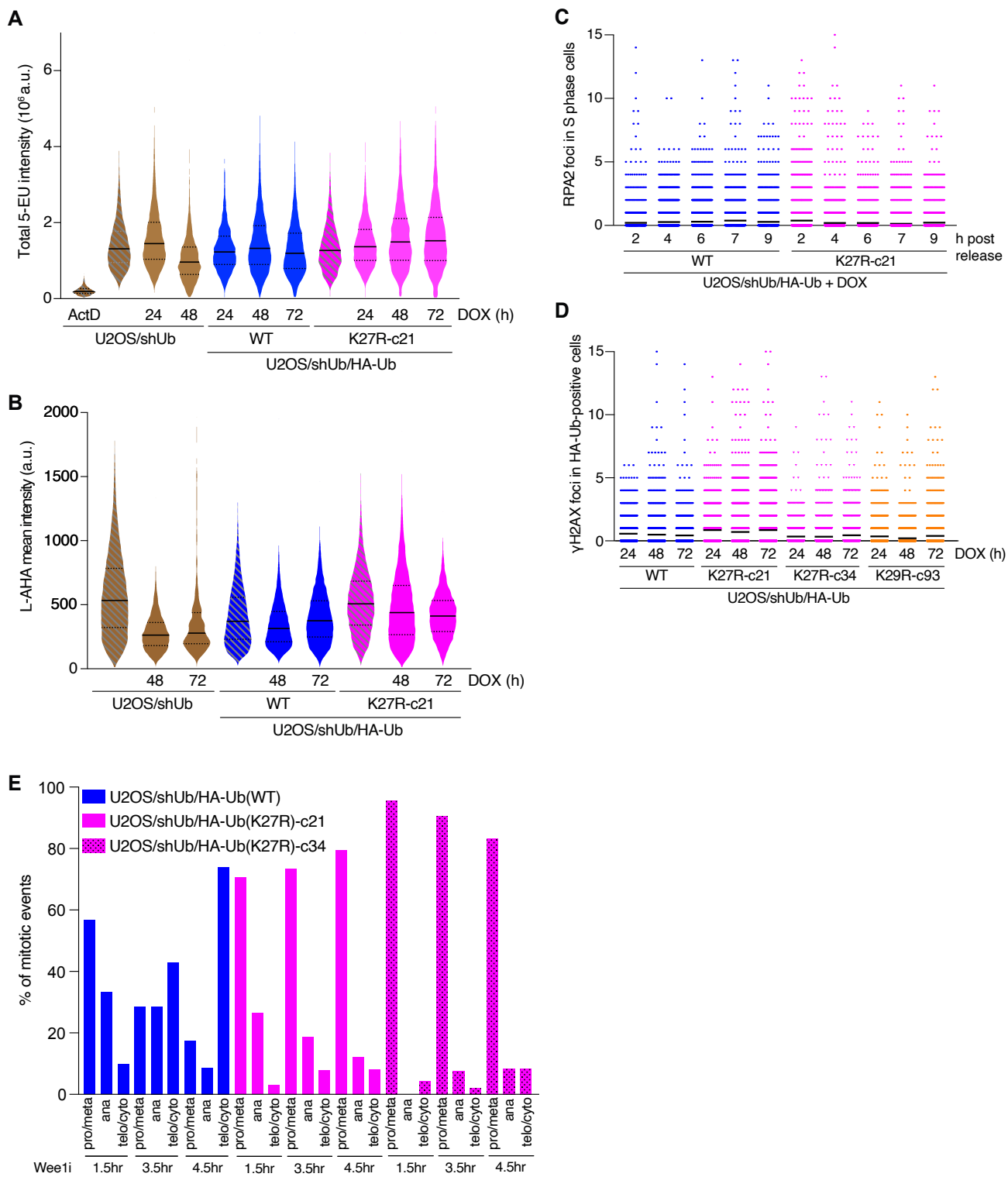


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Appendix Figure S1.....2



Appendix Figure S1.

Additional characterization of Ub replacement cell lines

A. Transcriptional activity of U2OS/shUb, U2OS/shUb/HA-Ub(WT) and U2OS/shUb/HA-Ub(K27R) cell lines treated or not with DOX, assayed by QIBC-based analysis of 5-ethynyl uridine (5-EU) incorporation (solid lines, median; dashed lines, quartiles (a.u., arbitrary units); >2000 cells analyzed per condition). The transcriptional inhibitor Actinomycin D (ActD) was used as a negative control. **B.** Translational activity of U2OS/shUb, U2OS/shUb/HA-Ub(WT) and U2OS/shUb/HA-Ub(K27R) cell lines treated or not with DOX, assayed by QIBC-based analysis of incorporation of the methionine analog L-Azidohomoalanine (L-AHA) into new proteins (solid lines, median; dashed lines, quartiles; >5000 cells analyzed per condition). **C.** Quantification of endogenous RPA2 foci in DOX-treated S phase (EdU-positive) U2OS/shUb/HA-Ub cell lines at the indicated time points after release from a double thymidine block (black bars, mean; >2000 S phase cells analyzed per condition). **D.** Quantification of endogenous γ H2AX foci of U2OS/shUb/HA-Ub(WT), U2OS/shUb/HA-Ub(K27R) and U2OS/shUb/HA-Ub(K29R) cell lines treated with DOX for the indicated times (black bars, mean; >1500 phase cells analyzed per condition). Cells were gated for Ub replacement based on HA signal positivity. **E.** Live-cell imaging-based quantification of DOX-treated U2OS/shUb/HA-Ub cell lines in different stages of mitosis after treatment with Wee1i for the indicated times.

Data are representative of three (**A,E**) and two (**B,C,D**) independent experiments.