# Supplementary information for

# DDX39B promotes translation through regulation of pre-ribosomal RNA levels

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**Table S1. Primers used in qRT-PCR for various investigations**

| Gene Name | Sequence (5' to 3') | Investigation |
|---|---|---|
| DDX39B-FP | GAGCAAAGAGATCCGTCCAG | DDX39B mRNA level |
| DDX39B-RP | TTCCGGTTCTTCTCGTTGTC | DDX39B mRNA level |
| DDX49-FP | CTTCTTCTGGGAAGCACAGG | DDX49 mRNA level |
| DDX49-RP | TTCATCATGGAGTGCAGAGC | DDX49 mRNA level |
| GAPDH-FP | TCACCAGGGCTGCTTTTAAC | qPCR normalization |
| GAPDH-RP | TGACGGTGCCATGGAATTTG | qPCR normalization |
| 47S-FP | CTGTCCTCTGGCGACCTG | 47S rRNA level |
| 47S-RP | GAGAGAACAGCAGGCCCG | 47S rRNA level |
| H42-FP | GCACCGTTTGTGTGGGGTTGG | Chromatin Immunoprecipitation (ChIP) |
| H42-RP | CGAGACAGATCCGGCTGGCAG | |
| H0-FP | GGAGGTATATCTTTCGCTCCGAG | |
| H0-RP | GACGACAGGTCGCCAGAGGA | |
| H13-FP | ACCTGGCGCTAAACCATTCGT | |
| H13-RP | GGACAAACCCTTGTGTCGAGG | |
| H18-FP | GTTGACGTACAGGGTGGACTG | |
| H18-RP | GGAAGTTGTCTTCACGCCTGA | |
| YY2-FP | TATAGCGGCTGCGAAAAGAT | |
| YY2-RP | CTTTGCCACATTCTGCACAT | |
| CALML3-FP | GGCCTTCTCCCTGTTTGAC | |
| CALML3-FP | TCCGTGTCCTTCATCTTCCT | |

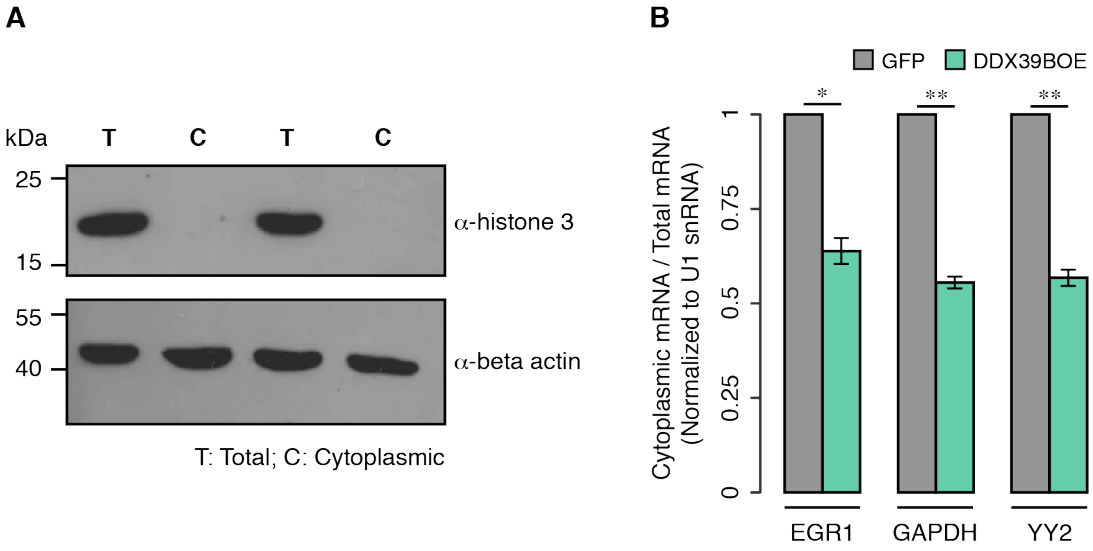


**Figure S1**: Overexpression of DDX39B inhibits mRNA export. HEK293 cells were transfected with pEGFP-C1 vector or pEGFP-DDX39B and cytoplasmic RNA and total RNA were isolated after 60 hours of transfection. **(A)** Western blot analysis of total (T) and cytoplasmic (C) extracts, used for RNA isolation. The immunoblotting was performed with histone 3 (nuclear protein) or beta actin antibody. The absence of histone 3 signal in cytoplasmic extracts confirms that there is no nuclear leakage in the cytoplasmic fractions. **(B)** Subcellular distribution of mRNAs of the indicated genes was quantified using qRT-PCR. The ratios of cytoplasmic to total mRNA were normalized to U1 small nuclear RNA (snRNA) levels and are presented relative to the control sample. Data are represented as mean of three independent experiments, with error bars representing standard deviations. The statistical significance was assessed by two tailed t-Test: paired two samples for means. * represents P-value < 0.05 and ** P-value < 0.01.

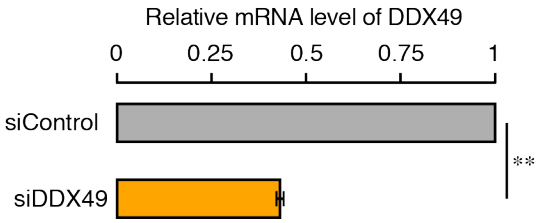


**Figure S2**: Knockdown efficiency of DDX49 siRNA. HEK293 cells were transfected with control siRNA or DDX49 and transcript levels of DDX49 were quantified using qRT-PCR. DDX49 transcripts levels were normalized to GAPDH expression and are presented relative to the control sample. Data are represented as mean of three independent experiments, with error bars representing standard deviation. Statistical significance was assessed by two tailed t-Test: paired two samples for means. ** represents P-value < 0.01.