Supporting information for Li (2002) *Proc. Natl. Acad. Sci. USA*, 10.1073/pnas.252466999

Table 2. Liquid-association pairs (LAPS) scouted by CYT1

Top 10 positive LAPs of CYT1	Top 11–20 positive LAPs of CYT1	Top 10 negative LAPs of CYT1	Top 11–20 negative LAPs of CYT1
ATP1 HTS1	**ATP5** KTR3	CEM1 YPR002W	YHR180W YPL238C
ATP1 SIR2	**ATP1** HPT1	YGL121C YNR046W	PRP43 YGL121C
ATP1 YER036C	**ATP1** YLR007W	YER036C YGL121C	TFB3 PTM1
ATP1 ERG10	YFR035C YNR013C	YGL121C YLR186W	YDR363W SEC12
ATP1 YNL232W	CDC19 RPA34	SER3 RPL33A	SAS3 ERG28
ATP1 ZUO1	**ATP1** YEL040W	YFL052W YMR233W	YDR363W YLR173W
YBL100C YPR126C	**ATP1** URA6	RPL4B YMR31	YMR31 YJR071W
LAS21 YNL313C	CDC19 YPL238C	YGL121C RPC40	YGL121C YPR169W
KTR3 YIL088C	RPS4A YPR123C	YOR193W YPL238C	YHR189W NDH1
TCM62 RPC19	**ATP1** YPL273W	YHR180W YNL303W	YGL121C AFG2

ATP1 F1F0 ATPASE COMPLEX F1 ALPHA SUBUNIT
ATP5 F1F0 ATPASE COMPLEX OSCP SUBUNIT
HTS1 HISTIDINE TRNA LIGASE
TCM62 CHAPERONE REQUIRED FOR ASSEMBLY OF MITOCHONDRIAL SUCCINATE DEHYDROGENASE
NDH1 MITOCHONDRIAL CYTOSOLICALLY DIRECTED NADH DEHYDROGENASE
CEM1 BETA-KETO-ACYL-ACP SYNTHASE MITOCHONDRIAL
ERG10 ACETYL-COA C-ACETYLTRANSFERASE, CYTOSOLIC
ERG28 involved in ergosterol biosynthesis
URA6 URIDINE MONOPHOSPHATE KINASE; pyrimidine biosynthesis
HPT1 HYPOXANTHINE GUANINE PHOSPHORIBOSYL TRANSFERASE; purine salvage
KTR3 ALPHA-1-2-MANNOSYLTRANSFERASE;
LAS21 SIMILARITY TO *Schizosaccharomyces pombe* SPAC13G6.3 PROTEIN

SER3 3 PHOSPHOGLYCERATE DEHYDROGENASE
CDC19 PYRUVATE KINASE
ZUO1 ZUOTIN A PUTATIVE Z DNA-BINDING PROTEIN chaperone; bind tRNA; ribosome-associated Dna-like protein
SIR2-SILENCING REGULATORY PROTEIN AND DNA-REPAIR PROTEIN
SAS3-SILENCING PROTEIN

RPS4A RIBOSOMAL PROTEIN S4.E.C10
RPL33A RIBOSOMAL PROTEIN L35A.E.C16
RPL4B RIBOSOMAL PROTEIN L4.E.B
YMR31 RIBOSOMAL PROTEIN MITOCHONDRIAL

RPA34 NONESSENTIAL COMPONENT OF RNA POLI
RPC19 DNA DIRECTED RNA POLYMERASE I III 16 KD SUBUNIT
RPC40 DNA DIRECTED RNA POLYMERASE I III 40 KD SUBUNIT
PRP43 INVOLVED IN SPLICEOSOME DISASSEMBLY
TFB3 TFIIH SUBUNIT, TRANSCRIPTION/REPAIR FACTOR
PTM1 MEMBER OF THE MAJOR FACILITATOR SUPERFAMILY
YDR363W REGULATOR OF EXOCYTOSIS AND PSEUDOHYPHAL DIFFERENTIATION
SEC12 GDP/GTP EXCHANGE FACTOR FOR SAR1P
AFG2 MEMBER OF THE SEC18P-PAS1P-CDC48P-TBP1 FAMILY OF ATPASES