagy	2	UBP3, BRE5
58	kmx00310	Lysine degradation	1	ALD5
59	kmx00300	Lysine biosynthesis	1	ACO2a
60	kmx00380	Tryptophan metabolism	1	ALD5
61	kmx00780	Biotin metabolism	1	BIO2
62	kmx00640	Propanoate metabolism	1	ACS2
63	kmx03440	Homologous recombination	1	RAD54
64	kmx00770	Pantothenate and CoA biosynthesis	1	PAN5
65	kmx00650	Butanoate metabolism	1	ERG13
66	kmx03430	Mismatch repair	1	EXO1
67	kmx00250	Alanine, aspartate and glutamate metabolism	1	URA2
68	kmx03060	Protein export	1	IMP2
69	kmx04933	AGE-RAGE signaling pathway in diabetic complications	1	KSS1
70	kmx04141	Protein processing in endoplasmic reticulum	1	SFB3
71	kmx00072	Synthesis and degradation of ketone bodies	1	ERG13
72	kmx00750	Vitamin B6 metabolism	1	PDX3

No	Code	Pathway	Genes number	Gene name
73	kmx00261	Monobactam biosynthesis	1	MET3
74	kmx00562	Inositol phosphate metabolism	1	TPI1
75	kmx00020	Citrate cycle (TCA cycle)	1	MDH1
76	kmx00510	N-Glycan biosynthesis	1	DPM1
77	kmx00040	Pentose and glucuronate interconversions	1	UGP1
78	kmx00053	Ascorbate and aldarate metabolism	1	ALD5

KEGG Mapper analysis of up-regulated DEGs

No	Code	Pathway	Genes number	Gene name
1	kmx01100	Metabolic pathways	80	KLMA_10012, CHA1, ECM38, HEM4, PGU1, INU1, GLY1, ECM31, DAL3, KLMA_20057, CIT1, ppr1, HST2, POT1, GPD2, AGX1, FAB1, ARO10, CTS2, ALD2, GDH2, KLMA_30011, CYB2, YPR1, KLMA_30124, KLMA_30282, ACO2b, KLMA_30365, DPL1, GAD1, ACS1, TH113, OXP1, LYS9, MDH3, UGA1, SPO14, KLMA_40359, LYS1, MDH2, IDP1, NPY1, THI4, ALD4, CAR1, ARO8, DAK1, CAR2, sdh, GLT1, SFA1, KLMA_50451, INO1, PUT1, GUD1, ACAD11, KLMA_60039, TDA10, TES1, gabD, KLMA_60206, ETR1, KLMA_60327, ARO9, FBP1, YMR1, ATH1, ICL1, ALG12, FAD1, ICL2, CIT3, lag1, KLMA_80136, SGA1, ADH3, ARO7, ADH6, GUT1
2	kmx01110	Biosynthesis of secondary metabolites	45	CHA1, HEM4, GLY1, ECM31, CIT1, ppr1, POT1, POX1, GPD2, AGX1, ALD2, KLMA_30011, KLMA_30124, ACO2b, DPP1, GAD1, ACS1, LYS9, MDH3, SPO14, LYS1, MDH2, IDP1, ALD4, CAR1, ARO8, CAR2, GLT1, SFA1, CIT1, PUT1, dpp1, ACAD11, TDA10, TES1, KLMA_60327, ARO9, FBP1, ICL1, FAD1, ICL2, CIT3, ADH3, ARO7, ADH6
3	kmx01130	Biosynthesis of antibiotics	33	CHA1, GLY1, CIT1, POT1, GPD2, AGX1, RAM1, KLMA_30124, ACO2b, ACS1, LYS9, MDH3, LYS1, MDH2, IDP1, ALD4, CAR1, ARO8, CAR2, GLT1, SFA1, CTT1, KLMA_50451, INO1, PUT1, ACAD11, TDA10, ARO9, FBP1, CIT3, ADH3, ARO7, ADH6
4	kmx01200	Carbon metabolism	19	CHA1, CIT1, GPD2, AGX1, KLMA_30124, ACO2b, ACS1, MDH3, MDH2, IDP1, DAK1, SFA1, CTT1, ACAD11, TDA10, FBP1, ICL1, ICL2, CIT3
5	kmx04138	Autophagy	18	ATG12, ATG27, YKT6, ATG17, RIM15, ATG14, ATG1, VTI1, KLMA_30673, ELM1, ATG4, PHO85, ATG3, YMR1, KLMA_70233, ATG9, VAM3, ATG8
6	kmx04011	MAPK signaling pathway	15	STE3, FUS3, STE4, PTP2, MSB2, CTT1, BAR1, GPA1, KLMA_60356, KLMA_60404, SST2, KLMA_70118, TEC1, SSK1, MSG5
7	kmx01230	Biosynthesis of amino acids	13	CHA1, GLY1, CIT1, GPD2, ACO2b, LYS9, LYS1, IDP1, CAR1, ARO8, GLT1, CIT3, ARO7
8	kmx04113	Meiosis	13	CDC7, SSP1, KLMA_10523, DMC1, RIM15, SPS4, ZIP1, IME2, REC8, RME1, HOP1, APC2, APC11
9	kmx04146	Peroxisome	12	YAT1, ECI1, PXA1, POT1, POX1, AGX1, CAT2, IDP1, PXA2, NPY1, CTT1, SPS19
10	kmx00630	Glyoxylate and dicarboxylate metabolism	11	CIT1, AGX1, ACO2b, ACS1, MDH3, MDH2, CTT1, TDA10, ICL1, ICL2, CIT3

No	Code	Pathway	Genes number	Gene name
11	kmx03040	Spliceosome	9	KLMA_10570, SMD1, CUS1, SYF2, SNU23, KLMA_40041, LEA1, PRP45, SAD1
12	kmx00071	Fatty acid degradation	8	ECI1, DIT2, POT1, POX1, ALD4, SFA1, ACAD11, ADH3
13	kmx00010	Glycolysis / Gluconeogenesis	8	GPD2, ALD2, ACS1, ALD4, SFA1, FBP1, ADH3, ADH6
14	kmx00561	Glycerolipid metabolism	8	YPR1, DPP1, ALD4, DAK1, dpp1, TDA10, ADH6, GUT1
15	kmx04144	Endocytosis	8	VTA1, IST1, VPS60, SNX4, SPO14, KLMA_50160, APS2, SNF8
16	kmx00330	Arginine and proline metabolism	8	ppr1, KLMA_20834, KLMA_40359, ALD4, CAR1, CAR2, PUT1, KLMA_80318
17	kmx00020	Citrate cycle (TCA cycle)	7	CIT1, KLMA_30124, ACO2b, MDH3, MDH2, IDP1, CIT3
18	kmx00260	Glycine, serine and threonine metabolism	7	CHA1, GLY1, DSD1, AGX1, sdh, TDA10, KLMA_60327
19	kmx00350	Tyrosine metabolism	7	ALD2, ARO8, SFA1, gabD, KLMA_60327, ARO9, ADH3
20	kmx00360	Phenylalanine metabolism	7	ARO10, ALD2, KLMA_20834, ARO8, KLMA_60327, ARO9, KLMA_80318
21	kmx04136	Autophagy	6	ATG12, ATG1, ATG4, ATG3, ATG9, ATG8
22	kmx00620	Pyruvate metabolism	6	CYB2, GLO4, ACS1, MDH3, MDH2, ALD4
23	kmx04120	Ubiquitin mediated proteolysis	6	HRD1, AOS1, UBC12, APC2, APC11, UBA3
24	kmx00760	Nicotinate and nicotinamide metabolism	6	URH1, HST2, KLMA_30282, SDT1, NPY1, gabD
25	kmx00380	Tryptophan metabolism	6	DIT2, KLMA_20834, ALD4, ARO8, CTT1, KLMA_80318
26	kmx00410	beta-Alanine metabolism	6	ALD2, GAD1, UGA1, ALD4, ACAD11, KLMA_60327
27	kmx00250	Alanine, aspartate and glutamate metabolism	6	AGX1, GDH2, GAD1, UGA1, GLT1, gabD
28	kmx01210	2-Oxocarboxylic acid metabolism	5	CIT1, ACO2b, IDP1, ARO8, CIT3
29	kmx03420	Nucleotide excision repair	5	RAD26, SRS2, DPB3, KIN28, RAD1
30	kmx00564	Glycerophospholipid metabolism	5	PLB, DPP1, SPO14, GDE1, dpp1
31	kmx04139	Mitophagy	5	MMM1, ATG1, ATG32, SSK1, ATG8
32	kmx00230	Purine metabolism	5	DAL3, KLMA_20057, GUD1, KLMA_60206, PDE1
33	kmx00680	Methane metabolism	5	AGX1, ACS1, DAK1, SFA1, FBP1

No	Code	Pathway	Genes number	Gene name
34	kmx04141	Protein processing in endoplasmic reticulum	4	HRD1, PNG1, HSP26, OTU1
35	kmx00480	Glutathione metabolism	4	KLMA_10012, ECM38, OXP1, IDP1
36	kmx00051	Fructose and mannose metabolism	4	SOU2, SOU1, DAK1, FBP1
37	kmx04130	SNARE interactions in vesicular transport	4	YKT6, VTI1, KLMA_30673, VAM3
38	kmx00640	Propanoate metabolism	4	ACS1, UGA1, ACAD11, PDH1
39	kmx04111	Cell cycle	4	CDC7, APC2, APC11, PHO85
40	kmx01212	Fatty acid metabolism	4	POT1, POX1, ACAD11, ETR1
41	kmx00500	Starch and sucrose metabolism	4	INU1, KLMA_30011, ATH1, SGA1
42	kmx04213	Longevity regulating pathway	4	HST2, RIM15, CTT1, HSP78
43	kmx00280	Valine, leucine and isoleucine degradation	4	POT1, UGA1, ALD4, ACAD11
44	kmx00562	Inositol phosphate metabolism	4	MIOX5, FAB1, INO1, YMR1
45	kmx00270	Cysteine and methionine metabolism	4	CHA1, MDH3, MDH2, ARO8
46	kmx00650	Butanoate metabolism	4	GAD1, UGA1, BDH2, gabD
47	kmx00310	Lysine degradation	4	LYS9, LYS1, ALD4, gabD
48	kmx00910	Nitrogen metabolism	3	GDH2, GLT1, NCE103
49	kmx00400	Phenylalanine, tyrosine and tryptophan biosynthesis	3	ARO8, ARO9, ARO7
50	kmx03410	Base excision repair	3	MAG1, APN1, DPB3
51	kmx00430	Taurine and hypotaurine metabolism	3	ECM38, GDH2, GAD1
52	kmx03430	Mismatch repair	3	MLH1, SRS2, MLH3
53	kmx03440	Homologous recombination	3	RAD55, MUS81, TEL1
54	kmx01040	Biosynthesis of unsaturated fatty acids	3	POT1, POX1, TES1
55	kmx02010	ABC transporters	3	PXA1, PDR5, PXA2

No	Code	Pathway	Genes number	Gene name
56	kmx00600	Sphingolipid metabolism	3	YDC1, DPL1, lag1
57	kmx00300	Lysine biosynthesis	3	LYS9, LYS1, ARO8
58	kmx04070	Phosphatidylinositol signaling system	3	FAB1, KLMA_40476, YMR1
59	kmx03030	DNA replication	2	RNH1, DPB3
60	kmx00062	Fatty acid elongation	2	TES1, ETR1
61	kmx00592	alpha-Linolenic acid metabolism	2	POT1, POX1
62	kmx00240	Pyrimidine metabolism	2	URH1, sdh
63	kmx00460	Cyanoamino acid metabolism	2	ECM38, KLMA_30011
64	kmx00340	Histidine metabolism	2	ALD2, ALD4
65	kmx00190	Oxidative phosphorylation	2	PMA1, KLMA_30124
66	kmx00040	Pentose and glucuronate interconversions	2	PGU1, ADH6
67	kmx00770	Pantothenate and CoA biosynthesis	2	ECM31, LYS5
68	kmx00053	Ascorbate and aldarate metabolism	2	MIOX5, ALD4
69	kmx00563	Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	2	KLMA_60039, KLMA_80136
70	kmx00520	Amino sugar and nucleotide sugar metabolism	2	CTS2, CHS1
71	kmx00730	Thiamine metabolism	2	THI13, THI4
72	kmx03022	Basal transcription factors	2	TFG2, KIN28
73	kmx00220	Arginine biosynthesis	2	GDH2, CAR1
74	kmx00030	Pentose phosphate pathway	1	FBP1
75	kmx00290	Valine, leucine and isoleucine biosynthesis	1	CHA1
76	kmx00860	Porphyrin and chlorophyll metabolism	1	HEM4
77	kmx00510	N-Glycan biosynthesis	1	ALG12

No	Code	Pathway	Genes number	Gene name
78	kmx00052	Galactose metabolism	1	INU1
79	kmx00130	Ubiquinone and other terpenoid-quinone biosynthesis	1	ARO8
80	kmx00740	Riboflavin metabolism	1	FAD1
81	kmx04122	Sulfur relay system	1	AHP1
82	kmx03450	Non-homologous end-joining	1	YKU80
83	kmx04392	Hippo signaling pathway	1	TEC1
84	kmx04145	Phagosome	1	FAB1
85	kmx03060	Protein export	1	IMP1
86	kmx03008	Ribosome biogenesis in eukaryotes	1	POP4
87	kmx00565	Ether lipid metabolism	1	SPO14
88	kmx00750	Vitamin B6 metabolism	1	KLMA_30365
89	kmx03013	RNA transport	1	POP4
90	kmx00311	Penicillin and cephalosporin biosynthesis	1	KLMA_50451
91	kmx04933	AGE-RAGE signaling pathway in diabetic complications	1	FUS3
92	kmx00900	Terpenoid backbone biosynthesis	1	RAM1
93	kmx00513	Various types of N-glycan biosynthesis	1	ALG12
94	kmx00052	Galactose metabolism	1	INU1
95	kmx03013	RNA transport	1	POP4
96	kmx00740	Riboflavin metabolism	1	FAD1