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The NORAD lncRNA assembles a topoisomerase complex critical for genome stability

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Supplementary Tables

Supplementary Table 1 | Proteins enriched in RMRP antisense purifications. RMRP RAP-MS iTRAQ data ($\log_2\text{FC} < -1.6$, $P < 0.05$) from two biological replicate experiments. Adjusted P value was estimated by two-tailed moderated t -test (Supplementary Note 2).

Supplementary Table 2 | Proteins enriched in NORAD antisense purifications. NORAD RAP-MS iTRAQ data ($\log_2\text{FC} > 1.6$, $P < 0.05$) from two biological replicate experiments. Adjusted P value was estimated by two-tailed moderated t -test (Supplementary Note 2).

Supplementary Table 3 | Transcriptome-wide RBMX binding sites. RBMX CLIP peaks enriched in two biological replicate experiments over size-matched input (fold change ≥ 2 , see Methods).

Supplementary Table 4 | NORAD-dependent RBMX protein-protein interactions. TMT quantification of RBMX co-IP in NORAD wt relative to NORAD kd cells. Two independent experiments were performed for each condition. Adjusted P value was estimated by two-tailed moderated t -test (Supplementary Note 2).

Supplementary Table 5 | NARC1 size-exclusion chromatography and mass spectrometry. Mass spectrometry validation of RBMX, RBMXL1, TOP1 and PRPF19 peptides in fractions 4-6 of size-fractionated RBMX co-IP samples.

Supplementary Table 6 | Analysis of alternative splicing. Alternative splicing events in NORAD CRISPRi knockdown cells at 24 h ($n=2$), 48 h ($n=3$) and 96 h ($n=3$) ($\text{PSI} > 20\%$, $\text{FDR} < 0.05$). P values across putative splicing events were corrected using the Benjamini–Hochberg procedure to derive an FDR. dPSI: delta percentage spliced in.

Supplementary Table 7 | Analysis of differentially expressed genes. Differentially expressed genes upon NORAD CRISPRi knockdown at 24 h ($n=2$), 48 h ($n=3$) and 96 h ($n=3$) ($\log_2$ fold change > 1 , $\text{FDR} < 0.05$). P values for differential gene expression were corrected using the Benjamini–Hochberg procedure to derive an FDR. lfcSE: log fold change Standard Error; stat: Wald statistic.

Supplementary Table 8 | DNA combing CldU + IdU measurements. DNA combing raw data (speed and track length). CldU: 5-Chloro-2'-deoxyuridine; IdU: 5-Iodo-2'-deoxyuridine.

Supplementary Table 9 | DNA combing CldU measurements.

DNA combing raw data (speed and track length). CldU: 5-Chloro-2'-deoxyuridine.

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41 **Supplementary Table 10 | DNA combing IdU measurements.**

42 DNA combing raw data (speed and track length). IdU: 5-Iodo-2'-deoxyuridine.

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44 **Supplementary Table 11 | Cell cycle analysis of NORAD and RBMX depleted cells.**

45 Raw measurements of EdU incorporation and total DNA content for NORAD and RBMX
46 CRISPRi knockdown experiments. EdU: 5-Ethynyl-2'-deoxyuridine.

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48 **Supplementary Table 12 | Cell cycle analysis of TOP1 depleted cells.**

49 Raw measurements of EdU incorporation and total DNA content for TOP1 RNAi knockdown
50 experiments. EdU: 5-Ethynyl-2'-deoxyuridine.

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