

1 **MALT1 controls attenuated rabies virus by inducing early**
2 **inflammation and T cell activation in the brain**

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4 **Running title:** MALT1 is required to control attenuated rabies virus

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32 **ABSTRACT**

33 MALT1 is involved in the activation of immune responses as well as in the proliferation and
34 survival of certain cancer cells. MALT1 acts as a scaffold protein for NF- κ B signalling and a
35 cysteine protease that cleaves substrates, further promoting the expression of
36 immunoregulatory genes. Deregulated MALT1 activity has been associated with
37 autoimmunity and cancer, implicating MALT1 as a new therapeutic target. While MALT1
38 deficiency has been shown to protect against experimental autoimmune encephalomyelitis,
39 nothing is known about the impact of MALT1 on virus infection in the central nervous
40 system. Here, we studied infection with an attenuated rabies virus (ERA) and observed
41 increased susceptibility with ERA in MALT1^{-/-} mice. Indeed, following intranasal infection
42 with ERA, wild-type mice developed mild transient clinical signs with recovery at 35 DPI.
43 Interestingly, MALT1^{-/-} mice developed severe disease requiring euthanasia around 17 DPI.
44 A decreased induction of inflammatory gene expression and cell infiltration and activation
45 was observed in MALT1^{-/-} mice at 10DPI as compared to MALT1^{+/+} infected mice. At 17
46 DPI, however, inflammatory cell activation was comparable to the one observed in
47 MALT1^{+/+} mice. Moreover, MALT1^{-/-} mice failed to produce virus-neutralizing antibodies.
48 Similar results were obtained with specific inactivation of MALT1 in T cells. Finally,
49 treatment of wild-type mice with mepazine, a MALT1 protease inhibitor, also led to mortality
50 upon ERA virus infection. These data emphasize the importance of early inflammation and
51 activation of T cells through MALT1 for controlling the virulence of an attenuated rabies
52 virus in the brain.

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57 **IMPORTANCE**

58 Rabies virus is a neurotropic virus which can infect any mammal. Annually, 59000 people die
59 from rabies. Effective therapy is lacking and hampered by gaps in the understanding of virus
60 pathogenicity. MALT1 is an intracellular protein involved in innate and adaptive immunity,
61 and an interesting therapeutic target because MALT1-deregulated activity has been
62 associated with autoimmunity and cancers. The role of MALT1 in viral infection is however
63 largely unknown. Here, we study the impact of MALT1 on virus infection in the brain, using
64 the attenuated ERA rabies virus in different models of MALT1 deficient mice. We reveal the
65 importance of MALT1-mediated inflammation and T cell activation to control ERA virus,
66 providing new insights in the biology of MALT1 and rabies virus infection.

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68 **KEYWORDS**

69 Rabies virus, ERA, MALT1, neuroinflammation, immunity

70 INTRODUCTION

71 The paracaspase MALT1 (mucosa-associated lymphoid tissue lymphoma translocation
72 gene 1) is an intracellular protein that mediates nuclear factor κ B (NF- κ B) and p38/JNK
73 MAP kinase signalling in response to multiple stimuli, including antigen receptor activation
74 in lymphocytes, dectin-driven dendritic cell activation, and thrombin- and angiotensin-
75 induced activation of fibroblasts and endothelial cells (1). In resting cells, MALT1 is
76 constitutively associated with the caspase recruitment domain (CARD)-containing protein
77 BCL10 and upon stimulation forms a complex with one of the CARD-containing proteins
78 CARD9, CARD10 (CARMA3), CARD11 (CARMA1), or CARD14 (CARMA2), depending
79 on the cell type and stimulus (2). The CARD-BCL10-MALT1 (CBM) complex acts as a
80 scaffold for other proteins, including TRAF6, which then mediates the activation of NF- κ B
81 and p38/JNK (3). In addition to its scaffold function, MALT1 holds proteolytic activity that
82 cleaves a limited number of proteins at well-defined sites (4). MALT1 substrates include
83 among others, NF- κ B family members (5), ubiquitin regulatory enzymes (6-8), and
84 ribonuclease and mRNA-destabilizing proteins (9,10). MALT1 proteolytic activity is not
85 essential for NF- κ B or p38/JNK activation but further fine-tunes gene expression that
86 contributes to immune cell activation, proliferation and survival. Because of its major role in
87 lymphocyte activation and proliferation, targeting MALT1 proteolytic activity via small
88 compound inhibitors is currently of high interest for the treatment of several autoimmune
89 diseases and lymphoma (11-13).

90 Genetic mouse models have provided key insights into the biology of MALT1. MALT1^{-/-}
91 mice are viable, fertile and born at the expected Mendelian ratios (14,15). Their total number
92 of T cells and the distribution of CD4⁺ and CD8⁺ T cells in the spleen, lymph nodes and
93 thymus is comparable to those of wild-type (WT) mice, but T cell activation, proliferation
94 and IL-2 production is decreased, leading to a lower number of activated T cells in the

95 periphery (15). MALT1 is also required for the development of regulatory T cells in the
96 thymus (16,17), as well as the development of marginal zone (MZ) and B1 B cells (14,15),
97 but is dispensable for the development of normal B2 B cells. MALT1^{-/-} mice present impaired
98 IgM- and CD40-induced proliferation, and lower basal serum immunoglobulin levels, with
99 IgM and IgG3 showing the most pronounced reduction. A limited number of patients
100 carrying MALT1 mutations leading to severe immunodeficiency have been reported (18-20),
101 further illustrating the key role of MALT1 in innate and adaptive immunity. Finally, knock-in
102 mice expressing a so-called ‘protease-dead’ mutant of MALT1 in which the catalytic activity
103 is disrupted, but which can still function as a scaffold for NF-κB activation, mimic all
104 immune defects that are observed in full MALT1^{-/-} mice, although to a lesser extent.
105 Surprisingly, these mice spontaneously develop autoimmunity because of a deregulated
106 effector T cell response (reviewed in (1)).

107 While genetic studies have indicated that MALT1 deficiency may lead to severe immune
108 defects, promising results upon pharmacological targeting of MALT1 in preclinical mouse
109 models of multiple sclerosis (12) and ABC-type diffuse large B cell lymphoma (11,13),
110 without obvious side effects, have stirred a lot of interest in the therapeutic targeting of
111 MALT1. However, a better understanding of the role of MALT1 in different tissues and
112 under different conditions is essential. Previous studies already showed that MALT1
113 deficiency protects against experimental autoimmune encephalitis (EAE) (12,16,17),
114 illustrating a role for MALT1 in the central nervous system (CNS). In the present study, we
115 focused on the impact of MALT1 deficiency on infection with a neurotropic virus. More
116 specifically, we investigated whether MALT1 deficiency affects the virulence of an
117 attenuated rabies virus.

118 Rabies virus is a highly neurotropic negative single-stranded RNA virus that belongs to
119 the *Genus Lyssavirus, Familia Rhabdoviridae* (21). Rabies virus normally causes a highly

120 lethal infection of the brain, which escapes control from the immune system (22). The virus
121 still kills at least 59000 humans each year and remains an important public health problem
122 (23). A small number of humans have survived clinical rabies virus infection (24,25),
123 suggesting that, at least under certain conditions, the immune system can clear rabies virus
124 from the brain. Evelyn–Rotnycki–Abelseth (ERA) virus is a highly attenuated rabies virus
125 laboratory strain that was first described in the sixties (26,27). In contrast to virulent rabies
126 virus strains, ERA virus induces a benign non-lethal infection of the nervous system that is
127 associated with an efficient immune response (28). The ERA strain has therefore been used
128 as a live vaccine for oral immunization of wildlife (29). Since the ERA virus strain causes a
129 non-lethal brain infection in mice and can mount protective immunity against rabies, it allows
130 to study the mechanisms by which the host can control rabies virus in the brain.

131 The role of T cell immunity in the control of rabies virus infection has been thoroughly
132 documented (30-32). To study the impact of MALT1 activity on rabies virus infection, we
133 compared the clinical and immunological effect of ERA virus infection in MALT1^{+/+} and
134 MALT1^{-/-} mice, as well as conditional MALT1^{-/-} mice, lacking MALT1 in specific cell types
135 such as T cells, neuroectodermal cells or myeloid cells. We also examined the effect of
136 treatment of mice with mepazine, a phenothiazine derivative and reversible MALT1 protease
137 activity inhibitor (33). Our results demonstrate that MALT1 plays an important role in the
138 control of infection by attenuated rabies virus in the CNS of laboratory mice by inducing
139 neuroinflammation and by recruiting and activating CD8⁺ and CD4⁺ T cells within the brain
140 in the early phase of infection.

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142 MATERIALS AND METHODS

143 *Mice*

144 MALT1^{-/-} mice were generated and provided generously provided by the team of Prof. Dr.
145 Tak Mak (15). Mice were backcrossed for more than 10 generations into the C57BL/6
146 background and were inter-crossed to generate MALT1^{+/+}, MALT1^{+/-} and MALT1^{-/-}
147 offspring. Mice lacking MALT1 specifically in T cells were generated by crossing the CD4-
148 Cre line (34) and mice in which the *MALT1* gene is flanked by two loxP Cre recombinase
149 recognition sites (MALT1^{FL/FL}) on a C57BL/6 background. MALT1^{FL/FL} mice were originally
150 derived from the EUCOMM Malt1^{tm1a(EUCOMM)Hmgu} strain. Mice lacking MALT1 specifically
151 in cells from neuroectoderm origin (neurons, astrocytes and oligodendrocytes) were
152 generated by crossing the Nestin-Cre line (35) and MALT1^{FL/FL}. Mice lacking MALT1
153 specifically in myeloid cells were generated by crossing the LysM-Cre line (36) and
154 MALT1^{FL/FL}. All mice were bred and housed in filter top cages in temperature-controlled, air
155 conditioned facilities with 14/10h light/dark cycles and food and water *ad libitum*, and used
156 at the age of 6–12 weeks. All experimental procedures were approved by the Local Ethical
157 Committee of the Scientific Institute of Public Health (WIV-ISP) and the Veterinary and
158 Agrochemical Research Center (CODA-CERVA) (advice n° 070515-05).

159 *Genotyping*

160 MALT1^{-/-}, ^{+/+} and ^{+/-} mice were genotyped using the primers P08_11 (GGG TAC ATC ATG
161 GCC TGA ACA GTT G), P08_12 (TCC ACT CCA GCT CTT CTG CTA ACCAG) and
162 P08_13 (GGG TGG GAT TAG ATA AAT GCC TGC TC), which resulted in PCR products of
163 900 bp for MALT1^{+/+}, 1000 bp for MALT1^{-/-}, or both for heterozygous MALT1^{+/-} mice. The
164 MALT1 Flox-allele was detected with the primers MALTcKO-F (GTT TCT CAG GTC TTT
165 AGT TCA TGT C), CoMLT-3-R (TAT ACT CTA CAT CTC CAT GGT), MALTcKO-R

166 (TTG TTT TGC AGA TCT CTG CC), which resulted in PCR products of 280 bp for
167 MALT1^{+/+}, 400 bp for MALT1^{FL/FL}, or 345 bp for MALT1^{-/-} mice. The Cre allele was
168 detected with the primers Cre-F (TGC CAC GAC CAA GTG ACA GCA ATG) and Cre-R
169 (AGA GAC GGA AAT CCA TCG CTC G), producing a 374 bp PCR fragment. Transgenic
170 mice were identified by PCR analysis of genomic DNA extracted from tails and amplification
171 of the selected fragments was performed using the GoTaq G2 DNA polymerase (Promega,
172 Madison, USA) master mix, with a typical PCR program: 5 minutes 95 °C denaturation, 35-
173 40 cycles [30s 95 °C | 30s 55-60 °C | 60s 72 °C] and 10 minutes 72 °C for final elongation.
174 Fragments were visualised on a 2% agarose gel.

175 *Virus*

176 The attenuated Evelyn-Rotnycki-Abelseth (ERA) virus, used as an oral vaccine for
177 immunisation of wild life, was obtained from the American Type Culture Collection (ATCC)
178 (Reference: VR322) (37). Viral stocks were produced in baby hamster kidney (BHK)-21 cells
179 (Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH, Braunschweig,
180 Germany). The lysates of infected cell cultures were centrifuged at 20,000g for 20 min at 4°C
181 and supernatants were stored at -80°C.

182 *Virus titration*

183 Infectious rabies virus particles were titrated by endpoint dilution assay in BHK-21 cells.
184 The measure of infectious virus titer was expressed as 50% tissue culture infective dose
185 (TCID₅₀)/ml and represents the the amount of virus per ml that gives rise to infection in
186 50% of inoculated tissue culture cells. Virus titration was performed according to the Manual
187 of Diagnostic Tests and Vaccines for Terrestrial Animals (Office International des
188 Epizooties, 2008).

189 *Virus inoculation, clinical follow up, euthanasia and sampling*

190 Mice were inoculated intranasally with ERA virus using 10^5 TCID₅₀ in 25µl of PBS,
191 during brief anaesthesia with isoflurane, as described by Rosseels *et al* (38). Intranasal
192 inoculation of virus was chosen, as administration by this route results in a quick invasion of
193 the CNS. Mice were monitored once a day for signs of disease throughout the experiment
194 until 35 days post inoculation (DPI). A cumulative daily clinical score per mouse was
195 obtained by adding the scores for each parameter and ranged from 0 (no disease) to 9 (severe
196 brain disease). Disease signs were scored as follows: no signs = 0, rough hair coat = 1,
197 depression / isolation from the group = 1, hunched back = 1, slow movement = 1, paresis in
198 the front paws = 1, uncoordinated movements = 1, no spontaneous movements = 1, paralysis
199 of hind legs = 1, no response to external stimuli (end stage) = 1. Disease progression is
200 represented by a curve of the mean cumulative score per group. Once mice reached a
201 minimum score of 6, or at pre-determined time points post virus inoculation (10DPI:
202 incubation phase and 17DPI: end stage of disease), mice were euthanized with an overdose of
203 ketamine (Ceva, Brussels, Belgium, 100 mg/kg) and xylazine (Rompun 2%, Bayer
204 Healthcare, Kiel, Germany, 9.9 mg/kg) (300µl/mouse, intraperitoneally (ip)). Upon terminal
205 anaesthesia, the blood was flushed from the circulatory system by transcardial perfusion with
206 a PBS solution. Brains were collected and divided in two halves according to a longitudinal
207 section. One half was stored at -80°C for further analysis by real time quantitative reverse
208 transcriptase polymerase chain reaction (RT-qPCR) or fluorescent antigen test (FAT), the
209 other half was submerged in 4% formaldehyde for fixation and further immunohistochemical
210 analysis. Serum was collected from mice at different time points post infection and upon
211 euthanasia for titration of virus-neutralizing antibodies. Mice that did not develop disease
212 signs were terminally anesthetised, perfused and euthanized at 35 DPI.

213 *RNA extraction and real time quantitative reverse transcriptase polymerase chain reaction*
214 *(RT-qPCR) assay for quantification of viral RNA and inflammatory gene expression.*

215 Seven mice per group were euthanized at each indicated time point. RNA extraction
216 was performed using the RNeasy Mini kit (Qiagen, Hilden, Germany) according to the
217 manufacturer's instructions. RNA concentration was calculated using Nano Vue
218 spectrophotometry (GE Healthcare, Bucks, UK) and 100 ng was used for reverse
219 transcription. Reverse transcription and q-PCR were performed as described by Rosseels *et*
220 *al.* (38). Two primers (forward and reverse), located in the nucleoprotein N genome region
221 were used for quantification of viral RNA. All primer sequences are listed in Table 1. All
222 samples were analysed in duplicates. Amplification was performed on an iCycler iQ (Biorad)
223 in a 96-well optical plate format, using the following program: 2 min at 95°C followed by
224 45 cycles of: 20 sec at 95°C and 30 sec at 62°C. A melting curve analysis was performed in
225 order to verify the specificity of amplicons. Expressions of inflammatory genes were
226 normalized using the cellular 18S rRNA housekeeping gene. Quantification of immune gene
227 expression was performed using the comparative $\Delta\Delta\text{Ct}$ method. The fold was calculated as $2^{-\Delta\Delta\text{Ct}}$
228 with $\Delta\Delta\text{Ct} = \Delta\text{Ct}_{\text{sample}} - \Delta\text{Ct}_{\text{ctrl}}$. $\Delta\text{Ct}_{\text{sample}} = \text{Ct}_{\text{gene}} - \text{Ct}_{18\text{S}}$ and $\Delta\text{Ct}_{\text{ctrl}} = \text{Ct}_{\text{ctrl}} - \text{Ct}_{18\text{S}}$ with
229 Ct_{ctrl} corresponding to the Ct of gene expression in non-infected brain. For the detection of
230 the viral N protein's gene, delta cycle thresholds (ΔCt) values were calculated using the
231 following formula: $\Delta\text{Ct} = \text{Ct}_{\text{ref}} - \text{Ct}_{\text{sample}}$, with Ct_{ref} equal to 45, which is the maximum number
232 of cycles of this qPCR program. A ΔCt value of 0 means no detection of viral RNA.

233 *Titration of neutralizing antibody by rapid fluorescent focus inhibition test (RFFIT)*

234 Mouse blood samples were used for measurement of neutralizing antibodies using the
235 RFFIT according to the Manual of Diagnostic Tests and Vaccines for Terrestrial Animals
236 (Office International des Epizooties, 2008). Neutralizing antibody titers are expressed as
237 International Units (IU)/ml in reference to "The Second International standard for Anti-rabies
238 Immunoglobulin", purchased from the United Kingdom National Institute for Biological

239 Standards and Control. Serum titer levels of 0.5 IU/ml or higher is an indication of
240 seroconversion.

241 *Detection of nucleocapsid antigen of rabies virus by fluorescent antigen test (FAT)*

242 The fluorescent antigen test (FAT) was performed according to the Manual of Diagnostic
243 Tests and Vaccines for Terrestrial Animals (Office International des Epizooties, 2008). Brain
244 smears were fixed with 75% acetone for 30 min at -20°C and incubated with FITC-coupled
245 anti-nucleocapsid rabbit antibody for 30 min at 37°C.

246 *Immunohistological analysis of mouse brains for expression of Iba-1, GFAP, B220, CD3 and*
247 *Mac-3*

248 Virus-inoculated mice and PBS-inoculated mice were transcardially perfused with PBS.
249 Brains were removed, immersed in 4% paraformaldehyde, dehydrated, and embedded in
250 paraffin blocks. Sections of 2µm were realized and microglial cells, astrocytes, B cells, T
251 cells and macrophages were detected using specific antibodies: rabbit anti-Iba-1 (WAKO
252 Chemicals, Fuggerstraße, Germany), rabbit anti-GFAP (DAKO - Agilent Technologies,
253 Santa Clara, CA, USA), rat anti-B220 (eBioscience - Thermo Fisher Scientific,
254 Waltham, MA USA), rabbit anti-CD3 (DAKO - Agilent Technologies, Santa Clara, CA,
255 USA) and rat anti-Mac-3 (BD Pharmingen, San Diego, CA, USA), respectively. Sections
256 were rehydrated and incubated in 10mM citrate buffer for 10 min at 95°C. To remove
257 endogenous peroxydase, tissue sections were treated with 3% H₂O₂ in methanol. To block
258 non-specific reactions, each section was treated with 5% goat serum in antibody diluent
259 (DAKO - Agilent Technologies, Santa Clara, CA, USA) for 30 min. Primary antibody was
260 diluted in 5% goat serum in antibody diluent with the dilution depending on the staining
261 realized (Iba-1: 1/1000, CD3: 1/200, MAC-3: 1/250, B220: 1/1000, GFAP: 1/200 000) and
262 incubated on brain sections overnight at 4°C. Goat anti-rabbit (DAKO - Agilent

263 Technologies, Santa Clara, CA, USA) or goat anti-rat (BD Pharmingen, San Diego, CA,
264 USA) secondary antibodies conjugated to biotin were diluted at 1:500 in block buffer and
265 added for 45 min-1h to the sections. Drops of avidin/biotin-based peroxidase system
266 Vectastrain[®] Elite[®] ABC (Vector laboratories, Burlingame, CA, USA) were added to each
267 section for 30 min. Finally antibody was visualized using 3-3'-diaminobenzidine (DAB,
268 DAKO - Agilent Technologies, Santa Clara, CA, USA) until specific staining appeared;
269 slides were counterstained with hematoxylin, dehydrated and mounted with a xylene-based
270 mounting medium. Sections without primary antibody were taken along as controls.

271 *Immunophenotyping of leukocytes*

272 Immune cells were extracted from the brain at 10 DPI as described (39). In brief, brains
273 were collected and single-cell suspensions were prepared by gently pressing the organs in
274 HBSS through a nylon mesh (mesh size 100 μ m). After centrifugation, cells were placed in
275 collagenase-DNase for 1h. After washing, the suspension was centrifuged in 25% Percoll
276 (Sigma Aldrich, St Louis, MO, USA), the myelin layer was removed and cells were
277 suspended in HBSS containing 10% FCS. Red blood cell lysis buffer was added to the cell
278 pellet to eliminate erythrocytes. Cells were washed twice with FACS buffer (PBS containing
279 10% FCS and 0.1% NaN₃) and incubated with Fc γ II/III receptor blocking anti-CD16/CD32
280 (clone 2.4G2, BD Biosciences, San Jose, CA, USA) for 15 minutes at 4°C. Cells were then
281 incubated for 30 minutes at 4°C protected from light with viability dye (Thermofisher) and
282 the appropriate dilutions of the following antibodies Alexa fluor 488-anti CD11b (clone
283 M1/70), Brilliant Violet-421 anti-CD45 (clone 104), PE-anti-CD49b (clone DX5), APC-Cy7-
284 anti-CD3 (clone 145-2C11), PerCP-Cy5.5-anti-CD8 (clone 53-6.7), APC-anti-CD4 (clone
285 GK1.5), PE-Cy7-anti-CD86 (clone GL1). The stained cells were washed twice in FACS
286 buffer, fixed with 4% paraformaldehyde and analyzed in a BD FACSV[®]VERSE Flow

287 cytometer. Data were analyzed using BD FACSuite software. Antibodies were from BD
288 Pharmingen or Thermofisher.

289 *Activation of T cells*

290 For analysis of T cell activation in the brain, collected leukocytes were cultured in the
291 presence of 1µg/ml anti-CD28 (clone 37.51), 1µg/ml of anti-CD49d (clone 9C10 (MFR4.B)),
292 10 µg/ml of ERA inactivated antigens and Brefeldin A (Thermofisher) for 5h at 37°C. Cells
293 were then harvested, washed twice and suspended in FACS buffer containing FcγII/III
294 receptor blocking anti-CD16/CD32 (clone 2.4G2, BD Biosciences, San Jose, CA, USA) for
295 15 min at 4°C. Cells were stained with viability dye and a cocktail of extracellular antibodies
296 (Brilliant Violet-421 anti-CD45 (clone 104), APC-Cy7-anti-CD3 (clone 145-2C11), APC-
297 anti-CD4 (clone GK1.5), PerCP-Cy5.5-anti-CD8 (clone 53-6.7)). Cells were then washed
298 twice with FACS buffer and permeabilized using Cytofix/Cytoperm kit (BD pharmingen).
299 Cells were subsequently suspended in 1X Perm Wash buffer (BD pharmingen) containing a
300 cocktail of PE-anti-IFNγ (clone XMG1.2), Alexa Fluor 488-anti-IL-17A (clone TC11-
301 18H10) and PE-Cy7-GranzymeB (NGZB)). Isotype control and Fluorescence Minus One
302 controls (FMO) staining were done in parallel. Cells were then washed twice and fixed with
303 4% paraformaldehyde. Samples were examined using BD FACSVERSERSE Flow cytometer and
304 analyzed with BD FACSuite software. Antibodies were from BD Pharmingen or
305 Thermofisher.

306 *Serum transfer by intraperitoneal injection*

307 Serum was collected at 35 DPI from immune C57BL/6 mice infected with 10⁵
308 TCID₅₀/25µl ERA virus. MALT1^{-/-} mice received 500µl of serum i.p. on day 10 after virus
309 challenge. Serum of naïve mice was used as a control. Mouse sera were heat-inactivated prior
310 to administration (30 min at 56°C).

311 *Treatment with mepazine*

312 Mice were randomly treated with either mepazine or 0.9% NaCl. Mepazine (Chembridge)
313 was solubilized in NaCl 0.9% at a concentration of 2 mg/ml. Mice were injected i.p. daily
314 with 200 μ l (16 mg/kg) starting 2 days before ERA virus inoculation until the end of the
315 experiment. Mice were monitored once a day for signs of disease throughout the experiment.

316 *Statistical analyses*

317 Statistical analysis was performed using the Student's t test for unpaired data or the 2-way
318 ANOVA followed by a Sidak multiple comparison test in GraphPad Prism7. Logrank test
319 was used to analyse Kaplan-Meier survival curves.

320

321 **RESULTS**322 *Attenuated ERA virus becomes virulent in MALT1^{-/-} mice*

323 Intranasal inoculation of ERA virus in wild-type C57BL/6 mice resulted in a clinically
324 benign infection with, as expected, complete survival (40) (Figure 1A-B). Minor clinical
325 signs were observed at day 10 (rough hair coat and a slightly reduced reactivity) and the
326 general appearance (rough hair coat) improved rapidly (11DPI). Nevertheless most mice
327 remained slightly less reactive throughout the follow-up period (35DPI) resulting in a clinical
328 score of 1. Differently, ERA virus inoculated MALT1^{-/-} mice presented the first clinical signs
329 around 15 DPI and developed severe disease, characterized by limb paralysis and depression,
330 requiring euthanasia at 17 or 18 DPI. These data indicate that MALT1 is necessary to control
331 infection with ERA. Viral loads were analysed in total brain, by RT-qPCR and FAT, and in
332 olfactory bulbs, cerebrum and cerebellum by RT-qPCR (Figure 2A-D). At 10 DPI, viral loads
333 were similar in the brains of MALT1^{-/-} and MALT1^{+/+} mice (Figure 2C). At 17 DPI, which
334 corresponds with the end stage of disease in MALT1^{-/-} mice, a significantly higher viral load
335 was observed in the different parts of MALT1^{-/-} mouse compared to MALT1^{+/+} brains (Figure
336 2D). Fluorescence staining of the viral N protein yielded a similar signal in MALT1^{-/-} and
337 MALT1^{+/+} brains at 10DPI, whereas at 17DPI more fluorescent foci were observed in
338 MALT1^{-/-} brains (Figure 2E), in agreement with the results obtained by RT-qPCR. These
339 results show that deficiency of MALT1 leads to a progressive and lethal increase of ERA
340 viral load in the brain, resulting in severe clinical signs.

341 *Anti-viral and inflammatory gene expression is severely disrupted in the brain of MALT1^{-/-}*
342 *mice at the pre-symptomatic phase of infection*

343 To further analyze the increased virulence of ERA virus in MALT1 deficient mice, virus-
344 induced expression of several immune response genes in the brain was assessed. The mRNA

345 levels of interferons (IFN β , IFN γ), pro-inflammatory cytokines (TNF, IL-1 β , IL-12, IL-23),
346 chemokines (MIP2, MCP1, CXCL10), Th1 associated genes (IFN γ , t-bet), T-reg associated
347 genes (Foxp3), inflammasome components (NLRP3, caspase-1), T cell markers (CD4 and
348 CD8), and iNOS enzyme were measured in the brains of MALT1^{+/+} or MALT1^{-/-} mice at
349 different time-points after infection and compared with mRNA levels in the corresponding
350 uninfected controls. As shown in figure 3, no upregulation of IL-12 could be observed. At 10
351 DPI, expression of all other investigated genes was higher following ERA virus infection in
352 infected compared to non-infected mice. In contrast, at comparable time points, virus-induced
353 expression of the same genes was much less pronounced in the brains of MALT1^{-/-} mice,
354 with the exception of MCP1, MIP2, CD4, and IL-23 that were expressed to a similar extent.
355 Absence of Foxp3 expression reflects the known lack of thymic regulatory T cells in
356 MALT1^{-/-} mice (41), while absence of CD8 and IFN γ indicates a defective cytotoxic T cell
357 response. The anti-viral IFN- β response and pro-inflammatory gene expression were also
358 almost completely absent. At 17 DPI, virus-induced gene expression was in most cases less
359 pronounced compared to 10 DPI and differences between MALT1^{+/+} and MALT1^{-/-} were
360 more gene-dependent: expression of IFN- β and Foxp3 was absent, whereas expression of
361 TNF and CXCL10 was significantly higher in the brains of MALT1^{-/-} mice compared to
362 MALT1^{+/+} mice. The latter results are in line with the high viral loads detected at 17DPI in
363 the brain of MALT1^{-/-} as compared to MALT1^{+/+} mice (Figure 2). Together, these results
364 suggest that at the early stage of infection (10 DPI) anti-viral and inflammatory immune
365 responses are severely disrupted in MALT1^{-/-} mice.

366 *MALT1 deficiency is associated with decreased infiltration and activation of inflammatory*
367 *and immune cells in the brain at the pre-symptomatic phase of infection*

368 To investigate if the above described defects in virus-induced cytokine and chemokine
369 expression in MALT1^{-/-} mice were also associated with an altered recruitment and activation
370 of inflammatory cells, immunohistological analysis for different inflammatory cell markers
371 was performed on brain sections obtained at 10 DPI and 17 DPI from ERA-infected
372 MALT1^{+/+} and MALT1^{-/-} mice in comparison to PBS-inoculated control mice (Figure 4).
373 Microglia cells, which are the resident macrophages of the CNS, and astrocytes, which are
374 the most abundant glial cell population, typically both respond to injury and infection by
375 acquiring an activated phenotype, defined by morphologic changes, migration and
376 proliferation (42,43). Staining for the microglia cell marker Iba1 revealed an increased
377 number of activated microglia at 10 and 17 DPI in MALT1^{+/+} mice compared to non-infected
378 brains. Microglia activation is demonstrated by the typically bigger cell body and shorter and
379 thicker branch processes. Resting microglial cells, observed mainly in non-infected mice,
380 were characterized by their smaller cell bodies and long and ramified branch processes. In
381 ERA-infected MALT1^{-/-} mice, the number of activated microglia cells was less pronounced at
382 both 10 and 17 DPI compared to MALT1^{+/+} mouse brains. Astrocyte activation was also
383 evident in ERA-infected MALT1^{+/+} mice as demonstrated by enhanced GFAP
384 immunoreactivity. At 10 DPI, GFAP staining was observed in the white matter of the
385 cerebellum, whereas at 17 DPI, GFAP staining was observed in the white matter and in the
386 outer layer of the grey matter. In ERA-infected MALT1^{-/-} mice, astrocyte activation in the
387 outer layer of the grey matter was slightly reduced at 17 DPI.

388 Infiltration of CD3⁺ T cells and Mac-3⁺ macrophages was observed at 10 DPI in ERA-
389 infected MALT1^{+/+} mice. The T cell infiltrates persisted at 17 DPI, whereas macrophage
390 infiltrates were no longer visible. T cell and macrophage infiltration was much less
391 pronounced in ERA-infected MALT1^{-/-} mice at 10 DPI, but similar levels of T cells were
392 detected in ERA-infected MALT1^{+/+} and MALT1^{-/-} mice at 17 DPI. B220⁺ B cells were

393 detectable around the blood vessels and in the choroid plexus, but not in the brain
394 parenchyma, at 10 DPI and 17 DPI in ERA-infected MALT1^{+/+}. In contrast, almost no B cells
395 were detected in ERA-infected MALT1^{-/-} mice, neither around blood vessels nor in the
396 choroid plexus. As expected, CD3⁺, B220⁺ or Mac-3⁺ staining was not detected in PBS-
397 inoculated control mice. For all stainings, results were similar in cerebellum and
398 hippocampus.

399 Inflammatory cell infiltration was also assessed by flow cytometric analysis of brain
400 leukocytes at 10 DPI. As shown in figure 5A, strong leukocyte infiltration was observed in
401 ERA-infected MALT1^{+/+} mice as compared to non-infected mice. A comparatively lower
402 number of leukocytes was detected in infected MALT1^{-/-} mice. Analysis of cell populations
403 revealed strong infiltration of microglial cells (CD45^{int}CD11b⁺),
404 monocytes/macrophages/DCs (CD45^{high}CD11b⁺), NK cells (CD49⁺CD3⁻), NKT cells
405 (CD49b⁺CD3⁺), and T cells (CD49b⁻CD3⁺) with a high proportion of CD8⁺ T cells and a few
406 CD4⁺ T cells (Figure 5B and C) in ERA-infected MALT1^{+/+} mice. Analysis of costimulatory
407 markers such as CD86 showed that microglia and monocytes/macrophages/DCs were highly
408 activated, which was confirmed by analysing the mean fluorescence intensity (M.F.I.) of the
409 CD86 marker (Figure 5C). In ERA-infected MALT1^{-/-} brains, the absolute number of total
410 leukocytes was much lower compared to ERA-infected MALT1^{+/+} brains (Figure 5A), which
411 is also reflected by lower numbers of CD8⁺ T cells, NK cells, NKT cells, activated
412 monocytes/macrophages/DCs and activated microglia. No significant difference was
413 observed for CD3⁺CD4⁺ T cells (Figure 5B and C), which is in line with equal CD4 mRNA
414 expression in MALT1^{+/+} and MALT1^{-/-} mouse brains (Figure 3). Furthermore, *in vitro*
415 stimulation of leukocytes isolated from ERA-infected MALT1^{+/+} brains with inactivated ERA
416 virus showed that T cells express IL-17, IFN- γ and granzyme B, suggesting the recruitment
417 of Th1, Th17 and CD8⁺ T cells. In contrast, leukocytes from ERA-infected MALT1^{-/-} mice

418 produced significantly less IL-17, granzyme B and IFN- γ (Figure 6). Altogether, these data
419 illustrate that MALT1 deficiency is associated with decreased infiltration and activation of
420 inflammatory and immune cells in the brain upon ERA virus infection.

421 *MALT1 deficiency is associated with a defective anti-viral humoral immune response*

422 To investigate if MALT1 deficiency also affects the humoral immune response against
423 ERA virus we measured rabies virus neutralising antibodies (VNA) in the serum. VNA were
424 detected in the blood of MALT1^{+/+} infected mice at 17 DPI (1.90 +- 1.30 IU/ml). This time
425 point was chosen because it is the end point of disease for MALT1^{-/-} mice. Titers increased
426 further at 35 DPI (6.53 +- 3.12 IU/ml) (Figure 7). However, most MALT1^{-/-} mice failed to
427 produce VNA (<0.5 IU/ml). Low levels of VNA (0.85 IU/ml) could be detected in two
428 MALT1^{-/-} mice at 17 DPI, but this made no difference on infection and disease outcome.

429 To further assess the role of antibodies in the protection against ERA virus in the brain, we
430 tested whether transfer of serum from immunized MALT1^{+/+} mice could confer protection in
431 MALT1^{-/-} mice. Pooled immune serum (4.8 IU/ml, 0.5 ml/mouse ip) was transferred to ERA-
432 infected MALT1^{-/-} mice at 10 DPI, which corresponds to the time point when MALT1^{+/+} mice
433 normally start to produce VNA after infection with ERA virus (Figure 8A). Transfer of
434 immune serum was unable to rescue the MALT1^{-/-} mice from lethal infection (Figure 8B).
435 These results suggest that antibodies alone are not sufficient to confer protection and that
436 cell-mediated immunity is also necessary.

437 *MALT1 deficiency in T cells is sufficient to render ERA virus neurovirulent*

438 MALT1^{-/-} mice were previously shown to have a normal number of T cells but their
439 capacity to be activated is impaired (15). We therefore hypothesized that MALT1 in T cells
440 might be important to control ERA virus. This was investigated by using T cell specific
441 MALT1^{-/-} mice that were generated by crossing CD4-Cre mice with mice in which the

442 MALT1 gene is flanked by two loxP Cre recombinase recognition sites (MALT1^{FL/FL})
443 (Figure 9A). In contrast to wild-type littermates (CD4-Cre^{+/+} MALT1^{FL/FL}), infection of T cell
444 specific MALT1^{-/-} mice (CD4-Cre^{tg/+} MALT1^{FL/FL}) with ERA virus led to severe disease and
445 death between 15 DPI and 17 DPI (Figure 9B), similarly to the phenotype observed in
446 MALT1 full knock-out mice (Figure 1). In addition, we observed that most of the T cell
447 specific MALT1^{-/-} mice did not mount an antibody response (Figure 9C). Indeed, only one
448 mouse developed a low level of VNA (0.99 IU/ml). Accordingly, we also observed a
449 significant increase of viral load in CD4-Cre^{tg/+} MALT1^{FL/FL} compared to their wild-type
450 littermates (CD4-Cre^{+/+} MALT1^{FL/FL}) (Figure 9D). These results confirm the importance of
451 the activation of CD4⁺ and CD8⁺ T cells through MALT1 to control ERA virus in the CNS.
452 Theoretically, impaired signalling in neurons or myeloid cells could also be responsible for
453 the increased pathogenicity of ERA virus in MALT1^{-/-} mice. Mice specifically lacking
454 MALT1 in myeloid cells (LysMCre^{tg/+} MALT1^{FL/FL}) or cells of neuro-ectodermal origin
455 (neurons, astrocytes or oligodendrocytes; Nestin-Cre^{tg/+} MALT1^{FL/FL}) were therefore also
456 generated and analyzed in similar infection experiments (Figure 9A). Infection of Nestin-
457 Cre^{tg/+} MALT1^{FL/FL} and LysMCre^{tg/+} MALT1^{FL/FL} mice gave survival results comparable to
458 those of wild-type littermates, excluding a role for MALT1 in neurons, astrocytes,
459 oligodendrocytes or myeloid cells (Figure 9B). Together, our data demonstrate the
460 importance of MALT1-mediated T cell activation to control infection with a live attenuated
461 rabies virus in the brain.

462 *Pharmacological inhibition of MALT1 increases virulence of ERA virus*

463 MALT1^{-/-} mice lack both MALT1 scaffold and MALT1 catalytic activities. To better
464 delineate the specific role of MALT1 proteolytic activity in the control of ERA virus, we also
465 tested the effect of inhibition of MALT1 catalytic activity using the small compound inhibitor
466 mepazine. Wild-type mice were treated daily with mepazine starting two days before virus

467 inoculation and lasting until the late stage of disease (Figure 10A). Control mice were treated
468 with 0.9% NaCl. Part of the mepazine-treated mice (4/7) developed severe disease and had to
469 be euthanized between 12 and 15 DPI, while the remaining mice developed only mild disease
470 and survived the infection (Figure 10B). At sacrifice, CNS viral loads of the mepazine-treated
471 mice with severe disease were significantly higher than in untreated mice and reached similar
472 levels as observed previously in MALT1^{-/-} mice (Figure 10C and 2B). At 35 DPI, surviving
473 mepazine-treated mice and control mice presented similarly low viral loads (Figures 10C).
474 High levels of virus neutralizing antibodies were detected in the blood of the surviving
475 mepazine-treated mice (>10 IU/ml) and control mice (8.86 +- 2.28 IU/ml), but not in the
476 mepazine-treated mice that developed severe disease and died (0.45 +- 0.30 IU/ml) (Figure
477 10D). These data demonstrate that MALT1 proteolytic activity is essential for a proper
478 immune response and the control of rabies virus infection in the CNS.

479 **DISCUSSION**

480 Although attenuated vaccines are often used to immunize man and animal, there always
481 remains a risk that they become pathogenic again either by acquisition of mutations or
482 because of increased susceptibility of the host, as has been reported for attenuated rabies
483 vaccines in wildlife (37,44-47). A better understanding of the immunological mechanisms
484 that control attenuated rabies virus in the CNS is therefore of immediate interest. Our data
485 demonstrate an important protective role for paracaspase MALT1-mediated signalling in the
486 response to infection with the attenuated rabies virus ERA by mediating neuroinflammation
487 at the early phase of infection. More specifically, we show that MALT1 deficiency in mice
488 decreases cerebral immune responses at the early phase of infection as evidenced by reduced
489 microglial, astroglial and T cell activation, less infiltration of macrophages and CD8⁺ T cells,
490 and diminished expression of NF- κ B regulated pro-inflammatory mediators in the brain at 10
491 DPI. At a later phase of infection (17 DPI), however, immune cell infiltration and activation
492 were comparable between MALT1^{+/+} and MALT1^{-/-} mice, indicating that immune cells can
493 still be activated and infiltrate the brain in MALT1^{-/-} infected mice, but with delayed kinetics
494 as compared to MALT1^{+/+} mice. In agreement with the curtailed immune response, MALT1^{-/-}
495 mice developed severe disease, characterized by severe depression and paralysis and
496 requiring human euthanasia, whereas MALT1^{+/+} mice developed only mild disease resolving
497 at 11 DPI, characterized by transiently reduced activity. Similar results were observed in
498 conditional knock-out mice lacking MALT1 specifically in T cells. In contrast, mice lacking
499 MALT1 specifically in neuroectodermal cells or myeloid cells survived the infection. Finally,
500 also pharmacological inhibition of MALT1 increased the pathogenicity of ERA virus.
501 Together, our results demonstrate a key role for MALT1-dependent T cell activation in the
502 control of attenuated rabies virus.

503 It is important to mention that T cell-specific MALT1^{-/-} mice lack MALT1 in both CD4⁺
504 and CD8⁺ T cells, since CD4-Cre is expressed during the double positive phase of T cell
505 development. CD8⁺ T cells were the most recruited T cell population in the brain during
506 ERA virus infection in wild-type mice. It has been shown before that CD8⁺T cells are
507 required for the early production of cytokines at the site of infection, contribute to the
508 clearance of rabies virus from the CNS by enhancing IFN- γ production and the CNS
509 inflammatory response, and kill infected cells by the release of granzyme B (48).
510 Consequently, viral loads were found to be higher in CD8⁺ T cell deficient mice (48). In
511 MALT1^{-/-} mice, significantly less CD8⁺ T cells were recruited, whereas the number of CD4⁺
512 T cells remained the same as in MALT1^{+/+} mice. In contrast with others who have shown that
513 rabies virus infection in CD8⁺ T cell deficient mice remains sub-lethal (48), we observed
514 lethal disease in MALT1^{-/-} mice, suggesting that decreased activation of CD4⁺ T cell subsets
515 also contributes to the observed sensitization in MALT1^{-/-} mice. In this context, ERA rabies
516 virus infection increased expression of the transcription factor t-bet and IFN- γ in the CNS,
517 which is indicative for infiltration of CD4⁺ Th1 cells. Th1 cells were previously shown to be
518 essential for the rapid clearance of attenuated rabies virus from the CNS (49), and the blunted
519 expression of t-bet and IFN- γ in MALT1^{-/-} mice may thus be associated with the increased
520 lethality. We also found evidence for increased Th17 infiltration and IL-17 production in the
521 CNS of ERA rabies virus infected mice. IL-17 in the brain of mice infected with a laboratory-
522 attenuated rabies virus has previously been reported to enhance blood-brain barrier
523 permeability and viral clearance (50-52). Interestingly, IL-17 levels in the brains of ERA-
524 infected MALT1^{-/-} mice were lower compared to MALT1^{+/+} mice, suggesting that MALT1
525 deficiency may decrease blood-brain barrier permeability, which on its turn may contribute to
526 the reduced infiltration of inflammatory cells in the brain of infected MALT1^{-/-} mice. Loss of
527 MALT1 has formerly been shown to also interfere with T cell infiltration and expression of

528 IL-17 in experimental autoimmune encephalitis (EAE) in mice, a well-known model of
529 multiple sclerosis (16,17). In this case, MALT1 inhibition was shown to protect against EAE
530 by blunting T-cell mediated autoimmunity.

531 Effective clearance of rabies virus requires the rapid production of neutralizing antibodies
532 (48). ERA-infected MALT1^{-/-} mice failed to mount neutralizing antibodies. The same was
533 true for conditional knock-out mice lacking MALT1 specifically in T cells, illustrating that
534 production of neutralizing antibodies against ERA virus is T cell dependent. Although rabies
535 virus neutralizing antibodies are important for virus clearance, passive immunisation of
536 MALT1^{-/-} mice failed to rescue the mice. *In situ* production of antibodies by B cells in the
537 brain (53) or active permeabilisation of the blood-brain barrier is most likely required for
538 antibodies to be effective against rabies virus (54). On the other hand, cellular immunity as
539 described above is probably also required to control the virus in the brain. Together, these
540 findings implicate that in the future, besides neutralizing antibodies, markers for cellular
541 immunity should also be considered to assess vaccine efficacy and anti-rabies immunity.

542 A hypothetical model for the impact of MALT1 inactivation on ERA rabies virus-induced
543 immune responses in the brain is depicted in figure 11. The high level of cytokines and
544 inflammation in wild-type mice at 10 DPI with ERA virus, which coincides with some mild
545 disease signs, together with the infiltration of activated T cells in the brain might be key for
546 effective control of the infection. MALT1^{-/-} mice presented less infiltration of activated T
547 cells and inflammatory cytokine production in the brain and a significant reduction of CD8⁺ T
548 cell, NK cell and NKT cell infiltration. We propose that the reduction of immune cell
549 infiltration in the brain, together with the lack of a peripheral humoral immune response, are
550 at the origin of the higher viral loads and severe disease in MALT1^{-/-} mice.

551 The fact that MALT1 deficiency reduces neuroinflammation in the brain might also be of
552 interest in the context of therapeutic modulation of other neurological pathologies involving

553 neuroinflammation such as Alzheimer's disease (55), Parkinson's disease (56), multiple
554 sclerosis (57), stroke (58) and neuropsychiatric diseases like depression, schizophrenia and
555 autism (59,60). In this context, the allosteric MALT1 inhibitor mepazine has already been
556 shown to have a therapeutic effect in EAE (12). At the same time, however, our results
557 indicate that MALT1 inhibitors can also increase the risk for severe virus infection in the
558 brain or severe adverse effects upon vaccination with attenuated rabies viruses. Indeed,
559 mepazine treatment of ERA-infected mice led to susceptibility to virulence of ERA virus in
560 more than half of the mice. It should be mentioned that, similar to Nagel *et al* (11), in our
561 study mice were treated with 16 mg mepazine/kg body weight every 24 hours. Considering
562 the relatively short half-life of mepazine, a more frequent treatment schedule may still lead to
563 stronger sensitizing effects for ERA infection. Next to pharmacological MALT1 inhibition,
564 also mutations in MALT1 leading to MALT1 deficiency may sensitize an attenuated rabies
565 virus to neurovirulence. To date, a limited number of MALT1 deficient patients have been
566 described (18-20), each presenting with severe combined immunodeficiency and being highly
567 susceptible to fungal, bacterial and viral infections. Moreover, other mutations may be less
568 disruptive and only become apparent under certain conditions. It should be mentioned,
569 however, that rabies vaccination in humans uses only inactivated vaccines. Therefore, the use
570 of MALT1 inhibitors or MALT1 deficiency in combination with rabies vaccination in
571 humans would not impose any risks. As it remains to be seen if our findings with an
572 attenuated rabies virus also apply to other attenuated viruses, it is currently premature to
573 generalize our findings to other attenuated virus vaccines. In future studies it will be
574 interesting to also analyse the effect of MALT1 deficiency on infection with virulent rabies
575 virus or other viruses.

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586 E.K., S.V.G. and R.B. conceived the study, designed experiments and wrote the manuscript.
587 E.K. performed experiments, analyzed data and designed the figures. J.S. generated the mouse models
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589 realized the genotyping and RT-qPCR experiments. K.L. performed the immunohistochemistry and
590 E.K. performed the analysis. E.K. and H.G.T. performed the flow cytometry experiments and
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825
826

827 **FIGURE LEGENDS**

828

829 **Figure 1. MALT1 is critical to control the pathogenicity of ERA virus.** MALT1^{-/-} (n = 10)
830 and MALT1^{+/+} littermates (n = 10) were infected intranasally with ERA virus. (A) Clinical
831 symptoms and (B) survival rates were assessed. All MALT1^{-/-} mice developed severe disease
832 and had to be euthanized. MALT1^{+/+} mice developed only mild symptoms. Results are
833 representative of 2 independent experiments.

834

835 **Figure 2. Virus spread in the brain of MALT1^{-/-} and MALT1^{+/+} mice following**
836 **intranasal inoculation.** (A) Schematic overview of the experiment. Mice were inoculated
837 intranasally with the ERA virus and sacrificed at 10, 17 and 35 DPI. (B) Profile of viral RNA
838 load in total brain determined by RT-qPCR. (C, D) Profile of viral RNA load in different
839 parts of the brain (**= P-value ≤ 0.01). (E) Immunofluorescence staining for viral
840 nucleocapsid in the brain tissue. At 10 DPI, green fluorescent spots indicate the abundant
841 spread of virus in the brain of MALT1^{-/-} and MALT1^{+/+} mice. At 17 DPI, only a small
842 amount of viral antigens were still visible in MALT1^{+/+} mice, whereas viral antigens were
843 still abundant in the brains of MALT1^{-/-} mice. These results are representative of 3 mice per
844 time point and per genotype. Scale bars represent 20µm, magnification 40×.

845

846 **Figure 3. Defective expression of anti-viral and inflammatory genes in the brain of ERA**
847 **virus-infected MALT1^{-/-} mice.** Quantitative RT-qPCR measurements of the indicated
848 mRNA expression levels in brains of MALT1^{+/+} (n=7) and MALT1^{-/-} littermate mice (n=7) at
849 10 DPI and 17 DPI are shown. Results are represented as fold increase compared to
850 respectively non-infected MALT1^{+/+} and MALT1^{-/-} littermate mice. Differences in the fold
851 increase at the same time point were determined by two-way ANOVA and Sidak's multiple-

852 comparison test and statistical differences between MALT1^{+/+} and MALT1^{-/-} mice are
853 denoted as ****, ***, **, and *, representing P-values of less than 0.0001, 0.001, 0.01 and
854 0.05, respectively.

855

856 **Figure 4. Reduced infiltration and activation of inflammatory cells in the brain of**
857 **MALT1^{-/-} mice at 10 DPI with ERA virus.** Immunohistochemical analysis of CNS sections
858 from ERA-infected MALT1^{+/+} and MALT1^{-/-} mice at 10 and 17 DPI. PBS-inoculated
859 MALT1^{+/+} mice were used as controls. Sections of cerebellum and hippocampus are shown.
860 Brain sections were immunostained for Iba-1 (microglial cells), CD3 (T cells), Mac-3
861 (macrophages), B220 (B cells) and GFAP (astrocytes). PBS-injected mice showed abundant
862 inactive ramified microglial cells and astrocytes, but no B cell, macrophage or T cell
863 infiltration. At 10 DPI, ERA virus-infected MALT1^{+/+} mice showed activation of microglia
864 and astroglia cells, infiltration of T lymphocytes and macrophages in the parenchyma, and
865 infiltration of B cells around the blood vessels and choroid plexus. In MALT1^{-/-} mice, T
866 lymphocyte and macrophage infiltration, as well as microglial activation, were reduced at 10
867 DPI. Moreover, B cells could not be observed around the blood vessels or choroid plexus in
868 MALT1^{-/-} mice. At 17 DPI, pronounced microglial activation and T lymphocyte infiltration
869 were observed in both MALT1^{+/+} and MALT1^{-/-} mice. Macrophages were no longer visible.
870 Astrogliosis increased further, but was more pronounced in MALT1^{+/+} than in MALT1^{-/-}
871 mice. Scale bars represent 20µm (magnification 20×), 50µm (magnification 10×) or 100µm
872 (magnification 4×). Data are representative of two mice per condition.

873

874 **Figure 5. Flow cytometric analysis of immune cell activation and infiltration in the**
875 **brain of ERA-infected mice.** Immune cells were isolated from the brains of naïve mice and
876 infected mice (MALT1^{+/+} and MALT1^{-/-}) at 10 DPI. (A) Absolute numbers of leukocytes

877 present in the brain were first determined and total numbers of each cell type were
878 determined by the percentage of marker expression on total number of leukocytes. A
879 significant decrease of total leukocytes was observed in ERA-infected MALT1^{-/-} mice
880 compared to infected MALT1^{+/+} mice. **(B)** CD49b and CD3 markers were used to distinguish
881 NK cells (CD49b⁺CD3⁻), NKT cells (CD49b⁺CD3⁺) and T cells (CD49b⁻CD3⁺). CD8 and
882 CD4 markers were also used. A significant decrease of NK cells, NKT cells and CD8⁺T cells
883 was observed in ERA infected MALT1^{-/-} mice compared to infected MALT1^{+/+} mice. **(C)**
884 CD45 and CD11b markers were used to distinguish T cells (CD3⁺CD11b⁻CD45^{high}),
885 microglial cells (CD11b⁺CD45^{int}) and monocytes/macrophages/DCs (CD11b⁺CD45^{high}).
886 CD45^{int} cells were selected to analyze microglial activation by using CD11b and CD86, a
887 stimulatory molecule expressed on activated antigen presenting cells. CD45^{high} cells were
888 selected to analyze monocyte, macrophage and DC activation. Activation of microglial cells
889 and monocytes/macrophages/DCs was determined by CD86 expression represented as mean
890 fluorescence intensity (MFI). A significant decrease of CD86 MFI was observed in ERA
891 infected MALT1^{-/-} mice compared to MALT1^{+/+} mice, which corresponds to the dot plots.
892 Dot plots are representative of 5 mice per condition. Statistical differences between
893 MALT1^{+/+} and MALT1^{-/-} mice were determined using student t-test and are denoted as
894 follows: ***, **, and *, representing P-values of less than 0.001, 0.01 and 0.05, respectively.

895

896 **Figure 6. Reduced granzyme B, IL-17 and IFN- γ production in T cells from ERA-**
897 **infected MALT1^{-/-} mice.** Immune cells were isolated from the brains of naïve mice and
898 infected mice (MALT1^{+/+} and MALT1^{-/-}) at 10 DPI and stained for the intracellular markers
899 IFN- γ , IL-17 and granzyme B. T cells were gated for their phenotypic marker CD3. **(A-B)**
900 FACS analysis revealed less production of IL-17, granzyme B and IFN- γ in T cells of ERA-
901 infected MALT1^{-/-} mice compared to ERA-infected MALT1^{+/+} mice. Dot plots are

902 representative of 5 mice per condition. (C) A significant decrease of T cells expressing IFN-
903 γ , granzyme B and IL-17 was observed in infected MALT1^{-/-} mice compared to infected
904 MALT1^{+/+} mice. Statistical differences between MALT1^{+/+} and MALT1^{-/-} mice were
905 determined using student t-test and are denoted as follows: ***, **, and *, representing P-
906 values of less than 0.001, 0.01 and 0.05, respectively.

907

908 **Figure 7. Defective humoral immune response in MALT1^{-/-} mice.** In MALT1^{+/+} mice,
909 antibody production was first detected in 1 out of 7 mice at 10 DPI. At 17 DPI, neutralizing
910 antibodies were detected in all MALT1^{+/+} mice (n=7) and antibody levels increased further at
911 35 DPI (n=7). Neutralizing antibodies were not detected in MALT1^{-/-} mice (n=7) at 10 DPI
912 and in 5 out of 7 mice at 17 DPI. The two remaining MALT1^{-/-} mice had low levels of
913 antibodies just above the cut off at 17 DPI.

914

915 **Figure 8. Transfer of neutralizing antibodies does not rescue MALT1^{-/-} mice.** (A)
916 Schematic overview of the experimental set-up. MALT1^{+/+} mice were inoculated intranasally
917 with the ERA virus and sacrificed at 35 DPI. Immune sera were collected, pooled, heat-
918 inactivated and titrated prior to i.p. transfer in MALT1^{-/-} mice at 10 DPI (500 μ l, 4.8 IU/ml).
919 (B) Survival of infected mice. All MALT1^{-/-} mice developed severe disease and had to be
920 euthanized, despite transfer of immune serum.

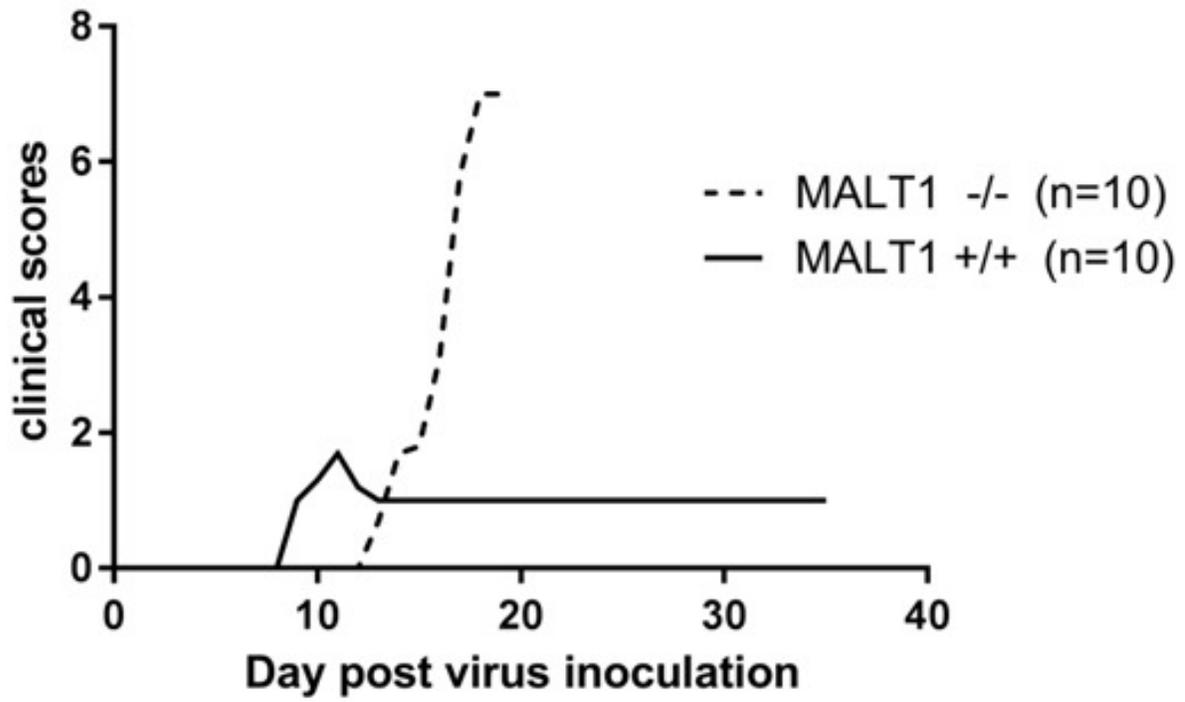
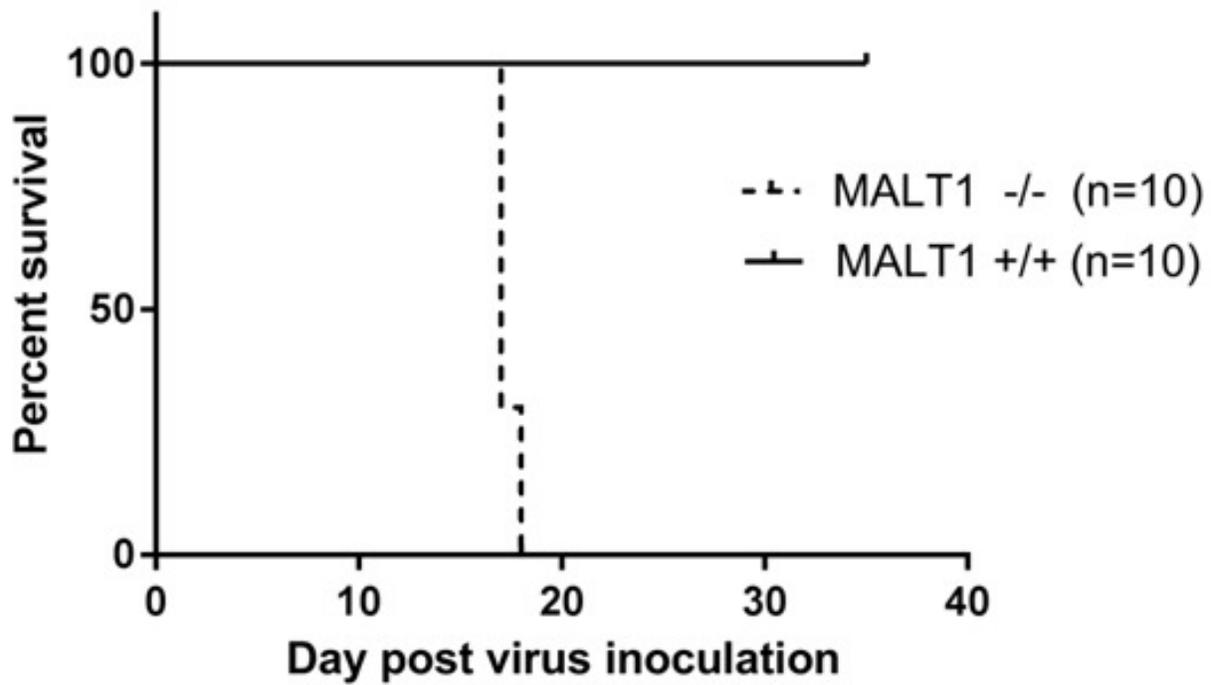
921 **Figure 9. Impact of specific MALT1 deficiency in T cells, myeloid cells or cells from**
922 **neuroectodermal origin on ERA virus infection.** (A) Schematic overview of conditional
923 MALT1^{-/-} mice generation. Mice expressing the CRE recombinase gene under the influence
924 of the CD4, LysM, or Nestin promoter, were crossed with MALT1^{FL/FL} mice to generate
925 conditional mice lacking MALT1 in T cells, myeloid cells, or cells from neuroectodermal
926 origin, respectively. Conditional mice and their wild-type littermates were genotyped and

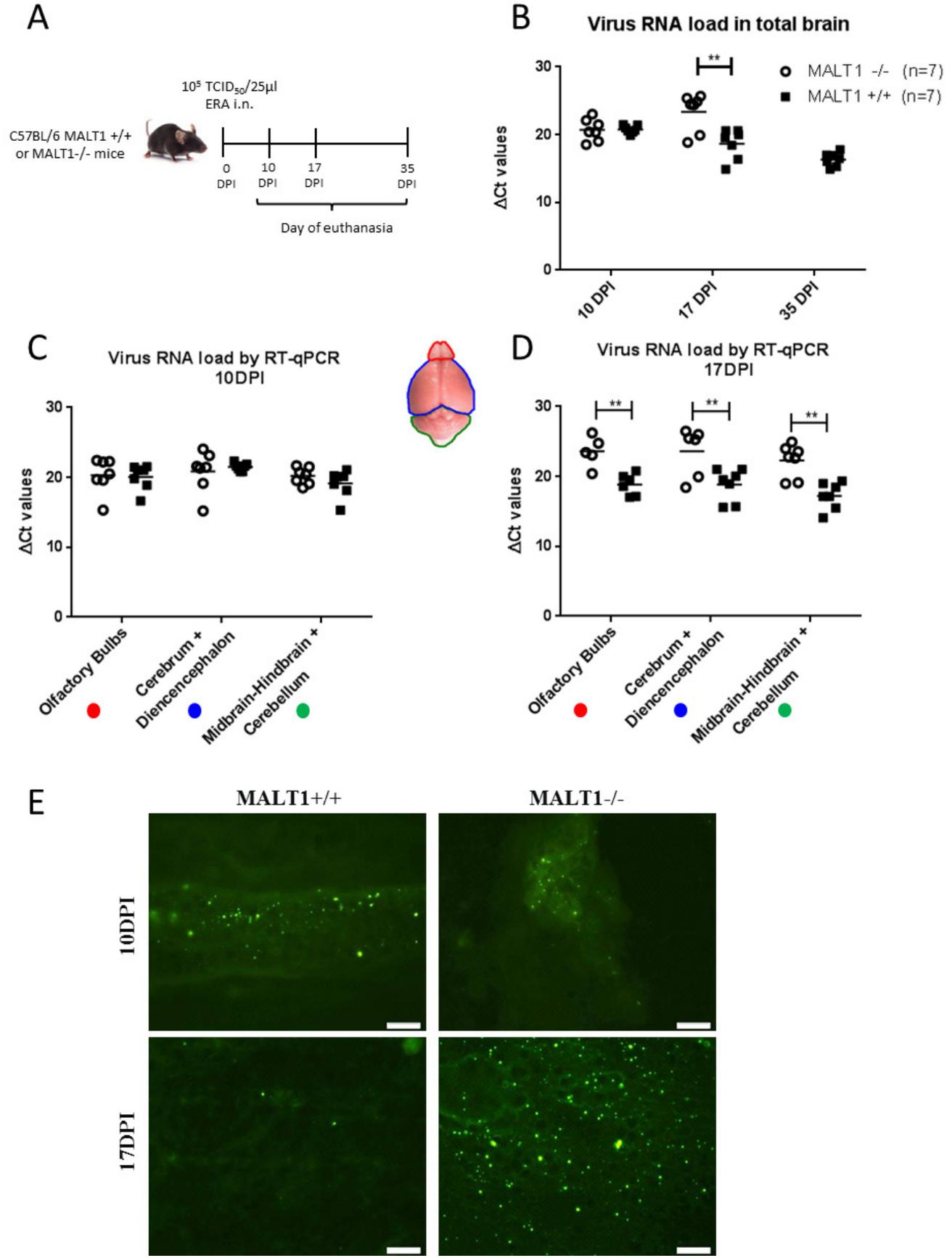
927 selected for each experiment. **(B)** Survival of infected mice. Mice were infected intranasally
928 with ERA virus and followed for disease development and survival. Mice lacking MALT1 in
929 cells from neuro-ectodermal origin (Nestin-Cre^{tg/+} MALT1^{FL/FL}) and myeloid cells (LysM-
930 Cre^{tg/+} MALT1^{FL/FL}) developed only mild disease, comparable to their wild-type littermates.
931 Mice lacking MALT1 in T-cells (CD4-Cre^{tg/+} MALT1^{FL/FL}) presented the same phenotype as
932 the full MALT1^{-/-} and developed severe disease requiring euthanasia at 15 DPI. **(C)** Virus
933 neutralizing antibodies in serum. Except for one, all CD4-Cre^{tg/+} MALT1^{FL/FL} mice failed to
934 mount protective levels of neutralizing antibodies. **(D)** Viral RNA in total brain. All T cell
935 specific MALT1^{-/-} mice (CD4-Cre^{tg/+} MALT1^{FL/FL}) presented a high viral load at 15 DPI,
936 comparable to full MALT1^{-/-} mice.

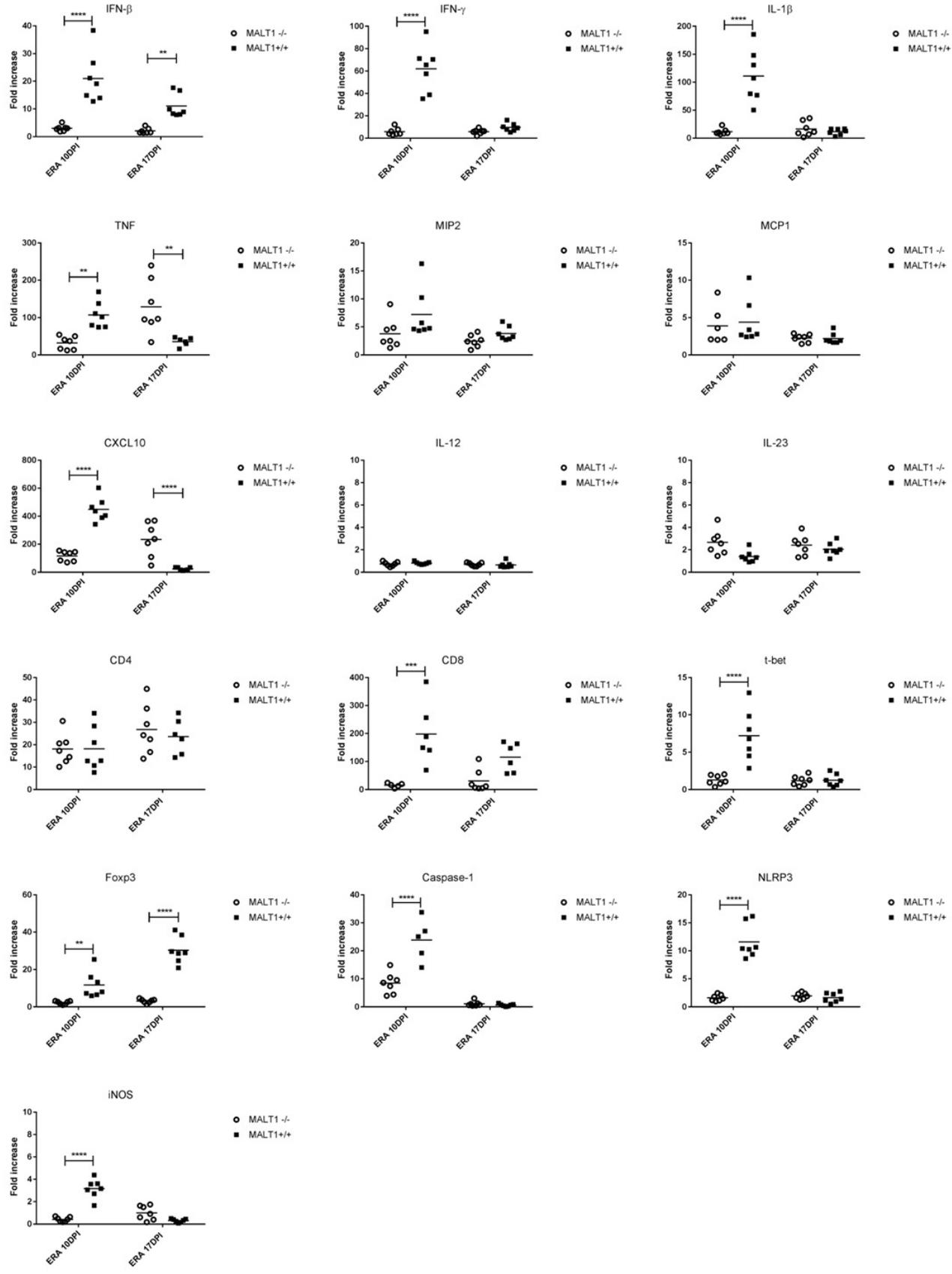
937 **Figure 10. Treatment with mepazine in ERA-infected MALT1^{+/+} mice: impact on**
938 **survival, viral load and neutralizing antibody production.** **(A)** Schematic overview of the
939 experimental set-up. MALT1^{+/+} mice were treated daily with mepazine (n=7) or a control
940 solution (0.9% NaCl) (n=7) starting at day -2 before virus inoculation until the end of the
941 experiment. Two days after the first treatment, mice were inoculated intranasally with ERA
942 virus and followed daily for signs of disease. **(B)** Survival curves. Four out of seven
943 mepazine-treated mice developed severe disease and had to be euthanized. Control mice and
944 the remaining 3 mepazine-treated mice survived the infection. **(C)** Profile of viral RNA in
945 total brain of mepazine-treated MALT1^{+/+} mice (n=7) and control mice (n=7) at sacrifice
946 determined by RT-qPCR. Mepazine-treated mice with severe disease had higher viral loads.
947 **(D)** Humoral immune response in mepazine-treated mice and control mice. Mepazine-treated
948 mice with severe disease had no neutralizing antibodies. Control mice and the 3 surviving
949 mepazine-treated mice had developed protective levels of neutralizing antibodies. Results are
950 obtained from one experiment.

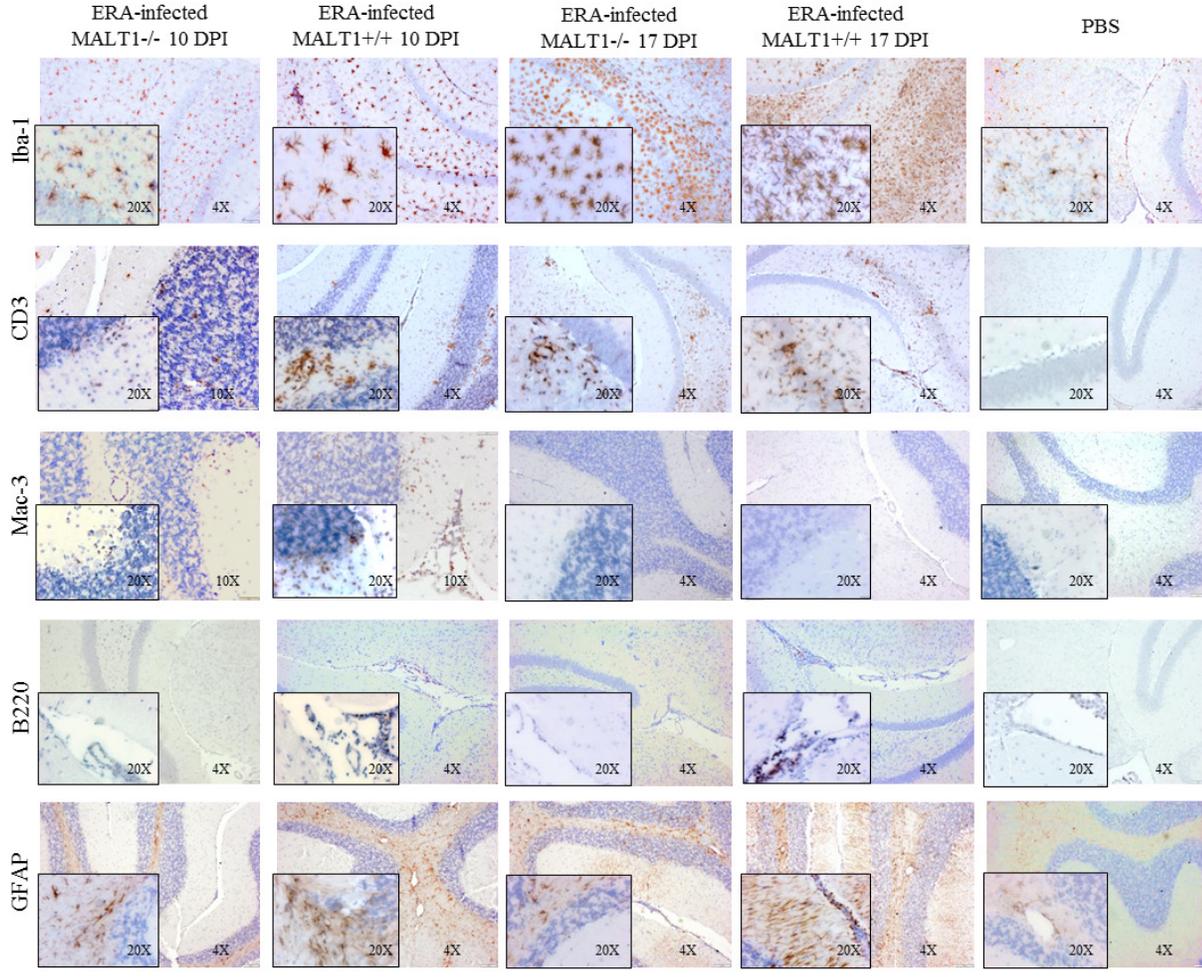
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952 **Figure 11. Hypothetical model for the impact of MALT1 inactivation on ERA virus-**
953 **induced immune responses in the brain.** In MALT1^{+/+} mice, virus-infected neuronal cells
954 produce CXCL10 (as shown in other studies), leading to the activation of microglia and
955 recruitment of CXCR3-expressing T cells and NK cells to the brain parenchyma. Activated
956 microglia and astrocytes start to produce pro-inflammatory cytokines, iNOS and CXCL10,
957 which amplifies the recruitment and activation of several immune cell types. Activated
958 macrophages migrate to the cervical lymph nodes, where they serve as antigen-presenting
959 cells for naïve T cells and trigger the differentiation to effector T cells, mainly CD4⁺ Th1 and
960 Th17 subsets and cytotoxic CD8⁺ T cells. Only activated T cells can infiltrate the brain. IFN-
961 γ producing CD8⁺T cells are the main T-cells recruited to the site of infection. Th1 cells and
962 CD8⁺T cells can further activate macrophages by IFN- γ production and antigen-presenting
963 cells can reactivate the T cells that have entered the brain. CD8⁺T cells also produce
964 granzyme B, mediating their cytotoxic activity and virus clearance. Th1 cells provide help for
965 B cell activation and Ig production outside the brain, whereas Th17 cells produce IL-17,
966 contributing to the activation of microglia and astrocytes, as well as enhancing blood brain
967 barrier permeability. The impact of MALT1 deficiency is represented by orange arrows.
968 MALT1 deficiency in T cells reduces their activation and differentiation by antigen-
969 presenting cells in the periphery, resulting in less effector T cells entering the brain. This does
970 not only cause less IFN- γ and IL-17 production, but also lower T cell help to activate B cells
971 and CD8⁺ cytotoxic T cells, leading to defective production of virus neutralizing antibodies
972 and reduced killing of virus-infected cells. As a consequence, viral load in the brain
973 increases, exacerbating disease development.

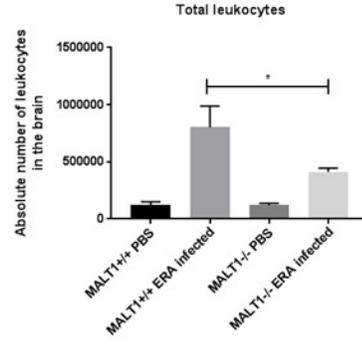
A**B**



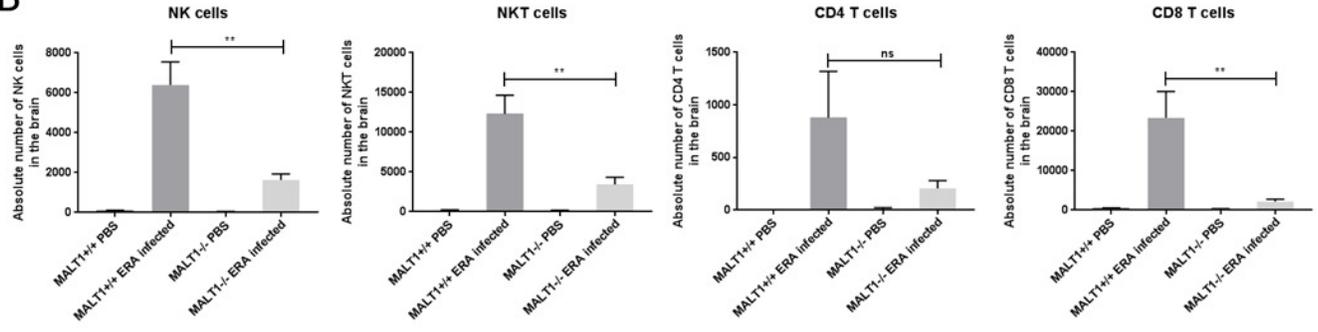




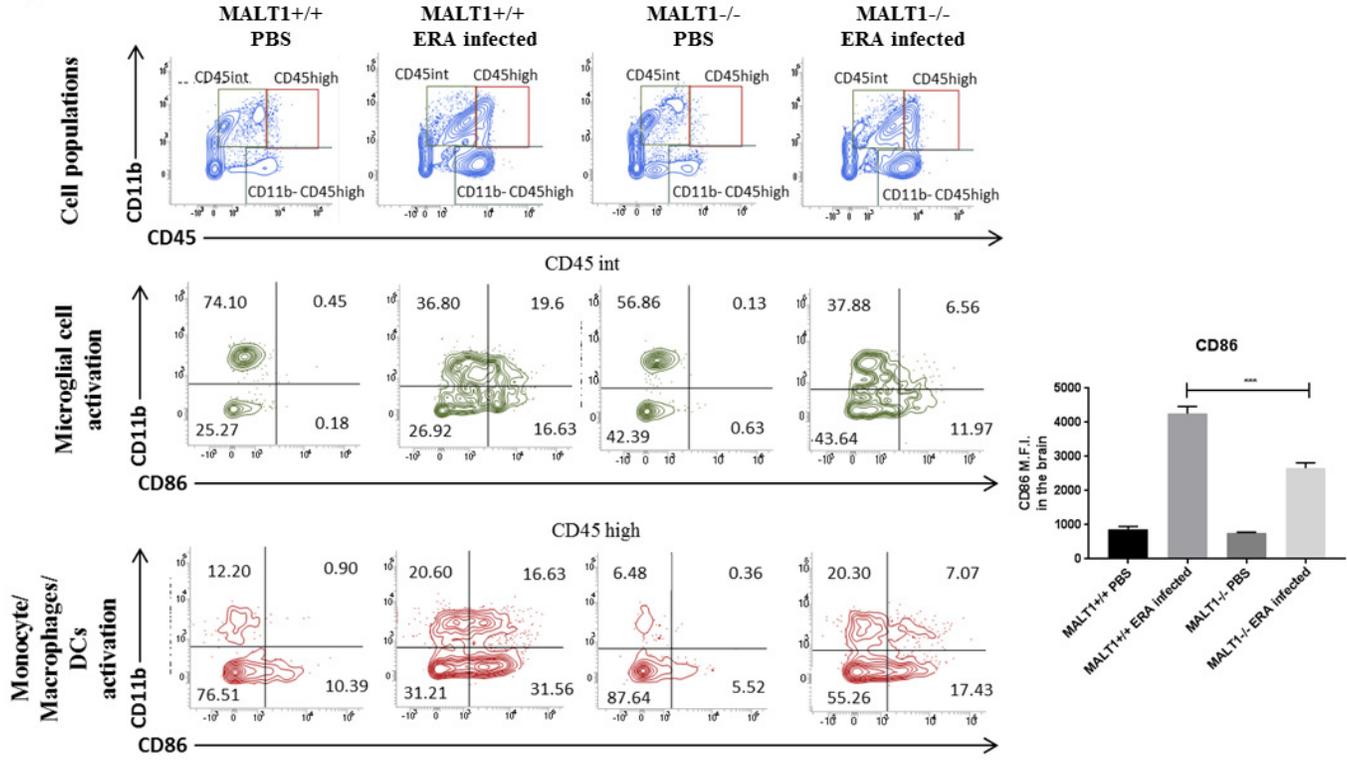
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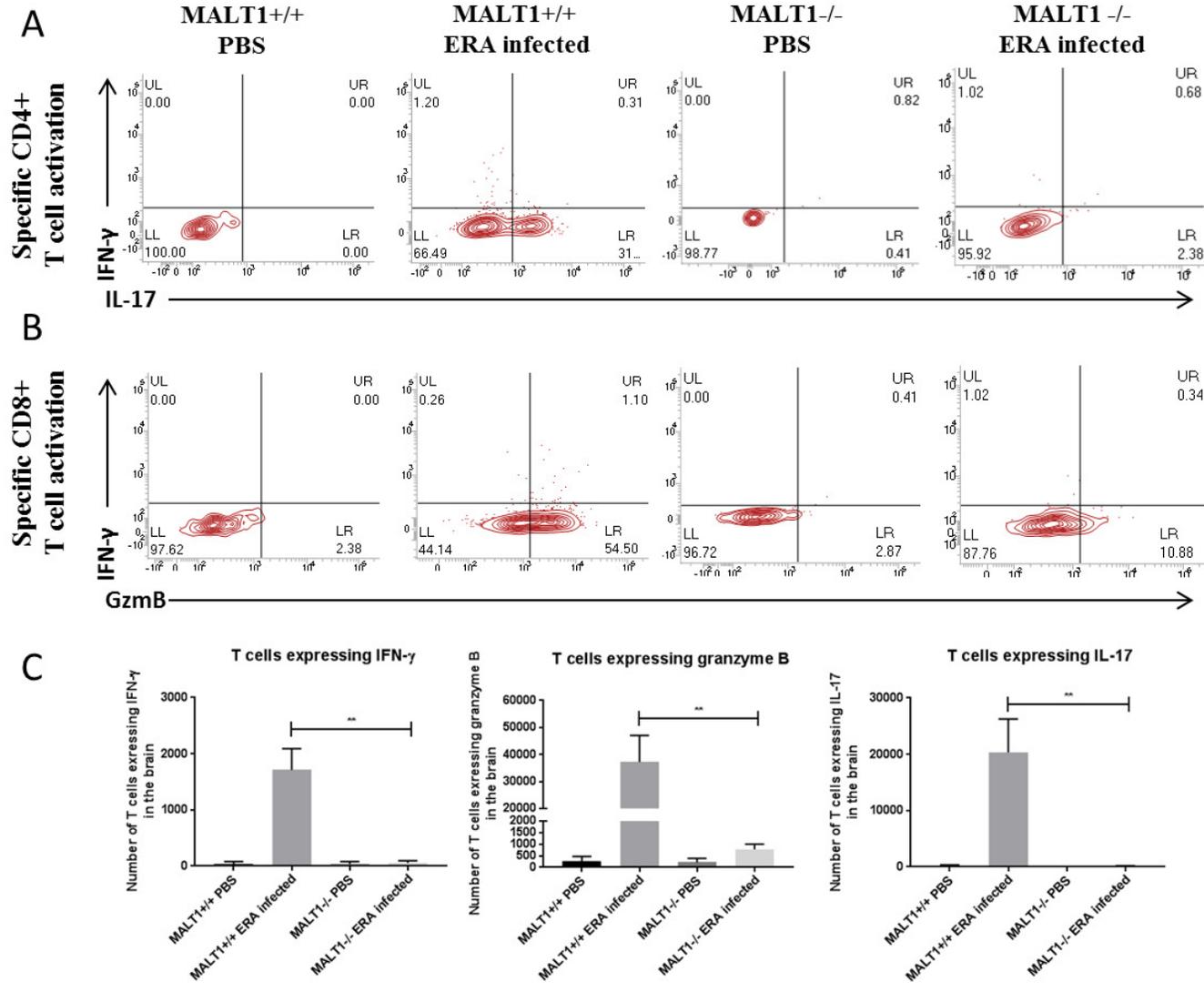


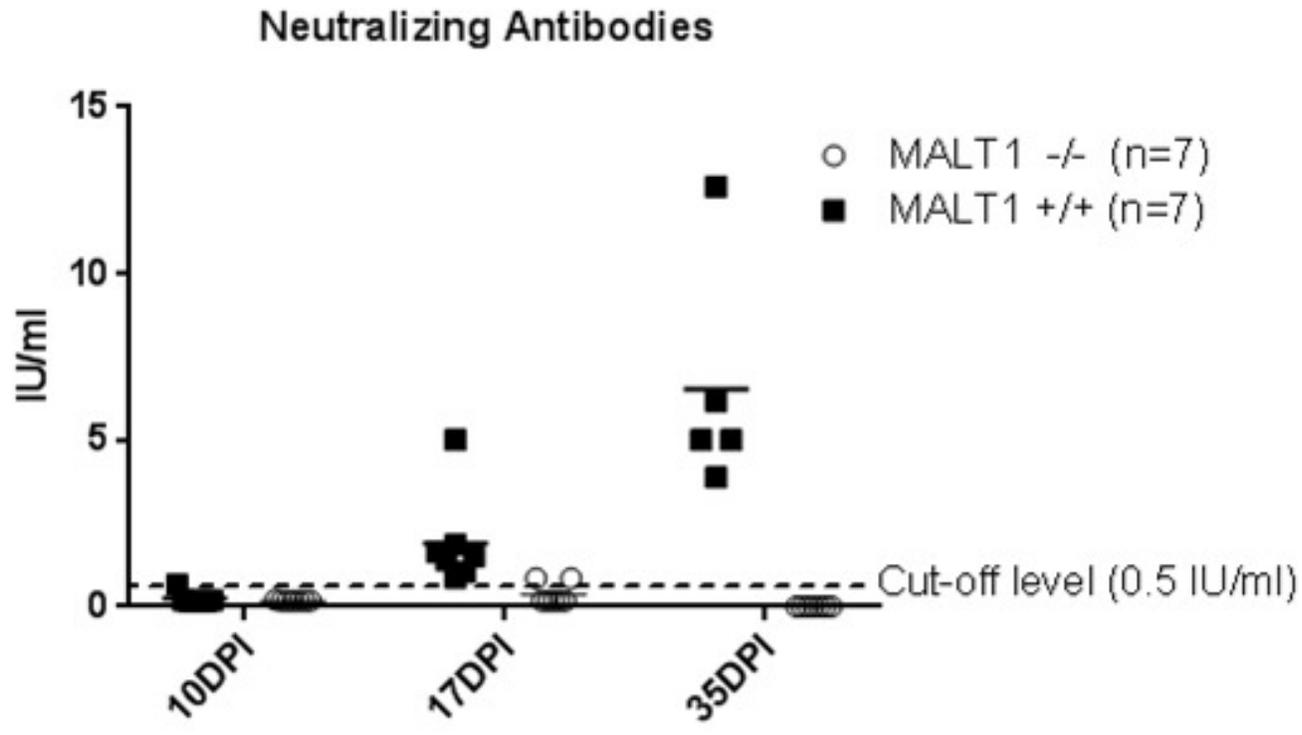
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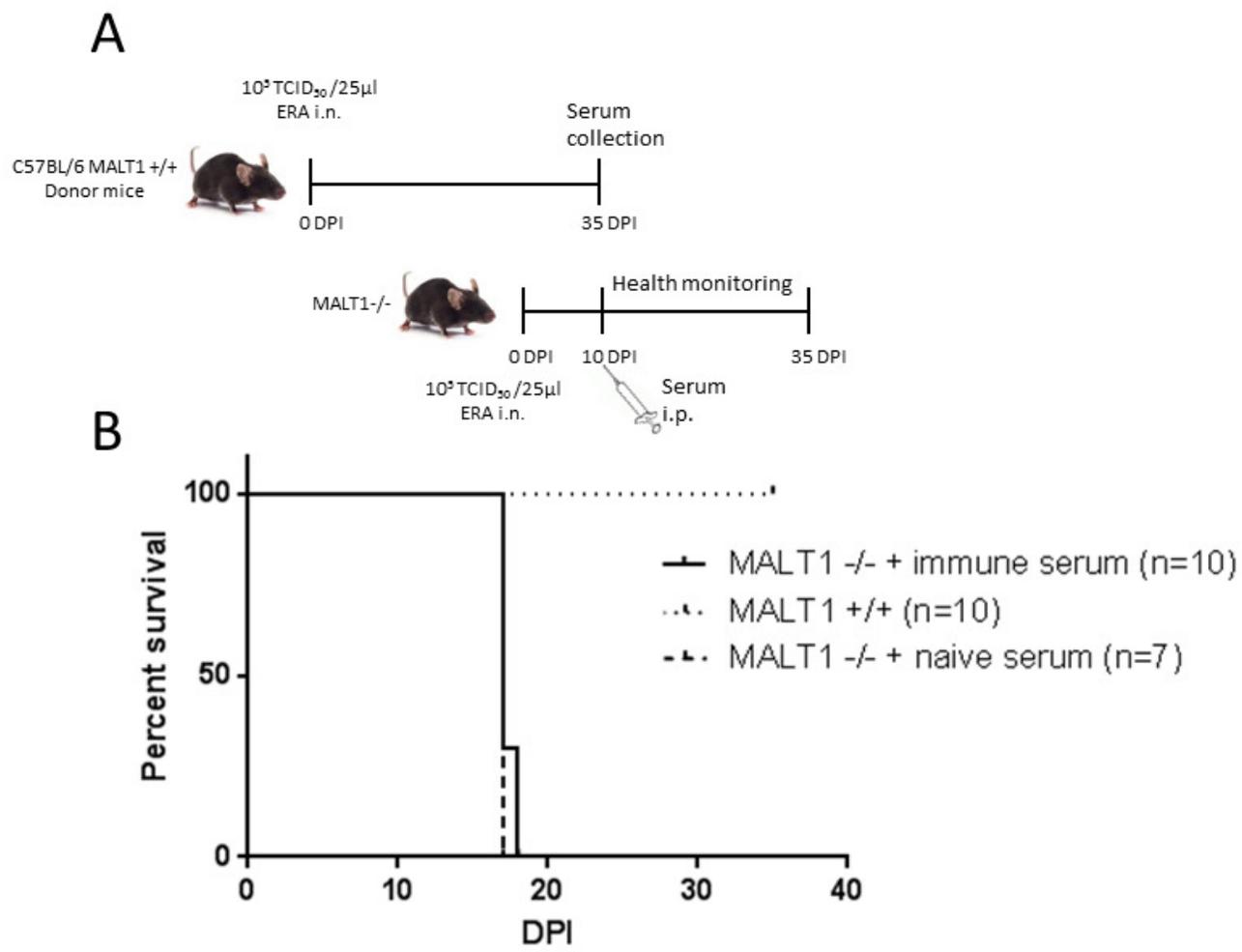


C

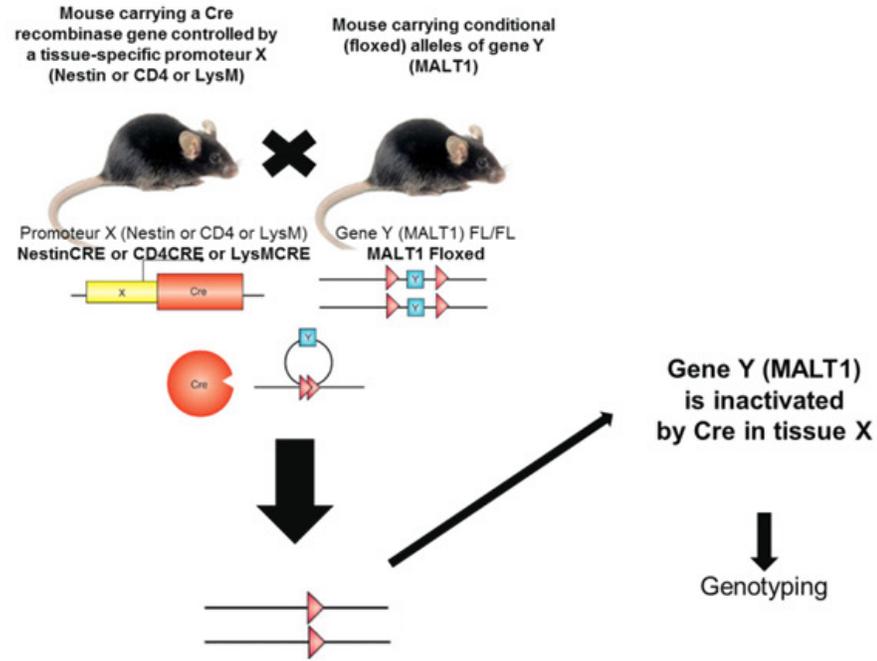




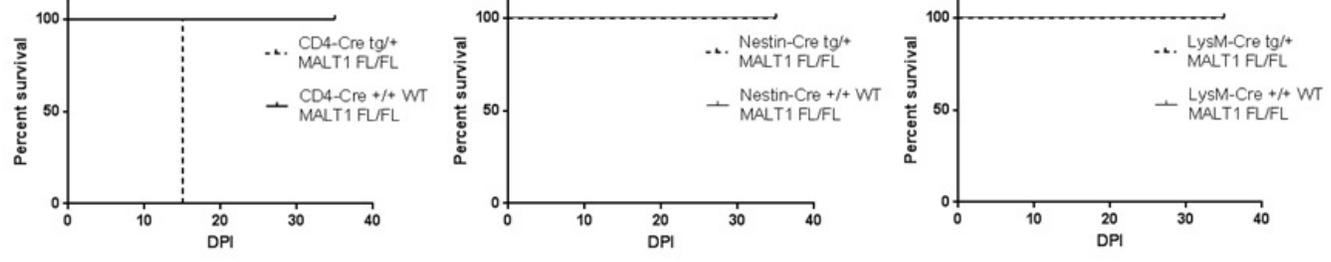




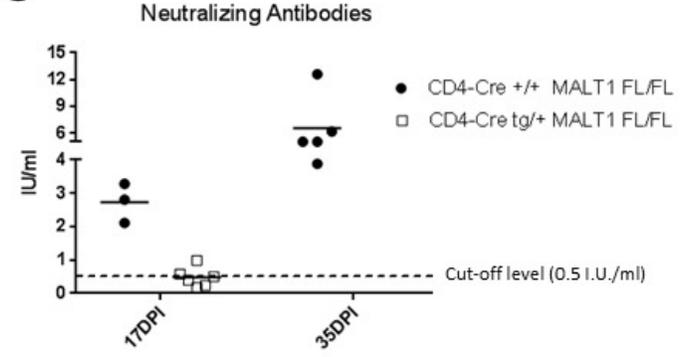
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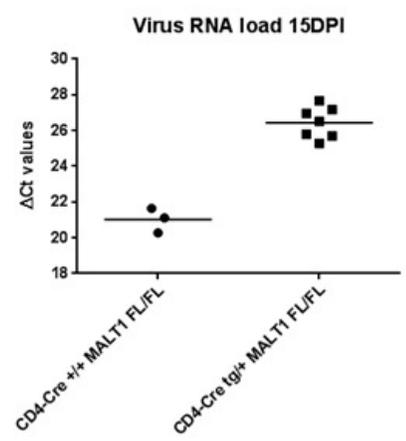
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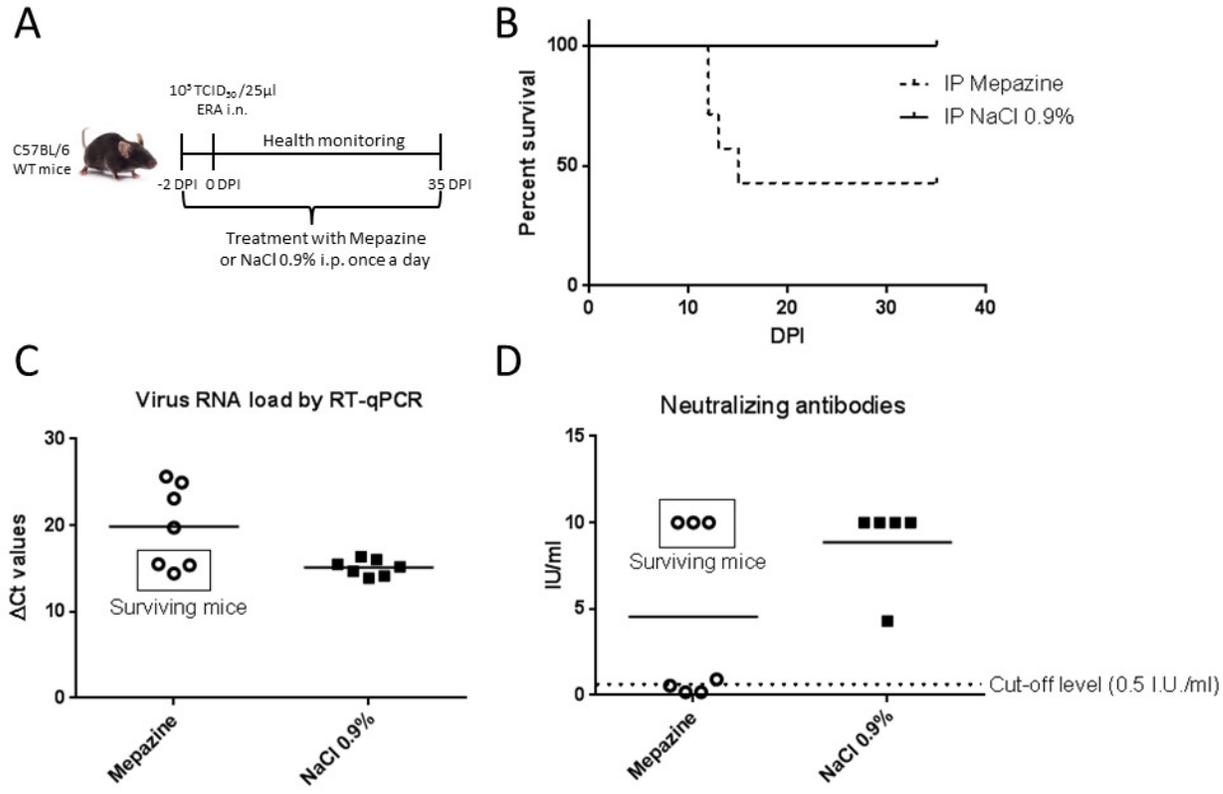


C



D





MALT1 deficiency

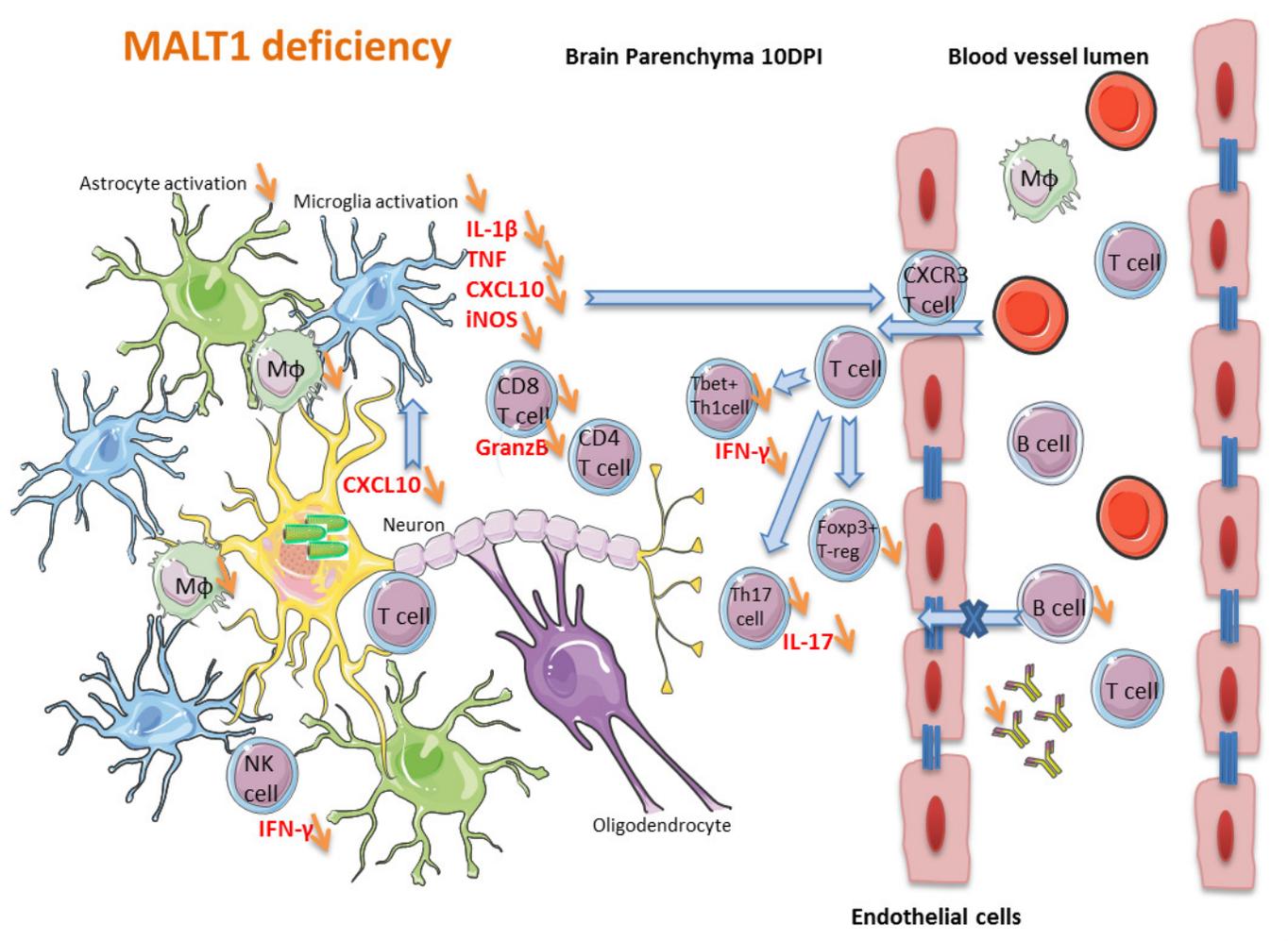


Table 1. List of primers used in real-time PCR

Gene	Definition	Primer sequences
RABV N	Rabies virus nucleoprotein	F : 5'-TGGGCATAGTTGTCAGTCTTA-3' R : 5'-CTCCTGCCCTGGCTCAA-3'
IFN-β	Interferon beta	F : 5'-GTTACACTGCCTTTGCCATCC-3' R : 5'-CAACAATAGTCTCATTCCACCCAG-3'
IFN-γ	Interferon gamma	F : 5'-GGCTGTCCCTGAAAGAAAGC-3' R : 5'-AGCGAGTTATTGTCAATTCGG-3'
IL-1β	Interleukin 1 beta	F : 5'-GCAACTGTTCTGAACTCAAC-3' R : 5'-ATCTTTGGGGTCCGTCAACT-3'
TNF	Tumor necrosis factor	F : 5'-ACCCTCACACTCAGATCATC-3' R : 5'-GAGTAGACAAGGTACAACCC-3'
IL-12p35	Interleukin 12A (p35 gene)	F : 5'-CCAAGGTCAGCGTTCCAACA-3' R : 5'-AGAGGAGGTAGCGTGATTGACA-3'
IL-23p19	Interleukin 23 p19 subunit	F : 5'-CCGGGAGACCAACAGATG-3' R : 5'-CGAAGGATCTTGGAACGGAGAAG-3'
MIP-2	Macrophage inflammatory protein 2 or chemokine (C-X-C motif) ligand 2 (CXCL2)	F : 5'-CCGTATGGATGTCTACGTG-3' R : 5'-CAGCAGCAGGATACCACTGA-3'
MCP-1	Monocyte chemoattractant protein 1 or chemokine (C-C motif) ligand 2 (CCL2)	F : 5'-AGTGTGAGGCAGAGGCCAGCAT-3' R : 5'-TGGATGGAAGTCTCCTGCGTGGA-3'
iNOS	Nitric oxide synthase 2, inducible	F : 5'-TGCATGGACCAGTATAAGGCAAGC-3' R : 5'-GCTTCTGGTCGATGTCATGAGCAA-3'
Foxp3	Forkhead box P3	F : 5'-TTCCTTCCCAGAGTTCTTCC-3' R : 5'-CTCAAATTCATCTACGGTCCAC-3'
NLRP3	NLR family pyrin domain containing 3	F : 5'-GCTCCAACCATTCTGACC-3' R : 5'-AAGTAAGGCCGAATTCACC-3'
Caspase-1	Caspase-1/Interleukin-1 converting enzyme (ICE)	F : 5'-TATGGACAAGGCACGGACCTATG-3' R : 5'-CCAGCAGCAACTTCATTTCTCTG-3'
CXCL10	Chemokine (C-X-C motif) 10 or Interferon gamma-induced protein 10 (IP-10)	F : 5'-TTCTGCCTCATCCTGCTG-3' R : 5'-AGACATCTCTGCTCATCATT-3'
t-bet	T-box transcription factor TBX21	F : 5'-AGAACGCAGAGATCACTCAG-3' R : 5'-GGATACTGGTTGGATAGAAGAGG-3'
CD4	Cluster of differentiation 4	F : 5'-TTAATTAGAGGAGGTTCCG-3' R : 5'-ACACTCGACCTCTGTCC-3'
CD8	Cluster of differentiation 8	F : 5'-GTATCATGAATGTGAAGCCA-3' R : 5'-CTGACCAACTACAGGAAG-3'