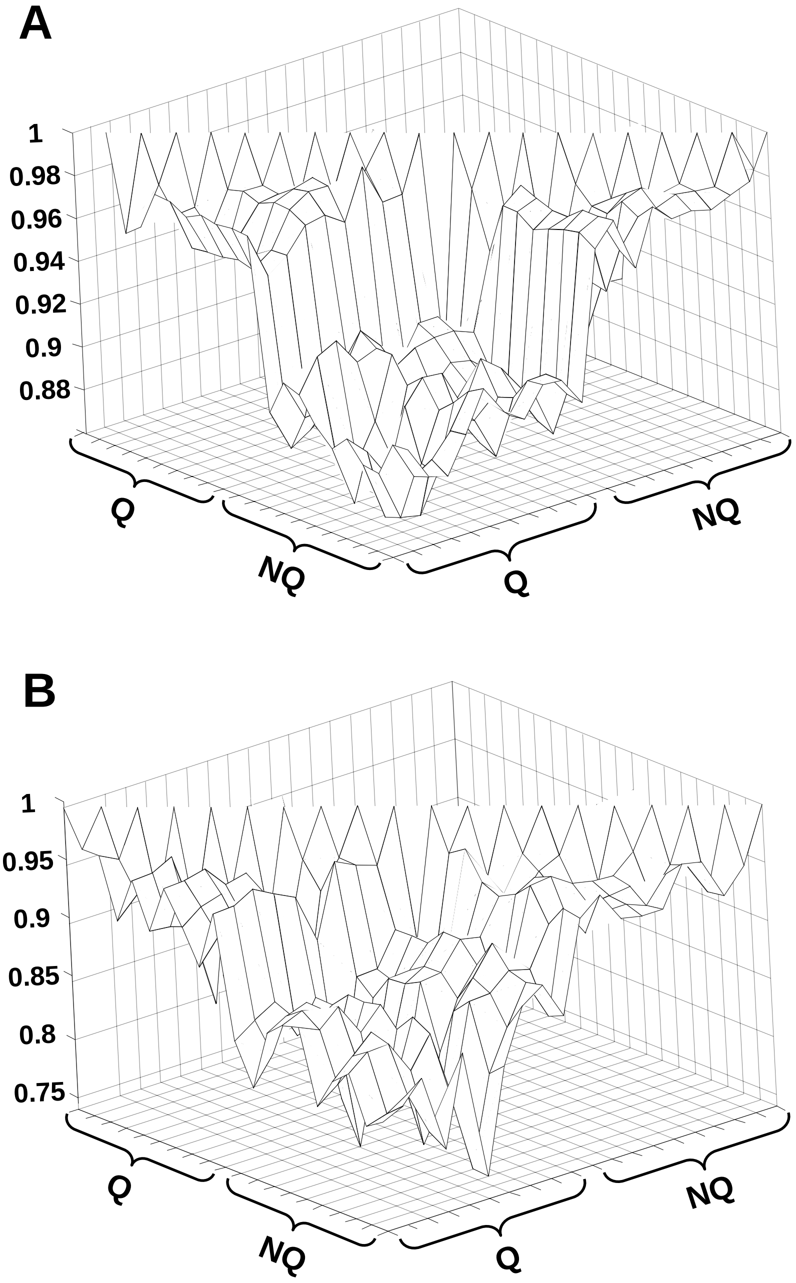
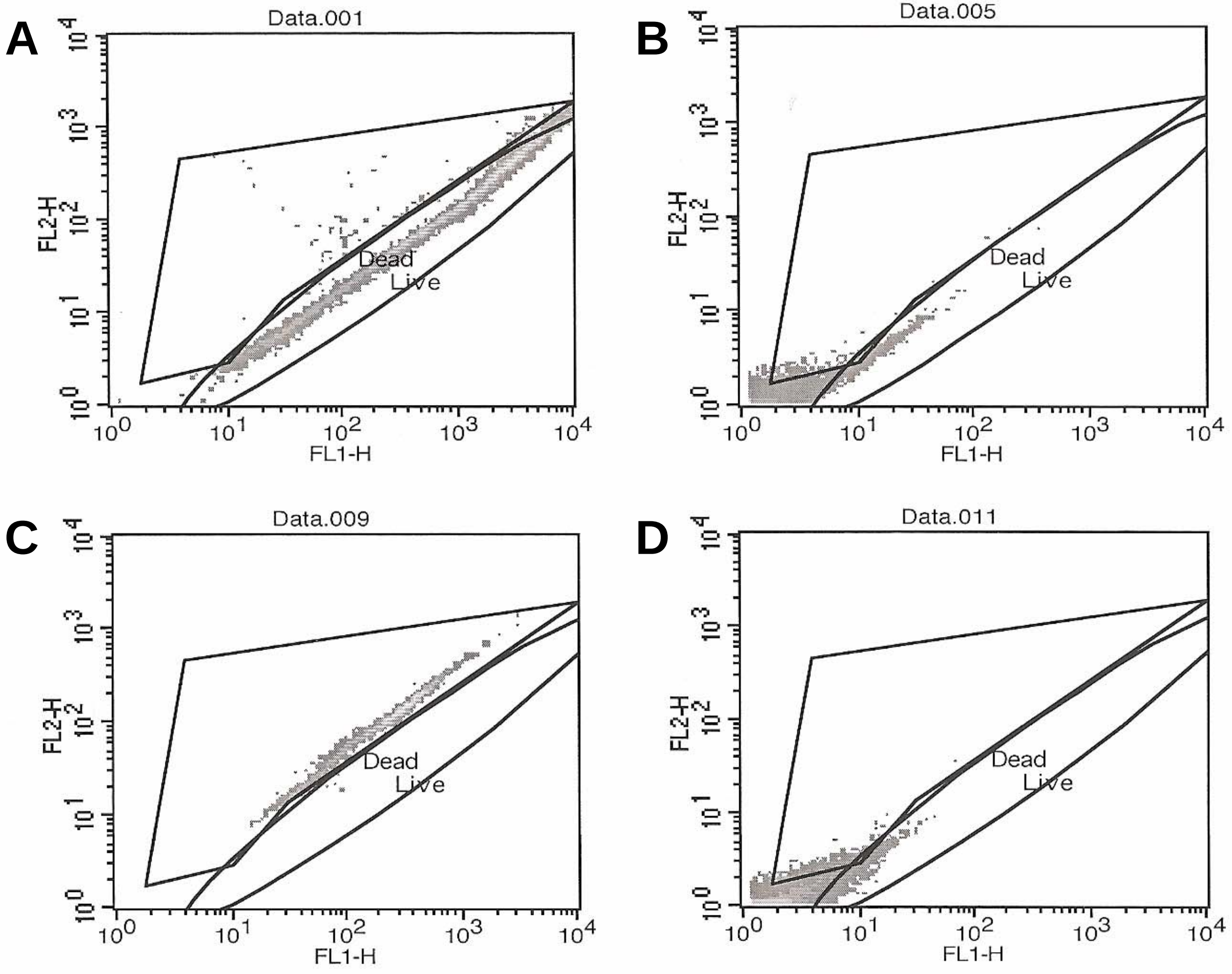
Mutants in this study

ACS1
ADH2
ADY2
AGX1
ALD2
ALD3
ALD4
ARD1
ATG8
ATP1
ATP18
ATP2
ATP3
CIT1
CIT2
COR1
COX6
COX7
COX8
CTA1
CTT1
DDR2
DOA4
ETR1
FAA1
FBP1
FMP16
FMP21
FMP45
GAD1
GAT2
GID8
GIS1
GLK1
GPD1
GPG1
GRE1
GTT1
GUT2
HAP4
HBT1
HSP104
HSP12
HSP26
HSP30
HXK1
HXT5
ICL1
JEN1
KGD1
MDH1
MLS1
MOH1
MPM1
MSC1
NAT1
NGR1
ODC1
OM45
PAI3
PBI2
PCK1
PNC1
POR1
POT1
PST2
QCR10
QCR7
QCR8
RBF9
RIP1
RTN2
SDH2
SDH4
SDS24
SFA1
SIP18
SNA2
SNZ1
SOD2
SPG1
SPG3
SPG4
SPG5
SPI1
SPS100
TIP1
UBI4
XBP1
YAT1
YMR31
YBL048W
YBR056W
YBR230C
YDL218W
YDR262W
YGR043C
YHR097C
YHR138C
YLR312C
YPL230W



Correlation plots of gene expression ratios from replicate hybridizations of the Q and NQ fraction. Correlation was determined using Matlab as described in the Materials and Methods. (A) Correlation map of pair wise R^2 values calculated for all replicate hybridizations of the Q and NQ fractions in the wild-type strain S288c. (B) Correlation map of pair wise R^2 values calculated for all replicate hybridizations of the Q and NQ fractions in the parental strain BY4742.



Flow cytometric viability assay using BY4742 haploid yeast cells. (A) Stained exponential cells grown overnight, positive viability control. (B) Unstained exponential cells, autofluorescence control. (C) Stained isopropanol “killed” cells from a non-separated stationary-phase culture, negative viability control. (D) Unstained isopropanol “killed” cells from a non-separated stationary-phase culture, autofluorescence control.

Q gene list
YAL001C
YAL008W
YAL049C
YAL051W
YAL056W
YAL064W-B
YBL001C
YBL003C
YBL027W
YBL048W
YBL064C
YBL092W
YBL108C-A
YBR004C
YBR026C
YBR050C
YBR056W
YBR072W
YBR089C-A
YBR090C
YBR094W
YBR117C
YBR126C
YBR129C
YBR140C
YBR149W
YBR150C
YBR167C
YBR189W
YBR216C
YBR225W
YBR230C
YBR255C-A
YBR265W
YBR269C
YBR280C
YBR287W
YBR295W
YBR296C
YCL001W
YCL032W
YCL033C
YCR007C
YCR030C
YCR079W
YCR083W
YCR094W
YDL019C
YDL022W
YDL027C
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YDL049C
YDL064W
YDL072C
YDL078C
YDL083C
YDL085W
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YDL110C
YDL112W
YDL113C
YDL124W
YDL130W-A
YDL131W
YDL133C-A
YDL133W
YDL134C
YDL135C
YDL136W
YDL137W
YDL174C
YDL183C
YDL184C
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YDL199C
YDL201W
YDL203C
YDL204W
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YDR025W
YDR032C
YDR034W-B
YDR070C
YDR074W
YDR099W
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YDR122W
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YDR155C
YDR161W
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YDR483W
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YDR513W
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YER020W
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YER022W
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YER042W
YER054C
YER063W
YER075C
YER101C
YER105C
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YER131W
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YGL190C
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YPR165W
YPR172W
YPR189W
YPR192W
YPR200C

Quiescent	Probability
vesicle-mediated transport	1.29E-09
vesicle docking during exocytosis	2.77E-06
oxygen and reactive oxygen species metabolism	9.11E-06
vesicle docking	9.41E-06
fatty acid oxidation	1.22E-05
exocytosis	1.55E-05
membrane organization and biogenesis	2.05E-05
response to oxidative stress	2.07E-05
membrane fusion	7.46E-05
lipid metabolism	9.20E-05
cellular lipid metabolism	9.55E-05
signal transduction	9.67E-05
establishment of localization	0.0001
transport	0.00011
post-Golgi vesicle-mediated transport	0.00013
Golgi to plasma membrane transport	0.00014
secretion	0.00014
cell communication	0.00016
fatty acid beta-oxidation	0.00023
bipolar bud site selection	0.00027
localization	0.00027
Golgi vesicle transport	0.00031
secretory pathway	0.00034
endocytosis	0.0004
response to stress	0.00049
cellular localization	0.00065
reproduction	0.00066
cell organization and biogenesis	0.00077
physiological process	0.00087
fatty acid metabolism	0.00092
intracellular transport	0.00106
establishment of cellular localization	0.00112
protein modification	0.00113
regulation of protein metabolism	0.0013
response to stimulus	0.00135
cell wall organization and biogenesis (sensu Fungi)	0.00153
cellular process	0.00164
actin polymerization and/or depolymerization	0.00175
response to abiotic stimulus	0.00199
cellular physiological process	0.00242
biopolymer biosynthesis	0.00243
vesicle fusion	0.00243
polysaccharide biosynthesis	0.00243
ethanol metabolism	0.00275
glucan biosynthesis	0.00314
cell wall biosynthesis	0.00314
cell wall biosynthesis (sensu Fungi)	0.00314
cell wall polysaccharide biosynthesis (sensu Fungi)	0.00321
protein localization	0.00336
endosome transport	0.00362
regulation of translational fidelity	0.00411
response to chemical stimulus	0.00436
establishment of protein localization	0.00436
age-dependent response to oxidative stress during chronological cell aging	0.00455
age-dependent general metabolic decline during chronological cell aging	0.00455
age-dependent response to oxidative stress	0.00455
asexual reproduction	0.00487
cell budding	0.00487

intracellular protein transport	0.00496
lipid biosynthesis	0.00511
Ras protein signal transduction	0.00584
Golgi to endosome transport	0.00588
protein amino acid phosphorylation	0.00645
regulation of proteolysis	0.00661
actin filament depolymerization	0.00661
beta-1,6 glucan biosynthesis	0.00661
protein transport	0.00711
beta-glucan biosynthesis	0.00723
age-dependent general metabolic decline	0.00723
cellular polysaccharide metabolism	0.00755
polysaccharide metabolism	0.00755
cell wall organization and biogenesis	0.00774
external encapsulating structure organization and biogenesis	0.00774
cell aging	0.00831
phosphate metabolism	0.00929
phosphorus metabolism	0.00929
carbohydrate biosynthesis	0.00955
aging	0.00964
steroid biosynthesis	0.01071
beta-glucan metabolism	0.01077
regulation of cellular biosynthesis	0.01121
regulation of biosynthesis	0.01121
intracellular signaling cascade	0.01179
beta-1,6 glucan metabolism	0.01206
glucose catabolism to ethanol	0.01206
protein retention in Golgi	0.01229
coenzyme metabolism	0.01277
development	0.01304
actin filament organization	0.014
ubiquitin-dependent protein catabolism via the multivesicular body pathway	0.01435
regulation of cell redox homeostasis	0.01527
response to desiccation	0.01527
cell redox homeostasis	0.01527
response to water	0.01527
response to water deprivation	0.01527
aromatic amino acid family catabolism	0.01548
actin filament capping	0.01548
age-dependent response to reactive oxygen species during chronological cell aging	0.01548
age-dependent response to reactive oxygen species	0.01548
barbed-end actin filament capping	0.01548
regulation of actin filament depolymerization	0.01548
regulation of cell shape	0.01548
negative regulation of actin filament depolymerization	0.01548
regulation of translation	0.01617
glucan metabolism	0.01669
late endosome to vacuole transport	0.01839
cortical cytoskeleton organization and biogenesis	0.01839
cortical actin cytoskeleton organization and biogenesis	0.01839
regulation of protein biosynthesis	0.01884
cell death	0.0189
glycolytic fermentation	0.01948
carbohydrate metabolism	0.01987
protein targeting	0.02007
maintenance of protein localization	0.02093
actin cytoskeleton organization and biogenesis	0.02104
death	0.02134
dephosphorylation	0.02182

energy reserve metabolism	0.02182
MAPKKK cascade	0.02311
regulation of physiological process	0.02327
vacuole fusion, non-autophagic	0.02704
cell adhesion	0.02856
maintenance of localization	0.02859
actin filament-based process	0.02866
peroxisome organization and biogenesis	0.02874
trehalose metabolism	0.0289
plasma membrane organization and biogenesis	0.0289
phospholipid translocation	0.0289
copper ion homeostasis	0.0289
regulation of transcription from RNA polymerase III promoter	0.0289
response to reactive oxygen species	0.0289
regulation of biological process	0.03156
generation of precursor metabolites and energy	0.03158
lipid transport	0.03202
reproductive cellular physiological process	0.03266
reproductive physiological process	0.03266
formation of catalytic spliceosome for first transesterification step	0.03278
regulation of actin polymerization and/or depolymerization	0.03278
aromatic compound catabolism	0.03278
regulation of actin filament length	0.03278
phosphorylation	0.03339
cofactor metabolism	0.03416
biopolymer modification	0.03486
cytokinesis, site selection	0.03507
bud site selection	0.03507
chronological cell aging	0.03519
steroid metabolism	0.03542
small GTPase mediated signal transduction	0.03709
replicative cell aging	0.03796
oxidoreduction coenzyme metabolism	0.03956
reproductive sporulation	0.04017
sporulation (sensu Fungi)	0.04017
cell cycle arrest in response to pheromone	0.04033
cell wall chitin metabolism	0.04033
protein depolymerization	0.04033
protein kinase cascade	0.04173
vacuole organization and biogenesis	0.04174
energy derivation by oxidation of organic compounds	0.0422
cellular macromolecule metabolism	0.04259
protein amino acid dephosphorylation	0.04369
actin cortical patch assembly	0.04408
regulation of cellular physiological process	0.04441
protein targeting to vacuole	0.04564
regulation of cellular process	0.04568
cell division	0.04607
cellular carbohydrate metabolism	0.04654
morphogenesis	0.05078
cellular morphogenesis	0.05078
growth	0.05096
protein import into mitochondrial inner membrane	0.0537
nonprotein amino acid metabolism	0.0537
negative regulation of protein metabolism	0.0537
protein targeting to peroxisome	0.05412
osmosensory signaling pathway	0.05412
MAPKKK cascade during cell wall biogenesis	0.05485
N-glycan processing	0.05485

proline catabolism	0.05485
disaccharide biosynthesis	0.05485
trehalose biosynthesis	0.05485
fatty acid transport	0.05485
sporulation	0.05506
mitochondrial genome maintenance	0.0577
cytokinesis	0.06098
pyridine nucleotide metabolism	0.06221
cell differentiation	0.06249
nitrogen compound catabolism	0.07412
sterol biosynthesis	0.07412
amine catabolism	0.07412
retrograde vesicle-mediated transport, Golgi to ER	0.07749
response to heat	0.07755
fermentation	0.07755
negative regulation of biological process	0.07929
ubiquitin cycle	0.08037
negative regulation of cell organization and biogenesis	0.08071
endoplasmic reticulum organization and biogenesis	0.08071
peptide or protein carboxyl-terminal blocking	0.08071
propionate metabolism	0.08071
metabolism	0.08142
negative regulation of cellular process	0.08358
negative regulation of cellular physiological process	0.08358
regulation of cell growth	0.08584
chitin metabolism	0.08584
cell cycle arrest	0.08584
negative regulation of progression through cell cycle	0.08584
organic acid metabolism	0.08664
carboxylic acid metabolism	0.08664
ergosterol metabolism	0.08838
ergosterol biosynthesis	0.08838
filamentous growth	0.09108
negative regulation of physiological process	0.09153
regulation of metabolism	0.09165
transcription initiation	0.0917
Not yet annotated	

NQ gene list
YAL004W
YAL012W
YAL020C
YAL023C
YAL039C
YAL040C
YAL042W
YAL058W
YAR018C
YAR028W
YAR029W
YAR031W
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YBL005W-A
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Non-quiescent

GO_term	Probability
Ty element transposition	4.19E-29
DNA transposition	3.01E-27
DNA recombination	1.94E-19
DNA metabolism	2.48E-06
nucleobase, nucleoside, nucleotide and nucleic acid metabolism	2.46E-05
amino acid metabolism	6.42E-05
amine metabolism	8.66E-05
nitrogen compound metabolism	9.58E-05
asparagine metabolism	0.00014
protein folding	0.00016
amino acid and derivative metabolism	0.00028
aspartate family amino acid metabolism	0.00058
cellular response to nitrogen starvation	0.00095
asparagine catabolism	0.00095
cellular response to nitrogen levels	0.00095
hexose transport	0.00135
monosaccharide transport	0.00135
carbohydrate transport	0.00191
phosphatidylcholine biosynthesis	0.0032
carboxylic acid metabolism	0.0042
organic acid metabolism	0.0042
amino acid activation	0.00459
tRNA aminoacylation	0.00459
tRNA aminoacylation for protein translation	0.00459
nuclear migration during conjugation with cellular fusion	0.00502
regulation of transcription, mating-type specific	0.00512
glutamine family amino acid catabolism	0.00542
cellular process	0.00587
physiological process	0.00656
sulfur amino acid metabolism	0.00666
cellular physiological process	0.00714
siderophore transport	0.00767
phosphatidylcholine metabolism	0.00767
snoRNA processing	0.00923
homologous chromosome segregation	0.00923
regulation of carbohydrate metabolism	0.0108
aspartate family amino acid catabolism	0.01096
karyogamy during conjugation with cellular fusion	0.01096
glutamine family amino acid metabolism	0.01229
cellular response to extracellular stimulus	0.01248
cellular response to stimulus	0.01248
response to starvation	0.01248
cellular response to starvation	0.01248
cellular response to nutrient levels	0.01248
pyrimidine ribonucleoside metabolism	0.01282
phenylalanyl-tRNA aminoacylation	0.01282
donor selection	0.01282
cytidine metabolism	0.01282
GMP metabolism	0.01282
sphingolipid metabolism	0.01287
regulation of transcription from RNA polymerase II promoter	0.01781
transcription from RNA polymerase II promoter	0.01836
karyogamy	0.01995
regulation of physiological process	0.02126
positive regulation of cellular metabolism	0.02191
positive regulation of metabolism	0.02191
cell separation during cytokinesis	0.02239

ceramide metabolism	0.02239
homoserine metabolism	0.02239
cellular metabolism	0.02241
biopolymer metabolism	0.02375
primary metabolism	0.02484
regulation of progression through cell cycle	0.02511
regulation of cell cycle	0.02511
glutamate biosynthesis	0.02575
glucose transport	0.0273
histone ubiquitination	0.0273
ion transport	0.02801
regulation of biological process	0.02857
pigment biosynthesis	0.02911
amino acid biosynthesis	0.0301
positive regulation of cellular physiological process	0.03125
positive regulation of physiological process	0.03125
positive regulation of cellular process	0.03125
regulation of metabolism	0.03199
amino acid catabolism	0.03379
pigment metabolism	0.03475
protein monoubiquitination	0.03475
positive regulation of transcription	0.03594
positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	0.03915
nuclear migration, microtubule-mediated	0.04012
microtubule-based movement	0.04012
regulation of exit from mitosis	0.04102
negative regulation of gluconeogenesis	0.04212
sphingoid metabolism	0.04212
negative regulation of carbohydrate metabolism	0.04212
membrane lipid biosynthesis	0.04256
metabolism	0.0434
regulation of cellular physiological process	0.04415
regulation of cellular process	0.04535
cysteine metabolism	0.04595
snoRNA 3'-end processing	0.04595
asparagine biosynthesis	0.04595
sex determination	0.04793
mating type determination	0.04793
methionine metabolism	0.04793
glutamate metabolism	0.04871
cytoskeleton-dependent intracellular transport	0.04871
inorganic anion transport	0.04871
positive regulation of transcription, DNA-dependent	0.04919
amine catabolism	0.05071
nitrogen compound catabolism	0.05071
membrane lipid metabolism	0.05155
phosphate transport	0.05439
response to desiccation	0.05439
response to water deprivation	0.05439
response to water	0.05439
ribonucleoside metabolism	0.05439
amine biosynthesis	0.05484
nitrogen compound biosynthesis	0.05484
response to nutrient levels	0.05549
response to extracellular stimulus	0.05549
secondary metabolism	0.05549
response to external stimulus	0.05549
metal ion transport	0.05691
positive regulation of biological process	0.05787

organelle fusion	0.05823
anion transport	0.05823
transcription	0.05827
sulfur metabolism	0.06199
regulation of mitosis	0.06592
carboxylic acid transport	0.06592
pyrimidine nucleoside metabolism	0.06799
pyrimidine salvage	0.06799
response to hexose stimulus	0.06799
response to glucose stimulus	0.06799
isocitrate metabolism	0.06799
regulation of gluconeogenesis	0.06815
chitin metabolism	0.06815
aspartate family amino acid biosynthesis	0.06867
transition metal ion transport	0.06944
negative regulation of transcription from RNA polymerase II promoter	0.06944
organic acid transport	0.07201
di-, tri-valent inorganic cation transport	0.07201
glycerophospholipid biosynthesis	0.07202
meiosis I	0.073
regulation of transcription	0.07409
regulation of cellular metabolism	0.07545
regulation of transcription, DNA-dependent	0.07632
transcription, DNA-dependent	0.07768
sphingolipid biosynthesis	0.08001
glutamine family amino acid biosynthesis	0.08205
G1/S-specific transcription in mitotic cell cycle	0.08333
external encapsulating structure organization and biogenesis	0.0841
cell wall organization and biogenesis	0.0841
organelle localization	0.08521
positive regulation of transcription from RNA polymerase II promoter	0.08521
response to stimulus	0.08694
heterocycle metabolism	0.09014
alcohol metabolism	0.0922
nucleus localization	0.09221
nuclear migration	0.09221
establishment of nucleus localization	0.09221
organic cation transport	0.09275
zinc ion transport	0.09275
mitochondrial signaling pathway	0.09275
purine base biosynthesis	0.09275
response to carbohydrate stimulus	0.09275
polyol transport	0.09275
cytokinesis, completion of separation	0.09275
siderophore-iron transport	0.09275
ammonium transport	0.09275
monosaccharide metabolism	0.09654
cation transport	0.09654
amino acid transport	0.09774
drug transport	0.0998
telomerase-dependent telomere maintenance	0.0998
DNA damage checkpoint	0.0998
Not yet annotated	

Q protease gene list

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Q Protease	Probability
Ty element transposition	2.21E-28
transposition	5.54E-27
transposition, DNA-mediated	5.54E-27
DNA recombination	3.15E-15
DNA metabolism	4.82E-06
protein targeting to mitochondrion	0.00014
homeostasis	0.00017
cellular localization	0.00027
ion homeostasis	0.00039
establishment of cellular localization	0.00041
protein folding	0.00042
intracellular transport	0.00044
cell homeostasis	0.00056
nitrogen compound biosynthesis	0.0012
amino acid and derivative metabolism	0.0012
amine biosynthesis	0.0012
establishment of protein localization	0.00143
cofactor metabolism	0.00164
cell ion homeostasis	0.00168
cation homeostasis	0.00194
regulation of pH	0.00198
protein localization	0.00207
protein targeting	0.00236
amino acid biosynthesis	0.00245
amine metabolism	0.00249
monovalent inorganic cation homeostasis	0.00271
intracellular protein transport	0.00286
nitrogen compound metabolism	0.00306
amino acid metabolism	0.00306
protein transport	0.00329
asparagine metabolism	0.00336
regulation of translation	0.00441
organic acid metabolism	0.00463
carboxylic acid metabolism	0.00463
regulation of protein biosynthesis	0.00553
aspartate family amino acid catabolism	0.00555
generation of precursor metabolites and energy	0.00583
aspartate family amino acid metabolism	0.00617
coenzyme metabolism	0.00677
cellular response to nitrogen levels	0.00856
asparagine catabolism	0.00856
cellular response to nitrogen starvation	0.00856
iron ion homeostasis	0.00917
threonine metabolism	0.00935
glutamine family amino acid metabolism	0.00963
biogenic amine biosynthesis	0.0116
glutamine family amino acid biosynthesis	0.01184
malate metabolism	0.01235
water-soluble vitamin metabolism	0.01408
vitamin metabolism	0.01408
ion transport	0.01452
amino acid derivative metabolism	0.01487
vacuolar acidification	0.0153
hydrogen ion homeostasis	0.0153
pH reduction	0.0153
proton transport	0.0153
serine family amino acid metabolism	0.0153
cellular pH reduction	0.0153

regulation of cellular pH	0.0153
hydrogen transport	0.0153
pyridine nucleotide metabolism	0.01616
ribosomal small subunit assembly and maintenance	0.0182
cation transport	0.01821
energy derivation by oxidation of organic compounds	0.01923
biogenic amine metabolism	0.01931
response to inorganic substance	0.01979
amino acid derivative biosynthesis	0.01979
regulation of protein metabolism	0.02023
tryptophan metabolism	0.0222
indole and derivative metabolism	0.0222
indolalkylamine biosynthesis	0.0222
indole derivative metabolism	0.0222
indole derivative biosynthesis	0.0222
indolalkylamine metabolism	0.0222
aromatic amino acid family biosynthesis, anthranilate pathway	0.0222
tryptophan biosynthesis	0.0222
SRP-dependent cotranslational protein targeting to membrane, translocation	0.0222
oxidoreduction coenzyme metabolism	0.02238
protein import	0.02268
regulation of biosynthesis	0.02341
regulation of cellular biosynthesis	0.02341
metal ion homeostasis	0.02475
protein import into mitochondrial matrix	0.02515
main pathways of carbohydrate metabolism	0.02537
cofactor biosynthesis	0.02537
homoserine metabolism	0.02582
signal peptide processing	0.02582
glyoxylate cycle	0.02611
ribosomal small subunit export from nucleus	0.02611
glyoxylate metabolism	0.02611
budding cell bud growth	0.02739
alcohol biosynthesis	0.02739
non-developmental growth	0.02739
coenzyme biosynthesis	0.02765
nucleotide metabolism	0.02796
cell budding	0.03545
asexual reproduction	0.03545
peptide metabolism	0.03906
protein secretion	0.03906
heterocycle metabolism	0.04008
spermidine biosynthesis	0.04027
nicotinate nucleotide salvage	0.04027
pyridine nucleotide salvage	0.04027
GDP-mannose biosynthesis	0.04027
S-adenosylmethionine transport	0.04027
glutathione biosynthesis	0.04027
nucleotide salvage	0.04027
nucleotide-sugar biosynthesis	0.04027
spermidine metabolism	0.04027
mannose biosynthesis	0.04027
GDP-mannose metabolism	0.04027
nicotinate nucleotide metabolism	0.04027
lysyl-tRNA aminoacylation	0.04027
SRP-dependent cotranslational protein targeting to membrane	0.04133
peroxisome organization and biogenesis	0.04146
growth	0.04212
serine family amino acid biosynthesis	0.04306

response to starvation	0.0431
branched chain family amino acid metabolism	0.0431
cellular response to starvation	0.0431
cellular response to extracellular stimulus	0.0431
cellular response to stimulus	0.0431
cellular response to nutrient levels	0.0431
protein modification	0.04387
ubiquitin cycle	0.04543
regulation of translational initiation	0.04553
response to copper ion	0.04553
protein import into mitochondrial intermembrane space	0.04553
proteasome assembly	0.04553
sulfur amino acid transport	0.04553
response to extracellular stimulus	0.04709
response to nutrient levels	0.04709
response to external stimulus	0.04709
di-, tri-valent inorganic cation homeostasis	0.05078
nucleobase biosynthesis	0.0511
ribosomal large subunit biogenesis	0.0511
monovalent inorganic cation transport	0.05111
protein processing	0.05385
response to metal ion	0.05462
siderophore transport	0.05552
protein import into mitochondrial inner membrane	0.05552
glycerol metabolism	0.05552
polyol metabolism	0.05552
ribonucleotide biosynthesis	0.05562
glutamate biosynthesis	0.05678
alcohol metabolism	0.05945
phosphorylation	0.06599
histone acetylation	0.0671
thiamin and derivative biosynthesis	0.06784
negative regulation of translation	0.07031
manganese ion transport	0.07031
cytokinesis, completion of separation	0.07031
negative regulation of cellular biosynthesis	0.07031
microautophagy	0.07031
L-amino acid transport	0.07031
negative regulation of protein biosynthesis	0.07031
poly(A)+ mRNA export from nucleus	0.07031
mitochondrial protein processing	0.07031
negative regulation of biosynthesis	0.07031
dicarboxylic acid metabolism	0.07031
invasive growth (sensu Saccharomyces)	0.07187
ribonucleotide metabolism	0.07268
NADPH regeneration	0.07273
cotranslational protein targeting to membrane	0.07468
protein catabolism	0.0747
iron-sulfur cluster assembly	0.07517
metallo-sulfur cluster assembly	0.07517
budding cell isotropic bud growth	0.07517
cell communication	0.07608
vacuolar transport	0.07674
hexose biosynthesis	0.0788
monosaccharide biosynthesis	0.0788
amino acid catabolism	0.0788
vesicle fusion	0.0788
nucleotide biosynthesis	0.0798
protein targeting to ER	0.0811

nucleobase metabolism	0.0811
proline biosynthesis	0.08188
mannose metabolism	0.08188
sodium ion homeostasis	0.08188
positive regulation of cellular biosynthesis	0.08188
vesicle coating	0.08188
glycerol catabolism	0.08188
positive regulation of protein biosynthesis	0.08188
homoserine biosynthesis	0.08188
positive regulation of translation	0.08188
positive regulation of protein metabolism	0.08188
polyol biosynthesis	0.08188
polyol catabolism	0.08188
threonine catabolism	0.08188
glycerol biosynthesis	0.08188
positive regulation of biosynthesis	0.08188
transition metal ion homeostasis	0.0819
purine ribonucleotide biosynthesis	0.08216
tricarboxylic acid cycle intermediate metabolism	0.08275
ribonucleoside triphosphate biosynthesis	0.08852
ribonucleoside triphosphate metabolism	0.08852
acetyl-CoA catabolism	0.09088
negative regulation of protein metabolism	0.09088
protein targeting to peroxisome	0.09088
pyrimidine base biosynthesis	0.09088
tricarboxylic acid cycle	0.09088
nicotinamide metabolism	0.09305
cellular protein catabolism	0.09447
phosphorus metabolism	0.09468
phosphate metabolism	0.09468
ubiquitin-dependent protein catabolism	0.09563
modification-dependent protein catabolism	0.09563
modification-dependent macromolecule catabolism	0.09563
regulation of cell redox homeostasis	0.09783
cell redox homeostasis	0.09783
thiamin and derivative metabolism	0.09934
protein refolding	0.09989
phosphatidylcholine biosynthesis	0.09989
NAD biosynthesis	0.09989
calcium-mediated signaling	0.09989
'de novo' protein folding	0.09989
Not yet annotated	

NQ Protease Gene list

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YJR161C
YKL206C
YDR258C
YEL045C
YNR017W
YGR198W
YBR236C
YGL173C

NQ Protease

GO_term	Probability
regulation of signal transduction	0.00096
1,6-beta-glucan biosynthesis	0.00375
transcription from RNA polymerase I promoter	0.0043
1,6-beta-glucan metabolism	0.00577
cortical cytoskeleton organization and biogenesis	0.00577
cortical actin cytoskeleton organization and biogenesis	0.00577
vitamin B6 metabolism	0.01415
beta-glucan biosynthesis	0.01415
pyridoxine metabolism	0.01415
phosphorus metabolism	0.01418
phosphate metabolism	0.01418
signal transduction	0.01647
beta-glucan metabolism	0.01766
protein amino acid phosphorylation	0.01802
phosphorylation	0.01827
ergosterol metabolism	0.01906
ergosterol biosynthesis	0.01906
endocytosis	0.03028
cell communication	0.03131
sterol biosynthesis	0.03302
biopolymer biosynthesis	0.03858
polysaccharide biosynthesis	0.03858
actin cortical patch assembly	0.03976
actin filament organization	0.04907
peroxisome organization and biogenesis	0.05443
steroid biosynthesis	0.05443
thiamin biosynthesis	0.05616
response to metal ion	0.05616
sterol metabolism	0.05792
transcription from RNA polymerase III promoter	0.05792
cellular lipid metabolism	0.06017
cell wall polysaccharide biosynthesis (sensu Fungi)	0.06207
thiamin and derivative biosynthesis	0.06207
thiamin metabolism	0.06207
protein deubiquitination	0.06818
cell surface receptor linked signal transduction	0.069
thiamin and derivative metabolism	0.07448
glucan biosynthesis	0.07448
lipid metabolism	0.07952
response to inorganic substance	0.08096
steroid metabolism	0.08941
translational initiation	0.09376
signal transduction during conjugation with cellular fusion	0.09441
regulation of conjugation with cellular fusion	0.09441
regulation of conjugation	0.09441
pheromone-dependent signal transduction during conjugation with cellular fusion	0.09441
Not yet annotated	

Stationary phase protease gene list

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Stationary phase protease	Probability
generation of precursor metabolites and energy	9.64E-13
main pathways of carbohydrate metabolism	3.94E-12
Ty element transposition	4.78E-10
transposition, DNA-mediated	7.30E-10
transposition	7.30E-10
energy derivation by oxidation of organic compounds	9.35E-10
cofactor metabolism	2.04E-09
coenzyme metabolism	2.44E-09
organic acid metabolism	1.77E-08
carboxylic acid metabolism	1.77E-08
carbohydrate metabolism	1.10E-07
acetyl-CoA metabolism	1.59E-07
tricarboxylic acid cycle intermediate metabolism	4.12E-07
cellular carbohydrate metabolism	5.03E-07
tricarboxylic acid cycle	6.56E-07
acetyl-CoA catabolism	6.56E-07
coenzyme catabolism	2.75E-06
cofactor catabolism	5.23E-06
pyruvate metabolism	8.83E-06
DNA recombination	1.14E-05
alcohol biosynthesis	1.37E-05
amino acid biosynthesis	2.05E-05
hydrogen transport	3.07E-05
proton transport	3.07E-05
glutamine family amino acid metabolism	3.45E-05
nucleotide metabolism	3.56E-05
hexose biosynthesis	4.86E-05
monosaccharide biosynthesis	4.86E-05
nitrogen compound biosynthesis	5.46E-05
amine biosynthesis	5.46E-05
glucose metabolism	5.96E-05
oxidative phosphorylation	8.79E-05
catabolism	8.83E-05
hexose metabolism	9.39E-05
cellular catabolism	9.95E-05
glutamine family amino acid biosynthesis	0.00011
glutamate metabolism	0.00015
monosaccharide metabolism	0.00017
alcohol metabolism	0.00019
gluconeogenesis	0.00025
monovalent inorganic cation transport	0.00033
pyridine nucleotide metabolism	0.00036
vitamin metabolism	0.00036
water-soluble vitamin metabolism	0.00036
carbohydrate biosynthesis	0.00052
cellular respiration	0.00053
glutamate biosynthesis	0.00055
purine ribonucleoside triphosphate metabolism	0.00061
purine ribonucleoside triphosphate biosynthesis	0.00061
purine nucleoside triphosphate metabolism	0.00061
purine nucleoside triphosphate biosynthesis	0.00061
cofactor biosynthesis	0.00064
glucose catabolism	0.00065
aerobic respiration	0.00078
hexose catabolism	0.00088
NADPH regeneration	0.00093
ATP metabolism	0.00095
nucleoside phosphate metabolism	0.00095

energy coupled proton transport, down electrochemical gradient	0.00095
ATP synthesis coupled proton transport	0.00095
ATP biosynthesis	0.00095
oxidoreduction coenzyme metabolism	0.00101
cell wall organization and biogenesis	0.00102
external encapsulating structure organization and biogenesis	0.00102
homeostasis	0.00107
alcohol catabolism	0.00112
nicotinamide metabolism	0.00117
ribonucleoside triphosphate biosynthesis	0.00127
ribonucleoside triphosphate metabolism	0.00127
monosaccharide catabolism	0.00132
purine ribonucleotide biosynthesis	0.00132
response to stress	0.00164
isocitrate metabolism	0.00201
coenzyme biosynthesis	0.00204
purine ribonucleotide metabolism	0.00219
ribonucleotide biosynthesis	0.00219
ribosomal small subunit assembly and maintenance	0.0023
nucleoside triphosphate biosynthesis	0.00244
phosphorylation	0.00269
amino acid metabolism	0.00275
endocytosis	0.00275
cell homeostasis	0.00283
cation transport	0.00288
protein targeting to mitochondrion	0.00297
ion transport	0.00315
nucleoside triphosphate metabolism	0.00329
amino acid and derivative metabolism	0.00334
NADP metabolism	0.00341
ribonucleotide metabolism	0.0035
nucleotide biosynthesis	0.00364
dicarboxylic acid metabolism	0.00434
purine nucleotide biosynthesis	0.00436
group transfer coenzyme metabolism	0.00436
response to oxidative stress	0.00437
mitochondrion distribution	0.00513
mitochondrion localization	0.00513
mitochondrion inheritance	0.00513
regulation of protein metabolism	0.0054
calcium-dependent cell-cell adhesion	0.00541
flocculation via cell wall protein-carbohydrate interaction	0.00541
asparagine metabolism	0.00541
flocculation	0.00541
mitochondrial electron transport, succinate to ubiquinone	0.00561
regulation of transcription from RNA polymerase I promoter	0.00561
glycolysis	0.00598
electron transport	0.00612
oxygen and reactive oxygen species metabolism	0.00621
ion homeostasis	0.00637
regulation of biosynthesis	0.0065
regulation of cellular biosynthesis	0.0065
protein folding	0.00653
protein catabolism	0.00667
cellular protein catabolism	0.0074
purine nucleotide metabolism	0.00802
regulation of transcription from RNA polymerase III promoter	0.00816
heterophilic cell adhesion	0.00851
aspartate family amino acid catabolism	0.00882

cellular macromolecule catabolism	0.00918
regulation of translation	0.00966
response to stimulus	0.01038
amine metabolism	0.01079
regulation of pH	0.01131
regulation of protein biosynthesis	0.01195
cellular response to nitrogen starvation	0.01197
asparagine catabolism	0.01197
cellular response to nitrogen levels	0.01197
regulation of translational initiation	0.01197
cell-cell adhesion	0.01236
cell redox homeostasis	0.01354
regulation of cell redox homeostasis	0.01354
pentose-phosphate shunt	0.01354
cellular localization	0.01364
ATP synthesis coupled electron transport (sensu Eukaryota)	0.01366
ATP synthesis coupled electron transport	0.01366
response to water deprivation	0.01385
response to water	0.01385
pyridoxine metabolism	0.01385
vitamin B6 metabolism	0.01385
response to desiccation	0.01385
phosphate metabolism	0.01525
phosphorus metabolism	0.01525
macromolecule catabolism	0.0157
malate metabolism	0.01606
cell ion homeostasis	0.01955
nitrogen compound metabolism	0.0197
serine family amino acid biosynthesis	0.0198
mitochondrial protein processing	0.0217
glycine metabolism	0.0217
mitochondrion organization and biogenesis	0.02174
translational initiation	0.02352
cellular response to stimulus	0.02355
response to starvation	0.02355
cellular response to extracellular stimulus	0.02355
cellular response to starvation	0.02355
cellular response to nutrient levels	0.02355
ubiquitin cycle	0.02552
cell adhesion	0.02571
amino acid catabolism	0.02706
proteolysis	0.02725
glutamine family amino acid catabolism	0.02778
proteolysis during cellular protein catabolism	0.03004
aromatic compound biosynthesis	0.03117
fermentation	0.03117
SRP-dependent cotranslational protein targeting to membrane, translocation	0.03205
budding cell isotropic bud growth	0.03205
vacuolar protein catabolism	0.03205
glyoxylate metabolism	0.03356
glyoxylate cycle	0.03356
citrate metabolism	0.03356
fatty acid metabolism	0.03368
NAD biosynthesis	0.0352
organelle inheritance	0.03716
ubiquitin-dependent protein catabolism	0.03828
modification-dependent protein catabolism	0.03828
modification-dependent macromolecule catabolism	0.03828
thiamin and derivative biosynthesis	0.04029

intracellular transport	0.04468
amine catabolism	0.04793
nitrogen compound catabolism	0.04793
positive regulation of gluconeogenesis	0.0481
glycine biosynthesis	0.0481
G-protein signaling, adenylate cyclase activating pathway	0.0481
acetyl-CoA biosynthesis from pyruvate	0.0481
nucleotide-sugar biosynthesis	0.0481
sequestering of metal ion	0.0481
lysyl-tRNA aminoacylation	0.0481
intracellular sequestering of iron ion	0.0481
mannose biosynthesis	0.0481
GDP-mannose metabolism	0.0481
GDP-mannose biosynthesis	0.0481
inositolphosphoceramide metabolism	0.0481
L-serine metabolism	0.0481
L-serine biosynthesis	0.0481
2-oxoglutarate metabolism	0.0481
negative regulation of protein metabolism	0.04947
heterocycle metabolism	0.05163
purine ribonucleoside metabolism	0.05263
cell separation during cytokinesis	0.05263
establishment of cellular localization	0.0539
DNA metabolism	0.05699
cation homeostasis	0.05701
propionate metabolism	0.05786
folic acid and derivative biosynthesis	0.05786
actin filament bundle formation	0.05786
actin cable formation	0.05786
intron homing	0.05786
attachment of GPI anchor to protein	0.05786
protein targeting	0.05881
vitamin biosynthesis	0.05889
water-soluble vitamin biosynthesis	0.05889
'de novo' pyrimidine base biosynthesis	0.06066
cellular pH reduction	0.06182
regulation of cellular pH	0.06182
hydrogen ion homeostasis	0.06182
pH reduction	0.06182
vacuolar acidification	0.06182
serine family amino acid metabolism	0.06182
pigment biosynthesis	0.06333
thiamin and derivative metabolism	0.06333
glucan biosynthesis	0.06333
branched chain family amino acid metabolism	0.06336
aromatic amino acid family biosynthesis	0.06336
carbohydrate catabolism	0.06374
cellular carbohydrate catabolism	0.06374
response to abiotic stimulus	0.06413
monovalent inorganic cation homeostasis	0.06665
protein modification	0.06698
aromatic compound metabolism	0.06976
actin filament organization	0.0723
polyol metabolism	0.07395
purine nucleoside metabolism	0.07395
glycerol metabolism	0.07395
ergosterol biosynthesis	0.0742
ergosterol metabolism	0.0742
response to external stimulus	0.0742

response to extracellular stimulus	0.0742
response to nutrient levels	0.0742
pigment metabolism	0.07733
nucleobase biosynthesis	0.07733
asexual reproduction	0.07889
cell budding	0.07889
NAD metabolism	0.07903
branched chain family amino acid biosynthesis	0.07903
Ras protein signal transduction	0.07933
thiamin biosynthesis	0.07933
transcription from RNA polymerase III promoter	0.0832
intracellular protein transport	0.0881
purine ribonucleoside salvage	0.08837
negative regulation of cellular biosynthesis	0.08837
negative regulation of translation	0.08837
negative regulation of biosynthesis	0.08837
poly(A)+ mRNA export from nucleus	0.08837
negative regulation of protein biosynthesis	0.08837
microautophagy	0.08837
organic cation transport	0.08837
ammonium transport	0.08837
nucleoside salvage	0.08837
cytokinesis, completion of separation	0.08837
protein processing	0.08949
biopolymer catabolism	0.09029
protein import into mitochondrial matrix	0.093
budding cell bud growth	0.09615
non-developmental growth	0.09615
regulation of phosphorylation	0.09681
actin nucleation	0.09681
glycosphingolipid metabolism	0.09681
isoleucine metabolism	0.09681
glycosphingolipid biosynthesis	0.09681
protein-tetrapyrrole linkage	0.09681
protein-heme linkage	0.09681
glycerol biosynthesis	0.09681
mannose metabolism	0.09681
homoserine biosynthesis	0.09681
glycolipid biosynthesis	0.09681
glycolipid metabolism	0.09681
negative regulation of phosphorylation	0.09681
polyol biosynthesis	0.09681
cytochrome c-heme linkage	0.09681
negative regulation of phosphate metabolism	0.09681
thiamin metabolism	0.09734
mRNA polyadenylylation	0.09734
RNA polyadenylation	0.09734
establishment of protein localization	0.09795
indolalkylamine metabolism	0.09896
indole derivative biosynthesis	0.09896
iron-sulfur cluster assembly	0.09896
indolalkylamine biosynthesis	0.09896
tryptophan biosynthesis	0.09896
ribonucleoside metabolism	0.09896
arginine biosynthesis	0.09896
tryptophan metabolism	0.09896
pyridine nucleotide biosynthesis	0.09896
metallo-sulfur cluster assembly	0.09896
indole derivative metabolism	0.09896

polyamine transport	0.09896
indole and derivative metabolism	0.09896
aromatic amino acid family biosynthesis, anthranilate pathway	0.09896
aspartate family amino acid metabolism	0.09906
Not yet annotated	

Aging Genes
YCL025C
YJL129C
YIL094C
YDR019C
YER091C-A
YHR204W
YDL173W
YDL172C
YLL007C
YGR057C
YGL197W
YGR027C
YML121W
YHL034C
YLL013C
YBR077C
YJR066W
YEL014C
YKL046C
YDR221W
YHR158C
YPL182C
YGL203C
YJL165C
YGR163W
YLR152C
YOR179C
YNL142W
YPR158W
YHR139C
YGR043C
YKR007W
YPL133C
YGR044C
YOL116W
YCR037C
YHR142W
YHR125W
YDR490C
YKL175W
YGL252C
YKR095W
YBL102W
YHR167W
YGL139W
YIL156W
YHR124W
YHR195W
YLR428C
YPR138C
YHR209W
YPR021C
YER040W
YKR034W
YFR041C
YGL033W
YGR237C
YKL027W
YGR054W
YNL021W
YKL015W
YDR262W
YBR019C
YHR126C
YML066C
YBL042C
YPR031W
YBR030W
YHR003C
YBR248C
YKL001C
YKL081W
YHR064C
YER132C
YGR289C
YPL042C
YGR153W
YNL014W
YDR515W
YGL195W
YGR045C
YIL056W
YKL068W
YGR059W
YBL103C
YKL216W
YHR111W
YGL083W
YNL016W
YLR455W
YBR012C
YGR108W
YMR015C
YDL034W
YML062C
YCR048W
YHR161C
YGL057C
YIL173W
YGR107W
YKR009C
YHR159W
YER137C
YKL044W
YPR156C
YHR157W
YBR028C
YPR011C
YIL157C
YPR114W
YIL058W
YDL215C
YBR220C
YPL145C
YBL066C
YNR049C
YPR157W
YER059W
YBR018C
YBR072W
YBL107C
YJL132W
YLR187W
YIL168W
YIL121W
YNR056C
YPR151C
YGL079W
YIR023W
YGR291C
YCL013W
YOL106W
YBR015C
YMR326C
YKL176C
YPL017C
YLR327C
YBR013C
YBR071W
YPL150W
YBR114W
YGL248W
YPR009W
YDL053C
YKR087C
YIL159W
YIL131C
YLL015W
YIL030C
YJL105W
YJL130C
YPR030W
YGR292W
YPL071C
YDR143C
YDL182W
YEL049W
YKR015C
YPL034W
YIL140W
YDL216C
YNL268W
YLR461W
YEL037C
YDR229W
YOR155C
YNL011C
YJL078C
YHR113W
YIL100W
YOR268C
YAL067C
YDR018C
YBR016W
YPR005C
YLR278C
YKL034W
YJL096W
YPR029C
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YMR118C
YDR357C
YKL184W
YBR116C
YFR017C
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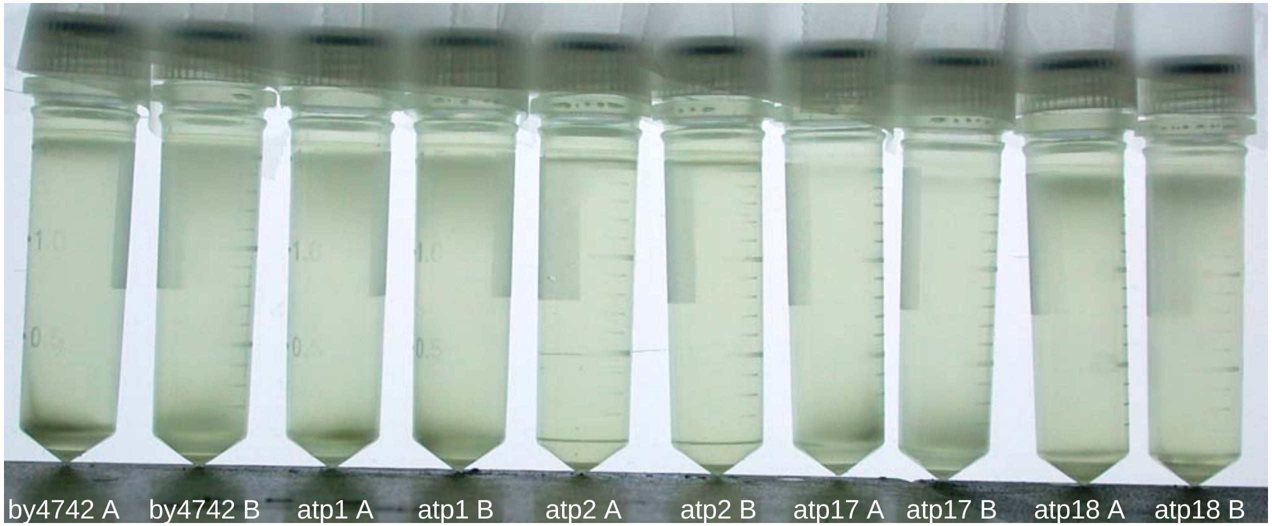
YJL094C
YFL055W
YLR422W
YPL026C
YDR443C
YPL009C
YER170W
YGR250C
YBL087C
YBR040W
YPR091C
YJL103C
YEL008W

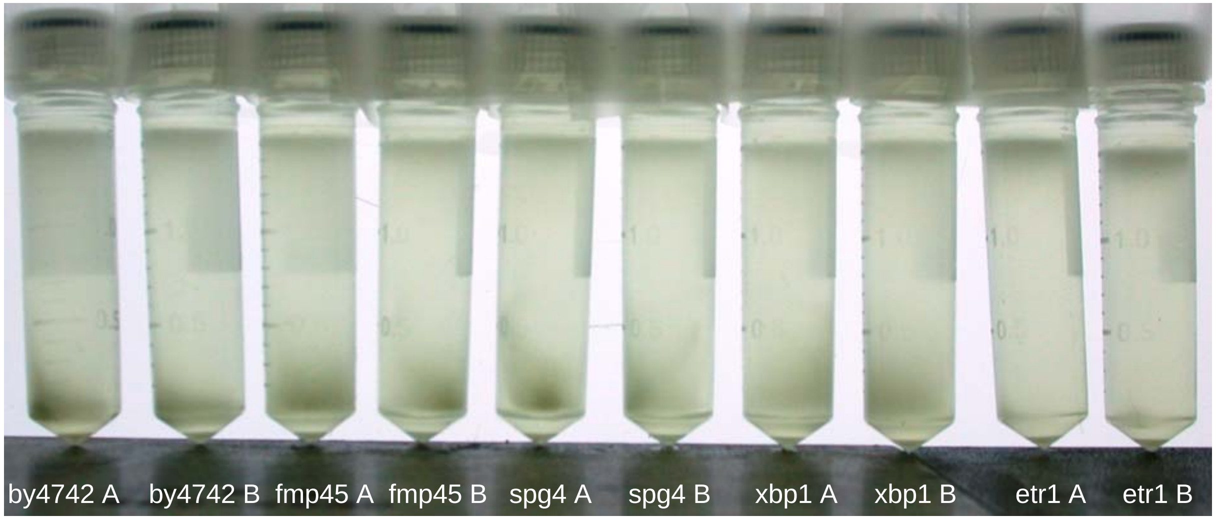
8/30/07



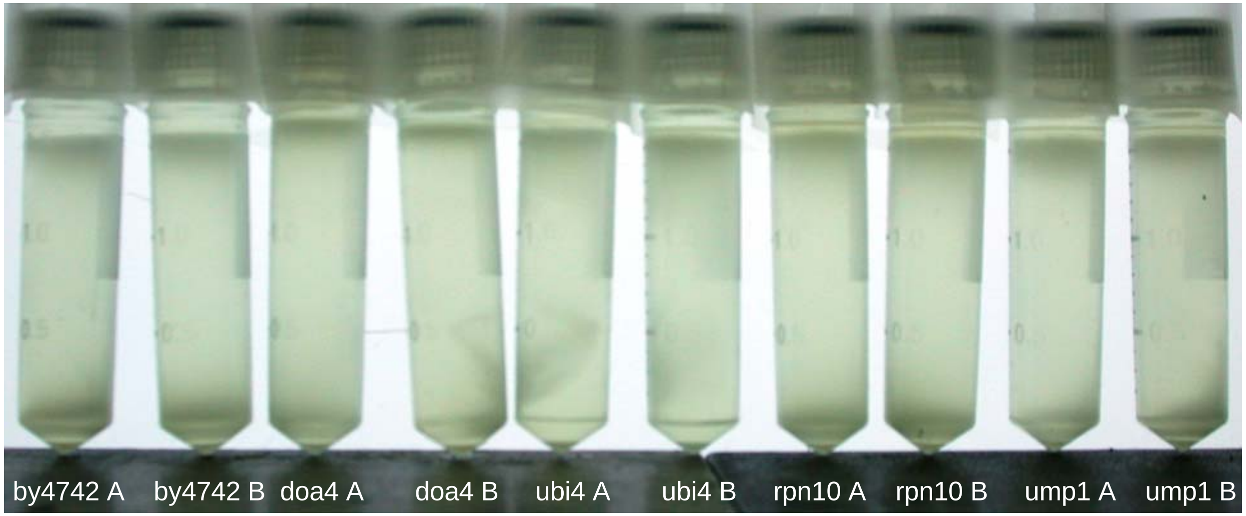
No lower band

*pictures were autocorrected

9/12/07

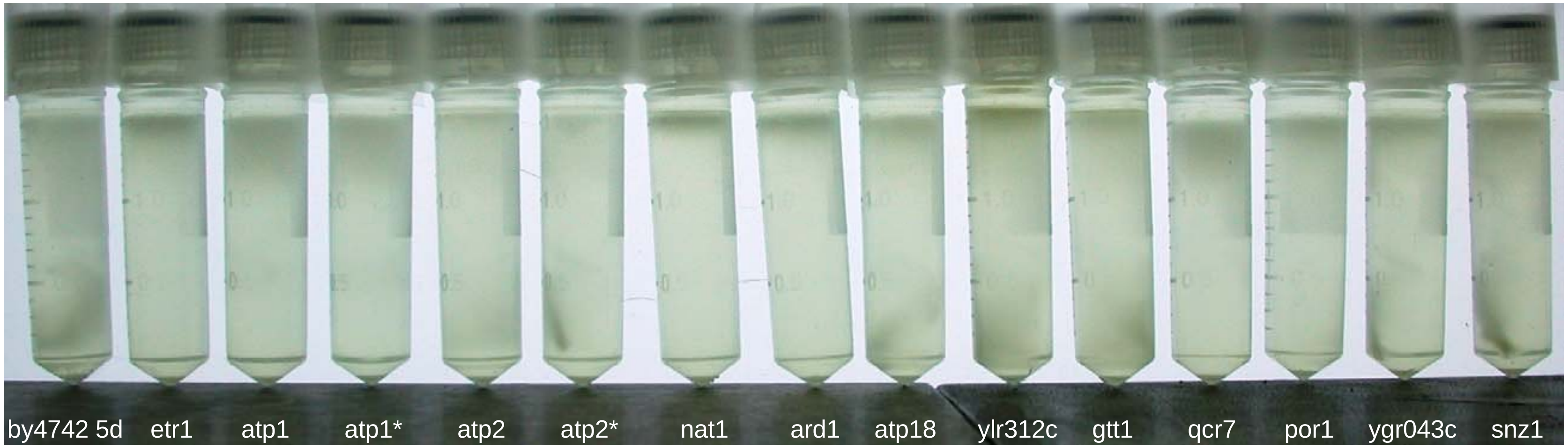


9/12/07



10/16/07

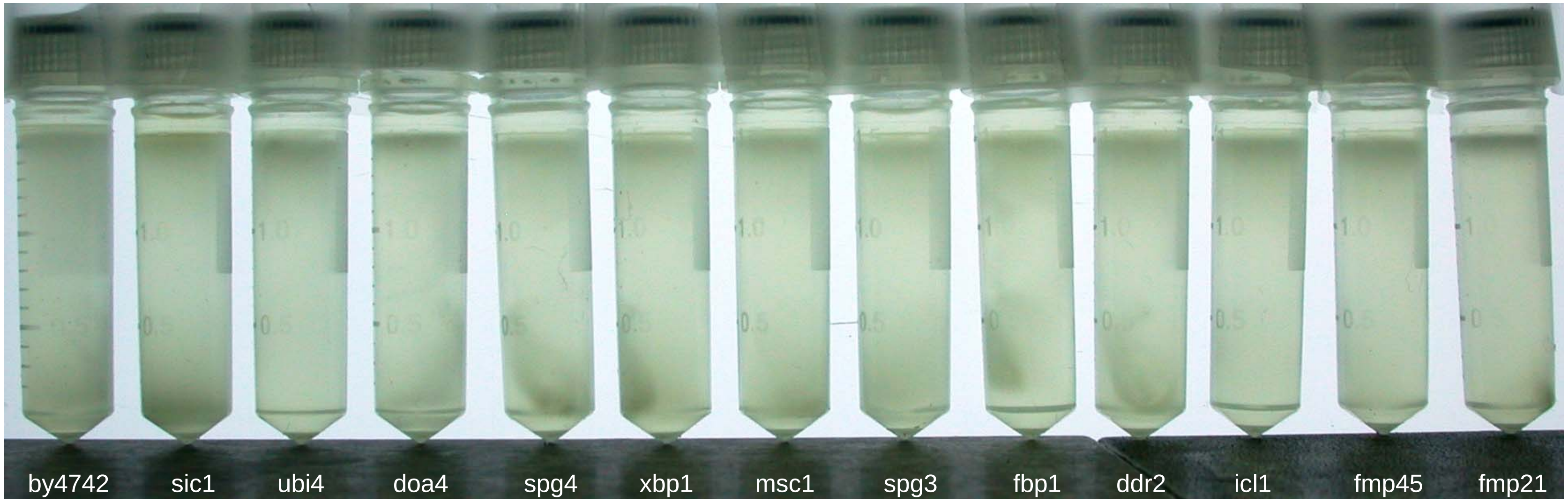
*pictures were autocorrected



No lower band for etr1, nat1, ard1

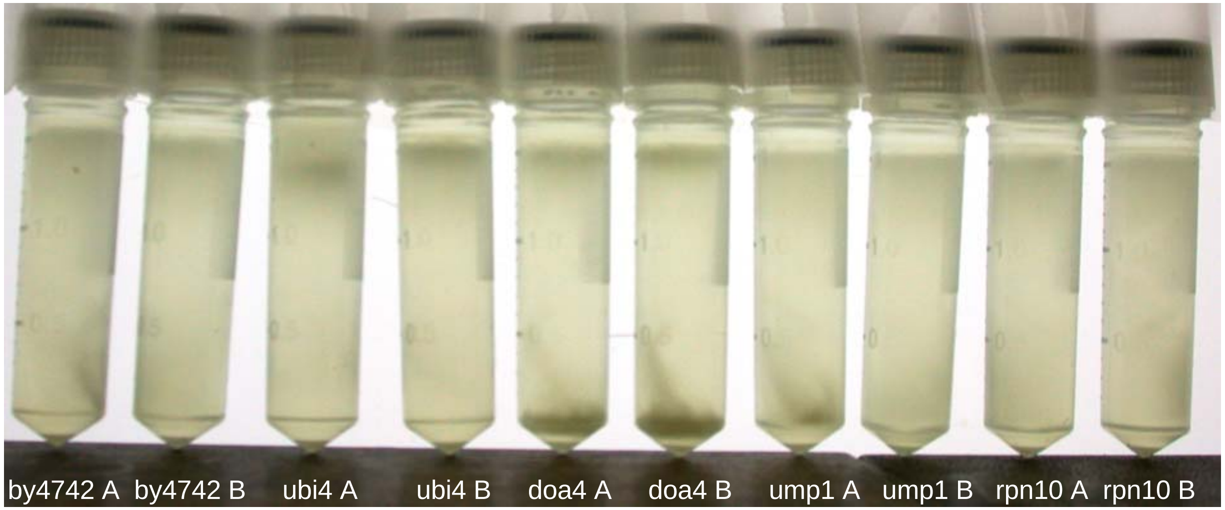
-atp1* and atp2* are from the micro titer dishes (deletion set)

10/16/07



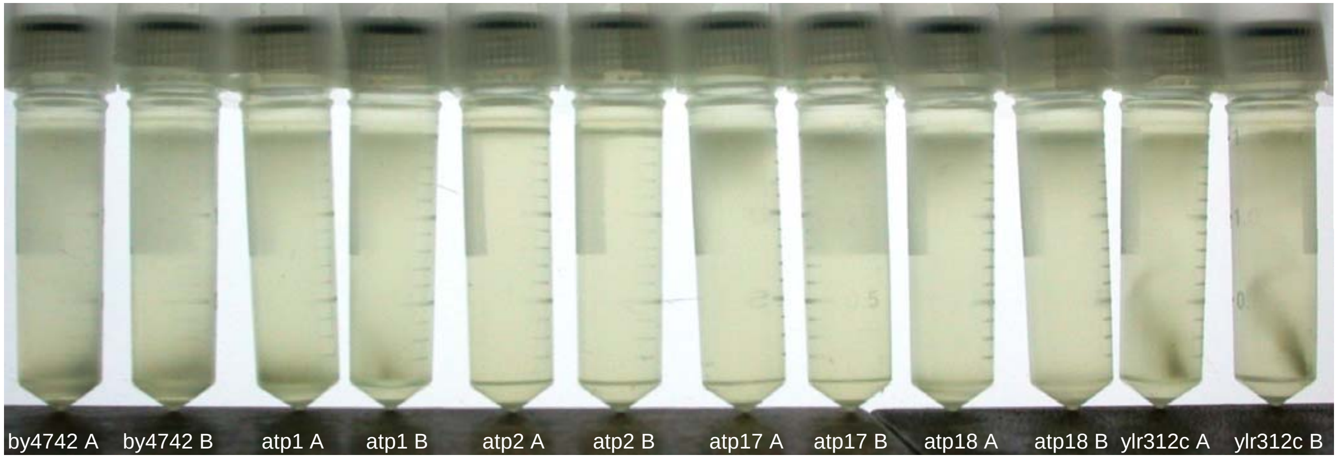
10/26/07

*pictures were autocorrected



Doa4 seems odd in this picture, look at the high concentration of cells *picture was autocorrected

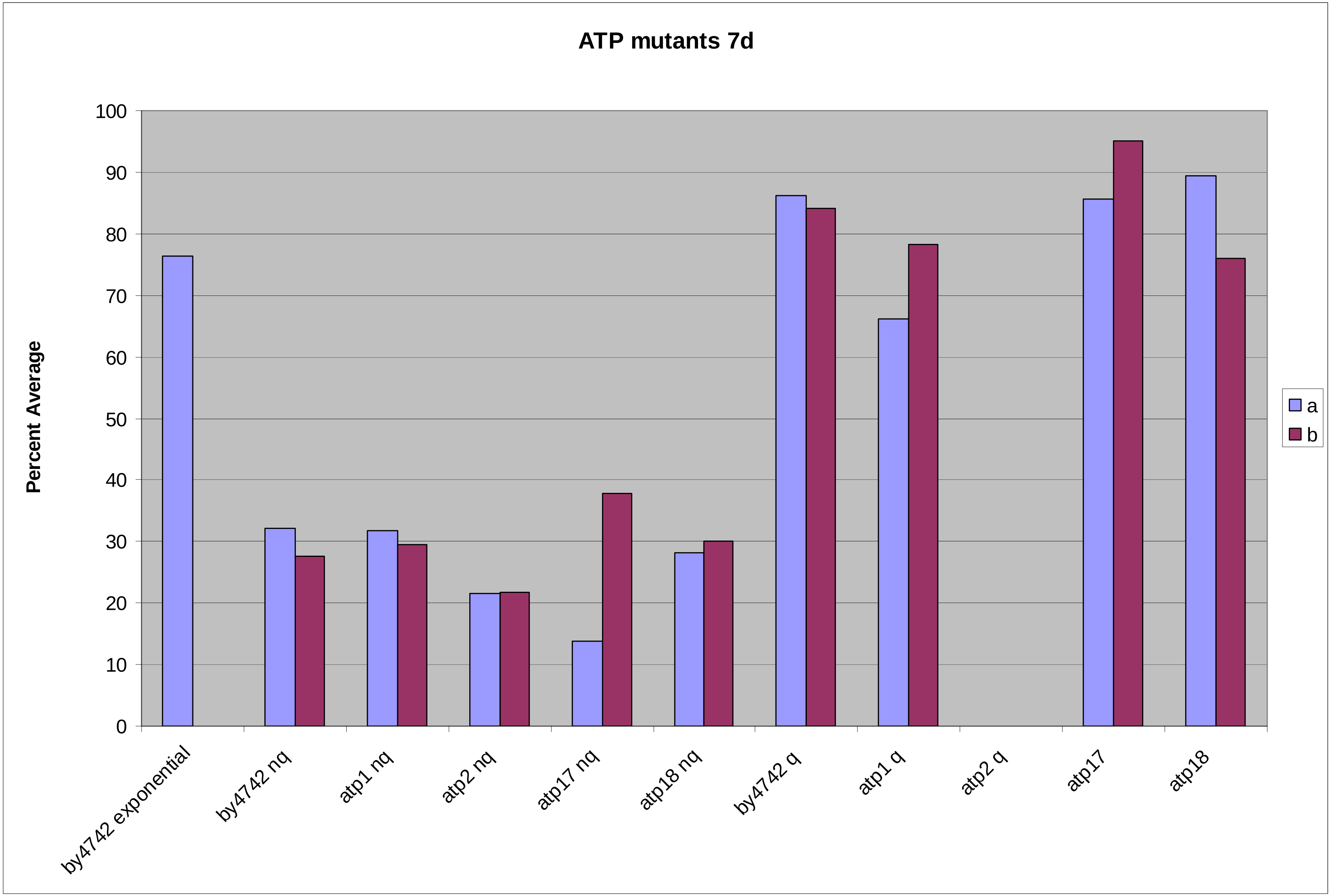
11/2/07

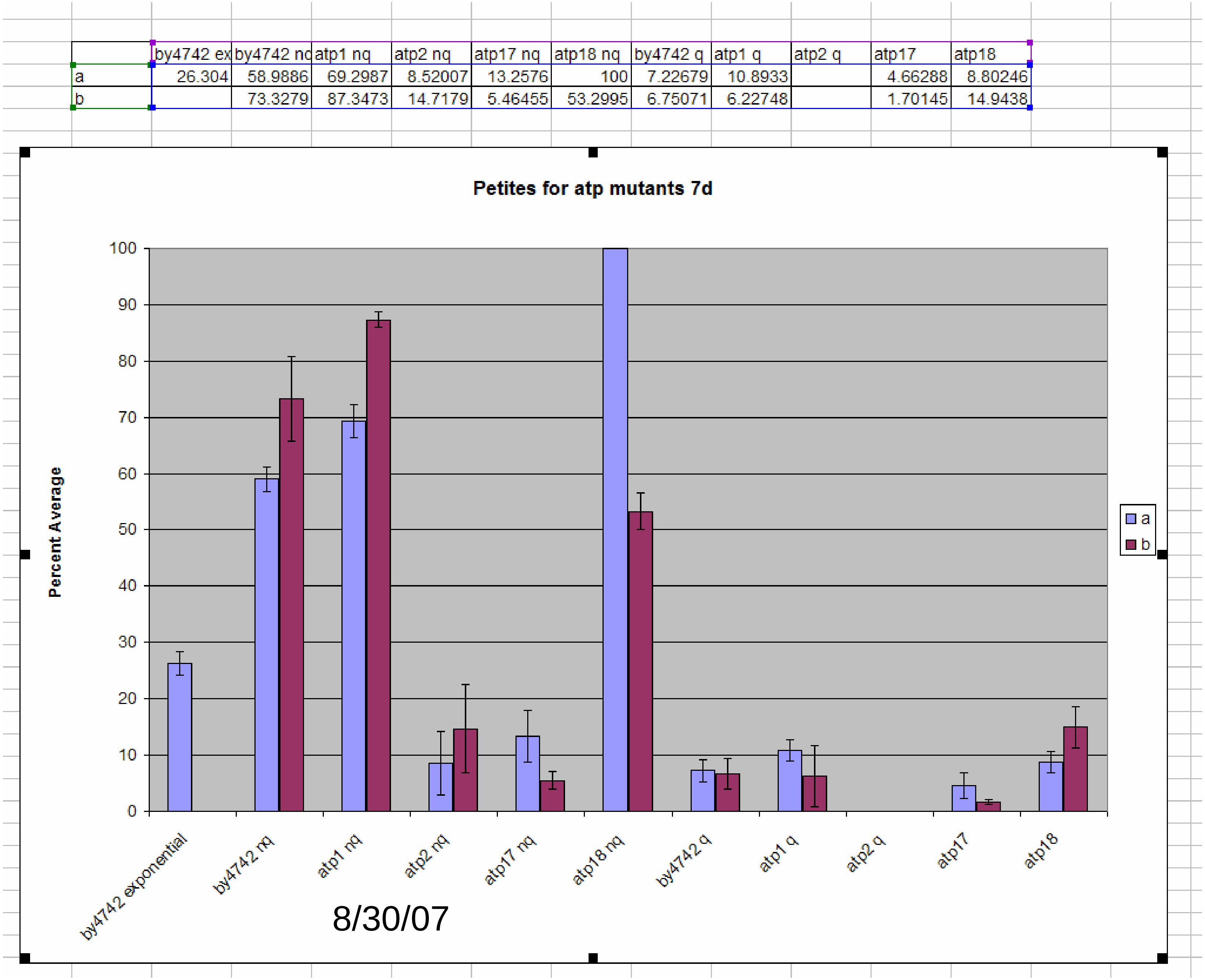


-No lower bands for atp2 and atp17 A&B

9/19/2007

Variability of ATP mutants

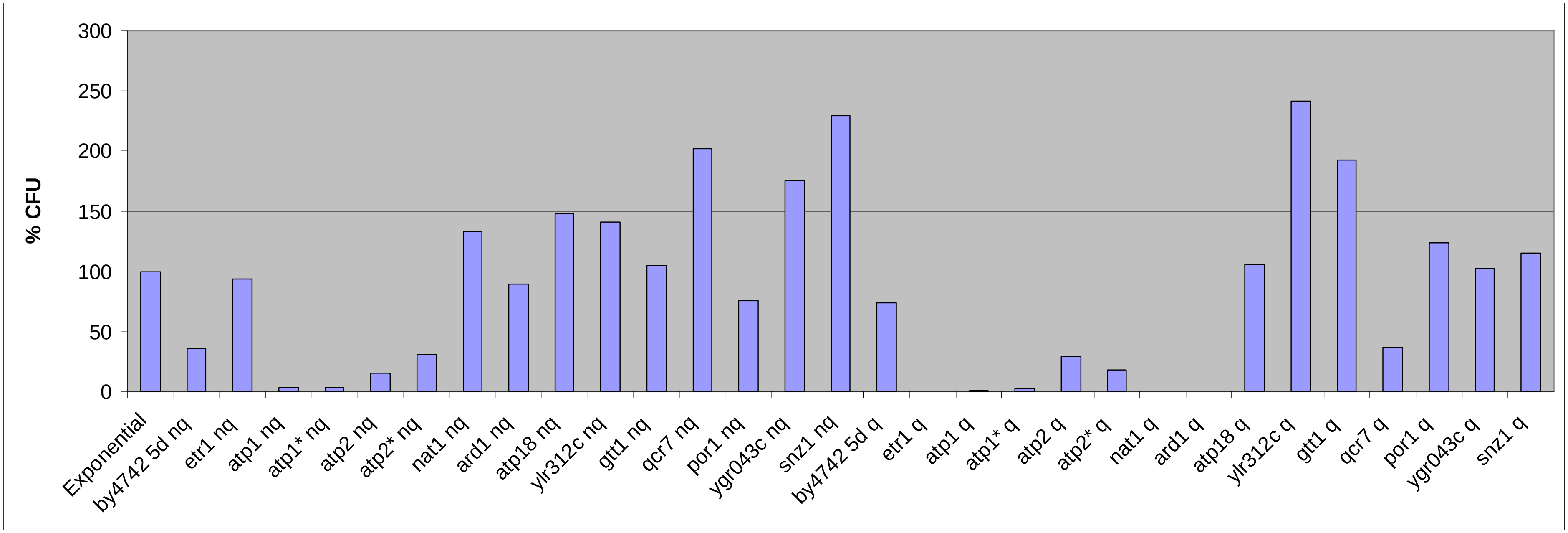




	by4742 ex	by4742 nq	atp1 nq	atp2 nq	atp17 nq	atp18 nq	by4742 q	atp1 q	atp2 q	atp17	atp18
a	26.304	58.9886	69.2987	8.52007	13.2576	100	7.22679	10.8933		4.66288	8.80246
b		73.3279	87.3473	14.7179	5.46455	53.2995	6.75071	6.22748		1.70145	14.9438

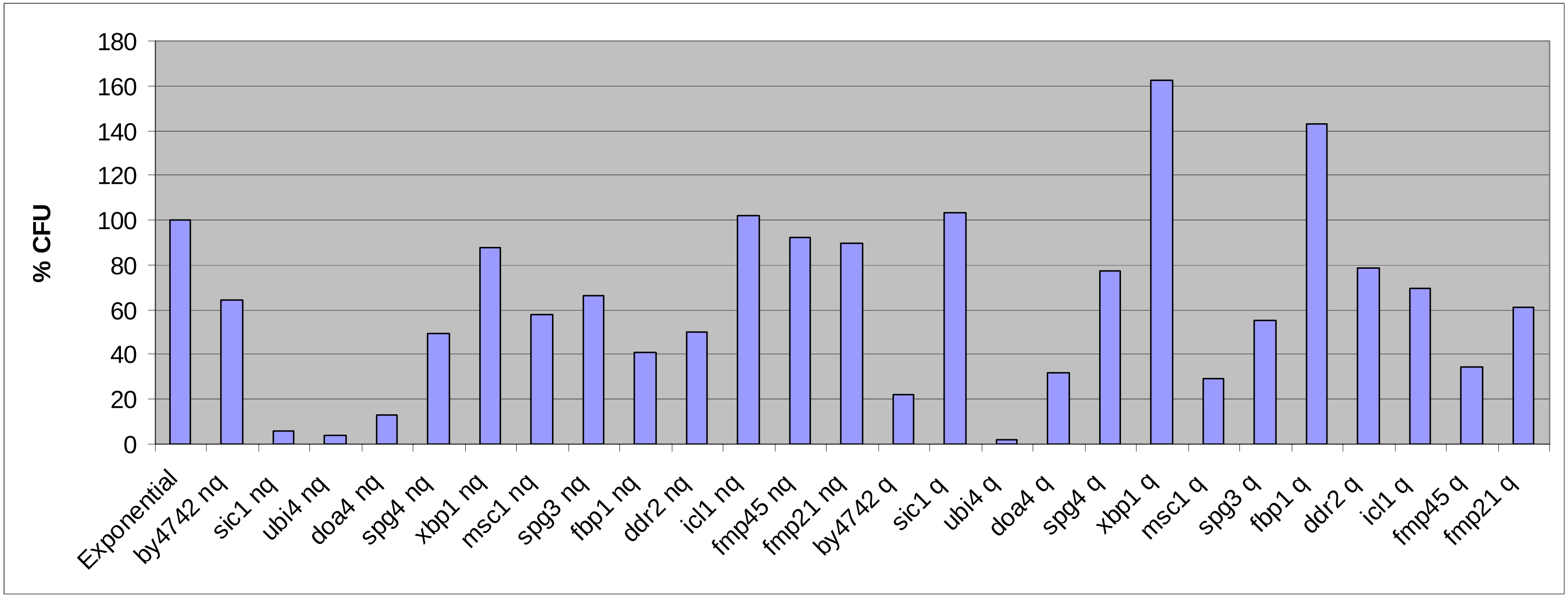
Petites for atp mutants 7d

8/30/07



From 10/16/2007 shows atp1,atp2 acting identically, atp18 different

From 10/18/2007



Shows appropriate xbp1 phenotype, ng parental q numbers

11/18/2007

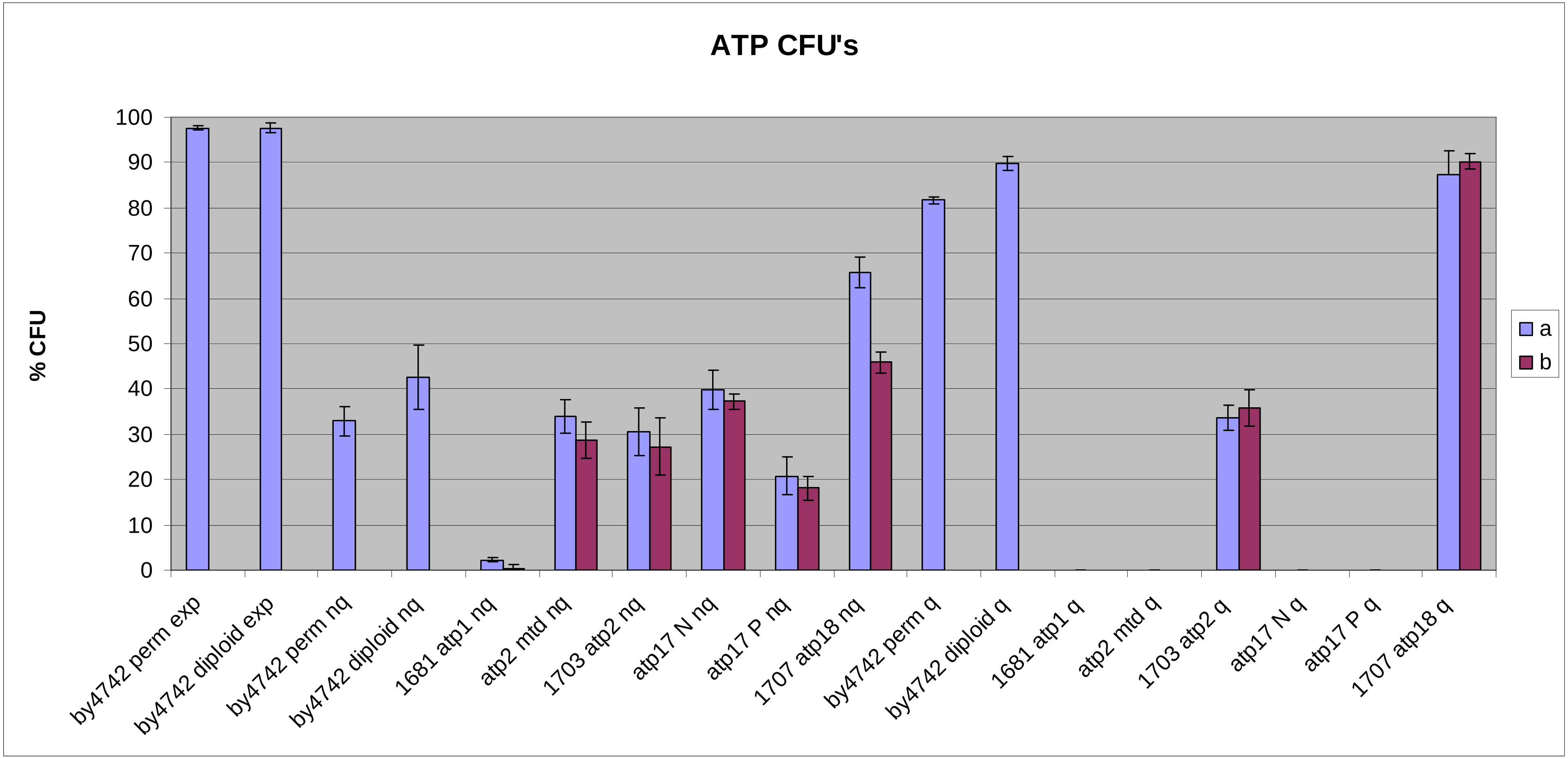

ATP CFU's
% CFU
100
90
80
70
60
50
40
30
20
10
0
a
b
by4742 perm exp
by4742 diploid exp
by4742 perm nq
by4742 diploid nq
1681 atp1 nq
atp2 mtd nq
1703 atp2 nq
atp17 N nq
atp17 P nq
1707 atp18 nq
by4742 perm q
by4742 diploid q
1681 atp1 q
atp2 mtd q
1703 atp2 q
atp17 N q
atp17 P q
1707 atp18 q

Table 1S. Change in viability and reproductive capacity of mutants from the parental strain

Group	Strain	Q viability	Q CFU	NQ viability	NQ CFU	Function[a]
1	*SPG4*	NC	**↓ 55% ± 5.2**	NC	NC	Unknown
2	YLR312C	NC	**↓ 79% ± 9.4**	NC	**↓ 75% ± 6.0**	Unknown
	GTT1		**↓ 71% ± 19.6**		**↓ 54% ± 11.6**	Glutathione transferase[c]
3	YGR043C	NC	NC	NC	**↓ 54% ± 13.4**	Unknown
	SNZ1				**↓ 52% ± 17.6**	Vitamin B6 biosynthesis
	MSC1				**↓ 57% ± 16.5**	Unknown
	FMP21				**↓ 50% ± 10.9**	Unknown[b]
4	*XBP1*	NC	NC	NC	**↑ 83% ± 50.0**	Transcriptional repressor
	FBP1				**↑ 81% ± 32.1**	Gluconeogenesis
	ATP18				**↑ 46% ± 26.8**	ATP synthesis[b]

[a] *Saccharomyces* Genome Database

[b] mitochondrial

[c] endoplasmic reticulum