Figure S1: RPA most strongly interacts with DEK following HU-treatment. HF-DEK transduced cells were treated with either HU or IR for the indicated time points and harvested using the TAP-protocol. After performing washes on the FLAG affinity beads, they were boiled in 2x Laemmli buffer, analyzed by Western blot. The interaction with RPA was strongest in the HU-treated samples and weakest in those treated with IR.

```
  1 MSASAPAAEG EGTPTQPASE KEPEMPGPRE ESEEEEDEDD EEEEEEEKEK
 51 SLIVEGKREK KKVERLTMQV SSLQREPFTI AQGKGQKLCE IERIHFFLSK
101 KKTDELRNLH KLLYNRPGTV SSLKKNVGQF SGFPFEKGSV QYKKKEEMLK
151 KFRNAMLKSI CEVLDLERSG VNSELVKRIL NFLMHPKPSG KPLPKSKKTC
201 SKGSKKERNS SGMARKAKRT KCPEILSDES SSDEDEKKNK EESSDDEDKE
251 SEEEPPKKTA KREKPKQKAT SKSKKSVKSA NVKKADSSTT KKNQNSSKKE
301 SESEDSSDDE PLIKKLKKPP TDEELKETIK KLLASANLEE VTMKQICKKV
351 YENYPTYDLT ERKDFIKTTV KELIS      Sequence Coverage: 77%
```

Figure S2: DEK peptide and phosphorylation sequences identified in HF-DEK TAP-MS. The sequence match score to human DEK was 7289. Matching peptides are shown in bold red, and identified phosphorylated sequences are shown in bold blue (<5% FDR and Significance Threshold at p<0.005).

```
  1 MSASAPAAEG EGTPTQPASE KEPEMPGPRE ESEEEEDEDD EEEEEEEKEK
 51 SLIVEGKREK KKVERLTMQV SSLQREPFTI AQGKGQKLCE IERIHFFLSK
101 KKTDELRNLH KLLYNRPGTV SSLKKNVGQF SGFPFEKGSV QYKKKEEMLK
151 KFRNAMLKSI CEVLDLERSG VNSELVKRIL NFLMHPKPSG KPLPKSKKTC
201 SKGSKKERNS SGMARKAKRT KCPEILSDES SSDEDEKKNK EESSDDEDKE
251 SEEEPPKKTA KREKPKQKAT SKSKKSVKSA NVKKADSSTT KKNQNSSKKE
301 SESEDSSDDE PLIKKLKKPP TDEELKETIK KLLASANLEE VTMKQICKKV
351 YENYPTYDLT ERKDFIKTTV KELIS      Sequence Coverage: 67%
```

Figure S3: DEK peptide and phosphorylation sequences identified in the untreated HF-DEK TAP-MS sample. The sequence match score to human DEK was 2503. Matching peptides are shown in bold red, and identified phosphorylated sequences are shown in bold blue (<5% FDR and Significance Threshold at p<0.005).

```
  1 MSASAPAAEG EGTPTQPASE KEPEMPGPRE ESEEEEDEDD EEEEEEEKEK
 51 SLIVEGKREK KKVERLTMQV SSLQREPFTI AQGKGQKLCE IERIHFFLSK
101 KKTDELRNLH KLLYNRPGTV SSLKKNVGQF SGFPFEKGSV QYKKKEEMLK
151 KFRNAMLKSI CEVLDLERSG VNSELVKRIL NFLMHPKPSG KPLPKSKKTC
201 SKGSKKERNS SGMARKAKRT KCPEILSDES SSDEDEKKNK EESSDDEDKE
251 SEEEPPKKTA KREKPKQKAT SKSKKSVKSA NVKKADSSTT KKNQNSSKKE
301 SESEDSSDDE PLIKKLKKPP TDEELKETIK KLLASANLEE VTMKQICKKV
351 YENYPTYDLT ERKDFIKTTV KELIS       Sequence Coverage: 57%
```

Figure S4: DEK peptide and phosphorylation sequences identified in the HU-treated HF-DEK TAP-MS sample. The sequence match score to human DEK was 2197. Matching peptides are shown in bold red, and identified phosphorylated sequences are shown in bold blue (<5% FDR and Significance Threshold at p<0.005).