

Supplementary table 1 the expression of proteins sugar related to metabolism in rat liver regeneration detected by iTRAQ

Recovery time points (h) after PH								Recovery time points (h) after PH							
Protein name	0h	2h	6h	12h	24h	30h	36h	Protein name	0h	2h	6h	12h	24h	30h	36h
A. Signaling pathways								B. carbohydrate metabolism							
a. PKA Signaling								d. HIF1α signaling							
GNB1	1.00	53.58	54.12	77.81	94.94	919.51	991.02	PSMA3	1.00	11.30	11.10	11.55	11.68	0.25	0.01
CLIC4	1.00	22.82	25.10	25.59	24.72	24.07	24.74	GMFG	1.00	0.11	3.46	3.33	3.46	1.64	3.56
ITPR2	1.00	5.52	4.82	4.99	4.38	5.04	4.53	AKT1	1.00	1.02	3.95	0.30	3.92	1.03	2.13
PTPN12	1.00	2.08	2.02	2.35	2.12	2.19	2.17	PIK3R4	1.00	20.29	32.04	2.10	27.49	22.85	34.79
AKAP13	1.00	40.39	5.26	10.37	5.57	4.26	1.05	PIK3R1	1.00	1.77	1.08	0.61	0.58	2.15	1.69
PTPN1	1.00	12.11	12.06	12.21	12.44	1.01	1.13	LDHB	1.00	0.00	0.10	0.04	0.10	0.71	0.72
PPP1CB	1.00	0.76	10.94	6.33	7.24	4.52	3.22	EGLN2	1.00	0.17	1.13	1.37	1.35	1.03	1.52
PTPRK	1.00	1.20	7.67	0.88	12.17	12.87	14.88	PIK3CB	1.00	1.03	0.03	0.88	1.07	1.05	1.08
TNNI3	1.00	2.90	2.20	0.77	2.09	1.77	0.83	AKT1	1.00	1.02	3.95	0.30	3.92	1.03	2.13
AKAP14	1.00	4.78	1.59	1.14	4.40	1.75	1.17	ARNT	1.00	1.08	0.93	1.80	0.18	2.18	0.82
PHKG2	1.00	3.29	1.23	0.83	1.09	1.67	1.63	e. HER-2 signaling							
CLIC6	1.00	0.38	0.31	0.05	0.07	0.10	0.46	GSK3A	1.00	0.07	0.07	0.95	1.06	0.28	0.04
MYL3	1.00	0.07	0.46	0.05	0.38	0.69	0.64	PRKCI	1.00	0.54	0.39	0.56	0.10	0.03	0.39
GSK3A	1.00	0.07	0.07	0.95	1.06	0.28	0.04	AKT1	1.00	1.02	3.95	0.30	3.92	1.03	2.13
PPP1R10	1.00	0.29	0.94	0.06	1.08	0.07	1.04	f. AMPK Signaling							
CACNA1A	1.00	1.62	0.86	0.53	0.49	1.01	0.08	GNB1	1.00	53.58	54.12	77.81	94.94	919.51	991.02
PTPN9	1.00	0.37	1.00	0.77	0.75	0.96	0.73	PIK3R4	1.00	20.29	32.04	2.10	27.49	22.85	34.79
MYL2	1.00	1.15	0.11	0.90	0.60	0.71	0.79	CRAT	1.00	8.98	7.91	7.78	7.59	3.09	0.81
PHKB	1.00	1.08	1.01	0.33	1.03	0.76	0.52	INSR	1.00	15.47	1.23	15.33	13.88	15.46	15.79
ANAPC5	1.00	1.36	0.69	0.10	1.05	0.57	0.91	PDPK1	1.00	1.23	2.02	2.14	0.87	2.10	0.81
PPP1R14A	1.00	0.94	1.09	1.11	0.04	0.97	1.09	PIK3R1	1.00	1.77	1.08	0.61	0.58	2.15	1.69
PTPN6	1.00	0.76	1.19	1.24	0.03	1.15	1.14	CHRNA4	1.00	1.13	1.06	1.13	1.13	0.05	0.05
RYR3	1.00	93.07	6.78	3.54	5.76	82.23	0.22	PIK3CB	1.00	1.03	0.03	0.88	1.07	1.05	1.08
PRKACA	1.00	7.58	0.41	7.59	3.04	2.92	2.33	PRKACA	1.00	7.58	0.41	7.59	3.04	2.92	2.33
PPP1R7	1.00	12.29	12.12	11.88	11.40	0.32	1.12	TFRC	1.00	6.42	0.50	6.55	6.55	3.73	1.76
SIRPA	1.00	13.15	0.12	8.01	13.59	0.39	11.35	GNA13	1.00	4.95	0.28	0.32	7.11	0.48	7.17
GNA13	1.00	4.95	0.28	0.32	7.11	0.48	7.17	AKT1	1.00	1.02	3.95	0.30	3.92	1.03	2.13
b. PPAR Signaling								c. p53 Signaling							
BMP15	1.00	36.70	46.90	57.66	32.92	11.49	12.42	PSMD2	1.00	536.75	553.64	555.59	15.97	35.90	487.43
GFER	1.00	24.37	5.10	556.00	37.29	560.26	553.54	PSMA1	1.00	213.96	202.78	204.83	212.72	214.45	214.03
PIK3R4	1.00	20.29	32.04	2.10	27.49	22.85	34.79	BMP15	1.00	36.70	46.90	57.66	32.92	11.49	12.42
IL1RAP	1.00	2.97	18.62	20.26	20.72	4.56	79.78	GFER	1.00	24.37	5.10	556.00	37.29	560.26	553.54
INSR	1.00	15.47	1.23	15.33	13.88	15.46	15.79	PIK3R4	1.00	20.29	32.04	2.10	27.49	22.85	34.79
PIK3R1	1.00	1.77	1.08	0.61	0.58	2.15	1.69	CASP6	1.00	4.73	6.30	6.52	5.73	5.54	6.17
SRA1	1.00	0.11	0.22	0.23	0.15	0.10	0.12	PSMB8	1.00	19.18	18.93	18.69	18.75	1.80	18.22
IL6	1.00	0.96	0.98	0.04	1.08	0.06	0.04	PIK3R1	1.00	1.77	1.08	0.61	0.58	2.15	1.69
MED1	1.00	1.15	1.12	0.04	1.17	0.05	1.18	PSMD3	1.00	0.03	0.05	0.08	0.06	0.51	0.10
PIK3CB	1.00	1.03	0.03	0.88	1.07	1.05	1.08	PSMC5	1.00	0.05	1.00	0.01	1.03	0.07	0.03
ITGA9	1.00	0.55	0.07	0.89	0.90	0.98	0.71	CDK4	1.00	0.06	0.86	0.94	0.83	1.06	1.09
PRKACA	1.00	7.58	0.41	7.59	3.04	2.92	2.33	BRCA1	1.00	0.62	0.13	0.63	1.87	0.76	1.30
GMFG	1.00	0.11	3.46	3.33	3.46	1.64	3.56	PIK3CB	1.00	1.03	0.03	0.88	1.07	1.05	1.08
IL1RN	1.00	12.05	0.60	11.73	1.21	0.33	6.19	IL6	1.00	0.96	0.98	0.04	1.08	0.06	0.04
AKT1	1.00	1.02	3.95	0.30	3.92	1.03	2.13	PIDD	1.00	1.03	0.94	0.79	0.40	0.92	0.05
NCOR1	1.00	0.94	0.14	1.84	1.84	1.94	2.12								

* The red bottom represent up-regulated (>2 fold) proteins, green bottom represent down-regulated (<0.5 fold) proteins