Supporting Information

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SI Methods

Mice. mCD4-ThPOK (line 198) mice, referred to as ThPOK^{const} mice throughout the study, have been described previously (1). To assess lymphoma development, animals were monitored by biweekly physical examinations and PBL analyses. Lymphoid and nonlymphoid organs were subjected to FACS analysis using antibodies against Thy1, TCRβ, γδTCR, CD4, CD8, CD25, and CD44. KN6^{+} RAG2$^{-/-}$ d/d and KN6^{+} RAG2$^{-/-}$ B2m$^{-/-}$ mice were described previously (2). hCD2-ThPOK transgenics have been reported previously (1). For transgenic expression of ThPOK cDNA under mProxLck regulatory elements, the full-length cDNA insert was cloned into a vector containing mouse proximal promoter/enhancer elements (3).

Immunohistochemical Staining. Hematoxylin/eosin staining was carried out according to standard procedures. Anti-CD3ε antibody (eBioscience) was used according to manufacturer's instructions.

Antibody Injection of RAG$^{-/-}$ Mice. Groups of juvenile ThPOK^{const} Rag$^{-/-}$ mice (2 wk of age) and control Rag$^{-/-}$ mice were injected either with anti-CD3ε antibody (clone 2C11, 9 μg of antibody per gram of mouse weight) or with PBS alone as a control. A mouse of each group at 3 wk was killed to verify occurrence of thymocyte expansion and also at 15 wk to check for persistence of post-DN3 cells generated by antibody stimulation. Remaining mice were monitored for 7 mo by biweekly physical examination for signs of lymphoma development.

Adoptive Transfer of Bone Marrow and Lymphoma Cells from ThPOK^{const} Donors. Bone marrow cells were isolated from tibias and femora of ThPOK^{const} mice (or control nontransgenic mice) and depleted of CD4^{+} and CD8^{+} cells by magnetic cell separation system (Miltenyi Biotec). One million cells in 0.2 mL of DMEM + Hepes media were injected i.v. into Rag2$^{-/-}$ recipients that had been irradiated (900 rads, delivered in two doses of 450 rads) 24 h previously. Peripheral blood samples were analyzed 6 wk after bone marrow transfer to verify hematopoietic reconstitution. Mice were monitored weekly by physical examination and monthly by PBL analysis for signs of lymphoma development. Adoptive transfers of 10^5 ThPOK^{const} tumor cells into Rag2$^{-/-}$ hosts were carried out according to the same protocol.

PCR Assays. Primers for PCR are as follows: Sequences of Notch1 gene were obtained from genomic DNA following PCR with specific primers: exon 26: F, GCGAGTCGCCAAGCACATTT and R, CACCTCCAGGGTTAAGCTGGT; exon 27: F, GGCTAGGGAGTCAGAGCTGGT and R, TTGAACCCTTGTCCTCTGCAA; exon 28: F, AGCCCACAGCATCACCAC and R, ATGGGCCTTCTGGAGCTAAG; exon 34 PEST: F, CACAGCAGCCTCTCCACCAA and R, CCCCAGCATCCTGAAGCACT; and exon 34 TAD: F, CATGCTGTCGCCTGTGGACT and R, CTGCCGAGCTCACACTGAGG.

In some cases Notch1 sequences were amplified from cDNA, using the same primers, except for exons 26–28 (F, ACTGTGACAGCCAGTGCAAC and R, CACAAAGAACAGGAGCACGA).

Dβ2-Jβ2.7 rearrangements were PCR amplified using specific primers for:

Dβ2 5′-GTAGGCACCTGTGGGGAAGAAACT-3′ and

Jβ2.7 5′-TGAGAGCTGTCTCCTACTATCGATT-3′.

Indicated commercial Taqman Gene expression assays were used to measure expression of the following murine genes: Mm00478361_m1 for Ptcra, Mm01345646_m1 for Notch3, Mm01342805_m1 for Hes1, Mm00492297_m1 for Dtx1, and Mm00490666_m1 for Runx3. For RT-PCR measurement of murine ThPOK expression, we designed the following primers and probe: F, AGAAGCCCTTTGCCTGTGA and R, TGTGGATCTTCAGCTTGTCATTC; P: 6fam-TCTGCGGCGTCCGCTTCAC-Bhq1.

Microarray Analysis. Gene expression profiling of mouse tumors. We profiled three Thpok transgenic-derived T-ALLs and an additional 11 T-cell lymphoblastic tumors from well-characterized T-ALL models including E2A knockout, TAL1 transgenic, TAL1 and LMO1 double transgenic, and Ikaros plastic mutant mice. Gene-expression profiling was performed using Affymetrix Mouse Genome 430A 2.0 Array following standard procedures (www.affymetrix.com/support/technical/manuals.affx). Raw data are available in GEO www.ncbi.nlm.nih.gov/geo/ (accession no. GSE33550). Array normalization was performed by DNA-Chip Analyzer (dChip) (4). Following interarray normalization the microarray data were preprocessed and analyzed for differential expression using the Genepattern platform (www.broadinstitute.org/cancer/software/genepattern/) for microarray analysis (5). Significant differentially expressed genes were calculated by using the Comparative Marker Selection Genepattern tool (6) and *t* test statistical test and nonparametric *P* value calculation (1,000 random permutations).

CGH Array Analysis. Genomic imbalances were identified using array-CGH (comparative genomic analysis), which was performed according to Agilent's oligonucleotide array-based CGH protocol for Genomic DNA Analysis, version 4.0. Genomic DNA (0.5–3 μg) from tumors that were digested with AluI and RsaI restriction endonucleases. The digested DNA was labeled using Agilent's Genomic DNA Labeling Kit PLUS. Tumor and normal (tail) reference DNA samples were labeled with either cyanine 5- or cyanine 3-dUTP, according to the manufacturer's suggestions. The labeled DNA products were purified using Microcon YM-30 filtration devices (Millipore). DNA yield and level of dye incorporation were measured using a ND-1000 spectrophotometer. Appropriate cyanine 5- and cyanine 3-labeled DNA sample pairs were combined and mixed with mouse Cot-1 DNA, Agilent 10× blocking agent, and Agilent 2× hybridization buffer. Then each labeled target solution was hybridized to an Agilent 244K Mouse Genome CGH Microarray (G4415A) using SureHyb chambers. Following hybridization, the microarrays were washed and dried as outlined in Agilent's protocol. Microarray slides were then scanned using an Agilent microarray scanner. Data for individual features were extracted from the scanned image using Agilent's Feature Extraction Software, and output files were imported into Agilent's CGH Analytics for DNA copy number analysis.

1. He X, et al. (2005) The zinc finger transcription factor Th-POK regulates CD4 versus CD8 T-cell lineage commitment. *Nature* 433(7028):826–833.
2. Haks MC, et al. (2005) Attenuation of gammadeltaTCR signaling efficiently diverts thymocytes to the alphabeta lineage. *Immunity* 22(5):595–606.
3. Chaffin KE, et al. (1990) Dissection of thymocyte signaling pathways by in vivo expression of pertussis toxin ADP-ribosyltransferase. *EMBO J* 9(12):3821–3829.
4. Li C, Wong WH (2001) Model-based analysis of oligonucleotide arrays: Expression index computation and outlier detection. *Proc Natl Acad Sci USA* 98(1):31–36.
5. Reich M, et al. (2006) GenePattern 2.0. *Nat Genet* 38(5):500–501.
6. Gould J, Getz G, Monti S, Reich M, Mesirov JP (2006) Comparative gene marker selection suite. *Bioinformatics* 22(15):1924–1925.

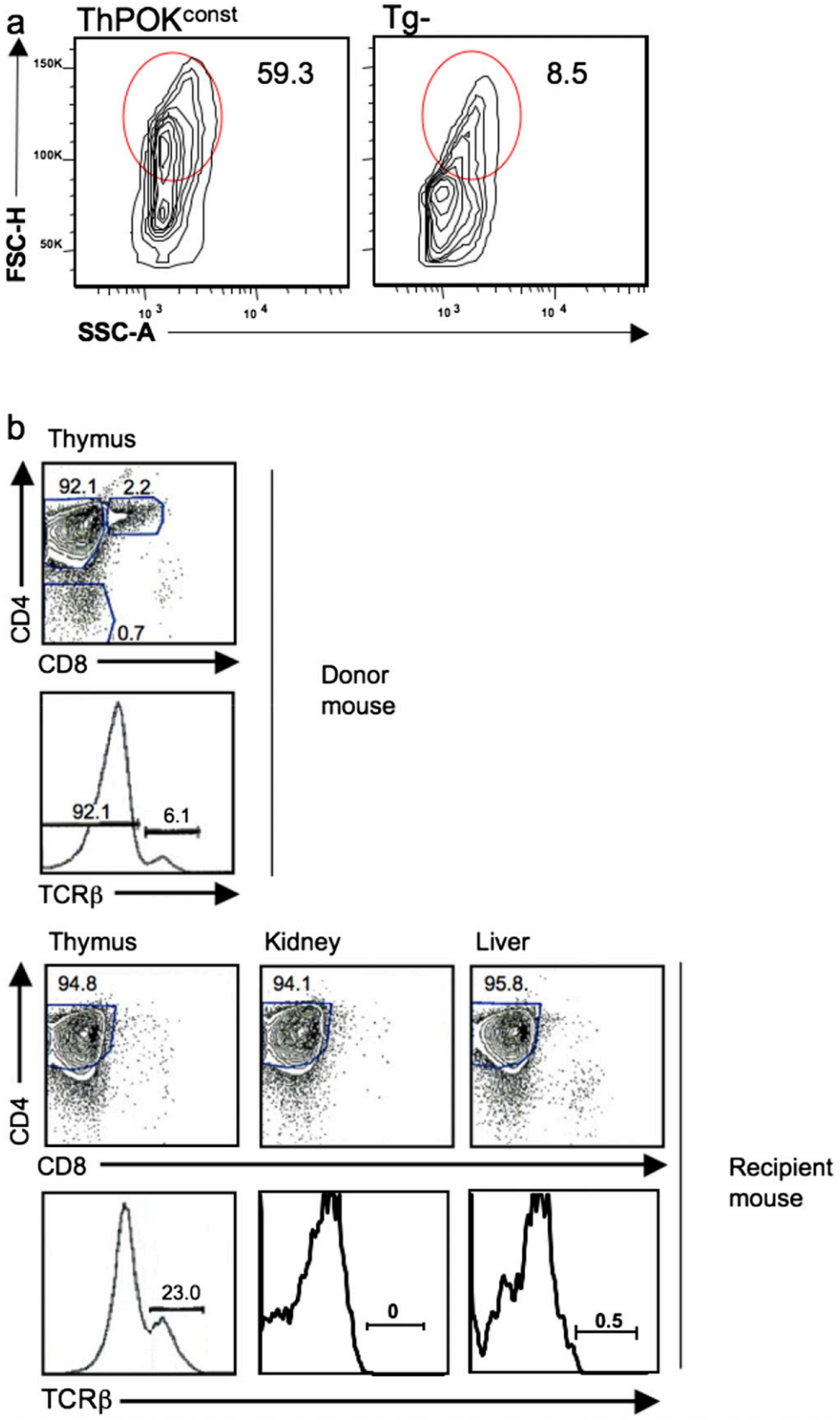


Fig. S1. ThPOK^{const} lymphomas exhibit increased cell size and can be adoptively transferred to immunodeficient hosts. (*A*) Forward/side scatterplots of Thy1^{+} PBLs from ThPOK^{const} and nontransgenic littermates. (*B*) The 10^5 Thy1^{+} cells from the thymus of a sick 4-mo-old ThPOK^{const} mouse were transferred i.v. into sublethally irradiated Rag2$^{-/-}$ hosts. Organs were harvested 6 wk after adoptive transfer and examined by flow cytometry for presence of lymphoma cells, based on expression of CD4, CD8, and TCRβ. Note high proportion of CD4^{+} TCRβ^{-} cells in all host organs after adoptive transfer (*Bottom* row), closely resembling the phenotype of original donor lymphoma cells (*Top* row) (no such cells were detected in Rag2$^{-/-}$ mice that did not receive tumor cell transplants). This experiment was repeated three times with similar results.

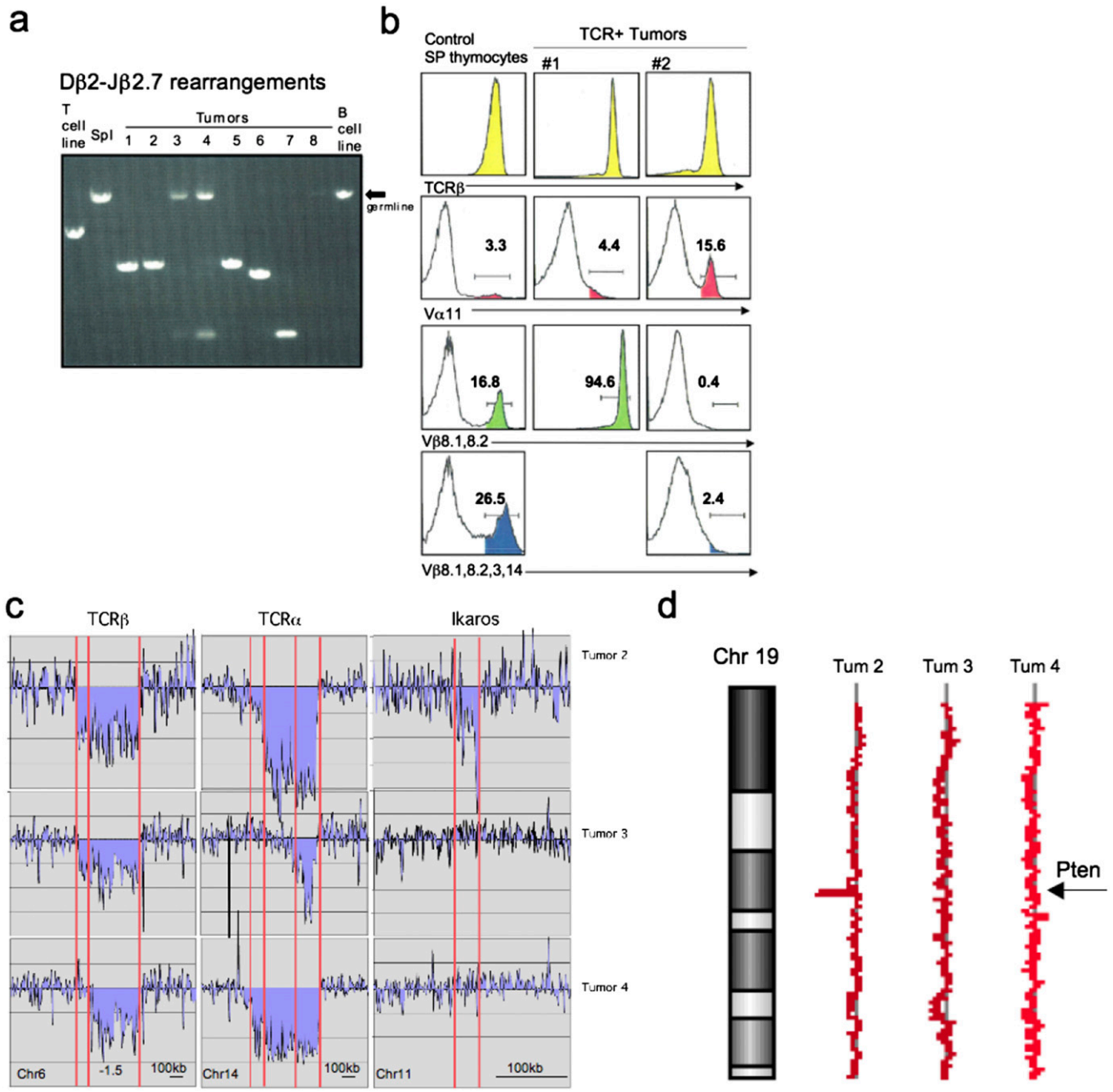


Fig. S2. Clonality of ThPOK^{const} T-cell lymphomas. (*A*) PCR analysis of Dβ2-Jβ2.7 rearrangement from eight independent ThPOK^{const} T-cell lymphomas. Note that each tumor sample exhibits a single rearrangement product (tumors 3 and 4 also retain some germ-line configuration TCRβ). (*B*) FACS analysis of two independent ThPOK^{const} T-cell lymphomas. Note that samples 1 and 2 express Vβ8 on 95% or <1% of all cells, compared with 17% by normal WT T cells (combined SP CD4 and CD8 populations from C57BL/6 mouse). (*C*) Comparative genomic hybridization (CGH) array analysis of representative ThPOK^{const} T-cell lymphoma samples showing deletions of TCRβ, TCRα, and Ikaros loci (plotted as Log2 ratio). (*D*) CGH array analysis of whole chromosome 19 in representative ThPOK^{const} T-cell lymphoma samples showing deletions of Pten locus in sample 2.

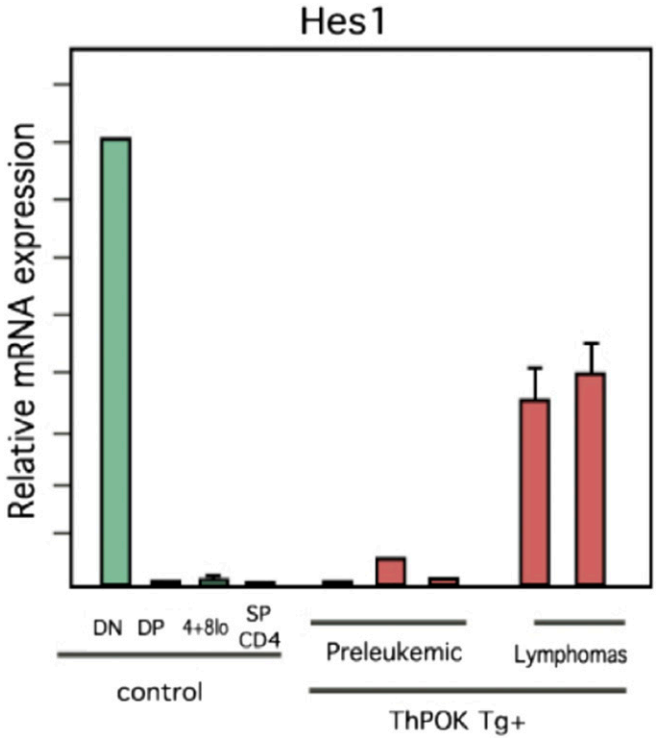


Fig. S3. Preleukemic ThPOK^{const} thymocytes do not show induction of Notch target gene Hes1. RT-PCR analysis of Hes1 mRNA expression in total thymocytes from different 2- to 3-mo-old ThPOK^{const} mice, typed as either "preleukemic" or "lymphoma-bearing," depending on relative size and subset distribution in the thymus. Data are shown for two representative lymphoma-bearing and three preleukemic mice, as well as sorted thymocyte subsets from a WT control mouse (green columns).

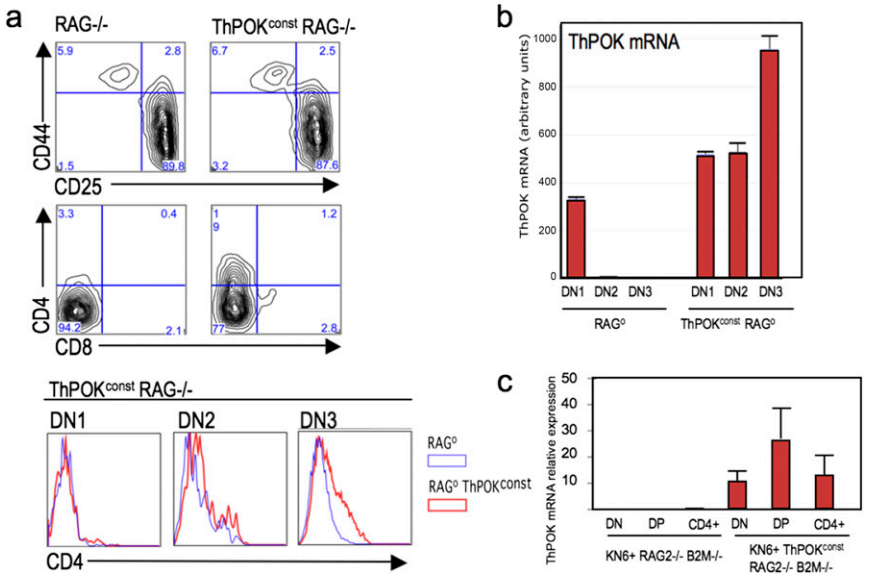


Fig. S4. ThPOK^{const} transgene affects gene expression from DN2 stage onwards. (*A*) FACS analysis of gated TCRβ^{-} DN (CD4^{-}CD8^{-}) thymocyte subsets from ThPOK^{const} Rag2$^{-/-}$ mice, compared with Rag2$^{-/-}$ mice, showing expression of CD4, CD8, CD25, and CD44 (*Top* two rows). FACS analysis of CD4 expression by gated DN1, DN2, and DN3 subsets from ThPOK^{const} Rag2$^{-/-}$ mice and Rag2$^{-/-}$ mice, as indicated. Note induction of CD4 at DN3 stage. (*B*) RT-PCR analysis of ThPOK mRNA expression in sorted DN1, DN2, and DN3 subsets from ThPOK^{const} Rag2$^{-/-}$ mice and Rag2$^{-/-}$ mice, as indicated. (*C*) RT-PCR analysis of ThPOK mRNA expression in sorted DN, DP, and SP CD4 subsets from ThPOK^{const} KN6^{+} Rag2$^{-/-}$ B2m$^{-/-}$ mice and KN6^{+} Rag2$^{-/-}$ B2m$^{-/-}$ mice, as indicated.

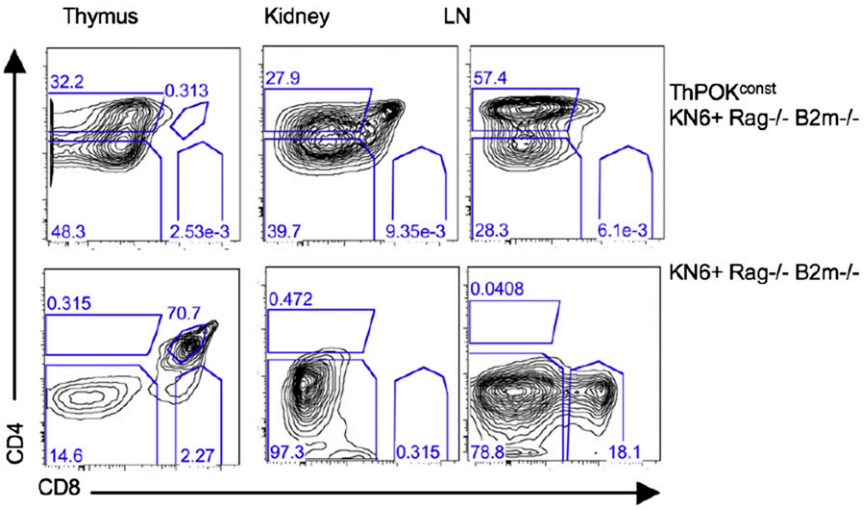
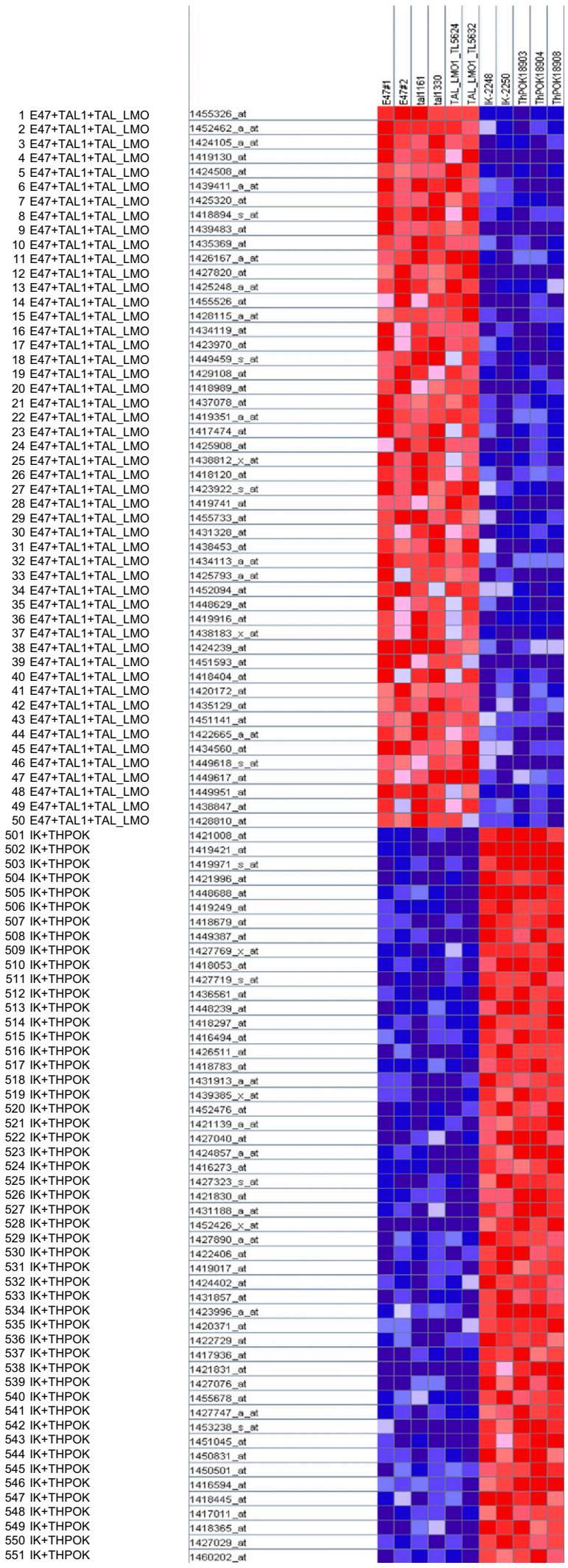
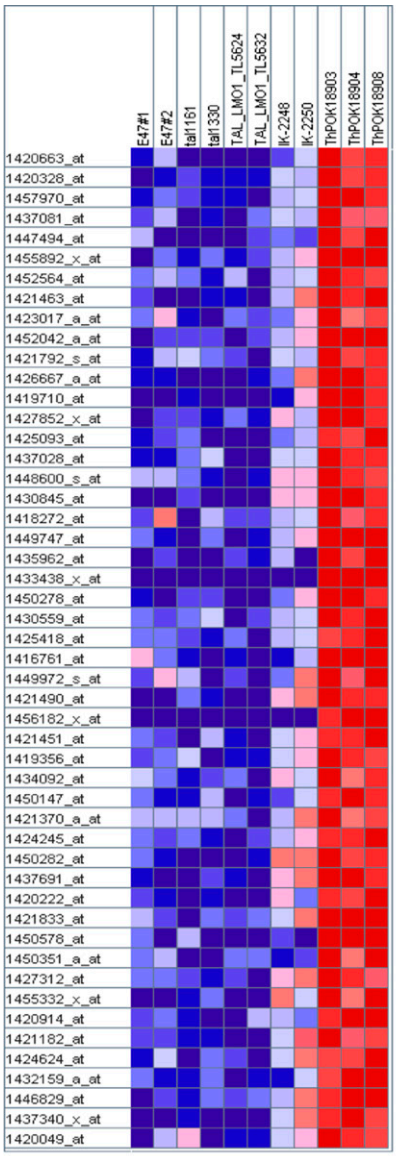


Fig. S5. γδTCR promotes ThPOK-mediated lymphomagenesis in the absence of strong ligand engagement. FACS analysis of thymus, kidney, and lymph nodes from 4-mo-old KN6^{+} B2m$^{-/-}$ Rag$^{-/-}$ mice with or without ThPOK^{const} transgene. Note presence of SP CD4^{lo} and CD4^{hi} tumor cells in kidney and lymph nodes of ThPOK^{const} transgenic mouse. SP CD8 cells in lymph node of control KN6^{+} Rag$^{-/-}$ B2m$^{-/-}$ mice represent normal γδTCR^{+} subset.



1	E47+TAL1+TAL_LMO	1455326_at	RIKEN cDNA 4932416N17 gene
2	E47+TAL1+TAL_LMO	1452462_a_at	Btg3 associated nuclear protein
3	E47+TAL1+TAL_LMO	1424105_a_at	pituitary tumor-transforming 1
4	E47+TAL1+TAL_LMO	1419130_at	deaminase domain containing 1
5	E47+TAL1+TAL_LMO	1424508_at	tetratricopeptide repeat domain 5
6	E47+TAL1+TAL_LMO	1439411_a_at	exportin 7
7	E47+TAL1+TAL_LMO	1425320_at	RIKEN cDNA A830023I12 gene
8	E47+TAL1+TAL_LMO	1418894_s_at	pre B-cell leukemia transcription factor 2
9	E47+TAL1+TAL_LMO	1439483_at	expressed sequence AI506816
10	E47+TAL1+TAL_LMO	1435369_at	expressed sequence C78212
11	E47+TAL1+TAL_LMO	1426167_a_at	calcium/calmodulin-dependent protein kinase IV
12	E47+TAL1+TAL_LMO	1427820_at	Mus musculus, clone IMAGE:3983821, mRNA, partial cds
13	E47+TAL1+TAL_LMO	1425248_a_at	TYRO3 protein tyrosine kinase 3
14	E47+TAL1+TAL_LMO	1455526_at	DIRAS family, GTP-binding RAS-like 1
15	E47+TAL1+TAL_LMO	1428115_a_at	RAB2B, member RAS oncogene family
16	E47+TAL1+TAL_LMO	1434119_at	DNA segment, Chr 2, Wayne State University 81, expressed
17	E47+TAL1+TAL_LMO	1423970_at	THO complex 3
18	E47+TAL1+TAL_LMO	1449459_s_at	ankyrin repeat and SOCS box-containing protein 13
19	E47+TAL1+TAL_LMO	1429108_at	ring finger protein 184
20	E47+TAL1+TAL_LMO	1418989_at	cathepsin E
21	E47+TAL1+TAL_LMO	1437078_at	vacuolar protein sorting 52 (yeast)
22	E47+TAL1+TAL_LMO	1419351_a_at	RIKEN cDNA 0610007P06 gene
23	E47+TAL1+TAL_LMO	1417474_at	RIKEN cDNA 1500035H01 gene
24	E47+TAL1+TAL_LMO	1425908_at	gb:BC003294.1 /DB_XREF=gi:13097008 /FEA=FLmRNA /CNT=2 /TID=
25	E47+TAL1+TAL_LMO	1438812_x_at	ubiquitin specific protease 19
26	E47+TAL1+TAL_LMO	1418120_at	RNA binding motif protein 8a
27	E47+TAL1+TAL_LMO	1423922_s_at	expressed sequence C77668
28	E47+TAL1+TAL_LMO	1419741_at	suppressor of Ty 16 homolog (S. cerevisiae)
29	E47+TAL1+TAL_LMO	1455733_at	RIKEN cDNA A430105I05 gene
30	E47+TAL1+TAL_LMO	1431328_at	protein phosphatase 1, catalytic subunit, beta isoform
31	E47+TAL1+TAL_LMO	1438453_at	Rad51 homolog c (S. cerevisiae)
32	E47+TAL1+TAL_LMO	1434113_a_at	XPMC2 prevents mitotic catastrophe 2 homolog (Xenopus laevis)
33	E47+TAL1+TAL_LMO	1425793_a_at	RAR-related orphan receptor gamma
34	E47+TAL1+TAL_LMO	1452094_at	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxyla
35	E47+TAL1+TAL_LMO	1448629_at	Hermansky-Pudlak syndrome 4 homolog (human)
36	E47+TAL1+TAL_LMO	1419916_at	Ring finger protein 20
37	E47+TAL1+TAL_LMO	1438183_x_at	sorbitol dehydrogenase 1
38	E47+TAL1+TAL_LMO	1424239_at	RIKEN cDNA 2310066E14 gene
39	E47+TAL1+TAL_LMO	1451593_at	Histocompatibility 2, D region locus 1
40	E47+TAL1+TAL_LMO	1418404_at	RAD9 homolog (S. pombe)
41	E47+TAL1+TAL_LMO	1420172_at	Myosin, heavy polypeptide 9, non-muscle
42	E47+TAL1+TAL_LMO	1435129_at	Protein tyrosine phosphatase 4a2
43	E47+TAL1+TAL_LMO	1451141_at	cDNA sequence BC004636
44	E47+TAL1+TAL_LMO	1422665_a_at	protein-L-isoaspartate (D-aspartate) O-methyltransferase 1
45	E47+TAL1+TAL_LMO	1434560_at	WD and tetratricopeptide repeats 1
46	E47+TAL1+TAL_LMO	1449618_s_at	RIKEN cDNA 2900092E17 gene
47	E47+TAL1+TAL_LMO	1449617_at	RIKEN cDNA 2900092E17 gene
48	E47+TAL1+TAL_LMO	1449951_at	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib
49	E47+TAL1+TAL_LMO	1438847_at	Max dimerization protein 3
50	E47+TAL1+TAL_LMO	1428810_at	RIKEN cDNA 2700097O09 gene
501	IK+THPOK	1421008_at	radical S-adenosyl methionine domain containing 2
502	IK+THPOK	1419421_at	ankyrin 1, erythroid
503	IK+THPOK	1419971_s_at	gb:C86506 /DB_XREF=gi:2918463 /DB_XREF=C86506 /CLONE=J022
504	IK+THPOK	1421996_at	transcription factor AP-2, alpha
505	IK+THPOK	1448688_at	podocalyxin-like
506	IK+THPOK	1419249_at	PFTAIRE protein kinase 1
507	IK+THPOK	1418679_at	granzyme F
508	IK+THPOK	1449387_at	RIKEN cDNA 2310015J09 gene
509	IK+THPOK	1427769_x_at	myosin, light polypeptide 3
510	IK+THPOK	1418053_at	synuclein, beta
511	IK+THPOK	1427719_s_at	keratin complex 2, basic, pseudogene 1 /// keratin complex 2, basic, ge
512	IK+THPOK	1436561_at	suppressor of variegation 3-9 homolog 2 (Drosophila)
513	IK+THPOK	1448239_at	heme oxygenase (decycling) 1
514	IK+THPOK	1418297_at	dihydropyrimidinase-like 4
515	IK+THPOK	1416494_at	NADH dehydrogenase (ubiquinone) Fe-S protein 5
516	IK+THPOK	1426511_at	sushi domain containing 2
517	IK+THPOK	1418783_at	transient receptor potential cation channel, subfamily M, member 5
518	IK+THPOK	1431913_a_at	phosphodiesterase 3A, cGMP inhibited
519	IK+THPOK	1439385_x_at	Solute carrier family 13 (sodium-dependent dicarboxylate transporter),
520	IK+THPOK	1452476_at	calcium channel, voltage-dependent, beta 2 subunit
521	IK+THPOK	1421139_a_at	zinc finger protein 386 (Kruppel-like)
522	IK+THPOK	1427040_at	MyoD family inhibitor domain containing
523	IK+THPOK	1424857_a_at	tripartite motif protein 34
524	IK+THPOK	1416273_at	tumor necrosis factor, alpha-induced protein 2
525	IK+THPOK	1427323_s_at	DNA segment, Chr 11, ERATO Doi 498, expressed
526	IK+THPOK	1421830_at	adenylate kinase 3 alpha-like 1
527	IK+THPOK	1431188_a_at	target of myb1 homolog (chicken)
528	IK+THPOK	1452426_x_at	gb:BC004065.1 /DB_XREF=gi:13278542 /FEA=mRNA /CNT=80 /TID=
529	IK+THPOK	1427890_a_at	RIKEN cDNA 5730427C23 gene
530	IK+THPOK	1422406_at	interferon alpha family, gene 9
531	IK+THPOK	1419017_at	corin
532	IK+THPOK	1424402_at	DNA segment, Chr 5, Brigham & Women's Genetics 0860 expressed
533	IK+THPOK	1431857_at	PHD finger protein 19
534	IK+THPOK	1423996_a_at	interleukin 4 receptor, alpha
535	IK+THPOK	1420371_at	syntrophin, basic 2
536	IK+THPOK	1422729_at	protocadherin beta 10
537	IK+THPOK	1417936_at	gb:NM_011338.1 /DB_XREF=gi:6755433 /GEN=Scya9 /FEA=FLmRNA
538	IK+THPOK	1421831_at	gb:NM_009647.1 /DB_XREF=gi:6753021 /GEN=Ak4 /FEA=FLmRNA /(
539	IK+THPOK	1427076_at	macrophage expressed gene 1
540	IK+THPOK	1455678_at	sema domain, immunoglobulin domain (Ig), transmembrane domain (TI
541	IK+THPOK	1427747_a_at	lipocalin 2
542	IK+THPOK	1453238_s_at	RIKEN cDNA 1200016E24 gene
543	IK+THPOK	1451045_at	synaptotagmin 13
544	IK+THPOK	1450831_at	POU domain, class 3, transcription factor 2
545	IK+THPOK	1450501_at	integrin alpha 2
546	IK+THPOK	1416594_at	secreted frizzled-related sequence protein 1
547	IK+THPOK	1418445_at	gb:NM_009197.1 /DB_XREF=gi:6677996 /GEN=Slc16a2 /FEA=FLmR
548	IK+THPOK	1417011_at	syndecan 2
549	IK+THPOK	1418365_at	cathepsin H
550	IK+THPOK	1427029_at	serine protease HTRA3
551	IK+THPOK	1460202_at	myozenin 1

Fig. S6. ThPOK^{const} lymphomas share a robust gene expression profile with Ikaros plastic tumors. Oligonucleotide microarray gene expression comparison of ThPOK^{const} lymphomas with other mouse T-cell lymphomas. Unsupervised hierarchical clustering indicates closest similarity to Ikaros DN lymphomas. This analysis is the same as in Fig. 2*C*, but limited to the 100 most robust gene expression differences.



1420663_at **T helper-inducing POZ/Krueppel factor**
1420328_at RIKEN cDNA 2210417D09 gene
1457970_at ARP1 actin-related protein 1 homolog A (yeast)
1437081_at Tissue inhibitor of metalloproteinase 2
1447494_at DNA segment, Chr 7, Brigham & Women's Genetics 0826 expressed
1455892_x_at gb:BB794742 /DB_XREF=gi:16964361 /DB_XREF=BB794742
1452564_at oncofetal antigen
1421463_at SIGLEC-like 1
1423017_a_at interleukin 1 receptor antagonist
1452042_a_at RIKEN cDNA 5730537D05 gene
1421792_s_at triggering receptor expressed on myeloid cells 2
1426667_a_at unc-84 homolog A (C. elegans)
1419710_at neurexophilin 3
1427852_x_at Immunoglobulin heavy chain (J558 family)
1425093_at purinergic receptor P2X, ligand-gated ion channel, 3
1437028_at surfactant associated protein B
1448600_s_at vav 3 oncogene
1430845_at RIKEN cDNA 2410018L13 gene
1418272_at 3-oxoacid CoA transferase 2A
1449747_at DNA segment, Chr 5, Wayne State University 46, expressed
1435962_at ribosomal protein S6 /// similar to 40S ribosomal protein S6 (Phosphoprotein NP33)
1433438_x_at melanoma antigen
1450278_at tachykinin receptor 3
1430559_at RIKEN cDNA C330027I04 gene
1425418_at WAP four-disulfide core domain 5
1416761_at gb:BC014753.1 /DB_XREF=gi:15928555 /FEA=FLmRNA /CNT=88 /TID=Mm.5079.1
1449972_s_at zinc finger protein 97 /// cDNA sequence BC018101
1421490_at proline-rich protein MP5
1456182_x_at melanoma antigen
1421451_at crumbs homolog 1 (Drosophila)
1419356_at Kruppel-like factor 7 (ubiquitous)
1434092_at nitric oxide synthase 3 antisense
1450147_at gb:BI733611 /DB_XREF=gi:15710624 /DB_XREF=603352495F1 /CLONE=IMAGE:5360063
1421370_a_at interleukin 1 family, member 5 (delta)
1424245_at carboxylesterase 2
1450282_at fibroblast growth factor 4
1437691_at annexin A2
1420222_at gb:T25554 /DB_XREF=gi:562875 /DB_XREF=EST00587 /CLONE=B0001C09
1421833_at phosphatidylinositol-4-phosphate 5-kinase, type 1 alpha
1450578_at sex determining region of Chr Y
1450351_a_at restin (Reed-Steinberg cell-expressed intermediate filament-associated protein)
1427312_at Cardiomyopathy associated 5
1455332_x_at Fc receptor, IgG, low affinity IIb
1420914_at solute carrier organic anion transporter family, member 2a1
1421182_at C-type lectin domain family 1, member b
1424624_at RIKEN cDNA 2900011O08 gene
1432159_a_at testis expressed gene 13
1446829_at DNA segment, Chr 12, ERATO Doi 216, expressed
1437340_x_at gastrokine 1
1420049_at expressed sequence C78859

Fig. S7. Genes most highly induced in ThPOK^{const} lymphomas. Oligonucleotide microarray gene expression comparison of ThPOK^{const} lymphomas with other mouse T-cell lymphomas. Comparative expression levels of 50 genes that are most highly overexpressed in ThPOK^{const} lymphomas relative to a panel of other mouse T-cell lymphomas.