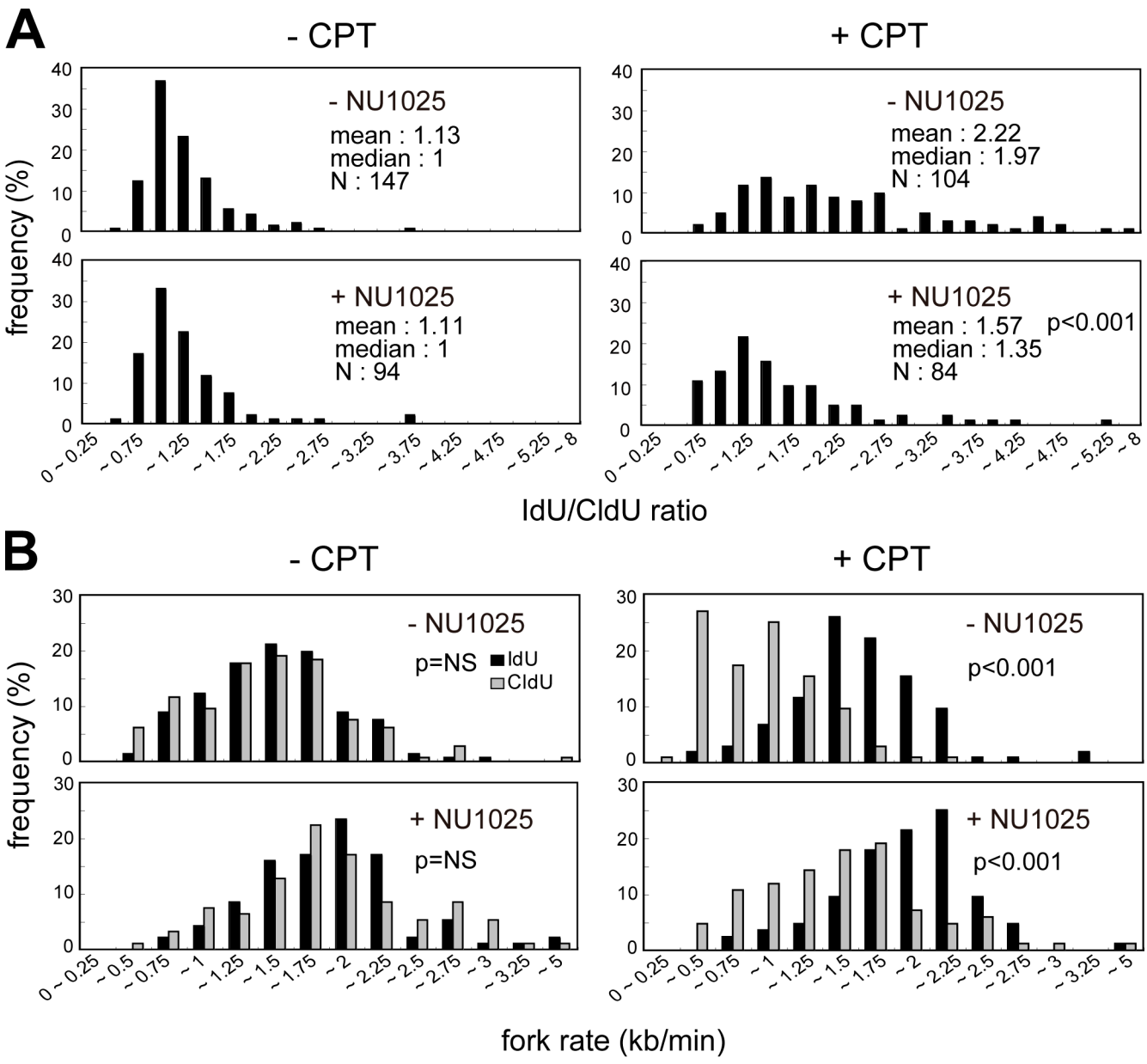
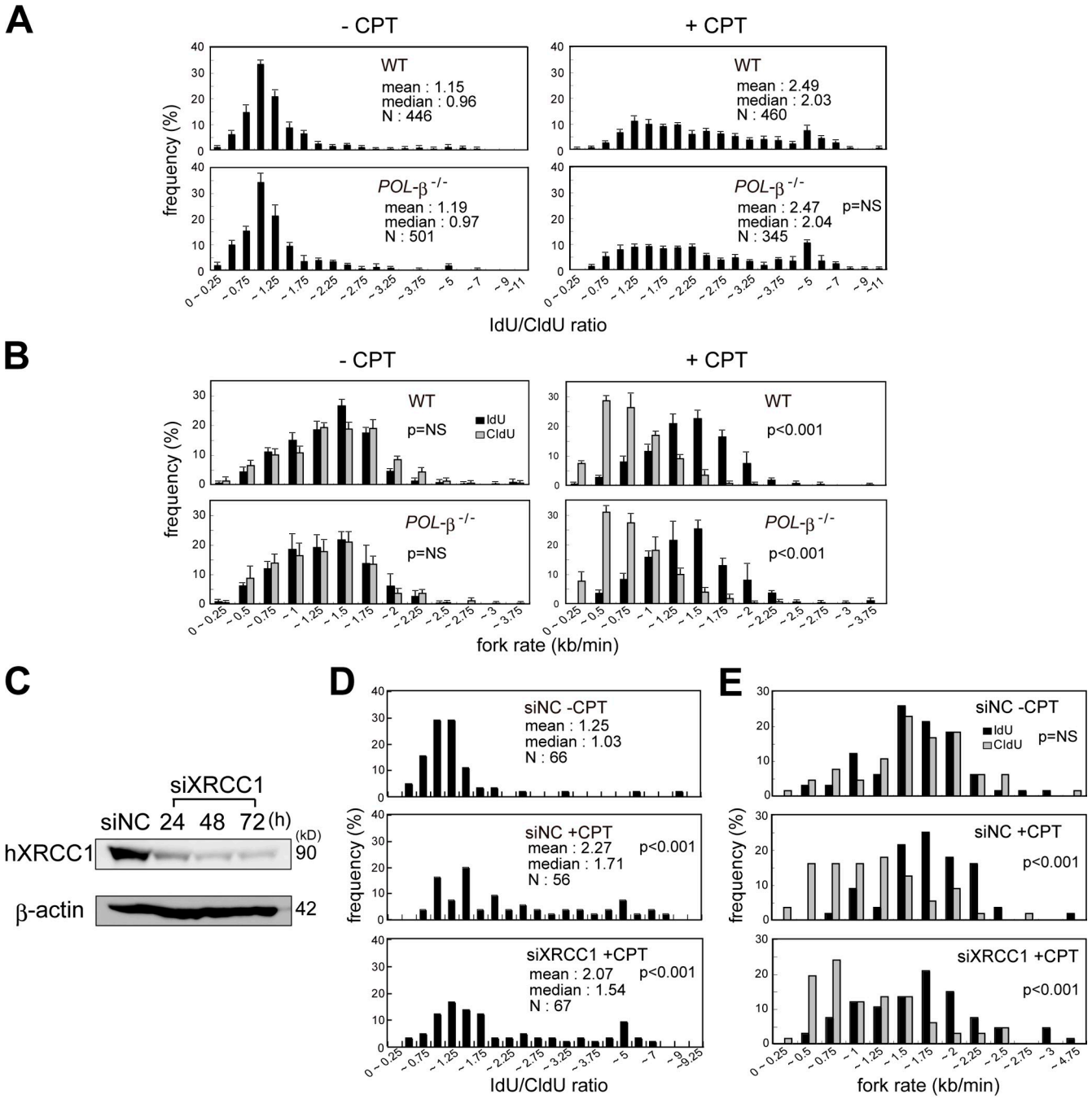


C

	fork rate (kb/min)	CPT	fork rate (kb/min)	CPT
control	1.36 ± 0.47	–	1.33 ± 0.55	–
control	1.53 ± 0.47	–	0.83 ± 0.40	+
NU1025	1.79 ± 0.61	–	1.77 ± 0.61	–
NU1025	1.84 ± 0.48	–	1.40 ± 0.60	+

Figure S1. **A PARP inhibitor abrogates the CPT-induced replication fork slowing in mouse m5S cells.** (A) Distribution of the ratio of the rate of fork progression in cells treated with or without CPT in the presence or absence of NU1025. The total number of forks analyzed in each cell treated as indicated is shown. (B) Distribution of the rate of fork progression during IdU and CldU pulse labeling in cells treated as indicated. (C) The tabular data are mean fork rates for each cell treated as indicated. The mean rates were calculated from the data described in B.



	fork rate (kb/min)	CPT	fork rate (kb/min)	CPT
siNC	1.49 ± 0.50	–	1.47 ± 0.58	–
siNC	1.67 ± 0.44	–	1.02 ± 0.53	+
XRCC1	1.55 ± 0.62	–	0.98 ± 0.56	+

Figure S2. **Base excision repair machineries are not involved in replication fork slowing in response to CPT-induced DNA damage.** (A and B) Distribution of the ratio of the rate of fork progression and the rate of fork progression during IdU and CldU pulse labeling in wild-type (WT) and *polymerase* $\beta^{-/-}$ DT40 cells. Data bars are the means of three independent experiments, and error bars represent SEM. The total number of the forks analyzed in each cell is also indicated. (C) Evaluation of XRCC1 knockdown in HeLa cells. The amount of XRCC1 in HeLa cells transfected with the siRNA duplex against XRCC1 and control siRNA was evaluated by Western blotting. β-Actin was detected as a loading control. (D and E) Distribution of the ratio of the rate of fork progression and the rate of fork progression during IdU and CldU pulse labeling in HeLa cells transfected with the siRNA duplex against XRCC1 and control siRNA. The total number of the forks analyzed in each cell is also indicated. (F) The tabular data are mean fork rates for each cell transfected with each siRNA. The mean rates were calculated from the data described in E. siNC, negative control siRNA.

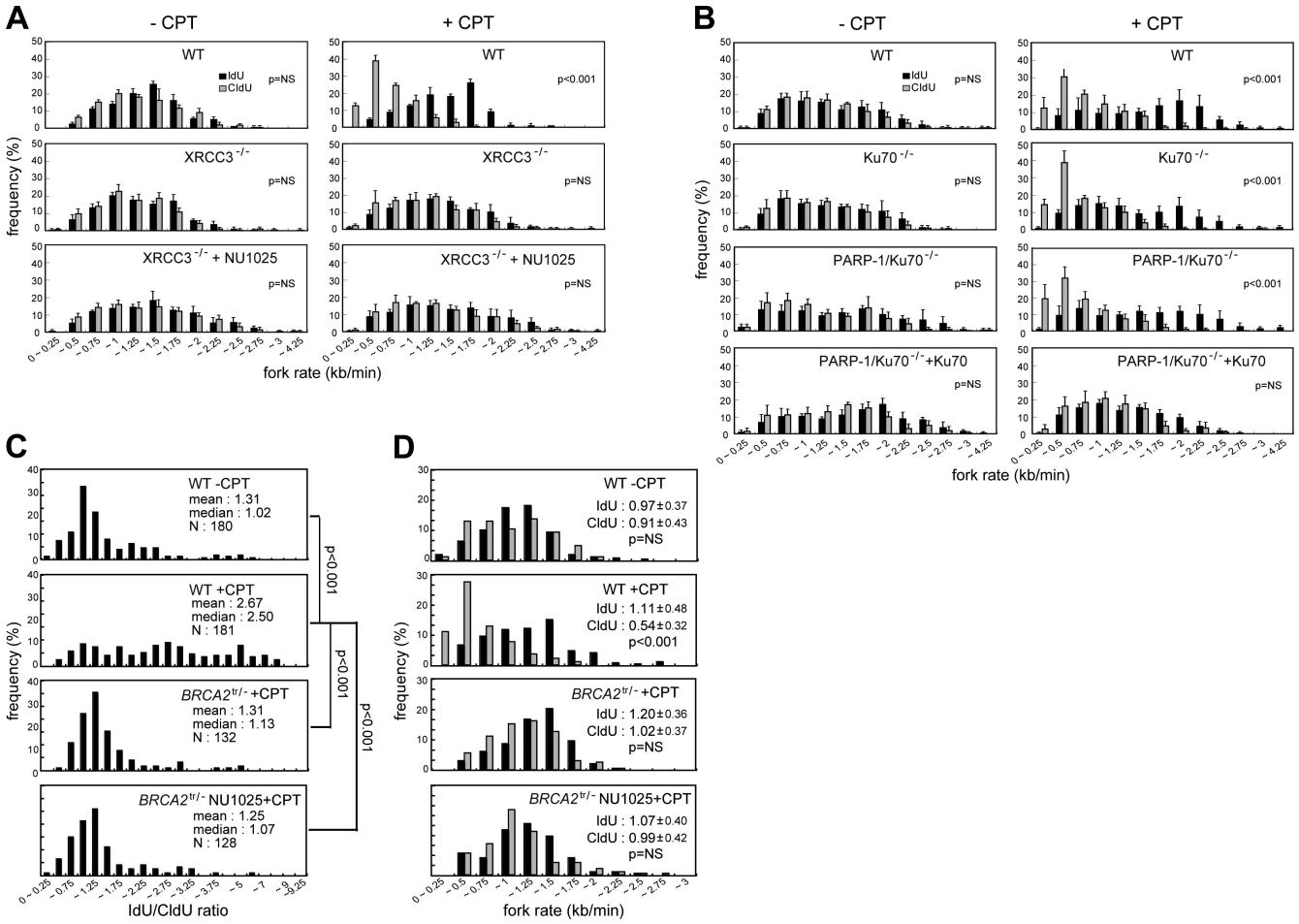


Figure S3. **Replication fork progression in each indicated DT40 cell.** (A and B) Distribution of the ratio of the rate of fork progression and the rate of fork progression during IdU and CldU pulse labeling in each indicated cell line. Cells were treated with CPT during CldU labeling. NU1025 was pretreated for 2 h before IdU pulse labeling and treated during IdU and CldU pulse labeling. (C and D) Distribution of the ratio of the rate of fork progression and the rate of fork progression during IdU and CldU pulse labeling in wild-type (WT) and *BRCA2*$^{tr/-}$ DT40 cells. The data are represented as described in A and B. The total number of the forks analyzed in each cell is also indicated. Data bars are the means of three independent experiments, and error bars represent SEM.