

## ***Supplementary Information***

A targeted *in vivo* SILAC approach for quantification of drug metabolism enzymes; regulation by the constitutive androstane receptor

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### Supplementary Tables

**Supplementary Table S-1:** Peptides/proteins identified in 13C6 liver lysate following in-gel digestion protocol. Data were exported from PEAKS (FDR = 0.1%,  $-10\text{LogP} = 17.3$ ).

**Supplementary Table S-2:** Peptides/proteins identified in 13C6 liver lysate following FASP protocol. Data were exported from PEAKS (FDR = 0.1%,  $-10\text{LogP} = 22.9$ ).

**Supplementary Table S-3:** Summary of DME identified by in-gel digestion versus FASP derived from Supplementary Table S-1 and 2.

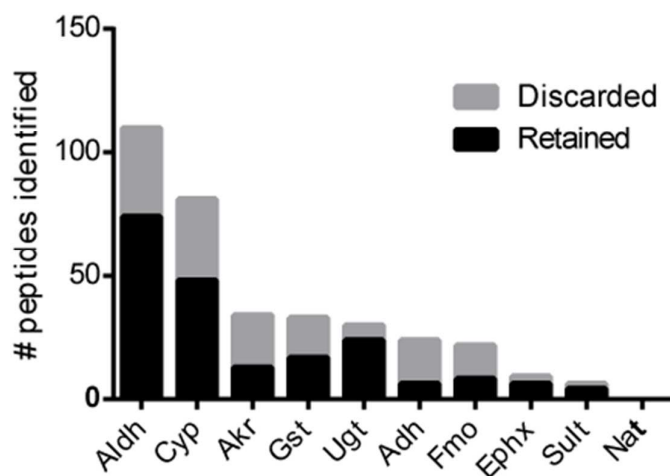
**Supplementary Table S-4:** Analysis of linearity of drug metabolism enzyme DME region 1 peptides (output from SIEVE). Integrated peak areas calculated by SIEVE are presented in columns Q-V, with two technical replicates for each of the four heavy: light sample input

ratios. Ratios of K0: K6 signals were then calculated, and values are shown in columns X-AC. Technical replicate ratios were averaged (columns AE-AG),  $\log_4$ -transformed (columns AI-AK) and  $R^2$  values calculated (column AM).

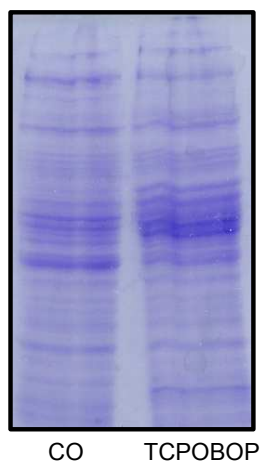
**Supplementary Table S-5:** Analysis of linearity of drug metabolism enzyme DME region 2 peptides (output from SIEVE). Integrated peak areas calculated by SIEVE are presented in columns Q-V, with two technical replicates for each of the four heavy: light sample input ratios. Ratios of K0: K6 signals were then calculated, and values are shown in columns X-AC. Technical replicate ratios were averaged (columns AE-AG),  $\log_4$ -transformed (columns AI-AK) and  $R^2$  values calculated (column AM).

**Supplementary Table S-6:** DME region 1 seed file

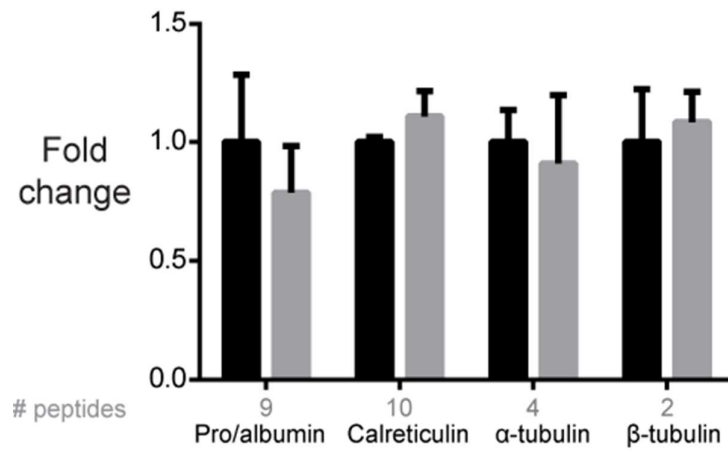
**Supplementary Table S-7:** DME region 2 seed file



**Supplementary Figure 1.** Distribution of the number of peptides in each DME protein retained or discarded after linearity filtering. Filtering of peptides was based on linearity of signal across heavy: light sample input ratios. Of the unique, lysine-containing peptides identified, approximately 57% demonstrated satisfactory linearity.



**Supplementary Figure 2.** Coomassie Brilliant Blue R-250 staining to confirm equality of microsomal protein sample loading on SDS-PAGE gels.



**Supplementary Figure 3.** Effect of TCPOBOP treatment to the expression of four proteins

(albumin, calreticulin,  $\alpha$ -tubulin and  $\beta$ -tubulin) in liver.

tHR/SIM-*in vivo* SILAC analysis of modulation of control protein/protein groups by

TCPOBOP. Black bars: corn oil, grey bars: TCPOBOP.

## Description of data deposited in ProteomeExchange.

Table / Figure / File	File name	File type
Supplementary Table S-1	DME region 1 replicate 1	RAW
	DME region 1 replicate 2	RAW
	DME region 2 replicate 1	RAW
	DME region 2 replicate 2	RAW
	In gel digest DME regions 1 and 2 combined PEAKS file	RESULT
Supplementary Table S-2	FASP replicate 1	RAW
	FASP replicate 2	RAW
	FASP replicate 3	RAW
	FASP replicate 4	RAW
	FASP PEAKS file	RESULT
Supplementary Table S-4	DME region 1, Heavy:light 1:1 replicate 1	RAW
	DME region 1, Heavy:light 1:1 replicate 2	RAW
	DME region 1, Heavy:light 1:0.25 replicate 1	RAW
	DME region 1, Heavy:light 1:0.25 replicate 2	RAW
	DME region 1, Heavy:light 1:0.0625 replicate 1	RAW
	DME region 1, Heavy:light 1:0.0625 replicate 2	RAW
	DME region 1 linearity SIEVE file	OTHER
Supplementary Table S-5	DME region 2, Heavy:light 1:1 replicate 1	RAW
	DME region 2, Heavy:light 1:1 replicate 2	RAW
	DME region 2, Heavy:light 1:0.25 replicate 1	RAW
	DME region 2, Heavy:light 1:0.25 replicate 2	RAW
	DME region 2, Heavy:light 1:0.0625 replicate 1	RAW
	DME region 2, Heavy:light 1:0.0625 replicate 2	RAW
	DME region 2 linearity SIEVE file	OTHER
Figure 3	DME region 1, corn oil 1 replicate 1	RAW
	DME region 1, corn oil 1 replicate 2	RAW
	DME region 1, corn oil 2 replicate 1	RAW
	DME region 1, corn oil 2 replicate 2	RAW
	DME region 1, corn oil 3 replicate 1	RAW
	DME region 1, corn oil 3 replicate 2	RAW
	DME region 1, TCPOBOP 1 replicate 1	RAW
	DME region 1, TCPOBOP 1 replicate 2	RAW
	DME region 1, TCPOBOP 2 replicate 1	RAW
	DME region 1, TCPOBOP 2 replicate 2	RAW
	DME region 1, TCPOBOP 3 replicate 1	RAW
	DME region 1, TCPOBOP 3 replicate 2	RAW
	DME region 2, corn oil 1 replicate 1	RAW
	DME region 2, corn oil 1 replicate 2	RAW
	DME region 2, corn oil 2 replicate 1	RAW
	DME region 2, corn oil 2 replicate 2	RAW
	DME region 2, corn oil 3 replicate 1	RAW
	DME region 2, corn oil 3 replicate 2	RAW
	DME region 2, TCPOBOP 1 replicate 1	RAW
	DME region 2, TCPOBOP 1 replicate 2	RAW
	DME region 2, TCPOBOP 2 replicate 1	RAW
	DME region 2, TCPOBOP 2 replicate 2	RAW
	DME region 2, TCPOBOP 3 replicate 1	RAW
	DME region 2, TCPOBOP 3 replicate 2	RAW
	DME region 1 corn oil versus TCPOBOP SIEVE file	OTHER
	DME region 2 corn oil versus TCPOBOP SIEVE file	OTHER
Supplementary File S-1	LTQ-Orbitrap_method file	OTHER
Supplementary File S-2	positive tune file_fibrinogen	OTHER