Supplementary Methods

siRNAs

siRNA target sequences used in this study were: Control (CTRL) (5'-GGGAUACCUAGACGUUCUA-3'); UBL5(#57) (5'-CGAUUUUUAAGGACCACGU-3'); UBL5(#58) (5'-CCUGGAGCUUUAUUAUCAA-3'); UBL5(#82) (5'-UGAAGAAGUGGUACACGAU-3'); SART1(#1)(5'-GCUCUAUCCUGUCCAAGUA-3'); SART1(#2) (5'-GCAUCGAGGAGACUAACAA-3'); EFTUD2(#1) (5'-CGACCCUUGAAGUUCAAUA-3'); EFTUD2(#2) (5'-GCAUGUAUUCCACUGAUGA-3'); WAPL (5'-CGGACUACCCUUAGCACAA-3'); Sororin (5'-GCCUAGGUGUCCUUGAGCU-3'); SGO1 (5'-CAGUAGAACCUGCUCAGAA-3'); and BubR1 (5'-GAUGGUGAAUUGUGGAAUA-3')

Primer sequences for RT-PCR analysis

Primer sequences used in this study were: *Sororin* exon1-forward, 5'-AACGCGGTCCGGAGGA-3'; *Sororin* exon2-reverse, 5'-TTCGGCCAGATTTCAGGGAG-3'; *Sororin* exon5-forward, 5'-AGTCTCGCCAGTGGTGTGCT-3'; *Sororin* exon6-reverse, 5'-TTCAACCAGGAGATCAAACTGC-3'.

Antibodies

Antibodies used in this study included: Rabbit polyclonals to SMC1, SMC3, RAD21, SA2, WAPL, PDS5B, ESCO2, and EFTUD2 (Bethyl), MFAP1, H2B and β-Tubulin (Abcam), SART1 (Sigma-Aldrich), Histone H3-pSer10 (06-570, Millipore), and ORC2 (BD Biosciences Pharmingen), mouse monoclonals to HA and GFP (Santa Cruz), Cyclin B1 (Abcam), FLAG (Sigma), SGO1 (Abnova), and XRCC3 (Novus Biologicals), goat polyclonals to MCM6 and LZTS2 (Santa Cruz). Rabbit polyclonals to *S. pombe* Hub1 and human Sororin were kind gifts

from Dr. Hideki Yashiroda (University of Tokyo, Japan) and Dr. Jan-Michael Peters (Institute of Molecular Pathology, Vienna, Austria), respectively.

Preparation of chromatin-enriched fractions

For the preparation of chromatin-enriched fractions, cells were resuspeded in lysis buffer (10 mM HEPES, pH 7.9; 10 mM KCl; 1.5 mM $MgCl_2$; 0.34 M Sucrose; 10% Glycerol; 0.1% Triton X-100) supplemented with protease inhibitor cocktail (Roche) and incubated on ice for 5 min. After centrifugation at 1,300g for 4 min at 4 ℃, the pellet was washed with the lysis buffer and centrifuged at 1,300g for 4 min. The pellet was incubated with 250 U/ml Benzonase Nuclease (Sigma) in modified RIPA buffer (50 mM Tris, pH 7.5; 150 mM NaCl; 1% NP-40; 0.1% Sodium Deoxycholate) supplemented with protease inhibitor cocktail (Roche) for 15 min at 37 ℃. Insoluble fraction was removed by centrifugation at 16,000g for 10 min at 4 ℃.

Analysis of alternative splicing

Identification of alternative splicing was done with spliceR software based on full-length transcripts, as described [19]. Briefly, for each gene the hypothetical pre-RNA was constructed from the exon information of all transcripts belonging to that gene. In a pairwise manner, these transcripts were then compared to this hypothetical pre-RNA and all alternative splicing events were classified and annotated. For each transcript and condition, spliceR also calculates an isoform fraction (IF) value. This IF value is calculated as (transcript expression) / (gene expression) x 100%, and represents the contribution of a transcript to the expression of the parent gene. Furthermore, a delta-IF (dIF) value, indicating absolute change in IF values between conditions, is also calculated. Isoform switches were identified by searching for genes, for which one transcript had a dIF value of ≥20 and another transcript a dIF value of ≥-20. The coding potential of transcripts was analyzed via spliceR as described [19]. Briefly, annotated ORFs from Gencode were retrieved from the UCSC Genome Browser repository. For each transcript, the

most upstream compatible start codon was identified, the downstream sequence was translated, and for the most upstream stop codon, the distance to final exon-exon junction was annotated. By consensus, transcripts are marked NMD-sensitive if a stop codon appears more than 50 nt upstream of the final exon-exon junction, indicating a pre-mature stop codon (PTC).