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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  $\geq 2$ , 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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