

**Transcriptomic profiling identifies novel mechanisms of transcriptional regulation of the
cytochrome P450 (*Cyp*)*3a11* gene**

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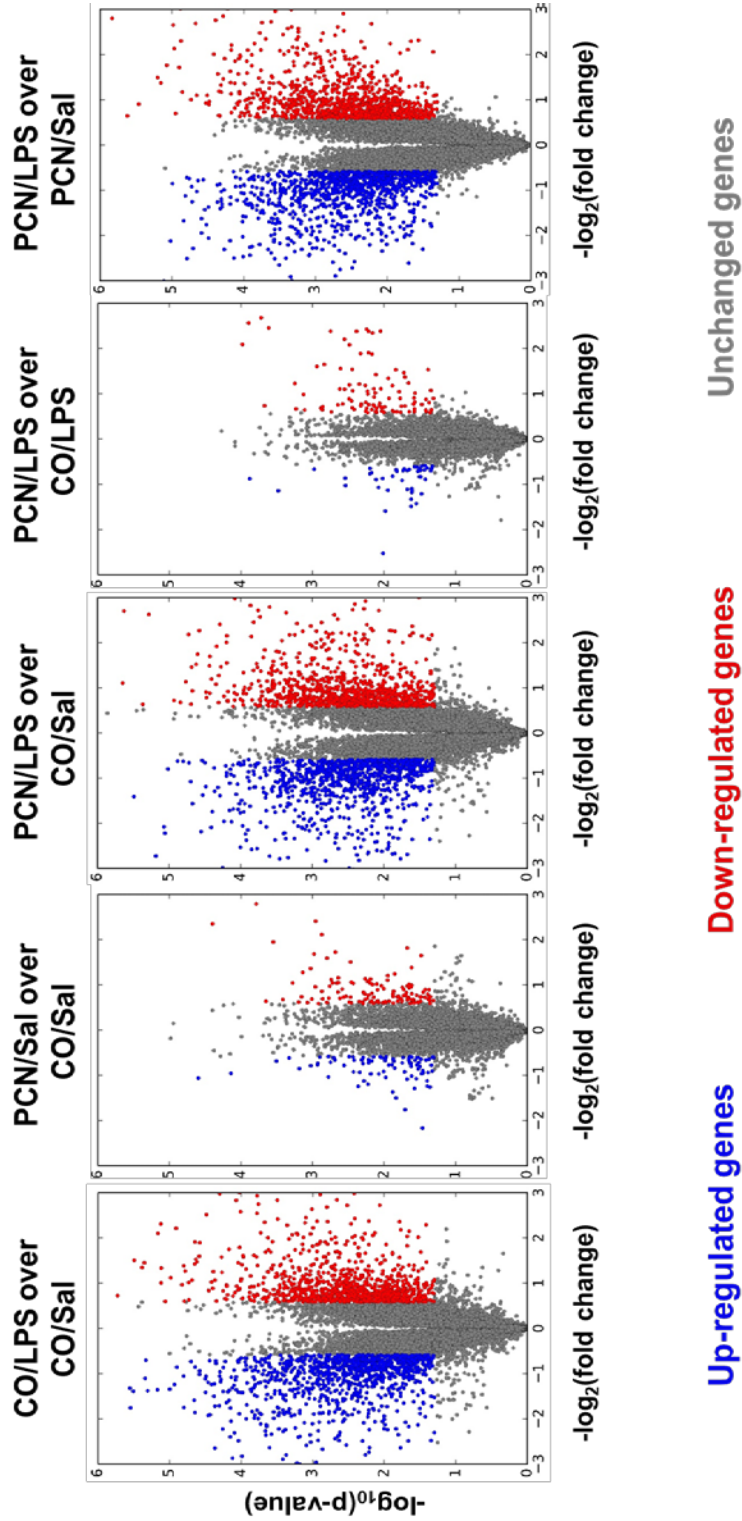
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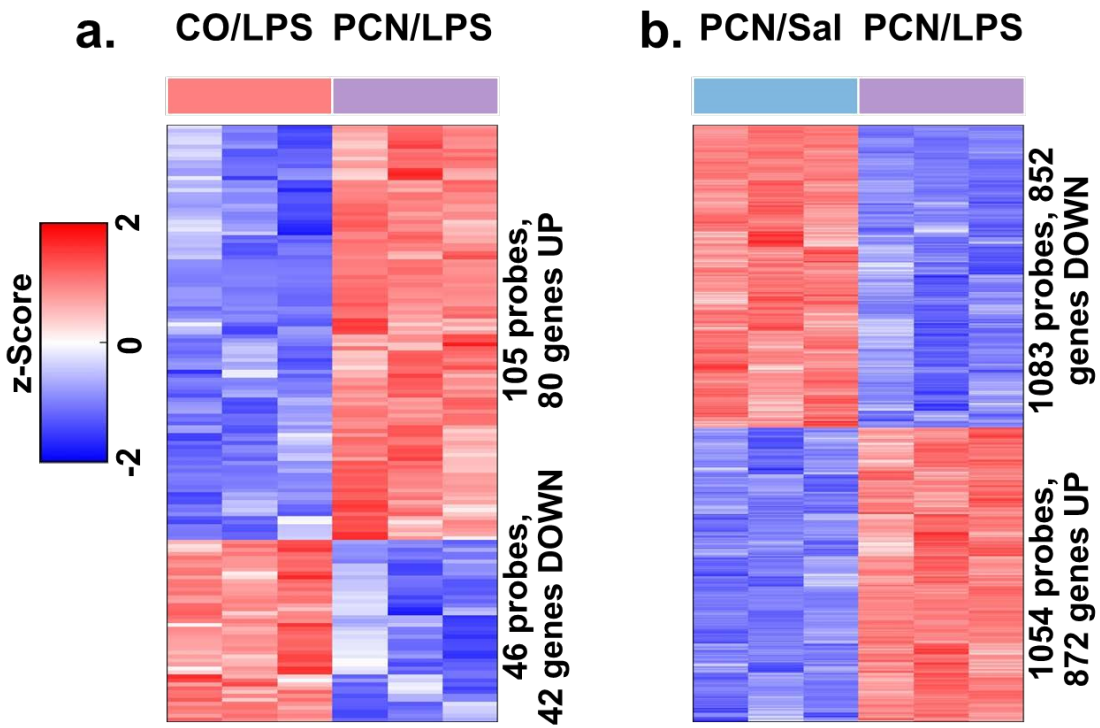
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Supplementary Figures

Supplementary Figure S1. Volcano plot showing the differentially regulated genes by PCN and LPS treatment.



Supplementary Figure S2. Heatmap showing the differentially regulated genes with the combined PCN and LPS treatment compared to A. LPS alone and B. PCN alone.



Supplementary Table S1. Fold changes in the gene expression of the top 15 genes with PCN and LPS treatment.

a. Significantly up-regulated genes ordered from highest to the lowest fold change w.r.t. PCN treatment.

Gene Symbol	Fold Change		
	PCN vs control	LPS vs control	PCN/LPS vs control
GSTM3	5.16	-1.59	1.54
CYP2C55	4.92	-1.14	1.24
CES6	3.88	-0.64	3.53
GSTA1	3.83	-2.24	
GSTA2	3.48	-2.48	
CYP3A11	2.41	-2.64	2.15
GSTM6	2.11	-2.89	-1.34
GSTM2	1.95	-1.87	
HSD17B6	1.72	-1.50	0.88
GSTM2	1.68	-1.22	0.66
CYP3A25	1.36	-2.40	0.94
GSTT3	1.13	-1.28	-0.90
EPHX1	1.12	-0.60	
GSTA4	1.20	-1.46	-0.78
INMT	1.05	-3.47	-2.24

b. Significantly down-regulated genes ordered from lowest to the highest fold change w.r.t. PCN treatment.

Gene Symbol	Fold Change		
	PCN vs control	LPS vs control	PCN/LPS vs control
SAA4	-0.92	2.68	2.26
2200001I15RIK	-0.85	1.05	0.89
LRG1	-0.74	1.45	1.50
LCAT	-0.67	0.83	0.86
LDHA	-0.64	1.15	1.12
IIGP2	-0.62	0.94	1.00
ACTB	-0.61	0.61	
IGTP	-0.59	1.05	0.98

Supplementary Table S2. Altered transcription factors predicted to have putative binding sites on the CYP3A4 promoter using TRANSFAC analysis.

PCN↓ LPS↓	PCN↑ LPS↑	PCN↓ LPS↑	PCN↑ LPS↓
SP1	NFE2	GABP	MEF2
FOXO4		CETS1P54	
MAZ		PEA3	
E12		STAT1	
FREAC2		NFKB	
NFAT		IRF	
LEF1		MYCMAX	
AP4		SP1	
MYC		AP1	
HNF3		HSF	
ETS2			
PAX4			
MYOD			
NFY			
CHX10			
ERR1			