

SUPPLEMENTARY INFORMATION

Mitochondrial ubiquinol oxidation is necessary for tumor growth

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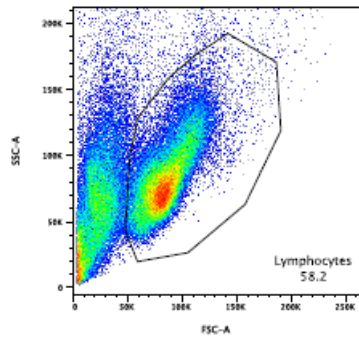
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Supplementary Figures 1–6 show source data for western blots.

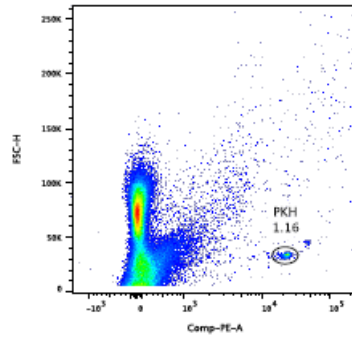
Supplementary Figure 7 shows the gating strategy for T-ALL experiments.

Supplementary Tables 1 shows the sequences of the sgRNAs used in this study.

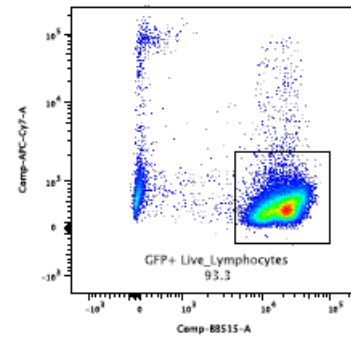
A. Count of Lymphocytes



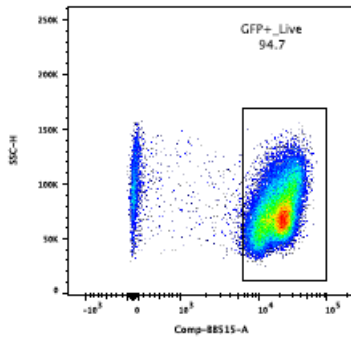
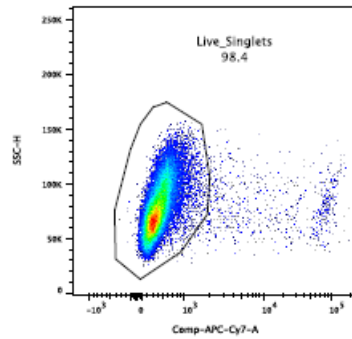
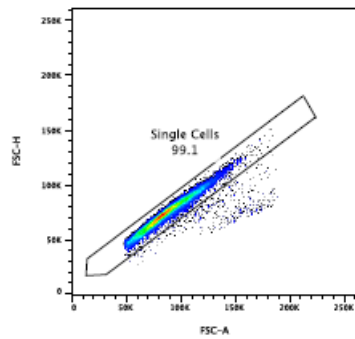
B. Count of PKH beads



C. % (GFP+ and live / Lymphocytes)



D. % (GFP+ / Live singlet)



Supplementary Figure 7. T-ALL Gating Strategy. Representative flow plots from the bone marrow cells of a QPC-WT recipient. To determine the number of GFP+ cells, the flow plots in the upper row of the figure were used. The number was calculated using the following equation: $(A / B) \times \text{PKH bead concentration (beads/ml)} \times \text{total volume of cell suspension (ml)} \times C$. To determine the percentage of GFP+ cells, the flow plots in the lower row of the figure were used. The percentage was calculated as D.

sgRNA ID	Strand	Sequence
Human-sgNDUFS_1	-	GGTCACTCACCATTCCAAGG
Human-sgNDUFS2_2	+	CTGCAGCCGGAGTAAGATGG
Human-sgSDHA_1	-	GCCCATCACCTCGACCACGG
Human-sgDHODH_1	-	ATAGAAACGCTCATCTCCCG
Human-sgDHODH_2	+	GCTGCAGGATTTGACAAGCA
Human- sgNon-targeting	NA	GTAGCGAACGTGTCCGGCGT
Mouse-sgQPC_1	-	GATCCCTACAGCGTTTGTAG
Mouse- sgNon-targeting	NA	GCGAGGTATTCGGCTCCGCG

Supplementary Table 1. sgRNA sequences.