

Ingenuity Canonical Pathways	-log(p-value)	p-value	Ratio	z-score	Genes	Number of genes
Prostanoid Biosynthesis	3,91	0,0001230	30%	NaN	HPGDS,PTGS1,TBXAS1	3
Oxidative Phosphorylation	2,42	0,0038019	5%	-2,236	ATP5MG,ATP5PO,NDUFB10,NDUFB2,UQCRFS1	5
Mitochondrial Dysfunction	2,20	0,0063096	4%	NaN	ATP5MG,ATP5PO,GPX4,NDUFB10,NDUFB2,UQCRFS1	6
Alanine Biosynthesis III	1,99	0,0102329	100%	NaN	NFS1	1
Chondroitin Sulfate Degradation (Metazoa)	1,94	0,0114815	13%	NaN	HEXB,HYAL2	2
Dermatan Sulfate Degradation (Metazoa)	1,89	0,0128825	12%	NaN	HEXB,HYAL2	2
Phagosome Maturation	1,82	0,0151356	4%	NaN	CTSB,CTSZ,HLA-DRB5,PRDX2,VPS18	5
Necroptosis Signaling Pathway	1,80	0,0158489	4%	-1,342	CAPNS1,CHUK,PPIF,RBCK1,TSPO	5
Glutathione Redox Reactions I	1,75	0,0177828	10%	NaN	GPX4,MGST3	2
L-cysteine Degradation III	1,69	0,0204174	50%	NaN	MPST	1
Sirtuin Signaling Pathway	1,67	0,0213796	3%	1,000	G6PD,NDUFB10,NDUFB2,PPIF,SOD1,TSPO,UQCRFS1	7
NAD Salvage Pathway II	1,67	0,0213796	9%	NaN	ACP1,NT5E	2
Autophagy	1,66	0,0218776	5%	NaN	CTSB,CTSZ,VPS18	3
Regulation of eIF4 and p70S6K Signaling	1,62	0,0239883	3%	NaN	ITGA3,ITGA9,RPS10,RPS17,RPS29	5
Eicosanoid Signaling	1,58	0,0263027	5%	NaN	HPGDS,PTGS1,TBXAS1	3
Glutathione-mediated Detoxification	1,57	0,0269153	8%	NaN	HPGDS,MGST3	2
GP6 Signaling Pathway	1,42	0,0380189	3%	NaN	COL6A1,COL6A2,COL6A3,FYB1	4
Regulation of Cellular Mechanics by Calpain Protease	1,42	0,0380189	4%	NaN	CAPNS1,ITGA3,ITGA9	3
Ferroptosis Signaling Pathway	1,41	0,0389045	3%	2,000	CTSB,GPX4,NFS1,TFRC	4
Pentose Phosphate Pathway (Oxidative Branch)	1,39	0,0407380	25%	NaN	G6PD	1
Spermine and Spermidine Degradation I	1,39	0,0407380	25%	NaN	PAOX	1
Methylmalonyl Pathway	1,39	0,0407380	25%	NaN	PCCA	1
2-oxobutanoate Degradation I	1,30	0,0501187	20%	NaN	PCCA	1