Table S2 GO IPA analysis results

Ingenuity Canonical Pathways	-log 10 (p-value)	Significant (>1.3 Log10 p-value)	Ratio	Activation z-score (> 0 pthway is activayed, < 0 pathway is inhibited)	Down regulated	No change	Up regulated	No overlap with dataset	Molecules
Systemic Lupus Erythematosus Signaling	7.96	YES	0.1	NA	14/229 (6%)	0/229 (0%)	9/229 (4%)	206/229 (90%)	C5,CBL,CD22,CD40,HLA-E,LSM5,LSM8,PIK3CG,PRPF4B,PRPF8,PTPN6,RNU1-1,RNU1-28P,RNU1-3,RNU11,RNU4-2,RNU4ATAC,RNU6-
CD40 Signaling	5.44	YES	0.154	2.828	1/65 (2%)	0/65 (0%)	9/65 (14%)	55/65 (85%)	CD40,FCER2,LTA,MAP2K2,MAPK11,NFKB1,NFKB2,PIK3CG,TANK,TRAF1
Salvage Pathways of Pyrimidine Ribonucleotides	5.37	YES	0.124	0	6/97 (6%)	0/97 (0%)	6/97 (6%)	85/97 (88%)	AICDA,AK1,CDK1,CDK6,IRAK1,MAP2K2,MAP3K8,NME3,PAK2,PRPF4B,PYCR3,SGK1
Crosstalk between Dendritic Cells and Natural Killer Cells	4.97	YES	0.124	0.816	2/89 (2%)	0/89 (0%)	9/89 (10%)	78/89 (88%)	CAMK2G,CCR7,CD40,CD69,FSCN1,HLA-DRB3,HLA-E,LTA,NFKB1,NFKB2,TLR9
Systemic Lupus Erythematosus In B Cell Signaling Pathway	4.82	YES	0.0727	0.894	4/275 (1%)	0/275 (0%)	16/275 (6%)	255/275 (93%)	BCL2L1,CBL,CD22,CD40,CSK,GSK3B,IRAK1,ISG20,LTA,MAP2K2,MYC,NFKB1,NFKB2,PIK3CG,PTPN6,RASGRP3,STAT2,TLR9,TNFSF4,TRAF1
EIF2 Signaling	4.42	YES	0.0759	0.632	8/224 (4%)	0/224 (0%)	9/224 (4%)	207/224 (92%)	AGO1,AGO2,ATF4,DDIT3,EIF3B,EIF3G,EIF4A2,GSK3B,MAP2K2,MYC,PIK3CG,RPL15,RPL26,RPL34,RPL7L1,RPS27L,RPS4X
Inhibition of ARE-Mediated mRNA Degradation Pathway	4.35	YES	0.0984	1	2/122 (2%)	0/122 (0%)	10/122 (8%)	110/122 (90%)	AGO1,AGO2,EXOSC8,LTA,MAPK11,PPP2R1A,PRKAR2A,PSME4,TIA1,TNFSF4,ZFP36,ZFP36L2
Dendritic Cell Maturation	4.35	YES	0.082	1.732	3/183 (2%)	0/183 (0%)	12/183 (7%)	168/183 (92%)	ATF4,CCR7,CD40,CD58,FSCN1,HLA-DQB1,HLA-DRB3,HLA-E,LTA,MAPK11,NFKB1,NFKB2,PIK3CG,STAT2,TLR9
Pyridoxal 5'-phosphate Salvage Pathway	3.75	YES	0.123	0.707	3/65 (5%)	0/65 (0%)	5/65 (8%)	57/65 (88%)	CDK1,CDK6,IRAK1,MAP2K2,MAP3K8,PAK2,PRPF4B,SGK1
Role of JAK1, JAK2 and TYK2 in Interferon Signaling	3.61	YES	0.208	NA	1/24 (4%)	0/24 (0%)	4/24 (17%)	19/24 (79%)	NFKB1,NFKB2,PTPN6,SOCS1,STAT2
Protein Ubiquitination Pathway	3.38	YES	0.0623	NA	10/273 (4%)	0/273 (0%)	7/273 (3%)	256/273 (94%)	ANAPC10,CBL,DNAJC12,DNAJC2,DNAJC27,DNAJC7,HLA-E,HSPB11,PSMA2,PSMC6,PSMD4,UBD,UBE2T,USP11,U
B Cell Receptor Signaling	3.2	YES	0.0703	0	3/185 (2%)	0/185 (0%)	10/185 (5%)	172/185 (93%)	ATF4,BCL2L1,CAMK2G,CD22,CSK,GSK3B,MAP2K2,MAP3K8,MAPK11,NFKB1,NFKB2,PIK3CG,PTPN6
Molecular Mechanisms of Cancer	3.18	YES	0.0537	NA	6/391 (2%)	0/391 (0%)	15/391 (4%)	370/391 (95%)	ARHGEF2,BCL2L1,BMP7,CAMK2G,CBL,CDK1,CDK6,CFLAR,CHEK2,GNAI2,GSK3B,HAT1,MAP2K2,MAPK11,MYC,NFKB1,NFKB2,PAK2,PIK3CG,PRKAR2A,RHOG
TNFR2 Signaling	3.14	YES	0.167	2	1/30 (3%)	0/30 (0%)	4/30 (13%)	25/30 (83%)	LTA,NFKB1,NFKB2,TANK,TRAF1

JAK/Stat Signaling	3.13	YES	0.1		0.707	1/80 (1%)	0/80 (0%)	7/80 (9%)	72/80 (90%)	BCL2L1,MAP2K2,NFKB1,NFKB2,PIK3CG,PTPN6,SOCS1,STAT2
4-1BB Signaling in T Lymphocytes	3.01	YES	0.156		2	0/32 (0%)	0/32 (0%)	5/32 (16%)	27/32 (84%)	MAP2K2,MAPK11,NFKB1,NFKB2,TRAF1
Oxidative Phosphorylation	2.85	YES	0.0826		-1	6/109 (6%)	0/109 (0%)	3/109 (3%)	100/109 (92%)	ATP5F1C,ATP5F1D,ATP5MG,COX11,COX4I1,COX7B,NDUFA4,NDUFB7,UQCRC1
NF-κB Signaling	2.82	YES	0.067		2.111	3/179 (2%)	0/179 (0%)	9/179 (5%)	167/179 (93%)	CD40,GSK3B,IGF2R,IRAK1,LTA,MAP3K8,NFKB1,NFKB2,PIK3CG,TANK,TLR9,TNFRSF17
Regulation of eIF4 and p70S6K Signaling	2.78	YES	0.0701	NA		2/157 (1%)	0/157 (0%)	9/157 (6%)	146/157 (93%)	AGO1,AGO2,EIF3B,EIF3G,EIF4A2,MAP2K2,MAPK11,PIK3CG,PPP2R1A,RPS27L,RPS4X
Small Cell Lung Cancer Signaling	2.77	YES	0.0986		2.449	1/71 (1%)	0/71 (0%)	6/71 (8%)	64/71 (90%)	BCL2L1,CDK6,MYC,NFKB1,NFKB2,PIK3CG,TRAF1
Lymphotoxin β Receptor Signaling	2.75	YES	0.113		2	0/53 (0%)	0/53 (0%)	6/53 (11%)	47/53 (89%)	BCL2L1,LTA,NFKB1,NFKB2,PIK3CG,TRAF1
FAK Signaling	2.65	YES	0.0842	NA		1/95 (1%)	0/95 (0%)	7/95 (7%)	87/95 (92%)	ASAP1,CAPNS1,CSK,HMMR,MAP2K2,PAK2,PIK3CG,WAS
Production of Nitric Oxide and Reactive Oxygen Species in Macrophages	2.64	YES	0.0638		0.632	2/188 (1%)	0/188 (0%)	10/188 (5%)	176/188 (94%)	ALB,CYBA,CYBB,MAP3K8,MAPK11,NFKB1,NFKB2,PIK3CG,PPP1R14B,PPP2R1A,PTPN6,RHOG
Cell Cycle Control of Chromosomal Replication	2.63	YES	0.107		-0.816	4/56 (7%)	0/56 (0%)	2/56 (4%)	50/56 (89%)	CDC45,CDK1,CDK6,CHEK2,MCM5,ORC3
Communication between Innate and Adaptive Immune Cells	2.62	YES	0.0833	NA		1/96 (1%)	0/96 (0%)	7/96 (7%)	88/96 (92%)	CCL3,CCL3L3,CCR7,CD40,HLA-DRB3,HLA-E,TLR9,TNFRSF17
April Mediated Signaling	2.61	YES	0.128		1	1/39 (3%)	0/39 (0%)	4/39 (10%)	34/39 (87%)	MAPK11,NFKB1,NFKB2,TNFRSF17,TRAF1
HMGB1 Signaling	2.61	YES	0.0667		1.667	2/165 (1%)	0/165 (0%)	9/165 (5%)	154/165 (93%)	HAT1,KAT2B,LTA,MAP2K2,MAPK11,NFKB1,NFKB2,PIK3CG,RHOG,SP1,TNFSF4
ILK Signaling	2.6	YES	0.0632		1.508	2/190 (1%)	0/190 (0%)	10/190 (5%)	178/190 (94%)	ATF4,GSK3B,ITGB2,MYC,MYH9,NFKB1,NFKB2,PIK3CG,PPP1R14B,PPP2R1A,RHOG,RPS6KA4
Erythropoietin Signaling	2.6	YES	0.0921	NA		0/76 (0%)	0/76 (0%)	7/76 (9%)	69/76 (91%)	CBL,MAP2K2,NFKB1,NFKB2,PIK3CG,PTPN6,SOCS1

Toll-like Receptor Signaling	2.6	YES	0.0921	NA	1/76 (1%)	0/76 (0%)	6/76 (8%)	69/76 (91%)	IRAK1,MAPK11,NFKB1,NFKB2,TLR9,TRAF1,UBD
B Cell Activating Factor Signaling	2.51	YES	0.122	1	1/41 (2%)	0/41 (0%)	4/41 (10%)	36/41 (88%)	MAPK11,NFKB1,NFKB2,TNFRSF17,TRAF1
FLT3 Signaling in Hematopoietic Progenitor Cells	2.47	YES	0.0875	0.816	2/80 (3%)	0/80 (0%)	5/80 (6%)	73/80 (91%)	ATF4,CBL,MAP2K2,MAPK11,PIK3CG,RPS6KA4,STAT2
Role of IL-17F in Allergic Inflammatory Airway Diseases	2.47	YES	0.119	1.342	1/42 (2%)	0/42 (0%)	4/42 (10%)	37/42 (88%)	ATF4,MAP2K2,NFKB1,NFKB2,RPS6KA4
Pentose Phosphate Pathway (Oxidative Branch)	2.46	YES	0.5	NA	0/4 (0%)	0/4 (0%)	2/4 (50%)	2/4 (50%)	G6PD,H6PD
BAG2 Signaling Pathway	2.42	YES	0.116	-0.447	1/43 (2%)	0/43 (0%)	4/43 (9%)	38/43 (88%)	MYC,NFKB1,NFKB2,PSME4,SP1
Apelin Pancreas Signaling Pathway	2.38	YES	0.114	-0.447	1/44 (2%)	0/44 (0%)	4/44 (9%)	39/44 (89%)	DDIT3,NFKB1,NFKB2,PIK3CG,PRKAR2A
Activation of IRF by Cytosolic Pattern Recognition Receptors	2.37	YES	0.0952	0	2/63 (3%)	0/63 (0%)	4/63 (6%)	57/63 (90%)	CD40,LTA,NFKB1,NFKB2,STAT2,TANK
PD-1, PD-L1 cancer immunotherapy pathway	2.35	YES	0.0755	-1.134	0/106 (0%)	0/106 (0%)	8/106 (8%)	98/106 (92%)	BCL2L1,CSK,GSK3B,HLA-DQB1,HLA-DRB3,HLA-E,PDCD4,PIK3CG
Role of PI3K/AKT Signaling in the Pathogenesis of Influenza	2.34	YES	0.0938	1.633	0/64 (0%)	0/64 (0%)	6/64 (9%)	58/64 (91%)	GNAI2,GSK3B,MAP2K2,NFKB1,NFKB2,PIK3CG
IL-17A Signaling in Airway Cells	2.34	YES	0.0938	2	0/64 (0%)	0/64 (0%)	6/64 (9%)	58/64 (91%)	GSK3B,MAP2K2,MAPK11,NFKB1,NFKB2,PIK3CG
FAT10 Cancer Signaling Pathway	2.29	YES	0.109	0.447	2/46 (4%)	0/46 (0%)	3/46 (7%)	41/46 (89%)	GSK3B,MAD2L1,NFKB1,NFKB2,UBD
Telomere Extension by Telomerase	2.28	YES	0.2	NA	0/15 (0%)	0/15 (0%)	3/15 (20%)	12/15 (80%)	TERF2,XRCC5,XRCC6
Adipogenesis pathway	2.25	YES	0.0672	NA	8/134 (6%)	0/134 (0%)	1/134 (1%)	125/134 (93%)	BMP7,CCNH,DDIT3,GTF2H2,HAT1,KAT2B,PAXIP1,SAP130,SAP30
Tetrahydrofolate Salvage from 5,10-methenyltetrahydrofolate	2.25	YES	0.4	NA	1/5 (20%)	0/5 (0%)	1/5 (20%)	3/5 (60%)	MTHFD1L,MTHFD2

RANK Signaling in Osteoclasts	2.24	YES	0.0795	1.633	1/88 (1%)	0/88 (0%)	6/88 (7%)	81/88 (92%)	CBL,MAP2K2,MAP3K8,MAPK11,NFKB1,NFKB2,PIK3CG
Type I Diabetes Mellitus Signaling	2.23	YES	0.0721	1.342	0/111 (0%)	0/111 (0%)	8/111 (7%)	103/111 (93%)	HLA-DQB1,HLA-E,IRAK1,LTA,MAPK11,NFKB1,NFKB2,SOCS1
Vitamin-C Transport	2.2	YES	0.188	NA	2/16 (13%)	0/16 (0%)	1/16 (6%)	13/16 (81%)	GLRX,SELENOT,SLC2A3
Altered T Cell and B Cell Signaling in Rheumatoid Arthritis	2.19	YES	0.0778	NA	1/90 (1%)	0/90 (0%)	6/90 (7%)	83/90 (92%)	CD40,HLA-DQB1,LTA,NFKB1,NFKB2,TLR9,TNFRSF17
OX40 Signaling Pathway	2.19	YES	0.0778	2	0/90 (0%)	0/90 (0%)	7/90 (8%)	83/90 (92%)	BCL2L1,HLA-DQB1,HLA-DRB3,HLA-E,NFKB1,NFKB2,TNFSF4
NGF Signaling	2.17	YES	0.0702	1.414	2/114 (2%)	0/114 (0%)	6/114 (5%)	106/114 (93%)	ATF4,MAP2K2,MAP3K8,NFKB1,NFKB2,PIK3CG,RHOG,RPS6KA4
IL-15 Signaling	2.12	YES	0.0845	NA	0/71 (0%)	0/71 (0%)	6/71 (8%)	65/71 (92%)	BCL2L1,MAP2K2,MAPK11,NFKB1,NFKB2,PIK3CG
Opioid Signaling Pathway	2.1	YES	0.0526	1.387	5/247 (2%)	0/247 (0%)	8/247 (3%)	234/247 (95%)	ATF4,CAMK2G,GNAI2,GSK3B,MAP2K2,MYC,NFKB1,NFKB2,PIK3CG,PRKAR2A,RGS1,RGS13,RPS6KA4
Senescence Pathway	2.1	YES	0.0509	0.832	5/275 (2%)	0/275 (0%)	9/275 (3%)	261/275 (95%)	ANAPC10,ASXL2,CAPNS1,CDK1,CDK6,CHEK2,DMTF1,KAT2B,MAP2K2,NFKB1,NFKB2,PIK3CG,PPP2R1A,RPS6KA4
Selenocysteine Biosynthesis II (Archaea and Eukaryotes)	2.08	YES	0.333	NA	1/6 (17%)	0/6 (0%)	1/6 (17%)	4/6 (67%)	PSTK,SARS2
Renin-Angiotensin Signaling	2.08	YES	0.0678	2.646	0/118 (0%)	0/118 (0%)	8/118 (7%)	110/118 (93%)	MAP2K2,MAPK11,NFKB1,NFKB2,PAK2,PIK3CG,PRKAR2A,PTPN6
FAT10 Signaling Pathway	2.05	YES	0.167	NA	1/18 (6%)	0/18 (0%)	2/18 (11%)	15/18 (83%)	PSMD4,PSME4,UBD
CD28 Signaling in T Helper Cells	2.04	YES	0.0667	1.134	0/120 (0%)	0/120 (0%)	8/120 (7%)	112/120 (93%)	CSK,HLA-DQB1,MAP2K2,NFKB1,NFKB2,PIK3CG,PTPN6,WAS
CD27 Signaling in Lymphocytes	2.03	YES	0.0943	1.342	1/53 (2%)	0/53 (0%)	4/53 (8%)	48/53 (91%)	BCL2L1,MAP2K2,MAP3K8,NFKB1,NFKB2
Hepatic Fibrosis Signaling Pathway	2.03	YES	0.0462	2.183	2/368 (1%)	0/368 (0%)	15/368 (4%)	351/368 (95%)	ATF4,CCL3,CD40,CYBB,GNAI2,GSK3B,IRAK1,MAP2K2,MAPK11,MYC,NFKB1,NFKB2,PDCD4,PIK3CG,PRKAR2A,RHOG,SP1

Th1 and Th2 Activation Pathway	2.03	YES	0.0585	NA	0/171 (0%)	0/171 (0%)	10/171 (6%)	161/171 (94%)	CD40,CHD4,HLA-DQB1,HLA-DRB3,ITGB2,LTA,NFKB1,PIK3CG,SOCS1,TNFSF4
ATM Signaling	2.02	YES	0.0722	0.816	3/97 (3%)	0/97 (0%)	4/97 (4%)	90/97 (93%)	ATF4,CDK1,CHEK2,H2AX,MAPK11,MDC1,PPP2R1A
Th1 Pathway	2.02	YES	0.0661	1.633	0/121 (0%)	0/121 (0%)	8/121 (7%)	113/121 (93%)	CD40,HLA-DQB1,HLA-DRB3,ITGB2,LTA,NFKB1,PIK3CG,SOCS1
TREM1 Signaling	2	YES	0.08	2.449	0/75 (0%)	0/75 (0%)	6/75 (8%)	69/75 (92%)	CCL3,CD40,IRAK1,NFKB1,NFKB2,TLR9
Role of IL-17A in Arthritis	2	YES	0.0926	NA	0/54 (0%)	0/54 (0%)	5/54 (9%)	49/54 (91%)	MAP2K2,MAPK11,NFKB1,NFKB2,PIK3CG
IL-17A Signaling in Fibroblasts	2	YES	0.114	NA	0/35 (0%)	0/35 (0%)	4/35 (11%)	31/35 (89%)	GSK3B,MAPK11,NFKB1,NFKB2
GNRH Signaling	2	YES	0.0578	-0.333	3/173 (2%)	0/173 (0%)	7/173 (4%)	163/173 (94%)	ATF4,CAMK2G,GNAI2,MAP2K2,MAP3K8,MAPK11,NFKB1,NFKB2,PAK2,PRKAR2A
IL-8 Signaling	1.99	YES	0.055	3	0/200 (0%)	0/200 (0%)	11/200 (6%)	189/200 (95%)	BCL2L1,CYBB,GNAI2,IRAK1,ITGB2,MAP2K2,NFKB1,PAK2,PIK3CG,RHOG,VASP
IL-7 Signaling Pathway	1.92	YES	0.0769	-1	1/78 (1%)	0/78 (0%)	5/78 (6%)	72/78 (92%)	CXCR5,GSK3B,MAPK11,MYC,PIK3CG,SOCS1
PTEN Signaling	1.92	YES	0.0635	-1.89	0/126 (0%)	0/126 (0%)	8/126 (6%)	118/126 (94%)	BCL2L1,CBL,GSK3B,IGF2R,MAP2K2,NFKB1,NFKB2,PIK3CG
Superpathway of Methionine Degradation	1.91	YES	0.108	0	2/37 (5%)	0/37 (0%)	2/37 (5%)	33/37 (89%)	AHCY,GOT1L1,MAT2A,MCEE
Sirtuin Signaling Pathway	1.9	YES	0.0481	0.632	5/291 (2%)	0/291 (0%)	9/291 (3%)	277/291 (95%)	ATP5F1C,ATP5F1D,BPGM,G6PD,GSK3B,MYC,NDUFA4,NDUFB7,NFKB1,NFKB2,POLR1C,SP1,XRCC5,XRCC6
P2Y Purigenic Receptor Signaling Pathway	1.9	YES	0.063	0.707	2/127 (2%)	0/127 (0%)	6/127 (5%)	119/127 (94%)	ATF4,GNAI2,MAP2K2,MYC,NFKB1,NFKB2,PIK3CG,PRKAR2A
Chronic Myeloid Leukemia Signaling	1.88	YES	0.068	NA	1/103 (1%)	0/103 (0%)	6/103 (6%)	96/103 (93%)	BCL2L1,CDK6,MAP2K2,MYC,NFKB1,NFKB2,PIK3CG
Huntington's Disease Signaling	1.86	YES	0.0506	0.816	3/237 (1%)	0/237 (0%)	9/237 (4%)	225/237 (95%)	ATF4,ATP5F1C,ATP5F1D,BCL2L1,CAPNS1,CTSD,DCTN1,PIK3CG,PSME4,SGK1,SP1,UBD

PEDF Signaling	1.82	YES	0.0732	0.447	0/82 (0%)	0/82 (0%)	6/82 (7%)	76/82 (93%)	BCL2L1,CFLAR,MAPK11,NFKB1,NFKB2,PIK3CG
Histidine Degradation III	1.82	YES	0.25	NA	1/8 (13%)	0/8 (0%)	1/8 (13%)	6/8 (75%)	MTHFD1L,MTHFD2
Aldosterone Signaling in Epithelial Cells	1.81	YES	0.057	2	4/158 (3%)	0/158 (0%)	5/158 (3%)	149/158 (94%)	AHCY,DNAJC12,DNAJC2,DNAJC27,DNAJC7,HSPB11,MAP2K2,PIK3CG,SGK1
IL-12 Signaling and Production in Macrophages	1.8	YES	0.0606	NA	2/132 (2%)	0/132 (0%)	6/132 (5%)	124/132 (94%)	ALB,CD40,MAP2K2,MAP3K8,MAPK11,NFKB1,NFKB2,PIK3CG
Pyrimidine Deoxyribonucleotides De Novo Biosynthesis I	1.8	YES	0.136	NA	2/22 (9%)	0/22 (0%)	1/22 (5%)	19/22 (86%)	AK1,NME3,RRM1
Integrin Signaling	1.8	YES	0.0516	1.508	1/213 (0%)	0/213 (0%)	10/213 (5%)	202/213 (95%)	ASAP1,CAPNS1,GSK3B,ITGAE,ITGB2,MAP2K2,PAK2,PIK3CG,RHOG,VASP,WAS
Neuroinflammation Signaling Pathway	1.8	YES	0.0467	2.309	1/300 (0%)	0/300 (0%)	13/300 (4%)	286/300 (95%)	ATF4,CCL3,CD40,CFLAR,CYBB,GSK3B,HLA-DQB1,HLA-E,IRAK1,MAPK11,NFKB1,NFKB2,PIK3CG,TLR9
Antioxidant Action of Vitamin C	1.76	YES	0.0642	NA	3/109 (3%)	0/109 (0%)	4/109 (4%)	102/109 (94%)	ABHD3,GLRX,MAPK11,NFKB1,NFKB2,SELENOT,SLC2A3
BMP signaling pathway	1.75	YES	0.0706	1.342	1/85 (1%)	0/85 (0%)	5/85 (6%)	79/85 (93%)	BMP7,MAP2K2,MAPK11,NFKB1,NFKB2,PRKAR2A
Androgen Signaling	1.73	YES	0.0588	1	4/136 (3%)	0/136 (0%)	4/136 (3%)	128/136 (94%)	CCNH,GNAI2,GTF2B,GTF2H2,KAT2B,NFKB1,NFKB2,PRKAR2A
Th2 Pathway	1.73	YES	0.0588	NA	0/136 (0%)	0/136 (0%)	8/136 (6%)	128/136 (94%)	CD40,CHD4,HLA-DQB1,HLA-DRB3,ITGB2,NFKB1,PIK3CG,TNFSF4
iCOS-iCOSL Signaling in T Helper Cells	1.72	YES	0.0631	1.134	1/111 (1%)	0/111 (0%)	6/111 (5%)	104/111 (94%)	CAMK2G,CD40,CSK,HLA-DQB1,NFKB1,NFKB2,PIK3CG
Folate Transformations I	1.72	YES	0.222	NA	1/9 (11%)	0/9 (0%)	1/9 (11%)	7/9 (78%)	MTHFD1L,MTHFD2
Agranulocyte Adhesion and Diapedesis	1.71	YES	0.0521	NA	2/192 (1%)	0/192 (0%)	8/192 (4%)	182/192 (95%)	C5,CCL17,CCL22,CCL3,CCL3L1,CCL3L3,CCL4L1/CCL4L2,GNAI2,ITGB2,MYH9
Rac Signaling	1.7	YES	0.0625	1.89	1/112 (1%)	0/112 (0%)	6/112 (5%)	105/112 (94%)	BRK1,CYBB,MAP2K2,NFKB1,NFKB2,PAK2,PIK3CG

PI3K Signaling in B Lymphocytes	1.7	YES	0.058		0.707	2/138 (1%)	0/138 (0%)	6/138 (4%)	130/138 (94%)	ATF4,CAMK2G,CBL,CD40,MAP2K2,NFKB1,NFKB2,PIK3CG
ERK/MAPK Signaling	1.69	YES	0.0518		0.632	2/193 (1%)	0/193 (0%)	8/193 (4%)	183/193 (95%)	ATF4,MAP2K2,MKNK2,MYC,PAK2,PIK3CG,PPP1R14B,PPP2R1A,PRKAR2A,RPS6KA4
Ceramide Signaling	1.69	YES	0.0682		1.633	0/88 (0%)	0/88 (0%)	6/88 (7%)	82/88 (93%)	CTSD,NFKB1,NFKB2,PIK3CG,PPP2R1A,S1PR4
ErbB2-ErbB3 Signaling	1.68	YES	0.0769		0.447	1/65 (2%)	0/65 (0%)	4/65 (6%)	60/65 (92%)	GSK3B,MAP2K2,MYC,PIK3CG,SP1
Endocannabinoid Developing Neuron Pathway	1.65	YES	0.0609		0.447	1/115 (1%)	0/115 (0%)	6/115 (5%)	108/115 (94%)	ATF4,GNAI2,GSK3B,MAP2K2,MAPK11,PIK3CG,PRKAR2A
Pentose Phosphate Pathway	1.63	YES	0.2	NA		0/10 (0%)	0/10 (0%)	2/10 (20%)	8/10 (80%)	G6PD,H6PD
fMLP Signaling in Neutrophils	1.63	YES	0.0603		2.646	0/116 (0%)	0/116 (0%)	7/116 (6%)	109/116 (94%)	CYBB,GNAI2,MAP2K2,NFKB1,NFKB2,PIK3CG,WAS
iNOS Signaling	1.63	YES	0.0889	NA		0/45 (0%)	0/45 (0%)	4/45 (9%)	41/45 (91%)	IRAK1,MAPK11,NFKB1,NFKB2
Prostate Cancer Signaling	1.62	YES	0.0659	NA		1/91 (1%)	0/91 (0%)	5/91 (5%)	85/91 (93%)	ATF4,GSK3B,MAP2K2,NFKB1,NFKB2,PIK3CG
IL-1 Signaling	1.62	YES	0.0659		2	0/91 (0%)	0/91 (0%)	6/91 (7%)	85/91 (93%)	GNAI2,IRAK1,MAPK11,NFKB1,NFKB2,PRKAR2A
Endocannabinoid Cancer Inhibition Pathway	1.62	YES	0.0559		0	3/143 (2%)	0/143 (0%)	5/143 (3%)	135/143 (94%)	ATF4,DDIT3,GNAI2,GSK3B,MAP2K2,MYC,PIK3CG,PRKAR2A
Mitochondrial Dysfunction	1.61	YES	0.0526	NA		6/171 (4%)	0/171 (0%)	3/171 (2%)	162/171 (95%)	ATP5F1C,ATP5F1D,ATP5MG,COX11,COX4I1,COX7B,NDUFA4,NDUFB7,UQCRC1
p38 MAPK Signaling	1.59	YES	0.0593		0	3/118 (3%)	0/118 (0%)	4/118 (3%)	111/118 (94%)	ATF4,DDIT3,IRAK1,MAPK11,MKNK2,MYC,RPS6KA4
Melanocyte Development and Pigmentation Signaling	1.56	YES	0.0638		0.816	1/94 (1%)	0/94 (0%)	5/94 (5%)	88/94 (94%)	ATF4,MAP2K2,PIK3CG,PRKAR2A,PTPN6,RPS6KA4
ERK5 Signaling	1.51	YES	0.0694		-0.447	3/72 (4%)	0/72 (0%)	2/72 (3%)	67/72 (93%)	ATF4,MAP3K8,MYC,RPS6KA4,SGK1

Cell Cycle: G2/M DNA Damage Checkpoint Regulation	1.51	YES	0.0816	NA	4/49 (8%)	0/49 (0%)	0/49 (0%)	45/49 (92%)	CDK1,CHEK2,CKS2,KAT2B
Acute Phase Response Signaling	1.5	YES	0.0503	1.89	2/179 (1%)	0/179 (0%)	7/179 (4%)	170/179 (95%)	ALB,C5,IRAK1,MAP2K2,MAPK11,NFKB1,NFKB2,PIK3CG, SOCS1
Granulocyte Adhesion and Diapedesis	1.5	YES	0.0503	NA	2/179 (1%)	0/179 (0%)	7/179 (4%)	170/179 (95%)	C5,CCL17,CCL22,CCL3,CCL3L1,CCL3L3,CCL4L1/CCL4L2 ,GNAI2,ITGB2
Caveolar-mediated Endocytosis Signaling	1.49	YES	0.0685	NA	2/73 (3%)	0/73 (0%)	3/73 (4%)	68/73 (93%)	ALB,COPA,HLA-E,ITGAE,ITGB2
Sonic Hedgehog Signaling	1.48	YES	0.103	NA	1/29 (3%)	0/29 (0%)	2/29 (7%)	26/29 (90%)	CDK1,GSK3B,PRKAR2A
TNFR1 Signaling	1.48	YES	0.08	2	1/50 (2%)	0/50 (0%)	3/50 (6%)	46/50 (92%)	NFKB1,NFKB2,PAK2,TANK
Assembly of RNA Polymerase II Complex	1.48	YES	0.08	NA	4/50 (8%)	0/50 (0%)	0/50 (0%)	46/50 (92%)	CCNH,GTF2B,GTF2H2,TAF9
Amyloid Processing	1.48	YES	0.08	NA	0/50 (0%)	0/50 (0%)	4/50 (8%)	46/50 (92%)	CAPNS1,GSK3B,MAPK11,PRKAR2A
Apoptosis Signaling	1.47	YES	0.0606	-1.633	1/99 (1%)	0/99 (0%)	5/99 (5%)	93/99 (94%)	BCL2L1,CAPNS1,CDK1,MAP2K2,NFKB1,NFKB2
Estrogen-Dependent Breast Cancer Signaling	1.46	YES	0.0676	1.342	1/74 (1%)	0/74 (0%)	4/74 (5%)	69/74 (93%)	ATF4,NFKB1,NFKB2,PIK3CG,SP1
Protein Kinase A Signaling	1.45	YES	0.0402	-0.577	4/398 (1%)	0/398 (0%)	12/398 (3%)	382/398 (96%)	ANAPC10,ATF4,CAMK2G,DUSP11,DUSP5,EBI3,GNAI2,G SK3B,MAP2K2,NFKB1,NFKB2,PDE12,PPP1R14B,PRKA R2A,PTPN6,VASP
Signaling by Rho Family GTPases	1.42	YES	0.0451	2.53	1/244 (0%)	0/244 (0%)	10/244 (4%)	233/244 (95%)	ARHGEF2,CYBB,GNAI2,MAP2K2,NFKB1,NFKB2,PAK2,PI K3CG,RHOG,WAS,WASF3
Mouse Embryonic Stem Cell Pluripotency	1.4	YES	0.0583	-0.447	2/103 (2%)	0/103 (0%)	4/103 (4%)	97/103 (94%)	GSK3B,ID2,MAP2K2,MAPK11,MYC,PIK3CG
Sumoylation Pathway	1.4	YES	0.0583	-1	1/103 (1%)	0/103 (0%)	5/103 (5%)	97/103 (94%)	ISG20,NFKB1,NFKB2,RANGAP1,RHOG,SP1
Role of Macrophages, Fibroblasts and Endothelial Cells in Rheumatoid	1.36	YES	0.0417	NA	4/312 (1%)	0/312 (0%)	9/312 (3%)	299/312 (96%)	ATF4,C5,CAMK2G,GSK3B,IRAK1,LTA,MAP2K2,MYC,NFK B1,PIK3CG,SOCS1,TLR9,TRAF1

T Cell Receptor Signaling	1.36	YES	0.0571	NA	0/105 (0%)	0/105 (0%)	6/105 (6%)	99/105 (94%)	CBL,CSK,MAP2K2,NFKB1,NFKB2,PIK3CG
DNA Double-Strand Break Repair by Non-Homologous End Joining	1.35	YES	0.143	NA	0/14 (0%)	0/14 (0%)	2/14 (14%)	12/14 (86%)	XRCC5,XRCC6
IL-17 Signaling	1.34	YES	0.0625	NA	0/80 (0%)	0/80 (0%)	5/80 (6%)	75/80 (94%)	GSK3B,MAP2K2,MAPK11,NFKB1,PIK3CG
IL-9 Signaling	1.34	YES	0.0909	NA	0/33 (0%)	0/33 (0%)	3/33 (9%)	30/33 (91%)	NFKB1,NFKB2,PIK3CG
Chemokine Signaling	1.34	YES	0.0625	1	1/80 (1%)	0/80 (0%)	4/80 (5%)	75/80 (94%)	CAMK2G,GNAI2,MAP2K2,MAPK11,PIK3CG
Telomerase Signaling	1.33	YES	0.0561	0	1/107 (1%)	0/107 (0%)	5/107 (5%)	101/107 (94%)	MAP2K2,MYC,PIK3CG,PPP2R1A,SP1,TERF2
RAR Activation	1.32	YES	0.0466	NA	3/193 (2%)	0/193 (0%)	6/193 (3%)	184/193 (95%)	CCNH,CSK,GTF2H2,KAT2B,MAPK11,NFKB1,NFKB2,PIK3CG,PRKAR2A
Prolactin Signaling	1.32	YES	0.0617	0.447	1/81 (1%)	0/81 (0%)	4/81 (5%)	76/81 (94%)	MAP2K2,MYC,PIK3CG,SOCS1,SP1
Cyclins and Cell Cycle Regulation	1.32	YES	0.0617	-1.342	2/81 (2%)	0/81 (0%)	3/81 (4%)	76/81 (94%)	CCNH,CDK1,CDK6,GSK3B,PPP2R1A
Spermidine Biosynthesis I	1.32	YES	0.5	NA	0/2 (0%)	0/2 (0%)	1/2 (50%)	1/2 (50%)	SRM
Tec Kinase Signaling	1.32	YES	0.0488	1.89	1/164 (1%)	0/164 (0%)	7/164 (4%)	156/164 (95%)	GNAI2,NFKB1,NFKB2,PAK2,PIK3CG,RHOG,STAT2,WAS
Paxillin Signaling	1.31	YES	0.0556	NA	1/108 (1%)	0/108 (0%)	5/108 (5%)	102/108 (94%)	CSK,ITGAE,ITGB2,MAPK11,PAK2,PIK3CG
DNA Methylation and Transcriptional Repression Signaling	1.31	YES	0.0882	NA	1/34 (3%)	0/34 (0%)	2/34 (6%)	31/34 (91%)	CHD4,SAP130,SAP30

Table S2 GONH2 IPA analysis results

Ingenuity Canonical Pathways	-log 10 (p-value)	Significant (>1.3 Log10 p-value)	Ratio	Activation z-score (> 0 pthway is activayed, < 0 pathway is inhibited)	Down regulated	No change	Up regulated	No overlap with dataset	Molecules
JAK/Stat Signaling	4.58	YES	0.112	0.333	1/80 (1%)	0/80 (0%)	8/80 (10%)	71/80 (89%)	KRAS,MAP2K1,PIAS1,PIK3C2A,PTPN11,PTPN6,RELA,SOCS1,STAT2
Chronic Myeloid Leukemia Signaling	4.46	YES	0.0971	NA	2/103 (2%)	0/103 (0%)	8/103 (8%)	93/103 (90%)	CDK6,HDAC8,KRAS,MAP2K1,MYC,PIK3C2A,PTPN11,RB1,RELA,SIN3A
EIF2 Signaling	4.42	YES	0.067	0	9/224 (4%)	0/224 (0%)	6/224 (3%)	209/224 (93%)	AGO2,ATF4,EIF2AK4,EIF2B3,EIF2B5,EIF4G3,KRAS,MAP2K1,MYC,PIK3C2A,RPL14,RPL28,RPS21,RPS4Y2,RPSA
Systemic Lupus Erythematosus Signaling	4.31	YES	0.0655	NA	9/229 (4%)	0/229 (0%)	6/229 (3%)	214/229 (93%)	C5,CBL,HLA-G,IL10,KRAS,PIK3C2A,PRPF8,PTPN6,RNU1-1,RNU1-28P,RNU11,RNU4-1,RNVU1-18,RNVU1-7,SNRPA1
Polyamine Regulation in Colon Cancer	4.25	YES	0.227	NA	2/22 (9%)	0/22 (0%)	3/22 (14%)	17/22 (77%)	KRAS,MYC,PSME4,SAT2,TCF4
Oxidative Phosphorylation	4.25	YES	0.0917	-2.53	9/109 (8%)	0/109 (0%)	1/109 (1%)	99/109 (91%)	ATP5F1C,COX11,COX7B,NDUFB10,NDUFB4,NDUFB9,NDUFS3,UQCR10,UQCRC1,UQCRC2
Prostate Cancer Signaling	4.13	YES	0.0989	NA	1/91 (1%)	0/91 (0%)	8/91 (9%)	82/91 (90%)	ATF4,CREB5,KLK3,KRAS,MAP2K1,PIK3C2A,RB1,RELA,SIN3A
Estrogen Receptor Signaling	4.08	YES	0.0803	NA	2/137 (1%)	0/137 (0%)	9/137 (7%)	126/137 (92%)	GTF2H1,GTF2H3,HNRNPD,KRAS,MAP2K1,POLR2A,PRKDC,SPEN,TAF4,TAF6L,TRRAP
Non-Small Cell Lung Cancer Signaling	4.05	YES	0.11	1.342	0/73 (0%)	0/73 (0%)	8/73 (11%)	65/73 (89%)	CDK6,FOXO3,ITPR1,KRAS,MAP2K1,PIK3C2A,RB1,SIN3A
ATM Signaling	3.92	YES	0.0928	0.707	2/97 (2%)	0/97 (0%)	7/97 (7%)	88/97 (91%)	ATF4,CCNB1,CREB5,HERC2,MDC1,PPP2R1A,SMC3,TLK2,TRRAP
FLT3 Signaling in Hematopoietic Progenitor Cells	3.77	YES	0.1	1.414	2/80 (3%)	0/80 (0%)	6/80 (8%)	72/80 (90%)	ATF4,CBL,CREB5,KRAS,MAP2K1,PIK3C2A,PTPN11,STAT2
Regulation of eIF4 and p70S6K Signaling	3.56	YES	0.0701	1	4/157 (3%)	0/157 (0%)	7/157 (4%)	146/157 (93%)	AGO2,EIF2B3,EIF2B5,EIF4G3,KRAS,MAP2K1,PIK3C2A,PPP2R1A,RPS21,RPS4Y2,RPSA
B Cell Receptor Signaling	3.52	YES	0.0649	1.155	3/185 (2%)	0/185 (0%)	9/185 (5%)	173/185 (94%)	ATF4,BTK,CD19,CREB5,DAPP1,KRAS,MAP2K1,PAG1,PIK3C2A,PTPN11,PTPN6,RELA

Adipogenesis pathway	3.5	YES	0.0746	NA	3/134 (2%)	0/134 (0%)	7/134 (5%)	124/134 (93%)	BMP7,EGR2,GTF2H1,GTF2H3,HDAC8,KAT6A,RB1,SAP130,SENP2,SIN3A
Systemic Lupus Erythematosus In B Cell Signaling Pathway	3.43	YES	0.0545	-0.775	5/275 (2%)	0/275 (0%)	10/275 (4%)	260/275 (95%)	BTK,CBL,CD19,FOXO3,IL10,KRAS,MAP2K1,MYC,PAG1,PIK3C2A,PTPN11,PTPN6,RELA,STAT2,TNFSF14
PI3K Signaling in B Lymphocytes	3.4	YES	0.0725	0.333	3/138 (2%)	0/138 (0%)	7/138 (5%)	128/138 (93%)	ATF4,BTK,CBL,CD19,DAPP1,FOXO3,ITPR1,KRAS,MAP2K1,RELA
Hereditary Breast Cancer Signaling	3.35	YES	0.0714	NA	3/140 (2%)	0/140 (0%)	7/140 (5%)	130/140 (93%)	ARID1A,CCNB1,CDK6,DDB2,HDAC8,KRAS,PIK3C2A,POLR2A,RB1,XPC
Nucleotide Excision Repair Pathway	3.25	YES	0.143	NA	1/35 (3%)	0/35 (0%)	4/35 (11%)	30/35 (86%)	GTF2H1,GTF2H3,POLR2A,RAD23B,XPC
Erythropoietin Signaling	3.14	YES	0.0921	NA	0/76 (0%)	0/76 (0%)	7/76 (9%)	69/76 (91%)	CBL,KRAS,MAP2K1,PIK3C2A,PTPN6,RELA,SOCS1
Neurotrophin/TRK Signaling	3.14	YES	0.0921	1.89	1/76 (1%)	0/76 (0%)	6/76 (8%)	69/76 (91%)	ATF4,CREB5,KLK3,KRAS,MAP2K1,PIK3C2A,PTPN11
VEGF Signaling	3.14	YES	0.0808	0.447	2/99 (2%)	0/99 (0%)	6/99 (6%)	91/99 (92%)	EIF2B3,EIF2B5,FOXO3,KRAS,MAP2K1,PIK3C2A,PTPN11,PTPN6
Role of JAK1, JAK2 and TYK2 in Interferon Signaling	2.95	YES	0.167	NA	1/24 (4%)	0/24 (0%)	3/24 (13%)	20/24 (83%)	PTPN6,RELA,SOCS1,STAT2
FGF Signaling	2.89	YES	0.0833	1.134	1/84 (1%)	0/84 (0%)	6/84 (7%)	77/84 (92%)	ATF4,CREB5,ITPR1,MAP2K1,PIK3C2A,PTPN11,PTPN6
Acute Myeloid Leukemia Signaling	2.74	YES	0.0787	1.134	2/89 (2%)	0/89 (0%)	5/89 (6%)	82/89 (92%)	ARAF,KRAS,MAP2K1,MYC,PIK3C2A,RELA,TCF4
Cholesterol Biosynthesis I	2.74	YES	0.231	NA	2/13 (15%)	0/13 (0%)	1/13 (8%)	10/13 (77%)	FDFT1,NSDHL,SC5D
Cholesterol Biosynthesis II (via 24,25-dihydrolanosterol)	2.74	YES	0.231	NA	2/13 (15%)	0/13 (0%)	1/13 (8%)	10/13 (77%)	FDFT1,NSDHL,SC5D
Cholesterol Biosynthesis III (via Desmosterol)	2.74	YES	0.231	NA	2/13 (15%)	0/13 (0%)	1/13 (8%)	10/13 (77%)	FDFT1,NSDHL,SC5D
Mitochondrial Dysfunction	2.69	YES	0.0585	NA	9/171 (5%)	0/171 (0%)	1/171 (1%)	161/171 (94%)	ATP5F1C,COX11,COX7B,NDUFB10,NDUFB4,NDUFB9,NDUFS3,UQCR10,UQCRC1,UQCRC2

Melanocyte Development and Pigmentation Signaling	2.6	YES	0.0745	1.134	1/94 (1%)	0/94 (0%)	6/94 (6%)	87/94 (93%)	ATF4,CREB5,KRAS,MAP2K1,PIK3C2A,PTPN11,PTPN6
Huntington's Disease Signaling	2.59	YES	0.0506	NA	4/237 (2%)	0/237 (0%)	8/237 (3%)	225/237 (95%)	ATF4,ATP5F1C,CREB5,CTSD,HDAC8,ITPR1,PIK3C2A,POLR2A,PSME4,SIN3A,TAF4,VTI1B
Small Cell Lung Cancer Signaling	2.58	YES	0.0845	1	1/71 (1%)	0/71 (0%)	5/71 (7%)	65/71 (92%)	CDK6,MYC,PIK3C2A,RB1,RELA,SIN3A
ERK5 Signaling	2.54	YES	0.0833	0	2/72 (3%)	0/72 (0%)	4/72 (6%)	66/72 (92%)	ATF4,CREB5,FOXO3,KRAS,MYC,PTPN11
Assembly of RNA Polymerase II Complex	2.54	YES	0.1	NA	2/50 (4%)	0/50 (0%)	3/50 (6%)	45/50 (90%)	GTF2H1,GTF2H3,POLR2A,TAF4,TAF6L
Thyroid Cancer Signaling	2.5	YES	0.098	NA	1/51 (2%)	0/51 (0%)	4/51 (8%)	46/51 (90%)	KLK3,KRAS,MAP2K1,MYC,TCF4
NER Pathway	2.38	YES	0.068	0.816	2/103 (2%)	0/103 (0%)	5/103 (5%)	96/103 (93%)	DDB2,GTF2H1,GTF2H3,POLR2A,RAD23B,TOP2B,XPC
IGF-1 Signaling	2.36	YES	0.0673	1.633	0/104 (0%)	0/104 (0%)	7/104 (7%)	97/104 (93%)	FOXO3,KRAS,MAP2K1,PIK3C2A,PTPN11,SOCS1,SRF
T Cell Receptor Signaling	2.34	YES	0.0667	NA	1/105 (1%)	0/105 (0%)	6/105 (6%)	98/105 (93%)	BTK,CBL,KRAS,MAP2K1,PAG1,PIK3C2A,RELA
ERK/MAPK Signaling	2.31	YES	0.0518	0.333	4/193 (2%)	0/193 (0%)	6/193 (3%)	183/193 (95%)	ARAF,ATF4,CREB5,KRAS,MAP2K1,MYC,PIK3C2A,PLA2G2D,PPP2R1A,SRF
Sirtuin Signaling Pathway	2.29	YES	0.0447	2.53	8/291 (3%)	0/291 (0%)	5/291 (2%)	278/291 (96%)	ATP5F1C,FOXO3,MYC,NDUFB10,NDUFB4,NDUFB9,NDUFS3,NFE2L2,POLR1C,PRKDC,RELA,UQCRC2,XPC
Telomerase Signaling	2.29	YES	0.0654	0.447	2/107 (2%)	0/107 (0%)	5/107 (5%)	100/107 (93%)	HDAC8,KRAS,MAP2K1,MYC,PIK3C2A,PPP2R1A,RB1
Prolactin Signaling	2.29	YES	0.0741	0.816	1/81 (1%)	0/81 (0%)	5/81 (6%)	75/81 (93%)	KRAS,MAP2K1,MYC,PIK3C2A,PTPN11,SOCS1
Cyclins and Cell Cycle Regulation	2.29	YES	0.0741	-1	2/81 (2%)	0/81 (0%)	4/81 (5%)	75/81 (93%)	CCNB1,CDK6,HDAC8,PPP2R1A,RB1,SIN3A
Interferon Signaling	2.28	YES	0.111	-2	1/36 (3%)	0/36 (0%)	3/36 (8%)	32/36 (89%)	PIAS1,RELA,SOCS1,STAT2

Pancreatic Adenocarcinoma Signaling	2.25	YES	0.0642	1.633	1/109 (1%)	0/109 (0%)	6/109 (6%)	102/109 (94%)	CYP2E1,KRAS,MAP2K1,PIK3C2A,RB1,RELA,SIN3A
Glioma Signaling	2.23	YES	0.0636	2	0/110 (0%)	0/110 (0%)	7/110 (6%)	103/110 (94%)	CDK6,IGF2R,KRAS,MAP2K1,PIK3C2A,RB1,SIN3A
Insulin Receptor Signaling	2.21	YES	0.0576	0.707	2/139 (1%)	0/139 (0%)	6/139 (4%)	131/139 (94%)	CBL,EIF2B3,EIF2B5,FOXO3,KRAS,MAP2K1,PIK3C2A,PTPN11
Endometrial Cancer Signaling	2.2	YES	0.0833	0.447	1/60 (2%)	0/60 (0%)	4/60 (7%)	55/60 (92%)	FOXO3,KRAS,MAP2K1,MYC,PIK3C2A
Glucocorticoid Receptor Signaling	2.17	YES	0.0417	NA	3/336 (1%)	0/336 (0%)	11/336 (3%)	322/336 (96%)	ARID1A,CCL3,FKBP5,FOXO3,GTF2H1,GTF2H3,IL10,KRAS,MAP2K1,PIK3C2A,POLR2A,RELA,TAF4,TAF6L
IL-2 Signaling	2.17	YES	0.082	1.342	0/61 (0%)	0/61 (0%)	5/61 (8%)	56/61 (92%)	KRAS,MAP2K1,PIK3C2A,PTPN11,SOCS1
NGF Signaling	2.14	YES	0.0614	1.89	1/114 (1%)	0/114 (0%)	6/114 (5%)	107/114 (94%)	ATF4,CREB5,KRAS,MAP2K1,PIK3C2A,PTPN11,RELA
Ceramide Signaling	2.12	YES	0.0682	1.633	0/88 (0%)	0/88 (0%)	6/88 (7%)	82/88 (93%)	CTSD,KRAS,MAP2K1,PIK3C2A,PPP2R1A,RELA
Thrombopoietin Signaling	2.11	YES	0.0794	1.342	1/63 (2%)	0/63 (0%)	4/63 (6%)	58/63 (92%)	KRAS,MAP2K1,MYC,PIK3C2A,PTPN11
Senescence Pathway	2.08	YES	0.0436	0.905	3/275 (1%)	0/275 (0%)	9/275 (3%)	263/275 (96%)	ARAF,ASXL2,CCNB1,CDC26,CDK6,EP400,FOXO3,KRAS,MAP2K1,PIK3C2A,PPP2R1A,RB1
Pyrimidine Deoxyribonucleotides De Novo Biosynthesis I	2.06	YES	0.136	NA	1/22 (5%)	0/22 (0%)	2/22 (9%)	19/22 (86%)	NME3,RRM1,RRM2
Role of IL-17F in Allergic Inflammatory Airway Diseases	2.05	YES	0.0952	1	1/42 (2%)	0/42 (0%)	3/42 (7%)	38/42 (90%)	ATF4,CREB5,MAP2K1,RELA
Mitotic Roles of Polo-Like Kinase	2.03	YES	0.0758	NA	2/66 (3%)	0/66 (0%)	3/66 (5%)	61/66 (92%)	CCNB1,CDC26,KIF11,PPP2R1A,SMC3
Cell Cycle: G1/S Checkpoint Regulation	2	YES	0.0746	1	2/67 (3%)	0/67 (0%)	3/67 (4%)	62/67 (93%)	CDK6,HDAC8,MYC,RB1,SIN3A
Inhibition of ARE-Mediated mRNA Degradation Pathway	1.99	YES	0.0574	-0.816	2/122 (2%)	0/122 (0%)	5/122 (4%)	115/122 (94%)	AGO2,CNOT6,EXOSC8,PPP2R1A,PSME4,TNFSF14,ZFP36L2

TCA Cycle II (Eukaryotic)	1.95	YES	0.125	NA	1/24 (4%)	0/24 (0%)	2/24 (8%)	21/24 (88%)	CS,FH,IDH3A
IL-6 Signaling	1.94	YES	0.056	1.89	0/125 (0%)	0/125 (0%)	7/125 (6%)	118/125 (94%)	KRAS,MAP2K1,PIK3C2A,PTPN11,RELA,SOCS1,SRF
NRF2-mediated Oxidative Stress Response	1.91	YES	0.0476	0.816	2/189 (1%)	0/189 (0%)	7/189 (4%)	180/189 (95%)	ATF4,DNAJC13,FKBP5,KRAS,MAP2K1,NFE2L2,PIK3C2A,PPIB,USP14
P2Y Purigenic Receptor Signaling Pathway	1.9	YES	0.0551	1.134	2/127 (2%)	0/127 (0%)	5/127 (4%)	120/127 (94%)	ATF4,CREB5,KRAS,MAP2K1,MYC,PIK3C2A,RELA
HOTAIR Regulatory Pathway	1.88	YES	0.0503	1.414	1/159 (1%)	0/159 (0%)	7/159 (4%)	151/159 (95%)	AEBP2,AGO2,MYC,PIK3C2A,RELA,SRF,SUZ12,TCF4
Estrogen-Dependent Breast Cancer Signaling	1.82	YES	0.0676	1.342	1/74 (1%)	0/74 (0%)	4/74 (5%)	69/74 (93%)	ATF4,CREB5,KRAS,PIK3C2A,RELA
Cell Cycle: G2/M DNA Damage Checkpoint Regulation	1.82	YES	0.0816	NA	2/49 (4%)	0/49 (0%)	2/49 (4%)	45/49 (92%)	CCNB1,CKS2,PRKDC,TOP2B
3-phosphoinositide Biosynthesis	1.8	YES	0.0488	1.414	2/164 (1%)	0/164 (0%)	6/164 (4%)	156/164 (95%)	DUSP11,DUSP5,MTMR4,MTMR9,PIK3C2A,PPFIBP2,PTPN11,PTPN6
Mouse Embryonic Stem Cell Pluripotency	1.8	YES	0.0583	1.633	1/103 (1%)	0/103 (0%)	5/103 (5%)	97/103 (94%)	KRAS,MAP2K1,MYC,PIK3C2A,PTPN11,TCF4
Melanoma Signaling	1.79	YES	0.08	1	0/50 (0%)	0/50 (0%)	4/50 (8%)	46/50 (92%)	KRAS,MAP2K1,PIK3C2A,RB1
Antiproliferative Role of Somatostatin Receptor 2	1.75	YES	0.0649	2.236	0/77 (0%)	0/77 (0%)	5/77 (6%)	72/77 (94%)	KRAS,MAP2K1,PIK3C2A,PTPN11,PTPN6
Superpathway of Cholesterol Biosynthesis	1.73	YES	0.103	NA	2/29 (7%)	0/29 (0%)	1/29 (3%)	26/29 (90%)	FDFT1,NSDHL,SC5D
Asparagine Biosynthesis I	1.71	YES	1	NA	1/1 (100%)	0/1 (0%)	0/1 (0%)	0/1 (0%)	ASNS
Renal Cell Carcinoma Signaling	1.69	YES	0.0625	2	1/80 (1%)	0/80 (0%)	4/80 (5%)	75/80 (94%)	FH,KRAS,MAP2K1,PIK3C2A,PTPN11
D-myo-inositol (1,4,5,6)-Tetrakisphosphate Biosynthesis	1.69	YES	0.05	1.134	2/140 (1%)	0/140 (0%)	5/140 (4%)	133/140 (95%)	DUSP11,DUSP5,MTMR4,MTMR9,PPFIBP2,PTPN11,PTPN6

D-myo-inositol (3,4,5,6)-tetrakisphosphate Biosynthesis	1.69	YES	0.05	1.134	2/140 (1%)	0/140 (0%)	5/140 (4%)	133/140 (95%)	DUSP11,DUSP5,MTMR4,MTMR9,PPFIBP2,PTPN11,PTPN6
T Cell Exhaustion Signaling Pathway	1.65	YES	0.0457	0	3/175 (2%)	0/175 (0%)	5/175 (3%)	167/175 (95%)	HLA-G,IL10,KRAS,PIK3C2A,PPP2R1A,PTPN11,PTPN6,STAT2
LPS-stimulated MAPK Signaling	1.65	YES	0.061	2.236	0/82 (0%)	0/82 (0%)	5/82 (6%)	77/82 (94%)	KRAS,MAP2K1,PIK3C2A,RELA,SRF
PEDF Signaling	1.65	YES	0.061	2.236	0/82 (0%)	0/82 (0%)	5/82 (6%)	77/82 (94%)	KRAS,PIK3C2A,RELA,SRF,TCF4
EGF Signaling	1.65	YES	0.0727	2	0/55 (0%)	0/55 (0%)	4/55 (7%)	51/55 (93%)	ITPR1,MAP2K1,PIK3C2A,SRF
Molecular Mechanisms of Cancer	1.64	YES	0.0358	NA	2/391 (1%)	0/391 (0%)	12/391 (3%)	377/391 (96%)	ARHGEF2,BMP7,CBL,CDK6,KRAS,MAP2K1,MYC,PIK3C2A,PRKDC,PTPN11,RB1,RELA,SIN3A,TCF4
Cell Cycle Control of Chromosomal Replication	1.62	YES	0.0714	2	0/56 (0%)	0/56 (0%)	4/56 (7%)	52/56 (93%)	CDK6,MCM4,MCM5,TOP2B
CNTF Signaling	1.6	YES	0.0702	2	0/57 (0%)	0/57 (0%)	4/57 (7%)	53/57 (93%)	KRAS,MAP2K1,PIK3C2A,PTPN11
Endocannabinoid Developing Neuron Pathway	1.59	YES	0.0522	0.816	2/115 (2%)	0/115 (0%)	4/115 (3%)	109/115 (95%)	ARAF,ATF4,CREB5,KRAS,MAP2K1,PIK3C2A
Cancer Drug Resistance By Drug Efflux	1.57	YES	0.069	NA	1/58 (2%)	0/58 (0%)	3/58 (5%)	54/58 (93%)	ARAF,FOXO3,KRAS,MAP2K1
PDGF Signaling	1.57	YES	0.0581	0.447	1/86 (1%)	0/86 (0%)	4/86 (5%)	81/86 (94%)	KRAS,MAP2K1,MYC,PIK3C2A,SRF
Fc Epsilon RI Signaling	1.56	YES	0.0513	0.816	2/117 (2%)	0/117 (0%)	4/117 (3%)	111/117 (95%)	BTK,KRAS,MAP2K1,PIK3C2A,PLA2G2D,PTPN11
Role of JAK2 in Hormone-like Cytokine Signaling	1.55	YES	0.0882	NA	0/34 (0%)	0/34 (0%)	3/34 (9%)	31/34 (91%)	PTPN11,PTPN6,SOCS1
Renin-Angiotensin Signaling	1.54	YES	0.0508	2.449	0/118 (0%)	0/118 (0%)	6/118 (5%)	112/118 (95%)	ITPR1,KRAS,MAP2K1,PIK3C2A,PTPN6,RELA
DNA Double-Strand Break Repair by Non-Homologous End Joining	1.53	YES	0.143	NA	1/14 (7%)	0/14 (0%)	1/14 (7%)	12/14 (86%)	DCLRE1C,PRKDC

Phospholipase C Signaling	1.51	YES	0.0389		0.333	4/257 (2%)	0/257 (0%)	6/257 (2%)	247/257 (96%)	ARHGEF2,ATF4,BTK,CREB5,HDAC8,ITPR1,KRAS,MAP2K1,PLA2G2D,RELA
CD28 Signaling in T Helper Cells	1.51	YES	0.05		0.816	0/120 (0%)	0/120 (0%)	6/120 (5%)	114/120 (95%)	ITPR1,MAP2K1,PIK3C2A,PTPN11,PTPN6,RELA
3-phosphoinositide Degradation	1.49	YES	0.0455		1.134	2/154 (1%)	0/154 (0%)	5/154 (3%)	147/154 (95%)	DUSP11,DUSP5,MTMR4,MTMR9,PPFIBP2,PTPN11,PTPN6
D-myo-inositol-5-phosphate Metabolism	1.48	YES	0.0452		1.134	2/155 (1%)	0/155 (0%)	5/155 (3%)	148/155 (95%)	DUSP11,DUSP5,MTMR4,MTMR9,PPFIBP2,PTPN11,PTPN6
Histidine Degradation VI	1.47	YES	0.133	NA		1/15 (7%)	0/15 (0%)	1/15 (7%)	13/15 (87%)	CYP2E1,UROC1
Activation of IRF by Cytosolic Pattern Recognition Receptors	1.46	YES	0.0635		-1	3/63 (5%)	0/63 (0%)	1/63 (2%)	59/63 (94%)	IL10,PPIB,RELA,STAT2
Aldosterone Signaling in Epithelial Cells	1.44	YES	0.0443		2	0/158 (0%)	0/158 (0%)	7/158 (4%)	151/158 (96%)	DNAJC13,DNAJC24,HSPH1,ITPR1,KRAS,MAP2K1,PIK3C2A
RAR Activation	1.44	YES	0.0415	NA		1/193 (1%)	0/193 (0%)	7/193 (4%)	185/193 (96%)	AKR1B1,ARID1A,GTF2H1,GTF2H3,MAP2K1,RDH10,RELA,TAF4
PTEN Signaling	1.42	YES	0.0476		-2.236	0/126 (0%)	0/126 (0%)	6/126 (5%)	120/126 (95%)	CBL,FOXO3,IGF2R,KRAS,MAP2K1,RELA
CD40 Signaling	1.41	YES	0.0615		1	0/65 (0%)	0/65 (0%)	4/65 (6%)	61/65 (94%)	MAP2K1,PIK3C2A,RELA,TNFAIP3
ErbB2-ErbB3 Signaling	1.41	YES	0.0615		1	1/65 (2%)	0/65 (0%)	3/65 (5%)	61/65 (94%)	KRAS,MAP2K1,MYC,PIK3C2A
Pyridoxal 5'-phosphate Salvage Pathway	1.41	YES	0.0615		1	1/65 (2%)	0/65 (0%)	3/65 (5%)	61/65 (94%)	ARAF,CDK6,FAM20B,MAP2K1
Epoxysqualene Biosynthesis	1.41	YES	0.5	NA		1/2 (50%)	0/2 (0%)	0/2 (0%)	1/2 (50%)	FDFT1
S-methyl-5'-thioadenosine Degradation II	1.41	YES	0.5	NA		0/2 (0%)	0/2 (0%)	1/2 (50%)	1/2 (50%)	MTAP
Spermidine Biosynthesis I	1.41	YES	0.5	NA		0/2 (0%)	0/2 (0%)	1/2 (50%)	1/2 (50%)	SRM

Cardiolipin Biosynthesis II	1.41	YES	0.5	NA		0/2 (0%)	0/2 (0%)	1/2 (50%)	1/2 (50%)	PGS1
Superpathway of Inositol Phosphate Compounds	1.39	YES	0.0406		1.414	2/197 (1%)	0/197 (0%)	6/197 (3%)	189/197 (96%)	DUSP11,DUSP5,MTMR4,MTMR9,PIK3C2A,PPFIBP2,PTPN11,PTPN6
p70S6K Signaling	1.38	YES	0.0465		0.816	1/129 (1%)	0/129 (0%)	5/129 (4%)	123/129 (95%)	BTK,CD19,KRAS,MAP2K1,PIK3C2A,PPP2R1A
Bladder Cancer Signaling	1.38	YES	0.0515	NA		1/97 (1%)	0/97 (0%)	4/97 (4%)	92/97 (95%)	KRAS,MAP2K1,MYC,RB1,SIN3A
Salvage Pathways of Pyrimidine Ribonucleotides	1.38	YES	0.0515		0.447	2/97 (2%)	0/97 (0%)	3/97 (3%)	92/97 (95%)	ARAF,CDK6,FAM20B,MAP2K1,NME3
RAN Signaling	1.37	YES	0.118	NA		0/17 (0%)	0/17 (0%)	2/17 (12%)	15/17 (88%)	RANGAP1,XPO1
Glioblastoma Multiforme Signaling	1.36	YES	0.0424		0.816	1/165 (1%)	0/165 (0%)	6/165 (4%)	158/165 (96%)	CDK6,ITPR1,KRAS,MAP2K1,MYC,PIK3C2A,RB1
Role of Macrophages, Fibroblasts and Endothelial Cells in Rheumatoid	1.35	YES	0.0353	NA		4/312 (1%)	0/312 (0%)	7/312 (2%)	301/312 (96%)	ATF4,C5,CREB5,IL10,KRAS,MAP2K1,MYC,PIK3C2A,RELA,SOCS1,TCF4
Mechanisms of Viral Exit from Host Cells	1.34	YES	0.0732	NA		1/41 (2%)	0/41 (0%)	2/41 (5%)	38/41 (93%)	PDCD6IP,SH3GL1,XPO1
Role of JAK1 and JAK3 in γc Cytokine Signaling	1.33	YES	0.058	NA		0/69 (0%)	0/69 (0%)	4/69 (6%)	65/69 (94%)	KRAS,PIK3C2A,PTPN11,SOCS1
Differential Regulation of Cytokine Production in Macrophages and T Helper	1.32	YES	0.111	NA		1/18 (6%)	0/18 (0%)	1/18 (6%)	16/18 (89%)	CCL3,IL10
Methylglyoxal Degradation III	1.32	YES	0.111	NA		1/18 (6%)	0/18 (0%)	1/18 (6%)	16/18 (89%)	AKR1B1,CYP2E1
GM-CSF Signaling	1.32	YES	0.0571		2	0/70 (0%)	0/70 (0%)	4/70 (6%)	66/70 (94%)	KRAS,MAP2K1,PIK3C2A,PTPN11
STAT3 Pathway	1.3		0.0444		0	1/135 (1%)	0/135 (0%)	5/135 (4%)	129/135 (96%)	IGF2R,KRAS,MAP2K1,MYC,PTPN6,SOCS1
IL-15 Signaling	1.3		0.0563	NA		0/71 (0%)	0/71 (0%)	4/71 (6%)	67/71 (94%)	KRAS,MAP2K1,PIK3C2A,RELA

Growth Hormone Signaling	1.3	0.0563	0	0/71 (0%)	0/71 (0%)	4/71 (6%)	67/71 (94%)	PIK3C2A,PTPN6,SOCS1,SRF
BAG2 Signaling Pathway	1.29	0.0698	NA	1/43 (2%)	0/43 (0%)	2/43 (5%)	40/43 (93%)	MYC,PSME4,RELA
mTOR Signaling	1.26	0.0381	1	2/210 (1%)	0/210 (0%)	6/210 (3%)	202/210 (96%)	EIF4B,EIF4G3,KRAS,PIK3C2A,PPP2R1A,RPS21,RPS4Y2,RPSA
Ovarian Cancer Signaling	1.25	0.0432	1	0/139 (0%)	0/139 (0%)	6/139 (4%)	133/139 (96%)	KRAS,MAP2K1,PIK3C2A,RB1,SIN3A,TCF4
Thyroid Hormone Biosynthesis	1.24	0.333	NA	0/3 (0%)	0/3 (0%)	1/3 (33%)	2/3 (67%)	CTSD
Angiopoietin Signaling	1.23	0.0533	NA	0/75 (0%)	0/75 (0%)	4/75 (5%)	71/75 (95%)	KRAS,PIK3C2A,PTPN11,RELA
Hepatic Fibrosis Signaling Pathway	1.22	0.0326	1.155	3/368 (1%)	0/368 (0%)	9/368 (2%)	356/368 (97%)	ARAF,ATF4,CCL3,CREB5,KRAS,MAP2K1,MYC,PDCD4,PIK3C2A,RELA,TCF4,TFRC
PFKFB4 Signaling Pathway	1.22	0.0652	NA	1/46 (2%)	0/46 (0%)	2/46 (4%)	43/46 (93%)	ATF4,CREB5,MAP2K1
GDNF Family Ligand-Receptor Interactions	1.21	0.0526	NA	0/76 (0%)	0/76 (0%)	4/76 (5%)	72/76 (95%)	ITPR1,KRAS,MAP2K1,PIK3C2A
Aryl Hydrocarbon Receptor Signaling	1.2	0.042	0.816	1/143 (1%)	0/143 (0%)	5/143 (3%)	137/143 (96%)	CDK6,CTSD,MYC,NFE2L2,RB1,RELA
Endocannabinoid Cancer Inhibition Pathway	1.2	0.042	-0.816	2/143 (1%)	0/143 (0%)	4/143 (3%)	137/143 (96%)	ATF4,CREB5,MAP2K1,MYC,PIK3C2A,TCF4
Acute Phase Response Signaling	1.2	0.0391	0.816	1/179 (1%)	0/179 (0%)	6/179 (3%)	172/179 (96%)	C5,KRAS,MAP2K1,PTPN11,RELA,SOCS1,TCF4
Systemic Lupus Erythematosus In T Cell Signaling Pathway	1.19	0.033	-0.302	3/333 (1%)	0/333 (0%)	8/333 (2%)	322/333 (97%)	ATF4,CBL,CREB5,HLA-G,IL10,ITPR1,KRAS,MAP2K1,PIK3C2A,PPP2R1A,STIM1
Role of NFAT in Regulation of the Immune Response	1.18	0.0387	1.342	1/181 (1%)	0/181 (0%)	6/181 (3%)	174/181 (96%)	BTK,ITPR1,KRAS,MAP2K1,PIK3C2A,RELA,XPO1
IL-7 Signaling Pathway	1.18	0.0513	NA	1/78 (1%)	0/78 (0%)	3/78 (4%)	74/78 (95%)	FOXO3,MYC,PIK3C2A,SOCS1

Rac Signaling	1.16	0.0446	1.342	1/112 (1%)	0/112 (0%)	4/112 (4%)	107/112 (96%)	BRK1,KRAS,MAP2K1,PIK3C2A,RELA
IL-3 Signaling	1.16	0.0506	1	0/79 (0%)	0/79 (0%)	4/79 (5%)	75/79 (95%)	KRAS,MAP2K1,PIK3C2A,PTPN6
IL-17 Signaling	1.14	0.05	NA	0/80 (0%)	0/80 (0%)	4/80 (5%)	76/80 (95%)	KRAS,MAP2K1,PIK3C2A,RELA
Role of MAPK Signaling in the Pathogenesis of Influenza	1.14	0.05	NA	2/80 (3%)	0/80 (0%)	2/80 (3%)	76/80 (95%)	KRAS,MAP2K1,PLA2G2C,PLA2G2D
Neuroinflammation Signaling Pathway	1.14	0.0333	1.265	4/300 (1%)	0/300 (0%)	6/300 (2%)	290/300 (97%)	ATF4,CCL3,CREB5,IL10,KLK3,MFGE8,NFE2L2,PIK3C2A,PLA2G2D,RELA
Differential Regulation of Cytokine Production in Intestinal Epithelial Cells	1.13	0.087	NA	1/23 (4%)	0/23 (0%)	1/23 (4%)	21/23 (91%)	CCL3,IL10
Primary Immunodeficiency Signaling	1.13	0.06	NA	2/50 (4%)	0/50 (0%)	1/50 (2%)	47/50 (94%)	BTK,CD19,DCLRE1C
Spermine and Spermidine Degradation I	1.12	0.25	NA	1/4 (25%)	0/4 (0%)	0/4 (0%)	3/4 (75%)	SAT2
Methylmalonyl Pathway	1.12	0.25	NA	1/4 (25%)	0/4 (0%)	0/4 (0%)	3/4 (75%)	MCEE
Fatty Acid β-oxidation III (Unsaturated, Odd Number)	1.12	0.25	NA	1/4 (25%)	0/4 (0%)	0/4 (0%)	3/4 (75%)	ECI2
Endothelin-1 Signaling	1.11	0.0372	-0.378	4/188 (2%)	0/188 (0%)	3/188 (2%)	181/188 (96%)	ARAF,ITPR1,KRAS,MYC,PIK3C2A,PLA2G2C,PLA2G2D
fMLP Signaling in Neutrophils	1.11	0.0431	2.236	0/116 (0%)	0/116 (0%)	5/116 (4%)	111/116 (96%)	ITPR1,KRAS,MAP2K1,PIK3C2A,RELA
UVC-Induced MAPK Signaling	1.11	0.0588	NA	1/51 (2%)	0/51 (0%)	2/51 (4%)	48/51 (94%)	ARAF,KRAS,MAP2K1
ILK Signaling	1.09	0.0368	0.378	2/190 (1%)	0/190 (0%)	5/190 (3%)	183/190 (96%)	ATF4,CREB5,MYC,MYH9,PIK3C2A,PPP2R1A,RELA
p38 MAPK Signaling	1.08	0.0424	-0.447	3/118 (3%)	0/118 (0%)	2/118 (2%)	113/118 (96%)	ATF4,CREB5,MYC,PLA2G2D,SRF

Role of Pattern Recognition Receptors in Recognition of Bacteria and Viruses	1.08	0.039	1.342	3/154 (2%)	0/154 (0%)	3/154 (2%)	148/154 (96%)	C5,IL10,PIK3C2A,RELA,RIPK2,TNFSF14
VEGF Family Ligand-Receptor Interactions	1.08	0.0476	1	1/84 (1%)	0/84 (0%)	3/84 (4%)	80/84 (95%)	KRAS,MAP2K1,PIK3C2A,PLA2G2D
Agranulocyte Adhesion and Diapedesis	1.08	0.0365	NA	1/192 (1%)	0/192 (0%)	6/192 (3%)	185/192 (96%)	C5,CCL22,CCL3,CCL3L1,CCL3L3,CCL4L1/CCL4L2,MYH9
Regulation of the Epithelial-Mesenchymal Transition Pathway	1.08	0.0365	NA	1/192 (1%)	0/192 (0%)	6/192 (3%)	185/192 (96%)	ARAF,KRAS,MAP2K1,PIK3C2A,PTPN11,RELA,TCF4
Natural Killer Cell Signaling	1.07	0.042	NA	0/119 (0%)	0/119 (0%)	5/119 (4%)	114/119 (96%)	KRAS,MAP2K1,PIK3C2A,PTPN11,PTPN6
Lymphotoxin β Receptor Signaling	1.07	0.0566	NA	1/53 (2%)	0/53 (0%)	2/53 (4%)	50/53 (94%)	PIK3C2A,RELA,TNFSF14
Role of JAK family kinases in IL-6-type Cytokine Signaling	1.07	0.08	NA	0/25 (0%)	0/25 (0%)	2/25 (8%)	23/25 (92%)	PTPN11,SOCS1
IL-4 Signaling	1.07	0.0471	NA	0/85 (0%)	0/85 (0%)	4/85 (5%)	81/85 (95%)	KRAS,PIK3C2A,PTPN6,SOCS1
BMP signaling pathway	1.07	0.0471	1	1/85 (1%)	0/85 (0%)	3/85 (4%)	81/85 (95%)	BMP7,KRAS,MAP2K1,RELA
Clathrin-mediated Endocytosis Signaling	1.07	0.0363	NA	1/193 (1%)	0/193 (0%)	6/193 (3%)	186/193 (96%)	AP3M1,CBL,PIK3C2A,SH3GL1,TFRC,USP9X,WASL
Role of IL-17A in Arthritis	1.05	0.0556	NA	0/54 (0%)	0/54 (0%)	3/54 (6%)	51/54 (94%)	MAP2K1,PIK3C2A,RELA
Antiproliferative Role of TOB in T Cell Signaling	1.04	0.0769	NA	0/26 (0%)	0/26 (0%)	2/26 (8%)	24/26 (92%)	PABPC4,RB1
Estrogen-mediated S-phase Entry	1.04	0.0769	NA	1/26 (4%)	0/26 (0%)	1/26 (4%)	24/26 (92%)	MYC,RB1
Protein Kinase A Signaling	1.03	0.0302	0.333	3/398 (1%)	0/398 (0%)	9/398 (2%)	386/398 (97%)	AKAP17A,ATF4,CDC26,CREB5,DUSP11,DUSP5,ITPR1,MAP2K1,PTPN11,PTPN6,RELA,TCF4
CMP-N-acetylneuraminate Biosynthesis I (Eukaryotes)	1.03	0.2	NA	0/5 (0%)	0/5 (0%)	1/5 (20%)	4/5 (80%)	CMAS

2-oxobutanoate Degradation I	1.03	0.2	NA	1/5 (20%)	0/5 (0%)	0/5 (0%)	4/5 (80%)	MCEE
RANK Signaling in Osteoclasts	1.03	0.0455	2	0/88 (0%)	0/88 (0%)	4/88 (5%)	84/88 (95%)	CBL,MAP2K1,PIK3C2A,RELA
CCR3 Signaling in Eosinophils	1.01	0.0403	1	1/124 (1%)	0/124 (0%)	4/124 (3%)	119/124 (96%)	ITPR1,KRAS,MAP2K1,PIK3C2A,PLA2G2D
Unfolded protein response	1.01	0.0536	NA	1/56 (2%)	0/56 (0%)	2/56 (4%)	53/56 (95%)	ATF4,HSPH1,NFE2L2
CTLA4 Signaling in Cytotoxic T Lymphocytes	1.01	0.0449	NA	0/89 (0%)	0/89 (0%)	4/89 (4%)	85/89 (96%)	PIK3C2A,PPP2R1A,PTPN11,PTPN6
Breast Cancer Regulation by Stathmin1	1	0.035	NA	0/200 (0%)	0/200 (0%)	7/200 (4%)	193/200 (97%)	ARHGEF2,ITPR1,KRAS,MAP2K1,PIK3C2A,PPP2R1A,UHMK1
Role of CHK Proteins in Cell Cycle Checkpoint Control	0.996	0.0526	NA	0/57 (0%)	0/57 (0%)	3/57 (5%)	54/57 (95%)	MDC1,PPP2R1A,TLK2
14-3-3-mediated Signaling	0.983	0.0394	NA	0/127 (0%)	0/127 (0%)	5/127 (4%)	122/127 (96%)	CBL,KRAS,MAP2K1,PDCD6IP,PIK3C2A
HMGB1 Signaling	0.975	0.0364	2.236	1/165 (1%)	0/165 (0%)	5/165 (3%)	159/165 (96%)	KAT6A,KRAS,MAP2K1,PIK3C2A,RELA,TNFSF14
Synaptic Long Term Potentiation	0.959	0.0388	1.342	1/129 (1%)	0/129 (0%)	4/129 (3%)	124/129 (96%)	ATF4,CREB5,ITPR1,KRAS,MAP2K1
Reelin Signaling in Neurons	0.959	0.0388	2.236	0/129 (0%)	0/129 (0%)	5/129 (4%)	124/129 (96%)	ARHGEF2,MAP2K1,PAFAH1B1,PIK3C2A,WASL
Role of p14/p19ARF in Tumor Suppression	0.959	0.069	NA	0/29 (0%)	0/29 (0%)	2/29 (7%)	27/29 (93%)	PIK3C2A,RB1
Gα12/13 Signaling	0.951	0.0385	1.342	1/130 (1%)	0/130 (0%)	4/130 (3%)	125/130 (96%)	BTK,KRAS,MAP2K1,PIK3C2A,RELA
Selenocysteine Biosynthesis II (Archaea and Eukaryotes)	0.951	0.167	NA	1/6 (17%)	0/6 (0%)	0/6 (0%)	5/6 (83%)	PSTK
Zymosterol Biosynthesis	0.951	0.167	NA	1/6 (17%)	0/6 (0%)	0/6 (0%)	5/6 (83%)	NSDHL

Tight Junction Signaling	0.947	0.0357	NA	1/168 (1%)	0/168 (0%)	5/168 (3%)	162/168 (96%)	ARHGEF2,CASK,MYH9,PPP2R1A,RELA,VTI1B
CREB Signaling in Neurons	0.947	0.0338	1.633	1/207 (0%)	0/207 (0%)	6/207 (3%)	200/207 (97%)	ATF4,CREB5,ITPR1,KRAS,MAP2K1,PIK3C2A,POLR2A
FAK Signaling	0.936	0.0421	NA	0/95 (0%)	0/95 (0%)	4/95 (4%)	91/95 (96%)	ASAP1,KRAS,MAP2K1,PIK3C2A
TNFR2 Signaling	0.936	0.0667	NA	0/30 (0%)	0/30 (0%)	2/30 (7%)	28/30 (93%)	RELA,TNFAIP3
Neuregulin Signaling	0.924	0.0417	1	1/96 (1%)	0/96 (0%)	3/96 (3%)	92/96 (96%)	KRAS,MAP2K1,MYC,PTPN11
Communication between Innate and Adaptive Immune Cells	0.924	0.0417	NA	2/96 (2%)	0/96 (0%)	2/96 (2%)	92/96 (96%)	CCL3,CCL3L3,HLA-G,IL10
Wnt/Ca+ pathway	0.917	0.0484	NA	1/62 (2%)	0/62 (0%)	2/62 (3%)	59/62 (95%)	ATF4,CREB5,RELA
PAK Signaling	0.91	0.0412	2	0/97 (0%)	0/97 (0%)	4/97 (4%)	93/97 (96%)	KRAS,MAP2K1,PIK3C2A,WASL
AMPK Signaling	0.907	0.033	0.447	1/212 (0%)	0/212 (0%)	6/212 (3%)	205/212 (97%)	ARID1A,ATF4,CREB5,FOXO3,PIK3C2A,PPP2R1A,RAB22A
GNRH Signaling	0.903	0.0347	0.816	1/173 (1%)	0/173 (0%)	5/173 (3%)	167/173 (97%)	ATF4,CREB5,ITPR1,KRAS,MAP2K1,RELA
p53 Signaling	0.9	0.0408	NA	0/98 (0%)	0/98 (0%)	4/98 (4%)	94/98 (96%)	PIAS1,PIK3C2A,PRKDC,RB1
4-1BB Signaling in T Lymphocytes	0.889	0.0625	NA	0/32 (0%)	0/32 (0%)	2/32 (6%)	30/32 (94%)	MAP2K1,RELA
Role of PI3K/AKT Signaling in the Pathogenesis of Influenza	0.886	0.0469	NA	0/64 (0%)	0/64 (0%)	3/64 (5%)	61/64 (95%)	MAP2K1,PIK3C2A,RELA
IL-17A Signaling in Airway Cells	0.886	0.0469	NA	0/64 (0%)	0/64 (0%)	3/64 (5%)	61/64 (95%)	MAP2K1,PIK3C2A,RELA
Myc Mediated Apoptosis Signaling	0.87	0.0462	NA	1/65 (2%)	0/65 (0%)	2/65 (3%)	62/65 (95%)	KRAS,MYC,PIK3C2A

Regulation of Cellular Mechanics by Calpain Protease	0.87	0.0462	NA	0/65 (0%)	0/65 (0%)	3/65 (5%)	62/65 (95%)	CDK6,KRAS,RB1
Circadian Rhythm Signaling	0.866	0.0606	NA	1/33 (3%)	0/33 (0%)	1/33 (3%)	31/33 (94%)	ATF4,CREB5
IL-9 Signaling	0.866	0.0606	NA	0/33 (0%)	0/33 (0%)	2/33 (6%)	31/33 (94%)	PIK3C2A,RELA
Retinoate Biosynthesis I	0.866	0.0606	NA	0/33 (0%)	0/33 (0%)	2/33 (6%)	31/33 (94%)	AKR1B1,RDH10
Granulocyte Adhesion and Diapedesis	0.854	0.0335	NA	1/179 (1%)	0/179 (0%)	5/179 (3%)	173/179 (97%)	C5,CCL22,CCL3,CCL3L1,CCL3L3,CCL4L1/CCL4L2
NF-κB Signaling	0.854	0.0335	0.816	1/179 (1%)	0/179 (0%)	5/179 (3%)	173/179 (97%)	ARAF,IGF2R,KRAS,PIK3C2A,RELA,TNFAIP3
DNA Methylation and Transcriptional Repression Signaling	0.845	0.0588	NA	0/34 (0%)	0/34 (0%)	2/34 (6%)	32/34 (94%)	SAP130,SIN3A
MIF-mediated Glucocorticoid Regulation	0.845	0.0588	NA	1/34 (3%)	0/34 (0%)	1/34 (3%)	32/34 (94%)	PLA2G2D,RELA
Ephrin Receptor Signaling	0.845	0.0333	1.633	1/180 (1%)	0/180 (0%)	5/180 (3%)	174/180 (97%)	ATF4,CREB5,KRAS,MAP2K1,PTPN11,WASL
ErbB4 Signaling	0.842	0.0448	NA	0/67 (0%)	0/67 (0%)	3/67 (4%)	64/67 (96%)	KRAS,MAP2K1,PIK3C2A
Sumoylation Pathway	0.842	0.0388	NA	0/103 (0%)	0/103 (0%)	4/103 (4%)	99/103 (96%)	PIAS1,RANGAP1,SENP2,SERBP1
Histidine Degradation III	0.836	0.125	NA	0/8 (0%)	0/8 (0%)	1/8 (13%)	7/8 (88%)	UROC1
Dendritic Cell Maturation	0.821	0.0328	0.816	3/183 (2%)	0/183 (0%)	3/183 (2%)	177/183 (97%)	ATF4,CREB5,IL10,PIK3C2A,RELA,STAT2
SPINK1 General Cancer Pathway	0.815	0.0435	NA	0/69 (0%)	0/69 (0%)	3/69 (4%)	66/69 (96%)	KRAS,MAP2K1,PIK3C2A
PD-1, PD-L1 cancer immunotherapy pathway	0.812	0.0377	1	1/106 (1%)	0/106 (0%)	3/106 (3%)	102/106 (96%)	HLA-G,PDCD4,PIK3C2A,PTPN11

Virus Entry via Endocytic Pathways	0.801	0.0374	NA	0/107 (0%)	0/107 (0%)	4/107 (4%)	103/107 (96%)	AP3M1,KRAS,PIK3C2A,TFRC
Hepatic Fibrosis / Hepatic Stellate Cell Activation	0.799	0.0323	NA	2/186 (1%)	0/186 (0%)	4/186 (2%)	180/186 (97%)	COL12A1,CYP2E1,IL10,KLF6,MYH9,RELA
Synaptogenesis Signaling Pathway	0.793	0.0288	1	3/312 (1%)	0/312 (0%)	6/312 (2%)	303/312 (97%)	ATF4,CREB5,ITPR1,KRAS,PAFAH1B1,PIK3C2A,THBS3,VTI1B,WASL
Cell Cycle Regulation by BTG Family Proteins	0.788	0.0541	NA	0/37 (0%)	0/37 (0%)	2/37 (5%)	35/37 (95%)	PPP2R1A,RB1
Pathogenesis of Multiple Sclerosis	0.788	0.111	NA	0/9 (0%)	0/9 (0%)	1/9 (11%)	8/9 (89%)	CCL3
Sucrose Degradation V (Mammalian)	0.788	0.111	NA	0/9 (0%)	0/9 (0%)	1/9 (11%)	8/9 (89%)	ALDOA
Leucine Degradation I	0.788	0.111	NA	0/9 (0%)	0/9 (0%)	1/9 (11%)	8/9 (89%)	BCAT1
Superpathway of Methionine Degradation	0.788	0.0541	NA	1/37 (3%)	0/37 (0%)	1/37 (3%)	35/37 (95%)	EEF1AKMT2,MCEE
Synaptic Long Term Depression	0.777	0.0317	0	2/189 (1%)	0/189 (0%)	4/189 (2%)	183/189 (97%)	ITPR1,KRAS,MAP2K1,PLA2G2C,PLA2G2D,PPP2R1A
Protein Ubiquitination Pathway	0.775	0.0293	NA	1/273 (0%)	0/273 (0%)	7/273 (3%)	265/273 (97%)	CBL,DNAJC13,DNAJC24,HSPH1,PSMA2,UBE2V2,USP14,USP9X
HGF Signaling	0.762	0.036	2	0/111 (0%)	0/111 (0%)	4/111 (4%)	107/111 (96%)	KRAS,MAP2K1,PIK3C2A,PTPN11
Type I Diabetes Mellitus Signaling	0.762	0.036	NA	1/111 (1%)	0/111 (0%)	3/111 (3%)	107/111 (96%)	HLA-G,PIAS1,RELA,SOCS1
Leptin Signaling in Obesity	0.752	0.0405	NA	0/74 (0%)	0/74 (0%)	3/74 (4%)	71/74 (96%)	MAP2K1,PIK3C2A,PTPN11
tRNA Charging	0.752	0.0513	NA	1/39 (3%)	0/39 (0%)	1/39 (3%)	37/39 (95%)	IARS2,RARS2
Hypoxia Signaling in the Cardiovascular System	0.752	0.0405	NA	1/74 (1%)	0/74 (0%)	2/74 (3%)	71/74 (96%)	ATF4,CREB5,UBE2V2

Epithelial Adherens Junction Signaling	0.75	0.0329	NA	0/152 (0%)	0/152 (0%)	5/152 (3%)	147/152 (97%)	CLINT1,KRAS,MYH9,TCF4,WASL
Dolichyl-diphosphooligosaccharide Biosynthesis	0.747	0.1	NA	1/10 (10%)	0/10 (0%)	0/10 (0%)	9/10 (90%)	ALG5
TREM1 Signaling	0.74	0.04	NA	1/75 (1%)	0/75 (0%)	2/75 (3%)	72/75 (96%)	CCL3,IL10,RELA
FcγRIIB Signaling in B Lymphocytes	0.74	0.04	NA	1/75 (1%)	0/75 (0%)	2/75 (3%)	72/75 (96%)	BTK,KRAS,PIK3C2A
Apelin Endothelial Signaling Pathway	0.724	0.0348	2	0/115 (0%)	0/115 (0%)	4/115 (3%)	111/115 (97%)	KRAS,MAP2K1,PIK3C2A,RELA
Adrenomedullin signaling pathway	0.721	0.0305	1.633	1/197 (1%)	0/197 (0%)	5/197 (3%)	191/197 (97%)	ARAF,ITPR1,KRAS,MAP2K1,PIK3C2A,RELA
Pyrimidine Ribonucleotides Interconversion	0.719	0.0488	NA	1/41 (2%)	0/41 (0%)	1/41 (2%)	39/41 (95%)	NME3,RECQL
Gαq Signaling	0.71	0.0318	1.342	1/157 (1%)	0/157 (0%)	4/157 (3%)	152/157 (97%)	BTK,ITPR1,MAP2K1,PIK3C2A,RELA
MIF Regulation of Innate Immunity	0.703	0.0476	NA	1/42 (2%)	0/42 (0%)	1/42 (2%)	40/42 (95%)	PLA2G2D,RELA
Cholecystokinin/Gastrin-mediated Signaling	0.688	0.0336	2	0/119 (0%)	0/119 (0%)	4/119 (3%)	115/119 (97%)	ITPR1,KRAS,MAP2K1,SRF
Role of NANOG in Mammalian Embryonic Stem Cell Pluripotency	0.688	0.0336	NA	1/119 (1%)	0/119 (0%)	3/119 (3%)	115/119 (97%)	BMP7,KRAS,MAP2K1,PIK3C2A
GP6 Signaling Pathway	0.688	0.0336	1	1/119 (1%)	0/119 (0%)	3/119 (3%)	115/119 (97%)	BTK,COL12A1,ITPR1,PIK3C2A
Oncostatin M Signaling	0.686	0.0465	NA	0/43 (0%)	0/43 (0%)	2/43 (5%)	41/43 (95%)	KRAS,MAP2K1
Pyrimidine Ribonucleotides De Novo Biosynthesis	0.686	0.0465	NA	1/43 (2%)	0/43 (0%)	1/43 (2%)	41/43 (95%)	NME3,RECQL
Role of BRCA1 in DNA Damage Response	0.684	0.0375	NA	0/80 (0%)	0/80 (0%)	3/80 (4%)	77/80 (96%)	ARID1A,MDC1,RB1

Assembly of RNA Polymerase I Complex	0.676	0.0833	NA	1/12 (8%)	0/12 (0%)	0/12 (0%)	11/12 (92%)	POLR1C
Glycogen Degradation II	0.676	0.0833	NA	0/12 (0%)	0/12 (0%)	1/12 (8%)	11/12 (92%)	MTAP
Opioid Signaling Pathway	0.676	0.0283	1.134	2/247 (1%)	0/247 (0%)	5/247 (2%)	240/247 (97%)	ATF4,CREB5,ITPR1,KRAS,MAP2K1,MYC,SRF
IL-15 Production	0.672	0.0331	NA	2/121 (2%)	0/121 (0%)	2/121 (2%)	117/121 (97%)	BTK,CLK1,MAP2K1,RELA
Apelin Pancreas Signaling Pathway	0.672	0.0455	NA	0/44 (0%)	0/44 (0%)	2/44 (5%)	42/44 (95%)	PIK3C2A,RELA
IL-23 Signaling Pathway	0.672	0.0455	NA	0/44 (0%)	0/44 (0%)	2/44 (5%)	42/44 (95%)	PIK3C2A,RELA
NF-κB Activation by Viruses	0.664	0.0366	NA	0/82 (0%)	0/82 (0%)	3/82 (4%)	79/82 (96%)	KRAS,PIK3C2A,RELA
Thrombin Signaling	0.65	0.0288	2.449	0/208 (0%)	0/208 (0%)	6/208 (3%)	202/208 (97%)	ARHGEF2,ITPR1,KRAS,MAP2K1,PIK3C2A,RELA
Role of Oct4 in Mammalian Embryonic Stem Cell Pluripotency	0.644	0.0435	NA	1/46 (2%)	0/46 (0%)	1/46 (2%)	44/46 (96%)	PHB,RB1
HER-2 Signaling in Breast Cancer	0.644	0.0357	NA	0/84 (0%)	0/84 (0%)	3/84 (4%)	81/84 (96%)	CDK6,KRAS,PIK3C2A
Pregnenolone Biosynthesis	0.644	0.0769	NA	1/13 (8%)	0/13 (0%)	0/13 (0%)	12/13 (92%)	CYP2E1
FAT10 Cancer Signaling Pathway	0.644	0.0435	NA	0/46 (0%)	0/46 (0%)	2/46 (4%)	44/46 (96%)	RELA,TCF4
Atherosclerosis Signaling	0.631	0.0317	NA	3/126 (2%)	0/126 (0%)	1/126 (1%)	122/126 (97%)	PLA2G2C,PLA2G2D,RELA,TNFSF14
Ephrin A Signaling	0.631	0.0426	NA	0/47 (0%)	0/47 (0%)	2/47 (4%)	45/47 (96%)	PIK3C2A,PTPN11
Glycogen Degradation III	0.616	0.0714	NA	0/14 (0%)	0/14 (0%)	1/14 (7%)	13/14 (93%)	MTAP

Germ Cell-Sertoli Cell Junction Signaling	0.613	0.0292	NA	0/171 (0%)	0/171 (0%)	5/171 (3%)	166/171 (97%)	CLINT1,KRAS,MAP2K1,PIK3C2A,WASL
White Adipose Tissue Browning Pathway	0.609	0.031	-1	3/129 (2%)	0/129 (0%)	1/129 (1%)	125/129 (97%)	ATF4,BMP7,CAMP,CREB5
Autoimmune Thyroid Disease Signaling	0.604	0.0408	NA	2/49 (4%)	0/49 (0%)	0/49 (0%)	47/49 (96%)	HLA-G,IL10
Regulation of IL-2 Expression in Activated and Anergic T	0.597	0.0337	NA	0/89 (0%)	0/89 (0%)	3/89 (3%)	86/89 (97%)	KRAS,MAP2K1,RELA
PI3K/AKT Signaling	0.593	0.0287	1	0/174 (0%)	0/174 (0%)	5/174 (3%)	169/174 (97%)	FOXO3,KRAS,MAP2K1,PPP2R1A,RELA
Actin Cytoskeleton Signaling	0.592	0.0275	1.633	1/218 (0%)	0/218 (0%)	5/218 (2%)	212/218 (97%)	BRK1,KRAS,MAP2K1,MYH9,PIK3C2A,WASL
TNFR1 Signaling	0.592	0.04	NA	0/50 (0%)	0/50 (0%)	2/50 (4%)	48/50 (96%)	RELA,TNFAIP3
Isoleucine Degradation I	0.59	0.0667	NA	0/15 (0%)	0/15 (0%)	1/15 (7%)	14/15 (93%)	BCAT1
IL-12 Signaling and Production in Macrophages	0.587	0.0303	NA	1/132 (1%)	0/132 (0%)	3/132 (2%)	128/132 (97%)	IL10,MAP2K1,PIK3C2A,RELA
Role of Osteoblasts, Osteoclasts and Chondrocytes in	0.58	0.0273	NA	2/220 (1%)	0/220 (0%)	4/220 (2%)	214/220 (97%)	BMP7,CBL,IL10,PIK3C2A,RELA,TCF4
Granzyme B Signaling	0.567	0.0625	NA	0/16 (0%)	0/16 (0%)	1/16 (6%)	15/16 (94%)	PRKDC
Chondroitin Sulfate Degradation (Metazoa)	0.567	0.0625	NA	1/16 (6%)	0/16 (0%)	0/16 (0%)	15/16 (94%)	HEXD
UVB-Induced MAPK Signaling	0.567	0.0385	NA	0/52 (0%)	0/52 (0%)	2/52 (4%)	50/52 (96%)	MAP2K1,PIK3C2A
Human Embryonic Stem Cell Pluripotency	0.565	0.0296	NA	1/135 (1%)	0/135 (0%)	3/135 (2%)	131/135 (97%)	BMP7,KLK3,PIK3C2A,TCF4
Sperm Motility	0.565	0.0269	NA	4/223 (2%)	0/223 (0%)	2/223 (1%)	217/223 (97%)	BTK,CLK1,ITPR1,MAP2K1,PLA2G2C,PLA2G2D

Androgen Signaling	0.558	0.0294	NA	1/136 (1%)	0/136 (0%)	3/136 (2%)	132/136 (97%)	GTF2H1,GTF2H3,POLR2A,RELA
CD27 Signaling in Lymphocytes	0.556	0.0377	NA	0/53 (0%)	0/53 (0%)	2/53 (4%)	51/53 (96%)	MAP2K1,RELA
ErbB Signaling	0.553	0.0319	NA	0/94 (0%)	0/94 (0%)	3/94 (3%)	91/94 (97%)	KRAS,MAP2K1,PIK3C2A
α-Adrenergic Signaling	0.545	0.0316	NA	0/95 (0%)	0/95 (0%)	3/95 (3%)	92/95 (97%)	ITPR1,KRAS,MAP2K1
Transcriptional Regulatory Network in Embryonic Stem Cells	0.545	0.037	NA	0/54 (0%)	0/54 (0%)	2/54 (4%)	52/54 (96%)	KAT6A,ZFHX3
Ubiquinol-10 Biosynthesis (Eukaryotic)	0.545	0.0588	NA	1/17 (6%)	0/17 (0%)	0/17 (0%)	16/17 (94%)	CYP2E1
Dermatan Sulfate Degradation (Metazoa)	0.545	0.0588	NA	1/17 (6%)	0/17 (0%)	0/17 (0%)	16/17 (94%)	HEXD
TGF-β Signaling	0.538	0.0312	NA	1/96 (1%)	0/96 (0%)	2/96 (2%)	93/96 (97%)	BMP7,KRAS,MAP2K1
Valine Degradation I	0.524	0.0556	NA	0/18 (0%)	0/18 (0%)	1/18 (6%)	17/18 (94%)	BCAT1
FAT10 Signaling Pathway	0.524	0.0556	NA	0/18 (0%)	0/18 (0%)	1/18 (6%)	17/18 (94%)	PSME4
Nitric Oxide Signaling in the Cardiovascular System	0.514	0.0303	NA	0/99 (0%)	0/99 (0%)	3/99 (3%)	96/99 (97%)	ITPR1,MAP2K1,PIK3C2A
Apoptosis Signaling	0.514	0.0303	NA	0/99 (0%)	0/99 (0%)	3/99 (3%)	96/99 (97%)	KRAS,MAP2K1,RELA
Production of Nitric Oxide and Reactive Oxygen Species in Macrophages	0.511	0.0266	1	0/188 (0%)	0/188 (0%)	5/188 (3%)	183/188 (97%)	MAP2K1,PIK3C2A,PPP2R1A,PTPN6,RELA
GADD45 Signaling	0.504	0.0526	NA	1/19 (5%)	0/19 (0%)	0/19 (0%)	18/19 (95%)	CCNB1
DNA damage-induced 14-3-3σ Signaling	0.504	0.0526	NA	1/19 (5%)	0/19 (0%)	0/19 (0%)	18/19 (95%)	CCNB1

MSP-RON Signaling Pathway	0.503	0.0345	NA	0/58 (0%)	0/58 (0%)	2/58 (3%)	56/58 (97%)	KLK3,PIK3C2A
PPARα/RXRα Activation	0.5	0.0263	NA	0/190 (0%)	0/190 (0%)	5/190 (3%)	185/190 (97%)	CKAP5,KRAS,MAP2K1,NCOA6,RELA
Corticotropin Releasing Hormone Signaling	0.5	0.0276	NA	1/145 (1%)	0/145 (0%)	3/145 (2%)	141/145 (97%)	ATF4,CREB5,ITPR1,MAP2K1
Cardiomyocyte Differentiation via BMP Receptors	0.485	0.05	NA	1/20 (5%)	0/20 (0%)	0/20 (0%)	19/20 (95%)	BMP7
The Visual Cycle	0.485	0.05	NA	0/20 (0%)	0/20 (0%)	1/20 (5%)	19/20 (95%)	RDH10
Cardiac Hypertrophy Signaling	0.481	0.025	2.449	2/240 (1%)	0/240 (0%)	4/240 (2%)	234/240 (98%)	EIF2B3,EIF2B5,KRAS,MAP2K1,PIK3C2A,SRF
PPAR Signaling	0.478	0.0288	NA	0/104 (0%)	0/104 (0%)	3/104 (3%)	101/104 (97%)	KRAS,MAP2K1,RELA
Putrescine Degradation III	0.469	0.0476	NA	1/21 (5%)	0/21 (0%)	0/21 (0%)	20/21 (95%)	SAT2
Endoplasmic Reticulum Stress Pathway	0.469	0.0476	NA	1/21 (5%)	0/21 (0%)	0/21 (0%)	20/21 (95%)	ATF4
Gαs Signaling	0.457	0.028	NA	1/107 (1%)	0/107 (0%)	2/107 (2%)	104/107 (97%)	ATF4,CREB5,MAP2K1
Phospholipases	0.456	0.0317	NA	2/63 (3%)	0/63 (0%)	0/63 (0%)	61/63 (97%)	PLA2G2C,PLA2G2D
Phosphatidylglycerol Biosynthesis II (Non-plastidic)	0.452	0.0455	NA	0/22 (0%)	0/22 (0%)	1/22 (5%)	21/22 (95%)	PGS1
Methionine Degradation I (to Homocysteine)	0.452	0.0455	NA	0/22 (0%)	0/22 (0%)	1/22 (5%)	21/22 (95%)	EEF1AKMT2
IL-8 Signaling	0.451	0.025	1.342	1/200 (1%)	0/200 (0%)	4/200 (2%)	195/200 (98%)	ARAF,KRAS,MAP2K1,PIK3C2A,RELA
CDK5 Signaling	0.451	0.0278	NA	0/108 (0%)	0/108 (0%)	3/108 (3%)	105/108 (97%)	KRAS,MAP2K1,PPP2R1A

Cardiac Hypertrophy Signaling (Enhanced)	0.447	0.0226	1	5/487 (1%)	0/487 (0%)	6/487 (1%)	476/487 (98%)	EIF2B3,EIF2B5,HDAC8,ITPR1,KRAS,MAP2K1,MYC,PIK3C2A,RELA,SRF,TNFSF14
Antioxidant Action of Vitamin C	0.444	0.0275	NA	2/109 (2%)	0/109 (0%)	1/109 (1%)	106/109 (97%)	PLA2G2C,PLA2G2D,RELA
PXR/RXR Activation	0.439	0.0308	NA	0/65 (0%)	0/65 (0%)	2/65 (3%)	63/65 (97%)	FOXO3,RELA
iCOS-iCOSL Signaling in T Helper Cells	0.432	0.027	NA	0/111 (0%)	0/111 (0%)	3/111 (3%)	108/111 (97%)	ITPR1,PIK3C2A,RELA
Eicosanoid Signaling	0.431	0.0303	NA	2/66 (3%)	0/66 (0%)	0/66 (0%)	64/66 (97%)	PLA2G2C,PLA2G2D
Colorectal Cancer Metastasis Signaling	0.426	0.0237	1.633	1/253 (0%)	0/253 (0%)	5/253 (2%)	247/253 (98%)	KRAS,MAP2K1,MYC,PIK3C2A,RELA,TCF4
Calcium Signaling	0.424	0.0243	NA	2/206 (1%)	0/206 (0%)	3/206 (1%)	201/206 (98%)	ATF4,CREB5,HDAC8,ITPR1,MYH9
Cysteine Biosynthesis III (mammalia)	0.423	0.0417	NA	0/24 (0%)	0/24 (0%)	1/24 (4%)	23/24 (96%)	EEF1AKMT2
IL-17A Signaling in Gastric Cells	0.409	0.04	NA	0/25 (0%)	0/25 (0%)	1/25 (4%)	24/25 (96%)	RELA
Bupropion Degradation	0.409	0.04	NA	1/25 (4%)	0/25 (0%)	0/25 (0%)	24/25 (96%)	CYP2E1
IL-10 Signaling	0.407	0.029	NA	1/69 (1%)	0/69 (0%)	1/69 (1%)	67/69 (97%)	IL10,RELA
Dopamine-DARPP32 Feedback in cAMP Signaling	0.402	0.0245	1	1/163 (1%)	0/163 (0%)	3/163 (2%)	159/163 (98%)	ATF4,CREB5,ITPR1,PPP2R1A
Neuroprotective Role of THOP1 in Alzheimer's Disease	0.401	0.0259	NA	2/116 (2%)	0/116 (0%)	1/116 (1%)	113/116 (97%)	HLA-G,KLK3,PRSS53
Osteoarthritis Pathway	0.401	0.0237	0.447	1/211 (0%)	0/211 (0%)	4/211 (2%)	206/211 (98%)	ATF4,CREB5,FOXO3,RELA,TCF4
Tec Kinase Signaling	0.398	0.0244	0	2/164 (1%)	0/164 (0%)	2/164 (1%)	160/164 (98%)	BTK,PIK3C2A,RELA,STAT2

Role of Tissue Factor in Cancer	0.396	0.0256	NA	0/117 (0%)	0/117 (0%)	3/117 (3%)	114/117 (97%)	KRAS,PIK3C2A,PTPN11
Glycolysis I	0.396	0.0385	NA	0/26 (0%)	0/26 (0%)	1/26 (4%)	25/26 (96%)	ALDOA
Gluconeogenesis I	0.396	0.0385	NA	0/26 (0%)	0/26 (0%)	1/26 (4%)	25/26 (96%)	ALDOA
Integrin Signaling	0.393	0.0235	2.236	0/213 (0%)	0/213 (0%)	5/213 (2%)	208/213 (98%)	ASAP1,KRAS,MAP2K1,PIK3C2A,WASL
Role of NFAT in Cardiac Hypertrophy	0.389	0.0234	2	1/214 (0%)	0/214 (0%)	4/214 (2%)	209/214 (98%)	HDAC8,ITPR1,KRAS,MAP2K1,PIK3C2A
CXCR4 Signaling	0.384	0.024	2	0/167 (0%)	0/167 (0%)	4/167 (2%)	163/167 (98%)	ITPR1,KRAS,MAP2K1,PIK3C2A
Melatonin Signaling	0.384	0.0278	NA	1/72 (1%)	0/72 (0%)	1/72 (1%)	70/72 (97%)	ARAF,MAP2K1
Basal Cell Carcinoma Signaling	0.384	0.0278	NA	1/72 (1%)	0/72 (0%)	1/72 (1%)	70/72 (97%)	BMP7,TCF4
Actin Nucleation by ARP-WASP Complex	0.384	0.0278	NA	0/72 (0%)	0/72 (0%)	2/72 (3%)	70/72 (97%)	KRAS,WASL
Th1 Pathway	0.374	0.0248	NA	1/121 (1%)	0/121 (0%)	2/121 (2%)	118/121 (98%)	IL10,PIK3C2A,SOCS1
Glioma Invasiveness Signaling	0.371	0.027	NA	0/74 (0%)	0/74 (0%)	2/74 (3%)	72/74 (97%)	KRAS,PIK3C2A
Sonic Hedgehog Signaling	0.361	0.0345	NA	1/29 (3%)	0/29 (0%)	0/29 (0%)	28/29 (97%)	CCNB1
Toll-like Receptor Signaling	0.357	0.0263	NA	0/76 (0%)	0/76 (0%)	2/76 (3%)	74/76 (97%)	RELA,TNFAIP3
Macropinocytosis Signaling	0.357	0.0263	NA	0/76 (0%)	0/76 (0%)	2/76 (3%)	74/76 (97%)	KRAS,PIK3C2A
G-Protein Coupled Receptor Signaling	0.356	0.0221	NA	1/272 (0%)	0/272 (0%)	5/272 (2%)	266/272 (98%)	ATF4,CREB5,KRAS,MAP2K1,PIK3C2A,RELA

Acetone Degradation I (to Methylglyoxal)	0.349	0.0333	NA	1/30 (3%)	0/30 (0%)	0/30 (0%)	29/30 (97%)	CYP2E1
Chemokine Signaling	0.332	0.025	NA	0/80 (0%)	0/80 (0%)	2/80 (3%)	78/80 (98%)	KRAS,MAP2K1
Fatty Acid β-oxidation I	0.329	0.0312	NA	1/32 (3%)	0/32 (0%)	0/32 (0%)	31/32 (97%)	ECI2
Cellular Effects of Sildenafil (Viagra)	0.324	0.0229	NA	0/131 (0%)	0/131 (0%)	3/131 (2%)	128/131 (98%)	ITPR1,MYH9,PABPC4
TR/RXR Activation	0.308	0.0238	NA	0/84 (0%)	0/84 (0%)	2/84 (2%)	82/84 (98%)	NCOA6,PIK3C2A
Xenobiotic Metabolism Signaling	0.307	0.0209	NA	0/287 (0%)	0/287 (0%)	6/287 (2%)	281/287 (98%)	KRAS,MAP2K1,NFE2L2,PIK3C2A,PPP2R1A,RELA
TWEAK Signaling	0.301	0.0286	NA	0/35 (0%)	0/35 (0%)	1/35 (3%)	34/35 (97%)	RELA
IL-17A Signaling in Fibroblasts	0.301	0.0286	NA	0/35 (0%)	0/35 (0%)	1/35 (3%)	34/35 (97%)	RELA
Allograft Rejection Signaling	0.298	0.0233	NA	2/86 (2%)	0/86 (0%)	0/86 (0%)	84/86 (98%)	HLA-G,IL10
Iron homeostasis signaling pathway	0.298	0.0219	NA	2/137 (1%)	0/137 (0%)	1/137 (1%)	134/137 (98%)	BMP7,LYRM4,TFRC
B Cell Development	0.293	0.0278	NA	0/36 (0%)	0/36 (0%)	1/36 (3%)	35/36 (97%)	CD19
Complement System	0.285	0.027	NA	1/37 (3%)	0/37 (0%)	0/37 (0%)	36/37 (97%)	C5
Signaling by Rho Family GTPases	0.283	0.0205	2.236	0/244 (0%)	0/244 (0%)	5/244 (2%)	239/244 (98%)	ARHGEF2,MAP2K1,PIK3C2A,RELA,WASL
Crosstalk between Dendritic Cells and Natural Killer Cells	0.282	0.0225	NA	1/89 (1%)	0/89 (0%)	1/89 (1%)	87/89 (98%)	HLA-G,RELA
Docosahexaenoic Acid (DHA) Signaling	0.277	0.0263	NA	0/38 (0%)	0/38 (0%)	1/38 (3%)	37/38 (97%)	PIK3C2A

Type II Diabetes Mellitus Signaling	0.277	0.0211	NA	0/142 (0%)	0/142 (0%)	3/142 (2%)	139/142 (98%)	PIK3C2A,RELA,SOCS1
Altered T Cell and B Cell Signaling in Rheumatoid Arthritis	0.277	0.0222	NA	1/90 (1%)	0/90 (0%)	1/90 (1%)	88/90 (98%)	IL10,RELA
OX40 Signaling Pathway	0.277	0.0222	NA	1/90 (1%)	0/90 (0%)	1/90 (1%)	88/90 (98%)	HLA-G,RELA
Th17 Activation Pathway	0.272	0.022	NA	1/91 (1%)	0/91 (0%)	1/91 (1%)	89/91 (98%)	IL10,RELA
April Mediated Signaling	0.269	0.0256	NA	0/39 (0%)	0/39 (0%)	1/39 (3%)	38/39 (97%)	RELA
Antigen Presentation Pathway	0.269	0.0256	NA	1/39 (3%)	0/39 (0%)	0/39 (0%)	38/39 (97%)	HLA-G
Leukocyte Extravasation Signaling	0.268	0.0203	1	1/197 (1%)	0/197 (0%)	3/197 (2%)	193/197 (98%)	BTK,PIK3C2A,PTPN11,WASL
Gap Junction Signaling	0.264	0.0202	NA	0/198 (0%)	0/198 (0%)	4/198 (2%)	194/198 (98%)	ITPR1,KRAS,MAP2K1,PIK3C2A
Factors Promoting Cardiogenesis in Vertebrates	0.263	0.0215	NA	1/93 (1%)	0/93 (0%)	1/93 (1%)	91/93 (98%)	BMP7,TCF4
Role of PKR in Interferon Induction and Antiviral Response	0.255	0.0244	NA	0/41 (0%)	0/41 (0%)	1/41 (2%)	40/41 (98%)	RELA
B Cell Activating Factor Signaling	0.255	0.0244	NA	0/41 (0%)	0/41 (0%)	1/41 (2%)	40/41 (98%)	RELA
Estrogen Biosynthesis	0.255	0.0244	NA	1/41 (2%)	0/41 (0%)	0/41 (0%)	40/41 (98%)	CYP2E1
Intrinsic Prothrombin Activation Pathway	0.249	0.0238	NA	0/42 (0%)	0/42 (0%)	1/42 (2%)	41/42 (98%)	KLK3
Retinol Biosynthesis	0.249	0.0238	NA	0/42 (0%)	0/42 (0%)	1/42 (2%)	41/42 (98%)	RDH10
Relaxin Signaling	0.248	0.02	NA	0/150 (0%)	0/150 (0%)	3/150 (2%)	147/150 (98%)	MAP2K1,PIK3C2A,RELA

Role of Hypercytokinemia/hyperchemokinemia in the	0.242	0.0233	NA	0/43 (0%)	0/43 (0%)	1/43 (2%)	42/43 (98%)	CCL3
tRNA Splicing	0.242	0.0233	NA	1/43 (2%)	0/43 (0%)	0/43 (0%)	42/43 (98%)	TSEN2
UVA-Induced MAPK Signaling	0.241	0.0204	NA	0/98 (0%)	0/98 (0%)	2/98 (2%)	96/98 (98%)	KRAS,PIK3C2A
Apelin Cardiomyocyte Signaling Pathway	0.237	0.0202	NA	0/99 (0%)	0/99 (0%)	2/99 (2%)	97/99 (98%)	ITPR1,PIK3C2A
Role of RIG1-like Receptors in Antiviral Innate Immunity	0.236	0.0227	NA	0/44 (0%)	0/44 (0%)	1/44 (2%)	43/44 (98%)	RELA
iNOS Signaling	0.23	0.0222	NA	0/45 (0%)	0/45 (0%)	1/45 (2%)	44/45 (98%)	RELA
Neuropathic Pain Signaling In Dorsal Horn Neurons	0.228	0.0198	NA	0/101 (0%)	0/101 (0%)	2/101 (2%)	99/101 (98%)	ITPR1,PIK3C2A
SAPK/JNK Signaling	0.225	0.0196	NA	0/102 (0%)	0/102 (0%)	2/102 (2%)	100/102 (98%)	KRAS,PIK3C2A
Stearate Biosynthesis I (Animals)	0.223	0.0217	NA	1/46 (2%)	0/46 (0%)	0/46 (0%)	45/46 (98%)	CYP2E1
Graft-versus-Host Disease Signaling	0.213	0.0208	NA	1/48 (2%)	0/48 (0%)	0/48 (0%)	47/48 (98%)	HLA-G
Hematopoiesis from Pluripotent Stem Cells	0.207	0.0204	NA	1/49 (2%)	0/49 (0%)	0/49 (0%)	48/49 (98%)	IL10
Axonal Guidance Signaling	0	0.0165	NA	1/485 (0%)	0/485 (0%)	7/485 (1%)	477/485 (98%)	BMP7,DPYSL2,HERC2,KRAS,MAP2K1,PIK3C2A,PTPN11,WASL
Amyotrophic Lateral Sclerosis Signaling	0	0.0103	NA	0/97 (0%)	0/97 (0%)	1/97 (1%)	96/97 (99%)	PIK3C2A
LPS/IL-1 Mediated Inhibition of RXR Function	0	0.00446	NA	0/224 (0%)	0/224 (0%)	1/224 (0%)	223/224 (100%)	XPO1
Hepatic Cholestasis	0	0.0109	NA	1/184 (1%)	0/184 (0%)	1/184 (1%)	182/184 (99%)	RELA,TNFSF14

LXR/RXR Activation	0	0.0165	NA	1/121 (1%)	0/121 (0%)	1/121 (1%)	119/121 (98%)	FDFT1,RELA
VDR/RXR Activation	0	0.0128	NA	1/78 (1%)	0/78 (0%)	0/78 (0%)	77/78 (99%)	CAMP
Regulation of Actin-based Motility by Rho	0	0.0106	NA	0/94 (0%)	0/94 (0%)	1/94 (1%)	93/94 (99%)	WASL
Fcγ Receptor-mediated Phagocytosis in Macrophages and	0	0.0106	NA	0/94 (0%)	0/94 (0%)	1/94 (1%)	93/94 (99%)	CBL
CCR5 Signaling in Macrophages	0	0.0106	NA	0/94 (0%)	0/94 (0%)	1/94 (1%)	93/94 (99%)	CCL3
Calcium-induced T Lymphocyte Apoptosis	0	0.0152	NA	0/66 (0%)	0/66 (0%)	1/66 (2%)	65/66 (98%)	ITPR1
Induction of Apoptosis by HIV1	0	0.0164	NA	0/61 (0%)	0/61 (0%)	1/61 (2%)	60/61 (98%)	RELA
T Helper Cell Differentiation	0	0.0137	NA	1/73 (1%)	0/73 (0%)	0/73 (0%)	72/73 (99%)	IL10
Role of Cytokines in Mediating Communication between Immune Cells	0	0.0185	NA	1/54 (2%)	0/54 (0%)	0/54 (0%)	53/54 (98%)	IL10
HIF1α Signaling	0	0.0177	NA	0/113 (0%)	0/113 (0%)	2/113 (2%)	111/113 (98%)	KRAS,PIK3C2A
Agrin Interactions at Neuromuscular Junction	0	0.0127	NA	0/79 (0%)	0/79 (0%)	1/79 (1%)	78/79 (99%)	KRAS
Semaphorin Signaling in Neurons	0	0.0167	NA	0/60 (0%)	0/60 (0%)	1/60 (2%)	59/60 (98%)	DPYSL2
G Beta Gamma Signaling	0	0.0164	NA	1/122 (1%)	0/122 (0%)	1/122 (1%)	120/122 (98%)	BTK,KRAS
Sphingosine-1-phosphate Signaling	0	0.00855	NA	0/117 (0%)	0/117 (0%)	1/117 (1%)	116/117 (99%)	PIK3C2A
Cdc42 Signaling	0	0.012	NA	1/167 (1%)	0/167 (0%)	1/167 (1%)	165/167 (99%)	HLA-G,WASL

IL-1 Signaling	0	0.011	NA	0/91 (0%)	0/91 (0%)	1/91 (1%)	90/91 (99%)	RELA
Role of Wnt/GSK-3β Signaling in the Pathogenesis of Influenza	0	0.0128	NA	0/78 (0%)	0/78 (0%)	1/78 (1%)	77/78 (99%)	TCF4
Nur77 Signaling in T Lymphocytes	0	0.0169	NA	0/59 (0%)	0/59 (0%)	1/59 (2%)	58/59 (98%)	SIN3A
PKCθ Signaling in T Lymphocytes	0	0.0194	NA	0/155 (0%)	0/155 (0%)	3/155 (2%)	152/155 (98%)	KRAS,PIK3C2A,RELA
Paxillin Signaling	0	0.0185	NA	0/108 (0%)	0/108 (0%)	2/108 (2%)	106/108 (98%)	KRAS,PIK3C2A
RhoGDI Signaling	0	0.0111	NA	0/180 (0%)	0/180 (0%)	2/180 (1%)	178/180 (99%)	ARHGEF2,WASL
Sertoli Cell-Sertoli Cell Junction Signaling	0	0.0162	NA	0/185 (0%)	0/185 (0%)	3/185 (2%)	182/185 (98%)	CLINT1,KRAS,MAP2K1
eNOS Signaling	0	0.0189	NA	1/159 (1%)	0/159 (0%)	2/159 (1%)	156/159 (98%)	AQP12A/AQP12B,ITPR1,PIK3C2A
Ephrin B Signaling	0	0.0139	NA	0/72 (0%)	0/72 (0%)	1/72 (1%)	71/72 (99%)	CBL
Nicotine Degradation III	0	0.0179	NA	1/56 (2%)	0/56 (0%)	0/56 (0%)	55/56 (98%)	CYP2E1
Melatonin Degradation I	0	0.0167	NA	1/60 (2%)	0/60 (0%)	0/60 (0%)	59/60 (98%)	CYP2E1
Nicotine Degradation II	0	0.0154	NA	1/65 (2%)	0/65 (0%)	0/65 (0%)	64/65 (98%)	CYP2E1
Superpathway of Melatonin Degradation	0	0.0154	NA	1/65 (2%)	0/65 (0%)	0/65 (0%)	64/65 (98%)	CYP2E1
Gαi Signaling	0	0.008	NA	0/125 (0%)	0/125 (0%)	1/125 (1%)	124/125 (99%)	KRAS
HIPPO signaling	0	0.0118	NA	0/85 (0%)	0/85 (0%)	1/85 (1%)	84/85 (99%)	PPP2R1A

Cardiac β-adrenergic Signaling	0	0.0142	NA	0/141 (0%)	0/141 (0%)	2/141 (1%)	139/141 (99%)	AKAP17A,PPP2R1A
Wnt/β-catenin Signaling	0	0.0173	NA	1/173 (1%)	0/173 (0%)	2/173 (1%)	170/173 (98%)	MYC,PPP2R1A,TCF4
Death Receptor Signaling	0	0.011	NA	0/91 (0%)	0/91 (0%)	1/91 (1%)	90/91 (99%)	RELA
Dopamine Receptor Signaling	0	0.013	NA	0/77 (0%)	0/77 (0%)	1/77 (1%)	76/77 (99%)	PPP2R1A
cAMP-mediated signaling	0	0.0175	NA	1/228 (0%)	0/228 (0%)	3/228 (1%)	224/228 (98%)	AKAP17A,ATF4,CREB5,MAP2K1
GPCR-Mediated Integration of Enteroendocrine Signaling Exemplified by	0	0.0137	NA	0/73 (0%)	0/73 (0%)	1/73 (1%)	72/73 (99%)	ITPR1
GPCR-Mediated Nutrient Sensing in Enteroendocrine Cells	0	0.00893	NA	0/112 (0%)	0/112 (0%)	1/112 (1%)	111/112 (99%)	ITPR1
Gustation Pathway	0	0.00649	NA	0/154 (0%)	0/154 (0%)	1/154 (1%)	153/154 (99%)	ITPR1
Phagosome Formation	0	0.008	NA	0/125 (0%)	0/125 (0%)	1/125 (1%)	124/125 (99%)	PIK3C2A
Phagosome Maturation	0	0.0132	NA	1/151 (1%)	0/151 (0%)	1/151 (1%)	149/151 (99%)	CTSD,VTI1B
Autophagy	0	0.0164	NA	0/61 (0%)	0/61 (0%)	1/61 (2%)	60/61 (98%)	CTSD
Th1 and Th2 Activation Pathway	0	0.0175	NA	1/171 (1%)	0/171 (0%)	2/171 (1%)	168/171 (98%)	IL10,PIK3C2A,SOCS1
Th2 Pathway	0	0.0147	NA	1/136 (1%)	0/136 (0%)	1/136 (1%)	134/136 (99%)	IL10,PIK3C2A
SPINK1 Pancreatic Cancer Pathway	0	0.0167	NA	0/60 (0%)	0/60 (0%)	1/60 (2%)	59/60 (98%)	KLK3
Endocannabinoid Neuronal Synapse Pathway	0	0.00781	NA	0/128 (0%)	0/128 (0%)	1/128 (1%)	127/128 (99%)	ITPR1

Table S2 IPA aggregates used for Figure 3c heatmaps

All Pathways	Annotation
Systemic Lupus Erythematosus Signaling	Systemic Lupus Erythematosus Sign.
NF-KB Signaling	NF/KB Sign.
JAK/Stat Signaling	JAK/STAT-IFN Sign.
Role of JAK1, JAK2 and TYK2 in Interferon Signaling	JAK/STAT-IFN Sign.
Crosstalk between Dendritic Cells and Natural Killer Cells	DC Maturation and Crosstolk Adaptive/Innate
Dendritic Cell Maturation	DC Maturation and Crosstolk Adaptive/Innate
Communication between Innate and Adaptive Immune Cells	DC Maturation and Crosstolk Adaptive/Innate
CD40 Signaling	CD40 Sign.
B Cell Receptor Signaling	B Cell Sign.
Systemic Lupus Erythematosus In B Cell Signaling Pathway	B Cell Sign.
PI3K Signaling in B Lymphocytes	B Cell Sign.