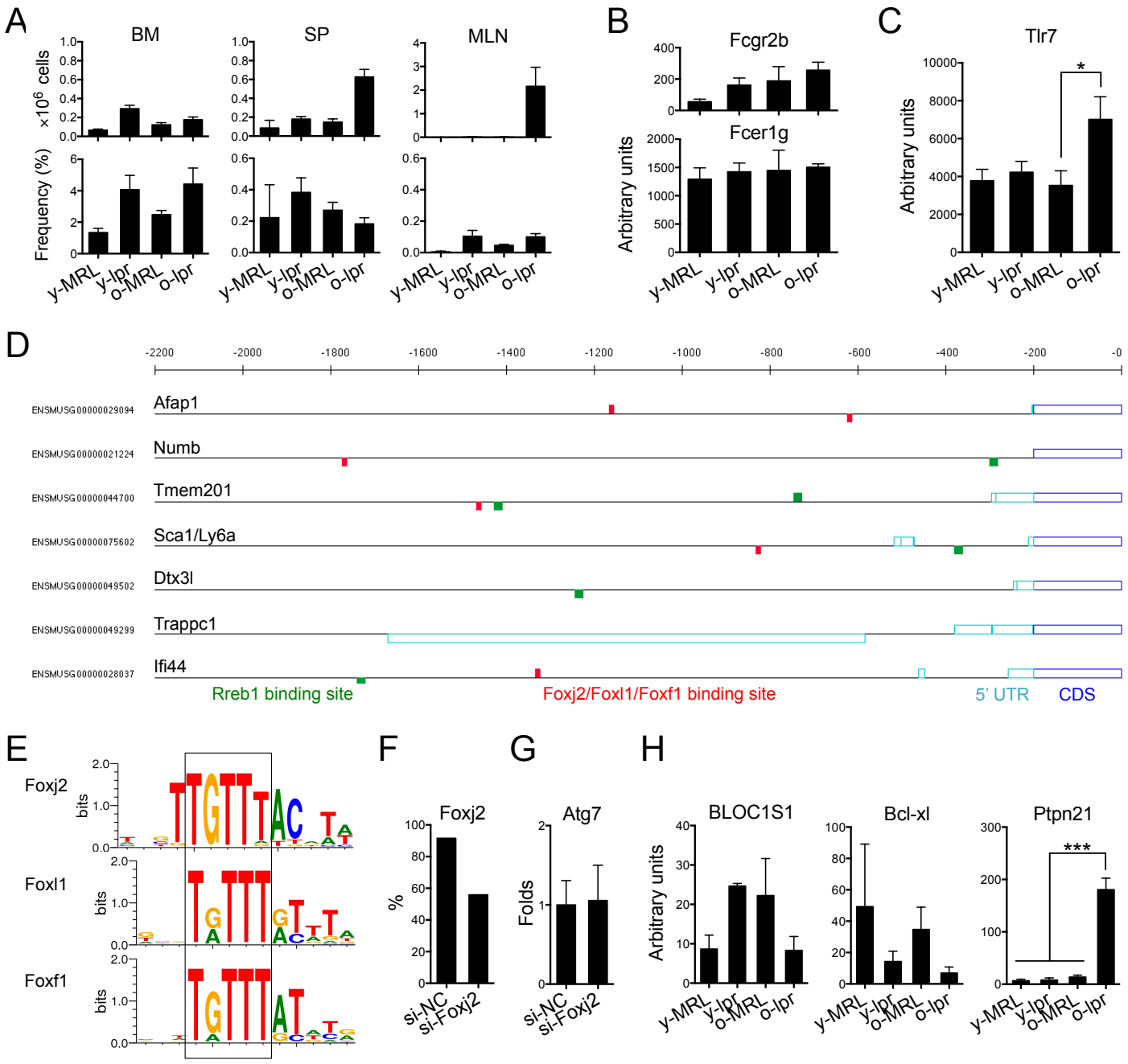
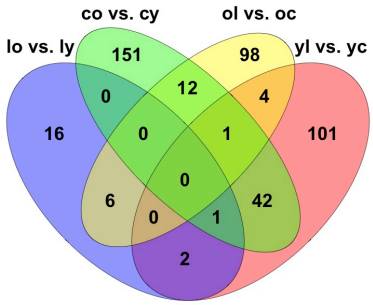


Supplemental Fig. 1. PDCs unable to produce IFNα in late-stage lupus mice. (**A**) Absolute cell numbers and frequencies of pDCs in bone marrow (BM), spleen (SP) and mesenteric lymph node (MLN). (**B**) Transcript levels of immune complex receptors Fcgr2b and Fcer1g. PDCs from these mice did not express Fcgr1 or Fcgr3. (**C**) Transcript levels of Tlr7. *P<0.05, Student's t-test, n=3 per group. (**D**) Promoter analysis by using TOUCAN (https://gbiomed.kuleuven.be/english/research/50000622/lcb/tools/toucan). (**E**) Shared binding motif of Foxj2, Foxl1 and Foxf1. Maps were provided by MotifMap (http://motifmap.ics.uci.edu/). Only Foxj2 was expressed in the pDCs. (**F**) Transcript level of Foxj2 with negative control siRNA (si-NC) or Foxj2-specific siRNAs (si-Foxj2) in bone marrow cells from *lpr* mice. Percentages from the untransfected control are shown. (**G**) Transcript level of Atg7 after transfection with siRNAs. (**H**) Transcript levels of BLOC1S1 (subunit 1 of the lysosome-related BLOC1 complex), Bcl-xl, and Ptpn21. n≥3 mouse per group. ***P<0.001, ANOVA.

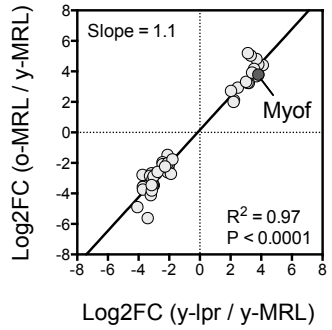
A



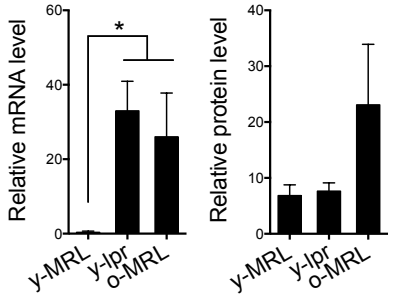
B

Gene	Ensembl ID	o-lpr vs. y-lpr	*P*-value
5730480H06Rik	ENSMUSG00000093459	-3.1	0.000000005
Ptpn21	ENSMUSG00000021009	2.9	0.00000001
Cd209d	ENSMUSG00000031495	-2.3	0.0000002
Ppif	ENSMUSG00000021868	-1.2	0.017
Maff	ENSMUSG00000042622	-1.9	0.017
Pde5a	ENSMUSG00000053965	-1.6	0.017
Sdc2	ENSMUSG00000022261	1.7	0.028
Ptpn11	ENSMUSG00000043733	-1.4	0.045
Arhgap12	ENSMUSG00000041225	-1.1	0.049

C



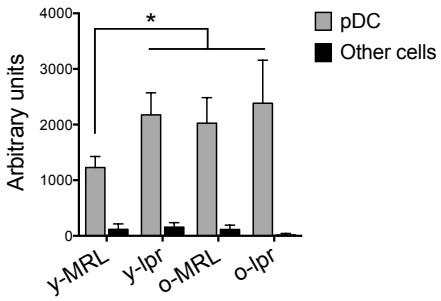
D



E

Gene	Chr	Start	End	y-lpr vs. y-MRL	*P*-value	o-MRL vs. y-MRL	*P*-value	Adjacent gene(s)
XLOC_002487	1	95337570	95338098	-6.5	0.046	-5.4	0.047	*Fam174a*
XLOC_002527	1	102628128	102628476	-4.2	0.036	-3.6	0.047	/
XLOC_002731	1	154729087	154732504	3.2	0.025	3.6	0.047	*Cacna1e*
XLOC_002785	1	154862037	154864052	4.2	0.018	4.2	0.002	*Cacna1e*
XLOC_030964	3	94949177	94949585	-7.1	0.027	-7.7	0.013	/
XLOC_031027	3	103006391	103008460	-5.4	0.018	-4.5	0.015	*Sike1*
XLOC_034788	4	155826772	155827415	5.4	0.041	6.2	0.003	*Ccnl2*
XLOC_037202	5	75045027	75045533	5.2	0.027	4.9	0.046	*Chic2*
XLOC_048769	9	13544086	13544924	5.3	0.018	5.1	0.023	/
XLOC_018942	16	49852204	49855405	-2.7	0.049	-3.4	0.003	*CD47*

F



Supplemental Fig. 2. Predisposed dysregulation of pDCs in lupus mice. (**A**) Venn diagram showing the number of differentially expressed genes in 4 comparisons (FDR<0.1). Blue: older vs. younger in MRL/lpr mice. Green: older vs. younger in MRL mice. Yellow: MRL/lpr vs. MRL in older mice. Red: MRL/lpr vs. MRL in younger mice. (**B**) Differentially expressed genes between pDCs of older vs. younger MRL/lpr mice (*P*<0.05). (**C**) Log2 fold changes (FC) of 44 overlapped, differentially expressed genes in both Green and Red. (**D**) Transcript levels of Myof in sorted pDCs and protein levels of Myof in bone marrow pDCs. For protein levels, percentage and mean fluorescence intensity of Myof$^+$ pDCs were measured by using flow cytometry and the numbers were multiplied to represent the total expression level. **P*<0.05, student's *t*-test. Data are shown as mean + SEM (n=3 mice per group). (**E**) List of predicted lncRNAs that were overlapped. (**F**) Transcript level of Cacna1e, a gene next to predicted lncRNAs XLOC_002731 and XLOC_2785 on Chromosome 1. This gene appeared to be pDC-specific, and was upregulated in lupus mice with either early or late disease. The two predicted lncRNAs were also upregulated during lupus progression. **P*<0.05, Student's *t*-test, n=3 per group.