

1 **CD27 is required for protective lytic EBV antigen specific CD8⁺ T cell expansion**

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22 Running title: CD27 mediated immune control of EBV

23

24 **KEY POINTS**

25 • Blockade of CD27/CD70 interaction compromises EBV-specific immune
26 control.

27 • CD27 is particularly required for the expansion and effector function of lytic
28 EBV antigen specific CD8⁺ T cells.

29

30 **ABSTRACT**

31 Primary immunodeficiencies in the co-stimulatory molecule CD27 and its ligand
32 CD70 predispose for pathologies of uncontrolled Epstein Barr virus (EBV) infection
33 in nearly all affected patients. We demonstrate that both depletion of CD27 positive
34 cells and antibody blocking of CD27 interaction with CD70 causes uncontrolled EBV
35 infection in mice with reconstituted human immune system components. While
36 overall CD8⁺ T cell expansion and composition is unaltered after antibody blocking
37 of CD27, only some EBV specific CD8⁺ T cell responses, exemplified by early lytic
38 EBV antigen BMLF1 specific CD8⁺ T cells are inhibited in their proliferation and
39 killing of EBV transformed B cells. This suggests that CD27 is not required for all
40 CD8⁺ T cell expansions and cytotoxicity, but for a subset of CD8⁺ T cell responses
41 that protect us from EBV infection.

42

43 Keywords: CD27; CD70; humanized mice; Epstein Barr virus; cytotoxicity

44 **INTRODUCTION**

45 Epstein Barr virus (EBV) is a common γ -herpesvirus that infects more than 95% of
46 the human population ¹. At the same time, it was the first human tumor virus
47 discovered in the 1960s ^{2,3}. It is also associated with a spectrum of pathologies in
48 humans ^{4,5}, ranging from B cell lymphomas and epithelial cell carcinomas to
49 immunopathologies like hemophagocytic lymphohistiocytosis (HLH) and infectious
50 mononucleosis (IM). The diverse manifestations of EBV pathology are connected to
51 the lytic and 4 latent (latency 0 to III) gene expression programs that EBV can switch
52 between in healthy virus carriers ⁶. These are also mirrored in EBV associated
53 malignancies, such as Burkitt's lymphoma (latency I) and Hodgkin's lymphoma
54 (latency II). Despite this high pathogenic potential and wide distribution of EBV in
55 the human populations the respective tumors are with an annual incidence of around
56 200'000, fortunately, quite rare ⁷.

57 A nearly perfect cell-mediated immune control protects us from EBV
58 associated pathologies. This becomes apparent under conditions of primary or
59 acquired immunodeficiencies, such as HIV co-infection ^{5,8,9}. They identify cytotoxic
60 lymphocytes, mainly CD8⁺ T cells, as the primary immune compartment for EBV
61 specific immune control ¹⁰⁻¹². Defects in T cell receptor signalling have been
62 identified in primary immunodeficiencies that predispose for EBV associated
63 pathologies. These affect among others interleukin-2 inducible T cell kinase (ITK),
64 ZAP70 and PI3K 110 δ . Furthermore, development and expansion of cytotoxic
65 lymphocytes is required for EBV specific immune control and this is compromised by
66 mutations in GATA2, MCM4, XIAP, STK4 and CTPS1. The last group of molecules
67 that are required for EBV associated immune control, affect co-stimulation of CD8⁺ T
68 cells. Among these, mutations in both CD27 and its ligand CD70 have been identified
69 as a nearly exclusive cornerstone of EBV specific immune control. Previous research
70 has shown that nearly all affected patients develop EBV associated pathologies, with
71 HLH-like immunopathologies more often observed in CD27 deficiencies and
72 Hodgkin's lymphoma more frequent in CD70 deficiencies ¹³⁻¹⁸.

73 Therefore, we investigated the requirement for CD27 positive lymphocytes
74 and CD27 engagement of CD70 during EBV infection in mice with reconstituted
75 human immune system components. We found that depletion of CD27 positive cells
76 and blocking of CD27 compromised EBV specific immune control resulting in

77 elevated viral titres and expansion of infected CD39⁺CD70⁺ B cells. Overall CD8⁺ T
78 cell expansion was not compromised by CD27 blocking. However, the expansion and
79 cytotoxicity of early lytic EBV antigen specific CD8⁺ T cells, exemplified by BMLF1
80 specific cytotoxic lymphocytes, was abolished, suggesting that CD27 is required for
81 an important part of the immune control of EBV.

82 **METHODS**83 **Humanized mouse generation and infection**

84 NOD-scid γ_c^{null} (NSG) mice and HLA-A2 transgenic NSG mice were maintained in
85 ventilated, specific pathogen-free condition at the Institute of Experimental
86 Immunology, University of Zurich. Newborn pups were reconstituted with human
87 CD34 $^+$ hematopoietic progenitor cells (HPCs). Mice with sufficient reconstitution of
88 human immune cells were injected with 10⁵ Raji Green units (RGU) of EBV. The
89 detailed procedure for NSG and NSG-A2 reconstitution and virus production are
90 provided in the Supplemental Methods. All animal work strictly followed the animal
91 protocols ZH209/2014 & ZH159/17, licensed by the veterinary office of the canton of
92 Zurich, Switzerland.

93

94 ***In vivo* anti-CD27 antibody depletion and blocking**

95 CD27 depleting mAB (clone: LG.3A10) and the corresponding Armenian hamster
96 IgG isotype control (Biolegend) were injected i.p. at 12.5 μ g/g of the mouse weight
97 two weeks post EBV infection and continued every 4 days until the termination of
98 experiment. CD27 blocking mAB (clone: LG.3A10) and the corresponding mouse
99 IgG1 isotype control (Absolute Antibody) were injected i.p. at 6.25 μ g/g of the mouse
100 weight two weeks post EBV infection and continued every 4 days until the
101 termination of experiment.

102

103 **ChipCytometry**

104 Splenic tissues harvested at the termination of experiments were embedded in OCT
105 (Tissue-Tek) at -80°C. Cryosections (5-6 μ m thick) were fixed and inserted into
106 ZellSafe T chips (Canopy Biosciences) for staining. Samples labeled with fluorescent
107 antibodies were acquired with a Zellkraftwerk ZellScanner One and its ZellExplorer
108 software. After each round of acquisition, the fluorescent signals were photobleached
109 and prepared for the next round of staining to accomplish a 27-marker panel.
110 Additional details are provided in the Supplemental Methods.

111

112 **Laboratory assays**

113 Multiple assays were conducted to analyse the experimental samples including flow
114 cytometry, *in vivo* IVIS imaging, LCL generation, cytotoxicity assay,

115 immunohistochemistry and immunofluorescence, serum cytokine quantification and
116 quantitative RT-PCR. Assay details are provided in the Supplemental Methods.

117

118 **Statistical analysis**

119 Statistical significance was calculated with 1) Mann-Whitney U test to analyze
120 unpaired data with a non-Gaussian distribution, 2) one-way ANOVA (Kruskal-Wallis
121 test) followed by Dunn's post hoc test or 3) two-way ANOVA with Sidak's (or
122 Tukey's) multiple comparisons as post hoc test or 4) two-tailed unpaired t test by
123 Prism 7 (GraphPad Software). D'Agostino-Pearson omnibus normality test was used
124 to determine normality of data. All data points in the graphs are displayed with
125 median and interquartile range, indicated with horizontal lines. N represents number
126 of biological replicates unless otherwise stated. High-dimensional analysis details are
127 provided in Supplemental Methods.

128

129 **RESULTS**130 **CD27 shows a similar expression pattern on T cells of humans and humanized**
131 **mice.**

132 To investigate the specific contribution of CD27 to EBV associated immune control,
133 we have primarily used a mouse model with reconstituted human immune system
134 compartments (humanized mice) that allows establishment of EBV infection,
135 lymphomagenesis and its cell-mediated immune control *in vivo*^{19,20} (Figure 1A). To
136 examine whether humanized mice are a suitable model to study CD27 function, we
137 characterized CD27 expression on single cell suspensions of peripheral blood
138 mononuclear cells (PBMCs) of healthy donors and humanized mice. The majority of
139 CD27⁺ cells of both PBMC sources were CD4⁺ and CD8⁺ T cells (Figure S1A, Figure
140 1B). There was a similarly high level of expression on T cells in individual cell
141 populations (Figure 1C). Slightly higher expression in the naïve population
142 (CCR7⁺CD45RA⁺) but lower expression in Temra (CCR7⁻CD45RA⁺) and Tem
143 (CCR7⁻CD45RA⁻) in CD3⁺CD27⁺ T cells was observed in humanized mice (Figures
144 1D and 1E). Taken together, these data demonstrate that CD27 has a similar
145 distribution pattern on T cells in humanized mice and humans. Thus, we conclude that
146 humanized mice are a suitable model to study the role of CD27 expression on human
147 T cells for EBV infection.

148

149 **CD27⁺ cells are important in the immune control of EBV viral loads and**
150 **tumorigenesis during EBV infection in humanized mice**

151 We next determined how important the CD3⁺CD27⁺ cells are to protect against EBV
152 infection. To this end, we adopted the acute (or IM-like) EBV infection model by
153 injecting humanized mice with 10⁵ Raji green unit (RGU) of B95-8 EBV²¹. In order
154 to allow priming of EBV specific T cell responses prior to depletion, CD27 positive
155 cells were depleted starting at week two post infection (Figure 2A). A depletion effect
156 of CD3⁺CD27⁺ T cells was observed and persisted for up to six days (Figure S2A).
157 Therefore, depleting antibody injection was repeated every four days. There was a
158 significant drop in CD3⁺ T cells in the peripheral blood under treatment (Figure 2B).
159 A clear reduction in total CD3⁺ T cell count was observed in both blood and spleen
160 samples (Figures 2C and 2D). There was no significant difference in total CD19⁺ B
161 cell counts (Figure 2B), consistent with low CD27 expression in this immune
162 compartment (Figure 1B and C). Loss of T cells in infected animals treated with

163 depleting antibody led to a higher frequency of tumor incidence (Figure 2E).
164 Furthermore, EBV viral burden was significantly elevated in both blood and spleen
165 after CD27 depletion (Figures 2F-H). The detected viral load is primarily cell-
166 associated ²². Consistently, the number of EBNA2-expressing cells, which indicates
167 early virus-transformed B cells ²³, was significantly increased in spleen (Figures 2I
168 and 2J). Altogether, these experiments suggest an essential role of CD27⁺ T cells in
169 providing EBV specific immunity and preventing development of EBV associated
170 malignancies.

171

172 **Blocking of CD27 diminishes the immune control of EBV infection**

173 We next sought to investigate the effect of CD27 co-stimulation on EBV-specific
174 immune control using HLA-A2 transgenic humanized mice reconstituted with HLA-
175 A2⁺ CD34⁺ HPCs (NSG-A2). To monitor both bulk T cell subsets and EBV antigen
176 specific CD8⁺ T cell responses, we adoptively transferred recombinant HLA-A2
177 restricted T cell receptor (TCR) transduced human T cells, previously isolated from
178 donor-mate NSG-A2 animals, which are specific for either 1) the early lytic EBV
179 antigen BMLF1 or 2) the latent EBV antigen LMP2 (Figures 3A and 3B). Both the
180 TCR transduced (both specificities) and bulk CD8⁺ T cells showed similar levels of
181 CD27 expression before transfer (Figure 3B). Following transfer, humanized NSG-A2
182 mice were infected with luciferase-expressing EBV (Luc-EBV) in order to monitor
183 the localization of infection by *in vivo* imaging and then treated with either CD27
184 blocking antibody or isotype control starting from week 2 after infection. There was
185 no depletion effect on CD3⁺ T and CD19⁺ B cells observed (Figures S3A and S3B).
186 The blocking effect of the antibody was checked by flow cytometry using two
187 fluorochrome conjugated anti-CD27 antibodies (Figure S3C). While the antibody
188 (clone: O323) derived from a different clone than the blocking antibody could still
189 detect CD27 (Figure S3D), the antibody (clone: LG.3A10) derived from the same
190 clone as the blocking antibody was inhibited from binding (Figure S3E).

191 Animals treated with CD27 blocking antibody exhibited splenomegaly 5
192 weeks post-infection (Figure 3C). However, CD27 blocking did not seem to have an
193 effect on animal weight (Figure S3F) and survival (Figure S3G). A significant
194 increase in blood viral loads was observed upon CD27 blocking (Figure 3D) as well
195 as in spleen and liver (Figure 3E). Viral loads of the groups transferred with BMLF1
196 or LMP2 specific T cells or mock transduced cells were not different (Figures S3H).

197 Additionally, the number of EBNA2 positive cells was significantly higher in splenic
198 sections upon CD27 blocking (Figures 3F and 3G) and CD27 expression on EBV
199 infected B cells in blood and spleen was also higher (Figure S3I). To assess the viral
200 burden and infection progression, mice were imaged with an IVIS Spectrum Imaging
201 System on a weekly basis. The bioluminescent signal showed a significantly higher
202 level due to CD27 blocking at week 5 post EBV infection (Figures 3H and 3I).
203 Moreover, with respect to individual EBV gene expression, both latent genes (EBER1,
204 EBNA2, LMP1, LMP2a and EBNA1_Wp) and lytic genes (BMLF1, BMRF1,
205 BGLF5, BNLF2a and BILF1) were higher expressed after blocking CD27 (Figure
206 S3J).

207 In order to examine if CD27 blocking has a selective effect on immune control
208 of latent or lytic EBV infection, humanized NSG mice were infected with wild type
209 EBV and compared with BZLF1 knock-out EBV (BZkoEBV) that cannot switch into
210 lytic replication. Interestingly, wild type EBV infected animals showed significantly
211 higher spleen weights (Figure 3J) and viral loads in both blood and spleen (Figures
212 3K and 3L) upon CD27 blocking, as compared to animals infected with BZkoEBV
213 with and without CD27 inhibition. Additionally, the number of EBNA2 positive cells
214 was significantly higher in wild type EBV infected animals treated with the anti-
215 CD27 antibody, as compared to the other groups (Figures S3K and S3L). Taken
216 together, these data reveal that CD27 blockade leads to loss of EBV specific immune
217 control, primarily against lytic EBV antigen expression.

218

219 **CD70⁺CD39⁺EBNA2⁺ B cells accumulate upon loss of CD27 mediated immune
220 control of EBV**

221 To better understand which EBV infected B cells accumulate in the absence of CD27
222 mediated immune control, we checked their phenotype on sacrifice day (Figure 3A).
223 It has been previously shown that expression of both CD70 and CD39 are up-
224 regulated on lymphoblastoid cell lines (LCLs), which consist of EBV transformed B
225 cells^{24,25}. Both markers were reported to be highly expressed in B-cell lymphomas
226 such as germinal center B-cell-like (GCB) and activated B-cell-like diffuse large B-
227 cell lymphomas (DLBCL)^{26,27}. We observed significantly increased expression of
228 CD70 and CD39 in the peripheral blood, spleen and liver (Figures 4A-C) upon CD27
229 blocking. No significant increase was seen in CD73⁺ and CD39⁺CD73⁺ populations
230 (Figure 4B). However, CD39 frequency positively correlated with EBV viral loads

231 (Figure 4D). Additionally, we found reduced expression of CXCR5 and CCR7 after
232 blocking CD27, two chemokine receptors important for B cell migration into
233 lymphoid organs (Figures 4E and 4F).

234 Next, we assessed the co-expression of CD70 and CD39, together with Ki67
235 for B cell proliferation and EBNA2 for EBV infection in blood (Figure S4A) and
236 spleen (Figure S4B). Two phenotypically distinct populations were identified with
237 respect to the expression of CD70 and CD39 (Figures 4F and 4G). In animals treated
238 with anti-CD27 blocking antibody, we found the CD70⁺CD39⁺ population was more
239 expanded and showed high co-expression of Ki67 and EBNA2 in blood (Figure 4H).
240 The same phenotypic difference was also observed in spleen (Figures S4C-4E). In
241 summary, these results suggest that CD27 blocking allows accumulation of
242 CD39⁺CD70⁺ DLBCL-like EBV infected B cells with possibly more aggressive
243 proliferative behavior.

244

245 **Early EBV lytic antigen BMLF1 specific CD8⁺ T cells require CD27 for
246 expansion and cytotoxicity**

247 We next addressed whether CD27 blocking affected particularly EBV specific CD8⁺
248 T cell responses *in vivo*. In line with CD27 deficient patient data, which showed
249 normal T cell differentiation compared to healthy controls in peripheral blood¹⁴, our
250 results demonstrated that CD27 blockade did not lead to a change in bulk T cell
251 differentiation (Figure 5A), as well as in the memory subset composition of EBV
252 specific CD8⁺ T cells (Figure S5A) in blood. No significant difference was also
253 observed in spleen, liver and bone marrow (Figure S5B). We next examined BMLF1
254 and LMP2 specific CD8⁺ T cells which were adoptively transferred into the animals
255 (Figure 5B). In line with CD27 blocking mainly affecting immune control of lytic
256 EBV infection, there was an impaired expansion of BMLF1 specific CD8⁺ T cells in
257 animals treated with CD27 blocking antibody longitudinally in blood (Figure 5C),
258 while such a difference was not observed for LMP2 specific CD8⁺ T cells (Figure 5D).
259 Further analysis in spleen and liver showed similar results with selective impairment
260 of BMLF1 specific, but not LMP2 specific CD8⁺ T cells (Figures 5E and 5F).
261 Moreover, significantly increased Ki67 expression on BMLF1 specific CD8⁺ T cells
262 (depicted as CD8 Pent⁺ cells), as compared to non-BMLF1 specific T cells (depicted
263 as CD8 Pent⁻ cells), was observed in the isotype antibody treated group. However,
264 CD27 blockade seemed to suppress proliferation of BMLF1 specific CD8⁺ T cells as

265 Ki67 expression was reduced comparable to bulk CD8⁺ T cell levels (Figures 5G-5H).
266 By contrast, LMP2 specific CD8⁺ T cells showed no difference (Figure 5I).

267 Given that cytotoxicity is the main protective T cell function during EBV
268 infection, we further assessed T cell cytolytic response by co-culturing LCLs with
269 BMLF1 and LMP2 specific CD8⁺ T cell clones, generated *ex vivo* from the
270 autologous healthy human donor ²⁸. We found that BMLF1 specific T cells showed
271 significantly reduced cytotoxic activity against LCLs after blocking CD27 at the
272 effector to target ratio of 10 to 1 (Figures 5J and 5K). However, the proliferation of
273 LCLs was not influenced by CD27 blocking (Figure S5B). In summary, these data
274 reveal a differential susceptibility of early lytic and latent EBV antigen-specific CD8⁺
275 T cells to CD27 blockade during EBV infection.

276

277 **CD27 blockade compromises CXCR5⁺EOMES⁺ CD8⁺ T cell accumulation 278 during EBV infection**

279 To interrogate the alterations in proinflammatory cytokine production after CD27
280 blockade, we examined terminal serum samples. Animals treated with the CD27
281 blocking antibody exhibited significantly elevated levels of IFN γ , IL-10 and highly
282 increased levels of TNF α (Figure 6A), suggesting that CD27 blocking increases the
283 inflammatory immune responses which might contribute to EBV associated
284 pathologies. Consistent with a more proinflammatory environment, CD27 blockade
285 also led to a moderately decreased expression of CXCR5 on CD8⁺ T cells in blood
286 and liver (Figure 6B).

287 We next assessed the differential expression of T-box transcription factors (T-
288 bet) and eomesodermin (EOMES), which are key drivers for effector functions and
289 long-term memory formation of T cells ^{29,30}. We found the frequency of EOMES^{bright}
290 T-bet^{dim} CD8⁺ T cells to be reduced after CD27 blockade (Figures 6C), indicating that
291 cytotoxic effector and effector memory T cell functions are decreased. In addition, the
292 expression of the activation/tissue residency marker CD69 was diminished (Figure
293 6D), whereas an upregulation in the expression of co-stimulatory 2B4 and inhibitory
294 PD1 was observed on CD8⁺ T cells (Figure 6E).

295 To obtain spatial information of activated CD8⁺ T cells in relation to EBV
296 infected B cells, we investigated splenic sections by ChipCytometry, a multiplexing
297 tissue imaging technology that allows for repeated rounds of immunofluorescence

298 staining and bleaching to assess multiple parameters in histological sections. CD20⁺ B
299 cells and CD8⁺ T cells were aggregated in white pulp areas of isotype control treated
300 spleens (Figure S6A). We assessed a 27-marker panel plus a nuclear staining (Table
301 S1, Figure S6C, D, E and F) by ChipCytometry and observed co-localization between
302 CD20 and EBNA2, CD8 and CD69, and CD8 and PD1 in splenic white pulp areas
303 (Figure 6F). Quantification of segmented cells showed higher frequencies of CD8⁺ T
304 cells and EBNA2⁺CD20⁺ cells after CD27 blockade (Figures S6B). The ratio of
305 CD8⁺/EBNA2⁺CD20⁺ cells was significantly higher upon CD27 blocking, suggesting
306 compromised immune control despite efficient CD8⁺ T cell expansion. However,
307 CD8⁺ T cells were similarly activated as judged by PD1 and CD69 expression (Figure
308 6G). Thus, these results suggested that CD27 blockade may compromise terminal
309 cytotoxic CD8⁺ T cell differentiation with homing capacity to germinal centers in
310 secondary lymphoid organs, where cytotoxic EBV specific immune control needs to
311 take place.

312

313 **DISCUSSION**

314 In this study, we performed *in vivo* experiments using humanized mice as an EBV
315 infection model to address CD27 deficiency during EBV specific immune responses.
316 Both CD27⁺ lymphocyte depletion and CD27 blocking compromised EBV specific
317 immune control. We deciphered that CD27 blockade had a dramatic effect on the
318 protective function of early lytic EBV antigen (BMLF1) specific CD8⁺ T cells, but to
319 a lesser extent on latent EBV antigen (LMP2) specific CD8⁺ T cells, despite the
320 elevated gene expression of BMLF1 in B cells of the CD27 blocking antibody treated
321 group (Figure 3J), which should have driven BMLF1 specific T cell expansion more
322 efficiently. In line with our findings, previous studies in CD27 deficient patients
323 showed a detectable level of EBV specific T cells against LMP2 and autologous LCL
324 restimulation^{13,17}, suggesting that CD27 signaling may be involved in expansion of
325 early lytic antigen specific cytotoxic CD8⁺ T cell responses. In line with these
326 findings CD27 was required for the immune control of wild-type but not lytic
327 replication deficient EBV infection.

328 Although CD27 has been reported to regulate T cell survival, expansion and
329 memory generation³¹⁻³³, its blocking did not seem to have an impact on overall T cell
330 differentiation during EBV infection in humanized mice. This is consistent with
331 clinical observations from both CD27 and CD70 deficient patients^{14,16,18}, in which

332 the T cell repertoire composition seems also largely unaltered compared to healthy
333 controls. Consistent with our findings, only some, but not other EBV specific CD8⁺ T
334 cell responses were diminished in the affected patients ^{16,18}. These CD27 dependent T
335 cell specificities might be stimulated by and target early EBV infected B cells in
336 which CD70 peaks at day 5 in mRNA and day 8 in protein expression after infection
337 ^{34,35}, and even earlier leaky lytic EBV antigen expression can be targeted by CD8⁺ T
338 cells to eliminate EBV infected B cells ³⁶. These data from both CD27 blocking in
339 humanized mice and CD27 or CD70 deficient patients argue that absence of
340 CD27/CD70 signaling does not alter T cell repertoire composition or even bulk CD8⁺
341 T cell expansion to EBV infection, but that a subset of protective CD8⁺ T cell
342 responses against lytic EBV antigens, exemplified by BMLF1 specific CD8⁺ T cells,
343 depends on CD27 for their expansion and cytotoxicity.

344 Interestingly, patients with RASGRP1 deficiency, the main activator of the
345 MAP kinase pathway, exhibited a reduced T cell expansion in a CD27 dependent
346 manner ³⁷. RASGRP1 deficient T cells failed to proliferate upon stimulation with
347 CD70^{high} LCLs ^{37,38}. This result further confirmed the importance of CD27/CD70 and
348 the downstream MAP kinase pathway in the expansion of EBV-specific T cells.

349 Other co-stimulatory molecules affecting T cell interactions with B cells also
350 seem to play a unique role in immunity to EBV. For instance, it has been discovered
351 that in X-linked lymphoproliferative disease type 1 (XLP-1) the deficiency of the
352 SLAM-associated protein (SAP) compromises co-stimulatory 2B4 function ³⁹. This
353 leads to a profound effect on cytotoxicity against EBV infected B cells ^{40,41}, however,
354 it still allows expansion of EBV specific CD8⁺ T cells ^{42,43}. Accordingly, humanized
355 mice present with similar CD8⁺ T cell expansion but less controlled EBV infection
356 after antibody blocking of 2B4, and SAP deficient patients suffer from EBV
357 pathology despite their normal frequencies of EBV specific CD8⁺ T cells ^{41,44}. This
358 implies that 2B4 might only be required for cytotoxic CD8⁺ T cell recognition of
359 EBV transformed B cells, while CD27 promotes expansion and cytotoxicity of a
360 subset of protective EBV specific CD8⁺ T cells. Possibly compensatory 2B4 up-
361 regulation was observed on CD8⁺ T cells in our experiments upon CD27 blocking,
362 but diminished expression of this co-receptor was reported in CD27 or CD70
363 deficient patients ¹⁸. In contrast to the better understood role of CD27 and 2B4, the
364 functions of 4-1BB, NKG2D, CTLA-4 and PD-1 that are required for EBV specific
365 immune control still need to be defined ^{21,45-49}. However, different EBV associated

366 pathologies were observed in primary immunodeficiencies affecting these molecules
367 suggest their non-redundant roles in controlling virus infection. A better
368 understanding of these underlying mechanisms should allow us to harness these co-
369 stimulatory and co-inhibitory functions for immune modulation.

370 The selective loss of expansion and cytotoxicity of a subset of EBV specific
371 CD8⁺ T cells was also associated with a significant up-regulation in the co-expression
372 of CD39 and CD70 on the EBV infected B cells in our study. This indicates more
373 activation of B cells after blocking CD27/CD70 interaction, which might promote
374 EBV mediated growth transformation and development of persistent infection in B
375 cells, ultimately resulting in DLBCL-like malignancies. This altered phenotype of
376 EBV infected B cells might be the result of higher EBV viral loads or selective
377 targeting of CD39⁺CD70⁺ EBV infected B cells by the CD27 dependent CD8⁺ T cell
378 response. However, in the absence of efficient cytotoxicity against B cells through the
379 CD27/CD70 axis, elevated proinflammatory cytokines might also provoke higher
380 expression of CD70 on EBV infected B cells. Similar results have also been reported
381 for CD48, the ligand of 2B4, which was up-regulated in SAP deficiency during EBV
382 infection ⁴⁰. Thus, not only overall EBV infection increases upon CD27 blocking, but
383 also the phenotype of the infected B cells seems to change.

384 These CD39⁺ B cells might be mainly involved in the expansion of BMLF1
385 specific CD8⁺ T cells and in turn be controlled by the subset of EBV specific
386 cytotoxic CD8⁺ T cell responses that fail to expand during CD27 blocking and
387 deficiency, indicating that this subset of EBV specific CD8⁺ T cells are particularly
388 sensitive to CD27 deficiency. In contrast, CD8⁺ T cell responses to the related β -
389 herpesvirus human cytomegalovirus (HCMV) that has with 50% also a high
390 prevalence in the human population have been shown to be CD27⁻CD28⁻ ⁵⁰. This
391 might at least explain why EBV, but not HCMV specific immune control by T cells is
392 sensitive to CD27 or CD70 deficiency. The near exclusive susceptibility of CD27 or
393 CD70 deficient patients to EBV pathology argues that most common infections apart
394 from EBV follow the HCMV example.

395 Collectively, these results suggest a unique and non-redundant role of CD27 to
396 EBV specific immunity, mainly emphasizing its function in T cell expansion and
397 cytotoxicity, primarily of a subset of EBV specific T cells, such as BMLF1 specific
398 CD8⁺ T cells. Absence of immune control by these CD27 dependent CD8⁺ T cells

399 leads to uncontrolled EBV infection. Our results also support a possibly protective
400 role of early antigen specific CD8⁺ T cell responses against EBV infection and
401 lymphomagenesis ¹. Moreover, restoration of the CD27/CD70 pathway by CD27
402 agonistic antibody could be a therapeutic approach for the treatment of EBV
403 associated lymphomas, especially in patients with a CD70 deficiency.

404

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409 **AUTHORSHIP CONTRIBUTIONS**

410 Contribution: Y.D. designed the study, performed the majority of the experiments and
411 analysed the data. B.C., K.Z., and H.Z. helped with design and perform experiments;
412 A.M., L.-A.L. and A.B. performed the ChipCyometry and its quantification; P.S., R.C.
413 and A.Z. established the quantification of viral loads; A.H. and H.S. generated the
414 TCR constructs; W.H. provided with the Luc-EBV and C.M. designed the study with
415 Y.D. and supervised the study; Y.D. and C.M. prepared the figures and wrote the
416 manuscript.

417

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419 Quell Therapeutics and shareholder of Kuur Therapeutics. All other authors declare
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421

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568

569 **FIGURE LEGENDS**570 **Figure 1. Comparison of CD27 expression between immune cell populations of**
571 **humans and humanized mice**

572 (A) Humanized mice (huMice) reconstitution scheme. Immunodeficient NOD mice
573 with a loss-of-function mutation in the *Prkdc* gene and common γ chain deficiency
574 (NOD-scid γ_c^{null} , NSG) were engrafted with human CD34 $^+$ hematopoietic progenitor
575 cells (HPCs) to reconstitute human immune system components and were tested for
576 human immune compartment reconstitution after three months.

577 (B) Pie charts show the distribution of CD27 $^+$ cells in different immune cell
578 populations examined in huMice blood (n=3) and human PBMCs (n=3).

579 (C) Frequency of CD27 $^+$ cells in different immune cell populations, comparing
580 huMice peripheral blood (n=3) and human PBMCs (n=3).

581 (D-E) Representative flow cytometry analysis illustrating the gating strategy to
582 differentiate memory T cell subsets characterized by CCR7 and CD45RA expression
583 within the CD3 $^+$ CD27 $^+$ population (D) and the frequency of each subset (E),
584 comparing huMice peripheral blood (n=3) and human PBMCs (n=3). See also related
585 Figure S1.

586

587 **Figure 2. CD27 $^+$ cells are essential for the immune control of EBV viral loads**
588 **and tumorigenesis during EBV infection**

589 (A) Workflow of CD27 depletion experiments. HuMice mice were infected (i.p.) with
590 10⁵ Raji Green Units (RGU) of B95-8 EBV. At week 2 post EBV infection, animals
591 were injected (i.p.) with 12.5 μ g/g of either anti-CD27 depletion antibody or isotype
592 control antibody consecutively every 4 days to ensure the depletion effect until
593 termination of experiment.

594 (B-E) Frequency of CD3 $^+$ T cells in anti-CD27 depleting antibody treated group (α -
595 CD27 depl.) and isotype control antibody treated group (IsoCtrl. depl.) (B), frequency
596 of CD3 $^+$ T cells at the termination of experiment (C), total CD3 $^+$ T cell count (D) and
597 tumor burden in the respective groups (E).

598 (F-H) EBV viral loads quantified by qPCR over time (F), and at termination of
599 experiment in peripheral blood (G) and spleen (H). The lower limit of quantification
600 (LLOQ) of 122 IU/ml is depicted as horizontal dashed line.

601 (I-J) Immunohistochemistry images of EBNA2 in the respective groups, original
602 magnification 200x (I), and the quantification of EBNA2⁺ cells/mm² in splenic
603 sections (J). Images are representative from one of two independent experiments.
604 Data (n=8-13 per group) are pooled from two independent mouse experiments in
605 graph (B-H) and (J) and displayed with median and interquartile range. Two-way
606 ANOVA analysis and Sidak's multiple comparisons as a post hoc test was used for
607 (B), (E) and (F), Mann-Whitney test was used for (C-H) and (J) to assess p values;
608 **p<0.01, ***p<0.001, ****p<0.0001. See also related Figure S2.

609

610 **Figure 3. Blocking of CD27 diminishes the immune control of EBV infection**

611 (A) Workflow of CD27 blocking experiments. One day before infection with 10⁵ Raji
612 Green Units (RGU) of luciferase encoding B95-8 EBV (Luc-EBV), huNSG-A2 mice
613 (HLA-A2 transgenic NSG mice reconstituted with HLA-A2⁺ human hematopoietic
614 progenitor cells) were adoptively transferred (AT) with 200'000 autologous T cells
615 expressing either BMLF1 or LMP2 specific TCRs that had been transduced *ex vivo*.
616 The anti-CD27 blocking antibody is the Fc domain re-engineered version of the anti-
617 CD27 depletion antibody of Figure 2 and can no longer engage antibody directed
618 cellular cytotoxicity (ADCC). At week 1 post EBV infection, animals were injected
619 (i.p.) with 6.5 μ g/g of either anti-CD27 blocking antibody or isotype control antibody
620 consecutively every 4 days until termination of experiment.

621 (B) Representative flow cytometry plots of BMLF1- and LMP2-specific TCR
622 transduced CD8⁺ T cells (left) using mouse TCR β specific antibodies (mTCR β) and
623 BMLF1 and LMP2 peptide plus HLA-A2 pentamers ²⁶. Frequency of CD27
624 expression on transduced and non-transduced CD8⁺ T cells (right).

625 (C) Spleen weight of animals treated with either anti-CD27 blocking antibody (α -
626 CD27 blo.) or isotype control antibody (IsoCtrl. blo.) upon different transfer
627 conditions.

628 (D-E) EBV viral loads quantified by qPCR over time during EBV infection (D), at the
629 termination of experiment in peripheral blood (E, left), spleen (E, middle) and liver (E,
630 right). Mice treated with either anti-CD27 blocking antibody or isotype control
631 antibody in different transfer conditions were compared.

632 (F-G) Representative immunohistochemistry images of EBNA2 in the respective
633 groups, original magnification 200x (F), and the quantification of EBNA2⁺ cells/mm²
634 in splenic sections (G).
635 (H-I) Representative IVIS image analysis at week 1 and week 5 post Luc-EBV
636 infection (H) and quantification of defined region of interest (ROI) of IVIS images (I).
637 (J) Spleen weight of animals infected with either wild type EBV or BZLF1 knock-out
638 EBV (BZkoEBV), treated with anti-CD27 blocking antibody or isotype control
639 antibody without adoptive transfer.
640 (K-L) EBV viral loads of animals over time during EBV infection (K), at the
641 termination of experiment in peripheral blood (L, left) and spleen (L, right) in the
642 respective groups.
643 Data (n= 14-16 per group) are pooled from two independent mouse experiments in
644 graphs (C-E), (G) and (I-L) and displayed with median and interquartile range.
645 Graphs (F-I) (n= 7-8 per group) are representative from one out of two independent
646 experiments. Graphs (K-L) (n=4-6 per group) are from one experiment. One-way
647 ANOVA analysis (Kruskal-Wallis test) followed by Tukey's post hoc test was used
648 for (J) and (L). Two-way ANOVA analysis and Sidak's multiple comparisons as a
649 post hoc test was used for (D), (I) and (K), and Mann-Whitney test for (C), (E) and (G)
650 to assess p values; *p<0.05, **p<0.01. See also related Figure S3.

651

652 **Figure 4. CD70⁺CD39⁺EBNA2⁺ B cells accumulate upon loss of CD27 mediated
653 immune control of EBV**

654 (A) Frequency of CD70 expression on CD19⁺ B cells in multiple organs (blood,
655 spleen and liver) in anti-CD27 blocking antibody versus isotype control antibody
656 treated group.
657 (B) Flow cytometry plots of CD39 and CD73 expression on CD19⁺ B cells in
658 multiple organs (blood, spleen and liver) in the indicated experimental groups.
659 (C) Frequency of CD39 expression on CD19⁺ B cells.
660 (D) Correlation between the CD39 expression on CD19⁺ B cells and EBV viral loads
661 in blood.
662 (E) Frequency of CXCR5 expression on CD19⁺ B cells.
663 (F) Representative UMAP analysis depicts clusters with co-expression of CD39,
664 CD70, Ki67 and EBNA2 on CD19⁺ B cells in blood.

665 (G) Data from (F) were transformed and shown in percentile of each population in
666 anti-CD27 blocking antibody versus isotype control antibody treated group.
667 (H) Representative heatmap analysis of co-expression of CD39, CD70, Ki67 and
668 EBNA2 on CD19⁺ B cells in blood.
669 Data (n= 14-16 per group) are pooled from two independent mouse experiments in
670 graph (A) and (C-E) and displayed with median and interquartile range. Graphs (F-H)
671 (n= 7-8 per group) are representative from one of two independent experiments.
672 Mann-Whitney test was used for (A), (C) and (E) to assess p values; Spearman
673 correlation examining rank correlation was used for D. *p<0.05, **p<0.01,
674 ***p<0.001. See also related Figure S4.

675

676 **Figure 5. Early EBV lytic antigen BMLF1 specific CD8⁺ T cells require CD27 for**
677 **expansion and cytotoxicity**

678 (A) CD8⁺ T cell memory subsets characterized by CD45RA and CD62L expression
679 and depicted as naïve, Tcm, Tem and Temra in groups treated with either anti-CD27
680 blocking antibody or isotype control antibody *in vivo*.
681 (B) Weekly representative flow cytometry plots showing the gating strategy and
682 circulating BMLF1 and LMP2 specific CD8⁺ T cells in blood *in vivo*.
683 (C-D) Longitudinal data examining the expansion of BMLF1 (C) and LMP2 (D)
684 specific CD8⁺ T cells in blood over time post Luc-EBV infection, treated with anti-
685 CD27 blocking antibody versus isotype control antibody.
686 (E-F) Frequency of BMLF1 (E) and LMP2 (F) specific CD8⁺ T cells in multiple
687 organs (blood, spleen and liver) at termination of experiment.
688 (G) Representative flow cytometry plot of EBV specific TCR transduced CD8⁺ T
689 cells (depicted as CD8 Pent⁺) and the rest of the T cells (depicted as CD8 Pent⁻) using
690 mouse TCR β specific antibodies (mTCR β) and either BMLF1 or LMP2 peptide plus
691 HLA-A2 pentamers²⁶.
692 (H-I) Frequency of Ki67 expressing cells showing the cell proliferation of EBV
693 specific BMLF1 (H) and LMP2 (I) specific CD8⁺ T cells (depicted as CD8 Pent⁺ cells)
694 versus the rest of CD8⁺ T cells (depicted as CD8 Pent⁻ cells) in blood in different
695 experimental groups.
696 (J-K) *In vitro* killing assay with BMLF1 and LMP2 specific T cell clones generated
697 from healthy EBV carriers *ex vivo*. T cells were pre-treated with either anti-CD27

698 blocking antibody or isotype control antibody and co-cultured with PHK-26 pre-
699 labeled autologous LCLs for 21h at the indicated effector-to-target ratios (J), and at
700 the ratio of 10:1 (K).

701 Data (n= 5-6 per group) are pooled from two independent mouse experiments in
702 graph (A) and (C-I) and displayed with median and interquartile range. Two-way
703 ANOVA analysis and Sidak's multiple comparisons as a post hoc test was used for (C)
704 and (D) and Mann-Whitney test for (A) and (E-I). Data shown in (J-K) are pooled
705 from three experiments and analyzed using two-tailed unpaired t test, dashed line
706 signifies target cell only. (p values; *p<0.05, **p<0.01, ns: not significant)

707 See also related Figure S5.

708

709 **Figure 6. CD27 blockade compromises CXCR5⁺EOMES⁺ CD8⁺ T cell
710 accumulation during EBV infection**

711 (A) Cytokine production from serum samples harvested at termination of experiment.
712 Each individual cytokine is presented in the separate transfer conditions in the upper
713 panel. In the lower panel, pooled data of α -CD27 blocking antibody treated or isotype
714 control antibody treated groups is shown.

715 (B) Frequency of CXCR5 expression on CD8⁺ T cells in the respective groups in
716 blood, spleen and liver.

717 (C) Frequency of EOMES bright T-bet dim and EOMES dim T-bet bright populations
718 in the respective group in blood.

719 (D) Frequency of CD69 expression on CD8⁺ T cells in spleen.

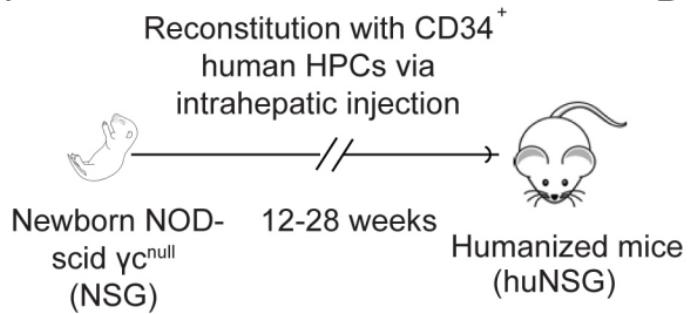
720 (E) Frequency of 2B4 (left) and PD1 (right) expression on CD8⁺ T cells in Spleen.

721 (F) Representative ChipCytometry immunofluorescence images for CD20, EBNA2,
722 CD8, CD69 and PD1 in splenic sections of the respective treatment groups. Scale bars
723 are 50 μ m.

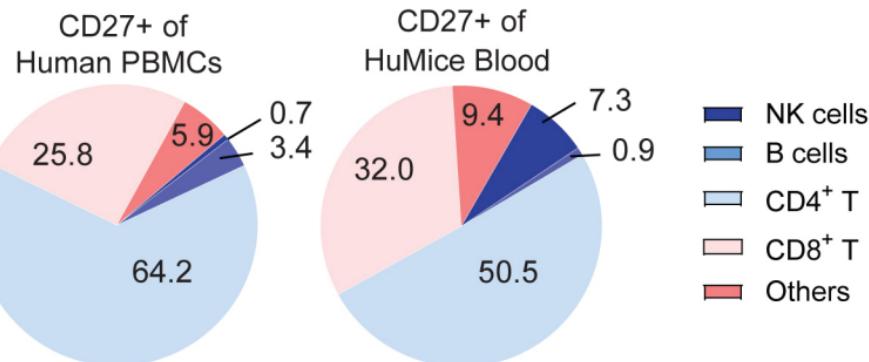
724 (G) Quantification of the CD8⁺/EBNA2⁺CD20⁺ ratio, as well as the frequency of
725 CD8⁺CD69⁺ and CD8⁺PD1⁺ cells in 5 to 7 randomly selected fields in splenic
726 sections of isotype control or CD27 blocking antibody treated animals.

727 Data (n= 14-16 per group) are pooled from two independent mouse experiments in
728 graphs (A), (B) and (D-F) and displayed with median and interquartile range. Mann-
729 Whitney test for was used for (A), (B) and (D-F) and (G) to assess p values; *p<0.05,
730 **p<0.01, ***p<0.001.

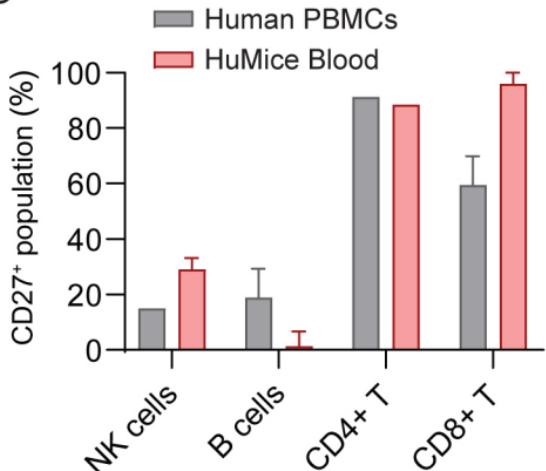
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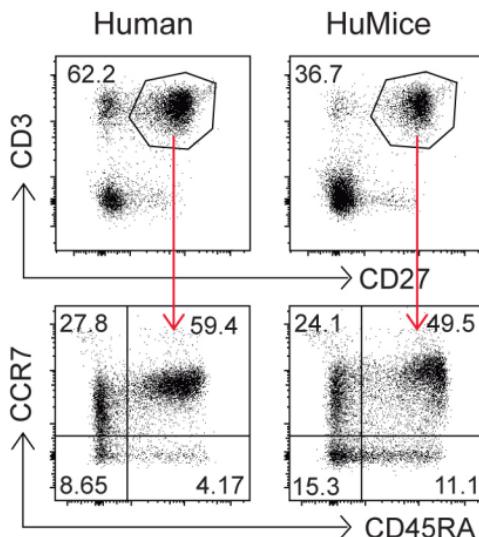
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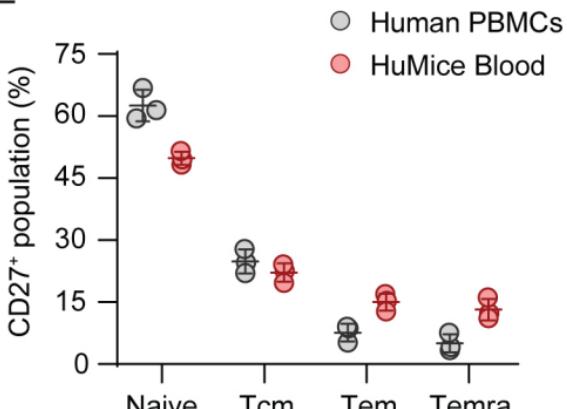
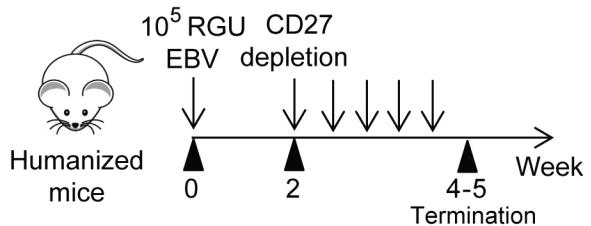
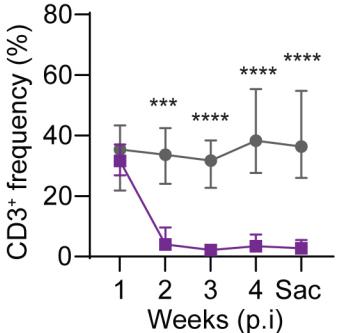
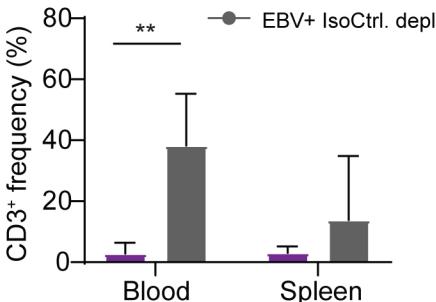
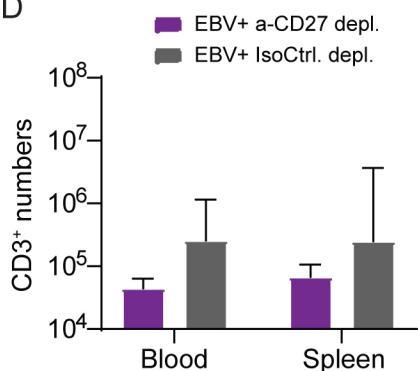
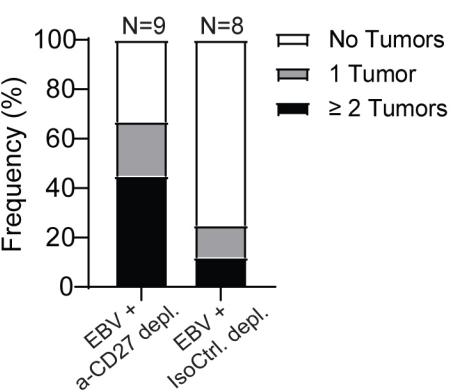
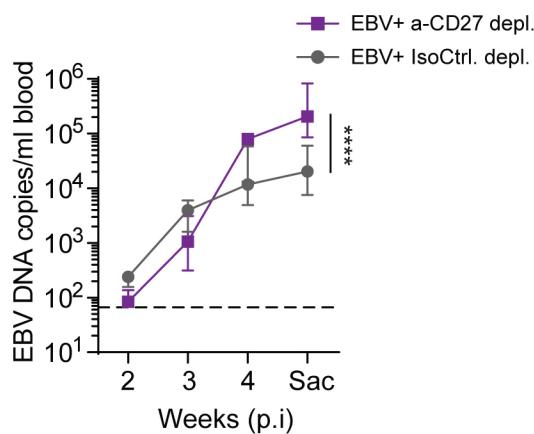
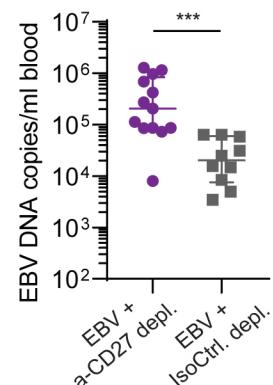
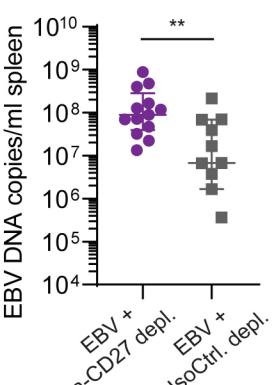
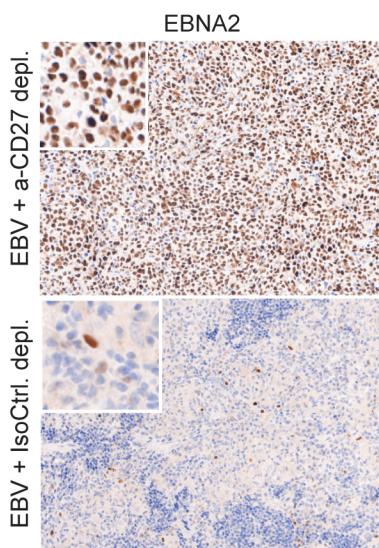
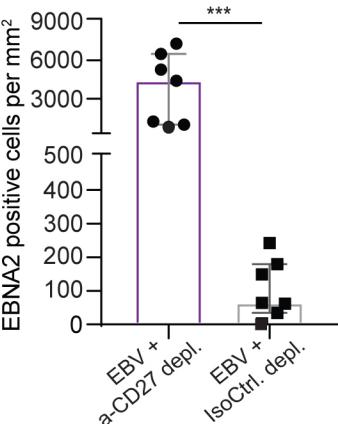


Figure 1

A

CD27 depletion experiment scheme

**B****C****D****E****F****G****H****I****J****Figure 2**

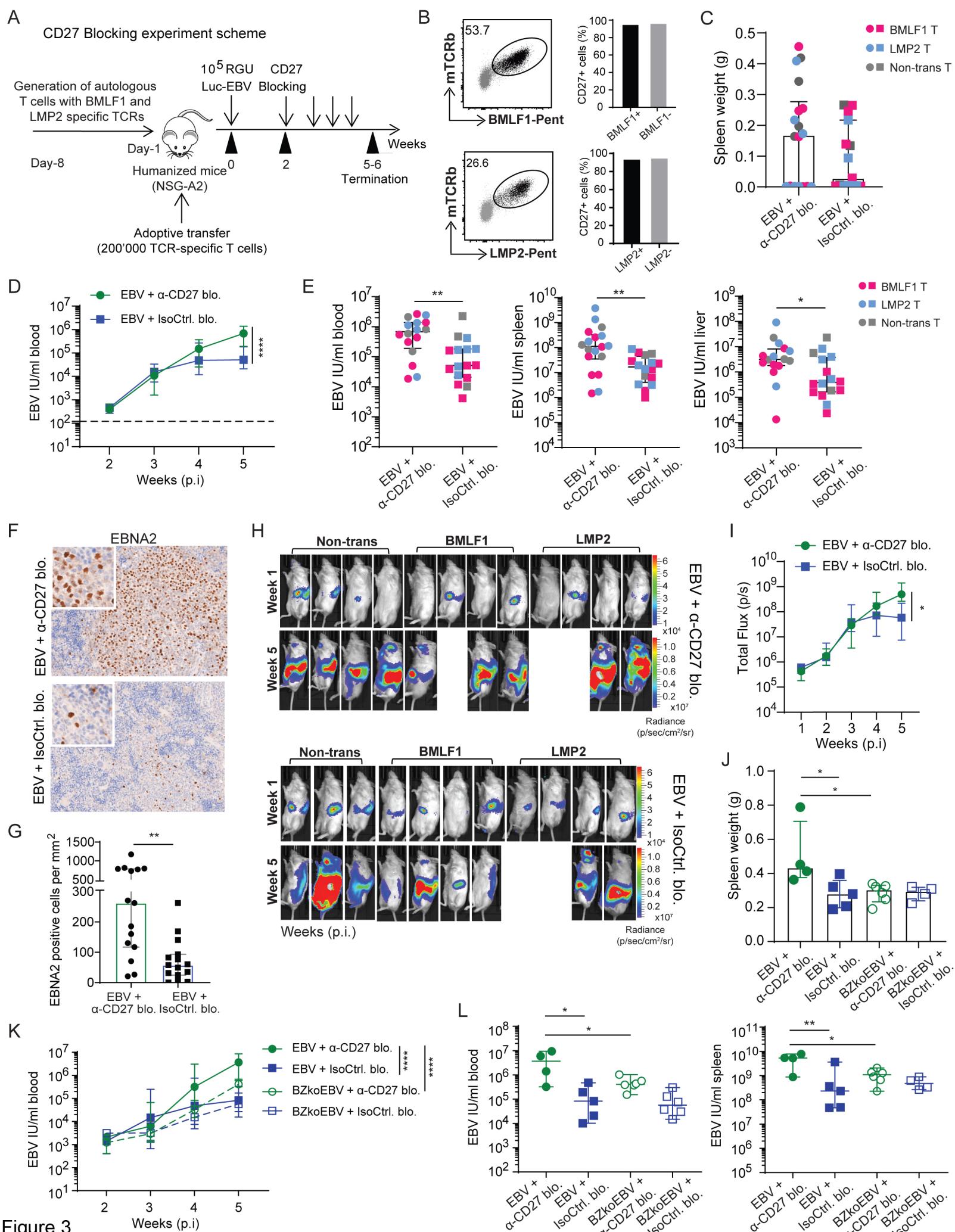


Figure 3

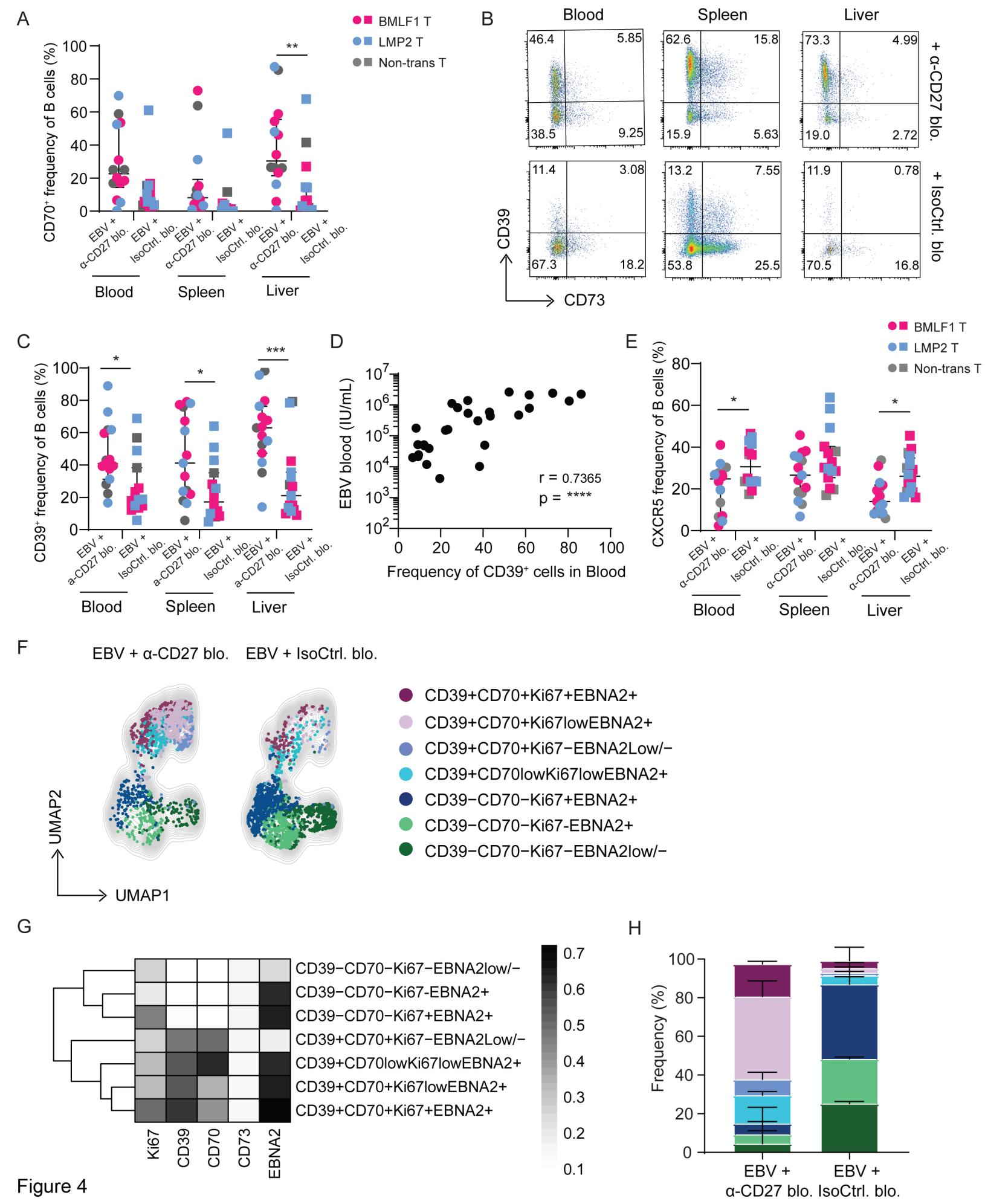


Figure 4

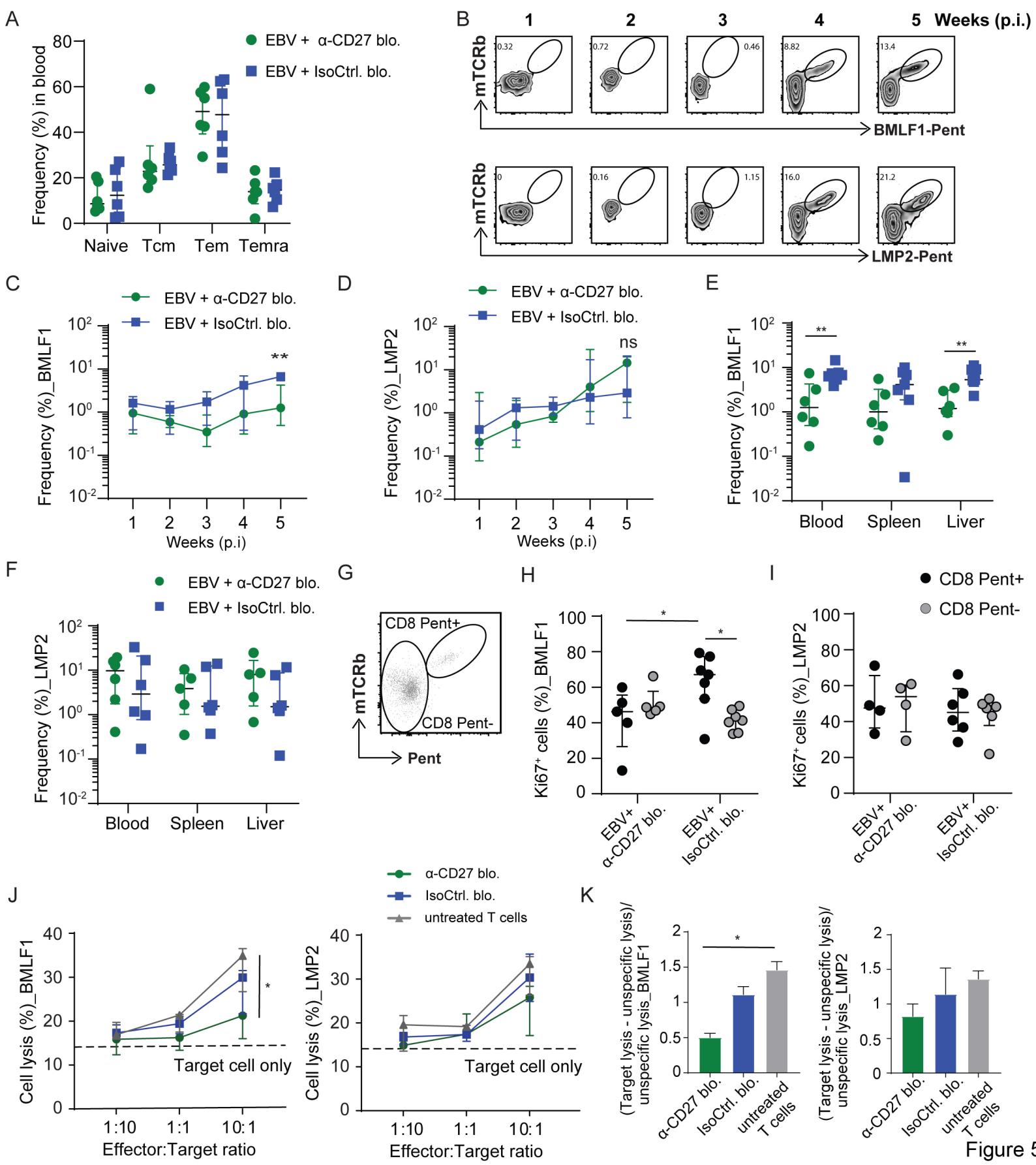


Figure 5

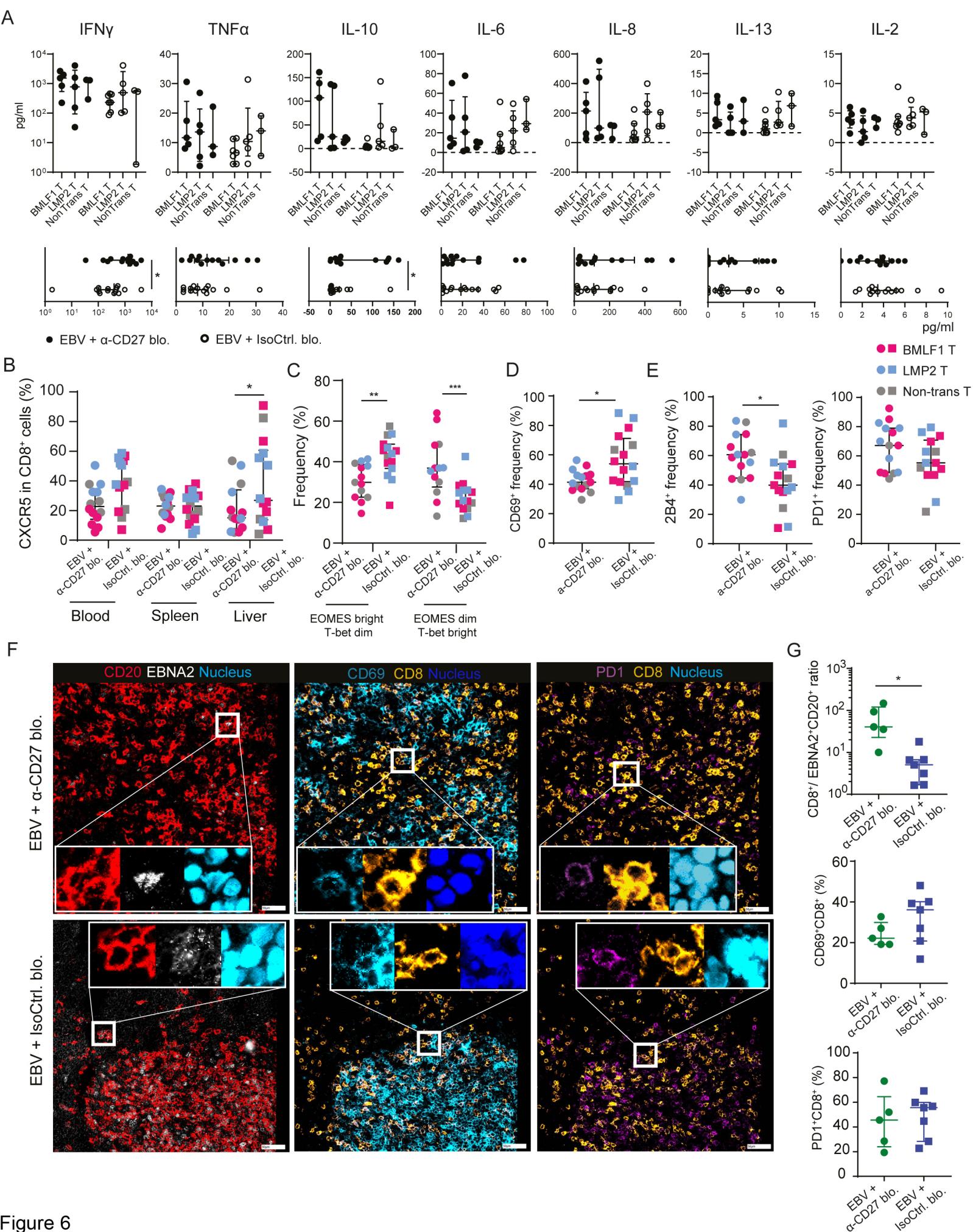


Figure 6

1 **CD27 is required for protective lytic EBV antigen specific CD8⁺ T cell expansion**2
3 Yun Deng, Bithi Chatterjee, Kyra Zens, Hana Zdimerova, Anne Müller, Patrick Schumachers,
4 Laure-Anne Ligeon, Antonino Bongiovanni, Riccarda Capaul, Andrea Zbinden, Angelika Holler,
5 Hans Stauss, Wolfgang Hammerschmidt and Christian Münz
67 **Supplementary Figure Legends**8 **Figure S1. Related to Figure 1. Gating strategy of CD27⁺ cells in huMice**9 (A) Representative flow cytometry gating strategy of CD27⁺ cells in different immune cell
10 populations in huMice.
1112 **Figure S2. Related to Figure 2. CD27 depletion effect on T and B cells**13 (A) Flow cytometry analysis of CD3⁺ T cells -1 (before), 1 and 6 days post injection of anti-
14 CD27 depletion antibody.15 (B) Total numbers of CD19⁺ B cells at the end of experiment as compared between anti-CD27
16 depletion antibody-treated group (n= 9-13 per group) and isotype control antibody-treated group
17 (n= 8-11 per group). Mann-Whitney test was used to analyze the p value; ns: not significant.
18 Data are pooled from two independent experiments.
1920 **Figure S3. Related to Figure 3. CD27 blocking antibody does not deplete CD27⁺ cells, and
21 no significant difference in EBV viral loads between groups with transferred BMLF1 and
22 LMP2 specific T cells could be observed.**23 (A-B) Frequency of CD3⁺ T cells (A) and CD19⁺ B cells (B) in the respective group (left) and
24 total cell count (right) in peripheral blood and spleen at termination of experiment.25 (C) Graphical illustration describing the working principle of using two fluorochrome-
26 conjugated anti-CD27 antibodies to check the blocking effect of the blocking antibody.27 (D) Frequency of CD27⁺ CD8⁺ T cells detected by anti-CD27 antibody derived from a different
28 clone to the injected anti-CD27 blocking antibody.29 (E) Frequency of CD27⁺ CD8⁺ T cells detected by anti-CD27 antibody derived from the same
30 clone as the injected anti-CD27 blocking antibody.

31 (F) Longitudinal data of animal weight over time until termination in the respective groups.

32 (G) Animal survival over time until experiment termination in the respective groups.
33 (H) Comparison of EBV viral loads in different transfer conditions in blood (left), spleen
34 (middle) and liver (right).
35 (I) Frequency of CD27 positive of EBNA2⁺ B cells in blood (left) and spleen (right).
36 (J) qRT-PCR analysis shows relative gene expression of the representative five EBV latent genes
37 and five lytic genes in the anti-CD27 blocking antibody-treated group versus isotype control
38 antibody treated group. Data are normalized to housekeeping gene SDHA expression. n= 4 from
39 one out of three independent experiments.
40 (K-L) Representative immunohistochemistry images of EBNA2 in the respective groups,
41 original magnification 200x (K), and the quantification of EBNA2⁺ cells/mm² in splenic sections
42 (L).
43 Data (n= 14-16 per group) are pooled from two independent mouse experiments in graph (A) and
44 (C-H) and displayed with median and interquartile range. Two-way ANOVA analysis and
45 Sidak's multiple comparisons as a post hoc test was used for (C -F) and (I), Mann-Whitney test
46 for (A), two-way ANOVA analysis and Tukey's multiple comparisons for (H) to assess p values.
47 Log-rank (Mantel-Cox) test for (G) was used to compare the survival curves. One-way ANOVA
48 analysis (Kruskal-Wallis test) followed by Tukey's post hoc test was used for (L). Graph I (n=4-
49 6 per group) is from one experiment and Mann-Whitney test was used to assess the p values:
50 *p<0.05, **p<0.01, ***p<0.001. ns: not significant.
51

52 **Figure S4. Related to Figure 4. Individual expression and co-expression of CD39, CD70,
53 Ki67 and EBNA2 in blood and spleen under CD27 blockade**

54 (A-B) UMAP presentation overlaid expression of each individual marker in blood (A) and spleen
55 (B).
56 (C) Representative UMAP analysis depicts clusters, showing the co-expression of CD39, CD70,
57 Ki67 and EBNA2 on the CD19⁺ B cells in spleen.
58 (D) Transformed data from (C) are shown in frequency of each population in different
59 experimental groups.
60 (E) Representative heatmap analysis of co-expression of CD39, CD70, Ki67 and EBNA2 on
61 CD19⁺ B cells in spleen.

62 Graphs (A-E) (n= 7-8 per group) are representative from one out of two independent
63 experiments.

64

65 **Figure S5. Related to Figure 5. Treatment with anti-CD27 blocking antibody shows no**
66 **effect on T cell memory subsets *in vivo* and LCL proliferation *ex vivo***

67 (A) Comparison of T cell memory subsets characterized by CD45RA and CD62L expression and
68 depicted as naïve, Tcm, Tem and Temra cells in different transfer conditions (BMLF1 and
69 LMP2) in blood (from one representative experiment).

70 (B) T cell memory subsets in groups treated with either anti-CD27 blocking antibody or isotype
71 control antibody *in vivo*. Cells were harvested at termination of experiment from spleen, liver
72 and bone marrow.

73 (C) Flow cytometry plots of LCL proliferation. Three LCLs generated from human cells and
74 huNSG/huNSG-A2 mice, respectively, were labeled with Cell Trace Violet and incubated with
75 either anti-CD27 blocking antibody (10 μ g/mL) or isotype control antibody (10 μ g/mL) for 3 and
76 10 days.

77 Data (n=3 per group) in graph A is from one representative experiment. Data (n= 5-6 per group)
78 in graph B are pooled from two independent experiments and displayed with median and
79 interquartile range. Mann-Whitney test was used to assess p values; *p<0.05, **p<0.01.

80

81 **Figure S6. Related to Figure 6.**

82 (A) Overview of the CD20, CD8 and EBNA2 stainings in whole spleen sections after anti-CD27
83 blocking or isotype control antibody treatment, acquired by ChipCytometry. Big bright red and
84 green spots in the isotype treatment condition are artifacts during acquisition.

85 (B) Frequency of CD8 $^{+}$ T cells and EBNA2 $^{+}$ CD20 $^{+}$ B cells as quantified in 5 to 7 randomly
86 chosen positions.

87 (C) Immunofluorescence images for human CD45, CD7, CD38, the lineage markers CD3, CD4,
88 CD8, CD21 and CD11c.

89 (D) Immunofluorescence images for CD45RA, CD45RO and CD62L used to define T cell
90 subsets.

91 (E) Immunofluorescence images for co-stimulatory/inhibitory molecules CD27, CD28, CD30,
92 TIM3, CD278, CD40, CD134 (OX40 receptor) and the transcription factor FoxP3.

93 (F) Immunofluorescence images for CD39, HLADR, and Ki67.

94 Scale bars for (A), (C)-(F) are 50 μ m.

A

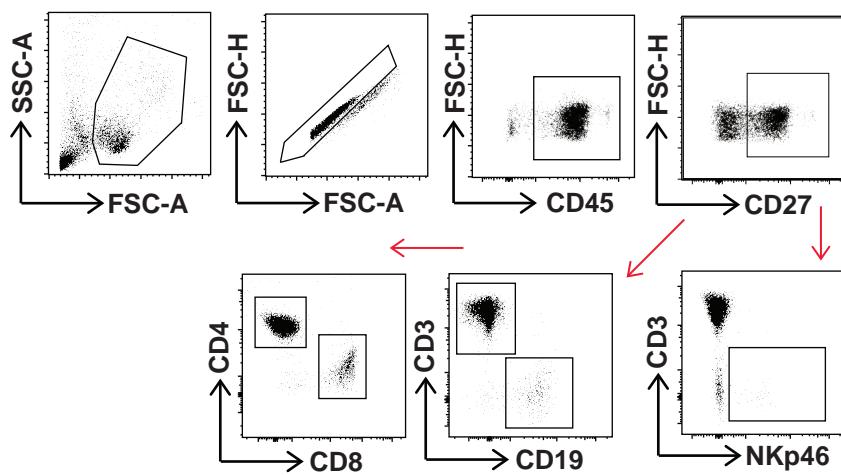
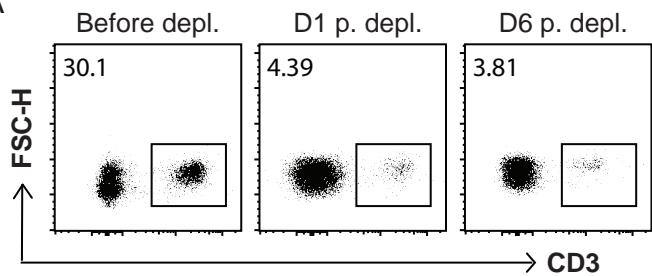


Figure S1

A



B

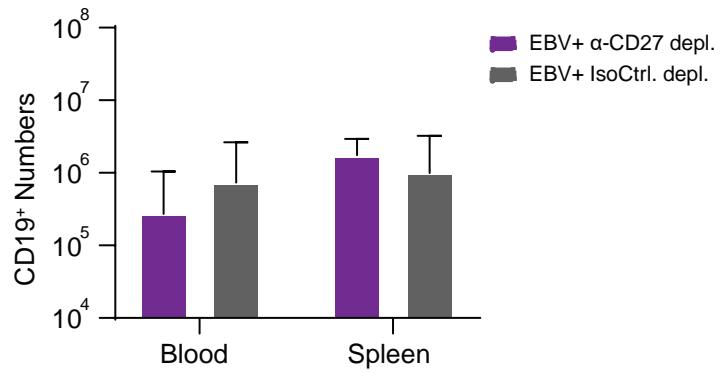


Figure S2

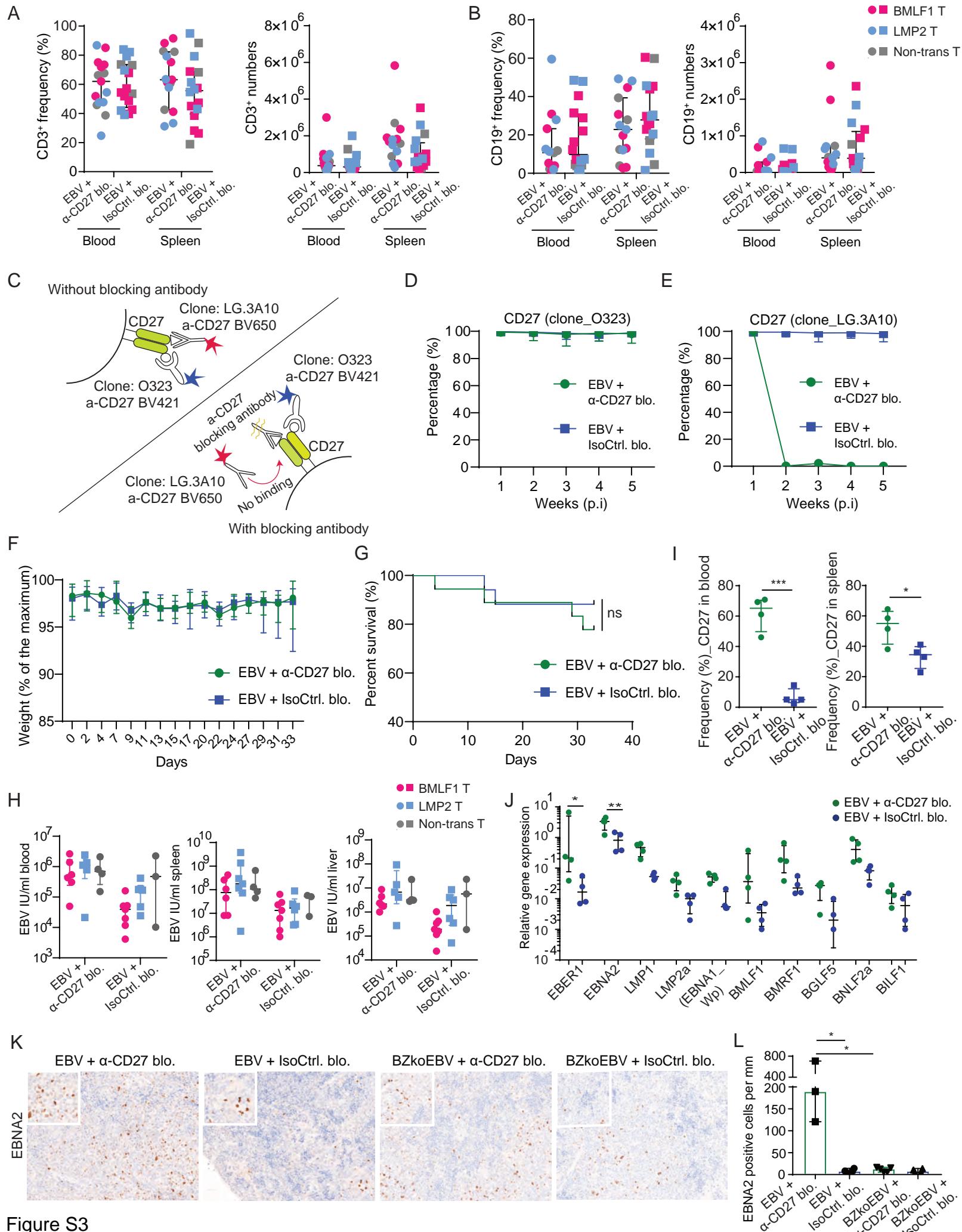
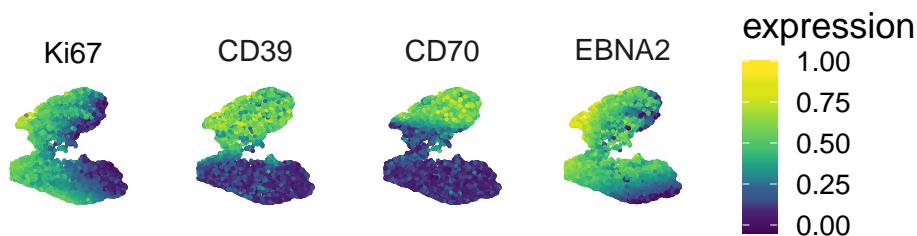
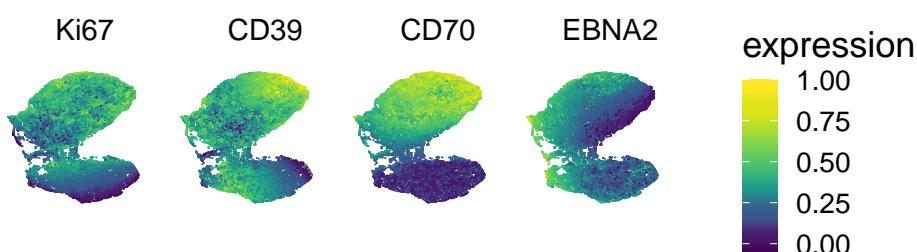
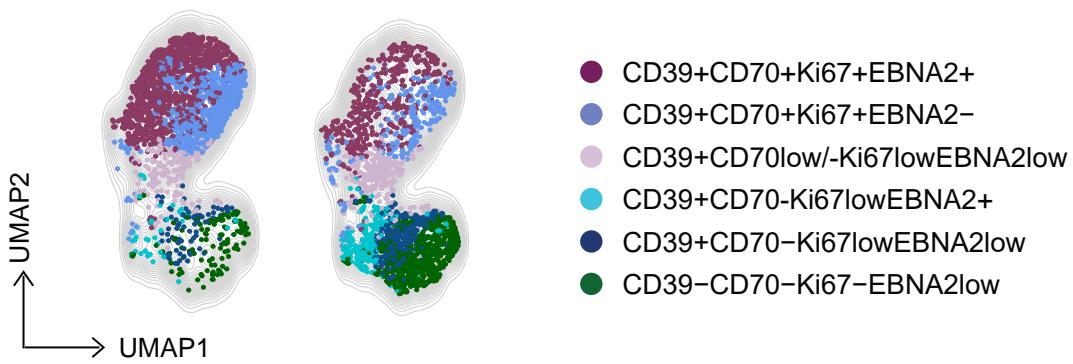


Figure S3

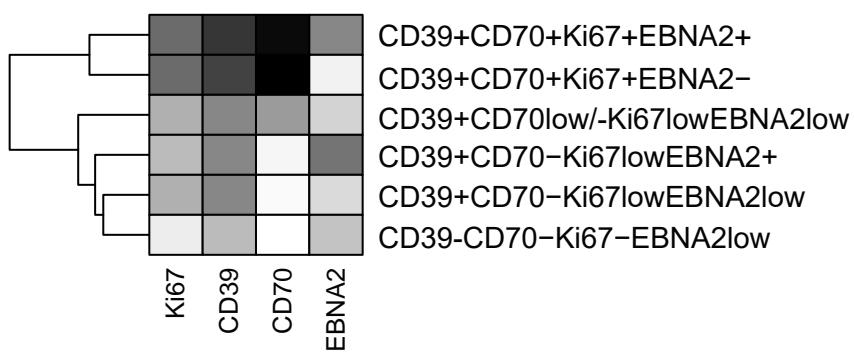
A



B

C EBV + α -CD27 blo. EBV + IsoCtrl. blo.

D



E

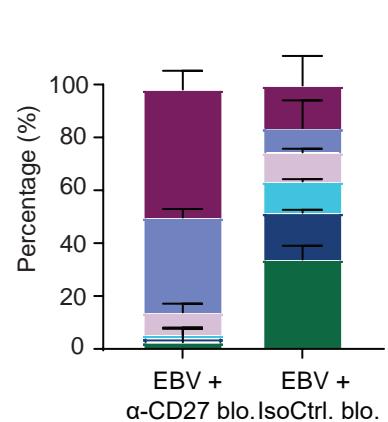


Figure S4

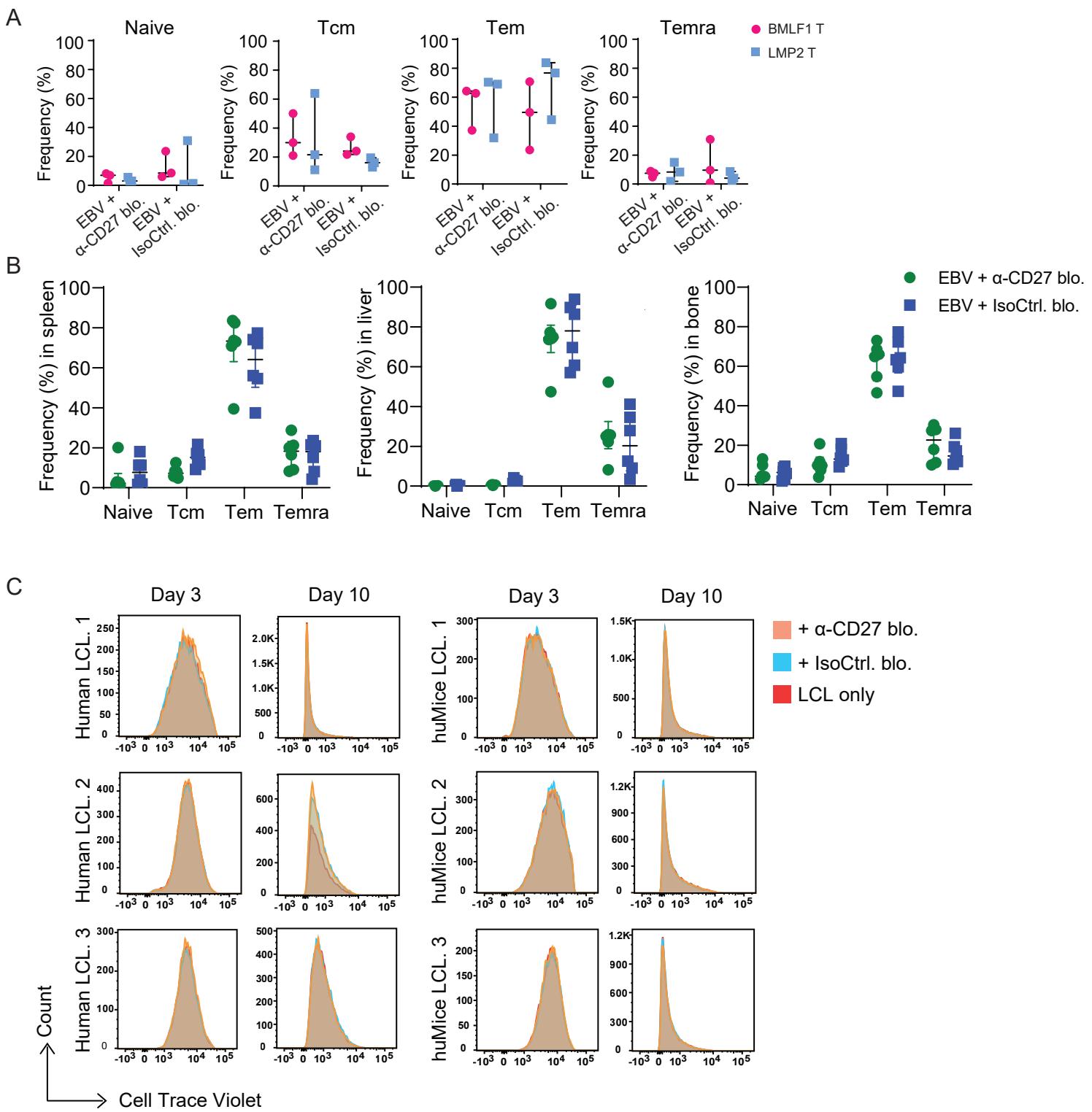
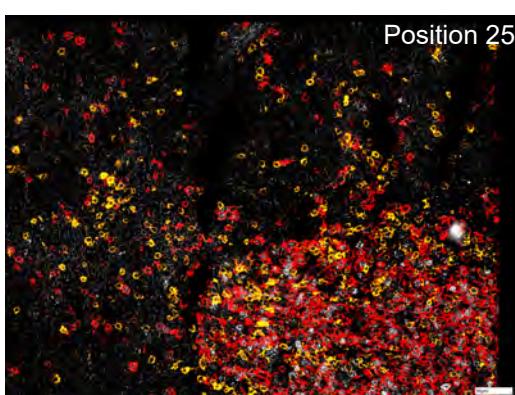
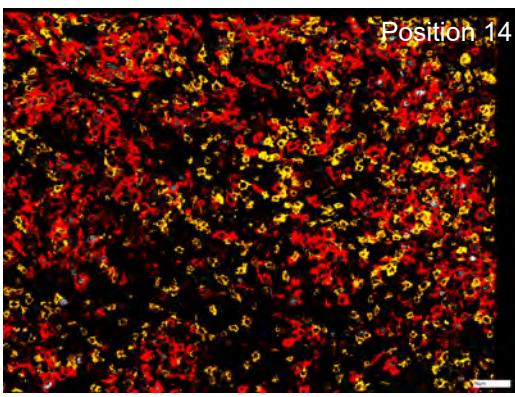
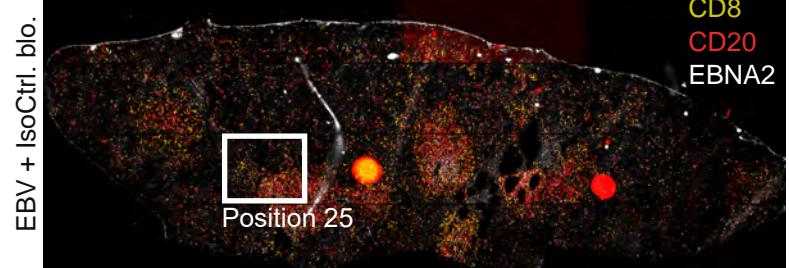
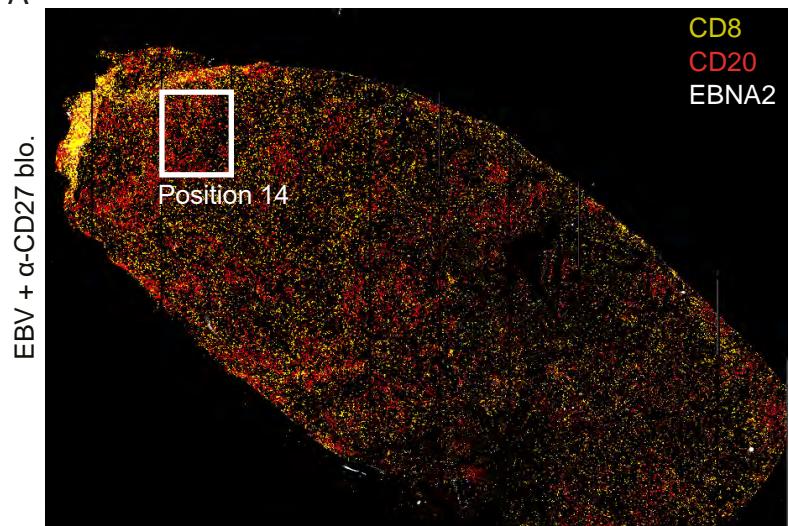
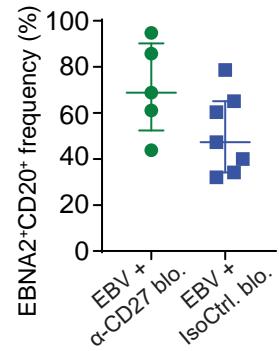
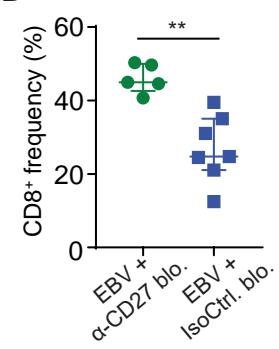


Figure S5

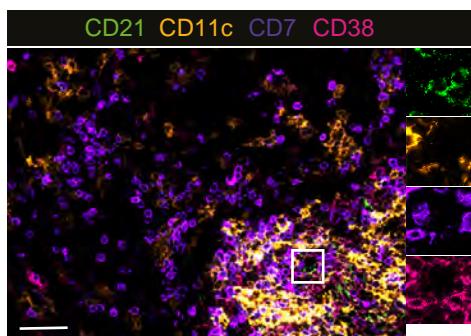
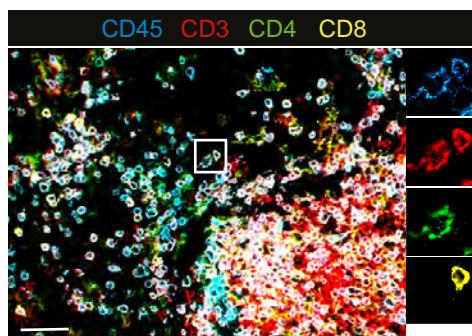
A



B



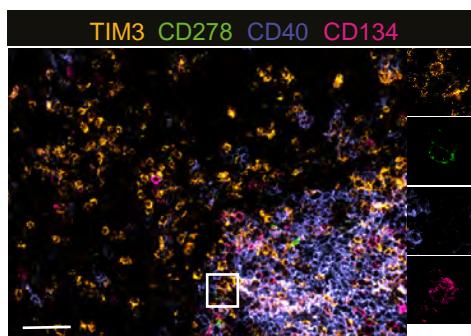
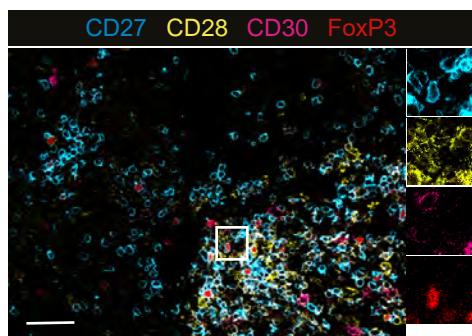
C



D



E



F

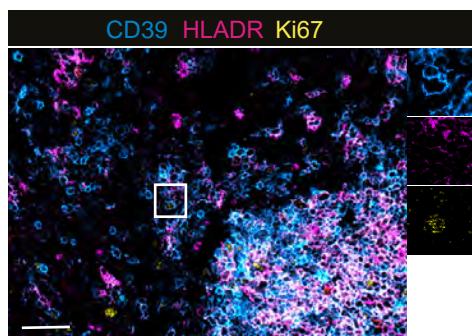


Figure S6

Table S1: Antibodies and dyes for ChipCytometry

	Markers	Color	Clone	Company	Cat#
1	CD8	PerCP	SK1	Biolegend	344708
2	CD4	PE	RPA-T4	Biolegend	300508
3	CD45	BUV395	HI30	BD	563792
4	CD45RA	FITC	HI100	BD	555488
5	CD11c	PE	S-HCl-3	Biolegend	371504
6	CD27	PerCP	LG.3A10	Biolegend	124213
7	CD134 (OX40)	PE	Ber-Act35	Biolegend	350003
8	CD278 (ICOS)	PerCP	C398.4A	Biolegend	313517
9	CD45RO	FITC	UCHL1	BD	555492
10	CD3	PE	SK7	Biolegend	344805
11	CD56	PE	MEM-188	BL	304605
12	CD69	PE	FN50	Biolegend	310905
13	CD38	PE	HIT2	Biolegend	303506
14	CD30	PE	Ber-H8	BD	550041
15	CD20	PE	1412	Biolegend	340510
16	CD40	FITC	HB14	Biolegend	313004
17	CD7	FITC	CD7-6B7	Biolegend	343104
18	CD62L	PE	FMC46	BioRad	MCA1076PET
19	CD279 (PD1)	PE	EH12.1	BD	560795
20	HLA-DR	FITC	G46.6	BD	555811
21	CD28	PE	CD28.2	BD	5585729
22	CD21	PE	Bu32	Biolegend	354921
23	CD366 (TIM3)	PE	D5D5R	RD	FAB2365P
24	Ki67	PE	B56	BD	BD 556027
25	FOXP3	PE	236A/E7	BD	560852
26	CD39	FITC	A1	Biolegend	328207
27	EBNA2	PE	R3	Sigma	MABE8
28	Helix NP Green	FITC		Biolegend	425303

Table S2. Quantitative RT-PCR primer list in the paper.

Name	Primer/Probe	Source	Sequence
EBER1	F	Tierney et al., 2015	TGCTAGGGAGGAGACGTGTGT
	R		TGACCGAAGACGGCAGAAAG
	probe		AGACAACCACAGACACCGTCCTCACCA
EBNA2	F	Bell et al., 2006	GCTTAGCCAGTAACCCAGCACT
	R		TGCTTAGAAGGTTGTTGGCATG
	probe		CCCAACCACAGGTTCAGGCAAAACTT
LMP1	F	Bell et al., 2006	AATTTCACGGACAGGCATT
	R		AAGGCCAAAAGCTGCCAGAT
	pobe		TCCAGATACTAACAGACAAGTAAGCACCCGAAGAT
LMP2a	F	Bell et al., 2006	CGGGATGACTCATCTAACACATA
	R		GGCGGTACAACACGGTACTAACT
	probe		CAGTATGCCTGCCTGTAATTGTTGCGC
EBNA1 (Wp)	F	Bell et al., 2006	TGCCTGAACCTGTGGTTGG
	R		CATGATTTCACACTAAAGGAGACGG
	probe		TCCTCTGGAGCCTGACCTGTGATCG
BMLF1	F	Tierney et al., 2015	CCCGAACTAGCAGCATTCCCT
	R		GACCGCTTCGAGTTCCAGAA
	probe		AACGAGGATCCCGCAGAGAGCCA
BMRF1	F	Tierney et al., 2015	GAGGAACGAGCAGATGATTGG
	R		TGCCCACTTCTGCAACGA
	probe		TGCTGTTGATGCCAAGACGGCTT
BGLF5	F	Tierney et al., 2015	GCAAGCCCAGGAGAGACT
	R		GAGGCGACCCTTCGAA
	probe		CGGGTGAACATTGTGACGGCCTTC
BNLF2a	F	Tierney et al., 2015	TGGAGCGTGCTTGCTAGAG
	R		GGCCTGGTCTCCGTAGAAGAG
	probe		CCTCTGCCTGCAGGCTGCC
BILF1	F	Tierney et al., 2015	TGCCTTTGACCCAGAACATG
	R		CAACGCCATACCCAAGTGAGT
	probe		TACGGAGCACATCAGGCCAAGAACAA

1 **Supplementary Methods**

2 **Humanized mouse generation and infection**

3 NOD-scid γ_c^{null} (NSG) mice and HLA-A2 transgenic NSG mice were originally
4 purchased from Jackson Laboratories (Bar Harbor, Maine, USA) and maintained in
5 ventilated, specific pathogen-free cages at the Institute of Experimental Immunology,
6 University of Zurich. To assist with the engraftment of human CD34 $^+$ hematopoietic
7 progenitor cells (HPCs), newborn pups (1-5 days) were irradiated with 1Gy prior to
8 reconstitution ^{1,2}. Five to seven hours later, irradiated pups were intrahepatically
9 injected with 2×10^5 CD34 $^+$ human hematopoietic progenitor cells (HPCs) isolated
10 from human fetal livers (HFL) (Advanced Bioscience Resources, USA). The HFL
11 samples were procured during termination between gestational weeks 14 and 22. Use
12 of human tissue was approved by the cantonal ethics committee of Zurich (KEK-ZH-
13 Nr. 2010-0057 and 2019-00837). After 12 weeks of reconstitution, peripheral blood
14 was collected via tail vein bleeding and cells were checked for immune cell
15 populations through expression of human CD45, CD3, CD4, CD8, CD19, NKp46 and
16 HLA-DR, as previously described ³. All procedures were strictly followed in
17 accordance with the animal protocols ZH209/2014 & ZH159/17, licensed by the
18 veterinary office of the canton of Zurich, Switzerland. Mice were immune phenotyped
19 again prior to the start of the experiments and showed the following mean frequencies
20 of different cell populations; huCD45 $^+$ $81.5\% \pm 8.5\%$, huCD3 $^+$ T cells of huCD45 $^+$
21 $33.6\% \pm 10.9\%$, huCD19 $^+$ B cells of huCD45 $^+$ $53.9\% \pm 12.1\%$, huCD4 $^+$ T cells of
22 human T cells $74.5\% \pm 8.6\%$, huCD8 $^+$ T cells of human T cells $22.4\% \pm 8.2\%$ and
23 NKp46 $^+$ NK cells of huCD45 $^+$ $3.2\% \pm 1.9\%$. Animals were used between 12 and 28
24 weeks old (Mean \pm SD, n = 80; female 43 and male 37). Mice were then injected with
25 10^5 Raji Green units (RGU) of wild type Epstein Barr virus (EBV) or Luciferase-
26 expressing EBV (Luc-EBV) intraperitoneally (i.p.) and monitored for 4 to 6 weeks. In
27 each experimental group, 3 to 6 biological replicates were tested. For each individual
28 experiment, animals were reconstituted from a single HFL donor and distributed into
29 different experimental groups with a similar ratio of males and females, as well as
30 similar reconstitution levels of human immune cell populations.

31

32 **Wild type EBV, BZLF1 knock-out EBV and Luciferase-expressing EBV
33 production**

34 Wild type EBV B95-8 strain-producing cells were a generous gift of Prof. Dr. Henri-

35 Jacques Delecluse (DKFZ, Heidelberg, Germany). The recombinant EBV B95-8
36 DNA was stored as a bacmid and encompassed the gene for hygromycin resistance
37 and green fluorescent protein (GFP) in HEK293 cells. Similarly, EBV B95-8-delta
38 BZLF1 knock-out EBV (BZkoEBV) was produced in HEK293 cells. Those cells
39 were cultured in DMEM (1X) medium supplemented with 10% heat inactivated FBS,
40 20 μ g/ml gentamycin and 20 μ g/ml hygromycin. Cell transfection was performed using
41 3 μ g of BZLF1 (p509) and BALF4 (p2670) plasmids each, together with 32 μ l of
42 METAFECTENE® PRO (Biontex) in 10 cm petri dishes ³⁻⁵. The virus supernatant
43 was harvested 3 days after transfection and concentrated through centrifugation at
44 30,000g for 2 hours at 4 °C. Prior to animal infection, the GFP expressing virus was
45 titrated on Raji cells *in vitro* by analyzing the GFP positive cells 48h after infection
46 with flow cytometry. Based on the serial dilution of the virus on Raji cells, Raji Green
47 units (RGU) were calculated for each virus preparation. Luciferase-expressing EBV
48 (Luc-EBV) producer cells were kindly provided by Prof. Dr. Wolfgang
49 Hammerschmidt (HelmholtzZentrum, Munich, Germany). Luc-EBV genome was
50 originally derived from the B95-8 EBV with bioluminescent firefly luciferase protein
51 incorporated as an EBV EBNA2 fusion construct and produced in HEK293 cells. It
52 was produced and titrated in the same way as described above for wild type and
53 BZLF1 knock-out EBV, if not stated otherwise.

54

55 **EBV-specific T cell receptor (TCR) generation and adoptive T cell transfer**

56 Phoenix-AMPHO packaging cells were transfected with envelope vector pCl-Ampho
57 construct and either LMP2-TCR or BMLF1-TCR to produce retrovirus supernatants
58 encoding EBV-specific TCRs. Subsequently, CD3/CD28 Dynabeads (Thermofisher
59 Scientific) activated splenocytes derived from donor-mate animals were transduced
60 with either LMP2-TCR or BMLF1-TCR encoding retroviruses. Transduction
61 efficiency was determined by flow cytometry 48 hours after the second transduction.
62 A total of 200'000 TCR⁺CD3⁺ T cells were transferred intravenously into donor-
63 matched recipient mice and monitored longitudinally during the course of EBV
64 infection.

65

66 ***In vivo* bioluminescence imaging**

67 The progression of EBV infection was monitored longitudinally every week and
68 quantitatively measured by *in vivo* bioluminescence imaging with the IVIS Spectrum

69 Imaging System (PerkinElmer). Animals were anesthetized by isofluorane with the
70 flow of 3 liters per minute and injected i.p. with 150mg/kg D-Luciferin (Promega) 10
71 minutes before imaging. Mice were placed inside the IVIS imaging box and imaged
72 dorsally and ventrally. Representative images were acquired at 2 minutes for each
73 mouse during the entire experiment to illustrate the virus progression within the host.
74 Images for quantification were captured at various time points before the luminescent
75 signal reached the saturation intensity and analyzed with Living image 4.3.1 software
76 (PerkinElmer). Regions of interest (ROI) were set to include the regions with
77 luminescent signal in mice and photon flux (p/s) of light emitted per second within
78 the ROI was measured as the readout.

79

80 **Preparation of tissue sections for ChipCytometry**

81 Splenic tissues from EBV infected mice treated with either anti-CD27 blocking
82 antibody or the corresponding isotype control antibody were collected at the
83 termination of experiment. Vertically dissected fresh tissues, up to 0.5cm in thickness
84 were embedded in OCT (Tissue-Tek) and preserved at -80°C. Tissue sectioning was
85 prepared on a cryostat (Leica) instrument by placing the frozen tissue block facing up
86 on a freezing-temperature steel well and adjusting the temperature of the chamber and
87 cutting knife to -16°C and -17°C, respectively. The section thickness was set to 5-
88 6µm. Each individual section was collected on a room temperature microscope cover
89 slide and assembled into a ZellSafe_T chip (Canopy Biosciences). Tissue on the cover
90 slide was fixed using 100% acetone for 5 minutes, 90% ethanol for 3 minutes, 70%
91 ethanol for 3 minutes on ice and washed twice with PBS.

92

93 **Antibody staining and tissue immunofluorescence imaging in ChipCytometry**

94 Prior to staining of the samples, individual antibodies were filtered and titrated to
95 their optimal dilution to achieve a good signal-to-background staining, known as the
96 optimal Fisher's discrimination ratio (FDR). Tissues on the chips were blocked using
97 blocking buffer (1% fetal bovine serum, 10% normal mouse serum and 0.1% Tween-
98 20 in PBS) for one hour at room temperature. For surface staining, the relevant
99 monoclonal antibodies were prepared in 400µl of blocking buffer and incubated with
100 the sample for 15 minutes at either four degrees or at room temperature, depending on
101 the optimized staining condition per antibody. Followed by a continuous wash step
102 with PBS containing 0.1% Tween-20 controlled by an automated Ismatec pump

103 system for 5 minutes and washing the chip twice with PBS, the chip was ready to be
104 acquired. For the intranuclear staining, tissue was permeabilized using 1X perm
105 buffer from the FoxP3 Transcription factor staining buffer set (Invitrogen), washed
106 with PBS and incubated with antibodies for intranuclear markers for 15 minutes
107 before washing. For the EBNA2 staining, tissue was blocked with blocking buffer
108 containing 10% normal mouse serum, 1% FCS, 0.1% Tween 20 in 1X perm buffer for
109 1 hour. Purified primary EBNA2 rat anti-human antibody was applied in blocking
110 buffer for 1 hour at 4°C. Followed by washing with 0.1% Tween 20, tissue was
111 incubated with secondary mouse anti-rat IgG2a PE antibody (Biolegend) in blocking
112 buffer for 15 minutes at room temperature, and then washed with PBS-0.1% Tween
113 20 before acquisition.

114 Combining Zellkraftwerk ZellScanner One and ZellExplorer software, fluorescent
115 antibody-labeled tissue samples were acquired. Briefly, each chip was photobleached
116 in all channels and scanned for background fluorescence. A whole slide scan was
117 ordered in the beginning in order to have full spatial information about the tissue.
118 After staining with the corresponding antibodies, the fluorescent signals were
119 acquired and then photobleached preparing for the next round of acquisition of
120 background fluorescence and fluorescent signals of antigens of interest. In the end,
121 the net fluorescent signal was achieved and calculated by deducting the background
122 fluorescence in each staining round. 28 parameters were assessed in the splenic tissue
123 sections (Table S1).

124

125 **Quantification of EBV DNA genome in blood and tissue**

126 Total DNA from whole blood and small pieces of spleen and liver was extracted
127 using NucliSENS easyMag (Biomerieux) and DNeasy Blood & Tissue Kit
128 (QIAGEN) respectively, according to manufacturer's instructions. TaqMan (Applied
129 Biosystems) real-time PCR was used to quantify EBV DNA as previously described⁶,
130 with modified primers for the BamH1 W fragment (50-
131 CTTCTCAGTCCAGCGCGTT-30 and 50-CAGTGGTCCCCCTCCCTAGA-30)
132 and a fluorogenic probe (50-FAM CGTAAGCCAGACAGCAGCCAATTGTCAG-
133 TAMRA-30). All samples were performed in duplicates and measured on either
134 ViiATM 7 Real-Time PCR System (ThermoFisher Scientific) or ABI Prism 7300
135 Sequence Detector (Applied Biosystems) at the Institute of Medical Virology,
136 University of Zurich. Samples below the lower limit of quantification (LLOQ) of 122

137 International Units (IU)/ml were defined as negative for EBV DNA. EBV-inoculated
138 animals with blood and splenic EBV DNA genome below the LLOQ were considered
139 non-infected and excluded from further analysis.

140

141 **Cell isolation and tissue preparation**

142 Peripheral blood cells were obtained from the animals by tail vein bleeding and lysed
143 with 1xACK lysis buffer for 5 minutes, followed by washing with PBS. Splenocytes
144 were prepared as described above. Liver tissues were mechanically chopped into
145 small pieces and enzymatically digested in 2ml of digestion buffer (1mg Collagenase
146 D (Roche) and 0.2mg DNase I (Roche) in 2ml DMEM) at 37°C for 30 minutes with
147 agitation. Dissociated livers were then passed through a 70µm cell strainer and
148 subjected to centrifugation in a discontinuous Percoll gradient (40% and 70%, Sigma-
149 Aldrich) for 20 minutes at 1000rpm. Cells aggregated at the interface between 40%
150 and 70% Percoll gradient were harvested and washed twice with PBS. Bone marrow
151 cells were flushed out of the femur by short centrifugation. Cells were washed with
152 PBS and passed through a 70µm cell strainer if necessary. Cells from different organs
153 were counted using the Beckman Coulter AcT diff Analyzer to aliquot the optimal
154 number of cells for staining and calculation of the total cell numbers for different
155 experimental purposes.

156

157 **Antibody, pentamer labeling and flow cytometry**

158 Surface staining was performed by incubating cells with the relevant mAbs for 20
159 minutes at 4°C, followed by washing with PBS twice and resuspending in fixation
160 buffer (1% paraformaldehyde) before acquisition. For intracellular staining, cells were
161 labeled with mAbs against surface markers and fixed in fixation buffer as stated
162 above. Then, cells were permeabilized by two washes with PBS+0.05% saponin (PS),
163 resuspended with mAbs against intracellular markers diluted in PS and incubated for
164 20 minutes at 4°C. For intranuclear staining, cells labeled with mAbs against surface
165 markers were fixed and permeabilized with Foxp3/Transcription Factor Staining
166 Buffer Set (eBioscience) and stained with mAbs against intranuclear markers for 1
167 hour at 4°C. To detect EBV specific CD8⁺ T cells, PE-conjugated pentamers specific
168 for BMLF1 and LMP2 antigens, restricted by HLA-A*0201 (Proimmune), were
169 incubated with the cells prior to surface staining for 10 minutes at room temperature ².
170 Labeled cells were acquired on either the BD FACSCantoII, BD LSRII or BD

171 FACSymphony. The data analysis was performed using FlowJo software (FlowJo
172 LLC).

173

174 **In vitro-transformed LCL generation**

175 To generate NSG LCLs *ex vivo*, CD19⁺ B cells were isolated from the spleen using
176 positive selection with CD19 microbeads according to the manufacturer's
177 recommendations (Miltenyi Biotec). A total of 5x10⁵ cells/well were plated in a 96-
178 well U-bottom plate and cultured with EBV supernatants with a MOI of 0.5. Cells
179 were cultured in RPMI 1640 medium supplemented with 10% heat inactivated FBS,
180 50U/ml penicillin-streptomycin and 1% L-glutamine. Cell growth was monitored by
181 light microscopy and clusters of cells were normally visible 2 weeks post EBV
182 infection. Outgrowing cells were further expanded by seeding at 3-5x10⁵ cells/ml and
183 splitting at a concentration of 10⁶ cells/ml.

184

185 **Generation of EBV specific CD8⁺ T cell clones and T cell re-stimulation**

186 EBV specific T cell clones for BMLF1 and LMP2 were generated from a healthy
187 HLA-A*0201 positive EBV carrier using BMLF1 and LMP2-specific dextramers, as
188 described previously ³. Briefly, dextramer positive CD8⁺ T cells were single-cell
189 sorted and co-cultured with irradiated autologous LCLs and PBMC feeder cells in
190 complete T cell medium supplemented with 1 μ g/ml PHA and 150U/ml IL-2 ⁷. IFN γ
191 secretion was analyzed upon re-stimulation with 1 μ M of the relevant peptides using
192 enzyme-linked immunosorbent assays (ELISA; MABTECH). Only the T cells, which
193 showed specific responses to the relevant peptide were used for further phenotypic
194 characterization and functional T cell avidity tests in peptide titration assays to
195 confirm the specificity of the respective clones.

196 For re-stimulation, autologous LCLs were pulsed with either BMLF1 or
197 LMP2 specific peptide (1 μ M), PBMC feeder cells were stimulated with PHA
198 (5 μ g/ml) overnight and they were irradiated at 20Gy and 60Gy, respectively. T cell
199 clones specific for BMLF1 and LMP2 were co-cultured with irradiated LCLs and
200 PBMC feeder cells at the ratio of 1:5:50 in complete T cell medium (as stated above)
201 for stimulation and expansion for 1 to 2 weeks before conducting the described
202 experiments.

203

204 *In vitro* cytotoxicity assay

205 Cytotoxic activity of BMLF1 and LMP2 specific T cell clones against autologous
206 LCLs was evaluated as previously described ¹. In brief, target cells (LCLs) were
207 labeled with PKH-26 (Sigma-Aldrich) for 5 minutes and washed with PBS according
208 to the manufacturer's instructions. T cells, pretreated with either anti-CD27 blocking
209 antibody or the corresponding isotype control antibody for a week at the
210 concentration of 5 μ g/ml, were co-cultured with the labeled target cells at 10:1, 1:1
211 and 1:10 effector/target ratios. After 21 hours of incubation, TO-PRO-3-iodide
212 (ThermoFisher Scientific), a membrane-impermeable nuclear counterstain for dead
213 cells, was added to each culture (0.5 μ M final concentration) and cells were analyzed
214 by flow cytometry. Background and maximum TO-PRO-3-iodide staining was
215 obtained by incubation of target cells with medium and/or heating the cells at 90°C
216 for 15 minutes, respectively. The percentage of specific lysis was calculated with the
217 following formula: ((%TO-PRO-3-iodide⁺PKH26⁺ cells in co-culture - %TO-PRO-3-
218 iodide⁺PKH26⁺ cells in medium) / (%TO-PRO-3-iodide⁺PKH26⁺ cells in max kill -
219 %TO-PRO-3-iodide⁺PKH26⁺ cells in medium)) x 100%.

220

221 Histology, immunohistochemistry and immunofluorescence

222 Tissue sections were excised and fixed in 4% formalin overnight before paraffin
223 embedding (SophistoLab). For immunohistochemistry and immunofluorescence,
224 tissue was prepared in 3 μ m sections with Leica BOND-MAX or Bond-III automated
225 immunohistochemistry system. Tissue sections were treated with BOND Epitope
226 Retrieval Solution 2 (Leica Biosystem) for antigen retrieval at 100°C for 30 minutes.
227 Stainings were performed with Leica HRP Refine Kit (Leica Biosystem). Briefly,
228 samples were incubated with mAb mouse anti-EBNA2 (Abcam) for 30 minutes,
229 followed by incubation with Post Primary Rabbit anti mouse IgG for 20 minutes and
230 anti-rabbit Poly-HRP-IgG for 15 minutes. 3,3'-Diaminobenzidine tetrahydrochloride
231 (DAB) was the substrate chromogen used to visualize the complex via brown
232 precipitate and hematoxylin counterstaining was performed for the visualization of
233 cell nuclei. All stainings were acquired with a Vectra3 automated quantitative
234 pathology imaging system (PerkinElmer) and analyzed with InForm software to
235 quantify positive staining ⁸.

236

237 Serum cytokine quantification

238 Serum samples harvested from cardiac puncture at the termination of experiments
239 were preserved at -20°C until use. Concentration of each individual cytokine
240 (prepared 1:2.5 with dilution buffer) were measured in duplicates using V-PLEX
241 Proinflammatory Panel 1 kits (Mesoscale) following the manufacturer's instructions.
242 Standard dilutions for the calibrator blend for standard curve generation were
243 prepared in parallel in duplicates. Plates were read with a Meso Quickplex SQ120 and
244 analyzed with Discovery Workbench 4.0.12 (Mesoscale) ^{2,9}.

245

246 **B cell isolation and quantitative RT-PCR (qRT-PCR)**

247 Total RNA was isolated with MACS sorting for B cells using CD19 human
248 MicroBeads (Miltenyi Biotec) and extracted using RNeasy Mini Kit (QIAGEN)
249 according to the manufacturer's recommendations. To avoid genomic DNA
250 contamination, the on-column DNase processing was included during the RNA
251 isolation (RNase-Free DNase Set, QIAGEN). cDNA was synthesized in a 20µl
252 volume mixed with reverse transcriptase (Promega) and primer mix at concentrations
253 of 10µM each. qRT-PCR was performed with a CFX384 Touch Real-Time PCR
254 Detection System (Bio-Rad) using a program of 2 minutes at 50°C and 10 minutes at
255 95°C, followed by 50 cycles of amplification (95°C for 15 seconds and 60°C for 1
256 minute) ⁹. Primers used in this manuscript are listed in Table S2 ^{10,11}. Transcript level
257 of each gene of interest was calculated relative to the geometric mean of the reference
258 gene *SDHA* (TaqMan Applied Biosystems Gene Expression Assay (Hs00417200))
259 and presented as relative gene expression.

260

261 **Fluorescence image segmentation and quantification**

262 Quantification of cells positive for EBNA2, CD8, CD20, CD69 and PD1 (single
263 and/or double-positive) was performed using a homemade semiautomatic plugin
264 designed on ImageJ. For every image the channels were separated and cell
265 segmentation were performed on the nuclei channels, then the average of fluorescence
266 intensity for each single protein was measured (the threshold is selected manually for
267 each channel), and followed by quantification. The lineage markers and markers that
268 are expressed on many different types of immune cells are show in Figure S6C; the
269 markers used to characterize the T cell subsets are shown in Figure S6D; the stainings
270 for co-stimulatory molecules and their receptors, as well as FoxP3 that are all positive

271 for CD27 are shown in Figure S6D; the markers that have high expression on B cells
272 are shown in Figure S6F.

273

274 **High-dimensional analysis**

275 Flow cytometry data was processed using FlowJo software and imported into
276 Cytobank to generate cell density plots and histograms (Beckman Coulter). All the
277 parameters were displayed with an arcsinh transformation with an argument ranging
278 from 50 to 500 on different biomarkers. The exported FCS files, together with the
279 argument information, were uploaded into Rstudio. The FlowSom algorithm was used
280 for automated clustering of cell populations for UMAP and heatmap ¹². Individual
281 cluster frequencies generated in the R environment were exported and used for further
282 analysis.

283

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