

Differential stoichiometry among core ribosomal proteins

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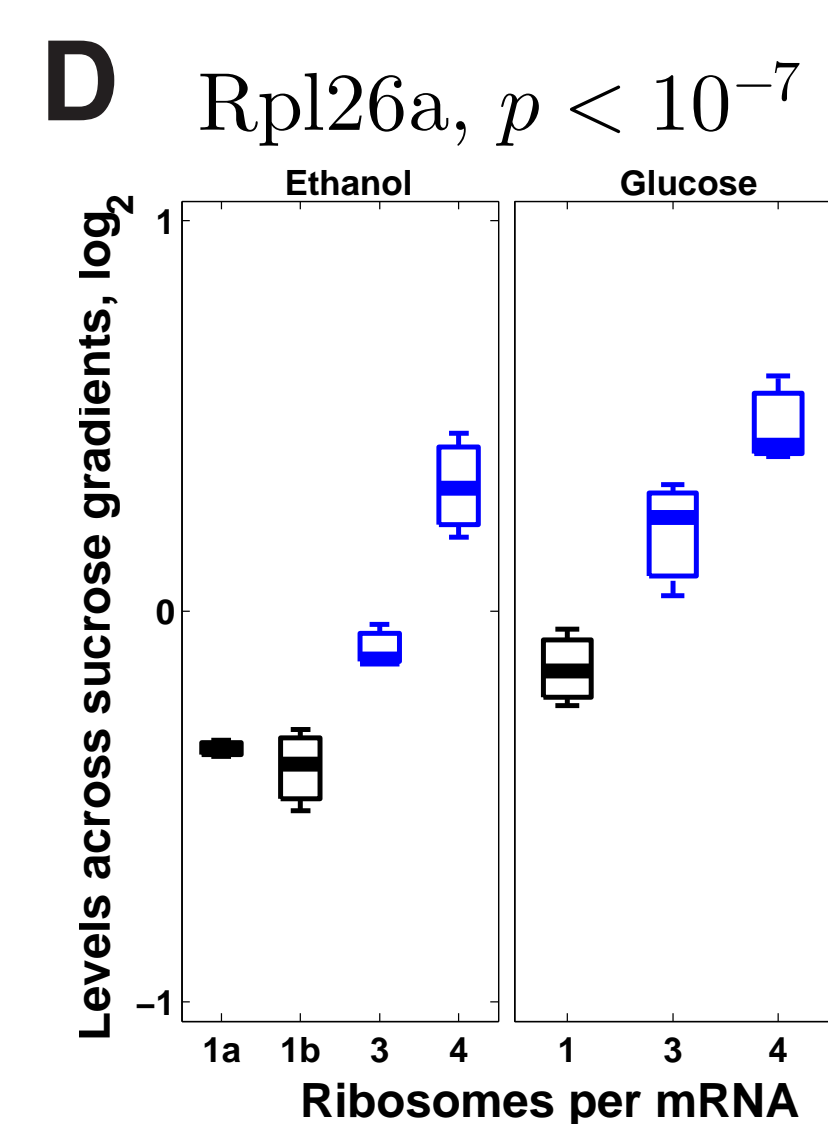
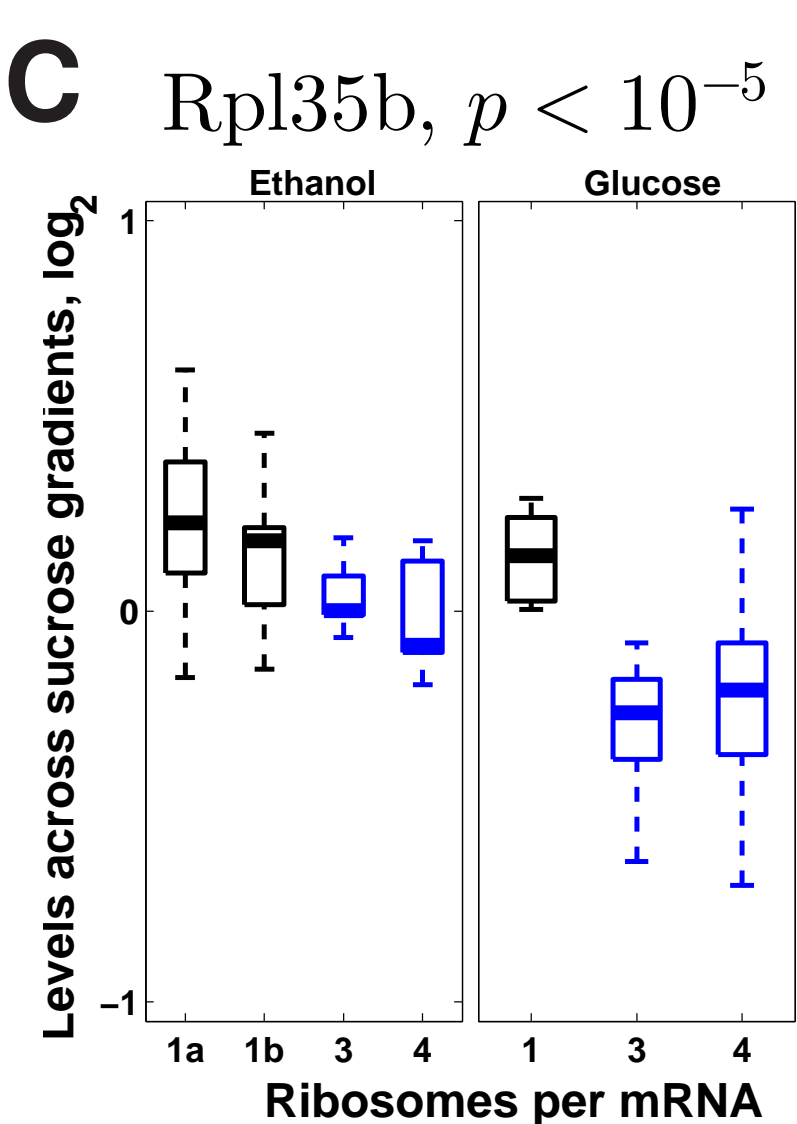
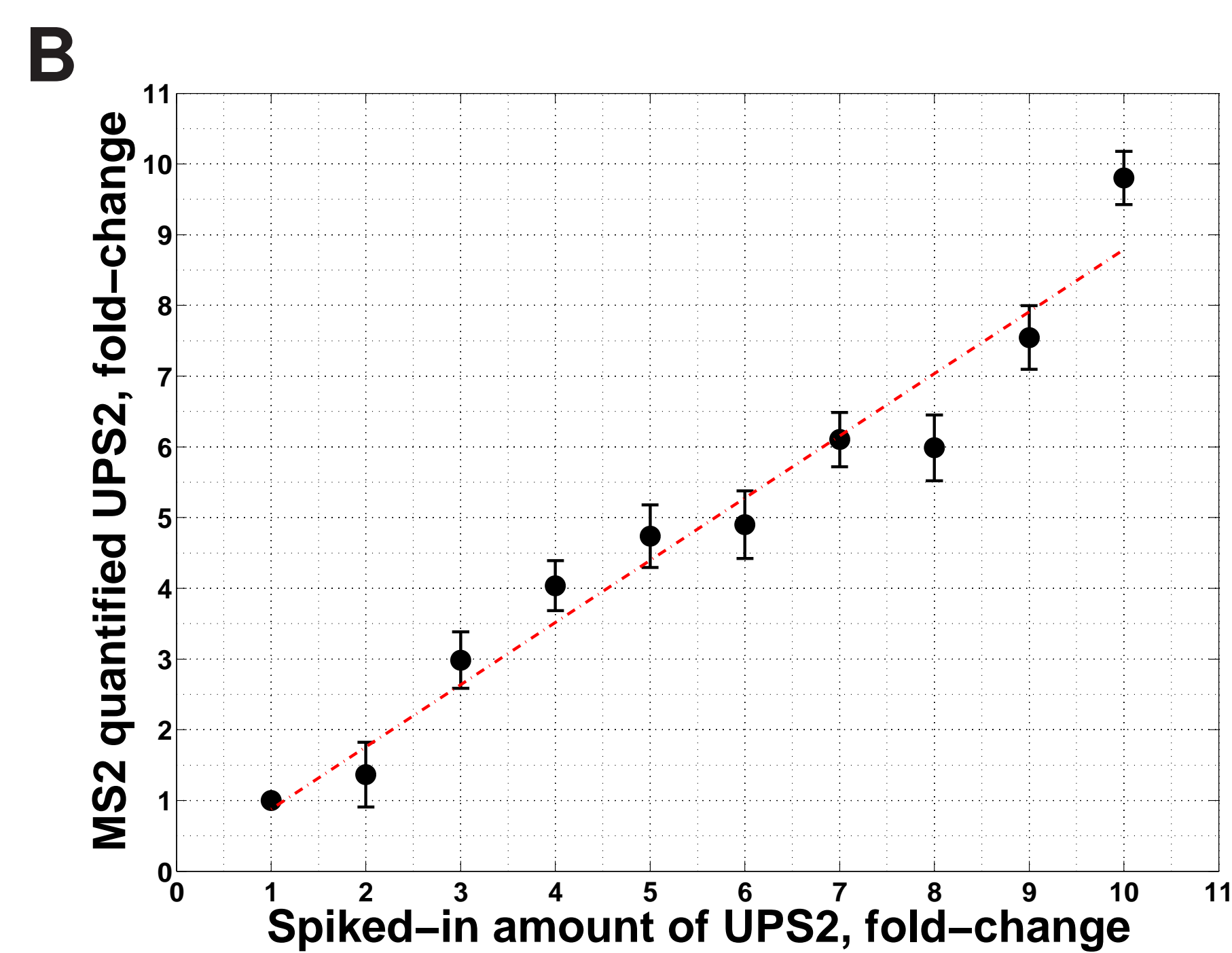
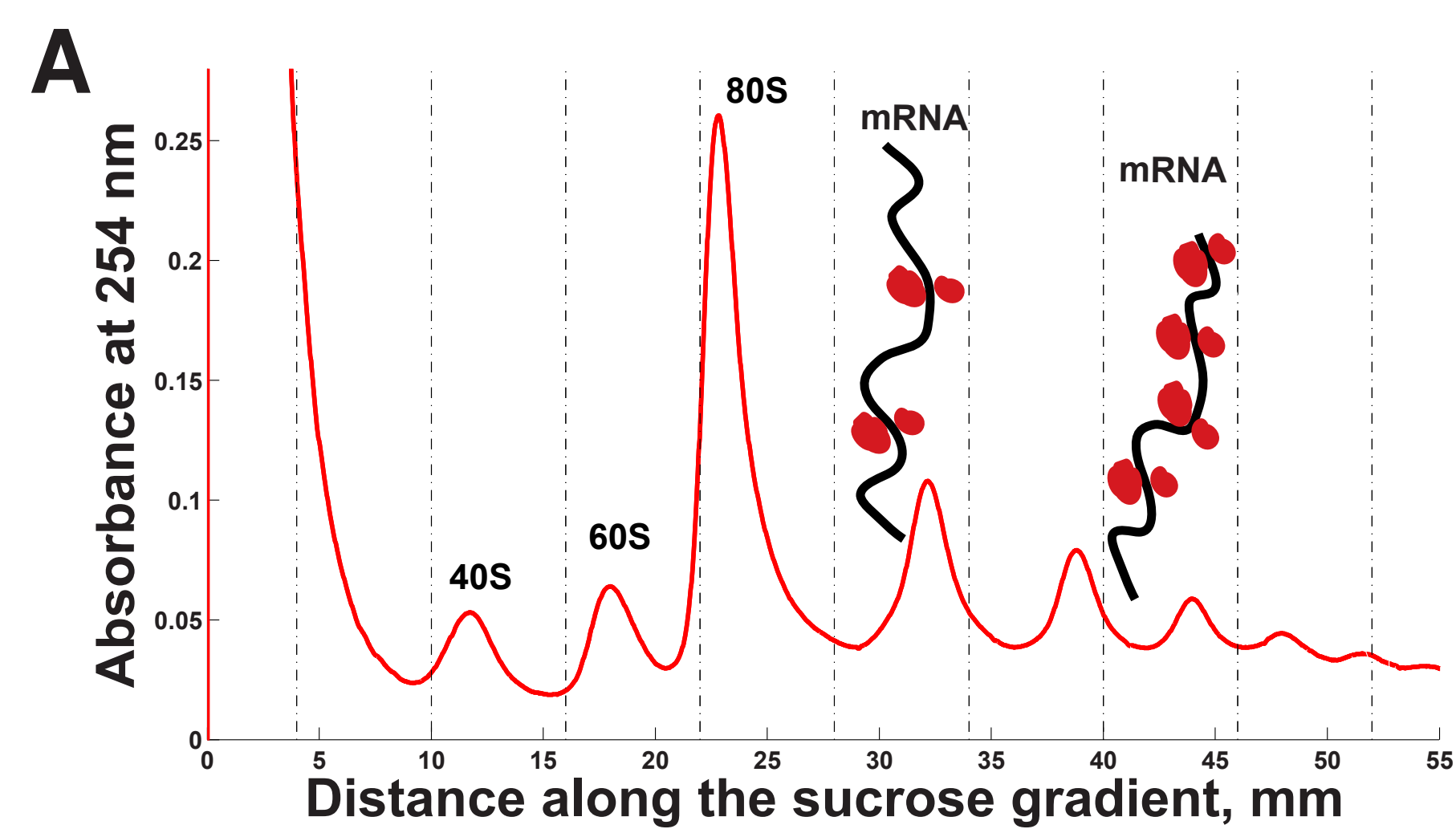
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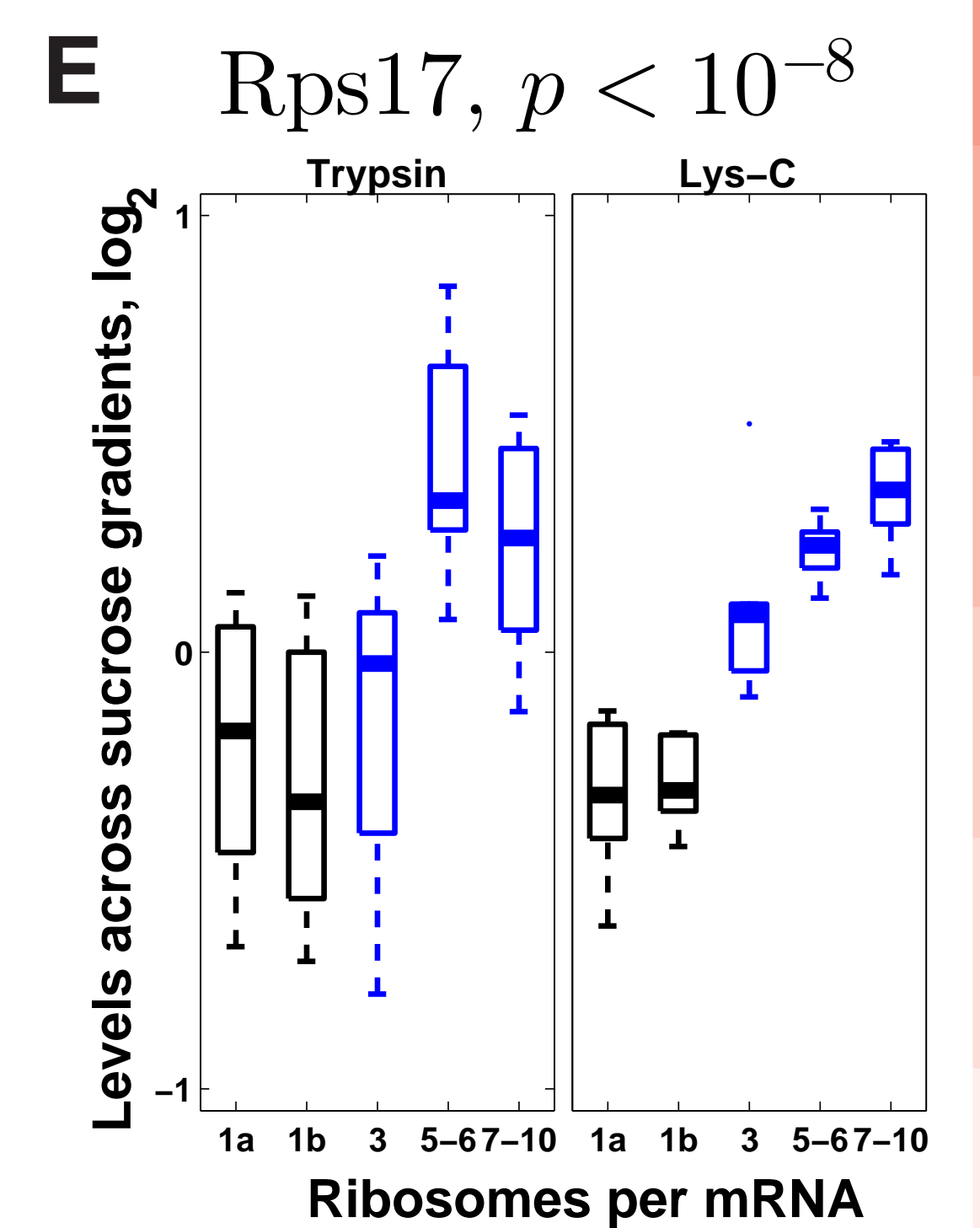
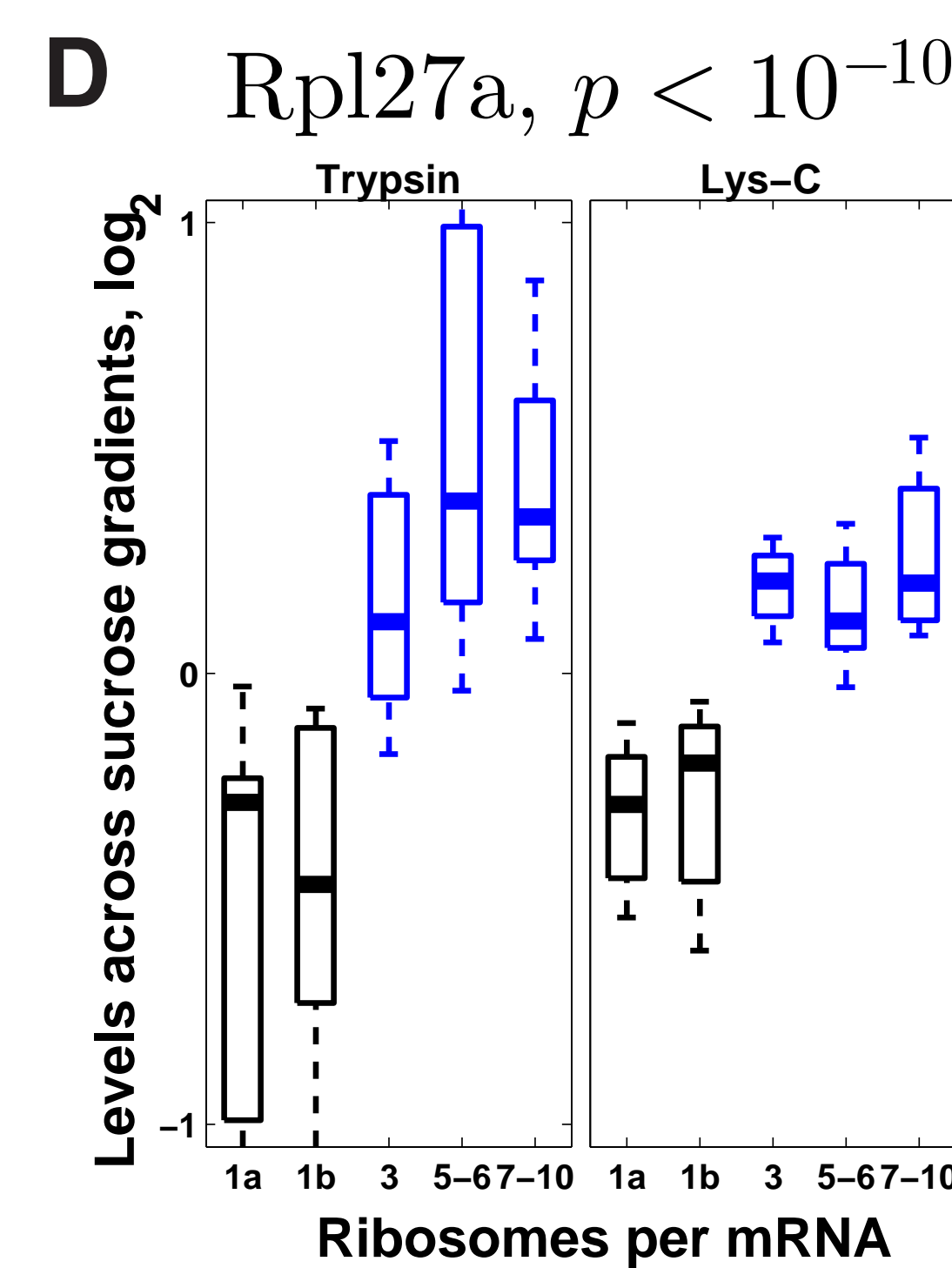
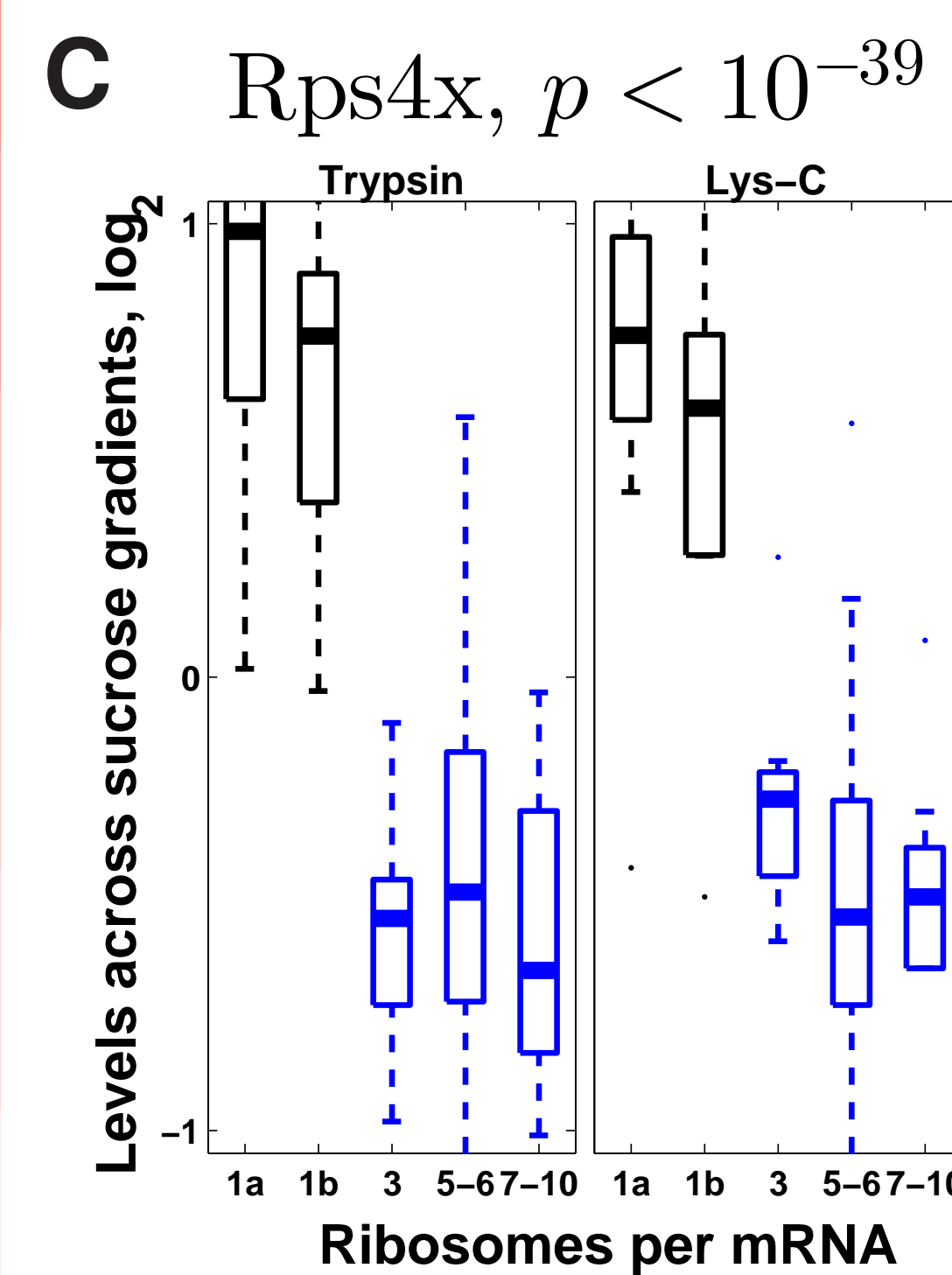
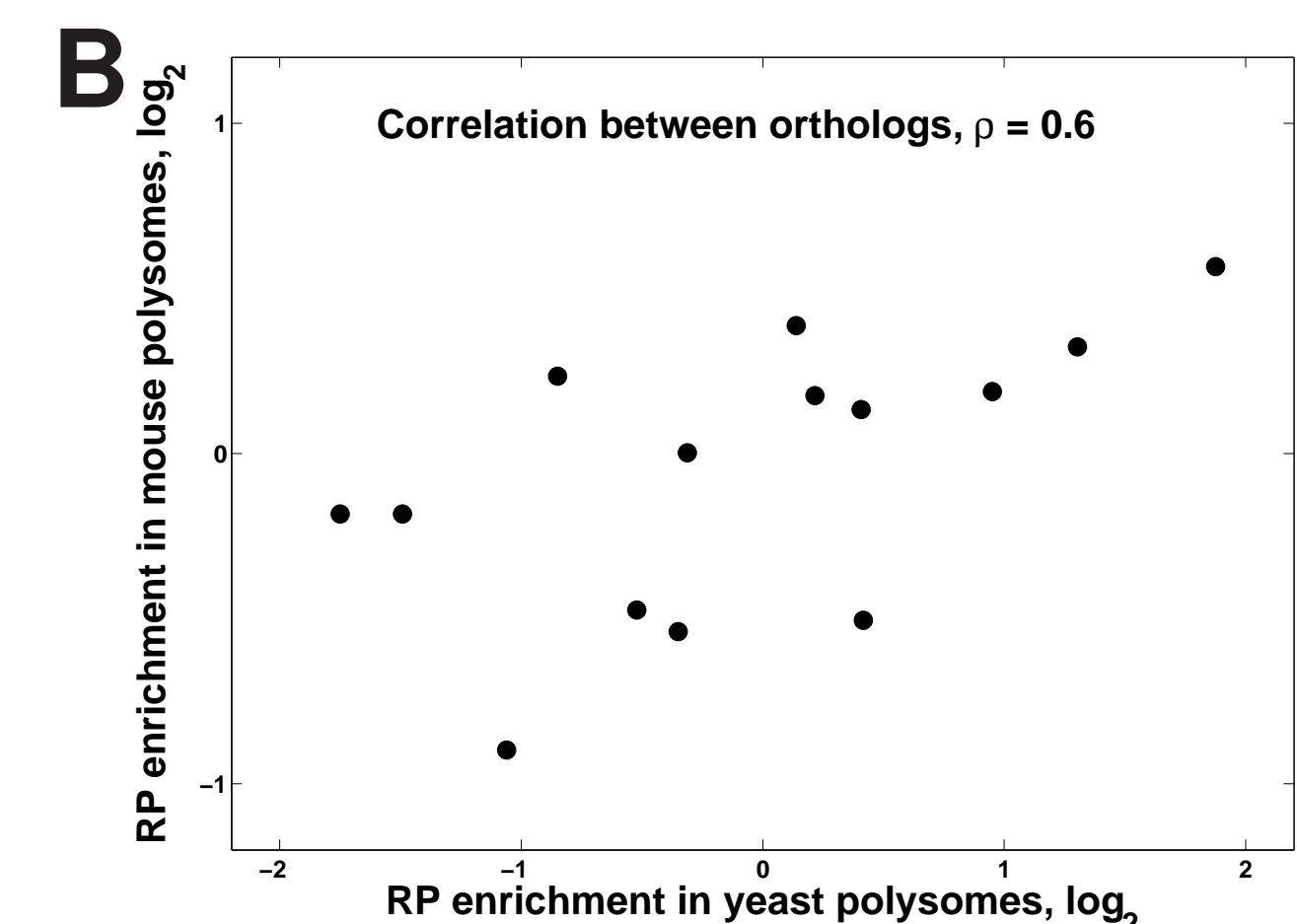
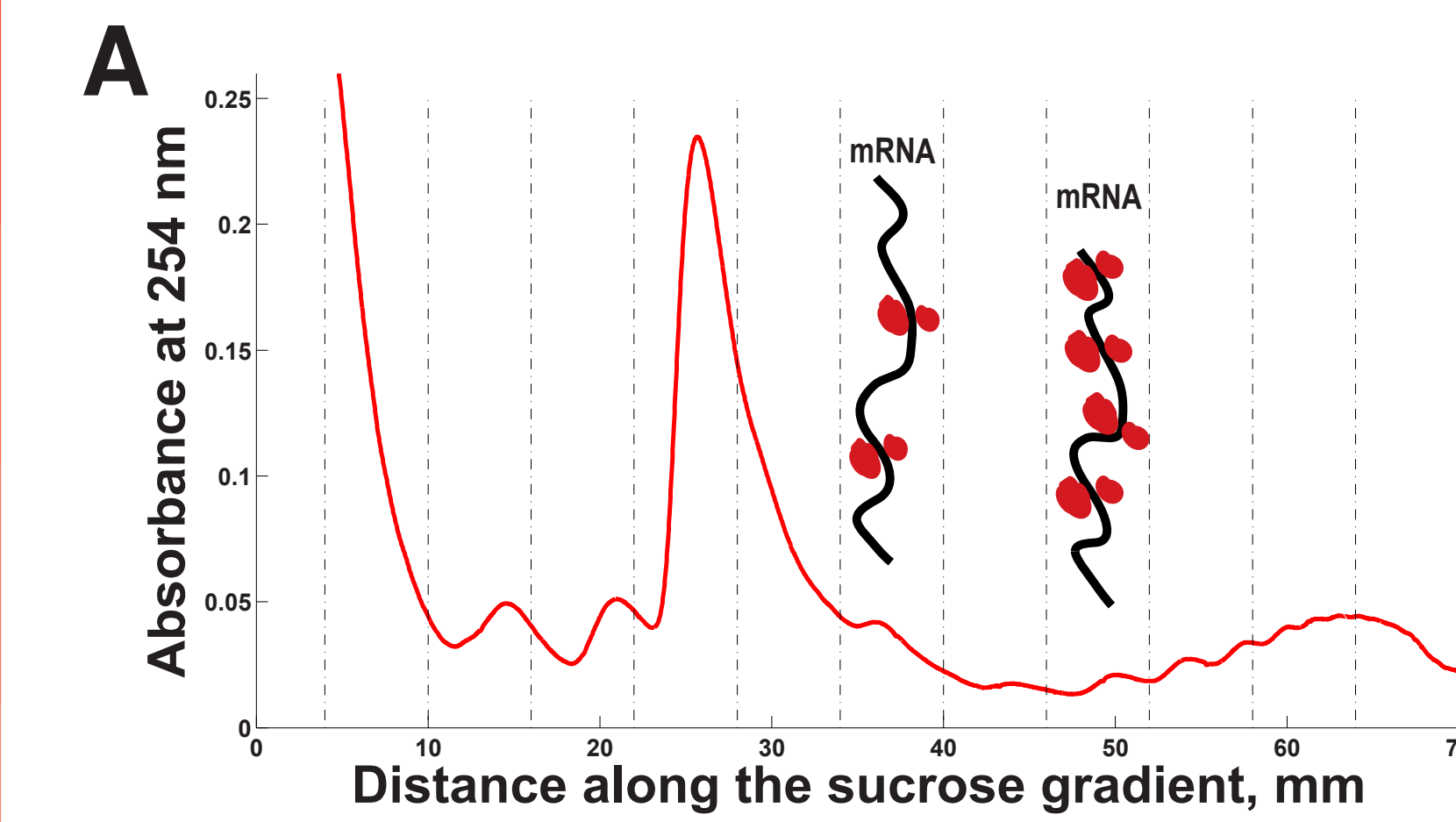
ABSTRACT

Understanding the regulation and structure of the ribosome is essential to understanding protein synthesis and its deregulation in disease. While ribosomes are believed to have a fixed stoichiometry among their core ribosomal proteins (RPs), some experiments suggest a more variable composition. Reconciling these views requires direct and precise quantification of RPs. We used mass-spectrometry to directly quantify RPs across monosomes and polysomes of budding yeast and mouse embryonic stem cells (ESC). Our data show that the stoichiometry among core RPs in wild-type yeast cells and ESC depends both on the growth conditions and on the number of ribosomes bound per mRNA. Furthermore, we find that the fitness of cells with a deleted RP-gene is inversely proportional to the enrichment of the corresponding RP in ribosomes bound to multiple mRNAs. Together, our findings support the existence of ribosomes with distinct protein composition and physiological function.

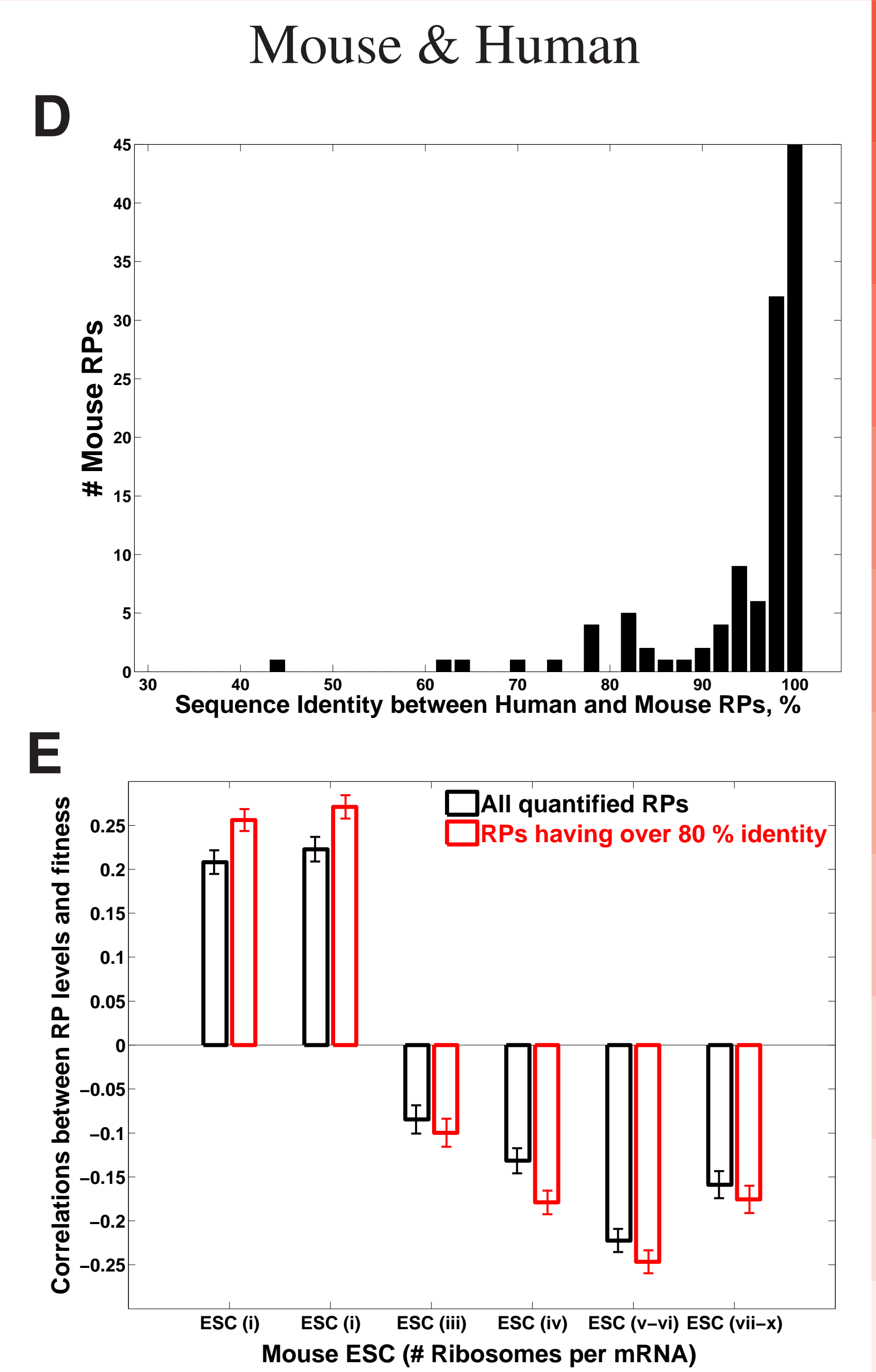
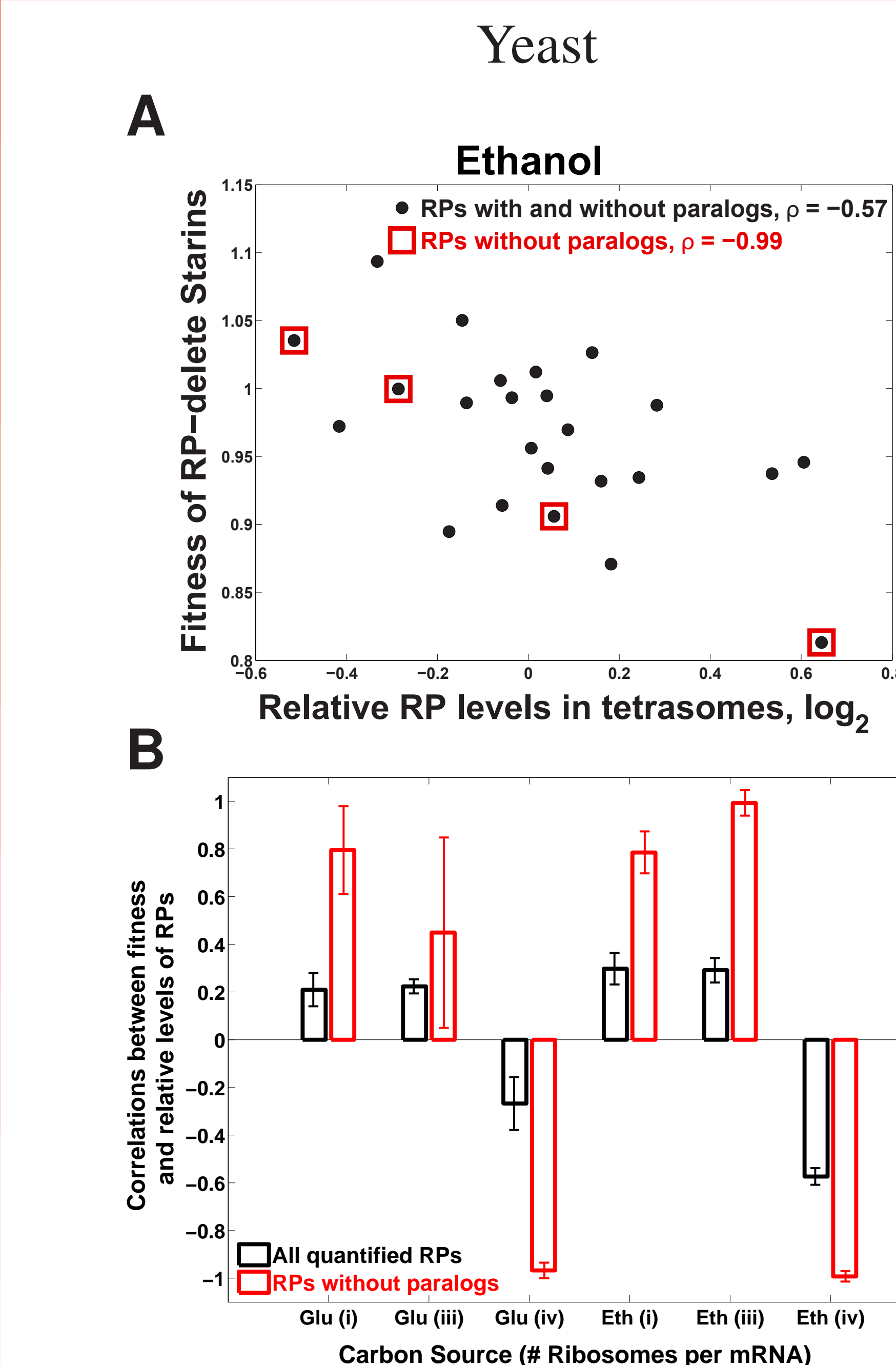
YEAST RPs



DIFFERENTIAL STOICHIOMETRY AMONG CORE RPs IN MOUSE ESCS



RP STOICHIOMETRY CORRELATES WITH FITNESS



REFERENCES

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