Global Phosphoproteomic Analysis Reveals Significant Metabolic Reprogramming in the

Termination of Liver Regeneration in Mice

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Figure S-1. Quality control of MS data.

Figure S-2. Functional characterization of proteins with dysregulated phosphosites in PH-WT/Sham-WT in the termination of liver regeneration.

Figure S-3. Two representative KEGG pathways significantly changed in PH-WT/Sham-WT or PH-KO/PH-WT respectively in the termination of liver regeneration.

Table S-1. Combined MS identification and quantification information of all experiments (Provide as separate table).

Table S-2. List of proteins with significantly dysregulated phosphosites in PH-WT/Sham-WT in the termination of liver regeneration (Provide as separate table).

Table S-3. List of significantly dysregulated phosphoproteins selected for validation and discussion.









Figure S-3



Table S-3

Accession	Position	PH/Sham Ratio	P value	Regulated Type	Amino Acid	Protein Name
Pyruvate dehydroge	enase F1 compon	ent subunit alpha, som	atic form, mitoch	ondrial		
P35486	293	0 72	0 000079335	Down	S	PDHA1
P35486	295	0.676	0 000104949	Down	ŝ	PDHA1
P35486	300	0 634	7 478F-08	Down	s	PDHA1
P35486	232	0.443	0.000019824	Down	S	PDHA1
Acetyl_CoA carboxy	lase 1					
05SWU9	29	1 793	0 00029844	Un	S	ACACA
05SWU9	25	1 707	0.006899	Un	s	ACACA
05SWU9	1258	1.553	0.0061814	Un	S	ACACA
05SWU9	79	1.535	0.000058851	Un	ŝ	
05SWU9	1200	1.340	0.00062423	Un	s	ACACA
Q5SWU9	1215	1.269	0.0134613	Up	S	ACACA
Fotty agid syntheses						
	2402	2 112	0 000104597	Lln	e	EAGN
P 19090	976	1 336	0.000104507	Up	т	FASN
1 15050	570	1.550	0.0100020	00	1	TASIN
1,4-alpha-glucan-bra	anching enzyme					
Q9D6Y9	ັ189໌	0.427	0.0035234	Down	S	GBE1
Mitogen-activated p	rotein kinase kina	ase kinase kinase 4				
P97820	629	2.493	0.000123172	Up	S	MAP4K4
P97820	621	1.808	0.031736	Up	S	MAP4K4
P97820	701	1.639	0.000042532	Up	S	MAP4K4
Stathmin						
P54227	63	3 851	5 3632E-07	Un	S	Stathmin
P54227	16	2 771	0.0001773	Un	ŝ	Stathmin
P54227	25	2.578	0.00156267	Un	s	Stathmin
P54227	38	2.096	0.00058462	Un	s	Stathmin
1 04221		2.000	0.00000402			Otdimin
BCL2/adenovirus E1	IB 19 kDa protein	-interacting protein 3				
O55003	88	0.785	0.00170241	Down	S	BNIP3
O55003	85	0.782	2.8593E-06	Down	S	BNIP3
O55003	66	0.719	0.0106834	Down	Т	BNIP3
O55003	79	0.715	0.0016445	Down	S	BNIP3
O55003	60	0.653	0.000023154	Down	S	BNIP3
O55003	64	0.611	0.00021723	Down	S	BNIP3
I. I	****					
L-lactate denydroge	mase A chain	4.400	0.0000007	11-	-	L D L
P06151	309	1.498	0.0020007	Up	I	LDH

* Not validated by Western blot