Fig. S8 ERCC6L2 determines directional CSR. a Distribution of S junctions in CSR-activated B cells. Top, AID targeting (black arrow) in Sμ, Sγ1 and Sϵ, and HTGTS bait site (blue arrow) are depicted. Bottom, linear distribution of pooled junctions along *IgH* locus recovered from LPS/IL4-stimulated B cells. Grey circles indicate S regions. Blue, orientated from left to right; Red, orientated from right to left.

b Percentages of resection and inversional/deletional joining ratio of Sμ-Sε joining are plotted from top to bottom for the indicated primary B cells. Data are from 3-5 mice.

c Schematic illustration of IgH gene structure in CH12F3 and CH12F3-derived NCDel cells. Two sgRNAs used in deletion the DJ non-productive allele are showed by red arrows. **d** Distribution of S junctions in CH12F3-DJ allele knockout (NCDel) cells. Top, AID targeting (black arrow) in Sμ and Sα, and HTGTS bait site (blue arrow) are depicted. Bottom, linear distribution of pooled junctions along IgH locus recovered from CIT-activated NCDel cells. Grey boxes indicate S regions. Blue, orientated from left to right; Red, orientated from right to left. **e** CSR level, end resection and inversional/deletional joining ratios of Sμ-Sα joining are plotted for the indicated genotypes. Data are summarized as mean ±SD in Panels (**b**) and (**e**). Two-tail unpaired *t*-test was performed. Data from *Ercc6l2* knockout are compared with those from other genotypes. ****: $p<0.0001$, ***: $p<0.001$, **: $p<0.01$, *: $p<0.05$. ns: $p>0.05$.