Supplementary Figures

Nanopore sequencing reveals endogenous NMD-targeted isoforms in human cells

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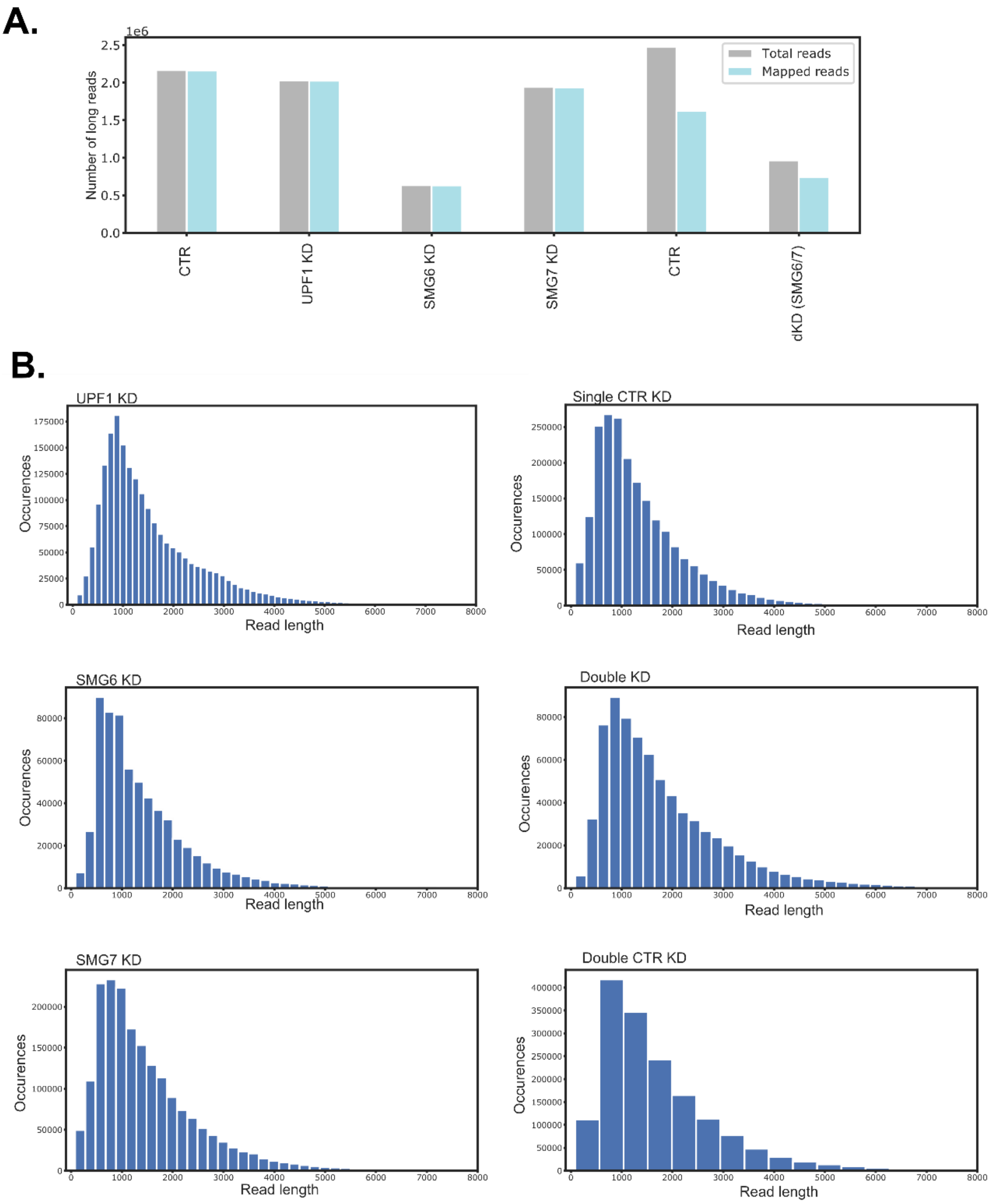
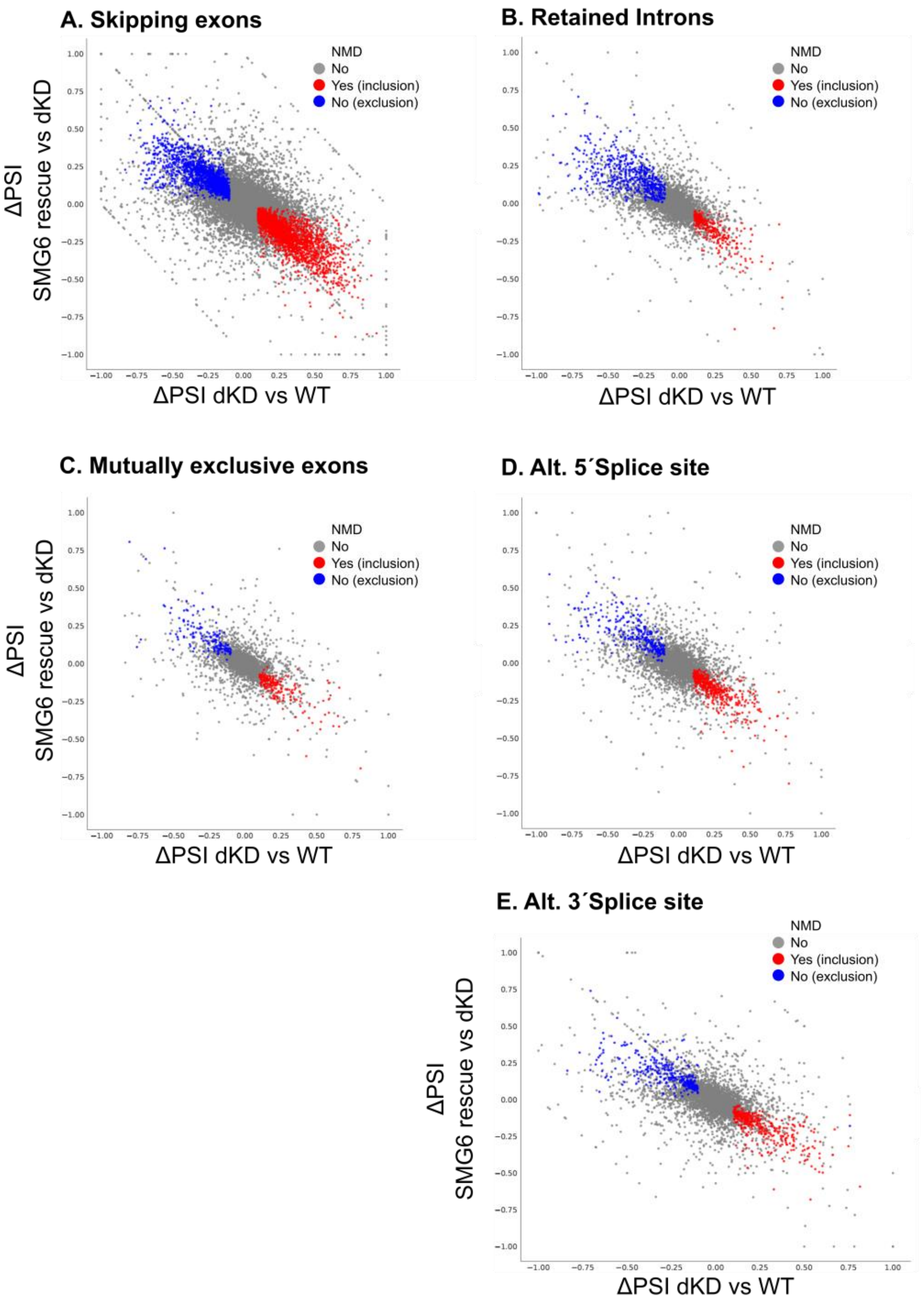


Figure S1 (A) Number of totally sequenced (grey) and mapped Nanopore reads (light blue) in the different cDNA sequencing experiments of reverse-transcribed total RNA from cells with the indicated knockdowns. **(B)** Read length distribution of mapped reads from the long-read cDNA sequencing experiments indicated in (A).



A. Skipping exons

B. Retained Introns

C. Mutually exclusive exons

D. Alt. 5´Splice site

E. Alt. 3´Splice site

Figure S2 (A-E) Scatter plots comparing the change in "percent spliced in" (deltaPSI) of exons in CTR versus dKD (*x*-axis) and SMG6 rescue versus dKD (*y*-axis). Coloured in red are significant exon inclusion and in blue significant exon exclusion events. Non-significant events are depicted in grey.

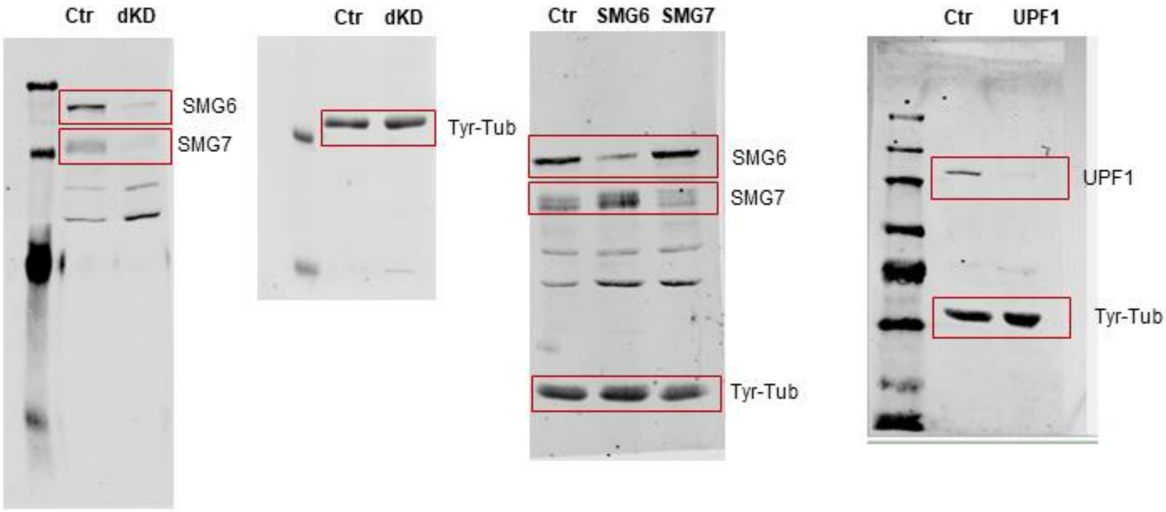


Figure S3 Uncropped Western blots