Supplemental Figure Legends

Supplemental Figure 1, related to Figure 1. Primary T-ALL utilizes aerobic glycolysis that is required for cell survival.

A-D. Primary human T-ALL samples and naïve human CD4 T cells were compared for **(A)** expression of Glut1, **(B)** Hexokinase II and **(C)** Hexokinase I by intracellular flow cytometry and **(D)** extracellular acidification rate (ECAR). **E-F.** Primary human T-ALL samples were treated with vehicle or 2-deoxyglucose (2DG) and the percentage of viable cells that were T-ALL cells (CD4+CD8+) or CD4+ T cells was measured by propidium iodide exclusion flow cytometry. **G.** Naïve human CD4+ T cells were isolated from healthy independent donor blood and were treated with vehicle or 10 mM 2-deoxyglucose (2DG) and viability was measured over time by propidium iodide exclusion flow cytometry. Data are the mean and standard deviation of six independent samples (**A-C**), two independent experiments **(D),** are representative of the mean and standard deviation of technical triplicates of independent human T-ALL samples (**E-F**) or are representative of the mean and standard deviation of three independent experiments (**G**). (* $p<0.05$)

Supplemental Figure 2, related to Figure 1. Glycolysis supports disease progression in primary T-ALL.

A-G. Primary T-ALL was generated on a **(A)** $Glut1^{flox/flox}$;$Rosa26CreER^{T2}$ or **(B-G)** $HK2^{flox/flox}$;$Rosa26CreER^{T2}$ inducible deletion background and transplanted into sublethally irradiated recipient mice. Mice were treated with vehicle or

tamoxifen 10 days after transplant and **(A, B, D-G)** sacrificed 2 days after treatment completion or treated with tamoxifen to measure **(C)** overall survival in mice with $HK2^{flox/flox}$;$Rosa26CreER^{T2}$ T-ALL. T-ALL cells were isolated and the deletion efficiency of **(A)** Glut1 or **(B)** Hexokinase II was measured by immunoblot. **(D)** T-ALL burden was measured in the spleens of mice treated with vehicle or tamoxifen to delete HK2. **(E)** Pentose phosphate pathway activity was measured by production of $^{14}CO_2$ from 1-^{14}C-Glucose in T-ALL cells isolated from the spleens of mice treated with vehicle or tamoxifen to delete HK2. **F-G.** T-ALL cells were extracted from the spleens of mice treated with vehicle or tamoxifen to delete HK2 and analyzed using high-resolution LC-QE-MS for metabolomics analysis. Select analytes are shown. Data are representative of two independent experiments (**A-D**) or the mean and standard deviation of four independent samples (**E-G**). (* $p<0.05$)

Supplemental Figure 3, related to Figure 1. Cre activation alone does not alter T-ALL disease severity or metabolic traits *in vivo*.

Primary T-ALL was generated on a wild type (no floxed alleles);$Rosa26CreER^{T2}$ background and transplanted into sublethally irradiated recipient mice. Mice were treated with vehicle or tamoxifen for 4 consecutive days to induce Cre activity 4 days after T-ALL transplant and **(A)** survival was monitored. Other mice were treated with vehicle or tamoxifen 10 days after transplant, sacrificed 2 days after treatment completion **(B)** and the **(C)** cellularity of the spleen, **(D)** number of T-ALL cells in the spleen and **(E)** percentage of T-ALL cells in the

spleen was assessed. T-ALL cells were isolated and the **(E)** pentose phosphate pathway activity was measured by production of $^{14}CO_2$ from 1-^{14}C-Glucose. Isolated cells were also assayed for **(F)** extracellular acidification rate and **(G)** oxygen consumption rate. Data are representative of two independent experiments with at least 5 mice per group **(A-E)**, two independent experiments with four samples per group **(F)** or two independent experiments with three samples per group **(G-H).** (ns. Not Significant)

Supplemental Figure 4, related to Figure 2. Primary T-ALL glycolytic metabolism is limited, with increased oxidative metabolism.
Naïve T cells, T cells that were activated *in vitro* for 24 or 48 hrs, and purified primary T-ALL cells mitotracker green and TMRE staining. Data is representative of at least 4 independent experiments and are shown as the mean and standard deviation. (* $p<0.05$, ns. Not Significant)

Supplemental Figure 5, related to Figures 3-4. The PI3K pathway and c-Myc mediate oncogenic Notch induced metabolic changes. Murine lineage negative hematopoietic cells were isolated from the bone marrow of wild type **(A-D, F-G)** or Glut1^{myc} expressing **(E)** mice and retrovirally transduced with ICN1 or vector control. **(A)** Mitotracker green **(B)**, TMRE **(C)** and DCFDA staining were measured by flow cytometry. **D-F.** Cells were treated with vehicle, rapamycin (20 nM), LY29004 (10 μM), PP242 (1 μM) or JQ1 (1 μM) for 16 hrs and **(D)** cell size, **(E)** surface Glut1^{myc} expression and **(F)** hexokinase 2 expression were

measured by flow cytometry. **(G)** ICN1 and vector control transduced cell lysates were analyzed by immunoblot. Data are representative of at least three independent experiments. Data is shown as the mean and standard deviation. (* $p<0.05$, ns. Not Significant)

Supplemental Figure 6, related to Figure 6. AMPK regulates mitochondrial Complex I in T-ALL.

Primary T-ALL was generated on an AMPKα1 inducible deletion background and transplanted into sublethally irradiated recipient mice. Mice were treated with vehicle or tamoxifen 10 days after transplant and sacrificed 2 days after treatment completion. Purified T-ALL cells from vehicle and tamoxifen treated groups were isolated for **(A)** rtPCR examination of select mitochondrial energy pathway gene expression, **(B)** immunblot examination of select mitochondrial proteins and **(C)** colorimetric analysis of Complex I activity in cell lysate. Data represent an experiment with four independent T-ALL samples per group. (* $p<0.05$, ns. Not Significant)

Supplemental Figure 7, related to Figure 7. Loss of AMPK or pharmacological inhibition of mitochondrial Complex I inhibits T-ALL growth and progression.

A-C. Primary T-ALL was generated on an AMPKα1 inducible deletion background and transplanted into sublethally irradiated recipient mice. **A.** Mice were treated with vehicle or tamoxifen for 4 days beginning 10 days after

transplant and sacrificed 2 days after treatment completion. Ki67 expression was analyzed by flow cytometry. **B-C.** Mice were treated with vehicle or tamoxifen for 4 days beginning 10 days after transplant and sacrificed 7 days after treatment completion. **(B)** T-ALL cell burden and percentage present in the bone marrow and **(C)** Annexin V and propidium iodide staining were measured by flow cytometry. **D.** Published datasets were examined for AMPKα1 (PRKAA1) expression in primary human T-ALL compared with control cells (naïve T cells or whole bone marrow). **E.** Primary T-ALL was generated on a wild type background. T-ALL was isolated and was treated for 45 minutes with 100 μM phenformin or PBS vehicle and the oxygen consumption rate (OCR)/ extracellular acidification rate (ECAR) ratio was measured. **F.** Primary T-ALL was generated on a wild type background and transplanted into sublethally irradiated recipient mice. Mice were dosed daily with vehicle (PBS) or phenformin (100 mg/kg body weight) for 10 consecutive days starting two days after T-ALL transplant and survival was recorded. Data is representative of an experiment with seven mice per group **(A)** an experiment with eight mice per group **(B-C)** two independent experiments **(E)** and an experiment with at least seven mice per group. (* $p<0.05$)

Supplemental Table Legends

Supplemental Table 1, related to Figure 1: Primary HK2flox/flox;Rosa26CreER^{T2} T-ALL was transplanted into secondary recipient

mice. Mice were treated with vehicle or tamoxifen ten days after transplant and sacrificed five days after tamoxifen treatment. T-ALL cells were isolated and extracted for high resolution LC-QE-MS metabolomics. Range scaled area counts normalized using Metaboanalyst are reported.
Data are provided in separate Supplemental Data File in Excel format.

Supplemental Table 2, related to Figure 2: Naïve T cells, T cells that were activated on plate bound α-CD3 and α-CD28 for 24 or 48 hrs and primary T-ALL cells were isolated and extracted for high resolution LC-QE-MS metabolomics. Range scaled area counts normalized using Metaboanalyst are reported.
Data are provided in separate Supplemental Data File in Excel format.

Supplemental Table 3, related to Figure 2. Metabolic pathways altered in T-ALL cells relative to naïve T cells. Naïve T cells and primary TALL cells were isolated and extracted for high resolution LC-QE-MS metabolomics. Metabolites altered by 1.5-fold or more ($p<0.05$) were analyzed using Metaboanalyst Pathway Analysis and are listed below in respective pathways. Metabolites found to be significantly enriched in T-ALL cells compared to naïve T cells are indicated in red, while those significantly depleted in T-ALL cells compared to naïve T cells are indicated in green.

Supplemental Table 4, related to Figure 2. Metabolic pathways altered in T-

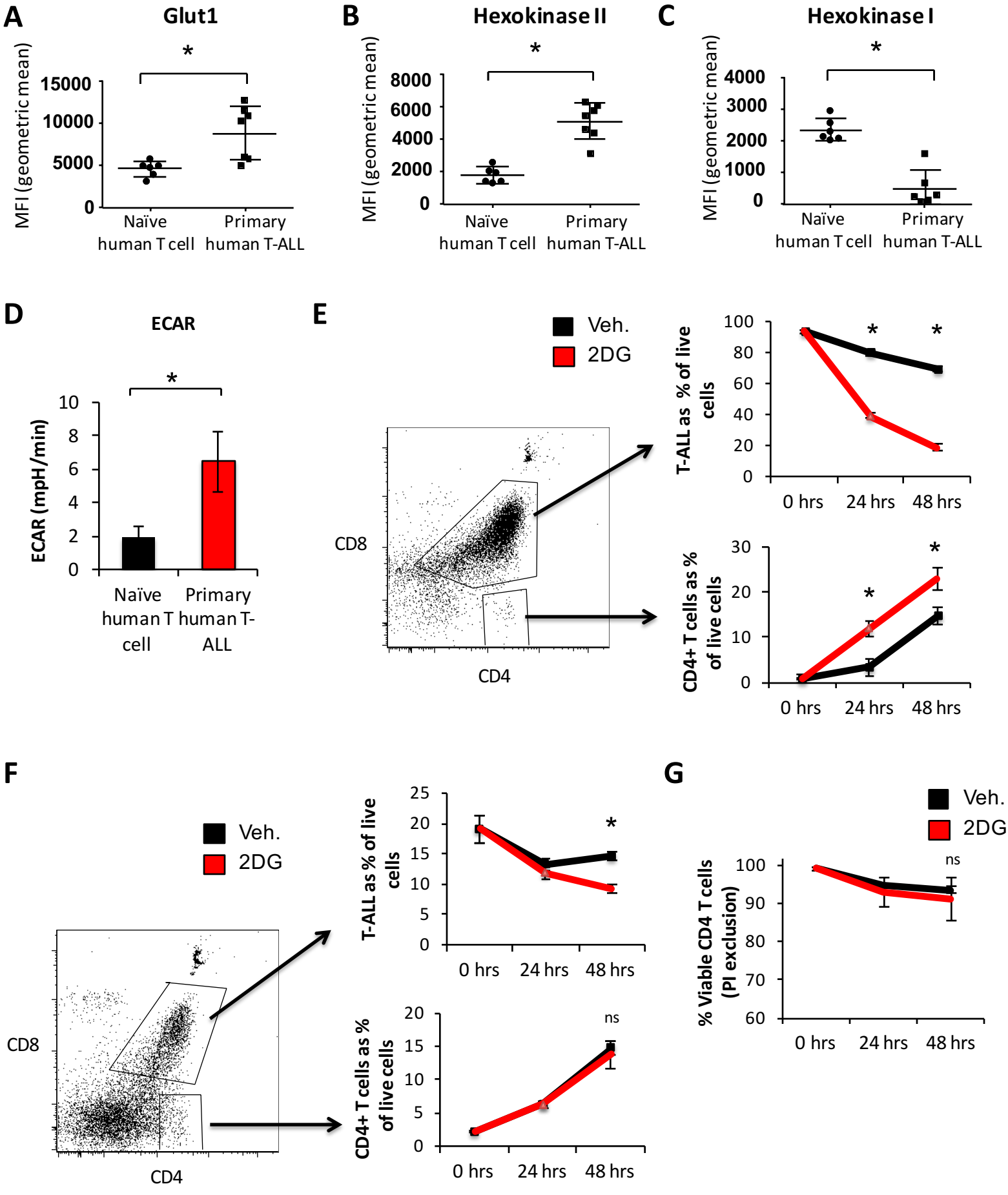
ALL cells relative to 48 hour activated T cells. T cells activated for 48 hours with anti-CD3 + anti-CD28 and primary TALL cells were isolated and extracted for high resolution LC-QE-MS metabolomics. Metabolites altered by 1.5-fold or more ($p<0.05$) were analyzed using Metaboanalyst Pathway Analysis and are listed below in respective pathways. Metabolites found to be significantly enriched in T-ALL cells compared to naïve T cells are indicated in red, while those significantly depleted in T-ALL cells compared to activated T cells are indicated in green.

Supplemental Table 5, related to Figure 5: Glucose metabolism qPCR Array Ct values for Figure 5D. Secondary recipient mice were transplanted with T-ALL from an AMPKα1$^{flox/flox}$;Rosa26CreER^{T2} background primary cancer and treated with vehicle or tamoxifen. T-ALL cell were isolated and metabolic gene expression was determined by qrt-PCR array. Ct values for each independent mouse are provided.

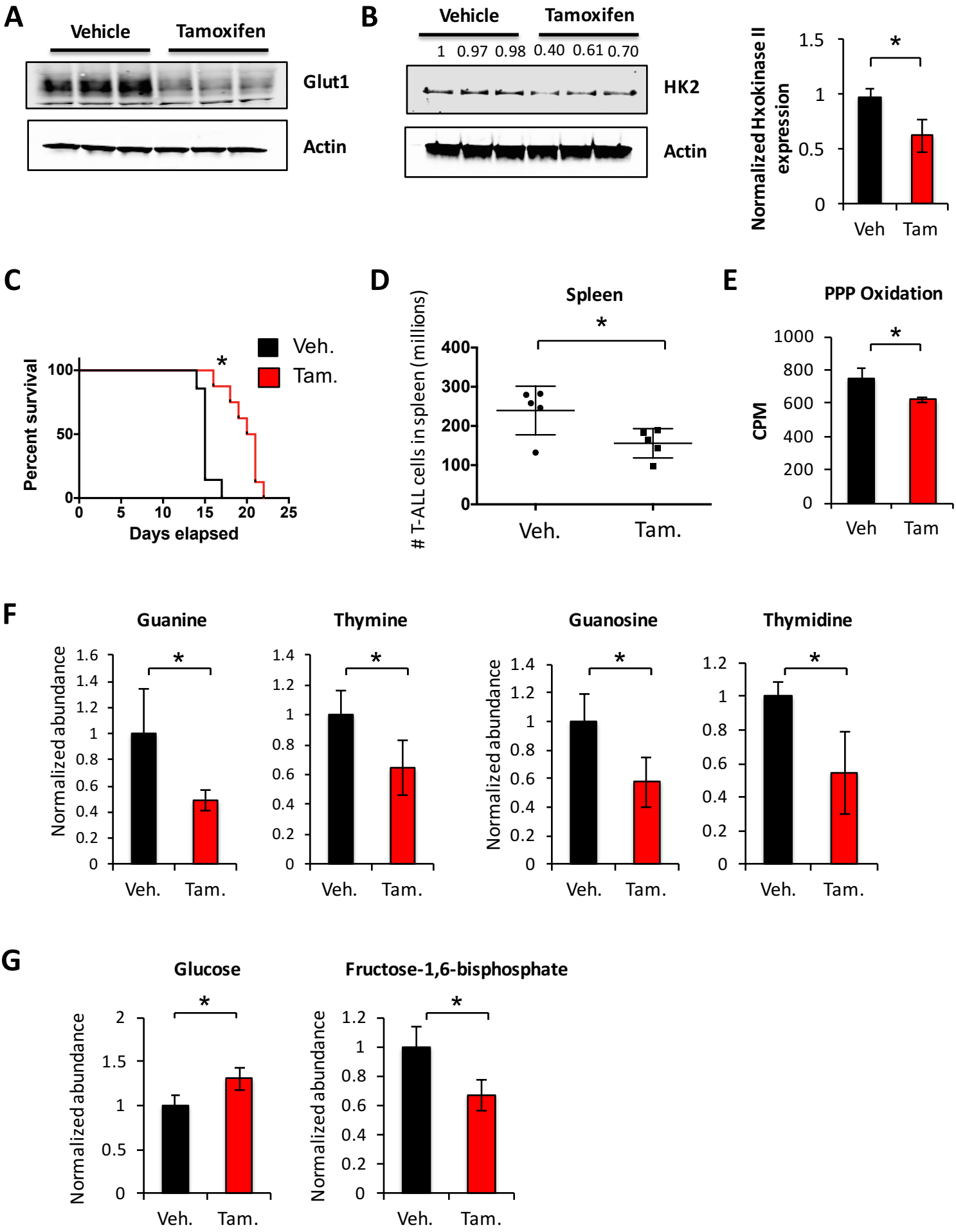
Supplemental Table 6, related to Figures 5-6: Primary AMPKα1$^{flox/flox}$;Rosa26CreER^{T2} T-ALL was transplanted into secondary recipient mice. Mice were treated with vehicle or tamoxifen ten days after transplant and sacrificed five days after tamoxifen treatment. T-ALL cells were isolated and extracted for high resolution LC-QE-MS metabolomics. Range scaled area counts normalized using Metaboanalyst are reported.

Data are provided in separate Supplemental Data File in Excel format.

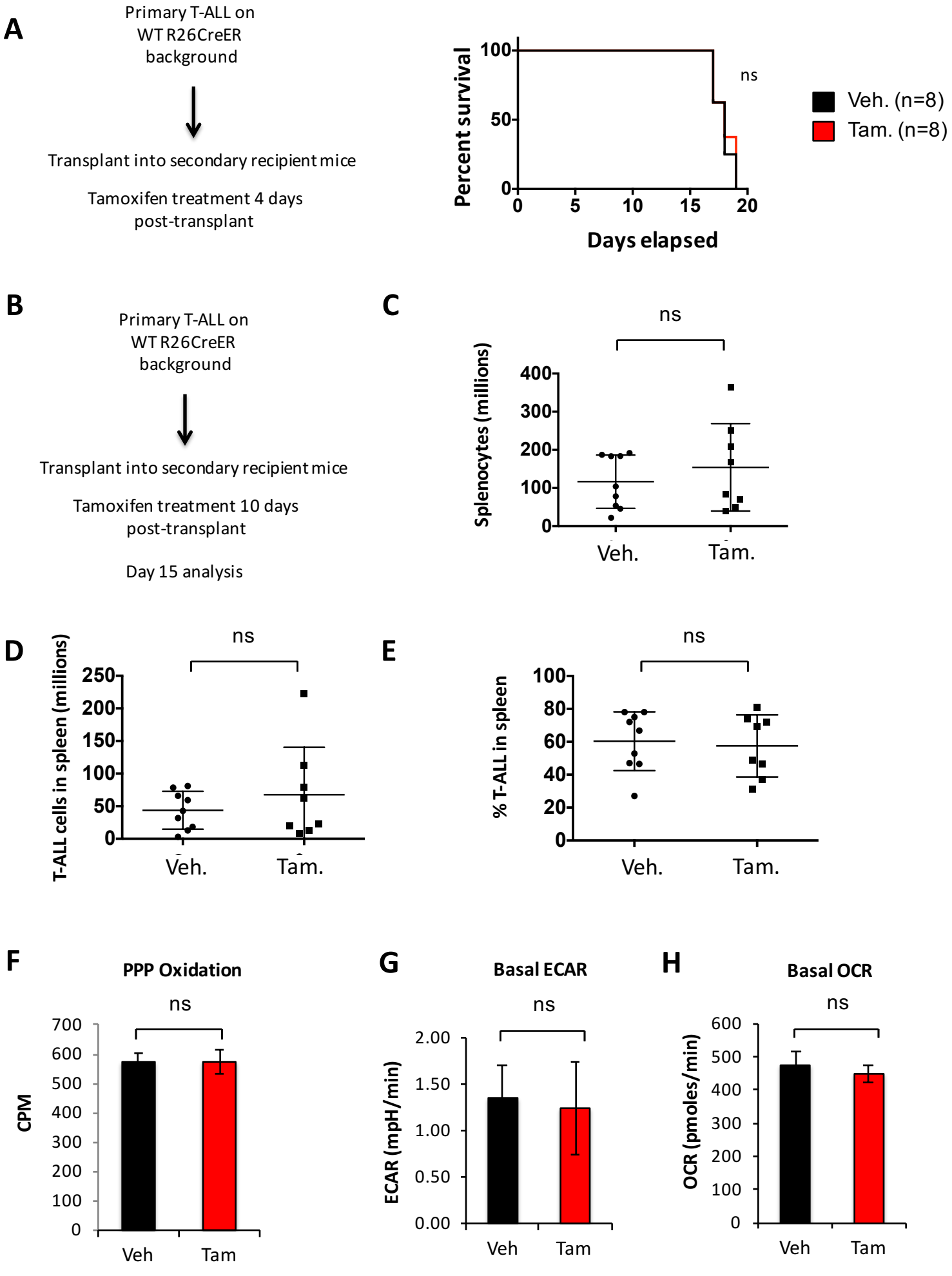
Supplemental Table 7, related to Figure 6: Mitochondrial energy metabolism qPCR Array Ct values for Figure 6F, S6A. Secondary recipient mice were transplanted with T-ALL from an AMPKα1$^{flox/flox}$;Rosa26CreER^{T2} background primary cancer and treated with vehicle or tamoxifen. T-ALL cell were isolated and metabolic gene expression was determined by qrt-PCR array. Ct values for each independent mouse are provided.


A
Glut1
MFI (geometric mean)
15000
10000
5000
0
*
Naïve human T cell
Primary human T-ALL
B
Hexokinase II
MFI (geometric mean)
8000
6000
4000
2000
0
*
Naïve human T cell
Primary human T-ALL
C
Hexokinase I
MFI (geometric mean)
4000
3000
2000
1000
0
*
Naïve human T cell
Primary human T-ALL
D
ECAR
ECAR (mpH/min)
10
8
6
4
2
0
*
Naïve human T cell
Primary human T-ALL
E
Veh.
2DG
CD8
CD4
T-ALL as % of live cells
100
80
60
40
20
0
*
*
0 hrs
24 hrs
48 hrs
CD4+ T cells as % of live cells
30
20
10
0
*
*
0 hrs
24 hrs
48 hrs
F
Veh.
2DG
CD8
CD4
T-ALL as % of live cells
25
20
15
10
5
0
*
0 hrs
24 hrs
48 hrs
CD4+ T cells as % of live cells
20
15
10
5
0
ns
0 hrs
24 hrs
48 hrs
G
Veh.
2DG
% Viable CD4 T cells (PI exclusion)
100
90
80
70
60
ns
0 hrs
24 hrs
48 hrs

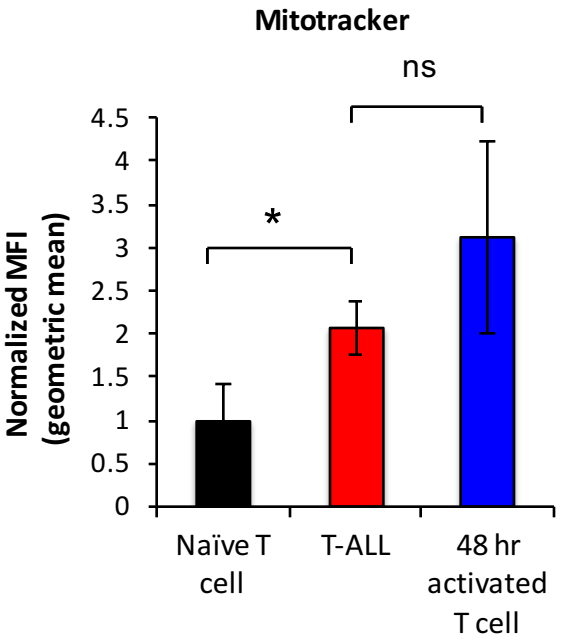
Sup. Figure 1

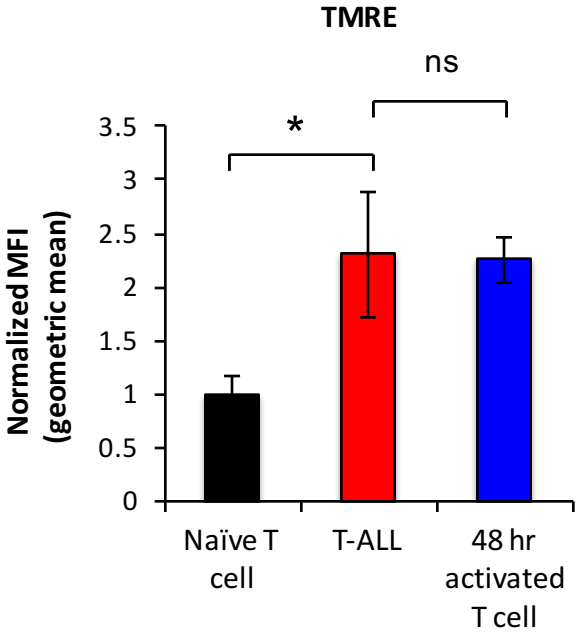

A
Vehicle
Tamoxifen
Glut1
Actin
B
Vehicle
Tamoxifen
1 0.97 0.98 0.40 0.61 0.70
HK2
Actin
Normalized Hxokinase II expression
1.5
1
0.5
0
*
Veh
Tam
C
Percent survival
100
50
0
0 5 10 15 20 25
Days elapsed
*
Veh.
Tam.
D
Spleen
T-ALL cells in spleen (millions)
400
300
200
100
0
*
Veh.
Tam.
E
PPP Oxidation
CPM
1000
800
600
400
200
0
*
Veh
Tam
F
Guanine
Thymine
Guanosine
Thymidine
Normalized abundance
Veh.
Tam.
G
Glucose
Fructose-1,6-bisphosphate
Normalized abundance
Veh.
Tam.

Sup. Figure 2

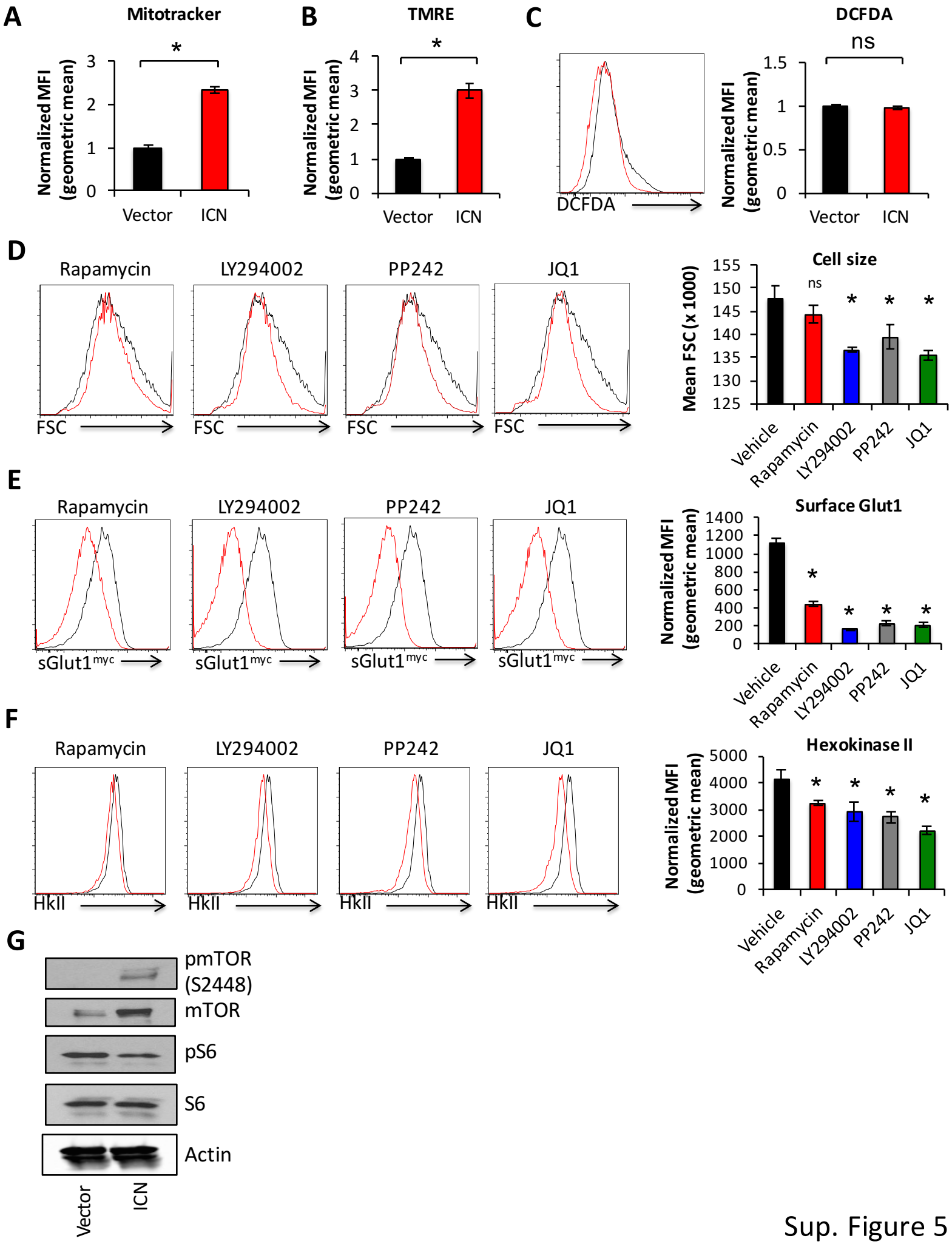

A
Primary T-ALL on WT R26CreER background
Transplant into secondary recipient mice
Tamoxifen treatment 4 days post-transplant
Percent survival
100
50
0
0
5
10
15
20
Days elapsed
ns
Veh. (n=8)
Tam. (n=8)
B
Primary T-ALL on WT R26CreER background
Transplant into secondary recipient mice
Tamoxifen treatment 10 days post-transplant
Day 15 analysis
C
ns
Splenocytes (millions)
400
300
200
100
0
Veh.
Tam.
D
ns
T-ALL cells in spleen (millions)
250
200
150
100
50
0
Veh.
Tam.
E
ns
% T-ALL in spleen
100
80
60
40
20
0
Veh.
Tam.
F
PPP Oxidation
ns
CPM
700
600
500
400
300
200
100
0
Veh
Tam
G
Basal ECAR
ns
ECAR (mpH/min)
2.00
1.50
1.00
0.50
0.00
Veh
Tam
H
Basal OCR
ns
OCR (pmoles/min)
600
500
400
300
200
100
0
Veh
Tam

Sup. Figure 3

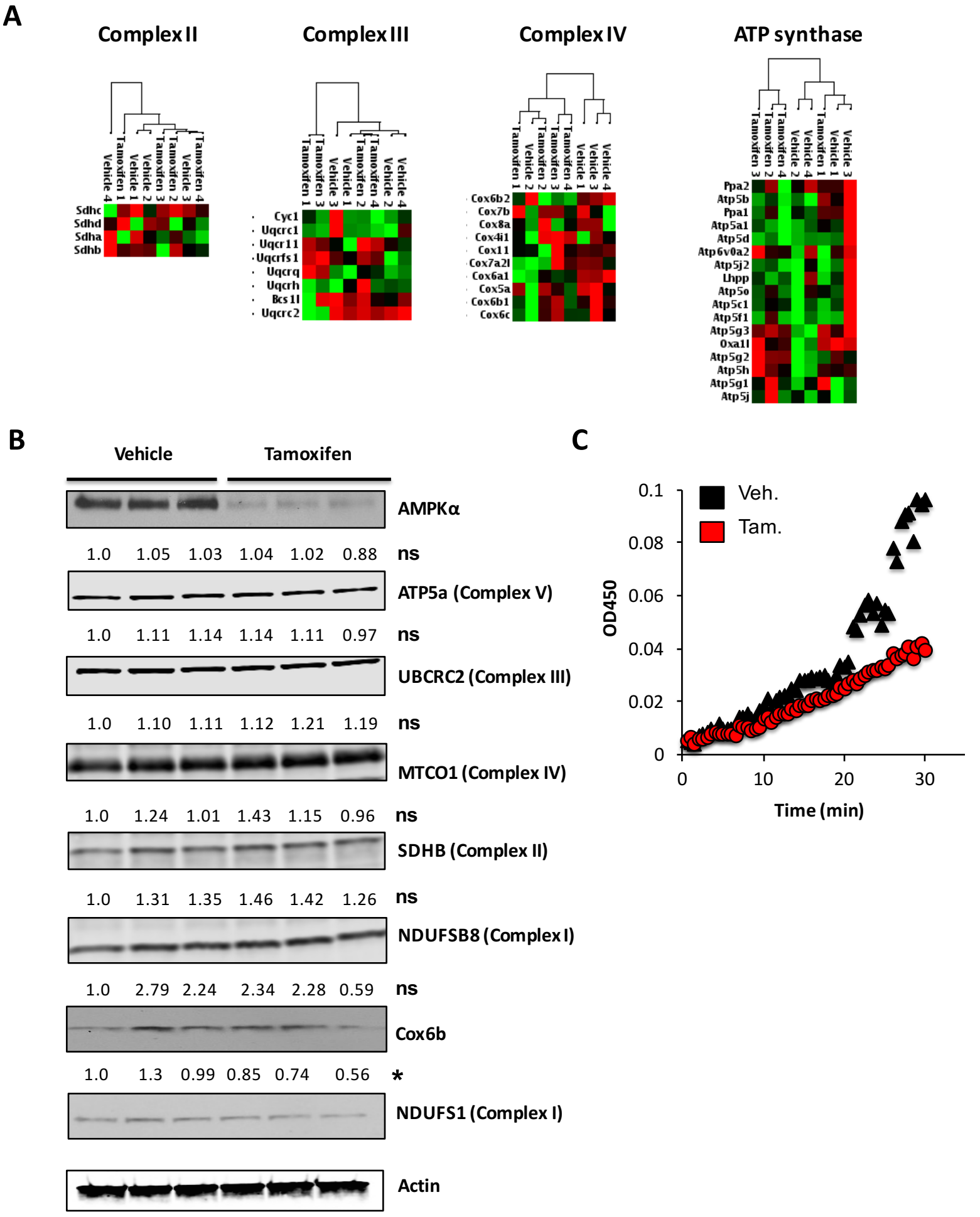

Mitotracker
ns
*
Normalized MFI (geometric mean)
4.5
4
3.5
3
2.5
2
1.5
1
0.5
0
Naïve T cell
T-ALL
48 hr activated T cell


TMRE
ns
*
Normalized MFI (geometric mean)
3.5
3
2.5
2
1.5
1
0.5
0
Naïve T cell
T-ALL
48 hr activated T cell

Sup. Figure 4

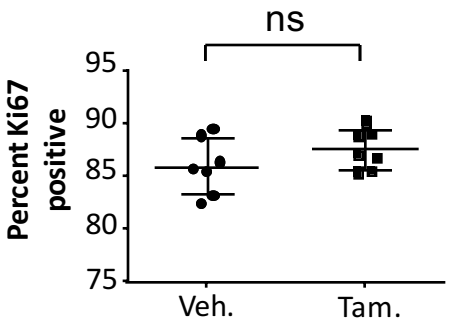

A
Mitotracker
Normalized MFI (geometric mean)
Vector
ICN
B
TMRE
C
DCFDA
ns
D
Rapamycin
LY294002
PP242
JQ1
FSC
Cell size
Mean FSC (x 1000)
Vehicle
E
sGlut1myc
Surface Glut1
F
HkII
Hexokinase II
G
pmTOR (S2448)
mTOR
pS6
S6
Actin

Sup. Figure 5


A
Complex II
Complex III
Complex IV
ATP synthase
Vehicle 4
Tamoxifen 1
Vehicle 1
Vehicle 2
Tamoxifen 3
Tamoxifen 2
Vehicle 3
Tamoxifen 4
Sdhc
Sdhd
Sdha
Sdhb
Tamoxifen 1
Tamoxifen 3
Vehicle 3
Vehicle 1
Tamoxifen 2
Tamoxifen 4
Vehicle 2
Vehicle 4
Cyc1
Uqcrc1
Uqcr11
Uqcrfs1
Uqcrq
Uqcrh
Bcs1l
Uqcrc2
Tamoxifen 1
Vehicle 2
Tamoxifen 2
Tamoxifen 3
Tamoxifen 4
Vehicle 1
Vehicle 3
Vehicle 4
Cox6b2
Cox7b
Cox8a
Cox4i1
Cox11
Cox7a2l
Cox6a1
Cox5a
Cox6b1
Cox6c
Tamoxifen 3
Tamoxifen 2
Tamoxifen 4
Vehicle 2
Vehicle 4
Tamoxifen 1
Vehicle 1
Vehicle 3
Ppa2
Atp5b
Ppa1
Atp5a1
Atp5d
Atp6v0a2
Atp5j2
Lhpp
Atp5o
Atp5c1
Atp5f1
Atp5g3
Oxa1l
Atp5g2
Atp5h
Atp5g1
Atp5j
B
Vehicle
Tamoxifen
AMPKα
1.0 1.05 1.03 1.04 1.02 0.88 ns
ATP5a (Complex V)
1.0 1.11 1.14 1.14 1.11 0.97 ns
UBCRC2 (Complex III)
1.0 1.10 1.11 1.12 1.21 1.19 ns
MTCO1 (Complex IV)
1.0 1.24 1.01 1.43 1.15 0.96 ns
SDHB (Complex II)
1.0 1.31 1.35 1.46 1.42 1.26 ns
NDUFSB8 (Complex I)
1.0 2.79 2.24 2.34 2.28 0.59 ns
Cox6b
1.0 1.3 0.99 0.85 0.74 0.56 *
NDUFS1 (Complex I)
Actin
C
Veh.
Tam.
OD450
0.1
0.08
0.06
0.04
0.02
0
0
10
20
30
Time (min)

Sup. Figure 6

A



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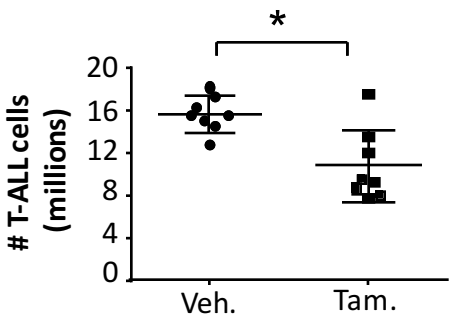
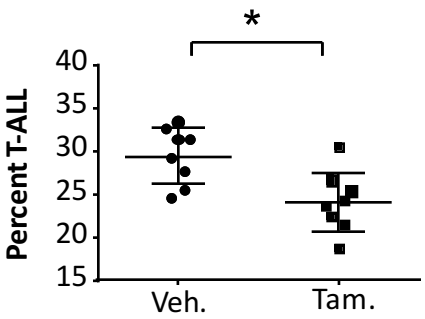
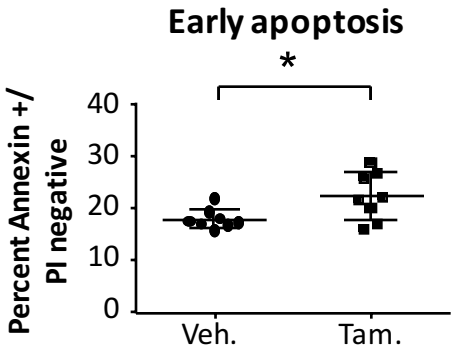
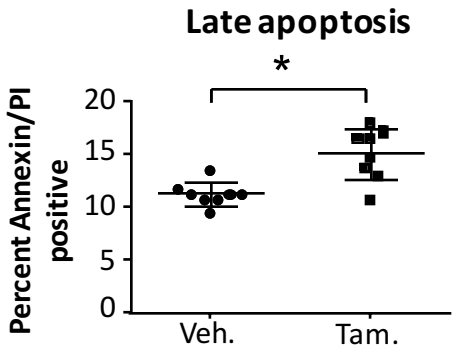
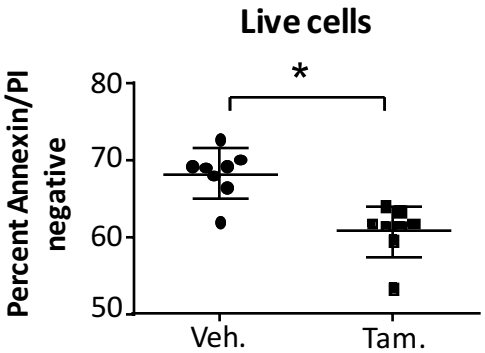




C



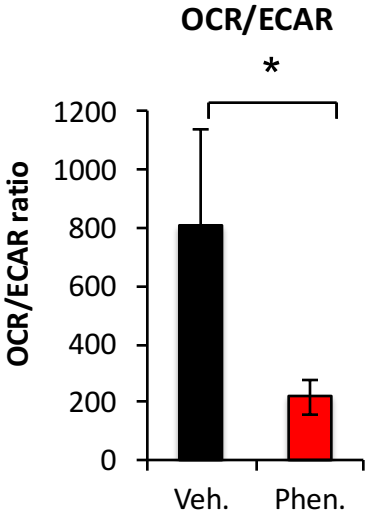




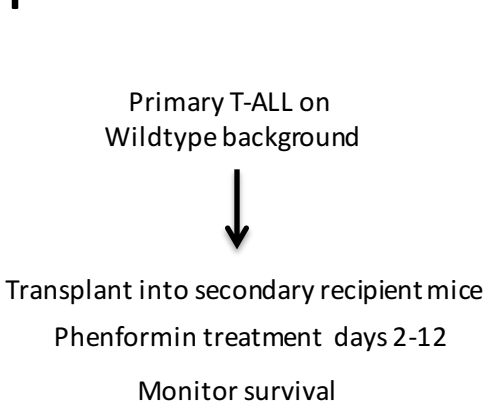
D

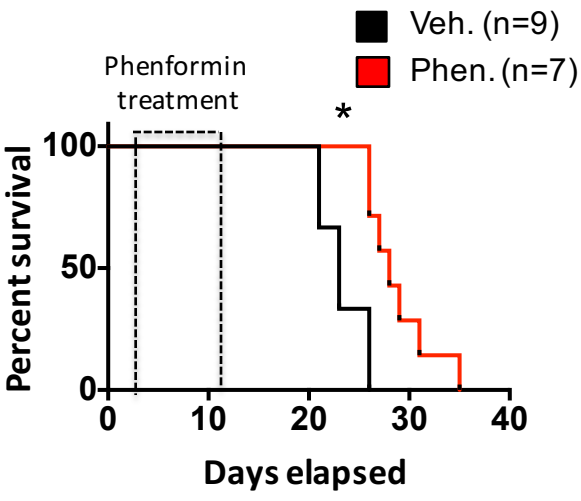
Study design	Control cells	Gene title	Control mean	T-ALL mean	Log FC	p value	Adj. p value	Reference	GEO Accession
RNAseq	T cells	PRKAA1	2727.551	3332.801	0.289	0.308	0.499	Sanghvi *et al* 2014	GSE63602
Microarray	Bone marrow	PRKAA1	7.6016	7.0166	0.585	0.069	0.210	Homminga *et al* 2011	GSE26713

E



F





Sup. Figure 7

Supplemental Table 3, related to Figure 2. Metabolic pathways altered in T-ALL cells relative to naïve T cells. Naïve T cells and primary TALL cells were isolated and extracted for high resolution LC-QE-MS metabolomics. Metabolites altered by 1.5-fold or more ($p<0.05$) were analyzed using Metaboanalyst Pathway Analysis and are listed below in respective pathways. Metabolites found to be significantly enriched in T-ALL cells compared to naïve T cells are indicated in red, while those significantly depleted in T-ALL cells compared to naïve T cells are indicated in green.

Citric acid cycle	Citric acid, Fumaric acid, L-Malic acid, oxalacetic acid, NAD, guanosine diphosphate, ADP, Coenzyme A, NADH, ATP, FAD
Glutathione metabolism	Glycine, Glutathione, Pyroglutamic acid, gamma-glutamylcysteine, oxidized glutathione
Pyrimidine metabolism	Cytidine triphosphate, cytidine, cytidine monophosphate, Uridine 5'monophosphate, uridine 5'-diphosphate, uracil, dCTP, dCMP, 5-thymidylic acid, CDP
Aspartate metabolism	Fumaric acid, oxalacetic acid, N-acetyl-L-aspartic acid, citrulline, D-Aspartic acid
Oxidation of branched chain amino acids	L-carnitine, L-acetylcarnitine, pristanic acid, propionyl carnitine, coenzyme A
Methionine metabolism	Betaine, glycine, L-serine, L-homoserine, S-adenosylhomocysteine, 5'-methylthioadenosine, S-adenosylmethionine
Urea cycle	Fumaric acid, L-alanine, ornithine, oxalacetic acid, citrulline, ADP
Glutamate metabolism	Glutathione, NAD, gamma-glutamylcysteine, 5-phosphoribosylamine, oxidized glutathione
Amino sugar metabolism	N-acetyl-D-glucosamine, N-

	acetylneuraminic acid, glucosamine
Glycerol phosphate shuttle	FAD, glyceric acid 1,3-biphosphate
Glycolysis	Phosphoenolpyruvate, ATP, Glycerate 1,3-bisphosphate

Supplemental Table 4, related to Figure 2. Metabolic pathways altered in T-ALL cells relative to 48 hour activated T cells. T cells activated for 48 hours with anti-CD3 + anti-CD28 and primary TALL cells were isolated and extracted for high resolution LC-QE-MS metabolomics. Metabolites altered by 1.5-fold or more ($p<0.05$) were analyzed using Metaboanalyst Pathway Analysis and are listed below in respective pathways. Metabolites found to be significantly enriched in T-ALL cells compared to naïve T cells are indicated in red, while those significantly depleted in T-ALL cells compared to activated T cells are indicated in green.

Oxidation of branched chain amino acids	L-carnitine, L-acetylcarnitine, propionyl carnitine, coenzyme A
Aspartate metabolism	L-aspartic acid, n-acetyl-L-aspartic acid, citrulline
Beta oxidation of very long chain fatty acids	L-carnitine, L-acetylcarnitine, coenzyme A
Gluco-neogenesis	D-glucose, oxoglutaric acid, oxalacetic acid, pyruvic acid, phosphoenolpyruvic acid, ATP, 3-phosphoglyceric acid, NAD, glyceraldehyde 3-phosphate, GDP, glyceric acid 1,3-bisphosphate, ADP, glucose 6-phosphate, dihydroxyacetone phosphate, NADH
Citric acid cycle	cis-aconitic acid, citric acid, fumaric acid, L-malic acid, oxoglutaric acid, oxalacetic acid, pyruvic acid, ATP, NAD, GDP, ADP, NADH
Glycolysis	D-glucose, pyruvic acid, phosphoenolpyruvic acid, ATP, 3-phosphoglyceric acid, NAD, glyceraldehyde 3-phosphate, glyceric acid 1,3-bisphosphate, ADP, glucose 6-phosphate, dihydroxacetone phosphate, NADH
Mitochondrial electron transport chain	Glycerol 3-phosphate, fumaric acid, ATP, NAD, glyceraldehyde 3-phosphate, glyceric acid 1,3-bisphosphate, ADP, dihydroxyacetone phosphate, NADH
Alanine metabolism	glyoxylic acid, L-alanine, oxoglutaric acid, oxalacetic acid, pyruvic acid
Ammonia recycling	glycine, L-histidine, L-serine, oxoglutaric acid, pyruvic acid, ATP, NAD, ADP, NADH
Glucose-alanine cycle	L-alanine, oxoglutaric acid, NADP, NADPH, pyruvic acid, NAD, NADH
Glutathione metabolism	cysteinylglycine, glycine, glutathione, NADP, NADPH, gamma-glutamylcysteine
Urea cycle	argininosuccinc acid, fumaric acid, L-alanine, oxoglutaric acid, oxalacetic acid, pyruvic acid, arginine, ATP, ADP
Glycerol phosphate shuttle	glycerol 3-phosphate, NAD, glyceraldehyde 3-phosphate, glyceric acid 1,3-bisphosphate, dihydroxyacetone phosphate
Methionine metabolism	glycine, L-serine, ATP, L-methionine, S-adenyosylhomocysteine, 5'-methylthioadenosine, S-adenosylmethionine, 2-oxo-4-methylthiobutanoic acid, methionine sulfoxide
Histidine metabolism	1-methylhistidine, carnosine, L-histidine, formiminoglutamic acid, methylimidazoleacetic acid

Pyrimidine metabolism	deoxycytidine, ureidopropionic acid, dihydrothymine, CTP, orotic acid, uridine triphosphate, Uridine 5'-diphosphate, uracil, ureidosuccinic acid, CDP, ureidoisobutyric aid
Malate-aspartate shuttle	oxoglutaric acid, oxalacetic acid, NAD, NADH
Nucleotide sugars metabolism	uridine diphosphate glucose, uridine diphophate glucuronic acid, UDP-D-xylose, glucose 6-phosphate

Supplemental Table 5, related to Figure 5: Glucose metabolism qPCR Array Ct values for Figure 5D. Secondary recipient mice were transplanted with T-ALL from an AMPKα1flox/flox;Rosa26CreERT2 background primary cancer and treated with vehicle or tamoxifen. T-ALL cell were isolated and metabolic gene expression was determined by qrt-PCR array. Ct values for each independent mouse are provided.

Symbol	Vehicle 1	Vehicle 2	Vehicle 3	Vehicle 4	Tamoxifen 1	Tamoxifen 2	Tamoxifen 3	Tamoxifen 4
Acly	23.37	23.22	23.54	23.24	23.71	24.04	23.6	23.36
Aco1	26.57	26.54	26.63	26.48	26.87	27.04	26.5	26.65
Aco2	24.03	24.01	24.05	24.16	24.18	24.6	24.19	24.28
Agl	28.61	28.62	28.54	28.39	28.4	28.95	28.22	28.47
Aldoa	22.04	21.89	21.57	21.89	22.2	22.88	22.16	22.29
Aldob	35	35	35	35	35	35	35	35
Aldoc	31.46	32.07	32.09	31.28	31.37	31.95	31.91	31.57
Bpgm	26.01	26.22	26.18	25.91	26.28	26.59	26.03	26.23
Cs	27.83	27.94	27.45	27.79	27.85	28.32	27.71	28.05
Dlat	26.06	25.74	26.05	25.63	26.05	26.27	26.21	26.09
Dld	24.19	23.84	23.62	23.68	24.22	24.58	23.79	24.04
Dlst	24.41	24.81	24.32	24.39	24.6	25.36	24.27	24.55
Eno1	21.35	21.23	21.16	21.31	21.34	21.63	21.42	21.57
Eno2	32.31	32.73	33.25	32.93	33.26	33.39	33.02	32.42
Eno3	29.2	29.18	29.35	29.03	29.52	29.66	28.97	29.2
Fbp1	35	34.52	34.32	30.42	32.2	31.31	33.06	33.57
Fbp2	34.84	35	35	34.74	35	35	35	35
Fh1	24.4	24.22	24.19	24.26	24.59	24.75	24.43	24.6
G6pc	35	35	35	35	35	35	35	35
G6pc3	26.55	26.71	26.55	26.88	27.06	27.28	26.67	26.82
G6pdx	24.57	24.56	24.31	24.45	24.97	25.3	24.4	24.63
Galm	28.65	28.26	28.66	27.93	28.57	28.49	28.45	28.24
Gapdhs	34.23	35	35	34.25	34.72	35	34.33	34.57
Gbe1	28.24	28.32	28.12	28.15	28.29	28.55	27.64	28.05
Gck	35	35	35	35	35	35	35	35
Gpi1	22.57	22.59	22.48	22.54	22.93	23.31	22.52	22.7
Gsk3a	23.75	23.85	24.06	23.74	24.05	24.2	24.01	24.02
Gsk3b	25.36	25.34	25.54	25.36	25.61	25.91	25.19	25.39
Gys1	27.63	27.78	28.09	27.69	28.09	28.13	27.87	28.27
Gys2	35	35	35	35	35	35	35	35
H6pd	28.08	28.09	28.12	28.07	28.57	28.51	27.72	28.16
Hk2	28.85	28.32	28.39	28.18	28.49	29.21	28.9	29.06
Hk3	30.32	30.64	31	30.61	30.91	31.03	29.58	30.03
Idh1	27.95	28.07	27.93	28.2	28.53	29.02	27.86	27.98
Idh2	24.89	24.95	25.09	24.85	25.23	25.34	24.95	24.91
Idh3a	23.33	23.07	23.04	23.17	23.46	23.75	23.48	23.55
Idh3b	23.85	23.68	23.57	23.79	23.67	24.11	23.64	23.99
Idh3g	23.1	23.23	23.19	23.59	23.38	23.67	23.14	23.28
Mdh1	23.34	23.13	23.27	23.52	23.39	23.77	23.52	23.55
Mdh1b	35	35	35	35	35	35	35	35
Mdh2	23.1	23.01	22.94	23.22	23.23	23.42	23.27	23.31

Ogdh	24.09	24.08	24.2	24.16	24.41	24.62	24.16	24.29
Pck1	33.23	33.42	31.16	32.55	32.07	31.44	31.47	32.15
Pck2	30.15	29.97	31.41	30.58	30.62	30.47	29.95	30
Pcx	30.52	30.94	31.44	30.54	31.24	31.52	31.19	31.41
Pdha1	23.16	23.35	22.92	23.22	23.3	23.59	23.11	23.5
Pdhb	24.29	24.36	24.25	24.36	24.49	24.78	24.39	24.53
Pdk1	25.61	25.51	25.34	25.67	25.59	26.08	25.59	25.55
Pdk2	34.33	34.17	35	34.21	34.46	34.86	33.84	34.25
Pdk3	25.51	25.37	25.6	25.61	25.67	25.99	25.67	25.89
Pdk4	35	35	35	35	33.92	35	34.49	35
Pdp2	26.56	26.84	27.02	26.76	27.19	27.28	26.87	27.04
Pdpr	26.52	26.53	26.58	26.71	26.81	27.08	26.39	26.93
Pfkl	25.85	25.46	25.34	25.61	25.81	26.3	25.78	26.32
Pgam2	28.75	28.77	28.78	28.7	28.85	29.14	28.43	28.86
Pgk1	22.7	22.46	22.28	22.83	22.82	23.23	22.8	23.01
Pgk2	35	35	35	35	35	35	35	35
Pgm1	25.83	25.87	26.08	26.12	26.27	26.32	25.87	26.07
Pgm2	27.43	27.39	27.3	27.19	27.47	27.96	27.29	27.39
Pgm3	27.19	27.13	27.28	27.3	27.64	27.82	27.05	27.43
Phka1	35	35	34.56	35	34.1	33.95	32.84	34.48
Phkb	27.43	27.46	27.88	27.4	27.73	27.78	27.53	27.78
Phkg1	32.82	33.79	33.58	33.49	34.91	33.98	34.29	35
Phkg2	25.83	25.97	25.96	25.96	26.23	26.4	25.7	25.71
Pklr	32.13	32.26	31.13	31.34	31.45	31.47	30.28	30.6
Prps1	24.31	24.06	24.12	24.56	24.45	24.87	24.34	24.54
Prps1l1	35	35	35	35	35	35	35	35
Prps2	23.29	23.35	23.46	23.45	23.49	23.92	23.55	23.52
Pygl	31.71	31.41	31.71	31.64	31.98	32.11	30.81	31.27
Pygm	30.09	30.47	30.33	30.36	31.01	30.95	29.62	29.83
Rbks	27.17	27.04	26.79	26.91	27.39	27.43	26.89	27.01
Rpe	24.68	24.5	24.8	24.93	24.91	25.21	24.74	25.05
Rpia	24.43	24.25	24.5	24.33	24.68	24.78	24.29	24.52
Sdha	23.43	23.34	23.37	23.45	23.74	24.01	23.44	23.73
Sdhb	24.5	24.36	24.35	24.5	24.57	24.83	24.61	24.6
Sdhc	24.06	23.94	24.11	24.14	24.34	24.5	24.26	24.23
Sdhd	27.63	27.49	27.54	27.55	28.04	28.21	27.71	27.83
Sucla2	25.25	25.29	25.29	25.4	25.56	25.87	25.41	25.63
Suclg1	27.72	27.38	26.62	27.22	27.72	27.99	27.9	27.8
Suclg2	24.96	24.82	24.66	25.12	25.09	25.4	25.05	25.18
Taldo1	25.16	25.08	26.53	24.97	25.27	25.44	26.65	25.22
Tkt	21.72	21.52	21.26	21.51	21.97	22.08	21.58	21.63
Tpi1	23.93	23.42	23.31	23.67	23.73	24.25	24.07	24.11
Ugp2	25.42	25.6	25.45	25.43	25.64	25.88	25.33	25.54
Actb	18.44	18.48	19.5	18.48	18.8	18.98	18.28	18.82
B2m	19.21	19.22	19.51	18.75	19.55	19.72	19.24	19.31
Gapdh	20.79	20.68	20.55	20.55	20.9	21.24	20.85	20.9
Gusb	25.59	25.59	25.62	25.92	25.91	26.05	25.75	25.99
Hsp90ab1	19.64	19.45	19.33	19.65	19.84	20.06	19.8	19.89

Supplemental Table 7, related to Figure 6: Mitochondrial energy metabolism qPCR Array Ct values for Figure 6F, S6A. Secondary recipient mice were transplanted with T-ALL from an AMPKα1flox/flox;Rosa26CreERT2 background primary cancer and treated with vehicle or tamoxifen. T-ALL cell were isolated and metabolic gene expression was determined by qrt-PCR array. Ct values for each independent mouse are provided.

Symbol	Vehicle 1	Vehicle 2	Vehicle 3	Vehicle 4	Tamoxifen 1	Tamoxifen 2	Tamoxifen 3	Tamoxifen 4
Atp12a	35	35	35	35	35	35	35	35
Atp4a	33.75	33.28	33.78	34.13	33.65	33.22	32.73	33.51
Atp4b	35	35	34.84	34.9	35	35	35	34.93
Atp5a1	21.49	21.44	21.72	22.08	21.3	21.58	21.63	21.75
Atp5b	20.63	20.55	20.95	21.39	20.41	20.67	20.88	20.89
Atp5c1	22.21	22.2	22.46	22.78	22.18	22.15	22.36	22.27
Atp5d	23.2	23.09	23.39	23.78	23.09	23.19	23.4	23.41
Atp5f1	22.35	22.27	22.44	22.85	22.25	22.11	22.48	22.45
Atp5g1	22.9	22.68	23.21	23.23	22.31	22.44	22.79	22.77
Atp5g2	22.41	22.54	22.97	23.2	22.43	22.36	22.4	22.46
Atp5g3	21.25	21.23	21.6	22.01	21.03	21.16	21.34	21.31
Atp5h	21.62	21.97	22.03	22.56	21.44	21.5	21.43	21.73
Atp5j	21.89	21.54	22.23	22.41	21.57	21.52	21.86	21.87
Atp5j2	22.29	22.24	22.49	22.75	22.27	22.25	22.42	22.46
Atp5o	23.01	22.94	23.3	23.5	22.83	22.93	23.14	23.11
Atp6v0a2	24.25	24.37	24.57	24.7	24.46	24.25	24.19	24.36
Atp6v0d2	33.28	33.63	33.17	33.22	33.47	32.6	32.54	32.42
Atp6v1c2	32.88	32.57	32.99	32.87	33.22	33.12	32.32	32.88
Atp6v1e2	35	35	35	35	35	35	35	35
Atp6v1g3	35	35	34.21	35	35	34.85	35	35
Bcs1l	27.63	27.73	27.9	28.19	28.43	27.48	27.59	27.92
Cox11	28.65	28.74	29.16	29.15	28.74	29.93	28.37	28.88
Cox4i1	21.48	21.32	21.73	21.9	21.2	21.19	21.32	21.3
Cox4i2	31.01	31.47	31.38	30.88	31.77	30.6	30.86	31.41
Cox5a	22.71	22.9	23.15	23.43	22.62	22.73	22.96	23.01
Cox5b	31.79	31.54	31.54	31.8	31.33	31.19	31.57	31.54
Cox6a1	22.1	22.25	22.59	22.6	22.33	22.21	22.41	22.34
Cox6a2	34.24	33.77	33.26	34.35	33.7	34.22	32.37	32.72
Cox6b1	22.27	22.21	22.66	22.83	22.17	22.25	22.34	22.4
Cox6b2	28.13	27.83	28.56	28.58	28.14	28.47	28.46	28.48
Cox6c	21	21	21.26	21.53	20.9	20.91	20.97	21.08
Cox7a2	33.17	34.58	33.73	33.9	33.35	33.24	32.96	33.66
Cox7a2l	22.53	22.76	23.02	23.24	22.73	22.83	22.55	22.67
Cox7b	22.86	23	23.52	23.82	22.71	22.92	23.06	23.14
Cox8a	23.71	23.71	24.18	24.51	23.65	23.63	24.03	23.87
Cox8c	35	35	35	35	35	35	35	35
Cyc1	23.92	23.76	23.91	24.35	23.64	23.89	24.06	24.16
Lhpp	28.36	28.63	28.4	28.64	28.57	28.62	28.5	28.52
Ndufa1	23.12	23.11	23.41	23.74	23.21	23.22	23.3	23.3
Ndufa10	23.75	23.72	24.2	24.3	23.68	24.05	23.85	23.89
Ndufa11	24.35	24.26	24.64	25.01	24.26	24.39	24.4	24.49

Ndufa2	24.91	24.97	25.37	25.65	25.05	25.03	25.18	25.16
Ndufa3	23.42	23.62	23.75	24.06	23.71	23.36	23.72	23.51
Ndufa4	22.11	21.99	22.29	22.65	21.98	22.02	22.13	22.14
Ndufa5	23.71	23.72	24.12	24.41	23.62	23.7	23.9	24.03
Ndufa6	23.14	23.24	23.56	23.9	23.32	23.26	23.42	23.42
Ndufa7	23.78	23.76	24.13	24.26	23.86	23.89	23.78	23.91
Ndufa8	23.79	23.81	24.16	24.18	23.86	23.71	24.04	23.82
Ndufab1	29.28	29.07	29.4	29.72	29.02	28.88	29.4	29.44
Ndufb10	24.81	24.7	25.15	25.59	24.75	24.86	25.01	25.08
Ndufb2	23.43	23.39	23.98	24.09	23.66	23.56	23.76	23.78
Ndufb3	23.55	23.68	24.13	24.31	23.48	23.38	23.66	23.64
Ndufb4	24.23	24.25	24.57	24.82	23.99	24.34	24.28	24.32
Ndufb5	23.79	23.78	24.25	24.28	23.74	23.58	23.85	23.86
Ndufb6	23.94	23.92	24.23	24.47	24.01	24.14	24.31	24.29
Ndufb7	23.48	23.56	24.09	24.15	23.23	23.23	23.34	23.33
Ndufb8	23.24	23.12	23.42	23.61	23.05	23.05	23.27	23.21
Ndufb9	23.15	23.15	23.38	23.8	23.12	23.33	23.33	23.32
Ndufc1	23.32	23.31	23.35	23.94	23.32	23.11	23.5	23.48
Ndufc2	22.39	22.28	22.73	23.03	22.19	22.35	22.47	22.51
Ndufs1	24.97	24.98	25.24	25.46	24.74	25.18	25.26	25.41
Ndufs2	23.66	23.7	24.19	24.31	23.72	23.86	24.01	24.05
Ndufs3	24.07	24.04	24.34	24.63	24.06	24.18	24.28	24.2
Ndufs4	24.2	24.13	24.64	24.66	24.14	24.14	24.44	24.29
Ndufs5	23.36	23.22	23.9	24.1	23.1	23.03	23.49	23.35
Ndufs6	23.17	22.99	23.46	23.71	22.85	23.13	23.25	23.16
Ndufs7	24.33	24.2	24.79	24.98	24.09	24.41	24.56	24.46
Ndufs8	24.64	24.62	25.09	25.27	24.47	24.59	24.79	24.66
Ndufv1	24.58	24.35	24.84	24.9	24.19	24.6	24.67	24.66
Ndufv2	23.42	23.33	23.76	23.87	23.36	23.56	23.45	23.65
Ndufv3	24.04	24.11	24.41	24.57	23.87	23.88	23.89	23.99
Oxa1l	24.7	25.18	25.23	25.73	24.65	24.96	24.84	25
Ppa1	24.54	24.49	24.82	25.34	24.4	24.57	24.92	25.1
Ppa2	25.58	25.45	25.9	26.04	25.44	25.49	25.78	25.94
Sdha	23.36	23.31	24.03	23.91	23.52	23.44	23.67	23.7
Sdhb	24.39	24.24	24.91	24.91	24.28	24.36	24.67	24.53
Sdhc	24.17	24.15	24.69	24.99	24.1	24.17	24.35	24.35
Sdhd	27.91	27.54	28.24	28.32	27.52	27.9	27.85	27.93
Uqcr11	26.74	26.33	27	27.13	26.25	26.31	26.56	26.46
Uqcrc1	23.06	22.97	23.3	23.49	22.93	23.06	23.22	23.19
Uqcrc2	23.29	23.06	23.64	23.71	24.23	23.2	24.38	23.39
Uqcrfs1	22.73	22.69	23.17	23.35	22.5	22.64	22.74	22.76
Uqcrh	25.11	24.98	25.72	25.72	25.1	24.97	25.3	25.24
Uqcrq	22.66	22.45	23.07	23.15	22.27	22.52	22.57	22.62
Actb	18.51	18.34	19.12	19.16	18.52	18.38	18.54	18.28
B2m	19.17	19.24	19.5	19.7	19.59	18.82	19.15	19.15
Gapdh	20.61	20.5	20.88	21.35	20.35	20.49	20.91	20.96
Gusb	25.43	25.3	25.86	25.86	25.35	25.46	25.64	25.6
Hsp90ab1	19.67	19.48	20.02	20.24	19.35	19.75	19.83	20.01