

Ingenuity Canonical Pathways	-log(p-value)	p-value	Ratio	z-score	Genes	Number of genes
Oxidative Phosphorylation	12,00	1,00E-12	23,0%	-4,379	Atp5e,ATP5MC1,ATPAF1,COX4I2,COX7A2,CYC1,MT-CO3,MT-ND3,MT-ND4L,NDUFA10,NDUFA11,NDUFA2,NDUFA3,NDUFA4,NDUFA7,NDUFB1,NDUFB6,NDUFV2,SDHC,SDHD,UQCR10,UQCRC1,UQCRQ	23
Mitochondrial Dysfunction	11,30	5,01E-12	17,5%	NaN	APH1A,Aph1c,Atp5e,ATP5MC1,ATPAF1,COX4I2,COX7A2,CYC1,FIS1,MT-CO3,MT-ND3,MT-ND4L,NDUFA10,NDUFA11,NDUFA2,NDUFA3,NDUFA4,NDUFA7,NDUFB1,NDUFB6,NDUFV2,PRDX3,SDHC,SDHD,UQCR10,UQCRC1,UQCRQ,VDAC3	28
Sirtuin Signaling Pathway	5,71	1,95E-06	10,1%	1,807	ATP5MC1,CYC1,GADD45G,GLUD1,H3C14,MAP1LC3A,MT-ND3,MT-ND4L,NDUFA10,NDUFA11,NDUFA2,NDUFA3,NDUFA4,NDUFA7,NDUFB1,NDUFB6,NDUFV2,PAM16,POLR2F,PPID,SDHC,SDHD,SIRT3,TIMM8A,TOMM22,TSPO,VDAC3	27
EIF2 Signaling	3,69	2,04E-04	9,2%	-3,162	RPL10,RPL15,RPL17,Rpl22l1,RPL24,RPL3,RPL37A,RPL38,RPL39,RPL41,RPS14,RPS18,RPS19,RPS20,RPS25,RPS27L,RPS29,RPS4Y1,RPS5	19
Huntington's Disease Signaling	3,16	6,92E-04	8,4%	NaN	ATP5MC1,CAPN11,CREB5,DNM1,GNB2,GNG10,GNG4,GOSR2,HDAC9,HSPA1A/HSPA1B,Hspa1b,NCOR1,POLR2B,POLR2F,POLR2I,PRKCB,SIN3A,TCERG1,VAMP3	19
D-glucuronate Degradation I	2,41	3,89E-03	66,7%	NaN	CRYL1,DCXR	2
Caveolar-mediated Endocytosis Signaling	2,37	4,27E-03	11,3%	NaN	ACTG1,CD55,DYRK3,ITGA2B,ITGA4,ITGA9,ITGAL,ITGB5	8
Protein Kinase A Signaling	2,26	5,50E-03	6,4%	0,471	AKAP8,ANAPC11,CREB5,CTNNB1,DUSP10,EPM2A,GDE1,GNB2,GNG10,GNG4,H3C14,NFAT5,NFKBID,PD4A,PPP1R7,PRKCB,PTPN22,PTPN5,PTPN6,PTPRC,PTPRS,PTPRT,YWHAH,YWHAQ	24
Phospholipase C Signaling	1,85	1,41E-02	6,7%	3,464	CD3G,CREB5,GNB2,GNG10,GNG4,HDAC9,ITGA4,ITK,LAT,LCK,LCP2,NFAT5,PLA2G6,PRKCB,RHOF,ZAP70	16
Isoleucine Degradation I	1,80	1,58E-02	20,0%	NaN	ACAA2,ECHS1,HADHB	3
Regulation of eIF4 and p70S6K Signaling	1,68	2,09E-02	7,4%	NaN	ITGA4,PPP2R2C,RPS14,RPS18,RPS19,RPS20,RPS25,RPS27L,RPS29,RPS4Y1,RPS5	11
Superpathway of Geranylgeranyldiphosphate Biosynthesis I (via Mevalonate)	1,65	2,24E-02	17,6%	NaN	ACAA2,FDPS,HADHB	3
Eicosanoid Signaling	1,60	2,51E-02	9,7%	NaN	ALOX12,ALOX15,CYSLTR2,PLA2G6,PTGER1,PTGIS	6
Valine Degradation I	1,58	2,63E-02	16,7%	NaN	BCKDHA,ECHS1,HADHB	3
Fatty Acid beta-oxidation I	1,55	2,82E-02	12,5%	-1	ACAA2,ACADM,ECHS1,HADHB	4
Methionine Degradation I (to Homocysteine)	1,52	3,02E-02	15,8%	NaN	EEF1AKMT1,EHMT1,PRMT1	3
Glutamate Biosynthesis II	1,44	3,63E-02	100,0%	NaN	GLUD1	1
Glutamate Degradation X	1,44	3,63E-02	100,0%	NaN	GLUD1	1
Cysteine Biosynthesis III (mammalia)	1,40	3,98E-02	14,3%	NaN	EEF1AKMT1,EHMT1,PRMT1	3
Ketolysis	1,39	4,07E-02	22,2%	NaN	ACAA2,HADHB	2
Ephrin B Signaling	1,35	4,47E-02	8,5%	NaN	AXIN1,CFL2,CTNNB1,GNB2,GNG10,GNG4	6
TCA Cycle II (Eukaryotic)	1,30	5,01E-02	13,0%	NaN	SDHAF4,SDHC,SDHD	3
p53 Signaling	0,89	1,29E-01	6,4%	2	BBC3,CTNNB1,GADD45G,HDAC9,KAT2B,ST13	6
Unfolded protein response	0,85	1,40E-01	7,3%	2	CALR,CEBPD,HSPA1A/HSPA1B,Hspa1b	4
Wnt/Ca+ pathway	0,72	1,90E-01	6,5%	2	AXIN1,CREB5,DVL3,NFAT5	4
Netrin Signaling	0,69	2,05E-01	6,3%	2	CACNA1A,CACNA1I,CACNB4,NFAT5	4
Calcium Signaling	0,00	1,00E+00	3,6%	2,236	CACNA1A,CACNA1I,CACNB4,CALR,CREB5,HDAC9,NFAT5	7