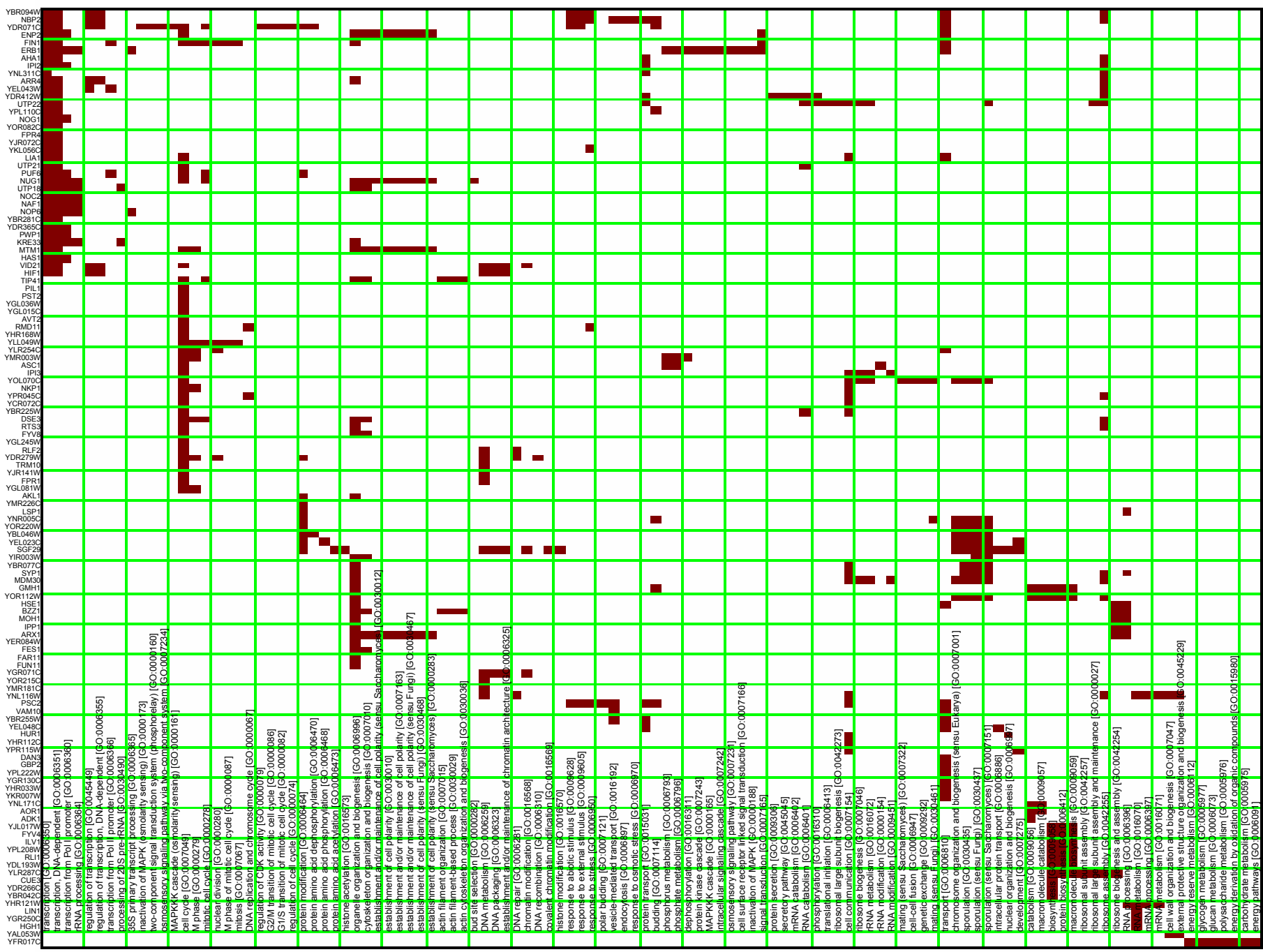


- transcription**
  - transcription, DNA-dependent
  - transcription from Pol I promoter
  - rRNA processing
  - regulation of transcription
  - regulation of transcription, DNA-dependent
  - transcription from Pol II promoter
  - processing of 20S pre-rRNA
  - 35S primary transcript processing
  - inactivation of MAPK (osmolarity sensing)
  - two-component signal transduction system (phosphorelay)
  - osmosensory signaling pathway via two-component system
  - MAPKKK cascade (osmolarity sensing)
- cell cycle**
  - M phase
  - mitotic cell cycle
  - nuclear division
  - M phase of mitotic cell cycle
  - mitosis
  - DNA replication and chromosome cycle
  - regulation of CDK activity
  - G2/M transition of mitotic cell cycle
  - G1/S transition of mitotic cell cycle
  - regulation of cell cycle
- protein modification**
  - protein amino acid dephosphorylation
  - protein amino acid phosphorylation
  - protein amino acid acetylation
  - histone acetylation
- organelle organization and biogenesis**
  - cytoskeleton organization and biogenesis
  - establishment and/or maintenance of cell polarity (sensu Saccharomyces)
  - establishment of cell polarity
  - establishment and/or maintenance of cell polarity
  - establishment and/or maintenance of cell polarity (sensu Fungi)
  - establishment of cell polarity (sensu Fungi)
  - establishment of cell polarity (sensu Saccharomyces)
  - actin filament organization
  - actin filament-based process
  - actin cytoskeleton organization and biogenesis
  - bud site selection
- DNA metabolism**
  - DNA packaging
  - establishment and/or maintenance of chromatin architecture
  - DNA repair
  - chromatin modification
  - DNA recombination
  - covalent chromatin modification
  - histone modification



YBR084W  
NB23  
YDR071C  
ENP2  
FIN1  
ERB1  
AHA1  
IPB2  
YNL31C  
ARR4  
YEL043W  
YDR124W  
UTP22  
YPL110C  
NOC5  
YOR082C  
FPR4  
YJR072C  
YKL058C  
LIA1  
UTP21  
PUF8  
NUG1  
UTP18  
NOC2  
NAF1  
NOP6  
YBR281C  
YDR365C  
PWP1  
KRE33  
MTM1  
HAS1  
VID21  
HIF1  
TIP41  
PLL1  
PS12  
YGL036W  
YGL015C  
AVT2  
RMD11  
YHR168W  
YFL049W  
YLR254C  
YMR003W  
ASC1  
IPB1  
YOL070C  
NKP1  
YPR045C  
YCR072C  
YBR225W  
DSE3  
RTS3  
FYV8  
YGL245W  
RLF2  
YDR279W  
RPM1  
YJR141W  
FPR1  
YGL081W  
AK1  
YMR226C  
LSP1  
YNR005C  
YOR220W  
YBL046W  
YGL003C  
SGF28  
YIR003W  
YBR077C  
SVY1  
MDM30  
GMH1  
MOM1  
YOR112W  
HSE1  
BZZ1  
YOL117W  
IPP1  
ARX1  
YER084W  
FES1  
FAR11  
FUN1  
YGR071C  
YOR216C  
YMR181C  
YNL110W  
PSC2  
VAM10  
YBR255W  
YEL049C  
HUR1  
YHR110C  
YPR115W  
DAN5  
GAS1  
YPL222W  
YGR130C  
YHR033W  
YGR040C  
YNL171C  
AOR1  
RPL1  
YPL200W  
CUE3  
YDR265C  
YBR121W  
YHR121W  
LNU1  
YHR121W  
GH1  
YAL053W  
YFR017C

transcription, DNA-dependent [GO:0006351]  
transcription from Pol I promoter [GO:0006361]  
RNA processing [GO:0006381]  
regulation of transcription [GO:0042449]  
regulation of transcription, DNA-dependent [GO:0006385]  
transcription from Pol I promoter [GO:0006396]  
processing of 23S rRNA [GO:0006397]  
35S primary transcript processing [GO:0006398]  
transcription of small subunit rRNA [GO:0006399]  
transcription of large subunit rRNA [GO:0006400]  
transcription of 5.8S rRNA [GO:0006401]  
transcription of 5S rRNA [GO:0006402]  
MAPK cascade (osmolarity sensor) [GO:0006416]  
cell cycle [GO:0006418]  
M phase [GO:0006419]  
mitotic cell cycle [GO:0006420]  
nuclear division [GO:0006421]  
M phase of mitotic cell cycle [GO:0006422]  
DNA replication [GO:0006423]  
DNA replication and chromosome cycle [GO:0006424]  
regulation of G1/S activity [GO:0006425]  
S2/M transition of mitotic cell cycle [GO:0006426]  
G1/S transition of mitotic cell cycle [GO:0006427]  
regulation of cell cycle [GO:0006428]  
protein modification [GO:0006429]  
protein amino acid dephosphorylation [GO:0006430]  
protein amino acid phosphorylation [GO:0006431]  
protein amino acid acetylation [GO:0006432]  
histone acetylation [GO:0006433]  
organelle organization and biogenesis [GO:0006434]  
cytoskeleton organization and biogenesis [GO:0006435]  
establishment and/or maintenance of cell polarity [sensu Sarcophaga] [GO:0006436]  
establishment and/or maintenance of cell polarity [sensu Drosophila] [GO:0006437]  
establishment and/or maintenance of cell polarity [sensu Anopheles] [GO:0006438]  
establishment and/or maintenance of cell polarity [sensu Culex] [GO:0006439]  
establishment and/or maintenance of cell polarity [sensu Aedes] [GO:0006440]  
actin filament organization [GO:0006441]  
actin filament-based process [GO:0006442]  
actin cytoskeleton organization and biogenesis [GO:0006443]  
bud site selection [GO:0006444]  
DNA metabolism [GO:0006445]  
DNA packaging [GO:0006446]  
establishment and/or maintenance of chromatin architecture [GO:0006447]  
DNA repair [GO:0006448]  
chromatin modification [GO:0006449]  
chromatin organization [GO:0006450]  
DNA recombination [GO:0006451]  
covalent chromatin modification [GO:0006452]  
histone modification [GO:0006453]  
response to abiotic stimulus [GO:0006454]  
response to external stimulus [GO:0006455]  
response to stress [GO:0006456]  
polar budding [GO:0006457]  
vesicle-mediated transport [GO:0006458]  
endocytosis [GO:0006459]  
response to osmotic stress [GO:0006460]  
protein transport [GO:0006461]  
budding [GO:0006462]  
phosphorus metabolism [GO:0006463]  
nitrogen metabolism [GO:0006464]  
biogenic amine metabolism [GO:0006465]  
lipid metabolism [GO:0006466]  
lipid synthesis [GO:0006467]  
MAPK cascade [GO:0006468]  
intracellular signaling cascade [GO:0006469]  
cell surface receptor linked signal transduction [GO:0006470]  
inactivation of MAPK [GO:0006471]  
signal transduction [GO:0006472]  
protein secretion [GO:0006473]  
secretory pathway [GO:0006474]  
mRNA metabolism [GO:0006475]  
RNA catabolism [GO:0006476]  
phosphorylation [GO:0006477]  
translational initiation [GO:0006478]  
ribosomal large subunit biogenesis [GO:0006479]  
cell communication [GO:0006480]  
ribosome biogenesis [GO:0006481]  
RNA metabolism [GO:0006482]  
RNA modification [GO:0006483]  
RNA maturation [GO:0006484]  
RNA processing [GO:0006485]  
mating [sensu Saccharomycetes] [GO:0006486]  
cell-cell fusion [GO:0006487]  
genetic exchange [GO:0006488]  
mating [sensu Ascomycota] [GO:0006489]  
mating [sensu Basidiomycota] [GO:0006490]  
transcription of protein-coding genes and biogenesis (sensu Eukarya) [GO:0006491]  
sporulation (sensu Eukarya) [GO:0006492]  
sporulation (sensu Sarcophagales) [GO:0006493]  
sporulation (sensu Streptomyces) [GO:0006494]  
intracellular protein transport [GO:0006495]  
nuclear organization and biogenesis [GO:0006496]  
development [GO:0006497]  
catabolism [GO:0006498]  
macromolecule catabolism [GO:0006499]  
protein biosynthesis [GO:0006500]  
protein biosynthesis [GO:0006501]  
macromolecule biosynthesis [GO:0006502]  
ribosomal subunit assembly [GO:0006503]  
ribosomal large subunit assembly and maintenance [GO:0006504]  
ribosome assembly [GO:0006505]  
ribosome biogenesis and assembly [GO:0006506]  
RNA processing [GO:0006507]  
RNA processing [GO:0006508]  
mRNA processing [GO:0006509]  
cell wall organization and biogenesis [GO:0006510]  
external protective structure organization and biogenesis [GO:0006511]  
energy reserve metabolism [GO:0006512]  
glycogen metabolism [GO:0006513]  
glucan metabolism [GO:0006514]  
polysaccharide metabolism [GO:0006515]  
energy storage [GO:0006516]  
energy storage [GO:0006517]  
energy storage [GO:0006518]  
energy storage [GO:0006519]  
energy storage [GO:0006520]  
energy storage [GO:0006521]  
energy storage [GO:0006522]  
energy storage [GO:0006523]  
energy storage [GO:0006524]  
energy storage [GO:0006525]  
energy storage [GO:0006526]  
energy storage [GO:0006527]  
energy storage [GO:0006528]  
energy storage [GO:0006529]  
energy storage [GO:0006530]

## Supplementary Figure 1

A high-resolution version of Figure 1C in the text. It shows the 122 genes with predictions supported by three or more data types in at least one of the 114 categories with precision  $\geq 50\%$ . Five major functional categories (transcription, cell cycle, protein modification, organelle organization and biogenesis, and DNA metabolism) encompass 90 of the 122 uncharacterized genes ( $\sim 74\%$ ), although these categories encompass only  $\sim 42\%$  of the genes with GO-BP annotations. The broad categories *cell organization and biogenesis*; *nucleobase, nucleoside, nucleotide, and nucleic acid metabolism*; *protein metabolism*; and *cytoplasm organization and biogenesis* were omitted.