Pathway	Oncogene/Tumor Supressor	Type of Alteration	WT (n=12)	KrasLA1 (n=8)	p53+/-(n=4)	NIR p53 -/- (n=7)
Notch Signaling	5					
Notch1	Oncogene	Mutation	75.0%	62.5%	25.0%	28.6%
lkzf1	Tumor Supressor	CNVs	75.0%	62.5%	50.0%	28.6%
lkzf1	Tumor Supressor	Mutation	50.0%	37.5%	25.0%	0.0%
PI3K/AKT/mTO						
Akt1	Oncogene	Mutation	8.3%	12.5%	0.0%	0.0%
Pten	Tumor Supressor	CNVs	25.0%	0.0%	25.0%	42.9%
Pten	Tumor Supressor	Mutation	16.7%	0.0%	50.0%	14.3%
Mtor	Oncogene	CNVs	8.3%	0.0%	75.0%	28.6%
Mtor	Oncogene	Mutation	0.0%	0.0%	0.0%	14.3%
MEK/ERK Pathy	•					
Kras	Oncogene	Mutation	8.3%	100.0%	0.0%	0.0%
Flt3	Oncogene	CNVs	0.0%		25.0%	
Ptpn11	Oncogene	Mutation	8.3%		0.0%	
Cxcr4	Oncogene	Mutation	8.3%	0.0%	0.0%	0.0%
Ackr3	Oncogene	Mutation	0.0%		0.0%	0.0%
Epigenetic Mod	•					
Chd4	Oncogene	Mutation	8.3%	0.0%	0.0%	0.0%
Dnmt3a	Tumor Supressor	CNVs	0.0%		25.0%	
Esr1	Oncogene	Mutation	0.0%		0.0%	
Bcl11b	Tumor Supressor	CNVs	50.0%		75.0%	
Bcl11b	Tumor Supressor	Mutation	8.3%		0.0%	
Dicer1	Tumor Supressor	CNVs	66.7%		50.0%	
Ezh2	Oncogene	Mutation	8.3%		0.0%	
Kmt2c	Tumor Supressor	Mutation	0.0%		0.0%	0.0%
Hippo Pathway						
Nf2	Tumor Supressor	CNVs	50.0%	62.5%	50.0%	28.6%
Fat1	Tumor Supressor	Mutation	0.0%		0.0%	
Wnt Signaling						
Lrig3	Tumor Supressor	CNVs	25.0%	0.0%	25.0%	57.1%
Lrig3	Tumor Supressor	Mutation	8.3%		0.0%	
Cdh11	Tumor Supressor	CNVs	50.0%		0.0%	
Rspo3	Oncogene	CNVs	25.0%		50.0%	
Lrp1b	Tumor Supressor	Mutation	0.0%	12.5%	0.0%	
DNA Damage Re						
p53	Tumor Supressor	CNVs	8.3%	12.5%	100.0%	100.0%
p53	Tumor Supressor	Mutation	16.7%		0.0%	
Fancg	Tumor Supressor	CNVs	58.3%		100.0%	
RpI5	Tumor Supressor	Mutation	8.3%	0.0%	0.0%	
Хра	Tumor Supressor	Mutation	0.0%	0.0%	25.0%	0.0%
Others	•					
Ncoa4	Tumor Supressor	Mutation	0.0%	0.0%	0.0%	14.3%
Stil	Oncogene	Mutation	8.3%		0.0%	
Pold1	Tumor Supressor	CNVs	33.3%		75.0%	
Ptprb	Tumor Supressor	Mutation	8.3%		0.0%	
Ptprc	Tumor Supressor	Mutation	8.3%		0.0%	
Tdpoz5	Tumor Supressor	CNVs	16.7%		0.0%	71.4%
Tdpoz3	Tumor Supressor	Mutation	0.0%		0.0%	14.3%

Table S5. Summary of mutations and copy number variations in COSMIC genes among different cohorts of thymic lymphomas. Note: the frequency of Kras mutation and p53 mutation in Kras^{LA1} and p53 deficient mice, respectively, is defined as 100%.