IDENTIFICATION OF NOVEL TOXICITY-ASSOCIATED METABOLITES BY METABOLOMICS AND MASS ISOTOPOMER ANALYSIS OF ACETAMINOPHEN METABOLISM IN WILD-TYPE AND CYP2E1-NULL MICE Chi Chen¹, Kristopher W. Krausz¹, Jeffrey R. Idle², Frank J. Gonzalez¹

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Supplemental Tables and Figures

Supplemental Table 1. Comparison of major APAP metabolites in the serum of wild-type (Cyp2e1+/+) and Cyp2e1-null (Cyp2e1-/-) mice. Data were processed by MarkerLynx software. Relative abundances of APAP and its metabolites (mean ± SD in parts per ten thousand) were determined by normalizing the single ion counts (SIC) of each metabolite *versus* the total ion counts (TIC) of each serum sample (n=4, * for P < 0.05, ** for P < 0.01, ND for not detected).

Metabolites	1 h		2 h		4 h	
	<i>Cyp2e1+/+</i>	Cyp2e1-/-	<i>Cyp2e1+/+</i>	Cyp2e1-/-	<i>Cyp2e1+/+</i>	Cyp2e1-/-
APAP (I)	224.12±44.11	228.54 ±8.12	114.00 ±5.19	111.37±7.43	22.51±8.62**	1.75±3.14 ^{**}
Cys-APAP (II)	6.83±2.19	7.19±1.32	$8.09{\pm}0.58^{*}$	5.26±1.65*	2.82±1.21 [*]	$0.55 \pm 0.89^{*}$
NAC-APAP (III)	15.42±3.97	14.93±3.26	8.17±0.77	10.24±2.47	2.66±1.89	1.62±1.50
APAP-G (IV)	10.81±1.56	11.55±2.15	7.47±0.36	8.23±0.93	0.97±0.66	0.18±0.35
APAP-S (V)	5.91±1.29	6.48±0.59	4.59±0.93*	6.81±1.11 [*]	2.72±0.96**	ND
GS-APAP	12.57±2.11	13.46±9.56	44.37±5.58 [*]	21.11±15.50 [*]	12.50±5.76 ^{**}	ND

SUPPLEMENTAL FIGURE LEGENDS

Supplemental Figure 1. Influence of APAP treatment on the GSSG level in liver and GSH level in mitochondria of wild-type and *Cyp2e1*-null mice. Liver samples collected at 0, 1, 2, 4, 24 h after i.p. administration of 400 mg/kg APAP were processed as described in the *Experimental procedures* (n=4, * for P < 0.05 and ** for P < 0.01). Both oxidized and reduced glutathione levels were determined by LC-MS analysis, and normalized by liver weight. *A*. GSSG level in the liver of wild-type and *Cyp2e1*-null mice. *B*. Relative GSH level in the liver mitochondria of wildtype and *Cyp2e1*-null mice. Determined mitochondrial GSH level in control wild-type mice was arbitrarily set as 100%.

Supplemental Figure 2. 3-D scores plot of a PCA model on 24-h urine samples from control and APAP-treated wild-type and *Cyp2e1*-null mice. A three-component PCA model was constructed to characterize the relationship among 6 mouse groups (8 mice/group), including wild-type mice (control, 200 mg/kg APAP, 400 mg/kg APAP) and *Cyp2e1*-null mice (control, 200 mg/kg APAP, 400 mg/kg APAP). The t[1], t[2] and t[3] values represent the scores of each sample in principal component 1, 2 and 3, respectively.

Supplemental Figure 3. *A*. MS^2 fragmentation of APAP (I). *B*. MS^2 fragmentation of Cys-APAP (II). *C*. MS^2 fragmentation of NAC-APAP (III). *D*. MS^2 fragmentation of APAP-G (IV). Major fragment ions were interpreted in the inlaid structural diagrams.

Supplemental Figure 4. MS^2 fragmentation of *N*-acetylamino-1,4-benzothiazine formed by HRP-catalyzed reaction between Cys-APAP and H₂O₂.

Supplemental Figure 1





 \blacktriangle WT_Control \blacktriangle KO_Control \bigstar WT_200 \bigstar KO_200 \bigstar WT_400 \bigstar KO_400

Supplemental Figure 3





Supplemental Figure 4

