

Research article

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1 Turncoat antibodies unmasked in a model of autoimmune 2 demyelination: from biology to therapy

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32 **Abstract**

33 Autoantibodies contribute to many autoimmune diseases, yet there is no approved therapy to
34 neutralize them selectively. A popular mouse model, experimental autoimmune encephalomyelitis
35 (EAE), could serve to develop such a therapy, provided we can better understand the nature and
36 importance of the autoantibodies involved. Here we report the discovery of autoantibody-secreting
37 extrafollicular plasmablasts in EAE induced with specific myelin oligodendrocyte glycoprotein (MOG)
38 antigens. Single-cell RNA sequencing reveals that these cells produce non-affinity-matured IgG
39 antibodies. These include pathogenic antibodies competing for shared binding space on MOG's
40 extracellular domain. Interestingly, the synthetic anti-MOG antibody 8-18C5 can prevent the binding of
41 pathogenic antibodies from either EAE mice or people with MOG antibody disease (MOGAD).
42 Moreover, an 8-18C5 variant carrying the NNAS mutation, which inactivates its effector functions, can
43 reduce EAE severity and promote functional recovery. In brief, this study provides not only a
44 comprehensive characterization of the humoral response in EAE models, but also a proof of concept
45 for a novel therapy to antagonize pathogenic anti-MOG antibodies.

46 **Introduction**

47 B cells can play a dual role in autoimmune diseases. Firstly, they can capture protein antigens with their
48 immunoglobulins in a membrane-bound form called the B cell receptor¹. These antigens can then be
49 processed and presented to autoreactive T cells, key players in autoimmunity, resulting in their
50 activation. Secondly, activated B cells can differentiate into short-lived plasmablasts or long-lived
51 plasma cells, which secrete the same immunoglobulins in a soluble form, lacking the transmembrane
52 domain, called antibodies^{2,3}. During this process, the immunoglobulin genes can undergo class-switch
53 recombination, generating antibody isotypes with different properties^{4,5}, as well as somatic
54 hypermutation, creating antibodies with greater affinity for the cognate antigen⁶. Ultimately and
55 accidentally, these antibodies can cross-react with normal body components, leading to their

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56 destruction by the complement system and/or Fc gamma receptor (FcγR)-mediated cellular
57 mechanisms^{7,8}.

58 Typical examples of autoantibodies are those directed against myelin oligodendrocyte glycoprotein
59 (MOG) and aquaporin-4. These autoantibodies serve as diagnostic markers for rare neurological
60 autoimmune diseases, namely MOG antibody diseases (MOGAD) and neuromyelitis optica spectrum
61 disorder (NMOSD)⁹⁻¹³. In contrast, no specific antibody has been validated as a marker for the most
62 common neurological autoimmune disease, multiple sclerosis (MS)¹⁴. However, MS is characterized by
63 the presence, in the cerebrospinal fluid, of a mixture of antibodies, detected by electrophoresis as
64 oligoclonal bands¹⁵. Unfortunately, there is currently no approved drug to selectively eliminate or
65 counteract these antibodies.

66 Autoantibodies such as anti-MOG are heterogeneous and not functionally equal¹⁶. Some recognize
67 accessible epitopes, exposed on the cell surface or in the extracellular environment, making them
68 pathogenic¹⁷. Others target epitopes that are normally inaccessible due to intracellular localization,
69 protein folding, or proximity to the plasma membrane, preventing them from being directly
70 pathogenic¹⁷. Pathogenic anti-MOG antibodies generate a positive signal in a cell-based assay used to
71 diagnose MOGAD^{11,13,18-22}. Accordingly, anti-MOG antibodies that are negative in this assay are thought
72 to be non-pathogenic. These are nevertheless detectable by ELISA or Western blotting in several
73 conditions such as MS^{17,23,24}, MOGAD²⁵, NMOSD²⁶, and genetic leukoencephalopathies²⁷. The function
74 of these “non-pathogenic” antibodies, if any, is unknown.

75 Much of our knowledge on autoimmune demyelination comes from a mouse model called
76 experimental autoimmune encephalomyelitis (EAE)²⁸. EAE can be induced by immunization with myelin
77 antigens such as MOG-derived polypeptides. When a short polypeptide is used (e.g. the
78 immunodominant epitope MOG₃₅₋₅₅, which is presented to T cells by dendritic cells²⁹), EAE develops in
79 a B cell-independent manner^{30,31}. In this context, some B cells even exert a beneficial role, as their

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80 depletion exacerbates EAE³⁰⁻⁴⁰. These anti-inflammatory B cells (also called regulatory B cells or Bregs)
81 can attenuate EAE via IL-10 secretion^{31,37,41,42}. In contrast, when EAE is induced with a longer
82 polypeptide (e.g. mouse MOG₁₋₁₂₅, corresponding to the extracellular domain), B cells adopt a
83 detrimental role: they process and present antigenic epitopes^{43,44} and secrete IL-6^{43,45}, both leading to
84 encephalitogenic T cell activation⁴⁶. Under these conditions, B cell deficiency attenuates EAE^{30,47-51}.
85 Proinflammatory B cells are even essential for EAE induction with either human MOG₁₋₁₂₅
86 (hMOG)^{47,48,52,53} or mouse MOG₁₋₁₂₅ carrying the humanizing mutation S42P abolishing the 35-55
87 epitope (an antigen called bMOG)⁵⁴. These two antigens are termed B cell-dependent because they do
88 not induce EAE if B cells are depleted.

89 While there is ample evidence that some EAE models involve proinflammatory B cells as antigen
90 presenters and cytokine secretors, little is known about the involvement of autoantibodies other than
91 the observation that immunization with hMOG induces the production of anti-MOG IgG antibodies with
92 pathogenic potential^{53,55}. In the present study, we report the discovery of a population of antibody-
93 secreting B cells that transiently proliferate in lymph nodes of mice immunized with bMOG or hMOG.
94 Our objectives were to: 1) characterize these cells comprehensively by single-cell RNA sequencing and
95 mass cytometry; 2) examine how their antibodies can influence EAE by administering selected
96 recombinant antibodies or bMOG antiserum; and 3) develop an approach to block pathogenic
97 autoantibodies.

98 Results

99 Prominent expansion of extrafollicular plasmablasts in B cell-dependent EAE

100 To determine whether antibody-secreting cells are generated in B cell-dependent EAE, we quantified
101 cells expressing the canonical marker CD138 (syndecan-1) by flow cytometry in various tissues and at
102 different time points (days 0, 8, 12, 24) after immunization with bMOG. These cells were significantly

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103 increased in number in the draining inguinal lymph nodes on day 8 as well as in the bone marrow and
104 spinal cord on day 24, but not in the spleen at any time point (**Figure 1A** and **1B**). A similar increase was
105 observed in lymph nodes of mice immunized with hMOG (**Figure 1C**), but not with mouse MOG₃₅₋₅₅ or
106 adjuvants alone (**Figure 1D**). A replicate of the experiment using Vert-X mice, which express EGFP under
107 the control of the IL-10 promoter⁵⁶, revealed that 62 ± 16 % of bMOG-induced CD138⁺ cells were IL-10
108 producers (**Figure 1E** and **1F**). A similar percentage was observed in mice immunized with MOG₃₅₋₅₅ or
109 adjuvants alone (**Figure 1F**), suggesting that IL-10 production by CD138⁺ cells is antigen-independent.
110 However, the total number of CD138⁺ cells expressing IL-10 was much lower under these conditions
111 compared to bMOG (**Figure 1G**). For comparison, only 7 ± 4 % of CD19⁺CD138⁻ B cells expressed IL-10
112 (**Figure 1F**).

113 To further determine the anatomical distribution of CD138⁺ cells, we examined confocal images of
114 lymph node sections from CD19^{cre} × Ai14 mice, which express tdTomato specifically in the B cell
115 lineage^{57,58}. Numerous tdTomato⁺CD138⁺ cells were observed on day 8 after bMOG injection, mainly
116 outside the germinal centers, in the vicinity of Lyve-1⁺ lymphatic vessels (**Figure 1H**). Furthermore,
117 microscopic examination of spinal cords on day 24 confirmed the presence of CD138⁺ cells, but only in
118 the leptomeninges (**Figure 1I**). Some were individually scattered (not shown), while others were
119 clustered in follicles containing several dozen cells (**Figure 1J**), as observed in people with progressive
120 MS⁵⁹⁻⁶¹ and transgenic mice expressing a MOG-specific B cell receptor^{43,62}. Taken together, these results
121 indicate that a population of extrafollicular plasmablasts, phenotypically similar to the IL-10-producing
122 regulatory plasmablasts described in MOG₃₅₋₅₅-induced EAE⁴², expand to a much greater extent when
123 EAE is induced with B cell-dependent antigens.

124 **Single-cell transcriptomic and protein profiling of bMOG-induced plasmablasts**

125 To characterize the transcriptome and antibody repertoire of bMOG-induced plasmablasts, we
126 enriched these cells from lymph nodes of four mice on day 8 post-immunization and analyzed them by

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127 scRNAseq using 10× Genomics technology. The four gene expression datasets were pooled to produce
128 a single tSNE plot of all the isolated cells that met our quality criteria (**Figure 2A** and **Supplementary**
129 **Dataset 1**). Using this plot in combination with cell-specific markers, we identified 6 unambiguous
130 subsets of leukocytes (**Figure 2A**). Plasmablasts were distinguished by the expression of *Sdc1* (CD138)
131 and *Tnfrsf17* (BCMA) (**Figure 2B**). A significant proportion of plasmablasts (~25 %) expressed
132 proliferation markers such as *Birc5* (**Figure 2C**) and several others (e.g. *Mki67*, *Pclaf*, *Ube2c*, *Cdk1*,
133 *Hist1h2ap*, *Top2a*; **Supplementary Dataset 1**). Strikingly, compared with B cells, plasmablasts had
134 upregulated many genes associated with the protein/antibody synthesis machinery, while they had
135 downregulated many genes associated with antigen presentation (**Figure 2D**). This was confirmed at
136 the protein level by mass cytometry, except for MHCII which remained elevated (**Figure 2E–2G**).
137 Furthermore, plasmablasts appear to be poor producers of cytokines, as only *Il15* and *Il10* were
138 detectable, and only in very low amounts (**Supplementary Dataset 1** and **Figure 2D**). Interestingly, they
139 did not express *Aicda* (**Supplementary Dataset 1**), which encodes the enzyme AID, essential for
140 antibody maturation by somatic hypermutation⁶³. Consistent with published observations^{42,64,65}, they
141 expressed higher levels of *Cd44*, *Cd93*, *Irf4*, and *Prdm1*, while they had lost expression of *Sell* (**Figure**
142 **2D**). Overall, our results support the concept that CD138⁺ cells are extrafollicular plasmablasts engaged
143 in a primary antibody response, and not fully matured plasma cells, notably because they still
144 proliferate and express MHCII².

145 We next analyzed the four V(D)J datasets by selecting only high-quality plasmablasts (**Figure 3A**). Cells
146 with similarly rearranged V(D)J sequences (with or without mutations), most likely arising from a
147 common ancestor, were algorithmically combined into clonotypes, regardless of their constant region
148 (isotypes were considered subclonotypes). Clonotype abundance (**Figure 3B**) and immunoglobulin gene
149 segment usage (**Figure 3C–3E**) were similar between mice. Most clonotypes (93 ± 3 %) had undergone
150 class-switch recombination resulting in the expression of IgG antibodies (**Figure 3D**) lacking the
151 transmembrane exon (**Figure 3F**). IgG1 was the most abundant isotype (75 ± 10 %), followed by IgG2b

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152 (10 ± 5 %) and IgG2c (6 ± 3 %). However, these antibodies had not undergone somatic hypermutation,
153 as mutations were infrequent (median = 0; mean = 0.014–0.039 %; **Figure 3G**) and corresponded mainly
154 to junctional additions or deletions in the CDR3 regions, especially that of the heavy chain (**Figure 3H**).
155 Although the clonotype profile was similar between the mice (**Figure 3B–3G**), the percentage of
156 clonotypes shared between at least two mice was only 2.5 % (75 out of 2,974; **Figure 3I**). Among the
157 shared clonotypes, a few had the same V(D)J segments, but different junctional additions or deletions
158 in the CDR3 regions, suggesting that they originated from different ancestors that converged to produce
159 identical or nearly identical antibodies. This was the case for a set of clonotypes, collectively called
160 clonotype 2, which were present in all mice and produced the most prominent antibody, mainly in the
161 form of IgG1 (**Figure 3H** and **3J**). These results indicate that bMOG-induced plasmablasts secrete a
162 complex cocktail of non-affinity-matured IgG antibodies.

163 **Binding capability of recombinant bMOG-induced antibodies**

164 To determine whether bMOG-induced antibodies cross-react with endogenous MOG, we selected 6
165 clonotypes based on their isotype and size in terms of cell number. Clonotypes 1–3 were the largest
166 and produced mainly IgG1, while clonotypes 4–6 comprised fewer cells, but were the largest to express
167 IgG2b and/or IgG2c (**Figure 3J** and **Supplementary Table 1**). The *Ighv* and *Iglv* gene segments of these
168 clonotypes were cloned to produce the corresponding antibodies (clones C1 to C6) as IgG1, regardless
169 of their original isotype. ELISA results showed that only the IgG1 antibodies (C1–C3) bound to bMOG
170 and that only C1 cross-reacted with mouse and human MOG₁₋₁₂₅ (**Figure 4A**). Western blots confirmed
171 these findings and showed that C1 could also react with denatured full-length mMOG from spinal cord
172 lysates (**Figure 4B**). However, C1 did not react with either fixed full-length mMOG in spinal cord sections
173 (**Figure 4C**) or native full-length mMOG on live cells in culture (**Figure 4D**), presumably because the
174 epitope is masked due to the protein conformation and/or its proximity to the plasma membrane.

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175 Similar results were obtained using C1 in an IgG2b or IgG2c format (**Figure 4D**), ruling out an effect of
176 the isotype on the binding capacity.

177 To directly demonstrate that C1 is non-pathogenic, we administered this antibody to mice on day 8
178 post-immunization with MOG₃₅₋₅₅, i.e. just before the onset of disease and opening of the blood-brain
179 barrier^{66,67}. We chose to use MOG₃₅₋₅₅ instead of bMOG because the former does not induce the
180 production of anti-MOG antibodies (data not shown), which could have had a confounding effect in this
181 experiment. As a positive control, we used the anti-MOG IgG1 clone 8-18C5, which has been repeatedly
182 shown to be pathogenic^{55,68-78}. As expected, only 8-18C5 increased EAE severity (**Figure 4E**) and
183 incidence (**Figure 4F**) as compared to the control group. We can therefore conclude that an anti-MOG
184 antibody that is negative in live cell-based assay is not pathogenic, at least by a classic mechanism
185 involving its binding to CNS myelin.

186 **Pathogenic anti-MOG IgG antibodies are secreted in B cell-dependent EAE**

187 As we could only characterize a few clonotypes out of hundreds, we wondered whether bMOG could
188 nevertheless induce the production of pathogenic anti-MOG antibodies. To answer this question, we
189 first quantified serum anti-MOG antibodies over weeks after bMOG immunization using an isotype-
190 specific ELISA. High titers of anti-MOG IgG1, IgG2b, and IgG2c were detected from day 14 onwards, with
191 IgG1 being clearly the most abundant (**Figure 5A**), corroborating our scRNAseq results (**Figure 3D**).
192 Further analysis of sera on day 14, using an isotype-specific live cell-based assay, revealed the presence
193 of IgG1, IgG2b, and IgG2c antibodies capable of binding to membrane-bound MOG (**Figure 5B**),
194 suggesting that they are pathogenic^{11,18,79}. These observations were replicated with sera from mice
195 immunized against hMOG, except that the IgG1/IgG2b ratio was lower (**Figure 5A and 5B**).

196 We next sought to confirm the pathogenicity of bMOG antiserum by adoptive transfer into mice on day
197 8 post-immunization with MOG₃₅₋₅₅. As expected, EAE severity was increased in mice administered with
198 bMOG antiserum (**Figure 5C–E**), which is consistent with previous results obtained with hMOG

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199 antiserum⁵⁵. Overall, these results indicate that anti-MOG IgG1, IgG2b, and IgG2c are released into the
200 bloodstream from the second week after bMOG immunization and contribute to disease progression.

201 **8-18C5 can block the binding of pathogenic antibodies from EAE mice or MOGAD** 202 **patients**

203 To characterize the binding site of pathogenic bMOG-induced autoantibodies, we performed a
204 competitive live cell-based assay, pre-incubating MOG-expressing cells with 8-18C5 before adding
205 bMOG antiserum. We found that 8-18C5 blocked the binding of anti-MOG IgG2b and IgG2c from all
206 serum samples in a dose-dependent manner (**Figure 6A**). Interestingly, similar results were obtained
207 with serum from hMOG-immunized mice (**Figure 6B**) as well as patients diagnosed with MOGAD and
208 confirmed to be positive for anti-MOG IgG (**Figure 6C**). These findings indicate that pathogenic anti-
209 MOG antibodies, in both mice and humans, bind to MOG by occupying a shared space, and that this
210 binding can be prevented by obstructing this space with a synthetic antibody.

211 **An inactive 8-18C5 variant can attenuate bMOG-induced EAE**

212 Having demonstrated that 8-18C5 competes with pathogenic anti-MOG antibodies, we wondered
213 whether an effector function-deficient 8-18C5 variant could be therapeutically beneficial. To test this,
214 we engineered 8-18C5Mut with the NNAS mutation, which relocates the Fc glycosylation site and blocks
215 binding to FcγRs⁸⁰. This IgG1 variant was unable to bind to mouse or human FcγRs in vitro, unlike 8-
216 18C5, which bound to two mouse and two human FcγRs (mFcγRIIb, mFcγRIII, hFcγRIIIa, hFcγRIIb/c), and
217 unlike an irrelevant mouse IgG2a, which bound to all tested FcγRs (**Table 1** and **Supplementary**
218 **Figure 1**). These results confirm the effect of the NNAS mutation in a mouse antibody context and are
219 consistent with the literature^{80,81}.

220 Next, we administered mice with either 8-18C5Mut, 8-18C5, isotype control IgG1 or PBS on day 9 post-
221 immunization with bMOG. This time point was chosen because it coincides with the increase in blood-

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222 brain barrier permeability^{66,67,82} and the appearance of autoantibodies in the bloodstream, which is
223 observable in a fraction of mice as early as day 7 (**Figure 5A**). Interestingly, 8-18C5Mut markedly
224 reduced EAE severity (**Figure 7A**), resulting in a higher rate of complete recovery of locomotor function
225 (**Figure 7B**). Histological examination of spinal cords on day 43 post-immunization revealed clear signs
226 of demyelination (e.g. weak or granular luxol fast blue staining, presence of inflammatory lesions) in
227 mice with a score ≥ 0.5 , but not in fully recovered mice (**Figure 7C**). A protective effect of 8-18C5Mut
228 was also observed in another experiment comparing it with C1 (**Supplementary Figure 2**). These results
229 provide proof of concept that a pathogenic autoantibody, once inactivated, can counter the progression
230 of an autoimmune disease by acting as an antagonist.

231 Discussion

232 This study aimed to improve our understanding of the humoral response in EAE with a view to finding
233 a strategy to combat autoantibodies. Our results indicate that pathogenic anti-MOG antibodies in B
234 cell-dependent EAE models resemble those in MOGAD patients, targeting a common binding space on
235 the antigen surface. Based on this insight, we came up with the idea of exploiting the NNAS mutation,
236 which is known to inactivate all effector functions of human IgG antibodies⁸⁰. For the first time, we
237 demonstrate the validity of this mutation in a mouse antibody context and, more importantly, its utility
238 in the design of an autoantibody antagonist capable of mitigating an autoimmune disease. More
239 specifically, our inert 8-18C5Mut antibody is directly translatable for the treatment of MOGAD.

240 The humoral response we observed in bMOG EAE is typical of a primary acute extrafollicular response,
241 in which short-lived plasmablasts massively expand without entering follicular germinal centers and
242 without undergoing affinity maturation, to quickly produce as many antibodies as possible in the short
243 time that they are allotted^{2,3,83}. This response bypasses tolerance checkpoints that control the germinal
244 center response^{6,84}, thus running a greater risk of generating autoantibodies. This is the first report of

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245 a pathogenic extrafollicular response in B cell-dependent EAE. Extrafollicular plasmablasts have been
246 reported in MOG₃₅₋₅₅ EAE, as we observed here in small numbers, but these cells play an anti-
247 inflammatory role in this B cell-independent model, apparently via IL-10^{41,42,85}. Although bMOG-
248 induced plasmablasts also express IL-10, they should not be considered protective as they secrete
249 pathogenic autoantibodies. Rather than acting as a general suppressor of inflammation, IL-10 may
250 contribute to the development of the extrafollicular response, as reported in lupus erythematosus⁸⁶.
251 Furthermore, a pathogenic extrafollicular response is likely to occur in human autoimmune neurological
252 diseases⁸⁷. It may even be favored at the expense of a germinal center response by pathogens such as
253 Epstein-Barr virus⁸⁸⁻⁹¹, which has been linked to autoantibodies in MS⁹². Of course, proving this in
254 humans remains challenging due to the difficulty of obtaining the necessary tissues.

255 The fate of extrafollicular plasmablasts in our model is unclear. First, some may undergo affinity
256 maturation before differentiating into long-lived plasma cells that would help perpetuate the disease.
257 The increased number of CD138⁺ cells in the bone marrow on day 24 after bMOG immunization
258 supports this possibility. This most likely occurred in two studies that found anti-MOG antibodies with
259 somatic hypermutation in mice immunized against hMOG⁵⁵ or rat cerebellar glycoproteins⁶⁸. In both
260 cases, the mice were immunized several times and sacrificed weeks later. This probably also occurs in
261 people with MOGAD or MS, in whom affinity-matured antibodies have been detected in cerebrospinal
262 fluid⁹³. Second, other cells may migrate to meningeal lymphoid follicles, where they would expand to
263 release antibodies inside the CNS. The clusters of CD138⁺ cells that we observed in the leptomeninges
264 28 days post-immunization may correspond to those reported in ~40 % of people with secondary
265 progressive MS, which correlate with gray matter demyelination and disease progression⁶¹.

266 In conclusion, this study provides the most comprehensive characterization to date of the humoral
267 response occurring in B cell-dependent EAE, which is a more representative model of neurological
268 autoimmune diseases, especially MOGAD, compared with B cell-independent EAE. Our model proves

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269 advantageous for studying the mechanisms involved in humoral autoimmunity (e.g. plasmablast
270 development, isotype class switching, somatic hypermutation, ectopic follicle formation, antibody
271 effector functions) as well as for exploring novel therapies targeting them. The NNAS mutation holds
272 promise for the development of autoantibody antagonists, with potential applications extending
273 beyond demyelinating diseases to encompass a range of conditions involving tissue-destructive
274 autoantibodies.

275 **Materials and Methods**

276 **Human samples**

277 Serum was collected from MOGAD patients (3 male and 2 female children aged 5–17 years, and 10 male
278 and 12 female adults aged 21–72 years) at the Mayo Clinic (Rochester, USA), Hôpital Neurologique
279 Pierre Wertheimer (Bron, France), and University of Montreal Hospital Center (Montreal, Canada) with
280 the approval of the respective ethics committees. All patients gave their informed consent and met the
281 2023 diagnosis criteria for MOGAD, including a clear positive MOG-IgG cell-based assay on serum¹³.

282 **Mice**

283 C57BL/6J, Vert-X⁵⁶, CD19-Cre⁵⁷, and Ai14⁵⁸ mice were obtained from The Jackson Laboratory. CD19-Cre
284 and Ai14 mice were crossed to produce CD19^{Cre} × Ai14 mice. Genotypes were confirmed by PCR as
285 recommended by the supplier. Experiments were performed on males aged 8 to 12 weeks under
286 specific pathogen-free conditions with the approval of the Laval University Animal Protection
287 Committee and in accordance with the guidelines of the Canadian Council on Animal Care. Groups were
288 formed so that there were no significant differences in age between them.

289 **EAE induction**

290 Mice received a total of 200 μ l of emulsion, injected subcutaneously into each flank. Emulsion was
291 made by mixing equal volumes of Freund's adjuvant (BD Difco) supplemented with 5 mg/ml of killed
292 *Mycobacterium tuberculosis* H37Ra (BD Difco), and PBS containing 3.0–4.5 mg/ml of either MOG₃₅₋₅₅
293 (Medicinal Chemistry Platform, *CHU de Québec*), bMOG, or hMOG. The latter two antigens were
294 produced as previously described⁹⁴. Mice were injected intraperitoneally with 20 μ g/kg of pertussis
295 toxin (List Biological Laboratories) immediately before immunization and 2 days later.

296 **EAE scoring**

297 Mice were weighed and scored daily and blindly as follows: 0, no visual sign of disease; 0.5, partial tail
298 paralysis; 1, complete tail paralysis; 1.5, weakness in one hind limb; 2, weakness in both hind limbs; 2.5,
299 partial hind limb paralysis; 3, complete hind limb paralysis; 3.5, partial forelimb paralysis; 4, complete
300 forelimb paralysis; 5, dead or sacrificed for ethical reasons.

301 **Administration of serum or antibodies**

302 Serum was collected via cardiac puncture and administered via the retro-orbital sinus at a dose of 150
303 μ l per mouse. Recombinant antibodies (see below) were administered via the retro-orbital sinus at a
304 dose of 200 μ g per mouse.

305 **Recombinant antibody production**

306 Antibodies were cloned and produced in HEK293 cells by MediMab (Montreal) or in CHO cells by Evitria
307 (Zurich) using the variable domain sequences in **Supplementary Table 1**. HEK293 productions were
308 used for in vitro assays, whereas CHO productions were used for in vivo experiments.

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309 **Single-cell RNA sequencing**

310 Single-cell suspensions were prepared from inguinal lymph nodes on day 8 post-immunization with
311 bMOG. CD138⁺ cells were enriched using the EasySep Mouse CD138 Positive Selection Kit (Stemcell
312 Technologies). After determining cell purity (41 % ± 7 SD) and viability (90 % ± 3 SD) by flow cytometry,
313 cells were counted using a TC10 Automated Cell Counter (Bio-RAD) and processed with the Chromium
314 Single Cell Chip A and Chromium Controller (10× Genomics) with the goal of analyzing ~6,000 cells per
315 mouse. RNA samples were pooled for reverse transcription and amplification to generate gene
316 expression and V(D)J libraries using the Single Cell 5' Library Kit and Single Cell V(D)J Enrichment Kit
317 (10× Genomics). Libraries were pooled in equimolar ratio and sequenced using both Illumina Hiseq 2500
318 PE100 technology (low pass) at the University Hospital Center of Quebec and Illumina NovaSeq 6000
319 S4 PE150 technology (high pass) at Genome Quebec. The mean number of reads per cell was 48,201
320 (SD ± 8,842) for the gene expression libraries and 16,448 (SD ± 2197) for the V(D)J libraries.

321 For gene expression libraries, sequencing data were processed, aligned to the mm10 reference
322 genome, and aggregated into a single file using Cell Ranger 4.0 (10× Genomics) with default settings.
323 This file was examined using Loupe Browser 4.2 (10× Genomics) and filtered to remove ambiguous cells
324 (e.g. doublets, phagocytosed cells) based on colocalized cell-specific markers (e.g. *Sdc1* [CD138], *Ighd*,
325 *Cd19*, *Cd3e*, *C1qa*, *Siglech*, *Ccr7*, *Ly6g*, *Hbb-bt*). Downstream analyses were performed on the filtered
326 data reanalyzed with Cell Ranger. Cell subsets were identified using tSNE distribution, K-means, and cell
327 type-specific markers. Differentially expressed mRNAs were identified by significant feature
328 comparison. Heatmaps were generated with Clustvis⁹⁵.

329 For V(D)J libraries, sequencing data were processed and aligned to the GRCh38 reference genome
330 using Cell Ranger with default settings. Each sample was separately examined using Loupe V(D)J
331 Browser v3.0 (10× Genomics). Clonotype and lineage data were obtained using Enclone v.0.5.9 (10×
332 Genomics), first using each sample individually, and then by combining the samples using the

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333 *MIX_DONORS* argument to identify interindividual differences and similarities. *MIN_CELLS* was used to
334 keep only clonotypes with ≥ 5 cells, while *PLOT_BY_ISOTYPE* was used to generate honeycomb graphs.

335 **Flow cytometry**

336 Mice were anesthetized and exsanguinated by transcardial perfusion with saline. Inguinal lymph nodes
337 and spleens were minced, while bone marrow was flushed out from femurs with 10 ml of HBSS (Wisent
338 Bioproducts). The resulting suspensions were filtered through 70- μ m cell strainers and treated with
339 RBC lysis buffer (eBioscience). Spinal cords were minced in DPBS containing calcium and magnesium,
340 then digested 45 min at 37 °C in DPBS supplemented with 0.13 U/ml Liberase TM (Roche Diagnostics)
341 and 50 U/ml DNase (Millipore Sigma), filtered through 70- μ m cell strainers, and centrifuged for 30 min
342 at room temperature on a 35 % Percoll gradient (GE Healthcare) to remove myelin debris. For
343 immunostaining, cells were incubated on ice for 5 min with rat anti-CD16/CD32 antibody (BD
344 Biosciences, clone 2.4G2, 5 μ g/ml) and Fixable Viability Dye eFluor 660 or UV455 (eBioscience, 1:1000),
345 followed by a 30-min incubation with primary antibodies (**Supplementary Table 2**). Cells were washed
346 and resuspended in PBS supplemented with BSA (Cytivia) and EDTA before being analyzed with an LSR
347 II or FACSCanto II flow cytometer (BD Biosciences). For data analysis, the following quality control
348 checks were performed using FlowJo (Tree Star): 1) debris were removed using FSC-A and SSC-A; 2)
349 doublets were removed using FSC-A and FSC-H; and 3) dead cells positive for the viability dye were
350 removed. Gates were based on fluorescence-minus-one controls. Cell counts were normalized to
351 sample volume using 123count eBeads (Thermo Fisher).

352 **Mass cytometry**

353 Inguinal lymph node cells were isolated as for flow cytometry. For each mouse, 3×10^6 cells were
354 stained with Cell-ID Cisplatin and metal-conjugated antibodies (**Supplementary Table 2**) following the
355 MaxPar Cell Surface Staining with Fresh Fix protocol (Fluidigm). Cells were counted and resuspended at
356 a concentration of 1×10^6 cells/ml in a 9:1 ratio of MaxPar Cell Acquisition Buffer and EQ Four Element

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357 Calibration Beads (Fluidigm). Data were acquired using a Helios mass cytometer equipped with a wide-
358 bore injector (Fluidigm), then analyzed using FlowJo (BD Bioscience). Data cleaning was performed
359 according to the technical note Approach to Bivariate Analysis of Data (Fluidigm). After excluding
360 unwanted cells (CD45⁻ cells, TER119⁺ erythrocytes, CD3e⁺ T cells, Ly6G⁺ neutrophils, NK1.1⁺ natural
361 killer cells), data from each mouse were combined to create a single tSNE plot using the following
362 parameters: CD19⁺CD138⁻ B cells limited to 10,000; perplexity of 110; 3,000 iterations; learning rate of
363 1,889; exact k-nearest neighbors algorithm, Barnes-Hut gradient algorithm.

364 ELISA

365 The binding of recombinant anti-MOG antibodies to MOG antigens was analyzed using in-house ELISAs.
366 Microplates (Corning #9018) were coated overnight at 4 °C with 5 µg/ml of either bMOG (produced in-
367 house) or MOG₁₋₁₂₅ (Anaspect). BSA-6His-coated wells were used to control for binding to bMOG and
368 MOG₁₋₁₂₅ tags. The plates were then washed and blocked with 1 % BSA in PBS before adding serial
369 dilutions of recombinant antibodies (50–5000 ng/ml) and incubating for 2 h at room temperature. After
370 washes, a 1:5000 dilution of alkaline phosphatase-conjugated anti-mouse antibody (Jackson
371 Immunoresearch) was added to the plates and incubated 1 h at room temperature. Finally, after
372 additional washes, 1 mg/ml pNPP substrate (MilliporeSigma) was added for up to 30 min at room
373 temperature and absorbance was read at 405 nm using a SpectraMax i3x microplate reader (Molecular
374 Devices). Data shown are those of the weakest dilution for which no signal saturation was observed.

375 Anti-MOG antibodies were quantified in mouse sera collected via the submandibular vein at a 1:1000
376 dilution using an anti-mouse MOG₁₋₁₂₅ ELISA kit (Anaspec). For isotype-specific anti-MOG ELISA, the
377 HRP-conjugated secondary antibody from this kit was replaced by HRP-conjugated goat anti-mouse
378 IgG1, IgG2b, or IgG2c secondary antibody (Abcam). Data are presented as raw absorbance value minus
379 background.

380 **Western blotting**

381 Spinal cords were collected from saline-perfused mice and homogenized in RIPA buffer (50 mM Tris-
382 HCl, 150 mM NaCl, 1 % Triton X-100, 0.5 % sodium deoxycholate, 0.1 % sodium dodecyl sulfate, 1×
383 protease and phosphatase inhibitor cocktails [Sigma-Aldrich]). Tissue extracts and recombinant MOG
384 samples were diluted, respectively, at 2 mg/ml or 2 ng/ml in Laemmli buffer and boiled for 5 min. Ten
385 µl of each sample were resolved on 10 % SDS-polyacrylamide gel (Bio-Rad Mini-Protean II) and
386 transferred to a nitrocellulose membrane for 1 h at 4 °C and 100 V in transfer buffer (25 mM Tris,
387 200 mM glycine, 20 % methanol). The membranes were blocked for 30 min at room temperature and
388 incubated overnight at 4 °C in primary antibody, followed by washes and 1 h of incubation at room
389 temperature in HRP-conjugated goat anti-mouse IgG heavy chain (1:5000, ABClonal). Additional washes
390 were done before incubating the membranes 60 sec in Clarity Max ECL substrate (Bio-Rad) and
391 capturing chemiluminescent signal via ChemiDoc XRS+ Imaging System (Bio-Rad).

392 **Live cell-based assay**

393 The binding of antibodies to membrane-bound MOG was tested using mouse GL261 cells stably
394 transfected with a pCMV vector expressing either full-length mMOG or hMOG isoform 1. Cells were
395 incubated 15 min on ice in PBS supplemented with 2 % FBS and Fixable Viability Dye (eBioscience,
396 1:1000). For competition assays only, 8-18C5 was included in this first incubation step at 0.01, 1, or 10
397 µg/ml. Cells were then incubated with either recombinant anti-MOG antibodies (1 µg/ml), mouse
398 serum (1:40 dilution) collected 2 weeks after bMOG immunization, or MOGAD patient serum (1:40) for
399 30 min. Finally, cells were washed, incubated 15 min with secondary antibodies (**Supplementary Table**
400 **2**), and analyzed with a FACSCanto II flow cytometer (BD Biosciences). Non transfected cells and
401 conditions without recombinant primary antibody or serum were used as controls. Prior to analysis, the
402 following quality control checks were performed using FlowJo (Tree Star): 1) debris were removed using
403 FSC-A and SSC-A; 2) doublets were removed using FSC-A and FSC-H; and 3) dead cells positive for the

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404 viability dye were removed. Data are presented as mean fluorescence intensity for all live cells, from
405 which the mean fluorescence intensity of control cells was deducted.

406 **Analysis of antibody-FcγR binding using surface plasmon resonance**

407 Analysis of antibody binding to mouse and human FcγRs was performed on a Biacore T200 (GE
408 Healthcare) using anti-His or anti-mouse Fab capture. Briefly, His-tagged recombinant human and
409 mouse FcγRs (R&D Systems) were diluted to 2 μg/ml in HBS-EP+ (10 mM HEPES, pH 7.4, 150 mM NaCl,
410 3 mM EDTA, 0.05 % surfactant P20) and captured to anti-tetra His mIgG1 (Qiagen) amine-coupled to a
411 CM5 chip (Cytiva) for 30 sec at a flow rate of 10 μl/min. Antibodies were serially diluted 2- or 3-fold
412 from 3000 nM and injected over the captured FcγRs for 1 min in duplicate at 30 μl/min. To measure
413 binding to human FcγRI, antibodies were serially diluted 2-fold from 300 nM and injected for 3 min
414 followed by 10 min dissociation. The surface was regenerated with 10 mM glycine, pH 1.5. Alternately,
415 human and mouse FcγRII binding was measured by capturing ~100 RU of antibody to a CM5 chip
416 immobilized with goat anti-mouse IgG, F(ab')₂ (Jackson ImmunoResearch) and injecting receptors
417 serially diluted 2-fold from 3000 nM in HBS-EP+ buffer for 1 min at 30 μl/min. Dissociation was
418 measured for 1 min and the surface was regenerated with 0.85 % phosphoric acid. Steady state analysis
419 was used to determine the binding affinity of low affinity receptors and kinetic fits using a 1:1 binding
420 model were performed on high affinity receptor sensorgrams to calculate K_D.

421 **Histology**

422 For lymph nodes, mice were transcardially perfused with saline for 5 min. Lymph nodes were fixed
423 overnight at 4 °C in PLP solution (1 % PFA, 0.1M L-lysine, 0.01 M sodium periodate in PBS), and mounted
424 in blocks of M-1 Embedding Matrix (Thermo Fisher). Series of 8 μm-thick sections were cut using a
425 cryostat (CryoStar NX70), mounted on slides, and stored at -80 °C.

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426 For spinal cords, mice were transcardially perfused with ice-cold saline, followed by 4 % PFA in
427 phosphate buffer, pH 7.4, over 10 min. Spinal cords were post-fixed 4 h at 4 °C in 4 % PFA and
428 cryoprotected overnight in 20 % sucrose. 25 µm-thick sections were cut with a microtome (Leica
429 SM2000R) and stored at -20 °C in cryoprotectant solution (PBS with 20 % glycerol and 30 % ethylene
430 glycol).

431 Immunofluorescence was performed as previously described⁹⁶. Briefly, slides were blocked and
432 incubated overnight at 4 °C in primary antibodies (**Supplementary Table 2**). After washing, sections
433 were incubated at room temperature for 2 h in secondary antibodies (**Supplementary Table 2**). Slides
434 were counterstained for 1 min with 2 µg/ml DAPI, then mounted with coverslips no. 1.5H and ProLong
435 Glass Antifade Mountant (Molecular Probes).

436 Sections of lumbar spinal cords were stained for myelin with 0.3 % Black-Gold II (Histo-Chem) in 0.9 %
437 NaCl at 60 °C for 15 min, then differentiated in 1 % sodium thiosulphate at 60 °C for 3 min as
438 described⁹⁷. Brightfield tiled images were captured at 20× magnification using a Zeiss Axio Scan.Z1 slide
439 scanner.

440 **Confocal microscopy**

441 Confocal images were acquired with a Leica TCS SP8 STED 3X microscope by sequential scanning using
442 the following settings: objective, HC/PL/APO 63×/1.40 oil; immersion oil, Leica Type F; scan speed, 600
443 Hz; line average, 2-4; time gate, 0.3-6.0 ns. Laser power and gain were set to optimize signal-to-noise
444 ratio and avoid saturation using the QLUT Glow mode. Sizes of pixel, pinhole and z-step were set to
445 optimize resolution or to oversample in the case of images to be deconvolved. Deconvolution was
446 performed with Huygens Professional (Scientific Volume Imaging) using a theoretical point spread
447 function, manual settings for background intensity and default signal-to-noise ratio. Color balance,
448 contrast and brightness were adjusted with Photoshop (Adobe). CD138⁺ and CD3⁺ cells were
449 systematically counted in the meninges of five serial sections per mouse.

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450 **Statistics**

451 Data are expressed as mean \pm standard error. In general, groups were compared using either
452 nonparametric (Mann-Whitney, Kruskal-Wallis with Dunn's test) or parametric tests (one-way ANOVA,
453 two-way ANOVA with Tukey's or Dunnett's test), when data were continuous, normally distributed
454 (Anderson-Darling test), and of equal variance (Levene's test). EAE incidence curves were constructed
455 using the Kaplan-Meier method and compared by log-rank analysis. EAE severity curves were compared
456 by: 1) two-way ANOVA with repeated measures, followed by Fisher's LSD test, using rank-transformed
457 scores; and 2) parametric tests using the area under the curve. Analyses were performed with GraphPad
458 Prism 9.1 (GraphPad Software). A *P* value less than 0.05 was considered significant.

459 **Data availability**

460 The raw and processed scRNAseq data generated in this study are available in the NCBI GEO repository
461 under the accession code [GSE260585](#).

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714 Author contributions

715 L.V. was responsible for conceptualization, funding acquisition, project administration, supervision,
716 methodology, data analysis, and writing. R.T.M. carried out most of the experiments and contributed
717 to data analysis and writing with the help of F.M. Y.Z. performed the mass cytometry experiment, while
718 L.B. performed the analysis of plasmablasts in spinal cord sections, with the help and supervision of
719 L.C.B. Q.Z, J.J., and A.P. provided the NNAS sequence and performed the antibody-FcγR binding analysis.
720 J.M.D. processed and analyzed scRNAseq data under the supervision of J.C. E.F., R.M., and C.L. provided
721 human serum samples. S.K. contributed to conceptualization and provided bMOG. All authors reviewed
722 the manuscript and gave final approval.

723 Table

724 **Table 1:** Antibody binding affinity to FcγRs determined by surface plasmon resonance.

| | K_D (M) | | |
|-----------------|--------------------------|--------------------------|-------------------------|
| | 8-18C5 (mIgG1) | 8-18C5Mut (mIgG1) | Irrelevant mIgG2 |
| mFcγRI | n/d | n/d | 2.7×10^{-8} |
| mFcγRIIb | 3.5×10^{-7} | n/d | 6.2×10^{-7} |
| mFcγRIII | 2.9×10^{-6} | n/d | 3.0×10^{-6} |
| mFcγRIV | n/d | n/d | 9.0×10^{-8} |
| hFcγRI | n/d | n/d | 6.5×10^{-9} |
| hFcγRIIa (R167) | 8.7×10^{-8} | n/d | 8.2×10^{-7} |
| hFcγRIIb/c | 2.5×10^{-6} | n/d | 1.9×10^{-6} |

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| | | | |
|------------------|-----|-----|----------------------|
| hFcγRIIIa (V158) | n/d | n/d | 1.7×10^{-6} |
| hFcγRIIIa (F158) | n/d | n/d | 2.7×10^{-6} |

725 Figure legends

726 **Figure 1.** Extrafollicular plasmablasts expand greatly and transiently in EAE induced with B cell-
727 dependent antigens. **(A)** Representative flow cytometry plot of lymph node cells from a mouse
728 immunized with bMOG 8 days earlier. Gating strategy used to identify plasmablasts ($CD138^{hi}CD19^{+/-}$)
729 and B cells ($CD138^{-}CD19^{+}$) is shown. Dead cells, doublets, and other leukocytes ($CD3^{+}$, $Ly6G^{+}$, $CD11b^{+}$,
730 $CD11c^{+}$) were excluded. **(B)** Quantification of plasmablasts in different tissues and at different time
731 points after bMOG immunization. *Significantly different from the other time points (ANOVA, $P <$
732 0.0001 ; post hoc Tukey's test, $P < 0.0001$). Sample size: 4 day 0, 11 day 8, 10 day 16, 10 day 24. **(C, D)**
733 Quantification of plasmablasts in lymph nodes 8 days after immunization with B cell-dependent (bMOG,
734 hMOG) or -independent (MOG_{35-55}) antigens. Mice untreated (naive) or injected with adjuvants alone
735 (sham) were used as controls. *Significantly different from the controls (C: Kruskal-Wallis, $P = 0.014$;
736 post hoc Dunn's test, $P \leq 0.018$; D: ANOVA, $P < 0.0001$; post hoc two-tailed Student's *t*-test, $P < 0.0001$).
737 Sample size: C, 3 naive, 10 hMOG1-125, 10 bMOG; D, 2 naive, 3 sham, 5 MOG_{35-55} , 5 bMOG. **(E)** Flow
738 cytometric gating strategy used to identify plasmablasts and B cells expressing the IL-10 reporter EGFP
739 in lymph nodes of $Vert-X^{+/+}$ mice 8 days after bMOG immunization. **(F, G)** Percentage and relative
740 number of plasmablasts and B cells expressing IL-10 in lymph nodes of $Vert-X^{+/+}$ mice after the indicated
741 treatments. *Significantly different from the other groups (ANOVA, $P \leq 0.01$; post hoc two-tailed
742 Student's *t*-test, $P \leq 0.05$). †Tends to be significant (ANOVA, $P = 0.0588$; Student's *t*-test: $P \leq 0.0477$).
743 Sample size: 2 naive, 3 sham, 5 MOG_{35-55} , 5 bMOG. **(H)** Confocal images at low (top) or high (bottom)
744 magnification showing the distribution of $CD138^{+}$ plasmablasts (red) in a lymph node of a $CD19^{cre} \times Ai14$
745 mouse expressing the B cell reporter tdTomato (false color green) on day 8 after bMOG immunization.
746 Note that these plasmablasts: 1) are predominantly located near lymphatic vessels (blue) outside the

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747 follicles (delineated by dashed lines); and 2) express lower amount of tdTomato than CD138⁻ B cells.
748 Arrowheads: tdTomato^{lo}CD138⁺ plasmablasts. Arrows: tdTomato^{hi}CD138⁻ B cells. Abbreviation: GC,
749 germinal center. Scale bars: top, 100 μ m; bottom, 10 μ m. **(I)** Counts of plasmablasts and T cells in the
750 spinal cord meninges from mice sacrificed on day 28 after immunization with bMOG or adjuvants alone
751 (sham). *Significantly different from sham (two-tailed Student's *t*-test, $P < 0.0001$). Sample size: 4 sham,
752 6 bMOG. **(J)** Confocal image of a spinal cord section on day 28 post-immunization showing a cluster of
753 CD138⁺ plasmablasts (red) counterstained with DAPI (blue, nuclei) outside the parenchyma (P), within
754 the meninges (M; delineated by a dashed line). Scale bar: 10 μ m.

755 **Figure 2.** Transcriptomic and protein profiles of bMOG-induced plasmablasts. **(A)** tSNE plot of lymph
756 node cells enriched in CD138⁺ cells from four mice on day 8 after bMOG immunization. Cells were
757 analyzed using 10 \times Genomics 5' Single-Cell Gene Expression technology. The indicated cell subsets were
758 identified using the tSNE distribution, K-means, and cell type-specific markers. Encircled cells were
759 those selected for V(D)J profiling in Figure 3. Descriptive data on each subset are provided in table.
760 Abbreviations: pDCs, plasmacytoid dendritic cells; cDCs, conventional dendritic cells. **(B)** Cells
761 expressing the plasmablast markers CD138 and BCMA (blue). **(C)** Log₂ expression of *Birc5* revealing
762 proliferating plasmablasts (encircled). **(D)** Heat map showing the expression profile of genes
763 differentially regulated in plasmablasts compared to B cells, as identified by significant feature
764 comparison in Loupe Cell Browser ($P \leq 0.04$). Median-normalized mean UMI counts were Ln(x+1)-
765 transformed and centered without row scaling using Clustvis. **(E)** tSNE plot generated from mass
766 cytometry data on lymph node cells on day 8 after bMOG immunization. **(F)** Markers used to identify
767 plasmablasts (CD138), B cells (CD19), and type-2 cDCs (cDC2s; CCR7) in E. **(G)** Comparison of expression
768 levels of proteins involved in antigen presentation between plasmablasts, B cells, and cDC2s.
769 *Significantly different from plasmablast group (ANOVA, $P < 0.0001$; post hoc Tukey's test ($P \leq 0.0004$)).

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770 **Figure 3.** Profile of antibodies produced by bMOG-induced plasmablasts. **(A)** tSNE plots of gene
771 expression data in Figure 2 showing plasmablasts selected for V(D)J analysis (colors). **(B)** Abundance
772 distribution of the top-100 clonotypes, as analyzed using 10× Genomics Single-Cell V(D)J technology.
773 **(C–E)** Comparison of immunoglobulin gene segment usage between mice. **(F)** Sequencing data from
774 gene expression libraries showing the presence of the transmembrane domain (blue) in *Ighm*, *Igha*, and
775 *Ighe*, but not *Ighg* transcripts. **(G)** Percentage of somatic mutations in the *Ighv* gene segment of the
776 main clonotypes with ≥ 5 cells ($n = 89$ -123 clonotypes per mouse). Two outliers with mutation rates of
777 16 and 18 % were excluded in mouse 4. **(H)** Comparison of the CDR3 region of the heavy and light chains
778 of nine highly similar clonotypes from mouse 1, collectively referred to as clonotype 2 in J. These
779 clonotypes were identical except for the CDR3 regions. Alignment was performed with webPRANK. **(I)**
780 Number of clonotypes shared between mice. **(J)** Honeycomb plots showing clonotypes (dot clusters)
781 with ≥ 5 cells (dots) of any isotypes. Numbers indicate clonotypes selected for further analysis.

782 **Figure 4.** C1 can react with wild-type MOG, but not when the latter is in its native, plasma membrane-
783 bound form, making it a non-pathogenic antibody. In all panels, anti-MOG IgG1 clone 8-18C5 was used
784 as a positive control. Antibodies were IgG1, except in D where three C1 isotypes were tested. **(A)** ELISA
785 against bMOG (left) or wild-type mouse and human MOG₁₋₁₂₅ (mMOG and hMOG; right). Quantity of
786 bound IgG is expressed as either raw absorbance minus background (left) or absorbance normalized to
787 8-18C5 (right). **(B)** Western blot for bMOG, mouse MOG₁₋₁₂₅ or full-length MOG from mouse spinal cord
788 extracts. **(C)** Spinal cord sections stained with anti-MOG antibodies (red) and DAPI (blue). Scale bar: 25
789 μm . CC = central canal. **(D)** Flow cytometry of live GL261 cells transfected to produce full-length MOG
790 (red), incubated with anti-MOG antibodies, and stained with anti-mouse IgG antibody. Non-transfected
791 cells (blue) were used as a negative control. **(E)** Severity of EAE in mice immunized with MOG₃₅₋₅₅ and
792 injected intravenously 8 days later with PBS or 200 μg of the indicated antibody. Data from two
793 independent experiments are expressed as either daily scores from the day of disease onset (left) or
794 area under the curve (right). Left panel: *significantly different from PBS (two-way ANOVA with

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795 repeated measures using rank-transformed data, $P < 0.0001$; post hoc Mann-Whitney tests, $P \leq 0.049$).
796 Right panel: *significantly different from the other groups (one-way ANOVA, $P < 0.0001$; post hoc
797 Tukey's test, $P \leq 0.0012$). Sample size: 9 PBS; 20 clonotype 1; 20 8-18C5. **(F)** Disease incidence of
798 experiments in E. Log-rank test, $P = 0.0003$. Sample size: 10 PBS; 20 clonotype 1; 20 8-18C5.

799 **Figure 5.** Pathogenic anti-MOG IgG antibodies are produced in B cell-dependent EAE models. **(A)** ELISA
800 detection of anti-MOG IgG1, IgG2b, and IgG2c in serum from mice immunized with either bMOG (top)
801 or hMOG (bottom) through time. Sample size per group: bMOG, 16-20 mice; hMOG, 10 mice. **(B)**
802 Detection of anti-MOG antibodies by live cell-based assay in serum from mice immunized with either
803 bMOG (left) or hMOG (right). GL261 cells transfected to produce full-length mMOG were incubated
804 with serum collected before or after immunization (days 0 and 14), and stained with isotype-specific
805 secondary antibodies. Data are expressed as delta mean fluorescence intensity (Δ MFI). *Significantly
806 different from day 0 group from same isotype (Mann-Whitney test, $P < 0.0001$). Sample size per group:
807 bMOG, 12 mice; hMOG, 9 mice. **(C)** Severity of EAE in MOG₃₅₋₅₅-immunized mice injected with 150 μ l of
808 serum from either naive mice or mice sacrificed 8 days after immunization with bMOG. Data are
809 expressed as either daily scores from the day of disease onset (left) or area under the curve (right). Left
810 panel: *significantly different from naive group as determined by two-way ANOVA with repeated
811 measures using rank-transformed data ($P = 0.002$), followed by post hoc Mann-Whitney tests ($P \leq$
812 0.007). Right panel: Mann-Whitney test, $P = 0.006$. Data are from two independent experiments.
813 Sample size: 12 naive serum; 14 bMOG serum. **(D)** Survival and **(E)** disease incidence rates for the
814 experiment in C. P -values shown were calculated using the log-rank test. Sample size: as in C.

815 **Figure 6.** 8-18C5 competes with mouse and human pathogenic anti-MOG antibodies for binding to
816 plasma membrane-bound MOG. **(A)** Live cell-based assay in which mMOG-expressing cells were
817 sequentially incubated with 8-18C5 at the indicated concentrations, mouse serum collected on day 14
818 post-immunization with bMOG, and secondary antibodies to mouse IgG2b and IgG2c. Data are

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819 expressed as delta mean fluorescence intensity (Δ MFI). *Significantly different from the other
820 concentrations (Kruskal-Wallis test, $P \leq 0.0003$ for both IgG2b and IgG2c; post hoc Dunn's test, $P \leq$
821 0.0028). Sample size: 12 sera. **(B)** Same analysis as in A, except that the sera were from hMOG-
822 immunized mice. *Significantly different from the other concentrations (Kruskal-Wallis test, $P \leq 0.0072$;
823 post hoc Dunn's test, $P \leq 0.0042$). Sample size: 6 sera. **(C)** Same analysis as in A, except that hMOG-
824 expressing cells were incubated with serum from MOGAD patients and stained with an anti-human IgG
825 secondary antibody. *Significantly different from the other concentrations (Kruskal-Wallis test, $P <$
826 0.0001; post hoc Dunn's test, $P < 0.0001$). Sample size: 25.

827 **Figure 7.** bMOG-induced EAE can be attenuated with 8-18C5Mut. **(A)** Severity of EAE in mice
828 intravenously injected with PBS or 200 μ g of the indicated antibody on day 9 post-immunization. Data
829 are expressed as either daily scores from the day of disease onset (left) or area under the curve (right).
830 Left panel: *significantly different from the isotype group, as determined by two-way ANOVA with
831 repeated measures ($P = 0.049$), followed by Fisher's LSD tests ($P \leq 0.0451$), using rank-transformed
832 scores. Right panel: *significantly different from the other groups (one-way ANOVA, $P = 0.0036$; post
833 hoc Tukey tests, $P \leq 0.0220$). Data are from two independent experiments. Sample Size: 18 8-18C5, 16
834 8-18C5Mut, 19 isotype, 17 PBS. **(B)** Kaplan-Meier plot showing the percentage of mice from panel A
835 that had completely recovered by the end of experiment (log-rank test: overall, $P = 0.0331$; PBS vs 8-
836 18C5Mut, $P = 0.0412$; isotype vs 8-18C5Mut, $P = 0.0229$; 8-18C5 vs 8-18C5Mut, $P = 0.0680$). Shaded
837 areas: 95 % pointwise confidence interval. **(C)** Black gold-stained spinal cord sections on day 43 post-
838 immunization at low (top) or high (bottom) magnification. Evidence of demyelination (lost or granular
839 staining) is observable in a mouse treated with isotype antibody, but not in a mouse treated with 8-
840 18C5Mut or not immunized (naive). The clinical score at the time of sacrifice is indicated for each
841 mouse. Scale bars: top, 200 μ m; bottom, 50 μ m.

842

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843 **Supplementary Materials**

844 **Supplementary Dataset 1.** scRNAseq of bMOG-induced plasmablasts.

845 **Supplementary Figure 1.** Surface plasmon resonance sensorgrams comparing the binding of mouse
846 antibodies to mouse and human FcγRs.

847 **Supplementary Figure 2.** bMOG-induced EAE can be attenuated with 8-18C5Mut.

848 **Supplementary Table 1.** Antibody clones selected for further analysis.

849 **Supplementary Table 2.** Antibodies used in this study.

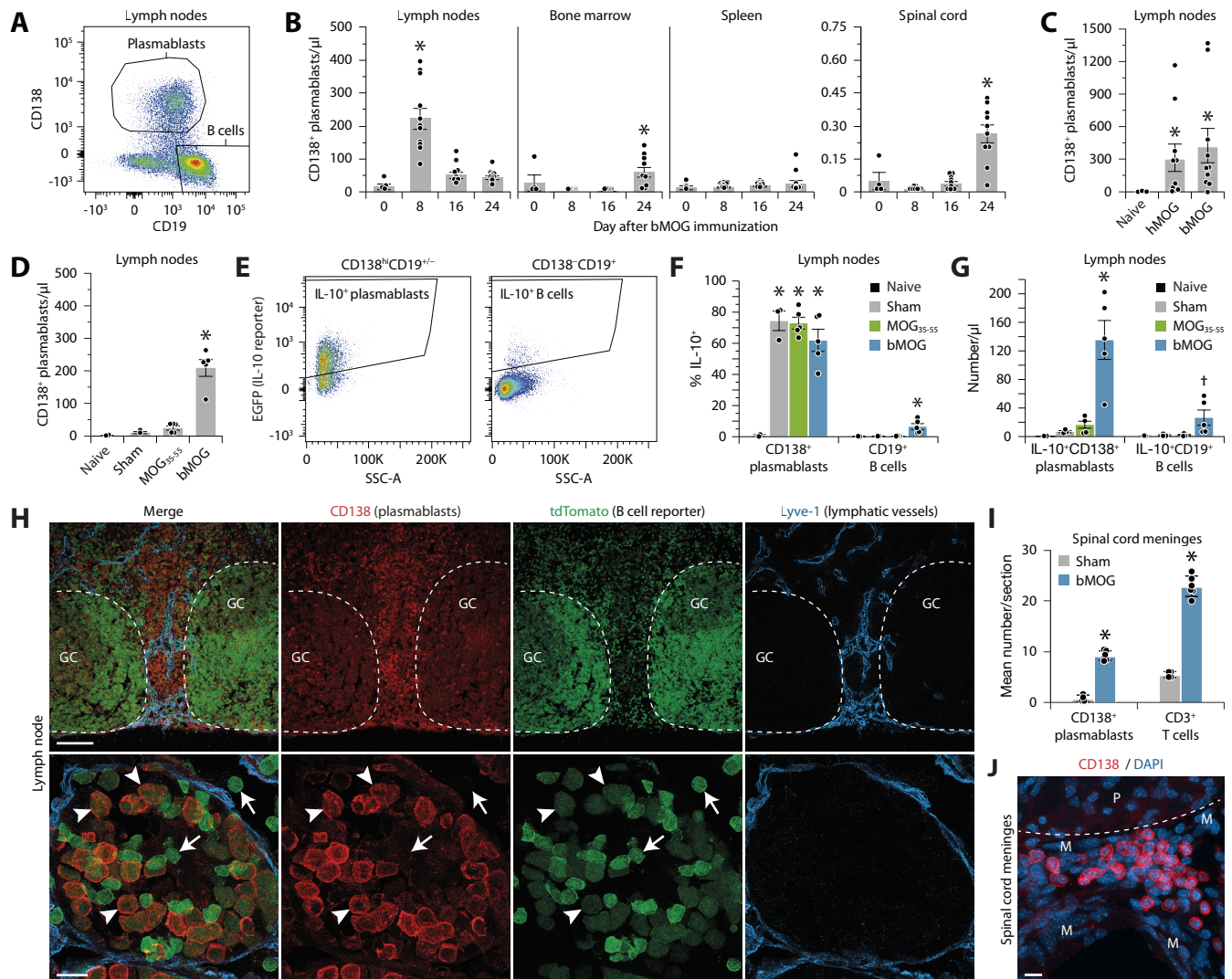


Figure 1. Extrafollicular plasmablasts expand greatly and transiently in EAE induced with B cell-dependent antigens. **(A)** Representative flow cytometry plot of lymph node cells from a mouse immunized with bMOG 8 days earlier. Gating strategy used to identify plasmablasts ($CD138^{hi}CD19^{-/-}$) and B cells ($CD138^{-}CD19^{+}$) is shown. Dead cells, doublets, and other leukocytes ($CD3^{+}$, $Ly6G^{+}$, $CD11b^{+}$, $CD11c^{+}$) were excluded. **(B)** Quantification of plasmablasts in different tissues and at different time points after bMOG immunization. *Significantly different from the other time points (ANOVA, $P < 0.0001$; post hoc Tukey's test, $P < 0.0001$). Sample size: 4 day 0, 11 day 8, 10 day 16, 10 day 24. **(C, D)** Quantification of plasmablasts in lymph nodes 8 days after immunization with B cell-dependent (bMOG, hMOG) or -independent (MOG_{35-55}) antigens. Mice untreated (naive) or injected with adjuvants alone (sham) were used as controls. *Significantly different from the controls (C: Kruskal-Wallis, $P = 0.014$; post hoc Dunn's test, $P \leq 0.018$; D: ANOVA, $P < 0.0001$; post hoc two-tailed Student's t -test, $P < 0.0001$). Sample size: C, 3 naive, 10 hMOG₁₋₁₂₅, 10 bMOG; D, 2 naive, 3 sham, 5 MOG_{35-55} , 5 bMOG. **(E)** Flow cytometric gating strategy used to identify plasmablasts and B cells expressing the IL-10 reporter EGFP in lymph nodes of Vert- $X^{+/+}$ mice 8 days after bMOG immunization. **(F, G)** Percentage and relative number of plasmablasts and B cells expressing IL-10 in lymph nodes of Vert- $X^{+/+}$ mice after the indicated treatments. *Significantly different from the other groups (ANOVA, $P \leq 0.01$; post hoc two-tailed Student's t -test, $P \leq 0.05$). †Tends to be significant (ANOVA, $P = 0.0588$; Student's t -test: $P \leq 0.0477$). Sample size: 2 naive, 3 sham, 5 MOG_{35-55} , 5 bMOG. **(H)** Confocal images at low (top) or high (bottom) magnification showing the distribution of $CD138^{+}$ plasmablasts (red) in a lymph node of a $CD19^{cre} \times Ai14$ mouse expressing the B cell reporter tdTomato (false color green) on day 8 after bMOG immunization. Note that these plasmablasts: 1) are predominantly located near lymphatic vessels (blue) outside the follicles (delineated by dashed lines); and 2) express lower amount of tdTomato than $CD138^{-}$ B cells. Arrowheads: $tdTomato^{lo}CD138^{+}$ plasmablasts. Arrows: $tdTomato^{hi}CD138^{-}$ B cells. Abbreviation: GC, germinal center. Scale bars: top, 100 μm ; bottom, 10 μm . **(I)** Counts of plasmablasts and T cells in the spinal cord meninges from mice sacrificed on day 28 after immunization with bMOG or adjuvants alone (sham). *Significantly different from sham (two-tailed Student's t -test, $P < 0.0001$). Sample size: 4 sham, 6 bMOG. **(J)** Confocal image of a spinal cord section on day 28 post-immunization showing a cluster of $CD138^{+}$ plasmablasts (red) counterstained with DAPI (blue, nuclei) outside the parenchyma (P), within the meninges (M; delineated by a dashed line). Scale bar: 10 μm .

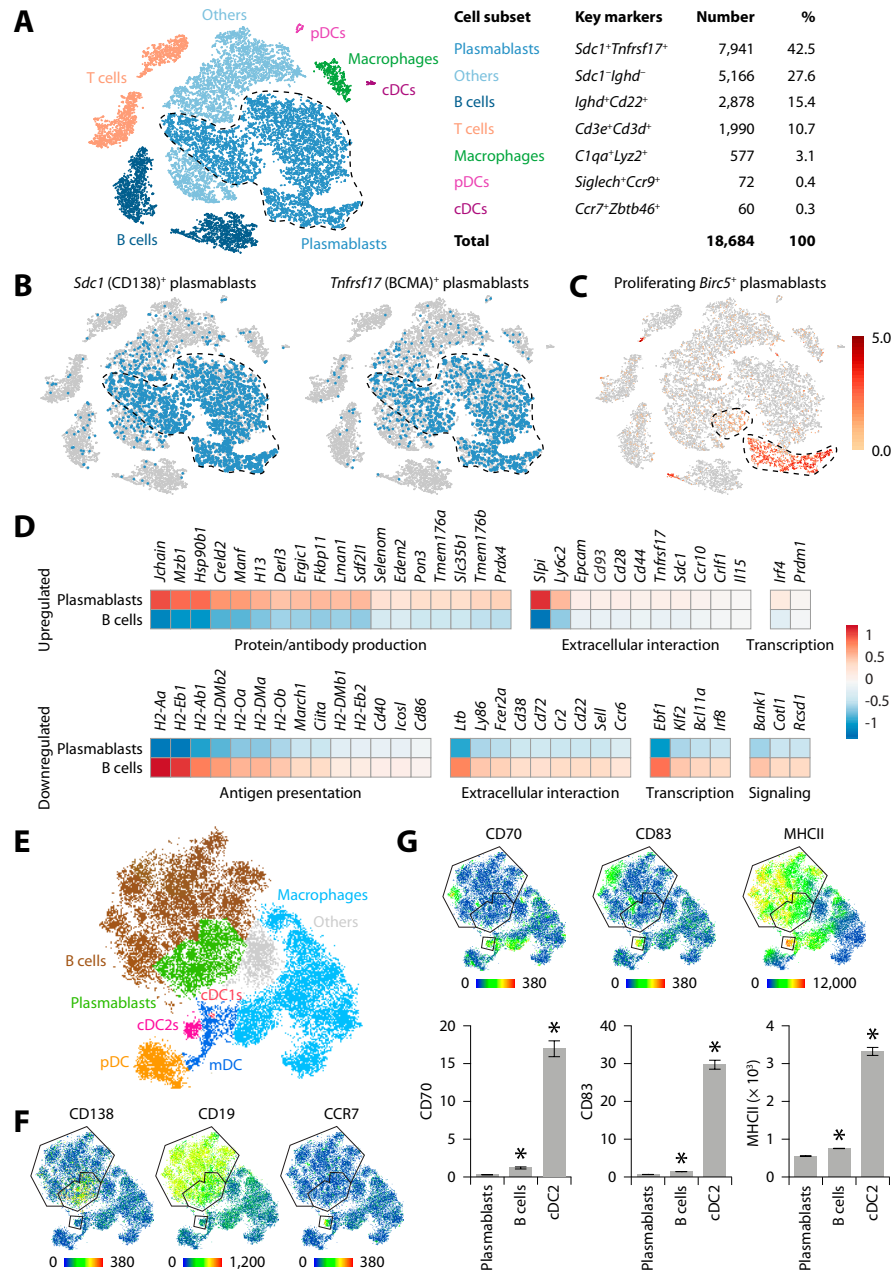


Figure 2. Transcriptomic and protein profiles of bMOG-induced plasmablasts. **(A)** tSNE plot of lymph node cells enriched in CD138⁺ cells from four mice on day 8 after bMOG immunization. Cells were analyzed using 10× Genomics 5′ Single-Cell Gene Expression technology. The indicated cell subsets were identified using the tSNE distribution, K-means, and cell type-specific markers. Encircled cells were those selected for V(D)J profiling in Figure 3. Descriptive data on each subset are provided in table. Abbreviations: pDCs, plasmacytoid dendritic cells; cDCs, conventional dendritic cells. **(B)** Cells expressing the plasmablast markers CD138 and BCMA (blue). **(C)** Log₂ expression of *Birc5* revealing proliferating plasmablasts (encircled). **(D)** Heat map showing the expression profile of genes differentially regulated in plasmablasts compared to B cells, as identified by significant feature comparison in Loupe Cell Browser ($P \leq 0.04$). Median-normalized mean UMI counts were Ln(x+1)-transformed and centered without row scaling using Clustvis. **(E)** tSNE plot generated from mass cytometry data on lymph node cells on day 8 after bMOG immunization. **(F)** Markers used to identify plasmablasts (CD138), B cells (CD19), and type-2 cDCs (cDC2s; CCR7) in E. **(G)** Comparison of expression levels of proteins involved in antigen presentation between plasmablasts, B cells, and cDC2s. *Significantly different from plasmablast group (ANOVA, $P < 0.0001$; post hoc Tukey’s test ($P \leq 0.0004$)).

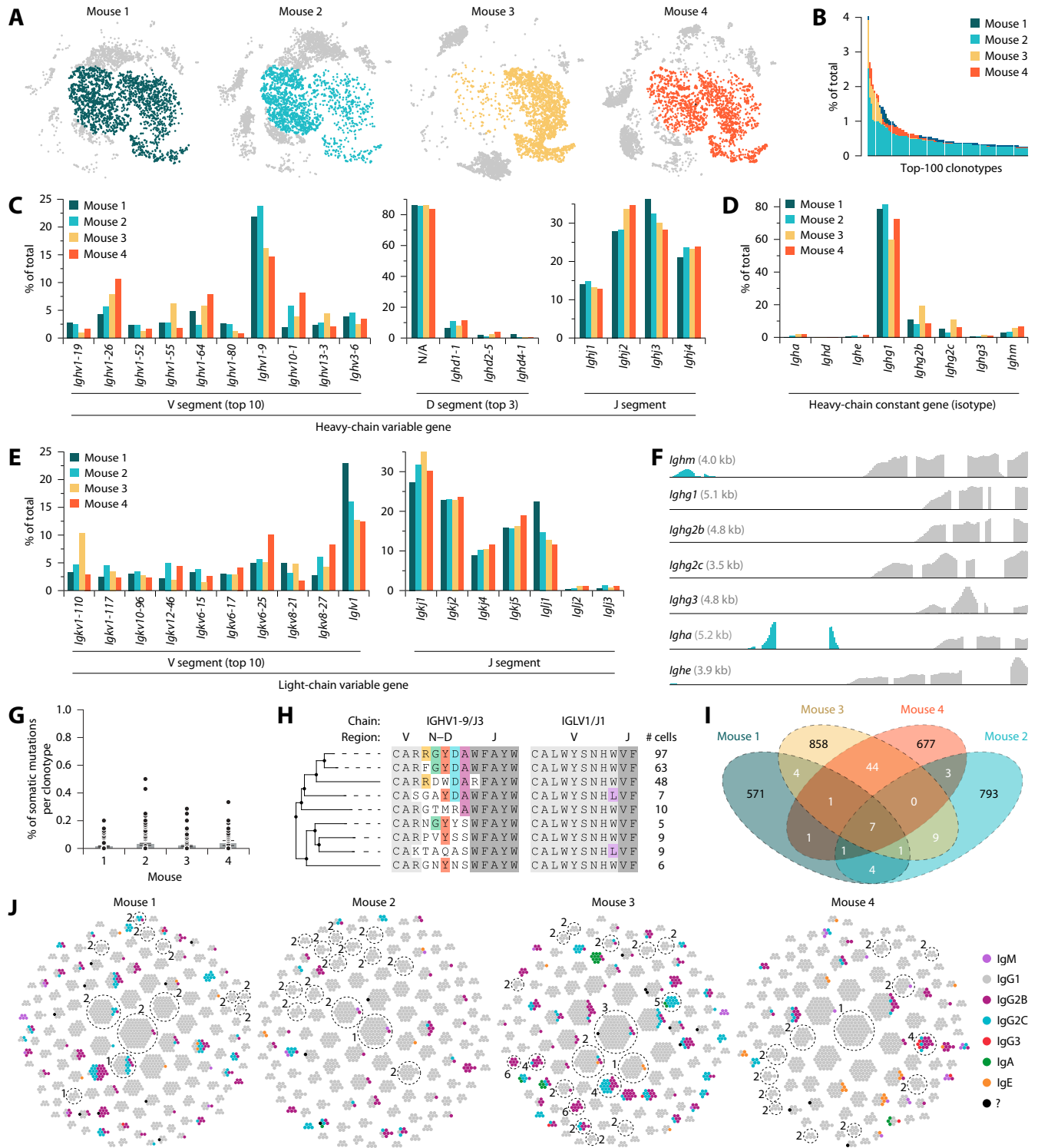


Figure 3. Profile of antibodies produced by bMOG-induced plasmablasts. **(A)** tSNE plots of gene expression data in Figure 2 showing plasmablasts selected for V(D)J analysis (colors). **(B)** Abundance distribution of the top-100 clonotypes, as analyzed using 10x Genomics Single-Cell V(D)J technology. **(C–E)** Comparison of immunoglobulin gene segment usage between mice. **(F)** Sequencing data from gene expression libraries showing the presence of the transmembrane domain (blue) in *Ighm*, *Igha*, and *Ighe*, but not *Ighg* transcripts. **(G)** Percentage of somatic mutations in the *Ighv* gene segment of the main clonotypes with ≥ 5 cells ($n = 89$ –123 clonotypes per mouse). Two outliers with mutation rates of 16 and 18% were excluded in mouse 4. **(H)** Comparison of the CDR3 region of the heavy and light chains of nine highly similar clonotypes from mouse 1, collectively referred to as clonotype 2 in J. These clonotypes were identical except for the CDR3 regions. Alignment was performed with webPRANK. **(I)** Number of clonotypes shared between mice. **(J)** Honeycomb plots showing clonotypes (dot clusters) with ≥ 5 cells (dots) of any isotypes. Numbers indicate clonotypes selected for further analysis.

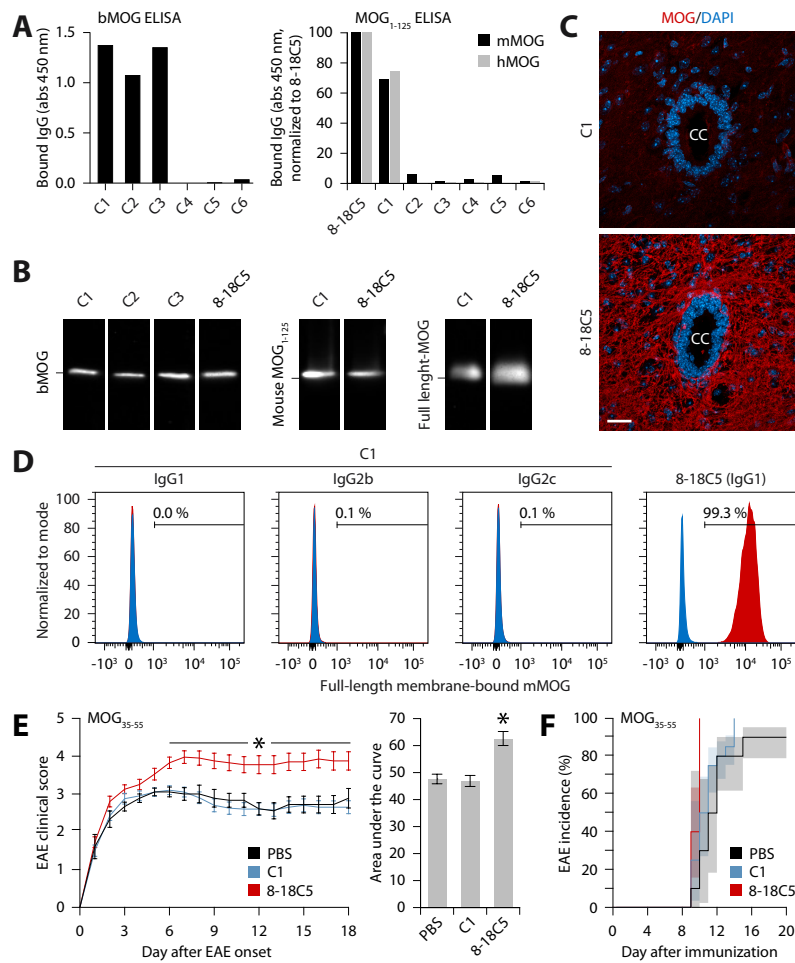


Figure 4. C1 can react with wild-type MOG, but not when the latter is in its native, plasma membrane-bound form, making it a non-pathogenic antibody. In all panels, anti-MOG IgG1 clone 8-18C5 was used as a positive control. Antibodies were IgG1, except in D where three C1 isotypes were tested. **(A)** ELISA against bMOG (left) or wild-type mouse and human MOG₁₋₁₂₅ (mMOG and hMOG; right). Quantity of bound IgG is expressed as either raw absorbance minus background (left) or absorbance normalized to 8-18C5 (right). **(B)** Western blot for bMOG, mouse MOG₁₋₁₂₅ or full-length MOG from mouse spinal cord extracts. **(C)** Spinal cord sections stained with anti-MOG antibodies (red) and DAPI (blue). Scale bar: 25 μm. CC = central canal. **(D)** Flow cytometry of live GL261 cells transfected to produce full-length MOG (red), incubated with anti-MOG antibodies, and stained with anti-mouse IgG antibody. Non-transfected cells (blue) were used as a negative control. **(E)** Severity of EAE in mice immunized with MOG₃₅₋₅₅ and injected intravenously 8 days later with PBS or 200 μg of the indicated antibody. Data from two independent experiments are expressed as either daily scores from the day of disease onset (left) or area under the curve (right). Left panel: *significantly different from PBS (two-way ANOVA with repeated measures using rank-transformed data, $P < 0.0001$; post hoc Mann-Whitney tests, $P \leq 0.049$). Right panel: *significantly different from the other groups (one-way ANOVA, $P < 0.0001$; post hoc Tukey's test, $P \leq 0.0012$). Sample size: 9 PBS; 20 clonotype 1; 20 8-18C5. **(F)** Disease incidence of experiments in E. Log-rank test, $P = 0.0003$. Sample size: 10 PBS; 20 clonotype 1; 20 8-18C5.

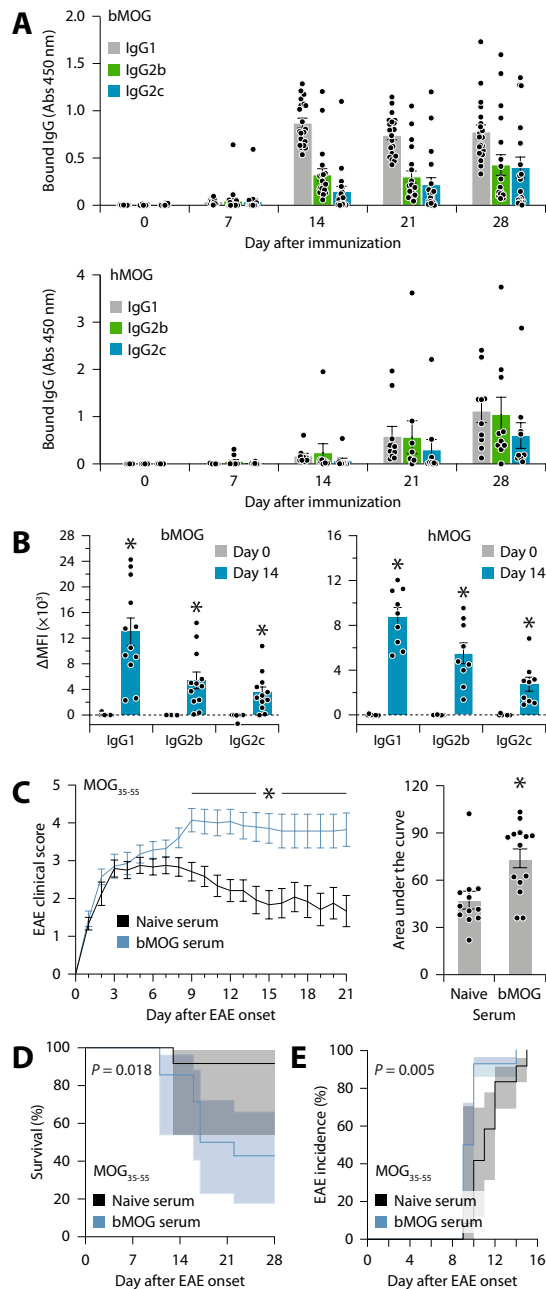


Figure 5. Pathogenic anti-MOG IgG antibodies are produced in B cell-dependent EAE models. **(A)** ELISA detection of anti-MOG IgG1, IgG2b, and IgG2c in serum from mice immunized with either bMOG (top) or hMOG (bottom) through time. Sample size per group: bMOG, 16-20 mice; hMOG, 10 mice. **(B)** Detection of anti-MOG antibodies by live cell-based assay in serum from mice immunized with either bMOG (left) or hMOG (right). GL261 cells transfected to produce full-length mMOG were incubated with serum collected before or after immunization (days 0 and 14), and stained with isotype-specific secondary antibodies. Data are expressed as delta mean fluorescence intensity (Δ MFI). *Significantly different from day 0 group from same isotype (Mann-Whitney test, $P < 0.0001$). Sample size per group: bMOG, 12 mice; hMOG, 9 mice. **(C)** Severity of EAE in MOG₃₅₋₅₅-immunized mice injected with 150 μ l of serum from either naive mice or mice sacrificed 8 days after immunization with bMOG. Data are expressed as either daily scores from the day of disease onset (left) or area under the curve (right). Left panel: *significantly different from naive group as determined by two-way ANOVA with repeated measures using rank-transformed data ($P = 0.002$), followed by post hoc Mann-Whitney tests ($P \leq 0.007$). Right panel: Mann-Whitney test, $P = 0.006$. Data are from two independent experiments. Sample size: 12 naive serum; 14 bMOG serum. **(D)** Survival and **(E)** disease incidence rates for the experiment in C. P -values shown were calculated using the log-rank test. Sample size: as in C.

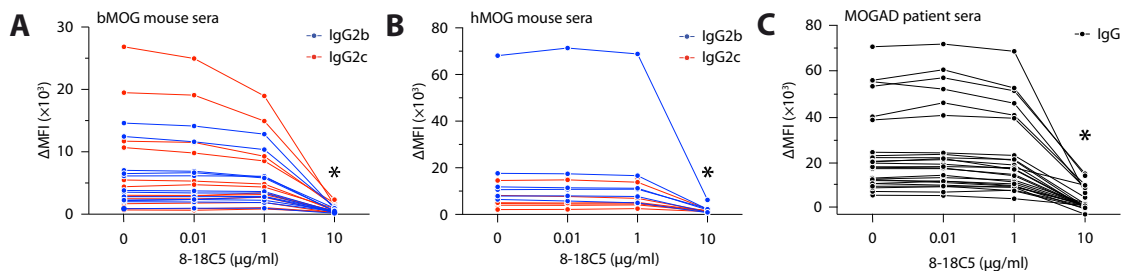


Figure 6. 8-18C5 competes with mouse and human pathogenic anti-MOG antibodies for binding to plasma membrane-bound MOG. **(A)** Live cell-based assay in which mMOG-expressing cells were sequentially incubated with 8-18C5 at the indicated concentrations, mouse serum collected on day 14 post-immunization with bMOG, and secondary antibodies to mouse IgG2b and IgG2c. Data are expressed as delta mean fluorescence intensity (ΔMFI). *Significantly different from the other concentrations (Kruskal-Wallis test, $P \leq 0.0003$ for both IgG2b and IgG2c; post hoc Dunn's test, $P \leq 0.0028$). Sample size: 12 sera. **(B)** Same analysis as in A, except that the sera were from hMOG-immunized mice. *Significantly different from the other concentrations (Kruskal-Wallis test, $P \leq 0.0072$; post hoc Dunn's test, $P \leq 0.0042$). Sample size: 6 sera. **(C)** Same analysis as in A, except that hMOG-expressing cells were incubated with serum from MOGAD patients and stained with an anti-human IgG secondary antibody. *Significantly different from the other concentrations (Kruskal-Wallis test, $P < 0.0001$; post hoc Dunn's test, $P < 0.0001$). Sample size: 25.

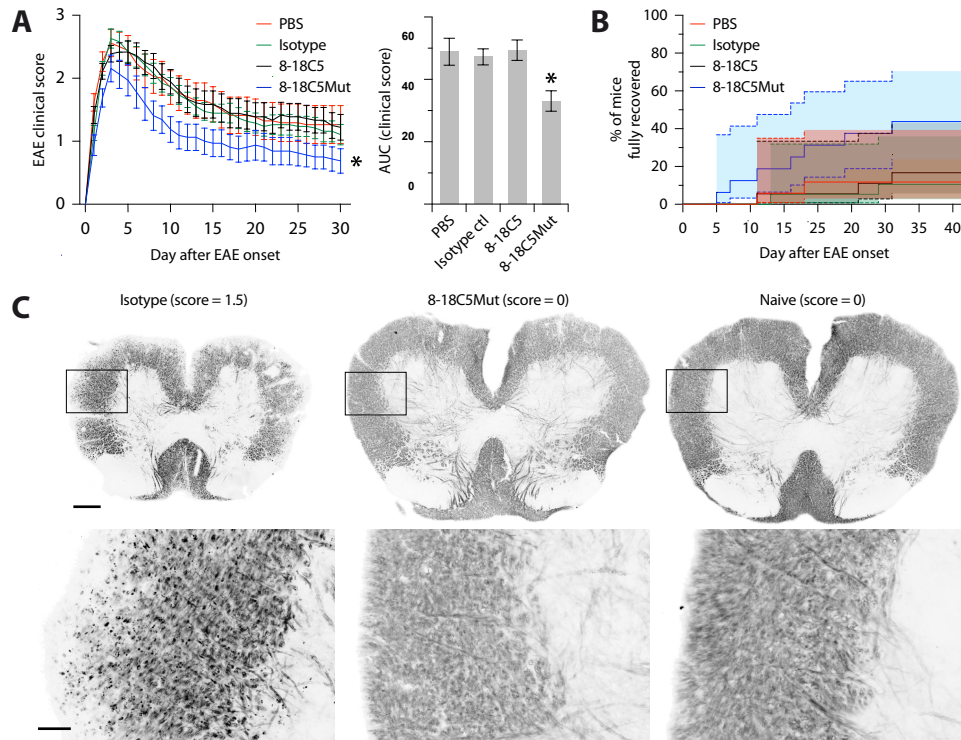


Figure 7. bMOG-induced EAE can be attenuated with 8-18C5Mut. **(A)** Severity of EAE in mice intravenously injected with PBS or 200 μ g of the indicated antibody on day 9 post-immunization. Data are expressed as either daily scores from the day of disease onset (left) or area under the curve (right). Left panel: *significantly different from the isotype group, as determined by two-way ANOVA with repeated measures ($P = 0.049$), followed by Fisher's LSD tests ($P \leq 0.0451$), using rank-transformed scores. Right panel: *significantly different from the other groups (one-way ANOVA, $P = 0.0036$; post hoc Tukey tests, $P \leq 0.0220$). Data are from two independent experiments. Sample Size: 18 8-18C5, 16 8-18C5Mut, 19 isotype, 17 PBS. **(B)** Kaplan-Meier plot showing the percentage of mice from panel A that had completely recovered by the end of experiment (log-rank test: overall, $P = 0.0331$; 8-18C5Mut vs isotype, $P = 0.0229$). Shaded areas: 95 % pointwise confidence interval. **(C)** Black gold-stained spinal cord sections on day 43 post-immunization at low (top) or high (bottom) magnification. Evidence of demyelination (lost or granular staining) is observable in a mouse treated with isotype antibody, but not in a mouse treated with 8-18C5Mut or not immunized (naive). The clinical score at the time of sacrifice is indicated for each mouse. Scale bars: top, 200 μ m; bottom, 50 μ m.