

Supplemental Tables

SUPPLEMENTAL TABLE 1: 234 genes, found to be differentially expressed with at least fold change of 2 in at least 1 of the mouse models.

FILE: Table_S1_234genes_agilentMED-CENT_LIMMA_DE_Union_FC2-0_withAllFC_allvalues_RAWedit

SUPPLEMENTAL TABLE 2: Pathways and GO processes.

FILE: Table_S2_NetworkPathwayEnrichment_GOanalyses

SUPPLEMENTAL TABLE 3:

	GSE33561	GSE33512	GSE52509	GSE17737	GSE55127	GSE18344
PLA2G7	1.59	1.52	1.56	2.1	1.87	2.73
CYP1B1	3.18	13.07	3.28	3.07	7.95	6.66
MMP12	3.44	3.16	8.83	18.37	13.45	26.29
TREM2	1.92	1.77	3.45	2.22	4.02	2.05
GDF15	Yes	2.6	3.48	2.57	2.28	2.29
NQO1	Yes	4.03	Yes	1.88	3.78	7.44
AHRR	Yes	8.95	Yes	2.63	5.48	3.36
ATP6V0D2	Yes	1.82	Yes	3.45	2.72	3.48
ALDH3A1	Yes	3.38	Yes	Yes	4.14	6.3
ACP5	Yes	Yes	Yes	2.7	2	2.19
LCN2	3.39	Yes	3.18	5.01	4.38	6.22
CLEC5A	Yes	Yes	2.21	4.05	3.35	4.01
SPP1			3.17	2.57	4.25	2.71
NEK6	Yes	Yes	1.36	1.74	1.63	1.69
GSTA2		Yes			1.66	1.95

SUPPLEMENTAL TABLE 3: Leading edge genes belonging to the gene set regulated by cigarette smoke in both mice and humans.

Genes belonging to the leading edge but not found to be differentially expressed in pair-wise comparisons are marked with "Yes"

Genes belonging to the leading edge and found to be differentially expressed in pair-wise comparisons are marked in gray, with fold change written in white. The gray scale is correlating with the fold change value (from light gray to black). Genes not belonging to the leading edge are marked in white. There were no genes that were differentially expressed but did not belong to the leading edge.

SUPPLEMENTAL TABLE 4: Full name and function of differentially expressed genes shared between all smoke exposure systems.

FILE: Table_S4_GenesNamesFunctions