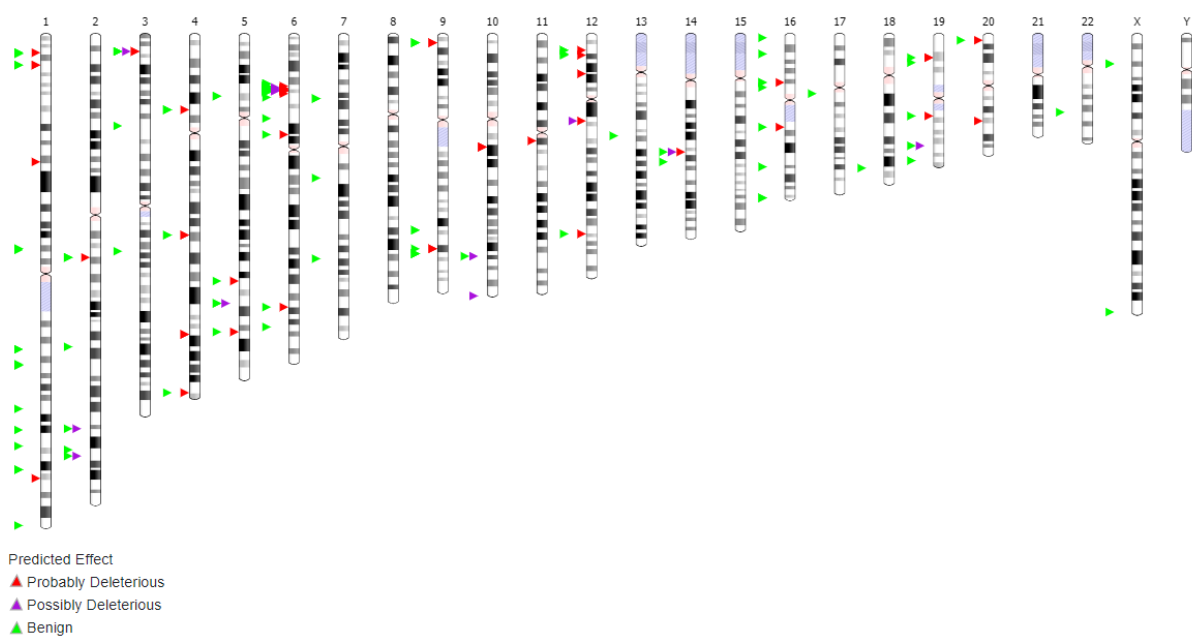


Biological Process	P.Value	FDR	Percentag
Innate immune response	4.28E-57	3.51E-54	29.31
Intracellular signal transduction	6.30E-48	2.58E-45	16.37
Immune response	3.57E-44	9.74E-42	19.23
Regulation of defense response	2.76E-43	5.65E-41	28.52
Intracellular protein kinase cascade	4.36E-43	7.15E-41	20.70
Regulation of immune response	1.16E-42	1.44E-40	24.62
Regulation of apoptotic process	1.23E-42	1.44E-40	18.51
Regulation of programmed cell death	1.48E-42	1.51E-40	18.52
Positive regulation of defense response	3.05E-42	2.78E-40	37.73
Positive regulation of immune system process	2.05E-40	1.68E-38	23.95
Regulation of immune system process	2.42E-40	1.81E-38	20.00
I kappaB kinase/NF kappaB cascade	5.30E-40	3.62E-38	38.62
Regulation of protein metabolic process	7.06E-40	4.45E-38	17.20
Programmed cell death	8.27E-40	4.84E-38	16.20
Immune system process	8.98E-40	4.91E-38	15.07
Regulation of molecular function	2.30E-39	1.18E-37	15.96
Apoptotic process	5.72E-39	2.61E-37	16.20
Apoptotic process	5.72E-39	2.61E-37	16.20
Multi organism process	2.21E-38	9.52E-37	17.31
Interaction with host	6.43E-38	2.64E-36	29.34
Positive regulation of protein metabolic process	2.34E-37	9.15E-36	20.19
Epidermal growth factor receptor signaling pathway	4.01E-37	1.50E-35	44.91
Response to stress	5.10E-37	1.82E-35	13.11
Regulation of protein modification process	5.84E-37	2.00E-35	19.04
Positive regulation of immune response	1.22E-36	4.01E-35	27.31
Regulation of catalytic activity	2.83E-36	8.93E-35	16.99
Activation of immune response	3.62E-36	1.10E-34	29.57
Enzyme linked receptor protein signaling pathway	4.79E-36	1.40E-34	19.24
Regulation of cellular protein metabolic process	6.61E-36	1.87E-34	17.50
Transmembrane receptor protein tyrosine kinase signaling pathway	2.96E-35	8.09E-34	22.25
Regulation of I kappaB kinase/NF kappaB cascade	4.88E-35	1.29E-33	39.05
Positive regulation of catalytic activity	2.75E-34	7.04E-33	19.63
Positive regulation of response to stimulus	5.39E-34	1.34E-32	17.29
Positive regulation of cellular protein metabolic process	2.73E-32	6.59E-31	19.94
Response to wounding	5.83E-32	1.37E-30	17.94
Viral reproduction	1.32E-31	3.01E-30	21.17
Viral reproductive process	2.28E-31	5.04E-30	23.62
Response to organic substance	4.44E-31	9.58E-30	14.56
Positive regulation of protein modification process	7.40E-31	1.55E-29	20.42
Defense response	2.89E-30	5.92E-29	16.82
Positive regulation of metabolic process	9.77E-30	1.95E-28	14.13
Positive regulation of cellular metabolic process	2.30E-29	4.49E-28	14.31
Negative regulation of protein metabolic process	1.21E-28	2.30E-27	23.70
Intracellular receptor mediated signaling pathway	2.34E-28	4.37E-27	31.48
Regulation of signal transduction	3.64E-28	6.63E-27	14.30
Positive regulation of signal transduction	3.93E-28	7.01E-27	18.84
Positive regulation of I kappaB kinase/NF kappaB cascade	1.80E-27	3.15E-26	40.67
Protein catabolic process	3.37E-27	5.76E-26	21.74
Cellular response to stress	1.13E-26	1.90E-25	15.93
Positive regulation of NF kappaB transcription factor activity	3.01E-26	4.94E-25	45.22

Supplementary Figure 1: Top 50 biological processes from BINGO analysis of Exonic SNPs

a



b

Variant	UniProt ID	Mutation	Polyphen2	SIFT	SNPeffect
VAR_024500	RAGE HUMAN	G82S			
VAR_029135	GHRL HUMAN	Q90L			
VAR_050095	GHRL HUMAN	L72M			
VAR_025846	HS71L HUMAN	E602K			
VAR_058287	IL17F HUMAN	E126G			
VAR_012988	LEG3 HUMAN	P64H			
VAR_004182	MBL2 HUMAN	G54D			
VAR_004183	MBL2 HUMAN	G57E			
VAR_008543	MBL2 HUMAN	R52C			
VAR_022127	NOS2 HUMAN	S608L			
VAR_020641	PADI4 HUMAN	G112A			
VAR_049843	PD1L2 HUMAN	I241T			
VAR_015076	SO1B1 HUMAN	V174A			
VAR_036795	SPIT4 HUMAN	G73S			
VAR_031237	TLR2 HUMAN	R753Q			
VAR_021976	TLR3 HUMAN	L412F			
VAR_020171	TENX HUMAN	G2555S			
VAR_048291	GPAN1 HUMAN	R41L			
VAR_022878	CF010 HUMAN	P128L			
VAR_022877	CF010 HUMAN	Y69C			
VAR_039560	CE110 HUMAN	P216L			
VAR_029754	IL23R HUMAN	R381Q			
VAR_039564	LY66D HUMAN	L9V			

Supplementary Figure 2: RA associated exonic SNPs predicted **a.** probably deleterious, possibly deleterious, and benign by SNP Nexus tool and **b.** predicted deleterious by Polyphen2, SIFT, SNPeffect and tools

WBC Count					
Variation ID	Gene	Chromosome	Trait	p-Value	PubMed ID
rs2476601	PTPN22	chr1	White blood cell count	1.00E-64	32888493
rs2476601	PTPN22	chr1	White blood cell count	1.00E-47	30595370
rs2476601	PTPN22	chr1	White blood cell count	2.00E-21	27863252
rs11052877	CD69	chr12	White blood cell count	4.00E-43	32888493
rs3184504	SH2B3	chr12	White blood cell count	8.00E-290	32888493
rs3184504	SH2B3	chr12	White blood cell count	8.00E-222	30595370
rs3184504	SH2B3	chr12	White blood cell count (eosinophil)	0.000002	28158719
rs3184504	SH2B3	chr12	White blood cell count	9.00E-70	27863252
rs3822733	IL7R	chr5	White blood cell count	6.00E-14	30595370
rs2631367	SLC22A5	chr5	White blood cell count	2.00E-56	30595370
rs2416804	TRAF1	chr9	White blood cell count	7.00E-14	30595370
rs10118357	TRAF1	chr9	White blood cell count	2.00E-11	32888493

Platelet Count					
Variation ID	Gene	Chromosome	Trait	p-Value	PubMed ID
rs3184504	SH2B3	chr12	Platelet count	0.000005	31217584
rs3184504	SH2B3	chr12	Plateletcrit	5.00E-216	27863252
rs3184504	SH2B3	chr12	Platelet count	6.00E-180	27863252
rs3184504	SH2B3	chr12	Platelet count	5.00E-11	24026423
rs3184504	SH2B3	chr12	Platelet count	1.00E-26	22139419
rs2631367	SLC22A5	chr5	Mean platelet volume	6.00E-111	32888493
rs399604	HLA-DOA	chr6	Platelet count	1.00E-10	22139419
rs513349	BAK1	chr6	Platelet count	7.00E-24	31217584
rs513349	BAK1	chr6	Platelet count	2.00E-12	23263863
rs5745582	BAK1	chr6	Platelet count	2.00E-53	32888493
rs3757385	IRF5	chr7	Platelet count	1.00E-15	32888493

Homocysteine levels					
Variation ID	Gene	Chromosome	Trait	p-Value	PubMed ID
rs1801133	MTHFR	chr1	Homocysteine levels	4.00E-104	23824729
rs1801133	MTHFR	chr1	Homocysteine levels	2.00E-11	23696881
rs1801133	MTHFR	chr1	Homocysteine levels	8.00E-35	20031578
rs1801133	MTHFR	chr1	Plasma homocysteine levels	1.00E-19	30339177

MCV					
Variation ID	Gene	Chromosome	Trait	p-Value	PubMed ID
rs4149056	SLCO1B1	chr12	Mean corpuscular volume	1.00E-24	32888493
rs4149056	SLCO1B1	chr12	Mean corpuscular volume	6.00E-25	32888493
rs5754217	UBE2L3	chr22	Mean corpuscular volume	2.00E-10	28017375
rs26232	MAC1R	chr5	Mean corpuscular volume	7.00E-30	32888493
rs10225965	CDK6	chr7	Mean corpuscular volume	5.00E-09	27863252

Hematocrit					
Variation ID	Gene	Chromosome	Trait	p-Value	PubMed ID
rs3184504	SH2B3	chr12	Hematocrit	8.00E-72	27863252
rs833070	VEGFA	chr6	Hematocrit	3.00E-22	27863252

Blood Protein Levels					
Variation ID	Gene	Chromosome	Trait	p-Value	PubMed ID
rs11209026	IL23R	chr1	Blood protein levels	3.00E-16	28240269
rs7522061	FCRL3	chr1	Blood protein levels	7.00E-182	30072576
rs7522061	FCRL3	chr1	Blood protein levels	5.00E-57	28240269
rs7528684	FCRL3	chr1	Blood protein levels	1.00E-112	29875488
rs1801274	FCGR2A	chr1	Blood protein levels	1E-2102	29875488
rs1061170	CFH	chr1	Blood protein levels	2.00E-52	29875488
rs1800451	MBL1	chr10	Blood protein levels	2.00E-51	29875488
rs2255336	KLK1	chr12	Blood protein levels	1.00E-13	28240269
rs3184504	SH2B3	chr12	Blood protein levels	2.00E-14	29875488
rs3184504	SH2B3	chr12	Blood protein levels	8.00E-07	27532455
rs4810485	CD40	chr20	Blood protein levels	5.00E-19	28915241
rs4704846	HAVCR2	chr5	Blood protein levels	2.00E-39	28240269
rs6457374	HLA-B	chr6	Blood protein levels	2.00E-34	29875488
rs2239705	ATP6V1G2	chr6	Blood protein levels	8.00E-09	27532455
rs2242653	LY6G6F	chr6	Blood protein levels	3.00E-10	28915241
rs1042663	C2	chr6	Blood protein levels	5.00E-18	29875488
rs550513	NELFE	chr6	Blood protein levels	1.00E-19	28240269
rs387608	STK19	chr6	Blood protein levels	3.00E-25	28240269
rs8111	ATF6B	chr6	Blood protein levels	1.00E-15	29875488
rs9296009	FKBP1	chr6	Blood protein levels	7.00E-13	29875488
rs9296009	FKBP1	chr6	Blood protein levels	3.00E-37	29875488
rs2070600	AGER	chr6	Blood protein levels	4.00E-33	29875488
rs2070600	AGER	chr6	Blood protein levels	3.00E-22	27532455
rs775228	HLA-DQB1	chr6	Blood protein levels	0.000003	28240269
rs1794282	HLA-DQB1	chr6	Blood protein levels	3.00E-19	28240269
rs7854413	PDCD1LG2	chr9	Blood protein levels	5.00E-12	29875488
rs4986790	TLR4	chr9	Blood protein levels	3.00E-70	29875488
rs4986791	TLR4	chr9	Blood protein levels	2.00E-50	28240269
rs1035029	C5	chr9	Blood protein levels	2.00E-13	30072576
rs1801274	FCGR2A	chr1	Serum total protein level	4.00E-12	29403010
rs204999	FKBP1	chr6	Serum total protein level	4.00E-11	23022100
rs204999	FKBP1	chr6	Serum total protein level	3.00E-09	23022100

RBC Count					
Variation ID	Gene	Chromosome	Trait	p-Value	PubMed ID
rs1801133	MTHFR	chr1	Red cell distribution width	1.00E-23	30595370
rs3184504	SH2B3	chr12	Red blood cell count	1.00E-102	30595370
rs3184504	SH2B3	chr12	Red blood cell count	2.00E-43	27863252
rs3184504	SH2B3	chr12	Red blood cell traits	4.00E-19	23222517
rs5754217	UBE2L3	chr22	Red blood cell traits	9.00E-10	23222517
rs322353	ACO222.17.4	chr5	Red cell distribution width	7.00E-11	30595370
rs833070	VEGFA	chr6	Red blood cell count	3.00E-16	27863252

CRP Levels					
Variation ID	Gene	Chromosome	Trait	p-Value	PubMed ID
rs2239704	LTA	chr6	C-reactive protein levels	1.00E-14	31900758
rs209474	BRD2	chr6	C-reactive protein levels	7.00E-09	31900758
rs6920220	TNFAIP3	chr6	C-reactive protein levels	7.00E-18	31900758

ANA Levels					
Variation ID	Gene	Chromosome	Trait	p-Value	PubMed ID
rs2395185	CD40	chr6	Antinuclear antibody levels	1.00E-11	25186300

Platelet Count					
Variation ID	Gene	Chromosome	Trait	p-Value	PubMed ID
rs3184504	SH2B3	chr12	Platelet count	0.000005	31217584
rs3184504	SH2B3	chr12	Plateletcrit	5.00E-216	27863252
rs3184504	SH2B3	chr12	Platelet count	6.00E-180	27863252
rs3184504	SH2B3	chr12	Platelet count	5.00E-11	24026423
rs3184504	SH2B3	chr12	Platelet count	1.00E-26	22139419
rs2631367	SLC22A5	chr5	Mean platelet volume	6.00E-111	32888493
rs399604	HLA-DOA	chr6	Platelet count	1.00E-10	22139419
rs513349	BAK1	chr6	Platelet count	7.00E-24	31217584
rs513349	BAK1	chr6	Platelet count	2.00E-12	23263863
rs5745582	BAK1	chr6	Platelet count	2.00E-53	32888493
rs3757385	IRF5	chr7	Platelet count	1.00E-15	32888493

ACPA Levels					
Variation ID	Gene	Chromosome	Trait	p-Value	PubMed
rs883220	AL390839.1	chr1	RA (ACPA-positive)	0.00000002	24532676
rs883220	AL390839.1	chr1	RA (ACPA-positive)	0.00000002	23143596
rs2476601	PTPN22	chr1	RA (ACPA-positive)	2.00E-126	24532676
rs2476601	PTPN22	chr1	RA (ACPA-positive)	8.00E-77	23143596
rs3761959	FCRL3	chr1	RA (ACPA-positive)	0.00000001	24532676
rs4936059	ETS1-FL11	chr11	RA (ACPA-positive)	7.00E-10	24532676
rs13031237	REL	chr2	RA (ACPA-positive)	1.00E-11	23143596
rs11893432	STAT4	chr2	RA (ACPA-positive)	2.00E-11	23143596
rs1980422	CD28	chr2	RA (ACPA-positive)	0.00000003	23143596
rs3087243	CTLA4	chr2	RA (ACPA-positive)	9.00E-15	24532676
rs3087243	CTLA4	chr2	RA (ACPA-positive)	4.00E-11	23143596
rs4810485	CD40	chr20	RA (ACPA-positive)	9.00E-11	23143596
rs3129890	HLA-DRA	chr6	ACPA-positive RA (smoking interaction)	1.00E-10	26272072
rs660895	HLA-DRB1	chr6	RA (ACPA-positive)	1.00E-300	23143596
rs660895	HLA-DRB1	chr6	RA (ACPA-negative)	0.00000002	23143596
rs10484565	TAP2	chr6	ACPA-positive RA (smoking interaction)	7.00E-10	26272072
rs6920220	AL356234.2	chr6	RA (ACPA-positive)	2.00E-18	24532676
rs6920220	AL356234.2	chr6	RA (ACPA-positive)	4.00E-18	23143596
rs4728142	IRF5	chr7	RA (ACPA-positive)	5.00E-12	24532676
rs3807306	IRF5	chr7	RA (ACPA-positive)	5.00E-10	23143596
rs2812378	CCL21	chr9	RA (ACPA-positive)	5.00E-11	24532676
rs2812378	CCL21	chr9	RA (ACPA-positive)	0.000000001	23143596
rs10739580	TRAF1	chr9	RA (ACPA-positive)	0.000002	23143596
rs1980493	BTNL2	chr6	Anti-cyclic Citrullinated Peptide Antibody	0.00000005	19287509

Hemoglobin Levels					
Variation ID	Gene	Chromosome	Trait	p-Value	PubMed ID
rs3184504	SH2B3	chr12	Hemoglobin levels	3.00E-175	32327693
rs3184504	SH2B3	chr12	Hemoglobin levels	1.00E-10	28017375
rs3184504	SH2B3	chr12	Hemoglobin concentration	1.00E-74	27863252
rs3132580	DPCR1	chr6	Hemoglobin levels	3.00E-34	32327693
rs1150752	TNXB	chr6	Hemoglobin levels	7.00E-35	32327693
rs7775397	Gcorf10	chr6	Hemoglobin levels	1.00E-35	32327693
rs833061	VEGFA	chr6	Hemoglobin concentration	1.00E-12	32888493
rs833070	VEGFA	chr6	Hemoglobin concentration	1.00E-20	27863252
rs833070	VEGFA	chr6	Hemoglobin levels	1.00E-50	32327693

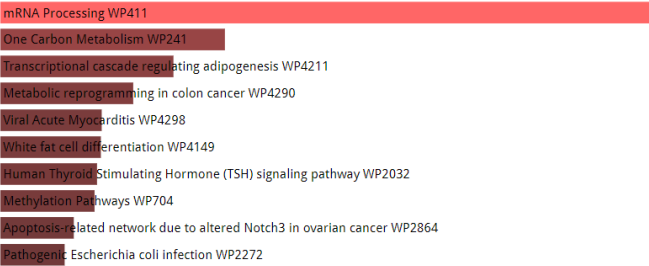
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rs2476601	PTPN22	chr1	IgM levels	2.00E-12	28628107
rs3184504	SH2B3	chr12	IgA levels	1.00E-08	28628107
rs1801275	IL4R	chr16	IgE levels	1.00E-07	22075330
rs2858331	HLA-DQA2	chr6	IgE levels	0.000006	23146381
rs2858331	HLA-DQA2	chr6	IgE levels	1.00E-08	22075330
rs6498142	CLEC16A	chr16	Immunoglobulin A	2.00E-07	20694011
rs1990760	IFIH1	chr2	Immunoglobulin A	7.00E-10	20694011
rs9271366	HLA-DRB1	chr6	Immunoglobulin A	3.00E-33	20694011
rs2187668	HLA-DRB1	chr6	Immunoglobulin A	2.00E-33	20694011

Supplementary Figure 3: SNPs associated with the Clinical Outcomes of RA

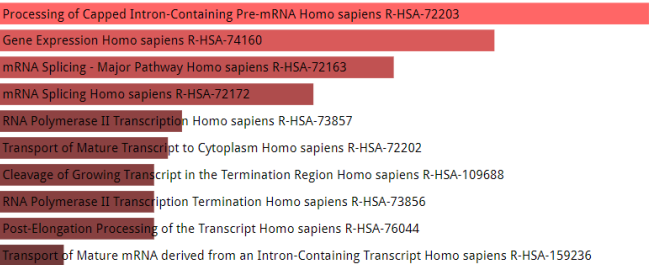
Mutation	AA variant	Gene	Func. Impact	FI score
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MBL2_HUMAN G54D	G54D	MBL2	high	4.485
MBL2_HUMAN G57E	G57E	MBL2	high	4.150
SPIT4_HUMAN G73S	G73S	SPIT4	high	3.515
SO1B1_HUMAN V174A	V174A	SLCO1B1	medium	3.350
MBL2_HUMAN R52C	R52C	MBL2	medium	3.335
TLR2_HUMAN P631H	P631H	TLR2	medium	2.850
IL17F_HUMAN E126G	E126G	IL17F	medium	2.720
IL1A_HUMAN R85Q	R85Q	IL1A	medium	2.515
CY24A_HUMAN Y72H	Y72H	CYBA	medium	2.470
MTHFR_HUMAN A222V	A222V	MTHFR	medium	2.425
GHRL_HUMAN L72M	L72M	GHRL	medium	2.340
LEG3_HUMAN P64H	P64H	LGALS3	medium	2.340
TYK2_HUMAN I684S	I684S	TYK2	medium	2.310
TLR10_HUMAN N241H	N241H	TLR10	medium	2.280
RAGE_HUMAN G82S	G82S	AGER	medium	2.255
PTN22_HUMAN R620W	R620W	PTPN22	medium	2.255
TLR2_HUMAN R753Q	R753Q	TLR2	medium	2.175
IL6RA_HUMAN D358A	D358A	IL6R	medium	2.140
CF010_HUMAN K400Q	K400Q	C6orf10	medium	2.140
ITPA_HUMAN P32T	P32T	ITPA	medium	2.130
PARP1_HUMAN V762A	V762A	PARP1	medium	2.110
GHRL_HUMAN Q90L	Q90L	GHRL	medium	2.075
DNASE1_HUMAN R2S	R2S	DNASE1	medium	1.995
DOB_HUMAN R18Q	R18Q	HLA-DOB	medium	1.950
GCR_HUMAN R23K	R23K	NR3C1	medium	1.950

Supplementary Figure 4: Functional Impact of Exonic SNPs by Mutation Assessor Tool

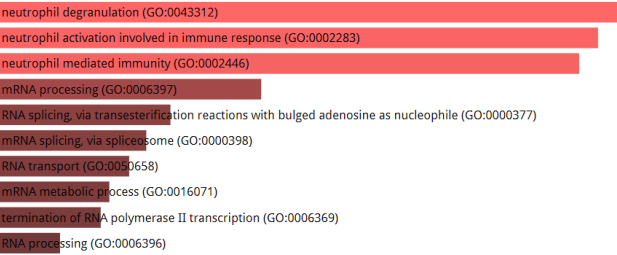
WIKI Pathways



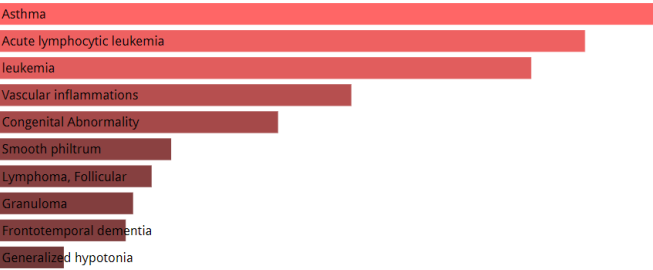
REACTOME Pathways



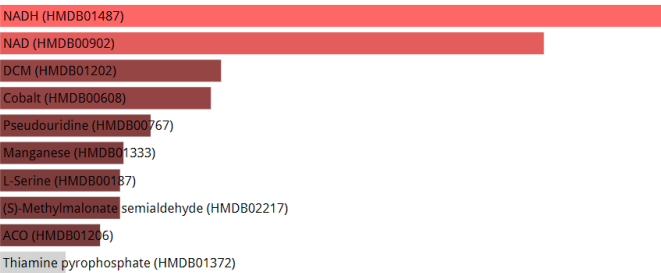
GO Biological Processes



DisGeNET

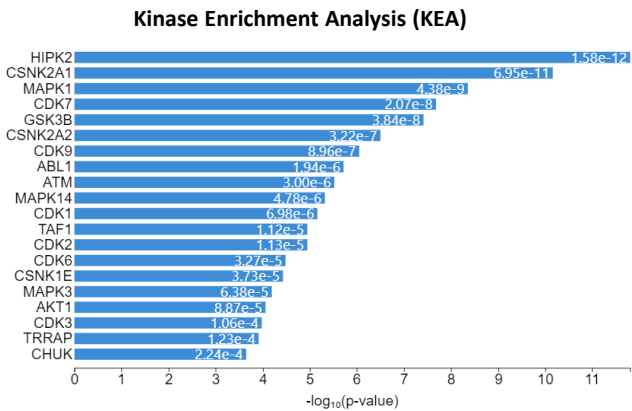
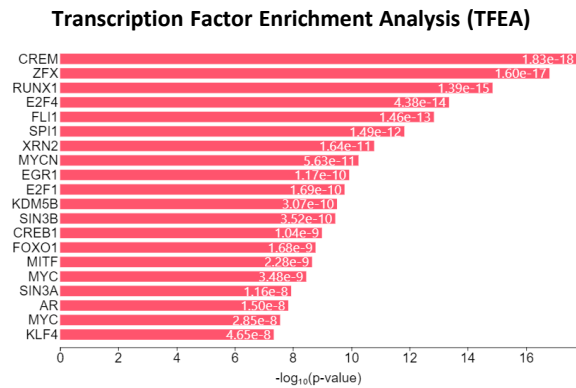


HMDB

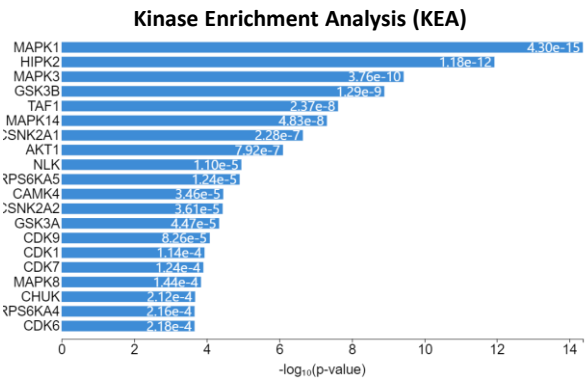
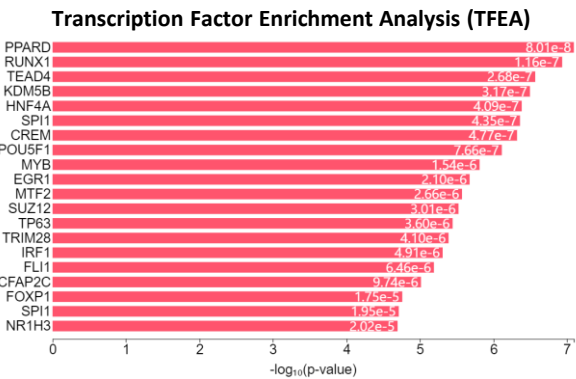


Supplementary Figure 5: Transcriptomics analysis of GSE15573 dataset : Enrichr analysis showing significant pathways, processes, diseases and metabolites Wiki and Reactome Pathways, Gene Ontlogy (Biological Processes), DiGeNET, and HMDB databases

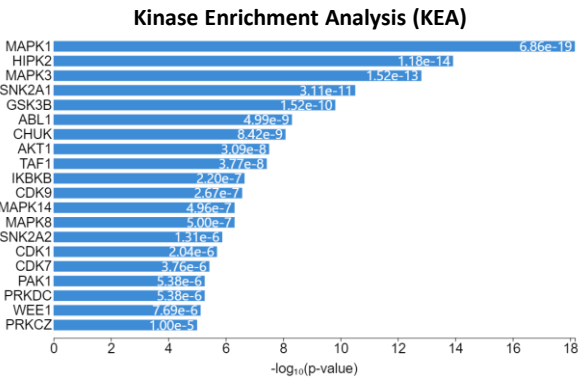
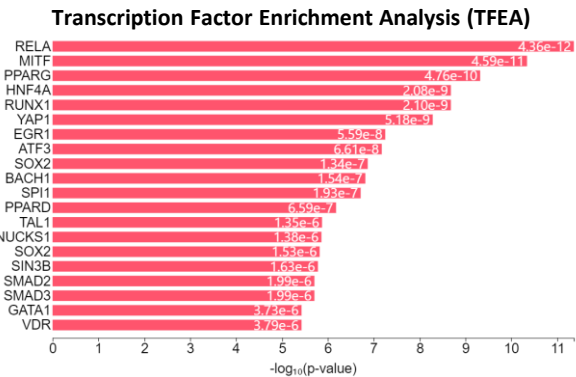
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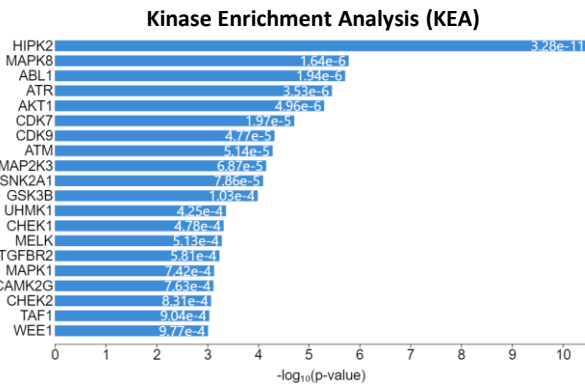
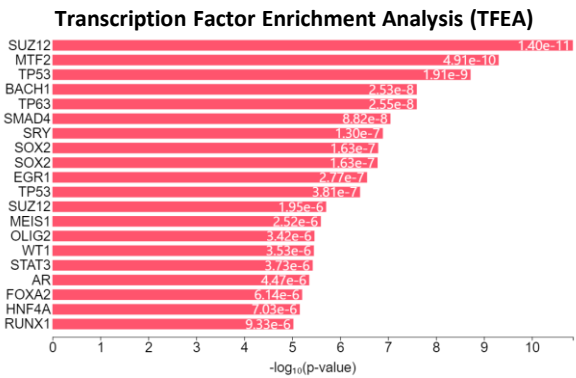
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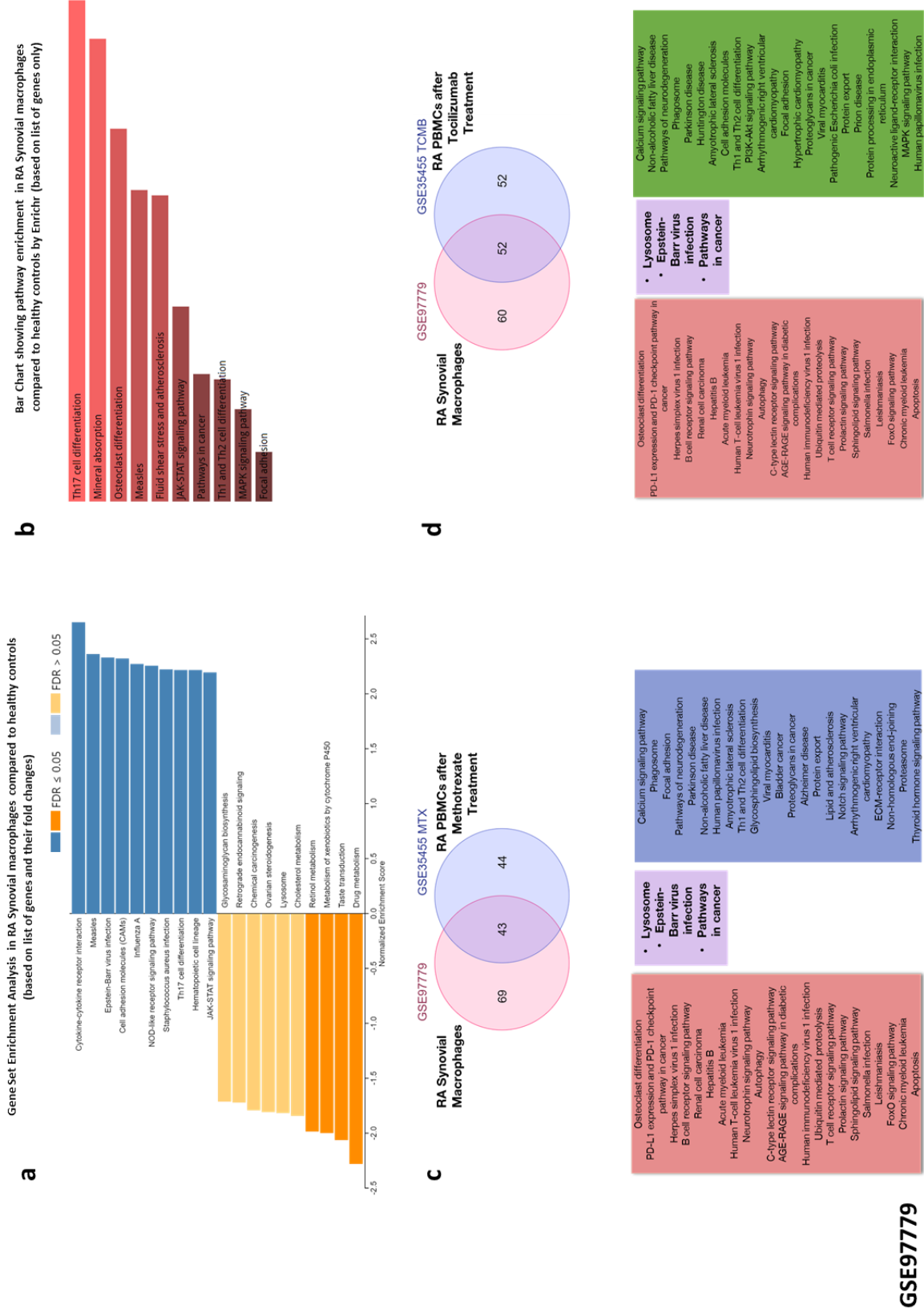
GSE10500



GSE77298



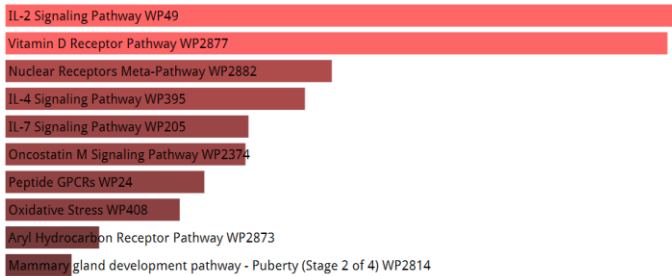
Supplementary Figure 6: X2K analysis of Transcriptomics datasets showing enriched critical transcription factors and kinases



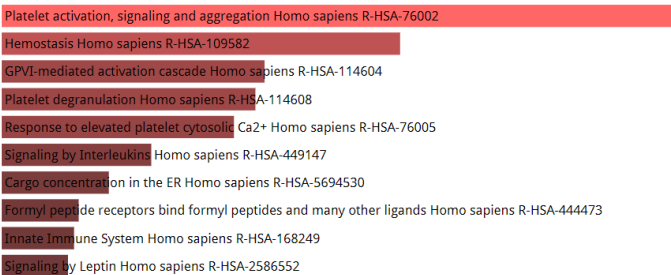
GSE97779

Supplementary Figure 7: Gene expression data analysis of GSE97779 GEO dataset (Synovial Macrophages): a) Gene set enrichment analysis (GSEA) of differentially expressed genes, b) Transcription factor enrichment analysis (through X2K analysis from iLINC database), c) Kinase enrichment analysis, d) Enrichment analysis of genes by Enrichr tool, e and f) commonality analysis of significant pathways that were found to be common between GSE97779 dataset and GSE35455 dataset with DMARDs and biologics treatment of RA patients.

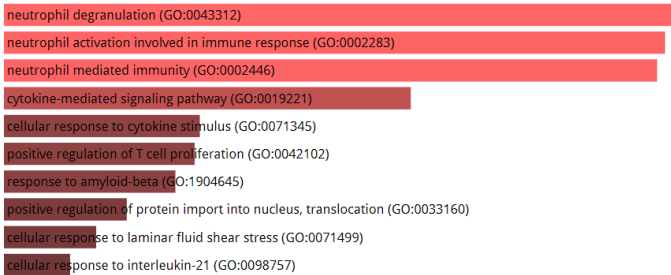
WIKI Pathways



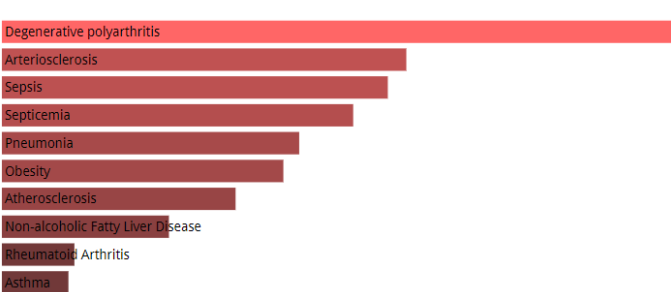
REACTOME Pathways



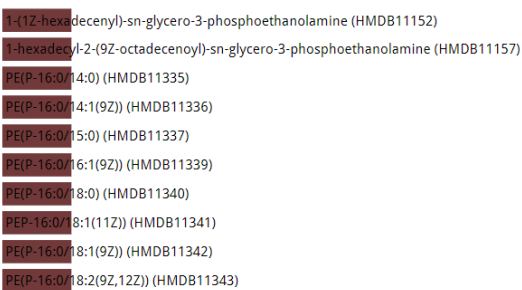
GO Biological Processes



DisGeNET



HMDB



Supplementary Figure 8: Transcriptomics analysis of GSE97779 dataset : Enrichr analysis showing significant pathways, processes, diseases and metabolites Wiki and Reactome Pathways, Gene Ontology (Biological Processes), DiGeNET, and HMDB databases



WIKI Pathways

Pathway
Hypertrophy Model WP516
Apoptosis Modulation and Signaling WP1772
Signaling Pathways in Glioblastoma WP2261
Breast cancer pathway WP4262
Aryl Hydrocarbon Receptor Pathway WP2873
Photodynamic therapy-induced AP-1 survival signalling. WP3611
DNA Damage Response (only ATM dependent) WP710
Osteopontin Signaling WP1434
Prader-Willi and Angelman Syndrome WP3998
TYROBP Causal Network WP3945

REACTOME Pathways

Pathway
TP53 Regulates Transcription of Caspase Activators and Caspases Homo sapiens R-HSA-6803207
Cytosolic tRNA aminoacylation Homo sapiens R-HSA-379716
G1 Phase Homo sapiens R-HSA-69236
Cyclin D associated events in G1 Homo sapiens R-HSA-69231
Class A/1 (Rhodopsin-like receptors) Homo sapiens R-HSA-373076
GPCR ligand binding Homo sapiens R-HSA-500792
tRNA Aminoacylation Homo sapiens R-HSA-379724
TP53 Regulates Transcription of Cell Death Genes Homo sapiens R-HSA-5633008
Immune System Homo sapiens R-HSA-168256
Sensing of DNA Double Strand Breaks Homo sapiens R-HSA-5693548

GO Biological Processes

Process
regulation of apoptotic process (GO:0042981)
positive regulation of protein kinase activity (GO:0045860)
extrinsic apoptotic signaling pathway (GO:0097191)
negative regulation of programmed cell death (GO:0043069)
mast cell activation involved in immune response (GO:0002279)
mast cell degranulation (GO:0043303)
positive regulation of gene expression (GO:0010628)
T cell differentiation (GO:0030217)
T cell activation (GO:0042110)
mast cell mediated immunity (GO:0002448)

DisGeNET

Disease
Carcinoma of lung
leukemia
Primary malignant neoplasm of lung
Malignant neoplasm of lung
Secondary malignant neoplasm of lung
Glioblastoma
Carcinogenesis
Mammary Neoplasms
B-Cell Lymphomas
Malignant neoplasm of prostate

HMDB

Metabolite
C3H7NO2Se (HMDB03288)
Selenium (HMDB01349)
L-Glutamine (HMDB00641)
NAP (HMDB00217)
NADPH (HMDB00221)
Glycine (HMDB00123)
Gamma-Aminobutyric acid (HMDB00112)
Phosphoric acid (HMDB02142)
Pyrophosphate (HMDB00250)
D-Galactose (HMDB00143)

Supplementary Figure 10: Transcriptomics analysis of GSE10500 dataset :
Enrichr analysis showing significant pathways, processes, diseases and
metabolites Wiki and Reactome Pathways, Gene Ontology (Biological Processes),
DiGeNET, and HMDB databases

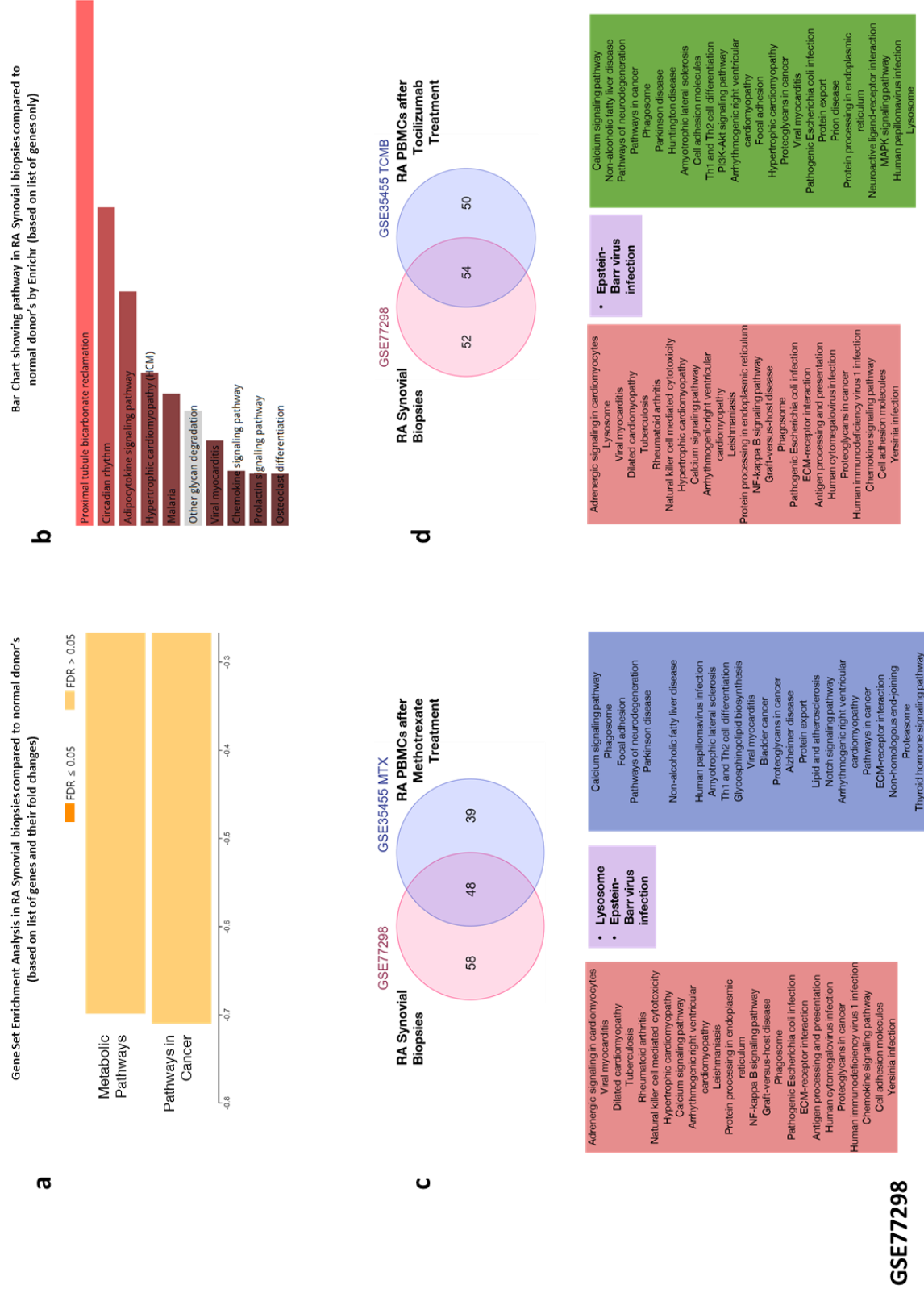
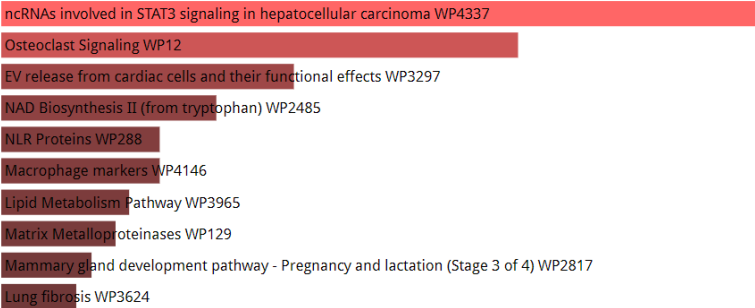
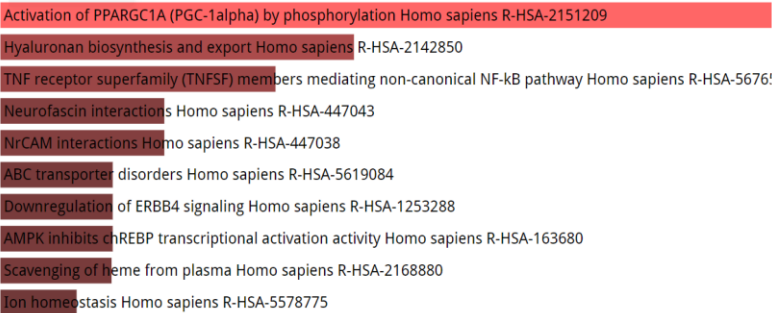


Figure 11: Gene expression data analysis of GSE77298 GEO dataset (Synovial Biopsies): a) Gene set enrichment analysis (GSEA) of differentially expressed genes, b) Transcription factor enrichment analysis (through X2K analysis from iLINC5 database), c) Kinase enrichment analysis of genes by Enrichr tool, e and f) commonality analysis of significant pathways that were found to be common between GSE77298 dataset and GSE35455 dataset with DMARDs and biologics treatment of RA patients.

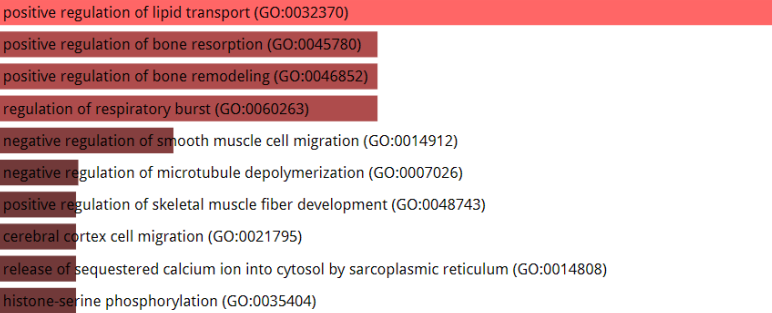
WIKI Pathways



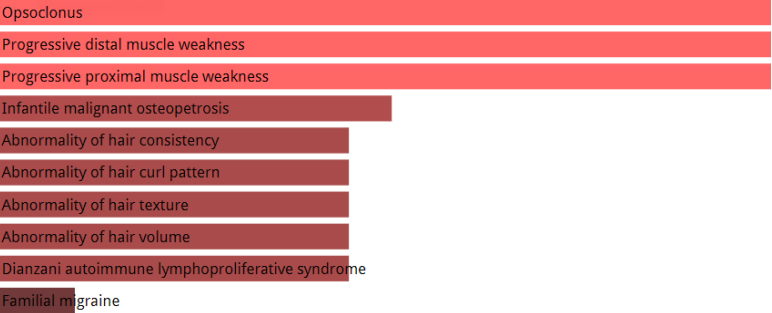
REACTOME Pathways



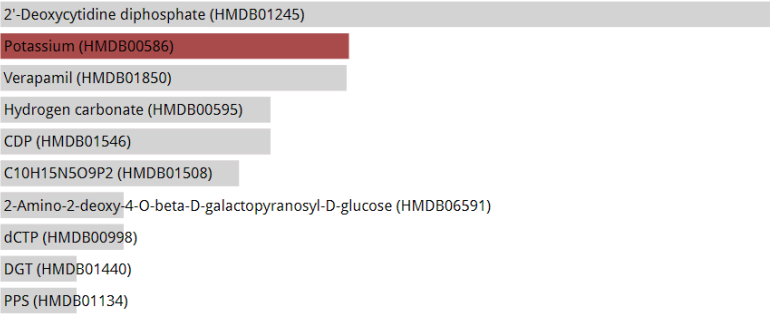
GO Biological Processes



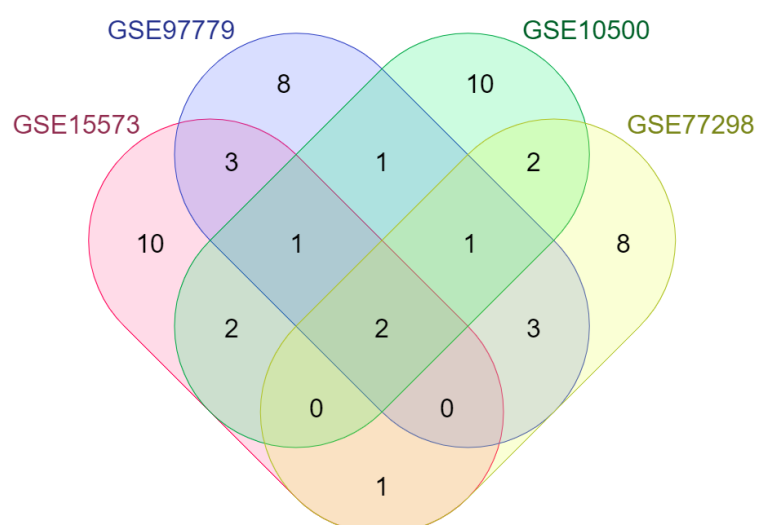
DisGeNET



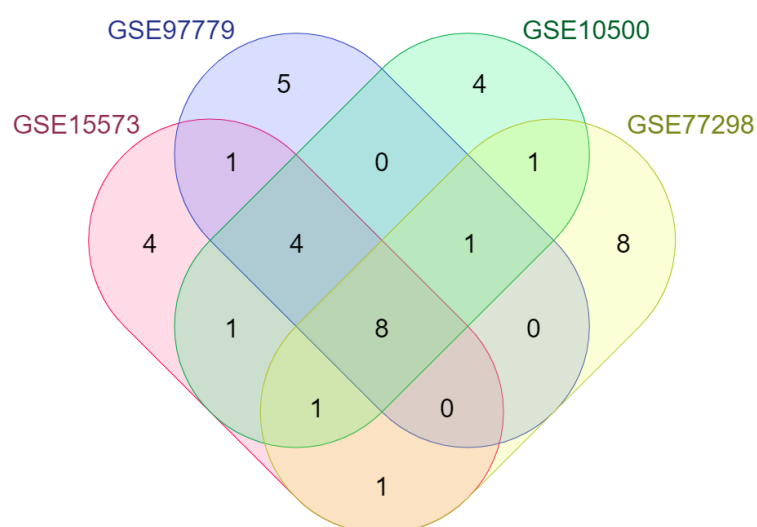
HMDB



Supplementary Figure 12: Transcriptomics analysis of GSE77298 dataset :
Enrichr analysis showing significant pathways, processes, diseases and
metabolites Wiki and Reactome Pathways, Gene Ontology (Biological Processes),
DiGeNET, and HMDB databases



Transcription Factor	Common among Datasets
EGR1	GSE15573, GSE97779, GSE10500, GSE77298
RUNX1	GSE15573, GSE97779, GSE10500, GSE77298
HNF4A	GSE97779, GSE10500, GSE77298
SPI1	GSE15573, GSE97779, GSE10500
AR	GSE15573, GSE77298
BACH1	GSE10500, GSE77298
CREM	GSE15573, GSE97779
FLI1	GSE15573, GSE97779
KDM5B	GSE15573, GSE97779
MITF	GSE15573, GSE10500
MTF2	GSE97779, GSE77298
PPARD	GSE97779, GSE10500
SIN3B	GSE15573, GSE10500
SOX2	GSE10500, GSE77298
SUZ12	GSE97779, GSE77298
TP63	GSE97779, GSE77298



KINASES	Common among Datasets
AKT1	GSE15573, GSE97779, GSE10500, GSE77298
CDK7	GSE15573, GSE97779, GSE10500, GSE77298
CDK9	GSE15573, GSE97779, GSE10500, GSE77298
CSNK2A1	GSE15573, GSE97779, GSE10500, GSE77298
GSK3B	GSE15573, GSE97779, GSE10500, GSE77298
HIPK2	GSE15573, GSE97779, GSE10500, GSE77298
MAPK1	GSE15573, GSE97779, GSE10500, GSE77298
TAF1	GSE15573, GSE97779, GSE10500, GSE77298
ABL1	GSE15573, GSE10500, GSE77298
CDK1	GSE15573, GSE97779, GSE10500
CHUK	GSE15573, GSE97779, GSE10500
CSNK2A2	GSE15573, GSE97779, GSE10500
MAPK14	GSE15573, GSE97779, GSE10500
MAPK8	GSE97779, GSE10500, GSE77298
ATM	GSE15573, GSE77298
CDK6	GSE15573, GSE97779
MAPK3	GSE15573, GSE10500
WEE1	GSE10500, GSE77298

Supplementary Figure 13: Transcription factor and Kinase analyses of GSE15573, GSE97779, GSE10500, and GSE77298 datasets : Venn diagram showing the overlap of Transcription factors and Kinases