

Figure S1

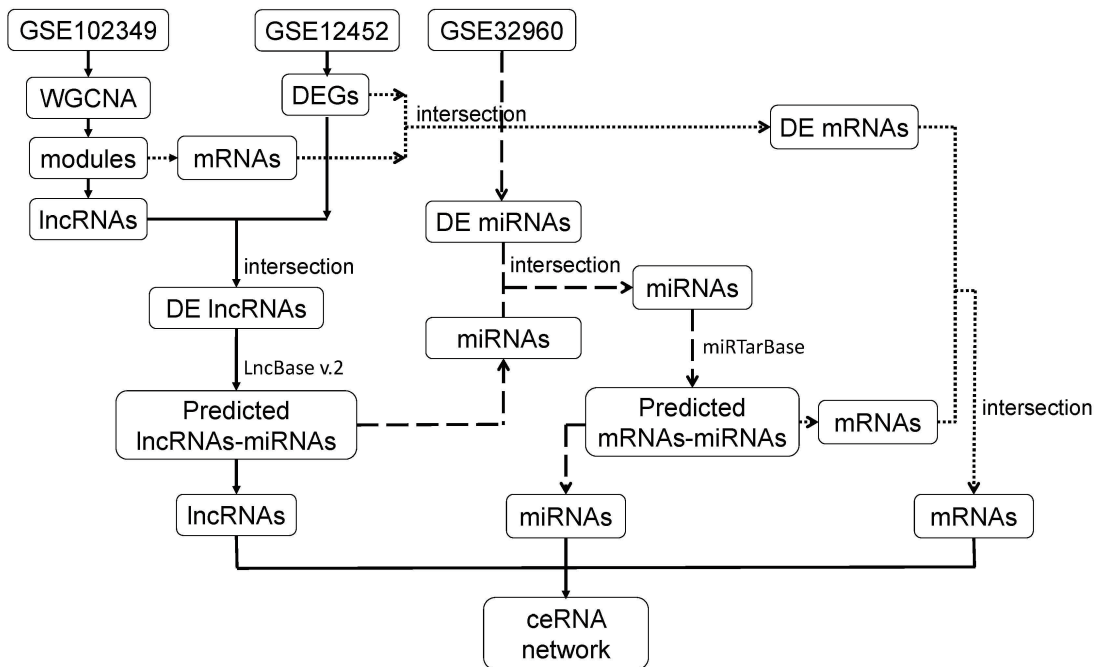


Figure S3

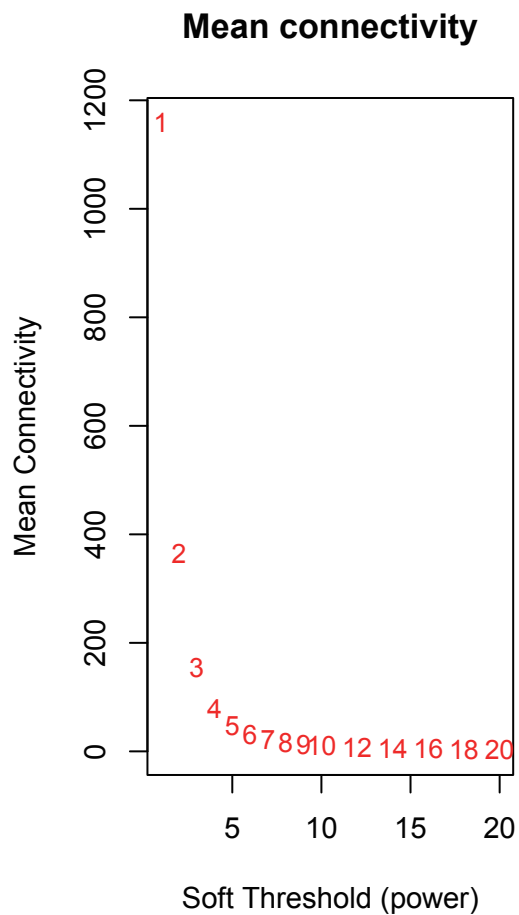
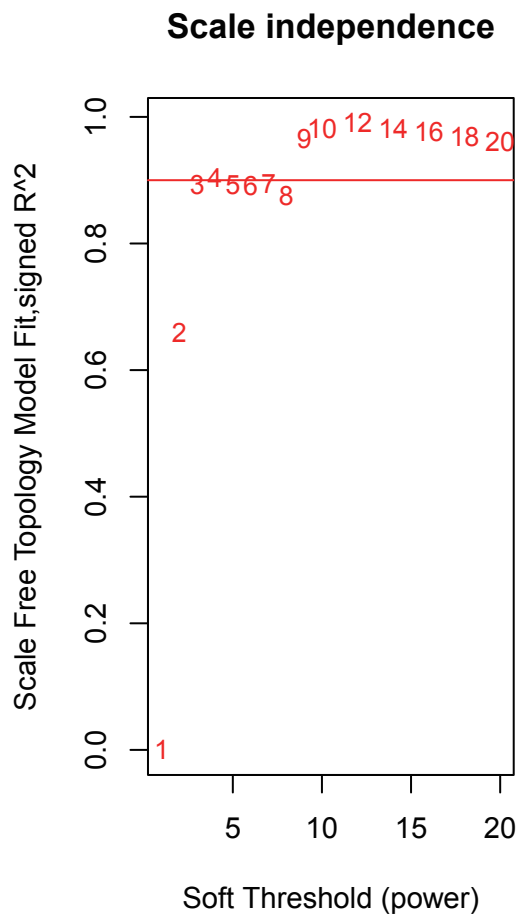
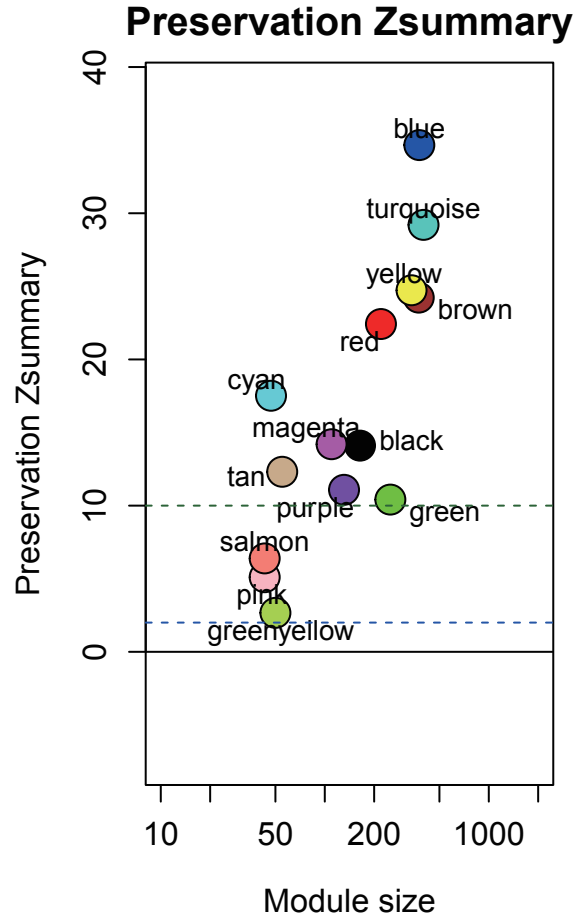
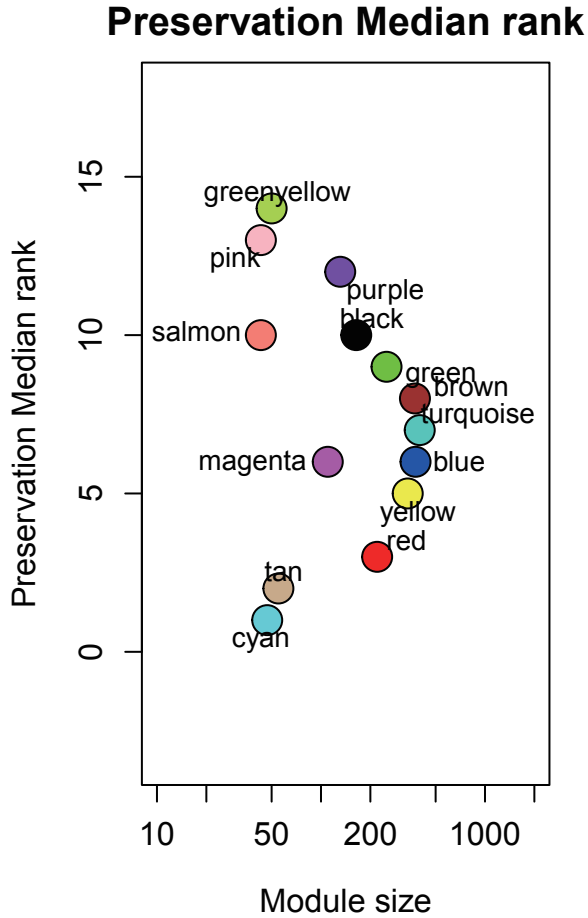


Figure S4



DEmiRNAs in the ceRNA network

Symbol	logFC	AveExpr	t	P. Value	adj. P. Val	B	group	type
hsa-miR-125a-5p	-1.859889215	10.34313524	-14.46967381	3.63E-37	6.66E-35	73.71851782	downregulate	miRNA
hsa-miR-140-3p	-1.278153043	9.233931313	-11.76881169	5.60E-27	3.67E-25	50.47093093	downregulate	miRNA
hsa-miR-140-5p	-0.679776875	8.61002063	-8.87942616	4.22E-17	8.60E-16	27.99496683	downregulate	miRNA
hsa-miR-142-3p	-3.310699599	9.570592987	-16.95503002	6.11E-47	1.87E-44	96.03669615	downregulate	miRNA
hsa-miR-142-5p	-1.395608336	8.928458681	-11.81431373	3.83E-27	2.70E-25	50.84849332	downregulate	miRNA
hsa-miR-146b-5p	-0.86037352	9.433394673	-5.859195665	1.12E-08	8.12E-08	8.982019323	downregulate	miRNA
hsa-miR-28-5p	-0.557666756	8.665958377	-6.903641834	2.57E-11	2.43E-10	14.90795275	downregulate	miRNA
hsa-miR-342-3p	-1.479852746	9.262921776	-13.07559494	7.95E-32	6.63E-30	61.528846	downregulate	miRNA
hsa-miR-34c-5p	-1.443074117	8.85615501	-9.59741277	2.02E-19	5.15E-18	33.26331809	downregulate	miRNA
hsa-miR-361-3p	-0.640823507	10.13378732	-3.990416058	8.11E-05	3.38E-04	0.434521413	downregulate	miRNA
hsa-miR-361-5p	-0.717123599	8.908437512	-8.203011735	5.14E-15	7.61E-14	23.26550627	downregulate	miRNA
hsa-miR-421	-1.122229324	9.411207315	-8.098008649	1.06E-14	1.50E-13	22.55328205	downregulate	miRNA
hsa-miR-449a	-0.75204128	8.886929824	-7.840224353	6.12E-14	7.60E-13	20.83106808	downregulate	miRNA
hsa-miR-564	-0.75543993	9.61438955	-3.91195101	1.11E-04	4.40E-04	0.138770045	downregulate	miRNA
hsa-miR-574-5p	0.860834024	12.74338187	5.734293032	2.20E-08	1.54E-07	8.325333022	upregulated	miRNA

DEmRNAs in the ceRNA network

Symbol	logFC	AveExpr	t	P. Value	adj. P. Val	B	group	moduleColor
MYC	1.221070851	8.808032021	3.785372339	4.84E-04	0.004306487	-0.540282105	upregulated	salmon
NPM1	0.640885388	12.04801949	4.542466409	4.68E-05	7.02E-04	1.693775438	upregulated	salmon
CDK4	1.439838722	9.85770533	6.647218013	4.79E-08	2.45E-06	8.37858912	upregulated	turquoise
ATL2	0.874078369	7.014891468	3.761027835	5.21E-04	0.00455857	-0.609156039	upregulated	turquoise
NOP2	0.669241973	9.167533038	4.015685613	2.41E-04	0.002524064	0.121431036	upregulated	turquoise
XPOT	1.243547995	9.798126402	6.839642198	2.54E-08	1.48E-06	8.996837804	upregulated	turquoise
KIAA1549L	0.536931105	6.800755122	3.213792126	0.002527051	0.015595936	-2.09470596	upregulated	turquoise
UCK2	0.682872613	7.483707611	4.807357198	2.01E-05	3.59E-04	2.508943829	upregulated	turquoise
TFRC	0.520498319	7.554836097	5.965970222	4.54E-07	1.56E-05	6.185475301	upregulated	turquoise
TPI1	0.721345846	9.646985336	4.283292689	1.06E-04	0.001333046	0.911027683	upregulated	turquoise
GGCT	1.085088371	10.94257157	5.610064818	1.47E-06	4.27E-05	5.043618731	upregulated	turquoise
FERMT1	0.996010276	8.279014772	5.772781789	8.59E-07	2.73E-05	5.564887767	upregulated	turquoise
LAMB1	2.315728145	7.256558426	7.317460385	5.31E-09	4.07E-07	10.52459798	upregulated	turquoise
UNG	1.022193356	8.226059252	5.757386979	9.04E-07	2.84E-05	5.515505422	upregulated	turquoise
TMTC3	0.718289391	8.060036576	3.054976896	0.003911756	0.021723813	-2.500423884	upregulated	turquoise
TWSG1	0.99847215	7.561078418	3.821466852	4.35E-04	0.003961936	-0.437774991	upregulated	turquoise
FJX1	1.505847335	7.520104665	5.767304365	8.75E-07	2.76E-05	5.547316295	upregulated	turquoise
IFNG	1.163718662	6.996755616	4.618357219	3.68E-05	5.75E-04	1.925887284	upregulated	turquoise
ZNRF3	1.477360629	7.193780095	5.56070606	1.73E-06	4.85E-05	4.885832662	upregulated	turquoise
LAMC1	0.658408205	8.78349495	4.216674176	1.30E-04	0.001562873	0.712563907	upregulated	turquoise
GLCE	0.840745114	7.592239922	2.665670541	0.010879997	0.046720791	-3.43789224	upregulated	turquoise
FZD7	1.46644514	7.286328522	4.19511826	1.39E-04	0.001650514	0.64860572	upregulated	turquoise
ECT2	0.719969628	6.881106107	5.328127671	3.71E-06	9.13E-05	4.145017172	upregulated	turquoise
PHB2	0.684971543	10.86247757	3.272978957	0.002141595	0.013713934	-1.94034929	upregulated	turquoise
TM7SF3	1.138785743	8.636023627	4.240006555	1.21E-04	0.00148122	0.78193723	upregulated	turquoise
BLMH	0.713112045	8.075104735	4.112979338	1.79E-04	0.001995607	0.406098924	upregulated	turquoise
PTPN14	0.644201499	7.204456877	3.05289499	0.003933944	0.021818582	-2.505657764	upregulated	turquoise
AHCY	0.921096337	9.344512483	4.441215093	6.44E-05	9.00E-04	1.386069753	upregulated	turquoise
VANGL2	0.986451529	7.520729116	4.208124298	1.34E-04	0.001599242	0.68718029	upregulated	turquoise
ZNF738	0.739737575	6.845256784	2.657180062	0.011116338	0.047470734	-3.457362522	upregulated	turquoise
CPS1	0.609868409	5.540628317	2.666567083	0.010855313	0.046691334	-3.435833744	upregulated	turquoise
FNDC3B	0.756511446	7.430682517	4.836731582	1.83E-05	3.32E-04	2.600153151	upregulated	turquoise

SOX4	0.735307863	7.942177378	4.031773313	2.30E-04	0.002429249	0.168301442	upregulated	turquoise
IGF2BP3	0.941337942	6.459476325	3.357402424	0.001687227	0.011419083	-1.717348556	upregulated	turquoise
JAK2	0.774128797	7.099387187	3.128669031	0.003198139	0.018692305	-2.313733639	upregulated	turquoise
LDHA	1.020697726	12.39917782	5.63603087	1.35E-06	3.99E-05	5.126692764	upregulated	turquoise
LMNB2	0.969277056	7.946167817	5.464283149	2.37E-06	6.30E-05	4.578130301	upregulated	turquoise
FKBP5	0.618867401	8.04032831	5.24889518	4.80E-06	1.13E-04	3.89383255	upregulated	turquoise
PAX5	-0.948595788	7.2846298	-4.453384231	6.20E-05	8.77E-04	1.422927947	downregulate	turquoise
PRKCB	-0.547731869	7.003481117	-3.150808437	0.003008991	0.017865988	-2.257110854	downregulate	turquoise

Enriched GO terms and KEGG pathways for the genes in the ceRNA network

ONTOLOGY	ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
BP	GO:0006913	nucleocytoplasmic transport	8/39	357/18493	6.51E-07	0.000550687	0.00036991	NPM1/XPOT/FERMT1/IFNG/ECT2/PHB2/PTPN14/JAK2	8
BP	GO:0051169	nuclear transport	8/39	360/18493	6.93E-07	0.000550687	0.00036991	NPM1/XPOT/FERMT1/IFNG/ECT2/PHB2/PTPN14/JAK2	8
BP	GO:0046822	regulation of nucleocytoplasmic transport	5/39	112/18493	3.64E-06	0.001927288	0.001294605	FERMT1/IFNG/ECT2/PTPN14/JAK2	5
BP	GO:0042306	regulation of protein import into nucleus	4/39	64/18493	9.80E-06	0.003738317	0.002511115	FERMT1/IFNG/ECT2/JAK2	4
BP	GO:1904589	regulation of protein import	4/39	67/18493	1.18E-05	0.003738317	0.002511115	FERMT1/IFNG/ECT2/JAK2	4
BP	GO:0006606	protein import into nucleus	5/39	157/18493	1.89E-05	0.004997154	0.003356705	FERMT1/IFNG/ECT2/PHB2/JAK2	5
BP	GO:0051170	import into nucleus	5/39	178/18493	3.45E-05	0.007829094	0.005258986	FERMT1/IFNG/ECT2/PHB2/JAK2	5
BP	GO:0000060	protein import into nucleus, translocation	3/39	38/18493	6.95E-05	0.012775392	0.008581529	IFNG/PHB2/JAK2	3
BP	GO:2000027	regulation of organ morphogenesis	5/39	208/18493	7.24E-05	0.012775392	0.008581529	MYC/ZNRF3/FZD7/PHB2/VANGL2	5
BP	GO:0017038	protein import	5/39	214/18493	8.28E-05	0.01281893	0.008610775	FERMT1/IFNG/ECT2/PHB2/JAK2	5
BP	GO:0042307	positive regulation of protein import into nucleus	3/39	42/18493	9.40E-05	0.01281893	0.008610775	IFNG/ECT2/JAK2	3
BP	GO:0000096	sulfur amino acid metabolic process	3/39	44/18493	0.000108175	0.01281893	0.008610775	BLMH/AHCY/CPS1	3
BP	GO:1904591	positive regulation of protein import	3/39	44/18493	0.000108175	0.01281893	0.008610775	IFNG/ECT2/JAK2	3
BP	GO:1900180	regulation of protein localization to nucleus	4/39	121/18493	0.00012015	0.01281893	0.008610775	FERMT1/IFNG/ECT2/JAK2	4
BP	GO:0033157	regulation of intracellular protein transport	5/39	232/18493	0.000121009	0.01281893	0.008610775	FERMT1/IFNG/ECT2/PTPN14/JAK2	5
BP	GO:1905330	regulation of morphogenesis of an epithelium	4/39	134/18493	0.000178072	0.01688805	0.011344097	ZNRF3/FZD7/PHB2/VANGL2	4
BP	GO:0051222	positive regulation of protein transport	6/39	402/18493	0.000180678	0.01688805	0.011344097	FERMT1/IFNG/ECT2/TM7SF3/SOX4/JAK2	6
BP	GO:0050673	epithelial cell proliferation	6/39	420/18493	0.000228936	0.019151203	0.012864311	MYC/FERMT1/LAMB1/LAMC1/FZD7/PHB2	6
BP	GO:0032386	regulation of intracellular transport	6/39	422/18493	0.000234871	0.019151203	0.012864311	FERMT1/IFNG/ECT2/PTPN14/JAK2/PRKCB	6
BP	GO:0034504	protein localization to nucleus	5/39	269/18493	0.000241047	0.019151203	0.012864311	FERMT1/IFNG/ECT2/PHB2/JAK2	5
BP	GO:0033160	positive regulation of protein import into nucleus, translocation	2/39	12/18493	0.000282232	0.020466883	0.013748084	IFNG/JAK2	2
BP	GO:1904951	positive regulation of establishment of protein localization	6/39	437/18493	0.000283368	0.020466883	0.013748084	FERMT1/IFNG/ECT2/TM7SF3/SOX4/JAK2	6
BP	GO:0060071	Wnt signaling pathway, planar cell polarity pathway	3/39	63/18493	0.000315495	0.021170514	0.014220729	ZNRF3/FZD7/VANGL2	3
BP	GO:0090068	positive regulation of cell cycle process	5/39	286/18493	0.000319756	0.021170514	0.014220729	NPM1/CDK4/ECT2/PHB2/SOX4	5
BP	GO:0090175	regulation of establishment of planar polarity	3/39	65/18493	0.000346019	0.021992943	0.014773174	ZNRF3/FZD7/VANGL2	3
BP	GO:0046824	positive regulation of nucleocytoplasmic transport	3/39	67/18493	0.000378384	0.022840552	0.015342532	IFNG/ECT2/JAK2	3
BP	GO:0050667	homocysteine metabolic process	2/39	14/18493	0.000388103	0.022840552	0.015342532	BLMH/CPS1	2
BP	GO:0032024	positive regulation of insulin secretion	3/39	70/18493	0.000430487	0.024051191	0.016155747	TM7SF3/SOX4/JAK2	3
BP	GO:0050796	regulation of insulin secretion	4/39	172/18493	0.000461019	0.024051191	0.016155747	IFNG/TM7SF3/SOX4/JAK2	4
BP	GO:0002009	morphogenesis of an epithelium	6/39	479/18493	0.00046207	0.024051191	0.016155747	MYC/ZNRF3/FZD7/PHB2/VANGL2/SOX4	6
BP	GO:0030111	regulation of Wnt signaling pathway	5/39	311/18493	0.000469218	0.024051191	0.016155747	FERMT1/ZNRF3/FZD7/VANGL2/SOX4	5
BP	GO:0033158	regulation of protein import into nucleus, translocation	2/39	16/18493	0.000510421	0.025345602	0.017025233	IFNG/JAK2	2
BP	GO:0007369	gastrulation	4/39	181/18493	0.000558702	0.025666543	0.017240816	LAMB1/TWEG1/FZD7/VANGL2	4
BP	GO:0046209	nitric oxide metabolic process	3/39	77/18493	0.000569435	0.025666543	0.017240816	IFNG/CPS1/JAK2	3
BP	GO:1900182	positive regulation of protein localization to nucleus	3/39	78/18493	0.000591351	0.025666543	0.017240816	IFNG/ECT2/JAK2	3
BP	GO:0034404	nucleobase-containing small molecule biosynthetic process	4/39	184/18493	0.000594303	0.025666543	0.017240816	UCK2/TPI1/UNG/LDHA	4
BP	GO:0001736	establishment of planar polarity	3/39	79/18493	0.0006138	0.025666543	0.017240816	ZNRF3/FZD7/VANGL2	3
BP	GO:0007164	establishment of tissue polarity	3/39	79/18493	0.0006138	0.025666543	0.017240816	ZNRF3/FZD7/VANGL2	3
BP	GO:2001057	reactive nitrogen species metabolic process	3/39	80/18493	0.000636787	0.025945001	0.017427863	IFNG/CPS1/JAK2	3
BP	GO:0031589	cell-substrate adhesion	5/39	338/18493	0.000684388	0.027187326	0.018262362	FERMT1/LAMB1/LAMC1/FZD7/JAK2	5
BP	GO:0034446	substrate adhesion-dependent cell spreading	3/39	87/18493	0.000813199	0.030994021	0.020819408	LAMB1/LAMC1/FZD7	3
BP	GO:0030073	insulin secretion	4/39	203/18493	0.000858236	0.030994021	0.020819408	IFNG/TM7SF3/SOX4/JAK2	4
BP	GO:0050679	positive regulation of epithelial cell proliferation	4/39	203/18493	0.000858236	0.030994021	0.020819408	MYC/LAMB1/LAMC1/FZD7	4
BP	GO:0090276	regulation of peptide hormone secretion	4/39	203/18493	0.000858236	0.030994021	0.020819408	IFNG/TM7SF3/SOX4/JAK2	4
BP	GO:0006790	sulfur compound metabolic process	5/39	362/18493	0.000931411	0.032889169	0.022092423	GGCT/GLCE/BLMH/AHCY/CPS1	5
BP	GO:0090277	positive regulation of peptide hormone secretion	3/39	93/18493	0.000986923	0.033699295	0.022636604	TM7SF3/SOX4/JAK2	3
BP	GO:0050678	regulation of epithelial cell proliferation	5/39	368/18493	0.001002398	0.033699295	0.022636604	MYC/LAMB1/LAMC1/FZD7/PHB2	5

BP	GO:0060993	kidney morphogenesis	3/39	94/18493	0.001017977	0.033699295	0.022636604	MYC/VANGL2/SOX4	3
BP	GO:0001738	morphogenesis of a polarized epithelium	3/39	95/18493	0.001049645	0.033832187	0.022725871	ZNRF3/FZD7/VANGL2	3
BP	GO:1903532	positive regulation of secretion by cell	5/39	373/18493	0.001064575	0.033832187	0.022725871	FERMT1/IFNG/TM7SF3/SOX4/JAK2	5
BP	GO:0048103	somatic stem cell division	2/39	24/18493	0.001161526	0.034947931	0.023475342	FZD7/VANGL2	2
BP	GO:0050855	regulation of B cell receptor signaling pathway	2/39	24/18493	0.001161526	0.034947931	0.023475342	PAX5/PRKCB	2
BP	GO:1901989	positive regulation of cell cycle phase transition	3/39	100/18493	0.001217343	0.034947931	0.023475342	NPM1/CDK4/PHB2	3
BP	GO:0072527	pyrimidine-containing compound metabolic process	3/39	101/18493	0.001252787	0.034947931	0.023475342	UCK2/UNG/CPS1	3
BP	GO:0015012	heparan sulfate proteoglycan biosynthetic process	2/39	25/18493	0.001260849	0.034947931	0.023475342	GLCE/VANGL2	2
BP	GO:0060330	regulation of response to interferon-gamma	2/39	25/18493	0.001260849	0.034947931	0.023475342	IFNG/JAK2	2
BP	GO:0060334	regulation of interferon-gamma-mediated signaling pathway	2/39	25/18493	0.001260849	0.034947931	0.023475342	IFNG/JAK2	2
BP	GO:0035567	non-canonical Wnt signaling pathway	3/39	102/18493	0.001288876	0.034947931	0.023475342	ZNRF3/FZD7/VANGL2	3
BP	GO:0045787	positive regulation of cell cycle	5/39	390/18493	0.001297626	0.034947931	0.023475342	NPM1/CDK4/ECT2/PHB2/SOX4	5
BP	GO:0045830	positive regulation of isotype switching	2/39	27/18493	0.001471272	0.038664814	0.025972059	TFRC/UNG	2
BP	GO:0060828	regulation of canonical Wnt signaling pathway	4/39	236/18493	0.001497839	0.038664814	0.025972059	FERMT1/ZNRF3/FZD7/SOX4	4
BP	GO:0051047	positive regulation of secretion	5/39	404/18493	0.001516363	0.038664814	0.025972059	FERMT1/IFNG/TM7SF3/SOX4/JAK2	5
BP	GO:0030099	myeloid cell differentiation	5/39	405/18493	0.001532966	0.038664814	0.025972059	MYC/TFRC/IFNG/JAK2/PRKCB	5
BP	GO:0007050	cell cycle arrest	4/39	241/18493	0.001617493	0.040159326	0.026975958	MYC/CDK4/IFNG/SOX4	4
BP	GO:0030072	peptide hormone secretion	4/39	244/18493	0.001692402	0.041372725	0.027791026	IFNG/TM7SF3/SOX4/JAK2	4
BP	GO:0050714	positive regulation of protein secretion	4/39	246/18493	0.001743665	0.041980045	0.028198977	FERMT1/TM7SF3/SOX4/JAK2	4
BP	GO:0030201	heparan sulfate proteoglycan metabolic process	2/39	31/18493	0.001938776	0.045081409	0.030282235	GLCE/VANGL2	2
BP	GO:1902751	positive regulation of cell cycle G2/M phase transition	2/39	31/18493	0.001938776	0.045081409	0.030282235	NPM1/CDK4	2
BP	GO:0001704	formation of primary germ layer	3/39	118/18493	0.001957594	0.045081409	0.030282235	LAMB1/TWSG1/FZD7	3
BP	GO:0051091	positive regulation of DNA binding transcription factor activity	4/39	255/18493	0.001987783	0.045122679	0.030309958	NPM1/PHB2/JAK2/PRKCB	4
BP	GO:0045727	positive regulation of translation	3/39	120/18493	0.002053743	0.045963349	0.030874655	NPM1/CDK4/SOX4	3
BP	GO:0050708	regulation of protein secretion	5/39	438/18493	0.002160125	0.047084881	0.031628015	FERMT1/IFNG/TM7SF3/SOX4/JAK2	5
BP	GO:0046883	regulation of hormone secretion	4/39	261/18493	0.002163119	0.047084881	0.031628015	IFNG/TM7SF3/SOX4/JAK2	4
BP	GO:0002793	positive regulation of peptide secretion	4/39	265/18493	0.00228579	0.049082708	0.032970002	FERMT1/TM7SF3/SOX4/JAK2	4
BP	GO:0010922	positive regulation of phosphatase activity	2/39	34/18493	0.002329727	0.049359158	0.0331557	IFNG/JAK2	2
CC	GO:0034399	nuclear periphery	4/42	134/19659	0.000188963	0.01757358	0.015713784	XPOT/PHB2/JAK2/LMNB2	4
MF	GO:0043024	ribosomal small subunit binding	2/38	16/17632	0.000532491	0.047309582	0.038063358	NPM1/UNG	2
MF	GO:0035173	histone kinase activity	2/38	17/17632	0.00060267	0.047309582	0.038063358	JAK2/PRKCB	2

Gene set enrichment analysis (GSEA) for ZNF667-AS1 using GSE102349

ID	setSize	enrichmentScore	NES	pvalue	p.adjust	qvalues	rank	leading edge	core enrichment
KEGG_CYTOKINE_CYTOKINE_REC EPTOR_INTERACTION	260	0.612102228	1.9795786	0.001067236	0.011027659	0.007341315	3261	tags=41%, list=13%, signal=36%	CCL21/CCL14/CXCL14/TNFRSF13B/CXCR5/CCL19/CXCL12/TGFBR2/TNFRSF17/CCR7/P DGFRB/TNFRSF13C/IL1R1/CCR6/CD27/CXCL13/IL18/CCL28/TNFSF12/TNFSF13B/CCL 24/CD40LG/TGFB3/IL10RA/TNFSF8/IL7R/LTB/CCR2/CXCL9/TNFSF11/CXCR3/LTA/PL EKH02/CCL11/IL21R/CSF1R/IL2RB/IL3RA/TGFB1/TNFSF13/CCR4/IL6R/IL12RB1/CX CR6/TNFRSF1B/VEGFC/ACVRL1/FLT3/CSF2RA/FLT3LG/CCL15/CCL18/TNFSF14/CSF3R /LEPR/CCR5/CCL4L2/CCR1/CCL13/IL2RG/IFNLR1/IL5RA/CLCF1/IL9R/KDR/FLT4/IL 2RA/XCL2/IFNAR2/PDGFC/CXCR4/INHBB/CXCR2/XCR1/CCL2/CXCL16/TNFRSF6B/TNFR SF19/TNFRSF10D/CSF2RB/TNFRSF10C/IL6ST/CCL22/CXCL11/CCL3L1/IL4R/CCL26/I L18RAP/IFNAR1/IL18R1/CCL23/CCL3L3/TNFRSF14/TNFRSF25/CCL5/FASLG/IL21/HG F/PDGFB/PDGFR/TNFRSF18/IL10RB/CX3CR1/TGFBR1/CCL17/CNTF
KEGG_OLFACTORY_TRANSDUCTIO N	249	0.478581809	1.542215299	0.001072961	0.011027659	0.007341315	3729	tags=4%, list=15%, signal=4%	PRKACB/CALM1/CLCA4/ARRB2/CLCA2/CNGA4/PRKG1/GNAL/CAMK2D/GUCA1A/OR52N4
KEGG_CHEMOKINE_SIGNALING_P ATHWAY	184	0.639644324	2.016701669	0.001114827	0.011027659	0.007341315	3240	tags=43%, list=13%, signal=38%	CCL21/CCL14/CXCL14/RASGRP2/CXCR5/CCL19/CXCL12/CCR7/PRKCB/NCF1/CCR6/CXC L13/CCL28/WAS/CCL24/PLCB2/GNG11/PREX1/GNG7/PIK3CD/ITK/CCR2/FGR/VAV1/CX CL9/ADCY7/PIK3CG/ELM01/GNB4/PRKACB/LYN/CXCR3/DOCK2/PIK3R5/CCL11/ADCY4/ CCR4/CXCR6/ARRB2/CSK/GNA12/GRK5/PTK2B/CCL15/SHC2/CCL18/GNG2/STAT5B/PRK CD/RAC2/CCR5/CCL4L2/CCR1/CCL13/GNGT2/MAPK3/RAP1A/STAT1/XCL2/CXCR4/GRK6 /CXCR2/XCR1/CCL2/CXCL16/PIK3R1/CCL22/CXCL11/CCL3L1/SOS2/VAV3/CCL26/CCL 23/CCL3L3/CCL5/GNG10/ROCK1/RHOA/CX3CR1/CCL17
KEGG_CALCIUM_SIGNALING_PAT HWAY	176	0.504091104	1.588369872	0.001119821	0.011027659	0.007341315	3465	tags=30%, list=14%, signal=26%	ATP2A3/PLCG2/PDGFRB/PRKCB/P2RX5/CD38/MYLK/PLCB2/GNA14/F2R/CYSLTR1/ADCY 7/EDNRA/PRKACB/ADCY4/CALM1/EDNRB/PPP3CC/P2RX1/BST1/ITPR2/PTK2B/PLCD1/P TGER3/PTAFR/ITPR1/NOS3/P2RX7/SLC8A1/PTGFR/PLCE1/GNAL/SPHK1/CAMK2D/PDE1 B/HRH1/OXTR/PRKCA/TNNC1/CACNA1C/CAMK4/NOS2/ADORA2A/TRPC1/GNAQ/PDGFR/T NNC2/PDE1A/LTB4R2/TBXA2R/PPP3CA/ADRB2/CACNA1H
KEGG_NATURAL_KILLER_CELL_M EDIATED_CYTOTOXICITY	132	0.601581433	1.839628229	0.001176471	0.011027659	0.007341315	3760	tags=43%, list=15%, signal=37%	CD48/PLCG2/PRKCB/NCR3/ITGAL/KLRK1/ITGB2/HGST/PIK3CD/VAV1/PTPN6/LCK/CD2 47/PIK3CG/LAT/HLA-E/SH2D1A/FYN/PIK3R5/ZAP70/LCP2/TYROBP/HLA- C/NFATC2/PPP3CC/PTK2B/HLA-G/NFATC1/NFATC4/SHC2/HLA- B/RAC2/MAPK3/RAET1E/FCER1G/HLA- A/IFNAR2/KLRD1/CD244/MICB/TNFRSF10D/PIK3R1/FCGR3A/ICAM2/TNFRSF10C/SOS2 /VAV3/PRKCA/KLRC3/IFNAR1/FASLG/KLRC1/PPP3CA/RAET1G/GRB2/SHC1/SYK C3/C1S/C7/C2/CD40LG/CTSG/HLA-DQA2/CD28/FCGR2B/C1QA/C1QC/C1R/CD86/HLA- DOB/C1QB/ACTN1/HLA-DMA/HLA-DMB/HLA-DOA/HLA- DPA1/FCGR2C/HIST2H2BE/FCGR1A/HLA-DPB1/H2AFJ/HLA- DRA/FCGR3A/CD80/HIST2H2AA4/HIST2H4A/HLA-DRB1/TRIM21/HIST1H2AC/FCGR2A CD22/SELL/SELP/ITGA4/PTPRC/CD6/ITGAL/ICAM3/CD40LG/CADM3/ITGB2/HLA- DQA2/JAM3/CD28/PECAM1/JAM2/SELPLG/CD4/CD2/CD34/HLA- E/CD86/CD8B/ITGB7/CDH5/SPN/ICOS/HLA-DOB/CD8A/PDCD1/HLA-C/ESAM/HLA- DMA/HLA-DMB/HLA-DOA/HLA-DPA1/HLA-G/CLDN23/CLDN10/CD226/HLA- B/CLDN11/CTLA4/CLDN5/HLA-F/ITGA8/PDCD1LG2/HLA-A/VCAN/HLA- DPB1/PTPRM/SIGLEC1/HLA- DRA/NFASC/ICAM2/NEGR1/CD80/CLDN3/SDC2/CD99/CDH2/HLA-DRB1
KEGG_SYSTEMIC_LUPUS_ERYTHE MATOSUS	124	0.537187019	1.634244652	0.001184834	0.011027659	0.007341315	3653	tags=27%, list=15%, signal=23%	CTSK/FUCA1/LAPTM5/CTSG/CTSS/CD68/CTSZ/ACP5/GALC/CTSC/CTSF/CTSH/LGMN/AP 1S2/IDS/CTSB/ATP6VOD1/LIPA/SMPD1/CTSD/TPP1/NAGA/TCIRG1/NPC2/SLC17A5/CT SA/CTSW/PLA2G15/PSAP/GBA/AP1M2/HEXA/CTNS/ARSA/GNPTG/PPT1/AP4S1/HYAL1/A TP6V0A4/GM2A/ATP6AP1/ARSG/ACP2/GNPTAB/CTSO/GALNS/AP1G1/NEU1/HEXB/GLB1/ LAPTM4A/ATP6V0A1/GNS/AP4B1/MAN2B1/ASAH1/ATP6VOD2/ATP6VOC/SORT1
KEGG_CELL_ADHESION_MOLECUL ES_CAMS	128	0.615629301	1.872884903	0.001190476	0.011027659	0.007341315	3135	tags=48%, list=13%, signal=42%	
KEGG_LYSOSOME	119	0.574686245	1.735776254	0.001201923	0.011027659	0.007341315	4695	tags=50%, list=19%, signal=40%	

KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY	107	0.566725816	1.692478382	0.001218027	0.011027659	0.007341315	3753	tags=44%, list=15%, signal=37%	PTPRC/CARD11/CD3E/CD40LG/CD28/PIK3CD/ITK/CD3D/CD3G/VAV1/PTPN6/CD4/LCK/CD247/PIK3CG/LAT/CD8B/FYN/ICOS/PIK3R5/ZAP70/CD8A/LCP2/GRAP2/PDCD1/NFATC2/PPP3CC/PRKCQ/NFATC1/NFATC4/CTLA4/RASGRP1/FOS/MAPK3/MAP3K8/CBL/PIK3R1/SOS2/VAV3/TEC/RHOA/MAPK14/PPP3CA/PAK2/GRB2/IL2/CBLB/CXCL12/MMP2/PLCG2/ITGA4/MYL9/PRKCB/NCF1/RHOH/CYBB/ITGAL/ITGB2/JAM3/PIK3CD/SIPA1/ITK/PECAM1/CYBA/VAV1/JAM2/MMP9/PIK3CG/CDH5/PIK3R5/ACTN1/ESAM/THY1/TXK/GNAI2/PTK2B/CLDN23/CLDN10/CLDN11/CLDN5/RAC2/RAP1A/NCF4/VASP/CXCR4/PIK3R1/NCF2/RASSF5/VAV3/CLDN3/PRKCA/RAPGEF3/CD99/ROCK1/RHOA/MAPK14/ACTB
KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION	115	0.617231688	1.853976465	0.001219512	0.011027659	0.007341315	3366	tags=43%, list=14%, signal=38%	PLA2G2D/RAMP3/MYL9/PRKCB/MYLK/PLCB2/ADCY7/EDNRA/ARHGEF1/PRKACB/ACTA2/RAMP2/MYH11/ADCY4/CALM1/PLA2G2A/PRKCQ/MRVI1/ITPR2/CALCRL/PRKCH/PRKCD/MAPK3/ITPR1/NPR2/PRKG1/CALD1/PPP1R12B/PPP1R14A/PRKCA/CACNA1C/ADORA2A/ROCK1/GNAQ/NPR1/RHOA/PLA2G10
KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRACTION	113	0.554375529	1.660843367	0.00122399	0.011027659	0.007341315	3192	tags=33%, list=13%, signal=29%	HLA-DQA2/CTSS/CD4/HLA-E/CD8B/LTA/HLA-DOB/CD8A/LGMN/HLA-C/HLA-DMA/HLA-DMB/HLA-DOA/CTSB/HLA-DPA1/HLA-G/HLA-B/B2M/HLA-F/IFI30/HLA-A/HLA-DPB1/KLRD1/CD74/HLA-DRA/KLRC3/HLA-DRB1/KLRC1
KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION	80	0.610697234	1.772233527	0.001257862	0.011027659	0.007341315	3175	tags=35%, list=13%, signal=31%	MS4A1/CR2/CD22/CD19/CD37/ITGA4/IL1R1/CD38/CR1/FCER2/CD5/CD3E/IL7R/CD3D/CD3G/CD1C/CD4/CD55/CD2/CD34/ITGA1/CD8B/GP1BA/CD1D/CD7/CD8A/CSF1R/IL3RA/IL6R/CD14/FLT3/CSF2RA/FLT3LG/CSF3R/MME/CD1E/IL5RA/ITGA5/IL9R/FCGR1A/IL2RA/CD36/CD33/HLA-DRA/IL4R
KEGG_HEMATOPOIETIC_CELL_LINEAGE	84	0.73632525	2.14111201	0.001262626	0.011027659	0.007341315	2599	tags=54%, list=11%, signal=48%	CD79A/CR2/CD22/CD19/CD79B/CD72/PLCG2/BTK/PRKCB/CARD11/RASGRP3/PIK3AP1/PIK3CD/VAV1/FCGR2B/PTPN6/PIK3CG/LYN/PIK3R5/NFATC2/PPP3CC/IFITM1/INPP5D/NFATC1/NFATC4/RAC2/FOS/MAPK3/PIK3R1/SOS2/VAV3/LILRB3/CD81/BLNK
KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY	75	0.668235344	1.927123046	0.001264223	0.011027659	0.007341315	2919	tags=45%, list=12%, signal=40%	C3/ITGA4/PRKCB/NCF1/CR1/TGFB3/ITGB2/HLA-DQA2/CYBA/TLR4/PTPN6/HLA-DOB/TGFB1/HLA-DMA/HLA-DMB/HLA-DOA/HLA-DPA1/FCGR2C/FOS/MAPK3/MYD88/FCGR1A/STAT1/HLA-DPB1/NCF4/HLA-DRA/NCF2/FCGR3A/JAK1/TLR2/NOS2/HLA-DRB1/MAPK14
KEGG_LEISHMANIA_INFECTION	70	0.629671665	1.799886943	0.001277139	0.011027659	0.007341315	3295	tags=47%, list=13%, signal=41%	GSTA1/ALDH1A3/ALDH3A1/AKR1C3/ADH1B/ALDH3B1/ADH1C/CYP1B1/GSTA2/ADH7/MGST1/GSTM3/CYP2F1/GSTM5/GSTM2/EPHX1/GSTK1/UGT2A1/GSTM4/GSTA3/GSTM1/GSTT1
KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P450	70	0.617602495	1.765387786	0.001277139	0.011027659	0.007341315	3176	tags=31%, list=13%, signal=27%	CR2/C3/SERPING1/CFH/C1S/CFI/C7/F13A1/A2M/CR1/C2/PROS1/F2R/SERPINA1/MASP1/C1QA/F3/CD55/C1QC/C1R/CFB/THBD/C1QB/VWF/F10/C3AR1
KEGG_COMPLEMENT_AND_COAGULATION_CASCADES	68	0.793716221	2.263206549	0.00128041	0.011027659	0.007341315	1494	tags=38%, list=6%, signal=36%	GSTA1/FMO2/ALDH1A3/ALDH3A1/MAOB/ADH1B/ALDH3B1/ADH1C/GSTA2/ADH7/MGST1/GSTM3/FMO3/FMO1/FMO5/GSTM5/GSTM2/GSTK1/AOX1/UGT2A1/GSTM4/GSTA3/GSTM1/GSTT1
KEGG_DRUG_METABOLISM_CYTOCHROME_P450	72	0.632120592	1.812924413	0.00128041	0.011027659	0.007341315	3176	tags=33%, list=13%, signal=29%	CD40LG/HLA-DQA2/CD28/HLA-E/CD86/HLA-DOB/HLA-C/HLA-DMA/HLA-DMB/HLA-DOA/HLA-DPA1/HLA-G/HLA-B/CTLA4/HLA-F/HLA-A/HLA-DPB1/HLA-DRA/CD80/FASLG/HLA-DRB1/IL2/PRF1/IL10/HLA-DQB1/TSHR/HLA-DQA1
KEGG_AUTOIMMUNE_THYROID_DISEASE	50	0.721516754	1.965440377	0.001321004	0.011027659	0.007341315	4983	tags=54%, list=20%, signal=43%	PIGR/TNFRSF13B/CXCL12/TNFRSF17/ITGA4/TNFRSF13C/CCL28/TNFSF13B/CD40LG/HLA-DQA2/CD28/CD86/ITGB7/ICOS/HLA-DOB/TGFB1/TNFSF13/HLA-DMA/AICDA/HLA-DMB/HLA-DOA/HLA-DPA1/HLA-DPB1/CXCR4/HLA-DRA/CD80
KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	45	0.774684005	2.082738993	0.001335113	0.011027659	0.007341315	2644	tags=58%, list=11%, signal=52%	HLA-DQA2/CD28/HLA-E/CD86/HLA-DOB/HLA-C/HLA-DMA/HLA-DMB/HLA-DOA/HLA-DPA1/HLA-G/HLA-B/HLA-F/HLA-A/HLA-DPB1/KLRD1/HLA-DRA/CD80/FASLG/HLA-DRB1/KLRC1/IL2/PRF1/TNF/HLA-DQB1/HLA-DQA1/KIR3DL2/IFNG
KEGG_GRAFT_VERSUS_HOST_DISEASE	37	0.694149021	1.787917407	0.001385042	0.011027659	0.007341315	5255	tags=76%, list=21%, signal=60%	CD40LG/HLA-DQA2/CD28/HLA-E/CD86/HLA-DOB/HLA-C/HLA-DMA/HLA-DMB/HLA-DOA/HLA-DPA1/HLA-G/HLA-B/HLA-F/HLA-A/HLA-DPB1/HLA-DRA/CD80/FASLG/HLA-DRB1/IL2/PRF1/IL12B/IL10/TNF/HLA-DQB1/HLA-DQA1
KEGG_ALLOGRAFT_REJECTION	35	0.73183931	1.866659265	0.001396648	0.011027659	0.007341315	4983	tags=77%, list=20%, signal=62%	CD79A/CD19/TNFRSF13B/BTK/PTPRC/TNFRSF13C/CD3E/CD40LG/IL7R/CD3D/CD4/LCK/CD8B/ICOS/ZAP70/CD8A/AICDA/IL2RG
KEGG_PRIMARY_IMMUNODEFICIENCY	35	0.783243433	1.997772723	0.001396648	0.011027659	0.007341315	1748	tags=51%, list=7%, signal=48%	

KEGG_ASTHMA	28	0.741195043	1.818231914	0.001430615	0.011027659	0.007341315	4983	tags=64%, list=20%, signal=51%	CD40LG/HLA-DQA2/HLA-DOB/CCL11/HLA-DMA/HLA-DMB/HLA-DOA/HLA-DPA1/FCER1G/HLA-DPB1/MS4A2/HLA-DRA/PRG2/HLA-DRB1/IL10/TNF/HLA-DQB1/HLA-DQA1 S1PR1/ADRA2A/P2RY8/P2RX5/S1PR4/GABRP/P2RY10/P2RY13/CNR2/CTSG/LPAR1/F2R/CYSLTR1/EDNRA/APLNR/EDNRB/P2RY14/FPR1/P2RX1/C3AR1/CALCRL/PTGER3/PTGER2/F2RL2/LEPR/P2RY11/FPR3/PTAFR/P2RX7/F2RL1/P2RY6/GIPR/VIPR1/PTGFR/GRIN3B/CHRNA1/HRH1/OXTR/PRSS3/ADORA2A/LTB4R2/GZMA/TBXA2R/F2RL3/SSTR3/LTB4R/OPRL1/GPR35/ADRB2/CNR1/TACR1/NR3C1/PTH1R/MC1R/GRID1/PTGDR/THRA/C5AR1/CHRN1/FPR2/GRIA3/GRIN3A/HRH2/ADORA3/GRIN2D/ADRA2C/NPY1R/GLRB/CYSLTR2/TSHR/NPFFR1/AVPR2/GRM5/AVPR1A/LPAR6/ADRB1/PTGER1 COL6A3/COL3A1/COL1A2/PDGFRB/ITGA4/MYL9/PRKCB/PARVG/THBS2/COL1A1/COL6A2/MYLK/PIK3CD/COL5A2/VAV1/LAMA4/PIK3CG/THBS1/COL6A1/TNC/ITGA1/TNXB/ITGB7/FYN/PIK3R5/COMP/ACTN1/VWF/LAMA2/VEGFC/IGF1/SHC2/ITGA11/RAC2/COL11A1/MAPK3/ITGA5/FN1/ITGA8/RAP1A/TLN1/CCND3/KDR/FLT4/ZYX/FLNC/COL5A3/VASP/PDGFC/LAMB2/PIK3R1/PARVB/SOS2/VAV3/PRKCA/DIAPH1/COL6A6/HGF/ROCK1/PDGFB/PDGFR/PTGFR/PTGFR2/RHOA/PARVA/ITGB3/RAPGEF1/ACTB/PAK2/ITGA9/GRB2/BCAR1/SHC1
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION	266	0.468512827	1.516013339	0.002134472	0.015794416	0.010514633	5438	tags=29%, list=22%, signal=23%	SSBP1/MSH2/RFC3/RFC2/LIG1/RFC4/MSH6/EXO1/POLD2/PCNA/POLD1/RFC5 XRCC3/MUS81/RPA1/TOP3B/BRCA2/NBN/RAD51D/RPA3/BLM/SSBP1/RAD51C/RAD52/XRCC2/RAD54B/RAD54L/EME1/RAD51/POLD2/POLD1 POLR2G/POLR2J3/POLR1E/POLR3C/POLR2B/POLR2L/POLR3F/POLR3K/POLR2J2/POLR3D/POLR2E/POLR3A/POLR2J/POLR1B/POLR2K/POLR1C/POLR1D/POLR3B/POLR3H/POLR1A/POLR2D/POLR2F/POLR2I/POLR2H APEX2/MUTYH/POLL/POLB/PARP1/POLE3/XRCC1/TDG/LIG3/SMUG1/POLE2/NEIL3/FEN1/LIG1/POLE/POLD2/NTHL1/PCNA/POLD1/UNG TAF4/TAF11/GTF2E2/TAF6L/GTF2F1/TAF5L/GTF2H4/GTF2A2/TAF5/GTF2I/GTF2H1/TBP/TBPL1/GTF2F2/TAF4B/GTF2H3/GTF2IRD1 RPA3/POLA2/RNASEH1/SSBP1/MCM5/PRIM2/POLA1/POLE2/MCM6/PRIM1/FEN1/DNA2/MCM3/RFC3/RFC2/LIG1/POLE/RFC4/MCM7/POLD2/PCNA/POLD1/RFC5/MCM2/RNASEH2A/MCM4 AARS/AARS2/TARS2/DARS2/RARS/PSTK/RARS2/VARS/DARS/CARS2/IARS2/WARS2/EPRS/SARS/CARS/YARS/PARS2/NARS/MARS2/GARS/FARSB/IARS/TARS/MARS/FARSA/LARS/YARS2/EARS2/SARS2 GTF2H5/RBX1/DBP1/GTF2H4/CUL4A/RAD23B/CDK7/POLE3/RPA3/ERCC3/GTF2H1/DBP2/POLE2/GTF2H3/RAD23A/RFC3/RFC2/LIG1/POLE/RFC4/POLD2/PCNA/POLD1/RFC5 PSME4/PSMC2/POMP/PSMD12/PSMB5/PSMD4/PSME3/PSMA5/PSMB3/PSMC5/PSMA6/PSMA4/PSMD8/PSMB1/PSMC3/PSMB2/PSMD11/PSMB4/PSMD2/PSMA7/PSMA1/PSMA2/PSMD3/PSMB7/PSMD14/PSMC4 SKIV2L/CNOT4/LSM3/CNOT7/LSM1/EXOSC9/EXOSC1/EDC3/EXOSC7/PATL1/CNOT3/WDR61/XRN2/CNOT6/LSM6/LSM7/EXOSC2/PNPT1/HSPA9/LSM2/EXOSC4/ENO1/LSM5/ENO2/LSM4/EXOSC5/HSPD1 SESN1/CDKN1A/BBC3/CCND2/DBP2/FAS/EI24/BID/TP53/SFN/CHEK1/CCNE2/MDM2/STEAP3/GTSE1/GADD45A/TNFRSF10B/CYCS/CHEK2/RRM2/TP73/CCND1/CCNB1/CDK4/PERP/PMAIP1/CDK1/CCNB2 RPS15A/RPL3/RPS20/RPL30/RPL23A/RPS9/RPL28/RPL9/RPL22/RPL2/RPS23/RPL37/RPS27A/RPL10A/UBA52/RPL39/RSL24D1/RPL26L1/RPL12/RPL19/RPS2/RPL27A/RPL23/RPL27/RPL4/RPL7A/RPL36A/RPS13/RPS3/RPS11/RPL35/RPL7/RPS10/RPS8/RPL41/RPS28/MRPL13/RPL31/RPS4X/RPLP1/RPS3A/RPL38/RPS16/RPL8/RPL13A/RPL17/RPL18/RPL36/RPS18/RPL35A/RPS26/RPS12/RPL22L1/RPL18A/RPL37A/RPS15/RPS24/RPS7/RPL24/RPS21/RPS5/RPS19/RPLP0
KEGG_FOCAL_ADHESION	197	0.461085845	1.459695851	0.002219756	0.015794416	0.010514633	3715	tags=37%, list=15%, signal=31%	
KEGG_MISMATCH_REPAIR	23	-0.703948891	-1.896726496	0.002873563	0.019689229	0.013107481	2467	tags=57%, list=10%, signal=51%	
KEGG_HOMOLOGOUS_RECOMBINATION	26	-0.649811876	-1.798685687	0.00304878	0.020143728	0.01341005	5259	tags=77%, list=21%, signal=60%	
KEGG_RNA_POLYMERASE	29	-0.643017111	-1.794584315	0.003344482	0.020487265	0.013638748	6125	tags=86%, list=25%, signal=65%	
KEGG_BASE_EXCISION_REPAIR	33	-0.56956501	-1.652580776	0.003460208	0.020487265	0.013638748	4644	tags=64%, list=19%, signal=52%	
KEGG_BASAL_TRANSCRIPTION_FACTORS	35	-0.640821048	-1.881168456	0.003496503	0.020487265	0.013638748	5100	tags=51%, list=21%, signal=41%	
KEGG_DNA_REPLICATION	36	-0.770098588	-2.266655581	0.003584229	0.020487265	0.013638748	3375	tags=75%, list=14%, signal=65%	
KEGG_AMINOACYL_TRNA_BIOSYNTHESIS	41	-0.671280404	-2.019557464	0.003831418	0.020487265	0.013638748	4960	tags=73%, list=20%, signal=58%	
KEGG_NUCLEOTIDE_EXCISION_REPAIR	44	-0.613224348	-1.872606502	0.003846154	0.020487265	0.013638748	4759	tags=57%, list=19%, signal=46%	
KEGG_PROTEASOME	43	-0.645455604	-1.960484601	0.003875969	0.020487265	0.013638748	4686	tags=63%, list=19%, signal=51%	
KEGG_RNA_DEGRADATION	52	-0.488481516	-1.551407151	0.004065041	0.020889792	0.013906718	6049	tags=54%, list=25%, signal=41%	
KEGG_P53_SIGNALING_PATHWAY	65	-0.50297341	-1.663776396	0.004444444	0.022222222	0.014793741	3226	tags=45%, list=13%, signal=39%	
KEGG_RIBOSOME	85	-0.795730299	-2.795456505	0.004784689	0.023293881	0.015507164	3009	tags=75%, list=12%, signal=66%	

KEGG_VIRAL_MYOCARDITIS	68	0.547347031	1.560708164	0.005121639	0.023874048	0.015893392	4983	tags=56%, list=20%, signal=45%	ITGAL/CD40LG/ITGB2/HLA-DQA2/CD28/CD55/HLA-E/CD86/FYN/HLA-DOB/MYH11/HLA-C/LAMA2/HLA-DMA/HLA-DMB/HLA-DOA/HLA-DPA1/HLA-G/HLA-B/RAC2/HLA-F/HLA-A/HLA-DPB1/HLA-DRA/SGCB/CD80/HLA-DRB1/ACTB/SGCD/MYH10/CASP8/PRF1/EIF4G3/CASP9/SGCA/CAV1/HLA-DQB1/HLA-DQA1
KEGG_PYRIMIDINE_METABOLISM	98	-0.518307527	-1.853248488	0.005208333	0.023874048	0.015893392	3556	tags=48%, list=14%, signal=41%	POLR2J2/POLR3D/POLE3/POLR2E/ENTPD6/POLR3A/POLA2/POLR2J/CANT1/CTPS2/POLR1B/POLR2K/UCLL1/POLR1C/POLR1D/PRIM2/UMPS/POLR3B/POLA1/POLE2/PNPT1/POLR3H/POLR1A/DCTD/NME1-NME2/NME4/POLR2D/POLR2F/PRIM1/RRM1/UCLL2/POLR2I/DUT/CAD/POLR2H/POLE/NT5M/RRM2/CTPS1/TYMS/POLD2/NME2/POLD1/DTYMK/NME1/TK1
KEGG_OXIDATIVE_PHOSPHORYLATION	101	-0.488252151	-1.761012739	0.005291005	0.023874048	0.015893392	5569	tags=62%, list=23%, signal=48%	NDUFB2/NDUFV2/COX8A/ATP6V1E1/COX10/COX15/NDUFS1/NDUFC1/NDUFA3/SDHB/UQCRB/UQCRC1/NDUFB6/NDUFA2/COX4I1/NDUFS7/NDUFB10/NDUFB5/NDUFS3/NDUFA1/NDUFS2/NDUFA5/UQCRC2/UQCR10/ATP6V1C2/COX7C/COX5A/COX11/NDUFA10/NDUFA6/PPA1/PPA2/NDUFA8/NDUFB3/ATP6V1E2/UQCR11/NDUFA4/NDUFAB1/NDUFS4/UQCRFS1/NDUFA11/UQCRQ/COX7A2L/COX6C/NDUFS5/COX7A2/COX17/COX5B/NDUFB4/COX7B/NDUFB7/COX6B1/NDUFA7/COX6A1/NDUFS6/NDUFS8/NDUFV1/NDUFA9/CYC1/UQCRH/NDUFB9/COX6B2
KEGG_PARKINSONS_DISEASE	99	-0.532047382	-1.888270426	0.005434783	0.023938923	0.015936581	5569	tags=65%, list=23%, signal=50%	NDUFB2/NDUFV2/COX8A/GPR37/PARK7/NDUFS1/NDUFC1/NDUFA3/SDHB/UQCRB/UQCRC1/NDUFB6/NDUFA2/COX4I1/NDUFS7/NDUFB10/NDUFB5/NDUFS3/NDUFA1/NDUFS2/NDUFA5/UQCRC2/UQCR10/PPID/VDAC3/COX7C/UBE2L3/COX5A/SLC25A4/NDUFA10/NDUFA6/NDUFA8/NDUFB3/UQCR11/SLC25A5/NDUFA4/NDUFAB1/NDUFS4/UQCRFS1/UQCRQ/COX7A2L/COX6C/NDUFS5/COX7A2/COX5B/NDUFB4/COX7B/NDUFB7/COX6B1/VDAC2/NDUFA7/COX6A1/SLC25A6/NDUFS6/VDAC1/NDUFS8/NDUFV1/NDUFA9/CYCS/CYC1/UQCRH/NDUFB9/COX6B2
KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS	130	-0.432094801	-1.598048922	0.00625	0.026353276	0.01754386	6106	tags=51%, list=25%, signal=38%	BTRC/FBXW11/STUB1/UBE2G2/UBE2J2/UBA1/HUWE1/UBE2F/RNF7/UBE2B/FBXO4/BIRC3/PIAS1/UBOX5/AIRE/UBE4B/RBX1/UBE2N/CUL1/UBE2K/ANAPC10/CUL2/DDB1/FZR1/PIAS2/UBE2W/UBE2D4/PIAS4/TRIM37/SMURF1/CUL4A/SKP1/FANCL/CDC23/UBE2L3/ANAPC1/UBE3B/UBE20/UBE3C/SAE1/ANAPC5/CUL7/UBE3A/UBE2E3/CDC34/PRPF19/UBE2Z/FBXW8/ANAPC7/DDB2/HERC2/ANAPC11/KEAP1/UBE2M/MDM2/UBA2/BRCA1/KLHL13/NEDD4L/SKP2/CDC20/CBLC/UBE2S/SOCS1/UBE2C
KEGG_CELL_CYCLE	124	-0.603265139	-2.210454942	0.006329114	0.026353276	0.01754386	4497	tags=62%, list=18%, signal=51%	MAD1L1/CUL1/ANAPC10/HDAC1/ORC3/FZR1/SMAD4/ORC2/E2F5/SKP1/SMAD3/SMC3/CDK7/CCNE1/YWHAQ/ORC4/DBF4/E2F2/CDK2/BUB3/CDC23/ANAPC1/CDKN1A/RAD21/ANAPC5/RBL1/YWHAQ/ORC5/MCM5/CDC7/SMC1A/CCND2/ANAPC7/YWHAG/BUB1/ANAPC11/TFDP1/TP53/MCM6/SFN/CHEK1/CCNE2/HDAC2/MDM2/ORC6/MCM3/GADD45A/CDC25C/PLK1/ORC1/PKMYT1/CCNA2/PRKDC/CDC25A/ESPL1/MYC/BUB1B/TTK/SKP2/WEE1/CHEK2/MCM7/CCND1/CDC20/PCNA/PTTG1/CCNB1/CDK4/MCM2/MCM4/E2F1/CDK1/CCNB2/MAD2L1/CDK6/CDC45
KEGG_SPLICEOSOME	123	-0.658269234	-2.40118824	0.006410256	0.026353276	0.01754386	6126	tags=72%, list=25%, signal=55%	PLRG1/DDX39B/SNRPB2/PRPF3/SNRNP200/XAB2/LSM3/BCAS2/HNRNPC/RBM8A/NCBP1/HNRNPU/CRNKL1/PP1E/CTNBL1/HNRNPA3/TRA2A/TCERG1/RBM17/DDX23/SART1/SRSF10/DDX46/SF3B5/PP1L1/SMNDC1/U2AF1/SF3B4/TRA2B/DHX15/THOC1/SF3A3/SNRNP70/PRPF6/THOC2/PRPF4/SRSF1/EIF4A3/LSM6/HNRNPM/ISY1/RBMX/PQBP1/SNRNP40/FTUD2/DDX42/PP1H/SRSF7/PRPF40A/SRSF3/U2AF2/BUD31/NCBP2/SF3B2/MAGO8/PRPF19/SRSF2/SNRPA1/SRSF6/SRSF9/PRPF31/PUF60/CHERP/LSM7/SNRPC/SF3A2/SNRPG/WBP11/USP39/U2SURP/HNRNPA1/LSM2/PHF5A/SNRPB/SNRPD3/TXNL4A/ALYREF/SNRPA/LSM5/SNRPD1/SNRPE/HSPA1B/THOC3/PRPF40B/LSM4/SNRPD2/MAGO8B/SNRPF
KEGG_TYPE_I_DIABETES_MELLITUS	41	0.61816036	1.623641832	0.006747638	0.027137241	0.018065759	4410	tags=63%, list=18%, signal=52%	HLA-DQA2/CD28/HLA-E/CD86/LTA/HLA-DOB/PTPRN2/HLA-C/HLA-DMA/HLA-DMB/HLA-DOA/HLA-DPA1/HLA-G/HLA-B/HLA-F/HLA-A/HLA-DPB1/CPE/HLA-DRA/CD80/FASLG/HLA-DRB1/IL2/PRF1/IL12B/TNF

KEGG_ALZHEIMERS_DISEASE	145	-0.390345951	-1.474949332	0.007194245	0.028317771	0.01885166	5569	tags=53%, list=23%, signal=41%	NDUFB2/APH1A/PLCB3/NDUFV2/COX8A/CAPN1/IL1B/CALML6/IDE/NDUFS1/ATP2A2/NDUFC1/NDUFA3/SDHB/UQCRB/UQCRC1/NDUFB6/NDUFA2/COX4I1/NDUFS7/NDUFB10/NDUFB5/NDUFS3/NDUFA1/NDUFS2/MAPT/CALML3/NDUFA5/APP/UQCRC2/UQCR10/LPL/HSD17B10/PLCB1/COX7C/COX5A/NDUFA10/NDUFA6/PPP3R1/NDUFA8/CDK5/NDUFB3/RYR3/UQCR11/FADD/NDUFA4/FAS/GRIN2A/NDUFAB1/BID/NDUFS4/UQCRFS1/UQCRQ/COX7A2L/COX6C/NDUFS5/COX7A2/COX5B/NDUFB4/ITPR3/COX7B/NDUFB7/BAD/COX6B1/NDUFA7/COX6A1/NDUFS6/NDUFS8/NDUFV1/NDUFA9/CYCS/CYC1/UQCRH/NDUFB9/GAPDH/COX6B2PLCG2/PTPRC/PRKCB/NCF1/WAS/PIK3CD/VAV1/FCGR2B/PIK3CG/LAT/LYN/DOCK2/PIK3R5/SCIN/INPP5D/FCGR2C/ARPC1B/PRKCD/RAC2/GAB2/MAPK3/FCGR1A/VASP/PIK3R1/FCGR3A/MARCKS/VAV3/SPHK1/WASF3/DNM1/PRKCA/GSN
KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS	93	0.511510987	1.504936957	0.007434944	0.028655514	0.019076502	2858	tags=34%, list=12%, signal=31%	FUCA1/FUCA2/GBA/HEXA/NEU1/MAN2B2/HEXB/GLB1/MAN2B1/ENGASE
KEGG_OTHER_GLYCAN_DEGRADATION	16	0.74202667	1.601876183	0.008169935	0.030327869	0.020189819	5266	tags=62%, list=21%, signal=49%	NDUFC1/POLR2L/TAF4/NDUFA3/SDHB/UQCRB/UQCRC1/NDUFB6/HDAC1/NDUFA2/COX4I1/NDUFS7/NDUFB10/NDUFB5/NDUFS3/NDUFA1/NDUFS2/NDUFA5/AP2A1/SP1/UQCRC2/UQCR10/PPID/VDAC3/POLR2J2/POLR2E/PLCB1/COX7C/COX5A/SLC25A4/NDUFA10/NDUFA6/DCTN2/POLR2J/AP2S1/TBP/BBC3/POLR2K/NDUFA8/TFAM/NDUFB3/TBPL1/UQCR11/SLC25A5/TAF4B/NDUFA4/DNAL4/NDUFAB1/CLTB/NDUFS4/BDNF/UQCRFS1/UQCRQ/COX7A2L/COX6C/TP53/SOD1/NDUFS5/COX7A2/POLR2D/COX5B/POLR2F/NDUFB4/HDAC2/COX7B/NDUFB7/COX6B1/VDAC2/NDUFA7/COX6A1/SLC25A6/NDUFS6/VDAC1/NDUFS8/NDUFV1/POLR2I/NDUFA9/POLR2H/CYCS/CYC1/UQCRH/NDUFB9/COX6B2
KEGG_HUNTINGTONS_DISEASE	160	-0.459299355	-1.76893552	0.008196721	0.030327869	0.020189819	4847	tags=52%, list=20%, signal=42%	CTSK/LY96/TLR7/TLR9/PIK3CD/CXCL9/TLR4/PIK3CG/TLR8/CD86/PIK3R5/CD14/FOS/IRF7/MAPK3/MYD88/MAP3K8/STAT1/IFNAR2/PIK3R1/CXCL11/CD80/TLR2/TICAM2/IFNAR1/CCL5/IRF5/MAP2K3/MAPK14/RIPK1/TLR1/TLR6/CASP8/IL12B/TNF/AKT1/IRAK4/TIRAP/TRAF3
KEGG_TOLL LIKE RECEPTOR SIGNALING PATHWAY	101	0.498584879	1.478670271	0.008610086	0.031232665	0.020792158	5003	tags=39%, list=20%, signal=31%	PIAS2/PIAS4/COL4A6/RELA/RXRA/CCNE1/E2F2/ITGA2/CDK2/LAMC2/COL4A2/TP53/PIK3CB/CCNE2/TRAF2/LAMB1/ITGA6/PIK3R2/BCL2/TRAF4/LAMA3/LAMB3/NFKBIA/PTK2/CYCS/MYC/SKP2/CCND1/CKS1B/CDK4/E2F1/LAMA5/ITGAV/PTGS2
KEGG_SMALL_CELL_LUNG_CANCER	84	-0.422265999	-1.482718258	0.00952381	0.033882784	0.022556391	4155	tags=42%, list=17%, signal=35%	PLA2G2D/PLCG2/BTK/PRKCB/PIK3CD/VAV1/PIK3CG/LAT/FYN/LYN/PIK3R5/LCP2/PLA2G2A/INPP5D/PRKCD/RAC2/GAB2/MAPK3/FCER1G/MS4A2/PIK3R1/SOS2/VAV3/PRKCA/PLA2G10/MAP2K3/MAPK14/GRB2/SYK
KEGG_FC_EPSILON_RI_SIGNALING_PATHWAY	79	0.524996285	1.524102046	0.010050251	0.035081066	0.023354109	3760	tags=37%, list=15%, signal=31%	IL10RA/IL7R/PIK3CD/PTPN6/IRF9/PIK3CG/STAT4/PIK3R5/PIM1/IL21R/IL2RB/IL3RA/IL6R/IL12RB1/CSF2RA/STAT5B/CSF3R/LEPR/IL2RG/IFNLR1/IL5RA/CLCF1/IL9R/CCND3/STAT1/IL2RA/IFNAR2/CBL/CSF2RB/PIK3R1/JAK1/IL6ST/IL4R/SOS2/IFNAR1/IL21/IL10RB/CNTF/STAT5A/IL12RB2/CISH/GRB2/IL24/IL2/CBLB/JAK3/SPRY1/C
KEGG_JAK_STAT_SIGNALING_PATHWAY	154	0.458437416	1.427214701	0.010344828	0.035440613	0.023593466	4550	tags=36%, list=19%, signal=29%	TF1/IL12B/IL10/OSM/IL7/IL22RA2/SOCS3/AKT1
KEGG_CYSTEINE_AND_METHIONINE_METABOLISM	34	-0.536499986	-1.569000809	0.010600707	0.035656923	0.023737468	3958	tags=68%, list=16%, signal=57%	AHCYL1/MTR/GOT2/LDHC/AMD1/SRM/LDHB/DNMT3B/DNMT3L/MAT1A/APIP/ADI1/MAT2A/SMS/DNMT1/DNMT3A/ENOPH1/MPST/GOT1/CBS/LDHA/AHCY
KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_GANGLIO_SERIES	15	0.740204794	1.571910849	0.012965964	0.042833989	0.028515373	4252	tags=73%, list=17%, signal=61%	ST6GALNAC4/ST3GAL5/ST6GALNAC6/B3GALT4/ST3GAL1/ST6GALNAC5/HEXA/ST6GALNAC3/HEXB/GLB1/ST3GAL2
KEGG_PURINE_METABOLISM	151	-0.372369533	-1.424783249	0.014285714	0.046365915	0.03086664	3891	tags=37%, list=16%, signal=31%	NT5C/HPRT1/POLR3K/POLR2J2/POLR3D/ADCY3/POLE3/POLR2E/ENTPD6/POLR3A/PAPS1/DGUOK/POLA2/POLR2J/CANT1/POLR1B/POLR2K/IMPDH2/AK2/PKM/POLR1C/POLR1D/PRIM2/ADSL/PDE9A/POLR3B/POLA1/POLE2/PNPT1/POLR3H/POLR1A/NME1-NME2/NME4/GART/ADK/PPAT/POLR2D/POLR2F/ADCY10/PRIM1/RRM1/GMPS/POLR2I/AK4/ATIC/POLR2H/POLE/PAICS/NT5M/RRM2/POLD2/NME2/POLD1/NME1/PAPSS2
KEGG_ECM_RECEPTOR_INTERACTION	83	0.508055175	1.475058125	0.015151515	0.048328109	0.032172909	2267	tags=33%, list=9%, signal=30%	COL6A3/COL3A1/COL1A2/ITGA4/THBS2/COL1A1/COL6A2/COL5A2/LAMA4/THBS1/COL6A1/TNC/ITGA1/TNXB/ITGB7/GP1BA/COMP/VWF/LAMA2/ITGA11/COL11A1/ITGA5/FN1/ITGA8/COL5A3/LAMB2/CD36

Gene set enrichment analysis (GSEA) for ZNF667-AS1 using GSE12452.

ID	setSize	enrichmentScore	NES	pvalue	p.adjust	qvalues	rank	leading edge	core enrichment
KEGG_PATHWAYS_IN_CANCER	319	-0.409967305	-1.656121601	0.001567398	0.013814217	0.008646167	3932	tags=27%, list=18%, signal=22%	HIF1A/RAC1/WNT10B/CRK/NFKBIA/CCDC6/STAT1/CDK6/PTCH1/CDKN1B/CRKL/SOS1/EP300/TPR/KRAS/BIRC2/LAMC2/SMAD2/PIK3CA/EGLN1/TP53/RBX1/WNT2/TFG/BRCA2/JUN/BIRC3/CDKN1A/MDM2/PIK3CB/PTEN/IGF1R/ITGB1/SMAD4/KITLG/HSP90B1/HDAC1/FAS/MAPK8/PTK2/VEGFA/RALA/BCL2/RAD51/FGF1/SKP2/GSTP1/FZD3/FH/CHUK/AKT3/E2F3/MSH6/HSP90AB1/ITGA6/LAMC1/CYCS/BIRC5/BID/FZD6/FADD/HDAC2/CUL2/FGF2/ITGAV/NRAS/LAMA1/CCNE2/MSH2/LAMB3/ARNT2/CKS1B/COL4A2/CDK4/PTGS2/CXCL8/BMP2/WNT5A/COL4A1/MYC/FZD7/FN1/KIT/LAMB1/MMP1 ROCK2/RAC1/CRK/FLNA/KDR/ITGA1/CRKL/SOS1/BIRC2/DOCK1/LAMC2/PIK3CA/COL6A6/PPP1R12A/JUN/VCL/BIRC3/PDGFRC/PIK3CB/PTEN/PAK3/IGF1R/ITGB8/ITGB1/RAP1B/MAPK8/PTK2/VEGFA/THBS4/BCL2/AKT3/CAV2/PPP1CC/ITGA6/LAMC1/CCND2/CAV1/ITGAV/COL11A1/COL5A1/COL1A1/THBS2/LAMA1/COL6A3/LAMB3/IBSP/COL4A2/COL1A2/COL4A1/COL3A1/FN1/SPP1/COL5A2/LAMB1 PDE6D/POLR2G/PRPS1/POLR2F/DGUOK/PDE8A/POLR3C/POLR2I/POLR3G/PKM/RRM2B/POLD1/PRIM2/PNP/NT5M/DCK/POLR3F/POLR1D/PRPS2/NUDT9/AK4/POLR2B/POLE3/PFAS/GART/POLD2/NUDT5/ADK/AK2/POLR1B/NME4/NT5C3A/POLR2K/HPRT1/GMPS/POLR1C/POLA1/RRM1/POLE2/POLR2D/POLR2H/PRIM1/ADSL/ATIC/PAICS/PPAT/PNPT1/PAPSS2/RRM2/ADA/NME1 YWHAH/YWHAZ/RBL1/SKP1/CDK6/MCM5/CDKN1B/EP300/CDK7/SMAD2/SMC1A/TFDP2/TP53/RBX1/CDKN1A/MDM2/STAG2/BUB1/YWHAE/SMAD4/TFDP1/CDC25B/ANAPC1/BUB3/CUL1/CCNB2/HDAC1/CDC27/CHEK1/ANAPC7/WEE1/RAD21/ANAPC10/CDC23/ANAPC5/YWHAQ/ESPL1/SKP2/ORC5/ORC4/ORC1/ORC6/E2F3/ATR/MCM4/CCND2/CDC25A/HDAC2/ORC2/YWHAG/CDC20/E2F5/ORC3/MCM6/CCNA2/GADD45A/PRKDC/CHEK2/CCNE2/MCM7/MCM3/PTTG1/MCM2/CDC7/CDC45/CDK1/PCNA/CDC6/CDK4/DBF4/MYC/MAD2L1/TTK/BU B1B/CCNB1 CDC16/UBE2E2/PML/PRPF19/ANAPC13/UBE2R2/UBE2E1/UBE2Q1/TRIM37/UBE2M/CUL4B/MID1/CBLB/PIAS4/UBE2D1/KLHL9/HERC4/FBXW11/UBE2G2/ANAPC11/PIAS1/PIAS2/KEAP1/UBE2I/UBE2B/SAE1/UBE3C/UBA3/CUL4A/SKP1/UBA6/RNF7/TRIP12/UBE2N/BIRC2/UBE3A/UBE2L6/UBR5/UBE2QL1/RBX1/UBE2K/SOCS1/UBE2Z/HERC2/BIRC3/UBE2W/FBXW7/MDM2/UBE2L3/DDB2/UBE2G1/UBE2D2/ANAPC1/RCHY1/CUL1/CDC27/ANAPC7/ANAPC10/CDC23/ANAPC5/WWP1/SKP2/UBE2F/UBA2/BRCA1/BIRC6/NEDD4L/NEDD4/CUL2/CDC20/UBE2E3/FANCL/KLHL13/UBE2C PRPF31/SNRNP27/DHX16/LSM4/DDX42/SF3B1/CDC40/LSM3/SF3A2/DDX5/EFTUD2/PP1H/PRPF38A/TRA2B/SNRNP40/PRPF4/SNRPB2/SNRPC/SF3B6/HNRNPC/DDX46/PRPF38B/TCERG1/TRA2A/SRSF1/SF3B4/PLRG1/AQR/USP39/SRSF6/NCBP1/THOC2/RBMX/HNRNPU/DDX23/EIF4A3/SRSF3/SRSF7/SMNDC1/PRPF40A/PPIL1/SNRPA/SNRPB/PHF5A/BCAS2/HNRNPA3/NCBP2/LSM7/SNRPA1/PRPF3/LSM6/LSM8/SF3A3/DHX15/SNRPD2/LSM2/SNRPD3/SRSF9/WBP11/MAGOH/TXNL4A/SNRPE/SRSF2/SNRPG/HNRNPA1/SRSF10/CRNKL1/THOC1/ALYREF/SNRPF/U2SURP/MAGOH/SNRPD1/LSM5 UPP1/POLR3C/POLR2I/DTYMK/POLR3G/TYMP/RRM2B/POLD1/PRIM2/PNP/NT5M/DCK/C TPS2/POLR3F/POLR1D/POLR2B/UMPS/POLE3/POLD2/POLR1B/NME4/NT5C3A/POLR2K/ POLR1C/DCTD/POLA1/RRM1/POLE2/POLR2D/CMPK2/UCK2/AK3/POLR2H/DUT/PRIM1/T K1/TYMS/PNPT1/RRM2/CTPS1/NME1
KEGG_FOCAL_ADHESION	196	-0.434579023	-1.674098484	0.00170068	0.013814217	0.008646167	3981	tags=28%, list=19%, signal=23%	
KEGG_PURINE_METABOLISM	149	-0.475619965	-1.794410551	0.001718213	0.013814217	0.008646167	3613	tags=35%, list=17%, signal=29%	
KEGG_CELL_CYCLE	123	-0.684992958	-2.509617213	0.00174216	0.013814217	0.008646167	3981	tags=62%, list=19%, signal=51%	
KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS	128	-0.512255002	-1.890791791	0.001760563	0.013814217	0.008646167	5723	tags=59%, list=27%, signal=43%	
KEGG_SPLICEOSOME	121	-0.706658359	-2.577274513	0.001763668	0.013814217	0.008646167	3873	tags=62%, list=18%, signal=51%	
KEGG_PYRIMIDINE_METABOLISM	95	-0.575030315	-2.016658973	0.001766784	0.013814217	0.008646167	3074	tags=44%, list=14%, signal=38%	

KEGG_PARKINSONS_DISEASE	98	-0.540984303	-1.905747412	0.001776199	0.013814217	0.008646167	4921	tags=56%, list=23%, signal=43%	PPID/SNCAIP/NDUFC2/UBE2G2/SDHC/NDUFS4/NDUFB3/SDHB/COX6A1/CASP3/NDUFB10/NDUFV2/NDUFA7/VDAC3/NDUFA1/SLC25A5/COX6B1/NDUFB6/NDUFV1/UQCRB/UBE2L6/UQCRQ/COX5B/GPR37/COX5A/NDUFB5/NDUFA6/COX7C/NDUFA5/NDUFB4/UBE2L3/COX7B/COX7A2L/NDUFA4/NDUFV3/NDUFS2/UBE2G1/COX7A2/NDUFS8/VDAC2/NDUFAB1/PARK7/NDUFS6/COX6C/UQCRC2/VDAC1/UQCRFS1/NDUFA8/NDUFS5/CYCS/UQCRH/CYC1/NDUFB9/NDUFA9
KEGG_RNA_DEGRADATION	53	-0.636311663	-2.057256188	0.001808318	0.013814217	0.008646167	4073	tags=58%, list=19%, signal=47%	PATL1/EXOSC4/LSM1/LSM4/CNOT6/PAPOLG/EXOSC2/LSM3/TTC37/ZCCHC7/C1D/DIS3/EXOSC3/EXOSC9/ENO2/WDR61/PARN/CNOT7/EXOSC5/ENO1/EXOSC8/HSPA9/LSM7/XRN2/LSM6/LSM8/LSM2/HSPD1/LSM5/PNPT1
KEGG_CYSTEINE_AND_METHIONINE_METABOLISM	33	-0.659471928	-1.956417798	0.001821494	0.013814217	0.008646167	4637	tags=55%, list=22%, signal=43%	LDHC/SDS/SRM/GOT1/DNMT3B/ADI1/IL4I1/MAT2A/APIP/DNMT1/AMD1/SMS/ENOPH1/MTR/AHCY/LDHA/LDHB
KEGG_AMINOACYL_TRNA_BIOSYNTHESIS	41	-0.687863796	-2.147688858	0.001834862	0.013814217	0.008646167	3338	tags=56%, list=16%, signal=47%	TARSL2/WARS2/EPRS/HARS2/FARSA/MTFMT/SARS/NARS/RARS/EARS2/YARS/MARS2/TARS/IARS2/LARS/FARSB/MARS/GARS/IARS/DARS/YARS2/NARS2
KEGG_PROTEASOME	41	-0.747410863	-2.33361022	0.001834862	0.013814217	0.008646167	3998	tags=78%, list=19%, signal=64%	IFNG/PSMD4/PSMD3/PSME1/PSMB6/PSMB1/PSME2/PSMB7/PSMA3/PSMB4/PSMD13/PSME4/PSMC3/PSMD8/PSME3/PSMC5/PSMD2/PSMD1/PSMD11/PSMB5/PSMC4/POMP/PSMA5/PSMC2/PSMA7/PSMA2/PSMB3/PSMD14/PSMA4/PSMD12/PSMA1
KEGG_P53_SIGNALING_PATHWAY	67	-0.594368599	-1.982317917	0.001841621	0.013814217	0.008646167	3410	tags=43%, list=16%, signal=36%	BBC3/TP53/SERPINE1/IGFBP3/CDKN1A/MDM2/PTEN/RRM2B/EI24/DDB2/RCHY1/CCNB2/FAS/CHEK1/SESNI/ATR/CYCS/CCND2/BID/CCNG1/GADD45A/CHEK2/CCNE2/CDK1/CDK4/RRM2/CCNB1/PMAIP1
KEGG_BASAL_TRANSCRIPTION_FACTORS	31	-0.644653418	-1.876642714	0.001851852	0.013814217	0.008646167	5158	tags=61%, list=24%, signal=47%	TAF11/TAF4/TAF7/TAF5L/TAF2/GTF2A2/TAF13/GTF2E1/TBP/GTF2H4/GTF2E2/STON1/GTF2H1/TBPL1/TAF5/GTF2H3/TAF4B/GTF2F2
KEGG_DNA_REPLICATION	36	-0.778539216	-2.348458481	0.001851852	0.013814217	0.008646167	2845	tags=72%, list=13%, signal=63%	RNASEH1/POLD1/PRIM2/RPA1/POLE3/POLD2/RPA3/RFC2/SSBP1/RPA4/MCM4/POLA1/POLE2/FEN1/RNASEH2A/RFC3/PRIM1/MCM6/MCM7/RFC5/MCM3/MCM2/PCNA/RFC4/DNA2
KEGG_SMALL_CELL_LUNG_CANCER	84	-0.563349751	-1.92866877	0.001858736	0.013814217	0.008646167	3336	tags=35%, list=16%, signal=29%	LAMC2/PIK3CA/TP53/BIRC3/PIK3CB/PTEN/ITGB1/PTK2/BCL2/SKP2/CHUK/AKT3/E2F3/ITGA6/LAMC1/CYCS/ITGAV/LAMA1/CCNE2/LAMB3/CKS1B/COL4A2/CDK4/PTGS2/COL4A1/MYC/FN1/LAMB1
KEGG_ECM_RECEPTOR_INTERACTION	82	-0.657383035	-2.247807435	0.001865672	0.013814217	0.008646167	879	tags=26%, list=4%, signal=25%	LAMC1/ITGAV/COL11A1/COL5A1/COL1A1/THBS2/LAMA1/COL6A3/LAMB3/IBSP/SDC2/COL4A2/COL1A2/HMMR/COL4A1/COL3A1/FN1/SPP1/COL5A2/LAMB1
KEGG_RIBOSOME	81	-0.52197189	-1.780655911	0.001869159	0.013814217	0.008646167	5840	tags=60%, list=27%, signal=44%	RPS10/RPL41/RPL23A/RPS15/RPS2/RPL14/RPL13A/UBA52/RPS4X/RPL10A/RPS8/RPS28/RPS3/FAU/RPL12/RPL19/RPS3A/RPL23/RPL30/RPS13/RPS19/RPS27A/RPS12/RPS23/RPS20/RPL35/RPL5/RPL24/RPL35A/RPS17/RPL7/RPL22/RPL4/RPL8/RPS5/RPL37A/RPS15A/RPLP0/RPL36/RPS7/RPS27L/RSL24D1/RPL31/RPS24/RPS21/RPL22L1/RPL26L1/MRPL13
KEGG_NUCLEOTIDE_EXCISION_REPAIR	43	-0.591845465	-1.853271775	0.001876173	0.013814217	0.008646167	4630	tags=60%, list=22%, signal=47%	POLE/CCNH/LIG1/CUL4A/GTF2H5/CDK7/RAD23B/RBX1/RFC1/POLD1/GTF2H4/DDB2/GTF2H1/RPA1/POLE3/POLD2/RPA3/RFC2/RPA4/POLE2/GTF2H3/RFC3/RFC5/PCNA/RFC4
KEGG_MISMATCH_REPAIR	22	-0.752037876	-2.029395919	0.001912046	0.013814217	0.008646167	2845	tags=68%, list=13%, signal=59%	POLD1/RPA1/POLD2/RPA3/RFC2/SSBP1/RPA4/MSH6/RFC3/RFC5/MSH2/EXO1/PCNA/RFC4
KEGG_HOMOLOGOUS_RECOMBINATION	26	-0.696557159	-1.959606827	0.001926782	0.013814217	0.008646167	2913	tags=58%, list=14%, signal=50%	POLD1/BLM/RPA1/RAD50/POLD2/RPA3/RAD51/EME1/SSBP1/RPA4/NBN/RAD54L/RAD51C/RAD54B
KEGG_ASTHMA	27	0.648171175	1.810920818	0.002074689	0.013814217	0.008646167	3450	tags=52%, list=16%, signal=44%	HLA-DMA/HLA-DMB/HLA-DRB1/TNF/HLA-DPB1/HLA-DOB/HLA-DQB1/FCER1A/HLA-DPA1/HLA-DRA/HLA-DOA/RNASE3/CD40LG/HLA-DRB4
KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	44	0.645745927	2.006385502	0.002150538	0.013814217	0.008646167	2738	tags=50%, list=13%, signal=44%	PIGR/TNFRSF17/CXCL12/TNFRSF13C/HLA-DMA/HLA-DMB/AICDA/CCL28/HLA-DRB1/HLA-DPB1/ITGB7/HLA-DOB/HLA-DQB1/HLA-DPA1/ITGA4/HLA-DRA/TNFRSF13B/TNFSF13/IL2/HLA-DOA/CCL27/CD28
KEGG_HEMATOPOIETIC_CELL_LINEAGE	84	0.544230633	1.928947295	0.002155172	0.013814217	0.008646167	3279	tags=45%, list=15%, signal=38%	MS4A1/CD19/CD1C/CD1D/IL1R2/CD55/CR2/CR1/CD22/CD3D/IL7R/HLA-DRB1/TNF/IL6R/CD37/CD2/CD59/ITGA4/FCER2/CD8A/IL4R/GP1BA/HLA-DRA/CD3G/FLT3LG/TP0/CSF1R/IL7/IL1R1/CD1E/CD38/CSF2RA/CD8B/CD3E/IL5RA/CD5/CD7/FLT3

KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY	74	0.583146783	2.009818718	0.002164502	0.013814217	0.008646167	3054	tags=45%, list=14%, signal=38%	CD19/CD72/CR2/BTK/PLCG2/FOS/PTPN6/CD79A/PRKCB/VAV1/LYN/CD22/CD79B/SYK/PIK3CD/CHP2/PPP3CA/CARD11/RAC2/BLNK/PIK3CG/INPP5D/RASGRP3/MAPK3/FCGR2B/PPP3CC/PIK3AP1/AKT1/CHP1/NFATC1/NFATC2/GRB2/NFAT5
KEGG_RETINOL_METABOLISM	48	0.580725057	1.832629649	0.002164502	0.013814217	0.008646167	2785	tags=27%, list=13%, signal=24%	DHRS9/ALDH1A1/ADH1C/ADH7/CYP2C18/ADH1B/UGT2B28/RDH10/RDH12/CYP2A7/ADH1A/CYP2C8/ADH6
KEGG_DRUG_METABOLISM_CYTOCHROME_P450	59	0.649869614	2.134587796	0.002192982	0.013814217	0.008646167	2785	tags=41%, list=13%, signal=35%	GSTA1/ALDH3A1/ADH1C/GSTA3/ADH7/FMO2/CYP2E1/ALDH1A3/FMO3/MAOA/ALDH3B1/CYP2C18/ADH1B/ALDH3B2/UGT2B28/GSTK1/FMO5/GSTM1/CYP2A7/ADH1A/GSTO2/CYP2C8/MAOB/ADH6
KEGG_METABOLISM_OF_XENOBOTICS_BY_CYTOCHROME_P450	57	0.648976021	2.103887486	0.002207506	0.013814217	0.008646167	2785	tags=39%, list=13%, signal=34%	GSTA1/ALDH3A1/AKR1C3/ADH1C/GSTA3/ADH7/CYP2E1/CYP2F1/ALDH1A3/CYP1B1/ALDH3B1/CYP2C18/ADH1B/ALDH3B2/EPHX1/UGT2B28/GSTK1/GSTM1/ADH1A/GSTO2/CYP2C8/ADH6
KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION	113	0.498352227	1.855892058	0.002257336	0.013814217	0.008646167	3281	tags=35%, list=15%, signal=29%	CLDN10/RHOH/NCF1/ITGAL/PLCG2/CXCL12/CLDN3/CLDN23/ITGB2/PRKCB/VAV1/CLDN8/MMP9/CLDN7/EZR/SIPA1/ITK/CYBA/NCF4/PIK3CD/CLDN11/RASSF5/JAM2/RAC2/PIK3CG/ITGA4/GNAI2/CLDN4/MYL12B/JAM3/CLDN9/TXK/RHOA/CD99/GNAI1/MYLPF/CYBB/PECAM1/CLDN15
KEGG_CELL_ADHESION_MOLECULES_CAMS	126	0.454653345	1.716117136	0.002314815	0.013814217	0.008646167	3336	tags=40%, list=16%, signal=34%	CLDN10/SELL/ITGAL/PTPRC/ICAM3/CLDN3/HLA-DMA/CLDN23/HLA-DMB/ITGB2/CD22/CLDN8/CLDN7/HLA-E/HLA-DRB1/HLA-DPB1/ITGB7/HLA-DOB/HLA-DQB1/ALCAM/CLDN11/SELP/JAM2/CD2/HLA-DPA1/ITGA4/HLA-F/HLA-B/CD8A/HLA-DRA/HLA-G/ITGA8/CLDN4/SELPLG/GLG1/ITGA9/CDH3/JAM3/HLA-A/NRXN3/CLDN9/SDC1/HLA-DOA/CD28/HLA-C/CD99/CD8B/ICAM2/PECAM1/CLDN15/CD40LG
KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	126	0.432408288	1.632151795	0.002314815	0.013814217	0.008646167	3190	tags=33%, list=15%, signal=28%	ITGAL/PLCG2/PTPN6/ITGB2/PRKCB/VAV1/LCK/CD48/HLA-E/SYK/LAT/TNF/FYN/ZAP70/PIK3CD/CHP2/PPP3CA/RAC2/PIK3CG/HCSST/CD247/NCR3/HLA-B/SH2D1B/MAPK3/PPP3CC/HLA-G/SH2D1A/TNFRSF10D/IFNGR1/RAET1E/CHP1/HLA-A/LCP2/NFATC1/HLA-C/NFATC2/GRB2/NFAT5/ICAM2/IFNAR1
KEGG_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI_ANCHOR_BIOSYNTHESIS	24	-0.635045047	-1.752957552	0.003816794	0.02143809	0.013417866	4450	tags=50%, list=21%, signal=40%	PIGP/PIGB/PIGK/PIGC/PIGU/PIGN/PIGX/PIGF/PIGW/PIGA/PGAP1
KEGG_PROTEIN_EXPORT	22	-0.683203077	-1.843643227	0.003824092	0.02143809	0.013417866	5643	tags=82%, list=26%, signal=60%	SRP68/SPCS3/OXA1L/SEC61B/SRP54/SEC61A1/SPCS2/IMMP1L/HSPA5/SEC63/SRP19/SEC61A2/SRP72/SEC11A/IMMP2L/SRP9/SEC61G
KEGG_LEISHMANIA_INFECTION	68	0.483172352	1.639465015	0.004310345	0.023453347	0.014679193	1741	tags=29%, list=8%, signal=27%	C3/NCF1/FOS/PTPN6/HLA-DMA/HLA-DMB/ITGB2/CR1/PRKCB/HLA-DRB1/TNF/HLA-DPB1/CYBA/HLA-DOB/HLA-DQB1/NCF4/HLA-DPA1/ITGA4/MAPK3/HLA-DRA
KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY	107	0.421656562	1.542489909	0.004716981	0.024932615	0.01560505	3580	tags=38%, list=17%, signal=32%	PTPRC/FOS/PTPN6/VAV1/LCK/CD3D/LAT/TNF/FYN/ITK/ZAP70/PIK3CD/CHP2/MAP3K8/PPP3CA/CARD11/PIK3CG/CD247/CD8A/RASGRP1/MAPK3/CD3G/PPP3CC/AKT1/CHP1/LCP2/IL2/NFATC1/RHOA/CBL/PDPK1/CD28/NFATC2/CD8B/GRB2/CD3E/NFAT5/PAK6/CD40LG/PRKCQ/MAP3K14
KEGG_HUNTINGTONS_DISEASE	158	-0.426029245	-1.626321532	0.005025126	0.025823562	0.016162685	5110	tags=51%, list=24%, signal=39%	CLTC/TAF4/SP1/NDUFS1/PPID/HIP1/NDUFC2/SDHC/NDUFS4/NDUFB3/SDHB/CREB1/COX6A1/CASP3/BAX/NDUFB10/NDUFV2/AP2S1/NDUFA7/VDAC3/NDUFA1/SLC25A5/COX6B1/NDUFB6/POLR2G/NDUFV1/EP300/BBC3/POLR2F/UQCRB/UQCRQ/COX5B/COX5A/PLCB1/NDUFB5/DCTN4/TP53/BDNF/POLR2I/NDUFA6/COX7C/NDUFA5/NDUFB4/SOD2/COX7B/COX7A2L/SOD1/NDUFA4/TBP/NDUFV3/NDUFS2/COX7A2/NDUFS8/VDAC2/NDUFAB1/NDUFS6/HDAC1/COX6C/UQCRC2/POLR2B/TBPL1/AP2B1/CREB5/VDAC1/UQCRFS1/NDUFA8/TFAM/NDUFS5/POLR2K/CYCS/HDAC2/PLCB4/UQCRH/POLR2D/TAF4B/POLR2H/CYC1/NDUFB9/NDUFA9

KEGG_ALZHEIMERS_DISEASE	143	-0.406785935	-1.524797272	0.005190311	0.025951557	0.016242795	4735	tags=44%, list=22%, signal=34%	SDHC/NDUFS4/NDUFB3/PSEN2/SDHB/ATP2A2/COX6A1/CASP3/ADAM17/NDUFB10/NDUFV2/GRIN2A/GSK3B/NDUFA7/NDUFA1/COX6B1/NDUFB6/RYR3/NDUFV1/ATF6/UQCRB/UQCRQ/COX5B/COX5A/PLCB1/CDK5/NDUFB5/NDUFA6/COX7C/NDUFA5/NDUFB4/APP/COX7B/COX7A2L/IL1B/NDUFA4/NDUFV3/NDUFS2/COX7A2/PPP3R1/NDUFS8/NDUFAB1/TNFRSF1A/NDUFS6/FAS/COX6C/UQCRC2/HSD17B10/NAE1/UQCRFS1/NDUFA8/NDUFS5/CYCS/BID/FADD/PLCB4/UQCRH/CYC1/NDUFB9/GAPDH/NDUFA9/LPL
KEGG_BLADDER_CANCER	41	-0.560088753	-1.748742094	0.005504587	0.026798648	0.01677298	3363	tags=29%, list=16%, signal=22%	TP53/TYMP/CDKN1A/MDM2/VEGFA/E2F3/NRAS/CDK4/CXCL8/MYC/MMP1
KEGG_STEROID_HORMONE_BIO SYNTHESIS	43	0.537092687	1.65891046	0.006396588	0.028479064	0.017824734	1528	tags=23%, list=7%, signal=22%	AKR1C3/SRD5A2/HSD17B2/CYP1B1/SULT1E1/SRD5A3/STS/SULT2B1/UGT2B28/HSD17B8
KEGG_PRIMARY_IMMUNODEFICIENCY	35	0.561784346	1.649877206	0.006437768	0.028479064	0.017824734	1970	tags=40%, list=9%, signal=36%	CD19/BTK/PTPRC/TNFRSF13C/CD79A/LCK/AICDA/CD3D/IL7R/ZAP70/IL2RG/BLNK/CD8A/TNFRSF13B
KEGG_ALLOGRAFT_REJECTION	34	0.587822588	1.723509041	0.006465517	0.028479064	0.017824734	3774	tags=62%, list=18%, signal=51%	HLA-DMA/HLA-DMB/HLA-E/HLA-DRB1/TNF/HLA-DPB1/HLA-DOB/HLA-DQB1/HLA-DPA1/HLA-F/HLA-B/HLA-DRA/HLA-G/HLA-A/IL2/HLA-DOA/CD28/HLA-C/CD40LG/HLA-DRB4/IL12B
KEGG_GRAFT_VERSUS_HOST_DISEASE	34	0.580452918	1.701901001	0.006465517	0.028479064	0.017824734	2752	tags=53%, list=13%, signal=46%	HLA-DMA/HLA-DMB/HLA-E/HLA-DRB1/TNF/HLA-DPB1/HLA-DOB/HLA-DQB1/HLA-DPA1/HLA-F/HLA-B/HLA-DRA/HLA-G/HLA-A/IL2/HLA-DOA/CD28/HLA-C
KEGG_AUTOIMMUNE_THYROID_DISEASE	49	0.52094842	1.646002594	0.008695652	0.036963037	0.02313476	3450	tags=41%, list=16%, signal=34%	HLA-DMA/HLA-DMB/HLA-E/HLA-DRB1/HLA-DPB1/HLA-DOB/HLA-DQB1/HLA-DPA1/HLA-F/HLA-B/HLA-DRA/HLA-G/TPO/HLA-A/IL2/HLA-DOA/CD28/HLA-C/CD40LG/HLA-DRB4
KEGG_FC_EPSILON_RI_SIGNALING_PATHWAY	75	0.45366536	1.566656921	0.008791209	0.036963037	0.02313476	1714	tags=25%, list=8%, signal=23%	BTK/PLCG2/PRKCB/PRKCD/VAV1/LYN/SYK/LAT/PLA2G10/TNF/FYN/PLA2G2D/PIK3CD/FCER1A/RAC2/PIK3CG/MAP2K3/INPP5D/MAPK3
KEGG_RNA_POLYMERASE	29	-0.614176806	-1.768839316	0.009416196	0.037785948	0.023649811	3613	tags=48%, list=17%, signal=40%	POLR2G/POLR2F/POLR3C/POLR2I/POLR3G/POLR3F/POLR1D/POLR2B/POLR1B/POLR2K/POLR1C/POLR2D/POLR2H
KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	105	0.407675295	1.486932916	0.009456265	0.037785948	0.023649811	2738	tags=28%, list=13%, signal=24%	C3/HIST2H2BE/HLA-DMA/HLA-DMB/C7/H2AFJ/HLA-DRB1/TNF/HLA-DPB1/HLA-DOB/HLA-DQB1/C6/HIST1H2AE/HIST1H2BD/HLA-DPA1/HIST1H2BG/HIST1H2AC/HLA-DRA/FCGR2B/HIST1H2BC/C1R/H3F3A/HIST1H2AJ/C1S/HIST1H2AI/HLA-DOA/CTSG/C1QA/CD28
KEGG_GLYOXYLATE_AND_DICARBOXYLATE_METABOLISM	16	-0.675203727	-1.690927482	0.009803922	0.037785948	0.023649811	4553	tags=56%, list=21%, signal=44%	PGP/MTHFD2L/MDH2/MTHFD1L/GRHPR/MDH1/CS/MTHFD2
KEGG_ONE_CARBON_POOL_BY_FOLATE	16	-0.679506372	-1.701702688	0.009803922	0.037785948	0.023649811	2371	tags=56%, list=11%, signal=50%	MTFMT/GART/MTHFD2/DHFR/MTR/ATIC/TYMS/SHMT2
KEGG_BASE_EXCISION_REPAIR	33	-0.592109261	-1.756576809	0.010928962	0.040838852	0.02556059	4845	tags=58%, list=23%, signal=45%	POLD3/POLE/HMGB1/LIG1/SMUG1/PARP2/POLD1/PARP1/POLE3/POLD2/APEX1/TDG/NEIL3/POLE2/FEN1/NTHL1/UNG/PCNA
KEGG_ARACHIDONIC_ACID_METABOLISM	52	0.489231285	1.547409276	0.011037528	0.040838852	0.02556059	2944	tags=33%, list=14%, signal=28%	AKR1C3/PTGDS/GGT6/ALOX15/CYP2E1/GPX3/PLA2G10/GPX1/CYP2C18/PLA2G2D/CBR1/TBXAS1/CYP2U1/CYP2C8/HPGDS/ALOX5/ALOX12
KEGG_OXIDATIVE_PHOSPHORYLATION	100	-0.440650783	-1.566848635	0.012259194	0.044469627	0.027833052	5112	tags=55%, list=24%, signal=42%	NDUFB2/ATP6V1E1/COX17/NDUFS1/NDUFA11/ATP6V1B2/NDUFC2/SDHC/NDUFS4/NDUFB3/SDHB/COX6A1/NDUFB10/ATP6V1E2/NDUFV2/PPA2/NDUFA7/NDUFA1/COX6B1/NDUFB6/ATP6V1C2/COX15/NDUFV1/COX10/UQCRB/UQCRQ/COX5B/COX5A/NDUFB5/NDUFA6/COX7C/NDUFA5/NDUFB4/COX7B/COX7A2L/NDUFA4/NDUFV3/NDUFS2/COX7A2/NDUFS8/NDUFAB1/ATP6V1C1/NDUFS6/COX6C/UQCRC2/UQCRFS1/NDUFA8/NDUFS5/COX11/UQCRH/CYC1/PPA1/NDUFB9/NDUFA9
KEGG_CALCIUM_SIGNALING_PATHWAY	174	0.35574996	1.406727564	0.012594458	0.044807208	0.028044341	4147	tags=26%, list=19%, signal=21%	P2RX5/CALML5/OXTR/PLCG2/PRKCB/CALML3/CYSLTR1/GNAL/CHP2/GNA14/PPP3CA/ADR1/ADCY7/ITPR1/ATP2A3/PLCE1/PRKACB/PPP3CC/HTR5A/PLCB2/TNCC1/EDNRB/TRPC1/CHP1/CACNA1F/P2RX1/CD38/CAMK2D/TNCC2/CACNA1H/ITPR2/HRH1/ADRA1B/GNAQ/CHRM1/MYLK2/GNAS/HTR2B/ERBB2/CACNA1A/CAMK2A/ADCY2/CHRM5/P2RX7/PTK2B
KEGG_VIRAL_MYOCARDITIS	67	0.468421662	1.579566323	0.013071895	0.045628314	0.028558262	3510	tags=39%, list=16%, signal=33%	CD55/ITGAL/HLA-DMA/HLA-DMB/ITGB2/HLA-E/HLA-DRB1/FYN/HLA-DPB1/HLA-DOB/HLA-DQB1/RAC2/HLA-DPA1/HLA-F/HLA-B/HLA-DRA/HLA-G/MYH14/HLA-A/HLA-DOA/CD28/HLA-C/CD40LG/SGCA/HLA-DRB4/MYH13

KEGG_VALINE_LEUCINE_AND_
ISOLEUCINE BIOSYNTHESIS

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-0.726070133 -1.654210401 0.014256619 0.048842121 0.030569749

2022 tags=45%, list=9%,
signal=41%

PDHA1/IARS2/LARS/IARS
