

Supplemental File

The Effect of Air Pollution on the Transcriptomics of the Immune Response to Respiratory Infection

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Sensitivity Analysis of Smokers

As a sensitivity analysis, we reran the individual gene analysis for Delta C at 0-6 hours stratified by smoking status. The differences observed when accounting for smoking were small. For example, the only change observed in smokers was that TUT4 (mRNA decay in oocytes) and not POC1B (centrosome proteins related to cilia formation) was significantly associated with increased concentrations of Delta-C and gene expression. **(Supplemental Table S10)**

Sensitivity Analysis of Individual Genes within Significant Pathways

We then performed an exploratory cross-reference analysis to understand which differentially expressed genes were present within the gene pathways associated with specific pollutants.

We observed multiple differentially expressed genes associated with increased air pollution concentrations, which were also present in the gene pathways associated with specific pollutants. For example, for increased concentrations of Delta-C at the 0-6 lag day, upregulation in the gene HMBS participates in multiple upregulated gene pathways pertaining to iron homeostasis. At later lag times, RPS4Y1 (codes for ribosomal subunit) was the most common gene upregulated across multiple pathways pertaining to ribosomal structure and function at multiple lag times. Finally, for increases in Delta-C concentrations in the 0-6 lag days, there were associations with multiple genes participating in the negative regulation of the viral life cycle were also observed (TRIM8, ISG15, OAS2) **(Supplemental Table S12).**

Though there were no individual genes associated with increases in BC, there were several gene pathways associated with increases in BC (**Table 3**). We then explored which differentially expressed genes were present in specific gene pathways (**Supplemental Table S13**). For example, for exposure to BC at 0-6 days, there were multiple differentially expressed genes present in both the specific pathway, Response To Type I Interferon and individual gene analysis, including IFI27, ISG15, OAS2, and OAS1. For BC at 0-28 days, several gene pathways related to protein folding (endoplasmic reticulum) shared a common gene, RPS4Y1. For PM_{2.5} at the 7-13 and 14-20 lag day, the RPS4Y1 gene was also observed within the ER specific pathways (**Supplemental Table S14**). For the later lag times of UFP (lag days 14-28), the RPS4Y1 gene was also present in the ER related pathways along with a variety of immune related genes (**Supplemental Table S15**). For all lag times of UFP, the gene STXBP2, which regulates cytotoxic granule exocytosis in natural killer cells, was the dominant gene present in immune pathways. For AMP, there were multiple genes across a variety of pathways (ER and immune) represented within the 0-6 and 21-28 day lag times. For AMP, iron homeostasis genes were also present at the 21-28 day lag period (**Supplemental Table S16**). Although there were common pathways associated with multiple different pollutants, each pollutant appeared to have unique patterns of association.

By comparing the differentially expressed genes from the individual gene analysis (LIMMA) with the significant gene pathways from the CAMERA analysis we could identify key genes that may be involved in the overall air pollution/respiratory infection association (**Table S6**). An iron homeostasis gene (HBMS) was the most frequently associated with increased concentrations of DC. Despite observing no individual genes associated with increases in BC concentrations, several genes related to the immune response to respiratory infection were identified as part of the individual gene/pathway cross-analysis. One particular gene, IFI27, appears to be differentially expressed in association with RVI, as well as in viral related pathways in association with BC exposure. What remains unclear is whether the expression of IFI27, or other genes, are part of the mechanistic pathway for the effect of air pollution on the immune response to RVI, or whether these genes are simply expressed in response to both RVI and air pollution. In this way, our analytic approach can help spotlight certain genes and pathways for further exploration in prospective exposure studies. In addition to focusing on specific immune related gene responses, future research will also need to focus on broader areas that could impair immune responses such as the aforementioned protein folding (ER) and iron homeostasis pathways.

Table S1. Description of Respiratory Infections

Infection Type	N(%)
Viral infections	
Influenza A	22(33.3)
Influenza B	5(7.6)
RSV (Respiratory Syncytial Virus Infection)	19(28.8)
Other viruses (Parainfluenza Virus (1-3), Human Metapneumovirus, H1N1 virus (swine flu), Rhinovirus, Coronavirus OC43)	20(30.3)
Bacteria	
Streptococcus pneumonia	12(60.0)
Other bacteria (Haemophilus influenzae, Moraxella catarrhalis, Mycoplasma pneumonia, Staphylococcus aureus)	8(40.0)

Table S2. Individual genes in Cluster 2 of the 150 most differentially expressed genes

Illumina Number	Gene name	Illumina Number	Gene name
ILMN_1733811	JUP	ILMN_2239754	IFIT3
ILMN_2058782	IFI27	ILMN_1664543	IFIT3
ILMN_1658247	OAS1	ILMN_1674811	OASL
ILMN_1663347	OTOF	ILMN_1675640	OAS1
ILMN_1699331	NA	ILMN_2410826	OAS1
ILMN_1783621	CMPK2	ILMN_1760062	IFI44
ILMN_1835092	IFI44L	ILMN_1723912	IFI44L
ILMN_1795181	DDX60	ILMN_1745397	OAS3
ILMN_1736729	OAS2	ILMN_2054019	ISG15
ILMN_2248970	OAS2	ILMN_1674063	OAS2
ILMN_2173975	RTP4	ILMN_1742618	XAF1
ILMN_1683678	SPATS2L	ILMN_1657871	RSAD2
ILMN_1678422	DHX58	ILMN_1695404	LY6E
ILMN_1718558	PARP12	ILMN_2388547	EPSTI1
ILMN_1654639	HERC6	ILMN_1662358	MX1
ILMN_2370573	XAF1	ILMN_1707695	IFIT1
ILMN_1701789	IFIT3	ILMN_1729749	HERC5
ILMN_1739428	IFIT2	ILMN_2347798	IFI6

Table S3 Individual gene analysis (Gene expression from infection alone-independent of air pollution).

Illumina ID	Gene	Log Fold change	Average Expression	*Adjusted p- value	Beta	Standard Deviation
ILMN_2054019	ISG15	3.3	10.5	<0.001	14.4	1.6
ILMN_1765332	TIMM10	2.2	7.4	<0.001	14.3	1.1
ILMN_1660079	RNF44	-0.7	7.9	<0.001	13.6	0.3
ILMN_1723912	IFI44L	4.0	8.9	<0.001	12.6	2.1
ILMN_1760062	IFI44	2.8	9.2	<0.001	12.4	1.4
ILMN_1674063	OAS2	2.5	9.5	<0.001	12.1	1.3
ILMN_2058782	IFI27	3.9	11.2	<0.001	11.6	2.1
ILMN_1679929	KLF13	-0.6	8.5	<0.001	11.4	0.3
ILMN_1703263	SP140	1.2	5.6	<0.001	11.4	0.7
ILMN_1708991	CCNY	-0.8	6.9	<0.001	11.2	0.4

*Adjusted p value uses the FDR metric to control for testing thousands of genes simultaneously

Table S4 Association between pollution and gene expression. Log fold change of gene expression in all patients with respiratory infection (all types combined) associated with a one unit increase of Delta Carbon concentrations at the 0-6 day lag period.

Illumina ID	Gene	Log Fold Change	Average Expression	*Adjusted p-value	Beta	Standard Deviation
ILMN_1659024	TMCC2	5.2	5.8	0.004	6.6	0.9
ILMN_1714461	RNF14	3.5	7.3	0.004	5.6	0.6
ILMN_2164242	UBE2F	2.4	9.8	0.004	5.5	0.4
ILMN_1747227	ADORA1	2.9	5.9	0.004	5.1	0.6
ILMN_2351241	RNF14	3.2	6.6	0.004	5.1	0.6
ILMN_1726308	ST13P4	3.5	8.0	0.004	5.0	0.7
ILMN_2174884	XPO7	3.3	7.3	0.004	5.0	0.6
ILMN_1694476	HMBS	5.2	6.5	0.005	4.5	1.0
ILMN_1783156	MAP2K3	3.1	10.3	0.006	4.2	0.6
ILMN_1667201	POC1B	2.6	7.0	0.006	4.2	0.5

*Adjusted p value uses the FDR metric to control for testing thousands of genes simultaneously

Supplemental Table S5 Timing and pattern of association between gene pathways and increased concentrations of Delta-C (red-upregulated, blue-downregulated).

DC	Gene Pathway Name
0-6	GO_SPLICEOSOMAL_COMPLEX
21-27	GO_NEGATIVE_REGULATION_OF_CALCIUM_ION_TRANSPORT_INTO_CYTOSOL
21-27	GO_NEGATIVE_REGULATION_OF_RYANODINE_SENSITIVE_CALCIUM_RELEASE_CHANNEL_ACTIVITY
21-27	GO_POSITIVE_REGULATION_OF_SEQUESTERING_OF_CALCIUM_ION
0-6	GO_HEME_METABOLIC_PROCESS
0-6	GO_HEMOGLOBIN_COMPLEX
0-6	GO_NEURAL_PLATE_ANTERIOR_POSTERIOR_REGIONALIZATION
0-6	GO_NEURAL_PLATE_PATTERN_SPECIFICATION
0-6	GO_NEURAL_PLATE_REGIONALIZATION
0-6	GO_PROTEIN GLUTAMINE GAMMA GLUTAMYLTRANSFERASE_ACTIVITY
7-13	GO_HYDROGEN_PEROXIDE_CATABOLIC_PROCESS
7-13	GO_NASCENT_POLYPEPTIDE_ASSOCIATED_COMPLEX
7-13	GO_THIOREDOXIN_PEROXIDASE_ACTIVITY
14-20	GO_EUKARYOTIC_48S_PREINITIATION_COMPLEX
14-20	GO_EUKARYOTIC_TRANSLATION_INITIATION_FACTOR_3_COMPLEX
14-20	GO_EUKARYOTIC_TRANSLATION_INITIATION_FACTOR_3_COMPLEX EIF3M
14-20	GO_FORMATION_OF_CYTOPLASMIC_TRANSLATION_INITIATION_COMPLEX
14-20	GO_TRANSLATION_ELONGATION_FACTOR_ACTIVITY

Supplemental Table S6. Timing and pattern of association between gene pathways and increased concentrations of Black carbon (red-upregulated, blue-downregulated).

BC	Gene Pathway Name
7-13	GO_MHC_CLASS_I_PROTEIN_COMPLEX_BINDING
14-20	GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_PEPTIDE_ANTIGEN_VIA_MHC_CLASS_I_TAP_INDEPENDENT
14-20	GO_MHC_CLASS_I_PROTEIN_COMPLEX
14-20	GO_NATURAL_KILLER_CELL_CYTOKINE_PRODUCTION
14-20	GO_POSITIVE_REGULATION_OF_NATURAL_KILLER_CELL_MEDIATED_IMMUNITY
0-6	GO_DEFENSE_RESPONSE_TO_VIRUS
0-6	GO_INTERFERON_GAMMA_MEDIATED_SIGNALING_PATHWAY
0-6	GO_ISG15_PROTEIN_CONJUGATION
0-6	GO_NADPLUS_ADP_RIBOSYLTRANSFERASE_ACTIVITY
0-6	GO_NEGATIVE_REGULATION_OF_MULTI_ORGANISM_PROCESS
0-6	GO_NEGATIVE_REGULATION_OF_VIRAL_GENOME_REPLICATION
0-6	GO_NEGATIVE_REGULATION_OF_VIRAL_LIFE_CYCLE
0-6	GO_NEGATIVE_REGULATION_OF_VIRAL_PROCESS
0-6	GO_POSITIVE_REGULATION_OF_ENDOTHELIAL_CELL_CHEMOTAXIS
0-6	GO_POSITIVE_REGULATION_OF_TYPE_I_INTERFERON_MEDIATED_SIGNALING_PATHWAY
0-6	GO_PROTEIN_ADP_RIBOSYLASE_ACTIVITY
0-6	GO_PROTEIN_AUTO_ADP_RIBOSYLATION
0-6	GO_REGULATION_OF_RIBONUCLEASE_ACTIVITY
0-6	GO_REGULATION_OF_VIRAL_GENOME_REPLICATION
0-6	GO_REGULATION_OF_VIRAL_LIFE_CYCLE
0-6	GO_RESPONSE_TO_INTERFERON_ALPHA
0-6	GO_RESPONSE_TO_TYPE_I_INTERFERON
0-6	GO_RESPONSE_TO_VIRUS
0-6	GO_VIRAL_GENOME_REPLICATION
7-13	GO_CCR2_CHEMOKINE_RECEPTOR_BINDING
7-13	GO_EOSINOPHIL_ACTIVATION
7-13	GO_HEMATOPOIETIC_STEM_CELL_MIGRATION
7-13	GO_REGULATION_OF_LEUKOCYTE_TETHERING_OR_ROLLING

Supplemental Table S7. Timing and pattern of association between gene pathways and increased concentrations of PM_{2.5} (red-upregulated, blue-downregulated).

PM25	Gene Pathway Name
0-6	GO_CYTOLYSIS_IN_OTHER_ORGANISM
0-6	GO_DISRUPTION_BY_HOST_OF_SYMBIONT_CELLS
0-6	GO_DISRUPTION_OF_CELLS_OF_OTHER_ORGANISM_INVOLVED_IN_SYMBIOTIC_INTERACTION
0-6	GO_NADPH_OXIDASE_COMPLEX
0-6	GO_PEROXISOME_TARGETING_SEQUENCE_BINDING
0-6	GO_PHAGOLYSOSOME
0-6	GO_SUPEROXIDE_GENERATING_NADPH_OXIDASE_ACTIVATOR_ACTIVITY
7-13	GO_MITOCHONDRIAL_PROTEIN_COMPLEX
7-13	GO_MITOCHONDRIAL_SMALL_RIBOSOMAL_SUBUNIT
7-13	GO_MITOCHONDRIAL_TRANSLATIONAL_TERMINATION
7-13	GO_ORGANELLAR_RIBOSOME
7-13	GO_RIBOSOME_ASSEMBLY
7-13	GO_RIBOSOME_BIOGENESIS
7-13	GO_ROUGH_ENDOPLASMIC_RETICULUM_MEMBRANE
7-13	GO_RRNA_METABOLIC_PROCESS
7-13	GO_TRANSLATIONAL_TERMINATION
14-20	GO_CYTOPLASMIC_SIDE_OF_ENDOPLASMIC_RETICULUM_MEMBRANE
14-20	GO_MITOCHONDRIAL_LARGE_RIBOSOMAL_SUBUNIT
14-20	GO_NCRNA_METABOLIC_PROCESS
14-20	GO_NCRNA_PROCESSING
14-20	GO_POSITIVE_REGULATION_OF_CELL_CELL_ADHESION_MEDIATED_BY_INTEGRIN
14-20	GO_PRERIBOSOME
21-27	GO_ADENYL_NUCLEOTIDE_EXCHANGE_FACTOR_ACTIVITY
21-27	GO_BETA_CATENIN_TCF_COMPLEX_ASSEMBLY
21-27	GO_POST_MRNA_RELEASE_SPLICEOSOMAL_COMPLEX
21-27	GO_RNA_POLYMERASE_II_GENERAL_TRANSCRIPTION_INITIATION_FACTOR_ACTIVITY
0-6	GO_CELLULAR_RESPONSE_TO_COPPER_ION
0-6	GO_DETOXIFICATION_OF_INORGANIC_COMPOUND
0-6	GO_MINERALOCORTICOID_SECRETION
0-6	GO_REGULATION_OF_MDA_5_SIGNALING_PATHWAY

Supplemental Table S8 Timing and pattern of association between gene pathways and increased concentrations of ultrafine particles (red-upregulated, blue-downregulated).

UFP	Gene Pathway Name
7-13	GO_FICOLIN_1_RICH_GRANULE_MEMBRANE
7-13	GO_GLUCOSYLCERAMIDE_METABOLIC_PROCESS
7-13	GO_MYELOID_LEUKOCYTE_ACTIVATION
7-13	GO_PODOSOME
7-13	GO_REGULATION_OF_LEUKOCYTE_DEGRANULATION
7-13	GO_REGULATION_OF_NEUTROPHIL_ACTIVATION
7-13	GO_REGULATION_OF_SUPEROXIDE_ANION_GENERATION
7-13	GO_TERTIARY_GRANULE_MEMBRANE
0-6	GO_1_PHOSPHATIDYLINOSITOL_4_PHOSPHATE_5_KINASE_ACTIVITY
0-6	GO_2_IRON_2_SULFUR_CLUSTER_BINDING
0-6	GO_ANTERIOR_HEAD_DEVELOPMENT
0-6	GO_CELLULAR_MAGNESIUM_ION_HOMEOSTASIS
0-6	GO_REGULATION_BY_VIRUS_OF_VIRAL_PROTEIN_LEVELS_IN_HOST_CELL
0-6	GO_REGULATION_OF_MITOCHONDRIAL_ATP_SYNTHESIS_COUPLED_ELECTRON_TRANSPORT
0-6	GO_TETRAPYRROLE_BIOSYNTHETIC_PROCESS
7-13	GO_METAL_CLUSTER_BINDING
14-20	GO_RIBOSOMAL_LARGE_SUBUNIT_BIOGENESIS
14-20	GO_RRNA_BINDING

Supplemental Table S9 Timing and pattern of association between gene pathways and increased concentrations of Accumulation mode particles (red-upregulated, blue-downregulated).

AMP	Gene Pathway Name
14-20	GO_POSITIVE_REGULATION_OF_PHOSPHOLIPID_TRANSPORT
21-27	GO_AZUROPHIL_Granule_LUMEN
21-27	GO_RNA_METHYLATION
21-27	GO_VESICLE_LUMEN
21-27	GO_SEQUESTERING_OF_IRON_ION
21-27	GO_SEQUESTERING_OF_METAL_ION

Supplemental Table S10. Genes present within each cluster of the Type 1 Interferon/ Black carbon 0-6 day lag heatmap

ILMN_1806056	CEACAM8	cluster1
ILMN_1687384	IFI6	cluster1
ILMN_1653466	HES4	cluster1
ILMN_1652199	NA	cluster1
	IGKV1ORY-	
ILMN_3240375	1	cluster1
ILMN_2389590	PRKAR1A	cluster1
ILMN_2105441	JCHAIN	cluster1
ILMN_1680652	SELENBP1	cluster1
ILMN_1683093	GYPB	cluster1
ILMN_1733811	JUP	cluster1
ILMN_2305407	ZBTB16	cluster1
ILMN_1670305	SERPING1	cluster1
ILMN_1662358	MX1	cluster1
ILMN_1771385	GBP4	cluster1
ILMN_2388547	EPSTI1	cluster1
ILMN_1807919	TNS1	cluster1
ILMN_1759155	IFIT1B	cluster1
ILMN_3243112	RNF182	cluster1
ILMN_1712522	CEACAM6	cluster1
ILMN_1697499	HLA-DRB5	cluster1
ILMN_1674811	OASL	cluster1
ILMN_1795181	DDX60	cluster1
ILMN_1664543	IFIT3	cluster1
ILMN_1675640	OAS1	cluster1
ILMN_1739508	NA	cluster1
ILMN_1814397	EPB42	cluster1
ILMN_1725661	NA	cluster1
ILMN_2193233	MZB1	cluster1
ILMN_1755537	EIF1AY	cluster1
ILMN_1781966	OSBP2	cluster1
ILMN_1735712	KRT1	cluster1

ILMN_1716733	MYOM2	cluster1
ILMN_1781700	IL18R1	cluster1
ILMN_1753347	DEFA4	cluster1
ILMN_1652431	CA1	cluster1
ILMN_1693262	NA	cluster1
ILMN_2402817	ZBTB16	cluster1
ILMN_1815527	HBD	cluster1
ILMN_1658247	OAS1	cluster1
ILMN_1742618	XAF1	cluster1
ILMN_2066060	HLA-DRB6	cluster1
ILMN_1766896	ZDHHC19	cluster1
ILMN_1701789	IFIT3	cluster1
ILMN_1772809	SLC4A1	cluster1
ILMN_1776519	RAP1GAP	cluster1
ILMN_2054019	ISG15	cluster1
ILMN_2415529	CDK5RAP2	cluster1
ILMN_1810752	C4BPA	cluster1
ILMN_1774091	FECH	cluster1
ILMN_3235221	LOC644936	cluster2
ILMN_1685122	COL9A2	cluster2
ILMN_1812281	ARG1	cluster2
ILMN_1774071	CD177	cluster2
ILMN_1654875	CLC	cluster2
ILMN_1696584	ORM1	cluster2
ILMN_2393765	IGLL1	cluster2
ILMN_1707695	IFIT1	cluster2
ILMN_2271875	ALAS2	cluster2
ILMN_2370573	XAF1	cluster2
ILMN_2347798	IFI6	cluster2
ILMN_1695404	LY6E	cluster2
ILMN_1679357	NA	cluster2
ILMN_1701114	GBP1	cluster2
ILMN_1812433	HP	cluster2
ILMN_1723436	PFKFB2	cluster3
ILMN_1688423	FCER1A	cluster3
ILMN_2148785	GBP1	cluster3
ILMN_1663347	OTOF	cluster3
ILMN_1722622	CD163	cluster3
ILMN_1693192	PI3	cluster3
ILMN_2114568	GBP5	cluster3
ILMN_2165289	NA	cluster3
ILMN_1651950	TPST1	cluster3
ILMN_1748090	SLC2A11	cluster3

ILMN_2072178	ECHDC3	cluster3
ILMN_1733259	TMIGD3	cluster3
ILMN_2102721	NA	cluster3
ILMN_3285762	SLC4A1	cluster3
ILMN_1663640	MAOA	cluster3
ILMN_1674063	OAS2	cluster3
ILMN_1768016	TNFRSF17	cluster3
ILMN_2058782	IFI27	cluster3
ILMN_3251610	CD177	cluster3
ILMN_1815895	NA	cluster3
ILMN_2410826	OAS1	cluster4
ILMN_1699331	NA	cluster4
ILMN_2352921	BPGM	cluster4
ILMN_2239754	IFIT3	cluster4
ILMN_2403965	NA	cluster4
ILMN_1680274	NA	cluster4
ILMN_2173975	RTP4	cluster4
ILMN_1804601	NA	cluster4
ILMN_2193213	NA	cluster4
ILMN_1835092	IFI44L	cluster4
ILMN_2116877	OLFM4	cluster4
ILMN_1708580	PDZK1IP1	cluster4
ILMN_1706635	ELANE	cluster4
ILMN_1677920	LTF	cluster4
ILMN_1729749	HERC5	cluster4
ILMN_1678422	DHX58	cluster4
ILMN_1736026	MMP8	cluster4
ILMN_1756715	RUNDC3A	cluster4
ILMN_1657871	RSAD2	cluster4
ILMN_1680424	CTSG	cluster4
ILMN_1765332	TIMM10	cluster4
ILMN_1739428	IFIT2	cluster4
ILMN_2166457	HPGD	cluster4
ILMN_1745397	OAS3	cluster5
ILMN_1699214	NA	cluster5
ILMN_1723912	IFI44L	cluster5
ILMN_2159694	HLA-DRB4	cluster5
ILMN_1783142	RPS4Y1	cluster5
ILMN_1766736	BPI	cluster5
ILMN_2399463	VAV3	cluster5
ILMN_1683678	SPATS2L	cluster5
ILMN_1736729	OAS2	cluster5
ILMN_2165753	HLA-A	cluster5

ILMN_3203189	MAP2K3	cluster5
ILMN_1675190	RETN	cluster5
ILMN_3238417	RPS4Y1	cluster5
ILMN_2038775	TUBB2A	cluster5
ILMN_1760062	IFI44	cluster5
ILMN_1715169	HLA-DRB1	cluster5
ILMN_1772131	IL1R2	cluster5
ILMN_1708323	ALAS2	cluster5

Table S11 Pollution effect of DC 0-6 lag period, with Smoking Status

Log fold change of gene expression in all patients with respiratory infection (all types combined) associated with a one unit increase of Delta Carbon concentrations at the 0-6 day lag period. These results control for smoking status of patient.

[illegible]

Table S12 Differentially expressed genes present in specific gene pathways associated with increased concentrations of Delta-C at multiple lag periods

DC 0-6					
Gene Symbols	Gene Pathway	NGenes	Direction	PValue	FDR
HMBS	GO_TETRAPYRROLE_BIOSYNTHETIC_PROCESS	37	Up	<0.0001	0.0077
HMBS	GO_PORPHYRIN_CONTAINING_COMPOUND_METABOLIC_PROCESS	41	Up	<0.0001	0.0018
HMBS	GO_TETRAPYRROLE_METABOLIC_PROCESS	59	Up	0.0018	0.0962
HMBS	GO_HEME_BIOSYNTHETIC_PROCESS	30	Up	<0.0001	0.0067
XPO7	GO_RNA_LOCALIZATION	328	Down	0.0002	0.0274
FABP5 SERPING1	GO_VESICLE_LUMEN	397	Down	0.0011	0.0748
DERL2 RPS4Y1 RPS4Y2	GO_RIBONUCLEOPROTEIN_COMPLEX	1147	Down	0.001	0.072
TIMM10	GO_MITOCHONDRIAL_PROTEIN_COMPLEX	298	Down	<0.0001	0.008
EIF1AY RPS4Y1 RPS4Y2 OAS2	GO_RNA_BINDING	2299	Down	0.0013	0.0804
HMBS	GO_PROTOPORPHYRINOGEN_IX_BIOSYNTHETIC_PROCESS	13	Up	<0.0001	<0.0001
HMBS	GO_PROTEIN_COFACTOR_LINKAGE	15	Up	0.0009	0.0692
XPO7	GO_ESTABLISHMENT_OF_RNA_LOCALIZATION	277	Down	0.0011	0.0741
HMBS	GO_HEME_METABOLIC_PROCESS	34	Up	<0.0001	0.0046
HMBS	GO_PROTOPORPHYRINOGEN_IX_METABOLIC_PROCESS	17	Up	<0.0001	<0.0001
TRIM8 ISG15 OAS2	GO_NEGATIVE_REGULATION_OF_VIRAL_LIFE_CYCLE	107	Up	0.001	0.0705
DC 7-13					
Gene Symbols	Gene Pathway	NGenes	Direction	PValue	FDR
EIF1AY RPS4Y1	GO_TRANSLATIONAL_INITIATION	497	Up	<0.0001	0.0004
RPS4Y1	GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	396	Up	<0.0001	<0.0001
RPS4Y1	GO_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	423	Up	<0.0001	0.0002
RPS4Y1	GO_PROTEIN_TARGETING_TO_MEMBRANE	473	Up	<0.0001	0.001
RPS4Y1	GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_NONSENSE_MEDIATED_DECAY	411	Up	<0.0001	<0.0001
RPS4Y1 RPS4Y2	GO_RIBOSOME	536	Up	<0.0001	0.001
RPS4Y1 RPS4Y2	GO_CYTOSOLIC_SMALL_RIBOSOMAL_SUBUNIT	174	Up	<0.0001	0.001
RPS4Y1 RPS4Y2	GO_SMALL_RIBOSOMAL_SUBUNIT	210	Up	<0.0001	0.0168
STXBP2	GO_SPECIFIC_GRANULE	214	Down	<0.0001	0.0123
RPS4Y1 RPS4Y2	GO_RIBOSOMAL_SUBUNIT	490	Up	<0.0001	0.0002
RPS4Y1 RPS4Y2	GO_CYTOSOLIC_RIBOSOME	384	Up	<0.0001	<0.0001
RPS4Y1 RPS4Y2	GO_STRUCTURAL_CONSTITUENT_OF_RIBOSOME	462	Up	<0.0001	0.0002
RPS4Y1 RPS4Y2	GO_STRUCTURAL_MOLECULE_ACTIVITY	791	Up	0.0003	0.0612
RPS4Y1	GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS	513	Up	<0.0001	0.0046
RPS4Y1	GO_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE	382	Up	<0.0001	<0.0001
TRIM8 RPS4Y1	GO_VIRAL_GENE_EXPRESSION	503	Up	<0.0001	0.0008
DC 14-20					
Gene Symbols	Gene Pathway	NGenes	Direction	PValue	FDR
EIF1AY RPS4Y1	GO_TRANSLATIONAL_INITIATION	497	Up	<0.0001	<0.0001

OAS2 ISG15 OAS1 RSAD2	GO_RESPONSE_TO_TYPE_I_INTERFERON	125	Down	0.0006	0.0937
RPS4Y1	GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	396	Up	<0.0001	<0.0001
RPS4Y1	GO_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	423	Up	<0.0001	0.0001
RPS4Y1	GO_PROTEIN_TARGETING_TO_MEMBRANE	473	Up	<0.0001	0.0024
RPS4Y1	GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_NONSENSE_MEDIATED_DECAY	411	Up	<0.0001	<0.0001
RPS4Y1 RPS4Y2	GO_RIBOSOME	536	Up	<0.0001	0.0004
RPS4Y1 RPS4Y2	GO_CYTOSOLIC_SMALL_RIBOSOMAL_SUBUNIT	174	Up	<0.0001	0.0011
RPS4Y1 RPS4Y2	GO_SMALL_RIBOSOMAL_SUBUNIT	210	Up	<0.0001	0.0212
RPS4Y1	GO_POLYSOME	179	Up	<0.0001	0.008
RPS4Y1 RPS4Y2	GO_RIBOSOMAL_SUBUNIT	490	Up	<0.0001	0.0004
RPS4Y1 RPS4Y2	GO_CYTOSOLIC_RIBOSOME	384	Up	<0.0001	<0.0001
RPS4Y1 RPS4Y2	GO_STRUCTURAL_CONSTITUENT_OF_RIBOSOME	462	Up	<0.0001	0.0002
EIF1AY	GO_TRANSLATION_FACTOR_ACTIVITY_RNA_BINDING	128	Up	0.0001	0.0278
RPS4Y1 RPS4Y2	GO_RRNA_BINDING	119	Up	0.0003	0.0662
EIF1AY	GO_TRANSLATION_REGULATOR_ACTIVITY	200	Up	0.0002	0.046
EIF1AY	GO_TRANSLATION_REGULATOR_ACTIVITY_NUCLEIC_ACID_BINDING	152	Up	0.0004	0.0695
RPS4Y1 RPS4Y2	GO_STRUCTURAL_MOLECULE_ACTIVITY	791	Up	0.0003	0.0608
RPS4Y1	GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS	513	Up	<0.0001	0.0033
RPS4Y1	GO_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE	382	Up	<0.0001	<0.0001
TRIM8 RPS4Y1	GO_VIRAL_GENE_EXPRESSION	503	Up	<0.0001	0.0001
DC 21-27					
Gene Symbols	Gene Pathway	NGenes	Direction	PValue	FDR
EIF1AY RPS4Y1	GO_TRANSLATIONAL_INITIATION	497	Up	<0.0001	0.002
RPS4Y1	GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	396	Up	<0.0001	0.0027
RPS4Y1	GO_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	423	Up	<0.0001	0.0111
RPS4Y1	GO_PROTEIN_TARGETING_TO_MEMBRANE	473	Up	0.0001	0.0284
RPS4Y1	GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_NONSENSE_MEDIATED_DECAY	411	Up	<0.0001	0.0009
STXBP2 SERPING1	GO_PLATELET_DEGRANULATION	120	Down	0.0003	0.0542
RPS4Y1 RPS4Y2	GO_RIBOSOME	536	Up	0.0001	0.0269
RPS4Y1 RPS4Y2	GO_CYTOSOLIC_SMALL_RIBOSOMAL_SUBUNIT	174	Up	<0.0001	0.0009
RPS4Y1 RPS4Y2	GO_SMALL_RIBOSOMAL_SUBUNIT	210	Up	<0.0001	0.019
SERPING1	GO_PLATELET_ALPHA_GANULE_LUMEN	59	Down	0.0007	0.0844
STXBP2	GO_SPECIFIC_GANULE	214	Down	<0.0001	0.0087
RPS4Y1	GO_POLYSOME	179	Up	0.0002	0.0302
RPS4Y1 RPS4Y2	GO_RIBOSOMAL_SUBUNIT	490	Up	<0.0001	0.0237
RPS4Y1 RPS4Y2	GO_CYTOSOLIC_RIBOSOME	384	Up	<0.0001	0.0005
RPS4Y1 RPS4Y2	GO_STRUCTURAL_CONSTITUENT_OF_RIBOSOME	462	Up	<0.0001	0.019
EIF1AY	GO_TRANSLATION_FACTOR_ACTIVITY_RNA_BINDING	128	Up	0.0003	0.0459
EIF1AY	GO_TRANSLATION_REGULATOR_ACTIVITY	200	Up	0.0009	0.0926

EIF1AY	GO_TRANSLATION_REGULATOR_ACTIVITY_NUCLEIC_ACID_BINDING	152	Up	0.0005	0.0718
RPS4Y1	GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS	513	Up	0.0001	0.0273
RPS4Y1	GO_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE	382	Up	<0.0001	0.0009
TRIM8 RPS4Y1	GO_VIRAL_GENE_EXPRESSION	503	Up	<0.0001	0.015
STXBP2	GO_CYTOLYTIC_GRANULE	7	Down	0.0002	0.0425

Table S13 Differentially expressed genes present in specific gene pathways associated with increased concentrations of black carbon at multiple lag periods

BC 0-6					
GeneSymbols	Gene Pathway	NGenes	Direction	PValue	FDR
TRIM8 ISG15 OAS2 RSAD2 OAS1	GO_NEGATIVE_REGULATION_OF_VIRAL_PROCESS	124	Up	<0.0001	<0.0001
IFI27 ISG15 OAS2 RSAD2 OAS1	GO_RESPONSE_TO_TYPE_I_INTERFERON	125	Up	<0.0001	<0.0001
IFI27 ISG15 OAS2 IFI44L RSAD2 OAS1	GO_DEFENSE_RESPONSE_TO_VIRUS	296	Up	<0.0001	<0.0001
IFI27 TRIM8 ISG15 OAS2 RSAD2 OAS1	GO_REGULATION_OF_SYMBIOSIS_ENCOMPASSING_MUTUALISM_THROUGH_PARASITISM	282	Up	0.0005	0.0975
IFI27 ISG15 OAS2 RSAD2 OAS1	GO_VIRAL_GENOME_REPLICATION	184	Up	<0.0001	0.0029
TRIM8 OAS2 OAS1	GO_INTERFERON_GAMMA_MEDIATED_SIGNALING_PATHWAY	111	Up	<0.0001	0.0002
TRIM8 OAS2 OAS1	GO_RESPONSE_TO_INTERFERON_GAMMA	214	Up	0.0004	0.0884
SERPING1 TRIM8 ISG15 OAS2 RSAD2 OAS1	GO_NEGATIVE_REGULATION_OF_MULTIORGANISM_PROCESS	260	Up	<0.0001	0.0015
IFI27 ISG15 OAS2 RSAD2 OAS1	GO_REGULATION_OF_VIRAL_GENOME_REPLICATION	139	Up	<0.0001	<0.0001
ISG15 OAS2 RSAD2 OAS1	GO_NEGATIVE_REGULATION_OF_VIRAL_GENOME_REPLICATION	81	Up	<0.0001	<0.0001
TRIM8	GO_REGULATION_OF_VIRAL_ENTRY_INTO_HOST_CELL	33	Up	<0.0001	0.012
IFI27 ISG15 OAS2 IFI44 IFI44L RSAD2 OAS1	GO_RESPONSE_TO_VIRUS	398	Up	<0.0001	0.0002
OAS2 OAS1	GO_ADENYLYLTRANSFERASE_ACTIVITY	32	Up	<0.0001	0.0073
OAS2 OAS1	GO_DOUBLE_STRANDED_RNA_BINDING	101	Up	0.0002	0.0451
ISG15	GO_ISG15_PROTEIN_CONJUGATION	8	Up	<0.0001	0.0012
RSAD2	GO_TOLL LIKE RECEPTOR 7 SIGNALING PATHWAY	15	Up	0.0001	0.0397
OAS2 OAS1	GO_REGULATION_OF_RIBONUCLEASE_ACTIVITY	22	Up	<0.0001	<0.0001
IFI27 TRIM8 ISG15 OAS2 RSAD2 OAS1	GO_REGULATION_OF_VIRAL_LIFE_CYCLE	192	Up	<0.0001	<0.0001
CARD17	GO_CASPASE_BINDING	10	Up	<0.0001	0.0262
TRIM8 ISG15 OAS2 RSAD2 OAS1	GO_NEGATIVE_REGULATION_OF_VIRAL_LIFE_CYCLE	107	Up	<0.0001	<0.0001
BC 21-27					
GeneSymbols	Gene Pathway	NGenes	Direction	PValue	FDR
EIF1AY RPS4Y1	GO_TRANSLATIONAL_INITIATION	497	Up	<0.0001	<0.0001
RPS4Y1 TIMM10	GO_PROTEIN_TARGETING	739	Up	0.0003	0.0627
RPS4Y1	GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	396	Up	<0.0001	<0.0001
RPS4Y1	GO_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	423	Up	<0.0001	<0.0001
RPS4Y1	GO_PROTEIN_TARGETING_TO_MEMBRANE	473	Up	<0.0001	<0.0001
RPS4Y1 TIMM10	GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_MEMBRANE	626	Up	<0.0001	0.0332
RPS4Y1	GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_NONSENSE_MEDIATED_DECAY	411	Up	<0.0001	<0.0001
ISG15 OAS2 OAS1	GO_NEGATIVE_REGULATION_OF_VIRAL_GENOME_REPLICATION	81	Up	0.0003	0.0635

RPS4Y1 RPS4Y2	GO_RIBOSOME	536	Up	<0.0001	<0.0001
RPS4Y1 RPS4Y2	GO_CYTOSOLIC_SMALL_RIBOSOMAL_SUBUNIT	174	Up	<0.0001	<0.0001
RPS4Y1 RPS4Y2	GO_SMALL_RIBOSOMAL_SUBUNIT	210	Up	<0.0001	<0.0001
STXBP2	GO_SPECIFIC_GRANULE	214	Down	0.0001	0.0378
RPS4Y1	GO_POLYSOME	179	Up	<0.0001	0.0052
RPS4Y1 RPS4Y2	GO_RIBOSOMAL_SUBUNIT	490	Up	<0.0001	<0.0001
RPS4Y1 RPS4Y2	GO_CYTOSOLIC_RIBOSOME	384	Up	<0.0001	<0.0001
RPS4Y1 RPS4Y2	GO_STRUCTURAL_CONSTITUENT_OF_RIBOSOME	462	Up	<0.0001	<0.0001
RPS4Y1	GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCES S	513	Up	<0.0001	<0.0001
RPS4Y1	GO_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMB RANE	382	Up	<0.0001	<0.0001
TRIM8 RPS4Y1	GO_VIRAL_GENE_EXPRESSION	503	Up	<0.0001	<0.0001
OAS2 OAS1	GO_REGULATION_OF_RIBONUCLEASE_ACTIVITY	22	Up	0.0001	0.0403
STXBP2	GO_CYTOLYTIC_GRANULE	7	Down	0.0002	0.0501

Table S14. Differentially expressed genes present in specific gene pathways associated with increased concentrations of PM_{2.5} at multiple lag periods

PM25 0-6					
GeneSymbols	Differentially Expressed Gene	NGenes	Direction	PValue	FDR
ORM1 STXBP2	GO_SPECIFIC_GRANULE	214	Down	<0.0001	0.0808
ORM1	GO_SPECIFIC_GRANULE_LUMEN	73	Down	<0.0001	0.0102
PM25 7-13					
GeneSymbols	Differentially Expressed Gene	NGenes	Direction	PValue	FDR
ISG15	GO_MYELOID_CELL_HOMEOSTASIS	204	Up	0.0019	0.0955
RPS4Y1 EIF1AY	GO_TRANSLATIONAL_INITIATION	497	Down	0.0001	0.0199
MRPS34	GO_MITOCHONDRIAL_TRANSLATION	154	Down	<0.0001	0.0001
RPS4Y1	GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	396	Down	<0.0001	0.0014
TSPO	GO_TETRAPYRROLE_BIOSYNTHETIC_PROCESS	37	Up	0.0006	0.0528
MRPS34	GO_TRANSLATIONAL_TERMINATION	129	Down	<0.0001	0.0005
TSPO	GO_PORPHYRIN_CONTAINING_COMPOUND_METABOLIC_PROCESS	41	Up	<0.0001	0.0076
RPS4Y1	GO_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	423	Down	<0.0001	0.0039
RPS4Y1	GO_PROTEIN_TARGETING_TO_MEMBRANE	473	Down	0.0002	0.024
RPS4Y1 TIMM10	GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_MEMBRANE	626	Down	0.0016	0.0879
MRPS34	GO_TRANSLATIONAL_ELONGATION	187	Down	<0.0001	0.0057
RPS4Y1	GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_NONSENSE_MEDIATED_DECAY	411	Down	<0.0001	0.0086
TSPO	GO_HEME_BIOSYNTHETIC_PROCESS	30	Up	<0.0001	0.0122
RPS4Y1 OAS2	GO_RNA_CATABOLIC_PROCESS	768	Down	0.0016	0.0879
MRPS34 RPS4Y1 RPS4Y2	GO_RIBOSOME	536	Down	<0.0001	0.0028
USPL1	GO_CAJAL_BODY	67	Down	0.0004	0.0362
RPS4Y1 RPS4Y2	GO_CYTOSOLIC_SMALL_RIBOSOMAL_SUBUNIT	174	Down	<0.0001	0.0076
MRPS34 RPS4Y1 RPS4Y2	GO_SMALL_RIBOSOMAL_SUBUNIT	210	Down	<0.0001	0.0012
MRPS34	GO_ORGANELLAR_RIBOSOME	103	Down	<0.0001	0.0001
TIMM10	GO_INNER_MITOCHONDRIAL_MEMBRANE_PROTEIN_COMPLEX	143	Down	<0.0001	0.0144
RPS4Y1	GO_POLYSOME	179	Down	0.0009	0.0629
MRPS34 RPS4Y1 RPS4Y2	GO_RIBOSOMAL_SUBUNIT	490	Down	<0.0001	0.0009
MRPS34 RPS4Y1 RPS4Y2	GO_RIBONUCLEOPROTEIN_COMPLEX	1147	Down	0.0001	0.0181
MRPS34 TIMM10	GO_MITOCHONDRIAL_PROTEIN_COMPLEX	298	Down	<0.0001	0.0006
RPS4Y1 RPS4Y2	GO_CYTOSOLIC_RIBOSOME	384	Down	<0.0001	0.0076
MRPS34 RPS4Y1 RPS4Y2	GO_STRUCTURAL_CONSTITUENT_OF_RIBOSOME	462	Down	<0.0001	0.0006
RPS4Y1 RPS4Y2	GO_RRNA_BINDING	119	Down	0.0002	0.024
RPS4Y1	GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS	513	Down	<0.0001	0.0086
RPS4Y1	GO_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE	382	Down	<0.0001	0.0026
TRIM8 RPS4Y1	GO_VIRAL_GENE_EXPRESSION	503	Down	0.0004	0.0419
MRPS34 RPS4Y1 EIF1AY RPS4Y2	GO_PEPTIDE_BIOSYNTHETIC_PROCESS	1052	Down	0.0012	0.0735
MRPS34	GO_MITOCHONDRIAL_TRANSLATIONAL_TERMINATION	109	Down	<0.0001	0.0001
MRPS34	GO_MITOCHONDRIAL_GENE_EXPRESSION	190	Down	<0.0001	0.0006
TSPO	GO_HEME_METABOLIC_PROCESS	34	Up	<0.0001	0.0118
TSPO	GO_NEGATIVE_REGULATION_OF_ATP_METABOLIC_PROCESSES	27	Up	0.0017	0.0898
MRPS34	GO_MITOCHONDRIAL_SMALL_RIBOSOMAL_SUBUNIT	33	Down	<0.0001	0.0016
PM25 14-20					
GeneSymbols	Gene Pathway	NGenes	Direction	PValue	FDR
RPS4Y1 RPS4Y2	GO_RIBOSOME	536	Down	0.0012	0.0923
RPS4Y1 RPS4Y2	GO_CYTOSOLIC_SMALL_RIBOSOMAL_SUBUNIT	174	Down	0.0006	0.0622

RPS4Y1 RPS4Y2	GO_SMALL_RIBOSOMAL_SUBUNIT	210	Down	<0.0001	0.0186
RPS4Y1 RPS4Y2	GO_RIBOSOMAL_SUBUNIT	490	Down	0.0004	0.0523
RPS4Y1 RPS4Y2	GO_RIBONUCLEOPROTEIN_COMPLEX	1147	Down	<0.0001	0.0196
RPS4Y1 RPS4Y2	GO_STRUCTURAL_CONSTITUENT_OF_RIBOSOME	462	Down	0.0007	0.0625
EIF1AY RPS4Y1 RPS4Y2	GO_RNA_BINDING	2299	Down	0.0004	0.0512

Table S15. Differentially expressed genes present in specific gene pathways associated with increased concentrations of ultrafine particles at multiple lag periods

UFP 0-6					
GeneSymbols	Gene Pathway	NGenes	Direction	PValue	FDR
STXBP2	GO_MYELOID_LEUKOCYTE_MEDIATED_IMMUNITY	760	Down	0.0003	0.0577
STXBP2	GO_REGULATION_OF_LEUKOCYTE_DEGRANULATION	65	Down	0.0005	0.0858
STXBP2	GO_SPECIFIC_GRANULE	214	Down	<0.0001	0.0022
STXBP2	GO_AZUROPHIL_GRANULE	209	Down	0.0005	0.0858
STXBP2	GO_TERTIARY_GRANULE	224	Down	0.0003	0.0653
UFP 7-13					
GeneSymbols	Gene Pathway	NGenes	Direction	PValue	FDR
STXBP2 RARA	GO_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	928	Down	0.0002	0.0573
STXBP2	GO_MYELOID_LEUKOCYTE_ACTIVATION	867	Down	<0.0001	0.0422
STXBP2	GO_MYELOID_LEUKOCYTE_MEDIATED_IMMUNITY	760	Down	<0.0001	0.013
STXBP2	GO_REGULATION_OF_LEUKOCYTE_DEGRANULATION	65	Down	<0.0001	0.0449
STXBP2 LHFPL2	GO_EXOCYTOSIS	1042	Down	0.0001	0.0512
STXBP2 LHFPL2	GO_SECRETORY_GRANULE	918	Down	0.0003	0.0641
STXBP2	GO_SPECIFIC_GRANULE	214	Down	<0.0001	<0.0001
STXBP2 LHFPL2	GO_SECRETORY_GRANULE_MEMBRANE	361	Down	<0.0001	0.0049
RPS4Y1 RPS4Y2	GO_CYTOSOLIC_RIBOSOME	384	Up	0.0001	0.0512
MAPK3	GO_REGULATION_OF_CYCLASE_ACTIVITY	30	Down	0.0002	0.052
STXBP2	GO_AZUROPHIL_GRANULE	209	Down	0.0002	0.0512
STXBP2	GO_TERTIARY_GRANULE	224	Down	<0.0001	0.0024
UFP 14-20					
GeneSymbols	Gene Pathway	NGenes	Direction	PValue	FDR
SHKBP1	GO_REGULATION_OF_ERBB_SIGNALING_PATHWAY	116	Down	0.0055	0.0971
SCARB2	GO_ENDOSOME_ORGANIZATION	77	Down	0.0004	0.0187
SCARB2	GO_VESICLE_ORGANIZATION	359	Down	0.0003	0.0143
STXBP2	GO_REGULATION_OF_MAST_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	34	Down	0.0005	0.0211
EIF1AY RPS4Y1	GO_TRANSLATIONAL_INITIATION	497	Up	<0.0001	<0.0001
SCARB2 RPS4Y1					
TIMM10	GO_PROTEIN_TARGETING	739	Up	<0.0001	<0.0001
STXBP2	GO_REGULATION_OF_EXOCYTOSIS	190	Down	<0.0001	0.0002
OAS2	GO_REGULATION_OF_BODY_FLUID_LEVELS	452	Down	0.0002	0.0113
RPS4Y1	GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	396	Up	<0.0001	<0.0001
ORM1 STXBP2	GO_CELL_ACTIVATION	1616	Down	0.0007	0.0282
SCARB2	GO_REGULATION_OF_VACUOLE_ORGANIZATION	61	Down	<0.0001	0.006
SCARB2 RPS4Y1	GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ORGANELLE	904	Up	<0.0001	0.0011
TIMM10					
ORM1	GO_INTERLEUKIN_1_PRODUCTION	127	Down	0.0003	0.0146
ORM1 BTN3A3					
STXBP2	GO_LEUKOCYTE_MEDIATED_IMMUNITY	988	Down	<0.0001	0.0035
STXBP2	GO_REGULATION_OF_VESICLE_MEDIATED_TRANSPORT	511	Down	0.0001	0.0083
ORM1	GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_6_PRODUCTION	49	Down	0.0007	0.0268
RPS4Y1	GO_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	423	Up	<0.0001	<0.0001
EIF1AY RPS4Y1					
RPS4Y2	GO_PEPTIDE_METABOLIC_PROCESS	1190	Up	<0.0001	<0.0001
ORM1 OAS2					
STXBP2 ISG15	GO_SECRETION	1645	Down	0.0003	0.0138
ORM1 STXBP2	GO_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	928	Down	<0.0001	0.0028
SCARB2	GO_CELLULAR_CARBOHYDRATE_CATABOLIC_PROCESS	50	Down	0.0004	0.0179
STXBP2	GO_MAST_CELL_ACTIVATION	63	Down	0.0003	0.0152
RPS4Y1	GO_PROTEIN_TARGETING_TO_MEMBRANE	473	Up	<0.0001	<0.0001
RPS4Y1 TIMM10	GO_PROTEIN_LOCALIZATION_TO_MEMBRANE	896	Up	0.0004	0.0175
OAS2 ISG15 IFI44	GO_RESPONSE_TO_BACTERIUM	543	Down	0.0017	0.0504
ORM1 OAS2					
STXBP2	GO_REGULATION_OF_SECRETION	701	Down	0.0051	0.0941
ORM1	GO_ACUTE_INFLAMMATORY_RESPONSE	88	Down	<0.0001	0.0019
ORM1 STXBP2	GO_MYELOID_LEUKOCYTE_ACTIVATION	867	Down	<0.0001	0.0002
TIMM10	GO_INNER_MITOCHONDRIAL_MEMBRANE_ORGANIZATION	58	Up	0.0002	0.0102

EIF1AY RPS4Y1 RPS4Y2	GO_CELLULAR_AMIDE_METABOLIC_PROCESS	1444	Up	<0.0001	0.0046
STXBP2	GO_LYSOSOME_LOCALIZATION	87	Down	<0.0001	0.0019
STXBP2	GO_REGULATION_OF_MAST_CELL_ACTIVATION	41	Down	<0.0001	0.0063
EIF1AY RPS4Y1 RPS4Y2	GO_AMIDE_BIOSYNTHETIC_PROCESS	1194	Up	<0.0001	<0.0001
ORM1	GO_POSITIVE_REGULATION_OF_INTERLEUKIN_1_PRODUCTI ON	69	Down	0.0024	0.0597
RPS4Y1 TIMM10	GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ME MBRANE	626	Up	<0.0001	<0.0001
ORM1	GO_INFLAMMATORY_RESPONSE	698	Down	0.0005	0.0214
STXBP2	GO_REGULATION_OF_REGULATED_SECRETORY_PATHWAY	137	Down	<0.0001	0.0007
ORM1	GO_POSITIVE_REGULATION_OF_CYTOKINE_SECRETION	151	Down	0.0024	0.0604
ORM1 STXBP2	GO_MYELOID_LEUKOCYTE_MEDIATED_IMMUNITY	760	Down	<0.0001	<0.0001
ORM1 ISG15	GO_CYTOKINE_SECRETION	250	Down	0.0011	0.0374
OAS2 RPS4Y1	GO_ORGANIC_CYCLIC_COMPOUND_CATABOLIC_PROCESS	968	Up	<0.0001	0.0005
TRIM8 OAS2 SCARB2 RPS4Y1 ISG15	GO_INTERSPECIES_INTERACTION_BETWEEN_ORGANISMS	1432	Up	0.0018	0.0517
TRIM8 SCARB2 RPS4Y1 TIMM10	GO_PROTEIN_LOCALIZATION_TO_ORGANELLE	1306	Up	0.003	0.0685
STXBP2	GO_MAST_CELL_MEDIATED_IMMUNITY	55	Down	0.0008	0.0295
SCARB2	GO_LYTIC_VACUOLE_ORGANIZATION	69	Down	0.0053	0.0947
RPS4Y1	GO_MRNA_METABOLIC_PROCESS	1313	Up	0.0008	0.029
EIF1AY RPS4Y1 RPS4Y2	GO_ORGANONITROGEN_COMPOUND_BIOSYNTHETIC_PROCE SS	2133	Up	0.001	0.0359
RPS4Y1	GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS _NONSENSE_MEDIATED_DECAY	411	Up	<0.0001	<0.0001
STXBP2	GO_REGULATION_OF_LEUKOCYTE_DEGRANULATION	65	Down	<0.0001	<0.0001
ORM1 STXBP2	GO_EXOCYTOSIS	1042	Down	<0.0001	0.0003
STXBP2	GO_VESICLE_DOCKING	68	Down	0.002	0.0542
SCARB2	GO_RECEPTOR_MEDIATED_ENDOCYTOSIS	234	Down	0.001	0.0351
ORM1 STXBP2	GO_PLATELET_DEGRANULATION	120	Down	<0.0001	0.0003
ISG15	GO_INTEGRIN_MEDIATED_SIGNALING_PATHWAY	121	Down	<0.0001	0.0013
OAS2 RPS4Y1	GO_RNA_CATABOLIC_PROCESS	768	Up	<0.0001	<0.0001
SCARB2	GO_ENDOCYTOSIS	522	Down	0.0021	0.0551
ORM1	GO_POSITIVE_REGULATION_OF_SECRETION	387	Down	0.0043	0.0849
ISG15	GO_DEFENSE_RESPONSE_TO_BACTERIUM	177	Down	0.004	0.0809
ORM1	GO_ACUTE_PHASE_RESPONSE	34	Down	0.0001	0.0069
ORM1 BTN3A3 OAS2 STXBP2 ISG15 IFIT3	GO_IMMUNE_EFFECTOR_PROCESS	1454	Down	0.0052	0.0946
STXBP2	GO_PHAGOCYTIC_VESICLE	166	Down	<0.0001	<0.0001
ORM1 STXBP2	GO_SECRETORY_GRANULE	918	Down	<0.0001	0.0006
STXBP2 SCARB2	GO_VESICLE_MEMBRANE	828	Down	<0.0001	0.0048
ORM1	GO_PLATELET_ALPHA_GRANULE	82	Down	0.0001	0.0069
RPS4Y1 RPS4Y2	GO_RIBOSOME	536	Up	<0.0001	<0.0001
ORM1 STXBP2	GO_SECRETORY_VESICLE	1039	Down	<0.0001	0.0012
ORM1	GO_VESICLE_LUMEN	397	Down	0.0019	0.0525
RPS4Y1 RPS4Y2	GO_CYTOSOLIC_SMALL_RIBOSOMAL_SUBUNIT	174	Up	<0.0001	<0.0001
TIMM10	GO_ORGANELLE_INNER_MEMBRANE	537	Up	0.0041	0.0824
RPS4Y1 RPS4Y2	GO_SMALL_RIBOSOMAL_SUBUNIT	210	Up	<0.0001	<0.0001
ORM1	GO_PLATELET_ALPHA_GRANULE_LUMEN	59	Down	0.0004	0.0179
ORM1 STXBP2	GO_SPECIFIC_GRANULE	214	Down	<0.0001	<0.0001
SCARB2	GO_VACUOLAR_LUMEN	201	Down	0.0054	0.0963
TIMM10	GO_INNER_MITOCHONDRIAL_MEMBRANE_PROTEIN_COMPL EX	143	Up	0.0013	0.0422
STXBP2	GO_SECRETORY_GRANULE_MEMBRANE	361	Down	<0.0001	<0.0001
RPS4Y1	GO_POLYSOME	179	Up	<0.0001	<0.0001
RPS4Y1 RPS4Y2	GO_RIBOSOMAL_SUBUNIT	490	Up	<0.0001	<0.0001
NARF KDM5D	GO_NUCLEOLUS	1177	Up	0.0049	0.0914
RPS4Y1 RPS4Y2	GO_RIBONUCLEOPROTEIN_COMPLEX	1147	Up	<0.0001	<0.0001
TIMM10	GO_MITOCHONDRIAL_PROTEIN_COMPLEX	298	Up	<0.0001	0.0013
RPS4Y1 RPS4Y2	GO_CYTOSOLIC_RIBOSOME	384	Up	<0.0001	<0.0001
EIF1AY	GO_TRANSLATION_INITIATION_FACTOR_ACTIVITY	71	Up	0.0007	0.0279
RPS4Y1 RPS4Y2	GO_STRUCTURAL_CONSTITUENT_OF_RIBOSOME	462	Up	<0.0001	<0.0001
EIF1AY	GO_TRANSLATION_FACTOR_ACTIVITY_RNA_BINDING	128	Up	<0.0001	0.0001

SCARB2	GO_CARGO_RECEPTOR_ACTIVITY	51	Down	0.003	0.0682
RPS4Y1 RPS4Y2	GO_RRNA_BINDING	119	Up	<0.0001	<0.0001
EIF1AY	GO_TRANSLATION_REGULATOR_ACTIVITY	200	Up	<0.0001	0.0003
EIF1AY	GO_TRANSLATION_REGULATOR_ACTIVITY_NUCLEIC_ACID_BINDING	152	Up	<0.0001	0.0003
EFEMP2 RPS4Y1 RPS4Y2	GO_STRUCTURAL_MOLECULE_ACTIVITY	791	Up	<0.0001	<0.0001
OAS2 EIF1AY RPS4Y1 RPS4Y2	GO_RNA_BINDING	2299	Up	0.0003	0.016
RPS4Y1	GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS	513	Up	<0.0001	<0.0001
STXBP2	GO_REGULATION_OF_MYELOID_LEUKOCYTE_MEDIATED_IMMUNITY	71	Down	<0.0001	0.0008
RPS4Y1	GO_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE	382	Up	<0.0001	<0.0001
TRIM8 RPS4Y1	GO_VIRAL_GENE_EXPRESSION	503	Up	<0.0001	<0.0001
ORM1	GO_INTERLEUKIN_1_BETA_PRODUCTION	114	Down	0.0008	0.0293
ORM1	GO_INTERLEUKIN_6_PRODUCTION	170	Down	0.0006	0.023
EIF1AY RPS4Y1 RPS4Y2	GO_PEPTIDE_BIOSYNTHETIC_PROCESS	1052	Up	<0.0001	<0.0001
ORM1	GO_INTERLEUKIN_1_SECRETION	76	Down	0.0014	0.0443
STXBP2	GO_EXOCYTIC_PROCESS	77	Down	0.0024	0.0604
TIMM10	GO_TIM23_MITOCHONDRIAL_IMPORT_INNER_MEMBRANE_TRANSLOCASE_COMPLEX	18	Up	0.0012	0.0388
ORM1	GO_SPECIFIC_GRANULE_LUMEN	73	Down	<0.0001	<0.0001
STXBP2	GO_AZUROPHIL_GRANULE	209	Down	<0.0001	0.0015
ORM1 STXBP2	GO_TERTIARY_GRANULE	224	Down	<0.0001	<0.0001
STXBP2 SCARB2	GO_WHOLE_MEMBRANE	1768	Down	0.0052	0.0947
ORM1	GO_TERTIARY_GRANULE_LUMEN	76	Down	<0.0001	0.0044
OAS2 RPS4Y1	GO_CELLULAR_NITROGEN_COMPOUND_CATABOLIC_PROCESS	943	Up	<0.0001	0.0004
ORM1	GO_REGULATION_OF_INTERLEUKIN_1_SECRETION	64	Down	0.001	0.0341
UFP 21-27					
GeneSymbols	Gene Pathway	NGenes	Direction	PValue	FDR
SERPING1	GO_REGULATION_OF_WOUND_HEALING	134	Down	0.0022	0.0901
SERPING1	GO_RESPONSE_TO_WOUNDING	627	Down	0.0014	0.0703
EIF1AY RPS4Y1	GO_TRANSLATIONAL_INITIATION	497	Up	<0.0001	<0.0001
RPS4Y1 TIMM10	GO_PROTEIN_TARGETING	739	Up	<0.0001	<0.0001
STXBP2	GO_REGULATION_OF_EXOCYTOSIS	190	Down	<0.0001	0.0025
OAS2 SERPING1	GO_REGULATION_OF_BODY_FLUID_LEVELS	452	Down	0.0023	0.0932
RPS4Y1	GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	396	Up	<0.0001	<0.0001
STXBP2	GO_CELL_ACTIVATION	1616	Down	0.0017	0.0775
RPS4Y1 TIMM10	GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ORGANELLE	904	Up	<0.0001	0.0087
STXBP2 BTN3A3	GO_LEUKOCYTE_MEDIATED_IMMUNITY	988	Down	0.0003	0.0243
SERPING1					
STXBP2					
SERPING1					
RPS4Y1	GO_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	423	Up	<0.0001	<0.0001
SERPING1	GO_NEGATIVE_REGULATION_OF_COAGULATION	44	Down	0.0025	0.0997
EIF1AY RPS4Y1 RPS4Y2	GO_PEPTIDE_METABOLIC_PROCESS	1190	Up	0.0001	0.0117
STXBP2 OAS2	GO_SECRETION	1645	Down	0.0024	0.0955
SERPING1 ISG15					
STXBP2	GO_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	928	Down	0.0002	0.0175
RPS4Y1	GO_PROTEIN_TARGETING_TO_MEMBRANE	473	Up	<0.0001	<0.0001
RPS4Y1 TIMM10	GO_PROTEIN_LOCALIZATION_TO_MEMBRANE	896	Up	0.0004	0.0319
STXBP2	GO_MYELOID_LEUKOCYTE_ACTIVATION	867	Down	<0.0001	0.0094
EIF1AY RPS4Y1 RPS4Y2	GO_CELLULAR_AMIDE_METABOLIC_PROCESS	1444	Up	0.0021	0.0881
EIF1AY RPS4Y1 RPS4Y2	GO_AMIDE_BIOSYNTHETIC_PROCESS	1194	Up	<0.0001	0.0096
RPS4Y1 TIMM10	GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_MEMBRANE	626	Up	<0.0001	<0.0001
STXBP2	GO_REGULATION_OF_REGULATED_SECRETORY_PATHWAY	137	Down	<0.0001	0.0043
STXBP2	GO_MYELOID_LEUKOCYTE_MEDIATED_IMMUNITY	760	Down	<0.0001	0.0025

OAS2 RPS4Y1	GO_ORGANIC_CYCLIC_COMPOUND_CATABOLIC_PROCESS	968	Up	<0.0001	0.0089
RPS4Y1	GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_NONSENSE_MEDIATED_DECAY	411	Up	<0.0001	<0.0001
STXBP2	GO_REGULATION_OF_LEUKOCYTE_DEGRANULATION	65	Down	<0.0001	0.0002
STXBP2 SERPING1	GO_EXOCYTOSIS	1042	Down	<0.0001	0.0034
STXBP2 SERPING1	GO_PLATELET_DEGRANULATION	120	Down	<0.0001	0.0048
ISG15	GO_INTEGRIN_MEDIATED_SIGNALING_PATHWAY	121	Down	<0.0001	0.0116
OAS2 RPS4Y1	GO_RNA_CATABOLIC_PROCESS	768	Up	<0.0001	0.0003
STXBP2	GO_PHAGOCYTIC_VESICLE	166	Down	<0.0001	0.0066
STXBP2 SERPING1	GO_SECRETORY_GRANULE	918	Down	0.0002	0.0185
STXBP2	GO_VESICLE_MEMBRANE	828	Down	0.0009	0.0541
SERPING1	GO_PLATELET_ALPHA_GRANULE	82	Down	0.0025	0.0989
RPS4Y1 RPS4Y2	GO_RIBOSOME	536	Up	<0.0001	<0.0001
STXBP2 SERPING1	GO_SECRETORY_VESICLE	1039	Down	0.0003	0.0233
SERPING1	GO_VESICLE_LUMEN	397	Down	0.0005	0.0331
RPS4Y1 RPS4Y2	GO_CYTOSOLIC_SMALL_RIBOSOMAL_SUBUNIT	174	Up	<0.0001	<0.0001
RPS4Y1 RPS4Y2	GO_SMALL_RIBOSOMAL_SUBUNIT	210	Up	<0.0001	<0.0001
STXBP2	GO_SPECIFIC_GRANULE	214	Down	<0.0001	<0.0001
STXBP2	GO_SECRETORY_GRANULE_MEMBRANE	361	Down	<0.0001	0.0003
RPS4Y1	GO_POLYSOME	179	Up	<0.0001	<0.0001
RPS4Y1 RPS4Y2	GO_RIBOSOMAL_SUBUNIT	490	Up	<0.0001	<0.0001
RPS4Y1 RPS4Y2	GO_RIBONUCLEOPROTEIN_COMPLEX	1147	Up	<0.0001	0.0074
RPS4Y1 RPS4Y2	GO_CYTOSOLIC_RIBOSOME	384	Up	<0.0001	<0.0001
RPS4Y1 RPS4Y2	GO_STRUCTURAL_CONSTITUENT_OF_RIBOSOME	462	Up	<0.0001	<0.0001
RPS4Y1 RPS4Y2	GO_RRNA_BINDING	119	Up	<0.0001	<0.0001
RPS4Y1 RPS4Y2	GO_STRUCTURAL_MOLECULE_ACTIVITY	791	Up	<0.0001	<0.0001
RPS4Y1	GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS	513	Up	<0.0001	<0.0001
STXBP2	GO_REGULATION_OF_MYELOID_LEUKOCYTE_MEDIATED_IMMUNITY	71	Down	<0.0001	0.0082
RPS4Y1	GO_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE	382	Up	<0.0001	<0.0001
TRIM8 RPS4Y1	GO_VIRAL_GENE_EXPRESSION	503	Up	<0.0001	<0.0001
EIF1AY RPS4Y1 RPS4Y2	GO_PEPTIDE_BIOSYNTHETIC_PROCESS	1052	Up	<0.0001	0.0012
SERPING1	GO_COAGULATION	334	Down	0.0004	0.0303
STXBP2	GO_AZUROPHIL_GRANULE	209	Down	<0.0001	0.0036
STXBP2	GO_TERTIARY_GRANULE	224	Down	<0.0001	0.0018
OAS2 RPS4Y1	GO_CELLULAR_NITROGEN_COMPOUND_CATABOLIC_PROCESS	943	Up	<0.0001	0.0077

Table S16. Differentially expressed genes present in specific gene pathways associated with increased concentrations of accumulation mode particles at multiple lag periods

AMP 0-6					
GeneSymbols	Gene Pathway	NGenes	Direction	PValue	FDR
TRIM8 ISG15 RSAD2	GO_NEGATIVE_REGULATION_OF_VIRAL_PROCESS	124	Up	0.0015	0.0625
EIF1AY RPS4Y1	GO_TRANSLATIONAL_INITIATION	497	Up	<0.0001	<0.0001
IFI27 ISG15 RSAD2	GO_RESPONSE_TO_TYPE_I_INTERFERON	125	Up	0.0022	0.0803
RPS4Y1	GO_PROTEIN_TARGETING	739	Up	0.0003	0.0232
MAPK3	GO_LUNG_MORPHOGENESIS	47	Down	0.0002	0.0191
RPS4Y1	GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	396	Up	<0.0001	<0.0001
IFI27 ISG15 RSAD2	GO_DEFENSE_RESPONSE_TO_VIRUS	296	Up	0.0015	0.0625
RPS4Y1	GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ORGANELLE	904	Up	0.0011	0.0519
FABP5 STXBP2 RSAD2	GO_LEUKOCYTE_MEDIATED_IMMUNITY	988	Down	0.0002	0.014
RPS4Y1	GO_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	423	Up	<0.0001	0.0001
RARA EIF1AY RPS4Y1 RPS4Y2 CPQ MAPK3	GO_PEPTIDE_METABOLIC_PROCESS	1190	Up	0.0006	0.0333
FABP5 STXBP2 MAPK3 ISG15 RSAD2	GO_SECRETION	1645	Down	0.0007	0.0388
FABP5 STXBP2 RARA	GO_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	928	Down	<0.0001	0.0058
RPS4Y1	GO_PROTEIN_TARGETING_TO_MEMBRANE	473	Up	<0.0001	0.001
FABP5 STXBP2	GO_MYELOID_LEUKOCYTE_ACTIVATION	867	Down	<0.0001	0.0008
RARA EIF1AY RPS4Y1 RPS4Y2 MAPK3	GO_AMIDE_BIOSYNTHETIC_PROCESS	1194	Up	0.0003	0.0237
MAPK3	GO GRANULOCYTE MIGRATION	113	Down	<0.0001	0.0075
RARA MAPK3	GO_FACE_DEVELOPMENT	43	Down	0.0029	0.0967
RPS4Y1	GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_MEMBRANE	626	Up	<0.0001	0.0083
IFI27 ISG15 RSAD2	GO_VIRAL_GENOME_REPLICATION	184	Up	0.0008	0.0431
STXBP2	GO_REGULATION_OF_REGULATED_SECRETORY_PATHWAY	137	Down	0.0019	0.0714
FABP5 STXBP2	GO_MYELOID_LEUKOCYTE_MEDIATED_IMMUNITY	760	Down	<0.0001	0.0001
UPB1 RPS4Y1	GO_ORGANIC_CYCLIC_COMPOUND_CATABOLIC_PROCESS	968	Up	0.0005	0.03
MAPK3	GO_TRACHEA_MORPHOGENESIS	15	Down	0.0002	0.0172
RPS4Y1	GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_NONSENSE_MEDIATED_DECAY	411	Up	<0.0001	<0.0001
STXBP2	GO_REGULATION_OF_LEUKOCYTE_DEGRANULATION	65	Down	<0.0001	0.0017
FABP5 STXBP2	GO_EXOCYTOSIS	1042	Down	<0.0001	0.0035
IFI27 ISG15 RSAD2	GO_REGULATION_OF_VIRAL_GENOME_REPLICATION	139	Up	<0.0001	0.0009
ISG15	GO_INTEGRIN_MEDIATED_SIGNALING_PATHWAY	121	Down	0.0012	0.0547
ISG15 RSAD2	GO_NEGATIVE_REGULATION_OF_VIRAL_GENOME_REPLICATION	81	Up	<0.0001	0.0058
RPS4Y1	GO_RNA_CATABOLIC_PROCESS	768	Up	<0.0001	0.0043
SLC9A1	GO_AMINOGLYCAN_CATABOLIC_PROCESS	48	Down	0.0006	0.0368
RARA MAPK3	GO_PHAGOCYTOSIS	322	Down	<0.0001	0.0078
RARA	GO_NEGATIVE_REGULATION_OF_TUMOR_NECROSIS_FACTOR_SUPERFAMILY_CYTOKINE_PRODUCTION	75	Down	0.0027	0.0911
MAPK3	GO_THYROID_GLAND_DEVELOPMENT	15	Down	0.0023	0.0805
MAPK3	GO_NEURAL_CREST_CELL_DIFFERENTIATION	62	Down	0.0017	0.0689
MAPK3	GO_ACTIVATION_OF_MAPKK_ACTIVITY	55	Down	0.0009	0.0437
STXBP2	GO_PHAGOCYTIC_VESICLE	166	Down	<0.0001	0.0028
FABP5 STXBP2	GO_SECRETORY_GRANULE	918	Down	<0.0001	0.0032
RPS4Y1 RPS4Y2	GO_RIBOSOME	536	Up	<0.0001	<0.0001
FABP5 STXBP2	GO_SECRETORY_VESICLE	1039	Down	<0.0001	0.0069
FABP5	GO_VESICLE_LUMEN	397	Down	0.0009	0.0443
RPS4Y1 RPS4Y2	GO_CYTOSOLIC_SMALL_RIBOSOMAL_SUBUNIT	174	Up	<0.0001	0.0017
RPS4Y1 RPS4Y2	GO_SMALL_RIBOSOMAL_SUBUNIT	210	Up	<0.0001	0.0008
STXBP2	GO_SPECIFIC_GRANULE	214	Down	<0.0001	<0.0001

FABP5 STXBP2	GO_SECRETORY_GRANULE_MEMBRANE	361	Down	<0.0001	<0.0001
RPS4Y1	GO_POLYSOME	179	Up	<0.0001	0.0065
RPS4Y1 RPS4Y2	GO_RIBOSOMAL_SUBUNIT	490	Up	<0.0001	<0.0001
MAPK3	GO_PSEUDOPODIUM	16	Down	<0.0001	0.0059
RPS4Y1 RPS4Y2	GO_RIBONUCLEOPROTEIN_COMPLEX	1147	Up	<0.0001	0.0067
RPS4Y1 RPS4Y2	GO_CYTOSOLIC_RIBOSOME	384	Up	<0.0001	<0.0001
ALPL	GO_ANCHORED_COMPONENT_OF_MEMBRANE	90	Down	0.001	0.0471
EIF1AY	GO_TRANSLATION_INITIATION_FACTOR_ACTIVITY	71	Up	0.002	0.0753
MAPK3	GO_MAP_KINASE_ACTIVITY	16	Down	<0.0001	0.0076
RPS4Y1 RPS4Y2	GO_STRUCTURAL_CONSTITUENT_OF_RIBOSOME	462	Up	<0.0001	<0.0001
EIF1AY	GO_TRANSLATION_FACTOR_ACTIVITY_RNA_BINDING	128	Up	0.0004	0.0262
RSAD2	GO_METAL_CLUSTER_BINDING	67	Up	<0.0001	0.0082
RPS4Y1 RPS4Y2	GO_RRNA_BINDING	119	Up	<0.0001	0.0017
RARA EIF1AY	GO_TRANSLATION_REGULATOR_ACTIVITY	200	Up	0.0017	0.0665
RARA EIF1AY	GO_TRANSLATION_REGULATOR_ACTIVITY_NUCLEIC_ACID_BINDING	152	Up	0.0012	0.0553
RPS4Y1 RPS4Y2	GO_STRUCTURAL_MOLECULE_ACTIVITY	791	Up	0.0001	0.0126
RPS4Y1	GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS	513	Up	<0.0001	<0.0001
MAPK3	GO_FC_RECEPTOR_MEDIATED_STIMULATORY_SIGNALING_PATHWAY	127	Down	0.0009	0.0442
STXBP2	GO_REGULATION_OF_MYELOID_LEUKOCYTE_MEDIATED_IMMUNITY	71	Down	0.0001	0.0116
RPS4Y1	GO_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE	382	Up	<0.0001	<0.0001
TRIM8 RPS4Y1	GO_VIRAL_GENE_EXPRESSION	503	Up	<0.0001	0.0002
RARA EIF1AY RPS4Y1 RPS4Y2 MAPK3	GO_PEPTIDE_BIOSYNTHETIC_PROCESS	1052	Up	<0.0001	0.0065
MAPK3	GO_ANIMAL_ORGAN_FORMATION	35	Down	0.0012	0.0543
MAPK3	GO_BERGMANN_GLIAL_CELL_DIFFERENTIATION	10	Down	0.0007	0.0388
MAPK3	GO_TRACHEA_FORMATION	13	Down	0.0001	0.0126
MAPK3	GO_CARDIAC_NEURAL_CRESCENT_CELL_DIFFERENTIATION_INVOLVED_IN_HEART_DEVELOPMENT	11	Down	0.0004	0.025
MAPK3	GO_CAVEOLIN_MEDIATED_ENDOCYTOSIS	14	Down	0.0014	0.0606
IFI27 TRIM8 ISG15 RSAD2	GO_REGULATION_OF_VIRAL_LIFE_CYCLE	192	Up	0.0003	0.022
MAPK3	GO_REGULATION_OF_METALLOPEPTIDASE_ACTIVITY	28	Down	<0.0001	0.002
MAPK3	GO_POSITIVE_REGULATION_OF_METALLOPEPTIDASE_ACTIVITY	19	Down	0.0002	0.0161
FABP5	GO_AZUROPHIL_GRANULE_LUMEN	121	Down	0.0011	0.0498
FABP5 STXBP2	GO_AZUROPHIL_GRANULE	209	Down	<0.0001	0.0017
STXBP2	GO_TERTIARY_GRANULE	224	Down	<0.0001	<0.0001
RARA	GO_MRNA_5_UTR_BINDING	58	Up	0.0001	0.0116
UPB1 RPS4Y1	GO_CELLULAR_NITROGEN_COMPOUND_CATABOLIC_PROCESS	943	Up	0.0003	0.0201
TRIM8 ISG15 RSAD2	GO_NEGATIVE_REGULATION_OF_VIRAL_LIFE_CYCLE	107	Up	0.0005	0.03
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GeneSymbols	Gene Pathway	NGenes	Direction	PValue	FDR
RPS12 RPS4Y1	GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	396	Up	0.0008	0.0914
FTH1	GO_NEGATIVE_REGULATION_OF_FIBROBLAST_PROLIFERATION	45	Up	0.0005	0.0699
FTH1	GO_SEQUESTERING_OF_METAL_ION	26	Up	<0.0001	0.0155
HNRNPM	GO_RNA_SPLICING_VIA_TRANSESTERIFICATION_REACTIONS	448	Down	0.0006	0.0751
RPS12 RPS4Y1	GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_NONSENSE_MEDIATED_DECAY	411	Up	0.0003	0.056
USPL1	GO_CAJAL_BODY	67	Down	<0.0001	0.0193
SERPING1	GO_VESICLE_LUMEN	397	Down	<0.0001	0.0193
RPS12 RPS4Y1 RPS4Y2	GO_CYTOSOLIC_SMALL_RIBOSOMAL_SUBUNIT	174	Up	<0.0001	0.0193
STXBP2	GO_SPECIFIC_GRANULE	214	Down	<0.0001	0.0222
HNRNPM	GO_CATALYTIC_STEP_2_SPLICEOSOME	141	Down	<0.0001	0.0057
HNRNPM	GO_SPLICEOSOMAL_COMPLEX	267	Down	0.0001	0.0317
TIMM10	GO_MITOCHONDRIAL_PROTEIN_COMPLEX	298	Down	0.0007	0.0836

RPS12 RPS4Y1 RPS4Y2	GO_CYTOSOLIC_RIBOSOME	384	Up	<0.0001	0.0218
FTH1	GO_OXIDOREDUCTASE_ACTIVITY_OXIDIZING_METAL_IONS	27	Up	<0.0001	0.0016
FTH1	GO_FERROUS_IRON_BINDING	34	Up	<0.0001	<0.0001
RPS12 RPS4Y1	GO_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBR ANE	382	Up	0.0002	0.0462
FTH1	GO_SEQUESTERING_OF_IRON_ION	20	Up	<0.0001	0.0016
FTH1	GO_SECONDARY_LYSOSOME	37	Up	<0.0001	0.0193
HNRNPM	GO_PARASPECKLES	10	Down	<0.0001	0.0219
STXBP2	GO_AZUROPHIL_GRANULE	209	Down	0.0006	0.0751
FTH1	GO_AUTOLYSOSOME	30	Up	<0.0001	0.0018
HNRNPM	GO_POST_MRNA_RELEASE_SPLICEOSOMAL_COMPLEX	20	Down	0.0001	0.03
FTH1	GO_FERRIC_IRON_BINDING	17	Up	<0.0001	<0.0001
FTH1	GO_OXIDOREDUCTASE_ACTIVITY_OXIDIZING_METAL_IONS _OXYGEN_AS_ACCEPTOR	17	Up	<0.0001	<0.0001