Supplementary Material (ESI) for Molecular BioSystems
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SUPPLEMENTARY TABLE I. Comparison of over-represented functional clusters of genes and protein levels from MLY61 WT YPM vs SLAM ($p < 0.01$). Red highlighting indicates shared in common with the same comparison in the *gpa2Δ* strain. () = Ratio metric change of iTRAQ-generated differentially expressed proteins.

Common biological process	Down-regulated genes	Decreased protein level	Up-regulated genes	Increased protein level
Cellular organization and biogenesis Ribosome biogenesis/assembly rRNA processing processing 20S pre-RNA processing 35S primary transcript ribosome assembly/maintenance	*ESF1 MAK5 UTP21 UTP22 UTP7 BRX1 RPL3 RPL40B RPS0A RRP5 ASC1*	*RPL5* (0.72)		*SNU13* (1.78) *NOP1* (1.48) *PAB1* (1.53) *RPS19A* (1.81) *RPS18B* (1.80) *RPL23B* (2.42) *RPL4B* (2.10) *RPL28* (1.82) *RPS12* (1.73) *RPS8B* (2.17) *ASC1* (1.52) *RPP0* (1.37) *RPS5* (2.27) *RPS17A* (3.01) *RPS24B* (2.07) *RPL25* (2.72) *RPS0B* (1.68) *RPL20B* (1.40)
RNA metabolism RNA processing RNA methylation/modification tRNA metabolism	*ESF1 LSM5 MAK5 MSE1 MST1 MSW1 RRP5 SNR44 SNR56 SNR63 SNR68 SNR72 SUP35 TAD2 TIS11 UTP21 UTP22 UTP7 DBP2 NCL1 PUS7 SNR75 TRM1*			*KRS1* (1.31) *GUS1* (1.16)
Nucleotide/nucleobase metabolism nucleobase, nucleoside, nucleotide nucleic acid metabolism/transport		*ATP1* (0.74) *ATP2* (0.73)		*ADE6* (1.21)
Protein biosynthesis Amino acid activation Regulation of translation Translational elongation	*MCD4 MRP4 MRPL7 MRPL8 MSE1 MST1 MSW1 RPL18A RPL7B RPS29B RPS9A RSM26 SUF5 SUP35 MIS1 MRPL3 RPL15A RPL22A RPL3 RPL31B RPL34A RPL36A RPL40B RPL7A RPL9A RPL9B RPS0A RPS13 RPS22B RPS23A RPS23B RPS28B RPS7B RPS9B SUP45 TEF4*			*EFB1* (1.76) *EFT2* (1.20) *CDC33* (1.25) *TEF1* (1.29)
Carbon source utilization Transport/Synthesis/Metabolism	*SUC2 SUC4*	*TDH3* (0.84) *TAL1* (0.87) *TPI1* (0.74)	*PCKI*	*FBA1* (1.42) *ENO2* (1.48) *CDC19* (1.16) *PFK2* (1.29) *TDH1* (2.70) *PSA1* (1.38) *PDC1* (1.24) *GPM1* (1.19) *PGK1* (1.66)
Nitrogen source utilization Transport Synthesis	*ALD6 ARN1 ARN2 ASC1 BAP2 CCC2 CTR1 CTR3 ENB1 FRE1 FTR1 GNP1 MIS1 MSE1 MST1 MSW1 PHO84 RPS23A RPS23B RPS9A RPS9B SUF5 SUP35 SUP4 SUP45 TAT1 TAT2 TEF4*	*ILV3* (0.67) *LEU1* (0.28) *HIS4* (0.73) *PEP4* (0.68) *URA2* (0.79)	*ARG5,6 GAT1 SDL1 STR3 CAT2 CPA1 DAL3 DAL80 ECM40 LEU1 LYS5 MET13 MET6 SHC1 UGA3*	*CYS4* (1.27) *HYP2* (1.22) *CCT5* (1.37)

Metabolism				
DNA replication initiation				
Organelle biosynthesis structure/function		*QCR2* (0.45) *CYB5* (0.60) *IDP1* (0.59) *ACO1* (0.45)		*ILV5* (1.39)
Mitochondrial iron import				
Other metabolic functions	*APT1 COX10 DFR1 URA7*	*ERG13* (0.63) *SOD1* (0.80) *PIL1* (0.57) *SOD2* (0.39) *SSC1* (0.87)	*BIO4 CRC1 MLS1 FYV10*	