An essential role for CtIP in chromosomal translocation formation through an alternative end-joining pathway

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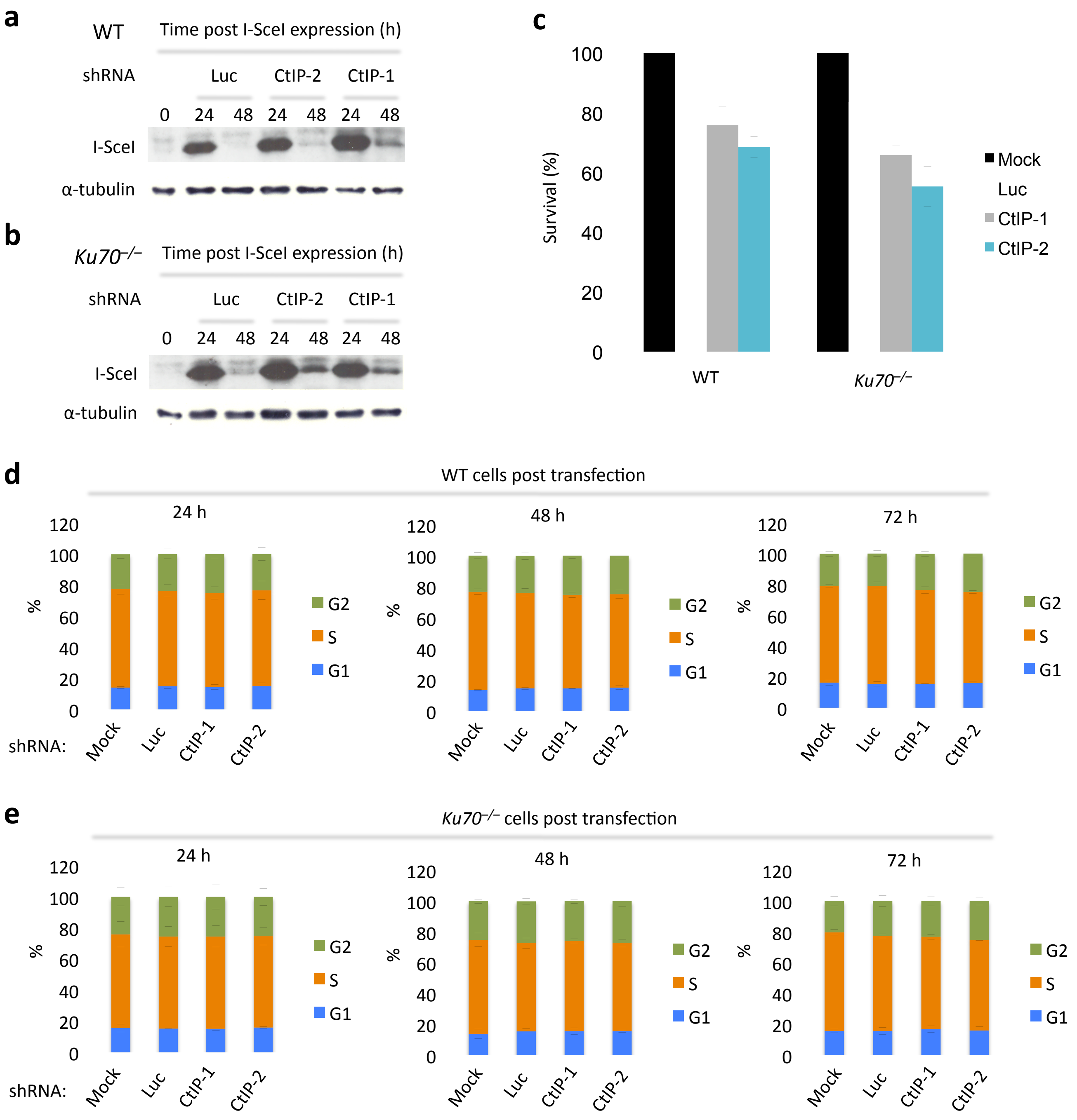
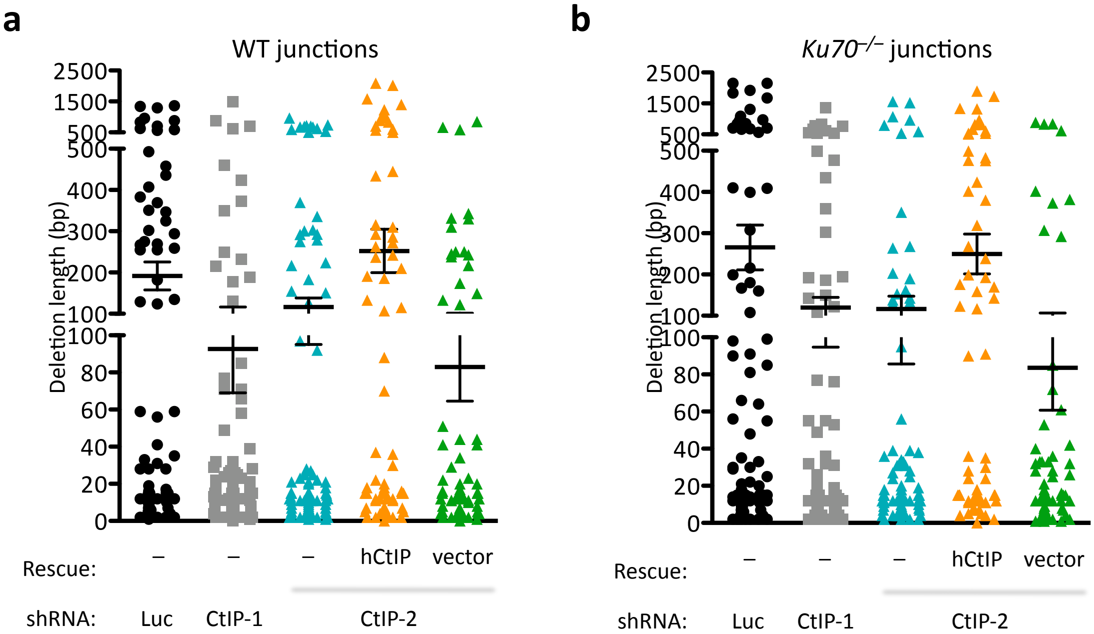


Supplementary Figure 1. The effect of CtIP depletion on I-SceI expression, cell survival, and cell cycle. (**a–b**) Representative Western blots showing I-SceI expression in shRNA-treated wild-type (**a**) and *Ku70−/−* (**b**) pCr15 cells. (**c**) Cell survival measured by colony formation assay upon treatment of the control Luc shRNA (white bar), CtIP-1 shRNA (gray bar), and CtIP-2 shRNA (blue bar) compared to mock treated cells (black bar). Note that CtIP depletion has a small effect on survival relative to the Luc shRNA (dotted line). (**d–e**) Cell cycle distribution of wild-type (**d**) and *Ku70−/−* (**e**) pCr15 cells after indicated treatment. Data represent the mean ± 1 S.D. from 3 independent experiments.



Supplementary Figure 2. Scatter plot of deletions at translocation breakpoint junctions. (**a**–**b**) Scatter plot showing deletion lengths for der(17) breakpoint junctions from wild-type (**a**) and *Ku70*$^{-/-}$ (**b**) pCr15 cells. Each value represents the combined deletion from both ends of an individual junction. The mean and the standard error of mean (SEM) of each group are indicated on the graph.

Supplementary Table 1. Summary of translocation frequencies

Treatment		Translocation frequency (10^{-5})		*P* value	
shRNA	rescue	WT	*Ku70*$^{-/-}$	WT	*Ku70*$^{-/-}$
–	–	6.05 ± 1.20	26.3 ± 4.38	–	–
Luc		5.95 ± 0.33	25.9 ± 1.25	0.655	0.597
CtIP-1		1.40 ± 0.13	6.43 ± 0.89	<0.001	<0.001
CtIP-2		1.05 ± 0.25	4.58 ± 0.81	<0.001	<0.001
Luc	vector	5.85 ± 0.31	26.2 ± 1.90	–	–
	hCtIP	6.25 ± 0.36	26.4 ± 1.92	0.218	0.891
CtIP-1	vector	1.57 ± 0.32	7.33 ± 1.05	–	–
	hCtIP	5.83 ± 1.67	23.1 ± 1.63	0.013	<0.001
CtIP-2	vector	1.39 ± 0.19	6.32 ± 0.81	–	–
	hCtIP	4.75 ± 0.55	19.8 ± 0.60	<0.001	<0.001

All translocation frequencies are normalized for colony survival after shRNA transfection (Supplementary Fig. 1c). Translocation frequencies are presented as the mean ± S.D. from three or more independent experiments. *P* values are determined by a two-tailed unpaired *t* test, derived from a comparison with mock treated control for non-rescue groups, and derived from a comparison with the correlated empty vector control for human CtIP rescue groups.