

1 **Germline deletion reveals a non-essential role of the atypical MAPK6/ERK3**

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21

22 Materials and Methods: 1149 words

23 Rest of the text: 3289 words

24 **Abstract (200 words)**

25 MAPK6/ERK3 is an atypical member of the MAPKs. An essential role has been suggested by the
26 perinatal lethal phenotype of ERK3 knockout mice carrying a lacZ insertion in exon 2 due to
27 pulmonary disfunction and by defects in function, activation and positive selection of T cells. To
28 study the role of ERK3 *in vivo*, we generated mice carrying a conditional *Erk3* allele with exon3
29 flanked by LoxP sites. Loss of ERK3 protein was validated after deletion of *Erk3* in the female
30 germ line using zona pellucida 3 (*Zp3*)-*cre* and a clear reduction of the protein kinase MK5 is
31 detected, providing first evidence for the existence of the ERK3/MK5 signaling complex *in vivo*.
32 In contrast to the previously reported *Erk3* knockout phenotype, these mice are viable and
33 fertile, do not display pulmonary hypoplasia, acute respiratory failure, abnormal T cell
34 development, reduction of thymocyte numbers or altered T cells selection. Hence, ERK3 is
35 dispensable for pulmonary and T-cell functions. The perinatal lethality, lung and T-cell defects of
36 the previous ERK3 knockout mice are likely due to ERK3-unrelated effects of the inserted lacZ-
37 neomycin-resistance-cassette. The knockout mouse of the closely related atypical MAPK
38 ERK4/MAPK4 is also normal suggesting redundant functions of both protein kinases.

39 **Introduction (630 words)**

40
41 Mitogen-activated protein kinase (MAPK) cascades are conserved eukaryote signaling modules
42 where the downstream effector kinases regulate cell proliferation, differentiation and cell death
43 by phosphorylation of protein substrates. MAPK are also regulators in many physiological
44 processes including development and immune response. Multiple MAPKs were described in
45 mammalian cells, which can be divided in five groups, the 'classical' mitogen-responsive MAPKs
46 (ERK1 and ERK2), the stress-activated JNKs (JNK1-3) and p38^{MAPK} ($\alpha, \beta, \gamma, \delta$), the big MAPK ERK5,
47 and the atypical MAPKs ERK3, ERK4 and ERK7 (1). MAPKs activity is classically regulated by dual
48 phosphorylation on a TXY motif in the activation loop of the kinase by MAPK-kinases.

49
50 ERK3/MAPK6/p97^{MAPK} and the closely-related ERK4/MAPK4/p63^{MAPK} are the only two MAPKs
51 carrying long C-terminal extensions and lacking the dual TXY-phosphorylation motif in the
52 activation loop (2-4). Instead of the canonical dual phosphorylation motif, ERK3 and ERK4
53 contain only a single phospho-acceptor serine (SEG motif) in the activation loop which can be
54 phosphorylated by p21-activated kinases *in vitro* and in transfected cells (5, 6). Apart from this
55 little is known about the mechanisms of regulation, substrate specificity, and the physiological
56 functions of atypical MAP kinases. Especially, mitogen and stress stimuli resulted in only weak
57 phosphorylation at the SEG motif and the only biological relevant regulator of ERK3 and ERK4
58 identified so far is the MAP kinase-activated protein kinase MK5 (7-10). MK5 forms a complex
59 with ERK3/4 and is phosphorylated at its activating site T182 within this complex. In turn and
60 still in the complex, ERK3 also auto-phosphorylates at various sites in its C-terminal extension. It
61 is suggested that the ERK3/MK5 complex is involved in the regulation of dendrite morphology

62 and septin function (11). However, it is not clear whether and how the productive complex
63 formation between ERK3/4 and MK5 is regulated by extracellular stimuli or whether it just
64 depends on their expression levels.

65
66 Additional functions described for ERK3 include its interaction with the cell cycle regulator
67 Cdc14 (12), its contribution to meiotic spindle stability and metaphase-anaphase transition in
68 mouse oocyte maturation (13) and its interaction with the steroid receptor coactivator 3 (SRC-
69 3), an oncogenic protein overexpressed in multiple human cancers (14). ERK3 seemingly
70 phosphorylates SRC-3 at S857 and regulates its interaction with the ETS- and SP1-type
71 transcription factors (14, 15). Recently, the tyrosyl DNA phosphodiesterase 2 (TDP2), which
72 repairs topoisomerase 2-linked DNA damage, was also described as a substrate of ERK3, and it
73 was suggested that ERK3 phosphorylates TDP2 at S60 and stimulates its phosphodiesterase
74 activity during the DNA damage response (16).

75
76 A major contribution to the understanding of the functions of ERK3 and ERK4 was the
77 generation of constitutive knockout alleles of ERK3 (17) and ERK4 (18). Although both kinases
78 are similar in structure and display similar molecular interactions, the phenotypes of both kinase
79 knockouts differed significantly. While ERK4 knockout mice appeared normal, ERK3 knockout
80 mice were not viable, displayed retarded intrauterine growth and pulmonary hypoplasia leading
81 to acute perinatal respiratory failure (17). Furthermore, T cell development, selection and
82 activation was impaired only in the ERK3, but not in the ERK4 knockout mice (19-21). The lack of
83 phenocopy between both knockouts suggested distinct and non-redundant functions of the
84 ERK3/MK5 and ERK4/MK5 signaling complexes.

85 The perinatal lethality of the constitutive ERK3 knockout mice limits the use of this mouse strain
86 in disease models, which are mostly established for adult mice. To overcome this limitation we
87 generated a conditional allele where exon 3 of *Erk3* is flanked by loxP sites. Here we describe
88 the unexpected finding that germ line deletion of exon 3 in mice causes the complete loss of
89 ERK3 protein but does not lead to any of the phenotypes described for the ERK3 knockout
90 mouse carrying the lacZ insertion. Mice lacking ERK3 protein are viable allowing for the further
91 analysis of ERK3 function in post-natal development and adult mice.

92 **Materials and Methods (1149 words)**

93

94 **Generation of ERK3 (MAPK6) conditional knockout mice**

95 *Erk3^{ex3lox}*;mice (Mapk6^{tm1Mgl}) were generated as indicated in Figure 1A. Briefly, the targeting

96 vector containing lox sites flanked exon3 of mouse *Erk3* gene and FRT sites flanked neomycin

97 cassette was linearized with AsiSI and electroporated in 129Ola ES-cells. Two positive clones

98 (2H3 and 2B5) were obtained by PCR screen and homologous recombination was confirmed by

99 Southern blot analysis. DNA samples were digested with Scal and probed with a 5' external

100 probe (PCR product, that amplified 846 bp genomic fragment 5'probe-ERK3-FW: 5'-

101 GTACAGACATGCCTGTACTCATGC-3' and 5'probe-ERK3-RC: 5'-

102 CTATGCTAACCGACTTAACATGGGAC-3'). Positive clones were injected into blastocysts for the

103 generation of chimeric mice. Agouti germ line pups were derived from the mating of chimeric

104 male mice, obtained following the blastocyst injection of *Erk3* targeted ES cell clone 2H3, with

105 C57Bl/6 Flip females. The resulting *Erk3^{ex3loxNeo}*; mice were crossed with C57BL/6-(C3)-Tg(Pgk1-

106 FLPo)10Sykr/J Flippase - expressing mice (22) to delete the neomycin cassette retaining the lox-

107 P-flanked (floxed) exon3 leading to *Erk3^{ex3lox}*; mice. Subsequent Cre-recombinase expression will

108 then catalyze exon3-excision resulting in an additional frameshift mutation downstream to this

109 exon. For generation of Oocyte specific knockout animals, *Erk3* homozygous floxed mice were

110 crossed with B6-Zp3Cre^{tmTgCre}(23). *Erk3^{wt/ex3lox}*::Zp3Cre mice were bred to generate

111 *Erk3^{wt/Δex3}*;mice. *Erk3^{wt/Δex3}*mice were crossed and littermates of different resulting genotypes

112 (*Erk3^{wt/wt}* (+/+), *Erk3^{wt/Δex3}* (+/-) and *Erk3^{Δex3/Δex3}* (-/-)) were analyzed. All mice were maintained

113 at the animal facility of the Hannover Medical School under individually ventilated cages (IVC)

114 conditions with free access to food and water. Mice were handled according to the European

115 guideline (2010/63/EU) as well as the German Animal Welfare Act. All animal experiments were
116 approved by the Lower Saxony State Office for Consumer Protection and Food Safety (file
117 Z2017/47).

118

119 **DNA isolation and genotyping**

120 Tail biopsies, cells and colonies were overnight digested at 55°C in lysis buffer (50 mM Tris-Cl
121 (pH 8.0), 100 mM EDTA, 100 mM NaCl and 1% SDS) containing proteinase-K (0.5 mg/mL). For
122 tissue samples proteins were salted out with extra NaCl. DNA was precipitated with isopropanol,
123 washed with 70% ethanol and dissolved in water. Genotyping PCR was performed with Hotstar
124 Taq (Qiagen) with extra Mg²⁺ under standard conditions. The primers used were: 1) ERK3-1-
125 genotyping-FW: CCGTTTGAGTTTCTTGAGTG, 2) ERK3-3-genotyping-RV: CGTGGTATCGTTATGCG.
126 1+2 primer combination amplifies 2,4 kb fragment in case of homology recombination (short
127 arm integration).

128 3) long arm FW: CAGCTTTTGTTCCTTTAGTGCTCGAC, 4) long arm RC:

129 AGGACTCCTACATCCTGAGCTACCTCTCTAG. 3+4 primer combination amplifies 10,2 kb fragment
130 in case of homology recombination (long arm integration).

131 5) ERK3_1-target-seq.-FW: TGGACAGAGCACTGGAAG, 6) ERK3-loxP-RC:

132 CTTAAGACAGGAGTGTGGATC. 5+6 primer combination amplifies 943 bp of WT, 1055 bp of
133 exon3 floxed or 336 bp of exon3 deleted fragment.

134 PCR reactions were separated on 2% agarose gels and images acquired using INTAS Gel
135 documentation system.

136

137

138 **Cell culture**

139 To generate bone marrow-derived macrophages (BMDM), bone marrow cells were flushed from
140 the femurs of mice. Cells were cultured on 10 cm dishes in DMEM supplemented with 10% fetal
141 bovine serum, penicillin/streptomycin, and 50 ng/ml recombinant macrophage colony-
142 stimulating factor (M-CSF) (Wyeth, Boston, MA) under humidified conditions with 5% CO₂ at
143 37°C for 7 days.

144

145 **Analysis of ERK3 mRNA expression**

146 Total RNA was isolated from BMDM of ERK3^{+/+} and ERK3^{-/-} mice. RNA was purified using the
147 Extractme Total RNA extraction kit (BioScience) according to the manufacturer's instructions.
148 cDNA from 500 ng RNA was synthesized using the first strand cDNA synthesis kit
149 (Fermentas/Thermo) in combination with random hexamer primers. Sense and antisense
150 oligonucleotides (ERK3-mRNA-FW: 5'- TGGACAGAGCACTGGAAG -3' and ERK3-mRNA-RC: 5'-
151 CTTAAGACAGGAGTGTGGATC-3') specific for *Erk3* were used to amplify a 619 bp ERK3 mRNA
152 fragment spanning exons 2-4 from ERK3^{+/+} or a 474 bp fragment lacking the 145 bases of exon
153 3 from ERK3^{-/-} cells. Amplification of GAPDH mRNA fragment was used as a loading control
154 (GAPDH-fw: 5'-CATGGCCTTCCGTGTTCTTA-3'; GAPDH-rc: 5'-CCTGCTTCACCACCTTCTTGAT-3').
155

156 **SDS-PAGE, Western blot and antibodies**

157 Protein extracts were prepared by direct lysis of the cells in the culture plate with 2x Laemmli's
158 SDS sample buffer. Protein lysates were separated by sodium dodecyl sulfate polyacrylamide gel
159 electrophoresis (SDS-PAGE) on 7.5%-16% gradient gels and transferred by semi-dry blotting to
160 Hybond ECL nitrocellulose membranes (GE Healthcare). Primary antibodies used were: anti-

161 ERK3 [EP1720Y] ab53277 from Abcam, MK5 [HPA015515] from Atlas antibody, GAPDH from
162 Millipore. Secondary HRP-conjugated antibodies (Santa Cruz Biotechnologies) were used.
163 Antigen-antibody complexes were detected with enhanced chemiluminescence (ECL) detection
164 solution (solution A: 1.2 mM luminol in 0.1 M Tris-HCl (pH 8.6); solution B: 6.7 mM p-coumaric
165 acid in DMSO; 35% H₂O₂ solution; ratio 3333 : 333 : 1) using the Luminescent Image Analyzer
166 LAS-3000 (Fujifilm).

167

168 **Histology**

169 Mice were euthanized individually with carbon dioxide in a standard mouse IVC. Lungs were
170 harvested and inflation-fixed with 10% neutral buffered formalin after euthanasia. Lung was cut
171 at different levels, processed through a gradient of alcohols and xylene and embedded in
172 paraffin. For histological examination, 2-3 μm thick sections were cut and stained with
173 hematoxylin and eosin.

174

175 **Flow cytometry and cell sorting**

176 Monoclonal antibodies specific for CCR7 (4B12), CD4 (GK1.5), CD5 (53-7.3), CD8α (53-6.7), CD19
177 (6D5), CD25 (PC61.5), CD44 (IM7), CD62L (MEL-14), CD69 (H1.2F3), Foxp3 (MF23), TCRβ (H57-
178 597), TCRγδ (GL3) were used as AmCyan, Brilliant Violet 510 (BV510), BV421, Pacific Blue (PB),
179 eFluor450, fluorescein isothiocyanate (FITC), Alexa488, Alexa647, phycoerythrin (PE), peridinin
180 chlorophyll protein-Cy5.5 (PerCP-Cy5.5), PE-Cy7, APC, APC-Cy7 and were purchased from
181 eBioscience, BD Biosciences, or Biolegend. Cells were acquired using a BD FACSCanto II and data
182 was analyzed using FlowJo software (Tree Star). Discrimination of dead cells were performed

183 using either the Zombie Aqua Fixable Viability kit or 7-amino-actinomycin D according to the
184 manufacturer's instructions and doublets were excluded.

185

186 **Cell preparations**

187 Thymus and spleen were crushed through a 70 μm cell strainer (Corning) to obtain single-cell
188 suspensions. For spleen, red blood cells (RBCs) were lysed using Qiagen RBC Lysis Solution
189 according to manufacturer's instructions.

190

191 **Statistical analysis**

192 All analysis was performed using GraphPad Prism software (version 7). Data are represented as
193 mean plus or minus SEM. Analysis of significance between 3 groups of mice was performed
194 using one-way analysis of variance followed by Tukey's test.

195

196 **Analysis of T cell proliferation**

197 Splenic and peripheral lymph node single cell suspensions were pooled and stained with cell
198 proliferation dye eFluor670 (eBioscience). Staining was performed at a cell concentration of
199 1×10^7 cells/ml in PBS with 1.25 μM eFluor670 for 10 min at 37°C. For in vitro activation 0.15×10^6
200 labeled cells in 200 μl medium (RPMI-1640 supplemented with 10% FCS, 1% PenStrep, 1.75 μl β -
201 MercaptoEtOH/500 ml medium, and freshly added rhIL-2 100 U/ml) were seeded into coated
202 round bottom 96-well plates. Plates were coated overnight at 4°C with anti-CD3 (clone 17.A2,
203 final concentration 0.5 $\mu\text{g}/\text{ml}$) and anti-CD28 (clone 37.51, final concentration 1 $\mu\text{g}/\text{ml}$) in a
204 volume of 100 μl per well. After 48h incubation at 37°C 5% CO₂ cells were splitted 1:2 into non-
205 coated 96-well plates and supplemented with fresh rhIL-2. 72h and 96h after start of the culture

206 cells were harvested, stained with anti-CD4 (clone RM4-5, Biolegend) and anti-CD8b (clone
207 RMCD8, homemade) antibodies, and proliferation was analyzed by flow cytometry. For live
208 dead discrimination DAPI was used.

209 **Results (1143 words)**

210

211 **Conditional targeting of the ERK3 allele**

212

213 The murine *Erk3* gene is comprised of 6 exons spanning 20 kb of genomic sequence (24). Exons
214 2 to 6 encode the ORF sequence of ERK3. A targeting vector was designed to flank exon 3 of
215 *Erk3* coding for the activation loop and catalytic kinase subdomains VIII-X (amino acids 186-233)
216 with loxP sites in ES cells (*Erk3^{ex3lox}*; Fig. 1 A). The Neo selection cassette flanked by FRT sites was
217 inserted in intron 2. The correct integration of this vector was screened by PCR (Fig. 1B,C) and
218 validated by Southern blot analysis (Fig. 1D) of genomic DNA. Germline transmission was
219 obtained with targeted *Erk3^{ex3lox}* ES cell clone 2H3, and the neomycin resistance cassette was
220 removed by breeding with Flp-deleter mice (22). Recombination was confirmed by PCR (Fig. 1E).

221

222 **Germline deletion of exon 3 of ERK3 leads to viable mice with the complete loss of ERK3 and**
223 **reduced MK5 expression**

224

225 To validate that our targeting strategy results in a null allele we first generated a germ line
226 deletion of exon 3 (*Erk3^{Δex3}*) by breeding mice with the floxed exon 3 to Zp3-*Cre* mice that
227 express CRE-recombinase in oocytes (23) which eliminates ERK3 in all cells of the body, i.e.
228 generates a constitutive knockout. Unexpectedly and in contrast to the previously described
229 knockout (17) matings of heterozygous *Erk3^{Δex3}* mice gave rise to viable homozygous offspring at
230 the expected Mendelian ratio (n=105 of six crosses and 15 litters (Fig. 2A), 25 WT mice, 45 HETs,
231 35 ERK3 KO, $\chi^2=4.04<5.99$ (p<0.05)). PCR analysis of bone marrow-derived macrophages

232 (BMDMs) demonstrated absence of WT mRNA in *Erk3* ^{Δ ex3x} homozygotes and the presence of a
233 reduced level of mRNA lacking Exon 3 (Fig. 1F). Western blot analysis of BMDM lysates using
234 various antibodies including the N-terminal specific one, which could detect the C-terminal
235 truncations, revealed the lack of ERK3 in homozygous mutant mice (Fig. 1G). Detection of a very
236 faint band at about 28 kDa could represent some remaining rather instable protein fragment of
237 only part of the catalytic domain (subdomains I-VII) encoded by exon 2 (aa 1-185). Deletion of
238 exon 3 leads to a frame shift and immediate translation stop in potential alternatively spliced
239 transcripts of the targeted allele. Interestingly, the protein level of the ERK3 interaction partner
240 MK5 was also decreased in the ERK3 knockout (Fig. 1G).

241

242 **Early and transient growth retardation of *Erk3* ^{Δ ex3/ Δ ex3} mice**

243

244 We determined body weight of male and female *Erk3* ^{Δ ex3/ Δ ex3} mice and their littermates 3 to 20
245 weeks after birth. Male *Erk3* ^{Δ ex3/ Δ ex3} mice displayed significantly lower body weight 3 weeks after
246 birth indicating some early growth retardation (Fig. 2B). However, subsequently all *Erk3* ^{Δ ex3/ Δ ex3}
247 mice gradually caught up in weight, developed normally, were apparently healthy and became
248 indistinguishable from wild type and heterozygous littermates in the age of about 20 weeks.
249 Examination of tissue sections stained with hematoxylin and eosin revealed no obvious
250 abnormalities in the lungs of WT, *Erk3*^{+/ Δ ex3} and *Erk3* ^{Δ ex3/ Δ ex3} mice (Fig. 2C). At present, several
251 mice reached already an age of one year or more, and several males and two females tested
252 were fertile.

253 **Loss of ERK3 does not impair T-cell development and proliferation**

254

255 Because of the published effects of the previous ERK3 deletion on T-cell development,
256 activation and function (19-21), we analyzed T-cell development and function in our *Erk3*^{*Δe3x/Δex3*}
257 mice. We first compared T cell populations of the thymus of 5-6 weeks old WT, ERK3+/- and
258 ERK3-deficient mice. We did not detect significant differences in total thymus cellularity. In
259 addition, no differences were observed in the frequencies of any of the major thymocyte
260 populations, CD4 and CD8 double negatives (DN), DP, $\gamma\delta$ TCR⁺, as well as CD4 and CD8 SP cells
261 (Fig. 3A). This is in contrast to the *Erk3-lacZ* allele, which strongly reduced numbers of
262 thymocytes, most prominently within the CD4 and CD8 double positive (DP) and CD8 single-
263 positive (SP) subsets (19).

264 It has been proposed that *Erk3* contributes to positive selection of thymocytes (21). At steady
265 state, DP thymocytes undergoing selection can be discriminated based on expression of the
266 surface marker CD5 and TCR β . Pre-selection DP cells are CD5^{lo}TCR β ^{lo} (DP1), selecting DP cells
267 are CD5^{hi}TCR β ^{int}, and CD5^{hi}TCR β ^{hi} cells (DP3) are precursors of CD8 SP thymocytes (25). We did
268 not observe any alterations in ratios between the 3 DP thymocyte fractions, suggesting that also
269 positive selection in the thymus is unaffected by loss of ERK3 (Fig. 3B). These data are consistent
270 with normal frequencies of CD4 and CD8 SP cells in the absence of ERK3. In order to assess
271 potential consequences of *Erk3* deletion at the SP stages of T-cell development, we employed
272 the same staining strategy. Again, we found no difference in surface phenotype in CD4 and CD8
273 SP cells (Fig. 3B). An alternative strategy to monitor thymocyte maturation is staining for the
274 activation marker CD69 and chemokine receptor CCR7. Selection induces upregulation of CD69,
275 followed by CCR7. CD69 is then rapidly downregulated, leaving a mature CD69⁻CCR7⁺ mature

276 thymocyte population. We detected a statistically significant lower frequency of transitory
277 CD69⁺CCR7⁺ thymocytes within the CD8 lineage that had no impact on the frequency of fully
278 mature CD69⁻CCR7⁺ CD8 SP cells in ERK3-deficient thymi (Fig. 3C). We detected no ERK3-
279 dependent differences in frequencies of CD4 SP subsets.

280 Next, we assessed development of Foxp3⁺ regulatory T cells (Treg) in the absence of functional
281 ERK3. We found no Erk3-dependent differences in Treg cell frequencies in either thymus or
282 spleen (Fig. 4A). The total cellularity of splenocytes was unaltered in the absence of ERK3 (Fig.
283 4B). Consistent with normal T cell development in the thymus, we also did not detect any
284 alteration in the ratio of T vs. B cells in spleen, although we noted a marginal, but statistically
285 significant increase in the frequency of splenic B cells. In addition, we found no changes in the
286 ratio between CD4⁺ and CD8⁺ T cells upon deletion of ERK3. Expression of CD44 and CD62L
287 allows for discrimination of naïve (CD44⁻CD62L⁺), central memory (CD44⁺CD62L⁺) and effector
288 memory (CD44⁺CD62L⁻) T cell subsets. We found no differences in the frequencies of naïve,
289 central memory or effector T cells within the CD4 and CD8 T-cell compartments in spleen when
290 comparing ERK3-sufficient and ERK3-deficient mice (Fig. 4C). These data suggest that loss of
291 Erk3 expression does not result in aberrant T-cell activation at steady-state. T cells from
292 conventional ERK3 KO mice had reduced proliferation capacity upon unspecific TCR stimulation
293 using anti-CD3 and anti-CD28 antibodies (4). Although T-cell activation was not altered in our
294 newly generated ERK3 knockout mice at steady state, we compared proliferation capacity of WT
295 and ERK3-deficient cells upon CD3/CD28 stimulation. In contrast to the conventional ERK3 KO
296 we could not observe any differences in T cell proliferation, neither in CD4 nor CD8 T cells, for
297 our new ERK3 KO (Fig. 4D). Together, we conclude from these data that ERK3 is dispensable for
298 intrathymic T cell development, T cell homeostasis as well as T cell proliferation.

299 **Discussion (603 words)**

300

301 Here, we report the generation and analysis of a novel *Erk3* null allele, and show that deletion of
302 ERK3 is not essential for viability, pulmonary function or T-cell development in contrast to
303 previously described mice carrying a lacZ insertion into exon2 of *Erk3* (17, 19-21). The reason for
304 these differences likely lie in the different targeting strategies used to disrupt *Erk3*. The
305 constitutive ERK3 knockout was generated by insertion of a lacZ in frame with the translation
306 start of exon 2 of the ERK3 gene 12 amino acids downstream of the initiation codon and a
307 neomycin-resistance-cassette downstream of lacZ. The conditional allele reported here removes
308 exon 3 of *Erk3* and leaves only a single FRT and a single loxP sites in intron 2. The insertion of a
309 lacZ-neomycin-resistance-cassette often altered transcription of genes in the flanking DNA
310 around the targeted gene, and accordingly the phenotype of the mutation (26-29). This may be
311 due to the loss or disruption of intragenic regulatory elements, the constitutive promoter
312 driving the neomycin gene, removal of insulating DNA in the targeted alleles, and local silencing
313 due to disruption of normal chromatin organization by the exogenous construct (26). The
314 detailed transcriptome analysis of 29 targeted alleles in mice revealed that down-regulated
315 genes flanking the targets were rather equally distributed 5' and 3' of the target and the median
316 distance from the target was 34kb (26). In this regard, it is interesting that on chromosome 9 the
317 gene for an essential subunit of RNA polymerase II, *leo1*, is 40 kb 3' to the *Erk3* gene. Hence, one
318 may speculate that down regulation of essential genes, such as *leo1*, may severely compromise
319 cell viability and contribute to the previously reported *Erk3* mutant phenotype. In contrast to
320 effects of insertion cassettes and to the best of our knowledge no effects of insertions of single
321 loxP and FRT sites into intronic sequences are described. Therefore, a likely explanation for the

322 perinatal lethality, lung and T-cell defects observed in the previous ERK3 knockout mice is ERK3-
323 unrelated effects of the inserted lacZ-neomycin-resistance-cassette.

324 We and others have described the ERK3/MK5 and ERK4/MK5 signaling modules (7, 9, 10, 30).

325 Deletion of MK5 and ERK4 in mice resulted in some mild growth retardation (31, 32) and no

326 significant phenotype at all (18), respectively. In contrast, disruption of *Erk3* had a lethal

327 phenotype (17). So far, it was difficult to understand that deletion of different components of

328 these modules do not mutually phenocopy, but display completely different phenotypes. This

329 also questioned the physiological relevance of these signaling modules. However, the

330 phenotype of slight and transient male growth retardation described for deletion of exon 3 of

331 *Erk3* here phenocopies the MK5 knockout and reconciles the genetic analysis of these signaling

332 complexes with their existence in a specific signaling module. Furthermore, the observation that

333 the level of the interaction partner MK5 is significantly reduced in the *Erk3^{Δex3/Δex3}* BMDMs

334 strongly supports the existence of the ERK3/MK5 signaling complex *in vivo*. Possibly the

335 remaining MK5 in our *Erk3^{Δex3/Δex3}* mice is stabilized by its interaction with ERK4.

336 So far, the differences between the phenotypes of the conventional knockouts of ERK3 and

337 ERK4 were explained by specific non-redundant functions of these closely related atypical

338 MAPKs (18), which contrasts with the similarities in structure and molecular interactions of both

339 kinases (5, 33, 34). The viability and fertility of mice with deletion of exon 3 of *Erk3* is much

340 more similar to the phenotype of the conventional ERK4 knockout. Hence, one cannot exclude a

341 redundant function of both atypical MAPKs, which could be revealed in the future by generation

342 of the exon 3 ERK3/ERK4 double knockout mouse.

343 **Acknowledgements (9 words)**

344 The work of M.G. is supported by Deutsche Forschungsgemeinschaft.

345 **Legends to the Figures (633 words)**

346

347 **Figure 1: Generation of the conditional ERK3 knockout mouse and deletion of ERK3 mRNA and**

348 **protein.** A) Targeting strategy. B-D) ES cell screening by PCR (B,C) and Southern hybridization

349 (D). B,C) PCR using primer combination P1/P2 and P3/P4 (cf. A) to detect *Erk3^{ex3loxneo}* allele. D)

350 Southern blot analysis using probe (cf. A) and *ScaI* digested DNA. E) Detection of Flp- and Cre-

351 mediated recombination by PCR using primer combinations (P5,P6) leading to fragments as

352 indicated in A. F) ERK3 mRNA was amplified by PCR from total RNA of BMDMs using primers for

353 exons 2 and 4. The ERK3 KO displays a single band weaker and smaller than WT indicating loss of

354 exon 3. G) Western blot analysis of total protein of BMDMs by an N-terminal-ERK3 antibody

355 (Abcam 53277) and a MK5 antibody. Equal loading is demonstrated by GAPDH detection.

356

357 **Figure 2: Characterization of the viable ERK3 KO mice.** A) Mendelian ratio of the offspring of

358 heterozygous *Erk3^{Δex3}* mice. 15 litters of six crosses (total n=105) were analyzed. No statistical

359 significant deviation from Mendelian ratio is detected $\chi^2=4.04<5.99$ ($p<0.05$). B) Slight and

360 transient growth retardation of male but not female ERK3 KO mice (4-6 mice per group, **

361 $p<0.05$, *** $p<0.01$). C) Histopathology of the lungs from 35 day old WT (a), ERK3+/- (b) and

362 ERK3 KO (c) mice revealed no significant pathological alterations. Hematoxylin eosin staining,

363 bars = 50 μ m.

364

365 **Figure 3: ERK3 is largely dispensable for intrathymic T-cell development.** A) Representative flow

366 cytometric analysis of thymi from WT and *Erk3^{-/-}* mice stained with antibodies against CD4 and

367 CD8 α . Numbers in quadrants represent frequencies. Total cellularity of thymi from WT, ERK3+/-

368 and ERK3^{-/-} mice. Statistical analysis of flow cytometric results from WT, ERK3^{+/-} and ERK3^{-/-} mice,
369 cells were defined as DN (CD4⁻, CD8α⁻), DP (CD4⁺, CD8α⁺), SP4 (CD4⁺,
370 CD8α⁻), SP8 (CD4⁻, CD8α⁺) and γδ T cells (CD4⁻, CD8α⁻, TCRγδ⁺). B) Representative flow cytometric
371 analysis of thymi from WT and ERK3^{-/-} mice stained with antibodies against CD4, CD8α, TCRβ and
372 CD5. Numbers adjacent to gates represent frequencies. Statistical analysis of flow cytometric
373 results, cells were defined as DP1 (TCRβ^{lo}, CD5^{lo}), DP2 (TCRβ^{int}, CD5^{hi}) and DP3 (TCRβ^{hi}, CD5^{int})
374 thymocytes. C) Representative flow cytometric analysis of thymi from WT and ERK3^{-/-} mice
375 stained with antibodies against CD4, CD8α, CCR7 and CD69. Numbers in quadrants represent
376 frequencies. Statistical analysis of flow cytometric results, cells were defined as described in A)
377 and CD69⁺CCR7⁻, CD69⁺CCR7⁺ and CD69⁻CCR7⁺ thymocytes. A-C) Pooled data of two independent
378 experiments, n=5-6 per genotype.

379
380 **Figure 4: ERK3 is largely dispensable for T-cell homeostasis and proliferation.** A) Treg cell
381 numbers in thymus and spleen. Dot plots show representative flow cytometric analysis of thymi
382 and spleen from WT and ERK3^{-/-} mice stained with antibodies against CD4, TCRβ, Foxp3 and CD25.
383 Numbers adjacent to gates represent frequencies. Graphs display statistical analysis of flow
384 cytometric results from WT, ERK3^{+/-} and ERK3^{-/-} mice. B) Representative flow cytometric analysis
385 of spleen from WT and ERK3^{-/-} mice stained with antibodies against CD19, TCRβ, CD4 and CD8.
386 Numbers in quadrants represent frequencies. Total cellularity of spleen from WT, ERK3^{+/-} and
387 ERK3^{-/-} mice. Statistical analysis of flow cytometric results from WT, ERK3^{+/-} and ERK3^{-/-} mice, cells
388 were defined as T cells (TCRβ⁺), B cells (CD19⁺), SP4 (TCRβ⁺, CD4⁺) and SP8 (TCRβ⁺, CD8⁺). C)
389 Representative flow cytometric analysis of SP4 and SP8 splenic T cells from WT and ERK3^{-/-} mice
390 stained with antibodies against CD4, CD8, CD44 and CD62L to identify naïve (CD44⁻CD62L⁺),

391 central memory (CD44⁺CD62L⁺) and effector memory (CD44⁺CD62L⁻) T cell subsets. A-C) Pooled
392 data of two independent experiments, n=5-6 per genotype. D) Flow cytometric analysis of CD4
393 (upper panel) and CD8 (lower panel) T cell proliferation from WT and ERK3^{-/-} mice after 3 and 4
394 days of culture. Shown are representative contour plots of 1 – 2 experiments with each n = 2 mice
395 per genotype.

396 References

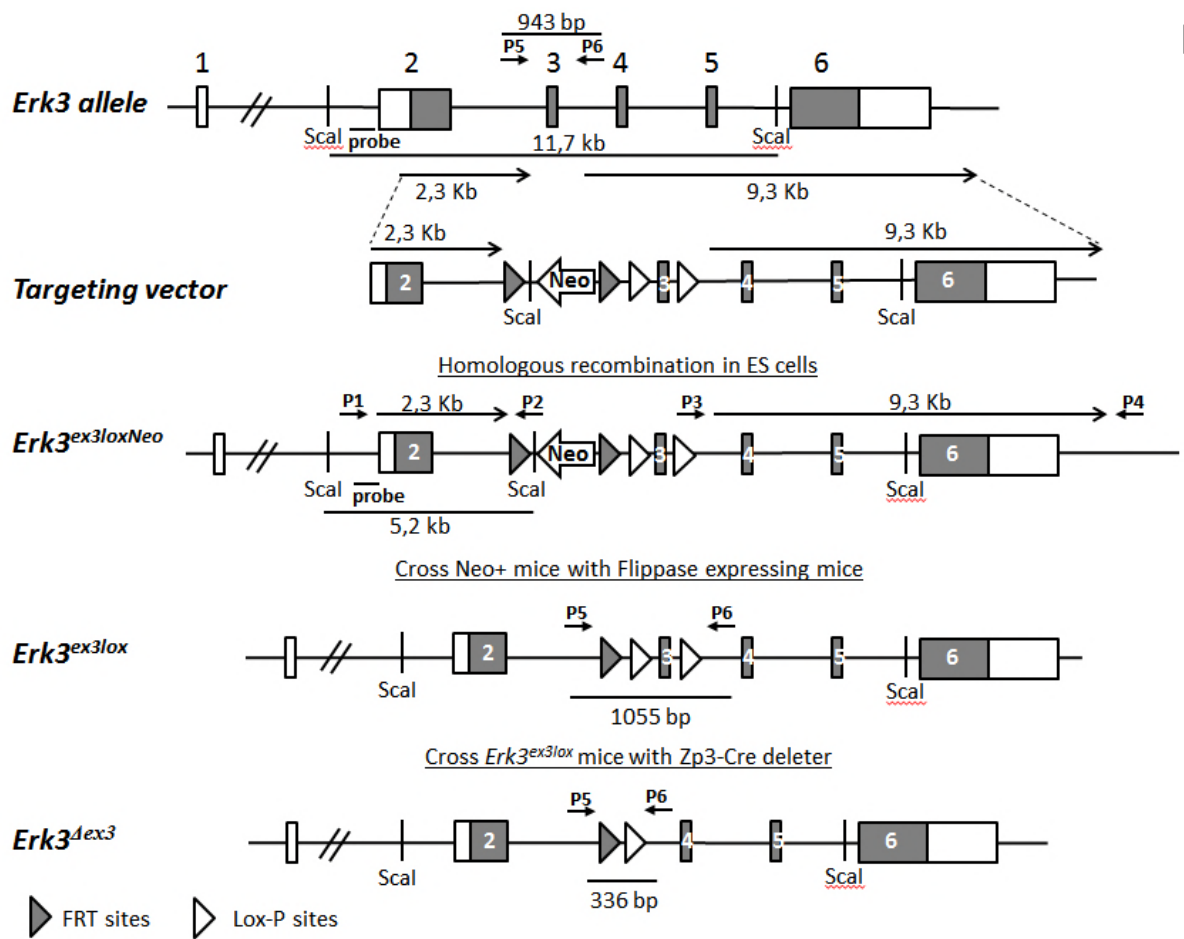
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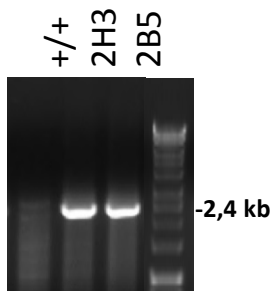
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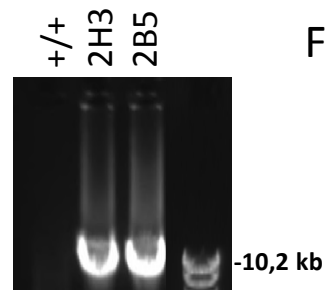
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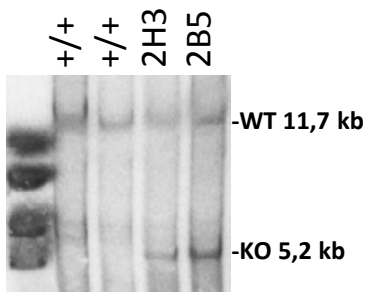
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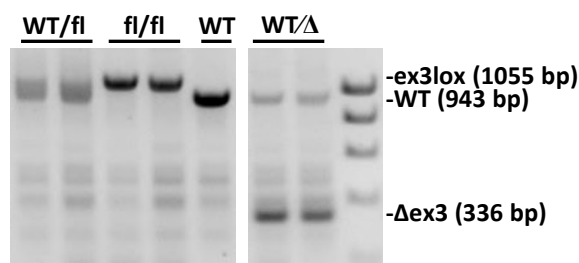
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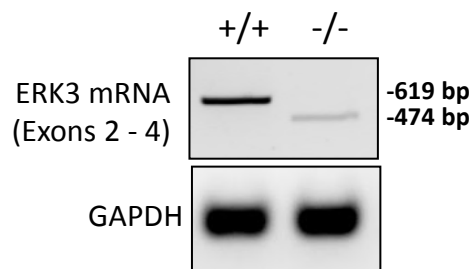
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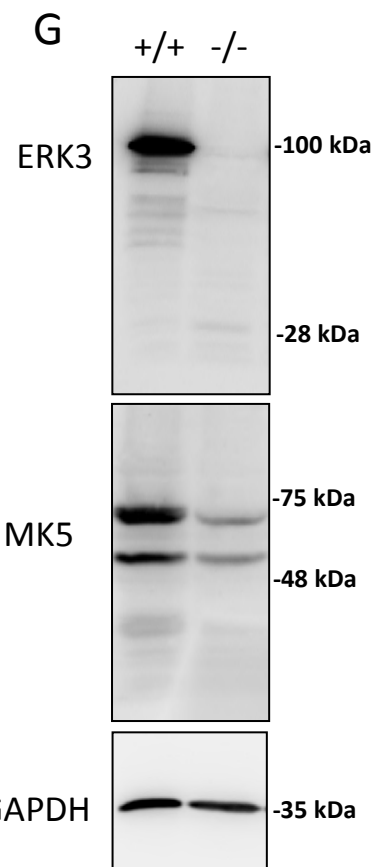
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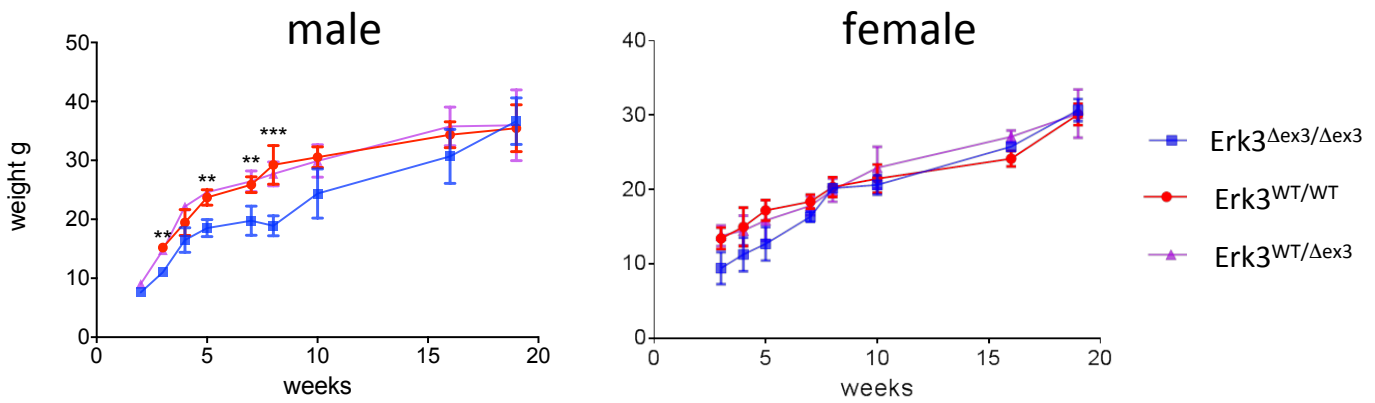
G



A

Mating #	Litter #	WT	HE	KO
13124	2	2	7	7
13125	1	1	2	2
13542	3	7	11	9
13541	2	5	8	4
18676	3	4	9	9
18675	4	6	8	4
total	15	25	45	35

B



C

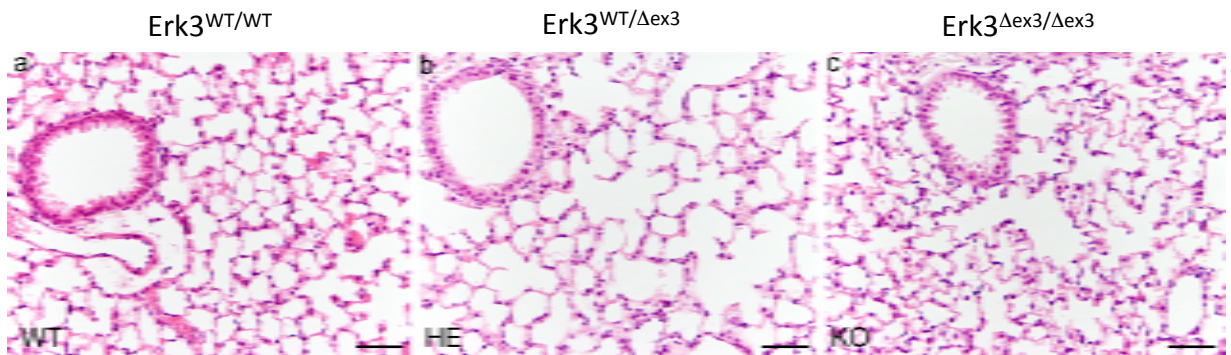
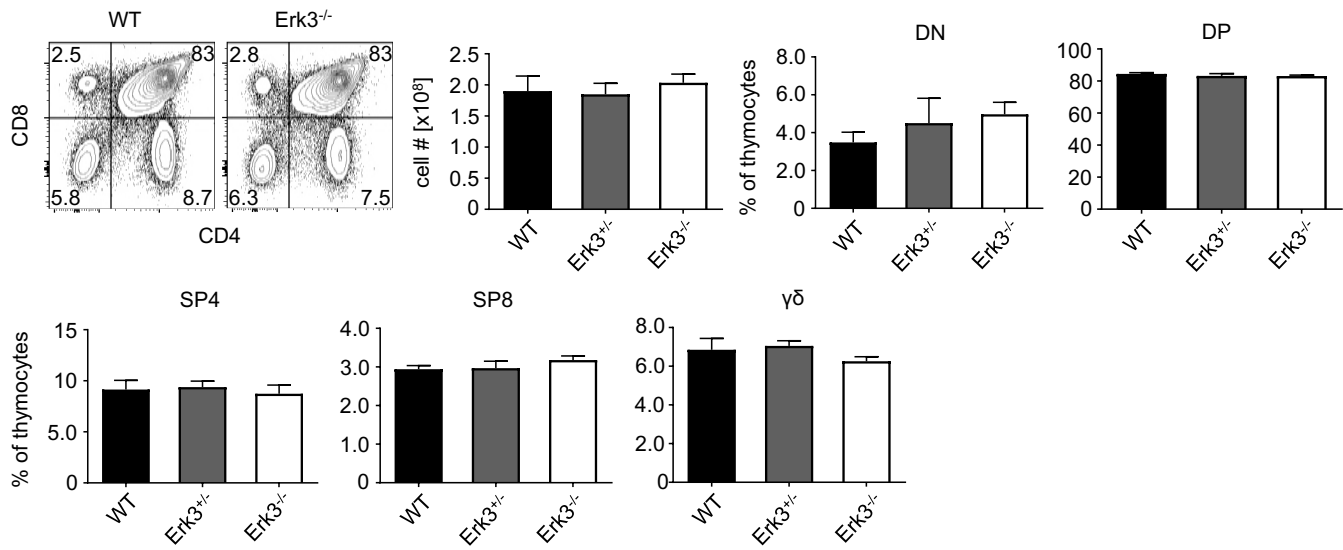


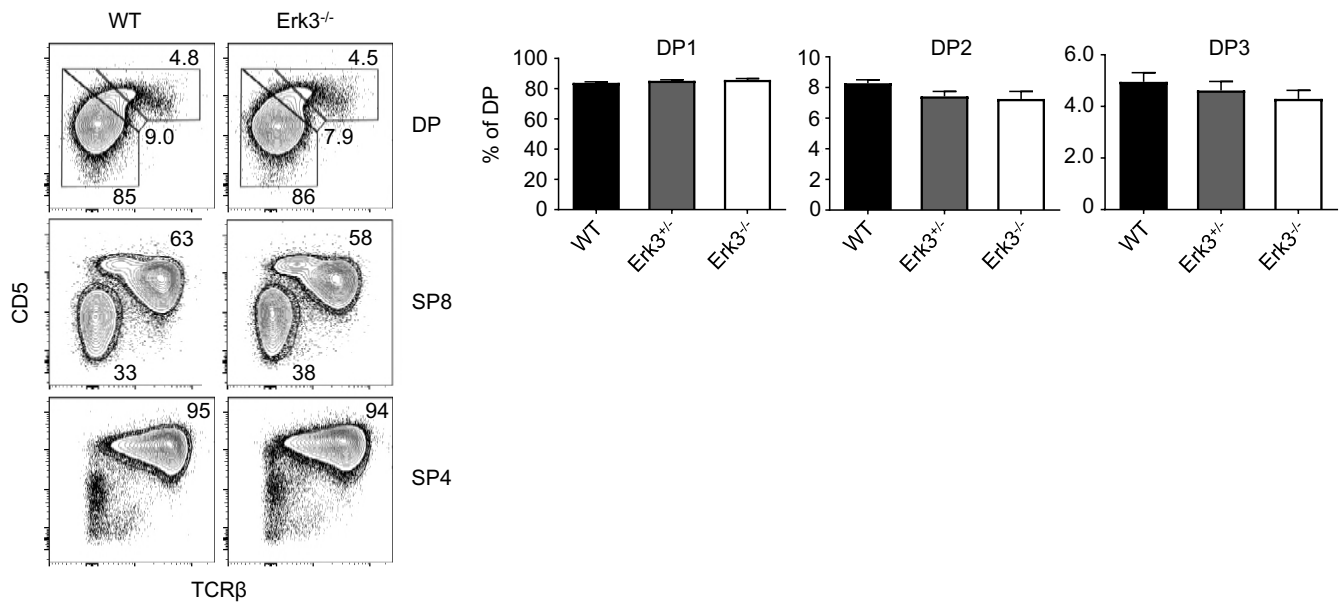
Fig. 2

Fig. 3

A



B



C

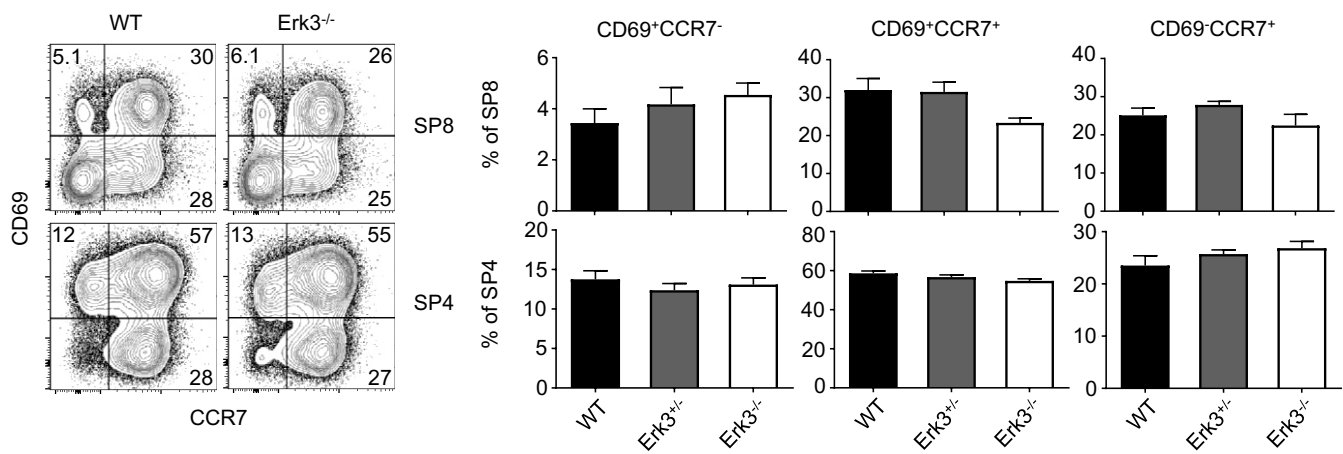
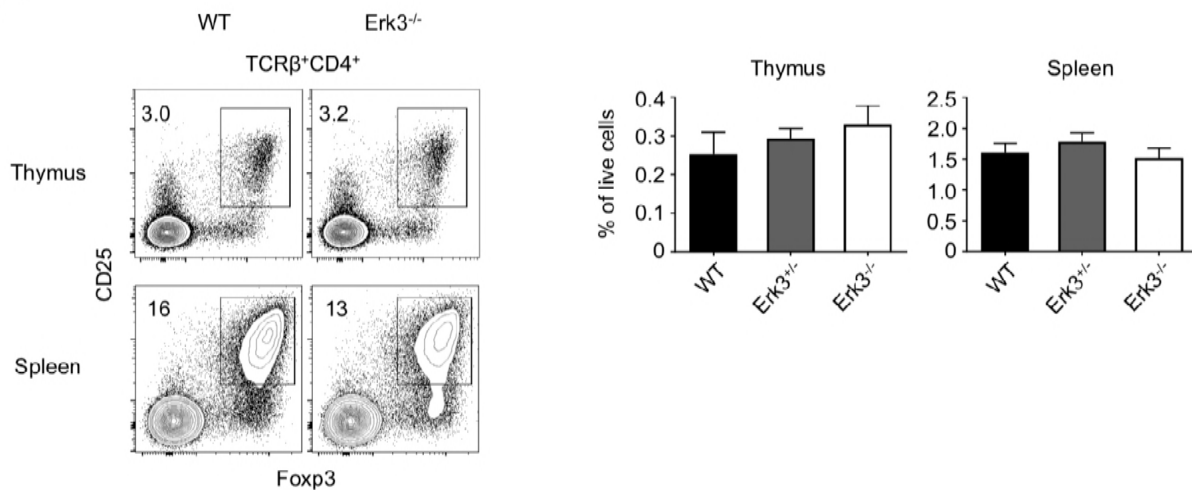
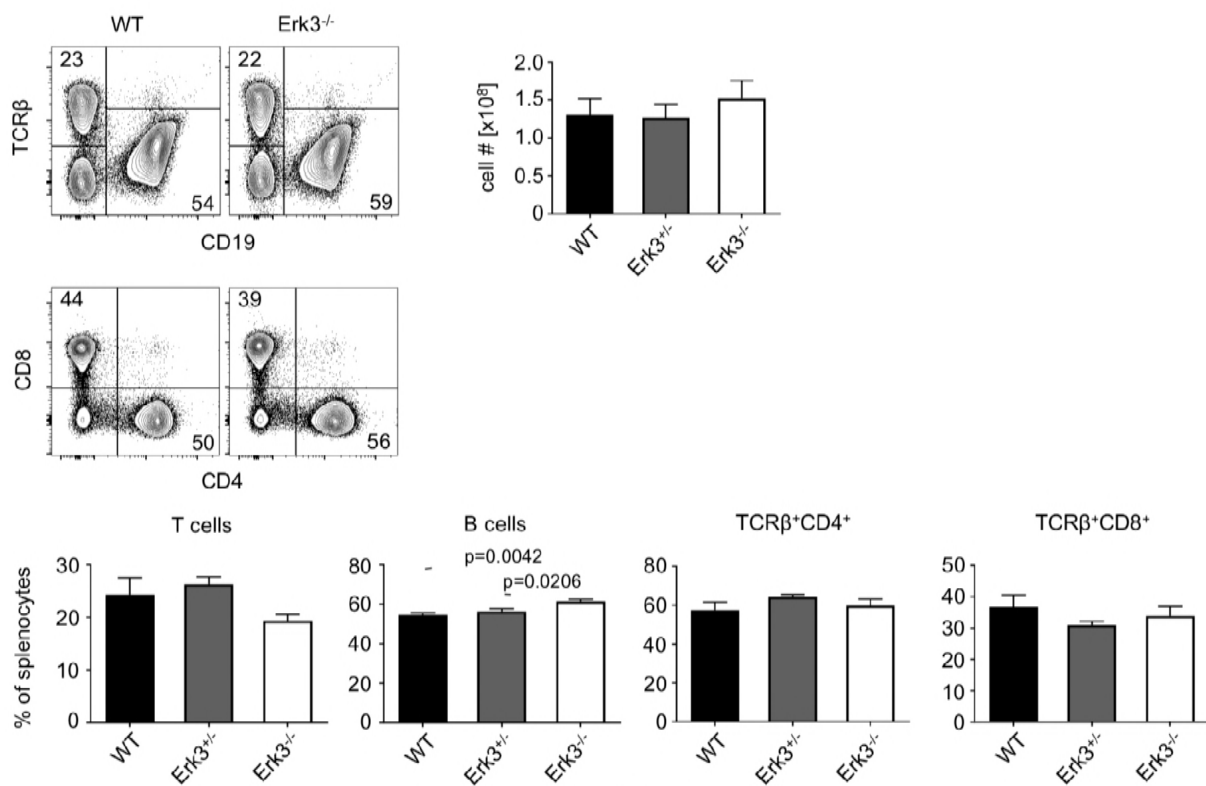


Fig. 4

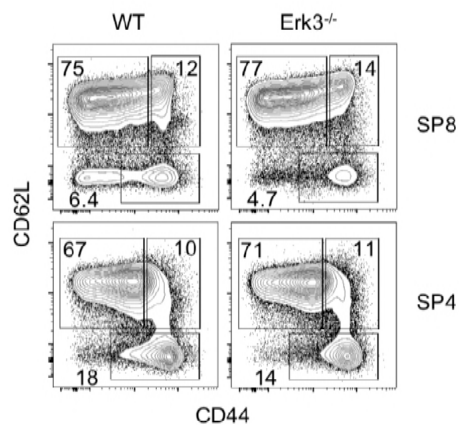
A



B



C



D

