

Coordinated Activities of Multiple Myc-Dependent and Myc-Independent Biosynthetic Pathways in Hepatoblastoma

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Running Title: *Coordinated Biosynthetic Pathways in Hepatoblastoma*

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Key words: β -catenin, YAP, metabolism, oxidative phosphorylation, hepatocellular carcinoma

SUPPLEMENTAL FIGURE LEGENDS

Supplemental Figure S1. Expression of potential Myc surrogates in WT and KO hepatocytes and HBs. *A*, Transcript levels for the indicated genes was obtained from RNA seq data performed on WT and KO HBs. *B*, Immuno-blotting for the indicated proteins of WT and KO livers (L) and HBs (T)

Supplemental Figure S2. Structure and function of ETC complexes in livers and HBs. *A*, Top panel: Representative BNGE of ETC complexes from paired WT and KO livers (L) and HBs (T) stained with Coomassie Blue. Bottom panels: Representative examples of *in situ* enzymatic activities for ETC complexes I, III, IV and V. SC=super-complexes composed of varying stoichiometries of Complexes I, II and IV. *B*, Quantification of relative specific activities of *in situ* enzymatic activities after normalizing to total protein content. N=4-7 samples/group. Note that Complex II assays were performed upon total mitochondrial lysates as *in situ* gel-based assays proved unreliable(1,2).

Supplemental Figure S3. Low-magnification transmission electron micrographs of WT and KO livers (L) and HBs (T). *A*, Representative photos (magnification x 10,000) emphasizing the relative paucity of mitochondria (white arrows) in HBs. *B*, Quantification of mitochondrial

number and size in WT livers and tumors.

Supplemental Figure S4. RNA seq analysis of differential gene expression in WT and KO HBs. Red=up-regulated; green=down-regulated. The transcripts depicted here represent all those identified with $q < 0.05$ after correction for false discovery rates.

Supplemental Figure S5. Transcripts encoding RPs. The depicted heat map is same as shown in Figure 3B. Absolute levels of expression are included.

Supplemental Figure S6. Transcripts encoding proteins involved in the regulation of translation. The depicted heat map is the same as shown in Figure 3A and includes members involved in signaling by eIF2, eIF4, p70S6K and mTOR(3,4). Absolute levels of expression are indicated thus permitting a direct comparison of transcript level differences among WT and KO hepatocytes and HBs. Note the ~11-25-fold down-regulation in both WT and KO HBs of transcripts encoding eIF4EBP3, a negative regulator of pre-initiation complex formation.

Supplemental Figure S7. Transcripts encoding glycolytic enzymes. *A*, The depicted heat map is the same as shown in Fig. 3C. Absolute levels of expression are included. *B*, The glycolytic pathway depicting key enzymes encoded by transcripts listed in *A*.

Supplemental Figure S8. IPA of the top categories of transcript variation between WT and KO HBs. We have previously shown that several of these pathways, which regulate functions associated with white blood cells, including “granulocyte adhesion and diapedesis” and “leukocyte extravasation signaling” are likely to be up-regulated in KO livers in response to the accumulation of lipids by hepatocytes (1). Excluding these and the already discussed pathways pertaining to protein translation, 8 of the remaining pathways (asterisks) were associated with lipid, sterol and eicosanoid biosynthesis.

Supplemental Figure S9. Differential expression of transcripts related to fatty acid biosynthesis. The data are taken from the heat map depicted in Figure 4A with actual levels of expression indicated. ND=not detected.

Supplemental Figure S10. Differential expression of transcripts related to FAO. The data are taken from the heat map depicted in Figure 4B with actual levels of expression indicated

Supplemental Figure S11. Differential expression of transcripts related to cholesterol biosynthesis. The data are taken from the heat map depicted in Figure 4C with actual levels of expression indicated.

Supplemental Figure S12. Reduced conversion of glutamine to α -ketoglutarate. *A*, In the liver Slc1A5 is the major glutamine transporter, whereas Gls2 and Glud1 catalyze the sequential two step deamination of glutamine to α -ketoglutarate. Glud1 also catalyzes the conversion of oxaloacetate and pyruvate to α -ketoglutarate via the actions of Got1/2 and Gpt, respectively. *B*, Transcript levels encoding each of the above-mentioned enzymes in WT and KO livers and HBs. Each bar represents the mean of five individual RNAseq results \pm 1 S.E. *C*, Immunoblots for Gls2 and Glud1 in WT and KO livers and HBs. *D*, The conversion of glutamine to α -ketoglutarate via the actions of Gls2 and Glud1. Each result was normalized to equivalent protein concentrations.

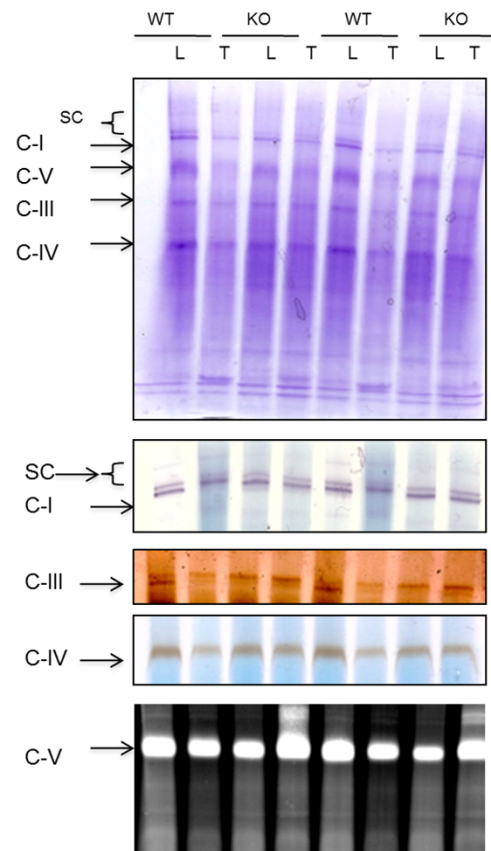
1. Edmunds, L. R., Otero, P. A., Sharma, L., D'Souza, S., Dolezal, J. M., David, S., Lu, J., Lamm, L., Basantani, M., Zhang, P., Sipula, I. J., Li, L., Zeng, X., Ding, Y., Ding, F., Beck, M. E., Vockley, J., Monga, S. P., Kershaw, E. E., O'Doherty, R. M., Kratz, L. E., Yates, N. A., Goetzman, E. P., Scott, D., Duncan, A. W., and Prochownik, E. V. (2016) Abnormal lipid processing but normal long-term repopulation potential of myc^{-/-} hepatocytes. *Oncotarget* **7**, 30379-30395
2. Edmunds, L. R., Sharma, L., Wang, H., Kang, A., d'Souza, S., Lu, J., McLaughlin, M., Dolezal, J. M., Gao, X., Weintraub, S. T., Ding, Y., Zeng, X., Yates, N., and Prochownik, E. V. (2015) c-Myc and AMPK Control Cellular Energy Levels by Cooperatively Regulating Mitochondrial Structure and Function. *PLoS One* **10**, e0134049
3. Klann, E., and Dever, T. E. (2004) Biochemical mechanisms for translational regulation in synaptic plasticity. *Nat. Rev. Neurosci.* **5**, 931-942
4. Livingstone, M., Atas, E., Meller, A., and Sonenberg, N. (2010) Mechanisms governing the control of mRNA translation. *Phys. Biol.* **7**, 021001

Supplemental Table S1. Antibodies utilized in the current study

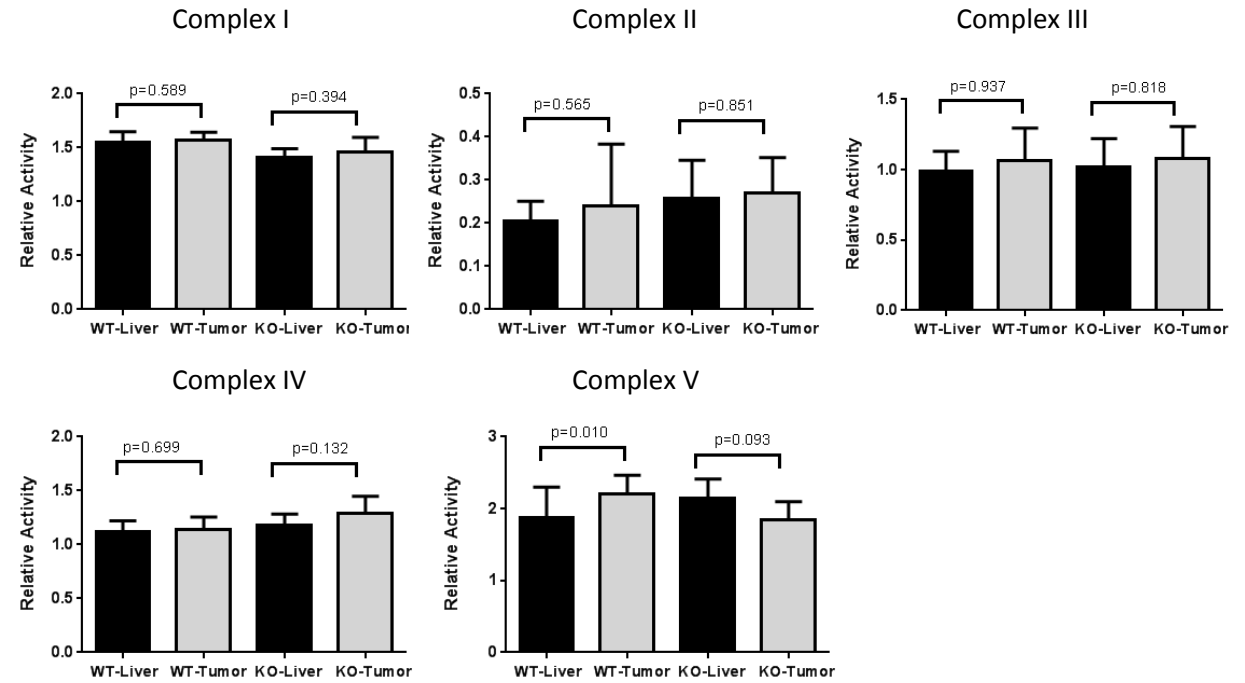
Antibody	Species	Vendor and ID no.	Dilution used
Myc	Rabbit	Cell Signaling(13987)	1:1,000
N-Myc	Rabbit	Santa Cruze(sc791)	1:500
L-Myc	Rabbit	Santa Cruze(sc790)	1:1,000
AMPK	Rabbit	Cell Signaling (3532)	1:1,000
pAMPK (Thr172)	Rabbit	Cell Signaling (4188)	1:1,000
Histone H3	Rabbit	Cell Signaling (9715)	1:1,000
Glutaminase 2	Rabbit	Abcam(ab113509)	1:1,000
Glutamine dehydrogenase	Rabbit	Cell signaling(12793)	1:1,000
Acetyl-histone-H3 (K9/K14)	Rabbit	Santa Cruz (sc8655-R)	1:500
GAPDH	Mouse	Sigma-Aldrich(G8795)	1:20,000
HRP anti-mouse	Horse	Cell Signaling(7076)	1:10,000
HRP anti-ribbit	Goat	Cell Signaling(7074)	1:5,000
Alexa Fluor 488 anti-rabbit	Goat	Thermo Fisher(A-11008)	1:1,000

Supplemental Fig. S2

A

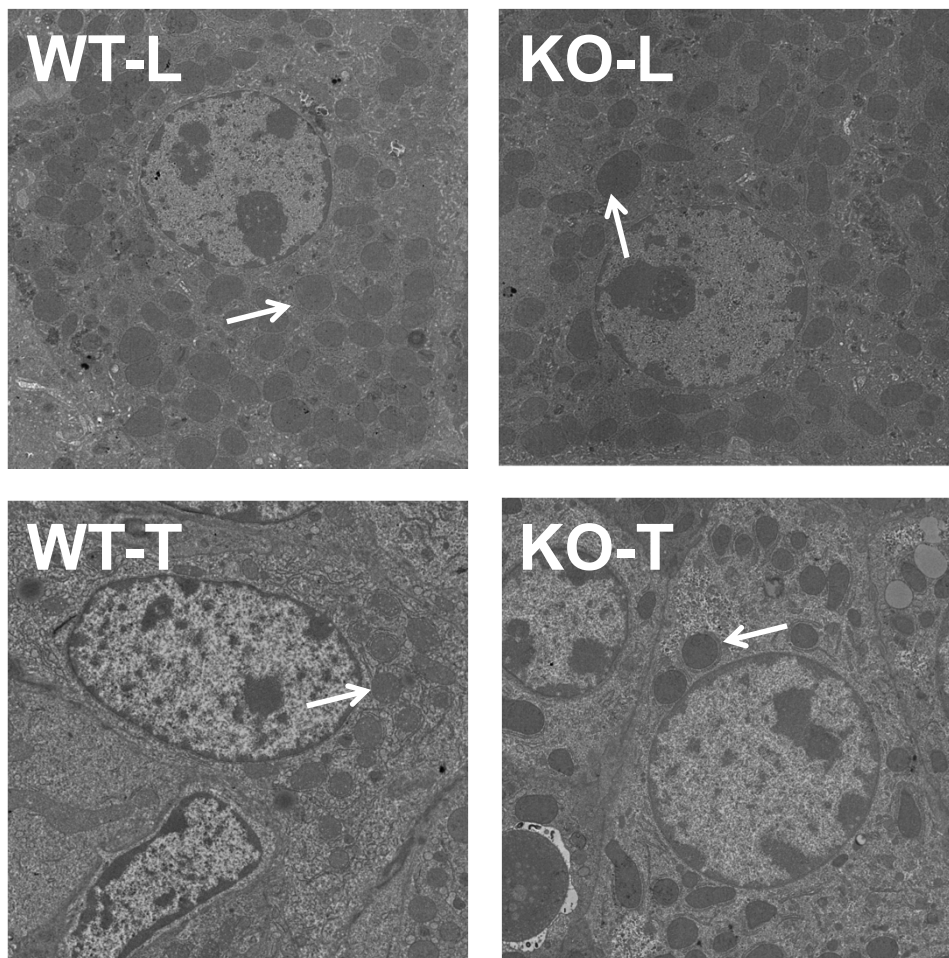


B

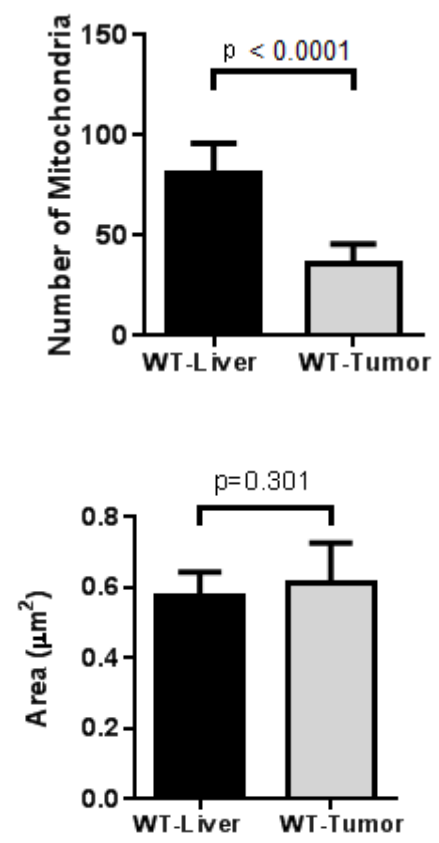


Supplemental Fig. S3

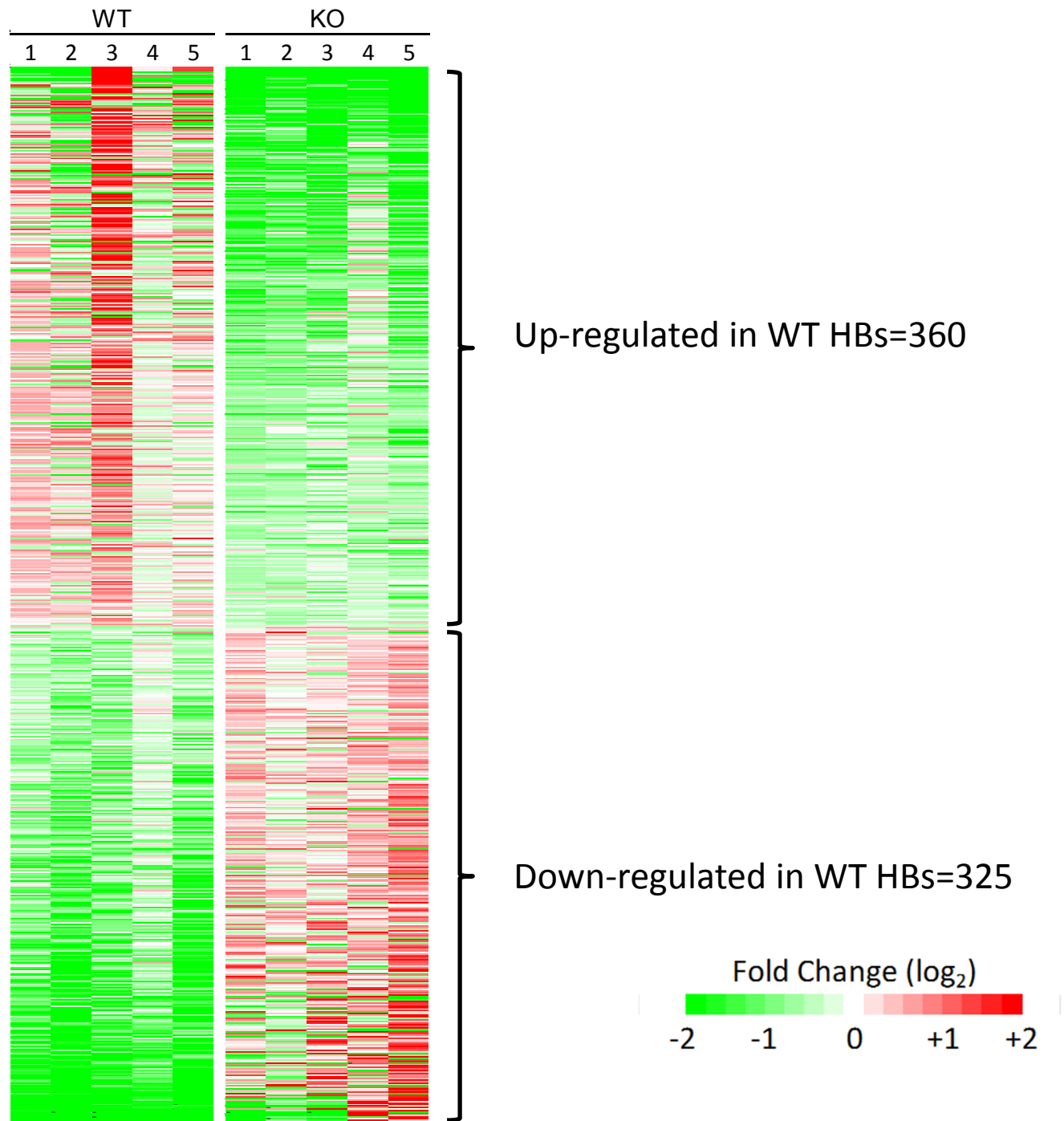
A



B

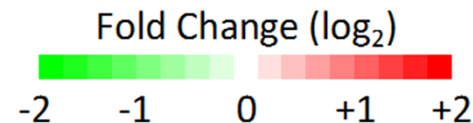


Supplemental Fig. S4



Supplemental Fig. S6

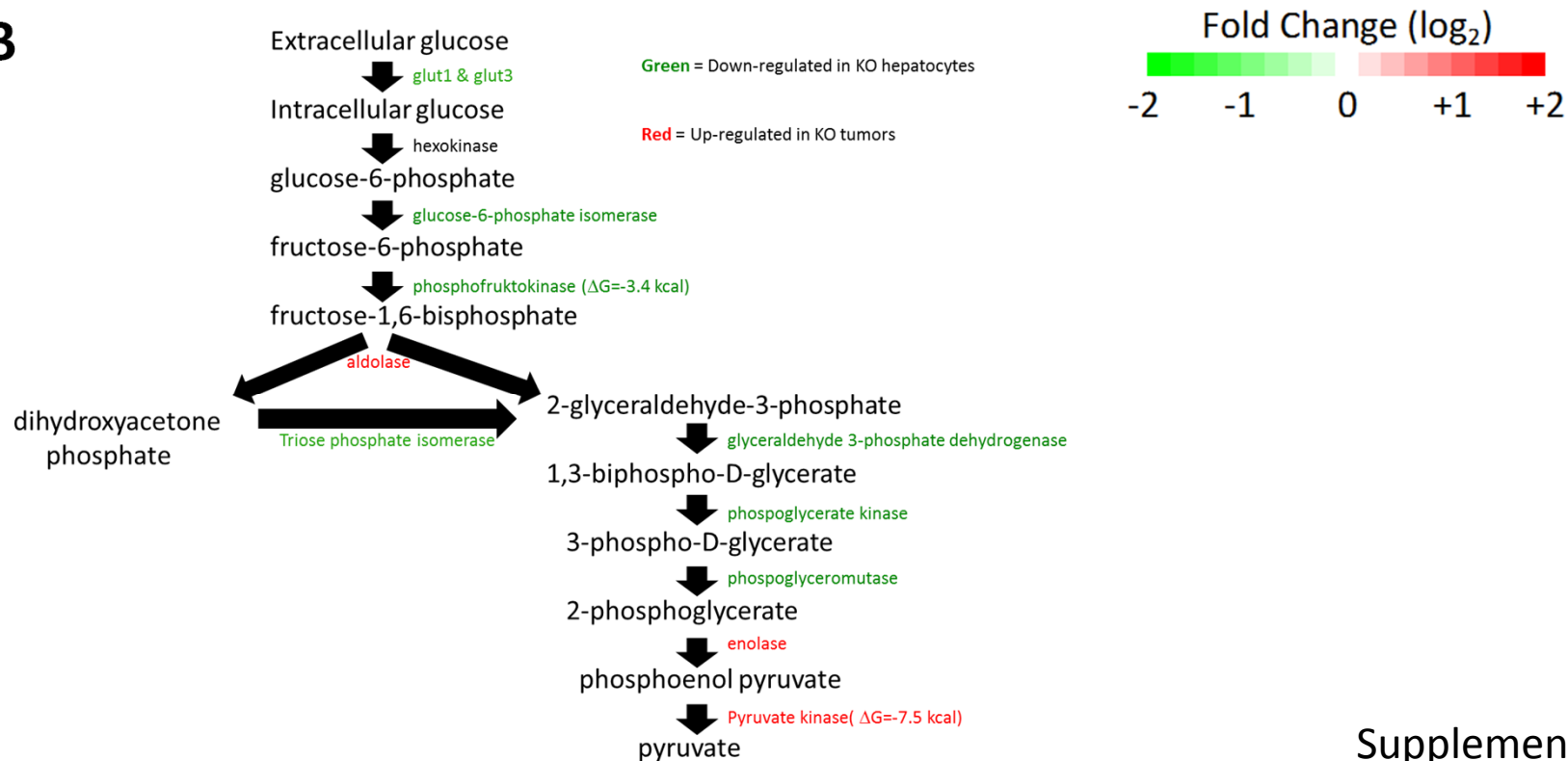
Gene ID	Gene Symbol	Tumor vs Hepatocyte				WT vs KO					Hepatocytes				HBs										
		WT		KO		Hepatocyte		Tumor			WT		KO		WT		KO								
		Log2 Diff	P value	Log2 Diff	P value	Log2 Diff	P value	Fold DI	Log2 Diff	P value	1	2	3	4	1	2	3	4	5	1	2	3	4	5	
381404	Pabpc1l	5.18419	0.0044	5.44632	0.0014	-0.487956	1	0.595	1	1															
12877	Cpeb1	3.60576	0.0006	3.86504	<0.0001	0.134924	0.57265	0.917	0.57265	0.63645															
66892	Eif4e3	3.30828	0.002	3.64597	<0.0001	-0.318557	0.217	0.635	0.217	0.0193															
208691	Eif5a2	3.18944	0.0001	4.09914	0.03338	0.789505	1	0.92	1	1															
13666	Eif2ak3	2.36478	0.0006	2.73397	<0.0001	0.051071	0.7085	0.802	0.7085	0.1845															
66085	Eif3f	1.83995	0.0003	1.59386	0.0001	0.205563	0.2084	1.368	0.2084	0.03335															
16418	Eif6	1.7709	0.0003	1.61567	0.0002	0.068107	0.62815	1.167	0.62815	0.24445															
27103	Eif2ak4	1.66115	0.0001	1.90368	<0.0001	0.051175	0.80485	0.876	0.80485	0.543															
19106	Eif2ak2	1.56325	0.0054	1.38913	0.00022	-0.22614	0.2213	0.965	0.2213	0.9113															
74203	Eif4enif1	1.54449	0.0001	1.17337	0.00031	-0.035643	0.9691	1.262	0.9691	0.5489															
245474	Dkc1	1.45613	0.0131	1.48565	0.00023	0.232899	0.47105	1.151	0.47105	0.65855															
226982	Eif5b	1.40429	0.0001	1.38709	<0.0001	0.064316	0.65395	1.058	0.65395	0.65185															
67204	Eif2s2	1.308	0.0027	1.00081	0.0005	0.086927	0.52175	1.314	0.52175	0.0555															
68135	Eif3h	1.2953	0.0036	0.67602	0.00484	-0.098261	0.5891	1.435	0.5891	0.0148															
13685	Eif4ebp1	1.28911	0.0042	0.73167	0.00967	0.179898	0.23065	1.667	0.23065	0.00075															
56347	Eif3c	1.26837	0.0014	1.1763	0.00023	0.051679	0.74695	1.105	0.74695	0.4966															
13681	Eif4a1	1.26802	0.0001	1.07561	0.00246	0.10727	0.4779	1.231	0.4779	0.2294															
98221	Eif3m	1.26096	0.0035	0.83999	0.00085	0.044256	0.75875	1.381	0.75875	0.0259															
16341	Eif3e	1.14567	0.0012	0.68289	0.00491	0.078112	0.5846	1.455	0.5846	0.00725															
54196	Pabpn1	1.13078	0.0039	1.64202	<0.0001	0.514931	0.0042	1.003	0.0042	0.9615															
13669	Eif3a	1.12092	0.0018	1.22362	0.00015	0.192415	0.22535	1.064	0.22535	0.61375															
13665	Eif2s1	1.11395	0.0034	0.87035	0.00404	-0.076339	0.66695	1.123	0.66695	0.30255															
192170	Eif4a3	1.11412	0.0004	1.16742	0.00019	-0.01933	0.84395	0.951	0.84395	0.88675															
229317	Eif2a	1.08897	0.0008	0.79767	0.00077	0.134344	0.7067	1.343	0.7067	0.50565															
26905	Eif2s3x	1.08087	0.0021	1.05913	0.00081	0.087628	0.59635	1.079	0.59635	0.5039															
16865	Eif2d	1.07727	0.0002	1.06373	0.00076	0.090473	0.5123	1.075	0.5123	0.52285															
54709	Eif3i	1.05754	0.0035	0.37621	0.03789	0.04637	0.72375	1.656	0.72375	0.00075															
20918	Eif1	0.99224	0.0004	0.731	0.01625	0.047096	0.86015	1.238	0.86015	0.22545															
18458	Pabpc1	0.97786	0.001	0.87378	0.00158	0.337305	0.03755	1.358	0.03755	0.0565															
217715	Eif2b2	0.94981	0.0032	0.74883	0.00039	0.073033	0.6451	1.209	0.6451	0.1702															
73830	Eif3k	0.89395	0.0135	0.50165	0.00101	0.096759	0.5041	1.404	0.5041	0.0168															
53356	Eif3g	0.88924	0.0033	0.79203	0.00031	0.099563	0.55925	1.146	0.55925	0.29265															
56717	Mtor	0.8912	0.0269	1.08441	0.00038	0.157115	0.38675	0.975	0.38675	0.89835															
13690	Eif4g2	0.84925	0.0098	0.99134	0.00172	-0.022613	0.86865	0.892	0.86865	0.67695															
22384	Eif4h	0.84096	0.0037	0.84816	0.00018	-0.011214	0.9054	0.987	0.9054	0.9829															
66711	Sbds	0.76935	0.0024	0.36713	0.1107	-0.083208	0.66225	1.247	0.66225	0.10385															
224045	Eif2b5	0.74574	0.0009	0.66133	0.0012	0.075137	0.64175	1.117	0.64175	0.36885															
13664	Eif1a	0.73861	0.0032	0.77716	0.00181	0.168335	0.25915	1.094	0.25915	0.4171															
276770	Eif5a	0.68884	0.0046	0.39079	0.05671	0.012764	0.8643	1.24	0.8643	0.1675															
230721	Pabpc4	0.65381	0.015	0.31733	0.14409	0.373499	0.0282	1.636	0.0282	0.0012															
26987	Eif4e2	0.63721	0.0002	0.52102	0.00247	-0.059228	0.80365	1.04	0.80365	0.67365															
27979	Eif3b	0.62351	0.0087	0.65144	0.00074	0.26852	0.08245	1.181	0.08245	0.2347															
223691	Eif3l	0.5532	0.0027	0.47252	0.03367	0.006755	0.90065	1.062	0.90065	0.56505															
78655	Eif3j1	0.53259	0.029	0.38252	0.07399	0.004449	0.9396	1.113	0.9396	0.5093															
108067	Eif2b3	0.51112	0.0316	0.24144	0.17994	0.193109	0.2942	1.378	0.2942	0.0708															
209354	Eif2b1	0.46272	0.0191	0.37733	0.03552	0.092252	0.5617	1.131	0.5617	0.3859															
13667	Eif2b4	0.46276	0.0006	0.61481	0.0016	0.162229	0.27765	1.007	0.27765	0.8645															
231207	Cpeb2	-0.79246	0.0288	-0.3848	0.15123	0.250075	0.1413	0.897	0.1413	0.601															
108112	Eif4ebp3	-3.45449	0.0051	-4.48411	0.00885	-0.045688	0.6816	1.978	0.6816	0.00015															



A

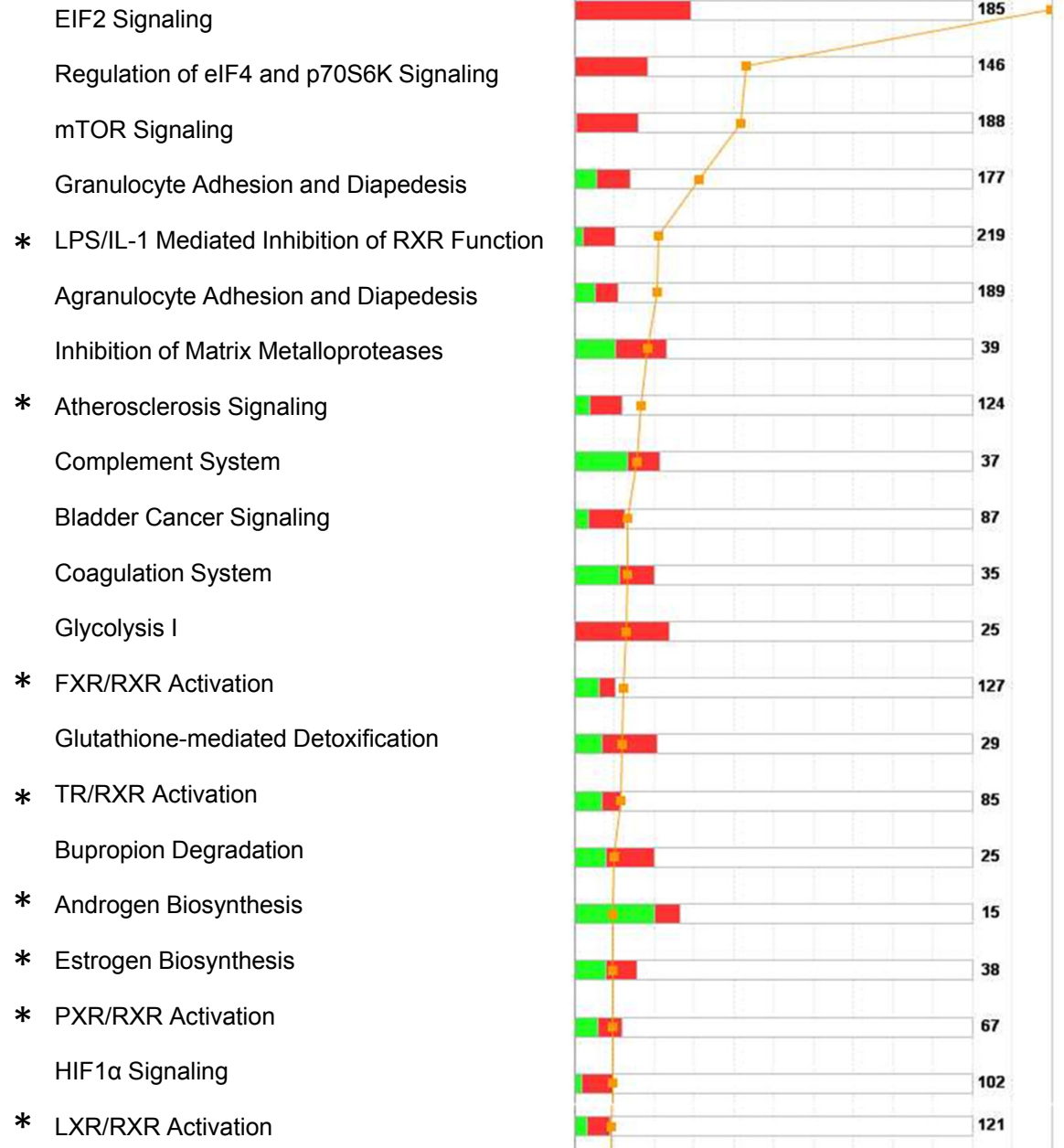
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		WT		KO		Hepatocyte		Tumor		WT		KO		WT		KO			
		Log2 Diff	P value	Log2 Diff	P value	Log2 Diff	P value	Fold D	Log2 Diff	P value	1	2	3	4	1	2	3	4	5
20525	SLC2A1	1.58506	0.1198	0.47423	0.19863	-0.20369	0.1633	2.487	0.1633	0.00005									
20526	SLC2A2	1.31565	0.0258	0.51479	0.12053	-0.524995	0.0025	1.211	0.0025	0.22935									
20527	SLC2A3	4.85613	0.1233	4.83753	0.00706	1.387674	1	2.651	1	0.00805									
20528	SLC2A4	6.07493	0.0198	6.56371	<0.0001	0.619948	1	1.095	1	0.78									
15275	HK1	3.63795	0.0783	2.5991	0.02999	-0.191743	1	1.799	1	0.02255									
15277	HK2	5.75422	0.045	4.49358	0.00307	-0.606021	1	1.574	1	0.0651									
212032	HK3	3.03876	0.0134	3.53789	0.01232	0.679162	1	1.133	1	0.5318									
14751	GPII	1.46372	0.0015	0.71571	0.00077	0.150086	0.30745	1.864	0.30745	0.0002									
18641	PFKL	2.57103	0.0066	2.04986	<0.0001	0.131595	0.50285	1.572	0.50285	0.0022									
18642	PFKM	0.15914	0.5869	0.505	0.03512	0.219948	0.3057	0.916	0.3057	0.7656									
56421	PFKP	4.07116	0.0243	3.0525	0.00121	-0.121706	1	1.862	1	0.1705									
11674	ALDOA	1.84761	0.0628	0.54645	0.00773	0.121555	0.3214	2.681	0.3214	0.00005									
230163	ALDOB	-1.16576	0.002	-1.51574	0.00099	-0.20247	0.47945	1.108	0.47945	0.6644									
11676	ALDOC	3.64566	0.0012	2.65665	<0.0001	-0.552653	0.019	1.353	0.019	0.05335									
14433	GAPDH	-0.04584	0.8477	-0.72266	0.0124	-0.019563	0.9564	1.577	0.9564	0.0145									
14447	GAPDHS	3.1865	0.0059	3.77327	0.00029	0.976888	1	1.31	1	0.4964									
18655	PGK1	0.47065	0.2311	-0.47368	0.02162	-0.053085	0.7048	1.855	0.7048	0.0003									
12183	BPGM	0.02313	0.8975	-0.0589	0.72372	-0.06457	0.77035	1.107	0.77035	0.4815									
18648	PGAM1	0.77814	0.0288	0.2355	0.26493	0.063955	0.6586	1.523	0.6586	0.0077									
13806	ENO1	0.07807	0.853	-0.592	0.11035	-0.079343	0.75145	1.506	0.75145	0.1079									
433182	ENO1B	1.79967	0.0014	1.13356	0.00137	0.009521	0.81115	1.597	0.81115	0.22245									
13808	ENO3	1.17718	0.0213	1.61451	0.00492	0.702704	0.0042	1.202	0.0042	0.40945									
18770	PKLR	1.78039	0.0679	1.09927	0.00254	-0.428274	0.00815	1.192	0.00815	0.2756									
18746	PKM	5.48674	0.0598	3.72967	0.00661	0.029697	0.9775	3.45	0.9775	0.00005									
18597	PDHA1	0.32312	0.1644	0.158	0.46156	0.036679	0.77515	1.15	0.77515	0.29025									
68263	PDHB	-0.13949	0.49	-0.29326	0.14184	-0.059054	0.7536	1.068	0.7536	0.5415									

B



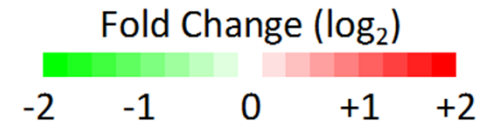
Supplemental Fig. S7

Supplemental Fig. S8



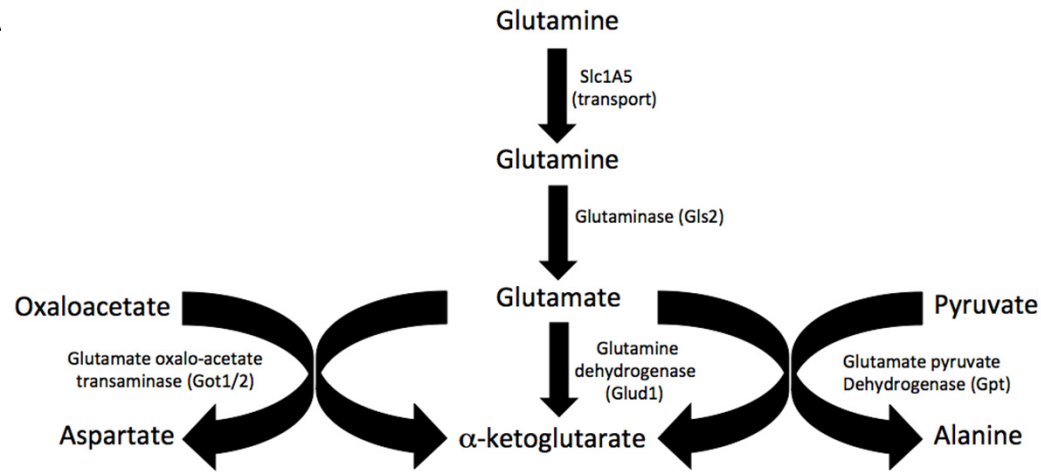
Supplemental Fig.S9

Gene ID	Gene Symbol	Tumor vs Hepatocyte				WT vs KO					Hepatocytes				HBs									
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		Log2 Diff	P value	Log2 Diff	P value	Log2 Diff	P value	Fold D	Log2 Diff	P value	1	2	3	4	1	2	3	4	5	1	2	3	4	5
99035	Olah	ND	0.0099	ND	0.40708	ND	1	1.895	1	1														
20250	Scd2	5.35496	0.0357	6.44417	0.32818	-0.260133	1	0.392	1	0.00675														
14104	Fasn	2.73821	0.03	2.61305	0.00181	-0.280659	0.11165	0.898	0.11165	0.59545														
107476	Acaca	1.98298	0.0341	2.11802	<0.0001	0.187243	0.21625	1.037	0.21625	0.7744														
76267	Fads1	1.52696	0.0037	1.6504	0.00061	-0.238732	0.15505	0.778	0.15505	0.2096														
104112	Acly	1.42411	0.0483	1.26471	0.05286	-0.500834	0.0032	0.789	0.0032	0.2267														
70757	Hacd2	0.66957	0.0055	0.85006	0.00118	0.033325	0.8002	0.903	0.8002	0.62485														
106529	Tecr	0.56436	0.0296	0.75321	0.00332	-0.047017	0.7814	0.849	0.7814	0.354														
30963	Hacd1	0.39742	0.0233	0.78949	0.0056	0.178589	0.29595	0.862	0.29595	0.55785														

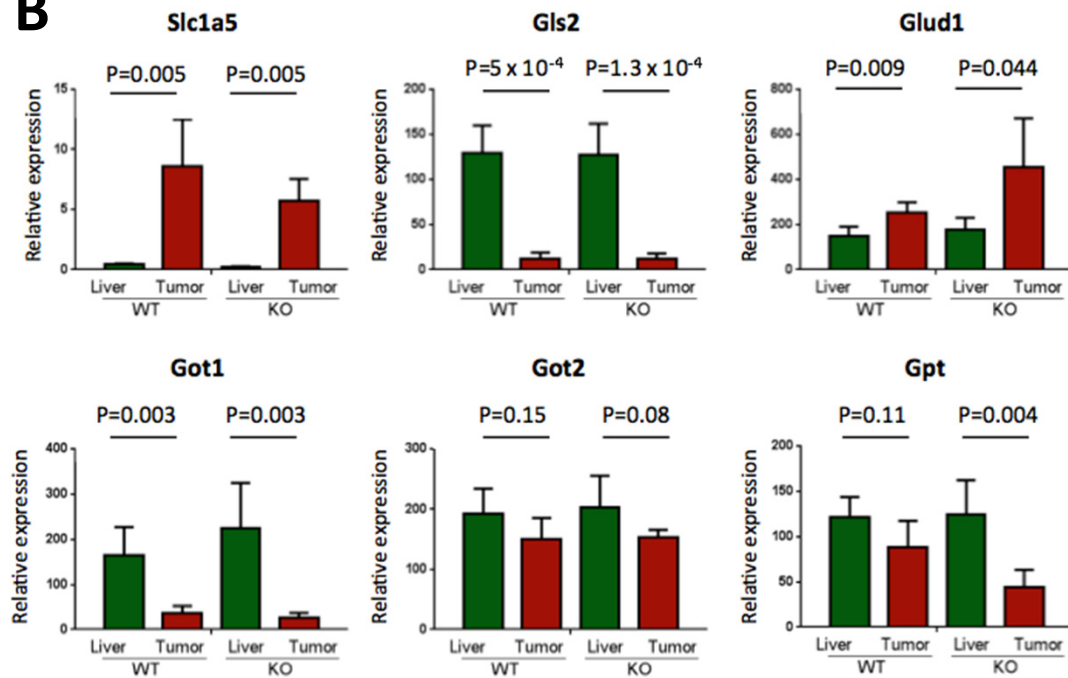


Supplemental Fig. S12

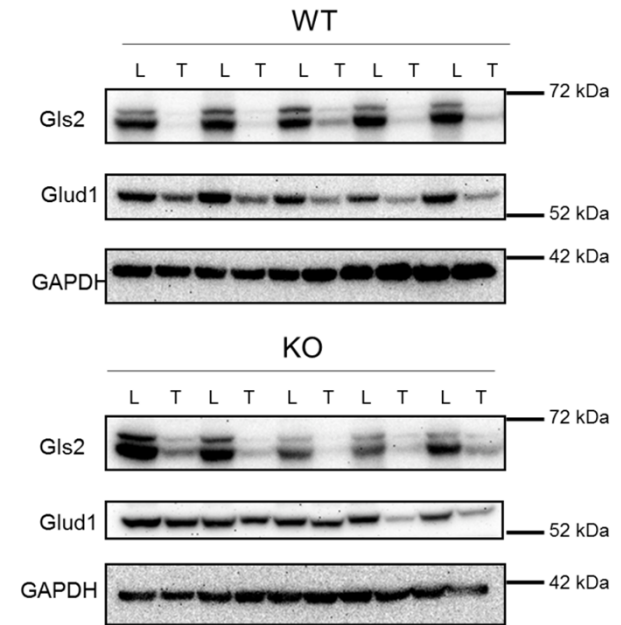
A



B



C



D

