Metabolic flux with [U-13C]Lactate - [12C]Glutamine in primary hepatocytes



Supplemental figure 1. Metabolic flux with $[U^{-13}C]$ Lactate - $[^{12}C]$ Glutamine in primary hepatocytes (**a-h**) Primary isolated hepatocytes were treated with with $[U^{-13}C]$ Lactate - $[^{12}C]$ Glutamine and either PBS (NT) or glucagon and (**a**) $[^{13}C_3]$ Pyruvate, (**b**) $[^{13}C_3]$ malate, (**c**) $[^{13}C_3]$ aspartate, (**d**) $[^{13}C3]$ citrate, (**e**) $[^{13}C2_3]\alpha$ ketoglutarate, (**f**) $[^{13}C_2]$ glutamate, (**g**) $[^{13}C_2]$ glycerol-phosphate, and (**h**) $[^{13}C_3]$ hexose-phosphate. Top plots are kinetic timecourses following addition of glucagon. Bottom plots show the isotopomer distribution at the 20 minute time point.

Metabolic flux with [¹²C]Lactate - [U-¹³C]Glutamine in primary hepatocytes



Supplemental figure 2. Metabolic flux with [¹²C]Lactate - [U-¹³C]Glutamine in primary hepatocytes (**a-h**) Primary isolated hepatocytes were treated with with [U-¹³C]Lactate - [¹²C]Glutamine and either PBS (NT) or glucagon and (**a**) [¹³C₃]Pyruvate, (**b**) [¹³C₄]malate, (**c**) [¹³C₄]aspartate, (**d**) [¹³C₄]citrate, (**e**) [¹³C₅] α ketoglutarate, (**f**) [¹³C₅]glutamate, (**g**) [¹³C₃]glycerol-phosphate, and (**h**) [¹³C₃]hexose-phosphate. Top plots are kinetic timecourses following addition of glucagon. Bottom plots show the isotopomer distribution at the 20 minute time point.



Supplemental figure 3. Modeling results from metabolic flux studies based on experiments presented in figure 1 and supplemental figures 1-2. Flux map with best fit flux values for untreated and glucagon stimulated fluxes.

Intracellular glutamine in primary hepatocytes treated with glucagon



Supplemental figure 4. Intracellular glutamine in primary hepatocytes treated with glucagon or PBS vehicle. Primary hepatocytes were incubated with (**a**) lactate or (**b**) lactate and $[^{13}C_6]$ glutamine and the intracellular glutamine was measured by mass spectrometry.



Supplemental figure 5. Mechanistic and signaling studies in primary mouse hepatocytes. (a) a-ketoglutarate levels following treatment of primary hepatocytes with PBS (vehicle), glucagon, or db-cAMP and measured enzymatically. (b) Liver a-ketoglutarate levels following treatment with a bolus injection of glucagon or PBS and and measured by mass spectrometry. (c) Measurement of a-kgdh enzymatic activity in primary hepatocytes treated with PBS or glucagon. (d) Primary hepatocytes isolated from mice infected with AAV-TBG-GFP or AAV-TBG-PKA-DN were isolated and treated with PBS, glucagon, or phenylephrine for 10 minutes and the resulting protein lysates were probed by western blot for phosphorylated or total Phosphofructokinase/FBPase1(PFKFB1), phosphorylated or total Inositol 3-Phosphate Receptor (IP3R), phosphorylated or total CREB, and the PKA regulatory subunit used to inhibit PKA activity (PKA-R1a). (e-f) Primary hepatocytes were treated with PBS (NT) or glucagon in the presence or absence of the PKA inhibitor H89 and (e) glucose output or (f) a-ketoglutarate levels were measured. (g) Primary hepatocytes were isolated and the levels of intracellular calcium were measured using calcium sensitive dyes in distinct hepatocytes. (h-l) Kinetic metabolic flux studies using [¹²C]Lactate - [U-¹³C]Glutamine in hepatocytes treated with PBS vehicle, glucagon, or phenylephrine were performed. The isotopomer pattern in extracellular glucose was measured and represented as a (h) total amount or (I) the fraction of the total glucose pool. Intracellular metabolite labeling patterns are shown for (j) [¹³C₃]a-ketoglutarate, (k) [¹³C₃]glutamate, and (j) [¹³C₄]malate.

Mechanistic and signaling studies in mouse liver



Supplemental figure 6. Mechanistic and signaling studies in mouse liver. (**a-b**) Animals infected with AAV-GFP or AAV-GLS2-sh were infused with $[U^{-13}C]$ Glutamine and PBS vehicle or glucagon. Hepatic enrichment of (**a**) $[^{13}C_5]$ glutamate and (**b**) $[^{13}C_4]$ malate. Values are corrected for plasma enrichment of glutamine. (**c**) Western blot evaluation of GLS2 protein levels in livers from GLS2-KO and litter mate control animals.

Supplemental Figure 7 Original Scan of Western Blots



Supplemental Figure 8. Original Scan of Western Blots

A. Original Scan for figure 3a and supplemental figure 6a. B. Original Scan for supplemental figure 6d

Supplemental Table 1 Best fit fluxes and lower and upper bounds of modeling

	95% confidence interval		Basal			Glucagon	
	nmol/mg protein/min	LB	BEST	UB	LB	BEST	UB
Net	Glc secretion	9.5	10.0	10.0	16.0	17.0	17.5
Net	Pyr secretion	1.3	1.7	1.7	0.9	0.9	1.4
Net	FA degradation	4.4	4.8	5.5	5.9	6.3	6.8
Net	Glycogenolysis	1.6	1.9	1.9	3.1	3.4	3.7
Net	Lactate uptake	15.4	15.7	18.9	17.3	18.3	19.5
Net	Gln uptake	3.2	3.2	3.9	9.6	10.3	10.8
Net	aKG→Succ-CoA+CO2	8.4	8.9	10.3	16.0	17.2	17.7
Reverse	aKG→Succ-CoA+CO2	0.0	0.3	0.7	0.7	1.0	1.4
Net	Ac-CoA+OA→Cit	5.4	5.8	5.8	6.7	6.9	7.3
Net	PEP+H2O→2PG	16.2	16.2	16.8	26.6	27.2	27.7
Reverse	PEP+H2O→2PG	49.2	983.3	1000.0	0.0	0.0	0.1
Net	GAP+DHAP→FBP	8.1	8.1	8.4	13.3	13.6	13.9
Net	2 Fum + 2 H2O \rightarrow 2 Mal	4.2	4.5	5.1	7.7	8.6	9.1
Net	Lac→Pyr	15.4	15.7	18.9	17.3	18.3	19.5
Net	Mal→OA	16.9	17.6	17.6	27.2	28.7	31.3
Net	OA→Mal (mitochondria)	8.6	8.6	11.3	13.1	14.1	15.1
Reverse	OA→Mal (mitochondria)	32.7	41.4	65.8	43.3	55.6	67.2
Net	Mal→Pyr+CO2	0.0	0.0	0.0	0.0	2.5	4.0
Net	Pyr+CO2→OA	14.4	14.4	16.6	19.5	21.0	22.2
Net	Pyr→Ac-CoA+CO2	0.9	1.0	1.3	0.4	0.5	0.6
Net	PEP→Pyr	0.6	1.4	1.4	0.0	1.6	5.0

Supplemental table 1. Best fit and upper/lower bounds from modeling results from metabolic flux studies based on experiments presented in figure 1 and supplemental figures 1-2.