Gene Expression Analysis

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GSE3397- RSV gene expression

Respiratory syncytial virus (RSV) causes infections of the lungs and respiratory tract. It's so common that most children have been infected with the virus by age 2. Respiratory syncytial (sin-SISH-ul) virus can also infect adults.

Expression profiling of bronchial epithelial cells following treatment with respiratory syncytial virus (RSV) at 1.0 MOI.

RSV is the most common cause of bronchiolitis and pneumonia among infants.

Group	Accession	Title	Source name	Vehicle treated 4 hours	RSV gene expression	Characteristics
controlled	GSM76392	Control 1	BEAS cells			
controlled	GSM76393	Control 2	BEAS cells			
controlled	GSM76394	Control 3	BEAS cells			
controlled	GSM76395	Control 4	BEAS cells			
-	GSM76396	RSV1-4H	BEAS cells			RSV 1.0 MOI 4 hours
-	GSM76397	RSV2-4H	BEAS cells			RSV 1.0 MOI 4 hours
-	GSM76398	RSV3-4H	BEAS cells			RSV 1.0 MOI 4 hours
-	GSM76399	RSV4-4H	BEAS cells			RSV 1.0 MOI 4 hours
RSV	GSM76400	RSV1-24H	BEAS cells			RSV 1.0 MOI 24 hours
RSV	GSM76401	RSV2-24H	BEAS cells			RSV 1.0 MOI 24 hours
RSV	GSM76402	RSV3-24H	BEAS cells			RSV 1.0 MOI 24 hours
RSV	GSM76403	RSV4-24H	BEAS cells			RSV 1.0 MOI 24 hours

The grouping is taken as normal genes vs infected patient of RSV

Analysation Tactics :

Benjamini & Hochberg (False discovery rate)

Significance level cut-off : 0.05

Top differentially expressed genes

ID	adj.P.Val	P.Value	t	B	logFC	Gene.symbol	Gene.title
201009_s_at	0.0107	3.93e-07	15.23	5.54	2.822	TXNIP	thioredoxin interacting ...
37028_at	0.0107	4.32e-07	-15.04	5.493	-2.931	PPP1R15A	protein phosphatase 1 ...
202014_at	0.0107	7.37e-07	-14.03	5.212	-3.89	PPP1R15A	protein phosphatase 1 ...
201010_s_at	0.0107	7.81e-07	13.92	5.181	3.192	TXNIP	thioredoxin interacting ...
201008_s_at	0.011	1.01e-06	13.46	5.04	3.479	TXNIP	thioredoxin interacting ...
214757_at	0.0154	1.69e-06	12.57	4.737	2.794	PMS2P2	PMS1 homolog 2, mis...
209383_at	0.0189	2.74e-06	-11.79	4.44	-3.676	DDIT3	DNA damage inducible...
232017_at	0.0189	2.76e-06	-11.78	4.436	-5.351	TJP2	tight junction protein 2
203574_at	0.0243	4.00e-06	-11.21	4.194	-2.469	NFIL3	nuclear factor, interleuk...
235251_at	0.0263	4.81e-06	10.94	4.073	2.97		
209892_at	0.0267	5.41e-06	10.77	3.993	2.906	FUT4	fucosyltransferase 4
200769_s_at	0.0267	5.86e-06	10.65	3.938	2.196	MAT2A	methionine adenosyltra...
229358_at	0.0275	6.54e-06	-10.49	3.862	-1.808	IHH	indian hedgehog
232869_at	0.0292	7.47e-06	-10.31	3.77	-2.481	SRGAP3	SLIT-ROBO Rho GTPa...
225283_at	0.0327	1.02e-05	9.88	3.546	2.266	ARRDC4	arrestin domain contai...
227908_at	0.0327	1.04e-05	9.85	3.532	2.584	TBC1D24	TBC1 domain family m...
1554508_at	0.0327	1.05e-05	-9.84	3.527	-2.315	PIK3AP1	phosphoinositide-3-kin...
221840_at	0.0327	1.11e-05	9.77	3.488	2.347	PTPRE	protein tyrosine phosp...
239377_at	0.0327	1.14e-05	9.74	3.471	1.629	EIF1AD	eukaryotic translation i...
1562969_at	0.0408	1.58e-05	-9.31	3.227	-2.809	DNMBP	dynamin binding protein
213449_at	0.0408	1.62e-05	9.27	3.207	1.65	POP1	POP1 homolog, ribonu...

Visualisations:
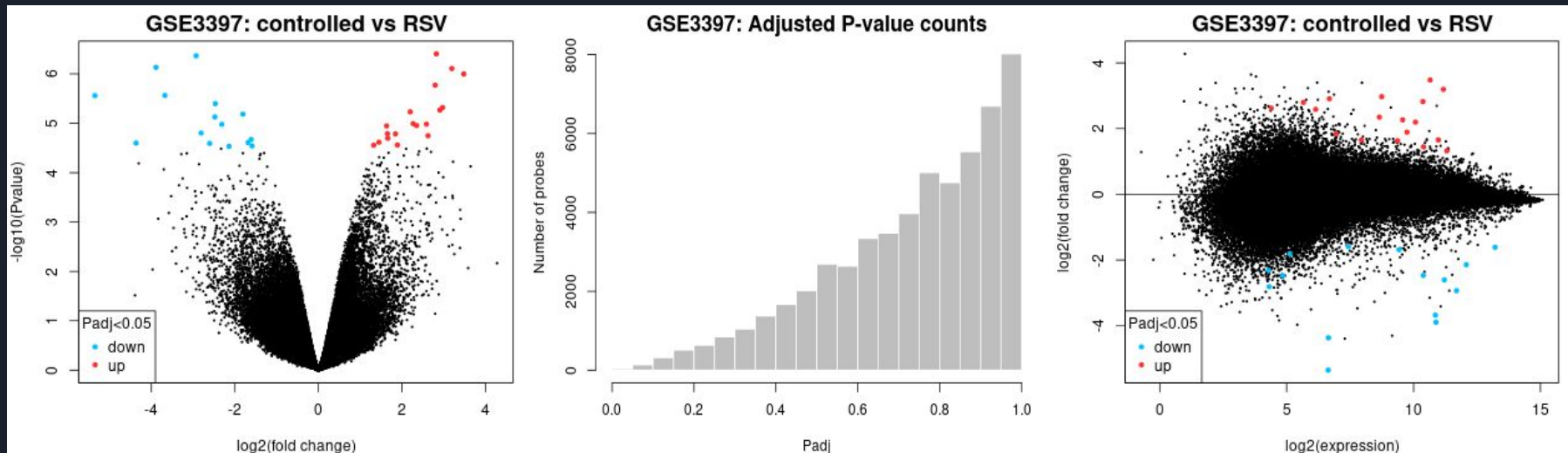
GSE18816- Expression data of influenza-A infected human macrophages

Influenza (commonly called flu) is an infection of the nose, throat and lungs, which are part of the respiratory system.

There are four types of influenza viruses: A, B, C and D. Influenza A viruses are the only influenza viruses known to cause flu pandemics. Influenza A viruses are divided into subtypes based on two proteins on the surface of the virus: hemagglutinin (H) and neuraminidase (N).

Macrophages are innate immune cells present in every tissue they sense and respond to pathogens and other environmental challenges and participate in tissue repair after injury.

Influenza A virus subtype **H1N1** (A/H1N1) is a subtype of influenza A virus (commonly called swine flu).

It is a respiratory disease that occurs in pigs. (Not common in humans)

Influenza A virus subtype **H5N1** (A/H5N1) is a subtype of influenza A virus (commonly called bird flu).

It is a highly pathogenic. (common in humans)

- **Database - Macrophage response to H1N1 and H5N1 influenza viral infections**
- Analysis of macrophages at 1, 3, and 6 hours post-infection with H1N1 or H5N1 viruses in vitro. The avian H5N1 virus is highly pathogenic, while the swine H1N1 virus is less so. Alveolar macrophages are targets of H5N1. Results provide insight into the host response to H1N1 and H5N1 infections.
- **Grouping** - It was done by taking 3 groups into account i.e mock, H1N1 and H5N1

Group	Accession	Title	Source name	Individual	Infection	Time point	Cell type
-	GSM466570	donor 1, mock infected macrophages at 1h	macrophages from donor 1 infected with mock at 1h post-infection time	donor 1	mock	1h post-infection time	monocyte-derived macrophages
-	GSM466571	donor 1, H1N1 infected macrophages at 1h	macrophages from donor 1 infected with H1N1 at 1h post-infection time	donor 1	H1N1	1h post-infection time	monocyte-derived macrophages
-	GSM466572	donor 1, H5N1 infected macrophages at 1h	macrophages from donor 1 infected with H5N1 at 1h post-infection time	donor 1	H5N1	1h post-infection time	monocyte-derived macrophages
mock	GSM466573	donor 1, mock infected macrophages at 3h	macrophages from donor 1 infected with mock at 3h post-infection time	donor 1	mock	3h post-infection time	monocyte-derived macrophages
H1N1	GSM466574	donor 1, H1N1 infected macrophages at 3h	macrophages from donor 1 infected with H1N1 at 3h post-infection time	donor 1	H1N1	3h post-infection time	monocyte-derived macrophages
H5N1	GSM466575	donor 1, H5N1 infected macrophages at 3h	macrophages from donor 1 infected with H5N1 at 3h post-infection time	donor 1	H5N1	3h post-infection time	monocyte-derived macrophages
-	GSM466576	donor 1, mock infected macrophages at 6h	macrophages from donor 1 infected with mock at 6h post-infection time	donor 1	mock	6h post-infection time	monocyte-derived macrophages
-	GSM466577	donor 1, H1N1 infected macrophages at 6h	macrophages from donor 1 infected with H1N1 at 6h post-infection time	donor 1	H1N1	6h post-infection time	monocyte-derived macrophages
-	GSM466578	donor 1, H5N1 infected macrophages at 6h	macrophages from donor 1 infected with H5N1 at 6h post-infection time	donor 1	H5N1	6h post-infection time	monocyte-derived macrophages
-	GSM466579	donor 2, mock infected macrophages at 1h	macrophages from donor 2 infected with mock at 1h post-infection time	donor 2	mock	1h post-infection time	monocyte-derived macrophages
-	GSM466580	donor 2, H1N1 infected macrophages at 1h	macrophages from donor 2 infected with H1N1 at 1h post-infection time	donor 2	H1N1	1h post-infection time	monocyte-derived macrophages
-	GSM466581	donor 2, H5N1 infected macrophages at 1h	macrophages from donor 2 infected with H5N1 at 1h post-infection time	donor 2	H5N1	1h post-infection time	monocyte-derived macrophages
mock	GSM466582	donor 2, mock infected macrophages at 3h	macrophages from donor 2 infected with mock at 3h post-infection time	donor 2	mock	3h post-infection time	monocyte-derived macrophages
H1N1	GSM466583	donor 2, H1N1 infected macrophages at 3h	macrophages from donor 2 infected with H1N1 at 3h post-infection time	donor 2	H1N1	3h post-infection time	monocyte-derived macrophages
H5N1	GSM466584	donor 2, H5N1 infected macrophages at 3h	macrophages from donor 2 infected with H5N1 at 3h post-infection time	donor 2	H5N1	3h post-infection time	monocyte-derived macrophages
	GSM466585	donor 2, mock infected macrophages at 6h	macrophages from donor 2 infected with mock at 6h post-infection time	donor 2	mock	6h post-infection time	monocyte-derived macrophages

Analysation Tactics :

Benjamini & Hochberg (False discovery rate)

Significance level cut-off : 0.05
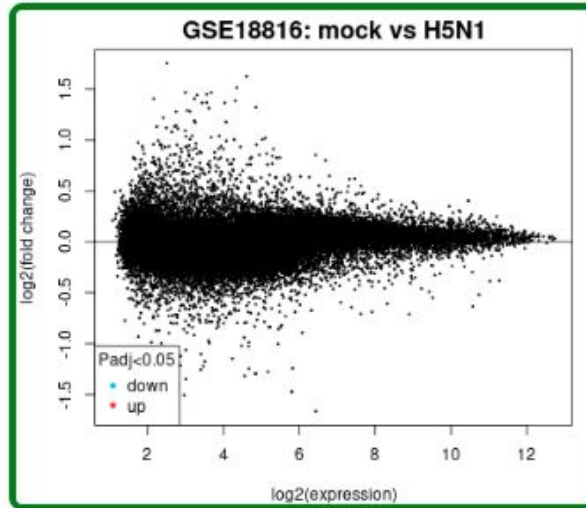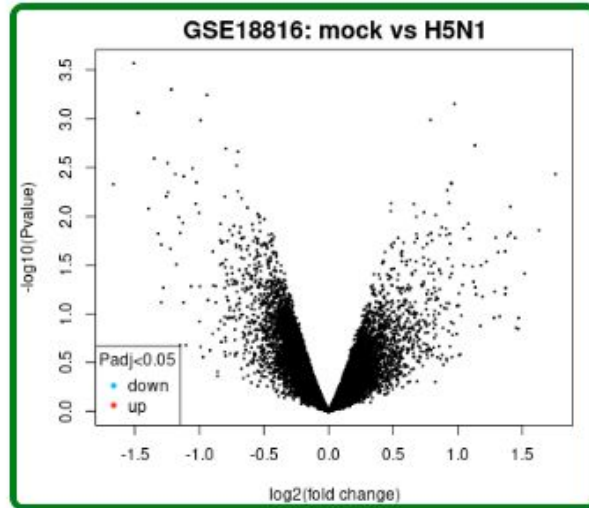
GSE24533- Expression data of influenza A-infected human type I-like alveolar epithelial cells

Diseases :**Seasonal H1N1 virus:** The H1N1 flu, commonly known as swine flu, is primarily caused by the H1N1 strain of the flu (influenza) virus. H1N1 is a type of influenza A virus, and H1N1 is one of several flu virus strains that can cause the seasonal flu. Symptoms of the H1N1 flu are the same as those of the seasonal flu. **Pandemic influenza H1N1** (pdmH1N1) virus: It causes mild disease in humans but occasionally leads to severe complications and even death, especially in those who are pregnant or have underlying disease. The remarkable feature of A/(H1N1)pdm09, compared with seasonal strains, is its high fatality rate and its higher incidence among younger people.

Database: We carried out a comprehensive gene expression profiling using a platform to compare the primary human alveolar type I-like alveolar epithelial cells infected with pdmH1N1 or seasonal H1N1 virus taken after 8 hours.

Grouping: It was done by taking two groups into consideration i.e mock and pdm H1N1. (6 out of 9 samples)

GEO accession [GSE24533] Set Expression data of influenza A-infected human type I-like alveolar epithelial cells

▾ **Samples**   ▸ Define groups   Selected **6** out of **9** samples

Group	Accession	Title	Source name	Individu
mock	GSM604841	Donor 1, mock-infected human type I-like alveolar epithelial cells at 8h	Differentiated human type I-like alveolar epithelial cells mock infected at 8h post-infection time	donor 1
-	GSM604842	Donor 1, seasonal H1N1-infected human type I-like alveolar epithelial cells at 8h	Differentiated human type I-like alveolar epithelial cells infected by seasonal H1N1 virus at 8h post-infection time	donor 1
pdmh1n1	GSM604843	Donor 1, pdmH1N1-infected human type I-like alveolar epithelial cells at 8h	Differentiated human type I-like alveolar epithelial cells infected by pdmH1N1 virus at 8h post-infection time	donor 1
mock	GSM604844	Donor 2, mock-infected human type I-like alveolar epithelial cells at 8h	Differentiated human type I-like alveolar epithelial cells mock infected at 8h post-infection time	donor 2
-	GSM604845	Donor 2, seasonal H1N1-infected human type I-like alveolar epithelial cells at 8h	Differentiated human type I-like alveolar epithelial cells infected by seasonal H1N1 virus at 8h post-infection time	donor 2
pdmh1n1	GSM604846	Donor 2, pdmH1N1-infected human type I-like alveolar epithelial cells at 8h	Differentiated human type I-like alveolar epithelial cells infected by pdmH1N1 virus at 8h post-infection time	donor 2
mock	GSM604847	Donor 3, mock-infected human type I-like alveolar epithelial cells at 8h	Differentiated human type I-like alveolar epithelial cells mock infected at 8h post-infection time	donor 3
-	GSM604848	Donor 3, seasonal H1N1-infected human type I-like alveolar epithelial cells at 8h	Differentiated human type I-like alveolar epithelial cells infected by seasonal H1N1 virus at 8h post-infection time	donor 3
pdmh1n1	GSM604849	Donor 3, pdmH1N1-infected human type I-like alveolar epithelial cells at 8h	Differentiated human type I-like alveolar epithelial cells infected by pdmH1N1 virus at 8h post-infection time	donor 3

Analysis Tactics :

Benjamini & Hochberg (False discovery rate)

Significance rate (Adj.P value) <= 0.05

GSE27973 - Human airway epithelial responses to rhinovirus infection and cigarette smoke extract alone and in combination

- Rhinovirus is a common viral infectious agent in human and predominant cause of common cold. It has been linked to sinus and ear infection and may also trigger asthma attacks
- Database - Cultured epithelial cells exposed to rhinovirus 16 (RV16) , medium alone, CSE alone and RV16 in the presence of CSE. Taken after 24hrs
- Grouping - It was done by taking 2 groups into account i.e medium alone and RV16

Group	Accession	Title	Source name	Donor	Tissue	Cell type	Growth	Stress
Medium	GSM692115	Donor 1 - medium	Human bronchial epithelial cells - 24h medium	1	bronchi	epithelial cell	primary cultures	medium
RV16	GSM692116	Donor 1 - RV16	Human bronchial epithelial cells - 24 h RV16	1	bronchi	epithelial cell	primary cultures	RV16
-	GSM692117	Donor 1 - CSE	Human bronchial epithelial cells - 24 h CSE	1	bronchi	epithelial cell	primary cultures	CSE
-	GSM692118	Donor 1 - RV16+CSE	Human bronchial epithelial cells - 24 h RV16+CSE	1	bronchi	epithelial cell	primary cultures	RV16+CSE
Medium	GSM692119	Donor 2 - medium	Human bronchial epithelial cells - 24h medium	2	bronchi	epithelial cell	primary cultures	medium
RV16	GSM692120	Donor 2 - RV16	Human bronchial epithelial cells - 24 h RV16	2	bronchi	epithelial cell	primary cultures	RV16
-	GSM692121	Donor 2 - CSE	Human bronchial epithelial cells - 24 h CSE	2	bronchi	epithelial cell	primary cultures	CSE
-	GSM692122	Donor 2 - RV16+CSE	Human bronchial epithelial cells - 24 h RV16+CSE	2	bronchi	epithelial cell	primary cultures	RV16+CSE
Medium	GSM692123	Donor 3 - medium	Human bronchial epithelial cells - 24h medium	3	bronchi	epithelial cell	primary cultures	medium
RV16	GSM692124	Donor 3 - RV16	Human bronchial epithelial cells - 24 h RV16	3	bronchi	epithelial cell	primary cultures	RV16
-	GSM692125	Donor 3 - CSE	Human bronchial epithelial cells - 24 h CSE	3	bronchi	epithelial cell	primary cultures	CSE
-	GSM692126	Donor 3 - RV16+CSE	Human bronchial epithelial cells - 24 h RV16+CSE	3	bronchi	epithelial cell	primary cultures	RV16+CSE
Medium	GSM692127	Donor 4 - medium	Human bronchial epithelial cells - 24h medium	4	bronchi	epithelial cell	primary cultures	medium
RV16	GSM692128	Donor 4 - RV16	Human bronchial epithelial cells - 24 h RV16	4	bronchi	epithelial cell	primary cultures	RV16
-	GSM692129	Donor 4 - CSE	Human bronchial epithelial cells - 24 h CSE	4	bronchi	epithelial cell	primary cultures	CSE

Analysation Tactics :

Benjamini & Hochberg (False discovery rate)

Significance level cut-off : 0.05

Top Significant Genes

ID	adj.P.Val	P.Value	t	B	logFC	Gene.symbol	Gene.title
233390_at	0.0426	0.00000226	-12.5	4.08728	-3.41		
214059_at	0.0426	0.0000024	-12.4	4.05648	-5.71	IFI44	interferon induced protein 44
218986_s_at	0.0426	0.00000279	-12.15	3.97631	-5.46	DDX60	DEXD/H-box helicase 60
204655_at	0.0426	0.00000311	-11.96	3.91637	-7.08	CCL5	C-C motif chemokine ligand 5
1552503_at	0.0516	0.00000587	-10.97	3.5567	-2.31	FRAS1	Fraser extracellular matrix c...
219364_at	0.0516	0.00000612	-10.9	3.53288	-5.71	DHX58	DEXH-box helicase 58
214453_s_at	0.0516	0.00000661	-10.79	3.48654	-6.11	IFI44	interferon induced protein 44
1561654_at	0.0578	0.00000846	-10.43	3.33714	-3.08		
1553765_a_at	0.0588	0.00001103	-10.05	3.17089	-4.37	KLHL32	kelch like family member 32
242020_s_at	0.0588	0.00001149	-9.99	3.14489	-5.18	ZBP1	Z-DNA binding protein 1
210362_x_at	0.0588	0.00001388	-9.73	3.02364	-3.01	PML	promyelocytic leukemia
237675_at	0.0588	0.00001507	-9.62	2.96975	-2.66	LINC01351	long intergenic non-protein c...
201601_x_at	0.0588	0.00001749	-9.42	2.87132	-3.46	IFITM2///IFITM1	interferon induced transmem...
207218_at	0.0588	0.00001761	-9.41	2.86683	-2.72	F9	coagulation factor IX
229839_at	0.0588	0.00001777	-9.4	2.86075	-3.72	SCARA5	scavenger receptor class A ...
215650_at	0.0588	0.00001819	-9.37	2.8449	-4.04		
1570099_at	0.0588	0.00001828	9.36	2.84192	3.81		
1562413_at	0.0644	0.00002261	-9.09	2.69802	-3.73	LINC00167	long intergenic non-protein c...
202086_at	0.0644	0.0000239	-9.02	2.65985	-6.31	MX1	MX dynamin like GTPase 1
204211_x_at	0.0644	0.00002712	-8.86	2.57263	-1.89	EIF2AK2	eukaryotic translation initiati...
219209_at	0.0644	0.0000282	-8.81	2.54524	-4.17	IFIH1	interferon induced with helic...
205483_s_at	0.0644	0.00002822	-8.81	2.54488	-5.52	ISG15	ISG15 ubiquitin-like modifier
		0.00002859	-8.79	2.53586	-2.72	SAMHD1	SAM and HD domain contai...