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2 **Fig. S1. *Bank1* deficiency barely modifies the survival rate in the TLR7.Tg6 and in**

3 **IMQ-treated mice. (A)** Survival curve was monitored in both models. TLR7.Tg6 model

4 with WT (n = 12), T7 (n = 21) and T7.B1^{-/-} (n = 15) mice up to 32 weeks; and IMQ-

5 induced model with WT (n = 12), WT + IMQ (n = 15), B1^{-/-} (n = 12) and B1^{-/-} + IMQ

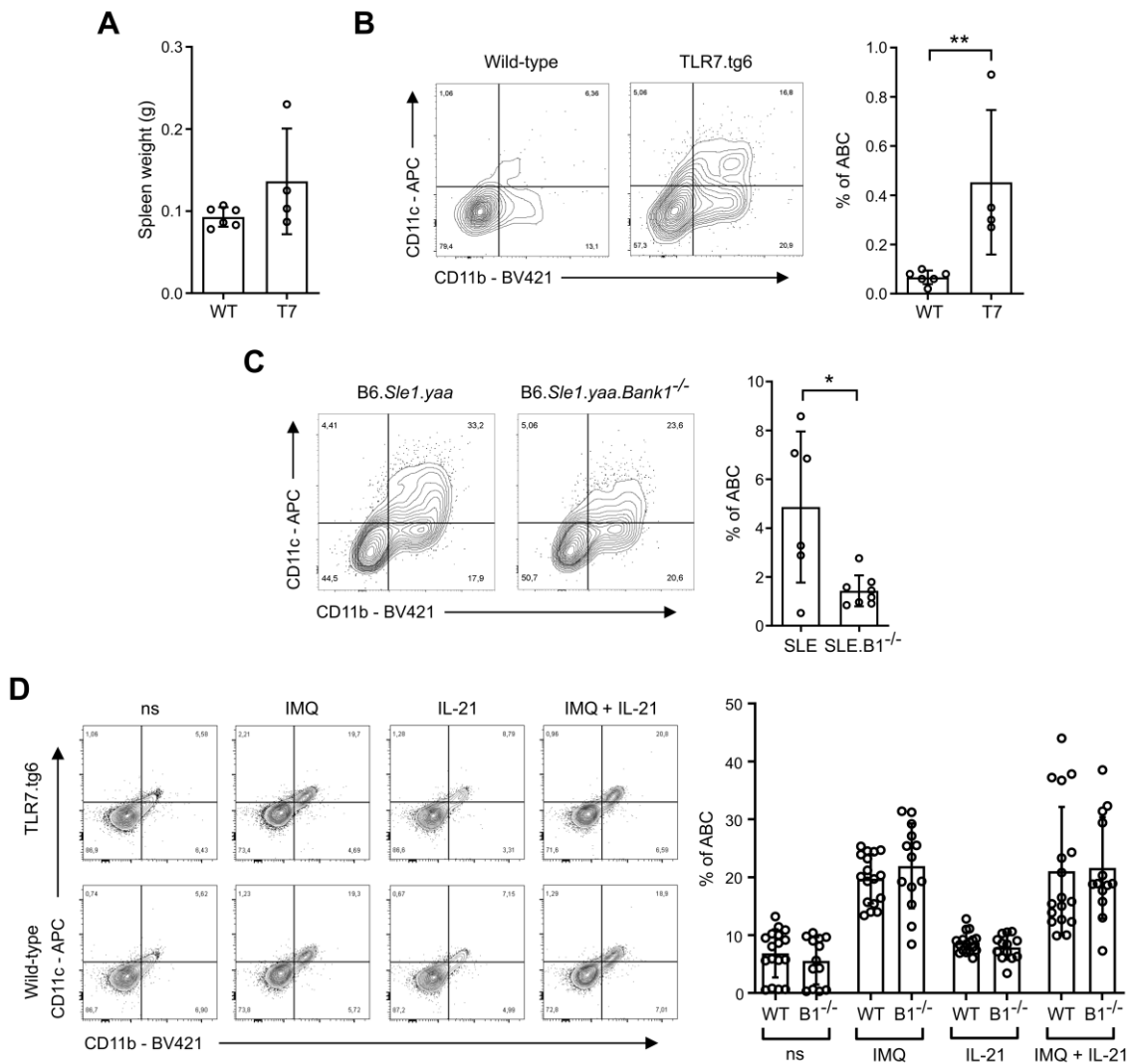
6 (n = 15) mice up to 20 weeks. A Kaplan-Meier survival plot is shown. **(B)** Serum levels

7 of IgG1 (μg/ml) at 1:10000 dilutions. Total mice analyzed: WT (n = 12), T7 (n = 12),

8 T7.B1^{-/-} (n = 14); and WT (n = 8), WT + IMQ (n = 9), B1^{-/-} (n = 8), B1^{-/-} + IMQ (n = 11).

9 Each point represents one individual mouse. Data are shown as mean ± SEM. Mann-

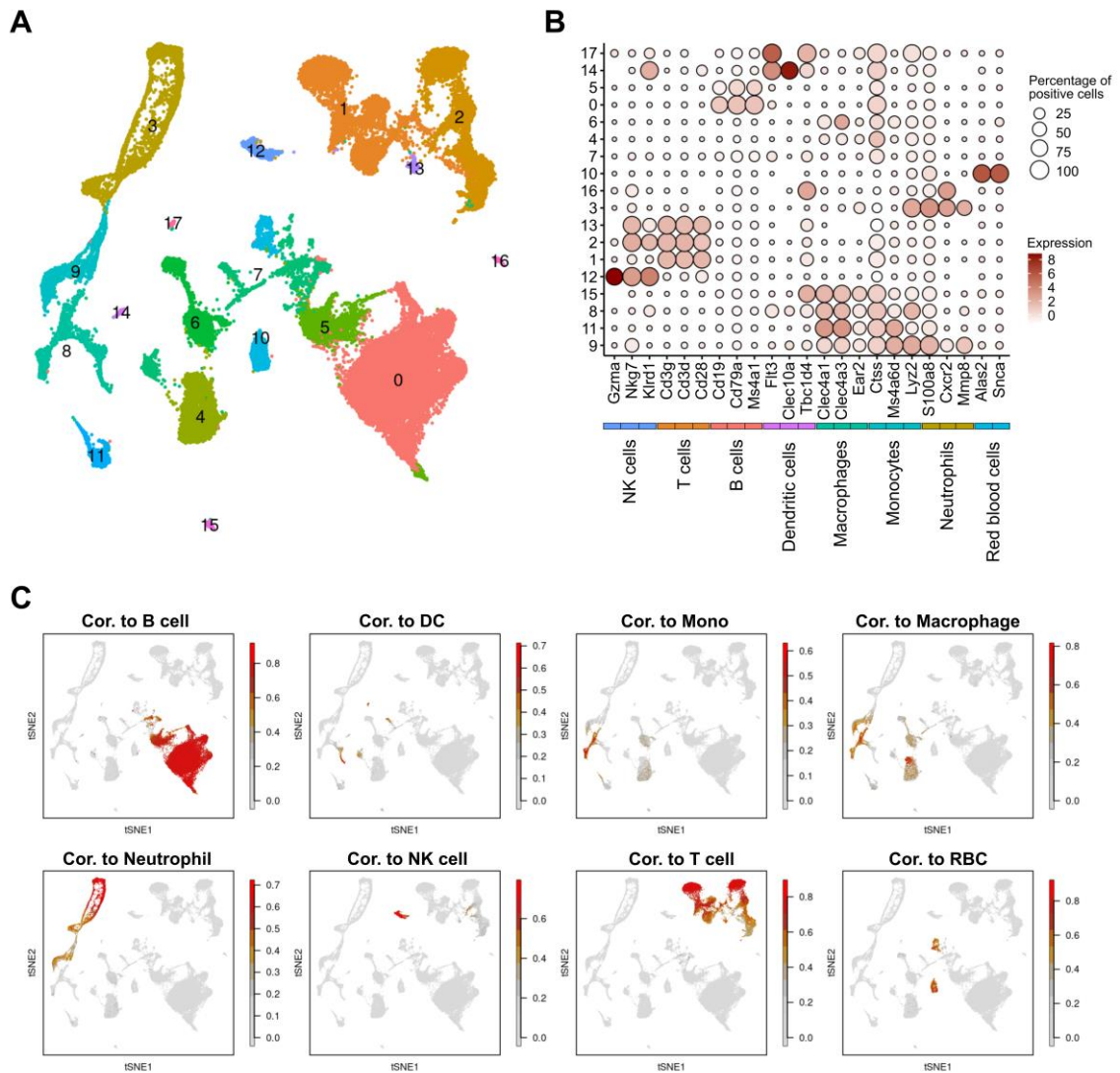
10 Whitney U test with Welch's correction was used to test statistical significance.



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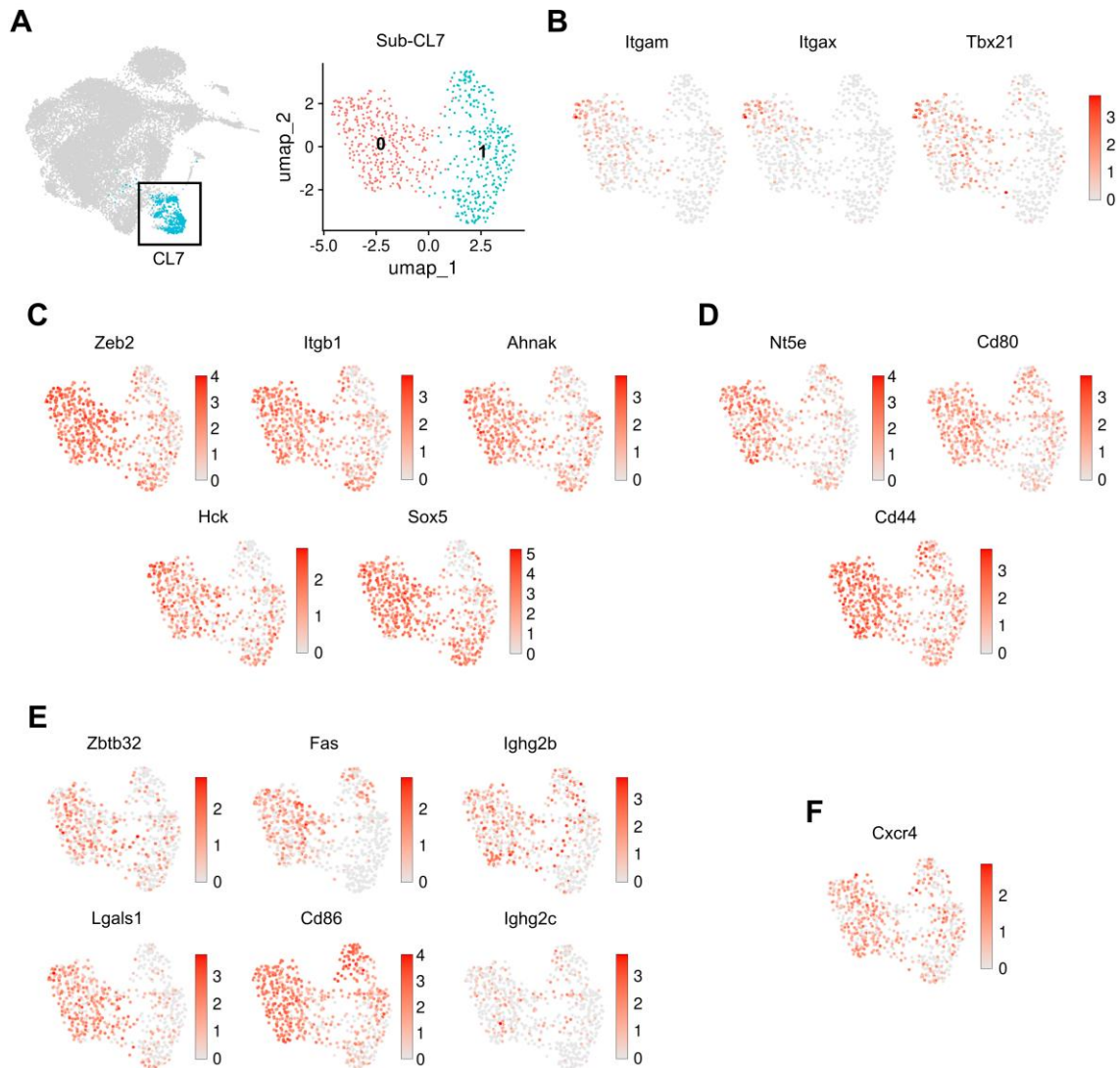
12 **Fig. S2. Frequency of ABCs at early ages, in the B6.Sle1.yaa model and *in vitro***
 13 **differentiation. (A)** Spleen weight from wild-type (n = 6) and TLR7.tg6 (n = 4) mice at
 14 10 weeks of age. **(B)** Frequency of ABCs among CD19⁺ B cells from the spleens of
 15 wild-type and TLR7.tg6 mice at 10 weeks of age. Total mice analyzed: WT (n = 6), T7
 16 (n = 4). **(C)** Frequency of ABCs among CD19⁺ B cells from the spleens of B6.Sle1.yaa
 17 and B6.Sle1.yaa.Bank1^{-/-} mice at 36 weeks of age. Total mice analyzed: SLE (n = 6),
 18 SLE.B1^{-/-} (n = 8). **(D)** Frequency of ABCs (CD11b⁺ CD11c⁺) among CD19⁺ T-bet⁺ B
 19 cells from cultures of B cells purified from wild-type and TLR7.tg6 10 week-old mice,
 20 stimulated with 5 µg/ml F(ab')₂-goat anti-mouse IgM, 5 µg/ml Ultra-LEAF purified anti-

21 mouse CD40, in presence or absence of 2.5 $\mu\text{g/ml}$ imiquimod, 25 ng/ml mouse IL-21
22 recombinant, and the combination of both, for 72 hours. Graph shows mean and
23 individual values of 3 independent experiments. Total mice analyzed: WT ($n = 17$), B1^{-/-}
24 ($n = 13$). Each point represents one individual mouse. Data are shown as mean \pm SEM.
25 Mann-Whitney U test with Welch's correction was used to test statistical significance.



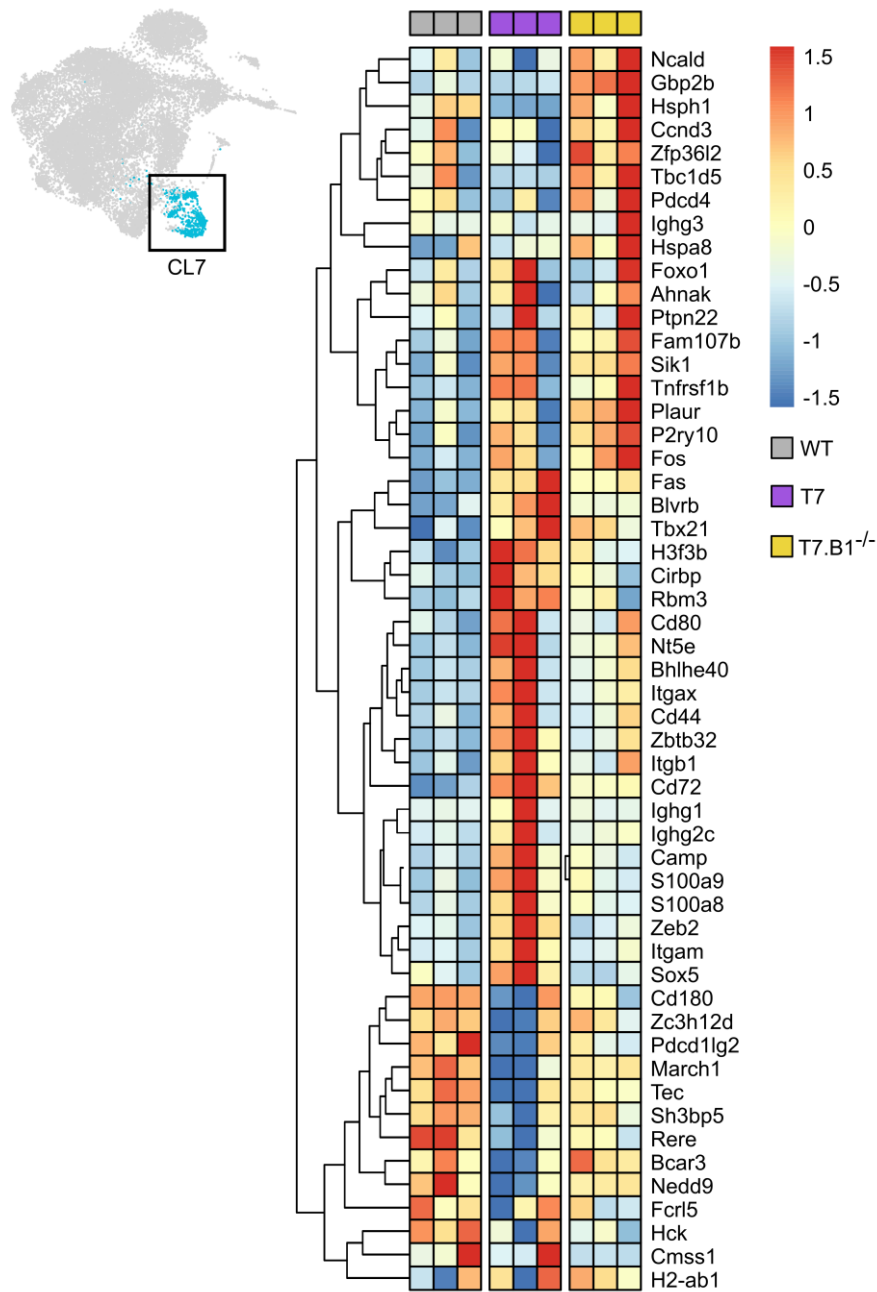
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27 **Fig. S3. Clustering of scRNA-Seq data.** (A) UMAP showing clusters of main cell types
 28 of spleen. Each point is a cell and the colours represent the different clusters. (B)
 29 Percentage of cells with the positive expression for cell type-specific markers (circle size)
 30 and their mean of expression (colour) across cells from each clusters. The markers are in
 31 columns and clusters are in rows. (C) Correlation between a panel of cell-specific markers
 32 and their expression by cells. Correlation is represented by the colour scale.



33

34 **Fig. S4. Subclusterization of CL7.** (A) UMAP showing two different subclusters
 35 (subCL7-0 and subCL7-1) obtained from the subclusterization of CL7. (B) Individual
 36 UMAPs showing the expression levels of typical markers of ABCs. (C) Individual
 37 UMAPs showing the expression levels of typical markers of: ABCs and atypical memory
 38 B cells (atMBCs), (D) memory B cells (MBCs), (E) plasma cells (PCs) and (F)
 39 extrafollicular cells.



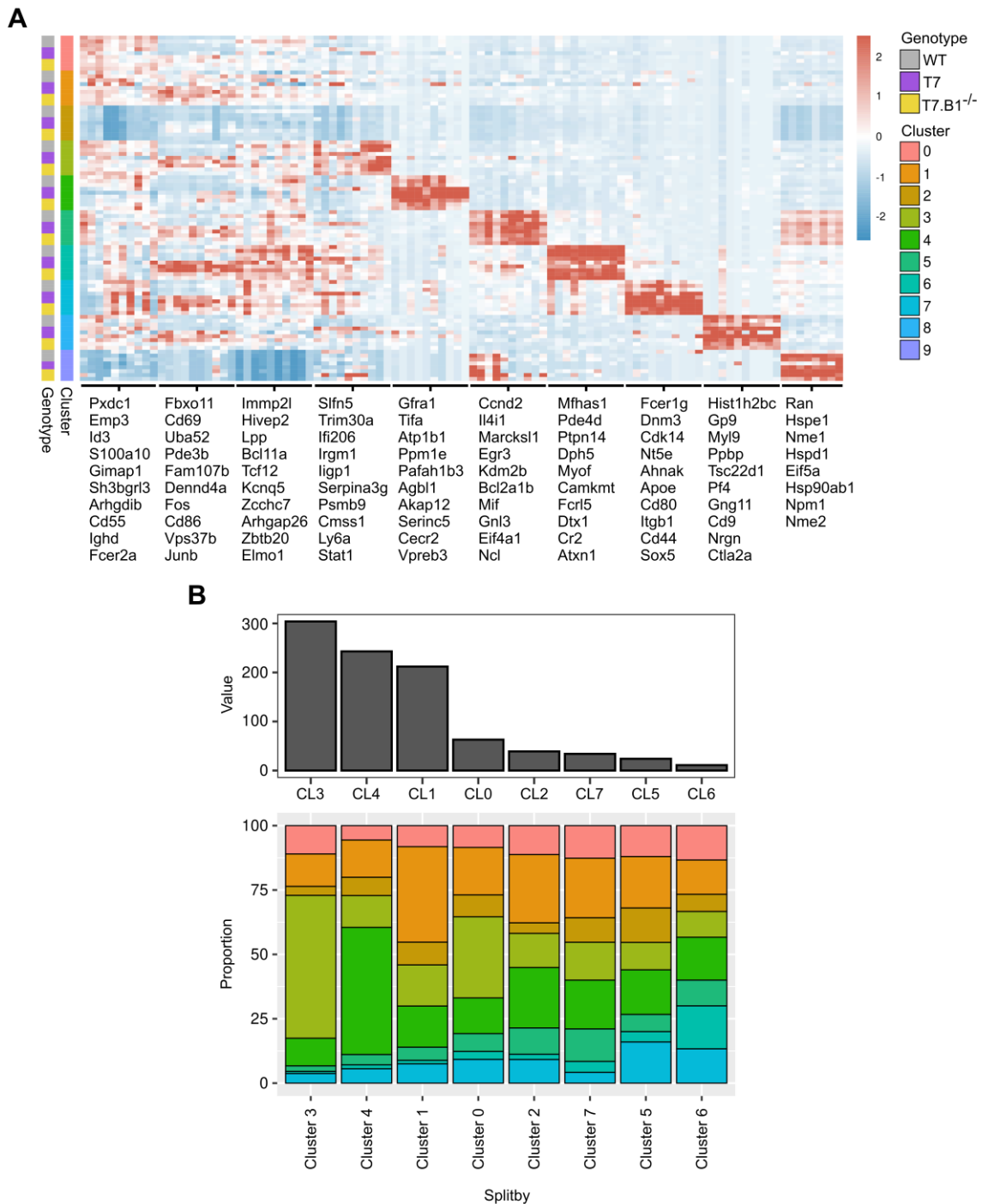
40

41 **Fig. S5. *Bank1* deficiency modified the differentially expressed genes in cluster 7.**

42 Heatmap showing the differentially expressed genes between wild-type, TLR7.tg6 and

43 TLR7.tg6.*Bank1*^{-/-} mice, in cluster 7. Colour represent the gene expression normalized

44 by z-score.

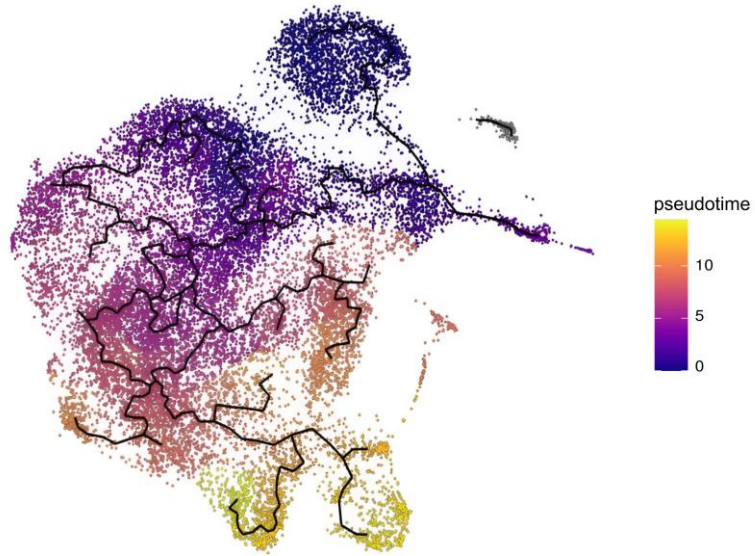


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46 **Fig. S6. scRNA-Seq transcriptome data from 10 clusters among CD19⁺ B cells. (A)**

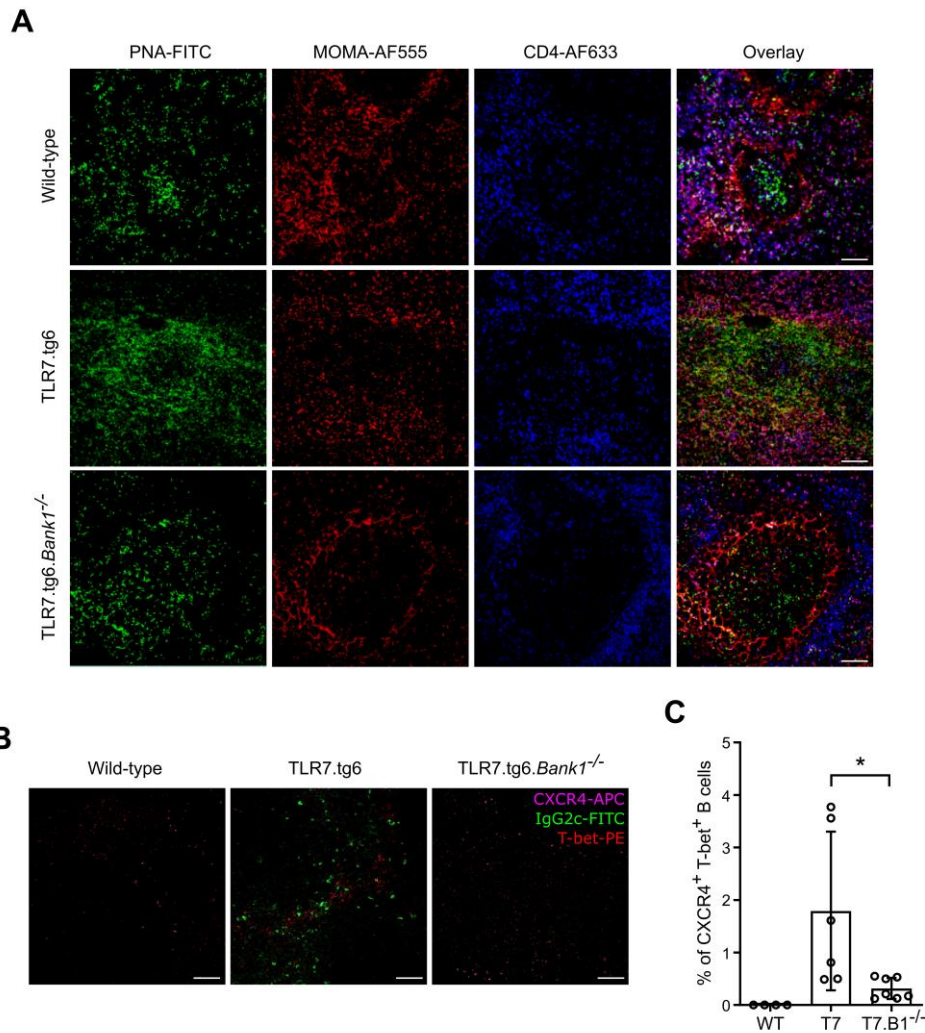
47 Top 10 most differentially expressed genes comparing each B cell clusters against the rest
 48 of B cell clusters. Colour scale represent the gene expression normalized by z-score. (B)

49 Above is the number of DEGs comparing each cluster against the rest. The proportion of
 50 significant genes unique and shared with other clusters is shown below.



51

52 **Fig. S7. Alternative trajectory of splenic B cells from the TLR7.tg6 model.** UMAP
53 visualization of the clusters arranged along trajectories, with CL2 as initial pseudotime
54 (root), coloured by inferred pseudotime, calculated by Monocle3.



55

56 **Fig. S8. T-bet⁺ extrafollicular B cells are increased in TLR7.tg6 mice compared to**
 57 **Bank1-deficient and wild-type mice.** (A) Representative cryosections of spleens from
 58 32 week-old wild-type, TLR7.tg6 and TLR7.tg6.*Bank1*^{-/-} mice, stained with anti-PNA
 59 FITC, anti-MOMA-1 conjugated with Alexa Fluor 555, and anti-CD4 conjugated with
 60 Alexa Fluor 633. Scale bar: 100 μm. This representative experiment was conducted 3
 61 different times. (B) Representative cryosections of spleens from 32 week-old wild-type,
 62 TLR7.tg6 and TLR7.tg6.*Bank1*^{-/-} mice, stained with anti-CXCR4 APC, anti-IgG2c FITC
 63 and anti-T-bet PE. Scale bar: 100 μm. This representative experiment was conducted 3
 64 different times. (C) Frequency of CXCR4⁺ T-bet⁺ cells among IgG2c⁺ CD138⁺ B220⁻

65 cells from the spleens of 32 week-old TLR7.tg6 model. Total mice analyzed: WT (n = 4),
66 T7 (n = 6), T7.B1^{-/-} (n = 7). Each point represents one individual mouse. Data are shown
67 as mean ± SEM. Mann-Whitney U test with Welch's correction was used to test statistical
68 significance.

69 **Legends for data files (Excel files):**

70 **Data file S1. Significantly expressed genes comparing between clusters.**

71 ClusterReference: cluster for which the rest of the values of the same row refer; GeneID:
72 Gene symbol identifier; PvalAdj: p-value adjusted by Bonferroni; AvgLog2FC: fold
73 change in base 2 logarithmic scale; pct1: percentage of cells expressing the gene in the
74 studied cluster; pct2: percentage of cells expressing the gene in the reference
75 cluster/clusters.

76

77 **Data file S2. Significantly expressed genes comparing between subclusters from**

78 **CL7.** ClusterReference: cluster for which the rest of the values of the same row refer;
79 GeneID: Gene symbol identifier; PvalAdj: p-value adjusted by Bonferroni; AvgLog2FC:
80 fold change in base 2 logarithmic scale; pct1: percentage of cells expressing the gene in
81 the studied cluster; pct2: percentage of cells expressing the gene in the reference
82 cluster/clusters.

83

84 **Data file S3. Significantly expressed genes comparing TLR7.tg6 and**
85 **TLR7.tg6.Bank1^{-/-} by cluster.** Each excel sheet contains the results obtained for a

86 cluster. GeneID: Gene symbol identifier; PvalAdj: p-value adjusted by Bonferroni;
87 AvgLog2FC: fold change in base 2 logarithmic scale; Comparison: group of mice
88 compared. Second group as used as reference for the statistical test.

89

90 **Data file S4. Significant biological pathways comparing between clusters.**

91 ClusterReference: cluster for which the rest of the values of the same row refer; PvalAdj:
92 p-value adjusted by Bonferroni; Direction: significant biological pathway for up-

93 regulated or downregulated genes; Description: pathway description; AnnotationID:
94 Gene Ontology identifier.

95

96 **Data file S5. Significant biological pathways comparing TLR7.tg6 and**
97 **TLR7.tg6.Bank1^{-/-} by cluster.** ClusterReference: cluster for which the rest of the values
98 of the same row refer; Direction: significant biological pathway for up-regulated or
99 downregulated genes; PvalAdj: p-value adjusted by Bonferroni; Description: pathway
100 description; AnnotationID: Gene Ontology identifier.