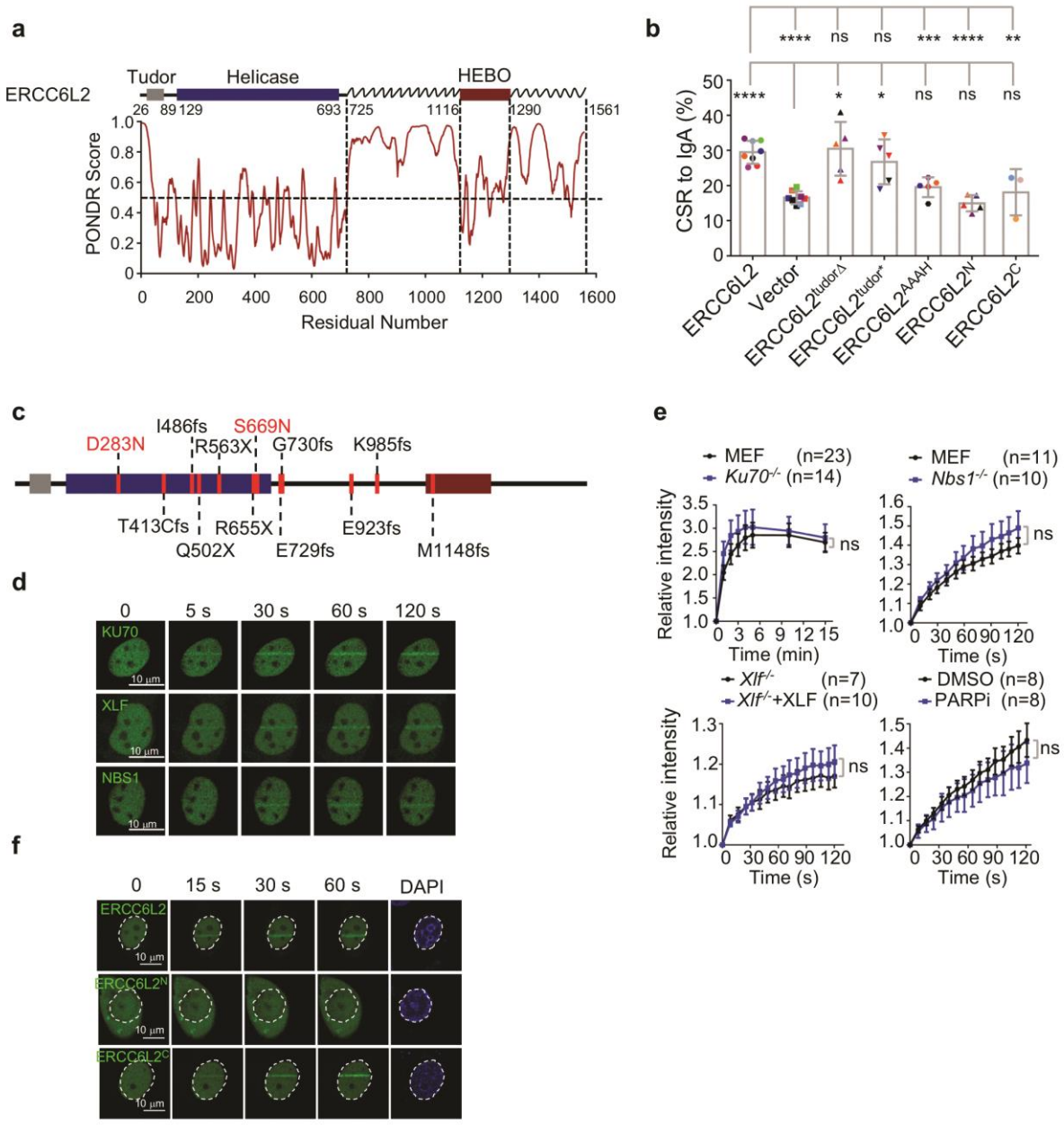

Fig. S4 Function dissection of ERCC6L2 mutants and their recruitments. a ERCC6L2 domain architecture is illustrated on top, and Predictor of Natural Disordered Regions (PONDR) score is plotted along full-length protein from N terminus to C terminus. **b** AID-initiated CSR to IgA level in ERCC6L2 mutants-complemented B cells are plotted. Two-tail unpaired *t*-test was performed. Data from WT ERCC6L2-complemented B cells and vector control are compared with those from other genotypes. ****: $p<0.0001$, ***: $p<0.001$, **: $p<0.01$; *: $p<0.05$, ns:

p>0.05. **c** Deleterious mutations identified in ERCC6L2-mutated BMF patients. Data are retrieved from previous reports[26,27,29,30,35]. **d** Representative time-lapse view of KU70/XLF/NBS1 recruitment to DNA damage sites in U2OS cells. **e** Relative fluorescent intensity of ERCC6L2 at DNA damage sites in MEFs of the indicated genotypes. Observed cell numbers (n) are listed. Data are represented as mean ± SEM. A *t*-test was performed as described in the method. ns: *p*>0.05. **f** Representative recruitment images of ERCC6L2 and its mutants in *ERCC6L2*$^{-/-}$ U2OS cells. Nucleus is circled based on DNA staining.