

```

1 import pandas as pd
2
3 pre = pd.read_excel(r"Master File - Pre Genes.xlsx")
4 fortyEight = pd.read_excel(r"Master File - 48 hours.xlsx")
5 dayEight = pd.read_excel(r"Master File - Day 8.xlsx")
6 dayFifteen = pd.read_excel(r"Master File - Day 15.xlsx")
7
8 timePointData = [pre,fortyEight,dayEight,dayFifteen]
9
10 geneSet = []
11
12 namesOfColumns = [" Pre"," 48 hours"," Day 8"," Day 15"]
13
14 def buildGeneSet():
15     for gene in geneSet:
16         resultFrame = pd.DataFrame()
17         for x in range(4):
18             timePoint = timePointData[x]
19             resultFrame = pd.concat([resultFrame, timePoint[timePoint['Unnamed: 0']==gene]])
20             resultFrame.columns = ['Gene Symbol','Group','GW','SW','BF','JL','JK','DC','PL','BR']
21             with pd.ExcelWriter(r"OutputDoc.xlsx",engine="openpyxl",mode='a',if_sheet_exists='overlay') as
writer:
22                 resultFrame.to_excel(writer,sheet_name=gene)
23
24 buildGeneSet()

```

Supplementary Figure 1 Contains the python code used to selectively parse and organize the data associated with specific gene subsets in a new Microsoft Office Excel Document. This code was developed using Anaconda Spyder (Python 3.9).

Supplementary Table 1 Contains a list of 25 cytokines that were studied and each is classified under the subheading of pro-inflammatory, anti-inflammatory, antiviral, immune cell activators/growth factors

Pro-inflammatory

IL-1 α / IL-1 β : Induce fever and inflammation; activate lymphocytes and promote Th17 differentiation.

IL-6: Stimulates acute phase response, B-cell differentiation, and inflammation.

IL-8 (CXCL8): Chemotactic for neutrophils; recruits immune cells to infection sites.

IL-17A: Recruits neutrophils and monocytes; amplifies inflammation.

TNF- α : Enhances vascular permeability, leukocyte recruitment, and systemic inflammation.

IFN- γ : Activates macrophages, enhances antigen presentation, and promotes Th1 responses.

MCP-1 (CCL2): Recruits monocytes to sites of inflammation.

MIP-1 α / MIP-1 β : Recruit and activate macrophages and T cells.

RANTES (CCL5): Attracts T cells, eosinophils, and basophils to inflammatory sites.

Anti-inflammatory

IL-10: Inhibits cytokine production by macrophages and dendritic cells; promotes immune tolerance.

IL-12 (p40/p70): Though often considered pro-inflammatory, it also can have anti-inflammatory effects

IL-22: Promotes epithelial cell survival and repair.

IL-37 / IL-38: Suppress inflammatory cytokine production and immune cell activation.

Antiviral

IFN- α 2: Induces antiviral state in cells, inhibits viral replication.

IFN- γ : Enhances antiviral immunity by activating macrophages and promoting cytotoxic T cell responses.

Immune Cell Activators/Growth Factors

IL-2: Promotes T cell proliferation and survival; activates NK cells.

IL-3: Stimulates hematopoietic stem cell differentiation.

IL-4: Drives Th2 differentiation; promotes B cell class switching to IgE.

IL-5: Stimulates eosinophil growth and activation.

IL-7: Essential for T and B cell development.

IL-9: Supports T cell growth and mast cell activation.

IL-13: Promotes Th2 responses and IgE production.

IL-15: Activates NK cells and memory T cells.

GM-CSF: Stimulates production of granulocytes and macrophages.

VEGF: Promotes angiogenesis; increases vascular permeability.

Supplementary Table 2 Contains a comprehensive list of all genes analyzed for this study, organized by their association with either the JAK-STAT, Wnt, RAS, or PI3K-AKT pathways

JAK-STAT	Wnt	Ras	PI3K-AKT
JAK1	APC	AKT1	AREG
JAK2	APC2	AKT2	DEPTOR
JAK3	AXIN1	AKT3	EFNA5
STAT1	AXIN2	ALK	ERBB3
STAT2	BAMBI	ARAF	ERBB4
STAT3	BTRC	ARHGAP35	EREG
STAT4	CACYBP	BRAF	GSK3B
STAT5b	CAMK2A	CDK4	IGF1
STAT5a	CAMK2B	CDK6	IGF1R
STAT6	CAMK2D	DUSP1	IGF2
TYK2	CAMK2G	DUSP2	IRS1
	CCND1	DUSP3	IRS2
	CCND2	DUSP4	IRS4
	CCND3	DUSP5	KIT
	CER1	DUSP6	NEDD4
	CHD8	EGFR	PDK1
	CREBBP	EIF4EBP1	PHLPP1
	CSNK1A1	ERBB2	PHLPP2
	CSNK1A1L	ETS1	PIK3CG
	CSNK1E	ETS2	PTENP1
	CSNK2A1	FGFR1	RICTOR
	CSNK2A2	FGFR2	SPRY2
	CSNK2A3	FGFR3	
	CSNK2B	FGFR4	
	CTBP1	FOS	

CTBP2	GRB2
CTNNB1	HRAS
CTNNBIP1	KRAS
CUL1	KSR1
CXXC4	KSR2
DAAM1	MAP2K1
DAAM2	MAP2K2
DKK1	MAPK1
DKK2	MAPK3
DKK4	MDM2
DVL1	MET
DVL2	MLST8
DVL3	MTOR
EP300	NF1
FBXW11	NRAS
FOSL1	PAK1
FRAT1	PAK2
FRAT2	PAK3
FZD1	PAK4
FZD10	PDGFRA
FZD2	PDGFRB
FZD3	PIK3CA
FZD4	PIK3CB
FZD5	PIK3CD
FZD6	PIK3R1
FZD7	PIK3R2
FZD8	PIK3R3
FZD9	PIK3R4

GPC4	PIK3R5
GSK3B	PIK3R6
INVS	PRKAA1
JUN	PRKAA2
LEF1	PRKAB1
LRP5	PRKAB2
LRP6	PRKAG1
MAP3K7	PRKAG2
MAPK10	PRKAG3
MAPK8	PTEN
MAPK9	RAF1
MMP7	RALA
MYC	RALB
NFATC1	RALGDS
NFATC2	RASA1
NFATC3	RASA2
NFATC4	RASA3
NKD1	RASAL1
NKD2	RASAL2
NLK	RASAL3
NOTUM	RASGRF2
PLCB1	RASGRP1
PLCB2	RASGRP2
PLCB3	RASGRP3
PLCB4	RASGRP4
PORCN	RB1
PPARD	RHEB
PPP3CA	RHOB

PPP3CB	RHOC
PPP3CC	ROCK1
PPP3R1	ROS1
PPP3R2	RPS6KA1
PRICKLE1	RPS6KA2
PRICKLE2	RPS6KA3
PRKACA	RPS6KA4
PRKACB	RPS6KA5
PRKACG	RPS6KA6
PRKCA	RPTOR
PRKCB	SHC1
PRKCG	SHC2
PSEN1	SHC3
RAC1	SHC4
RAC2	SOS1
RAC3	SOS2
RBX1	SPRED1
RHOA	SPRED2
ROCK2	SPRED3
RUVBL1	SPRY1
SEN2	SPRY2
SERPINF1	SPRY3
SFRP1	SPRY4
SFRP2	STK11
SFRP4	TIAM1
SFRP5	TIAM2
SIAH1	TSC1
SKP1	TSC2

SMAD3
SMAD4
SOST
SOX17
TBL1X
TBL1XR1
TBL1Y
TCF7
TCF7L1
TCF7L2
TP53
VANGL1
VANGL2
WIF1
WNT1
WNT10A
WNT10B
WNT11
WNT16
WNT2
WNT2B
WNT3
WNT3A
WNT4
WNT5A
WNT5B
WNT6
WNT7A

WNT7B

WNT8A

WNT8B

WNT9A

WNT9B

Supplementary Table 3 Contains a comprehensive list of significantly altered genes associated with the Ras pathway at 48 hours, day 8, and day 15

Significant Genes	48 hours	Day 8	Day 15
<i>ATK1</i>	2.83 (p = 0.00399)	1.08	1.28
<i>ALK</i>	0.76 (p = 0.04315)	1.03	0.92
<i>ARAF</i>	2.36 (p = 0.023536)	1.02	1.65
<i>BRAF</i>	2.84 (p = 0.050262)	0.68 (p = 0.036939)	0.83
<i>DUSP1</i>	2.65 (p = 0.004534)	1.74	1.18
<i>DUSP2</i>	0.94	1.1	0.88 (p = 0.02233)
<i>DUSP3</i>	0.86 (p = 0.024525)	0.92	0.85
<i>DUSP6</i>	1.73 (p = 0.037783)	1.36 (p = 0.034566)	2.4
<i>ETS2</i>	4.4 (p = 0.000483)	0.95	0.1
<i>GRB2</i>	2.08 (p = 0.024787)	1.91	2.26
<i>NRAS</i>	1.15	0.65 (p = 0.014252)	0.79 (p = 0.034829)
<i>RASA2</i>	0.64 (p = 0.002995)	0.78 (p = 0.026427)	0.87
<i>RASGRP2</i>	1.04	1.14 (p = 0.05209)	1.11
<i>RASGRP3</i>	1.05	0.98	0.86 (0.034863)
<i>RHOC</i>	1.74 (p = 0.003294)	0.71 (p = 0.000412)	0.79
<i>RPS6KA4</i>	1.3 (p = 0.023887)	1.15 (p = 0.041733)	1.41 (p = 0.000378)
<i>RPS6KA6</i>	1.25	1.32 (p = 0.045981)	1.48 (p = 0.04018)
<i>STK11</i>	1.14	1.44 (p = 0.0466)	1.31
<i>TIAM2</i>	0.9	1.03	0.81 (p = 0.014591)

Values shaded in red contain significantly downregulated (p < 0.05) fold changes.

Values shaded in green contain significantly upregulated (p < 0.05) fold changes

Supplementary Table 4 Contains a comprehensive list of significantly altered genes associated with the JAK-STAT pathway at 48 hours, day 8, and day 15

Significant			
Genes	48 hours	Day 8	Day 15
<i>JAK1</i>	1.44	1.21	2.07 (p = 0.03538)
<i>JAK2</i>	0.52 (p = 0.01758)	1.28	0.79
<i>STAT3</i>	2.07 (p = 0.007879)	1.58 (p = 0.050305)	2.02 (p = 0.027039)
<i>STAT4</i>	1.2	1.46 (p = 0.015613)	1.11
<i>STAT6</i>	0.9	1.25 (p = 0.032542)	1.12

Values shaded in red contain significantly downregulated (p < 0.05) fold changes.

Values shaded in green contain significantly upregulated (p < 0.05) fold changes.

Supplementary Table 5 Contains a comprehensive list of significantly altered genes associated with the PI3K-AKT pathway at 48 hours, day 8, and day 15

Significant			
Genes	48 hours	Day 8	Day 15
<i>ERBB3</i>	0.99	0.88 (p = 0.037388)	0.75 (p = 0.012752)
	0.78 (p = 0.023155)		
<i>EREG</i>		1.03	1.03
	3.82 (p = 0.030088)		
<i>GSK3b</i>		0.55 (p = 0.007948)	0.78 (p = 0.034592)
<i>IGF2</i>	0.95	0.78 (p = 0.016721)	0.84
	0.84 (p = 0.055014)		
<i>IRS2</i>		0.78 (p = 0.024555)	0.95
<i>PDK1</i>	1.2 (p = 0.047985)	1.78	1.01
	1.33 (p = 0.024888)		
<i>PIK3CG</i>		1.3 (p = 0.020653)	1.11
	1.57 (p = 0.018876)		
<i>PTENP1</i>		1.01	1.18
	0.88 (p = 0.043031)		
<i>RICTOR</i>		0.86 (p = 0.038213)	0.92

Values shaded in red contain significantly downregulated (p < 0.05) fold changes.

Values shaded in green contain significantly upregulated (p < 0.05) fold changes.

Supplementary Table 6 Contains a comprehensive list of significantly altered genes associated with the Wnt pathway at 48 hours, day 8, and day 15

Significant Genes	48 hours	Day 8	Day 15
<i>APC</i>	1.29	1.57	1.44 (p = 0.054)
	0.77 (p = 0.047)		
<i>AXIN1</i>		0.79 (p = 0.0078)	0.89
<i>CACYBP</i>	0.77	0.72 (p = 0.04)	0.86
<i>CAMK2A</i>	1.23	1.15 (p = 0.04)	1.16
<i>CAMK2B</i>	1.11	1.7 (p = 0.01)	1.2
<i>CAMK2D</i>	0.76 (p = 0.05)	0.19	1.05
<i>CCND1</i>	0.8 (p = 0.03)	0.87	0.87
<i>CCND2</i>	0.92 (p = 0.01)	1.04	1.07
<i>CCND3</i>	0.65	0.67 (p = 0.01)	0.67 (p = 0.05)
<i>CREBBP</i>	1.77 (p = 0.02)	1.48	0.96
	6.72 (p = 0.0003)		
<i>CSNK1A1</i>		1.43	0.79
<i>CSNK1A1L</i>	1.03	1.16 (p = 0.03)	1.1
<i>CSNK1E</i>	0.98	1.15	0.8 (p = 0.046)
<i>CSNK2A1</i>	2.47	1.1	1.98 (p = 0.035)
	2.95 (p = 0.007)		
<i>CSNK2A2</i>		1.32	2.61
<i>CTBP1</i>	1.38	1.38 (p = 0.01)	1.88
	1.36 (p = 0.015)		
<i>CTBP2</i>		1.4 (p = 0.00145)	1.48 (p = 0.010847)
<i>DVL3</i>	1.29	1.14	1.53 (p = 0.006)
<i>FRAT1</i>	0.99	0.98	0.92 (p = 0.042)
<i>FZD1</i>	0.88 (p = 0.02)	0.82 (p = 0.0013)	0.81 (p = 0.0057)
<i>FZD10</i>	1.24 (p = 0.05)	1.29	1.14

<i>FZD7</i>	0.84 (p = 0.03)	1.03	0.93
<i>GSK3B</i>	3.82 (p = 0.03)	0.55 (p = 0.008)	0.78 (p = 0.03)
<i>JUN</i>	0.91	1.16	0.69 (p = 0.04)
<i>LRP6</i>	0.87	0.75 (p = 0.05)	0.85
<i>MAPK8</i>	0.83	1.48	8.13 (p = 0.003)
<i>MAPK9</i>	5.02 (p = 0.02)	1.66	1.49
<i>NFATC1</i>	1.23 (p = 0.02)	0.97	1.27
<i>PLCB1</i>	0.64 (p = 0.03)	0.99	0.9
<i>PLCB2</i>	1.07	1.46 (p = 0.04)	1.52 (p = 0.05)
<i>PLCB4</i>	0.66 (p = 0.03)	0.83 (p = 0.05)	0.92
<i>PPP3R2</i>	0.85	0.83 (p = 0.02)	0.93
	7.18 (p = 0.008)		
<i>PRKCB</i>		2.94 (p = 0.05)	5.98 (p = 0.02)
<i>RAC2</i>	1.86 (p = 0.05)	1.1	2.15
<i>RAC3</i>	1.2 (p = 0.04)	1.06	0.99
<i>RBX1</i>	8.71 (p = 0.04)	0.49 (p = 0.0006)	0.71
<i>ROCK2</i>	1.8 (p = 0.003)	1.47	2.49
<i>SKP1</i>	5.26	0.66 (p = 0.009)	0.73 (p = 0.01)
<i>SOX17</i>	0.89	0.85 (p = 0.05)	0.96
	1.73 (p = 0.046)		
<i>TBL1XR1</i>		1.04	1.08
<i>TCF7L2</i>	1.29 (p = 0.02)	1.14 (p = 0.01)	1.17
	0.81 (p = 0.047)		
<i>VANGL2</i>		0.92	0.94
<i>WNT8A</i>	0.96	0.87 (p = 0.046)	1.19
<i>WNT8B</i>	0.86 (p = 0.04)	1	0.9

Values shaded in red contain significantly downregulated (p < 0.05) fold changes.

Values shaded in green contain significantly upregulated (p < 0.05) fold changes.