

1 *Type of the Paper (Research Paper)*  
2 Leaky severe combined immunodeficiency in mice lacking non-  
3 homologous end joining factors XLF and MRI  
4  
5 Sergio Castañeda-Zegarra<sup>1,2,†</sup>, Qindong Zhang<sup>1,3,†</sup>, Amin Alirezaylavasani<sup>1</sup>, Marion Fernandez-  
6 Berrocal<sup>1</sup>, Rouan Yao<sup>1</sup>, Valentyn Oksenyч<sup>1,4,5,\*</sup>

7 <sup>1</sup> Department of Clinical and Molecular Medicine (IKOM), Norwegian University of Science  
8 and technology, 7491 Trondheim, Norway;

9 <sup>2</sup> Science for Life Laboratory, Department of Oncology-Pathology, Karolinska Institutet, S-  
10 17176 Stockholm, Sweden;

11 <sup>3</sup> Department of Cancer Immunology, Institute for Cancer Research, The Norwegian Radium  
12 Hospital, Oslo University Hospital, N-0379 Oslo, Norway

13 <sup>4</sup> Department of Biosciences and Nutrition (BioNut), Karolinska Institutet, 14183 Huddinge,  
14 Sweden

15 <sup>5</sup> Institute of Clinical Medicine, UiT The Arctic University of Norway, Tromsø, Norway

16 <sup>†</sup> These authors contributed equally

17 <sup>\*</sup> Correspondence: Valentyn.oksenych@uit.no;

18 **Abstract:** Non-homologous end-joining (NHEJ) is a DNA repair pathway required to detect,  
19 process, and ligate DNA double-stranded breaks (DSBs) throughout the cell cycle. The NHEJ  
20 pathway is necessary for V(D)J recombination in developing B and T lymphocytes. During  
21 NHEJ, Ku70 and Ku80 form a heterodimer that recognizes DSBs and promotes recruitment  
22 and function of downstream factors PAXX, MRI, DNA-PKcs, Artemis, XLF, XRCC4, and LIG4.  
23 Mutations in several known NHEJ genes result in severe combined immunodeficiency (SCID).  
24 Inactivation of *Mri*, *Paxx* or *Xlf* in mice results in normal or mild phenotype, while combined  
25 inactivation of *Xlf/Mri*, *Xlf/Paxx*, or *Xlf/Dna-pkcs* leads to late embryonic lethality. Here, we  
26 describe three new mouse models. We demonstrate that deletion of *Trp53* rescues embryonic  
27 lethality in mice with combined deficiencies of *Xlf* and *Mri*. Furthermore, *Xlf<sup>-/-</sup>Mri<sup>-/-</sup>Trp53<sup>+/+</sup>* and  
28 *Xlf<sup>-/-</sup>Paxx<sup>-/-</sup>Trp53<sup>+/+</sup>* mice possess reduced body weight, severely reduced mature lymphocyte  
29 counts, and accumulation of progenitor B cells. We also report that combined inactivation of  
30 *Mri/Paxx* results in live-born mice with modest phenotype, and combined inactivation of  
31 *Mri/Dna-pkcs* results in embryonic lethality. Therefore, we conclude that XLF is functionally  
32 redundant with MRI and PAXX during lymphocyte development *in vivo*. Moreover, *Mri*  
33 genetically interacts with *Dna-pkcs* and *Paxx*.

34 **Keywords:** NHEJ; Cernunnos; Cyren; pro-B cells; lymphocyte; genetic interaction

---

## 35 1. Introduction

37 Non-homologous end-joining (NHEJ) is a DNA repair pathway that recognizes,  
38 processes and ligates DNA double-stranded breaks (DSB) throughout the cell cycle. NHEJ is  
39 required for lymphocyte development; in particular, to repair DSBs induced by the  
40 recombination activating genes (RAG) 1 and 2 in developing B and T lymphocytes, and by  
41 activation-induced cytidine deaminase (AID) in mature B cells [1]. NHEJ is initiated when Ku70

42 and Ku80 (Ku) are recruited to the DSB sites. Ku, together with DNA-dependent protein kinase,  
43 catalytic subunit (DNA-PKcs), forms the DNA-PK holoenzyme [2]. Subsequently, the nuclease  
44 Artemis is recruited to the DSB sites to process DNA hairpins and overhangs [3]. Finally, DNA  
45 ligase IV (LIG4), X-ray repair cross-complementing protein 4 (XRCC4) and XRCC4-like factor  
46 (XLF) mediate DNA end ligation. The NHEJ complex is stabilized by a parologue of XRCC4 and  
47 XLF (PAXX) and a modulator of retroviral infection (MRI/CYREN) [4, 5].

48 Inactivation of *Ku70*, *Ku80*, *Dna-pkcs* or *Artemis* results in severe combined immunodeficiency  
49 (SCID) characterized by lack of mature B and T lymphocytes [2, 3, 6-8]. Deletion of both alleles  
50 of *Xrcc4* [9] or *Lig4* [10] results in late embryonic lethality in mice, which correlates with  
51 increased apoptosis in the central nervous system (CNS). Inactivation of *Xlf* (*Cernunnos*) only  
52 results in modest immunodeficiency in mice [11-13], while mice lacking *Paxx* [14-17] or *Mri* [5,  
53 18] display no overt phenotype.

54 The mild phenotype observed in mice lacking XLF could be explained by functional redundancy  
55 between XLF and multiple DNA repair factors, including *Ataxia telangiectasia* mutated (ATM),  
56 histone H2AX [19], Mediator of DNA Damage Checkpoint 1 (MDC1) [20, 21], p53-binding  
57 protein 1 (53BP1) [17, 22], RAG2 [23], DNA-PKcs [20, 24, 25], PAXX [4, 14, 15, 20, 26-28] and  
58 MRI [5]. However, combined inactivation of *Xlf* and *Paxx* [4, 14, 15, 20], as well as *Xlf* and *Mri*  
59 [5], results in late embryonic lethality in mice, presenting a challenge to the study of B and T  
60 lymphocyte development *in vivo*. It has also been shown that both embryonic lethality and  
61 increased levels of CNS neuronal apoptosis in mice with deficiency in *Lig4* [9, 10, 29, 30], *Xrcc4*  
62 [9, 31], *Xlf* and *Paxx* [20], or *Xlf* and *Dna-pkcs* [24, 25] is p53-dependent.

63 In this study, we rescue synthetic lethality from *Xlf* and *Mri* by inactivating one or two alleles  
64 of *Trp53*. We also show that both *Xlf*<sup>-/-</sup>*Mri*<sup>-/-</sup>*Trp53*<sup>+/+</sup> and *Xlf*<sup>-/-</sup>*Paxx*<sup>-/-</sup>*Trp53*<sup>+/+</sup> mice possess a leaky  
65 SCID phenotype with severely reduced mature B and T lymphocyte counts in the spleen, low  
66 mature T cell counts in the thymus, and accumulated progenitor B cells in the bone marrow.  
67 Finally, we demonstrate that MRI is functionally redundant with DNA-PKcs and PAXX.

## 68 2. Results

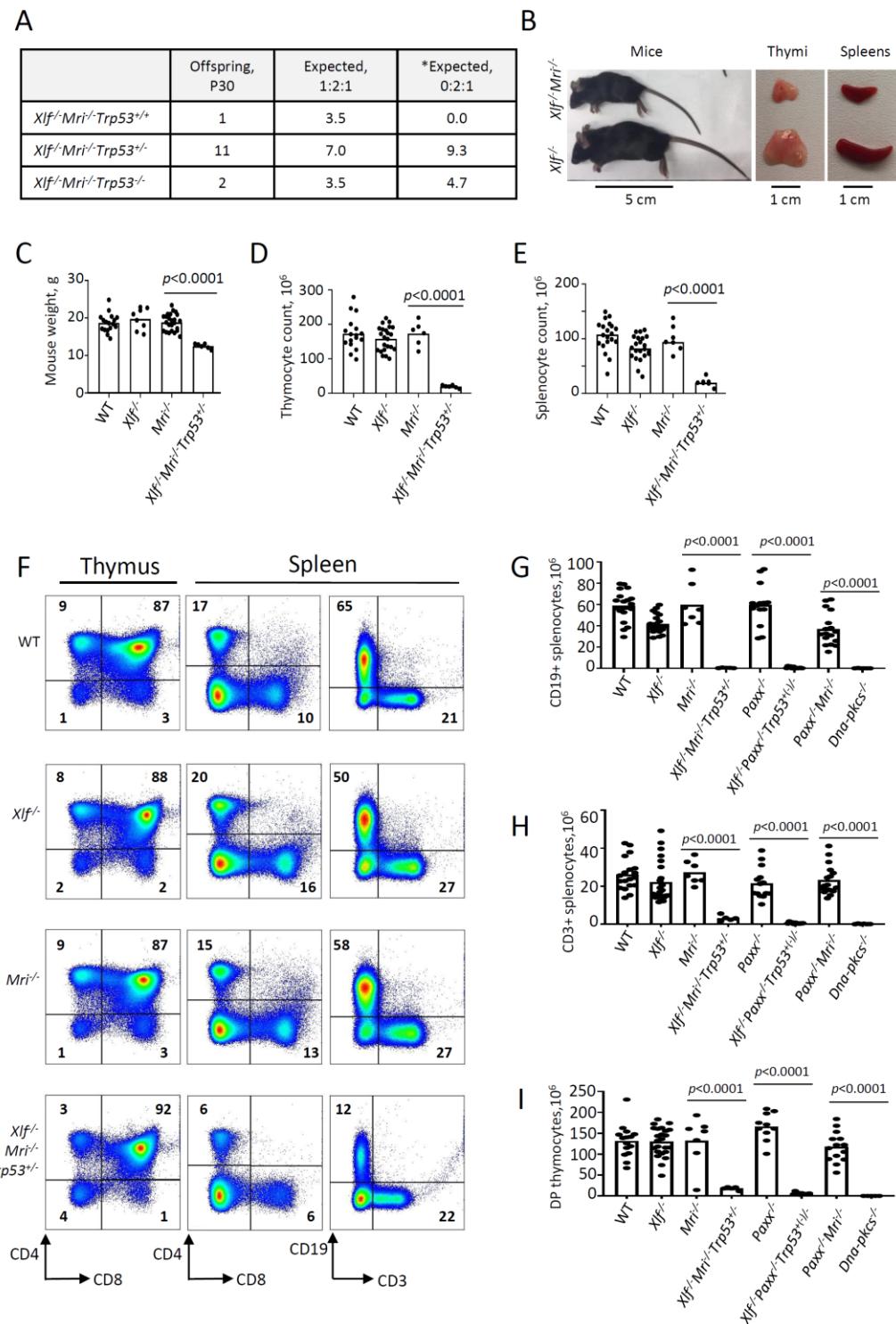
### 69 2.1. Inactivation of *Trp53* gene rescued embryonic lethality in mice lacking XLF and MRI

70        Combined inactivation of *Xlf* and *Mri* has previously been shown to result in synthetic  
71 lethality in mice [5]. To generate XLF/MRI deficient mice with altered expression of *Trp53*, we  
72 intercrossed an *Mri*<sup>-/-</sup> strain [18] with an *Xlf*<sup>-/-</sup>*Trp53*<sup>+/+</sup> [20] strain. Next, we selected and  
73 intercrossed triple heterozygous (*Xlf*<sup>+/+</sup>*Mri*<sup>+/+</sup>*Trp53*<sup>+/+</sup>), and later, *Xlf*<sup>-/-</sup>*Mri*<sup>+/+</sup>*Trp53*<sup>+/+</sup> mice. With  
74 PCR screening, we identified *Xlf*<sup>-/-</sup>*Mri*<sup>-/-</sup>*Trp53*<sup>+/+</sup> (n=11), *Xlf*<sup>-/-</sup>*Mri*<sup>-/-</sup>*Trp53*<sup>-/-</sup> (n=2), and *Xlf*<sup>-/-</sup>*Mri*<sup>-/-</sup>  
75 *Trp53*<sup>+/+</sup> (n=1) (Figure 1A) among the resulting offspring. Mice lacking both XLF and MRI  
76 possessed reduced weight (12 g on average, *p*<0.0001) when compared with gender- and age-  
77 matched WT (19 g), *Xlf*<sup>-/-</sup> (19 g) and *Mri*<sup>-/-</sup> (20 g) controls (Figure 1B and 1C). In addition, *Xlf*<sup>-/-</sup>  
78 *Mri*<sup>-/-</sup>*Trp53*<sup>+/+</sup> and *Xlf*<sup>-/-</sup>*Mri*<sup>-/-</sup>*Trp53*<sup>-/-</sup> mice were viable up to 63 days and died for unknown  
79 reasons. We used *Xlf*<sup>-/-</sup>*Mri*<sup>-/-</sup>*Trp53*<sup>+/+</sup> mice to further characterize the development of B and T  
80 lymphocytes *in vivo*.

81

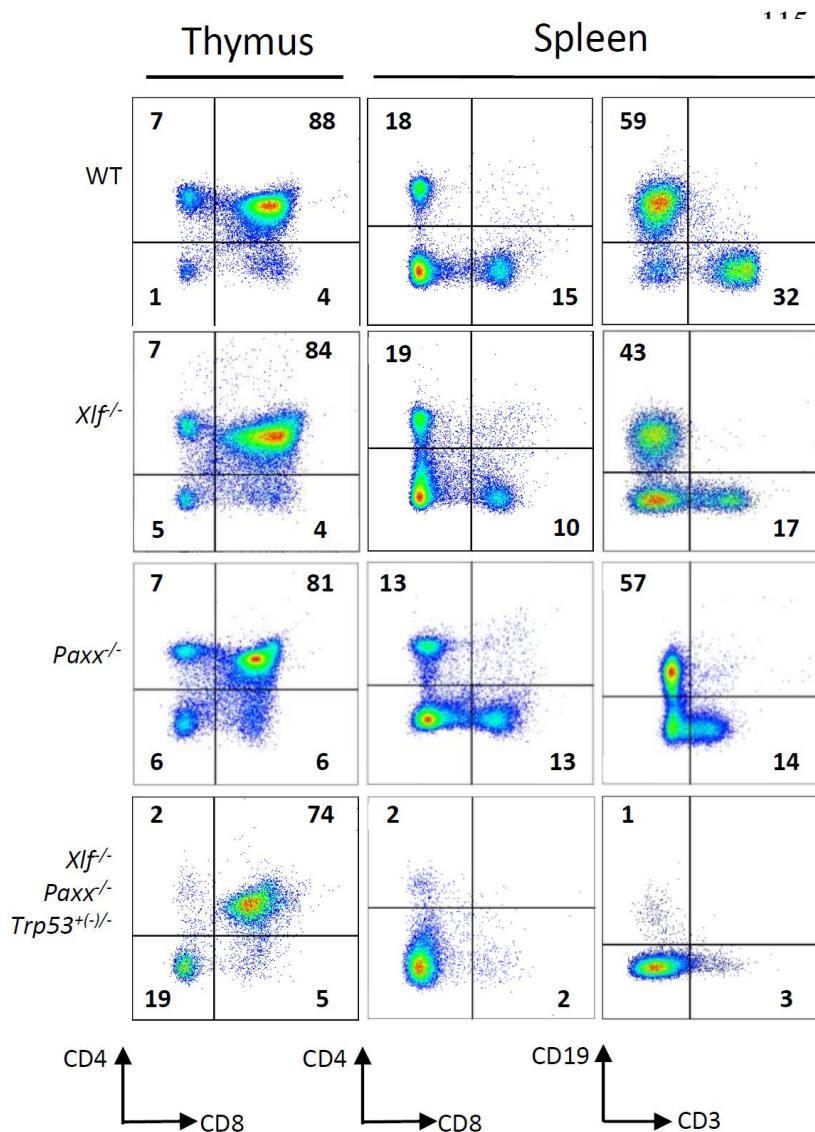
## 82 2.2. Leaky SCID in *Xlf*<sup>-/-</sup>*Mri*<sup>-/-</sup>*Trp53*<sup>+/+</sup> mice

83        To determine the roles of XLF and MRI in lymphocyte development *in vivo*, we isolated  
84 the thymus, spleen, and femur from *Xlf*<sup>-/-</sup>*Mri*<sup>-/-</sup>*Trp53*<sup>+/+</sup> mice, as well as from *Xlf*<sup>-/-</sup>, *Mri*<sup>-/-</sup>, *Trp53*<sup>+/+</sup>  
85 and WT controls. Combined deficiency for XLF and MRI resulted in a 3-fold reduction in thymus  
86 size (32 mg on average, *p*<0.0001) and a 9-fold reduction in thymocyte count (1.9x10<sup>7</sup>,  
87 *p*<0.0001) when compared to single deficient or WT controls (Figure 1D). Similarly, both  
88 average spleen weight (22 mg, *p*<0.0001) and splenocyte count (2.0x10<sup>7</sup>, *p*<0.0001) in *Xlf*<sup>-/-</sup>*Mri*  
89 *-/-**Trp53*<sup>+/+</sup> mice decreased approximately 4-5 fold when compared with WT and single deficient  
90 controls (Figure 1E). The reduced number of splenocytes in XLF/MRI double-deficient mice  
91 could be explained by decreased populations of B and T lymphocytes observed in the *Xlf*<sup>-/-</sup>*Mri*  
92 *-/-**Trp53*<sup>+/+</sup> mice (Figure 1F-H). Specifically, CD3+ T cells were reduced 6-fold (*p*<0.0001), while  
93 CD19+ B cells were reduced 50-fold (*p*<0.0001) when compared with single deficient and WT  
94 controls (Figure 1F-H). Likewise, counts of CD4+ and CD8+ T cells in the spleen, were all  
95 dramatically reduced when compared with single deficient and WT controls (about 4-fold,  
96 *p*<0.0001; Figure 1F, 1H) as well as counts of CD4+, CD8+ and CD4+CD8+ T cells in the thymus  
97 (Figure 1F,I). From these observations, we conclude that XLF and MRI are functionally  
98 redundant during B and T lymphocytes development in mice.



101 **Figure 1. Development of B and T lymphocytes in *Xlf<sup>-/-</sup>Mri<sup>-/-Trp53<sup>+/+</sup></sup>*** mice. (A) Number of  
 102 thirty-day-old mice (P30) of indicated genotypes. \*Expected distribution assuming lethality. (B)  
 103 Comparison of body size, thymi and spleens of XLF/MRI-deficient and XLF-deficient mice of  
 104 the same age. (C) Weights of WT, *Xlf<sup>-/-</sup>*, *Mri<sup>-/-</sup>*, *Xlf<sup>-/-</sup>Mri<sup>-/-Trp53<sup>+/+</sup></sup>* mice. (D, E) Number ( $\times 10^6$ ) of  
 105 thymocytes (D) and splenocytes (E) in WT, *Xlf<sup>-/-</sup>*, *Mri<sup>-/-</sup>*, *Xlf<sup>-/-</sup>Mri<sup>-/-Trp53<sup>+/+</sup></sup>* mice. (F) Flow

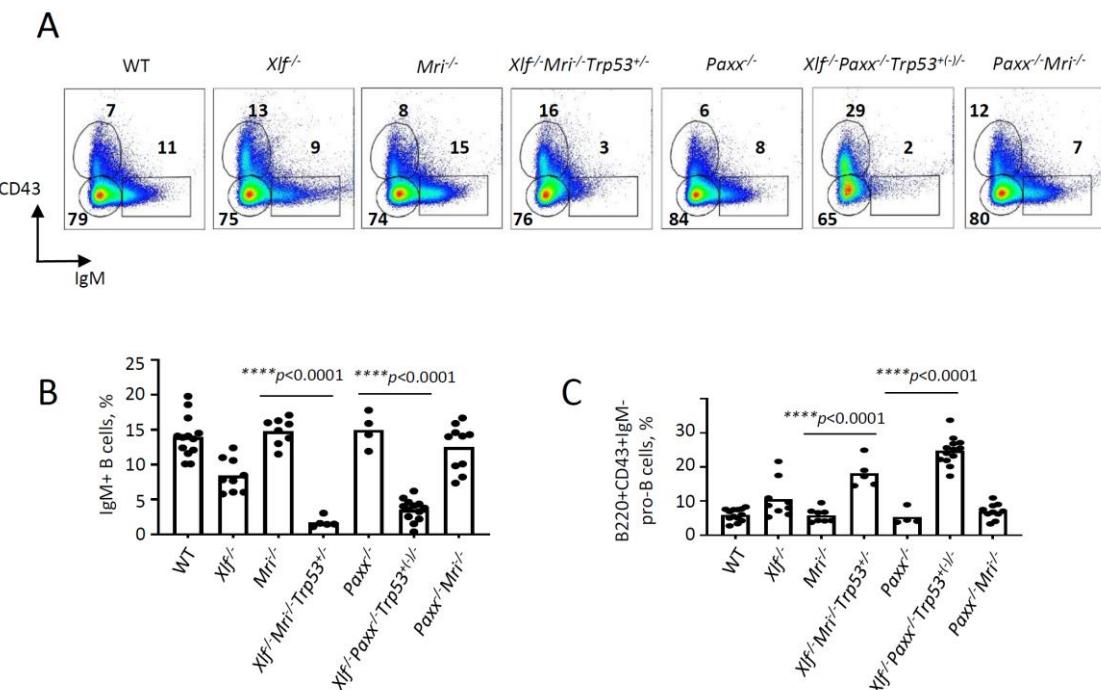
106 cytometric analysis of thymic and splenic T cell subsets and splenic B cells. (G,H,I) Number  
 107 ( $\times 10^6$ ) of splenic CD19+ B cells (G), splenic CD3+ T cells (H) and thymic CD4+CD8+ double  
 108 positive (DP) T cells (I) in WT, *Xlf<sup>-/-</sup>*, *Mri<sup>-/-</sup>*, *Xlf<sup>-/-</sup>Mri<sup>-/-</sup>Trp53<sup>+/+</sup>*, *Paxx<sup>-/-</sup>*, *Xlf<sup>-/-</sup>Paxx<sup>-/-</sup>Trp53<sup>+/(-)</sup>* and *Paxx<sup>-/-</sup>Mri<sup>-/-</sup>* mice. *Dna-pkcs<sup>-/-</sup>* mice were used as an immunodeficient control. Comparisons between  
 109 every two groups were made using one-way ANOVA, GraphPad Prism 8.0.1. *Xlf<sup>-/-</sup>Paxx<sup>-/-</sup>Trp53<sup>+/(-)</sup>*  
 110 is a combination of *Xlf<sup>-/-</sup>Paxx<sup>-/-</sup>Trp53<sup>+/+</sup>* and *Xlf<sup>-/-</sup>Paxx<sup>-/-</sup>Trp53<sup>-/-</sup>*. Not shown in the graph for (G):  
 111 WT vs *Paxx<sup>-/-</sup>Mri<sup>-/-</sup>*,  $p<0.0001$  (\*\*\*\*), *Paxx<sup>-/-</sup>* vs *Paxx<sup>-/-</sup>Mri<sup>-/-</sup>*,  $p<0.0001$  (\*\*\*\*), *Mri<sup>-/-</sup>* vs *Paxx<sup>-/-</sup>Mri<sup>-/-</sup>*,  
 112  $p<0.0025$  (\*\*), *Xlf<sup>-/-</sup>* vs *Paxx<sup>-/-</sup>Mri<sup>-/-</sup>*,  $p=0.9270$  (n.s), *Xlf<sup>-/-</sup>Mri<sup>-/-</sup>Trp53<sup>+/+</sup>* vs *Paxx<sup>-/-</sup>Mri<sup>-/-</sup>*,  $p<0.0001$  (\*\*\*\*),  
 113 and *Xlf<sup>-/-</sup>Paxx<sup>-/-</sup>Trp53<sup>+/(-)</sup>* vs *Paxx<sup>-/-</sup>Mri<sup>-/-</sup>*,  $p<0.0001$  (\*\*\*\*).  
 114



133 **Supplementary Figure 1. Development of B and T cells in *Xlf<sup>-/-</sup>Paxx<sup>-/-</sup>Trp53<sup>+/(-)</sup>* mice.** Examples  
 134 of flow cytometric analysis of thymic and splenic T cell subsets and splenic CD19+ B cells. *Xlf<sup>-/-</sup>*  
 135 *Paxx<sup>-/-</sup>Trp53<sup>+/(-)</sup>* is a combination of *Xlf<sup>-/-</sup>Paxx<sup>-/-</sup>Trp53<sup>+/+</sup>* and *Xlf<sup>-/-</sup>Paxx<sup>-/-</sup>Trp53<sup>-/-</sup>*.  
 136  
 137  
 138

## 139 2.3. Leaky SCID in mice lacking XLF and PAXX

140 Combined inactivation of XLF and PAXX has been shown to result in embryonic lethality  
 141 in mice [4, 14, 15, 20]. To determine the impact of XLF and PAXX on B and T cell development  
 142 *in vivo*, we rescued the synthetic lethality by inactivating one allele of *Trp53*, as described  
 143 previously [20]. We did not detect any direct influence of altered *Trp53* genotype on  
 144 lymphocyte development. The resulting *Xlf*<sup>−/−</sup>*Paxx*<sup>−/−</sup>*Trp53*<sup>+/−</sup> and *Xlf*<sup>−/−</sup>*Paxx*<sup>−/−</sup>*Trp53*<sup>−/−</sup> mice possess  
 145 30- to 40-fold reduced thymocyte count ( $4.0 \times 10^6$ ,  $p < 0.0001$ ) when compared to WT ( $1.3 \times 10^8$ ),  
 146 *Xlf*<sup>−/−</sup> ( $1.4 \times 10^8$ ) and *Paxx*<sup>−/−</sup> ( $1.7 \times 10^8$ ) mice. This is reflected in decreased levels of double-positive  
 147 CD4+CD8+ cells, as well as decreased levels of single-positive CD4+ and CD8+ T cells (Figure 1,  
 148 Supplementary Figure 1). Spleen development was dramatically affected in mice lacking XLF  
 149 and PAXX compared to WT and single-deficient controls, due to the lack of B cells and  
 150 decreased T cell count (Figure 1, Supplementary Figure 1). When compared with the WT and  
 151 single knockout controls, *Xlf*<sup>−/−</sup>*Paxx*<sup>−/−</sup>*Trp53*<sup>+/−</sup> and *Xlf*<sup>−/−</sup>*Paxx*<sup>−/−</sup>*Trp53*<sup>−/−</sup> mice had a 100- to 600-fold  
 152 reduction in CD19+ B splenocyte count ( $0.7 \times 10^6$ ,  $p < 0.0001$ ) and a 50- to 90-fold reduction in  
 153 CD3+ splenocyte count (to  $0.5 \times 10^6$ ) (Figure 1F-H and Supplementary Figure 1). From these  
 154 results, we concluded that XLF and PAXX are functionally redundant during the B and T  
 155 lymphocyte development *in vivo*.



156 **Figure 2. Development of B cells is abrogated in bone marrow of *Xlf*<sup>−/−</sup>*Mri*<sup>−/−</sup>*Trp53*<sup>+/−</sup> and *Xlf*<sup>−/−</sup>  
 157 *Paxx*<sup>−/−</sup>*Trp53*<sup>+/−</sup> mice.** (A) Flow cytometric analysis of developing B cells. Upper left boxes mark

158 B220+CD43+IgM- progenitor B cell populations, and lower right boxes mark the B220+CD43-  
159 IgM+ B cells. (B, C) Frequencies (%) of B220+CD43-IgM+ B cells (B) and B220+CD43+IgM-  
160 progenitor B cells (C) in WT, *Xlf*<sup>-/-</sup>, *Mri*<sup>-/-</sup>, *Xlf*<sup>-/-</sup>*Mri*<sup>-/-</sup>*Trp53*<sup>+/+</sup>, *Paxx*<sup>-/-</sup>, *Xlf*<sup>-/-</sup>*Paxx*<sup>-/-</sup>*Trp53*<sup>+/+</sup> and *Paxx*<sup>-/-</sup>*Mri*<sup>-/-</sup> mice. Comparisons between groups were made using one-way ANOVA, GraphPad  
161 Prism 8.0.1. *Xlf*<sup>-/-</sup>*Paxx*<sup>-/-</sup>*Trp53*<sup>+/+</sup> is a combination of *Xlf*<sup>-/-</sup>*Paxx*<sup>-/-</sup>*Trp53*<sup>+/+</sup> and *Xlf*<sup>-/-</sup>*Paxx*<sup>-/-</sup>*Trp53*<sup>-/-</sup>.  
162

163

164 **2.4. Early B cell development is abrogated in mice lacking XLF and MRI, or XLF and PAXX**

165 Reduced counts and proportions of mature B lymphocytes in *Xlf*<sup>-/-</sup>*Mri*<sup>-/-</sup>*Trp53*<sup>+/+</sup> mice  
166 suggest a blockage in B cell development in the bone marrow. To investigate this further, we  
167 isolated the bone marrow cells from femora of mice lacking XLF, MRI or both XLF/MRI, and  
168 analyzed the proportions of B220+CD43+IgM- progenitor B cells and B220+CD43-IgM+  
169 immature and mature B cells. We detected only background levels of B220+CD43-IgM+ B cells  
170 in bone marrows isolated from *Xlf*<sup>-/-</sup>*Mri*<sup>-/-</sup>*Trp53*<sup>+/+</sup> mice (Figure 2A, 2B). However, these mice  
171 exhibited a 2- to 3-fold higher proportion of pro-B cells when compared with WT, *Xlf*<sup>-/-</sup> and *Mri*<sup>-/-</sup>  
172 controls (Figure 2A, 2C). Similarly, *Xlf*<sup>-/-</sup>*Paxx*<sup>-/-</sup>*Trp53*<sup>+/+</sup> and *Xlf*<sup>-/-</sup>*Paxx*<sup>-/-</sup>*Trp53*<sup>-/-</sup> mice also possess  
173 background levels of IgM+ B cells ( $p<0.0001$ ; Figure 2A,B) while having 3- to 4-fold higher  
174 proportion of pro-B cells when compared with WT, *Xlf*<sup>-/-</sup> and *Paxx*<sup>-/-</sup> controls ( $p<0.0001$ ;  
175 Figure 2A,C). Therefore, we conclude that B cell development is blocked at the pro-B cell stage  
176 of *Xlf*<sup>-/-</sup>*Mri*<sup>-/-</sup>*Trp53*<sup>+/+</sup> and *Xlf*<sup>-/-</sup>*Paxx*<sup>-/-</sup>*Trp53*<sup>+/+</sup> mice.  
177

178

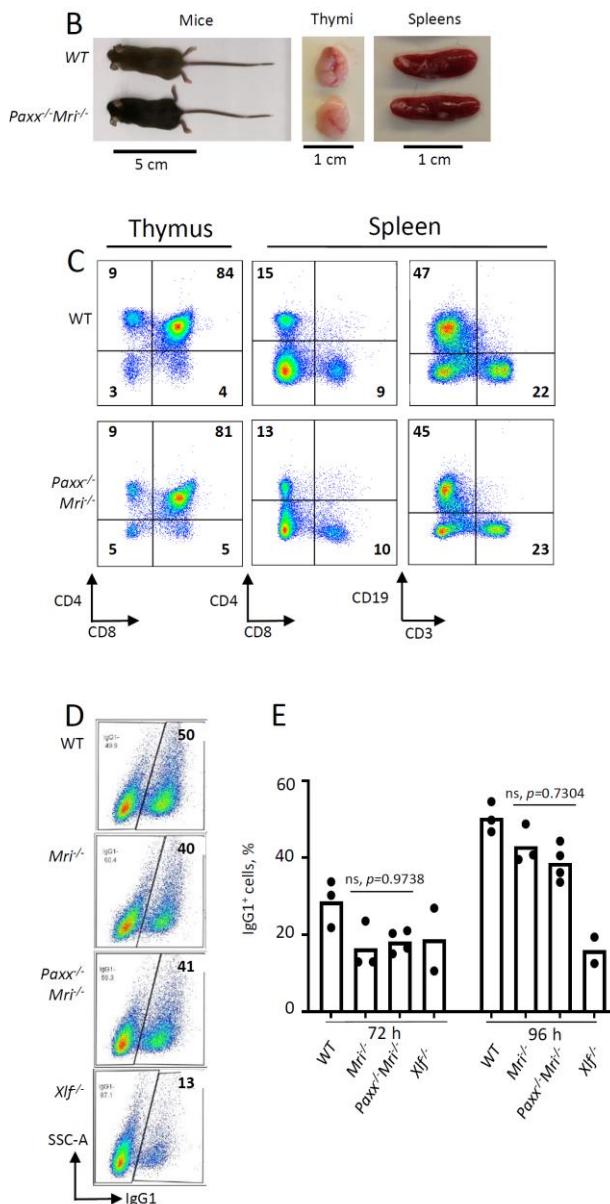
179 **2.5. *Paxx*<sup>-/-</sup>*Mri*<sup>-/-</sup> mice possess a modest phenotype**

180 Both PAXX and MRI are NHEJ factors that are functionally redundant with XLF in mice.  
181 Combined inactivation of *Paxx* and *Xlf* [4, 14, 15, 20], or *Mri* and *Xlf* ([5]; this study) results in  
182 synthetic lethality in mice, as well as in abrogated V(D)J recombination in vAbl pre-B cells [4, 5,  
183 14, 15, 27]. To determine if *Paxx* genetically interacts with *Mri*, we intercrossed mice that are  
184 heterozygous or null for both genes (such as *Paxx*<sup>-/-</sup>*Mri*<sup>+/+</sup> and *Paxx*<sup>+/+</sup>*Mri*<sup>-/-</sup>). We found that  
185 resulting *Paxx*<sup>-/-</sup>*Mri*<sup>-/-</sup> mice are live-born, fertile, and are similar in size to WT littermates (17 g,  
186  $p>0.9999$ ) (Figure 3A and 3B). Specifically, we observe that *Paxx*<sup>-/-</sup>*Mri*<sup>-/-</sup> mice have normal  
187 thymocyte and splenocyte counts. Furthermore, *Paxx*<sup>-/-</sup>*Mri*<sup>-/-</sup> mice underwent normal T cell  
188 development that was indistinguishable from the WT, *Paxx*<sup>-/-</sup>, and *Mri*<sup>-/-</sup> controls (Figure 1H, 1I  
and 3C). However, *Paxx*<sup>-/-</sup>*Mri*<sup>-/-</sup> mice had reduced CD19+ B cell counts (Figure 1G) when were

189 compared to WT, *Paxx*<sup>-/-</sup> and *Mri*<sup>-/-</sup> controls ( $p<0.0025$ ). Moreover, CD19+ B cell counts were  
190 similar in *Paxx*<sup>-/-</sup>*Mri*<sup>-/-</sup> and *Xlf*<sup>-/-</sup> mice ( $p>0.9270$ ), suggesting that combined depletion of PAXX  
191 and MRI has modest phenotype similar to the one in XLF-deficient mice. CSR to IgG1 was  
192 performed in order to determine if DNA repair-dependent immunoglobulin production is  
193 affected in mature B cells lacking PAXX and MRI [16, 18]. *Paxx* inactivation did not affect Ig  
194 switch to IgG1 in MRI-deficient B cells (Figure 3D and 3E). The quantity of IgG1+ cells after CSR  
195 stimulation was similar between *Paxx*<sup>-/-</sup>*Mri*<sup>-/-</sup> and *Mri*<sup>-/-</sup> naïve B cells ( $p>0.73$ ). From this, we can  
196 conclude that there is a genetic interaction between *Paxx* and *Mri* *in vivo*, and it is only detected  
197 in B cells.

Figure 3

	Offspring, P30	Expected, 1:2:1
<i>Paxx</i> <sup>+/-</sup> <i>Mri</i> <sup>+/+</sup>	2	3.25
<i>Paxx</i> <sup>+/-</sup> <i>Mri</i> <sup>+-</sup>	4	6.50
<i>Paxx</i> <sup>-/-</sup> <i>Mri</i> <sup>+-</sup>	7	3.25
Total	13	13.00



198

199 **Figure 3. Development of B and T cells in *Paxx*<sup>+/-</sup>*Mri*<sup>+-</sup> mice.** (A) Number of thirty-day-old mice  
200 (P30) of indicated genotypes. Parents were *Paxx*<sup>+/+</sup>*Mri*<sup>+/+</sup> and *Paxx*<sup>+/-</sup>*Mri*<sup>+-</sup>. (B) Example of thirty-day-old  
201 *Paxx*<sup>+/-</sup>*Mri*<sup>+-</sup> and WT male littermates with their respective thymi and spleens. (C) Example of  
202 flow cytometry analyzes of B and T cells in *Paxx*<sup>+/-</sup>*Mri*<sup>+-</sup> and WT mice. (D,E) Class switching  
203 analyzes of *in vitro* activated naïve B cells of indicated genotypes.

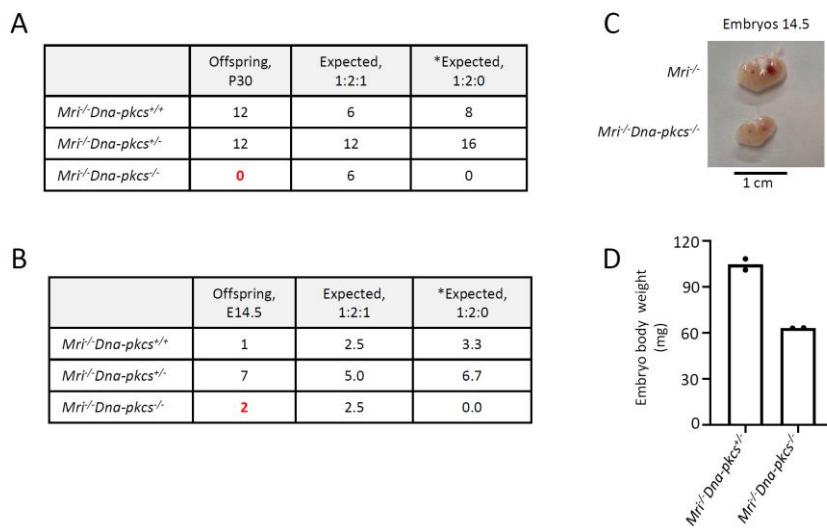
204 **2.6. Synthetic lethality between *Mri* and *Dna-pkcs* in mice**

205 Both MRI and DNA-PKcs are functionally redundant with XLF in mouse development

206 [5, 24]. Combined inactivation of *Paxx* and *Mri* (this study), or *Paxx* and *Dna-pkcs* [20] genes

207 results in live-born mice that are indistinguishable from single deficient controls. To determine  
 208 if *Mri* genetically interacts with *Dna-pkcs*, we crossed *Mri*<sup>+/−</sup> and *Dna-pkcs*<sup>+/−</sup> mouse strains, then  
 209 intercrossed the double-heterozygous *Mri*<sup>+/−</sup>*Dna-pkcs*<sup>+/−</sup>, and then *Mri*<sup>−/−</sup>*Dna-pkcs*<sup>+/−</sup> mice (Figure  
 210 4A). We identified 12 *Mri*<sup>−/−</sup>*Dna-pkcs*<sup>+/−</sup> and 12 *Mri*<sup>−/−</sup>*Dna-pkcs*<sup>+/−</sup>, but no *Mri*<sup>−/−</sup>*Dna-pkcs*<sup>−/−</sup> mice  
 211 (out of 6 expected). To determine if double-deficient *Mri*<sup>−/−</sup>*Dna-pkcs*<sup>−/−</sup> embryos are present at  
 212 day E14.5, we intercrossed *Mri*<sup>−/−</sup>*Dna-pkcs*<sup>+/−</sup> mice, extracted and genotyped the embryos  
 213 (Figure 4B). We identified two *Mri*<sup>−/−</sup>*Dna-pkcs*<sup>−/−</sup> mice at E14.5 (63mg), which were about 40%  
 214 lighter than *Mri*<sup>−/−</sup> littermates (108mg) (Figure 4C and 4D). A Chi-Square test ( $\chi^2$ ) was performed  
 215 to determine if the embryonic distribution data fits the mendelian ratio of 1:2:1 that is  
 216 expected from *Mri*<sup>−/−</sup>*Dna-pkcs*<sup>+/−</sup> parents. With DF=2 and  $\chi^2=1.8$ , the corresponding p-value lies  
 217 within the range 0.25

0.5. This affirms that our data fit the expected 1:2:1 distribution and  
 218 suggests that *Mri*<sup>−/−</sup>*Dna-pkcs*<sup>−/−</sup> is synthetic lethal. Therefore, we can conclude that there is  
 219 genetic interaction between *Mri* and *Dna-pkcs* *in vivo*.



229 **Figure 4. Genetic interaction between *Mri* and *Dna-pkcs* *in vivo*.** (A) No live-born *Mri*<sup>−/−</sup>*Dna-pkcs*<sup>−/−</sup>  
 230 mice were detected. (B,C) *Mri*<sup>−/−</sup>*Dna-pkcs*<sup>−/−</sup> embryos were detected at day E14.5. (D) Body weight  
 231 in milligrams (mg) from two E14.5 *Mri*<sup>−/−</sup>*Dna-pkcs*<sup>−/−</sup> and *Mri*<sup>−/−</sup>*Dna-pkcs*<sup>+/−</sup> embryos from the same  
 232 litter. The mendelian ratio 1:2:1 in embryos was verified by the Chi-Square test ( $\chi^2$ ). The  $\chi^2$  was 1.8  
 233 and its corresponding probability was between 25 and 50%. \*Expected distribution assuming  
 234 lethality.

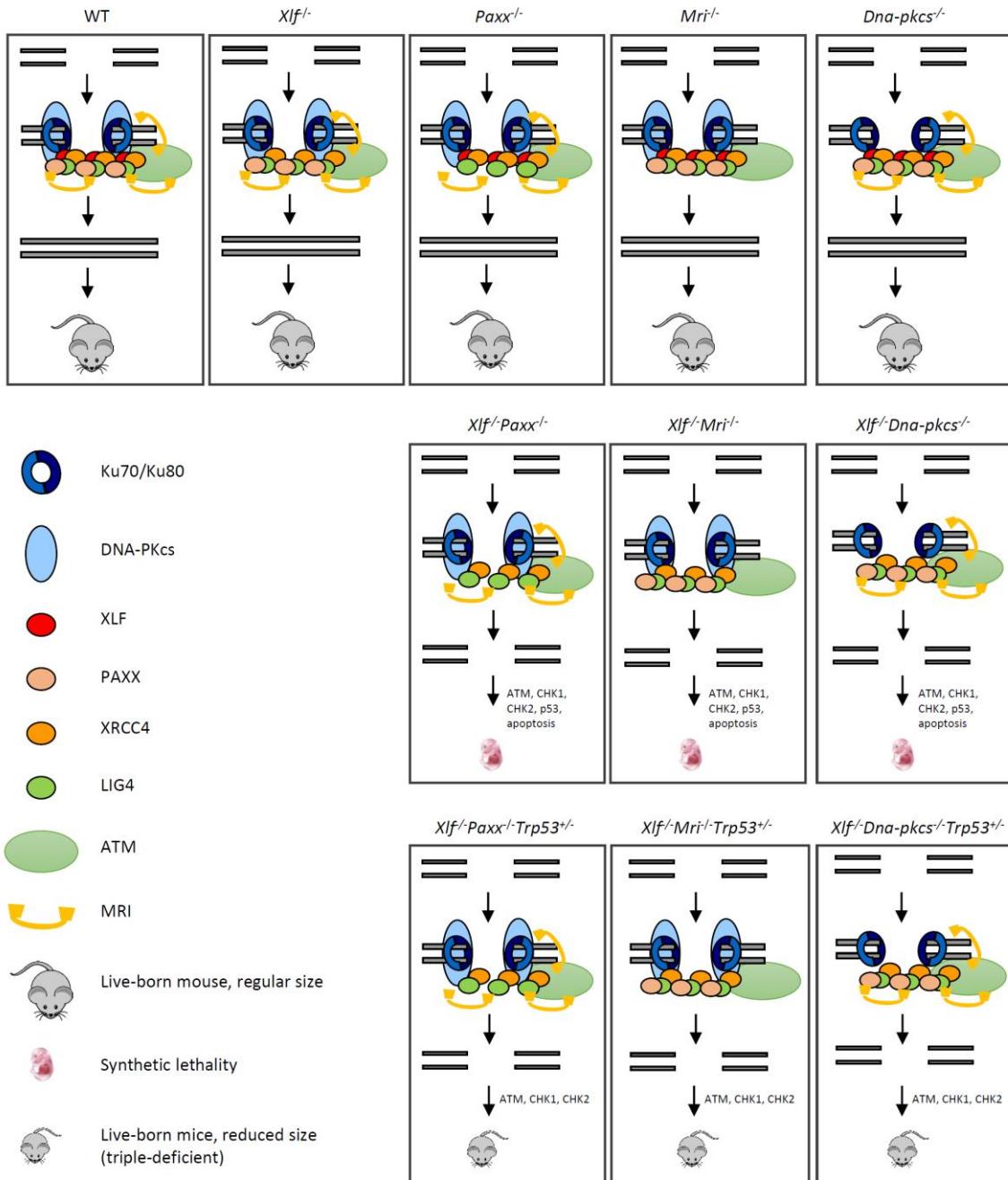
235

236

237 **3. Discussion**

238       Recent findings by our and other research groups suggest that MRI forms  
239       heterogeneous complexes involving PAXX or XLF, which function during DNA DSB repair by  
240       NHEJ [5]. Furthermore, genetic inactivation of *Xlf* [11], *Paxx* [4, 14-16], or *Mri* [5, 18] in mice  
241       leads to development of modest or no detectable phenotype. However, combined inactivation  
242       of *Xlf* and *Mri* [5] or *Xlf* and *Paxx* [4, 14, 15] results in embryonic lethality, which correlates with  
243       increased levels of neuronal apoptosis in the CNS (Figure 5). Here, we show that synthetic  
244       lethality produced by combined inactivation of *Xlf* and *Mri* can be rescued by altered *Trp53*  
245       expression, similar to our previous *Xlf*<sup>−/−</sup>*Paxx*<sup>−/−</sup>*Trp53*<sup>+/−</sup> [20] mouse model. Furthermore, we  
246       have developed and presented here *Paxx*<sup>−/−</sup>*Mri*<sup>−/−</sup> and *Mri*<sup>−/−</sup>*Dna-pkcs*<sup>−/−</sup> double deficient models.

247       Our findings have demonstrated that mice lacking XLF, MRI and p53, although live-  
248       born, possess a leaky SCID phenotype. *Xlf*<sup>−/−</sup>*Mri*<sup>−/−</sup>*Trp53*<sup>+/−</sup> mice have a clear fraction of mature  
249       B cells in the spleens (CD19+) and bone marrow (B220+CD43-IgM+) (Figures 1 and 2), as well  
250       as clear fractions of double- and single-positive T cells in the thymus (CD4+CD8+, CD4+, CD8+)  
251       and single-positive T cells in the spleen (CD4+ and CD8+) (Figure 1). However, the cell fractions  
252       from these mice are noticeably smaller than those of WT or single-deficient mice. Strikingly,  
253       we were able to identify one *Xlf*<sup>−/−</sup>*Mri*<sup>−/−</sup>*Trp53*<sup>+/−</sup> mouse at day P30 post-birth. This mouse  
254       resembled *Xlf*<sup>−/−</sup>*Mri*<sup>−/−</sup>*Trp53*<sup>+/−</sup> mice of similar age with respect of B and T cell development,  
255       although this mouse was generally sicker than its littermates and had to be euthanized.  
256       Similarly, one live-born *Xlf*<sup>−/−</sup>*Paxx*<sup>−/−</sup> mouse was reported by *Balmus et al.* (2016) [15], indicating  
257       that, exceptionally, embryonic lethality in NHEJ ligation-deficient mice can be overcome, likely  
258       due to activity of alternative end-joining. Previously, in 2018, *Hung et al.* [5] reported that  
259       combined inactivation of *Xlf* and *Mri* in vAbl pre-B cells results in a severe block in V(D)J  
260       recombination and accumulation of unrepaired DSBs *in vitro*, although it was unclear whether  
261       this combined inactivation would lead to a deficiency in B lymphocytes when translated to a  
262       mouse model [5]. Similarly, double deficient vAbl pre-B cells lacking *Xlf* and *Paxx* are also unable  
263       to sustain V(D)J recombination. Importantly, the lack of a progenitor T cell model system left  
264       the question of T cell development in *Xlf*<sup>−/−</sup>*Mri*<sup>−/−</sup> and *Xlf*<sup>−/−</sup>*Paxx*<sup>−/−</sup> mice completely unexplored.



265 **Figure 5. Mutations in NHEJ genes result in distinct phenotypes. Suggested models.** Inactivation of  
 266 *Paxx* or *Mri* results in live-born mice with nearly no DNA repair defects. Inactivation of *Xlf* or *Dna-pkcs*  
 267 results in live-born mice with increased levels of genomic instability due to reduced NHEJ activity.  
 268 Combined inactivation of *Xlf/Paxx*, *Xlf/Mri* or *Xlf/Dna-pkcs* leads to embryonic lethality in mice that  
 269 correlate with high levels of genomic instability and nearly no NHEJ. Accumulated DSBs activate the  
 270 ATM-dependent DNA damage response (DDR) pathway; ATM phosphorylates CHK checkpoint  
 271 proteins that further trigger cell cycle arrest and apoptosis. Alternative end-joining is blocked by  
 272 presence of Ku70/Ku80. Inactivation of one or two alleles of *Trp53* rescues embryonic lethality of *Xlf/Paxx*,  
 273 *Xlf/Mri* and *Xlf/Dna-pkcs* mice. While in these mice the levels of DSBs are increased and ATM-dependent  
 274 DDR response is activated, lack of p53 prevents massive apoptosis and thus results in alive mice. Sizes  
 275 of the triple-deficient mice are reduced, as one option, due to DNA damage-dependent cell cycle arrest

276 in multiple cells of the body. The embryonic lethality in mice lacking *Xlf/Paxx* and *Xlf/Mri* is likely to be  
277 rescued by inactivation of *Ku70* or *Ku80*.

278

279 Previously, we showed that mice lacking XLF, PAXX and p53 were live-born and had  
280 nearly no B and T cells, reduced size of spleen and hardly detectable thymus [20] (Figure 5).

281 Consistent with this model, a conditional knockout mouse model, which results in double-  
282 deficiency of XLF/PAXX in early hematopoietic progenitor cells, was also able to overcome the  
283 embryonic lethality of *Xlf<sup>f/f</sup>/Paxx<sup>-/-</sup>* mice [32]. With this model, impairment of V(D)J  
284 recombination in *Xlf<sup>f/f</sup>/Paxx<sup>-/-</sup>* cells, as well as the resulting depletion of mature B cells and lack  
285 of a visible thymus could also be observed *in vivo* [32]. Our new data provide evidence that *Xlf<sup>f/f</sup>*  
286 */Paxx<sup>-/-</sup>/Trp53<sup>+/+</sup>* and *Xlf<sup>f/f</sup>/Paxx<sup>-/-</sup>/Trp53<sup>-/-</sup>* mice possess a very small number of mature B cells in  
287 the spleen and bone marrow, as well as very minor fractions of single positive T cells in thymus  
288 and spleen (Figure 2, 5 and Supplementary Figure 1). Therefore, both mature B and T cells are  
289 present in mice lacking XLF/PAXX and XLF/MRI. This can be explained by incomplete blockage  
290 in NHEJ and V(D)J recombination, in which the process is dramatically reduced but still possible.

291 We also detected more mature T cells than B cells in these double-deficient mice. Potential  
292 explanations include longer lifespan of T cells, which accumulate over time following low  
293 efficiency of V(D)J recombination, while B cells are eliminated faster from the pool due to the  
294 different physiology [33, 34]. It is also possible that the T cells we detected are a resultant  
295 subpopulation that is descendent from the few cells that were able to bypass V(D)J  
296 recombination [12]. In this case, the repertoire of T cells based on T cell receptor in mice lacking  
297 XLF/PAXX and XLF/MRI would be significantly lower than in control mice, even if normalized to  
298 the total cell count. Due to the small presence of mature B and T cells in *Xlf<sup>f/f</sup>/Mri<sup>-/-</sup>/Trp53<sup>+/+</sup>*, *Xlf<sup>f/f</sup>*  
299 */Paxx<sup>-/-</sup>/Trp53<sup>+/+</sup>* and *Xlf<sup>f/f</sup>/Paxx<sup>-/-</sup>/Trp53<sup>-/-</sup>* mice, we categorize the observed immunodeficient  
300 phenotypes as “leaky SCID”. Previously, leaky SCID has been described in mice lacking other  
301 NHEJ factors, such as *Ku70<sup>-/-</sup>* [6], *Artemis<sup>-/-</sup>* [3], *Lig4<sup>-/-</sup>/Trp53<sup>+/+</sup>* [10, 30], *Xrcc4<sup>-/-</sup>/Trp53<sup>-/-</sup>* [9, 31], *Xlf<sup>-/-</sup>*  
302 */Atm<sup>-/-</sup>* [19] and *Xlf<sup>-/-</sup>/Rag2<sup>c/c</sup>* [23].

303 In addition to XLF/MRI and XLF/PAXX deficient mice, inactivation of one or two alleles  
304 of *Trp53* also rescues the embryonic lethality of *Xrcc4<sup>-/-</sup>* [9, 31], *Lig4<sup>-/-</sup>* [10, 30] and *Xlf<sup>-/-</sup>Dna-*  
305 *pkcs<sup>-/-</sup>* [20] mice. We propose a model (Figure 5), when single deficiency for DNA-PKcs, PAXX or

306 MRI results in no or modest phenotypes, and DSBs are efficiently repaired. Combined  
307 inactivation of *Xlf/Dna-pkcs*, *Xlf/Paxx* and *Xlf/Mri* results in inefficient DSB ligation,  
308 accumulation of DNA breaks, activation of ATM-dependent DDR, checkpoint protein CHK2,  
309 stabilization of p53 and massive apoptosis. This results in embryonic lethality in mice.  
310 Furthermore, inactivation of *Trp53* results in *Xlf/Dna-pkcs/Trp53*, *Xlf/Paxx/Trp53* and  
311 *Xlf/Mri/Trp53* triple-deficient mice. While DNA breaks in these mice are not repaired, ATM-  
312 dependent DDR response and activation of CHK proteins takes place. However, without p53,  
313 apoptosis is not activated, allowing survival of mice (Figure 5). Moreover, we propose that  
314 inactivation of *Atm* will also rescue embryonic lethality of *Xlf/Paxx* and *Xlf/Mri* mice due to the  
315 mechanisms proposed above. However, inactivation of *Atm* will not rescue embryonic lethality  
316 of *Xlf/Dna-pkcs* mice, due to synthetic lethality between *Atm* and *Dna-pkcs*.

317 It is important to note that altered *Trp53* expression is not always sufficient to rescue  
318 embryonic lethality in mice; for example, PLK1-interacting checkpoint helicase (PICH)-deficient  
319 mice possess developmental defects in the presence or absence of p53 [35], and ATR mutants  
320 (Seckel syndrome) are not completely rescued from embryonic lethality with the inactivation  
321 of *Trp53* [36]. Embryonic lethality of XLF/PAXX and XLF/MRI double-deficient mice can be  
322 explained by the presence of Ku70/Ku80 heterodimer at the DSBs sites, which blocks DNA  
323 repair by alternative end-joining pathway(s), leading to massive apoptosis and cell cycle arrest  
324 [37]. Previously, it was shown that embryonic lethality of LIG4-deficient [38] and XLF/DNA-PKcs  
325 double-deficient mice [25] could be rescued by inactivating *Ku70* or *Ku80* genes. Similarly, we  
326 propose that inactivation of either *Ku70* or *Ku80* gene will rescue the embryonic lethality of  
327 XLF/PAXX and XLF/MRI double-deficient mice and will result in mice indistinguishable from  
328 *Ku70*- or *Ku80*-deficient controls (Figure 5).

329 Recent studies have shown that *Xlf* genetically interacts with *Rag2* [23] and DDR  
330 factors, such as *Atm*, *53bp1*, *H2ax*, and *Mdc1* [17, 19-22, 37]. *Xlf<sup>-/-</sup>Rag2<sup>c/c</sup>* mice almost  
331 completely lack mature B cells and have significantly fewer mature T cells than single deficient  
332 controls [23]. *Xlf<sup>-/-</sup>Atm<sup>-/-</sup>* and *Xlf<sup>-/-</sup>53bp1<sup>-/-</sup>* mice are live-born and exhibit reduced body weight,  
333 increased genomic instability, and severe lymphocytopenia as a result of V(D)J recombination  
334 impairment in developing B and T cells [1, 17, 19, 22]. *Xlf<sup>-/-</sup>H2ax<sup>-/-</sup>* and *Xlf<sup>-/-</sup>Mdc1<sup>-/-</sup>*, on the other

335 hand, are embryonic lethal [19-21]. There are several possible explanations for the functional  
336 redundancy observed between DNA repair genes. For instance, the two factors could have  
337 identical (e.g., if both proteins are involved in ligation or DNA end tethering) or complementary  
338 (e.g., if one protein stimulates ligation while the other is required for DNA end tethering)  
339 functions. To date, XLF has been shown to genetically interact with multiple DNA repair factors  
340 [1, 4, 5, 14, 15, 19, 20, 24, 25], and this list is likely to grow [37, 39]. However, no clear genetic  
341 interaction has been shown between *Xlf* and *Artemis* or *Xrcc4* in the context of mouse  
342 development and V(D)J recombination [24], meaning that it remains difficult to predict genetic  
343 interactions without developing and characterizing genetic models.

344 We found that mice with combined inactivation of *Paxx* and *Mri* (*Paxx*<sup>-/-</sup>*Mri*<sup>-/-</sup>) are live-  
345 born, fertile, and undergo almost normal B and T cell development (Figure 3), where only the  
346 number of splenic B cells is affected, giving rise to a modest phenotype. Moreover, inactivation  
347 of *Paxx* did not affect the CSR efficiency in *in vitro* stimulated MRI-deficient B cells (Figure 3),  
348 thereby confirming our observations *in vitro*. It has been also shown that combined inactivation  
349 of *Paxx* and *Mri* genes in vAbl pre-B cells lead to similar V(D)J recombination efficiency to single-  
350 deficient *Mri*<sup>-/-</sup>, *Paxx*<sup>-/-</sup> and WT controls [5]. Thus, we conclude that there is a genetic interaction  
351 between *Paxx* and *Mri*, which results in a modest phenotype.

352 Lastly, we found that combined inactivation of *Mri* and *Dna-pkcs* (*Mri*<sup>-/-</sup>*Dna-pkcs*<sup>-/-</sup>)  
353 leads to embryonic lethality, and that E14.5 *Mri*<sup>-/-</sup>*Dna-pkcs*<sup>-/-</sup> murine embryos were about 40%  
354 smaller than single-deficient siblings (Figure 4). DNA-PKcs is associated with the N-terminus of  
355 the MRI and Ku heterodimer in the process of recognizing DSBs [5], which may account for  
356 genetic interaction between *Mri* and *Dna-pkcs*. Thus, inactivation of *Trp53*, *Ku70* or *Ku80* may  
357 be a viable method to rescue synthetic lethality from *Mri*<sup>-/-</sup>*Dna-pkcs*<sup>-/-</sup> mice.

358 In conclusion, we have developed and described several complex genetic mouse  
359 models (Figure 5). *Xlf*<sup>-/-</sup>*Mri*<sup>-/-</sup>*Trp53*<sup>+/+</sup> and *Xlf*<sup>-/-</sup>*Paxx*<sup>-/-</sup>*Trp53*<sup>+/+/-</sup> mice possessed severely impaired  
360 B and T lymphocyte development, leaky SCID; *Paxx*<sup>-/-</sup>*Mri*<sup>-/-</sup> mice develop a modest B cell  
361 phenotype; and *Mri*<sup>-/-</sup>*Dna-pkcs*<sup>-/-</sup> mice are embryonic lethal.

362

363

364 **4. Materials and Methods**365 **4.1. Mice**

366 All experiments involving mice were performed according to the protocols approved  
367 by the Comparative Medicine Core Facility (CoMed) at the Norwegian University of Science and  
368 Technology (NTNU, Trondheim, Norway). *Xif<sup>−/−</sup>* [11] and *Dna-pkcs<sup>−/−</sup>* [2] mice were imported  
369 from the laboratory of Professor Frederick W. Alt at Harvard Medical School. *Trp53<sup>−/−</sup>* mice [40]  
370 were imported from Jackson Laboratories. *Paxx<sup>−/−</sup>* [16] and *Mri<sup>−/−</sup>* [18] mice were generated by  
371 the Oksenych group and described previously.

372 **4.2. Lymphocyte development**

373 Lymphocyte populations were analyzed by flow cytometry [16, 18, 19, 22]. In summary,  
374 cells were isolated from the spleen, thymus, and femur of 5-7-week-old mice and treated with  
375 red blood cell lysis buffer Hybri-Max™ (Sigma Aldrich, St. Louis, MO, USA; #R7757). The cells  
376 were resuspended in PBS (Thermo Scientific, Basingstoke, UK; #BR0014G) containing 5% Fetal  
377 bovine serum, FCS (Sigma Life Science, St. Louis, Missouri, United States; #F7524), and counted  
378 using a Countess™ II Automated Cell Counter (Invitrogen, Carlsbad, CA, United States;  
379 #A27977). Then, the cell suspension was diluted with PBS to get a final cell concentration of  
380 2.5 x 10<sup>7</sup> cells/mL. Finally, surface markers were labeled with fluorochrome-conjugated  
381 antibodies and the cell populations were analyzed using flow cytometry.

382 **4.3. Class switch recombination (CSR)**

383 Spleens were isolated from 5-7-week-old mice and stored in cold PBS. Splenocytes were  
384 obtained by mincing the spleens, and naïve B cells were negatively selected using an EasySep  
385 Isolation kit (Stemcell™, Cambridge, UK; #19854). Lipopolysaccharide (LPS; 40 µg/mL; Sigma  
386 Aldrich, St. Louis, MO, USA; #437627-5MG) and interleukin 4 (IL-4; 20 ng/mL; PeproTech,  
387 Stockholm, Sweden; #214-14) were used to induce CSR to IgG1. Expression of IgG1 was  
388 analyzed by flow cytometry.

389 **4.4. Antibodies**

390 The following antibodies were used for flow cytometric analysis: rat anti-CD4-PE-Cy7  
391 (BD Pharmingen™, Allschwil, Switzerland, #552775; 1:100); rat anti-CD8-PE-Cy5  
392 (BD Pharmingen™, Allschwil, Switzerland, #553034; 1:100); anti-CD19-PE-Cy7 (Biolegend, San

393 Diego, CA, USA, #115520; 1:100); hamster anti-mouse anti-CD3-FITC (BD Pharmingen™,  
394 Allschwil, Switzerland, #561827; 1:100); rat anti-mouse anti-CD43-FITC (BD Pharmingen™,  
395 Allschwil, Switzerland, #561856; 1:100); rat anti-mouse anti-CD45R/B220-APC  
396 (BD Pharmingen™, Allschwil, Switzerland; #553092; 1:100); rat anti-mouse anti-IgM-PE-Cy7  
397 (BD Pharmingen™, Allschwil, Switzerland, #552867; 1:100); rat anti-mouse IgG1-APC  
398 (BD Pharmingen™, Allschwil, Switzerland; #550874; 1:100). A LIVE/DEAD™ fixable violet dead  
399 cell stain kit (ThermoFisher Scientific, Waltham, MA, USA; #L34955; 1:1000) was used to  
400 identify dead cells.

#### 401 4.5. Statistics

402 Statistical analyses were performed using one-way ANOVA, GraphPad Prism 8.0.1.244  
403 (San Diego, CA, USA). In all statistical tests,  $p<0.05$  were taken to be significant (\* $p<0.05$ ;  
404 \*\* $p<0.01$ ; \*\*\* $p<0.001$ ; \*\*\*\* $p<0.0001$ ).

405 **Author Contributions:** Conceptualization, V.O., S.C. and Q.Z.; methodology, V.O., S.C. and Q.Z.;  
406 software, V.O., S.C. and Q.Z.; validation, V.O., S.C., A.A. and Q.Z.; formal analysis, V.O., S.C., A.A. and Q.Z.;  
407 investigation, V.O., S.C., A.A., M.F. and Q.Z.; resources, V.O.; data curation, V.O., S.C., A.A., M.F. and Q.Z.;  
408 writing—original draft preparation, V.O. and S.C.; writing— V.O., S.C., A.A., M.F., R.Y. and Q.Z.;  
409 supervision, V.O. and S.C.; project administration, V.O.; funding acquisition, V.O. All authors have read  
410 and agreed to the published version of the manuscript.

411 **Funding:** This work was supported by the Research Council of Norway Young Talent Investigator grant  
412 (#249774) to V.O. In addition, VO group was supported by the Liaison Committee for Education, Research,  
413 and Innovation in Central Norway (#13477; #38811); the Norwegian Cancer Society (#182355); the Research  
414 Council of Norway FRIMEDBIO grants (#270491 and #291217), and The Outstanding Academic Fellow  
415 Program at NTNU (2017–2021).

416 **Conflicts of Interest:** The authors declare no conflict of interest

#### 417 References

- 418 1. Kumar, V., F.W. Alt, and V. Oksenych, *Functional overlaps between XLF and the ATM-dependent*  
419 *DNA double strand break response.* DNA Repair (Amst), 2014. **16**: p. 11-22.
- 420 2. Gao, Y., et al., *A targeted DNA-PKcs-null mutation reveals DNA-PK-independent functions for KU in*  
421 *V(D)J recombination.* Immunity, 1998. **9**(3): p. 367-76.
- 422 3. Rooney, S., et al., *Leaky Scid phenotype associated with defective V(D)J coding end processing in Artemis-*  
423 *deficient mice.* Mol Cell, 2002. **10**(6): p. 1379-90.
- 424 4. Liu, X., et al., *PAXX promotes KU accumulation at DNA breaks and is essential for end-joining in XLF-*  
425 *deficient mice.* Nat Commun, 2017. **8**: p. 13816.
- 426 5. Hung, P.J., et al., *MRI Is a DNA Damage Response Adaptor during Classical Non-homologous End*  
427 *Joining.* Mol Cell, 2018. **71**(2): p. 332-342 e8.
- 428 6. Gu, Y., et al., *Growth retardation and leaky SCID phenotype of Ku70-deficient mice.* Immunity, 1997.  
429 **7**(5): p. 653-65.

430 7. Nussenzweig, A., et al., *Requirement for Ku80 in growth and immunoglobulin V(D)J recombination*.  
431 Nature, 1996. **382**(6591): p. 551-5.

432 8. Ma, Y., et al., *Hairpin opening and overhang processing by an Artemis/DNA-dependent protein kinase*  
433 *complex in nonhomologous end joining and V(D)J recombination*. Cell, 2002. **108**(6): p. 781-94.

434 9. Gao, Y., et al., *A critical role for DNA end-joining proteins in both lymphogenesis and neurogenesis*. Cell,  
435 1998. **95**(7): p. 891-902.

436 10. Frank, K.M., et al., *Late embryonic lethality and impaired V(D)J recombination in mice lacking DNA*  
437 *ligase IV*. Nature, 1998. **396**(6707): p. 173-7.

438 11. Li, G., et al., *Lymphocyte-specific compensation for XLF/cernunnos end-joining functions in V(D)J*  
439 *recombination*. Mol Cell, 2008. **31**(5): p. 631-40.

440 12. Vera, G., et al., *Cernunnos deficiency reduces thymocyte life span and alters the T cell repertoire in mice*  
441 *and humans*. Mol Cell Biol, 2013. **33**(4): p. 701-11.

442 13. Roch, B., et al., *Cernunnos/Xlf Deficiency Results in Suboptimal V(D)J Recombination and Impaired*  
443 *Lymphoid Development in Mice*. Front Immunol, 2019. **10**: p. 443.

444 14. Abramowski, V., et al., *PAXX and Xlf interplay revealed by impaired CNS development and*  
445 *immunodeficiency of double KO mice*. Cell Death Differ, 2018. **25**(2): p. 444-452.

446 15. Balmus, G., et al., *Synthetic lethality between PAXX and XLF in mammalian development*. Genes Dev,  
447 2016. **30**(19): p. 2152-2157.

448 16. Gago-Fuentes, R., et al., *Normal development of mice lacking PAXX, the parologue of XRCC4 and XLF*.  
449 FEBS Open Bio, 2018. **8**(3): p. 426-434.

450 17. Liu, X., et al., *Overlapping functions between XLF repair protein and 53BP1 DNA damage response factor*  
451 *in end joining and lymphocyte development*. Proc Natl Acad Sci U S A, 2012. **109**(10): p. 3903-8.

452 18. Castaneda-Zegarra, S., et al., *Generation of a Mouse Model Lacking the Non-Homologous End-Joining*  
453 *Factor Mri/Cyren*. Biomolecules, 2019. **9**(798).

454 19. Zha, S., et al., *ATM damage response and XLF repair factor are functionally redundant in joining DNA*  
455 *breaks*. Nature, 2011. **469**(7329): p. 250-4.

456 20. Castaneda-Zegarra, S., et al., *Synthetic lethality between DNA repair factors Xlf and Paxx is rescued by*  
457 *inactivation of Trp53*. DNA Repair (Amst), 2019. **73**: p. 164-169.

458 21. Beck, C., et al., *Mediator of DNA Damage Checkpoint Protein 1 Facilitates V(D)J Recombination in Cells*  
459 *Lacking DNA Repair Factor XLF*. Biomolecules, 2019. **10**(1).

460 22. Oksenychn, V., et al., *Functional redundancy between repair factor XLF and damage response mediator*  
461 *53BP1 in V(D)J recombination and DNA repair*. Proc Natl Acad Sci U S A, 2012. **109**(7): p. 2455-60.

462 23. Lescale, C., et al., *RAG2 and XLF/Cernunnos interplay reveals a novel role for the RAG complex in DNA*  
463 *repair*. Nat Commun, 2016. **7**: p. 10529.

464 24. Oksenychn, V., et al., *Functional redundancy between the XLF and DNA-PKcs DNA repair factors in*  
465 *V(D)J recombination and nonhomologous DNA end joining*. Proc Natl Acad Sci U S A, 2013. **110**(6): p.  
466 2234-9.

467 25. Xing, M., et al., *Synthetic lethality between murine DNA repair factors XLF and DNA-PKcs is rescued*  
468 *by inactivation of Ku70*. DNA Repair (Amst), 2017. **57**: p. 133-138.

469 26. Lescale, C., et al., *Specific Roles of XRCC4 Paralogs PAXX and XLF during V(D)J Recombination*. Cell  
470 Rep, 2016. **16**(11): p. 2967-2979.

471 27. Kumar, V., F.W. Alt, and R.L. Frock, *PAXX and XLF DNA repair factors are functionally redundant*  
472 *in joining DNA breaks in a G1-arrested progenitor B-cell line*. Proc Natl Acad Sci U S A, 2016. **113**(38):  
473 p. 10619-24.

474 28. Hung, P.J., et al., *Deficiency of XLF and PAXX prevents DNA double-strand break repair by non-*  
475 *homologous end joining in lymphocytes*. *Cell Cycle*, 2017. **16**(3): p. 286-295.

476 29. Barnes, D.E., et al., *Targeted disruption of the gene encoding DNA ligase IV leads to lethality in embryonic*  
477 *mice*. *Curr Biol*, 1998. **8**(25): p. 1395-8.

478 30. Frank, K.M., et al., *DNA ligase IV deficiency in mice leads to defective neurogenesis and embryonic*  
479 *lethality via the p53 pathway*. *Mol Cell*, 2000. **5**(6): p. 993-1002.

480 31. Gao, Y., et al., *Interplay of p53 and DNA-repair protein XRCC4 in tumorigenesis, genomic stability and*  
481 *development*. *Nature*, 2000. **404**(6780): p. 897-900.

482 32. Musilli, S., et al., *An in vivo study of the impact of deficiency in the DNA repair proteins PAXX and XLF*  
483 *on development and maturation of the hemolymphoid system*. *J Biol Chem*, 2020. **295**(8): p. 2398-2406.

484 33. Di Rosa, F., et al., *On the lifespan of virgin T lymphocytes*. *J Immunol*, 1999. **163**(3): p. 1253-7.

485 34. Fulcher, D.A. and A. Basten, *B cell life span: a review*. *Immunol Cell Biol*, 1997. **75**(5): p. 446-55.

486 35. Albers, E., et al., *Loss of PICH Results in Chromosomal Instability, p53 Activation, and Embryonic*  
487 *Lethality*. *Cell Rep*, 2018. **24**(12): p. 3274-3284.

488 36. Murga, M., et al., *A mouse model of ATR-Seckel shows embryonic replicative stress and accelerated aging*.  
489 *Nat Genet*, 2009. **41**(8): p. 891-8.

490 37. Castaneda-Zegarra, S., et al., *Genetic interaction between the non-homologous end joining factors during*  
491 *B and T lymphocyte development: in vivo mouse models*. *Scand J Immunol*, 2020: p. e12936.

492 38. Karanjawala, Z.E., et al., *The embryonic lethality in DNA ligase IV-deficient mice is rescued by deletion*  
493 *of Ku: implications for unifying the heterogeneous phenotypes of NHEJ mutants*. *DNA Repair (Amst)*,  
494 2002. **1**(12): p. 1017-26.

495 39. Wang, X., B. Lee, and S. Zha, *The recent advances in non-homologous end-joining through the lens of*  
496 *lymphocyte development*. *DNA Repair (Amst)*, 2020.

497 40. Jacks, T., et al., *Tumor spectrum analysis in p53-mutant mice*. *Curr Biol*, 1994. **4**(1): p. 1-7.

498



© 2020 by the authors. Submitted for possible open access publication under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).