# SUPPLEMENTAL TABLES

## Table S1: Functional predictions of unknown genes from yeast cell cycling dataset.

| Systematic name | Syn | Predicted biological pathway/localization | Baikai's modules (2, 4) | Other predictions | SGD information | # of Links |
|---|---|---|---|---|---|---|
| YBL051C | PIN4 | cytoplasmic, protein fate (folding, modification, destination) | | | cytoplasmic; mdt1, modulate DNA damage tolerance and G2/M cell cycle | 2 |
| YBR108W | | cytoplasmic, protein fate (folding, modification, destination) | not present | | synthetic sick with gim3,5, components of bovine prefoldin for tubulin folding and cytokinesis | 3 |
| YBR124W | | cytoplasmic, protein fate (folding, modification, destination) | not present | | | 2 |
| YDR134C | | amino acid biosynthesis or energy transport | not present | | | 1 |
| YOR248W | | cytoplasmic, protein fate (folding, modification, destination) | cell cycle; module 63 | | | 2 |
| YPL067C | | cytoplasmic, protein fate (folding, modification, destination) | module 59 | | | 1 |
| YKL153W | | gluconeogenesis | module 60: glycolysis | | | 1 |
| YCR013C | | gluconeogenesis | module 60: glycolysis | | | 5 |
| YDR279W | RNH202 | cell cycle or cell fate | cell cycle; module 13 | | ribonuclease H2 subunit for DNA replication | 2 |
| YGR086C | PIL1 | cell cycle | module 24 | cell cycle (3); | | 1 |
| YGR151C | | cell cycle | cell cycle; module 15 | | synthetic lethal to Cde42p | 12 |
| YGR189C | CRH1 | cell cycle | cell cycle; module 63 | | Putative glycosidase of the cell wall, may have a role in cell wall architecture | 5 |
| YGR221C | TOS2 | cell cycle | cell cycle; module 63 | | Protein of unknown function that localizes to the bud neck and bud tip; potentially phosphorylated by Cdc28p | 12 |
| YBR070C | | cell cycle | cell cycle; module 77 | | | 3 |
| YBR071W | | cell cycle | cell cycle; module 77 | cell cycle (3); | | 1 |
| YHR098C | SFB3 | metabolism | | | Member of the Sec24p family; forms a complex, with Sec23p, that is involved in sorting of Pma1p into COPII vesicles; peripheral ER membrane protein; potential Cdc28p substrate | 1 |
| YHR149C | | cell cycle | cell cycle; module 77 | | Protein of unknown function found in the bud tip and bud | 1 |

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|---|---|---|---|---|---|---|
| | | | | | neck, potential Cdc28p substrate | |
| YBR089W | | cell cycle | cell cycle; module 77 | | | 9 |
| YIL158W | | cell cycle | module 40 | | | 6 |
| YJL051W | | cell cycle | module 63 | | localized to the bud tip | 6 |
| YJL181W | | cell cycle | cell cycle; module 77 | | | 3 |
| YKR012C | | cell cycle | mating; module 77 | | | 3 |
| YKR013W | PRY2 | cell cycle | cell cycle; module 82 | | | 9 |
| YKR077W | | cell cycle | cell cycle; module 82 | | | 2 |
| YKR090W | PXL1 | cell cycle | cell cycle; module 82 | | required for selection and/or maintenance of polarized growth sites, may modulate signaling by the GTPases Cdc42p and Rho1p; has similarity to metazoan paxillin | 1 |
| YLL022C | HIF1 | cell cycle | cell cycle; module 82 | | Non-essential component of the HAT-B histone acetyltransferase complex (Hat1p-Hat2p-Hif1p), localized to the nucleus; has a role in telomeric silencing | 14 |
| YLR049C | | cell cycle | cell cycle; module 85 | | | 3 |
| YLR154C | RNH203 | cell cycle | cell cycle | | Ribonuclease H2 subunit, required for RNase H2 activity | 1 |
| YLR183C | TOS4 | cell cycle | cell cycle; module 36 | | Transcription factor; promoters of some genes involved in pheromone response and cell cycle; | 25 |
| YLR190W | MMR1 | cytokinesis | module 63: cell wall integrity | | localized to small buds, bud neck, and incipient bud sites; mRNA is targeted to the bud via the mRNA transport system involving She2p | 11 |
| YML119W | | cell cycle | module 47 | | potential Cdc28p substrate | 10 |
| YMR031C | | metabolism | not present | | | 1 |
| YCL012W | | cytokinesis or cell cycle | module 64 | | | 1 |
| YCL013W | | cytokinesis or cell cycle | module 64 | | "=YCL012W" | 1 |
| YNL058C | | cell cycle | module 42 | Cell cycle (1) | potential Cdc28p substrate | 6 |
| YCL022C | | cell cycle | cell cycle; module 13 | | | 5 |
| YOL007C | | cell cycle | cell cycle; module 82 | | structural component of the chitin synthase 3 complex | 19 |
| YOL017W | ESC8 | cell cycle | cell cycle; module 77 | | Protein involved in telomeric and mating-type locus silencing, interacts with Sir2p and also interacts with the Gal11p, which is a component | 19 |

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
|  |  |  |  |  | of the RNA pol II mediator complex |  |
| YOL019W |  | cell cycle | cell cycle; module 82 |  |  | 4 |
| YCL060C |  | cell cycle | cell cycle; module 13; 15; 77 |  | S-phase checkpoint protein found at replication forks, required for DNA replication; also required for Rad53p activation during DNA replication stress, where it forms a replication-pausing complex with Tof1p and is phosphorylated by Mec1p | 10 |
| YOR066W |  | cell cycle | module 42 |  | potential Cdc28p substrate | 2 |
| YOR112W |  | metabolism | not present |  |  | 1 |
| YPL208W |  | cell cycle | cell cycle; module 77 |  |  | 7 |
| YPR174C |  | cell cycle | cell cycle; module 82 |  | potential Cdc28p substrate | 15 |
| YDL157C |  | cell cycle | cell cycle |  |  | 1 |
| YLL064C |  | stress response | not present |  |  | 2 |
| YKL177W |  | cell differentiation | not present |  |  | 1 |
| YPL158C |  | cytokinesis or cell fate | module 42 |  |  | 2 |
| YDL117W | CYK3 | cytokinesis | module 42 |  | SH3-domain protein located in the mother-bud neck and the cytokinetic actin ring; mutant phenotype and genetic interactions suggest a role in cytokinesis | 1 |
| YOR135C |  | energy transport | module 21 |  | exhibits growth defect on a non-fermentable (respiratory) carbon source | 3 |
| YDR361C | BCP1 | ribosome biogenesis | protein synthesis |  |  | 9 |
| YDR413C |  | ribosome biogenesis | not present |  |  | 3 |
| YDR417C |  | protein synthesis | protein synthesis |  |  | 5 |
| YDR494W | RSM28 | mitochondrial protein | module 12 |  | Mitochondrial ribosomal protein of the small subunit | 5 |
| YGL102C |  | protein synthesis | protein synthesis |  |  | 5 |
| YGR123C | PPT1 | ribosome biogenesis | protein synthesis |  | Protein serine/threonine phosphatase with similarity to human phosphatase PP5 | 8 |
| YGR173W | GIR1 | ribosome biogenesis | protein synthesis |  | GTPase, interacts with ribosomes | 5 |
| YGR187C | HGH1 | ribosome biogenesis | protein synthesis |  |  | 2 |
| YBR056W |  | metabolism | stress |  |  | 5 |
| YGR248W | SOL4 | metabolism | stress; module 34 |  | 6-phosphogluconolactonase activity by sequence analysis | 1 |
| YHL021C | FMP12 | stress response | stress; module 34 |  |  | 8 |
| YHR052W | CIC1 | ribosome biogenesis | protein |  |  | 2 |

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
|  |  |  | synthesis; module 10 |  |  |  |
| YHR116W |  | mitochondrial protein | module 12 |  | Protein that functions in mitochondrial copper homeostasis and is essential for functional cytochrome oxidase expression; homologous to COX17, localized to the mitochondrial intermembrane space | 1 |
| YIL127C |  | ribosome biogenesis | protein synthesis |  |  | 26 |
| YJL009W |  | ribosome biogenesis | not present |  |  | 1 |
| YJL122W |  | ribosome biogenesis | protein synthesis |  |  | 23 |
| YKL030W |  | mitochondrial protein | not present |  |  | 1 |
| YKL169C |  | mitochondrial protein | module 12 |  |  | 1 |
| YAL036C | FUN11 | ribosome biogenesis | protein synthesis |  | RiBosome interacting Gtpase | 6 |
| YKR016W | FMP13 | respiration | module 5: energy transport |  |  |  |
| YKR047W |  | protein synthesis | not present |  | synthetic lethal to Bni1p involved in spindle formation | 1 |
| YLL037W |  | metabolism | not present |  |  | 2 |
| YLR016C |  | ribosome biogenesis | not present |  |  | 1 |
| YLR051C |  | ribosome biogenesis | protein synthesis |  |  | 3 |
| YLR062C | BUD28 | protein synthesis | protein synthesis |  |  | 2 |
| YLR074C | BUD20 | ribosome biogenesis | protein synthesis |  | Protein involved in bud-site selection; diploid mutants display a random budding pattern instead of the wild-type bipolar pattern | 11 |
| YLR090W | XDJ1 | mitochondrial protein | not present |  | mitochondrial protein | 2 |
| YLR149C |  | metabolism | stress; module 37 |  |  | 1 |
| YLR196W | PWP1 | ribosome biogenesis | protein synthesis; module 10 |  | nucleolar protein | 16 |
| YLR198C |  | ribosome biogenesis | protein synthesis |  |  | 2 |
| YLR217W |  | protein chaperone, response to heat shock | module 50: protein chaperone |  |  | 1 |
| YLR221C | RSA3 | ribosome biogenesis | protein synthesis |  | Protein with a likely role in ribosomal maturation, required for accumulation of wild-type levels of large (60S) ribosomal subunits; binds to the helicase Dbp6p in pre-60S ribosomal particles in the nucleolus | 13 |
| YLR257W |  | mitochondrial protein | not present |  |  | 1 |

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|---|---|---|---|---|---|---|
| YLR270W | DCS1 | metabolism | stress | | interact with stress response protein Nth1p | 1 |
| YLR339C | | protein synthesis | module 70 | | | 2 |
| YLR397C | AFG2 | ribosome biogenesis | module 71 | | ATPase of the CDC48/PAS1/SEC18 (AAA) family, forms a hexameric complex; may be involved in degradation of aberrant mRNAs | 4 |
| YLR449W | FPR4 | ribosome biogenesis | protein synthesis | | Nuclear protein, putative peptidyl-prolyl cis-trans isomerase (PPIase) with similarity to Fpr3p; overproduction suppresses the growth defect resulting from the absence of E3 ubiquitin-protein ligase Tom1p | 18 |
| YBR266C | | ribosome biogenesis | protein synthesis | | endocytosis | 4 |
| YBR271W | | ribosome biogenesis | protein synthesis | | | 4 |
| YML128C | MSC1 | metabolism | stress; module 34 | | mutant has sporulation defect | 1 |
| YMR014W | BUD22 | ribosome biogenesis | protein synthesis | | Protein involved in bud-site selection | 19 |
| YMR269W | | ribosome biogenesis | not present | | protein possibly involved in protein synthesis | 6 |
| YMR290C | HAS1 | ribosome biogenesis | protein synthesis; module 10 | | Putative ATP-dependent RNA helicase; localizes to both the nuclear periphery and nucleolus; highly enriched in nuclear pore complex fractions | 17 |
| YNL023C | FAP1 | cell cycle | not present | | Protein that binds to Fpr1p (FKBP12), conferring rapamycin resistance by competing with rapamycin for Fpr1p binding; has similarity to putative transcription factors, including D. melanogaster shuttle craft and human NFX1 | 2 |
| YNL050C | | ribosome biogenesis | not present | | | 8 |
| YNL132W | KRE33 | ribosome biogenesis | protein synthesis; module 10 | | | 12 |
| YNL174W | | ribosome biogenesis | protein synthesis; module 10 | | | 1 |
| YNR046W | | ribosome biogenesis | protein synthesis | | nucleolar protein | 8 |
| YNR054C | | ribosome biogenesis | protein synthesis | | transcription regulator activity | 1 |
| YCL042W | | metabolism | stress | | | 1 |
| YOL022C | | ribosome biogenesis | protein synthesis | | | 8 |
| YOL032W | | mitochondrial protein | stress; | | | 1 |

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|---|---|---|---|---|---|---|
| | | | module 56 | | | |
| YOL048C | | cytoplasmic, protein or nucleotide degradation | stress | | | 2 |
| YOL079W | | ribosome biogenesis | not present | | | 6 |
| YOL124C | | ribosome biogenesis | protein synthesis | | | 6 |
| YOR042W | CUE5 | mitochondrial protein | module 35 | | Protein containing a CUE domain that binds ubiquitin, which may facilitate intramolecular monoubiquitination | 1 |
| YOR051C | | ribosome biogenesis | not present | | | 1 |
| YOR090C | PTC5 | mitochondrial protein | not present | | Phosphatase type Two C | 1 |
| YOR146W | | ribosome biogenesis | not present | | | 16 |
| YOR154W | | ribosome biogenesis | not present | | | 7 |
| YOR169C | | ribosome biogenesis | not present | | | 2 |
| YOR277C | | ribosome biogenesis | module 41 | | | 2 |
| YPL044C | | ribosome biogenesis | protein synthesis; module 76 | | | 6 |
| YCR016W | | ribosome biogenesis | protein synthesis | | nucleolar protein | 10 |
| YPL142C | | protein synthesis | protein synthesis | | | 2 |
| YPL146C | | ribosome biogenesis | protein synthesis | | nucleolar protein | 12 |
| YPL202C | AFT2 | ribosome biogenesis | not present | | Activator of Iron (Fe) Transcription; response to oxidative stress | 2 |
| YPL207W | | ribosome biogenesis | protein synthesis | | | 8 |
| YPL212C | PUS1 | ribosome biogenesis | protein synthesis | | Involved in tRNA biogenesis | 1 |
| YPL225W | | proteolytic degradation | not present | | | 1 |
| YPL238C | | ribosome biogenesis | protein synthesis | | | 1 |
| YPL239W | YAR1 | ribosome biogenesis | protein synthesis | | Null mutant is viable, grow slowly at low temperature | 5 |
| YPL273W | SAM4 | metabolism | amino acid metabolism; module 68 | | sulfur amino acid metabolism | 1 |
| YPR048W | TAH18 | ribosome biogenesis | not present | | | 2 |
| YPR136C | | ribosome biogenesis | module 76 | | | 1 |
| YPR142C | | ribosome biogenesis | not present | | | 1 |
| YPR143W | | ribosome biogenesis | protein synthesis | | nucleolar protein | 7 |
| YPR169W | JIP5 | ribosome biogenesis | not present | | nucleolar protein; interact with ubiquitin-ligase Bre1p | 7 |
| YCR051W | | ribosome biogenesis | module 70 | | | 1 |
| YCR055C | | ribosome biogenesis | protein synthesis | | "=PWP2" | 9 |
| YCR072C | | ribosome biogenesis | protein synthesis | | co-purified with 60S ribosome subunit | 9 |

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|---|---|---|---|---|---|---|
| YCR096C | HMRA2 | transcriptional regulator, phenomone response | not present | | Silenced copy of A2, encoding a protein of with similarity to Alpha2p that is required along with A1p for inhibiting expression of the HO endonuclease in a/alpha HO/HO diploid cells with an active mating-type interconversion system | 2 |
| YDL023C | SRF4 | metabolism | not present | | unlike to encode a protein | 1 |
| YDL063C | | ribosome biogenesis | ribosome biogenesis | | | 17 |
| YDR056C | | metabolism | protein synthesis | | synthetic lethal to Nbp2p, a Nap1p-binding protein | 1 |
| YDR152W | GIR2 | ribosome biogenesis | not present | | Genetically Interacts with Ribosomal genes | 4 |

## Table S2: Functional predictions of unknown genes from *Shewanella* heat/cold shock dataset.

| Gene designation | Prediction | TIGR Annotation | # of Links |
|---|---|---|---|
| SO1789 | energy metabolism; transport | conserved hypothetical protein | 1 |
| SO2391 | energy metabolism; transport | conserved hypothetical protein | 1 |
| SO3725 | central intermediate metabolism; protein modification | hypothetical protein | 3 |
| SO4150 | sulfur metabolism | transporter, putative | 2 |
| SO0119 | metabolism | conserved hypothetical protein | 2 |
| SO0126 | metabolism | conserved hypothetical protein | 3 |
| SO2011 | metabolism | conserved hypothetical protein | 3 |
| SO2017 | heat shcok response | conserved hypothetical protein | 8 |
| SO2042 | heat shcok response | conserved hypothetical protein | 3 |
| SO2064 | flagellar biosynthesis | conserved domain protein | 3 |
| SO2354 | metabolism | conserved hypothetical protein | 3 |
| SO2375 | metabolism | membrane protein, putative | 8 |
| SO2474 | metabolism | carbonic anhydrase family protein | 3 |
| SO2500 | flagellar biosynthesis | conserved hypothetical protein | 1 |
| SO3000 | flagellar biosynthesis | conserved hypothetical protein | 5 |
| SO3015 | flagellar biosynthesis | conserved hypothetical protein | 3 |
| SO3164 | metabolism | conserved hypothetical protein | 3 |
| SO3288 | flagellar biosynthesis | Transglycosylase, Slt family | 2 |
| SO3298 | metabolism | conserved hypothetical protein | 10 |
| SO3336 | metabolism | hypothetical protein | 4 |
| SO3896 | heat shcok response | outer membrane porin, putative | 3 |
| SO4492 | metabolism | conserved hypothetical protein | 2 |
| SO4556 | metabolism | transcriptional regulator, LysR family | 2 |
| SO4565 | flagellar biosynthesis | transporter, putative | 3 |
| SO0490 | metabolism | transcriptional regulator | 3 |
| SO0591 | metabolism | conserved hypothetical protein | 3 |
| SO0595 | metabolism | hypothetical protein | 2 |
| DsbD | metabolism | thiol:disulfide interchange protein | 5 |
| SO1125 | heat shcok response | Integral membrane domain protein | 3 |
| SO2862 | amino acid metabolism | HDIG domain protein | 2 |
| SO4051 | amino acid metabolism | HlyD family secretion protein | 2 |
| SO3696 | sulfur metabolism | hypothetical protein | 1 |

## Table S3: Functional predictions of unknown genes from *E.coli* datasets.

| Gene designation | Prediction | Annotation* | # of Links |
|---|---|---|---|
| b1155 | biosynthesis of small molecules | hypothetical protein | 2 |
| b1156 | biosynthesis of small molecules | hypothetical protein | 1 |
| yafJ | biosynthesis of small molecules | conserved protein with N-terminal nucleophile aminohydrolase domain | 1 |
| b0224 | biosynthesis of small molecules | hypothetical protein | 2 |
| b2353 | biosynthesis of small molecules | hypothetical protein | 2 |
| b2354 | biosynthesis of small molecules | hypothetical protein | 2 |
| b2596 | degradation of amino acids | hypothetical protein | 2 |
| b2853 | degradation of amino acids | hypothetical protein | 2 |
| b3263 | degradation of amino acids | hypothetical protein | 2 |
| cspH | degradation of small molecules | cold shock-like protein, nucleic acid-binding domain | 2 |
| b1088 | protein synthesis | conserved protein of unknown function | 5 |
| b1815 | transport of small molecule | conserved protein of unknown function | 2 |
| b1933 | function related to cell surface structure | hypothetical protein | 5 |
| yaeC | metabolism, cell surface structure | D-methionine transport protein (ABC superfamily, peri_bind) | 8 |
| b1983 | nucleotide metabolism | hypothetical protein | 2 |
| yejM | translation, post-translational modification | putative sulfatase | 12 |
| b0303 | carbon compound catabolism | hypothetical protein | 2 |
| agaA | post-translational modification | putative N-acetylgalactosamine-6-phosphate deacetylase | 13 |
| envR | function related to cell surface structure | transcriptional repressor for multiple drug efflux pump (TetR/AcrR family) | 3 |
| rhlB | amino acid metabolism | putative ATP-dependent helicase with nucleoside triP hydrolase domain | 3 |
| yihK | nucleotide metabolism | putative GTP-binding factor | 4 |
| yajC | amino acid biosynthesis | preprotein translocase, auxillary membrane component (General Secretory Pathway) | 6 |
| b4066 | function related to cell surface structure | hypothetical protein | 2 |
| b4103 | function related to cell surface structure | hypothetical protein | 4 |
| b4243 | protein translation and modification | hypothetical protein | 5 |
| ybgF | protein synthesis | putative periplasmic protein with protein prenylyltransferase domain | 9 |
| b1194 | flagellar biosynthesis | hypothetical protein | 2 |
| b1148 | carbon compound catabolism | hypothetical protein | 3 |
| b1505 | transport protein | putative outer membrane protein | 9 |
| b1644 | transport protein | putative multidrug resistance membrane protein | 3 |
| b1645 | transport protein | hypothetical protein | 2 |

| | | | |
|---|---|---|---|
| b1673 | transport of small molecule | putative aldehyde ferridoxin oxidoreductase | 7 |
| yeeP | transport protein | CP4-44 prophage; putative GTP-binding factor | 2 |
| b2459 | energy metabolism; transport protein | putative cobalamin adenosyltransferase with winged helix domain, in ethanolamine utilization | 7 |
| b2506 | function related to cell surface structure | putative membrane protein | 3 |
| yqcB | energy metabolism | pseudouridine synthase | 6 |
| yggR | energy metabolism; transport protein | putative protein transport | 3 |
| yghD | transport protein | putative secretion pathway protein | 5 |
| b2970 | transport protein | putative protein exporter (General Secretory Pathway) | 4 |
| b2973 | energy metabolism; transport protein | hypothetical protein | 5 |
| yraL | energy metabolism | putative enzyme with Cobalt precorrin-4 methyltransferase domain | 2 |
| yhfP | transport protein | conserved protein with Xylose isomerase-like domain | 6 |
| yhjQ | transport protein; amin acid metabolism | putative cell division protein, nucleotide triphosphate hydrolase domain | 4 |
| b3832 | transport protein | hypothetical protein | 8 |
| b4212 | energy metabolism; transport protein | hypothetical protein | 6 |
| b4256 | transport protein | hypothetical protein | 3 |
| b0960 | transport protein | putative efflux transport protein (PET family) | 2 |

*: annotation is based on information from TIGR's *E.coli* annotation database and personal communication with Margrethe Serres, Marine Biological Laboratory, Woods Hole, MA, 02543)

## References

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