Supplementary Table S2

BioCarta Pathways

Term	P-value	Z-score	Combined Score	Genes
repression of pain sensation by the transcriptional regulator dream	0.00303293	-1.605495601	2.014786426	RPS6KA3;CREB1;FOS
pdgf signaling pathway	0.01197648	-1.938116718	1.938347571	MAP2K4;STAT3;FOS
no2-dependent il-12 pathway in nk cells	0.01394357	-0.685077496	0.685159097	IL12A;IL12RB2
mapkinase signaling pathway	0.01696817	-1.360420771	1.360582813	MAP2K4;CREB1;FOS;MAP4K5
ceramide signaling pathway	0.02160869	-1.484490263	1.484667084	MAP2K4;KSR1;BAX
calcium signaling by hbx of hepatitis b virus	0.03237351	-1.274253048	1.274404827	CREB1;FOS
il12 and stat4 dependent signaling pathway in th1 development	0.03237351	-0.797633026	0.797728034	IL12A;IL12RB2
atm signaling pathway	0.04383133	-0.769852661	0.769944359	CHEK1;MDM2
regulation of cell cycle progression by plk3	0.04383133	-0.719236943	0.719322612	CHEK1;BAX
oxidative stress induced gene expression via nrf2	0.04383133	-0.618396593	0.618470252	CREB1;FOS
egf signaling pathway	0.05218983	-0.976654046	0.976770377	MAP2K4;STAT3
hypoxia and p53 in the cardiovascular system	0.05656825	-0.581381436	0.581450686	MDM2;BAX
inhibition of cellular proliferation by gleevec	0.06107229	-1.086624219	1.086753649	MAP2K4;FOS
cell cycle: g2/m checkpoint	0.06107229	-0.494267533	0.494326406	CHEK1;MDM2
induction of apoptosis through dr3 and dr4/5 death receptors	0.06569677	-0.354871579	0.354913849	DFFB;TNFSF12
ctcf: first multivalent nuclear factor	0.06569677	-0.248115809	0.248145363	TGFB2;MDM2
hiv-1 nef: negative effector of fas and tnf	0.06689068	-0.624751732	0.624826147	DFFB;MDM2;PSEN1
tpo signaling pathway	0.07043661	-0.782100669	0.782193827	STAT3;FOS
signaling pathway from g-protein families	0.08024272	-0.701597183	0.64816596	RPS6KA3;CREB1
fc epsilon receptor i signaling in mast cells	0.09569751	-0.731973819	0.633731096	MAP2K4;FOS
p38 mapk signaling pathway	0.10102998	-0.359894391	0.311590744	MAP2K4;CREB1
proteolysis and signaling pathway of notch	0.11321881	6.09028385	-5.272869278	PSEN1
multi-drug resistance factors	0.11321881	7.51843151	-6.509336428	ABCB4
p53 signaling pathway	0.12026195	-0.177057602	0.153293609	CHEK1;MDM2;BAX
angiotensin ii mediated activation of jnk pathway via pyk2 dependent signaling	0.12315202	-0.622926913	0.539320049	MAP2K4;FOS
tsp-1 induced apoptosis in microvascular endothelial cell	0.12834625	3.552363877	-3.075579203	FOS
cdc25 and chk1 regulatory pathway in response to dna damage	0.12834625	6.159490733	-5.332787477	CHEK1
toll-like receptor pathway	0.12886074	0.032497042	-0.028135413	MAP2K4;FOS
signal transduction through il1r	0.13463317	0.060161981	-0.052087271	TGFB2;FOS
g-secretase mediated erbb4 signaling pathway	0.14322439	4.04556395	-3.502583851	PSEN1
stat3 signaling pathway	0.14322439	5.769332183	-4.994994514	STAT3
ca-calmodulin-dependent protein kinase activation	0.14322439	6.365176681	-5.510867045	CREB1
pertussis toxin-insensitive ccr5 signaling in macrophage	0.15785719	4.160554713	-3.41987065	FOS
il22 soluble receptor signaling pathway	0.18640232	5.195641303	-4.270685624	STAT3
apoptotic dna-fragmentation and tissue homeostasis	0.18640232	6.23979288	-5.128951787	DFFB
il 3 signaling pathway	0.20032228	3.579765804	-2.942476869	FOS
tnfr2 signaling pathway	0.20032228	5.044933086	-4.146807285	TNFRSF1B
granzyme a mediated apoptosis pathway	0.20032228	6.282508835	-5.164063221	DFFB
il 6 signaling pathway	0.21401216	3.843427798	-3.159200354	STAT3
erythropoietin mediated neuroprotection through nf-kb	0.21401216	4.198307601	-3.450902568	CREB1
melanocyte development and pigmentation pathway	0.21401216	4.207674701	-3.458602087	CREB1
role of mitochondria in apoptotic signaling	0.21401216	5.390078629	-4.430508184	BAX
rb tumor suppressor/checkpoint signaling in response to dna damage	0.21401216	5.529889403	-4.545429101	CHEK1
apoptotic signaling in response to dna damage	0.22747563	4.381701152	-3.601647425	BAX
transcription regulation by methyltransferase of carm1	0.22747563	4.59226472	-3.774725347	CREB1
sumoylation by ranbp2 regulates transcriptional repression	0.22747563	5.454307875	-4.483302998	MDM2
keratinocyte differentiation	0.23936608	0.734391975	-0.603651612	MAP2K4;FOS
gamma-aminobutyric acid receptor life cycle pathway	0.24071629	4.640591773	-3.814448962	DNM1
mechanisms of transcriptional repression by dna methylation	0.24071629	6.155072399	-5.059313697	MBD1
human cytomegalovirus and map kinase pathways	0.25373772	3.241550013	-2.664472051	CREB1
cadmium induces dna synthesis and proliferation in macrophages	0.25373772	4.090855834	-3.362579936	FOS
bone remodeling	0.25373772	4.243485949	-3.488038026	FOS
hypoxia-inducible factor in the cardivascular system	0.25373772	4.781389934	-3.930181485	CREB1
endocytotic role of ndk phosphins and dynamin	0.25373772	5.571766739	-4.579851211	DNM1
map kinase inactivation of smrt corepressor	0.2665434	3.420859945	-2.811860276	MAP2K4
nerve growth factor pathway (ngf)	0.2665434	3.563556134	-2.929152931	FOS
tnfr1 signaling pathway	0.2665434	5.134266812	-4.220237346	MAP2K4
mets affect on macrophage differentiation	0.27913679	4.277257329	-3.39272714	FOS
gata3 participate in activating the th2 cytokine genes expression	0.29152129	4.305333805	-3.374055732	JUNB
er associated degradation (erad) pathway	0.29152129	4.975862916	-3.899544044	CANX
igf-1 signaling pathway	0.30370024	3.2094659	-2.50973253	FOS
fas signaling pathway (cd95)	0.30370024	4.501728608	-3.520253862	MAP2K4
erk1/erk2 mapk signaling pathway	0.32745459	3.332861941	-2.606225551	STAT3
role of brca1 brca2 and atr in cancer susceptibility	0.32745459	3.988123189	-3.118625595	CHEK1
how progesterone initiates the oocyte maturation	0.33903643	3.383671551	-2.645957561	CDC25C

regulation of bad phosphorylation	0.33903643	3.49315269	-2.73156943	BAX
tumor suppressor arf inhibits ribosomal biogenesis	0.33903643	3.758739346	-2.939252419	MDM2
tnf/stress related signaling	0.33903643	3.790798076	-2.964321648	MAP2K4
caspase cascade in apoptosis	0.33903643	4.420578919	-3.45679657	DFFB
regulation of ck1/cdk5 by type 1 glutamate receptors	0.35042558	3.938744273	-3.080012357	DRD2
proteasome complex	0.35042558	4.437924528	-3.470360459	PSMD12
segmentation clock	0.35042558	4.650591815	-3.636661653	PSEN1
skeletal muscle hypertrophy is regulated via akt-mtor pathway	0.36162514	3.696163666	-2.825021446	INPPL1
role of erk5 in neuronal survival pathway	0.37263815	3.055188807	-2.32603978	CREB1
links between pyk2 and map kinases	0.37263815	3.444603138	-2.622516784	MAP2K4
transcription factor creb and its extracellular signals	0.38346761	3.155197479	-2.394828819	CREB1
alk in cardiac myocytes	0.38346761	4.133046948	-3.137027082	TGFB2
role of erbb2 in signal transduction and oncology	0.39411647	3.004428046	-2.275138781	STAT3
?-arrestins in gpcr desensitization	0.39411647	4.040599332	-3.059791781	DNM1
nfkb activation by nontypeable hemophilus influenzae	0.40458764	3.949325367	-2.93679238	TGFB2
role of ?-arrestins in the activation and targeting of map kinases	0.41488398	3.429016026	-2.507270449	DNM1
bcr signaling pathway	0.4250083	3.036627364	-2.220358842	FOS
erk and pi-3 kinase are necessary for collagen binding in corneal epithelia	0.4250083	3.312592783	-2.422142658	ZYX
bioactive peptide induced signaling pathway	0.44475195	2.955151953	-2.15607229	STAT3
role of egf receptor transactivation by gpcrs in cardiac hypertrophy	0.44475195	3.003605981	-2.191424241	FOS
integrin signaling pathway	0.44475195	3.257256954	-2.376487427	ZYX
antigen processing and presentation	0.44620159	3.605033849	-2.630224676	CREB1;CANX
roles of ? arrestin dependent recruitment of src kinases in gpcr signaling	0.45437669	3.249736795	-2.349139629	DNM1
tgf beta signaling pathway	0.5092162	3.603838524	-2.235187816	TGFB2;SKIL
il-2 receptor beta chain in t cell activation	0.58079346	2.876590863	-1.437935762	FOS
mtor signaling pathway	0.63612513	3.353165271	-1.426319997	RPS6KA3
t cell receptor signaling pathway	0.63962612	3.59364422	-1.528611386	MAP2K4;FOS
insulin signaling pathway	0.90849223	3.606149495	-0.307509553	FBP2
wnt signaling pathway	0.93707317	3.766949264	-0.244828771	PSEN1