Supplementary Figure 1: Adoptive transfer of lymphoma cells gives rise to tumors in WT hosts
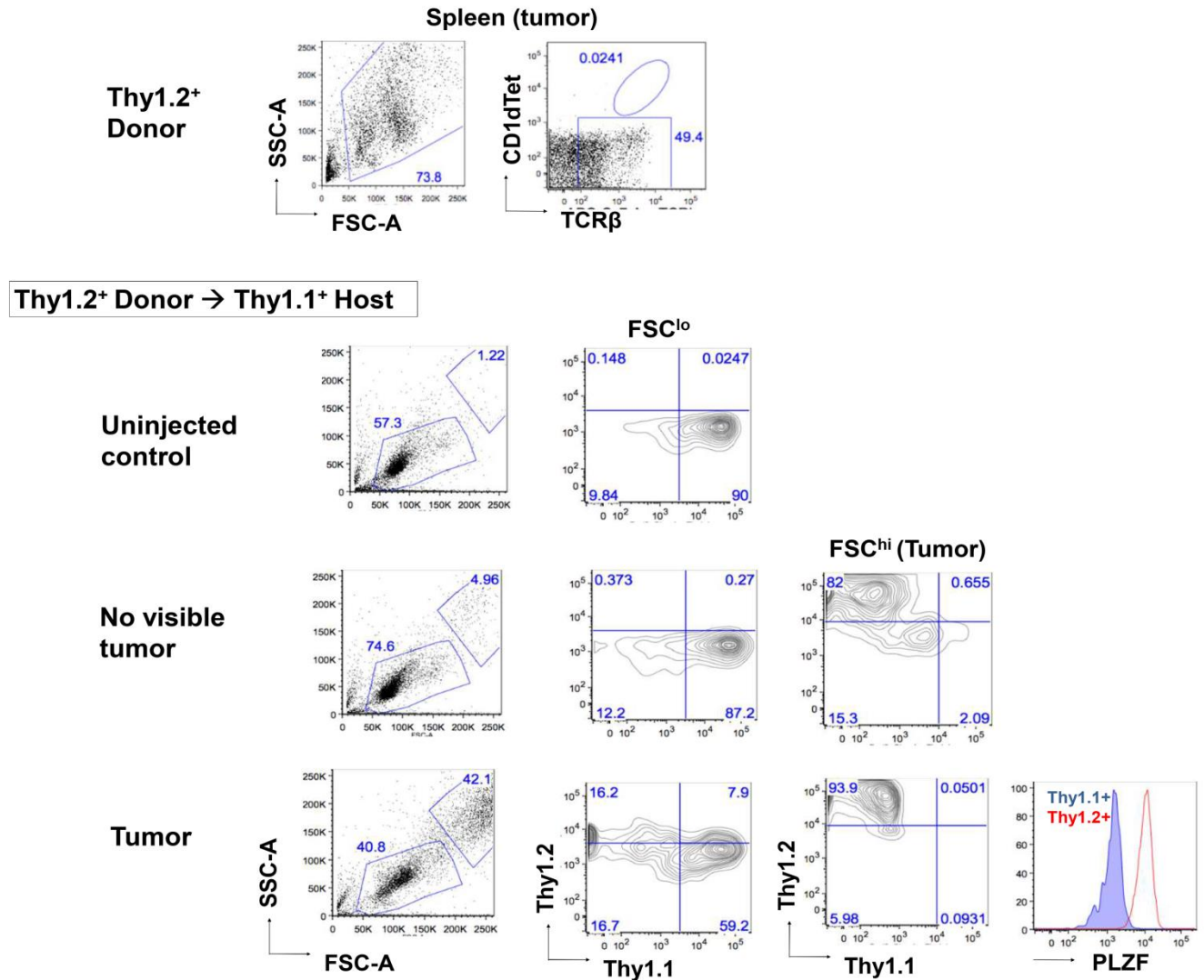
(A) Tumor incidence (left) in WT hosts (N = 10) after receiving 5×10^6 lymphoma cells from L-DKO donor mice with CD1dTet$^-$ tumor (N = 2). Representative picture of host with tumor in liver, spleen and LN (marked with arrows). (B) Representative flow cytometry analysis of CD1dTet$^-$ lymphoma donor cells from spleen (top panel), and cells recovered from spleen of Thy1.1$^+$ WT hosts, 10 weeks after receiving Thy1.2$^+$ lymphoma donor cells, or uninjected control. Retention of the innate-like phenotype of lymphoma donor cells was verified by upregulated PLZF expression in FSC^{hi} TCRβ$^+$Thy1.2$^+$ cells (large lymphoma cells) as compared to FSC^{lo}TCRβ$^+$Thy1.1$^+$ cells.
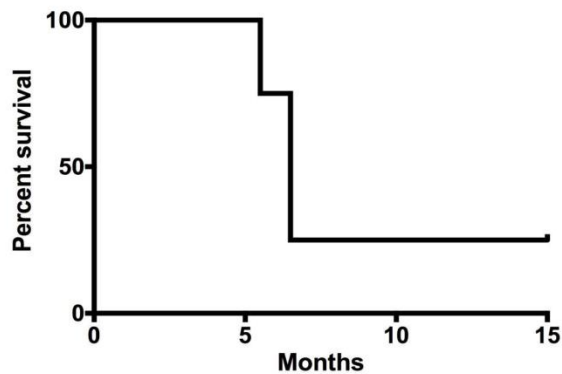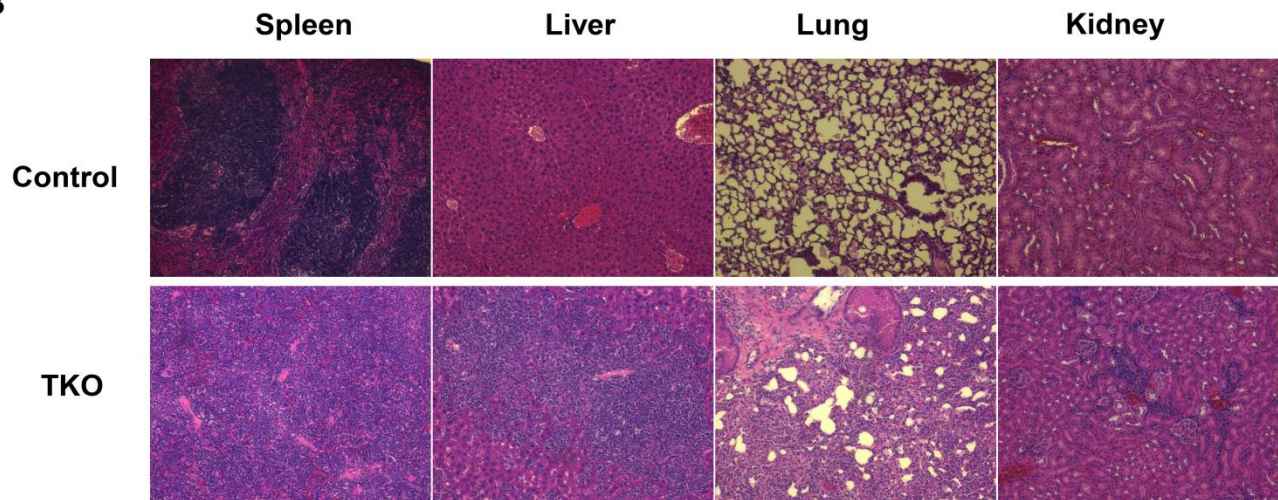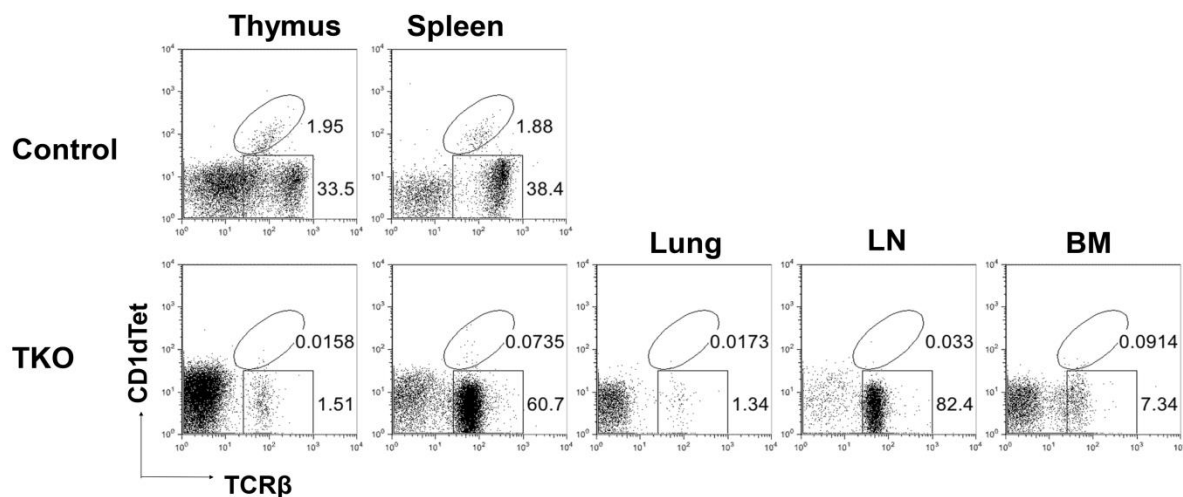
Supplementary Figure 2: CD1d-independent CD1dTet⁻TCRβ⁺ T cells give rise to lymphomas in TKO mice

(A) Survival curve for TKO mice (N=4) along with details of mice that developed tumor. (B) Representative pictures of H&E staining of spleen, lung, liver and kidney tissue sections from Cre⁻ control and TKO mice (100X). (C) Representative distribution of TCRβ⁺CD1dTet⁺ and TCRβ⁺CD1dTet⁻ cells in thymus, spleen, lung, lymph node (LN) and bone marrow (BM) of Cre⁻ mice and TKO mice with tumors.
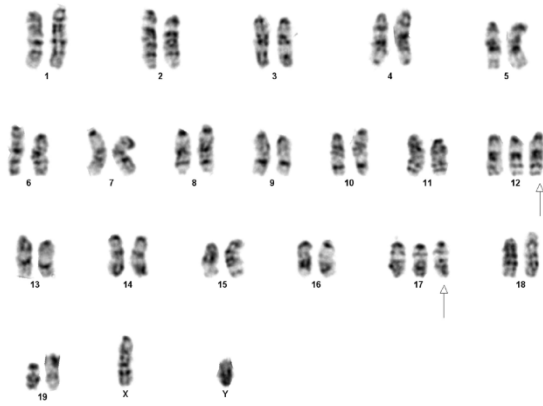
Slide10-PP cells 2/26-3   Cell: 32
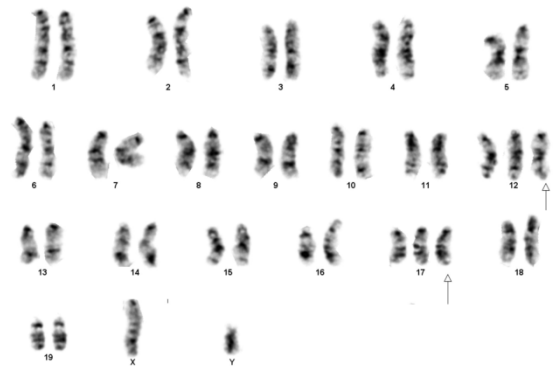
Slide: 3_PP cells   Cell: 8

Mouse 57 : Cd1dTet+ tumor (Abnormal karyotype)
42,XY,+12,+17[8]/43,XY,+Y,+12,+17[4]/41,X,-Y,+12,+17[4]/40,XY[27]

Tissues

Lymph Node (LN) (10 cells)	Normal	4 cells
	Abnormal	42,XY,+12,+17_2 cell
		43,XY,+Y,+12,+17_3 cells
Spleen (SP) (11 cells)	Normal	7 cells
	Abnormal	42,XY,+12,+17_2 cells
		41,X,-Y,+12,+17_2 cells
Peyer's patch (PP)(23 cells)	Normal	16 cells
	Abnormal	42,XY,+12,+17_4 cell
		43,XY,+Y,+12,+17_1 cell
		41,X,-Y,+12,+17_2 cell

Mouse 75 : CD1dTet- tumor (Normal karyotype)
40,XY[20]

Lymph Node (LN)	Normal	4 cells
Peyer's patch (PP)	Normal	6 cells
Thymus	Normal	10 cells

Supplementary Figure 3: Karyotyping analysis of lymphoma samples
Karyotyping analysis of lymphoma samples from one mouse with CD1dTet+ tumor and one with CD1dTet- tumor. Karyotypes for individual tissue samples are described.

Supplementary Table I: Cluster definitions according to Self-Organizing Map (SOM) analysis[1]

Cluster ID	Row	Column	Gene Names
1	1	1	Ifit1, Sh3bgrl2, Secisbp2l, Ifih1, Cmpk2, Irgm2, Irf7
2	1	2	Scn11a, Rps4y2, Hivep3, Ddx24, AY036118, Tprgl
3	1	3	F2rl1, Btg2, Coro2a, Atg14, Chd7, Rasa1, Osbpl5
4	1	4	Arl4d, Itgae, Trip4, Pcgf2, Rgs3
5	1	5	Marveld2, Ahnak, Smpdl3a, Fgd6
6	2	1	Phxr4, Brdt, Arl4c, Ndrg3, Dgka, Ifi27l2a, Vangl2
7	2	2	Parg, H2-T24, Cox6b2, Ccs, Hmbox1, Ldlrap1, Emilin1, Fam189b, Ndrg4
9	2	4	Cxcr3, Rhob, Cd244
10	2	5	Adam19, Hip1, Ctsd
11	3	1	Ccr7, Igfbp4, Rag2
13	3	3	Tmem176a, Tnc, Pld4, Lgals1, Wbp5, Colec12, Ggta1, Cdh5, Vcam1, Mmp2, Rab34, Sdc1, Rhoj
14	3	4	Pygl, Cst7, Slc39a4, Ifngr1, Syngr2
15	3	5	Ifitm3, Ms4a6c, Ccl5, Swap70, Il10ra, Ccr5, Naip2
16	4	1	Fignl1, Cdk1, Emp3
17	4	2	Tbc1d24, Sepp1, Fhl1
18	4	3	Cpe, Adm, Cfp, Slc15a3, Cd83, Cd86, Ms4a1, Cd79b, Fabp5, Ccl11
19	4	4	Frmd4b, Grn, Mt2, Ctsz, Hgfac
20	4	5	Icosl, Naip5, Irf5, Txndc5
21	5	1	Prss23, Cd81, Pdzd3, Slc27a2
22	5	2	Myh3, Fscn1, Mertk, Cd74, Lepr, Lpcat1, H2-DMa
23	5	3	Ms4a7, Spon1, Papss2, Bgn, Ccdc88a, Relb, Gns, Procr, Mospd2, Ankrd33b, Nfkbie, Pawr
24	5	4	Csf2rb, Lpl, 2610528A11Rik, Ryr1, Cebpd, Ly6d, Myadm, Ncf1, Serpina10, Cp, Slc4a8
25	5	5	Chi3l3, Mrc1, Gja1, Rsph1, Pkd2, Lrrk1, Steap4, Emp1, Rgs18, Uap1, Ccr1, Prcp

[1]List of genes in each cluster (identified by row and column number in map) as defined by the Self-Organizing Map (SOM) analysis shown in Figure 7B.