

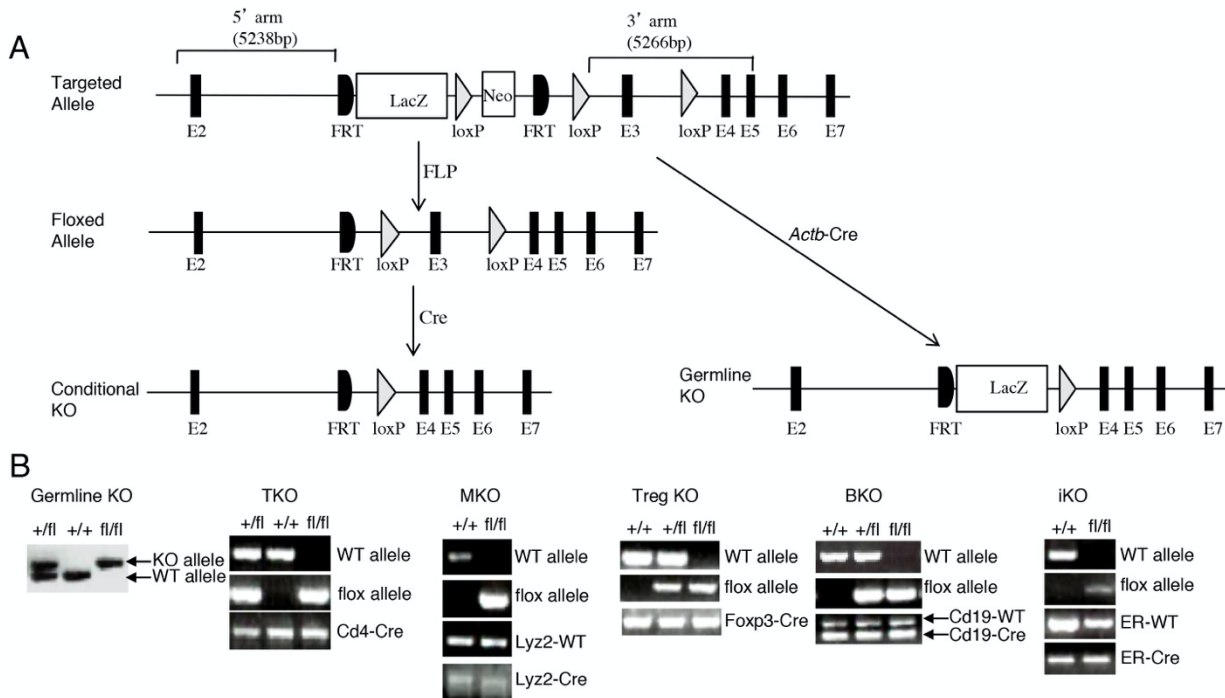
Peli1 regulates T cell metabolism and antitumor immunity by regulating mTORC1 activation

Chun-Jung Ko, Lingyun Zhang, Zuliang Jie, Lele Zhu, Xiaofei Zhou, Xiaoping Xie, Tianxiao Gao, Xuhong Cheng, and Shao-Cong Sun

Appendix

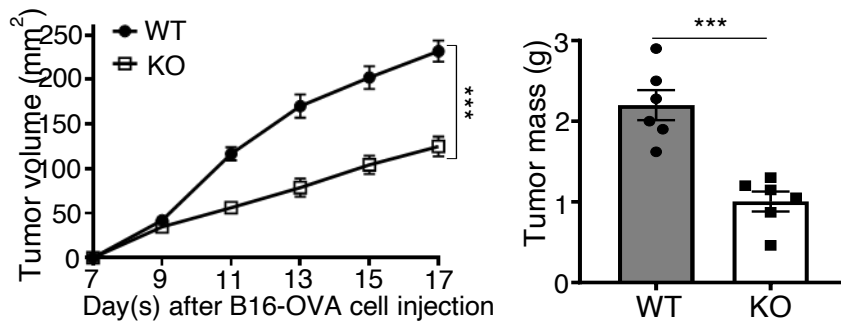
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Appendix Figures



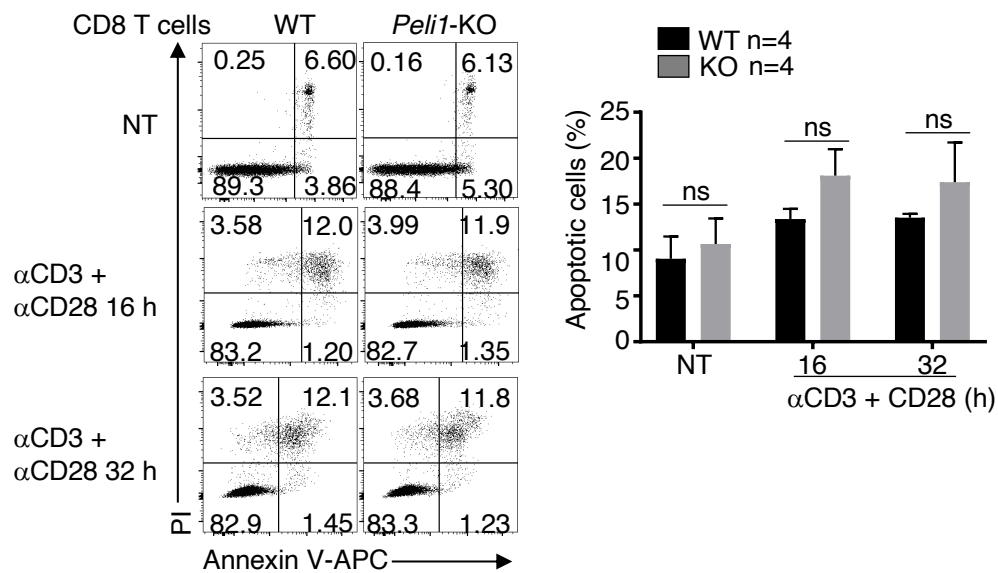
Appendix Figure S1. Generation of *Pelil* germline KO and conditional KO mice.

Schematic picture of *Pelil* gene targeting (A) and genotyping PCR analyses (B) of the generated mice. Mice carrying the *Pelil* targeted allele were crossed with FLP deleter (*Rosa26-FLPe*) mice to generate *Pelil-flox* mice, which were further crossed with *Cd4-Cre*, *Lyz2-Cre*, *Foxp3-Cre*, *Cd19-Cre*, and *CreER* mice to generate T cell-conditional KO (TKO), myeloid cell-conditional KO (MKO), Treg cell-conditional (Treg KO), B cell-conditional (BKO), and tomoxifen-inducible KO (iKO) mice, respectively. *Pelil* germline KO mice (obtained from KOMP) were created by crossing *Pelil*-targeted mice with *Actb-Cre* mice.



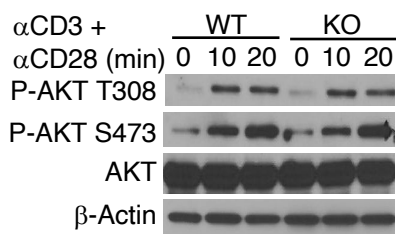
Appendix Figure S2. *Pel1* deficiency suppresses tumor growth.

Tumor growth curve (left) and summary of end-point tumor masses (right) of 6-8 week-old wildtype (WT) and *Pel1*-KO (KO) mice inoculated s.c. with B16-OVA tumor cells. Data are presented as mean±SEM with P values being determined by a two-way ANOVA analysis with Bonferroni correction (left panel) and two-tailed unpaired Student's t-test (right panel). ***P<0.001.



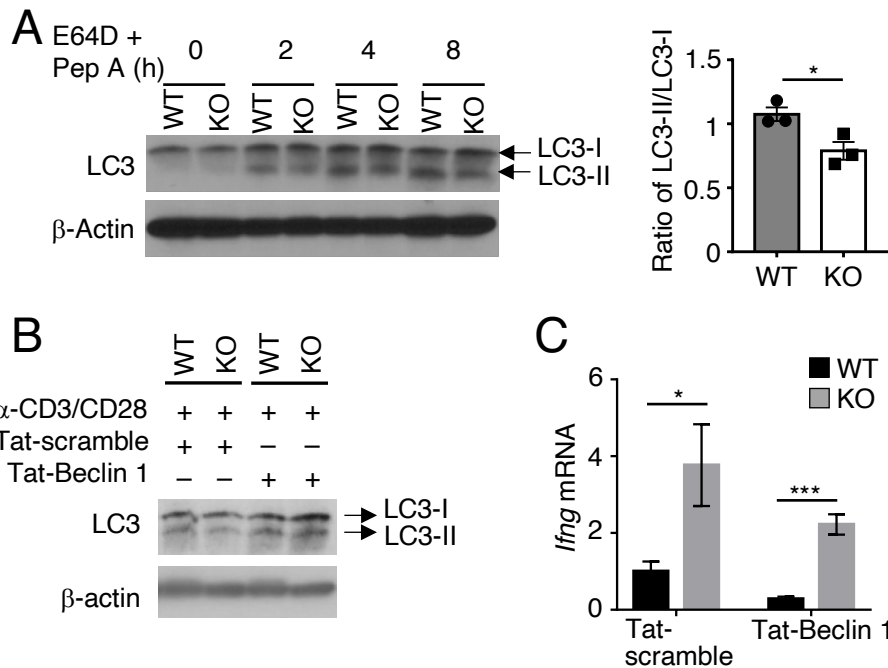
Appendix Figure S3. Effect of *Peli1* deficiency on apoptosis induction.

Flow cytometric analysis of apoptotic cells in wildtype (WT) or *Peli1*-KO (KO) CD8 T cells stimulated with anti-CD3 plus anti-CD28 for the indicated time points. Data are presented as representative FACS plot or summary graph based on 4 different pairs of mice. P values were determined by two-tailed unpaired Student's t-test. ns, not significant.



Appendix Figure S4. Dispensable role of Peli1 in AKT regulation.

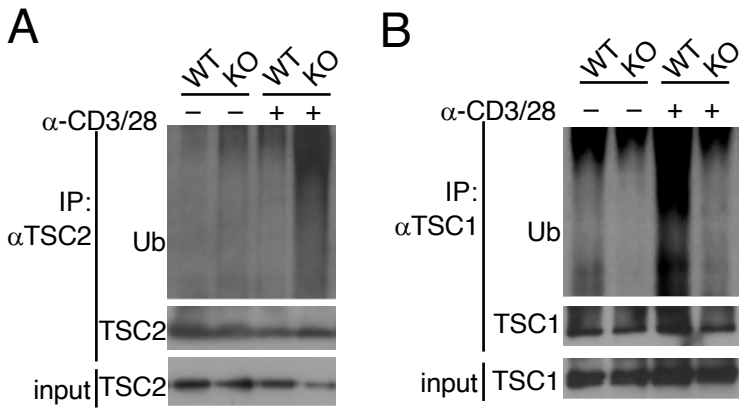
Immunoblot analysis of AKT phosphorylation at serine 473 (S473) and threonine 308 (T308), total AKT expression level, and loading control β -Actin expression level in whole-cell lysates of wildtype (WT) and Peli1-KO (KO) OT-I CD8 T cells, stimulated with anti-CD3 plus anti-CD28 for the indicated time points.



Appendix Figure S5. Autophagy is partially involved in the hyper-induction of IFN γ in Peli1-deficient CD8 T cells.

A. Immunoblot analysis of LC3 in wildtype (WT) and Peli1-KO (KO) CD8 T cells that were activated for 2 h with plate-bound anti-CD3 and anti-CD28 and then treated for the indicated time points with lysosomal protease inhibitors, E64D (10 μ g/ml) and pepstatin (10 μ g/ml). Data are presented as a representative plot (left panel) and a summary graph of LC3-II/LC3-I ratio based on the 8 h time point of E64D/PepA treatment.

B,C. Immunoblot analysis of LC3 (**b**) and qRT-PCR analysis of *Ifng* induction (**c**) in wildtype (WT) and Peli1-KO (KO) CD8 T cells that were activated for 2 h with anti-CD3 and anti-CD28 and then treated for additional 6 h with the autophagy-stimulating peptide Tat-Beclin 1 or the Tat-scrambled control peptide (Tat-scr). P values were determined by two-tailed unpaired Student's t-test. *P<0.05; ***P<0.001.



Appendix Figure S6. Ubiquitination of TSC2 and TSC1 in CD8 T cells.

TSC2 (A) and TSC1 (B) were immunoprecipitated from wildtype (WT) or Peli1-KO (KO) naïve CD8 T cells that were either untreated (-) or stimulated for 2h with anti-CD3 plus anti-CD28 (+) and subjected to immunoblotting using anti-ubiquitin (Ub) and anti-TSC2 or anti-TSC1. Cell lysates (input) were also subjected to immunoblotting using anti-TSC2 or anti-TSC1.

Appendix Tables

Appendix Table S1. Primers for mouse genotyping

Mice	Primer Sequence (5' to 3')	Amplicon
Peli1 KO		
WT allele	Forward GCTTCCTGGGTGTGTGATACATGC Reverse GGATCTGTCTGGCTATGTTTTGAACC	425 bp
KO allele	Forward GCTACCATTACCAGTTGGTCTGGTGTC Reverse AGAGAAATTCCAAGGCAAAATGAGG	560 bp
Peli1 flox		
WT allele	Forward TGAGTGTAGGGTTAATTGACGTAG Reverse AGTCCTAACTACCTGAATAGAGCAC	249 bp
Flox	Forward TGAGTGTAGGGTTAATTGACGTAG Reverse TGC GACTATAGAGATATCAACCAC	500 bp
Cd4-Cre	Forward CCCAACCAACAAGAGCTC Reverse CCCAGAAATGCCAGATTACG	600 bp
Lyz2-Cre		
WT allele	Forward CTTGGGCTGCCAGAATTTCTC Reverse TTACAGTCGGCCAGGCTGAC	350 bp
Cre allele	Forward CTTGGGCTGCCAGAATTTCTC Reverse CCCAGAAATGCCAGATTACG	700 bp
Cd19-Cre		
WT allele	Forward AGAGGGAGGCAATGTTGTGC Reverse GTCCAGGTCCTGACGTCTG	588 bp
Cre allele	Forward AGAGGGAGGCAATGTTGTGC Reverse GACGATGAAGCATGTTTAGCTGG	420 bp
Foxp3-Cre	Forward ACGTAAACGGCCACAAGTTCAGC Reverse GTCGCCGATGGGGGTGTTCT	509 bp
Rosa CreER		
WT allele	Forward AAAGTCGCTCTGAGTTGTTAT Reverse GGAGCGGGAGAAATGGATATG	650 bp
CreER allele	Forward AAAGTCGCTCTGAGTTGTTAT Reverse CCTGATCCTGGCAATTTTCG	825 bp

Appendix Table S2. Primers for human TSC1 site-directed mutagenesis

Mutation	Primers (5' to 3')
K30A	Forward ACAGCTGTCTTTGCAGAGAACCTCAAT Reverse ATTGAGGTTCTCTGCAAAGACAGCTGT
K632A	Forward TTAAAGAAAGCAGCAGGAAACACAGAG Reverse CTCTGTGTTTCCTGCTGCTTTCTTTAA

Appendix Table S3. Gene-specific primers for qRT-PCR analysis of mouse gene expression

Gene	Primers (5' to 3')	Amplicon
<i>Tsc1</i>	Forward ACTCTCCCTTCTACCGAGACA Reverse GAGGCTGCCGAATGAGTCTTC	61 bp
<i>Tsc2</i>	Forward TGCCGCAGCATCAGTGTATC Reverse TGCCAGGAGGAACTCTCCC	231 bp
<i>Hk2</i>	Forward GATCGCCGGATTGGAACAGA Reverse GGTCTAGCTGCTTAGCGTCC	97 bp
<i>Glut1</i>	Forward GCTGTGCTTATGGGCTTCTC Reverse CACATACATGGGCACAAAGC	114 bp
<i>Hif1a</i>	Forward AAGTGGCAACTGATGAGCAA Reverse GCGGAGAACGAGAAGAAAA	123 bp
<i>Myc</i>	Forward AAACGACAAGAGGGCGGACAC Reverse TGGTCACGCAGGGCAAAA	84 bp
<i>Pgk1</i>	Forward TGTCGCTTTCCAACAAGCTG Reverse GCTCCATTGTCCAAGCAGAAT	163 bp
<i>Eno1</i>	Forward TGCGTCCACTGGCATCTAC Reverse CAGAGCAGGCGCAATAGTTTTA	118 bp
<i>Pfkip</i>	Forward GAAACATGAGGCGTTCTGTGT Reverse CCCGGCACATTGTTGGAGA	66 bp
<i>Pkm</i>	Forward GCCGCCTGGACATTGACTC Reverse CCATGAGAGAAATTCAGCCGAG	145 bp
<i>Aldoa</i>	Forward GCGCCTTTAAATGTCCGGG Reverse TAGGGTCACCAGAACCTCGT	103 bp
<i>Pel1l</i>	Forward CGTGAAACCAGATCAGCTCAGC Reverse GAGCTGCATTGATCTCCTGTCTT	181 bp
<i>Ifng</i>	Forward CAGCAACAGCAAGGCGAAA Reverse CTGGACCTGTGGGTTGTTGAC	73 bp
<i>Actb</i>	Forward CGTGAAAAGATGACCCAGATCA Reverse CACAGCCTGGATGGCTACGT	72 bp