

1 Protective Humoral Immunity in the CNS Requires Peripheral CD19-Dependent  
2 Germinal Center Formation Following Coronavirus Encephalomyelitis

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11 Running Head: CD19-Dependent Humoral Immunity to CNS Viral Infection

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15 Word Count:

16 Abstract: 243

17 Importance: 149

18 Text: 6,549

19 **Abstract**

20 B cell subsets with phenotypes characteristic of naïve, non-isotype-switched,  
21 memory (B<sub>mem</sub>), and antibody-secreting cells (ASC) accumulate in various  
22 models of central nervous system (CNS) inflammation, including viral  
23 encephalomyelitis. During neurotropic coronavirus JHMV infection infiltration of  
24 protective ASC occurs after T cell mediated viral control, and is preceded by  
25 accumulation of non-isotype switched IgD<sup>+</sup> and IgM<sup>+</sup> B cells. However, the  
26 contribution of peripheral activation events in cervical lymph nodes (CLN) in  
27 driving humoral immune responses in the infected CNS is poorly defined. CD19,  
28 a signaling component of the B cell receptor complex, is one of multiple  
29 regulators driving B cell differentiation and germinal center (GC) formation by  
30 lowering the threshold of antigen-driven activation. JHMV infected CD19<sup>-/-</sup> mice  
31 were thus used to determine how CD19 affects CNS recruitment of B cell  
32 subsets. Early polyclonal ASC expansion, GC formation, and virus-specific ASC  
33 were all significantly impaired in CLN of CD19<sup>-/-</sup> mice compared to wild type (wt)  
34 mice, consistent with lower and unsustainable virus-specific serum Ab. ASC were  
35 also significantly reduced in the CNS resulting in increased infectious virus during  
36 persistence. Nevertheless, CD19 deficiency did not affect early CNS IgD<sup>+</sup> B cell  
37 accumulation. The results support that CD19 independent factors drive early B  
38 cell mobilization and recruitment to the infected CNS, while delayed  
39 accumulation of virus-specific, isotype switched ASC requires CD19 dependent  
40 GC formation in CLN. CD19 is thus essential for both sustained serum Ab as well  
41 as protective local Ab within the CNS following JHMV encephalomyelitis.

42 **Importance**

43 CD19 activation is known to promote GC formation and sustain serum Ab  
44 responses following antigen immunization and viral infections. However, the  
45 contribution of CD19 in the context of CNS infections has not been evaluated.  
46 This study demonstrates that antiviral protective ASC in the CNS are dependent  
47 on CD19 activation and peripheral GC formation, while accumulation of early-  
48 recruited IgD<sup>+</sup> B cells is CD19-independent. This indicates that IgD<sup>+</sup> B cells  
49 commonly found early in the CNS do not give rise to local ASC differentiation and  
50 that only antigen-primed, peripheral GC-derived ASC infiltrate the CNS, thereby  
51 limiting potentially harmful non-specific Ab secretion. Expanding our  
52 understanding of activation signals driving CNS migration of distinct B cell  
53 subsets during neuroinflammatory insults is critical for preventing and managing  
54 acute encephalitic infections, as well as preempting reactivation of persistent  
55 viruses during immune suppressive therapies targeting B cells in multiple  
56 sclerosis (MS), such as Rituximab and Ocrelizumab.

57 **Introduction**

58 Infections of the central nervous system (CNS) commonly require a  
59 humoral immune component for effective long-term control (1-4). However, little  
60 is known about the signals driving B cell activation and differentiation during  
61 neurotropic infections or how peripheral factors affect local immunity in the CNS.  
62 Following CNS infection with a glial tropic sub-lethal variant of mouse hepatitis  
63 virus (MHV), designated JHMV-v2.2-1, both T and B cell priming occurs in  
64 draining cervical lymph nodes (CLN) (5-7). While virus specific CD4 and CD8 T  
65 cells are essential to clear infectious virus, virus specific ASC and sustained  
66 neutralizing IgG antibody (Ab) are required for long term control of persisting  
67 virus, which is only detectable by the ongoing presence of low levels of viral RNA  
68 (5, 8, 9). Virus-specific ASC in CLN are CD4-dependent (10) and reach peak  
69 frequencies at ~14 days post infection (p.i.) (7, 11), coincident with germinal  
70 center (GC) formation (12). However, their accumulation in the CNS is not robust  
71 until day 21 p.i., when more mature GC characterized by dark and light zones  
72 become evident (12). Irrespective of the temporal and spatial ASC organization  
73 in CLN, chemokine guidance mediated via CXCR3 ligands, predominantly  
74 CXCL10, is essential for protective ASC accumulation in the CNS (11, 13).

75 The extent to which peripheral mature GC formation imprints ASC  
76 migration to the CNS is still unclear despite the temporal correlation between GC  
77 formation and ASC accumulation in the CNS. Key lymphoid chemokines  
78 organizing B cell compartmentalization in follicles and GCs are CXCL12,  
79 CXCL13, as well as CCL19 and CCL21, which act through their cognate

80 receptors CXCR4, CXCR5, and CCR7, respectively (9, 14). Specifically CXCL13  
81 contributes to GC formation by recruiting activated B and follicular helper CD4<sup>+</sup> T  
82 (T<sub>FH</sub>) cells expressing CXCR5 (15-17). CXCL13 is also associated with lymphoid  
83 neogenesis in non-lymphoid tissue, such as joints during rheumatoid arthritis (18)  
84 and CNS meninges during some neuroinflammatory diseases, including multiple  
85 sclerosis (MS) and Lyme disease (19-23). However, despite impaired GC  
86 formation, CXCL13<sup>-/-</sup> mice infected with glia tropic JHMV mounted effective  
87 peripheral ASC and serum Ab responses (24). Importantly, the specific deficit in  
88 ASC and B<sub>mem</sub> in the CNS did not affect virus control during persistence.  
89 Moreover, initial non-isotype-switched B cell recruitment into the CNS was not  
90 affected (24), similar to studies in Sindbis virus infection and experimental  
91 allergic encephalomyelitis (EAE) (25).

92         These results questioned the nature of activation signals required not only  
93 for effective ASC responses in the CNS, but also to mobilize early activated IgD<sup>+</sup>  
94 cells to the CNS, whose function and specificity is unknown. One critical  
95 signaling component promoting B cell receptor (BCR)-mediated activation and  
96 GC formation under conditions of low antigen (Ag) dose and/or limited pro-  
97 inflammatory stimuli is the BCR co-receptor CD19 (26). Together with CD21, also  
98 known as complement receptor type 2 (CR2), and CD81, CD19 forms a  
99 multimeric signal transduction complex on mature B cells (27-29). Activation and  
100 attachment of complement C3d, a cleavage product of complement C3, to Ag  
101 forms a covalent complex, which can lower the threshold for B cell activation by  
102 colligation of the BCR and coreceptor complex (28, 30, 31). The C3d-Ag complex

103 also acts directly on activated B cells in follicles and GC to enhance their survival  
104 (28, 32). Complement-mediated retention of Ag on follicular dendritic cells further  
105 promotes clonal selection of activated B cells in GCs. While many studies  
106 assessing the role of CD19 have focused on CD19<sup>-/-</sup> mice immunized with protein  
107 or inactivated virus, reports describing responses to replicating viruses are  
108 limited (26, 31). The latter revealed that CD19 is required for T cell-dependent  
109 responses such LCMV infection, but this requirement is overcome by infections  
110 associated with high viral dose exemplified by VSV (26). While a direct role of  
111 CD19 was not determined following peripheral HSV-1 infection, efficient humoral  
112 responses were dependent on complement C3 and CD21 (33). Overall both Ag  
113 and viral studies support a co-stimulatory role for CD19 in inducing long-term B  
114 cell memory, with CD19 playing a more prominent role in GC formation under  
115 limiting Ag conditions (26, 28, 31, 34).

116 The studies above focused largely on ASC and Ab responses to  
117 peripheral infections leaving the impact of CD19-dependent activation on B cell  
118 migration to inflamed tissue unclear. CNS inflammation is associated with  
119 accumulation of B cells in various differentiation and activation stages,  
120 independent of the insult, suggesting a common denominator in driving their  
121 initial activation (12, 35). Using the JHMV-induced encephalomyelitis model this  
122 study set out to identify a role of CD19 in driving early-activated B cells into the  
123 CNS as well as promoting antiviral ASC. Coincident with severely impaired GC  
124 formation, virus-specific ASC were significantly reduced in CLN and barely  
125 detectable in the CNS compared to wild type (wt) mice. While infected CD19<sup>-/-</sup>

126 mice mounted virus-specific serum Ab, they were not sustained. Surprisingly,  
127 early polyclonal ASC expansion prior to GC formation was also significantly  
128 reduced. However, absence of BCR-CD19 co-ligation did not appear to affect  
129 early CNS B cell accumulation. The results further demonstrate that elevated  
130 persisting virus in the CNS, as a result of impaired humoral immunity, can still be  
131 effectively controlled by re-emerging T cell activity without causing increased  
132 clinical disease.

133 **Methods**

134 **Mice, virus infection, and virus titer.** C57BL/6 were purchased from the  
135 National Cancer Institute (Frederick, MD). B6.129P2(C)-*Cd19<sup>tm1(cre)Cgn</sup>*/J mice  
136 (36) were purchased from The Jackson Laboratory (Bar Harbor, ME) and  
137 homozygous mice were utilized as CD19<sup>-/-</sup> mice. Female and male mice were  
138 housed at the Cleveland Clinic Lerner Research Institute under pathogen-free  
139 conditions. All animal procedures were executed in accordance with approved  
140 guidelines by the Cleveland Clinic Lerner Research Institute Institutional Animal  
141 Care and Use Committee. Mice of 6-7 weeks of age were infected by intracranial  
142 injection with 1,000 PFU of the gliotropic JHMV variant designated v2.2-1 (37).  
143 Infected animals were evaluated daily for clinical signs utilizing the following  
144 scale: 0, healthy; 1, hunched back and ruffled fur; 2, inability to correct to upright  
145 position or partial hind limb paralysis; 3, complete hind limb paralysis and  
146 wasting; 4, moribund or deceased. Virus titers within the CNS were determined in  
147 clarified supernatants via plaque assay with the murine delayed brain tumor  
148 (DBT) astrocytoma as previously described (37). Plaques were quantified  
149 following a 48 hour incubation at 37°C.

150

151 **Quantitative real-time polymerase chain reaction (PCR) gene expression**

152 **analysis.** Spinal cords and brains harvested from individual mice were snap-  
153 frozen, treated with 1 mL Trizol (Invitrogen, Grand Island, NY) and homogenized  
154 using a TissueLyser and stainless steel beads (Qiagen, Valenica, CA). RNA was  
155 extracted according to the manufacturer's instructions. DNA contamination was

156 eliminated via DNase I treatment for 30 minutes at 37°C (DNA-free kit; Ambion,  
157 Austin, TX). cDNA was synthesized from RNA using Moloney murine leukemia  
158 virus (MMLV) reverse transcriptase (Invitrogen) and a 1:1 mixture of oligo (dT)  
159 primers and random primers (Promega, Madison, WI). Quantitative real-time  
160 PCR was performed using either SYBR Green Master Mix or Applied Biosystems  
161 Gene Expression Assays with Universal Taqman Master Mix on a 7500 Fast  
162 Real-Time PCR System (Applied Biosystems, Foster City, CA). Primers used for  
163 transcripts encoding glyceraldehyde 3-phosphate dehydrogenase (GAPDH),  
164 Tumor necrosis factor (TNF), a proliferation-inducing ligand (APRIL, TNFSF13),  
165 IL-21, CXCL9, CXCL10, viral nucleocapsid, and C3 (5'-  
166 AAGCATCAACACACCCAACA-3', 5'-CTTGAGCTCCATTCGTGACA-3') were  
167 used in conjunction with SYBR Green Master mix as described previously (8, 24,  
168 38). GAPDH, activation-induced cytidine deaminase (AID), immunoglobulin  
169 gamma (IgG), gamma interferon (IFN $\gamma$ ), CXCR5, CCL19, CCL21, CXCL13, B-  
170 cell activating factor (BAFF, TNFSF13B), and IL-10 mRNA levels were  
171 determined using Taqman primers (Applied Biosystems). Transcript levels were  
172 calculated relative to the housekeeping gene GAPDH using the following  
173 formula:  $2^{[CT(GAPDH) - CT(Target\ Gene)]} \times 1000$ .

174

#### 175 **Mononuclear cell isolation and flow cytometric analysis**

176 Cells were isolated from the CNS as described (24, 39). Briefly, brains harvested  
177 from PBS-perfused mice were mechanically homogenized in Dulbecco's PBS  
178 using ice-cold Tenbroeck grinders. The resulting suspension was centrifuged at

179 450 x g for 7 minutes at 4°C, supernatants stored at -80°C for subsequent  
180 analysis, and cells resuspended in RPMI medium. Cells were adjusted to 30%  
181 percoll (Pharmacia, Piscataway, NJ), underlayered with 1 ml 70% Percoll and  
182 collected from the 30%/70% Percoll interface following centrifugation at 850 xg  
183 for 30 minutes at 4°C. After washing cells were resuspended in fluorescence-  
184 activated cell sorter (FACS) buffer and incubated with a mixture of mouse, goat,  
185 and horse serum (1:1:1) and rat anti-mouse FcγIII/II mAb (2.4G2: BD Bioscience,  
186 San Diego, CA) for 20 minutes on ice. Cells were then stained with specific  
187 monoclonal Ab (mAb) to determine expression of cell surface markers for CD45  
188 (30-F11), CD4 (L3T4), B220 (RA3-6B2), CD138 (281-2), CD95 (Jo2), CXCR4  
189 (2B11), T-cell and B-cell activation antigen (GL7) (all from BD Pharmingen), CD8  
190 (53-6.7), PD-1 (RMP1-30) (all from eBioscience), and CXCR3 (R&D Systems).  
191 Cell surface expression of CXCR5 was determined via staining with biotin rat  
192 anti-mouse CXCR5 mAb and streptavidin phycoerythrin (both from BD  
193 Bioscience). Cells were then washed with FACS buffer, fixed with 2%  
194 paraformaldehyde, and analyzed on a BD LSR II flow cytometer. Resulting data  
195 was analyzed with FlowJo software (Tree Star Inc., Ashland, OR).

196

#### 197 **Serum, brain supernatant, and neutralizing Ab quantification**

198 JHMV-specific IgG and IgM in serum and brain supernatant was quantified by  
199 ELISA using plates coated with serum-free supernatant from infected DBT cells  
200 and biotinylated goat anti-mouse IgG2a and IgM as detection Ab as described (7,  
201 38). Ab titers are expressed as the log of the highest dilution with an optical

202 density value exceeding 3 standard deviations above the mean background.  
203 Titers for brain supernatants are expressed using the following formula:  
204 (absorbance at 450nm / 0.1) x dilution factor x total volume of clarified CNS  
205 supernatant. Neutralizing serum Ab was measured by incubation of serial 2-fold  
206 dilutions of heat inactivated serum from individual mice with 50 PFU JHMV in 96-  
207 well plates for 90 min at 37°C. DBT cells were added, and plates incubated at  
208 37°C for 48 h. Neutralization titers represent the log of the highest average  
209 serum dilution that inhibited cytopathic effect.

210

#### 211 **ELISPOT**

212 ASC were determined by ELISPOT as described previously (12, 24). Briefly,  
213 sterile, white 96-well filter plates with 0.45 µm pore size hydrophobic PVDF  
214 membrane (Merck Millipore, Billerica, MA) were stripped with 70% ethanol for 2  
215 minutes, washed with 0.1M sodium bicarbonate buffer, and coated with either  
216 polyclonal goat anti-mouse Ig (Life Technologies, Eugene, OR) at a  
217 concentration of 2 mg/ml or undiluted virus supernatant for approximately 16  
218 hours at 4°C. Wells were washed with washing buffer (0.05% Tween20 in  
219 1xPBS) and blocked with 5% FCS in RPMI medium for 2 hours at 37°C.  
220 Blocking buffer was replaced with cell suspensions at serial dilutions in triplicate  
221 in RPMI medium. Plates were incubated at 37°C for 4 hours, then washed  
222 thoroughly to remove cells. After addition of biotinylated rabbit anti-mouse IgG  
223 (Southern Biotech, Birmingham, AL) at a concentration of 0.5 µg/mL, plates were  
224 incubated for ~16 hours at 4°C, subsequently washed with washing buffer, and

225 incubated with streptavidin horseradish peroxidase for 1 hour at 25°C. Following  
226 washes with washing buffer and 1xPBS, respectively, diaminobezadine (DAB)  
227 solution was added to visualize spots. Once spots had developed sufficiently, the  
228 reaction was stopped by flushing wells with H<sub>2</sub>O and plates left to dry in the dark.  
229 Plates were scanned and spots quantified via Immunospot (Cellular  
230 Technologies Ltd., Shaker Heights, OH). Threshold criteria for spot size was  
231 defined as between 0.0009 and .2257 mm<sup>2</sup>.

232

### 233 **Immunohistochemistry**

234 CLN from PBS-perfused mice were snap-frozen in Tissue-Tek OCT compound  
235 (Sakura Finetex, Torrance, CA) and sectioned at 10 μm using a Thermo  
236 Shandon cryostat. Slide-mounted tissue sections were fixed with ice cold 70%  
237 acetone for 5 min, blocked with 5% bovine serum albumin and 10% goat serum  
238 for 1 h, and stained with rat anti-mouse B220 mAb (BD biosciences), and rabbit  
239 anti-mouse CD3 polyclonal Ab (Abcam, Cambridge, MA), and rat anti-mouse  
240 FITC conjugated GL7 mAb (BD Biosciences) overnight at 4°C. Sections were  
241 then incubated with secondary Ab using Alexa Fluor 594 goat anti-rat (Life  
242 Technologies, Grand Island, NY) and Cy5 goat anti-rabbit (Life Technologies,  
243 Grand Island, NY) Ab for 1 h at room temperature. Sections were mounted with  
244 Vectashield Hard Set Mounting Medium with DAPI (4,6-diamidino-2-  
245 phenylindole) (Vector Laboratories, Burlingame, CA) and examined using a Leica  
246 TCS SP5 II confocal microscope (Leica Microsystems, Exton, PA).

247

248 **Statistical analysis**

249 All results are expressed as the mean  $\pm$  standard error of the mean (SEM). Data  
250 were plotted and statistical significance determined utilizing GraphPad Prism 6  
251 software. Statistically significant differences are denoted by \* $p < 0.05$ , \*\* $p < 0.01$ ,  
252 \*\*\* $p < 0.001$ , unless otherwise noted.

253 **Results**

254 **CD19 deficiency abrogates peripheral GC formation following CNS**

255 **infection**

256 CLN are the predominant site of both T cell and ASC expansion following  
257 JHMV infection, consistent with CLN as the draining site for CNS-derived Ag (5,  
258 40-42). Temporal analysis of GC formation in CLN following JHMV infection  
259 using GL7 to identify GC B cells previously showed formation of GL7<sup>+</sup> foci as  
260 early as day 7 p.i., more defined structures by day 14 p.i., and segregation into  
261 light and dark zones by day 21 p.i. (12). To assess whether accumulation of ASC  
262 within the CNS is dependent on CD19 signaling and GC formation in the  
263 periphery, JHMV infected CD19<sup>-/-</sup> and wt mice were initially compared for GC  
264 formation in CLN. In wt CLN, defined structures of GL7<sup>+</sup> B220<sup>+</sup> B cells started to  
265 form at day 14 p.i. and were robust by day 21 p.i. (Fig. 1A), confirming previous  
266 results (12). By contrast, in the absence of CD19, GL7<sup>+</sup> cells were very sparse  
267 and scattered at day 14 p.i. Although GC were evident in some follicles by day  
268 21.p.i., they were small in size and disorganized compared to those in wt mice  
269 (Fig. 1A). GL7<sup>+</sup> B cells were scattered within the follicle (white arrows) without  
270 forming structures resembling GC architecture. Quantitative evaluation of GL7<sup>+</sup>  
271 area by immunofluorescence highlights significantly reduced reactivity in CD19<sup>-/-</sup>  
272 compared to wt mice, especially at day 21 p.i. , when pixels per frame were 18-  
273 fold reduced (Fig. 1B). Impaired GC formation could not be attributed to disrupted  
274 lymphoid organization as B cell follicle formation and lymphoid architecture is  
275 intact in naïve CD19<sup>-/-</sup> mice (43).

276           The extent of impaired GC formation was further confirmed by flow  
277 cytometry using the B220<sup>+</sup> GL7<sup>+</sup> CD95<sup>+</sup> phenotype to identify GC B cells (Fig.  
278 1C). The population of GL7<sup>+</sup> CD95<sup>+</sup> B cells in CLN of both naive wt and CD19<sup>-/-</sup>  
279 mice was below 0.5%, consistent with no or sparse GC activity. In wt mice GL7<sup>+</sup>  
280 CD95<sup>+</sup> B cells started to emerge at day 5 and continued to increase to ~3% by  
281 day 14.p.i., consistent with anatomical GC formation. The frequency of GC  
282 phenotype B cells was maintained at ~3-4% throughout days 21 and 28 p.i. In  
283 contrast, GL7<sup>+</sup> CD95<sup>+</sup> B cells were only slightly elevated to <1% in CD19<sup>-/-</sup> mice  
284 and remained barely detectable throughout infection (Fig. 1C). Functionally, GC  
285 B cells are characterized by upregulation of activation-induced cytidine  
286 deaminase (AICDA), an enzyme required for somatic hypermutation and class  
287 switch recombination to increase Ab diversity and affinity. As B cell maturation  
288 can occur in the absence of GC (24, 25, 44), we also assessed transcript levels  
289 of the gene encoding AICDA (*aicda*). In CLN of infected wt mice, the progressive  
290 increase of *aicda* mRNA levels from day 7 to 21 p.i. correlated with GC formation  
291 and maturation (Fig. 1D). While CD19<sup>-/-</sup> mice exhibited modestly increased *aicda*  
292 mRNA levels in CLN between days 7 and 21 p.i., these levels did not significantly  
293 differ from naïve CD19<sup>-/-</sup> mice until day 21 p.i. (Fig. 1D). These results  
294 demonstrate a retarded and diminished capacity to initiate GC reactions in  
295 JHMV-infected CD19<sup>-/-</sup> relative to wt mice. Nevertheless, the relative population  
296 of GL7<sup>+</sup> CD95<sup>+</sup> B cells in CD19<sup>-/-</sup> CLN only reached ~15% of wt levels at day 21  
297 p.i., while *aicda* mRNA levels reached ~40% of wt levels, suggesting that CD19<sup>-/-</sup>

298 B-cells exhibit modest maturation capacity despite severely impaired GC  
299 formation.

300 To support the notion that deficient GC formation is a result of poor B cell  
301 activation in the absence of CD19 rather than extrinsic factors related to GC  
302 formation, we assessed transcript levels for several chemokines and cytokines  
303 regulating B cell migration and differentiation (Fig. 2). Compared to infected wt  
304 mice, CD19<sup>-/-</sup> mice exhibited no significant changes in relative levels or kinetics of  
305 mRNAs encoding CXCL13, CCL19 or CCL21, lymphoid chemokines regulating B  
306 cell migration within follicles (14) (Fig. 2). The CXCL13 chemokine receptor  
307 CXCR5 is up-regulated on B cells migrating to and forming GC (15, 45). It is also  
308 highly expressed by follicular helper T cells (T<sub>FH</sub>), which are essential for GC  
309 formation, maintenance, B cell differentiation and survival by producing IL-21.  
310 Although *cxcr5* transcripts were elevated in CLN of CD19<sup>-/-</sup> mice throughout  
311 infection, differences only reached statistical significance at day 21 p.i. (Fig. 2).  
312 *Il21* mRNA levels were not significantly altered in the absence of CD19 (Fig. 2),  
313 consistent with similar T<sub>FH</sub> cell frequencies characterized by their PD-1<sup>+</sup>CXCR5<sup>+</sup>  
314 phenotype using flow cytometry in both wt and CD19<sup>-/-</sup> mice (data not shown).  
315 Furthermore, transcript levels of the *Tnfrsf13b* gene, which encodes the survival  
316 factor B-cell activation factor (BAFF), were also similar between both groups  
317 suggesting no deficits in retaining B cell viability. We also assessed upregulation  
318 of transcripts encoding complement protein C3. C3-Ag adducts not only lower the  
319 threshold for B cell activation by co-ligation of the CD21/CD19/CD81 BCR co-  
320 receptor, but also enhance B cell survival in follicles and GC (32). CNS infection

321 indeed resulted in significant upregulation of c3 mRNA in both groups at day 7 to  
322 14 p.i. and remained elevated to day 21 p.i. Overall these results suggested that  
323 the absence of CD19 did not impair cues for B cell localization to and trafficking  
324 between anatomical structures of the CLN. The deficit in GC formation more  
325 likely resides in deficient CD19 engagement either directly or indirectly via the  
326 complement C3d binding receptor CD21 (27, 32).

327 **Impaired GC formation is associated with induction of, but reduced and**  
328 **rapid decline in, virus-specific humoral responses in the periphery**

329 Impaired GC formation in CLN was also a hallmark of CXCL13<sup>-/-</sup> mice  
330 infected with JHMV. However, differentiation of B cells into virus specific IgG  
331 ASC was only reduced by ~25% in the CLN and 50% in in the CNS (24).  
332 Modestly impaired, but not abrogated, virus-specific serum Ab in the absence of  
333 CXCL13 confirmed that formation of mature GC in CLN is not an absolute  
334 requirement for development of peripheral or CNS humoral immunity. We  
335 therefore assessed how severely impaired GC formation in CD19<sup>-/-</sup> affects JHMV-  
336 specific serum Ab throughout infection. Virus-specific IgM levels were below  
337 detection at day 7 p.i. in CD19<sup>-/-</sup> mice, but reached similar levels to wt mice by  
338 day 14 p.i. (Fig. 3A). However, while wt mice sustained virus-specific IgM levels  
339 out to day 28 p.i., they were progressively lost after day 14 p.i. in CD19<sup>-/-</sup> mice.  
340 Virus-specific IgG2a was induced in both mouse groups by day 7 p.i. and  
341 increased by day 14 p.i. (Fig. 3A). However, the levels were lower in the absence  
342 of CD19 reaching ~3 log<sub>10</sub> relative to ~4-4.5 log<sub>10</sub> in wt mice. Furthermore, while  
343 virus-specific serum IgG2a increased slightly in wt mice by day 21 p.i. and then

344 stabilized, it already started to decline by day 28 p.i. in CD19<sup>-/-</sup> mice. Importantly,  
345 although neutralizing serum Ab was initially reduced in infected CD19<sup>-/-</sup> relative to  
346 wt mice at day 7 p.i., it reached levels found in wt mice by day 14 p.i. However,  
347 distinct from the gradual increase of neutralizing Ab throughout infection in wt  
348 mice, it significantly declined by day 28 p.i. in CD19<sup>-/-</sup> mice (Fig. 3A). Thus,  
349 despite impaired GC formation in the absence of CD19, virus-specific serum Ab  
350 responses were induced, albeit with delayed kinetics, at lower levels, and shorter  
351 longevity. The inability of serum Ab to be maintained supported a critical role for  
352 CD19 in generation of both IgM and isotype switched long-lived ASC (31).

353 Induction, but not maintenance of virus-specific serum Ab prompted us to  
354 investigate the kinetics of virus-specific IgG ASC accumulation in CLN and bone  
355 marrow (BM) by ELISPOT analysis (Fig. 3B, C). Virus specific IgG ASC emerged  
356 at day 7 in CLN of wt mice, reached peak frequencies at day 14 p.i., and declined  
357 by day 21 p.i., consistent with previous data (7, 11, 46). Although virus-specific  
358 IgG ASC followed similar kinetics in CD19<sup>-/-</sup> mice, peak frequencies were  
359 reduced by ~70% compared to wt mice and dropped to barely detectable levels  
360 by day 21 p.i. Furthermore, contrasting the modest increase in virus-specific ASC  
361 in BM by day 21 p.i., virus-specific IgG ASC remained at baseline levels in BM of  
362 CD19<sup>-/-</sup> mice (Fig. 3C). Impaired ASC maturation was supported by assessment  
363 of spot size as an indicator for ASC Ab secretion rate (Fig. 3B, C). On average,  
364 ASC derived from WT CLN and BM at day 14 and 21 p.i., respectively, formed  
365 more intense spots with an increased diameter compared to CD19<sup>-/-</sup>  
366 counterparts, suggesting higher rates of IgG secretion. Sparse GC formation

367 following JHMV infection of CD19<sup>-/-</sup> mice thus coincides with reduced virus-  
368 specific ASC maturation and longevity. These results indicated CD19 is essential  
369 to drive activation and differentiation of high affinity virus-specific ASC competent  
370 to egress CLN and migrate to survival niches in BM (47).

371 **CD19 deficiency severely diminishes peripheral ASC expansion following**  
372 **CNS infection**

373 Impaired virus-specific ASC and serum responses as early as day 7 p.i.  
374 were consistent with a defect in early activation potentially due to the absence of  
375 complement mediated costimulation through CD21. Moreover, the peak of virus-  
376 specific ASC at day 14 p.i. in CLN following JHMV infection is preceded by a  
377 peak in polyclonal ASC expansion at day 7 p.i. (11, 12). To assess whether  
378 CD19 deficiency specifically affected virus-specific ASC, overall ASC expansion  
379 in CLN was monitored by flow cytometry using CD138 as a phenotypic marker  
380 (Fig. 4A, B). The frequency of CD138<sup>+</sup> B cells was reduced by ~70 % relative to  
381 wt mice at day 7 p.i. prior to expansion of virus specific ASC and remained low  
382 throughout days 14 to 28 p.i. (Fig. 4). Similar numbers of B220<sup>+</sup> B cells in CLN of  
383 both groups during infection indicated no overall deficiencies in the B cell  
384 compartment or recruitment to CLN following infection (data not shown). These  
385 data were consistent with a polyclonal defect in early B cell activation in CD19<sup>-/-</sup>  
386 mice following JHMV infection preceding impaired generation of virus specific  
387 ASC. Taken together, these results demonstrate a diminished capacity to initiate  
388 GC reactions resulting in impaired differentiation of long-lived ASC in the  
389 absence of CD19 in the periphery.

390 **CD19 deficiency severely diminishes CNS humoral responses**

391           ASC expanding prior to GC formation in CLN appear not to have egress or  
392 migration capacity, as ASC do not emerge in the CNS until 14 days p.i. and only  
393 prominently increase thereafter (7, 11, 24, 46). This observation suggests  
394 accumulation of ASC in the CNS is dependent on differentiation in GCs.  
395 Moreover, unlike CXCR4 driven migration of ASC to BM, ASC accumulation in  
396 the CNS is dependent on CXCR3 expression (11). We therefore assessed  
397 whether the few ASC primed in CLN of CD19<sup>-/-</sup> mice nevertheless traffic to the  
398 infected CNS, as observed in CXCL13<sup>-/-</sup> mice (21). Measurement of virus-specific  
399 IgG ASC by ELISPOT revealed similar frequencies at day 14 p.i. when  
400 comparing brain or spinal cords of wt and CD19<sup>-/-</sup> mice, respectively (Fig. 5A).  
401 However, while frequencies in wt mice increased by day 21 p.i. and remained  
402 steady at day 28 p.i., they never increased in the CNS of CD19<sup>-/-</sup> mice. Overall,  
403 virus-specific ASC frequencies were significantly higher in spinal cords than  
404 brains in wt mice at day 21 and 28 p.i., consistent with their preferential  
405 accumulation at the site of persistence and elevated inflammation (48). The  
406 differences between ASC frequencies were therefore especially pronounced in  
407 spinal cords, amounting to an almost 10-fold disparity, whereas differences were  
408 only 3-4 fold in the brain (Fig. 5A). Similar to CLN, average spot sizes of virus-  
409 specific CD19<sup>-/-</sup> ASC were also reduced at days 21 and 28 p.i. compared to wt  
410 ASC, reflecting poor affinity maturation and differentiation. The paucity in virus-  
411 specific ASC in the brain was supported by direct analysis of supernatants from  
412 brain homogenates for virus-specific IgG2a Ab, the most abundant and protective

413 Ab isotype during JHMV infection (7, 49, 50). Compared to the progressive  
414 increase of virus-specific IgG2a from day 14 to 28 p.i. in wt mice, the levels were  
415 barely above background in CD19<sup>-/-</sup> mice (Fig. 5B).

416 To ascertain that CD19 deficiency affected overall ASC CNS migration  
417 independent of specificity we monitored accumulation of ASC via expression of  
418 mRNA encoding IgG and IgM heavy chains, which are expressed highly in ASC  
419 compared to non Ab secreting B cells (8). Both brains and spinal cords of  
420 infected wt mice exhibited a significant increase in IgG heavy chain mRNA by 14  
421 days p.i., which was further elevated at days 21 through 28 p.i. (Fig 6A). As  
422 anticipated CD19<sup>-/-</sup> mice exhibited significantly decreased transcript levels  
423 throughout days 14 p.i. to 28 p.i. (Fig. 6A). Although a slight trend towards  
424 elevated transcript levels was noted in spinal cords, the levels at day 28 p.i. did  
425 not even reach those of wt mice at day 14 p.i. To delineate potential factors  
426 abrogating accumulation of ASCs within the CNS of CD19<sup>-/-</sup> mice, we used flow  
427 cytometry to assess CXCR3 expression on CD138<sup>+</sup> ASCs in the CLN (Fig. 6B).  
428 CXCR3 is upregulated by IFN $\gamma$  and essential in driving ASC migration to and  
429 entry into the CNS parenchyma (11). CD19<sup>-/-</sup> mice expressed significantly  
430 reduced frequencies of CXCR3<sup>+</sup> ASCs in the CLN throughout infection, with  
431 differences most prominent at day 14 p.i. (Fig. 6B). However, the mean  
432 fluorescent intensity (MFI) of CXCR3<sup>+</sup> was similar between wt and CD19<sup>-/-</sup> ASCs  
433 (Fig. 6C). These data suggest that there is no inherent deficit in the ability of  
434 CD19<sup>-/-</sup> ASCs to express CXCR3. Similarly to CXCR3, CXCR4 is upregulated  
435 during ASC differentiation (11, 51). Interactions with its ligand, CXCL12, are

436 important in mediating ASC homing to, and retention within, the BM (47, 51).  
437 CD19<sup>-/-</sup> mice also demonstrated a significant reduction in the frequency of ASCs  
438 expressing CXCR4 in the CLN, beginning at day 14 p.i. and continuing  
439 throughout infection (data not shown). As was the case with CXCR3, the MFI of  
440 CXCR4 on ASCs did not differ between wt and CD19<sup>-/-</sup> mice (data not shown).

441 We further assessed how CD19 deficiency affects overall B cell  
442 recruitment using CD45<sup>hi</sup> and B220 as expression markers of infiltrating B cells.  
443 There were no differences in total CNS cell yields or frequencies of CD45<sup>hi</sup>  
444 infiltrating bone marrow derived cells. CD8<sup>+</sup> and CD4<sup>+</sup> T cells were also similar  
445 between the groups (data not shown), confirming no overall deficits in leukocyte  
446 trafficking to the CNS. Although a ~40% reduction in the frequency of B220<sup>+</sup> B  
447 cells in the CNS was noted at 7 days p.i., frequencies were similar to wt mice by  
448 days 14 and 21 (Fig. 7). Moreover, ~60% of B220<sup>+</sup> B cells expressed IgD<sup>+</sup> in both  
449 groups at days 7 and 14 p.i., indicating that a majority of these B cells are  
450 undifferentiated. By day 21 p.i., the proportions decreased similarly to ~25%.  
451 These results suggest that CD19 has a minor impact on migration of IgD<sup>+</sup> early-  
452 activated B cells into the CNS following JHMV infection, but specifically affects  
453 overall ASC accumulation at day 14 p.i. and thereafter.

454 **The deficit in CNS humoral immunity is associated with increased**  
455 **infectious virus balanced by reactivation of T cell responses**

456 The severe deficit in virus-specific ASC and antiviral IgG2a in the CNS of  
457 JHMV-infected mice predicted loss of virus control during the persistent phase of  
458 infection, which requires local ASC (7, 49, 50, 52). Infectious virus load was

459 similar and even lower in the CNS of CD19<sup>-/-</sup> compared to wt mice at day 7 and  
460 14 p.i. (Fig. 8A), consistent with T cell-mediated control. However, whereas wt  
461 mice reduced infectious virus to below detection by day 21 p.i., it remained  
462 detectable between day 14 and 28 p.i. in the absence of CD19 (Fig. 8A). The  
463 inability to maintain effective virus control was confirmed by elevated, and even  
464 increasing, transcript levels of viral RNA encoding nucleocapsid protein in both  
465 brain and spinal cord comparing day 21 and 28 p.i. (Fig. 8B), although the  
466 increase was modest. Importantly however, mice also did not show signs of  
467 increased clinical disease (data not shown), distinct from mice totally deficient in  
468 virus specific Ab production, in which vastly increasing virus is associated with  
469 worsening clinical disease (52-54). Although T cells did not increase in the CNS  
470 during persistence in CD19<sup>-/-</sup> mice (data not shown), we assessed reemergence  
471 of T cell effector activity to explain partial ongoing viral control during persistence.  
472 IFN $\gamma$  is the most critical cytokine essential for JHMV control (5, 55, 56). IFN $\gamma$   
473 transcripts peaked to similar levels at day 7 p.i. in both the brain and spinal cord  
474 of CD19<sup>-/-</sup> and wt mice, confirming effective T cell stimulation by virus Ag  
475 presentation (Fig. 8C). IFN $\gamma$  mRNA levels dropped by days 10 and 14 p.i.  
476 coincident with viral control and were similarly low in both groups at day 21 p.i.,  
477 implying minimal *in vivo* stimulation and antiviral T cell activity. However, by day  
478 28 p.i. IFN $\gamma$  mRNA levels were significantly elevated in both brains and spinal  
479 cords of CD19<sup>-/-</sup> mice. These results indicated that elevated persisting viral load  
480 triggers retained or reemerging T cells to produce IFN $\gamma$  and exert antiviral  
481 activity.

482 To provide evidence for reemergence of other T cell functions as well as  
483 IFN $\gamma$ -dependent activities, both brains and spinal cords were temporally  
484 screened for expression of factors associated with increased T cell function (Fig.  
485 9). IL-21 not only enhances B cell differentiation in CLN, but also enhances and  
486 prolongs CD8 T cell function within the CNS (10). While IL-21 was similarly  
487 regulated in the CNS of wt and CD19<sup>-/-</sup> mice out to day 14 p.i., it was sustained  
488 and even increased in both brain and spinal cord of CD19<sup>-/-</sup> compared to wt mice  
489 during persistence, reaching statistically significant differences by day 28 p.i.  
490 Surprisingly, transcript levels of the lymphoid chemokine CXCL13, which  
491 regulates migration of IL-21 expressing CXCR5<sup>+</sup> T cells was also notably  
492 elevated at day 28 p.i. in the CNS of CD19<sup>-/-</sup> mice. Increased functional IFN $\gamma$   
493 activity in the CNS of CD19<sup>-/-</sup> mice *in vivo* was supported by elevated IFN $\gamma$   
494 inducible *Tnfsf13b* and *cxcl9* mRNA relative to wt mice, specifically at day 28 p.i.  
495 By contrast, *C3* mRNA as an activation marker peaked in the brain at day 7, and  
496 was only marginally increased at day 28 p.i. in the absence of CD19.  
497 Surprisingly, spinal cords revealed increasing *C3* mRNA levels throughout  
498 persistence on both groups. Lastly, *IL-10* mRNA, expressed most prominently by  
499 CD4 T cells during JHMV infection (57), peaked in both groups and organs at  
500 day 7 p.i., and declined during persistence, but was sustained at higher levels in  
501 CD19<sup>-/-</sup> mice, indicative of elevated regulatory T cell activity (58, 59). Assessment  
502 of the CCR7 binding lymphoid chemokines CCL19 and CCL21, known to be  
503 expressed in the inflamed CNS (60), revealed surprisingly distinct patterns  
504 between wt and CD19<sup>-/-</sup> mice. Compared to wt mice, CCL19 mRNA was

505 consistently elevated in brains of CD19<sup>-/-</sup> mice throughout infection, whereas it  
506 was mainly increased at day 28 in spinal cords. Unexpectedly, *CCL21* mRNA  
507 levels were vastly increased at basal levels in the CNS of CD19<sup>-/-</sup> mice, but  
508 remained unaltered by infection, similar to naïve wt mice. Overall the data imply  
509 that re-triggering of T cell activity by elevated virus replication in settings of  
510 impaired humoral immunity potentially contributes to steady-state viral control  
511 during JHMV persistence.

512 **Discussion**

513 A variety of human viral CNS infections, including those caused by  
514 measles, mumps, rubella, polio, varicella zoster, herpes simplex and Japanese  
515 encephalitis virus (JEV), are characterized by intrathecal Ab in the cerebral spinal  
516 fluid (CSF), consistent with local ASC (2, 61-64). Overall Ab detection is more  
517 transient in cases of acute encephalitis, but persists during chronic disease such  
518 as measles virus-associated subacute sclerosing panencephalitis (65, 66).  
519 Although the role of intrathecal humoral responses in humans is difficult to  
520 assess, they correlate with protective functions during JEV encephalitis (67),  
521 CNS retrovirus infection (68-70) and HTLV-I-associated myelopathy  
522 (70). Experimental CNS infections in rodents support an essential local  
523 protective role of ASC, as evidenced by infections established by Sindbis, rabies,  
524 and neurotropic coronaviruses (3, 11, 54, 71-75). Sustained Ab output by local  
525 ASC provides a potent non-lytic mechanism of immune control potentially  
526 beneficial for a variety of neurotropic infections prone to persist. However, little is  
527 known about peripheral activation signals and the necessity of GC formation in  
528 regulating B cell migration and accumulation to the CNS.

529 Expression of the lymphoid chemokines CXCL13 and CCL19/21 within the  
530 CNS has been associated with formation of ectopic follicle-like structures  
531 harboring multiple B cell differentiation phenotypes giving rise to *de novo* local Ab  
532 production (76-78). Upregulation of B cell survival factors (8, 79, 80) is thought to  
533 contribute to clonal B cell expansion and local humoral responses distinct from  
534 those occurring systemically. However, follicle-like structures have not been

535 observed in experimental viral encephalomyelitis (12, 81) suggesting activation  
536 and GC formation in draining lymphoid organs imprints activated B cells for  
537 migration to the inflamed site. As CD19 is a key signaling component initiating B  
538 cell activation as well as driving GC formation, we assessed the relevance of  
539 CD19 in humoral responses to neurotropic JHMV infection. As anticipated,  
540 based on sparse peripheral replication and consequently Ag load (82), GC  
541 formation was significantly impaired in the absence of CD19. Despite induction of  
542 virus-specific serum IgG and neutralizing Ab, both IgM and IgG responses were  
543 overall reduced and not sustained. Reduced anti-virus serum Ab, lower virus-  
544 specific ASC and very scant accumulation of IgG ASC in BM are consistent with  
545 lesser differentiation and longevity of isotype-switched CD19<sup>-/-</sup> ASC compared to  
546 wt ASC.

547         Contrasting scant migration to BM, virus-specific ASC trafficking to the  
548 CNS was initially similar to wt mice. However, their ongoing accumulation was  
549 significantly impaired after day 14 p.i. The more prominent defect in spinal cord  
550 reflects the overall enhanced ASC accumulation in spinal cord relative to brain  
551 associated with increased and sustained expression of ASC promoting factors  
552 (Fig. 9), as shown previously in wt mice (48). Initial recruitment of virus-specific  
553 ASC to the CNS, but not BM, supports the notion that CXCR3 driven recruitment  
554 to the inflamed site overrides CXCR4 driven recruitment to BM (46). Similar  
555 CXCR3 expression levels on CD19<sup>-/-</sup> vs wt ASC in CLN, irrespective of their low  
556 numbers, implies that defective progressive accumulation of ASC is due to their  
557 less differentiated, short-lived phenotype as a result of impaired GC formation,

558 rather than an inherent defect in migration or ASC promoting factors in the CNS  
559 of CD19<sup>-/-</sup> mice.

560 JHMV infection of CXCL13<sup>-/-</sup> mice also revealed impaired GC formation  
561 with reduced frequencies of GL7<sup>+</sup> B cells (24). Nevertheless, distinct from CD19<sup>-/-</sup>  
562 mice, virus-specific serum Ab responses were not significantly impaired  
563 throughout day 21 p.i., consistent with similar ASC in BM and only slightly  
564 reduced ASC in CLN. Although ASC in the CNS were reduced by 50% in  
565 CXCL13<sup>-/-</sup> mice they were sufficient to control persisting viral RNA. Potential  
566 differences may reside in lymphoid structure. While CXCL13<sup>-/-</sup> mice are devoid of  
567 most lymph nodes, they retain cervical lymph nodes (45). However, the absence  
568 of B cell follicles and disrupted lymphoid architecture likely alters typical migration  
569 patterns. By contrast, CD19<sup>-/-</sup> mice exhibit normal lymphoid architecture with  
570 intact B cell follicles (34), which may put more restraints on CD4 T cell-B cell  
571 interactions. Irrespectively, the absence of CD19 leads to more severely impaired  
572 generation of protective ASC during JHMV infection compared to CXCL13<sup>-/-</sup>  
573 mice. An early defect in B cell activation was already noted by reduced overall  
574 expansion of ASC, prior to detection of virus-specific ASC. While the early  
575 increase in ASC was previously attributed to IFN $\alpha$ / $\beta$ -induced bystander activation  
576 similar to influenza virus and WNV (83, 84), our results implicate a role for CD19  
577 co-receptor activation via CD21 co-ligation by virus/C3d adducts. JHMV infection  
578 resulted in a robust increase of C3 mRNA in both CLN and the CNS. Viral  
579 Ag/C3d mediated activation of the BCR co-receptor can thus reduce the  
580 threshold for B cell activation in the periphery as well as the CNS, where

581 astrocytes, microglia, and potentially neurons and oligodendrocytes are likely  
582 sources of C3 (85-87). Surprisingly however, early-activated IgD<sup>+</sup> B cells  
583 recruited to the CNS were not altered by CD19 deficiency, suggesting BCR  
584 independent signals drive their trafficking to the CNS. *In vitro* stimulation to  
585 assess virus specificity in this population provided no evidence for these early B  
586 cells as precursors of ASC (88). The nature of signals driving IgD<sup>+</sup> B cells to the  
587 CNS during infection, as well as their role, thus remains to be determined, but  
588 likely involves TLR driven signals (89, 90).

589 The biological impact of significantly impaired ASC within the CNS was  
590 manifested by the inability of CD19<sup>-/-</sup> mice to control infectious virus during  
591 persistence. Surprisingly, elevated viral load triggered T cell re-activation as  
592 evidenced by reemerging IFN $\gamma$  mRNA in both brains and spinal cords. Biological  
593 IFN $\gamma$  function was directly reflected by coincidentally increased expression of IFN $\gamma$   
594 inducible CXCL9 and CXCL10 mRNA (8). Although retention of both CD4 and  
595 CD8 T cells in the CNS during persistence make them likely sources of IFN $\gamma$ , *de*  
596 *novo* recruitment of T cells cannot be excluded. In this context it is interesting to  
597 note that *IL-21* mRNA levels were also increased, suggesting IL-21 contributes to  
598 reinvigorating local CD8 T cell effector function (10). Together these data  
599 suggest that persisting viral replication in the absence of protective ASC is kept  
600 in check by reemerging T cell activity. The significantly higher constitutive levels  
601 of the CCR7 binding chemokine CCL21 in both the brain and spinal cord, but not  
602 CLN, of CD19<sup>-/-</sup> mice is also of interest. Elevated CCL21 mRNA was also noted  
603 in CXCL13<sup>-/-</sup> and CXCR3<sup>-/-</sup> mice (11, 24). Following infection with the JHMV

604 heterologous MHV-A59 strain, CCR7 ligands produced by CNS stromal cells  
605 were crucial to support recruitment and local re-activation of antiviral CD8+ T  
606 cells (91). The latter studies indicated that CNS stromal cells generate confined  
607 microenvironments that control T cell immunity and protect the host from lethal  
608 neuroinflammatory disease. Surprisingly CD19<sup>-/-</sup> mice did not exhibit increased  
609 clinical symptoms or disability at day 28.p.i., suggesting CNS pathology  
610 manifested in demyelination and axonal damage was not significantly worsened.  
611 Possible explanations reside in CCR7-mediated restraint of T cell function to  
612 perivascular spaces and or elevated protective IL-10. In summary, the effect of  
613 CD19 deficiency on JHMV-induced humoral responses was overall similar to  
614 reduced GC formation in peripheral infection models associated with limited viral  
615 antigen (26, 31). Moreover, the results are the first to demonstrate that protective  
616 ASC in the CNS are dependent on CD19 activation. By contrast, CD19-  
617 independent accumulation of early recruited IgD<sup>+</sup> B cells to the CNS suggests  
618 independent activation mechanisms drive the emergence of early versus more  
619 differentiated, isotype-switched B cells accumulating in the CNS as GCs are  
620 formed in the periphery. A better understanding of distinct B cell subsets in the  
621 CNS is essential to preempt reactivation of persistent viruses in the CNS during  
622 immune suppressive therapies (92, 93) as well as combat disease susceptibility  
623 to acute encephalitic arboviral infections.

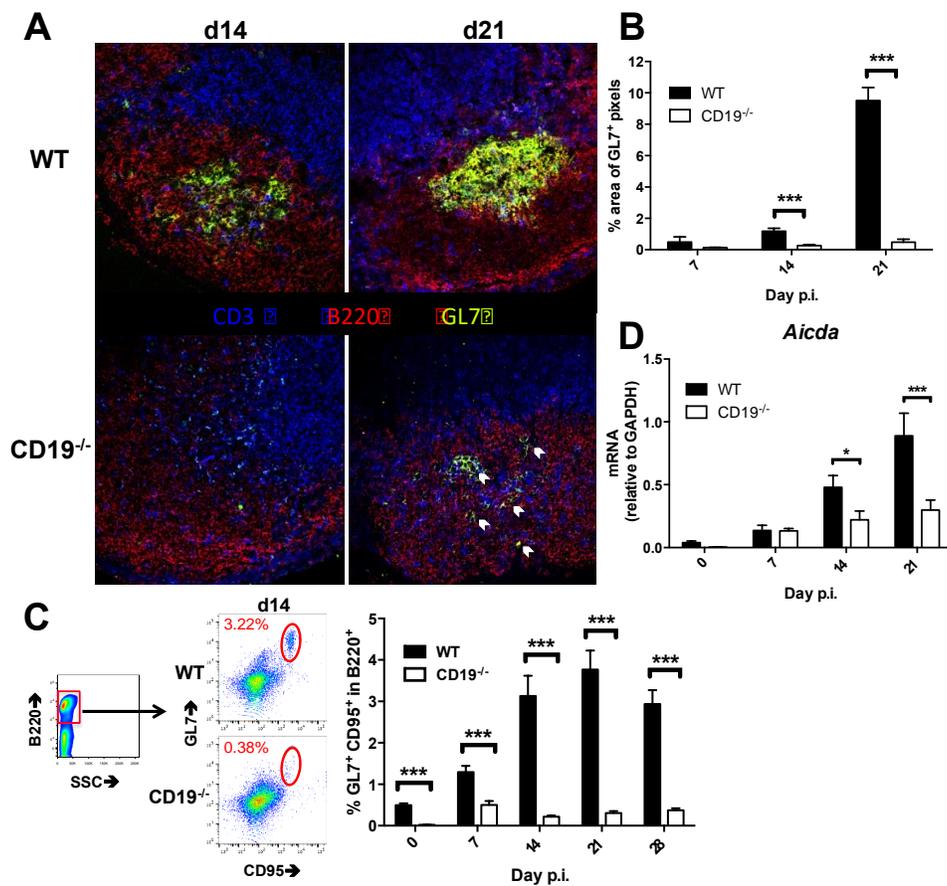
624 **Acknowledgements**

625 This work was supported by US National Institutes of Health grant NS086299.

626 The funding source had no involvement in the study design, writing of the

627 manuscript, decision to submit, or collection, analysis, and interpretation of data.

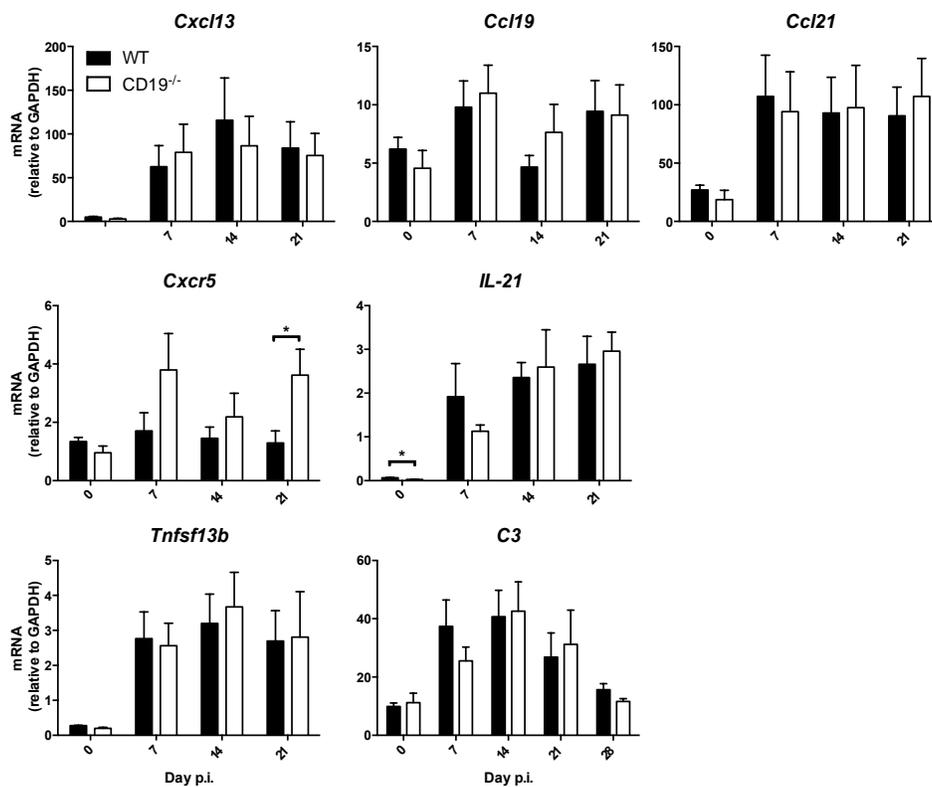
628 We sincerely thank Dr. Mi-Hyun Hwang for viral CNS infection.



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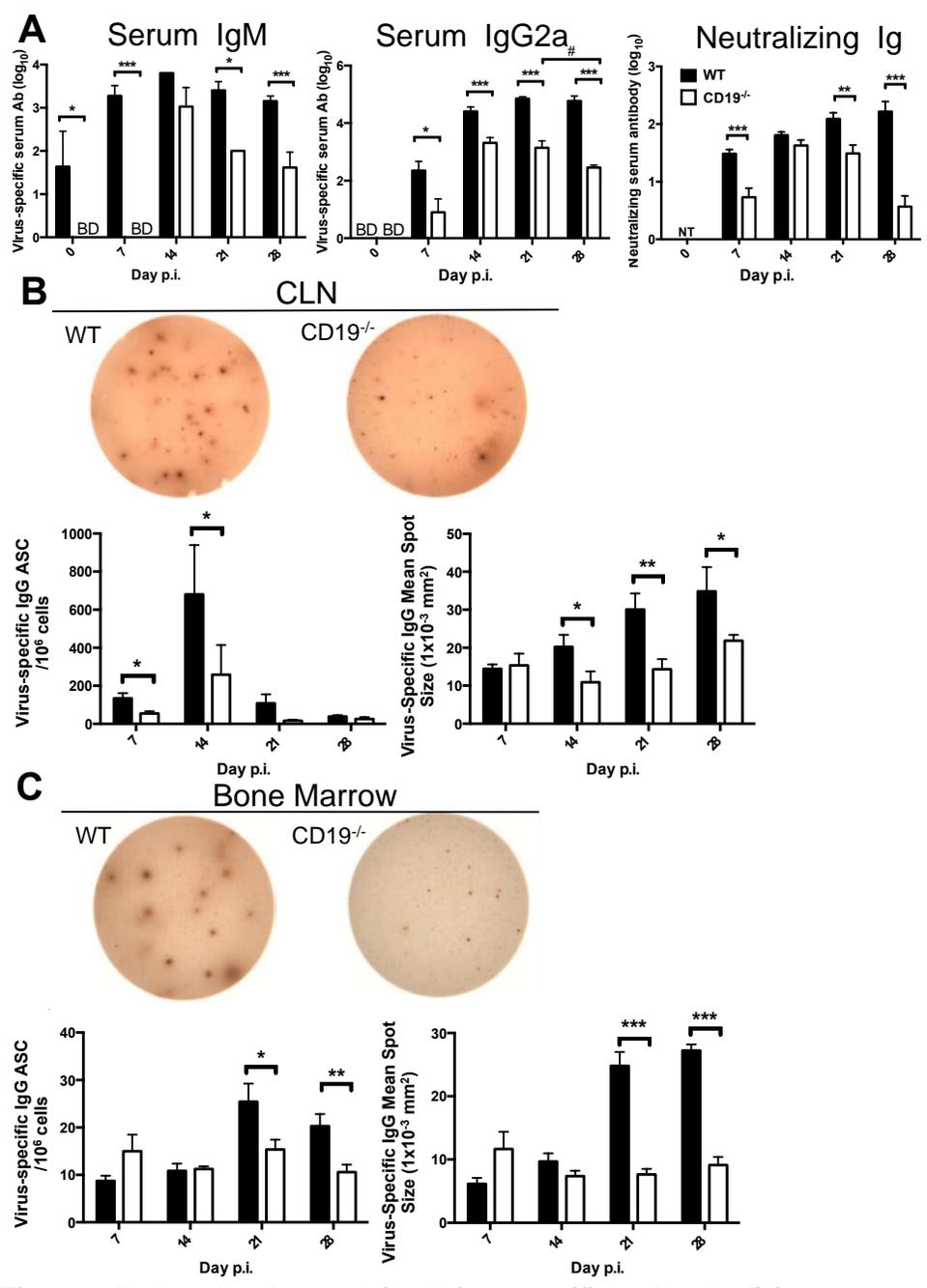
630 **Figure 1. Infected CD19<sup>-/-</sup> mice exhibit diminished GC in CLN.** WT and CD19<sup>-/-</sup>  
 631 <sup>-/-</sup> mice were infected with sublethal JHMV and CLN harvested at indicated times  
 632 for histology, flow cytometric analysis and gene expression. A) Representative  
 633 images of fluorescent immunohistochemistry performed at days 14 and 21 p.i..  
 634 Sections were stained for T cells (CD3, blue), B cells (B220, red), and activated  
 635 GC B cells (GL7, green). Images were taken at 40x magnification. B) Percentage  
 636 of pixels per image frame resulting from GL7<sup>+</sup> staining in CLN follicles. Bars  
 637 represent the mean percentage  $\pm$  SEM of GL7<sup>+</sup> pixels per frame from 2-3 frames  
 638 per mouse from 2-6 mice per time point. C) Flow cytometry of CLN suspensions  
 639 stained for B220, GL7, and CD95, and gated as indicated. The bar graph shows  
 640 percentages of GL7<sup>+</sup> CD95<sup>+</sup> cells within total B cells over time. Data represent  
 641 the mean  $\pm$  SEM of 2-4 individual mice per time point per group from 4 separate  
 642 experiments. D) CLN tissue was assessed for *Aicda* RNA transcript levels by rt-  
 643 PCR over time. Data represent the mean  $\pm$  SEM transcript levels relative to  
 644 *gapdh* mRNA of individual mice from 2 separate experiments, each comprising 3-

645 5 individual mice per time point and group. Statistically significant differences  
646 between wt and CD19<sup>-/-</sup> mice denoted by \*p < 0.05, \*\*\*p < 0.001.



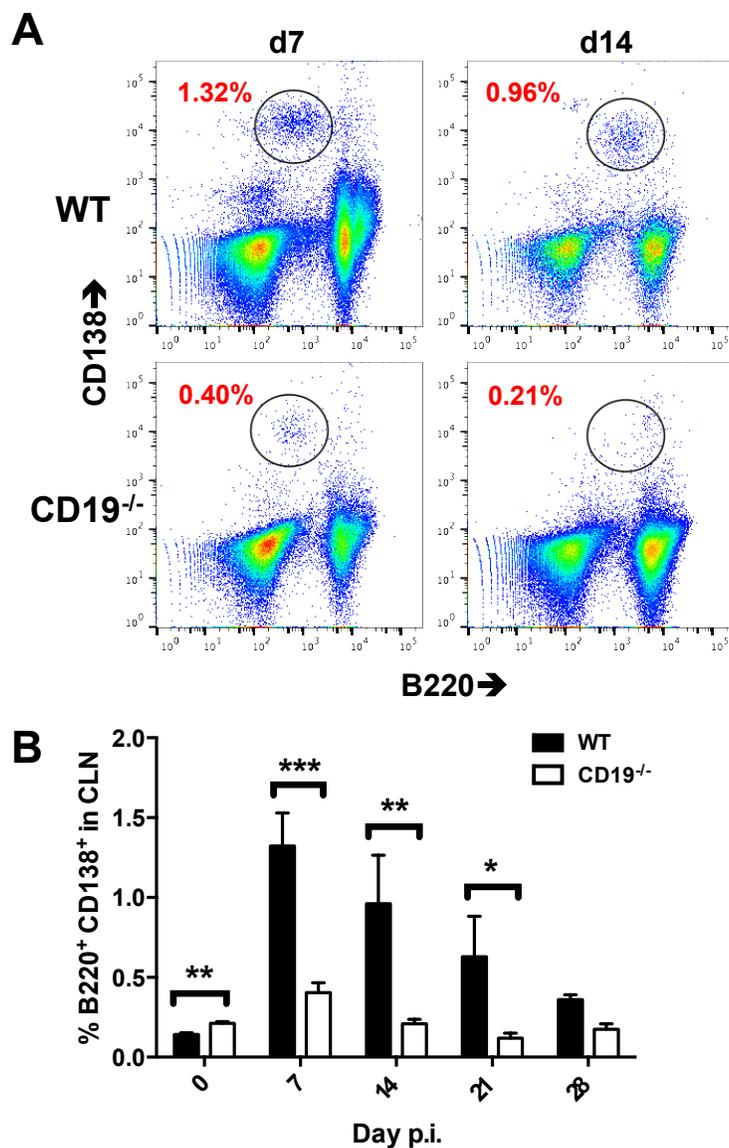
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**Figure 2. CD19 deficiency does not impair expression of factors promoting GC formation within CLN.** CLN harvested from infected wt and CD19<sup>-/-</sup> mice at the indicated times p.i. were analyzed for mRNA expression levels of *Cxcl13*, *Ccl19*, *Ccl21*, *Cxcr5*, *Il-21*, *Tnfsf13b* (BAFF), and complement *C3*. Data represent the mean  $\pm$  SEM transcript levels relative to *gapdh* mRNA of individual mice from 2 separate experiments, each comprising 3-5 individual mice per time point and group. Statistically significant differences between wt and CD19<sup>-/-</sup> mice, determined by unpaired *t* test, are denoted by \**p* < 0.05, \*\**p* < 0.01.



656  
 657 **Figure 3. Reduced and unsustainable virus-specific and neutralizing serum**  
 658 **Ab coincides with decreased virus-specific ASC in the absence of CD19. A)**  
 659 **Virus-specific IgM, IgG, and neutralizing Ab in sera of uninfected (Day 0 p.i.) and**

660 infected mice at indicated times p.i. CLN (B) and bone marrow (C) were analyzed  
661 for virus specific IgG ASC by ELISPOT. Representative wells are shown for CLN  
662 at day 14 and bone marrow (BM) at day 21 p.i.. Graphs show frequencies of  
663 virus-specific IgG ASC spots and spot diameter. Data represent the mean  $\pm$  SEM  
664 of individual mice from 3 separate experiments, each comprising 2-4 individual  
665 mice per time point and group. Statistically significant differences between WT  
666 and CD19<sup>-/-</sup> mice, determined by unpaired t test, are denoted by \*p < 0.05, \*\*p <  
667 0.01, \*\*\*p < 0.001. Significant differences between time-points within the same  
668 group are denoted by # p < 0.05.  
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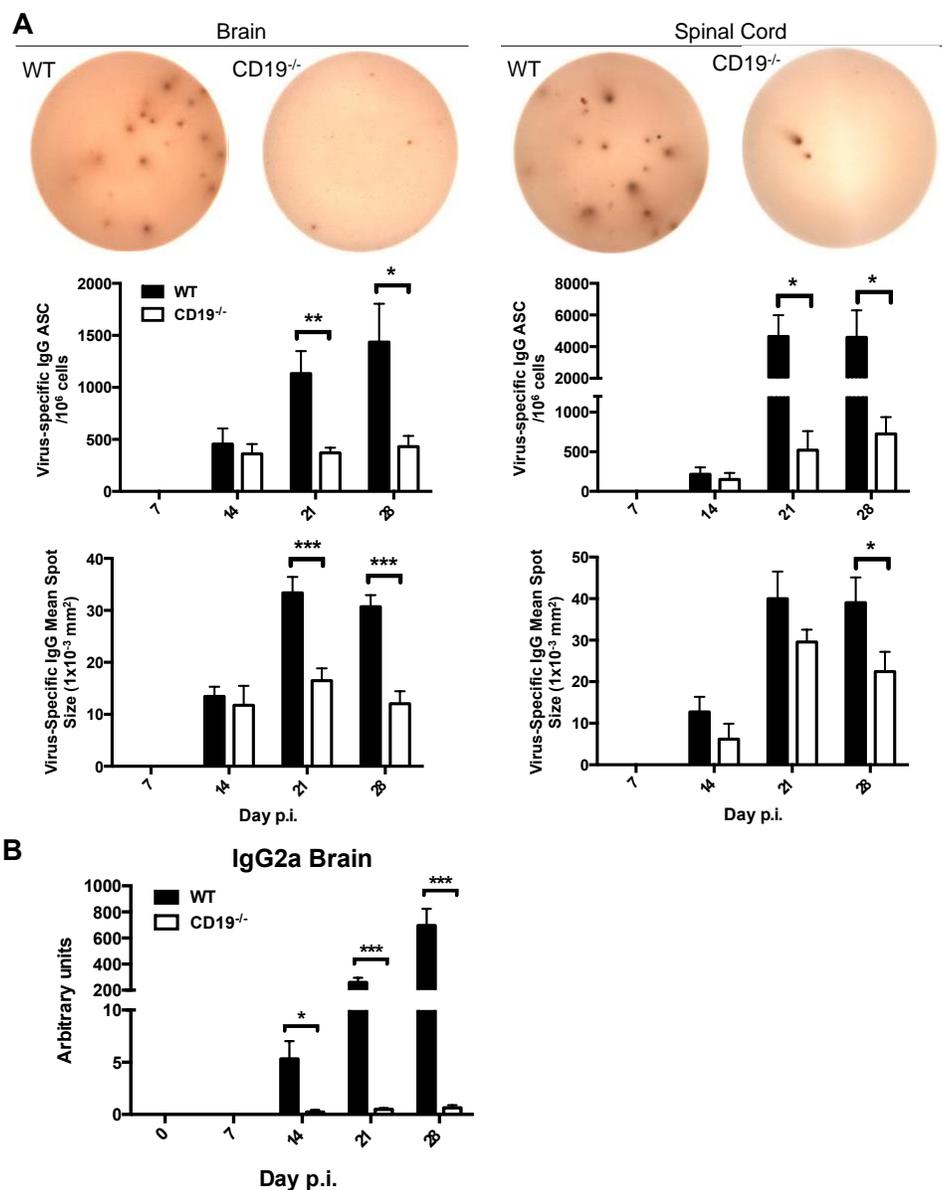


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671 **Figure 4. CD138<sup>+</sup> ASCs are decreased in CLN of CD19<sup>-/-</sup> mice following**  
 672 **infection.** Pooled CLN cells from infected wt and CD19<sup>-/-</sup> mice (n=2-3 mice per  
 673 time point per group from 3 separate experiments) were stained for B220 and the  
 674 ASC marker CD138. A) Representative density plots depicting CD138<sup>+</sup> and  
 675 B220<sup>+</sup> B cells at 7 and 14 days p.i. (gated on live cells). Numbers represent  
 676 percentages of CD138<sup>+</sup> B220<sup>+</sup> ASCs within total cells. B) The bar graph shows  
 677 mean  $\pm$  SEM. percentages of CD138<sup>+</sup> B220<sup>+</sup> ASCs within total CLN cells over

678 time. Statistically significant differences between wt and CD19<sup>-/-</sup> mice are  
679 denoted by \*p < 0.05, \*\*\* p < 0.001.  
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685 **Figure 5. Virus-specific ASC and Ab are severely decreased in the CNS of**686 **CD19<sup>-/-</sup> mice.** A) Brain and spinal cord of infected wt and CD19<sup>-/-</sup> were analyzed

687 for virus-specific IgG ASC by ELISPOT. Representative wells are shown from

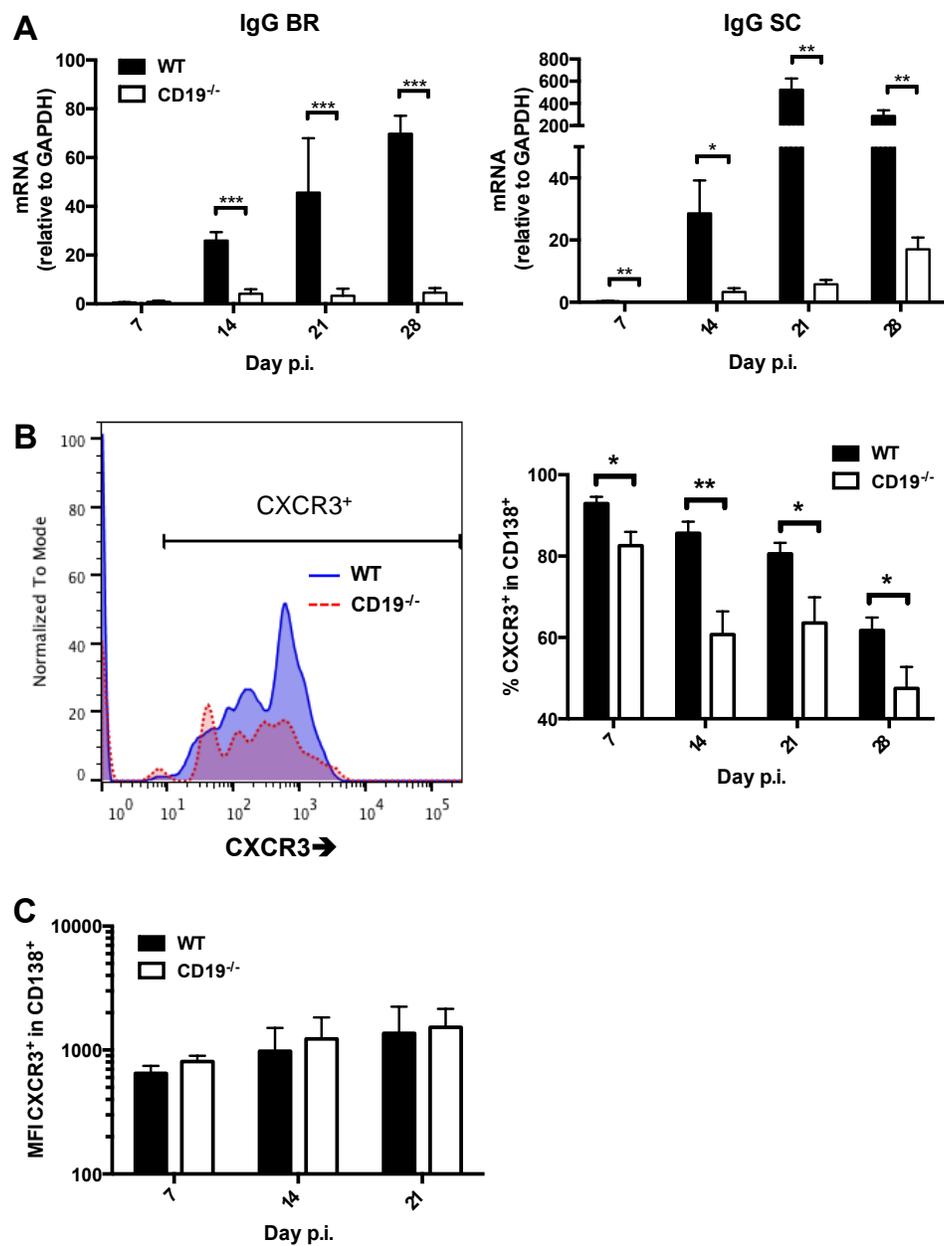
688 day 28 p.i.. Graphs show frequencies of virus-specific IgG ASC spots as well as

689 spot diameter. Statistically significant differences between WT and CD19<sup>-/-</sup> mice

(n=individual brains and pooled spinal cords from 2-6 mice per group per time

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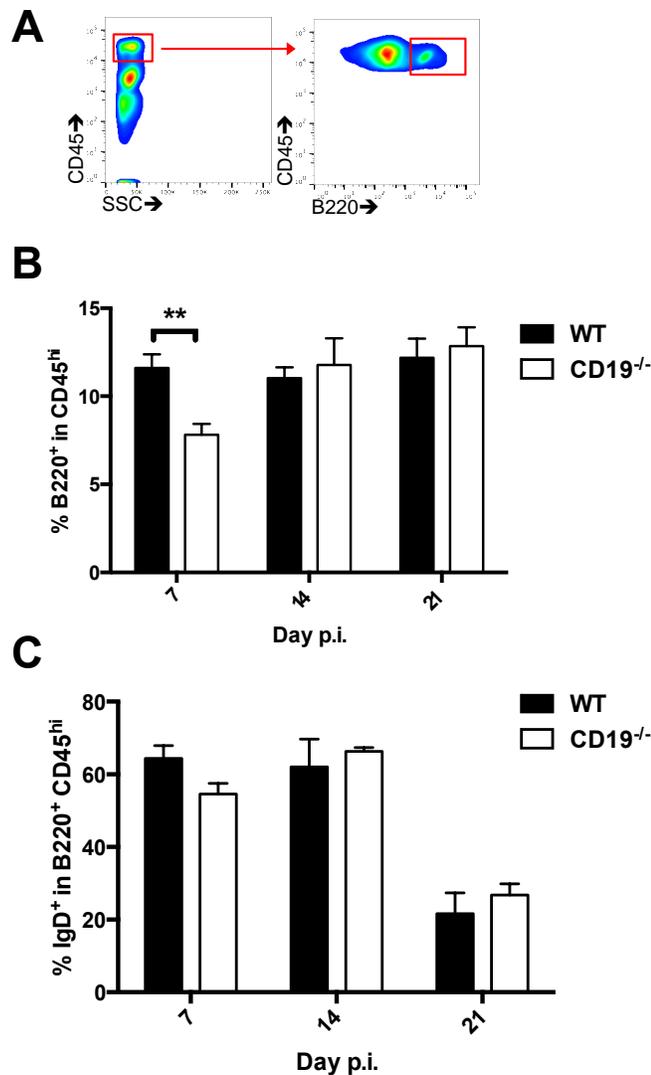
690 point from 4 separate experiments), determined by unpaired *t* test, are denoted  
691 by \**p* < 0.05, \*\* *p* < 0.01, \*\*\* *p* < 0.001. B) Virus-specific IgG2a in brain  
692 supernatants. Individual titers from 2-6 mice per group per time point from 2  
693 separate experiments are shown. Statistically significant differences between WT  
694 and CD19<sup>-/-</sup> mice, determined by unpaired *t* test, are denoted by \**p* < 0.05, \*\* *p* <  
695 0.01, \*\*\* *p* < 0.001.  
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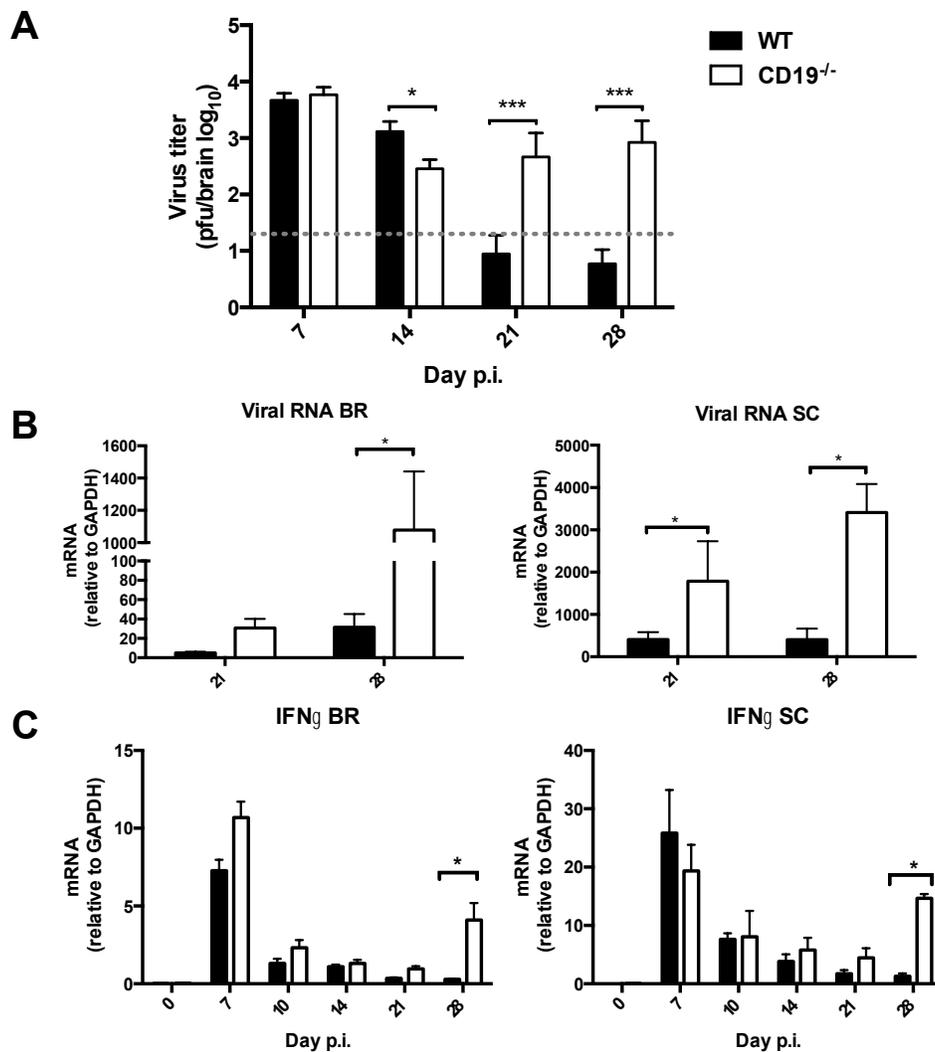
**Figure 6. Total CXCR3<sup>+</sup> ASC are reduced in CLN of CD19<sup>-/-</sup> mice.** A) Brains (BR) and spinal cords (SC) harvested from infected wt and CD19<sup>-/-</sup> mice at the indicated times p.i. were analyzed for expression of IgG heavy chain (*Ighg*) mRNA. Data represent the mean  $\pm$  SEM transcript levels relative to *gapdh* mRNA of individual mice from 2 separate experiments, each comprising 2-6 individual

703 mice per time point and group. B) CLN cells pooled from infected mice were  
704 stained for CD138 and CXCR3. Representative histograms gated on B220<sup>+</sup>  
705 CD138<sup>+</sup> ASCs at 21 days p.i. are shown for wt (blue, solid line) and CD19<sup>-/-</sup> mice  
706 (red, dotted line); the graph depicts mean  $\pm$  SEM percentages of CXCR3<sup>+</sup> cells  
707 within ASC (n= 2-4 individual mice per group per time point from 3 separate  
708 experiments). Statistically significant differences between WT and CD19<sup>-/-</sup> mice  
709 are denoted by \*p < 0.05, \*\*p < 0.01. C) Mean fluorescent intensity (MFI) of  
710 CXCR3<sup>+</sup> ASCs from cells depicted in B).  
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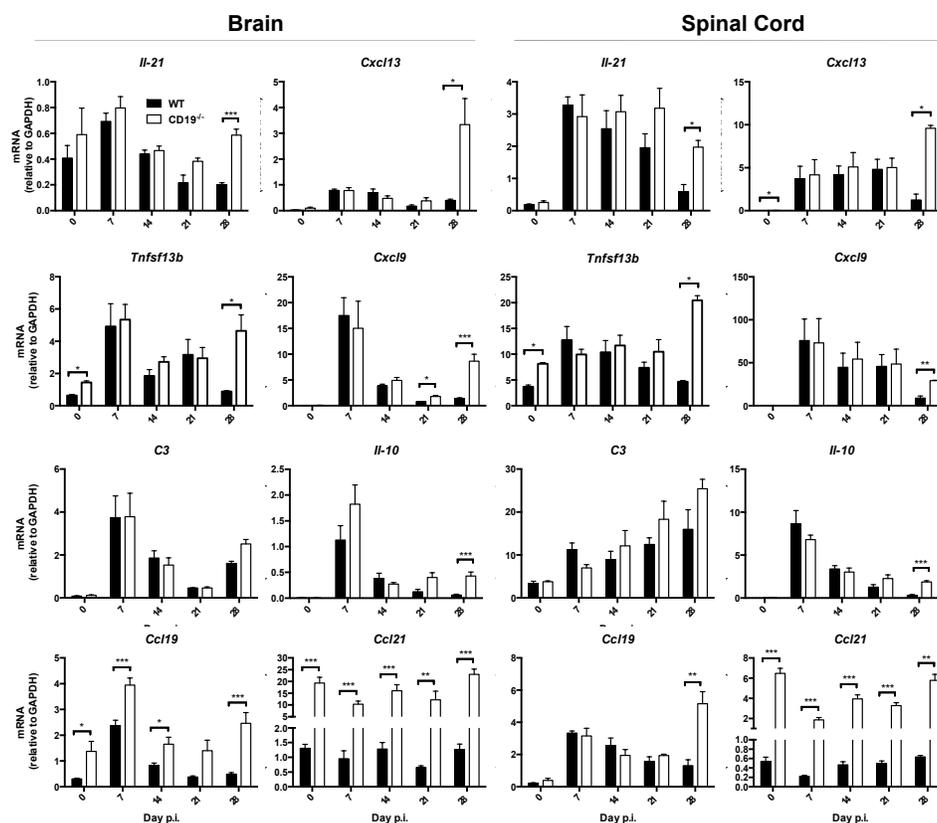
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**Figure 7. CD19 deficiency does not impair recruitment of IgD<sup>+</sup> B cells into the CNS.** Brains from infected wt and CD19<sup>-/-</sup> mice were analyzed for accumulation of total CD45<sup>hi</sup> expressing cells, as well as undifferentiated IgD<sup>+</sup> B220<sup>+</sup> B cells by flow cytometry. A) Representative density plots showing CD45 staining and side scatter (SSC) pattern and gating strategy for B220<sup>+</sup> cells within infiltrating CD45<sup>hi</sup> cells. Bar graphs depicts percentages of B220<sup>+</sup> cells within the CD45<sup>hi</sup> infiltrating population (B) and percentages of IgD<sup>+</sup> cells within CD45<sup>hi</sup> B220<sup>+</sup> B cells (C) over time. Data represent the mean  $\pm$  SEM of individual mice from 2 separate experiments, each comprising 2-4 individual mice per time point and group. Statistically significant differences between wt and CD19<sup>-/-</sup> mice are denoted by \*\*p < 0.01.



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**Figure 8. Impaired virus control associated with sparse local humoral immunity re-invigorates T-cell effector function.** A) Infectious virus within the brains of WT and CD19<sup>-/-</sup> mice (n= 2-6 mice per group per time point from 4 separate experiments) determined by plaque assay. Dashed line indicates limit of detection. Levels of viral RNA encoding nucleocapsid protein (B) and IFN $\gamma$  (C) in brains (BR) and spinal cords (SC) determined by real-time PCR. Data represent the mean  $\pm$  SEM transcript levels relative to *gapdh* mRNA of individual mice from 2-3 separate experiments, each comprising 2-6 individual mice per time point and group. Statistically significant differences between wt and CD19<sup>-/-</sup> mice, determined by unpaired *t* test, are denoted by \**p* < 0.05, \*\*\* *p* < 0.001.



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738 **Figure 9. CD19 deficiency leads to re-emergence of T cell associated**739 **functions.** Brains and spinal cords harvested from uninfected (Day 0 p.i.) and740 infected wt and *CD19<sup>-/-</sup>* mice at the indicated times p.i. were analyzed for mRNA

741 encoding cytokines and chemokines associated with regulation of humoral

742 responses. Data represent the mean  $\pm$  SEM transcript levels relative to *gapdh*

743 mRNA of individual mice from 2-3 separate experiments, each comprising 2-6

744 individual mice per time point and group. Statistically significant differences

745 between wt and *CD19<sup>-/-</sup>* mice, determined by unpaired *t* test, are denoted by \*p <

746 0.05, \*\*p &lt; 0.01, \*\*\* p &lt; 0.001.

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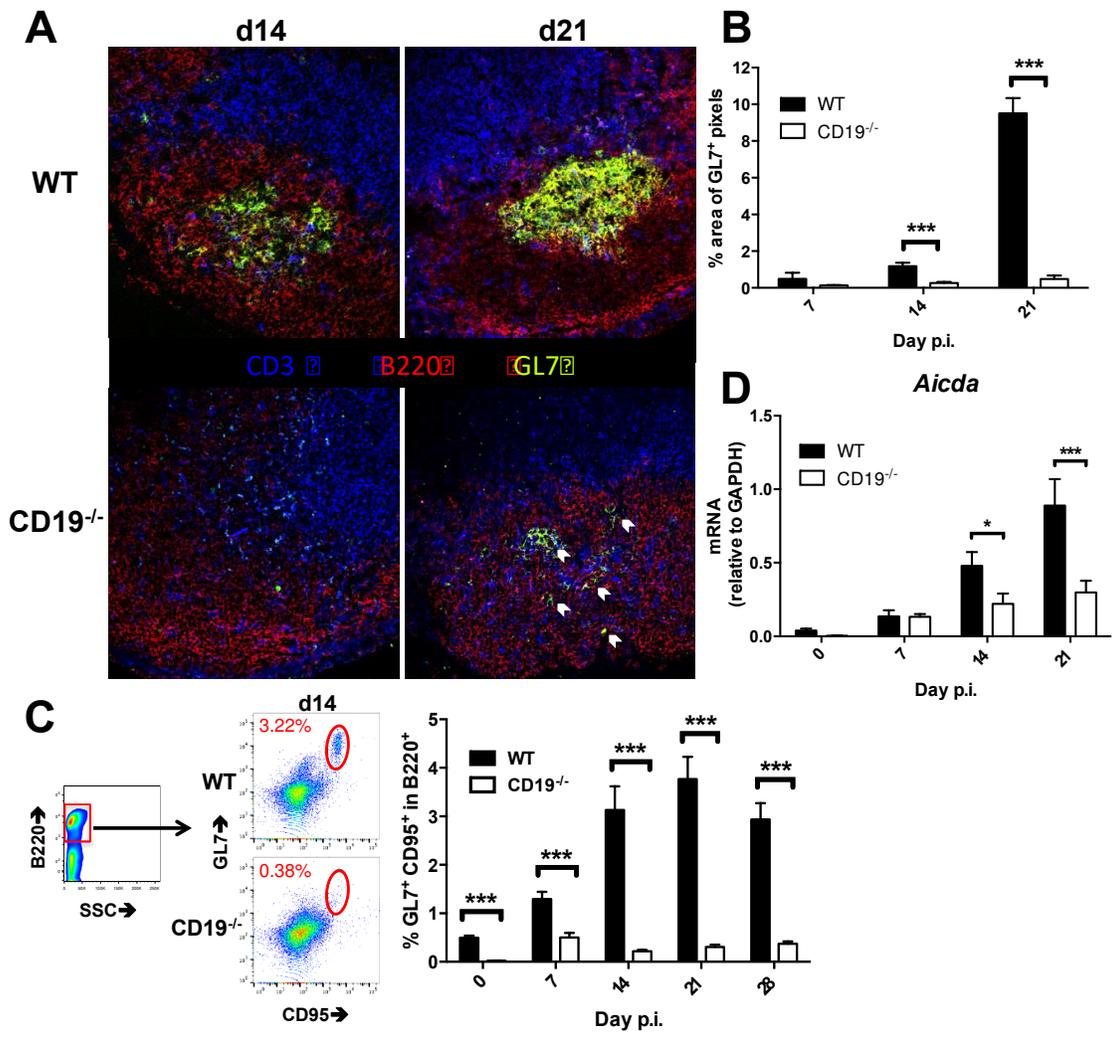
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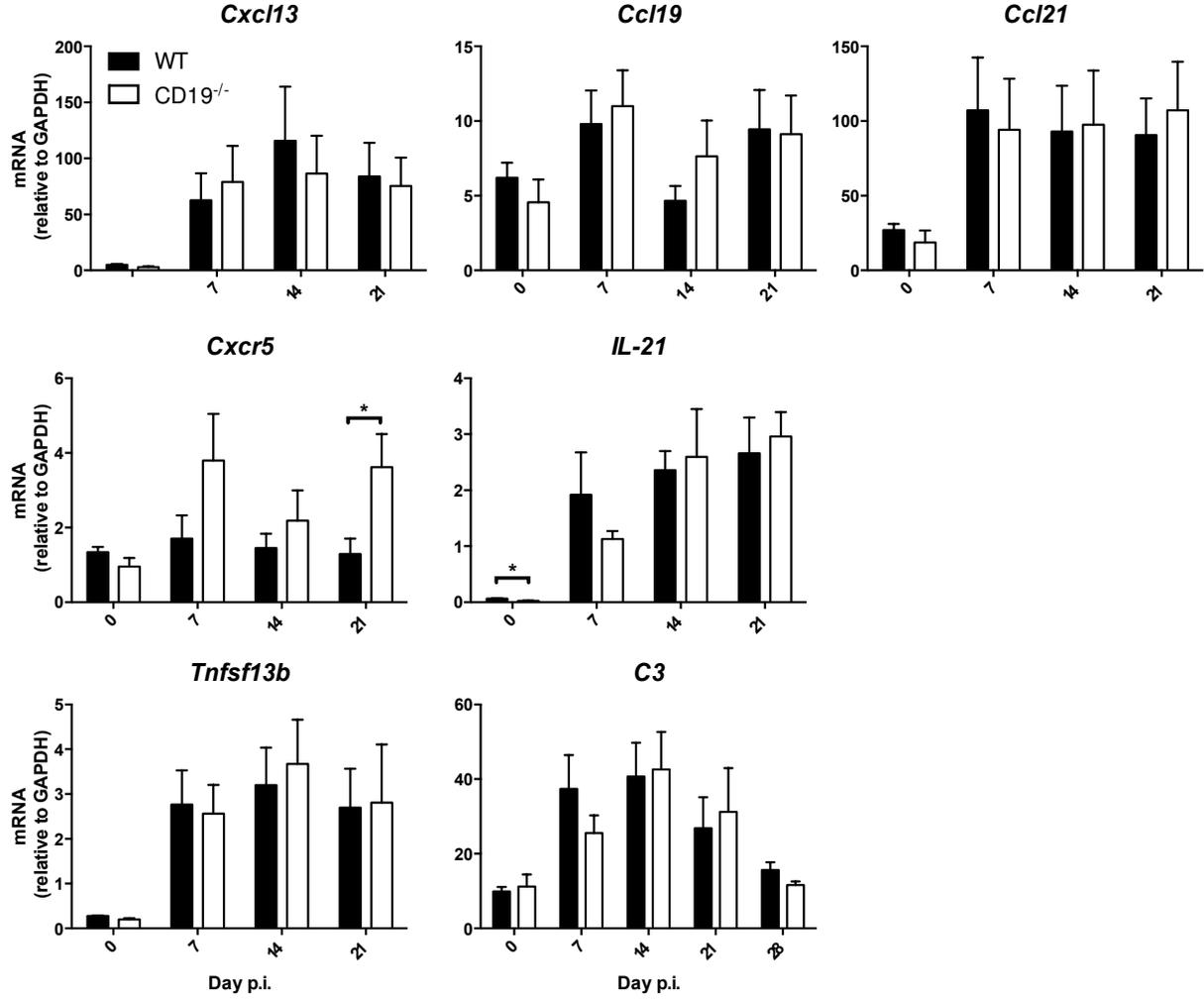
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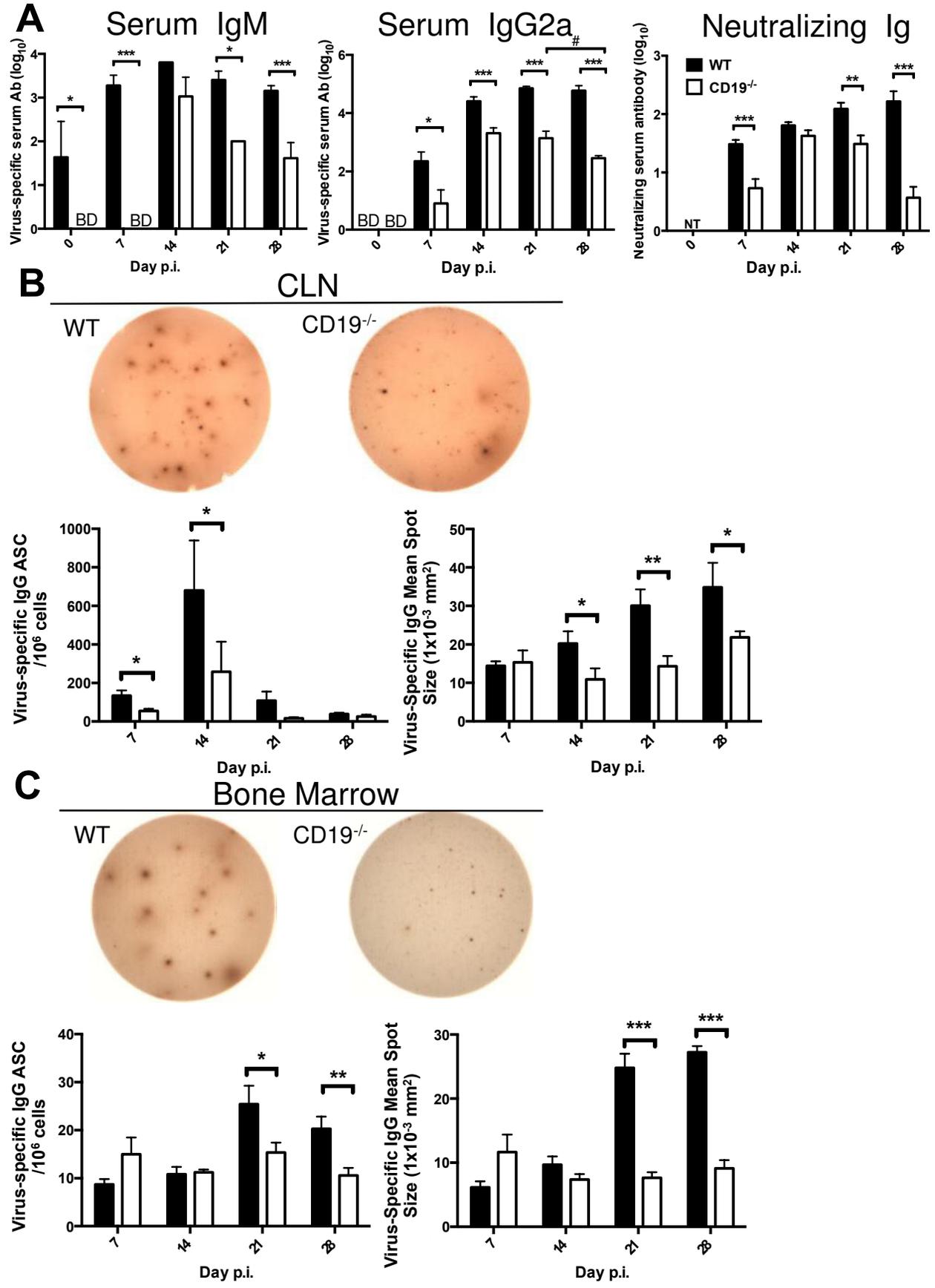
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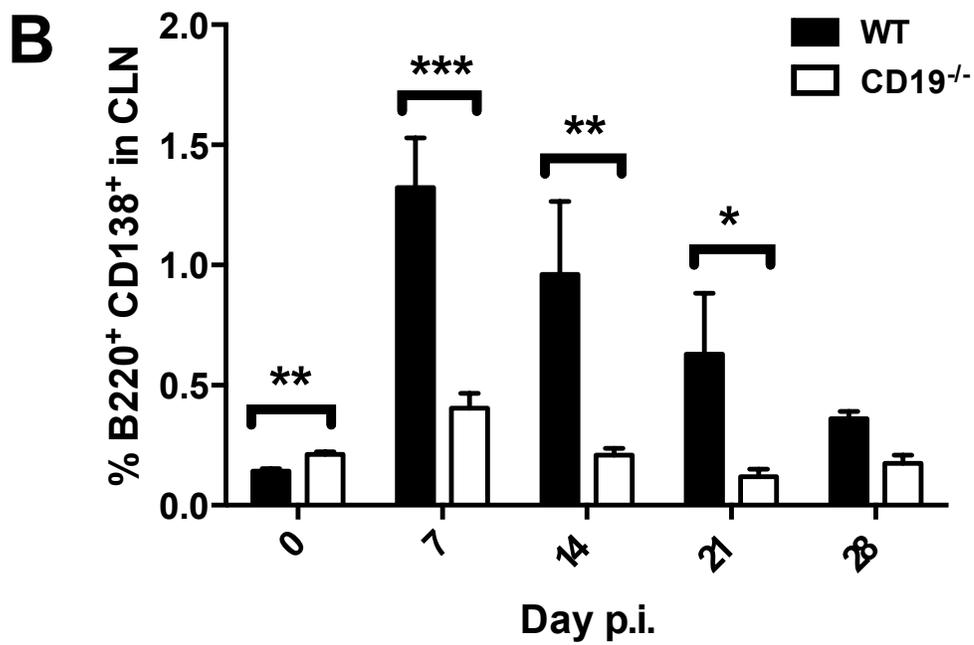
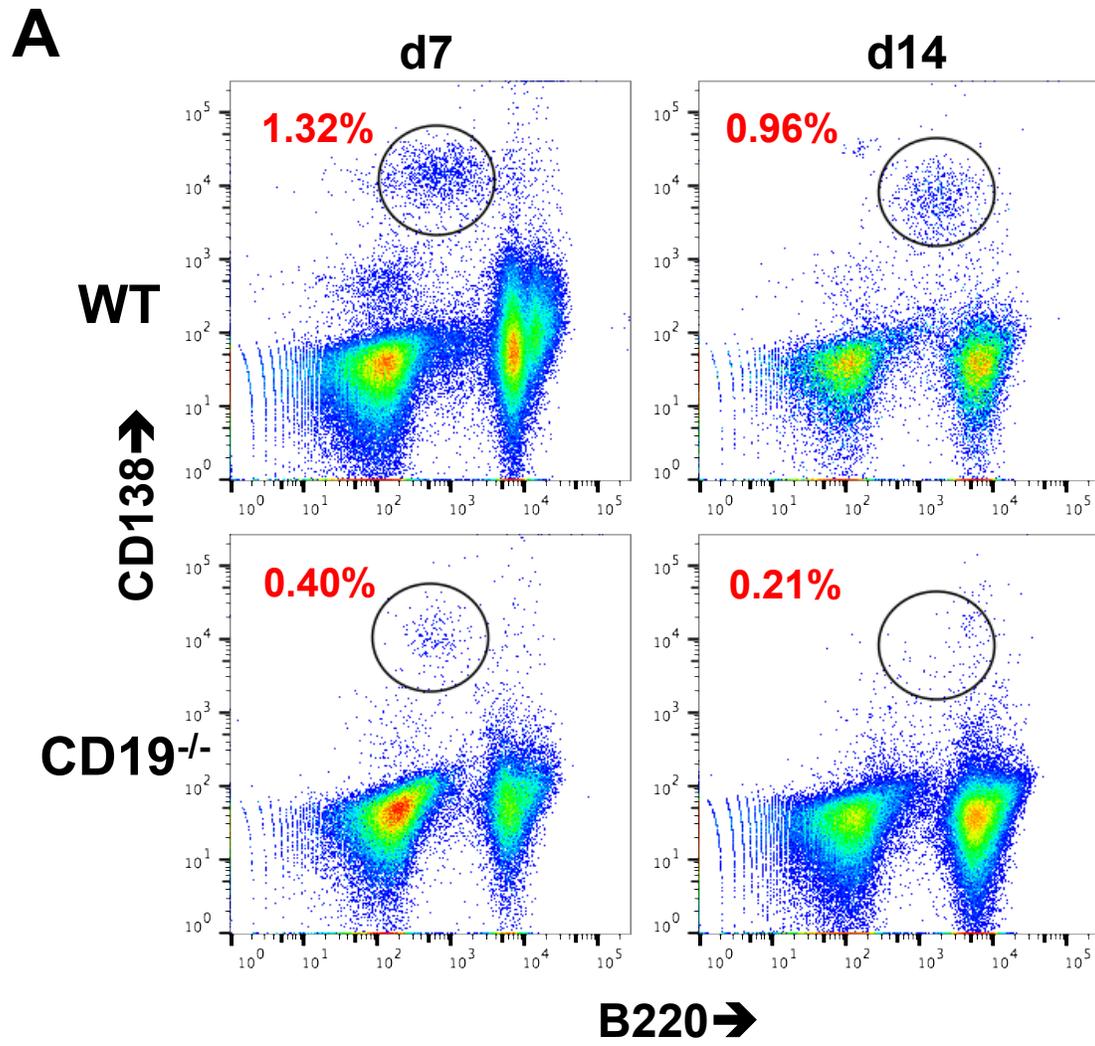
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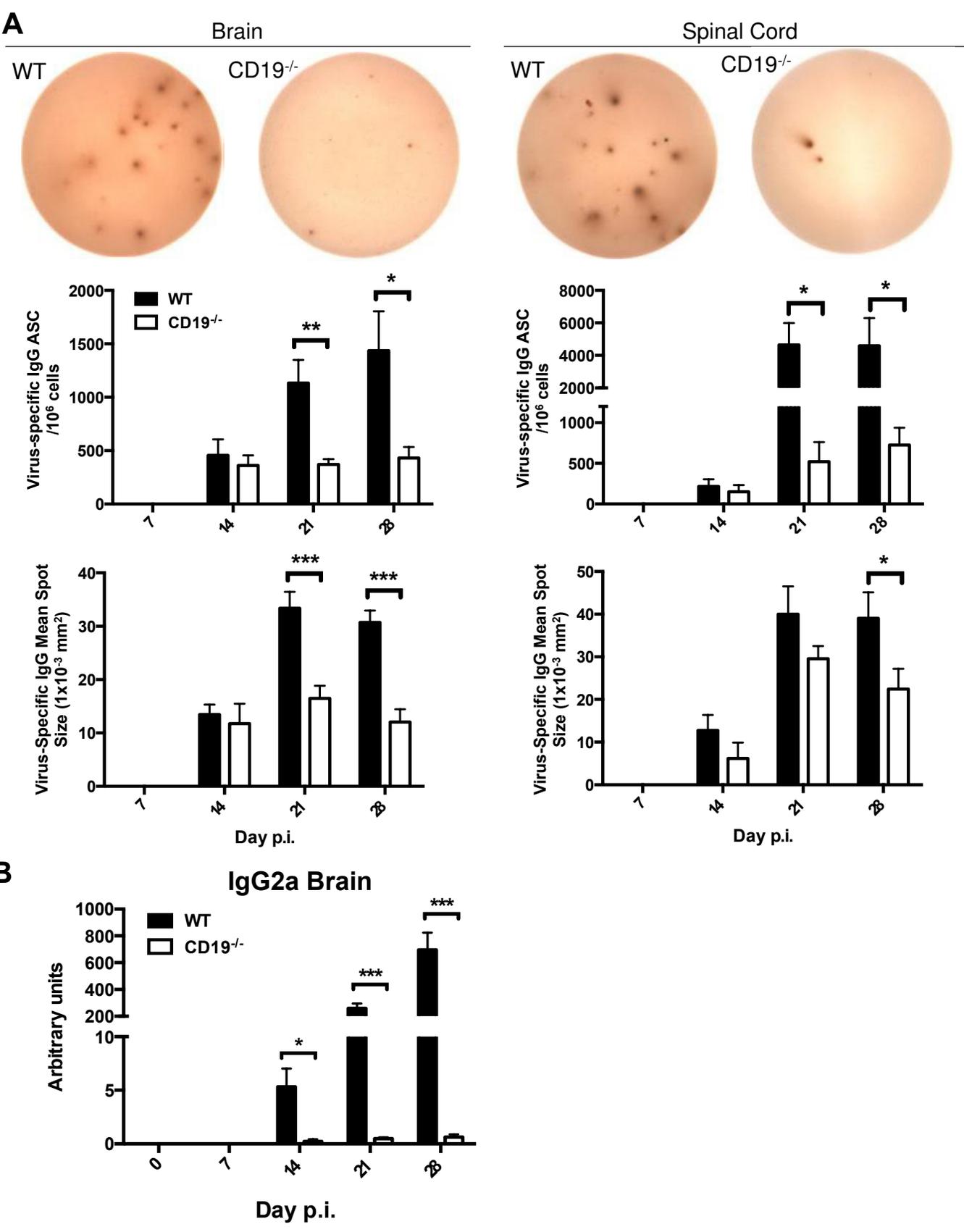
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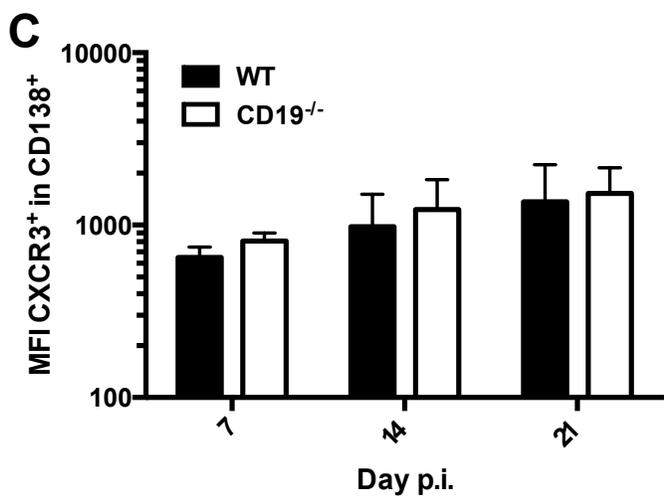
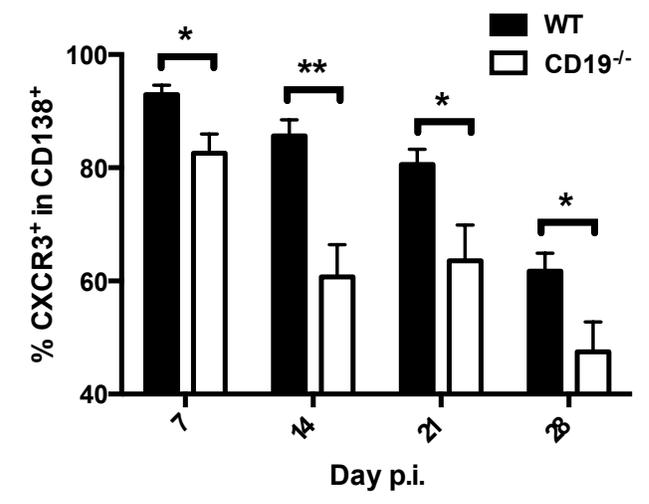
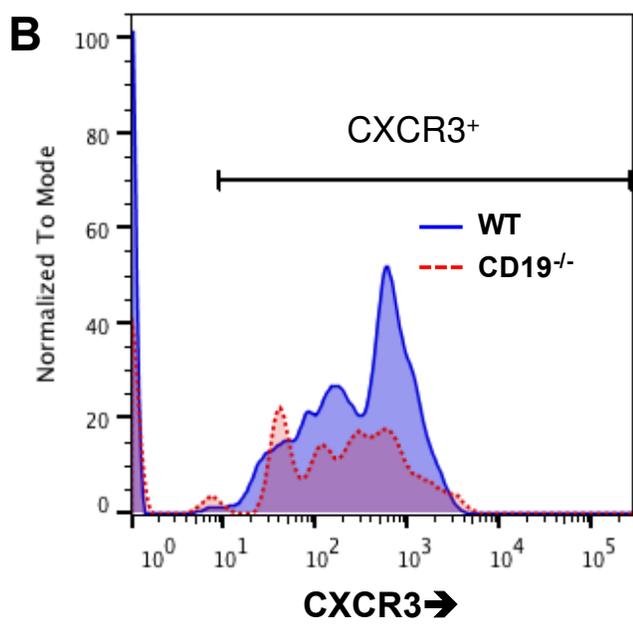
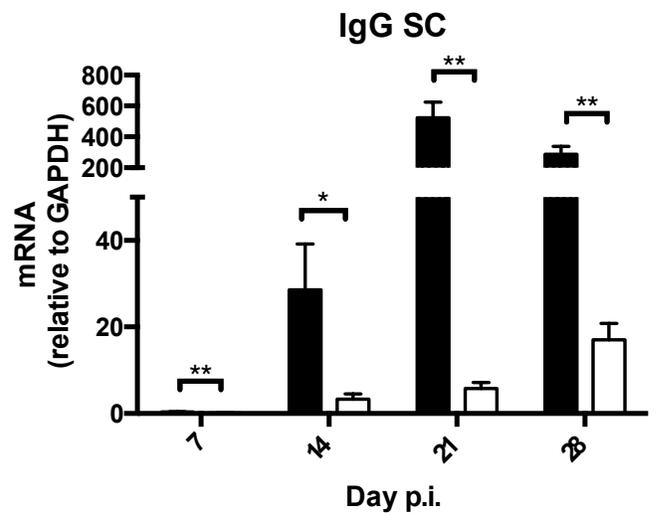
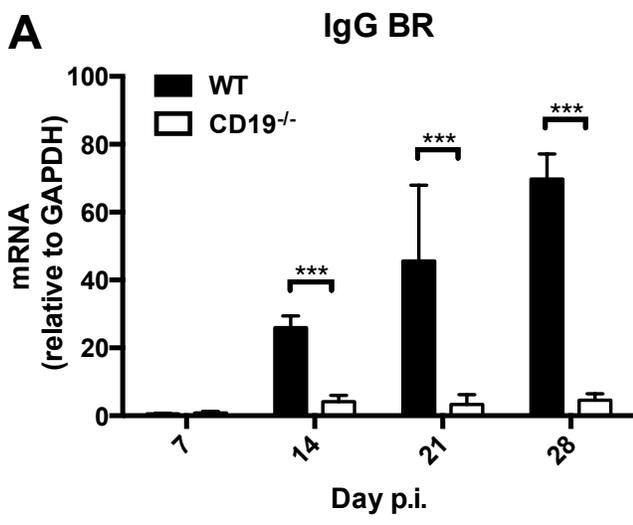


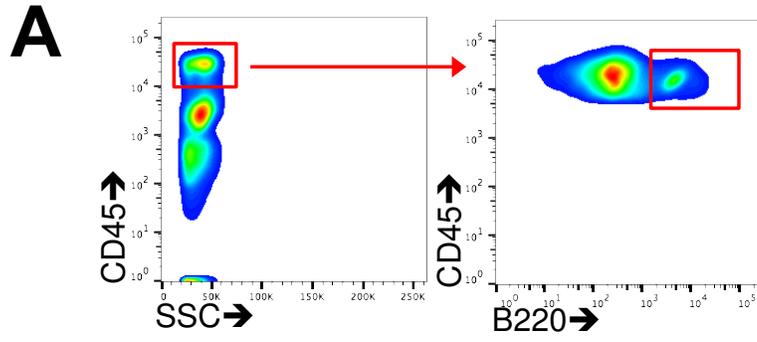




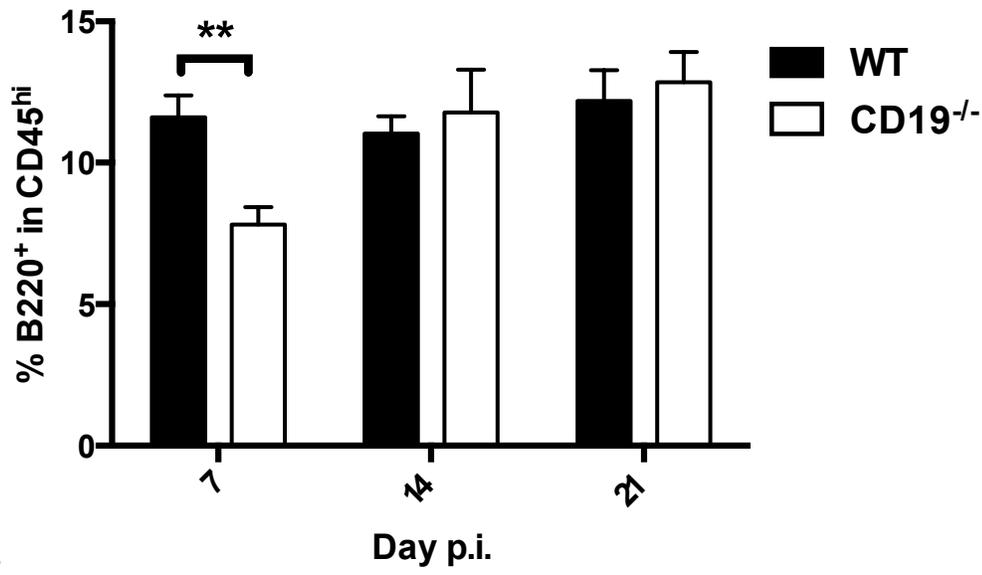




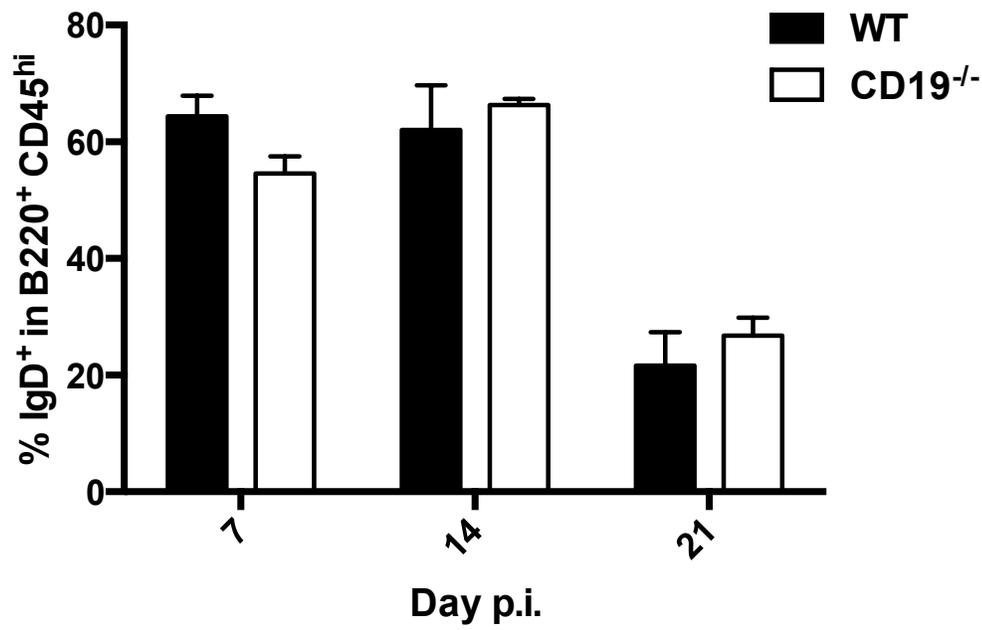


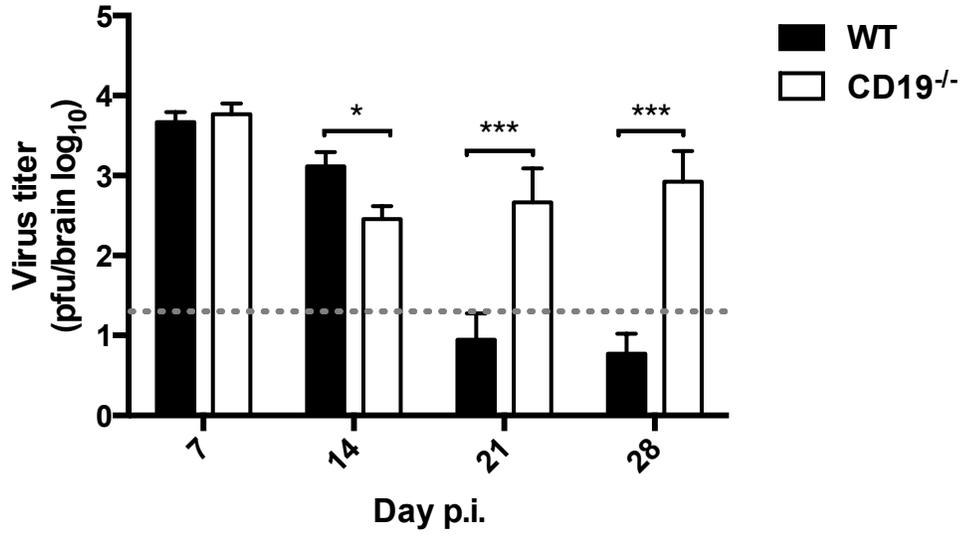
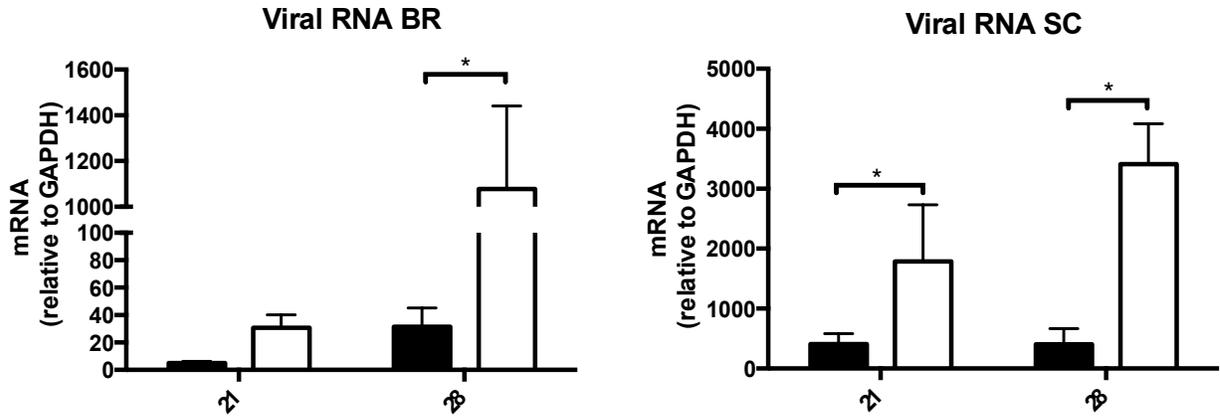


**B**



**C**



**A****B****C**