Table S1. Primers used for qRT-PCR analysis.

bcrp	Forward	5' -TTGGACTCAAGCACAGCAAAT-3'
	Reverse	5' -ATGGAATACCGAGGCTGGTGA-3'
cyp3a2	Forward	5' -GATTCTAAGCATAAGCACCGAGT-3'
	Reverse	5' -ACAGGGCTTTATGAGACACTTCGTCTT-3'
gapdh	Forward	5' -GCTCTCTGCTCCTCCCTGTTC-3'
	Reverse	5' -GAGGCTGGCACTGCACAA-3'
il-6	Forward	5' -GATGGATGCTTCCAAACTGGATAT-3'
	Reverse	5' -TCCAGAAGACCAGAGCAGATTTT-3'
mdr1a	Forward	5' -GCAGGTTGGCTGGACAGATT-3'
	Reverse	5' -GGAGCGCAATTCCATGGATA-3'
mdr1b	Forward	5' -AAACATGGCACGTAACCAAAGTT-3'
	Reverse	5' -AAAATGTGGCCCTGTTTAATGATT-3'
oatp2b1	Forward	5' -TGCCGCTCTTCTTCATTGG-3'
	Reverse	5' -GGGCACCCAGGTCTTGTG-3'
tnf-α	Forward	5' -GGTCCCAACAAGGAGGAGAAGT-3'
	Reverse	5' -TGGGCCATGGAACTGATGA-3'

Table S2. Maternal and Fetal Parameters

	GD17		GD18	
	CT	PE	CT	PE
Maternal Weight (g)	291±45	291±33	327±22	328±20
Number of Fetuses	11±1	11±1.5	11.5±1.5	11.5±1
Fetal Weight (g)	0.443±0.176	0.419±0.163	1.036±0.038	1.018±0.049
Placental Weight (g)	0.305±0.082	0.296±0.075	0.429±0.028	0.431±0.027

Table S3. Excel spreadsheet of all differentially expressed proteins in the PE rat model, ordered by percent fold-change.

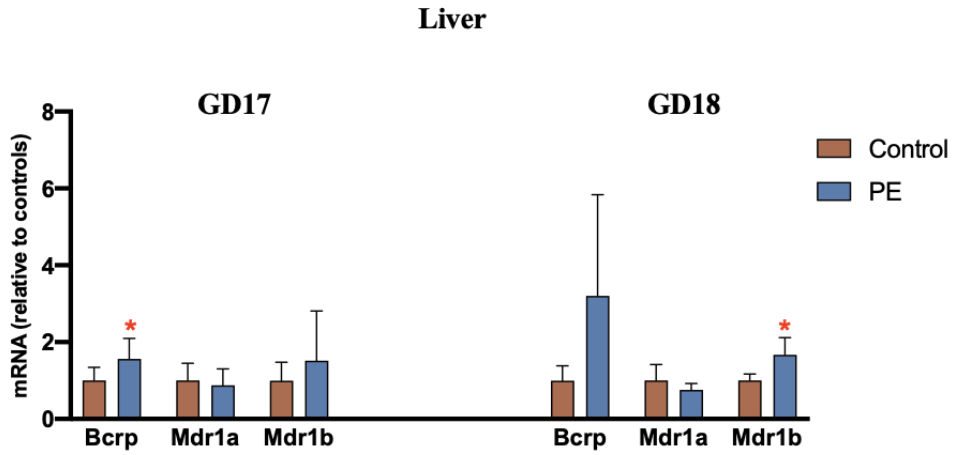

Figure S1. Impact of PE on mRNA levels in maternal liver. Relative mRNA levels was measured in maternal liver from PE or control dams on GD17 and GD18. Levels were measured by qRT-PCR, normalized to GAPDH, and are presented as mean ± S.D. relative to saline controls (n=7-8 per group). Significance was determined using Student's unpaired t test (*p < 0.05, **p<0.01, ***p<0.001).

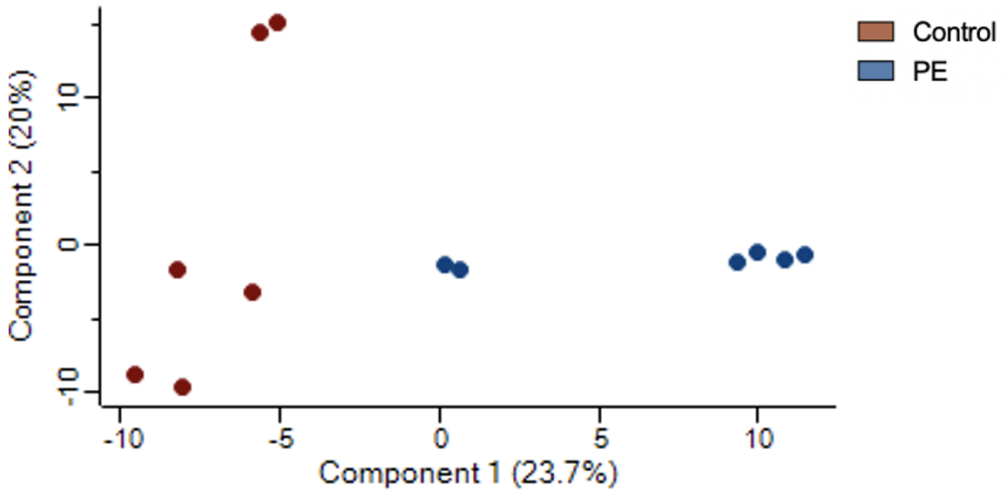

Figure S2. Principal component analysis (PCA) of control and PE rats. Differential protein expression was determined by LC-MS/MS in placental samples obtained from PE or control dams on GD18. Relative clustering of Control and PE groups indicate differences between their respective proteomes (n=3, run in technical duplicates). Plot generated using Perseus software.