

SUPPLEMENTARY DATA

Eukaryotic translation initiation factor eIF5 promotes the accuracy of start codon recognition by regulating P_i release and conformational transitions of the preinitiation complex

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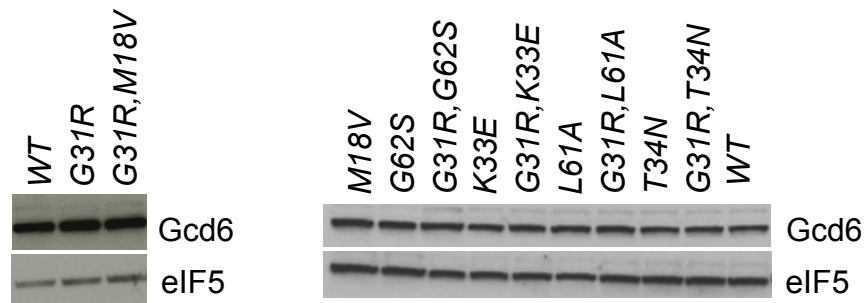


Figure S1. *TIF5* Ssu⁻ substitutions do not alter steady-state levels of eIF5 in vivo. Derivatives of *his4-301 tif5Δ* strain ASY100 containing the indicated *TIF5* alleles on sc *LEU2* plasmids except *T34N*, which was expressed from a hc *LEU2* plasmid to match the expression level of FLAG-tagged WT eIF5 and containing (*left panel*) or lacking (*right panel*) *TIF5*⁺ on a *URA3* plasmid were cultured in synthetic complete medium lacking leucine and uracil (SC-LU) or SC-L, respectively. WCEs were prepared under denaturing conditions, resolved by SDS-PAGE and subjected to Western blot analysis using antibodies against FLAG (eIF5) and Gcd6.

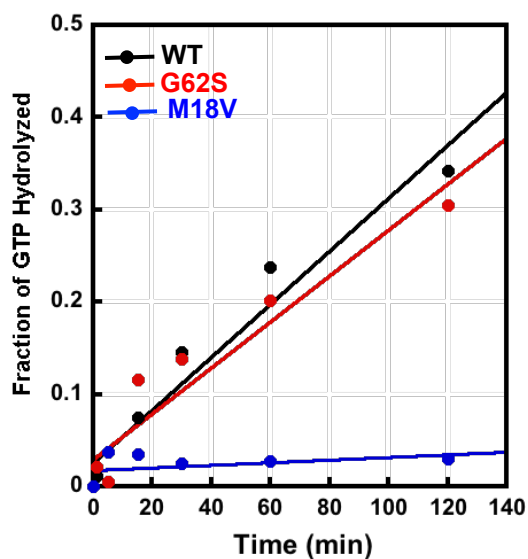


Figure S2. Effects of eIF5 Ssu⁻ mutants G62S and M18V on GTP hydrolysis by isolated eIF2•GTP•Met-tRNA_i ternary complexes. TC was assembled with [γ -³²P]-GTP and GTP hydrolysis was initiated by addition of a saturating concentration of WT, G62S or M18V forms of eIF5. Reactions were stopped at different times with EDTA. The amount of P_i formed over time was analyzed as described in Material and Methods. Rates of GTP hydrolysis are shown for TC with WT eIF5 (black circles; 0.0028 min⁻¹), G62S eIF5 (red circles; 0.0024 min⁻¹), and M18V eIF5 (blue circles; 0.00013 min⁻¹).