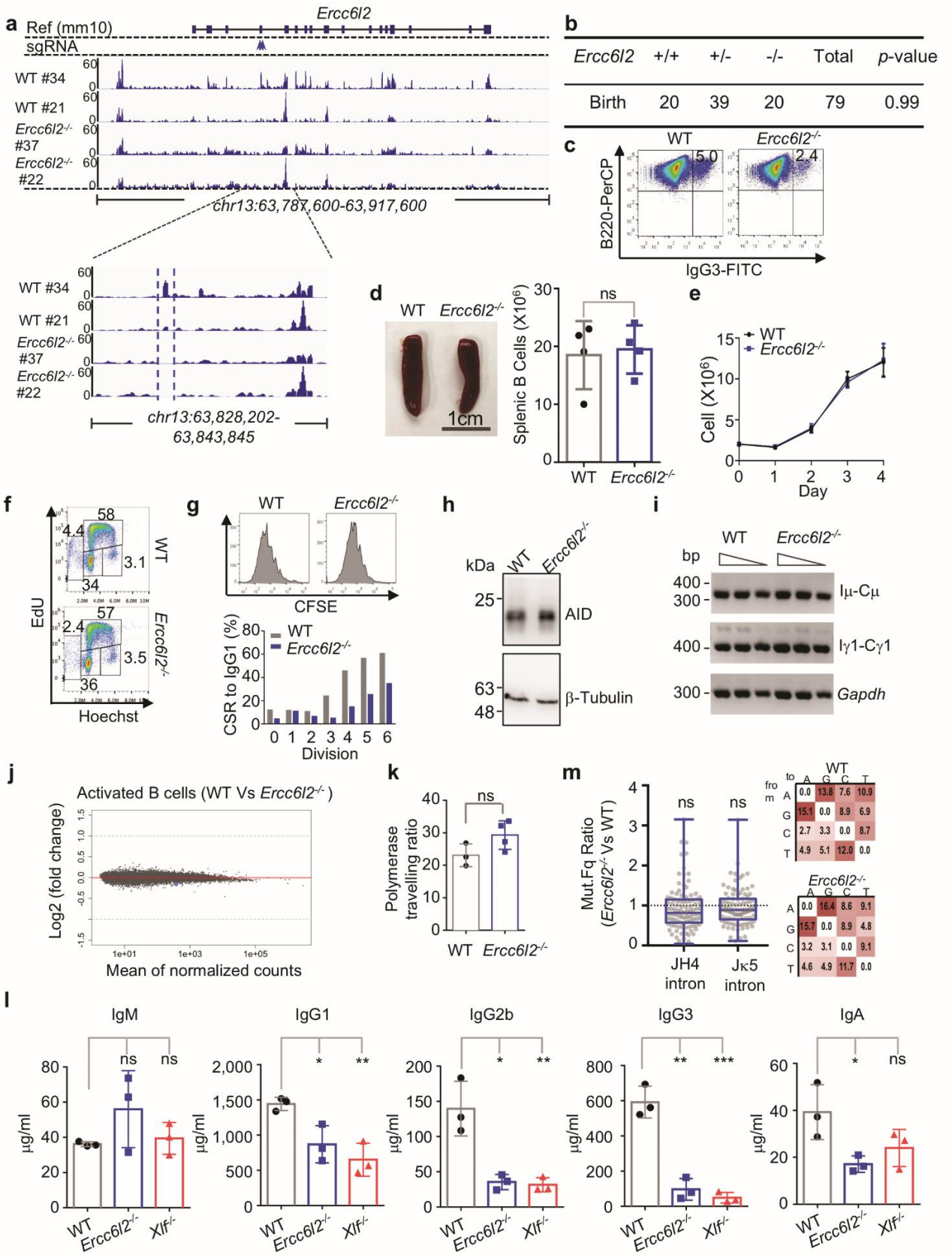
a
Ref (mm10)
Ercc6l2
sgRNA
WT #34
WT #21
Ercc6l2-/- #37
Ercc6l2-/- #22
chr13:63,787,600-63,917,600
chr13:63,828,202-63,843,845
b
Ercc6l2 +/+ +/- -/- Total p-value
Birth 20 39 20 79 0.99
c
WT
Ercc6l2-/-
5.0
2.4
B220-PerCP
IgG3-FITC
d
WT
Ercc6l2-/-
1cm
Splenic B Cells (X10^6)
ns
e
WT
Ercc6l2-/-
Cell (X10^6)
Day
f
58
4.4
3.1
34
57
2.4
3.5
36
WT
Ercc6l2-/-
EdU
Hoechst
g
WT
Ercc6l2-/-
CFSE
CSR to IgG1 (%)
Division
h
kDa
WT
Ercc6l2-/-
25
AID
63
48
β-Tubulin
i
WT
Ercc6l2-/-
bp
400
300
Iμ-Cμ
Iγ1-Cγ1
Gapdh
j
Activated B cells (WT Vs Ercc6l2-/-)
Log2 (fold change)
Mean of normalized counts
k
ns
Polymerase travelling ratio
WT
Ercc6l2-/-
m
Mut.Fq Ratio (Ercc6l2-/- Vs WT)
ns
JH4 intron
Jκ5 intron
WT
Ercc6l2-/-
l
IgM
IgG1
IgG2b
IgG3
IgA
μg/ml
WT
Ercc6l2-/-
Xlf-/-

Fig. S2 ERCC6L2 deficiency leads to defective CSR. a RNA-Seq data of *Ercc6l2* gene in *ex vivo* LPS/IL4-activated B cells with the indicated genotypes are showed with zoom-in views of the knockout-regions at bottom. **b** ERCC6L2 is not required for mouse viability. Numbers of pups are listed, and chi-square test was applied. **c** CSR to IgG3 in *ex vivo* LPS-activated B cells with the indicated genotypes. Representative flow cytometry plots are showed. **d** Size of *Ercc6l2*$^{-/-}$ spleen is comparable to the WT spleen (left), and the splenic B cell numbers are not affected by ERCC6L2-deficiency (right). Four pairs of *Ercc6l2*$^{-/-}$ and WT mice are tested, and no significant difference was identified (mean ± SD, two-tail unpaired *t*-test). **e** Growth curves of *ex vivo* LPS/IL4-activated B cells with the indicated genotypes. Data are represented as mean ± SEM from five pairs of *Ercc6l2*$^{-/-}$ and WT mice. **f** Cell cycle of *ex vivo* LPS/IL4-activated B cells with the indicated genotypes. Cell cycle was determined by flow cytometry analysis of incorporated EdU and DNA content. Representative flow cytometry plots of three repeats are showed. **g** Cell division of *ex vivo* LPS/IL4-activated B cells with the indicated genotypes. Cell division was monitored by CFSE-incorporation analysis. CSR for each cell division is plotted at bottom. **h** AID protein levels in *ex vivo* LPS/IL4-activated B cells with the indicated genotypes. Representative western blot of three repeats is showed. **i** *IgH C* gene germline transcript levels in *ex vivo* LPS/IL4-activated B cells with the indicated genotypes. Representative semi-quantitative RT-PCR result of three repeats is showed. **j** MA plot shows global RNA expression changes between WT and *Ercc6l2*$^{-/-}$ activated B cells. X axis indicates mean count of normalized reads, while y axis is log2-transformed fold