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## Supplementary files

## Tissue metabolomics study to reveal the toxicity of a Traditional Tibetan

## medicines 'Renqing Changjue' in rat

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Fig. S1. Histopathological examination of control and HD group liver and kidney tissues by H&E staining  $(10 \times)$ .



Fig. S2.Standard two-dimensional (2D) NMR spectra of liver, kidney and spleen

Parameters: For COSY and HSQC, 64 transients per increment and 128 increments were collected in the indirect dimension. A SINE function with 2048 and 1024 digital points was used for processing. Exponential multiplications of 0.20 and 0.30 Hz in the direct and indirect dimension were used, respectively. HSQC was processed using the SINE function. Exponential multiplications of 0.20 and 0.30 Hz in the direct and indirect dimension were used, respectively. In addition, a Gaussian multiplication of 0.1 Hz in the indirect dimension was applied for the HSQC. Two dimensional J-resolved spectra were also recorded to aid the assignments of the metabolites. The pulse sequence is of the form -RD-90-t1-180-t1-ACQ. The RD was 2 s, and the number of scans was 1 for all experiments.



**Fig. S3.** Representative PLS-DA score plots (t1 vs. t2) derived from the 1H NMR data of liver extract (A and B), kidney extract (C and D), and spleen extract (E and F) from control and dosed groups at day 15 and day 30



**Fig. S4.** OPLS-DA scores plots (A, C, E and G) and coefficient loading plots (B, D, F and H) derived from 1H NMR spectra of liver from LD/ NC and MD/ NC group at day 15 and day 30.



**Fig. S5.** OPLS-DA scores plots (A, C, E and G) and coefficient loading plots (B, D, F and H) derived from 1H NMR spectra of kidney from LD/ NC and MD/ NC group at day 15 and day 30.



**Fig. S6.** OPLS-DA scores plots (A, C, E and G) and coefficient loading plots (B, D, F and H) derived from 1H NMR spectra of spleen from LD/ NC and MD/ NC group at day 15 and day 30.

	Biochemical indices	HD group	MD group	LD group	NC group
	AST (IU/L)	224.28±35.0	190.6±56.91	136.8±14.1	152.9±52.3
2	ALT (IU/L)	61.33±8.33	56.67±10.0	52.06±2.82*	54.85±10.7
ay 1	ALP (IU/L)	327.3±73.1*	293.2±28.5*	323.6±29.6	347.8±15.28
D	BUN (mmol/L)	7.717±1.28*	$7.933 \pm 0.42^{*}$	6.880±1.18	9.432±1.54
	CHE (IU/L)	28.45±9.12	26.35±6.11	19.34±1.38*	28.67±15.28
	AST (IU/L)	203.0±58.2	196.3±48.67	177.4±41.4	193.6±43.0
0	ALT (IU/L)	60.13±10.3	48.62±4.13*	57.22±3.98	57.18±9.16
Day 3	ALP(IU/L)	265.6±34.1	259.7±33.0	252.7±47.8	268.3±84.03
	BUN (mmol/L)	$8.935 \pm 0.87$	7.517±0.95	9.020±1.40	9.395±0.44
	CHE (IU/L)	28.47±4.06	31.15±5.68	32.86±4.86	33.67±4.08

Table S1. The level of serum biochemical indices of RQCJ successive administration  $(x \pm s)$ .

Note:\* compared with control group, p<0.05

Pathway Name	Total	Hits	Raw p	=-LOG(p)	Holm P	FDR	Impact
D-Glutamine and D-	5	2	0.000363	7 0214	0.020022	0.012544	1
glutamate metabolism	5	2	0.000303	7.9214	0.029033	0.015544	1
Phenylalanine, tyrosine							
and tryptophan	4	1	0.025458	3.6707	1	0.34369	0.5
biosynthesis							
Alanine, aspartate and	24	2	0.0004	16671	0 72270	0 15229	0 40029
glutamate metabolism	24		0.0094	4.0071	0.72378	0.13228	0.40928
Phenylalanine metabolism	9	1	0.05647	2.874	1	0.50823	0.40741
Histidine metabolism	15	2	0.003685	5.6034	0.28745	0.074627	0.24194
Nicotinate and	12	1	0.000645	2 5177	1	0 65222	0 2291
nicotinamide metabolism	15		0.080045	2.31//		0.03322	0.2381
Glyoxylate and	16	1	0.009412	2 2 1 9 6	1	0 72441	0 11111
dicarboxylate metabolism	16	1	0.098413	2.3180	1	0./2441	0.11111

Table S2. Results from Pathway Analysis with MetPA from liver.

Total is the total number of compounds in the pathway; the hits is the actually matched number from the user uploaded data; the raw p is the original p value calculated from the enrichment analysis; the impact is the pathway impact value calculated from pathway topology analysis.

Pathway Name	Total	Hits	Raw p	=-LOG(p)	Holm P	FDR	Impact
Phenylalanine, tyrosine							
and tryptophan	4	2	0.000472	7.6595	0.037252	0.012732	1
biosynthesis							
D-Glutamine and D-	5	1	0.045574	2 0884	1	0 24068	1
glutamate metabolism	5	1	0.045574	5.0004	1	0.24908	1
Valine, leucine and	11	2	0.004167	5 1906	0 2125	0.049214	0 66666
isoleucine biosynthesis	11	2	0.00410/	3.4800	0.3125	0.048214	0.00000
Alanine, aspartate and	24	1	4 27E 05	10.061	0.003/10	0.001731	0 45253
glutamate metabolism	24	4	4.27E-03	10.001	0.003419	0.001/31	0.75255
Taurine and hypotaurine	Q	1	0.071001	2 6212	1	0 22206	0 12857
metabolism	0	1	0.071991	2.0312	1	0.32390	0.42037
Phenylalanine metabolism	9	2	0.002756	5.894	0.21221	0.037206	0.40741
Glycine, serine and	22	2	0.002647	5 02 42	0 20648	0.027206	0 20107
threonine metabolism	52	3	0.002047	5.9542	0.20048	0.037200	0.29197
Tyrosine metabolism	42	1	0.32775	1.1155	1	1	0.14045
Arginine and proline	11	2	0.006624	5 0171	0.40019	0.067069	0 10545
metabolism	44	3	0.000024	3.01/1	0.49018	0.00/008	0.10343

Table S3. Results from Pathway Analysis with MetPA from kidney.

Total is the total number of compounds in the pathway; the hits is the actually matched number from the user uploaded data; the raw p is the original p value calculated from the enrichment analysis; the impact is the pathway impact value calculated from pathway topology analysis.

Pathway Name	Total	Hits	Raw p	=-LOG(p)	Holm P	FDR	Impact
Phenylalanine, tyrosine							
and tryptophan	4	2	0.000723	7.2316	0.057147	0.019531	1
biosynthesis							
D-Glutamine and D-	5	1	0.055852	2 8851	1	0 41127	1
glutamate metabolism	5	1	0.055852	2.0031	1	0.41127	1
Valine, leucine and	11	2	0.006228	5 0628	0.48004	0.08543	0 66666
isoleucine biosynthesis	11	2	0.000328	5.0028	0.46094	0.06545	0.00000
Alanine, aspartate and	24	1	0.000105	0 1608	0.008406	0.004256	0 45560
glutamate metabolism	24	4	0.000105	9.1008	0.008400	0.004230	0.+3309
Taurine and hypotaurine	Q	1	0.087045	2 /21	1	0 40822	0 12857
metabolism	0	1	0.087943	2.431	1	0.49822	0.42637
Phenylalanine metabolism	9	2	0.004198	5.4732	0.32322	0.068003	0.40741
Tryptophan metabolism	41	1	0.37965	0.96849	1	1	0.15684
Tyrosine metabolism	42	2	0.080649	2.5176	1	0.49822	0.14045
Glyoxylate and	16	1	0 1696	1 7900	1	0 75960	0 11111
dicarboxylate metabolism	sm		0.1080	1.7802	1	0./3809	0.11111
Arginine and proline	11	1	0.001169	67504	0.001114	0 022655	0 105 45
metabolism	44	4	0.001108	0.7324	0.091114	0.023033	0.10343

Table S4. Results from Pathway Analysis with MetPA from spleen.

Total is the total number of compounds in the pathway; the hits is the actually matched number from the user uploaded data; the raw p is the original p value calculated from the enrichment analysis; the impact is the pathway impact value calculated from pathway topology analysis.

sample	time points	Element	Control group	Low dosed group	Medium dosed group	High dosed group
Liver	15 day	As	$0.593 \pm 0.05$	1.816±0.21*	$3.696 \pm 0.50^*$	9.963±1.53*
		Hg	0.658±0.19	1.749±0.21*	4.039±1.09*	$9.891{\pm}1.52^*$
	30 day	As	0.970±0.14	1.923±0.29	4.099±0.41*	8.938±1.48
		Hg	$0.332 \pm 0.05$	0.451±0.11	0.632±0.27*	$0.839 \pm 0.56*$
Kidney	15 day	As	$1.208 \pm 0.28$	$2.942{\pm}0.14^*$	$6.862 \pm 0.62^*$	19.75±5.67*
		Hg	0.159±0.03	2.173±0.38*	3.909±1.28*	$8.840{\pm}1.79^*$
	30 day	As	1.397±0.35	$2.982{\pm}0.58^{*}$	6.711±0.54*	$16.04 \pm 2.60^{*}$
		Hg	$0.105 \pm 0.04$	2.553±0.71*	4.463±0.88*	$6.266 \pm 0.95^*$
Spleen	15 day	As	5.037±1.21	13.90±3.75*	28.46±4.04*	58.13±16.17*
	15 day	Hg	Non-Detected	Non-Detected	Non-Detected	Non-Detected
	30 day	As	5.307±1.38	13.52±2.83*	33.29±8.06*	77.59±15.36*
		Hg	Non-Detected	Non-Detected	Non-Detected	Non-Detected

Table S5. Concentrations of As and Hg in control and dosed-group tissues sample.

Data were presented as mean±SD of n=8 animals per groups. Statistical analysis was performed by one-way ANOVA followed by Dunnett's test.

\* P<0.05 versus control group. \* \*P<0.01 versus control group.