Roaming Around AML

Reza Asakereh[a]

[a]*CE Department, Sharif University of Technology*

Abstract

Some random words placeholding the abstract

1. Introduction

This article conducts an unplanned investigation of bunch of data and research results about AML decease. As indicated by **?**, the fifth most affected site in body by cancer is the circulatory system, with about a hundred thousands estimated cases in total of a million cancer in the US, 2002. AML is one of the most suffered and fatal one with almost 35% of the cases resulting into death. Hence, piling up some results in this area will accelerate more experienced scientists toward a working solution. However, this field is not abandoned, and has been worked on extensively. Therefore, they are considered as rich sources of result validation. The process of the investigation begins with a beginner level differential expression analysis resulting in some gene lists with significant gene expression alterations. These lists are used as the input of the next pipeline component, gene enrichment. Extracting some pieces of information in this step will be the basis of some fact finding endeavors.

2. Differential Expression Analysis

This article has employed **?** data set and Limma tools **?**. The data set primarily consists of 170 samples having their expressions measured by 32321 probes and classified in two categories, having self-explanatory labels, "Normal" and "Leukemia." These samples were first examined in three prospectives, respectively independent of the cell source, cells of type T, cells of type B(Table 1.)

After having the data in this format, a basic visualization was employed to form an intuition about the comparability of the data. The data needed no normalization (figure1.) However, the heatmap and its interensic hierarchical clustering failed to assure the validity of the data.

extract some genes with significantly different expression levels in normal versus affected cells.

Email address: `rasakereh@ce.sharif.edu` (Reza Asakereh)

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Table 1: The samples were studied dependant and independant of their source.

Source Dependancy	Normal Sources	Leukemia Sources
Independent	B Cells, CD34+HSPC, Granulocytes, Monocytes, T Cells	AML Cell Line, AML Patient, B ALL Cell Line, B ALL Patient, T ALL Cell Line, T ALL Patient
T cells	T Cells	T ALL Cell Line, T ALL Patient
B cells	B Cells	B ALL Cell Line, B ALL Patient

3. Gene Set Enrichment Analysis

As the gene sets extracted, they were passed to EnrichR to find possible causes and cures for AML. The GSEA results were truncated not to be represent ideas elusive to naked eyes. So only results with adjusted p-value less than .05 were selected. Moreover, at most 5 top cases extracted from each database were kept and the rest were eliminated. The results were sorted by combined score before the elimination process. The databases that were exploited for each purpose are listed in Table B.48 . Appendix A would explain the reason of each database choice.

Table 2: Databases in Use for GSEA

Analysis	Databases
Transcription Factors	TRANSFAC and JASPAR PWMs, miRTarBase 2017
Pathways	KEGG2019 Human, NCI-Nature 2016, Reactome 2016
Gene Ontology	GO Biological Process 2018, GO Molecular Function 2018, GO Cellular Component 2018
Drugs	ARCHS4 IDG Coexp

The comprehensive genes outputed by GSEA can be viewed inAppendix B. Amongth the extracted genes, pathways, etc, some were more attractive and listed here with some details. The headers are represented in the format of ([Source_Change], Name, Adjusted P-value, Z-score, Combined Score, database.)

3.1. Transcription Factors (TF)
This section has been widely influenced by proteinatlas and KEGG.

3.1.1. ETV4
Transcription regulator, e.g is unfavorable to liver cancer while favorable to thyroid cancer.

3.1.2. E2F4
Transcription facator, significant role in cell cycle regulation.

3.1.3. E2F1
Transcription factor of the E2F TF family.

3.1.4. NRF1
Nuclear respiratory factor 1, TF regulating key metabolic genes.

3.1.5. NFIC
TF in cells and replication factor for adenovirus.

3.1.6. NFYA
TF associated with a subunit of a high specified and affined DNA binding complex.

3.1.7. POU2F1
Of the same group of oct4 i.e octamer transcription factors.

3.2. Pathways (PW)

3.2.1. Glycosaminoglycan degradation
Glycosaminoglycans are polar molecules found in extracellular matrix and interact with growth factors

3.2.2. Glycosphingolipid biosynthesis
Glycosphingolipids form a major part of lipid rafts in cell membrane, in which some receptors lay

3.2.3. RIG-I-like receptor signaling pathway
RIG-I-like receptors have accepted the role of pathogen sensing of RNA viruses

3.2.4. Autoimmune thyroid disease
A disease in which thyroid cells are defected and secrete antigens consequently, attracting B and T cells toward themselves, therefore, driven to necrosis/apoptosis.

3.2.5. Graft-versus-host disease
Allogeneic hematopoietic transplantations causes some disorders invoking donor cells against the host ones.

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Appendix A. GSEA Dataset Selection

place holder

Appendix B. GSEA Full Selected Genes

Table B.3: Databases in Use for GSEA

Name	Adj. P-value	Z-score	Combined Score
ETV4 (human)	0.043	-1.74	15.24

Table B.4: Databases in Use for GSEA

Name	Adj. P-value	Z-score	Combined Score
E2F4 (human)	6.248e-9	-1.97	48.40
E2F1 (human)	0.00002605	-1.55	23.43
NRF1 (human)	0.0001446	-1.71	22.44
NFIC (human)	0.001465	-1.69	18.00
NFYA (human)	0.002248	-1.60	16.03

Table B.5: Databases in Use for GSEA

Name	Adj. P-value	Z-score	Combined Score
hsa-miR-193b-3p	8.760050e-64	-6.364176	973.9777
hsa-miR-192-5p	2.501043e-31	-6.765765	522.3863
hsa-miR-215-5p	2.718386e-34	-5.184328	437.7653
hsa-miR-34a-5p	9.159129e-21	-5.117180	269.1568
hsa-miR-92a-3p	1.886866e-08	-9.381637	223.6528

Author biography

Reza Asakereh A good guy with bad fruits

Table B.6: Databases in Use for GSEA

Name	Adj. P-value	Z-score	Combined Score
E2F4 (human)	0.006586	-1.95	18.87
E2F1 (human)	0.002198	-1.57	18.41

Table B.7: Databases in Use for GSEA

Name	Adj. P-value	Z-score	Combined Score
hsa-miR-193b-3p	1.574e-35	-6.36	558.85
hsa-miR-192-5p	4.991e-29	-6.77	485.40
hsa-miR-215-5p	6.399e-30	-5.18	384.69
hsa-miR-34a-5p	1.639e-7	-5.12	112.13
hsa-let-7b-5p	0.008490	-7.90	85.63

Table B.8: Databases in Use for GSEA

Name	Adj. P-value	Z-score	Combined Score
POU2F1 (human)	0.03246	-1.74	15.68

Table B.9: Databases in Use for GSEA

Name	Adj. P-value	Z-score	Combined Score
E2F4 (human)	3.861e-8	-1.97	44.58
E2F1 (human)	0.005012	-1.55	15.12
NRF1 (human)	0.01787	-1.71	14.02

Table B.10: Databases in Use for GSEA

Name	Adj. P-value	Z-score	Combined Score
hsa-miR-193b-3p	1.275e-39	-6.36	618.57
hsa-miR-192-5p	4.036e-18	-6.77	315.22
hsa-miR-215-5p	2.494e-19	-5.18	258.08
hsa-miR-34a-5p	5.211e-14	-5.12	188.50
hsa-let-7b-5p	0.00006949	-7.90	121.79

Name	Adj. P-value	Z-score	Combined Score
Glycosaminoglycan degradation	0.02246	-613.78	3210.85
Glycosphingolipid biosynthesis	0.4322	-900.86	1321.91
RIG-I-like receptor signaling pathway	0.004278	-97.67	704.97
Autoimmune thyroid disease	0.002948	-78.88	653.40
Graft-versus-host disease	0.001461	-68.48	636.28

Name	Adj. P-value	Z-score	Combined Score
Endosomal/Vacuolar pathway_Homo sapiens_R-HSA-1236977	0.000001320	-1.98	37.94
Interferon alpha/beta signaling_Homo sapiens_R-HSA-909733	0.00001904	-1.86	29.37
Antigen Presentation: Folding, assembly and peptide loading of class I MHC_Homo sapiens_R-HSA-983170	0.00002778	-1.93	28.99
Immune System_Homo sapiens_R-HSA-168256	0.0001276	-2.20	28.61
Interferon gamma signaling_Homo sapiens_R-HSA-877300	0.00008257	-1.76	24.06

Name	Adj. P-value	Z-score	Combined Score
DNA replication 6.096e-17	-49.69	1855.26	
Homologous recombination	5.327e-9	-49.65	1100.04
Oocyte meiosis	1.312e-10	-26.82	704.47
Fanconi anemia pathway	0.000001224	-41.92	687.64
Small cell lung cancer	0.0006399	-63.94	602.21

Table B.14: Databases in Use for GSEA

Name	Adj. P-value	Z-score	Combined Score
E2F transcription factor network_Homo sapiens_bb4d0fd3-6191-11e5-8ac5-06603eb7f303	1.616e-20	-1.73	85.49
PLK1 signaling events_Homo sapiens_e5e87977-6194-11e5-8ac5-06603eb7f303	1.127e-20	-1.66	83.87
FOXM1 transcription factor network_Homo sapiens_c51cda49-6192-11e5-8ac5-06603eb7f303	2.769e-16	-1.51	58.67
Aurora B signaling_Homo sapiens_304a75af-618c-11e5-8ac5-06603eb7f303	5.779e-18	-1.26	54.28
ATR signaling pathway_Homo sapiens_8991cbac-618b-11e5-8ac5-06603eb7f303	4.751e-15	-1.18	42.36

Table B.15: Databases in Use for GSEA

Name	Adj. P-value	Z-score	Combined Score
Cell Cycle_Homo sapiens_R-HSA-1640170	1.426e-117	-2.46	677.98
Cell Cycle, Mitotic_Homo sapiens_R-HSA-69278	1.227e-106	-2.47	616.03
M Phase_Homo sapiens_R-HSA-68886	2.552e-50	-2.43	290.68
Cell Cycle Checkpoints_Homo sapiens_R-HSA-69620	6.168e-44	-2.34	244.94
G2/M Checkpoints_Homo sapiens_R-HSA-69481	2.432e-40	-2.32	222.45

Table B.16: Databases in Use for GSEA

Name	Adj. P-value	Z-score	Combined Score
Glycosaminoglycan degradation	0.1424	-585.89	2091.24
Autoimmune thyroid disease	0.00003361	-80.82	1151.46
Th17 cell differentiation	0.00002734	-69.21	1041.32
Graft-versus-host disease	0.00004041	-68.48	923.26
Allograft rejection	0.00003361	-54.70	767.09

Table B.17: Databases in Use for GSEA

Name	Adj. P-value	Z-score	Combined Score
TNF receptor signaling pathway_Homo sapiens__316be05e-6196-11e5-8ac5-06603eb7f303	0.0001737	-1.53	19.39
TRAIL signaling pathway_Homo sapiens_3a79fddf-6196-11e5-8ac5-06603eb7f303	0.0001737	-1.41	18.49
IL12-mediated signaling events_Homo sapiens__7acdea19-6193-11e5-8ac5-06603eb7f303	0.0008804	-1.54	16.39
Downstream signaling in naive CD8+ T cells_Homo sapiens__92180cef-6191-11e5-8ac5-06603eb7f303	0.0009973	-1.43	14.59
IL2-mediated signaling events_Homo sapiens_a2a1883c-6193-11e5-8ac5-06603eb7f303	0.002484	-1.55	14.07

Table B.18: Databases in Use for GSEA

Name	Adj. P-value	Z-score	Combined Score
Immune System_Homo sapiens__R-HSA-168256	0.00001975	-2.23	37.84
Cytokine Signaling in Immune system_Homo sapiens__R-HSA-1280215	0.00003972	-2.40	37.28
Endosomal/Vacuolar pathway_Homo sapiens_R-HSA-1236977	0.00004649	-1.90	28.15
Interferon alpha/beta signaling_Homo sapiens_R-HSA-909733	0.00004649	-1.84	27.00
Interferon gamma signaling_Homo sapiens__R-HSA-877300	0.00006090	-1.75	24.90

Table B.19: Databases in Use for GSEA

Name	Adj. P-value	Z-score	Combined Score
Glyoxylate and dicarboxylate metabolism	0.5917	-701.48	867.99
Glycosaminoglycan biosynthesis	0.3410	-406.31	856.52
Homologous recombination	0.00001242	-50.16	744.50
Small cell lung cancer	0.001191	-67.62	628.70
DNA replication	0.00006099	-49.02	624.51

Table B.20: Databases in Use for GSEA

Name	Adj. P-value	Z-score	Combined Score
PLK1 signaling events_Homo sapiens_e5e87977-6194-11e5-8ac5-06603eb7f303	1.853e-13	-1.66	55.78
FOXM1 transcription factor network_Homo sapiens_c51cda49-6192-11e5-8ac5-06603eb7f303	1.887e-11	-1.65	46.63
E2F transcription factor network_Homo sapiens_bb4d0fd3-6191-11e5-8ac5-06603eb7f303	3.319e-11	-1.68	45.91
p73 transcription factor network_Homo sapiens_a88c505e-6194-11e5-8ac5-06603eb7f303	8.821e-10	-1.38	32.22
ATR signaling pathway_Homo sapiens_8991cbac-618b-11e5-8ac5-06603eb7f303	1.914e-10	-1.24	31.11

Table B.21: Databases in Use for GSEA

Name	Adj. P-value	Z-score	Combined Score
Cell Cycle_Homo sapiens_R-HSA-1640170	3.743e-54	-2.46	317.68
Cell Cycle, Mitotic_Homo sapiens_R-HSA-69278	5.027e-44	-2.47	259.31
Mitotic Prometaphase_Homo sapiens_R-HSA-68877	1.905e-22	-2.03	111.73
M Phase_Homo sapiens_R-HSA-68886	2.687e-18	-2.41	107.58
Resolution of Sister Chromatid Cohesion_Homo sapiens_R-HSA-2500257	1.644e-20	-2.06	103.70
Intestinal immune network for IgA production	0.000003880	-99.15	1739.13

Table B.22: Databases in Use for GSEA

Name	Adj. P-value	Z-score	Combined Score
Glycosphingolipid biosynthesis	0.8842	-781.54	574.04
TNF signaling pathway	0.06974	-74.45	391.55
Autoimmune thyroid disease	0.08780	-77.59	383.98
Asthma	0.09760	-81.53	76.60

Table B.23: Databases in Use for GSEA

Name	Adj. P-value	Z-score	Combined Score
Immune System_Homo sapiens_R-HSA-168256	0.0003718	-2.23	31.24
Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell_Homo sapiens_R-HSA-198933	0.0006682	-2.00	25.45
Adaptive Immune System_Homo sapiens_R-HSA-1280218	0.006699	2.27	22.67
CD22 mediated BCR regulation_Homo sapiens_R-HSA-5690714	0.009758	-1.94	17.65
TNF receptor superfamily (TNFSF) members mediating non-canonical NF-kB pathway_Homo sapiens_R-HSA-5676594	0.009595	-1.88	17.61

Table B.24: Databases in Use for GSEA

Name	Adj. P-value	Z-score	Combined Score
Small cell lung cancer	0.002421	-64.35	525.51
DNA replication	0.0004052	-48.35	515.36
Homologous recombination	0.0005634	-48.79	488.48
Fanconi anemia pathway	0.001818	-40.98	355.37
Human T-cell leukemia virus 1 infection	0.00003497	-18.10	242.43

Table B.25: Databases in Use for GSEA

Name	Adj. P-value	Z-score	Combined Score
E2F transcription factor network_Homo sapiens_bb4d0fd3-6191-11e5-8ac5-06603eb7f303	6.635e-13	-1.78	57.97
FOXM1 transcription factor network_Homo sapiens_c51cda49-6192-11e5-8ac5-06603eb7f303	6.102e-9	-1.65	37.63
PLK1 signaling events_Homo sapiens_e5e87977-6194-11e5-8ac5-06603eb7f303	2.976e-7	-1.47	26.78
Aurora B signaling_Homo sapiens_304a75af-618c-11e5-8ac5-06603eb7f303	9.910e-8	-1.26	24.67
Regulation of retinoblastoma protein_Homo sapiens_407a3468-6195-11e5-8ac5-06603eb7f303	0.000003482	-1.52	23.55

Table B.26: Databases in Use for GSEA

Name	Adj. P-value	Z-score	Combined Score
Cell Cycle_Homo sapiens_R-HSA-1640170	1.430e-40	-2.46	241.02
Cell Cycle, Mitotic_Homo sapiens_R-HSA-69278	7.756e-36	-2.47	213.08
Mitotic G1-G1/S phases_Homo sapiens_R-HSA-453279	1.077e-18	-2.11	98.22
G1/S Transition_Homo sapiens_R-HSA-69206	2.942e-15	-2.11	80.21
Mitotic Prometaphase_Homo sapiens_R-HSA-68877	1.569e-15	-2.02	78.71

Table B.27: Databases in Use for GSEA

Name	Adj. P-value	Z-score	Combined Score
antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-independent (GO:0002480)	0.0001851	-2.33	35.76
type I interferon signaling pathway (GO:0060337)	0.0002905	-2.32	30.11
retrograde transport, vesicle recycling within Golgi (GO:0000301)	0.02414	-4.03	29.32
regulation of necrotic cell death (GO:0010939)	0.003712	-2.48	23.91
regulation of necroptotic process (GO:0060544)	0.0002905	-1.62	20.96

Table B.28: Databases in Use for GSEA

Name	Adj. P-value	Z-score	Combined Score
death-inducing signaling complex (GO:0031264)	0.01076	-3.30	22.26
recycling endosome membrane (GO:0055038)	0.00003093	-1.46	21.80
integral component of lumenal side of endoplasmic reticulum membrane (GO:0071556)	0.001205	-1.95	20.60
COPII-coated ER to Golgi transport vesicle (GO:0030134)	0.001228	-2.06	19.47
MHC protein complex (GO:0042611)	0.001980	-2.05	17.74

Table B.29: Databases in Use for GSEA

Name	Adj. P-value	Z-score	Combined Score
DNA metabolic process (GO:0006259)	1.366e-44	-1.36	147.85
DNA replication (GO:0006260)	1.493e-35	-1.56	135.24
DNA repair (GO:0006281)	3.977e-26	-1.71	109.74
mitotic cell cycle phase transition (GO:0044772)	2.146e-32	-1.17	92.67
chromatin remodeling at centromere (GO:0031055)	1.246e-15	-2.28	88.85

Table B.30: Databases in Use for GSEA

Name	Adj. P-value	Z-score	Combined Score
DNA helicase activity (GO:0003678)	7.421e-10	-2.66	66.98
ATPase activity (GO:0016887)	4.563e-9	-2.31	53.57
DNA-dependent ATPase activity (GO:0008094)	3.454e-13	-1.53	51.82
DNA binding (GO:0003677)	1.223e-16	-1.20	50.97
3'-5' DNA helicase activity (GO:0043138)	0.000003135	-2.82	44.63

Table B.31: Databases in Use for GSEA

Name	Adj. P-value	Z-score	Combined Score
nuclear chromosome part (GO:0044454)	4.133e-37	-1.25	111.11
chromosome, centromeric region (GO:0000775)	5.429e-20	-2.25	108.81
microtubule organizing center (GO:0005815)	1.986e-18	-2.02	88.76
spindle (GO:0005819)	1.837e-29	-1.18	83.06
chromatin (GO:0000785)	1.158e-19	-1.66	78.42

Table B.32: Databases in Use for GSEA

Name	Adj. P-value	Z-score	Combined Score
retrograde transport, vesicle recycling within Golgi (GO:0000301)	0.009160	-4.03	37.61
cytokine-mediated signaling pathway (GO:0019221)	6.018e-9	-1.35	35.45
type I interferon signaling pathway (GO:0060337)	0.001496	-2.32	29.10
regulation of lymphocyte activation (GO:0051249)	0.005443	-2.70	27.84
antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-independent (GO:0002480)	0.001988	-2.33	27.55

Table B.33: Databases in Use for GSEA

Name	Adj. P-value	Z-score	Combined Score
cytokine receptor activity (GO:0004896)	0.0002861	-1.84	25.68
tumor necrosis factor-activated receptor activity (GO:0005031)	0.04099	-2.56	20.28

Table B.34: Databases in Use for GSEA

Name	Adj. P-value	Z-score	Combined Score
clathrin vesicle coat (GO:0030125)	0.03999	-3.52	19.54
integral component of lumenal side of endoplasmic reticulum membrane (GO:0071556)	0.002593	-1.94	19.08
MHC protein complex (GO:0042611)	0.003483	-2.08	18.73
T cell receptor complex (GO:0042101)	0.02267	-2.55	16.46
clathrin coat of trans-Golgi network vesicle (GO:0030130)	0.05913	-3.12	15.73

Table B.35: Databases in Use for GSEA

Name	Adj. P-value	Z-score	Combined Score
strand displacement (GO:0000732)	1.727e-11	-2.58	75.45
kinetochore organization (GO:0051383)	2.163e-11	-2.56	73.81
mitotic nuclear division (GO:0140014)	1.157e-11	-2.22	65.92
DNA biosynthetic process (GO:0071897)	1.520e-12	-1.97	62.81
DNA replication (GO:0006260)	2.687e-15	-1.55	61.43

Table B.36: Databases in Use for GSEA

Name	Adj. P-value	Z-score	Combined Score
DNA helicase activity (GO:0003678)	0.000009750	-2.62	38.96
microtubule motor activity (GO:0003777)	1.938e-7	-1.85	37.43
ATPase activity (GO:0016887)	0.000003774	-2.31	37.41
motor activity (GO:0003774)	2.992e-7	-1.58	30.62
DNA-dependent ATPase activity (GO:0008094)	4.744e-7	-1.52	28.12

Table B.37: Databases in Use for GSEA

Name	Adj. P-value	Z-score	Combined Score
chromosome, centromeric region (GO:0000775)	4.185e-16	-2.26	89.52
condensed chromosome, centromeric region (GO:0000779)	5.224e-12	-2.09	61.06
spindle microtubule (GO:0005876)	5.953e-12	-1.95	56.22
condensed chromosome kinetochore (GO:0000777)	3.066e-10	-2.22	54.12
spindle (GO:0005819)	1.758e-16	-1.18	48.64

Table B.38: Databases in Use for GSEA

Name	Adj. P-value	Z-score	Combined Score
renal filtration (GO:0097205)	0.002162	-3.50	38.03
phagocytosis, engulfment (GO:0006911)	0.0001266	-2.39	35.59
regulation of immune effector process (GO:0002697)	0.001193	-2.89	34.48
glomerular filtration (GO:0003094)	0.001895	-3.00	33.73
positive regulation of lymphocyte activation (GO:0051251	0.0001266	-2.21	32.93

Table B.39: Databases in Use for GSEA

Name	Adj. P-value	Z-score	Combined Score
immunoglobulin receptor binding (GO:0034987)	0.00008611	-2.41	36.35

Table B.40: Databases in Use for GSEA

Name	Adj. P-value	Z-score	Combined Score
DNA metabolic process (GO:0006259)	1.976e-20	-1.36	71.65
microtubule cytoskeleton organization involved in mitosis (GO:1902850)	4.370e-12	-1.65	53.05
sister chromatid segregation (GO:0000819)	3.095e-9	-2.04	50.33
mitotic spindle organization (GO:0007052)	3.027e-13	-1.39	49.10
DNA replication (GO:0006260)	1.211e-11	-1.55	47.77

Table B.41: Databases in Use for GSEA

Name	Adj. P-value	Z-score	Combined Score
histone kinase activity (GO:0035173)	0.0001513	-3.09	41.13
DNA helicase activity (GO:0003678)	0.0001706	-2.67	34.36
DNA polymerase binding (GO:0070182)	0.0004986	-2.31	25.27
3'-5' DNA helicase activity (GO:0043138)	0.004400	-2.80	22.77
DNA-dependent ATPase activity (GO:0008094)	0.00006878	-1.53	22.22

Table B.42: Databases in Use for GSEA

Name	Adj. P-value	Z-score	Combined Score
microtubule organizing center (GO:0005815)	1.411e-10	-2.07	54.44
chromosome, centromeric region (GO:0000775)	2.555e-8	-2.21	45.55
nuclear chromosome part (GO:0044454)	1.751e-13	-1.25	42.91
centrosome (GO:0005813), 1.411e-10	-1.61	42.58	
condensed chromosome kinetochore (GO:0000777)	5.286e-7	-2.27	39.74

Table B.43: Databases in Use for GSEA

Name	Adj. P-value	Z-score	Combined Score
STK17A_IDG_kinase_ARCHS4_coexpression	5.174e-28	-1.62	110.43
P2RY10_IDG_GPCR_ARCHS4_coexpression	1.710e-25	-1.55	95.41
MAP3K14_IDG_kinase_ARCHS4_coexpression	9.806e-18	-1.54	66.84
GPR25_IDG_GPCR_ARCHS4_coexpression	1.197e-15	-1.77	66.61
GPR174_IDG_GPCR_ARCHS4_coexpression	8.520e-17	-1.58	63.96

Table B.44: Databases in Use for GSEA

Name	Adj. P-value	Z-score	Combined Score
UCK2_IDG_kinase_ARCHS4_coexpression	9.315e-75	-1.61	283.39
PKMYT1_IDG_kinase_ARCHS4_coexpression	2.303e-65	-1.53	235.44
CHRNA9_IDG_ionchannel_ARCHS4_coexpression	2.957e-46	-1.54	168.06
RIOK1_IDG_kinase_ARCHS4_coexpression	7.258e-36	-1.60	136.09
PKN3_IDG_kinase_ARCHS4_coexpression	7.575e-35	-1.55	127.31

Table B.45: Databases in Use for GSEA

Name	Adj. P-value	Z-score	Combined Score
STK17A_IDG_kinase_ARCHS4_coexpression	6.729e-22	-1.62	88.38
GPR174_IDG_GPCR_ARCHS4_coexpression	2.546e-21	-1.62	84.65
P2RY10_IDG_GPCR_ARCHS4_coexpression	2.546e-21	-1.54	80.07
DYRK2_IDG_kinase_ARCHS4_coexpression	8.547e-12	-1.60	47.72
GPR171_IDG_GPCR_ARCHS4_coexpression	3.522e-10	-1.72	44.50

Table B.46: Databases in Use for GSEA

Name	Adj. P-value	Z-score	Combined Score
UCK2_IDG_kinase_ARCHS4_coexpression	1.384e-31	-1.60	121.31
PKMYT1_IDG_kinase_ARCHS4_coexpression	1.384e-31	-1.54	117.12
CHRNA9_IDG_ionchannel_ARCHS4_coexpression	1.934e-23	-1.54	87.25
PKN3_IDG_kinase_ARCHS4_coexpression	3.962e-15	-1.55	57.22
CSNK2A2_IDG_kinase_ARCHS4_coexpression	3.962e-15	-1.47	54.49

Table B.47: Databases in Use for GSEA

Name	Adj. P-value	Z-score	Combined Score
P2RY10_IDG_GPCR_ARCHS4_coexpression	2.375e-20	-1.56	79.30
MAP3K14_IDG_kinase_ARCHS4_coexpression	3.895e-7	-1.55	30.67
STK38L_IDG_kinase_ARCHS4_coexpression	0.000007491	-1.61	26.45
GPR174_IDG_GPCR_ARCHS4_coexpression	0.00002773	-1.60	23.70
GPR152_IDG_GPCR_ARCHS4_coexpression	0.003520	-1.98	17.89

Table B.48: Databases in Use for GSEA

Name	Adj. P-value	Z-score	Combined Score
PKMYT1_IDG_kinase_ARCHS4_coexpression	8.882e-32	-1.54	118.82
UCK2_IDG_kinase_ARCHS4_coexpression	1.443e-24	-1.60	95.40
CHRNA9_IDG_ionchannel_ARCHS4_coexpression	9.312e-17	-1.54	63.51
PKN3_IDG_kinase_ARCHS4_coexpression	9.496e-14	-1.56	52.99
CSNK2A2_IDG_kinase_ARCHS4_coexpression	6.583e-11	-1.46	39.83