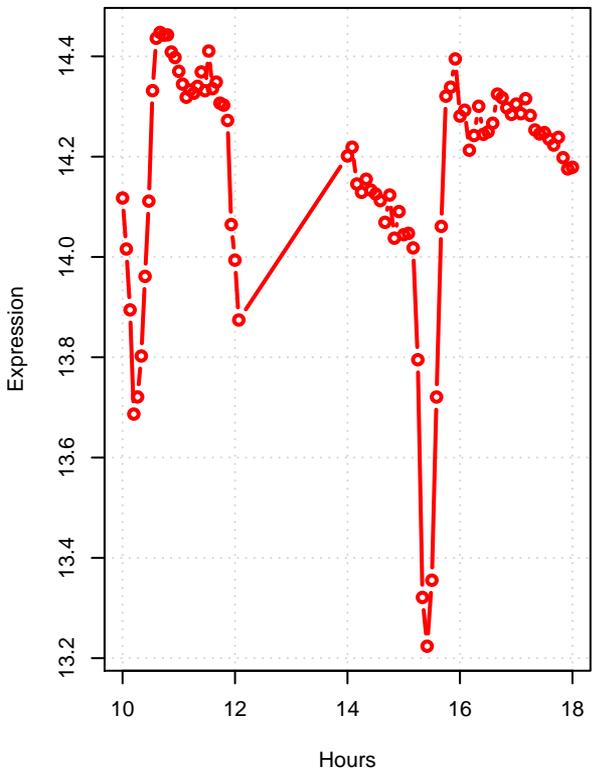


—⊖— ccTP81

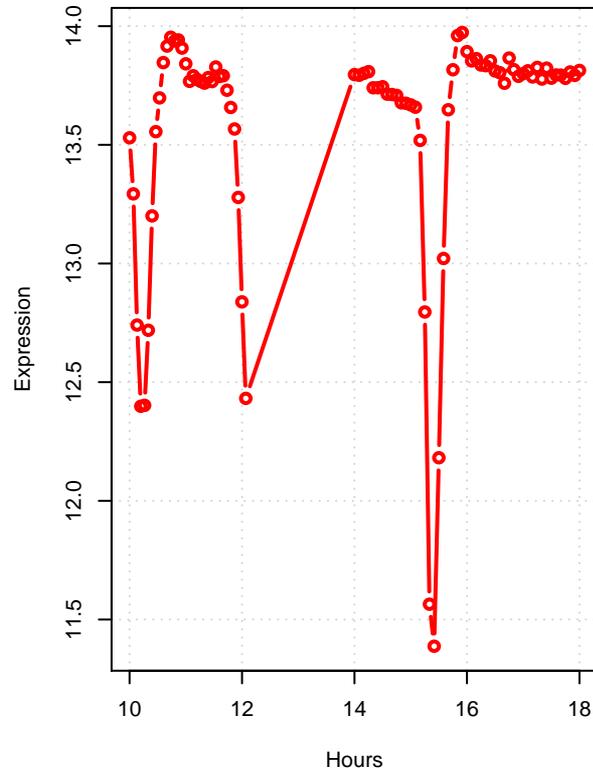
## 2-ketoglutarate dehydrogenase complex

# 2-ketoglutarate dehydrogenase complex

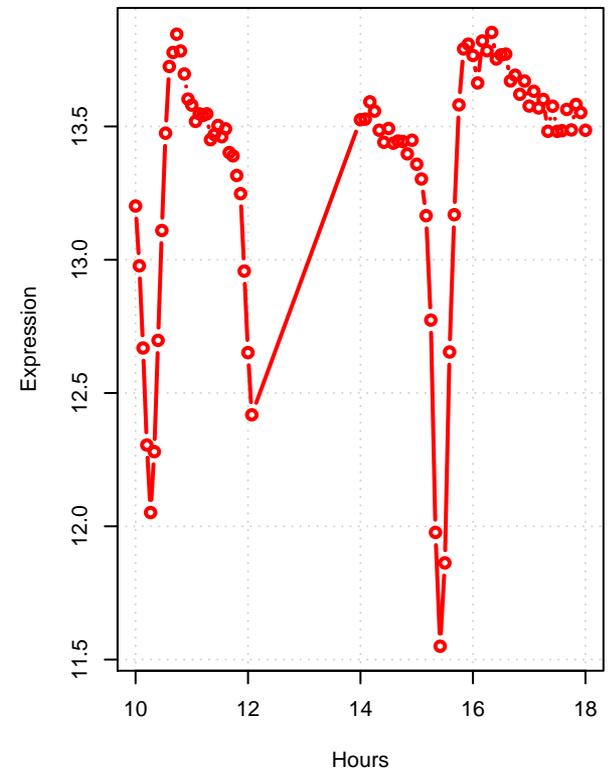
lpd1 YFL018C  
Dihydrolipoamide dehydrogenase



kgd2 YDR148C  
Dihydrolipoyl transsuccinylase

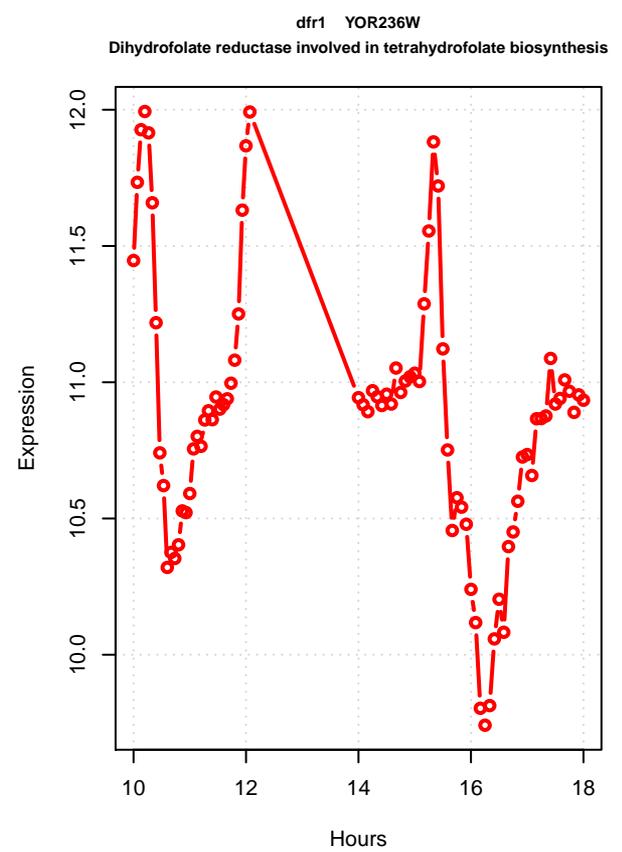
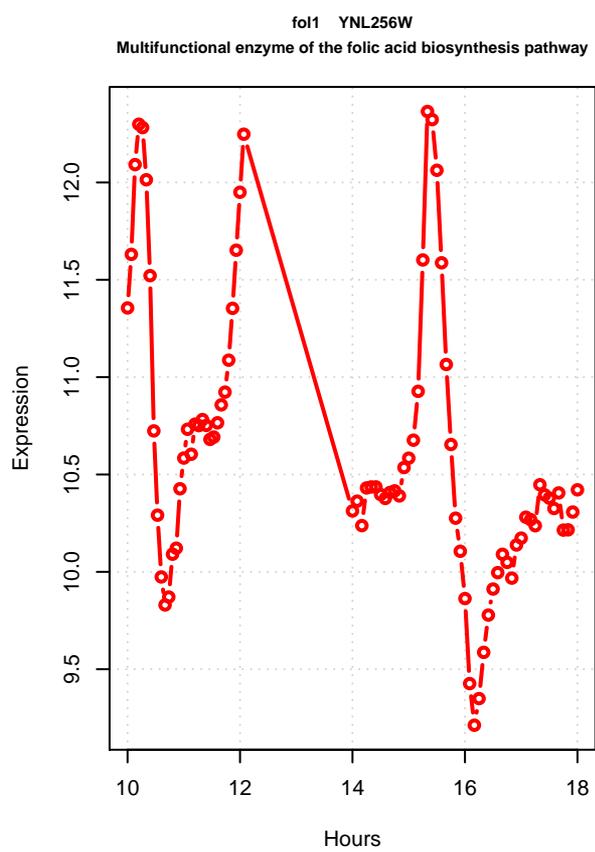
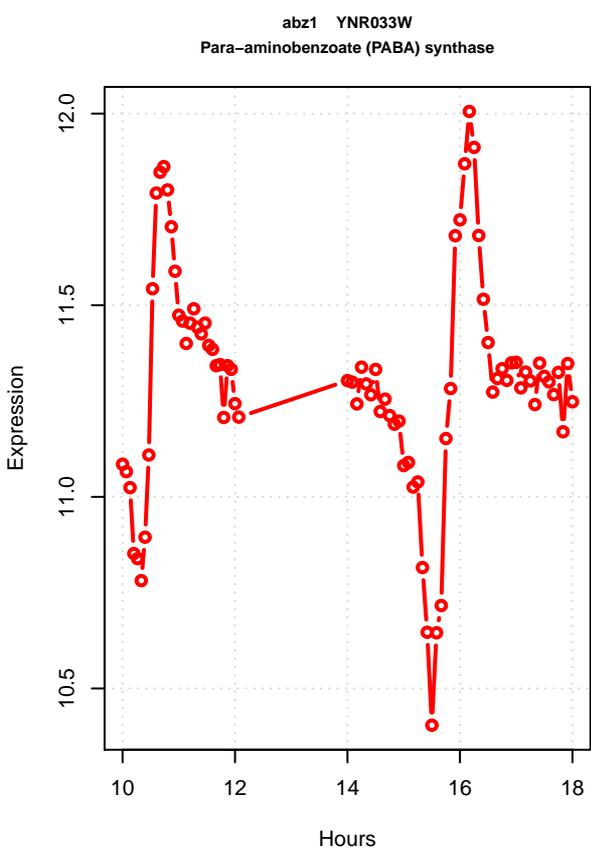
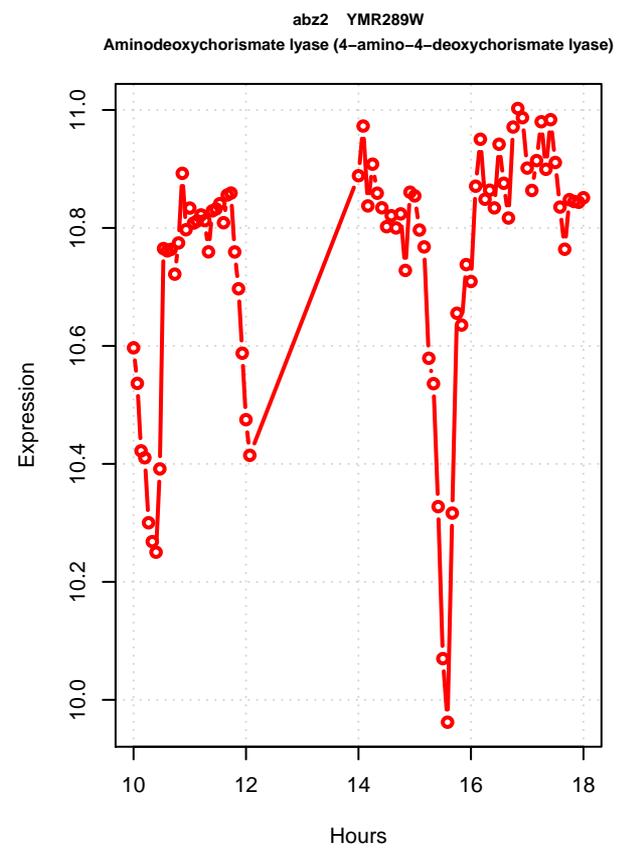
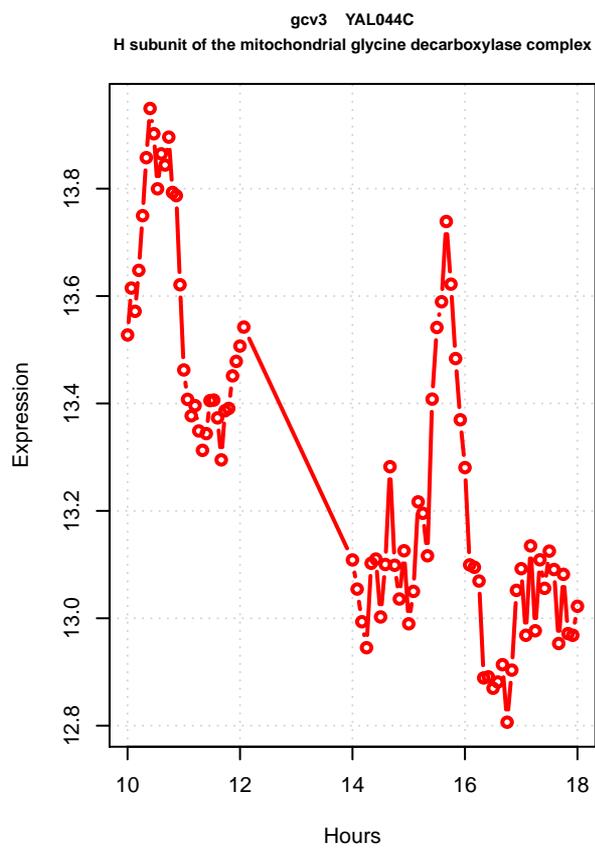
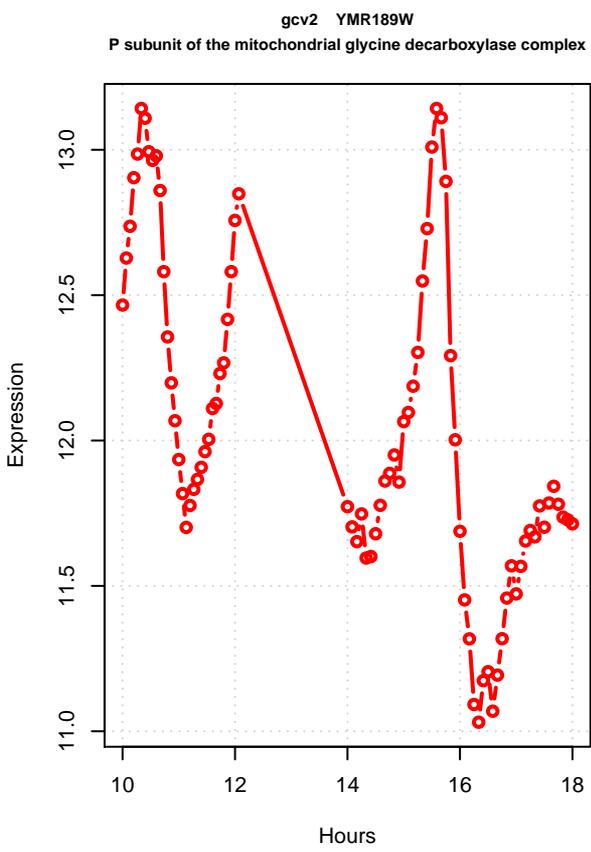
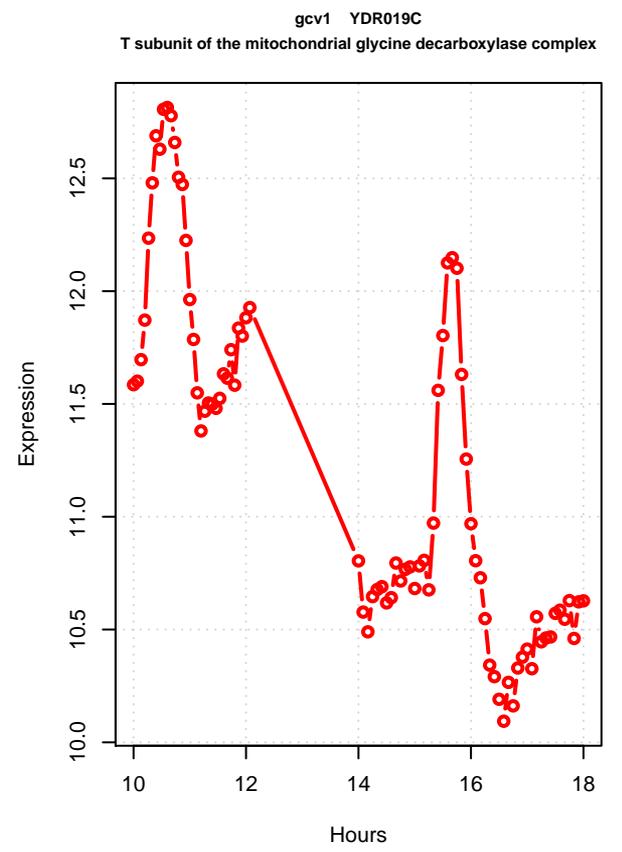
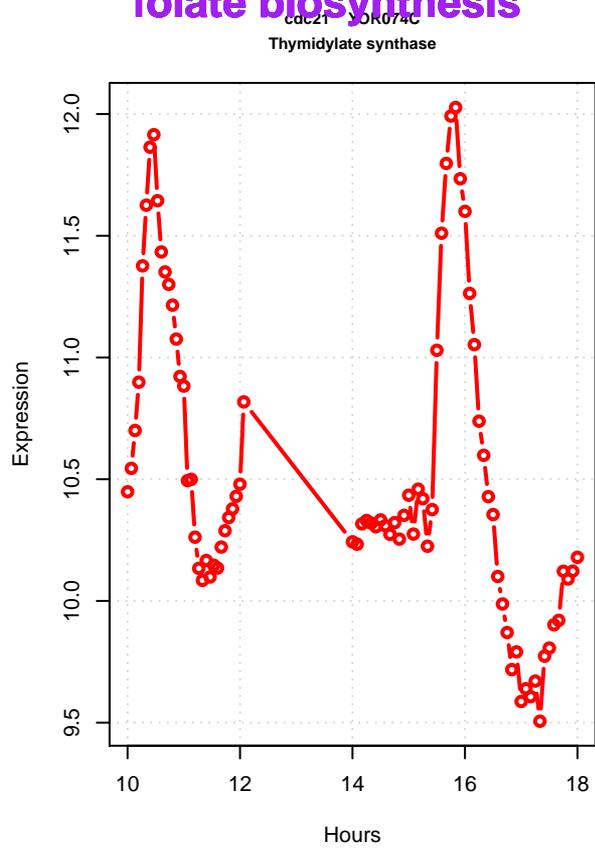
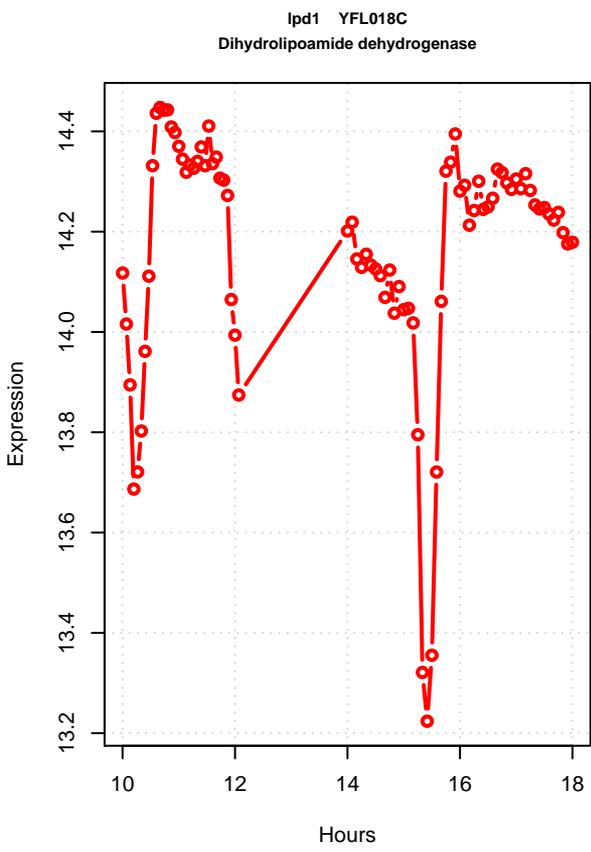


kgd1 YIL125W  
Subunit of the mitochondrial alpha-ketoglutarate dehydrogenase complex



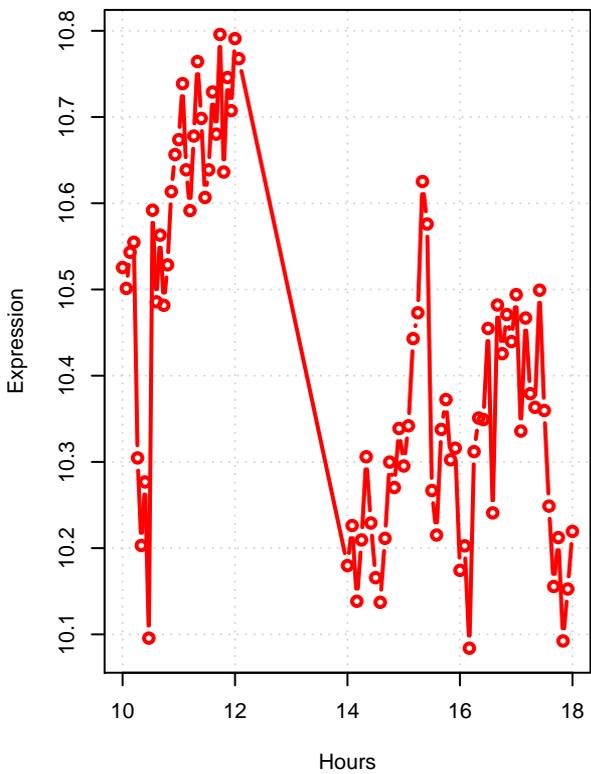
# folate biosynthesis

# folate biosynthesis

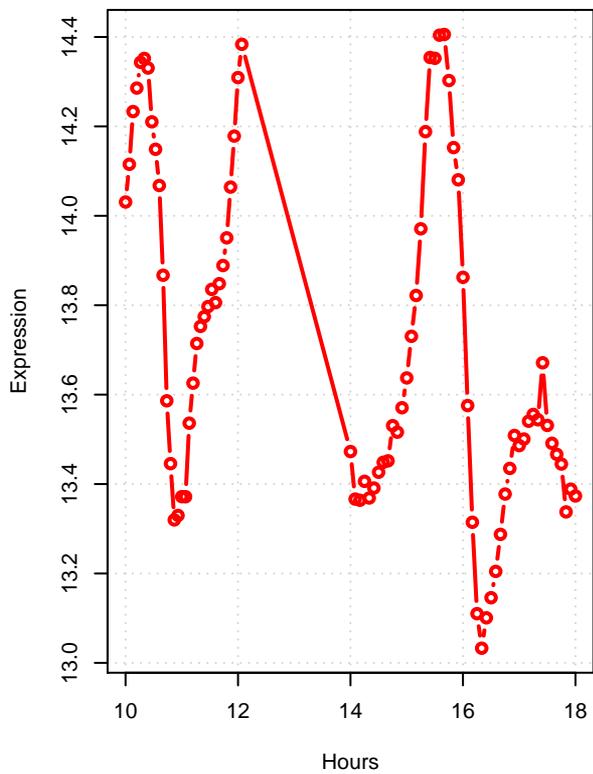


# folate biosynthesis

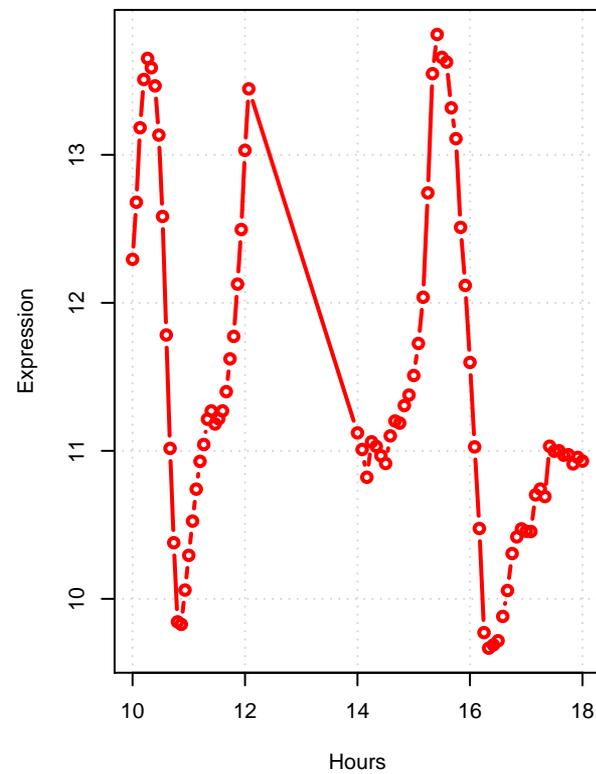
**fol3 YMR113W**  
Dihydrofolate synthetase, involved in folic acid biosynthesis



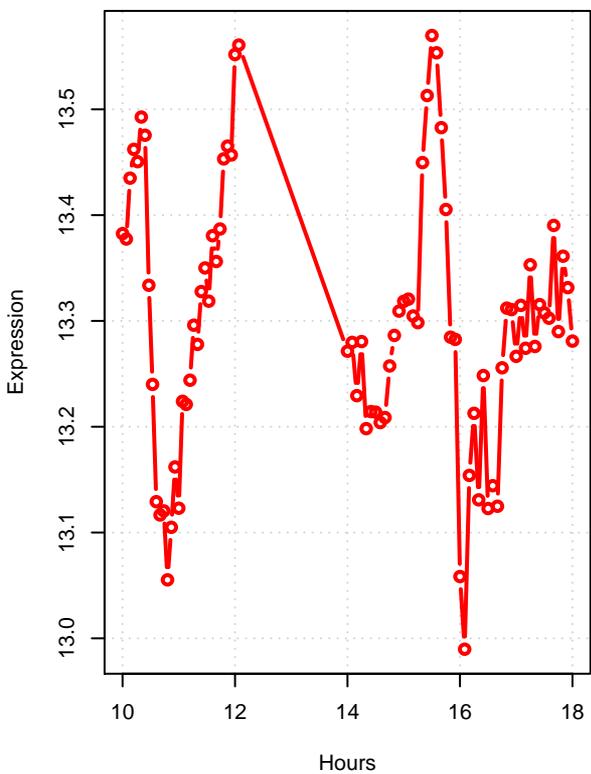
**ade3 YLR204W**  
Cytoplasmic trifunctional enzyme C1-tetrahydrofolate synthase



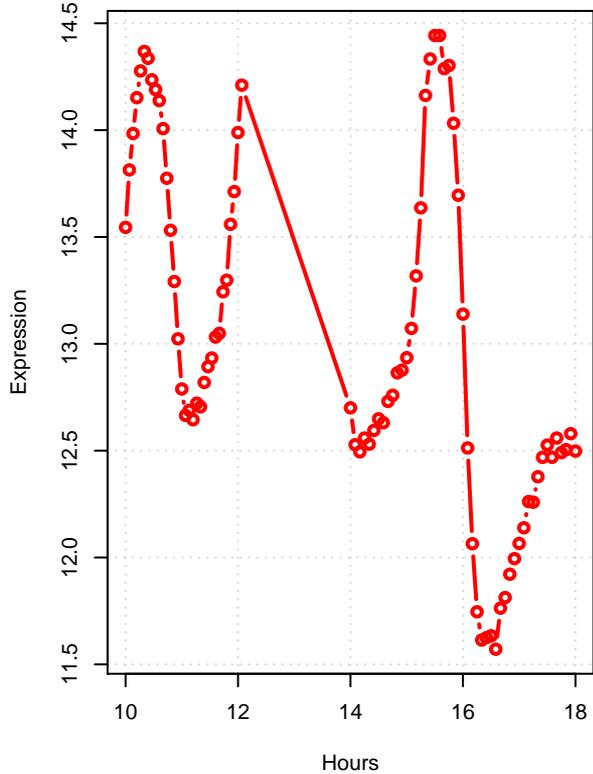
**mis1 YBR084W**  
Mitochondrial C1-tetrahydrofolate synthase



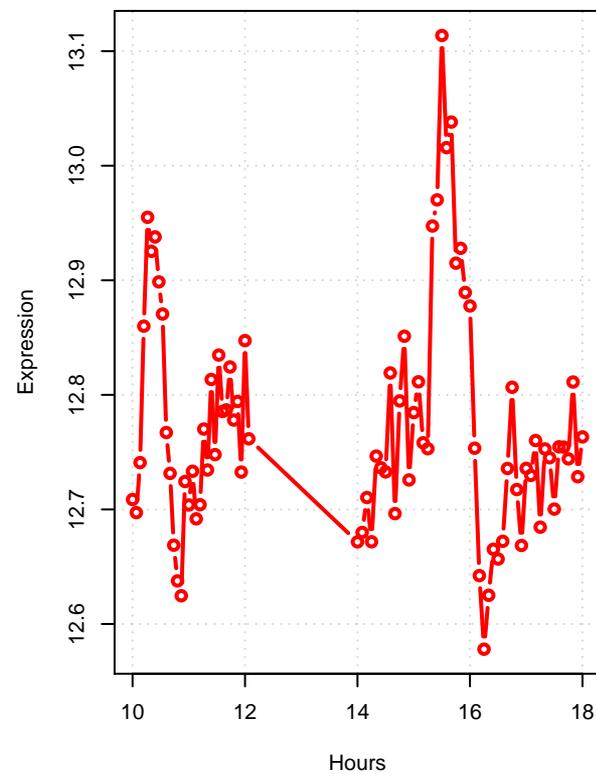
**shm1 YBR263W**  
Mitochondrial serine hydroxymethyltransferase



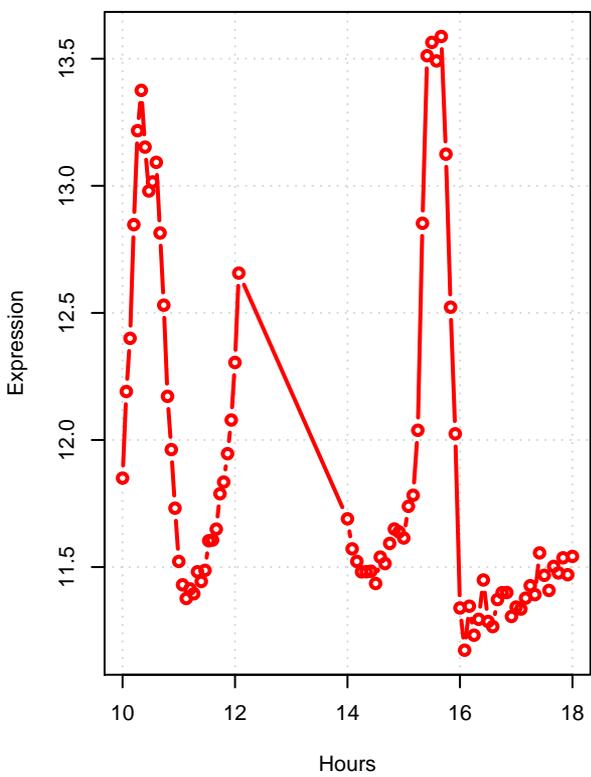
**shm2 YLR058C**  
Cytosolic serine hydroxymethyltransferase



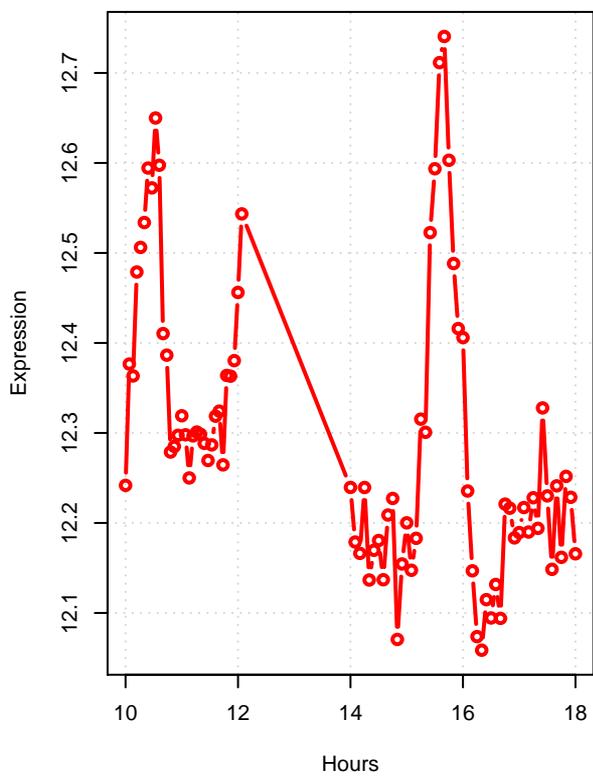
**fol2 YGR267C**  
GTP-cyclohydrolase I, catalyzes first step in folic acid biosynthesis



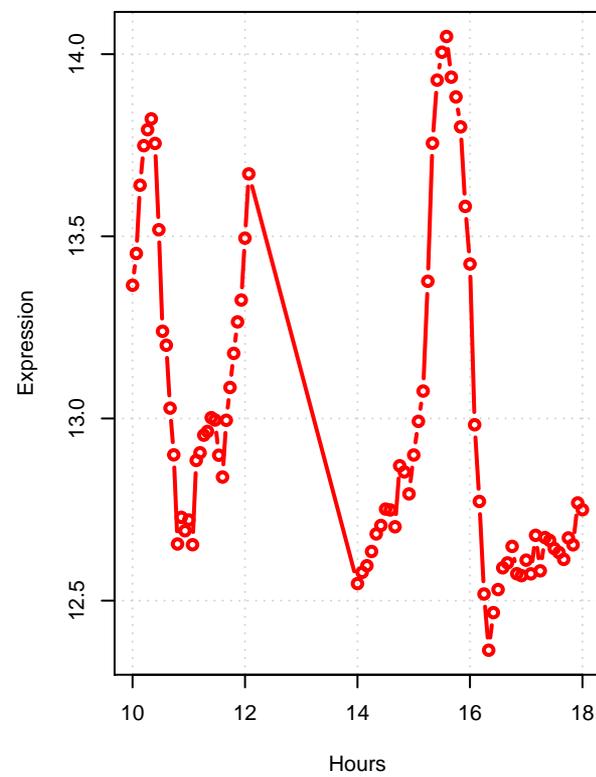
**mtd1 YKR080W**  
NAD-dependent 5,10-methylenetetrahydrofolate dehydrogenase



**met12 YPL023C**  
Protein with MTHFR activity in vitro

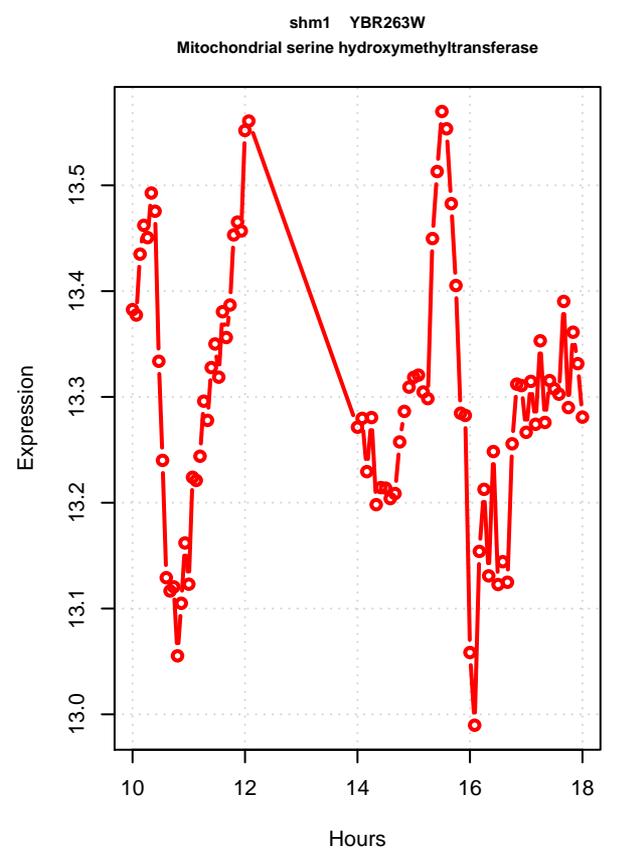
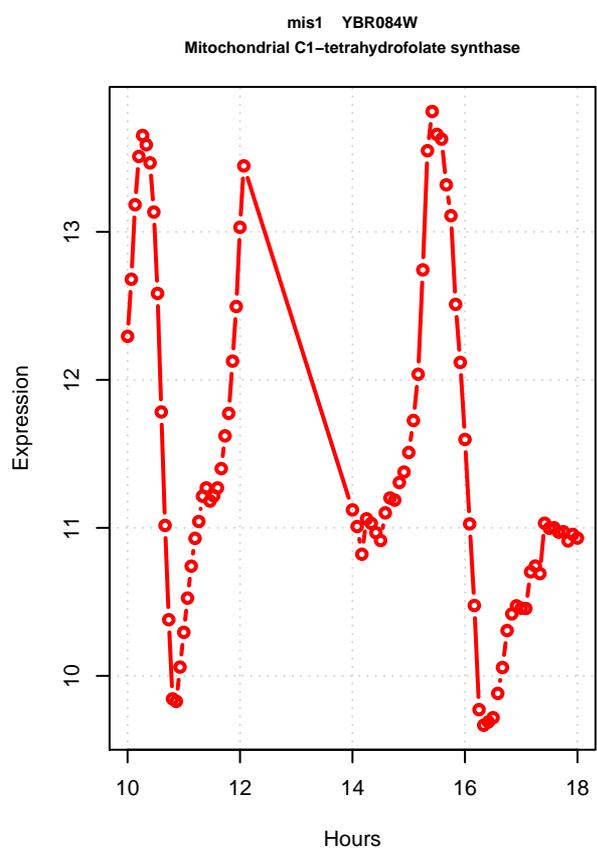
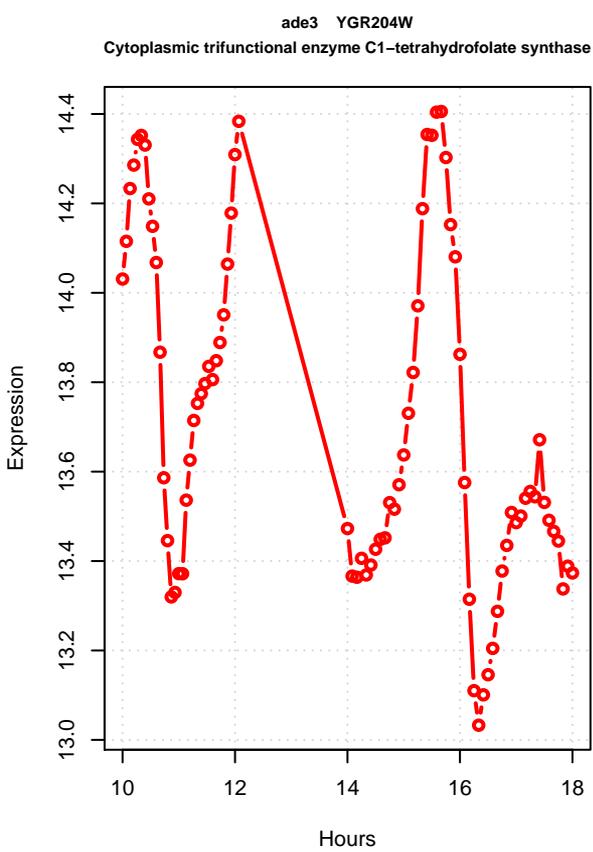
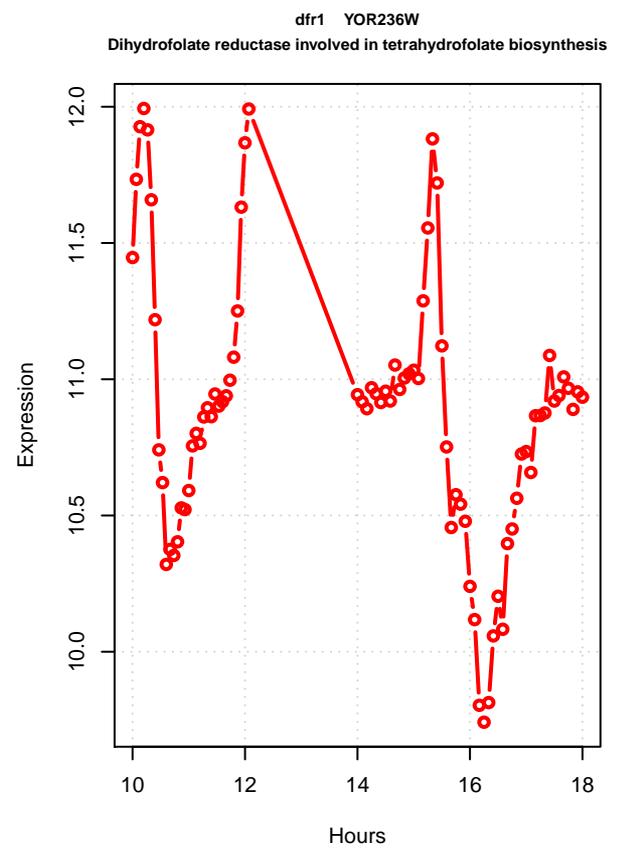
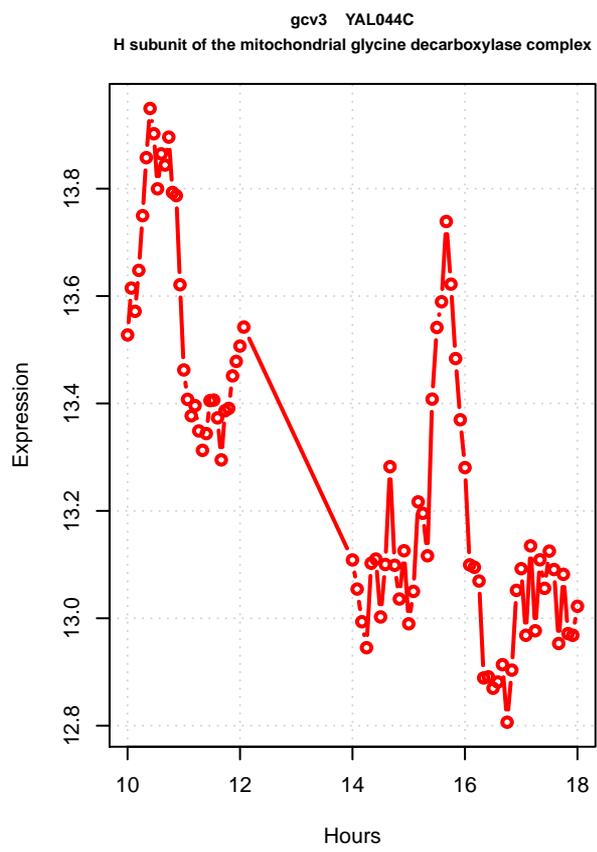
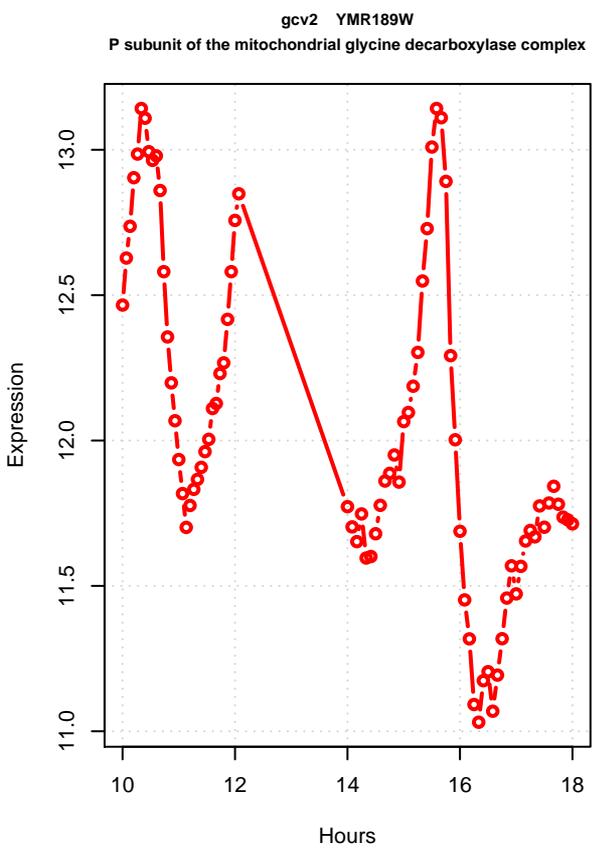
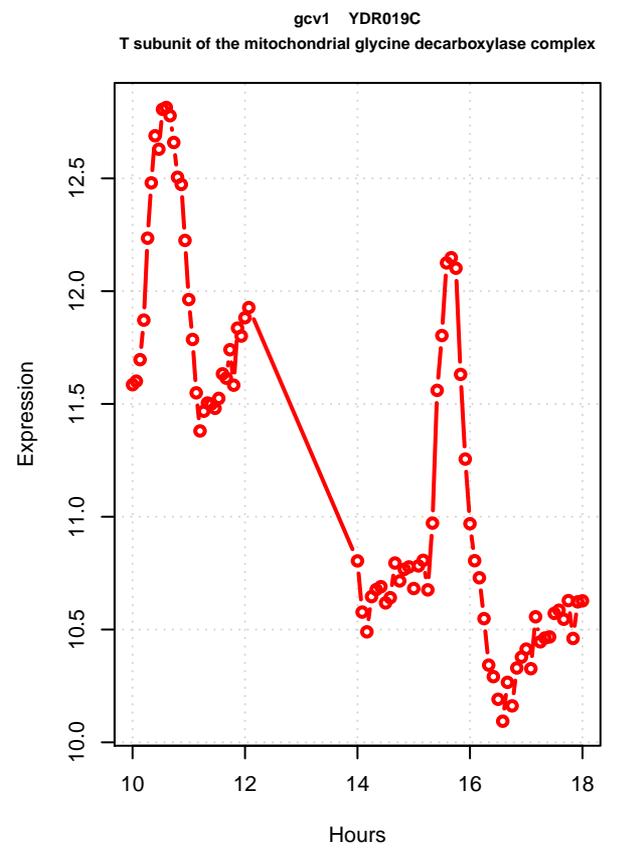
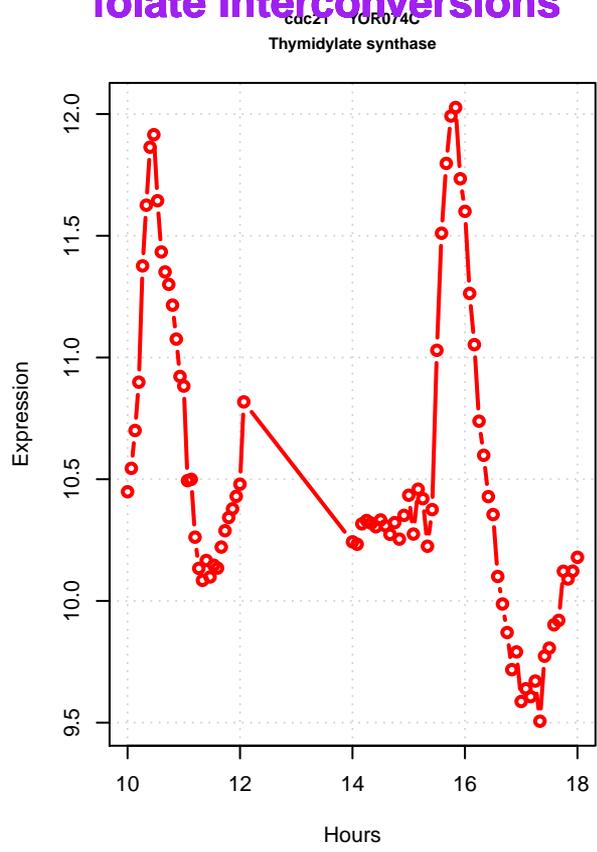
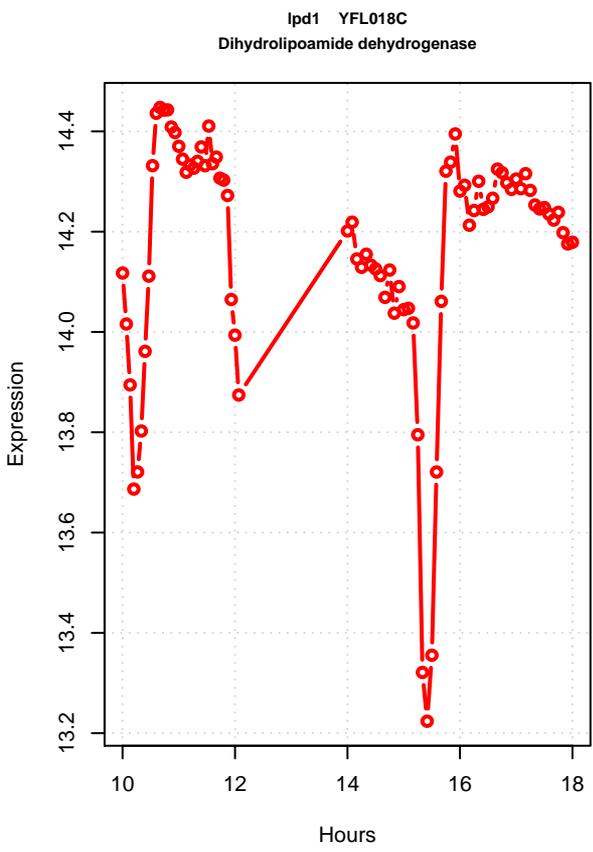


**met13 YGL125W**  
Major isozyme of methylenetetrahydrofolate reductase

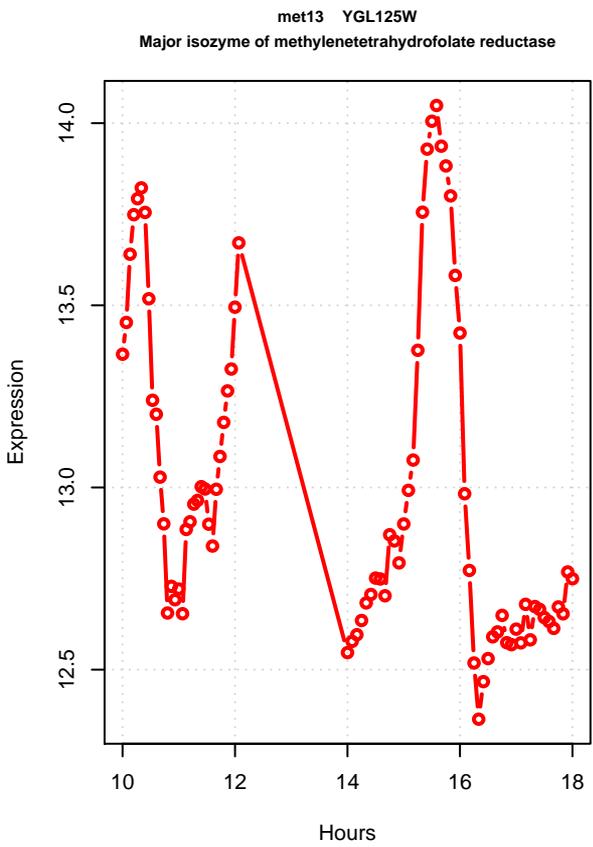
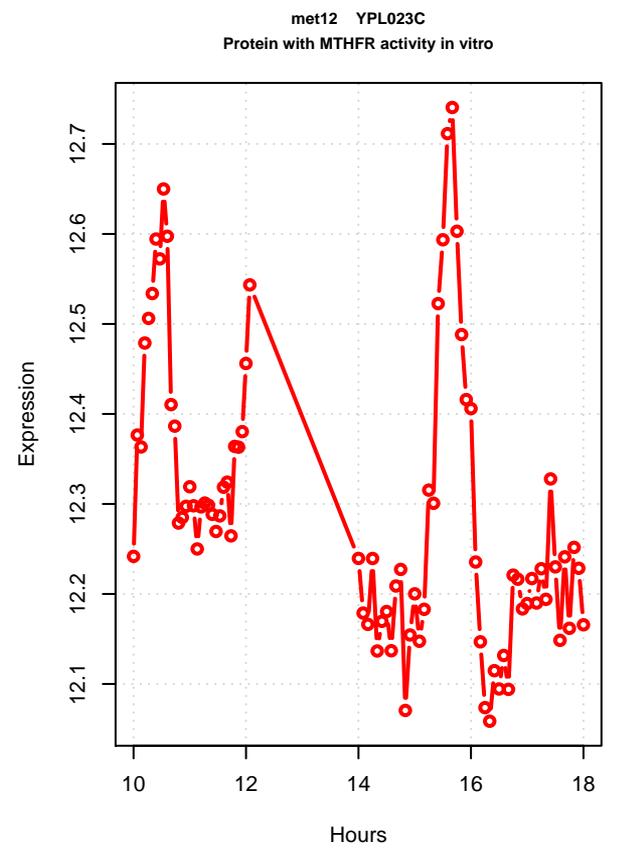
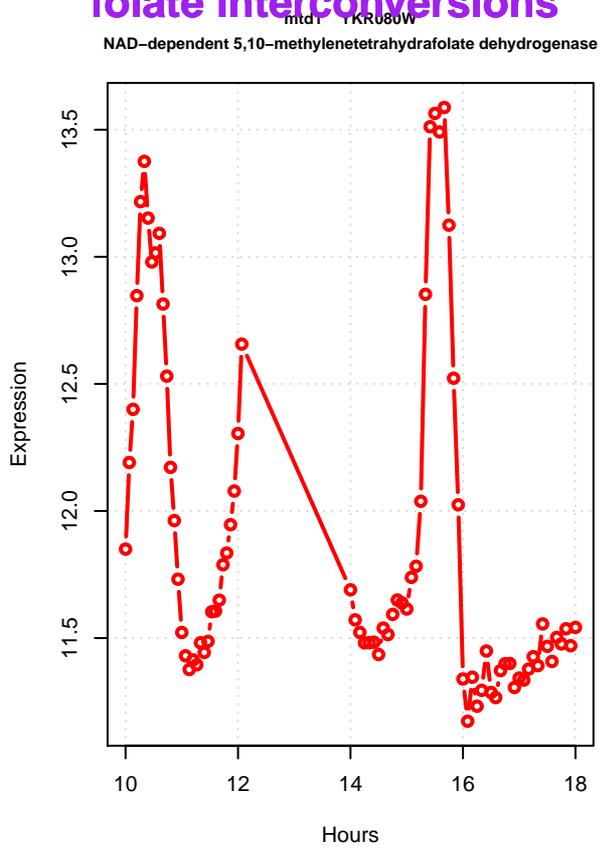
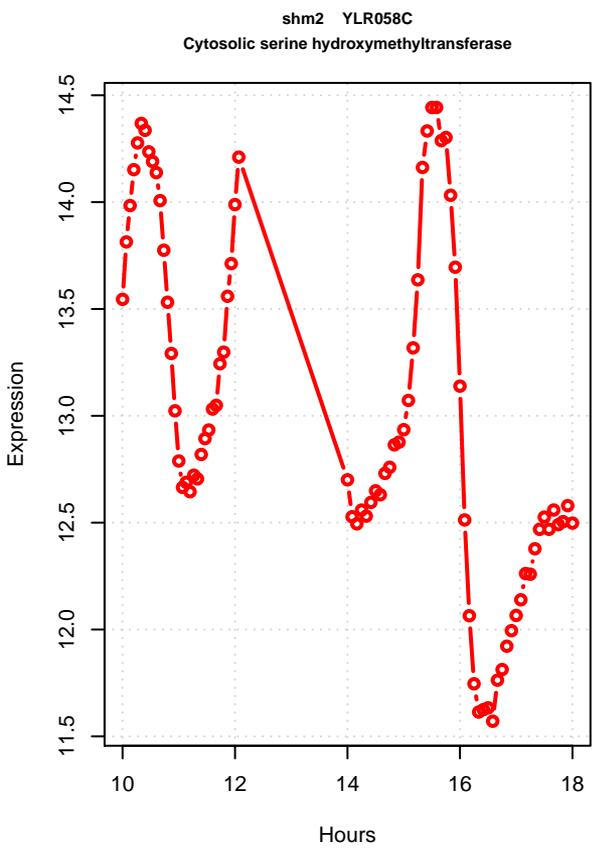


## **folate interconversions**

# folate interconversions

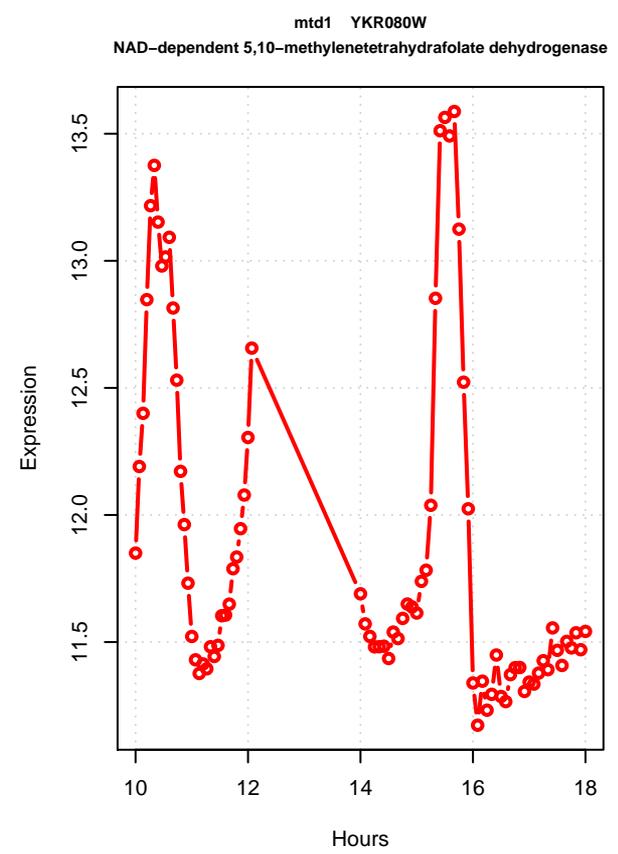
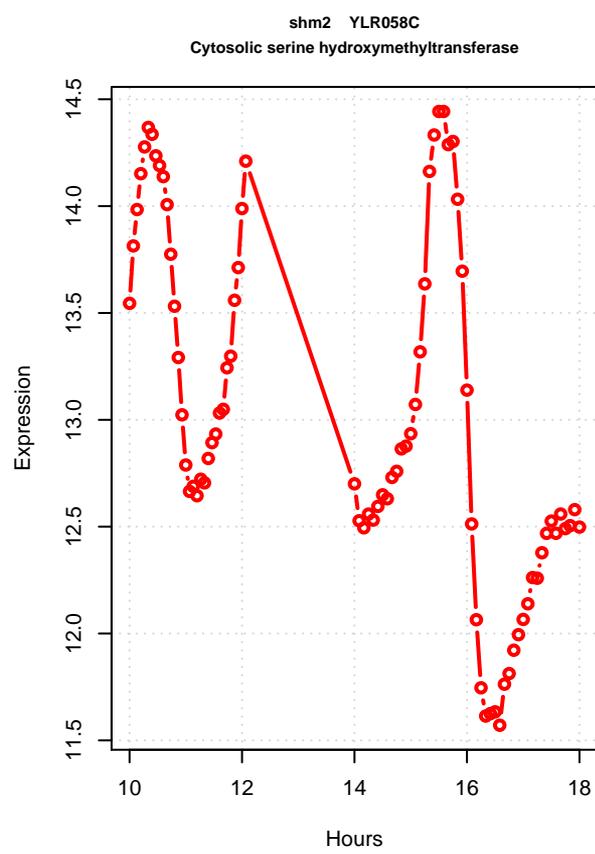
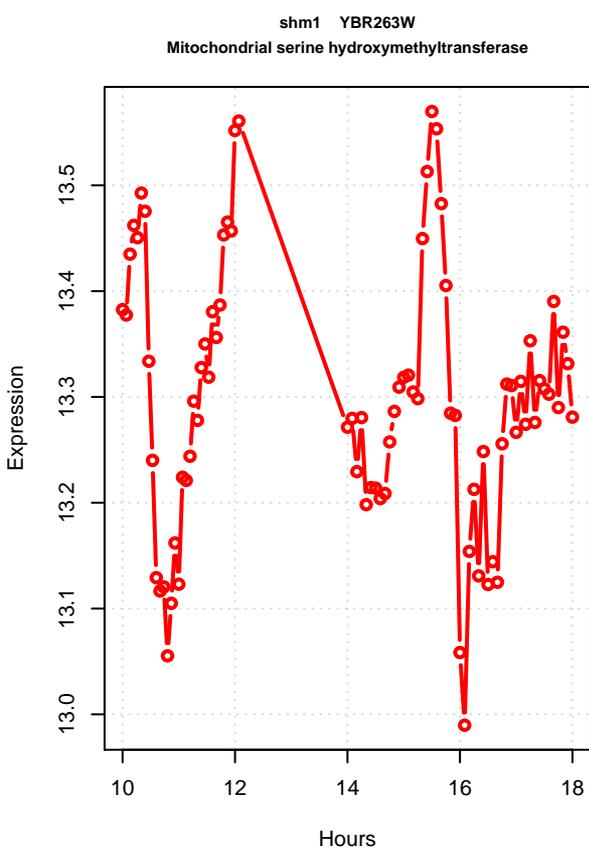
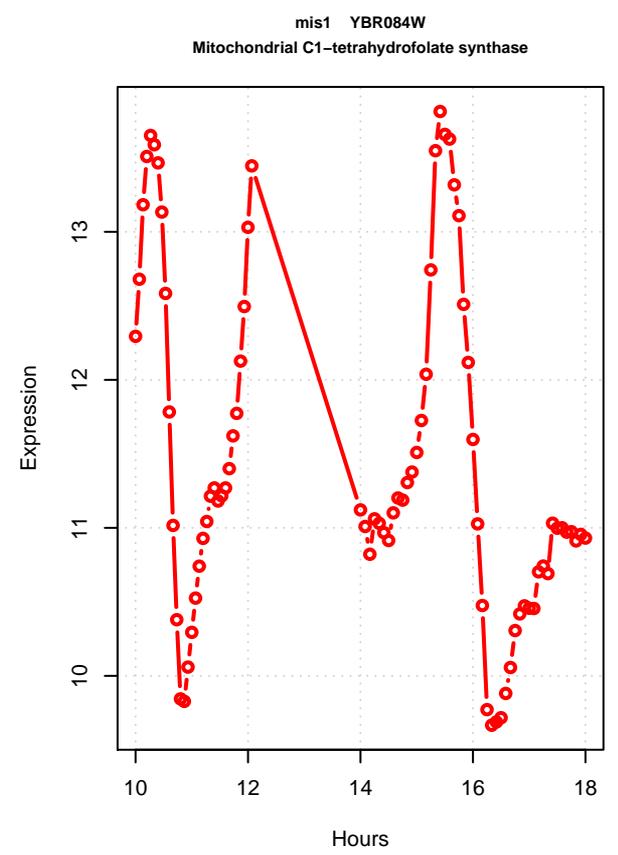
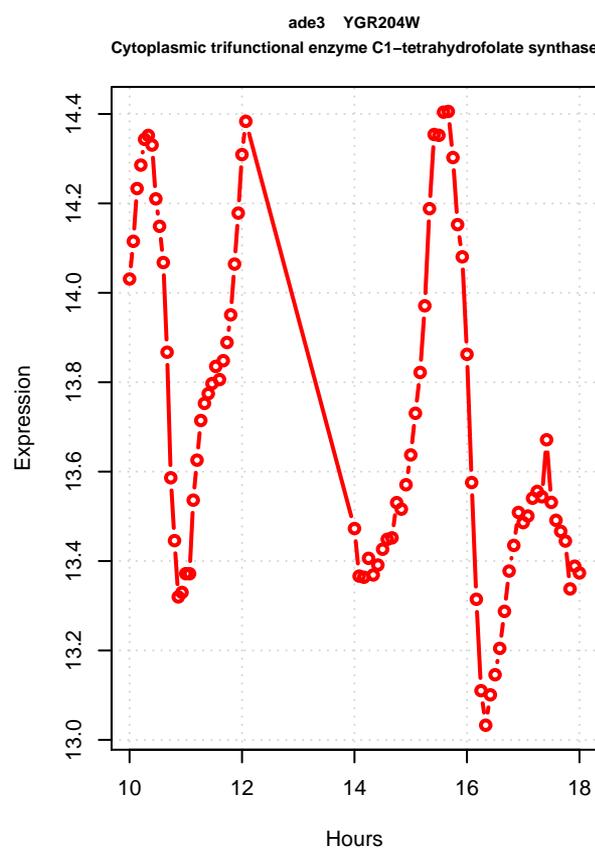
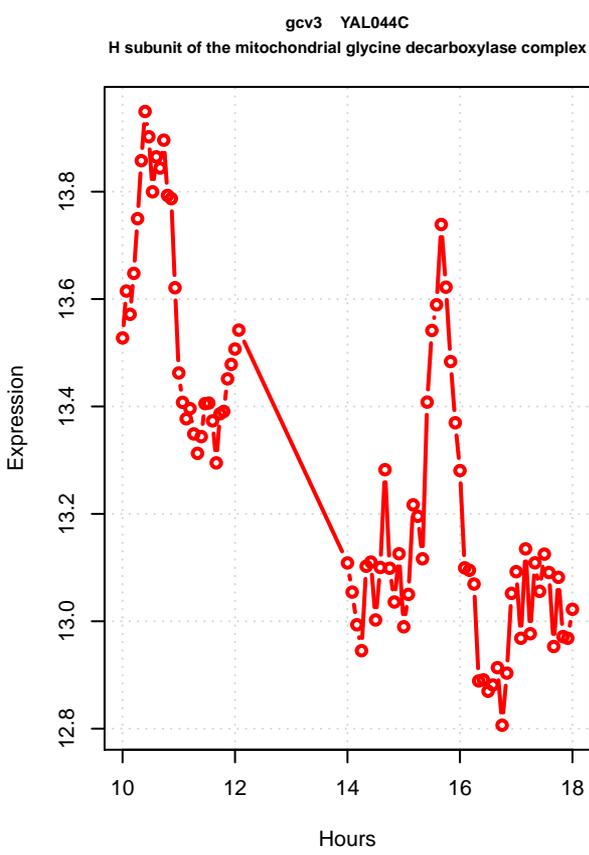
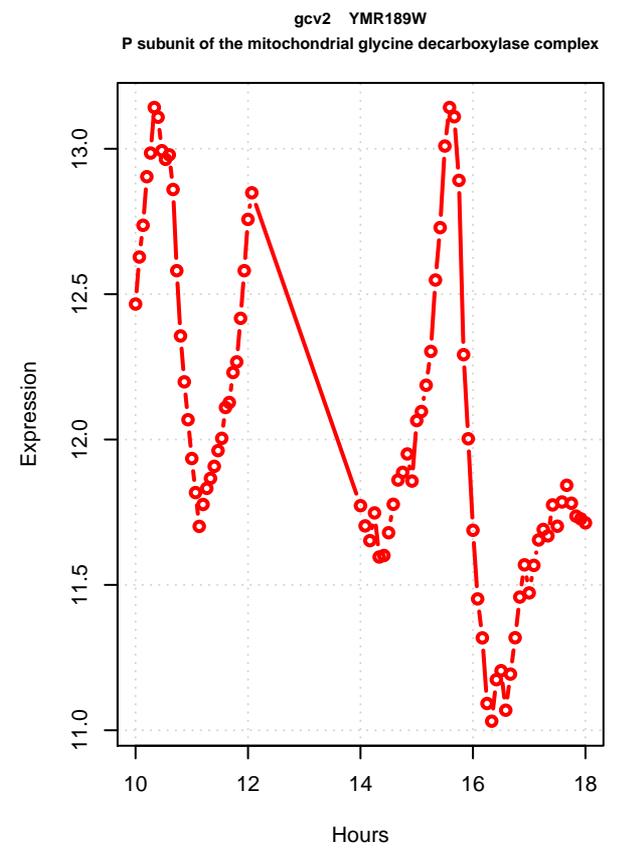
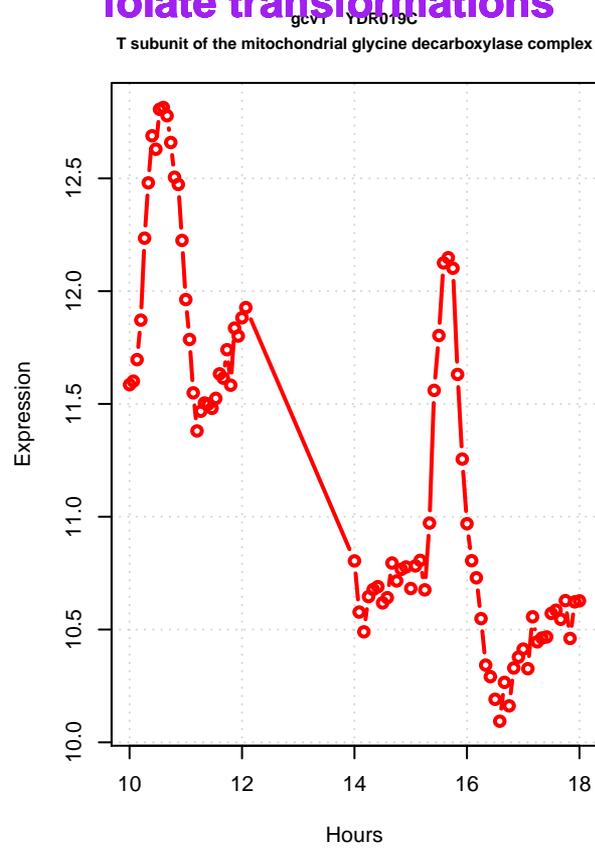
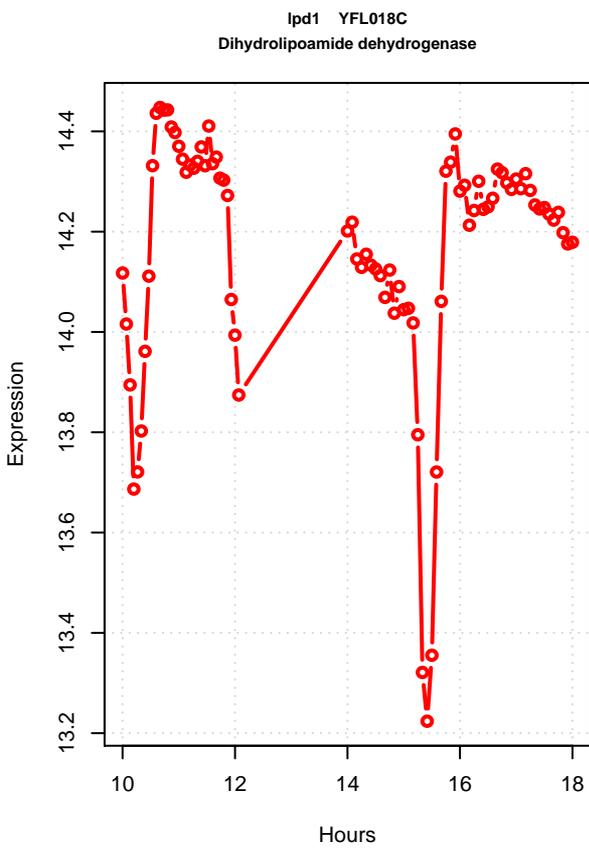


# folate interconversions



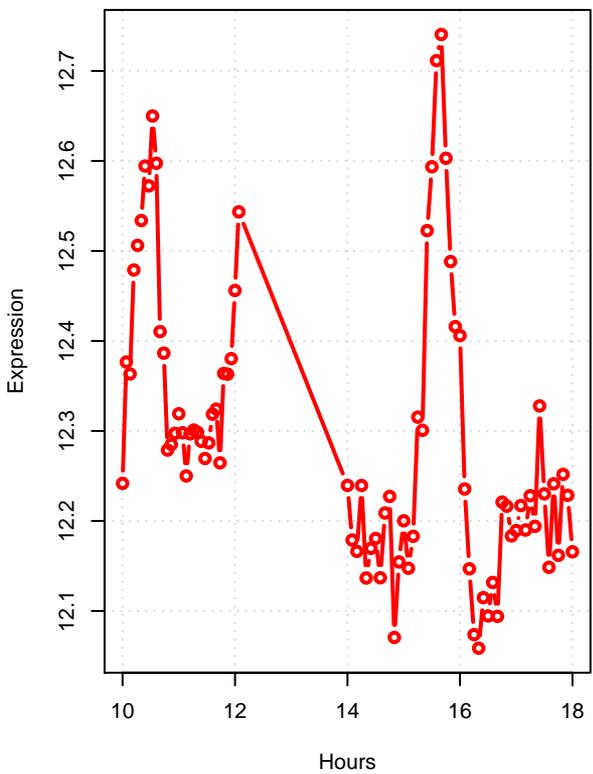
## **folate transformations**

# folate transformations

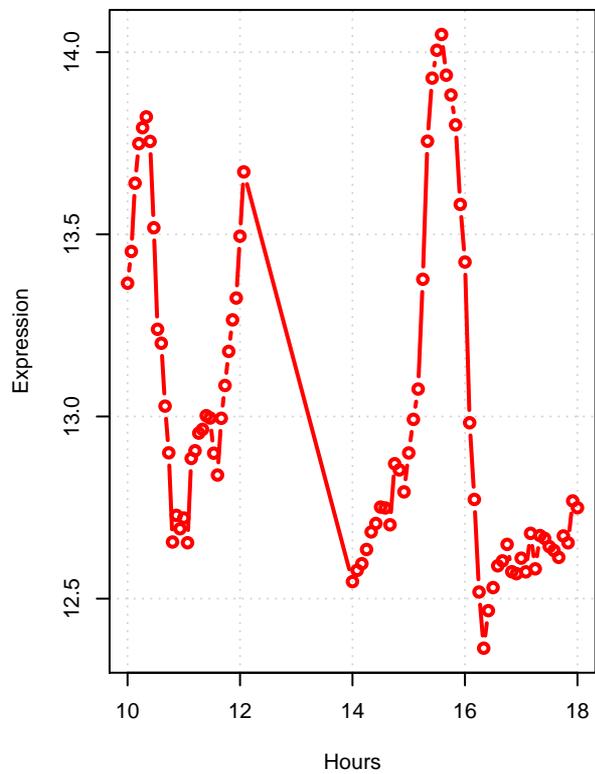


# folate transformations

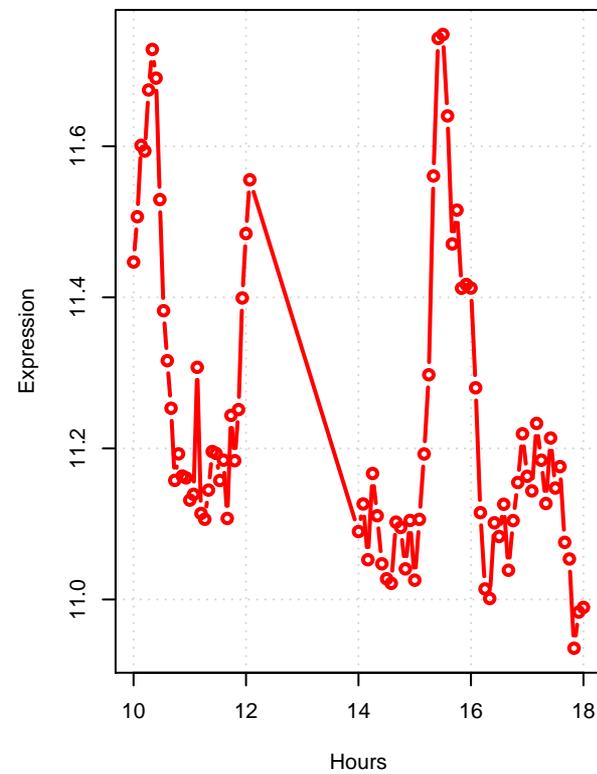
met12 YPL023C  
Protein with MTHFR activity in vitro



met13 YGL125W  
Major isozyme of methylenetetrahydrofolate reductase



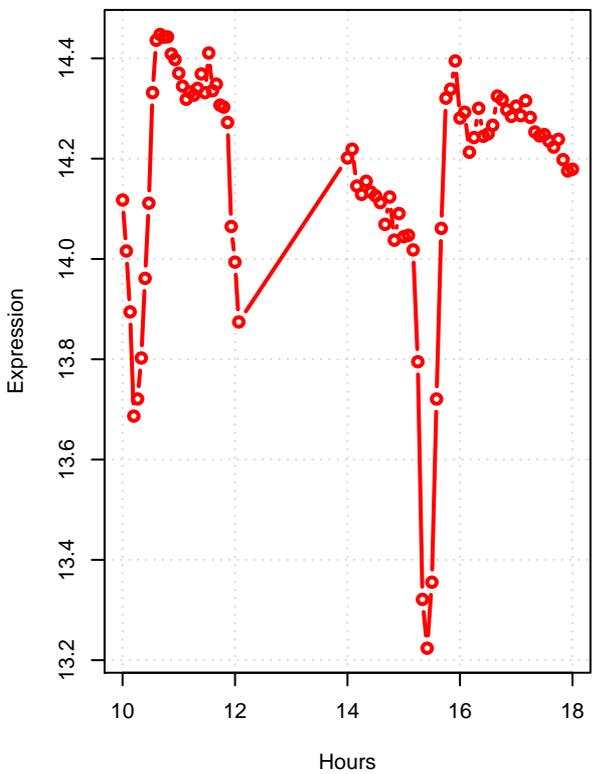
fau1 YER183C  
5,10-methenyltetrahydrofolate synthetase



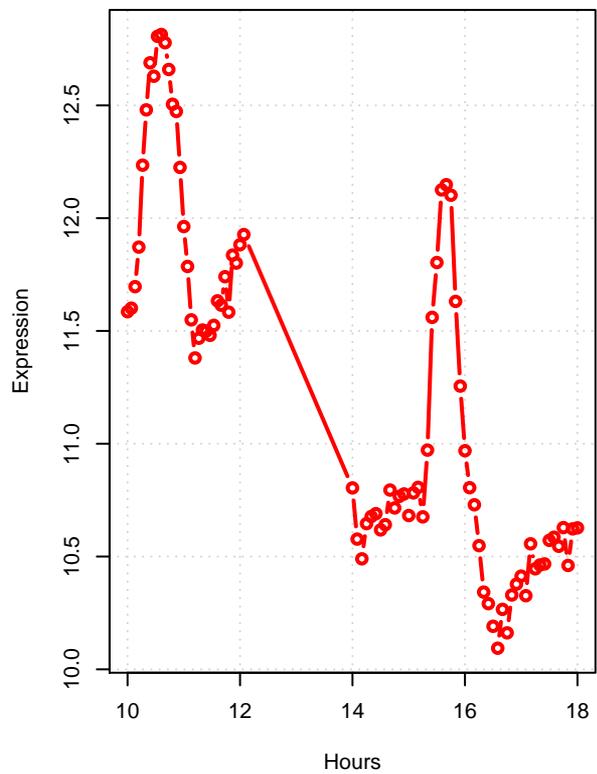
**glycine cleavage complex**

# glycine cleavage complex

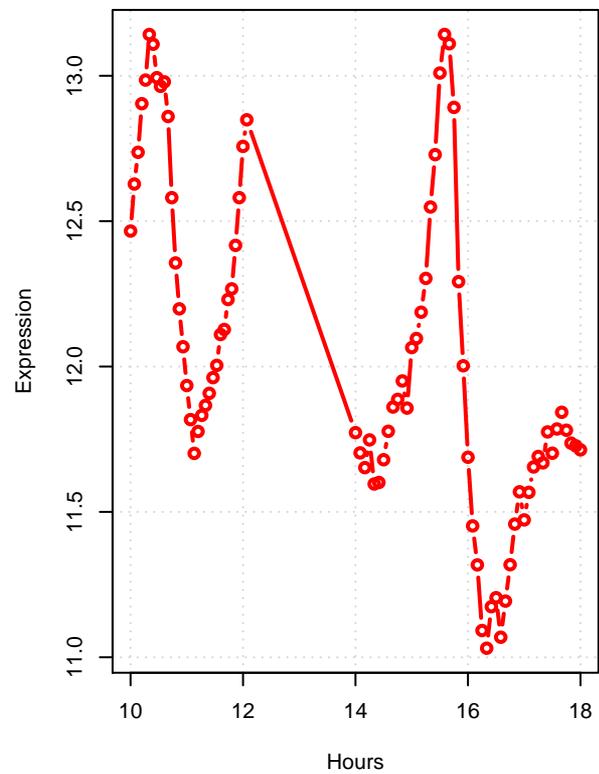
lpd1 YFL018C  
Dihydropyrimidine dehydrogenase



gcv1 YBR019C  
T subunit of the mitochondrial glycine decarboxylase complex

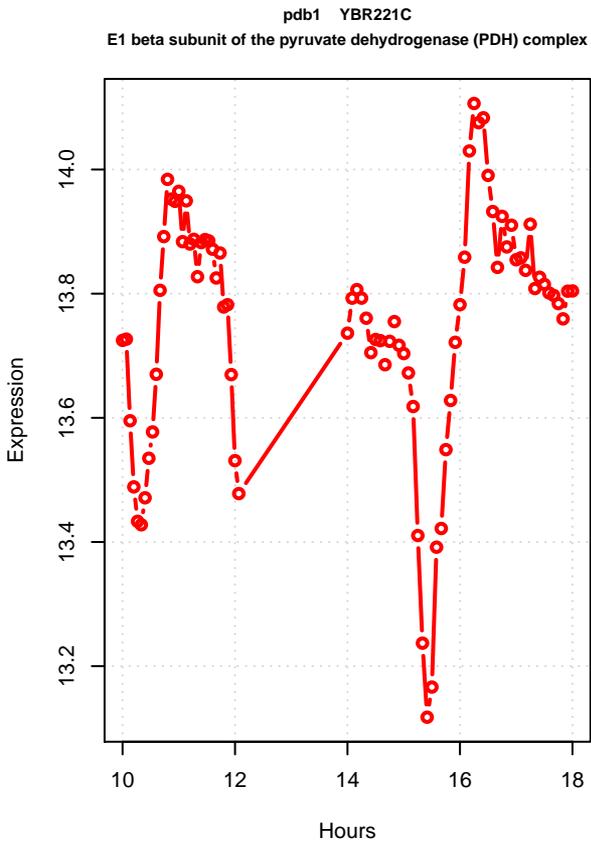
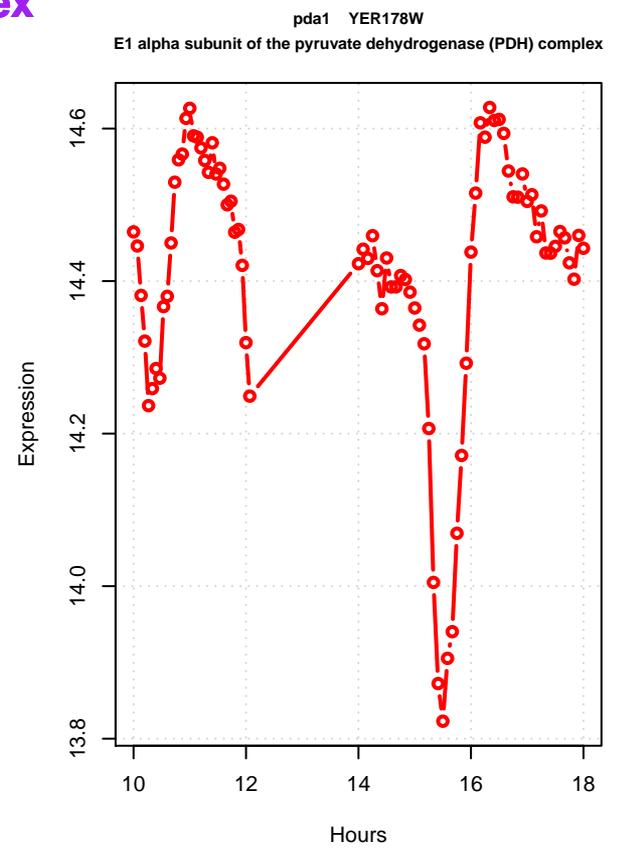
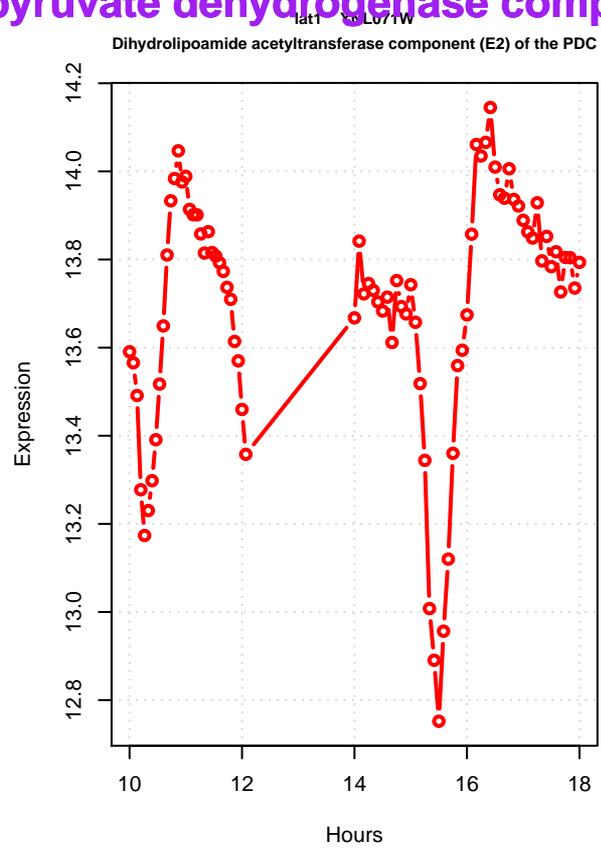
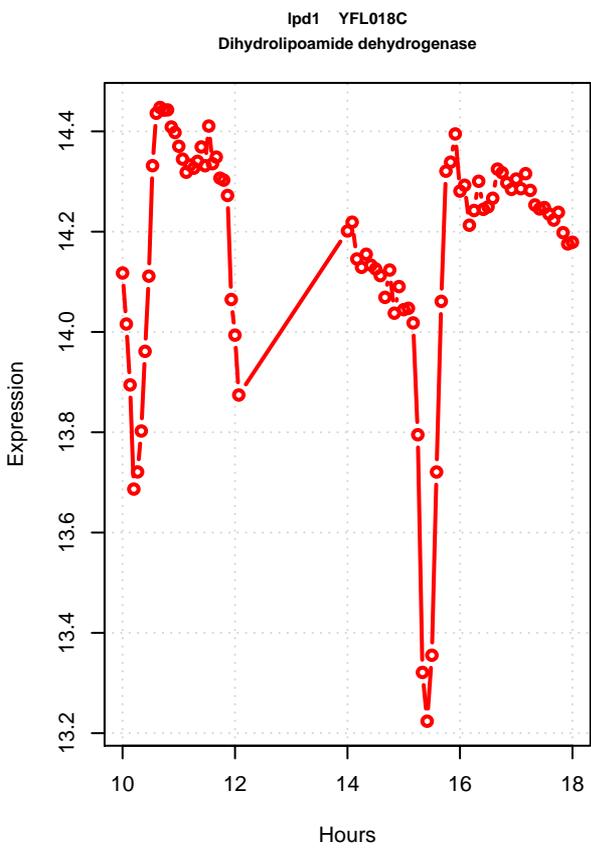


gcv2 YMR189W  
P subunit of the mitochondrial glycine decarboxylase complex



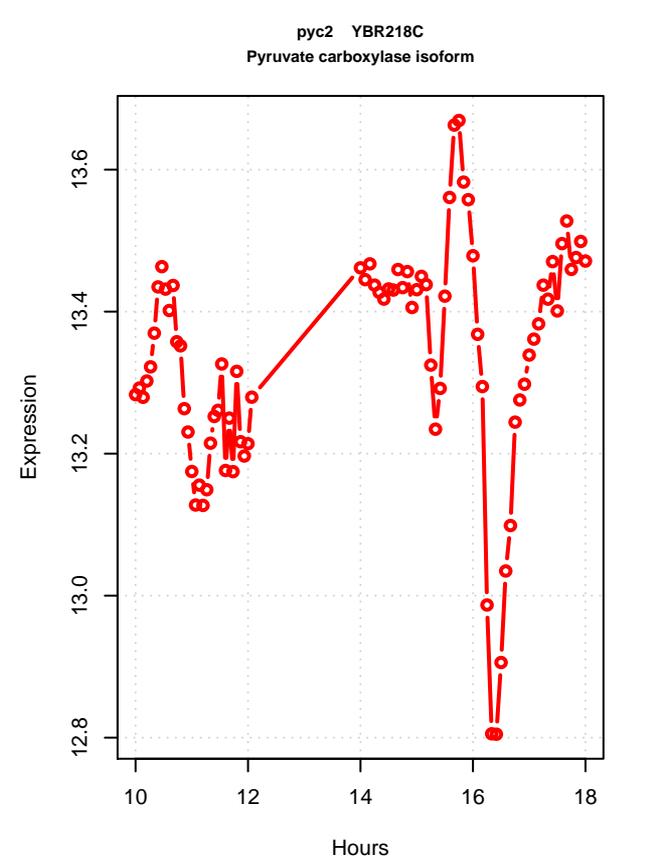
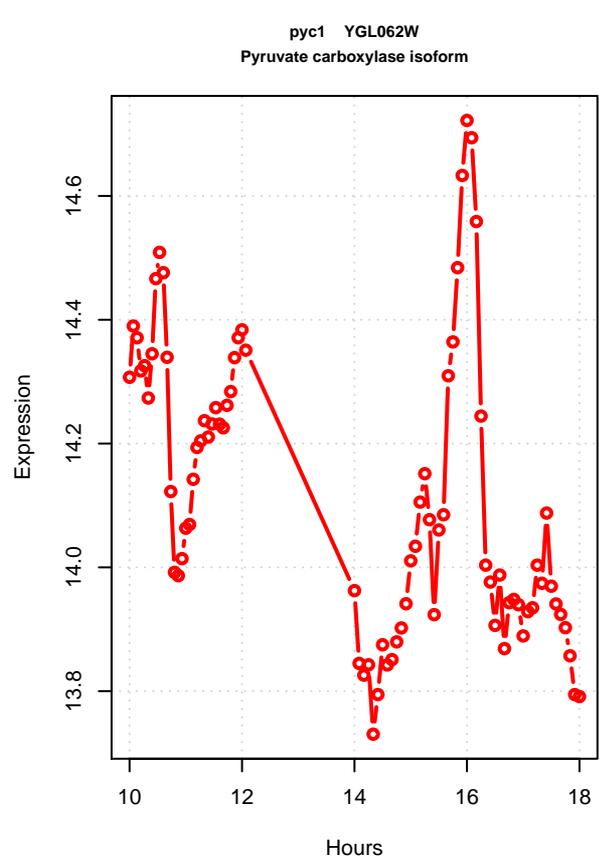
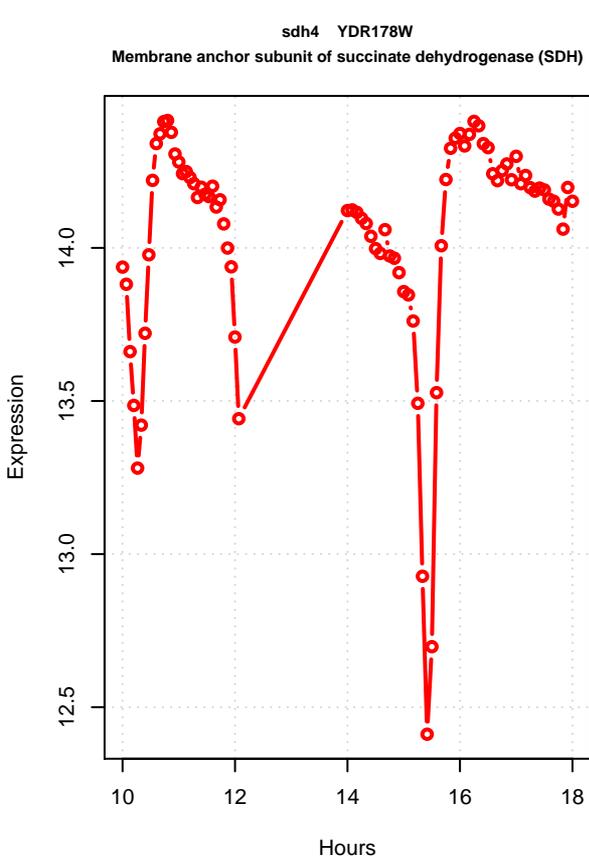
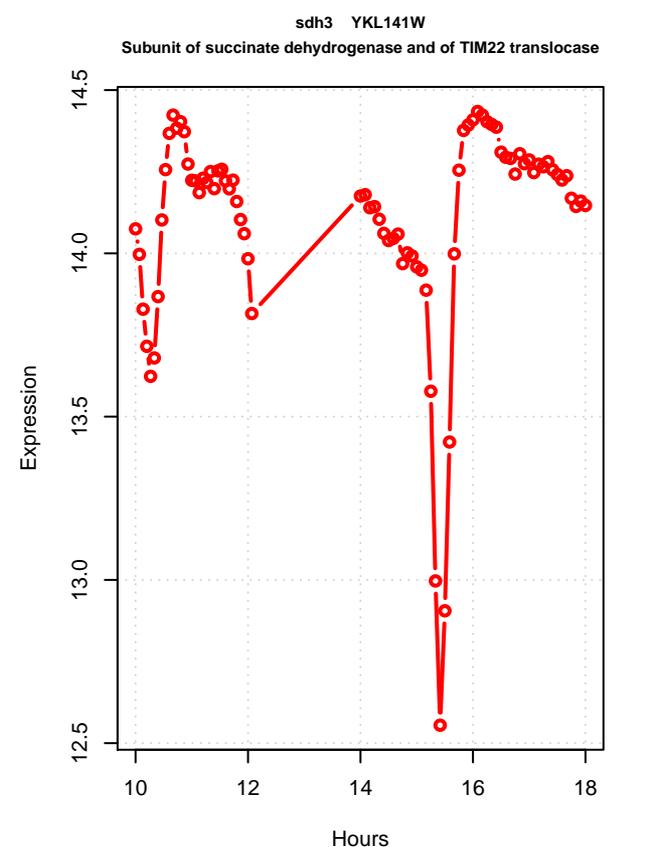
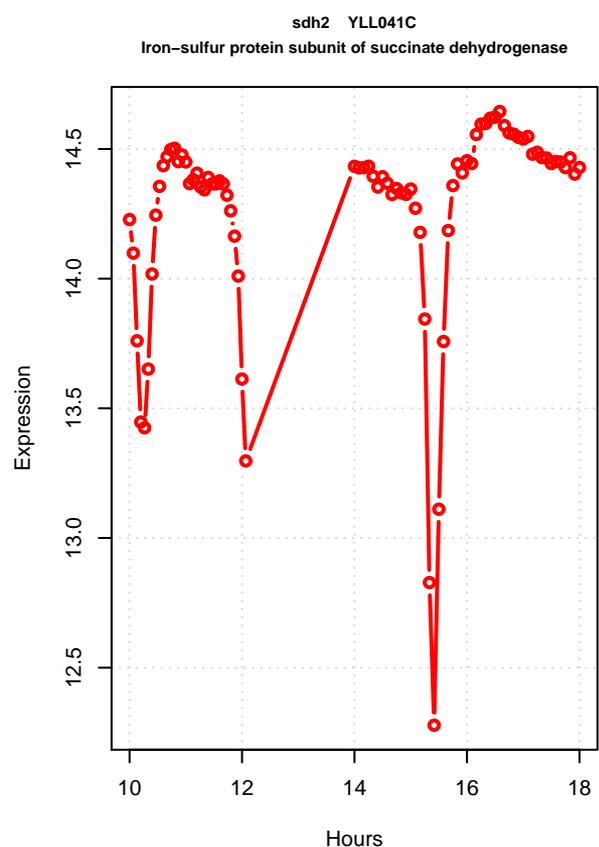
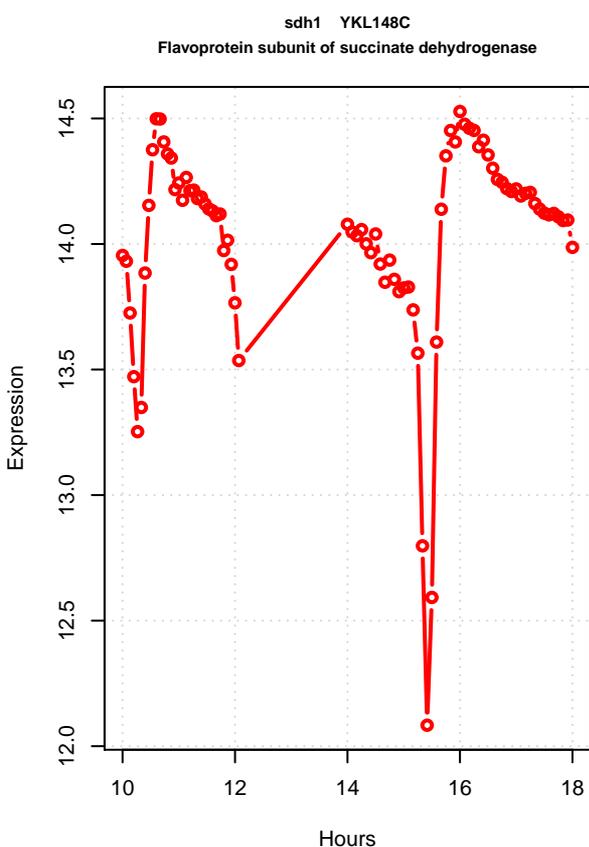
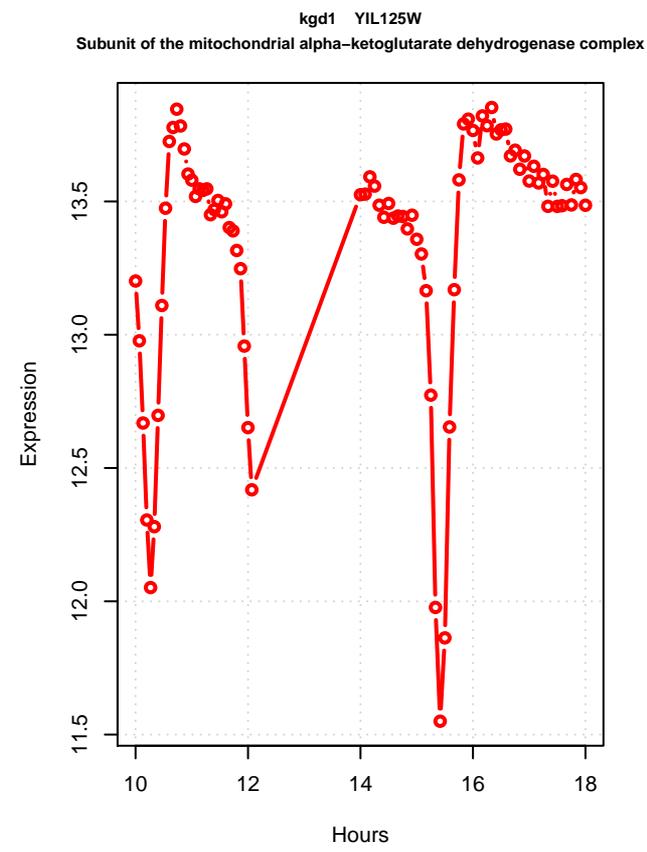
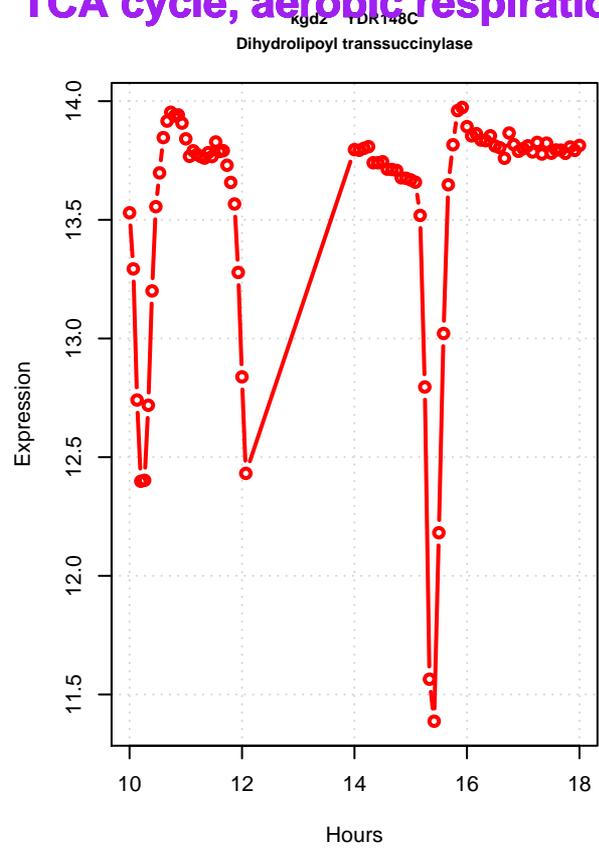
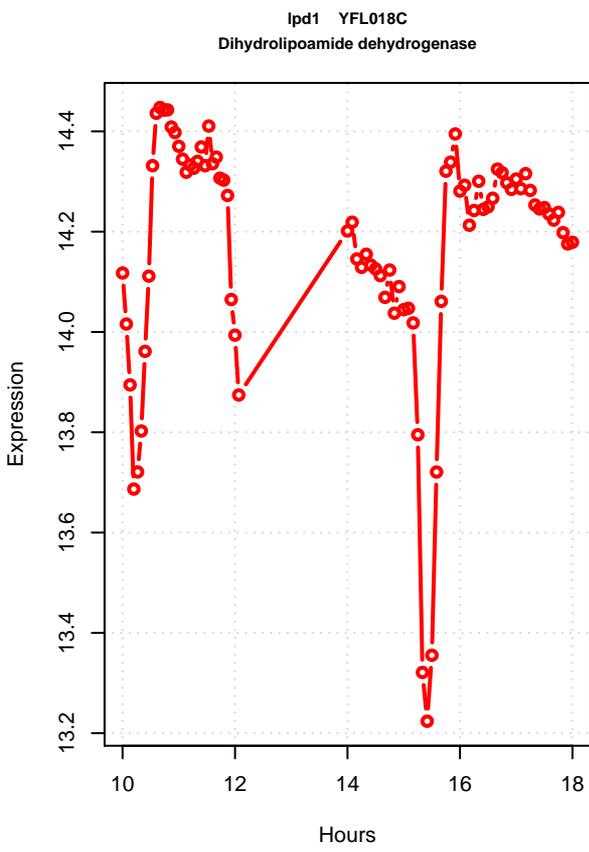
**pyruvate dehydrogenase complex**

# pyruvate dehydrogenase complex

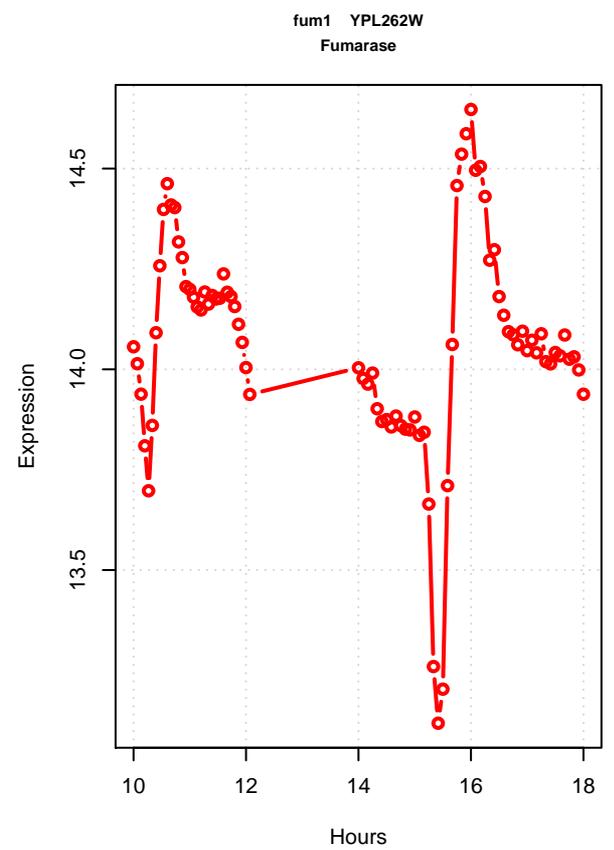
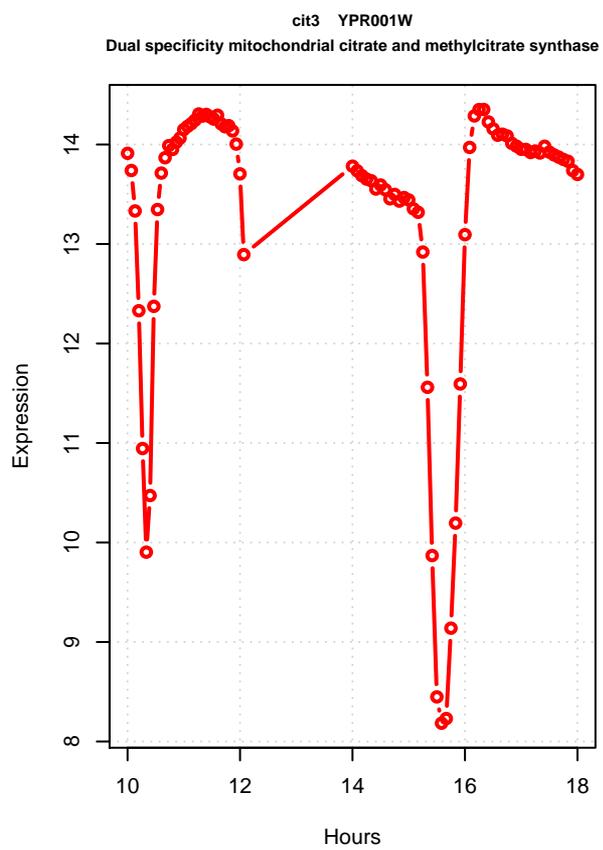
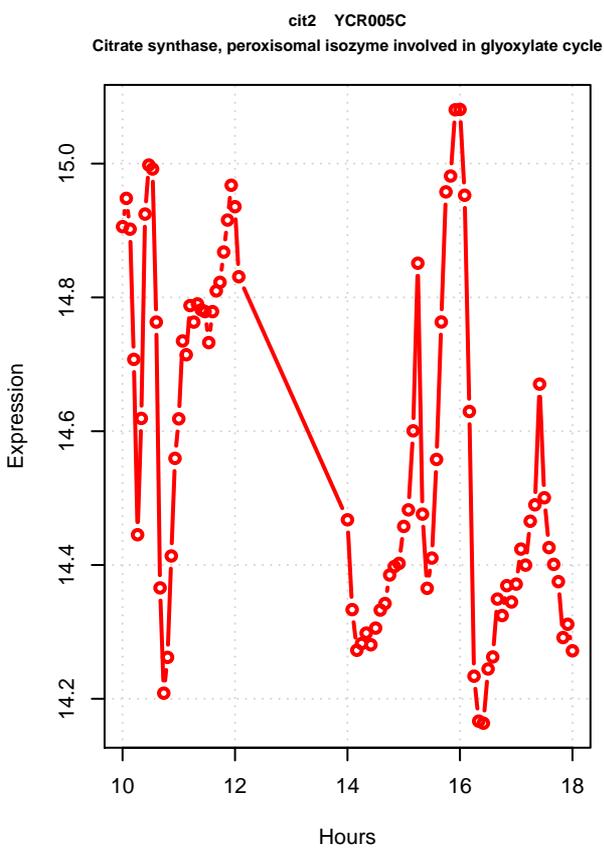
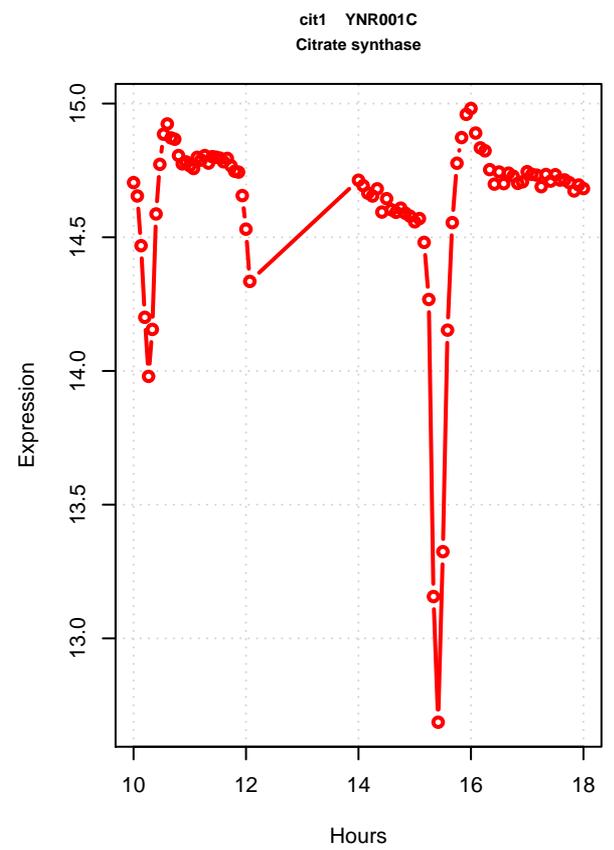
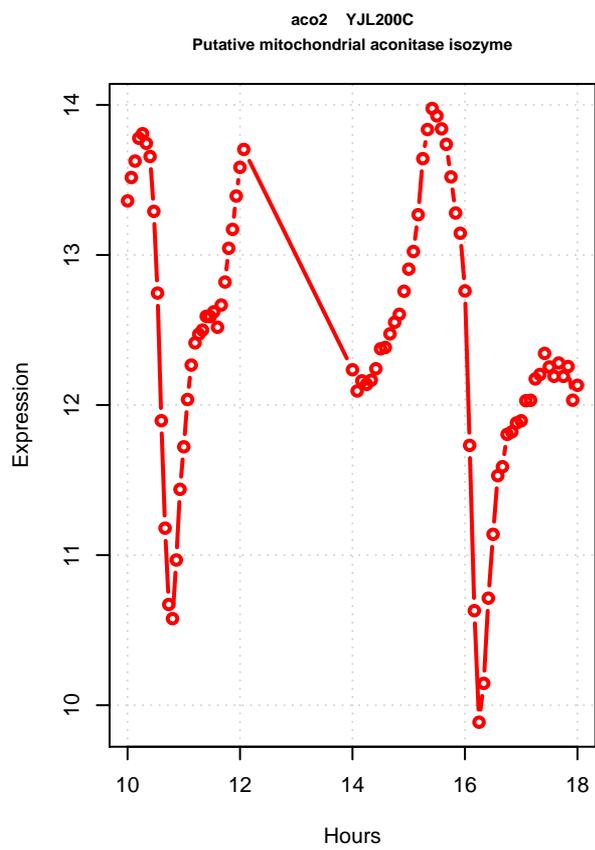
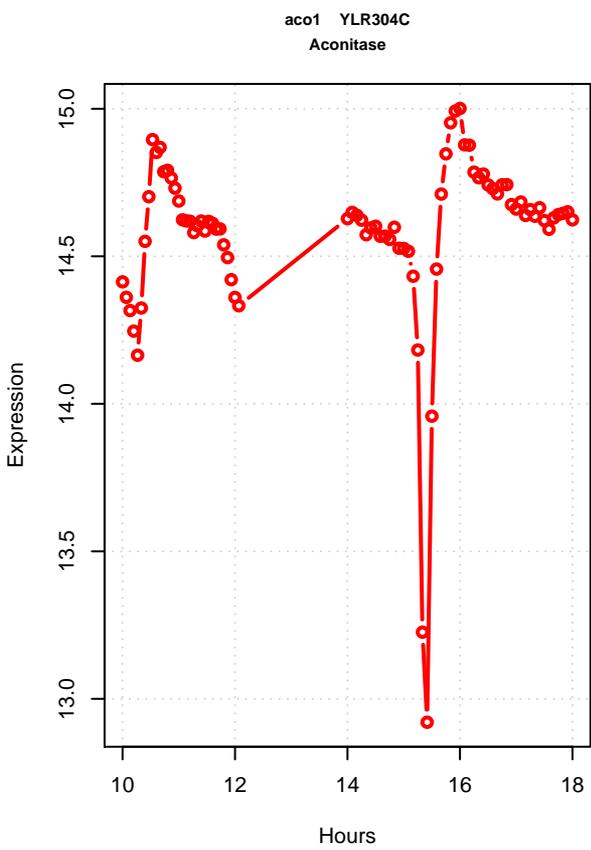
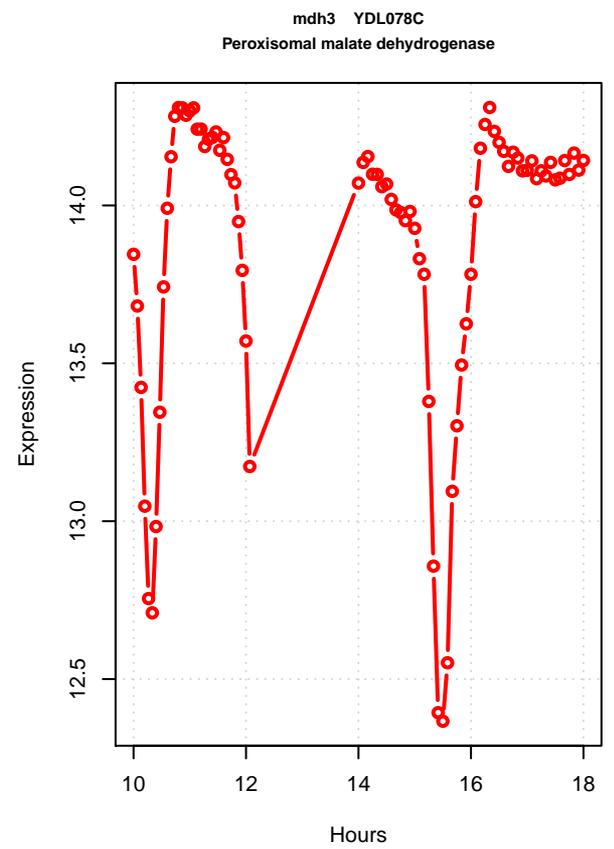
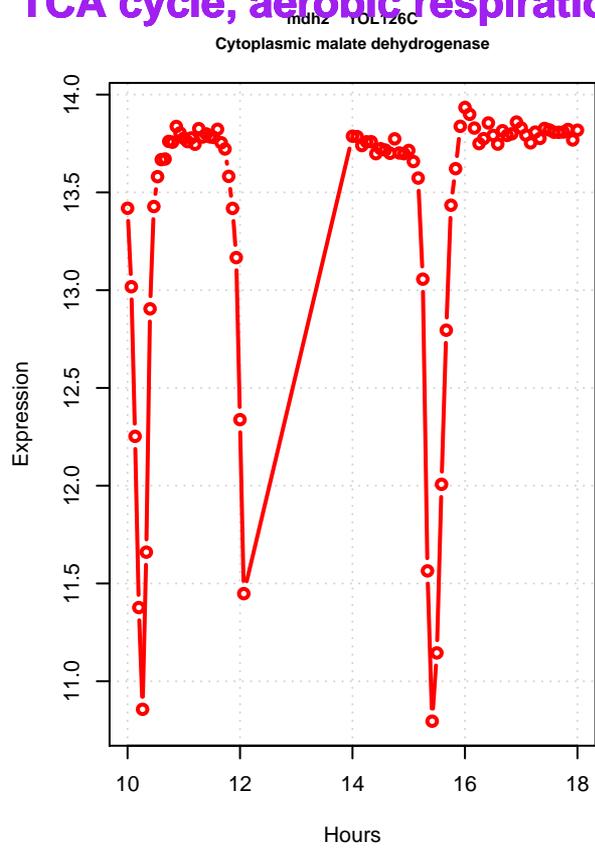
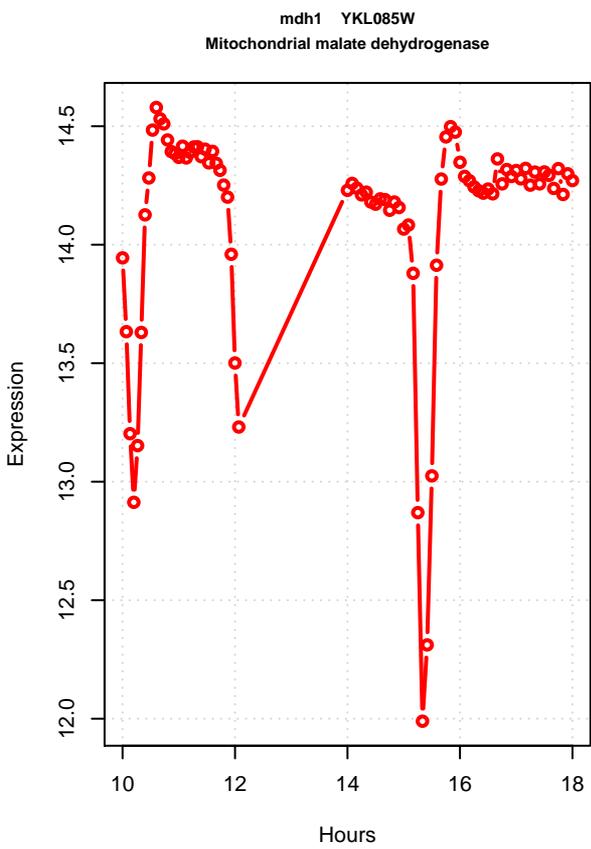


## **TCA cycle, aerobic respiration**

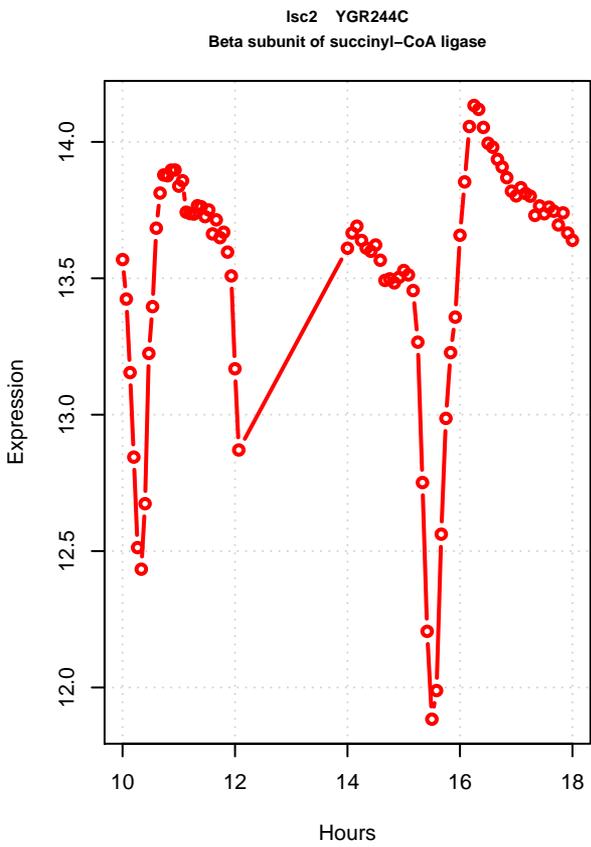
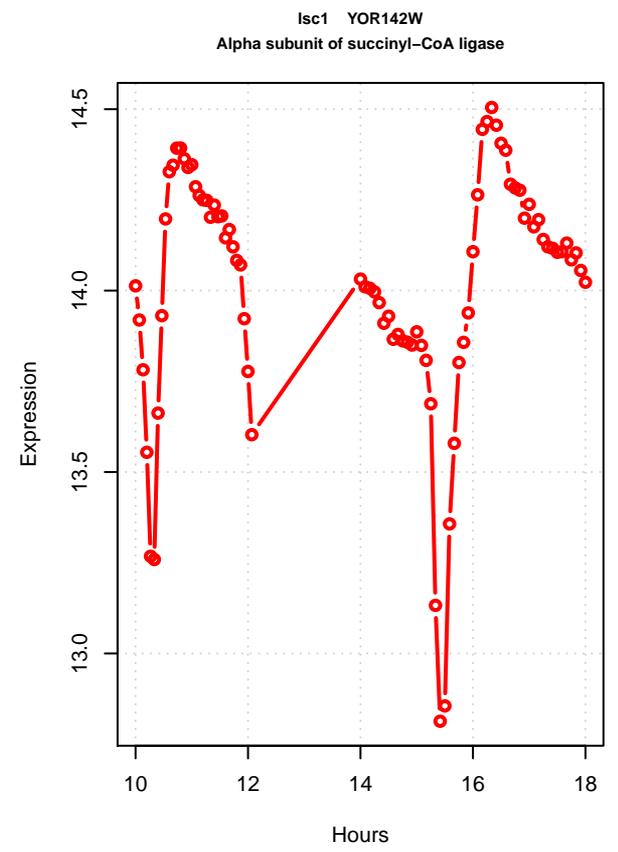
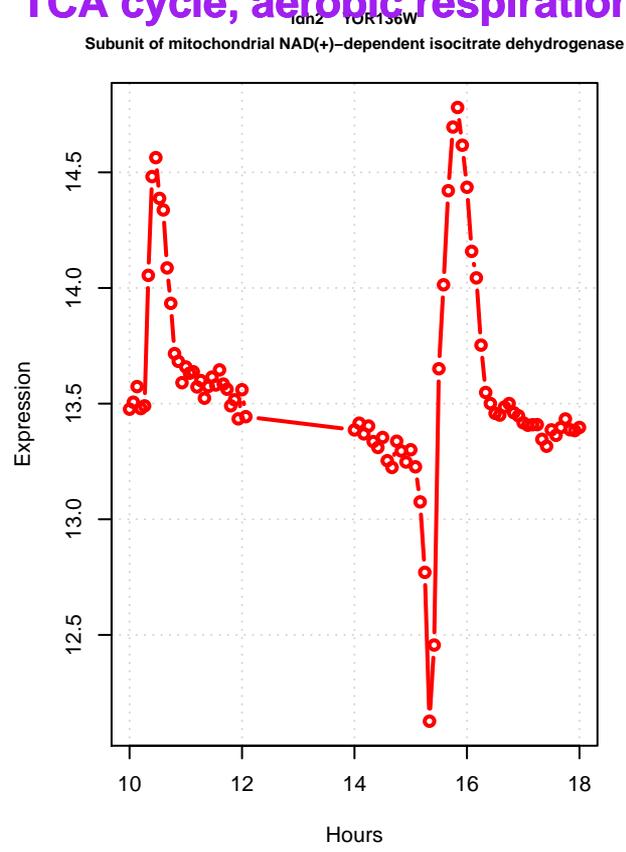
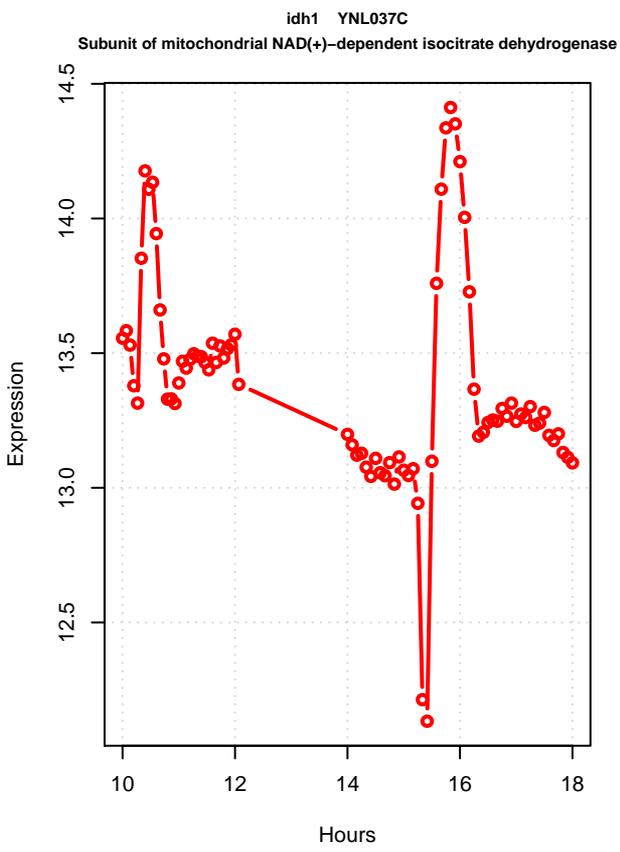
# TCA cycle, aerobic respiration



# TCA cycle, aerobic respiration



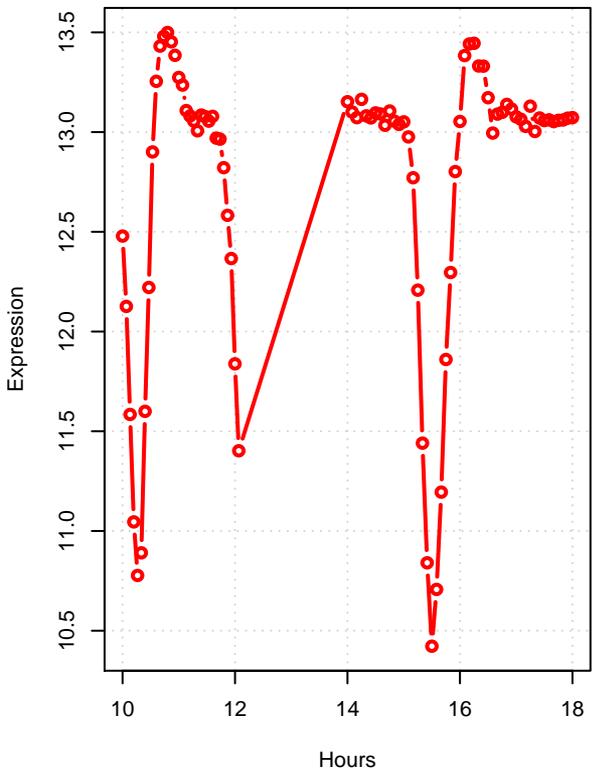
# TCA cycle, aerobic respiration



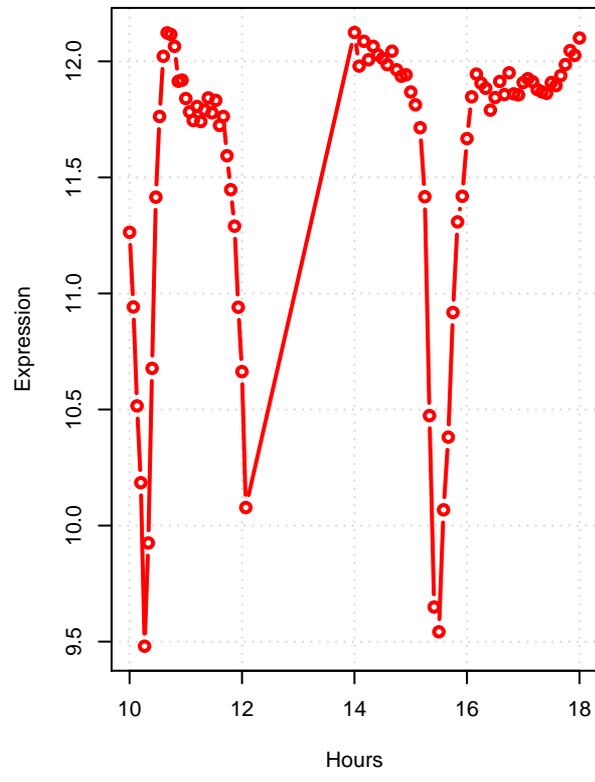
## 4-aminobutyrate degradation

# 4-aminobutyrate degradation

uga1 YGR019W  
Gamma-aminobutyrate (GABA) transaminase



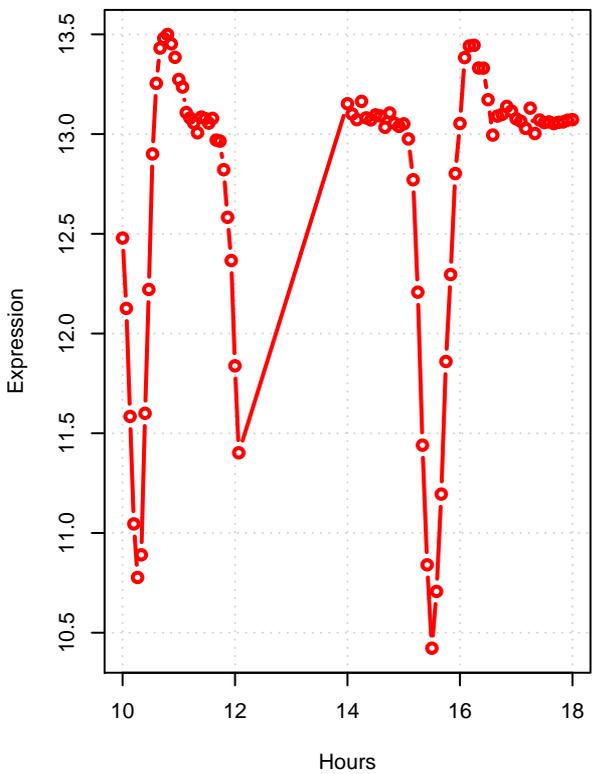
uga2 YBR006W  
Succinate semialdehyde dehydrogenase



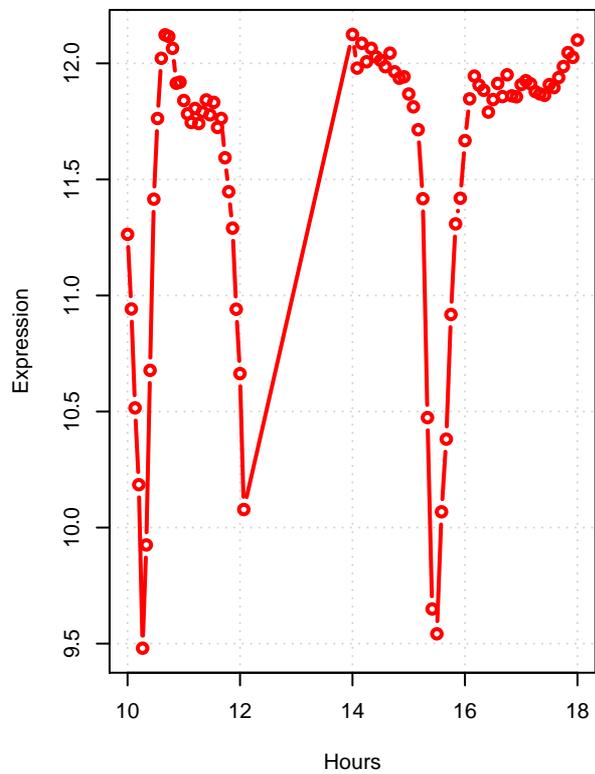
## glutamate degradation I

# glutamate degradation I

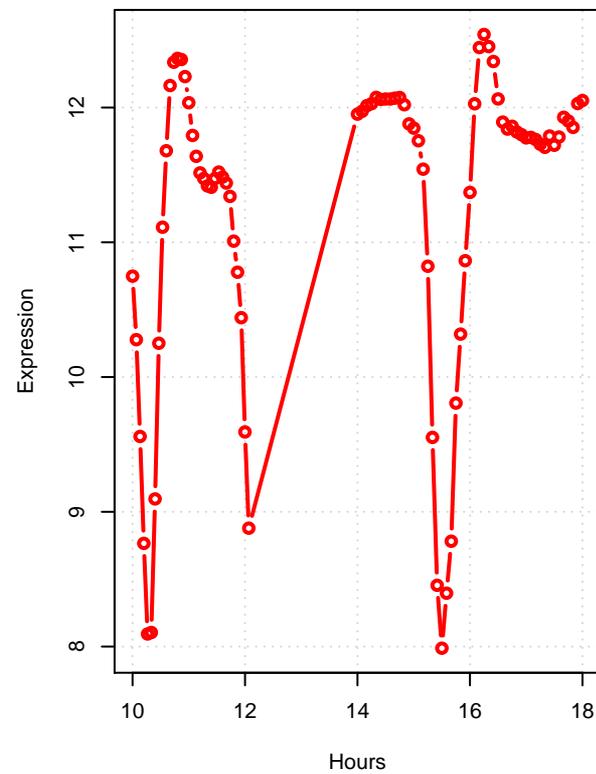
uga1 YGR019W  
Gamma-aminobutyrate (GABA) transaminase



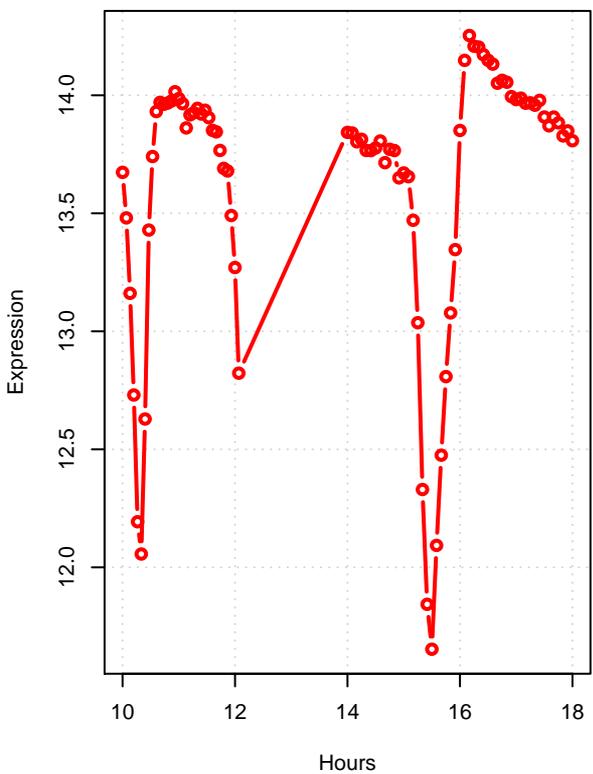
ugaz YSL006W  
Succinate semialdehyde dehydrogenase



gad1 YMR250W  
Glutamate decarboxylase



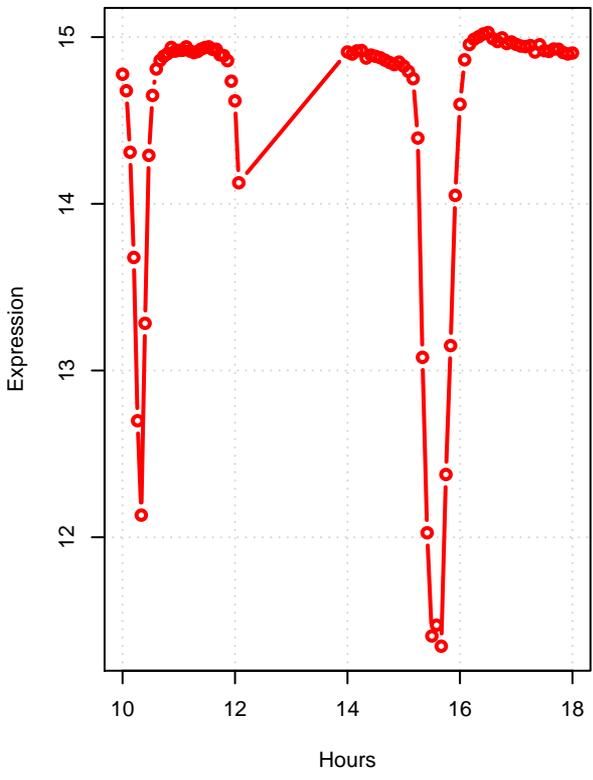
gdh2 YDL215C  
NAD(+)-dependent glutamate dehydrogenase



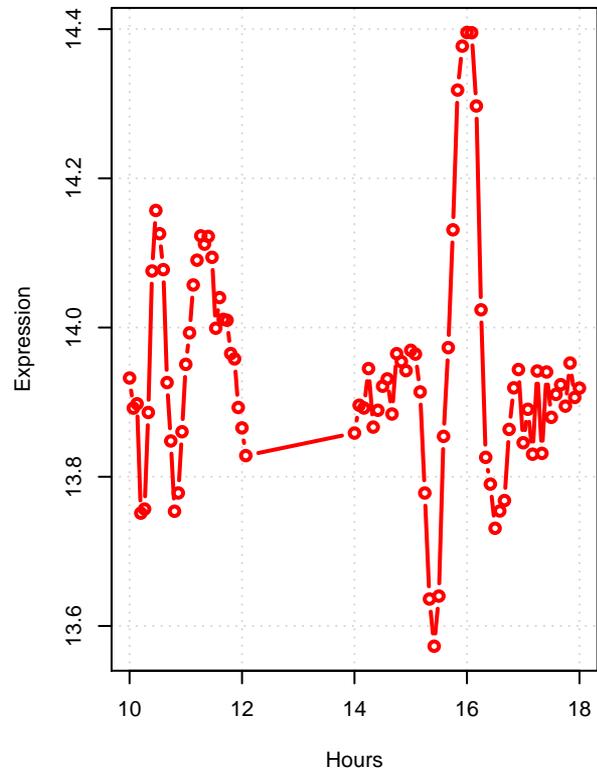
**acetate utilization**

# acetate utilization

acs1 YAL054C  
Acetyl-coA synthetase isoform

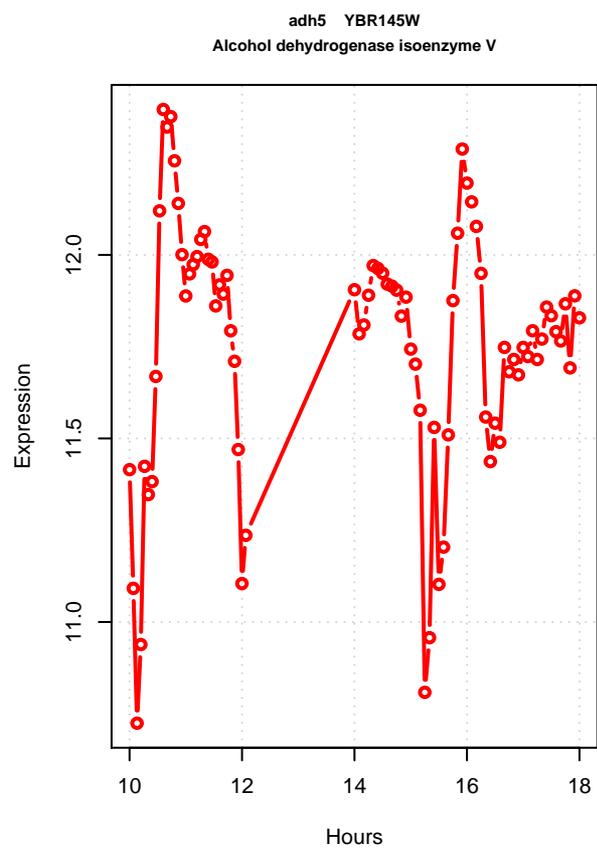
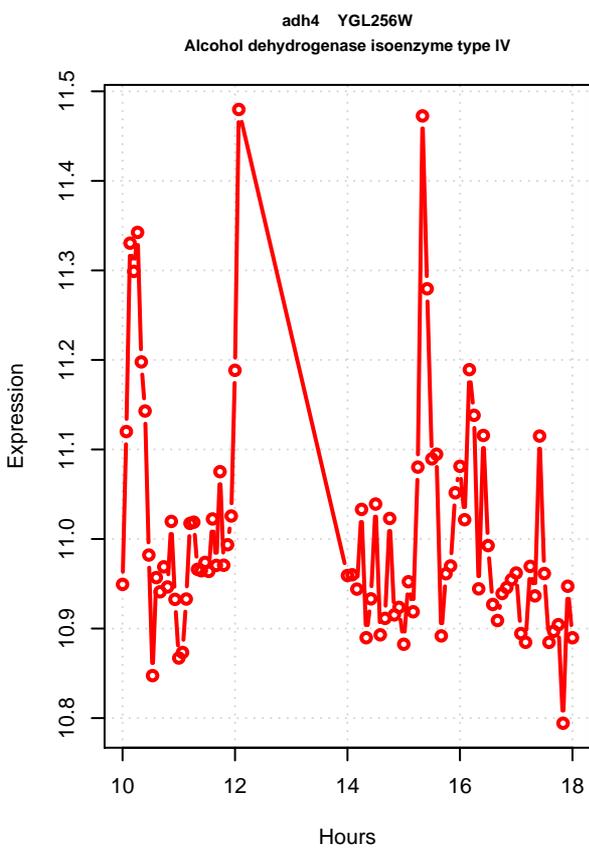
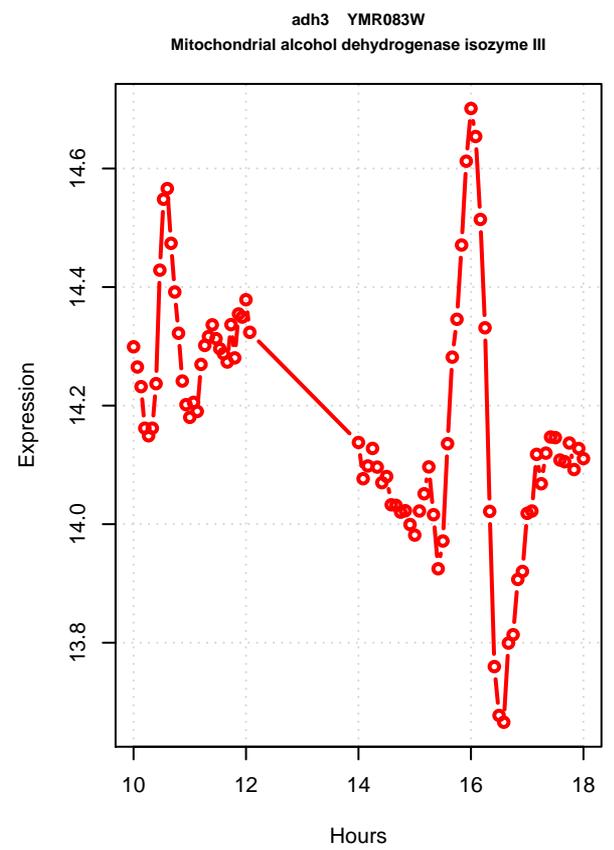
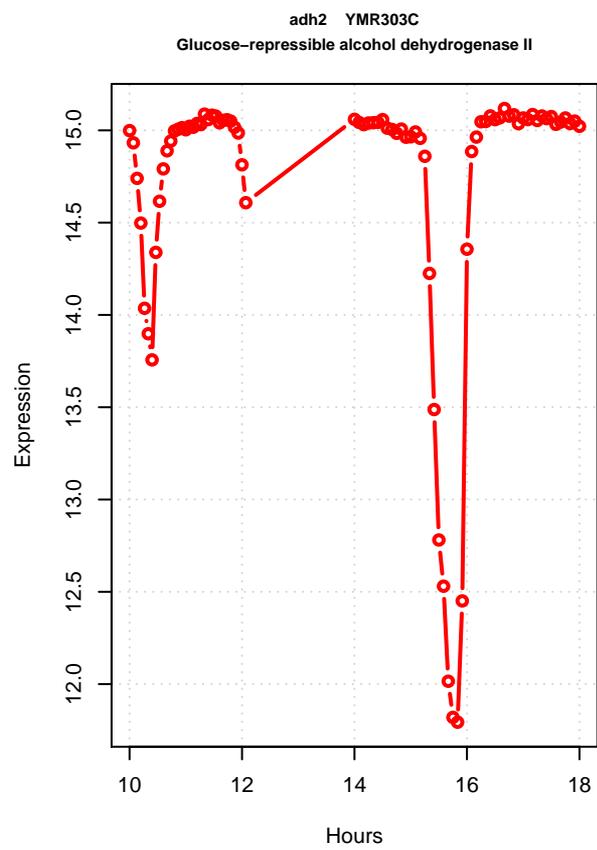
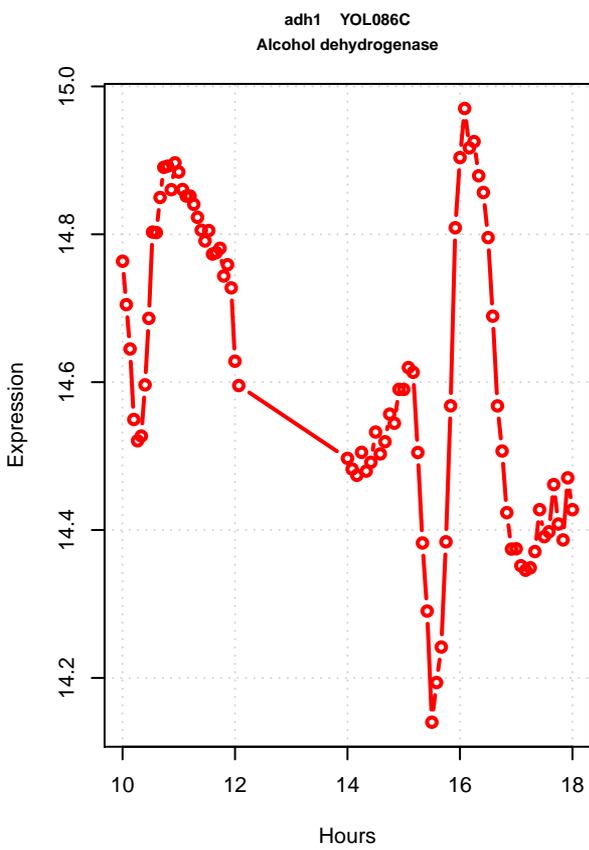
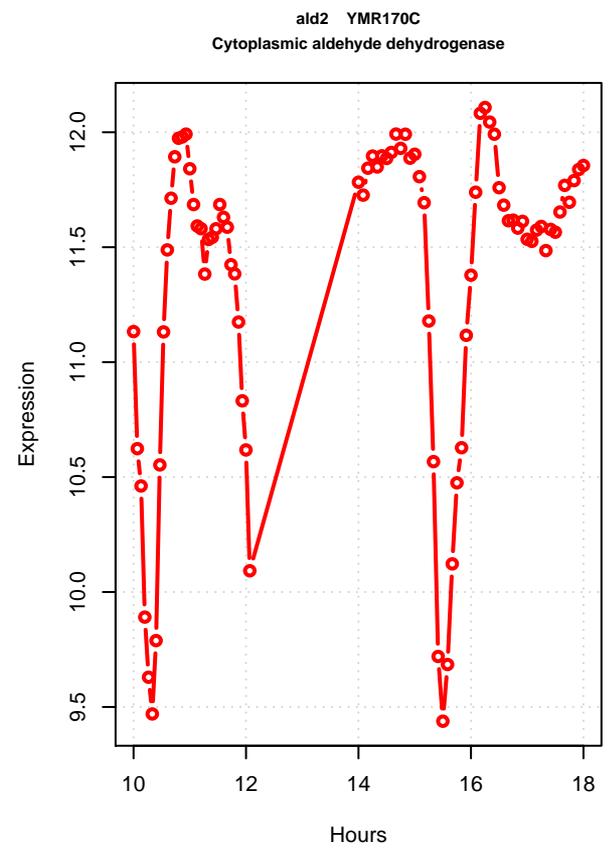
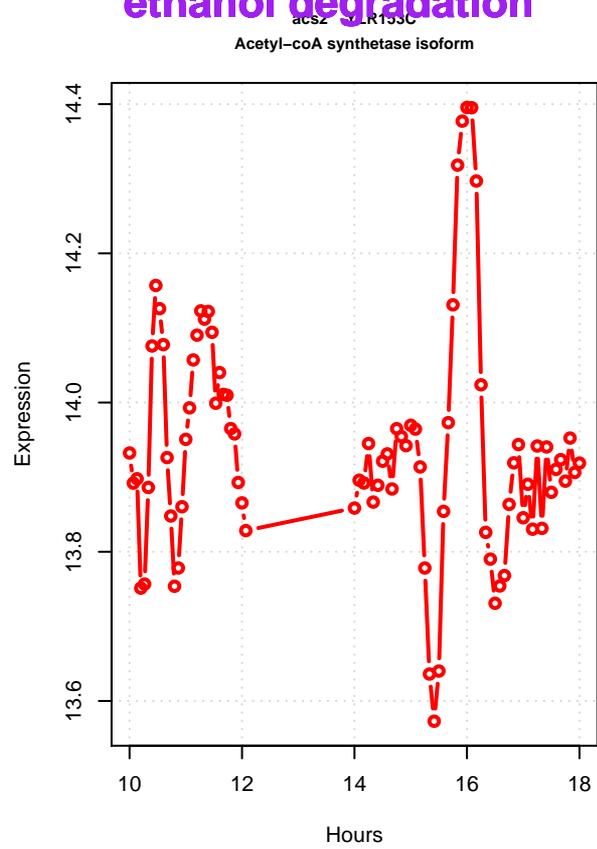
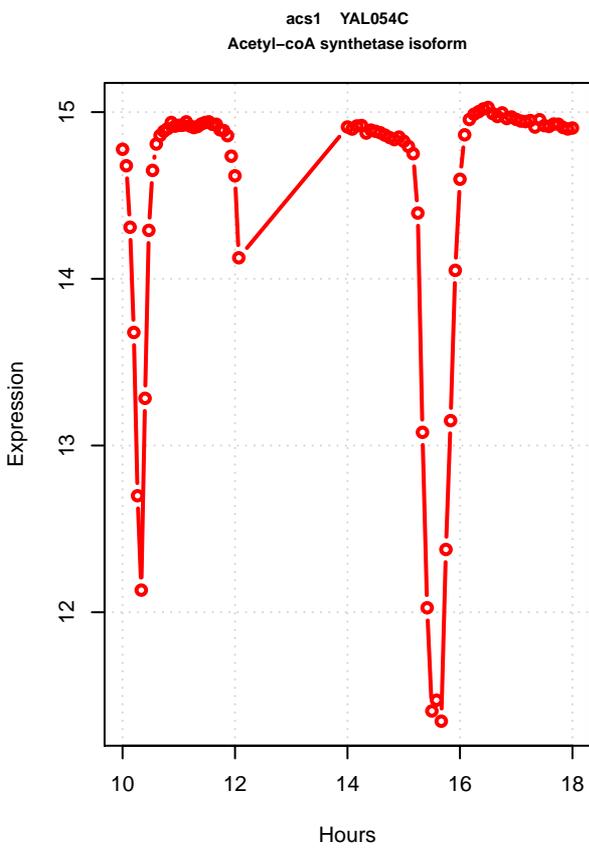


acs2 YLR153C  
Acetyl-coA synthetase isoform



**ethanol degradation**

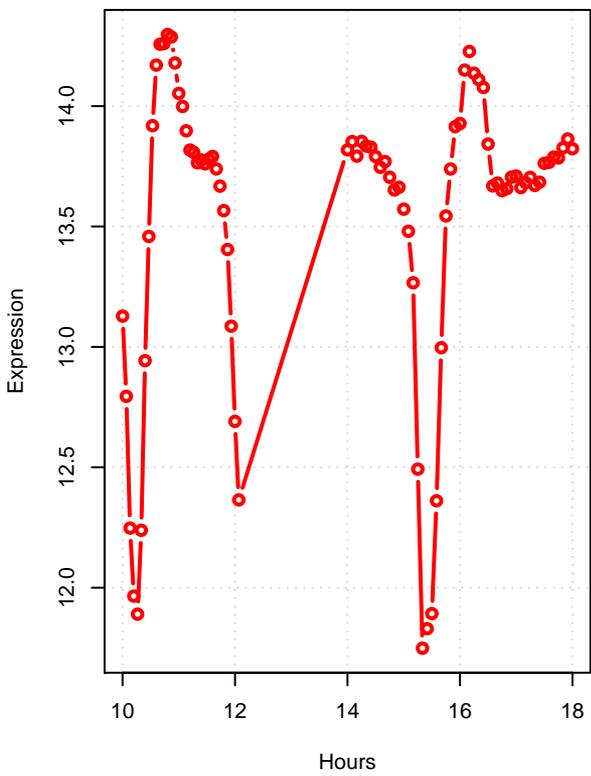
# ethanol degradation



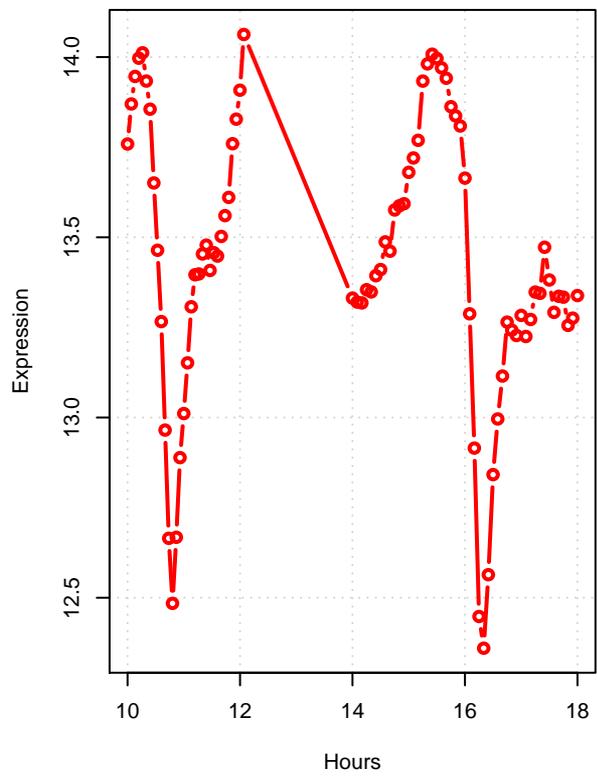
## **acetoin biosynthesis**

# acetoin biosynthesis

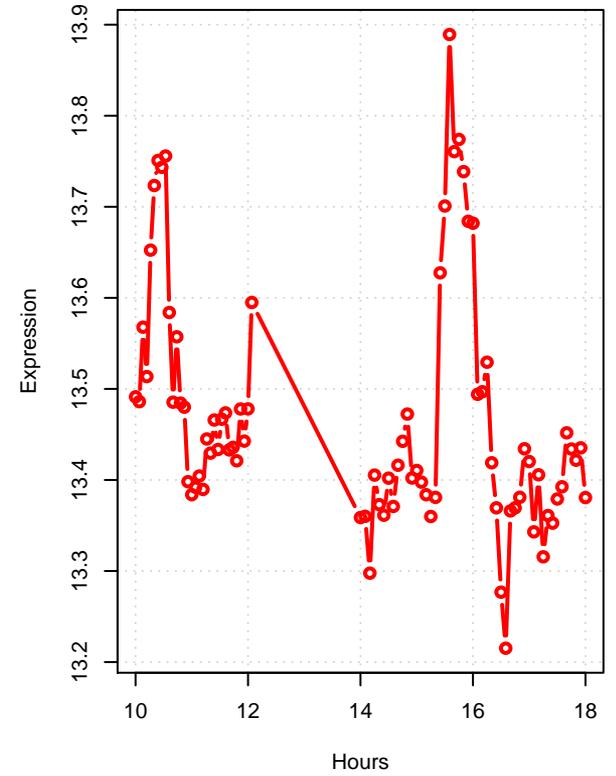
**bdh1 YAL060W**  
NAD-dependent (R,R)-butanediol dehydrogenase



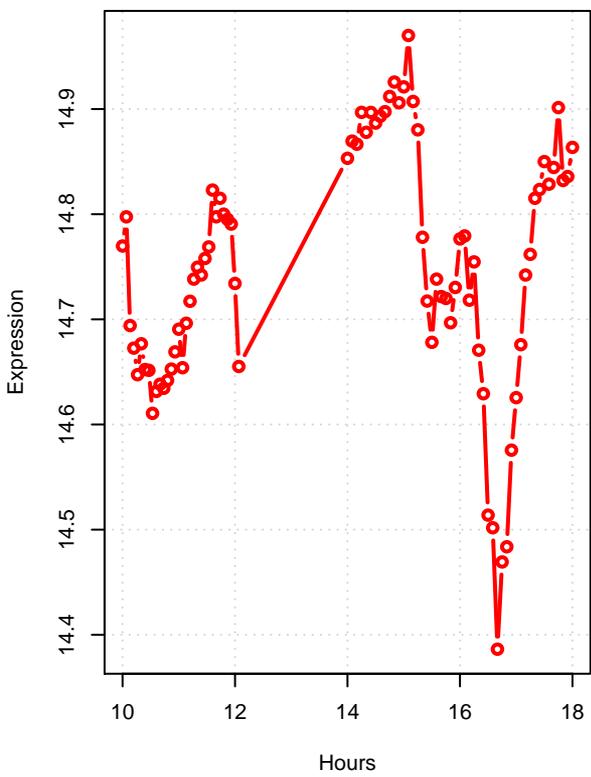
**ilv2 YMR08W**  
Acetolactate synthase



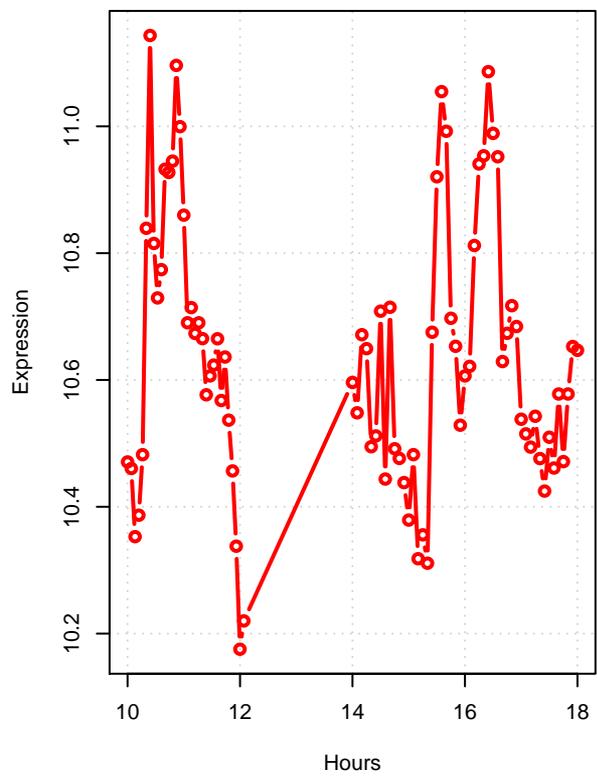
**ilv6 YCL009C**  
Regulatory subunit of acetolactate synthase



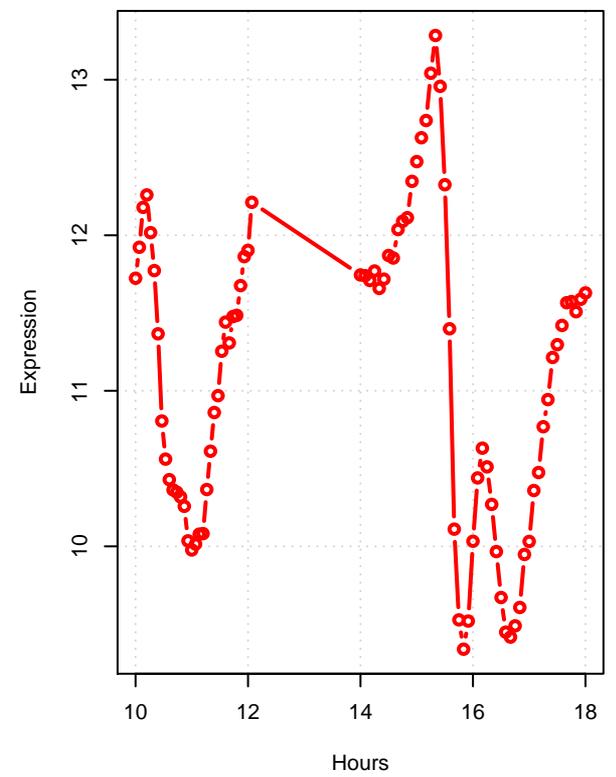
**pdh1 YLR044C**  
Major of three pyruvate decarboxylase isozymes



**pdh5 YLR134W**  
Minor isoform of pyruvate decarboxylase



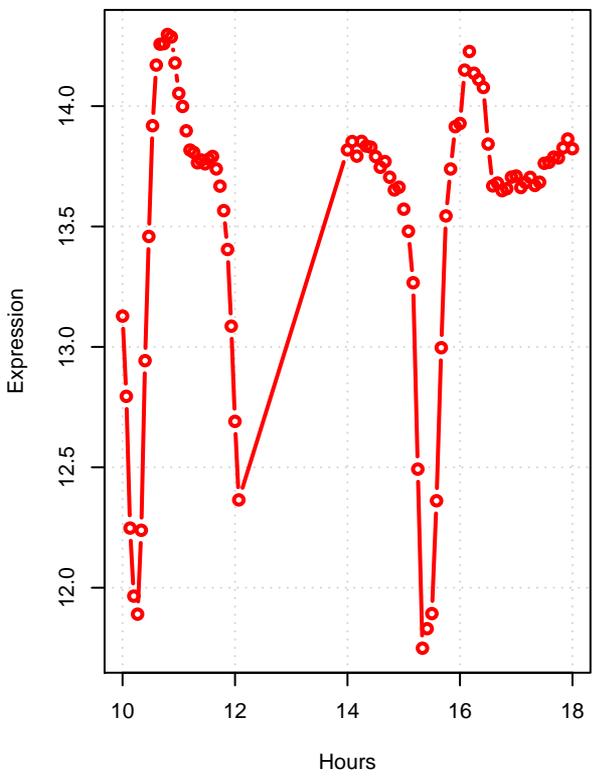
**pdh6 YGR087C**  
Minor isoform of pyruvate decarboxylase



## butanediol biosynthesis

# butanediol biosynthesis

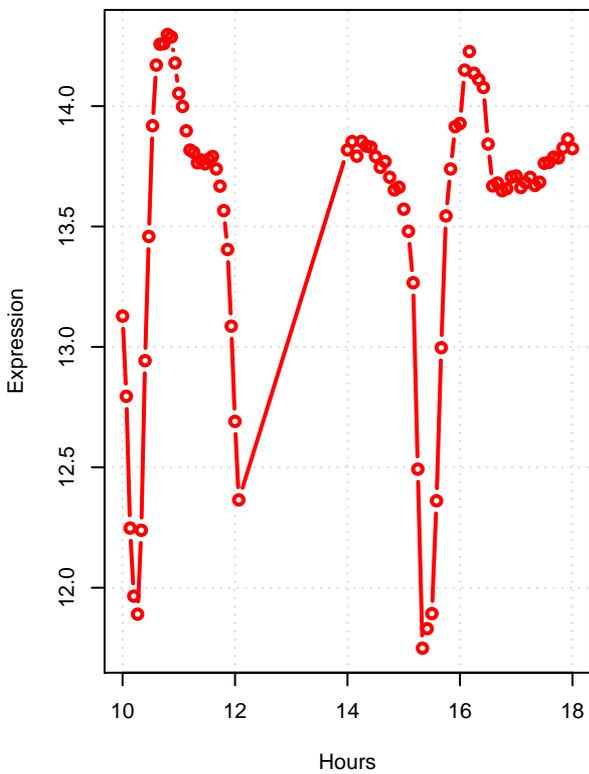
bdh1 YAL060W  
NAD-dependent (R,R)-butanediol dehydrogenase



## butanediol degradation

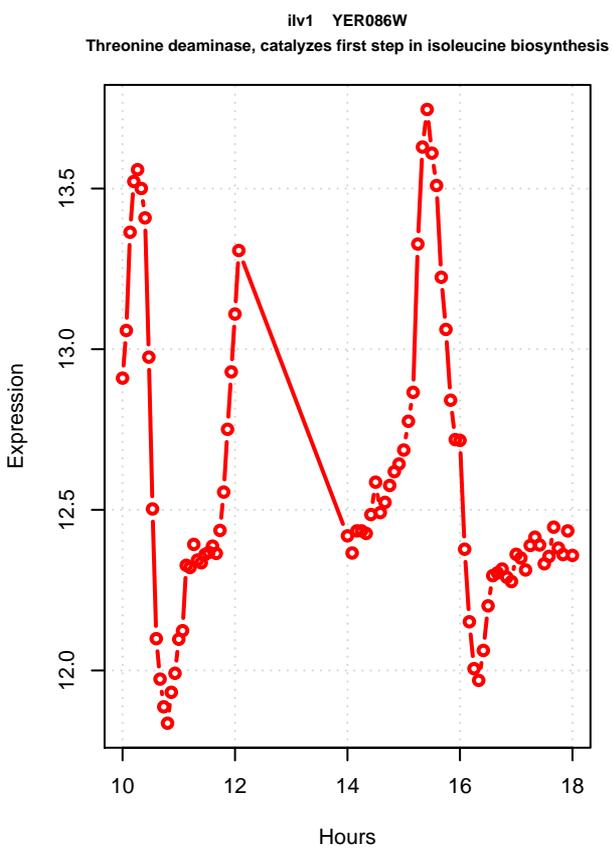
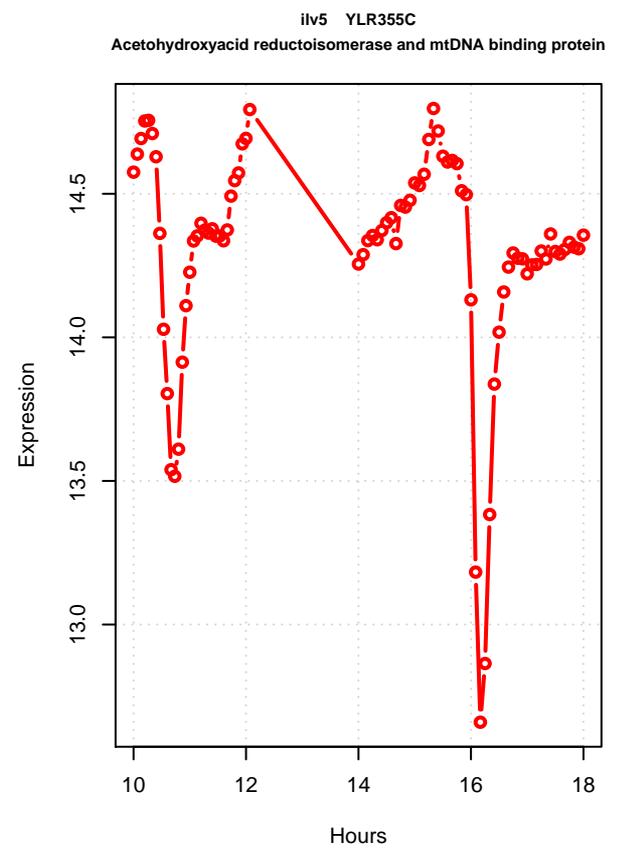
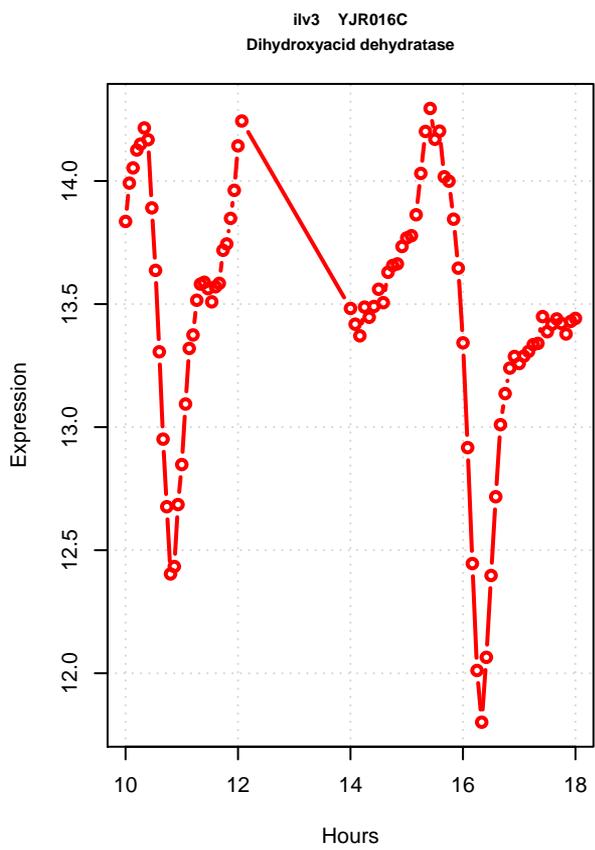
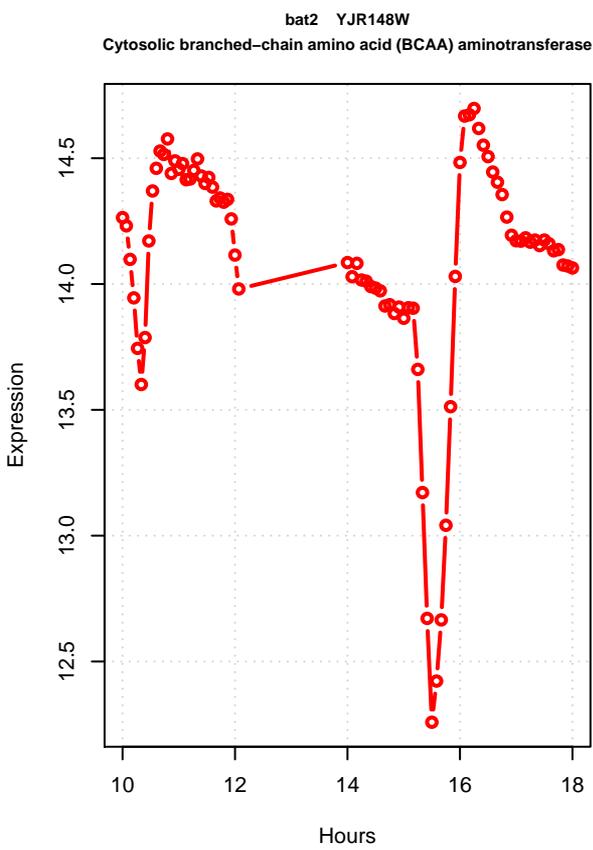
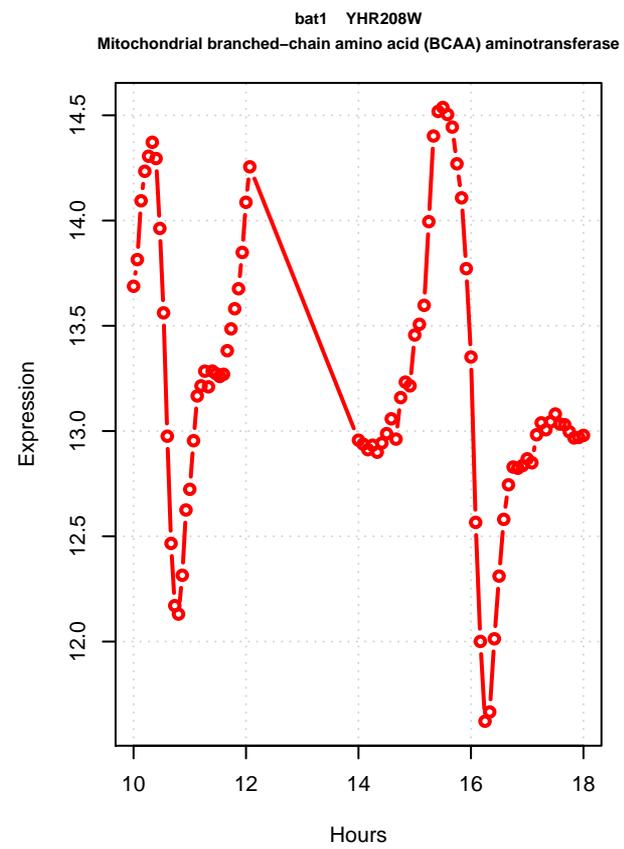
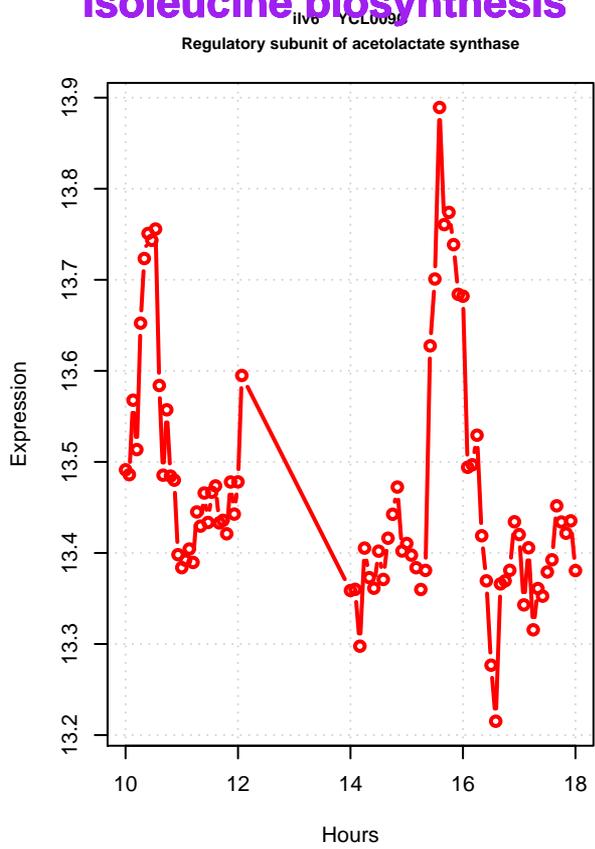
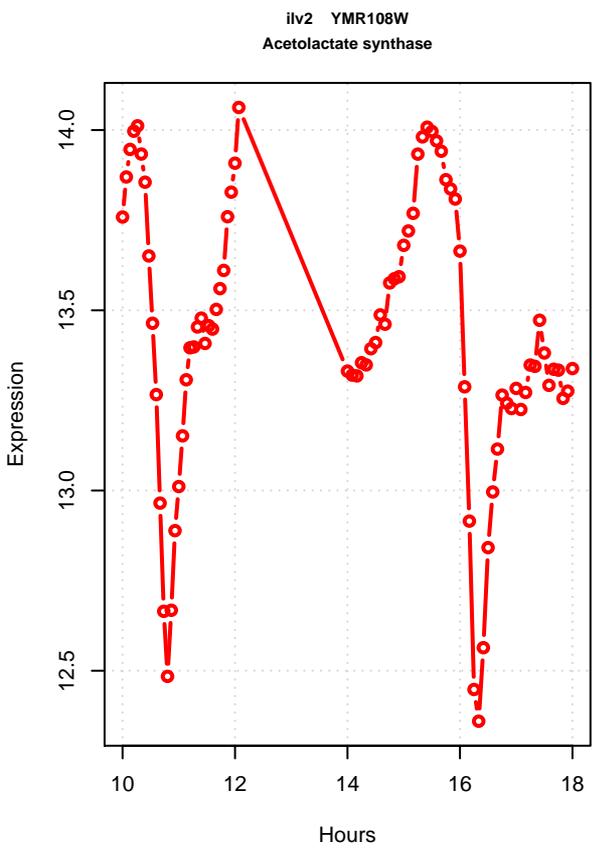
# butanediol degradation

bdh1 YAL060W  
NAD-dependent (R,R)-butanediol dehydrogenase



## isoleucine biosynthesis

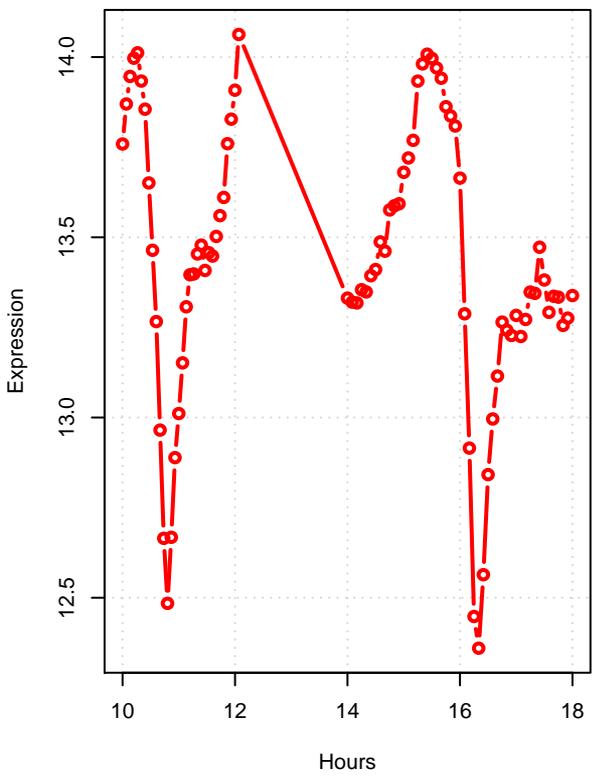
# isoleucine biosynthesis



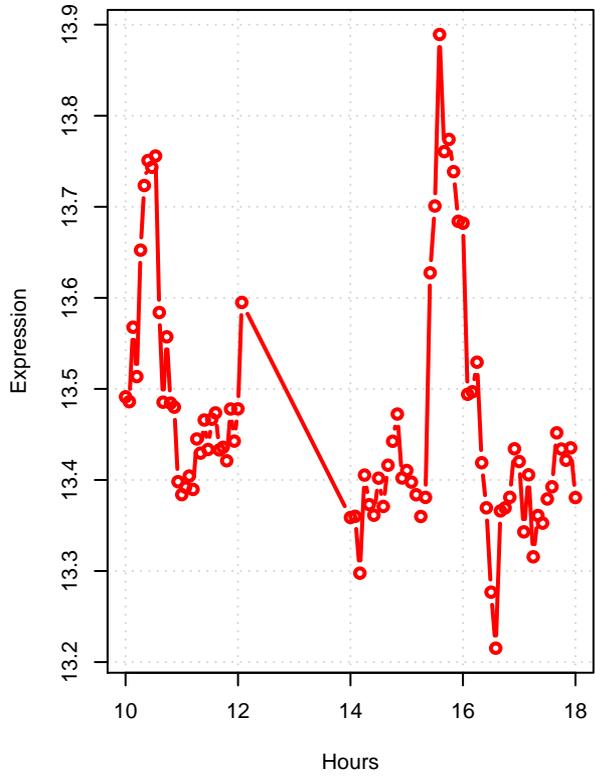
## **valine biosynthesis**

# valine biosynthesis

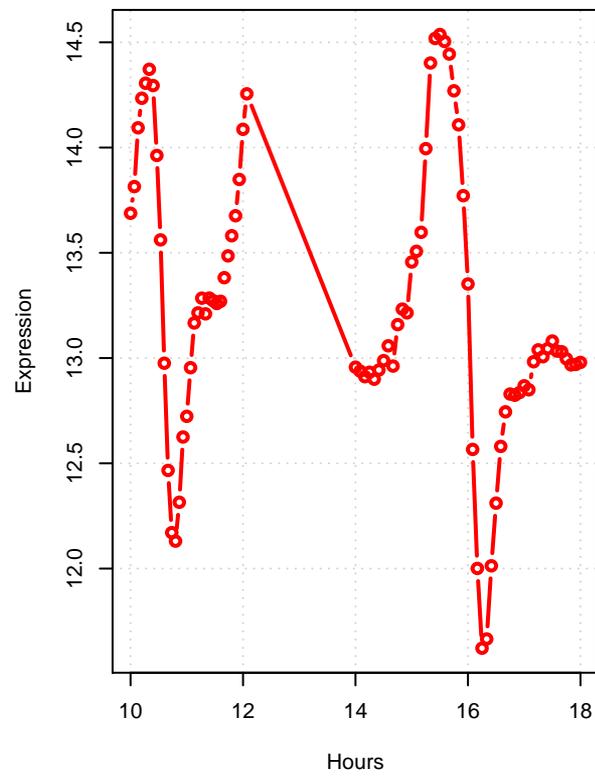
ilv2 YMR108W  
Acetolactate synthase



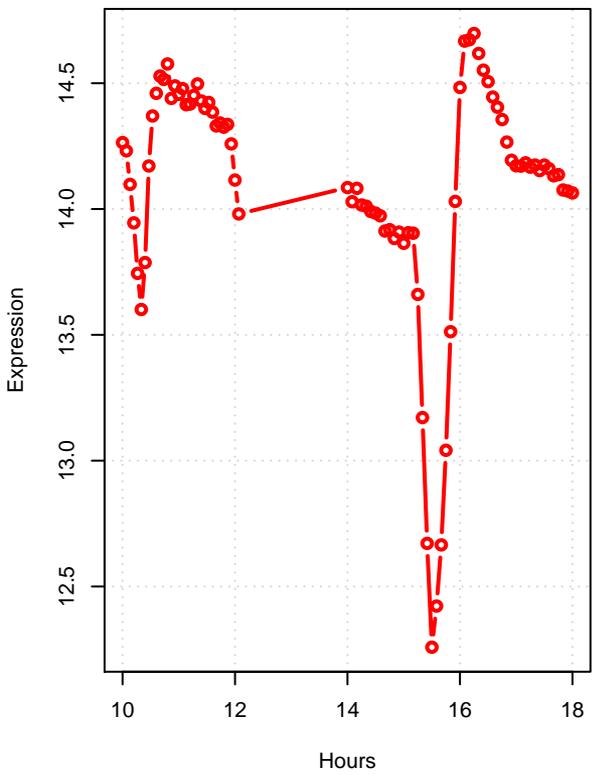
ilv6 YCL009C  
Regulatory subunit of acetolactate synthase



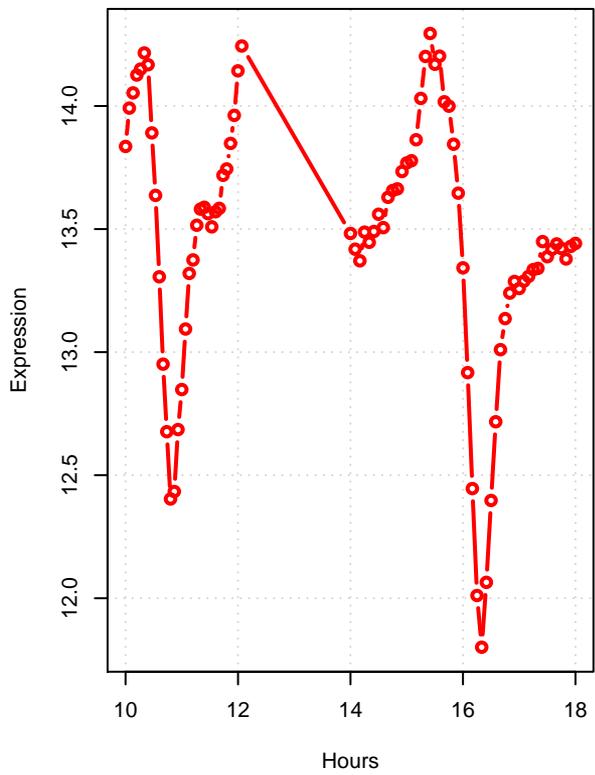
bat1 YHR208W  
Mitochondrial branched-chain amino acid (BCAA) aminotransferase



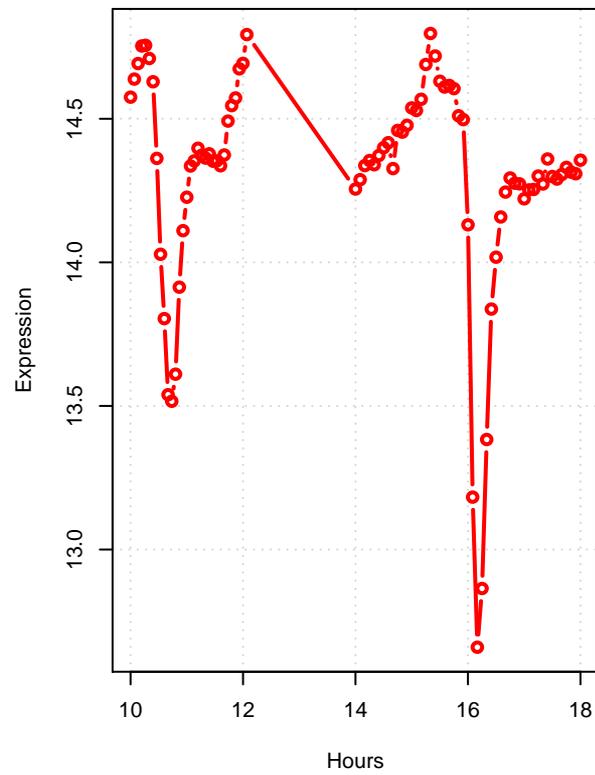
bat2 YJR148W  
Cytosolic branched-chain amino acid (BCAA) aminotransferase



ilv3 YJR016C  
Dihydroxyacid dehydratase



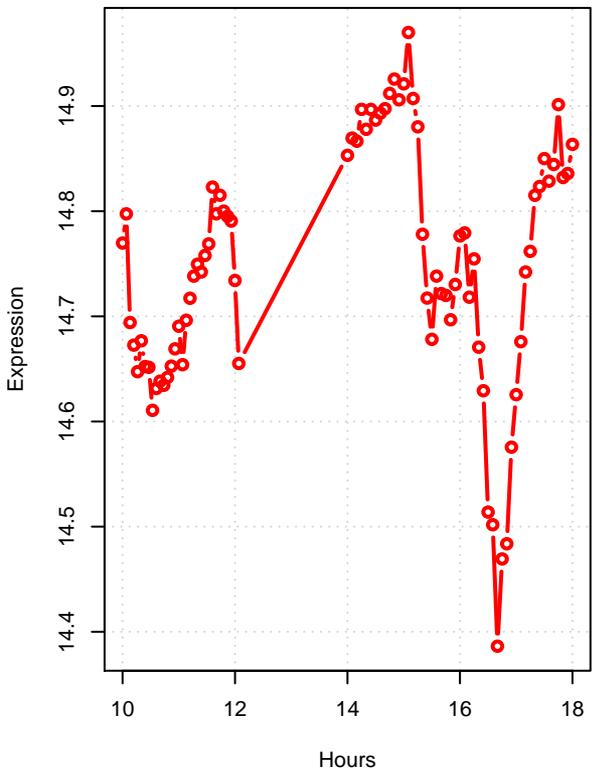
ilv5 YLR355C  
Acetoacetyl-CoA reductoisomerase and mtDNA binding protein



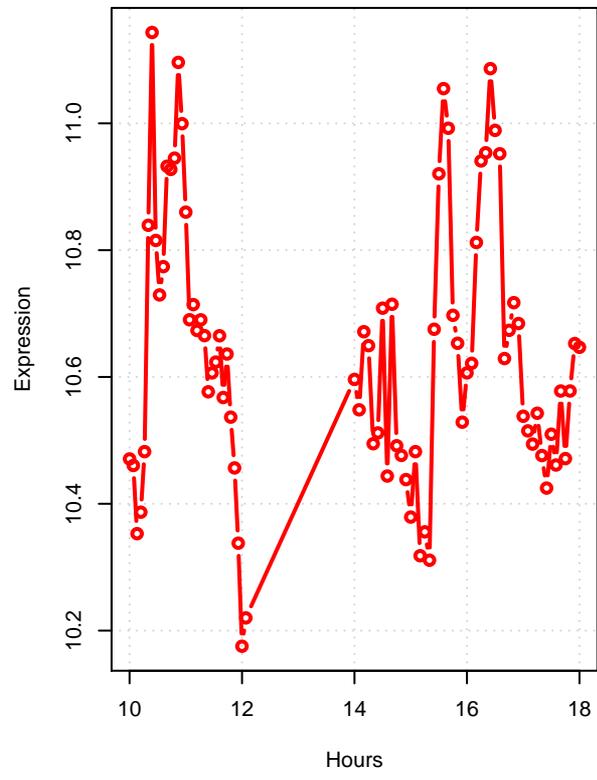
## acetoin biosynthesis II

# acetoin biosynthesis II

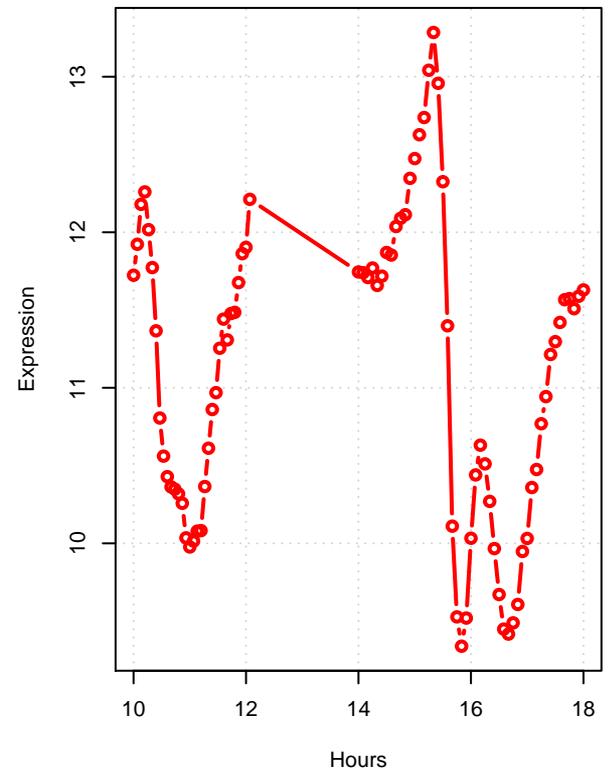
pdc1 YLR044C  
Major of three pyruvate decarboxylase isozymes



pdc5 YLR134W  
Minor isoform of pyruvate decarboxylase



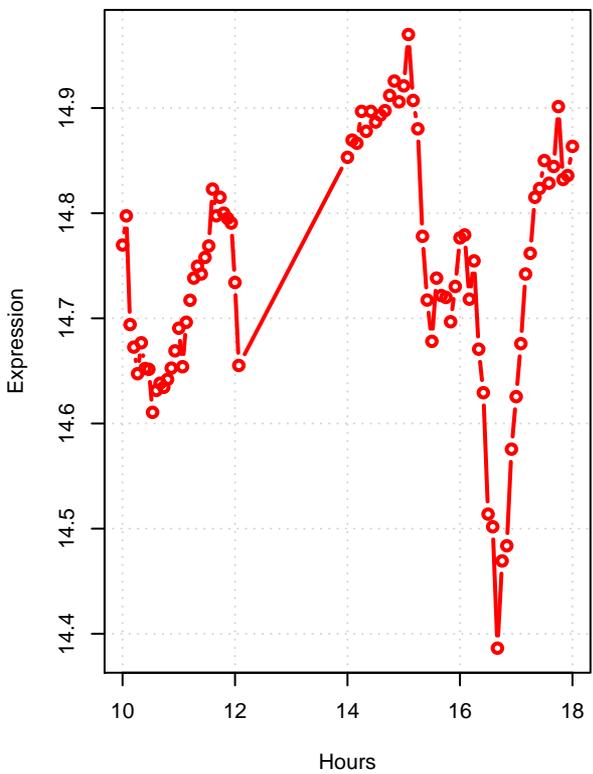
pdc6 YGR087C  
Minor isoform of pyruvate decarboxylase



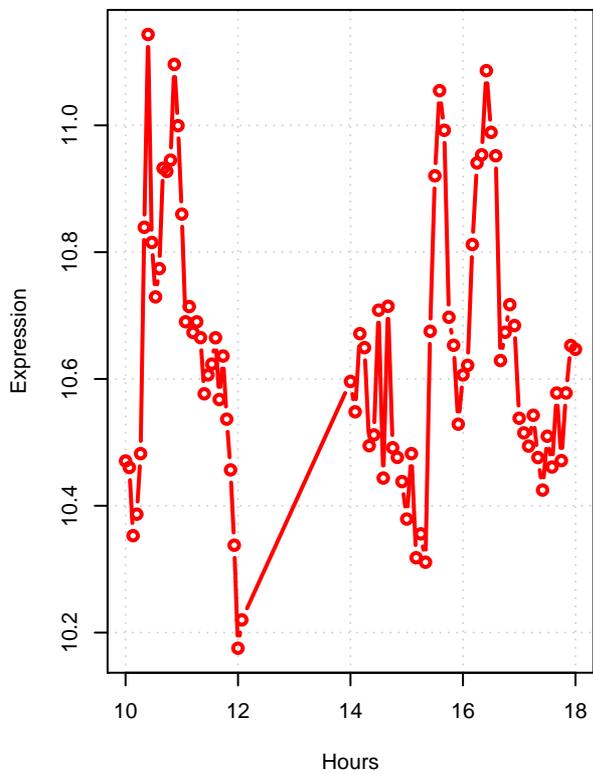
## isoleucine degradation

# isoleucine degradation

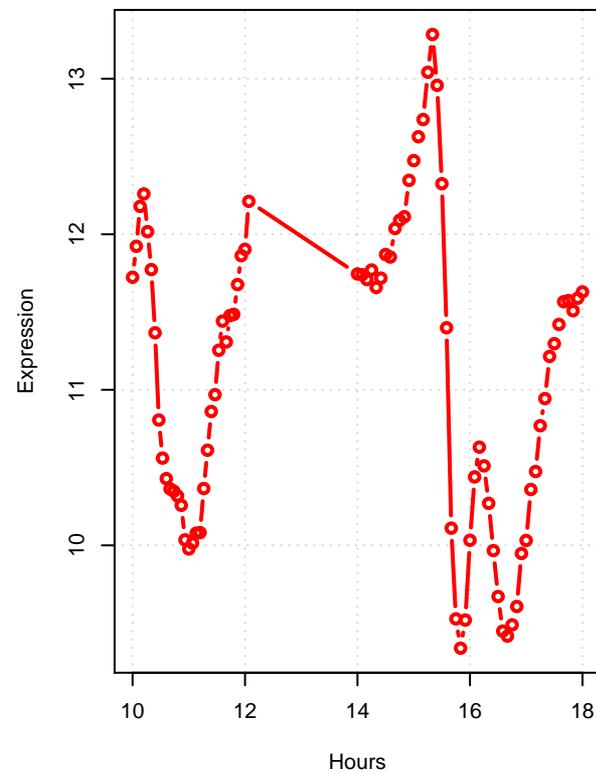
**pdc1 YLR044C**  
Major of three pyruvate decarboxylase isozymes



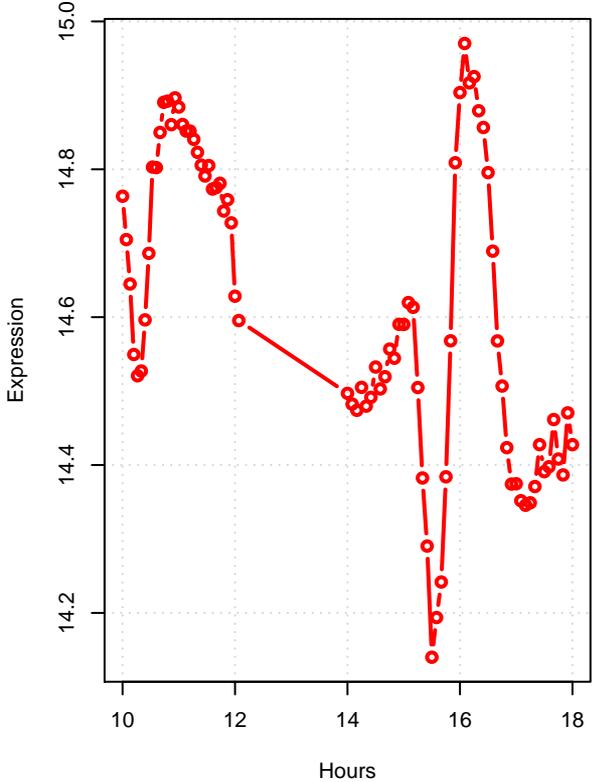
**pdcs YLR114W**  
Minor isoform of pyruvate decarboxylase



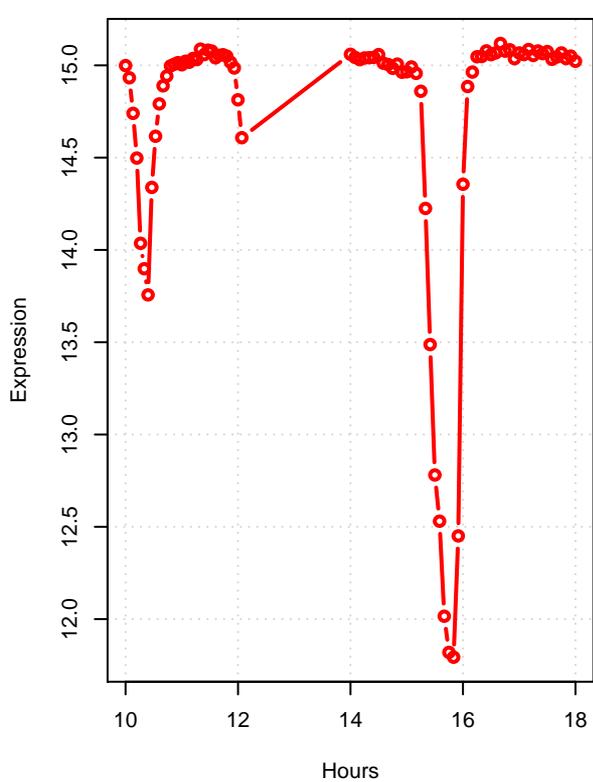
**pdcs6 YGR087C**  
Minor isoform of pyruvate decarboxylase



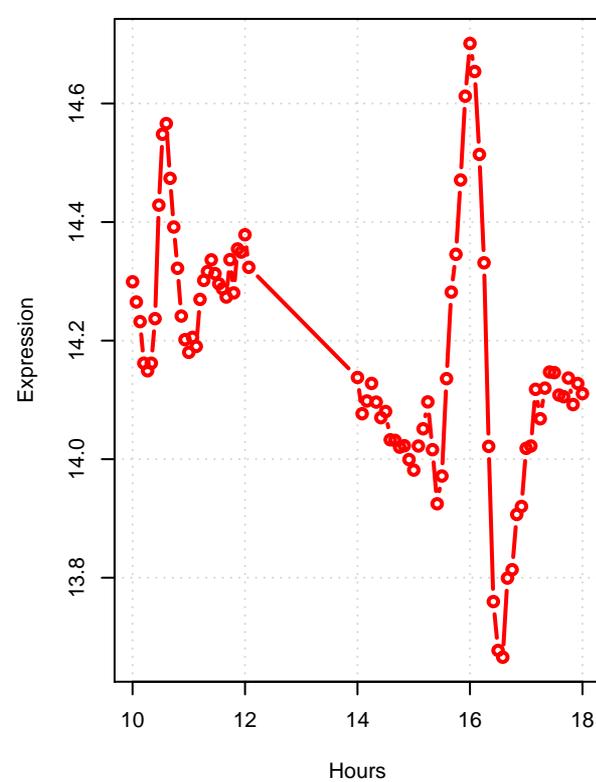
**adh1 YOL086C**  
Alcohol dehydrogenase



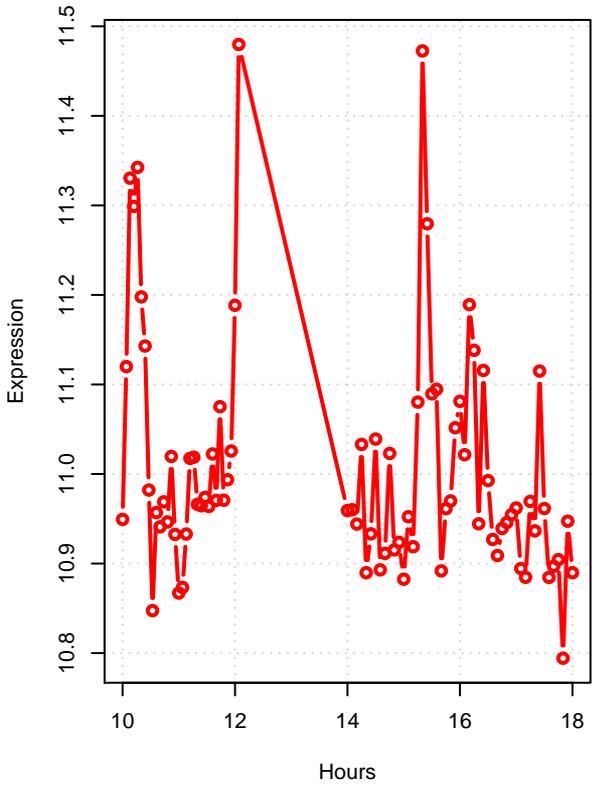
**adh2 YMR303C**  
Glucose-repressible alcohol dehydrogenase II



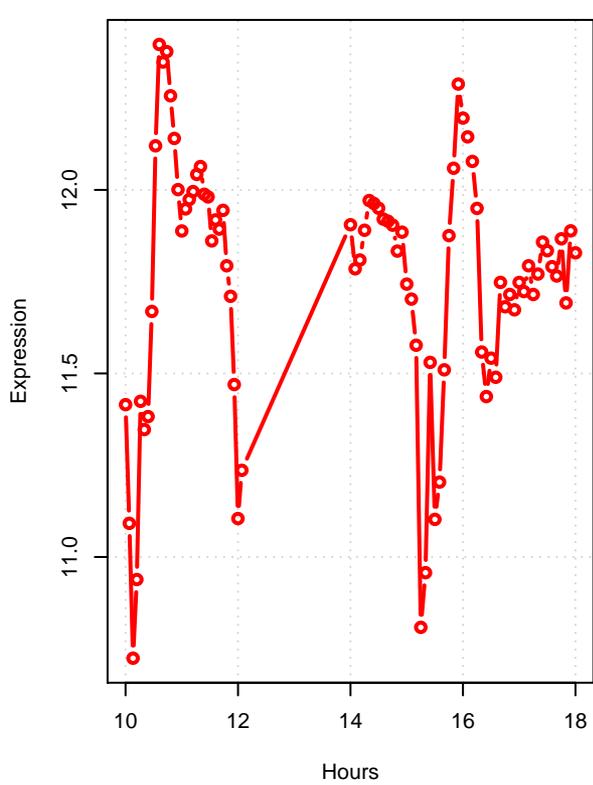
**adh3 YMR083W**  
Mitochondrial alcohol dehydrogenase isozyme III



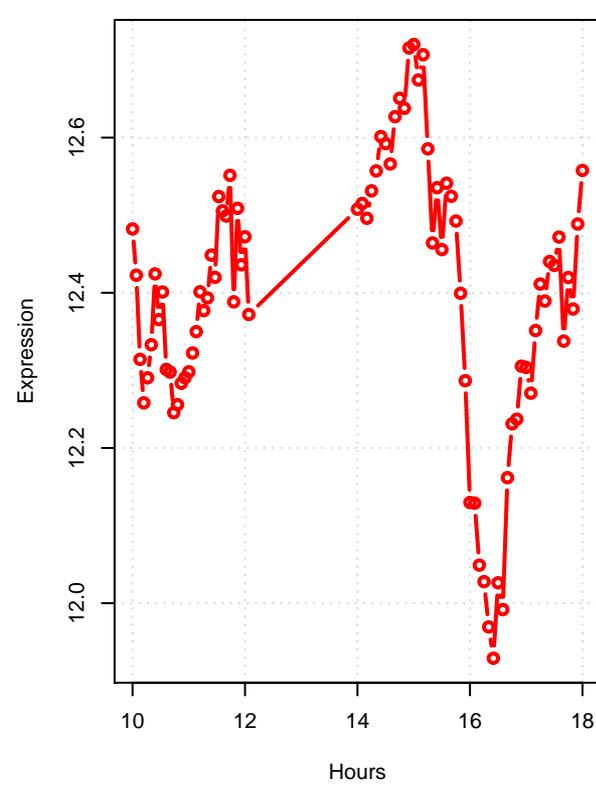
**adh4 YGL256W**  
Alcohol dehydrogenase isoenzyme type IV



**adh5 YBR145W**  
Alcohol dehydrogenase isoenzyme V

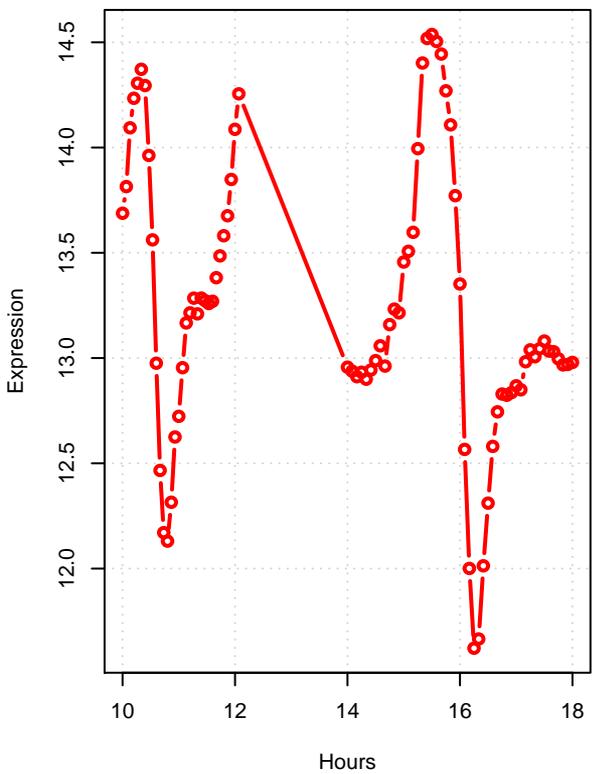


**sfa1 YDL168W**  
Bifunctional alcohol dehydrogenase and formaldehyde dehydrogenase

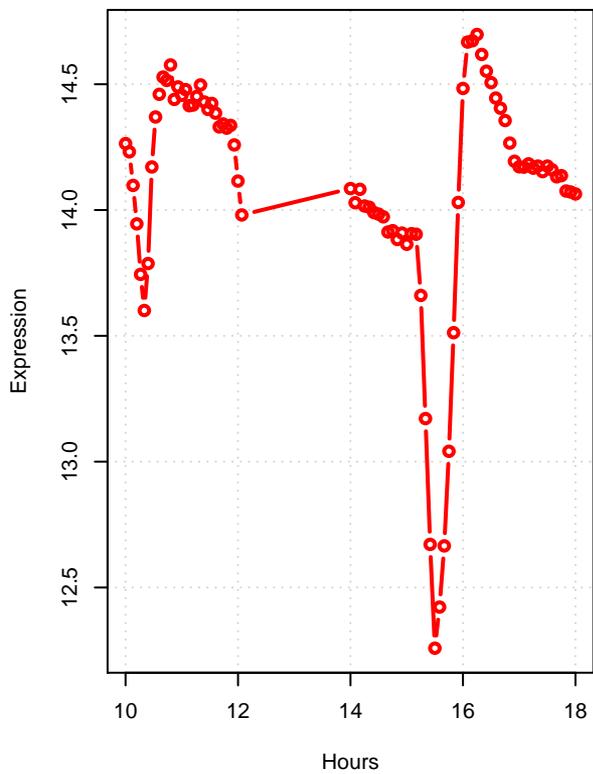


# isoleucine degradation

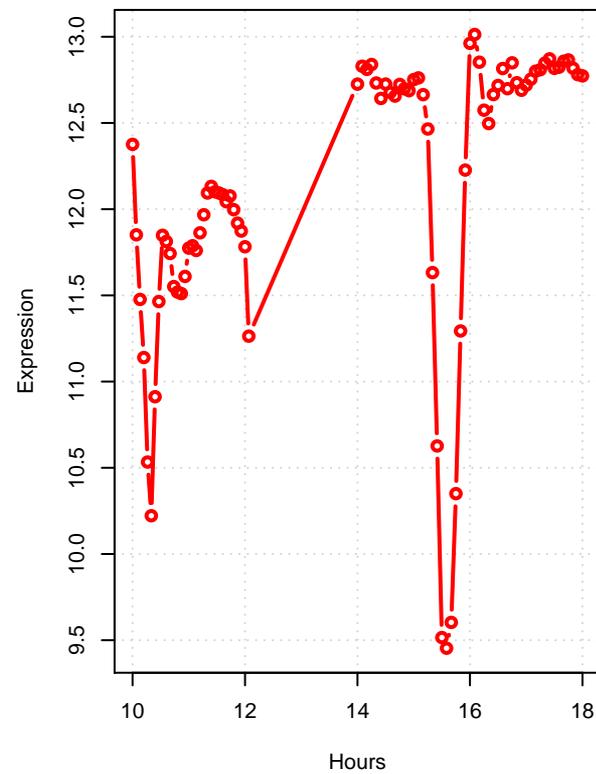
bat1 YHR208W  
Mitochondrial branched-chain amino acid (BCAA) aminotransferase



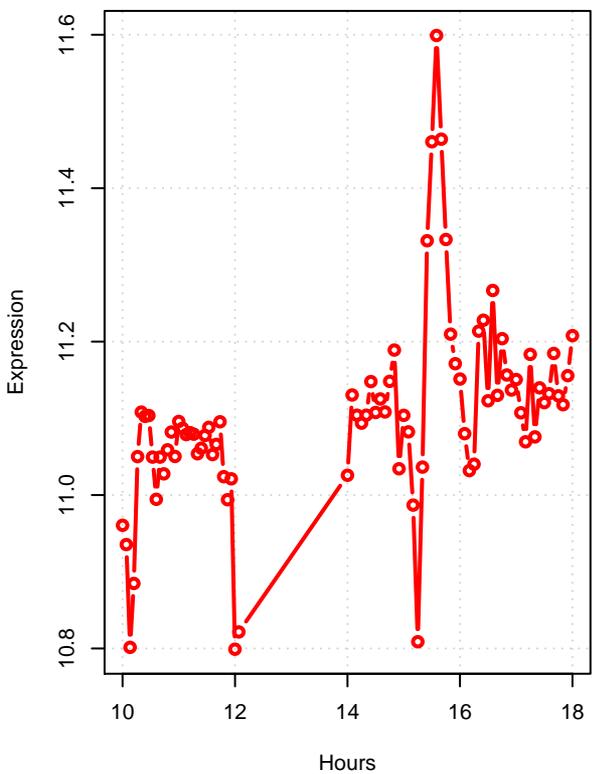
bat2 YJR18W  
Cytosolic branched-chain amino acid (BCAA) aminotransferase



aro10 YDR380W  
Phenylpyruvate decarboxylase



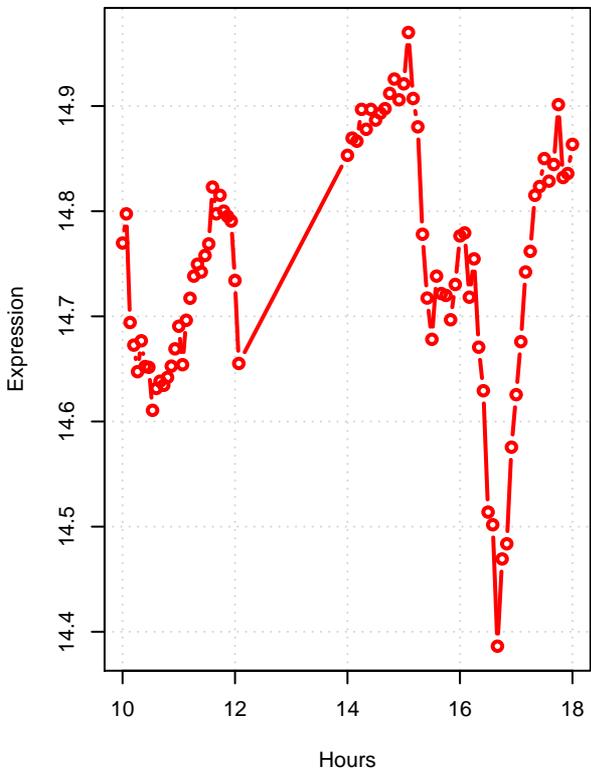
thi3 YDL080C  
Regulatory protein that binds Pdc2p and Thi2p transcription factors



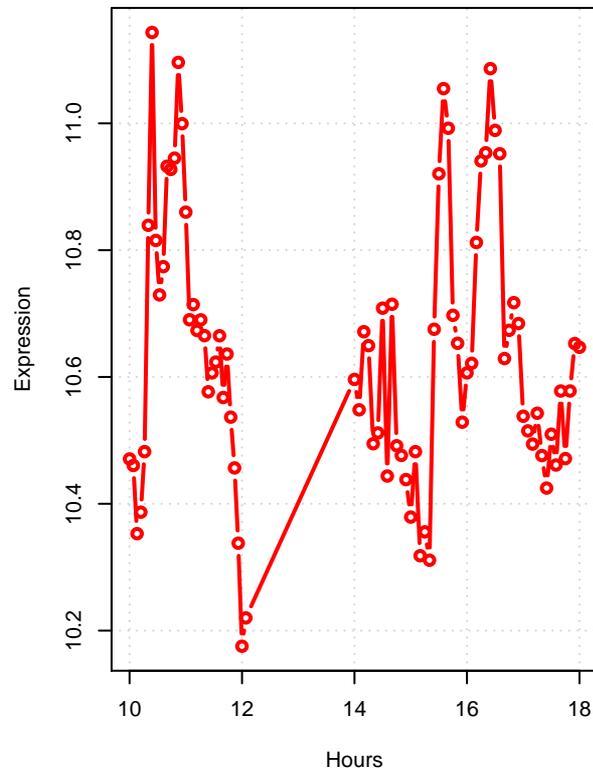
## phenylalanine degradation

# phenylalanine degradation

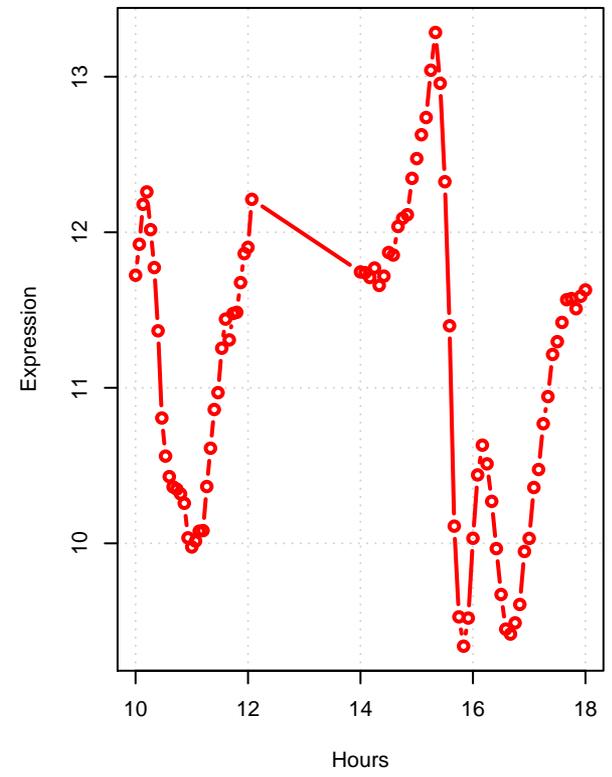
**pdc1 YLR044C**  
Major of three pyruvate decarboxylase isozymes



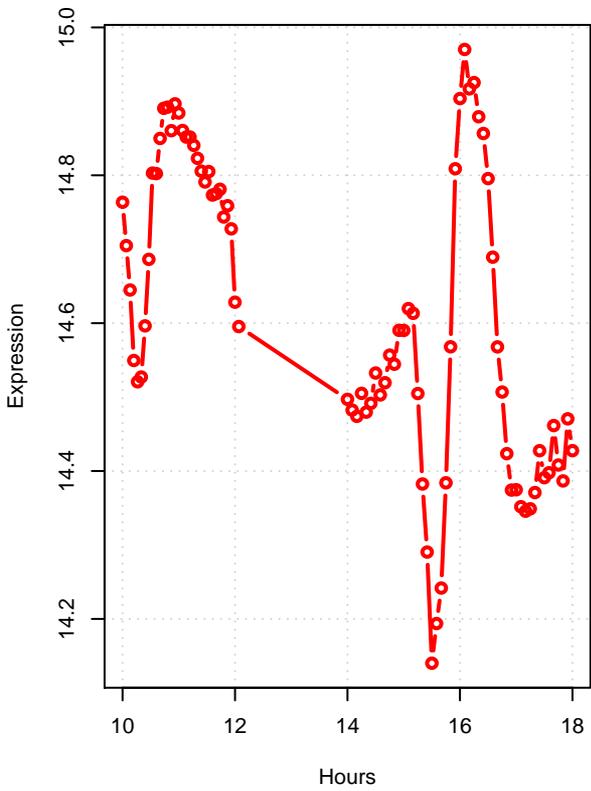
**pdc5 YLR134W**  
Minor isoform of pyruvate decarboxylase



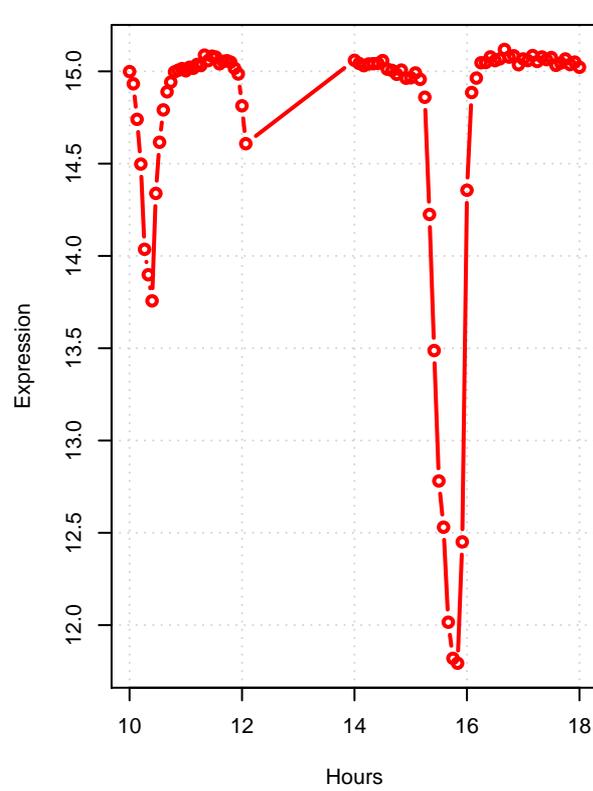
**pdc6 YGR087C**  
Minor isoform of pyruvate decarboxylase



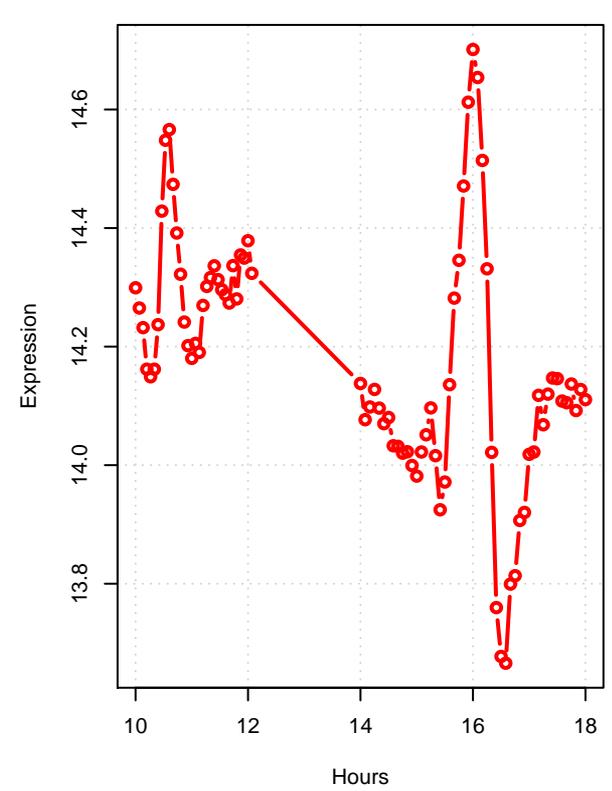
**adh1 YOL086C**  
Alcohol dehydrogenase



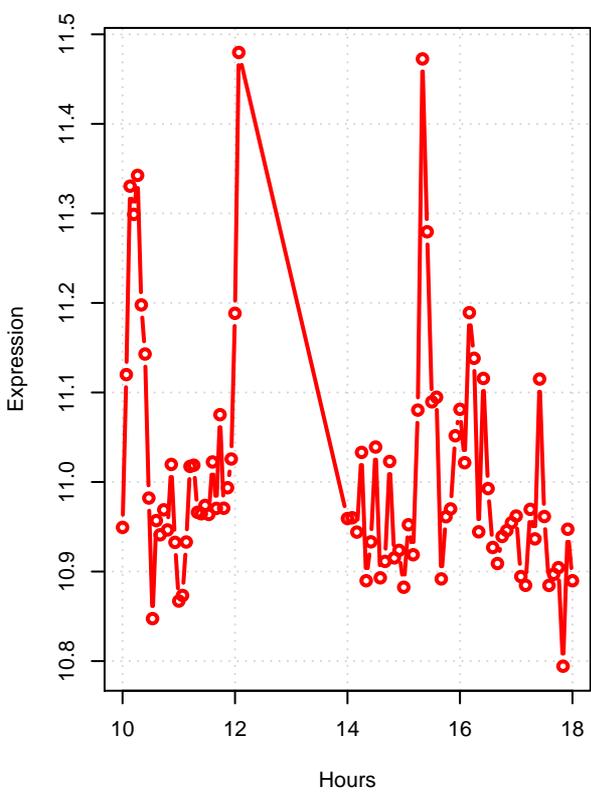
**adh2 YMR303C**  
Glucose-repressible alcohol dehydrogenase II



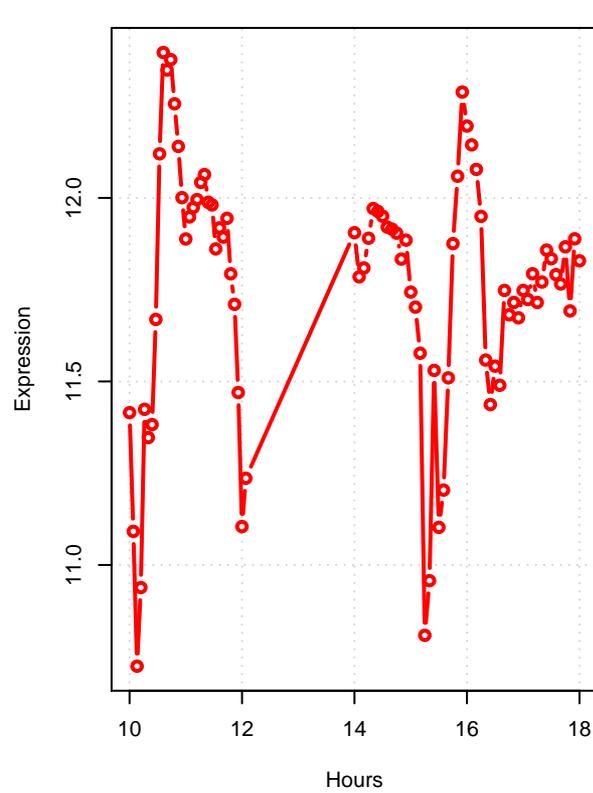
**adh3 YMR083W**  
Mitochondrial alcohol dehydrogenase isozyme III



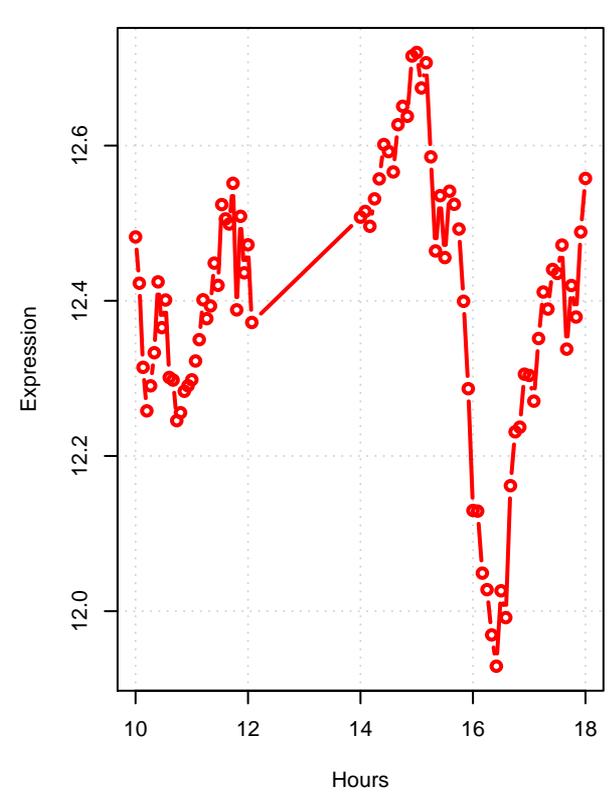
**adh4 YGL256W**  
Alcohol dehydrogenase isoenzyme type IV



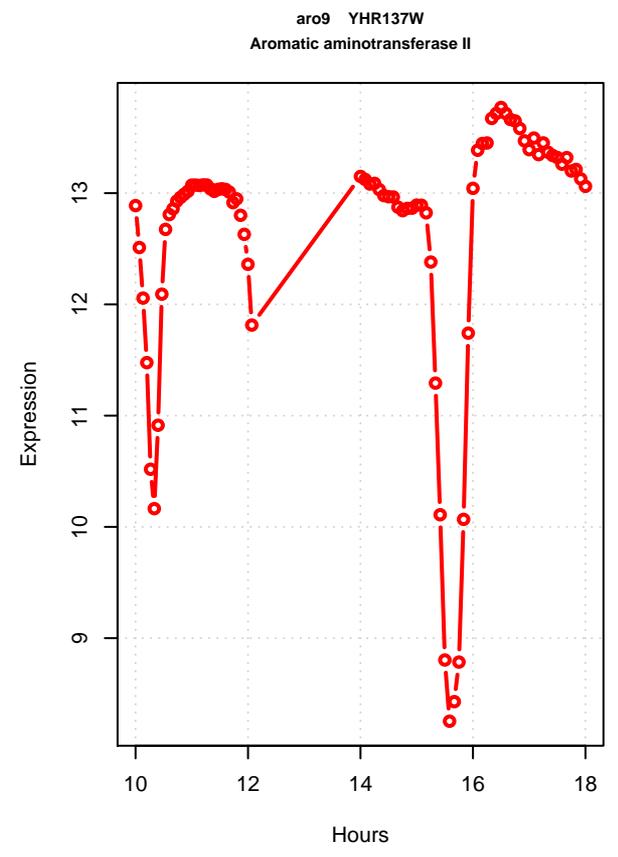
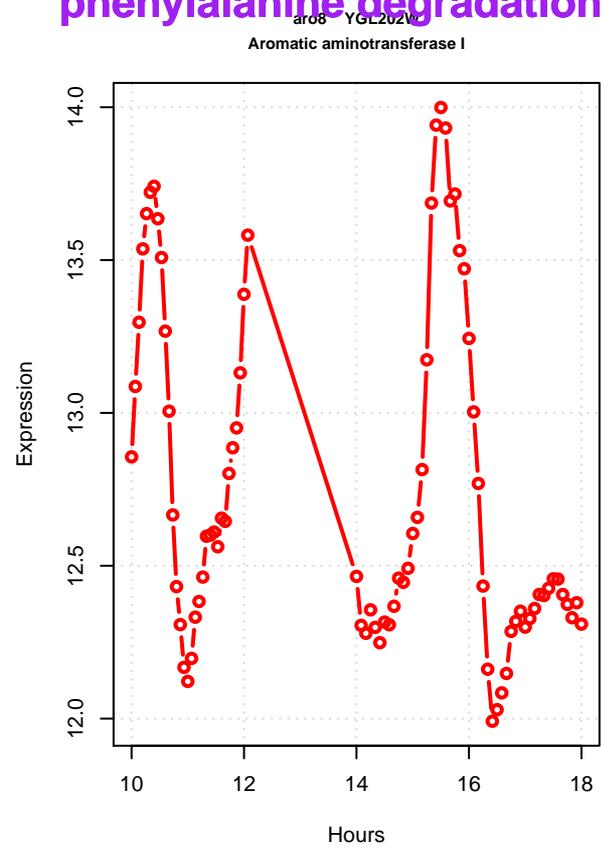
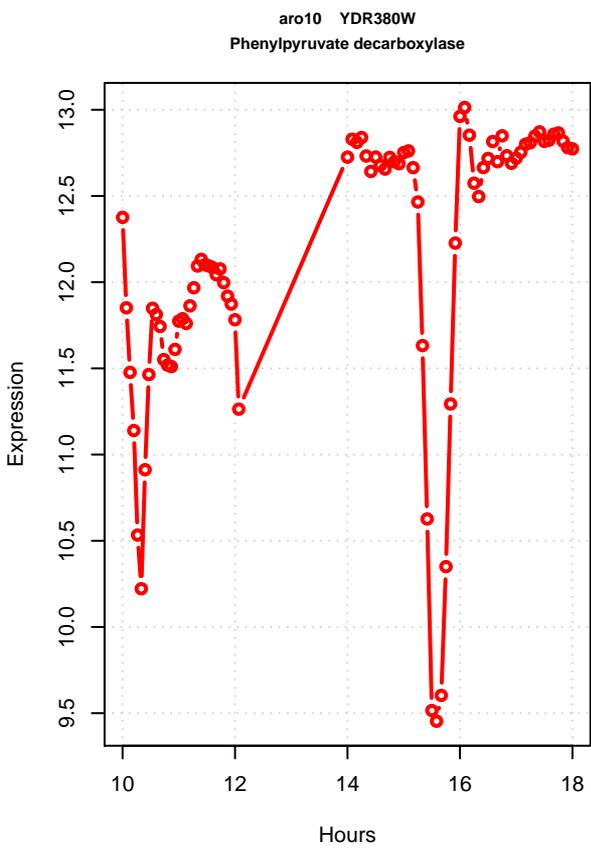
**adh5 YBR145W**  
Alcohol dehydrogenase isoenzyme V



**sfa1 YDL168W**  
Bifunctional alcohol dehydrogenase and formaldehyde dehydrogenase

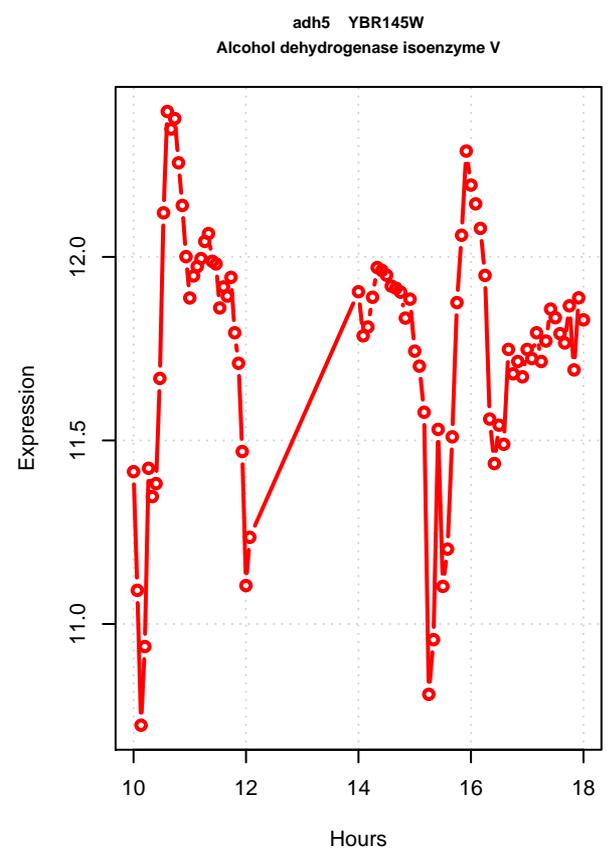
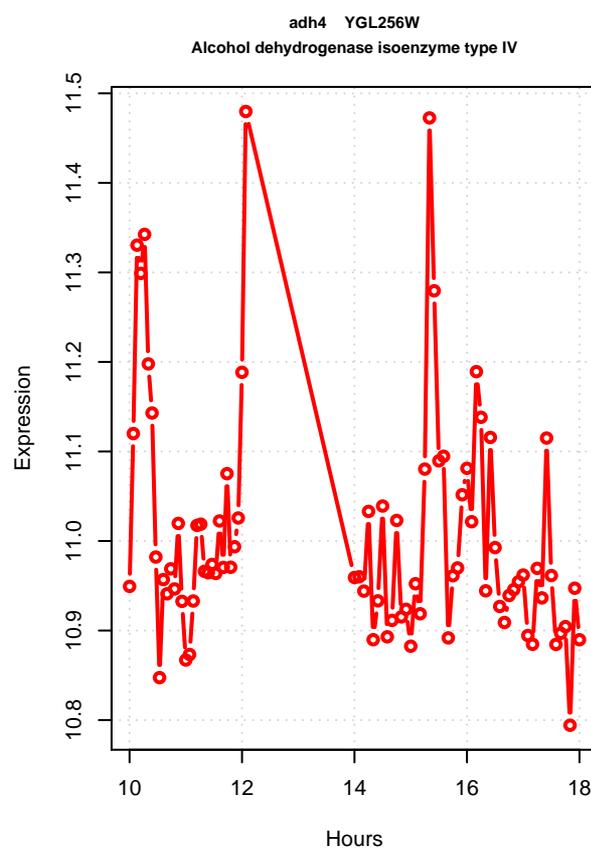
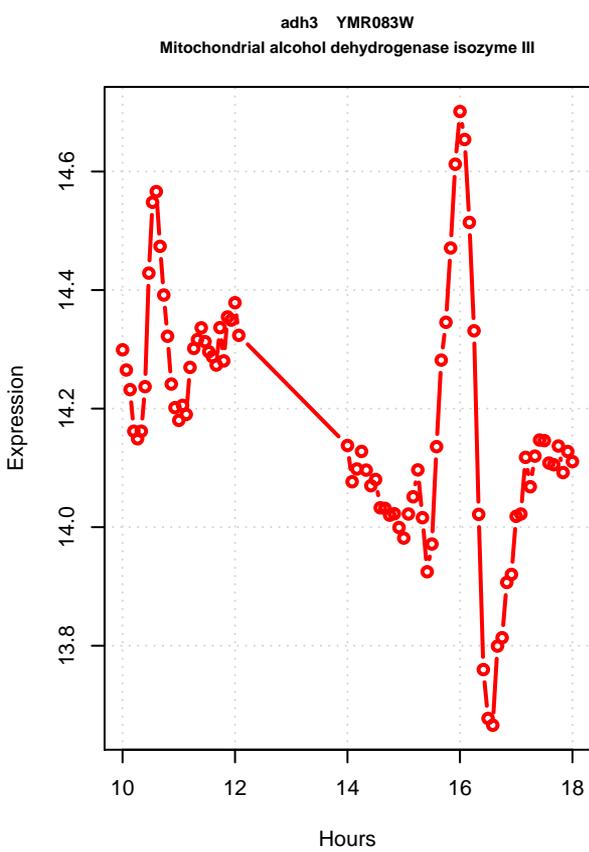
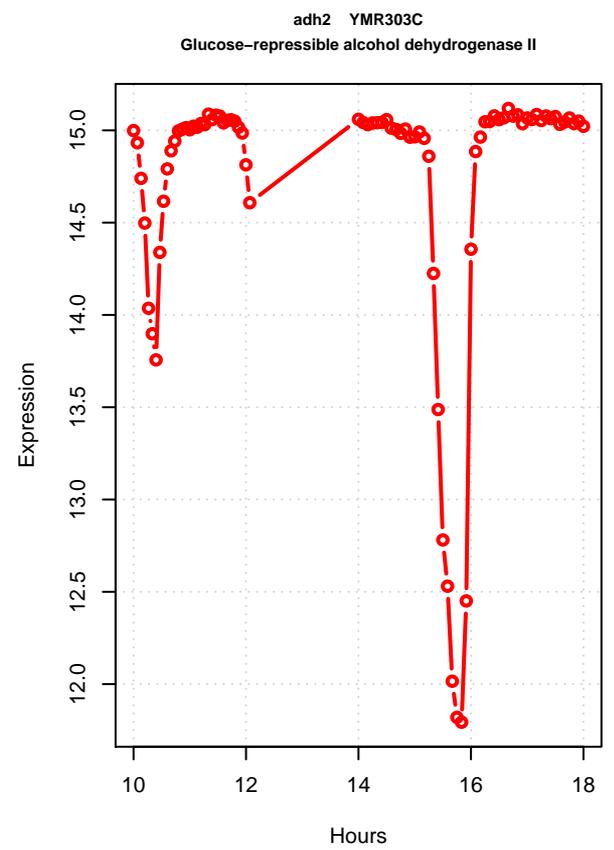
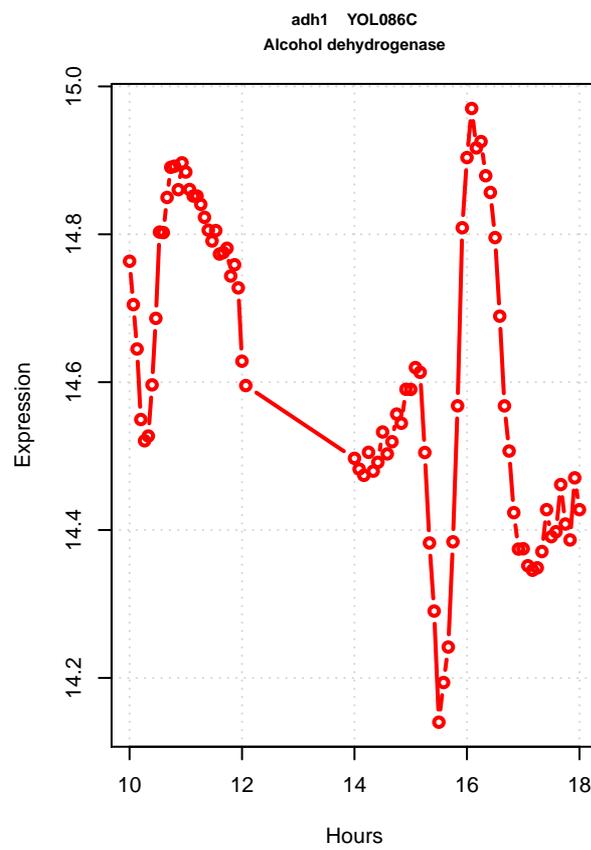
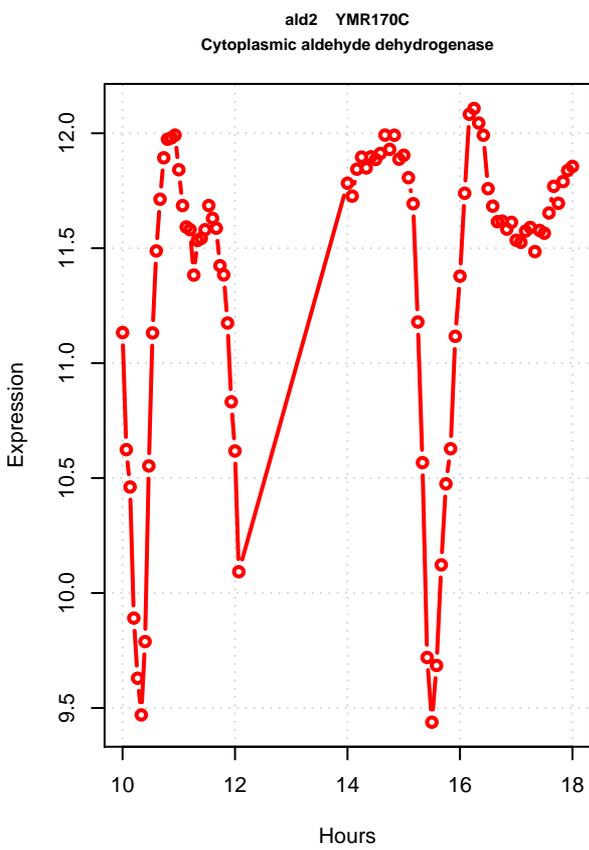
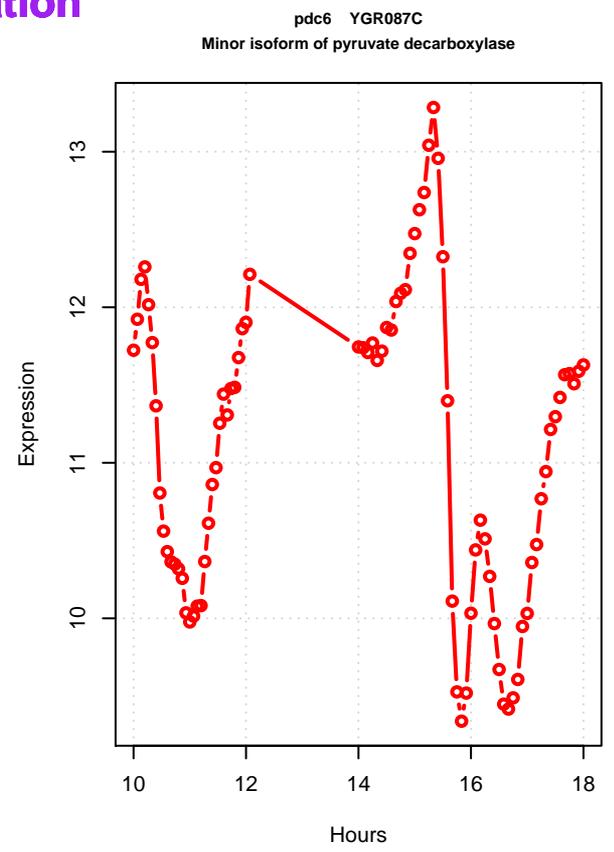
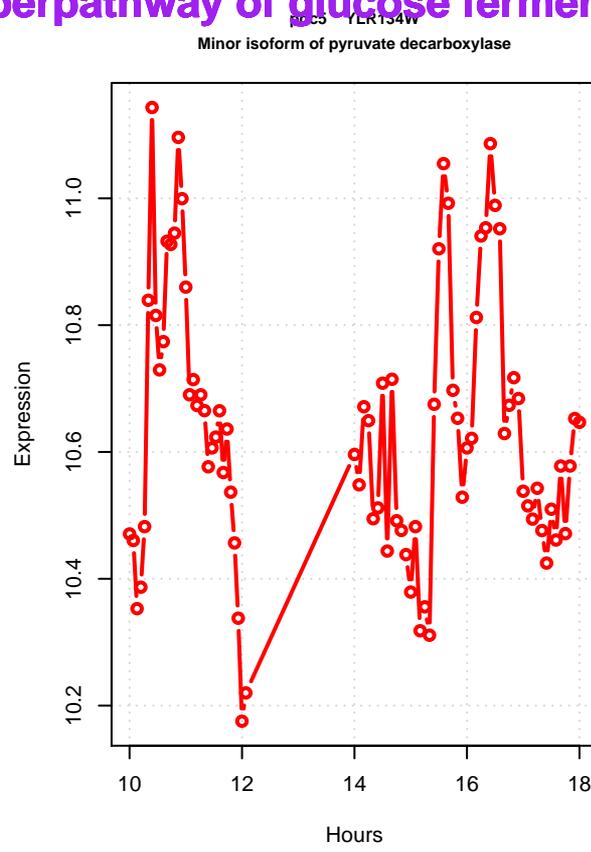
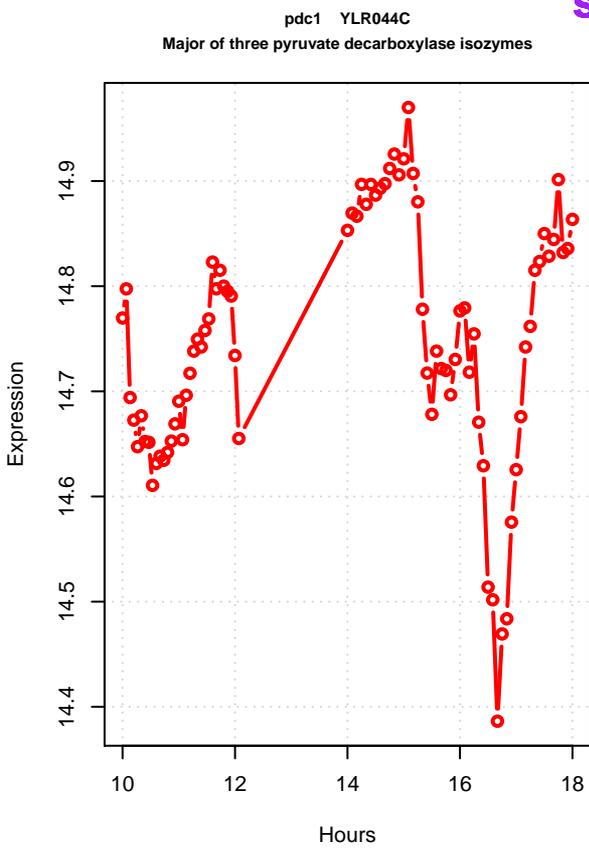


# phenylalanine degradation



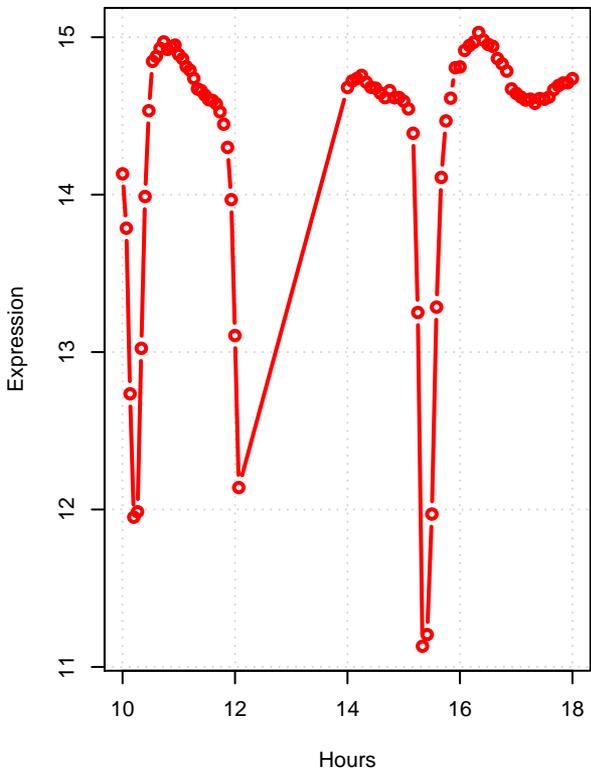
## **superpathway of glucose fermentation**

# superpathway of glucose fermentation

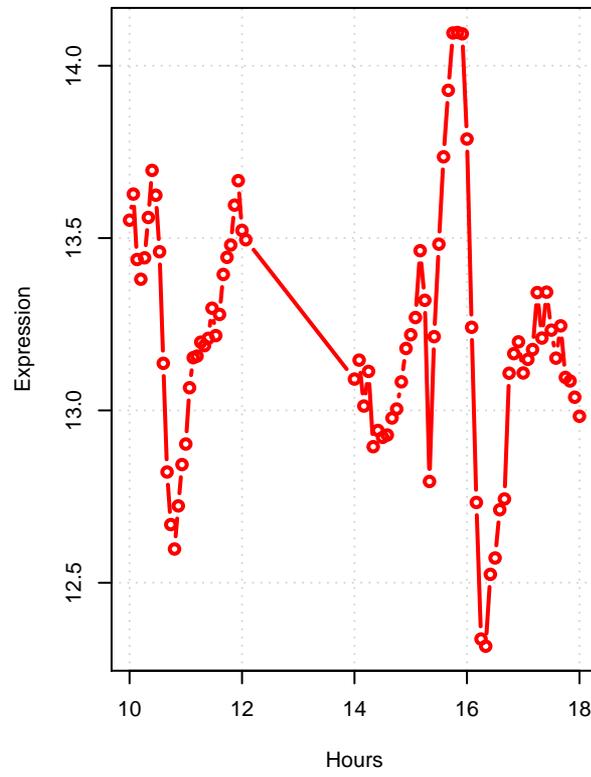


# superpathway of glucose fermentation

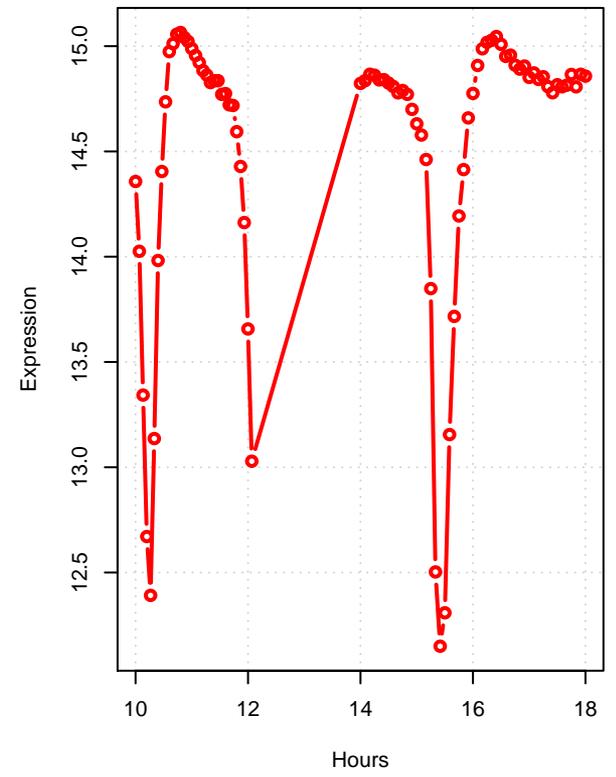
hvk1 YFR053C  
Hexokinase isoenzyme 1



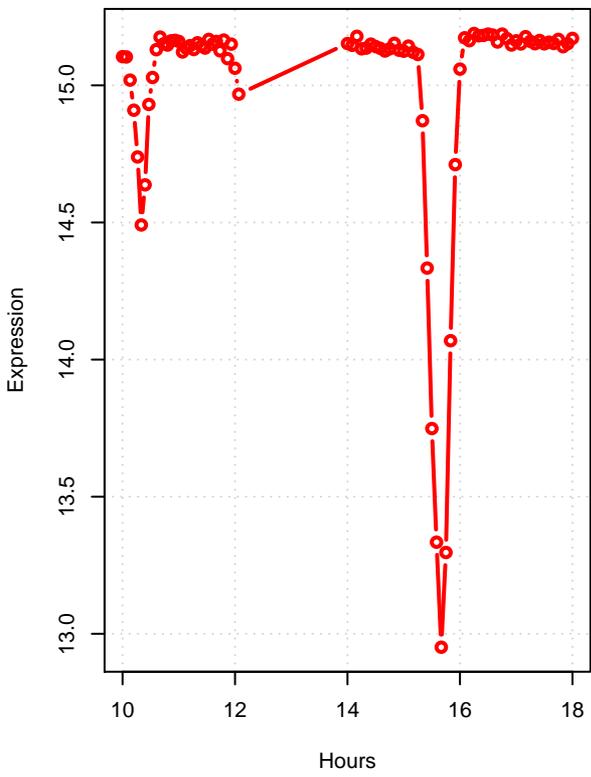
hvk2 YGL233W  
Hexokinase isoenzyme 2



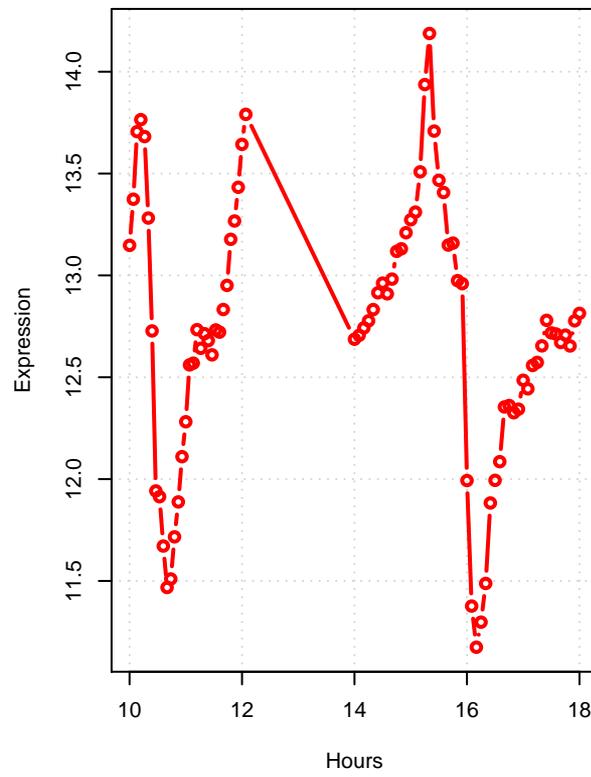
glk1 YCL040W  
Glucokinase



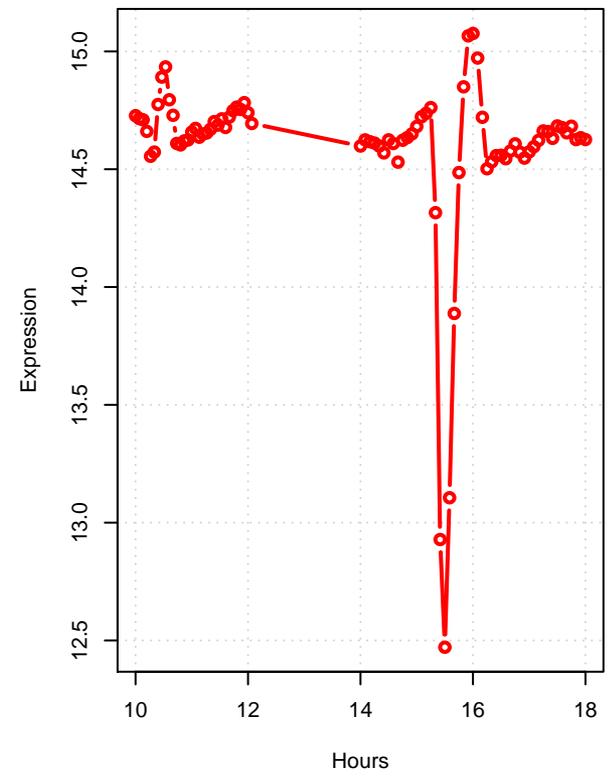
ald4 YOR374W  
Mitochondrial aldehyde dehydrogenase



ald5 YER073W  
Mitochondrial aldehyde dehydrogenase

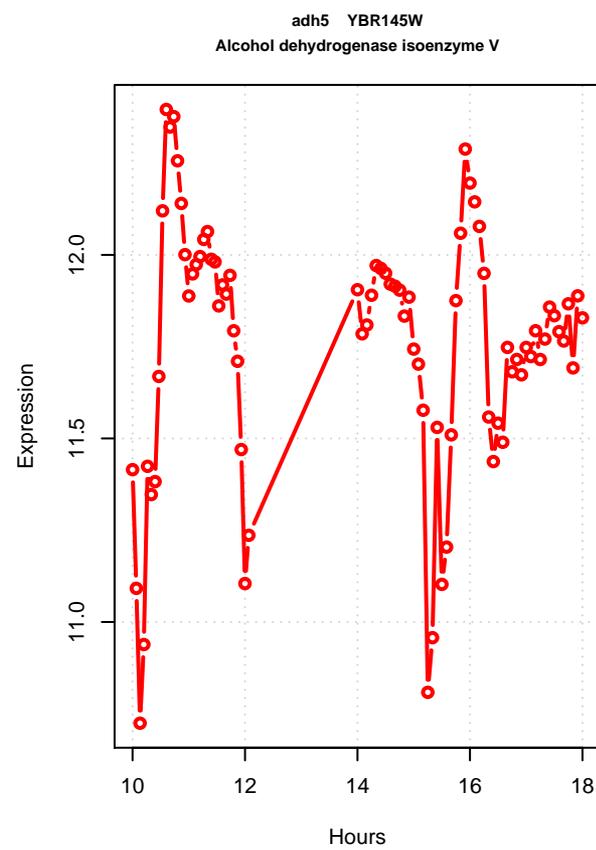
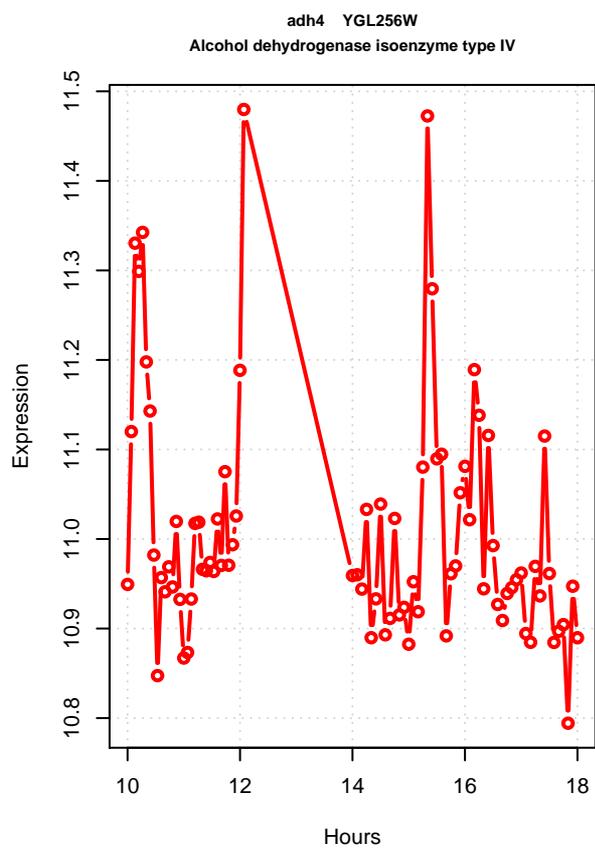
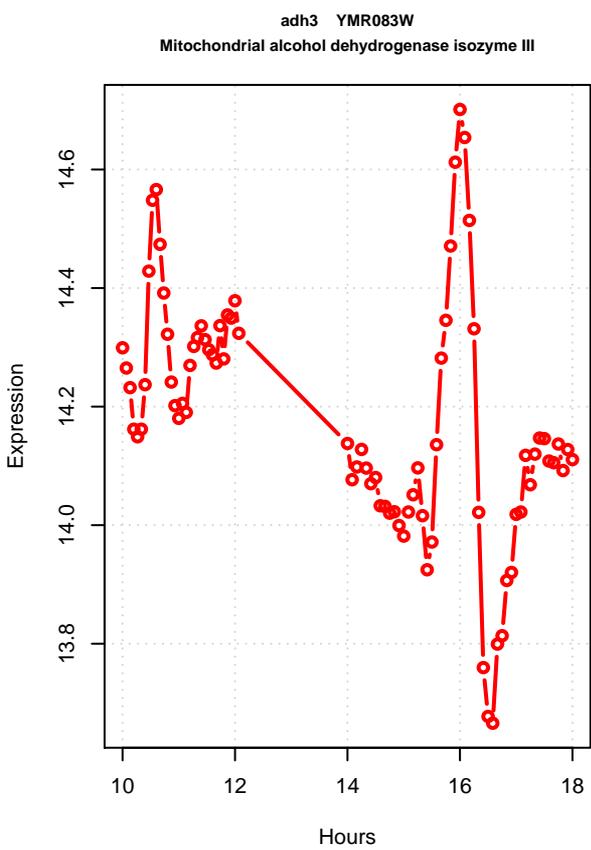
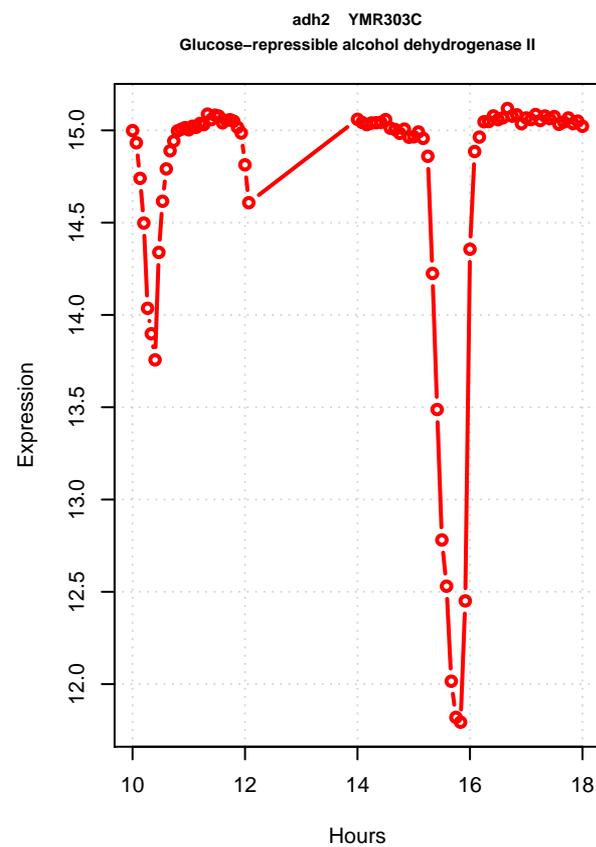
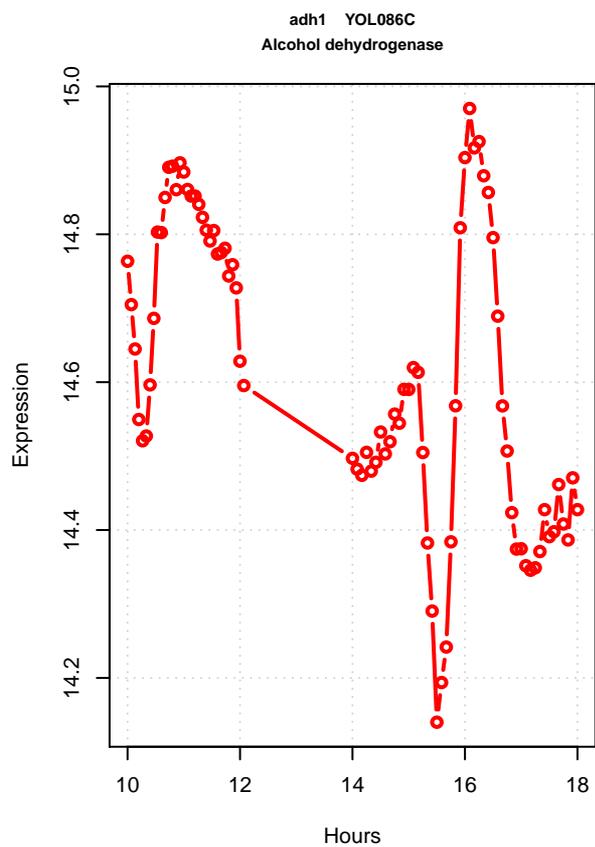
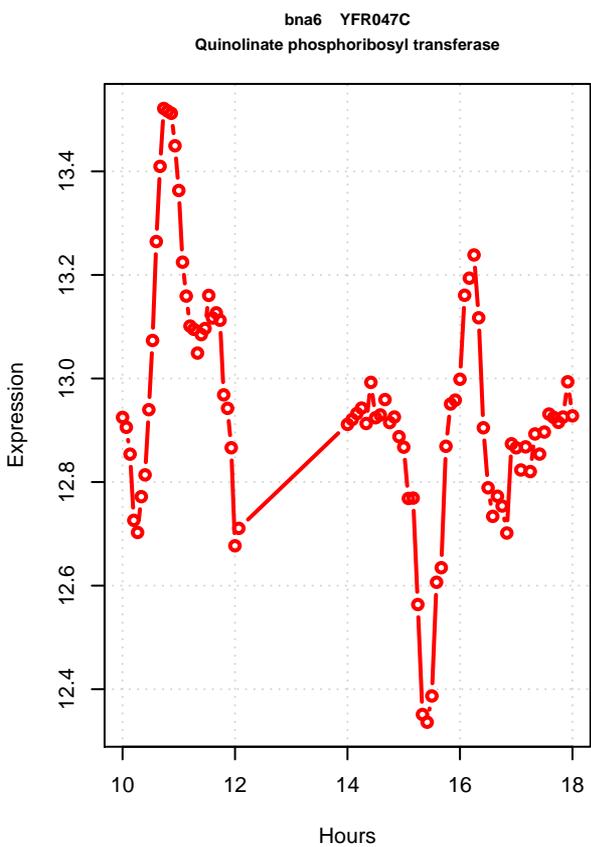
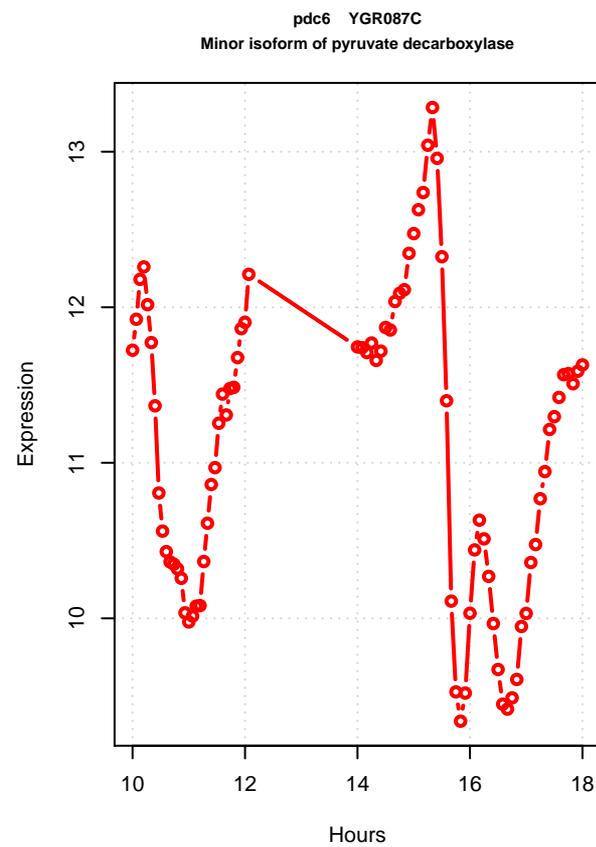
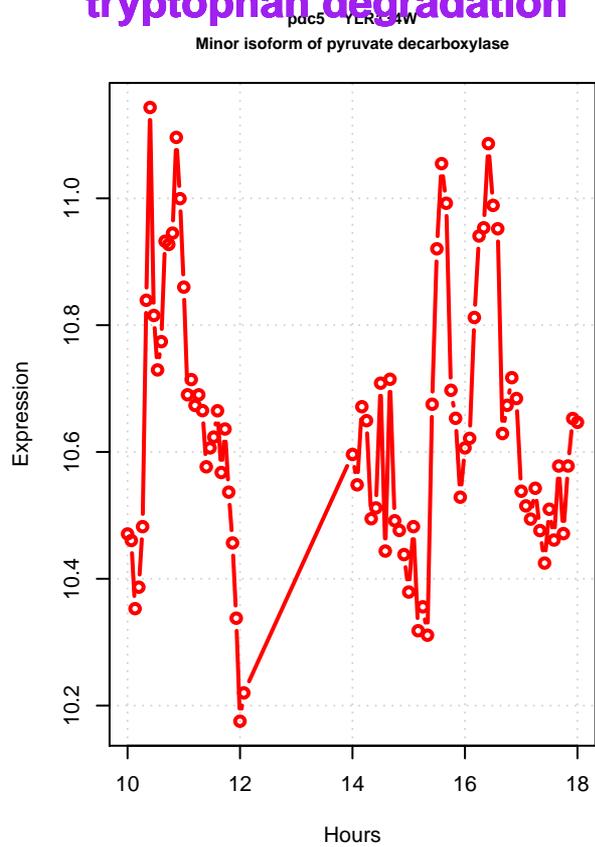
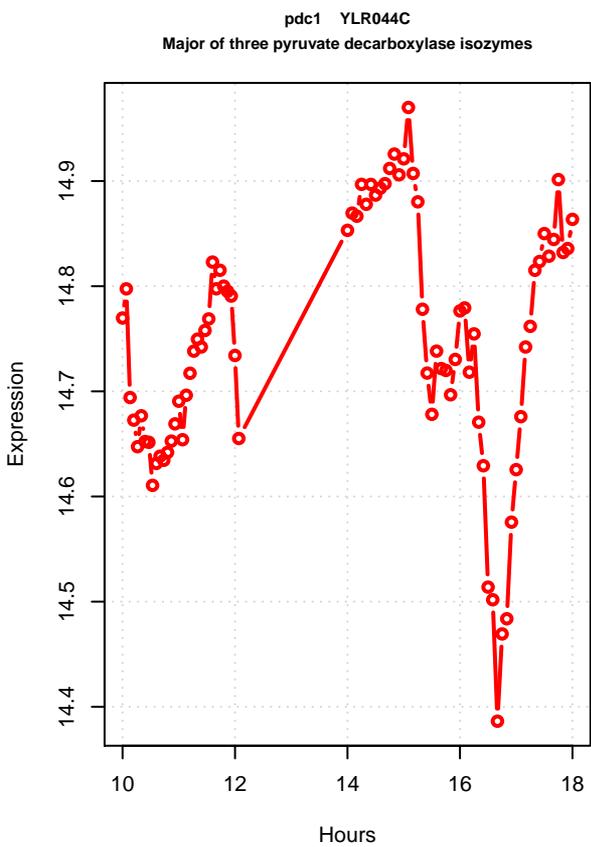


ald6 YPL061W  
Cytosolic aldehyde dehydrogenase



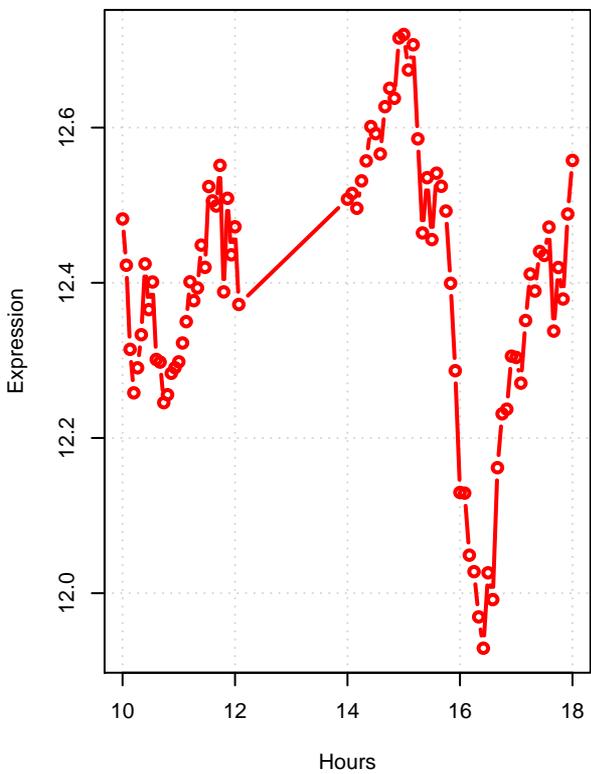
**tryptophan degradation**

# tryptophan degradation

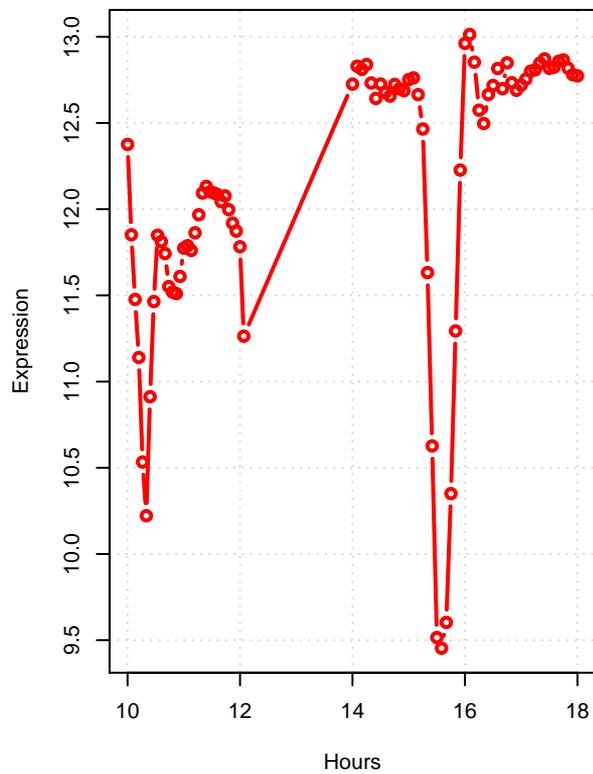


# tryptophan degradation

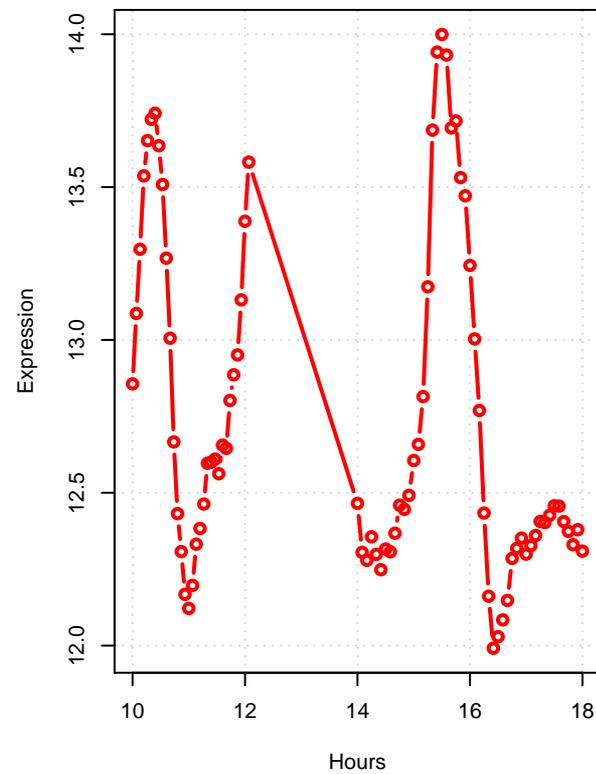
**sfa1 YDL168W**  
Bifunctional alcohol dehydrogenase and formaldehyde dehydrogenase



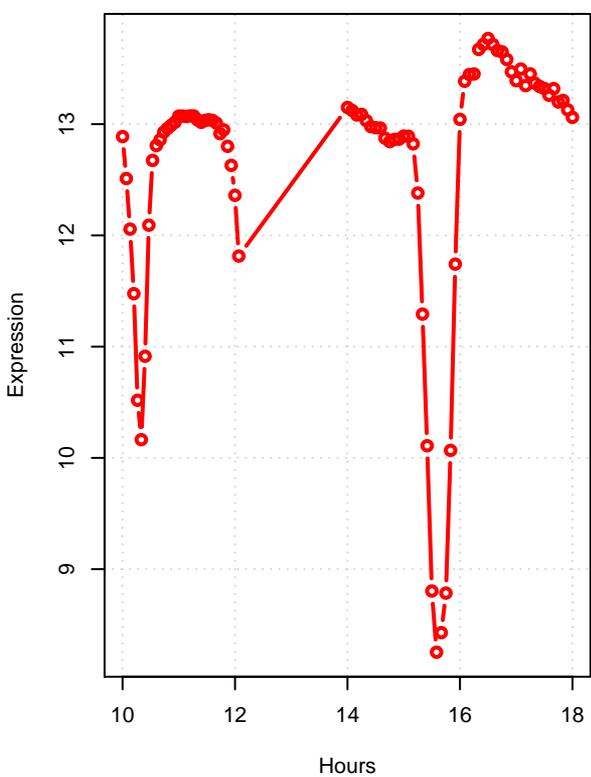
**aro10 YDR310W**  
Phenylpyruvate decarboxylase



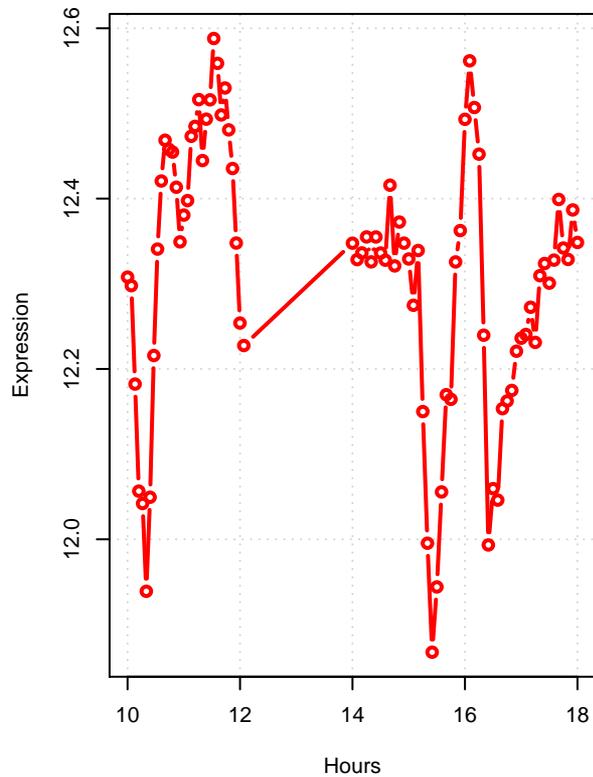
**aro8 YGL202W**  
Aromatic aminotransferase I



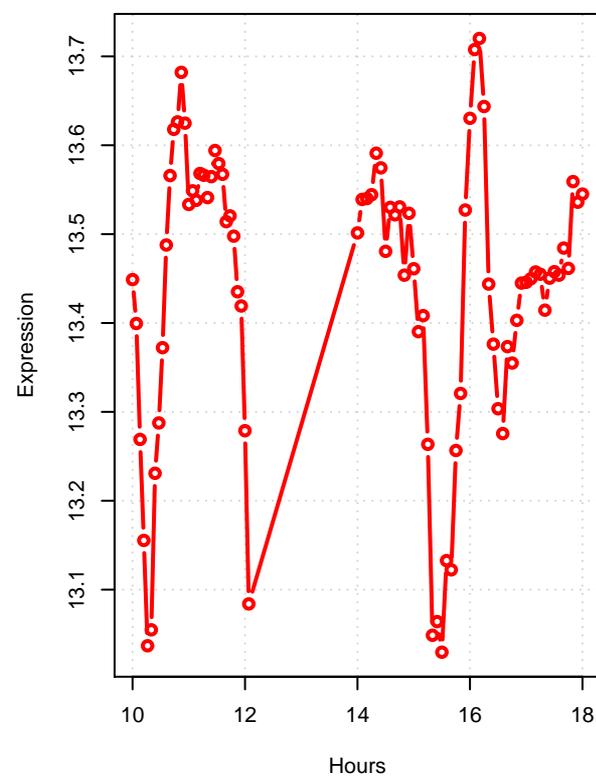
**aro9 YHR137W**  
Aromatic aminotransferase II



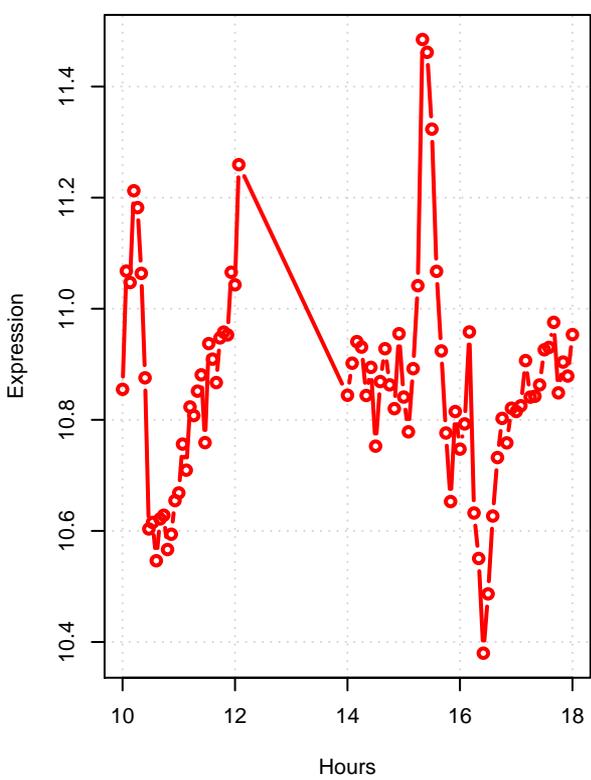
**bna5 YLR231C**  
Kynureninase



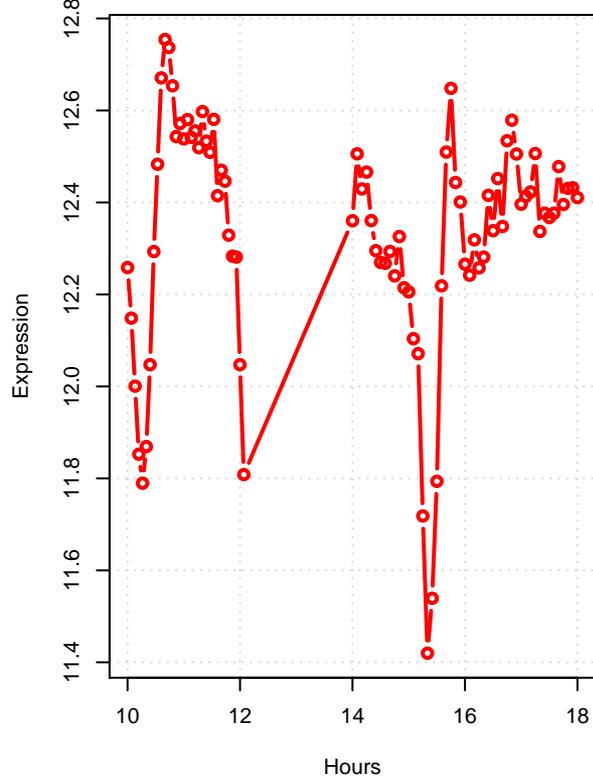
**bna1 YJR025C**  
3-hydroxyanthranilic acid dioxygenase



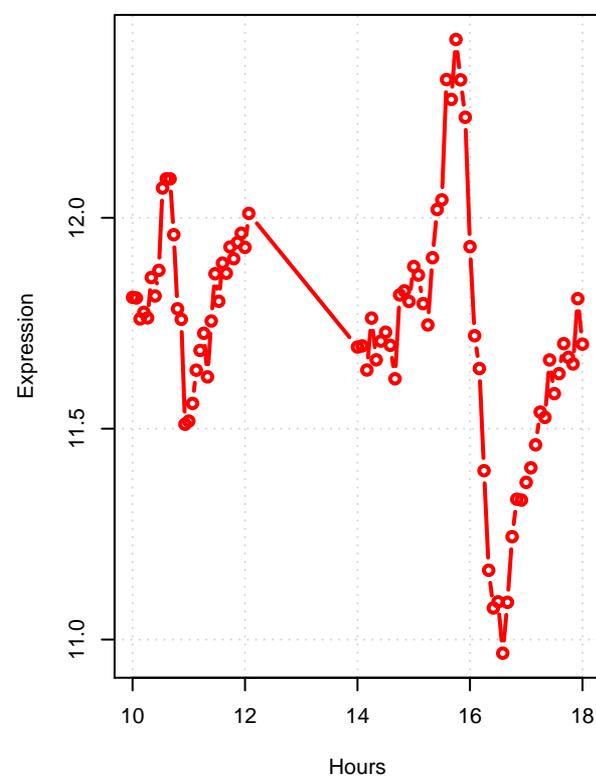
**bna7 YDR428C**  
Formylkynurenine formamidase



**bna4 YBL098W**  
Kynurenine 3-monooxygenase



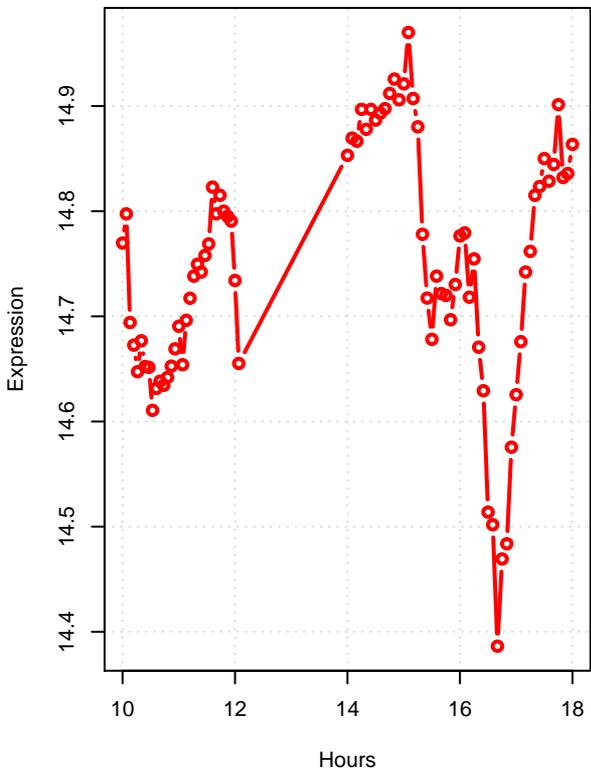
**bna2 YJR078W**  
Tryptophan 2,3-dioxygenase or indoleamine 2,3-dioxygenase



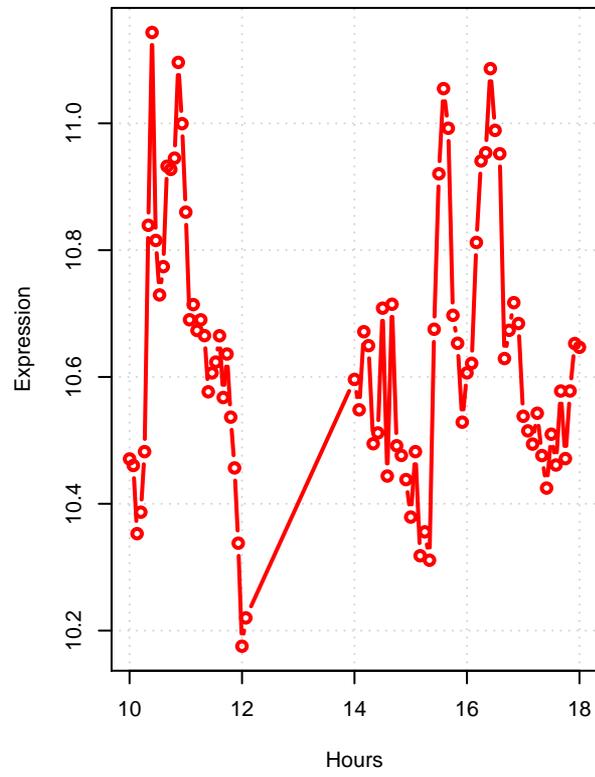
**valine degradation**

# valine degradation

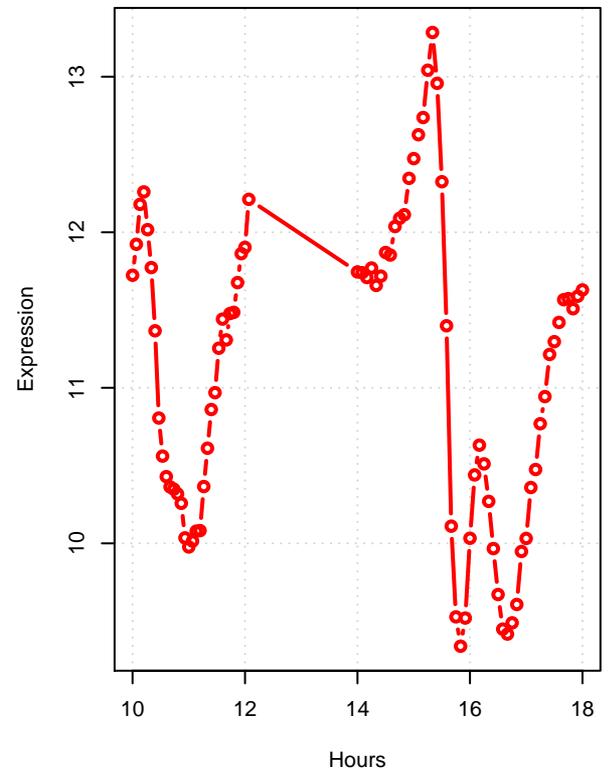
**pdc1 YLR044C**  
Major of three pyruvate decarboxylase isozymes



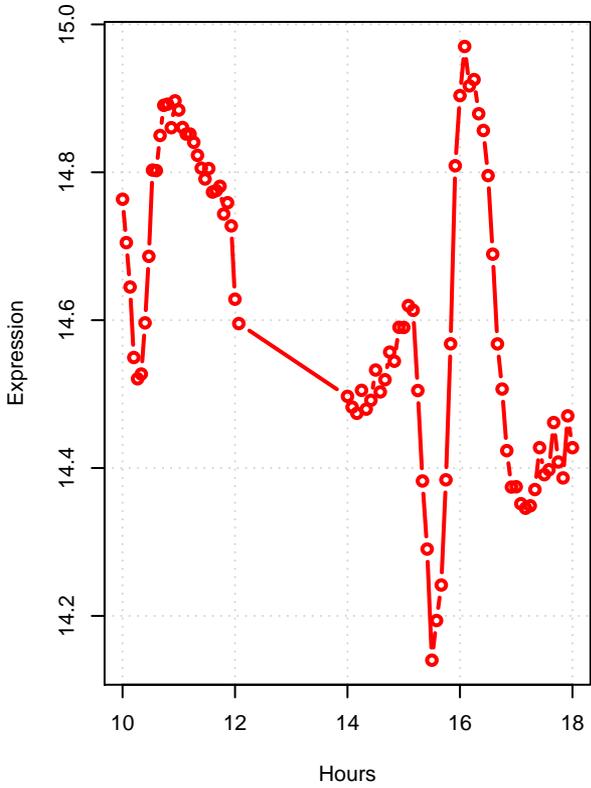
**pdc5 YLR134W**  
Minor isoform of pyruvate decarboxylase



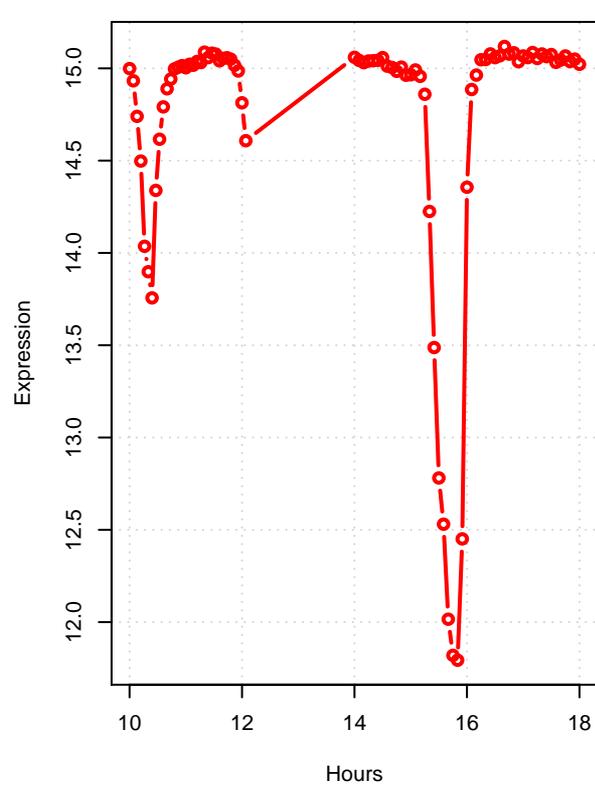
**pdc6 YGR087C**  
Minor isoform of pyruvate decarboxylase



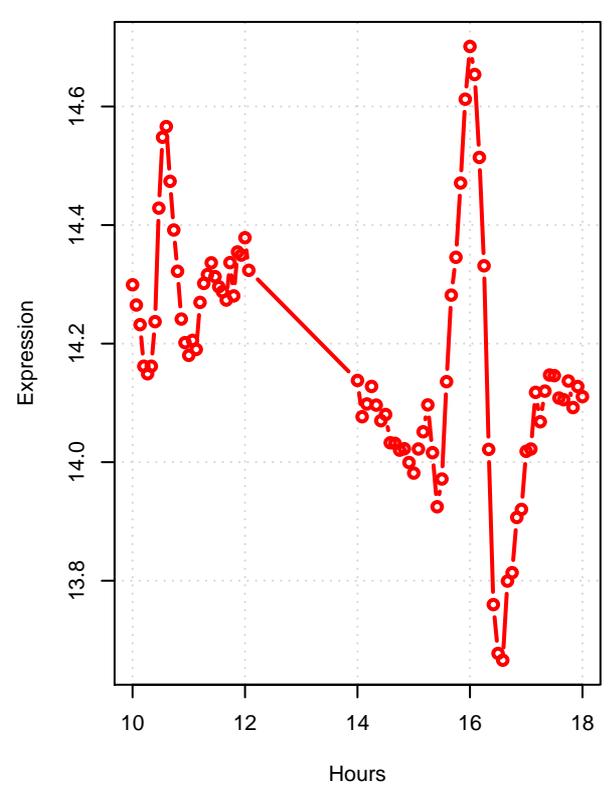
**adh1 YOL086C**  
Alcohol dehydrogenase



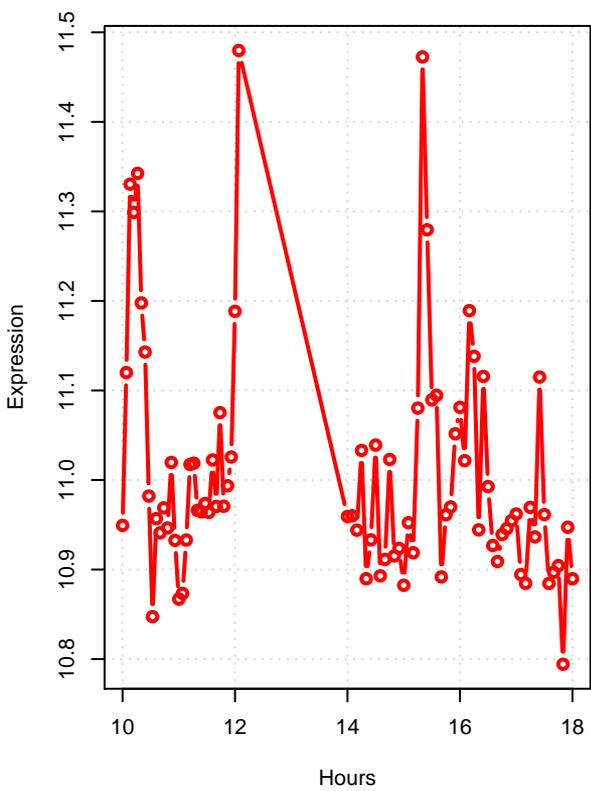
**adh2 YMR303C**  
Glucose-repressible alcohol dehydrogenase II



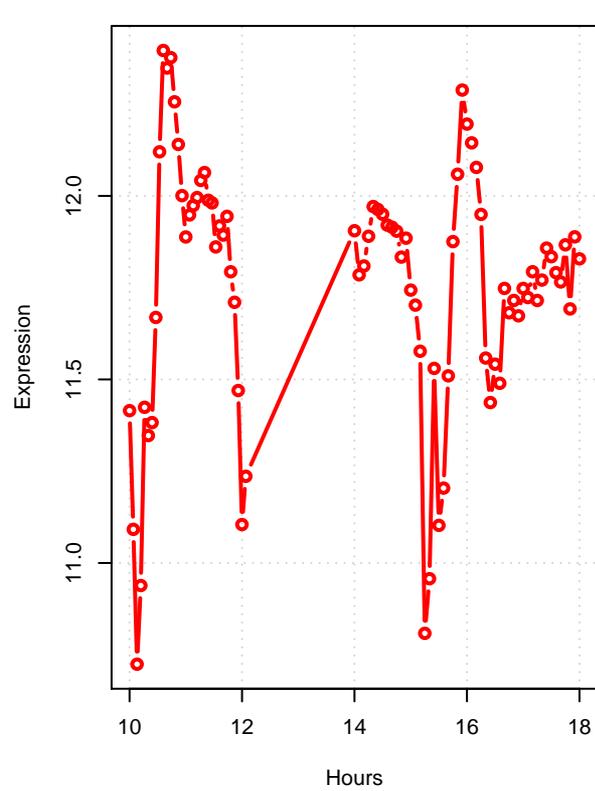
**adh3 YMR083W**  
Mitochondrial alcohol dehydrogenase isozyme III



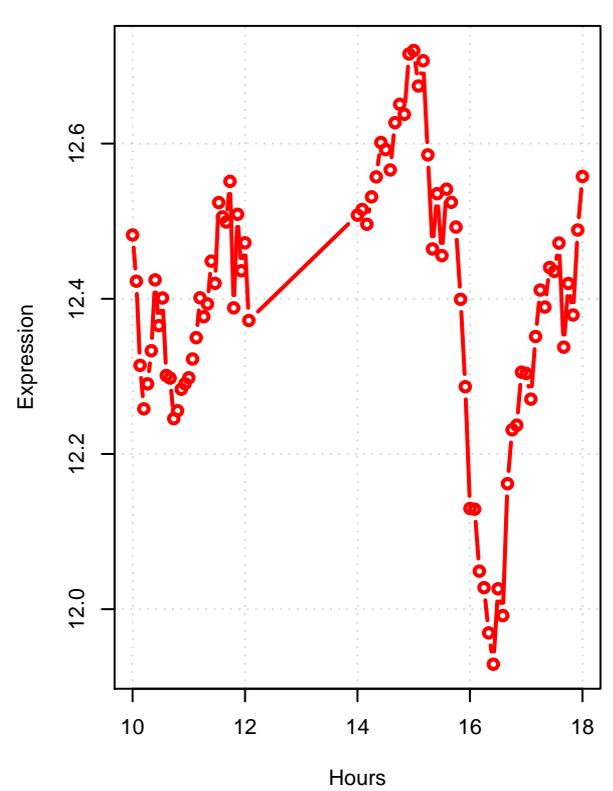
**adh4 YGL256W**  
Alcohol dehydrogenase isoenzyme type IV



**adh5 YBR145W**  
Alcohol dehydrogenase isoenzyme V

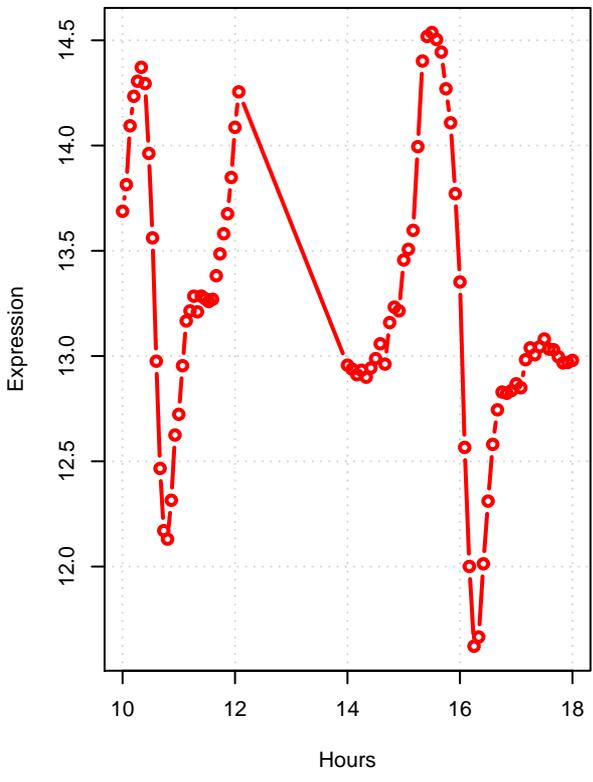


**sfa1 YDL168W**  
Bifunctional alcohol dehydrogenase and formaldehyde dehydrogenase

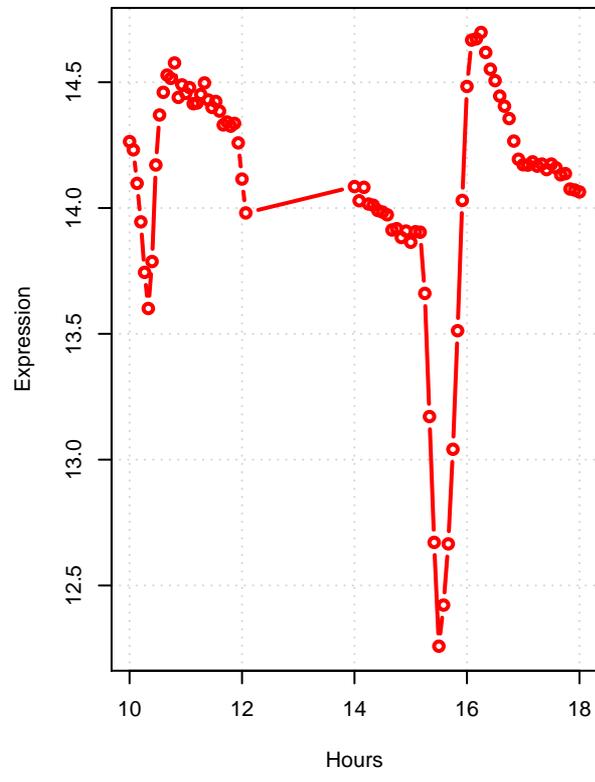


# valine degradation

bat1 YHR208W  
Mitochondrial branched-chain amino acid (BCAA) aminotransferase



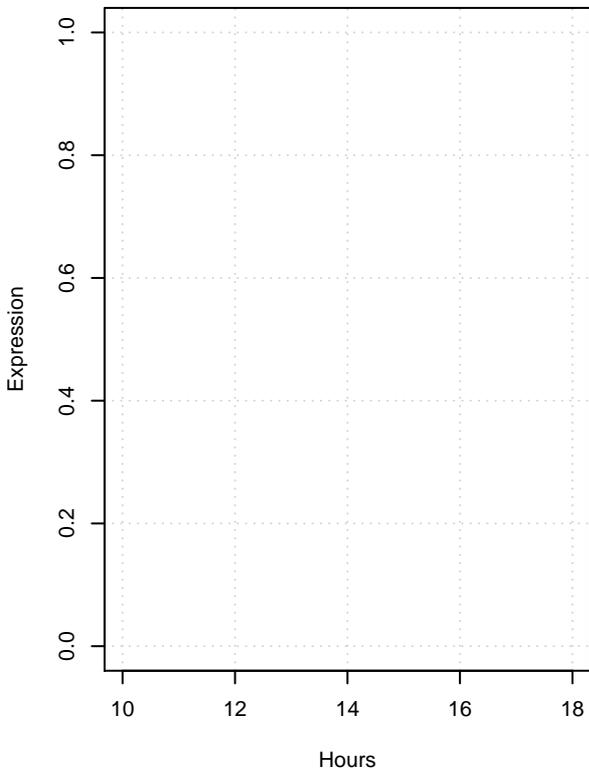
bat2 YJK148W  
Cytosolic branched-chain amino acid (BCAA) aminotransferase



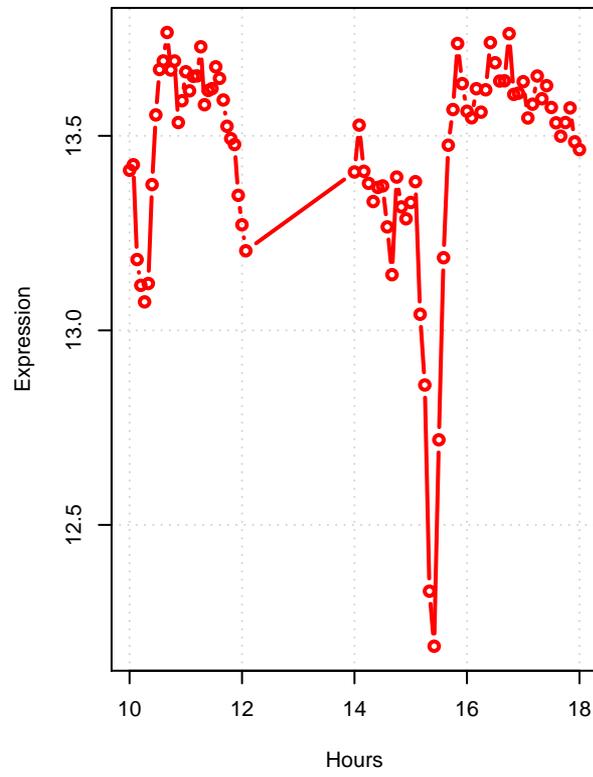
**aerobic respiration, electron transport chain**

# aerobic respiration, electron transport chain

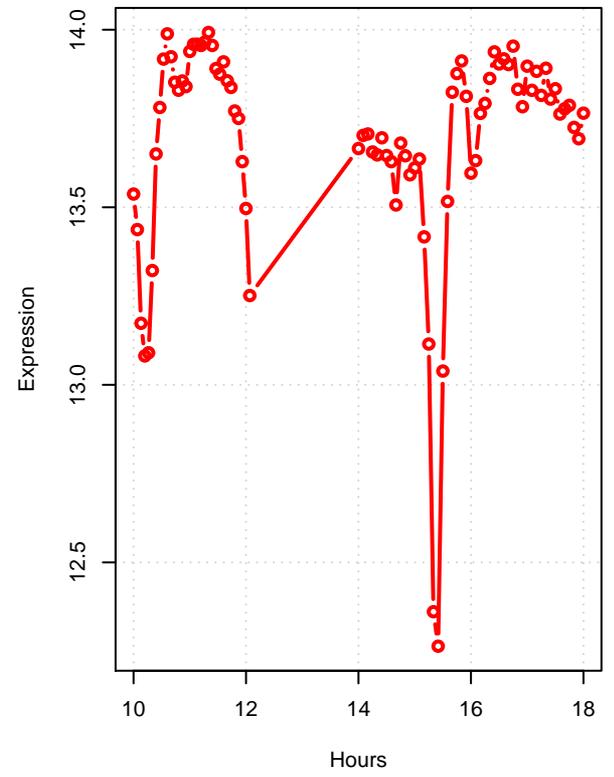
**cob Q0105**  
Cytochrome b



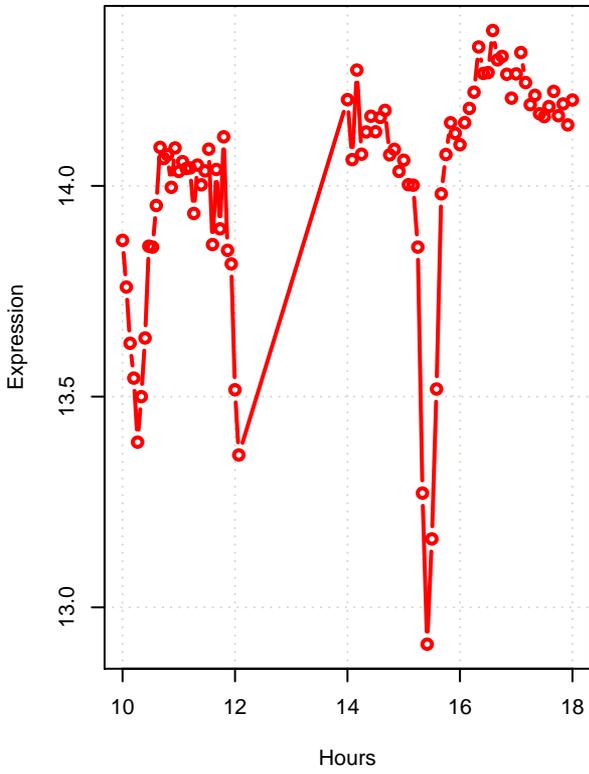
**cob1 YBL045C**  
Core subunit of the ubiquinol-cytochrome c reductase complex



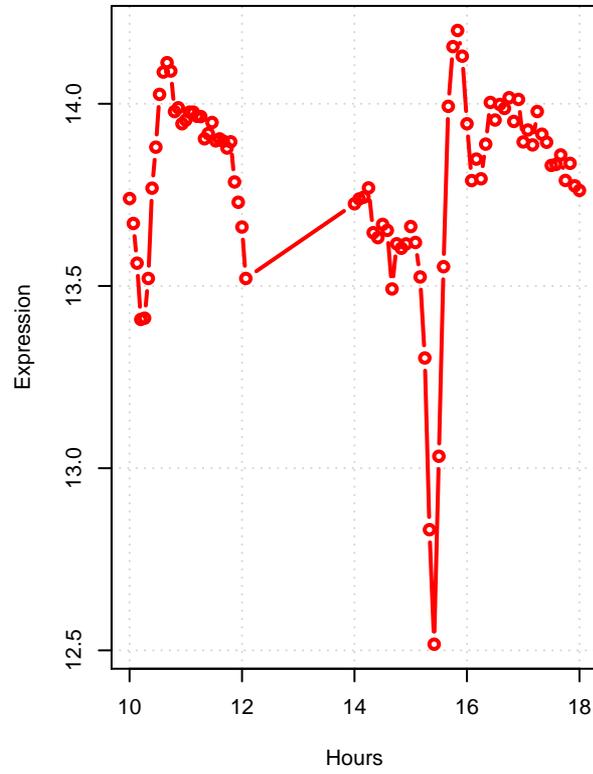
**cyt1 YOR065W**  
Cytochrome c1



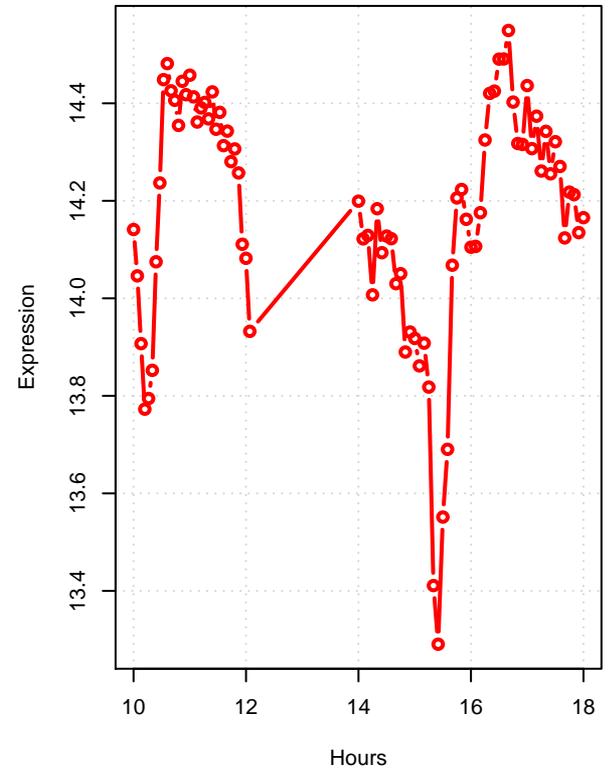
**qcr10 YHR001W-A**  
Subunit of the ubiquinol-cytochrome c oxidoreductase complex



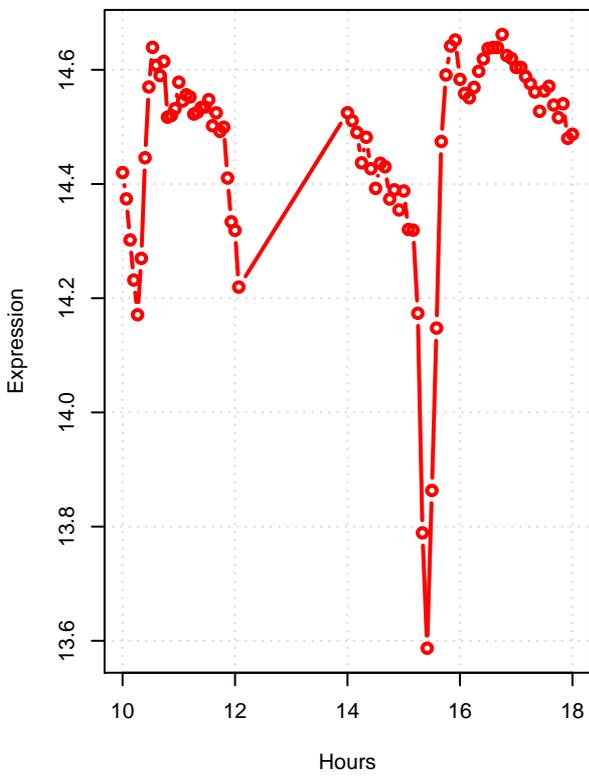
**qcr2 YPR191W**  
Subunit 2 of ubiquinol cytochrome-c reductase (Complex III)



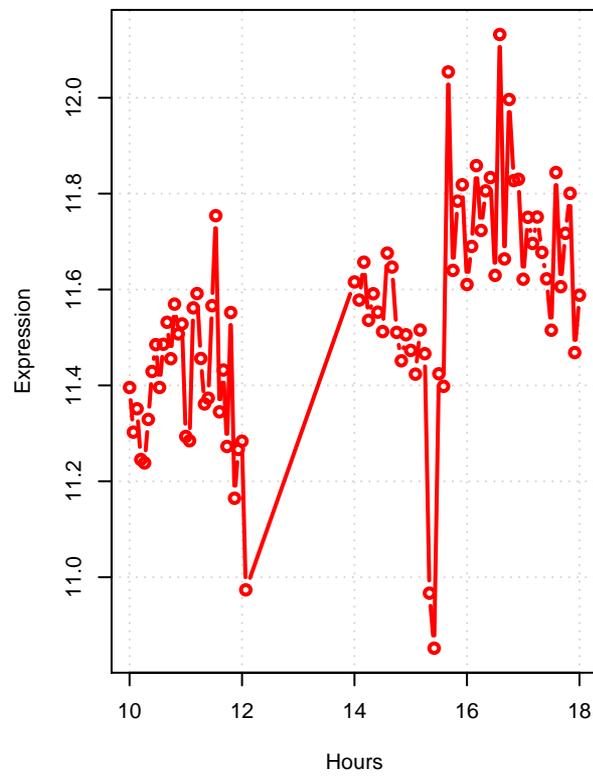
**qcr6 YFR033C**  
Subunit 6 of the ubiquinol cytochrome-c reductase complex



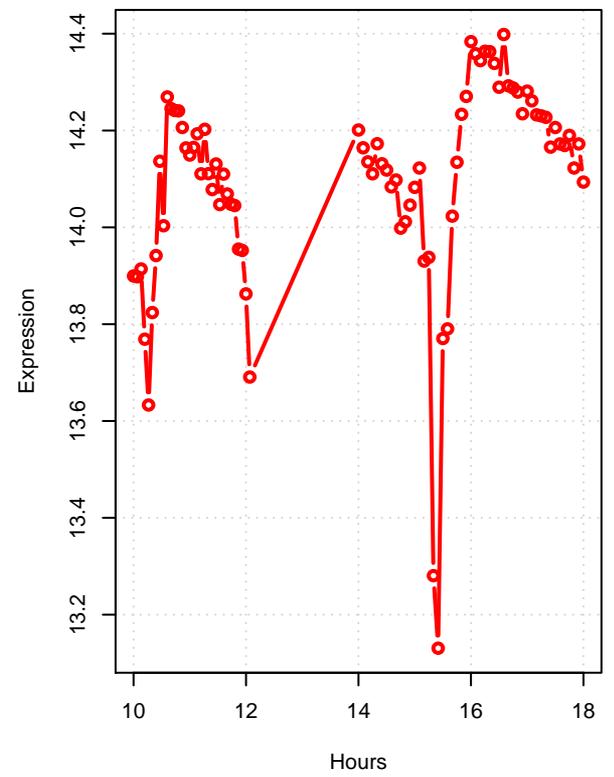
**qcr7 YDR529C**  
Subunit 7 of ubiquinol cytochrome-c reductase (Complex III)



**qcr8 YJL166W**  
Subunit 8 of ubiquinol cytochrome-c reductase (Complex III)

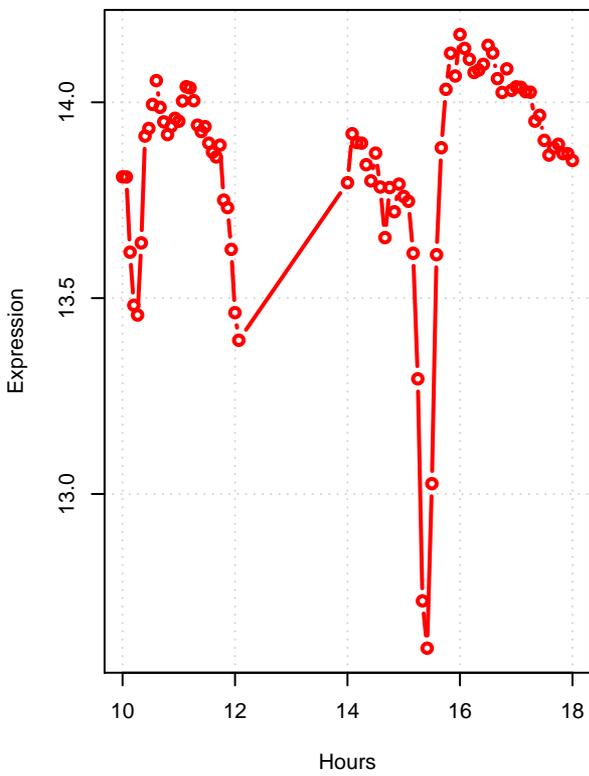


**qcr9 YGR183C**  
Subunit 9 of ubiquinol cytochrome-c reductase (Complex III)

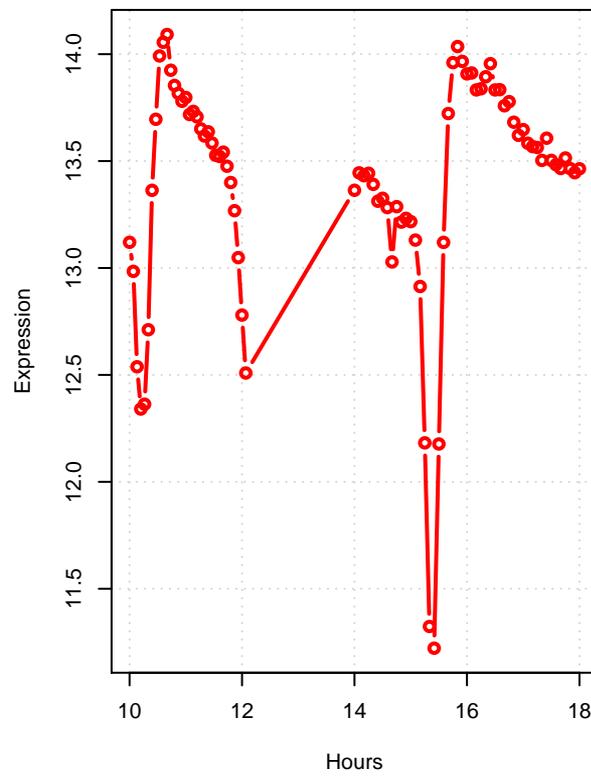


# aerobic respiration, electron transport chain

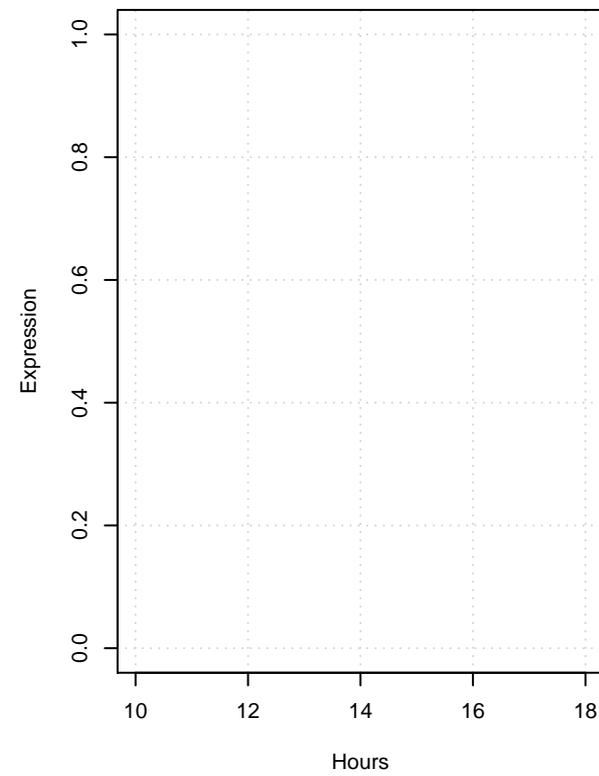
**rip1 YEL024W**  
Ubiquinol-cytochrome-c reductase



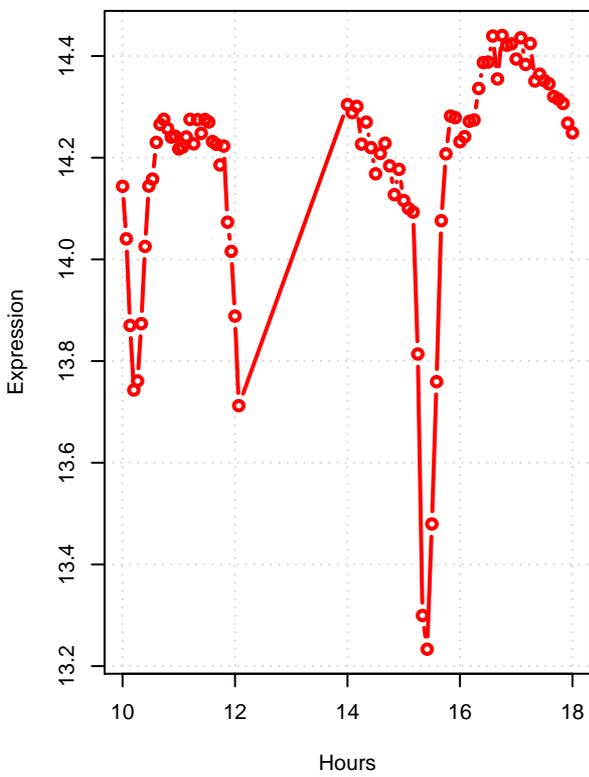
**ndh1 YML120C**  
NADH:ubiquinone oxidoreductase



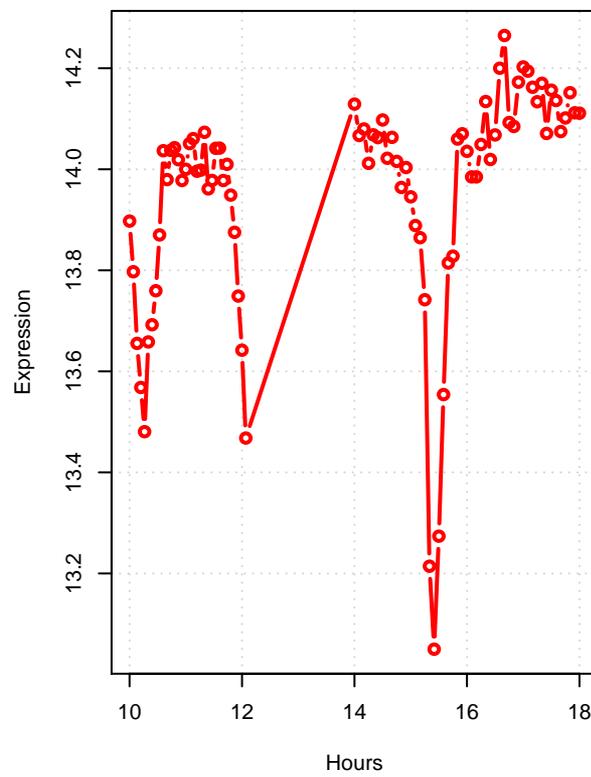
**cox1 Q0045**  
Subunit I of cytochrome c oxidase (Complex IV)



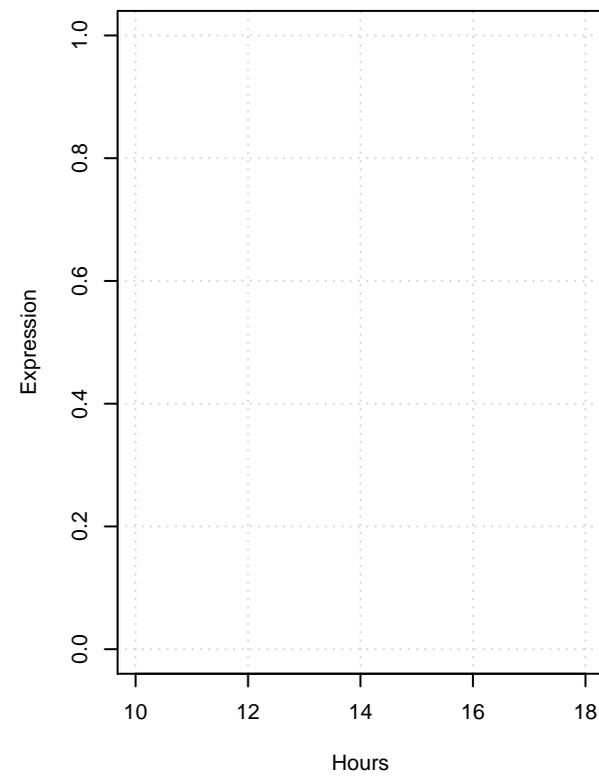
**cox12 YLR038C**  
Subunit VIb of cytochrome c oxidase



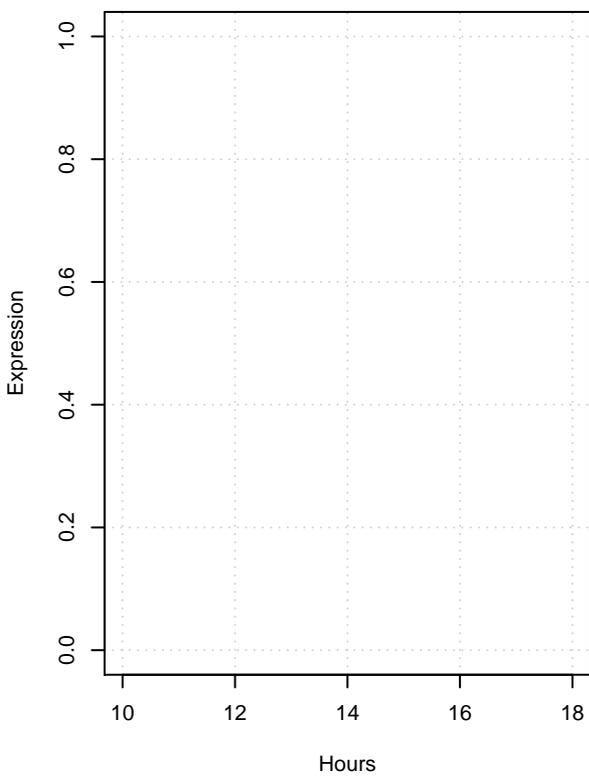
**cox13 YGL191W**  
Subunit VIa of cytochrome c oxidase



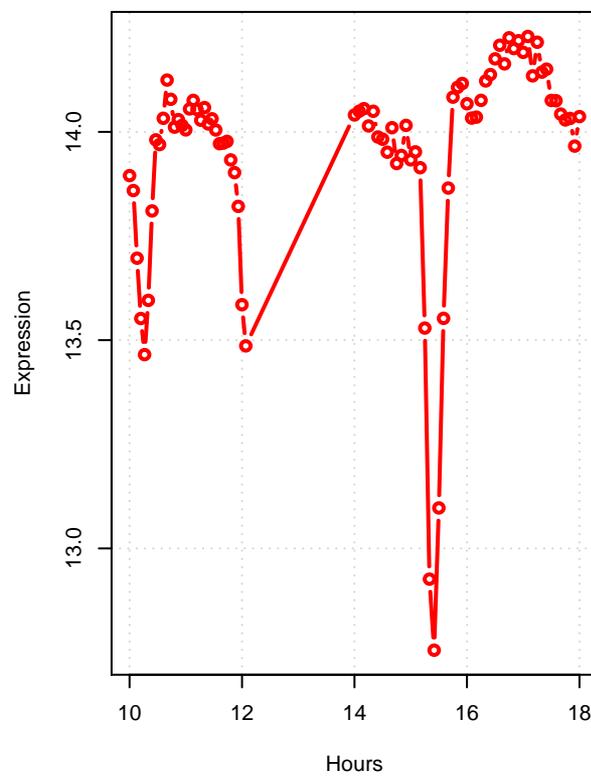
**cox2 Q0250**  
Subunit II of cytochrome c oxidase (Complex IV)



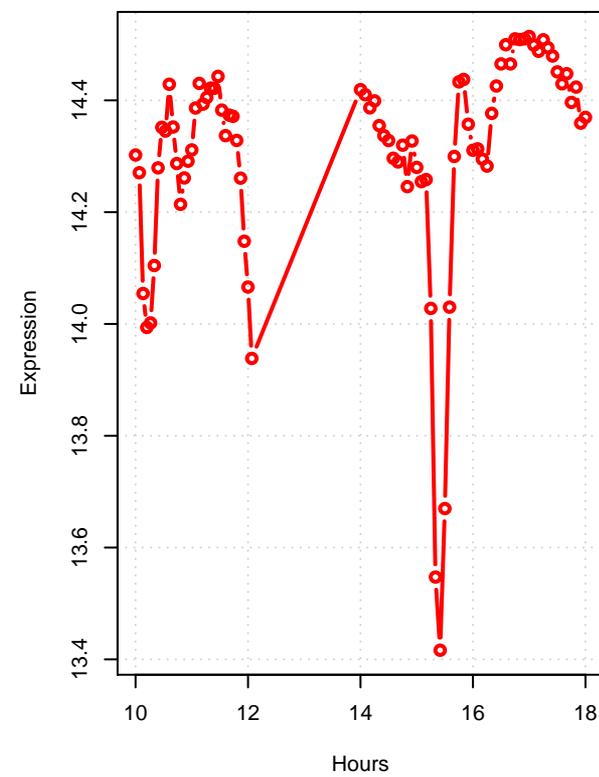
**cox3 Q0275**  
Subunit III of cytochrome c oxidase (Complex IV)



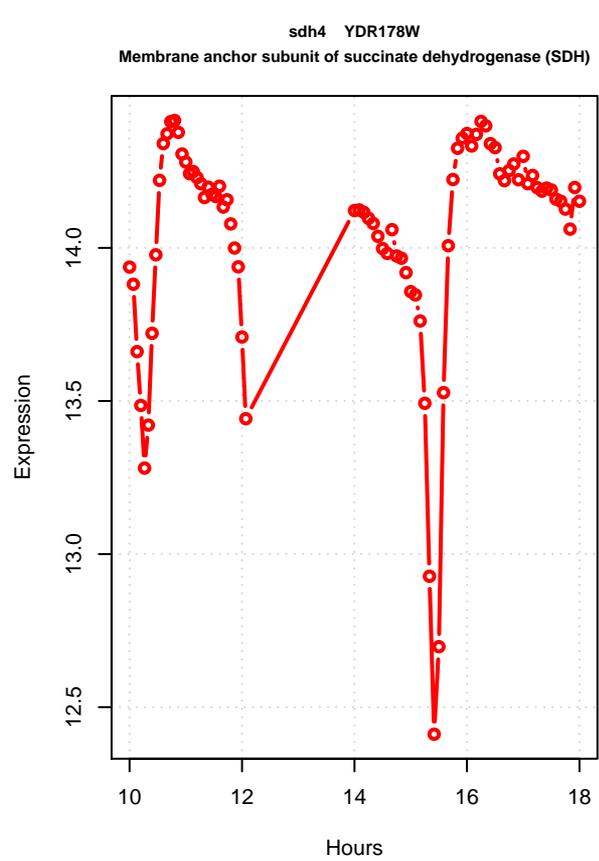
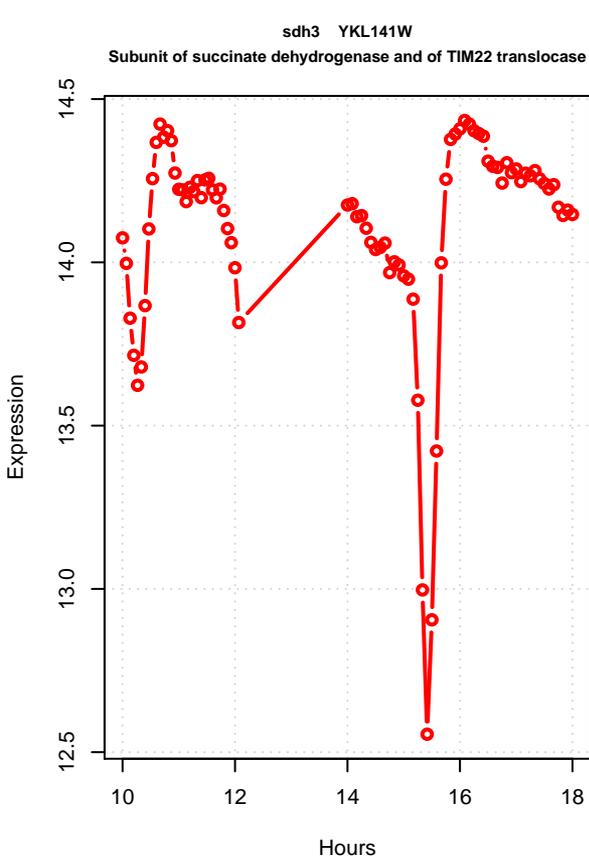
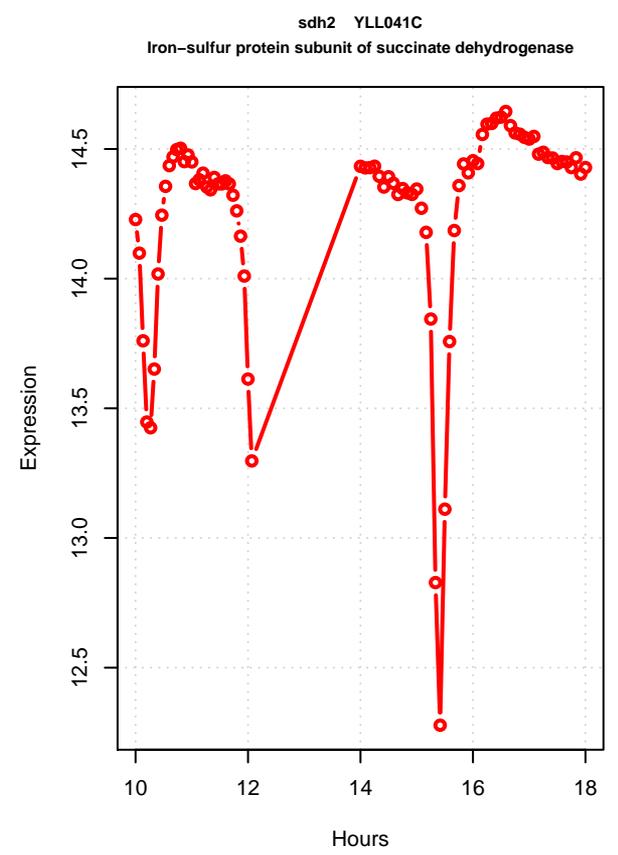
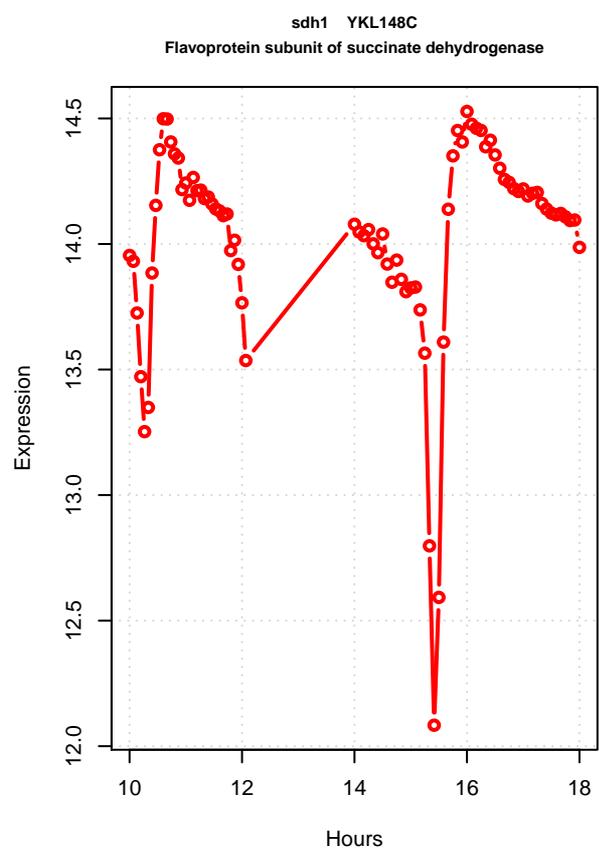
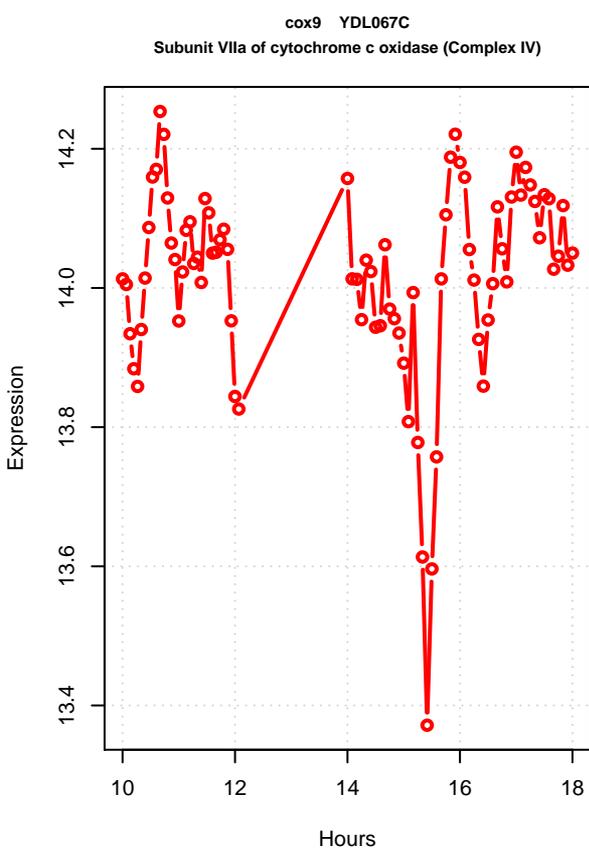
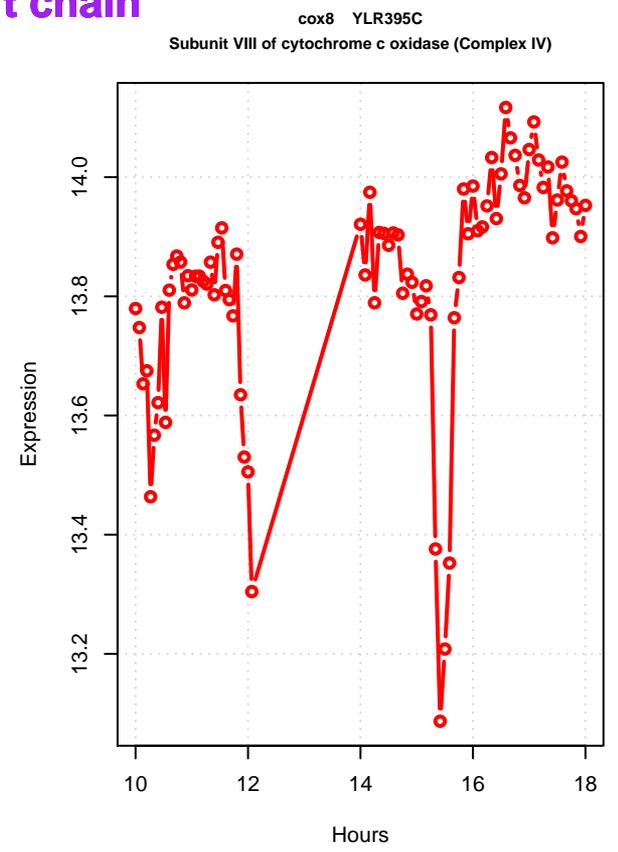
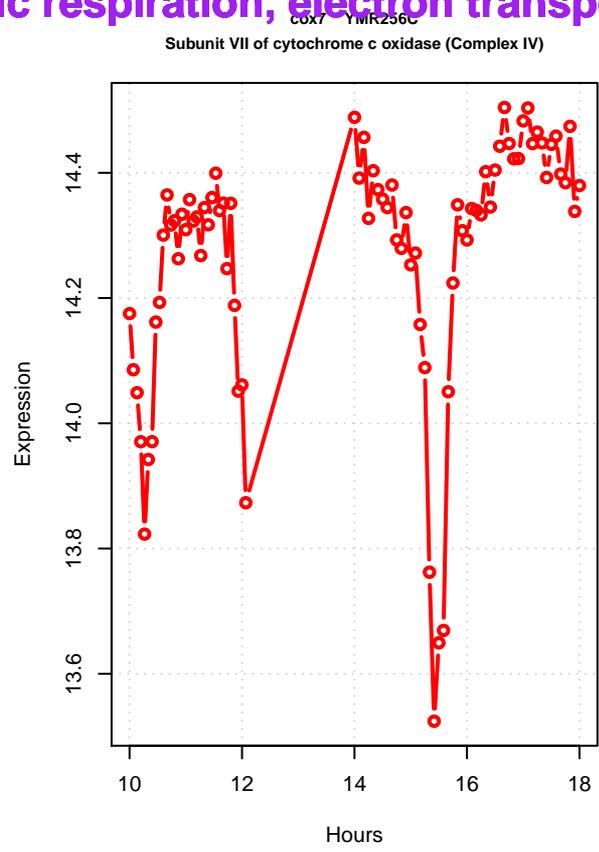
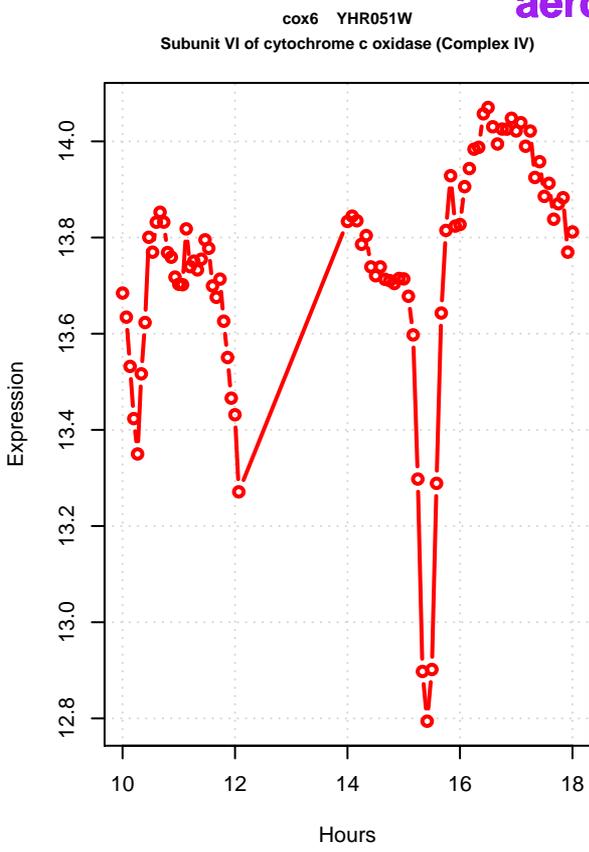
**cox4 YGL187C**  
Subunit IV of cytochrome c oxidase



**cox5a YNL052W**  
Subunit Va of cytochrome c oxidase



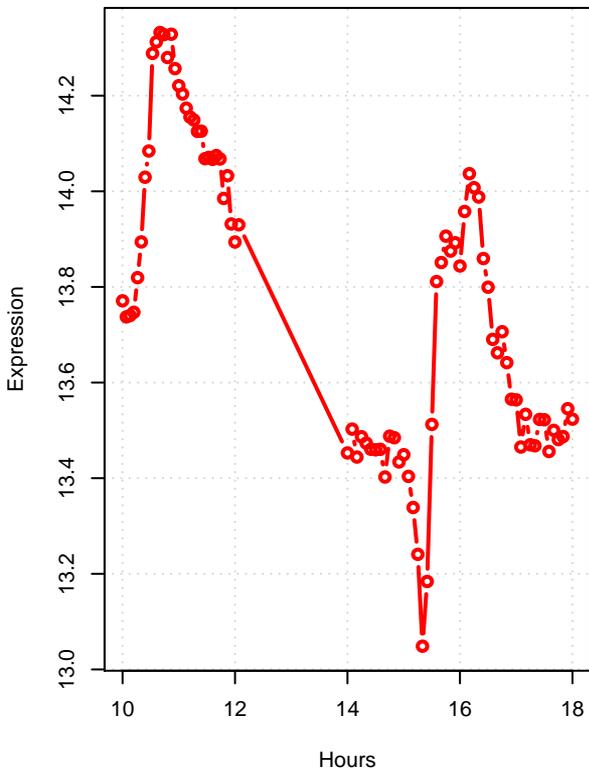
# aerobic respiration, electron transport chain



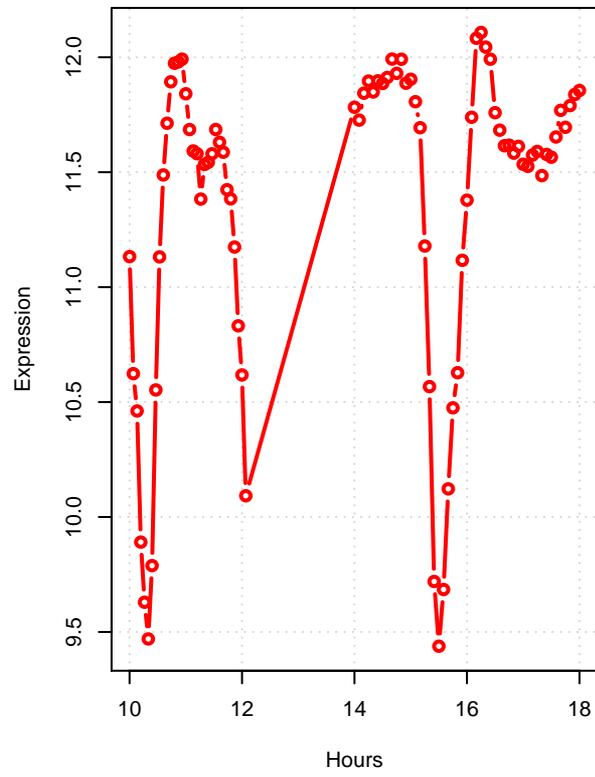
## alanine biosynthesis

# alanine biosynthesis

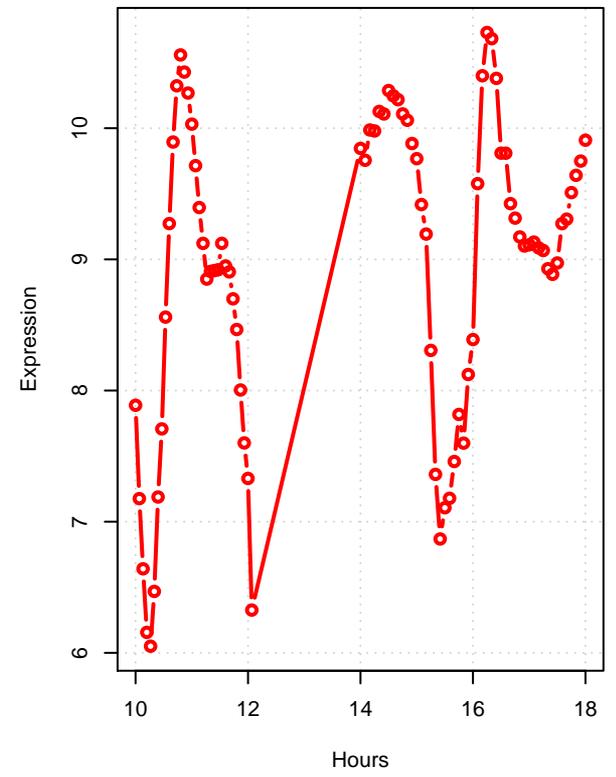
alt1 YLR089C  
Alanine transaminase (glutamic pyruvic transaminase)



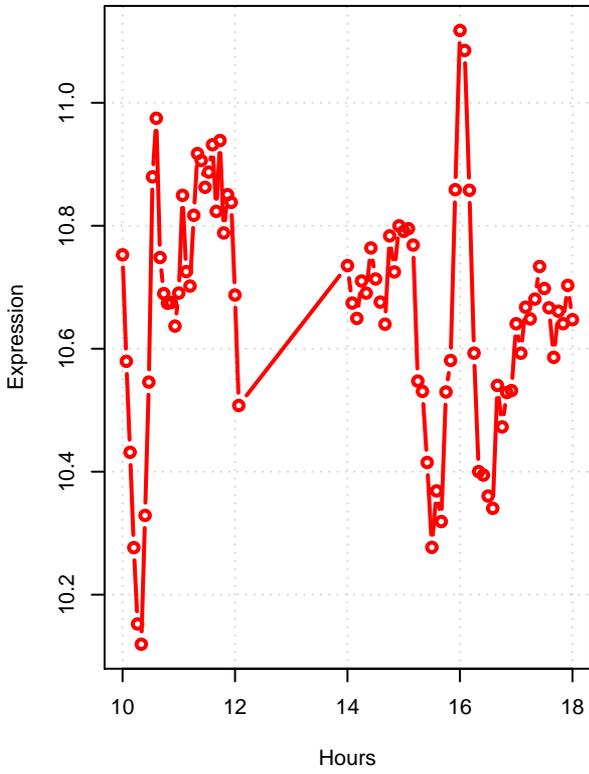
ald2 YMF170C  
Cytoplasmic aldehyde dehydrogenase



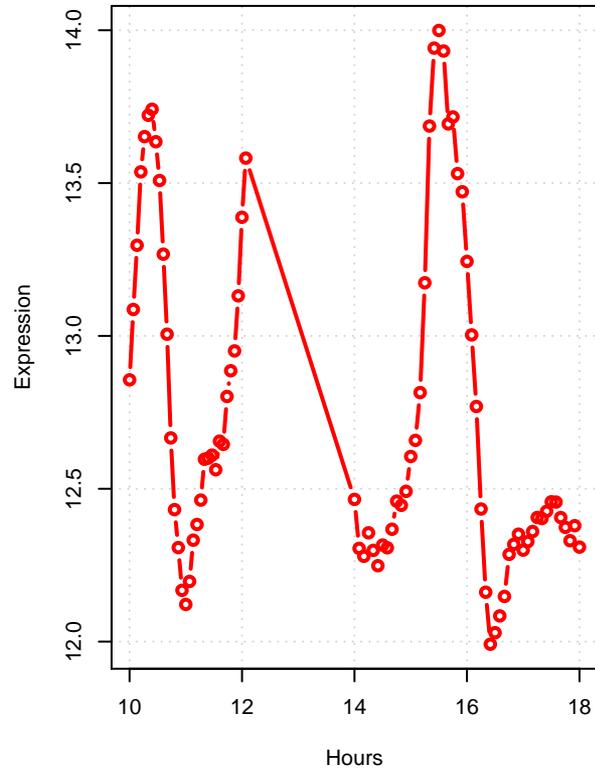
ald3 YMR169C  
Cytoplasmic aldehyde dehydrogenase



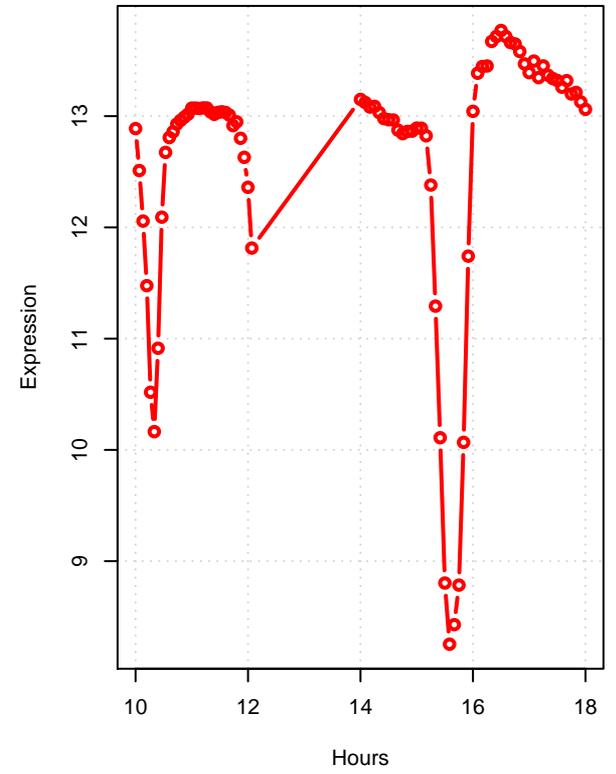
fms1 YMR020W  
Polyamine oxidase



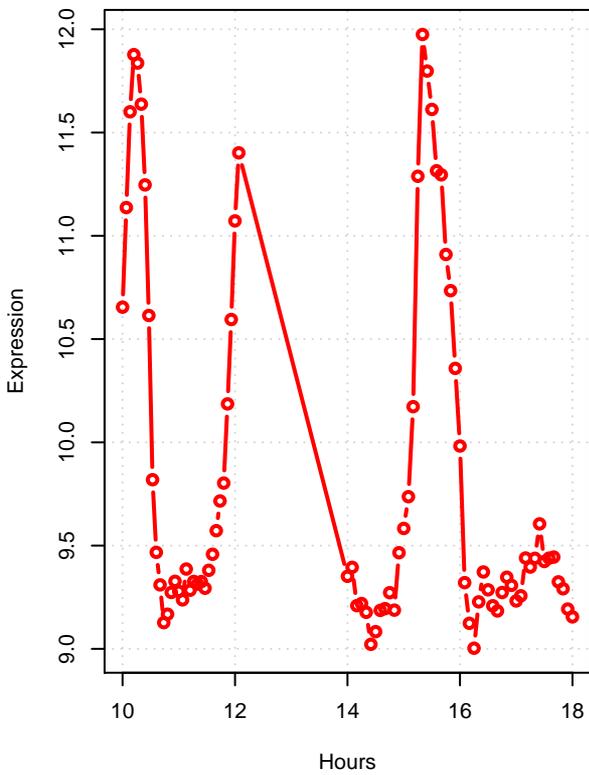
aro8 YGL202W  
Aromatic aminotransferase I



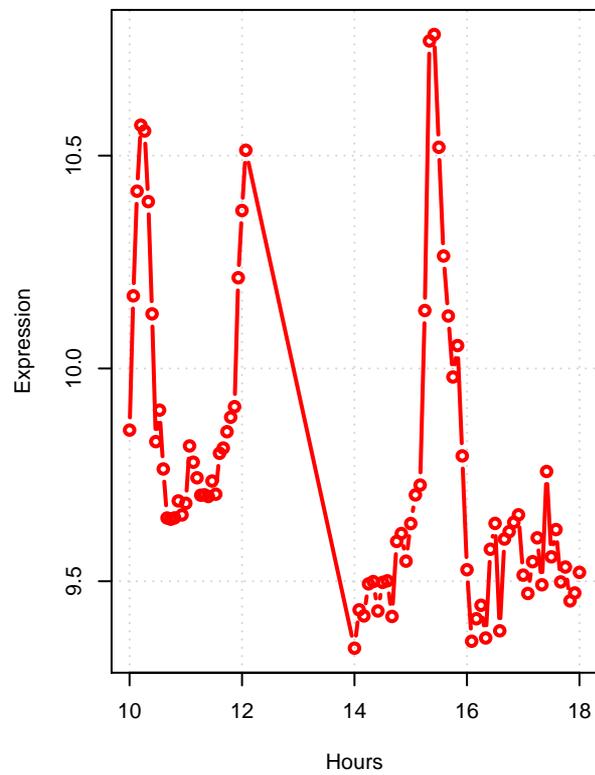
aro9 YHR137W  
Aromatic aminotransferase II



aro7 YPR060C  
Chorismate mutase



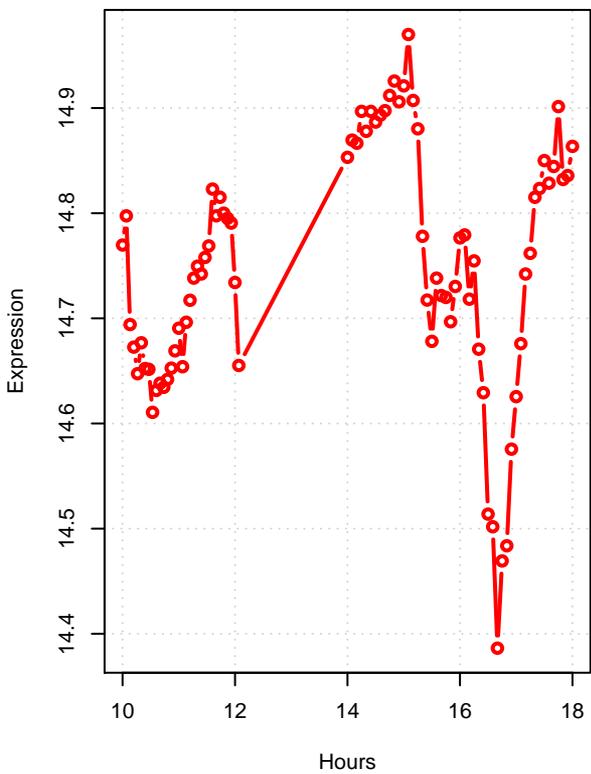
pha2 YNL316C  
Prephenate dehydratase



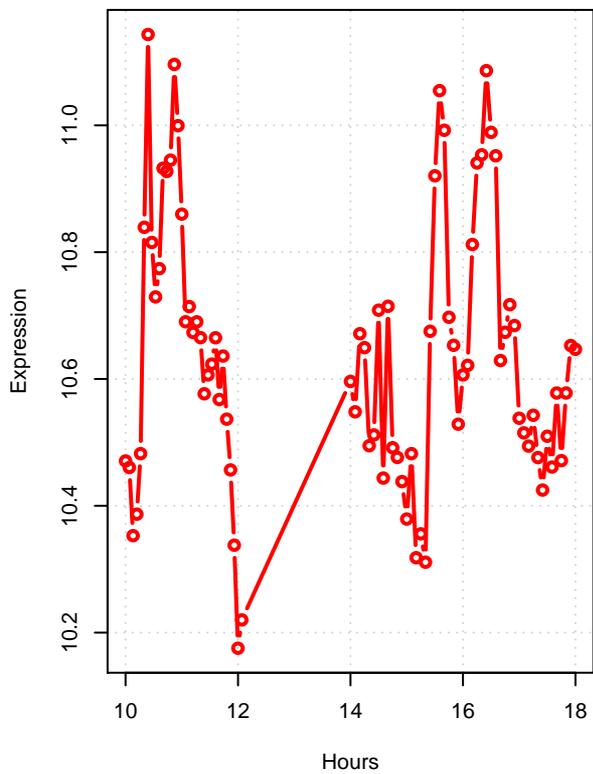
## alanine degradation

# alanine degradation

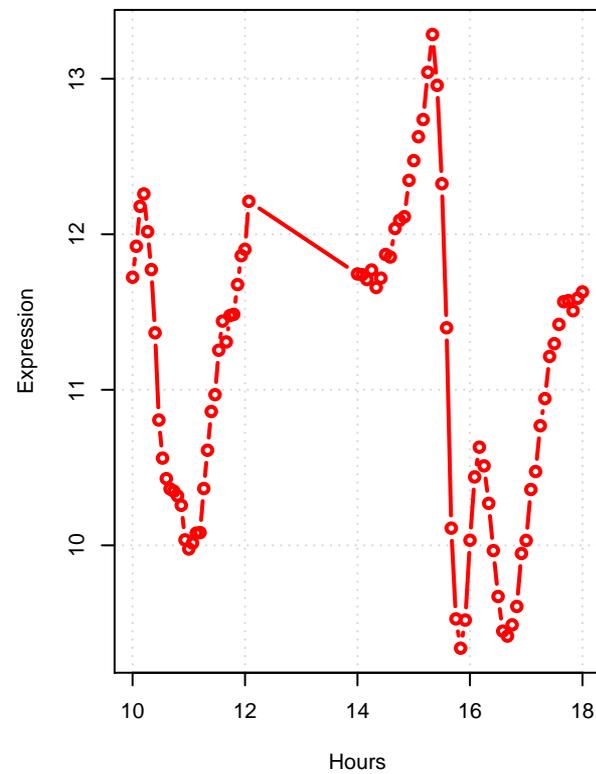
**pdc1 YLR044C**  
Major of three pyruvate decarboxylase isozymes



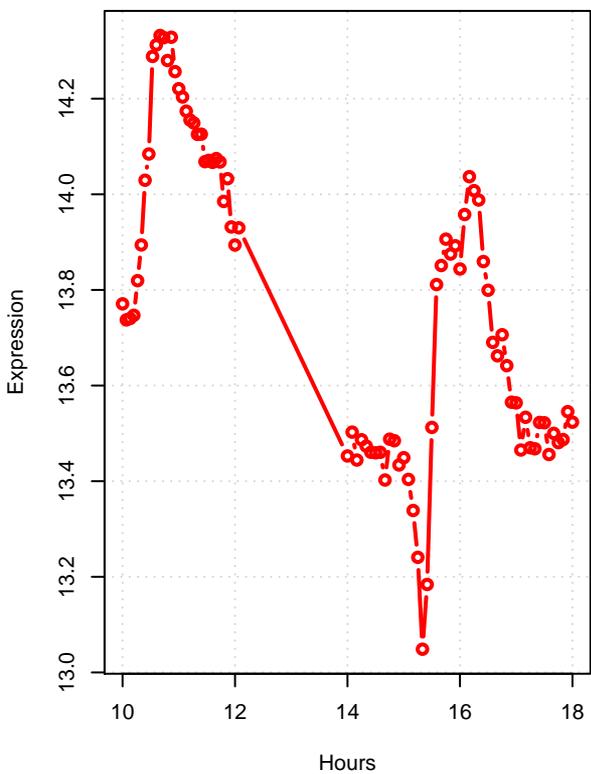
**pdcs YLR134W**  
Minor isoform of pyruvate decarboxylase



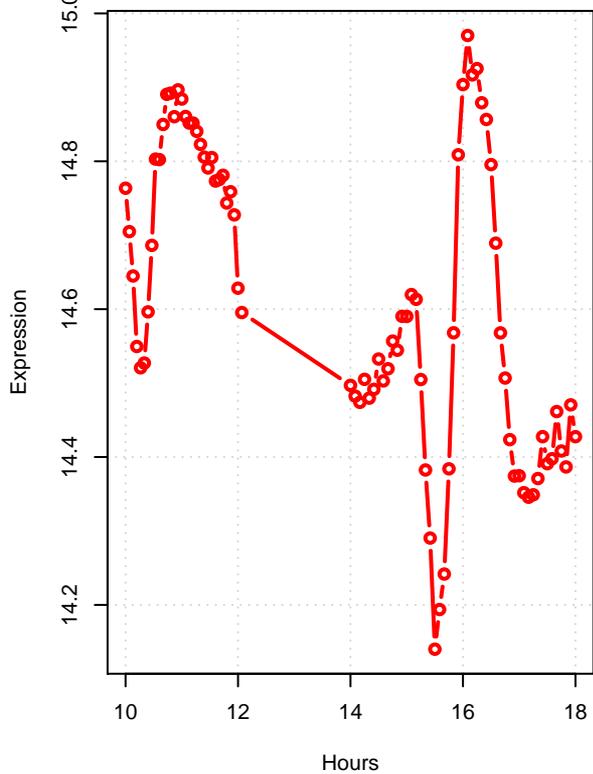
**pdcs6 YGR087C**  
Minor isoform of pyruvate decarboxylase



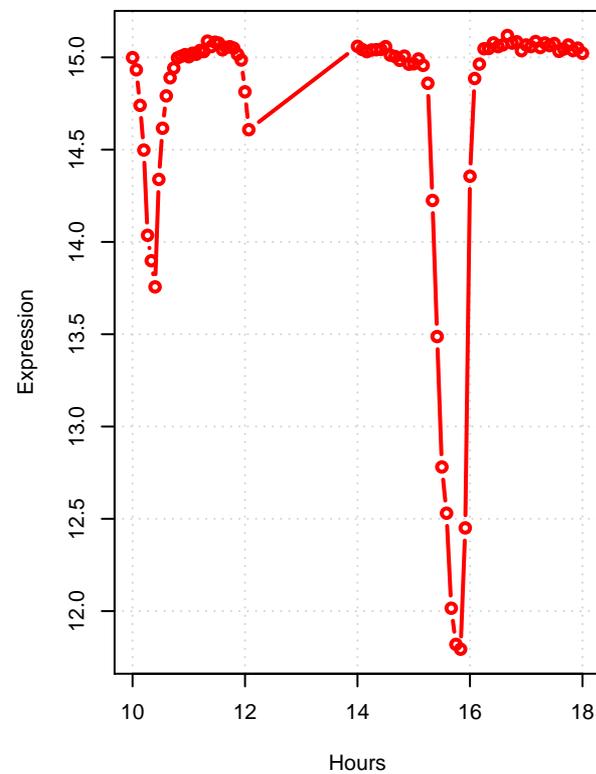
**alt1 YLR089C**  
Alanine transaminase (glutamic pyruvic transaminase)



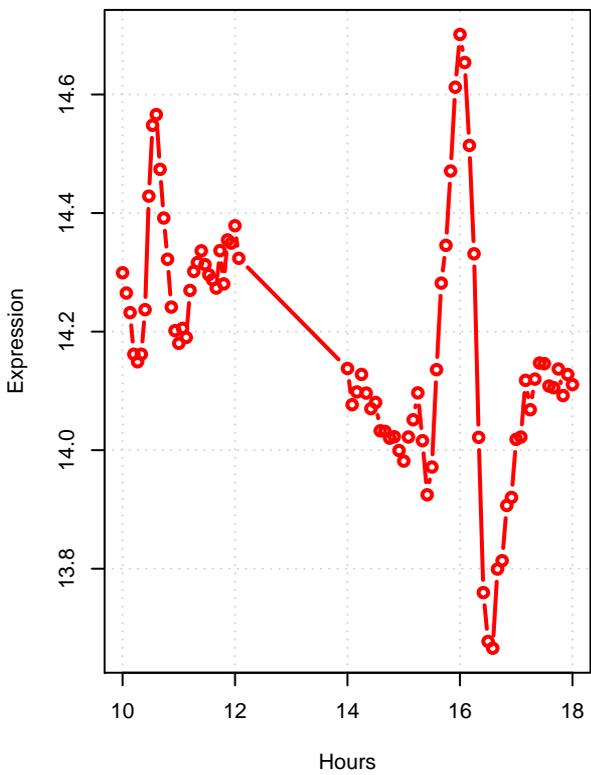
**adh1 YOL086C**  
Alcohol dehydrogenase



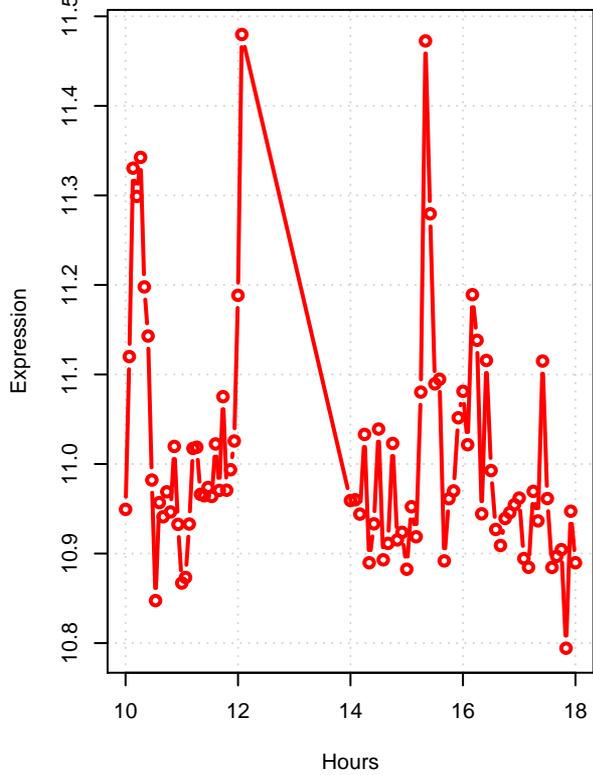
**adh2 YMR303C**  
Glucose-repressible alcohol dehydrogenase II



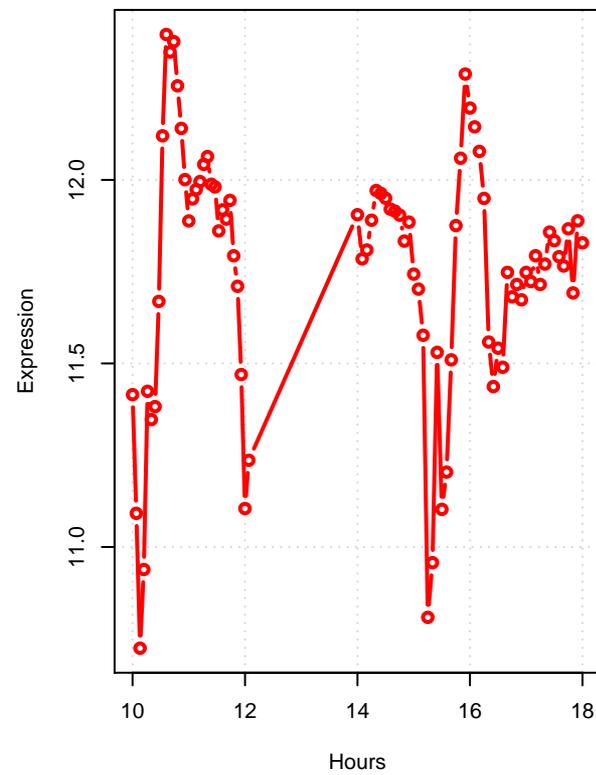
**adh3 YMR083W**  
Mitochondrial alcohol dehydrogenase isozyme III



**adh4 YGL256W**  
Alcohol dehydrogenase isoenzyme type IV

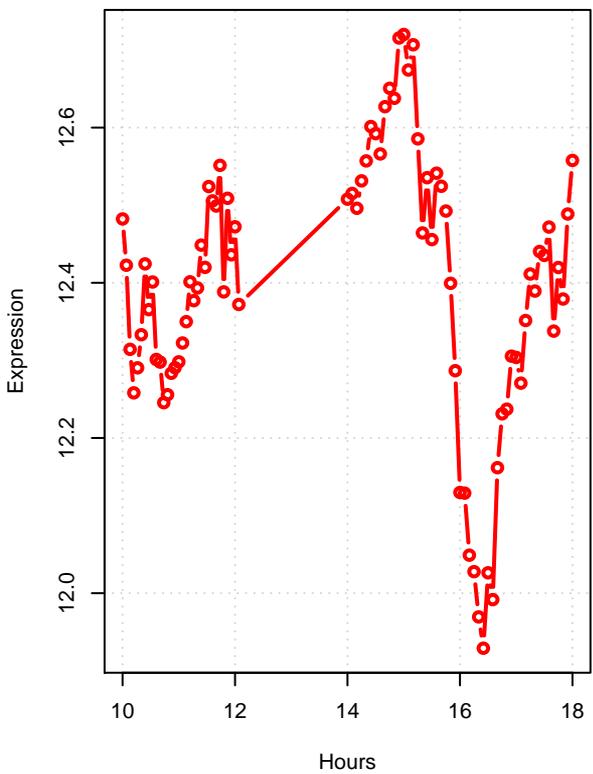


**adh5 YBR145W**  
Alcohol dehydrogenase isoenzyme V

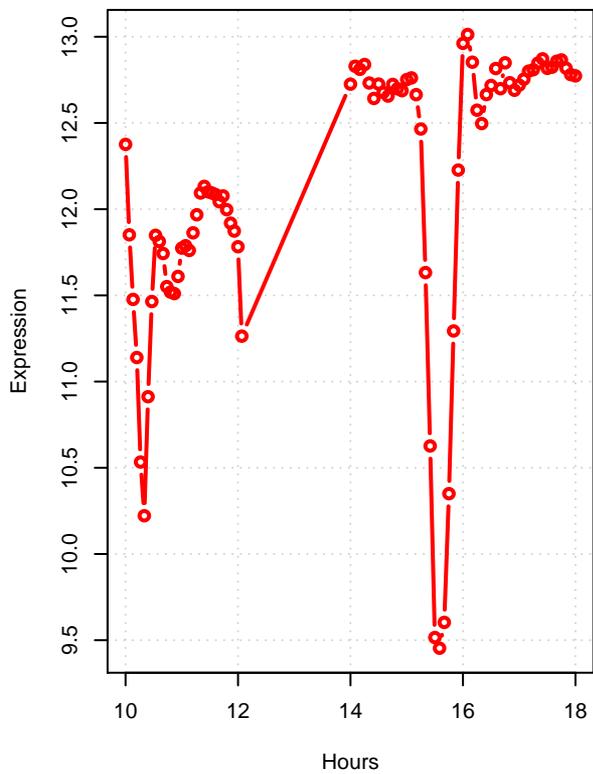


# alanine degradation

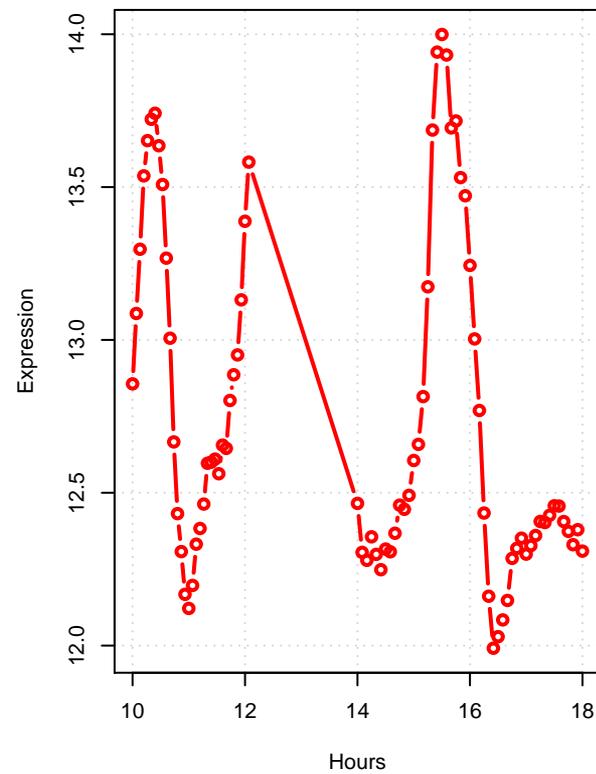
sfa1 YDL168W  
Bifunctional alcohol dehydrogenase and formaldehyde dehydrogenase



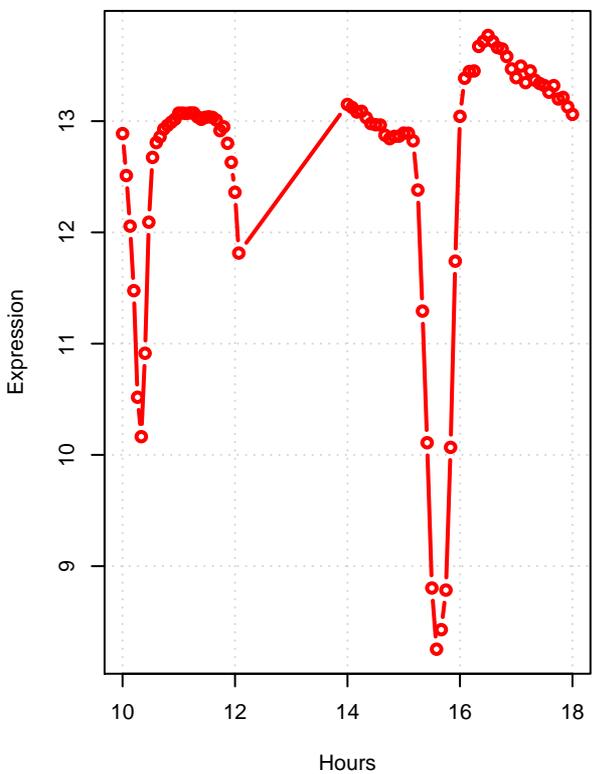
aro10 YDR380W  
Phenylpyruvate decarboxylase



aro8 YGL202W  
Aromatic aminotransferase I



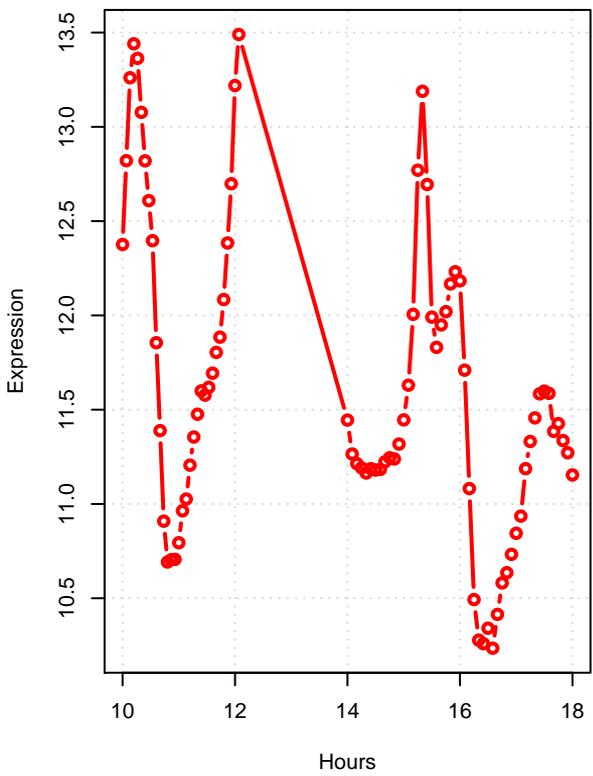
aro9 YHR137W  
Aromatic aminotransferase II



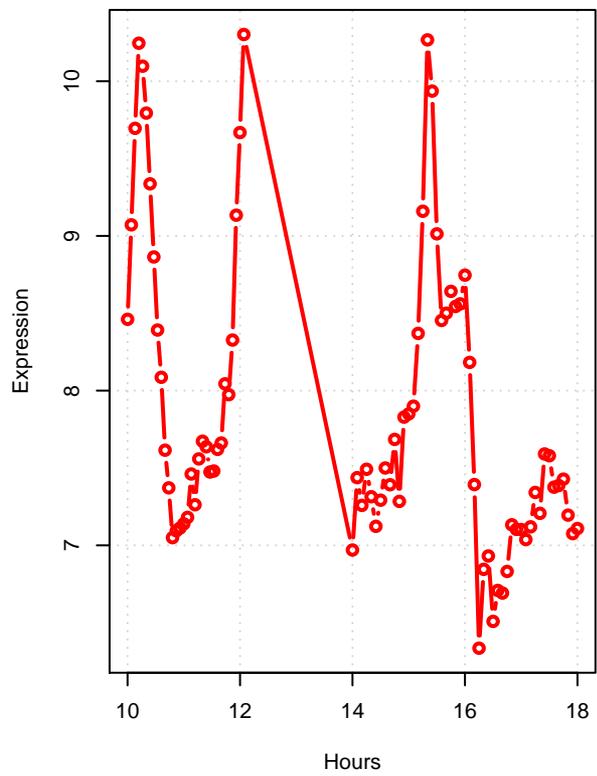
## **allantoin degradation**

# allantoin degradation

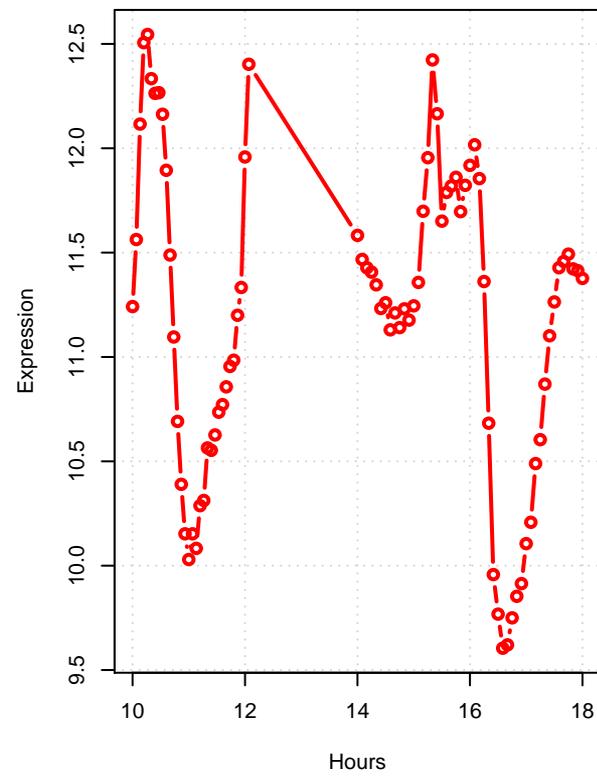
dal2 YIR029W  
Allantoicase



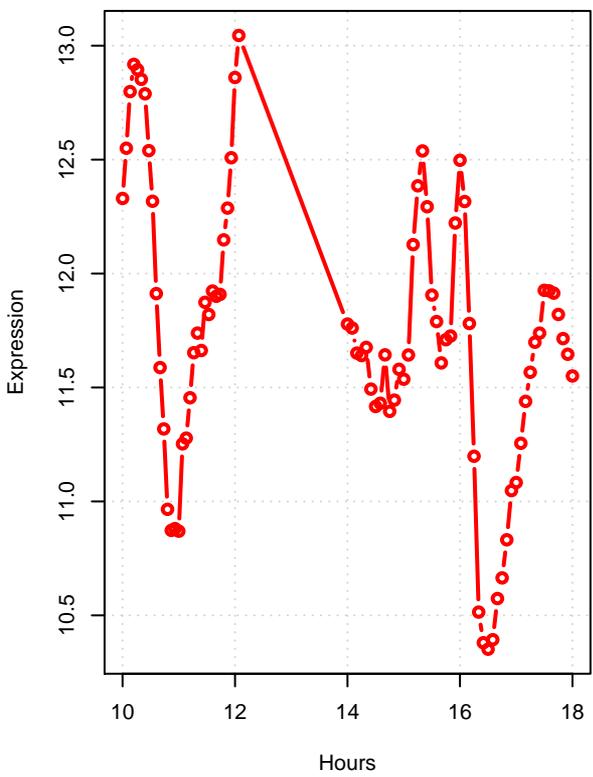
dal1 YIR027C  
Allantoinase



dur12 YBR208C  
Urea amidolyase



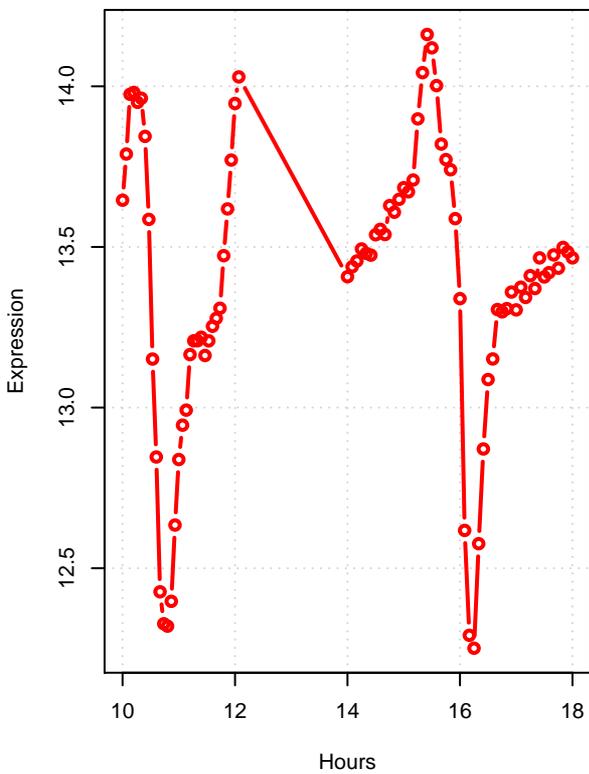
dal3 YIR032C  
Ureidoglycolate lyase



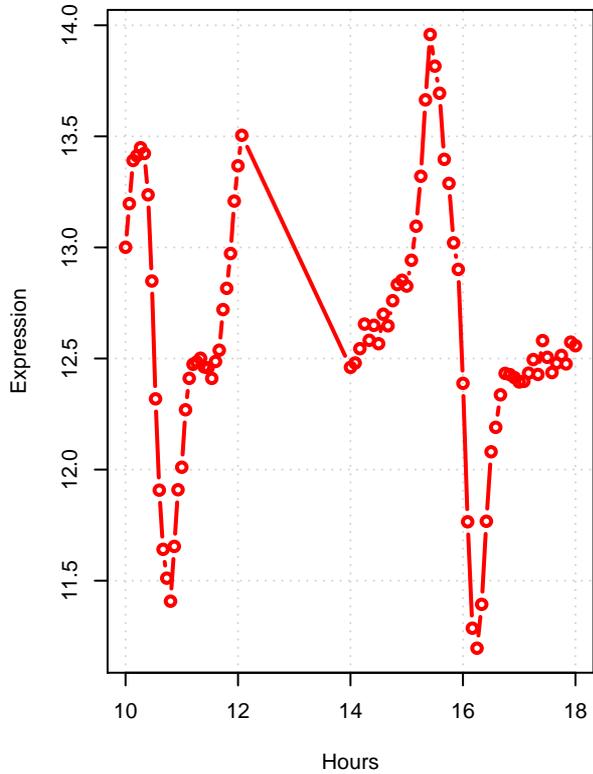
## **arginine biosynthesis**

# arginine biosynthesis

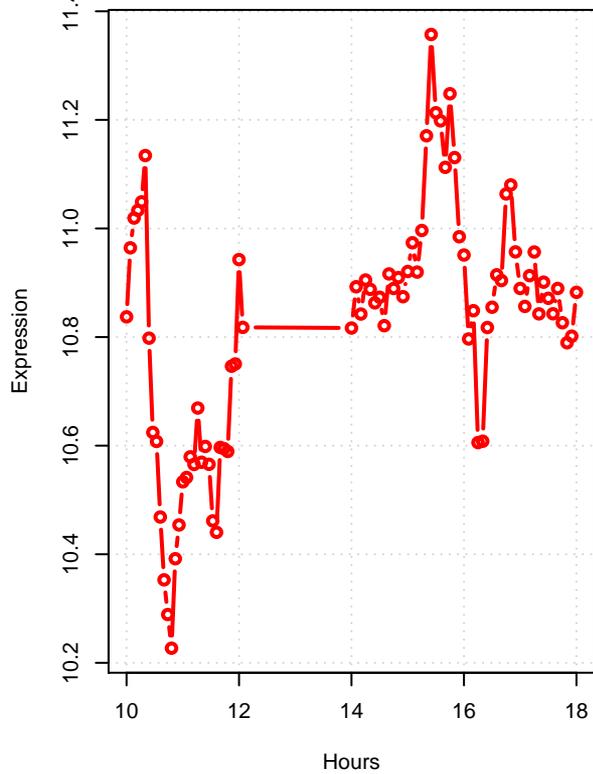
**arg56 YER069W**  
Acetylglutamate kinase and N-acetyl- $\gamma$ -glutamyl-phosphate reductase



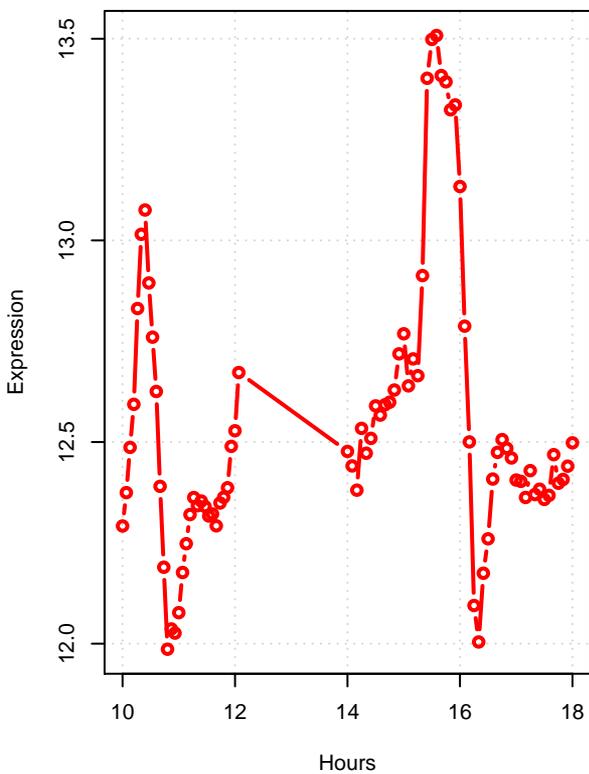
**arg6 YOL140W**  
Acetylmithine aminotransferase



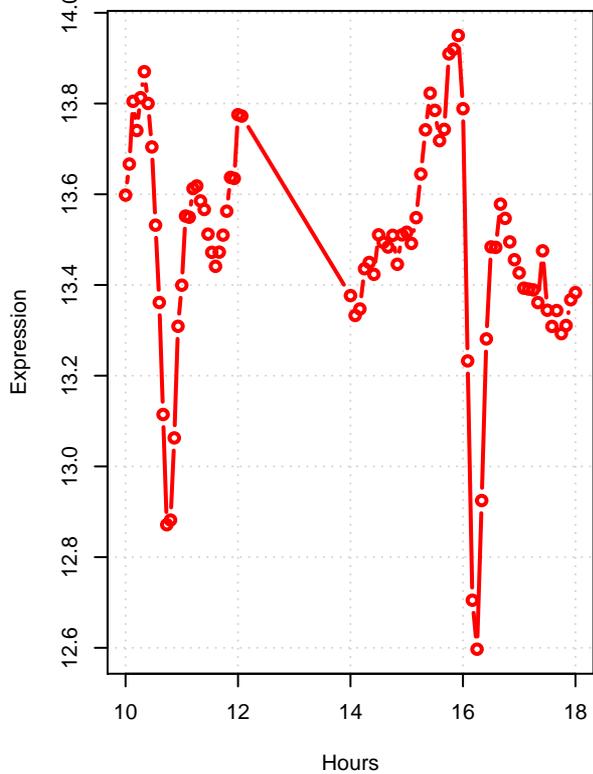
**arg2 YJL071W**  
Acetylglutamate synthase (glutamate N-acetyltransferase)



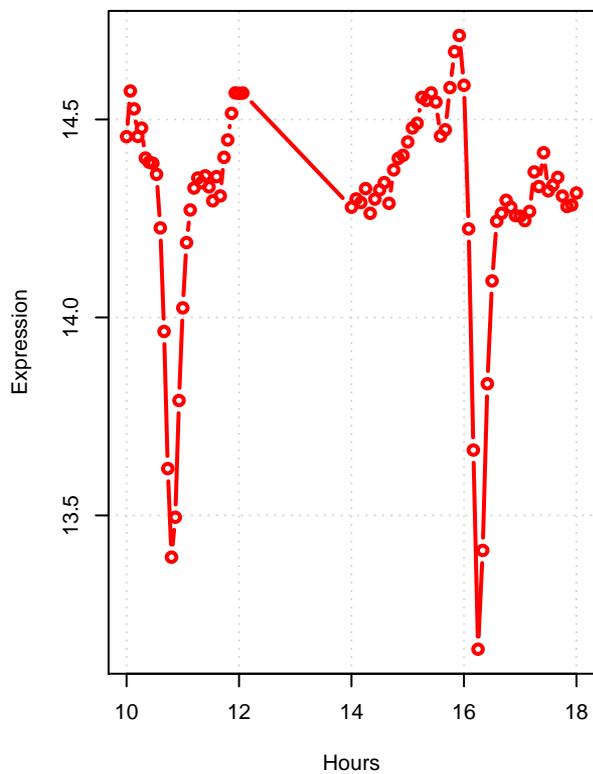
**arg7 YMR062C**  
Mitochondrial ornithine acetyltransferase



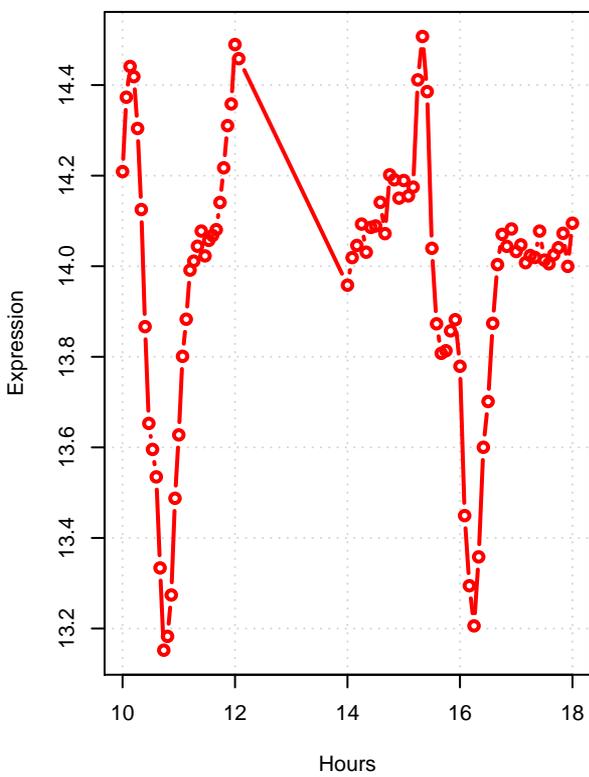
**arg4 YHR018C**  
Argininosuccinate lyase



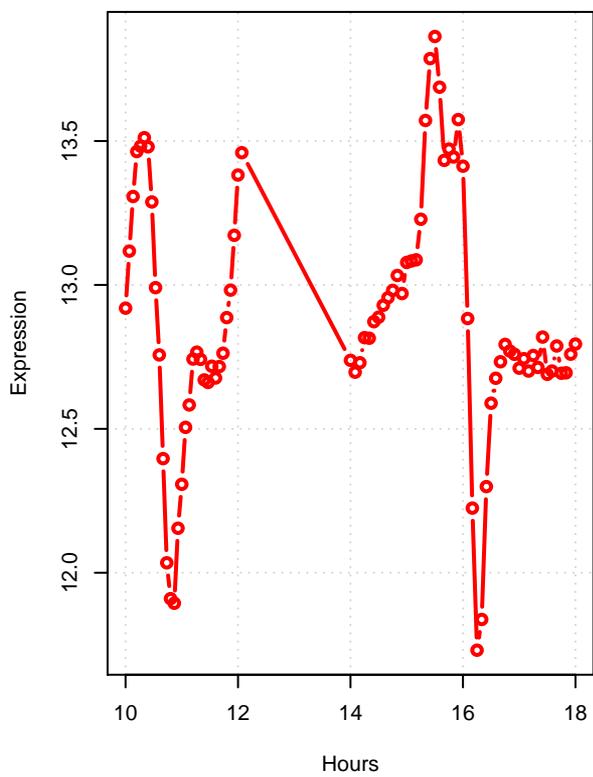
**arg1 YOL058W**  
Argininosuccinate synthetase



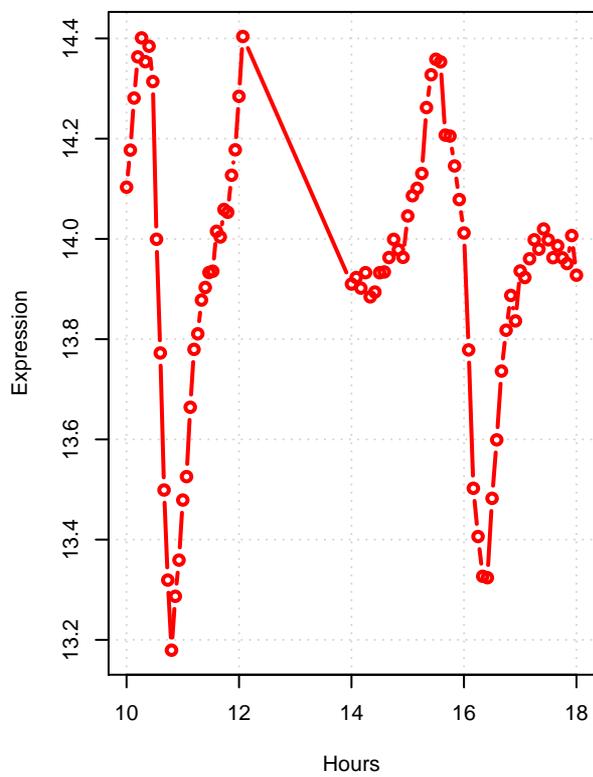
**cpa1 YOR303W**  
Small subunit of carbamoyl phosphate synthetase



**cpa2 YJR109C**  
Large subunit of carbamoyl phosphate synthetase

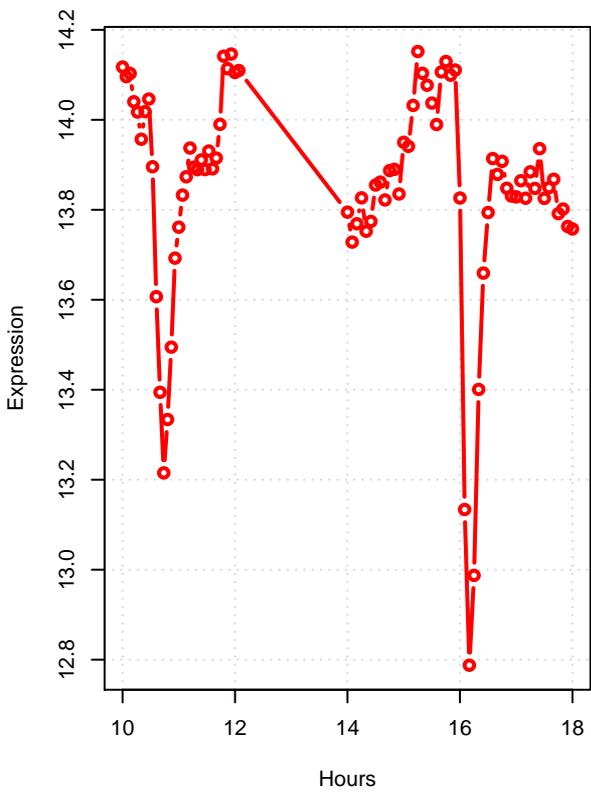


**ura2 YJL130C**  
Bifunctional carbamoylphosphate synthetase/aspartate transcarbamylase



# arginine biosynthesis

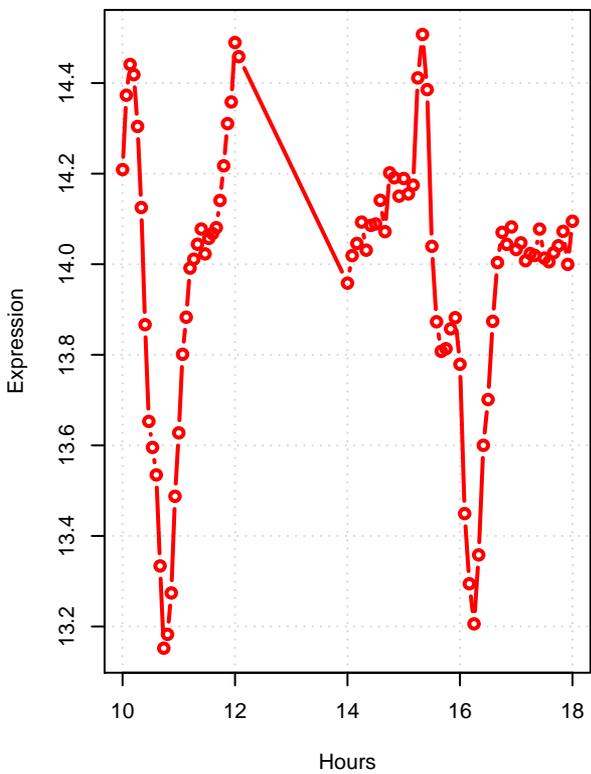
arg3 YJL088W  
Ornithine carbamoyltransferase



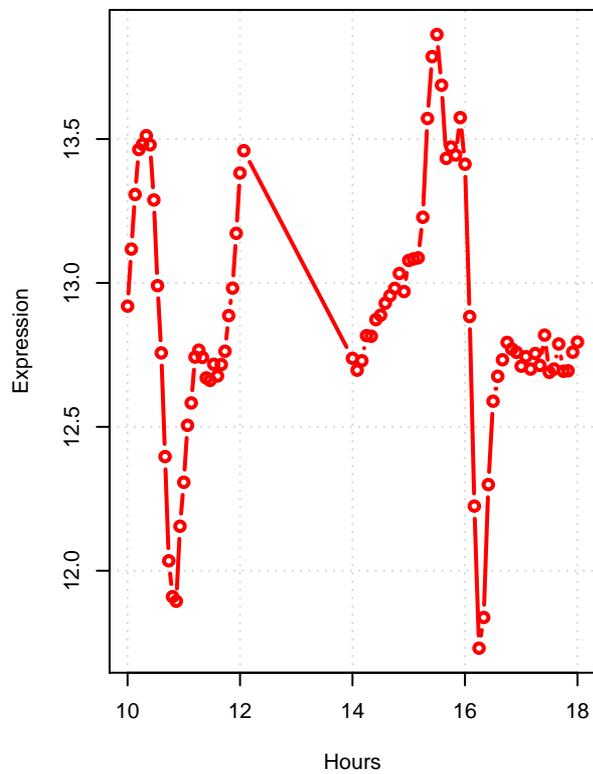
## **citrulline biosynthesis**

# citrulline biosynthesis

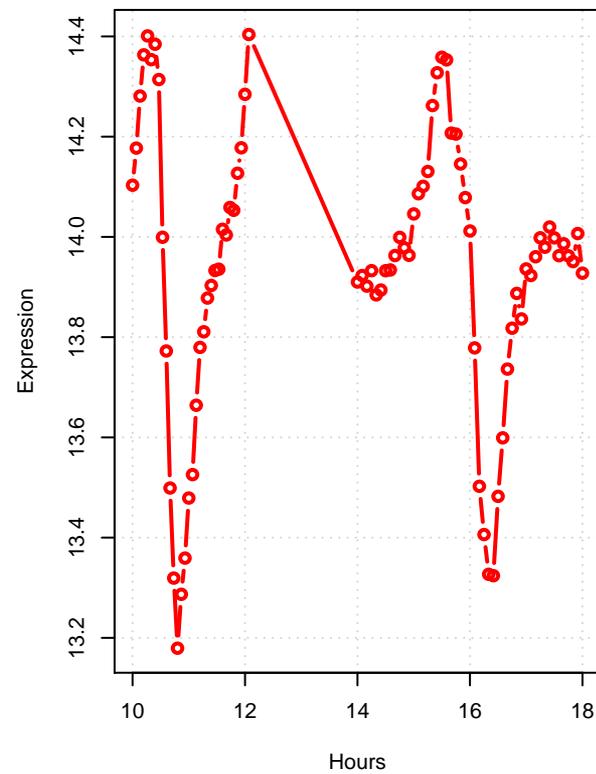
**cpa1 YOR303W**  
Small subunit of carbamoyl phosphate synthetase



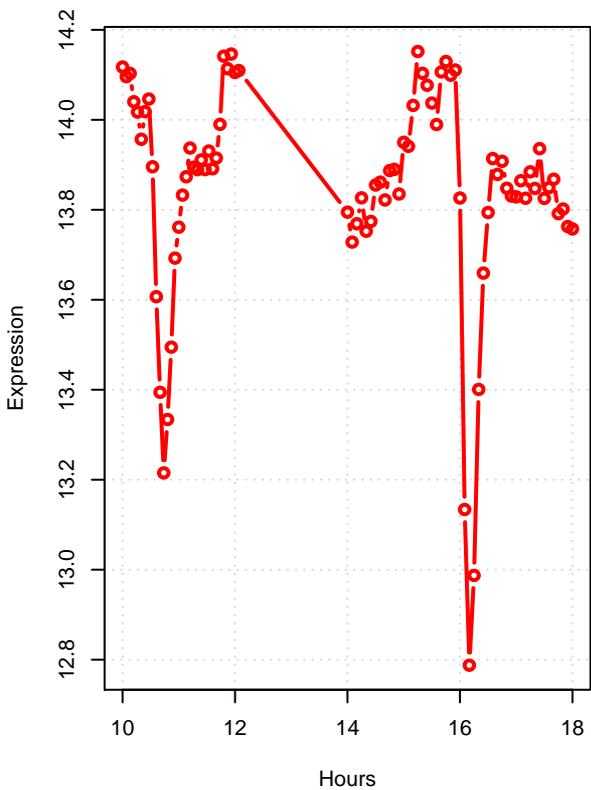
**cpa2 YJR119C**  
Large subunit of carbamoyl phosphate synthetase



**ura2 YJL130C**  
Bifunctional carbamoylphosphate synthetase/aspartate transcarbamylase

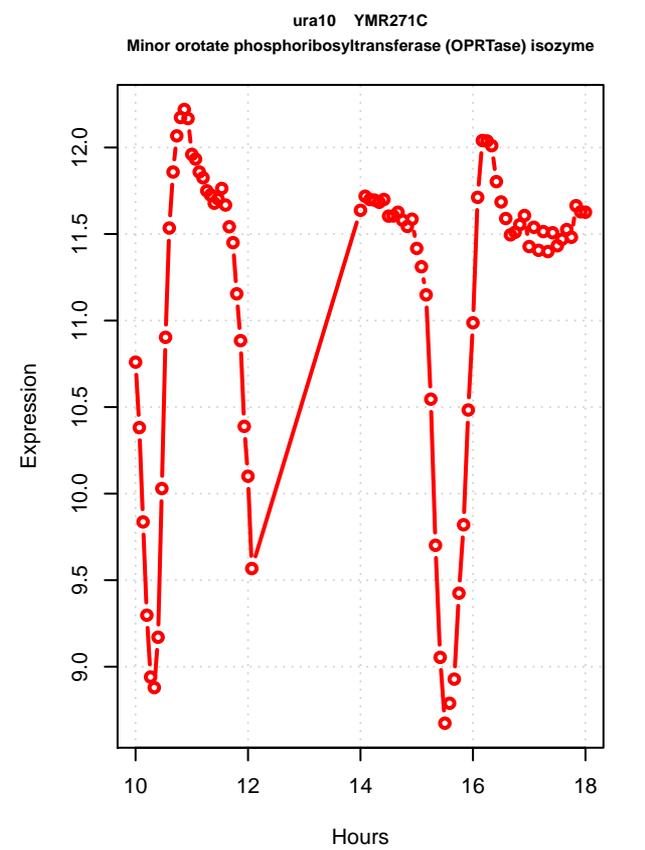
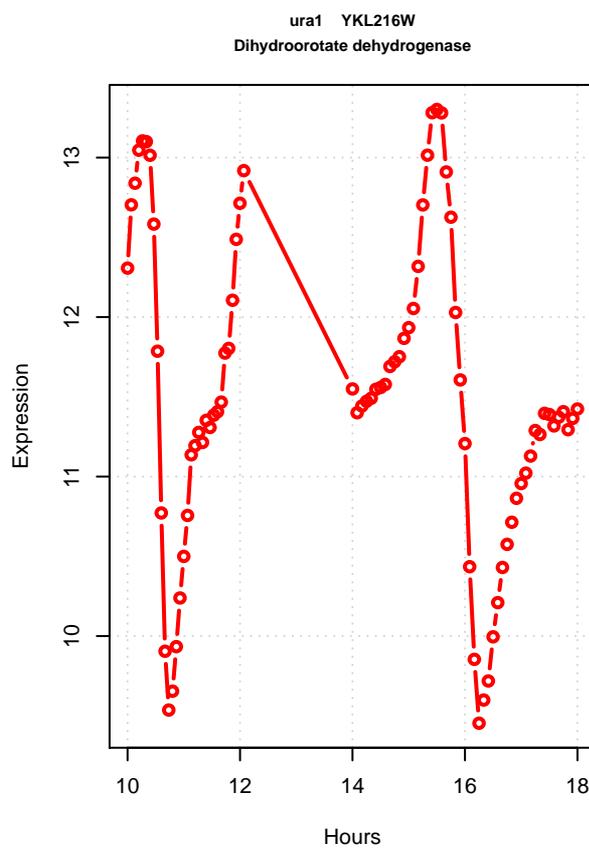
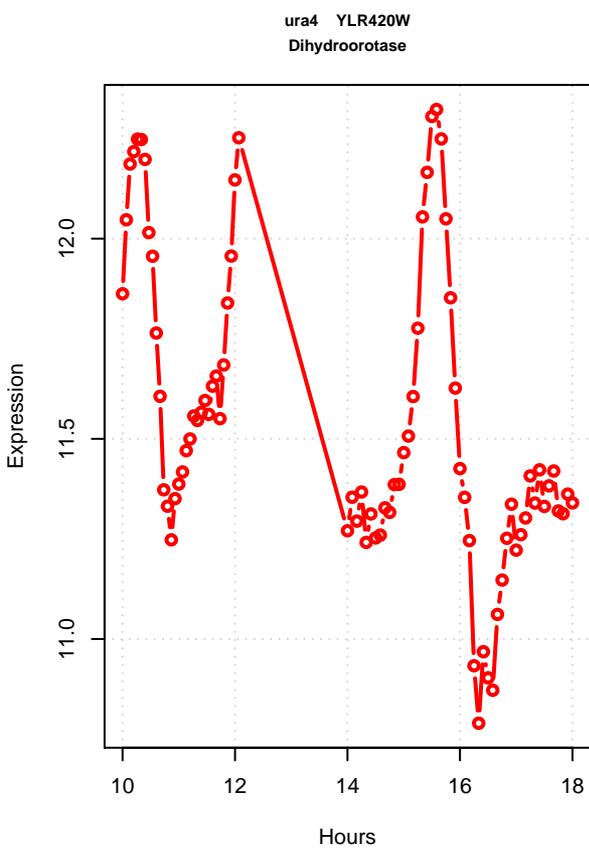
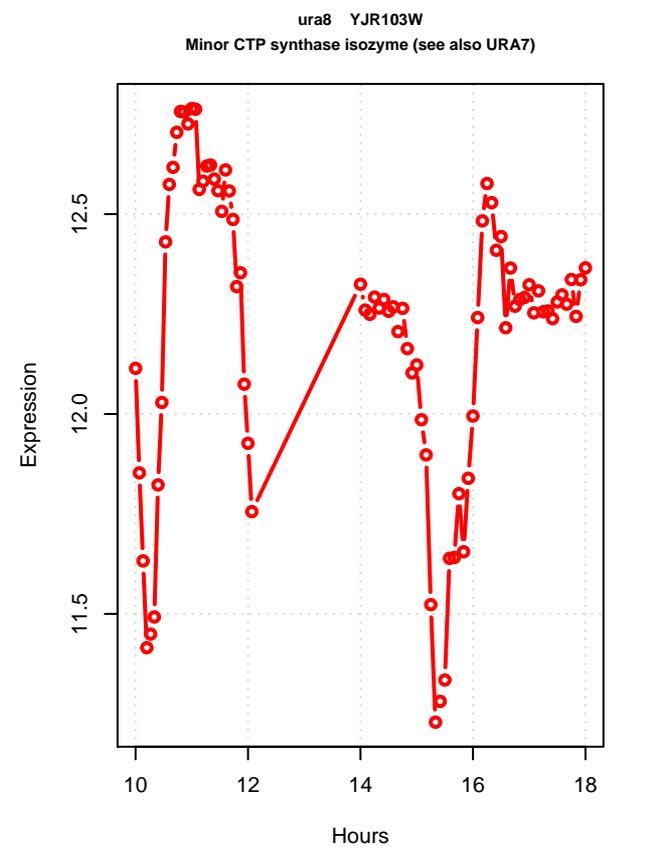
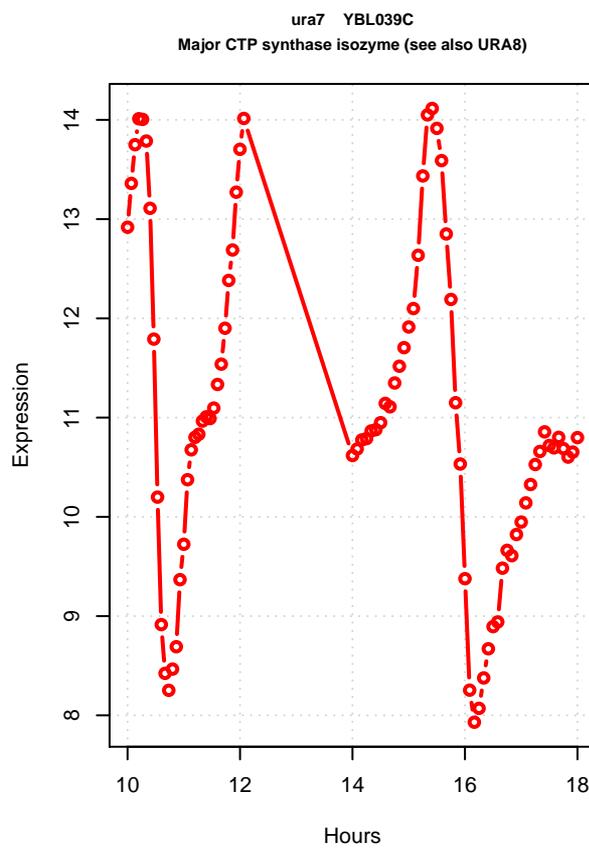
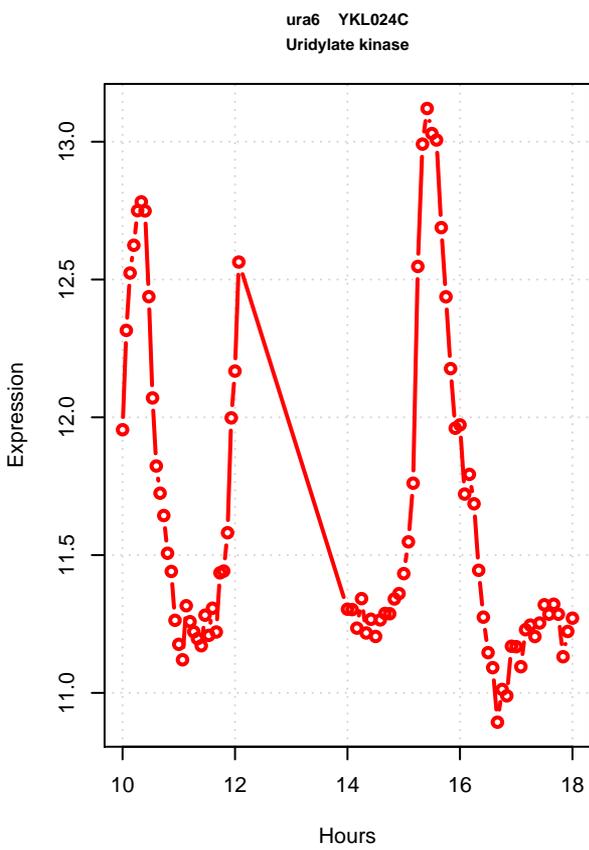
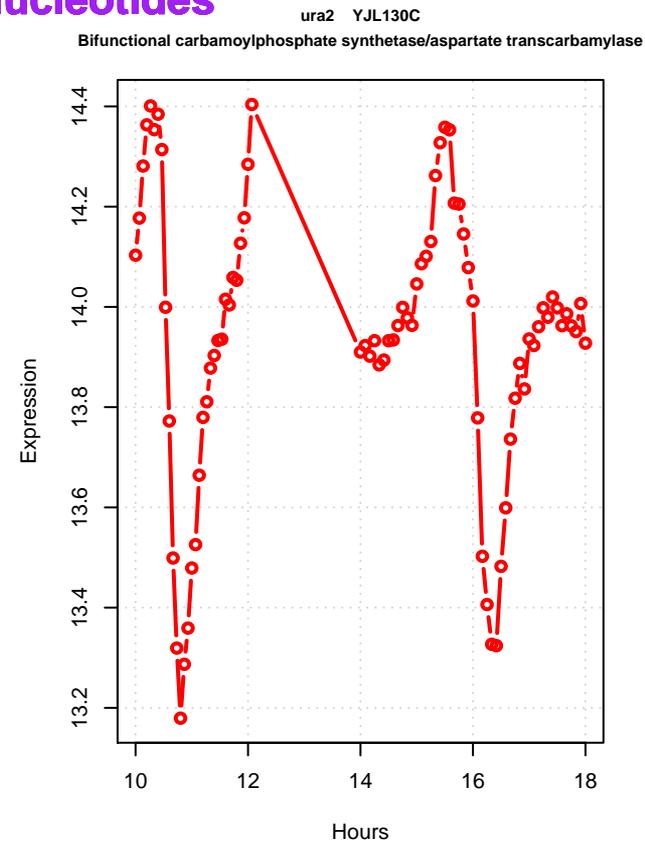
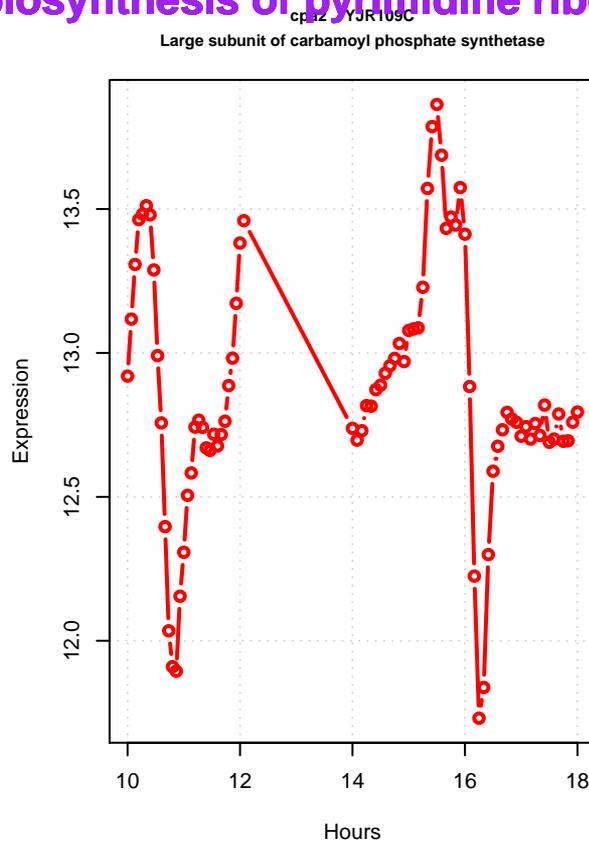
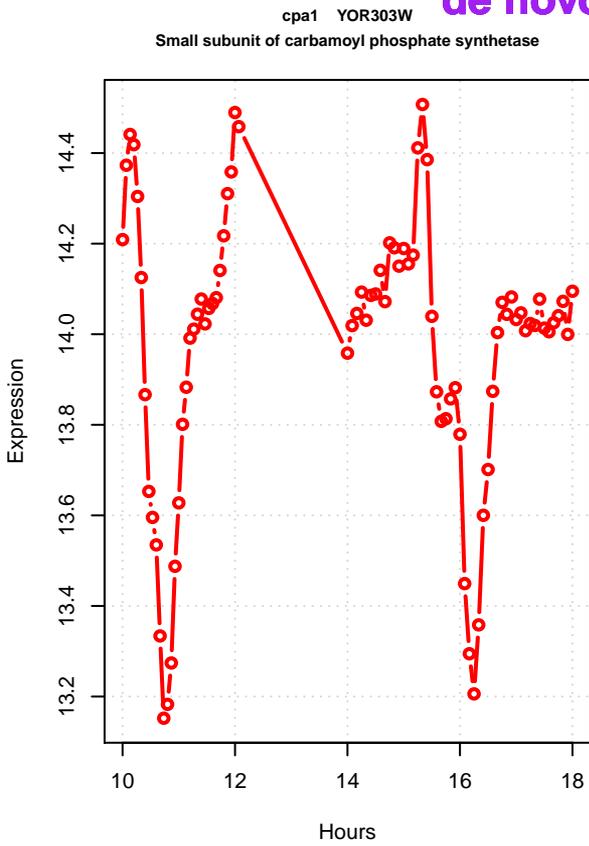


**arg3 YJL088W**  
Ornithine carbamoyltransferase



**de novo biosynthesis of pyrimidine ribonucleotides**

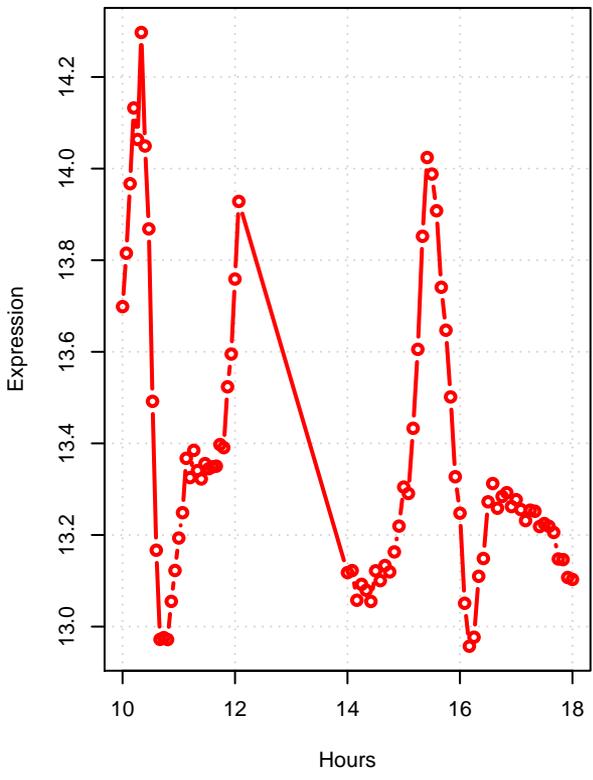
# de novo biosynthesis of pyrimidine ribonucleotides



# de novo biosynthesis of pyrimidine ribonucleotides

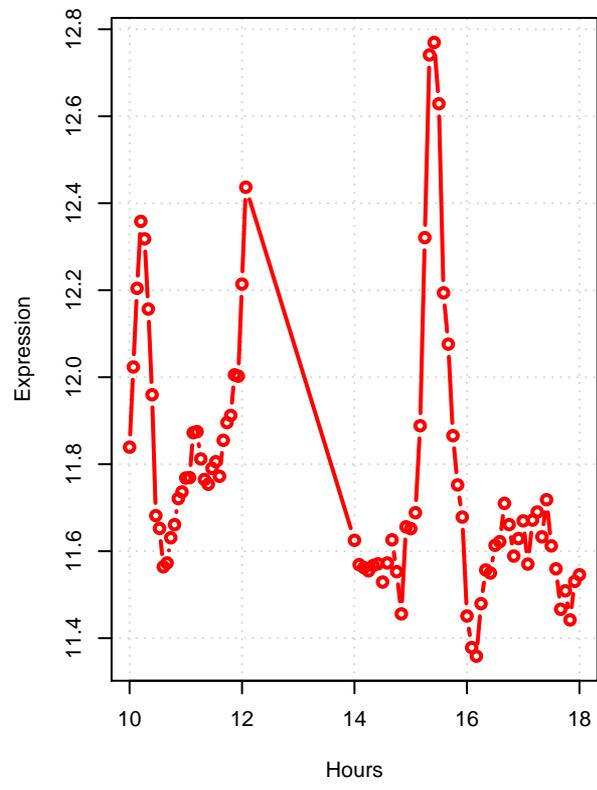
ura5 YML106W

Major orotate phosphoribosyltransferase (OPRTase) isozyme



ura5 YEL021W

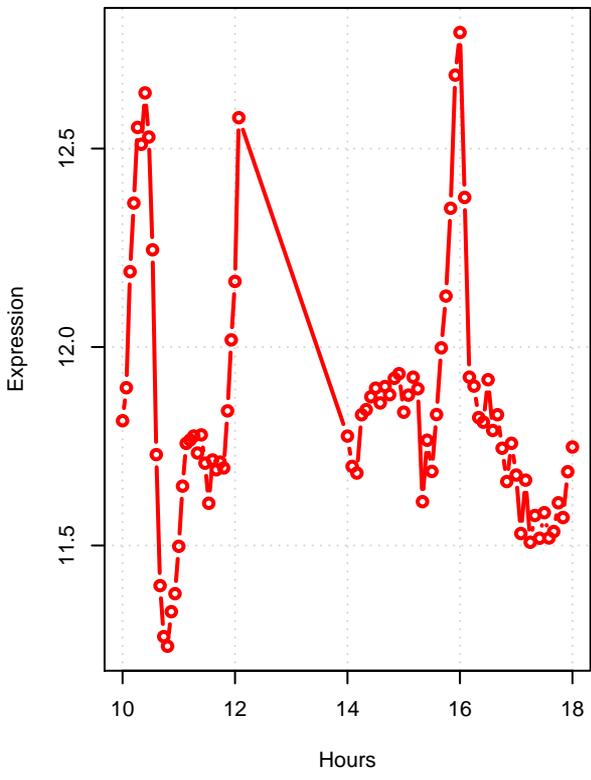
Orotidine-5'-phosphate (OMP) decarboxylase



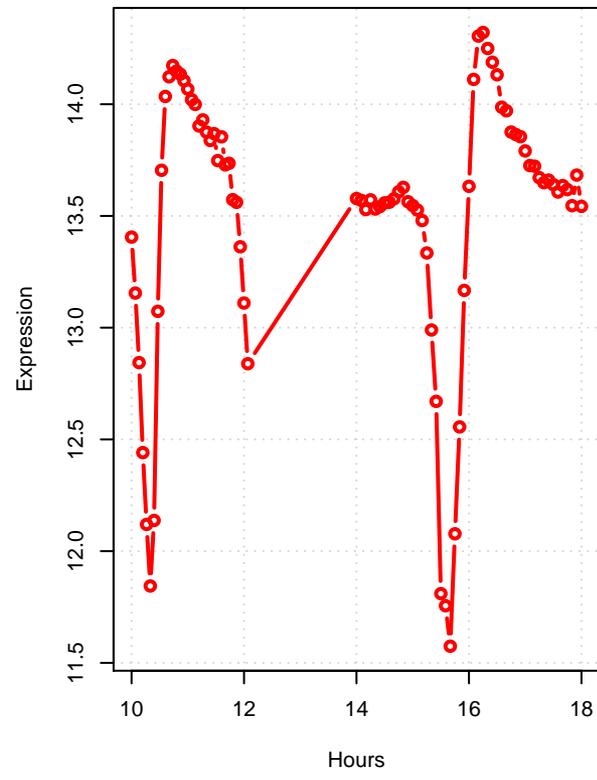
**arginine degradation (anaerobic)**

# arginine degradation (anaerobic)

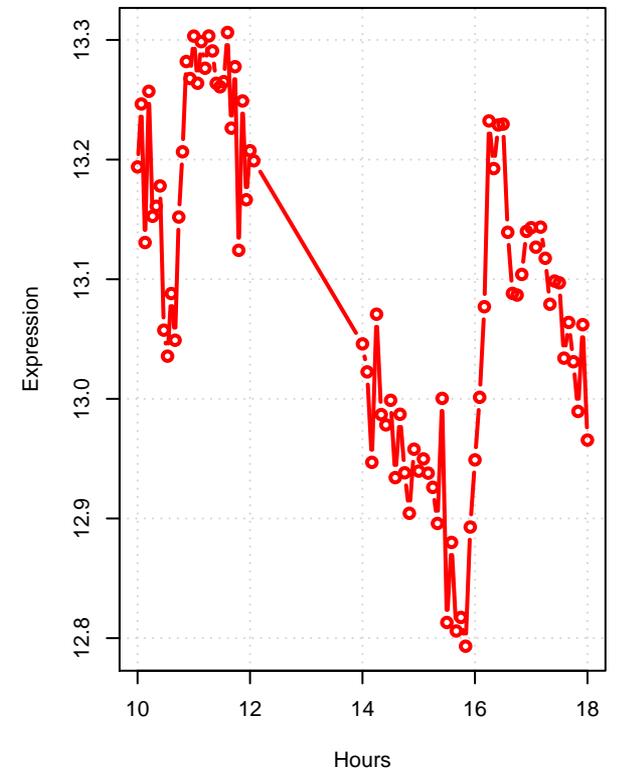
car1 YPL111W  
Arginase, catabolizes arginine to ornithine and urea



car2 YLR438W  
L-ornithine transaminase (OTase)

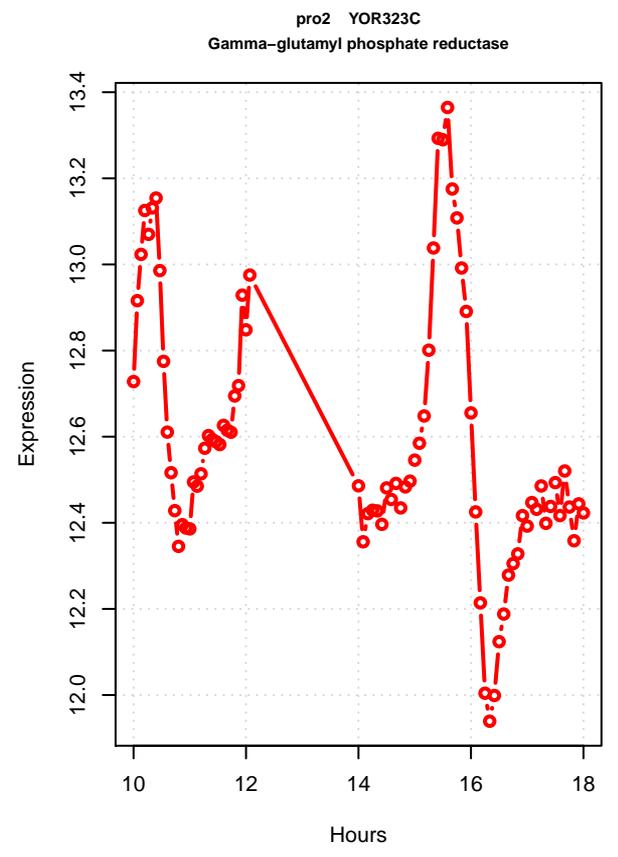
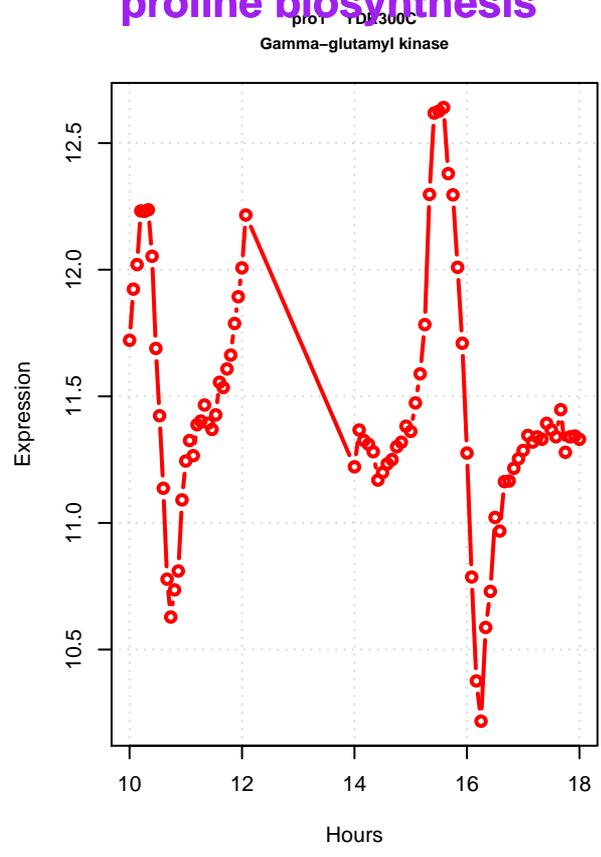
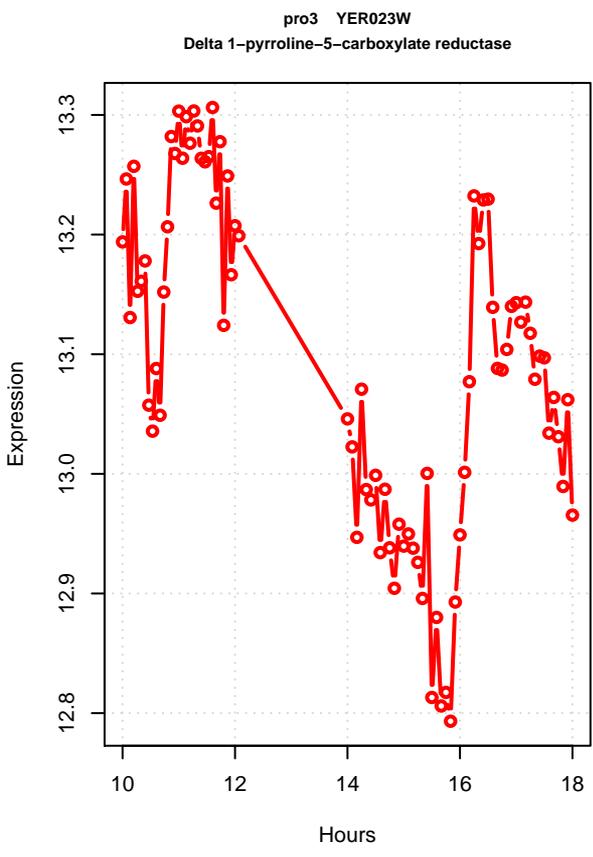


pro3 YER023W  
Delta 1-pyrroline-5-carboxylate reductase



## **proline biosynthesis**

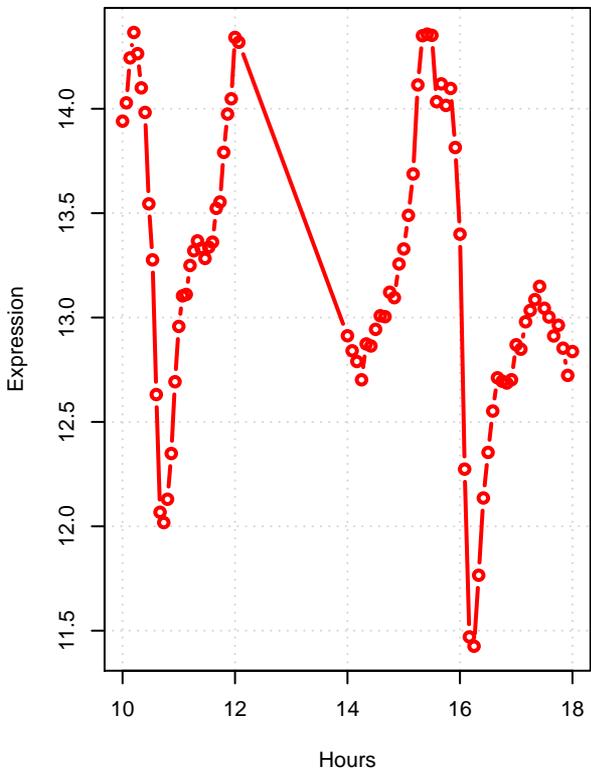
# proline biosynthesis



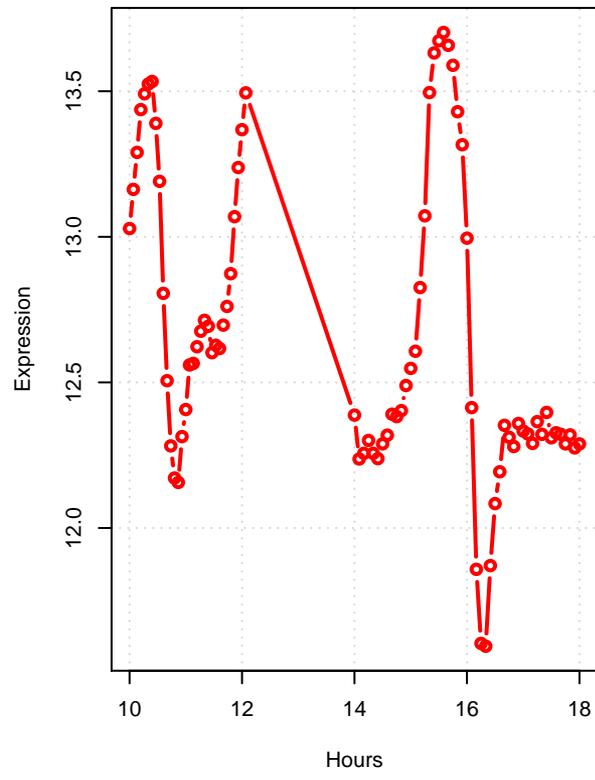
## asparagine biosynthesis

# asparagine biosynthesis

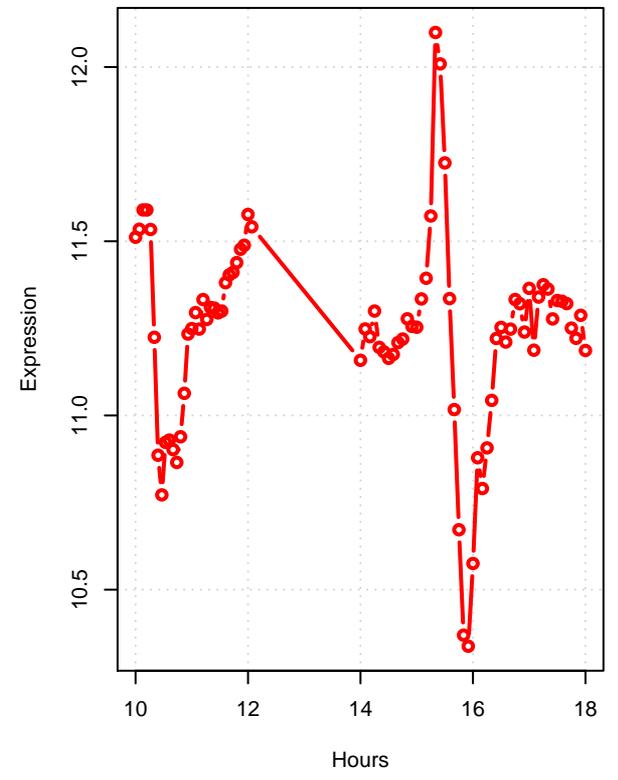
asn1 YPR145W  
Asparagine synthetase



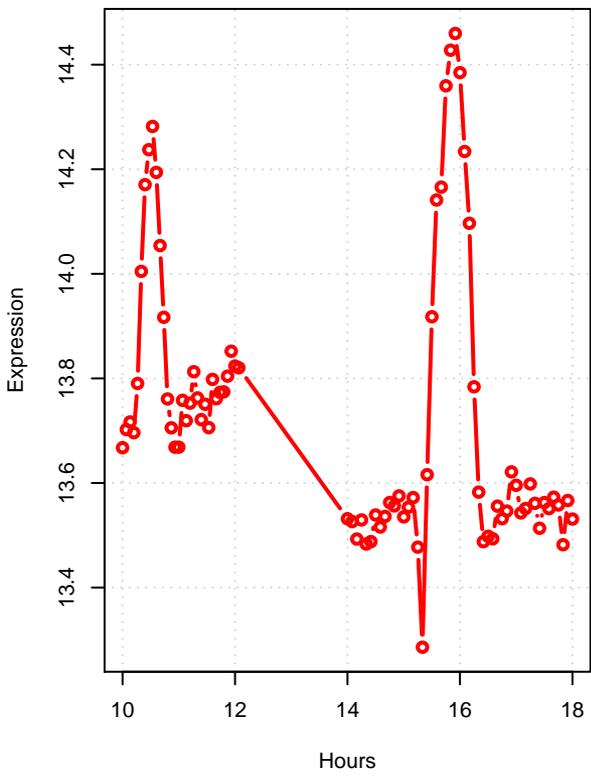
asn2 YGR124W  
Asparagine synthetase



aat1 YKL106W  
Mitochondrial aspartate aminotransferase

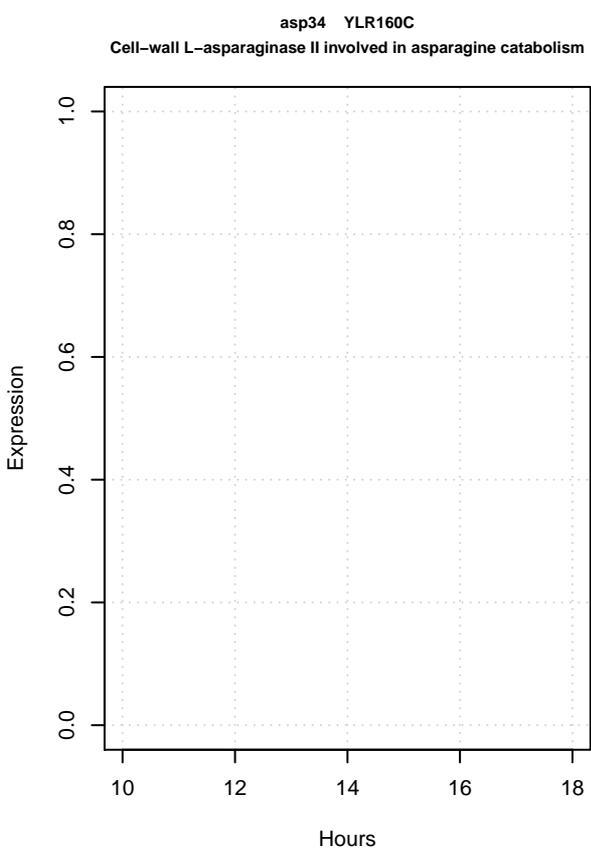
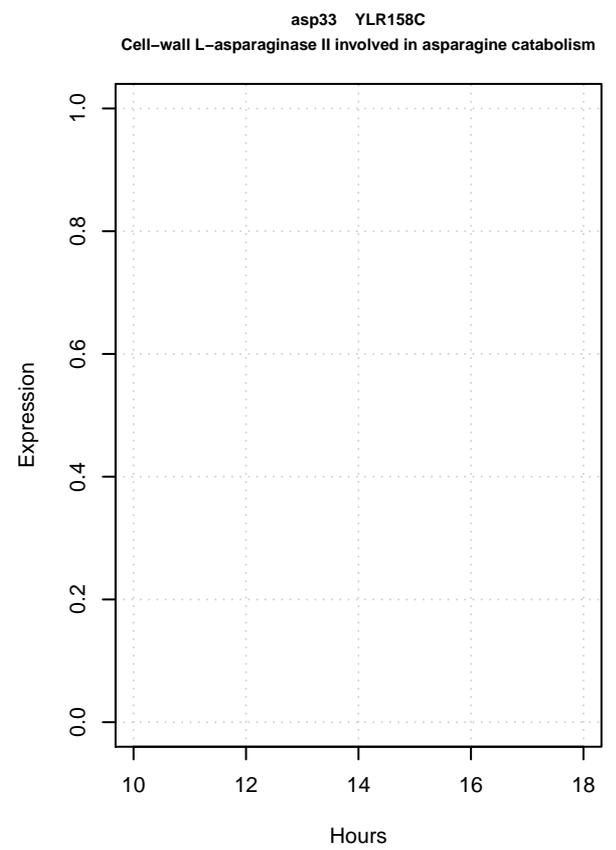
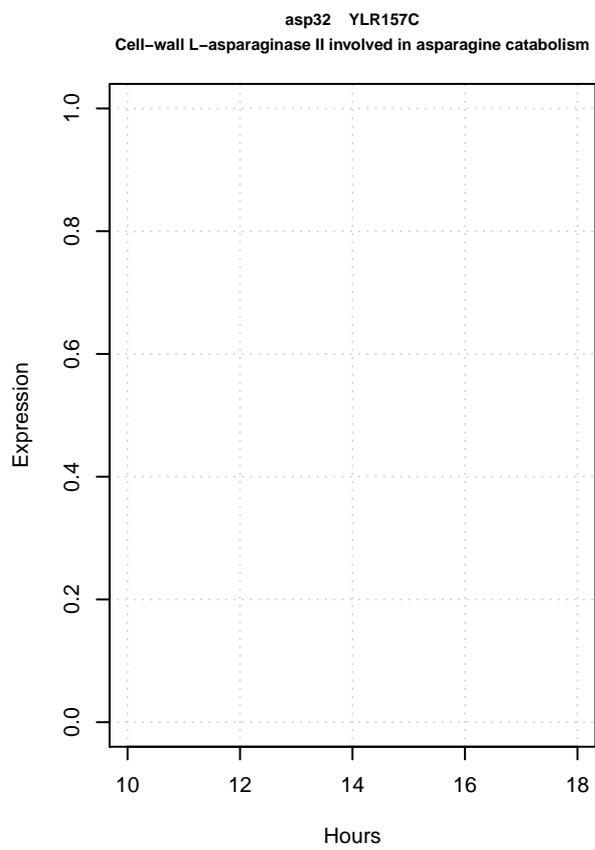
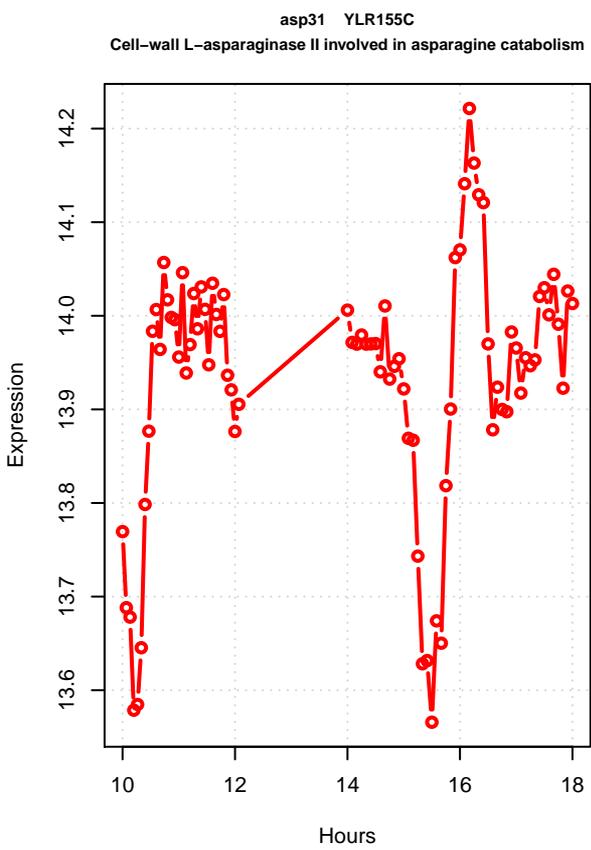
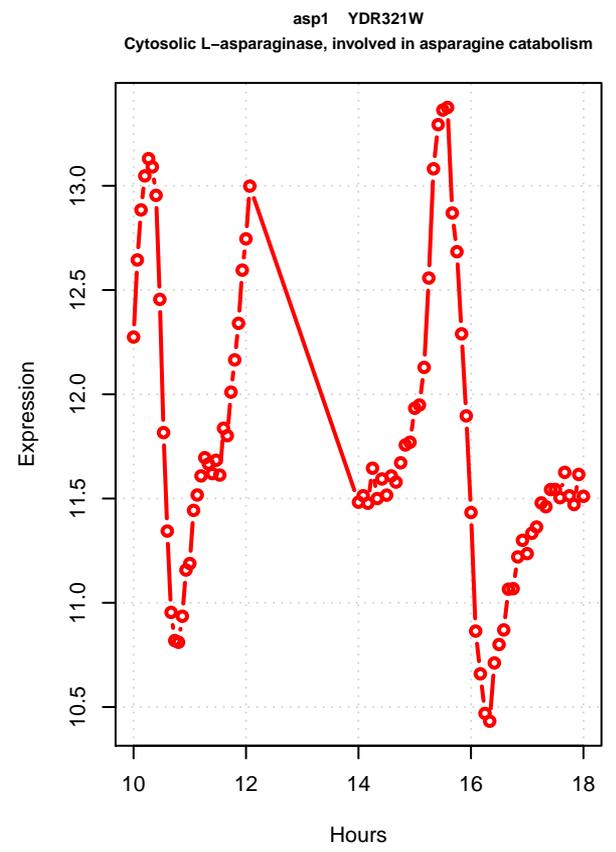
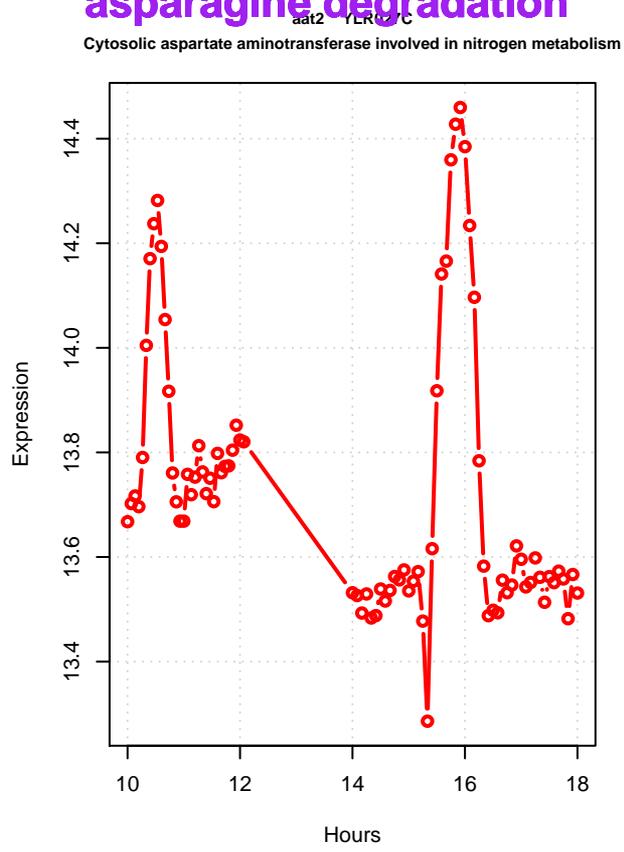
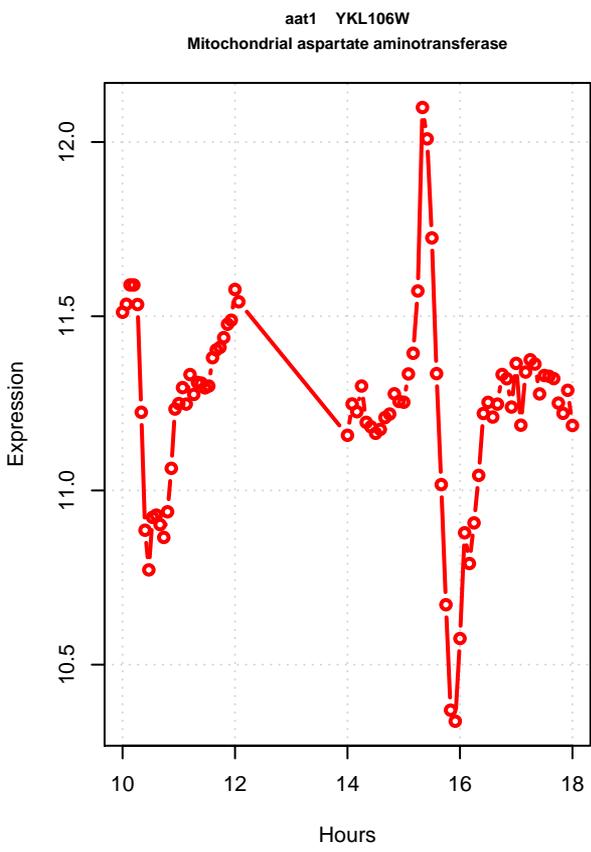


aat2 YLR027C  
Cytosolic aspartate aminotransferase involved in nitrogen metabolism



## asparagine degradation

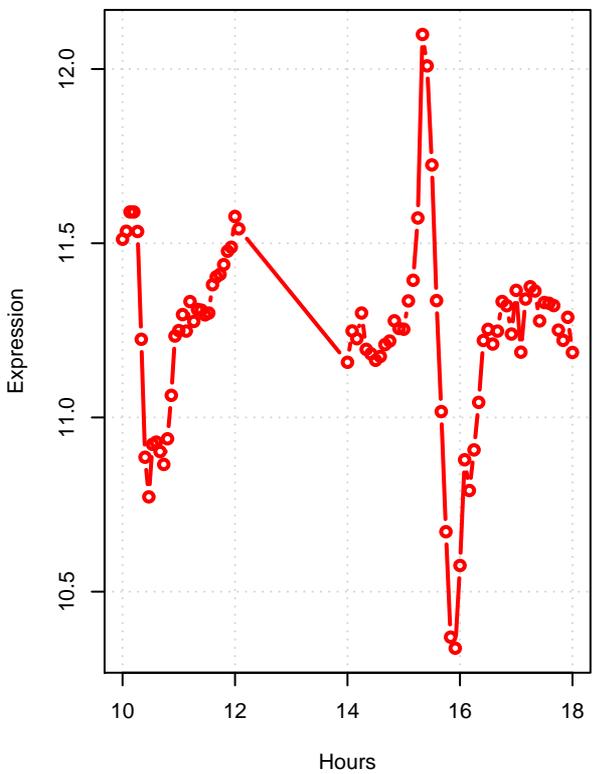
# asparagine degradation



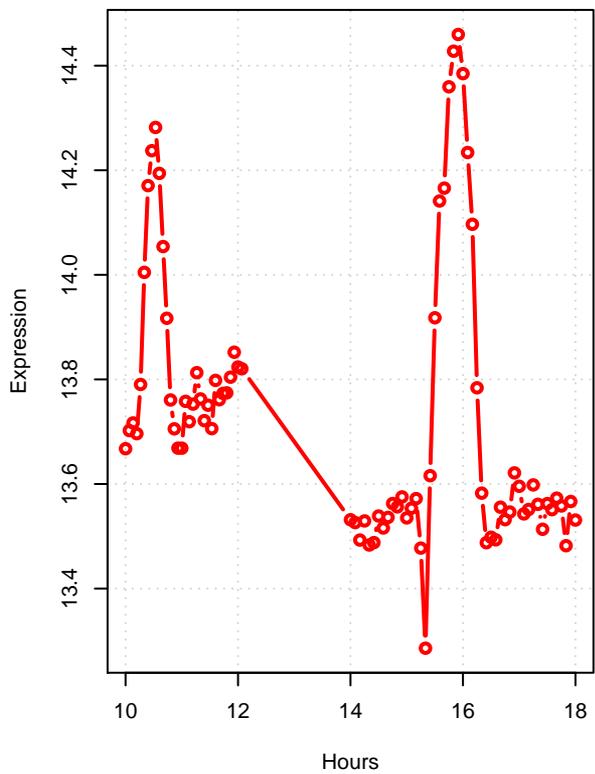
## **aspartate biosynthesis**

# aspartate biosynthesis

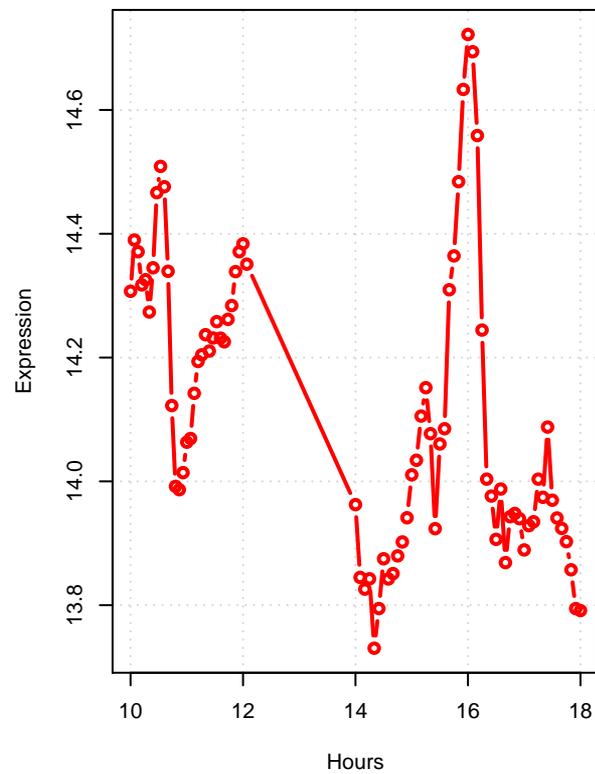
aat1 YKL106W  
Mitochondrial aspartate aminotransferase



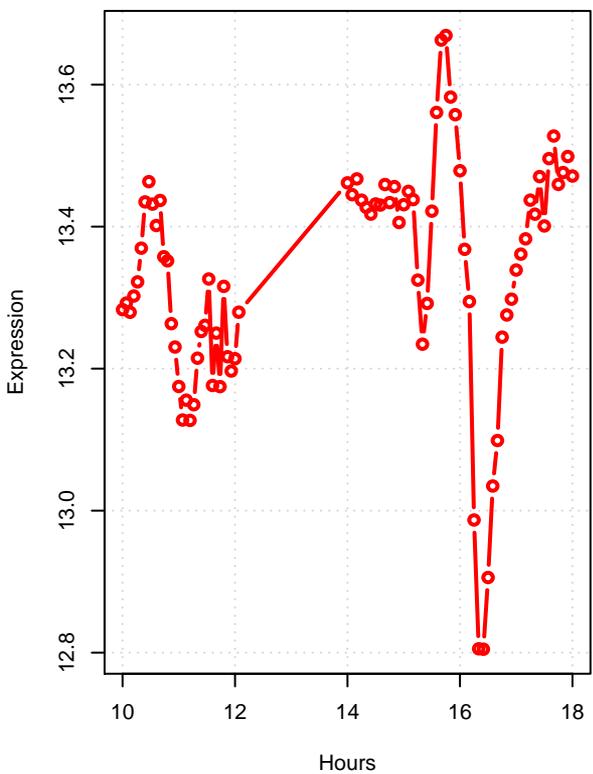
aat2 YLR027C  
Cytosolic aspartate aminotransferase involved in nitrogen metabolism



pyc1 YGL062W  
Pyruvate carboxylase isoform

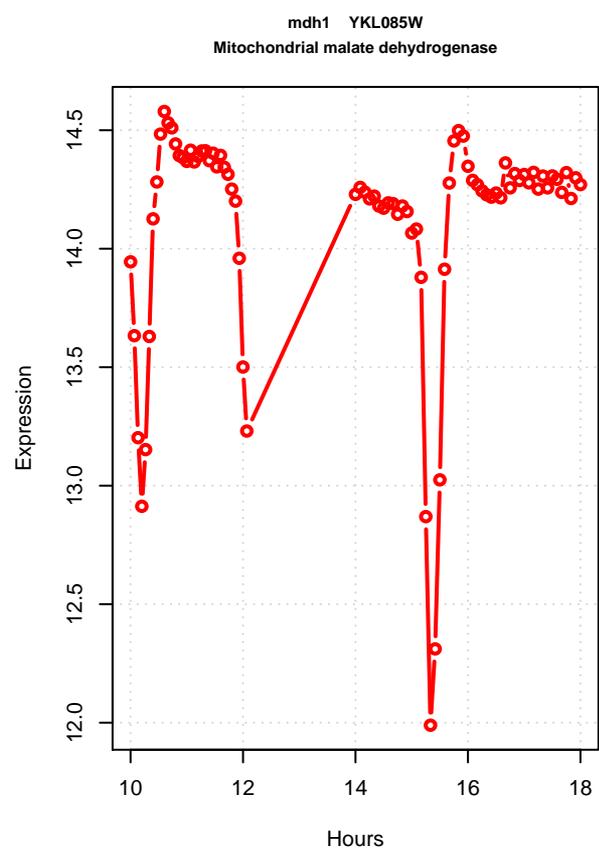
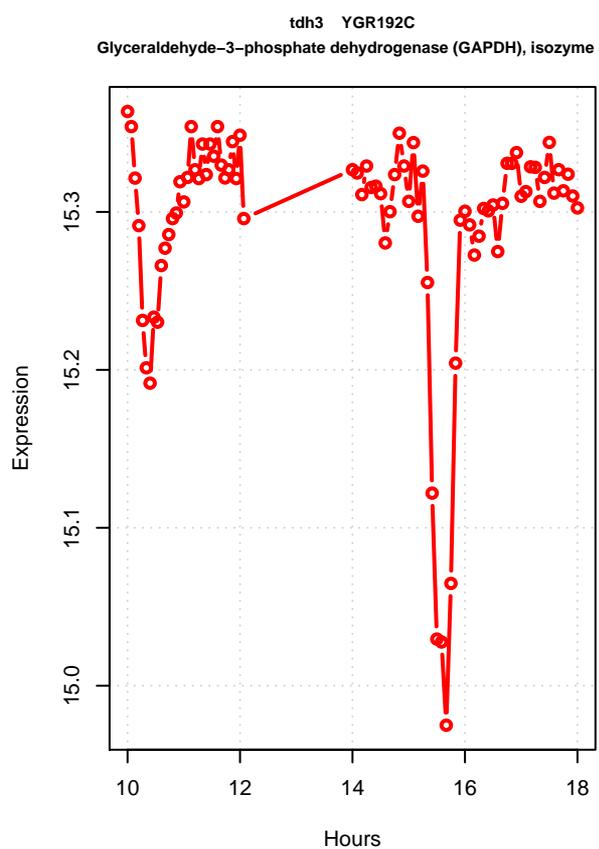
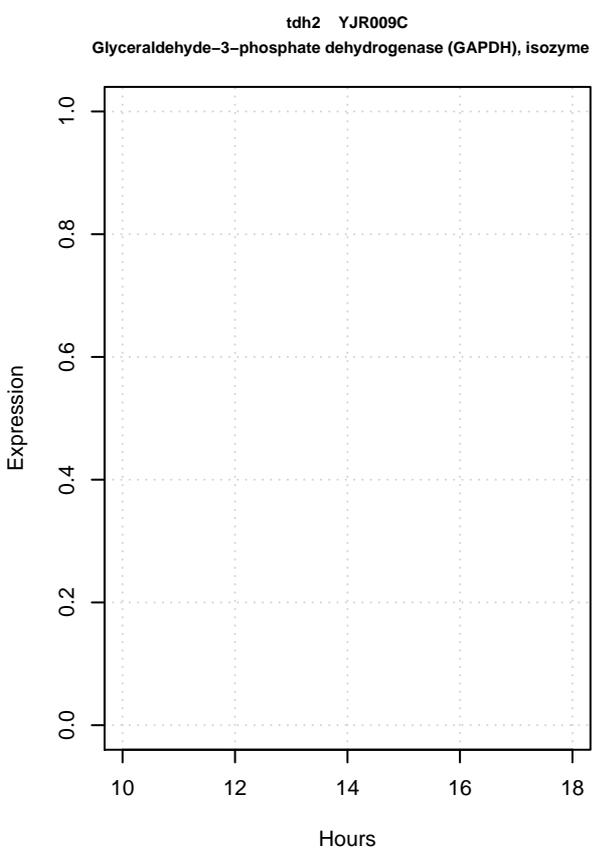
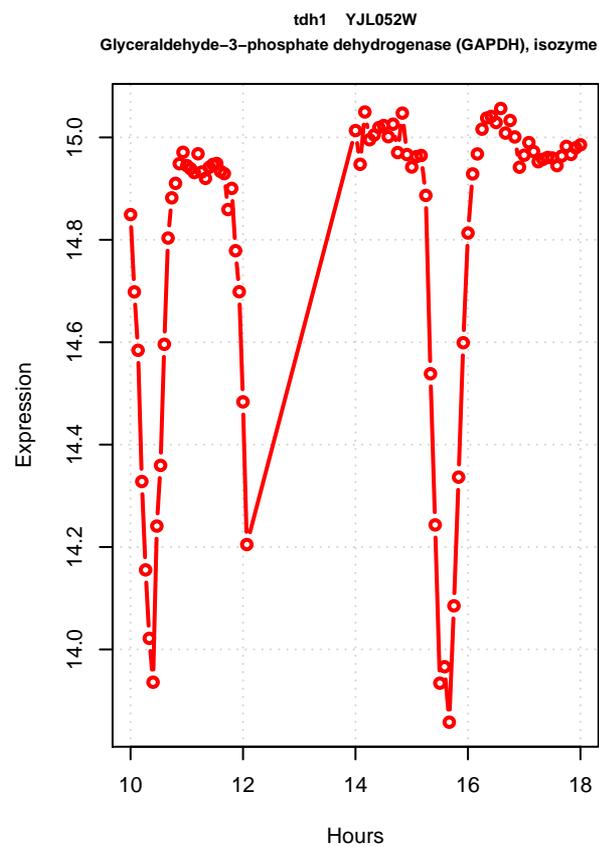
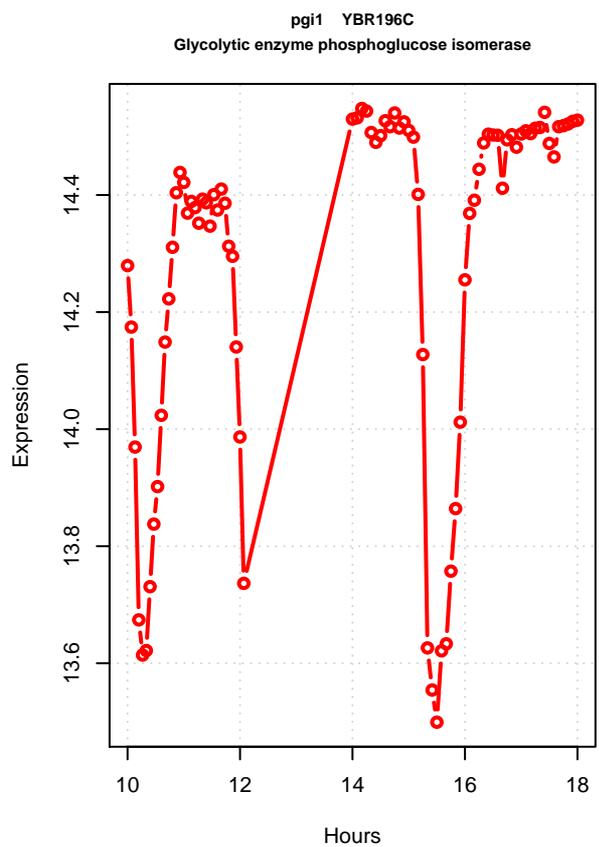
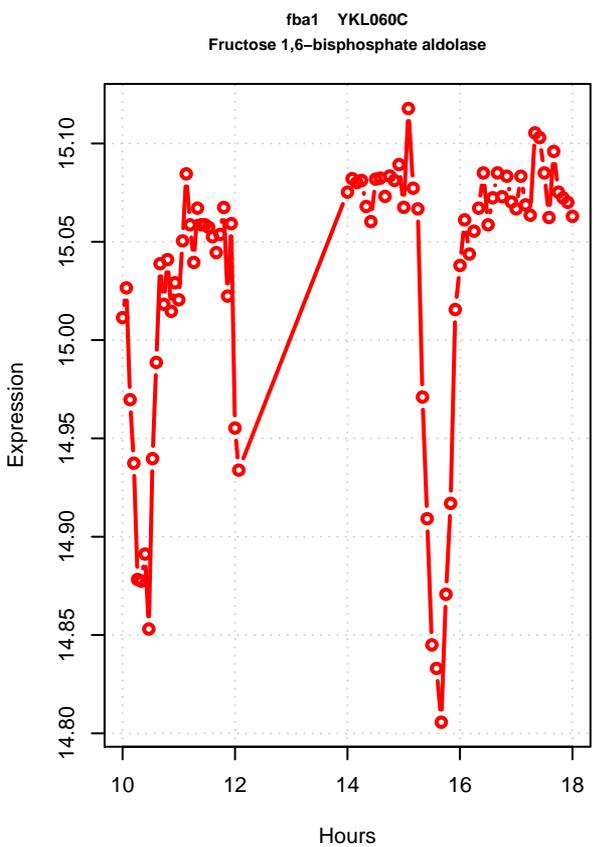
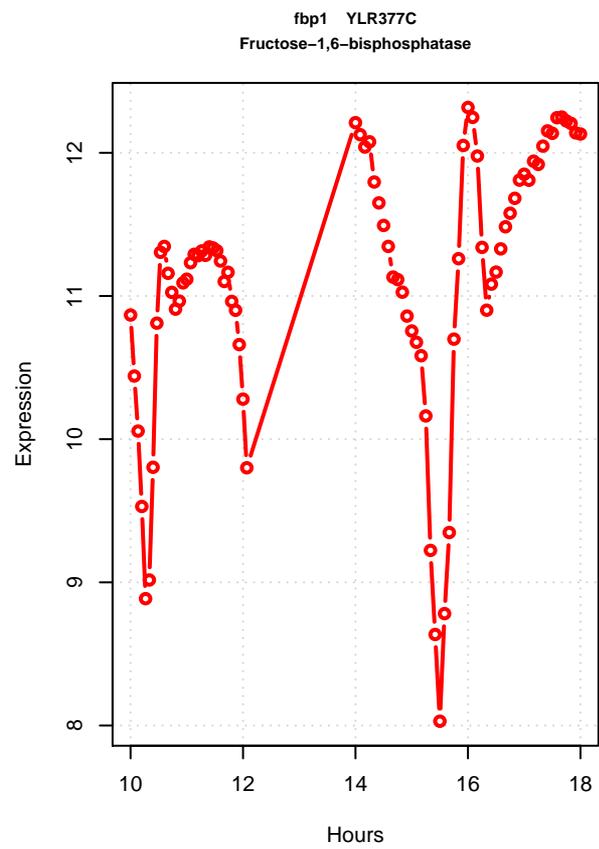
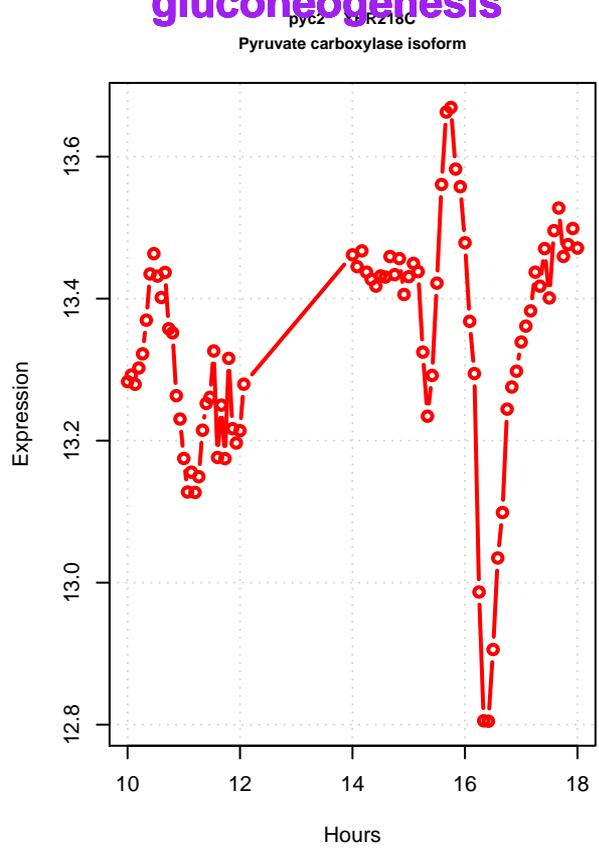
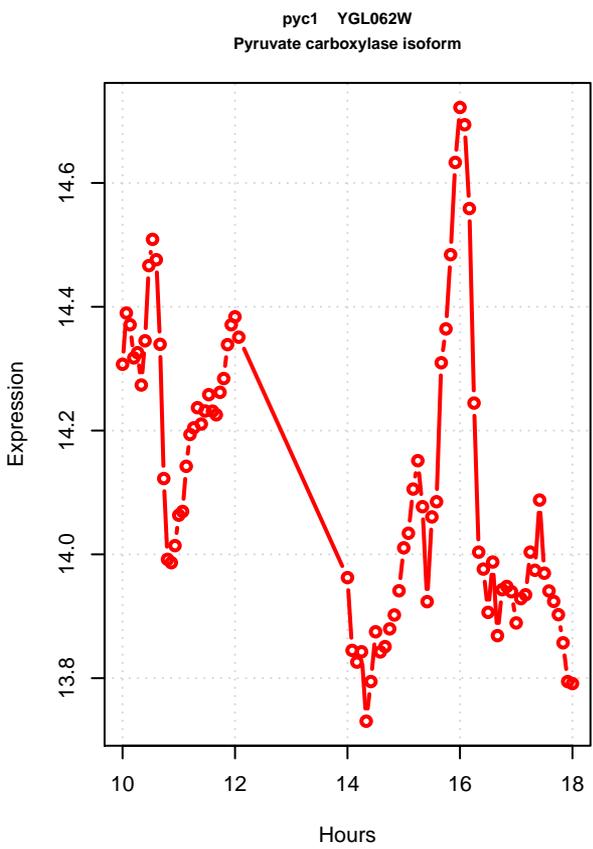


pyc2 YBR218C  
Pyruvate carboxylase isoform

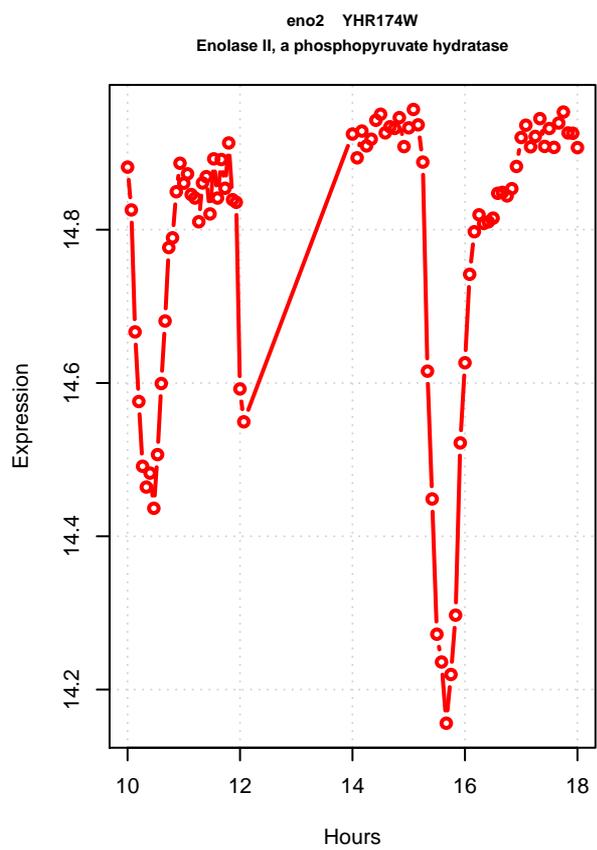
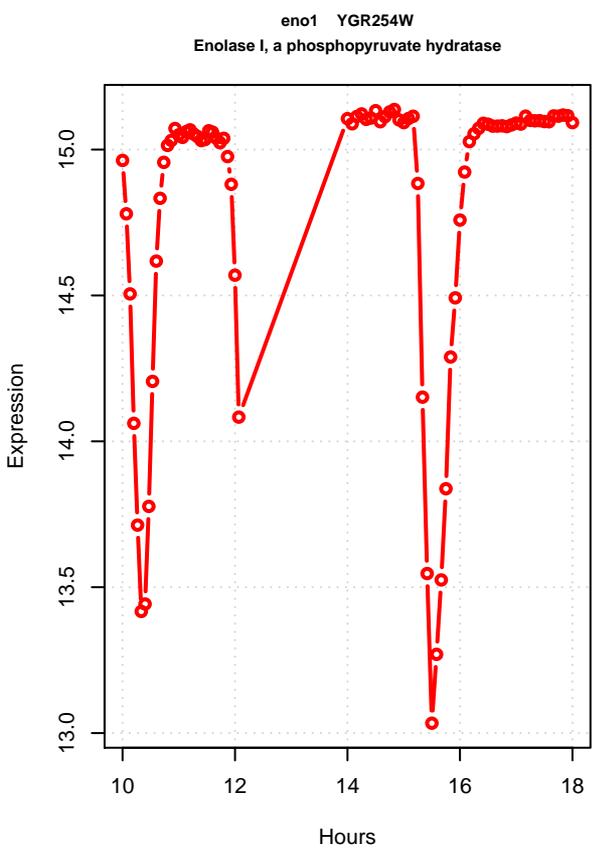
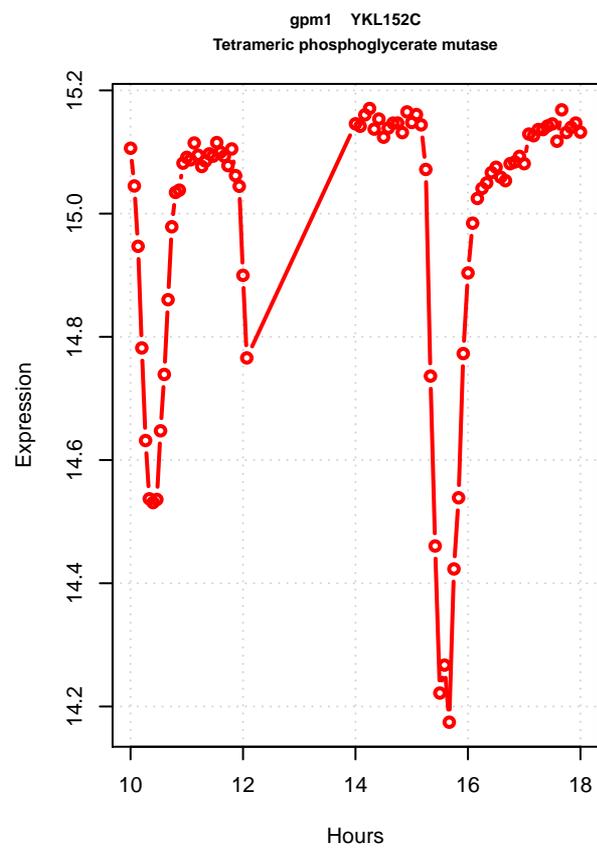
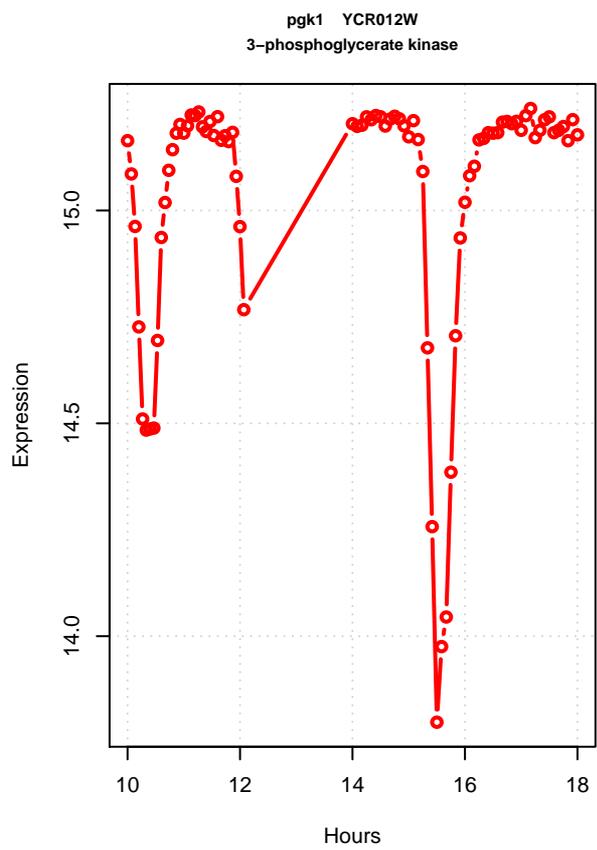
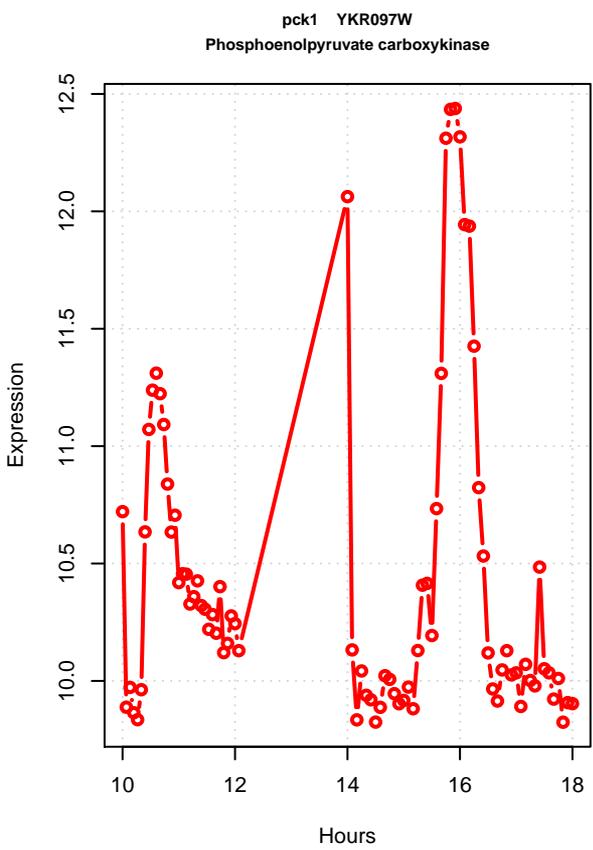
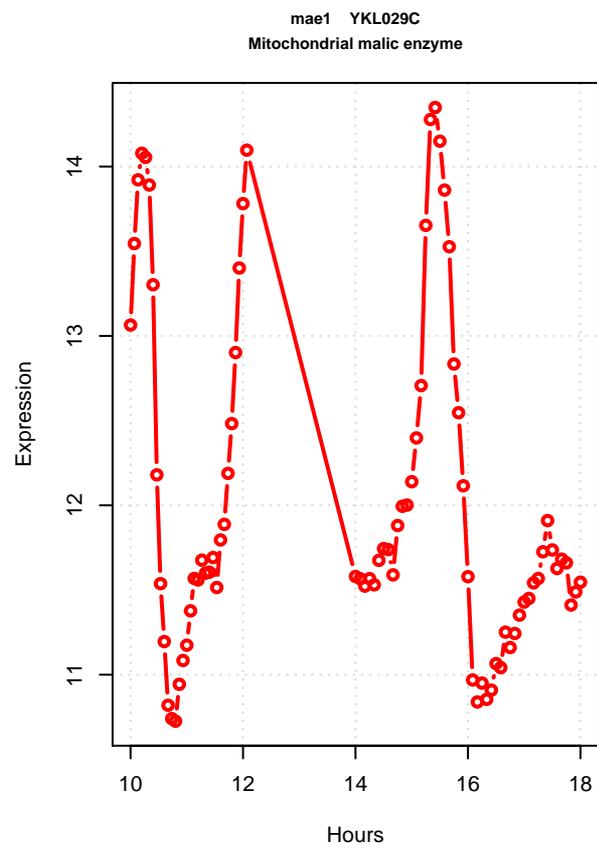
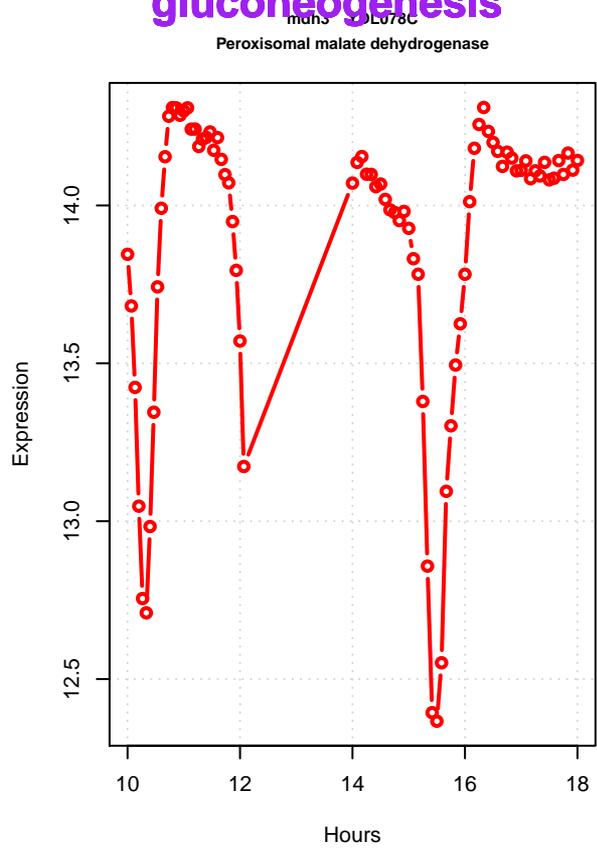
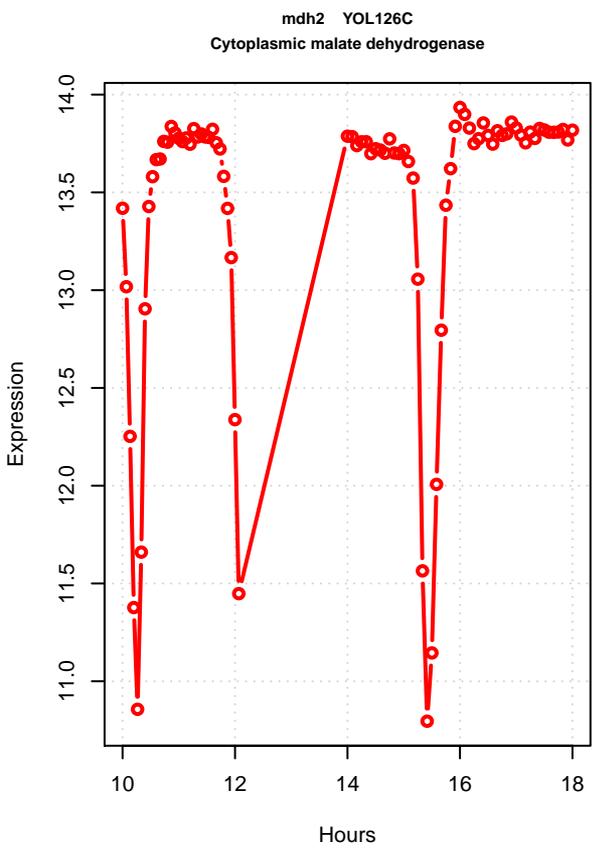


**gluconeogenesis**

# gluconeogenesis

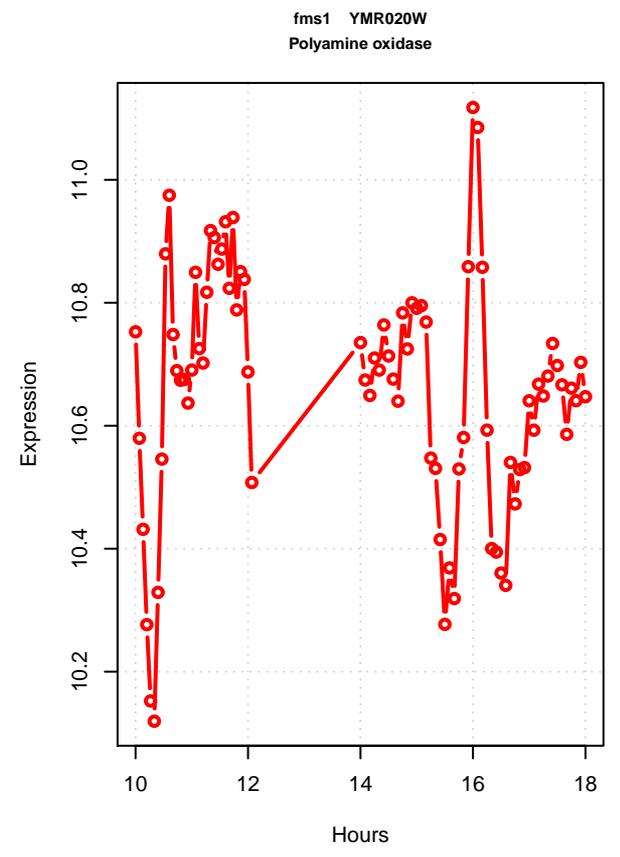
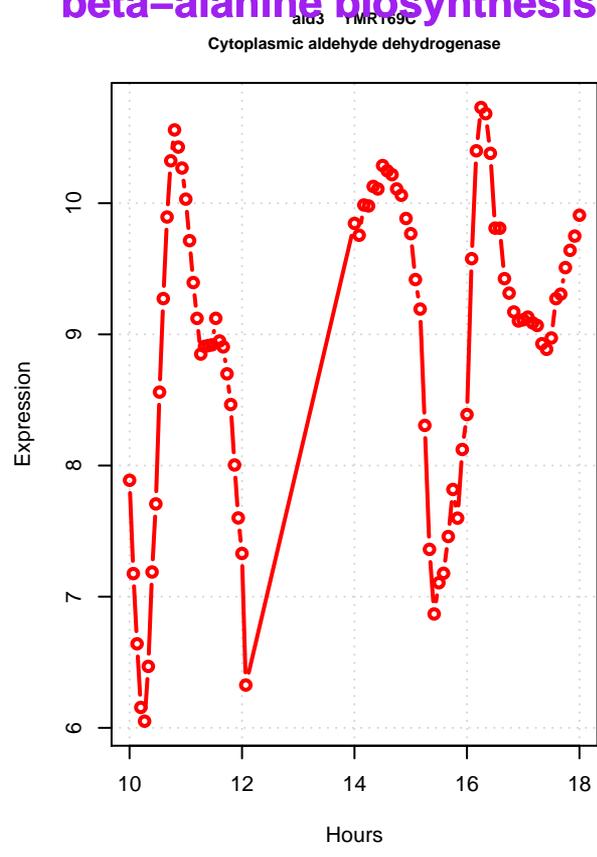
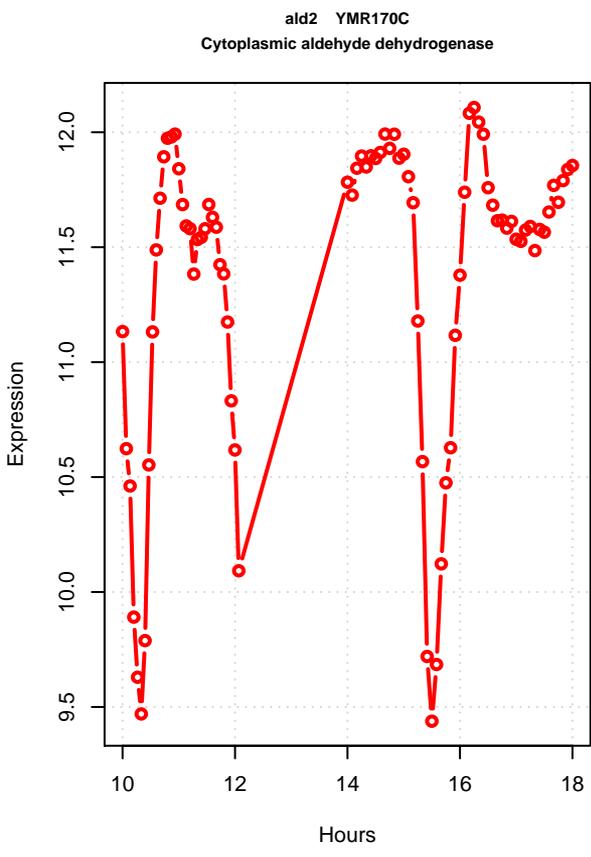


# gluconeogenesis



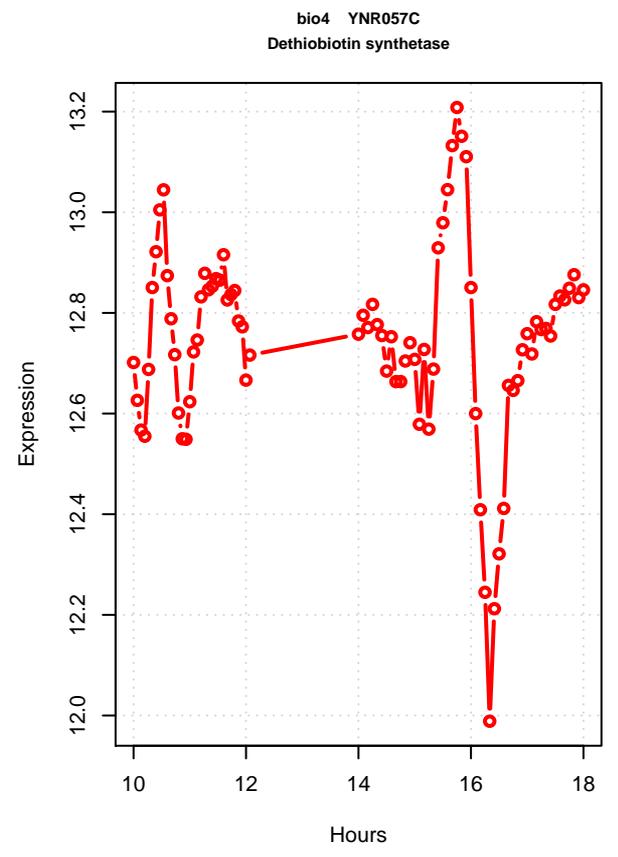
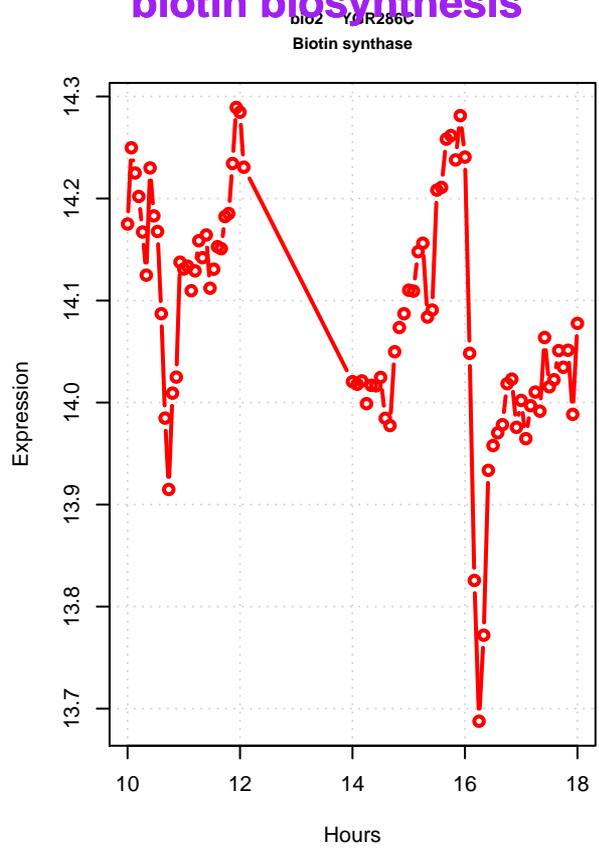
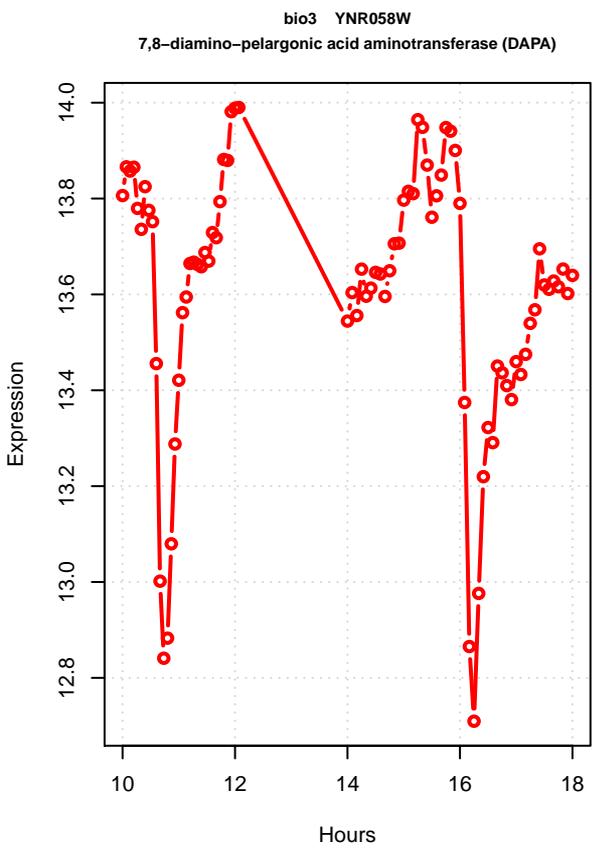
## **beta-alanine biosynthesis**

# beta-alanine biosynthesis



## **biotin biosynthesis**

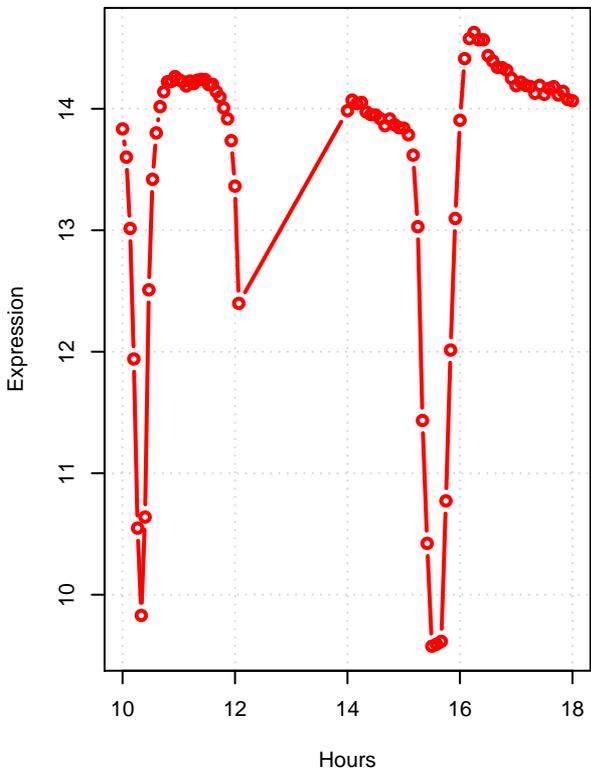
# biotin biosynthesis



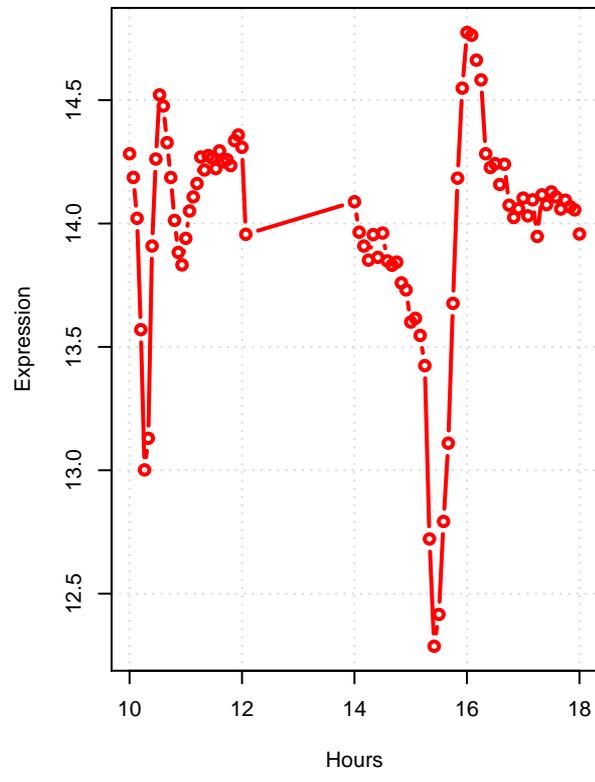
**carnitine shuttle**

# carnitine shuttle

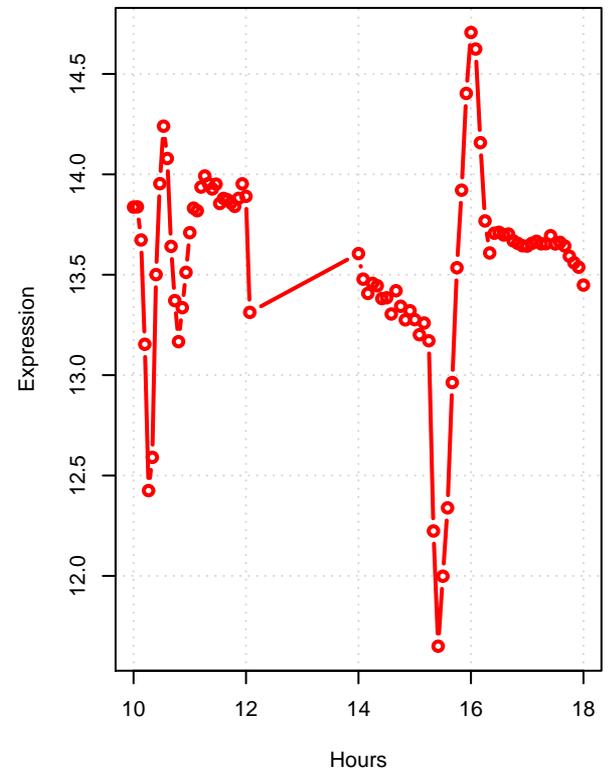
cat2 YML042W  
Carnitine acetyl-CoA transferase



yat1 YAK035W  
Outer mitochondrial carnitine acetyltransferase



yat2 YER024W  
Carnitine acetyltransferase

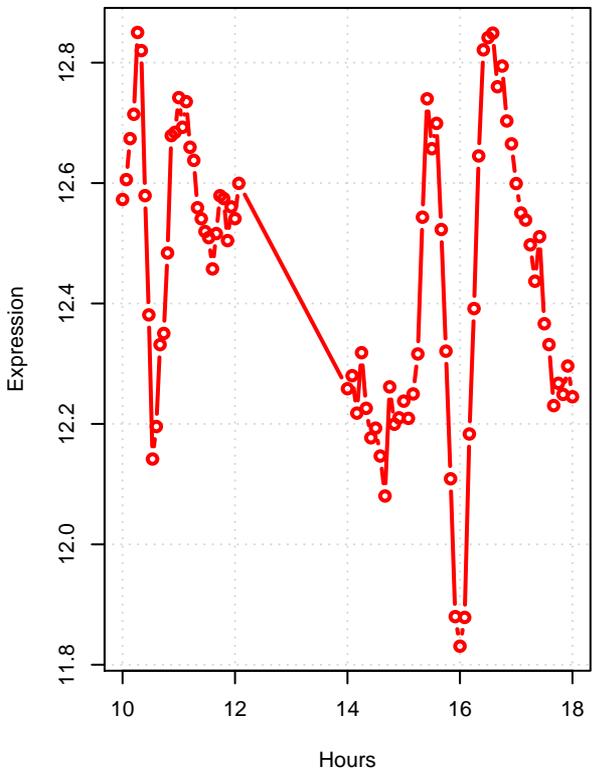


## **CDP–diacylglycerol biosynthesis**

# CDP-diacylglycerol biosynthesis

cds1 YBR029C

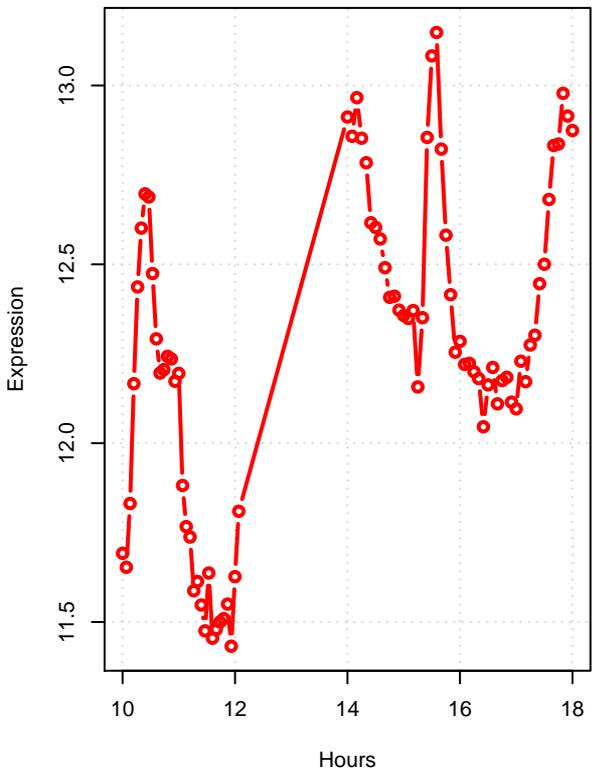
Phosphatidate cytidylyltransferase (CDP-diglyceride synthetase)



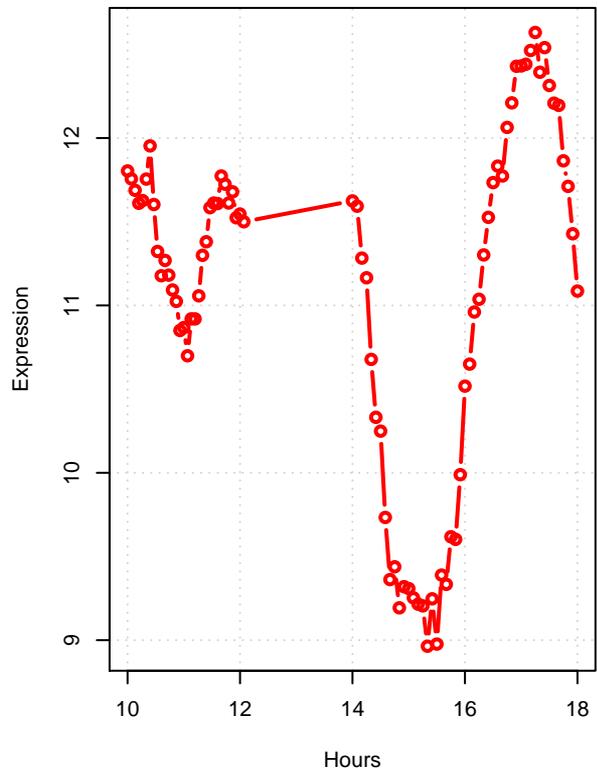
# chitin biosynthesis

# chitin biosynthesis

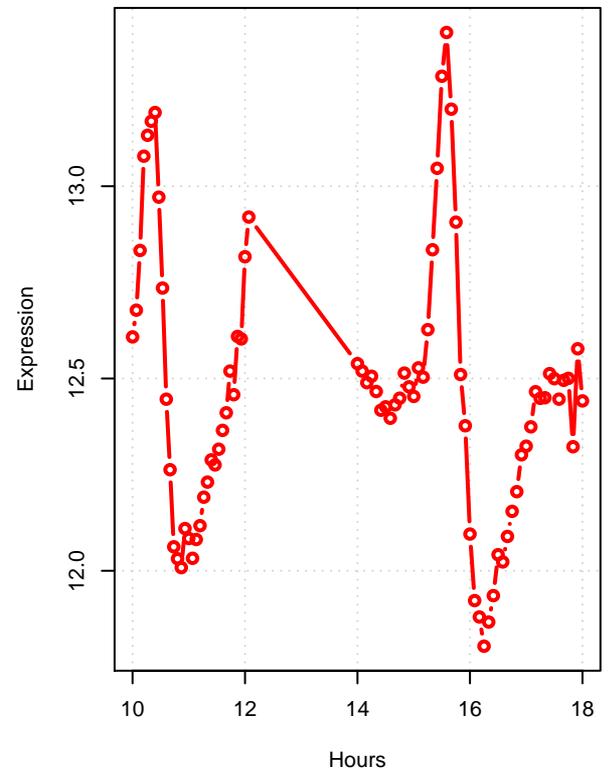
chs1 YNL192W  
Chitin synthase I



chs2 YLR038W  
Chitin synthase II



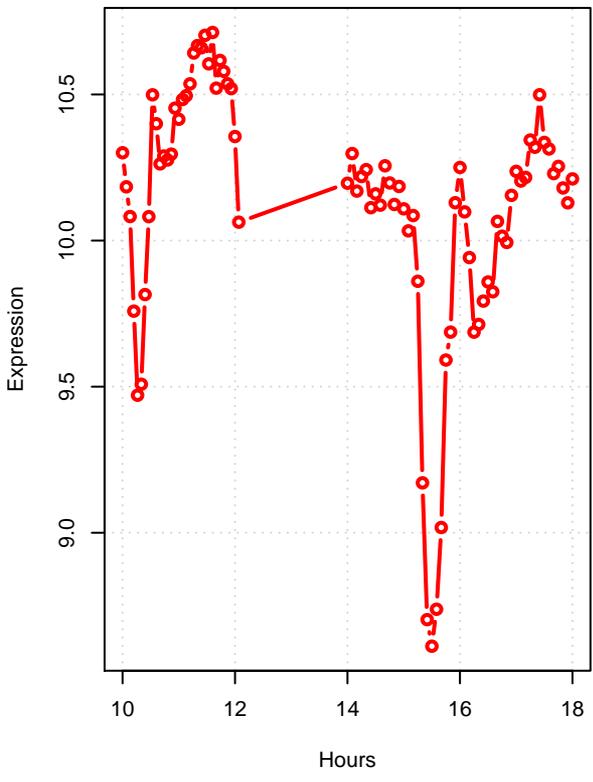
chs3 YBR023C  
Chitin synthase III



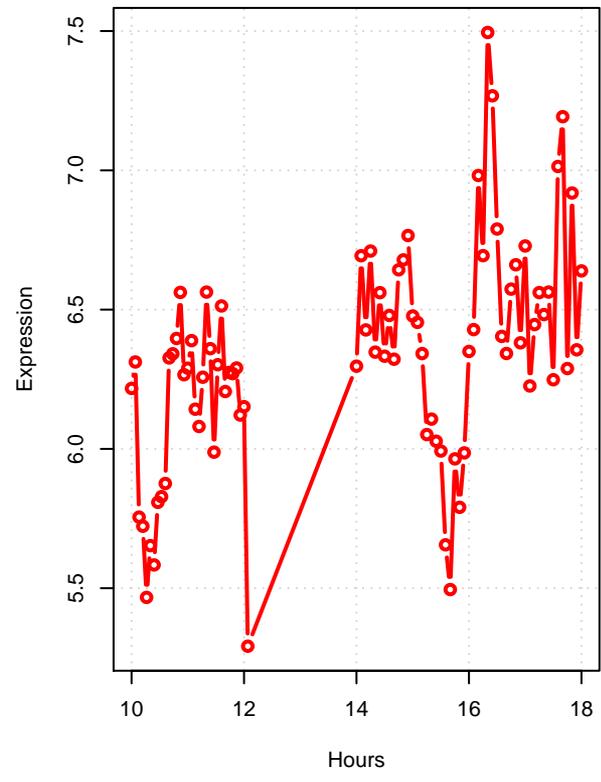
# chitosan biosynthesis

# chitosan biosynthesis

*cda1* YLR307W  
Chitin deacetylase



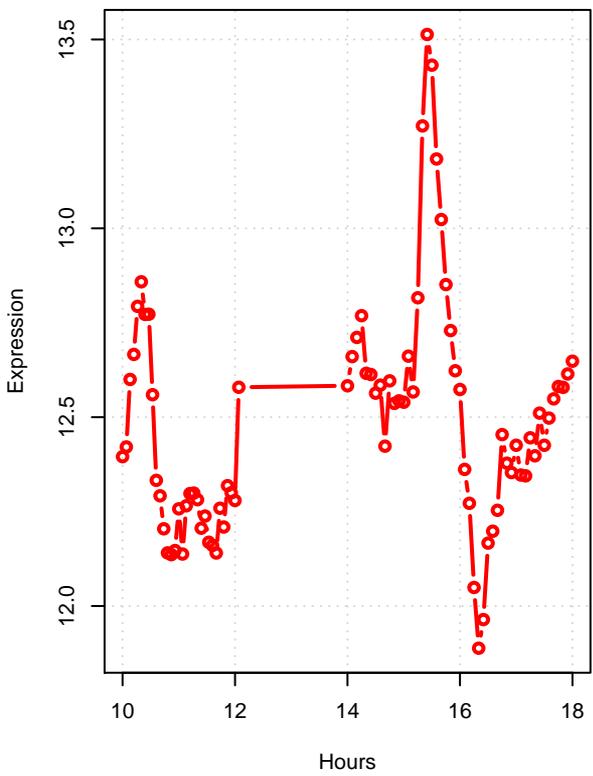
*cua2* YLR318W  
Chitin deacetylase



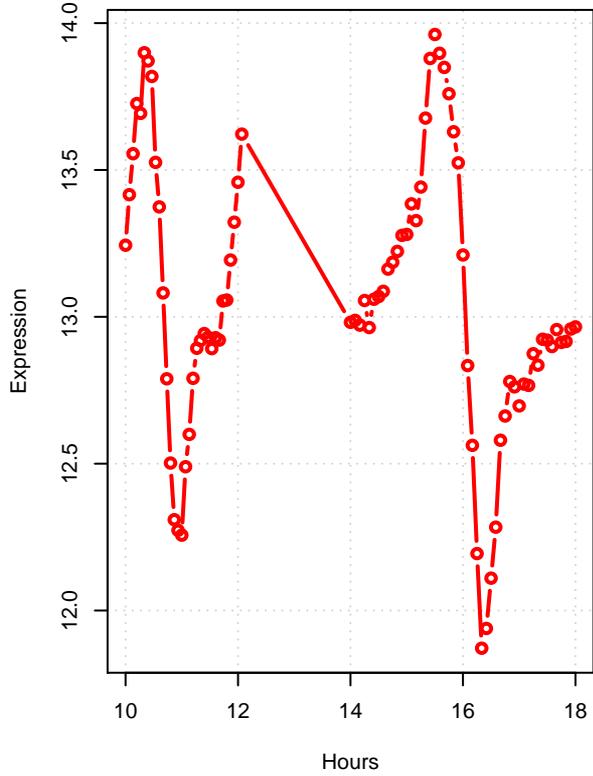
## **chorismate biosynthesis**

# chorismate biosynthesis

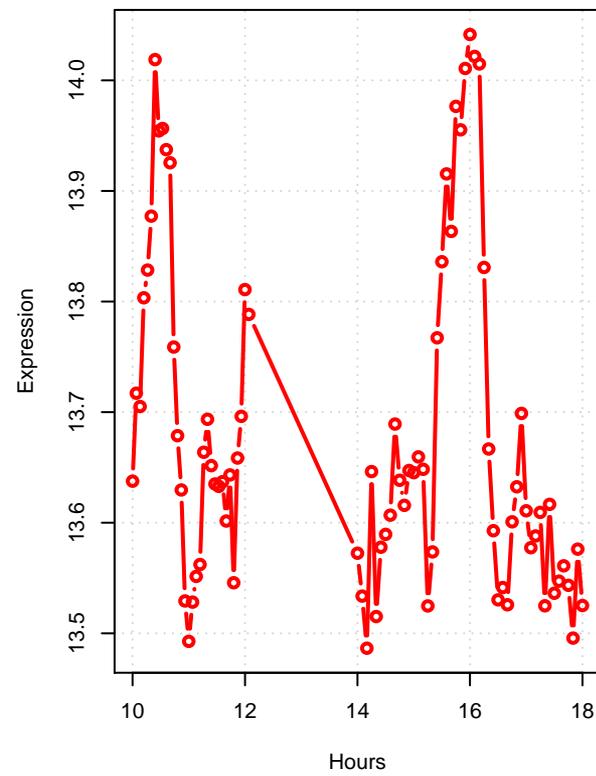
aro3 YDR035W  
3-deoxy-D-arabino-heptulosonate-7-phosphate (DAHP) synthase



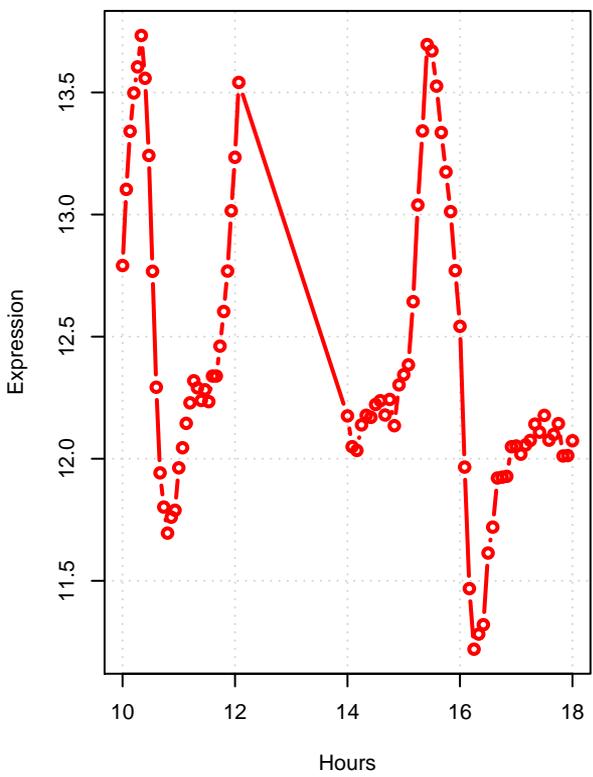
aro4 YBR249C  
3-deoxy-D-arabino-heptulosonate-7-phosphate (DAHP) synthase



aro1 YDR127W  
Pentafunctional arom protein



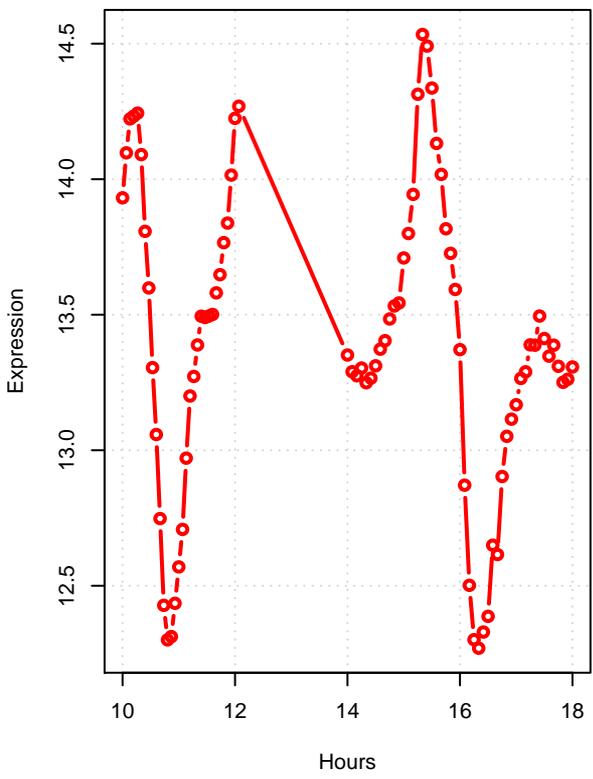
aro2 YGL148W  
Bifunctional chorismate synthase and flavin reductase



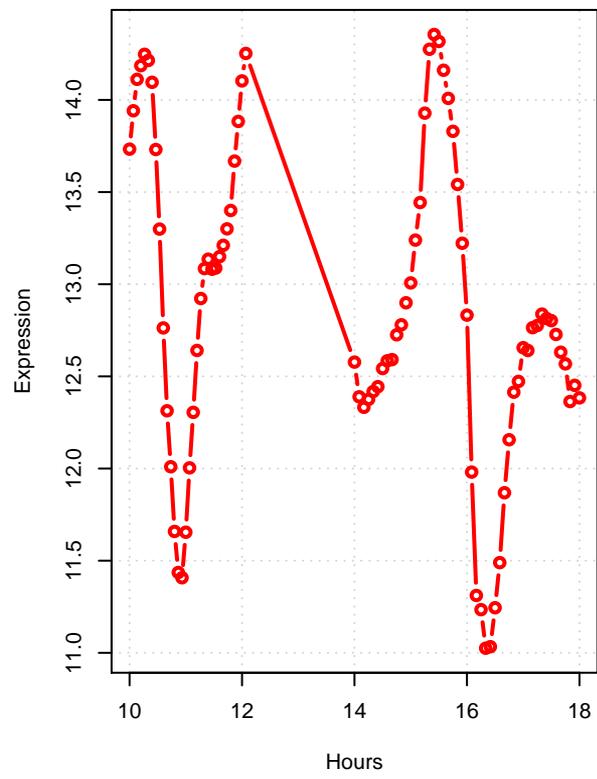
**cysteine biosynthesis from homocysteine**

# cysteine biosynthesis from homocysteine

*cys4* YGR155W  
Cystathionine beta-synthase



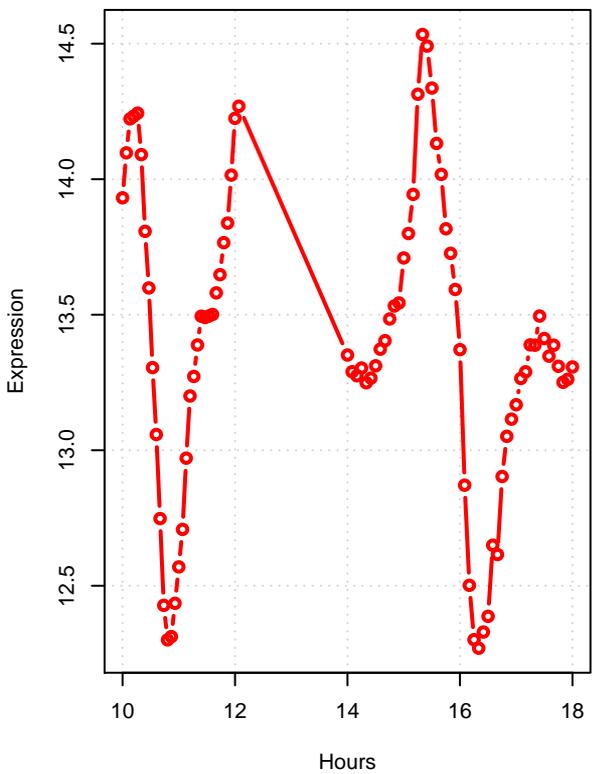
*cys3* YAL012W  
Cystathionine gamma-lyase



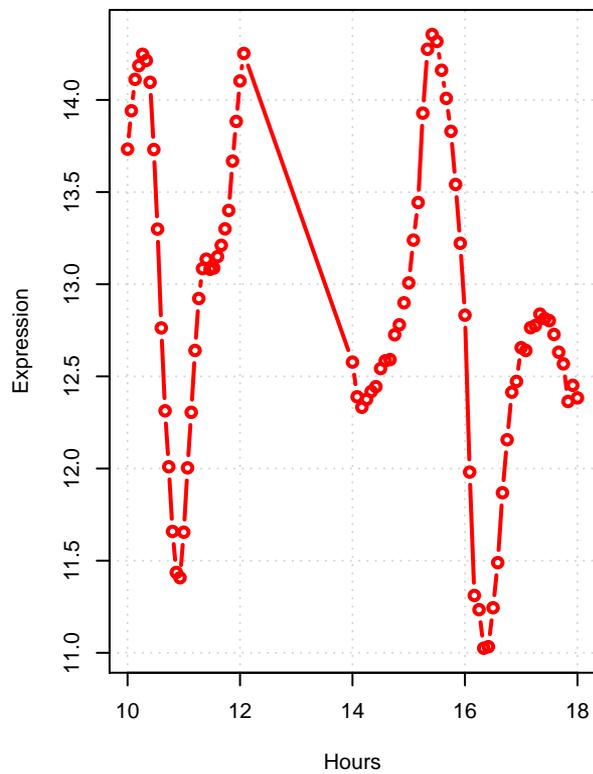
**cysteine biosynthesis/homocysteine degradation**

# cysteine biosynthesis/homocysteine degradation

cys4 YGR155W  
Cystathionine beta-synthase



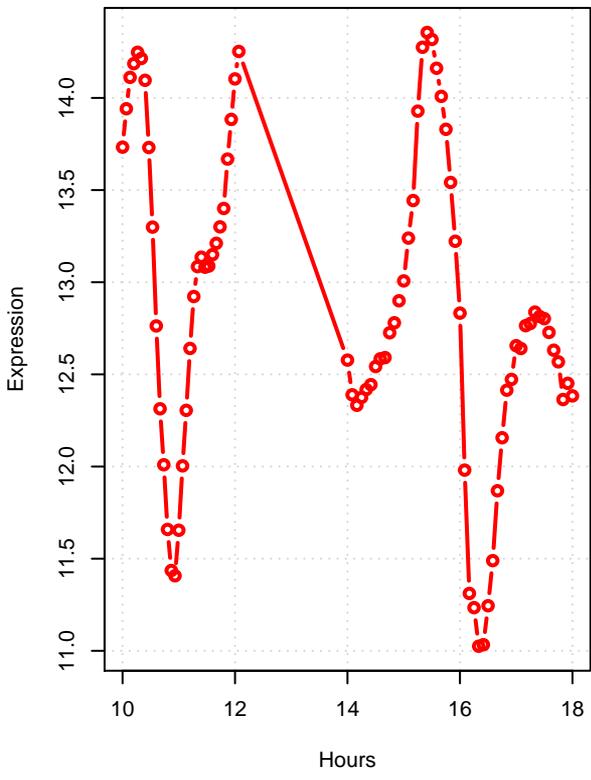
cys3 YAL012W  
Cystathionine gamma-lyase



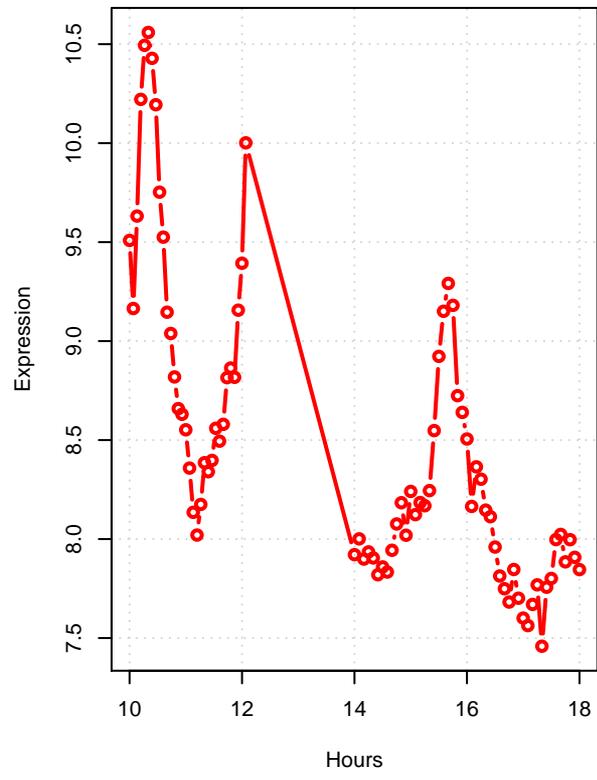
## threonine degradation

# threonine degradation

cys3 YAL012W  
Cystathionine gamma-lyase

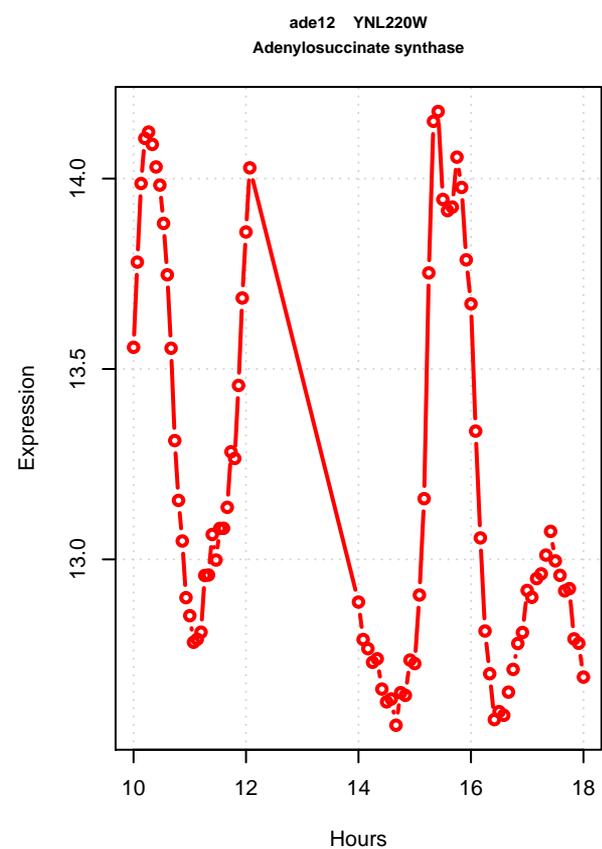
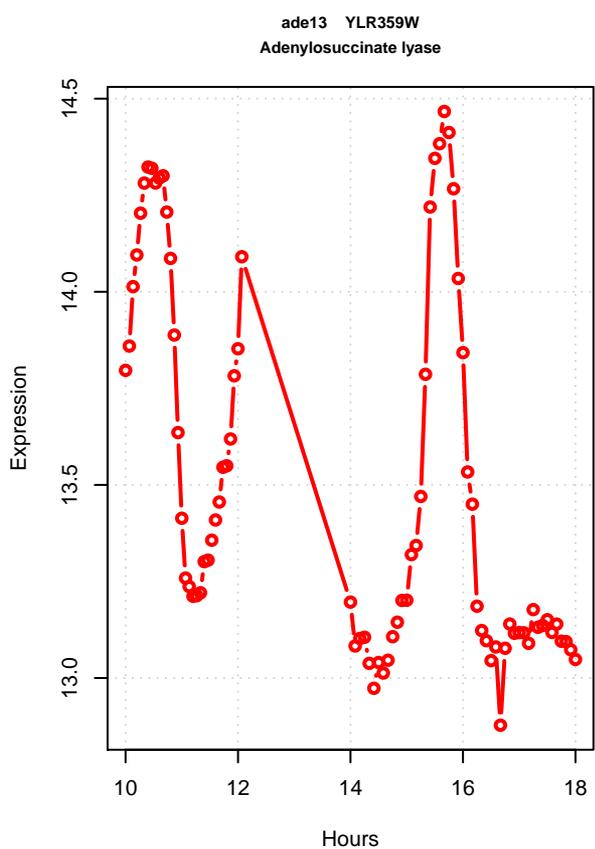
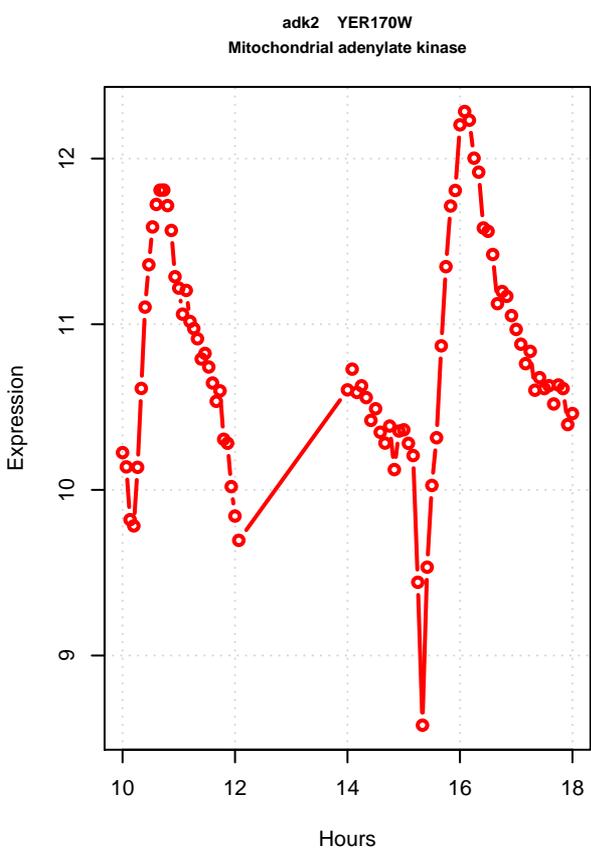
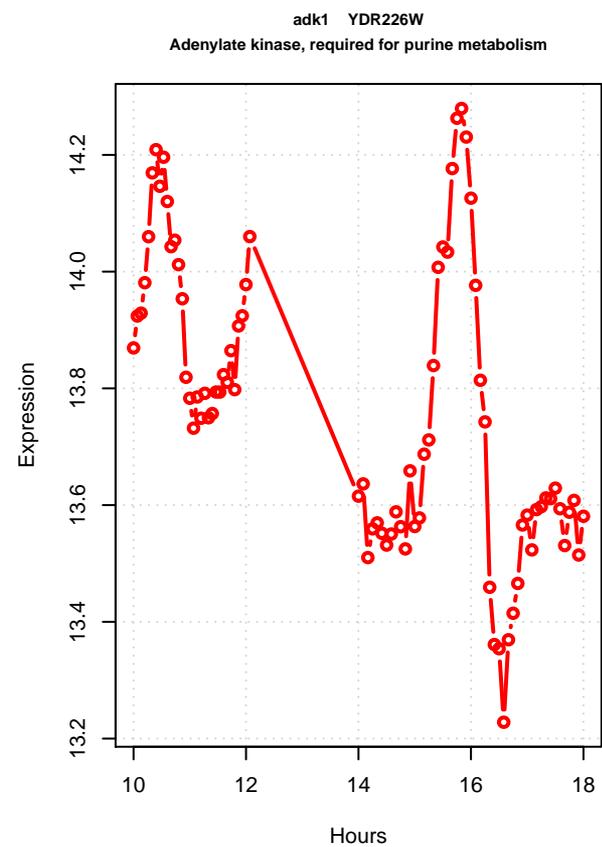
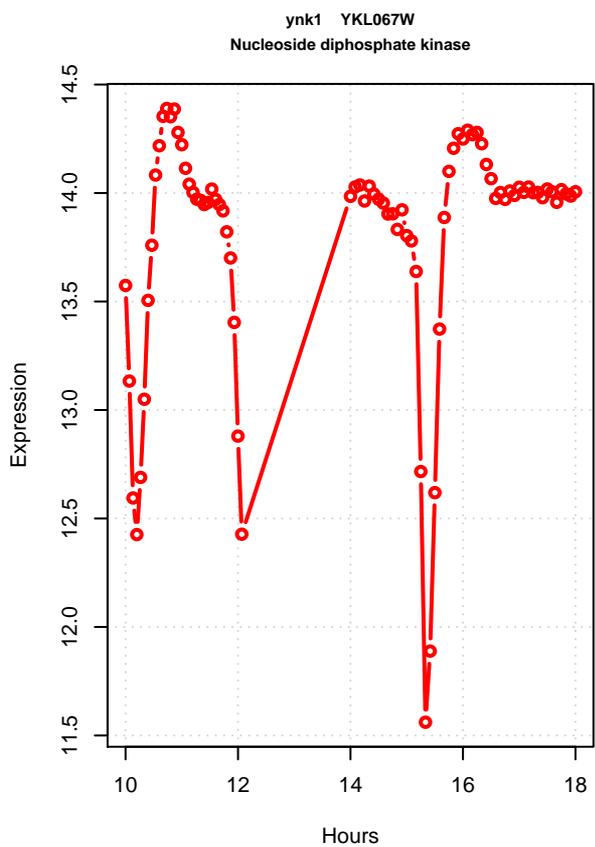
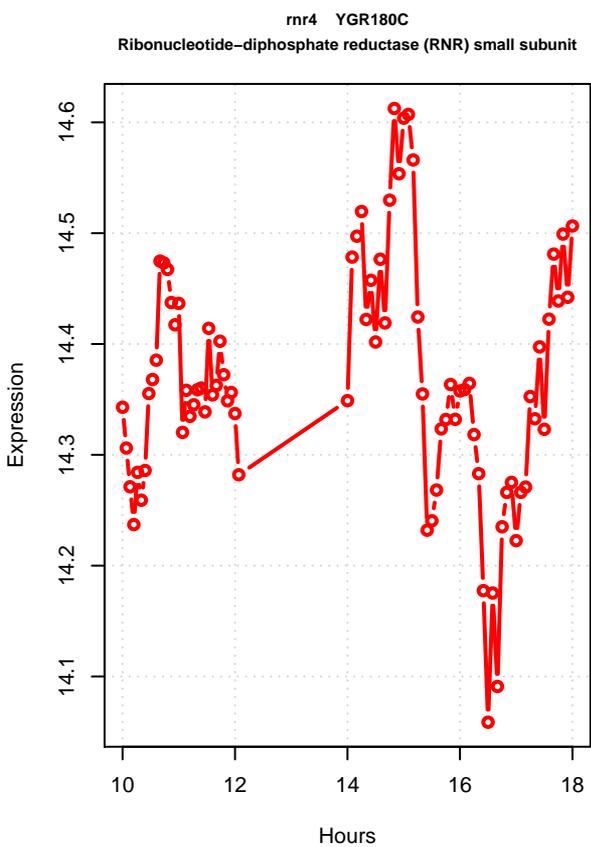
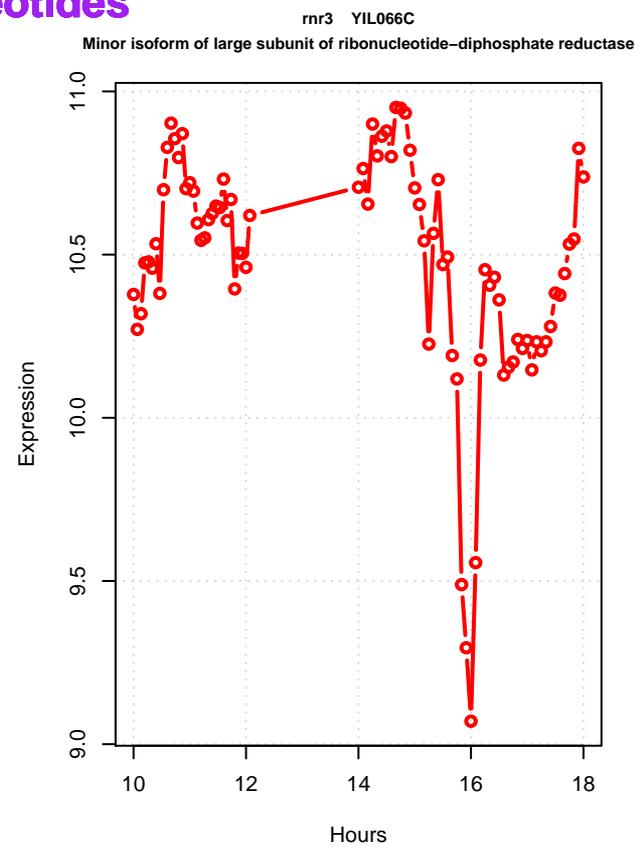
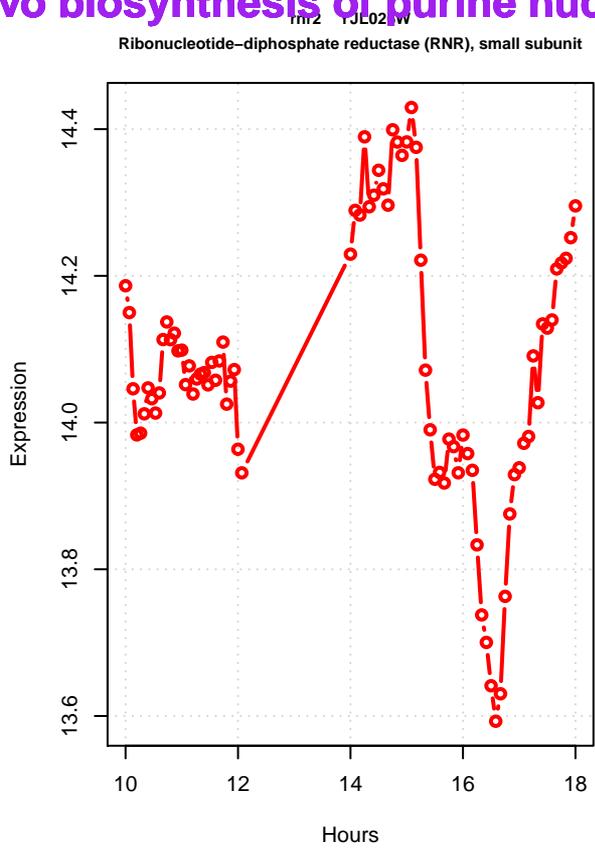
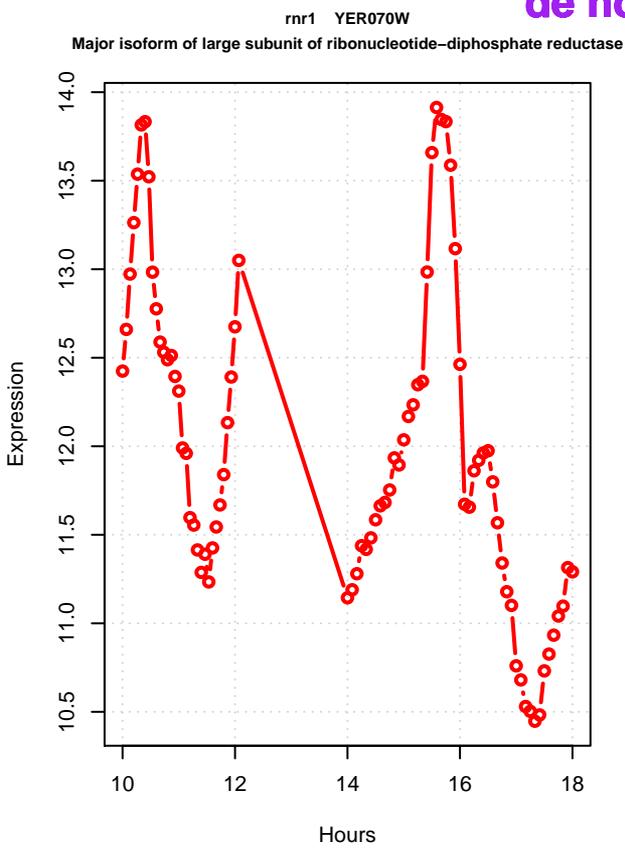


cha1 YC1064C  
Catabolic L-serine (L-threonine) deaminase

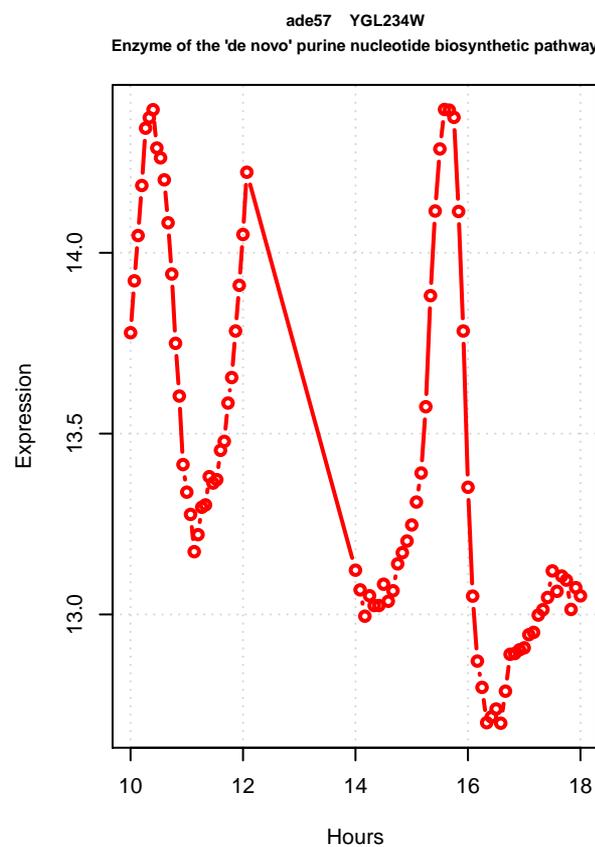
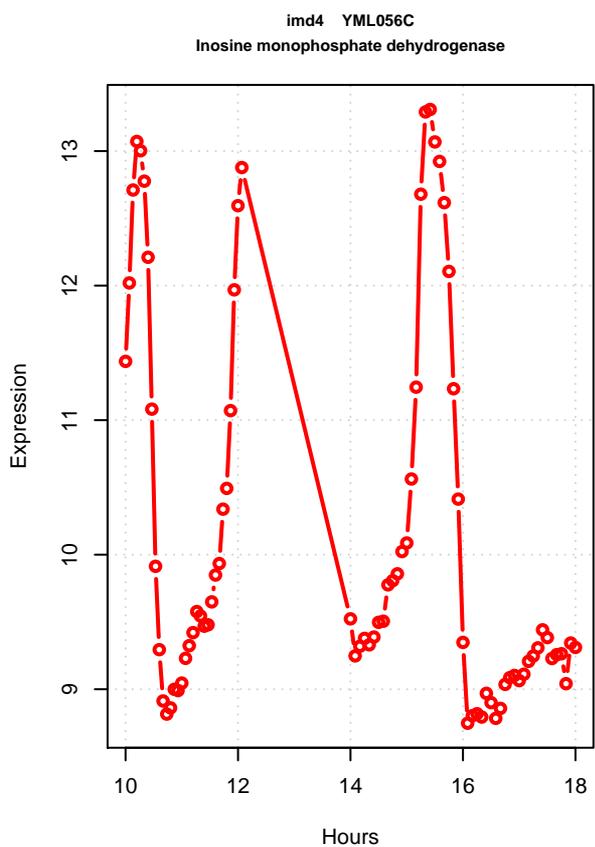
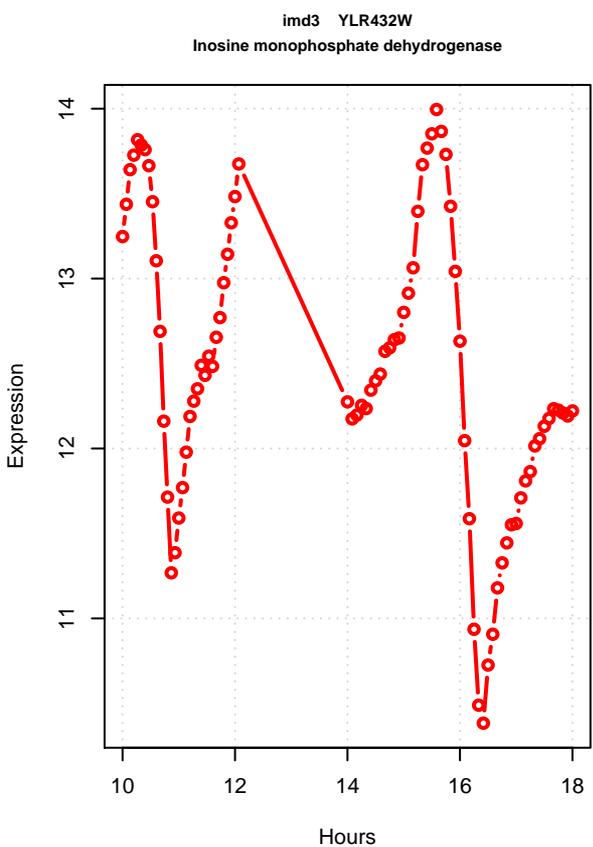
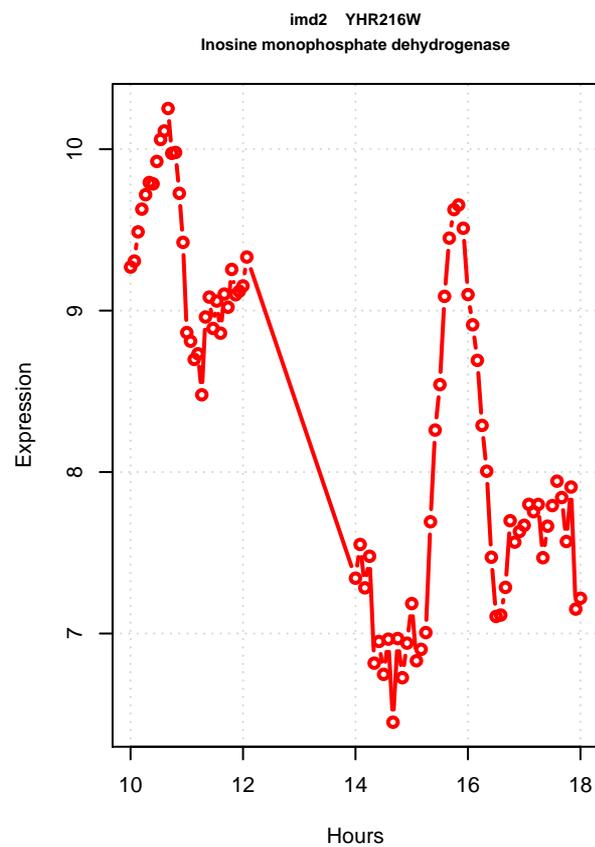
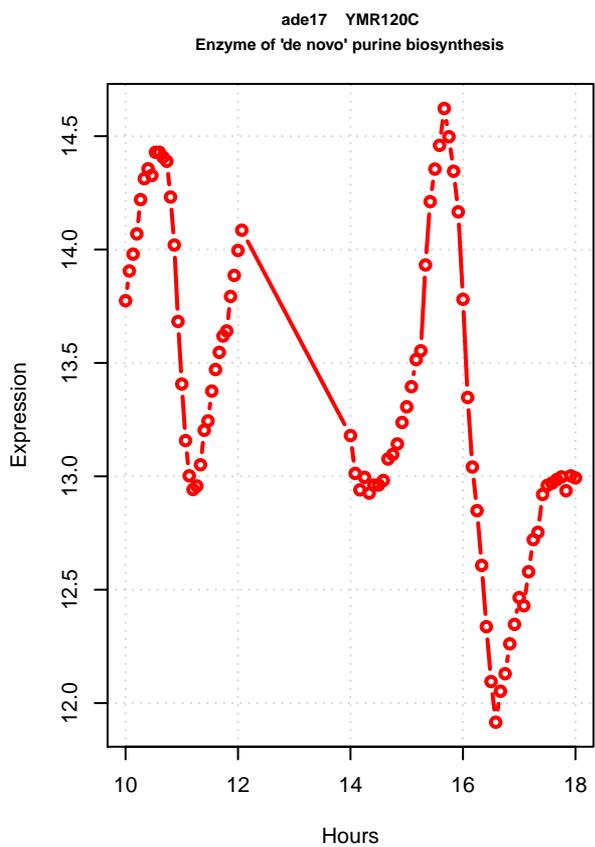
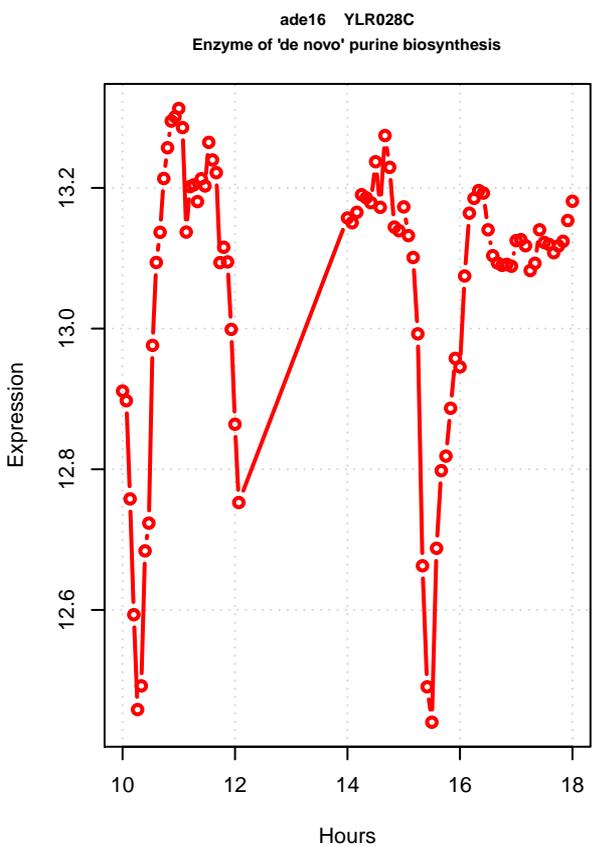
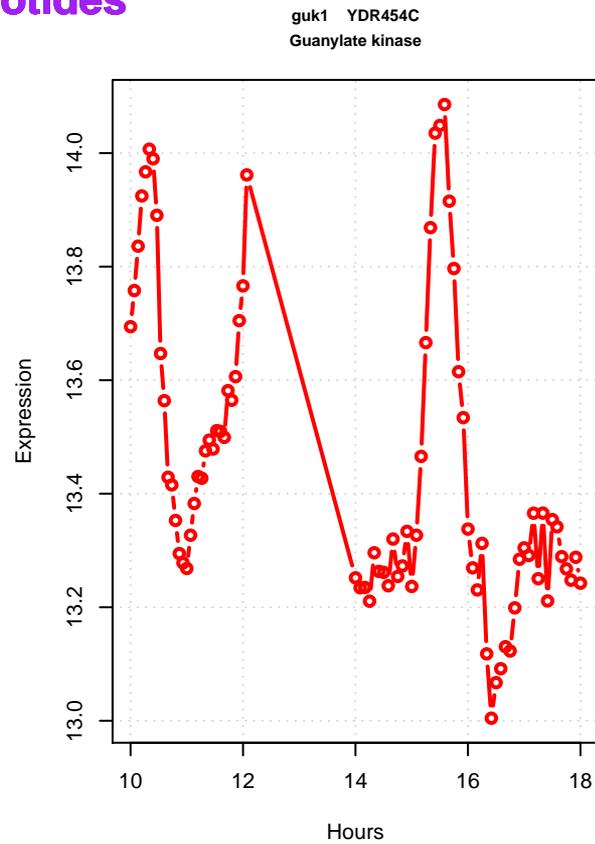
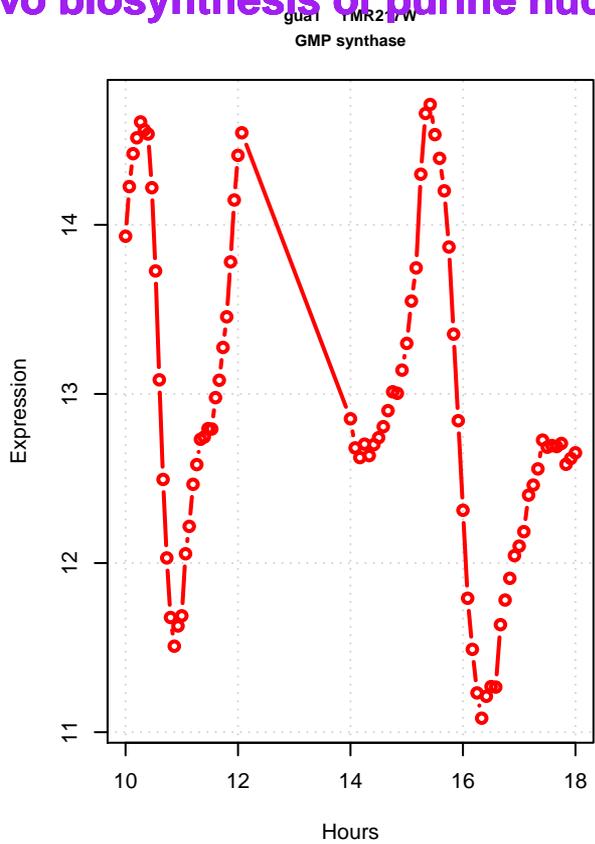
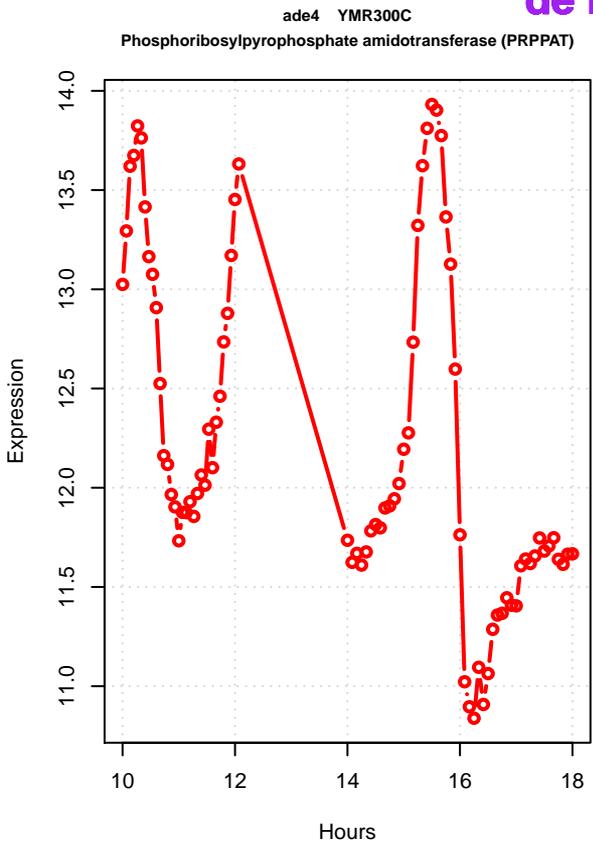


## de novo biosynthesis of purine nucleotides

# de novo biosynthesis of purine nucleotides



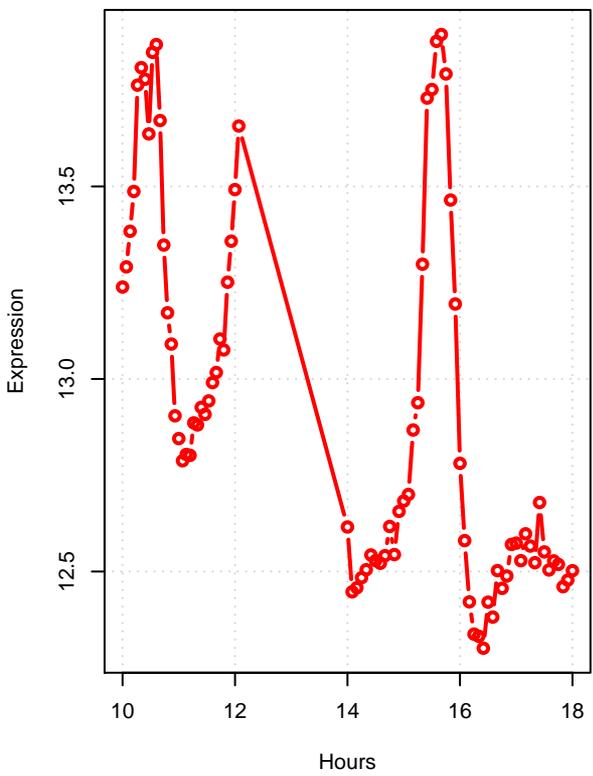
# de novo biosynthesis of purine nucleotides



# de novo biosynthesis of purine nucleotides

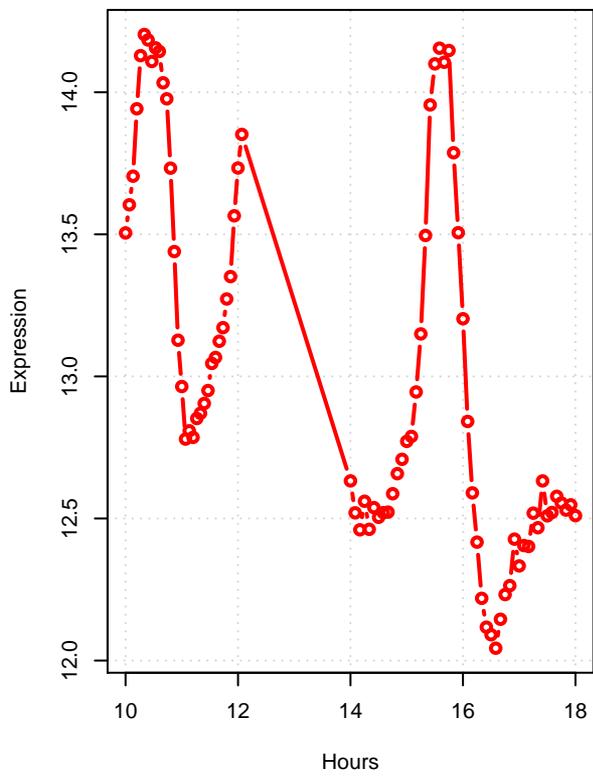
ade2 YOR128C

Phosphoribosylaminoimidazole carboxylase



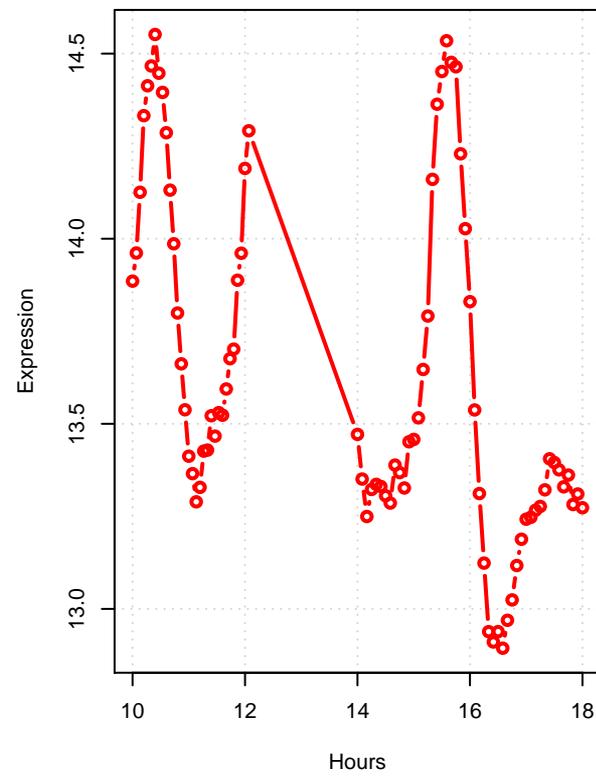
ade1 YAR015W

N-succinyl-5-aminoimidazole-4-carboxamide ribotide synthetase



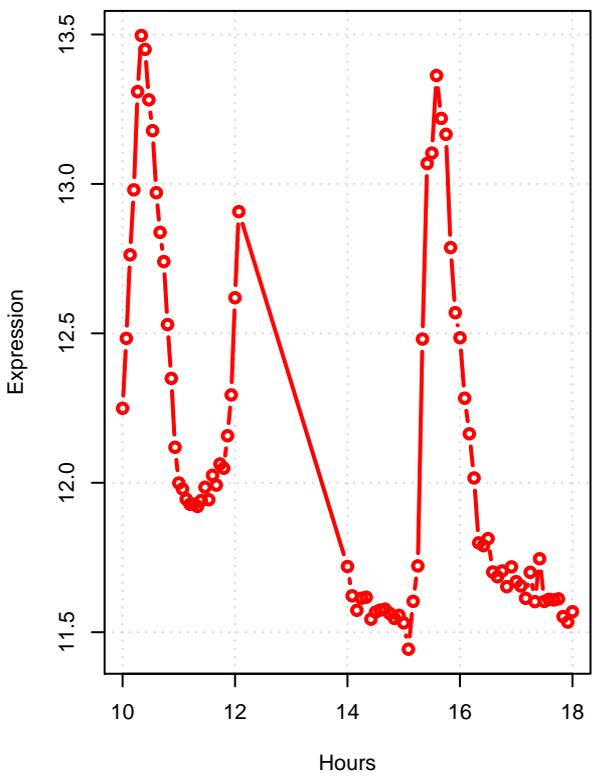
ade6 YGR061C

Formylglycinamide-ribonucleotide (FGAM)-synthetase



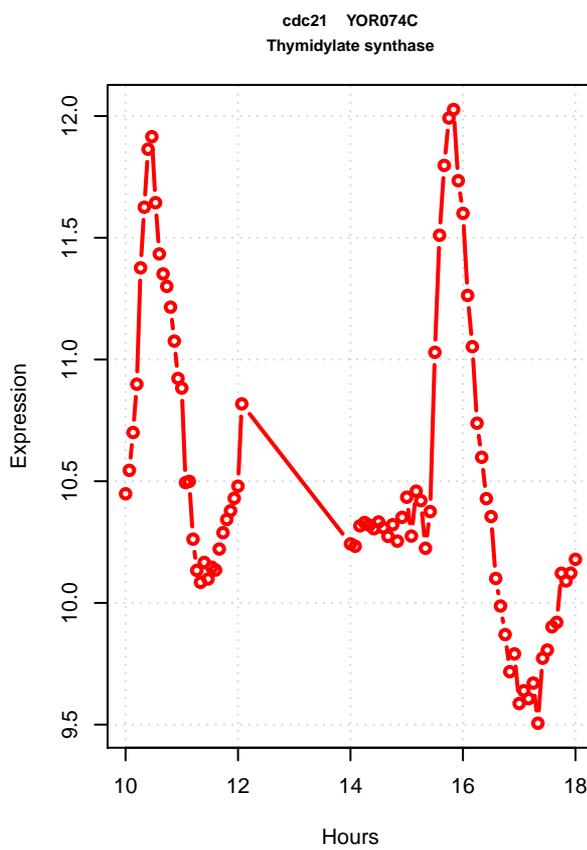
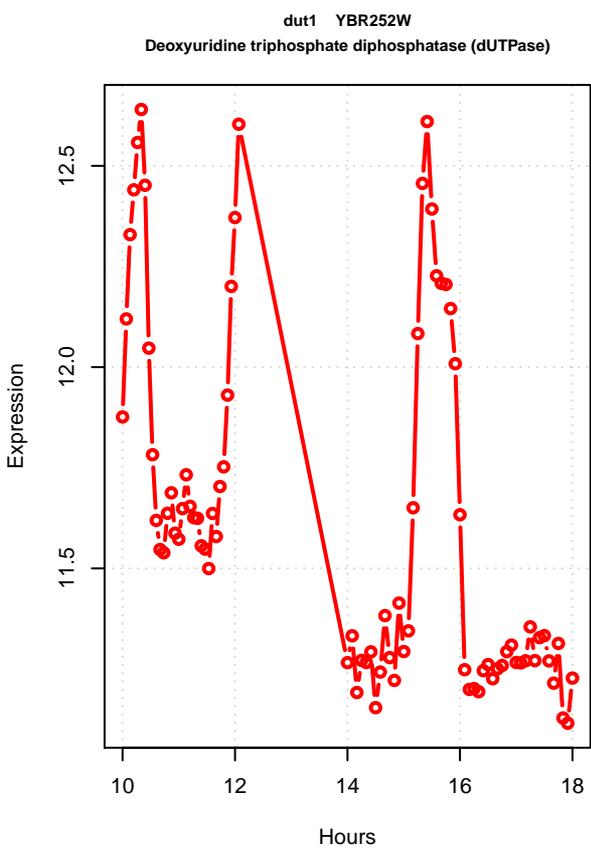
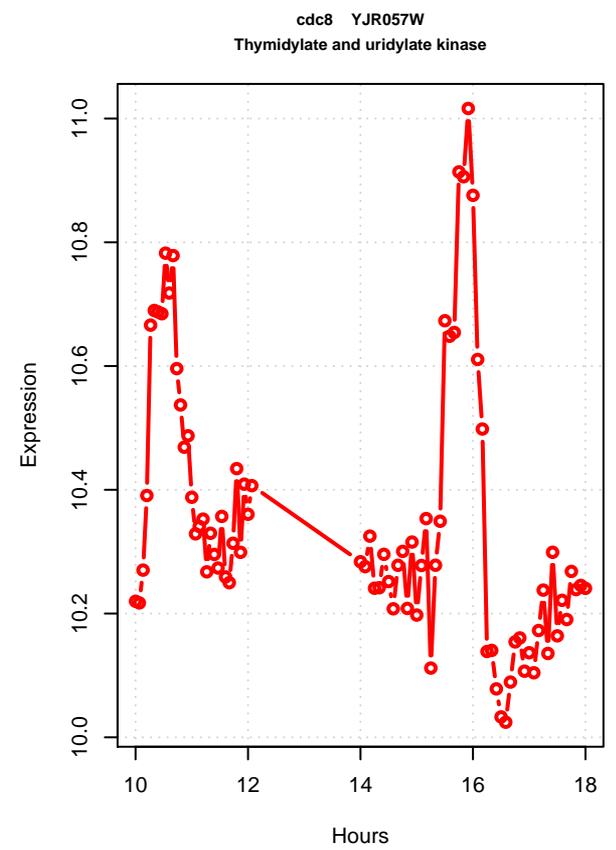
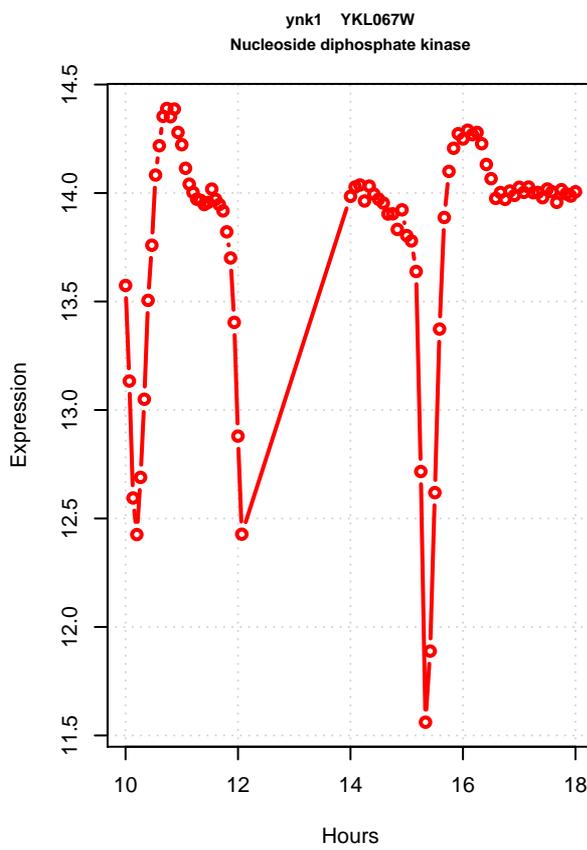
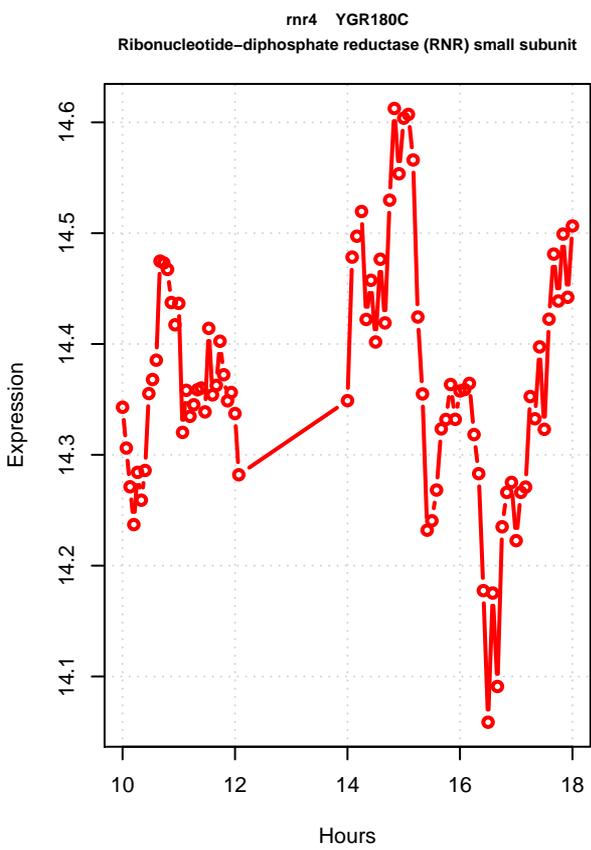
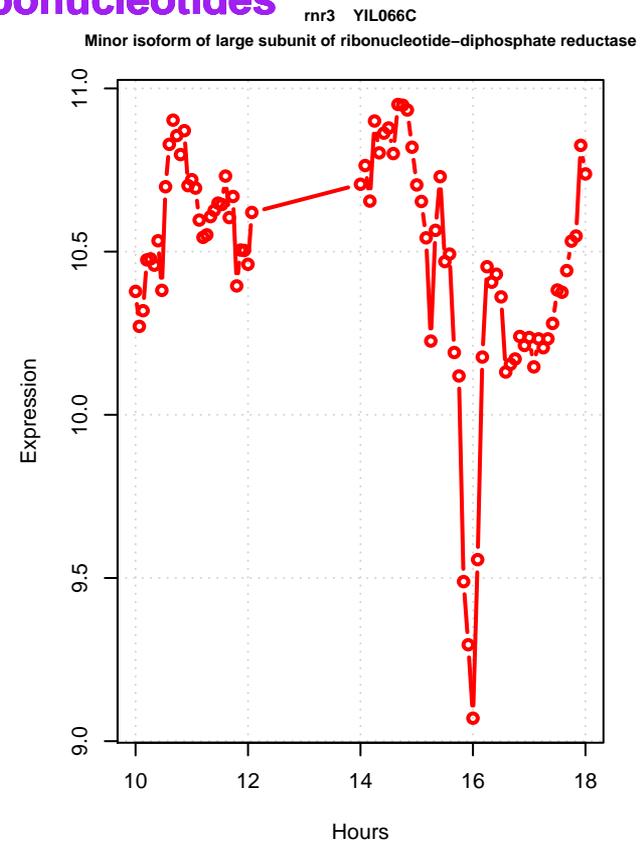
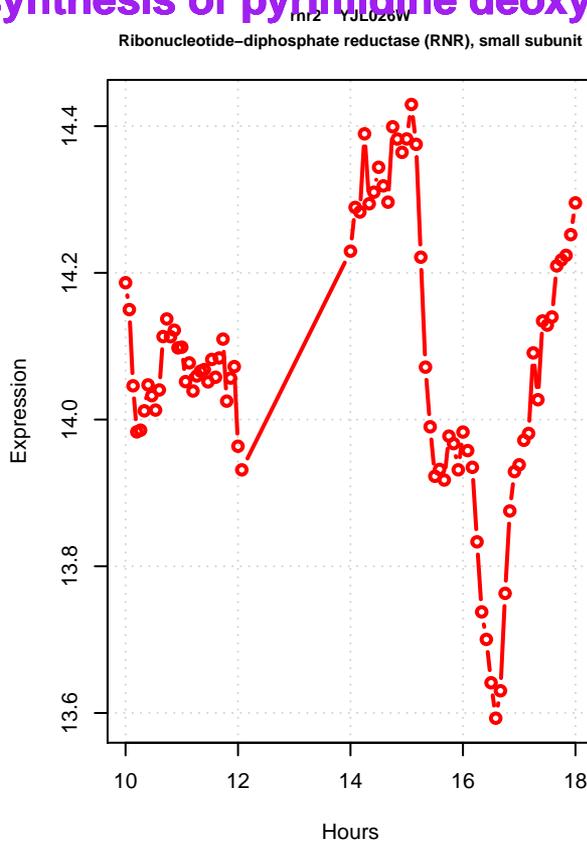
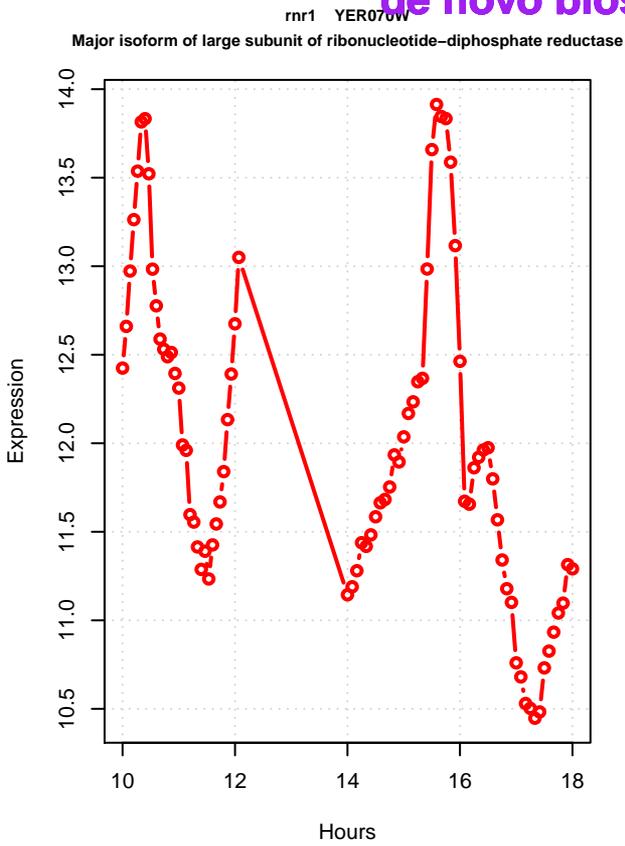
ade8 YDR408C

Phosphoribosyl-glycinamide transformylase



**de novo biosynthesis of pyrimidine deoxyribonucleotides**

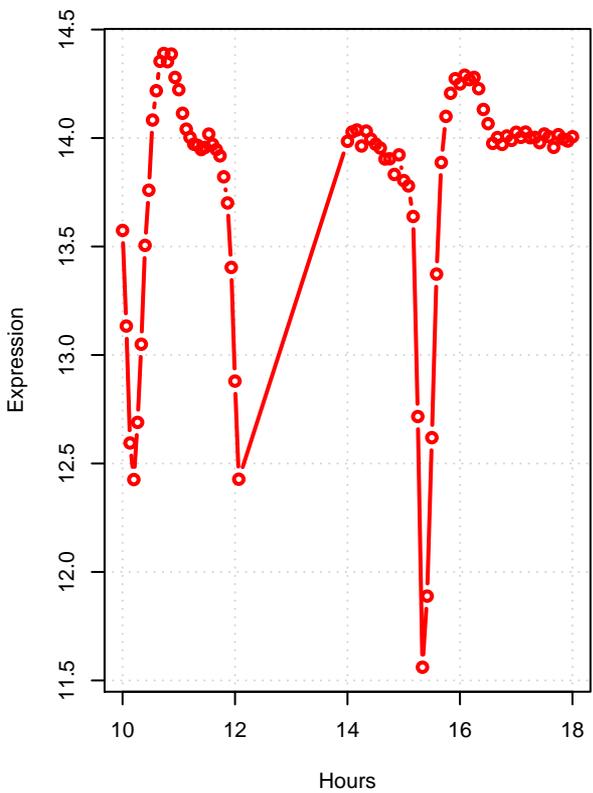
# de novo synthesis of pyrimidine deoxyribonucleotides



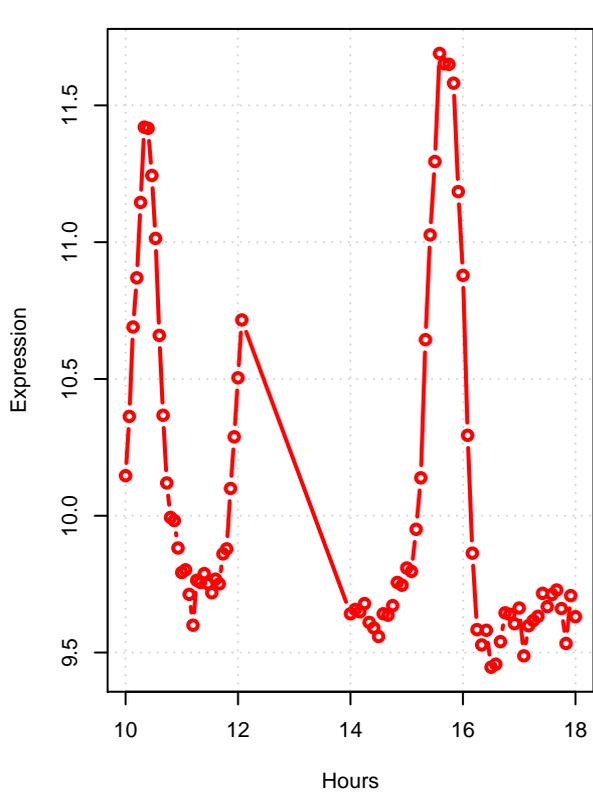
**salvage pathways of pyrimidine ribonucleotides**

# salvage pathways of pyrimidine ribonucleotides

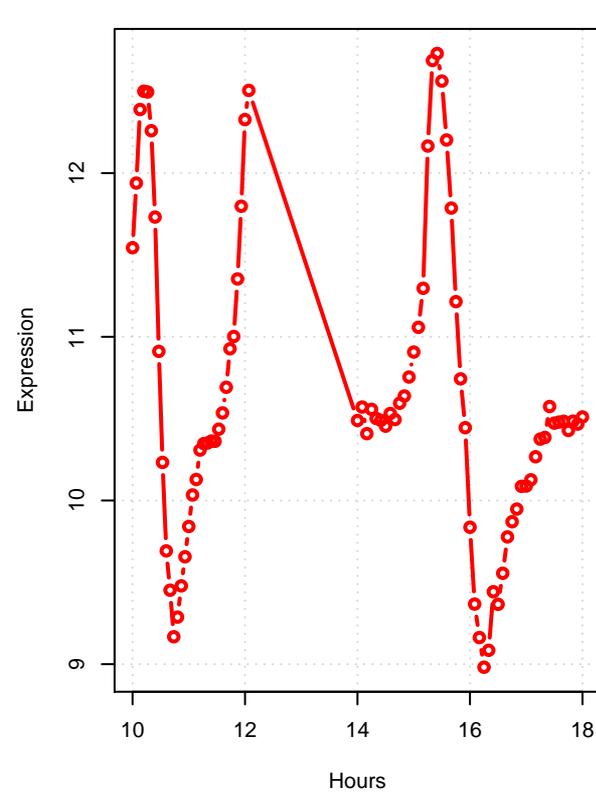
ynk1 YKL067W  
Nucleoside diphosphate kinase



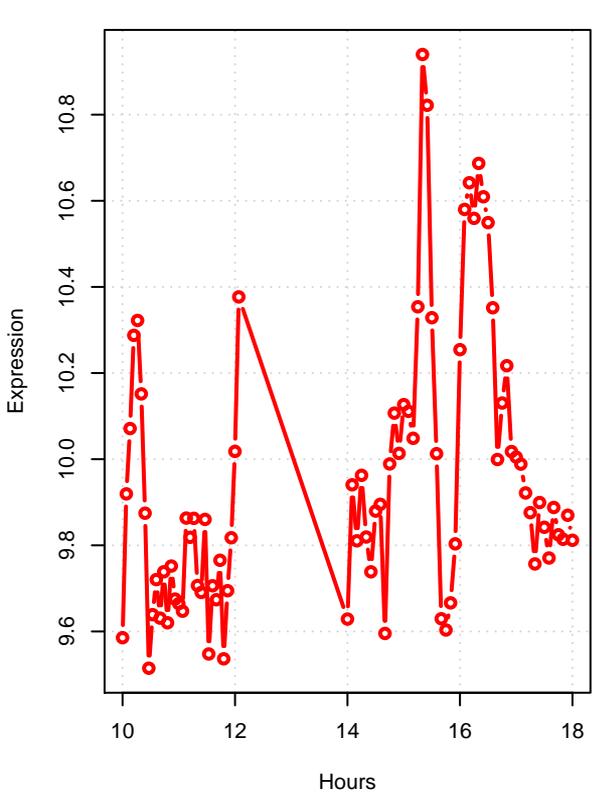
urh1 YDR400W  
Uridine nucleosidase (uridine-cytidine N-ribohydrolase)



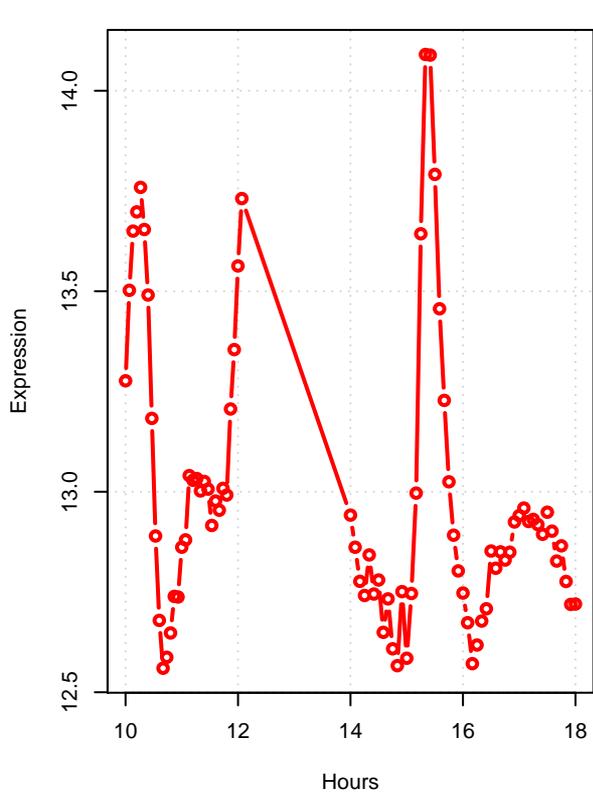
urk1 YNR012W  
Uridine/cytidine kinase



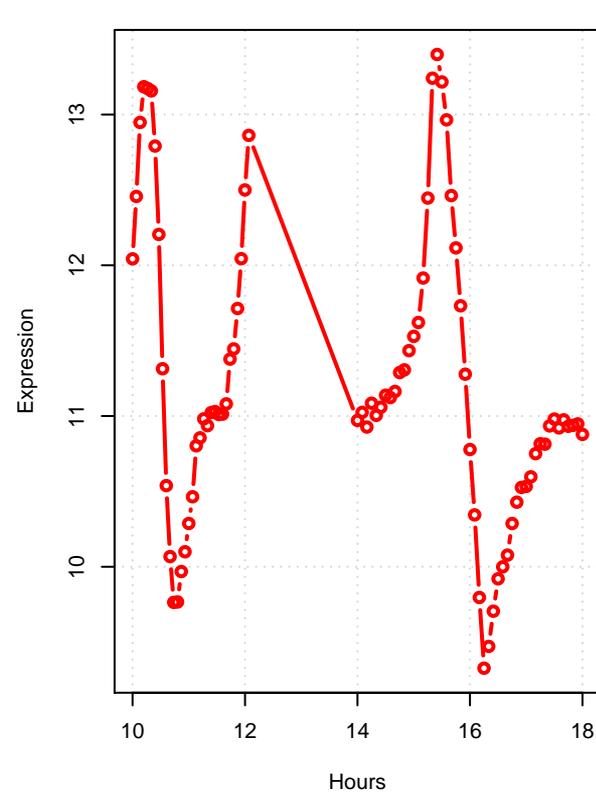
cdd1 YLR245C  
Cytidine deaminase



fcy1 YPR062W  
Cytosine deaminase

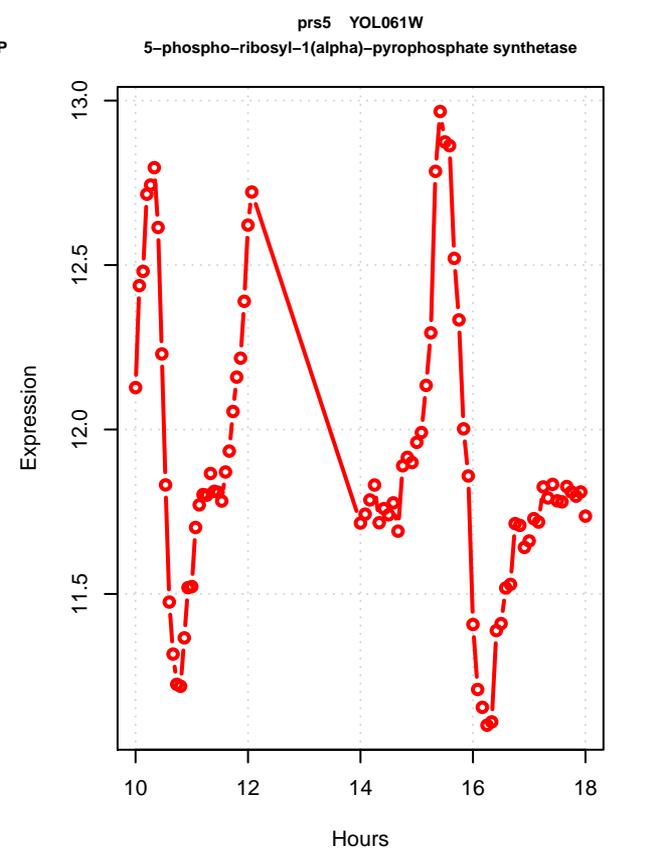
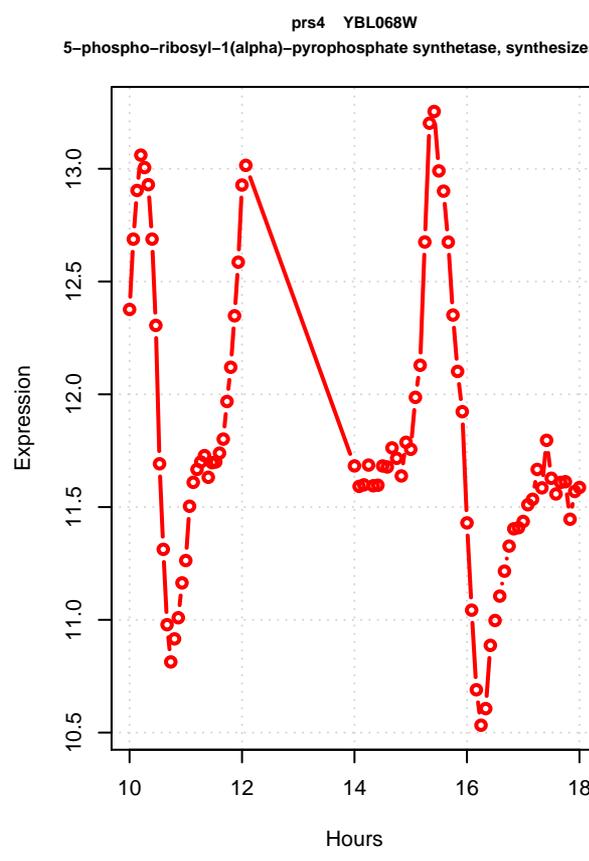
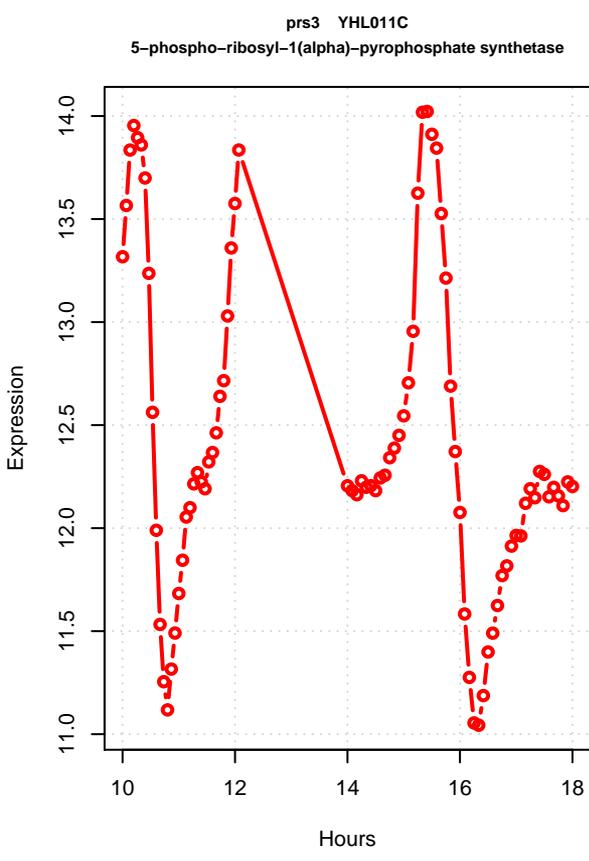
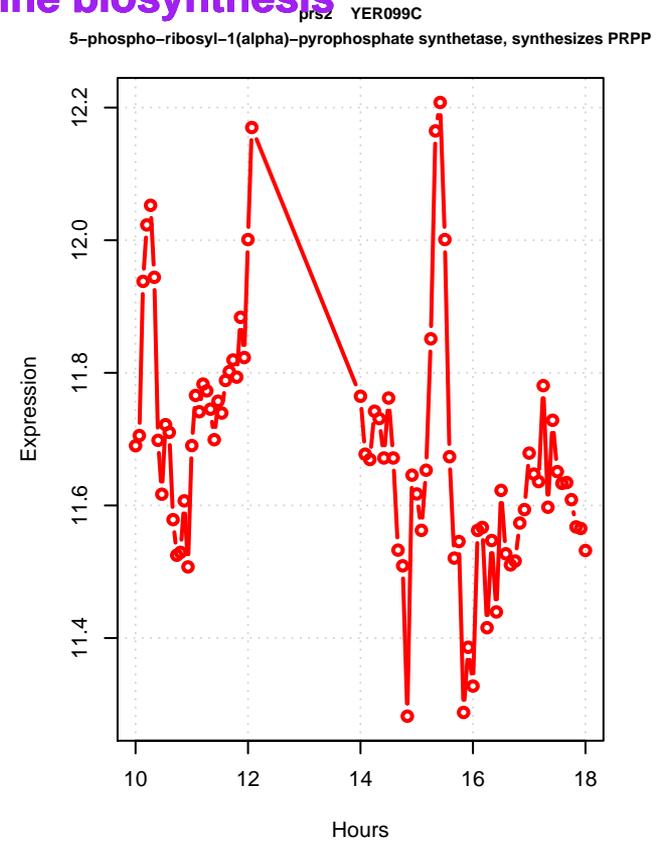
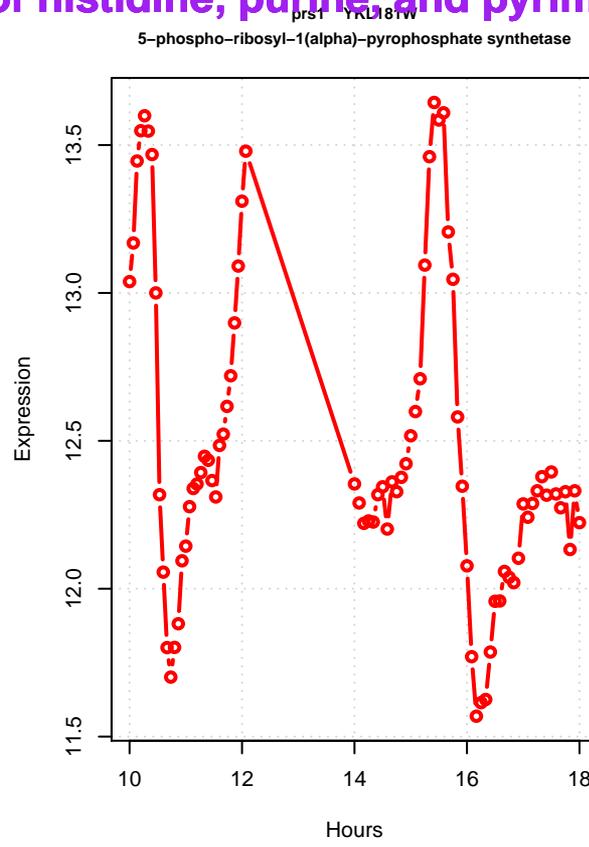
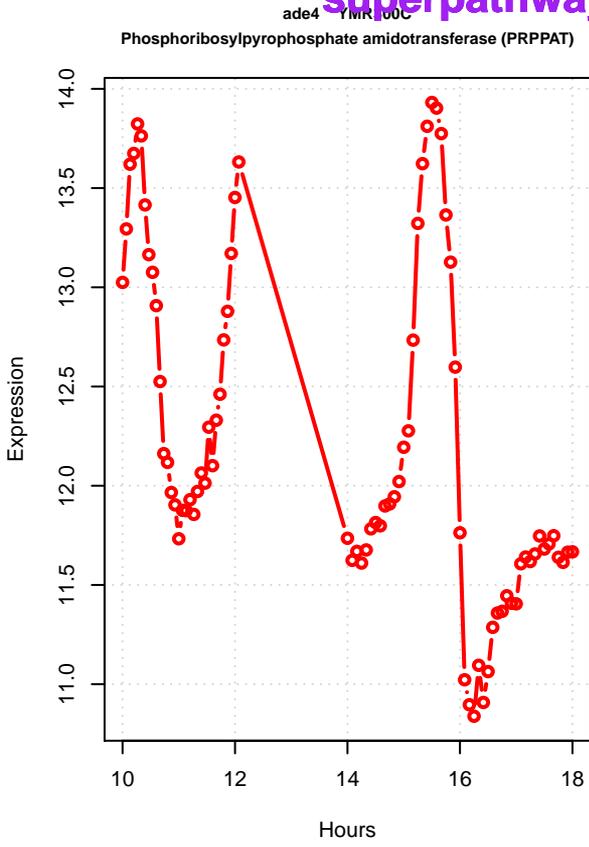


fur1 YHR128W  
Uracil phosphoribosyltransferase



**superpathway of histidine, purine, and pyrimidine biosynthesis**

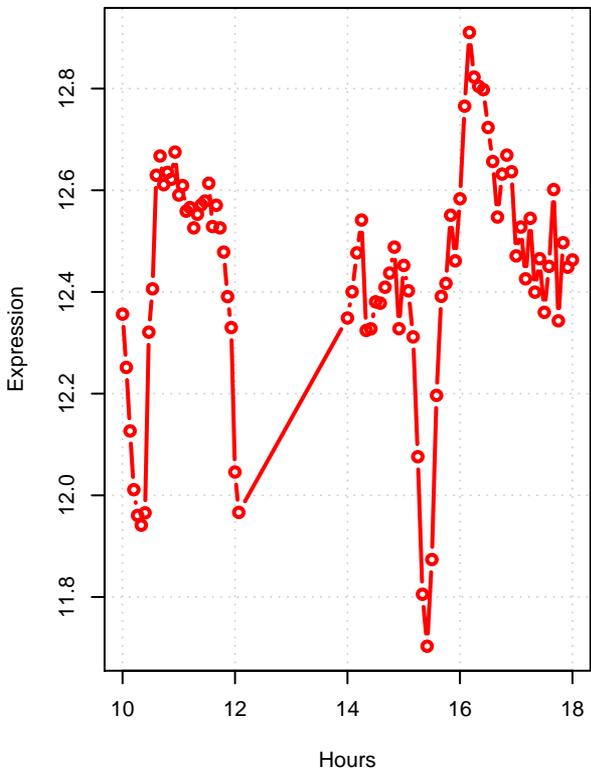
# superpathway of histidine, purine, and pyrimidine biosynthesis



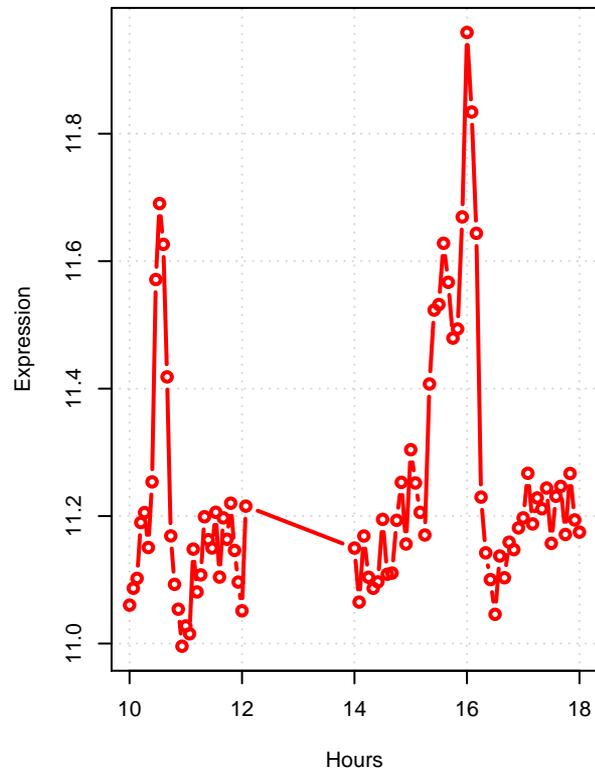
**de novo NAD biosynthesis**

# de novo NAD biosynthesis

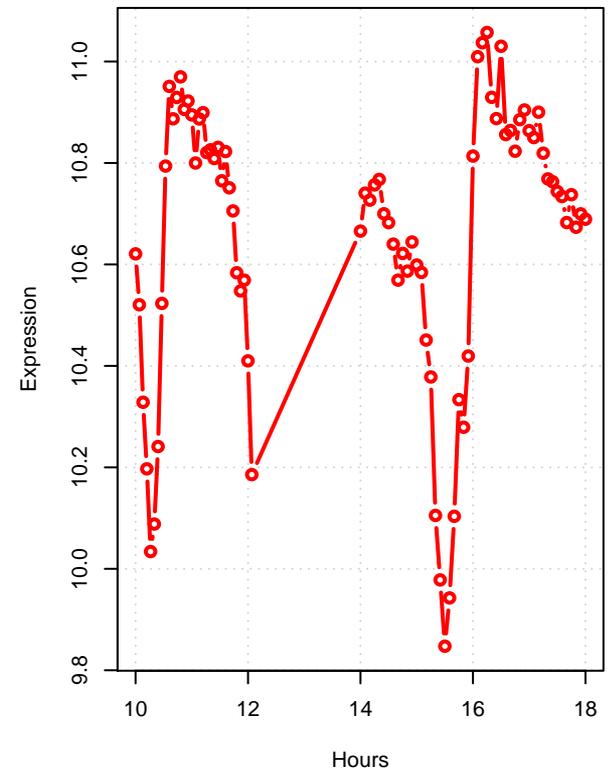
**qns1 YHR074W**  
Glutamine-dependent NAD(+) synthetase



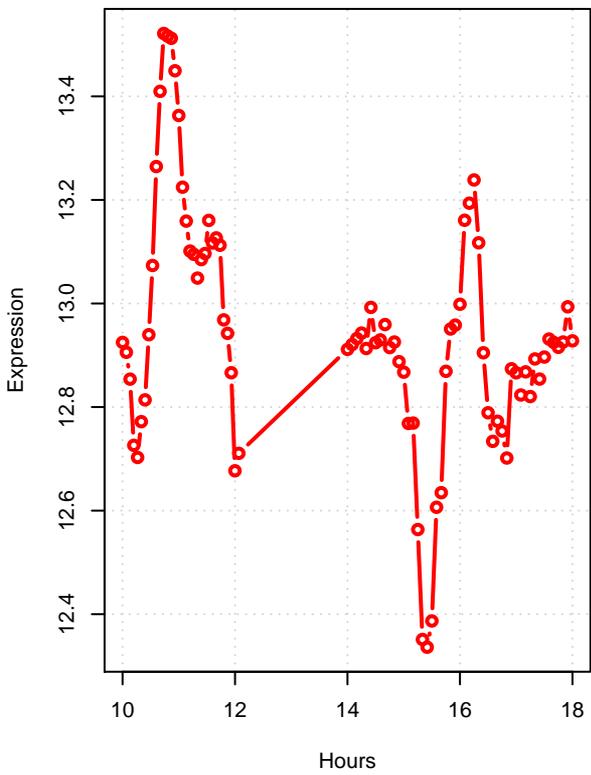
**nma1 YLR528W**  
Nicotinic acid mononucleotide adenyltransferase



**nma2 YGR010W**  
Nicotinic acid mononucleotide adenyltransferase



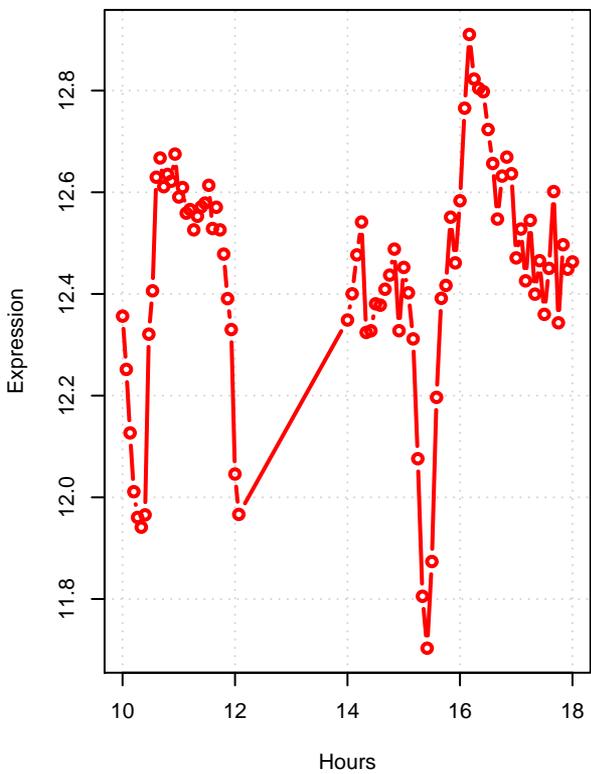
**bna6 YFR047C**  
Quinolinate phosphoribosyl transferase



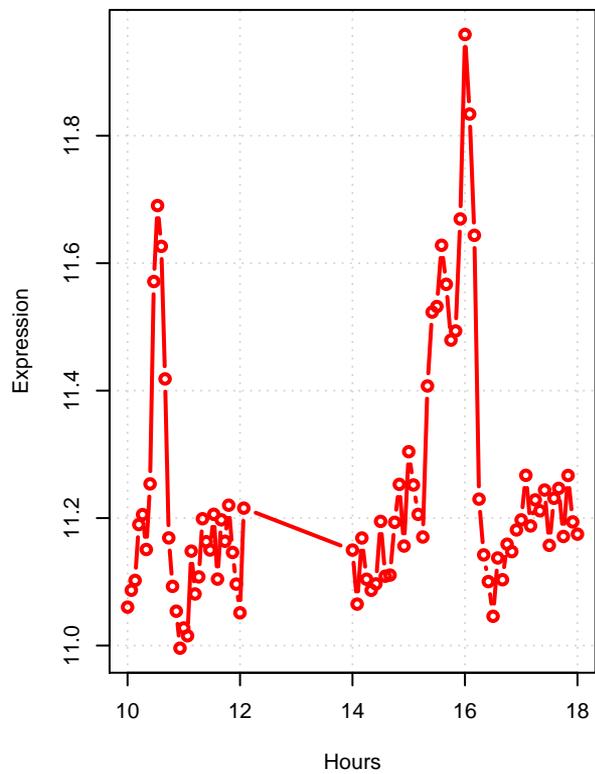
## NAD salvage pathway

# NAD salvage pathway

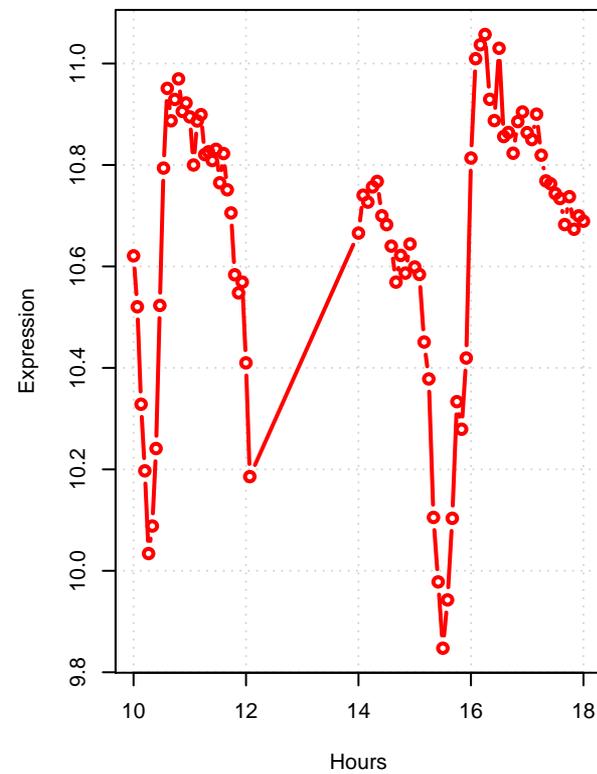
**qns1 YHR074W**  
Glutamine-dependent NAD(+) synthetase



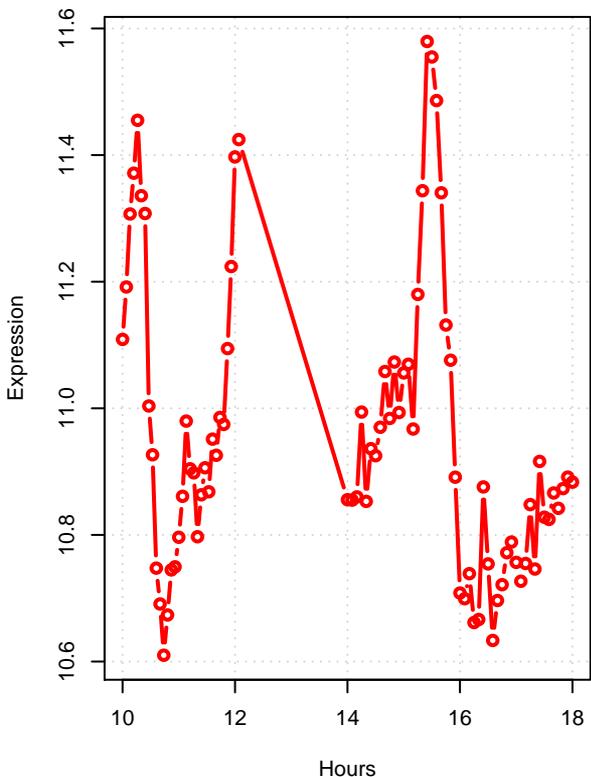
**nma1 YLR28W**  
Nicotinic acid mononucleotide adenyltransferase



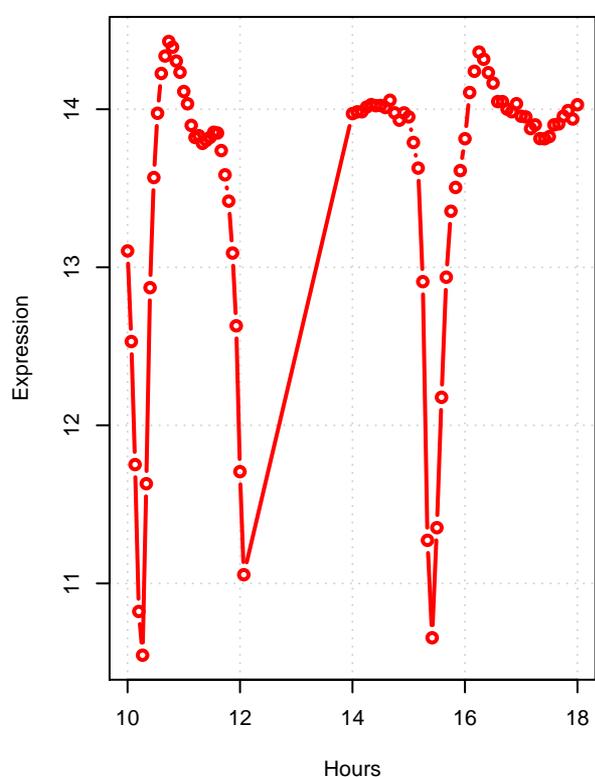
**nma2 YGR010W**  
Nicotinic acid mononucleotide adenyltransferase



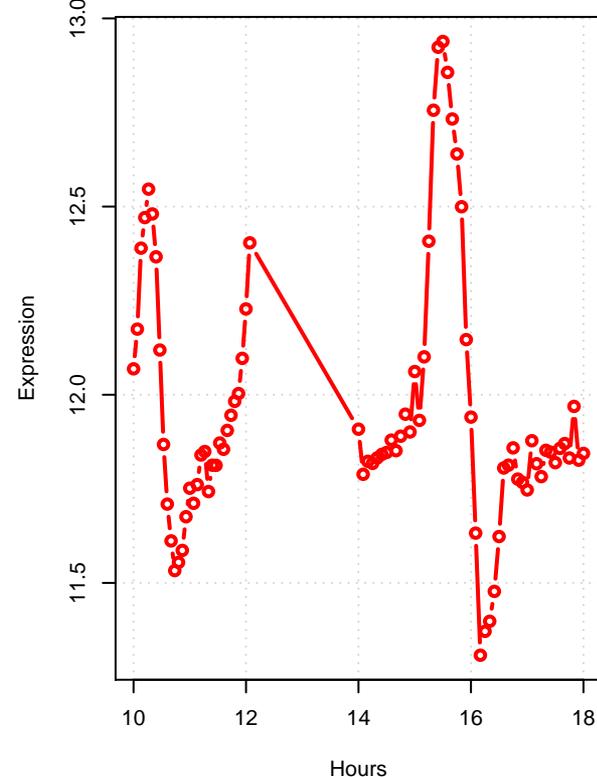
**sir2 YDL042C**  
Conserved NAD+ dependent histone deacetylase of the Sirtuin family



**pnc1 YGL037C**  
Nicotinamide that converts nicotinamide to nicotinic acid



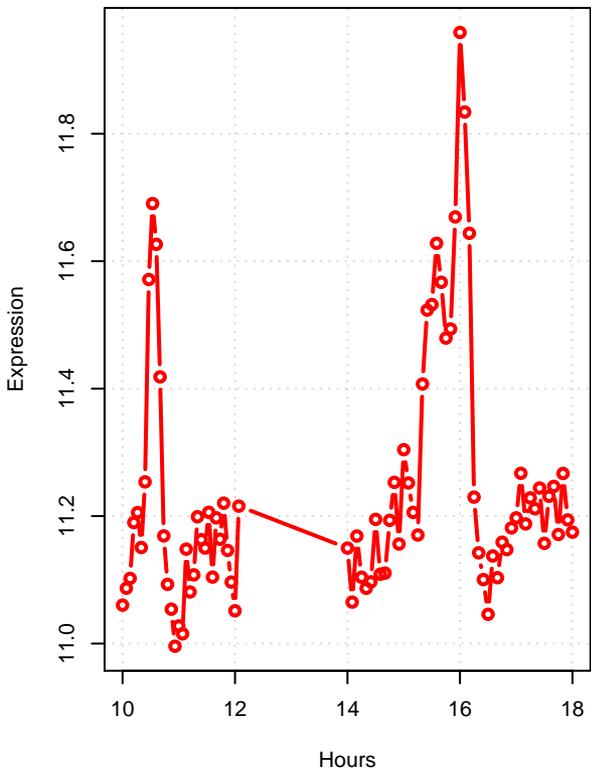
**npt1 YOR209C**  
Nicotinate phosphoribosyltransferase



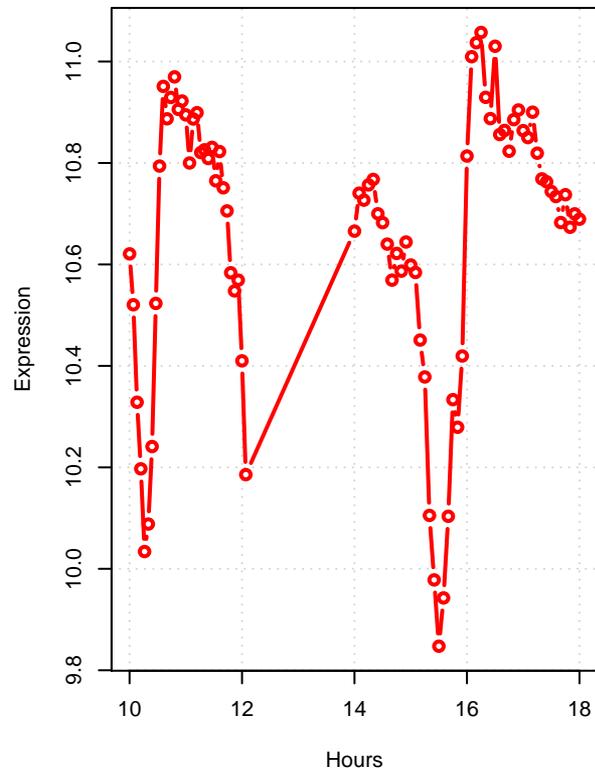
## nicotinamide riboside salvage pathway I

# nicotinamide riboside salvage pathway I

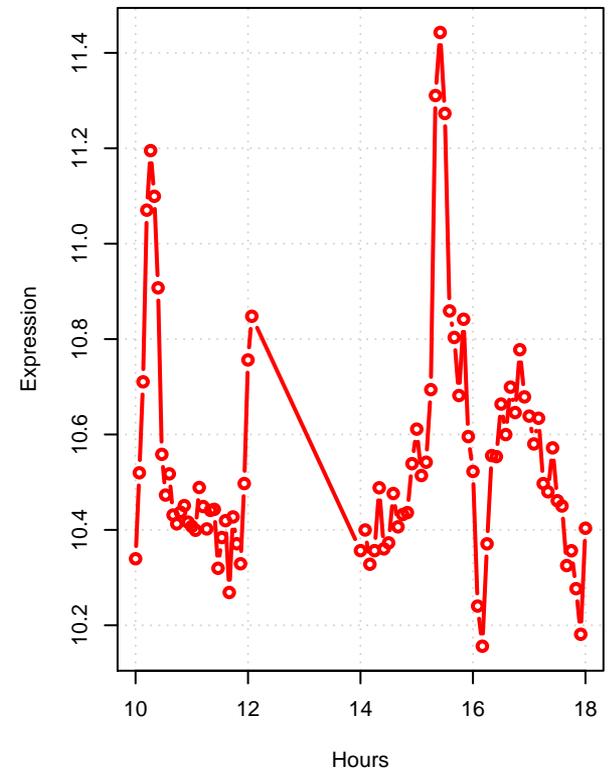
**nma1 YLR328W**  
Nicotinic acid mononucleotide adenyltransferase



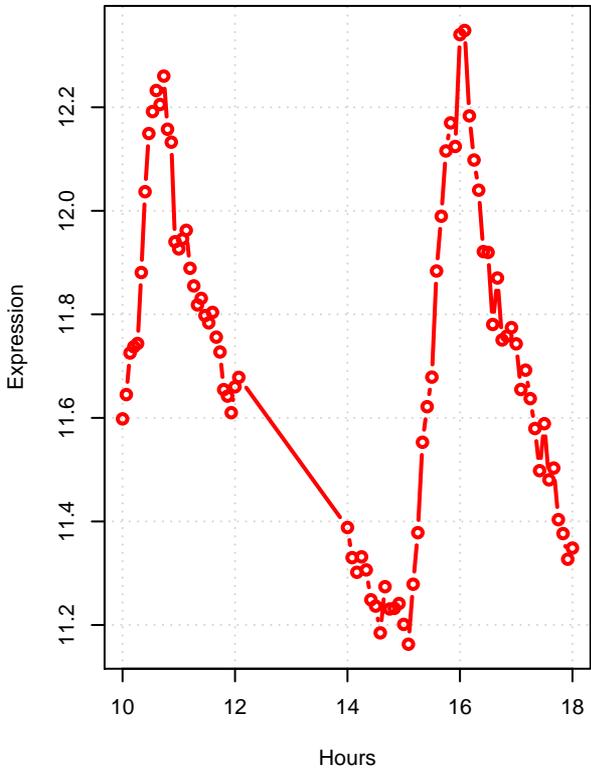
**nma2 YGR010W**  
Nicotinic acid mononucleotide adenyltransferase



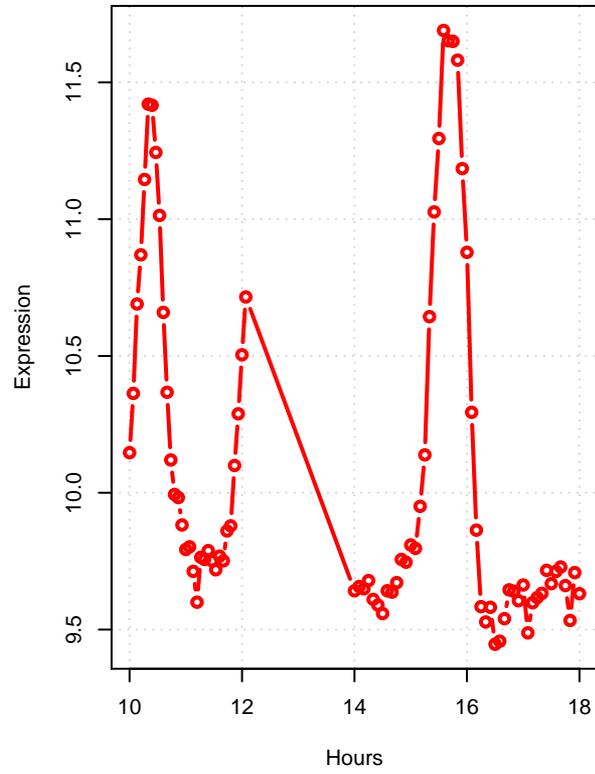
**nrk1 YNL129W**  
Nicotinamide riboside kinase



**pnp1 YLR209C**  
Purine nucleoside phosphorylase

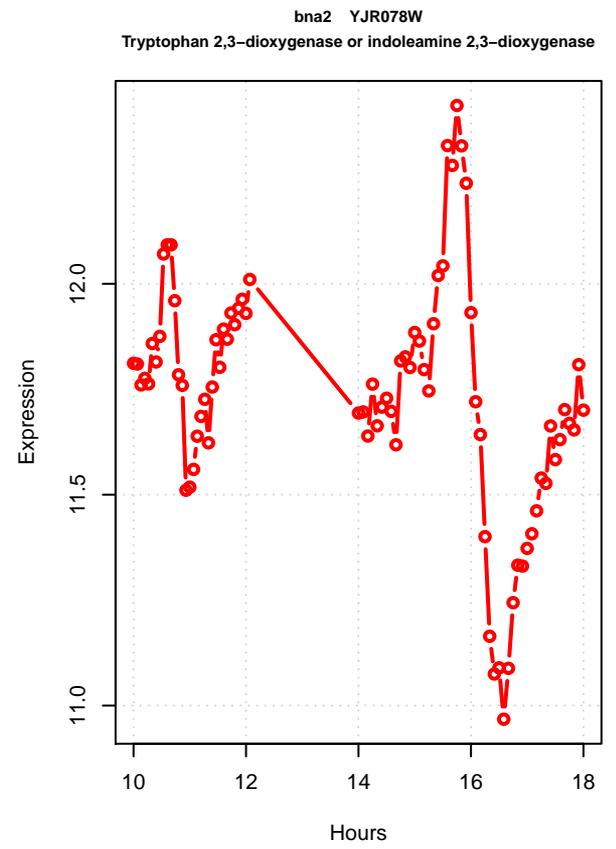
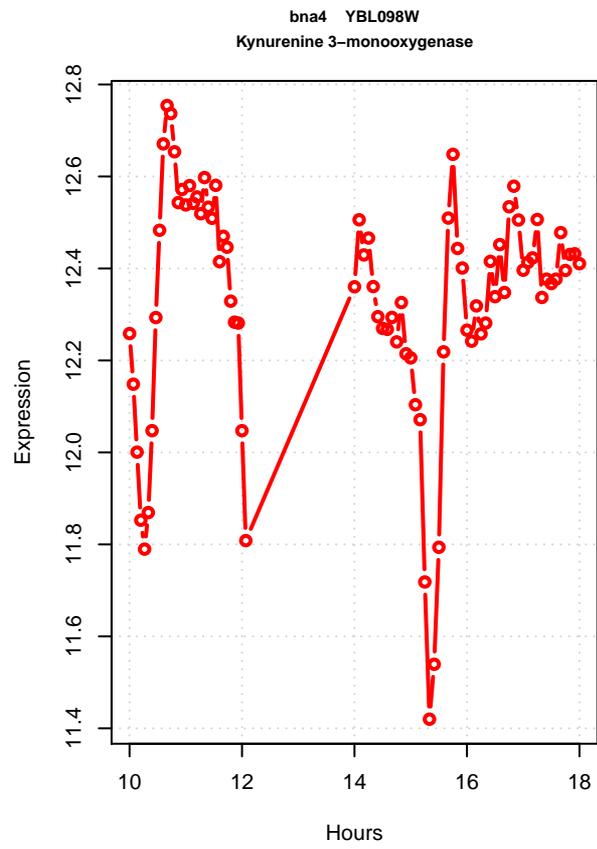
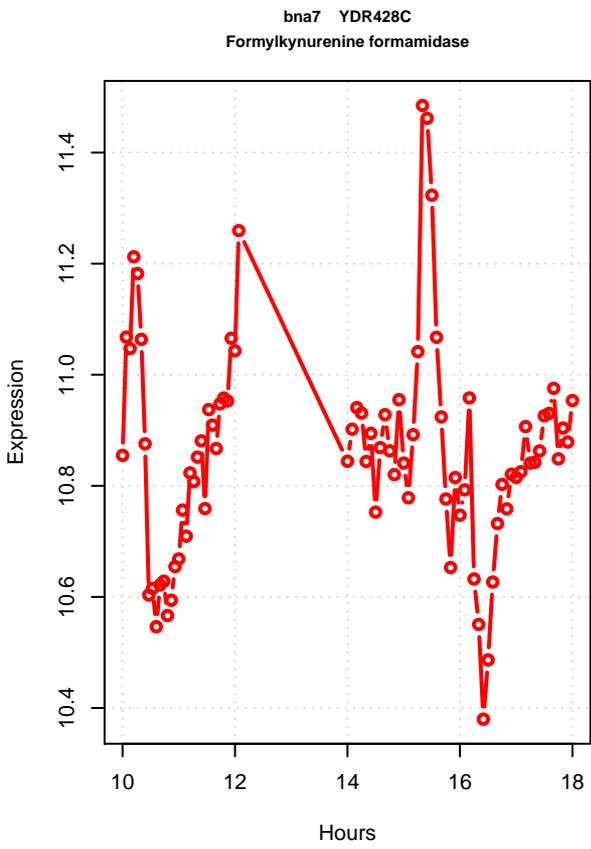
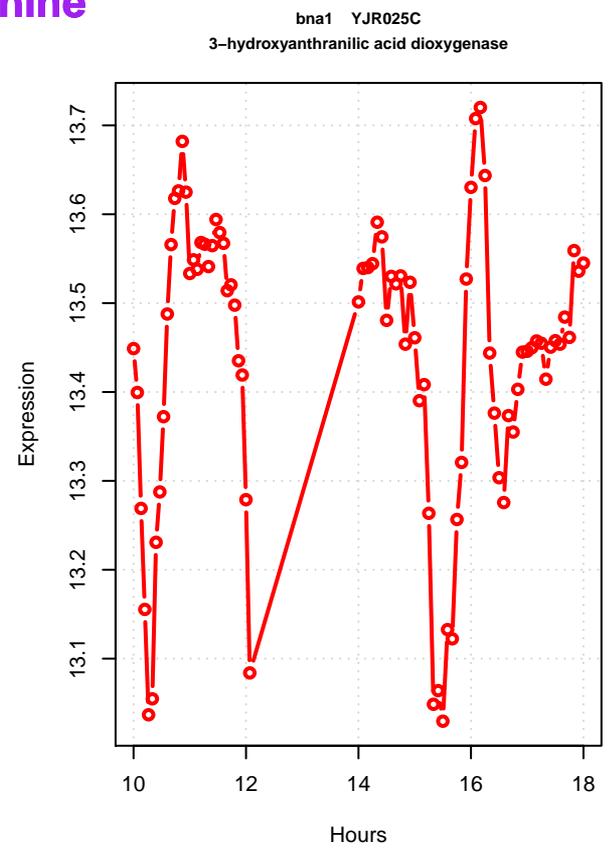
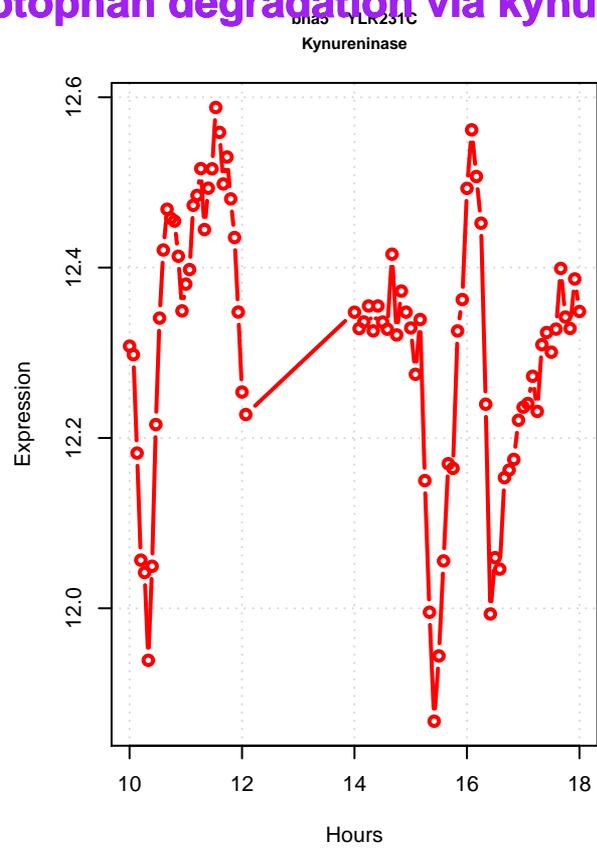
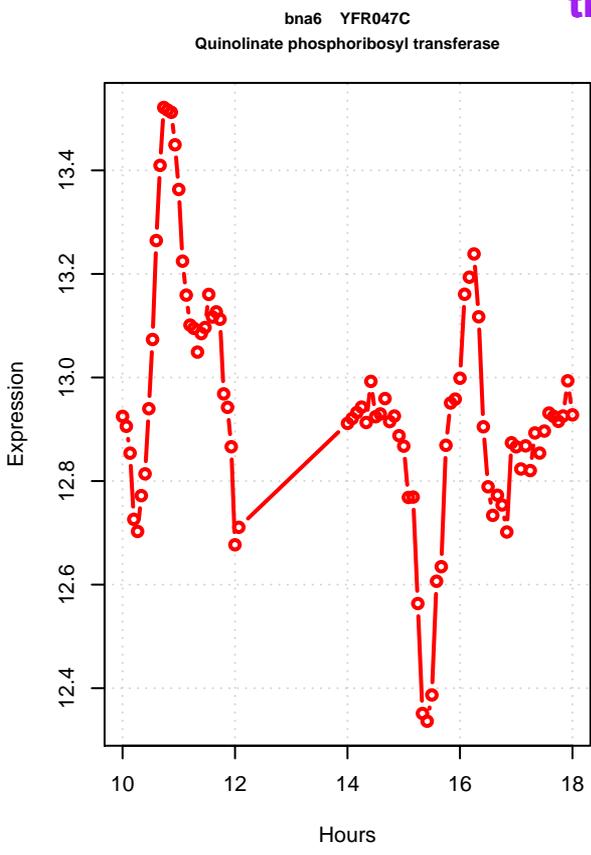


**urh1 YDR400W**  
Uridine nucleosidase (uridine-cytidine N-ribohydrolase)



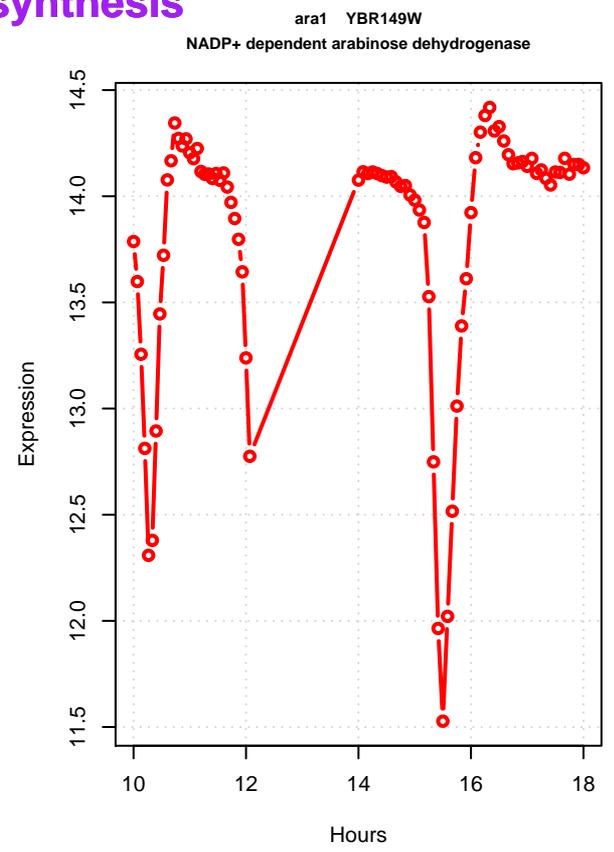
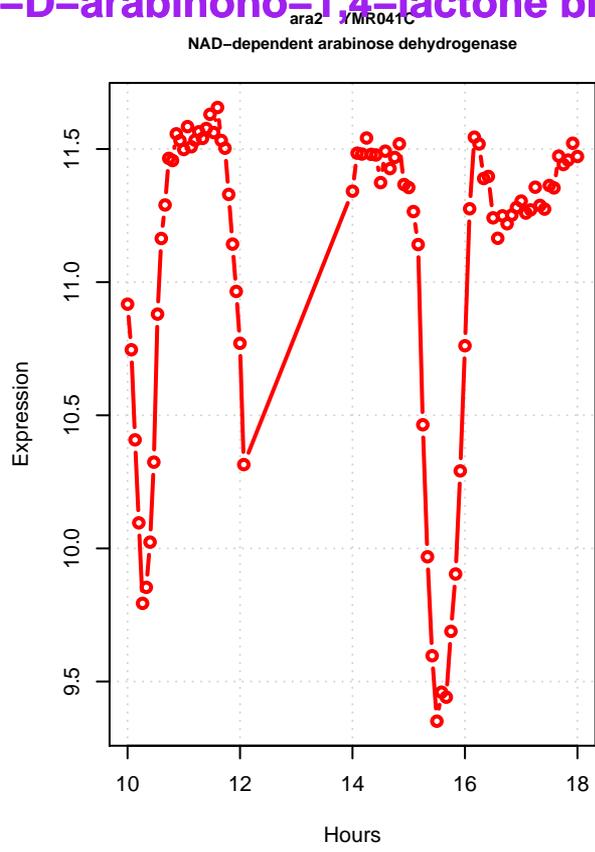
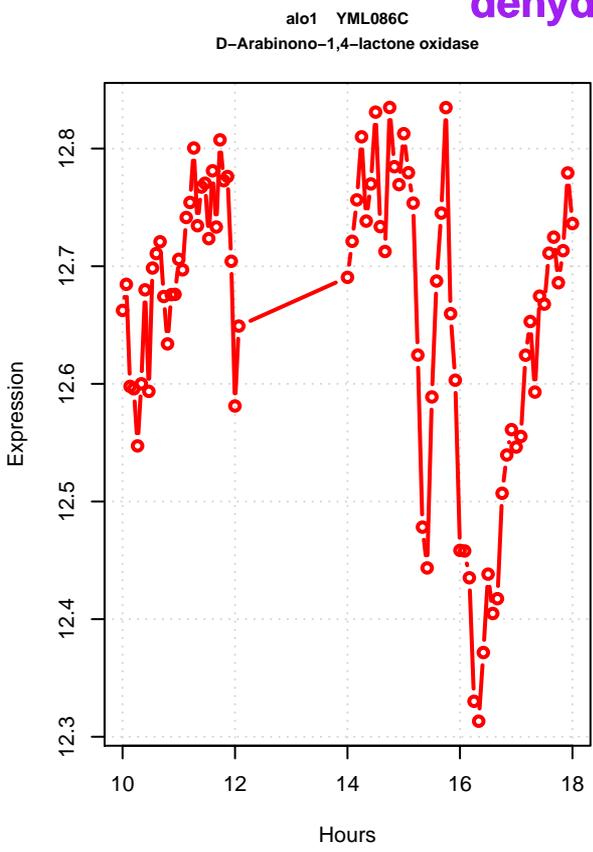
**tryptophan degradation via kynurenine**

# tryptophan degradation via kynurenine



**dehydro-D-arabinono-1,4-lactone biosynthesis**

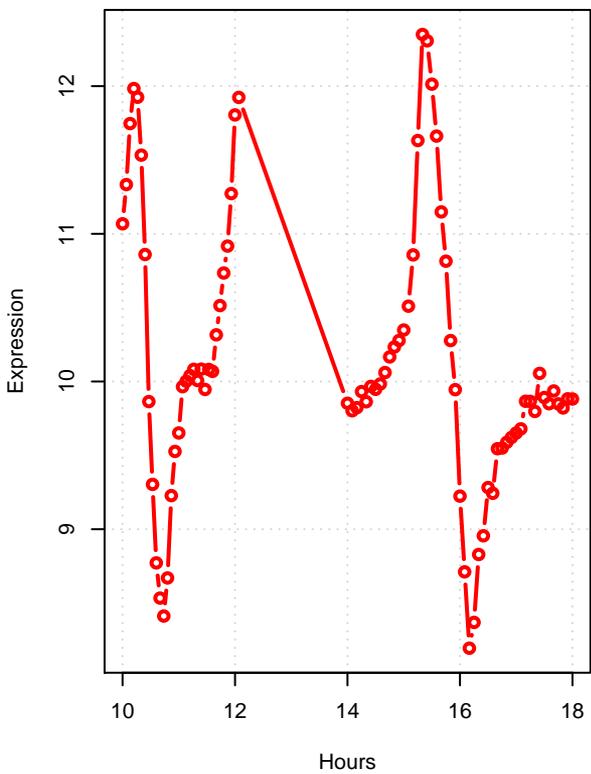
# dehydro-D-arabino-1,4-lactone biosynthesis



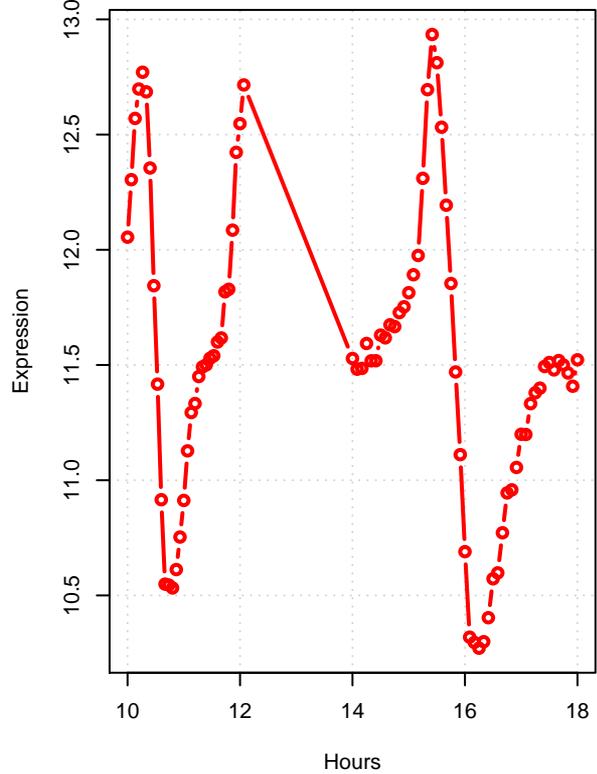
## **diphthamide biosynthesis**

# diphthamide biosynthesis

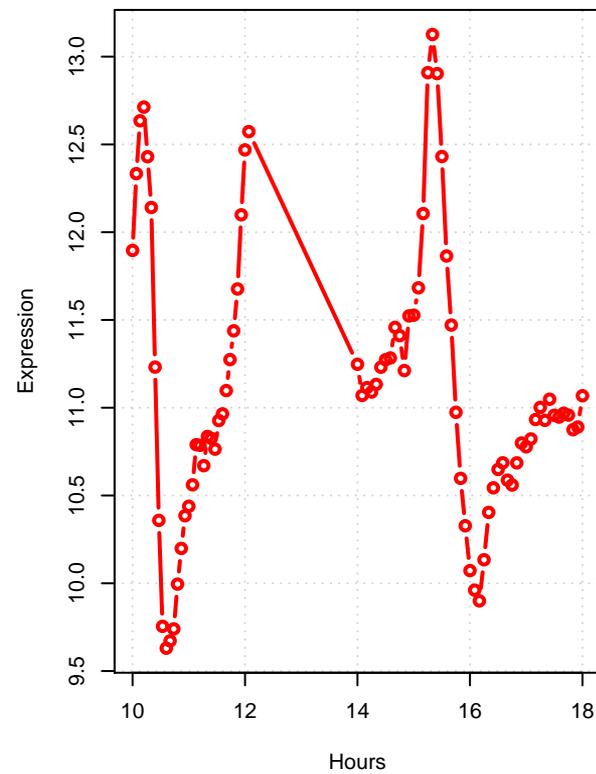
**dph1 YIL103W**  
Protein required for synthesis of diphthamide



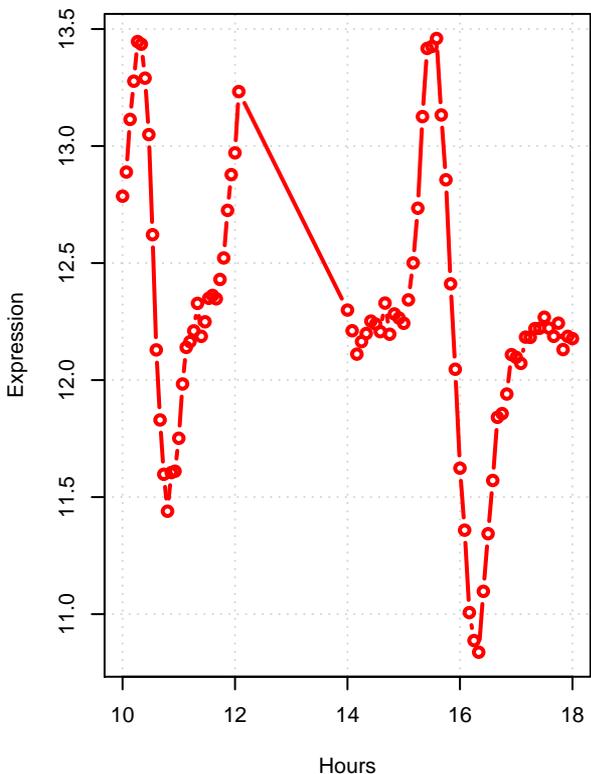
**dph2 YAL191W**  
Protein required for synthesis of diphthamide



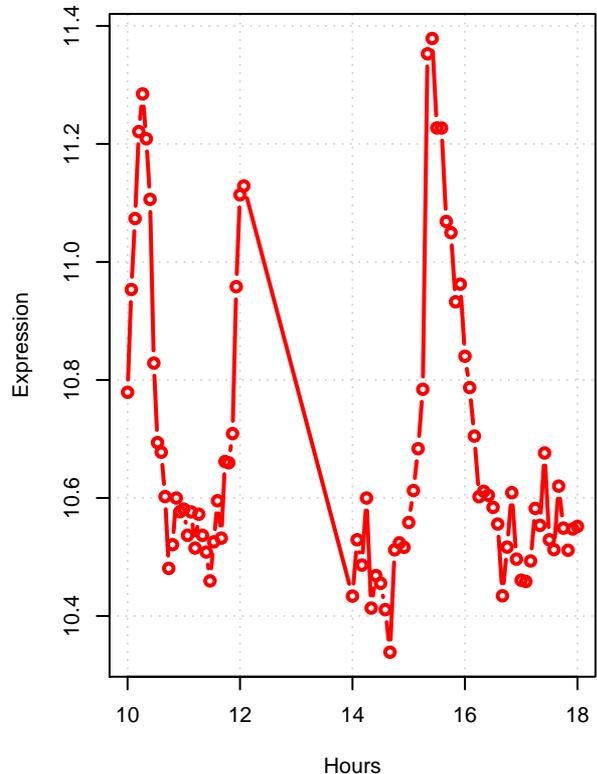
**kti11 YBL071W-A**  
Zn-ribbon protein that co-purifies with Dph1 and Dph2



**dph5 YLR172C**  
Methyltransferase required for synthesis of diphthamide

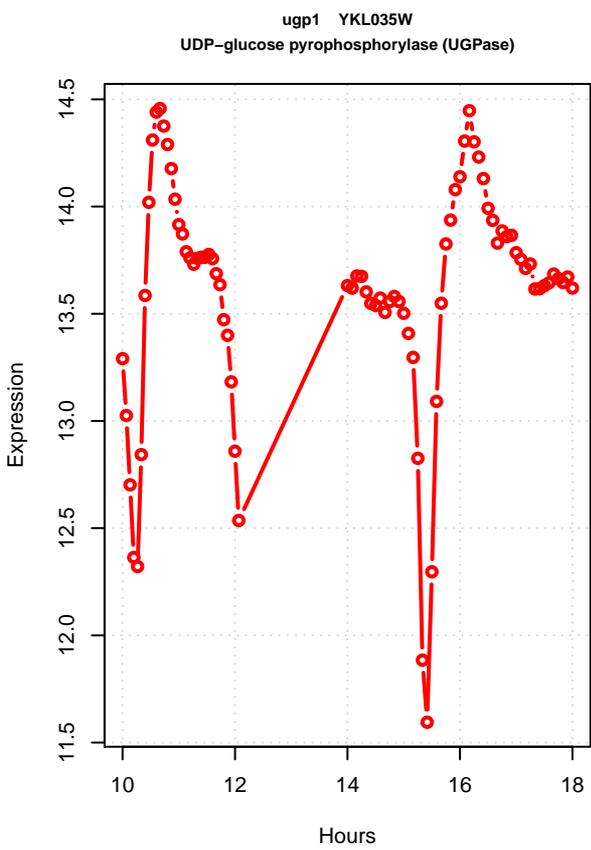
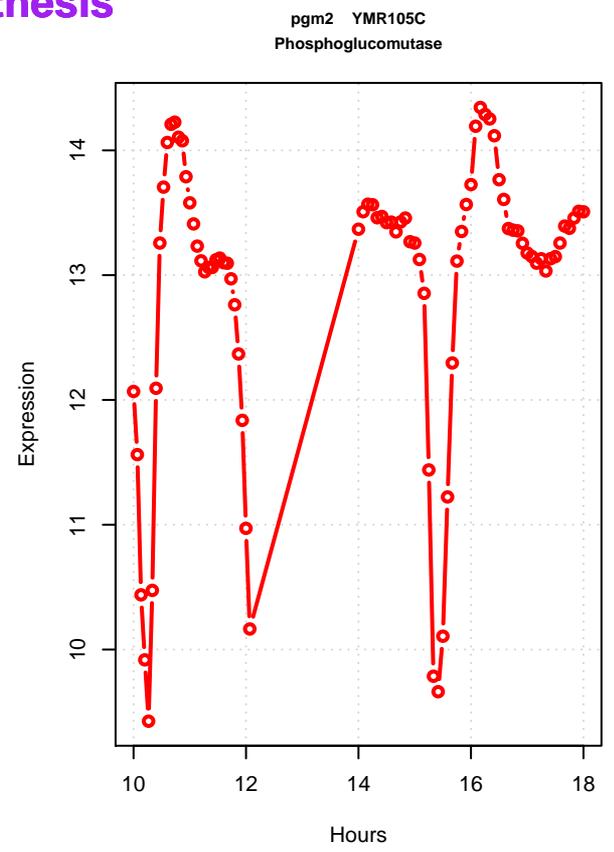
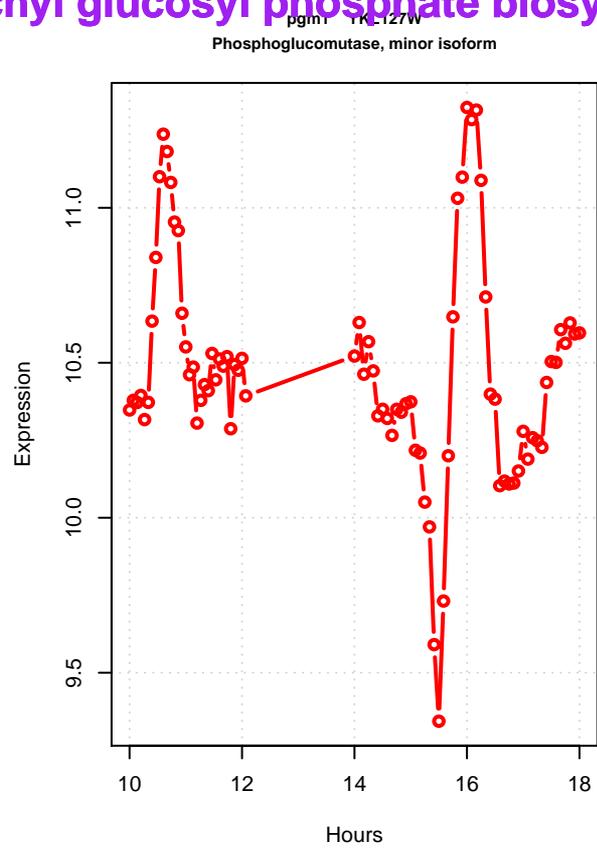
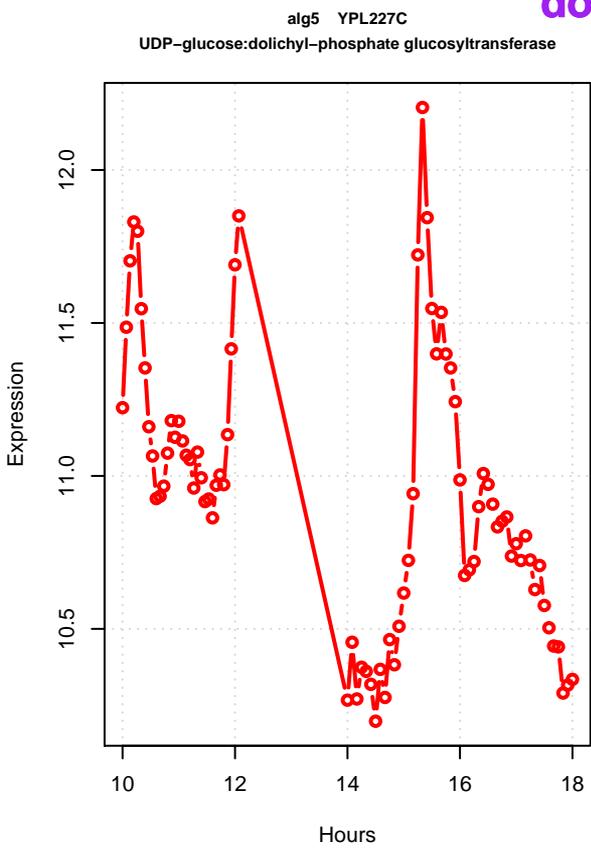


**rrt2 YBR246W**  
Methylesterase performing penultimate step of diphthamide biosynthesis



## **dolichyl glucosyl phosphate biosynthesis**

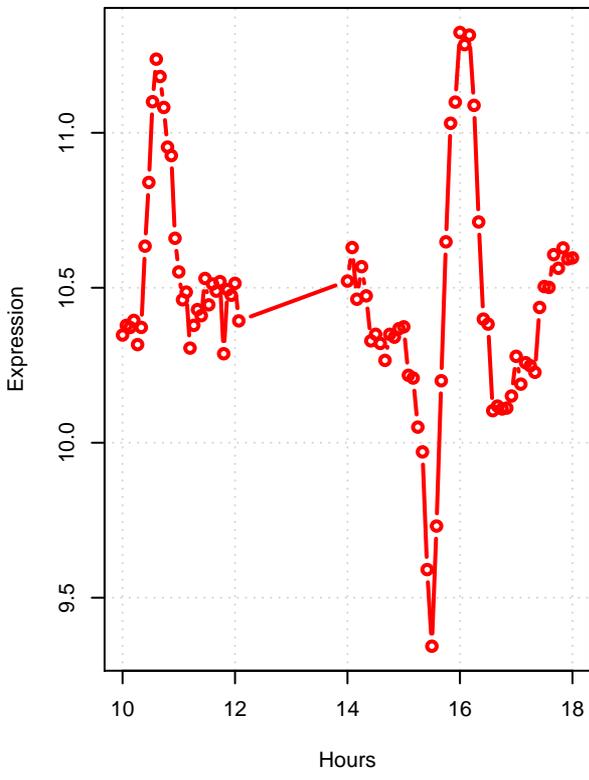
# dolichyl phosphate biosynthesis



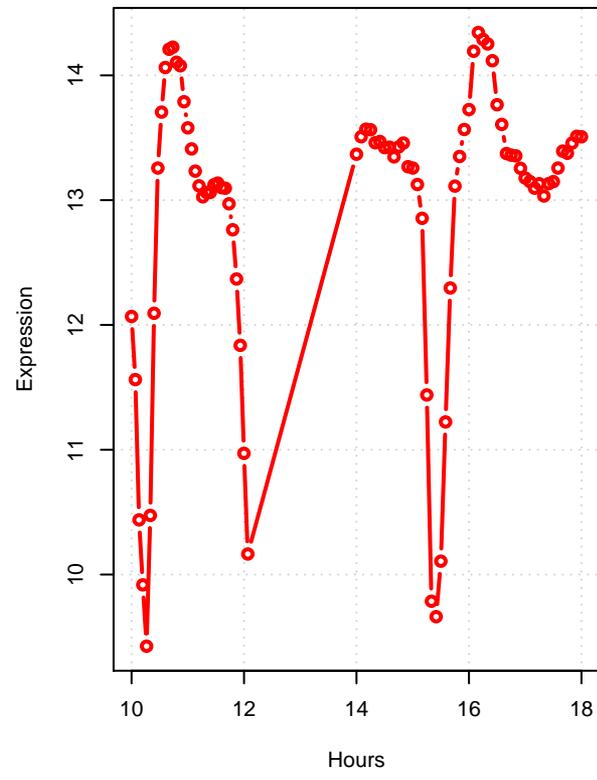
## galactose degradation

# galactose degradation

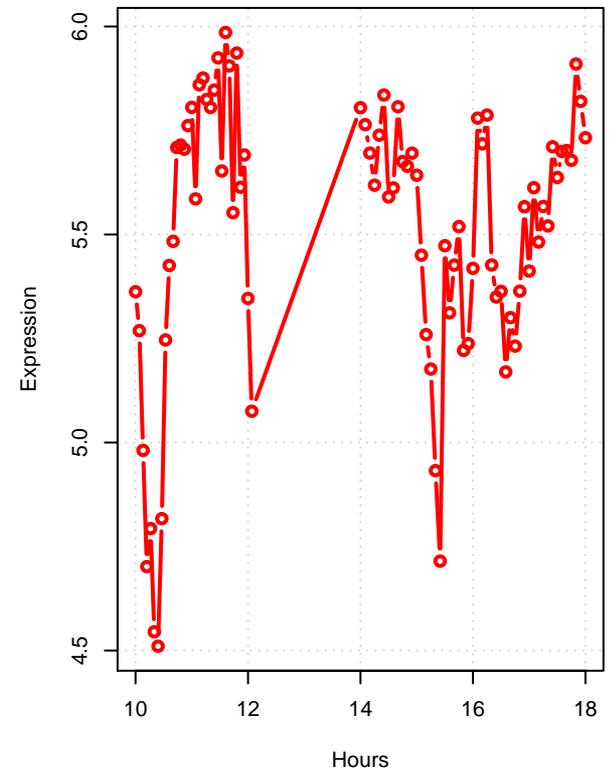
pgm1 YKL127W  
Phosphoglucomutase, minor isoform



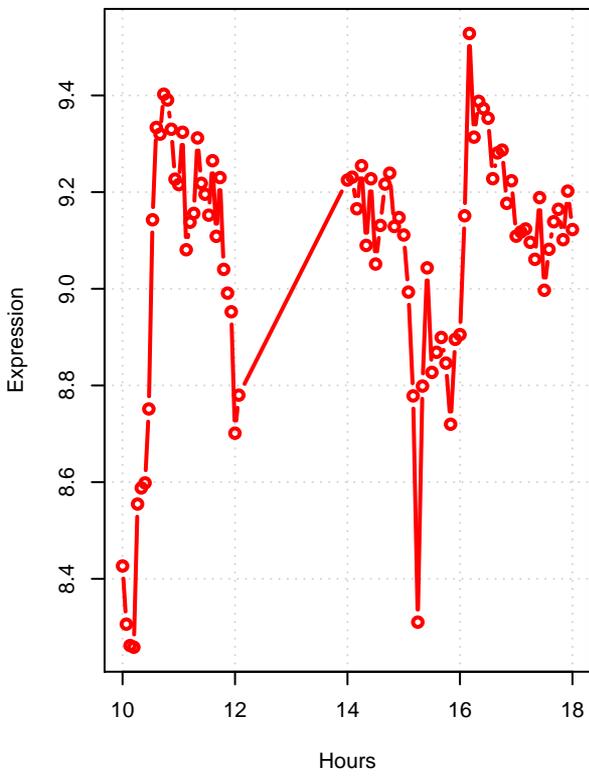
pgm2 YKL105C  
Phosphoglucomutase



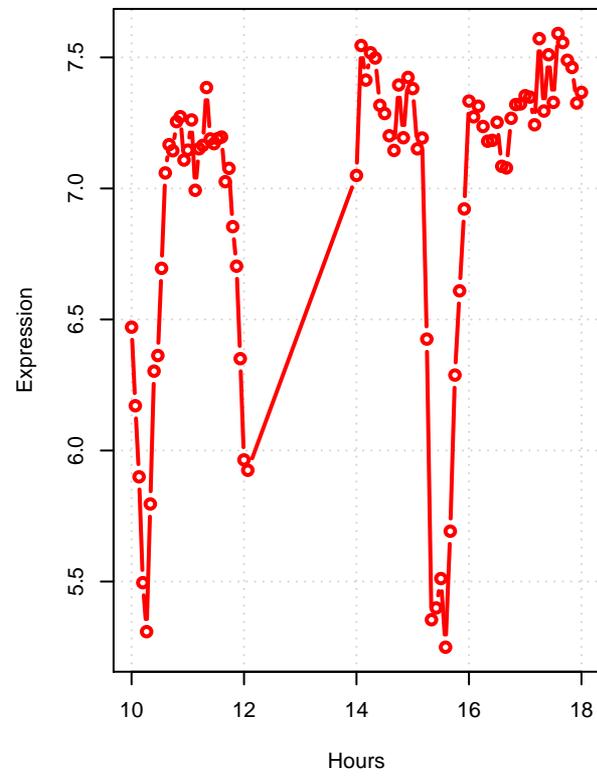
gal10 YBR019C  
UDP-glucose-4-epimerase



gal1 YBR020W  
Galactokinase

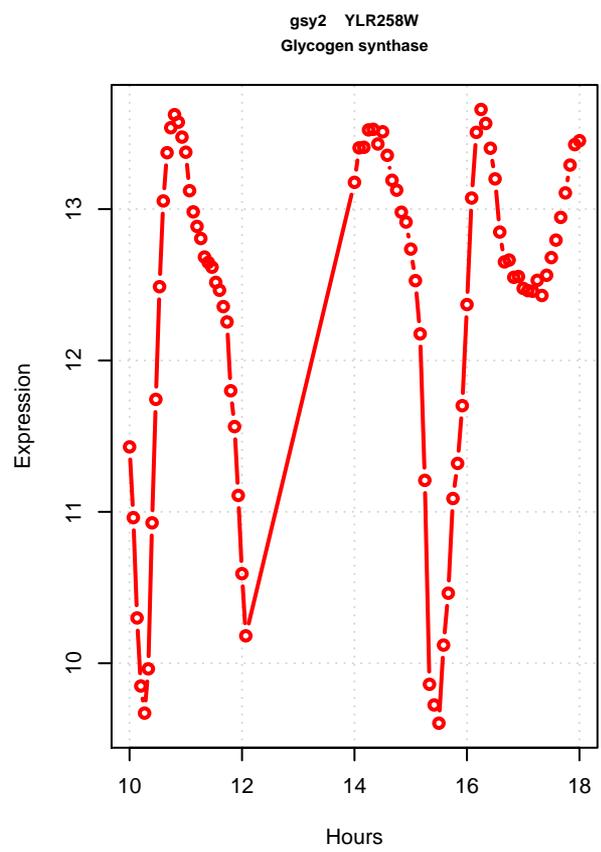
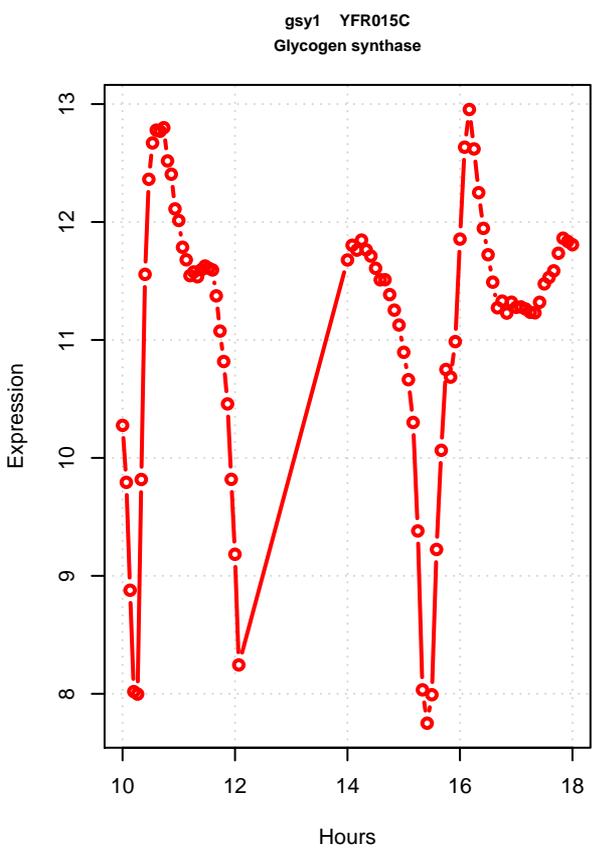
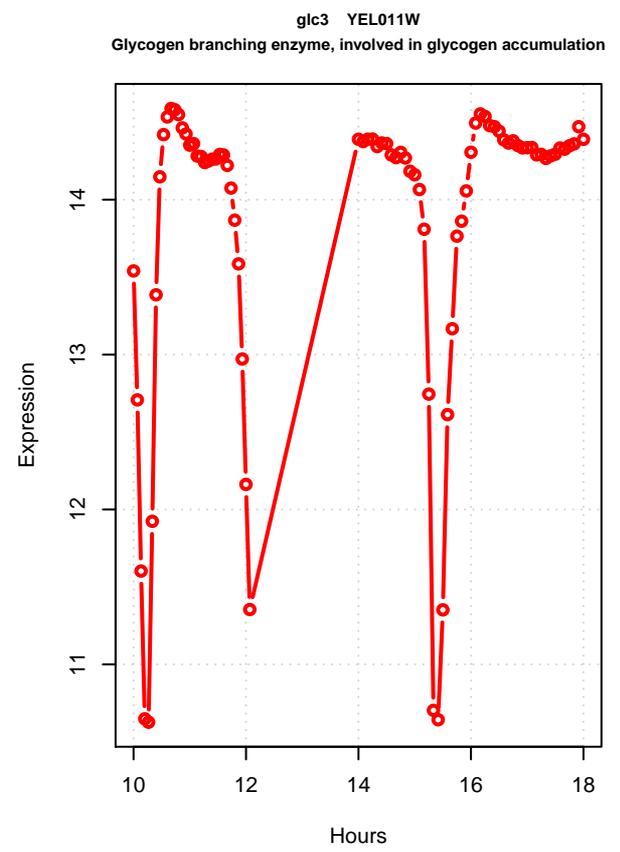
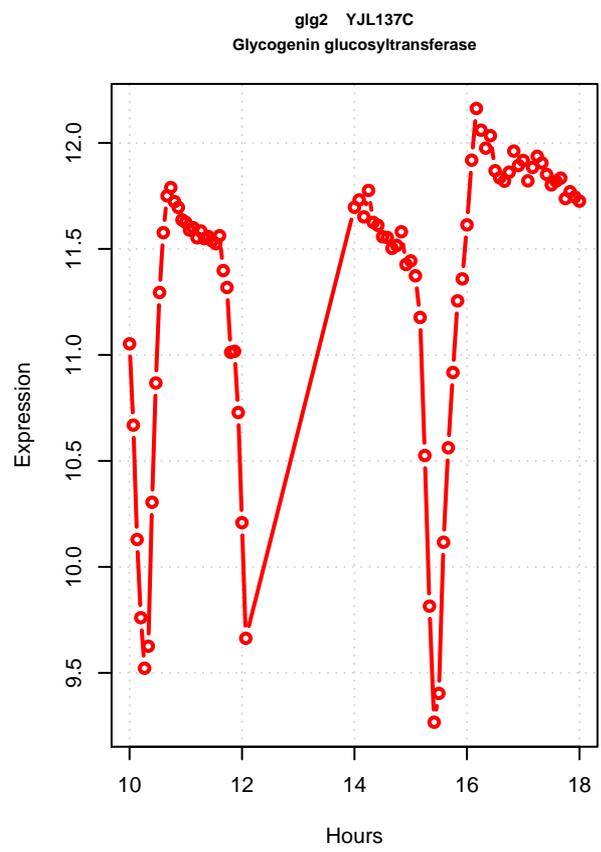
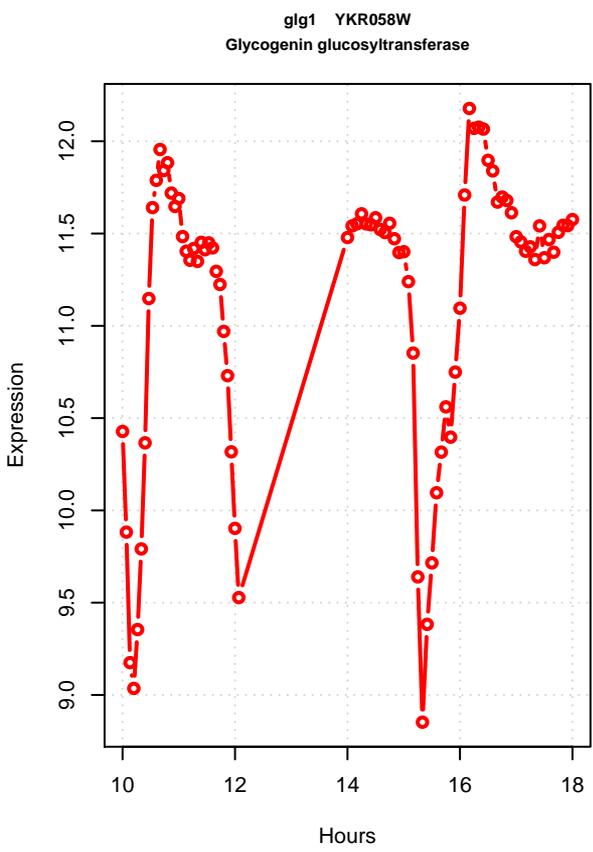
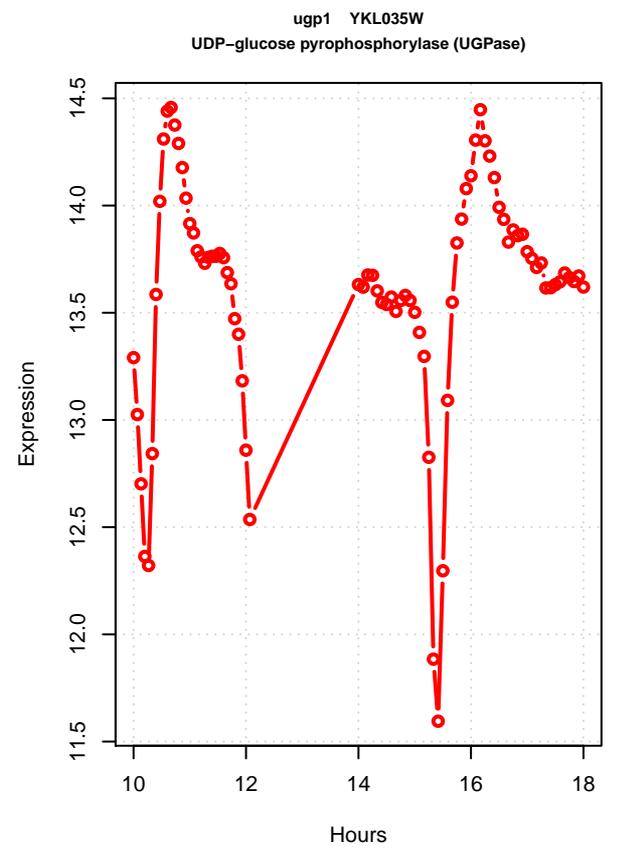
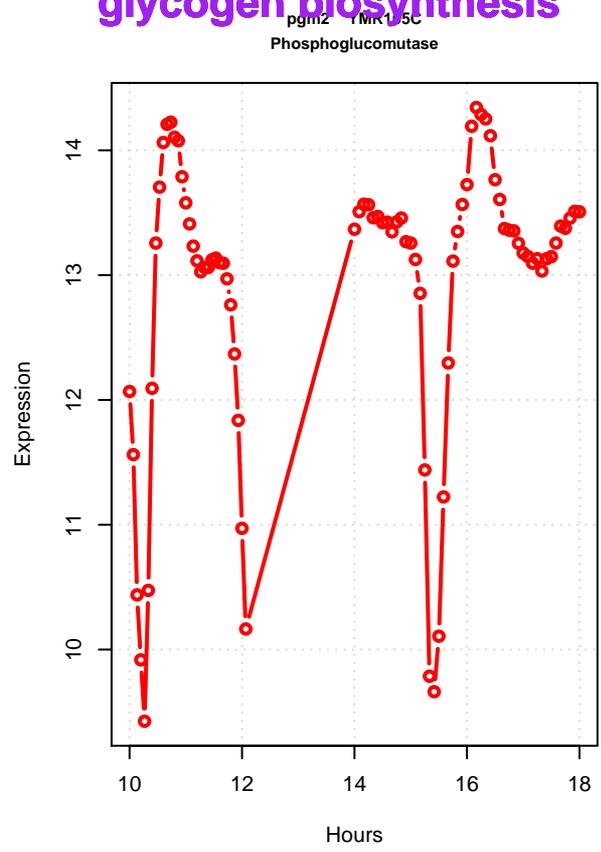
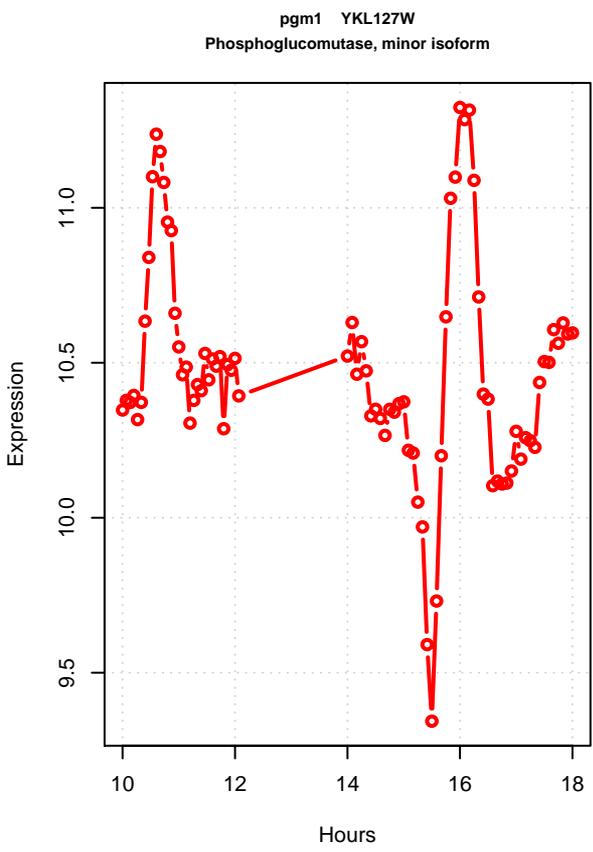


gal7 YBR018C  
Galactose-1-phosphate uridyl transferase



## **glycogen biosynthesis**

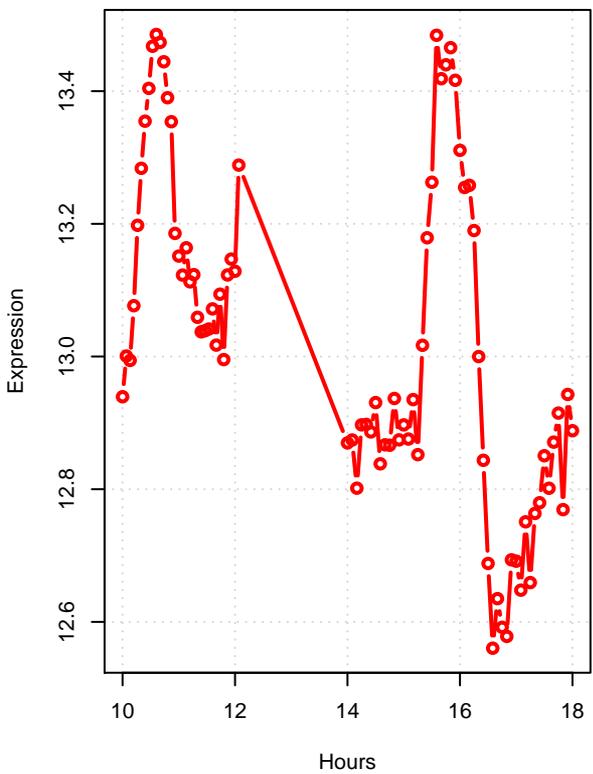
# glycogen biosynthesis



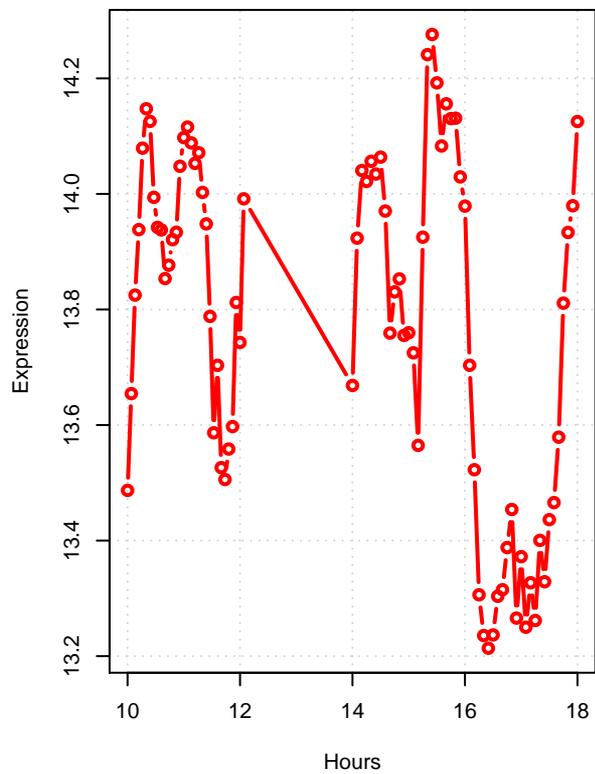
**dolichyl phosphate D-mannose biosynthesis**

# dolichyl phosphate D-mannose biosynthesis

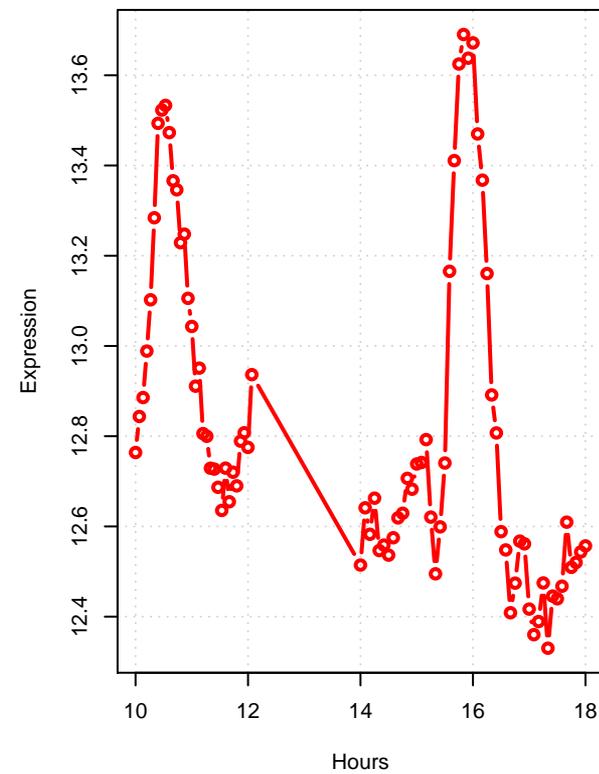
dpm1 YPR183W  
Dolichol phosphate mannose (Dol-P-Man) synthase of ER membrane



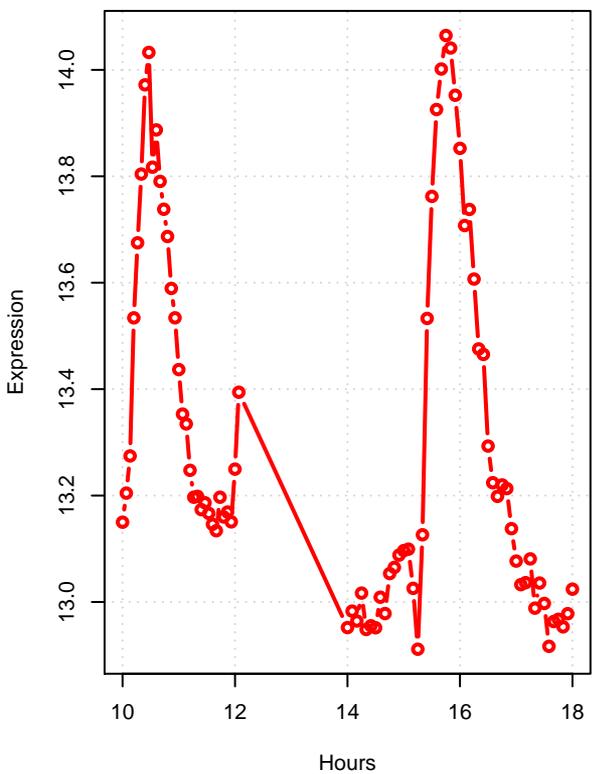
psa1 YDL055C  
GDP-mannose pyrophosphorylase (mannose-1-phosphate guanyltransferase)



pmi40 YER003C  
Mannose-6-phosphate isomerase



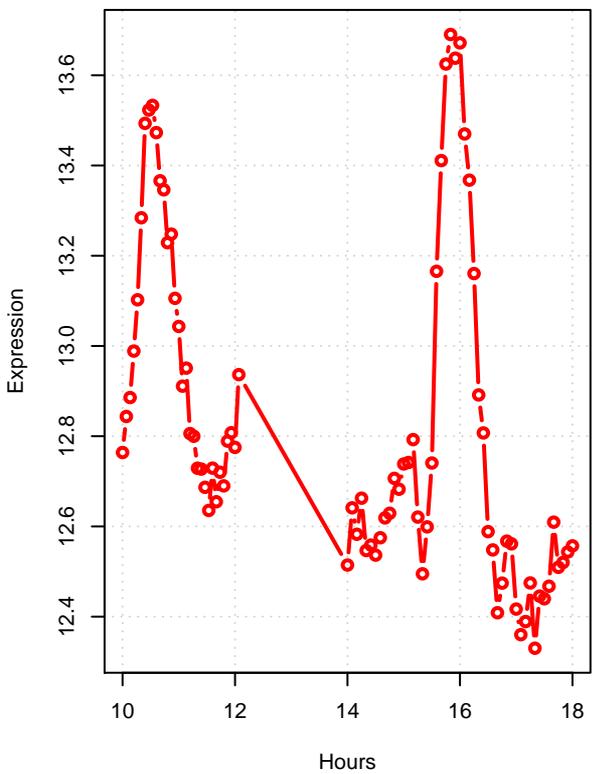
sec53 YFL045C  
Phosphomannomutase



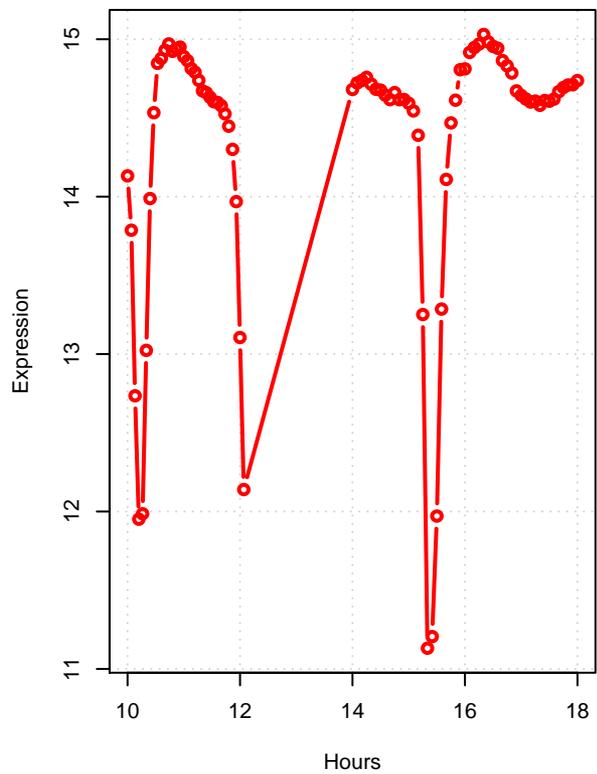
**mannose degradation**

# mannose degradation

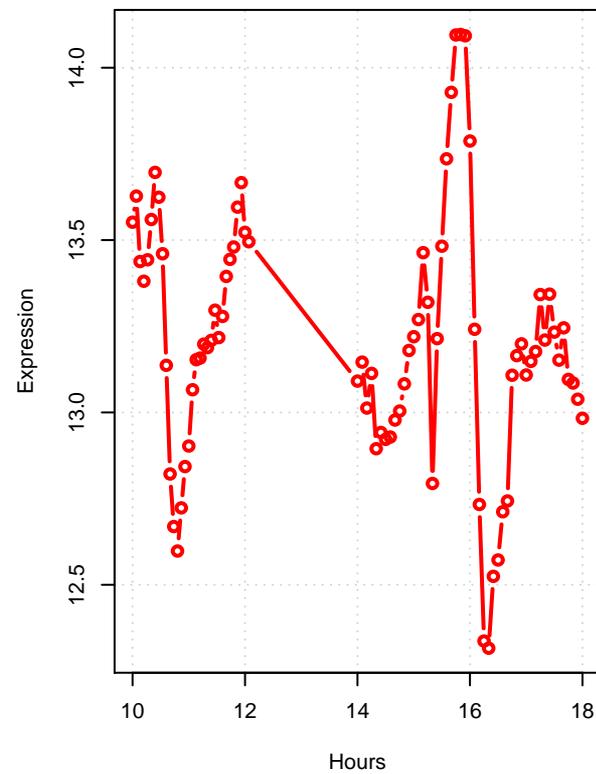
pmi40 YER003C  
Mannose-6-phosphate isomerase



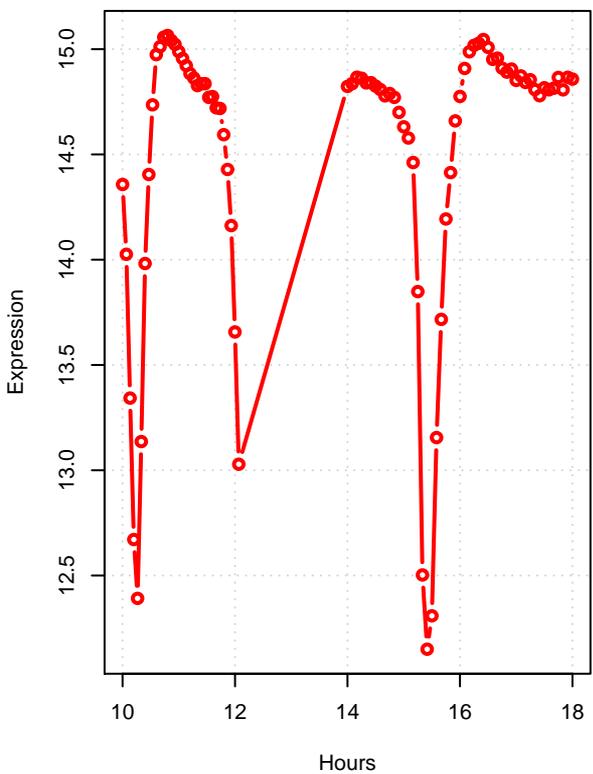
hxx1 YER053C  
Hexokinase isoenzyme 1



hxx2 YGL253W  
Hexokinase isoenzyme 2

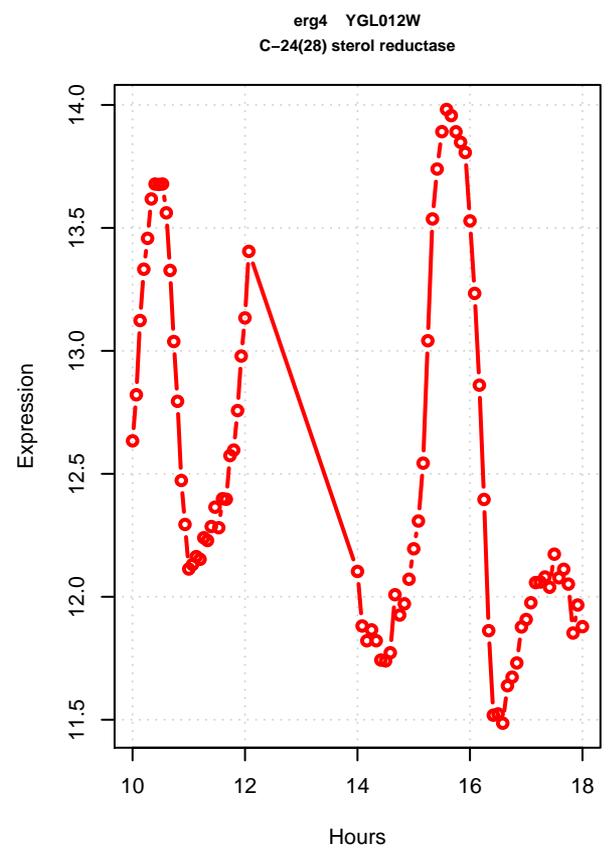
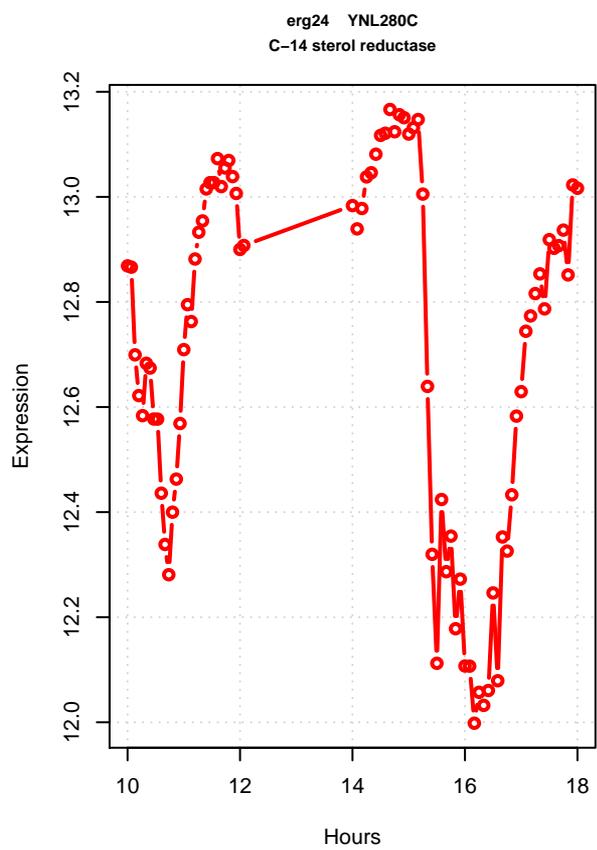
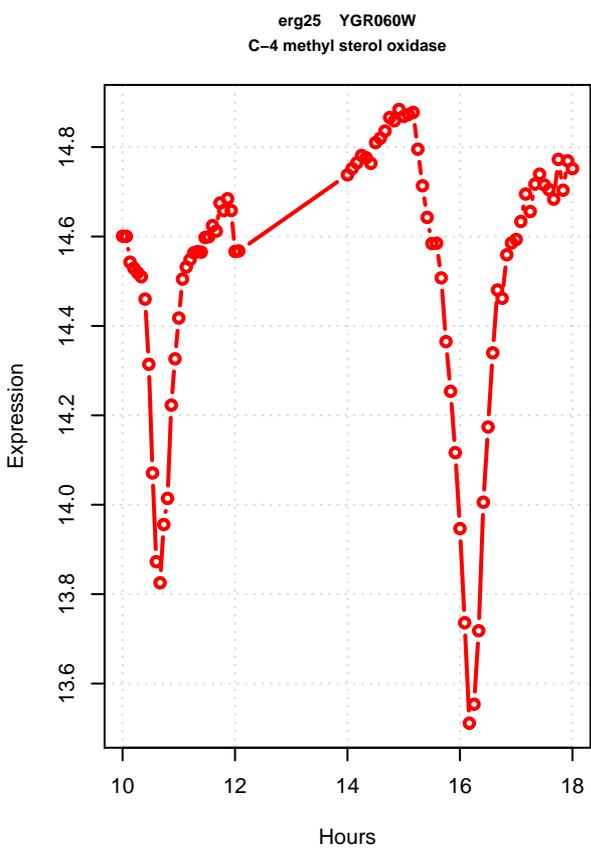
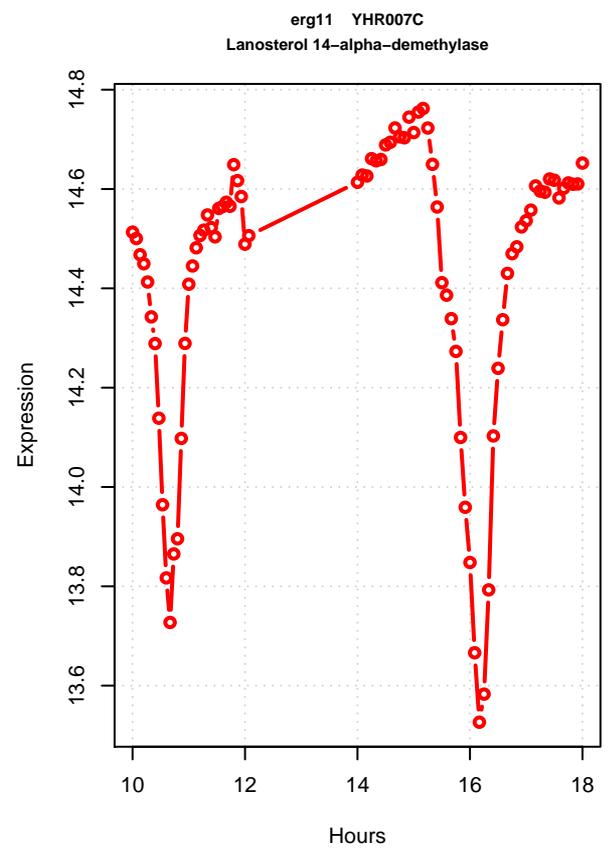
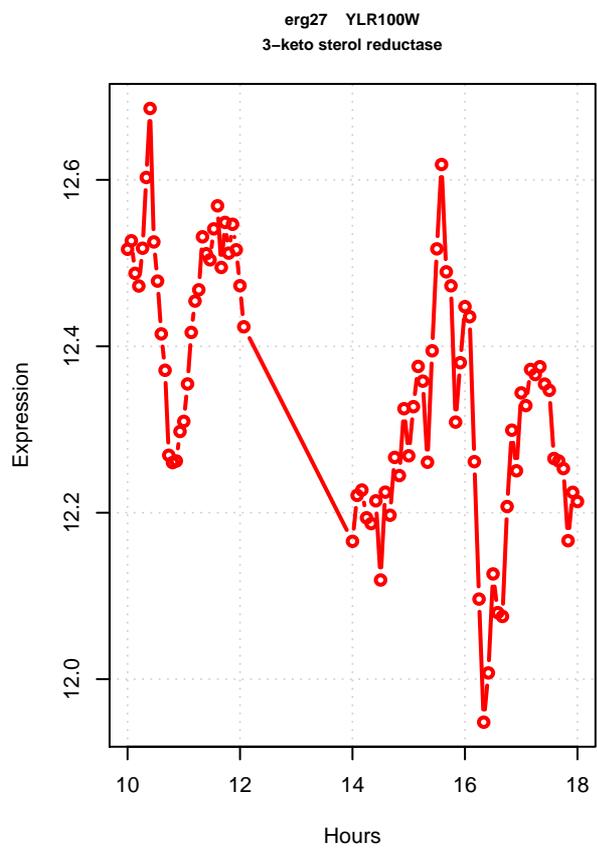
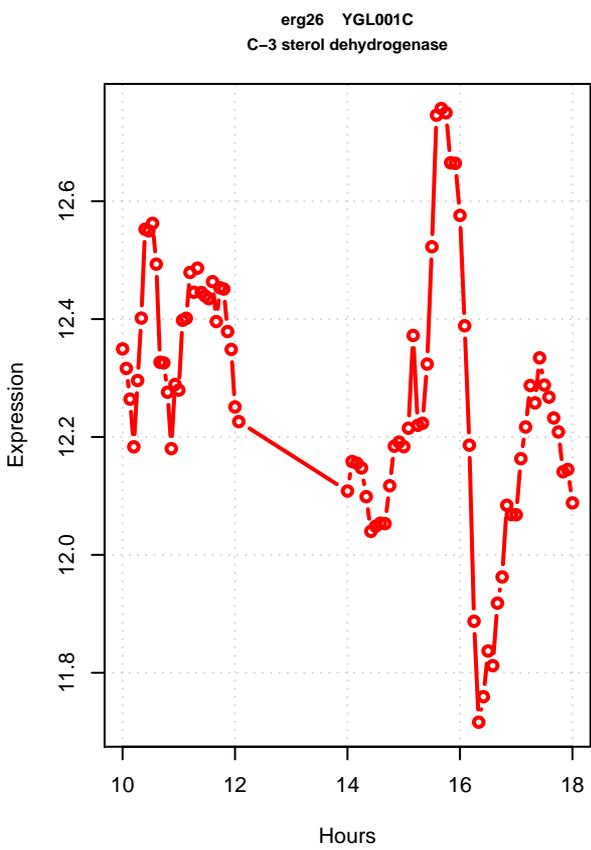
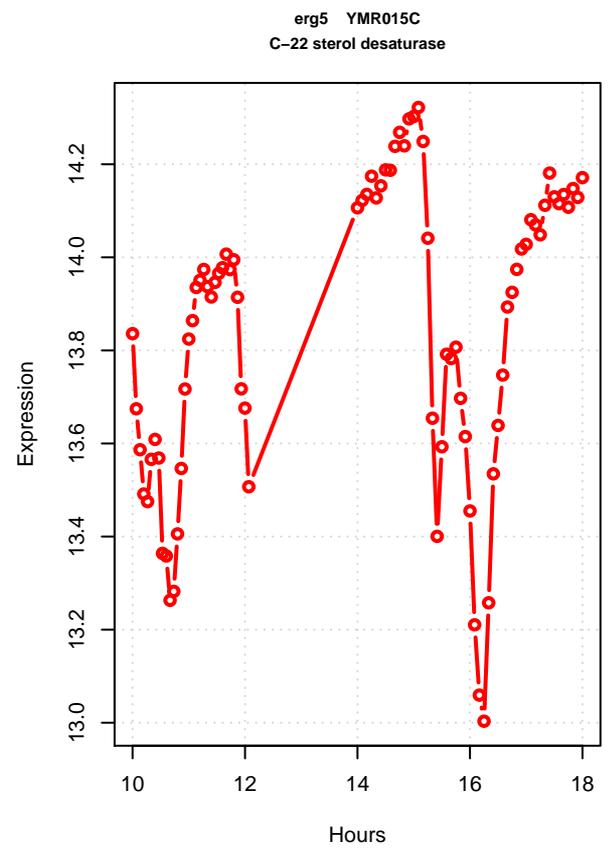
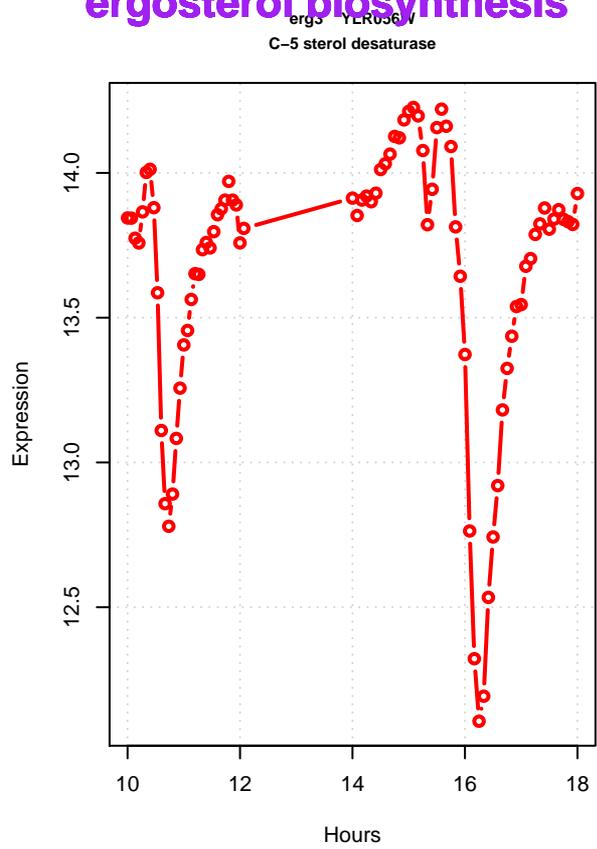
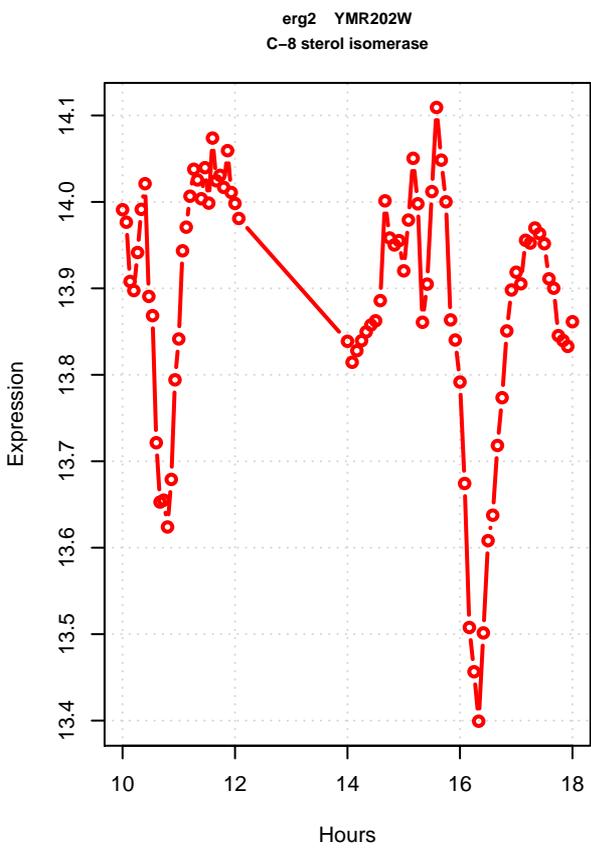


glk1 YCL040W  
Glucokinase

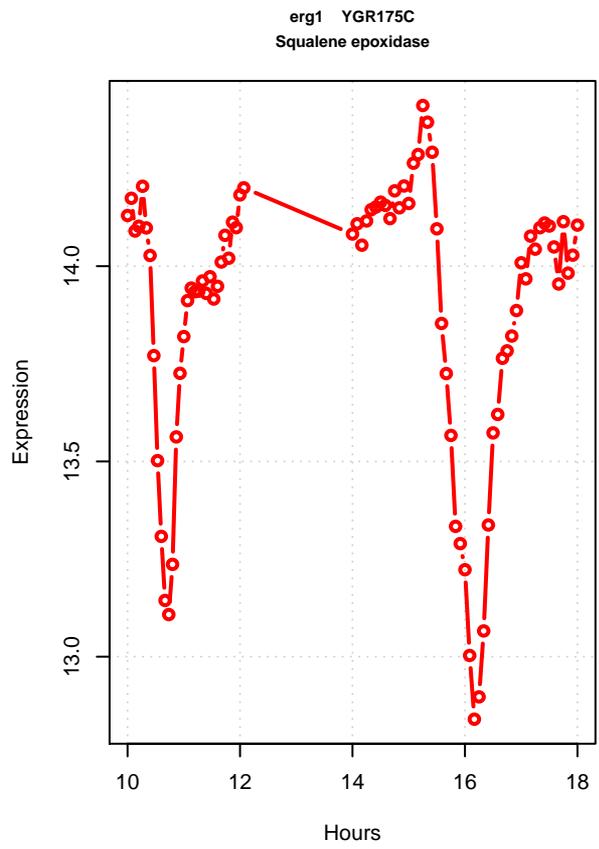
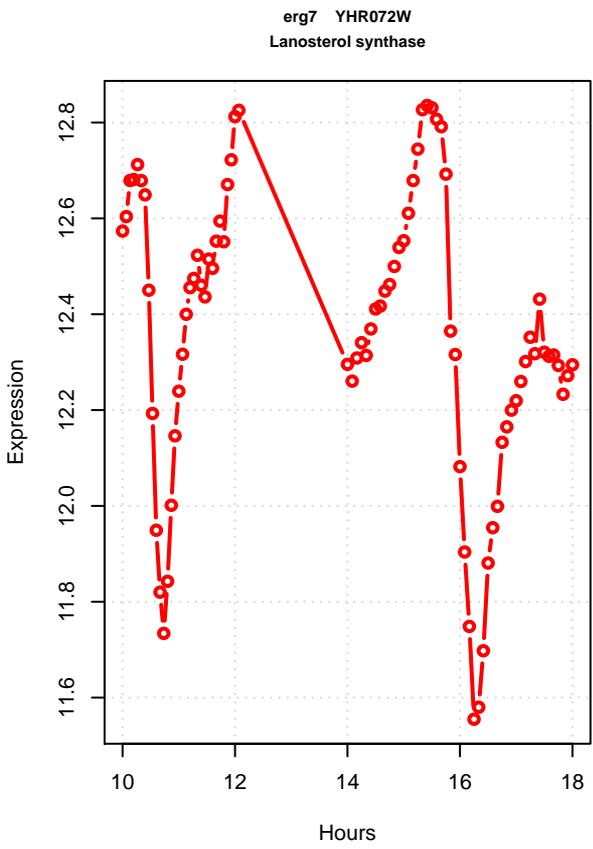
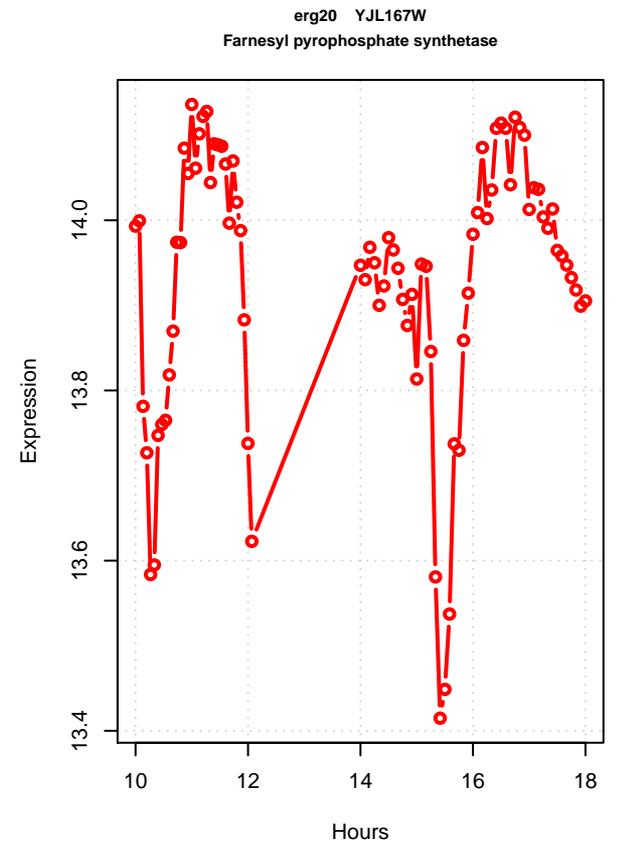
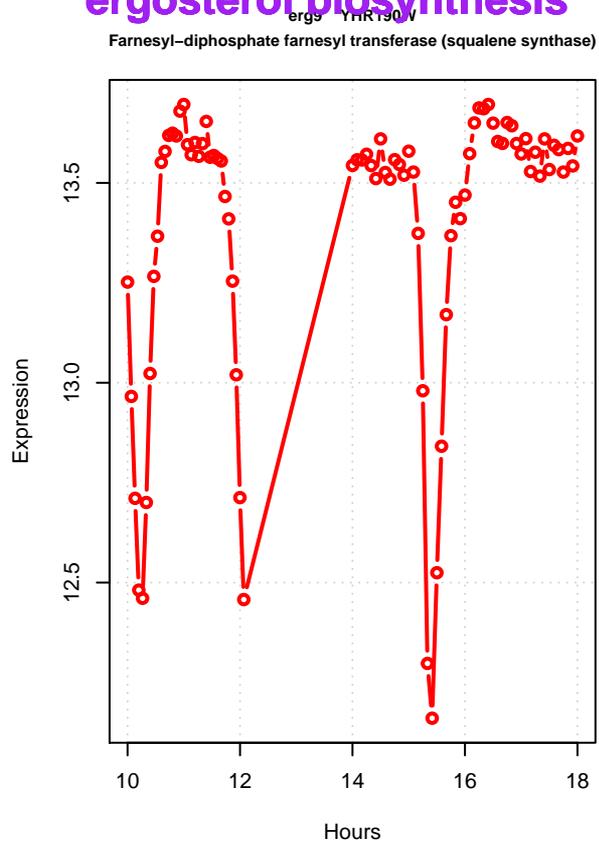
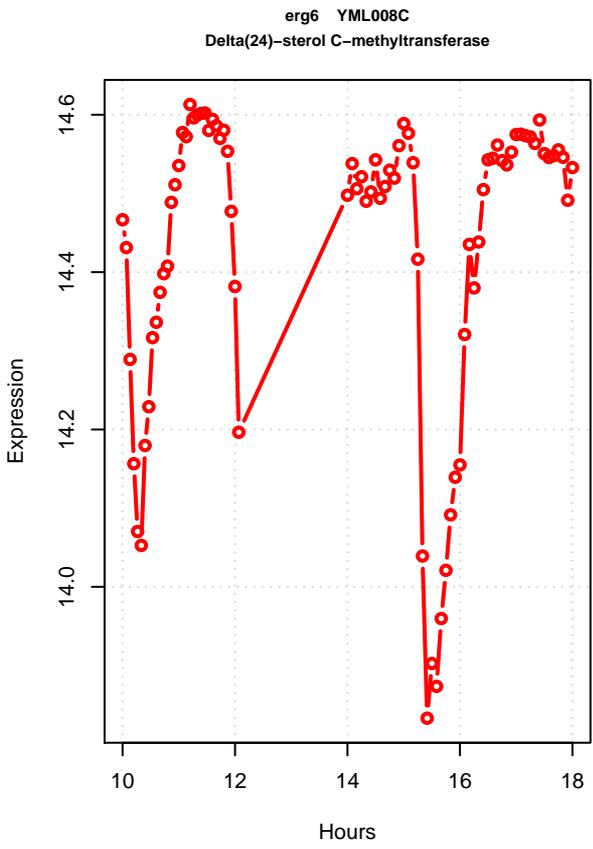


## **ergosterol biosynthesis**

# ergosterol biosynthesis



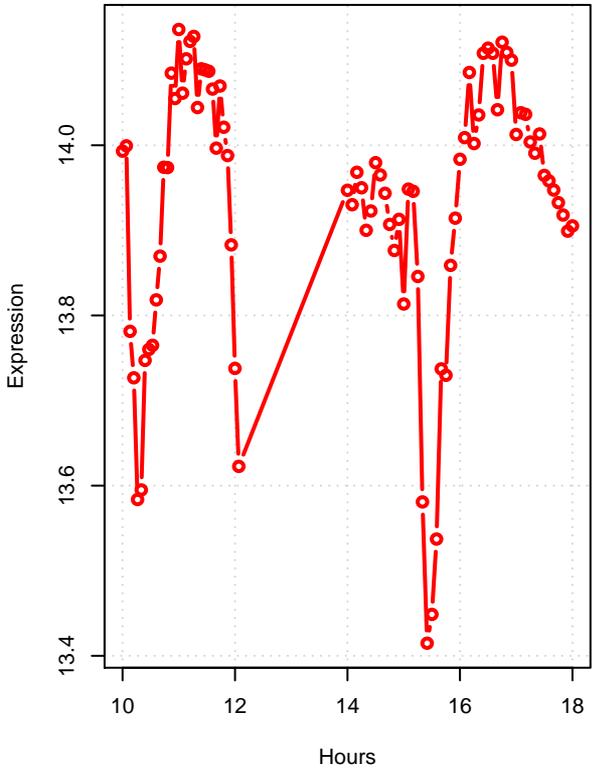
# ergosterol biosynthesis



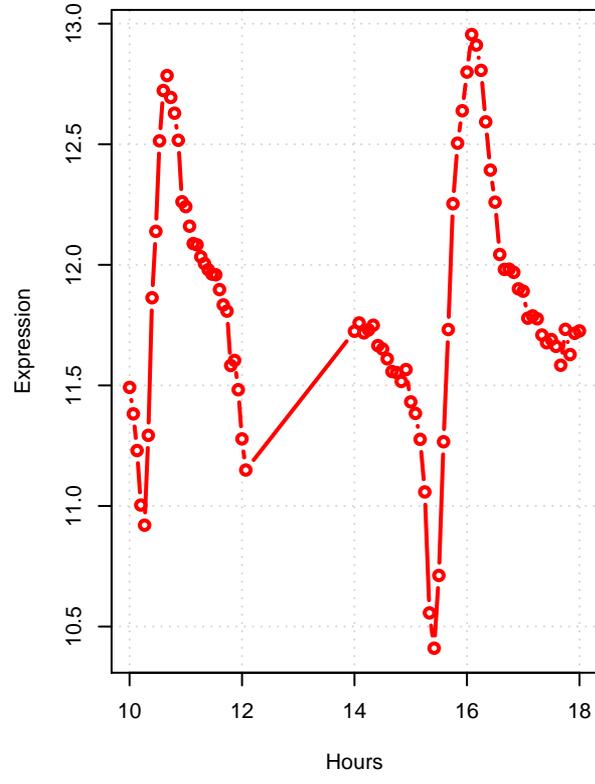
## hexaprenyl diphosphate biosynthesis

# hexaprenyl diphosphate biosynthesis

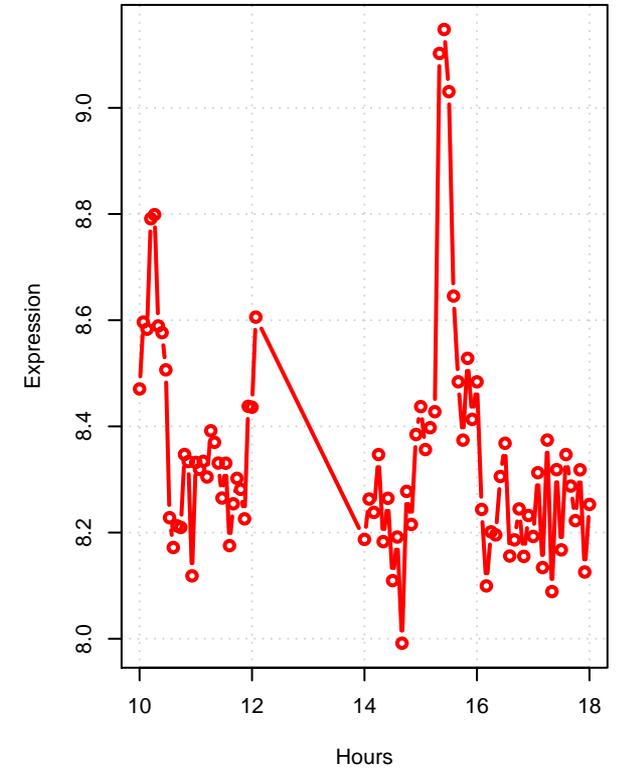
erg20 YJL167W  
Farnesyl pyrophosphate synthetase



coq1 YBR003W  
Hexaprenyl pyrophosphate synthetase



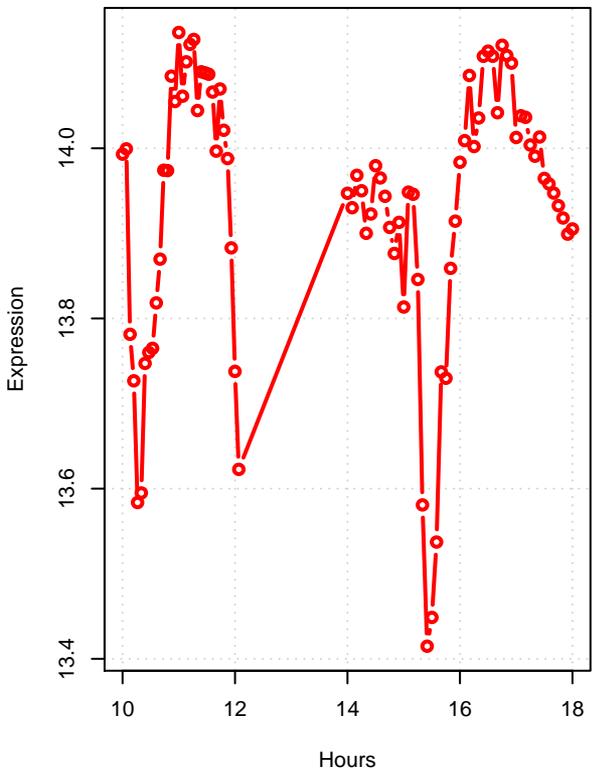
bts1 YPL069C  
Geranylgeranyl diphosphate synthase (GGPS)



**superpathway of ergosterol biosynthesis**

# superpathway of ergosterol biosynthesis

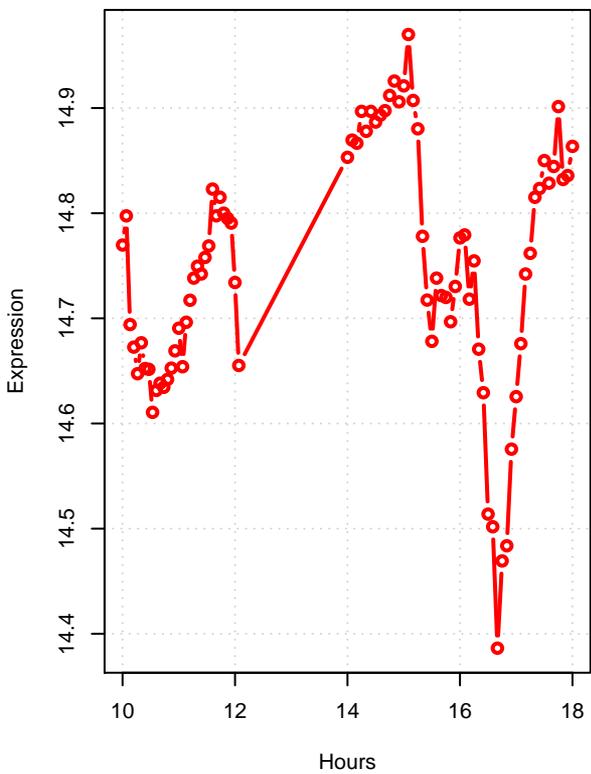
erg20 YJL167W  
Farnesyl pyrophosphate synthetase



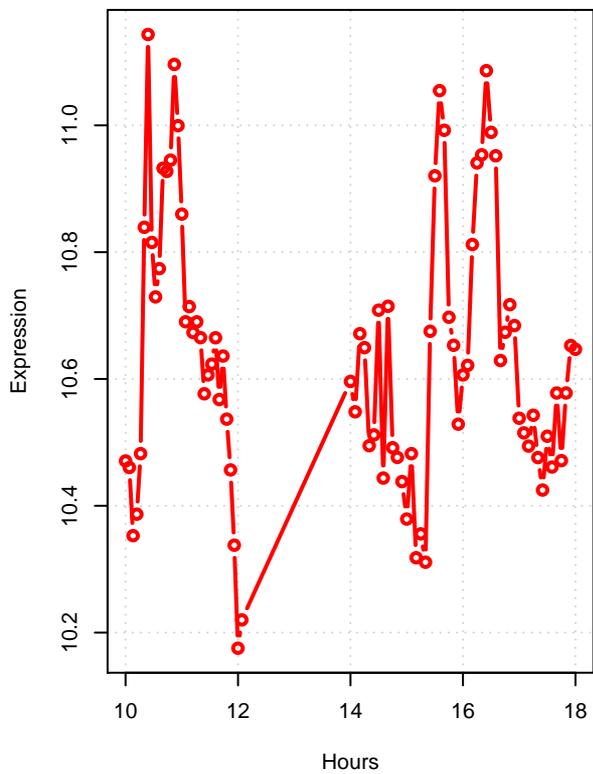
## leucine degradation

# leucine degradation

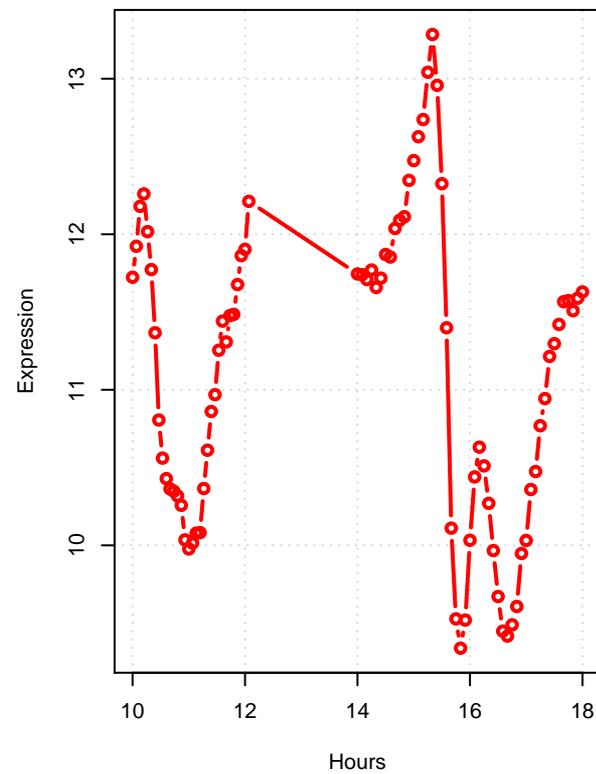
**pdc1 YLR044C**  
Major of three pyruvate decarboxylase isozymes



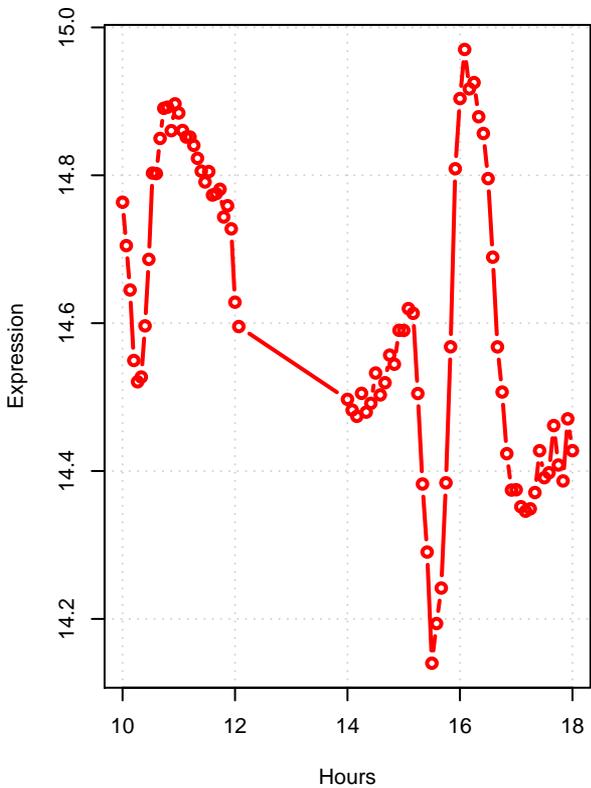
**pdcs YLR134W**  
Minor isoform of pyruvate decarboxylase



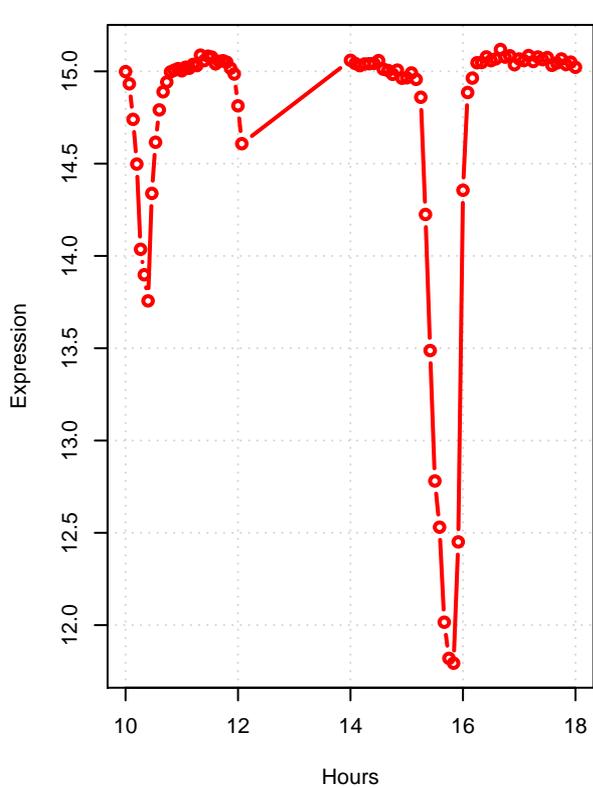
**pdcs6 YGR087C**  
Minor isoform of pyruvate decarboxylase



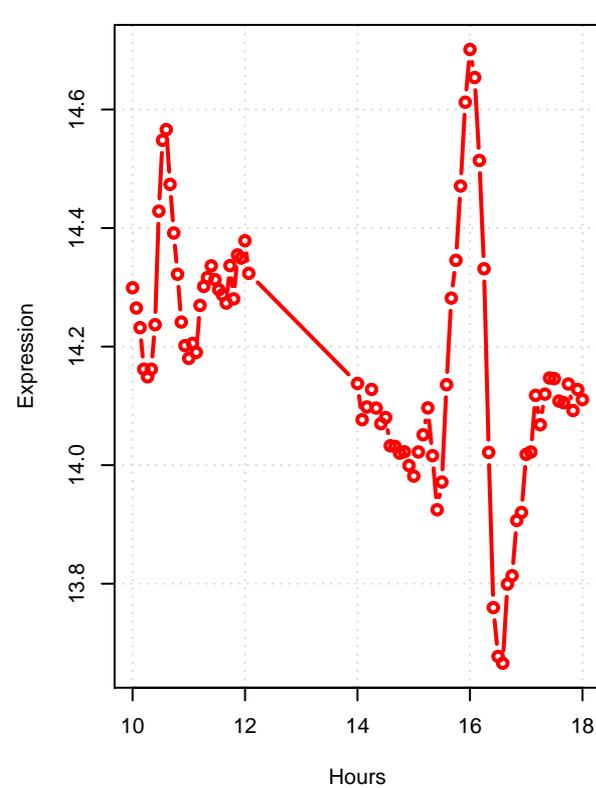
**adh1 YOL086C**  
Alcohol dehydrogenase



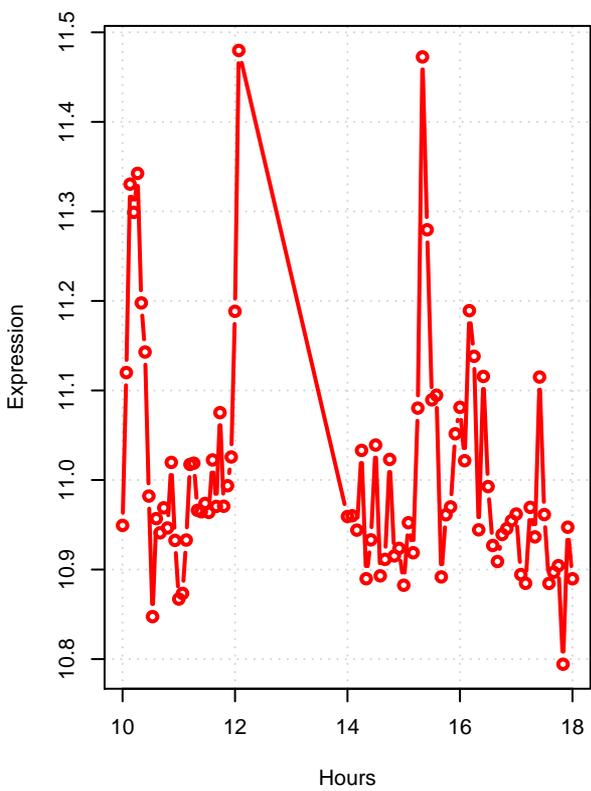
**adh2 YMR303C**  
Glucose-repressible alcohol dehydrogenase II



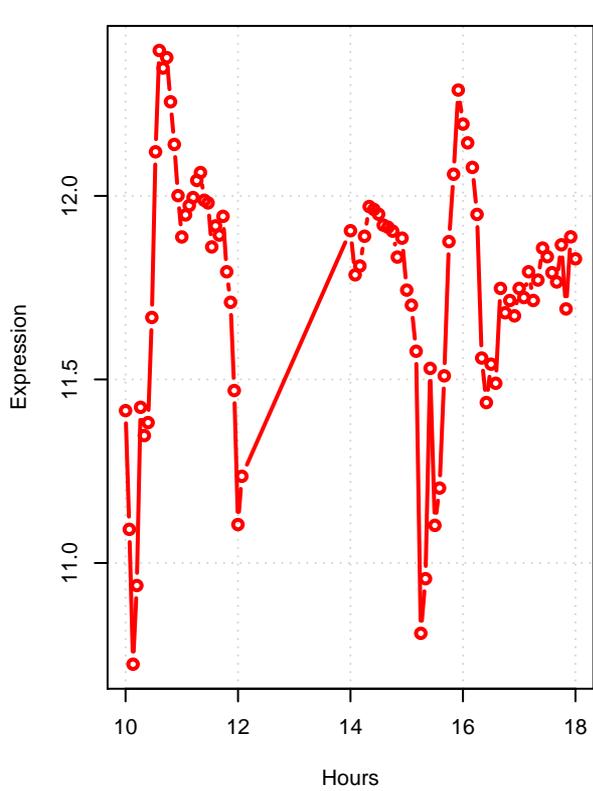
**adh3 YMR083W**  
Mitochondrial alcohol dehydrogenase isozyme III



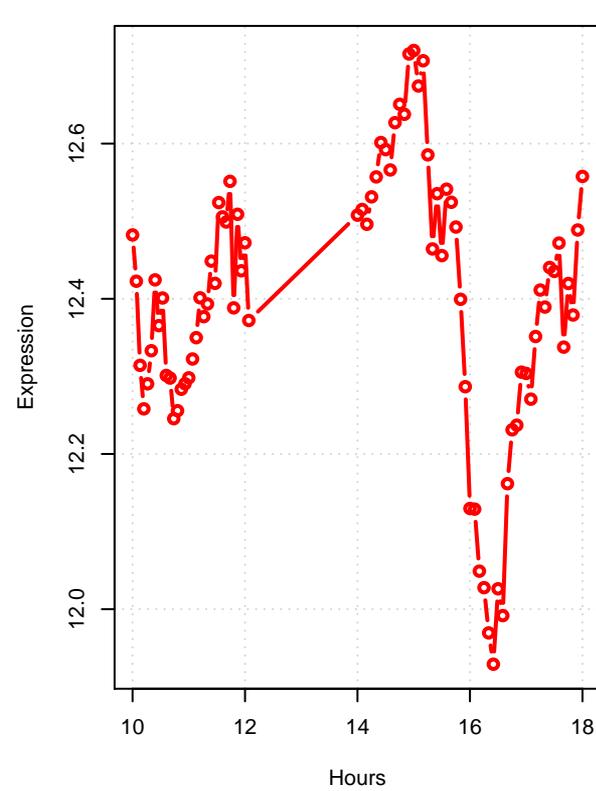
**adh4 YGL256W**  
Alcohol dehydrogenase isoenzyme type IV



**adh5 YBR145W**  
Alcohol dehydrogenase isoenzyme V

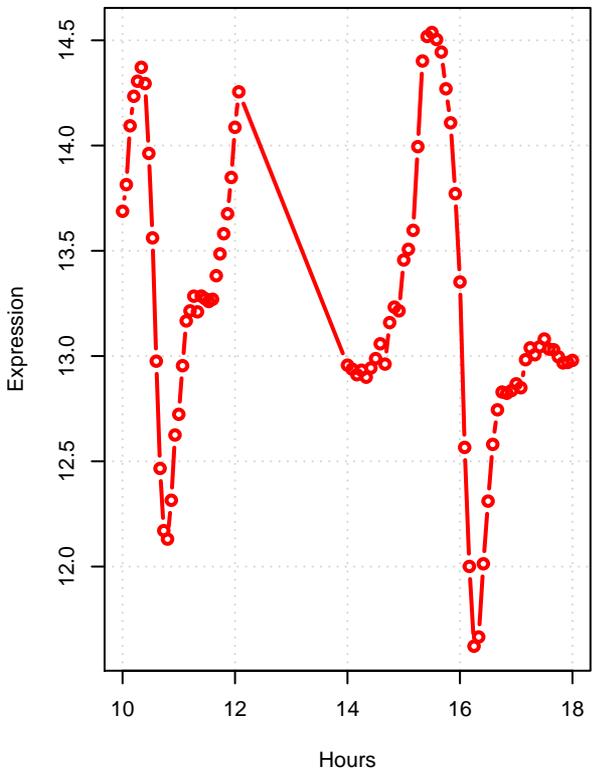


**sfa1 YDL168W**  
Bifunctional alcohol dehydrogenase and formaldehyde dehydrogenase

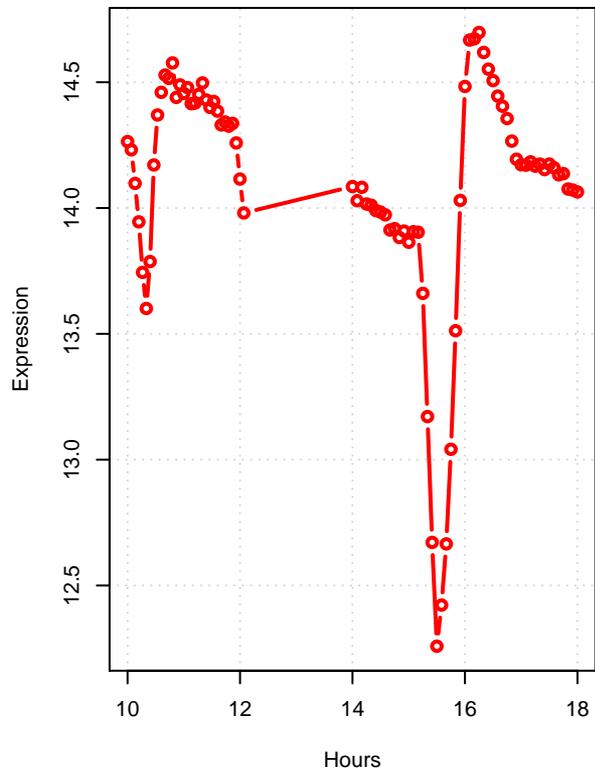


# leucine degradation

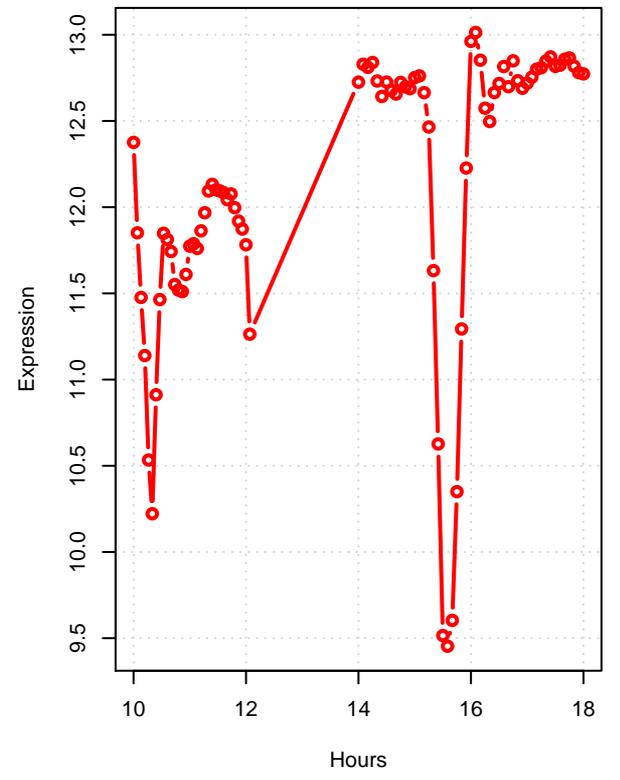
bat1 YHR208W  
Mitochondrial branched-chain amino acid (BCAA) aminotransferase



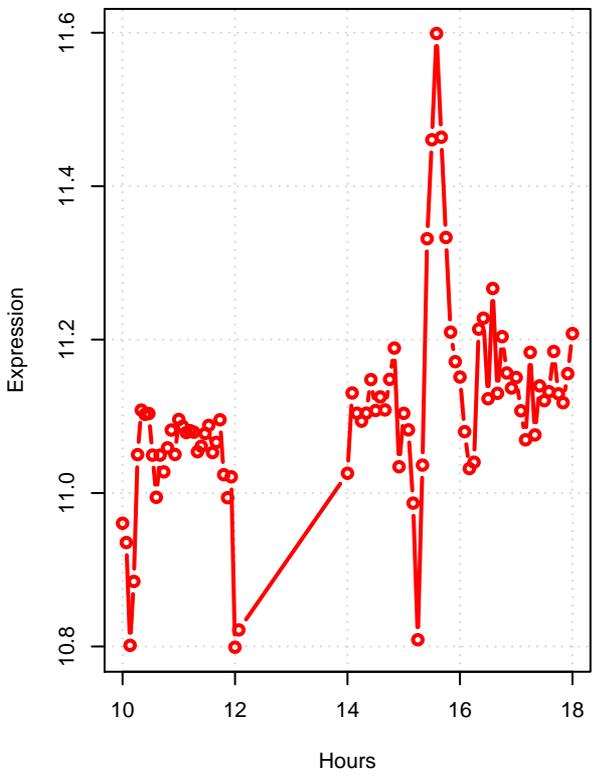
bat2 YJR148W  
Cytosolic branched-chain amino acid (BCAA) aminotransferase



aro10 YDR380W  
Phenylpyruvate decarboxylase



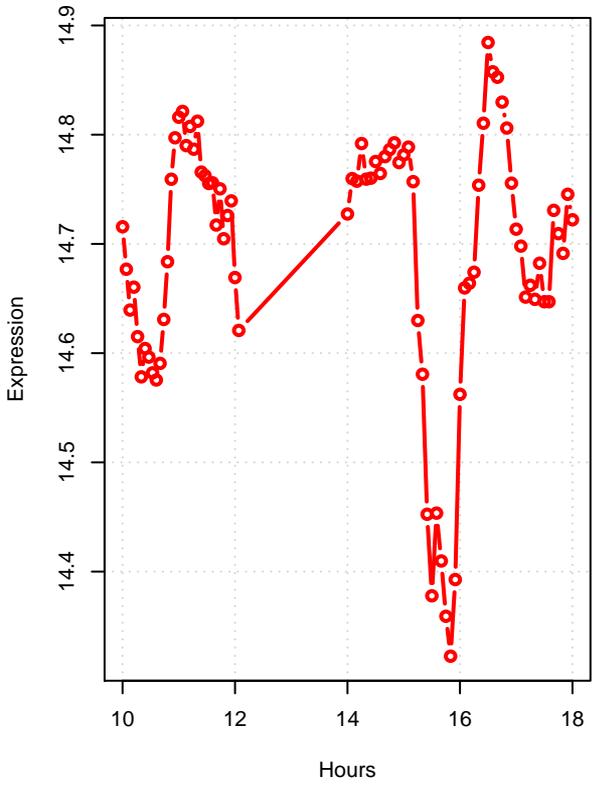
thi3 YDL080C  
Regulatory protein that binds Pdc2p and Thi2p transcription factors



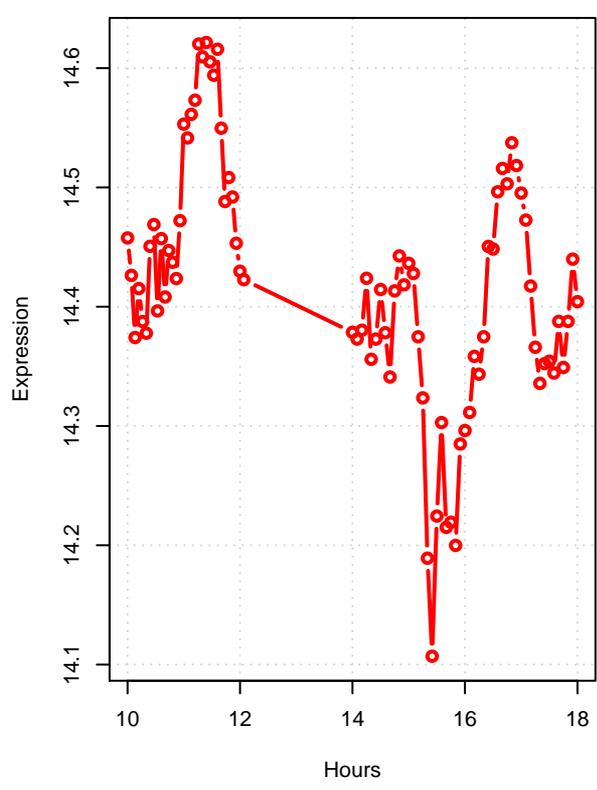
## **fatty acid biosynthesis (concise)**

# fatty acid biosynthesis (concise)

fas1 YKL182W  
Beta subunit of fatty acid synthetase

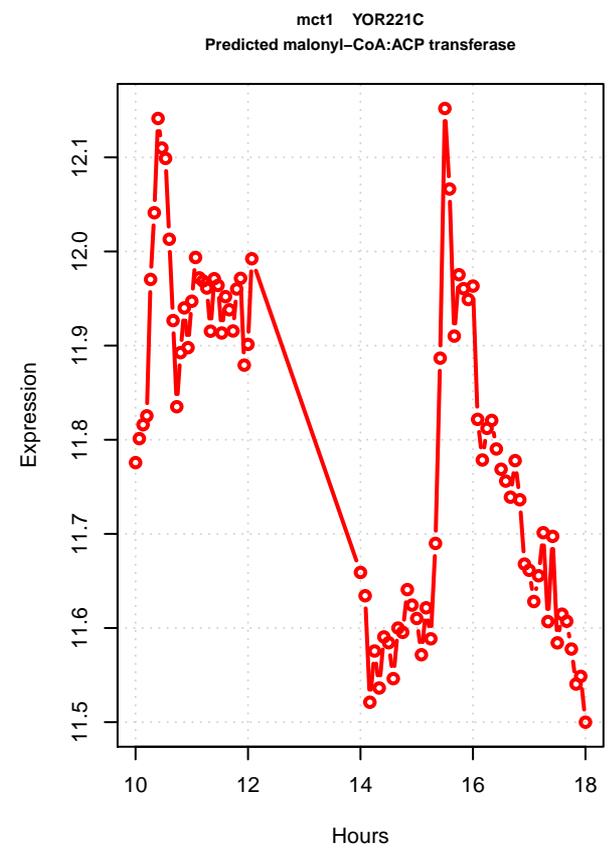
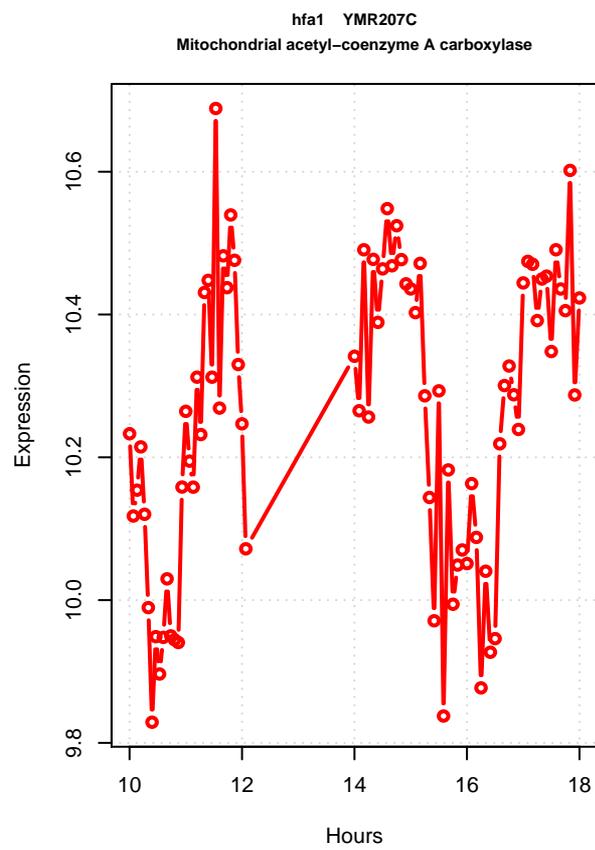
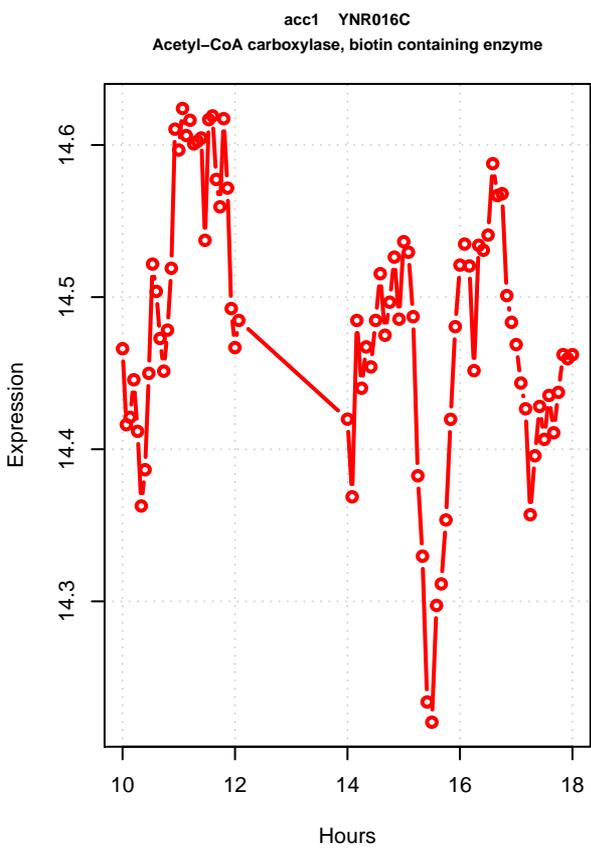
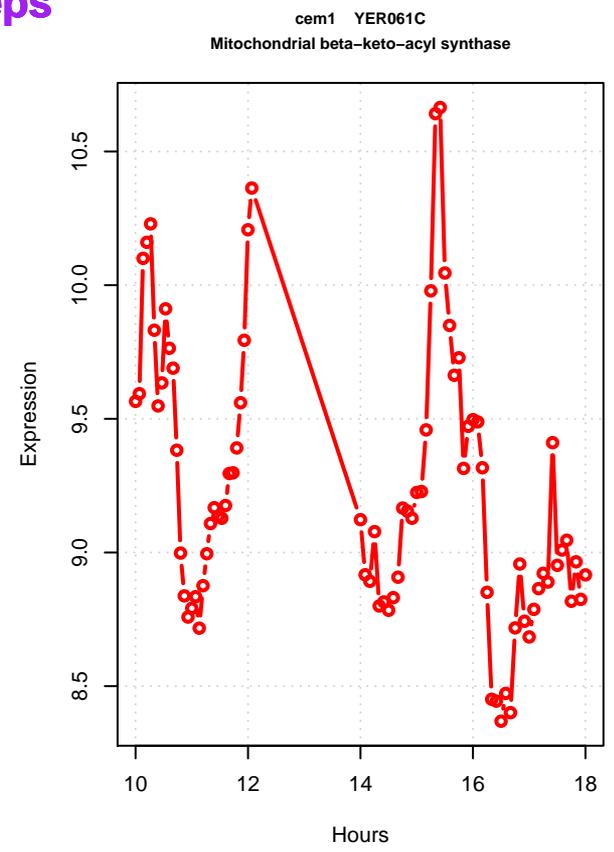
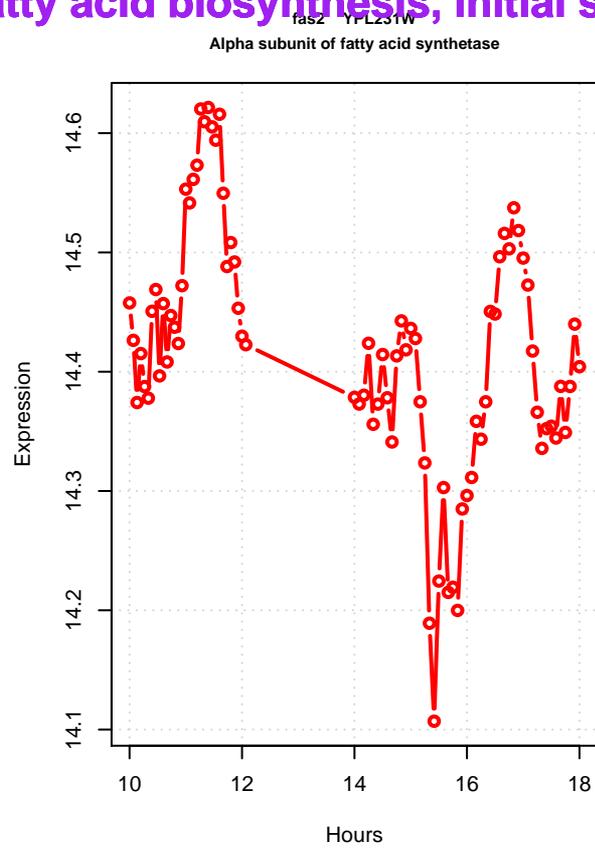
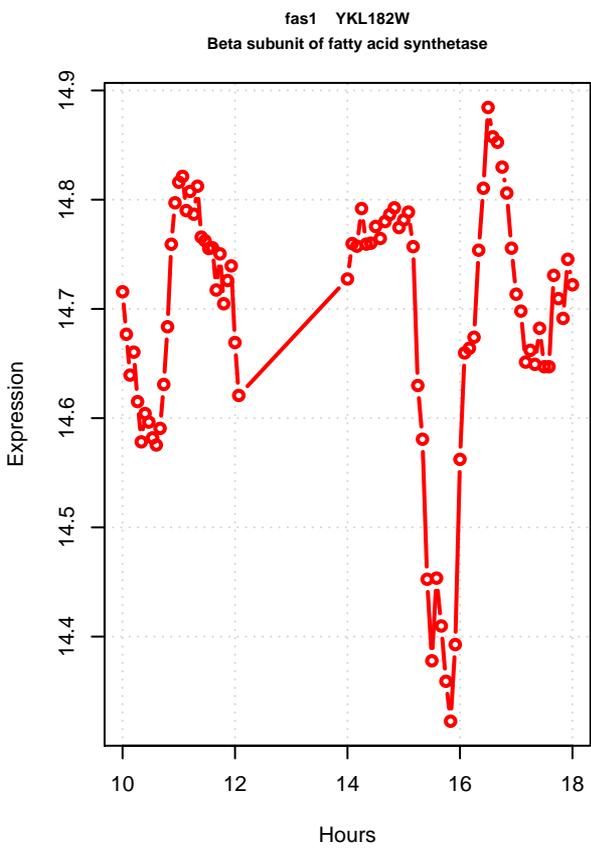


fas2 YPL251W  
Alpha subunit of fatty acid synthetase



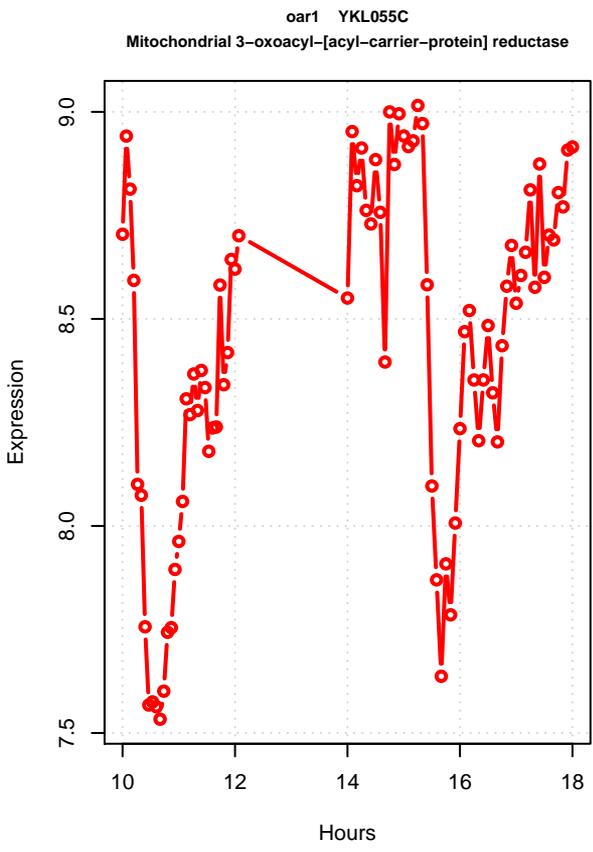
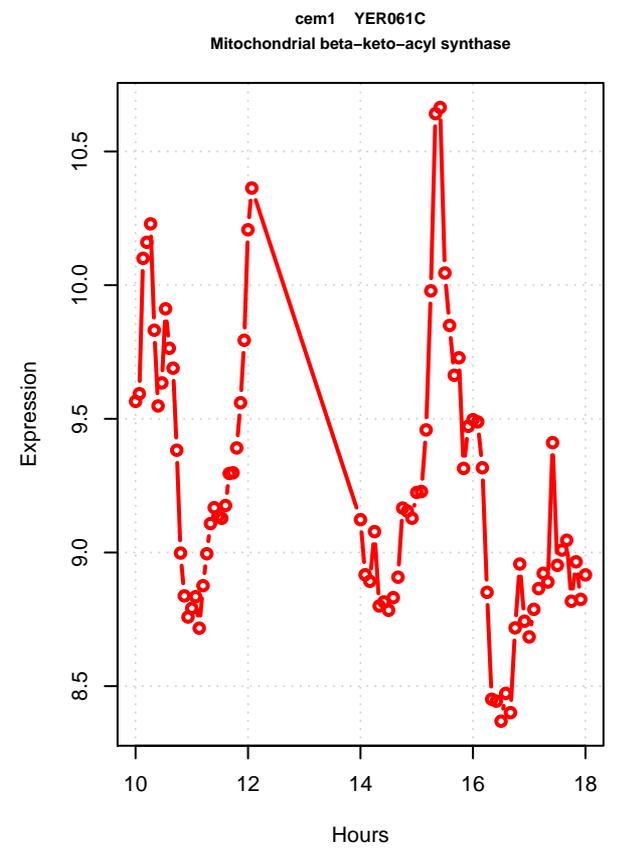
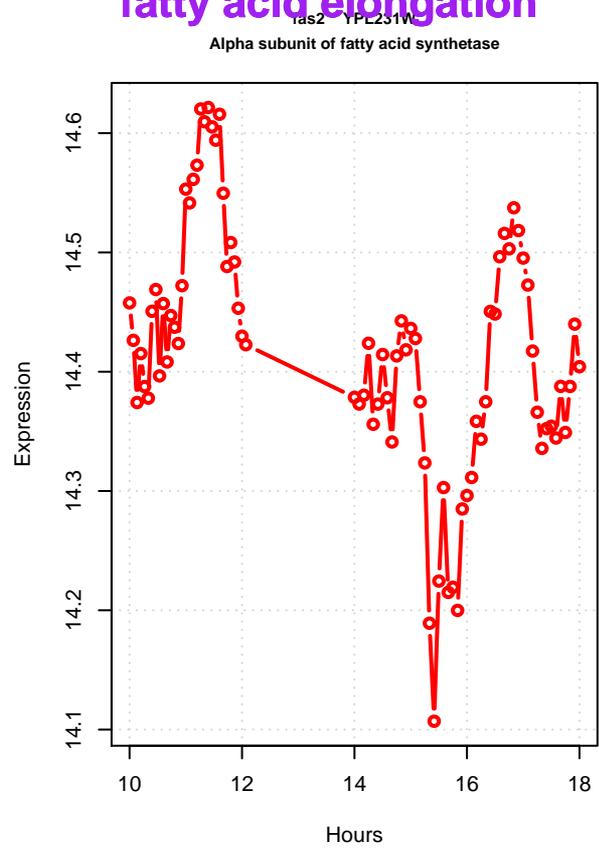
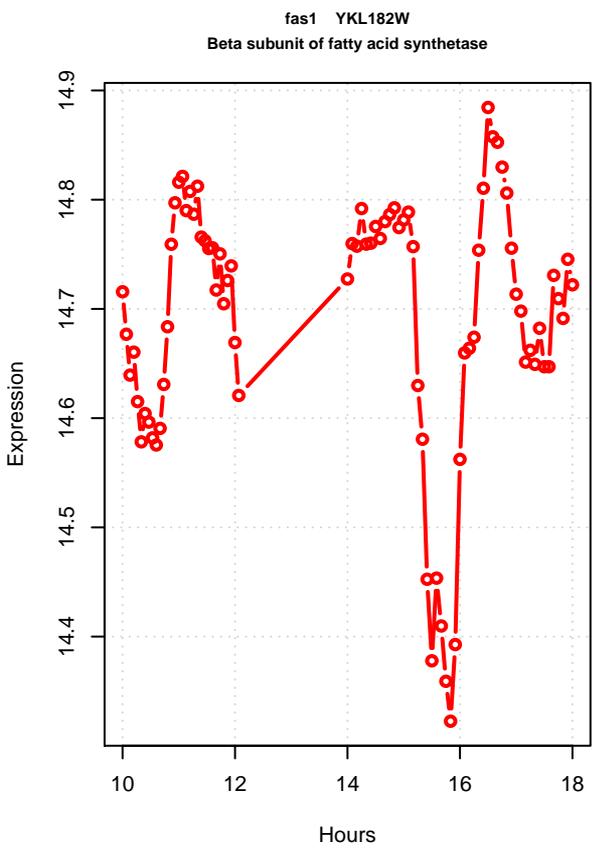
## **fatty acid biosynthesis, initial steps**

# fatty acid biosynthesis, initial steps



**fatty acid elongation**

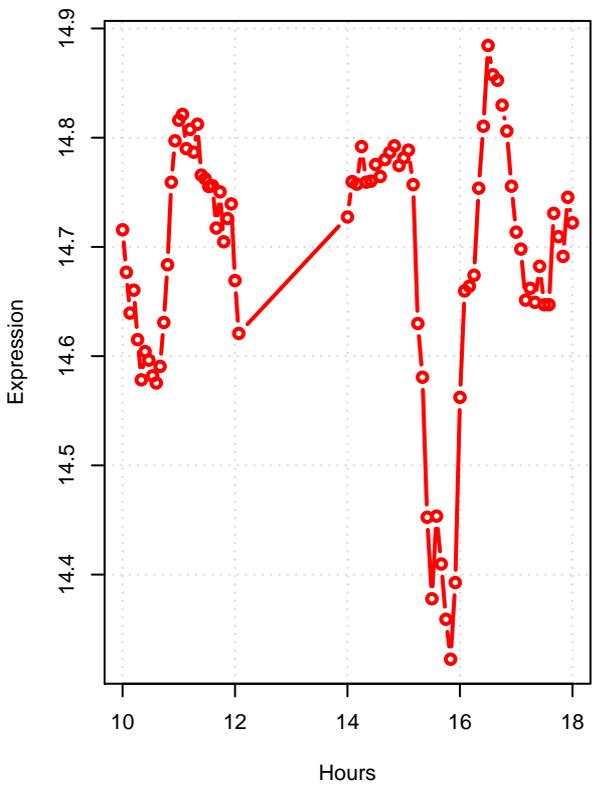
# fatty acid elongation



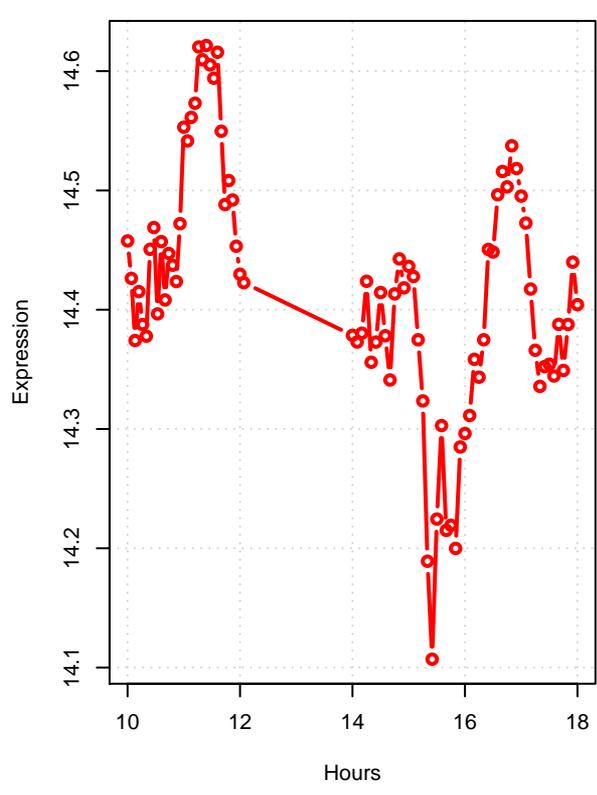
## myristate biosynthesis

# myristate biosynthesis

fas1 YKL182W  
Beta subunit of fatty acid synthetase



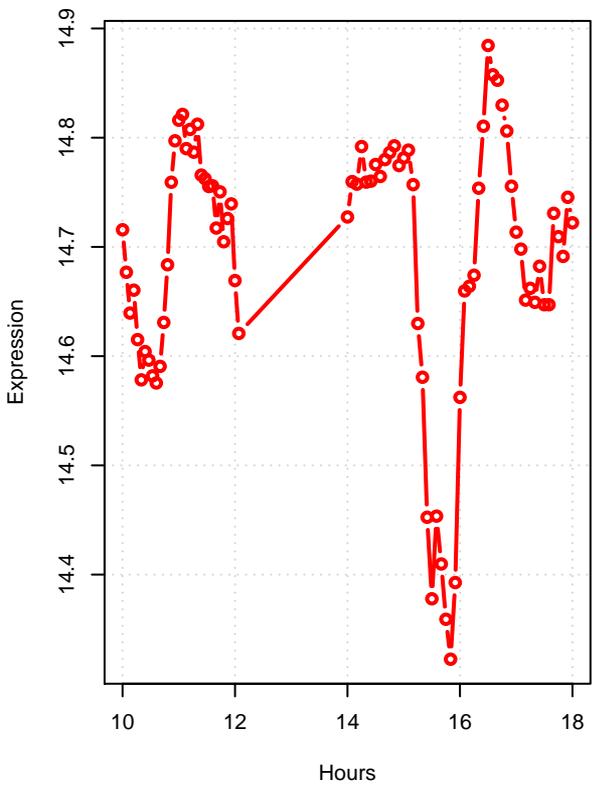
fas2 YPL237W  
Alpha subunit of fatty acid synthetase



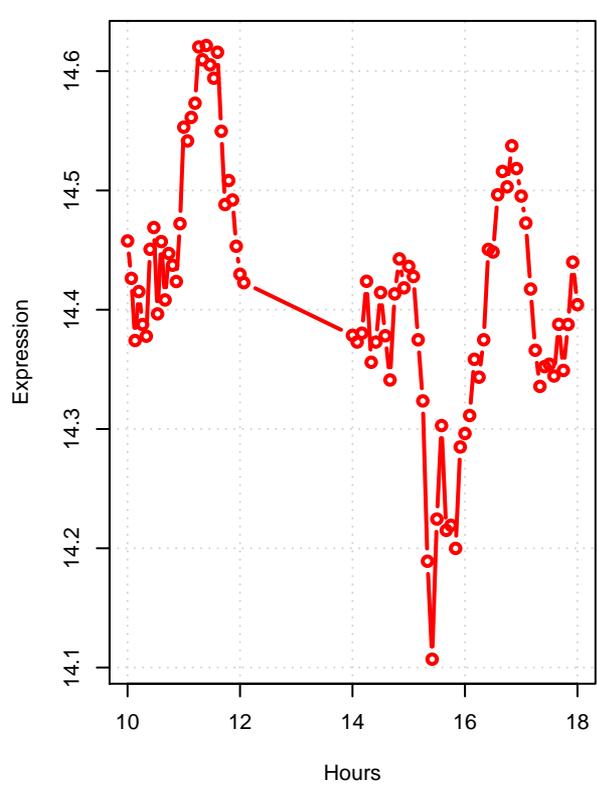
## palmitate biosynthesis

# palmitate biosynthesis

fas1 YKL182W  
Beta subunit of fatty acid synthetase



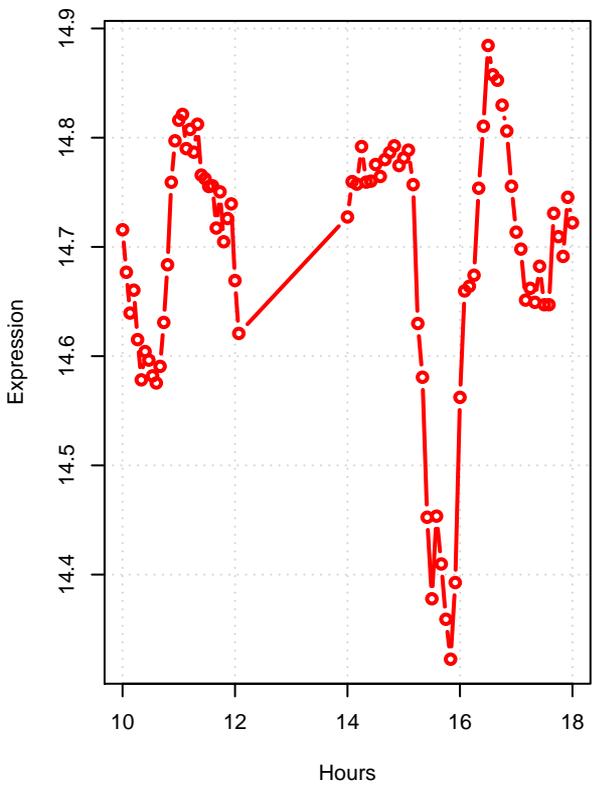
fas2 YPL23.W  
Alpha subunit of fatty acid synthetase



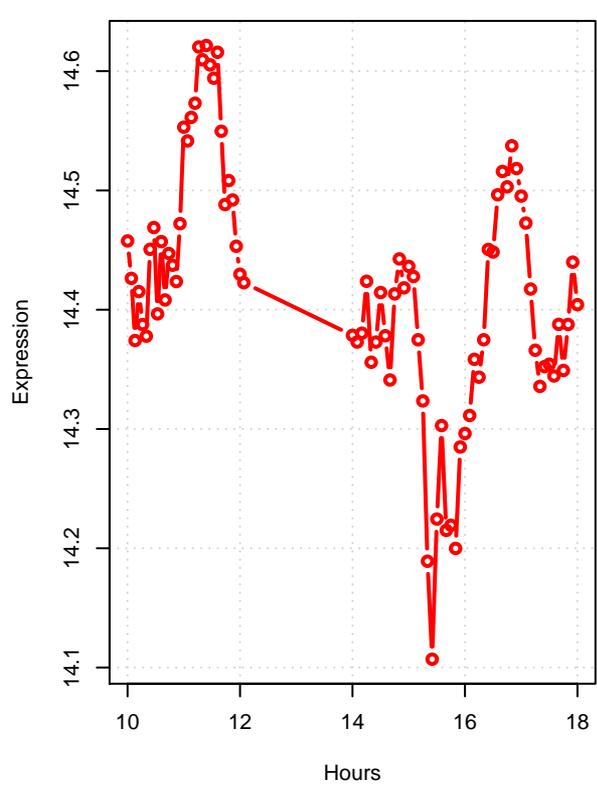
# stearate biosynthesis

# stearate biosynthesis

fas1 YKL182W  
Beta subunit of fatty acid synthetase



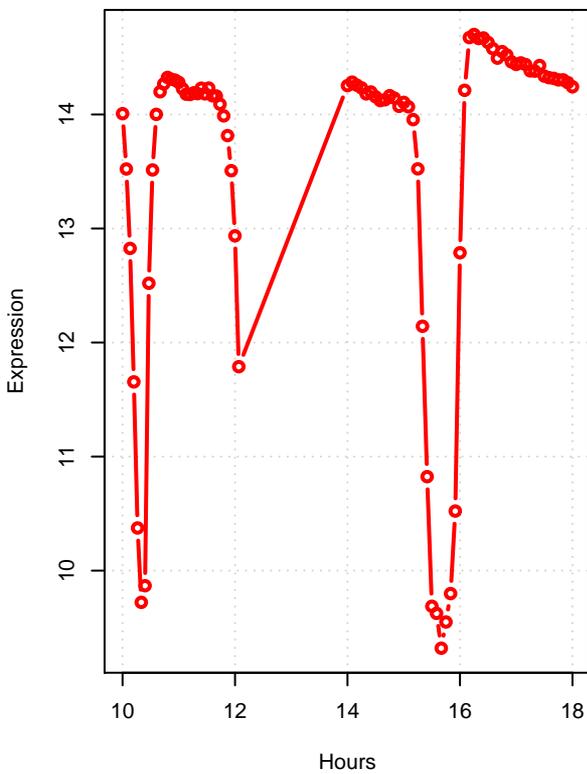
fas2 YPL231W  
Alpha subunit of fatty acid synthetase



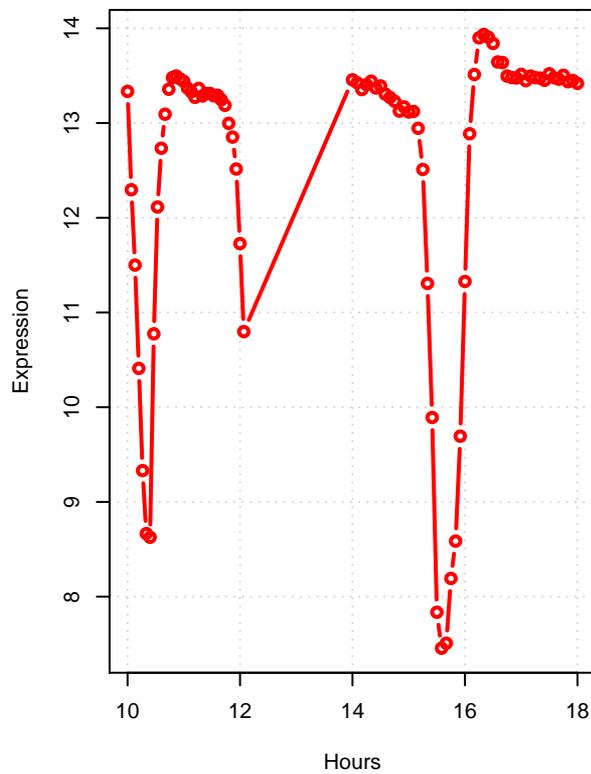
## **fatty acid oxidation pathway**

# fatty acid oxidation pathway

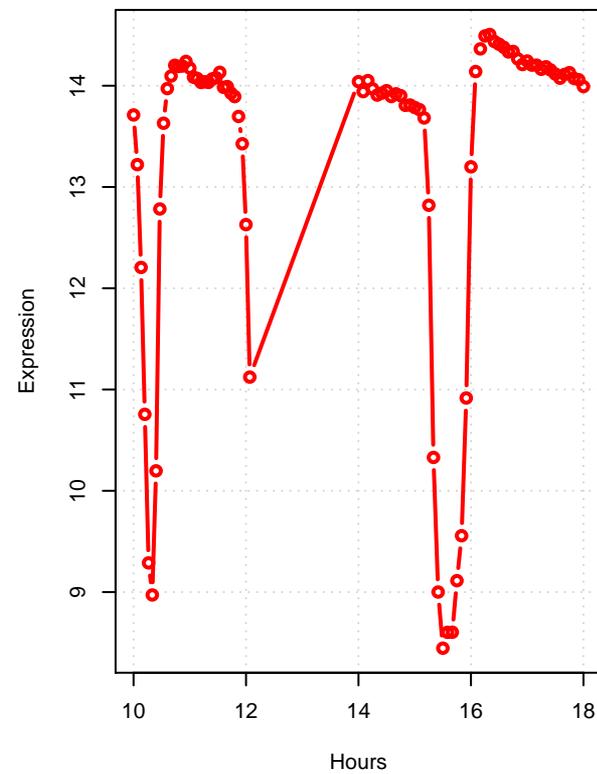
**fox2 YKR009C**  
3-hydroxyacyl-CoA dehydrogenase and enoyl-CoA hydratase



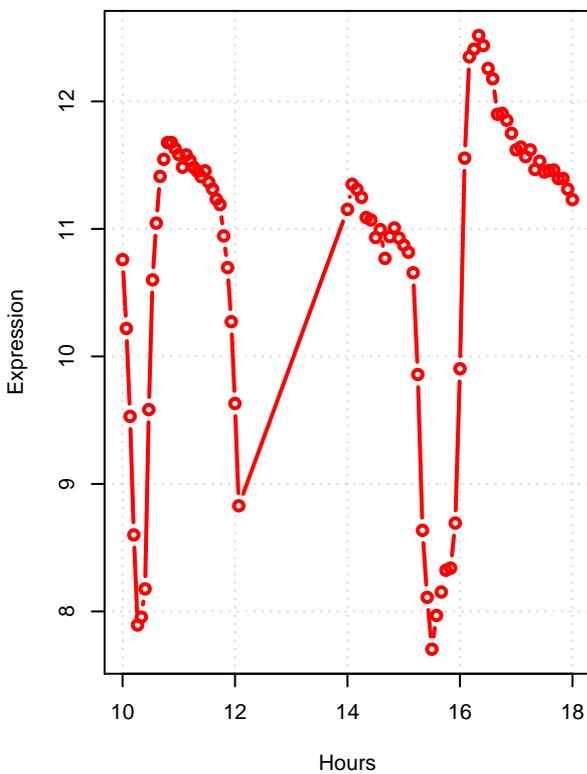
**por1 YL160C**  
3-ketoacyl-CoA thiolase with broad chain length specificity



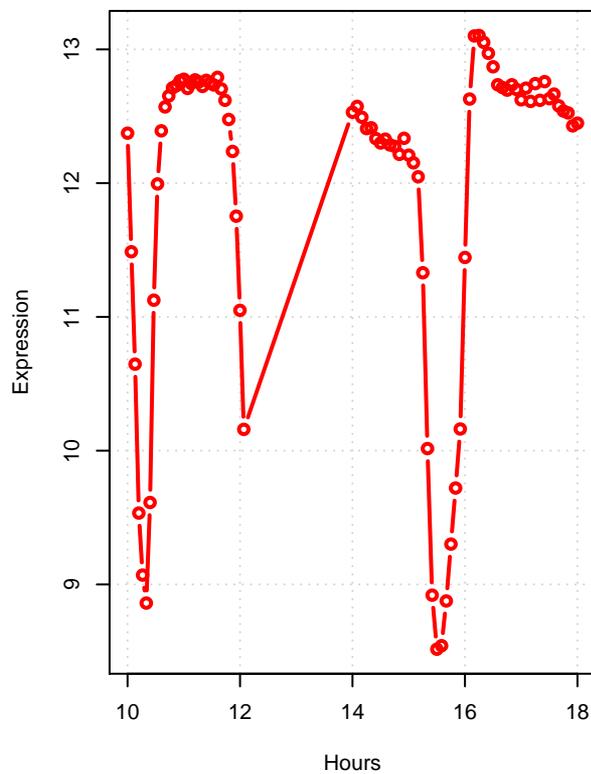
**pox1 YGL205W**  
Fatty-acyl coenzyme A oxidase



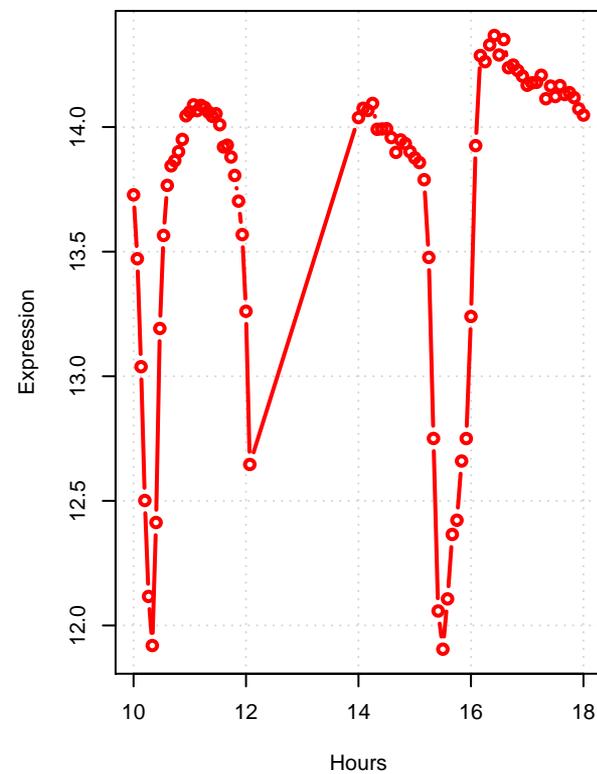
**dci1 YOR180C**  
Peroxisomal protein



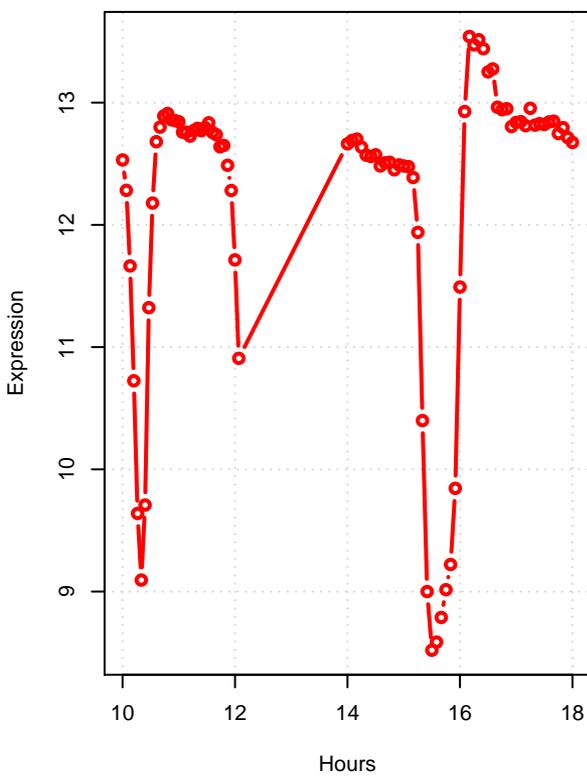
**eci1 YLR284C**  
Peroxisomal delta3,delta2-enoyl-CoA isomerase



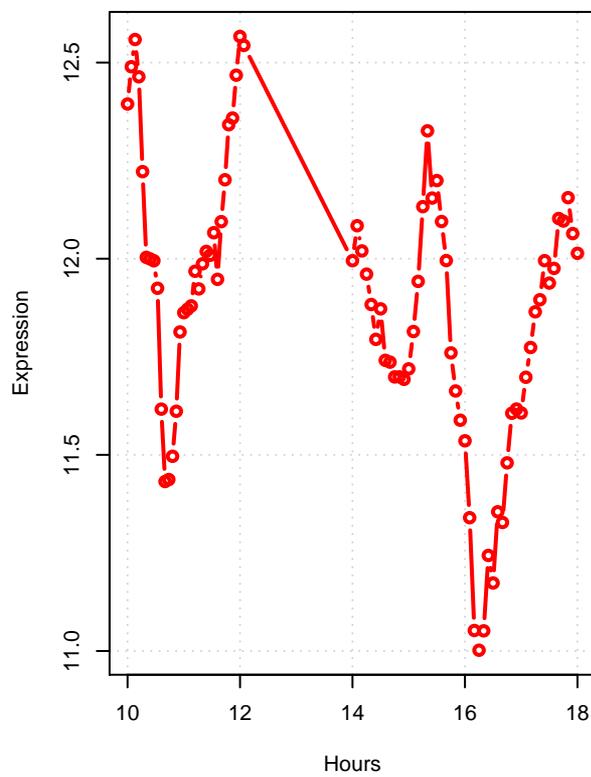
**faa1 YOR317W**  
Long chain fatty acyl-CoA synthetase



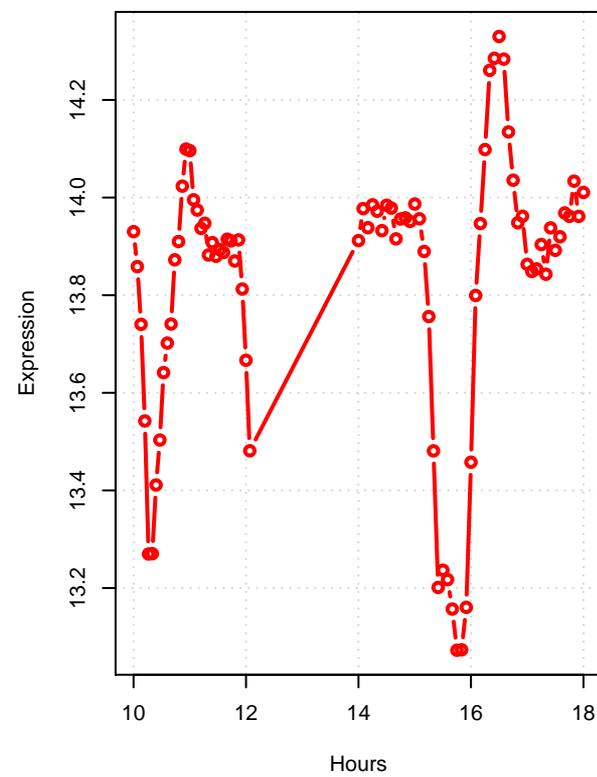
**faa2 YER015W**  
Medium chain fatty acyl-CoA synthetase



**faa3 YIL009W**  
Long chain fatty acyl-CoA synthetase



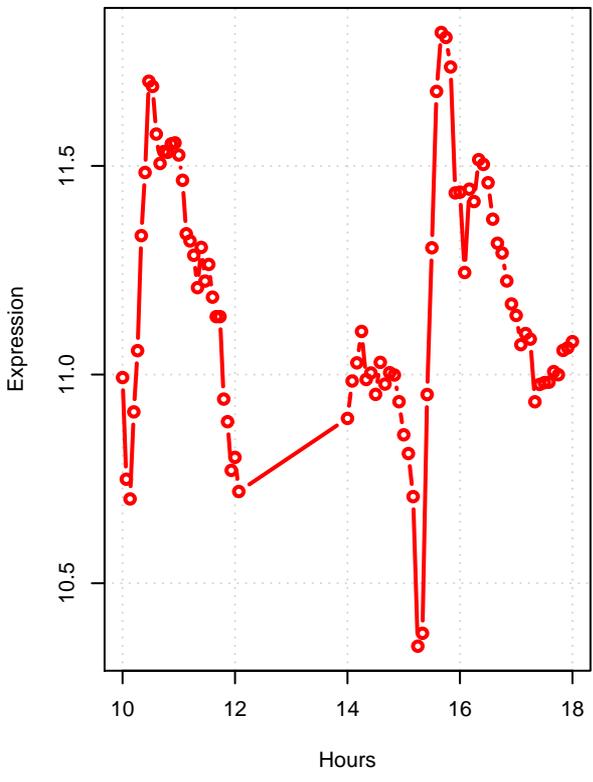
**faa4 YMR246W**  
Long chain fatty acyl-CoA synthetase



# fatty acid oxidation pathway

fat1 YBR041W

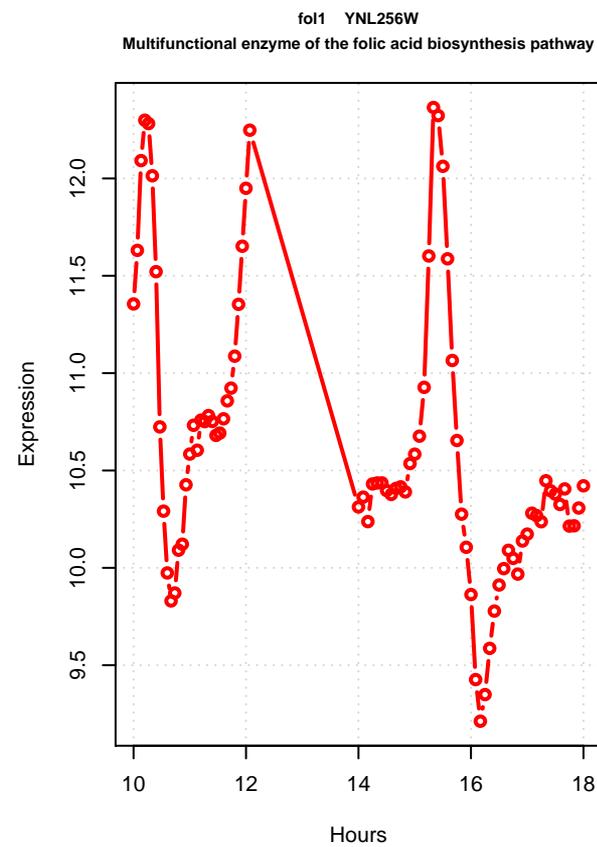
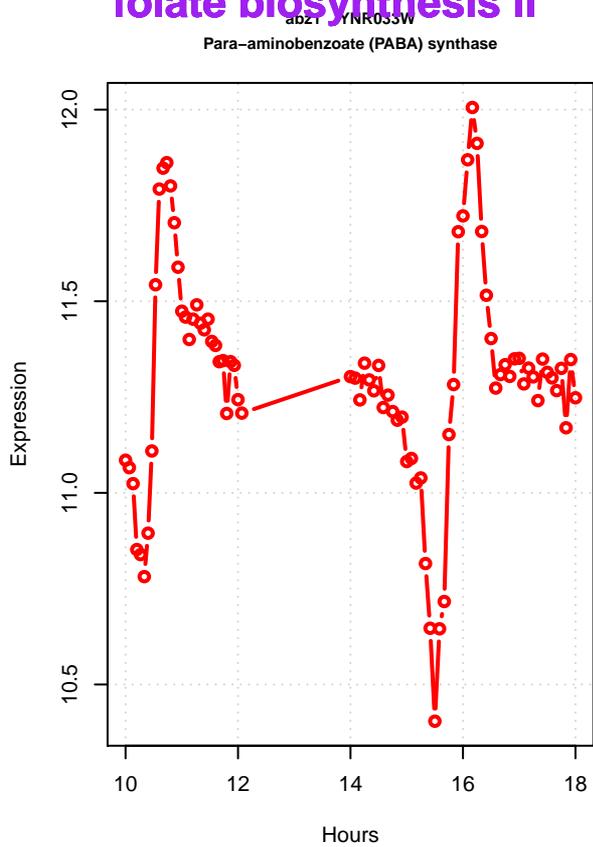
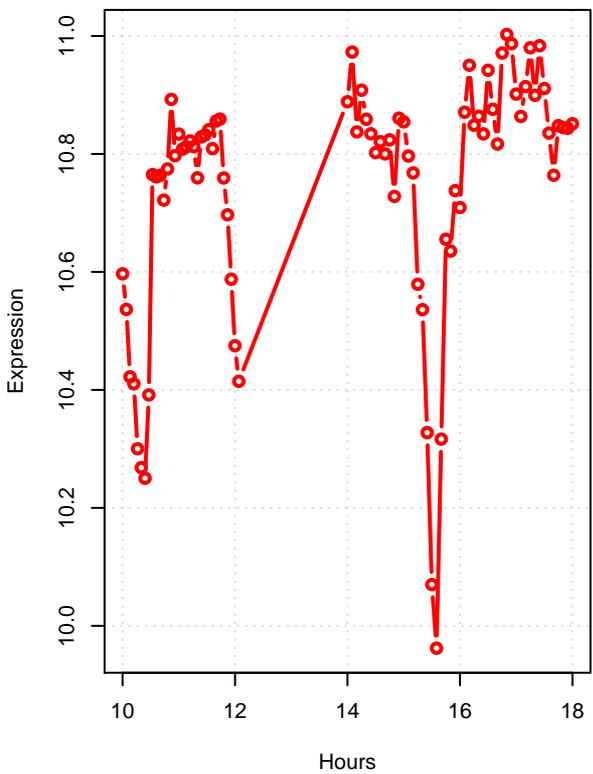
Very long chain fatty acyl-CoA synthetase and fatty acid transporter



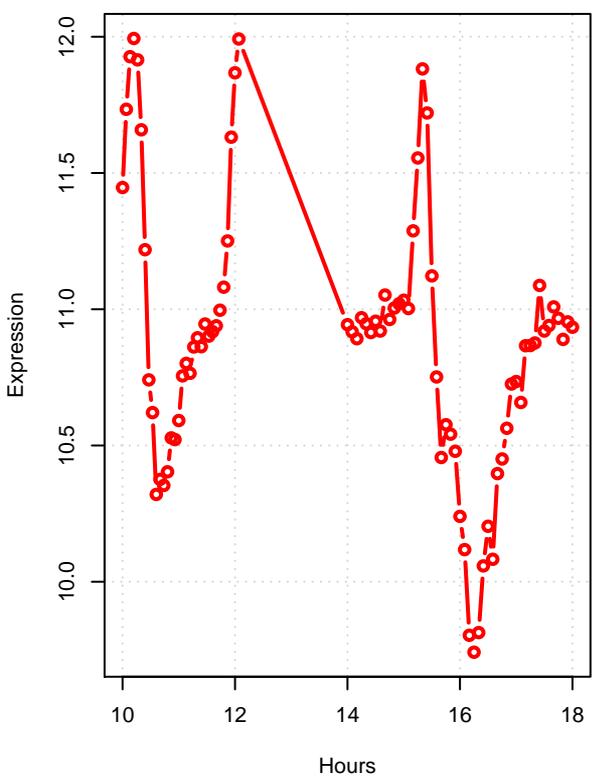
## folate biosynthesis II

# folate biosynthesis II

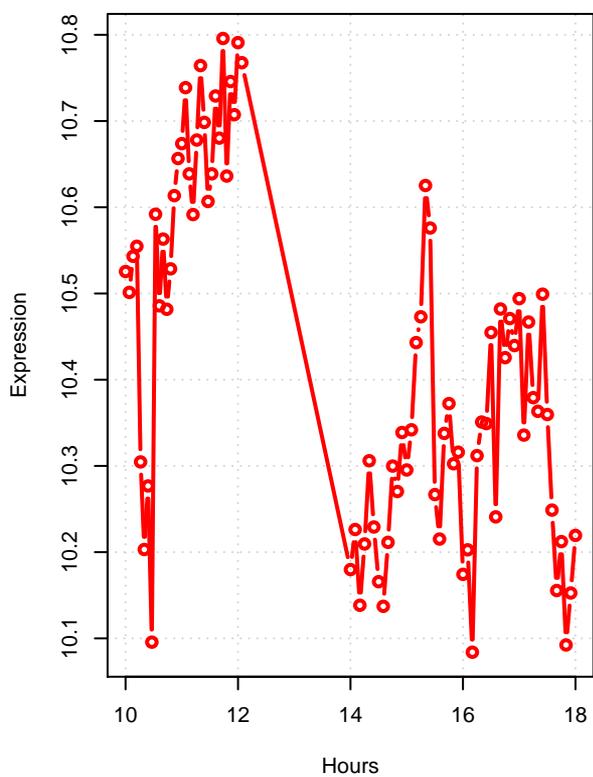
abz2 YMR289W  
Aminodeoxychorismate lyase (4-amino-4-deoxychorismate lyase)



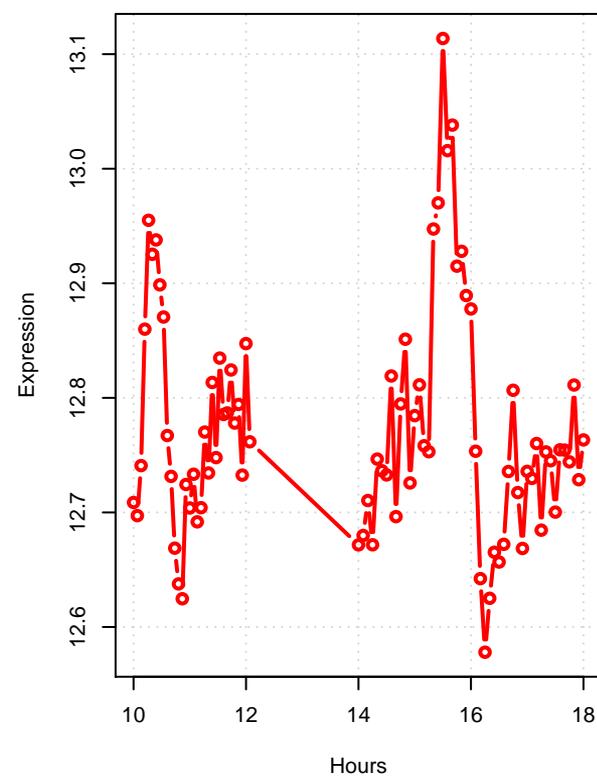
dfr1 YOR236W  
Dihydrofolate reductase involved in tetrahydrofolate biosynthesis



fol3 YMR113W  
Dihydrofolate synthetase, involved in folic acid biosynthesis



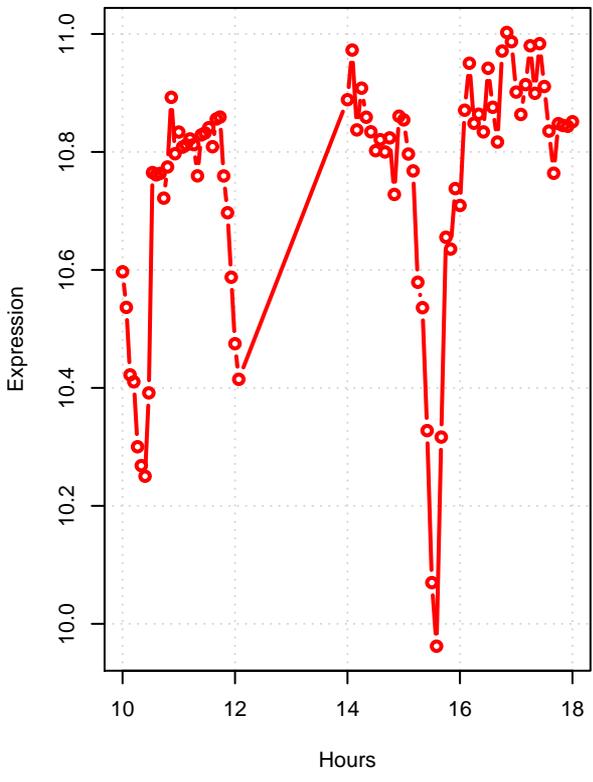
fol2 YGR267C  
GTP-cyclohydrolase I, catalyzes first step in folic acid biosynthesis



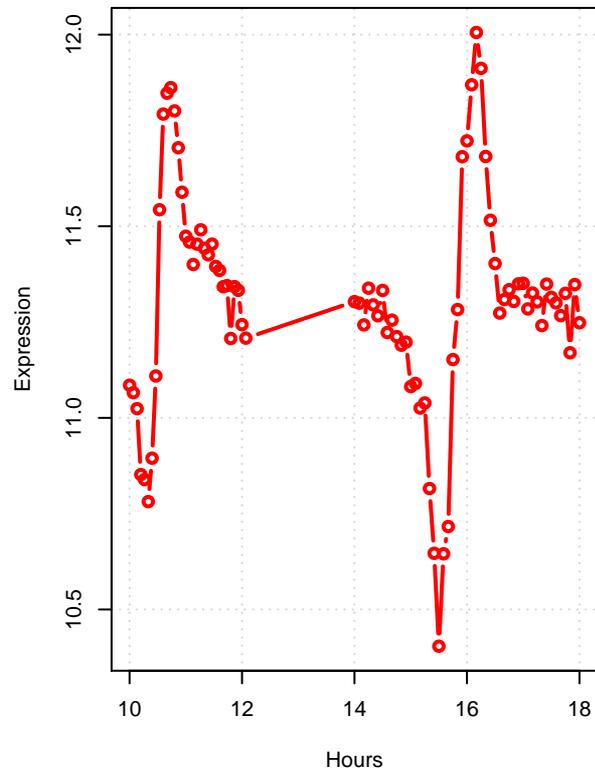
## **p-aminobenzoate biosynthesis**

# p-aminobenzoate biosynthesis

abz2 YMR289W  
Aminodeoxychorismate lyase (4-amino-4-deoxychorismate lyase)

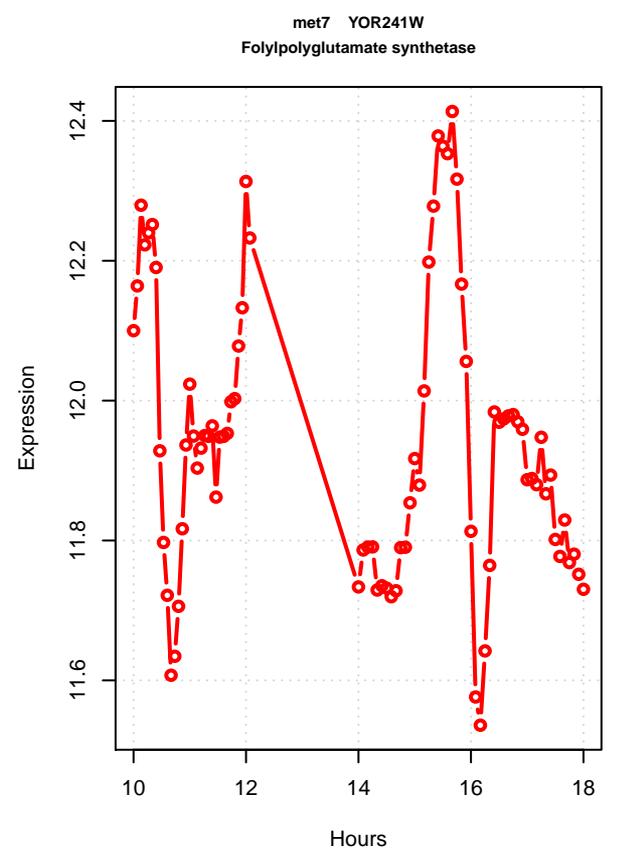
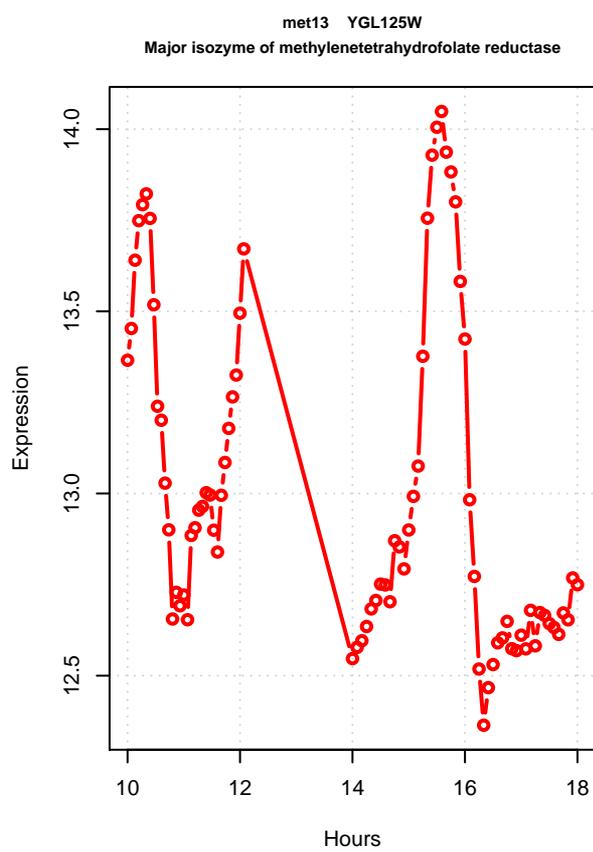
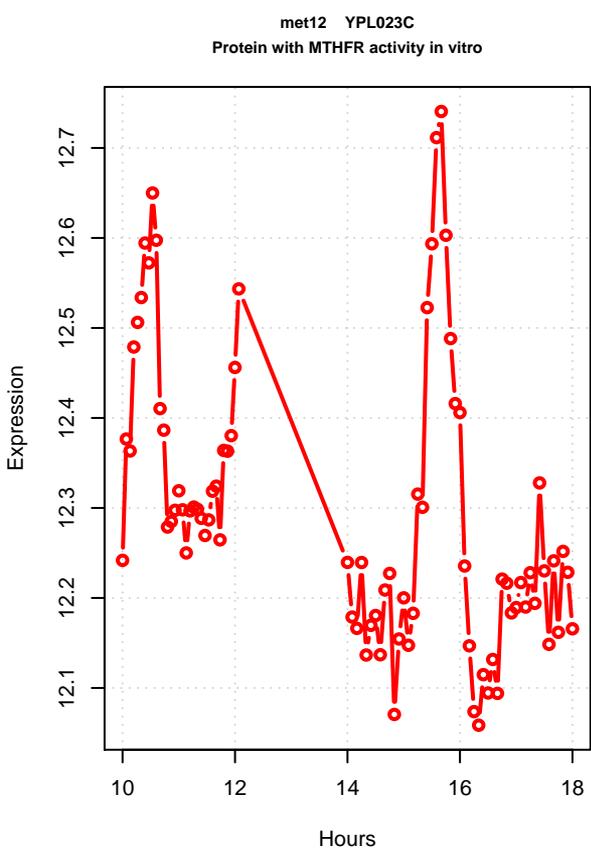
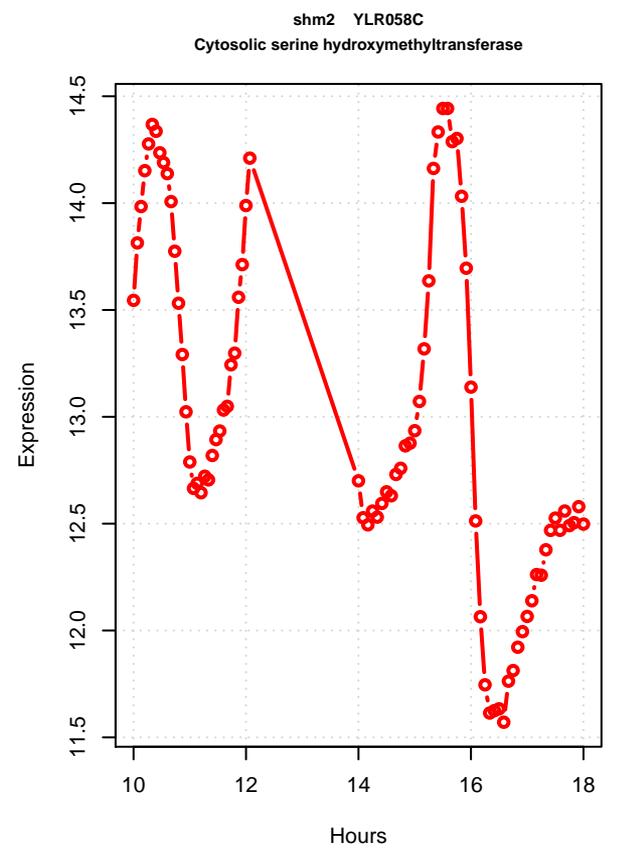
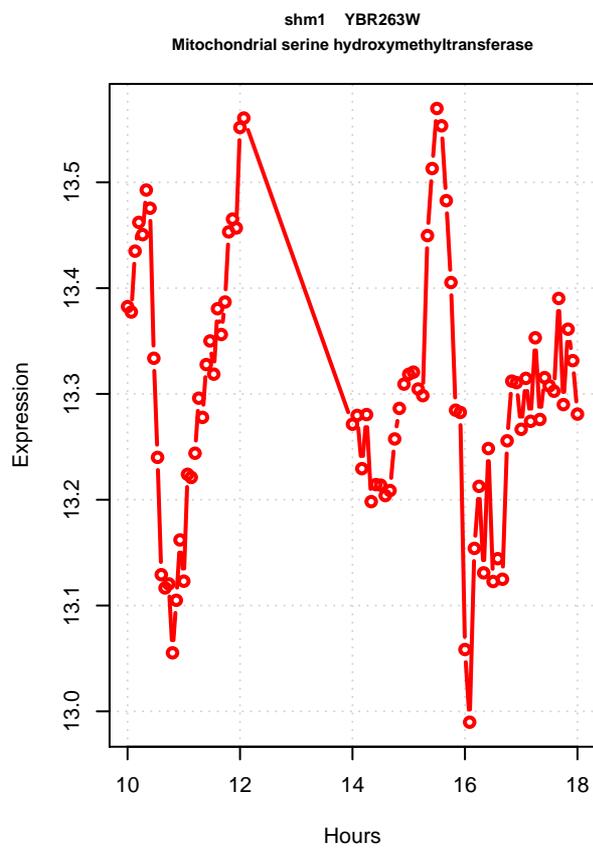
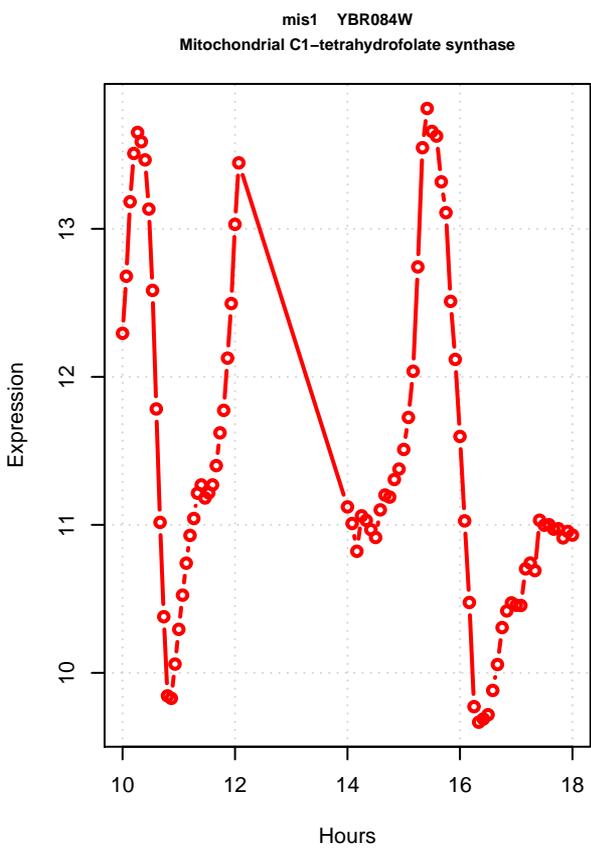
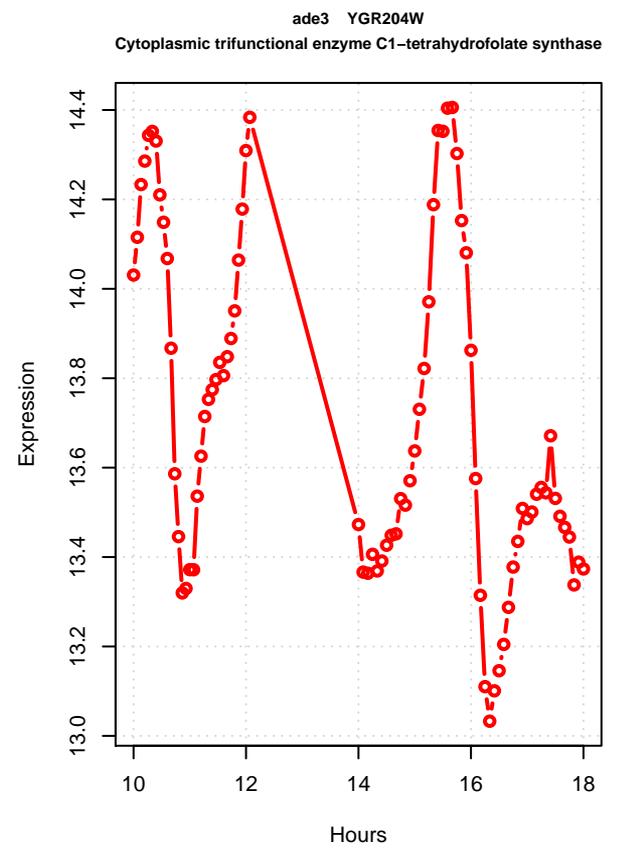
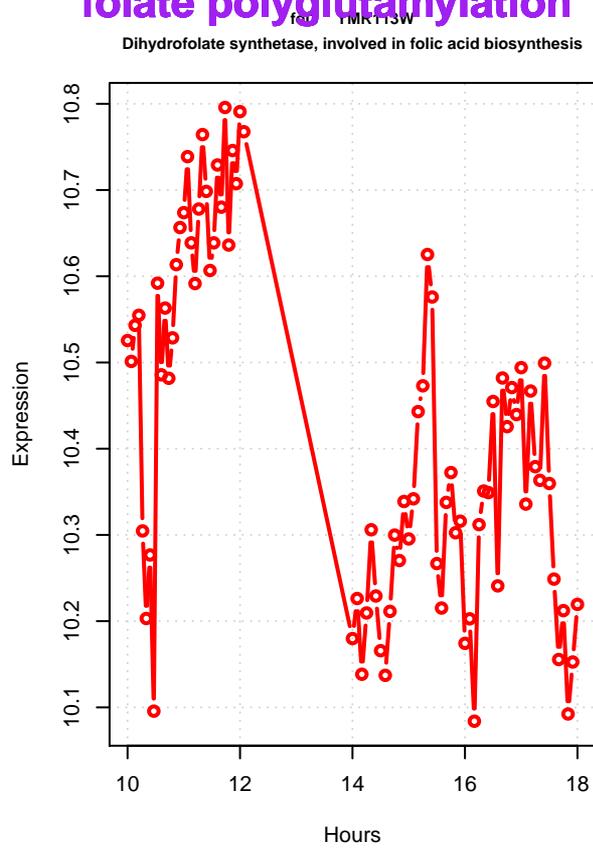
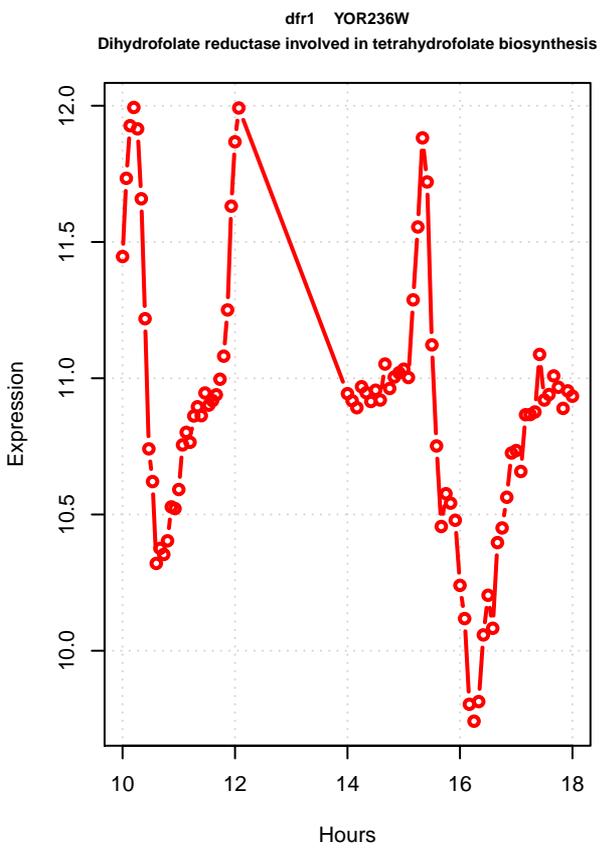


abz1 YNR035W  
Para-aminobenzoate (PABA) synthase



**folate polyglutamylation**

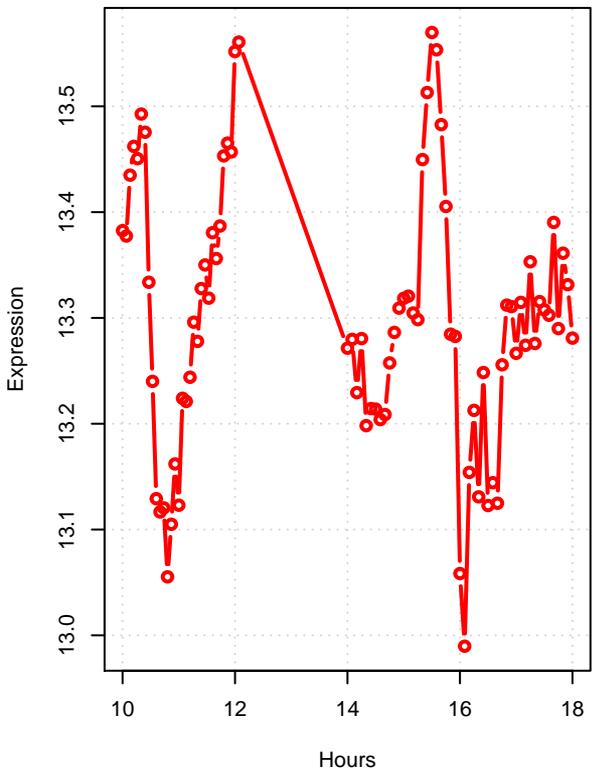
# folate polyglutamylation



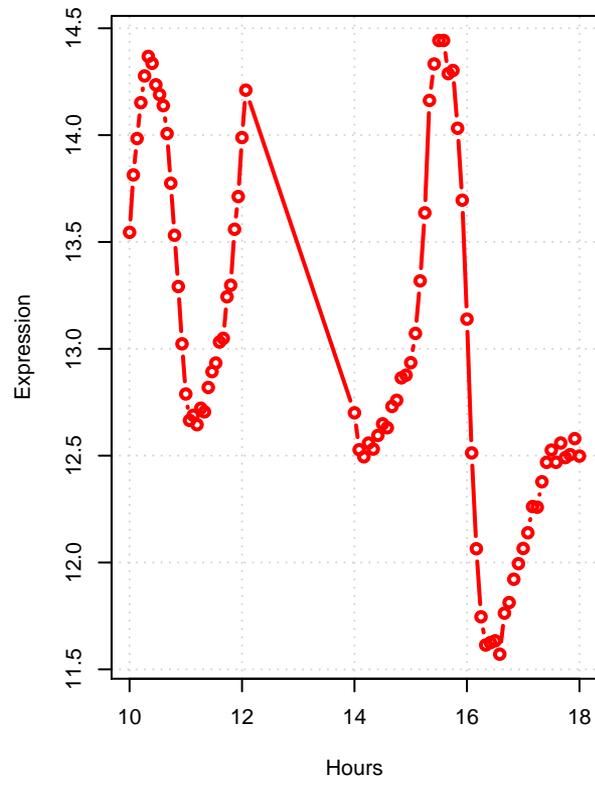
**glycine biosynthesis from serine**

# glycine biosynthesis from serine

shm1 YBR263W  
Mitochondrial serine hydroxymethyltransferase



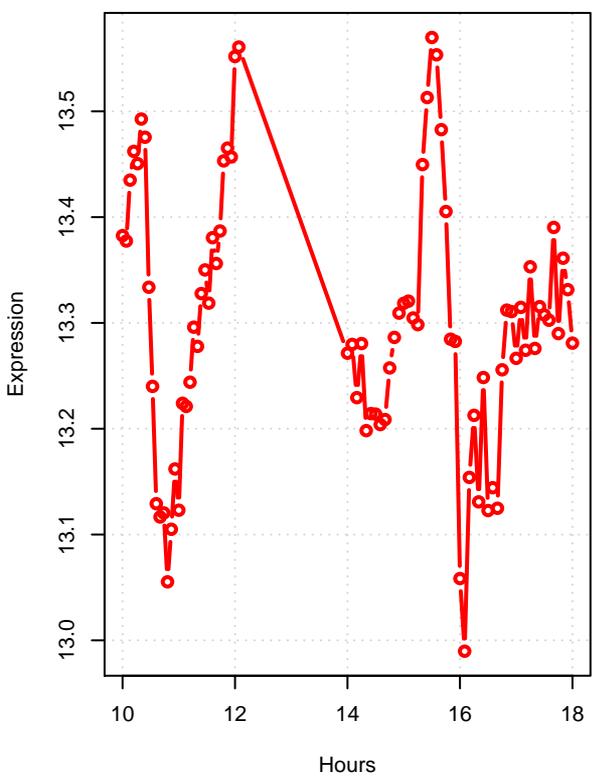
shm2 YLR058C  
Cytosolic serine hydroxymethyltransferase



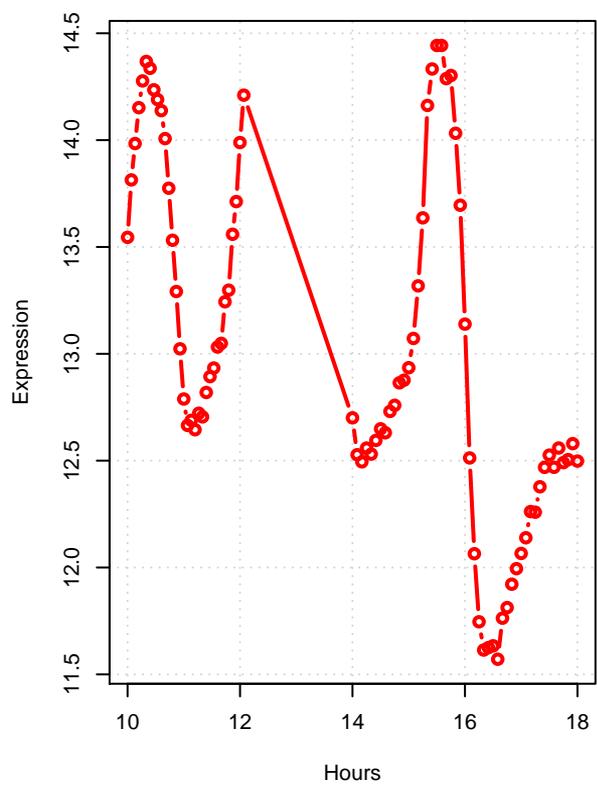
**serine biosynthesis from glyoxylate**

# serine biosynthesis from glyoxylate

shm1 YBR263W  
Mitochondrial serine hydroxymethyltransferase



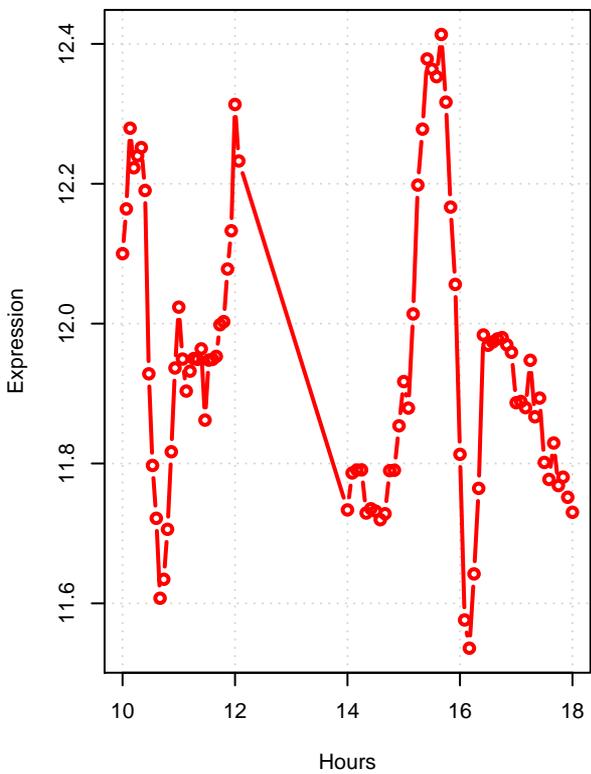
shm2 YLR058C  
Cytosolic serine hydroxymethyltransferase



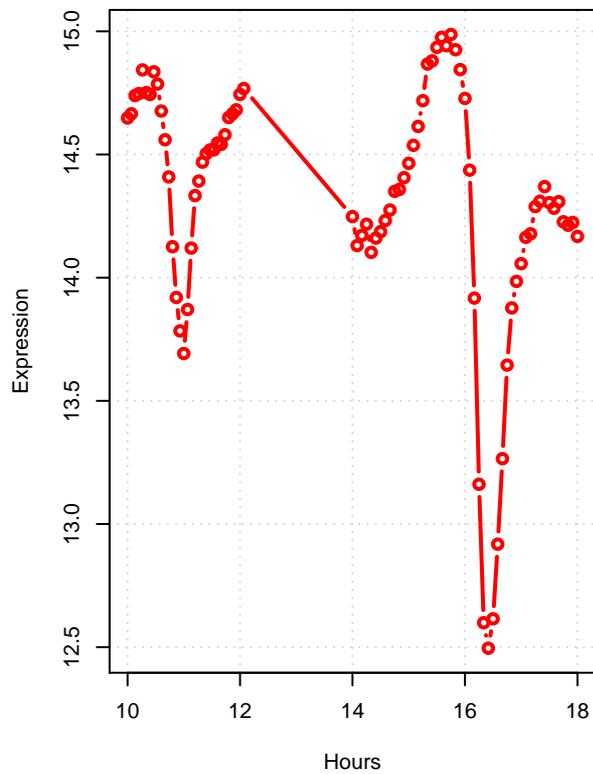
## **methionine biosynthesis**

# methionine biosynthesis

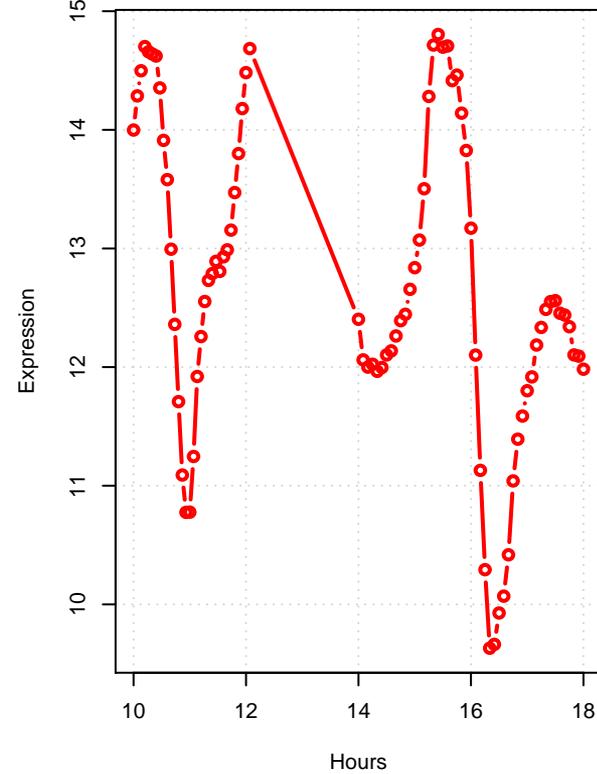
met7 YOR241W  
Folylpolyglutamate synthetase



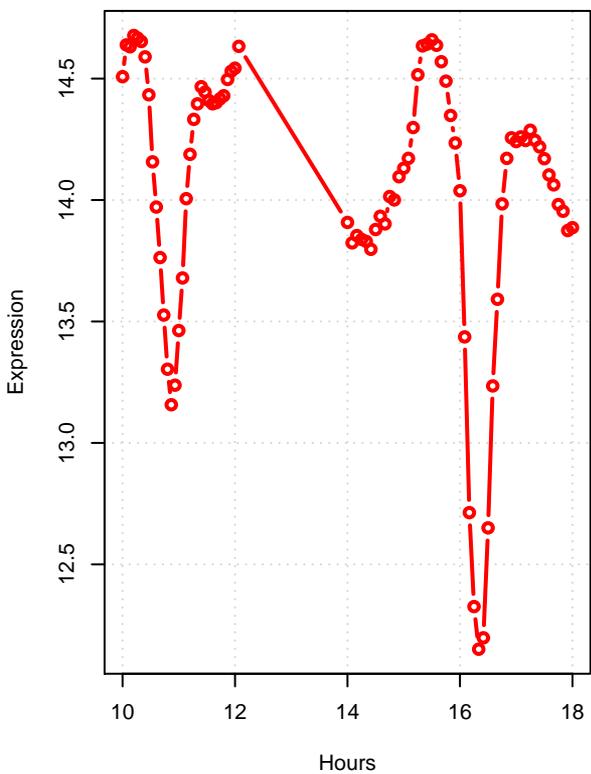
met8 YER0510  
Cobalamin-independent methionine synthase



sam1 YLR180W  
S-adenosylmethionine synthetase



sam2 YDR502C  
S-adenosylmethionine synthetase



**formaldehyde oxidation II (glutathione-dependent)**

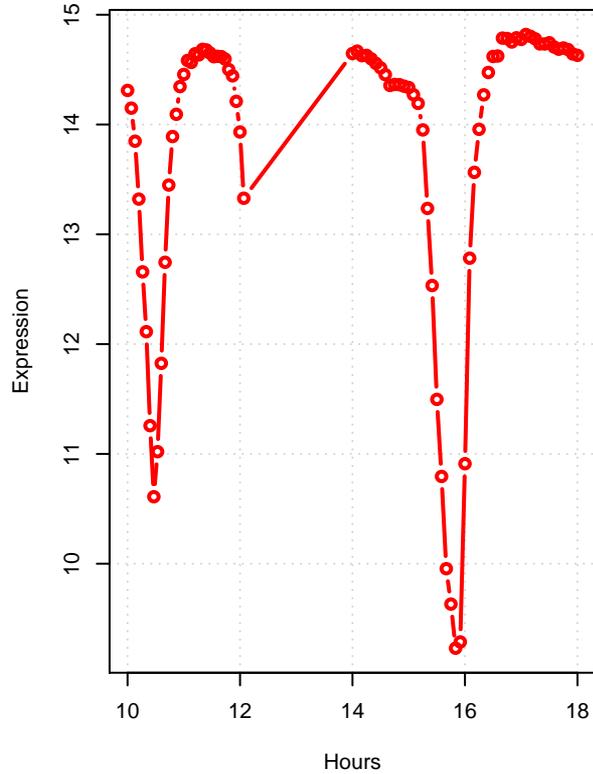
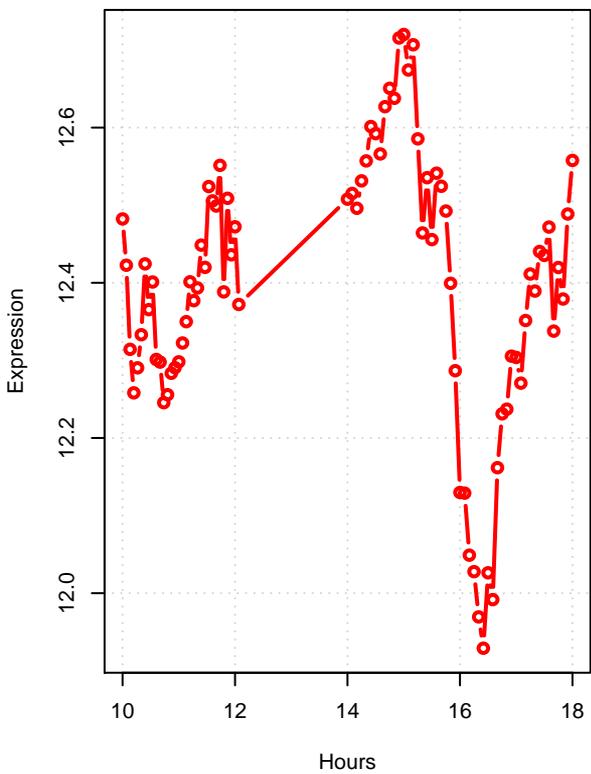
# formaldehyde oxidation II (glutathione-dependent)

sfa1 YDL168W

Bifunctional alcohol dehydrogenase and formaldehyde dehydrogenase

fdh1 OR388C

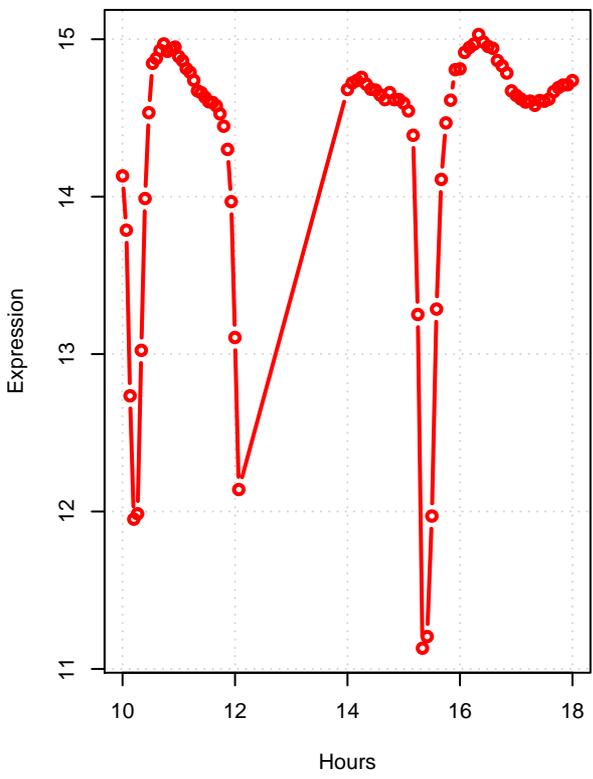
NAD(+)-dependent formate dehydrogenase



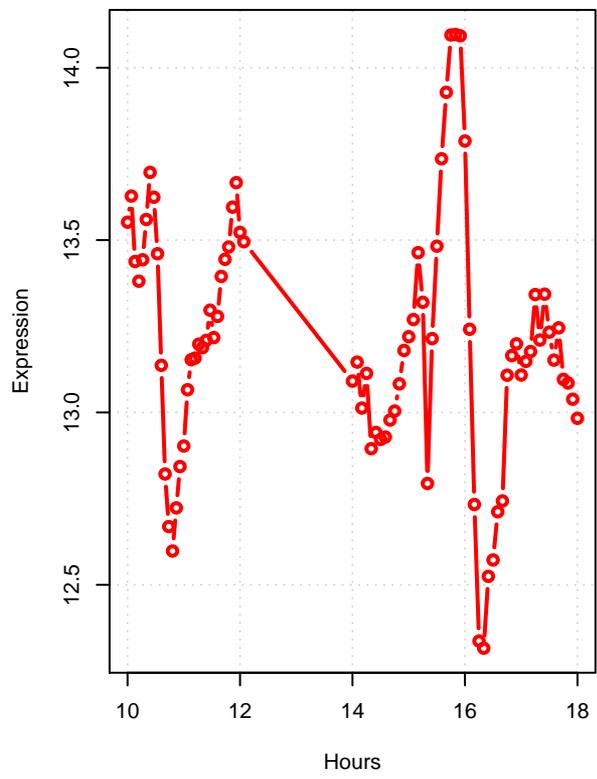
## fructose degradation

# fructose degradation

hxx1 YFR053C  
Hexokinase isoenzyme 1

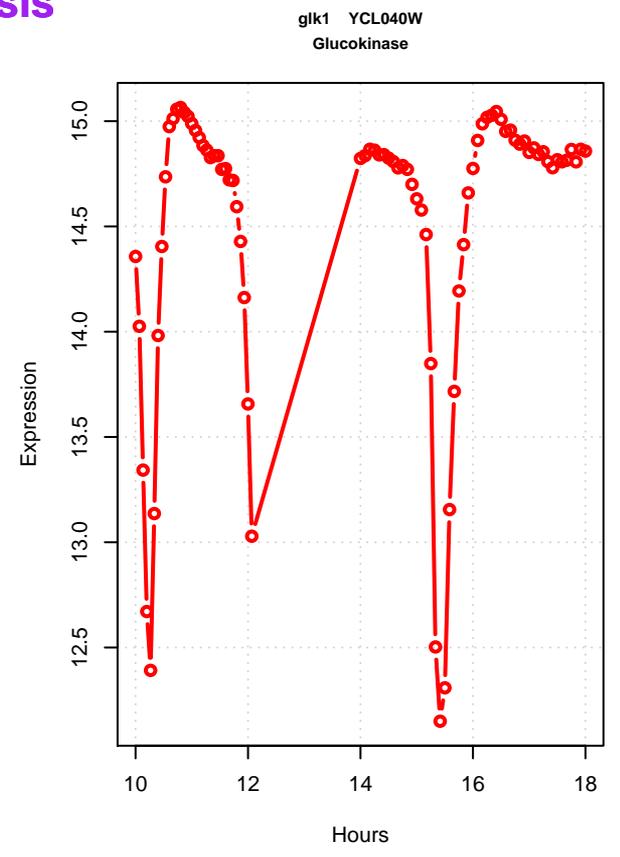
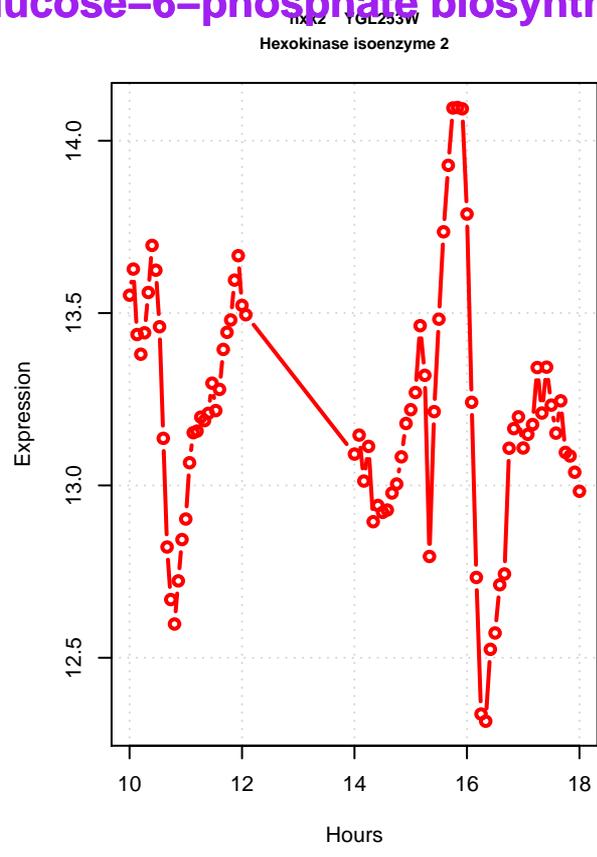
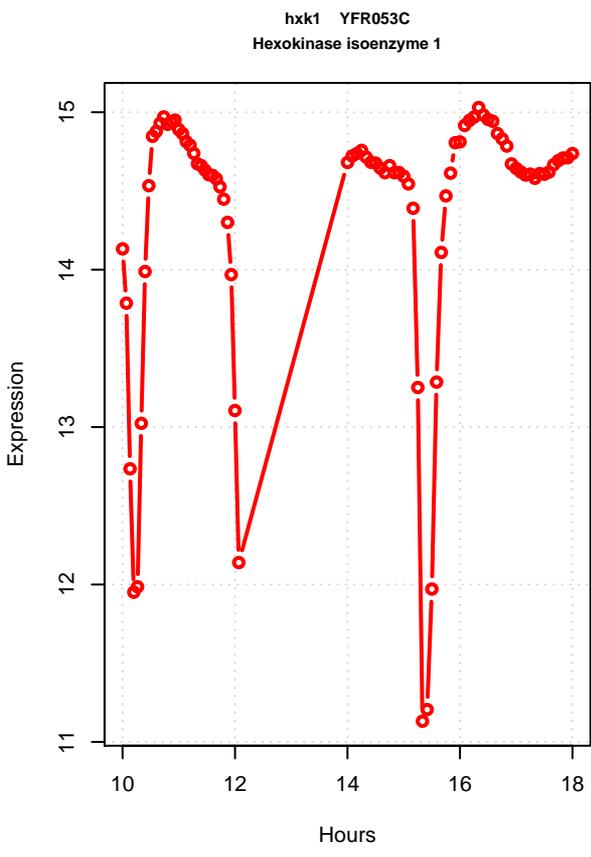


hxx2 YC\_255W  
Hexokinase isoenzyme 2



## glucose-6-phosphate biosynthesis

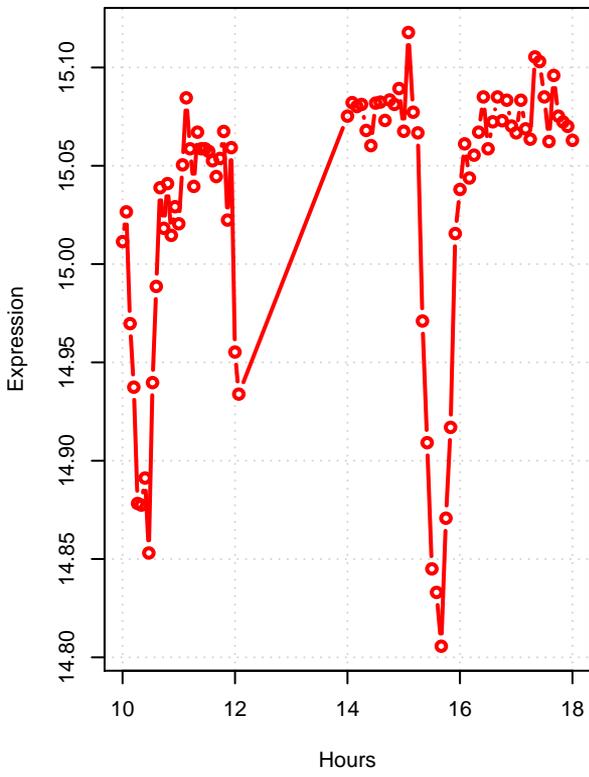
# glucose-6-phosphate biosynthesis



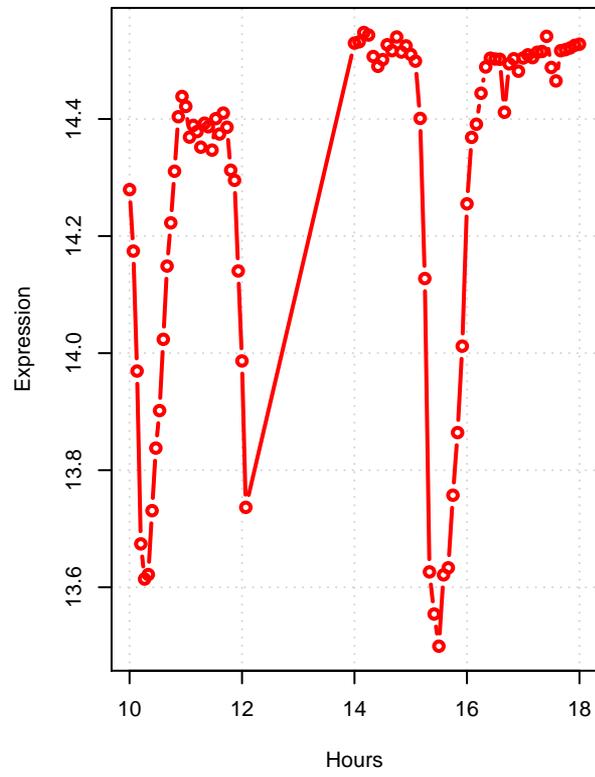
**glycolysis**

# glycolysis

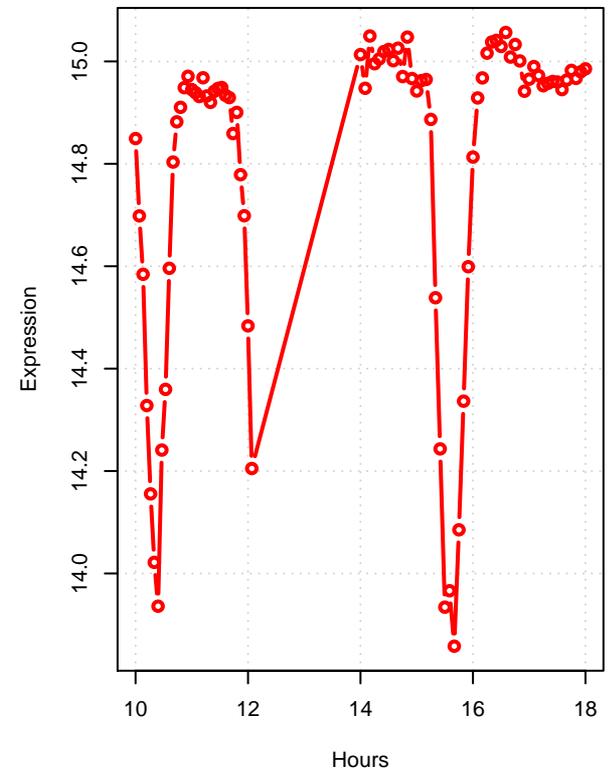
**fba1\_YKL060C**  
Fructose 1,6-bisphosphate aldolase



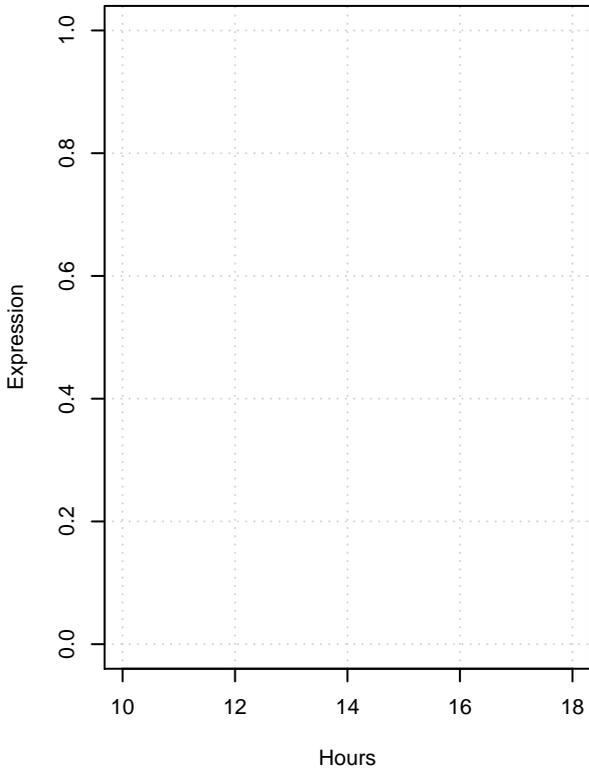
**pgi1\_YJR196C**  
Glycolytic enzyme phosphoglucose isomerase



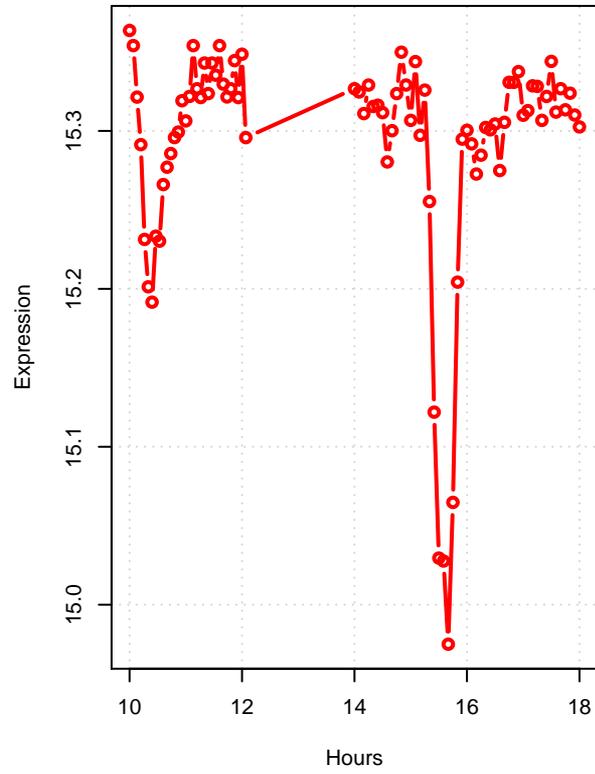
**tdh1\_YJL052W**  
Glyceraldehyde-3-phosphate dehydrogenase (GAPDH), isozyme 1



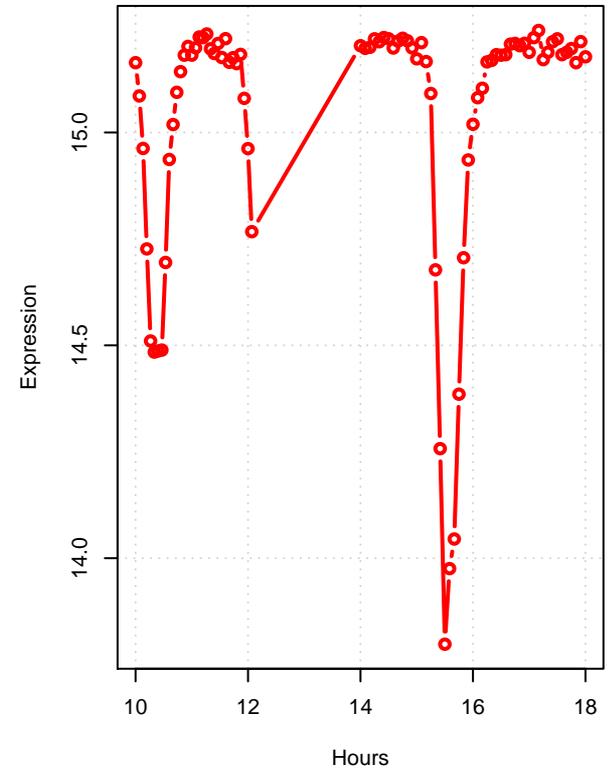
**tdh2\_YJR009C**  
Glyceraldehyde-3-phosphate dehydrogenase (GAPDH), isozyme 2



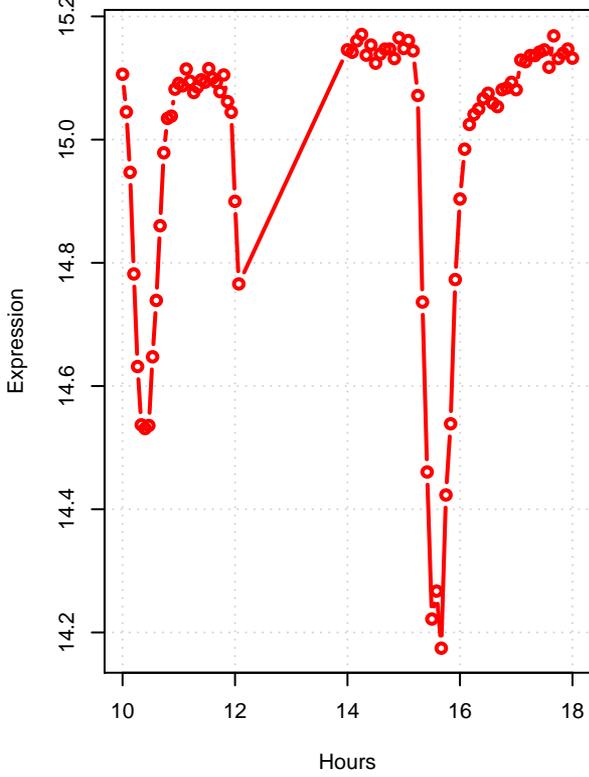
**tdh3\_YGR192C**  
Glyceraldehyde-3-phosphate dehydrogenase (GAPDH), isozyme 3



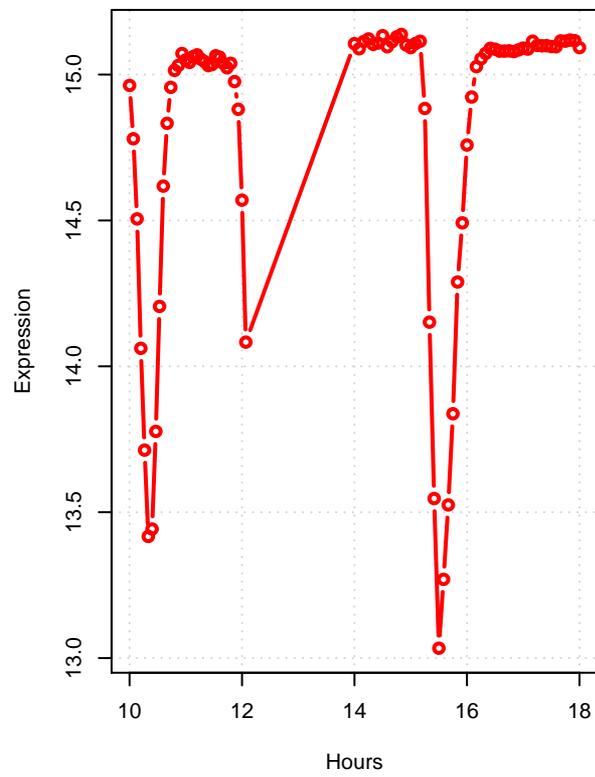
**pgk1\_YCR012W**  
3-phosphoglycerate kinase



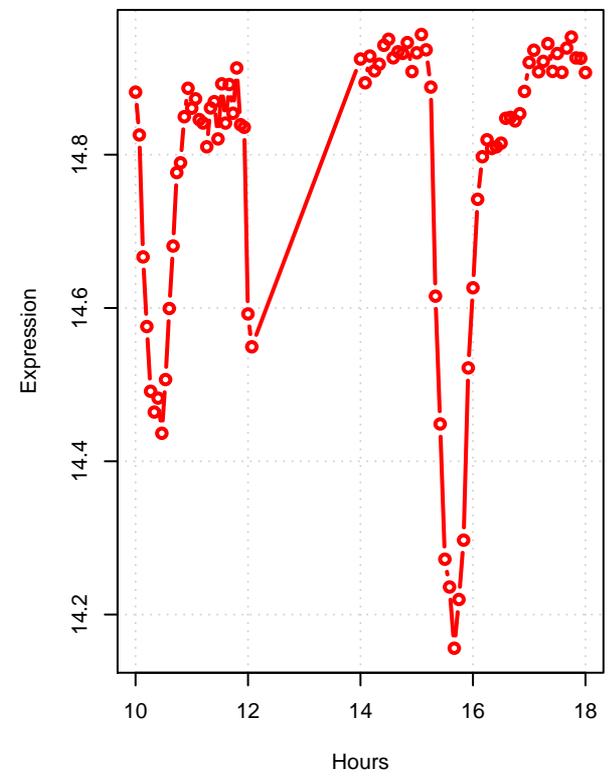
**gpm1\_YKL152C**  
Tetrameric phosphoglycerate mutase



**eno1\_YGR254W**  
Enolase I, a phosphopyruvate hydratase

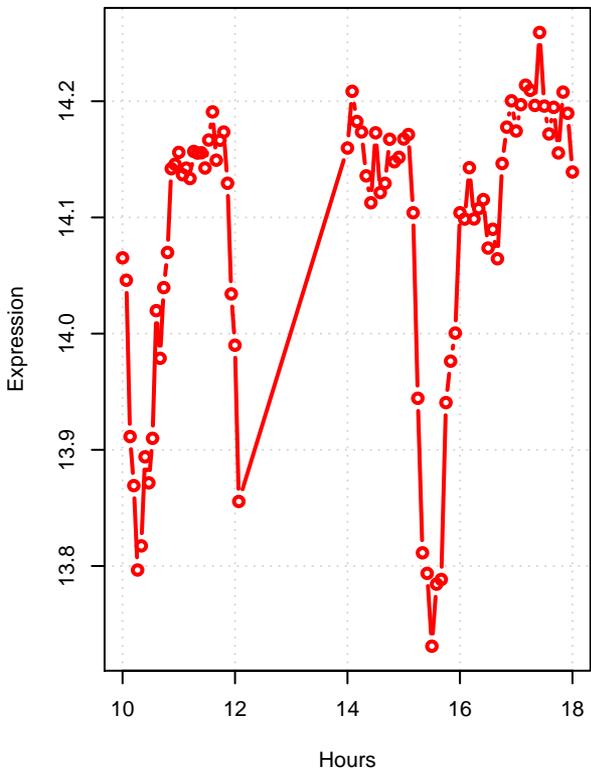


**eno2\_YHR174W**  
Enolase II, a phosphopyruvate hydratase

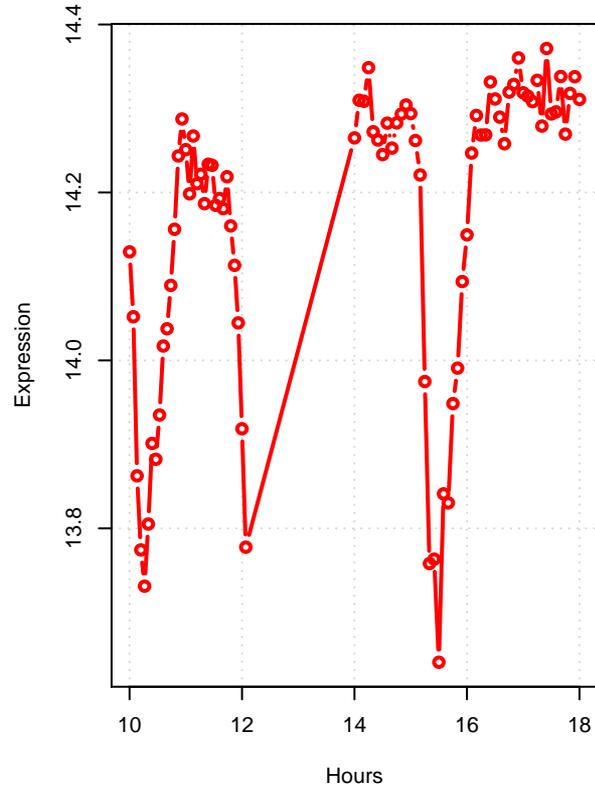


# glycolysis

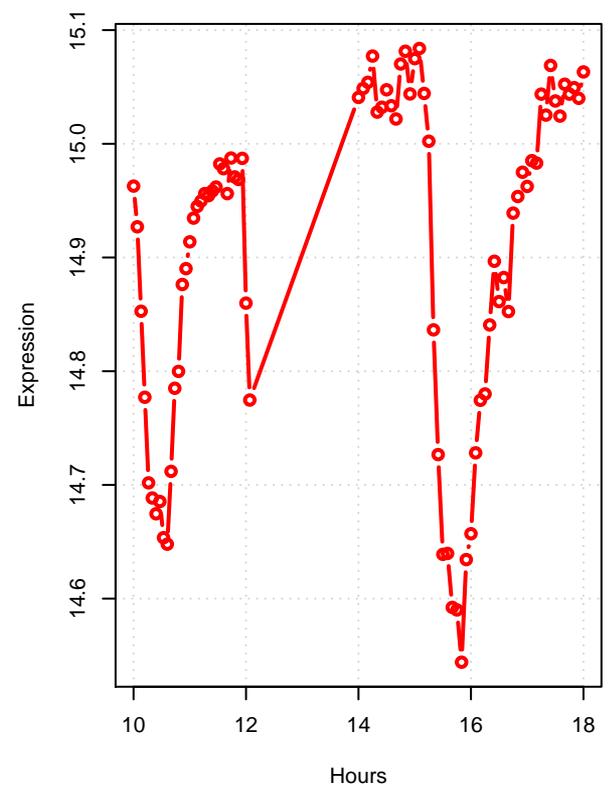
**pfk1 YGR240C**  
Alpha subunit of heterooctameric phosphofructokinase



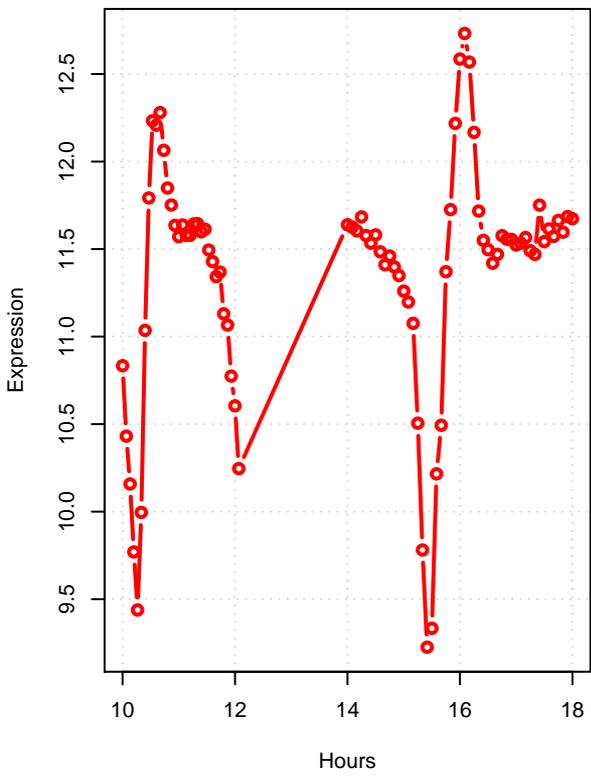
**pfk2 YLR205C**  
Beta subunit of heterooctameric phosphofructokinase



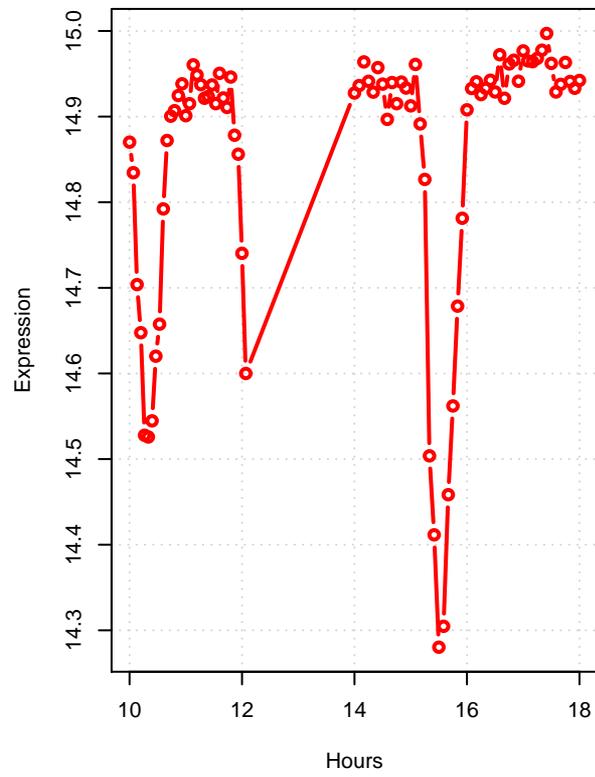
**cdc19 YAL038W**  
Pyruvate kinase



**pyk2 YOR347C**  
Pyruvate kinase

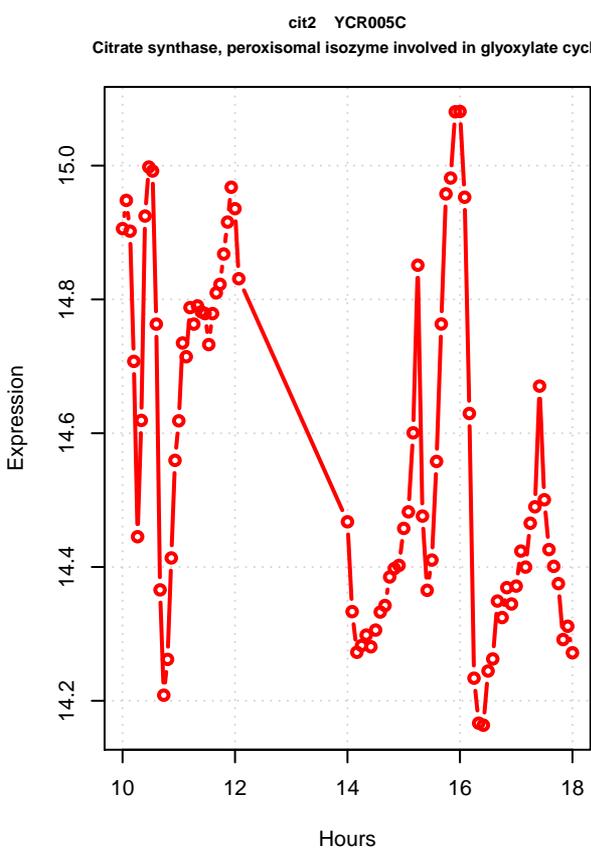
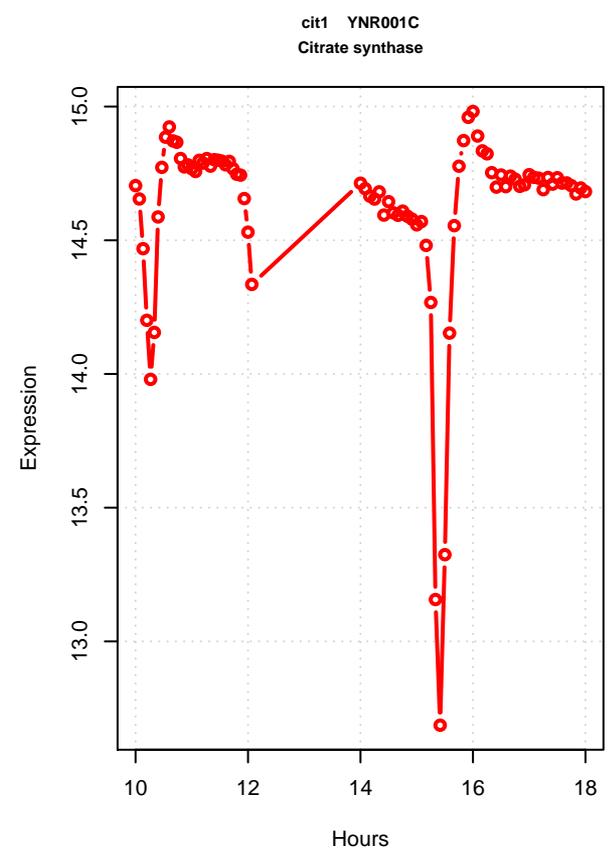
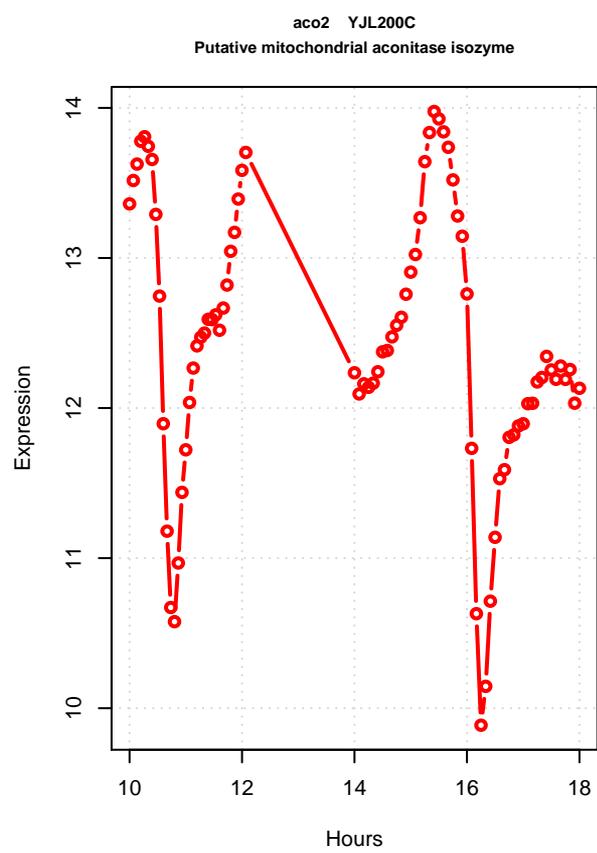
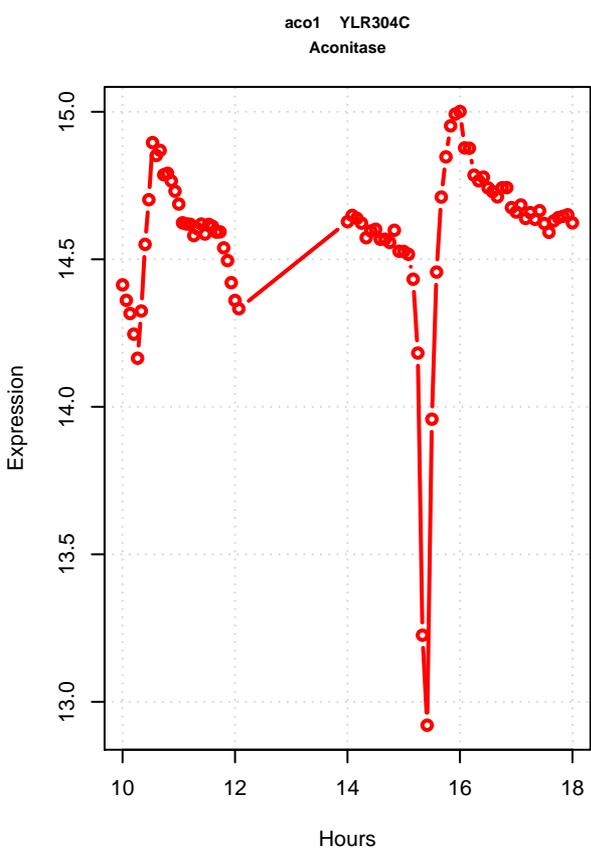
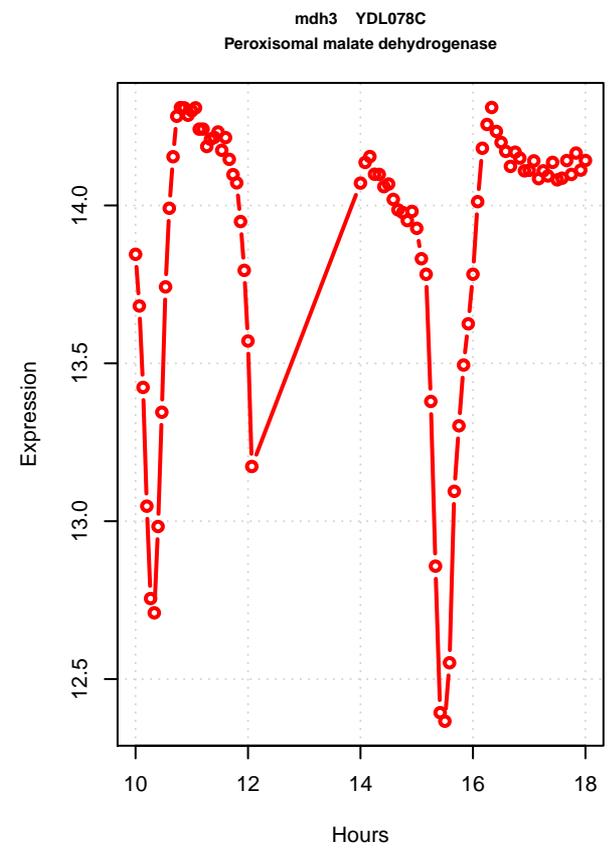
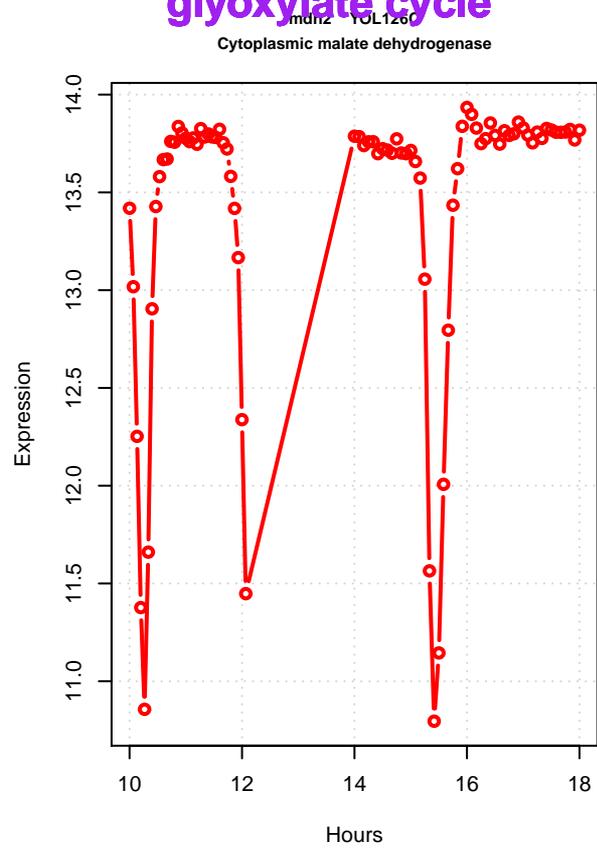
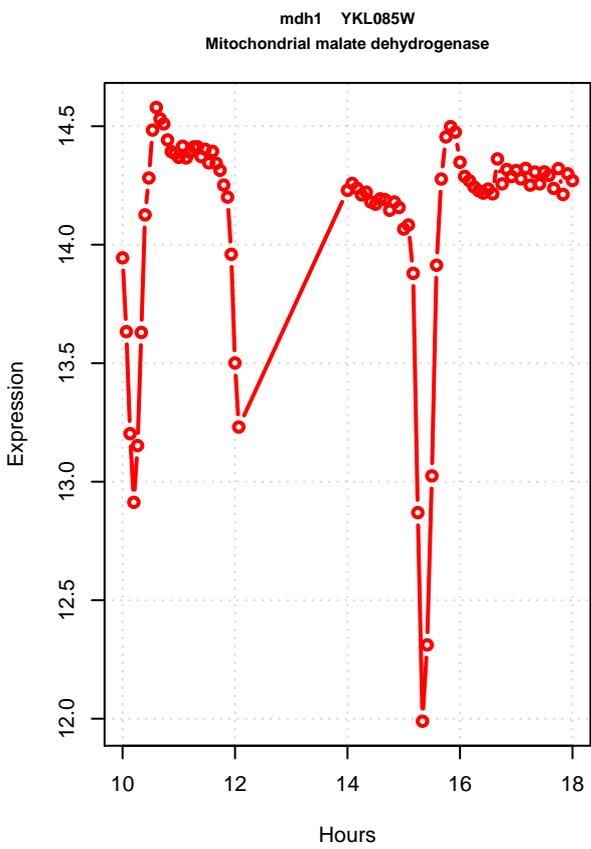


**tpi1 YDR050C**  
Triose phosphate isomerase, abundant glycolytic enzyme

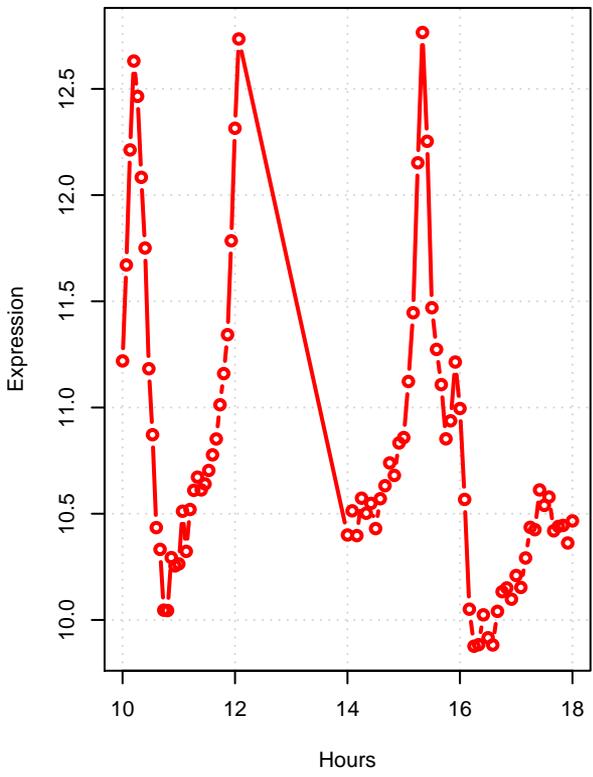


## glyoxylate cycle

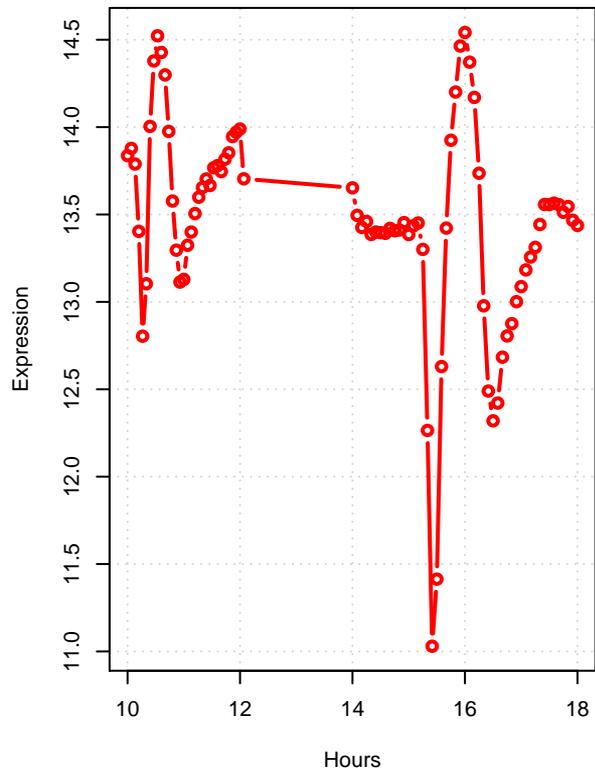
# glyoxylate cycle



dal7 YIR031C  
Malate synthase



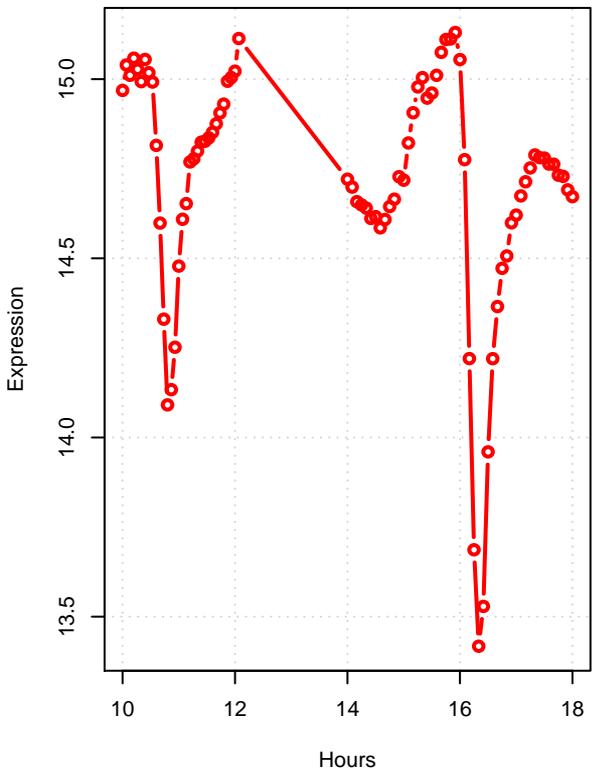
glyoxylate cycle  
mis1 YNL117W  
Malate synthase, enzyme of the glyoxylate cycle



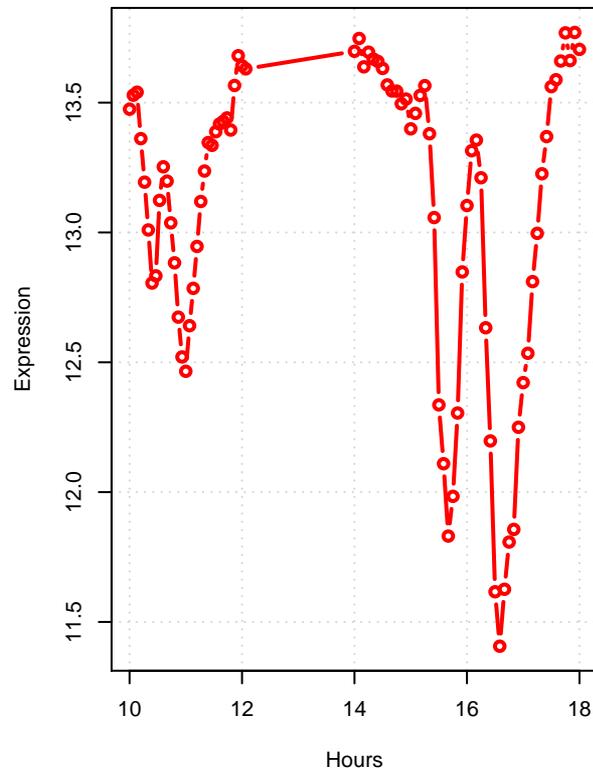
**glutamate biosynthesis from ammonia**

# glutamate biosynthesis from ammonia

gdh1 YOR375C  
NADP(+)-dependent glutamate dehydrogenase



gdh3 YAL062W  
NADP(+)-dependent glutamate dehydrogenase

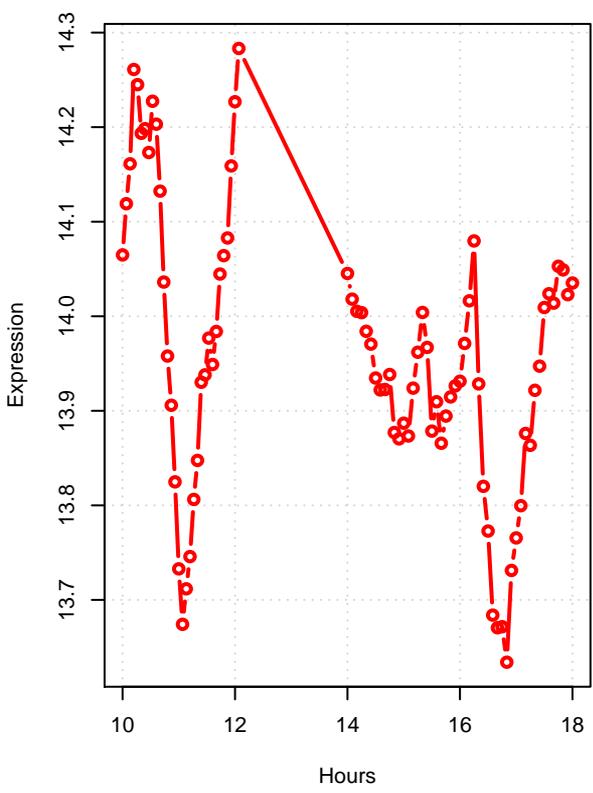


**glutamate biosynthesis from glutamine**

# glutamate biosynthesis from glutamine

glt1 YDL171C

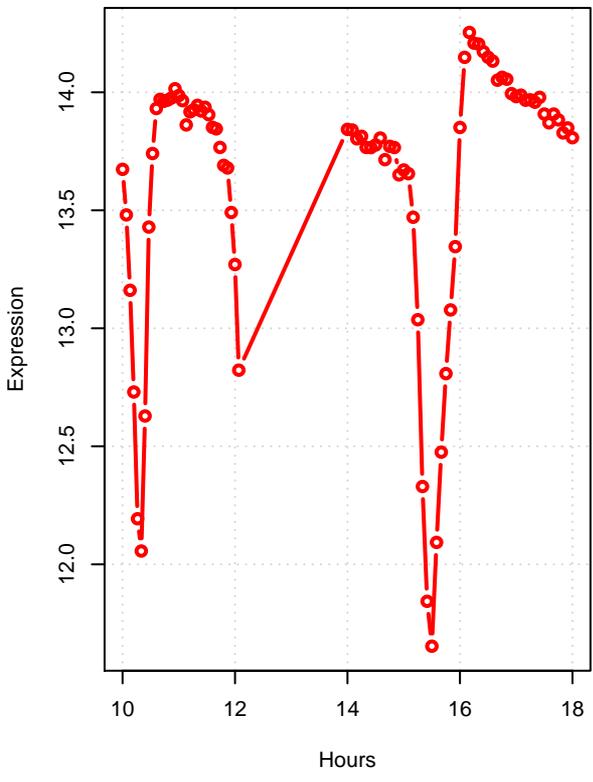
NAD(+)-dependent glutamate synthase (GOGAT)



## glutamate degradation IX

# glutamate degradation IX

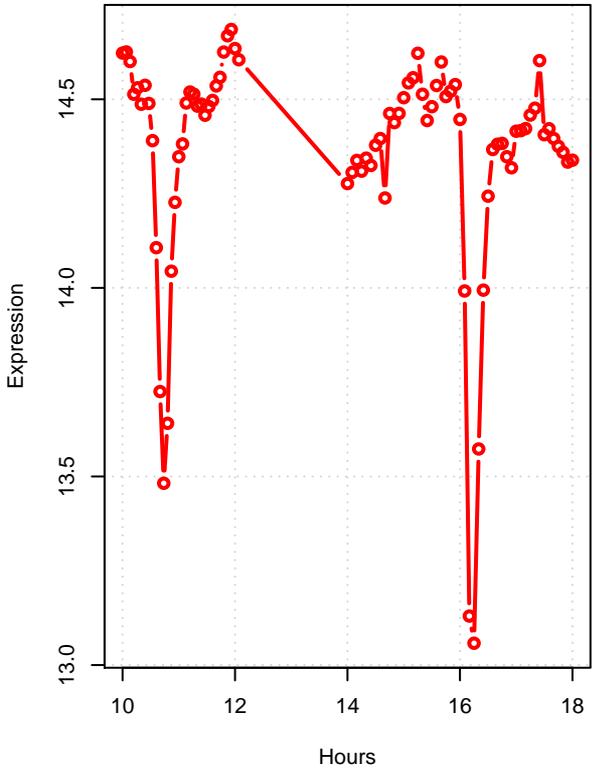
gdh2 YDL215C  
NAD(+)-dependent glutamate dehydrogenase



## **glutamine biosynthesis**

# glutamine biosynthesis

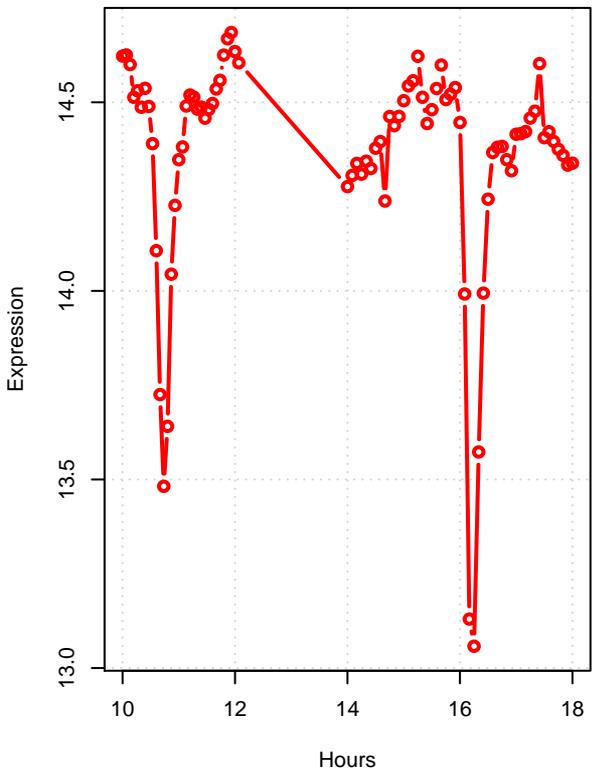
gln1 YPR035W  
Glutamine synthetase (GS)



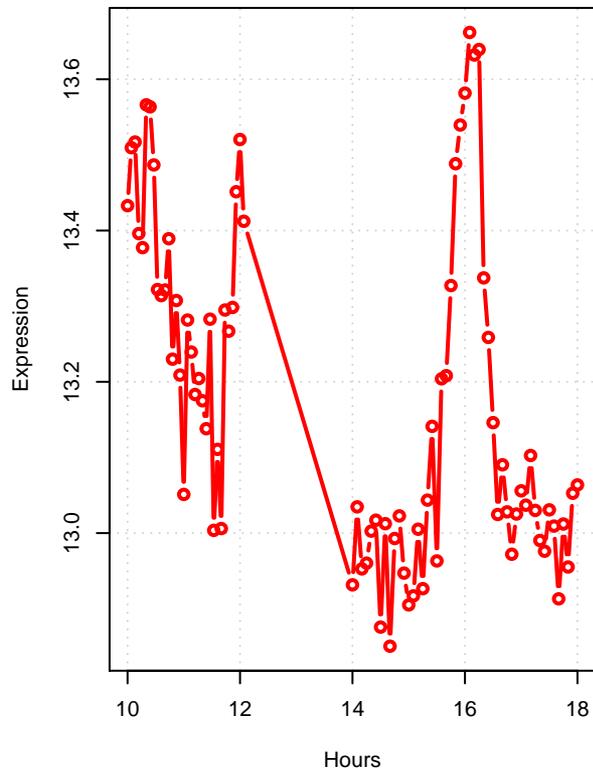
**superpathway of glutamate biosynthesis**

# superpathway of glutamate biosynthesis

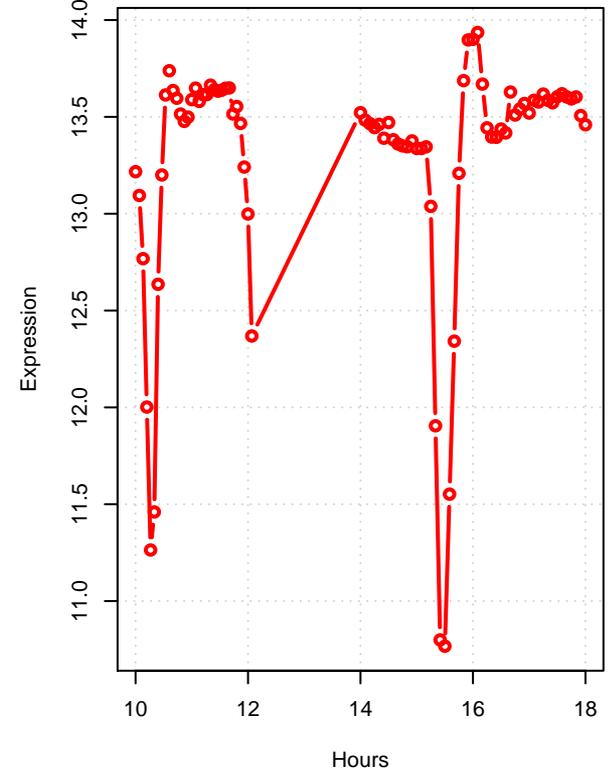
gln1 YPR035W  
Glutamine synthetase (GS)



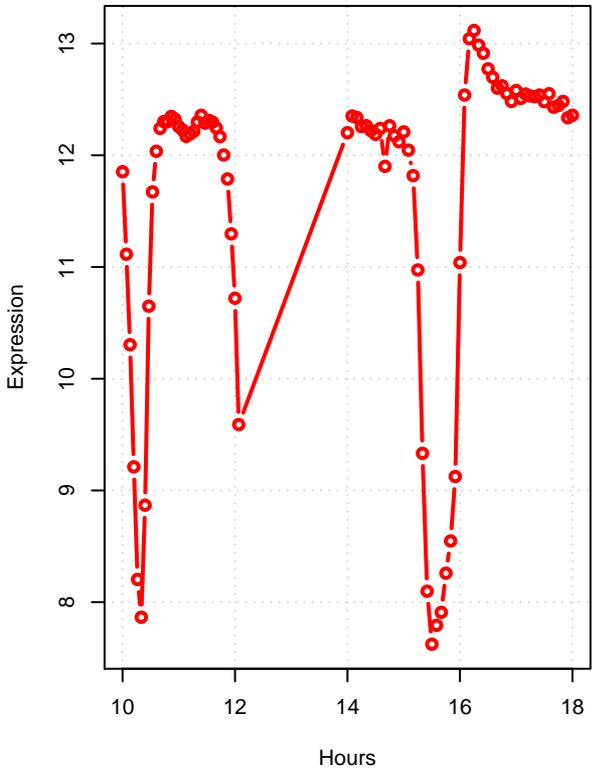
idp1 YDL066W  
Mitochondrial NADP-specific isocitrate dehydrogenase



idp2 YLR174W  
Cytosolic NADP-specific isocitrate dehydrogenase



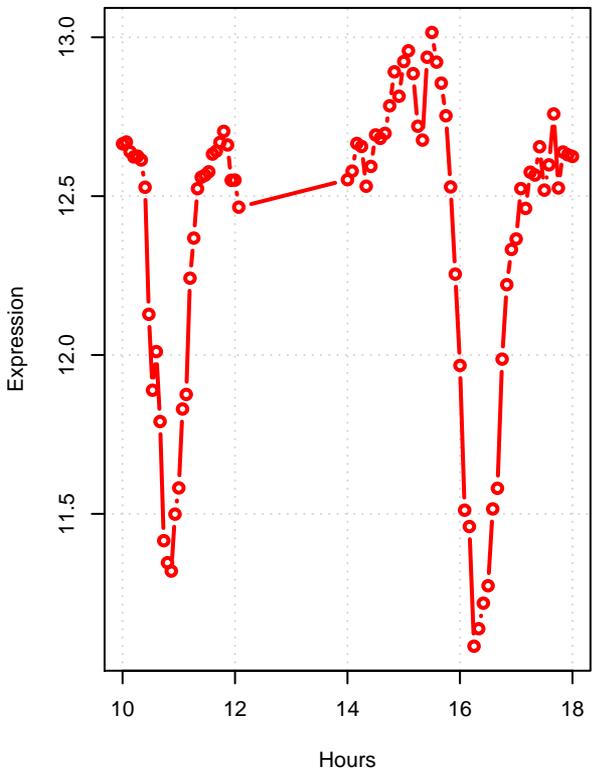
idp3 YNL009W  
Peroxisomal NADP-dependent isocitrate dehydrogenase



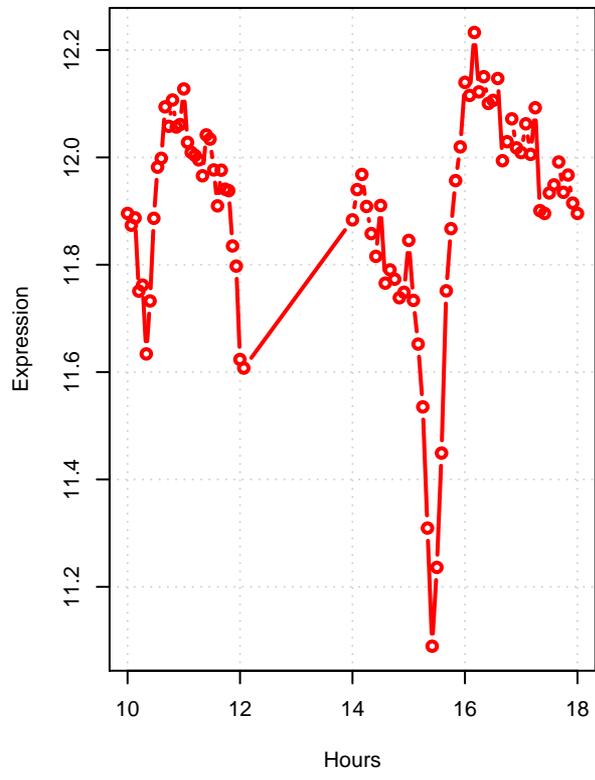
## glutathione biosynthesis

# glutathione biosynthesis

gsh1 YJL101C  
Gamma glutamylcysteine synthetase

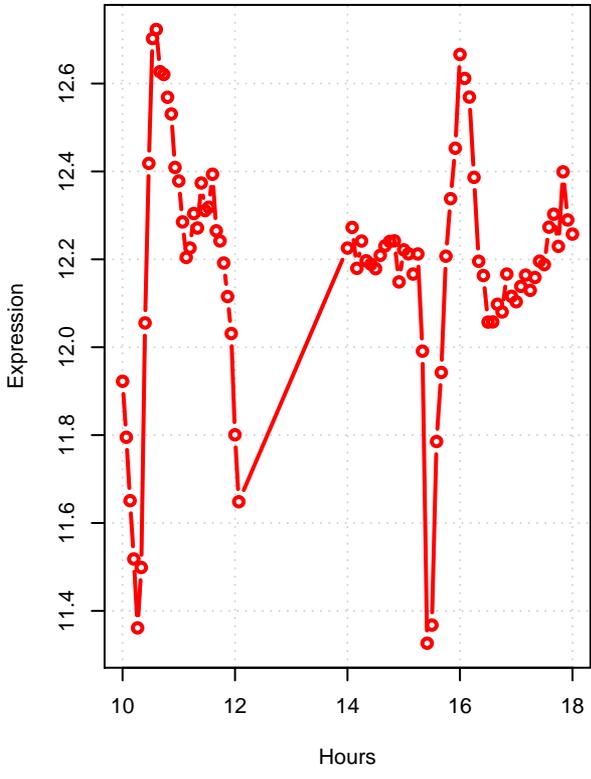


gsh2 YOL049W  
Glutathione synthetase

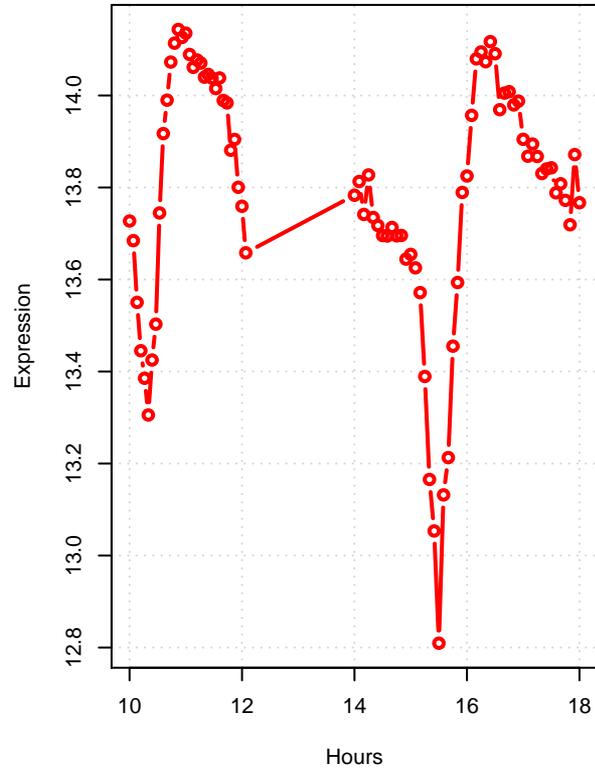


# glutathione degradation

ecm38 YLR299W  
Gamma-glutamyltranspeptidase



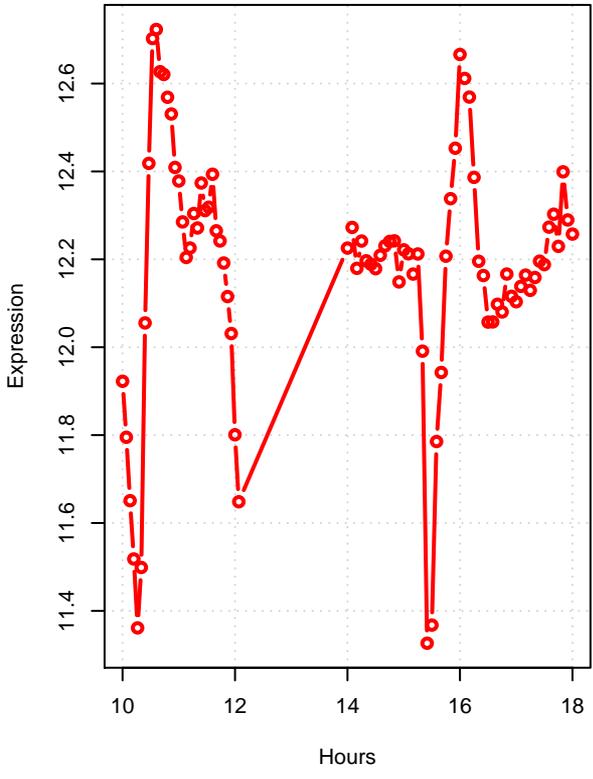
glutathione degradation  
aug1 YFR024C  
Cys-Gly metallo-di-peptidase



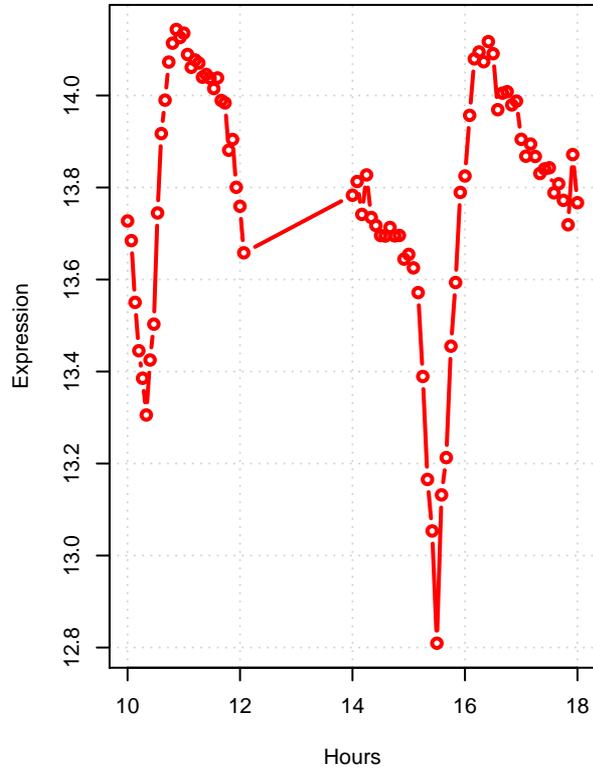
pathway of glutathione metabolism (truncated & gamma;-glutamyl

# superpathway of glutathione metabolism (truncated & gamma;-glutamyl cycle)

*elm38* YLR299W  
Gamma-glutamyltranspeptidase

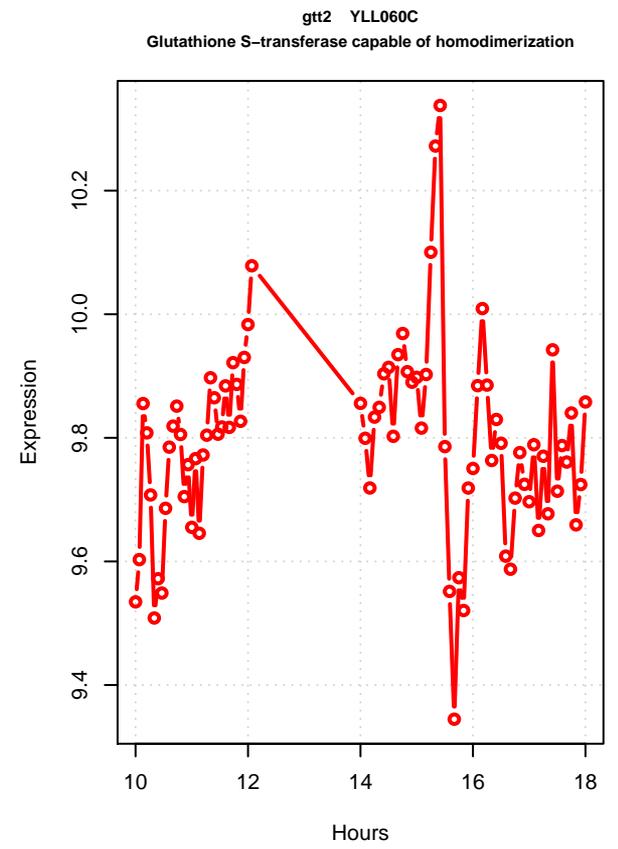
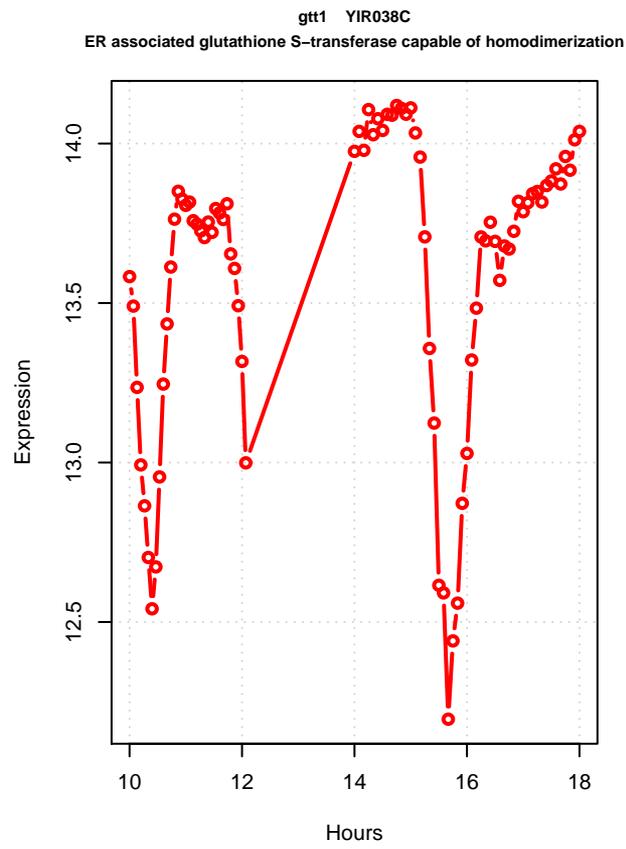
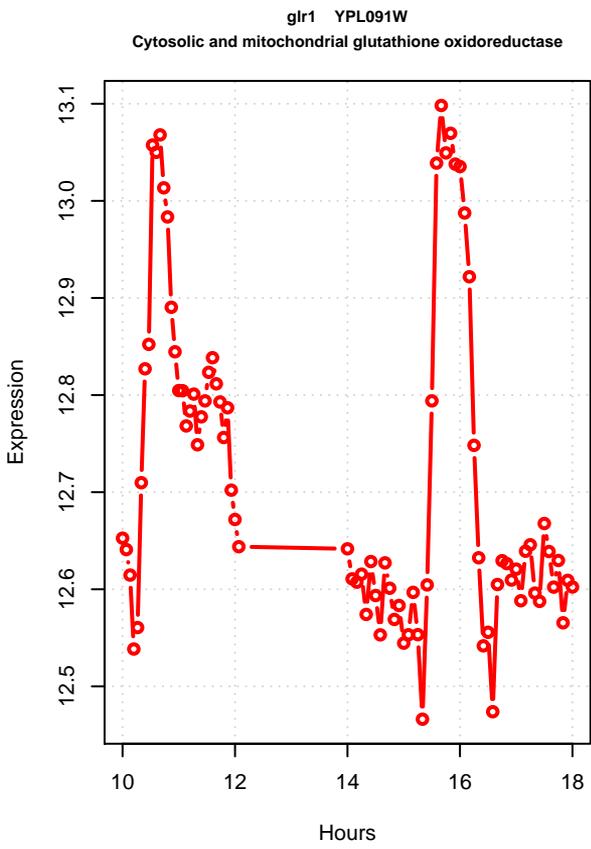
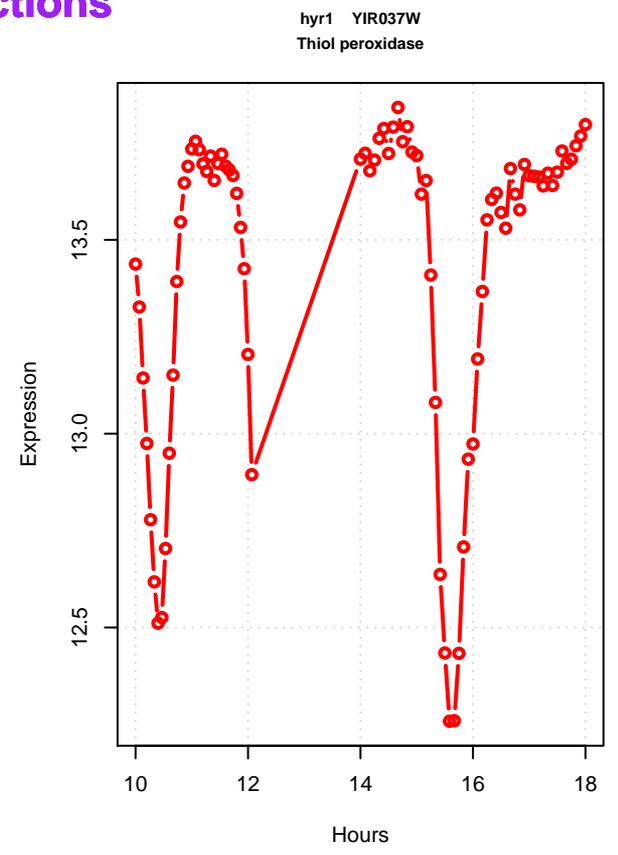
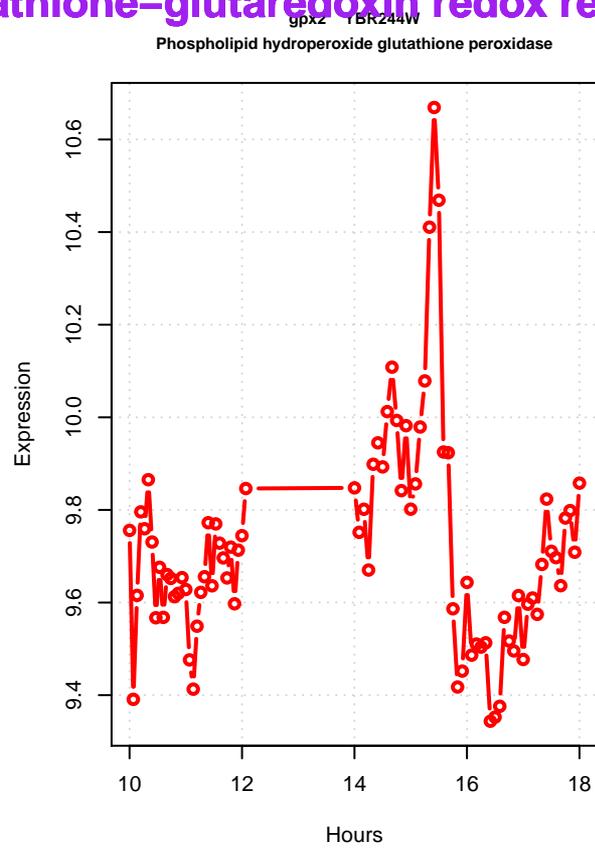
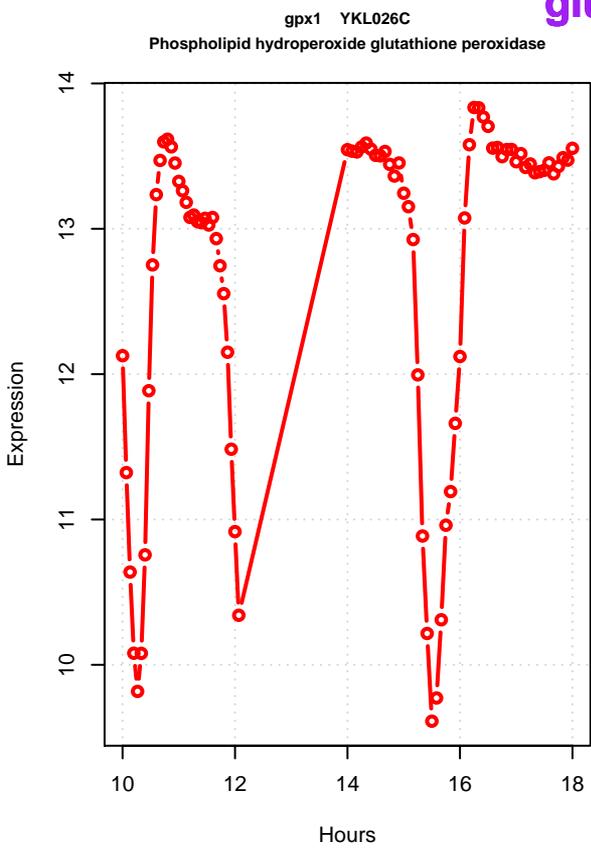


*dug1* YFR144C  
Cys-Gly metallo-di-peptidase



**glutathione–glutaredoxin redox reactions**

# glutathione-glutaredoxin redox reactions

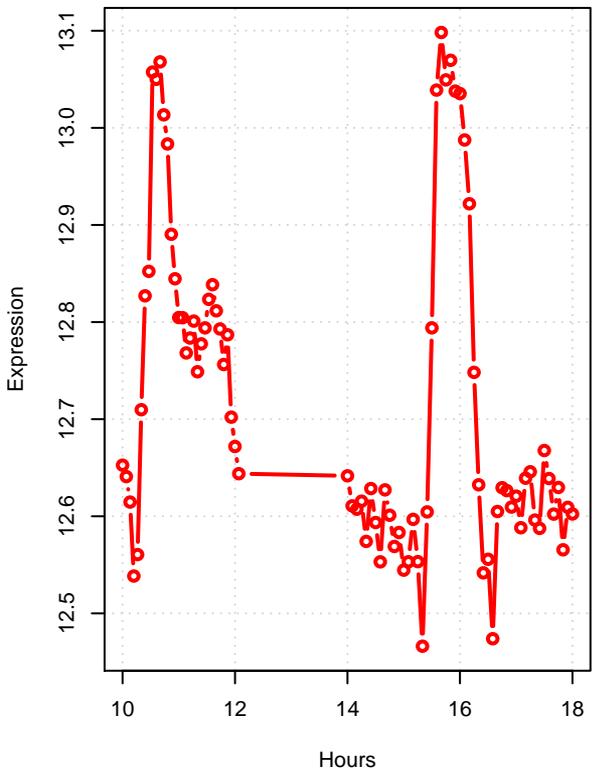


**glutathione–glutaredoxin system**

# glutathione-glutaredoxin system

glr1 YPL091W

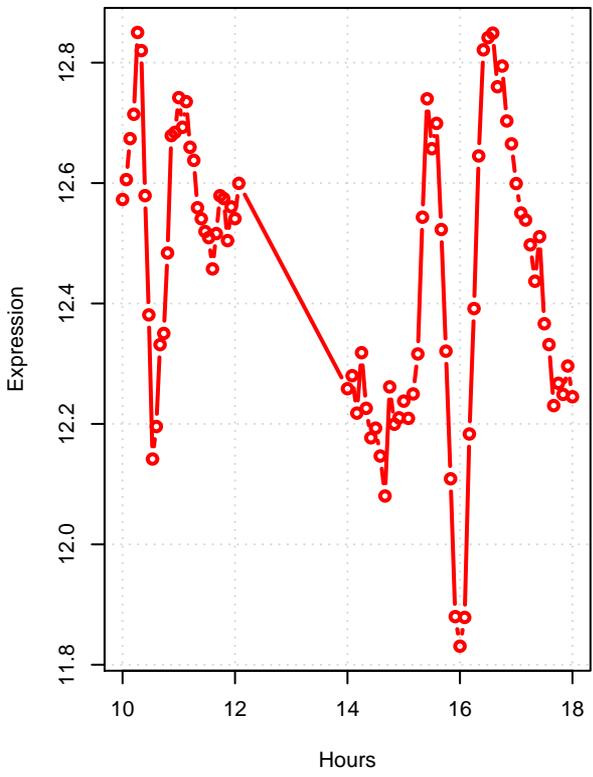
Cytosolic and mitochondrial glutathione oxidoreductase



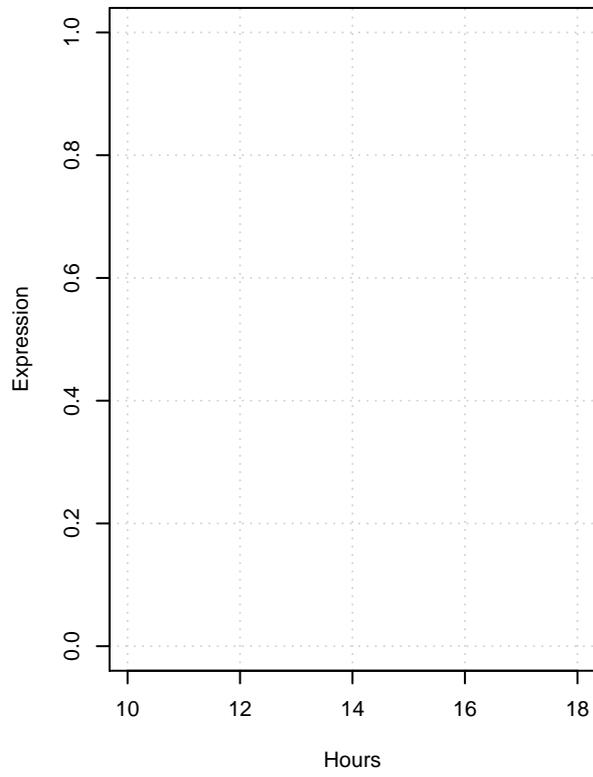
## glycerol biosynthesis

# glycerol biosynthesis

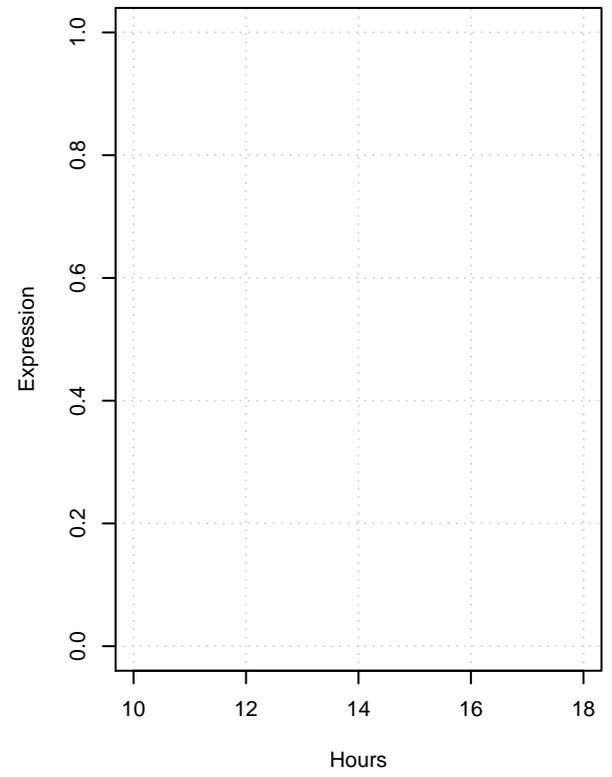
**cds1** YBR029C  
Phosphatidate cytidyltransferase (CDP-diglyceride synthetase)



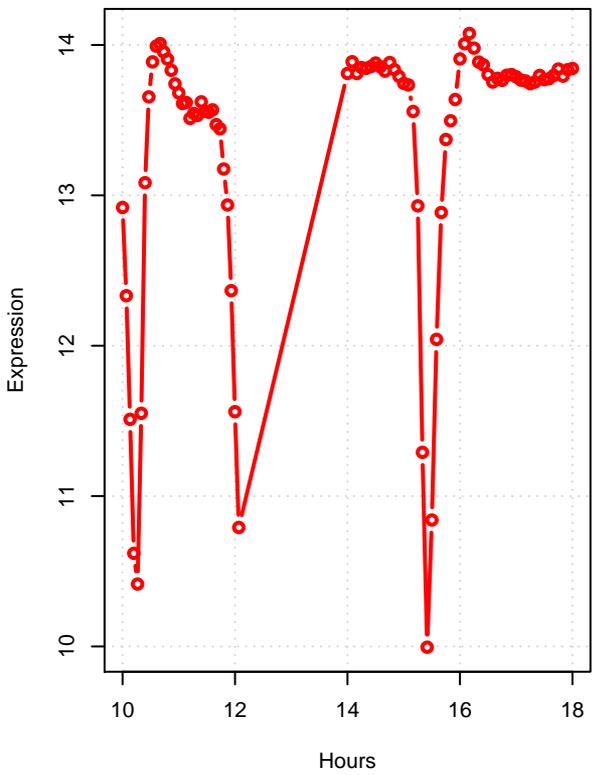
**hor2** Missing ORF  
Missing Function



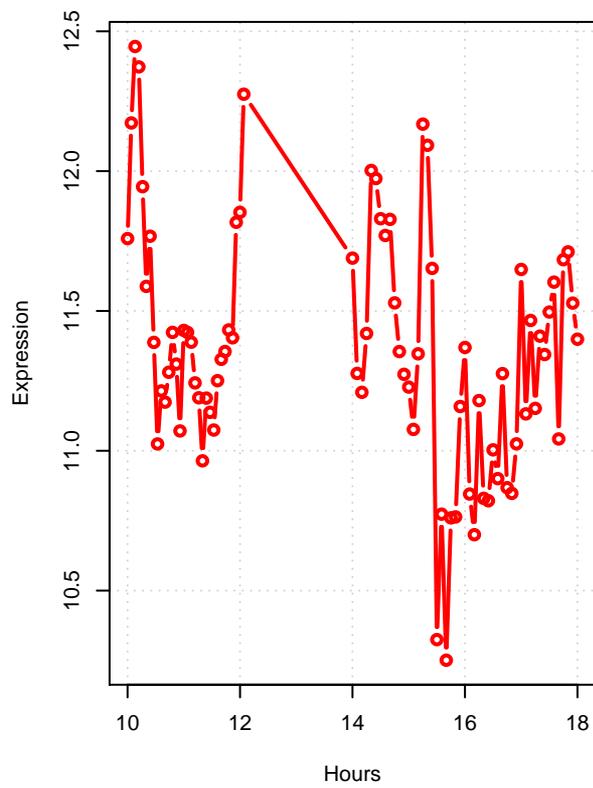
**rhr2** Missing ORF  
Missing Function



**gpd1** YDL022W  
NAD-dependent glycerol-3-phosphate dehydrogenase



**gpd2** YOL059W  
NAD-dependent glycerol 3-phosphate dehydrogenase

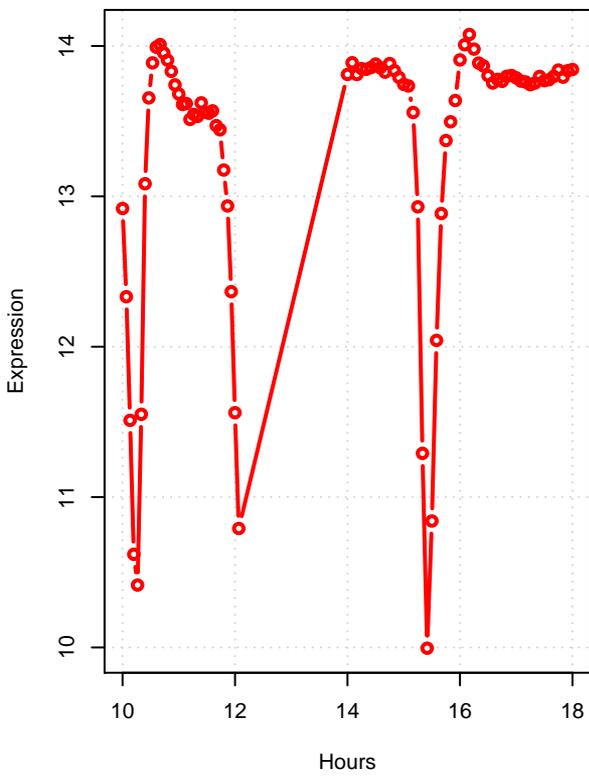


phosphatidate biosynthesis II (the glycerol-3-phosphate pathway)

# Phosphatidate biosynthesis II (the glycerol-3-phosphate pathway)

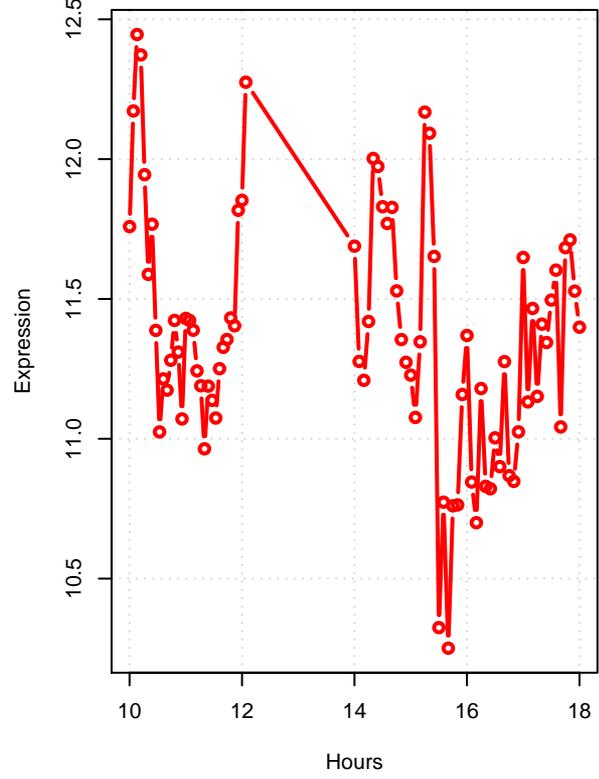
gpd1 YDL022W

NAD-dependent glycerol-3-phosphate dehydrogenase



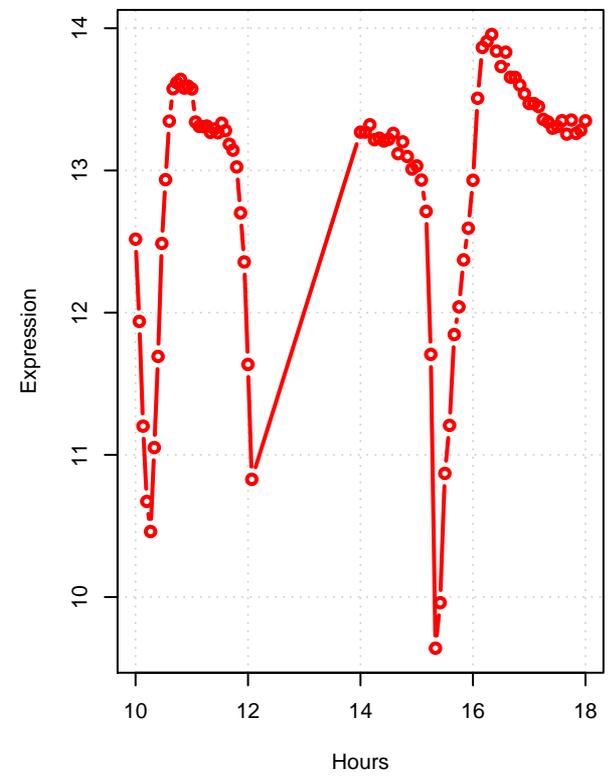
gpd2 YCU059W

NAD-dependent glycerol 3-phosphate dehydrogenase



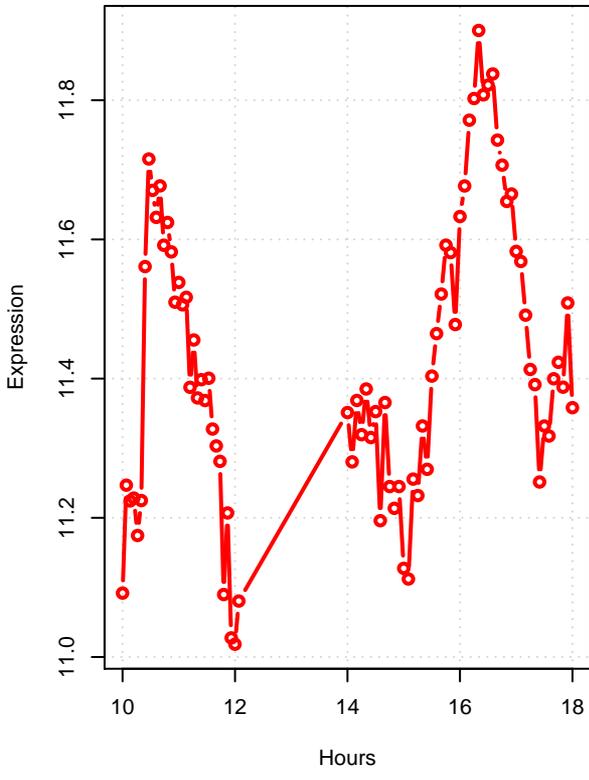
gpt2 YKR067W

Glycerol-3-phosphate/dihydroxyacetone phosphate sn-1 acyltransferase



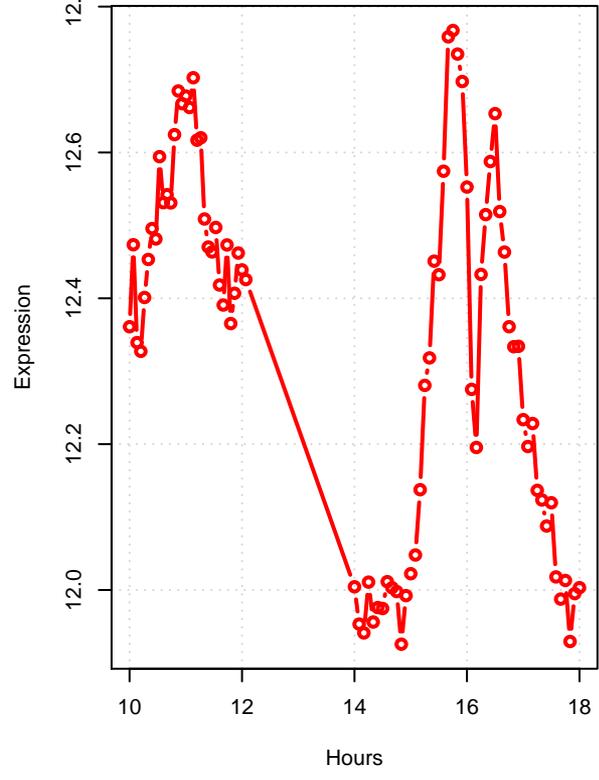
sct1 YBL011W

Glycerol 3-phosphate/dihydroxyacetone phosphate sn-1 acyltransferase



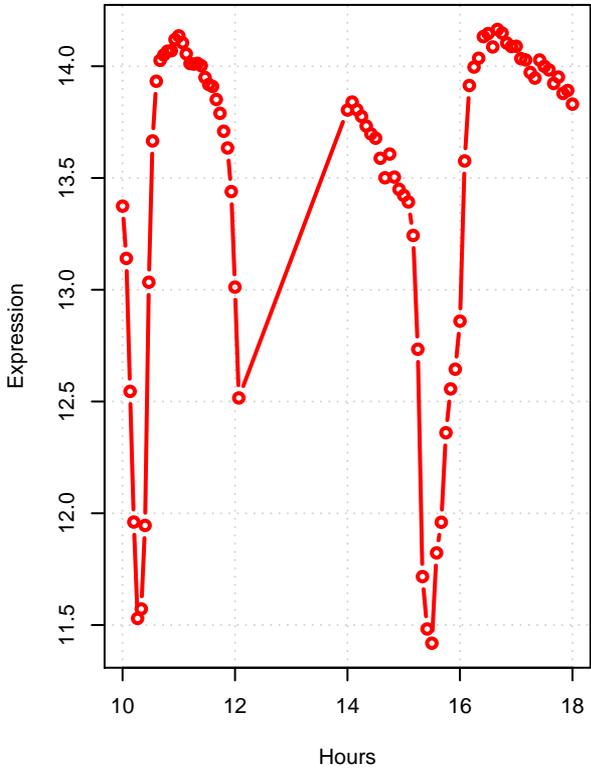
slc1 YDL052C

1-acyl-sn-glycerol-3-phosphate acyltransferase

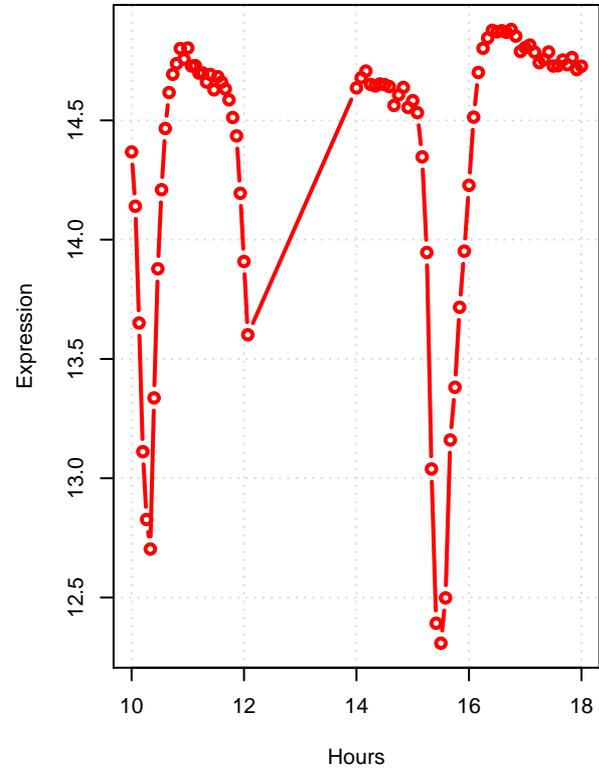


## glycerol degradation

gut1 YHL032C  
Glycerol kinase



gut2 YL155C  
Mitochondrial glycerol-3-phosphate dehydrogenase

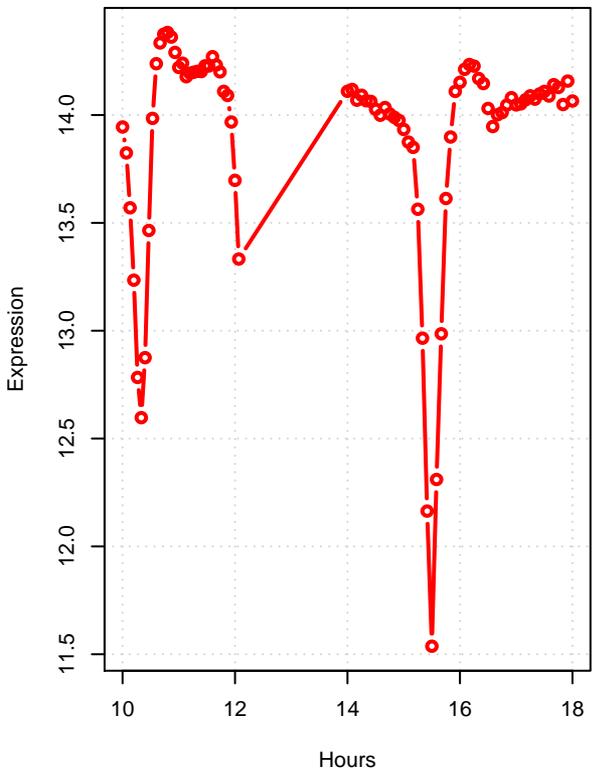


**glycine biosynthesis from glyoxylate**

# glycine biosynthesis from glyoxylate

agx1 YFL030W

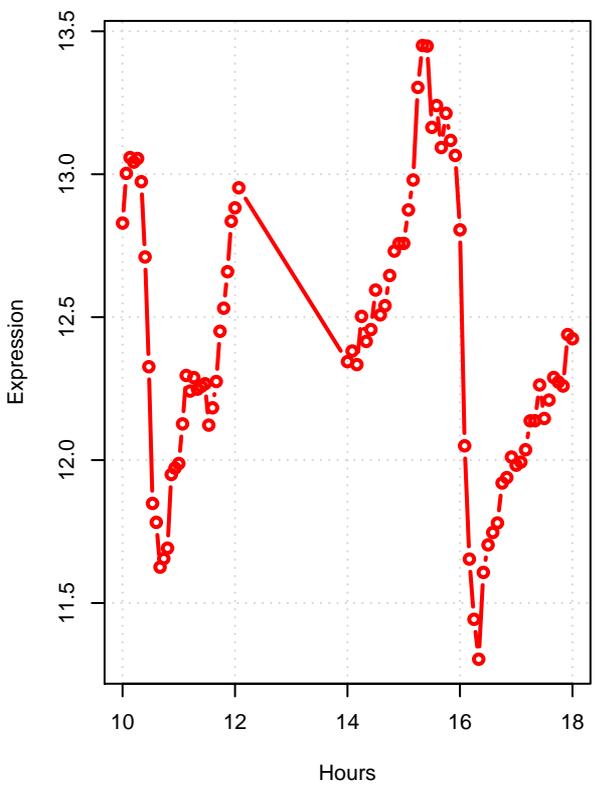
Alanine:glyoxylate aminotransferase (AGT)



**glycine biosynthesis from threonine**

# glycine biosynthesis from threonine

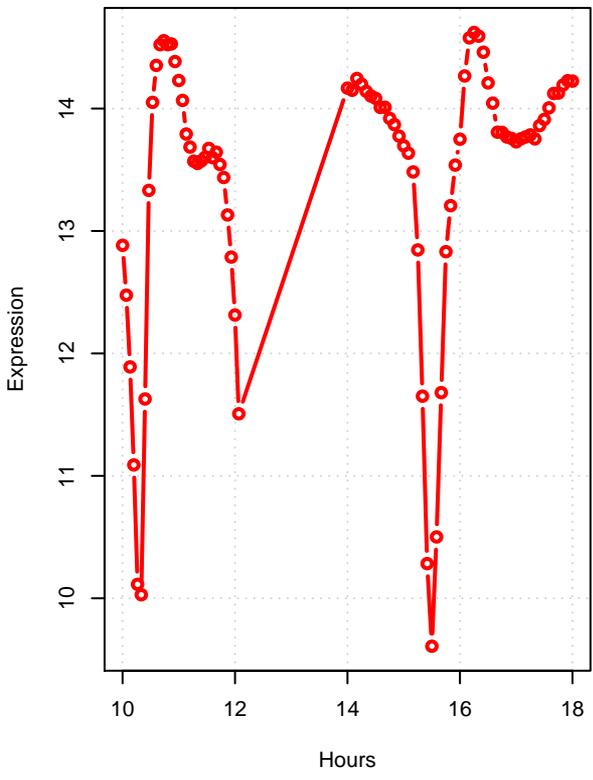
gly1 YEL046C  
Threonine aldolase



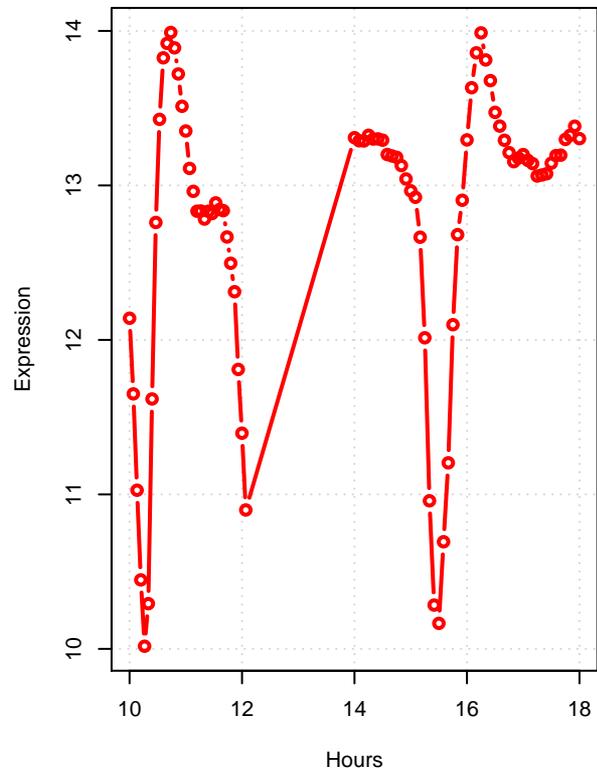
## glycogen catabolism

# glycogen catabolism

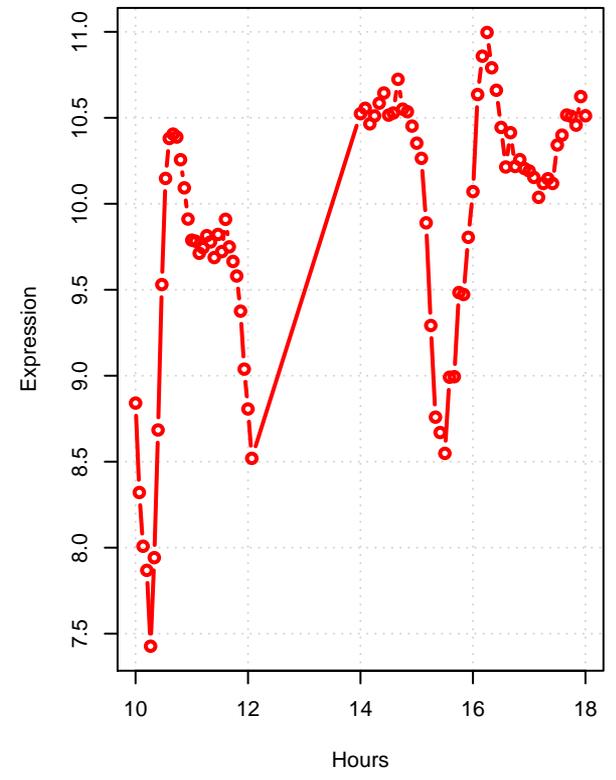
**gph1 YPR160W**  
Glycogen phosphorylase required for the mobilization of glycogen



**gdb1 YPR164W**  
Glycogen debranching enzyme



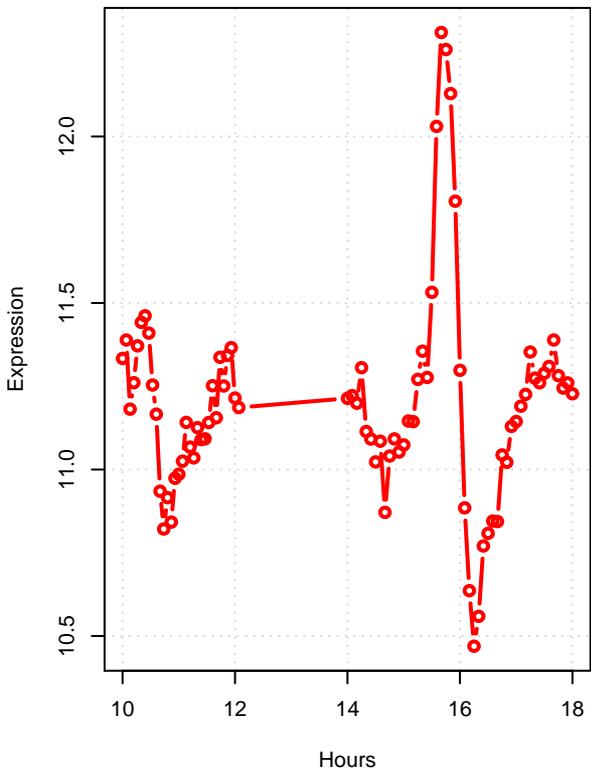
**sga1 YIL099W**  
Intracellular sporulation-specific glucoamylase



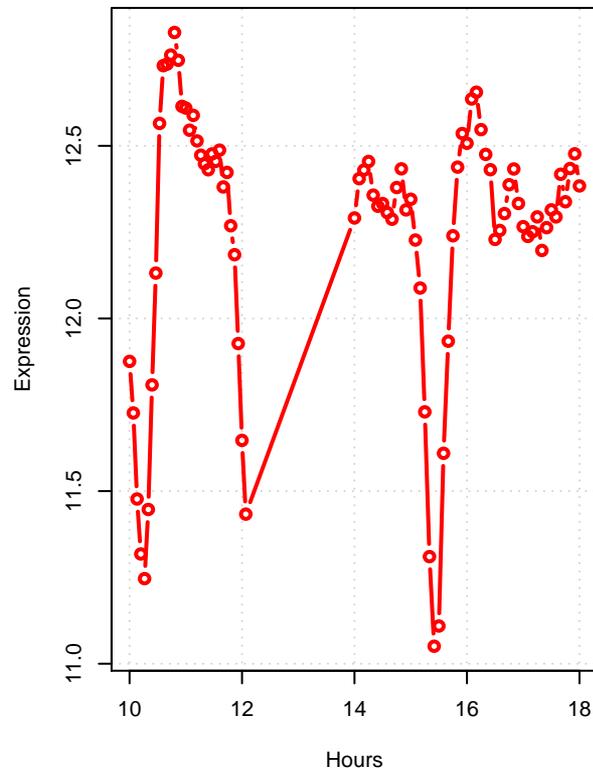
# **heme biosynthesis**

# heme biosynthesis

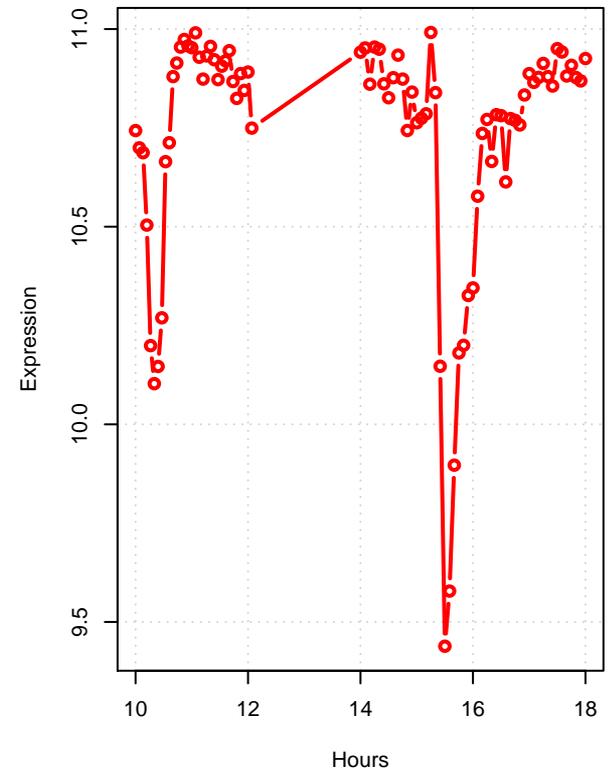
hem13 YDR044W  
Coproporphyrinogen III oxidase



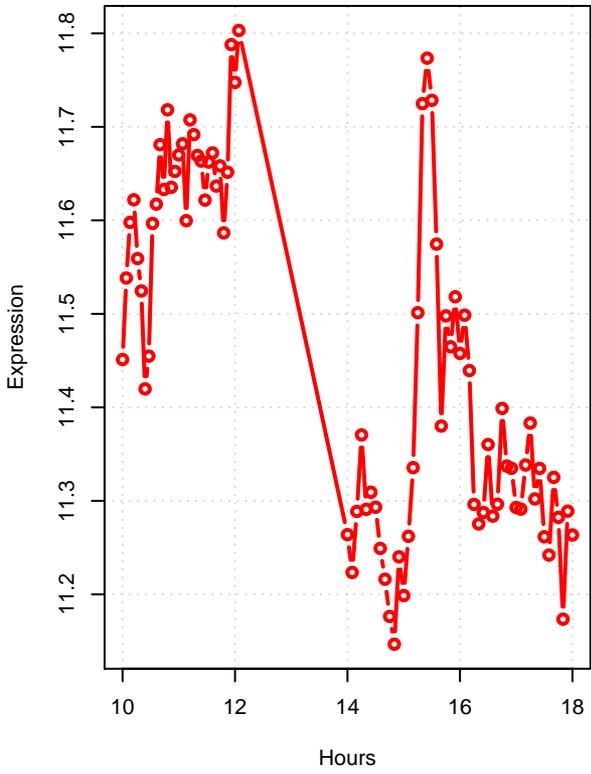
hem15 YOR176W  
Ferrochelatase



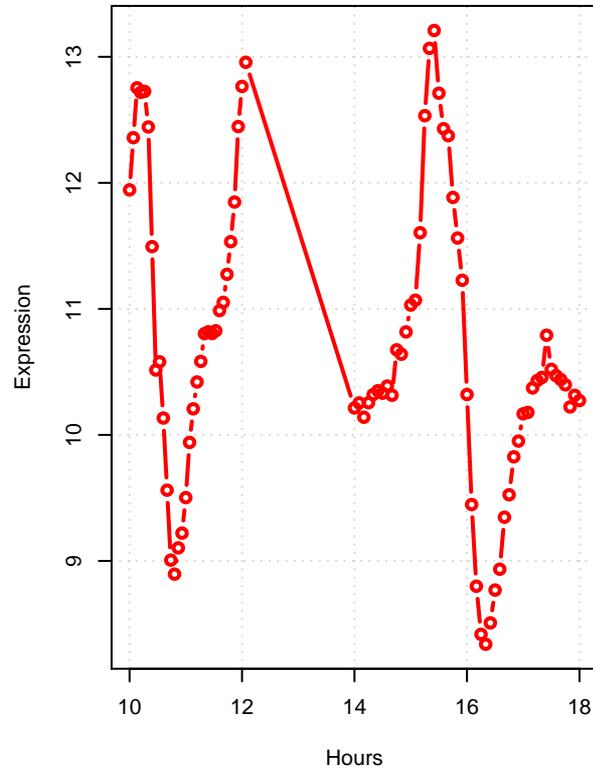
hem14 YER014W  
Protoporphyrinogen oxidase



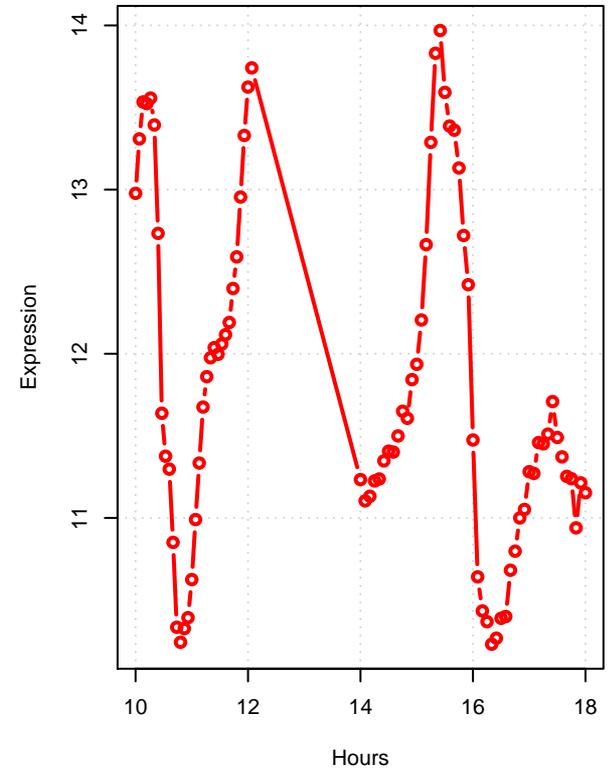
hem12 YDR047W  
Uroporphyrinogen decarboxylase



met8 YBR213W  
Bifunctional dehydrogenase and ferrochelatase

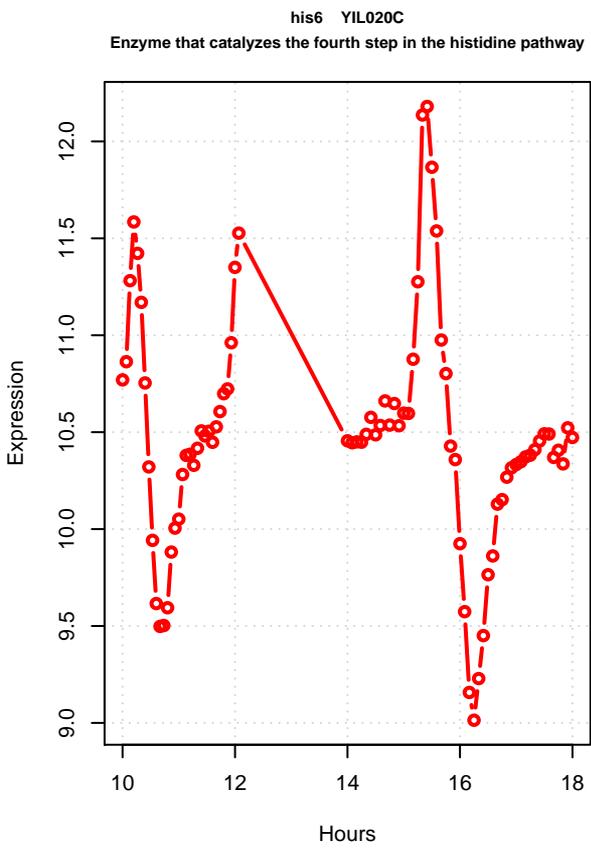
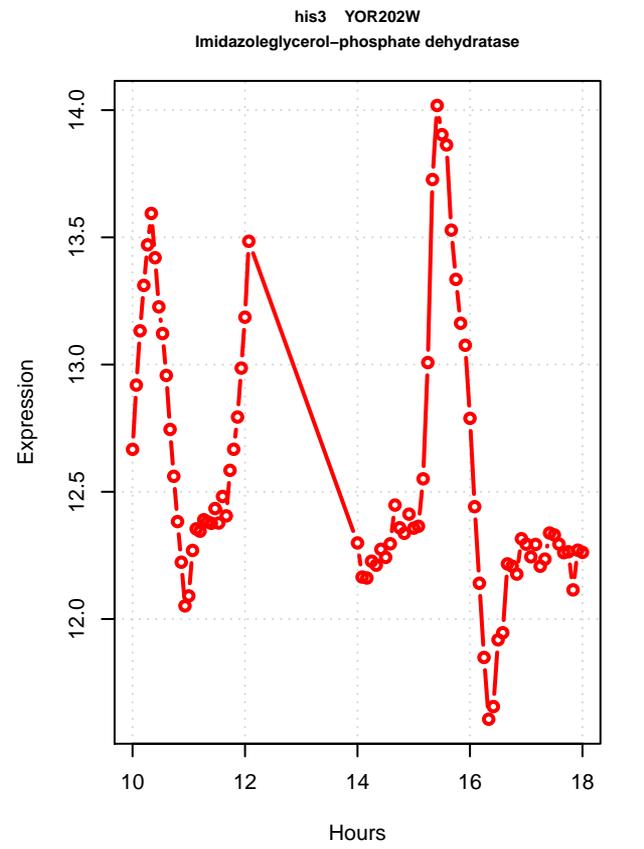
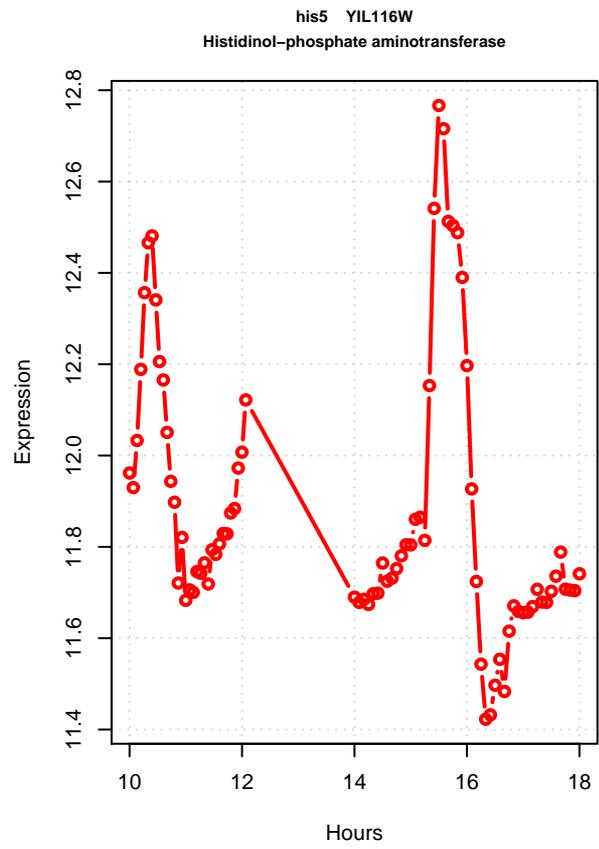
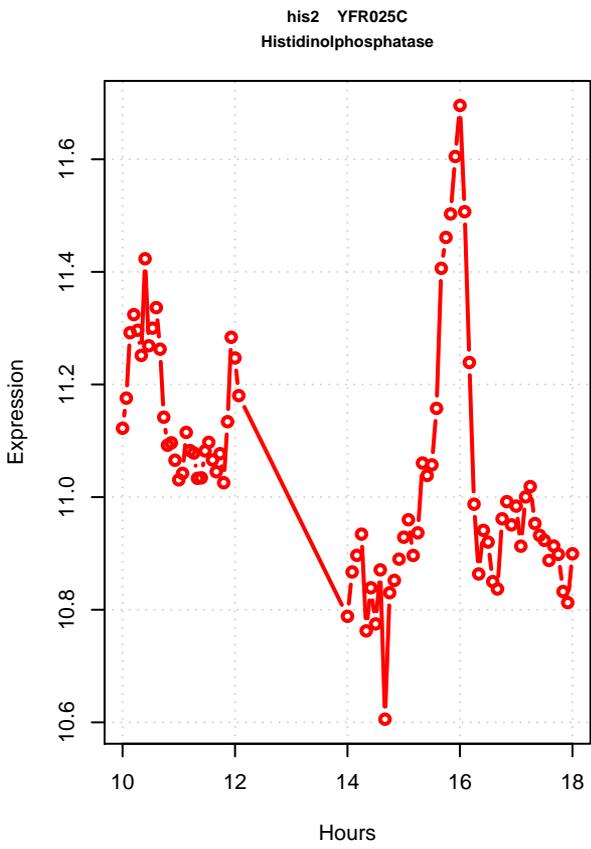
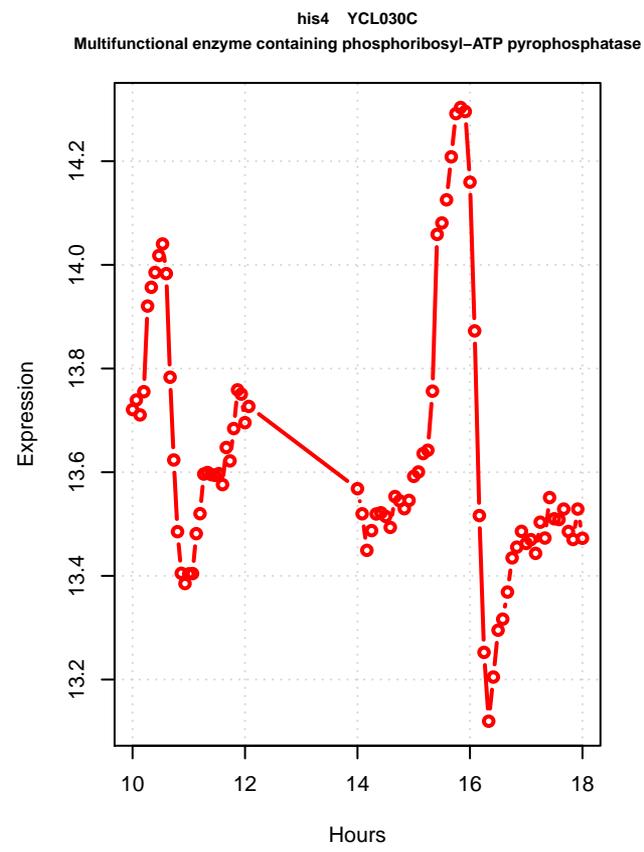
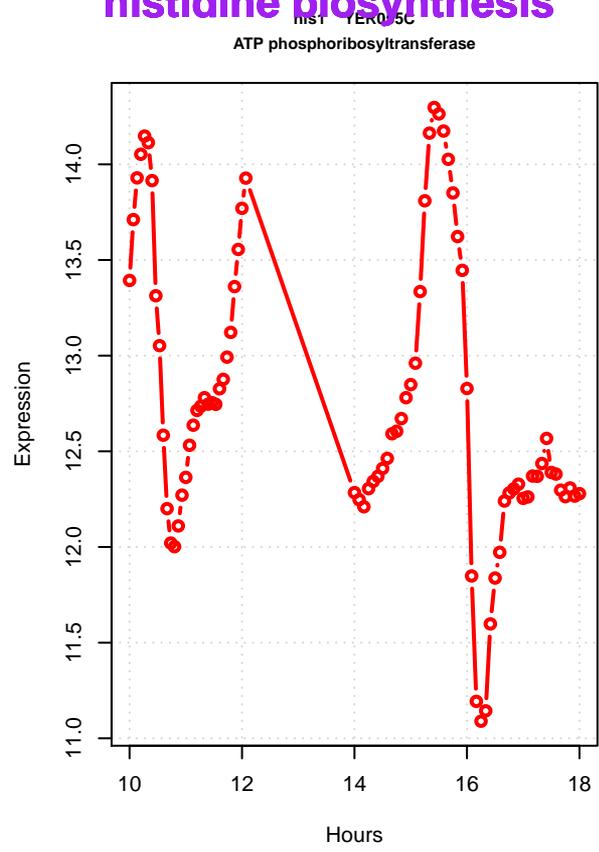
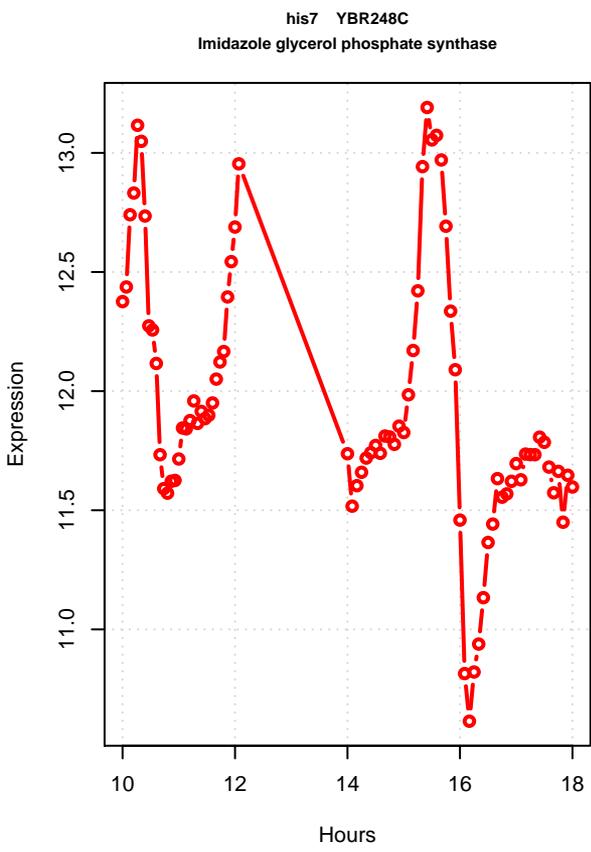


met1 YKR069W  
S-adenosyl-L-methionine uroporphyrinogen III transmethylase



## histidine biosynthesis

# histidine biosynthesis

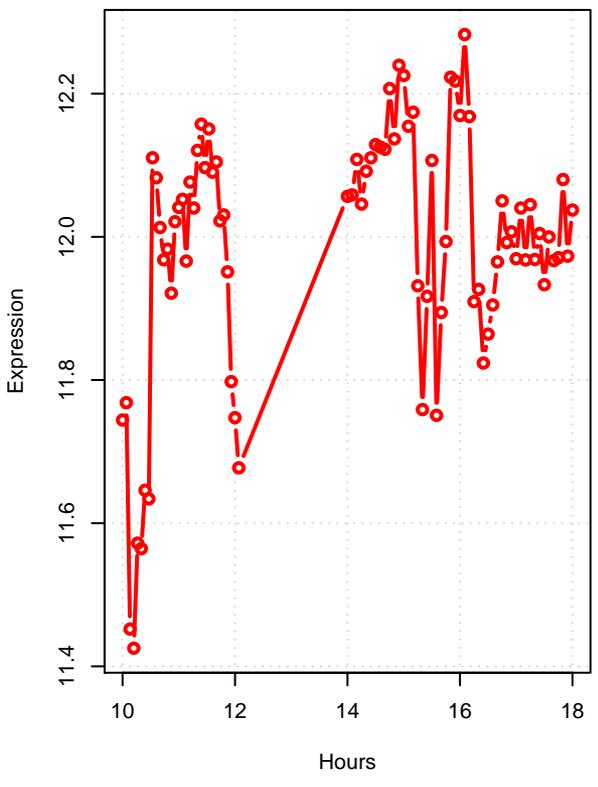


## homocysteine and cysteine interconversion

# homocysteine and cysteine interconversion

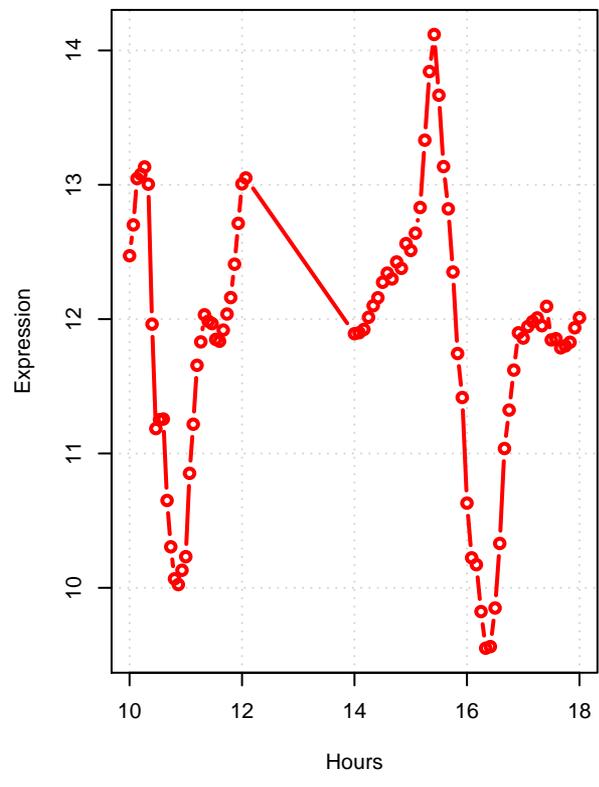
str2 YJR130C

Cystathionine gamma-synthase, converts cysteine into cystathionine



str3 YGL184C

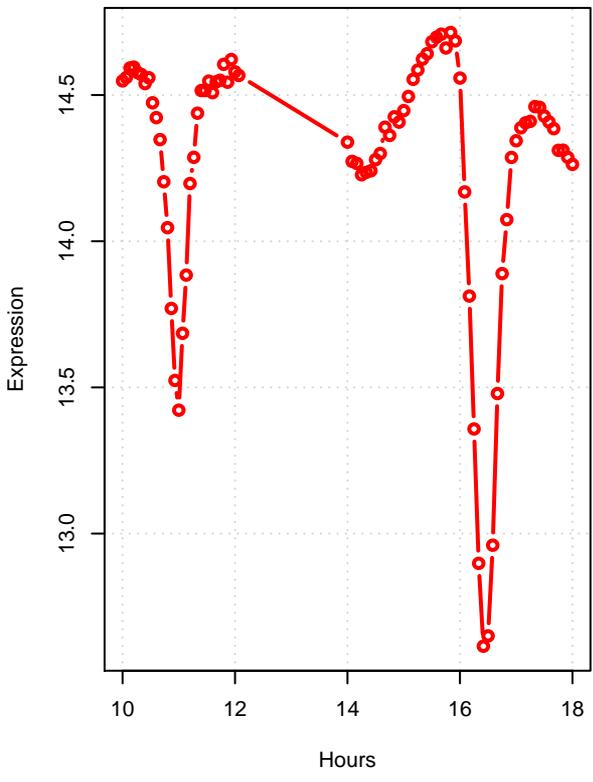
Peroxisomal cystathionine beta-lyase



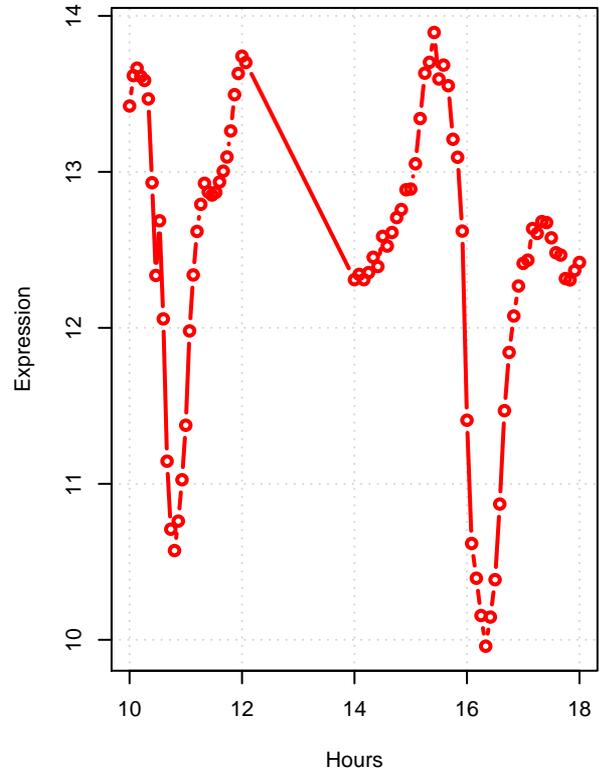
## homocysteine biosynthesis

# homocysteine biosynthesis

met17 YLR303W  
O-acetyl homoserine-O-acetyl serine sulfhydrylase



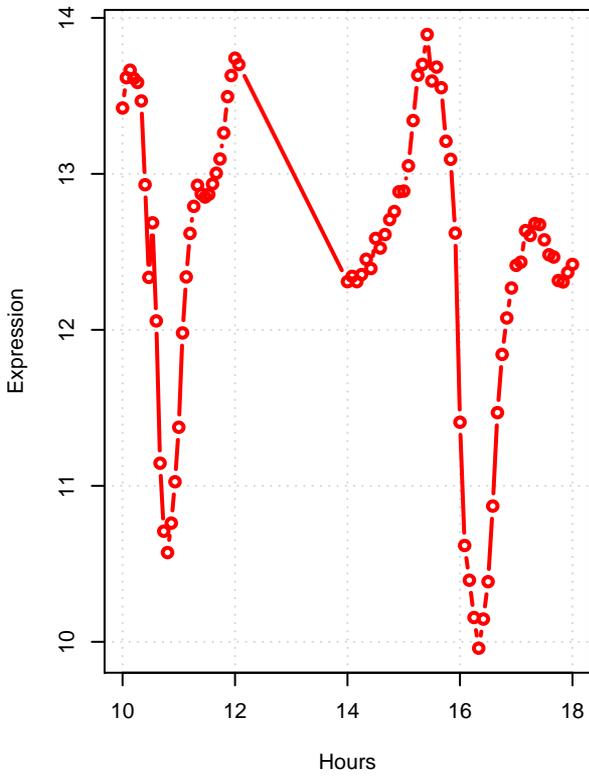
met2 YNL277W  
L-homoserine-O-acetyltransferase



**superpathway of sulfur amino acid biosynthesis**

# superpathway of sulfur amino acid biosynthesis

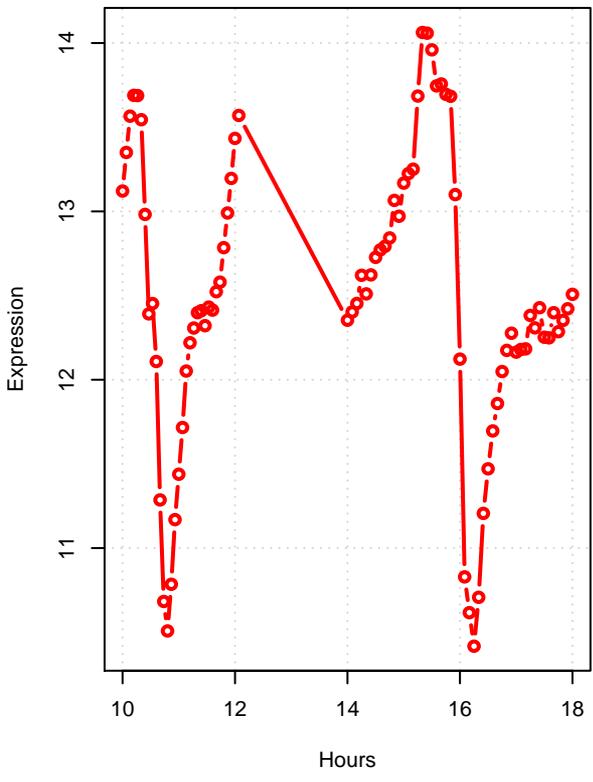
met2 YNL277W  
L-homoserine-O-acetyltransferase



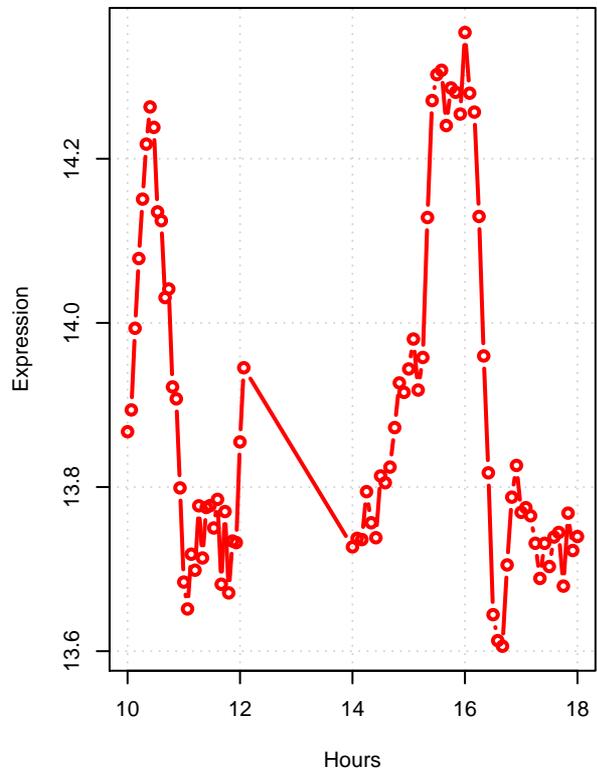
## homoserine biosynthesis

# homoserine biosynthesis

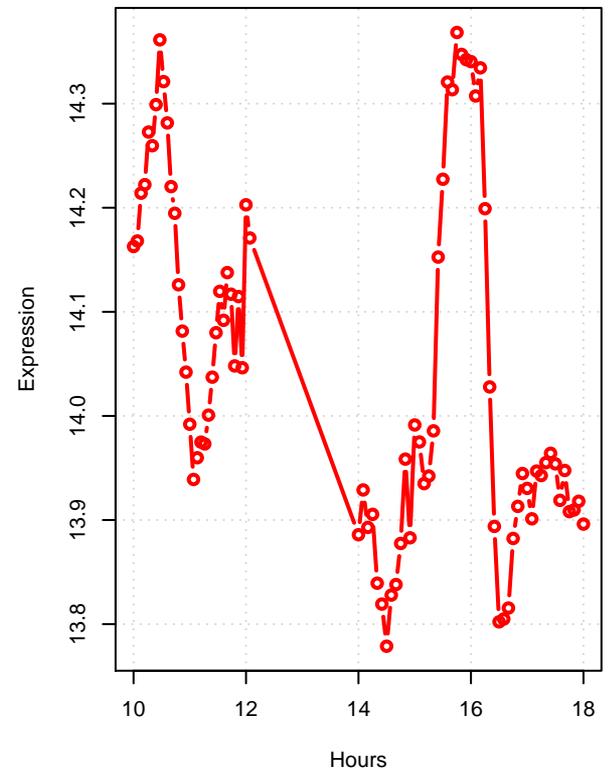
hom3 YER052C  
Aspartate kinase (L-aspartate 4-P-transferase)



hom2 YDR156W  
Aspartic beta semi-aldehyde dehydrogenase



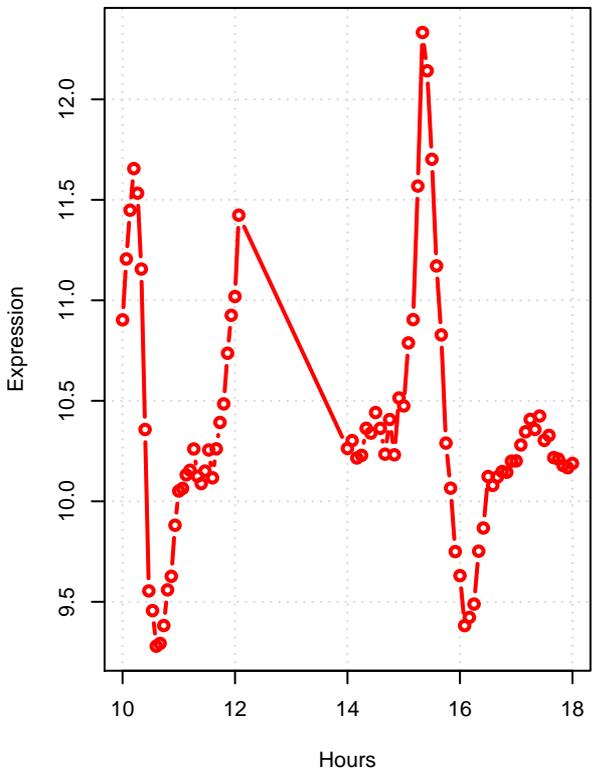
hom6 YJR139C  
Homoserine dehydrogenase (L-homoserine:NADP oxidoreductase)



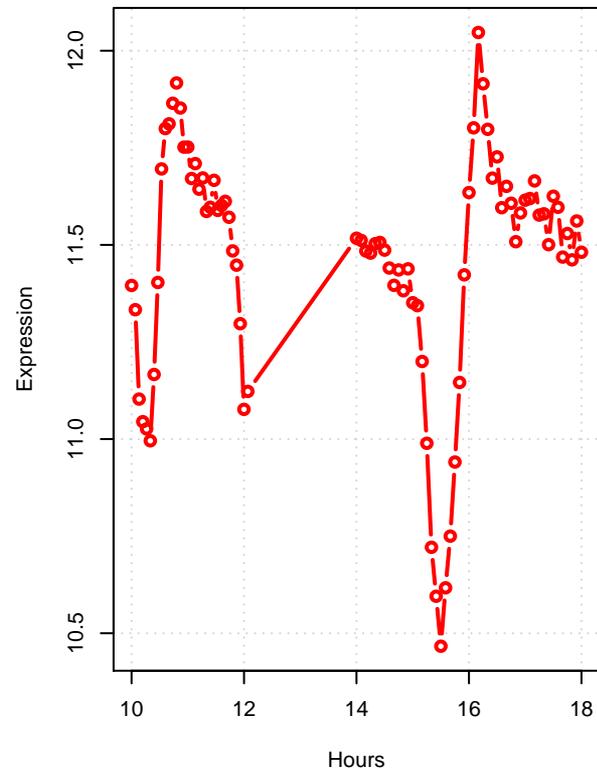
**<i>myo</i>-inositol biosynthesis**

# *ino*-inositol biosynthesis

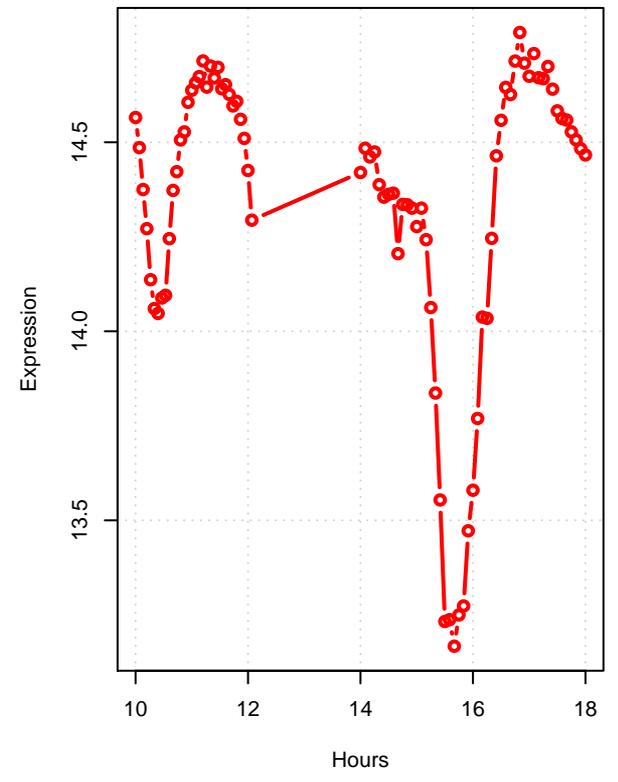
ino1 YHR046C  
Inositol monophosphatase



ino2 YDR287W  
Inositol monophosphatase

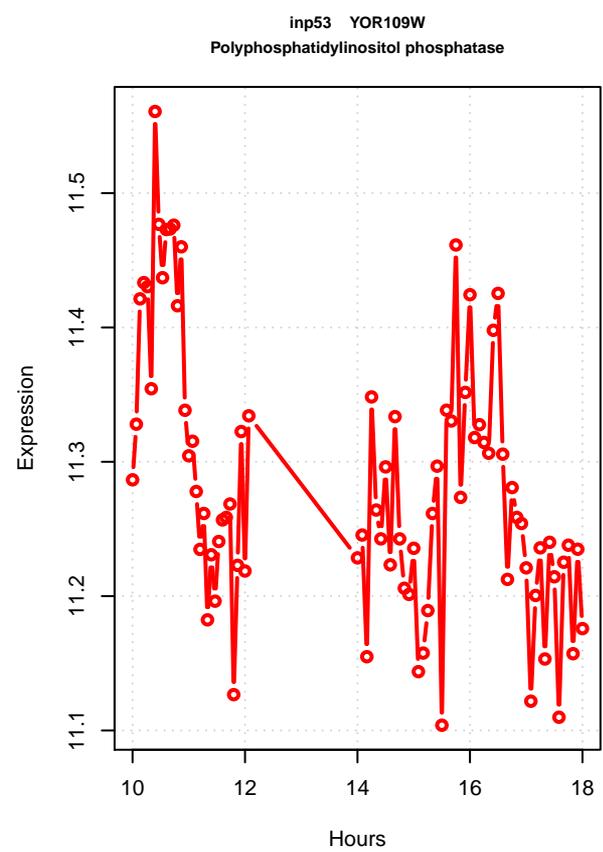
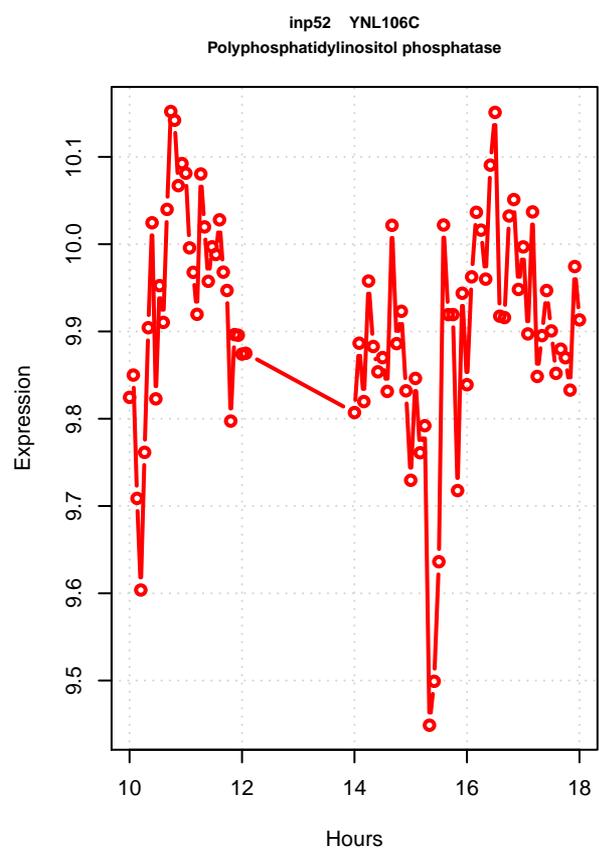
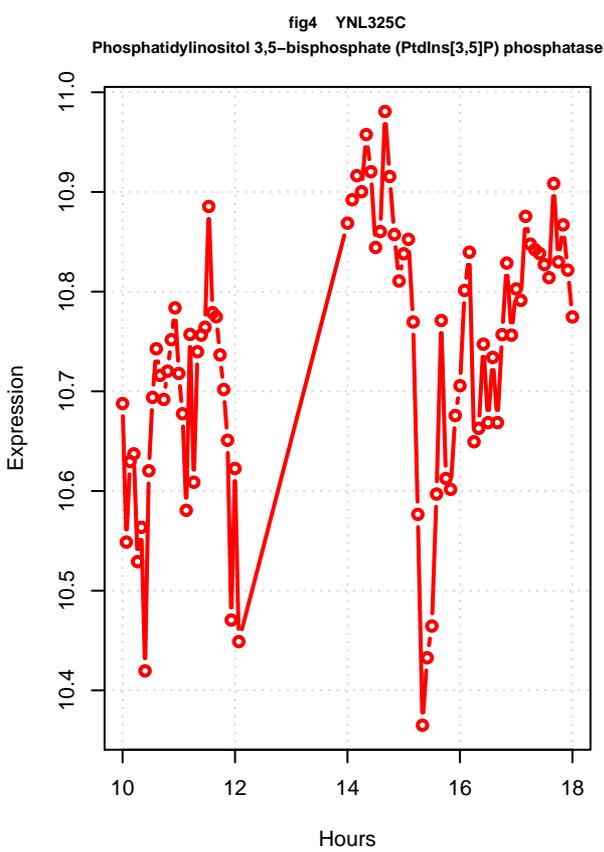
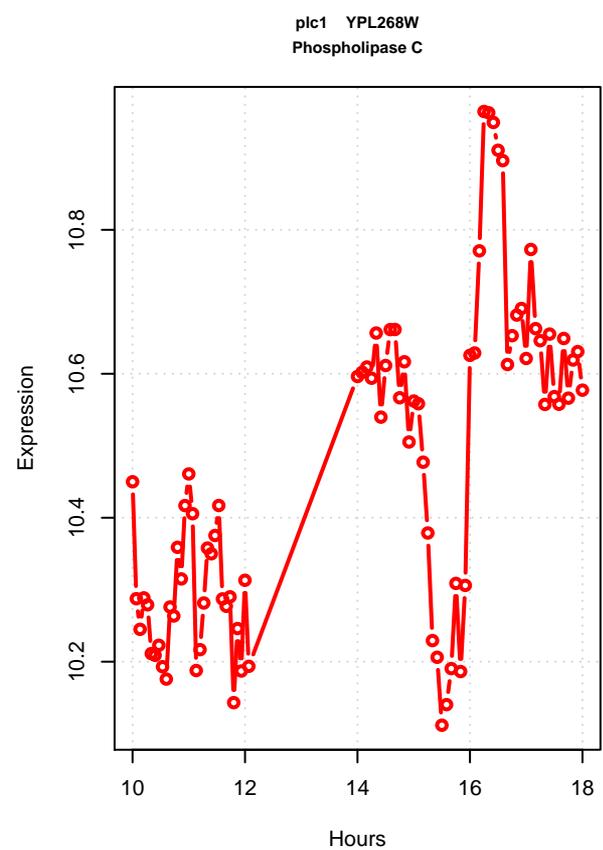
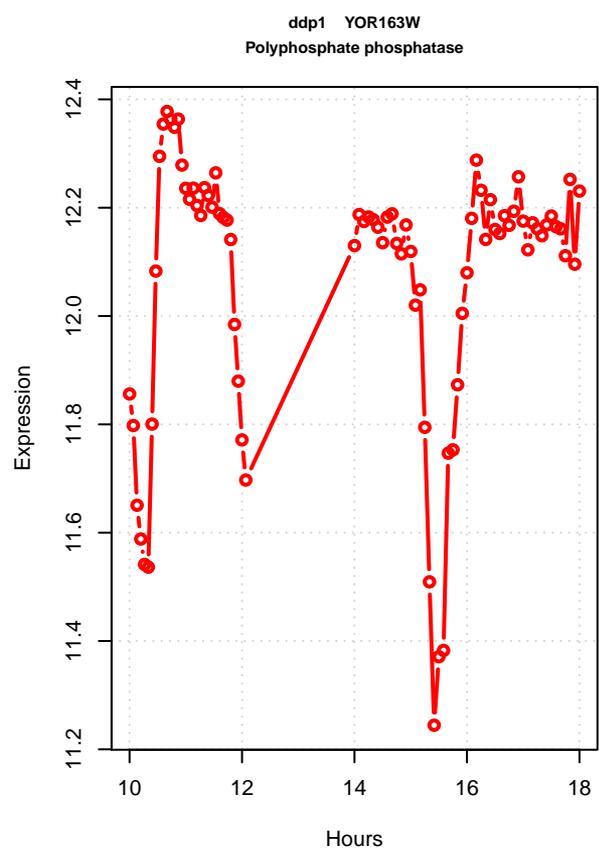
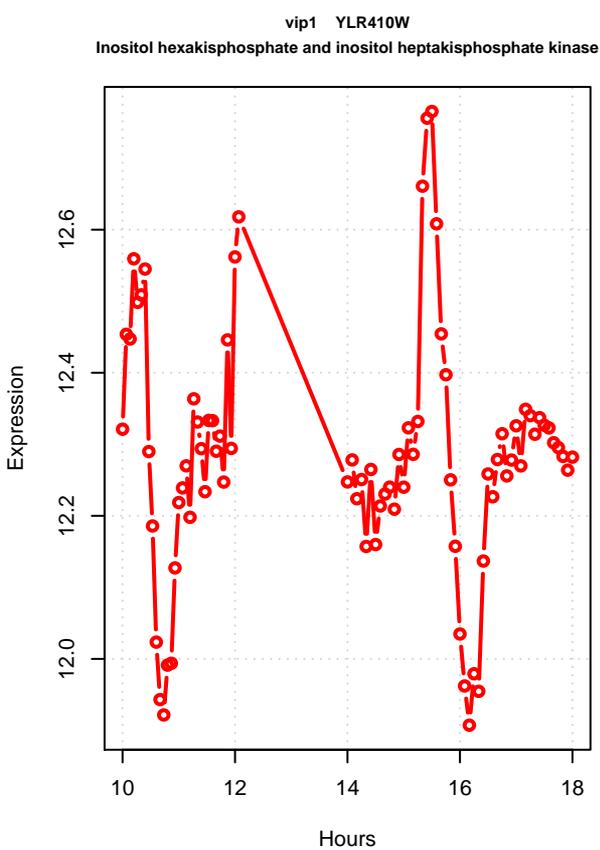
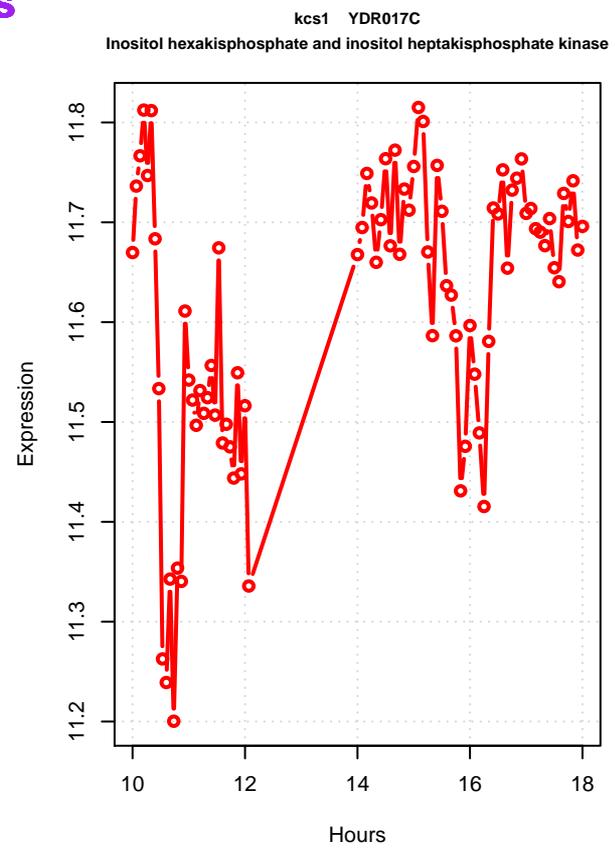
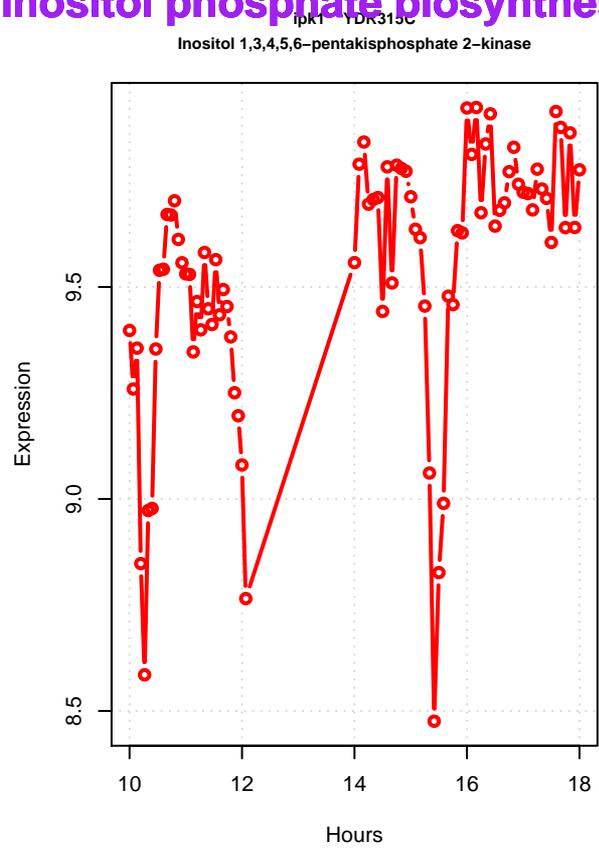
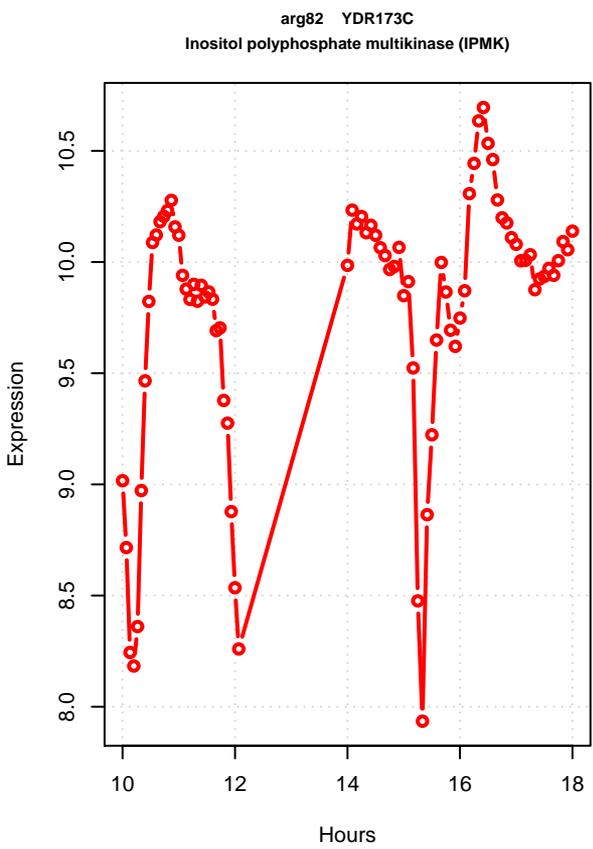


ino1 YJL153C  
Inositol-3-phosphate synthase



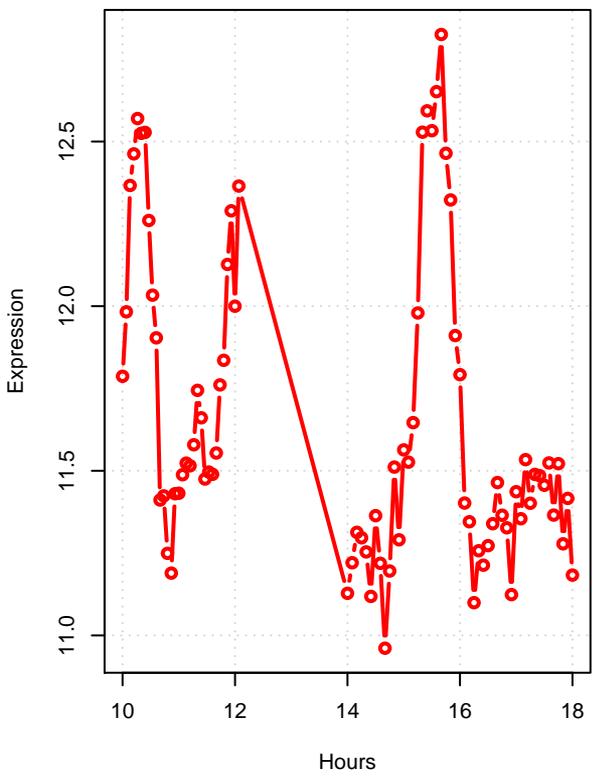
## **inositol phosphate biosynthesis**

# inositol phosphate biosynthesis

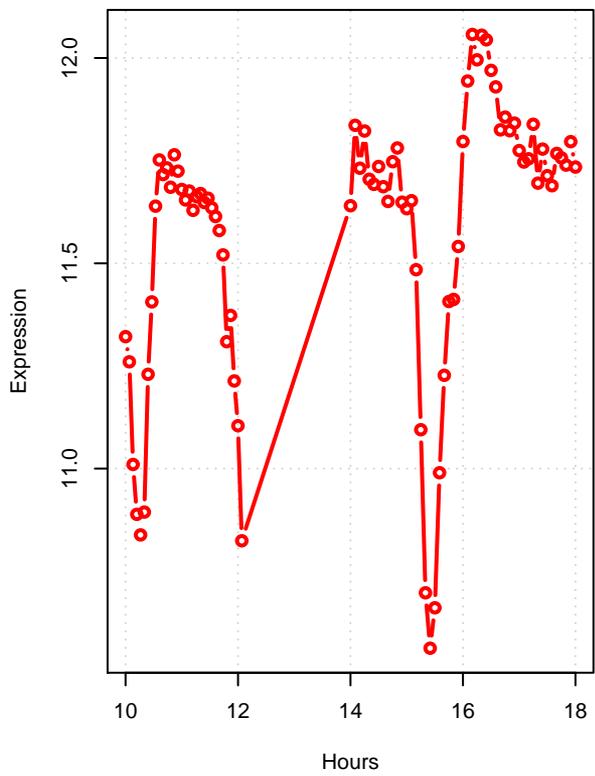


# inositol phosphate biosynthesis

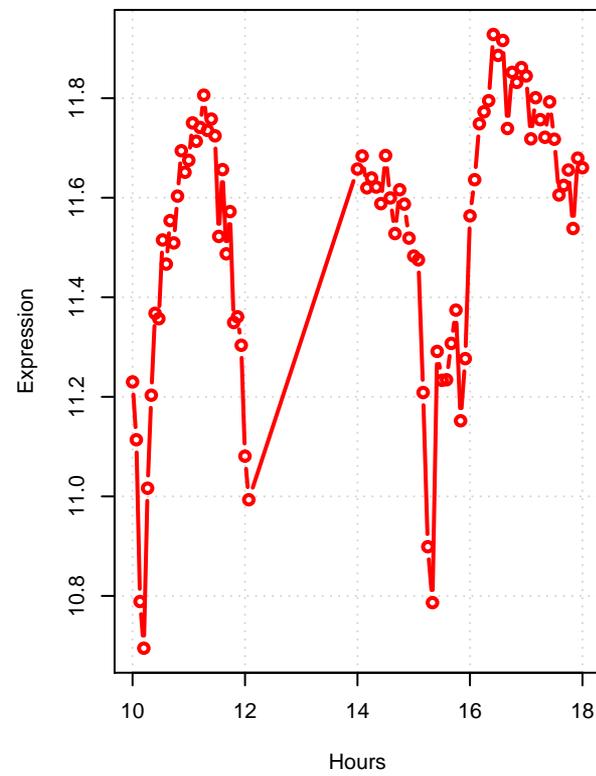
**sac1 YKL212W**  
Phosphatidylinositol phosphate (PtdInsP) phosphatase



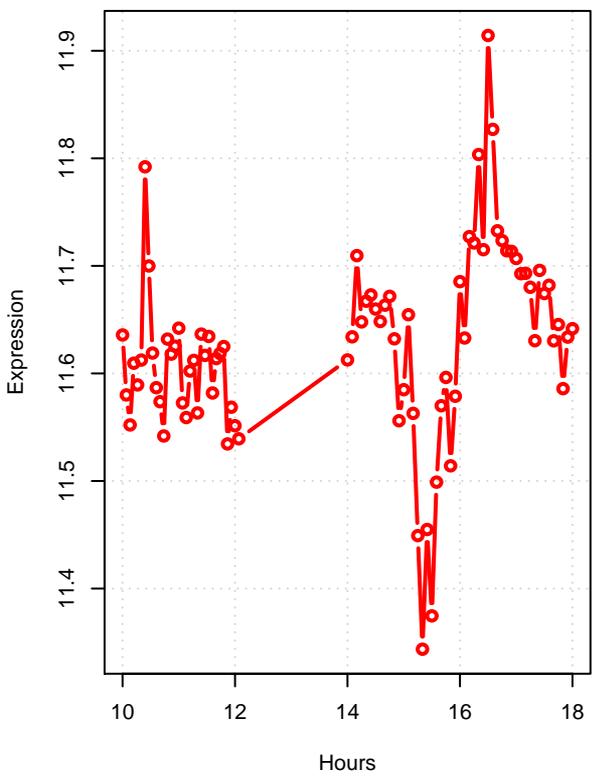
**vps34 YLR240W**  
Phosphatidylinositol (PI) 3-kinase that synthesizes PI-3-phosphate



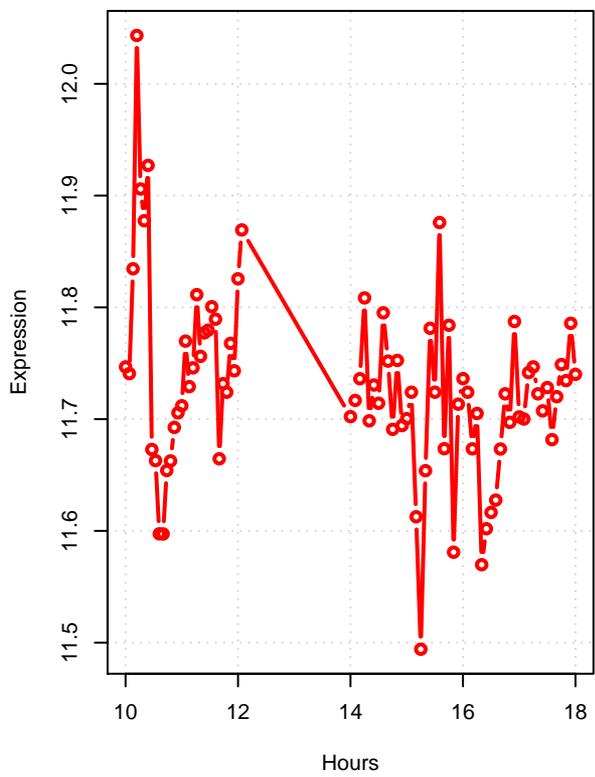
**Isb6 YJL100W**  
Type II phosphatidylinositol 4-kinase



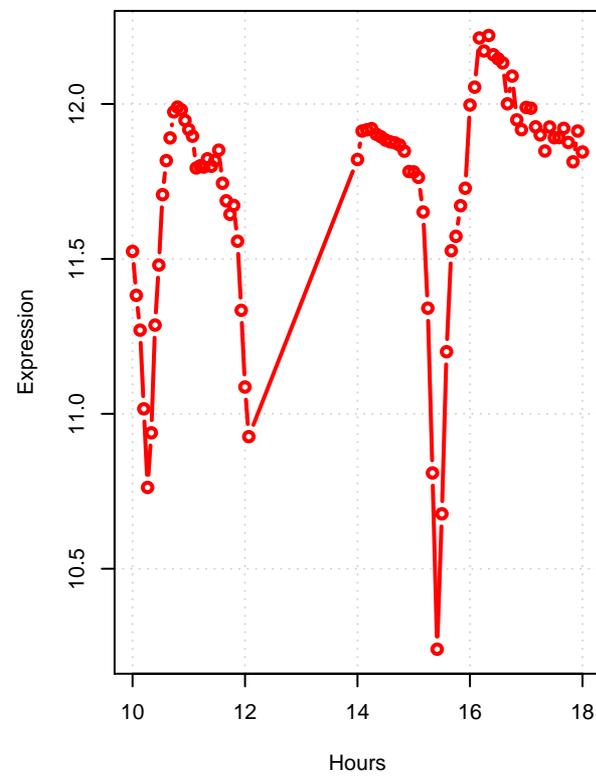
**pik1 YNL267W**  
Phosphatidylinositol 4-kinase



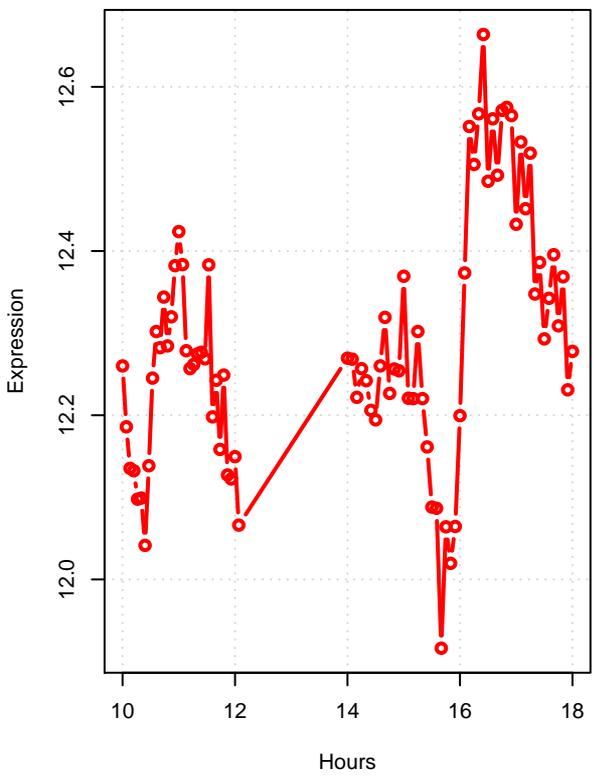
**stt4 YLR305C**  
Phosphatidylinositol-4-kinase



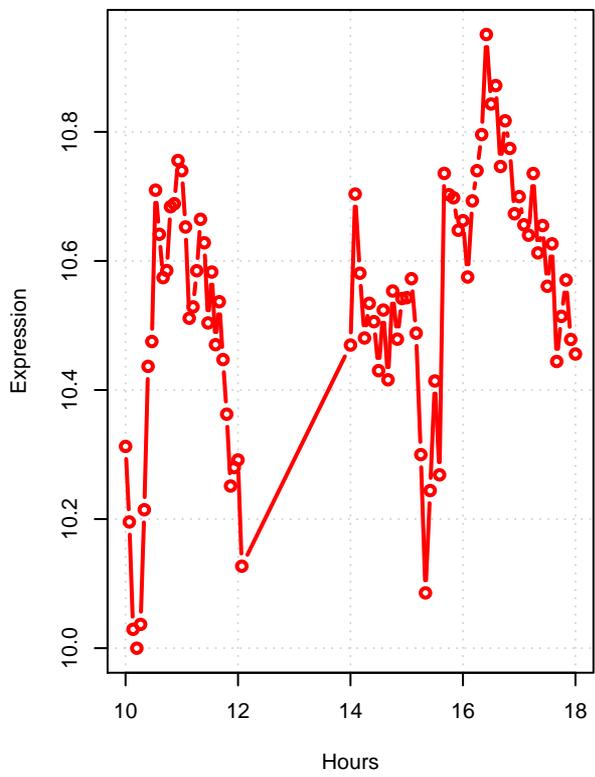
**fab1 YFR019W**  
1-phosphatidylinositol-3-phosphate 5-kinase



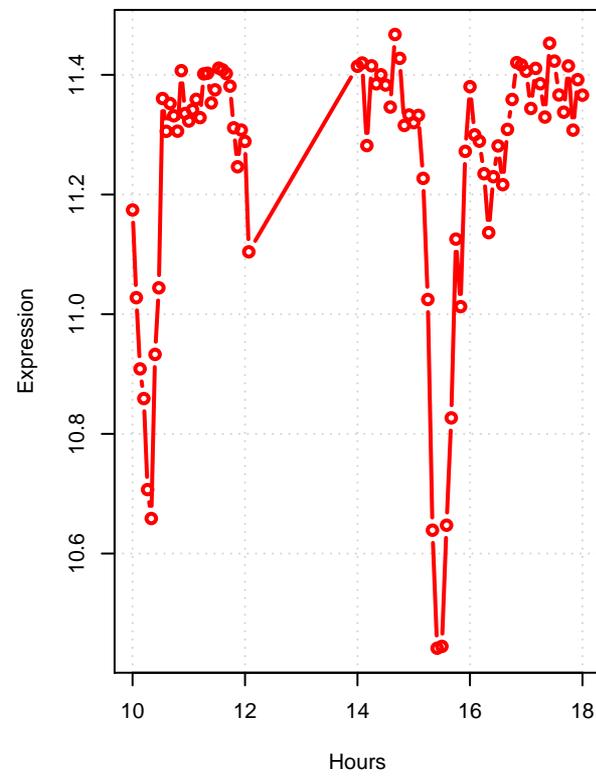
**mss4 YDR208W**  
Phosphatidylinositol-4-phosphate 5-kinase



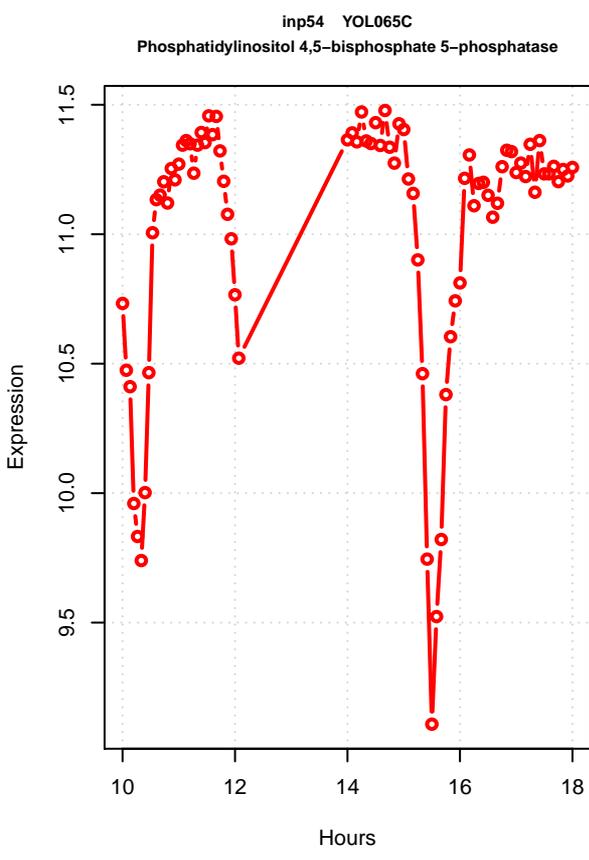
**ymr1 YJR110W**  
Phosphatidylinositol 3-phosphate (PI3P) phosphatase



**inp51 YIL002C**  
Phosphatidylinositol 4,5-bisphosphate 5-phosphatase



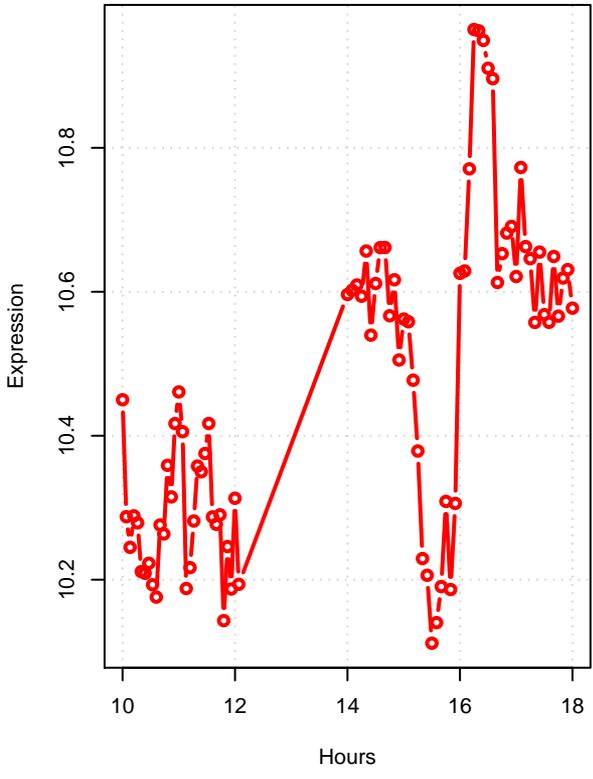
# inositol phosphate biosynthesis



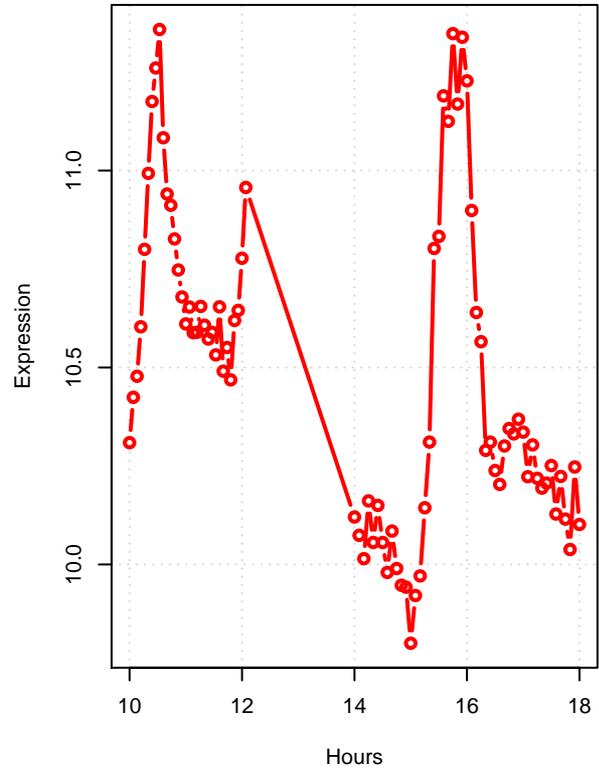
## phospholipids degradation

# phospholipids degradation

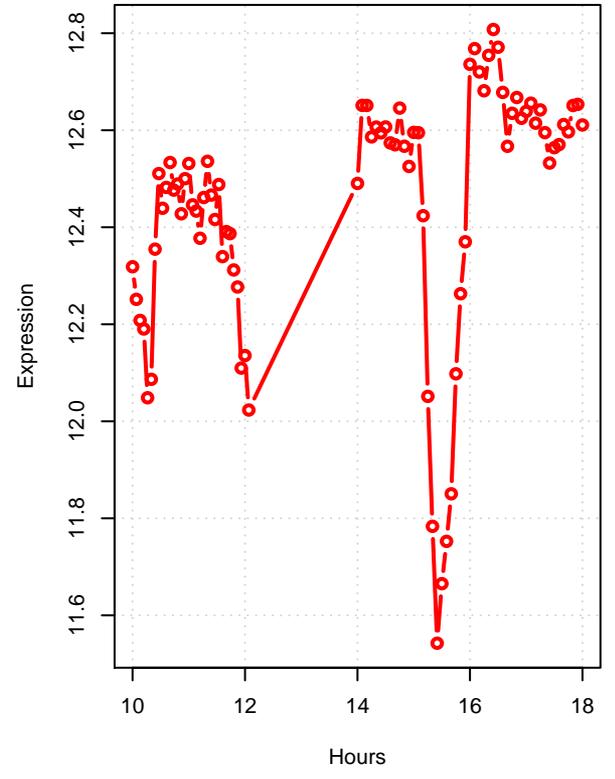
plc1 YPL268W  
Phospholipase C



isc1 YEK019W  
Inositol phosphosphingolipid phospholipase C

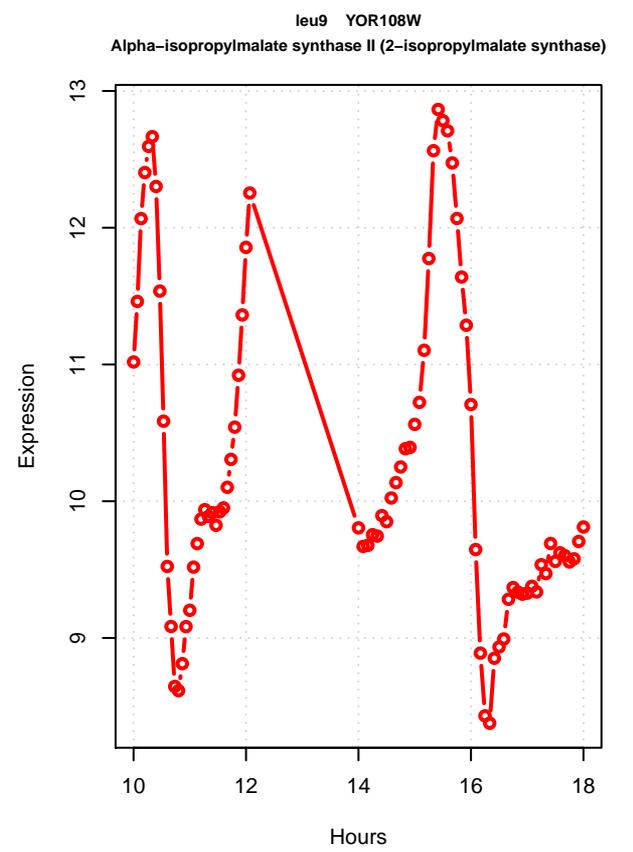
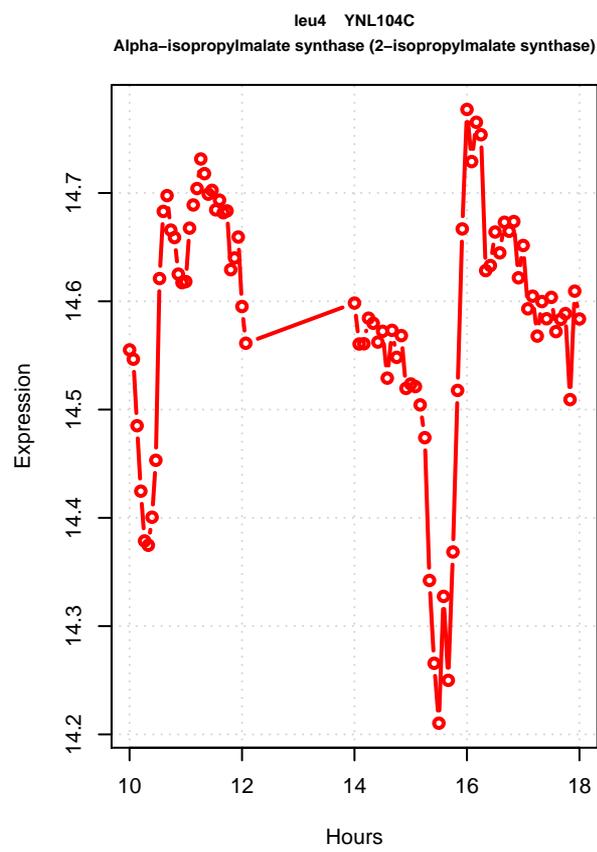
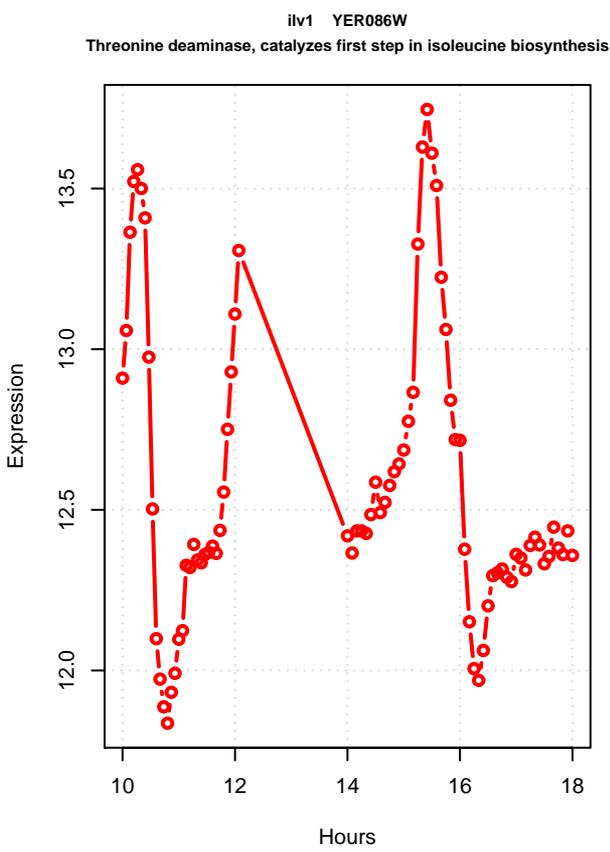
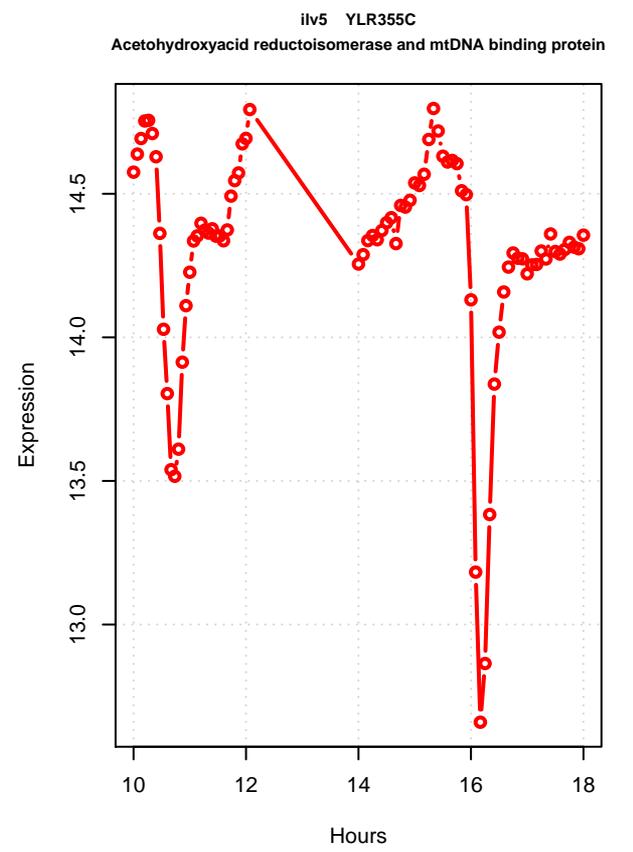
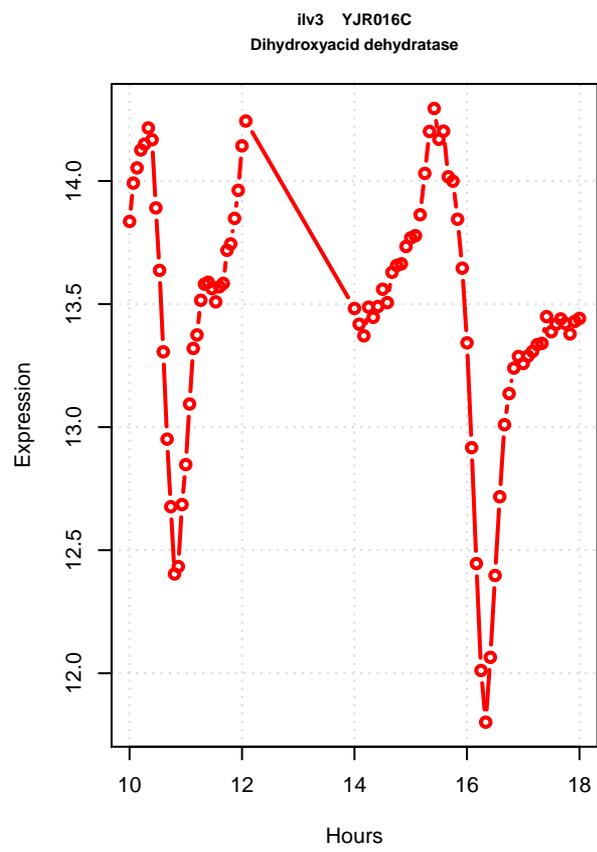
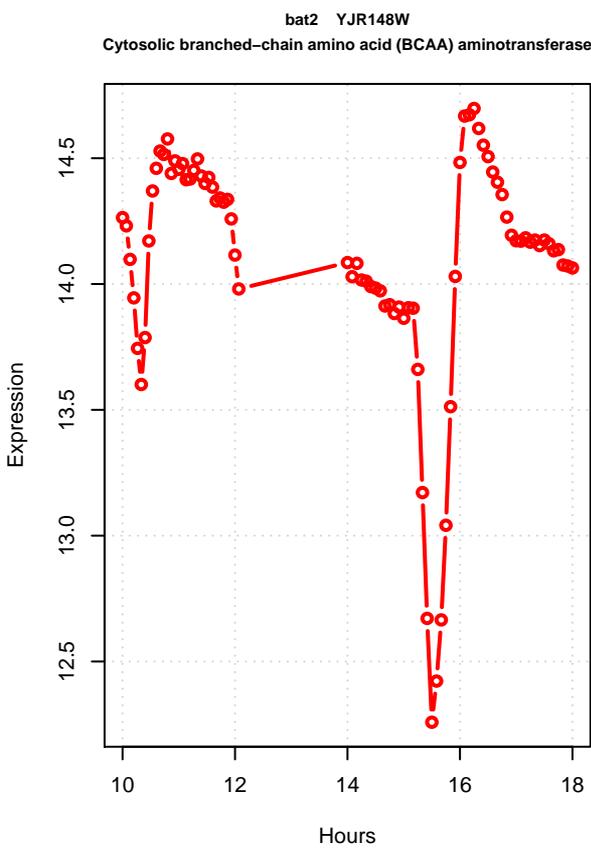
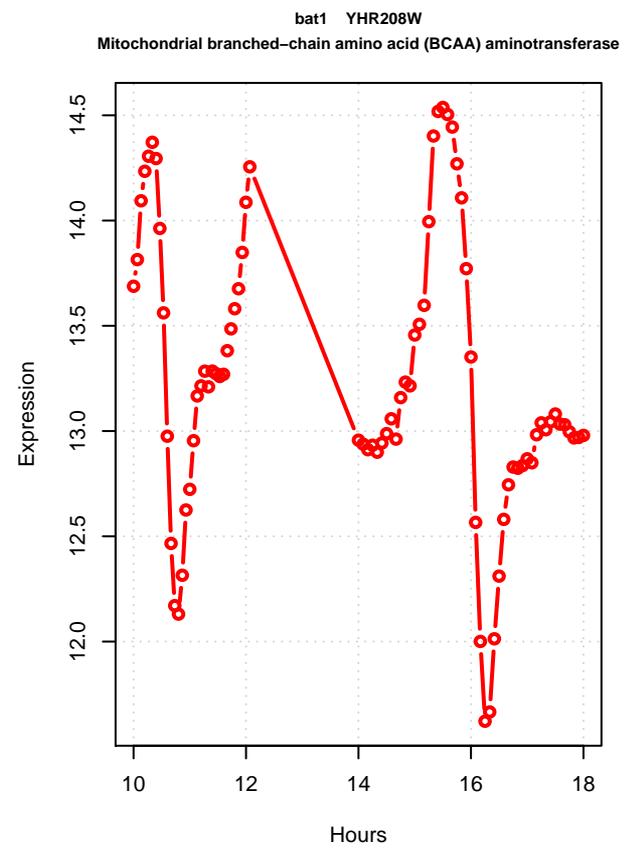
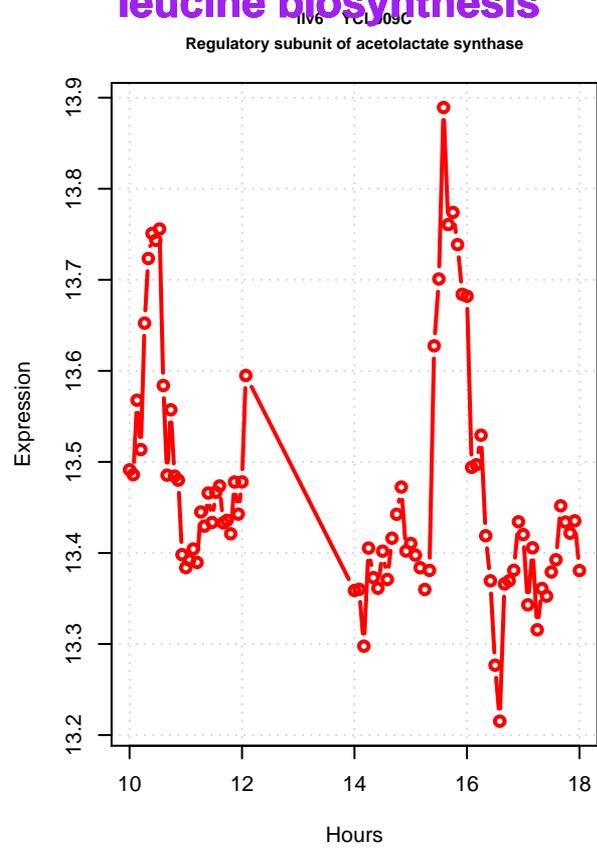
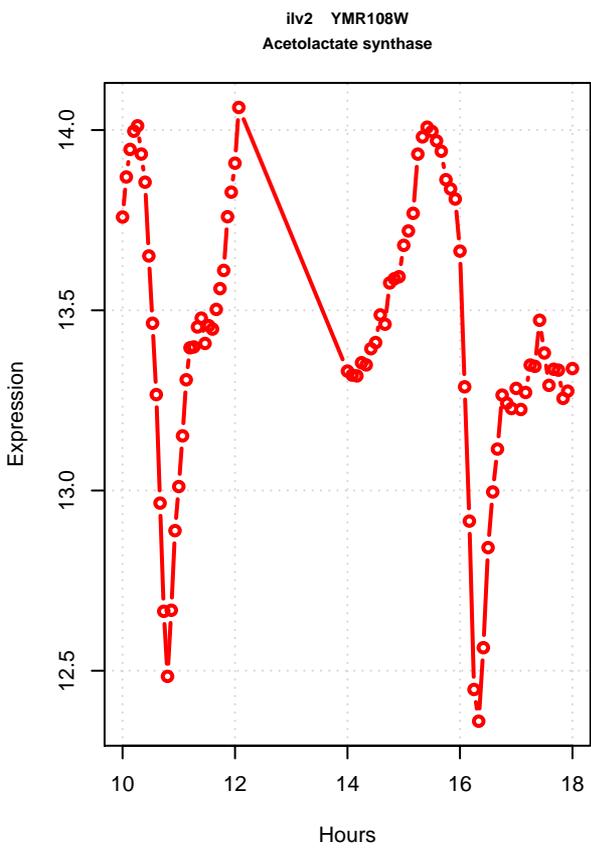


spo14 YKR031C  
Phospholipase D



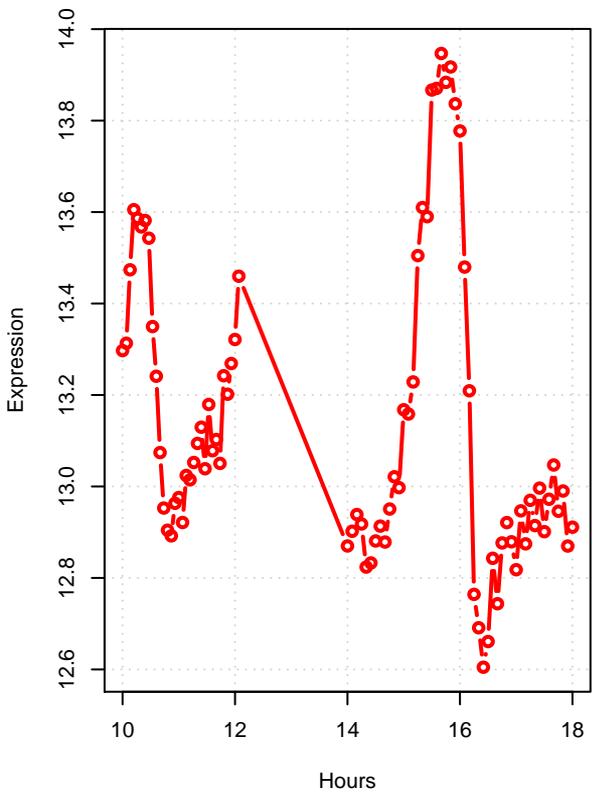
## leucine biosynthesis

# leucine biosynthesis

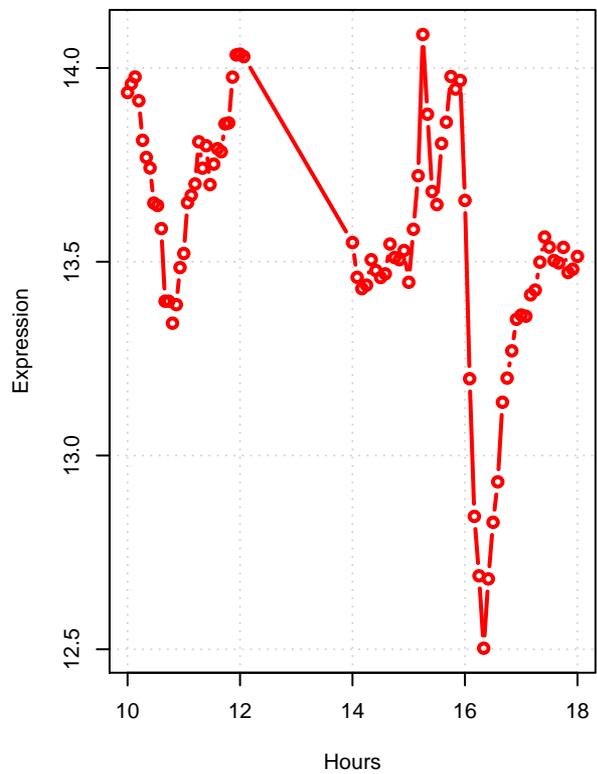


# leucine biosynthesis

leu1 YGL009C  
Isopropylmalate isomerase

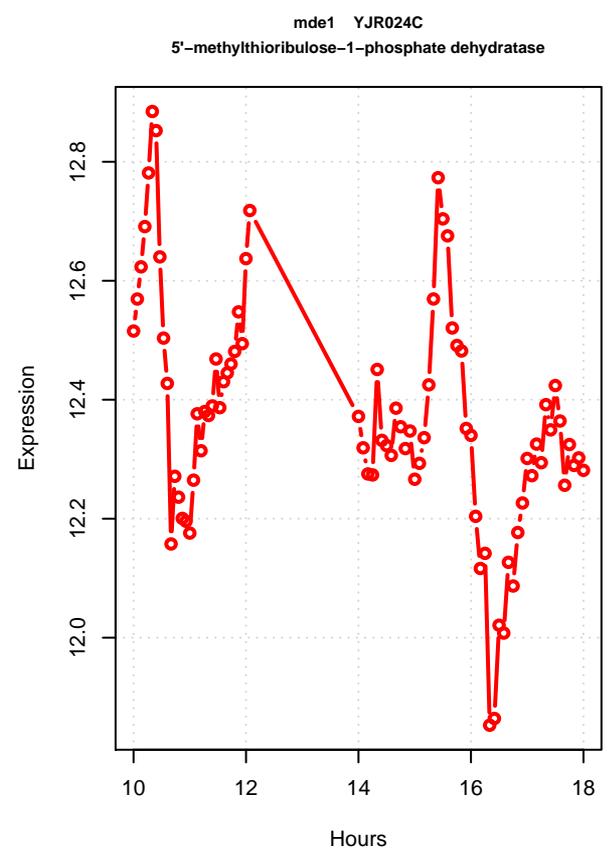
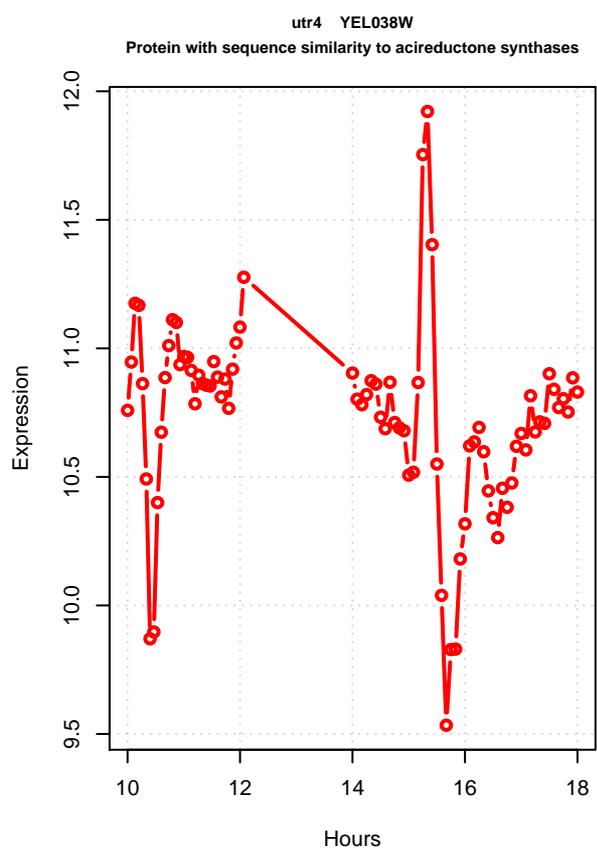
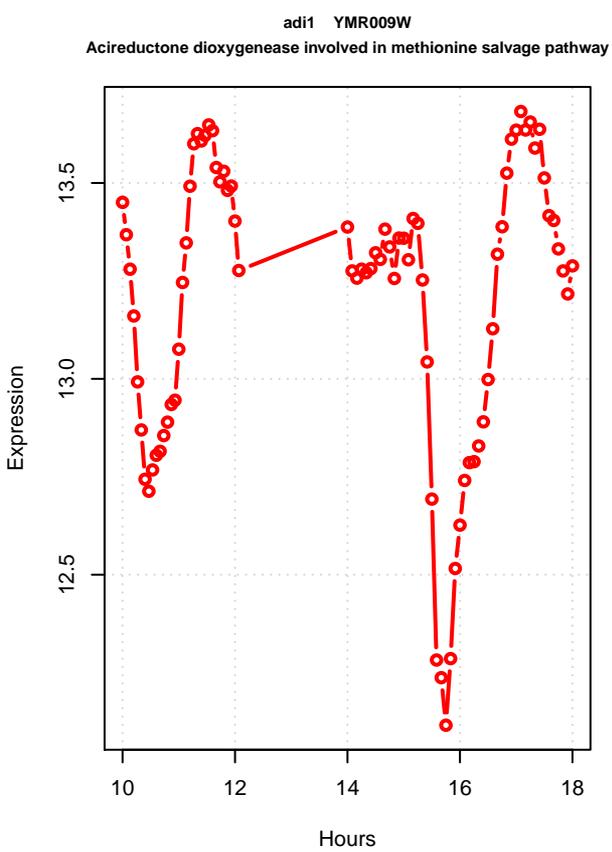
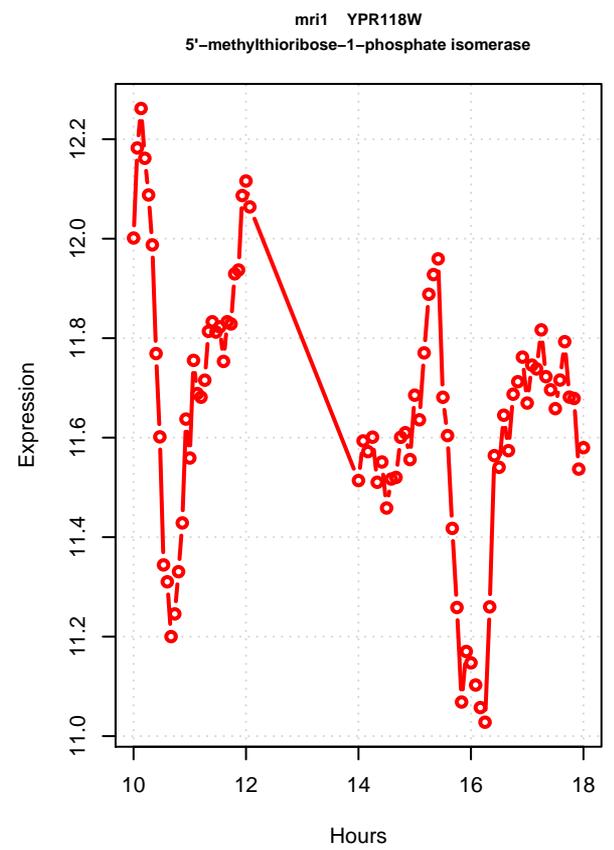
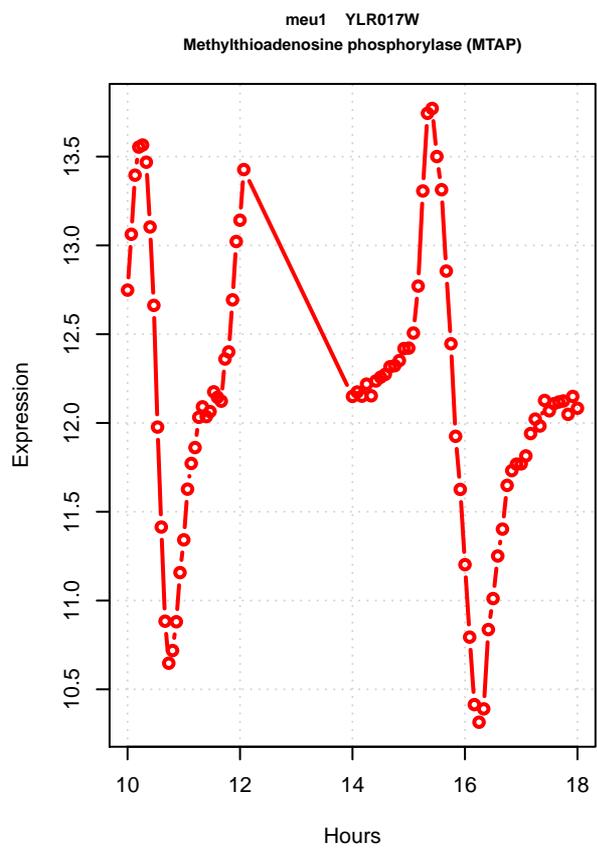
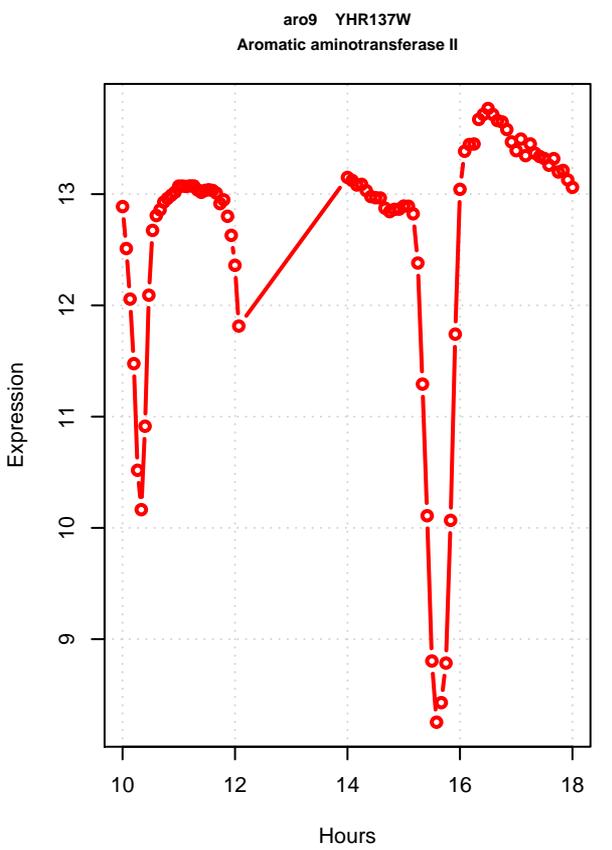
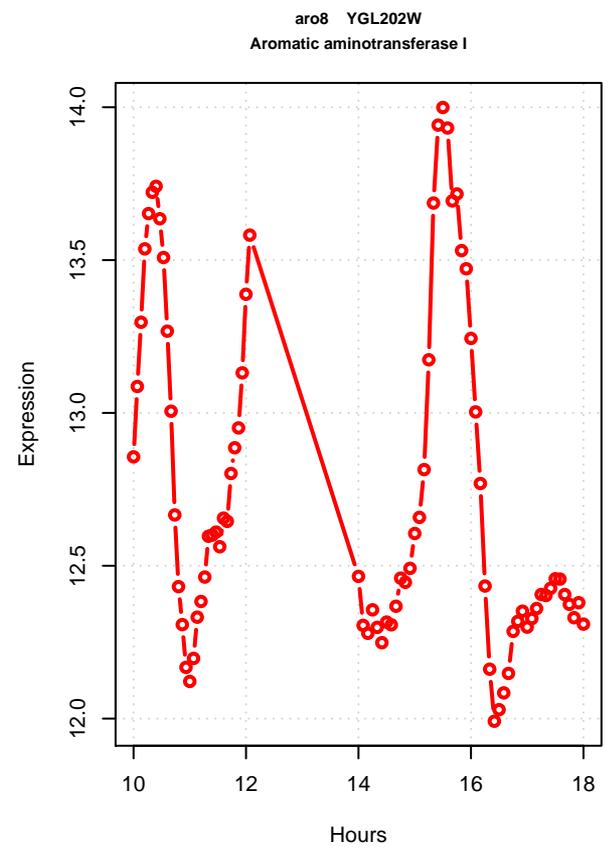
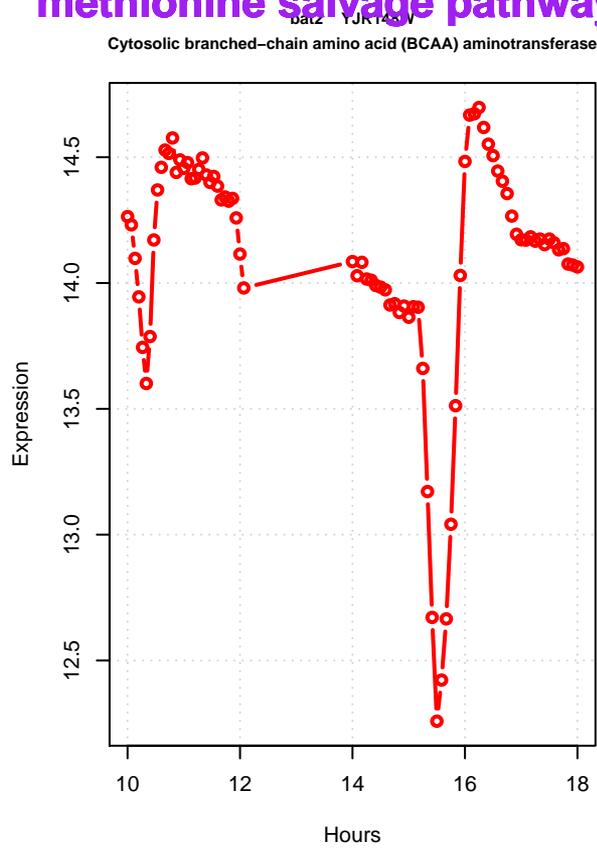
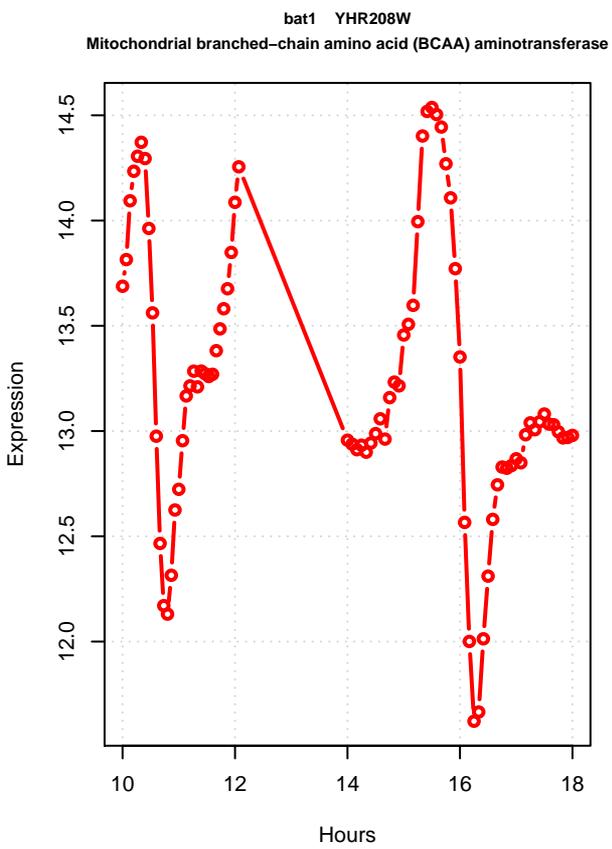


leu2 YCL118W  
Beta-isopropylmalate dehydrogenase (IMDH)



**methionine salvage pathway**

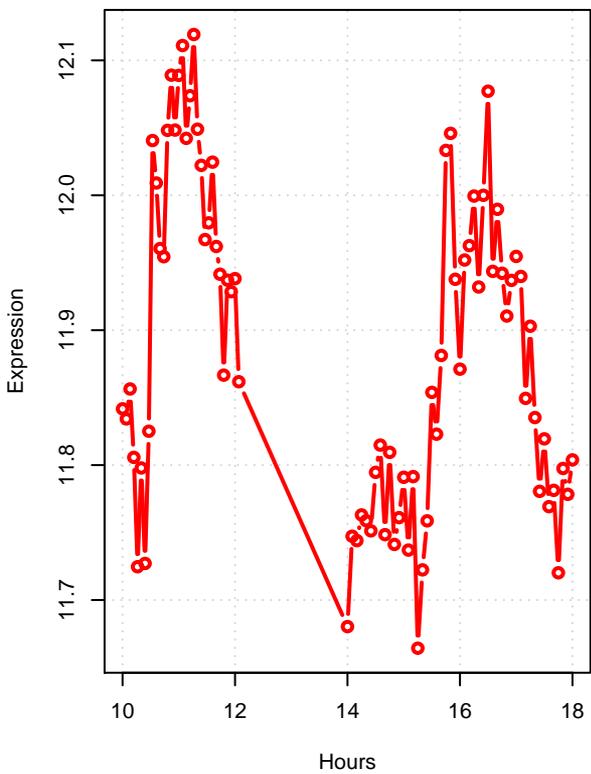
# methionine salvage pathway



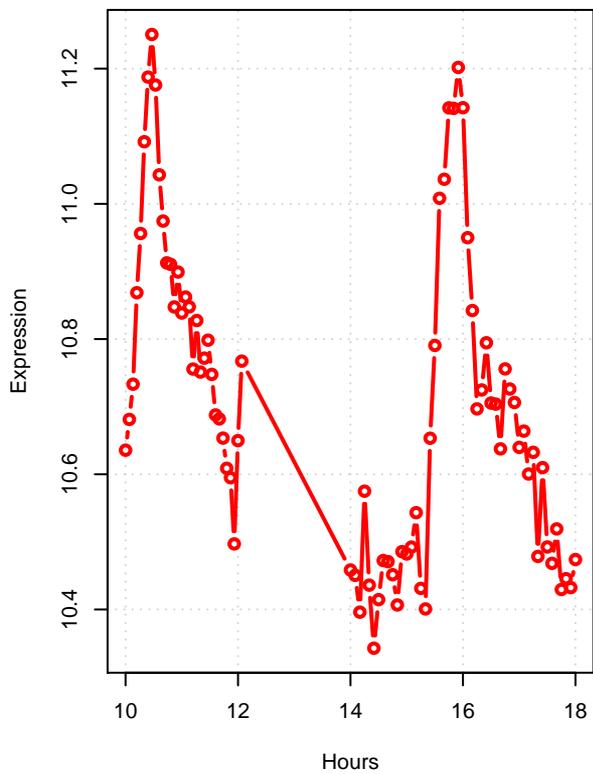
## lipid-linked oligosaccharide biosynthesis

# lipid-linked oligosaccharide biosynthesis

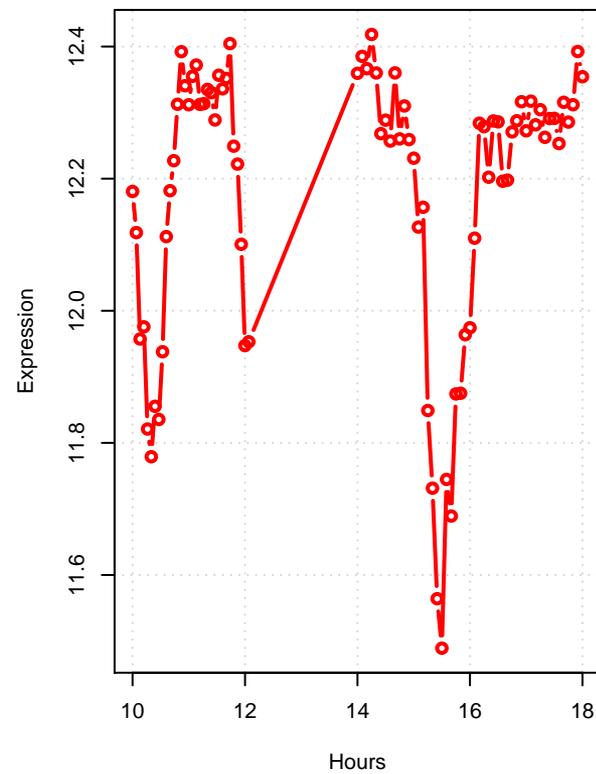
alg11 YNL048W  
Alpha-1,2-mannosyltransferase



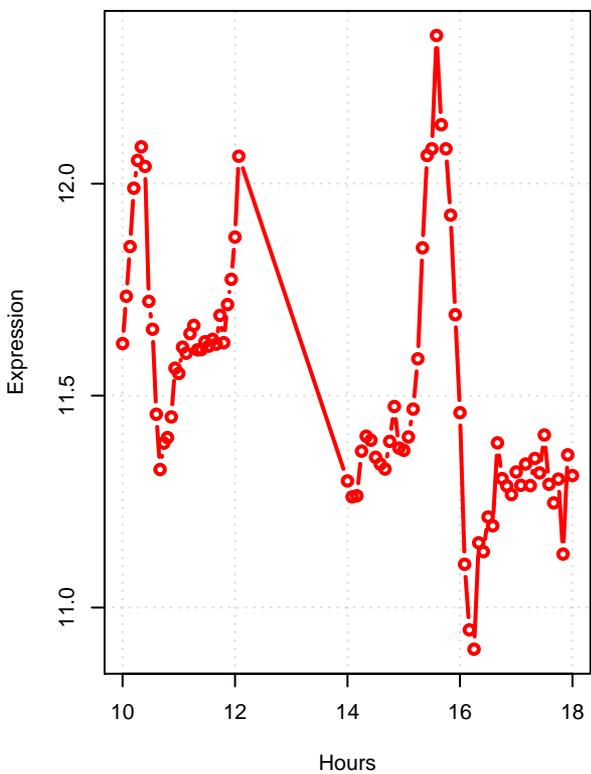
alg2 YGL065C  
Mannosyltransferase in the N-linked glycosylation pathway



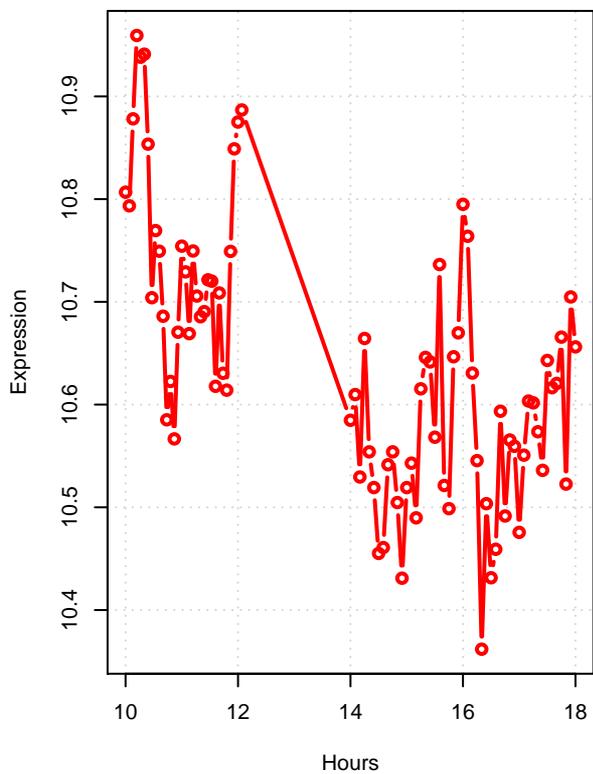
alg6 YOR002W  
Alpha 1,3 glucosyltransferase



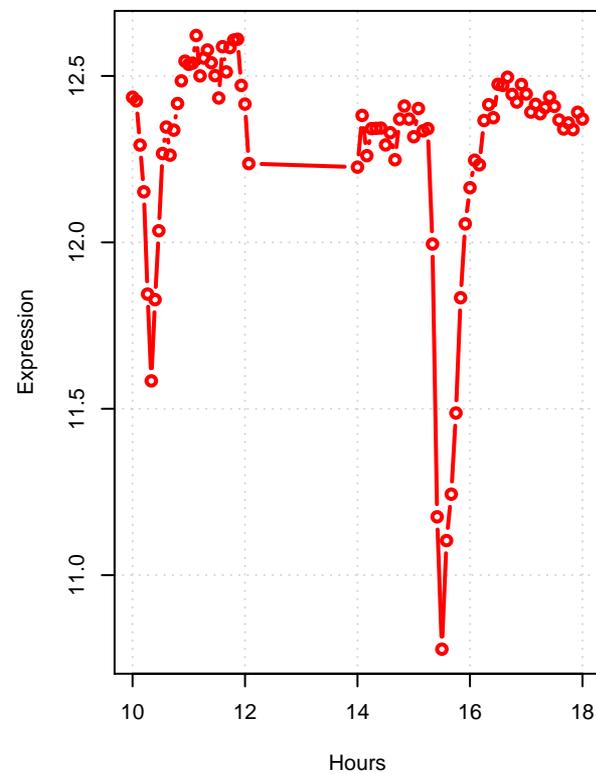
alg8 YOR067C  
Glucosyl transferase



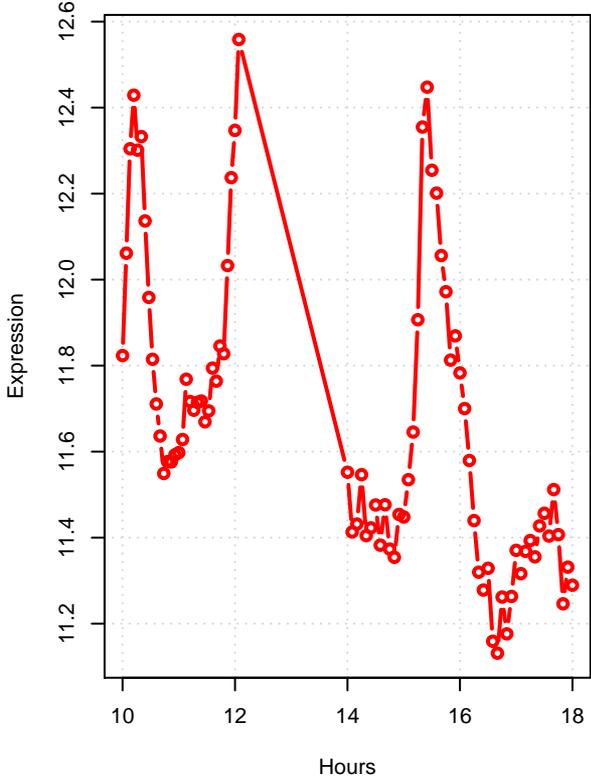
die2 YGR227W  
Dolichyl-phosphoglucose-dependent alpha-1,2-glycosyltransferase



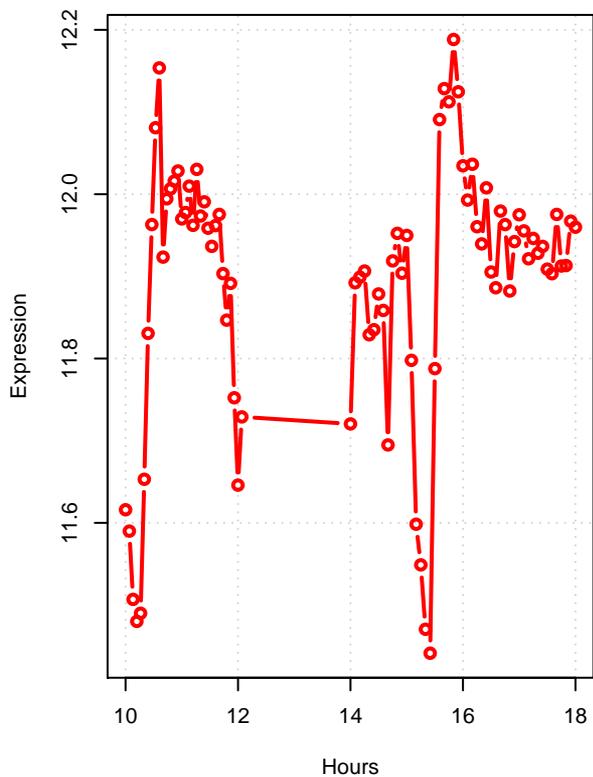
alg12 YNR030W  
Alpha-1,6-mannosyltransferase localized to the ER



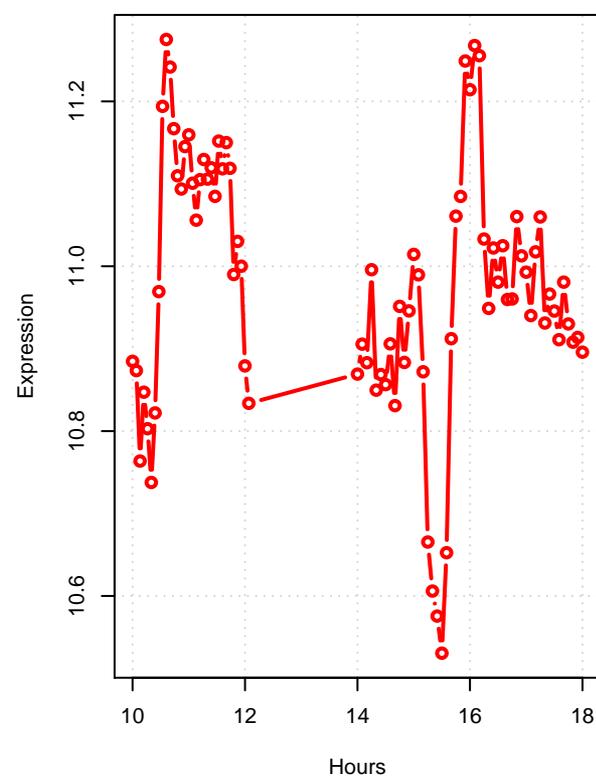
alg3 YBL082C  
Dolichol-P-Man dependent alpha(1-3) mannosyltransferase



alg9 YNL219C  
Mannosyltransferase, involved in N-linked glycosylation



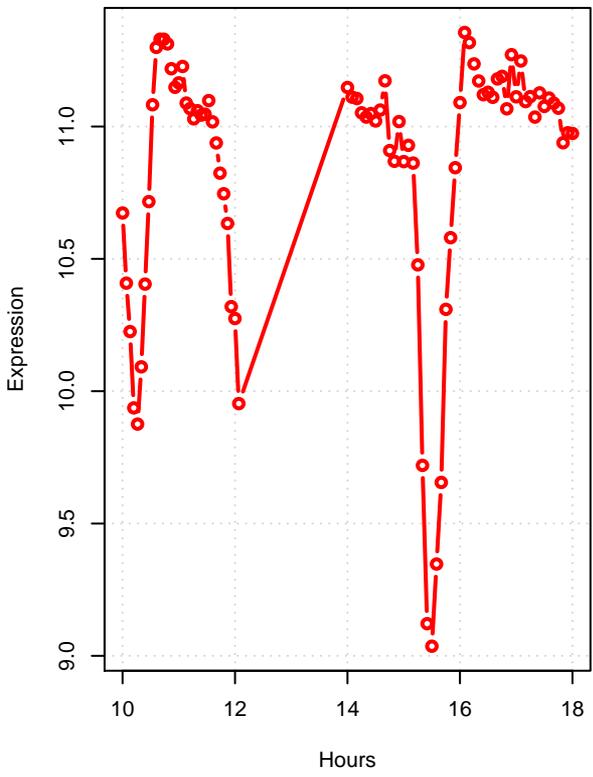
alg1 YBR110W  
Mannosyltransferase



# lipid-linked oligosaccharide biosynthesis

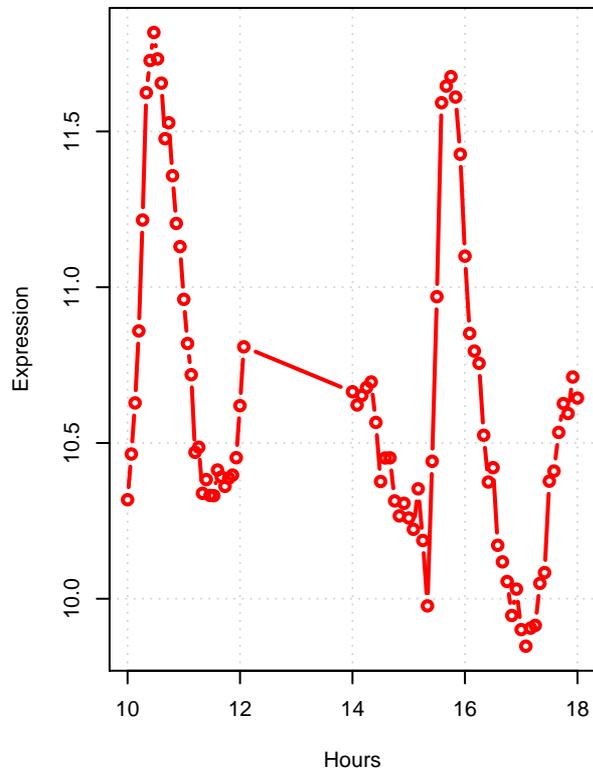
alg13 YGL047W

Catalytic component of UDP-GlcNAc transferase



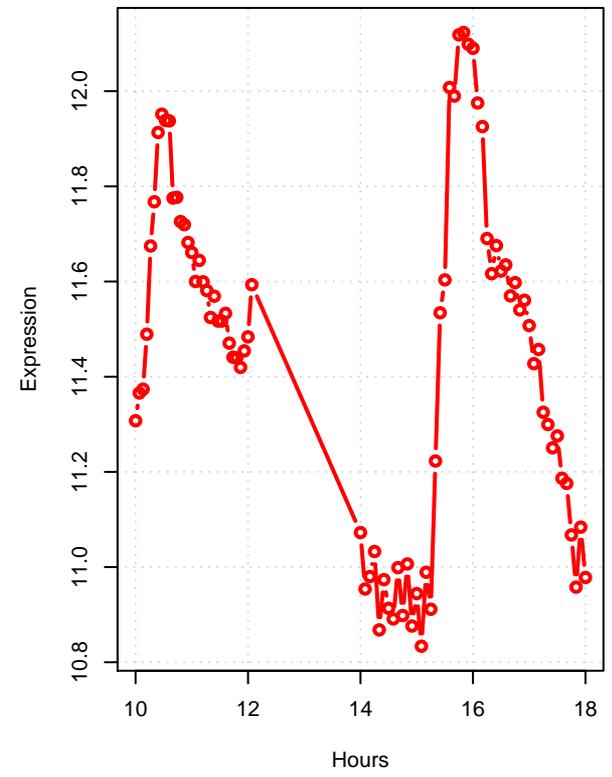
alg14 YBR070C

Component of UDP-GlcNAc transferase



alg7 YBR243C

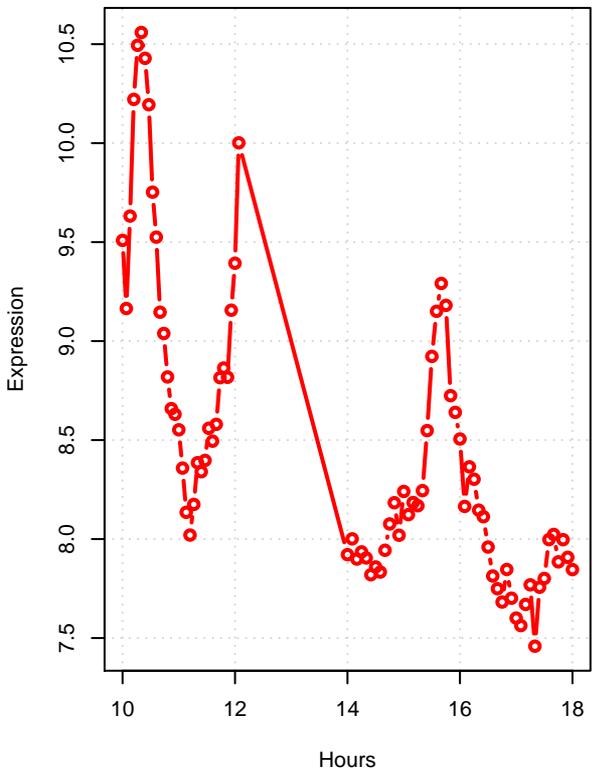
UDP-N-acetyl-glucosamine-1-P transferase



## **L-serine degradation**

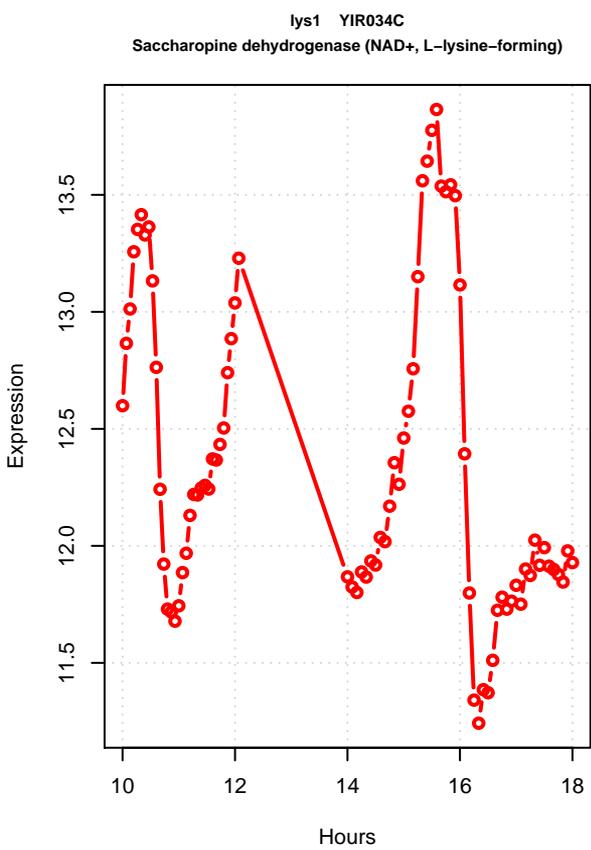
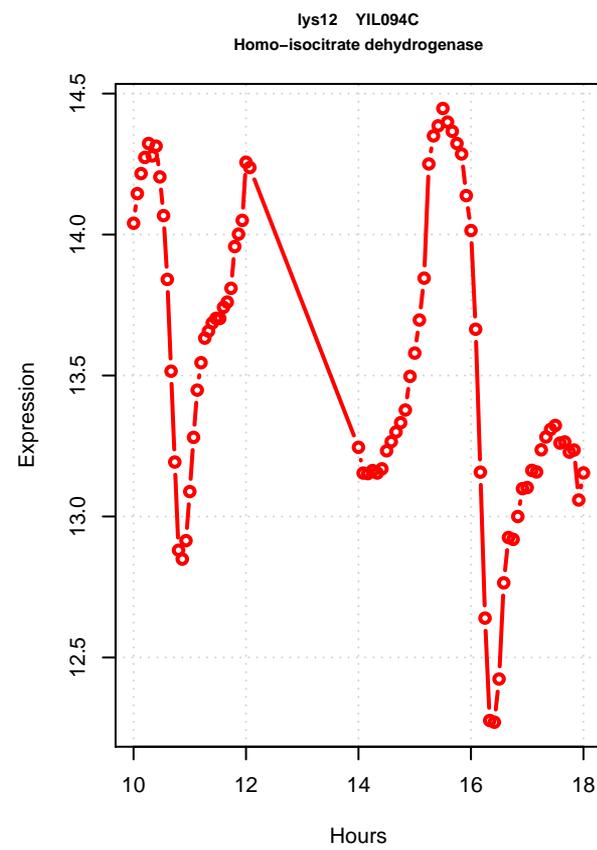
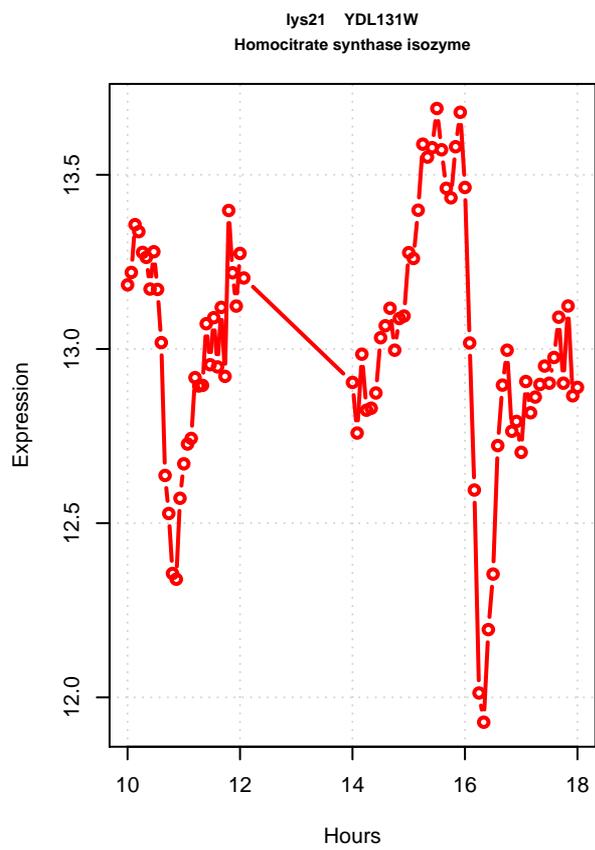
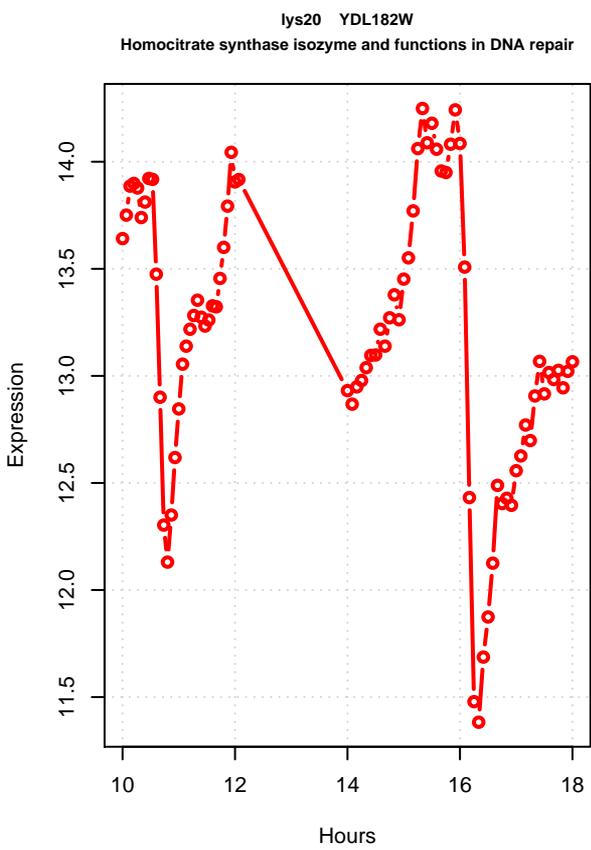
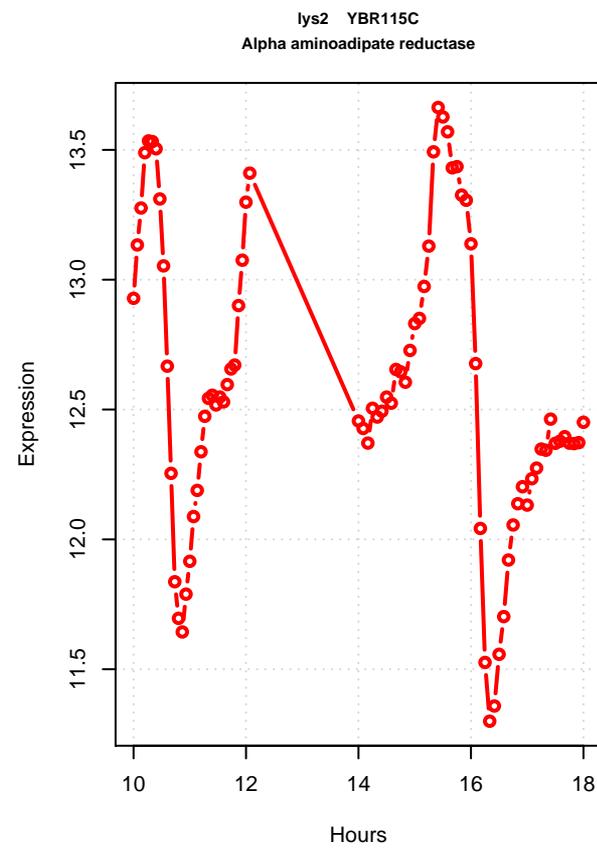
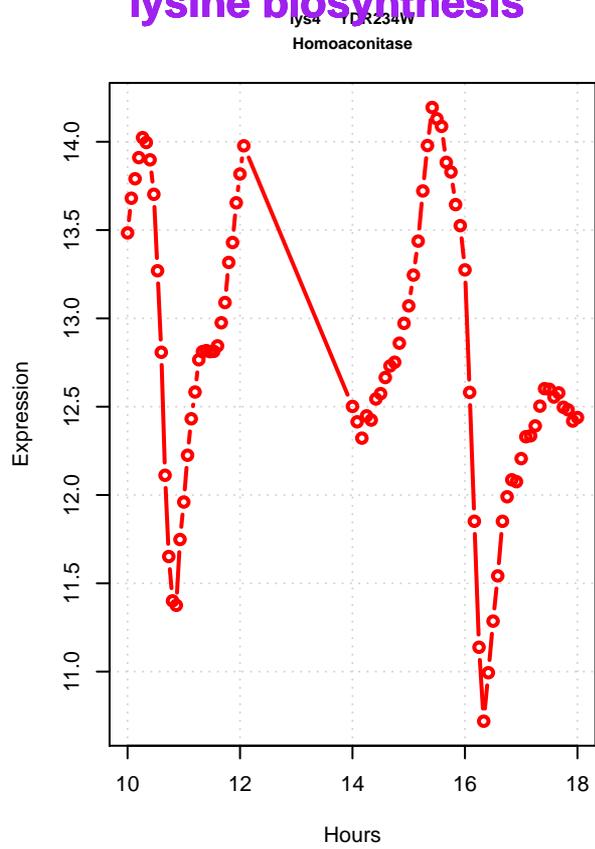
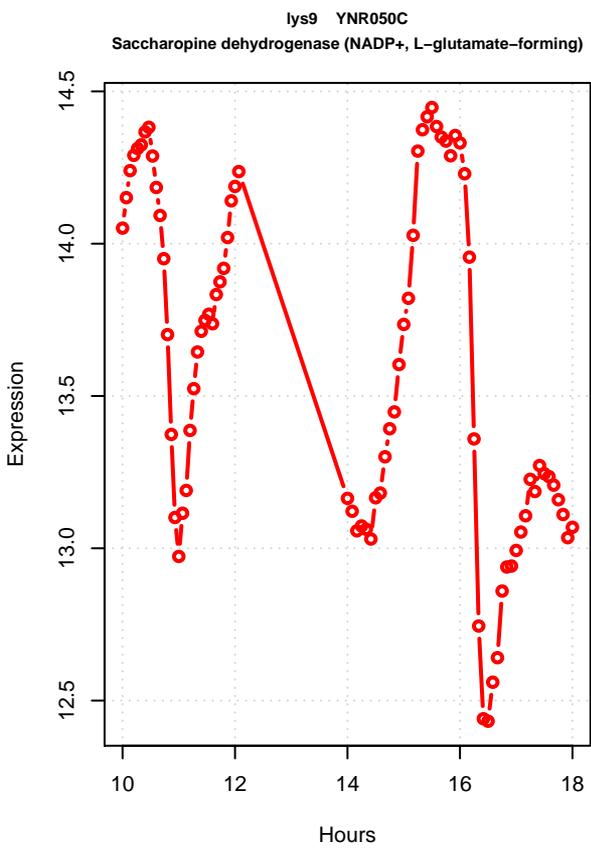
# L-serine degradation

cha1 YCL064C  
Catabolic L-serine (L-threonine) deaminase



## lysine biosynthesis

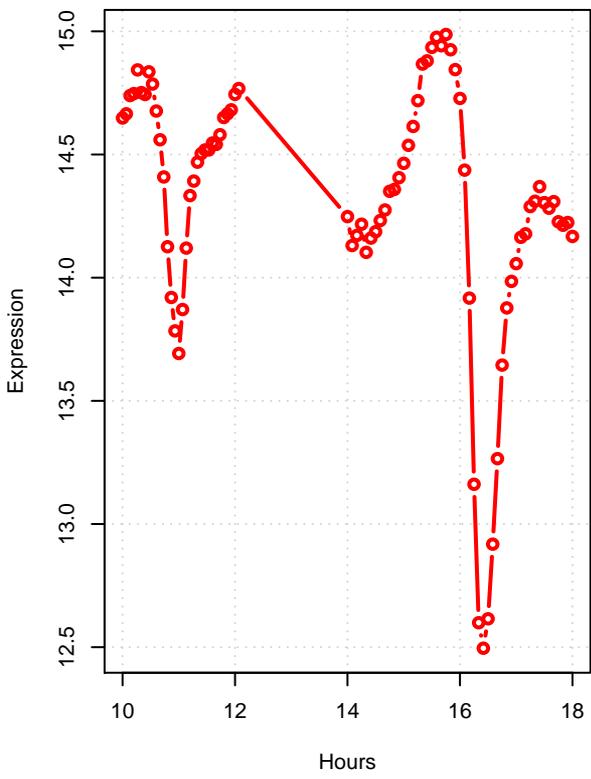
# lysine biosynthesis



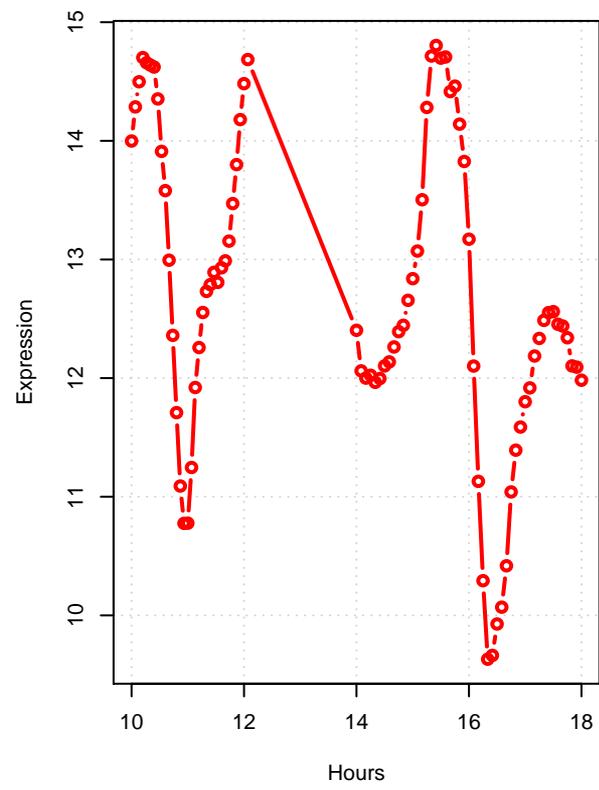
## **S-adenosylmethionine cycle**

# S-adenosylmethionine cycle

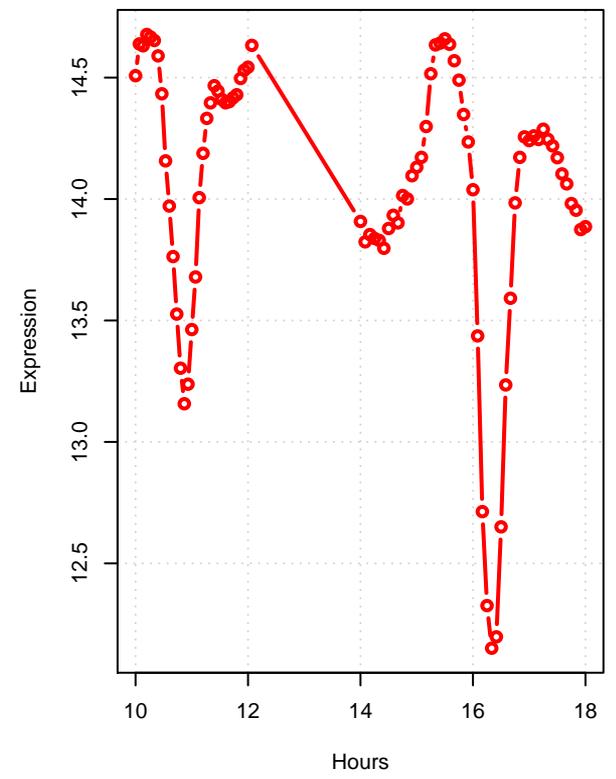
met6 YER091C  
Cobalamin-independent methionine synthase



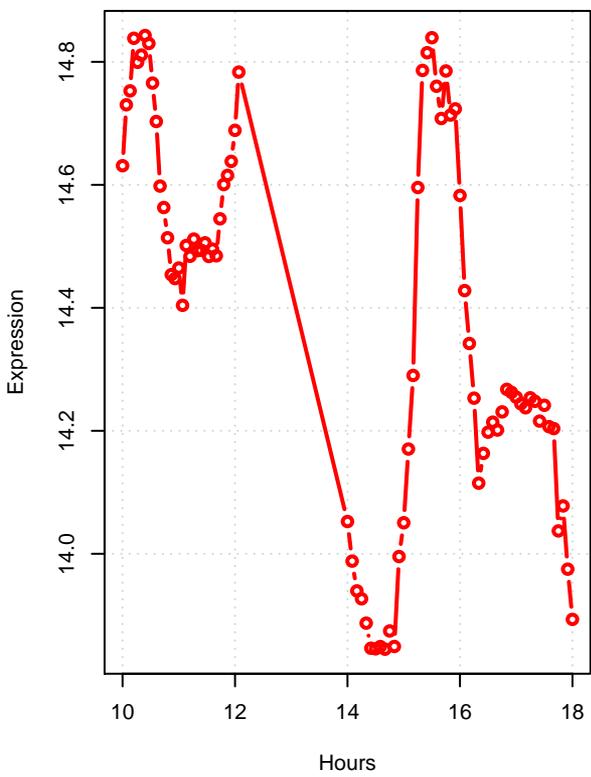
sam1 YLR180W  
S-adenosylmethionine synthetase



sam2 YDR502C  
S-adenosylmethionine synthetase



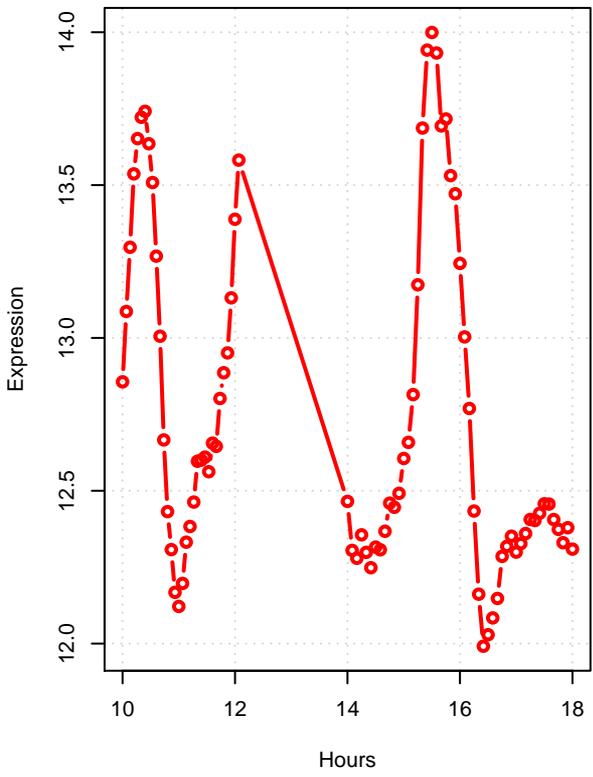
sah1 YER043C  
S-adenosyl-L-homocysteine hydrolase



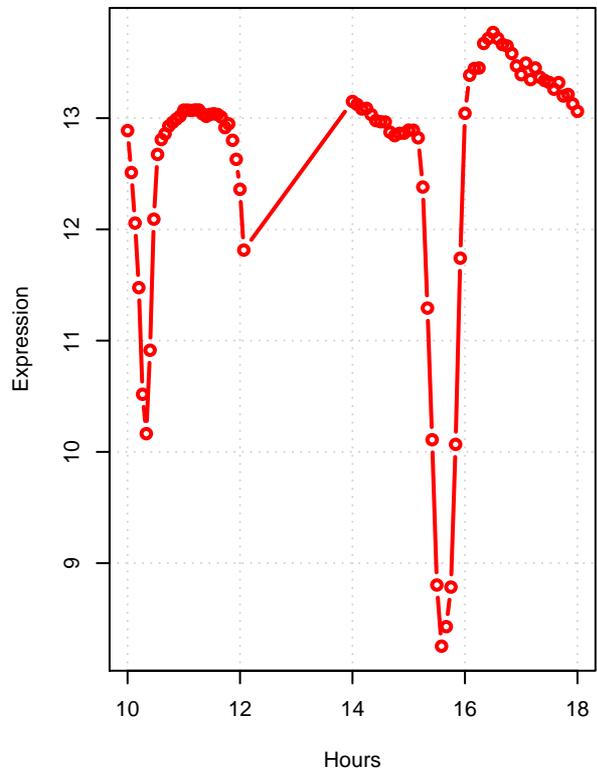
## phenylalanine biosynthesis

# phenylalanine biosynthesis

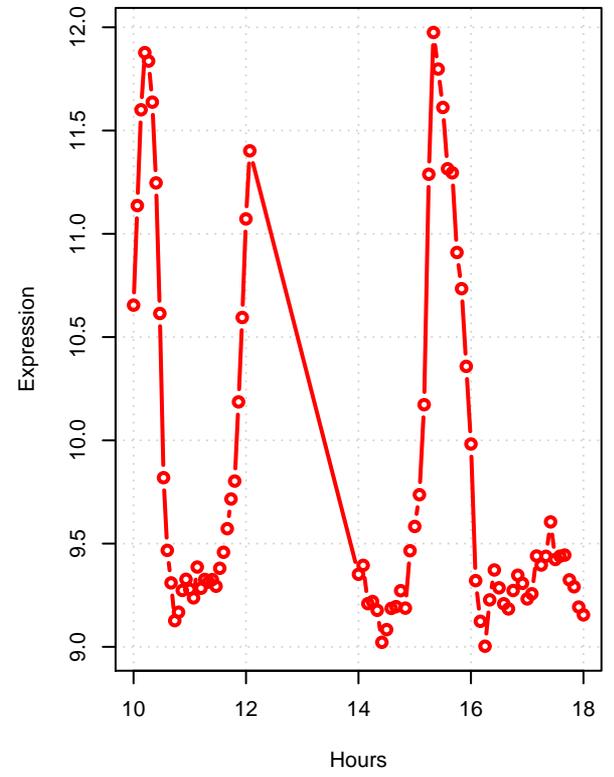
aro8 YGL202W  
Aromatic aminotransferase I



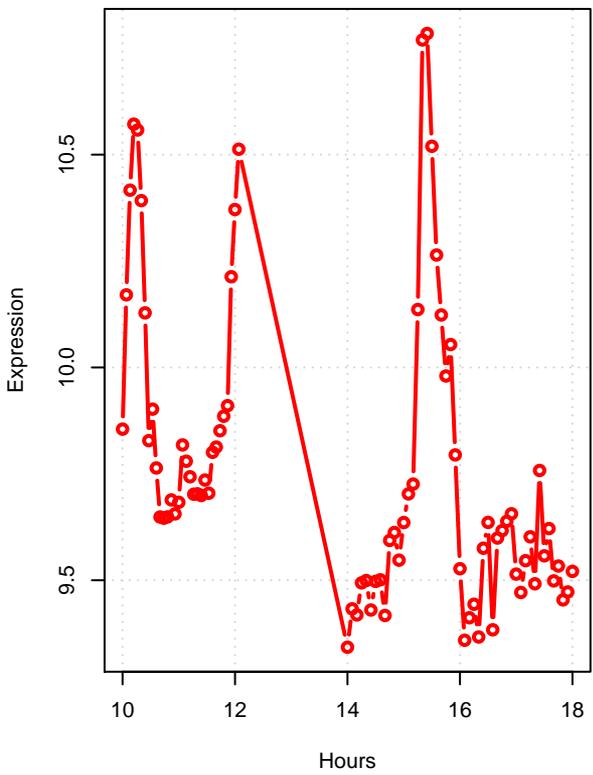
aro9 YHR137W  
Aromatic aminotransferase II



aro7 YPR060C  
Chorismate mutase



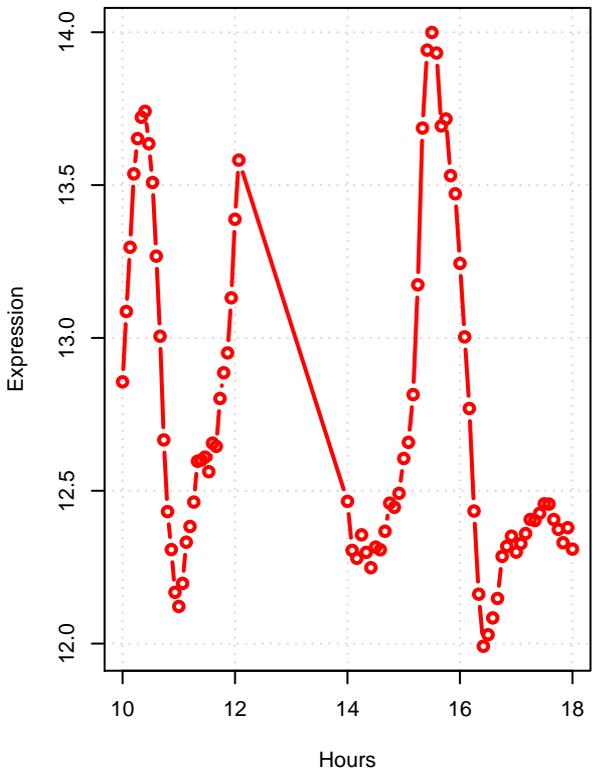
pha2 YNL316C  
Prephenate dehydratase



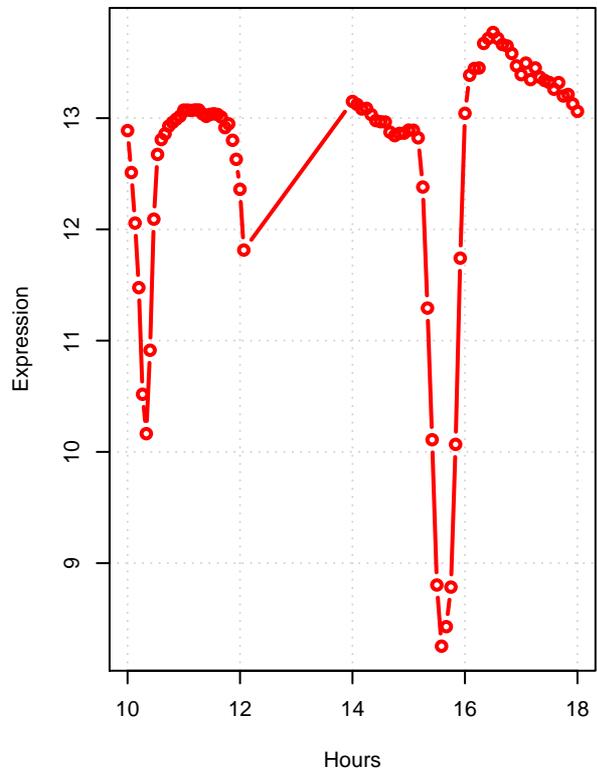
## tyrosine biosynthesis

# tyrosine biosynthesis

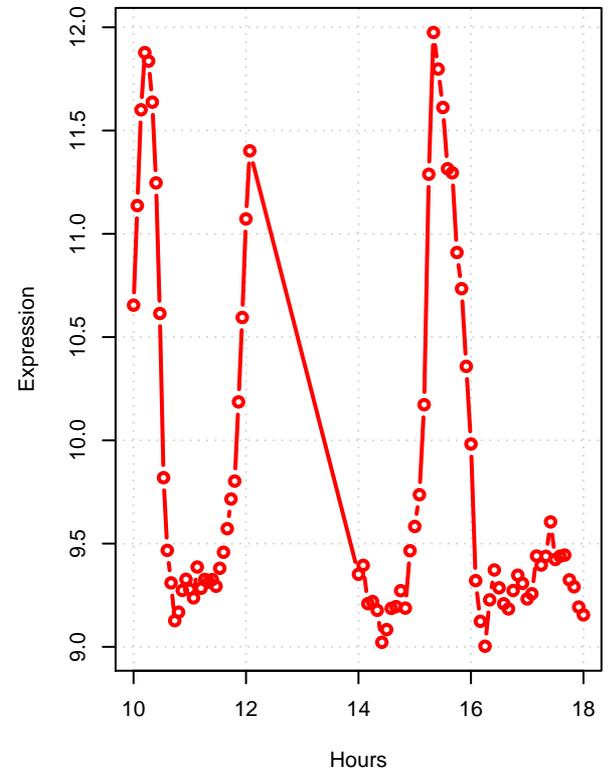
aro8 YGL202W  
Aromatic aminotransferase I



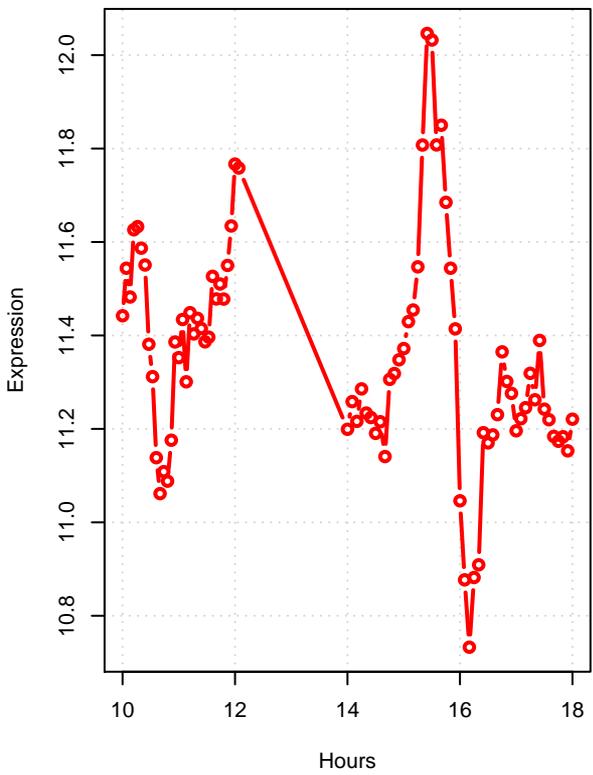
aro9 YNR137W  
Aromatic aminotransferase II



aro7 YPR060C  
Chorismate mutase



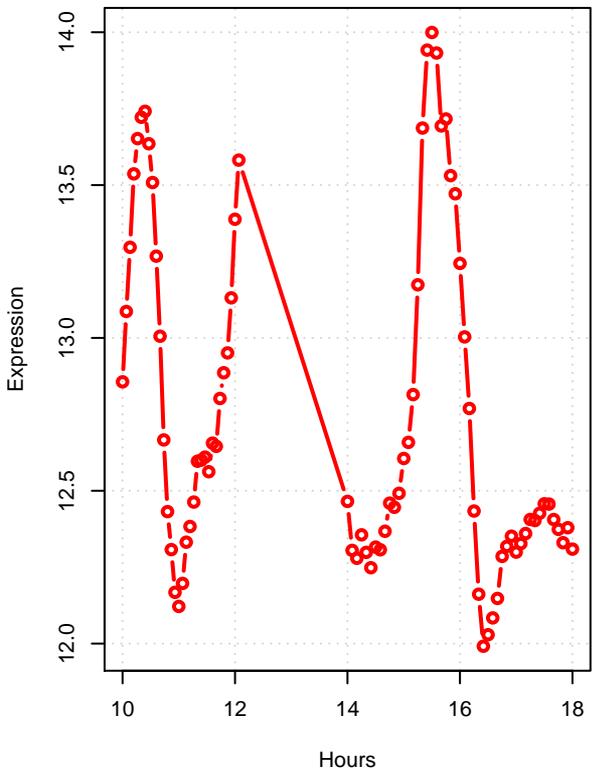
tyr1 YBR166C  
Prephenate dehydrogenase involved in tyrosine biosynthesis



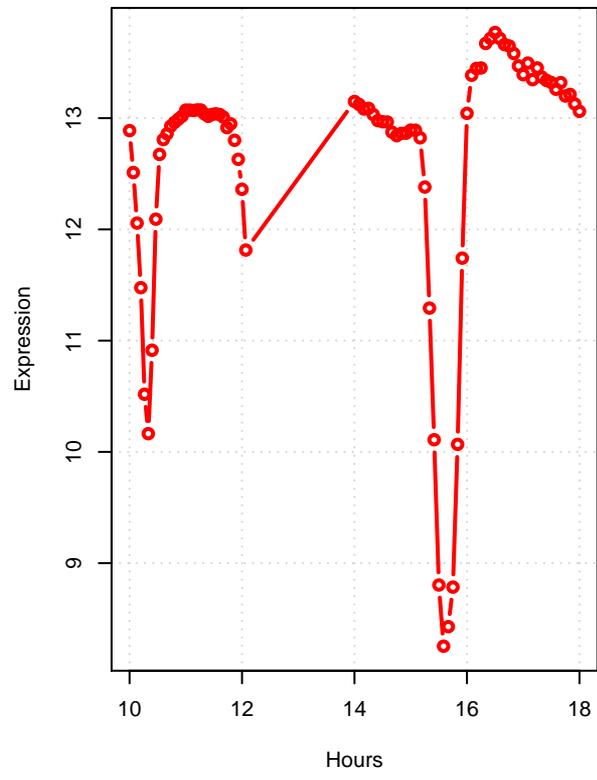
## tyrosine degradation

# tyrosine degradation

aro8 YGL202W  
Aromatic aminotransferase I



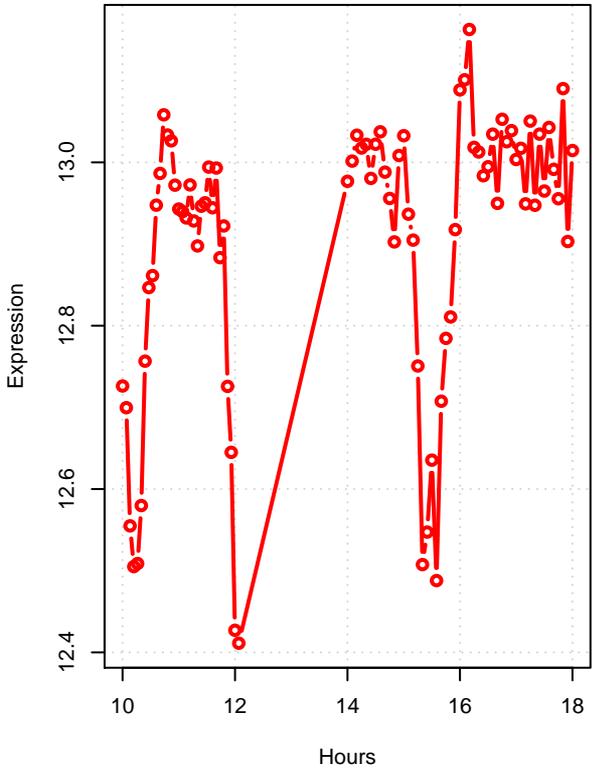
aro9 YLR137W  
Aromatic aminotransferase II



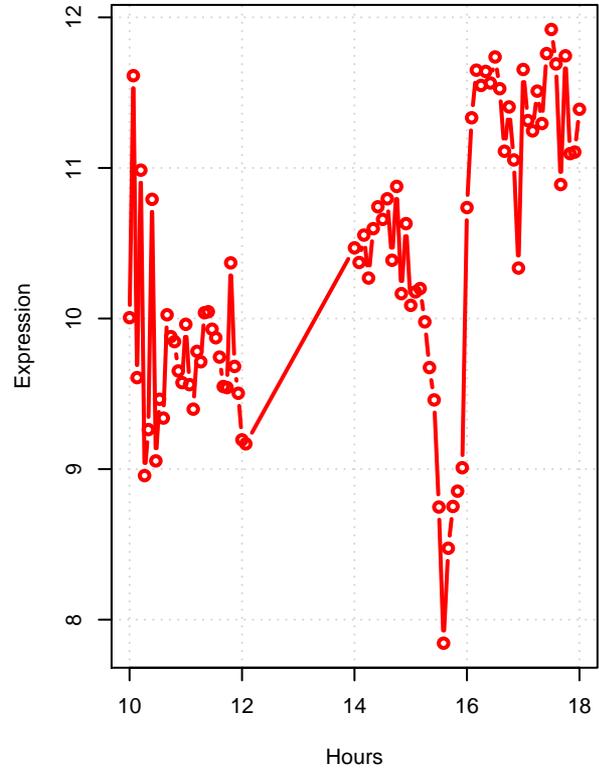
**methylglyoxal catabolism**

# methylglyoxal catabolism

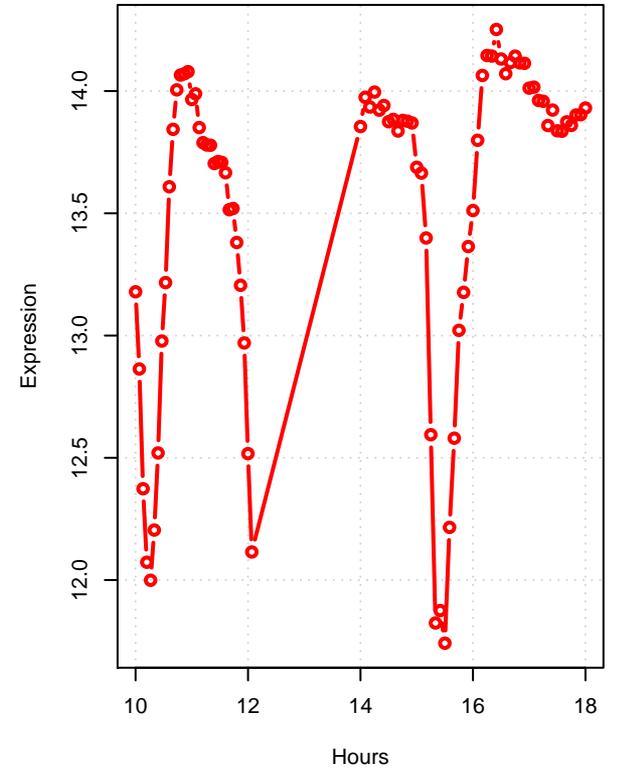
glo2 YDR272W  
Cytoplasmic glyoxalase II



glo4 YOR040W  
Mitochondrial glyoxalase II

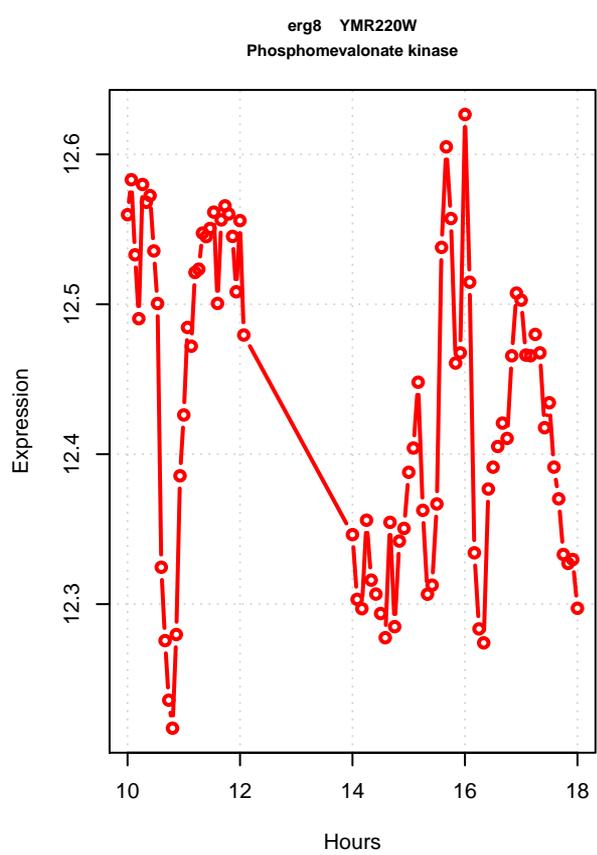
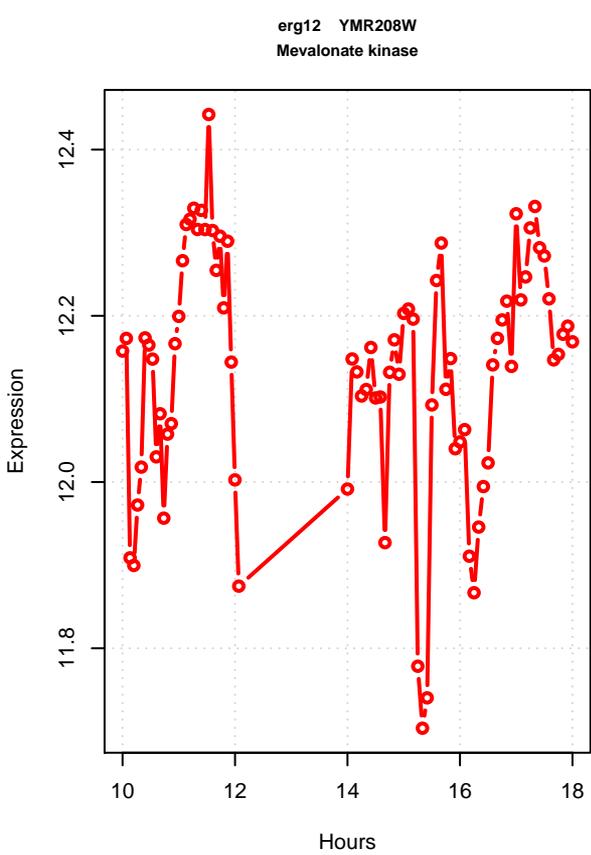
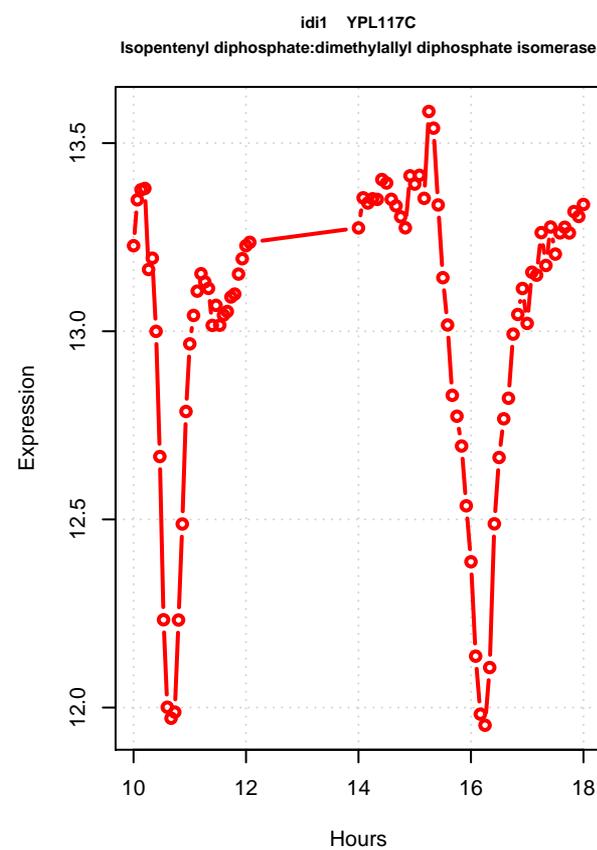
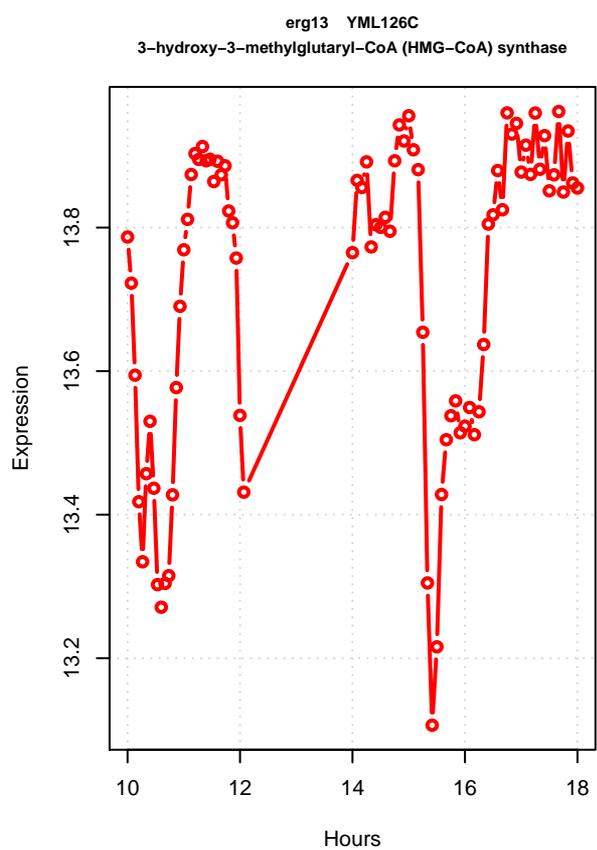
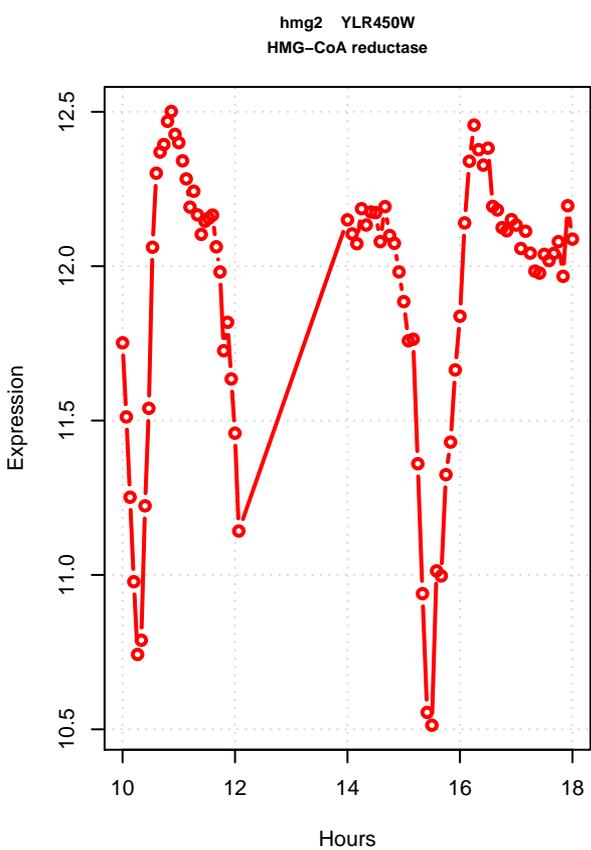
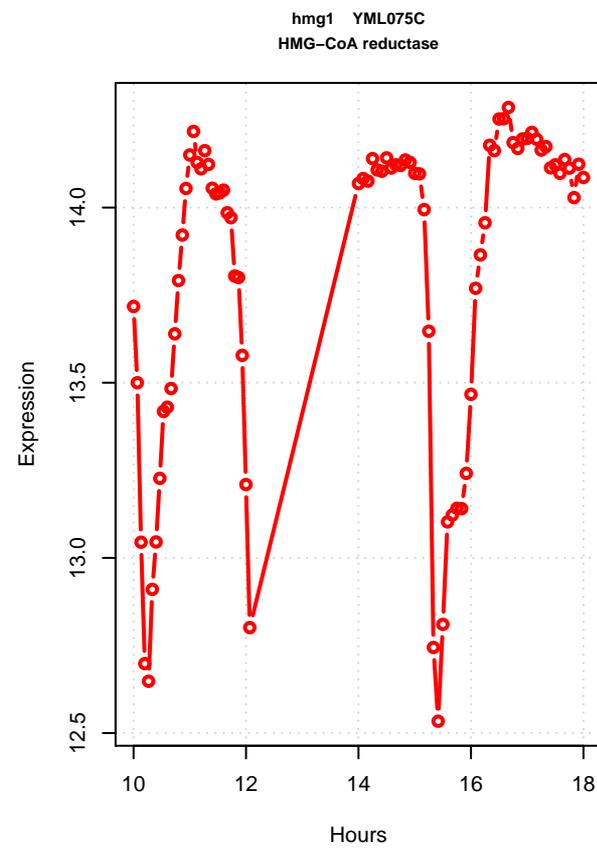
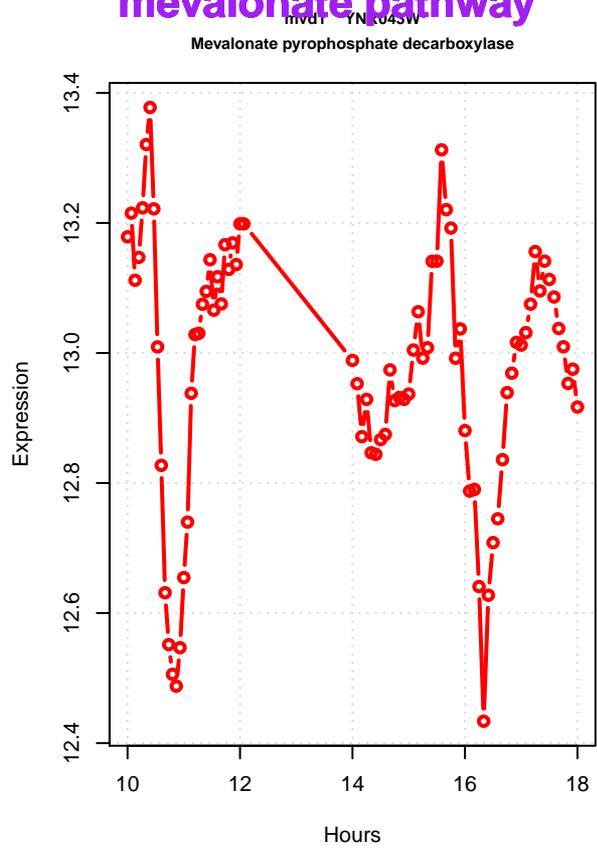
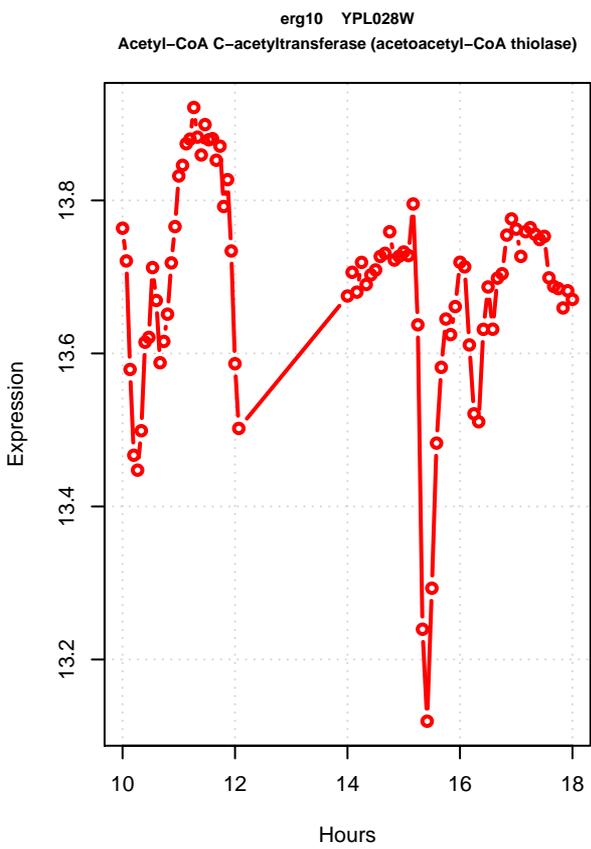


glo1 YML004C  
Monomeric glyoxalase I



**mevalonate pathway**

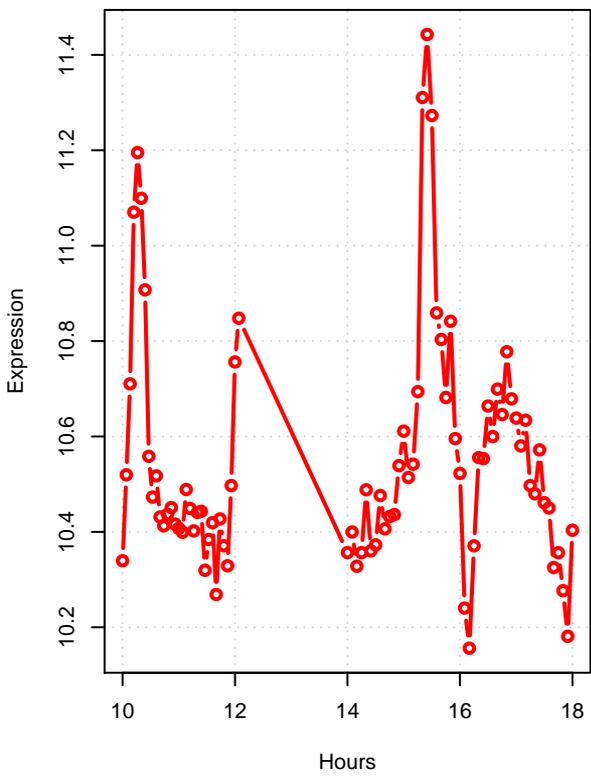
# mevalonate pathway



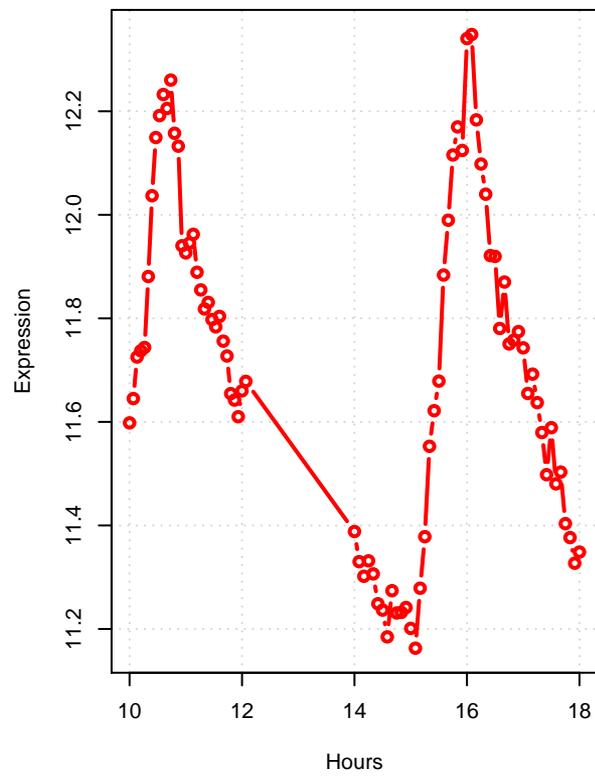
**nicotinate riboside salvage pathway I**

# nicotinate riboside salvage pathway I

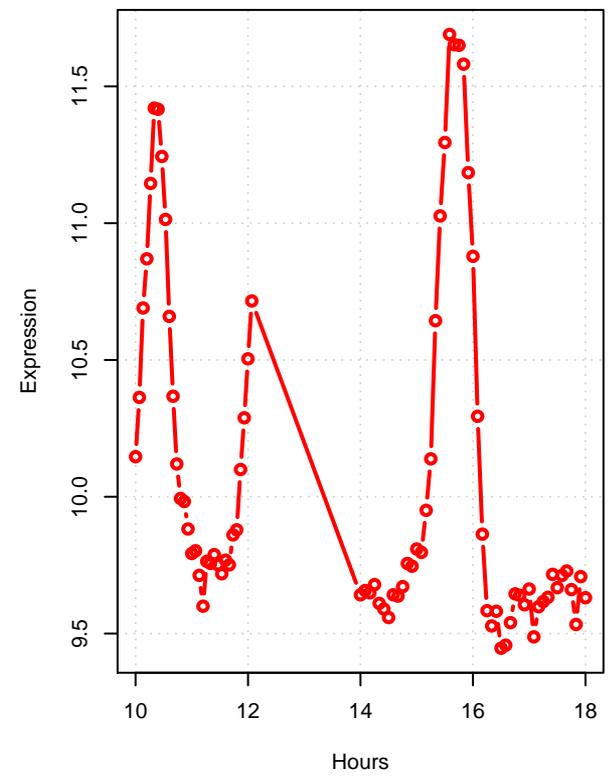
nrk1 YNL129W  
Nicotinamide riboside kinase



phr1 YLR209C  
Purine nucleoside phosphorylase



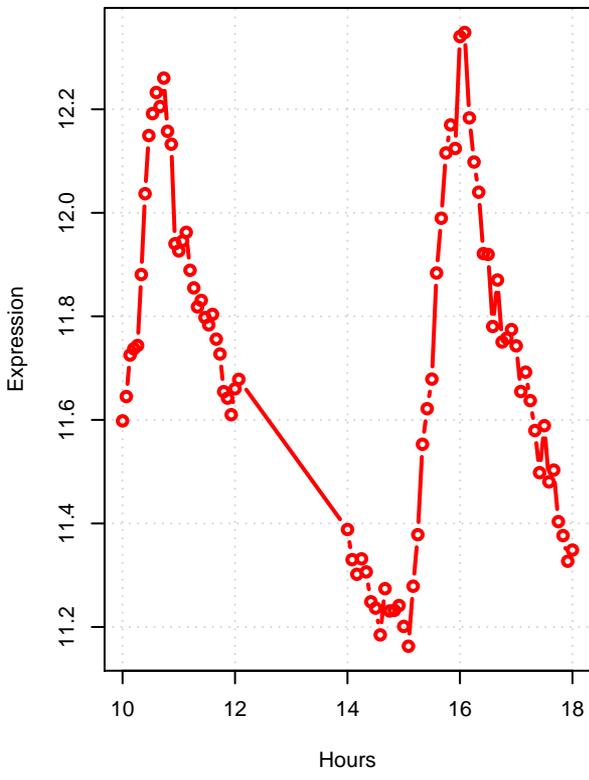
urh1 YDR400W  
Uridine nucleosidase (uridine-cytidine N-ribohydrolase)



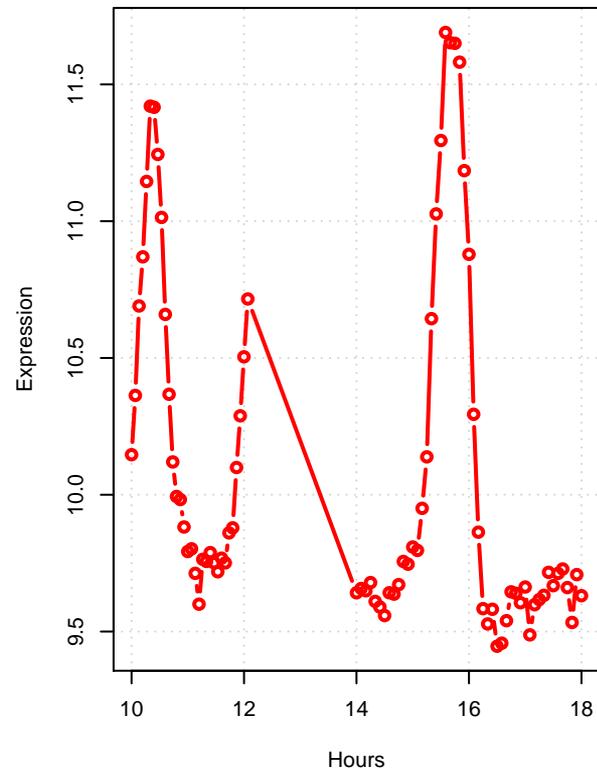
## nicotinamide riboside salvage pathway II

# nicotinamide riboside salvage pathway II

pnp1 YLR209C  
Purine nucleoside phosphorylase



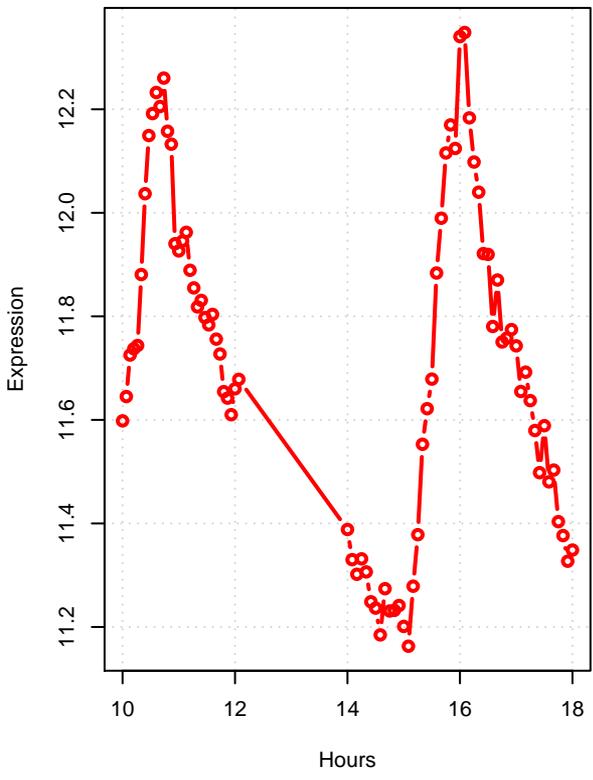
urn1 YDR400W  
Uridine nucleosidase (uridine-cytidine N-ribohydrolase)



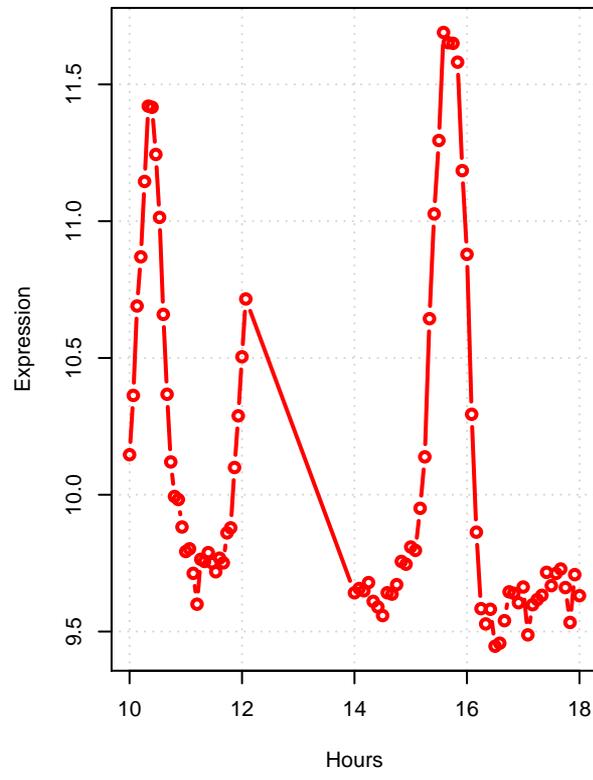
## nicotinate riboside salvage pathway II

# nicotinate riboside salvage pathway II

pnp1 YLR209C  
Purine nucleoside phosphorylase



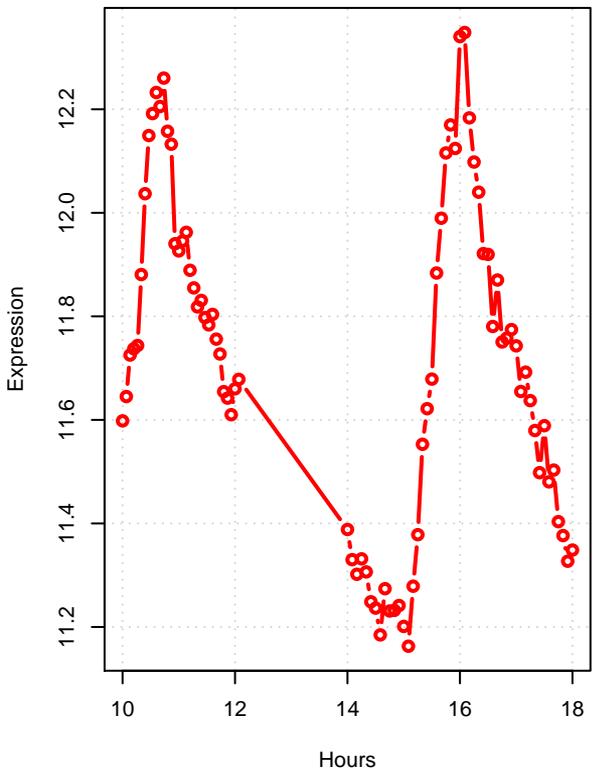
urn1 YDR400W  
Uridine nucleosidase (uridine-cytidine N-ribohydrolase)



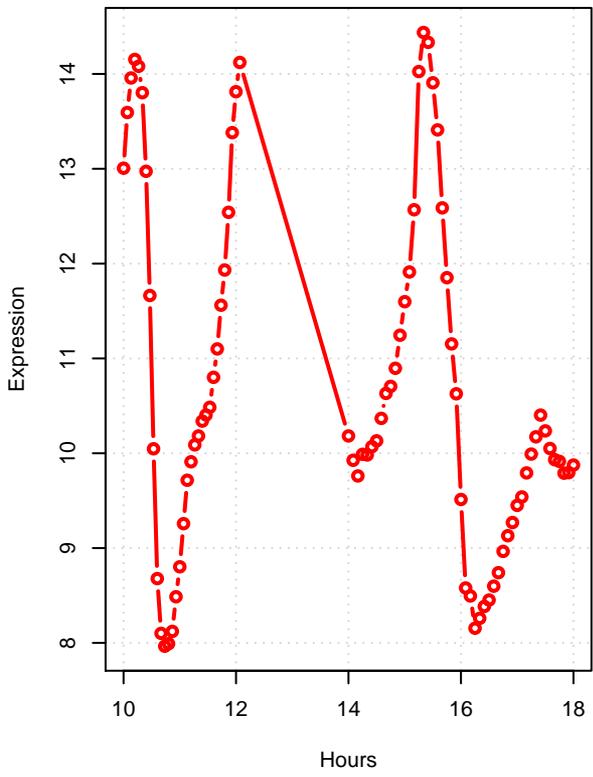
**salvage pathways of adenine, hypoxanthine and their nucleoside**

# salvage pathways of adenine, hypoxanthine and their nucleosides

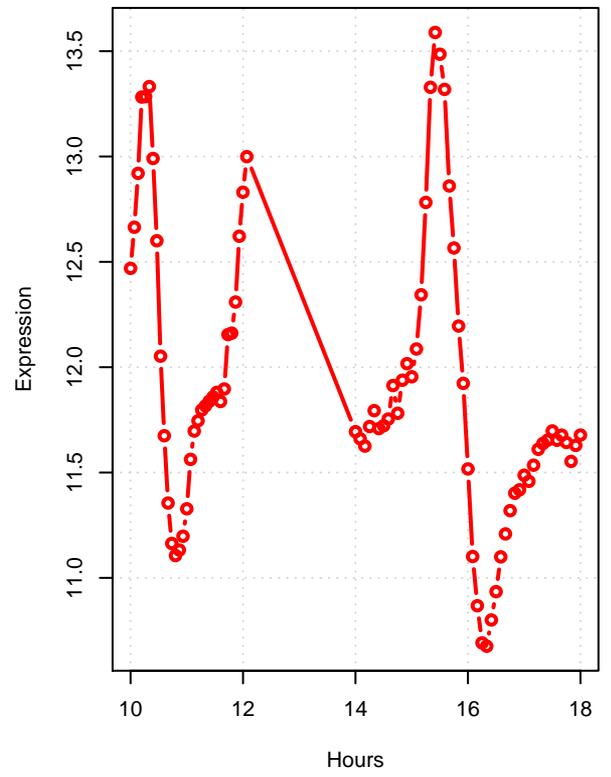
**php1 YLR209C**  
Purine nucleoside phosphorylase



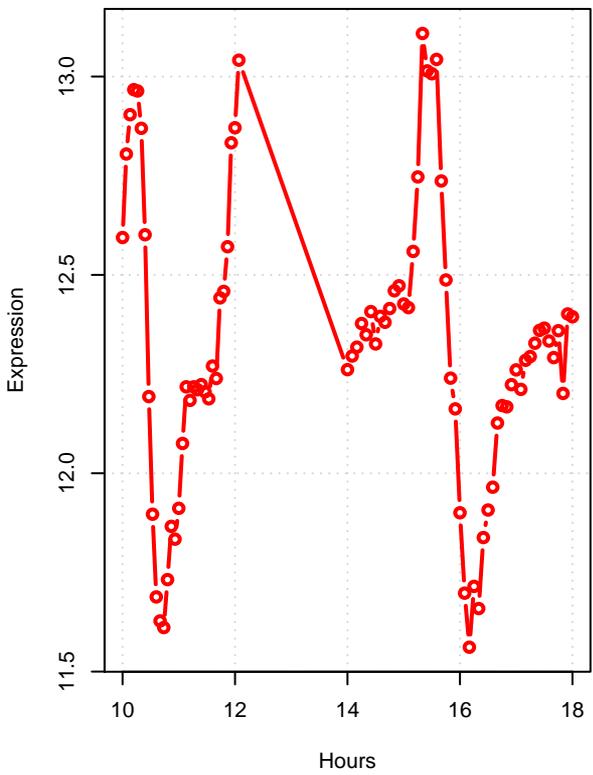
**ada1 YNL141W**  
Adenine deaminase (adenine aminohydrolase)



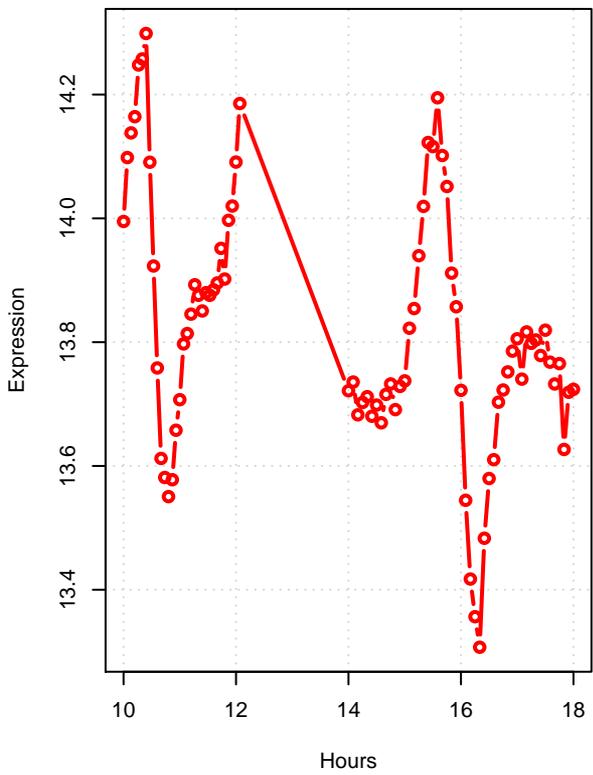
**apt1 YML022W**  
Adenine phosphoribosyltransferase



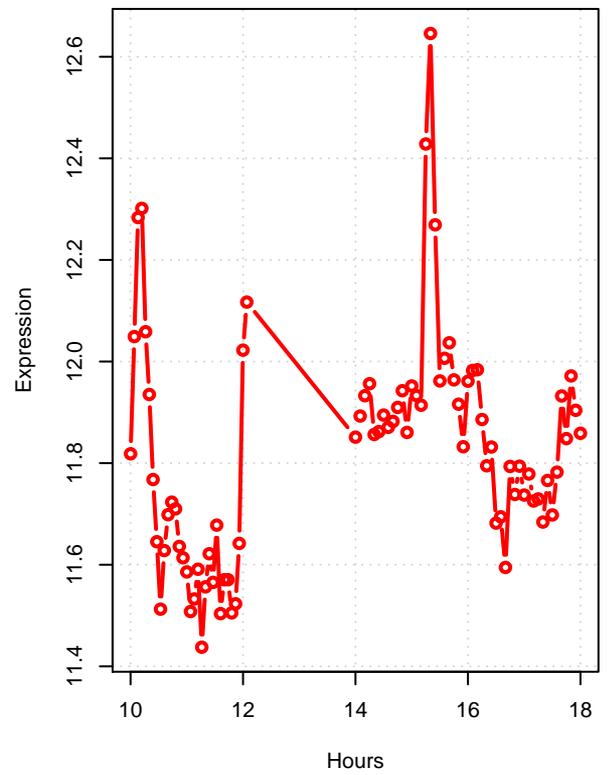
**apt2 YDR441C**  
Potential adenine phosphoribosyltransferase



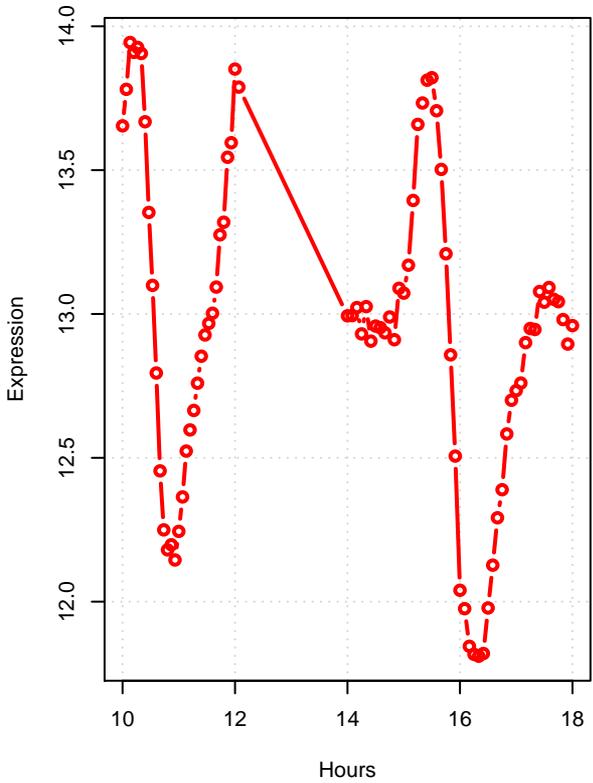
**ado1 YJR105W**  
Adenosine kinase



**amd1 YML035C**  
AMP deaminase



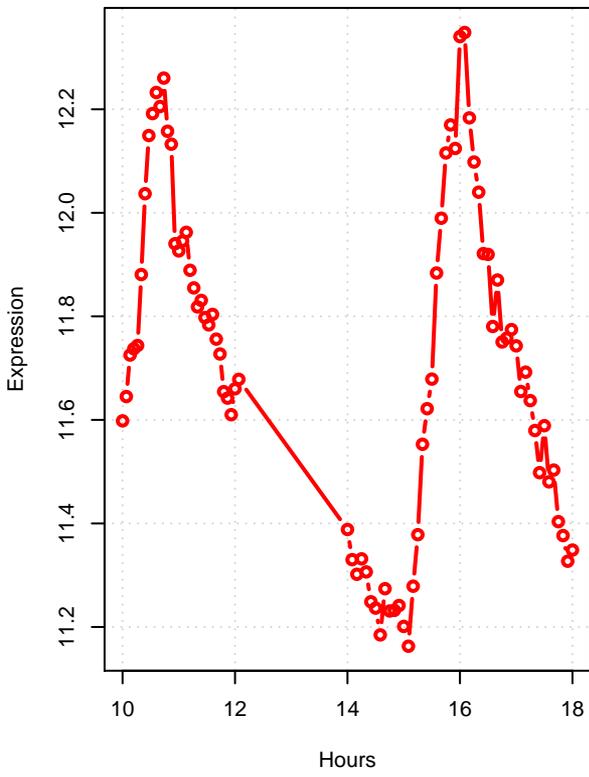
**hpt1 YDR399W**  
Dimeric hypoxanthine-guanine phosphoribosyltransferase



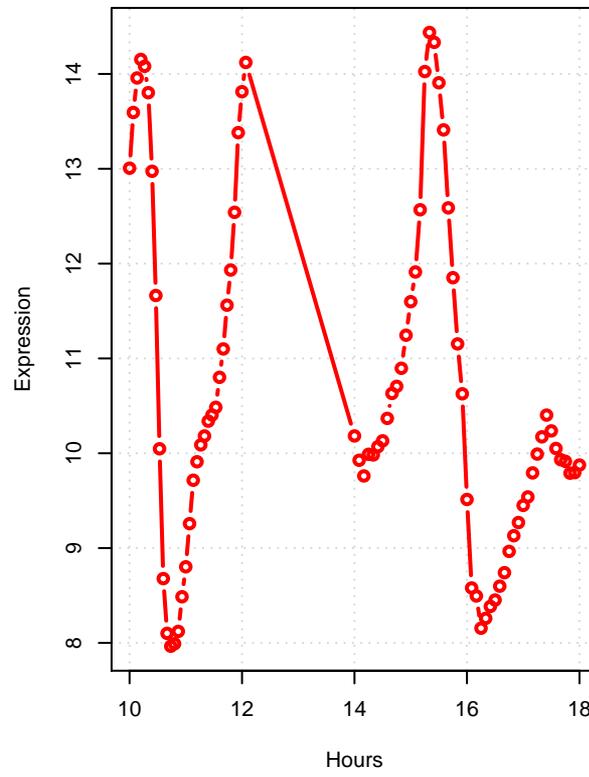
**salvage pathways of purines and their nucleosides**

# salvage pathways of purines and their nucleosides

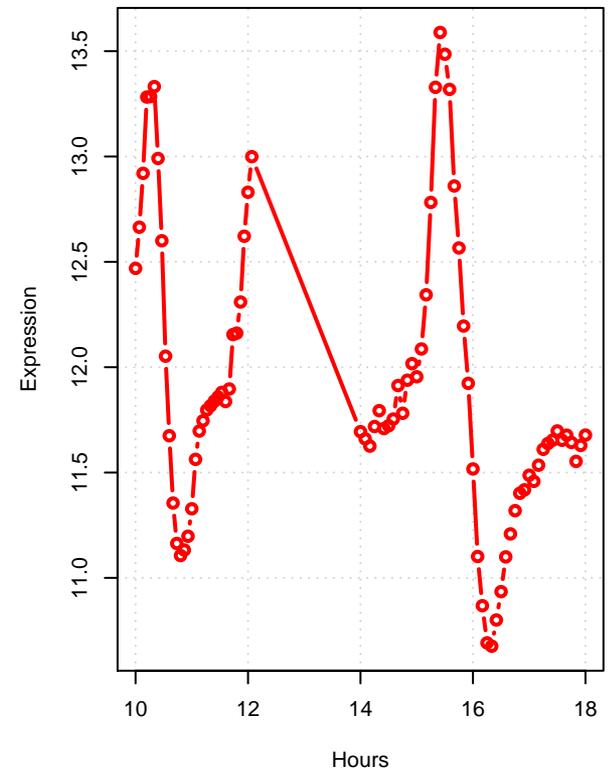
**pnp1 YLR209C**  
Purine nucleoside phosphorylase



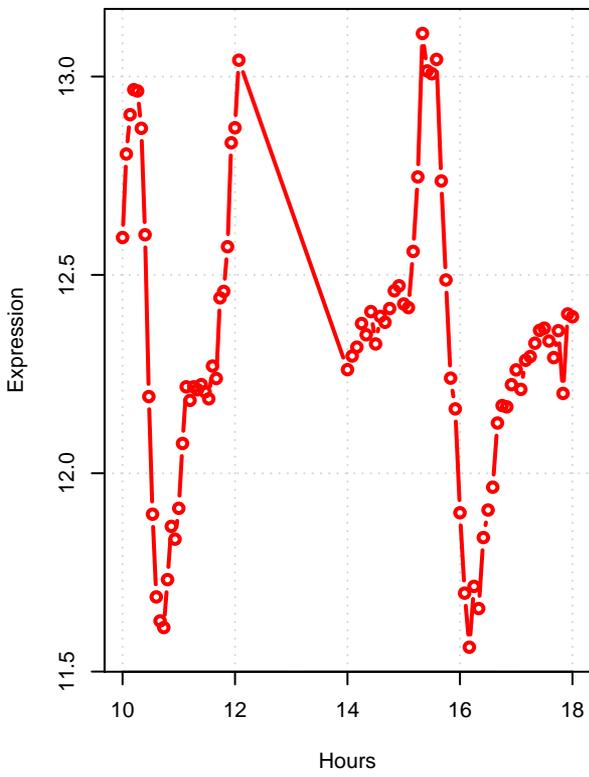
**ada1 YNL141W**  
Adenine deaminase (adenine aminohydrolase)



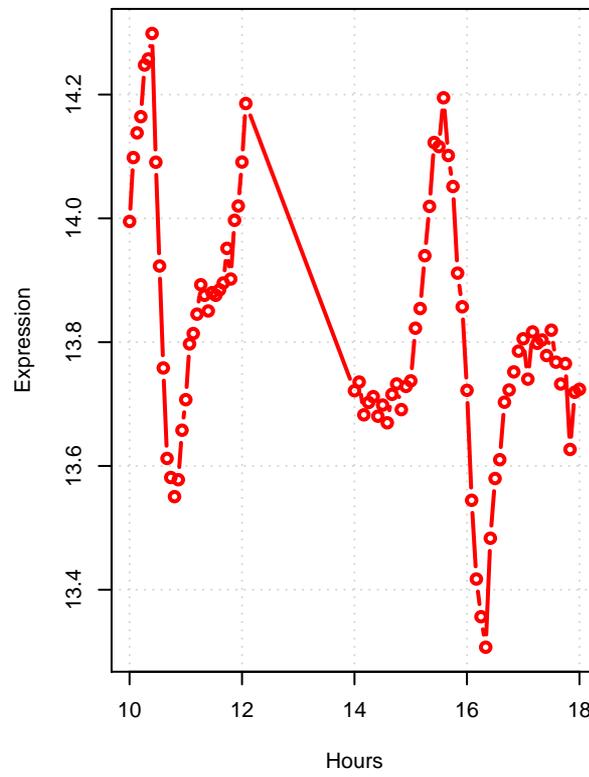
**apt1 YML022W**  
Adenine phosphoribosyltransferase



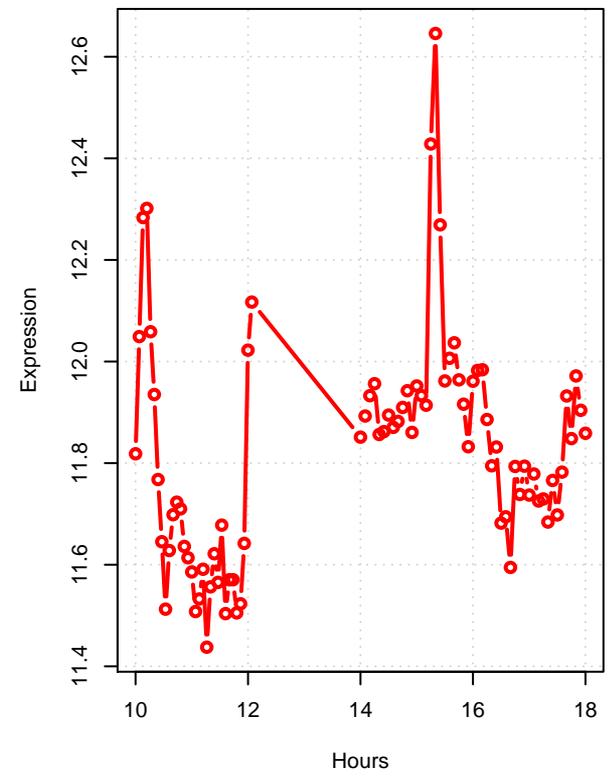
**apt2 YDR441C**  
Potential adenine phosphoribosyltransferase



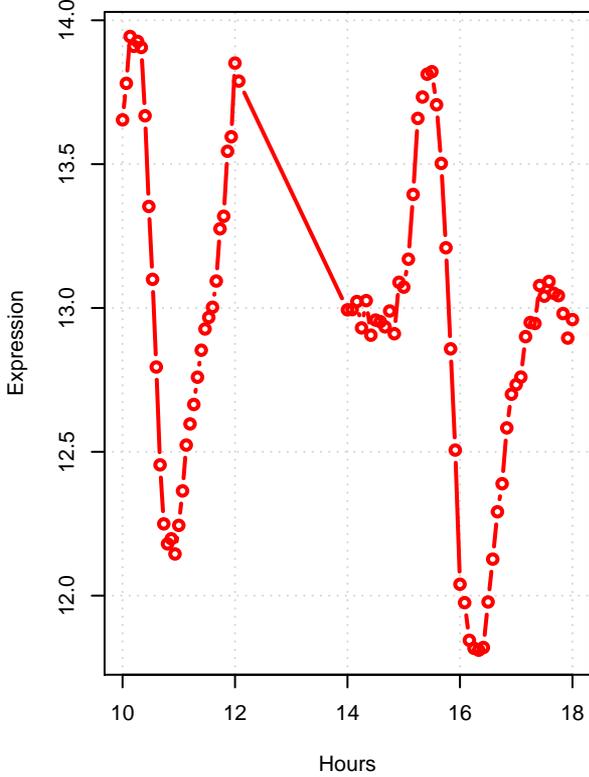
**ado1 YJR105W**  
Adenosine kinase



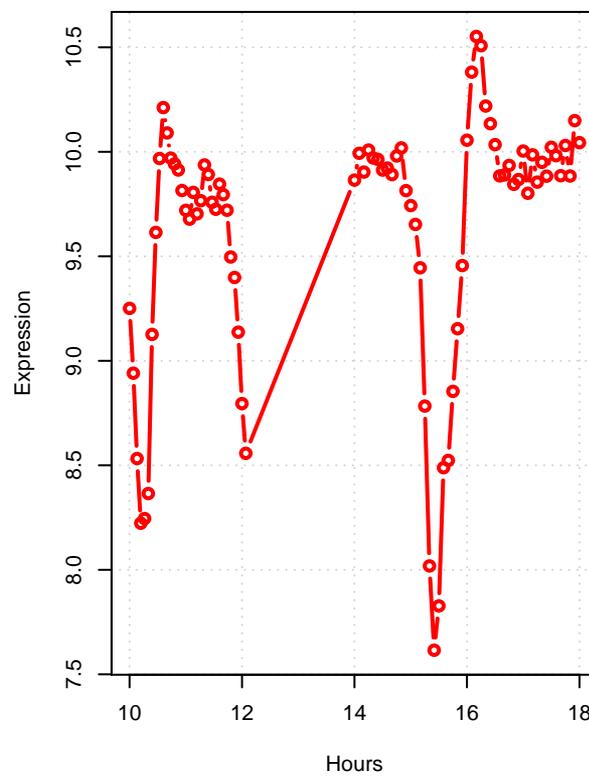
**amd1 YML035C**  
AMP deaminase



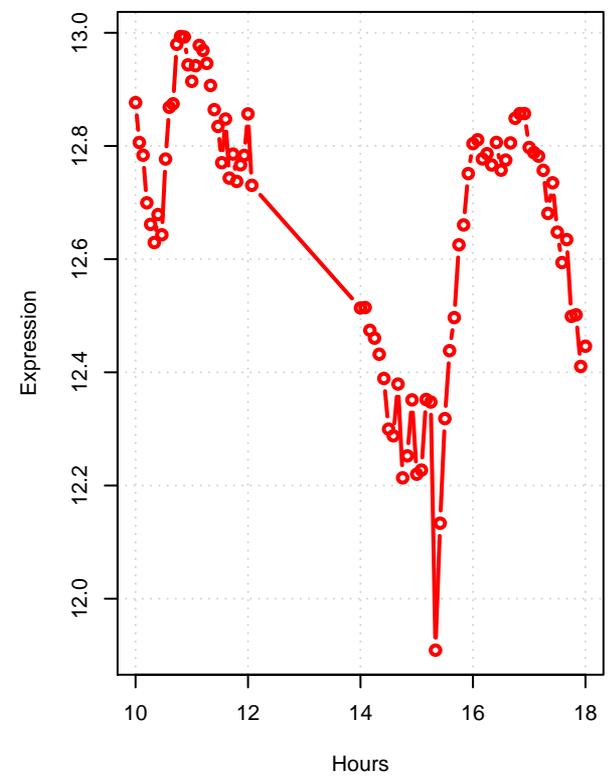
**hpt1 YDR399W**  
Dimeric hypoxanthine-guanine phosphoribosyltransferase



**gud1 YDL238C**  
Guanine deaminase



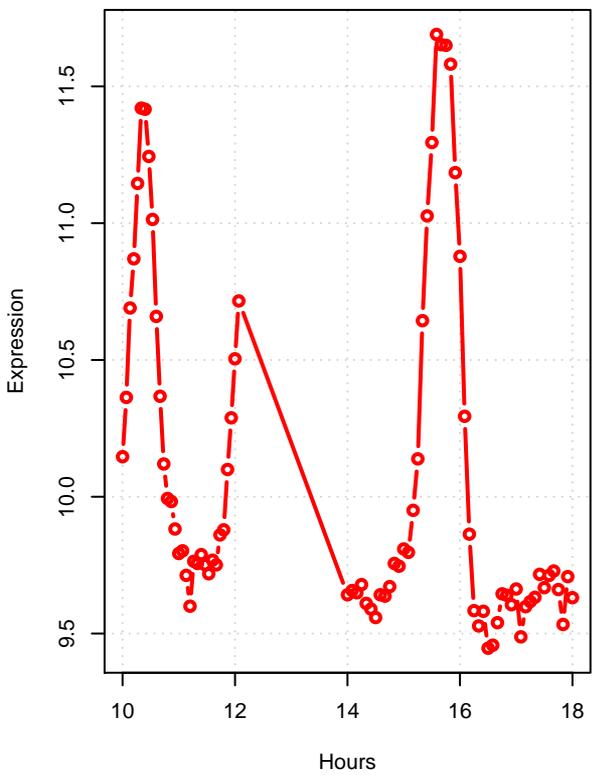
**xpt1 YJR133W**  
Xanthine-guanine phosphoribosyl transferase



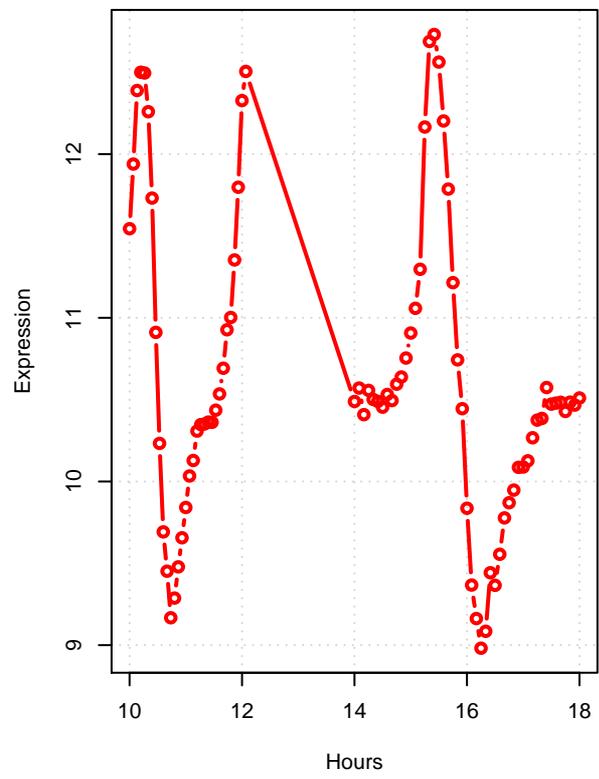
**salvage pathways of pyrimidine deoxyribonucleotides**

# salvage pathways of pyrimidine deoxyribonucleotides

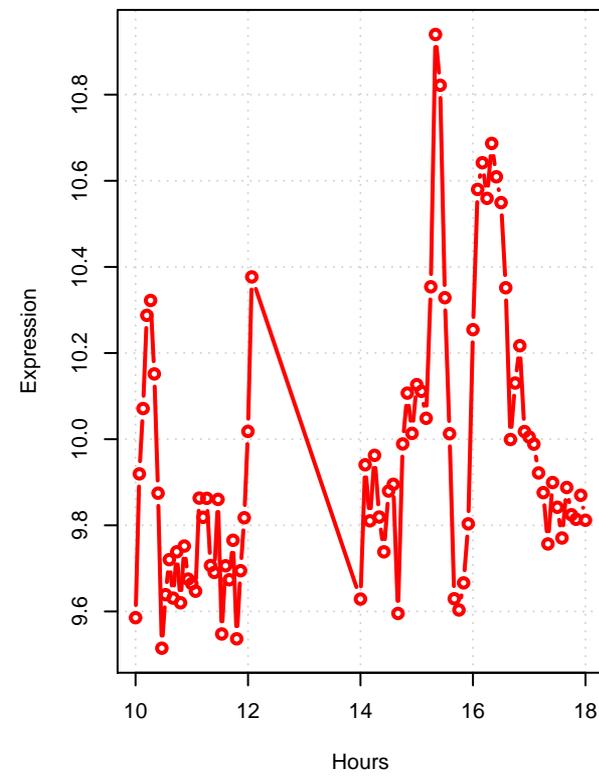
urh1 YDR400W  
Uridine nucleosidase (uridine-cytidine N-ribohydrolase)



urk1 YNR012W  
Uridine/cytidine kinase



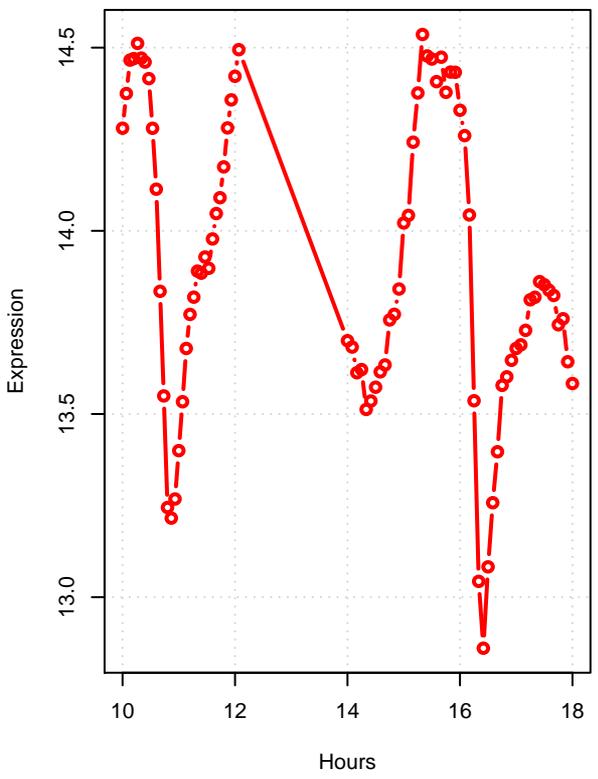
cdd1 YLR245C  
Cytidine deaminase



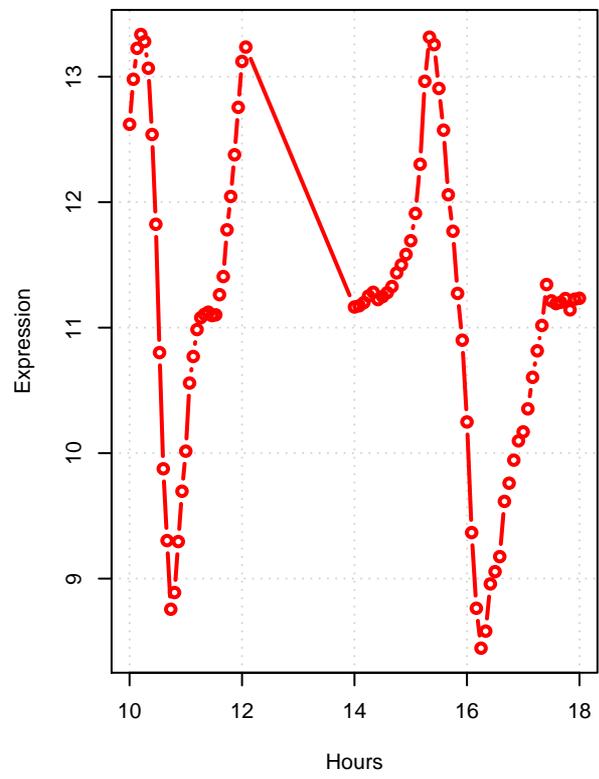
**non-oxidative branch of the pentose phosphate pathway**

# non-oxidative branch of the pentose phosphate pathway

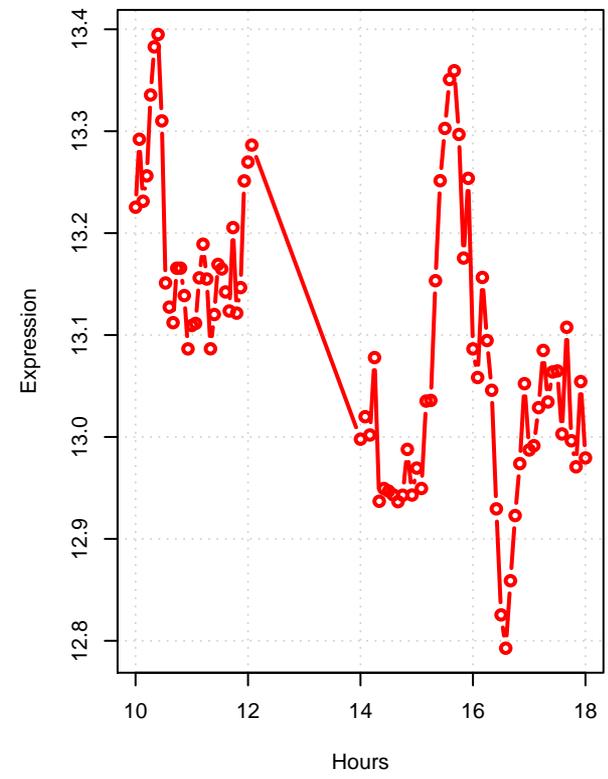
tkl1 YPR074C  
Transketolase



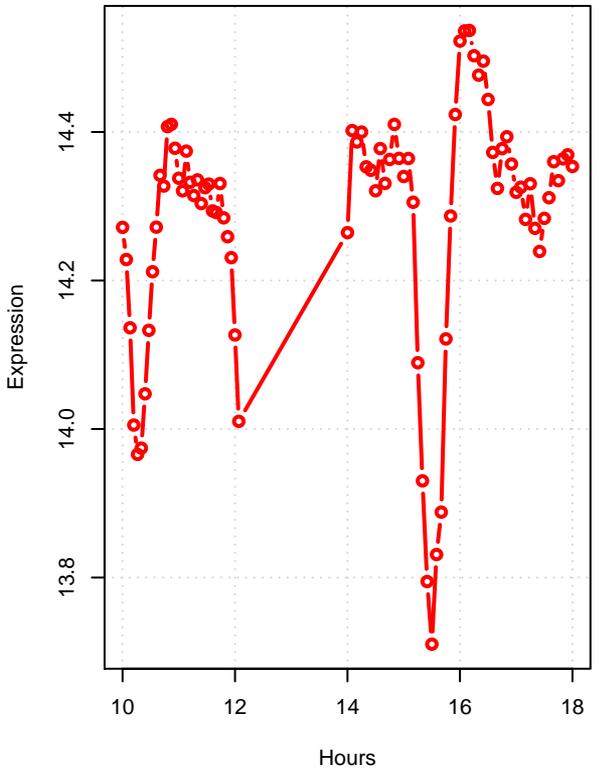
rki1 YOR095C  
Ribose-5-phosphate ketol-isomerase



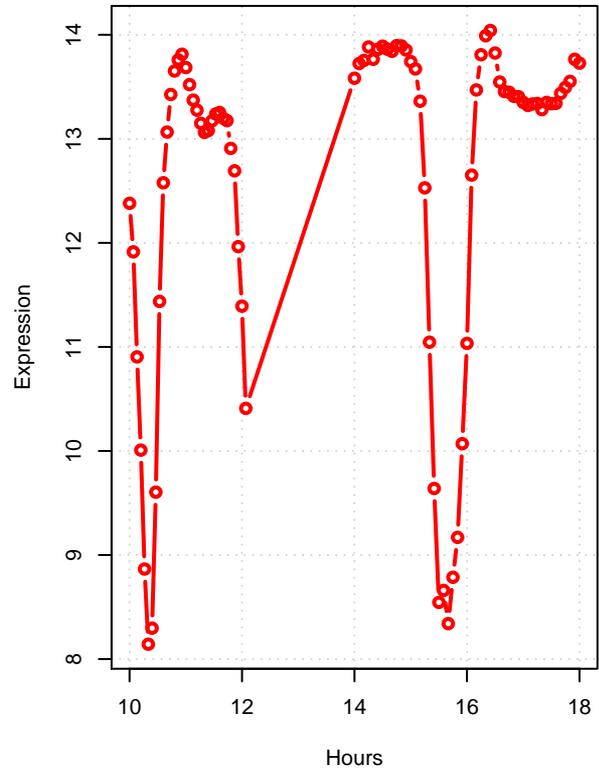
rpe1 YJL121C  
D-ribulose-5-phosphate 3-epimerase



tal1 YLR354C  
Transaldolase, enzyme in the non-oxidative pentose phosphate pathway



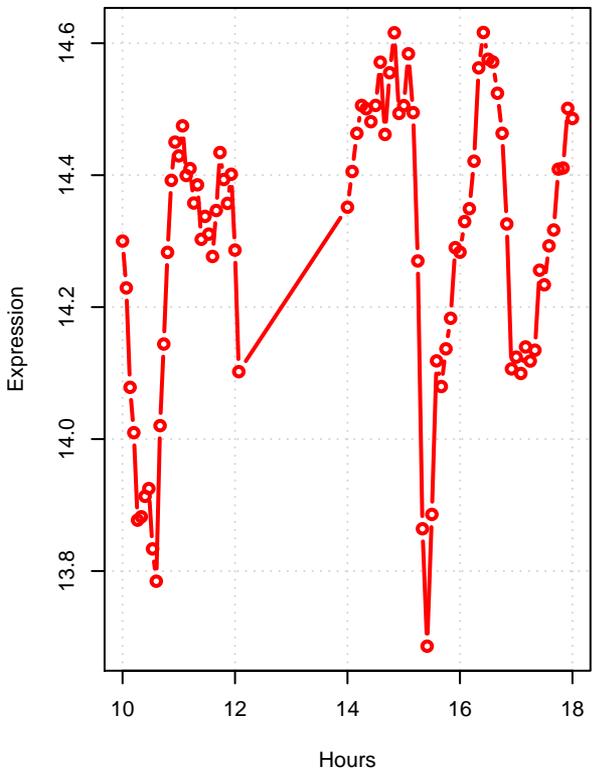
tkl2 YBR117C  
Transketolase



## **oleate biosynthesis**

# oleate biosynthesis

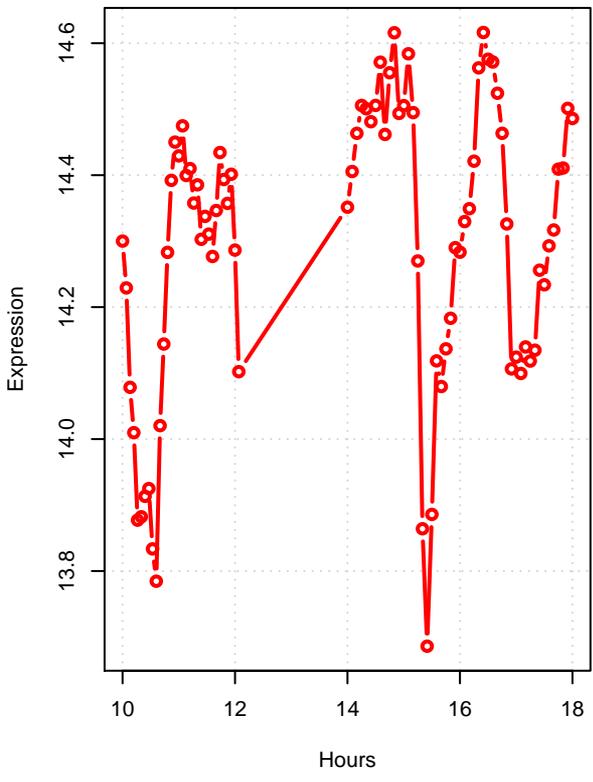
ole1 YGL055W  
Delta(9) fatty acid desaturase



## palmitoleate biosynthesis

# palmitoleate biosynthesis

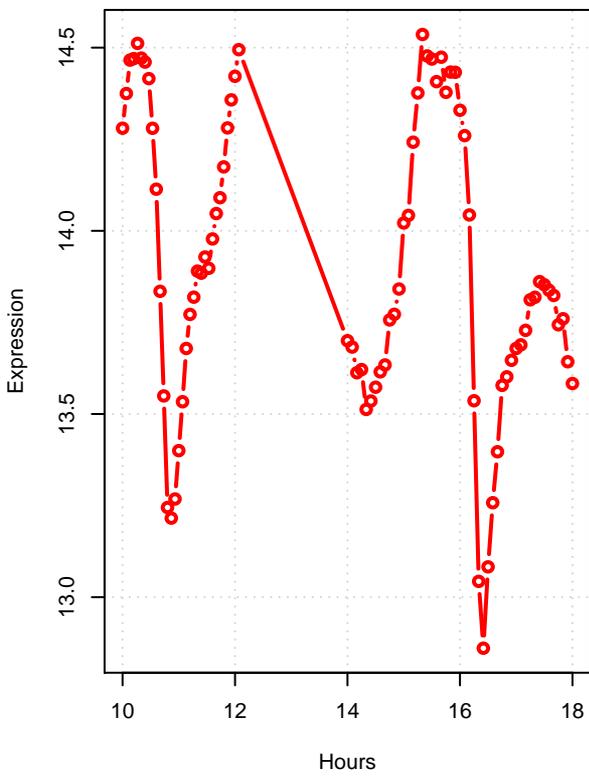
ole1 YGL055W  
Delta(9) fatty acid desaturase



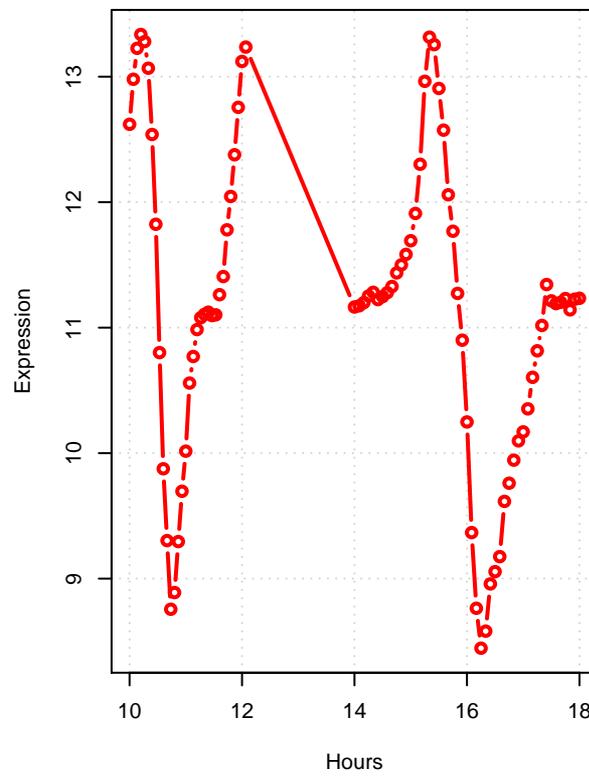
**oxidative branch of the pentose phosphate pathway**

# oxidative branch of the pentose phosphate pathway

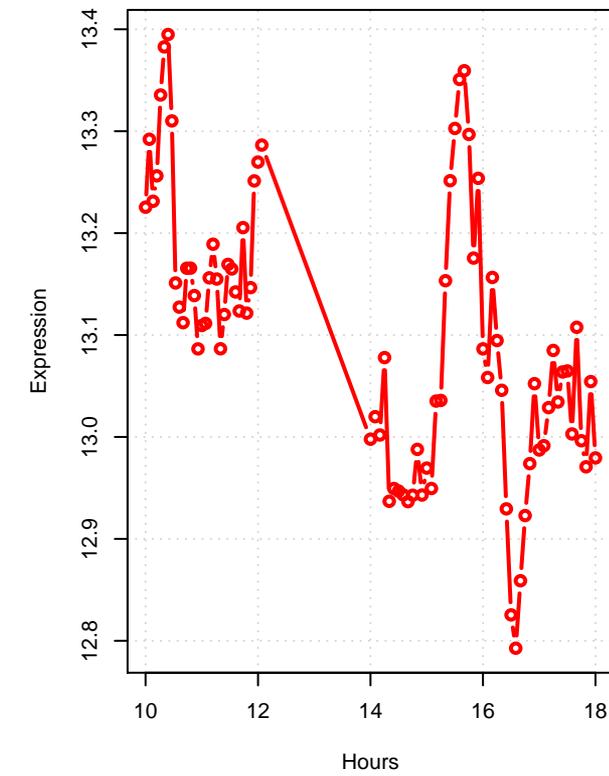
tkl1 YPR074C  
Transketolase



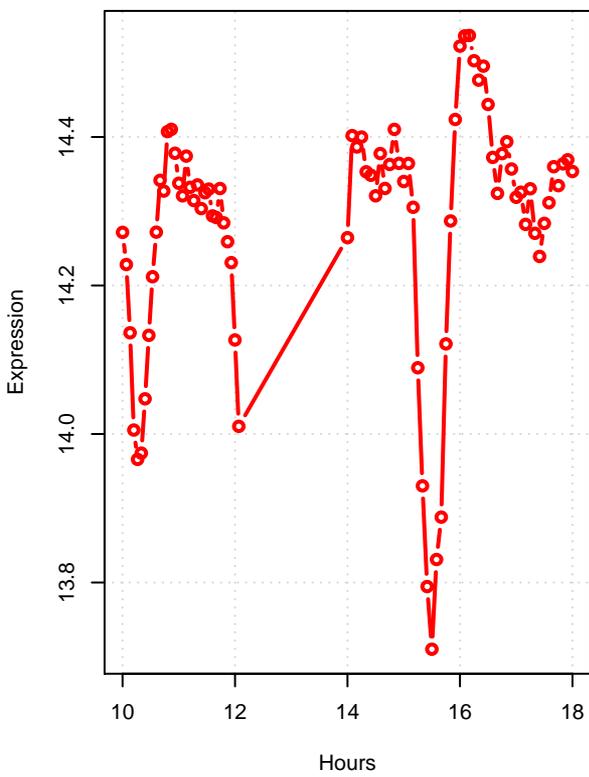
tkl1 YOR095C  
Ribose-5-phosphate ketol-isomerase



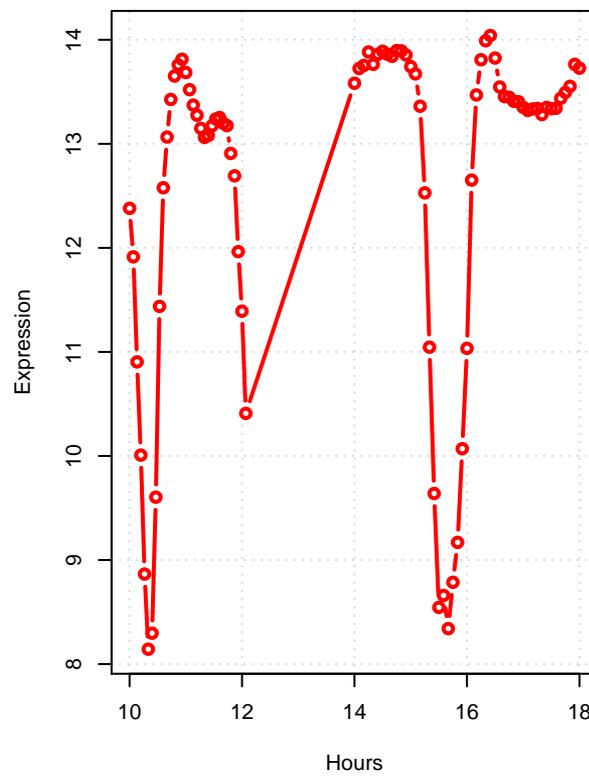
rpe1 YJL121C  
D-ribulose-5-phosphate 3-epimerase



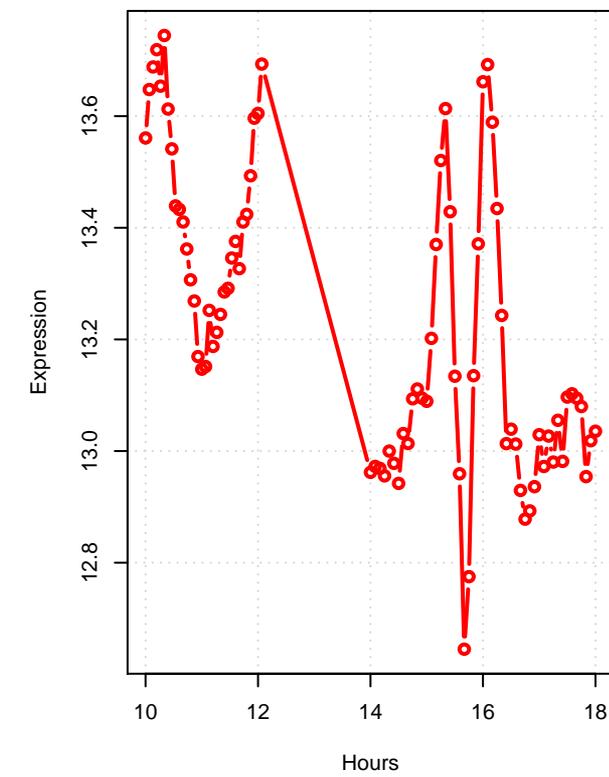
tal1 YLR354C  
Transaldolase, enzyme in the non-oxidative pentose phosphate pathway



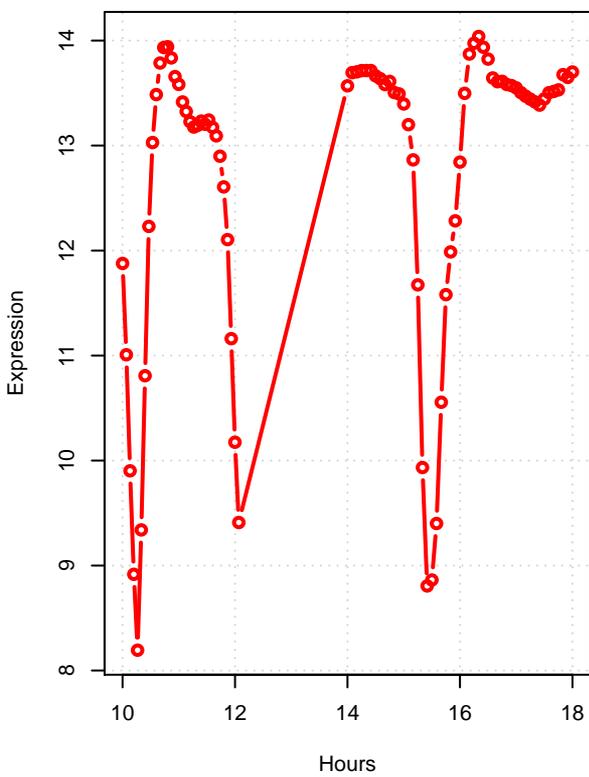
tkl2 YBR117C  
Transketolase



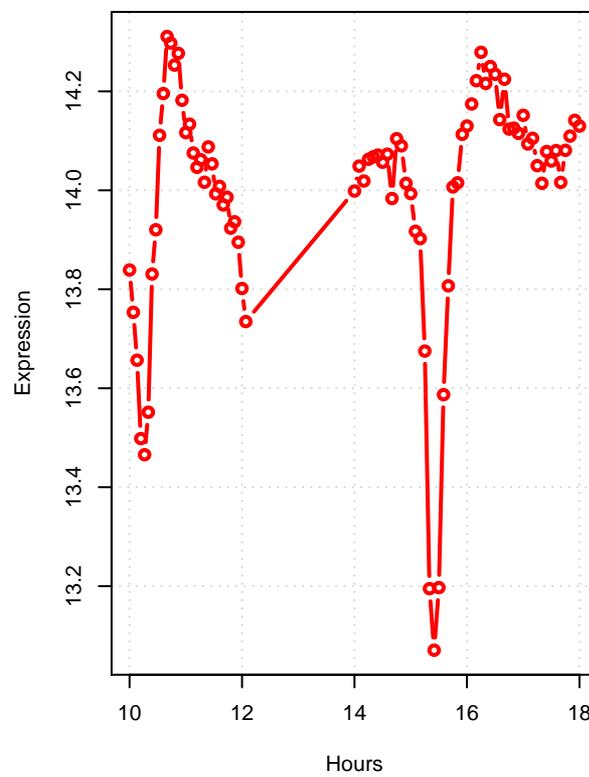
sol3 YHR163W  
6-phosphogluconolactonase



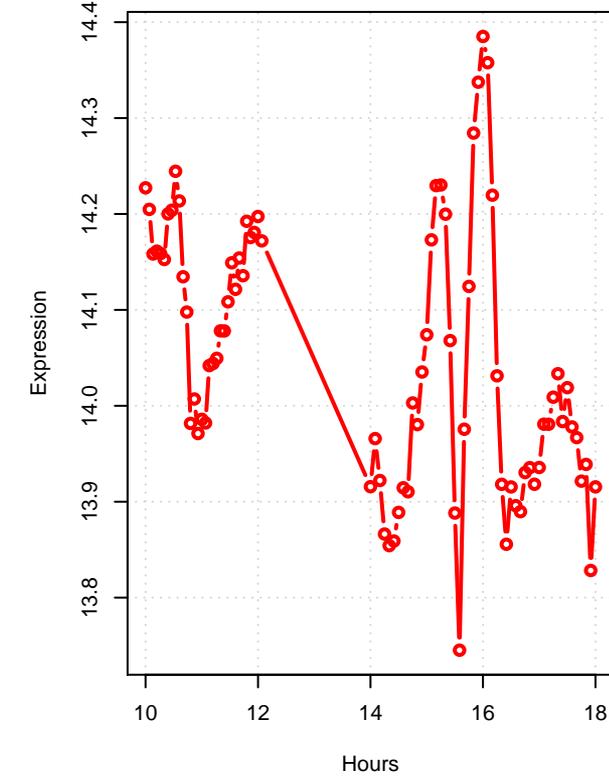
sol4 YGR248W  
6-phosphogluconolactonase



zwf1 YNL241C  
Glucose-6-phosphate dehydrogenase (G6PD)



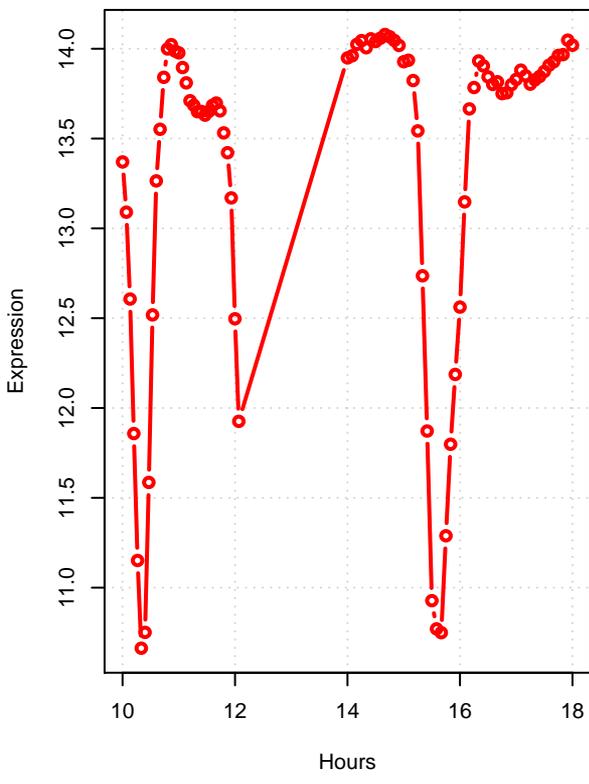
gnd1 YHR183W  
6-phosphogluconate dehydrogenase (decarboxylating)



# oxidative branch of the pentose phosphate pathway

gnd2 YGR256W

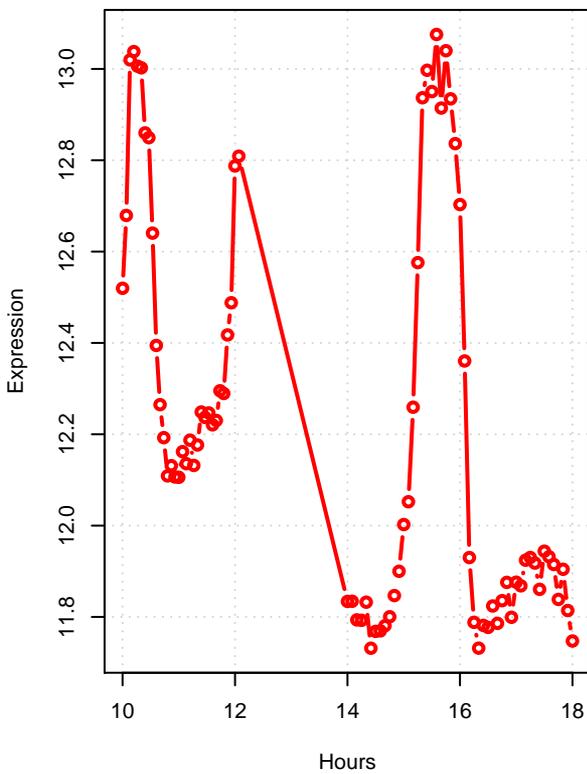
6-phosphogluconate dehydrogenase (decarboxylating)



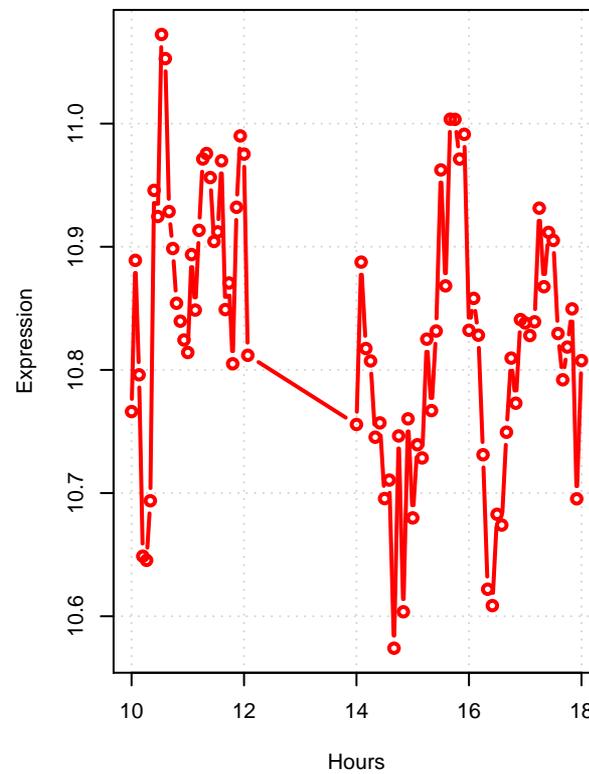
## **pantothenate and coenzyme A biosynthesis**

# pantothenate and coenzyme A biosynthesis

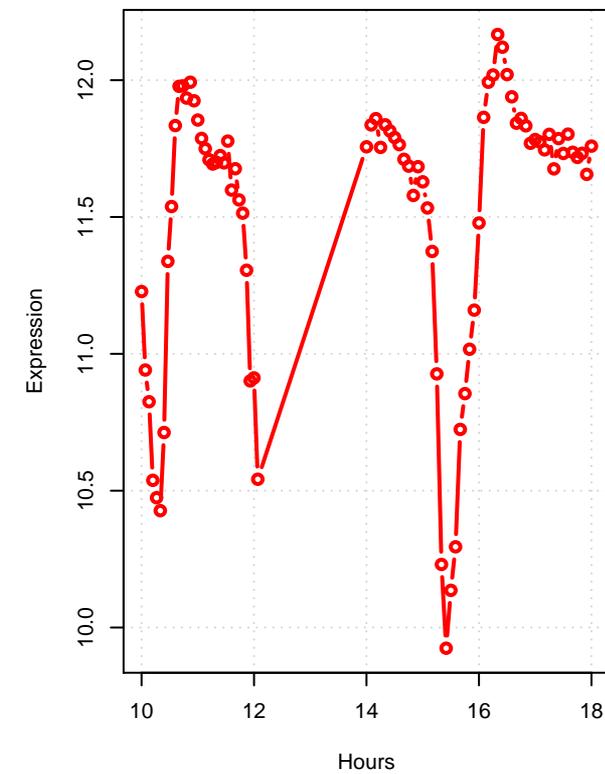
pan5 YHR063C  
2-dehydropanoate 2-reductase



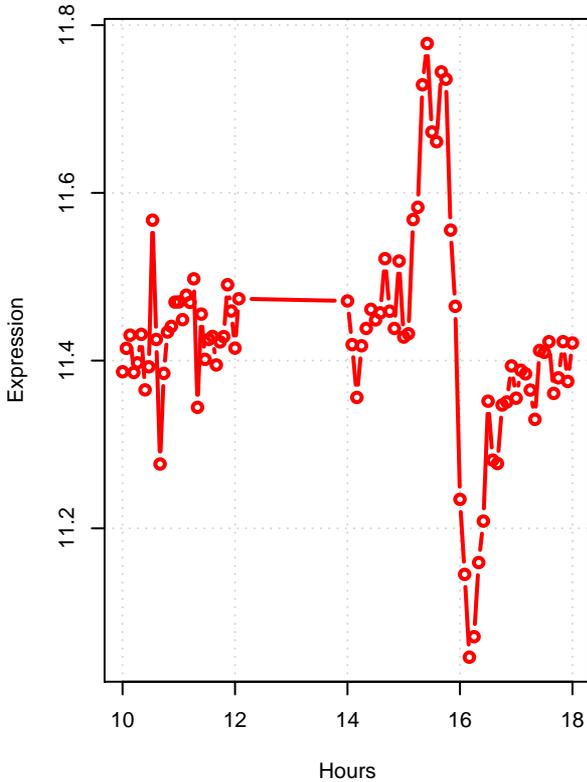
ecm31 YBB176W  
Ketopantoate hydroxymethyltransferase



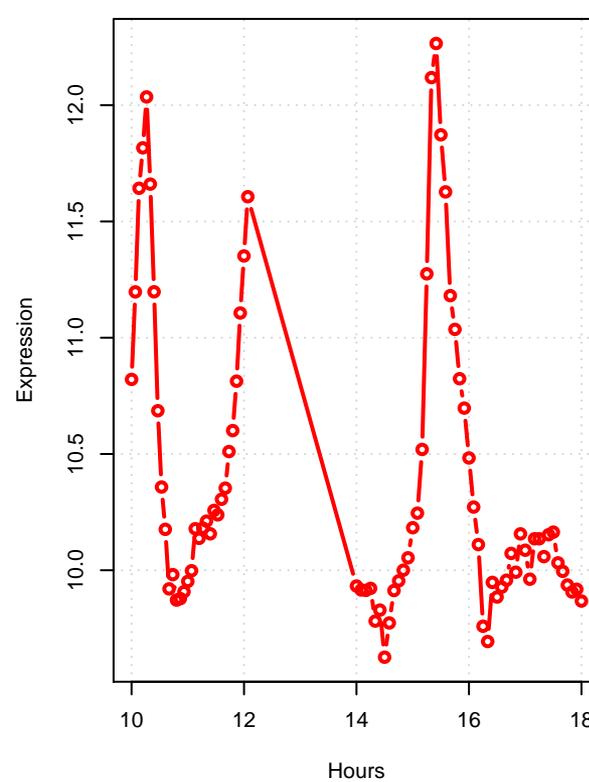
cab5 YDR196C  
Subunit of the CoA-Synthesizing Protein Complex (CoA-SPC)



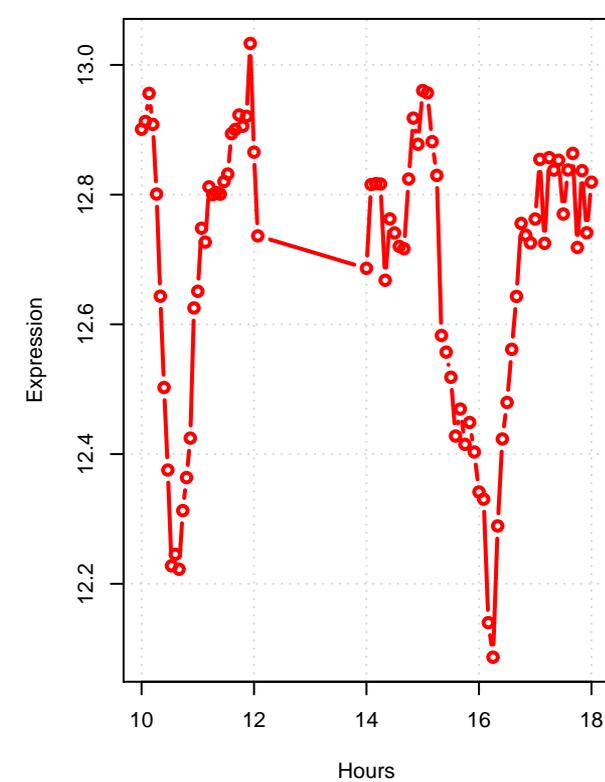
cab4 YGR277C  
Subunit of the CoA-Synthesizing Protein Complex (CoA-SPC)



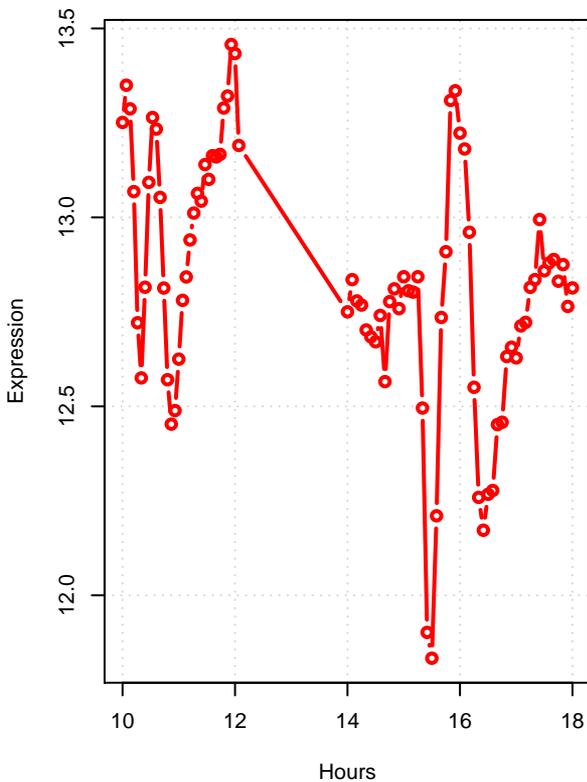
pan6 YIL145C  
Pantothenate synthase



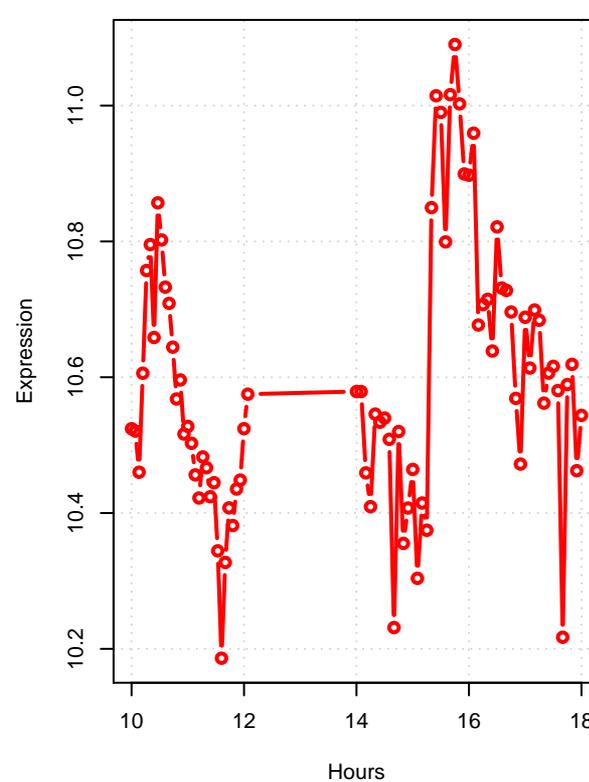
cab1 YDR531W  
Pantothenate kinase, ATP:D-pantothenate 4'-phosphotransferase



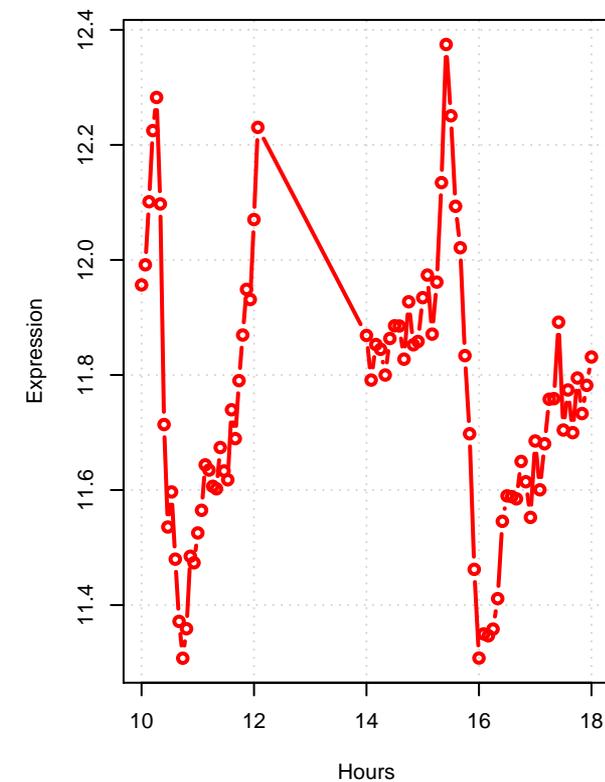
cab2 YIL083C  
Subunit of the CoA-Synthesizing Protein Complex (CoA-SPC)



cab3 YKL088W  
Subunit of PPCDC and CoA-SPC complexes involved in CoA biosynthesis



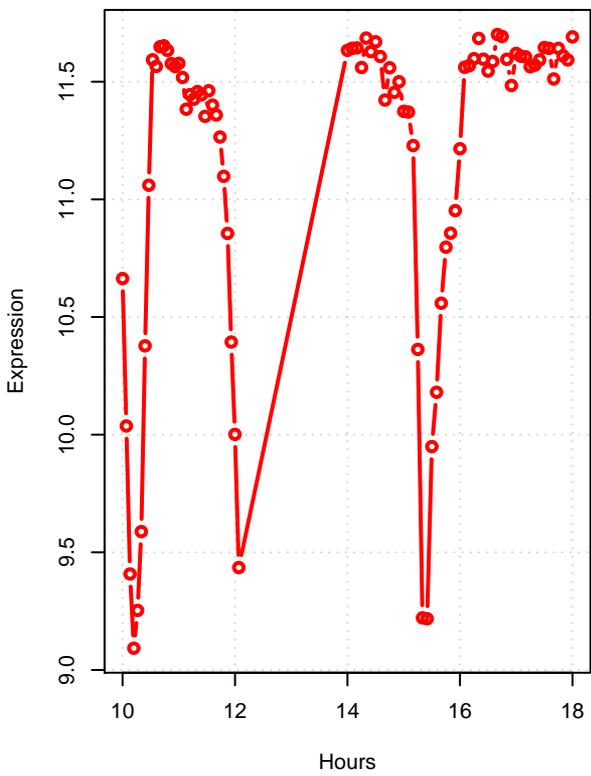
sis2 YKR072C  
Negative regulatory subunit of protein phosphatase 1 (Ppz1p)



# pantothenate and coenzyme A biosynthesis

vhs3 YOR054C

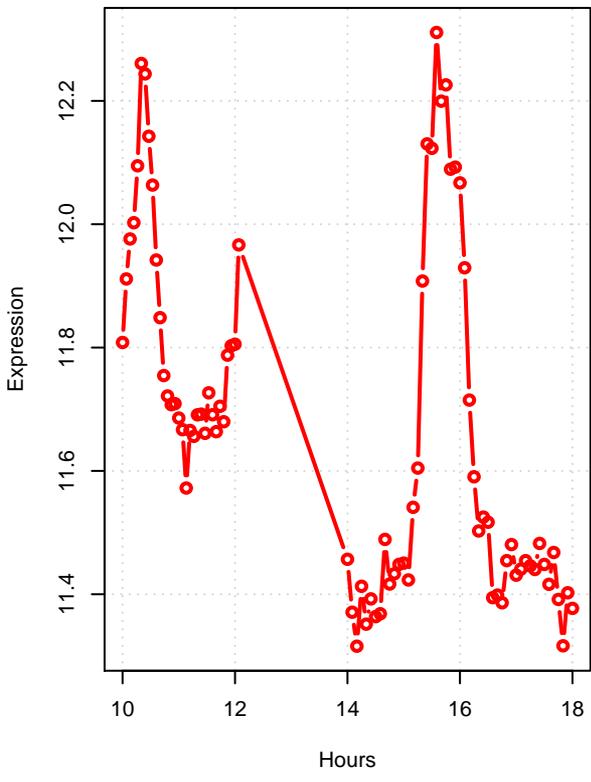
Negative regulatory subunit of protein phosphatase 1 Ppz1p



**periplasmic NAD degradation**

# periplasmic NAD degradation

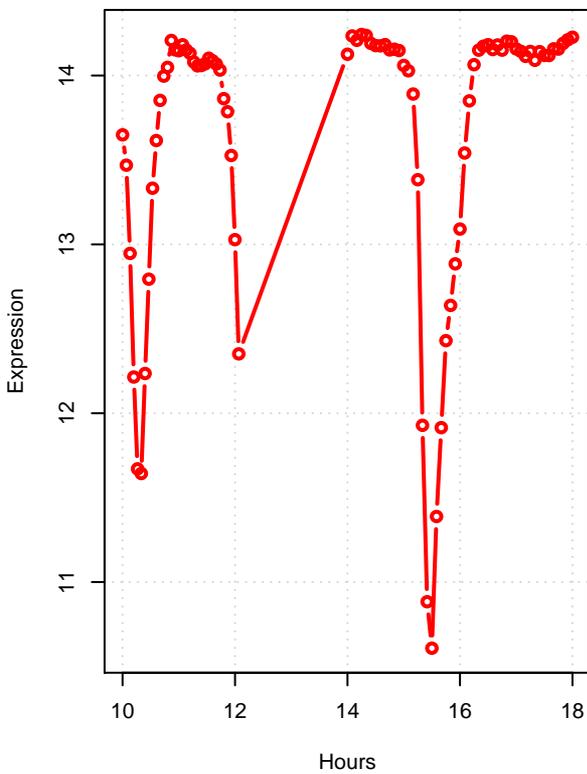
npv1 YGL067W  
NADH diphosphatase (pyrophosphatase)



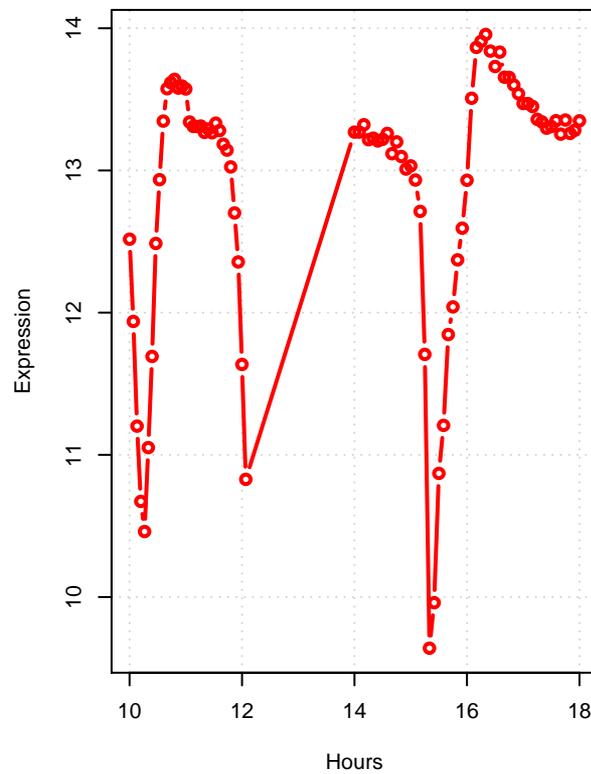
**phosphatidate biosynthesis I (the dihydroxyacetone pathway)**

# phosphatidate biosynthesis I (the dihydroxyacetone pathway)

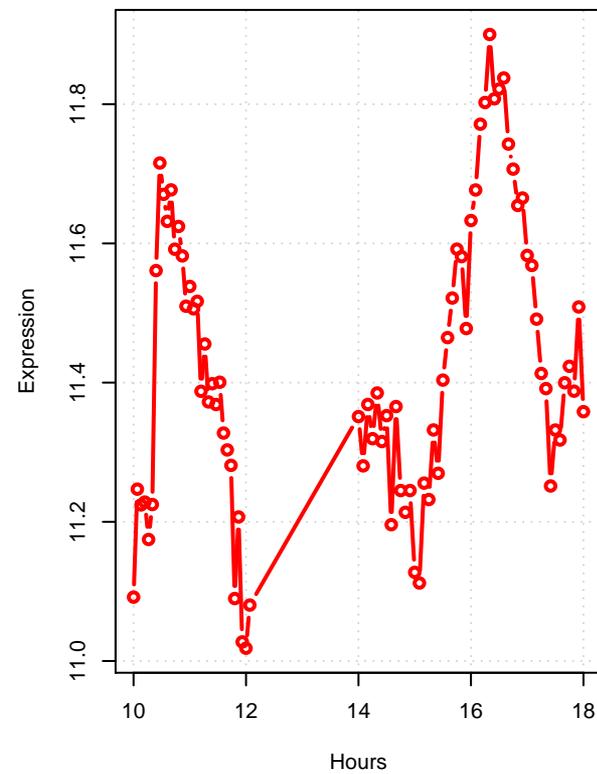
ayr1 YL124W  
Bifunctional triacylglycerol lipase and 1-acyl DHAP reductase



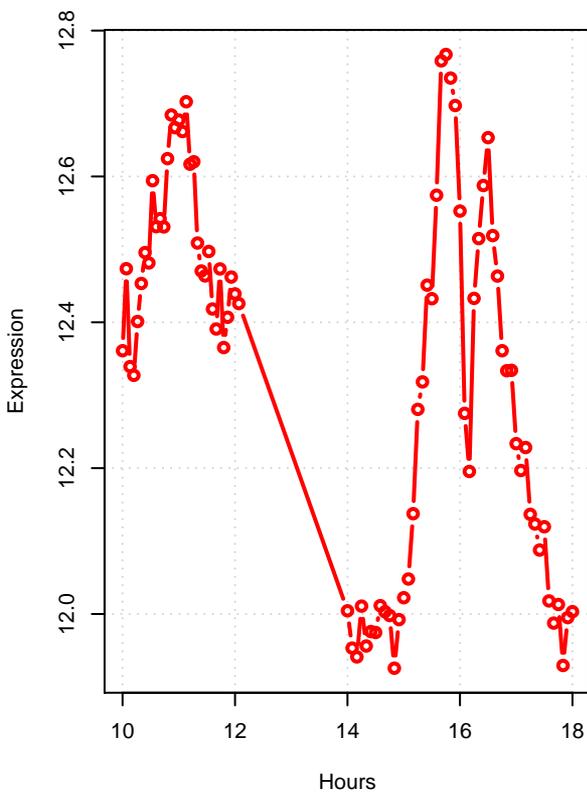
gpi2 YKR067W  
Glycerol-3-phosphate/dihydroxyacetone phosphate sn-1 acyltransferase



slc1 YBL011W  
Glycerol 3-phosphate/dihydroxyacetone phosphate sn-1 acyltransferase



slc1 YDL052C  
1-acyl-sn-glycerol-3-phosphate acyltransferase

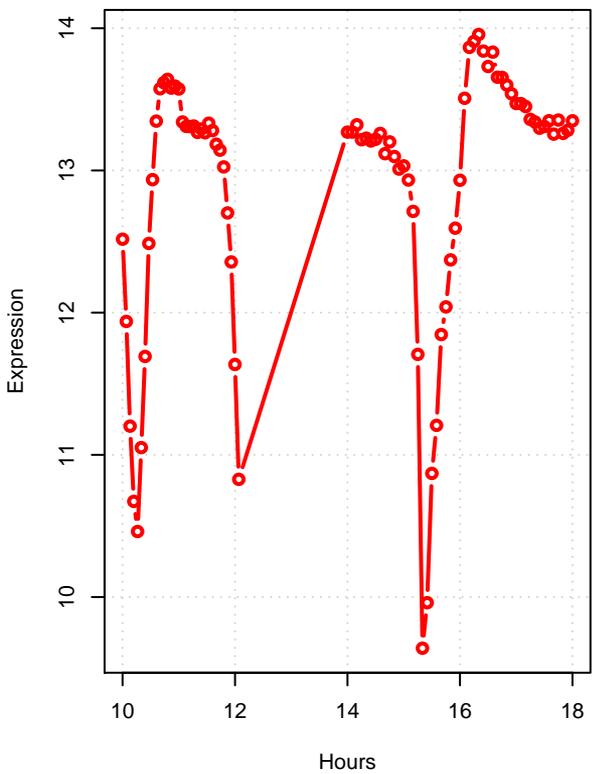


## **triglyceride biosynthesis**

# triglyceride biosynthesis

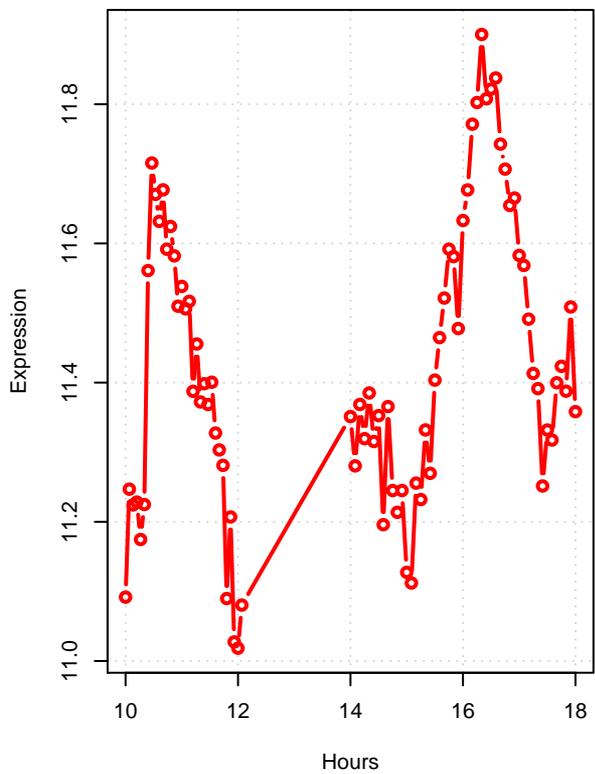
*gpt2* YKR067W

Glycerol-3-phosphate/dihydroxyacetone phosphate sn-1 acyltransferase



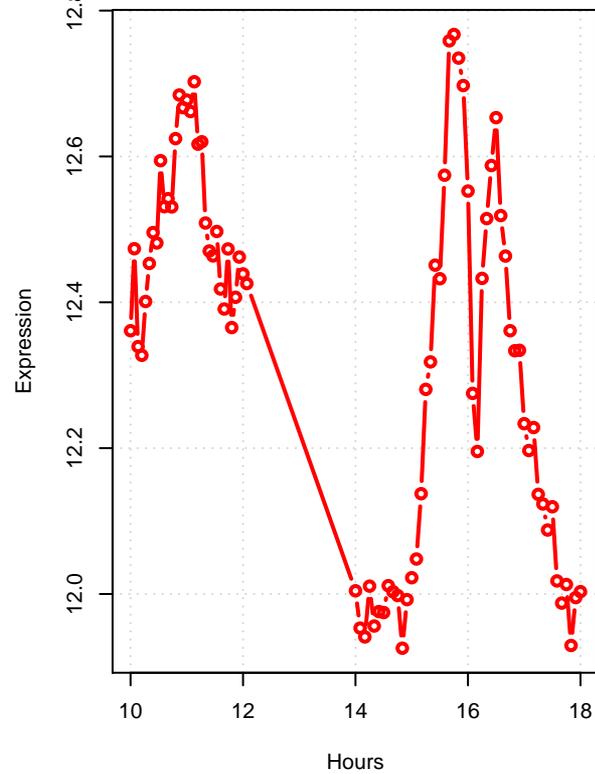
*sct1* YBL011W

Glycerol 3-phosphate/dihydroxyacetone phosphate sn-1 acyltransferase



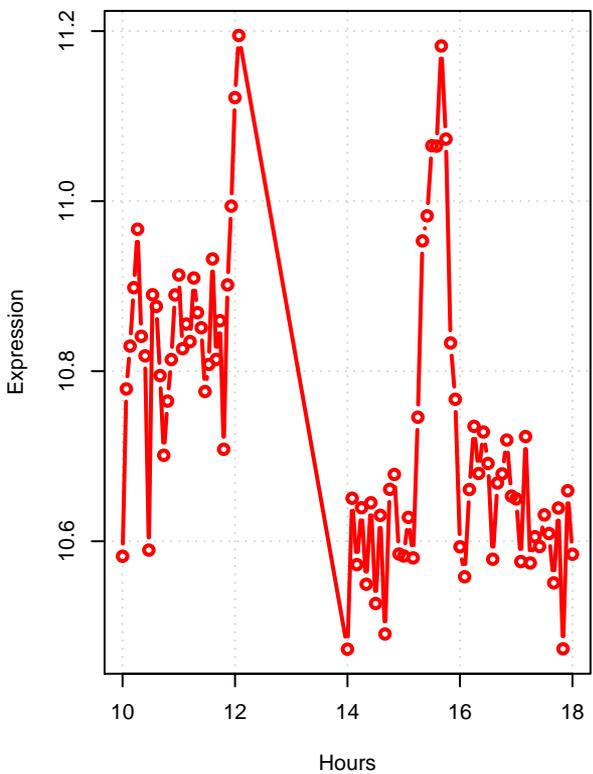
*slc1* YDL052C

1-acyl-sn-glycerol-3-phosphate acyltransferase



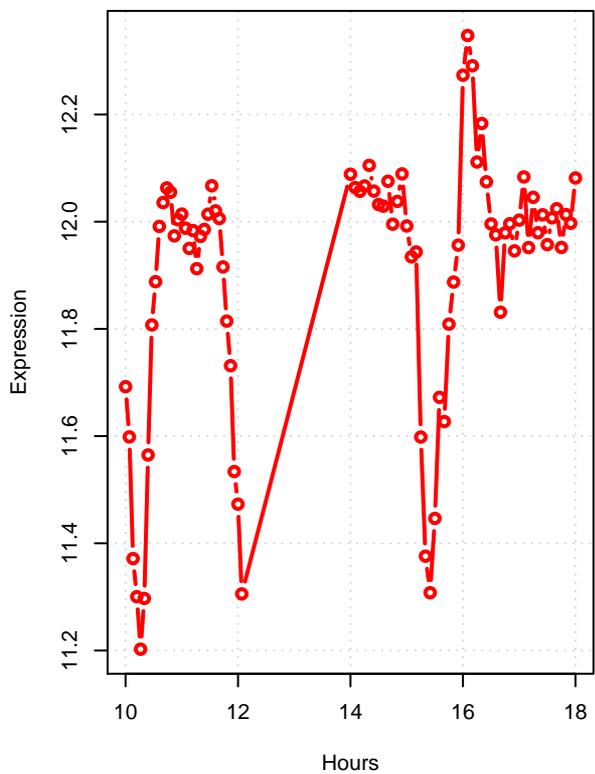
*Iro1* YNR008W

Acyltransferase that catalyzes diacylglycerol esterification



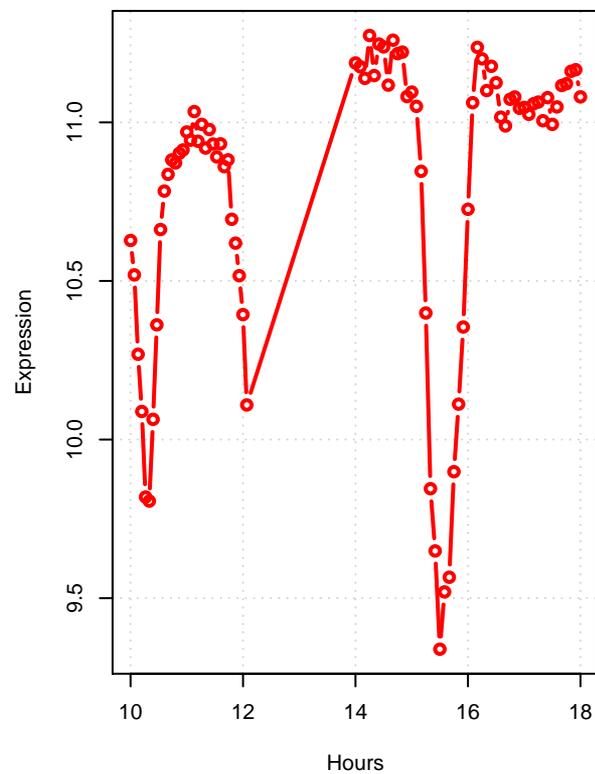
*dga1* YOR245C

Diacylglycerol acyltransferase



*pah1* YMR165C

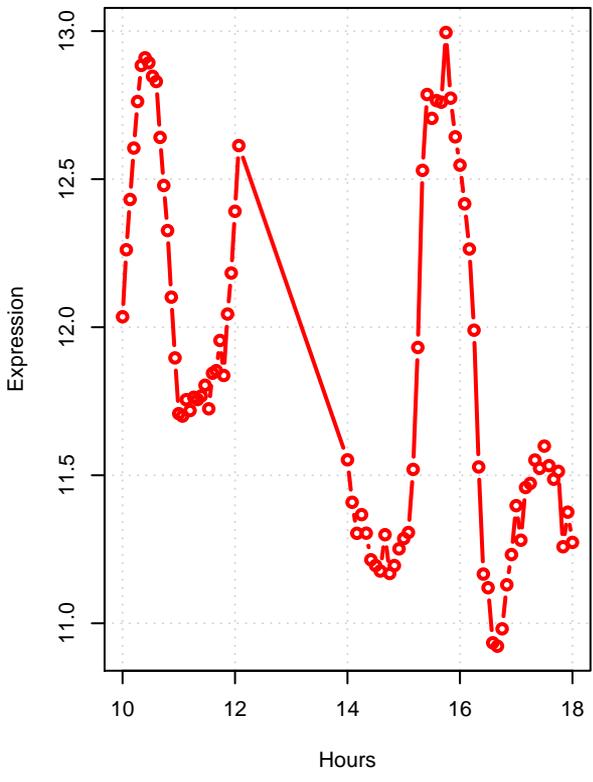
Mg<sup>2+</sup>-dependent phosphatidate (PA) phosphatase



# phosphatidylinositol biosynthesis

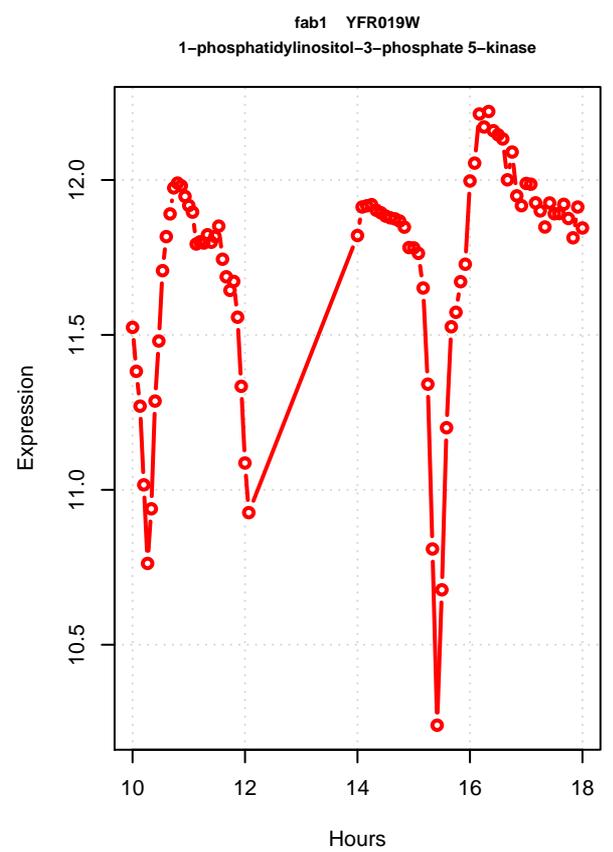
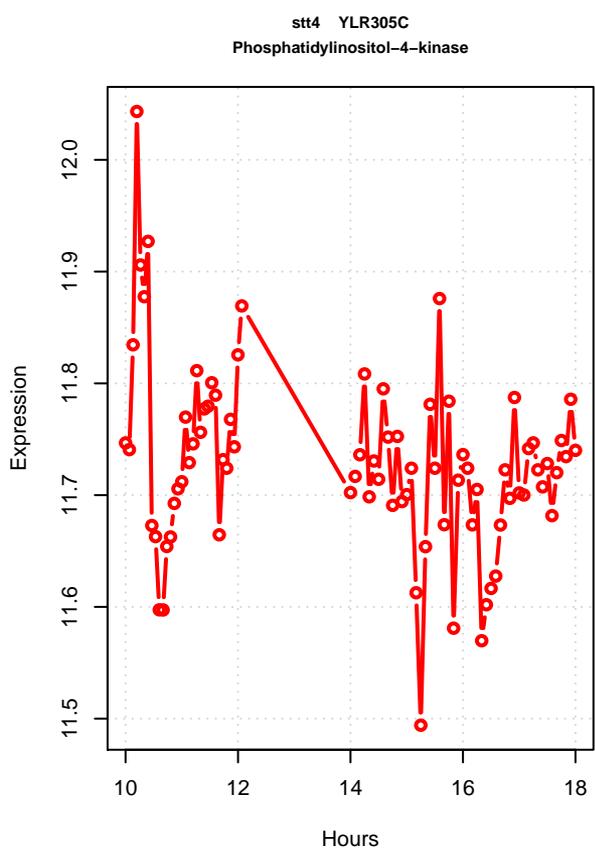
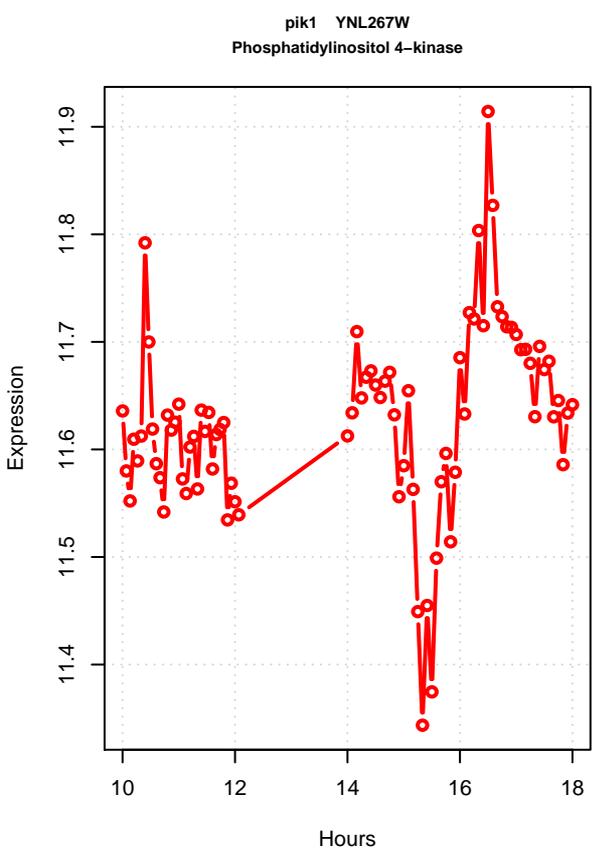
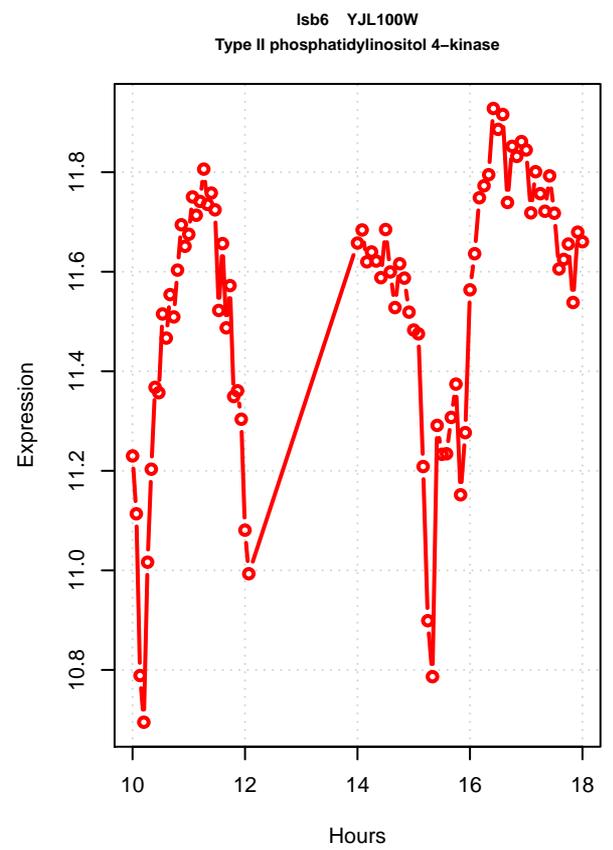
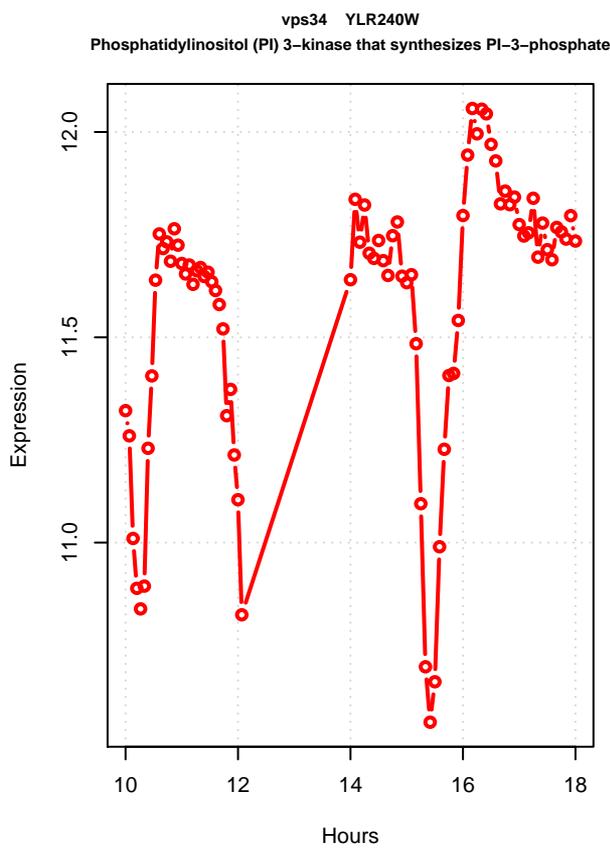
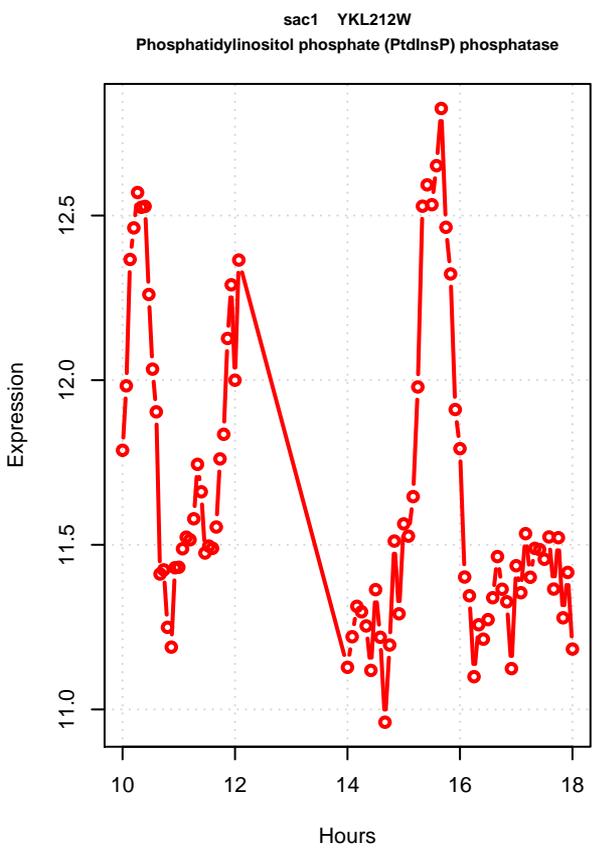
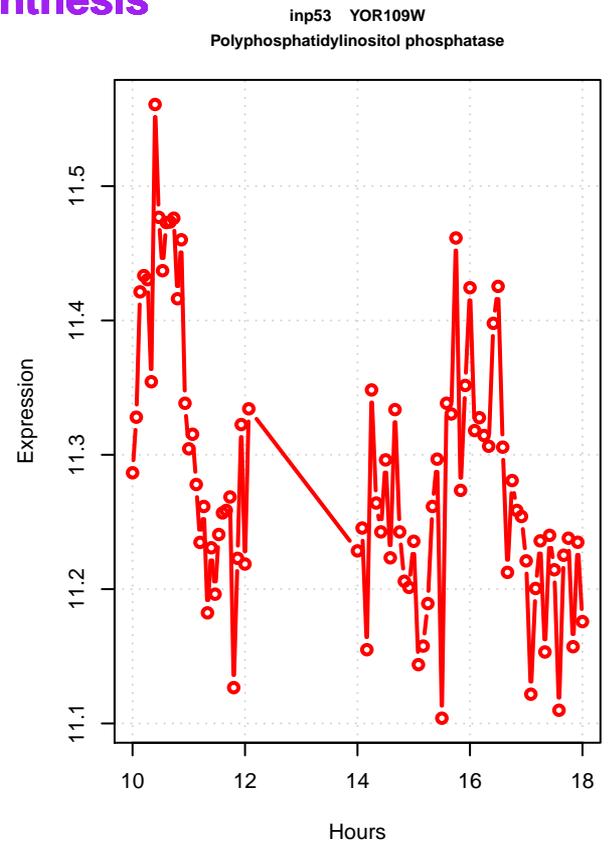
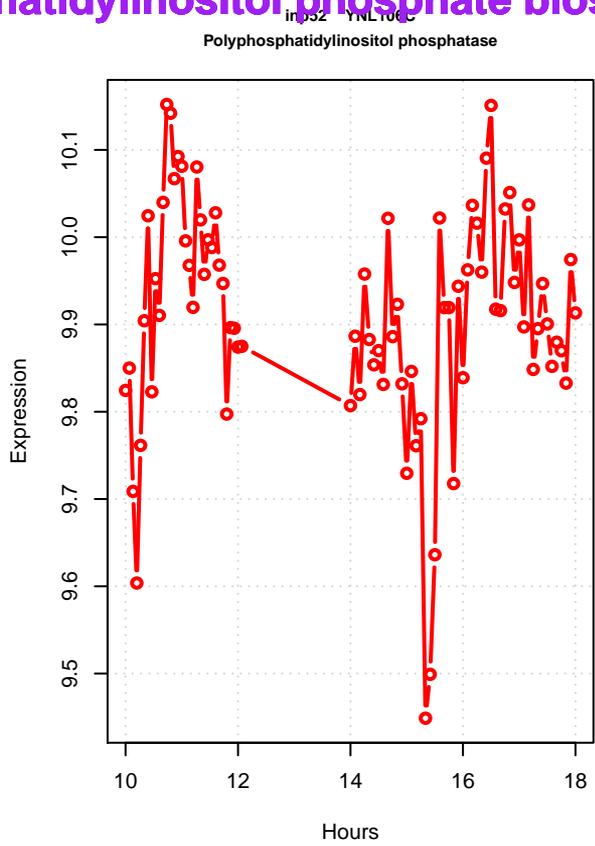
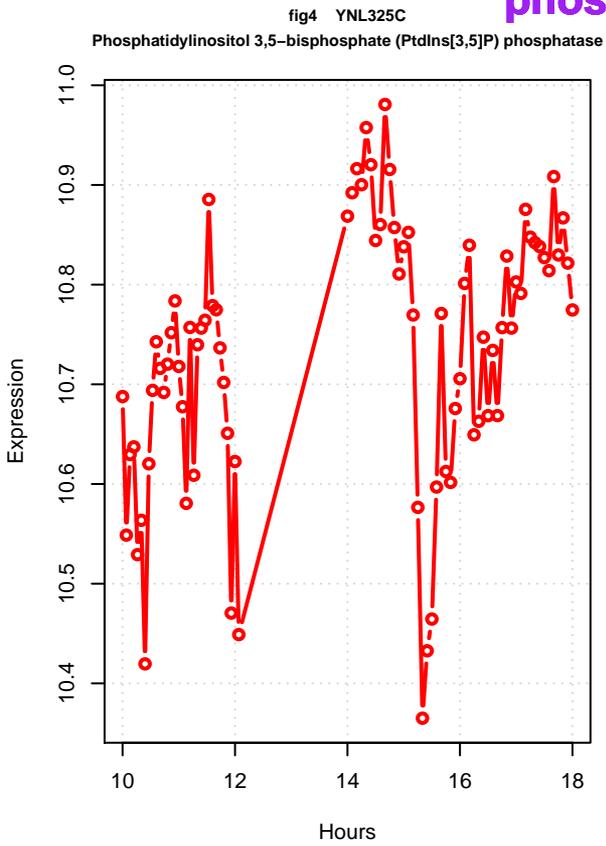
# phosphatidylinositol biosynthesis

pis1 YPR113W  
Phosphatidylinositol synthase



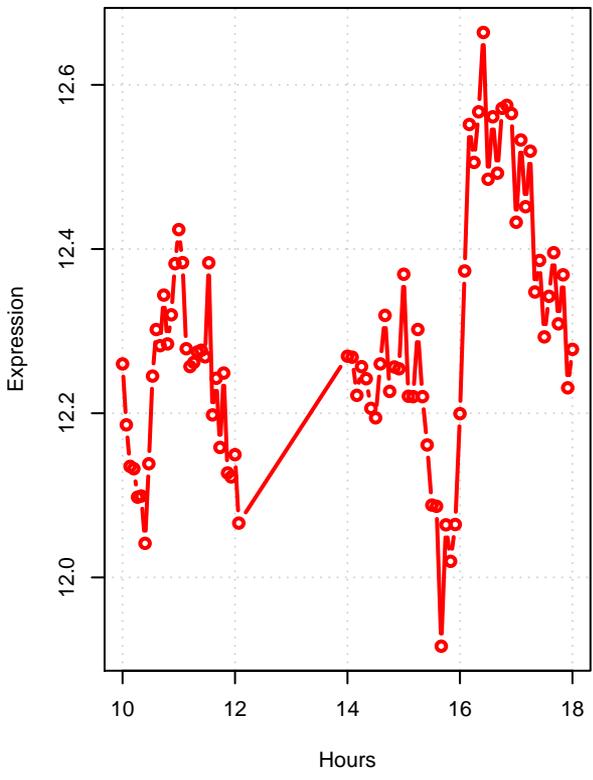
**phosphatidylinositol phosphate biosynthesis**

# phosphatidylinositol biosynthesis

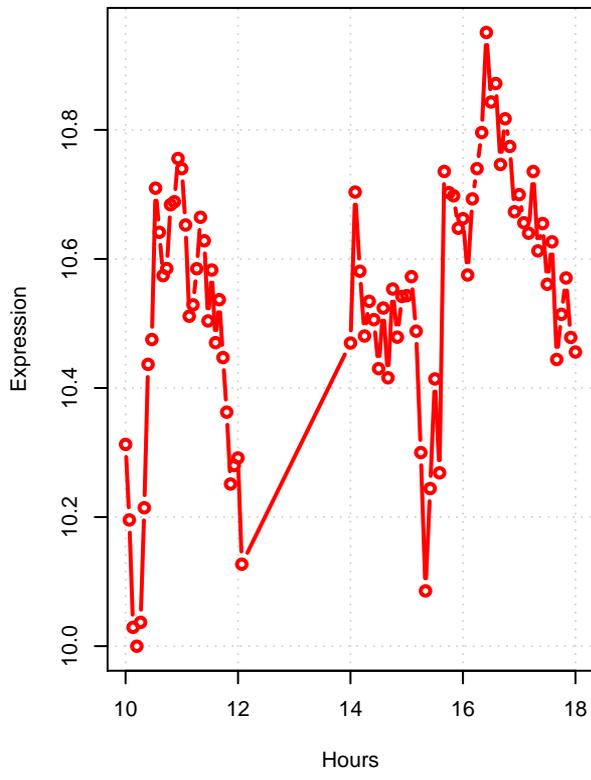


# phosphatidylinositol phosphate biosynthesis

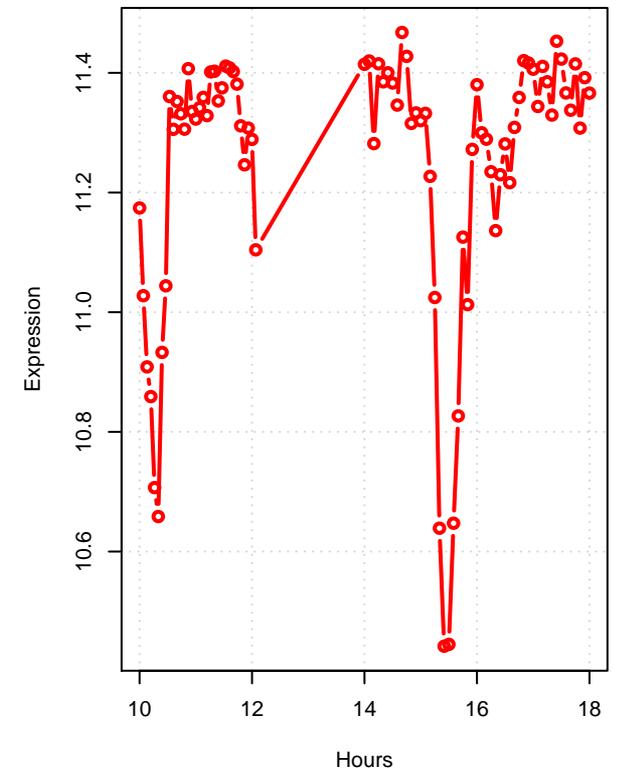
mss4 YDR208W  
Phosphatidylinositol-4-phosphate 5-kinase



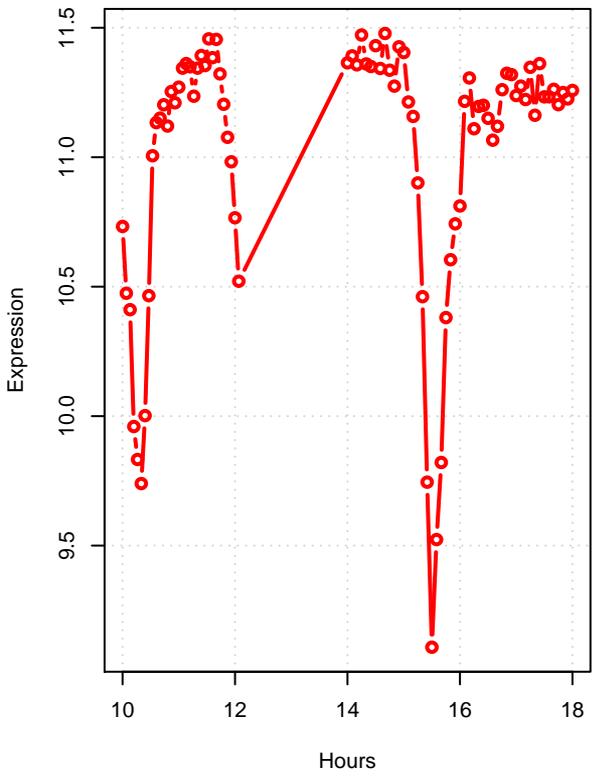
yup1 YJR1101  
Phosphatidylinositol 3-phosphate (PI3P) phosphatase



inp51 YIL002C  
Phosphatidylinositol 4,5-bisphosphate 5-phosphatase

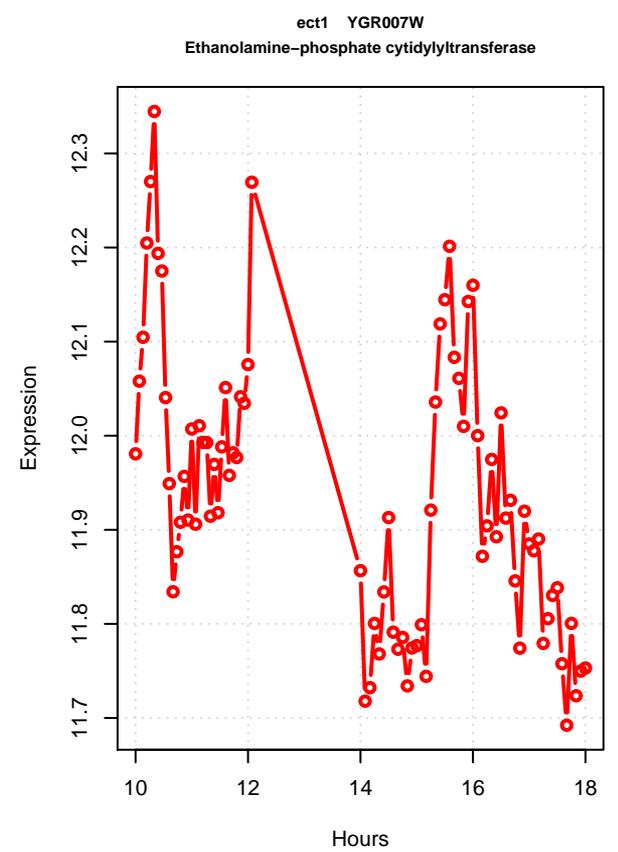
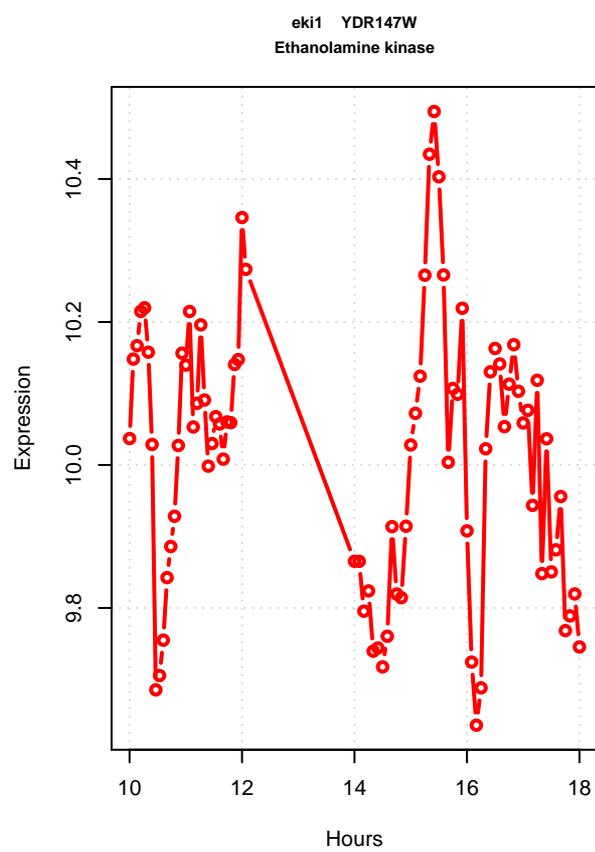
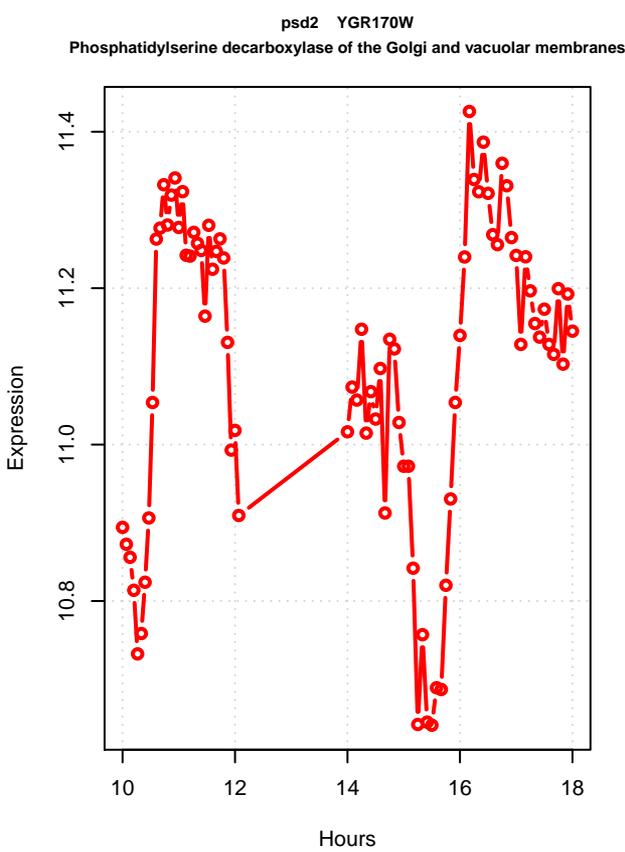
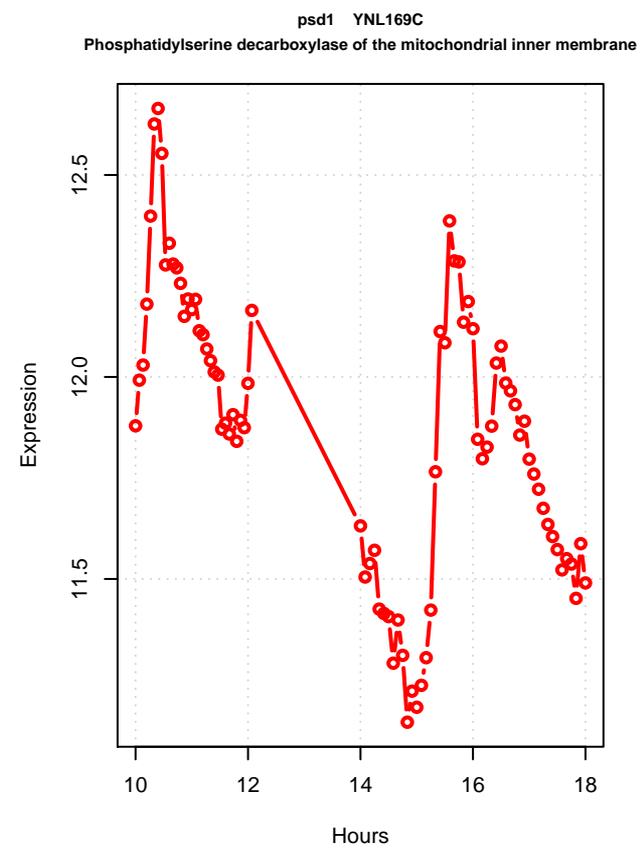
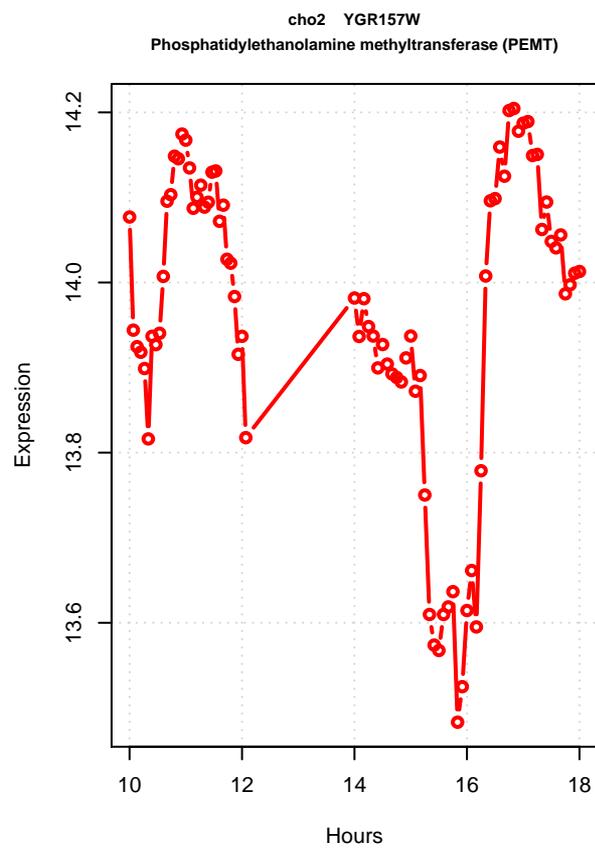
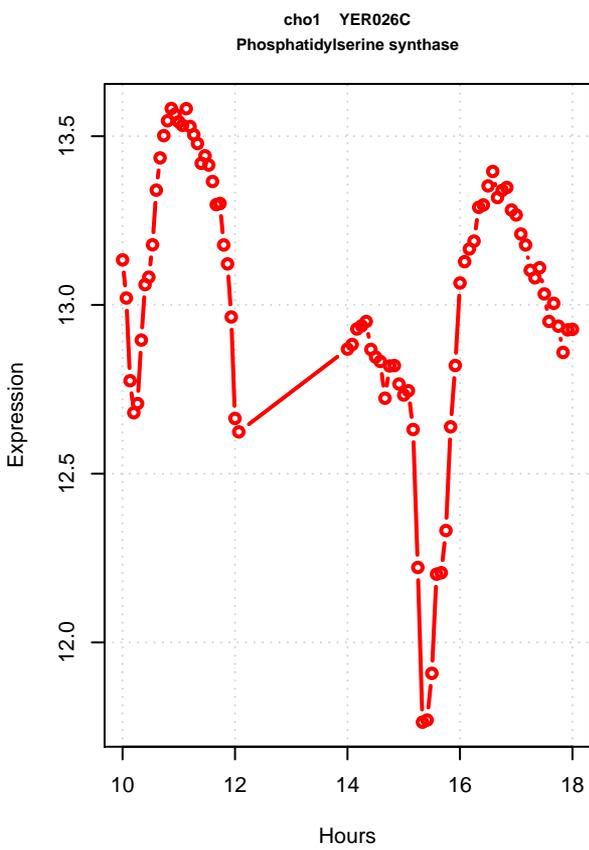
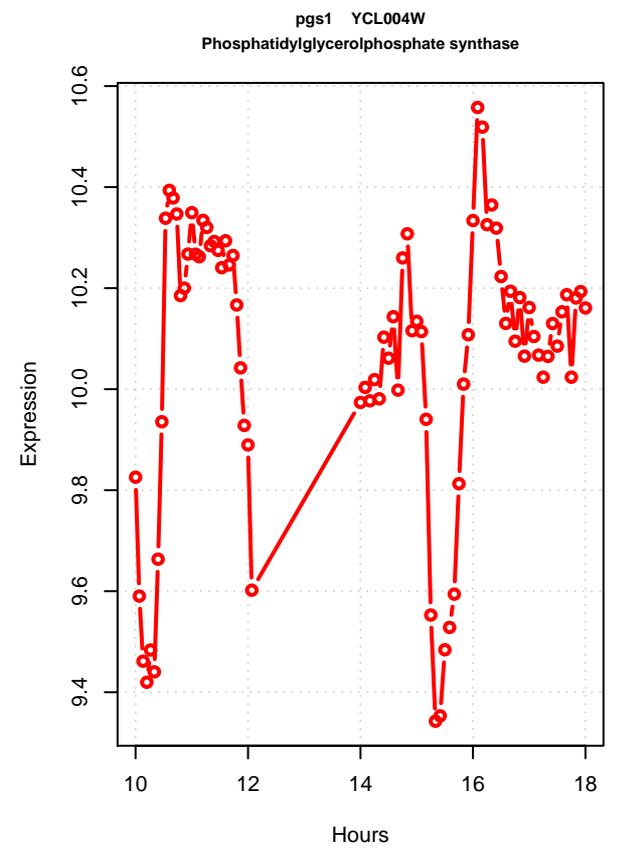
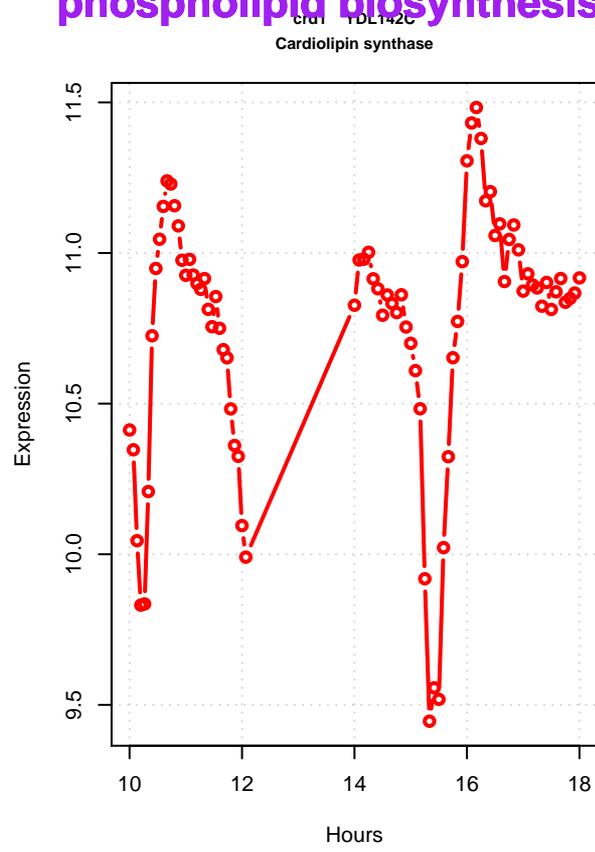
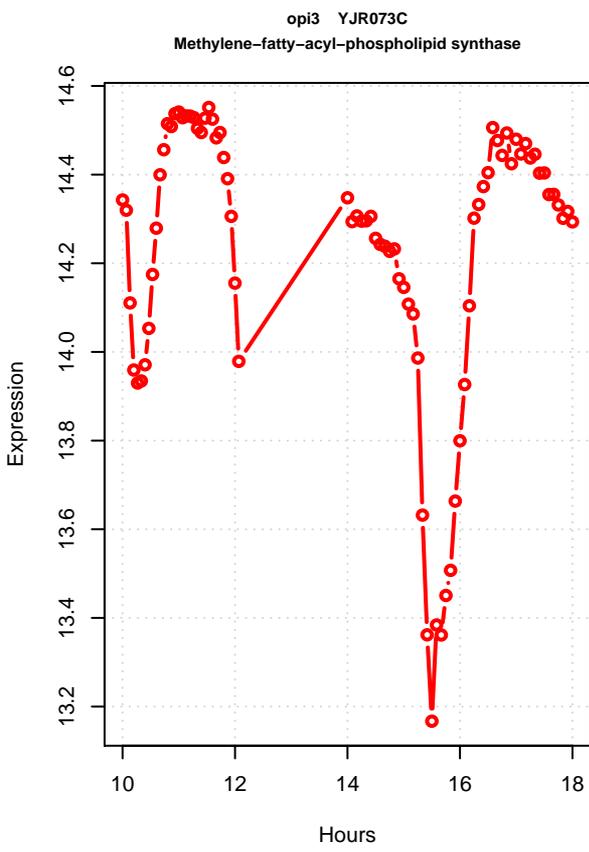


inp54 YOL065C  
Phosphatidylinositol 4,5-bisphosphate 5-phosphatase

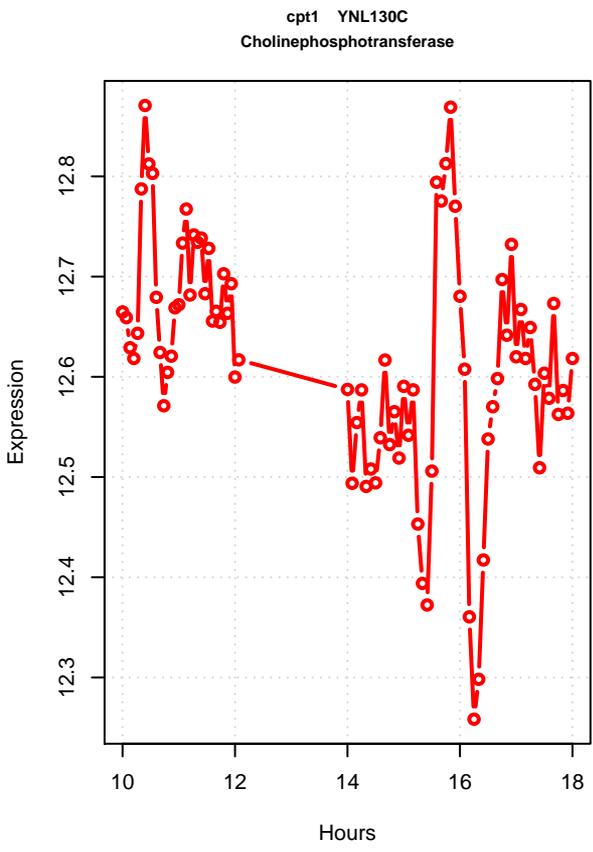
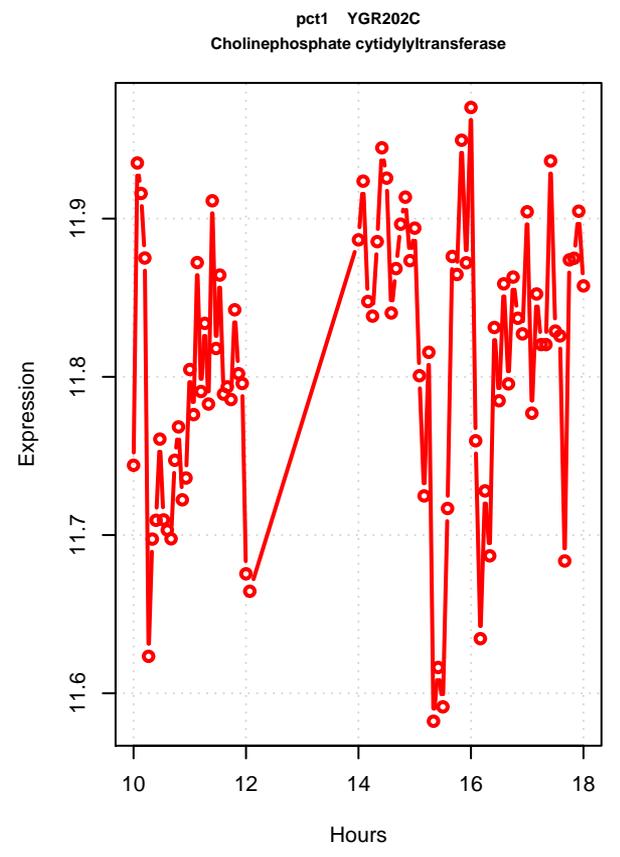
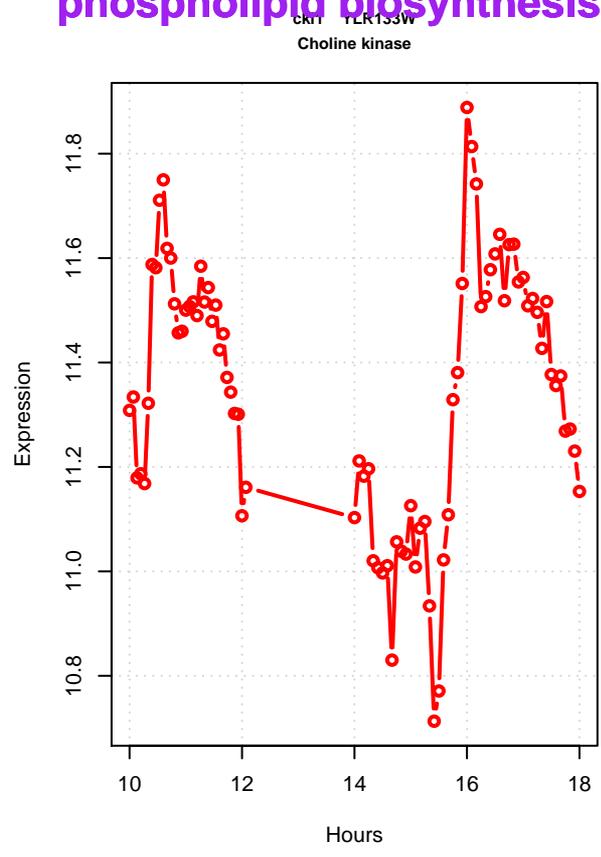
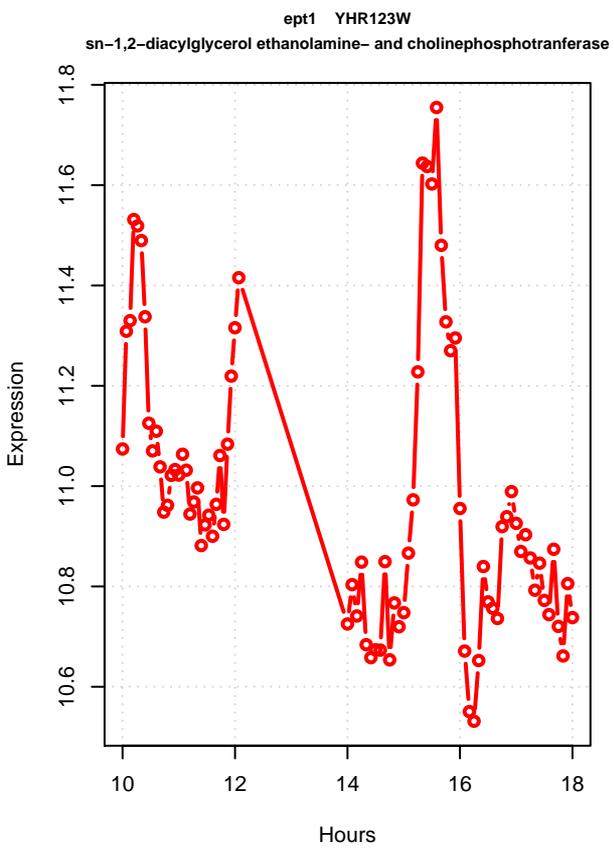


## **phospholipid biosynthesis**

# phospholipid biosynthesis



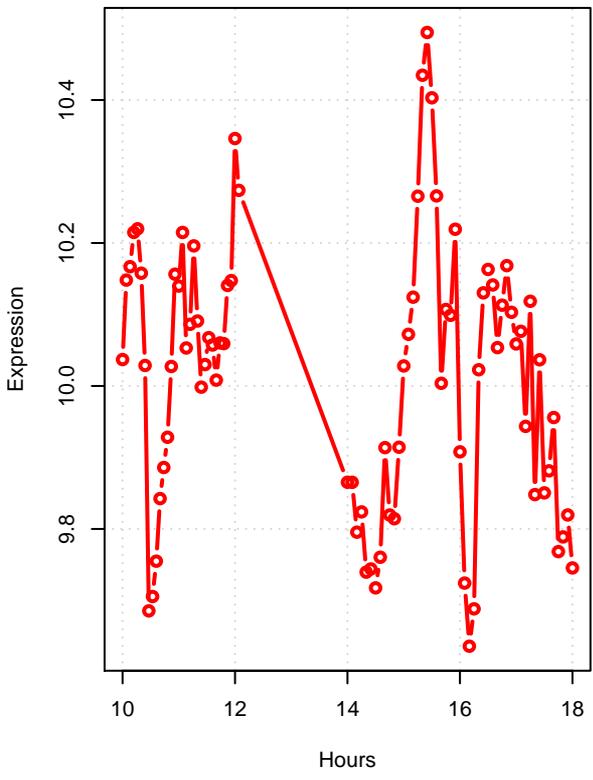
# phospholipid biosynthesis



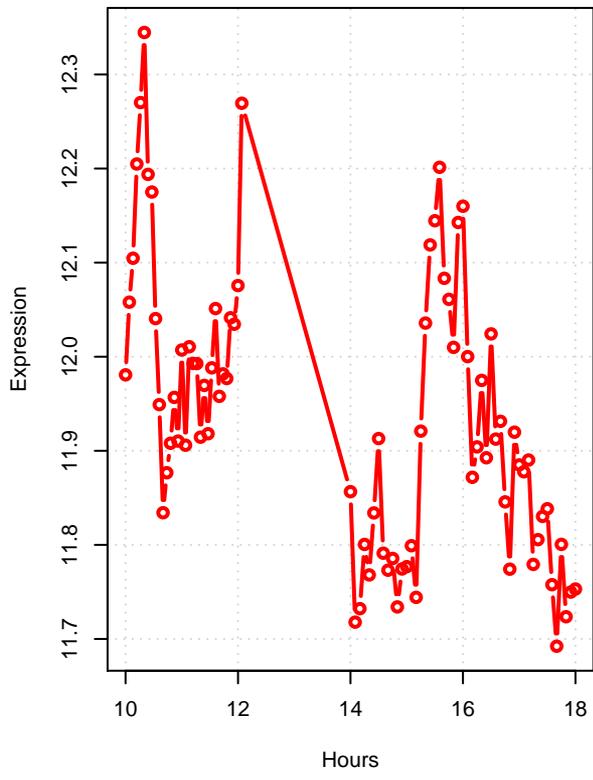
## phospholipid biosynthesis II (Kennedy pathway)

# phospholipid biosynthesis II (Kennedy pathway)

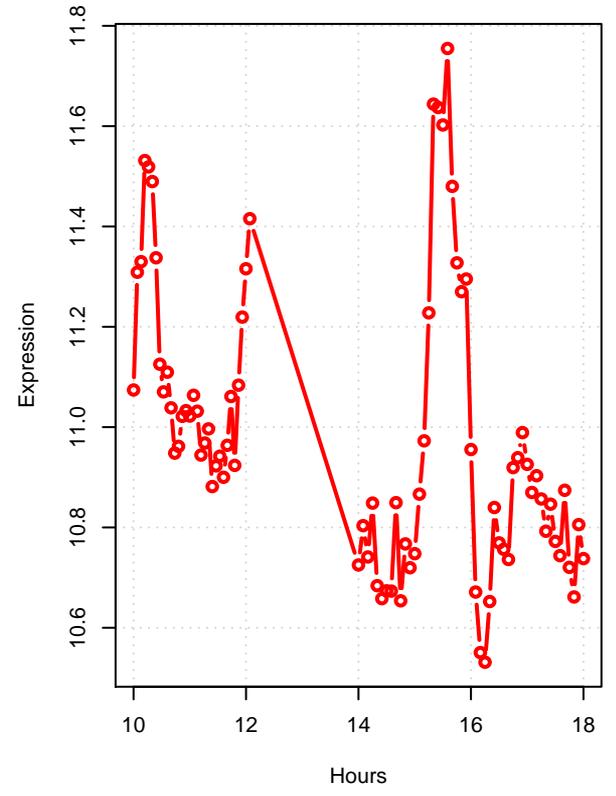
eki1 YDR147W  
Ethanolamine kinase



ect1 YGR007W  
Ethanolamine-phosphate cytidylyltransferase



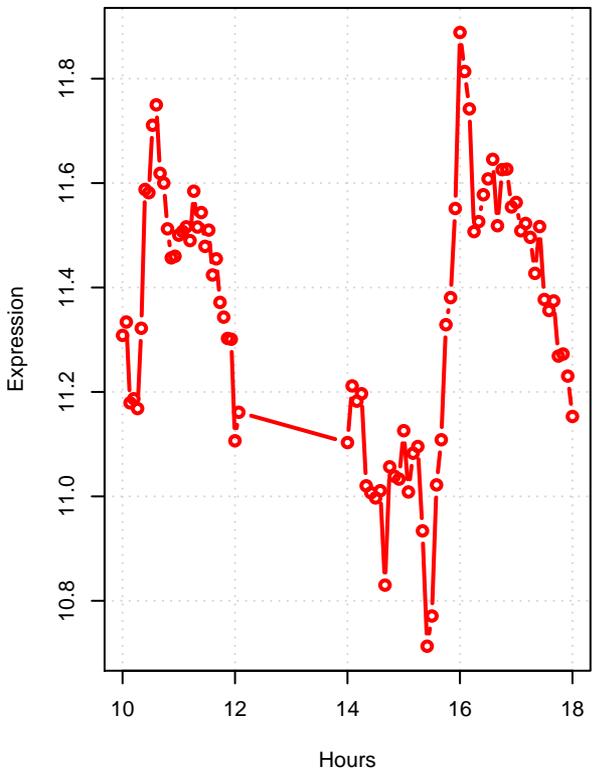
ept1 YHR123W  
sn-1,2-diacylglycerol ethanolamine- and cholinephosphotranferase



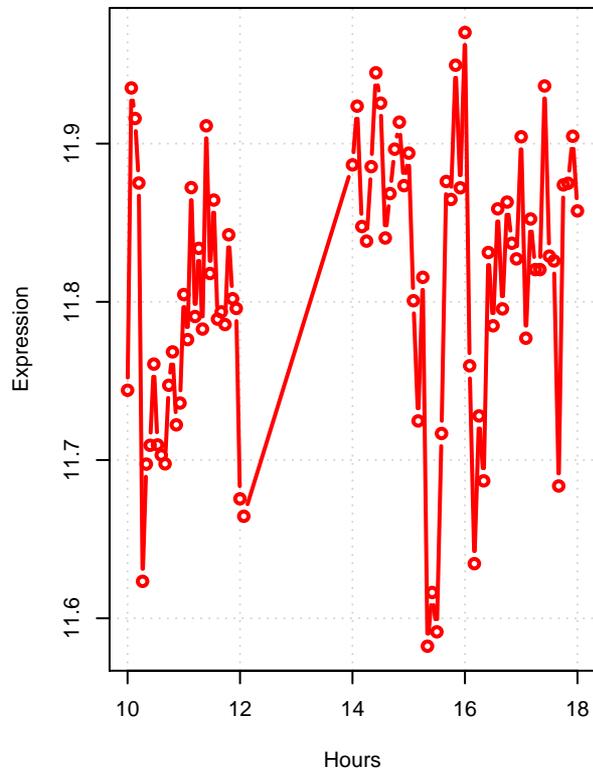
## phospholipid biosynthesis (Kennedy pathway)

# phospholipid biosynthesis (Kennedy pathway)

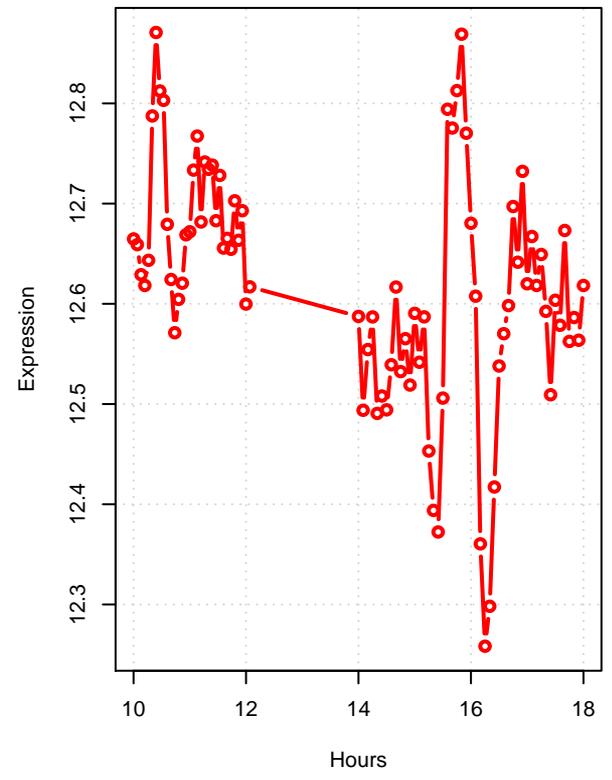
cki1 YLR133W  
Choline kinase



pct1 YGR202C  
Cholinephosphate cytidylyltransferase



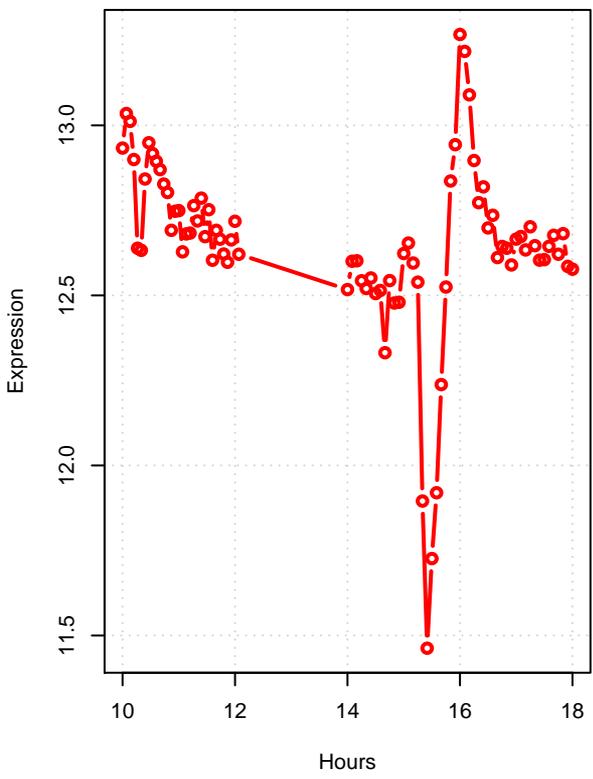
cpt1 YNL130C  
Cholinephosphotransferase



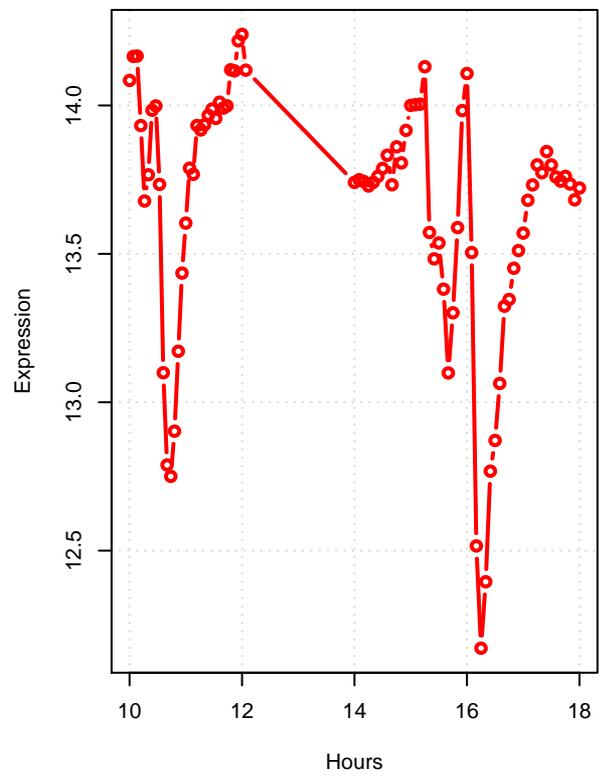
**proline utilization**

# proline utilization

put2 YHR037W  
Delta-1-pyrroline-5-carboxylate dehydrogenase



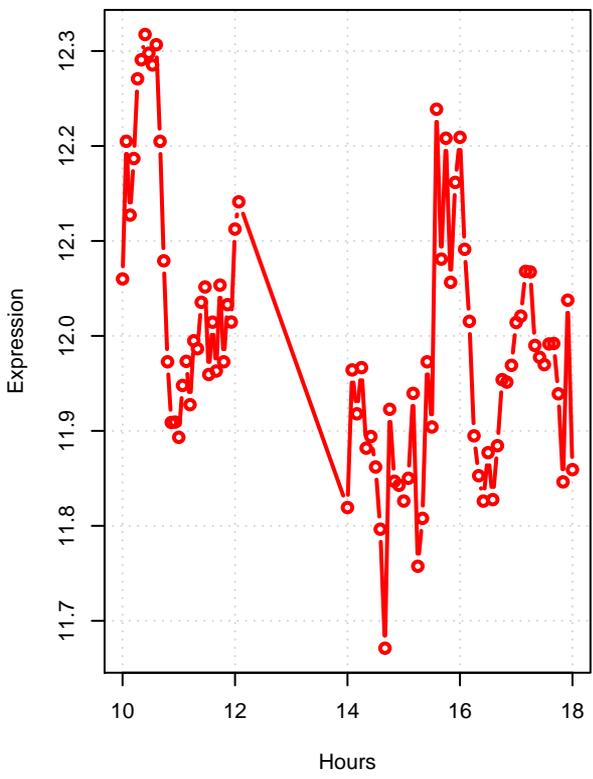
put1 YLR142W  
Proline oxidase



## **putrescine biosynthesis**

# putrescine biosynthesis

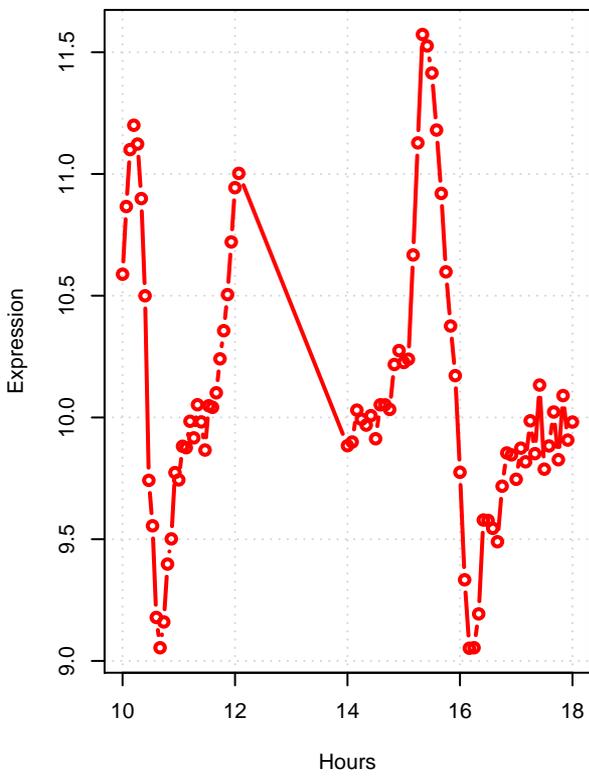
spe1 YKL184W  
Ornithine decarboxylase



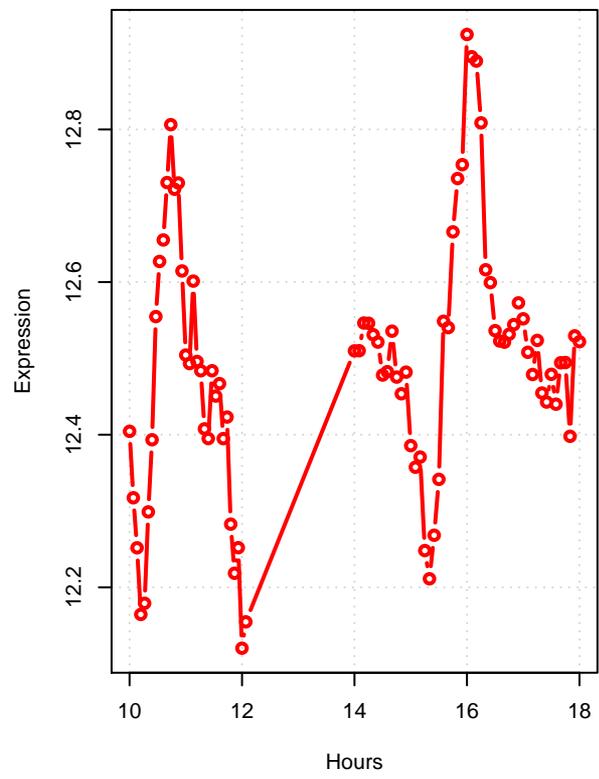
**pyridoxal 5'-phosphate salvage pathway**

# pyridoxal 5'-phosphate salvage pathway

bud16 YEL029C  
Putative pyridoxal kinase



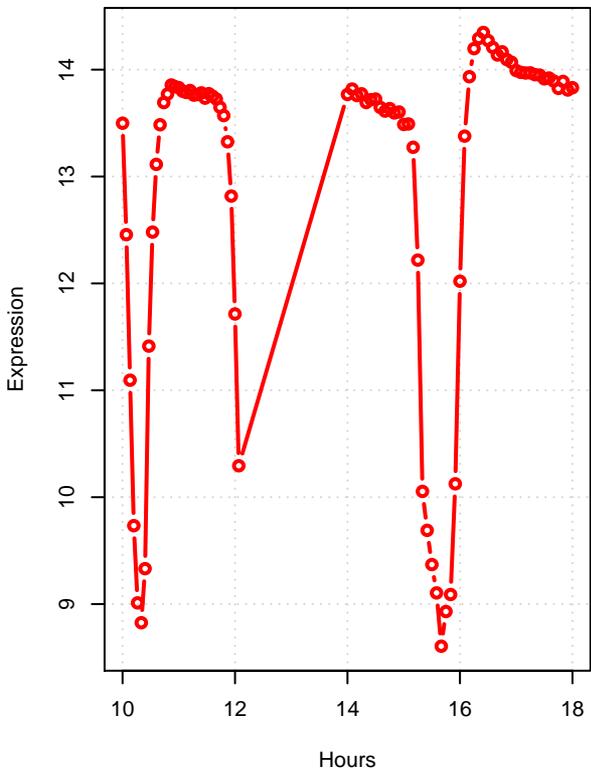
pox3 YBR035C  
Pyridoxine (pyridoxamine) phosphate oxidase



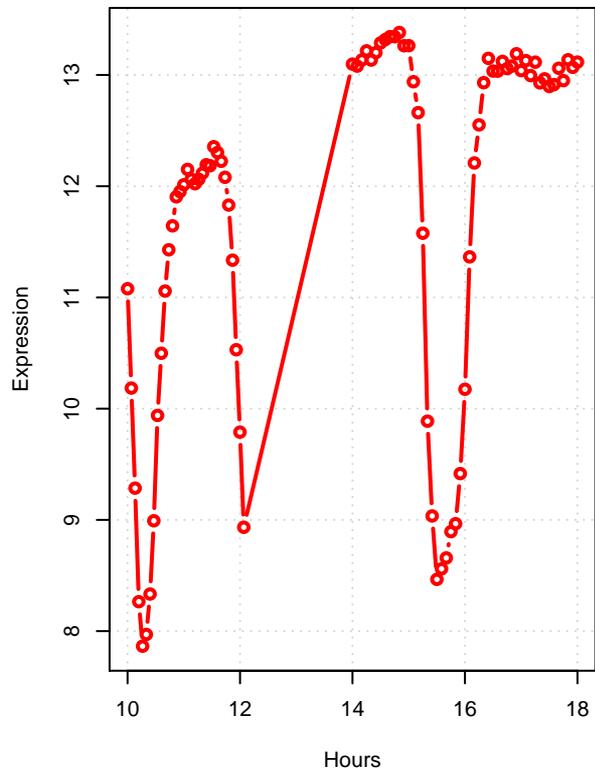
**removal of superoxide radicals**

# removal of superoxide radicals

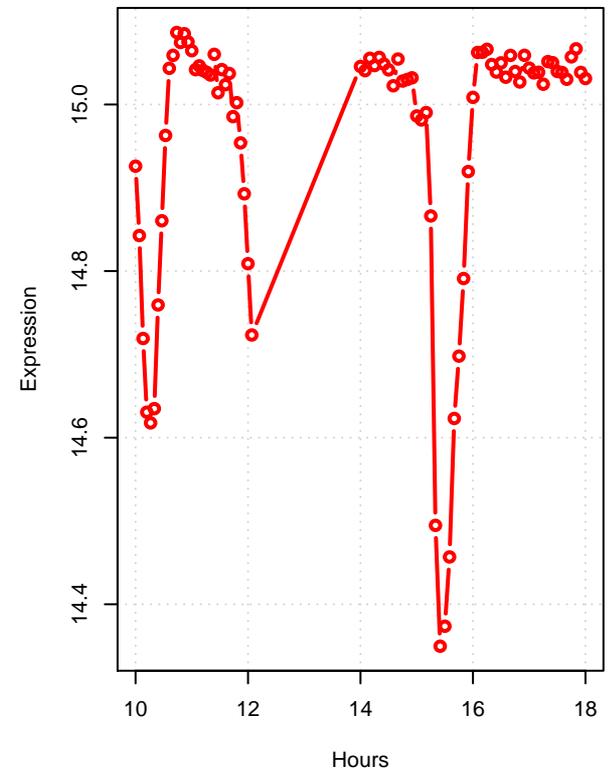
*cta1* YDR256C  
Catalase A



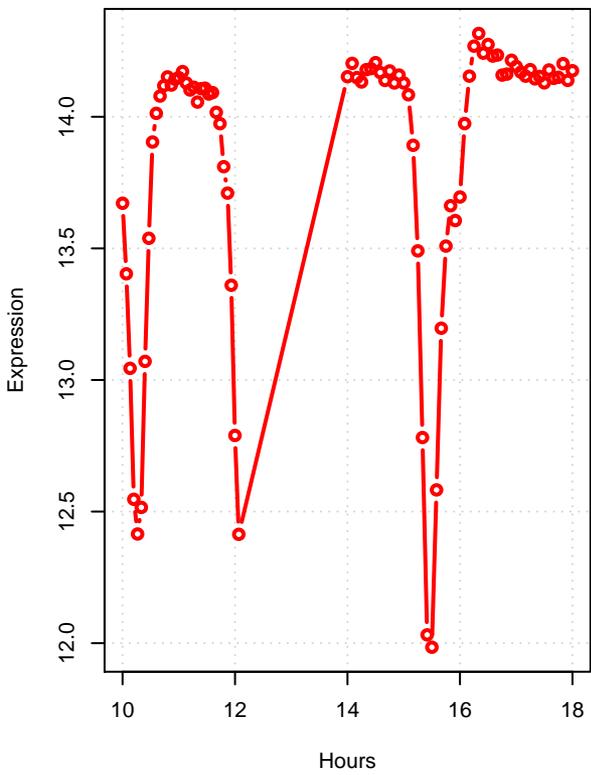
*ctt1* YGR088W  
Cytosolic catalase T



*sod1* YJR104C  
Cytosolic copper-zinc superoxide dismutase

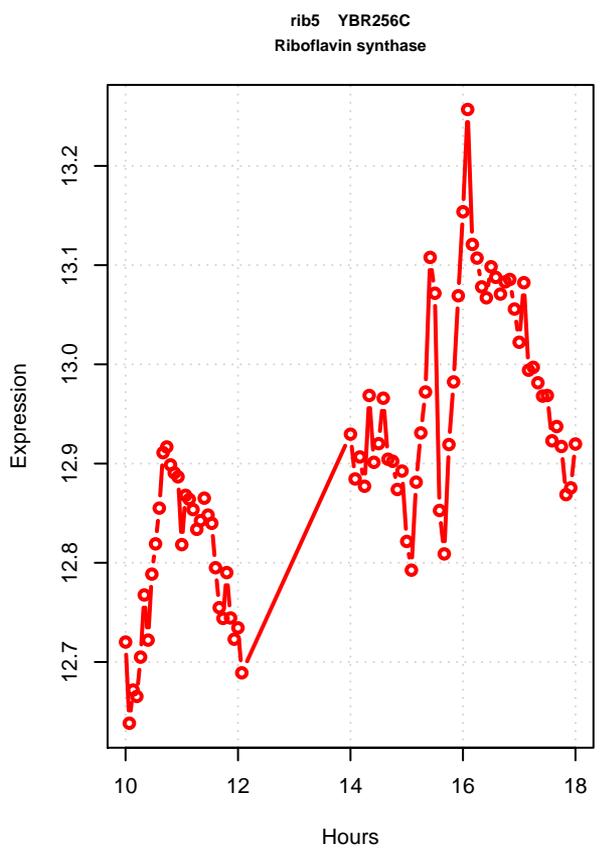
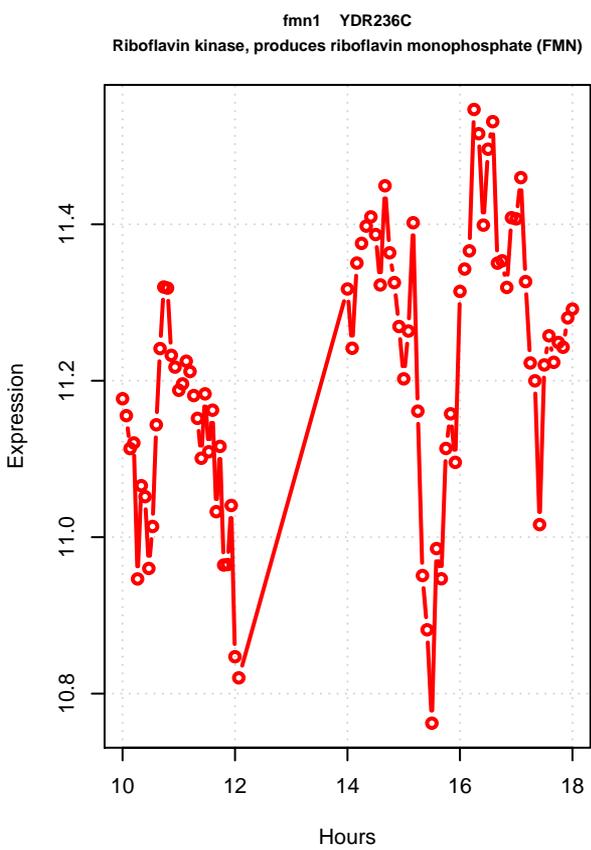
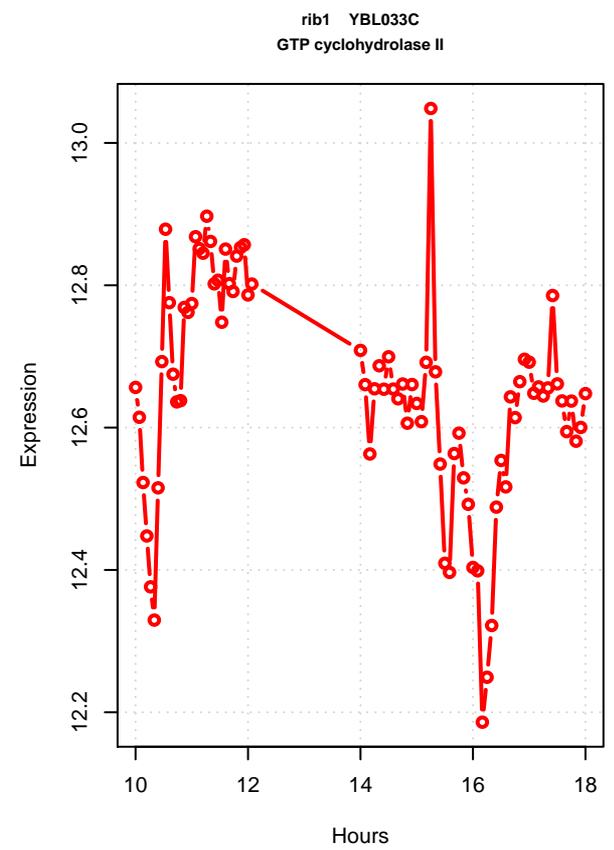
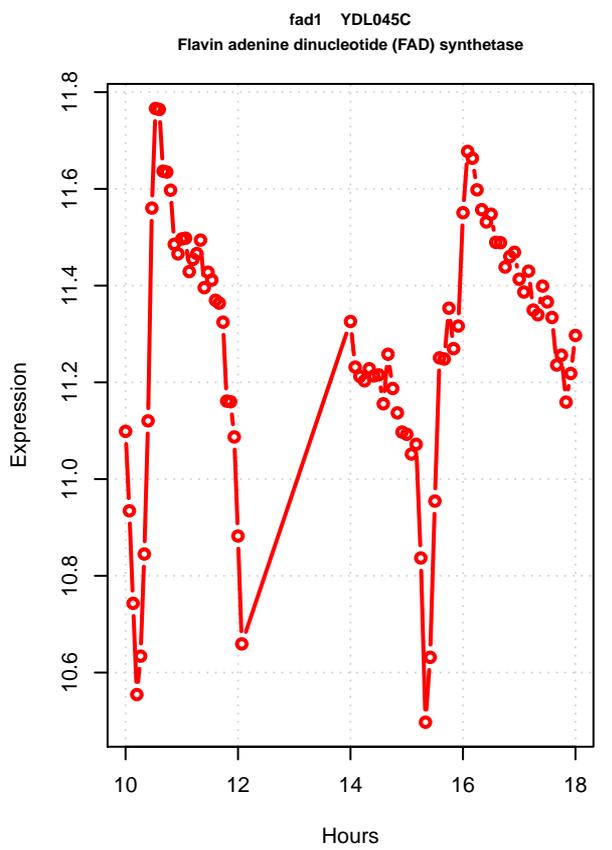
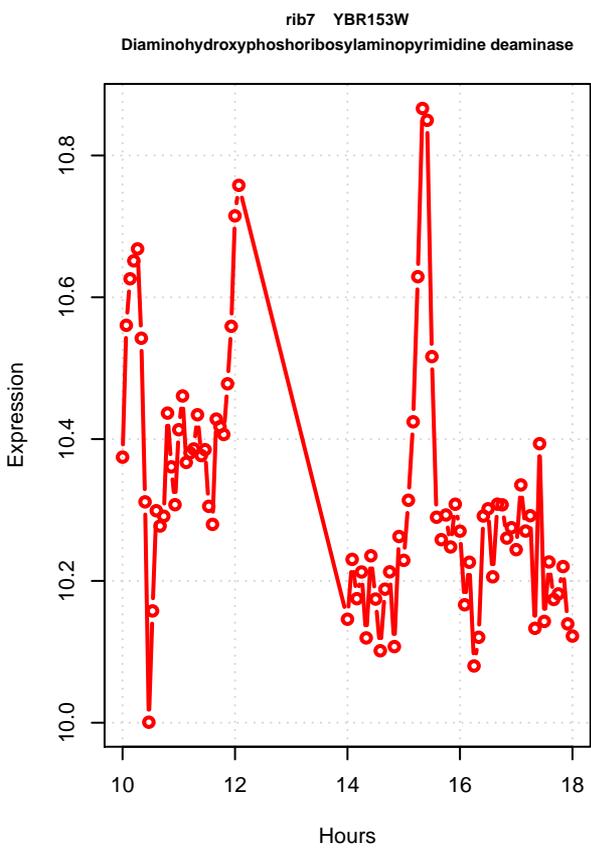
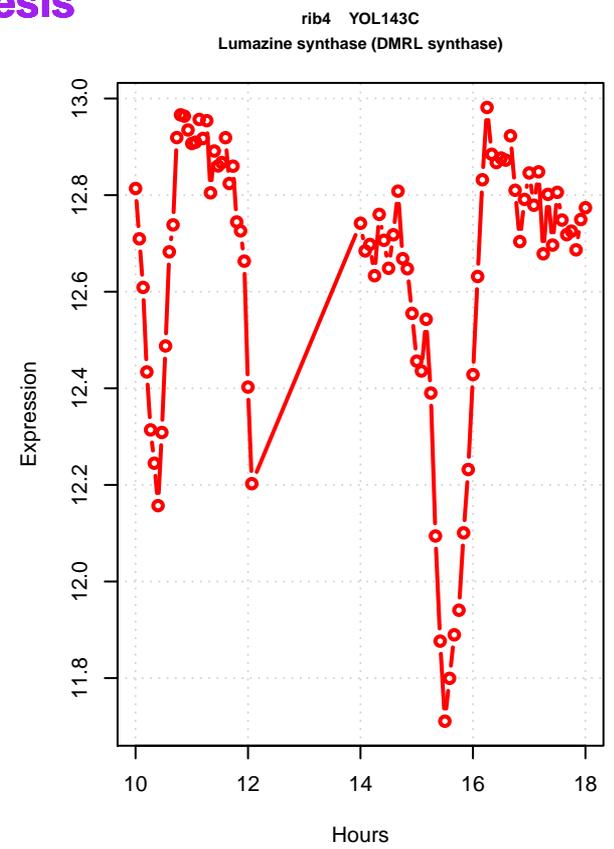
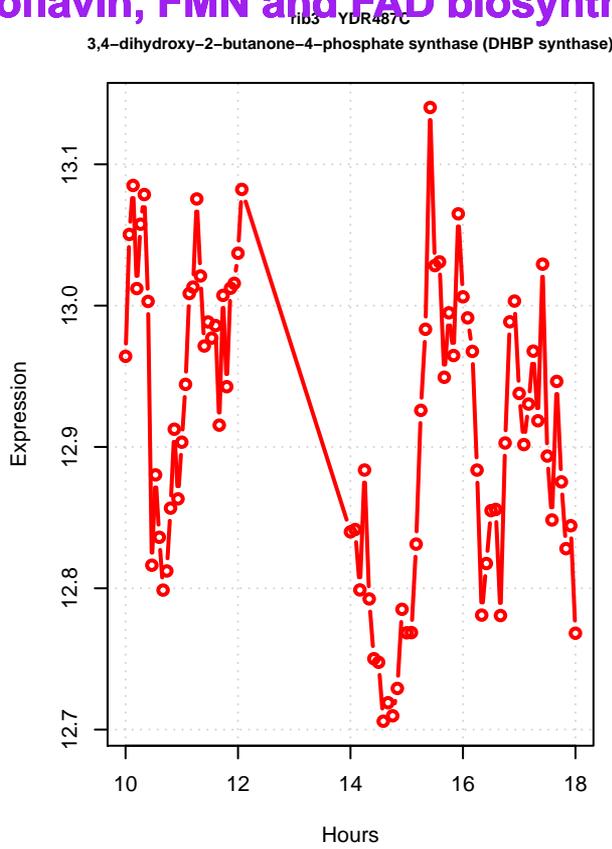
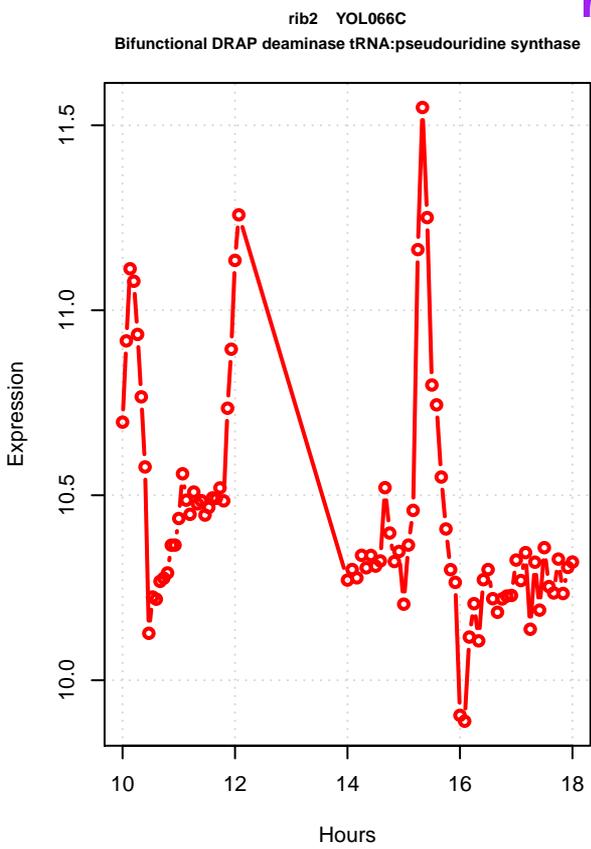


*sod2* YHR008C  
Mitochondrial manganese superoxide dismutase



## **riboflavin, FMN and FAD biosynthesis**

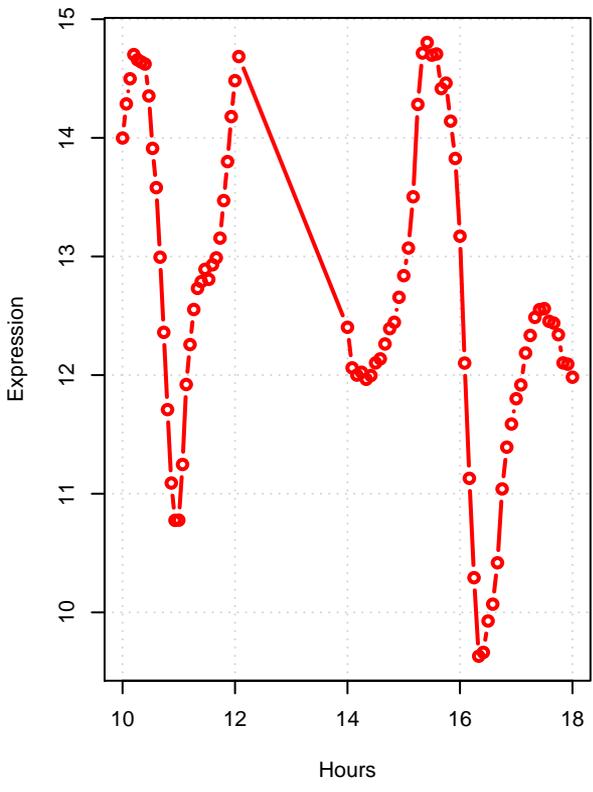
# riboflavin, FMN and FAD biosynthesis



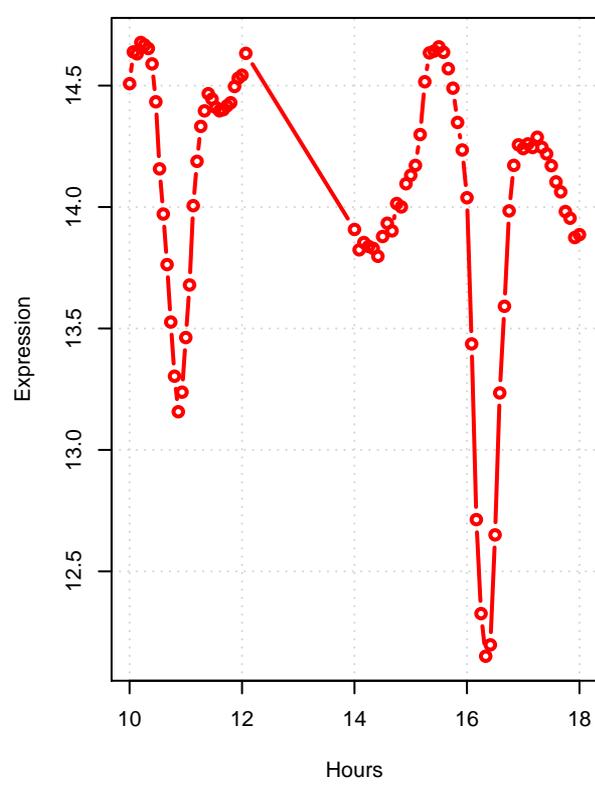
## **S-adenosylmethionine biosynthesis**

# S-adenosylmethionine biosynthesis

sam1 YLR180W  
S-adenosylmethionine synthetase

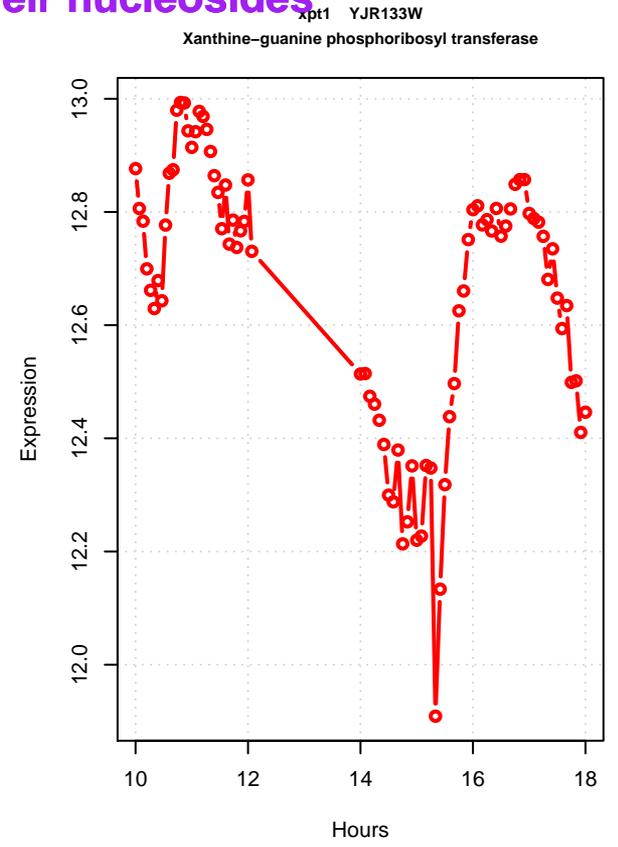
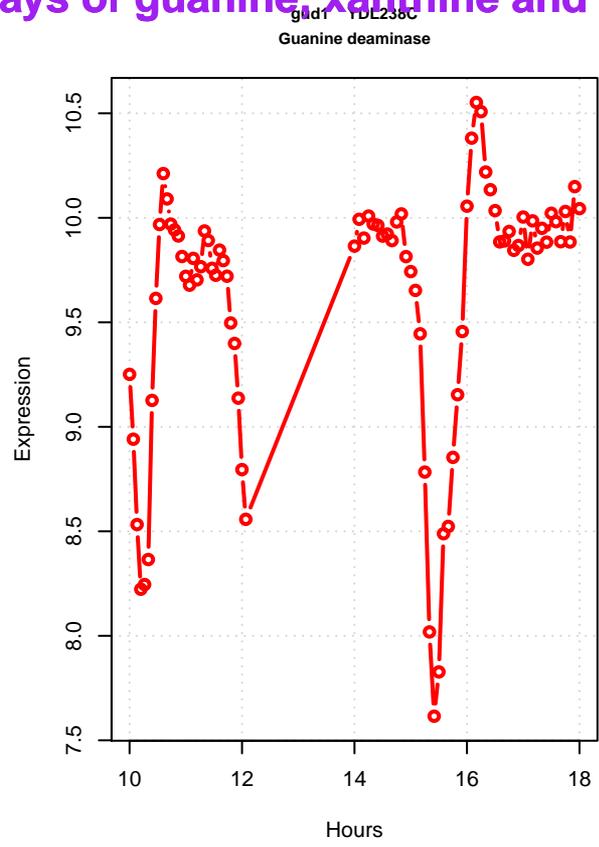
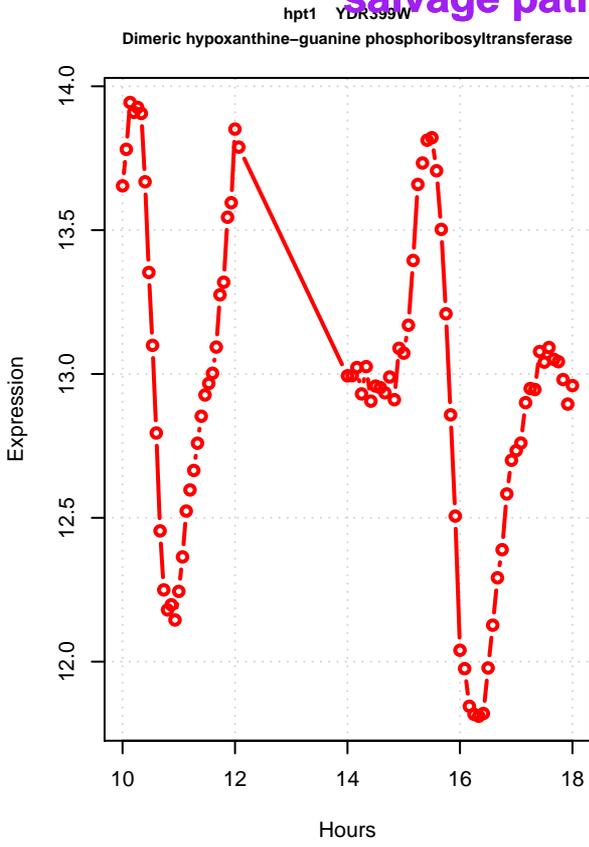


sam2 YDR502C  
S-adenosylmethionine synthetase



**salvage pathways of guanine, xanthine and their nucleosides**

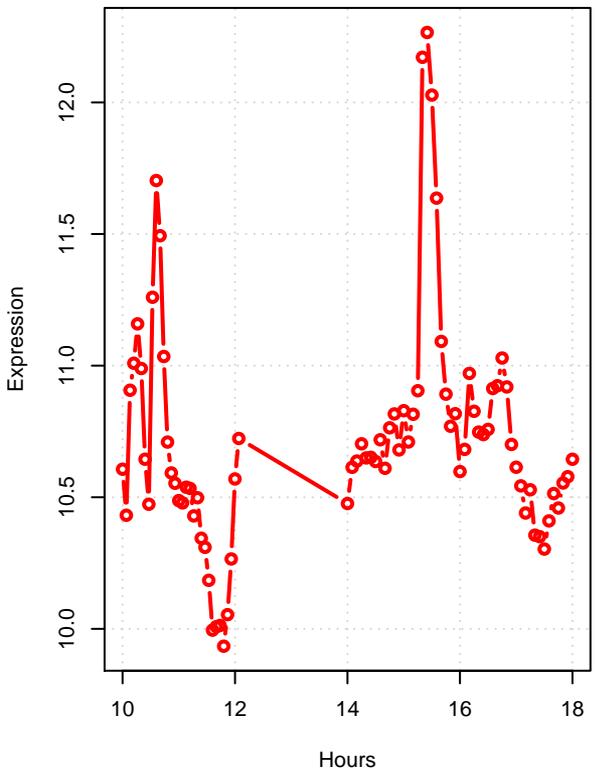
# salvage pathways of guanine, xanthine and their nucleosides



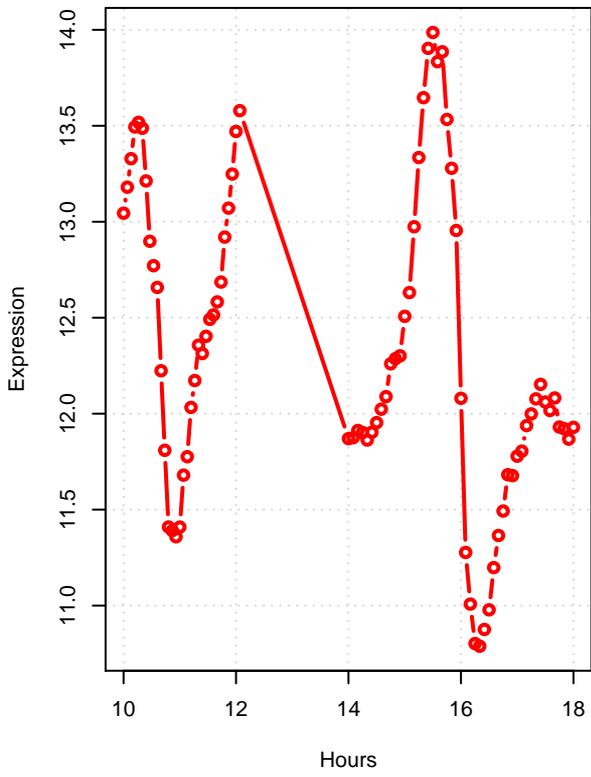
**serine biosynthesis from 3-phosphoglycerate**

# serine biosynthesis from 3-phosphoglycerate

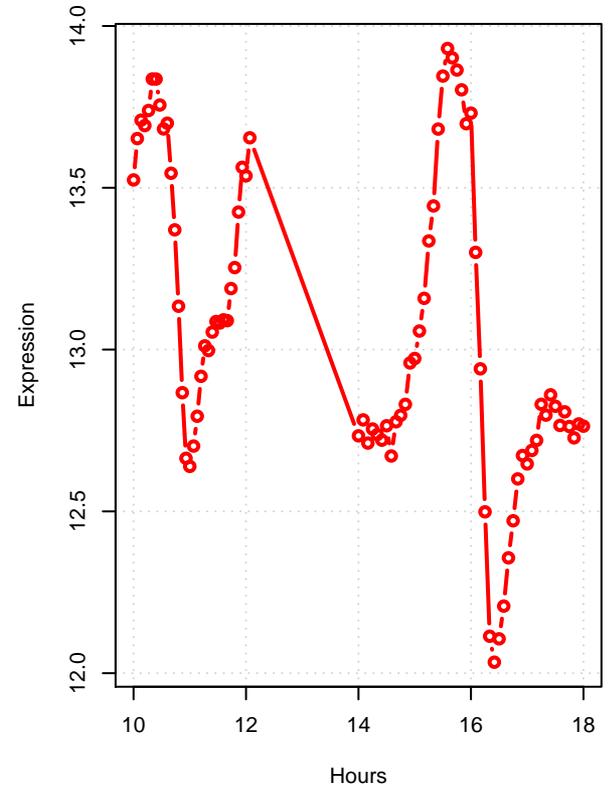
ser3 YER081W  
3-phosphoglycerate dehydrogenase and alpha-ketoglutarate reductase



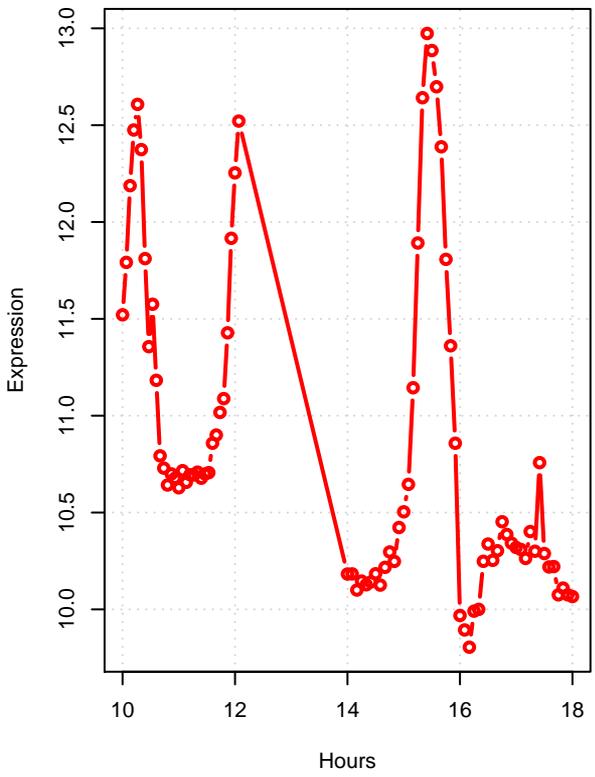
ser33 YIL074C  
3-phosphoglycerate dehydrogenase and alpha-ketoglutarate reductase



ser1 YOR184W  
3-phosphoserine aminotransferase



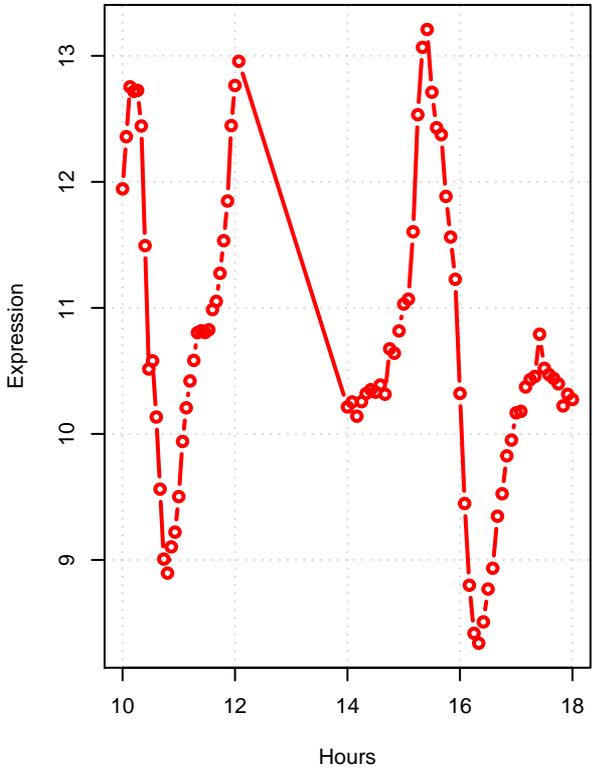
ser2 YGR208W  
Phosphoserine phosphatase of the phosphoglycerate pathway



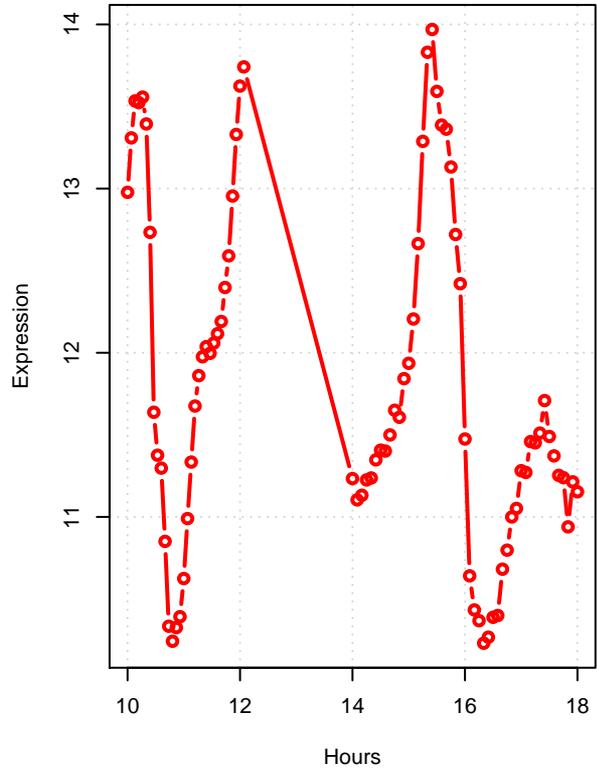
## **siroheme biosynthesis**

# siroheme biosynthesis

met8 YBR213W  
Bifunctional dehydrogenase and ferrochelatase



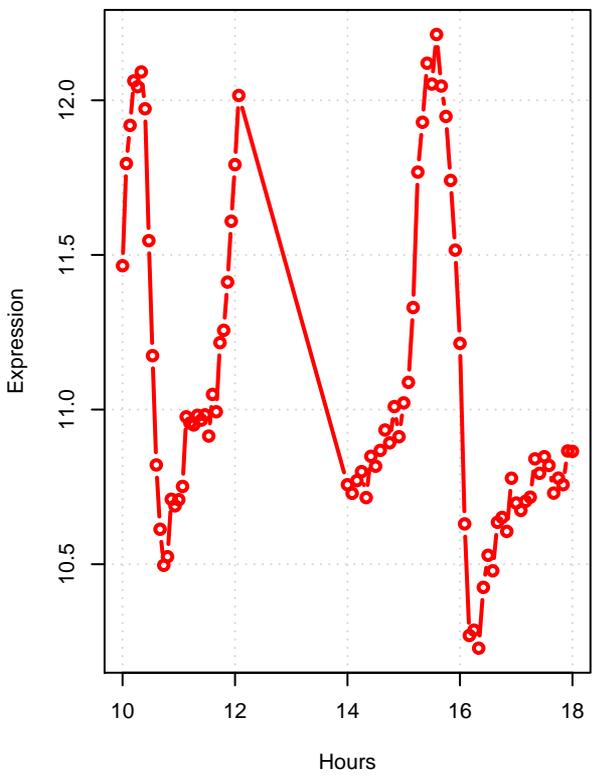
met1 YKR063W  
S-adenosyl-L-methionine uroporphyrin III transmethylase



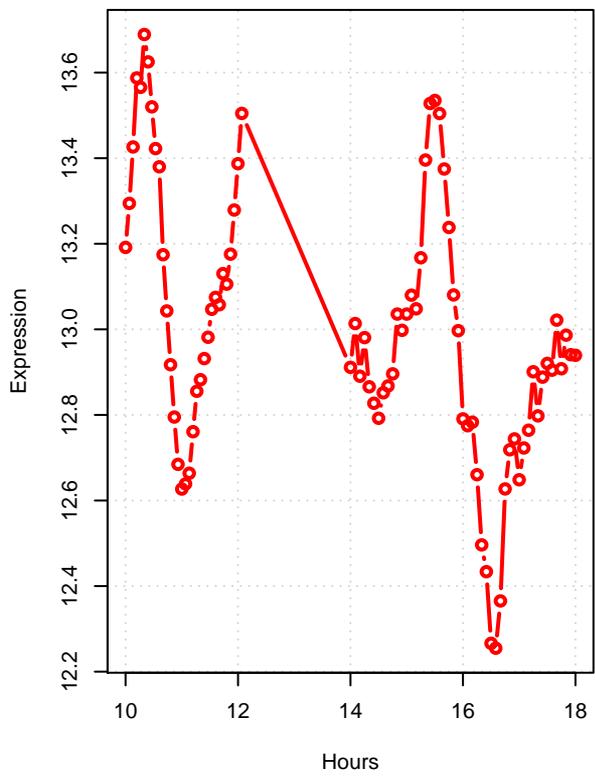
## **spermidine and methylthioadenosine biosynthesis**

# spermidine and methylthioadenosine biosynthesis

spe2 YOL052C  
S-adenosylmethionine decarboxylase



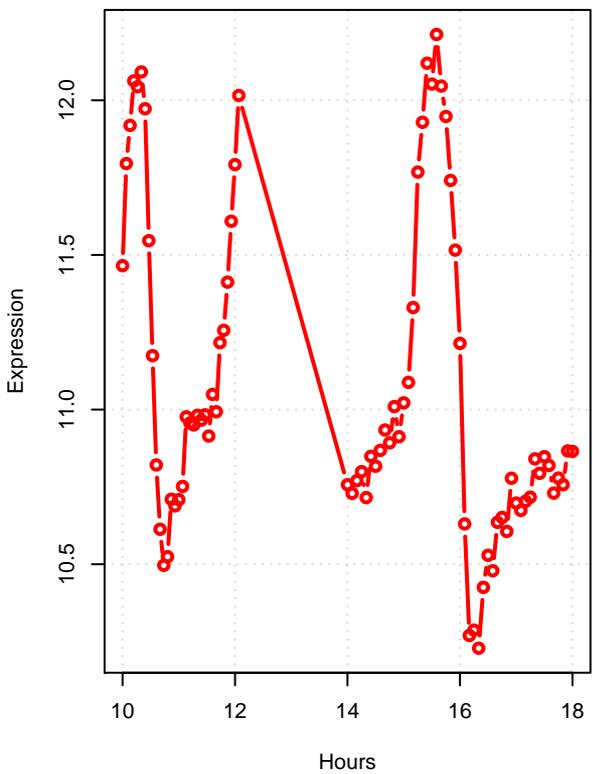
spe3 YPR069C  
Spermidine synthase



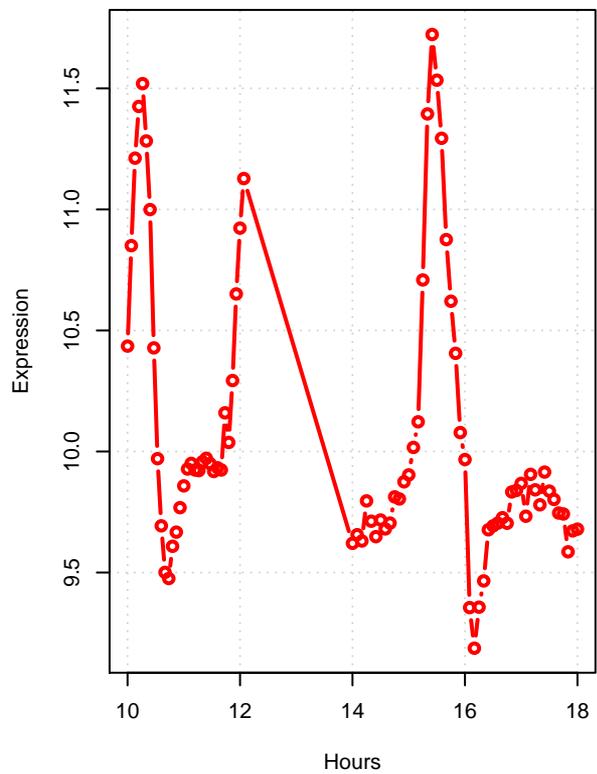
## **spermine and methylthioadenosine biosynthesis**

# spermine and methylthioadenosine biosynthesis

spe2 YOL052C  
S-adenosylmethionine decarboxylase



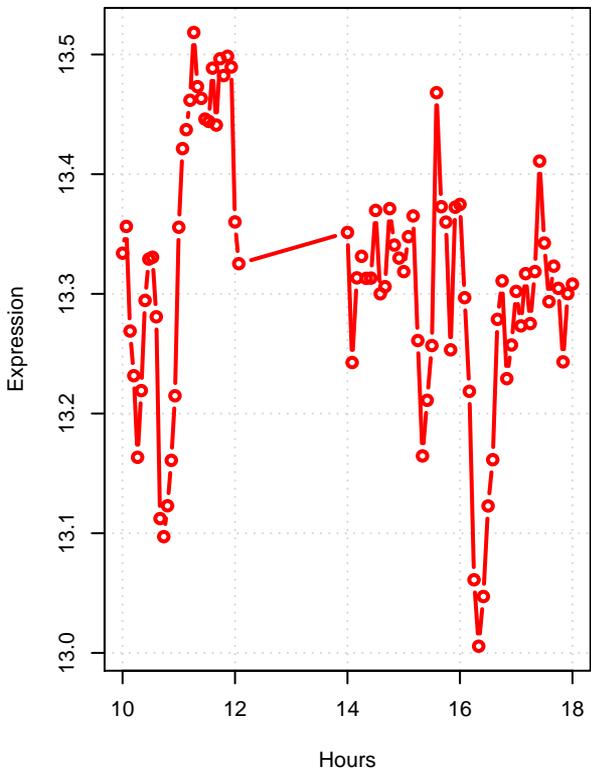
spe4 YLR146C  
Spermine synthase



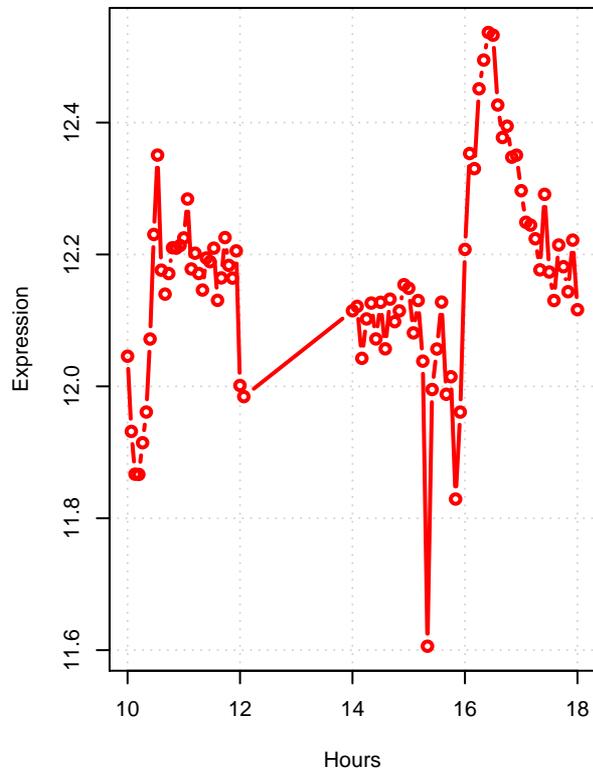
## **sphingolipid metabolism**

# sphingolipid metabolism

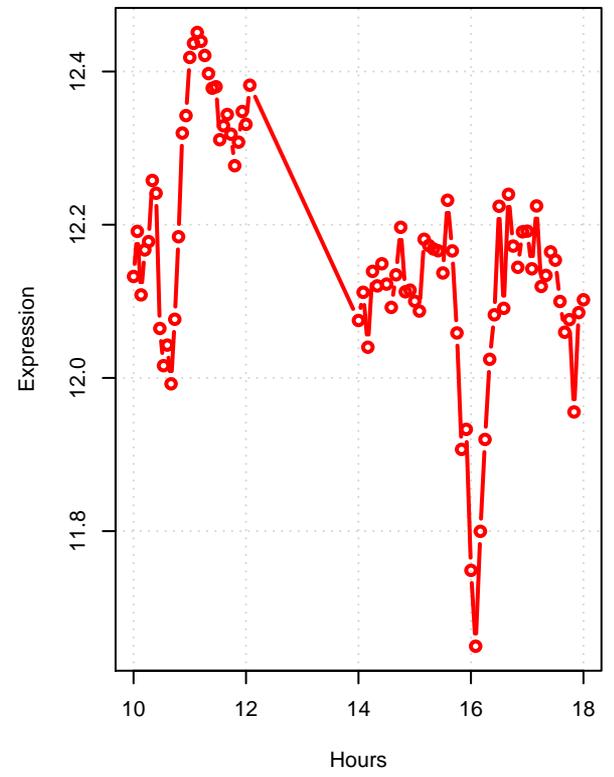
scs7 YMR272C  
Sphingolipid alpha-hydroxylase



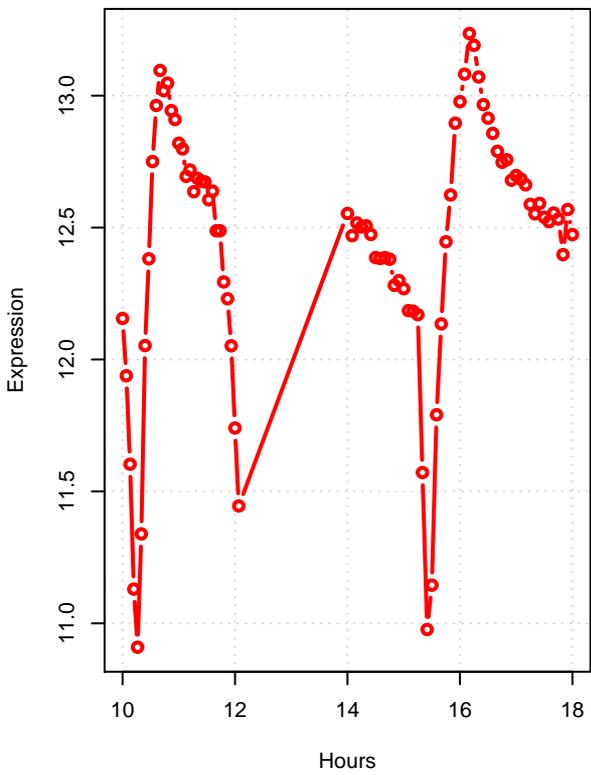
ipt1 YDR072C  
Inositolphosphotransferase



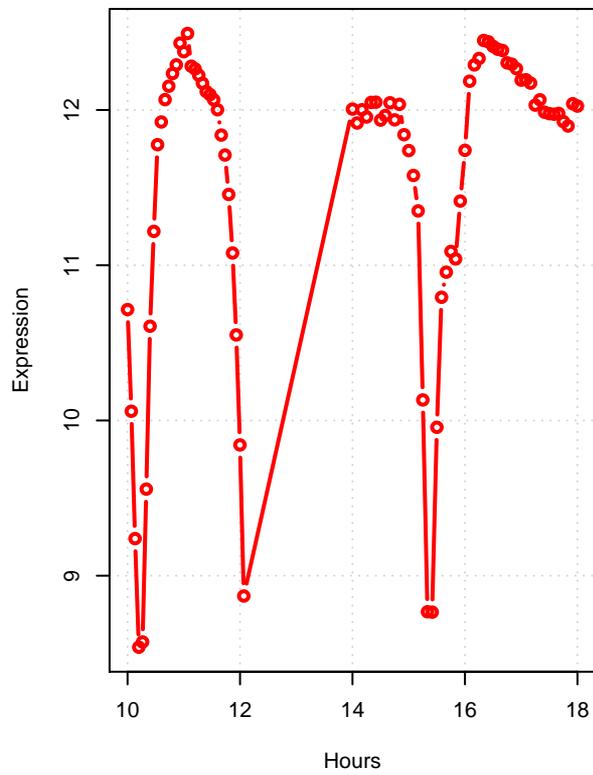
tsc10 YBR265W  
3-ketosphinganine reductase



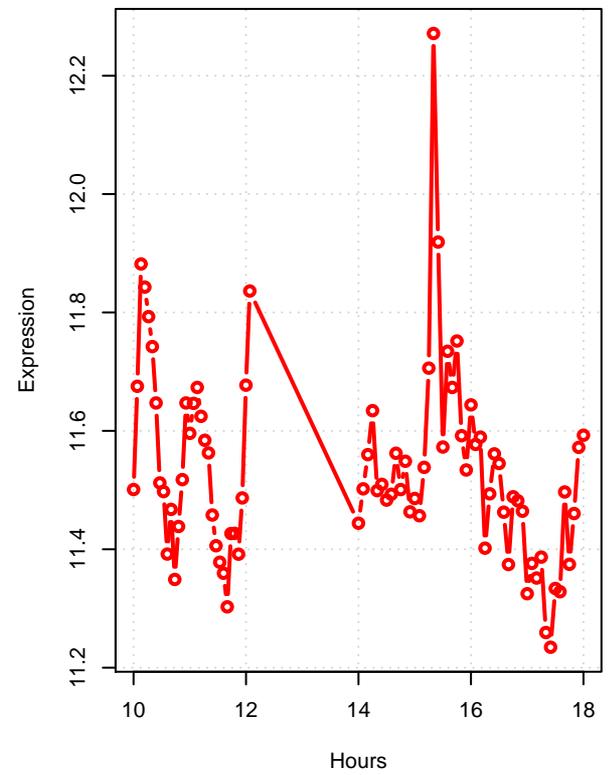
ycd1 YPL087W  
Alkaline dihydroceramidase, involved in sphingolipid metabolism



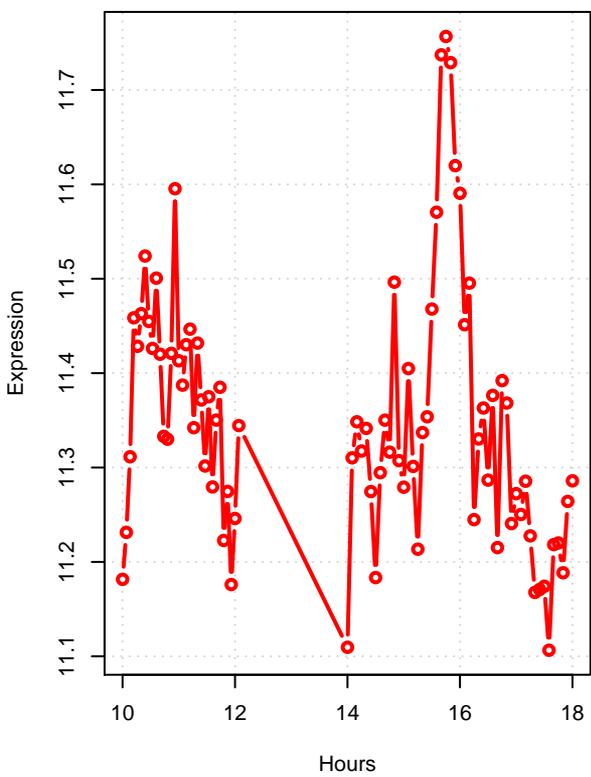
ypc1 YBR183W  
Alkaline ceramidase



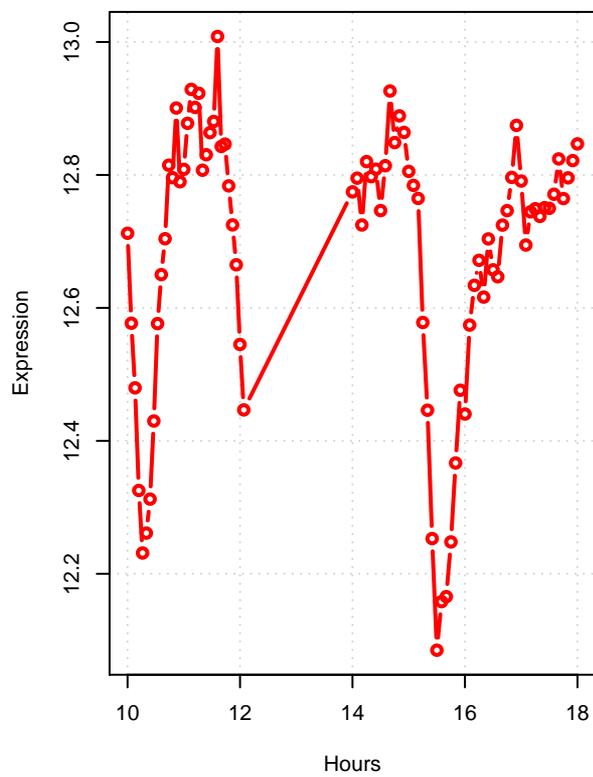
lac1 YKL008C  
Ceramide synthase component



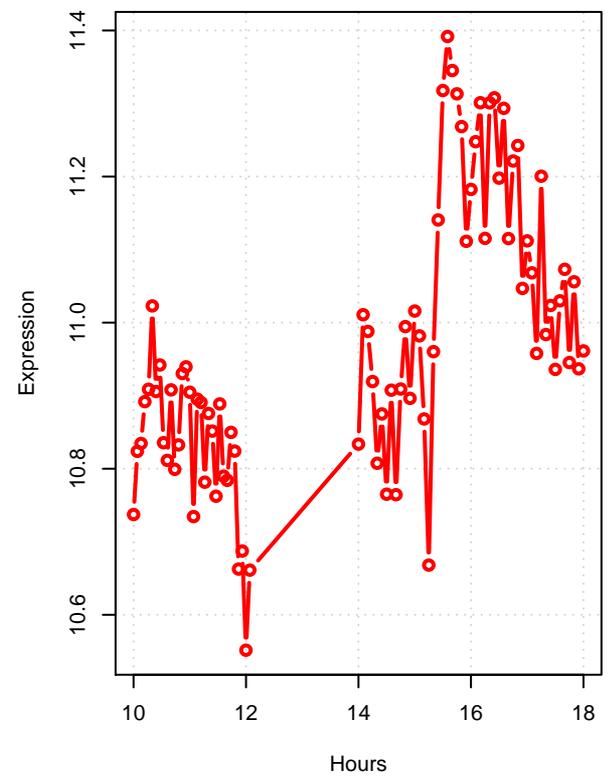
lag1 YHL003C  
Ceramide synthase component



lip1 YMR298W  
Ceramide synthase subunit

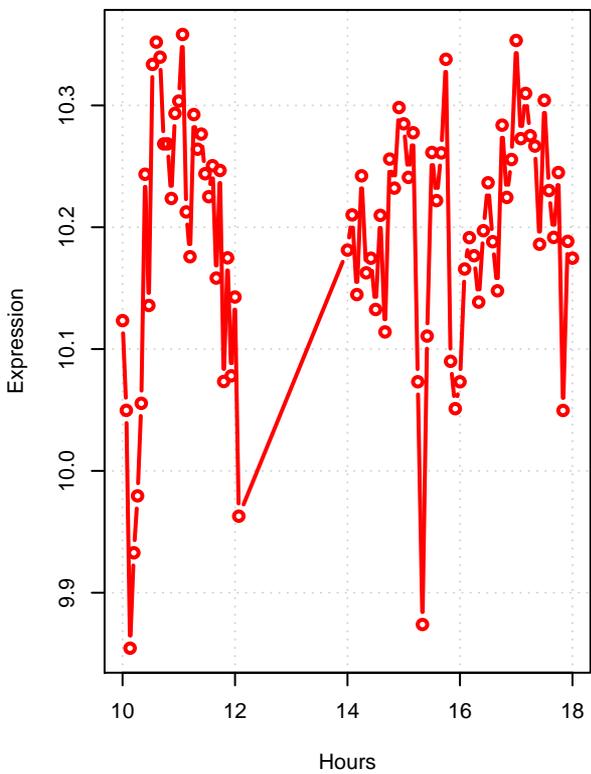


lcb4 YOR171C  
Sphingoid long-chain base kinase

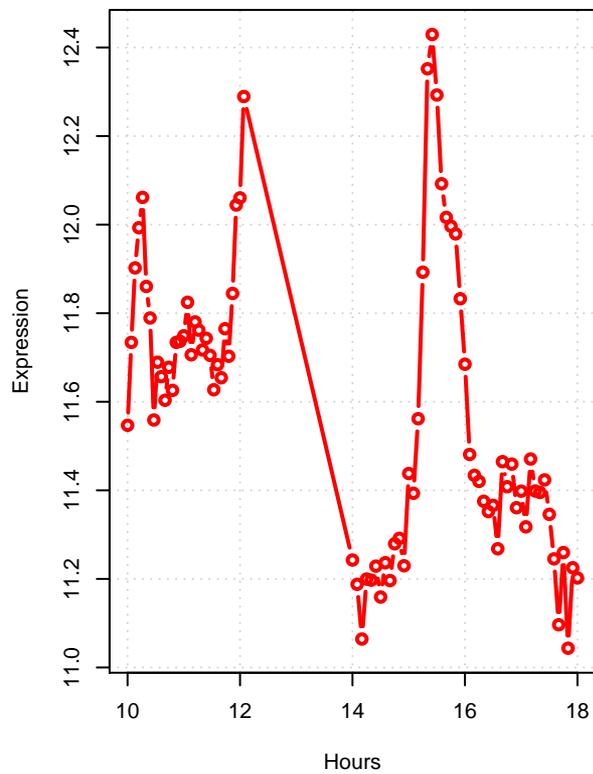


# sphingolipid metabolism

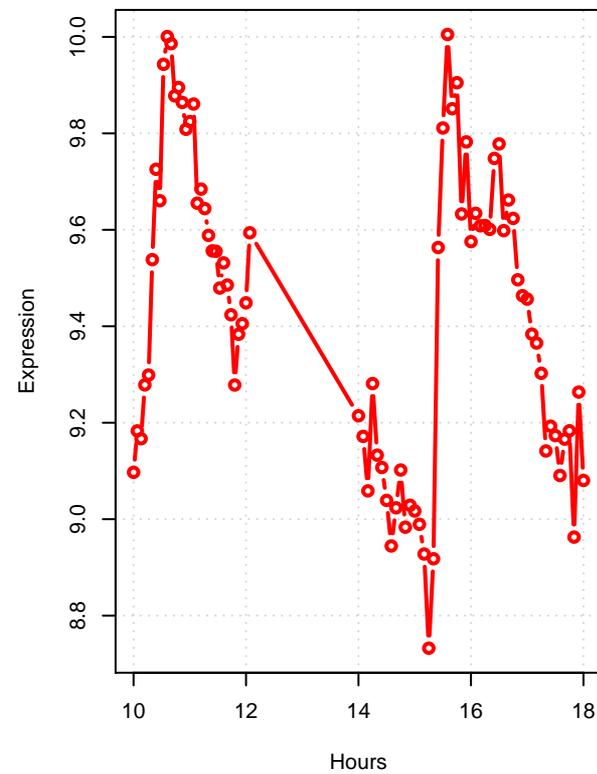
**lcb5 YLR260W**  
Minor sphingoid long-chain base kinase



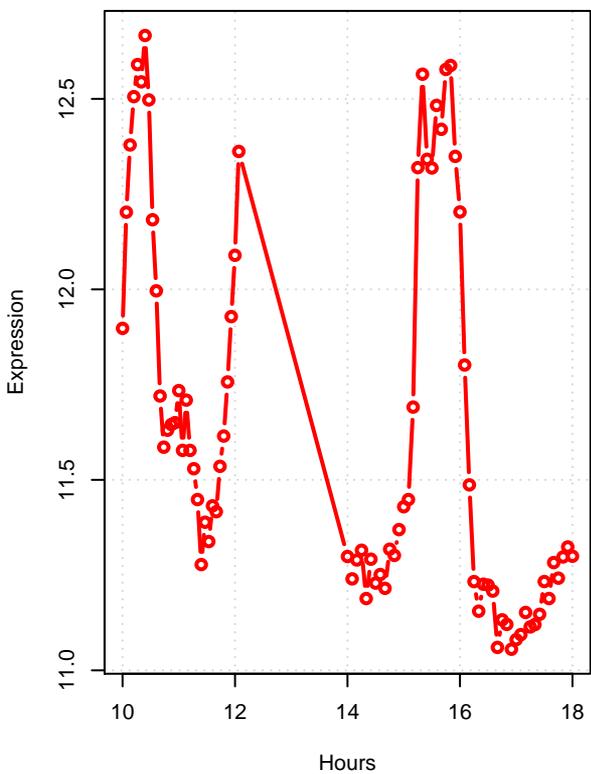
**lcb3 YJL134W**  
Long-chain base-1-phosphate phosphatase



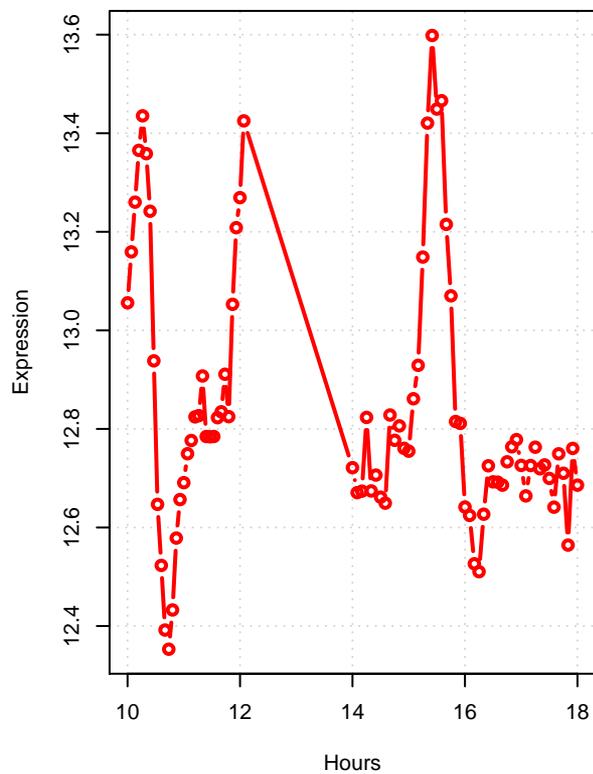
**ysr3 YKR053C**  
Dihydrosphingosine 1-phosphate phosphatase



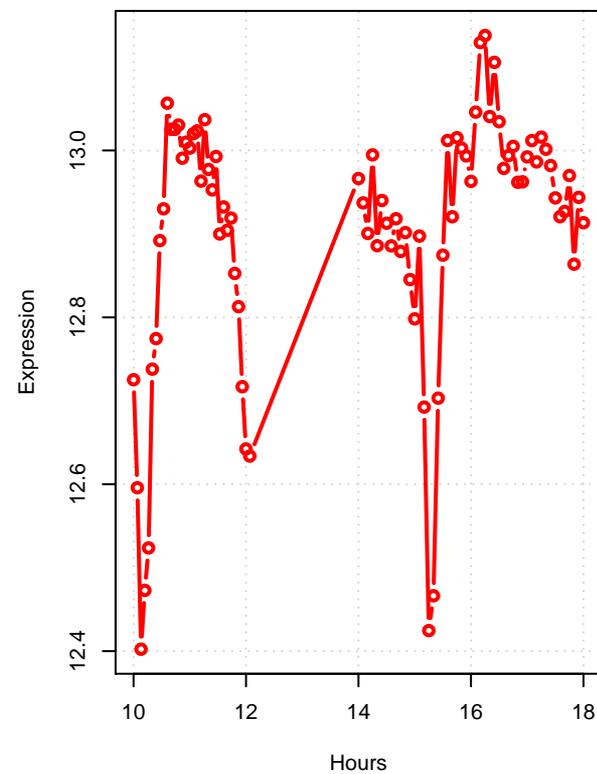
**sur2 YDR297W**  
Sphinganine C4-hydroxylase



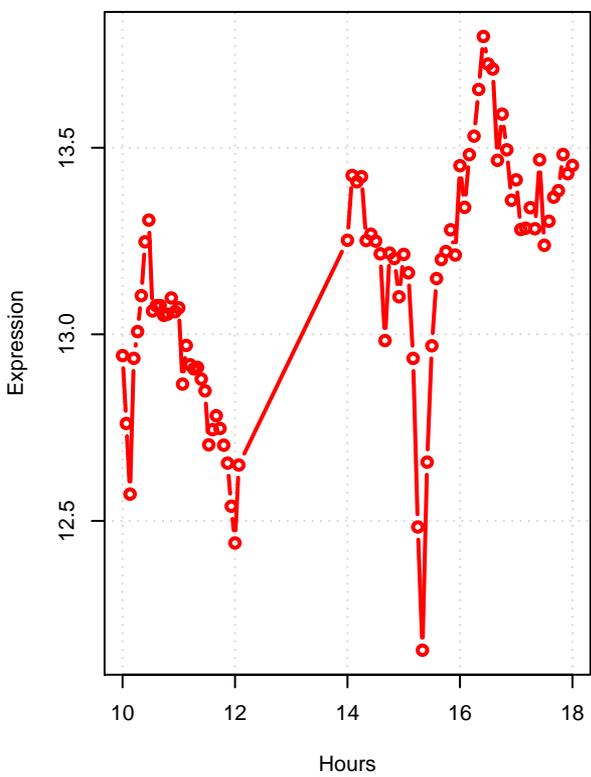
**aur1 YKL004W**  
Phosphatidylinositol:ceramide phosphoinositol transferase



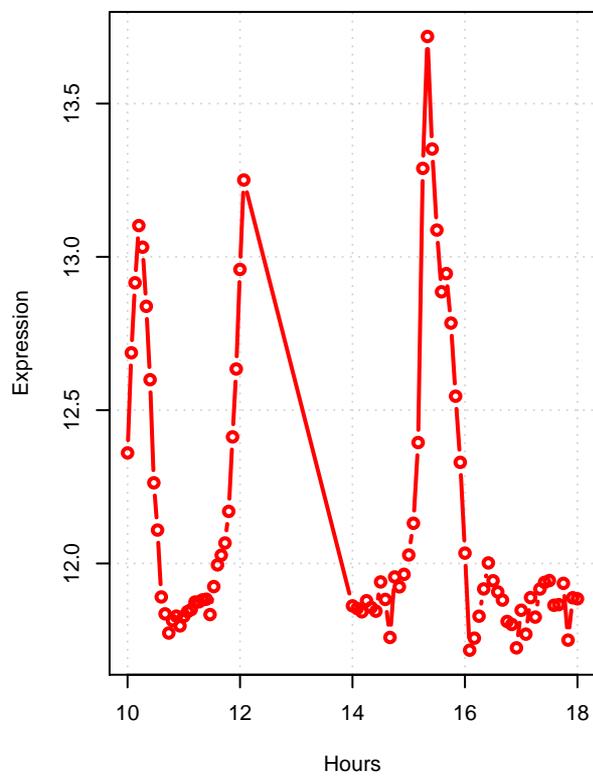
**csg2 YBR036C**  
Endoplasmic reticulum membrane protein



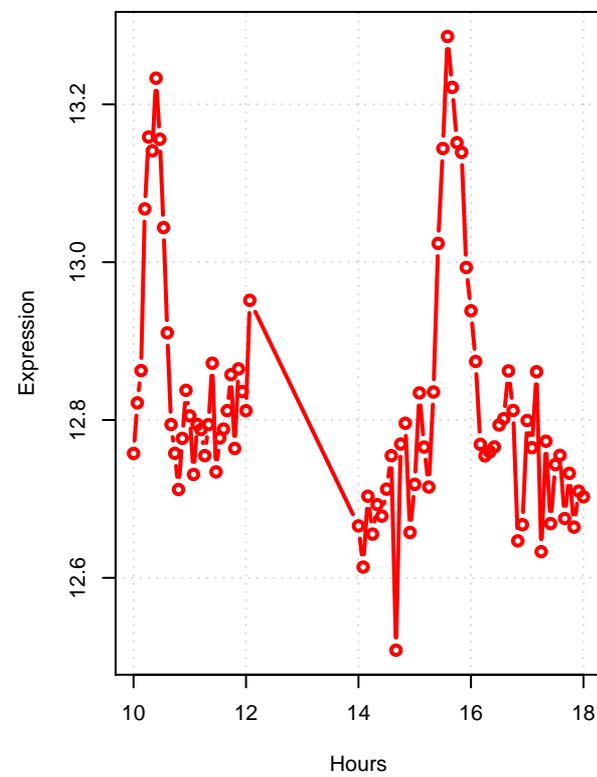
**sur1 YPL057C**  
Mannosylinositol phosphorylceramide (MIPC) synthase catalytic subunit



**lcb1 YMR296C**  
Component of serine palmitoyltransferase

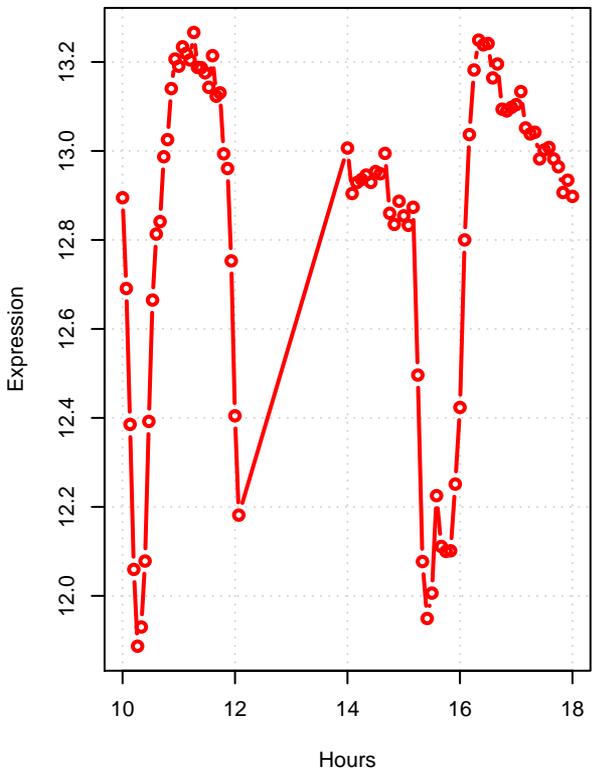


**lcb2 YDR062W**  
Component of serine palmitoyltransferase



# sphingolipid metabolism

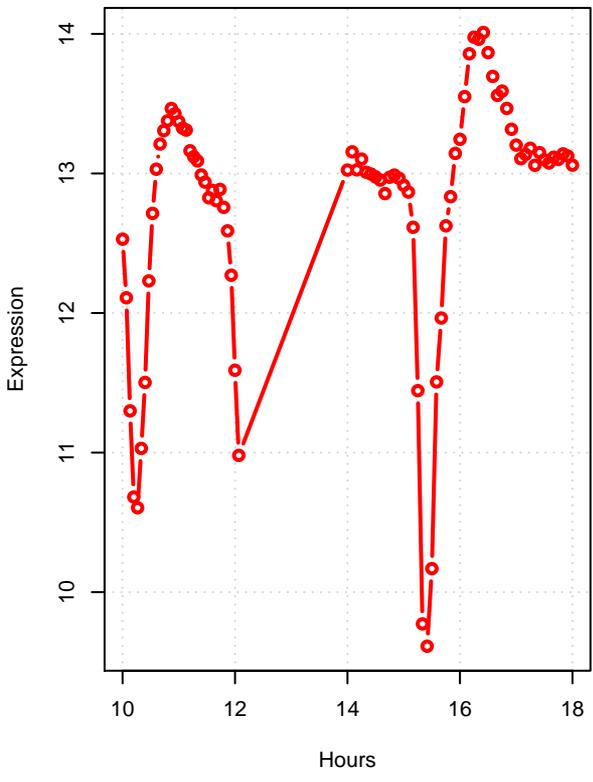
dp11 YDR294C  
Dihydrosphingosine phosphate lyase



## **sucrose degradation**

# sucrose degradation

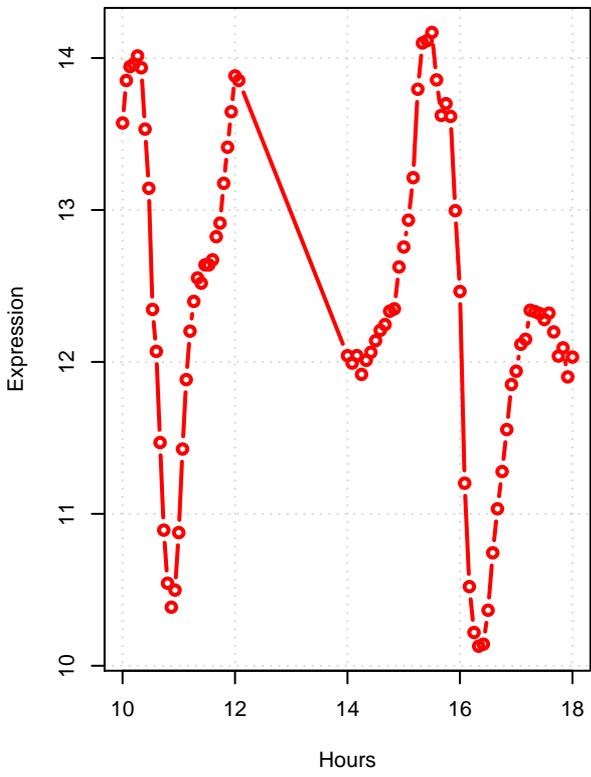
suc2 YIL162W  
Invertase



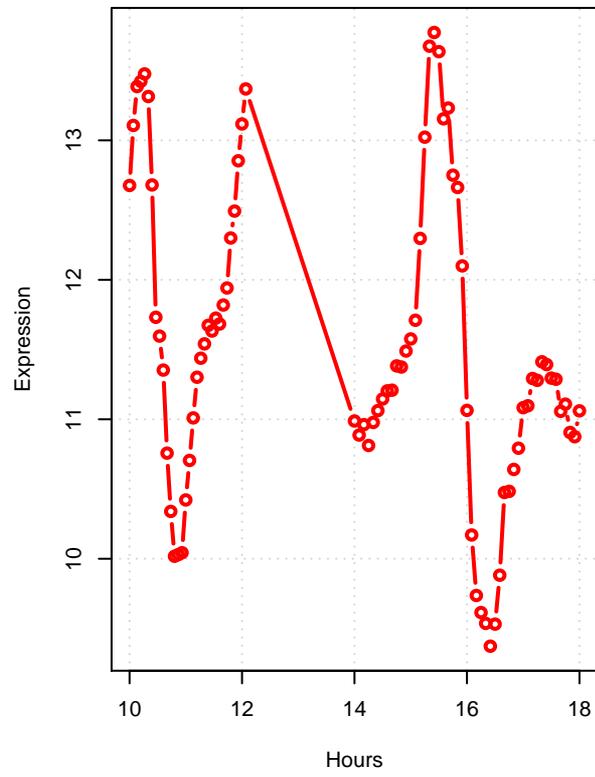
## sulfate assimilation pathway

# sulfate assimilation pathway

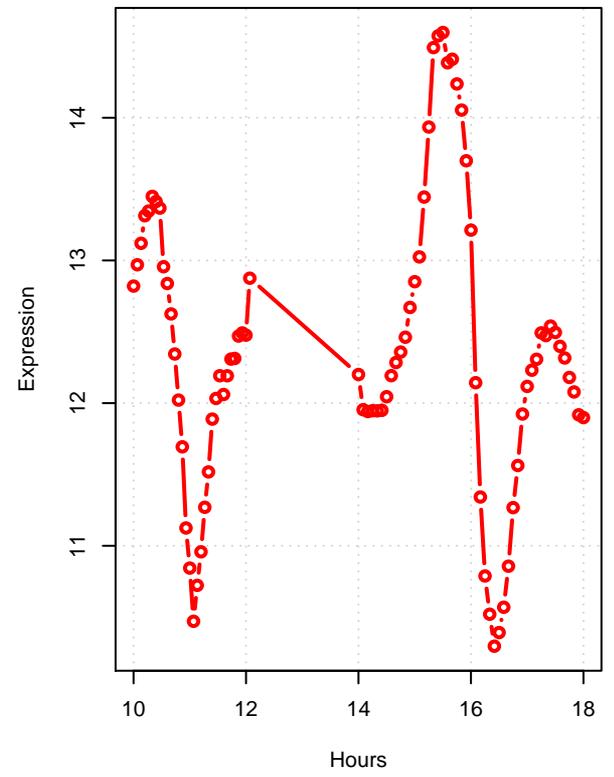
met14 YKL001C  
Adenylylsulfate kinase



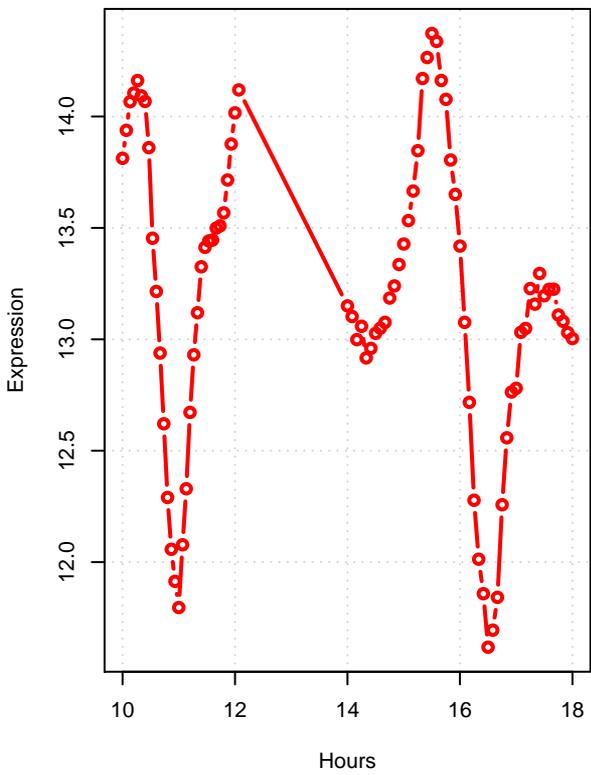
met16 YPR167C  
3'-phosphoadenylylsulfate reductase



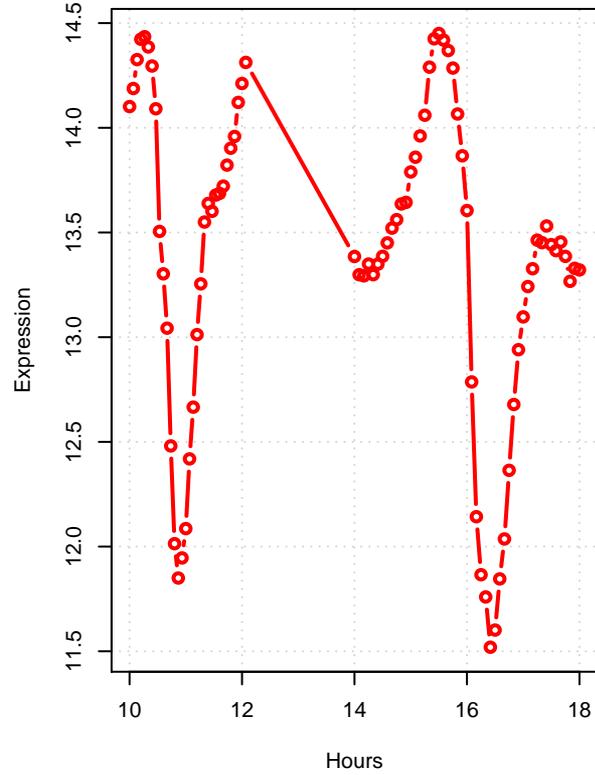
met3 YJR010W  
ATP sulfurylase



met10 YFR030W  
Subunit alpha of assimilatory sulfite reductase



met5 YJR137C  
Sulfite reductase beta subunit

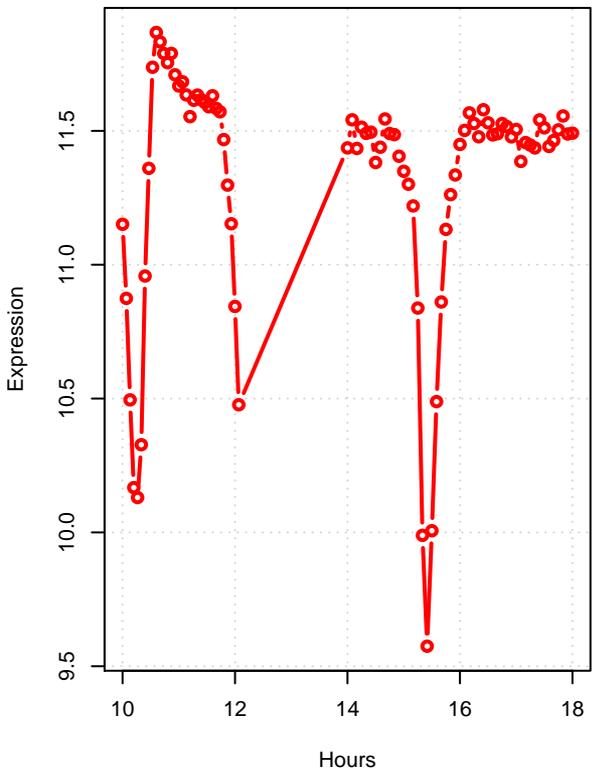


**superpathway of purine biosynthesis and salvage pathways**

# superpathway of purine biosynthesis and salvage pathways

isn1\_YOR155C

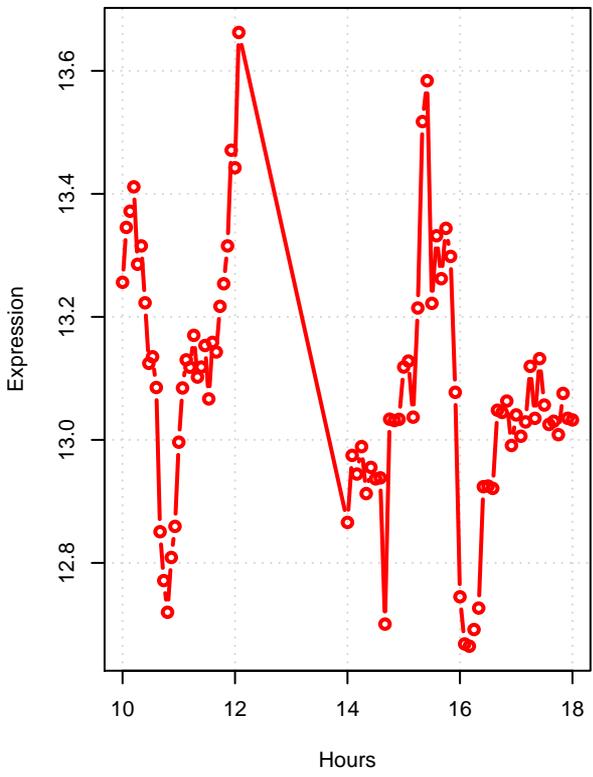
Inosine 5'-monophosphate (IMP)-specific 5'-nucleotidase



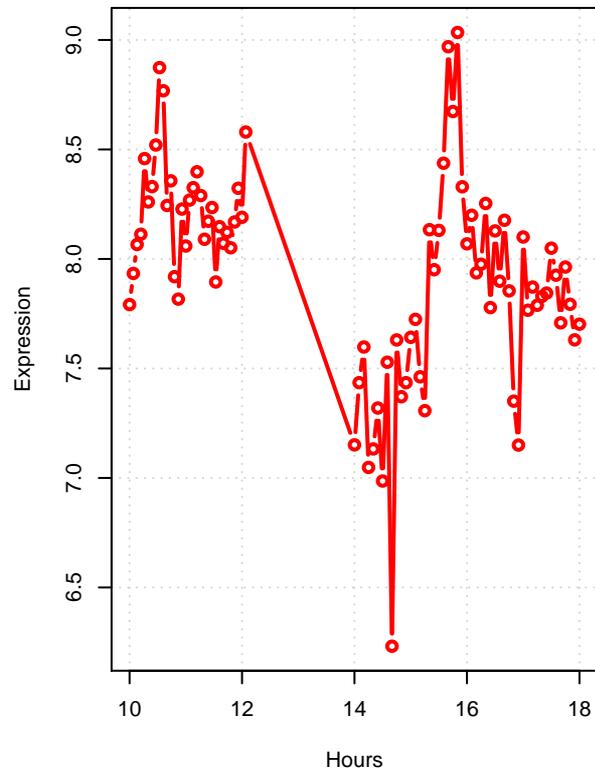
## **tetrapyrrole biosynthesis**

# tetrapyrrole biosynthesis

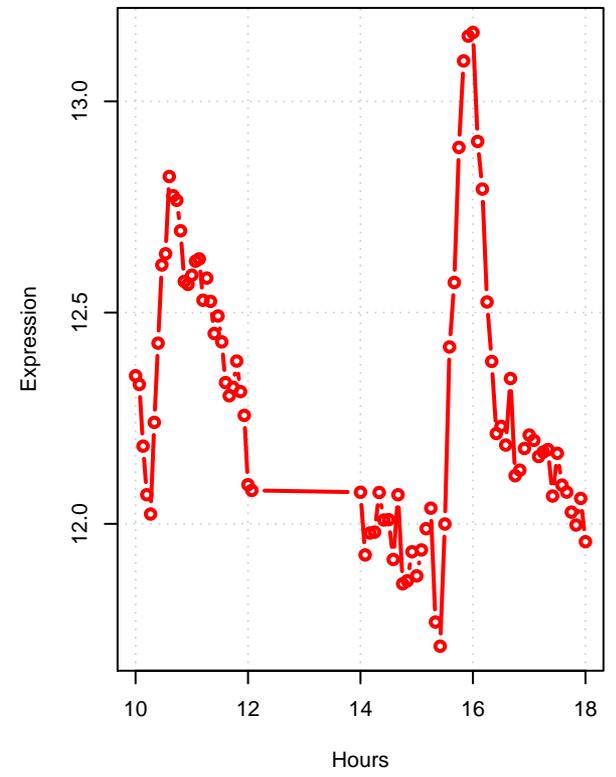
hem1 YDR232W  
5-aminolevulinic synthase



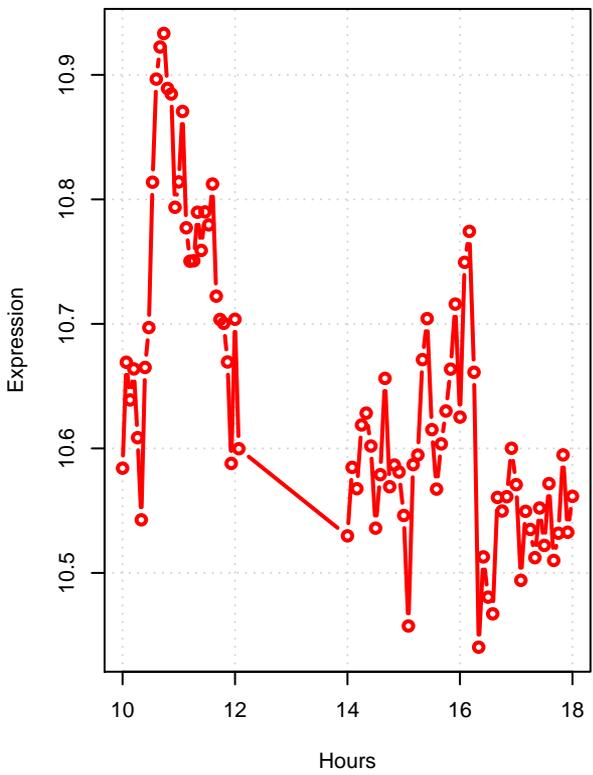
hem3 YDL203C  
Porphobilinogen deaminase



hem2 YGL040C  
Aminolevulinic dehydratase

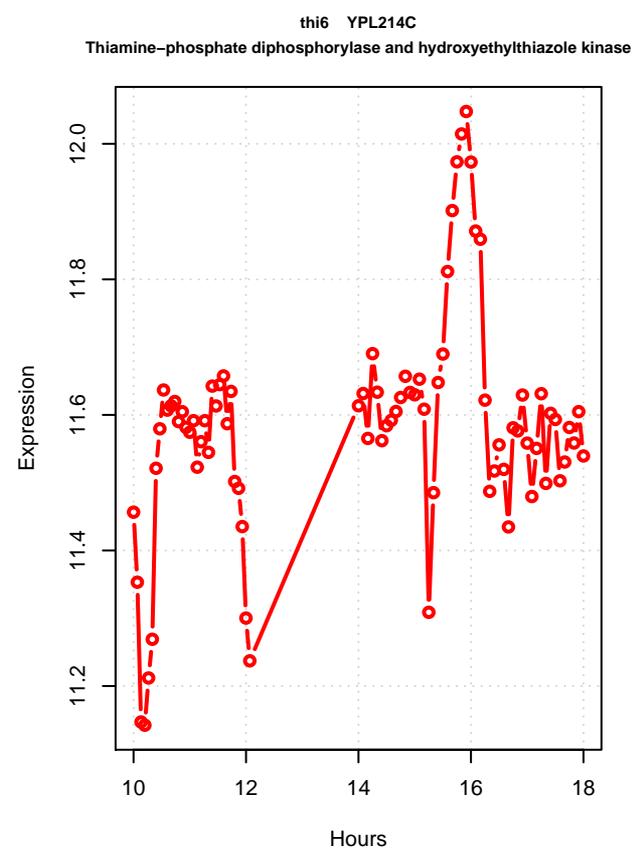
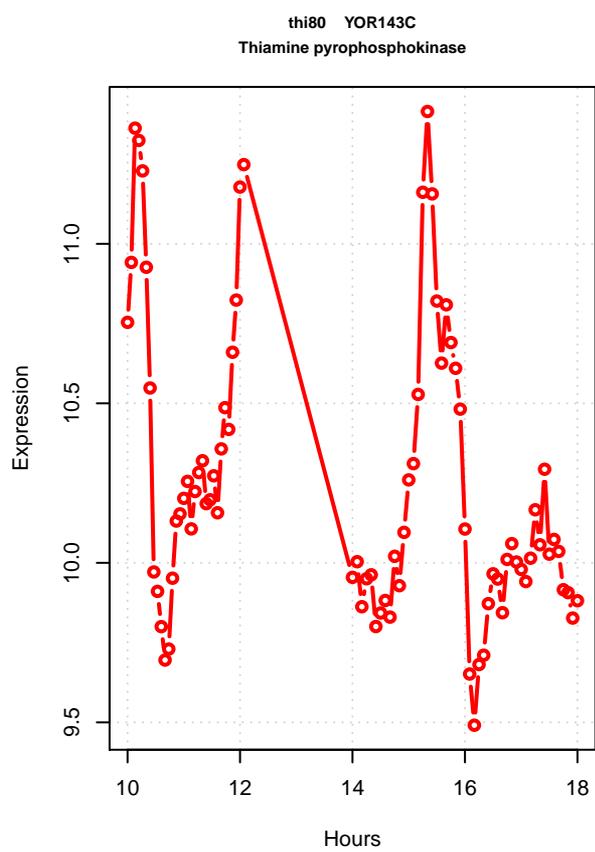
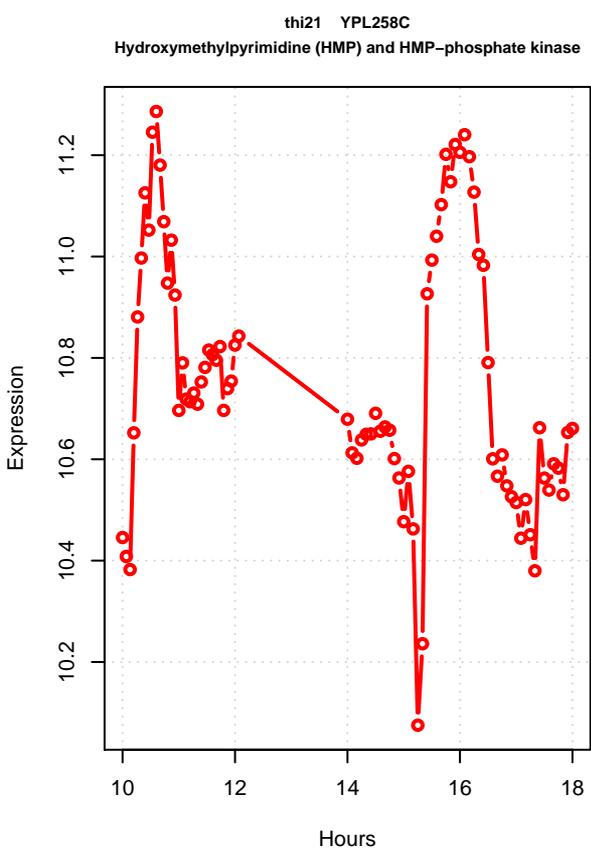
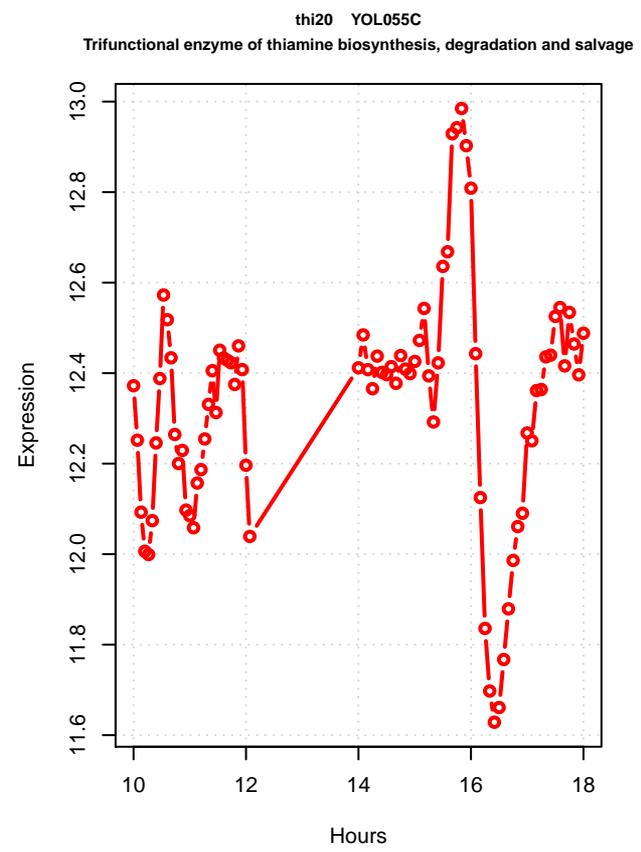
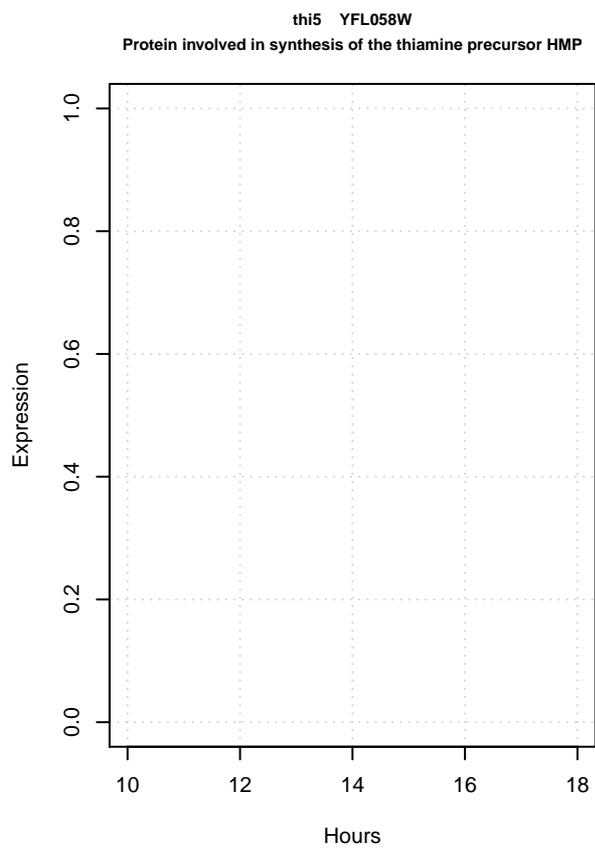
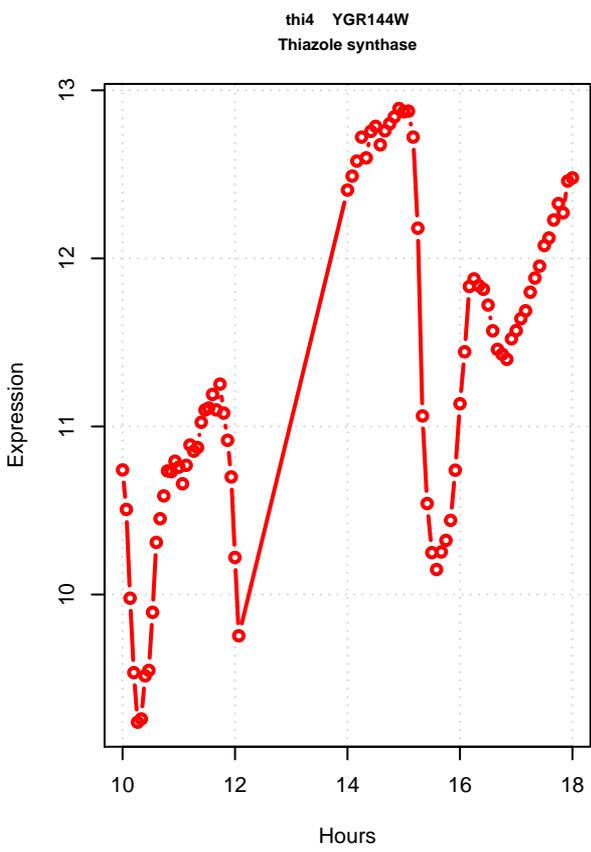
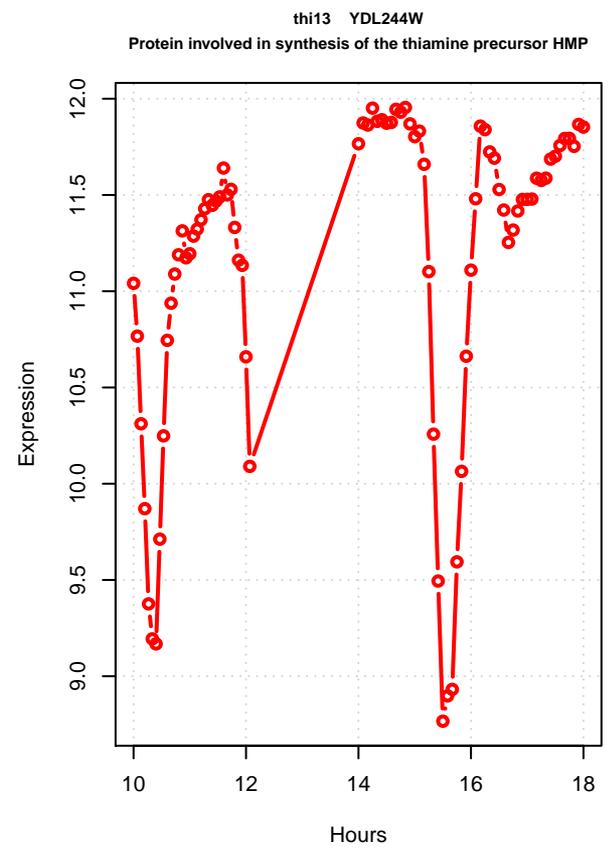
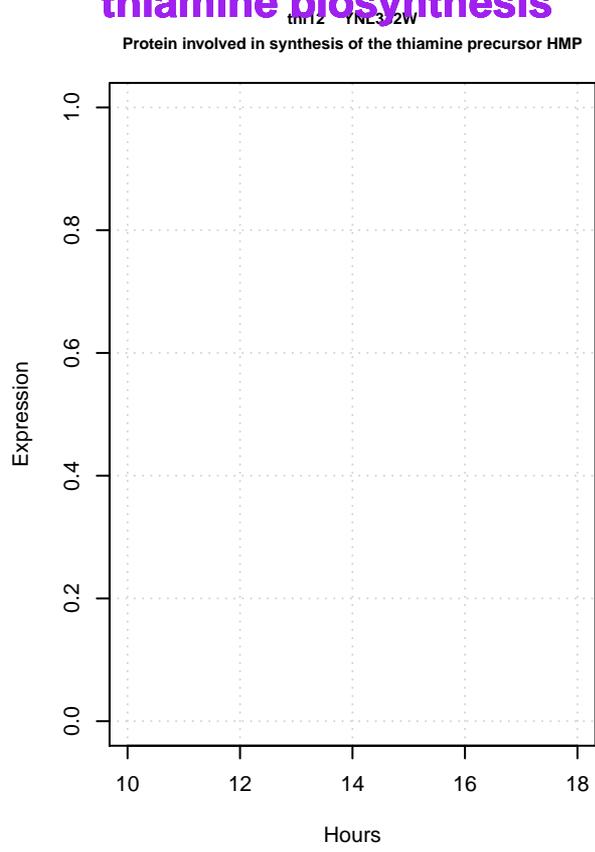
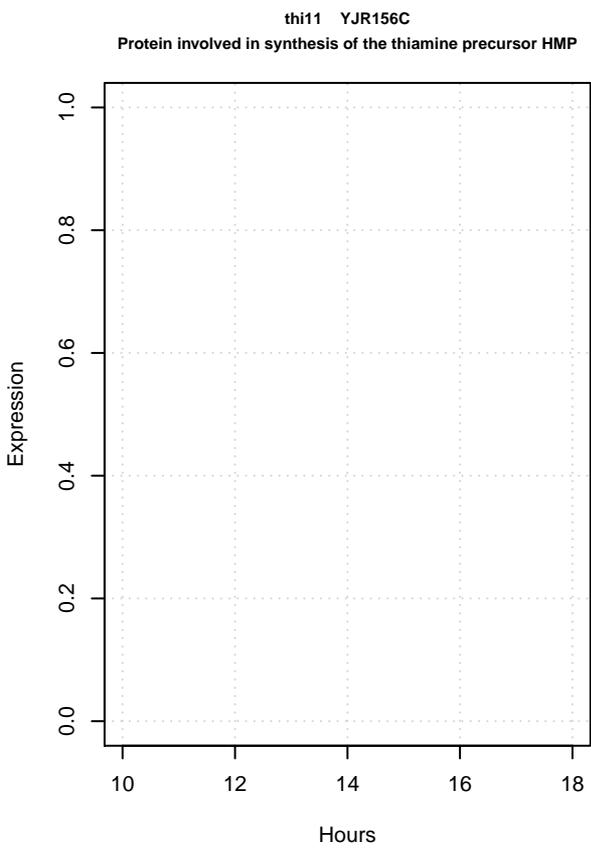


hem4 YOR278W  
Uroporphyrinogen III synthase



# thiamine biosynthesis

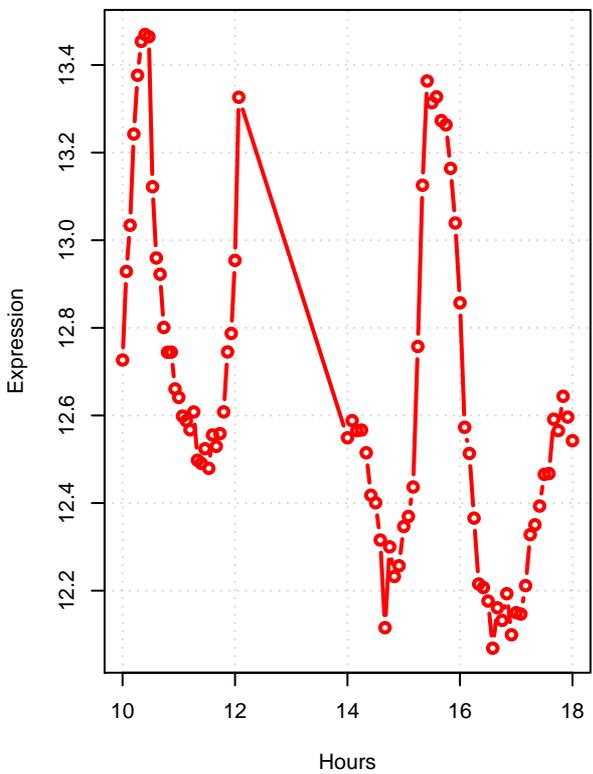
# thiamine biosynthesis



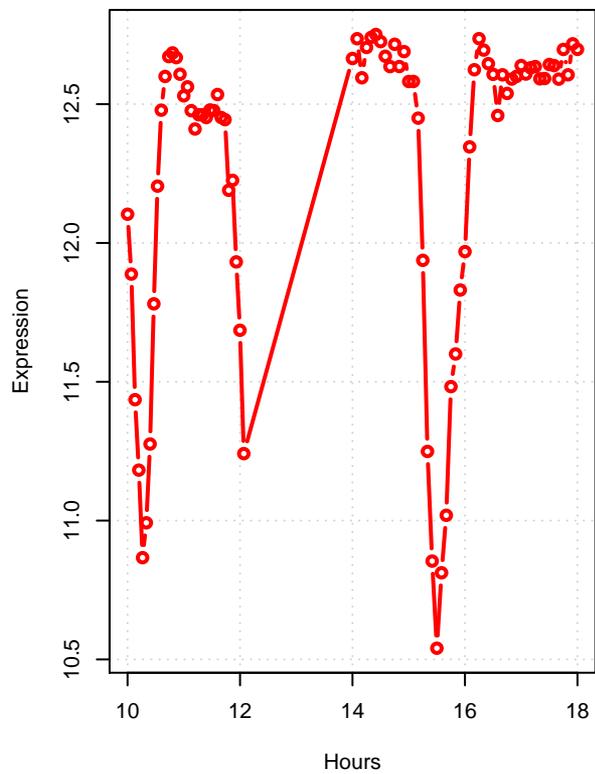
**thioredoxin system**

# thioredoxin system

trr1 YDR353W  
Cytoplasmic thioredoxin reductase



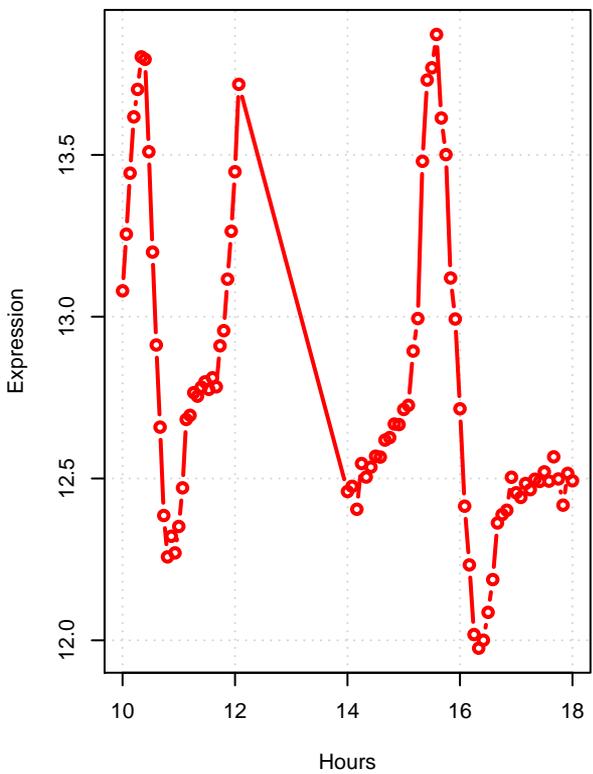
trr2 YHR106W  
Mitochondrial thioredoxin reductase



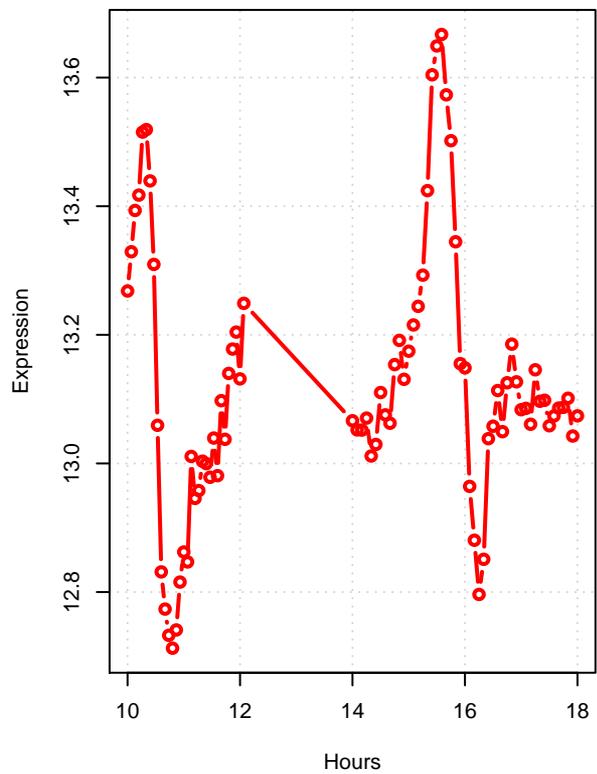
## **threonine biosynthesis**

# threonine biosynthesis

thr1 YHR025W  
Homoserine kinase



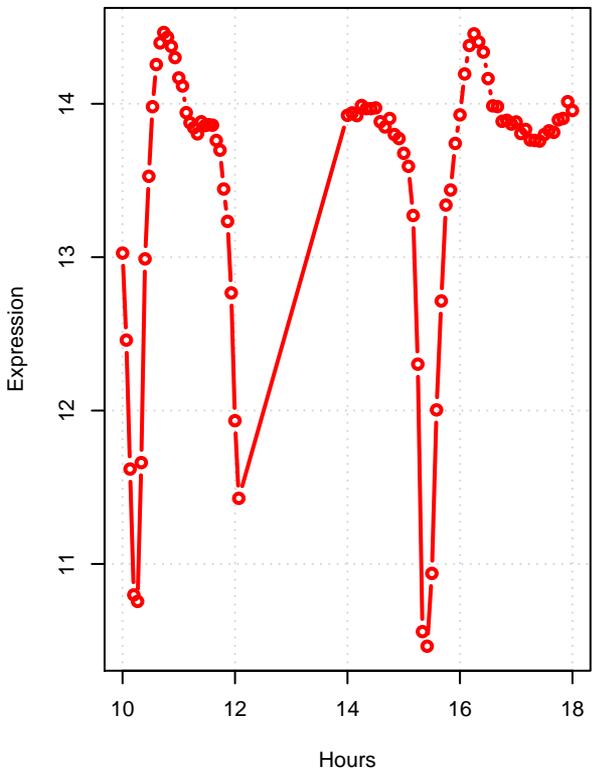
thr4 YCR053W  
Threonine synthase



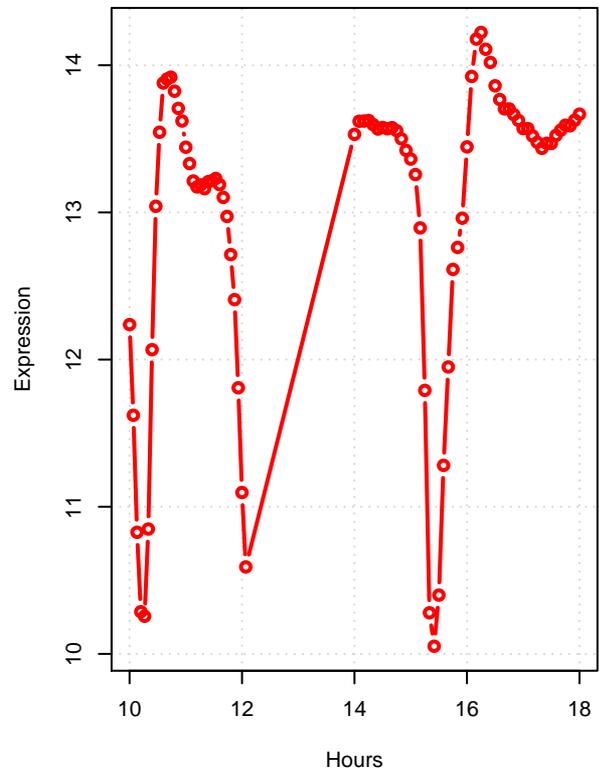
## **trehalose biosynthesis**

# trehalose biosynthesis

tps1 YBR126C  
Synthase subunit of trehalose-6-P synthase/phosphatase complex



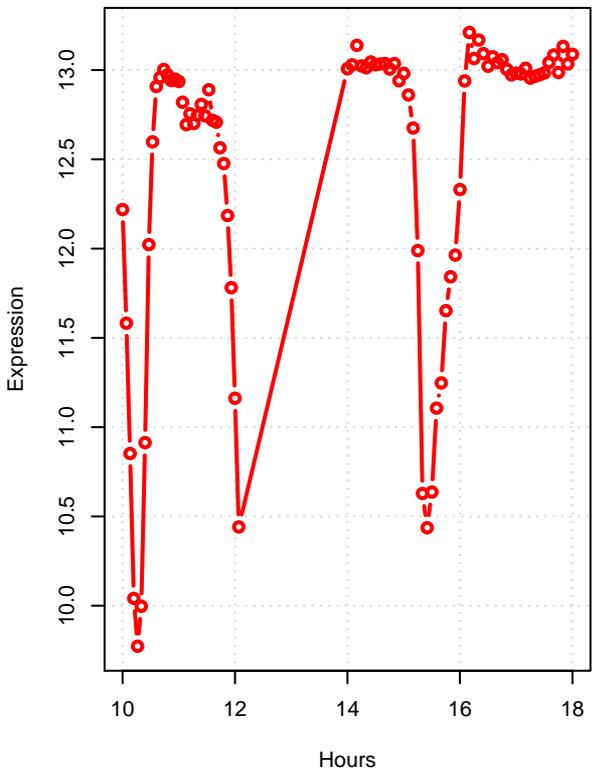
tps2 YDR071W  
Phosphatase subunit of the trehalose-6-P synthase/phosphatase complex



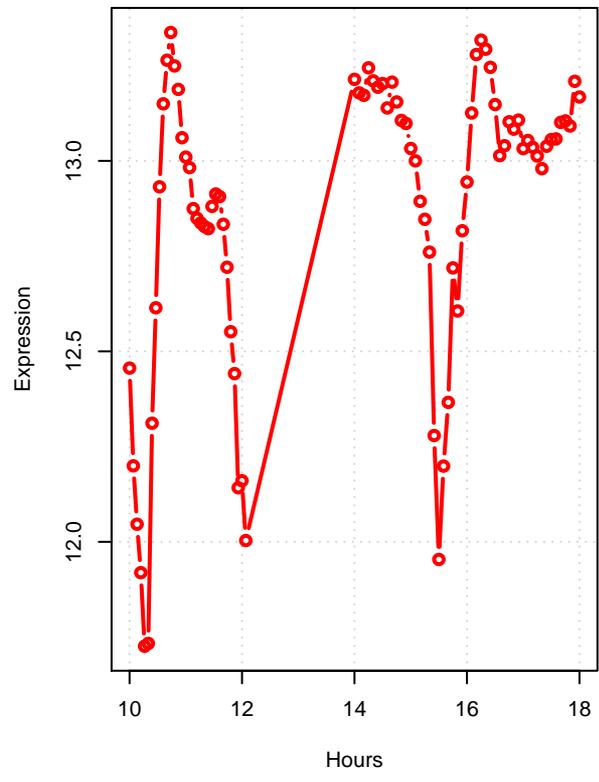
**trehalose degradation**

# trehalose degradation

ath1 YPR026W  
Acid trehalase required for utilization of extracellular trehalose



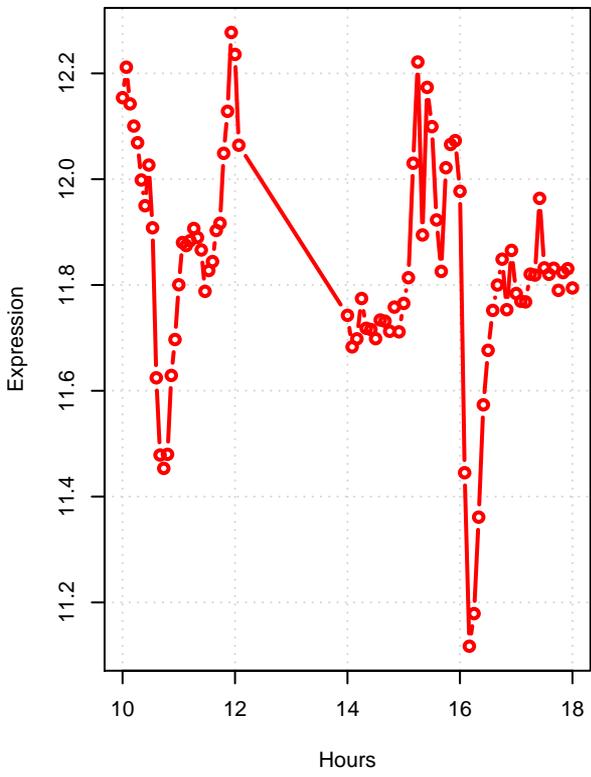
nth1 YPR001C  
Neutral trehalase, degrades trehalose



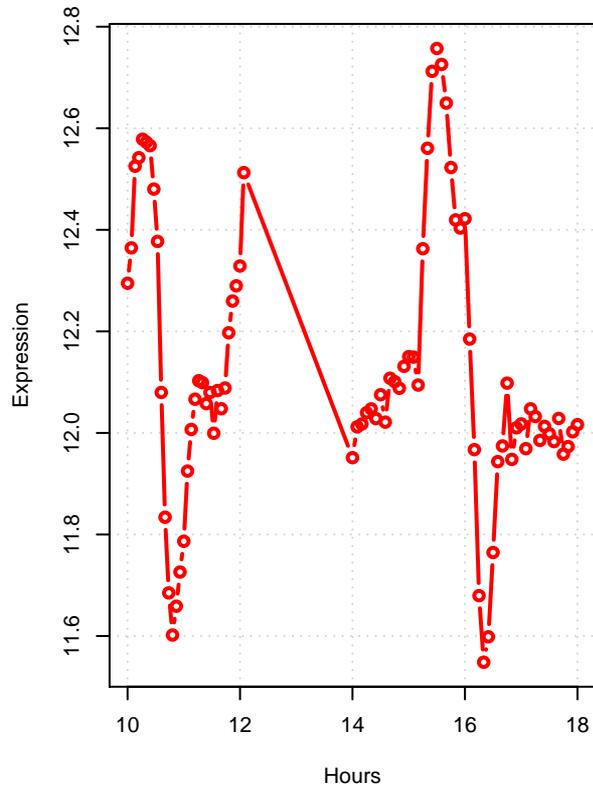
## tryptophan biosynthesis

# tryptophan biosynthesis

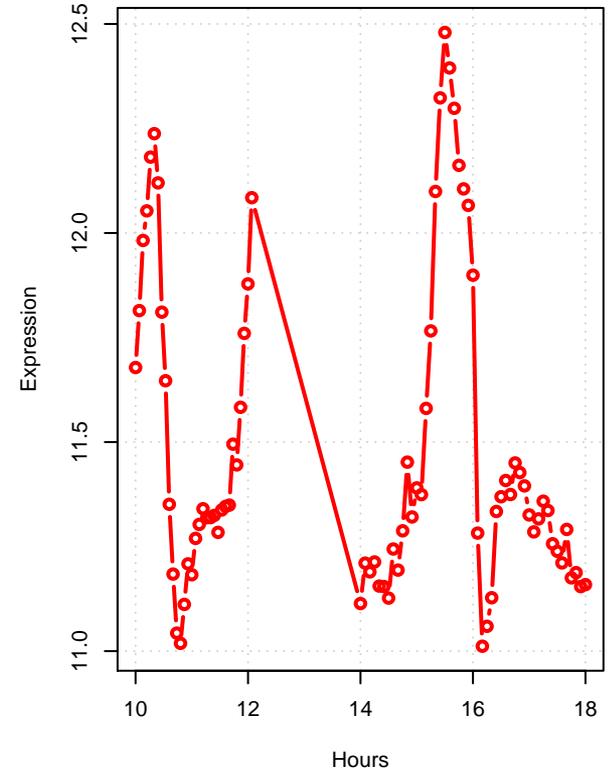
trp4 YDR354W  
Anthranilate phosphoribosyl transferase



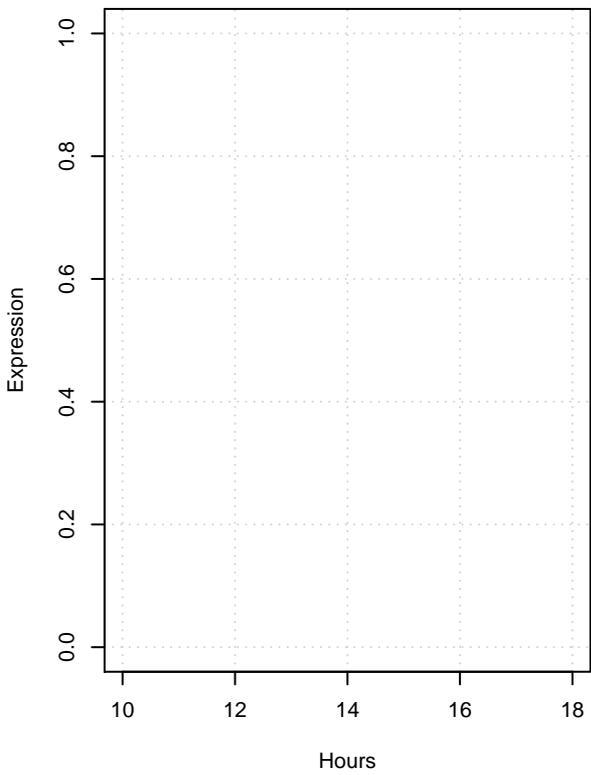
trp2 YER090W  
Anthranilate synthase



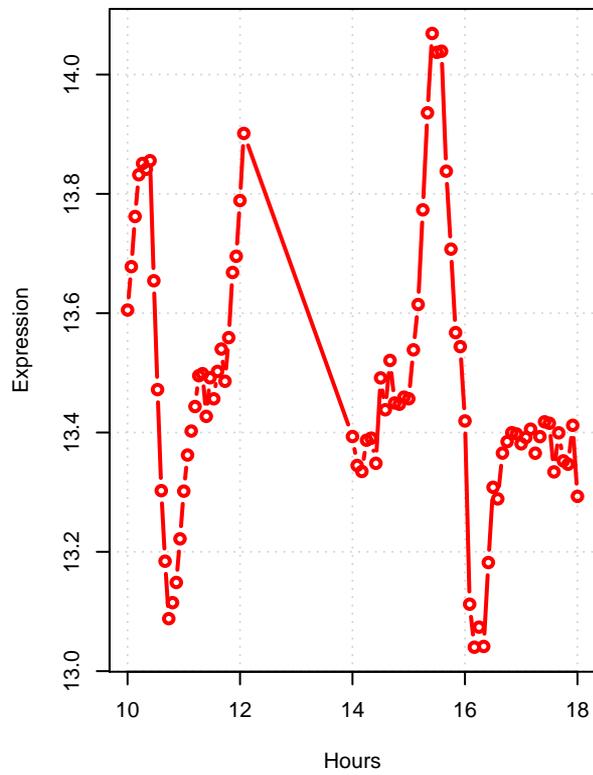
trp3 YKL211C  
Indole-3-glycerol-phosphate synthase



trp1 YDR007W  
Phosphoribosylanthranilate isomerase



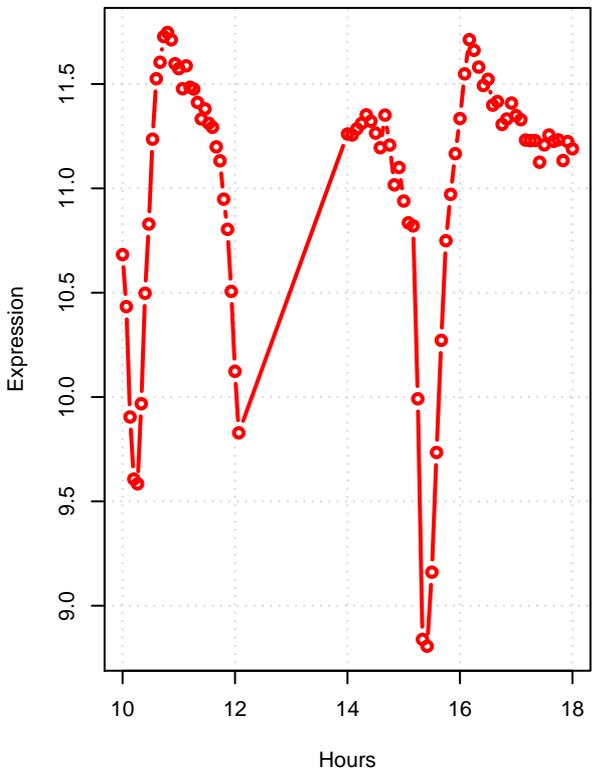
trp5 YGL026C  
Tryptophan synthase



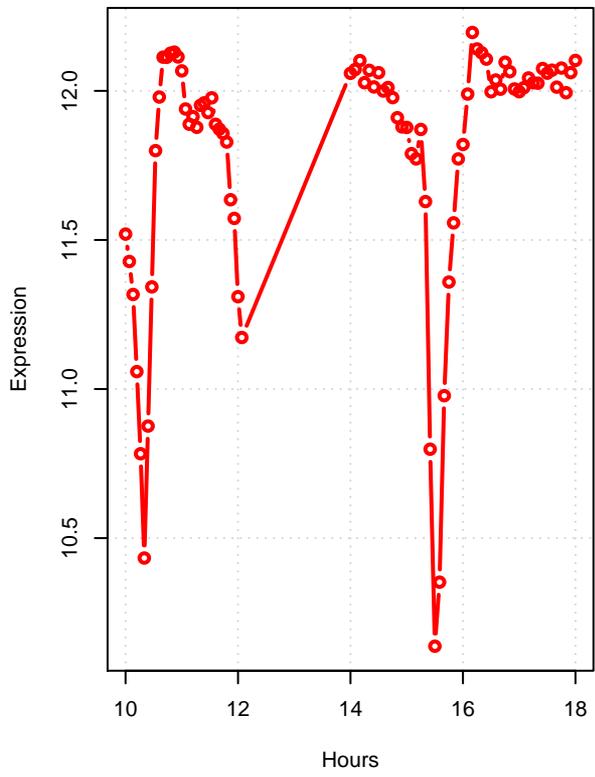
**ubiquinone biosynthesis from 4-hydroxybenzoate**

# ubiquinone biosynthesis from 4-hydroxybenzoate

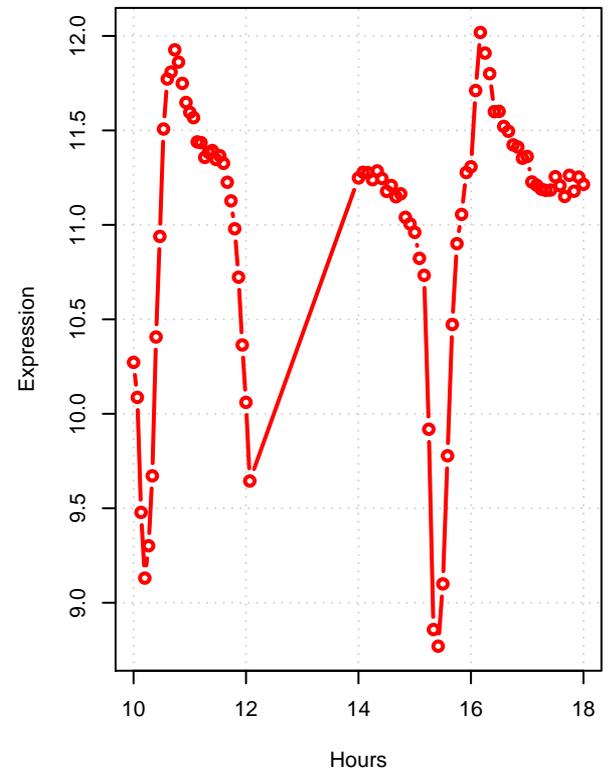
cat5 YOR125C  
Protein required for ubiquinone (Coenzyme Q) biosynthesis



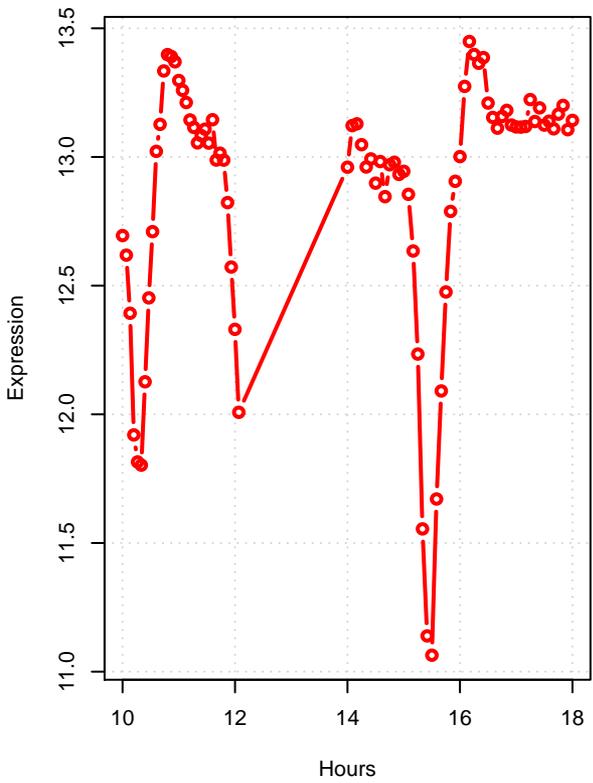
coq6 YGR255C  
Flavin-dependent monooxygenase involved in ubiquinone biosynthesis



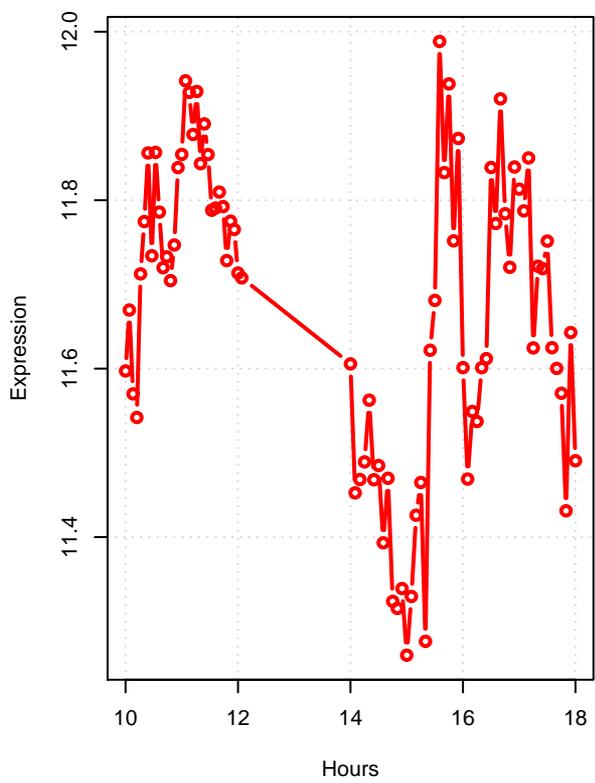
coq3 YOL096C  
O-methyltransferase



coq5 YML110C  
2-hexaprenyl-6-methoxy-1,4-benzoquinone methyltransferase



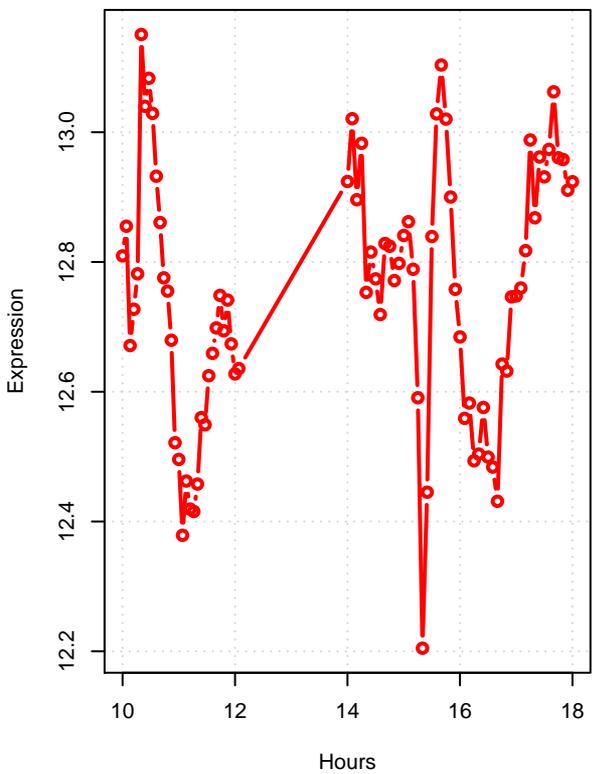
coq2 YNR041C  
Para hydroxybenzoate polyprenyl transferase



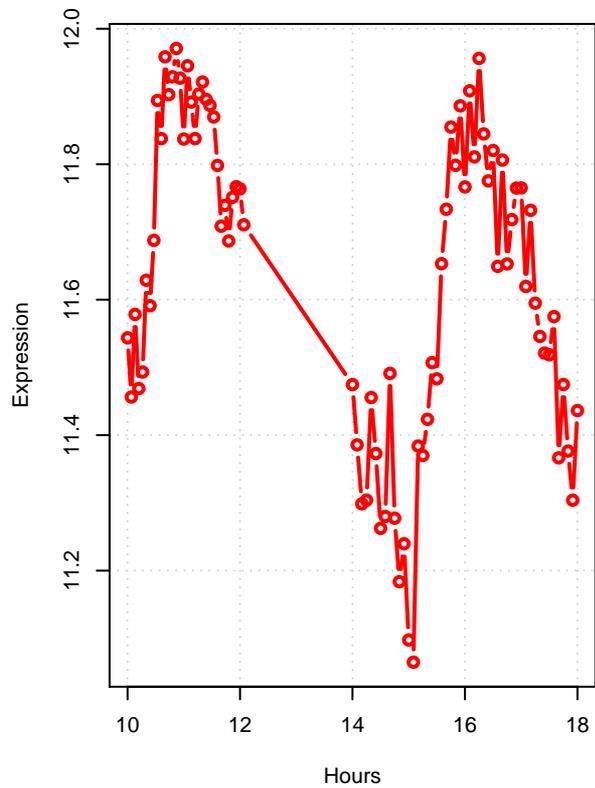
## UDP–N–acetylglucosamine biosynthesis

# UDP-N-acetylglucosamine biosynthesis

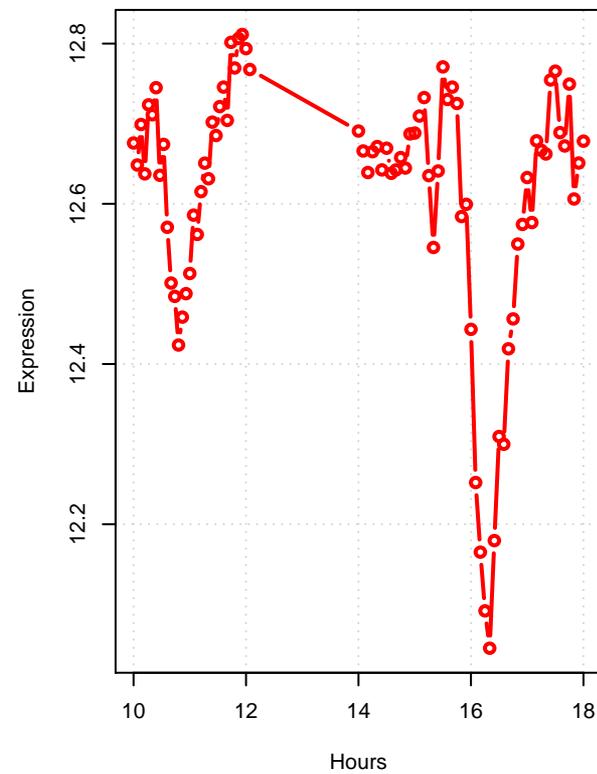
*gfa1* YKL104C  
Glutamine-fructose-6-phosphate amidotransferase



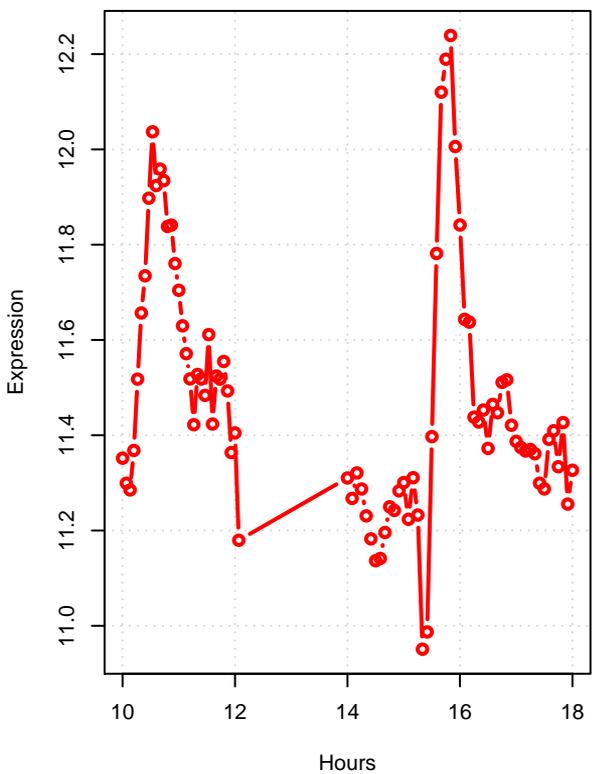
*gna1* YPL017C  
Glucosamine-6-phosphate acetyltransferase



*pcm1* YEL058W  
Essential N-acetylglucosamine-phosphate mutase



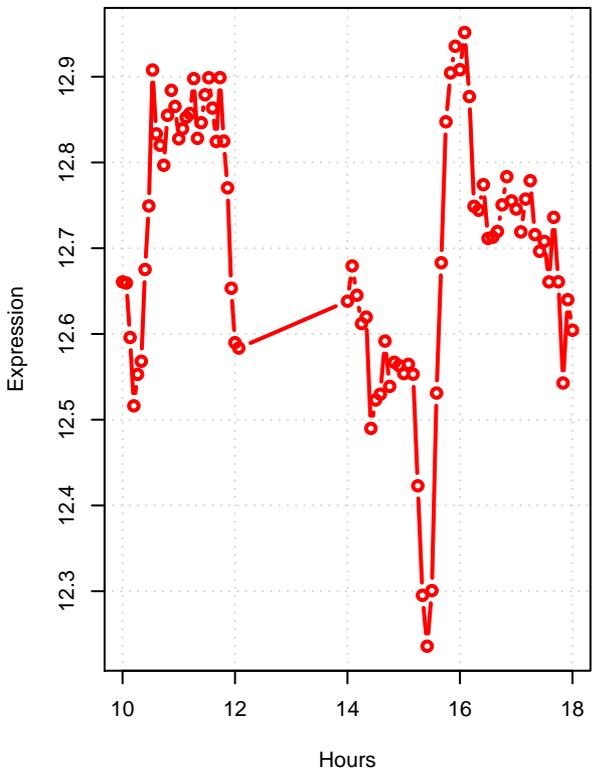
*qri1* YDL103C  
UDP-N-acetylglucosamine pyrophosphorylase



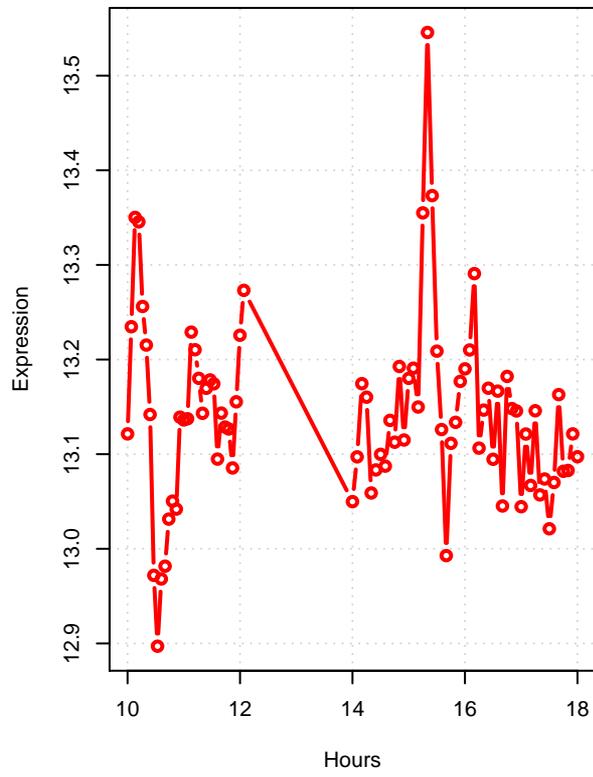
**very long chain fatty acid biosynthesis**

# very long chain fatty acid biosynthesis

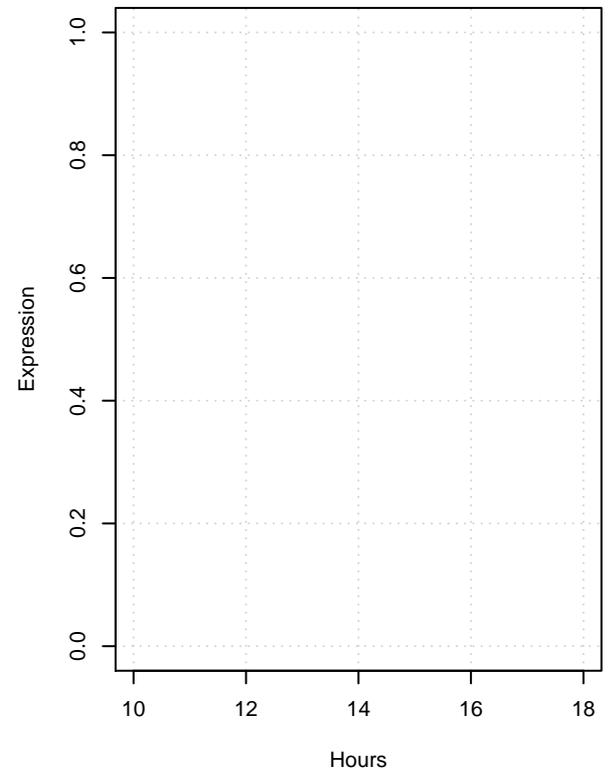
**ifa38 YBR159W**  
Microsomal beta-keto-reductase



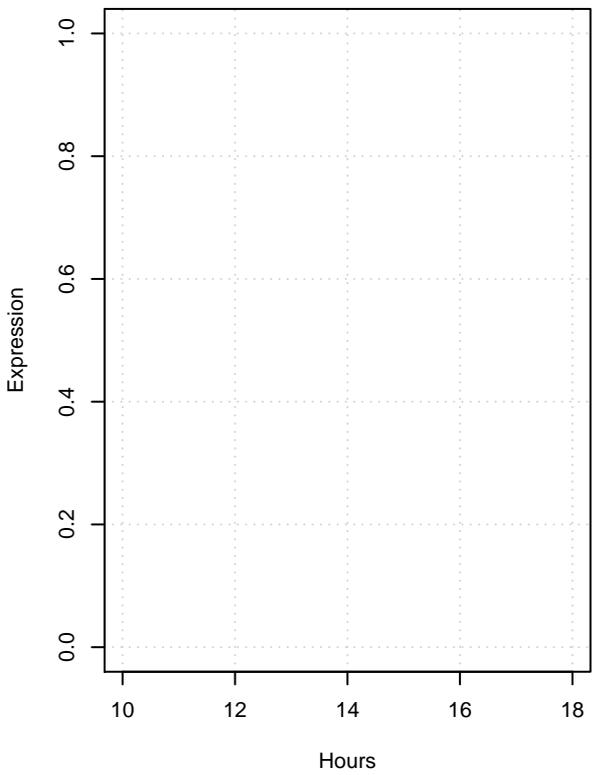
**tsc13 YDL015C**  
Enoyl reductase



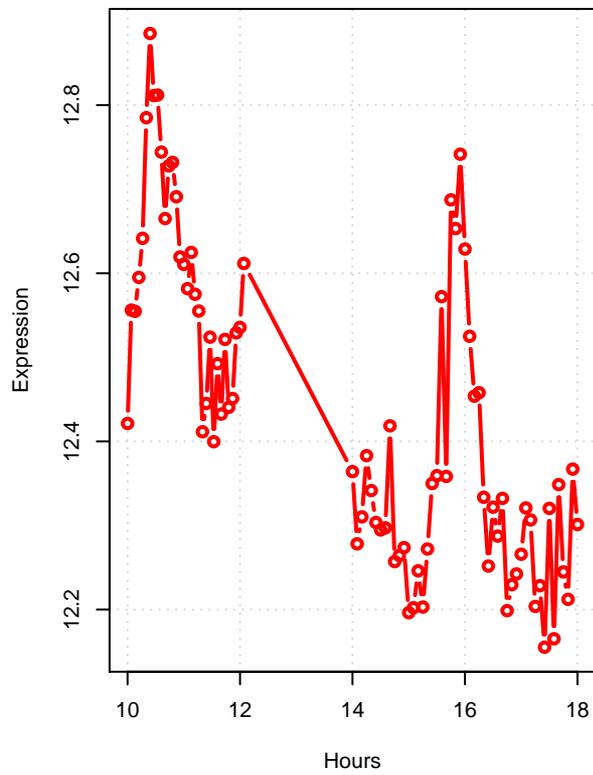
**fen1** Missing ORF  
Missing Function



**sur4** Missing ORF  
Missing Function

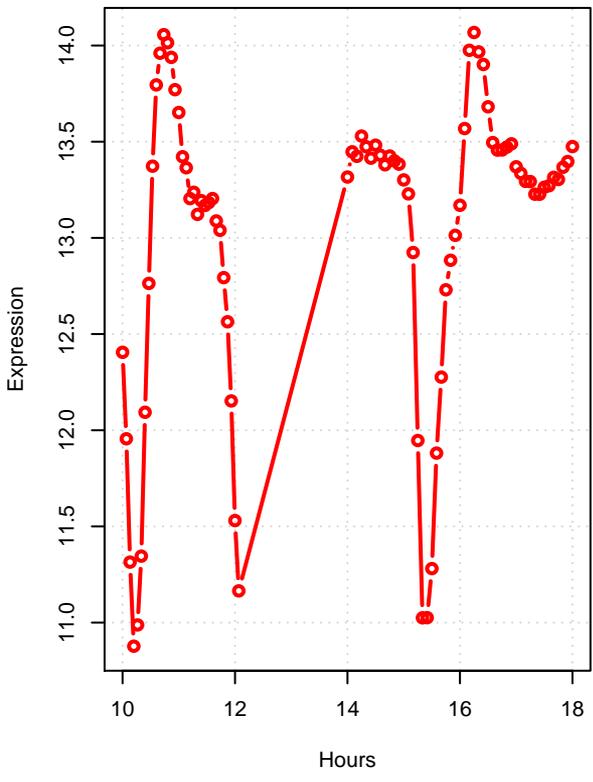


**phs1 YJL097W**  
Essential 3-hydroxyacyl-CoA dehydratase of the ER membrane

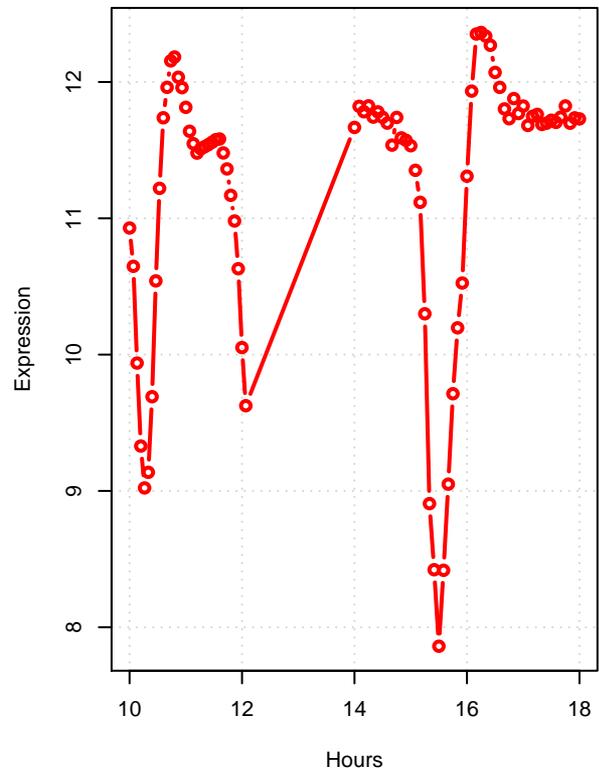


## xylose metabolism

gre3 YHR104W  
Aldose reductase



xy12 YLR070C  
Xylitol dehydrogenase



## xylulose degradation

# xylulose degradation

xks1 YGR194C  
Xylulokinase

