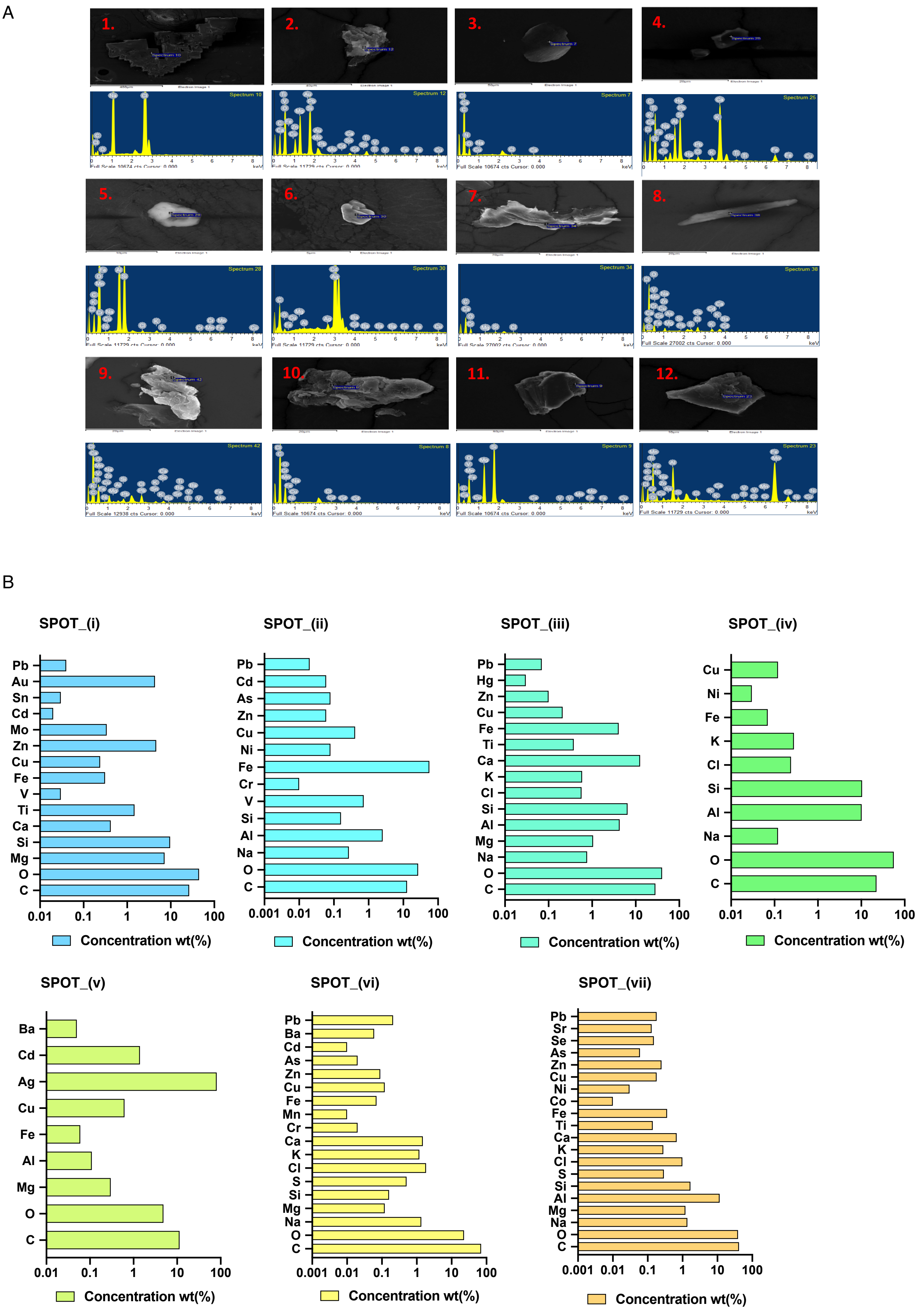
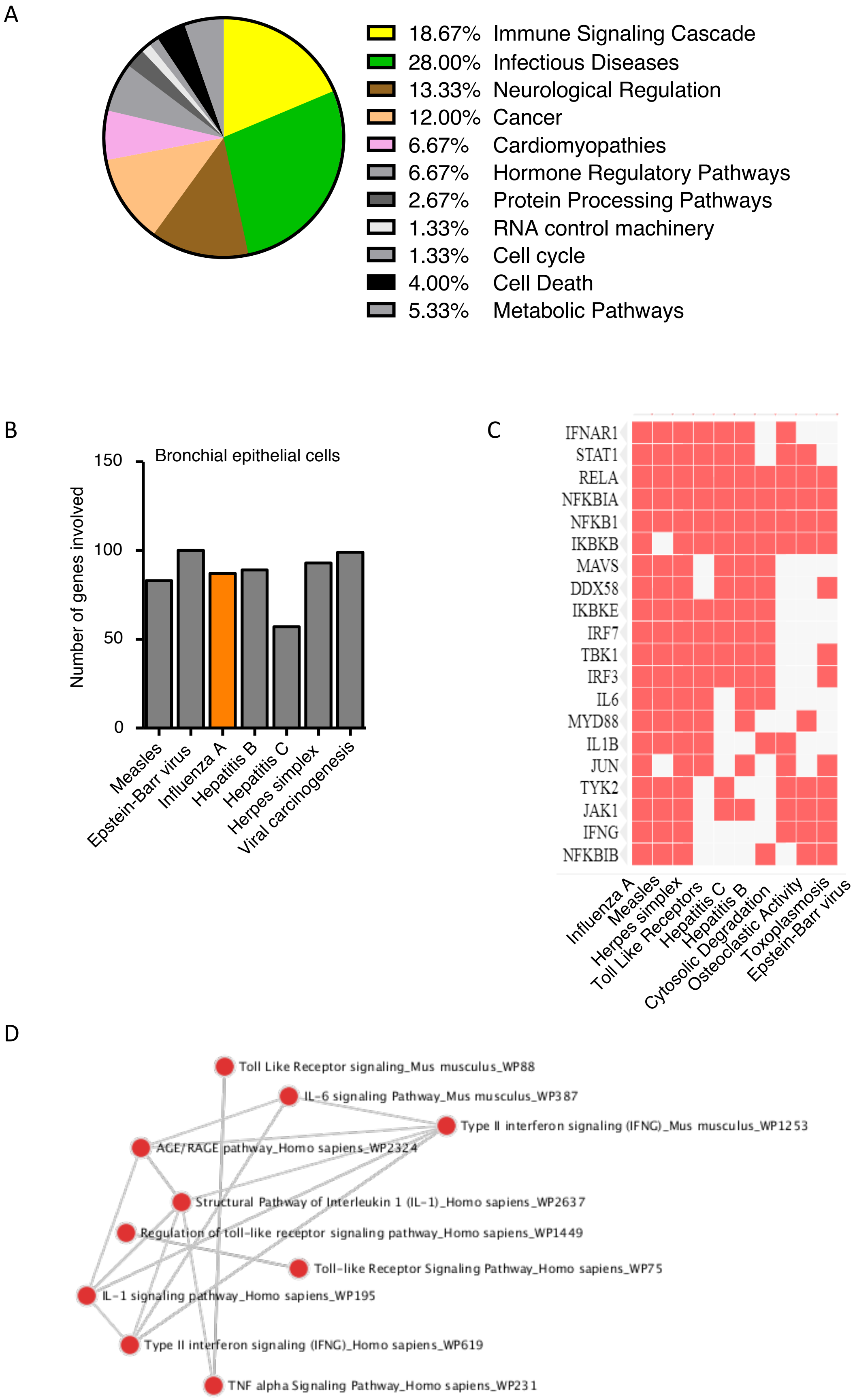
Figure S1.


A
1.
2.
3.
4.
Spectrum 10
Spectrum 12
Spectrum 7
Spectrum 25
5.
6.
7.
8.
Spectrum 28
Spectrum 30
Spectrum 34
Spectrum 38
9.
10.
11.
12.
Spectrum 42
Spectrum 8
Spectrum 9
Spectrum 23
B
SPOT_(i)
Pb
Au
Sn
Cd
Mo
Zn
Cu
Fe
V
Ti
Ca
Si
Mg
O
C
0.01
0.1
1
10
100
Concentration wt(%)
SPOT_(ii)
Pb
Cd
As
Zn
Cu
Ni
Fe
Cr
V
Si
Al
Na
O
C
0.001
0.01
0.1
1
10
100
Concentration wt(%)
SPOT_(iii)
Pb
Hg
Zn
Cu
Fe
Ti
Ca
K
Cl
Si
Al
Mg
Na
O
C
0.01
0.1
1
10
100
Concentration wt(%)
SPOT_(iv)
Cu
Ni
Fe
K
Cl
Si
Al
Na
O
C
0.01
0.1
1
10
100
Concentration wt(%)
SPOT_(v)
Ba
Cd
Ag
Cu
Fe
Al
Mg
O
C
0.01
0.1
1
10
100
Concentration wt(%)
SPOT_(vi)
Pb
Ba
Cd
As
Zn
Cu
Fe
Mn
Cr
Ca
K
Cl
S
Si
Mg
Na
O
C
0.001
0.01
0.1
1
10
100
Concentration wt(%)
SPOT_(vii)
Pb
Sr
Se
As
Zn
Cu
Ni
Co
Fe
Ti
Ca
K
Cl
S
Si
Al
Mg
Na
O
C
0.001
0.01
0.1
1
10
100
Concentration wt(%)

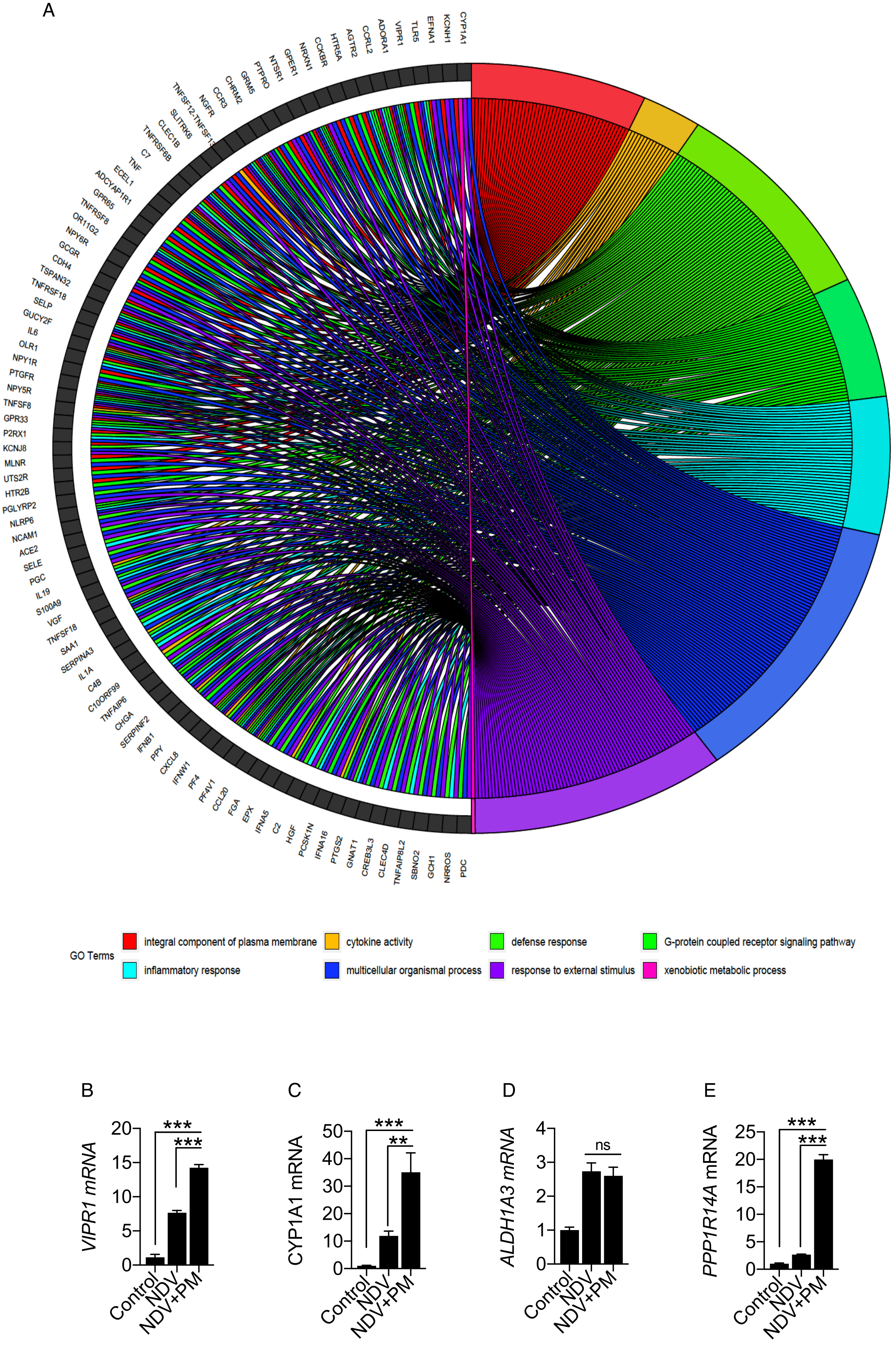
Supplementary Figure 1: SEM-EDS analysis of PM$_{10}$ - Scanning electron images and energy – dispersive X-ray spectra of coarse airborne particulate matter PM$_{10.}$ (A) 12 different spots of PM$_{10}$ shows 12 different types of spectral peaks corresponding to the presence of specific elements at that point. (B) Representation of elemental composition (% weight) of PM$_{10}$ at few other spots in bar graph having metal name on *y-axis* and respective concentration (%weight) on *x-axis*.

Figure S2.


A
18.67% Immune Signaling Cascade
28.00% Infectious Diseases
13.33% Neurological Regulation
12.00% Cancer
6.67% Cardiomyopathies
6.67% Hormone Regulatory Pathways
2.67% Protein Processing Pathways
1.33% RNA control machinery
1.33% Cell cycle
4.00% Cell Death
5.33% Metabolic Pathways
B
Bronchial epithelial cells
Number of genes involved
150
100
50
0
Measles
Epstein-Barr virus
Influenza A
Hepatitis B
Hepatitis C
Herpes simplex
Viral carcinogenesis
C
IFNAR1
STAT1
RELA
NFKBIA
NFKB1
IKBKB
MAVS
DDX58
IKBKE
IRF7
TBK1
IRF3
IL6
MYD88
IL1B
JUN
TYK2
JAK1
IFNG
NFKBIB
Influenza A
Measles
Herpes simplex
Toll Like Receptors
Hepatitis C
Hepatitis B
Cytosolic Degradation
Osteoclastic Activity
Toxoplasmosis
Epstein-Barr virus
D
Toll Like Receptor signaling_Mus musculus_WP88
IL-6 signaling Pathway_Mus musculus_WP387
Type II interferon signaling (IFNG)_Mus musculus_WP1253
AGE/RAGE pathway_Homo sapiens_WP2324
Structural Pathway of Interleukin 1 (IL-1)_Homo sapiens_WP2637
Regulation of toll-like receptor signaling pathway_Homo sapiens_WP1449
Toll-like Receptor Signaling Pathway_Homo sapiens_WP75
IL-1 signaling pathway_Homo sapiens_WP195
Type II interferon signaling (IFNG)_Homo sapiens_WP619
TNF alpha Signaling Pathway_Homo sapiens_WP231

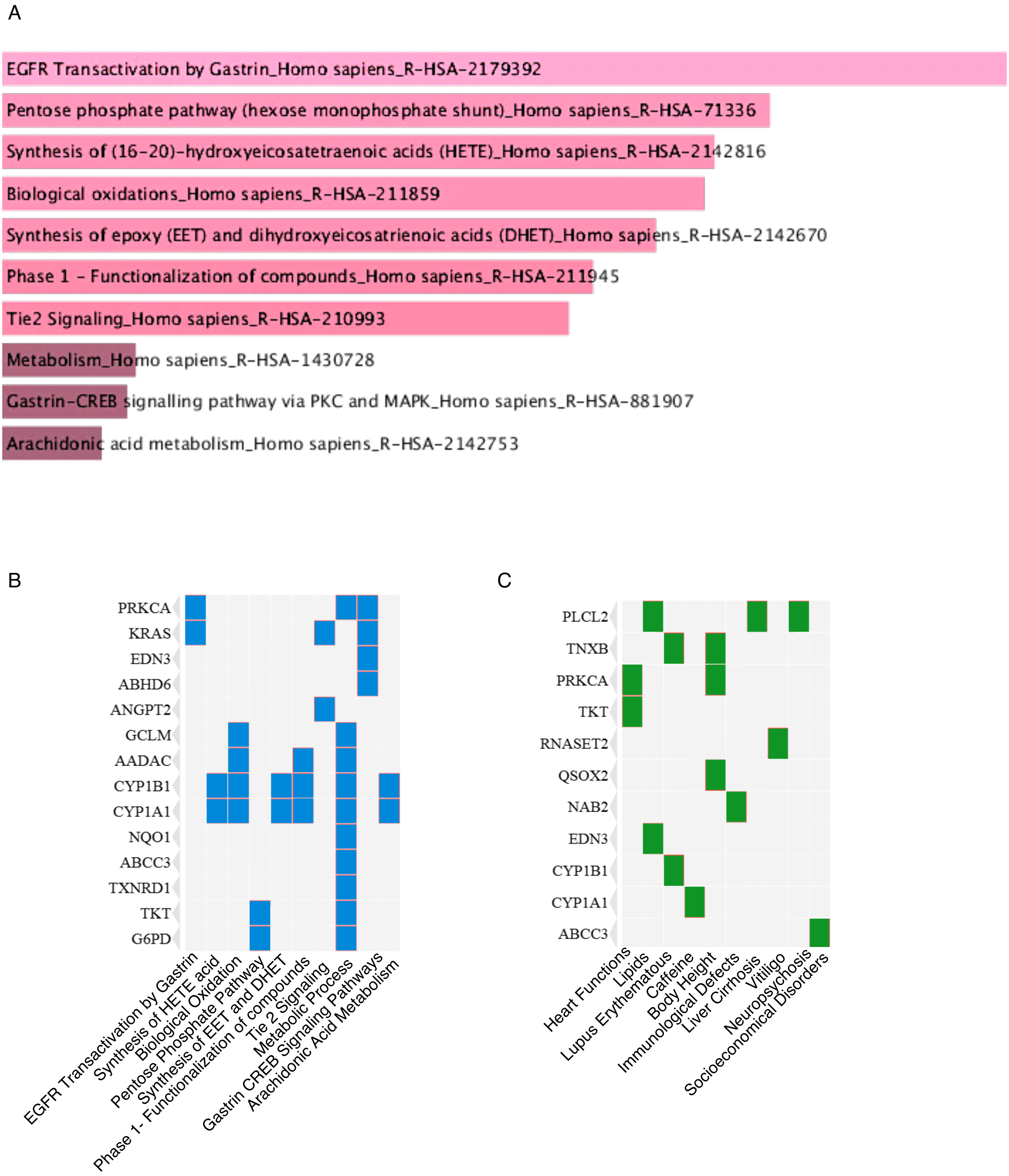
Supplementary Figure 2: Re-analysis of GEO dataset GSE27973 – (A) Cellular pathways dysregulated in presence of CSE (cigarette smoke extract) exposure and RV (rhinovirus) infection in human bronchial epithelial cells. (B) Number of genes involved in various diseases. (C) Exact gene plotted against the disease in which it is involved, represented by the heat map generated through the Enrichr software. (D) Connecting network between the pathways dysregulated, represented by the dot network analysis generated through the Enrichr software.

Figure S3.


A
CYP1A1
KCNH1
EFNA1
TLR5
VIPR1
ADORA1
CCRL2
AGTR2
HTR5A
CCKBR
NRXN1
GPER1
NTSR1
PTPRO
GRM5
CHRM2
CCR3
NGFR
TNFSF12-TNFSF13
SLITRK6
CLEC1B
TNFRSF6B
C7
TNF
ECEL1
ADCYAP1R1
GPR65
TNFRSF8
OR11G2
NPY6R
GCGR
CDH4
TSPAN32
TNFRSF18
SELP
GUCY2F
IL6
OLR1
NPY1R
PTGFR
NPY5R
TNFSF8
GPR33
P2RX1
KCNJ8
MLNR
UTS2R
HTR2B
PGLYRP2
NLRP6
NCAM1
ACE2
SELE
PGC
IL19
S100A9
VGF
TNFSF18
SAA1
SERPINA3
IL1A
C4B
C10ORF99
TNFAIP6
CHGA
SERPINF2
IFNB1
PPY
CXCL8
IFNW1
PF4
PF4V1
CCL20
FGA
EPX
IFNA5
C2
HGF
PCSK1N
IFNA16
PTGS2
GNAT1
CREB3L3
CLEC4D
TNFAIP8L2
SBNO2
GCH1
NRROS
PDC
GO Terms
integral component of plasma membrane
cytokine activity
defense response
G-protein coupled receptor signaling pathway
inflammatory response
multicellular organismal process
response to external stimulus
xenobiotic metabolic process
B
VIPR1 mRNA
0
5
10
15
20
***
***
Control
NDV
NDV+PM
C
CYP1A1 mRNA
0
10
20
30
40
50
***
**
Control
NDV
NDV+PM
D
ALDH1A3 mRNA
0
1
2
3
4
ns
Control
NDV
NDV+PM
E
PPP1R14A mRNA
0
5
10
15
20
25
***
***
Control
NDV
NDV+PM

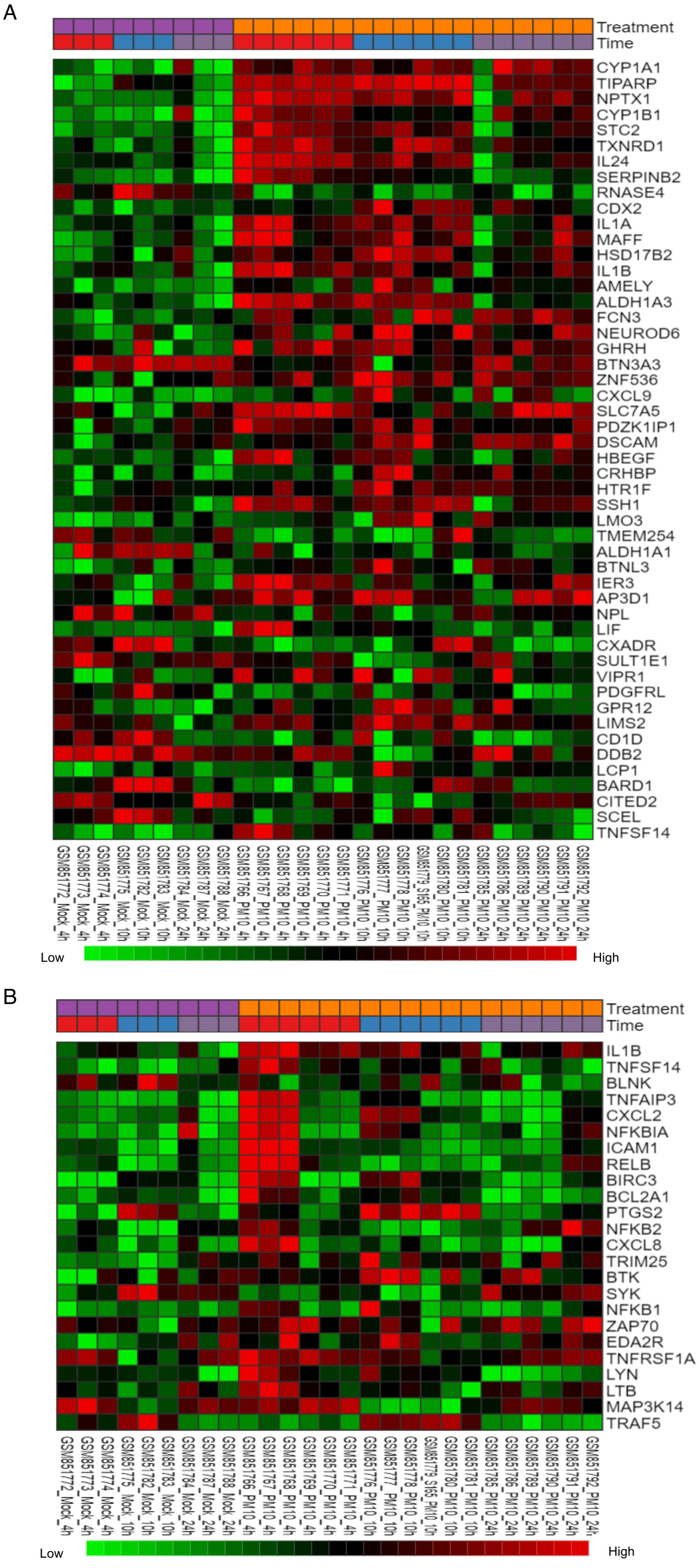
Supplementary Figure 3: Gene Ontology analysis of PM_{10} treated and H5N1 infected A549 cells – (A) Gene Ontology analysis represented by the chord plot that connects the common differentially expressed genes with the top significantly enriched ontology terms. (B-E) Quantification (measured by qRT-PCR) of the expression levels of metabolic pathways-related transcripts: *VIPR1*, *CYP1A1*, *ALDH1A3* and *PPP1R14A* in A549 cells exposed with PM_{10} (labelled as PM; corresponds to PM(I) dosage form - details are mentioned in the methods section) and infected with NDV. Sample labeled as untreated (control), mock NDV infected (NDV) and PM_{10} exposed plus NDV infected (NDV+PM). Data are mean +/- SEM of triplicate samples from single experiment and are representative of three independent experiments. ***$P<0.001$, **$P<0.01$ and ns = non-significant by one-way ANOVA Tukey test and unpaired t-test.

Figure S4.


A
EGFR Transactivation by Gastrin_Homo sapiens_R-HSA-2179392
Pentose phosphate pathway (hexose monophosphate shunt)_Homo sapiens_R-HSA-71336
Synthesis of (16-20)-hydroxyeicosatetraenoic acids (HETE)_Homo sapiens_R-HSA-2142816
Biological oxidations_Homo sapiens_R-HSA-211859
Synthesis of epoxy (EET) and dihydroxyeicosatrienoic acids (DHET)_Homo sapiens_R-HSA-2142670
Phase 1 - Functionalization of compounds_Homo sapiens_R-HSA-211945
Tie2 Signaling_Homo sapiens_R-HSA-210993
Metabolism_Homo sapiens_R-HSA-1430728
Gastrin-CREB signalling pathway via PKC and MAPK_Homo sapiens_R-HSA-881907
Arachidonic acid metabolism_Homo sapiens_R-HSA-2142753
B
PRKCA
KRAS
EDN3
ABHD6
ANGPT2
GCLM
AADAC
CYP1B1
CYP1A1
NQO1
ABCC3
TXNRD1
TKT
G6PD
EGFR Transactivation by Gastrin
Synthesis of HETE acid
Biological Oxidation
Pentose Phosphate Pathway
Synthesis of EET and DHET
Phase 1- Functionalization of compounds
Tie 2 Signaling
Metabolic Process
Gastrin CREB Signaling Pathways
Arachidonic Acid Metabolism
C
PLCL2
TNXB
PRKCA
TKT
RNASET2
QSOX2
NAB2
EDN3
CYP1B1
CYP1A1
ABCC3
Heart Functions
Lipids
Lupus Erythematous
Caffeine
Body Height
Immunological Defects
Liver Cirrhosis
Vitiligo
Neuropsychosis
Socioeconomical Disorders

Supplementary Figure 4: Re-analysis of GEO dataset GSE27973 to depict the pathways and genes upregulated in presence of CSE and RV infection – Enrichr software is used for the depiction of related genes and pathways. (A) Representation of enriched pathways by bar graph. (B) Representation of upregulated genes involved in enriched pathways by heat map. (C) Representation of upregulated genes involved in various diseases by heat map. Here, human bronchial epithelial cell lines were exposed to CSE (cigarette smoke extract) and infected with RV (rhinovirus).

Figure S5.


A
Treatment
Time
CYP1A1
TIPARP
NPTX1
CYP1B1
STC2
TXNRD1
IL24
SERPINB2
RNASE4
CDX2
IL1A
MAFF
HSD17B2
IL1B
AMELY
ALDH1A3
FCN3
NEUROD6
GHRH
BTN3A3
ZNF536
CXCL9
SLC7A5
PDZK1IP1
DSCAM
HBEGF
CRHBP
HTR1F
SSH1
LMO3
TMEM254
ALDH1A1
BTNL3
IER3
AP3D1
NPL
LIF
CXADR
SULT1E1
VIPR1
PDGFRL
GPR12
LIMS2
CD1D
DDB2
LCP1
BARD1
CITED2
SCEL
TNFSF14
GSM851772_Mock_4h
GSM851773_Mock_4h
GSM851774_Mock_4h
GSM851775_Mock_10h
GSM851782_Mock_10h
GSM851783_Mock_10h
GSM851784_Mock_24h
GSM851787_Mock_24h
GSM851788_Mock_24h
GSM851766_PM10_4h
GSM851767_PM10_4h
GSM851768_PM10_4h
GSM851769_PM10_4h
GSM851770_PM10_4h
GSM851771_PM10_4h
GSM851776_PM10_10h
GSM851777_PM10_10h
GSM851778_PM10_10h
GSM851779_S165_PM10_10h
GSM851780_PM10_10h
GSM851781_PM10_10h
GSM851785_PM10_24h
GSM851786_PM10_24h
GSM851789_PM10_24h
GSM851790_PM10_24h
GSM851791_PM10_24h
GSM851792_PM10_24h
Low
High
B
Treatment
Time
IL1B
TNFSF14
BLNK
TNFAIP3
CXCL2
NFKBIA
ICAM1
RELB
BIRC3
BCL2A1
PTGS2
NFKB2
CXCL8
TRIM25
BTK
SYK
NFKB1
ZAP70
EDA2R
TNFRSF1A
LYN
LTB
MAP3K14
TRAF5
GSM851772_Mock_4h
GSM851773_Mock_4h
GSM851774_Mock_4h
GSM851775_Mock_10h
GSM851782_Mock_10h
GSM851783_Mock_10h
GSM851784_Mock_24h
GSM851787_Mock_24h
GSM851788_Mock_24h
GSM851766_PM10_4h
GSM851767_PM10_4h
GSM851768_PM10_4h
GSM851769_PM10_4h
GSM851770_PM10_4h
GSM851771_PM10_4h
GSM851776_PM10_10h
GSM851777_PM10_10h
GSM851778_PM10_10h
GSM851779_S165_PM10_10h
GSM851780_PM10_10h
GSM851781_PM10_10h
GSM851785_PM10_24h
GSM851786_PM10_24h
GSM851789_PM10_24h
GSM851790_PM10_24h
GSM851791_PM10_24h
GSM851792_PM10_24h
Low
High

Supplementary Figure 5: Re-analysis of GEO dataset GSE34607 to depict the modulation of metabolic pathways-related genes in BEAS-2B bronchial epithelial cells in presence PM_{10} - (A) Heat map showing the expression of top most differentially expressed genes)based on the adjusted *p -values*) at varied time points upon exposure to PM_{10} in BEAS-2B cell compared with mock (untreated) cells. (B) Heat map showing the modulation of inflammatory genes via *NFkB* pathway.