Supplementary Notes

Note S1: Proteins interacting with NORAD *in vitro*

While this paper was under review, an independent study reported an *in vitro* association between NORAD and the partially cytoplasmic protein KHDRBS1, inferred from mixing of exogenous NORAD fragments with cytoplasmic extracts[1]. Our quantitative RAP-MS data demonstrates that endogenous NORAD interacts strongly with the nuclear protein KHDRBS3 (a paralog of KHDRBS1) in intact cells.

Note S2: Assessing statistical significance in RAP-MS and co-IP MS data

We have used a moderated *t*-test for determining statistical significance in RAP-MS and co-IP MS experiments. The limma library we have used for this purpose applies an empirical Bayes approach to effectively use variance shrinkage to make the test robust even with very few samples[2,3]. Ritchie *et al*., 2015[3] demonstrate that this method is applicable to a small number of samples — in fact the example presented in their study uses two groups with two replicates each. This approach is widely used for the analysis of quantitative mass spectrometry experiments[4,5].

Note S3: Promiscuous RNA binders in RAP-MS data

Promiscuous RNA binders were defined by intersecting the results of 9 different lncRNA RAP experiments, including MALAT1, U1, CRNDE, NORAD, RMRP, PVT1, DANCR, RN7SK, RPPH1.

Note S4: Detection of NARC1 components by size-exclusion chromatography and western blot

While we detected PRPF19 as a component of NARC1 by size-exclusion chromatography (SEC) and western blot, we did not manage to probe for the PRPF19/CDC5L complex subunit CDC5L due to a lack of high quality antibodies. With available antibodies the detection of CDC5L in cellular extracts proved challenging. At the same time, material recovered from RBMX co-IP and SEC experiments was highly limiting and did not allow comprehensive characterization of protein content beyond several key components.

References

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