

Figure S1. Prediction of secondary structure dynamics of TRF2 using the IUPred predictor (<http://iupred.enzim.hu>). IUPred2 scores characterize the disordered tendency of each position along the sequence, residues with a predicted score above 0.5 are considered disordered; ANCHOR2 scores characterize the probability of each residue being part of a binding region.

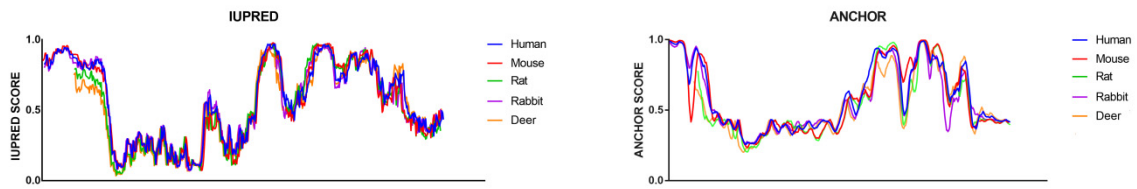


Table S1. Mass spectrometric analysis reveals that peptides are common to lamins A and C or immature prelamin A/C. Peptides in the first column were detected at least once in two independent runs.

Peptide	Residues in prelamin A/C
LQEKEDLQELNDR	29–41
LQTLKEELDFQK	198–210
LADALQELR	241–250
NSNLVGAAHEELQQR	280–296
VAVEEVDEEGKFVR	439–453
AQNTWGCSSLR	516–529