Table S1. Primer sequences used in the study for the relative quantification of porcine gene expression.

Gene			GenBank Accession number
P450 1A1	sense primer (*1*)	CCTTCACCATCCCTCACAGT	NM214412
	antisense primer (*1*)	CATGTCCACCTTCACACCAG	
P450 1A2	sense primer	TCGGGACTTTGACAAGAACT	NM001159614
	antisense primer	TAATTGTATCAAATCCGGCTC	
UGTs	sense primer (*1*)	GATGGGAGCCACTGGTTTAC	XM001927649
	antisense primer (*1*)	AAACATACTCATTTGCCGGG	
GSTAs	sense primer	AGAAGGTGTGGCAGATTTGG	NM001078684
	antisense primer	CATCCGCCTGCTCCTGGA	
MRP1	sense primer	CAACTGCATCGTCCTGTTTG	AF403246
	antisense primer	TCAAGTATGCGGTGATCTGC	
AhR	sense primer	TGATCCATACTGAAGACC	AY484399
	antisense primer	GGCCACTCGCTTCATCAAT	
Cyclophilin A	sense primer	TTATCCTGAAGCATACGGGTC	NM214353
	antisense primer	GCCATCCAACCACTCAGTCT	
TBP	sense primer	CAACAGTTCAGTAGTTATGAGCCA	DQ845178
	antisense primer	GCTCTGACTTTAGCACCTGTTAAT	

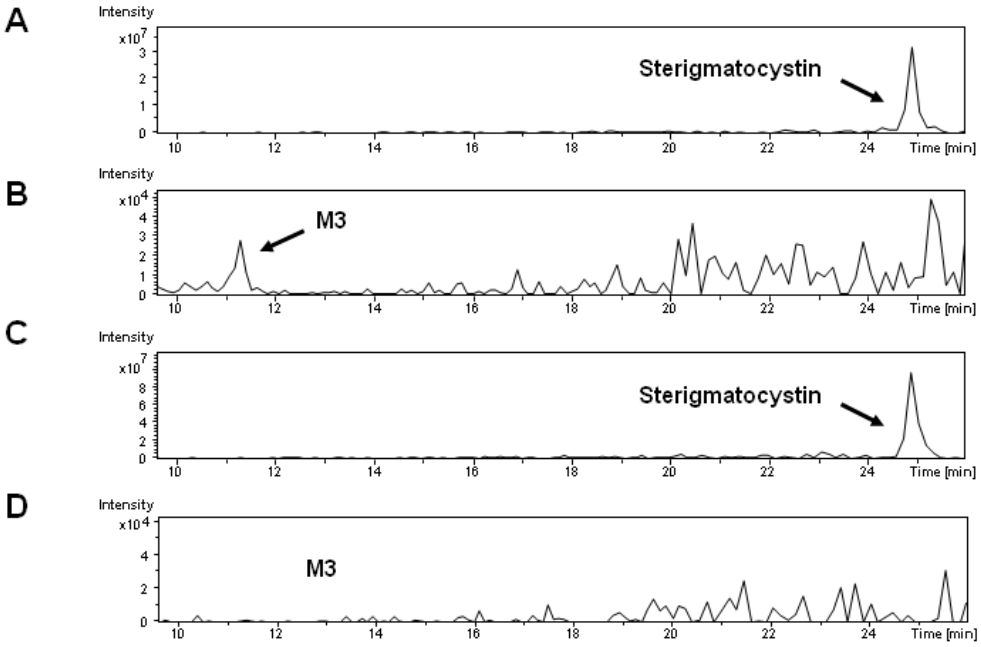

Figure 1S. Representative HPLC/MS chromatograms showing disappearance of the sterigmatocystin-glutathione adduct M3 after 30 min incubation *in vitro* in presence of 20 µM α-naphthoflavone. (A) chromatogram of the ion at *m/z* 325 in positive ionization mode (sterigmatocystin) without α-naphthoflavone, (B) *m/z* 644 in negative ionization mode (M+321, metabolite M3) without α-naphthoflavone, (C) *m/z* 325 in positive ionization mode (sterigmatocystin) in presence of α-naphthoflavone and (D) *m/z* 644 in negative ionization mode (M+321, metabolite M3) in presence of α-naphthoflavone.

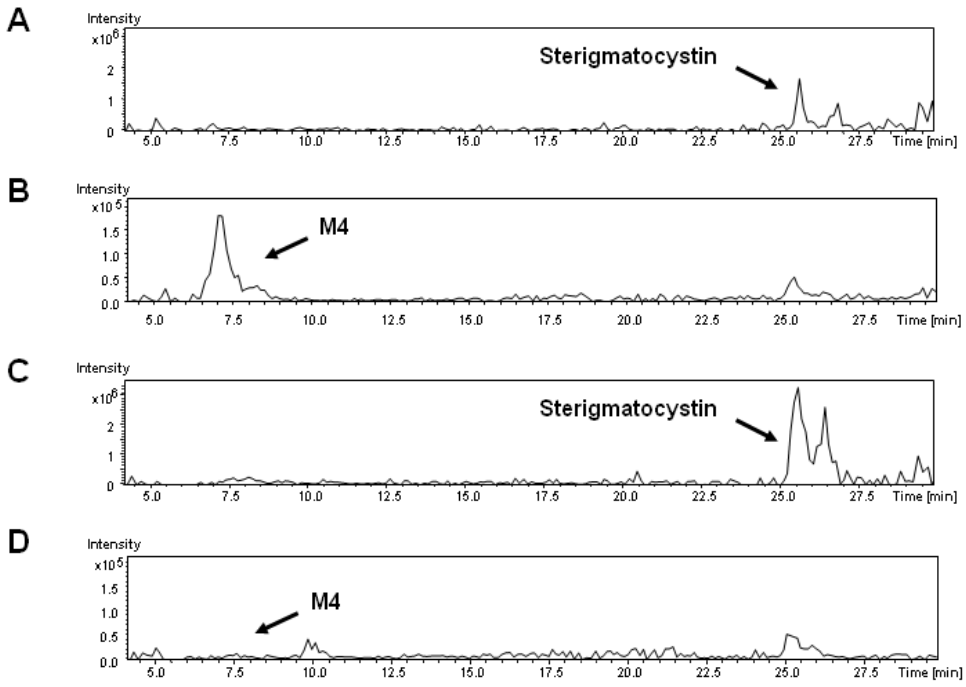

Figure 2S. Representative HPLC/MS chromatograms showing the conversion of sterigmatocystin glucuroconjugate (M4) to sterigmatocystin after digestion with β-glucuronidase. (A) chromatogram of the ion at *m/z* 325 in positive ionization mode (sterigmatocystin) without digestion, (B) *m/z* 499 in negative ionization mode (M4) without digestion, (C) chromatogram of the ion at *m/z* 325 in positive ionization mode (sterigmatocystin) after digestion with β-glucuronidase, (D) *m/z* 499 in negative ionization mode (M4) after digestion with β-glucuronidase.

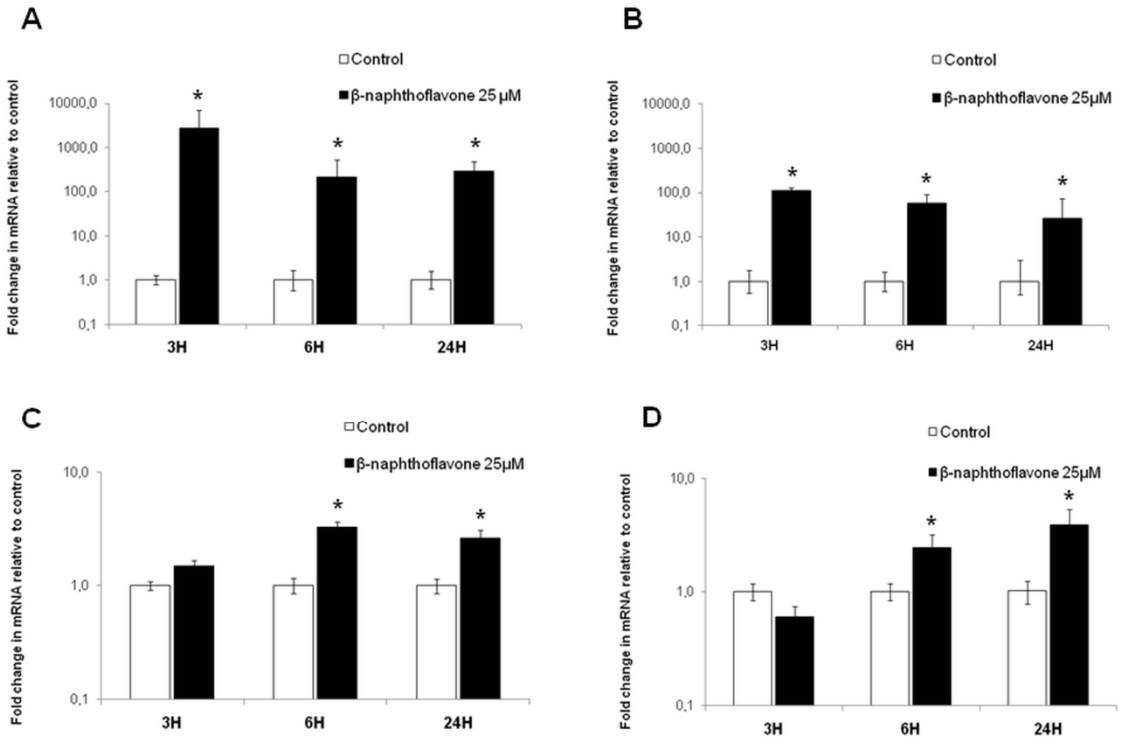

Figure 3S. Standardised mRNA expression of the genes encoding P450 1A1 (A), P450 1A2 (B), GSTAs (C), UGTs (D) after 3, 6 and 24 h exposure of PTEC to 25 µM β-naphthoflavone, calculated with the ΔΔCt method with porcine *TATA box binding protein* as the reference gene and presented according to Willems *et al*., 2008 (*2*). Significant overexpression was analysed by Wilcoxon paired *t* test. * $p < 0.05$ compared with control. Data are average (histograms) and 95% CI (error bars) after the sequential standardization steps from two separate experiments, each performed in duplicate.

References

(1) Wolf, A., Kutz, A., Plottner, S., Behm, C., Bolt, H. M., Follmann, W. and Kuhlmann, J. (2005) The effect of benzo(a)pyrene on porcine urinary bladder epithelial cells analyzed for the expression of selected genes and cellular toxicological endpoints. *Toxicology 207*, 255-269.

(2) Willems, E., Leyns, L. and Vandesompele, J. (2008) Standardization of real-time PCR gene expression data from independent biological replicates. *Anal. Biochem. 379*, 127-129.