**Figure Legends - Supplement**

**Fig.S1 DNA damage causes formation of nuclear actin filaments that associate with γH2AX and are required for an efficient DDR** (**A**) Representative IF image showing over-expression of mCherry-Exportin 6 (red) in U2OS+GFP-nAC. Nuclear actin (green) is exported into the cytoplasm (white arrows). DNA is stained with DAPI (blue). (**B**, **C and D**) Quantification of WB shown in Fig. 1E, showing expression of exportin 6 reduces nuclear actin (**B**) and simultaneously increases levels of DNA damage (H2AX) (**C**) and pKAP1 (**D**), n = 3. Data are presented as mean ± SEM and were analysed by parametric Student *t* test. \*\* = *p* < 0.01 and \*\*\* *p* < 0.001.

**Fig.S2 PML NBs localise along nuclear actin filaments** (**A**) Line-scan plot of IF data shown in Fig.2A showing extent of PML (red) and nuclear actin (green) colocalisation. Graph (right) shows colocalised regions as blue peaks. (**B**) 3D confocal microscopy image of PML in U2OS+GFP-nAC. PML foci (red) are distributed along nuclear F-actin (green). (**C**) IF representative image of recombinant mCherry-PML and nuclear actin (green) in U2OS expressing GFP-nAC. Localisation of PML along nuclear F-actin is evident (white arrows). DNA is stained with DAPI (blue). Scale bar = 10 µm. (**D**) Timelapse of PML (red) and nuclear actin (green) in U2OS expressing GFP-nAC. Images were taken every 2 minutes for 1.5 hours then frameshift adjusted.

**Fig.S3 Prelamin A causes mislocalisation of nuclear actin** (**A**) Quantification of IF data investigating the effect of prelamin A expression on nuclear F-actin polymerisation in U2OS+GFP-nAC treated with various inducers of DNA damage (etoposide (1 mM for 3 hrs), hydrogen peroxide (H2O2) (200 µM for 2 hours, ultra-violet (UV) irradiation (fixed 1 hour after 50 J/m2 irradiation) or serum starved. Data taken from 3 independent experiments (> 100 cells). (**B-C**) Representative WB and quantification of biochemical cell fractionations investigating the effect of prelamin A on nuclear actin cellular localisation. Cy = cytoplasmic fraction, Ns = nuclear soluble fraction, Ch = chromatin fraction, Ne = nuclear envelope fraction. U2OS+GFP-nAC were also transduced to express prelamin A. Prelamin A caused nuclear actin to shift from chromatin fraction into the nuclear envelope fraction as indicated by probing with GFP (actin chromobody). Quantification of this shift is shown in (**C**). (**D**) Quantification of experiments shown in Fig. 3C, showing prelamin A expression reduces localisation of γH2AX on nuclear F-actin in U2OS+GFP-nAC cells in the presence or absence of DNA double-strand breaks caused by 3 hr 1 mM etoposide treatment (n = 4). Data are presented as mean ± SEM and were analysed by one-way ANOVA and Tukey’s test or parametric Student *t* test. \* = *p* < 0.05, \*\* = *p* < 0.01 and \*\*\* *p* < 0.001. ns = not significantly different.

**Fig.S4 Expression of prelamin A ablates PML localisation on nuclear F-actin** (**A**) Representative IF showing PML in a U2OS+GFP-nAC cell also expressing prelamin A. Prelamin A (red) localises to the NE and causes nuclear actin (green) to also localise at the nuclear periphery. PML (magenta) no longer associates with nuclear F-actin. DNA is stained with DAPI (blue), scale bar is 10 µm. (**B**) Quantification of WB shown in Fig. 4D showing no change in either PML isoform upon prelamin A expression (adPLA) in U2OS cells, n = 4. Data are presented as mean ± SEM and were analysed by parametric Student *t* test.

**Fig.S5 Leptomycin B restores nuclear F-actin networks in prelamin A expressing cells and improves genomic integrity when used in combination with Remodelin** (**A**) WB analysis of whole cell lysates from U2OS cells expressing prelamin A through siRNA directed depletion of Face1 (siFace1) (causing prelamin A to accumulate). These cells were further treated with adenovirus to over-express wild-type lamin A (WTLA) to examine if mature lamin A could out-compete prelamin A to reduce levels of DNA damage (H2AX), however no improvement was seen, n = 3. (**B**) WB analysis of lysates from U2OS cells expressing prelamin A that were treated with retinoic acid receptor agonist AC261066 (AC) and antagonist BMS453 (BMS) and further treated with etoposide. Levels of DNA damage were assessed by quantifying H2AX, n = 3. (**C**) WB and IF analysis examining the over-expression of the dominant negative nesprin KASH (Klarsicht, ANC-1, Syne-Homology domain) domain in U2OS cells over-expressing prelamin A. There was no decrease in H2AX detected either in WB or IF (magenta staining), suggesting disruption of mechanotransduction was insufficient to restore genomic instability induced by prelamin A. (**D**) Representative IF and quantification showing LMB treatment increases levels of nucleoplasmic mDia2 (green). Data was taken from 3 independent experiments and mDia2 intensity was measured in > 100 cells. (**E**) Quantification of results shown in Fig. 6A. 2 hours of LMB treatment resulted in a significant increase in nuclear F-actin in cells treated with etoposide (1 mM for 3 hrs), n = 3 (> 100 cells). (**F**) Line-scan plot of IF data shown in Fig.6E showing extent of PML and nuclear actin colocalisation. Graph (right) shows colocalisation of PML (magenta) and nuclear actin (green) as blue peaks. (**G**) Additional example IF showing restoration of PML (magenta) association with nuclear F-actin (green) in a U2OS+GFP-nAC cell expressing prelamin A (red) that has been treated with LMB. Scale bars = 10 µm. (**H**) Cell vitality data showing effect of Remodelin treatment on U2OS cells expressing prelamin A and quantification of ‘dead cells’ (indicated by red arrow) from experiment shown in Fig. 6H, n = 8. Data are presented as mean ± SEM and were analysed by one-way ANOVA and Tukey’s test. \* = *p* < 0.05, \*\* = *p* < 0.01 and \*\*\*\* *p* < 0.0001. ns = not significantly different.