

Table SI. KEGG pathways targeted by microRNAs in each factor.

A, Red								
ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	count
hsa04360	Axon guidance	177/7109	182/8105	3.81051E-06	0.001253657	0.000822268	PARD3/PAK3/PTK2/PIK3R1/MET/NFATC2/SRGAP1/NFATC4/EPHB2/CAMK2G/ABLIM2/BMPR1B/CFL2/PTCH1/PAK4/NEO1/TRPC4/NFATC3/ROBO1/RGS3/PLXNA4/EFNA5/SEMA6D/UNC5D/SLIT3/NRP1/SSH2/LRRC4C/PDPK1/ABLIM1/FYN/EPHA5/ARHGEF12/CAMK2D/CDC42/SEMA4F/NTNG1/SEMA4D/DCC/EPHA4/BOC/PLXNB1/SEMA5B/PIK3CB/FZD3/SEMA6A/SRGAP2/PIK3R3/RHOA/EFNA4/DPYSL2/WNT5A/MAPK1/PIK3CD/LIMK2/EPHA3/SEMA3B/SEMA3A/SLIT2/GSK3B/SEMA5A/TRPC5/ENAH/PLCG1/ROBO2/CXCL12/SEMA4A/MYL12A/SEMA4G/FES/SEMA7A/PLXNB3/SEMA3E/EFNA1/DPYSL5/ITGB1/RGMA/PPP3CB/PIK3CA/GNAI2/EPHA6/PAK6/L1CAM/CAM	177

							K2B/SEMA3C/PLCG2/SEMA3D/PAK5/NTN4/ILK/SRGAP3/SEMA3G/CAMK2A/SEMA6C/UNC5B/ROCK2/ABLIM3/PTPN11/EPHA7/PLXNB2/RYK/PPP3CA/RAF1/TRPC3/NTNG2/SSH1/KRAS/RASA1/EFNB1/TRPC1/ROBO3/SEMA3F/SEMA4B/EPHB4/LIMK1/PLXNC1/SEMA4C/SSH3/PPP3R2/SEMA6B/WNT5B/UNC5C/LRRC4/EFNB2/PAK2/LRIG2/PAK1/CFL1/PIK3R2/BUB1B-PAK6/WNT4/UNC5A/RAC2/PLXNA2/EFNA3/NGEF/EPHA8/EFNB3/RAC1/NCK2/EPHA2/NCK1/TRPC6/PLXNA1/ABL1/CXCR4/SRC/MAPK3/BMPR2/EPHB1/GDF7/MYL12B/ROCK1/NRAS/PPP3CC/PLXNA3/PARD6B/SMO/PARD6G/SLIT1/SHH/EPHB3/EPHB6/PARD6A/GNAI1/GNAI3/NTN1/MYL9/MYL5/NTN3/BMP7/HRAS/PPP3R1/RND1/CDK5/EFNA2/PRKCZ	
hsa04933	AGE-RAGE signaling pathway	99/7109	100/8105	2.81929E-05	0.003134295	0.002055769	MAPK10/PIK3R1/NOX4/VEGFA/FN1/BAX/PLCB2/TGFBR1/MAPK8/COL4A	99

	in diabetic complications						6/AKT2/AKT3/MAPK14/PLCB4/VCA M1/SMAD2/CDC42/PIK3CB/CASP3/NFKB1/PIK3R3/NFATC1/MAPK1/PIK3CD/RELA/SMAD3/MMP2/STAT5A/COL4A5/STAT3/NOX1/PLCG1/TGFB2/AGTR1/COL4A4/PIK3CA/AKT1/AGER/PLCB3/PLCG2/COL4A3/PLCE1/PRKCD/COL4A1/PRKCB/CYBB/KRAS/SELE/PRKCE/STAT1/PLCD4/IL6/COL4A2/VEGFB/COL3A1/IL1A/DIAPH1/BCL2/NO S3/CDK4/PIK3R2/MAPK9/JAK2/SMA D4/VEGFD/PLCD1/TGFB3/IL1B/MAPK12/THBD/CCND1/PLCD3/RAC1/ICAM1/AGT/FOXO1/COL1A2/MAPK3/VEGFC/STAT5B/CDKN1B/MAPK11/F3/TNF/NRAS/TGFBR2/MAPK13/PLCB1/SERPINE1/PIM1/CXCL8/COL1A1/HRAS/JUN/PRKCZ/TGFB1/EDN1/CCL2/EG R1	
hsa04144	Endocytosis	240/7109	252/8105	3.27789E-05	0.003134295	0.002055769	BIN1/AP2B1/PARD3/NEDD4L/CBLB/GIT2/ZFYVE27/IST1/PIP5K1A/ITCH/FGFR2/DNM1/TGFBR1/ZFYVE16/WIPF	240

							2/NEDD4/DNM3/PML/RBSN/SH3KBP 1/MDM2/WASHC2A/CAPZB/ARAP1/P SD3/SMAD2/CDC42/LDLR/SPART/RN F41/ZFYVE9/ARRB1/ARFGAP2/AP2S 1/SH3GLB1/SNX12/RHOA/STAMBP/A RRB2/ASAP1/TFRC/ACTR3/KIF5A/CA V1/CLTC/RAB11FIP1/CHMP3/SMAD3 /RAB5B/AGAP1/RAB11A/DNAJC6/AR F1/IQSEC1/SMAP1/GBF1/VPS37A/SM URF1/EPS15/ARAP3/TRAFF6/RAB11FI P4/VPS36/AGAP2/ARPC1B/DNM2/AR FGAP1/SH3GLB2/RAB5C/PIP5K1B/EP N2/SNX1/ARPC4/PDGFR4/IQSEC2/US P8/HSPA8/ACAP2/RAB5A/EPS15L1/S MAP2/AP2A2/AGAP4/FOLR1/CAV2/ WASHC2C/HLA- F/PSD2/SNX6/WIPF1/IGF2R/CYTH2/R UFY1/ARAP2/MVB12B/DAB2/SNX5/V PS26A/EGFR/CLTCL1/AMPH/FGFR4/ WASHC4/AGAP6/SNX3/AGAP3/SH3G L2/HSPA1L/VPS45/ARF6/PDCD6IP/SN F8/CAV3/ACTR2/EPN1/IGF1R/AGAP9	
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							/ACTR3B/RABEP1/ASAP3/CBLC/SPG 21/RAB35/RUFY2/PIP5KL1/GRK1/AC AP3/KIF5B/HLA- G/HSPA6/ARF3/IL2RB/CHMP6/CXCR 1/CYTH4/CLTB/PSD4/RAB8A/AP2M1/ STAM/FOLR2/CHMP2A/ARPC2/CBL/ VPS4B/RAB11FIP5/VPS35/PSD/EEA1/ ARFGEF1/SNX32/PRKCI/WIPF3/TSG1 01/WWP1/CHMP5/CCR5/HLA- A/CXCR2/STAM2/CXCR4/SRC/ACTR 3C/HLA-B/PLD2/HLA- C/RAB22A/ASAP2/CHMP7/ARF4/CH MP1A/CYTH1/RAB11FIP3/KIF5C/IL2 RG/HGS/VPS29/CHMP4A/SNX2/GIT1/ RAB31/RAB11FIP2/RNF103- CHMP3/VPS26B/FGFR3/TGFBR2/WA SHC5/VPS28/PARD6B/GRK2/PARD6G /VPS25/VPS4A/IZUMO1R/ACAP1/WA SHC1/RAB10/SNX4/GRK6/ARF5/CYT H3/ARFGEF2/RAB7A/HSPA2/AP2A1/P IP5K1C/LDLRAP1/PARD6A/IL2RA/A RPC5/EPN3/SH3GL1/ARPC1A/AGAP5/	
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							CHMP1B/GRK3/HLA-E/PLD1/EHD1/WASHC3/MVB12A/IQSEC3/HRAS/CAPZA2/CHMP4B/VT A1/EHD3/SH3GL3/EHD4/EHD2/PRKCZ/ARPC5L/HSPA1A/SMURF2/GRK7/VPS37D/FOLR3/HSPA1B/CAPZA1/VPS37C	
hsa05166	Human T-cell leukemia virus 1 infection	209/7109	219/8105	6.97885E-05	0.003134295	0.002055769	MAPK10/PRKACB/PIK3R1/JAK1/NFATC2/NFATC4/BAX/DLG1/TGFBR1/IL15RA/NFATC3/MAPK8/CHEK2/ETS1/CREB3L4/TP53/AKT2/BCL2L1/AKT3/ATF2/NRP1/CREB5/SMAD2/CDC27/ADCY3/CCNE1/CANX/ELK1/LCK/ADCY5/PIK3CB/NFKB1/CCNA1/XIAP/CREBBP/ADCY7/PIK3R3/FDPS/NFATC1/MAPK1/ATF4/PIK3CD/RELA/CREB1/ANAPC1/IL1R2/SMAD3/ATF6B/STAT5A/CCND3/LTBR/CDK2/MAP2K4/ITGAL/CHEK1/CDC16/TGFB2/ESPL1/HLA-DQB1/TBP/XPO1/MYC/E2F3/ATM/CRTC3/ADCY4/PRKACA/SPI1/IKBKG/PP3CB/ADCY8/ELK4/PIK3CA/AKT1/ATR/CCND2/EGR2/CREB3L2/E2F2/AD	209

							CY2/CREB3L3/IKBKB/KAT5/TCF3/ITGB2/HLA-F/PPP3CA/ADCY6/RAN/KRAS/SLC2A1/VDAC3/MAP2K1/RANBP3/FOSL1/MAD1L1/PTTG1/CRTC1/ANAPC5/IL15/EP300/BUB1B/IL6/NFKB2/IL1R1/TERT/CD4/PPP3R2/RANBP1/HLA-DQA1/CREB3/TRRAP/VDAC2/SLC25A4/ADCY9/CCNE2/CDK4/HLA-G/MAP3K14/CHUK/IL2RB/JAK3/PIK3R2/CSF2/CREB3L1/MAPK9/HLA-DPB1/ZFP36/TLN2/SMAD4/MAP3K1/FOS/TGFB3/MAD2L1/TBPL1/HLA-DMB/GPS2/CDC23/CCND1/HLA-A/CD3D/ICAM1/RB1/HLA-DPA1/MAP3K3/HLA-B/MAPK3/HLA-C/VDAC1/CD40/BUB3/NFKBIA/CDKN1A/STAT5B/IL2RG/PRKACG/ANAPC10/TNF/CRTC2/NRAS/TLN1/ANAPC2/HLA-DQA2/ANAPC7/TGFBR2/HLA-DRB1/LTA/PPP3CC/ANAPC11/MMP7/CDKN2A/TNFRSF1A/HLA-	
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							DOB/CD3E/ETS2/HLA- DOA/SRF/MSX2/E2F1/ADCY1/CDC20/ HLA- DMA/IL2RA/CCNB2/PTEN/RELB/TBP L2/HLA- E/MSX1/SLC25A31/CD3G/HLA- DRB5/HRAS/POLB/B2M/PTTG2/PPP3 R1/NFYB/CDC26/KAT2B/CCNA2/JUN /TGFB1/IL2/CDKN2C/TNFRSF13C/SL C25A5/KAT2A/EGR1	
hsa049 31	Insulin resistance	106/710 9	108/81 05	8.52129 E-05	0.00313 4295	0.00205 5769	MAPK10/RPS6KA3/PPARGC1B/PIK3R 1/NR1H3/CD36/TBC1D4/MAPK8/PRK AG2/CREB3L4/AKT2/AKT3/RPS6KB1/ CREB5/PDPK1/PPARA/OGT/GFPT1/C PT1A/PIK3CB/CPT1B/NFKB1/INSR/PP ARGC1A/PIK3R3/MLXIP/PIK3CD/RE LA/CREB1/GSK3B/STAT3/SLC27A6/S LC2A4/G6PC2/PTPA/PPP1R3E/SLC2A 2/SREBF1/RPS6KA2/PIK3CA/AKT1/P CK2/CREB3L2/IRS2/CREB3L3/IKBKB /PRKCD/PRKAG1/PPP1CB/PTPN11/PR KCB/PRKAA1/PPP1CC/RPS6KA6/SLC	106

							2A1/SLC27A5/PPP1R3B/PRKCE/PRKA A2/IL6/G6PC/CREB3/TRIB3/NOS3/PR KAB2/PYGB/SLC27A2/IRS1/MTOR/PI K3R2/CREB3L1/PYGL/MAPK9/PTPRF /SLC27A1/SLC27A3/PPP1R3A/PRKAB 1/RPS6KA1/PCK1/SOCS3/MLXIPL/AG T/FOXO1/NFKBIA/PPP1R3D/PRKCQ/ PTPN1/TNF/CRTC2/MLX/PPP1R3C/T NFRSF1A/G6PC3/GFPT2/SLC27A4/IN S/PTEN/NR1H2/PRKAG3/PYGM/GYS1 /GYS2/RPS6KB2/PRKCZ/ACACB	
hsa049 22	Glucagon signaling pathway	105/710 9	107/81 05	9.56235 E-05	0.00313 4295	0.00205 5769	ITPR1/PRKACB/PFKM/CAMK2G/ACA CA/PLCB2/GNAS/PRKAG2/CREB3L4/ AKT2/AKT3/ATF2/CREB5/PLCB4/PH KA1/PDHA1/PPP4R3B/CAMK2D/PPA RA/CALML4/PKM/CPT1A/CPT1B/CA LM3/CREBBP/PPARGC1A/ATF4/CRE B1/CPT1C/G6PC2/SLC2A2/LDHB/PRK ACA/PPP3CB/AKT1/PCK2/PLCB3/CA MK2B/CREB3L2/ADCY2/CREB3L3/G NAQ/PPP4C/CAMK2A/PRKAG1/PHK G2/PRKAA1/PPP3CA/SLC2A1/ITPR2/	105

							LDHC/SIK2/PRKAA2/EP300/PGAM1/ G6PC/PPP3R2/PHKA2/CREB3/GCK/PF KP/PPP4R3C/PDE3B/PRKAB2/PYGB/S IRT1/FBP1/PHKG1/CREB3L1/PYGL/P DHB/PRKAB1/LDHA/PCK1/PDHA2/F OXO1/PPP4R3A/PHKB/PRKACG/LDH AL6B/CRTC2/PFKFB1/CALM1/PPP3C C/CALML6/PFKL/PLCB1/G6PC3/CAL ML3/LDHAL6A/FBP2/GCGR/PRMT1/P RKAG3/PYGM/PGAM4/GYS1/CALML 5/CALM2/PPP3R1/GCG/GYS2/SIK1B/P GAM2/ACACB	
hsa054 10	Hypertrophic cardiomyopathy	89/7109	90/810 5	9.62939 E-05	0.00313 4295	0.00205 5769	CACNA1C/TTN/CACNB4/DMD/SLC8 A1/CACNB2/DAG1/ATP2A3/LMNA/IT GA7/TPM3/CACNA2D2/CACNA1D/PR KAG2/TNNT2/ITGB4/ITGB8/IGF1/CA CNA1F/ATP2A2/ITGA10/TPM4/SGCD/ CACNA2D1/SLC8A3/ITGAV/TPM1/IT GA6/ITGB6/TGFB2/ITGA4/LAMA2/IT GB1/CACNB1/RYR2/ATP2A1/CACNG 7/CACNA1S/CACNG6/ITGA2B/ITGA3 /PRKAG1/PRKAA1/ITGB7/LAMA1/IT	89

							GB3/CACNA2D4/PRKAA2/ITGB5/IL6/ITGA5/ITGA9/CACNB3/PRKAB2/CACNG4/ITGA2/CACNG8/ITGA1/SGCB/TGFB3/PRKAB1/MYH7/ACE/AGT/TNNI3/CACNA2D3/SLC8A2/CACNG5/TNF/ACTG1/EMD/ITGA8/TPM2/ITGA11/ACTC1/SGCG/MYH6/CACNG3/DES/CACNG2/SGCA/PRKAG3/MYL2/MYBPC3/TGFB1/EDN1/ACTB/TNNC1/MYL3	
hsa05417	Lipid and atherosclerosis	205/7109	215/8105	9.9488E-05	0.003134295	0.002055769	MAPK10/ITPR1/POU2F1/NLRP3/PTK2/PIK3R1/NFATC2/CAMK2G/BAX/PLCB2/NFATC3/CD36/MAPK8/TP53/AKT2/BCL2L1/AKT3/CASP7/MAPK14/CYP1A1/APAF1/CASP9/PLCB4/PDPK1/VCA M1/CYP2C8/CAMK2D/CDC42/POU2F2/IRAK4/CALML4/LDLR/ABCG1/TLR4/PIK3CB/CASP3/NFKB1/CALM3/CASP1/APOB/PIK3R3/RHOA/NFATC1/MA P2K6/MAPK1/ATF4/PIK3CD/VAV3/RELA/GSK3B/TANK/SELP/IRAK1/STAT3/MAP2K3/OLR1/NOX1/NFE2L2/MA P2K7/MAP2K4/MYD88/PLCG1/BID/T	205

							LR2/CCL5/CASP8/ARHGEF1/POU2F3/ TRAF6/VAV1/APOA1/HSP90AB1/SOD 2/IKBKG/VLDLR/IKBKE/PPP3CB/TA B2/TIRAP/RXRA/PIK3CA/AKT1/ABC A1/NCF2/AGER/DDIT3/IRF3/PLCB3/C AMK2B/HSPA8/TLR6/CYP2B6/IKBKB /CAMK2A/IL18/TAB1/FAS/ROCK2/HS P90AA1/CYP2C9/PPP3CA/CYBB/KRA S/RXRB/IRF7/ATF6/SELE/TNFRSF10B /HSPA1L/IL6/HSPA5/FASLG/RAP1B/P PP3R2/BCL2/NOS3/VAV2/TNFSF10/C ASP6/HSPA6/CHUK/PIK3R2/CYP2A7/ MMP9/CD14/ERN1/MAPK9/NCF4/IL1 2B/MMP1/RAP1A/JAK2/FOS/CYCS/PP ARG/IL1B/MAPK12/TRAF3/LYN/RAC 1/ICAM1/TRAF2/TBK1/IL12A/BAD/R XRG/SRC/MAPK3/CD40/HSPD1/CCL3 /CCL3L3/NFKBIA/IFNA2/LBP/MIB2/ MAPK11/TNF/CALM1/NRAS/EIF2AK 3/XBP1/MAPK13/PPP3CC/CALML6/M IB1/TNFRSF1A/EIF2S1/IFNB1/ERO1A/ PLCB1/CYBA/LY96/CALML3/CXCL8/	
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							TICAM2/HSPA2/TICAM1/CXCL2/MA P3K5/CYP2J2/IFNA4/HSPA4/CXCL3/H RAS/IFNA1/CALML5/IFNA21/IFNA14/ CXCL1/CALM2/CD40LG/PPP3R1/APO A4/MMP3/JUN/TNFRSF10A/NCF1/CC L2/HSPA1A/HSP90B1/IFNA16/CYP2A 6/IFNA6/HSPA1B	
hsa042 61	Adrenergic signaling in cardiomyocytes	145/710 9	150/81 05	0.00010 7237	0.00313 4295	0.00205 5769	CACNA1C/CACNB4/SLC8A1/PRKAC B/CACNB2/CREM/CAMK2G/ATP2A3/ KCNE1/PPP2R5C/ATP2B2/PLCB2/TP M3/ATP2B3/GNAS/CACNA2D2/CACN A1D/CREB3L4/AKT2/AKT3/ATF2/PPP 2R1B/MAPK14/CREB5/PLCB4/CAMK 2D/TNNT2/ADCY3/CALML4/CACNA1 F/ATP2A2/ADCY5/RAPGEF4/RPS6KA 5/TPM4/CALM3/PPP2R3A/ADCY7/RA PGEF3/PIK3R5/CACNA2D1/PPP2R2A/ MAPK1/ATF4/PPP2R2C/CREB1/SLC8 A3/ATF6B/SCN7A/ATP2B4/TPM1/PPP 2R5E/ATP2B1/AGTR1/ADCY4/PRKAC A/PIK3CG/CACNB1/ADCY8/AKT1/G NAI2/SCN1B/PPP2R5D/ADRA1A/RYR	145

							2/ATP2A1/PLCB3/CAMK2B/CREB3L2 /CACNG7/CACNA1S/CACNG6/ADCY 2/CREB3L3/GNAQ/CAMK2A/PPP1CB/ PPP2R2B/ATP1B4/PPP1CC/ATP1A2/A DCY6/SCN5A/SLC9A1/CACNA2D4/A TP1A1/CACNB3/CREB3/BCL2/CACN G4/ADCY9/ADRB2/PPP2CA/PPP2R2D/ ATP1B2/CACNG8/CREB3L1/KCNE1B/ PIK3R6/KCNQ1/MAPK12/ATP1A4/AT P1B3/AGTR2/SCN4B/MYH7/AGT/PPP 2R5A/MAPK3/TNNI3/CACNA2D3/PPP 1R1A/SLC8A2/CACNG5/PRKACG/MA PK11/CALM1/ADRA1B/MAPK13/CAL ML6/TPM2/ACTC1/PLCB1/PPP2CB/C ALML3/MYH6/PLN/ADCY1/ADRB1/C ACNG3/GNAI1/PPP2R3B/GNAI3/CAC NG2/MYL2/ATP1B1/ATP1A3/ADRA1 D/CALML5/CALM2/MYL4/PPP2R5B/P PP2R3C/TNNC1/MYL3	
hsa049 28	Parathyroid hormone synthesis, secretion and	104/710 9	106/81 05	0.00010 7288	0.00313 4295	0.00205 5769	ITPR1/PRKACB/MEF2C/PDE4D/PLCB 2/SP1/MEF2A/GNAS/AKAP13/CREB3 L4/ATF2/CREB5/GNA12/PLCB4/LRP6/	104

	action						ADCY3/PDE4A/ARRB1/MEF2D/ADCY5/PDE4B/PDE4C/ADCY7/RHOA/ARRB2/ARHGEF11/MAPK1/ATF4/CREB1/ATF6B/BRAF/GNA13/SLC34A2/ARAF/ARHGEF1/ADCY4/PRKACA/CASR/SLC34A1/TRPV5/ADCY8/SLC34A3/RXRA/GNAI2/PLCB3/CREB3L2/ADCY2/CREB3L3/GNAQ/FGFR1/TNFSF11/NR4A2/PRKCB/CYP27B1/MMP24/RAF1/ADCY6/RXRB/RUNX2/ITPR2/MAP2K1/EGFR/VDR/MMP16/NACA/CREB3/BCL2/MMP15/MMP13/ADCY9/PTH1R/SOST/CREB3L1/HBEGF/FOS/CYP24A1/GCM1/RXRG/GATA3/MAPK3/PLD2/FGF23/MMP14/MMP17/CDKN1A/PTHLH/PRKACG/PTH/PLCB1/GNA11/MAFB/GCM2/ADCY1/GNAI1/GNAI3/LRP5/PLD1/KL/JUND/MMP25/PRKCG/BGLAP/SLC9A3R1/EGR1	
hsa04211	Longevity regulating pathway	88/7109	89/8105	0.000108809	0.003134295	0.002055769	PRKACB/TSC2/EIF4E/PIK3R1/TSC1/BAX/CAMKK2/PRKAG2/CREB3L4/ATG13/TP53/AKT2/AKT3/ATF2/RPS6KB	88

							1/CREB5/FOXO3/ADCY3/EHMT1/EIF4E2/SESN1/IGF1/ADCY5/PIK3CB/NFKB1/INSR/PPARGC1A/ADCY7/PIK3R3/ATG5/ATF4/PIK3CD/RELA/ADIPOQ/CREB1/SESN3/ATF6B/ADIPOR2/ADCY4/PRKACA/SOD2/CAMK4/ADCY8/PIK3CA/AKT1/EHMT2/CREB3L2/IRS2/ADCY2/CREB3L3/PRKAG1/PRKAA1/ADCY6/KRAS/SESN2/PRKAA2/RB1C1/IGF1R/CREB3/PRKAB2/ADCY9/IRS1/MTOR/SIRT1/AKT1S1/PIK3R2/ATG101/CREB3L1/RHEB/PRKAB1/ULK1/PPARG/RPTOR/FOXO1/ADIPOR1/PRKACG/NRAS/CAT/ADCY1/INS/EIF4E1B/IRS4/PRKAG3/KL/HRAS/APPL1/RPS6KB2/STK11	
hsa04510	Focal adhesion	192/7109	201/8105	0.000115794	0.003134295	0.002055769	MAPK10/LAMA3/COL6A3/PAK3/CTNNB1/PPP1R12B/PTK2/MYLK/PIP5K1A/PIK3R1/MET/LAMA4/PXN/VEGFA/FN1/BCAR1/ITGA7/PAK4/MAPK8/COL4A6/THBS3/AKT2/TNC/AKT3/LAMC2/PDPK1/FYN/TNR/CDC42/ITGB4/ITG	192

							B8/IGF1/PPP1R12A/ERBB2/ELK1/EGF /ITGA10/MYLK3/PIK3CB/LAMB3/XIA P/PIK3R3/RHOA/LAMB1/LAMB2/MY LK4/MAPK1/PIK3CD/HGF/FLT1/LAM B4/VAV3/RASGRF1/ARHGAP5/CAV1/ PARVB/SHC1/ITGAV/GSK3B/CCND3/ COL4A5/BRAF/ITGA6/SPP1/ITGB6/M YL12A/ITGA4/LAMA2/FLNC/VWF/V AV1/ITGB1/COL4A4/COL9A1/VCL/PI K3CA/AKT1/PIP5K1B/RELN/PAK6/PD GFRA/CCND2/PAK5/COL4A3/ILK/IT GA2B/ITGA3/COL4A1/CAV2/PPP1CB/ ROCK2/COL6A6/PARVG/PRKCB/PPP 1CC/RAF1/ITGB7/LAMA1/ITGB3/MA P2K1/COL2A1/EGFR/FLNA/KDR/ITG B5/COL6A5/SHC4/LAMC1/ITGA5/CO L4A2/RAPGEF1/RAP1B/VEGFB/BIRC 3/ITGA9/LAMC3/CAV3/IGF1R/SOS1/ DIAPH1/BCL2/VAV2/CRK/MYL10/TN N/THBS1/THBS4/PAK2/PAK1/PIK3R2/ ITGA2/BUB1B- PAK6/MYL7/MAPK9/ITGA1/DOCK1/F	
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							LNB/PDGFRB/RAP1A/RAC2/TLN2/VE GFD/CRKL/LAMA5/CCND1/RAC1/PA RVA/BAD/SRC/COL1A2/MAPK3/COL 9A2/PDGFB/THBS2/VEGFC/SHC3/MY L12B/FLT4/ACTN1/ROCK1/COMP/AC TG1/CHAD/TLN1/PDGFC/ZYX/GRB2/ ITGA8/PPP1R12C/ITGA11/MYLK2/TN XB/IBSP/ARHGAP35/MYLPF/PIP5K1 C/PDGFD/SHC2/COL6A1/PTEN/MYL9 /MYL5/COL6A2/MYL2/PDGFA/COL1 A1/HRAS/VASP/PRKCG/JUN/ACTB/V TN	
hsa040 10	MAPK signaling pathway	277/710 9	294/81 05	0.00012 3848	0.00313 4295	0.00205 5769	MAPK10/CACNA1G/CACNA1C/MAP4 K4/FGF1/RPS6KA3/CACNB4/PRKACB /CACNB2/MEF2C/BDNF/FGFR2/MET/ VEGFA/NTRK2/TGFBR1/TGFA/DAX X/NFATC3/MAPT/MAPK8/CACNA2D 2/CACNA1D/ANGPT1/EFNA5/TP53/M RAS/AKT2/AKT3/ATF2/CDC25B/MAP K14/MAX/ERBB4/MAP3K12/GNA12/C ACNA1A/IL1RAP/RAPGEF2/CDC42/R ASGRP1/CACNA1E/CACNA1I/IRAK4/	277

							STMN1/IGF1/MECOM/CACNA1F/ERB B2/ELK1/EGF/ARRB1/NF1/TAOK3/M KNK1/ANGPT2/RPS6KA5/MAP3K20/ CASP3/NFKB1/INSR/FLT3LG/PPM1B/ CACNA2D1/EFNA4/ARRB2/NR4A1/M APKAPK3/NFATC1/MAP2K6/MAPK1/ ATF4/HGF/FLT1/RASGRF1/RELA/RA SGRP4/ECSIT/DUSP4/IRAK1/MAP2K3 /BRAF/TAOK1/TEK/MAP2K7/MAP2K 4/MAPK7/CSF1/MYD88/MAP3K13/KI TLG/PPM1A/TGFB2/ARAF/PTPRR/M YC/RASGRP2/FLNC/CACNA1H/FGF5/ TRAF6/STK4/EFNA1/MAP3K4/PRKA CA/IKBKG/RPS6KA2/LAMTOR3/CAC NB1/PPP3CB/TAB2/ELK4/AKT1/MAP K8IP3/TAOK2/RPS6KA4/PDGFR/DD IT3/HSPA8/CACNG7/CACNA1S/ERBB 3/CACNG6/MAP3K2/JMJD7- PLA2G4B/IKBKB/FGFR1/TAB1/FAS/R ASGRP3/MAP3K6/PRKCB/RPS6KA6/P PP3CA/RAF1/KRAS/FGF8/RASA1/MA P2K1/EGFR/NTF3/CACNA2D4/KIT/R	
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							ASGRF2/FGF2/FGFR4/FLNA/KDR/MA PKAPK5/HSPA1L/NFKB2/NTRK1/STK 3/DUSP6/IL1R1/FASLG/MAP4K3/RAP 1B/VEGFB/CACNB3/IL1A/IGF1R/PPP 3R2/FLT3/MAP4K2/SOS1/RRAS2/CRK /DUSP16/RASA2/CACNG4/DUSP10/PL A2G4D/PLA2G4F/NGFR/ANGPT4/PA K2/MAP2K5/PAK1/MAP3K14/HSPA6/ PLA2G4B/CHUK/PTPN5/CACNG8/CD 14/NLK/MAPK9/CSF1R/FLNB/PDGFR B/FGF9/RAP1A/RAC2/DUSP1/FGF4/V EGFD/MAP3K1/FOS/TGFB3/EFNA3/C RKL/DUSP7/IL1B/MAPK12/RPS6KA1/ MAPK8IP2/RAC1/EPHA2/TRAF2/MAP 3K3/CACNA1B/MAPK3/CACNA2D3/F GF23/PDGFB/IGF2/FGF21/GADD45B/ VEGFC/CACNG5/FLT4/MAPK8IP1/PR KACG/MAP4K1/FGF3/MAPK11/PTPN 7/TNF/EREG/FGF7/NRAS/FGFR3/TGF BR2/MAPK13/PDGFC/PPP3CC/GRB2/ NGF/TNFRSF1A/DUSP3/FGF6/MAPK APK2/SRF/DUSP5/GNG12/PLA2G4A/T	
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							RADD/INS/HSPA2/CACNG3/DUSP8/D USP2/MAP3K5/PDGFD/CACNG2/REL B/MAP3K11/PDGFA/FGF17/HRAS/GA DD45G/JUND/PLA2G4C/AREG/FGF20 /PPP3R1/PRKCG/JUN/EFNA2/HSPB1/ TGFB1/HSPA1A/MAP3K8/PPP5C/MK NK2/HSPA1B	
hsa046 70	Leukocyte transendothelial migration	111/710 9	114/81 05	0.00024 1716	0.00540 8563	0.00354 745	CTNND1/CTNNB1/PTK2/CTNNA2/PI K3R1/PXN/RHOH/BCAR1/CD99L2/RA SSF5/MAPK14/PTK2B/OCLN/VCAM1/ CDC42/AFDN/RAPGEF4/PIK3CB/RAP GEF3/PIK3R3/RHOA/CLDN2/PIK3CD/ VAV3/ARHGAP5/MMP2/SIPA1/ITGA M/ITGAL/PLCG1/CXCL12/MYL12A/J AM3/ITGA4/CLDN10/VAV1/ITGB1/V CL/PIK3CA/GNAI2/CLDN18/NCF2/PL CG2/MSN/THY1/CLDN14/ROCK2/PTP N11/ITGB2/PRKCB/CTNNA3/CYBB/P ECAM1/RAP1B/CLDN1/CLDN15/VAV 2/MYL10/CLDN19/CLDN6/PIK3R2/M MP9/MYL7/F11R/NCF4/RAP1A/RAC2/ CLDN8/MAPK12/RAC1/ICAM1/ESAM	111

							/CLDN24/CXCR4/CLDN7/ITK/MYL12 B/ACTN1/ROCK1/MAPK11/ACTG1/E ZR/CLDN3/TXK/CLDN16/MAPK13/CT NNA1/JAM2/CYBA/CLDN23/ARHGA P35/CLDN17/MYLPF/CDH5/CLDN4/G NAI1/GNAI3/MYL9/MYL5/CLDN22/M YL2/CLDN5/CLDN20/CLDN9/CLDN25 /CD99/VASP/PRKCG/CLDN11/NCF1/A CTB	
hsa003 10	Lysine degradation	63/7109	63/810 5	0.00024 9893	0.00540 8563	0.00354 745	NSD2/PRDM2/EZH1/NSD1/SMYD1/E HMT1/MECOM/KMT2A/SETDB2/KM T2D/SETDB1/KMT2B/ACAT1/SETD2/ EHHADH/KMT5B/SUV39H1/DLD/SET D1B/PRDM7/EZH2/SETMAR/EHMT2/ ASH1L/KMT2E/ALDH3A2/ALDH7A1/ PLOD2/ALDH1B1/HYKK/SETD7/HAD H/COLGALT2/AASS/AADAT/HADHA /KMT2C/PRDM6/DHTKD1/TMLHE/B BOX1/CAMKMT/ALDH9A1/ALDH2/P LOD3/PHYKPL/ECHS1/SUV39H2/PLO D1/KMT5C/PIPOX/PRDM16/NSD3/DO T1L/PRDM9/COLGALT1/SMYD3/ACA	63

							T2/KMT5A/GCDH/DLST/SETD1A/SM YD2	
hsa040 22	cGMP-PKG signaling pathway	160/710 9	167/81 05	0.00026 303	0.00540 8563	0.00354 745	KCNMA1/CACNA1C/SLC8A1/ITPR1/ MEF2C/MYLK/NFATC2/GUCY1A1/N FATC4/ATP2A3/MRVI1/ATP2B2/PLC B2/MEF2A/GTF2I/NFATC3/ATP2B3/C ACNA1D/CREB3L4/AKT2/AKT3/ATF 2/GTF2IRD1/PDE5A/CREB5/GNA12/P LCB4/ADCY3/PRKG2/CALML4/PPP1 R12A/CACNA1F/ATP2A2/MEF2D/KC NMB2/EDNRB/ADCY5/MYLK3/INSR/ CALM3/ADCY7/PIK3R5/RHOA/NFAT C1/MYLK4/MAPK1/ATF4/CREB1/SLC 8A3/GUCY1A2/ATF6B/ATP2B4/GNA1 3/ATP2B1/KCNMB3/AGTR1/PDE2A/A DCY4/KCNJ8/PIK3CG/PPP3CB/ADCY 8/AKT1/GNAI2/ADRA1A/ATP2A1/PL CB3/CREB3L2/IRS2/CACNA1S/ADCY 2/CREB3L3/GNAQ/CNGB1/PPP1CB/K NG1/GATA4/ROCK2/ATP1B4/PPP1CC /ATP1A2/PPP3CA/RAF1/ADCY6/ITPR 2/VDAC3/MAP2K1/GUCY1B1/PRKCE/	160

							ATP1A1/NPR2/PDE3A/PPP3R2/CREB3 /PRKG1/VDAC2/NOS3/SLC25A4/PDE3 B/ADCY9/ADRB2/IRS1/NPR1/ATP1B2 /BDKRB2/ADORA3/CREB3L1/PIK3R6 /PPIF/ATP1A4/ATP1B3/MYH7/CNGA1 /TRPC6/KCNMB4/BAD/ADRA2A/MA PK3/VDAC1/NPPA/SLC8A2/ROCK1/C ALM1/ADRA1B/PPP3CC/CALML6/PL CB1/MYLK2/MEF2B/GNA11/SRF/CAL ML3/MYH6/NPPC/PLN/RGS2/KCNU1/ ADCY1/ADRA2B/ADRB1/INS/ADRA2 C/BORCS8- MEF2B/GNAI1/GNAI3/MYL9/IRS4/SL C25A31/ATP1B1/ATP1A3/ADRA1D/N PPB/CALML5/CALM2/EDNRA/PPP3R 1/VASP/KCNMB1/OPRD1/SLC25A5	
hsa042 13	Longevity regulating pathway - multiple species	62/7109	62/810 5	0.00028 5212	0.00548 0334	0.00359 4524	PRKACB/PIK3R1/PRKAG2/AKT2/AK T3/RPS6KB1/FOXO3/ADCY3/CLPB/IG F1/ADCY5/PIK3CB/INSR/ADCY7/PIK 3R3/ATG5/PIK3CD/CRYAB/ADCY4/P RKACA/SOD2/HDAC2/ADCY8/PIK3C A/AKT1/HSPA8/IRS2/ADCY2/PRKAG	62

							1/PRKAA1/ADCY6/KRAS/EIF4EBP2/PRKAA2/HSPA1L/IGF1R/PRKAB2/ADCY9/IRS1/MTOR/SIRT1/AKT1S1/HSPA6/PIK3R2/SOD1/PRKAB1/FOXA2/RPTOR/FOXO1/PRKACG/NRAS/CAT/ADCY1/INS/HSPA2/IRS4/PRKAG3/HRAS/HDAC1/RPS6KB2/HSPA1A/HSPA1B	
hsa052 15	Prostate cancer	95/7109	97/810 5	0.00029 9836	0.00548 0334	0.00359 4524	CTNNB1/PIK3R1/FGFR2/TGFA/ERG/CREB3L4/TP53/AKT2/AKT3/CREB5/MDM2/CASP9/PDPK1/TCF7L2/AR/TCF7/CCNE1/IGF1/ERBB2/EGF/PIK3CB/NFKB1/CREBBP/PIK3R3/MAPK1/ATF4/PIK3CD/PLAU/RELA/CREB1/LEF1/IL1R2/ZEB1/GSK3B/BRAF/CDK2/ARAF/PALAT/E2F3/HSP90AB1/IKBKG/PIK3CA/AKT1/PDGFR/CREB3L2/E2F2/CREB3L3/IKBKB/FGFR1/HSP90AA1/TMPRSS2/RAF1/KRAS/MAP2K1/KLK3/EGFR/EP300/IGF1R/CREB3/SOS1/BCL2/INSRR/NKX3-1/MTOR/CCNE2/CHUK/PIK3R2/MMP9/CREB3L1/PDGFRB/CCND1/BAD/RB	95

							1/FOXO1/MAPK3/PDGFB/NFKBIA/CDKN1A/ETV5/CDKN1B/NRAS/PDGFC/GRB2/SRD5A2/E2F1/SPINT1/INS/PDGF/PTEN/PDGFA/HRAS/GSTP1/MMP3/TCF7L1/HSP90B1	
hsa05414	Dilated cardiomyopathy	94/7109	96/8105	0.000335783	0.005604375	0.003675882	CACNA1C/TTN/CACNB4/DMD/SLC8A1/PRKACB/CACNB2/DAG1/ATP2A3/LMNA/ITGA7/TPM3/GNAS/CACNA2D2/CACNA1D/TNNT2/ADCY3/ITGB4/ITGB8/IGF1/CACNA1F/ATP2A2/ADCY5/ITGA10/TPM4/SGCD/ADCY7/CACNA2D1/SLC8A3/ITGAV/TPM1/ITGA6/ITGB6/TGFB2/ITGA4/LAMA2/ADCY4/PRKACA/ITGB1/CACNB1/ADCY8/RYR2/ATP2A1/CACNG7/CACNA1S/CACNG6/ADCY2/ITGA2B/ITGA3/ADCY6/ITGB7/LAMA1/ITGB3/CACNA2D4/ITGB5/ITGA5/ITGA9/CACNB3/CACNG4/ADCY9/ITGA2/CACNG8/ITGA1/SGCB/TGFB3/MYH7/AGT/TNNI3/CACNA2D3/SLC8A2/CACNG5/PRKACG/TNF/ACTG1/EMD/ITGA8/TPM2/ITGA11/A	94

							CTC1/SGCG/MYH6/PLN/ADCY1/ADRB1/CACNG3/DES/CACNG2/SGCA/MYL2/MYBPC3/TGFB1/ACTB/TNNC1/MYL3	
hsa04915	Estrogen signaling pathway	133/7109	138/8105	0.000355142	0.005604375	0.003675882	ITPR1/PRKACB/PIK3R1/OPRM1/PLCB2/SP1/TGFA/FKBP5/ESR1/GNAS/GRM1/CREB3L4/AKT2/AKT3/ATF2/CREB5/PLCB4/KRT40/PGR/ESR2/ADCY3/CALML4/ADCY5/PIK3CB/CALM3/ADCY7/PIK3R3/MAPK1/ATF4/PIK3CD/GABBR1/CREB1/SHC1/MMP2/ATF6B/RARA/NCOA1/KRT23/NCOA3/ADCY4/PRKACA/HSP90AB1/ADCY8/GPER1/PIK3CA/AKT1/GNAI2/NCOA2/PLCB3/HSPA8/CREB3L2/KRT35/ADCY2/CREB3L3/GNAQ/PRKCD/HSP90AA1/RAF1/ADCY6/KRAS/ITPR2/MAP2K1/EGFR/POMC/KCNJ5/HSPA1L/SHC4/KRT24/CREB3/SOS1/BCL2/KRT27/EBAG9/NOS3/ADCY9/KRT26/KRT13/HSPA6/KRT33B/PIK3R2/MMP9/CREB3L1/KRT34/KCNJ6/KRT38/HBEGF/KRT12/FOS/	133

							KRT28/KRT36/FKBP4/KRT16/KCNJ9/ KRT14/KRT18/KRT15/KRT10/SRC/KR T9/MAPK3/GNAO1/SHC3/PRKACG/K RT39/KRT37/CALM1/NRAS/GRB2/CA LML6/KRT31/PLCB1/CALML3/KRT33 A/ADCY1/HSPA2/CTSD/KRT20/GNAI 1/GNAI3/SHC2/KCNJ3/HRAS/CALML 5/CALM2/GABBR2/KRT25/KRT32/KR T17/JUN/HSPA1A/HSP90B1/KRT19/H SPA1B	
hsa051 68	Herpes simplex virus 1 infection	460/710 9	498/81 05	0.00037 1933	0.00560 4375	0.00367 5882	ZNF133/POU2F1/TSC2/ZNF302/PIK3R 1/ZNF248/JAK1/TSC1/ZNF331/BAX/Z NF200/ZNF398/DAXX/ZNF268/ZNF2/Z NF473/PML/ZNF214/TP53/AKT2/BCL2 L1/CD74/AKT3/ZNF81/ZNF304/ZNF77 2/ZNF426/ZNF484/APAF1/ZNF33A/CA SP9/ZNF226/ZNF195/POU2F2/IRAK4/ EIF2B3/ZNF544/ZNF3/ZNF662/ZNF84/ PIK3CB/CASP3/NFKB1/ZNF557/ZNF5 66/ZNF570/PIK3R3/ZNF550/ZNF227/O AS2/MAVS/PIK3CD/ZNF189/C3/IFNA R2/ZNF334/ZNF555/RELA/ZNF285/ZN	460

							F619/ZNF283/OAS1/ZNF436/ZNF641/I RAK1/ZNF208/ZNF605/ZFP90/ZNF333 /ZIK1/ZNF235/ZNF621/ZNF778/TRAF5 /MYD88/ZNF419/BID/ZNF181/ZNF630 /HCFC1/ZNF562/RNASEL/ZNF701/ZN F320/EIF2AK2/TAPBP/ZNF233/HLA- DQB1/ZNF567/TLR2/NXF1/CCL5/ZNF 569/CASP8/ZNF793/ZNF300/IFNAR1/P OU2F3/ZNF184/ZNF418/ZNF250/TRAF 6/HCFC2/NECTIN1/ZNF286A/ZNF785/ ZNF205/ZNF610/ZNF688/ZNF561/ZNF 546/IKBKG/ZNF282/ZNF727/ZNF74/Z NF141/ZNF510/IKBKE/ZNF383/ZNF45 /TAB2/PIK3CA/AKT1/ZNF667/ZNF773 /ZNF611/ZNF514/ZNF620/ZNF317/IRF 3/ZNF607/ZNF354C/ZNF254/ZNF33B/ ZNF43/ZNF337/ZNF726/ZNF623/ZNF7/ ZNF689/SRSF6/ZNF780A/ZNF613/ZNF 658/IKBKB/ZNF829/TAB1/FAS/PPP1C B/ZNF180/OAS3/ZNF679/PTPN11/ZNF 764/ZFP1/HLA- F/SP100/ZNF587/ZNF568/PPP1CC/ZNF	
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							736/ZSCAN32/ZFP69/ZNF805/ZNF527/ TNFSF14/ZNF229/STAT2/IRF7/ITGB3/ TLR9/ZNF614/ZNF780B/RBAK/ZNF21 1/ZNF135/SRSF1/ZNF107/STAT1/ZNF 160/SYK/SRPK1/ZNF596/ZFP30/ZNF2 34/ZNF112/ZNF420/ZNF713/ZNF766/I L6/NXF2/NXF2B/ZNF777/ITGA5/FAS LG/ZNF460/ZNF37A/ZNF558/BIRC3/Z NF23/ZNF382/ZNF585A/ZNF597/ZFP1 4/ZNF768/ZNF746/EIF2AK4/ZNF417/H LA- DQA1/BCL2/IFNGR2/EIF2B4/ZNF548/ ZNF674/ZNF25/ZNF540/SRSF7/C5/ZN F606/DDX58/SRSF4/ZNF577/MTOR/Z NF79/ZNF311/ZNF182/TAP2/ZNF154/ HLA- G/ZNF551/CHUK/PIK3R2/ZNF12/ZNF 589/ZNF790/TLR3/ZNF175/ZNF559/ZN F432/HLA- DPB1/ZNF529/ZNF534/ZNF101/NECTI N2/ZNF624/PDIA3/IL12B/ZNF573/JAK 2/ZNF547/TYK2/ZNF649/ZNF275/ZNF	
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							343/ZNF316/ZNF578/ZNF888/RHEB/Z NF699/ZFP37/ZNF816/CYCS/NXF3/ZN F41/IL1B/ZNF140/HLA- DMB/TRAF3/ZNF600/TNFRSF14/HLA - A/SOCS3/ZNF324B/ZNF708/IFIH1/ZN F814/CARD9/TRAF2/ZNF490/SRSF3/Z NF556/ZNF705E/ZNF583/ZNF682/TBK 1/IL12A/ZNF99/ZNF212/ZNF480/ZNF1 7/ZNF549/BAD/ZNF114/HLA- DPA1/SRC/ZNF221/ZNF615/ZNF85/HL A-B/HLA- C/ZNF714/ZNF554/ZNF224/ZNF707/Z NF836/ZNF251/ZNF34/ZNF223/NFKBI A/IFNA2/ZNF543/ZNF530/ZNF670/ZN F470/ZNF845/ZNF324/ZNF582/ZFP28/ ZNF284/ZNF709/ZNF471/ZNF737/TNF/ ZNF684/ZNF57/ZNF433/ZNF799/ZNF7 92/ZFP82/ZNF528/HLA- DQA2/ZNF559- ZNF177/ZNF177/EIF2AK3/ZNF850/ZN F571/HLA-	
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							DRB1/LTA/SRSF5/ZNF8/ZNF717/ZNF730/SRSF2/ZNF132/ZNF404/PILRB/ZNF517/ZNF441/ZNF584/TNFRSF1A/EIF2S1/ZNF761/PILRA/IFNB1/HLA-DOB/ZNF468/ZNF665/IFNGR1/ZNF479/TAP1/ZNF879/HLA-DOA/IRF9/ZNF415/ZNF891/ZNF222/ZNF442/ZNF157/ZNF416/ZNF791/ZNF627/ZNF169/ZNF705D/TRADD/EIF2B2/ZNF560/ZNF519/ZNF729/EIF2B1/ZNF749/ZIM3/ZNF354A/NXF5/TICAM1/HLA-DMA/ZNF100/ZNF20/ZNF783/IFNG/ZNF454/ZNF718/ZNF716/ZNF225/HLA-E/IFNA4/ZNF267/ZNF155/ZNF808/ZNF30/ZNF700/ZNF44/SRSF8/ZNF93/EIF2AK1/HLA-DRB5/ZNF786/ZNF91/ZNF669/ZNF563/ZNF552/ZNF354B/IFNA1/ZNF585B/ZNF765/ZNF257/ZNF705A/ZNF10/ZNF439/ZNF19/B2M/ZNF616/ZNF26/ZNF461/IFNA21/IFNA14/ZNF846/ZNF782/SR	
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							SF9/ZFP57/ZNF565/CFP/ZNF492/ZNF860/ZNF429/ZNF813/ZNF721/ZNF77/FADD/EIF2B5/ZNF136/ZNF253/ZNF98/ZNF273/CCL2/ZNF853/ZNF677/ZNF671/ZNF256/ZNF425/ZNF347/ZNF680/CGAS/IFNA16/ZNF14/ZNF440/ZNF443/ZNF841/ZNF675/IFNA6/ZNF763		
hsa04140	Autophagy animal	-	132/7109	137/8105	0.000391795	0.005604375	0.003675882	MAPK10/ITPR1/PRKACB/TSC2/PIK3R1/TSC1/CAMKK2/MAPK8/ATG16L1/ATG13/MRAS/AKT2/BCL2L1/CFLAR/AKT3/RUBCN/CTSB/RPS6KB1/PDPK1/MTMR3/BECN1/PIK3CB/MTMR14/SH3GLB1/STX17/PIK3R3/ATG5/DAPK1/MAPK1/ATG2A/PIK3CD/TANK/LAMP2/AMBRA1/VMP1/ATG4A/CTSL/TP53INP2/TRAF6/PRKACA/RRAGB/C9orf72/PIK3CA/AKT1/MLST8/ATG4B/WIPI2/ATG7/RRAGD/SUPT20H/IRS2/PRKCD/PRKAA1/ULK2/RAB1A/ATG9A/NRBF2/RAF1/KRAS/WDR41/MAP2K1/ATG2B/UVRAG/PRKAA2/RB1CC1/IGF1R/EIF2AK4/BCL2/RRAS2/DEPTOR/IR	132

							S1/MTOR/AKT1S1/PPP2CA/PIK3R2/ATG101/MTMR4/ERN1/WIP1/ATG10/ MAPK9/RAB8A/HIF1A/SMCR8/RAB7B/HMGB1/RHEB/ULK1/PIK3R4/RPTOR/ZFYVE1/LAMP1/GABARAPL1/TBK1/BAD/GABARAP/ MAPK3/RAB33B/RAB39B/DAPK2/PRKCQ/DDIT4/PRKACG/NRAS/BECN2/EIF2AK3/IGBP1/EIF2S1/RRAGC/ATG16L2/PPP2CB/ATG14/ATG12/DAPK3/RAB7A/INS/CTSD/ATG4C/PTEN/PRAP1/IRS4/SQSTM1/PIK3C3/HRAS/RRAGA/ATG9B/SNAP29/RPS6KB2/VAMP8/BNIP3/STK11/ATG4D	
hsa04910	Insulin signaling pathway	132/7109	137/8105	0.000391795	0.005604375	0.003675882	MAPK10/PRKACB/TSC2/SORBS1/CBLB/EIF4E/PIK3R1/TSC1/ACACA/PRKAR1A/ MAPK8/PRKAG2/PRKAR2A/AKT2/AKT3/HK1/RPS6KB1/PDPK1/PHKA1/EXOC7/EIF4E2/CALML4/ELK1/MKNK1/PIK3CB/INSR/CALM3/PPARGC1A/PIK3R3/ MAPK1/PIK3CD/SHC1/GSK3B/SOCS2/BRAF/TRIP10/PKLR/SLC2A4/G6PC2/ARAF/PPP1R3E/SREBF	132

							1/PRKACA/PIK3CA/AKT1/PCK2/FLO T2/IRS2/IKBKB/PRKAG1/SOCS4/PPP1 CB/PHKG2/PRKAA1/PPP1CC/RAF1/K RAS/PPP1R3B/MAP2K1/PRKAA2/PRK AR1B/SHC4/LIPE/G6PC/RAPGEF1/PH KA2/SOS1/GCK/CRK/PDE3B/PRKAB2 /PYGB/RHOQ/IRS1/MTOR/PRKAR2B/ FBP1/HK3/PHKG1/FASN/PIK3R2/PYG L/MAPK9/PTPRF/CBL/PPP1R3A/HK2/ RHEB/PRKCI/PRKAB1/CRKL/PCK1/S OCS3/RPTOR/PPP1R3F/BAD/FOXO1/ MAPK3/PHKB/INPP5A/PPP1R3D/SHC 3/PTPN1/PRKACG/HKDC1/CALM1/N RAS/GRB2/CALML6/PPP1R3C/G6PC3/ CALML3/INS/FBP2/EIF4E1B/SHC2/IR S4/PRKAG3/PYGM/INPPL1/HRAS/GY S1/CALML5/CALM2/GYS2/RPS6KB2/ SOCS1/PRKCZ/ACACB/SH2B2/FLOT1 /MKNK2	
hsa045 14	Cell adhesion molecules	143/710 9	149/81 05	0.00043 1212	0.00591 1197	0.00387 7125	NFASC/NRXN1/NRXN3/NRCAM/NEO 1/CD276/CD99L2/NLGN3/NCAM1/CD 86/IGSF11/NLGN4X/CNTN1/CD28/LR	143

							RC4C/OCLN/MPZL1/VCAM1/MPZ/VC AN/NTNG1/ITGB8/NRXN2/CD6/VTC N1/CLDN2/NECTIN3/CADM3/ITGAV/ CD226/SELP/CADM1/ICOSLG/ITGAM /ITGAL/SDC1/ICAM2/ITGA6/HLA- DQB1/MAG/JAM3/ITGA4/SPN/NECTI N1/CLDN10/CD274/GLG1/TIGIT/NLG N4Y/ITGB1/CLDN18/L1CAM/PTPRM/ SDC2/SDC3/CDH3/CDH1/CLDN14/IT GB2/HLA- F/PTPRC/ITGB7/NTNG2/PVR/CNTN2/ SELE/CDH4/PECAM1/SELL/ITGA9/C LDN1/CD4/HLA- DQA1/CLDN15/CD80/LRRC4/ALCAM /NEGR1/CLDN19/CLDN6/CNTNAP2/H LA-G/CD22/F11R/HLA- DPB1/PTPRF/CNTNAP1/NECTIN2/SIG LEC1/CLDN8/NLGN2/HLA- DMB/HLA- A/ICAM1/NLGN1/CDH2/SELPLG/ICA M3/CD34/ESAM/CLDN24/HLA- DPA1/HLA-B/CD8A/CTLA4/HLA-	
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							C/CLDN7/CD40/VSIR/SDC4/CD8B/CLDN3/PDCD1LG2/HLA-DQA2/CLDN16/HLA-DRB1/ITGA8/LOC102723996/HLA-DOB/JAM2/HLA-DOA/CLDN23/CLDN17/CD8B2/CDH5/HLA-DMA/CLDN4/HLA-E/CLDN22/LRRC4B/HLA-DRB5/CLDN5/ICOS/PDCD1/CLDN20/CLDN9/CD40LG/CLDN25/CD58/NCA M2/CD99/CD2/CLDN11	
hsa054 12	Arrhythmogenic right ventricular cardiomyopathy	76/7109	77/810 5	0.00046 6522	0.00599 589	0.00393 2675	CACNA1C/CACNB4/DMD/SLC8A1/CACNB2/CTNNB1/CTNNA2/DAG1/ATP2A3/LMNA/ITGA7/CACNA2D2/CACNA1D/TCF7L2/TCF7/ITGB4/ITGB8/CACNA1F/ATP2A2/ITGA10/SGCD/CACNA2D1/SLC8A3/LEF1/ITGAV/ITGA6/DSP/ITGB6/DSC2/ITGA4/LAMA2/PKP2/ITGB1/CACNB1/RYR2/ATP2A1/CACNG7/CACNA1S/CACNG6/ITGA2B/ITGA3/ACTN2/CTNNA3/ITGB7/LAMA1/ITGB3/CACNA2D4/ITGB5/ITGA5/ITGA9/	76

							CACNB3/GJA1/CACNG4/ITGA2/CACNG8/ITGA1/SGCB/CDH2/JUP/CACNA2D3/SLC8A2/CACNG5/ACTG1/EMD/DSG2/ITGA8/ITGA11/SGCG/CTNNA1/CACNG3/DES/CACNG2/ACTN3/SGCA/ACTB/TCF7L1	
hsa04072	Phospholipase D signaling pathway	142/7109	148/8105	0.000473839	0.00599589	0.003932675	TSC2/DGKB/PIP5K1A/PIK3R1/TSC1/DNM1/AGPAT3/PLCB2/GAB1/GNAS/DNM3/SPHK2/DGKG/GRM1/DGKH/DGKI/MRAS/AKT2/AKT3/GNA12/PLCB4/PTK2B/FYN/RALGDS/ADCY3/GRM5/AGPAT1/GRM7/EGF/ADCY5/RAPGEF4/PIK3CB/INSR/ADCY7/RAPGEF3/PIK3R3/PIK3R5/RHOA/DGKZ/MAPK1/PIK3CD/SHC1/DGKK/DGKA/KITLG/PLCG1/ARF1/GNA13/LPAR3/AGTR1/LPAR5/LPAR1/ADCY4/DNM2/PIK3CG/ADCY8/GRM8/PIK3CA/AKT1/PIP5K1B/SPHK1/PDGFR/PLCB3/PLCG2/PTGFR/AVPR1A/LPAR2/ADCY2/JMJD7-PLA2G4B/GAB2/PTPN11/CYTH2/RAF1/ADCY6/KRAS/RALB/MAP2K1/AVP	142

							R1B/EGFR/SYK/KIT/F2/SHC4/GRM4/ARF6/MS4A2/SOS1/RRAS2/AGPAT4/DGKE/ADCY9/PLA2G4D/MTOR/PLA2G4F/PLA2G4B/PIK3R2/CXCR1/GRM2/CYTH4/PIK3R6/RALA/PDGFRB/GRM3/RHEB/CXCR2/AGT/AVPR2/MAPK3/PLD2/PLPP3/DGKD/PDGFB/CYTH1/SHC3/PLPP2/GRM6/NRAS/PDGFC/LPAR4/GRB2/AGPAT5/PLCB1/CYTH3/CXCL8/F2R/PLA2G4A/FCER1A/ADCY1/INS/LPAR6/PLPP1/PIP5K1C/PDGFD/SHC2/AGPAT2/PLD1/DGKQ/PDGFA/HRAS/PLA2G4C/AVP/FCER1G	
hsa04919	Thyroid hormone signaling pathway	117/7109	121/8105	0.000507601	0.006182686	0.004055193	PRKACB/TSC2/CTNNB1/PFKM/PIK3R1/ATP2A3/PLCB2/ESR1/TBC1D4/MED24/TP53/AKT2/AKT3/MDM2/THRB/CASP9/PLCB4/PDPK1/DIO1/ATP2A2/PIK3CB/PLCZ1/CREBBP/PIK3R3/MED13L/MED12L/MAPK1/PIK3CD/SLCO1C1/PFKFB2/RCAN2/ITGAV/SIN3A/GSK3B/NCOA1/NOTCH2/RCAN1/PLCG1/NCOR1/NCOA3/MYC/MED1/DIO2/PR	117

							KACA/HDAC2/RXRA/PIK3CA/AKT1/ NCOA2/ATP2A1/PLCB3/PLCG2/PLCE 1/GATA4/ATP1B4/PRKCB/ATP1A2/R AF1/KRAS/SLC2A1/MED27/RXRB/IT GB3/NOTCH4/SLC9A1/MAP2K1/STA T1/ATP1A1/EP300/PLCD4/PFKP/MTO R/BMP4/SLC16A10/THRA/DIO3/ATP1 B2/PIK3R2/SLC16A2/WNT4/MED4/HI F1A/NOTCH3/RHEB/MED13/PLCD1/A TP1A4/ATP1B3/CCND1/PLCD3/MYH7 /MED14/BAD/RXRG/SRC/FOXO1/MA PK3/MED12/PRKACG/ACTG1/NOTCH 1/NRAS/PFKL/PLCB1/MYH6/PLN/HD AC3/ATP1B1/ATP1A3/HRAS/MED17/ MED16/PRKCG/HDAC1/KAT2B/ACT B/KAT2A	
hsa051 33	Pertussis	75/7109	76/810 5	0.00052 6186	0.00618 2686	0.00405 5193	MAPK10/NLRP3/CFL2/C1S/MAPK8/C ASP7/MAPK14/C2/IRAK4/CALML4/C 1R/TLR4/CASP3/NFKB1/CALM3/CAS P1/RHOA/MAPK1/C3/RELA/IRAK1/IT GAM/MYD88/TRAFF6/C4BPB/SFTPA1/ ITGB1/C1QA/TIRAP/GNAI2/C4A/C1Q	75

							C/IRF3/ITGB2/IRF1/C4BPA/IL6/ITGA5 /IL1A/C5/CFL1/CD14/MAPK9/SERPIN G1/IL12B/FOS/NOS2/IL1B/MAPK12/IL 12A/C4B/MAPK3/SFTPA2/CXCL5/C1 QB/MAPK11/TNF/NOD1/CALM1/IRF8 /MAPK13/CALML6/LY96/CALML3/C XCL8/TICAM2/TICAM1/GNAI1/GNAI 3/IL10/CALML5/CALM2/JUN/IL23A/C XCL6	
hsa012 12	Fatty acid metabolism	57/7109	57/810 5	0.00055 2232	0.00626 4979	0.00410 9169	ACSL1/ACACA/HSD17B4/ACSL4/ACS L5/ELOVL5/ACSL3/CPT1A/CPT1B/AC ADVL/ACSL6/ACSBG2/ACADSB/AC AT1/ACOX1/EHHADH/CPT1C/HACD3 /ELOVL6/ACADM/FADS1/SCP2/ACA A1/HADH/SCD/HADHA/HTD2/HADH B/ACSF3/HACD2/ELOVL2/SCD5/HSD 17B8/ACOX3/FASN/FADS2/MECR/EL OVL1/PPT2/ELOVL7/ECHS1/CPT2/CB R4/HACD4/PPT1/OXSM/ACAA2/ELO VL4/ACAT2/ELOVL3/ACADS/MCAT/ HACD1/TECR/ACSBG1/HSD17B12/A CADL	57

hsa047 22	Neurotrophin signaling pathway	115/710 9	119/81 05	0.00062 1473	0.00659 5629	0.00432 604	MAPK10/RPS6KA3/BDNF/PIK3R1/CA MK2G/BAX/KIDINS220/NTRK2/PSEN 1/GAB1/MAPK8/TP53/AKT2/AKT3/NT RK3/MAPK14/PDPK1/FOXO3/CAMK2 D/CDC42/MAGED1/IRAK4/CALML4/S H2B1/RPS6KA5/PIK3CB/NFKB1/CAL M3/PIK3R3/SORT1/RHOA/MAPK1/AT F4/PIK3CD/RELA/ARHGDIA/SHC1/G SK3B/FRS2/IRAK1/BRAF/MAP2K7/M APK7/ZNF274/PLCG1/TRAF6/RPS6KA 2/CAMK4/PIK3CA/AKT1/CAMK2B/PL CG2/IKBKB/PRKCD/CAMK2A/IRAK3 /PTPN11/RPS6KA6/RAF1/PSEN2/KRA S/ARHGDIB/MAP2K1/NTF3/SH2B3/S HC4/NTRK1/RIPK2/FASLG/IRAK2/RA PGEF1/RAP1B/PRDM4/SOS1/BCL2/C RK/IRS1/NGFR/MAP2K5/PIK3R2/MA TK/MAPK9/RAP1A/MAP3K1/CRKL/M APK12/RPS6KA1/RAC1/BAD/ABL1/N FKBIE/MAP3K3/MAPK3/NFKBIA/SH C3/YWHAE/MAPK11/CALM1/NRAS/ MAPK13/GRB2/CALML6/NGF/MAPK	115
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							APK2/CALML3/MAP3K5/SHC2/NFKB IB/ARHGDIG/HRAS/CALML5/CALM2 /JUN/BEX3/SH2B2	
hsa049 35	Growth hormone synthesis, secretion and action	115/710 9	119/81 05	0.00062 1473	0.00659 5629	0.00432 604	MAPK10/CACNA1C/ITPR1/PRKACB/ GHR/PTK2/PIK3R1/PLCB2/BCAR1/GN AS/MAPK8/ADCY10/CACNA1D/CRE B3L4/AKT2/AKT3/ATF2/MAPK14/CR EB5/PLCB4/ADCY3/IGF1/CACNA1F/ ADCY5/PIK3CB/CREBBP/ADCY7/PIK 3R3/GHRL/MAP2K6/MAPK1/ATF4/PI K3CD/CREB1/SHC1/GSK3B/ATF6B/S OCS2/STAT5A/STAT3/MAP2K3/MAP2 K4/PLCG1/SSTR3/CSH2/ADCY4/PRK ACA/ADCY8/PIK3CA/AKT1/GNAI2/P LCB3/PLCG2/CREB3L2/IRS2/CACNA 1S/ADCY2/CREB3L3/GNAQ/IGFBP3/P RKCB/RAF1/GH2/ADCY6/KRAS/ITPR 2/MAP2K1/STAT1/EP300/SHC4/GH1/C REB3/SOS1/CRK/ADCY9/IRS1/MTOR/ GHSR/PIK3R2/CREB3L1/MAPK9/JAK 2/MAP3K1/FOS/CRKL/CSH1/MAPK12 /SOCS3/POU1F1/GHRH/MAPK3/IGFA	115

							LS/SHC3/STAT5B/PRKACG/MAPK11/ NRAS/MAPK13/GRB2/PLCB1/GNA11/ ADCY1/SSTR2/GNAI1/GNAI3/SHC2/S STR1/IRS4/HRAS/SST/JUNB/PRKCG/S OCS1/SSTR5/GHRHR	
hsa045 30	Tight junction	161/710 9	169/81 05	0.00066 862	0.00687 4252	0.00450 8788	MAPK10/DLG2/PRKACB/PARD3/NED D4L/MPDZ/TJAP1/TJP2/CD1E/DLG1/T JP1/NEDD4/RAPGEF6/MAPK8/CACN A1D/PRKAG2/NF2/PPP2R1B/PATJ/OC LN/SYNPO/AMOTL2/RAPGEF2/CDC4 2/AFDN/ERBB2/MAGI1/RHOA/MARV ELD3/CLDN2/PPP2R2A/ACTR3/PPP2R 2C/MARVELD2/MYH11/MYH10/MAP 2K7/HCLS1/ARHGEF2/AMOTL1/DLG 3/ARHGAP17/AMOT/MYL12A/JAM3/ LLGL2/CLDN10/EPB41L4B/ARPC1B/P RKACA/TIAM1/RDX/ITGB1/CLDN18/ ARPC4/MYL6B/MSN/CGN/CD1B/PRK AG1/CLDN14/GATA4/PPP2R2B/ROCK 2/TUBA1A/PRKAA1/TJP3/CD1C/LLG L1/PRKCE/SCRIB/PRKAA2/CFTR/AC TR2/CLDN1/BVES/ACTR3B/CLDN15/	161

							TUBAL3/RAB13/PRKAB2/RAB8B/TUBA1C/RUNX1/MPP4/PPP2CA/CLDN19/CLDN6/PPP2R2D/CDK4/F11R/MAPK9/RAP2C/RAB8A/MYL6/ARPC2/RAP1A/CLDN8/MAP3K1/PRKCI/PRKAB1/CND1/RAC1/YBX3/CLDN24/SRC/ACTR3C/CLDN7/CGNL1/WHAMM/MYL12B/CD1D/ACTN1/PRKACG/ROCK1/SYMPK/IGSF5/ACTG1/EZR/CLDN3/CLDN16/PARD6B/PARD6G/CTTN/JAM2/TUBA8/CD1A/WAS/PPP2CB/ARHGEF18/CLDN23/CLDN17/MYH9/PARD6A/TUBA4A/TUBA1B/MAP3K5/CLDN4/ARPC5/ARPC1A/MYL9/TUBA3E/PRKAG3/CLDN22/MYL2/CLDN5/HSPA4/CLDN20/CLDN9/CLDN25/VASP/CRB3/JUN/CLDN11/PRKCZ/ARPC5L/ACTB/TUBA3D/TUBA3C/STK11/SLC9A3R1	
hsa04660	T cell receptor signaling pathway	101/7109	104/8105	0.000703035	0.007009045	0.004597198	MAPK10/PAK3/CBLB/PIK3R1/NFATC2/DLG1/PAK4/NFATC3/MAPK8/AKT2/AKT3/CD28/MAPK14/PDPK1/FYN/DC42/RASGRP1/LCK/PIK3CB/NFKB1/	101

							PIK3R3/RHOA/NFATC1/MAPK1/PIK3CD/VAV3/RELA/GSK3B/MAP2K7/PLCG1/VAV1/IKBKG/PPP3CB/PIK3CA/AKT1/PAK6/PAK5/BCL10/IKBKB/PTPN6/LAT/PTPRC/LCP2/PPP3CA/RAF1/KRAS/MAP2K1/MALT1/CD4/PPP3R2/SOS1/VAV2/PAK2/PAK1/CDK4/MAP3K14/CHUK/PIK3R2/CSF2/BUB1B-PAK6/MAPK9/IL4/FOS/MAPK12/CD3D/NCK2/NCK1/CD247/NFKBIE/MAPK3/CD8A/CTLA4/NFKBIA/TEC/ZAP70/PRKCQ/ITK/MAPK11/TNF/CD8B/NRAS/MAPK13/PPP3CC/GRB2/CD3E/GRAP2/CD8B2/IFNG/IL10/CD3G/NFKBIB/ICOS/PDCD1/HRAS/IL5/CD40LG/PPP3R1/JUN/IL2/MAP3K8/CARD11	
hsa05142	Chagas disease	99/7109	102/8105	0.00086781	0.008397334	0.00550777	MAPK10/PIK3R1/PLCB2/TGFBR1/GNAS/MAPK8/AKT2/CFLAR/AKT3/PPP2R1B/MAPK14/PLCB4/GNAL/SMAD2/IRAK4/TLR4/PIK3CB/NFKB1/PIK3R3/PPP2R2A/MAPK1/PIK3CD/C3/RELA/PPP2R2C/IRAK1/MAP2K4/MYD88/TGFB	99

							2/TLR2/CCL5/CASP8/TRAF6/IKBKG/C1QA/PIK3CA/AKT1/GNAI2/C1QC/PLCB3/TLR6/GNAQ/IKBKB/FAS/KNG1/PPP2R2B/TLR9/IL6/FASLG/IFNGR2/PP2CA/PPP2R2D/CHUK/PIK3R2/BDKRB2/MAPK9/IL12B/FOS/TGFB3/NOS2/IL1B/MAPK12/CD3D/CD247/IL12A/ACE/MAPK3/GNAO1/CCL3/CCL3L3/NFKBIA/C1QB/MAPK11/TNF/GNA15/TGFBR2/MAPK13/TNFRSF1A/GNA14/IFNB1/PLCB1/IFNGR1/CD3E/PPP2CB/SERPINE1/GNA11/CXCL8/ADCY1/TICAM1/GNAI1/GNAI3/IFNG/IL10/CD3G/JUN/FADD/TGFB1/CCL2/IL2	
hsa04015	Rap1 signaling pathway	198/7109	210/8105	0.001054033	0.009345822	0.006129879	CTNND1/FGF1/PARD3/CTNNB1/PIK3R1/FGFR2/MET/VEGFA/PLCB2/BCAR1/GNAS/RAPGEF6/ANGPT1/EFNA5/MRAS/AKT2/SIPA1L1/AKT3/RASSF5/ADORA2A/MAPK14/GRIN2A/PLCB4/RALGDS/KRIT1/RAPGEF2/CDC42/ADCY3/AFDN/CALML4/IGF1/EGF/GRIN2B/PRKD2/MAGI1/ADCY5/RAPGEF4/A	198

							NGPT2/PIK3CB/INSR/CALM3/ADCY7 /RAPGEF3/PIK3R3/CNR1/RHOA/EFN A4/MAP2K6/MAPK1/PIK3CD/HGF/FL T1/VAV3/MAGI2/RAP1GAP/PRKD1/SI PA1/MAP2K3/BRAF/TEK/ITGAM/EN AH/ITGAL/CSF1/KITLG/PLCG1/LPAR 3/RASGRP2/FGF5/ARAP3/VAV1/EFN A1/LPAR5/LPAR1/ADCY4/TIAM1/ITG B1/PFN2/ADCY8/PIK3CA/AKT1/GNAI 2/GRIN1/EVL/FYB1/PDGFR/PLCB3/ LPAR2/ADCY2/ITGA2B/FARP2/CDH1 /PLCE1/GNAQ/FGFR1/RASGRP3/LAT/ ITGB2/PRKCB/RAPGEF5/DOCK4/LCP 2/RAF1/ADCY6/KRAS/DRD2/RALB/IT GB3/FGF8/MAGI3/MAP2K1/SIPA1L2/ EGFR/KIT/FGF2/FGFR4/P2RY1/KDR/ RAPGEF1/RAP1B/VEGFB/IGF1R/VAV 2/CRK/ADCY9/THBS1/ID1/NGFR/AN GPT4/PIK3R2/PRKD3/CSF1R/RALA/P DGFRB/FGF9/RAP1A/RAC2/TLN2/FG F4/VEGFD/PRKCI/EFNA3/CRKL/MAP K12/RAC1/EPHA2/FPR1/SRC/MAPK3/	
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							GNAO1/FGF23/SKAP1/PDGFB/FGF21/VEGFC/FLT4/FGF3/APBB1IP/MAPK11/ACTG1/FGF7/CALM1/NRAS/TLN1/FGFR3/MAPK13/PDGFC/LPAR4/CALML6/PARD6B/NGF/PARD6G/PLCB1/PFN1/FGF6/CALML3/F2R/ADORA2B/ADCY1/INS/RGS14/PARD6A/F2RL3/GNAI1/PDGFD/GNAI3/PDGFA/PFN4/FGF17/HRAS/CALML5/CALM2/FGF20/VASP/PRKCG/EFNA2/PRKCZ/ACTB	
hsa04914	Progesterone-mediated oocyte maturation	97/7109	100/8105	0.001070064	0.009345822	0.006129879	MAPK10/RPS6KA3/PRKACB/PIK3R1/CPEB2/CPEB4/MAPK8/CDC25C/AKT2/AKT3/CDC25B/MAPK14/PGR/CDC27/ADCY3/CPEB1/IGF1/ADCY5/PIK3CB/CCNA1/ADCY7/PIK3R3/MAPK1/PIK3CD/ANAPC1/BRAF/CDK2/KIF22/CDC16/PKMYT1/ARAF/SPDYE1/BUB1/ADCY4/PRKACA/HSP90AB1/RPS6KA2/ADCY8/PIK3CA/AKT1/GNAI2/ADCY2/HSP90AA1/RPS6KA6/RAF1/ADCY6/KRAS/MAP2K1/MAD1L1/ANAPC5/IGF1R/SPDYE2/SPDYE2B/FZR1/SPDYA/P	97

							DE3B/ADCY9/CCNB3/ANAPC13/MA D2L2/PIK3R2/SPDYE16/SPDYE5/SPD YE6/MAPK9/SPDYE17/MAD2L1/MAP K12/RPS6KA1/CDC23/CDC25A/CCNB 1/MAPK3/PRKACG/ANAPC10/MAPK1 1/AURKA/STK10/ANAPC2/ANAPC7/ MAPK13/CPEB3/ANAPC11/PLK1/SPD YE11/ADCY1/INS/CDK1/GNAI1/GNAI 3/CCNB2/MOS/CDC26/SPDYC/CCNA2 /SPDYE3/SPDYE4	
hsa051 20	Epithelial cell signaling in Helicobacter pylori infection	69/7109	70/810 5	0.00107 9457	0.00934 5822	0.00612 9879	MAPK10/MET/TJP1/MAPK8/PTPRZ1/ MAPK14/CDC42/CASP3/NFKB1/RELA /ATP6AP1/MAP2K4/PLCG1/JAM3/CC L5/ATP6V0A1/IKBKG/ATP6V0A4/AT P6V1C2/PLCG2/IKBKB/PTPN11/ATP6 V0D1/EGFR/ADAM10/CSK/PAK1/MA P3K14/ATP6V1E1/CHUK/ATP6V0B/A TP6V1H/CXCR1/F11R/MAPK9/ATP6V 1E2/ATP6V0E1/HBEGF/MAPK12/LYN /RAC1/ATP6V1D/CXCR2/ATP6V0A2/ SRC/ATP6V1C1/ATP6V1B2/NFKBIA/ MAPK11/IGSF5/ATP6V0E2/GIT1/NOD	69

							1/MAPK13/ADAM17/ATP6V1A/JAM2/ATP6V1G2/CXCL8/ATP6V1B1/CXCL2/TCIRG1/CXCL3/ATP6V1F/CXCL1/ATP6V1G3/ATP6V0D2/JUN/ATP6V1G1	
hsa052 30	Central carbon metabolism in cancer	69/7109	70/810 5	0.00107 9457	0.00934 5822	0.00612 9879	PFKM/PIK3R1/FGFR2/MET/TP53/AKT2/AKT3/HK1/NTRK3/PDHA1/PKM/ERBB2/PIK3CB/PIK3R3/MAPK1/PIK3CD/SIRT6/MYC/SLC2A2/LDHB/PIK3CA/AKT1/PDGFR/FGFR1/RAF1/KRAS/SLC2A1/MAP2K1/LDHC/EGFR/SCO2/GLS2/KIT/PDK1/GLS/PGAM1/NTRK1/IDH1/SLC16A3/FLT3/GCK/PFKP/MTOR/HK3/PIK3R2/HIF1A/PDHB/TIGAR/PDGFRB/SIRT3/HK2/RET/LDHA/G6PD/PDHA2/IDH2/MAPK3/SLC1A5/HKDC1/LDHAL6B/NRAS/FGFR3/PFKL/LDHAL6A/SLC7A5/PTEN/PGAM4/HRAS/PGAM2	69
hsa046 10	Complement and coagulation cascades	83/7109	85/810 5	0.00115 0157	0.00970 2607	0.00636 3892	CD59/SERPINA1/C1S/CR1/PLAUR/C2/MASP1/CD46/C6/C1R/C8B/CR2/C3/PLAU/CD55/KLKB1/ITGAM/PROS1/C7/PAT/VWF/F8/CFHR4/C4BPB/C3AR1/C	83

							1QA/F10/CFI/FGA/C4A/C1QC/VSIG4/TFPI/CPB2/SERPINB2/KNG1/CFH/ITGB2/A2M/PLG/F5/ITGAX/CFB/C4BPA/F2RL2/F2/F11/PROC/F9/CFD/C8A/F7/C5/BDKRB2/SERPINA5/SERPINF2/SERPING1/CFHR3/THBD/C4B/MASP2/C9/PROCR/C1QB/F3/MBL2/F12/F13B/BDKRB1/F13A1/FGG/FGB/C8G/SERPINE1/CFHR2/F2R/F2RL3/C5AR1/CFHR5/VTN/SERPINC1/SERPIND1/CR1L	
hsa05130	Pathogenic Escherichia coli infection	186/7109	197/8105	0.001203384	0.009757903	0.006400161	MAPK10/ABI1/PAK3/NLRP3/BAX/NAIP/TJP1/WIPF2/MYO10/MAPK8/MYO1C/CASP7/MYO5A/MAPK14/GNA12/CASP9/FYN/OCN/ARHGEF12/CDC42/IRAK4/TLR4/CASP3/NFKB1/CASP1/TAB3/TMBIM6/RHOA/CLDN2/ARHGEF11/MAPK1/RELA/ACTR3/MYH11/IRAK1/CYFIP2/MYH10/HCLS1/ARHGEF2/MYD88/ARF1/GNA13/SEC24B/CASP8/ARHGEF1/MYO1H/MYO1A/TRAF6/CLDN10/SEC24C/ARPC1B/NCKAP1L/LPAR5/LPAR1/RIPK1/IKBKG/ITGB1/	186

							CASP4/ABCF2/TAB2/TIRAP/CLDN18/ ARPC4/FCGR2A/LPAR2/CYFIP1/IKB KB/IL18/TAB1/FAS/PTPN6/CLDN14/R OCK2/PTPN11/TUBA1A/NCKAP1/RA B1A/WIPF1/CYTH2/BAIAP2/WASF1/T NFRSF10B/RPS3/TMED10/SEC24D/F2/ MYO6/IL6/IL1R1/FASLG/MYO5C/AR F6/ACTR2/CLDN1/ACTR3B/CLDN15/ TUBAL3/TNFSF10/SEC24A/TLR5/TU BA1C/MYO1D/TUBB3/CLDN19/CLDN 6/PAK2/PAK1/CHUK/CYTH4/MYO5B/ MAPK9/ARPC2/BRK1/TUBB6/CLDN8/ FOS/CYCS/WIPF3/IL1B/MAPK12/RAC 1/NCK2/TRAF2/NCK1/WASF2/CLDN2 4/ABL1/SRC/ACTR3C/MAPK3/MYO1 E/MYO1B/MYO1G/CLDN7/CYTH1/NF KBIA/MYO1F/GAPDH/ROCK1/MAPK 11/TNF/ACTG1/NCL/EZR/WASF3/CL DN3/CLDN16/MAPK13/LPAR4/TUBB/ TNFRSF1A/CTTN/TUBA8/TUBB4A/N LRP4/CYTH3/CXCL8/CLDN23/F2R/TR ADD/CLDN17/MYH9/TUBA4A/TUBA	
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							1B/CLDN4/ARPC5/ARPC1A/TUBA3E/ CLDN22/BAIAP2L1/NFKBIB/CLDN5/ TUBB8/TUBB4B/CLDN20/CLDN9/CL DN25/JUN/FADD/CLDN11/ARPC5L/T NFRSF10A/ACTB/TUBA3D/TUBA3C/ SLC9A3R1	
hsa049 20	Adipocytokine signaling pathway	68/7109	69/810 5	0.00121 6031	0.00975 7903	0.00640 0161	MAPK10/ACSL1/LEPR/CD36/CAMKK 2/MAPK8/PRKAG2/ACSL4/AKT2/AKT 3/ACSL5/PPARA/ACSL3/CPT1A/CPT1 B/NFKB1/PPARGC1A/ACSL6/ACSBG 2/RELA/ADIPOQ/STAT3/CPT1C/SLC2 A4/G6PC2/ADIPOR2/IKBKG/RXRA/A KT1/PCK2/IRS2/IKBKB/PRKAG1/PTP N11/PRKAA1/SLC2A1/RXRB/POMC/P RKAA2/G6PC/PRKAB2/IRS1/MTOR/C HUK/MAPK9/JAK2/PRKAB1/PCK1/SO CS3/TRAF2/TNFRSF1B/RXRG/NFKBI E/ADIPOR1/NFKBIA/PRKCQ/TNF/TN FRSF1A/G6PC3/TRADD/NPY/IRS4/PR KAG3/NFKBIB/ACSBG1/LEP/ACACB/ STK11	68
hsa046	TNF signaling	108/710	112/81	0.00125	0.00980	0.00642	MAPK10/PIK3R1/ITCH/CASP10/MAP	108

68	pathway	9	05	1265	1576	8805	K8/CREB3L4/AKT2/CFLAR/AKT3/DA B2IP/ATF2/CASP7/MAPK14/CREB5/V CAM1/TNFAIP3/RPS6KA5/PIK3CB/C ASP3/NFKB1/TAB3/PIK3R3/MAP2K6/ MAPK1/ATF4/PIK3CD/RELA/CREB1/ ATF6B/MAP2K3/MAP2K7/MAP2K4/C SF1/TRAF5/TRAF1/CCL5/CASP8/IL18 R1/RIPK1/IKBKG/TAB2/PIK3CA/AKT 1/RPS6KA4/CREB3L2/BAG4/DNM1L/ CREB3L3/IKBKB/TAB1/FAS/IRF1/SE LE/MAP2K1/IL15/NOD2/IL6/BIRC3/LI F/CREB3/MAP3K14/CHUK/PIK3R2/M MP9/CSF2/CREB3L1/MAPK9/VEGFD/ FOS/IL1B/MAPK12/TRAF3/CCL20/BC L3/SOCS3/ICAM1/TRAF2/TNFRSF1B/ MAPK3/MLKL/MMP14/NFKBIA/VEG FC/CXCL5/MAPK11/TNF/JAG1/MAPK 13/CXCL10/LTA/TNFRSF1A/IFNB1/C X3CL1/TRADD/PGAM5/RIPK3/CXCL 2/MAP3K5/CXCL3/CXCL1/JUNB/MM P3/JUN/FADD/EDN1/CCL2/MAP3K8/C XCL6	
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hsa04020	Calcium signaling pathway	225/7109	240/8105	0.001335656	0.010219322	0.006702803	CACNA1G/CACNA1C/FGF1/SLC8A1/ITPR1/PRKACB/ASPH/MYLK/FGFR2/MET/P2RX2/PDE1C/CAMK2G/VEGFA/ATP2A3/NTRK2/ATP2B2/PLCB2/HTR4/ATP2B3/GNAS/PTAFR/SPHK2/CACNA1D/HTR2C/GRM1/ADORA2A/NTRK3/GRIN2A/ERBB4/PLCB4/PHKA1/PTK2B/CACNA1A/GNAL/CAMK2D/ADCY3/CACNA1E/CACNA1I/GRM5/PDE1B/HTR7/CALML4/CAMK1G/CACNA1F/ERBB2/ATP2A2/EGF/NOS1/EDNRB/CYSLTR2/MYLK3/TPCN1/PLCZ1/STIM2/CALM3/RYR3/ADCY7/MYLK4/HGF/FLT1/SLC8A3/TRDN/CHRNA7/HTR2A/ATP2B4/PDE1A/PLCG1/CHRM2/ATP2B1/MST1R/AGTR1/CACNA1H/FGF5/HRH1/ADCY4/PRKACA/CAMK4/STIM1/ORAI2/PPP3CB/ADCY8/GDNF/CHRM1/GRIN1/SPHK1/ADRA1A/RYR2/ATP2A1/PDGFR/PLCB3/CAMK2B/PLCG2/PTGFR/CACNA1S/ERBB3/CHRM3/AVPR1A/ADCY2/PLCE1/GNAQ/	225
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							PTGER3/CAMK2A/FGFR1/CAMK1D/P HKG2/PRKCB/PPP3CA/FGF8/ITPR2/V DAC3/AVPR1B/EGFR/P2RX5/FGF2/F GFR4/MCOLN2/KDR/CHRM5/MCU/T ACR1/PLCD4/DRD1/ITPKB/NTRK1/M ST1/VEGFB/PPP3R2/PHKA2/RYR1/V DAC2/NOS3/SLC25A4/ADCY9/ADRB 2/P2RX6/GRIN2D/PHKG1/CASQ2/BD KRB2/TACR3/MCOLN3/LTB4R2/PPIF/ PDGFRB/FGF9/FGF4/RET/P2RX7/VEG FD/PLCD1/NOS2/PLCD3/P2RX1/TPCN 2/CXCR4/CACNA1B/LHCGR/VDAC1/ PHKB/FGF23/PDGFB/FGF21/NTSR1/C ASQ1/VEGFC/CYSLTR1/SLC8A2/GRP R/FLT4/PRKACG/FGF3/FGF7/TRHR/C ALM1/TACR2/ADRA1B/BDKRB1/GN A15/FGFR3/PDGFC/PPP3CC/CALML6/ NGF/GNA14/TNNC2/PLCB1/MYLK2/F GF6/HRH2/CAMK1/CD38/GNA11/MC OLN1/P2RX3/CALML3/F2R/PLN/GRI N2C/ADORA2B/ADCY1/HTR6/ADRB1 /TBXA2R/ITPKA/PDGFD/CCKAR/HT	
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							R2B/DRD5/SLC25A31/PDGFA/FGF17/ ADRA1D/HTR5A/CALML5/ORAI3/CA LM2/FGF20/EDNRA/PPP3R1/PRKCG/ TNNC1/PTGER1/SLC25A5/HRC	
hsa008 30	Retinol metabolism	67/7109	68/810 5	0.00136 9623	0.01024 1048	0.00671 7053	CYP1A1/CYP2C8/DHRS4/CYP2C18/U GT2A1/UGT2B28/CYP26B1/ADH7/AL DH1A2/CYP2B6/CYP2C9/UGT2B10/D HRS4L2/ADH6/PNPLA4/AWAT2/ADH 1B/UGT2B4/LRAT/RDH11/UGT2B7/D GAT1/ADH5/ALDH1A1/RDH12/CYP2 A7/DHRS9/ALDH1A3/UGT2B17/CYP1 A2/UGT2A2/AOX1/ADH1C/ADH4/DH RS3/UGT1A6/UGT1A1/HSD17B6/CYP 3A4/RDH16/CYP27C1/CYP3A5/CYP3 A7/CYP2W1/UGT1A5/RDH13/ADH1A/ RDH10/BCO1/RETSAT/RDH5/CYP3A7 - CYP3A51P/CYP2S1/UGT2B11/UGT1A 8/UGT1A9/UGT1A4/UGT1A10/UGT1A 7/UGT1A3/UGT2B15/RPE65/UGT2A3/ CYP2A6/RDH8/CYP26C1/SDR16C5	67
hsa040	cAMP signaling	203/710	216/81	0.00155	0.01139	0.00747	MAPK10/CACNA1C/PRKACB/BDNF/	203

24	pathway	9	05	8437	3907	3207	GRIA1/PDE4D/PIK3R1/CAMK2G/ATP2A3/ABCC4/ATP2B2/HTR4/PTCH1/PDE10A/ATP2B3/ADCYAP1R1/GNAS/MAPK8/ADCY10/CACNA1D/CREB3L4/AKT2/AKT3/ADORA2A/GRIN2A/CREB5/CAMK2D/PPARA/ADCY3/AFDN/PDE4A/CALML4/PPP1R12A/CACNA1F/ATP2A2/GRIN2B/ADCY5/RAPGEF4/PDE4B/PIK3CB/NFKB1/PDE4C/CALM3/CREBBP/ADCY7/RAPGEF3/PIK3R3/RHOA/GHRL/NFATC1/MAPK1/PIK3CD/GABBR1/VAV3/RELA/CREB1/GLI3/GRIA4/BRAF/ATP2B4/ACOX1/FSHB/CHRM2/GRIA3/ATP2B1/GLI1/ARAP3/VAV1/PPP1R1B/EDN3/GRIN3A/ADCY4/PRKACA/TIAM1/CAMK4/ADCY8/CHRM1/PIK3CA/AKT1/GNAI2/GRIN1/RYR2/ATP2A1/CAMK2B/CREB3L2/CACNA1S/FXYD1/ADCY2/CREB3L3/GLP1R/PLCE1/CNGB1/PTGER3/CAMK2A/PPP1CB/ROCK2/GIPR/ATP1B4/TSHR/PPP1CC/ATP1A2/HCN4/RAF1/ADC	
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							Y6/DRD2/SLC9A1/MAP2K1/POMC/H CAR1/ATP1A1/EP300/ADCYAP1/DRD 1/LIPE/CFTR/PDE3A/RAP1B/CREB3/R RAS2/VAV2/SUCNR1/PDE3B/CNGA3/ ADCY9/ADRB2/FSHR/GRIN2D/NPR1/ GHSR/PAK1/CNGA2/ATP1B2/ACOX3/ NPY1R/PIK3R2/CREB3L1/GRIA2/MA PK9/RAP1A/RAC2/VIPR2/HCAR2/FOS /ATP1A4/VIP/ATP1B3/HCAR3/RAC1/ CNGA1/BAD/PTGER2/MAPK3/PLD2/ HTR1A/LHCGR/TNNI3/NPPA/NFKBI A/HTR1B/MC2R/CNGA4/PRKACG/RO CK1/HTR1F/GPR119/CALM1/CALML 6/HTR1D/EDN2/HHIP/CALML3/F2R/P LN/GRIN2C/ADCY1/HTR6/NPY/ADR B1/GIP/SSTR2/GNAI1/GNAI3/SSTR1/ MYL9/CGA/SOX9/DRD5/AMH/PLD1/ ATP1B1/ATP1A3/CNGB3/CALML5/C ALM2/SST/GRIN3B/EDNRA/GCG/GA BBR2/LHB/JUN/EDN1/SSTR5	
hsa041 46	Peroxisome	80/7109	82/810 5	0.00160 1055	0.01145 1024	0.00751 067	PEX5L/ACSL1/HSD17B4/ACSL4/ACS L5/PEX5/HMGCLL1/ACSL3/PEX2/PE	80

							X26/ACSL6/AMACR/NUDT7/EPHX2/DHRS4/PEX11B/ECI2/FAR2/ACOX1/EHHADH/PEX1/AGPS/PXMP4/SOD2/SCP2/MPV17/HMGCL/PEX6/PEX11G/PEX11A/GSTK1/ACAA1/PEX16/PHYH/HAO1/IDH1/BAAT/MVK/NUDT12/XDH/SLC27A2/PEX19/SLC25A17/HACL1/ACOX3/ACOT8/ACOX2/PRDX1/SOD1/ABCD2/NOS2/PMVK/PRDX5/PEX10/PIPOX/ABCD3/IDH2/PEX13/ABCD4/HAO2/PECR/DAO/GNPAT/CROT/CAT/PEX3/ABCD1/DDO/ECH1/PEX12/AGXT/MPV17L2/PAOX/NUDT19/PEX14/DECR2/FAR1/PXMP2/MLYCD/PEX7	
hsa05165	Human papillomavirus infection	307/7109	331/8105	0.001703089	0.011921622	0.007819333	DLG2/UBE3A/PRKACB/PARD3/TSC2/LAMA3/COL6A3/CTNNB1/PTK2/PIK3R1/JAK1/TSC1/LAMA4/PXN/VEGFA/FN1/BAX/DLG1/PPP2R5C/PSEN1/ITGA7/GNAS/COL4A6/THBS3/CREB3L4/TP53/AKT2/TNC/AKT3/LAMC2/PPP2R1B/RPS6KB1/CREB5/MDM2/PATJ/TCF7L2/RBPJ/TNR/TCF7/CDC42/MAML2/	307

							CCNE1/ITGB4/ITGB8/PKM/HEY1/EGF /MAGI1/ITGA10/PIK3CB/CASP3/NFK B1/CCNA1/LAMB3/FZD3/CREBBP/PP P2R3A/PIK3R3/PPP2R2A/LAMB1/LA MB2/HES6/WNT5A/MAPK1/PIK3CD/L AMB4/IFNAR2/RELA/PPP2R2C/CREB 1/ATP6AP1/APC/ITGAV/GSK3B/CCN D3/COL4A5/CDK2/NOTCH2/ITGA6/W NT8A/WNT7B/PPP2R5E/FZD6/SPP1/D LG3/ITGB6/EIF2AK2/BCAP31/TBP/IT GA4/LAMA2/CASP8/VWF/IFNAR1/AT P6V0A1/LLGL2/ATM/PRKACA/IKBK G/ATP6V0A4/ITGB1/LFNG/FZD5/COL 4A4/HDAC2/IKBKE/MX1/TADA3/CO L9A1/PIK3CA/ATP6V1C2/AKT1/ATR/ WNT2/PPP2R5D/RELN/IRF3/CCND2/C REB3L2/COL4A3/MAML1/ITGA2B/C REB3L3/IKBKB/HEY1/ITGA3/COL4A 1/FAS/OASL/PPP2R2B/CHD4/COL6A6 /HLA- F/RAF1/ITGB7/STAT2/ATP6V0D1/LA MA1/KRAS/IRF1/ITGB3/LLGL1/NOTC	
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							H4/FZD4/MAP2K1/NFX1/COL2A1/EGFR/STAT1/SCRIB/EP300/ITGB5/COL6A5/LAMC1/ITGA5/COL4A2/FASLG/RBPJL/ITGA9/LAMC3/TERT/MFNG/DVL3/CREB3/SOS1/TNN/WNT5B/THBS1/MTOR/THBS4/UBR4/CCNE2/PPP2CA/FZD2/PPP2R2D/CDK4/HLA-G/ATP6V1E1/CHUK/ATP6V0B/PIK3R2/AXIN2/ATP6V1H/ITGA2/WNT3/CREB3L1/APC2/HES7/WNT4/RFNG/CSNK1A1/TLR3/ITGA1/CSNK1A1L/RBL2/CDK6/WNT10B/ATP6V1E2/PDGFRB/ATP6V0E1/TYK2/RBL1/NOTCH3/HEY2/RHEB/FZD7/PRKCI/WNT2B/TBPL1/TRAFF3/LAMA5/CCND1/HLA-A/ATP6V1D/WNT9B/WNT16/TBK1/ATP6V0A2/BAD/RB1/PPP2R5A/FOXO1/COL1A2/HLA-B/MAPK3/HLA-C/ATP6V1C1/COL9A2/ATP6V1B2/WNT10A/WNT11/IFNA2/THBS2/FZD1/CDKN1A/CDKN1B/PRKACG/DVL2/COMP/TNF/WNT7A/NOTCH1/WNT8B/ATP	
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							6V0E2/PTGER4/CHAD/NRAS/JAG1/PS MC1/GRB2/ITGA8/ITGA11/ATP6V1A/ PARD6B/FZD8/TNFRSF1A/PARD6G/I FNB1/TUBG1/PPP2CB/FZD9/ATP6V1 G2/IRF9/TNXB/IBSP/TRADD/E2F1/AT P6V1B1/TICAM1/PARD6A/PPP2R3B/T UBG2/COL6A1/PTEN/TBPL2/HLA- E/IFNA4/COL6A2/TCIRG1/HES1/MX2/ WNT1/COL1A1/HRAS/IFNA1/ATP6V1 F/IFNA21/IFNA14/ATP6V1G3/ATP6V0 D2/WNT9A/HES2/PPP2R5B/PPP2R3C/ HDAC1/CRB3/MAML3/RPS6KB2/CCN A2/FADD/PRKCZ/ATP6V1G1/TCF7L1/ VTN/IFNA16/SLC9A3R1/IFNA6	
hsa041 52	AMPK signaling pathway	115/710 9	120/81 05	0.00199 5512	0.01367 7569	0.00897 105	TSC2/PFKM/PIK3R1/TSC1/PPP2R5C/A CACA/LEPR/CD36/CAMKK2/STRAD A/PRKAG2/CREB3L4/AKT2/AKT3/PP P2R1B/RPS6KB1/HNF4A/CREB5/PDP K1/FOXO3/CAB39/IGF1/CPT1A/PIK3C B/CPT1B/CCNA1/INSR/PPARGC1A/PP P2R3A/PIK3R3/PPP2R2A/PIK3CD/ADI POQ/PPP2R2C/CREB1/PFKFB2/TBC1	115

							D1/STRADB/CAB39L/PPP2R5E/CPT1 C/SLC2A4/G6PC2/ADIPOR2/SREBF1/ PIK3CA/AKT1/PCK2/PPP2R5D/ADRA 1A/CREB3L2/IRS2/CREB3L3/PRKAG1 /PPP2R2B/PFKFB3/PRKAA1/RAB14/S CD/PRKAA2/LIPE/G6PC/CFTR/IGF1R/ CREB3/PFKP/PFKFB4/PRKAB2/SCD5/ IRS1/MTOR/SIRT1/AKT1S1/PPP2CA/F BP1/PPP2R2D/FASN/PIK3R2/CREB3L 1/RAB8A/HMGCR/RHEB/PRKAB1/UL K1/PPARG/PCK1/CCND1/RPTOR/PPP 2R5A/FOXO1/ADIPOR1/CRTC2/PFKF B1/ELAVL1/PFKL/EEF2K/G6PC3/RAB 10/PPP2CB/INS/FBP2/PPP2R3B/RAB2 A/IRS4/PRKAG3/GYS1/LEP/PPP2R5B/ PPP2R3C/GYS2/RPS6KB2/CCNA2/AC ACB/STK11/MLYCD	
hsa049 30	Type II diabetes mellitus	46/7109	46/810 5	0.00235 9128	0.01583 9859	0.01038 9285	MAPK10/CACNA1G/CACNA1C/PIK3 R1/MAPK8/CACNA1D/HK1/CACNA1 A/CACNA1E/PKM/ABCC8/PIK3CB/IN SR/PIK3R3/MAPK1/PIK3CD/ADIPOQ/ SOCS2/PKLR/SLC2A4/SLC2A2/PIK3C	46

							A/IRS2/IKBKB/PRKCD/SOCS4/PRKCE /GCK/IRS1/MTOR/HK3/PIK3R2/MAPK 9/HK2/SOCS3/CACNA1B/MAPK3/HK DC1/TNF/PDX1/MAFA/INS/KCNJ11/I RS4/SOCS1/PRKCZ	
hsa020 10	ABC transporters	45/7109	45/810 5	0.00269 1757	0.01764 4117	0.01157 2689	ABCC4/ABCC5/ABCA8/ABCC1/ABCA 2/ABCB5/ABCG2/ABCC11/ABCB7/AB CC8/ABCG1/ABCA12/ABCC6/ABCA5/ ABCB4/ABCB11/ABCA13/ABCC3/AB CA4/ABCB9/ABCB8/ABCB1/ABCA1/ ABCC10/ABCA6/ABCC9/ABCG4/CFT R/ABCC12/ABCA3/ABCB6/ABCC2/A BCG5/ABCA9/TAP2/ABCD2/ABCD3/ ABCA10/ABCD4/ABCA7/ABCB10/AB CD1/TAP1/DEFB1/ABCG8	45
hsa046 25	C-type lectin receptor signaling pathway	100/710 9	104/81 05	0.00273 5106	0.01764 4117	0.01157 2689	MAPK10/ITPR1/CD209/CBLB/NLRP3/ PIK3R1/CYLD/NFATC2/NFATC4/NFA TC3/MAPK8/MRAS/AKT2/AKT3/MAP K14/CLEC7A/CLEC4M/MDM2/ARHG EF12/CALML4/PIK3CB/NFKB1/CALM 3/CASP1/PIK3R3/RHOA/KSR1/NFATC 1/MAPK1/PIK3CD/RELA/CASP8/IKBK	100

							G/IKBKE/PPP3CB/PIK3CA/AKT1/PLC G2/EGR2/BCL10/IKBKB/PRKCD/PTP N11/PPP3CA/RAF1/STAT2/KRAS/IRF1 /ITPR2/LSP1/MALT1/STAT1/SYK/IL6/ NFKB2/PPP3R2/RRAS2/PAK1/MAP3K 14/CHUK/PIK3R2/PLK3/CLEC4D/CLE C1B/MAPK9/IL12B/CLEC4E/IL1B/MA PK12/BCL3/CARD9/IL12A/EGR3/SRC/ MAPK3/NFKBIA/MAPK11/TNF/CAL M1/NRAS/MAPK13/PPP3CC/CALML6/ MAPKAPK2/IRF9/CALML3/CCL17/CL EC6A/RELB/IL10/IL17D/HRAS/CALM L5/CALM2/PPP3R1/JUN/IL2/IL23A/CC L22/FCER1G	
hsa043 80	Osteoclast differentiation	122/710 9	128/81 05	0.00294 1042	0.01811 1911	0.01187 9513	MAPK10/MITF/PIK3R1/JAK1/CYLD/N FATC2/TGFBR1/TNFRSF11A/MAPK8/ AKT2/AKT3/MAPK14/FYN/BLNK/SIR PA/FOSB/LCK/PIK3CB/NFKB1/PIK3R 3/NFATC1/MAP2K6/MAPK1/PIK3CD/I FNAR2/RELA/CREB1/LILRB4/CALCR /NOX1/MAP2K7/SIRPG/CSF1/OSCAR/ LILRB1/TGFB2/IFNAR1/TRAF6/FCGR	122

							3B/FCGR3A/SPI1/IKBKG/CAMK4/PPP3CB/TAB2/FOSL2/PIK3CA/AKT1/LILRB3/NCF2/FCGR2A/PLCG2/IKBKB/BTK/GAB2/TNFSF11/TAB1/LILRB5/LCP2/PPP3CA/STAT2/ITGB3/MAP2K1/FOSL1/STAT1/SYK/NFKB2/IL1R1/IL1A/PPP3R2/SIRPB1/IFNGR2/TYROBP/MAP3K14/CHUK/PIK3R2/LILRA2/CTSK/MAPK9/CSF1R/NCF4/TYK2/FOS/PPARG/IL1B/MAPK12/FCGR2B/SOCS3/RAC1/TREM2/TRAF2/MAPK3/NFKBIA/TEC/MAPK11/TNF/ACP5/TNFRSF11B/TGFBR2/MAPK13/PPP3CC/GRB2/TNFRSF1A/IFNB1/LILRA1/IFNGR1/CYBA/IRF9/LILRB2/RELB/IFNG/LILRA5/SQSTM1/FCGR1A/FHL2/JUND/JUNB/PP3R1/JUN/SOCS1/NCF1/TGFB1	
hsa04976	Bile secretion	87/7109	90/8105	0.002997894	0.018111911	0.011879513	PRKACB/ABCC4/GNAS/SLC5A1/ADCY3/ABCG2/LDLR/ABCB4/ADCY5/SLC4A4/ABCB11/ADCY7/SLC22A8/UGT2A1/ABCC3/SLC22A1/SLC4A5/NR1H4/AQP4/SLC4A2/UGT2B28/ADCY4/PR	87

							KACA/ABCB1/ADCY8/RXRA/EPHX1/ SLCO1A2/ADCY2/ATP1B4/ATP1A2/A DCY6/UGT2B10/SLC2A1/SLC27A5/SL C9A1/UGT2B4/AQP9/ATP1A1/CFTR/S CARB1/ABCC2/SLC10A2/ABCG5/BA AT/NCEH1/UGT2B7/ADCY9/SLC9A3/ ATP1B2/SLC51A/CYP7A1/UGT2B17/U GT2A2/HMGCR/ATP1A4/ATP1B3/UG T1A6/UGT1A1/CYP3A4/AQP1/PRKAC G/KCNN2/SCTR/UGT1A5/SLCO1B3/S LC22A7/SLCO1B1/ADCY1/SLC51B/U GT2B11/CA2/AQP8/UGT1A8/UGT1A9/ UGT1A4/SLC10A1/ATP1B1/ATP1A3/N R0B2/ABCG8/UGT1A10/UGT1A7/UGT 1A3/UGT2B15/SLCO1B7/UGT2A3	
hsa049 74	Protein digestion and absorption	99/7109	103/81 05	0.00301 1609	0.01811 1911	0.01187 9513	SLC8A1/COL6A3/MME/COL4A6/ELN/ SLC36A1/COL12A1/COL25A1/COL11 A2/COL21A1/SLC7A8/SLC36A4/SLC7 A7/PRSS3/SLC8A3/COL16A1/COL4A5 /COL8A2/KCNN4/COL11A1/COL18A1 /COL10A1/SLC36A3/PRCP/SLC15A1/C OL4A4/COL9A1/CPB2/COL4A3/SLC3	99

							A2/COL20A1/COL4A1/COL6A6/SLC7A9/ATP1B4/SLC38A2/ATP1A2/DPP4/C PB1/COL7A1/KCNE3/COL2A1/COL26A1/ATP1A1/KCNJ13/COL6A5/COL23A1/SLC36A2/COL4A2/COL17A1/COL3A1/XPNPEP2/COL24A1/COL28A1/CO L8A1/SLC16A10/SLC9A3/ATP1B2/SLC1A1/COL14A1/COL5A3/COL27A1/COL5A1/KCNQ1/ATP1A4/COL19A1/ATP1B3/CELA3A/PGA5/COL1A2/COL22A1/COL5A2/COL9A2/SLC1A5/CTRL/P RSS1/SLC8A2/COL15A1/PGA3/PGA4/ACE2/KCNK5/SLC6A19/CPA3/CPA2/COL6A1/PRSS2/COL6A2/MEP1A/SLC3A1/MEP1B/ATP1B1/ATP1A3/COL1A1/CELA3B/COL13A1/CTRB1/CPA1/CTRB2	
hsa03320	PPAR signaling pathway	74/7109	76/8105	0.003079707	0.018111911	0.011879513	SORBS1/ACSL1/NR1H3/CD36/AQP7/ACSL4/ACSL5/PDPK1/PPARA/ACSL3/CPT1A/CPT1B/ACSL6/PPARD/ACSBG2/HMGCS1/ADIPOQ/GK/OLR1/ACOX1/EHHADH/APOA5/PLTP/SLC27A6/FA	74

							BP7/CPT1C/APOA1/ACADM/RXRA/PCK2/SCP2/ILK/LPL/FABP6/DBI/RXRB/PLIN4/SLC27A5/ACAA1/GK2/SCD/PLIN2/PLIN1/ANGPTL4/SLC27A2/SCD5/ACOX3/CYP7A1/ACOX2/FADS2/LOC100509620/CYP27A1/SLC27A1/MMP1/FABP3/HMGCS2/PPARG/APOA2/PCK1/CPT2/RXRG/PLIN5/FABP2/CYP8B1/ME3/ME1/FABP1/APOC3/UCP1/SLC27A4/UBC/ACSBG1/FABP4/ACADL	
hsa00140	Steroid hormone biosynthesis	60/7109	61/8105	0.003131176	0.018111911	0.011879513	LRTOMT/HSD11B1L/CYP1A1/HSD3B2/CYP11A1/CYP19A1/HSD3B1/UGT2A1/AKR1C2/UGT2B28/STS/UGT2B10/HSD17B3/CYP11B1/UGT2B4/HSD11B1/UGT2B7/CYP17A1/HSD17B8/HSD17B7/CYP7A1/CYP7B1/COMT/AKR1D1/UGT2B17/CYP1A2/UGT2A2/SULT1E1/DHRS11/CYP1B1/HSD17B2/AKR1C3/AKR1C4/UGT1A6/UGT1A1/HSD17B6/SULT2B1/CYP3A4/CYP21A2/CYP3A5/CYP3A7/CYP11B2/UGT1A5/SRD5A2/CYP3A7-	60

							CYP3A51P/AKR1C1/SRD5A3/UGT2B1 1/UGT1A8/UGT1A9/UGT1A4/HSD11B 2/SRD5A1/HSD17B12/UGT1A10/UGT1 A7/UGT1A3/UGT2B15/CYP2E1/UGT2 A3	
hsa051 32	Salmonella infection	232/710 9	249/81 05	0.00313 793	0.01811 1911	0.01187 9513	MAPK10/ABI1/PAK3/CTNNB1/NLRP3 /BAX/RHOH/NAIP/MAPK8/AKT2/AK T3/CASP7/MAPK14/NLRC4/ELMO1/D YNC1I2/DCTN5/TCF7L2/PODXL/KLC 2/EXOC7/TCF7/CDC42/IRAK4/DYNC2 H1/ELMO2/TLR4/PIK3CB/ARHGEF26/ CASP3/NFKB1/CASP1/TAB3/RHOA/M AP2K6/MAPK1/PIK3CD/RELA/ACTR3 /KIF5A/DYNC1LI2/LEF1/DCTN4/M6P R/IRAK1/CASP5/KLC4/RAB5B/CYFIP 2/MAP2K3/MAP2K7/MAP2K4/MYD88 /ARF1/EXOC5/STX10/TLR2/MYL12A/ CASP8/MYC/FLNC/FHOD1/VPS39/AH NAK/TRAF6/ANXA2/ARPC1B/NCKA P1L/PKN1/GCC2/DCTN2/DNM2/HSP9 0AB1/RIPK1/IKBKG/PFN2/PIK3CG/R AB5C/CASP4/TAB2/TIRAP/PIK3CA/A	232

							KT1/ARPC4/TLR6/RAB5A/DYNLL2/V PS11/RHOJ/CYFIP1/IKBKB/DCTN1/R AB9A/IL18/TAB1/TXN2/ROCK2/ARL8 A/TUBA1A/HSP90AA1/KPNA4/NCKA P1/PIK3C2A/PTPRC/CYTH2/RAF1/TL R9/PLEKHM2/TNFRSF10B/MAP2K1/R HOG/RPS3/VPS41/FLNA/MYO6/IL6/RI PK2/ARF6/BIRC3/SNX18/ACTR2/FBX O22/ACTR3B/TUBAL3/BCL2/DYNC1 LI1/VPS16/TNFSF10/MYL10/KPNA3/S NX9/TLR5/TUBA1C/TUBB3/SNX33/KI F5B/PAK1/CHUK/PIK3C2G/CYTH4/V PS18/CD14/MYL7/GSDMD/KPNA1/M APK9/DYNC1I1/FLNB/RAB7B/ARPC2 /DCTN3/RALA/SKP1/BRK1/TUBB6/F OS/CYCS/FYCO1/IL1B/MAPK12/RAB 9B/RAC1/VPS33A/TRAF2/PIK3C2B/E XOC4/ACTR3C/MAPK3/MLKL/DYNC 1H1/CYTH1/NFKBIA/MYL12B/KIF5C/ GAPDH/DYNLRB2/ACBD3/MAPK11/ TNF/ACTG1/DYNC2LI1/NOD1/DYNL L1/KLC1/WASF3/MAPK13/TUBB/TNF	
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							RSF1A/PFN1/TUBA8/LY96/TUBB4A/CYTH3/DYNLT3/CXCL8/ACTR1B/ARL8B/TXN/TRADD/RAB7A/MYLPF/RIPK3/TUBA4A/TUBA1B/ARPC5/ARPC1A/EXOC2/MYL9/ACTR10/TUBA3E/MYL5/PIK3C3/MYL2/PFN4/HRAS/TUBB8/TUBB4B/RILP/DYNLT1/AHNAK2/JUN/FADD/ARPC5L/TNFRSF10A/ACTB/TUBA3D/CSE1L/TCF7L1/TUBA3C/HSP90B1/ACTR1A/RHOB	
hsa05235	PD-L1 expression and PD-1 checkpoint pathway in cancer	86/7109	89/8105	0.00331751	0.018818287	0.012342822	PIK3R1/JAK1/NFATC2/NFATC3/AKT2/AKT3/CD28/RPS6KB1/MAPK14/RASGRP1/EGF/LCK/TLR4/PIK3CB/NFKB1/PIK3R3/NFATC1/MAP2K6/MAPK1/PIK3CD/RELA/STAT3/MAP2K3/MYD88/PLCG1/CSNK2A1/TLR2/TRAF6/CD274/IKBKG/PPP3CB/TIRAP/PIK3CA/AKT1/ALK/IKBKB/PTPN6/PTPN11/LAT/PPP3CA/RAF1/KRAS/TLR9/EML4/MAP2K1/EGFR/STAT1/CD4/PPP3R2/IFNGR2/MTOR/CHUK/PIK3R2/BATF2/HIF1A/JAK2/FOS/MAPK12/CD3D/CD247/N	86

							FKBIE/MAP3K3/MAPK3/NFKBIA/ZA P70/PRKCQ/MAPK11/NRAS/MAPK13/ PPP3CC/IFNGR1/CD3E/CSNK2A2/TIC AM2/BATF/TICAM1/PTEN/IFNG/CSN K2A3/CD3G/NFKBIB/PDCD1/HRAS/P PP3R1/RPS6KB2/JUN	
hsa000 71	Fatty acid degradation	43/7109	43/810 5	0.00350 4142	0.01954 0049	0.01281 6221	ACSL1/ACSL4/ACSL5/ACSL3/CPT1A/ CPT1B/ACADVL/ACSL6/ACSBG2/ECI 2/ACADSB/ACAT1/ACOX1/EHHADH/ CPT1C/ACADM/ADH7/ALDH3A2/AL DH7A1/ALDH1B1/ADH6/ACAA1/HA DH/ADH1B/HADHA/HADHB/ADH5/A COX3/ALDH9A1/ALDH2/ECHS1/CPT 2/ADH1C/ADH4/ADH1A/CYP2U1/AC AA2/ACAT2/ECI1/GCDH/ACADS/ACS BG1/ACADL	43
hsa045 12	ECM-receptor interaction	85/7109	88/810 5	0.00366 997	0.02012 3667	0.01319 9013	LAMA3/COL6A3/CD44/DAG1/LAMA4 /FN1/FREM1/ITGA7/NPNT/CD36/COL 4A6/THBS3/TNC/HMMR/LAMC2/TNR /ITGB4/ITGB8/ITGA10/FRAS1/LAMB3 /LAMB1/LAMB2/LAMB4/SV2B/ITGA V/COL4A5/SDC1/SV2C/CD47/ITGA6/S	85

							PP1/ITGB6/ITGA4/LAMA2/DMP1/VWF/ITGB1/COL4A4/COL9A1/RELN/COL4A3/FREM2/ITGA2B/ITGA3/COL4A1/COL6A6/ITGB7/LAMA1/ITGB3/COL2A1/ITGB5/COL6A5/LAMC1/ITGA5/COL4A2/ITGA9/LAMC3/HSPG2/TNN/THBS1/THBS4/ITGA2/ITGA1/GP1BA/LAMA5/GP5/COL1A2/COL9A2/SV2A/THBS2/SDC4/COMP/DSPP/CHAD/GP6/ITGA8/ITGA11/TNXB/IBSP/COL6A1/COL6A2/AGRN/COL1A1/VTN	
hsa05135	Yersinia infection	130/7109	137/8105	0.003756968	0.020262993	0.013290397	MAPK10/RPS6KA3/GIT2/NLRP3/PTK2/PI5K1A/PIK3R1/NFATC2/PXN/ARHGEF7/FN1/BCAR1/WIPF2/NFATC3/MAPK8/AKT2/AKT3/MAPK14/NLRC4/ELMO1/PTK2B/ARHGEF12/CDC42/ARHGEF28/IRAK4/ELMO2/LCK/TLR4/PIK3CB/NFKB1/CASP1/PIK3R3/RHOA/NFATC1/MAP2K6/MAPK1/PIK3CD/VA3/RELA/ACTR3/GSK3B/IRAK1/MAP2K3/MAP2K7/MAP2K4/MYD88/PLCG1/ITGA4/ARHGEF1/TRAF6/VAV1/A	130

							RPC1B/PKN1/IKBKG/RPS6KA2/ITGB1/TAB2/PIK3CA/AKT1/PIP5K1B/ARPC4/FYB1/FCGR2A/IRF3/GNAQ/IKBKB/IL18/TAB1/ROCK2/LAT/RPS6KA6/WIPF1/LCP2/BAIAP2/MAP2K1/RHOG/LIMK1/IL6/ITGA5/ARF6/ACTR2/CD4/ACTR3B/VAV2/CRK/MEFV/PKN2/CHUK/PIK3R2/MAPK9/DOCK1/ARPC2/RAC2/FOS/WIPF3/CRKL/IL1B/MAPK12/RPS6KA1/RAC1/TRAF2/TBK1/WASF2/SRC/ACTR3C/MAPK3/CD8A/NFKBIA/ZAP70/ROCK1/SKAP2/MAPK11/TNFI/CD8B/ACTG1/MAPK13/IFNB1/WAS/CXCL8/CD8B2/PIP5K1C/TICAM1/ARPC5/ARPC1A/IL10/JUN/ARPC5L/CCL2/IL2/ACTB	
hsa04611	Platelet activation	118/7109	124/8105	0.004173485	0.022146397	0.014525712	ITPR1/PRKACB/MYLK/PIK3R1/GUCY1A1/PLCB2/GNAS/AKT2/PTGS1/AKT3/MAPK14/PLCB4/TBXAS1/FYN/ARHGEF12/RASGRP1/ADCY3/PRKG2/PPP1R12A/ADCY5/MYLK3/PIK3CB/ADCY7/PIK3R3/PIK3R5/RHOA/MYLK4/M	118

								APK1/PIK3CD/GUCY1A2/GNA13/MY L12A/ARHGEF1/RASGRP2/VWF/ADC Y4/PRKACA/ITGB1/PIK3CG/STIM1/A DCY8/PIK3CA/AKT1/GNAI2/FGA/FC GR2A/PLCB3/PLCG2/ADCY2/ITGA2B /JMJD7- PLA2G4B/GNAQ/BTK/PPP1CB/ROCK 2/PPP1CC/LCP2/ADCY6/ITGB3/ITPR2/ GUCY1B1/SNAP23/SYK/P2RY1/F2/RA P1B/COL3A1/FERMT3/PRKG1/NOS3/ ADCY9/PLA2G4D/PLA2G4F/PLA2G4 B/PIK3R2/ITGA2/PIK3R6/RAP1A/TLN 2/GP1BA/PRKCI/MAPK12/LYN/P2RX 1/SRC/GP5/COL1A2/MAPK3/PTGIR/M YL12B/PRKACG/ROCK1/APBB1IP/M APK11/ACTG1/TLN1/GP6/FGG/MAPK 13/PLCB1/MYLK2/FGB/P2RY12/F2R/P LA2G4A/ADCY1/ARHGAP35/TBXA2 R/F2RL3/GNAI1/GNAI3/COL1A1/PLA 2G4C/VASP/PRKCZ/VAMP8/ACTB/FC ER1G	
hsa041	p53	signaling	71/7109	73/810	0.00425	0.02221	0.01457	TSC2/MDM4/BAX/RCHY1/CHEK2/TP	71

15	pathway		5	4228	6523	1708	53/STEAP3/BCL2L1/MDM2/APAF1/CASP9/SHISA5/CCNE1/SESN1/IGF1/SHAH1/CASP3/SESN3/CCND3/CDK2/ZMAT3/CHEK1/BID/BBC3/ADGRB1/CASP8/PIDD1/ATM/RRM2/TP53AIP1/ATR/CCND2/DDB2/FAS/IGFBP3/COP1/RPRM/TP53I3/TNFRSF10B/AIFM2/EI24/SESN2/PERP/BCL2/RRM2B/CCNG1/THBS1/CCNE2/CDK4/CD82/CDK6/CCNG2/CYCS/CCND1/CCNB1/GORAB/PMAIP1/SERPINB5/GADD45B/CDKN1A/GTSE1/CDKN2A/SERPINE1/CDK1/PPM1D/CCNB2/PTEN/SIVA1/GADD45G/TNFRSF10A/SFN	
hsa03440	Homologous recombination	41/7109	41/8105	0.004561391	0.023448401	0.01537969	BRCA1/RAD51B/BARD1/POLD1/RAD52/MRE11/UIMC1/BRCC3/RAD54B/ABAM1/BRIP1/PALB2/ATM/RAD51D/MUS81/BRCA2/NBN/EME1/TOP3B/RAD51C/RBBP8/RAD54L/ABRAXAS1/SYCP3/RPA2/POLD3/POLD4/POLD2/XRCC2/XRCC3/TOP3A/BLM/RAD50/TOPBP1/RAD51/RPA1/SSBP1/RPA3/RPA	41

							4/BABAM2/SEM1	
hsa047 50	Inflammatory mediator regulation of TRP channels	94/7109	98/810 5	0.00484 9085	0.02417 1952	0.01585 4264	MAPK10/ITPR1/PRKACB/PIK3R1/CA MK2G/PLCB2/PLA2G6/GNAS/MAPK8 /HTR2C/TRPV4/MAPK14/ASIC1/PLCB 4/IL1RAP/CAMK2D/ADCY3/CALML4/ IGF1/P2RY2/TRPV1/ADCY5/PIK3CB/ CALM3/ADCY7/PIK3R3/MAP2K6/PIK 3CD/TRPV3/MAP2K3/HTR2A/PRKCH/ PLCG1/HRH1/ADCY4/PRKACA/ADC Y8/PIK3CA/PLCB3/CAMK2B/PLCG2/ ADCY2/JMJD7- PLA2G4B/GNAQ/PRKCD/CAMK2A/P PP1CB/KNG1/PRKCB/PPP1CC/ADCY6 /ITPR2/PRKCE/NTRK1/IL1R1/ASIC5/ ASIC2/ADCY9/PLA2G4D/PLA2G4F/A SIC3/PLA2G4B/PIK3R2/ALOX12/BDK RB2/MAPK9/TRPM8/TRPA1/IL1B/MA PK12/SRC/PTGER2/ASIC4/TRPV2/PR KCQ/PRKACG/MAPK11/PTGER4/CAL M1/BDKRB1/MAPK13/CALML6/NGF/ PLCB1/CALML3/PLA2G4A/ADCY1/C YP2J2/HTR2B/F2RL1/CALML5/CALM	94

							2/PLA2G4C/PRKCG	
hsa049 25	Aldosterone synthesis and secretion	94/7109	98/810 5	0.00484 9085	0.02417 1952	0.01585 4264	CACNA1G/CACNA1C/ITPR1/PRKAC B/CAMK2G/ATP2B2/PLCB2/ATP2B3/ GNAS/CACNA1D/CREB3L4/ATF2/CR EB5/PLCB4/CAMK2D/ADCY3/CACN A1I/CALML4/LDLR/CAMK1G/HSD3B 2/CACNA1F/PRKD2/ADCY5/CYP11A1 /CALM3/ADCY7/NR4A1/ATF4/CREB1 /KCNK9/PRKD1/ATF6B/HSD3B1/ATP 2B4/ATP2B1/AGTR1/PDE2A/CACNA1 H/KCNK3/ADCY4/PRKACA/CAMK4/ ADCY8/PLCB3/CAMK2B/CREB3L2/C ACNA1S/ADCY2/CREB3L3/GNAQ/CA MK2A/CAMK1D/NR4A2/ATP1B4/PRK CB/ATP1A2/ADCY6/ITPR2/PRKCE/PO MC/ATP1A1/KCNJ5/LIPE/SCARB1/CR EB3/ADCY9/NPR1/ATP1B2/CREB3L1/ PRKD3/ATP1A4/ATP1B3/AGT/NPPA/ CYP21A2/MC2R/PRKACG/DAGLA/C ALM1/CYP11B2/CALML6/DAGLB/PL CB1/CAMK1/GNA11/CALML3/ADCY 1/ATP1B1/ATP1A3/CALML5/CALM2/	94

							STAR/PRKCG	
hsa04070	Phosphatidylinositol signaling system	93/7109	97/8105	0.00532797	0.025777972	0.016907644	PPIP5K1/ITPR1/SYNJ1/DGKB/PIP5K1A/PIK3R1/INPP4B/PLCB2/DGKG/DGKH/INPP5F/SYNJ2/DGKI/IP6K2/PLCB4/MTMR3/PIP4K2C/CALML4/PIK3CB/PLCZ1/MTMR14/PI4KB/CALM3/PPIP5K2/INPP5D/PIK3R3/DGKZ/CDIPT/PIK3CD/IP6K1/DGKK/DGKA/MTMR1/SACM1L/PIP4K2A/PLCG1/INPP4A/PIKFYVE/INPP5B/PIK3CA/PIP5K1B/PLCB3/PLCG2/OCRL/PLCE1/PRKCB/PIK3C2A/PI4KA/CDS2/ITPR2/ITPK1/MTMR2/IPPK/MTM1/PLCD4/ITPKB/PIP4P1/MTMR7/DGKE/PI4K2B/CDS1/PIK3R2/PIK3C2G/MTMR4/INPP1/IMPAD1/MTMR8/PLCD1/IMPA1/PLCD3/PI4K2A/PIK3C2B/DGKD/INPP5A/PIP4K2B/CALM1/PIP4P2/IP6K3/CALML6/PLCB1/CALML3/MTMR6/PIP5K1C/ITPKA/PTEN/IMPA2/PIK3C3/DGKQ/INPPL1/CALML5/CALM2/INPP5E/PRKCG	93
hsa046	Fc gamma R-	93/7109	97/810	0.00532	0.02577	0.01690	BIN1/PIP5K1A/PIK3R1/CFL2/PLA2G6/	93

66	mediated phagocytosis		5	797	7972	7644	MYO10/SPHK2/AKT2/AKT3/RPS6KB1 /CDC42/PIK3CB/INPP5D/PIK3R3/ASA P1/MAPK1/PIK3CD/VAV3/ACTR3/LI MK2/PLCG1/SCIN/VAV1/ARPC1B/FC GR3B/DNM2/FCGR3A/HCK/PIK3CA/ AKT1/PIP5K1B/SPHK1/ARPC4/FCGR2 A/PLCG2/JMJD7- PLA2G4B/PRKCD/GAB2/LAT/PRKCB/ PTPRC/RAF1/WASF1/MAP2K1/PRKC E/AMPH/SYK/LIMK1/ARF6/ACTR2/A CTR3B/GSN/ASAP3/VAV2/CRK/PLA2 G4D/PLA2G4F/PAK1/PLA2G4B/CFL1/ PIK3R2/DOCK1/ARPC2/MARCKSL1/R AC2/CRKL/MARCKS/FCGR2B/LYN/R AC1/WASF2/ACTR3C/MAPK3/PLD2/ ASAP2/PLPP3/PLPP2/WASF3/WAS/PL A2G4A/PLPP1/PIP5K1C/ARPC5/ARPC 1A/PLD1/FCGR1A/INPPL1/PLA2G4C/ VASP/PRKCG/RPS6KB2/ARPC5L/NCF 1	
hsa040 71	Sphingolipid signaling pathway	113/710 9	119/81 05	0.00641 2174	0.03057 3987	0.02005 3327	MAPK10/PIK3R1/ASAH2/BAX/PPP2R 5C/PLCB2/MAPK8/SPHK2/TP53/AKT2	113

							/ AKT3/PPP2R1B/MAPK14/GNA12/PLC B4/PDPK1/FYN/ABCC1/SGMS2/PIK3C B/NFKB1/PPP2R3A/PIK3R3/RHOA/PP P2R2A/MAPK1/PIK3CD/RELA/PPP2R 2C/ASAH1/BID/PPP2R5E/GNA13/CER S5/SGPL1/PIK3CA/AKT1/GNAI2/SPH K1/PPP2R5D/PLCB3/CERS4/SMPD2/G NAQ/SPTLC2/GAB2/KNG1/PPP2R2B/ ROCK2/S1PR3/PRKCB/RAF1/KRAS/S 1PR5/MAP2K1/SPTLC1/PRKCE/NSMA F/SPTLC3/MS4A2/BCL2/NOS3/PPP2C A/PPP2R2D/PIK3R2/BDKRB2/ADORA 3/MAPK9/CERS3/RAC2/MAPK12/RAC 1/TRAF2/PPP2R5A/MAPK3/SMPD1/PL D2/SGPP2/SGPP1/ACER2/ROCK1/MA PK11/TNF/NRAS/ACER1/S1PR1/MAP K13/CERS1/CERS2/TNFRSF1A/PLCB1 /PPP2CB/DEGS1/S1PR2/FCER1A/TRA DD/CTSD/MAP3K5/GNAI1/PPP2R3B/ GNAI3/PTEN/CERS6/PLD1/SGMS1/H RAS/PPP2R5B/PRKCG/PPP2R3C/S1PR 4/PRKCZ/OPRD1/FCER1G	
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hsa046	Th17 cell	102/710	107/81	0.00651	0.03062	0.02008	MAPK10/JAK1/NFATC2/RORA/TGFB	102
59	differentiation	9	05	5891	4688	6582	R1/IL6ST/NFATC3/MAPK8/STAT6/M APK14/IL1RAP/SMAD2/LCK/NFKB1/ FOXP3/NFATC1/MAPK1/RELA/SMAD 3/IL21R/STAT5A/RARA/STAT3/PLCG 1/HLA- DQB1/RORC/IL23R/HSP90AB1/IL6R/I KBKG/PPP3CB/RXRA/IKBKB/IL4R/L AT/HSP90AA1/PPP3CA/RXRB/IL12RB 1/STAT1/IL6/IL1R1/CD4/PPP3R2/HLA- DQA1/IFNGR2/RUNX1/MTOR/CHUK/ IL2RB/JAK3/MAPK9/HLA- DPB1/IL4/HIF1A/JAK2/TYK2/SMAD4/ IRF4/FOS/IL1B/HLA- DMB/MAPK12/AHR/IL27RA/CD3D/C D247/RXRG/HLA- DPA1/NFKBIE/GATA3/MAPK3/NFKB IA/ZAP70/PRKCQ/STAT5B/IL2RG/MA PK11/HLA-DQA2/TGFBR2/HLA- DRB1/MAPK13/PPP3CC/IL21/HLA- DOB/IFNGR1/CD3E/HLA-DOA/HLA- DMA/IL2RA/IFNG/CD3G/NFKBIB/IL2	

							2/HLA-DRB5/IL17D/TBX21/PPP3R1/JUN/TGFB1/IL2/IL23A	
hsa05205	Proteoglycans in cancer	191/7109	205/8105	0.007238672	0.033244694	0.02180503	ANK2/ITPR1/PRKACB/CTNNB1/PPP1R12B/PTK2/PIK3R1/CD44/MET/PXN/CAMK2G/VEGFA/FN1/EIF4B/PTCH1/ESR1/GAB1/PLAUR/ANK3/TP53/MRAS/AKT2/ANK1/DCN/AKT3/RPS6KB1/MAPK14/CD63/MDM2/ERBB4/PDPK1/ARHGEF12/CAMK2D/SMAD2/CDC42/IGF1/PPP1R12A/ERBB2/ELK1/TLR4/PIK3CB/CASP3/HPSE2/FZD3/PIK3R3/RHOA/WNT5A/MAPK1/PIK3CD/HGF/PLAU/VAV3/CAV1/ITGAV/MMP2/HPS1/FRS2/STAT3/BRAF/HCLS1/SDC1/WNT8A/PLCG1/WNT7B/FZD6/TGFB2/DROSHA/TLR2/ARAF/CTSL/MYC/ARHGEF1/FLNC/VAV1/PRKACA/TIAM1/RDX/ITGB1/FZD5/PIK3CA/AKT1/WNT2/GPC3/CAMK2B/PLCG2/MSN/DDX5/SDC2/ERBB3/NANOG/PLCE1/CAMK2A/FGFR1/CAV2/FAS/PPP1CB/PTPN6/	191

							ROCK2/PTPN11/PDCD4/PRKCB/PPP1 CC/RAF1/KRAS/ITGB3/NUDT16L1/SL C9A1/ITPR2/FZD4/MAP2K1/EGFR/FG F2/FLNA/KDR/ITGB5/ITGA5/FASLG/ CAV3/IGF1R/SOS1/RRAS2/VAV2/HSP G2/WNT5B/THBS1/MTOR/FZD2/PAK 1/PIK3R2/MMP9/ITGA2/WNT3/WNT4/ WNT10B/HIF1A/FLNB/CBL/IL12B/HB EGF/FZD7/WNT2B/NANOGP8/MAPK 12/CCND1/RAC1/WNT9B/WNT16/SRC /COL1A2/GPC1/MAPK3/IHH/LUM/IGF 2/WNT10A/WNT11/FZD1/CDKN1A/S DC4/PRKACG/ROCK1/MAPK11/TNF/ ACTG1/WNT7A/WNT8B/IQGAP1/EZR /NRAS/MAPK13/GRB2/PPP1R12C/FZ D8/SMO/CTTN/SHH/FZD9/HSPB2/TF AP4/WNT1/COL1A1/HRAS/TIMP3/W NT9A/PRKCG/RPS6KB2/HOXD10/TW IST2/TGFB1/ACTB/VTN	
hsa049 26	Relaxin signaling pathway	122/710 9	129/81 05	0.00727 5435	0.03324 4694	0.02180 503	MAPK10/PRKACB/PIK3R1/VEGFA/PL CB2/TGFBR1/GNAS/MAPK8/COL4A6/ CREB3L4/AKT2/AKT3/GNG2/ATF2/M	122

							APK14/CREB5/PLCB4/SMAD2/ADCY 3/NOS1/ARRB1/EDNRB/ADCY5/RXFP 1/PIK3CB/NFKB1/ADCY7/PIK3R3/AR RB2/MAPK1/ATF4/PIK3CD/RELA/CR EB1/SHC1/RXFP2/MMP2/ATF6B/COL 4A5/MAP2K7/MAP2K4/GNB5/ADCY4/ PRKACA/GNG4/COL4A4/ADCY8/PIK 3CA/AKT1/GNAI2/PLCB3/CREB3L2/C OL4A3/ADCY2/CREB3L3/COL4A1/RA F1/ADCY6/KRAS/GNGT2/MAP2K1/E GFR/SHC4/COL4A2/VEGFB/COL3A1/ CREB3/SOS1/NOS3/MMP13/ADCY9/G NG7/PIK3R2/MMP9/CREB3L1/MAPK9 /MMP1/VEGFD/FOS/INSL3/NOS2/MA PK12/GNB1/RXFP4/SRC/COL1A2/MA PK3/GNAO1/NFKBIA/VEGFC/SHC3/R LN3/PRKACG/MAPK11/NRAS/GNA15 /TGFB2/MAPK13/GRB2/GNB4/PLCB 1/GNG13/GNG12/ADCY1/GNB3/GNAI 1/GNAI3/SHC2/GNB2/GNGT1/COL1A 1/GNG3/HRAS/INSL5/ACTA2/RXFP3/J UN/PRKCZ/TGFB1/EDN1/RLN2/RLN1	
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hsa041 51	PI3K-Akt signaling pathway	325/710 9	354/81 05	0.00782 2512	0.03525 4885	0.02312 3505	BCL2L11/FGF1/BRCA1/GHR/TSC2/LA MA3/COL6A3/BDNF/EIF4E/PTK2/PIK 3R1/JAK1/TSC1/FGFR2/MET/YWHAZ/ LAMA4/VEGFA/FN1/NTRK2/PPP2R5 C/MYB/EIF4B/ITGA7/TGFA/COL4A6/ ANGPT1/THBS3/EFNA5/CREB3L4/TP 53/AKT2/BCL2L1/TNC/AKT3/GNG2/A TF2/LAMC2/PPP2R1B/RPS6KB1/CRE B5/MDM2/MCL1/ERBB4/CASP9/PRLR /PDPK1/SGK1/TNR/FOXO3/CCNE1/IT GB4/EIF4E2/ITGB8/IGF1/ERBB2/EGF/ MAGI1/TLR4/ITGA10/ANGPT2/PIK3C B/NFKB1/INSR/LAMB3/FLT3LG/PPP2 R3A/PIK3R3/PIK3R5/EFNA4/PPP2R2A /NR4A1/LAMB1/LAMB2/MAPK1/ATF 4/PIK3CD/HGF/FLT1/LAMB4/IFNAR2/ RELA/PPP2R2C/CREB1/MAGI2/PIK3A P1/ITGAV/GSK3B/ATF6B/CCND3/CO L4A5/TEK/CDK2/PHLPP2/CSF1/IL7R/ KITLG/ITGA6/CHRM2/PPP2R5E/SPP1/ ITGB6/TLR2/GNB5/G6PC2/ITGA4/LP AR3/LAMA2/MYC/VWF/IFNAR1/FGF	325
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							5/CSH2/EFNA1/PKN1/LPAR5/LPAR1/ CSF3R/HSP90AB1/IL6R/IKBKG/GNG4 /ITGB1/COL4A4/PIK3CG/COL9A1/RX RA/CHRM1/PIK3CA/AKT1/MLST8/PC K2/PPP2R5D/RELN/SGK3/PDGFR/C CND2/CREB3L2/COL4A3/ERBB3/LPA R2/ITGA2B/CREB3L3/IKBKB/ITGA3/ FGFR1/COL4A1/PPP2R2B/COL6A6/SG K2/IL4R/PRKAA1/HSP90AA1/RAF1/G H2/ITGB7/LAMA1/KRAS/ITGB3/FGF8 /GNGT2/MAP2K1/COL2A1/EGFR/NTF 3/SYK/KIT/FGF2/FGFR4/PRKAA2/KD R/ITGB5/COL6A5/GH1/IL6/LAMC1/N TRK1/ITGA5/COL4A2/G6PC/FASLG/C SF3/VEGFB/ITGA9/LAMC3/IGF1R/FL T3/CREB3/SOS1/BCL2/NOS3/TNN/TH BS1/IRS1/MTOR/THBS4/CCNE2/PPP2 CA/PKN2/NGFR/GNG7/ANGPT4/PPP2 R2D/CDK4/CHUK/IL2RB/JAK3/PIK3R 2/ITGA2/CREB3L1/ITGA1/RBL2/CSF1 R/CDK6/IL4/PIK3R6/PDGFRB/FGF9/J AK2/FGF4/THEM4/RHEB/VEGFD/EF	
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							NA3/CSH1/LAMA5/GNB1/PCK1/CCN D1/RAC1/C8orf44- SGK3/EPHA2/IL7/RPTOR/EPOR/CD19 /OSMR/BAD/PPP2R5A/COL1A2/MAP K3/IL3RA/COL9A2/PHLPP1/FGF23/PD GFB/IGF2/FGF21/IFNA2/THBS2/VEGF C/CDKN1A/DDIT4/IL2RG/CDKN1B/F LT4/FGF3/COMP/YWHAE/YWHAG/E REG/FGF7/CRTC2/CHAD/NRAS/FGFR 3/PDGFC/LPAR4/GRB2/ITGA8/GNB4/ TCL1A/ITGA11/NGF/IFNB1/FGF6/G6P C3/GNG13/PPP2CB/YWHAH/TNXB/IB SP/GNG12/F2R/INS/LPAR6/EIF4E1B/G NB3/IL2RA/PPP2R3B/PDGFD/CDC37/ COL6A1/PTEN/PKN3/GNB2/GNGT1/I FNA4/COL6A2/PDGFA/FGF17/COL1A 1/GNG3/HRAS/IFNA1/GYS1/OSM/IFN A21/IFNA14/AREG/FGF20/EPO/PPP2R 5B/YWHAB/MTCP1/PPP2R3C/GYS2/R PS6KB2/EFNA2/IL2/HSP90B1/STK11/ VTN/IFNA16/IFNA6	
hsa054	Fluid shear stress	131/710	139/81	0.00803	0.03529	0.02314	MAPK10/MEF2C/CTNNB1/PTK2/PIK3	131

18	and atherosclerosis	9	05	8209	2261	802	R1/ACVR1/VEGFA/BMPR1B/MEF2A/ACVR2A/MAPK8/TP53/AKT2/AKT3/TPRV4/MAPK14/NQO1/VCAM1/CALML4/PIK3CB/NFKB1/CALM3/PIK3R3/RHOA/MAP2K6/PIK3CD/RELA/CAV1/IL1R2/ITGAV/MMP2/NOX1/NFE2L2/MAP2K7/MAP2K4/MGST2/MAPK7/SDC1/ARHGEF2/PLAT/CTSL/HSP90AB1/IKBKG/PIK3CA/AKT1/GSTO1/KEAP1/NCF2/SDC2/ITGA2B/IKBKB/CAV2/TXN2/PRKAA1/HSP90AA1/BMPR1A/ACVR2B/GSTM5/ITGB3/SELE/PECAM1/PRKAA2/KDR/IL1R1/CAV3/IL1A/BCL2/NOS3/BMP4/MAP2K5/CHUK/PIK3R2/MMP9/MAPK9/GSTM3/RAC2/DUSP1/FOS/GSTA4/IL1B/MAPK12/THBD/RAC1/ICAM1/SRC/GPC1/BMPR2/GSTA1/PDGFB/MGST3/SDC4/MAPK11/TNFA/ACTG1/CALM1/MAPK13/GSTM4/GSTT2B/CALML6/TNFRSF1A/MGST1/CYBA/GSTO2/CALML3/NPPC/TXN/CDH5/GSTA2/MAP3K5/ASS1/IFNG/GS	
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							TM2/SQSTM1/SUMO2/PDGFA/SUMO1/GSTP1/CALML5/CALM2/GSTA3/GSTA5/JUN/KLF2/PRKCZ/NCF1/GSTM1/EDN1/CCL2/ACTB/HSP90B1/PIAS4	
hsa00010	Glycolysis / Gluconeogenesis	65/7109	67/8105	0.008045348	0.035292261	0.02314802	PFKM/HK1/PDHA1/ALDH3A1/PKM/PKLR/G6PC2/ALDH3B1/ACSS1/GPI/DLD/LDHB/ADH7/PCK2/ALDH3A2/ALDOC/ALDH7A1/ALDH1B1/MINPP1/ALDH3B2/GALM/ADH6/LDHC/ADH1B/PGAM1/ENO4/G6PC/DLAT/ENO1/GCK/PFKP/ALDOA/ADH5/PGK2/FBP1/HK3/ALDH9A1/ALDH2/PDHB/HK2/ENO3/LDHA/PCK1/PDHA2/ADH1C/ADH4/ADPGK/ENO2/GAPDH/PGK1/HKDC1/LDHAL6B/BPGM/ALDOB/GAPDHS/AKR1A1/PFKL/ADH1A/ACSS2/G6PC3/PGM1/LDHAL6A/FBP2/PGAM4/PGAM2	65
hsa04658	Th1 and Th2 cell differentiation	88/7109	92/8105	0.008483331	0.036723894	0.02408702	MAPK10/JAK1/NFATC2/NFATC3/MAPK8/IL12RB2/STAT6/MAPK14/RBPJ/MAML2/LCK/NFKB1/NFATC1/MAPK1/RELA/STAT5A/NOTCH2/PLCG1/HLA-	88

							DQB1/IKBKG/PPP3CB/MAML1/IKBK B/RUNX3/STAT4/IL4R/LAT/PPP3CA/I L13/IL12RB1/STAT1/RBPJL/CD4/PPP3 R2/HLA- DQA1/IFNGR2/MAF/CHUK/IL2RB/JA K3/JAG2/MAPK9/HLA- DPB1/IL4/IL12B/JAK2/TYK2/NOTCH3 /FOS/HLA- DMB/MAPK12/CD3D/CD247/IL12A/H LA- DPA1/NFKBIE/GATA3/MAPK3/NFKB IA/ZAP70/PRKCQ/STAT5B/IL2RG/MA PK11/NOTCH1/DLL3/JAG1/HLA- DQA2/HLA- DRB1/MAPK13/PPP3CC/HLA- DOB/IFNGR1/CD3E/HLA- DOA/DLL4/HLA- DMA/IL2RA/IFNG/CD3G/NFKBIB/HL A- DRB5/TBX21/IL5/PPP3R1/MAML3/JU N/IL2	
hsa049	Cortisol synthesis	63/7109	65/810	0.00992	0.04238	0.02780	CACNA1G/CACNA1C/ITPR1/PRKAC	63

27	and secretion		5	0308	677	1273	B/PLCB2/SP1/GNAS/CACNA1D/CREB3L4/ATF2/CREB5/PLCB4/ADCY3/CACNA1I/LDLR/HSD3B2/CACNA1F/KCNK2/ADCY5/CYP11A1/ADCY7/PDE8B/NR4A1/ATF4/CREB1/ATF6B/HSD3B1/PDE8A/AGTR1/CACNA1H/KCNK3/ADCY4/PRKACA/PBX1/ADCY8/PLCB3/CREB3L2/CACNA1S/ADCY2/CREB3L3/GNAQ/ADCY6/MRAP/ITPR2/CYP11B1/POMC/SCARB1/CREB3/NCEH1/CYP17A1/ADCY9/CREB3L1/KCNA4/AGT/CYP21A2/MC2R/PRKACG/NR5A1/PLCB1/GNA11/ADCY1/NR0B1/STAR	
hsa05146	Amoebiasis	97/7109	102/8105	0.010100454	0.042603198	0.027943227	PRKACB/LAMA3/PTK2/PIK3R1/LAMA4/FN1/CD1E/PLCB2/GNAS/COL4A6/LAMC2/PLCB4/GNAL/C8B/SERPINB6/TLR4/PIK3CB/CASP3/NFKB1/LAMB3/PIK3R3/LAMB1/LAMB2/PIK3CD/LAMB4/RELA/IL1R2/RAB5B/COL4A5/ITGAM/TGFB2/TLR2/LAMA2/PRKACA/COL4A4/RAB5C/VCL/PIK3CA/PLCB3/	97

							COL4A3/RAB5A/CD1B/GNAQ/ARG1/ COL4A1/ITGB2/PRKCB/ARG2/LAMA 1/CD1C/IL6/LAMC1/COL4A2/IL1R1/C OL3A1/LAMC3/C8A/PIK3R2/CSF2/PR DX1/CD14/RAB7B/SERPINB13/IL12B/ TGFB3/NOS2/IL1B/LAMA5/SERPINB4 /IL12A/COL1A2/C9/CD1D/ACTN1/PR KACG/TNF/GNA15/SERPINB10/GNA1 4/PLCB1/CD1A/SERPINB3/C8G/GNA1 1/CXCL8/SERPINB9/ADCY1/RAB7A/ CXCL2/IFNG/IL10/COL1A1/CXCL3/C XCL1/PRKCG/HSPB1/TGFB1	
hsa051 44	Malaria	49/7109	50/810 5	0.01120 8313	0.04667 7656	0.03061 5644	MET/CD36/CR1/THBS3/VCAM1/TLR4 /GYPA/HGF/SELP/ITGAL/SDC1/MYD 88/TGFB2/TLR2/ACKR1/LRP1/SDC2/I L18/ITGB2/SELE/TLR9/PECAM1/IL6/ CSF3/GYPC/THBS1/THBS4/TGFB3/IL 1B/KLRK1/ICAM1/IL12A/CD40/THBS 2/COMP/TNF/CXCL8/GYPB/IFNG/KL RB1/IL10/HBA2/CD40LG/TGFB1/CCL 2/HBB/CD81/HBA1/CR1L	49
hsa042	Cellular senescence	146/710	156/81	0.01150	0.04675	0.03066	ITPR1/TSC2/FOXM1/PIK3R1/TSC1/NF	146

18		9	05	0755	2731	4885	ATC2/NFATC4/TGFBR1/LIN54/NFATC3/HIPK3/RAD9B/CHEK2/HIPK1/CACNA1D/ETS1/TP53/MRAS/AKT2/AKT3/RASSF5/TRPV4/MAPK14/MDM2/MRE11/FOXO3/SMAD2/CCNE1/CALML4/HIPK2/CAPN1/PIK3CB/NFKB1/CCNA1/CALM3/PIK3R3/NFATC1/MAP2K6/MAPK1/PIK3CD/RELA/SMAD3/CCND3/MAP2K3/CDK2/CHEK1/TGFB2/BTRC/MYC/E2F3/ATM/RBBP4/MYBL2/TRAF3IP2/PPP3CB/PIK3CA/AKT1/ATR/CND2/NBN/E2F2/PPP1CB/GATA4/IGFBP3/HLA-F/PPP1CC/PPP3CA/RAF1/KRAS/LIN37/ITPR2/VDAC3/MAP2K1/LIN9/ZFP36L1/MCU/IL6/IL1A/PPP3R2/RRAS2/VDAC2/SLC25A4/FBXW11/MTOR/SIRT1/CNBB3/CCNE2/CDK4/HLA-G/PIK3R2/RBL2/CDK6/RBL1/RHEB/HIPK4/TGFB3/MAPK12/KIR2DL4/CCND1/HLA-A/CDC25A/CCNB1/RAD9A/RB1/FOX	
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							O1/HLA-B/MAPK3/HLA-C/RAD50/VDAC1/GADD45B/E2F4/CDKN1A/PPID/MAPK11/CALM1/NRAS/TGFBR2/MAPK13/PPP3CC/CALML6/C DKN2A/TRPM7/MAPKAPK2/SERPINE1/CALML3/CXCL8/E2F1/CDK1/CCNB2/PTEN/HLA-E/SQSTM1/HUS1/RAD1/SLC25A31/HRAS/GADD45G/CALML5/ZFP36L2/CALM2/PPP3R1/CCNA2/TGFB1/LIN52/SLC25A5	
hsa05145	Toxoplasmosis	106/7109	112/8105	0.011510551	0.046752731	0.030664885	MAPK10/LAMA3/JAK1/LAMA4/MAPK8/AKT2/BCL2L1/AKT3/LAMC2/MAPK14/CASP9/PDPK1/IRAK4/LDLR/CIITA/TLR4/CASP3/NFKB1/LAMB3/XIAP/PIK3R5/LAMB1/LAMB2/MAP2K6/MAPK1/LAMB4/RELA/IRAK1/STAT3/MAP2K3/MYD88/ITGA6/TGFB2/HLA-DQB1/TLR2/LAMA2/CASP8/TRAF6/IKBKG/ITGB1/PIK3CG/TAB2/AKT1/GNAI2/HSPA8/IKBKB/TAB1/LAMA1/SATAT1/IL10RA/HSPA1L/LAMC1/BIRC3	106

							/LAMC3/HLA- DQA1/BCL2/IFNGR2/HSPA6/CHUK/M APK9/HLA- DPB1/PIK3R6/PPIF/IL12B/JAK2/TYK2 /TGFB3/CYCS/NOS2/HLA- DMB/MAPK12/LAMA5/CCR5/IL12A/B AD/HLA- DPA1/MAPK3/GNAO1/CD40/NFKBIA/ MAPK11/TNF/IRGM/HLA- DQA2/HLA- DRB1/MAPK13/TNFRSF1A/HLA- DOB/IFNGR1/LY96/HLA- DOA/HSPA2/HLA- DMA/IL10RB/GNAI1/GNAI3/IFNG/IL1 0/NFKBIB/HLA- DRB5/ALOX5/CD40LG/SOCS1/TGFB1 /HSPA1A/HSPA1B	
hsa048 10	Regulation of actin cytoskeleton	202/710 9	218/81 05	0.01177 7986	0.04691 4137	0.03077 0751	FGF1/PAK3/PPP1R12B/PTK2/MYLK/S PATA13/PIP5K1A/PIK3R1/FGFR2/PX N/ARHGEF7/FN1/BCAR1/CFL2/ITGA7 /PAK4/DIAPH3/ABI2/MRAS/SSH2/GN A12/PIP4K2C/ARHGEF12/CDC42/ITG	202

							B4/ITGB8/PPP1R12A/EGF/ITGA10/MY LK3/PIK3CB/PIK3R3/RHOA/MYLK4/ MAPK1/PIK3CD/VAV3/ACTR3/LIMK 2/APC/ITGAV/FGD3/MYH11/CYFIP2/ MYH10/BRAF/ITGAM/ENAH/PIP4K2 A/ITGAL/ITGA6/CHRM2/ITGB6/CXC L12/GNA13/PIKFYVE/MYL12A/ARAF /ITGA4/ARHGEF1/ARHGEF6/FGF5/SC IN/VAV1/ARPC1B/NCKAP1L/LPAR5/ LPAR1/TIAM1/RDX/ITGB1/PFN2/VCL /CHRM1/PIK3CA/PIP5K1B/ARPC4/PA K6/PDGFRA/MSN/PAK5/CHRM3/LPA R2/ITGA2B/CYFIP1/ITGA3/FGFR1/PP P1CB/KNG1/ROCK2/ITGB2/PPP1CC/N CKAP1/ITGAD/RAF1/ITGB7/BAIAP2/ SSH1/KRAS/ITGB3/ITGAX/WASF1/F GF8/SLC9A1/MAP2K1/IQGAP2/EGFR/ FGF2/FGFR4/CHRM5/F2/ITGAE/LIMK 1/SSH3/ITGB5/TMSB4X/ITGA5/ITGA9 /ACTR2/ACTR3B/GSN/SOS1/DIAPH1/ RRAS2/VAV2/CRK/MYL10/INSRR/PA K2/PAK1/CFL1/PIK3R2/BDKRB2/ITG	
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							A2/BUB1B- PAK6/MYL7/IQGAP3/APC2/ITGA1/D OCK1/ARPC2/PDGFRB/FGF9/RAC2/B RK1/FGF4/CRKL/TMSB4Y/RAC1/WA SF2/CXCR4/SRC/ACTR3C/MAPK3/FG F23/PDGFB/FGF21/PIP4K2B/MYL12B/ ACTN1/ROCK1/FGF3/ACTG1/GIT1/F GF7/IQGAP1/EZR/NRAS/BDKRB1/AR HGEF4/FGFR3/PDGFC/LPAR4/ITGA8/ PPP1R12C/ITGA11/MYLK2/PFN1/FGF 6/FGD1/GNG12/F2R/ARHGAP35/INS/ MYLPF/MYH9/PIP5K1C/ARPC5/PDGF D/ARPC1A/DIAPH2/MYL9/MYL5/MY L2/PDGFA/PFN4/FGF17/HRAS/MOS/F GF20/ARPC5L/ACTB		
hsa049 71	Gastric secretion	acid	73/7109	76/810 5	0.01197 8078	0.04691 4137	0.03077 0751	ITPR1/PRKACB/MYLK/CAMK2G/PLC B2/GNAS/PLCB4/CAMK2D/ADCY3/C ALML4/KCNK2/ADCY5/MYLK3/CAL M3/ADCY7/MYLK4/KCNJ15/KCNJ10/ KCNJ16/KCNK10/SLC26A7/SLC4A2/A DCY4/PRKACA/ADCY8/GNAI2/PLCB 3/CAMK2B/KCNJ2/CHRM3/ADCY2/G	73

							NAQ/CAMK2A/ATP1B4/PRKCB/ATP1A2/ADCY6/KCNJ1/SLC9A1/ITPR2/ATP1A1/CFTR/ADCY9/ATP1B2/SLC9A4/KCNQ1/ATP1A4/ATP1B3/KCNE2/PRKACG/ACTG1/EZR/CALM1/ATP4A/CALML6/PLCB1/MYLK2/HRH2/CALML3/ADCY1/CA2/SSTR2/GNAI1/GNAI3/ATP1B1/ATP1A3/GAST/CALML5/CALM2/SST/PRKCG/ATP4B/ACTB	
hsa05212	Pancreatic cancer	73/7109	76/8105	0.011978078	0.046914137	0.030770751	MAPK10/PIK3R1/JAK1/VEGFA/BAX/TGFBF1/TGFA/MAPK8/TP53/AKT2/BCL2L1/AKT3/RPS6KB1/CASP9/RALGDS/SMAD2/CDC42/ERBB2/EGF/PIK3CB/NFKB1/PIK3R3/MAPK1/PIK3CD/RELA/SMAD3/STAT3/BRAF/TGFB2/ARAF/ARHGEF6/E2F3/IKBKG/PIK3CA/AKT1/BRCA2/E2F2/DDB2/IKBKB/RAF1/KRAS/RALB/MAP2K1/EGFR/STAT1/POLK/MTOR/CDK4/CHUK/PIK3R2/MAPK9/CDK6/RALA/RAC2/SMAD4/TGFB3/CCND1/RAC1/BAD/RB1/MAPK3/PLD2/GADD45B/CDKN1A/RAD51/TG	73

							FBR2/CDKN2A/RALBP1/E2F1/PLD1/G ADD45G/RPS6KB2/TGFB1	
hsa041 50	mTOR signaling pathway	145/710 9	155/81 05	0.01234 8401	0.04779 5577	0.03134 8883	RPS6KA3/TSC2/EIF4E/PIK3R1/TSC1/ GRB10/EIF4B/STRADA/LPIN1/PRR5/ AKT2/AKT3/RPS6KB1/PDPK1/SGK1/L RP6/SLC38A9/CAB39/EIF4E2/IGF1/PI K3CB/INSR/FZD3/PIK3R3/RHOA/WN T5A/MAPK1/PIK3CD/MAPKAP1/FNIP 1/TTI1/GSK3B/STRADB/BRAF/CAB39 L/WNT8A/WNT7B/FZD6/DEPDC5/RR AGB/RPS6KA2/FZD5/LAMTOR3/CLIP 1/PIK3CA/ATP6V1C2/AKT1/MLST8/W NT2/SKP2/RRAGD/SLC3A2/IKBKB/S EH1L/PRKCB/PRKAA1/ULK2/RPS6K A6/WDR59/RAF1/KRAS/TELO2/FZD4/ MAP2K1/SESN2/PRKAA2/LAMTOR4/ DVL3/IGF1R/SOS1/RICTOR/SEC13/W NT5B/DEPTOR/LPIN2/LPIN3/IRS1/MT OR/AKT1S1/FZD2/ATP6V1E1/CHUK/ PIK3R2/ATP6V1H/WNT3/FNIP2/WNT 4/WNT10B/ATP6V1E2/RHEB/FZD7/U LK1/WNT2B/RPS6KA1/CASTOR1/AT	145

							P6V1D/WNT9B/RPTOR/WNT16/MAPK3/ATP6V1C1/ATP6V1B2/MIOS/WDR24/WNT10A/WNT11/FZD1/DDIT4/DVL2/TNF/WNT7A/WNT8B/CASTOR2/NRAS/GRB2/FLCN/ATP6V1A/FZD8/TNFRSF1A/RRAGC/TBC1D7-LOC100130357/FZD9/ATP6V1G2/LAMTOR5/NPRL2/INS/ATP6V1B1/EIF4E1B/SLC7A5/PTEN/LRP5/RNF152/WNT1/HRAS/RRAGA/ATP6V1F/ATP6V1G3/WNT9A/PRKCG/NPRL3/RPS6KB2/ATP6V1G1/LAMTOR2/STK11/TBC1D7	
hsa05030	Cocaine addiction	48/7109	49/8105	0.012563957	0.048064439	0.031525228	PRKACB/BDNF/SLC18A1/DLG4/GNAS/CREB3L4/ATF2/GRIN2A/CREB5/PDYN/GRIN2B/FOSB/ADCY5/NFKB1/DDC/ATF4/RELA/CREB1/ATF6B/PPP1R1B/GRIN3A/PRKACA/RGS9/GNAI2/GRIN1/CREB3L2/CREB3L3/DRD2/DRD1/MAOA/CREB3/GPSM1/GRIN2D/GRM2/CREB3L1/GRIA2/GRM3/SLC6A3/CDK5R1/PRKACG/MAOB/GRIN2C/GNAI1/GNAI3/GRIN3B/CDK5/JUN/SLC	48

							18A2	
hsa049 21	Oxytocin signaling pathway	144/710 9	154/81 05	0.01325 3502	0.05011 9565	0.03287 3175	CACNA1C/CACNB4/ITPR1/PRKACB/ CACNB2/MEF2C/PPP1R12B/MYLK/N FATC2/GUCY1A1/NFATC4/CAMK2G/ PLCB2/NFATC3/CAMKK2/GNAS/CA CNA2D2/CACNA1D/PRKAG2/PLCB4/ CAMK2D/ADCY3/TRPM2/CALML4/C AMK1G/PPP1R12A/CACNA1F/ELK1/ ADCY5/MYLK3/CALM3/RYR3/ADCY 7/PIK3R5/RHOA/CACNA2D1/NFATC1 /MYLK4/MAPK1/GUCY1A2/MAPK7/R CAN1/ADCY4/PRKACA/CAMK4/PIK3 CG/CACNB1/PPP3CB/ADCY8/GNAI2/ RYR2/MYL6B/PLCB3/CAMK2B/KCNJ 2/CACNG7/CACNA1S/CACNG6/ADC Y2/JMJD7- PLA2G4B/GNAQ/CAMK2A/PRKAG1/ PPP1CB/CAMK1D/ROCK2/PRKCB/PR KAA1/PPP1CC/PPP3CA/KCNJ4/RAF1/ ADCY6/KRAS/ITPR2/MAP2K1/GUCY 1B1/EGFR/CACNA2D4/PRKAA2/NPR 2/KCNJ5/CACNB3/PPP3R2/RYR1/NOS	144

							3/KCNJ12/PRKAB2/CACNG4/ADCY9/PLA2G4D/PLA2G4F/NPR1/MAP2K5/PLA2G4B/CACNG8/MYL6/PIK3R6/KCNJ6/FOS/PRKAB1/CCND1/KCNJ9/SRC/MAPK3/GNAO1/CACNA2D3/NPPA/C DKN1A/CACNG5/PRKACG/ROCK1/A CTG1/CALM1/NRAS/PPP3CC/CALML 6/PPP1R12C/EEF2K/PLCB1/MYLK2/C AMK1/CD38/KCNJ14/CALML3/PLA2 G4A/RGS2/ADCY1/CACNG3/GNAI1/G NAI3/KCNJ18/CACNG2/KCNJ3/MYL9 /PRKAG3/HRAS/CALML5/CALM2/PL A2G4C/PPP3R1/PRKCG/JUN/ACTB	
hsa015 22	Endocrine resistance	93/7109	98/810 5	0.01423 5234	0.05322 0364	0.03490 6974	MAPK10/PRKACB/PTK2/PIK3R1/BAX /SP1/ESR1/GNAS/MAPK8/TP53/AKT2/ AKT3/RPS6KB1/MAPK14/MDM2/ESR 2/ADCY3/IGF1/ERBB2/ADCY5/PIK3C B/ABCB11/ADCY7/PIK3R3/MAPK1/PI K3CD/SHC1/MMP2/BRAF/NOTCH2/N COR1/ARAF/NCOA3/E2F3/MED1/AD CY4/PRKACA/ADCY8/GPER1/PIK3C A/AKT1/E2F2/ADCY2/RAF1/ADCY6/	93

							KRAS/NOTCH4/MAP2K1/EGFR/CYP2D6/SHC4/IGF1R/SOS1/BCL2/ADCY9/MTOR/CDK4/PIK3R2/MMP9/JAG2/MAPK9/CYP2D7/NOTCH3/HBEGF/FOS/MAPK12/CCND1/BAD/RB1/SRC/MAPK3/CDKN1A/SHC3/CDKN1B/PRKACG/MAPK11/NOTCH1/NRAS/DLL3/JAG1/MAPK13/GRB2/CDKN2A/BIK/E2F1/ADCY1/DLL4/SHC2/HRAS/CARM1/RPS6KB2/JUN/CDKN2C	
hsa04911	Insulin secretion	82/7109	86/8105	0.014623302	0.054056927	0.035455671	KCNMA1/CACNA1C/PRKACB/CAMK2G/PLCB2/RIMS2/ADCYAP1R1/GNAS/CACNA1D/KCNN3/CREB3L4/ATF2/CREB5/PLCB4/TRPM4/CAMK2D/ADCY3/CACNA1F/ABCC8/KCNMB2/ADCY5/RAPGEF4/PCLO/ADCY7/ATF4/CREB1/ATF6B/KCNN4/KCNMB3/SLC2A2/ADCY4/PRKACA/ADCY8/RYR2/PLCB3/CAMK2B/CREB3L2/CACNA1S/CHRM3/ADCY2/CREB3L3/GLP1R/GNAQ/CAMK2A/ATP1B4/PRKCB/ATP1A2/ADCY6/SLC2A1/ATP1A1/ADCYAP1/CR	82

							EB3/GCK/ADCY9/ATP1B2/CREB3L1/ VAMP2/CCK/ATP1A4/ATP1B3/KCNM B4/KCNN1/PRKACG/PDX1/GPR119/K CNN2/STX1A/PLCB1/GNA11/KCNU1/ ADCY1/INS/GIP/CCKAR/KCNJ11/ATP 1B1/ATP1A3/FFAR1/GCG/PRKCG/KC NMB1/RAB3A	
hsa040 68	FoxO signaling pathway	123/710 9	131/81 05	0.01479 7781	0.05409 4111	0.03548 006	MAPK10/BCL2L11/PIK3R1/TGFBR1/ MAPK8/PRKAG2/GRM1/AKT2/AKT3/ MAPK14/MDM2/PDPK1/SGK1/FOXO3 /IGF1/EGF/HOMER3/PIK3CB/INSR/BC L6/CREBBP/PIK3R3/MAPK1/PIK3CD/ SMAD3/STAT3/BRAF/CDK2/IL7R/TG FB2/SLC2A4/G6PC2/ARAF/ATM/AGA P2/STK4/FOXO4/SOD2/PIK3CA/AKT1 /PCK2/SKP2/SGK3/PLK4/CCND2/IRS2 /HOMER1/IKBKB/USP7/PRKAG1/CSN K1E/SGK2/PRKAA1/RAF1/KRAS/SET D7/MAP2K1/EGFR/PRKAA2/EP300/IL 6/G6PC/FASLG/IGF1R/FBXO32/SOS1/ TNFSF10/PRKAB2/IRS1/RAG1/SIRT1/ CCNB3/CHUK/PIK3R2/PLK3/PLK2/NL	123

							K/MAPK9/RBL2/RAG2/CCNG2/SMAD4/TGFB3/PRKAB1/MAPK12/FBXO25/PCK1/CCND1/C8orf44-SGK3/CCNB1/GABARAPL1/FOXO1/GABARAP/MAPK3/GADD45B/HOMER2/CDKN1A/CDKN1B/MAPK11/NRAS/S1PR1/TGFBR2/MAPK13/GRB2/PLK1/CAT/G6PC3/ATG12/INS/CCNB2/PTEN/PRMT1/IRS4/PRKAG3/IL10/HRAS/GADD45G/S1PR4/KLF2/TGFB1/BNIP3/STK11/FOXG1	
hsa00620	Pyruvate metabolism	46/7109	47/8105	0.015770941	0.05536741	0.036315211	PC/ACACA/PDHA1/PKM/ACAT1/PKL R/ACSS1/DLD/LDHB/ADH7/PCK2/ALDH3A2/ALDH7A1/HAGH/ALDH1B1/ADH6/LDHC/MDH2/ADH1B/DLAT/ADH5/LDHD/MDH1/ME2/ALDH9A1/ALDH2/PDHB/LDHA/PCK1/PDHA2/ADH1C/ADH4/GLO1/ACYP1/LDHAL6B/ACOT12/ME3/ME1/AKR1A1/ADH1A/ACSS2/LDHAL6A/ACAT2/GRHPR/ACYP2/ACACB	46
hsa049	Carbohydrate	46/7109	47/810	0.01577	0.05536	0.03631	PIK3R1/PLCB2/CACNA1D/AKT2/AKT	46

73	digestion and absorption		5	0941	741	5211	3/HK1/SLC5A1/PLCB4/SLC37A4/PIK3CB/PIK3R3/PIK3CD/G6PC2/AMY1B/SLC2A2/SI/PIK3CA/AKT1/PLCB3/ATP1B4/PRKCB/ATP1A2/AMY1A/MGAM/MGAM2/TAS1R2/ATP1A1/G6PC/HK3/ATP1B2/PIK3R2/LCT/HK2/SLC2A5/ATP1A4/ATP1B3/AMY2B/AMY1C/GNAT3/HKDC1/PLCB1/G6PC3/TAS1R3/AMY2A/ATP1B1/ATP1A3	
hsa04630	JAK-STAT signaling pathway	151/7109	162/8105	0.015791617	0.05536741	0.036315211	GHR/FHL1/PIK3R1/JAK1/LEPR/IL6ST/IL15RA/LIFR/IL12RB2/AKT2/BCL2L1/AKT3/STAT6/MCL1/PRLR/CSF2RA/IL5RA/IL24/EGF/PIK3CB/CREBBP/PIK3R3/IL20RA/THPO/PIK3CD/IFNAR2/SOCS7/SOCS2/IL21R/STAT5A/CCND3/STAT3/SOCS6/PIAS2/IL7R/IL22RA2/SOCS5/GFAP/MYC/IFNAR1/IL23R/CSH2/CSF3R/IL6R/CNTFR/IFNLR1/PTPN2/PIK3CA/AKT1/PDGFR/CCND2/IL20RB/SOCS4/STAT4/PTPN6/PTPN11/IL4R/RAF1/GH2/STAT2/IL13/CSF2RB/IL12RB1/EGFR/STAT1/IL15/IL10RA/EP300	151

							/GH1/IL6/CSF3/CRLF2/PIAS1/LIF/SOS 1/BCL2/IFNGR2/IL22RA1/MTOR/IL11/ IL2RB/JAK3/PIK3R2/CSF2/IL11RA/IL4 /STAM/PDGFRB/IL12B/IL19/JAK2/TY K2/AOX1/CSH1/IL13RA1/CCND1/IL27 RA/SOCS3/IL7/STAM2/EPOR/OSMR/I L12A/CISH/IL3RA/MPL/PDGFB/PIAS3 /IFNA2/CDKN1A/STAT5B/IL2RG/IL20 /GRB2/IL21/IFNB1/IFNGR1/PIM1/IRF9 /TSLP/IFNL2/IFNK/IL10RB/IL2RA/IFN G/IFNA4/IL9R/PDGFA/IL10/IL22/IFN W1/IL17D/HRAS/IFNA1/OSM/IL5/IFN A21/IFNA14/LEP/EPO/SOCS1/IL13RA 2/IL2/IFNE/IFNA16/IL9/IL23A/IFNA6/ PIAS4/CNTF/IFNL3	
hsa005 62	Inositol phosphate metabolism	70/7109	73/810 5	0.01595 1341	0.05536 741	0.03631 5211	SYNJ1/PIP5K1A/INPP5J/INPP4B/PLCB 2/INPP5F/SYNJ2/PLCH1/PLCB4/MTM R3/PIP4K2C/INPP5K/PIK3CB/PLCZ1/ MTMR14/PI4KB/INPP5D/CDIPT/PIK3 CD/MTMR1/SACM1L/PIP4K2A/PLCG 1/INPP4A/PIKFYVE/INPP5B/PIK3CG/ PIK3CA/PIP5K1B/PLCB3/PLCG2/OCR	70

							L/PLCH2/PLCE1/PIK3C2A/PI4KA/MIN PP1/ITPK1/MTMR2/IPPK/MTM1/PLC D4/ITPKB/MTMR7/PIP5KL1/PI4K2B/P IK3C2G/MTMR4/ALDH6A1/INPP1/IS YNA1/MTMR8/PLCD1/IMPA1/PLCD3/ PI4K2A/PIK3C2B/INPP5A/PIP4K2B/FI G4/PLCB1/MTMR6/PIP5K1C/ITPKA/M IOX/PTEN/IMPA2/PIK3C3/INPPL1/INP P5E	
hsa040 12	ErbB signaling pathway	81/7109	85/810 5	0.01598 755	0.05536 741	0.03631 5211	MAPK10/NRG1/ABL2/PAK3/CBLB/PT K2/PIK3R1/CAMK2G/TGFA/PAK4/GA B1/MAPK8/AKT2/AKT3/RPS6KB1/ER BB4/CAMK2D/ERBB2/ELK1/EGF/PIK 3CB/PIK3R3/MAPK1/PIK3CD/SHC1/G SK3B/STAT5A/BRAF/MAP2K7/MAP2 K4/NRG3/PLCG1/ARAF/MYC/PIK3CA /AKT1/PAK6/CAMK2B/PLCG2/BTC/P AK5/ERBB3/CAMK2A/PRKCB/RAF1/ KRAS/MAP2K1/EGFR/SHC4/NRG4/SO S1/CRK/MTOR/PAK2/PAK1/PIK3R2/B UB1B- PAK6/MAPK9/CBL/HBEGF/CRKL/NC	81

							K2/NCK1/BAD/ABL1/SRC/MAPK3/NRG2/CDKN1A/SHC3/STAT5B/CDKN1B/EREG/NRAS/GRB2/SHC2/HRAS/AREG/PRKCG/RPS6KB2/JUN	
hsa01523	Antifolate resistance	31/7109	31/8105	0.017030212	0.058226702	0.038190606	ABCC4/ABCC5/MTHFR/ABCC1/ABCG2/NFKB1/DHFR/RELA/ABCC3/FPGS/ATIC/DHFR2/IKBKG/GART/FOLR1/IKKB/SLC19A1/TYMS/SHMT1/IL6/ABCC2/CHUK/ALOX12/FOLR2/SHMT2/IL1B/SLC46A1/TNF/IZUMO1R/GGH/FOLR3	31
hsa04114	Oocyte meiosis	121/7109	129/8105	0.017167143	0.058226702	0.038190606	RPS6KA3/ITPR1/PRKACB/YWHAZ/CAMK2G/SGO1/PPP2R5C/CPEB2/CPEB4/CDC25C/STAG3/PPP2R1B/MAPK14/PGR/CAMK2D/AR/CDC27/ADCY3/CCNE1/CALML4/CPEB1/IGF1/ADCY5/PLCZ1/SMC1A/CALM3/ADCY7/SMC1B/MAPK1/ANAPC1/CDK2/PPP2R5E/CDK16/ESPL1/PKMYT1/BTRC/SPDYE1/BUB1/ADCY4/PRKACA/RPS6KA2/PPP3CB/ADCY8/PPP2R5D/REC8/CAMK2B/ADCY2/CAMK2A/PPP1CB/SLK/PPP1	121

							CC/RPS6KA6/PPP3CA/ADCY6/FBXO5 /ITPR2/MAP2K1/MAD1L1/PTTG1/AN APC5/IGF1R/PPP3R2/SPDYE2/SPDYE 2B/SPDYA/ADCY9/FBXW11/CCNE2/P PP2CA/ANAPC13/MAD2L2/CUL1/SPD YE16/SPDYE5/SPDYE6/SKP1/SPDYE1 7/MAD2L1/MAPK12/RPS6KA1/CDC23 /CCNB1/PPP2R5A/MAPK3/PRKACG/A NAPC10/YWHAE/YWHAG/MAPK11/ AURKA/CALM1/ANAPC2/ANAPC7/M APK13/PPP3CC/CPEB3/CALML6/ANA PC11/PLK1/SPDYE11/PPP2CB/YWHA H/SMC3/CALML3/ADCY1/INS/CDC20 /CDK1/CCNB2/FBXO43/CALML5/MO S/CALM2/PTTG2/PPP3R1/PPP2R5B/Y WHAB/CDC26/SPDYC/SPDYE3/SPDY E4	
hsa052 04	Chemical carcinogenesis	79/7109	83/810 5	0.01908 2736	0.06406 347	0.04201 8913	HSD11B1L/CYP1A1/CYP2C8/ALDH3 A1/ARNT/CYP2C18/SULT1A1/UGT2A 1/CHRNA7/MGST2/NAT1/CYP3A43/A LDH3B1/AKR1C2/KYAT1/UGT2B28/A DH7/GSTO1/EPHX1/CYP2C9/UGT2B1	79

							0/ALDH3B2/GSTM5/GSTK1/ADH6/ADH1B/UGT2B4/SULT1A2/HSD11B1/UGT2B7/ADH5/CYP2A7/GSTM3/UGT2B17/CYP1A2/UGT2A2/GSTA4/SULT1A4/CYP1B1/ADH1C/ADH4/UGT1A6/UGT1A1/KYAT3/GSTA1/CYP3A4/MGST3/CYP2C19/CYP3A5/CYP3A7/NAT2/SULT1A3/HPGDS/UGT1A5/GSTM4/GSTT2B/ADH1A/CYP2A13/MGST1/GSTO2/CBR1/CYP3A7-CYP3A51P/GSTA2/UGT2B11/UGT1A8/UGT1A9/UGT1A4/GSTM2/GSTP1/GSTA3/UGT1A10/UGT1A7/UGT1A3/GSTA5/UGT2B15/GSTM1/CYP2E1/UGT2A3/CYP2A6	
hsa00410	beta-Alanine metabolism	30/7109	30/8105	0.019426327	0.064558196	0.042343402	AOC3/ALDH3A1/ABAT/CNDP2/ACOX1/EHHADH/ALDH3B1/ALDH3A2/AOC2/ALDH7A1/ALDH1B1/ALDH3B2/GAD1/CARNS1/DPYD/HADHA/SMOX/GADL1/ACOX3/ALDH9A1/ALDH6A1/ALDH2/GAD2/ECHS1/CNDP1/UPB1/ACADS/HIBCH/DPYS/MLYCD	30

hsa05031	Amphetamine addiction	66/7109	69/8105	0.02321714	0.076384391	0.050100145	CACNA1C/PRKACB/GRIA1/CAMK2G/SLC18A1/GNAS/CACNA1D/CREB3L4/ATF2/GRIN2A/CREB5/PDYN/CAMK2D/CALML4/GRIN2B/FOSB/ADCY5/CALM3/DDC/ATF4/CREB1/ATF6B/GRIA4/GRIA3/PPP1R1B/GRIN3A/PRKACA/CAMK4/HDAC2/PPP3CB/GRIN1/CAMK2B/CREB3L2/CREB3L3/CAMK2A/PPP1CB/PRKCB/PPP1CC/PPP3CA/DRD1/MAOA/PPP3R2/CREB3/SIRT1/GRIN2D/CREB3L1/GRIA2/FOS/SLC6A3/PRKACG/CALM1/MAOB/PPP3CC/CALML6/STX1A/ARC/CALML3/GRIN2C/CALML5/CALM2/GRIN3B/PPP3R1/PRKCG/HDAC1/JUN/SLC18A2	66
hsa01240	Biosynthesis of cofactors	145/7109	156/8105	0.023521918	0.076620902	0.050255271	BCAT1/NME6/MPI/MOCS1/PANK2/AK4/NME4/CTPS2/NQO1/UROS/COASY/NMNAT2/LIAS/PKM/NMNAT3/AK2/FECH/CAD/DHFR/HMBS/NADK2/PPCDC/AK3/GSS/UGT2A1/PPOX/COQ5/BCAT2/FLAD1/ALAS2/CMPK1/PKLR/GCLC/PNPO/MAT2B/FPGS/ADSL/PA	145

							NK1/CTPS1/DLD/UGT2B28/DHFR2/C OX15/KMO/ALPL/GGCX/AK9/NME1/ ALAS1/ALDH3A2/MTHFD1L/AK5/RG N/NFS1/ALDH1B1/HPD/UGP2/UGT2B 10/MTHFD2L/AK1/SHMT1/GCLM/UG T2B4/VKORC1/AK8/PDXK/EARS2/RD H11/IDO2/UGT2B7/NMNAT1/PSAT1/ NADSYN1/UMPS/RDH12/ALAD/HAA O/AK7/ALDH2/UGT2B17/KYNU/NAP RT/COQ6/UGT2A2/COQ3/SHMT2/NA DK/MTHFD2/CMPK2/DHRS3/VKORC 1L1/UGT1A6/UGT1A1/PHOSPHO2/AK 6/GPHN/COQ7/HSD17B6/LIPT1/COQ2 /TPK1/PPCS/COX10/MOCS2/GMPPA/ QPRT/OXSM/UGT1A5/MMAB/RDH13 /AKR1A1/UGDH/NME1- NME2/BCO1/IDO1/GCH1/DHODH/GM PPB/ALPP/AFMID/PMM2/LIPT2/UGT2 B11/ALPI/UGT1A8/UGT1A9/UGT1A4/ MTHFD1/MAT1A/NME3/PMM1/RFK/ CPOX/PANK3/UGT1A10/UGT1A7/UG T1A3/MAT2A/PDXP/UGT2B15/GGH/N	
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							ME7/UROD/UGT2A3/SDR16C5	
hsa043 40	Hedgehog signaling pathway	54/7109	56/810 5	0.02494 016	0.08044 4242	0.05276 298	PRKACB/CSNK1G1/PTCH1/GPR161/S POP/IQCE/CSNK1G3/HHAT/CUL3/BO C/ARRB1/ARRB2/GLI3/GSK3B/PTCH 2/CDON/SCUBE2/SMURF1/GLI1/BTR C/EVC2/LRP2/PRKACA/CCND2/CSN K1E/EVC/DHH/CSNK1D/KIF3A/HHA TL/BCL2/MEGF8/KIF7/FBXW11/CUL1 /CSNK1A1/CSNK1A1L/CCND1/MOSM O/GAS1/IHH/PRKACG/SPOPL/GRK2/ SMO/CSNK1G2/SHH/HHIP/SUFU/GLI 2/EFCAB7/GRK3/MGRN1/SMURF2	54
hsa006 50	Butanoate metabolism	28/7109	28/810 5	0.02527 6051	0.08057 1119	0.05284 6198	ACSM2A/HMGCLL1/BDH1/ABAT/HM GCS1/ACSM1/ACAT1/EHHADH/ACS M2B/ACSM3/HMGCL/GAD1/HADH/A LDH5A1/HADHA/BDH2/ACSM5/OXC T1/L2HGDH/ACSM4/GAD2/HMGCS2/ ECHS1/AACS/ACAT2/OXCT2/ACSM6 /ACADS	28
hsa041 37	Mitophagy - animal	65/7109	68/810 5	0.02546 929	0.08057 1119	0.05284 6198	MAPK10/MITF/SP1/OPTN/NBR1/MAP K8/BCL2L13/TP53/MRAS/BCL2L1/CA LCOCO2/FOXO3/BECN1/ATG5/ATF4/	65

							RELA/MFN1/AMBRA1/CSNK2A1/USP15/TFEB/UBA52/PRKN/MFN2/TBC1D15/RHOT1/TAX1BP1/USP8/TBC1D17/ATG9A/RPS27A/KRAS/CITED2/RRAS2/PINK1/MAPK9/HIF1A/RAB7B/ULK1/TFE3/BNIP3L/GABARAPL1/TBK1/SRC/GABARAP/RHOT2/NRAS/BECN2/EI2F2/USP30/CSNK2A2/FIS1/FUNDC1/E2F1/RAB7A/PGAM5/UBC/SQSTM1/CSNK2A3/TOMM7/HRAS/ATG9B/JUN/BNIP3/UBB	
hsa00062	Fatty acid elongation	27/7109	27/8105	0.02883083	0.088648067	0.058143829	ELOVL5/HACD3/ELOVL6/HADH/HADHA/HADHB/HACD2/ELOVL2/MECR/ELOVL1/ACOT7/PPT2/ELOVL7/THM4/ECHS1/ACOT4/HACD4/PPT1/ACA2/ELOVL4/THEM5/ELOVL3/HACD1/ACOT2/TECR/HSD17B12/ACOT1	27
hsa00601	Glycosphingolipid biosynthesis - lacto and neolacto series	27/7109	27/8105	0.02883083	0.088648067	0.058143829	ST3GAL3/B3GALNT1/ST3GAL4/B3GALT5/B3GNT5/FUT6/ST3GAL6/GCNT2/FUT1/FUT3/FUT9/B4GALT4/FUT2/B3GNT2/B4GALT1/B4GALT3/FUT4/B3GNT4/ST8SIA1/B3GALT1/B4GALT2/A	27

							4GALT/FUT7/B3GALT2/B3GNT3/FUT5/ABO	
hsa01040	Biosynthesis of unsaturated fatty acids	27/7109	27/8105	0.02883083	0.088648067	0.058143829	HSD17B4/ELOVL5/ACOX1/HACD3/ELOVL6/FADS1/SCP2/ACAA1/SCD/BAT/HACD2/ELOVL2/SCD5/ACOX3/FADS2/ELOVL1/ACOT7/ELOVL7/ACOT4/HACD4/ELOVL4/ELOVL3/HACD1/ACOT2/TECR/HSD17B12/ACOT1	27
hsa04721	Synaptic vesicle cycle	74/7109	78/8105	0.029444802	0.089697591	0.058832207	SLC1A2/AP2B1/RIMS1/STX3/DNM1/SLC18A1/SLC6A1/DNM3/SYT1/SLC6A2/CACNA1A/AP2S1/SLC6A9/UNC13C/CPLX2/CLTC/UNC13A/STXBP1/SLC6A12/SLC1A3/ATP6V0A1/DNM2/ATP6V0A4/UNC13B/SLC1A6/ATP6V1C2/SLC6A11/SLC6A13/SLC1A7/AP2A2/SLC17A8/ATP6V0D1/SLC6A4/CLTCL1/CPLX3/NSF/SLC1A1/ATP6V1E1/ATP6V0B/ATP6V1H/STX1B/CLTB/AP2M1/ATP6V1E2/ATP6V0E1/VAMP2/SLC6A3/ATP6V1D/NAPA/CPLX1/ATP6V0A2/SLC6A7/CACNA1B/ATP6V1C1/ATP6V1B2/CPLX4/ATP6V0E2/SLC6A5/STX2/	74

							STX1A/ATP6V1A/SLC32A1/ATP6V1G2/ATP6V1B1/AP2A1/SLC17A7/TCIRG1/ATP6V1F/ATP6V1G3/ATP6V0D2/ATP6V1G1/SLC17A6/RAB3A/SLC18A2	
hsa00230	Purine metabolism	121/7109	130/8105	0.033640647	0.10070251	0.066050278	PDE4D/PDE1C/GUCY1A1/NME6/ADA2/IMPDH1/ENTPD1/PDE9A/PDE10A/ENTPD6/ADCY10/AK4/NME4/PDE5A/PRUNE1/ADCY3/PDE1B/PDE4A/PDE11A/PKM/PRPS1/AK2/ADCY5/NT5C3A/PDE4B/PDE4C/ADCY7/PDE8B/FHIT/GDA/AK3/NUDT16/GUK1/GUCY1A2/PDE6B/NT5C1B-RDH14/PDE8A/NT5E/PDE1A/PAPSS2/ENTPD5/ENTPD3/AMPD2/ADK/PKLR/DGUOK/ADSL/PDE2A/ATIC/ADCY4/PRPS2/AK9/GART/ADCY8/RRM2/NME1/NUDT9/NT5C1B/ENPP1/ENTPD2/ADCY2/AK5/ENTPD4/NUDT2/PDE7A/ADCY6/AK1/ENPP3/RRM1/GUCY1B1/AK8/NPR2/NT5C2/ALLC/ADA/PDE3A/RRM2B/ENPP4/PDE3B/XDH/PPAT/ADCY9/ADPRM/NPR1/CANT1/HDDC3/G	121

							MPR2/AK7/PAICS/AMPD3/ITPA/PAPS S1/NT5M/GUCY2C/NUDT5/IMPDH2/P DE6D/NT5C/AK6/NT5C3B/PFAS/GUC Y2F/PDE6A/PDE6H/NTPCR/NME1- NME2/PDE7B/GMPS/GUCY2D/PGM1/ ADCY1/ENTPD8/PDE6C/PDE6G/NME 3/PNP/NT5C1A/APRT/GMPR/NME7/H PRT1	
hsa040 66	HIF-1 signaling pathway	102/710 9	109/81 05	0.03392 2335	0.10070 251	0.06605 0278	EIF4E/PFKM/PIK3R1/CAMK2G/VEGF A/ELOC/ANGPT1/AKT2/AKT3/HK1/R PS6KB1/PDHA1/CAMK2D/EIF4E2/IGF 1/ERBB2/EGF/MKNK1/TLR4/ANGPT2 /PIK3CB/NFKB1/INSR/CREBBP/PIK3 R3/ARNT/MAPK1/PIK3CD/FLT1/TFR C/RELA/LTBR/STAT3/TEK/PLCG1/LD HB/IL6R/EGLN3/PIK3CA/AKT1/CAM K2B/PLCG2/CUL2/ALDOC/VHL/CAM K2A/EGLN2/PFKFB3/PRKCB/CYBB/S LC2A1/MAP2K1/LDHC/EGFR/PDK1/E P300/IL6/ENO4/IGF1R/ENO1/BCL2/IF NGR2/PFKP/ALDOA/NOS3/MTOR/PG K2/ANGPT4/HK3/PIK3R2/HIF1A/PDH	102

							B/TF/HK2/EGLN1/NOS2/ENO3/LDHA/ PDHA2/MAPK3/ENO2/NPPA/CDKN1 A/GAPDH/CDKN1B/PGK1/HKDC1/LD HAL6B/ALDOB/PFKL/IFNGR1/SERPI NE1/LDHAL6A/INS/EIF4E1B/IFNG/EL OB/EPO/PRKCG/RPS6KB2/EDN1/MK NK2	
hsa051 52	Tuberculosis	166/710 9	180/81 05	0.03442 6983	0.10070 251	0.06605 0278	MAPK10/CD209/JAK1/CAMK2G/BAX/ CASP10/MAPK8/SPHK2/CR1/AKT2/C D74/AKT3/MAPK14/CLEC7A/CLEC4 M/APAF1/CASP9/ARHGEF12/CAMK2 D/IRAK4/CALML4/CIITA/NFYA/TLR4 /CASP3/NFKB1/CALM3/CREBBP/RH OA/KSR1/MAPK1/C3/RELA/CREB1/A TP6AP1/CEBPG/CTSS/LAMP2/IRAK1/ RAB5B/ITGAM/MYD88/BID/TGFB2/H LA- DQB1/TLR2/CASP8/ATP6V0A1/RFX5/ PLA2R1/TRAF6/FCGR3B/FCGR3A/AT P6V0A4/RAB5C/NFYC/PPP3CB/TIRA P/AKT1/SPHK1/FCGR2A/CAMK2B/TL R6/RAB5A/BCL10/CAMK2A/IL18/ITG	166

							B2/CYP27B1/PPP3CA/RAF1/ATP6V0D 1/ITGAX/TLR9/LSP1/VDR/MALT1/ST AT1/SYK/IL10RA/MRC1/NOD2/EP300 /IL6/RIPK2/TLR1/IRAK2/IL1A/PPP3R2 /HLA- DQA1/BCL2/IFNGR2/ATP6V0B/ATP6 V1H/PLK3/CD14/MAPK9/HLA- DPB1/IL12B/CLEC4E/JAK2/EEA1/TGF B3/CYCS/NOS2/IL1B/HLA- DMB/MAPK12/HSPA9/FCGR2B/CAR D9/LAMP1/IL12A/ATP6V0A2/BAD/HL A- DPA1/SRC/MAPK3/HSPD1/IFNA2/LB P/CORO1A/MAPK11/TNF/CALM1/RF XANK/HLA-DQA2/HLA- DRB1/MAPK13/PPP3CC/CALML6/TN FRSF1A/IFNB1/HLA- DOB/IFNGR1/MRC2/HLA- DOA/CALML3/TRADD/RAB7A/CTSD/ HLA- DMA/IL10RB/IFNG/IFNA4/TCIRG1/PI K3C3/FCGR1A/IL10/HLA-	
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							DRB5/IFNA1/CALML5/IFNA21/IFNA14/CALM2/CAMP/ATP6V0D2/PPP3R1/NFYB/FADD/TGFB1/IFNA16/IL23A/IFNA6/FCER1G/CR1L	
hsa05033	Nicotine addiction	39/7109	40/8105	0.034529454	0.10070251	0.066050278	GRIA1/GABRB3/GRIN2A/CACNA1A/GRIN2B/GABRA2/GABRA1/GRIA4/GABRG3/CHRNA7/GABRG2/GRIA3/GABRR1/GRIN3A/GABRP/GRIN1/CHRNA6/SLC17A8/GABRB2/GABRA3/GABRA4/CHRNA4/GABRE/GRIN2D/GRIA2/GABRG1/CACNA1B/GABRR2/GABRQ/SLC32A1/GABRA5/GRIN2C/SLC17A7/GABRB1/CHRNA2/GABRD/GRIN3B/SLC17A6/GABRR3	39
hsa03015	mRNA surveillance pathway	92/7109	98/8105	0.0347819	0.10070251	0.066050278	PPP2R5C/GSPT1/CPSF7/NCBP2/RNMT/PPP2R1B/SMG6/RNPS1/ACIN1/HBS1L/PPP2R3A/SMG1/WDR33/PPP2R2A/MSI2/PPP2R2C/PABPN1/PAPOLA/PAPOLG/PPP2R5E/NXF1/FIP1L1/CPSF4/PABPC4/TARDBP/RNGTT/PPP2R5D/SMG7/UPF3A/CASC3/DAZAP1/PPP1CB/UPF2/PPP2R2B/PPP1CC/CSTF2/CSTF	92

							2T/FUS/PAPOLB/WDR82/NXF2/NXF2 B/NXT2/PCF11/PABPC1L2A/UPF1/DD X19A/GSPT2/PPP2CA/PPP2R2D/NUD T21/PABPC1L2B/SMG5/NCBP1/NXF3/ RBM8A/DDX19B/CPSF2/SAP18/PABP C3/PYM1/PPP2R5A/MAGOHB/GLE1/C PSF6/BCL2L2- PABPN1/PABPC5/SYMPK/PELO/NXT 1/CPSF1/PABPC4L/ETF1/SRRM1/PPP2 CB/UPF3B/MSI1/NXF5/CLP1/DDX39B /PPP2R3B/PNN/CPSF3/SSU72/CPSF4L/ EIF4A3/PABPN1L/CSTF3/NCBP2L/PP P2R5B/PPP2R3C/CSTF1	
hsa052 20	Chronic myeloid leukemia	72/7109	76/810 5	0.03489 3879	0.10070 251	0.06605 0278	PIK3R1/BAX/TGFBR1/TP53/AKT2/BC L2L1/AKT3/MDM2/CTBP2/MECOM/PI K3CB/NFKB1/PIK3R3/MAPK1/PIK3C D/RELA/SHC1/SMAD3/STAT5A/BRA F/TGFB2/ARAF/MYC/E2F3/IKBKG/H DAC2/PIK3CA/AKT1/E2F2/DDB2/IKB KB/GAB2/PTPN11/BCR/RAF1/KRAS/ MAP2K1/SHC4/POLK/SOS1/CRK/RUN X1/CDK4/CHUK/PIK3R2/CDK6/CBL/S	72

							MAD4/TGFB3/CRKL/CCND1/BAD/RB1/ABL1/MAPK3/GADD45B/NFKBIA/CDKN1A/SHC3/STAT5B/CDKN1B/NRAS/TGFBR2/GRB2/CDKN2A/E2F1/SHC2/HRAS/GADD45G/CTBP1/HDAC1/TGFB1	
hsa04080	Neuroactive ligand-receptor interaction	310/7109	341/8105	0.035930913	0.102793656	0.067421851	GHR/PARD3/NR3C1/GRIA1/P2RX2/OPRM1/GRIK1/HTR4/LEPR/GABRB3/ADCYAP1R1/PTAFR/HTR2C/GRM1/ADORA2A/GRIN2A/THRB/PRLR/PDYN/GRM5/HTR7/GRM7/P2RY2/GRIN2B/EDNRB/TRPV1/CYSLTR2/RXFP1/CNR1/GABRA2/GHRL/NPY4R2/GABBR1/C3/HCRT1/PRSS3/GABRA1/CALCR/RXFP2/FPR2/GRIK2/GRIA4/GABRG3/CHRNA7/HTR2A/FPR3/GABRG2/GPR156/FSHB/CHRM2/GRIA3/CALCA/LPAR3/GRID2/AGTR1/SSTR3/HRH1/GABRR1/EDN3/CSH2/GRIN3A/GLP2R/TAC3/LPAR1/GABRP/C3AR1/PTH2R/GRM8/CHRM1/GRIN1/GLRA2/ADRA1A/CHRNA6/PTGFR/HRH4/DRD3/NPY5R	310

							/CHRM3/AVPR1A/CHRNA4/LPAR2/L TB4R/GLP1R/PTGER3/OPRL1/KNG1/S 1PR3/GIPR/CHRNA4/TSHR/GABRB2/P 2RY14/PLG/PTGDR/GNRHR/GRID1/G ABRA3/APLNR/GH2/GRIK4/DRD2/S1 PR5/AVPR1B/VIPR1/POMC/P2RX5/NP Y4R/CRHR2/F2RL2/P2RY1/CHRM5/F2 /GABRA4/NMU/TACR1/ADCYAP1/G RM4/DRD1/GH1/GPR83/NPFFR2/CHR NE/UTS2B/CHRNA4/CRHR1/TAC4/C5 /CHRNA1/GRIK5/ADRB2/GABRE/CA LCRL/P2RX6/FSHR/GRIN2D/THRA/G HSR/PTH1R/NPY1R/MLN/NTS/BDKR B2/GRM2/ADORA3/TACR3/GRIA2/GL RB/LTB4R2/NMUR1/GRM3/VIPR2/P2 RX7/INSL3/GZMA/CCK/MCHR1/CSH 1/VIP/MAS1/AGTR2/CHRNA4/GLRA1/ P2RY6/P2RX1/CHRNA3/MCHR2/GAB RG1/TAC1/AGT/RXFP4/AVPR2/FPR1/ ADRA2A/UTS2/GHRH/PTGER2/P2RY 10/GPR50/HTR1A/LHCGR/TAAR1/GP R35/MTNR1A/PRSS1/NTSR1/CNR2/C	
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							YSLTR1/NTSR2/HTR1B/PTGIR/GRPR/ RLN3/MC2R/TAAR5/CHRNA2/TAAR2 /HTR1F/GABRR2/OPRK1/CHRNA3/G RM6/NMUR2/PTGER4/TRHR/P2RY4/I APP/SCTR/TACR2/ADRA1B/P2RY13/ BDKRB1/MC4R/NPFF/S1PR1/LPAR4/ GRP/MTNR1B/TAAR6/GABRQ/HTR1 D/PTH/GLRA3/APLN/EDN2/MC5R/HR H2/NMBR/CHRNA9/GABRA5/TAAR8/ MC1R/P2RX3/S1PR2/P2RY8/GRIK3/F2 R/GRIN2C/CHRNA10/ADORA2B/ADR A2B/HTR6/NPY/ADRB1/HCRTR2/LPA R6/GIP/GALR3/MC3R/MLNR/TBXA2 R/CHRNA1/ADRA2C/NPY2R/GCGR/F 2RL3/SSTR2/PENK/CCKAR/SSTR1/HT R2B/F2RL1/NMB/CGA/PRSS2/DRD5/C 5AR1/CORT/CRH/GABRB1/CHRNA2/ GABRD/ADRA1D/HTR5A/NPBWR1/P PY/UCN3/LEP/SST/INSL5/GRIN3B/AV P/EDNRA/TAAR9/GCG/PRLHR/GABB R2/LHB/BRS3/S1PR4/RXFP3/UCN2/P2 RY11/PMCH/EDN1/GNRH2/TRH/GAL/	
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							NPBWR2/OPRD1/GABRR3/CALCB/PTGER1/UCN/NPFFR1/RLN2/RLN1/PTH2/HCRT/SSTR5/GHRHR	
hsa04142	Lysosome	119/7109	128/8105	0.038436445	0.10901371	0.071501554	SLC11A2/ARSA/GBA/AP1G1/CTSB/C D63/HYAL1/LITAF/SPAM1/AP4S1/MFSD8/ABCA2/HYAL3/ARSG/GGA3/GALC/SORT1/AP4B1/AP4E1/LGMN/PLA2G15/ATP6AP1/CLTC/CTSV/CTSC/AP3M2/CTSS/ASAH1/GGA1/CTSA/LAMP2/M6PR/CTSE/CTNS/CTSL/CD164/ATP6V0A1/ABCB9/CLN3/ATP6V0A4/AP1B1/ACP2/GLB1/TPP1/SLC17A5/AP1M2/MAN2B1/GM2A/ENTPD4/IDS/AP3D1/SUMF1/IGF2R/AP3M1/NPC1/ATP6V0D1/PSAP/SLC11A1/NAPSA/ARSB/AP3B1/CLTCL1/GGA2/CD68/AP3B2/DNASE2B/HEXA/GNPTAB/HEXB/AP3S2/AP3S1/HGSNAT/ATP6V0B/ATP6V1H/CLTB/CTSK/SCARB2/PPT2/GALNS/FUCA1/NPC2/GLA/NAGA/LAMP1/FUCA2/AP4M1/ATP6V0A2/SMPD1/HYAL4/LAPTM5/HYAL2/PPT1/GNS/ACP5/	119

							PSAPL1/CTSW/DNASE2/AP1S3/LAPT M4A/MCOLN1/CTSO/CTSD/AP1S1/AP 1M1/GNPTG/GAA/MANBA/TCIRG1/C TSF/CLN5/SGSH/AP1G2/ATP6V0D2/L APTM4B/IDUA/LAMP3/CTSZ/CTSH/N AGPA	
hsa043 71	Apelin signaling pathway	127/710 9	137/81 05	0.04146 0623	0.11576 6943	0.07593 0966	SLC8A1/ITPR1/PRKACB/MEF2C/MYL K/PLCB2/TGFBR1/MEF2A/ADCY10/S PHK2/PRKAG2/MRAS/AKT2/AKT3/G NG2/RPS6KB1/PLCB4/SMAD2/ADCY 3/CALML4/BECN1/NOS1/MEF2D/AD CY5/MYLK3/CALM3/PPARGC1A/RY R3/ADCY7/PIK3R5/MYLK4/MAPK1/S LC8A3/SMAD3/SPP1/GNA13/GNB5/P LAT/AGTR1/ADCY4/PRKACA/GNG4/ CAMK4/PIK3CG/ADCY8/AKT1/GNAI 2/SPHK1/RYR2/PLCB3/HDAC4/ADCY 2/CDH1/GNAQ/NRF1/PRKAG1/HDAC 5/PRKAA1/RAF1/APLNR/ADCY6/KR AS/SLC9A1/ITPR2/GNGT2/MAP2K1/P RKCE/PRKAA2/LIPE/RYR1/PLIN1/RR AS2/NOS3/PDE3B/PRKAB2/ADCY9/M	127

							TOR/GNG7/PIK3R6/NOTCH3/SMAD4/PRKAB1/NOS2/PIK3R4/GNB1/CCND1/GABARAPL1/GABARAP/MAPK3/TFAM/SLC8A2/PRKACG/CALM1/NRAS/BECN2/JAG1/GNB4/CALML6/APLN/PLCB1/MYLK2/GNG13/MEF2B/SERPINE1/CALML3/GNG12/UCP1/ADCY1/BORCS8-MEF2B/GNB3/GNAI1/GNAI3/GNB2/GNGT1/PRKAG3/PIK3C3/MYL2/GNG3/HRAS/CALML5/CALM2/MYL4/ACTA2/RPS6KB2/KLF2/MYL3/EGR1	
hsa05160	Hepatitis C	145/7109	157/8105	0.041521275	0.115766943	0.075930966	CTNNB1/PIK3R1/JAK1/YWHAZ/BAX/PSME3/NR1H3/TP53/AKT2/CFLAR/AKT3/PPP2R1B/APAF1/CASP9/OCLN/PARA/LDLR/EGF/PIK3CB/CASP3/NFKB1/PIK3R3/CLDN2/PPP2R2A/OAS2/MAPK1/MAVS/PIK3CD/IFNAR2/RELA/PPP2R2C/OAS1/GSK3B/STAT3/BRAF/CDK2/BID/RNASEL/EIF2AK2/ARAF/CASP8/MYC/IFNAR1/TRAF6/E2F3/CLDN10/RIPK1/IKBKG/IKBKE/MX1/R	145

							XRA/PIK3CA/AKT1/CLDN18/IRF3/E2 F2/IFIT1/IFIT1B/IKBKB/FAS/CLDN14/ OAS3/PPP2R2B/RAF1/STAT2/KRAS/I RF7/MAP2K1/EGFR/STAT1/FASLG/S CARB1/PIAS1/CLDN1/EIF2AK4/CLD N15/SOS1/DDX58/PPP2CA/CLDN19/C LDN6/PPP2R2D/CDK4/CHUK/PIK3R2/ TLR3/CDK6/TYK2/CLDN8/CYCS/TRA F3/CCND1/SOCS3/TRAF2/TBK1/BAD/ RB1/CLDN24/MAPK3/CLDN7/NFKBI A/IFNA2/CDKN1A/YWHAE/YWHAG/ TNF/NRAS/CLDN3/CLDN16/EIF2AK3/ CXCL10/GRB2/TNFRSF1A/EIF2S1/EIF 3E/IFNB1/PPP2CB/YWHAH/IRF9/RSA D2/CLDN23/TRADD/E2F1/CLDN17/TI CAM1/CLDN4/IFNG/IFNA4/CLDN22/ EIF2AK1/MX2/CLDN5/HRAS/IFNA1/I FNA21/IFNA14/CLDN20/CLDN9/CLD N25/YWHAB/FADD/CLDN11/IFNA16/ CD81/IFNA6	
hsa042 10	Apoptosis	126/710 9	136/81 05	0.04416 4688	0.12210 2372	0.08008 6342	MAPK10/BCL2L11/ITPR1/PIK3R1/BA X/CASP10/LMNA/PTPN13/DAXX/MA	126

							PK8/TP53/AKT2/BCL2L1/CFLAR/AKT 3/DAB2IP/CTSB/CASP7/APAF1/MCL1 /CASP9/PDPK1/AIFM1/CAPN1/PIK3C B/CASP3/NFKB1/XIAP/PIK3R3/MAPK 1/ATF4/PIK3CD/RELA/CTSV/CTSC/C TSS/PRF1/TRAF1/BID/BBC3/CASP8/C TSL/PIDD1/ATM/RIPK1/IKBKG/TP53 AIP1/PIK3CA/AKT1/HTRA2/DDIT3/BI RC5/DFFA/IKBKB/FAS/TUBA1A/RAF 1/KRAS/CSF2RB/SPTA1/ITPR2/TNFR SF10B/MAP2K1/DIABLO/PARP4/NTR K1/FASLG/BIRC3/SPTAN1/TUBAL3/B CL2/CASP2/PARP3/TNFSF10/CASP6/T UBA1C/MAP3K14/CHUK/PIK3R2/ER N1/CTSK/MAPK9/GZMB/PARP1/FOS/ CYCS/PARP2/TRAF2/DFFB/HRK/BAD /MAPK3/IL3RA/PMAIP1/GADD45B/N FKBIA/LMNB1/TNF/ACTG1/NRAS/CT SW/EIF2AK3/NGF/TNFRSF1A/EIF2S1/ TUBA8/LMNB2/TRADD/CTSO/CTSD/ TUBA4A/TUBA1B/MAP3K5/TUBA3E/ CTSF/HRAS/GADD45G/ENDOG/JUN/	
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							FADD/TNFRSF10A/ACTB/TUBA3D/TUBA3C/CTSZ/CTSH	
hsa04934	Cushing syndrome	143/7109	155/8105	0.046742723	0.128152965	0.084054896	CACNA1G/CACNA1C/ITPR1/PRKACB/CTNNB1/CAMK2G/PLCB2/SP1/GNAS/CACNA1D/CREB3L4/AIPL1/ATF2/CREB5/PLCB4/TCF7L2/CAMK2D/TCF7/ADCY3/CCNE1/CACNA1I/PDE11A/LDLR/HSD3B2/CACNA1F/KCNK2/ADCY5/CYP11A1/FZD3/KMT2A/ADCY7/PDE8B/NR4A1/WNT5A/ARNT/MAPK1/ATF4/KMT2D/CREB1/LEF1/APC/GSK3B/ATF6B/HSD3B1/PDE8A/BRAF/CDK2/WNT8A/WNT7B/FZD6/AGTR1/CACNA1H/KCNK3/E2F3/ADCY4/PRKACA/FZD5/PBX1/ADCY8/GNAI2/WNT2/ARMC5/RBBP5/PLCB3/CAMK2B/USP8/CREB3L2/E2F2/CACNA1S/ADCY2/CREB3L3/GNAQ/CAMK2A/ADCY6/MRAP/ITPR2/FZD4/MAP2K1/CYP11B1/EGFR/POMC/CRHR2/RAP1B/SCARB1/DVL3/CREB3/NCEH1/CRHR1/WNT5B/CYP17A1/ADCY9/MEN1/CCNE2/FZ	143

							D2/CDK4/AXIN2/WNT3/CREB3L1/APC2/WNT4/CDK6/WNT10B/RAP1A/KCNA4/FZD7/WNT2B/AHR/CCND1/WNT9B/WNT16/AGT/RB1/MAPK3/WNT10A/WNT11/CYP21A2/FZD1/CDKN1A/AIP/MC2R/CDKN1B/PRKACG/DVL2/WNT7A/WNT8B/NR5A1/CDKN2A/FZD8/PLCB1/FZD9/GNA11/WDR5/E2F1/ADCY1/GNAI1/GNAI3/WDR5B/CRH/WNT1/STAR/WNT9A/TCF7L1/CDKN2C	
hsa00561	Glycerolipid metabolism	58/7109	61/8105	0.047945377	0.130363876	0.085505022	DGKB/AGPAT3/MGLL/LPIN1/DGKG/DGKH/DGKI/AGPAT1/AGK/DGKZ/GK/GLYCTK/DGKK/DGKA/PLPP5/LCLAT1/ALDH3A2/LIPG/MBOAT2/LPL/ALDH7A1/PNPLA3/LIPC/LIPF/ALDH1B1/MOGAT3/PNLIPRP1/GK2/DGAT2/MOGAT2/TKFC/DGAT1/AGPAT4/DGKE/LPIN2/LPIN3/AKR1B1/ALDH9A1/ALDH2/GPAT4/GPAT3/GLA/PNLIP/PLPP3/DGKD/GPAM/PLPP2/AKR1B10/MBOAT1/GPAT2/CEL/AKR1A1/AGPAT5/PLPP4/PLPP1/AGPAT2/DGKQ/MOGA	58

							T1	
hsa009 82	Drug metabolism - cytochrome P450	68/7109	72/810 5	0.04866 9441	0.13124 7919	0.08608 4861	FMO1/CYP2C8/ALDH3A1/FMO5/UGT 2A1/MGST2/ALDH3B1/FMO2/UGT2B 28/ADH7/GSTO1/CYP2B6/CYP2C9/UG T2B10/ALDH3B2/GSTM5/GSTK1/AD H6/CYP2D6/ADH1B/UGT2B4/MAOA/ UGT2B7/ADH5/CYP2A7/GSTM3/UGT 2B17/CYP1A2/CYP2D7/UGT2A2/AOX 1/GSTA4/ADH1C/ADH4/UGT1A6/UGT 1A1/FMO3/GSTA1/CYP3A4/MGST3/F MO4/CYP2C19/CYP3A5/HPGDS/UGT1 A5/MAOB/GSTM4/GSTT2B/ADH1A/M GST1/GSTO2/GSTA2/UGT2B11/UGT1 A8/UGT1A9/UGT1A4/GSTM2/GSTP1/ GSTA3/UGT1A10/UGT1A7/UGT1A3/G STA5/UGT2B15/GSTM1/CYP2E1/UGT 2A3/CYP2A6	68
hsa047 24	Glutamatergic synapse	106/710 9	114/81 05	0.04938 0409	0.13180 9306	0.08645 3072	CACNA1C/SLC1A2/ITPR1/PRKACB/G RIA1/DLGAP1/GRIK1/PLCB2/DLG4/G NAS/CACNA1D/GLUL/GRM1/GNG2/ GRIN2A/PLCB4/CACNA1A/SLC38A1/ SHANK2/ADCY3/GRM5/GRM7/GRIN	106

							2B/HOMER3/ADCY5/ADCY7/SHANK1/MAPK1/GRIK2/GRIA4/GRIA3/GNB5/SLC1A3/GRIN3A/ADCY4/PRKACA/NG4/SLC38A3/PPP3CB/ADCY8/SLC1A6/GRM8/GNAI2/GRIN1/PLCB3/SLC1A7/HOMER1/ADCY2/JMJD7-PLA2G4B/GNAQ/SLC17A8/PRKCB/SLC38A2/PPP3CA/ADCY6/GRIK4/ITPR2/GNGT2/TRPC1/GLS2/GLS/GRM4/PPP3R2/GRIK5/ADCY9/PLA2G4D/PLA2G4F/GRIN2D/GNG7/SLC1A1/PLA2G4B/GRM2/GRIA2/GRM3/GNB1/MAPK3/PLD2/GNAO1/HOMER2/PRKACG/GRM6/PPP3CC/GNB4/GRK2/PLCB1/GNG13/GNG12/GRIK3/GRIN2C/PLA2G4A/ADCY1/GNB3/SLC17A7/GNAI1/GNAI3/KCNJ3/GNB2/GRK3/GNGT1/PLD1/GNG3/PLA2G4C/GRIN3B/PPP3R1/PRKCG/SLC17A6	
hsa00600	Sphingolipid metabolism	47/7109	49/8105	0.049678887	0.131809306	0.086453072	ARSA/ASAH2/GBA/SPHK2/SMPD4/ACER3/SGMS2/GALC/ASAH1/CERS5/NEU4/CERK/B4GALT6/SGPL1/GAL3ST	47

							1/SPHK1/GLB1/CERS4/UGT8/SMPD2/SPTLC2/KDSR/PSAP/SPTLC1/GBA2/SPTLC3/UGCG/CERS3/GLA/SMPD1/SGPP2/SGPP1/PLPP3/SMPD3/ACER2/PLP2/PSAPL1/NEU3/ACER1/CERS1/CERS2/DEGS1/NEU2/PLPP1/CERS6/SGMS1/ENPP7	
hsa04912	GnRH signaling pathway	87/7109	93/8105	0.050415326	0.132693138	0.087032773	MAPK10/CACNA1C/ITPR1/PRKACB/CAMK2G/PLCB2/GNAS/MAPK8/CACNA1D/MAPK14/PLCB4/PTK2B/CAMK2D/CDC42/ADCY3/CALML4/CACNA1F/ELK1/ADCY5/CALM3/ADCY7/MAP2K6/MAPK1/ATF4/MMP2/MAP2K3/MAP2K7/MAP2K4/MAPK7/FSHB/MAP3K4/ADCY4/PRKACA/ADCY8/PLCB3/CAMK2B/CACNA1S/MAP3K2/ADCY2/JMJD7-PLA2G4B/GNAQ/PRKCD/CAMK2A/PRKCB/GNRHR/RAF1/ADCY6/KRAS/ITPR2/MAP2K1/EGFR/SOS1/ADCY9/PLA2G4D/PLA2G4F/PLA2G4B/MAPK9/HBEGF/MAP3K1/MAPK12/SRC/MAP3	87

							K3/MAPK3/PLD2/MMP14/PRKACG/MAPK11/CALM1/NRAS/MAPK13/GRB2/CALML6/PLCB1/GNA11/CALML3/PLA2G4A/ADCY1/CGA/PLD1/HRAS/CALML5/CALM2/PLA2G4C/LHB/JUN/GNRH2/EGR1	
hsa04060	Cytokine-cytokine receptor interaction	268/7109	295/8105	0.052861309	0.136206047	0.089336873	GHR/IL31RA/ACVR1/BMPR1B/TGFB R1/LEPR/IL6ST/TNFRSF11A/IL15RA/TNFSF13/LIFR/ACVR2A/IL12RB2/CCR3/IL17RC/TNFRSF19/IL16/PRLR/CSF2RA/IL17RE/IL1RAP/GDF9/EDA/IL5RA/IL24/ACVR1C/AMHR2/IL20RA/EDA2R/CXCR6/THPO/CCL4L2/IFNAR2/CCR9/IL1R2/EDAR/IL21R/TNFRSF25/CX3CR1/LTBR/RELT/CSF1/IL7R/CXCL12/TGFB2/CCL5/IFNAR1/ACVR1B/INHBA/IL18R1/IL23R/CSH2/IL32/CSF3R/IL6R/CNTFR/IL1RL2/IFNLR1/IL17RB/CCR2/ACVRL1/IL20RB/CCR7/IL18/TNFSF11/GDF11/FAS/IL4R/TNFSF13B/IL1RL1/BMPR1A/TNFSF14/ACVR2B/GH2/IL13/CSF2RB/IL12RB1/IL17RA/TNF	268

							RSF10B/TNFRSF21/IL15/IL10RA/CCR 1/TNFRSF10D/TNFRSF8/CXCL9/GH1/ IL6/IL1R1/FASLG/CCR4/CSF3/CRLF2/ INHBC/IL1A/CD4/LIF/NODAL/IL1F10/ IFNGR2/BMP3/CCR6/TNFSF10/TNFSF 15/IL22RA1/BMP4/CCL19/BMP8A/NG FR/BMP10/IL11/IL36B/IL2RB/TNFRSF 17/BMP2/CXCR1/TNFSF8/CSF2/IL36G /IL11RA/CSF1R/IL4/INHBE/IL12B/IL1 9/IL36RN/TGFB3/CXCR5/IL1B/CSH1/I L33/CCL25/CCL20/XCL1/TNFSF4/IL1 RN/CCR5/IL13RA1/TNFRSF14/IL27RA /INHA/CXCR2/IL7/EPOR/OSMR/IL12 A/TNFRSF1B/CCL28/IL34/CXCR4/TN FRSF18/IL3RA/CCL1/IL37/BMPR2/GD F7/CCL15/CD40/TNFRSF9/MPL/IL18R AP/CCL3/CCL3L3/CD27/BMP5/IFNA2/ TNFSF18/CCL8/GDF2/IL26/CXCL5/IL 2RG/CXCL17/TNF/CCL21/TNFRSF11B /INHBB/BMP8B/IL25/IL20/TGFBR2/G DF5/CXCL10/LTA/IL21/NGF/PPBP/TN FRSF1A/TNFSF12/IFNB1/IFNGR1/IL3	
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							6A/XCL2/BMP15/TNFSF9/CX3CL1/CXCL8/TSLP/CXCL14/CXCL11/CCL4/TNFRSF10C/GDF6/CCL17/GDF3/TNFRSF4/IFNL2/IFNK/ACKR3/CXCL2/IL10RB/CCL16/IL2RA/CCL27/IFNG/MSTN/CCL11/CXCL16/IFNA4/CCL14/GDF10/AMH/CXCR3/IL9R/BMP6/IL10/ACKR4/IL22/PF4/BMP7/IFNW1/IL17D/CXCL3/IL17C/IFNA1/CLCF1/OSM/IL5/IFNA21/IFNA14/LEP/CXCL1/CD40LG/EPO/EBI3/CCL18/IL31/CCR10/XCR1/TNFRSF12A/TNFRSF10A/IL13RA2/TGFB1/LTB/TNFRSF13B/CCL2/IL2/IFNE/GDF1/IFNA16/IL9/TNFRSF13C/IL23A/IFNA6/CCL22/CXCL6/CNTF/IFNL3	
hsa04550	Signaling pathways regulating pluripotency of stem cells	132/7109	143/8105	0.052992018	0.136206047	0.089336873	CTNNB1/RIF1/PIK3R1/ACVR1/JAK1/FGFR2/KAT6A/PAX6/BMP1B/IL6ST/LIFR/ACVR2A/SMARCA1/AKT2/AKT3/MAPK14/ESRRB/SMAD2/TCF7/SKIL/IGF1/ACVR1C/PIK3CB/FZD3/PIK3R3/WNT5A/MAPK1/PIK3CD/SETDB1/APC/SMAD3/GSK3B/STAT3/WNT8A/W	132

							NT7B/FZD6/TBX3/MYC/ACVR1B/INHB A/ZFHX3/FZD5/LEFTY2/PIK3CA/AK T1/WNT2/PCGF5/NANOG/FGFR1/TCF 3/BMPR1A/RAF1/ACVR2B/KRAS/FZD 4/SMAD1/MAP2K1/HOXA1/FGF2/FGF R4/POU5F1/ID4/INHBC/DVL3/ZIC3/IG F1R/LIF/NODAL/WNT5B/SMAD9/BM P4/ID1/FZD2/OTX1/JAK3/PIK3R2/AXI N2/WNT3/SMAD5/APC2/WNT4/WNT1 0B/INHBE/JAK2/SMAD4/FZD7/WNT2 B/ONECUT1/NANOGP8/MAPK12/MEI S1/PCGF2/WNT9B/WNT16/JARID2/PC GF6/MAPK3/LHX5/HAND1/BMPR2/W NT10A/WNT11/FZD1/DVL2/PCGF1/M APK11/WNT7A/WNT8B/NRAS/INHBB /FGFR3/MAPK13/GRB2/FZD8/FZD9/L EFTY1/ID3/ISL1/POU5F1B/KLF4/SOX 2/HOXB1/COMMD3- BMI1/HOXD1/WNT1/HRAS/HESX1/R EST/WNT9A/NEUROG1/MYF5/BMI1	
hsa050 17	Spinocerebellar ataxia	132/710 9	143/81 05	0.05299 2018	0.13620 6047	0.08933 6873	MAPK10/ITPR1/GRIA1/PIK3R1/OPA1/ ATP2A3/ATXN3/RORA/PLCB2/SP1/M	132

							APK8/SPTBN2/GRM1/ATG13/AKT2/A KT3/GRIN2A/PLCB4/ATXN2L/CACN A1A/KCND3/RBPJ/PDYN/BECN1/ATP 2A2/GRIN2B/NFYA/PIK3CB/PUM2/T WNK/PIK3R3/ATG2A/PIK3CD/PSMC4 /PSMD11/AMBRA1/CIC/GRIA3/PSMB 2/TBP/ATXN2/GRIN3A/VLDLR/AFG3 L2/ATXN1L/ATXN1/SLC1A6/PIK3CA/ AKT1/GRIN1/ATXN10/WIP1/RELN/A TP2A1/BEAN1/PLCB3/GNAQ/KAT5/P SMA5/PRKCB/ULK2/PSMD12/NRBF2/ TRPC3/ITPR2/VDAC3/ATG2B/MCU/P SMC5/RBPJL/RB1CC1/RYR1/PUM1/P SMA4/PSMA6/VDAC2/SLC25A4/MTO R/PSMD4/GRIN2D/PIK3R2/ATG101/G RIA2/ERN1/WIP1/ADRM1/PSMB5/M APK9/PPIF/PSMA2/FGF14/CYCS/ULK 1/TBPL1/PIK3R4/TRAF2/ATXN3L/PS MD1/PSMD6/VDAC1/OMA1/BECN2/P SMC1/XBP1/PSMD13/PSMC2/PLCB1/ ATG14/PSMB7/GRIN2C/MAP3K5/TBP L2/PSMA3/PSMD8/PIK3C3/SLC25A31/	
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							PSMB4/KCNC3/NOP56/PSMB6/PSMD14/GRIN3B/PSMB3/SEM1/PRKCG/GTF2B/PSMD3/MYOD1/PSMA1/PSMB1/SLC25A5/PSMD7	
hsa05161	Hepatitis B	149/7109	162/8105	0.054892979	0.138709239	0.090978704	MAPK10/PIK3R1/JAK1/YWHAZ/NFATC2/NFATC4/BAX/CASP10/TGFBR1/NFATC3/MAPK8/CREB3L4/TP53/AKT2/AKT3/ATF2/STAT6/MAPK14/CREB5/APAF1/CASP9/PTK2B/CCNE1/IRAK4/ELK1/TLR4/PIK3CB/CASP3/NFKB1/CNA1/CREBBP/PIK3R3/NFATC1/MAP2K6/MAPK1/MAVS/ATF4/PIK3CD/RELA/CREB1/ATP6AP1/SMAD3/ATF6B/STAT5A/IRAK1/STAT3/MAP2K3/BRAF/MAP2K7/CDK2/MAP2K4/MYD88/BID/DDX3X/TGFB2/TLR2/ARAF/CASP8/MYC/IFNAR1/TRAF6/E2F3/IKBKG/IKBKE/TAB2/TIRAP/PIK3CA/AKT1/IRF3/EGR2/CREB3L2/E2F2/BIRC5/DDB2/CREB3L3/IKBKB/TAB1/FAS/STAT4/PRKCB/RAF1/STAT2/KRAS/IRF7/VDAC3/MAP2K1/STAT1/EP300/IL6/FASL	149

							G/CREB3/SOS1/BCL2/HSPG2/DDX58/CCNE2/CHUK/JAK3/PIK3R2/MMP9/CREB3L1/MAPK9/TLR3/JAK2/TYK2/S MAD4/MAP3K1/FOS/TGFB3/CYCS/MAPK12/TRAF3/IFIH1/TBK1/EGR3/BAD/RB1/SRC/MAPK3/DDB1/NFKBIA/IFNA2/CDKN1A/STAT5B/MAPK11/TNF/NRAS/TGFBR2/MAPK13/GRB2/IFNB1/CXCL8/TICAM2/E2F1/TICAM1/SLC10A1/IFNA4/HRAS/IFNA1/IFNA21/IFNA14/PRKCG/YWHAB/CCNA2/JUN/FADD/TGFB1/IFNA16/IFNA6	
hsa002 20	Arginine biosynthesis	22/7109	22/810 5	0.05565 2339	0.13870 9239	0.09097 8704	GLUL/NOS1/ARG1/ARG2/GLUD2/ASL/GLS2/GLS/ACY1/NOS3/GOT2/GOT1L1/GPT/NAGS/NOS2/GOT1/GPT2/OTC/GLUD1/CPS1/ASS1/ABHD14A-ACY1	22
hsa003 40	Histidine metabolism	22/7109	22/810 5	0.05565 2339	0.13870 9239	0.09097 8704	HAL/ALDH3A1/CNDP2/ALDH3B1/AOC1/ALDH3A2/ALDH7A1/ALDH1B1/ALDH3B2/MAOA/CARNS1/HNMT/HDC/ALDH9A1/ALDH2/UROC1/CARNMT1/FTCD/CNDP1/MAOB/ASPA/AMDH D1	22

hsa00900	Terpenoid backbone biosynthesis	22/7109	22/8105	0.055652339	0.138709239	0.090978704	FDPS/HMGCS1/ACAT1/DHDDS/NUS1/FNTB/PDSS2/MVK/PCYOX1/IDI2/PDSS1/IDI1/HMGCR/HMGCS2/PMVK/GGPS1/MVD/FNTA/ZMPSTE24/ICMT/RCE1/ACAT2	22
hsa04728	Dopaminergic synapse	122/7109	132/8105	0.05659676	0.140002512	0.091826955	MAPK10/CACNA1C/ITPR1/PRKACB/GRIA1/SCN1A/LRTOMT/CAMK2G/PP2R5C/PLCB2/SLC18A1/ARNTL/GNAS/MAPK8/CACNA1D/CREB3L4/AKT2/AKT3/GNG2/ATF2/PPP2R1B/MAPK14/GRIN2A/CREB5/PLCB4/CACNA1A/GNAL/CAMK2D/CALML4/GRIN2B/ARRB1/ADCY5/CALM3/DDC/CLOCK/PP2R3A/PPP2R2A/ARRB2/ATF4/PPP2R2C/CREB1/KIF5A/GSK3B/ATF6B/GRIA4/PPP2R5E/GRIA3/GNB5/PPP1R1B/PRKACA/GNG4/PPP3CB/AKT1/GNAI2/PPP2R5D/PLCB3/CAMK2B/CREB3L2/DRD3/CREB3L3/GNAQ/CAMK2A/PPP1CB/PPP2R2B/PRKCB/PPP1CC/PPP3CA/DRD2/ITPR2/GNGT2/KCNJ5/DRD1/MAOA/CREB3/PPP2CA/GNG7/PPP2R2	122

							D/KIF5B/CREB3L1/GRIA2/COMT/MA PK9/KCNJ6/FOS/MAPK12/GNB1/SLC6 A3/KCNJ9/PPP2R5A/CACNA1B/GNA O1/KIF5C/PRKACG/MAPK11/CALM1/ MAOB/MAPK13/PPP3CC/GNB4/CAL ML6/PLCB1/GNG13/PPP2CB/CALML3 /GNG12/GNB3/GNAI1/PPP2R3B/GNAI 3/KCNJ3/GNB2/GNGT1/DRD5/GSK3A /GNG3/CALML5/CALM2/PPP2R5B/PR KCG/PPP2R3C/CALY/SLC18A2	
hsa049 17	Prolactin signaling pathway	66/7109	70/810 5	0.05727 0954	0.14061 3014	0.09222 7381	MAPK10/PIK3R1/TNFRSF11A/ESR1/ MAPK8/AKT2/AKT3/MAPK14/PRLR/F OXO3/ESR2/PIK3CB/NFKB1/PIK3R3/ MAPK1/PIK3CD/RELA/SOCS7/SHC1/ GSK3B/SOCS2/STAT5A/STAT3/SOCS 6/SOCS5/ELF5/SLC2A2/PIK3CA/AKT1 /CCND2/TNFSF11/SOCS4/RAF1/KRAS /IRF1/MAP2K1/STAT1/SHC4/SOS1/GC K/CYP17A1/PIK3R2/MAPK9/JAK2/FO S/MAPK12/CCND1/SOCS3/CISH/SRC/ MAPK3/GALT/LHCGR/SHC3/STAT5B /MAPK11/NRAS/MAPK13/GRB2/INS/	66

							CSN2/SHC2/CGA/HRAS/LHB/SOCS1	
hsa049 16	Melanogenesis	94/7109	101/81 05	0.05954 8564	0.14512 2057	0.09518 484	MITF/PRKACB/CTNNB1/CAMK2G/PL CB2/GNAS/CREB3L4/PLCB4/TCF7L2/ CAMK2D/TCF7/ADCY3/CALML4/ED NRB/ADCY5/CALM3/FZD3/CREBBP/ ADCY7/WNT5A/MAPK1/CREB1/LEF1 /GSK3B/KITLG/WNT8A/WNT7B/FZD 6/ADCY4/PRKACA/FZD5/ADCY8/GN AI2/WNT2/DCT/PLCB3/CAMK2B/CRE B3L2/ADCY2/CREB3L3/GNAQ/CAMK 2A/PRKCB/RAF1/ADCY6/KRAS/FZD4 /MAP2K1/POMC/KIT/EP300/DVL3/CR EB3/WNT5B/ADCY9/FZD2/WNT3/CR EB3L1/WNT4/WNT10B/FZD7/WNT2B/ WNT9B/WNT16/MAPK3/GNAO1/WN T10A/WNT11/TYRP1/FZD1/PRKACG/ DVL2/WNT7A/WNT8B/CALM1/NRAS /CALML6/FZD8/PLCB1/MC1R/FZD9/C ALML3/ADCY1/GNAI1/GNAI3/WNT1/ HRAS/CALML5/CALM2/WNT9A/PRK CG/EDN1/TCF7L1/ASIP	94
hsa049	Renin secretion	65/7109	69/810	0.06206	0.14905	0.09776	KCNMA1/CACNA1C/ITPR1/PRKACB/	65

24			5	6721	0739	1643	PDE1C/GUCY1A1/PLCB2/ADCYAP1R1/GNAS/CACNA1D/CTSB/PLCB4/PRKG2/PDE1B/CALML4/CACNA1F/ADCY5/CALM3/CREB1/GUCY1A2/PDE1A/AGTR1/EDN3/PRKACA/PPP3CB/GNAI2/PLCB3/KCNJ2/CACNA1S/GNAQ/CLCA1/PPP3CA/ADCY6/ITPR2/GUCY1B1/CLCA2/ADCYAP1/PDE3A/PPP3R2/PDE3B/ADRB2/NPR1/ACE/AGT/PTGER2/NPPA/AQP1/PRKACG/PTGER4/CALM1/PPP3CC/CALML6/EDN2/PLCB1/REN/CALML3/ADRB1/GNAI1/GNAI3/CALML5/CALM2/CLCA4/EDNRA/PPP3R1/EDN1	
hsa05211	Renal cell carcinoma	65/7109	69/8105	0.062066721	0.149050739	0.097761643	PAK3/PIK3R1/MET/VEGFA/TGFA/PAK4/GAB1/ELOC/ETS1/AKT2/AKT3/CD42/PIK3CB/CREBBP/PIK3R3/ARNT/MAPK1/PIK3CD/HGF/BRAF/TGFB2/ARAF/EGLN3/PIK3CA/AKT1/PAK6/PAK5/CUL2/VHL/EGLN2/PTPN11/RAF1/KRAS/SLC2A1/MAP2K1/EP300/RAPGEF1/RAP1B/SOS1/CRK/PAK2/PAK1/	65

							PIK3R2/BUB1B-PAK6/EPAS1/HIF1A/RAP1A/PRCC/TGFB3/EGLN1/CRKL/RAC1/TFE3/BAD/MAPK3/PDGFB/CDKN1A/NRAS/GRB2/FLCN/ARNT2/ELOB/HRAS/JUN/TGFB1	
hsa04120	Ubiquitin mediated proteolysis	129/7109	140/8105	0.063236201	0.150758769	0.098881932	UBE2D3/UBE3A/BRCA1/NEDD4L/CBLB/ITCH/MID1/RCHY1/UBE2I/TRIP12/ELOC/NEDD4/PML/UBE2H/MDM2/HUWE1/CUL4A/UBR5/CDC27/UBE2W/CUL4B/CUL3/SIAH1/UBOX5/XIAP/CUL7/UBE2F/HERC4/WWP2/UBE4A/RHOBTB2/ANAPC1/UBE3B/PIAS2/TRIM37/CDC16/SMURF1/FANCL/BTRC/UBA52/PRKN/BIRC6/TRAFF6/UBA7/SYVN1/FBXO4/UBE2E3/SAE1/UBA3/KEAP1/SKP2/CUL2/UBE2D4/VHL/KLHL13/DDB2/TRIM32/PPIL2/UBE2K/COP1/HERC1/STUB1/RPS27A/UBE2D2/NHLRC1/FBXW8/UBE4B/HERC3/UBE2E1/FBXW7/UBE2L3/ANAPC5/UBE2G2/UBE2QL1/BIRC3/PIAS1/FZR1/UBE2J2	129

							/CBL/UBE2Z/FBXW11/ANAPC13/CUL1/UBE2U/CDC34/UBE2Q2/CBL/UBE2J1/SKP1/UBE2O/RHOBTB1/MAP3K1/KLHL9/WWP1/UBA2/CDC23/SOCS3/ERCC8/UBE2L6/UBA1/UBE2D1/DDB1/PIAS3/UBE2G1/ANAPC10/UBE2A/ANAPC2/ANAPC7/ANAPC11/UBA6/UBE3C/HERC2/UBE2N/FBXO2/CDC20/UBE2C/UBC/UBE2Q1/MGRN1/CUL5/ELOB/UBE2B/CDC26/UBE2R2/SOCS1/RNF7/SMURF2/UBB/PIAS4	
hsa01521	EGFR tyrosine kinase inhibitor resistance	74/7109	79/8105	0.065240471	0.154418092	0.101282063	NRG1/BCL2L11/EIF4E/PIK3R1/JAK1/FGFR2/MET/VEGFA/BAX/TGFA/GAB1/AKT2/BCL2L1/AKT3/RPS6KB1/FOXO3/EIF4E2/IGF1/ERBB2/EGF/NF1/PIK3CB/PIK3R3/MAPK1/PIK3CD/HGF/SHC1/GSK3B/STAT3/BRAF/PLCG1/ARAF/IL6R/PIK3CA/AKT1/PDGFR/PLCG2/ERBB3/AXL/PRKCB/RAF1/KRAS/MAP2K1/EGFR/FGF2/KDR/SHC4/IL6/IGF1R/SOS1/BCL2/MTOR/PIK3R2/PDGFRB/JAK2/BAD/SRC/MAPK3/NRG2/PD	74

							GFB/SHC3/NRAS/FGFR3/PDGFC/GRB2/EIF4E1B/PDGFD/SHC2/PTEN/PDGF A/HRAS/GAS6/PRKCG/RPS6KB2	
hsa051 62	Measles	128/710 9	139/81 05	0.06701 0175	0.15747 3911	0.10328 636	MAPK10/CD209/CBLB/PIK3R1/JAK1/BAX/RCHY1/ADAR/MAPK8/TP53/AKT2/BCL2L1/AKT3/CD28/CLEC4M/APAF1/CASP9/CD46/CCNE1/IRAK4/TNF AIP3/TLR4/PIK3CB/CASP3/NFKB1/PIK3R3/OAS2/MAVS/PIK3CD/IFNAR2/RELA/OAS1/GSK3B/STAT5A/IRAK1/CND3/STAT3/CDK2/MYD88/CSNK2A1/BID/BBC3/EIF2AK2/TLR2/CASP8/IFNAR1/TRAF6/IKBKG/IKBKE/MX1/TAB2/PIK3CA/AKT1/IRF3/HSPA8/CCND2/MSN/SLAMF1/IKBKB/RAB9A/FAS/OAS3/STAT2/IRF7/TLR9/STAT1/HSPA1L/IL6/FASLG/IL1A/EIF2AK4/BCL2/DDX58/CCNE2/CDK4/HSPA6/CHUK/IL2RB/JAK3/PIK3R2/MAPK9/CDK6/IL12B/TYK2/FOS/CYCS/IL1B/TRAF3/RAB9B/FCGR2B/CCND1/IFIH1/CD3D/TBK1/IL12A/BAD/NFKBIA/IFNA2/STA	128

							T5B/IL2RG/CDKN1B/EIF2AK3/EIF2S1/EIF3H/IFNB1/RACK1/CD3E/CSNK2A2/IRF9/TRADD/HSPA2/IL2RA/IFNA4/CSNK2A3/EIF2AK1/CD3G/NFKBIB/MX2/IFNA1/IFNA21/IFNA14/JUN/FADD/IL2/HSPA1A/IFNA16/IFNA6/HSPA1B	
hsa051 34	Legionellosis	54/7109	57/810 5	0.06790 1455	0.15794 4022	0.10359 4703	NAIP/CR1/BCL2L13/CASP7/APAF1/NLRC4/CASP9/HBS1L/TLR4/CASP3/NFKB1/CASP1/C3/RELA/ITGAM/MYD88/ARF1/TLR2/CASP8/SAR1B/HSPA8/SAR1A/IL18/ITGB2/RAB1A/HSPA1L/IL6/NFKB2/TLR5/HSPA6/VCP/CD14/IL12B/CLK1/CYCS/IL1B/IL12A/SEC22B/HSPD1/EEF1A1/CLK4/NFKBIA/RAB1B/TNF/CXCL8/HSPA2/CXCL2/CXCL3/CXCL1/HSF1/HSPA1A/BNIP3/HSPA1B/CR1L	54
hsa046 40	Hematopoietic cell lineage	92/7109	99/810 5	0.06817 0368	0.15794 4022	0.10359 4703	CD59/CD44/CD1E/CD36/MME/CR1/CSF2RA/IL5RA/DNTT/FLT3LG/CR2/THPO/GYPA/TFRC/CD55/IL1R2/ITGAM/CSF1/IL7R/KITLG/ITGA6/HLA-DQB1/ITGA4/CSF3R/IL6R/CD1B/ITG	92

							A2B/ITGA3/FCER2/IL4R/CD37/CD1C/ITGB3/KIT/CD7/IL6/ITGA5/IL1R1/CSF3/IL1A/CD4/FLT3/HLA-DQA1/IL11/CD22/ITGA2/CSF2/CD14/IL11RA/ITGA1/HLA-DPB1/CSF1R/IL4/GP1BA/IL1B/HLA-DMB/CD3D/IL7/EPOR/CD19/CD34/HLA-DPA1/GP5/CD8A/IL3RA/CD1D/TNF/CD8B/MS4A1/HLA-DQA2/CD24/HLA-DRB1/ANPEP/HLA-DOB/CD1A/CD3E/CD38/HLA-DOA/CD5/CD8B2/HLA-DMA/IL2RA/CD33/IL9R/FCGR1A/CD3G/HLA-DRB5/IL5/CD2/EPO/CD9/CR1L	
hsa00670	One carbon pool by folate	20/7109	20/8105	0.072390415	0.166218673	0.109022006	MTHFR/ALDH1L1/MTR/DHFR/AMT/ATIC/DHFR2/GART/MTHFD1L/ALDH1L2/MTHFD2L/TYMS/SHMT1/MTHFS/ST20-MTHFS/SHMT2/MTHFD2/FTCD/MTFMT/MTHFD1	20

hsa047 20	Long-term potentiation	63/7109	67/810 5	0.07275 2246	0.16621 8673	0.10902 2006	CACNA1C/RPS6KA3/ITPR1/PRKACB/ GRIA1/CAMK2G/PLCB2/GRM1/GRIN 2A/PLCB4/CAMK2D/GRM5/CALML4/ GRIN2B/CALM3/CREBBP/RAPGEF3/ MAPK1/ATF4/BRAF/ARAF/PRKACA/ RPS6KA2/CAMK4/PPP3CB/ADCY8/G RIN1/PLCB3/CAMK2B/GNAQ/CAMK 2A/PPP1CB/PRKCB/PPP1CC/RPS6KA6 /PPP3CA/RAF1/KRAS/ITPR2/MAP2K1 /EP300/RAP1B/PPP3R2/GRIN2D/GRIA 2/RAP1A/RPS6KA1/MAPK3/PPP1R1A/ PRKACG/CALM1/NRAS/PPP3CC/CAL ML6/PLCB1/CALML3/GRIN2C/ADCY 1/HRAS/CALML5/CALM2/PPP3R1/PR KCG	63
hsa034 10	Base excision repair	32/7109	33/810 5	0.07387 0213	0.16646 096	0.10918 0921	SMUG1/POLL/NEIL2/POLD1/OGG1/M UTYH/NEIL1/APEX1/LIG3/LIG1/PAR P4/FEN1/TDG/NEIL3/NTHL1/XRCC1/ PARP3/POLD3/POLD4/MPG/POLD2/M BD4/POLE/POLE2/HMGB1/PARP1/AP EX2/PARP2/POLE3/UNG/POLE4/POL B	32

hsa041 30	SNARE interactions in vesicular transport	32/7109	33/810 5	0.07387 0213	0.16646 096	0.10918 0921	GOSR2/STX3/STX16/GOSR1/STX17/V AMP4/VAMP7/STX6/VAMP1/STX7/S NAP23/STX1B/STX5/USE1/VAMP2/V TI1A/BNIP1/BET1/SEC22B/BET1L/ST X18/STX4/STX2/STX1A/VAMP5/VAM P3/STX11/STX19/YKT6/STX8/SNAP29 /VAMP8	32
hsa047 13	Circadian entrainment	90/7109	97/810 5	0.07785 9712	0.17425 7452	0.11429 4601	CACNA1G/CACNA1C/ITPR1/PRKAC B/GRIA1/GUCY1A1/CAMK2G/PLCB2/ PER3/ADCYAP1R1/GNAS/ADCY10/C ACNA1D/GNG2/GRIN2A/PLCB4/CAM K2D/ADCY3/PRKG2/CACNA1I/CALM L4/GRIN2B/NOS1/ADCY5/RPS6KA5/C ALM3/RYR3/ADCY7/NOS1AP/MAPK 1/CREB1/GUCY1A2/GRIA4/GRIA3/G NB5/CACNA1H/ADCY4/PRKACA/GN G4/ADCY8/GNAI2/GRIN1/RYR2/PLC B3/CAMK2B/ADCY2/GNAQ/CAMK2 A/PRKCB/ADCY6/GNGT2/GUCY1B1/ KCNJ5/ADCYAP1/RYR1/PRKG1/PER1 /ADCY9/GRIN2D/GNG7/GRIA2/PER2/ KCNJ6/FOS/GNB1/KCNJ9/MAPK3/GN	90

							AO1/MTNR1A/PRKACG/CALM1/MTNR1B/GNB4/CALML6/PLCB1/GNG13/CALML3/GNG12/GRIN2C/ADCY1/GNB3/GNAI1/GNAI3/KCNJ3/GNB2/GNGT1/GNG3/CALML5/CALM2/PRKCG	
hsa05167	Kaposi sarcoma-associated herpesvirus infection	176/7109	193/8105	0.079493378	0.176157799	0.115541029	MAPK10/ITPR1/CTNNB1/PIK3R1/JAK1/NFATC2/NFATC4/VEGFA/BAX/IL6ST/NFATC3/CD86/MAPK8/CCR3/TP53/AKT2/AKT3/GNG2/MAPK14/CASP9/TCF7L2/TCF7/CALML4/BECN1/ANGPT2/PIK3CB/CASP3/NFKB1/CALM3/CREBBP/PIK3R3/PIK3R5/NFATC1/MAP2K6/MAPK1/PIK3CD/C3/IFNAR2/RELA/CREB1/LEF1/GSK3B/STAT3/MAP2K7/MAP2K4/RCAN1/PLCG1/BID/EIF2AK2/GNB5/CASP8/MYC/UBA52/IFNAR1/E2F3/HCK/IKBKG/GNG4/PIK3CG/IKBKE/PPP3CB/PIK3CA/AKT1/IRF3/PLCG2/E2F2/IKBKB/FAS/HLA-F/CD200R1/RPS27A/PPP3CA/RAF1/STAT2/KRAS/IRF7/ITPR2/GNGT2/MAP2K1/MICB/STAT1/SYK/FGF2/CCR1/EP	176

							300/IL6/CCR4/MICA/PPP3R2/MTOR/G NG7/CDK4/HLA- G/CHUK/PIK3R2/CSF2/MAPK9/TLR3/ CDK6/HIF1A/PIK3R6/ZFP36/JAK2/TY K2/FOS/CYCS/MAPK12/TRAF3/GNB1 /CCR5/LYN/CCND1/HLA- A/RAC1/ICAM1/TRAF2/GABARAPL1/ TBK1/RB1/SRC/GABARAP/HLA- B/MAPK3/CD200R1L/HLA- C/PDGFB/NFKBIA/IFNA2/CDKN1A/M APK11/CALM1/NRAS/BECN2/MAPK1 3/PPP3CC/GNB4/CALML6/TNFRSF1A /IFNB1/IFNGR1/GNG13/MAPKAPK2/ ATG14/IRF9/CALML3/CXCL8/GNG12/ TRADD/E2F1/TICAM1/CXCL2/GNB3/ UBC/GNB2/GNGT1/HLA- E/IFNA4/PIK3C3/PREX1/CXCL3/GNG 3/HRAS/IFNA1/CALML5/IFNA21/IFN A14/CXCL1/CALM2/PPP3R1/JUN/FAD D/TCF7L1/CLEC2B/IFNA16/UBB/IFN A6	
hsa049	Vasopressin-	42/7109	44/810	0.07977	0.17615	0.11554	PRKACB/GNAS/CREB3L4/CREB5/DY	42

62	regulated water reabsorption		5	9672	7799	1029	NC1I2/DCTN5/ADCY3/DYNC2H1/CREB1/DYNC1LI2/ARHGDIA/DCTN4/RAB5B/RAB11A/AQP4/AQP3/DCTN2/PRKACA/RAB5C/CREB3L2/RAB5A/DYNLL2/CREB3L3/DCTN1/ADCY6/ARHGDIB/CREB3/DYNC1LI1/ADCY9/NSF/CREB3L1/DYNC1I1/VAMP2/AQP2/AVPR2/DYNC1H1/PRKACG/STX4/DYNC2LI1/DYNLL1/ARHGDIG/AVP	
hsa05169	Epstein-Barr virus infection	184/7109	202/8105	0.080797503	0.177215857	0.116235005	MAPK10/BCL2L11/PIK3R1/CD44/JAK1/BAX/ENTPD1/NEDD4/MAPK8/TP53/AKT2/AKT3/MAPK14/MDM2/APAF1/CASP9/RBPJ/BLNK/CCNE1/IRAK4/TNFAIP3/PIK3CB/CASP3/NFKB1/CCNA1/CR2/PIK3R3/OAS2/MAP2K6/MAVS/PIK3CD/IFNAR2/RELA/PSMC4/OAS1/SIN3A/PSMD11/IRAK1/CCND3/STAT3/MAP2K3/MAP2K7/CDK2/MAP2K4/ITGAL/TRAF5/MYD88/ENTPD3/BID/NCOR2/EIF2AK2/TAPBP/HLA-DQB1/TLR2/CASP8/MYC/IFNAR1/SAP30L/TRAF6/E2F3/RIPK1/IKBKG/HD	184

							AC2/IKBKE/TAB2/PIK3CA/AKT1/SKP 2/IRF3/PLCG2/CCND2/E2F2/DDB2/IK BKB/USP7/BTK/RUNX3/TAB1/FAS/O AS3/FCER2/HLA- F/PSMD12/STAT2/IRF7/STAT1/SYK/P SMC5/IL6/NFKB2/RBPJL/POLK/HLA- DQA1/BCL2/DDX58/PSMD4/TAP2/CC NE2/CDK4/HLA- G/MAP3K14/CHUK/JAK3/PIK3R2/AD RM1/MAPK9/HLA- DPB1/CDK6/PDIA3/TYK2/CYCS/HLA- DMB/MAPK12/TRAF3/LYN/CCND1/H LA- A/RAC1/CD3D/ICAM1/TRAF2/CD247/ CD19/TBK1/PSMD1/RB1/HLA- DPA1/NFKBIE/HLA-B/PSMD6/HLA- C/CD40/GADD45B/NFKBIA/IFNA2/C DKN1A/CDKN1B/VIM/MAPK11/TNF/ HLA-DQA2/PSMC1/HLA- DRB1/MAPK13/CXCL10/PSMD13/IFN B1/HLA- DOB/PSMC2/TAP1/CD3E/HLA-	
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							DOA/IRF9/TRADD/E2F1/ENTPD8/HLA-DMA/RELB/HLA-E/IFNA4/PSMD8/HES1/SAP30/CD3G/NFKBIB/HLA-DRB5/IFNA1/PSMD14/CIR1/B2M/GADD45G/IFNA21/IFNA14/CD58/SEM1/SNW1/HDAC1/CCNA2/JUN/FADD/PSMD3/IFNA16/IFNA6/PSMD7	
hsa01210	2-Oxocarboxylic acid metabolism	19/7109	19/8105	0.082559788	0.179881922	0.117983663	BCAT1/IDH3B/BCAT2/ACO2/IDH1/ADAT/ACY1/GOT2/GOT1L1/GPT/NAAGS/IDH3A/IDH3G/GOT1/IDH2/CS/GPT2/ACO1/ABHD14A-ACY1	19
hsa03460	Fanconi anemia pathway	51/7109	54/8105	0.087511644	0.188202501	0.12344109	BRCA1/FANCM/FANCD2/ATRIP/PMS2/FANCI/MLH1/POLH/FAN1/FANCA/FANCC/BRIP1/REV3L/PALB2/FANCL/ERCC1/MUS81/ATR/BRCA2/REV1/EME1/TOP3B/POLI/RAD51C/FANCB/FANCE/TELO2/CENPSCORT/POLK/RPA2/SLX4/USP1/FAAP24/WDR48/FANCG/POLN/ERCC4/RMI1/TOP3A/BLM/FAAP100/RAD51/RPA1/FANCF/RPA3/RPA4/HES1/CENPX/E	51

							ME2/SLX1B/SLX1A	
hsa052 14	Glioma	70/7109	75/810 5	0.08752 2744	0.18820 2501	0.12344 109	PIK3R1/CAMK2G/BAX/TGFA/TP53/A KT2/AKT3/MDM2/CAMK2D/CALML4 /IGF1/CAMK1G/EGF/PIK3CB/CALM3/ PIK3R3/MAPK1/PIK3CD/SHC1/BRAF/ PLCG1/ARAF/E2F3/CAMK4/PIK3CA/ AKT1/PDGFR/CAMK2B/PLCG2/E2F 2/DDB2/CAMK2A/CAMK1D/PRKCB/ RAF1/KRAS/MAP2K1/EGFR/SHC4/PO LK/IGF1R/SOS1/MTOR/CDK4/PIK3R2 /CDK6/PDGFRB/CCND1/RB1/MAPK3/ PDGFB/GADD45B/CDKN1A/SHC3/CA LM1/NRAS/GRB2/CALML6/CDKN2A/ CAMK1/CALML3/E2F1/SHC2/PTEN/P DGFA/HRAS/GADD45G/CALML5/CA LM2/PRKCG	70
hsa041 10	Cell cycle	114/710 9	124/81 05	0.09076 8838	0.19381 2306	0.12712 0533	TFDP2/YWHAZ/ORC4/CHEK2/CDC25 C/TP53/CDC25B/MDM2/CDC14B/SMA D2/CDC27/CCNE1/CDC45/CCNA1/SM C1A/CREBBP/SMC1B/STAG2/CDC14 A/ANAPC1/SMAD3/GSK3B/CCND3/C DK2/CHEK1/ZBTB17/TTK/CDC16/TG	114

							FB2/ESPL1/PKMYT1/MYC/E2F3/ATM /MCM7/BUB1/HDAC2/ORC3/ATR/PR KDC/SKP2/CCND2/E2F2/MCM4/WEE 1/ORC1/MAD1L1/PTTG1/ANAPC5/EP 300/BUB1B/CCNH/MCM3/STAG1/FZR 1/CDC7/CCNB3/CCNE2/ANAPC13/MA D2L2/CUL1/RAD21/CDK4/WEE2/RBL 2/CDK6/SKP1/RBL1/SMAD4/TGFB3/ MAD2L1/CDC23/ORC2/CCND1/CDC2 5A/CCNB1/MCM2/RB1/ABL1/MCM6/ BUB3/GADD45B/E2F4/CDKN1A/CDK N1B/ANAPC10/YWHAE/YWHAG/TFD P1/ANAPC2/ANAPC7/ANAPC11/PLK1 /CDKN2A/YWHAH/SMC3/CDKN1C/D BF4/ORC6/E2F1/CDC20/CDK1/CDC6/ CCNB2/ORC5/GADD45G/PTTG2/YW HAB/CDC26/HDAC1/CCNA2/TGFB1/ CDKN2C/SFN	
hsa000 52	Galactose metabolism	30/7109	31/810 5	0.09130 9749	0.19381 2306	0.12712 0533	PFKM/HK1/G6PC2/SI/GANC/GLB1/U GP2/GALM/MGAM/MGAM2/G6PC/G CK/PFKP/B4GALT1/HK3/AKR1B1/LC T/GALE/HK2/GLA/GALT/HKDC1/AK	30

							R1B10/B4GALT2/PFKL/LALBA/G6PC 3/PGM1/GAA/GALK1	
hsa042 70	Vascular smooth muscle contraction	122/710 9	133/81 05	0.09391 4452	0.19605 925	0.12859 4293	KCNMA1/CACNA1C/ITPR1/PRKACB/ PPP1R12B/MYLK/GUCY1A1/MRVI1/P LCB2/CALD1/PLA2G6/GNAS/CACNA 1D/ADORA2A/GNA12/PLCB4/ARHGE F12/ADCY3/CALML4/PPP1R12A/CAC NA1F/KCNMB2/ADCY5/MYLK3/CAL M3/ADCY7/RHOA/ARHGEF11/MYLK 4/MAPK1/GUCY1A2/MYH11/MYH10/ BRAF/PRKCH/GNA13/CALCA/ARAF/ KCNMB3/ARHGEF1/AGTR1/EDN3/A DCY4/PRKACA/ADCY8/ADRA1A/MY L6B/PLCB3/CACNA1S/AVPR1A/ADC Y2/JMJD7- PLA2G4B/GNAQ/PRKCD/PPP1CB/RO CK2/PRKCB/PPP1CC/RAF1/ADCY6/IT PR2/MAP2K1/PLA2G2D/AVPR1B/GU CY1B1/PRKCE/RAMP1/NPR2/PLA2G1 2B/PRKG1/ADCY9/PLA2G4D/CALCR L/PLA2G4F/NPR1/PLA2G4B/MYL6/PL A2G10/PLA2G3/KCNMB4/AGT/MAPK	122

							3/NPPA/PRKCQ/PTGIR/PRKACG/ROCK1/RAMP2/CALM1/ADRA1B/CALML6/PPP1R12C/EDN2/PLCB1/MYLK2/GNA11/CALML3/PPP1R14A/NPPC/PLA2G4A/ADORA2B/KCNU1/ADCY1/ACTG2/MYH9/PLA2G2A/MYL9/RAMP3/PLA2G12A/ADRA1D/NPPB/CALML5/CALM2/PLA2G4C/AVP/EDNRA/ACTA2/PRKCG/KCNMB1/EDN1/PLA2G2F/CALCB	
hsa04145	Phagosome	139/7109	152/8105	0.093986628	0.19605925	0.128594293	CD209/CD36/FCAR/THBS3/CLEC7A/CLEC4M/DYNC1I2/DYNC2H1/CANX/C1R/NOS1/TLR4/MSR1/C3/TFRC/ATP6AP1/DYNC1LI2/SEC61A2/ITGAV/CTSS/LAMP2/M6PR/RAB5B/OLR1/ITGAM/HLA-DQB1/PIKFYVE/TLR2/CTSL/ATP6V0A1/PLA2R1/FCGR3B/FCGR3A/ATP6V0A4/SFTPA1/ITGB1/RAB5C/ATP6V1C2/NCF2/FCGR2A/TLR6/RAB5A/ITGB2/TUBA1A/HLA-F/CYBB/ATP6V0D1/ITGB3/STX7/COL	139

							EC11/MRC1/ITGB5/ITGA5/SCARB1/HLA- DQA1/TUBAL3/DYNC1LI1/TUBA1C/THBS1/THBS4/TAP2/TUBB3/HLA-G/ATP6V1E1/ATP6V0B/ATP6V1H/ITGA2/CD14/DYNC1I1/HLA-DPB1/ATP6V1E2/RAB7B/NCF4/ATP6V0E1/TUBB6/EEA1/HLA-DMB/SFTPD/FCGR2B/STX12/HLA-A/RAC1/ATP6V1D/LAMP1/ATP6V0A2/HLA-DPA1/SEC22B/HLA-B/SFTPA2/HLA-C/ATP6V1C1/DYNC1H1/ATP6V1B2/STX18/THBS2/CORO1A/HGS/COMP/MPO/ACTG1/MBL2/ATP6V0E2/HLA-DQA2/HLA-DRB1/TUBB/ATP6V1A/VAMP3/HLA-DOB/TUBA8/CYBA/MRC2/TAP1/TUBB4A/HLA-DOA/ATP6V1G2/COLEC12/RAB7A/ATP6V1B1/HLA-DMA/TUBA4A/TUBA1B/HLA-	
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							E/TUBA3E/TCIRG1/PIK3C3/FCGR1A/HLA-DRB5/TUBB8/TUBB4B/ATP6V1F/ATP6V1G3/RILP/ATP6V0D2/ATP6V1G1/NCF1/ACTB/TUBA3D/TUBA3C/MARCO	
hsa00061	Fatty acid biosynthesis	18/7109	18/8105	0.094156114	0.19605925	0.128594293	ACSL1/ACACA/ACSL4/ACSL5/ACSL3/ACSL6/ACSBG2/HTD2/ACSF3/HSD17B8/FASN/MECR/OLAH/CBR4/OXSM/MCAT/ACSBG1/ACACB	18
hsa04961	Endocrine and other factor-regulated calcium reabsorption	50/7109	53/8105	0.095092454	0.196763631	0.129056293	SLC8A1/AP2B1/PRKACB/DNM1/ATP2B2/PLCB2/ESR1/ATP2B3/GNAS/DNM3/PLCB4/AP2S1/SLC8A3/CLTC/ATP2B4/RAB11A/ATP2B1/KLK2/DNM2/PRKACA/TRPV5/PLCB3/AP2A2/GNAQ/ATP1B4/PRKCB/ATP1A2/ADCY6/VDNR/CLTCL1/ATP1A1/ADCY9/ATP1B2/PTH1R/BDKRB2/CLTB/AP2M1/ATP1A4/ATP1B3/KLK1/CALB1/SLC8A2/PRKACG/PTH/PLCB1/AP2A1/ATP1B1/KL/ATP1A3/PRKCG	50
hsa003	Tryptophan	40/7109	42/810	0.09593	0.19727	0.12938	CYP1A1/DDC/ALDH8A1/ACAT1/EHH	40

80	metabolism		5	7212	0891	9002	ADH/DLD/KYAT1/KMO/AOC1/ALDH3A2/ALDH7A1/ALDH1B1/AANAT/HA DH/ASMT/MAOA/INMT/IDO2/AADAT/HADHA/DHTKD1/HAAO/ALDH9A1/ALDH2/KYNU/CYP1A2/AOX1/ECHS1/CYP1B1/TPH2/KYAT3/MAOB/CAT/IDO1/AFMID/ACAT2/GCDH/DLST/IL4I1/TPH1	
hsa04725	Cholinergic synapse	104/7109	113/8105	0.098007619	0.200276438	0.131360326	CACNA1C/ITPR1/PRKACB/PIK3R1/CAMK2G/PLCB2/CACNA1D/CREB3L4/AKT2/AKT3/GNG2/KCNQ5/CREB5/PLCB4/FYN/CACNA1A/CAMK2D/ADCY3/CACNA1F/ADCY5/PIK3CB/KCNQ2/ADCY7/PIK3R3/KCNQ3/PIK3R5/MAPK1/ATF4/PIK3CD/CREB1/CHRNA7/CHRM2/GNB5/ADCY4/PRKACA/GNG4/CHAT/CAMK4/PIK3CG/ADCY8/CHRM1/PIK3CA/AKT1/GNAI2/PLCB3/CAMK2B/CHRNA6/KCNQ4/KCNJ2/CREB3L2/CACNA1S/CHRM3/CHRNA4/ADCY2/CREB3L3/GNAQ/CAMK2A/PRKCB/KCNJ4/ADCY6/KRAS/ITPR2/GNGT	104

							2/MAP2K1/ACHE/CHRM5/CHRNA4/C REB3/BCL2/KCNJ12/ADCY9/GNG7/PI K3R2/CREB3L1/PIK3R6/JAK2/KCNJ6/ FOS/KCNQ1/GNB1/CHRNA3/CACNA 1B/MAPK3/GNAO1/PRKACG/NRAS/G NB4/PLCB1/GNG13/KCNJ14/GNA11/G NG12/ADCY1/GNB3/GNAI1/GNAI3/K CNJ18/KCNJ3/GNB2/GNGT1/CHRNA2 /GNG3/HRAS/PRKCG	
hsa053 23	Rheumatoid arthritis	86/7109	93/810 5	0.10083 2212	0.20220 9401	0.13262 8147	VEGFA/TNFRSF11A/TNFSF13/CD86/ ANGPT1/CD28/TLR4/FLT1/ATP6AP1/ TEK/ITGAL/CSF1/CXCL12/TGFB2/HL A- DQB1/TLR2/CCL5/CTSL/ATP6V0A1/A TP6V0A4/ATP6V1C2/IL18/TNFSF11/T NFSF13B/ITGB2/ATP6V0D1/IL15/IL6/I L1A/HLA- DQA1/CD80/IL11/ATP6V1E1/ATP6V0 B/ATP6V1H/CSF2/CTSK/HLA- DPB1/ATP6V1E2/ATP6V0E1/MMP1/F OS/TGFB3/IL1B/HLA- DMB/CCL20/ATP6V1D/ICAM1/ATP6	86

							V0A2/HLA-DPA1/CTLA4/ATP6V1C1/ATP6V1B2/CCL3/CCL3L3/CXCL5/TNF/ACP5/ATP6V0E2/HLA-DQA2/HLA-DRB1/ATP6V1A/PTH/HLA-DOB/HLA-DOA/ATP6V1G2/CXCL8/ATP6V1B1/HLA-DMA/CXCL2/IFNG/TCIRG1/HLA-DRB5/CXCL3/ATP6V1F/CXCL1/ATP6V1G3/ATP6V0D2/MMP3/JUN/ATP6V1G1/TGFB1/LTB/CCL2/IL23A/CXCL6	
hsa01524	Platinum drug resistance	68/7109	73/8105	0.100961508	0.202209401	0.132628147	BRCA1/PIK3R1/ATP7B/BAX/TP53/AKT2/BCL2L1/AKT3/MDM2/APAF1/CASP9/PDPK1/ERBB2/MLH1/POLH/PIK3CB/CASP3/XIAP/PIK3R3/ATP7A/MAPK1/PIK3CD/MGST2/BID/BBC3/REV3L/CASP8/ERCC1/ATM/MSH2/PIK3CA/AKT1/GSTO1/BIRC5/FAS/GSTM5/SLC31A1/FASLG/BIRC3/ABCC2/BCL2/TOP2A/MSH3/PIK3R2/GSTM3/CYCS/GSTA4/BAD/TOP2B/MAPK3/GSTA1/PMAP1/XPA/MGST3/CDKN1A/GSTM4/GSTT2B/CDKN2A/MGST1/GSTO2/GSTA	68

							2/MAP3K5/GSTM2/GSTP1/GSTA3/GS TA5/FADD/GSTM1	
hsa000 20	Citrate cycle (TCA cycle)	29/7109	30/810 5	0.10141 201	0.20220 9401	0.13262 8147	PC/SDHC/OGDH/PDHA1/SDHD/IDH3 B/DLD/PCK2/SUCLG2/SDHA/MDH2/ ACO2/IDH1/DLAT/SUCLA2/MDH1/PD HB/IDH3A/IDH3G/PCK1/PDHA2/IDH2 /CS/OGDHL/ACLY/SUCLG1/DLST/AC O1/SDHB	29
hsa000 53	Ascorbate and aldarate metabolism	29/7109	30/810 5	0.10141 201	0.20220 9401	0.13262 8147	UGT2A1/UGT2B28/ALDH3A2/ALDH7 A1/RGN/ALDH1B1/UGT2B10/UGT2B4 /UGT2B7/ALDH9A1/ALDH2/UGT2B17 /UGT2A2/UGT1A6/UGT1A1/UGT1A5/ AKR1A1/UGDH/UGT2B11/UGT1A8/U GT1A9/UGT1A4/MIOX/KL/UGT1A10/ UGT1A7/UGT1A3/UGT2B15/UGT2A3	29
hsa052 19	Bladder cancer	39/7109	41/810 5	0.10507 9439	0.20673 5356	0.13559 6698	VEGFA/TP53/MDM2/ERBB2/EGF/RPS 6KA5/DAPK1/MAPK1/MMP2/BRAF/A RAF/MYC/E2F3/RASSF1/E2F2/CDH1/ RAF1/KRAS/MAP2K1/EGFR/THBS1/C DK4/MMP9/MMP1/HBEGF/CCND1/R B1/SRC/MAPK3/DAPK2/CDKN1A/NR AS/FGFR3/CDKN2A/CXCL8/DAPK3/E	39

							2F1/HRAS/UPK3A	
hsa001 20	Primary bile acid biosynthesis	17/7109	17/810 5	0.10737 9392	0.20673 5356	0.13559 6698	HSD17B4/AMACR/HSD3B7/SCP2/SLC 27A5/BAAT/ACOT8/CYP7A1/ACOX2/ CYP7B1/AKR1D1/CYP27A1/CYP39A1 /CYP46A1/AKR1C4/CH25H/CYP8B1	17
hsa003 60	Phenylalanine metabolism	17/7109	17/810 5	0.10737 9392	0.20673 5356	0.13559 6698	AOC3/ALDH3A1/DDC/ALDH3B1/AO C2/HPD/ALDH3B2/MAOA/TAT/GOT2/ GOT1L1/GLYAT/GOT1/MAOB/PAH/I L4I1/MIF	17
hsa009 10	Nitrogen metabolism	17/7109	17/810 5	0.10737 9392	0.20673 5356	0.13559 6698	CA1/GLUL/CA12/CA3/GLUD2/CA5B/ CA7/CA14/CA9/CA6/CA8/GLUD1/CPS 1/CA2/CA13/CA5A/CA4	17
hsa052 22	Small cell lung cancer	85/7109	92/810 5	0.10739 6738	0.20673 5356	0.13559 6698	LAMA3/PTK2/PIK3R1/LAMA4/FN1/B AX/COL4A6/TP53/AKT2/BCL2L1/AK T3/LAMC2/APAF1/MAX/CASP9/CCN E1/PIK3CB/CASP3/NFKB1/LAMB3/XI AP/RARB/PIK3R3/LAMB1/LAMB2/FH IT/PIK3CD/LAMB4/RELA/ITGAV/CO L4A5/CDK2/ZBTB17/TRAF5/TRAF1/I TGA6/LAMA2/MYC/TRAF6/E2F3/IKB KG/ITGB1/COL4A4/RXRA/PIK3CA/A KT1/SKP2/COL4A3/E2F2/DDB2/ITGA	85

							2B/IKBKB/ITGA3/COL4A1/LAMA1/RXRB/LAMC1/COL4A2/BIRC3/LAMC3/POLK/BCL2/CCNE2/CDK4/CHUK/PIK3R2/ITGA2/CDK6/CYCS/NOS2/TRAF4/TRAF3/LAMA5/CCND1/TRAF2/RB1/RXRG/GADD45B/NFKBIA/CDKN1A/CDKN1B/E2F1/PTEN/GADD45G/CKS1B	
hsa05225	Hepatocellular carcinoma	153/7109	168/8105	0.107624347	0.206735356	0.135596698	SMARCA4/CTNNB1/PIK3R1/MET/BAX/TGFBR1/TGFA/GAB1/ARID2/SMARCA2/TP53/AKT2/BCL2L1/AKT3/RPS6KB1/NQO1/PBRM1/TCF7L2/LRP6/DPF1/SMARCC2/SMAD2/TCF7/ELK1/TXNRD2/PIK3CB/FZD3/PIK3R3/WNT5A/DPF3/MAPK1/PIK3CD/HGF/LEF1/SHC1/APC/SMAD3/GSK3B/BRAF/NFE2L2/MGST2/WNT8A/PLCG1/WNT7B/FZD6/TGFB2/ARAF/MYC/SMARCD2/E2F3/FZD5/PIK3CA/AKT1/GSTO1/WNT2/KEAP1/PLCG2/SMARCC1/E2F2/DDB2/PKCB/RAF1/KRAS/GSTM5/TXNRD1/FRAT2/FZD4/MAP2K1/EGFR/TXNRD	153

							3/SHC4/TERT/POLK/DVL3/IGF1R/SO S1/WNT5B/MTOR/FZD2/CDK4/PIK3R 2/AXIN2/WNT3/APC2/WNT4/ARID1A/ CSNK1A1/CSNK1A1L/CDK6/WNT10B /ARID1B/GSTM3/SMAD4/BRD7/FZD7 /TGFB3/GSTA4/WNT2B/CCND1/WNT 9B/WNT16/PHF10/BAD/RB1/SMARCD 3/MAPK3/GSTA1/FRAT1/IGF2/WNT10 A/WNT11/GADD45B/MGST3/FZD1/C DKN1A/SHC3/DVL2/ACTG1/WNT7A/ WNT8B/NRAS/TGFBR2/GSTM4/GSTT 2B/GRB2/CDKN2A/FZD8/MGST1/GST O2/FZD9/E2F1/GSTA2/SHC2/PTEN/GS TM2/LRP5/SMARCD1/ACTL6A/WNT1 /HRAS/GSTP1/GADD45G/SMARCE1/ GSTA3/SMARCB1/WNT9A/PRKCG/G STA5/RPS6KB2/TGFB1/GSTM1/ACTB /TCF7L1	
hsa052 23	Non-small cell lung cancer	67/7109	72/810 5	0.10832 0417	0.20673 5356	0.13559 6698	PIK3R1/MET/BAX/TGFA/TP53/AKT2/ AKT3/RASSF5/CASP9/PDPK1/FOXO3/ ERBB2/EGF/PIK3CB/RARB/PIK3R3/F HIT/MAPK1/PIK3CD/HGF/KIF5A/STA	67

							T5A/STAT3/BRAF/PLCG1/ARAF/E2F3 /STK4/RASSF1/RXRA/PIK3CA/AKT1/ PLCG2/E2F2/ALK/DDB2/PRKCB/RAF 1/KRAS/RXRB/EML4/MAP2K1/EGFR/ POLK/SOS1/KIF5B/CDK4/JAK3/PIK3R 2/CDK6/RET/CCND1/BAD/RB1/RXRG /MAPK3/GADD45B/CDKN1A/STAT5B /KIF5C/NRAS/GRB2/CDKN2A/E2F1/H RAS/GADD45G/PRKCG	
hsa040 14	Ras signaling pathway	210/710 9	232/81 05	0.10870 8865	0.20673 5356	0.13559 6698	MAPK10/FGF1/PRKACB/ABL2/BDNF/ PAK3/PIK3R1/FGFR2/MET/VEGFA/N TRK2/TGFA/PAK4/PLA2G6/GAB1/MA PK8/ANGPT1/ETS1/EFNA5/MRAS/AK T2/BCL2L1/AKT3/RASSF5/GNG2/GRI N2A/RALGDS/CDC42/RASGRP1/AFD N/HTR7/CALML4/IGF1/ELK1/EGF/GR IN2B/NF1/ANGPT2/PIK3CB/NFKB1/I NSR/CALM3/FLT3LG/PIK3R3/RHOA/ EFNA4/KSR1/MAPK1/PIK3CD/HGF/F LT1/RASGRF1/RELA/SHC1/RASGRP4 /RAB5B/TEK/CSF1/RASA4/KITLG/PL CG1/RASAL2/RASAL1/GNB5/PLA1A/	210

							BRAP/RASGRP2/FGF5/SHOC2/STK4/ EFNA1/RASSF1/PRKACA/TIAM1/FO XO4/IKBKG/GNG4/RAB5C/PIK3CA/A KT1/RASA4B/SYNGAP1/GRIN1/PAK6 /PDGFR/PLCG2/PAK5/REL/RAB5A/J MJD7- PLA2G4B/PLCE1/IKBKB/FGFR1/GAB 2/RASGRP3/PTPN11/LAT/PRKCB/RA PGEF5/RAF1/KRAS/RALB/FGF8/RAS A1/RIN1/GNGT2/MAP2K1/PLA2G2D/ EGFR/NTF3/KIT/RASGRF2/FGF2/FGF R4/RGL1/KDR/SHC4/NTRK1/PLA2G1 2B/FASLG/RGL2/RAP1B/ARF6/VEGF B/IGF1R/FLT3/SOS1/RRAS2/RASA2/P LA2G4D/PLA2G4F/NGFR/GNG7/ANG PT4/PAK2/PAK1/PLA2G4B/CHUK/PIK 3R2/BUB1B- PAK6/MAPK9/CSF1R/PLA2G10/RALA /PDGFRB/FGF9/RAP1A/RAC2/FGF4/V EGFD/RASA3/EFNA3/PLA2G3/GNB1/ RAC1/EPHA2/TBK1/BAD/ABL1/MAP K3/PLD2/FGF23/PDGFB/IGF2/FGF21/	
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							ZAP70/VEGFC/SHC3/FLT4/PRKACG/FGF3/FGF7/CALM1/KSR2/NRAS/FGFR3/PDGFC/GRB2/GNB4/CALML6/RALBP1/NGF/FGF6/GNG13/ETS2/CALML3/GNG12/PLA2G4A/INS/GNB3/PDGF D/SHC2/EXOC2/PLA2G2A/GNB2/GNGT1/PLD1/PDGFA/FGF17/PLA2G12A/GNG3/HRAS/CALML5/CALM2/PLA2G4C/FGF20/PRKCG/EFNA2/RASAL3/PLA2G2F	
hsa04913	Ovarian steroidogenesis	48/7109	51/8105	0.112014878	0.211798246	0.138917423	PRKACB/GNAS/CYP1A1/ADCY3/IGF1/LDLR/HSD3B2/ADCY5/INSR/CYP11A1/ADCY7/CYP19A1/HSD3B1/FSHB/ADCY4/PRKACA/ADCY8/ADCY2/JMJD7-PLA2G4B/ADCY6/SCARB1/IGF1R/CYP17A1/ADCY9/PLA2G4D/PLA2G4F/FSHR/HSD17B7/PLA2G4B/CYP1B1/ACOT4/HSD17B2/AKR1C3/LHCGR/PRKACG/BMP15/PLA2G4A/ADCY1/INS/CYP2J2/CGA/BMP6/ACOT2/ALOX5/PLA2G4C/STAR/LHB/ACOT1	48

hsa043 10	Wnt pathway	signaling	151/710 9	166/81 05	0.11826 4198	0.22233 6691	0.14582 9537	MAPK10/PRKACB/TLE3/CTNNB1/PRI CKLE1/TBL1XR1/NFATC2/NFATC4/C AMK2G/PSEN1/PLCB2/RNF43/NFATC 3/MAPK8/TP53/PLCB4/TCF7L2/LRP6/ CHD8/TBL1X/PRICKLE2/CAMK2D/T CF7/CTBP2/RSP01/VANG11/SIAH1/F ZD3/CREBBP/RHOA/LGR5/PPARD/W NT5A/NFATC1/LEF1/DAAM2/APC/S MAD3/GSK3B/CCND3/CTNNBIP1/WN T8A/WNT7B/RSP02/CSNK2A1/FZD6/ CTNND2/SEN2/BTRC/MYC/RSP04/P RKACA/FZD5/ROR1/PPP3CB/WNT2/P LCB3/CAMK2B/INVS/CCND2/CAMK2 A/CSNK1E/CBY1/ROCK2/PRKCB/R YK/PPP3CA/LGR6/PORCN/FRAT2/FZD 4/FOSL1/LGR4/VANG12/SFRP4/EP300 /DKK4/DVL3/PPP3R2/ZNRF3/RUVBL 1/RSP03/WNT5B/SERPINF1/FBXW11/ FZD2/CUL1/AXIN2/SOST/WNT3/NLK/ APC2/WNT4/CSNK1A1/MAPK9/CSNK 1A1L/WNT10B/NKD1/SKP1/RAC2/SM AD4/TLE1/FZD7/WNT2B/CACYBP/D	151
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							AAM1/NKD2/CCND1/RAC1/WNT9B/ WNT16/GPC4/FRAT1/WNT10A/WNT1 1/FZD1/TLE2/PRKACG/DVL2/DKK2/ WNT7A/WNT8B/BAMBI/PRICKLE3/P PP3CC/TBL1Y/MMP7/FZD8/PLCB1/SF RP1/CSNK2A2/FZD9/ROR2/SFRP2/PRI CKLE4/SFRP5/SOX17/CSNK2A3/LRP5 /CXXC4/WNT1/NOTUM/WIF1/DKK1/ PPP3R1/CTBP1/WNT9A/PRKCG/JUN/ CER1/TCF7L1	
hsa002 70	Cysteine and methionine metabolism	47/7109	50/810 5	0.12142 3977	0.22442 971	0.14720 2338	BCAT1/DNMT3B/DNMT3A/MTR/GSS/ BCAT2/GCLC/MAT2B/KYAT1/LDHB/ AHCYL2/AMD1/LDHC/GCLM/TST/M DH2/CBSL/MTAP/AGXT2/PSAT1/TAT /BHMT/GOT2/APIP/GOT1L1/MDH1/A HCYL1/BHMT2/CDO1/CBS/GOT1/LD HA/MRI1/KYAT3/AHCY/LDHAL6B/D NMT1/ADI1/LDHAL6A/SMS/PHGDH/ ENOPH1/MAT1A/IL4I1/SDSL/MAT2A/ CTH	47
hsa005 10	N-Glycan biosynthesis	47/7109	50/810 5	0.12142 3977	0.22442 971	0.14720 2338	GANAB/MGAT4C/ALG13/ALG9/STT3 A/ALG1/ST6GAL1/MAN1B1/MGAT4B	47

							/ALG3/MAN2A2/FUT8/MGAT4A/TUS C3/ALG10B/ALG5/MAN2A1/DOLPP1/ MAN1C1/ST6GAL2/MGAT5/RPN2/B4 GALT1/MOGS/B4GALT3/ALG6/MGA T3/ALG10/ALG2/MAN1A2/MGAT5B/ ALG14/MGAT1/DPAGT1/DDOST/STT 3B/MAN1A1/DOLK/ALG8/B4GALT2/ DPM2/SRD5A3/DPM3/MGAT2/ALG11 /MGAT4D/DPM1	
hsa049 79	Cholesterol metabolism	47/7109	50/810 5	0.12142 3977	0.22442 971	0.14720 2338	CD36/VAPB/LDLR/APOB/ABCB11/SO RT1/PLTP/LRP2/APOA1/LRPAP1/ABC A1/CETP/VAPA/LIPG/LRP1/LPL/LIPC/ ANGPTL3/NPC1/OSBPL5/VDAC3/SC ARB1/ABCG5/NCEH1/VDAC2/ANGPT L4/SOAT2/CYP7A1/CYP27A1/SOAT1/ LPA/NPC2/APOA2/ANGPTL8/MYLIP/ VDAC1/APOC2/STARD3/PCSK9/APO C1/APOC3/LDLRAP1/LCAT/STAR/AB CG8/APOH/APOA4	47
hsa040 62	Chemokine signaling pathway	174/710 9	192/81 05	0.12652 7745	0.23255 6581	0.15253 2712	PRKACB/PARD3/PTK2/PIK3R1/PXN/P LCB2/BCAR1/CCR3/AKT2/AKT3/GNG 2/ELMO1/PLCB4/PTK2B/FGR/FOXO3/	174

							CDC42/ADCY3/ARRB1/ADCY5/PIK3C B/NFKB1/ADCY7/PIK3R3/PIK3R5/RH OA/ARRB2/CXCR6/CCL4L2/MAPK1/P IK3CD/VAV3/RELA/CCR9/SHC1/GSK 3B/CX3CR1/STAT3/BRAF/PLCG1/CX CL12/GNB5/CCL5/RASGRP2/VAV1/A DCY4/PRKACA/TIAM1/HCK/IKBKG/ GNG4/PIK3CG/CCR2/ADCY8/PIK3CA /AKT1/GNAI2/PLCB3/PLCG2/ADCY2/ GNAQ/IKBKB/PRKCD/CCR7/ROCK2/ PRKCB/RAF1/ADCY6/STAT2/KRAS/G NGT2/MAP2K1/STAT1/CCR1/DOCK2/ CXCL9/SHC4/CCR4/RAP1B/SOS1/VA V2/CCR6/CRK/ADCY9/GRK1/CCL19/ GNG7/PAK1/CHUK/JAK3/PIK3R2/CX CR1/PIK3R6/RAP1A/JAK2/RAC2/CXC R5/CRKL/CCL25/CCL20/XCL1/GNB1/ CCR5/LYN/RAC1/CXCR2/CCL28/BAD /CXCR4/SRC/MAPK3/CCL1/CCL15/C CL3/CCL3L3/NFKBIA/CCL8/ITK/SHC 3/STAT5B/CXCL5/PRKACG/ROCK1/C CL21/NRAS/CXCL10/GRB2/GNB4/PP	
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							BP/GRK2/PLCB1/WAS/XCL2/GNG13/GRK6/CX3CL1/CXCL8/GNG12/CXCL14/CXCL11/CCL4/ADCY1/CCL17/CXCL2/CCL16/GNB3/GNAI1/GNAI3/SHC2/CCL27/GNB2/GRK3/CCL11/CXCL16/GNGT1/CCL14/CXCR3/PREX1/NFKBIB/GSK3A/PF4/CXCL3/GNG3/HRAS/CXCL1/CCL18/CCR10/XCR1/PRKCZ/NCF1/CCL2/GRK7/CCL22/CXCL6	
hsa04727	GABAergic synapse	82/7109	89/8105	0.129260464	0.236259403	0.154961375	CACNA1C/PRKACB/SLC6A1/GABRB3/CACNA1D/GLUL/GNG2/CACNA1A/SLC38A1/ADCY3/CACNA1F/ADCY5/ADCY7/PLCL1/ABAT/GABRA2/GABBR1/GABRA1/GABRG3/GABRG2/SLC38A5/GNB5/SLC6A12/GABRR1/ADCY4/PRKACA/GNG4/GABRP/SLC38A3/ADCY8/GNAI2/SLC6A11/HAP1/SLC6A13/CACNA1S/ADCY2/SLC12A5/PRKCB/GABRB2/SLC38A2/GABRA3/ADCY6/GAD1/GNGT2/GLS2/GLS/TRAK2/GABRA4/ADCY9/GABRE/NSF/GNG7/GAD2/KCNJ6/GNB1/GABRG1/GABARAP	82

							L1/SRC/GABARAP/CACNA1B/GPHN/GNAO1/PRKACG/GABRR2/GNB4/GABRQ/SLC32A1/GNG13/GABRA5/GNG12/ADCY1/GNB3/GNAI1/GNAI3/GNB2/GNGT1/GABRB1/GABRD/GNG3/GABBR2/PRKCG/GABRR3	
hsa00564	Glycerophospholipid metabolism	90/7109	98/8105	0.133931171	0.242106348	0.158796357	DGKB/AGPAT3/TAZ/PLA2G6/LPIN1/DGKG/DGKH/DGKI/PLD3/PCYT1B/AGPAT1/ETNPPL/PLB1/GPD2/DGKZ/CDIPT/PLA2G15/DGKK/DGKA/GPD1/SELENOI/PLA1A/PCYT2/LPCAT4/LPGAT1/PLPP5/CHAT/LYPLA1/PNPLA7/LCLAT1/CHKA/MBOAT2/JMJD7-PLA2G4B/CDS2/GPCPD1/PLA2G2D/PLD4/ACHE/PCYT1A/PISD/ETNK1/PLA2G12B/CEPT1/AGPAT4/DGKE/PLA2G4D/LPIN2/LPIN3/ADPRM/PLA2G4F/CDS1/PLA2G4B/PHOSPHO1/GPAT4/PLA2G10/PEMT/GPAT3/PLA2G3/PTDSS1/PLD2/PTDSS2/PLPP3/DGKD/PNPLA6/GPAM/GNPAT/PLPP2/MBOAT1/LPCAT1/GPAT2/CRLS1/AGPAT5/PLA2	90

							G4A/LYPLA2/PLPP4/PLPP1/ETNK2/C HKB/MBOAT7/LCAT/PLA2G2A/AGP AT2/LPCAT2/PLD1/DGKQ/LPCAT3/P LA2G12A/PLA2G4C/PGS1/PLA2G2F	
hsa052 31	Choline metabolism in cancer	90/7109	98/810 5	0.13393 1171	0.24210 6348	0.15879 6357	MAPK10/TSC2/DGKB/PIP5K1A/PIK3R 1/TSC1/SP1/MAPK8/DGKG/DGKH/DG KI/AKT2/AKT3/RPS6KB1/SLC44A1/P DPK1/RALGDS/SLC22A5/PCYT1B/EG F/PIK3CB/PIK3R3/DGKZ/MAPK1/PIK 3CD/DGKK/DGKA/SLC22A1/PLCG1/S LC44A3/SLC44A4/LYPLA1/PIK3CA/A KT1/PIP5K1B/PDGFRA/CHKA/JMJD7- PLA2G4B/PRKCB/RAF1/GPCPD1/KR AS/SLC22A2/WASF1/MAP2K1/EGFR/ PCYT1A/SOS1/DGKE/PLA2G4D/MTO R/PLA2G4F/PLA2G4B/PIK3R2/SLC44 A2/SLC22A4/MAPK9/HIF1A/PDGFRB/ RAC2/SLC44A5/RHEB/FOS/RAC1/WA SF2/MAPK3/PLD2/PLPP3/DGKD/PDG FB/PLPP2/SLC22A3/WASF3/NRAS/PD GFC/GRB2/WAS/PLA2G4A/PLPP1/CH KB/PIP5K1C/PDGFD/PLD1/DGKQ/PD	90

							GFA/HRAS/PLA2G4C/PRKCG/RPS6K B2/JUN	
hsa045 40	Gap junction	81/7109	88/810 5	0.13731 2047	0.24686 1548	0.16191 5269	ITPR1/PRKACB/GUCY1A1/PLCB2/TJ P1/GNAS/HTR2C/GRM1/PLCB4/ADC Y3/PRKG2/GRM5/EGF/ADCY5/ADCY 7/MAPK1/GUCY1A2/HTR2A/MAPK7/ LPAR1/ADCY4/PRKACA/ADCY8/GN AI2/PDGFR/PLCB3/MAP3K2/ADCY2 /GNAQ/TUBA1A/PRKCB/RAF1/ADCY 6/KRAS/DRD2/ITPR2/CSNK1D/MAP2 K1/GUCY1B1/EGFR/DRD1/TUBAL3/S OS1/GJA1/PRKG1/TUBA1C/ADCY9/T UBB3/MAP2K5/PDGFRB/TUBB6/SRC/ MAPK3/PDGFB/PRKACG/GJD2/NRAS /PDGFC/GRB2/TUBB/PLCB1/TUBA8/ TUBB4A/GNA11/ADCY1/ADRB1/CD K1/TUBA4A/TUBA1B/GNAI1/PDGFD/ GNAI3/HTR2B/TUBA3E/PDGFA/HRA S/TUBB8/TUBB4B/PRKCG/TUBA3D/T UBA3C	81
hsa049 66	Collecting duct acid secretion	26/7109	27/810 5	0.13829 2738	0.24727 3428	0.16218 5419	CLCNKB/SLC12A7/ATP6V0A1/ATP6 V0A4/ATP6V1C2/ATP6V0D1/ATP6V1	26

							E1/ATP6V1E2/ATP6V0E1/SLC4A1/ATP6V1D/ATP6V0A2/ATP6V1C1/ATP6V1B2/ATP6V0E2/ATP4A/ATP6V1A/ATP6V1G2/ATP6V1B1/CA2/TCIRG1/ATP6V1F/ATP6V1G3/ATP6V0D2/ATP6V1G1/ATP4B	
hsa00280	Valine, leucine and isoleucine degradation	45/7109	48/8105	0.14230973	0.253080546	0.165994279	BCAT1/HMGCLL1/PCCA/ABAT/HMGCS1/ACADSB/ACAT1/EHHADH/BCAT2/DLD/ACADM/ALDH3A2/DBT/ALDH7A1/HMGCL/AUH/ALDH1B1/ACAA1/HADH/IVD/HADHA/AGXT2/HADHB/ACSF3/OXCT1/MCCC1/ALDH9A1/ALDH6A1/ALDH2/AOX1/HMGCS2/ECHS1/BCKDHB/PCCB/HSD17B10/MCCC2/HIBADH/ACAA2/AACS/ACAT2/OXCT2/ACADS/HIBCH/IL4I1/BCKDHA	45
hsa05163	Human cytomegalovirus infection	203/7109	225/8105	0.143488169	0.253804342	0.166469013	ITPR1/PRKACB/TSC2/CTNNB1/PTK2/PIK3R1/JAK1/TSC1/NFATC2/NFATC4/PXN/VEGFA/BAX/PLCB2/BCAR1/SP1/NFATC3/GNAS/AKAP13/CCR3/CREB3L4/TP53/AKT2/AKT3/GNG2/ATF2/	203

							RPS6KB1/MAPK14/CREB5/MDM2/GN A12/CASP9/PLCB4/PTK2B/ARHGEF1 2/ADCY3/CALML4/ELK1/ADCY5/PIK 3CB/CASP3/NFKB1/CALM3/ADCY7/P IK3R3/RHOA/ARHGEF11/CCL4L2/NF ATC1/MAP2K6/MAPK1/ATF4/PIK3CD /RELA/CREB1/ITGAV/GSK3B/ATF6B/ STAT3/TRAF5/BID/CXCL12/GNA13/T APBP/GNB5/CCL5/CASP8/MYC/ARH GEF1/E2F3/ADCY4/PRKACA/IL6R/RI PK1/IKBKG/GNG4/PPP3CB/ADCY8/PI K3CA/AKT1/GNAI2/PDGFRA/IRF3/PL CB3/CREB3L2/E2F2/ADCY2/CREB3L 3/GNAQ/IKBKB/PTGER3/FAS/ROCK2 /HLA- F/PRKCB/PPP3CA/RAF1/ADCY6/KRA S/ITGB3/ITPR2/GNGT2/MAP2K1/EGF R/IL10RA/CCR1/IL6/IL1R1/FASLG/PP P3R2/CREB3/SOS1/CRK/ADCY9/MTO R/TAP2/GNG7/CDK4/HLA- G/CHUK/PIK3R2/CREB3L1/CDK6/PDI A3/RAC2/RHEB/CYCS/CRKL/IL1B/M	
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							APK12/GNB1/CCR5/CCND1/HLA-A/RAC1/TRAF2/CXCR2/TBK1/RB1/CXCR4/SRC/HLA-B/PTGER2/MAPK3/HLA-C/GNAO1/CCL3/CCL3L3/NFKBIA/IFNA2/CDKN1A/PRKACG/ROCK1/MAPK11/TNF/PTGER4/CALM1/NRAS/MAPK13/PPP3CC/GRB2/GNB4/CALML6/CDKN2A/TNFRSF1A/IFNB1/PLCB1/TAP1/GNG13/GNA11/CX3CL1/CALML3/CXCL8/GNG12/CCL4/TRADD/E2F1/ADCY1/IL10RB/GNB3/GNAI1/GNAI3/GNB2/GNGT1/HLA-E/IFNA4/GNG3/HRAS/IFNA1/B2M/CALML5/IFNA21/IFNA14/CALM2/PPP3R1/PRKCG/RPS6KB2/FADD/CCL2/CGAS/IFNA16/PTGER1/IFNA6	
hsa00250	Alanine, aspartate and glutamate metabolism	35/7109	37/8105	0.149924876	0.26098034	0.171175715	GLUL/GFPT1/CAD/ABAT/ADSL/RIMKLB/ASRGL1/RIMKLA/GLUD2/GAD1/ASL/GLS2/GLS/ALDH5A1/AGXT2/PPAT/GOT2/GOT1L1/GPT/ASNS/GAD2/GOT1/GPT2/FOLH1/ALDH4A1/ASPA/	35

							DDO/GFPT2/GLUD1/CPS1/ASS1/AGX T/IL4I1/NIT2/NAT8L	
hsa049 60	Aldosterone- regulated sodium reabsorption	35/7109	37/810 5	0.14992 4876	0.26098 034	0.17117 5715	NEDD4L/PIK3R1/PDPK1/SGK1/IGF1/ NR3C2/PIK3CB/INSR/PIK3R3/MAPK1/ PIK3CD/SCNN1B/SCNN1A/PIK3CA/S CNN1G/ATP1B4/PRKCB/ATP1A2/KR AS/KCNJ1/ATP1A1/IRS1/ATP1B2/PIK 3R2/SLC9A3R2/ATP1A4/ATP1B3/MAP K3/INS/ATP1B1/ATP1A3/HSD11B2/FX YD4/PRKCG/SFN	35
hsa051 43	African trypanosomiasis	35/7109	37/810 5	0.14992 4876	0.26098 034	0.17117 5715	LAMA4/PLCB2/PLCB4/VCAM1/MYD 88/APOA1/THOP1/PLCB3/GNAQ/IL18/ FAS/KNG1/PRKCB/SELE/TLR9/IL6/F ASLG/IDO2/IL12B/APOL1/IL1B/ICAM 1/IL12A/NPPA/HPR/TNF/PLCB1/IDO1/ IFNG/F2RL1/IL10/HBA2/PRKCG/HBB/ HBA1	35
hsa052 21	Acute myeloid leukemia	62/7109	67/810 5	0.15226 1549	0.26359 2019	0.17288 8702	RUNX1T1/PIK3R1/PML/AKT2/AKT3/ RPS6KB1/TCF7L2/TCF7/PIK3CB/NFK B1/CCNA1/PIK3R3/PPARD/MAPK1/PI K3CD/RELA/LEF1/STAT5A/RARA/ST AT3/BRAF/ITGAM/ARAF/MYC/SPI1/I	62

							KBKG/PIK3CA/AKT1/ZBTB16/IKBKB /RAF1/KRAS/MAP2K1/KIT/DUSP6/FL T3/SOS1/RUNX1/MTOR/CHUK/PIK3R 2/CSF2/CD14/CEBPE/CSF1R/PIM2/PE R2/CCND1/JUP/BAD/MAPK3/STAT5B /MPO/NRAS/GRB2/PIM1/CEBPA/FCG R1A/HRAS/RPS6KB2/CCNA2/TCF7L1	
hsa005 63	Glycosylphosphati dylinositol (GPI)- anchor biosynthesis	25/7109	26/810 5	0.15309 8035	0.26359 2019	0.17288 8702	PIGN/PIGL/PIGO/MPPE1/PIGG/PGAP1 /PIGC/PIGW/PIGF/PIGV/PIGX/PIGM/P IGT/GPLD1/PIGP/PIGS/PIGK/PIGZ/PI GA/PIGH/PIGB/DPM2/PIGQ/PIGU/GP AA1	25
hsa005 14	Other types of O- glycan biosynthesis	44/7109	47/810 5	0.15385 5295	0.26359 2019	0.17288 8702	ST3GAL3/GALNT15/OGT/GALNT16/P OMT1/ST6GAL1/LFNG/GALNT14/PO FUT2/GALNTL5/XXYLT1/POFUT1/PO GLUT1/GALNT8/ST6GAL2/GALNTL6 /POC1B- GALNT4/GALNT5/COLGALT2/MFNG /B4GALT1/B4GALT3/GALNT11/B3GL CT/RFNG/GALNT10/GALNT2/GALNT 6/GALNT4/PLOD3/GALNT1/POMT2/G XYLT1/GALNT9/C1GALT1/GALNT13	44

							/COLGALT1/B4GALT2/GALNT7/C1G ALT1C1L/GALNT12/GALNT3/EOGT/ GXYLT2	
hsa052 10	Colorectal cancer	79/7109	86/810 5	0.15462 9969	0.26359 2019	0.17288 8702	MAPK10/BCL2L11/CTNNB1/PIK3R1/ BAX/TGFBR1/TGFA/MAPK8/TP53/AK T2/AKT3/RPS6KB1/CASP9/TCF7L2/R ALGDS/SMAD2/TCF7/DCC/MLH1/EG F/PIK3CB/CASP3/PIK3R3/RHOA/MAP K1/PIK3CD/LEF1/APC/SMAD3/GSK3 B/BRAF/BBC3/TGFB2/ARAF/MYC/M SH2/PIK3CA/AKT1/BIRC5/DDB2/RAF 1/KRAS/RALB/MAP2K1/EGFR/POLK/ SOS1/BCL2/MTOR/MSH3/PIK3R2/AXI N2/APC2/MAPK9/RALA/RAC2/SMAD 4/FOS/TGFB3/CYCS/CCND1/RAC1/B AD/MAPK3/PMAIP1/GADD45B/CDK N1A/EREG/NRAS/TGFBR2/GRB2/HR AS/APPL1/GADD45G/AREG/RPS6KB2 /JUN/TGFB1/TCF7L1	79
hsa040 64	NF-kappa B signaling pathway	95/7109	104/81 05	0.16186 5218	0.27439 9662	0.17997 7382	ERC1/CYLD/UBE2I/TNFRSF11A/BCL 2L1/CFLAR/VCAM1/BLNK/EDA/IRA K4/TNFAIP3/LCK/TLR4/NFKB1/XIAP/	95

							TAB3/EDA2R/CCL4L2/PLAU/RELA/EDAR/IRAK1/LTBR/TRAF5/MYD88/EDARADD/TRAF1/PLCG1/CSNK2A1/CXCL12/PIDD1/TRAF6/ATM/CARD14/RIPK1/IKBKG/TAB2/TIRAP/TRIM25/PLCG2/BCL10/IKBKB/BTK/TNFSF11/TAB1/LAT/TNFSF13B/PRKCB/TNFSF14/MALT1/SYK/NFKB2/IL1R1/BIRC3/BCL2/DDX58/CCL19/MAP3K14/CHUK/CD14/PARP1/IL1B/TRAF3/LYN/ICAM1/TRAF2/CARD10/CD40/GADD45B/NFKBIA/LBP/ZAP70/PRKCQ/TNF/CCL21/LTA/TNFRSF1A/LY96/CSNK2A2/CXCL8/TICAM2/CCL4/TRADD/TICAM1/CXCL2/RELB/CSNK2A3/CXCL3/GADD45G/CXCL1/CD40LG/LTB/CARD11/TNFRSF13C/PIAS4	
hsa00350	Tyrosine metabolism	34/7109	36/8105	0.163472139	0.274399662	0.179977382	TPO/LRTOMT/AOC3/ALDH3A1/DDC/ALDH3B1/GSTZ1/ADH7/DCT/AOC2/HPD/ALDH3B2/ADH6/ADH1B/MAOA/ADH5/TAT/GOT2/GOT1L1/COMT/AOX1/GOT1/ADH1C/ADH4/TYRP1/MAO	34

							B/ADH1A/DBH/FAH/IL4I1/HGD/PNMT/FAHD1/MIF	
hsa00500	Starch and sucrose metabolism	34/7109	36/8105	0.163472139	0.274399662	0.179977382	HK1/G6PC2/GPI/AMY1B/SI/GANC/AGL/ENPP1/GYG2/AMY1A/UGP2/MGAM/MGAM2/ENPP3/G6PC/GCK/PYGB/HK3/PYGL/HK2/PGM2L1/AMY2B/AMY1C/GYG1/HKDC1/TREH/G6PC3/PGM1/GBE1/AMY2A/GAA/PYGM/GYS1/GYS2	34
hsa00240	Pyrimidine metabolism	52/7109	56/8105	0.165317897	0.276089279	0.181085593	TK2/NME6/ENTPD1/ENTPD6/NME4/C TPS2/NT5C3A/CAD/UCK1/NT5C1B-RDH14/NT5E/ENTPD5/ENTPD3/CMPK1/CTPS1/AK9/RRM2/NME1/NT5C1B/ENPP1/UPP2/ENTPD4/NUDT2/ENPP3/RRM1/TYMS/NT5C2/DUT/UCKL1/DPLYD/RRM2B/DCTD/CANT1/UMPS/UPP1/NT5M/UCK2/NT5C/CMPK2/NT5C3B/CDA/DCTPP1/DTYMK/NME1-NME2/UPB1/DHODH/ENTPD8/NME3/PNP/NT5C1A/NME7/DPYS	52
hsa04350	TGF-beta signaling pathway	86/7109	94/8105	0.167734326	0.277887985	0.182265356	LTBP1/ACVR1/BMPRI1B/TGFBR1/SP1/NEO1/ZFYVE16/ACVR2A/TGIF1/DC	86

							N/HJV/PPP2R1B/RPS6KB1/NBL1/SMA D2/ZFYVE9/ACVR1C/AMHR2/CREBB P/RHOA/MAPK1/TGIF2/SMAD3/TGFB 2/GREM1/SMURF1/MYC/ACVR1B/IN HBA/THSD4/RGMA/LEFTY2/FBN1/B MPR1A/ACVR2B/FMOD/SMAD1/ID4/ EP300/INHBC/FST/NODAL/HAMP/TH BS1/SMAD9/BMP4/ID1/GREM2/PPP2 CA/BMP8A/CUL1/BMP2/SMAD5/INH BE/PITX2/SKP1/SMAD7/RBL1/SMAD 4/TGFB3/MAPK3/BMPR2/GDF7/BMP5 /E2F4/ROCK1/TNF/BAMBI/TFDP1/IN HBB/BMP8B/TGFBR2/GDF5/PPP2CB/ GDF6/LEFTY1/ID3/IFNG/AMH/BMP6/ BMP7/SMAD6/RGMB/RPS6KB2/TGFB 1/SMURF2	
hsa012 30	Biosynthesis of amino acids	69/7109	75/810 5	0.16892 8866	0.27788 7985	0.18226 5356	BCAT1/PFKM/PC/RPE/GLUL/PKM/M TR/PRPS1/IDH3B/TKTL1/BCAT2/PKL R/MAT2B/PRPS2/PYCR1/ALDOC/AR G1/ARG2/PYCR2/SHMT1/ASL/ACO2/ TKT/PGAM1/ENO4/CBSL/IDH1/ENO1 /PFKP/ACY1/ALDOA/PSAT1/PGK2/G	69

							OT2/GOT1L1/GPT/ASNS/NAGS/TKTL2/SHMT2/IDH3A/ENO3/IDH3G/CBS/GOT1/IDH2/PYCR3/CS/GPT2/ENO2/GAPDH/PGK1/OTC/ALDOB/RPEL1/PFKL/PAH/CPS1/PHGDH/ASS1/MAT1A/PSPH/ACO1/ABHD14A-ACY1/PGAM4/SDSL/MAT2A/PGAM2/CTH	
hsa04918	Thyroid hormone synthesis	69/7109	75/8105	0.168928866	0.277887985	0.182265356	ITPR1/PRKACB/TPO/PLCB2/IYD/GNAS/CREB3L4/ATF2/CREB5/PLCB4/ADCY3/ASGR2/CANX/ADCY5/PAX8/ADCY7/ATF4/CREB1/ATF6B/DUOX1/LRP2/TG/ADCY4/PRKACA/ADCY8/TTF1/ASGR1/PLCB3/GPX8/CREB3L2/ADCY2/CREB3L3/GNAQ/ATP1B4/TSHR/PRKCB/ATP1A2/TTF2/ADCY6/GSR/ALB/ITPR2/ATP1A1/HSPA5/CREB3/ADCY9/ATP1B2/CREB3L1/SERPINA7/ATP1A4/ATP1B3/PDIA4/GPX1/SLC5A5/PRKACG/GPX3/PLCB1/SLC26A4/DUOX2/DUOX2/ADCY1/GPX5/TTR/CGA/ATP1B1/ATP1A3/GPX6/PRKCG/HSP90	69

							B1	
hsa053 21	Inflammatory bowel disease	60/7109	65/810 5	0.17351 1268	0.28400 6006	0.18627 8135	RORA/IL12RB2/STAT6/SMAD2/TLR4/ NFKB1/FOXP3/NFATC1/RELA/SMAD 3/IL21R/STAT3/TGFB2/HLA- DQB1/TLR2/RORC/IL18R1/IL23R/IL18 /STAT4/IL4R/IL13/IL12RB1/STAT1/N OD2/IL6/IL1A/HLA- DQA1/IFNGR2/MAF/TLR5/HLA- DPB1/IL4/IL12B/TGFB3/IL1B/HLA- DMB/IL12A/HLA- DPA1/GATA3/IL18RAP/IL2RG/TNF/H LA-DQA2/HLA-DRB1/IL21/HLA- DOB/IFNGR1/HLA-DOA/HLA- DMA/IFNG/IL10/IL22/HLA- DRB5/TBX21/IL5/JUN/TGFB1/IL2/IL2 3A	60
hsa043 90	Hippo signaling pathway	142/710 9	157/81 05	0.17670 3448	0.28779 918	0.18876 606	FGF1/DLG2/YAP1/PARD3/CTNNB1/C RB1/CTNNA2/YWHAZ/DLG1/BMPR1 B/RASSF6/TGFBR1/DLG4/NF2/PPP2R 1B/PATJ/TCF7L2/WWTR1/SMAD2/TC F7/FRMD6/FZD3/WWC1/PPP2R2A/W NT5A/PPP2R2C/LEF1/APC/SMAD3/L	142

							ATS1/GSK3B/CCND3/WNT8A/WNT7 B/BBC3/FZD6/DLG3/TGFB2/AMOT/B TRC/MYC/LLGL2/RASSF1/FZD5/WN T2/TEAD2/MOB1A/CCND2/BIRC5/AJ UBA/CDH1/CSNK1E/PPP1CB/PPP2R2 B/ITGB2/PPP1CC/CTNNA3/BMPR1A/ DLG5/CRB2/LLGL1/FZD4/SMAD1/CS NK1D/TP53BP2/SCRIB/STK3/BIRC3/S NAI2/DVL3/FRMD1/WNT5B/LIMD1/F BXW11/BMP4/ID1/PPP2CA/BMP8A/F ZD2/PPP2R2D/BMP2/AXIN2/WNT3/A PC2/WNT4/WNT10B/NKD1/SMAD7/S MAD4/FZD7/PRKCI/TGFB3/WNT2B/ MOB1B/NKD2/CCND1/SAV1/WNT9B/ WNT16/BMPR2/GDF7/TEAD1/WNT10 A/BMP5/WNT11/FZD1/DVL2/YWHAE /YWHAG/ACTG1/WNT7A/WNT8B/B MP8B/TGFBR2/GDF5/TEAD4/PARD6 B/FZD8/PARD6G/CTNNA1/PPP2CB/F ZD9/SERPINE1/YWHAH/GLI2/GDF6/ LATS2/PARD6A/SOX2/AFP/AMH/BM P6/BMP7/WNT1/AREG/WNT9A/TEAD	
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							3/YWHAB/PRKCZ/TGFB1/ACTB/TCF7L1	
hsa03450	Non-homologous end-joining	13/7109	13/8105	0.181608104	0.294330375	0.193049838	DCLRE1C/POLL/POLM/MRE11/LIG4/DNTT/XRCC6/PRKDC/FEN1/XRCC4/XRCC5/RAD50/NHEJ1	13
hsa00534	Glycosaminoglycan biosynthesis - heparan sulfate / heparin	23/7109	24/8105	0.187100956	0.300274217	0.196948375	NDST3/HS3ST5/HS2ST1/EXT2/B3GAT3/NDST1/HS6ST3/HS6ST1/NDST2/EXTL2/GLCE/NDST4/HS3ST3B1/EXTL3/XYLT1/HS3ST2/EXT1/HS3ST3A1/XYLT2/EXTL1/B3GALT6/HS6ST2/B4GALT7	23
hsa04977	Vitamin digestion and absorption	23/7109	24/8105	0.187100956	0.300274217	0.196948375	ABCC1/PLB1/SLC5A6/APOB/SLC23A1/CUBN/BTD/APOA1/TCN2/MMACHC/SLC19A1/AWAT2/LRAT/SCARB1/SLC19A3/PNLIP/SLC46A1/FOLH1/SLC19A2/LMBRD1/SLC52A3/APOA4/RBP2	23
hsa00040	Pentose and glucuronate interconversions	32/7109	34/8105	0.193748938	0.307939133	0.201975755	RPE/UGT2A1/UGT2B28/UGP2/UGT2B10/XYLB/UGT2B4/CRYL1/UGT2B7/AKR1B1/UGT2B17/UGT2A2/UGT1A6/UGT1A1/DHDH/DCXR/AKR1B10/UGT1A5/RPEL1/AKR1A1/UGDH/SORD/UG	32

							T2B11/UGT1A8/UGT1A9/UGT1A4/KL/ UGT1A10/UGT1A7/UGT1A3/UGT2B1 5/UGT2A3	
hsa006 40	Propanoate metabolism	32/7109	34/810 5	0.19374 8938	0.30793 9133	0.20197 5755	ACACA/ECHDC1/PCCA/ABAT/ACAT 1/ACOX1/EHHADH/ACSS1/DLD/LDH B/ACSS3/DBT/SUCLG2/LDHC/HADH A/SUCLA2/ACOX3/ALDH6A1/ECHS1/ LDHA/BCKDHB/PCCB/SUCLG1/LDH AL6B/ACSS2/LDHAL6A/ACAT2/ACA DS/HIBCH/ACACB/BCKDHA/MLYCD	32
hsa005 15	Mannose type O- glycan biosynthesis	22/7109	23/810 5	0.20651 8856	0.32360 3134	0.21224 9696	ST3GAL3/FKTN/POMT1/CHST10/B3G AT1/LARGE2/POMGNT1/FUT9/B4GA LT1/POMGNT2/B4GALT3/B3GALNT2 /FUT4/MGAT5B/LARGE1/B4GAT1/PO MT2/FKRP/B4GALT2/RXYLT1/POMK /B3GAT2	22
hsa049 64	Proximal tubule bicarbonate reclamation	22/7109	23/810 5	0.20651 8856	0.32360 3134	0.21224 9696	SLC4A4/SLC38A3/PCK2/ATP1B4/ATP 1A2/GLUD2/GLS2/GLS/ATP1A1/SLC9 A3/ATP1B2/MDH1/ATP1A4/ATP1B3/P CK1/AQP1/GLUD1/CA2/SLC25A10/AT P1B1/ATP1A3/CA4	22
hsa041	Protein processing	154/710	171/81	0.20655	0.32360	0.21224	MAPK10/UBE2D3/GANAB/SEC31A/O	154

41	in endoplasmic reticulum	9	05	5192	3134	9696	S9/BAX/ATXN3/MAPK8/PDIA6/HSPB P1/NGLY1/SSR3/CANX/CAPN1/HSPH 1/STT3A/SIL1/SEL1L/ATF4/RAD23B/S EC61A2/ATF6B/DNAJB2/NFE2L2/MA P2K7/RRBP1/YOD1/SEC23B/DNAJB12 /CRYAB/SEC24B/EIF2AK2/ERP29/BC AP31/UBXN8/PRKN/DNAJC5G/SEC24 C/HYOU1/MAN1B1/UBXN1/HSP90AB 1/DERL2/SYVN1/SSR1/SAR1B/DERL1 /DDIT3/HSPA8/UBE2D4/SAR1A/SEC6 3/TUSC3/UGGT1/UBQLN3/HSP90AA1 /NSFL1C/STUB1/UBE2D2/MAN1C1/P LAA/DNAJB1/UBE4B/DERL3/ATF6/S EC31B/UBE2G2/TRAM1/MBTPS2/SEC 24D/SEC62/HSPA1L/PREB/HSPA5/ED EM1/FBXO6/EIF2AK4/UBE2J2/RPN2/ BCL2/MOGS/SEC13/SEC24A/SELENO S/TXNDC5/UBQLN1/CUL1/HSPA6/VC P/ERN1/UBXN4/MAPK9/DNAJC3/UB XN2A/HSPA4L/UBXN6/PDIA3/UBE2J 1/SKP1/MAN1A2/BAG2/SVIP/UBQLN 2/UGGT2/DNAJC5/EDEM3/TRAF2/RN	
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							F185/DNAJA2/ATXN3L/NPLOC4/PDI A4/DNAJC5B/PRKCSH/UBE2D1/SEL1 L2/ERO1B/DDOST/UBE2G1/STT3B/M AN1A1/CKAP4/SEC23A/EIF2AK3/XB P1/EDEM2/EIF2S1/ERO1A/UBQLN4/R NF5/FBXO2/P4HB/HSPA2/BAG1/LMA N1/MAP3K5/DNAJA1/UFD1/WFS1/EIF 2AK1/SSR2/DNAJC1/TRAM1L1/RAD2 3A/AMFR/SSR4/HSPA1A/DNAJB11/H SP90B1/PPP1R15A/CRYAA2/CRYAA/ HSPA1B/LMAN1L	
hsa049 40	Type I diabetes mellitus	40/7109	43/810 5	0.20816 5627	0.32458 0528	0.21289 0764	CD86/CD28/ICA1/PTPRN2/PRF1/PTPR N/HLA-DQB1/FAS/HLA- F/GAD1/FASLG/IL1A/HLA- DQA1/CD80/HLA-G/HLA- DPB1/GZMB/GAD2/IL12B/IL1B/HLA- DMB/HLA-A/IL12A/HLA-DPA1/HLA- B/HLA-C/HSPD1/TNF/HLA- DQA2/CPE/HLA-DRB1/LTA/HLA- DOB/HLA-DOA/INS/HLA- DMA/IFNG/HLA-E/HLA-DRB5/IL2	40
hsa045	Adherens junction	65/7109	71/810	0.21412	0.33229	0.21794	CTNND1/PARD3/SORBS1/CTNNB1/P	65

20			5	069	1071	8071	TPRB/LMO7/CTNNA2/MET/TGFBR1/TJP1/YES1/FER/FYN/TCF7L2/SSX2IP/TCF7/CDC42/AFDN/ERBB2/INSR/CREBBP/RHOA/NECTIN3/MAPK1/LEF1/SMAD3/CSNK2A1/NECTIN1/VCL/PTPRM/FARP2/CDH1/FGFR1/PTPN6/CTNNA3/ACP1/BAIAP2/WASF1/NECTIN4/EGFR/EP300/SNAI2/IGF1R/PTPRJ/NLK/PTPRF/NECTIN2/RAC2/SMAD4/RAC1/WASF2/SRC/MAPK3/PTPN1/ACTN1/ACTG1/IQGAP1/WASF3/TGFBR2/CTNNA1/WAS/CSNK2A2/CSNK2A3/ACCTB/TCF7L1	
hsa00983	Drug metabolism - other enzymes	73/7109	80/8105	0.217014624	0.335200992	0.219856674	TK2/NME6/IMPDH1/NME4/UCK1/UGT2A1/MGST2/NAT1/CMPK1/UGT2B28/RRM2/NME1/GSTO1/CES1/UPP2/UGT2B10/GSTM5/RRM1/UGT2B4/DUT/UCKL1/DPYD/RRM2B/UGT2B7/XDH/UMPS/CYP2A7/UPP1/GSTM3/UGT2B17/ITPA/UGT2A2/IMPDH2/GSTA4/UCK2/UGT1A6/UGT1A1/GSTA1/CYP3A4/CDA/CES2/MGST3/NAT2/MPO/UGT1A	73

							5/GSTM4/GSTT2B/MGST1/NME1-NME2/GSTO2/GMPS/UPB1/GSTA2/UGT2B11/UGT1A8/UGT1A9/UGT1A4/GSTM2/NME3/GSTP1/GSTA3/UGT1A10/UGT1A7/UGT1A3/GSTA5/UGT2B15/GSTM1/NME7/CYP2E1/UGT2A3/HPRT1/DPYS/CYP2A6	
hsa04136	Autophagy - other	30/7109	32/8105	0.228617413	0.350909602	0.230159874	ATG16L1/ATG13/BECN1/ATG5/ATG2A/ATG4A/MLST8/ATG4B/WIP1/ATG7/ULK2/ATG9A/ATG2B/MTOR/PPP2CA/ATG101/WIP1/ATG10/PIK3R4/RPTOR/GABARAPL1/GABARAP/BECN2/IGBP1/PPP2CB/ATG12/ATG4C/PIK3C3/ATG9B/ATG4D	30
hsa01200	Carbon metabolism	104/7109	115/8105	0.23038442	0.350909602	0.230159874	PFKM/PC/RPE/SDHC/HK1/OGDH/PDHA1/PCCA/PKM/PRPS1/SDHD/IDH3B/AMT/GLYCK/ACAT1/TKTL1/ACOX1/PKLR/ACSS1/GPI/DLD/PRPS2/ALDO/RGN/SUCLG2/GLUD2/SDHA/SHMT1/MDH2/ACO2/TKT/PGAM1/ENO4/HAO1/H6PD/IDH1/DLAT/ENO1/GCK/PFKP/ALDOA/TKFC/ADH5/IDNK/PSAT1	104

							/PGK2/FBP1/HK3/SUCLA2/ACOX3/GOT2/GOT1L1/MDH1/GPT/ME2/GLDC/ALDH6A1/PDHB/TKTL2/HK2/SHMT2/IDH3A/ENO3/ECHS1/IDH3G/GOT1/G6PD/PDHA2/IDH2/ADPGK/PCCB/CS/OGDHL/GPT2/HAO2/ESD/ENO2/GAPDH/PGK1/HKDC1/SUCLG1/ME3/ALDOB/ME1/RPEL1/CAT/PFKL/ACSS2/ACAT2/GLUD1/FBP2/CPS1/PHGDH/DLST/ACADS/AGXT/PSPH/HIBCH/ACO1/PGAM4/SDSL/PGD/PGAM2/SDHB	
hsa04726	Serotonergic synapse	104/7109	115/8105	0.23038442	0.350909602	0.230159874	CACNA1C/ITPR1/PRKACB/APP/PLCB2/SLC18A1/HTR4/GABRB3/GNAS/CACNA1D/HTR2C/PTGS1/GNG2/PLCB4/CACNA1A/CYP2C8/HTR7/CACNA1F/ADCY5/CASP3/DDC/RAPGEF3/MAPK1/CYP2C18/BRAF/HTR2A/GNB5/ARAF/HTR3E/PRKACA/GNG4/GNAI2/HTR3D/PLCB3/CACNA1S/JMJD7-PLA2G4B/GNAQ/PRKCB/GABRB2/CYP2C9/RAF1/KRAS/SLC6A4/ITPR2/NGT2/MAP2K1/TRPC1/CYP2D6/KCN	104

							D2/KCNJ5/MAOA/HTR3A/PLA2G4D/PLA2G4F/GNG7/PLA2G4B/ALOX15/ALOX12/CYP2D7/DUSP1/KCNJ6/GNB1/KCNJ9/TPH2/CACNA1B/MAPK3/GNAO1/HTR1A/CYP2C19/HTR1B/PRKACG/HTR1F/KCNN2/NRAS/MAOB/GNB4/HTR1D/ALOX15B/PLCB1/HTR3C/GNG13/GNG12/PLA2G4A/HTR6/ALOX12B/GNB3/GNAI1/GNAI3/KCNJ3/CYP2J2/HTR2B/GNB2/GNGT1/GABRB1/ALOX5/GNG3/HRAS/HTR5A/PLA2G4C/PKCG/CYP4X1/TPH1/SLC18A2/HTR3B	
hsa00130	Ubiquinone and other terpenoid-quinone biosynthesis	11/7109	11/8105	0.23615501	0.355917565	0.233444571	NQO1/COQ5/GGCX/HPD/VKORC1/TAT/COQ6/COQ3/VKORC1L1/COQ7/COQ2	11
hsa00430	Taurine and hypotaurine metabolism	11/7109	11/8105	0.23615501	0.355917565	0.233444571	GGT5/CSAD/GGT1/GAD1/BAAT/GADL1/GGT6/GAD2/CDO1/ADO/GGT7	11
hsa04730	Long-term depression	55/7109	60/8105	0.236917771	0.355917565	0.233444571	ITPR1/GRIA1/GUCY1A1/PLCB2/GNAS/GRM1/PPP2R1B/GNA12/PLCB4/CA	55

							CNA1A/PRKG2/IGF1/NOS1/MAPK1/GUCY1A2/PPP1R17/BRAF/GRIA3/GNA13/ARAF/GRID2/GNAI2/PLCB3/JMJD7-PLA2G4B/GNAQ/PRKCB/RAF1/KRAS/ITPR2/MAP2K1/GUCY1B1/IGF1R/RYR1/PRKG1/CRHR1/PLA2G4D/PLA2G4F/PPP2CA/PLA2G4B/GRIA2/LYN/MAPK3/GNAO1/NRAS/GNAZ/PLCB1/PPP2CB/GNA11/PLA2G4A/GNAI1/GNAI3/CRH/HRAS/PLA2G4C/PRKCG	
hsa04216	Ferroptosis	38/7109	41/8105	0.240618689	0.359501771	0.235795434	SLC11A2/ACSL1/NCOA4/PCBP2/SLC39A14/ACSL4/TP53/STEAP3/ACSL5/ACSL3/ACSL6/ATG5/TFRC/GSS/GCLC/PARNP/SLC39A8/ATG7/SLC3A2/CYBB/VDAC3/GCLM/SLC7A11/VDAC2/ALOX15/TF/CP/FTH1/FTL/MAP1LC3A/SLC40A1/MAP1LC3B/GPX4/SAT1/MAP1LC3C/LPCAT3/MAP1LC3B2/PCBP1	38
hsa00980	Metabolism of xenobiotics by cytochrome P450	71/7109	78/8105	0.241489031	0.359501771	0.235795434	HSD11B1L/CYP1A1/ALDH3A1/UGT2A1/MGST2/ALDH3B1/UGT2B28/ADH7/GSTO1/EPHX1/CYP2B6/AKR7A2/C	71

							YP2C9/UGT2B10/ALDH3B2/GSTM5/G STK1/ADH6/CYP2D6/ADH1B/UGT2B 4/HSD11B1/UGT2B7/ADH5/CYP2A7/G STM3/UGT2B17/CYP1A2/CYP2D7/UG T2A2/GSTA4/CYP1B1/ADH1C/ADH4/ CYP2F1/UGT1A6/UGT1A1/GSTA1/CY P3A4/DHHDH/MGST3/CYP3A5/HPGDS/ UGT1A5/GSTM4/GSTT2B/ADH1A/CY P2A13/MGST1/GSTO2/CBR1/AKR1C1/ GSTA2/CYP2S1/UGT2B11/UGT1A8/U GT1A9/UGT1A4/GSTM2/AKR7A3/GS TP1/GSTA3/UGT1A10/UGT1A7/UGT1 A3/GSTA5/UGT2B15/GSTM1/CYP2E1/ UGT2A3/CYP2A6	
hsa047 10	Circadian rhythm	29/7109	31/810 5	0.24789 4789	0.36737 5611	0.24095 9847	RORA/PER3/ARNTL/PRKAG2/CLOCK /CREB1/BTRC/RORC/BHLHE40/PRKA G1/CSNK1E/PRKAA1/CSNK1D/CRY2/ PRKAA2/NPAS2/PER1/PRKAB2/FBX W11/CUL1/NR1D1/SKP1/PER2/BHLH E41/PRKAB1/RORB/FBXL3/CRY1/PR KAG3	29
hsa007	Pantothenate and	20/7109	21/810	0.25074	0.36932	0.24223	BCAT1/PANK2/COASY/VNN2/PPCDC	20

70	CoA biosynthesis		5	7504	2536	6826	/BCAT2/PANK1/VNN1/ALDH3A2/ENP P1/ALDH1B1/ENPP3/DPYD/GADL1/A LDH2/PPCS/UPB1/AASDHPPT/PANK3 /DPYS	
hsa043 70	VEGF signaling pathway	54/7109	59/810 5	0.25145 3642	0.36932 2536	0.24223 6826	PTK2/PIK3R1/NFATC2/PXN/VEGFA/S PHK2/AKT2/AKT3/MAPK14/CASP9/C DC42/PIK3CB/PIK3R3/MAPKAPK3/M APK1/PIK3CD/PLCG1/SH2D2A/PPP3C B/PIK3CA/AKT1/SPHK1/PLCG2/JMJD 7- PLA2G4B/PRKCB/PPP3CA/RAF1/KRA S/MAP2K1/KDR/PPP3R2/NOS3/PLA2 G4D/PLA2G4F/PLA2G4B/PIK3R2/RAC 2/MAPK12/RAC1/BAD/SRC/MAPK3/ MAPK11/NRAS/MAPK13/PPP3CC/MA PKAPK2/PLA2G4A/SHC2/HRAS/PLA2 G4C/PPP3R1/PRKCG/HSPB1	54
hsa052 13	Endometrial cancer	53/7109	58/810 5	0.26662 4294	0.38986 3967	0.25570 9849	CTNNB1/CTNNA2/PIK3R1/BAX/TP53/ AKT2/AKT3/CASP9/PDPK1/TCF7L2/F OXO3/TCF7/ERBB2/MLH1/ELK1/EGF/ PIK3CB/PIK3R3/MAPK1/PIK3CD/LEF 1/APC/GSK3B/BRAF/ARAF/MYC/PIK	53

							3CA/AKT1/ILK/DDB2/CDH1/CTNNA3 /RAF1/KRAS/MAP2K1/EGFR/POLK/S OS1/PIK3R2/AXIN2/APC2/CCND1/BA D/MAPK3/GADD45B/CDKN1A/NRAS/ GRB2/CTNNA1/PTEN/HRAS/GADD45 G/TCF7L1	
hsa000 72	Synthesis and degradation of ketone bodies	10/7109	10/810 5	0.26928 7901	0.39201 6457	0.25712 1656	HMGCLL1/BDH1/HMGCS1/ACAT1/H MGCL/BDH2/OXCT1/HMGCS2/ACAT 2/OXCT2	10
hsa051 64	Influenza A	154/710 9	172/81 05	0.27389 2077	0.39620 489	0.25986 8829	NLRP3/PIK3R1/JAK1/BAX/ADAR/PM L/TMPRSS4/NLRX1/AKT2/HNRNPUL 1/AKT3/CALCOCO2/APAF1/CASP9/IR AK4/CIITA/NUP98/TLR4/PIK3CB/CAS P3/NFKB1/CASP1/CREBBP/PIK3R3/O AS2/FDPS/MAPK1/MAVS/PIK3CD/IF NAR2/RELA/PRSS3/OAS1/PABPN1/C CND3/RAB11A/MYD88/BID/RNASEL/ EIF2AK2/HLA- DQB1/NXF1/CCL5/CASP8/XPO1/IFNA R1/CPSF4/IKBKG/IKBKE/MX1/PIK3C A/AKT1/TRIM25/IRF3/KPNA6/IKBKB/ IL18/FAS/OAS3/PRKCB/PLG/TMPRSS	154

							2/RAF1/STAT2/DNAJB1/IRF7/TNFRSF 10B/MAP2K1/STAT1/TMPRSS11D/EP 300/IL6/NXF2/NXF2B/FASLG/NXT2/I L1A/HLA- DQA1/IFNGR2/TNFSF10/SLC25A4/DD X58/KPNA2/CDK4/CHUK/PIK3R2/KP NA1/TLR3/HLA- DPB1/CDK6/DNAJC3/IL12B/JAK2/TY K2/CYCS/NXF3/IL1B/HLA- DMB/TRAF3/IL33/RAE1/SOCS3/IFIH1 /ICAM1/TBK1/IL12A/HLA- DPA1/MAPK3/VDAC1/PRSS1/NFKBI A/IFNA2/BCL2L2- PABPN1/TNF/ACTG1/NXT1/HLA- DQA2/HLA- DRB1/CXCL10/TNFRSF1A/EIF2S1/IF NB1/HLA-DOB/IFNGR1/KPNA5/HLA- DOA/IRF9/RSAD2/CXCL8/TRADD/NX F5/TICAM1/HLA- DMA/IFNG/KPNA7/PRSS2/IFNA4/SLC 25A31/NFKBIB/MX2/HLA- DRB5/CPSF4L/IFNA1/PABPN1L/IFNA	
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							21/IFNA14/TPSB2/FADD/TNFRSF10A/CCL2/ACTB/IFNA16/SLC25A5/IFNA6	
hsa00100	Steroid biosynthesis	19/7109	20/8105	0.275777872	0.39620489	0.259868829	FDFT1/NSDHL/SC5D/CYP27B1/CYP51A1/LSS/LBR/SQLE/MSMO1/SOAT2/HSD17B7/SOAT1/DHCR7/CYP24A1/DHCR24/TM7SF2/CYP2R1/CEL/EBP	19
hsa00532	Glycosaminoglycan biosynthesis - chondroitin sulfate / dermatan sulfate	19/7109	20/8105	0.275777872	0.39620489	0.259868829	CHST11/DSE/CHST15/CSGALNACT1/B3GAT3/CHST3/UST/CHPF2/CHSY3/CHST7/CHSY1/XYL1/CHST14/XYL2/B3GALT6/CHPF/CHST12/B4GALT7/CSGALNACT2	19
hsa04392	Hippo signaling pathway - multiple species	27/7109	29/8105	0.290340147	0.413514755	0.271222284	YAP1/RASSF6/NF2/FAT4/WWTR1/FRMD6/WWC1/DCHS2/LATS1/RASSF2/RASSF1/TEAD2/MOB1A/AJUBA/CSNK1E/STK3/FRMD1/LIMD1/PAK1/RASSF4/MOB1B/SAV1/TEAD1/TEAD4/DCHS1/LATS2/TEAD3	27
hsa04744	Phototransduction	27/7109	29/8105	0.290340147	0.413514755	0.271222284	SLC24A1/CALML4/CALM3/PDE6B/RGS9/GNAT1/CNGB1/GRK1/GNB1/RHO/CNGA1/GUCA1A/GUCY2F/PDE6A/CALM1/CALML6/SAG/RCVRN/GUCY2D/GUCA1B/CALML3/PDE6G/GNGT1	27

							/GUCA1C/CALML5/CALM2/GRK7	
hsa051 70	Human immunodeficiency virus 1 infection	189/710 9	212/81 05	0.30058 1696	0.42532 5533	0.27896 8914	MAPK10/ITPR1/PAK3/PTK2/PIK3R1/N FATC2/NFATC4/PXN/BAX/CFL2/PAK 4/NFATC3/ELOC/MAPK8/CDC25C/AK T2/BCL2L1/AKT3/AP1G1/GNG2/RPS6 KB1/MAPK14/CASP9/CUL4A/PTK2B/ TRIM5/IRAK4/CALML4/CUL4B/TLR4 /PIK3CB/CASP3/NFKB1/CALM3/PIK3 R3/NFATC1/MAP2K6/MAPK1/PIK3CD /RELA/LIMK2/IRAK1/MAP2K3/MAP2 K7/CHEK1/TRAF5/MYD88/PLCG1/BI D/TAPBP/TLR2/GNB5/CASP8/BTRC/T RAF6/ATM/RIPK1/IKBKG/AP1B1/GN G4/PPP3CB/TAB2/PIK3CA/AKT1/GNA I2/ATR/PAK6/IRF3/PLCG2/PAK5/AP1 M2/GNAQ/IKBKB/TAB1/FAS/APOBE C3B/HLA- F/PRKCB/WEE1/PPP3CA/APOBEC3F/ RAF1/KRAS/ITPR2/GNGT2/MAP2K1/ LIMK1/FASLG/CD4/PPP3R2/BCL2/CR K/FBXW11/MTOR/CCNB3/TAP2/GNG 7/PAK2/PAK1/CUL1/HLA-	189

							G/CHUK/CFL1/PIK3R2/BUB1B-PAK6/MAPK9/WEE2/PDIA3/SKP1/RAC2/DCAF1/FOS/CYCS/CRKL/MAPK12/GNB1/CCR5/HLA-A/RAC1/CCNB1/CD3D/TRAF2/CD247/TBK1/TNFRSF1B/BAD/CXCR4/HLA-B/MAPK3/HLA-C/GNAO1/DDB1/NFKBIA/IFNA2/SAMHD1/MAPK11/TNF/CALM1/NRAS/APOBEC3H/APOBEC3D/MAPK13/PPP3C/C/GNB4/CALML6/TNFRSF1A/IFNB1/AP1S3/TAP1/CD3E/GNG13/GNA11/CALML3/GNG12/TRADD/AP1S1/CDK1/AP1M1/GNB3/GNAI1/GNAI3/CCNB2/GNB2/GNGT1/HLA-E/IFNA4/CUL5/CD3G/ELOB/GNG3/HRAS/IFNA1/B2M/CALML5/IFNA21/IFNA14/CALM2/AP1G2/PPP3R1/APOBEC3C/PRKCG/RPS6KB2/JUN/FADD/APOBEC3G/RNF7/CGAS/IFNA16/IFNA6	
hsa04061	Viral protein interaction with	90/7109	100/8105	0.301218386	0.425325533	0.278968914	IL6ST/CCR3/IL24/IL20RA/CCL4L2/CCR9/CX3CR1/LTBR/CSF1/CXCL12/CCL	90

	cytokine and cytokine receptor						5/IL18R1/IL6R/CCR2/IL20RB/CCR7/IL18/TNFSF14/TNFRSF10B/IL10RA/CCR1/TNFRSF10D/CXCL9/IL6/CCR4/CCR6/TNFSF10/IL22RA1/CCL19/IL2RB/CXCR1/CSF1R/IL19/CXCR5/CCL25/CCL20/XCL1/CCR5/TNFRSF14/CXCR2/TNFRSF1B/CCL28/IL34/CXCR4/CCL1/IL37/CCL15/IL18RAP/CCL3/CCL3L3/CCL8/CXCL5/IL2RG/TNF/CCL21/IL20/CXCL10/LTA/PPBP/TNFRSF1A/XCL2/CX3CL1/CXCL8/CXCL14/CXCL11/CCL4/TNFRSF10C/CCL17/ACKR3/CXCL2/IL10RB/CCL16/IL2RA/CCL27/CCL11/CCL14/CXCR3/IL10/ACKR4/PF4/CXCL3/CXCL1/CCL18/CCR10/XCR1/TNFRSF10A/CCL2/IL2/CCL22/CXCL6	
hsa05032	Morphine addiction	82/7109	91/8105	0.304601476	0.428264469	0.280896548	PRKACB/PDE4D/PDE1C/OPRM1/GABRB3/PDE10A/GNAS/GNG2/CACNA1A/ADCY3/PDE1B/PDE4A/PDE11A/ARRB1/ADCY5/PDE4B/PDE4C/ADCY7/GABRA2/PDE8B/ARRB2/GABBR1/GABRA1/GABRG3/PDE8A/PDE1A/GABRG2/	82

							GNB5/PDE2A/GABRR1/ADCY4/PRKACA/GNG4/GABRP/ADCY8/GNAI2/ADCY2/PRKCB/GABRB2/PDE7A/GABRA3/ADCY6/GNGT2/GABRA4/KCNJ5/DRD1/PDE3A/PDE3B/ADCY9/GABRE/GNG7/KCNJ6/GNB1/KCNJ9/GABRG1/CACNA1B/GNAO1/PRKACG/GABRR2/GNB4/GABRQ/GRK2/SLC32A1/PDE7B/GNG13/GABRA5/GRK6/GNG12/ADCY1/GNB3/GNAI1/GNAI3/KCNJ3/GNB2/GRK3/GNGT1/GABRB1/GABRD/GNG3/GABBR2/PRKCG/GABRR3	
hsa05216	Thyroid cancer	34/7109	37/8105	0.317007781	0.443810894	0.291093371	CTNNB1/BAX/NCOA4/TPM3/TP53/TCF7L2/TCF7/PAX8/MAPK1/LEF1/BRAF/MYC/RXRA/DDB2/CDH1/KRAS/RXRB/TFG/MAP2K1/NTRK1/POLK/CCDC6/RET/PPARG/CCND1/RXRG/TPR/MAPK3/GADD45B/CDKN1A/NRAS/HRAS/GADD45G/TCF7L1	34
hsa03022	Basal transcription factors	41/7109	45/8105	0.336649657	0.469312445	0.307819713	GTF2I/GTF2IRD1/TAF8/TAF1/GTF2A1/TAF6/TBP/GTF2A1L/GTF2H2/MNAT1/TAF5L/TAF7L/TAF1L/CCNH/GTF2H	41

							1/GTF2E2/ERCC2/GTF2H3/TBPL1/TA F12/GTF2E1/TAF11/TAF7/GTF2A2/TA F4B/GTF2F1/TAF15/GTF2F2/TAF4/GT F2H4/TAF9/TAF13/TAF2/TAF5/TBPL2 /ERCC3/TAF3/TAF9B/GTF2H5/GTF2B /TAF6L	
hsa030 30	DNA replication	33/7109	36/810 5	0.33855 3979	0.46997 5776	0.30825 4789	POLD1/RNASEH2B/PRIM2/RFC2/POL A2/MCM7/LIG1/MCM4/FEN1/MCM3/ RPA2/POLD3/POLD4/POLD2/POLE/P OLE2/RFC1/MCM2/RNASEH1/MCM6/ POLE3/RPA1/RFC4/RNASEH2C/DNA2 /SSBP1/RPA3/RFC5/POLA1/RNASEH2 A/RPA4/POLE4/RFC3	33
hsa052 24	Breast cancer	131/710 9	147/81 05	0.35567 2595	0.49166 5058	0.32248 0681	FGF1/BRCA1/CTNNB1/PIK3R1/BAX/S P1/ESR1/TP53/AKT2/AKT3/RPS6KB1/ TCF7L2/LRP6/PGR/TCF7/ESR2/IGF1/E RBB2/HEY1/EGF/PIK3CB/FZD3/PIK3 R3/WNT5A/MAPK1/PIK3CD/LEF1/SH C1/APC/GSK3B/NCOA1/BRAF/NOTC H2/WNT8A/WNT7B/FZD6/ARAF/NCO A3/MYC/FGF5/E2F3/FZD5/PIK3CA/A KT1/WNT2/BRCA2/E2F2/DDB2/HEYL	131

							/FGFR1/TNFSF11/RAF1/KRAS/NOTCH4/FGF8/FRAT2/FZD4/MAP2K1/EGFR/KIT/FGF2/SHC4/NFKB2/POLK/DVL3/IGF1R/SOS1/WNT5B/MTOR/FZD2/CDK4/PIK3R2/AXIN2/WNT3/JAG2/APC2/WNT4/CSNK1A1/CSNK1A1L/CDK6/WNT10B/FGF9/FGF4/NOTCH3/HEY2/FZD7/FOS/WNT2B/CCND1/WNT9B/WNT16/RB1/MAPK3/FGF23/FRAT1/WNT10A/FGF21/WNT11/GADD45B/FZD1/CDKN1A/SHC3/FLT4/DVL2/FGF3/WNT7A/NOTCH1/WNT8B/FGF7/NRAS/DLL3/JAG1/GRB2/FZD8/FGF6/FZD9/E2F1/DLL4/SHC2/PTEN/LRP5/HES1/FGF17/WNT1/HRAS/GADD45G/FGF20/WNT9A/RPS6KB2/JUN/TCF7L1	
hsa00760	Nicotinate and nicotinamide metabolism	32/7109	35/8105	0.36107316	0.49659252	0.325712579	NNT/NMNAT2/NMNAT3/SIRT2/NADK2/NT5C1B-RDH14/NT5E/SIRT6/NT5C1B/ENPP1/ENPP3/SIRT5/NT5C2/NUDT12/NMNAT1/SIRT1/NADSYN1/NAPRT/NT5M/AOX1/SIRT3/NMRK2/NT5C/NADK/NMR	32

							K1/NAMPT/BST1/QPRT/CD38/NNMT/ PNP/NT5C1A	
hsa046 20	Toll-like receptor signaling pathway	93/7109	104/81 05	0.36225 5942	0.49659 252	0.32571 2579	MAPK10/PIK3R1/CD86/MAPK8/AKT2 /AKT3/MAPK14/IRAK4/TLR4/PIK3CB /NFKB1/PIK3R3/CCL4L2/MAP2K6/M APK1/PIK3CD/IFNAR2/RELA/IRAK1/ MAP2K3/MAP2K7/MAP2K4/MYD88/S PP1/TLR2/CCL5/CASP8/TLR8/IFNAR1 /TRAF6/RIPK1/IKBKG/IKBKE/IRF5/T AB2/TIRAP/PIK3CA/AKT1/IRF3/TLR6 /IKBKB/TAB1/IRF7/TLR9/MAP2K1/ST AT1/CXCL9/IL6/TLR1/CD80/TLR5/CH UK/PIK3R2/CD14/CTSK/MAPK9/TLR3 /IL12B/FOS/IL1B/MAPK12/TRAF3/RA C1/TBK1/IL12A/MAPK3/CD40/CCL3/ CCL3L3/NFKBIA/IFNA2/LBP/MAPK1 1/TNF/MAPK13/CXCL10/IFNB1/LY96/ CXCL8/TICAM2/CXCL11/CCL4/TICA M1/IFNA4/IFNA1/IFNA21/IFNA14/TO LLIP/JUN/FADD/MAP3K8/IFNA16/IF NA6	93
hsa008	Porphyrin and	39/7109	43/810	0.37761	0.51549	0.33811	HMOX2/UROS/HEPH/FECH/HMBS/U	39

60	chlorophyll metabolism		5	5455	9937	386	GT2A1/PPOX/ALAS2/UGT2B28/COX15/ALAS1/FXN/UGT2B10/HCCS/UGT2B4/EARS2/UGT2B7/HEPHL1/ALAD/BLVRA/UGT2B17/UGT2A2/CP/UGT1A6/UGT1A1/COX10/UGT1A5/MMAB/UGT2B11/UGT1A8/UGT1A9/UGT1A4/CP/OX/UGT1A10/UGT1A7/UGT1A3/UGT2B15/UROD/UGT2A3	
hsa05416	Viral myocarditis	54/7109	60/8105	0.382276477	0.519395133	0.3406687	DMD/ABL2/DAG1/EIF4G1/EIF4G3/CD86/CD28/CASP9/FYN/CASP3/SGCD/CD55/CAV1/PRF1/ITGAL/BID/HLA-DQB1/LAMA2/CASP8/ITGB2/HLA-F/LAMA1/HLA-DQA1/CD80/HLA-G/HLA-DPB1/SGCB/RAC2/CYCS/HLA-DMB/CCND1/HLA-A/RAC1/MYH7/ICAM1/CXADR/ABL1/HLA-DPA1/HLA-B/HLA-C/CD40/ACTG1/HLA-DQA2/HLA-DRB1/SGCG/HLA-DOB/HLA-DOA/MYH6/HLA-DMA/HLA-E/SGCA/HLA-DRB5/CD40LG/ACTB	54

hsa051 40	Leishmaniasis	69/7109	77/810 5	0.38362 6193	0.51939 5133	0.34066 87	JAK1/CR1/MAPK14/IRAK4/ELK1/TLR4/NFKB1/MAPK1/C3/RELA/IRAK1/ITGAM/MYD88/TGFB2/HLA-DQB1/TLR2/ITGA4/TRAFF6/FCGR3B/FCGR3A/ITGB1/TAB2/NCF2/FCGR2A/TAB1/PTPN6/ITGB2/PRKCB/CYBB/STAT1/IL1A/HLA-DQA1/IFNGR2/HLA-DPB1/IL4/NCF4/IL12B/MARCKSL1/JAK2/FOS/TGFB3/NOS2/IL1B/HLA-DMB/MAPK12/IL12A/HLA-DPA1/MAPK3/EEF1A1/NFKBIA/MAPK11/TNF/HLA-DQA2/HLA-DRB1/MAPK13/HLA-DOB/IFNGR1/CYBA/HLA-DOA/HLA-DMA/IFNG/FCGR1A/IL10/NFKBIB/HLA-DRB5/JUN/NCF1/TGFB1/CR1L	69
hsa049 72	Pancreatic secretion	91/7109	102/8105	0.38995 9888	0.52395 7238	0.34366 0962	KCNMA1/ITPR1/ATP2A3/ATP2B2/PLCB2/ATP2B3/GNAS/PLCB4/ADCY3/ATP2A2/ADCY5/SLC4A4/ADCY7/RHOA/PRSS3/ATP2B4/RAB11A/ATP2B1/AMY1B/SLC4A2/ADCY4/RAB27B/ADCY8/RYR2/ATP2A1/PLCB3/CPB2/CHR	91

							M3/ADCY2/GNAQ/CLCA1/ATP1B4/P RKCB/ATP1A2/AMY1A/RAB3D/ADC Y6/CPB1/SLC9A1/ITPR2/PLA2G2D/TR PC1/PNLIPRP1/CLCA2/ATP1A1/PLA2 G12B/CFTR/RAP1B/ADCY9/ATP1B2/ RAB8A/PLA2G10/RAP1A/CCK/PNLIP/ KCNQ1/ATP1A4/PLA2G3/ATP1B3/RA C1/TPCN2/CELA3A/AMY2B/SLC12A2 /AMY1C/BST1/CTRL/SLC26A3/PRSS1 /SCTR/CEL/PLCB1/CD38/ADCY1/CPA 3/CPA2/AMY2A/CA2/CCKAR/PLA2G2 A/PRSS2/ATP1B1/ATP1A3/PLA2G12A /CELA3B/CLCA4/PRKCG/CTRB1/PLA 2G2F/CPA1/CTRB2	
hsa003 30	Arginine and proline metabolism	46/7109	51/810 5	0.39036 3879	0.52395 7238	0.34366 0962	NOS1/CNDP2/P4HA2/P4HA1/PRODH/ CKMT1A/PYCR1/PRODH2/AOC1/AL DH3A2/ALDH7A1/ARG1/AMD1/ARG2 /ALDH1B1/P4HA3/PYCR2/MAOA/CA RNS1/SMOX/NOS3/AGMAT/GOT2/G OT1L1/ALDH9A1/CKMT1B/ALDH2/A ZIN2/NOS2/ODC1/GOT1/PYCR3/DAO/ GAMT/ALDH4A1/CNDP1/MAOB/CK	46

							MT2/SMS/CKB/GATM/SAT1/HOGA1/ CKM/L3HYPDH/OAT	
hsa046 64	Fc epsilon RI signaling pathway	61/7109	68/810 5	0.39177 3497	0.52395 7238	0.34366 0962	MAPK10/PIK3R1/MAPK8/AKT2/AKT3 /MAPK14/PDPK1/FYN/PIK3CB/INPP5 D/PIK3R3/MAP2K6/MAPK1/PIK3CD/ VAV3/MAP2K3/MAP2K7/MAP2K4/PL CG1/VAV1/PIK3CA/AKT1/PLCG2/JMJ D7- PLA2G4B/BTK/GAB2/LAT/LCP2/RAF 1/KRAS/IL13/MAP2K1/SYK/MS4A2/S OS1/VAV2/PLA2G4D/PLA2G4F/PLA2 G4B/PIK3R2/CSF2/MAPK9/IL4/RAC2/ MAPK12/LYN/RAC1/ALOX5AP/MAP K3/MAPK11/TNF/NRAS/MAPK13/GR B2/PLA2G4A/FCER1A/ALOX5/HRAS/ IL5/PLA2G4C/FCER1G	61
hsa043 30	Notch signaling pathway	53/7109	59/810 5	0.40063 1722	0.53363 4966	0.35000 8536	TLE3/PSEN1/RBPJ/NUMB/CTBP2/MA ML2/DTX4/HEY1/CREBBP/APH1B/DT X3/DTX2/NOTCH2/NUMBL/NCOR2/L FNG/ATXN1L/HDAC2/ATXN1/APH1A /MAML1/HEY1/PSEN2/NOTCH4/EP30 0/RBPJL/MFNG/DVL3/JAG2/RFNG/N	53

							OTCH3/HEY2/TLE1/PTCRA/TLE2/DVL2/NOTCH1/DLL3/JAG1/ADAM17/PS ENEN/DLL4/HES1/DTX1/CIR1/DTX3L /NCSTN/CTBP1/SNW1/HDAC1/MAML 3/KAT2B/KAT2A	
hsa00051	Fructose and mannose metabolism	30/7109	33/8105	0.408950301	0.542261854	0.35566687	PFKM/MPI/KHK/HK1/PFKFB2/ALDO C/FPGT/PFKFB3/PFKP/ALDOA/PFKF B4/TKFC/ENOSF1/FBP1/HK3/AKR1B1 /TIGAR/HK2/GMPPA/HKDC1/AKR1B 10/PFKFB1/ALDOB/PFKL/SORD/GMP PB/PMM2/FBP2/PMM1/GMDS	30
hsa05110	Vibrio cholerae infection	45/7109	50/8105	0.410404868	0.542261854	0.35566687	PRKACB/TJP2/TJP1/GNAS/ADCY3/A TP6AP1/SEC61A2/PLCG1/ARF1/ATP6 V0A1/PRKACA/ATP6V0A4/ATP6V1C 2/PLCG2/ATP6V0D1/CFTR/ADCY9/A TP6V1E1/ATP6V0B/ATP6V1H/ATP6V 1E2/ATP6V0E1/KCNQ1/ATP6V1D/AT P6V0A2/SLC12A2/PDIA4/ATP6V1C1/ KDEL2/ATP6V1B2/PRKACG/ACTG1 /ATP6V0E2/ATP6V1A/ERO1A/ATP6V 1G2/ATP6V1B1/KDEL1/TCIRG1/ATP 6V1F/KDEL3/ATP6V1G3/ATP6V0D2	45

							/ATP6V1G1/ACTB	
hsa052 26	Gastric cancer	132/710 9	149/81 05	0.43081 5732	0.56400 0107	0.36992 4882	FGF1/CTNNB1/CTNNA2/PIK3R1/FGF R2/MET/BAX/TGFBR1/GAB1/TP53/A KT2/AKT3/RPS6KB1/TCF7L2/LRP6/S MAD2/TCF7/CCNE1/ERBB2/MLH1/E GF/PIK3CB/FZD3/RARB/PIK3R3/WNT 5A/MAPK1/PIK3CD/HGF/LEF1/SHC1/ APC/SMAD3/GSK3B/BRAF/CDK2/WN T8A/WNT7B/FZD6/TGFB2/ARAF/MY C/FGF5/E2F3/REG4/FZD5/ABCB1/RX RA/PIK3CA/CDH17/AKT1/WNT2/E2F 2/DDB2/CDH1/CTNNA3/RAF1/KRAS/ RXRB/FGF8/FRAT2/FZD4/MAP2K1/E GFR/FGF2/SHC4/TERT/POLK/DVL3/S OS1/BCL2/WNT5B/MTOR/CCNE2/FZ D2/PIK3R2/AXIN2/WNT3/APC2/WNT 4/CSNK1A1/CSNK1A1L/WNT10B/FGF 9/FGF4/SMAD4/FZD7/TGFB3/CDX2/ WNT2B/CCND1/WNT9B/WNT16/JUP/ RB1/RXRG/MAPK3/FGF23/FRAT1/W NT10A/FGF21/WNT11/GADD45B/FZD 1/CDKN1A/SHC3/CDKN1B/DVL2/FGF	132

							3/WNT7A/WNT8B/FGF7/NRAS/TGFB R2/GRB2/FZD8/CTNNA1/FGF6/SHH/F ZD9/E2F1/SHC2/LRP5/FGF17/WNT1/H RAS/GADD45G/FGF20/WNT9A/RPS6 KB2/TGFB1/TCF7L1	
hsa046 72	Intestinal immune network for IgA production	44/7109	49/810 5	0.43096 9221	0.56400 0107	0.36992 4882	IL15RA/TNFSF13/CD86/CD28/CCR9/L TBR/ICOSLG/CXCL12/HLA- DQB1/ITGA4/TNFSF13B/ITGB7/IL15/I L6/HLA- DQA1/CD80/MAP3K14/TNFRSF17/HL A-DPB1/IL4/HLA- DMB/CCL25/AICDA/CCL28/CXCR4/H LA-DPA1/CD40/HLA-DQA2/HLA- DRB1/LOC102723996/HLA-DOB/HLA- DOA/HLA-DMA/IL10/HLA- DRB5/ICOS/IL5/PIGR/CD40LG/CCR10 /TGFB1/TNFRSF13B/IL2/TNFRSF13C	44
hsa006 03	Glycosphingolipid biosynthesis - globo and isoglobo series	14/7109	15/810 5	0.43371 4368	0.56400 0107	0.36992 4882	B3GALNT1/ST3GAL1/B3GALT5/FUT1 /FUT9/HEXA/FUT2/HEXB/GLA/NAG A/ST8SIA1/GBGT1/A4GALT/A3GALT 2	14
hsa006	Glycosphingolipid	14/7109	15/810	0.43371	0.56400	0.36992	ST6GALNAC6/ST3GAL1/ST3GAL5/G	14

04	biosynthesis - ganglio series		5	4368	0107	4882	LB1/B4GALNT1/HEXA/ST6GALNAC3/HEXB/ST6GALNAC5/SLC33A1/ST6GALNAC4/ST8SIA1/B3GALT4/ST8SIA5	
hsa04662	B cell receptor signaling pathway	73/7109	82/8105	0.43887156	0.568459618	0.372849854	PIK3R1/NFATC2/NFATC3/AKT2/AKT3/BLNK/PIK3CB/NFKB1/CR2/INPP5D/PIK3R3/NFATC1/MAPK1/PIK3CD/VAV3/RELA/PIK3AP1/LILRB4/GSK3B/LILRB1/VAV1/IKBKG/PPP3CB/PIK3CA/AKT1/LILRB3/PLCG2/BCL10/IKBKB/BTK/PTPN6/RASGRP3/LILRB5/PRKCB/PPP3CA/RAF1/KRAS/MAP2K1/MALT1/SYK/PPP3R2/SOS1/VAV2/CHUK/PIK3R2/CD22/LILRA2/DAPP1/RAC2/FOXS/FCGR2B/LYN/RAC1/CD79A/CD19/NFKBIE/MAPK3/CD72/NFKBIA/NRAS/PPP3CC/GRB2/LILRA1/LILRB2/LILRA5/CD79B/NFKBIB/INPPL1/HRAS/PPP3R1/JUN/CARD11/CD81	73
hsa00260	Glycine, serine and threonine metabolism	36/7109	40/8105	0.444300999	0.573235406	0.375982269	AOC3/AMT/GLYCTK/ALAS2/DLD/ALAS1/AOC2/ALDH7A1/SHMT1/PGAM1/CBSL/MAOA/AGXT2/PSAT1/BHMT/GLDC/SRR/SHMT2/CBS/PIPOX/DAO/	36

							SARDH/GAMT/BPGM/MAOB/DMGD H/GATM/PHGDH/AGXT/PSPH/PGAM 4/GCAT/GRHPR/SDSL/PGAM2/CTH	
hsa034 30	Mismatch repair	21/7109	23/810 5	0.45006 9944	0.57615 9579	0.37790 022	PMS2/POLD1/MLH3/MLH1/RFC2/MS H2/LIG1/RPA2/POLD3/POLD4/POLD2/ MSH3/RFC1/RPA1/RFC4/EXO1/SSBP1 /RPA3/RFC5/RPA4/RFC3	21
hsa046 14	Renin-angiotensin system	21/7109	23/810 5	0.45006 9944	0.57615 9579	0.37790 022	MME/CTSA/LNPEP/KLK2/AGTR1/PR CP/THOP1/NLN/ENPEP/MAS1/AGTR2 /ACE/AGT/KLK1/CMA1/ATP6AP2/PR EP/ACE2/ANPEP/REN/CPA3	21
hsa005 20	Amino sugar and nucleotide sugar metabolism	43/7109	48/810 5	0.45202 239	0.57641 6148	0.37806 8502	MPI/GNE/CHIA/HK1/PGM3/CYB5R3/ GFPT1/NPL/CHIT1/GPI/UXS1/UAP1/G NPDA1/FPGT/UGP2/AMDHD2/CYB5R L/HEXA/GCK/CYB5R1/HEXB/HK3/G ALE/CYB5R2/HK2/RENBPNANP/GA LT/NAGK/GMPPA/HKDC1/CYB5R4/U GDH/PGM1/CMAS/GFPT2/GMPPB/PM M2/GNPNAT1/PMM1/GNPDA2/GMDS /GALK1	43
hsa049 29	GnRH secretion	57/7109	64/810 5	0.46345 0988	0.58870 8011	0.38613 0675	CACNA1G/CACNA1C/ITPR1/PIK3R1/ PLCB2/TRPC4/CACNA1D/KCNN3/AK	57

							T2/AKT3/PLCB4/ESR2/CACNA1I/CACNA1F/ARRB1/PIK3CB/PIK3R3/ARRB2/MAPK1/PIK3CD/GABBR1/TRPC5/SP P1/KCNN4/CACNA1H/GPER1/PIK3CA/AKT1/PLCB3/CACNA1S/GNAQ/PRKCB/HCN3/RAF1/KRAS/ITPR2/MAP2K1/TRPC1/KCNJ5/PIK3R2/HCN1/KCNJ6/KCNJ9/KCNN1/MAPK3/KCNN2/NRAS/PLCB1/GNA11/KCNJ3/KCNJ11/CGA/HRAS/GABBR2/LHB/PRKCG/GNRH2	
hsa00513	Various types of N-glycan biosynthesis	35/7109	39/8105	0.467781285	0.589815459	0.386857044	ST3GAL3/MGAT4C/ALG13/ALG9/STT3A/ALG1/MAN1B1/MGAT4B/ALG3/MAN2A2/FUT8/MGAT4A/TUSC3/MAN2A1/MAN1C1/CHST9/HEXA/RPN2/CHST8/B4GALT1/HEXB/B4GALT3/ALG2/MAN1A2/ALG14/MGAT1/DDOST/STT3B/MAN1A1/B4GALNT4/B4GALT2/MGAT2/ALG11/MGAT4D/B4GALNT3	35
hsa05218	Melanoma	64/7109	72/8105	0.467908312	0.589815459	0.386857044	FGF1/MITF/PIK3R1/MET/BAX/TP53/AKT2/AKT3/MDM2/IGF1/EGF/PIK3CB/PIK3R3/MAPK1/PIK3CD/HGF/BRAF/ARAF/FGF5/E2F3/PIK3CA/AKT1/PDG	64

							FRA/E2F2/DDB2/CDH1/FGFR1/RAF1/KRAS/FGF8/MAP2K1/EGFR/FGF2/PO LK/IGF1R/CDK4/PIK3R2/CDK6/PDGF RB/FGF9/FGF4/CCND1/BAD/RB1/MA PK3/FGF23/PDGFB/FGF21/GADD45B/ CDKN1A/FGF3/FGF7/NRAS/PDGFC/C DKN2A/FGF6/E2F1/PDGFD/PTEN/PD GFA/FGF17/HRAS/GADD45G/FGF20	
hsa005 33	Glycosaminoglyca n biosynthesis - keratan sulfate	13/7109	14/810 5	0.47219 9024	0.59235 5859	0.38852 328	ST3GAL3/ST3GAL1/CHST6/FUT8/CH ST4/B4GALT4/B3GNT2/B4GALT1/B4 GALT3/B4GALT2/CHST2/CHST1/B3G NT7	13
hsa034 20	Nucleotide excision repair	42/7109	47/810 5	0.47352 4592	0.59235 5859	0.38852 328	POLD1/CUL4A/CUL4B/RAD23B/ERC C6/RFC2/ERCC1/DDB2/LIG1/GTF2H2/ MNAT1/CCNH/GTF2H1/RPA2/POLD3/ POLD4/ERCC2/POLD2/GTF2H3/POLE/ POLE2/ERCC4/RFC1/XPC/ERCC8/BIV M- ERCC5/DDB1/POLE3/XPA/GTF2H4/R PA1/ERCC5/RFC4/RPA3/RFC5/ERCC3 /RPA4/CETN2/POLE4/RAD23A/GTF2 H5/RFC3	42

hsa052 17	Basal cell carcinoma	56/7109	63/810 5	0.48215 0836	0.60086 2216	0.39410 2557	CTNNB1/BAX/PTCH1/TP53/TCF7L2/TCF7/FZD3/WNT5A/LEF1/GLI3/APC/GSK3B/PTCH2/WNT8A/WNT7B/FZD6/GLI1/FZD5/WNT2/DDB2/FZD4/POLK/DVL3/WNT5B/KIF7/BMP4/FZD2/BMP2/AXIN2/WNT3/APC2/WNT4/WNT10B/FZD7/WNT2B/WNT9B/WNT16/WNT10A/WNT11/GADD45B/FZD1/CDKN1A/DVL2/WNT7A/WNT8B/FZD8/SMO/SHH/HHIP/SUFU/FZD9/GLI2/WNT1/GADD45G/WNT9A/TCF7L1	56
hsa030 18	RNA degradation	70/7109	79/810 5	0.48857 7542	0.60600 6803	0.39747 6867	PFKM/DDX6/CNOT1/PARN/XRN1/DIS3/CNOT6L/CNOT8/CNOT4/NUDT16/PAN2/WDR61/EDC3/CNOT2/TTC37/CNOT7/DCP1A/TOB2/SKIV2L/PABPC4/CNOT9/LSM8/ZCCHC7/DCP2/PNLDC1/DHX36/EXOSC2/BTG4/ENO4/PABPC1L2A/CNOT10/ENO1/PFKP/EXOSC3/DCPS/BTG2/PABPC1L2B/ENO3/EXOSC9/HSPA9/PABPC3/DIS3L/EDC4/C1D/HSPD1/ENO2/EXOSC7/PABPC5/LSM6/PAN3/BTG1/MTREX/EXOSC10/PABP	70

							C4L/PFKL/PATL1/TOB1/CNOT3/LSM4/EXOSC5/LSM2/BTG3/MPHOSPH6/PNPT1/EXOSC1/DCP1B/EXOSC6/LSM5/EXOSC8/XRN2	
hsa053 30	Allograft rejection	34/7109	38/810 5	0.49180 4913	0.60600 6803	0.39747 6867	CD86/CD28/PRF1/HLA-DQB1/FAS/HLA-F/FASLG/HLA-DQA1/CD80/HLA-G/HLA-DPB1/IL4/GZMB/IL12B/HLA-DMB/HLA-A/IL12A/HLA-DPA1/HLA-B/HLA-C/CD40/TNF/HLA-DQA2/HLA-DRB1/HLA-DOB/HLA-DOA/HLA-DMA/IFNG/HLA-E/IL10/HLA-DRB5/IL5/CD40LG/IL2	34
hsa053 40	Primary immunodeficiency	34/7109	38/810 5	0.49180 4913	0.60600 6803	0.39747 6867	DCLRE1C/BLNK/CIITA/LCK/IL7R/RFX5/IKBKG/BTK/PTPRC/ADA/CD4/RAG1/TAP2/JAK3/RAG2/AICDA/CD3D/CD79A/CD19/CD8A/CD40/ZAP70/IL2RG/CD8B/RFXANK/UNG/TAP1/CD3E/CD8B2/IGLL1/ICOS/CD40LG/TNFRSF13B/TNFRSF13C	34
hsa046 57	IL-17 signaling pathway	83/7109	94/810 5	0.50918 8879	0.62508 6348	0.40999 1045	MAPK10/MAPK8/IL17RC/MAPK14/IL17RE/TNFAIP3/FOSB/CASP3/NFKB1/	83

							TAB3/MAPK1/RELA/GSK3B/USP25/MAPK7/TRAF5/CASP8/TRAF6/TRAF3IP2/HSP90AB1/IKBKG/IL17RB/IKBKE/TAB2/IKBKB/HSP90AA1/IL13/IL17RA/FOSL1/SRSF1/ANAPC5/IL6/CSF3/MMP13/CHUK/MMP9/CSF2/MAPK9/IL4/MMP1/S100A8/FOS/TRAF4/IL1B/MAPK12/TRAF3/CCL20/TRAF2/MAPK6/TBK1/MAPK3/MUC5B/S100A9/NFKBIA/CXCL5/MAPK11/TNF/IL25/ELAVL1/MAPK13/CXCL10/CXCL8/MUC5AC/TRADD/CCL17/CXCL2/MAPK4/IFNG/CCL11/IL17D/CXCL3/IL17C/MAPK15/IL5/CXCL1/LCN2/JUND/MMP3/JUN/FADD/CCL2/HSP90B1/CXCL6	
hsa04970	Salivary secretion	82/7109	93/8105	0.524757827	0.641804182	0.42095619	KCNMA1/ITPR1/PRKACB/GUCY1A1/DMBT1/ATP2B2/PLCB2/ATP2B3/GNAS/PLCB4/ADCY3/PRKG2/CALML4/NOS1/ADCY5/CALM3/RYR3/ADCY7/GUCY1A2/ATP2B4/KCNN4/ATP2B1/AMY1B/SLC4A2/ADCY4/PRKACA/ADCY8/ADRA1A/PLCB3/CHRM3/ADCY2	82

							/GNAQ/ATP1B4/PRKCB/ATP1A2/AMY1A/ADCY6/SLC9A1/ITPR2/GUCY1B1/ATP1A1/LPO/PRKG1/ADCY9/ADRB2/LYZL1/ATP1B2/MUC7/VAMP2/AQP5/ATP1A4/ATP1B3/TRPV6/CST3/AMY2B/SLC12A2/MUC5B/AMY1C/BEST2/BST1/PRKACG/CALM1/LYZ/ADRA1B/CALML6/PLCB1/PRH2/CD38/CALML3/ADCY1/ADRB1/AMY2A/STATH/ATP1B1/ATP1A3/ADRA1D/CALML5/CALML2/PRB2/CAMP/PRKCG/CST2	
hsa00531	Glycosaminoglycan degradation	17/7109	19/8105	0.581098799	0.708079648	0.464425941	HYAL1/SPAM1/HYAL3/HPSE2/HPSE/GLB1/IDS/ARSB/HEXA/HEXB/HGSNAT/GALNS/HYAL4/HYAL2/GNS/SGSH/IDUA	17
hsa04923	Regulation of lipolysis in adipocytes	50/7109	57/8105	0.598267967	0.726310558	0.476383505	PRKACB/PIK3R1/MGLL/AQP7/GNAS/AKT2/PTGS1/AKT3/ADCY3/PRKG2/ADCY5/PIK3CB/INSR/ADCY7/PIK3R3/PIK3CD/ADCY4/PRKACA/ADCY8/PIK3CA/AKT1/GNAI2/IRS2/ADCY2/PTGER3/TSHR/ADCY6/LIPE/PRKG1/PLIN1/PDE3B/ADCY9/ADRB2/IRS1/NPR1/	50

							NPY1R/PIK3R2/LOC100509620/NPPA/ PRKACG/ABHD5/ADCY1/NPY/ADRB 1/INS/GNAI1/GNAI3/CGA/IRS4/FABP 4	
hsa051 50	Staphylococcus aureus infection	84/7109	96/810 5	0.60112 3843	0.72709 4649	0.47689 7786	C1S/PTAFR/FCAR/C2/MASP1/KRT40/ C1R/C3/FPR2/SELP/ITGAM/FPR3/ITG AL/KRT23/HLA- DQB1/FCGR3B/FCGR3A/C3AR1/C1Q A/CFI/DSG1/C4A/C1QC/FCGR2A/KRT 35/CFH/ITGB2/PLG/CFB/CFD/KRT24/ HLA- DQA1/KRT27/C5/KRT26/KRT13/KRT3 3B/KRT34/HLA- DPB1/KRT38/KRT12/HLA- DMB/KRT28/KRT36/FCGR2B/KRT16/I CAM1/KRT14/KRT18/SELPLG/KRT15/ KRT10/FPR1/C4B/HLA- DPA1/KRT9/MASP2/C1QB/DEFB103A /KRT39/KRT37/MBL2/HLA- DQA2/FGG/HLA- DRB1/KRT31/DEFA4/HLA-DOB/HLA- DOA/KRT33A/DEFB103B/KRT20/HLA	84

							- DMA/DEFB1/C5AR1/FCGR1A/IL10/H LA- DRB5/CAMP/DEFA5/KRT25/KRT32/K RT17/KRT19	
hsa046 21	NOD-like receptor signaling pathway	158/710 9	181/81 05	0.62285 6669	0.75062 2139	0.49232 9351	MAPK10/ITPR1/TP53BP1/CARD8/NLR P3/JAK1/ERBIN/PLCB2/NAIP/MAPK8/ ATG16L1/NLRX1/BCL2L1/CTSB/MAP K14/NLRC4/PLCB4/IRAK4/TRPM2/NL RP12/TNFAIP3/RBCK1/NLRP1/TLR4/ NFKB1/CASP1/XIAP/TAB3/RHOA/OA S2/ATG5/MAPK1/MAVS/IFNAR2/REL A/OAS1/ANTXR2/ANTXR1/MFN1/TA NK/BRCC3/CASP5/TRAF5/GBP5/MYD 88/RNASEL/NLRP7/CCL5/CASP8/IFN AR1/TRAF6/PKN1/MFN2/HSP90AB1/ CASR/RIPK1/IKBKG/CASP4/IKBKE/T AB2/DHX33/IRF3/PLCB3/SHARPIN/D NM1L/IKBKB/PRKCD/IL18/TAB1/TX N2/OAS3/GPRC6A/HSP90AA1/CYBB/ STAT2/PSTPIP1/IRF7/ITPR2/VDAC3/S TAT1/GBP4/NOD2/MCU/IL6/RIPK2/BI	158

							RC3/GBP3/IFI16/BCL2/VDAC2/MEFV/ PKN2/CARD6/CHUK/GBP2/GSDMD/ MAPK9/TYK2/P2RX7/IL1B/MAPK12/ TRAF3/CARD9/TRAF2/GABARAPL1/ TBK1/TXNIP/GABARAP/MAPK3/NA MPT/RNF31/VDAC1/PANX1/TRPV2/N FKBIA/IFNA2/DEFB103A/YWHAE/M APK11/TNF/NOD1/MAPK13/TRPM7/I FNB1/DEFA4/PLCB1/CYBA/TRIP6/GB P1/SUGT1/IRF9/CXCL8/ATG12/TXN/ DEFB103B/TICAM1/RIPK3/CXCL2/NL RP6/IFNA4/NFKBIB/GBP7/CXCL3/IFN A1/IFNA21/IFNA14/CXCL1/CARD17/ CAMP/DEFA5/PYDC2/NEK7/JUN/FA DD/AIM2/CCL2/IFNA16/IFNA6	
hsa047 42	Taste transduction	75/7109	86/810 5	0.63466 7458	0.76206 421	0.49983 4148	CACNA1C/PRKACB/P2RX2/PDE1C/S CN3A/PLCB2/SCN2A/GRM1/PLCB4/C ACNA1A/SCN9A/PDE1B/GABRA2/GA BBR1/SCNN1B/GABRA1/PDE1A/SCN N1A/PKD1L3/HTR3E/ADCY4/PRKAC A/TAS1R1/ADCY8/HTR3D/PLCB3/EN TPD2/CHRM3/SCNN1G/HCN4/GABR	75

							A3/ADCY6/TAS1R2/PKD2L1/P2RY1/GABRA4/GRM4/HTR3A/ASIC2/TAS2R40/TAS2R4/HTR1A/GNAT3/HTR1B/PRKACG/TAS2R39/TAS2R16/HTR1F/TAS2R14/P2RY4/TRPM5/TAS2R30/TAS2R7/HTR1D/PLCB1/HTR3C/GNG13/TAS1R3/GABRA5/CALHM1/KCNK5/P2RX3/TAS2R13/TAS2R3/TAS2R38/TAS2R41/GNB3/TAS2R9/TAS2R50/GABBR2/TAS2R43/TAS2R42/TAS2R5/TAS2R60/HTR3B	
hsa00920	Sulfur metabolism	9/7109	10/8105	0.647049519	0.774106515	0.507732637	SELENBP1/PAPSS2/SUOX/SQOR/TST/BPNT1/IMPAD1/PAPSS1/ETHE1	9
hsa00450	Selenocompound metabolism	15/7109	17/8105	0.65133063	0.77640499	0.509240195	SEPHS1/MTR/TXNRD2/PAPSS2/KYAT1/TXNRD1/TXNRD3/INMT/PAPSS1/KYAT3/PSTK/MARS2/SEPHS2/SEPSECS/CTH	15
hsa03050	Proteasome	40/7109	46/8105	0.666086431	0.791127927	0.518896897	PSME3/PSMF1/PSMC4/PSMD11/PSMB2/PSMA5/PSMD12/PSMC5/PSMA4/PSMA6/PSMD4/PSME4/ADRM1/PSMB5/PSMA2/PSMB10/PSMD1/PSMD6/PSMB9/PSMC1/PSME1/PSMD13/PSMC2/PS	40

							MB7/PSMB11/IFNG/PSME2/PSMB8/PSMA3/PSMD8/POMP/PSMB4/PSMB6/PSMD14/PSMB3/SEM1/PSMD3/PSMA1/PSMB1/PSMD7	
hsa03020	RNA polymerase	27/7109	31/8105	0.668925139	0.791641622	0.519233827	POLR2F/POLR3E/POLR2E/POLR1D/POLR1A/POLR3A/POLR1B/POLR3C/ZNRD1/POLR3GL/POLR1C/POLR1E/POLR2J/POLR2G/POLR2H/POLR3D/POLR2B/POLR2J2/POLR2J3/POLR3H/TWISTNB/POLR3G/POLR3B/POLR2D/POLR2I/POLR3F/POLR2C	27
hsa00730	Thiamine metabolism	14/7109	16/8105	0.686885365	0.809716436	0.531089008	AK4/AK2/THTPA/ALPL/AK5/NFS1/ACP1/AK1/AK8/AK7/TPK1/NTPCR/ALPP/ALPI	14
hsa03060	Protein export	20/7109	23/8105	0.689120371	0.809716436	0.531089008	SEC61A2/SRPRA/SEC63/SEC11A/SRP54/IMMP2L/SRP19/SEC62/HSPA5/SPCS2/SPCS3/SRP68/SRP9/SRP14/SRP72/OXA1L/IMMP1L/SRPRB/SPCS1/SEC11C	20
hsa00630	Glyoxylate and dicarboxylate metabolism	26/7109	30/8105	0.694364528	0.812974839	0.533226178	GLUL/PCCA/AMT/GLYCTK/ACAT1/ACSS1/DLD/HYI/SHMT1/MDH2/ACO2/HAO1/MDH1/GLDC/SHMT2/PCCB/	26

							CS/HAO2/CAT/ACSS2/AFMID/ACAT2 /AGXT/HOGA1/ACO1/GRHPR	
hsa005 12	Mucin type O- glycan biosynthesis	31/7109	36/810 5	0.72301 9205	0.84352 2406	0.55326 2176	ST3GAL1/GALNT15/GALNT16/GALN T14/GALNTL5/GCNT1/GALNT8/GAL NTL6/POC1B- GALNT4/GCNT3/GALNT5/ST6GALN AC3/GALNT11/GALNT10/GALNT2/G ALNT6/GALNT4/B4GALT5/GALNT1/ B3GNT6/ST6GALNAC4/ST6GALNAC 1/GALNT9/C1GALT1/GALNT13/GAL NT7/C1GALT1C1L/GALNT12/GALNT 3/ST6GALNAC2/B3GNT3	31
hsa049 75	Fat digestion and absorption	37/7109	43/810 5	0.72760 201	0.84586 9475	0.55480 1607	CD36/AGPAT1/APOB/ACAT1/APOA1/ NPC1L1/ABCA1/MTTP/LIPF/MOGAT3 /PLA2G2D/PNLIPRP1/DGAT2/PLA2G1 2B/SCARB1/MOGAT2/ABCG5/DGAT1 /GOT2/SLC27A1/PLA2G10/PNLIP/PLA 2G3/PLPP3/FABP2/PLPP2/CEL/FABP1/ ACAT2/SLC27A4/PLPP1/PLA2G2A/A GPAT2/PLA2G12A/ABCG8/APOA4/PL A2G2F	37
hsa042	Cardiac muscle	75/7109	87/810	0.73234	0.84720	0.55567	CACNA1C/CACNB4/SLC8A1/CACNB	75

60	contraction		5	9013	4853	7475	2/ASPH/SLC9A6/ATP2A3/TPM3/CACNA2D2/CACNA1D/TNNT2/CACNA1F/ATP2A2/TPM4/CACNA2D1/SLC8A3/TRDN/TPM1/SLC9A7/CACNB1/RYR2/ATP2A1/CACNG7/CACNA1S/CACNG6/ATP1B4/ATP1A2/SLC9A1/UQCRB/CACNA2D4/ATP1A1/CACNB3/CACNG4/ATP1B2/CASQ2/CACNG8/COX7A2L/UQCR11/COX7A1/COX7B2/ATP1A4/ATP1B3/MYH7/COX4I2/TNNI3/UQCRC2/CACNA2D3/UQCRHL/SLC8A2/CACNG5/COX4I1/UQCR10/TPM2/ACTC1/COX5B/UQCRC1/MYH6/CACNG3/UQCRFS1/CYC1/CACNG2/UQCRQ/COX7C/MYL2/ATP1B1/ATP1A3/COX7A2/UQCRH/MYL4/COX5A/COX8A/TNNC1/COX6C/HRC/MYL3	
hsa04932	Non-alcoholic fatty liver disease	134/7109	155/8105	0.73390086	0.847204853	0.555677475	MAPK10/BCL2L11/PIK3R1/ITCH/BAX/LEPR/NR1H3/MAPK8/PRKAG2/AKT2/SDHC/AKT3/CASP7/MAPK14/NDUFS1/PPARA/NDUFC2-KCTD14/CDC42/SDHD/PIK3CB/CASP	134

							3/NFKB1/INSR/PIK3R3/MLXIP/ATF4/ PIK3CD/RELA/ADIPOQ/NDUFA5/GS K3B/NDUFC2/BID/PKLR/CASP8/ADIP OR2/SREBF1/IL6R/RXRA/PIK3CA/AK T1/DDIT3/IRS2/NDUFC1/IKBKB/PRK AG1/FAS/NDUFB4/PRKAA1/SDHA/U QCRB/PRKAA2/IL6/FASLG/IL1A/ND UFB6/PRKAB2/IRS1/PIK3R2/ERN1/C OX7A2L/NDUFB3/MAPK9/NDUFA9/U QCR11/FOS/CYCS/PRKAB1/PPARG/I L1B/COX7A1/COX7B2/MAPK12/SOC S3/RAC1/COX4I2/TRAF2/MLXIPL/ND UFB5/NDUFS2/UQCRC2/NDUFA3/AD IPOR1/UQCRHL/NDUFV3/COX4I1/M APK11/TNF/UQCR10/EIF2AK3/XBP1/ MAPK13/MLX/TNFRSF1A/EIF2S1/CO X5B/NDUFS6/NDUFB11/NDUFA10/U QCRC1/CXCL8/NDUFS4/INS/NDUFB8 /UQCRFS1/CYC1/MAP3K5/NDUFA2/C EBPA/MAP3K11/UQCRQ/COX7C/ND UFA6/PRKAG3/NDUFA4L2/GSK3A/C OX7A2/UQCRH/NDUFS7/LEP/NDUFB	
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							9/COX5A/NDUFA4/NDUFB7/JUN/NDUFA11/NDUFA13/TGFB1/COX8A/CYP2E1/COX6C/SDHB/NDUFB1/NDUFS3	
hsa00565	Ether lipid metabolism	42/7109	49/8105	0.75085951	0.863750974	0.566529994	PLA2G6/PLD3/PAFAH1B2/PLB1/SELENOI/AGPS/LPCAT4/GAL3ST1/PLA2G7/ENPP2/UGT8/PAFAH1B1/JMJD7-PLA2G4B/PAFAH2/PLA2G2D/PLD4/PLA2G12B/CEPT1/PAFAH1B3/ENPP6/PLA2G4D/PLA2G4F/PLA2G4B/GDPD1/PLA2G10/PLA2G3/PLD2/PLPP3/PLPP2/LPCAT1/TMEM189/TMEM189-UBE2V1/PLA2G4A/TMEM86B/PLPP1/PLA2G2A/GDPD3/LPCAT2/PLD1/PLA2G12A/PLA2G4C/PLA2G2F	42
hsa04622	RIG-I-like receptor signaling pathway	60/7109	70/8105	0.763524933	0.875260289	0.574078897	MAPK10/CYLD/CASP10/MAPK8/NLRX1/MAPK14/AZI2/NFKB1/SIKE1/ATG5/MAVS/RELA/TANK/OTUD5/DDX3X/CASP8/TRAF6/RIPK1/IKBKG/IKBKE/TRIM25/IRF3/IKBKB/IRF7/TKFC/DDX58/CHUK/MAPK9/IL12B/DHX58/MAP3K1/MAPK12/TRAF3/IFIH1/TRAF2/TB	60

							K1/IL12A/NFKBIA/IFNA2/MAPK11/TNF/MAPK13/CXCL10/IFNB1/TBKBP1/CXCL8/ATG12/TRADD/IFNK/RNF125/IFNA4/NFKBIB/IFNW1/IFNA1/IFNA21/IFNA14/FADD/IFNE/IFNA16/IFNA6	
hsa05100	Bacterial invasion of epithelial cells	66/7109	77/8105	0.768018976	0.877355011	0.575452815	CTNNB1/PTK2/CTNNA2/PIK3R1/MET/PXN/FN1/DNM1/BCAR1/GAB1/DNM3/ELMO1/CDC42/ELMO2/PIK3CB/ARHGEF26/PIK3R3/RHOA/PIK3CD/ACTR3/CAV1/CLTC/SHC1/HCLS1/ARPC1B/DNM2/ITGB1/VCL/PIK3CA/ARPC4/ILK/CDH1/CAV2/CTNNA3/WASF1/RHOG/CLTCL1/SHC4/ITGA5/CAV3/ACTR2/ACTR3B/CRK/MAD2L2/PIK3R2/CLTB/DOCK1/ARPC2/CBL/CRKL/RAC1/WASF2/SRC/ACTR3C/SHC3/ACTG1/CD2AP/ELMO3/CTNNA1/ARHGAP10/CTTN/ARPC5/SHC2/ARPC1A/ARPC5L/ACTB	66
hsa05022	Pathways of neurodegeneration - multiple diseases	412/7109	475/8105	0.772172937	0.879048084	0.576563293	MAPK10/CACNA1C/ITPR1/BDNF/CTNNB1/GRIA1/NOX4/CAMK2G/BAX/ATP2A3/ATXN3/APP/PSEN1/PLCB2/DL	412

							G4/OPTN/DAXX/MAPT/MAPK8/SPTB N2/CACNA1D/GRM1/ATG13/SPG11/B CL2L1/SDHC/SNCA/CASP7/MAPK14/ GRIN2A/DNAL1/APAF1/NDUFS1/CAS P9/PLCB4/DCTN5/ATXN2L/LRP6/PD YN/KLC2/CAMK2D/VAPB/NDUFC2- KCTD14/SNCAIP/GRM5/CALML4/LR RK2/BECN1/CACNA1F/CAPN1/ATP2 A2/SDHD/GRIN2B/NOS1/CASP3/NFK B1/CALM3/FZD3/DNAH8/RYR3/WNT 5A/MAP2K6/MAPK1/ATG2A/ATF4/RE LA/DNAH2/PSMC4/KIF5A/DCTN4/AP C/NDUFA5/GSK3B/MFN1/TANK/GRI A4/PSMD11/DNAH6/AMBRA1/KLC4/ MAP2K3/BRAF/CHRNA7/NOX1/MAP 2K7/NDUFC2/DNAI1/CSF1/WNT8A/P LCG1/WNT7B/CSNK2A1/BID/FZD6/G RIA3/PSMB2/ARAF/CASP8/PRNP/UB A52/PRKN/ATXN2/UBA7/DNAH3/HIP 1/MFN2/DCTN2/FZD5/C9orf72/ATXN1 L/DNAH7/TARDBP/ALS2/PPP3CB/AT XN1/CHRM1/WNT2/HAP1/GRIN1/DE	
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							RL1/WIPI2/RYR2/HTRA2/ATP2A1/TR AP1/AGER/DDIT3/PLCB3/GPX8/CAM K2B/RAB5A/NDUFC1/DNAH11/CACN A1S/CHRM3/DNAH17/GNAQ/DCTN1/ CAMK2A/CSNK1E/FAS/PSMA5/DNA H9/NDUFB4/TUBA1A/PRKCB/ULK2/ RAB1A/RPS27A/PSMD12/NRBF2/PPP 3CA/RAF1/PSEN2/SDHA/CYBB/NEF M/TRPC3/KRAS/WDR41/ATF6/FRAT2 /DNAH5/ITPR2/FZD4/UQCRB/VDAC3 /MAP2K1/ATG2B/UBE2L3/ATP5F1A/ UBE2G2/FUS/DNAH1/CHRM5/MCU/P SMC5/IL6/HSPA5/FASLG/DKK4/RB1C C1/DVL3/IL1A/PPP3R2/UBE2J2/TUBA L3/RYR1/BCL2/SIGMAR1/PSMA4/PS MA6/VDAC2/NDUFB6/WNT5B/SLC25 A4/TUBA1C/GPR37/ATP5PF/MTOR/P SMD4/TUBB3/GRIN2D/FZD2/KIF5B/A XIN2/VCP/ATG101/PINK1/IFT57/WNT 3/GRIA2/ERN1/WIPI1/ADRM1/SOD1/ DNAH12/PSMB5/APC2/WNT4/CSNK1 A1/COX7A2L/NDUFB3/MAPK9/CSNK	
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							1A1L/NDUFA9/WNT10B/RAB8A/PPIF /PARK7/SMCR8/DCTN3/PSMA2/UBE2 J1/TUBB6/DNAL1/UQCR11/FZD7/CY CS/ULK1/NOS2/WNT2B/IL1B/COX7A 1/COX7B2/MAPK12/PIK3R4/SLC6A3/ DNAH10/RAC1/COX4I2/TRAF2/WNT9 B/UBE2L6/ZFYVE1/WNT16/GABARA PL1/TBK1/NDUFB5/TNFRSF1B/BAD/ ATXN3L/PSMD1/GABARAP/CACNA1 B/UBA1/HSD17B10/MAPK3/NDUFS2/ ATP5PD/PSMD6/GPX1/CDK5R1/VDA C1/ATP5MC3/UQCRC2/NDUFA3/RAB 39B/FRAT1/WNT10A/UQCRHL/WNT1 1/NDUFV3/UBE2G1/FZD1/NEFH/TOM M40L/KIF5C/DVL2/PPID/DKK2/ATP5 PB/COX4I1/MAPK11/TNF/WNT7A/W NT8B/CALM1/KLC1/NRAS/BECN2/PS MC1/UQCR10/EIF2AK3/GPX3/XBP1/ MAPK13/PPP3CC/TUBB/CALML6/PS MD13/CAT/STX1A/FZD8/TNFRSF1A/ EIF2S1/COX5B/FIG4/PSMC2/PLCB1/T UBA8/NDUFS6/NDUFB11/TUBB4A/N	
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							DUFA10/DNAI2/CSNK2A2/FZD9/MAP 3K10/ATG14/PSMB7/CALML3/UQCR C1/ACTR1B/GRIN2C/NDUFS4/NEFL/ UCHL1/NDUFB8/UQCRFS1/ATP5MC2 /TUBA4A/TUBA1B/CYC1/MAP3K5/N DUFA2/GPX5/UBC/UQCRQ/PSMA3/C OX7C/TOMM40/ACTR10/TUBA3E/SQ STM1/NDUFA6/PSMD8/CSNK2A3/LR P5/HTT/PIK3C3/SLC25A31/NDUFA4L 2/PRPH/COX7A2/UQCRH/PSMB4/WN T1/DNAL4/ATP5MC1/HRAS/TUBB8/T UBB4B/PSMB6/PSMD14/ATP5F1B/ND UFS7/CALML5/ATP5F1D/CALM2/ND UFB9/COX5A/ATP5PO/PSMB3/DKK1/ PPP3R1/DNAH14/WNT9A/SEM1/GPX 6/NDUFA4/PRKCG/CDK5/NDUFB7/C CS/FADD/NDUFA11/PSMD3/NDUFA1 3/TUBA3D/COX8A/PSMA1/TUBA3C/P SMB1/COX6C/SDHB/ACTR1A/NDUF B1/SLC25A5/NDUFS3/UBB/PSMD7	
hsa007 90	Folate biosynthesis	22/7109	26/810 5	0.79174 7739	0.89513 7478	0.58711 6247	MOCS1/DHFR/FPGS/DHFR2/ALPL/A KR1B1/TPH2/AKR1C3/GPHN/MOCS2/	22

							AKR1B10/MOCOS/PCBD1/CBR1/GCH1/QDPR/PCBD2/ALPP/PAH/ALPI/TPH1/GGH	
hsa04950	Maturity onset diabetes of the young	22/7109	26/8105	0.791747739	0.895137478	0.587116247	PAX6/HNF4A/HNF1B/PKLR/SLC2A2/HNF1A/GCK/NR5A2/FOXA2/ONECUT1/FOXA3/NEUROD1/PDX1/IAPP/HNF4G/MAFA/INS/MNX1/HES1/RFX6/HHEX/NKX6-1	22
hsa04978	Mineral absorption	51/7109	60/8105	0.80382597	0.90568063	0.594031448	SLC8A1/SLC11A2/ATP7B/ATP2B2/HMOX2/ATP2B3/SLC26A6/STEAP2/SLC5A1/TRPM6/HEPH/CYBRD1/ATP7A/SLC8A3/ATP2B4/SLC34A2/ATP2B1/SLC26A9/CLCN2/SLC34A1/SLC34A3/ATP1B4/ATP1A2/VDR/ATP1A1/SLC31A1/HEPHL1/SLC9A3/ATP1B2/TF/ATP1A4/ATP1B3/STEAP1/SLC46A1/SLC39A4/TRPV6/SLC26A3/SLC8A2/MT1F/FTL/FTL/SLC30A1/TRPM7/S100G/SLC6A19/SLC40A1/MT1G/ATP1B1/MT1HL1/ATP1A3/MT1M	51
hsa04215	Apoptosis - multiple species	27/7109	32/8105	0.807290333	0.906479588	0.594555481	MAPK10/BCL2L11/BAX/MAPK8/BCL2L1/CASP7/APAF1/CASP9/BECN1/CA	27

							SP3/XIAP/BID/BBC3/CASP8/BIRC6/H TRA2/BIRC5/DIABLO/BIRC3/BCL2/N GFR/MAPK9/CYCS/PMAIP1/BECN2/T NFRSF1A/FADD	
hsa005 11	Other glycan degradation	15/7109	18/810 5	0.82807 1249	0.92665 1159	0.60778 5915	GBA/MAN2C1/MAN2B2/NEU4/GLB1/ MAN2B1/GBA2/HEXA/HEXB/FUCA1/ FUCA2/NEU3/ENGASE/NEU2/MANB A	15
hsa004 80	Glutathione metabolism	48/7109	57/810 5	0.84448 5074	0.93937 8396	0.61613 3646	GGT5/GSS/MGST2/GGT1/GCLC/RRM 2/GSTO1/GPX8/OPLAH/GSTM5/GSR/ RRM1/GSTK1/GCLM/IDH1/RRM2B/T XNDC12/NAT8/PRDX6/GGT6/GSTM3/ GSTA4/ODC1/G6PD/IDH2/CHAC1/GP X1/GSTA1/MGST3/GGT7/HPGDS/GPX 3/GSTM4/GSTT2B/ANPEP/MGST1/GS TO2/SMS/GPX4/GSTA2/GPX5/GSTM2 /GSTP1/GSTA3/GPX6/GSTA5/PGD/GS TM1	48
hsa000 30	Pentose phosphate pathway	25/7109	30/810 5	0.84515 5031	0.93937 8396	0.61613 3646	PFKM/RPE/PRPS1/GLYCTK/TKTL1/G PI/PRPS2/ALDOC/RGN/DERA/TKT/H6 PD/PFKP/ALDOA/IDNK/FBP1/TKTL2/ G6PD/RBKS/ALDOB/RPEL1/PFKL/PG	25

							M1/FBP2/PGD	
hsa05014	Amyotrophic lateral sclerosis	312/7109	364/8105	0.896018391	0.992559093	0.651014603	NRG1/SLC1A2/GRIA1/BAX/OPTN/DA XX/HDAC6/ATG13/SPG11/TP53/BCL2 L1/SDHC/HNRNPA2B1/POM121/NUP2 10L/HNRNPA3/MAPK14/NUP153/GRI N2A/DNAL1/APAF1/NDUFS1/ERBB4/ CASP9/DCTN5/ATXN2L/NUP155/KLC 2/VAPB/NDUFC2- KCTD14/MATR3/BECN1/SDHD/GRIN 2B/NOS1/NUP98/CASP3/CASP1/DNA H8/HNRNPA1/MAP2K6/ATG2A/ATF4/ DNAH2/NUP62/PSMC4/KIF5A/DCTN4 /NDUFA5/ANXA11/TANK/PSMD11/D NAH6/AMBRA1/KLC4/MAP2K3/NDU FC2/NRG3/DNAI1/BID/PSMB2/NXF1/ PRKN/NUP58/NUP160/ATXN2/DNAH 3/DCTN2/SETX/NUP214/PFN2/C9orf72 /DNAH7/TARDBP/ALS2/PPP3CB/ANX A7/HAP1/GRIN1/DERL1/WIPI2/DDIT3 /GPX8/RAB5A/NDUFC1/DNAH11/HN RNPA1L2/NUP107/DNAH17/DCTN1/S EH1L/UBQLN3/PSMA5/DNAH9/NDUF	312

							B4/TUBA1A/ULK2/RAB1A/PSMD12/N RBF2/PPP3CA/SDHA/NEFM/WDR41/P OM121C/ATF6/DNAH5/UQCRB/ATG2 B/NUP210/ATP5F1A/FUS/DNAH1/MC U/NUP50/PSMC5/NXF2/NXF2B/HSPA 5/NXT2/RB1CC1/NRG4/PPP3R2/TUBA L3/BCL2/SIGMAR1/PSMA4/RANBP2/ NUP85/PSMA6/NDUFB6/SEC13/SRSF 7/TUBA1C/ATP5PF/MTOR/PSMD4/TU BB3/GRIN2D/UBQLN1/KIF5B/POM12 1L2/VCP/ATG101/PINK1/GRIA2/ERN1 /WIPI1/ADRM1/SOD1/DNAH12/PSMB 5/COX7A2L/NDUFB3/NDUFA9/NUP3 5/RAB8A/ANG/SMCR8/NCBP1/DCTN 3/PSMA2/TUBB6/DNALI1/UQCR11/C YCS/NXF3/ULK1/NOS2/COX7A1/COX 7B2/MAPK12/UBQLN2/PIK3R4/RAE1/ DNAH10/RAC1/NUP54/COX4I2/TRAF 2/SRSF3/NUP205/GABARAPL1/TBK1/ NDUFB5/TNFRSF1B/BAD/PSMD1/NU P43/GABARAP/TPR/NUP88/NDUFS2/ NRG2/ATP5PD/PSMD6/GLE1/GPX1/N	
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							DC1/VDAC1/NUP93/ATP5MC3/UQCR C2/NDUFA3/RAB39B/UQCRHL/NDUF V3/NEFH/TOMM40L/KIF5C/ATP5PB/ COX4I1/MAPK11/TNF/ACTG1/NXT1/ KLC1/BECN2/NUP188/PSMC1/UQCR1 0/EIF2AK3/GPX3/XBP1/MAPK13/PPP3 CC/TUBB/PSMD13/CAT/TNFRSF1A/E IF2S1/COX5B/FIG4/PSMC2/PFN1/TUB A8/NDUFS6/NDUFB11/TUBB4A/NDU FA10/DNAI2/UBQLN4/ATG14/PSMB7/ UQCRC1/ACTR1B/GRIN2C/NDUFS4/ NEFL/NDUFB8/UQCRFS1/NXF5/ATP5 MC2/TUBA4A/TUBA1B/CYC1/MAP3 K5/NDUFA2/GPX5/UQCRQ/PSMA3/C OX7C/TOMM40/ACTR10/TUBA3E/SQ STM1/NDUFA6/PSMD8/NUP133/PIK3 C3/NDUFA4L2/PRPH/PFN4/COX7A2/ UQCRH/PSMB4/DNAL4/ATP5MC1/TU BB8/TUBB4B/PSMB6/PSMD14/ATP5F 1B/NDUFS7/ATP5F1D/NDUFB9/COX5 A/ATP5PO/PSMB3/PPP3R1/DNAH14/S EM1/GPX6/NDUFA4/NDUFB7/CCS/N	
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							DUFA11/PSMD3/NDUFA13/NUP37/A CTB/TUBA3D/COX8A/PSMA1/TUBA3 C/PSMB1/COX6C/SDHB/ACTR1A/ND UFB1/NDUFS3/PSMD7	
hsa053 10	Asthma	25/7109	31/810 5	0.92226 2042	1	0.65589 5057	HLA-DQB1/IL13/MS4A2/HLA- DQA1/HLA-DPB1/IL4/HLA- DMB/HLA- DPA1/CD40/EPX/TNF/HLA- DQA2/HLA-DRB1/HLA-DOB/HLA- DOA/FCER1A/HLA- DMA/PRG2/CCL11/IL10/HLA- DRB5/IL5/CD40LG/IL9/FCER1G	25
hsa053 32	Graft-versus-host disease	34/7109	42/810 5	0.93465 4028	1	0.65589 5057	KLRD1/CD86/CD28/PRF1/HLA- DQB1/FAS/HLA- F/IL6/FASLG/IL1A/HLA- DQA1/CD80/HLA-G/HLA- DPB1/GZMB/IL1B/HLA-DMB/HLA- A/HLA-DPA1/HLA-B/HLA- C/TNF/HLA-DQA2/HLA-DRB1/HLA- DOB/HLA-DOA/HLA- DMA/KLRC1/IFNG/KIR3DL1/HLA- E/HLA-DRB5/KIR2DL1/IL2	34

hsa005 91	Linoleic acid metabolism	23/7109	29/810 5	0.94285 8813	1	0.65589 5057	PLA2G6/CYP2C8/PLB1/JMJD7- PLA2G4B/CYP2C9/PLA2G2D/PLA2G1 2B/PLA2G4D/PLA2G4F/PLA2G4B/AL OX15/PLA2G10/CYP1A2/PLA2G3/CY P3A4/CYP2C19/PLA2G4A/CYP2J2/PL A2G2A/PLA2G12A/PLA2G4C/PLA2G2 F/CYP2E1	23
hsa046 23	Cytosolic DNA- sensing pathway	51/7109	63/810 5	0.95978 9245	1	0.65589 5057	ADAR/POLR2F/NFKB1/CASP1/CCL4L 2/MAVS/RELA/CCL5/RIPK1/IKBKG/P OLR3E/POLR2E/IKBKE/IRF3/POLR1D /POLR3A/IKBKB/IL18/IRF7/POLR3C/I L6/TREX1/DDX58/CHUK/POLR3GL/P OLR1C/IL1B/IL33/TBK1/POLR2H/POL R3D/NFKBIA/IFNA2/POLR3H/CXCL1 0/IFNB1/ZBP1/CCL4/RIPK3/POLR3G/P OLR3B/IFNA4/NFKBIB/POLR3F/IFNA 1/IFNA21/IFNA14/AIM2/CGAS/IFNA1 6/IFNA6	51
hsa050 10	Alzheimer disease	313/710 9	369/81 05	0.96189 3351	1	0.65589 5057	MAPK10/CACNA1C/ITPR1/BACE1/CT NNB1/RTN4/PIK3R1/NOX4/RTN3/AP BB1/ATP2A3/APP/PSEN1/PLCB2/IDE/ MAPT/MME/MAPK8/CACNA1D/ATG	313

							13/AKT2/SDHC/AKT3/SNCA/CASP7/G RIN2A/APAF1/NDUFS1/CASP9/PLCB 4/LRP6/KLC2/NDUFC2- KCTD14/GRM5/CALML4/BECN1/CAC NA1F/CAPN1/ATP2A2/SDHD/GRIN2B /NOS1/PIK3CB/CASP3/NFKB1/INSR/C ALM3/FZD3/RYR3/PIK3R3/WNT5A/B ACE2/MAPK1/ATG2A/ATF4/PIK3CD/ RELA/APH1B/PSMC4/KIF5A/APC/ND UFA5/GSK3B/PSMD11/AMBRA1/KLC 4/BRAF/CHRNA7/NOX1/MAP2K7/ND UFC2/CSF1/WNT8A/WNT7B/CSNK2A 1/BID/FZD6/PSMB2/EIF2AK2/ARAF/C ASP8/FZD5/PPP3CB/CHRM1/PIK3CA/ AKT1/WNT2/GRIN1/WIP1/APH1A/A TP2A1/AGER/DDIT3/PLCB3/IRS2/LRP 1/NDUFC1/CACNA1S/CHRM3/LPL/G NAQ/IKBKB/CSNK1E/FAS/PSMA5/N DUF4/TUBA1A/ULK2/PSMD12/NRB F2/PPP3CA/RAF1/PSEN2/SDHA/CYBB /KRAS/ATF6/FRAT2/ITPR2/FZD4/UQ CRB/VDAC3/MAP2K1/ATG2B/ATP5F	
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							1A/ADAM10/CHRM5/MCU/PSMC5/IL 6/GPR83/DKK4/RB1CC1/DVL3/IL1A/P PP3R2/TUBAL3/PSMA4/PSMA6/VDA C2/NDUFB6/WNT5B/SLC25A4/TUBA 1C/ATP5PF/IRS1/MTOR/PSMD4/TUB B3/GRIN2D/FZD2/KIF5B/CHUK/PIK3 R2/AXIN2/ATG101/WNT3/ERN1/WIPI 1/ADRM1/PSMB5/APC2/WNT4/CSNK 1A1/COX7A2L/NDUFB3/MAPK9/CSN K1A1L/NDUFA9/WNT10B/PPIF/PSMA 2/TUBB6/UQCR11/NAE1/FZD7/CYCS/ ULK1/NOS2/WNT2B/IL1B/COX7A1/C OX7B2/PIK3R4/COX4I2/TRAF2/WNT9 B/WNT16/NDUFB5/BAD/PSMD1/HSD 17B10/MAPK3/NDUFS2/ATP5PD/PSM D6/CDK5R1/VDAC1/ATP5MC3/UQCR C2/NDUFA3/FRAT1/WNT10A/UQCRH L/WNT11/NDUFV3/FZD1/KIF5C/GAP DH/DVL2/PPID/DKK2/ATP5PB/COX4I 1/TNF/WNT7A/WNT8B/CALM1/KLC1 /NRAS/BECN2/PSMC1/UQCR10/EIF2 AK3/XBP1/ADAM17/PPP3CC/TUBB/C	
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							ALML6/PSMD13/FZD8/TNFRSF1A/EI F2S1/COX5B/PSMC2/PLCB1/TUBA8/ NDUFS6/NDUFB11/TUBB4A/NDUFA1 0/PSENEN/CSNK2A2/FZD9/ATG14/PS MB7/CALML3/UQCRC1/GRIN2C/ND UFS4/INS/NDUFB8/UQCRFS1/ATP5M C2/TUBA4A/TUBA1B/CYC1/MAP3K5/ NDUFA2/UQCRQ/PSMA3/IRS4/COX7 C/TUBA3E/NDUFA6/PSMD8/CSNK2A 3/LRP5/PIK3C3/SLC25A31/NDUFA4L2 /COX7A2/UQCRH/PSMB4/WNT1/ATP 5MC1/HRAS/TUBB8/TUBB4B/PSMB6/ PSMD14/ATP5F1B/NDUFS7/CALML5/ ATP5F1D/CALM2/NDUFB9/COX5A/A TP5PO/PSMB3/NCSTN/DKK1/PPP3R1/ WNT9A/SEM1/NDUFA4/CDK5/NDUF B7/FADD/NDUFA11/PSMD3/NDUFA1 3/TUBA3D/COX8A/PSMA1/TUBA3C/P SMB1/COX6C/SDHB/NDUFB1/SLC25 A5/NDUFS3/PSMD7	
hsa052 02	Transcriptional misregulation in	160/710 9	192/81 05	0.97230 9872	1	0.65589 5057	PAX5/RUNX1T1/MITF/NSD2/MEF2C/ PTK2/KDM6A/MET/AFF1/ETV1/BAX/	160

	cancer						SP1/ERG/CD86/PML/TP53/BCL2L1/CC NT1/MDM2/JMJD1C/MAX/ETV4/MLF 1/IGF1/BAIAP3/PROM1/NFKB1/CCNA 1/PAX8/BCL6/KMT2A/SUPT3H/FLT1/ PLAU/RELA/SS18/NFKBIZ/IL1R2/ZEB 1/SIN3A/RARA/ITGAM/ZBTB17/TRA F1/EWSR1/GRIA3/PAX3/NCOR1/NR4 A3/PLAT/MYC/ETV6/MLLT3/ATM/C DK14/SPI1/PBX1/HDAC2/ELK4/RXRA /ZBTB16/FUT8/LDB1/DDIT3/CCND2/ REL/DDX5/NUPR1/DDB2/ASPSCR1/F LI1/ETV7/HPGD/EYA1/IGFBP3/TCF3/ SIX4/TMPRSS2/ITGB7/RXRB/RUNX2/ BCL11B/BMP2K/SMAD1/HMGA2/LM O2/FUS/KLF3/IL6/NTRK1/DUSP6/BIR C3/POLK/IGF1R/FLT3/CCNT2/MAF/R UNX1/MEN1/NGFR/IL2RB/MMP9/CSF 2/CD14/CEBPE/CSF1R/GZMB/SSX2/S SX2B/PER2/PRCC/PPARG/MEIS1/TFE 3/PTCRA/WNT16/JUP/RXRG/FOXO1/ MYCN/TAF15/DOT1L/CD40/SIX1/GA DD45B/CDK9/CDKN1A/ETV5/CDKN1	
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							B/MPO/PAX7/TGFBR2/HOXA9/PBX3/ TLX1/DEFA4/MLLT1/CXCL8/WT1/AR NT2/SPINT1/TSPAN7/SLC45A3/CEBP A/COMMD3- BMI1/FCGR1A/PDGFA/LYL1/GADD4 5G/TLX3/DEFA5/HHEX/FEV/HOXA10 /MMP3/HDAC1/CCNA2/BMI1/CDKN2 C/HOXA11	
hsa005 92	alpha-Linolenic acid metabolism	19/7109	25/810 5	0.97290 3722	1	0.65589 5057	PLA2G6/PLB1/ACOX1/JMJD7- PLA2G4B/PLA2G2D/ACAA1/PLA2G1 2B/PLA2G4D/PLA2G4F/ACOX3/PLA2 G4B/FADS2/PLA2G10/PLA2G3/PLA2 G4A/PLA2G2A/PLA2G12A/PLA2G4C/ PLA2G2F	19
hsa051 31	Shigellosis	206/710 9	246/81 05	0.97521 7862	1	0.65589 5057	MAPK10/UBE2D3/ITPR1/TNIP1/NLRP 3/PTK2/PIK3R1/CD44/UBE2V1/CAST/ PXN/BAX/PLCB2/BCAR1/NAIP/MAP K8/ATG16L1/TP53/AKT2/BCL2L1/AK T3/CALCOCO2/HK1/RPS6KB1/MAPK 14/MDM2/NLRC4/ELMO1/PLCB4/FO XO3/CDC42/ELMO2/RBCK1/BECN1/C APN1/TLR4/RPS6KA5/PIK3CB/PLCZ1	206

							/NFKB1/CASP1/TAB3/PIK3R3/RHOA/ ATG5/MAPK1/PIK3CD/C3/RELA/ACT R3/CAPNS1/GSK3B/FNBP1L/HCLS1/F NBP1/TRAF5/ARHGEF2/MYD88/PLC G1/ARF1/MYL12A/CCL5/BTRC/UBA5 2/TRAF6/ATM/ARPC1B/FOXO4/RRA GB/RIPK1/IKBKG/ITGB1/PFN2/CASP 4/TAB2/VCL/PIK3CA/AKT1/WIPI2/AR PC4/IRF3/PLCB3/PLCG2/RRAGD/GL MN/UBE2D4/ILK/SHARPIN/BCL10/PL CE1/IKBKB/PRKCD/IL18/TAB1/ROCK 2/U2AF1L4/RPS27A/CYTH2/UBE2D2/ WASF1/ITPR2/PRKCE/EGFR/MALT1/ CBX3/PLCD4/RIPK2/ITGA5/IL1R1/AR F6/ACTR2/ACTR3B/DIAPH1/BCL2/CR K/MYL10/TLR5/FBXW11/MTOR/AKT 1S1/HK3/CUL1/CHUK/PIK3R2/CSF2/C YTH4/CD14/WIPI1/MYL7/MAPK9/DO CK1/ARPC2/SKP1/TLN2/HK2/PLCD1/ CYCS/CRKL/IL1B/MAPK12/PIK3R4/P LCD3/RAC1/TRAF2/RPTOR/GABARA PL1/TBK1/WASF2/SRC/FOXO1/GABA	
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							RAP/ACTR3C/MAPK3/UBE2D1/RNF3 1/VDAC1/CYTH1/NFKBIA/PRKCQ/M YL12B/ACTN1/HKDC1/PPID/ROCK1/ MAPK11/TNF/ACTG1/NOD1/BECN2/T LN1/TECPR1/MAPK13/TNFRSF1A/RR AGC/IFNB1/CTTN/PLCB1/PFN1/UBE2 N/ATG14/CYTH3/CXCL8/ATG12/TRA DD/MYLPF/ARPC5/TIFA/ARPC1A/UB C/MYL9/MYL5/SQSTM1/PIK3C3/MYL 2/PFN4/NFKBIB/GSK3A/RRAGA/U2A F1/RPS6KB2/JUN/ARPC5L/ACTB/BNI P3/CGAS/UBB	
hsa053 20	Autoimmune thyroid disease	42/7109	53/810 5	0.97532 0975	1	0.65589 5057	TPO/CD86/CD28/PRF1/HLA- DQB1/TG/FAS/HLA- F/TSHR/FASLG/HLA- DQA1/CD80/HLA-G/HLA- DPB1/IL4/GZMB/HLA-DMB/HLA- A/HLA-DPA1/HLA-B/CTLA4/HLA- C/CD40/IFNA2/HLA-DQA2/HLA- DRB1/HLA-DOB/HLA-DOA/HLA- DMA/CGA/HLA-E/IFNA4/IL10/HLA- DRB5/IFNA1/IL5/IFNA21/IFNA14/CD4	42

							0LG/IL2/IFNA16/IFNA6	
hsa047 23	Retrograde endocannabinoid signaling	122/710 9	148/81 05	0.97806 8099	1	0.65589 5057	MAPK10/CACNA1C/ITPR1/PRKACB/ GRIA1/RIMS1/PLCB2/MGLL/GABRB3 /MAPK8/CACNA1D/GRM1/GNG2/MA PK14/NDUFS1/PLCB4/CACNA1A/ND UFC2- KCTD14/ADCY3/GRM5/CACNA1F/A DCY5/ADCY7/CNR1/GABRA2/NAPEP LD/MAPK1/GABRA1/NDUFA5/GRIA4 /GABRG3/NDUFC2/GABRG2/GRIA3/ GNB5/GABRR1/ADCY4/PRKACA/GN G4/GABRP/ADCY8/GNAI2/PLCB3/ND UFC1/CACNA1S/ADCY2/GNAQ/NDU FB4/SLC17A8/PRKCB/GABRB2/GAB RA3/ADCY6/ITPR2/GNGT2/GABRA4/ KCNJ5/NDUFB6/ADCY9/GABRE/GN G7/GRIA2/NDUFB3/MAPK9/NDUFA9/ KCNJ6/MAPK12/GNB1/KCNJ9/GABR G1/NDUFB5/CACNA1B/FAAH/MAPK 3/NDUFS2/GNAO1/NDUFA3/NDUFV3 /PRKACG/GABRR2/MAPK11/DAGLA/ MAPK13/GNB4/GABRQ/DAGLB/SLC	122

							32A1/PLCB1/NDUFS6/NDUFB11/ABH D6/NDUFA10/GNG13/GABRA5/GNG1 2/NDUFS4/ADCY1/NDUFB8/GNB3/SL C17A7/GNAI1/NDUFA2/GNAI3/KCNJ 3/GNB2/GNGT1/NDUFA6/NDUFA4L2/ GABRB1/GABRD/GNG3/NDUFS7/ND UFB9/NDUFA4/PRKCG/NDUFB7/ND UFA11/NDUFA13/SLC17A6/GABRR3/ NDUFB1/NDUFS3	
hsa046 50	Natural killer cell mediated cytotoxicity	107/710 9	131/81 05	0.98413 3412	1	0.65589 5057	PIK3R1/NFATC2/KLRD1/PTK2B/FYN/ LCK/PIK3CB/CASP3/PIK3R3/NFATC1 /MAPK1/PIK3CD/IFNAR2/VAV3/SH3 BP2/RAET1E/SHC1/PRF1/BRAF/ITGA L/CD244/ICAM2/PLCG1/BID/SH2D1A/ ARAF/IFNAR1/VAV1/FCGR3B/FCGR3 A/NCR1/PPP3CB/PIK3CA/PLCG2/FAS/ PTPN6/PTPN11/LAT/ITGB2/PRKCB/L CP2/PPP3CA/RAF1/KRAS/TNFRSF10B /MAP2K1/MICB/SYK/SHC4/FASLG/M ICA/PPP3R2/SOS1/IFNGR2/VAV2/TNF SF10/TYROBP/PAK1/HLA- G/PIK3R2/SH2D1B/CSF2/GZMB/RAC2	107

							/KLRK1/HLA-A/RAC1/NCR3/ICAM1/CD247/ULBP3/HLA-B/MAPK3/NCR2/HLA-C/IFNA2/ZAP70/SHC3/ULBP1/RAET1G/TNF/NRAS/PPP3CC/GRB2/IFNB1/IFNGR1/KLRC1/SHC2/KLRC3/IFNG/KIR3DL1/HLA-E/IFNA4/HRAS/IFNA1/ULBP2/IFNA21/IFNA14/PPP3R1/PRKCG/RAET1L/KIR2DL1/TNFRSF10A/IFNA16/HCST/IFNA6/FCER1G	
hsa00590	Arachidonic acid metabolism	48/7109	61/8105	0.985777201	1	0.655895057	PLA2G6/PTGS1/TBXAS1/GGT5/CYP2C8/PLB1/EPHX2/CYP4F3/GGT1/PTGES3/GPX8/CYP2B6/JMJD7-PLA2G4B/CYP2C9/PLA2G2D/PLA2G12B/PLA2G4D/PLA2G4F/PLA2G4B/ALOX15/ALOX12/CYP4F2/PLA2G10/PLA2G3/PTGES/PTGES2/AKR1C3/GPX1/CYP2C19/PTGIS/HPGDS/CYP4F8/GPX3/ALOX15B/CYP2U1/CBR1/PLA2G4A/ALOX12B/GPX5/CYP2J2/PLA2G2A/ALOX5/PLA2G12A/PLA2G4C/GPX6/PL	48

							A2G2F/CYP2E1/LTA4H	
hsa05016	Huntington disease	256/7109	306/8105	0.986592283	1	0.655895057	MAPK10/SLC1A2/AP2B1/ITPR1/BDNF/GRIA1/BAX/PLCB2/SP1/DLG4/MAPK8/CREB3L4/ATG13/TP53/SDHC/DNAL1/CREB5/APAF1/NDUFS1/CASP9/PLCB4/DCTN5/POLR2F/KLC2/NDUFC2-KCTD14/GRM5/BECN1/SDHD/GRIN2B/CASP3/AP2S1/DNAH8/CREBBP/PPARGC1A/ATG2A/DNAH2/CREB1/PSMC4/KIF5A/CLTC/DCTN4/NDUFA5/SIN3A/GRIA4/PSMD11/DNAH6/AMBR A1/KLC4/MAP2K7/NDUFC2/DNAI1/BC3/GRIA3/PSMB2/KCNJ10/TBP/CASP8/SLC1A3/DNAH3/HIP1/DCTN2/SOD2/POLR2E/DNAH7/HDAC2/HAP1/GRI N1/WIP1/PLCB3/GPX8/CREB3L2/NDUFC1/DNAH11/AP2A2/CREB3L3/DNAH17/GNAQ/NRF1/DCTN1/PSMA5/DNAH9/NDUFB4/TUBA1A/ULK2/PSMD12/NRBF2/SDHA/DNAH5/UQCRB/VDAC3/ATG2B/CLTCL1/ATP5F1A/DNAH1/EP300/PSMC5/RB1CC1/CREB3/TUBA	256

							L3/PSMA4/PSMA6/VDAC2/NDUFB6/S LC25A4/TUBA1C/ATP5PF/MTOR/PS MD4/TUBB3/KIF5B/ATG101/IFT57/CR EB3L1/GRIA2/CLTB/ERN1/WIP1/AD RM1/SOD1/DNAH12/PSMB5/COX7A2 L/NDUFB3/MAPK9/NDUFA9/AP2M1/ PPIF/DCTN3/PSMA2/TUBB6/DNAL1/ UQCR11/CYCS/ULK1/POLR2J/PPARG /COX7A1/COX7B2/TBPL1/PIK3R4/DN AH10/POLR2G/COX4I2/TRAF2/NDUF B5/PSMD1/POLR2H/TAF4B/CACNA1 B/POLR2B/NDUFS2/ATP5PD/PSMD6/ GPX1/RCOR1/TFAM/VDAC1/ATP5M C3/TAF4/UQCRC2/NDUFA3/TGM2/U QCRHL/NDUFV3/KIF5C/ATP5PB/CO X4I1/POLR2J2/KLC1/BECN2/POLR2J3 /PSMC1/UQCR10/GPX3/TUBB/PSMD1 3/STX1A/COX5B/PSMC2/PLCB1/TUB A8/NDUFS6/NDUFB11/TUBB4A/NDU FA10/DNAI2/MAP3K10/ATG14/PSMB 7/UQCRC1/ACTR1B/NDUFS4/UCP1/N DUFB8/UQCRFS1/AP2A1/ATP5MC2/T	
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							UBA4A/TUBA1B/CYC1/MAP3K5/ND UFA2/GPX5/TBPL2/UQCRQ/PSMA3/C OX7C/ACTR10/POLR2D/TUBA3E/ND UFA6/PSMD8/HTT/PIK3C3/SLC25A31 /NDUFA4L2/POLR2I/COX7A2/UQCR H/PSMB4/DNAL4/ATP5MC1/TUBB8/T UBB4B/PSMB6/PSMD14/ATP5F1B/ND UFS7/POLR2C/ATP5F1D/NDUFB9/RE ST/COX5A/ATP5PO/PSMB3/DNAH14/ SEM1/GPX6/NDUFA4/HDAC1/NDUFB 7/NDUFA11/PSMD3/NDUFA13/TUBA 3D/COX8A/PSMA1/TUBA3C/PSMB1/ COX6C/SDHB/ACTR1A/NDUFB1/SLC 25A5/NDUFS3/PSMD7	
hsa047 14	Thermogenesis	192/710 9	232/81 05	0.99020 6723	1	0.65589 5057	RPS6KA3/PRKACB/TSC2/SMARCA4/ TSC1/ACSL1/MGLL/COA1/GNAS/AD CY10/PRKAG2/SMARCA2/CREB3L4/ ACSL4/SDHC/ACSL5/ATF2/RPS6KB1/ MAPK14/CREB5/NDUFS1/DPF1/SMA RCC2/NDUFC2- KCTD14/ACSL3/ADCY3/PRKG2/SDH D/CPT1A/ADCY5/CPT1B/PPARGC1A/	192

							ACSL6/ADCY7/CNR1/DPF3/SLC25A2 9/CREB1/NDUFA5/FRS2/MAP2K3/SIR T6/NDUFC2/CPT1C/COA4/SMARCD2/ ADCY4/PRKACA/COX15/RPS6KA2/A DCY8/MLST8/CREB3L2/SMARCC1/N DUFC1/ATP5MF/ADCY2/CREB3L3/P RKAG1/FGFR1/NDUFB4/PRKAA1/RP S6KA6/SDHA/ADCY6/KRAS/UQCRB/ KDM3A/ATP5F1A/NDUFAF7/KDM3B/ PRKAA2/ZNF516/COX18/LIPE/COX11 /CREB3/SOS1/PRKG1/PLIN1/NDUFB6 /PRKAB2/ADCY9/ATP5PF/MTOR/AK T1S1/NPR1/BMP8A/CREB3L1/KLB/A RID1A/COX7A2L/NDUFB3/NDUFA9/ ARID1B/UQCR11/RHEB/PRKAB1/ND UFAF6/PPARG/COX7A1/COX7B2/MA PK12/RPS6KA1/CPT2/COX4I2/PRDM1 6/RPTOR/COX20/NDUFB5/SMARCD3/ NDUFS2/ATP5PD/ATP5MC3/UQCRC2 /NDUFA3/NPPA/UQCRHL/FGF21/ND UFV3/COX10/PRKACG/ATP5PB/COX 4I1/MAPK11/ACTG1/NRAS/BMP8B/U	
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							QCR10/MAPK13/GRB2/COA6/COX5B/NDUFS6/NDUFB11/NDUFA10/COX19/NDUFAF2/UQCRC1/ATP5MG/NDUFS4/KDM1A/UCP1/ADCY1/NDUFB8/UQCRFS1/ATP5MC2/COA7/CYC1/COX17/MAP3K5/NDUFA2/NDUFAF3/UQCRQ/COX7C/NDUFA6/PRKAG3/NDUFA4L2/SMARCD1/COA5/ACTL6A/COX7A2/UQCRH/ATP5MC1/HRAS/ATP5F1B/NDUFS7/NPPB/COA3/ATP5F1D/SMARCE1/NDUFB9/COX5A/ATP5PO/GCG/SMARCB1/NDUFAF4/NDUFA4/NDUFB7/RPS6KB2/NDUFA11/NDUFAF5/NDUFA13/NDUFAF8/ACTB/COX8A/S LC25A20/COX6C/SDHB/NDUFB1/NDUFS3/NDUFAF1	
hsa05020	Prion disease	227/7109	273/8105	0.990302704	1	0.655895057	MAPK10/CACNA1C/ITPR1/PRKACB/PIK3R1/BAX/NCAM1/MAPK8/CACNA1D/CREB3L4/SDHC/ATF2/MAPK14/GRIN2A/CREB5/APAF1/NDUFS1/CASP9/FYN/C6/KLC2/NDUFC2-KCTD14/CACNA1F/C8B/SDHD/GRIN	227

							2B/PIK3CB/CASP3/RYR3/PIK3R3/MA PK1/ATF4/PIK3CD/CREB1/PSMC4/KI F5A/CAV1/NDUFA5/GSK3B/ATF6B/P SMD11/KLC4/NDUFC2/CSNK2A1/PS MB2/C7/CCL5/PRNP/GRIN3A/PRKAC A/C1QA/PPP3CB/PIK3CA/GRIN1/RYR 2/NCF2/C1QC/DDIT3/HSPA8/CREB3L 2/NDUFC1/CACNA1S/CREB3L3/PRK CD/CAV2/PSMA5/NDUFB4/TUBA1A/ PSMD12/PPP3CA/SDHA/CYBB/ITPR2/ UQCRB/VDAC3/ATP5F1A/MCU/HSP A1L/PSMC5/IL6/HSPA5/LAMC1/CAV 3/IL1A/PPP3R2/C8A/CREB3/TUBAL3/ RYR1/PSMA4/PSMA6/VDAC2/NDUFB 6/SLC25A4/C5/TUBA1C/ATP5PF/PSM D4/TUBB3/GRIN2D/KIF5B/HSPA6/PI K3R2/CREB3L1/ADRM1/SOD1/PSMB 5/COX7A2L/NDUFB3/MAPK9/NDUFA 9/PPIF/NCF4/PSMA2/RAC2/TUBB6/U QCR11/CYCS/IL1B/COX7A1/COX7B2/ MAPK12/RAC1/STIP1/COX4I2/NDUF B5/BAD/PSMD1/CACNA1B/MAPK3/N	
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							DUF52/ATP5PD/PSMD6/VDAC1/ATP5 MC3/UQCRC2/NDUFA3/UQCRHL/C9/ NDUFV3/KIF5C/PRKACG/C1QB/ATP5 PB/COX4I1/MAPK11/TNF/NOTCH1/K LC1/PSMC1/UQCR10/EIF2AK3/MAPK 13/PPP3CC/TUBB/PSMD13/EIF2S1/CO X5B/PSMC2/TUBA8/CYBA/NDUFS6/ NDUFB11/C8G/TUBB4A/NDUFA10/C SNK2A2/PSMB7/UQCRC1/GRIN2C/N DUF54/HSPA2/NDUFB8/UQCRFS1/AT P5MC2/TUBA4A/TUBA1B/CYC1/NDU FA2/UQCRQ/PSMA3/COX7C/TUBA3E /NDUFA6/PSMD8/CSNK2A3/SLC25A3 1/NDUFA4L2/COX7A2/UQCRH/PSMB 4/ATP5MC1/TUBB8/TUBB4B/PSMB6/ PSMD14/ATP5F1B/NDUFS7/ATP5F1D /NDUFB9/GRIN3B/COX5A/NCAM2/A TP5PO/PSMB3/PPP3R1/SEM1/NDUFA 4/NDUFB7/NDUFA11/PSMD3/NDUFA 13/NCF1/TUBA3D/HSPA1A/COX8A/P SMA1/TUBA3C/PSMB1/COX6C/SDHB /NDUFB1/SLC25A5/NDUFS3/HSPA1B/	
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							PSMD7/EGR1	
hsa054 15	Diabetic cardiomyopathy	167/710 9	203/81 05	0.99157 2904	1	0.65589 5057	MAPK10/PIK3R1/CAMK2G/ATP2A3/P LCB2/TGFBR1/SP1/CD36/TBC1D4/MA PK8/AKT2/SDHC/AKT3/MAPK14/ND UFS1/PLCB4/PDHA1/CAMK2D/SMAD 2/PPARA/NDUFC2- KCTD14/GFPT1/ATP2A2/SDHD/PIK3 CB/CPT1B/NFKB1/INSR/PIK3R3/PIK3 CD/RELA/NDUFA5/SMAD3/MMP2/GS K3B/NDUFC2/PDK2/TGFB2/PDK3/SL C2A4/PTPA/AGTR1/PIK3CA/AKT1/R YR2/NCF2/ATP2A1/AGER/PLCB3/CA MK2B/NDUFC1/PRKCD/CAMK2A/PP P1CB/NDUFB4/PRKCB/PPP1CC/SDH A/CYBB/SLC2A1/GSR/UQCRB/VDAC 3/ATP5F1A/COL3A1/VDAC2/NOS3/N DUFB6/SLC25A4/ATP5PF/IRS1/MTOR /PIK3R2/MMP9/COX7A2L/NDUFB3/M APK9/NDUFA9/PDHB/PPIF/NCF4/RA C2/UQCR11/PARP1/TGFB3/COX7A1/ COX7B2/MAPK12/MPC2/CPT2/G6PD/ RAC1/PDHA2/COX4I2/ACE/NDUFB5/	167

							AGT/COL1A2/NDUFS2/ATP5PD/CMA1/TNNI3/VDAC1/ATP5MC3/UQCRC2/NDUFA3/UQCRHL/NDUFV3/GAPDH/ATP5PB/COX4I1/MAPK11/UQCR10/TGFBR2/MAPK13/COX5B/PLCB1/CYBA/NDUFS6/REN/NDUFB11/NDUFA10/PDK4/UQCRC1/PLN/GFPT2/NDUFS4/INS/CTSD/NDUFB8/UQCRFS1/ATP5MC2/CYC1/NDUFA2/PTEN/UQCRQ/COX7C/NDUFA6/SLC25A31/NDUFA4L2/COX7A2/UQCRH/COL1A1/ATP5MC1/GYS1/ATP5F1B/NDUFS7/ATP5F1D/NDUFB9/COX5A/ATP5PO/NDUFA4/PRKCG/GYS2/NDUFB7/NDUFA11/PRKCA/NDUFA13/NCF1/TGFB1/COX8A/COX6C/SDHB/MPC1/NDUFB1/SLC25A5/NDUFS3	
hsa03040	Spliceosome	122/7109	150/8105	0.991726839	1	0.655895057	SRSF10/HNRNPC/NCBP2/HNRNPA3/ACIN1/U2SURP/HNRNPA1/DDX42/RBMXL1/PRPF38B/CRNKL1/TRA2B/SNU13/CTNNBL1/HNRNPU/LSM8/U2AF2/HSPA8/RP9/DDX5/HNRNPA1L2/US	122

							P39/SRSF6/PQBP1/DDX46/U2AF1L4/R BM25/THOC2/WBP11/PUF60/SRSF1/F US/ISY1/HSPA1L/PPIL1/RBMX/DHX1 6/SRSF7/SRSF4/RBML3/SNRPE/PRP F38A/CDC5L/PPIE/SART1/HSPA6/SF3 B2/TXNL4A/SF3B3/RBM17/AQR/SF3 A3/NCBP1/TRA2A/HNRNPK/RBM8A/ CWC15/HNRNPM/SNRPC/SNRPD2/EF TUD2/SRSF3/PPIH/MAGOHB/SNRNP2 00/ISY1- RAB43/PRPF3/SF3B4/SF3A2/CCDC12/ XAB2/PRPF18/PRPF40B/RBML2/SL U7/DHX38/THOC3/LSM6/SNRPD3/SY F2/SF3A1/CHERP/SRSF5/DHX15/SRSF 2/RBM22/THOC1/ZMAT2/LSM4/BCAS 2/PRPF4/HSPA2/DDX23/PRPF40A/DD X39B/LSM2/SF3B1/SNRPA/SNRPB/D HX8/SRSF8/SNRPB2/EIF4A3/U2AF1/S RSF9/PHF5A/SNRPD1/NCBP2L/PRPF6 /SF3B6/SNW1/PCBP1/CDC40/SNRNP4 0/LSM5/SMNDC1/SNRNP27/HSPA1A/ PRPF8/SNRPG/SF3B5/HSPA1B	
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hsa046 12	Antigen processing and presentation	61/7109	78/810 5	0.99445 5517	1	0.65589 5057	PSME3/KLRD1/CD74/CTSB/CANX/CII TA/NFYA/LGMN/CREB1/CTSS/TAPB P/HLA- DQB1/CTSL/RFX5/HSP90AB1/NFYC/ HSPA8/HLA- F/HSP90AA1/HSPA1L/HSPA5/CD4/HL A-DQA1/TAP2/HLA-G/HSPA6/HLA- DPB1/PDIA3/HLA- DMB/KIR2DL4/HLA-A/HLA- DPA1/HLA-B/CD8A/HLA- C/TNF/CD8B/RFXANK/HLA- DQA2/IFI30/HLA-DRB1/PSME1/HLA- DOB/TAP1/HLA- DOA/HSPA2/CD8B2/HLA- DMA/KLRC1/KLRC3/IFNG/PSME2/KI R3DL1/HLA-E/HLA- DRB5/HSPA4/B2M/NFYB/KIR2DL1/H SPA1A/HSPA1B	61
hsa030 13	RNA transport	150/710 9	186/81 05	0.99813 8685	1	0.65589 5057	EIF4E/EIF4G1/EIF4G3/EIF4B/FXR1/U BE2I/NCBP2/FMR1/POM121/NUP210L /NUP153/NUP155/RNPS1/ACIN1/EIF4 E2/EIF2B3/NUP98/RPP38/NUP62/CYFI	150

							P2/SMN2/CLNS1A/PRMT5/SMN1/RA NGAP1/NXF1/SEN2/EIF3C/XPO1/NU P58/NUP160/NUP214/PABPC4/THOC5/ TARDBP/RPP40/EIF5/AAAS/RPP30/U PF3A/CASC3/NUP107/CYFIP1/GEMIN 4/SEH1L/UPF2/THOC2/RAN/ELAC2/P OM121C/KPNB1/NUP210/EIF4EBP2/T HOC6/FUS/NMD3/NUP50/NXF2/NXF2 B/EIF3CL/NXT2/PABPC1L2A/UPF1/D DX19A/EIF2B4/RANBP2/NUP85/EIF3I /SEC13/EIF2S2/POM121L2/EIF3A/PAB PC1L2B/GEMIN2/NUP35/NCBP1/SNU PN/NXF3/RBM8A/DDX19B/RAE1/SAP 18/GEMIN8/POP1/PABPC3/PYM1/NUP 54/TACC3/PHAX/RPP14/NUP205/GEM IN5/EIF5B/NUP43/TPR/NUP88/MAGO HB/GLE1/EIF2S3/XPOT/NDC1/XPO5/ RPP25/NUP93/EEF1A1/TRNT1/ELAC1 /EIF3B/THOC3/PABPC5/DDX20/POP5/ GEMIN7/NXT1/PAIP1/NUP188/PABPC 4L/POP4/EIF4A1/EIF2S1/EIF3E/EIF3H/ THOC1/EIF4EBP3/FXR2/SRRM1/EIF3J	
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							/UPF3B/EIF4A2/EIF2B2/EIF2B1/EIF4E1B/NXF5/EIF1B/DDX39B/PNN/SUMO2/NUP133/SUMO1/EIF4A3/NCBP2L/PO7/EIF2B5/TGS1/NUP37/GEMIN6/THOC7/EIF1/RPP25L/EIF3D	
hsa05012	Parkinson disease	203/7109	249/8105	0.998432145	1	0.655895057	MAPK10/ITPR1/PRKACB/CAMK2G/BAX/SLC18A1/DAXX/MAPT/GNAS/MAPK8/TP53/BCL2L1/SDHC/SNCA/ADORA2A/APAF1/NDUFS1/CASP9/GNAL/KLC2/CAMK2D/NDUFC2-KCTD14/SNCAIP/CALML4/LRRK2/SDHD/ADCY5/CASP3/CALM3/RYR3/ATF4/PSMC4/KIF5A/NDUFA5/MFN1/PSMD11/KLC4/NFE2L2/NDUFC2/PLCG1/PSMB2/UBA52/PRKN/UBA7/MFN2/PRKACA/GNAI2/HTRA2/TRAP1/DDIT3/CAMK2B/NDUFC1/CAMK2A/TXN2/PSMA5/NDUFB4/TUBA1A/RPS27A/PSMD12/SDHA/DRD2/ATF6/ITPR2/UQCRB/VDAC3/UBE2L3/ATP5F1A/UBE2G2/MCU/DRD1/PSMC5/HSPA5/MAOA/UBE2J2/TUBAL3/PSMA4/PSMA6/VD	203

							AC2/NDUFB6/SLC25A4/TUBA1C/GPR 37/ATP5PF/PSMD4/TUBB3/KIF5B/PIN K1/ERN1/ADRM1/PSMB5/COX7A2L/ NDUFB3/MAPK9/NDUFA9/PPIF/PAR K7/PSMA2/UBE2J1/TUBB6/DUSP1/U QCR11/CYCS/COX7A1/COX7B2/SLC6 A3/COX4I2/UBE2L6/NDUFB5/PSMD1/ UBA1/NDUFS2/ATP5PD/PSMD6/VDA C1/ATP5MC3/UQCRC2/NDUFA3/UQC RHL/NDUFV3/UBE2G1/KIF5C/PRKA CG/ATP5PB/COX4I1/CALM1/KLC1/PS MC1/UQCR10/EIF2AK3/MAOB/XBP1/ TUBB/CALML6/PSMD13/EIF2S1/COX 5B/PSMC2/TUBA8/NDUFS6/NDUFB11 /TUBB4A/NDUFA10/PSMB7/CALML3 /UQCRC1/TXN/NDUFS4/UCHL1/NDU FB8/UQCRFS1/ATP5MC2/TUBA4A/T UBA1B/CYC1/MAP3K5/GNAI1/NDUF A2/GNAI3/UBC/UQCRQ/PSMA3/COX 7C/TUBA3E/NDUFA6/PSMD8/SLC25A 31/NDUFA4L2/COX7A2/UQCRH/PSM B4/ATP5MC1/TUBB8/TUBB4B/PSMB	
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							6/PSMD14/ATP5F1B/NDUFS7/CALML5/ATP5F1D/CALM2/NDUFB9/COX5A/ATP5PO/PSMB3/SEM1/NDUFA4/NDUFB7/NDUFA11/PSMD3/NDUFA13/TUBA3D/COX8A/PSMA1/TUBA3C/PSMB1/COX6C/SDHB/NDUFB1/SLC25A5/NDUFS3/SLC18A2/UBB/PSMD7	
hsa05171	Coronavirus disease - COVID-19	188/7109	232/8105	0.998897637	1	0.655895057	MAPK10/NLRP3/PIK3R1/JAK1/IL6ST/ADAR/C1S/MAPK8/NRP1/MAPK14/C2/RPL15/MASP1/C6/IRAK4/C1R/C8B/TLR4/PIK3CB/NFKB1/CASP1/PIK3R3/OAS2/RPL10/MAPK1/MAVS/PIK3CD/C3/IFNAR2/RELA/OAS1/RPL28/SELP/RPS24/IRAK1/STAT3/MYD88/PLCG1/EI2F2/IRAK2/C7/TLR2/AGTR1/UBA52/VWF/TLR8/IFNAR1/RPS29/TRAF6/IL6R/IKBKG/C3AR1/C1QA/IKBKE/MX1/TAB2/PIK3CA/FGA/C4A/C1QC/FCGR2A/IRF3/PLCG2/RPL22L1/RPL36A-HNRNPH2/IKBKB/OAS3/PRKCB/RPL13A/RPS27A/TMPRSS2/CYBB/STAT2/RPL22/CFB/RPS3/EGFR/RPL17/STAT1	188

						/SYK/F2/IL6/CSF3/CFD/C8A/RPS14/C5 /DDX58/RPS4Y2/CHUK/PIK3R2/CSF2/ RPS10- NUDT3/MAPK9/TLR3/IL12B/MMP1/T YK2/HBEGF/FOS/IL1B/RPL27A/MAP K12/TRAF3/MAS1/IFIH1/TBK1/IL12A/ ACE/C4B/MAPK3/RPL13/MASP2/C9/N FKBIA/IFNA2/C1QB/MAPK11/TNF/RP L10L/MBL2/RPL32/F13B/F13A1/FGG/ ACE2/RPS20/MAPK13/CXCL10/ADA M17/RPL41/RPL19/RPL34/TNFRSF1A/ IFNB1/FGB/RPL29/RPL3/C8G/RPS23/I RF9/CXCL8/RPLP0/RPL23/RPS4X/RPL 37/RPL21/RPS15/RPS9/IFNA4/RPS10/C 5AR1/FAU/NFKBIB/MX2/RSL24D1/RP L27/IFNA1/RPL17- C18orf32/RPS17/RPS7/RPS8/RPL26/IF NA21/IFNA14/RPL36A/RPL36/RPL14/ RPS26/PRKCG/MMP3/JUN/RPL12/RPS 4Y1/CCL2/IL2/RPS27L/RPS18/RPL30/ RPL35A/CGAS/IFNA16/RPS5/RPL7A/ RPL38/RPL3L/IFNA6/RPL4/RPL11	
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hsa05203	Viral carcinogenesis	159/7109	204/8105	0.999975422	1	0.655895057	UBE3A/PRKACB/HDAC9/PIK3R1/JAK1/YWHAZ/HDAC8/PXN/BAX/DLG1/IL6ST/CCR3/CREB3L4/HDAC6/TP53/ATF2/HDAC7/CREB5/MDM2/RBPJ/CDC42/CCNE1/PKM/PIK3CB/CASP3/NFKB1/CCNA1/CREBBP/PIK3R3/RHOA/MAPK1/ATF4/PIK3CD/C3/RELA/GTF2A1/CREB1/ATF6B/STAT5A/CCND3/LTBR/STAT3/CDK2/CHEK1/TRAF5/TRAF1/DDX3X/EIF2AK2/TBP/CASP8/SCIN/HDAC11/PRKACA/IKBKG/HDAC2/PIK3CA/SKP2/IRF3/CCND2/EGR2/CREB3L2/HDAC4/REL/GTF2A1L/HDAC10/CREB3L3/USP7/HDAC5/CHD4/HLA-F/SP100/ATP6V0D1/KRAS/IRF7/GTF2H2/VDAC3/MAD1L1/SYK/SCRIB/EP300/NFKB2/CCR4/RBPJL/RANBP1/GSN/CREB3/GTF2H1/RASA2/DNAJA3/GTF2E2/UBR4/CCNE2/HPN/CDK4/HLA-G/JAK3/PIK3R2/CREB3L1/RBL2/CDK6/GTF2H3/RBL1/HNRNPK/TBPL1/TRAF3/CCR5/LYN/CCND1/HLA-	159
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							A/RAC1/GTF2E1/TRAF2/GTF2A2/EGR3/BAD/RB1/SRC/HLA-B/MAPK3/HLA-C/DDB1/PMAIP1/MRPS18B/NFKBIA/CDKN1A/GTF2H4/STAT5B/CDKN1B/ACTN1/PRKACG/YWHAE/YWHAG/NRAS/PSMC1/GRB2/CDKN2A/MAPKAPK2/YWHAH/SRF/IRF9/TRADD/CDC20/HDAC3/CDK1/TBPL2/HLA-E/HRAS/POLB/ATP6V0D2/YWHAB/SNW1/HDAC1/KAT2B/CCNA2/GTF2B/JUN/LOC102724334/SND1/KAT2A	
hsa04217	Necroptosis	120/7109	159/8105	0.99999462	1	0.655895057	MAPK10/NLRP3/JAK1/CYLD/CAMK2G/BAX/MAPK8/GLUL/CFLAR/STAT6/CAMK2D/PPIA/TNFAIP3/AIFM1/RBCK1/CAPN1/TLR4/CASP1/XIAP/IFNAR2/CHMP3/STAT5A/STAT3/TRAF5/USP21/BID/EIF2AK2/CASP8/IFNAR1/HSP90AB1/RIPK1/CAMK2B/SHARPIN/DNM1L/JMJD7-PLA2G4B/CAMK2A/FAS/STAT4/HSP90AA1/GLUD2/CYBB/STAT2/TNFRSF10B/VDAC3/STAT1/FASLG/BIRC3/IL1	120

							A/BCL2/IFNGR2/VDAC2/TNFSF10/SLC25A4/PYGB/PLA2G4D/PLA2G4F/PLA2G4B/JAK3/ALOX15/CHMP6/PYGL/MAPK9/TLR3/CHMP2A/JAK2/VPS4B/TYK2/HMGB1/PARP1/IL1B/IL33/CHMP5/TRAF2/SMPD1/MLKL/RNF31/VDAC1/CHMP7/CHMP1A/FAF1/IFNA2/STAT5B/SPATA2/PPID/TNF/CHMP4A/FTH1/RNF103-CHMP3/FTL/TRPM7/TNFRSF1A/IFNB1/VPS4A/IFNGR1/ZBP1/IRF9/SPATA2L/TICAM2/PLA2G4A/TRADD/GLUD1/PGAM5/TICAM1/RIPK3/IFNG/CHMP1B/IFNA4/SQSTM1/SLC25A31/PYGM/IFNA1/CHMP4B/IFNA21/IFNA14/PLA2G4C/FADD/TNFRSF10A/IFNA16/SLC25A5/IFNA6	
hsa00190	Oxidative phosphorylation	98/7109	133/8105	0.999997401	1	0.655895057	SDHC/NDUFS1/NDUFC2-KCTD14/SDHD/ATP6AP1/NDUFA5/NDUFC2/ATP6V0A1/COX15/ATP6V0A4/ATP6V1C2/NDUFC1/ATP5MF/PPA2/ATP12A/NDUFB4/SDHA/ATP6V0D1/	98

							UQCRB/ATP5F1A/COX11/NDUFB6/ATP5PF/ATP6V1E1/ATP6V0B/ATP6V1H/COX7A2L/NDUFB3/NDUFA9/ATP6V1E2/ATP6V0E1/UQCR11/COX7A1/COX7B2/ATP6V1D/COX4I2/NDUFB5/ATP6V0A2/NDUFS2/ATP5PD/ATP6V1C1/ATP6V1B2/ATP5MC3/UQCRC2/NDUFA3/UQCRHL/NDUFV3/COX10/ATP5PB/COX4I1/ATP6V0E2/UQCR10/ATP4A/LHPP/ATP6V1A/COX5B/NDUFS6/NDUFB11/NDUFA10/ATP6V1G2/UQCR1/ATP5MG/NDUFS4/ATP6V1B1/NDUFB8/UQCRFS1/ATP5MC2/CYC1/COX17/NDUFA2/UQCRQ/COX7C/NDUFA6/TCIRG1/NDUFA4L2/COX7A2/UQCRH/ATP5MC1/ATP5F1B/ATP6V1F/NDUFS7/ATP5F1D/ATP6V1G3/NDUFB9/COX5A/ATP5PO/ATP6V0D2/NDUFA4/NDUFB7/NDUFA11/ATP6V1G1/NDUFA13/ATP4B/COX8A/COX6C/SDHB/NDUFB1/NDUFS3	
hsa030	Ribosome	74/7109	110/81	0.99999	1	0.65589	REXO5/UTP15/TCOF1/XRN1/GNL3L/	74

08	biogenesis in eukaryotes		05	9996		5057	RPP38/RCL1/UTP14A/NOL6/CSNK2A1/DROSHA/MDN1/EFL1/NXF1/XPO1/HEATR1/SNU13/FCF1/IMP4/NVL/RPP40/BMS1/RPP30/WDR75/RBM28/GNL3/UTP4/RAN/SPATA5/NAT10/LSG1/NMD3/NXF2/NXF2B/NOB1/NXT2/RRP7A/FBL/EIF6/GAR1/WDR36/NXF3/RIOK1/POP1/AK6/RPP25/REXO1/POP5/NXT1/WDR3/UTP14C/POP4/REXO2/CSNK2A2/GTPBP4/DKC1/UTP6/WDR43/RIOK2/UTP18/NXF5/NOP58/NHP2/CSNK2A3/NOP56/IMP3/SBDS/PWP2/POP7/GNL2/TBL3/FBLL1/RPP25L/XRN2	
hsa03010	Ribosome	101/7109	158/8105	1	1	0.655895057	RPL15/RPL10/RPL28/RPS24/UBA52/RPS29/MRPS11/MRPL28/MRPL11/MRPL35/RPL22L1/RPL36A-HNRNPH2/RPL13A/RPS27A/MRPS21/RPL22/RPS3/MRPL22/MRPS12/RPL17/MRPS18A/MRPL19/MRPL15/MRPL9/RPS14/MRPL17/RPS4Y2/RPS10-NUDT3/MRPS18C/MRPL18/MRPL23/RPL27A/MRPL1/MRPL33/MRPL2/MRP	101

							L34/RPL13/MRPS5/MRPS7/MRPS6/MRPS14/RPL10L/RPL32/RPS20/RPL41/RPL19/MRPS9/RPL34/MRPS17/MRPL10/RPL29/RPL3/RPS23/MRPL3/MRPL20/RPLP0/MRPL4/RPL23/RPS4X/RPL37/RPL21/RPS15/MRPL21/RPS9/RPS10/FAU/MRPS10/MRPS16/RSL24D1/MRPL14/RPL27/RPL17-C18orf32/RPS17/RPS7/MRPL36/RPS8/MRPL12/RPL26/MRPS2/RPL36A/RPL36/RPL14/RPS26/MRPL16/RPL12/MRPL24/RPS4Y1/MRPL27/RPS27L/MRPL30/RPS18/RPL30/RPL35A/MRPS15/RPS5/RPL7A/RPL38/MRPL13/RPL3L/RPL4/RPL11	
hsa04740	Olfactory transduction	328/7109	443/8105	1	1	0.655895057	SLC8A1/PRKACB/PDE1C/CAMK2G/NCALD/GNAL/CAMK2D/ADCY3/PRKG2/PDE1B/CALML4/ARRB1/SLC24A4/CALM3/ARRB2/SLC8A3/PDE1A/OR2F1/OR3A1/PDE2A/PRKACA/CAMK2B/CNGB1/CAMK2A/OR4K3/OR10H1/OR10J3/OR2T10/OR8B3/OR10A3/OR13A1	328

							/PRKG1/OR3A3/OR5AP2/CNGA3/OR5 1E1/GNG7/OR4F16/OR52M1/CNGA2/ OR8A1/OR9Q1/OR6J1/OR5M9/OR3A2/ OR2S2/OR51G2/OR6P1/OR6S1/OR10K 1/OR4D5/OR8B2/OR1F1/OR2T8/OR2K 2/OR2D2/OR2A5/OR11H2/OR10G3/OR 4D9/GNB1/OR2T4/OR10A5/ANO2/OR 5C1/OR2A1/LOC102723532/OR1J1/OR 51F1/OR51G1/OR51I2/OR52E5/OR6K2 /OR6C76/OR8U1/OR10W1/OR4D6/OR 5AR1/OR5B2/OR14A2/OR4C5/OR56A4 /OR6X1/OR11H12/OR4K5/OR5AU1/O R2Z1/OR4C12/SLC8A2/OR51E2/OR10 S1/OR2H1/CNGA4/PRKACG/OR1Q1/O R52W1/OR4A16/OR1E1/OR2M4/OR4E 1/OR9I1/CALM1/OR2L13/OR2B11/OR 56A5/OR6N2/OR4M1/OR1G1/OR2T6/O R6N1/OR6B1/CALML6/OR13G1/OR13 F1/OR1B1/OR52B4/OR52A5/OR10A4/ OR10K2/OR6C70/OR4K17/GRK2/OR8 H2/OR8H3/OR10J1/OR10H4/OR4F3/O R2T1/OR2T7/OR4F29/OR13D1/OR52I2	
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						/OR51T1/OR52D1/OR2D3/OR4F21/OR 8D2/OR6C75/OR6C65/OR4K14/OR11G 2/OR1I1/OR10H3/OR11H1/OR5I1/OR5 M8/OR6Q1/OR4F15/GNG13/OR51L1/O R6K6/OR14J1/OR12D3/GUCY2D/OR4 D2/OR1L4/CALML3/OR2J1/OR7A5/O R5K4/OR52B2/RGS2/OR10G8/OR1E2/ OR2C3/OR2T5/OR4X2/OR6K3/OR2A4 2/OR1D5/OR1L8/OR2L2/OR52B6/OR1 0C1/OR5B21/OR10T2/OR4Q3/OR1A2/ OR1S2/OR2V1/OR2V2/OR14I1/OR4F5/ OR13C8/OR52R1/OR52J3/OR52E6/OR 8S1/OR2F2/OR2A12/OR2B2/OR2B6/O R11A1/OR4E2/OR4M2/OR1A1/OR9G4/ OR2T27/GRK3/OR51B4/OR10V1/OR4F 6/OR5K1/OR8J1/OR8B12/OR11H6/OR1 C1/OR2M2/OR2M3/OR1J4/OR51M1/O R52N5/OR10J4/OR4C15/OR2T11/OR14 K1/OR13C9/OR52I1/OR51A4/OR51A2/ OR2A14/OR10G2/OR7G3/OR6B3/OR2 C1/OR5D16/OR52N1/OR5A2/OR8D1/O R2AE1/OR10H2/OR10H5/OR4X1/OR51	
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							B5/OR10G4/OR4C46/CALML5/OR52H1/OR56B4/OR5AC2/OR5H1/OR4N4/OR7D2/CALM2/OR4N2/OR2T2/OR2T35/OR2G3/OR51D1/OR51B2/OR6V1/OR4F17/OR4C11/OR5W2/OR5AS1/OR8H1/OR8K3/OR1K1/OR52A1/OR6Y1/OR6M1/OR4K2/OR5H15/OR4A15/OR5M11/OR5B17/OR2W3/OR2AJ1/OR2L5/OR4B1/OR56B1/OR52N4/OR56A3/OR6A2/OR10A2/OR10X1/OR10Z1/OR2A2/OR8D4/OR10G6/OR8B8/OR10A7/OR6C3/OR11H4/OR1M1/OR7G1/OR5H14/OR4C6/OR5D14/OR10AG1/OR5J2/OR5M1/OR5A1/OR5L1/OR52K2/OR2L8/OR2L3/OR51S1/OR2AG2/OR2J3/OR4S2/OR4D11/OR52E1/OR11L1/OR1J2/OR1N2/OR1L3/OR51B6/OR56A1/OR10A6/OR10J5/OR9A2/OR9K2/OR6C74/OR7A10/OR2A4/OR52K1/OR4D10/OR13C4/OR52N2/OR5P2/OR2AT4/OR2J2/OR2H2/OR4A47/OR9A4/OR8K5/OR5B3	
hsa009	Aminoacyl-tRNA	25/7109	66/810	1	1	0.65589	TARS2/VARS2/GATC/FARS2/WARS2/	25

70	biosynthesis		5			5057	EARS2/AARS2/SARS2/LARS2/QRSL1/ RARS2/GATB/HARS2/FARSA/NARS2/ IARS2/YARS2/FARSB/PSTK/MARS2/ CARS2/MTFMT/DARS2/PARS2/SEPSE CS	
hsa046 13	Neutrophil extracellular trap formation	101/710 9	190/81 05	1	1	0.65589 5057	HDAC9/PIK3R1/HDAC8/CLCN3/CLC N5/PLCB2/CR1/HDAC6/AKT2/AKT3/ MAPK14/HDAC7/CLEC7A/PLCB4/TL R4/PIK3CB/NFKB1/CASP1/PIK3R3/M APK1/PIK3CD/C3/RELA/FPR2/SELP/C LCN4/ITGAM/FPR3/ITGAL/PLCG1/TL R2/VWF/TLR8/HDAC11/FCGR3B/FCG R3A/CASP4/HDAC2/PIK3CA/AKT1/F GA/NCF2/AGER/ATG7/FCGR2A/PLC B3/PLCG2/HDAC4/HDAC10/ITGA2B/ HDAC5/ITGB2/PRKCB/RAF1/CYBB/I TGB3/VDAC3/MAP2K1/SYK/AQP9/V DAC2/SLC25A4/C5/MTOR/PIK3R2/GS DMD/PPIF/NCF4/RAC2/HMGB1/GP1B A/MAPK12/RAC1/SELPLG/FPR1/SRC/ MAPK3/VDAC1/MPO/MAPK11/ACTG 1/FGG/MAPK13/SIGLEC9/AZU1/PLCB	101

							1/FGB/CYBA/PADI4/HDAC3/C5AR1/F CGR1A/SLC25A31/CAMP/PRKCG/HD AC1/NCF1/LOC102724334/ACTB/SLC 25A5/CR1L	
hsa050 34	Alcoholism	99/7109	187/81 05	1	1	0.65589 5057	PRKACB/BDNF/HDAC9/HDAC8/NTR K2/SLC18A1/CAMKK2/GNAS/CREB3 L4/HDAC6/GNG2/SLC29A1/ATF2/AD ORA2A/HDAC7/GRIN2A/CREB5/PDY N/CALML4/GRIN2B/FOSB/ADCY5/C ALM3/DDC/MAPK1/ATF4/CREB1/SH C1/ATF6B/BRAF/PKIA/SLC29A2/GNB 5/ARAF/CAMKK1/PPP1R1B/HDAC11/ GRIN3A/PRKACA/GNG4/CAMK4/HD AC2/GNAI2/GRIN1/CREB3L2/HDAC4/ HDAC10/CREB3L3/HDAC5/PPP1CB/P PP1CC/RAF1/KRAS/DRD2/GNGT2/M AP2K1/SHC4/DRD1/MAOA/CREB3/S OS1/GRIN2D/GNG7/CREB3L1/GNB1/ SLC6A3/SLC29A3/MAPK3/GNAO1/SH C3/PRKACG/CALM1/NRAS/MAOB/G RB2/GNB4/CALML6/GNG13/CALML3 /GNG12/GRIN2C/ADORA2B/NPY/HD	99

							AC3/GNB3/GNAI1/GNAI3/SHC2/GNB2/GNGT1/CRH/GNG3/HRAS/CALML5/CALM2/GRIN3B/HDAC1/LOC102724334/SLC18A2	
hsa05206	MicroRNAs in cancer	154/7109	310/8105	1	1	0.655895057	FOXP1/BCL2L11/BRCA1/TP63/PIK3R1/CD44/MET/MDM4/VEGFA/BMF/UBE2I/PAK4/EFNA5/CDC25C/TP53/TNC/IGF2BP1/DNMT3B/CDC25B/DICER1/MDM2/MCL1/TNR/DNMT3A/CCNE1/STMN1/ABCC1/ERBB2/RPS6KA5/PIK3CB/CASP3/NFKB1/FZD3/CREBBP/PIK3R3/RHOA/EFNA4/MAPK1/PIK3CD/PLAU/SHC1/ZEB2/ZEB1/APC/STAT3/MAPK7/TPM1/NOTCH2/PLCG1/TGFB2/MYC/E2F3/ATM/EFNA1/RASSF1/KIF23/RDX/ABCB1/EZH2/HDAC2/PIK3CA/TRIM71/PDGFR/PLCG2/CCND2/IRS2/HDAC4/E2F2/ERBB3/IKBKB/HDAC5/PDCD4/PRKCB/RAF1/KRAS/ITGB3/NOTCH4/MAP2K1/PRKCE/HMGA2/EGFR/GLS2/MMP16/GLS/EP300/BCL2L2/SHC4/ITGA5/SOS1/BCL2/CRK/T	154

							NN/CCNG1/THBS1/IRS1/MTOR/SIRT1 /CCNE2/PIK3R2/MMP9/WNT3/APC2/C DK6/PDGFRB/NOTCH3/HNRNPK/EF NA3/CRKL/MARCKS/CYP24A1/CCN D1/SOX4/CDC25A/CYP1B1/SPRY2/RP TOR/ABL1/MAPK3/BMP2/PDGFB/C DCA5/SERPINB5/CDKN1A/DDIT4/CD KN1B/VIM/ROCK1/NOTCH1/ZFPM2/ EZR/NRAS/FGFR3/GRB2/DNMT1/SLC 7A1/CDKN2A/PIM1/TNXB/E2F1/REC K/ST14/SLC45A3/PTEN/COMMD3- BMI1/PDGFA/HRAS/TIMP3/FSCN1/PR KCG/HDAC1/HOXD10/EFNA2/SOCS1/ BMI1	
hsa053 22	Systemic lupus erythematosus	48/7109	136/81 05	1	1	0.65589 5057	C1S/CD86/CD28/C2/GRIN2A/C6/C1R/ C8B/GRIN2B/C3/C7/HLA- DQB1/FCGR3B/FCGR3A/C1QA/C4A/C 1QC/FCGR2A/C8A/HLA- DQA1/CD80/C5/SSB/HLA-DPB1/HLA- DMB/C4B/HLA- DPA1/CD40/C9/ACTN1/C1QB/TNF/TR IM21/SNRPD3/HLA-DQA2/HLA-	48

							DRB1/HLA-DOB/C8G/HLA-DOA/HLA-DMA/IFNG/SNRPB/FCGR1A/IL10/HLA-DRB5/SNRPD1/CD40LG/LOC102724334	
B, Blue								
ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	count
hsa04360	Axon guidance	83/2512	182/8105	2.01809E-05	0.003321131	0.002475839	PTCH1/NFATC4/EPHA5/FZD3/PTK2/TRPC4/CAMK2B/ARHGEF12/CFL2/SSH2/FYN/SEMA7A/SLIT3/RGS3/SEMA6C/EPHA7/BMPR1B/UNC5D/EPHA6/PPP3CB/CAMK2G/ABLIM3/LRRC4C/EPHA3/ITGB1/EPHB4/MAPK3/PIK3CD/KRAS/MYL12B/PPP3CA/SLIT2/NFATC2/SEMA4D/SEMA3B/NEO1/L1CAM/ENAH/SRGAP2/PAK1/CXCL12/SRGAP1/SRGAP3/SEMA5B/PLXNA4/MET/RAF1/GSK3B/RYK/SEMA3D/RHOD/CXCR4/RASA1/PAK4/LIMK2/PIK3R3/GNAI3/RAC2/PPP3R1/SEMA5A/PLXNA1/	83

							SRC/BMPR2/NTNG1/CDC42/PAK5/WNT5A/SEMA3C/PLXNB2/PLXNA2/PLXNB1/BMP7/PIK3CA/PIK3R1/WNT5B/PLXNC1/LRRC4/MYL12A/ROCK1/EPHB3/EPHA4/TRPC5/DCC	
hsa04912	GnRH signaling pathway	48/2512	93/8105	2.50607E-05	0.003321131	0.002475839	CACNA1C/ITPR1/PRKACB/CAMK2B/CACNA1F/MAPK8/CAMK2G/SOS2/MAPK3/EGFR/KRAS/MAPK14/CACNA1D/MAP3K3/CGA/MAP2K4/ATF4/ADCY7/ADCY3/PLCB1/RAF1/ADCY8/CALM1/ITPR3/MAP2K6/JMJD7-PLA2G4B/PLD1/MMP14/MAP3K1/MAP3K4/PLA2G4F/SRC/GNAS/MAPK9/GNAQ/ADCY2/ITPR2/CDC42/PRKCB/GNRH1/CACNA1S/ADCY4/ADCY9/PLA2G4B/JUN/MAPK10/HBEGF/PLA2G4E	48
hsa04218	Cellular senescence	72/2512	156/8105	4.3319E-05	0.003321131	0.002475839	ITPR1/NFATC4/NFATC1/RASSF5/HIPK3/BTRC/SMAD2/FBXW11/MDM2/CDK2/ATM/CAPN1/E2F3/RBBP4/CCNE2/PPP3CB/FOXO1/MAPK3/PIK3CD/KRAS/MAPK14/ATR/CACNA1D/PPP3CA/CCND3/NFATC2/TSC2/CDK6/HIPK	72

							2/FOXO3/IL6/HIPK1/RAD1/RAF1/TRA F3IP2/ZFP36L1/CALM1/SMAD3/ITPR3 /TGFB1/MAP2K6/CDC25A/MRE11/C DKN2B/TRPM7/PIK3R3/ETS1/TP53/PP P3R1/CCNA2/RBL2/RB1/CCNB3/MRA S/ITPR2/E2F5/IL1A/CAPN2/ZFP36L2/ RBL1/PIK3CA/AKT2/PIK3R1/LIN9/SL C25A5/FOXO1/GADD45B/TGFB3/RA D9B/PPID/KIR2DL4/MYBL2	
hsa048 10	Regulation of actin cytoskeleton	95/2512	218/81 05	4.91757 E-05	0.00332 1131	0.00247 5839	ARHGEF7/DIAPH3/FGFR2/FGF1/PTK 2/RDX/IQGAP2/SPATA13/FN1/PPP1R1 2B/ARHGEF12/DIAPH1/CFL2/KNG1/S SH2/ITGB6/CYFIP1/PIP4K2C/WASF1/ EGF/CYFIP2/FGFR1/SOS2/LPAR4/ITG B1/MAPK3/EGFR/MYH10/PIK3CD/KR AS/ITGA6/ITGAM/MYL12B/ARHGEF 1/ENAH/PAK1/CXCL12/BRAF/CRKL/ GSN/ITGA5/ITGAD/F2R/ACTR3/IQGA P1/PDGFD/ITGA3/RAF1/TIAM1/ITGA 2/EZR/APC/GIT1/PIP5K1C/CXCR4/PA K4/ITGA10/LIMK2/VAV3/GNA13/PIK 3R3/MYLK3/SLC9A1/PIP4K2B/RAC2/	95

							ARPC3/SRC/PDGFRB/MRAS/ARHGA P35/FGF21/GNG12/CDC42/PAK5/PDG FC/PIP5K1B/PXN/CHRM5/ITGA11/MS N/FGF17/ITGB5/PIK3CA/PIK3R1/MYL K4/ITGAE/MYL12A/IQGAP3/NCKAP1 /ITGAL/ROCK1/PPP1R12C/CHRM1/IT GA4/ITGB3	
hsa054 10	Hypertrophic cardiomyopathy	46/2512	90/810 5	5.04731 E-05	0.00332 1131	0.00247 5839	CACNA1C/TTN/PRKAG2/CACNB4/C ACNB2/TNNT2/SLC8A1/CACNA1F/A TP2A1/ITGB6/CACNA2D2/LAMA2/AT P2A2/IGF1/ITGB1/ITGA6/CACNA1D/S GCD/IL6/ITGA5/TPM3/ITGA3/PRKAA 1/ITGA2/ITGA10/ACE/ATP2A3/MYH7 /LAMA1/CACNG8/DAG1/SLC8A2/ITG A11/ITGB5/PRKAG3/CACNA1S/CAC NA2D1/PRKAB2/TPM1/TGFB3/AGT/ MYBPC3/SGCB/ITGA4/ITGB3/MYH6	46
hsa054 14	Dilated cardiomyopathy	48/2512	96/810 5	7.18137 E-05	0.00393 7786	0.00293 5544	CACNA1C/TTN/CACNB4/CACNB2/PR KACB/TNNT2/SLC8A1/CACNA1F/AT P2A1/ITGB6/CACNA2D2/LAMA2/ATP 2A2/IGF1/ITGB1/ITGA6/CACNA1D/S GCD/ITGA5/ADCY7/ADCY3/TPM3/IT	48

							GA3/ITGA2/ADCY8/ITGA10/ATP2A3/MYH7/LAMA1/CACNG8/GNAS/ADCY2/DAG1/SLC8A2/ITGA11/ITGB5/CACNA1S/CACNA2D1/TPM1/TGFB3/AGT/MYBPC3/ADCY4/ADCY9/SGCB/ITGA4/ITGB3/MYH6	
hsa045 50	Signaling pathways regulating pluripotency of stem cells	66/2512	143/81 05	8.89697 E-05	0.00418 1576	0.00311 7284	CTNNB1/FGFR2/JAK1/FZD3/TCF7/SMAD2/RIF1/TCF3/BMPRI1/HOXA1/FGFR1/IGF1/MAPK3/PIK3CD/KRAS/IL6ST/MAPK14/WNT2B/SMARCA1/JARID2/ACVR2A/SETDB1/PCGF3/DVL3/DUSP9/ZFXH3/SKIL/KLF4/STAT3/RAF1/GSK3B/FZD4/SMAD3/ACVR1C/APC/LIFR/OTX1/PCGF5/WNT10B/PIK3R3/NODAL/HOXD1/WNT9B/AXIN2/FZD10/KAT6A/INHBC/BMPRI2/WNT5A/INHBB/INHBA/BMI1/LIF/PIK3CA/AKT2/PIK3R1/WNT8A/WNT5B/PAX6/ZIC3/ID4/ACVR2B/FZD5/FZD8/ONECUT1/HESX1	66
hsa054 12	Arrhythmogenic right ventricular	39/2512	77/810 5	0.00023 6273	0.00916 9666	0.00683 5809	CACNA1C/CTNNB1/CACNB4/CACNB2/SLC8A1/CTNNA2/CACNA1F/ATP2A	39

	cardiomyopathy						1/TCF7/ITGB6/CACNA2D2/LAMA2/ATP2A2/ITGB1/ITGA6/CACNA1D/ACTN2/SGCD/ITGA5/ITGA3/ITGA2/ITGA10/DSC2/ATP2A3/LAMA1/CACNG8/DAG1/SLC8A2/ITGA11/ACTN3/ITGB5/CACNA1S/CACNA2D1/PKP2/JUP/SGCB/ITGA4/ITGB3/DSG2	
hsa04918	Thyroid hormone synthesis	38/2512	75/8105	0.000280302	0.009169666	0.006835809	ITPR1/PRKACB/CREB5/SLC26A4/TSHR/TG/ATP1A1/IYD/CGA/ATF4/ADCY7/ADCY3/PLCB1/CREB1/PDIA4/ADCY8/GPX5/ATP1B1/ITPR3/ATP1B4/SLC5A5/ATF2/GNAS/CREB3L1/GNAQ/ADCY2/ITPR2/PRKCB/TTR/LRP2/GPX7/DUOXA2/DUOX1/ADCY4/ADCY9/DUOX2/CREB3L3/TTF2	38
hsa05205	Proteoglycans in cancer	87/2512	205/8105	0.000302293	0.009169666	0.006835809	ITPR1/CTNNB1/PRKACB/ANK2/PTCH1/FZD3/PTK2/RDX/CAMK2B/FN1/PPP1R12B/ARHGEF12/SMAD2/CD63/MDM2/HIF1A/ERBB2/GAB1/CAMK2G/ESR1/FGFR1/IGF1/SOS2/ITGB1/MAPK3/EGFR/PIK3CD/KRAS/PLAUR/CAV1/MAPK14/WNT2B/GPC3/HSPG2/ARH	87

							GEF1/CTTN/EIF4B/PAK1/BRAF/ITGA5/IQGAP1/STAT3/MET/RAF1/TIAM1/ITGA2/ANK3/EZR/FZD4/CBL/ITPR3/FLNC/WNT10B/CTSL/VAV3/PIK3R3/WNT9B/TP53/SLC9A1/ERBB3/FZD10/SRC/MMP9/IHH/MRAS/ITPR2/CDC42/PRKCB/WNT5A/PXN/MSN/TWIST2/ITGB5/HPSE2/PIK3CA/AKT2/PIK3R1/WNT8A/WNT5B/ANK1/RPS6/ROCK1/PPP1R12C/FZD5/HBEGF/FZD8/ITGB3	
hsa04072	Phospholipase D signaling pathway	66/2512	148/8105	0.000306585	0.009169666	0.006835809	DNM3/FYN/AGPAT3/LPAR6/GAB1/DGKH/EGF/GRM1/SOS2/DGKK/LPAR4/SPHK2/LPAR3/DGKA/MAPK3/EGFR/PIK3CD/KRAS/DGKZ/TSC2/RALA/DGKI/MS4A2/F2R/GRM7/ADCY7/ADCY3/PDGFD/PTGFR/PLCB1/RAF1/DGKB/ADCY8/PIP5K1C/PIK3R5/JMJD7-PLA2G4B/PLD1/GNA13/PIK3R3/PLA2G4F/RALB/GNAS/PDGFRB/MRAS/ADCY2/RAPGEF3/PIK3R6/ARF6/PDGFC/PIP5K1B/CYTH3/PIK3CA/AKT2/PIK3R1/DGKQ/SHC4/FCER1G/AGT/CYTH	66

							2/AVPR1A/ADCY4/AGPAT5/ADCY9/PLA2G4B/PLA2G4E/GRM2	
hsa045 10	Focal adhesion	85/2512	201/81 05	0.00040 5234	0.01111 0169	0.00828 2417	CTNNB1/PTK2/FN1/PPP1R12B/DIAPH1/ITGB6/FYN/LAMA3/MAPK8/FLT1/ERBB2/BIRC3/LAMA2/RASGRF1/EGF/IGF1/SOS2/ITGB1/MAPK3/EGFR/PIK3CD/CAV1/XIAP/ITGA6/MYL12B/CCND3/PAK1/BRAF/CRKL/ITGA5/PDGFD/ITGA3/MET/RAF1/GSK3B/ITGA2/RELN/COL6A6/LAMC2/FLNC/PIP5K1C/ARHGAP5/PAK4/ITGA10/VAV3/COL4A3/PIK3R3/COL9A1/MYLK3/RAC2/LAMA1/SRC/PDGFRB/MAPK9/ARHGAP35/CDC42/PRKCB/PAK5/PDGFC/BCL2/CAPN2/PIP5K1B/TNC/PXN/ITGA11/COL6A3/ITGB5/PIK3CA/AKT2/PIK3R1/SHC4/MYLK4/CHAD/COL9A2/MYL12A/TLN2/ROCK1/PPP1R12C/JUN/MAPK10/COL4A1/COL4A2/ITGA4/ITGB3/COL6A5	85
hsa041 20	Ubiquitin mediated proteolysis	62/2512	140/81 05	0.00057 646	0.01447 7154	0.01079 244	UBE2I/UBE3A/NEDD4L/NEDD4/UBE2D3/BTRC/CUL2/HERC4/FBXW11/PML	62

							/RCHY1/CDC16/MDM2/UBE2K/FBXW7/CUL4B/BRCA1/BIRC3/CUL3/UBE2O/XIAP/SKP2/SIAH1/PIAS2/CDC27/COP1/BIRC6/ANAPC13/NHLRC1/PIAS3/HUWE1/ANAPC4/WWP2/CBL/UBA3/UBA1/ANAPC1/CUL7/FBXO4/MID1/UBE2J1/UBE3C/MAP3K1/UBE3B/FBXW8/UBE2D1/RHOBTB1/UBE2E3/UBE2Q2/CBLB/UBE2D4/VHL/TRAF6/UBA6/ERRCC8/ANAPC2/UBE2C/UBE2J2/TRIM32/CBLC/UBE2Z/HERC1	
hsa04012	ErbB signaling pathway	41/2512	85/8105	0.000616049	0.014477154	0.01079244	NRG1/PTK2/CAMK2B/MAPK8/ABL2/ERBB2/GAB1/CAMK2G/EGF/SOS2/MAPK3/EGFR/PIK3CD/KRAS/NRG3/PAK1/BRAF/MAP2K4/CRKL/RAF1/GSK3B/CBL/PAK4/PIK3R3/STAT5B/ERBB3/SRC/NRG2/MAPK9/PRKCB/PAK5/TGFA/CBLB/NRG4/PIK3CA/AKT2/PIK3R1/SHC4/JUN/MAPK10/HBEGF	41
hsa04724	Glutamatergic synapse	52/2512	114/8105	0.000676958	0.014847945	0.011068857	CACNA1C/ITPR1/SLC1A2/PRKACB/HOMER1/KCNJ3/SLC38A2/SLC38A1/PPP3CB/GRM1/GLUL/MAPK3/SLC1A3/S	52

							LC1A7/CACNA1D/GRIK2/PPP3CA/GN G4/GLS/GRM7/ADCY7/GRIN2B/ADC Y3/GRIN2A/PLCB1/DLG4/GRIA3/AD CY8/ITPR3/JMJD7- PLA2G4B/GRIK1/PLD1/GNAI3/PPP3R 1/GNG2/PLA2G4F/GNAS/GNAQ/ADC Y2/ITPR2/GNG12/GRIK3/PRKCB/HO MER3/SLC17A6/GRIA2/DLGAP1/ADC Y4/ADCY9/PLA2G4B/PLA2G4E/GRM 2	
hsa003 10	Lysine degradation	32/2512	63/810 5	0.00078 4943	0.01614 0396	0.01203 2354	EHMT1/EZH2/KMT2E/PRDM2/KMT2 D/NSD1/PRDM6/EZH1/NSD3/HADH/A SH1L/SETDB1/KMT5B/PRDM16/AAS S/EHHADH/PRDM7/COLGALT1/KMT 2B/SETMAR/AADAT/NSD2/CAMKMT /KMT2C/HYKK/PIPOX/SETD7/HADH A/PRDM9/DOT1L/COLGALT2/SETD1 A	32
hsa040 68	FoxO signaling pathway	58/2512	131/81 05	0.00086 095	0.01666 1912	0.01242 1134	PRKAG2/HOMER1/SOD2/ATG12/USP 7/MAPK8/MDM2/CDK2/G6PC/ATM/E GF/GRM1/IGF1/SOS2/MAPK3/EGFR/P IK3CD/KRAS/AGAP2/MAPK14/SKP2/	58

							BRAF/IRS2/CCNG2/FOXO3/TNFSF10/IL6/S1PR1/FBXO32/STAT3/RAF1/C8orf44-SGK3/PRKAA1/SMAD3/TGFBR1/BCL2L11/CSNK1E/CDKN2B/PIK3R3/SLC2A4/RBL2/CCNB3/MAPK9/SETD7/HOMER3/RAG1/PIK3CA/AKT2/PIK3R1/PRKAG3/FOXO1/GADD45B/FOXG1/PRKAB2/TGFB3/GABARAP/MAPK10/IL7R	
hsa04921	Oxytocin signaling pathway	66/2512	154/8105	0.001137466	0.019284079	0.014375909	CACNA1C/ITPR1/PRKAG2/CACNB4/CACNB2/PRKACB/NFATC4/NFATC1/CAMK2B/PPP1R12B/CACNA1F/GUCY1A1/KCNJ3/CACNA2D2/PPP3CB/CAMK2G/MAPK3/EGFR/KRAS/CAMK4/RYR3/CACNA1D/PPP3CA/NFATC2/ADCY7/ADCY3/PLCB1/RAF1/PRKAA1/ADCY8/CALM1/ITPR3/KCNJ2/PIK3R5/JMJD7-PLA2G4B/GNAI3/MYLK3/EEF2K/PPP3R1/PLA2G4F/CACNG8/SRC/GNAS/GNAQ/ADCY2/KCNJ14/ITPR2/PIK3R6/	66

							RCAN1/TRPM2/PRKCB/MEF2C/CAMK1D/MYLK4/PRKAG3/NPR2/CACNA1S/CACNA2D1/PRKAB2/ADCY4/ADCY9/PLA2G4B/ROCK1/PPP1R12C/JUN/PLA2G4E	
hsa04935	Growth hormone synthesis, secretion and action	53/2512	119/8105	0.001196509	0.019284079	0.014375909	CACNA1C/ITPR1/PRKACB/SOCS2/PTK2/CACNA1F/MAPK8/CREB5/IGF1/SOS2/MAPK3/ADCY10/PIK3CD/KRAS/MAPK14/CACNA1D/IRS2/MAP2K4/CLKL/ATF4/ADCY7/ADCY3/STAT3/PLCB1/RAF1/GSK3B/CREB1/ADCY8/ITPR3/MAP2K6/POU1F1/PIK3R3/GNAI3/STAT5B/MAP3K1/ATF2/GNAS/MAPK9/CREB3L1/GNAQ/ADCY2/ITPR2/PRKCB/PIK3CA/AKT2/PIK3R1/SHC4/CACNA1S/STAT1/ADCY4/ADCY9/MAPK10/CREB3L3	53
hsa01522	Endocrine resistance	45/2512	98/8105	0.001277807	0.019284079	0.014375909	PRKACB/PTK2/ESR2/MAPK8/MDM2/E2F3/ERBB2/ESR1/IGF1/SOS2/MAPK3/EGFR/PIK3CD/KRAS/MAPK14/BRAF/ADCY7/ADCY3/RAF1/ADCY8/ABCB11/JAG2/PIK3R3/TP53/SRC/MMP9/GN	45

							AS/RB1/MAPK9/ADCY2/CYP2D7/BCL2/GPER1/MED1/PIK3CA/AKT2/PIK3R1/SHC4/NCOR1/CARM1/ADCY4/ADCY9/JUN/MAPK10/HBEGF	
hsa05231	Choline metabolism in cancer	45/2512	98/8105	0.001277807	0.019284079	0.014375909	SLC44A1/MAPK8/HIF1A/DGKH/WASF1/EGF/SOS2/DGKK/DGKA/MAPK3/EGFR/PIK3CD/KRAS/DGKZ/TSC2/LYPLA1/DGKI/PDGFD/RAF1/DGKB/SLC5A7/PIP5K1C/SLC22A1/JMJD7-PLA2G4B/PLD1/PIK3R3/RAC2/PLA2G4F/PDGFRB/MAPK9/PRKCB/PDGFC/IP5K1B/CHKA/PIK3CA/AKT2/PIK3R1/DGKQ/PCYT1A/SLC22A2/PLA2G4B/JUN/MAPK10/CHPT1/PLA2G4E	45
hsa04024	cAMP signaling pathway	88/2512	216/8105	0.001334855	0.019284079	0.014375909	CACNA1C/PRKACB/PTCH1/ATP2B1/PDE4A/PDE4D/NFATC1/ADCYAP1R1/CAMK2B/CACNA1F/ATP2A1/PDE4C/MAPK8/CREB5/GLI3/ABCC4/CAMK2G/ADORA2A/ATP2A2/TSHR/MAPK3/PTGER3/ADCY10/PIK3CD/CAMK4/ATP1A1/CACNA1D/GABBR1/PPP1R1B/PDE3A/CGA/PAK1/BRAF/CNGB3/F2R	88

							/ADCY7/CFTR/GRIN2B/ADCY3/GRIN2A/ADCYAP1/RAF1/TIAM1/ARAP3/CREB1/GRIA3/ADCY8/DRD5/ATP1B1/CALM1/GIPR/ATP2B4/EDNRA/PLD1/ATP1B4/PPARA/VAV3/PIK3R3/GNAI3/SLC9A1/RAC2/ATP2A3/GNAS/MAPK9/BDNF/CREB3L1/ADCY2/RAPGEF3/HTR1F/PIK3CA/AKT2/PIK3R1/CACNA1S/GRIA2/PDE10A/PDE3B/AMH/ADCY4/ADCY9/ROCK1/CHRM1/JUN/MAPK10/PDE4B/CNGA4/CREB3L3/NPY1R/LHCGR	
hsa04934	Cushing syndrome	66/2512	155/8105	0.001391381	0.019284079	0.014375909	CACNA1C/ITPR1/CACNA1G/CTNNB1/PRKACB/FZD3/CAMK2B/CACNA1F/USP8/TCF7/LDLR/PDE8B/CREB5/CDK2/KMT2D/E2F3/CCNE2/CAMK2G/PDE11A/MAPK3/EGFR/WNT2B/CACNA1D/CDK6/BRAF/DVL3/ATF4/ADCY7/ADCY3/PLCB1/GSK3B/CREB1/ADCY8/KCNK3/FZD4/ITPR3/APC/CDKN2B/WNT10B/CACNA1H/GNAI3/WNT9B/AXIN2/KCNA4/FZD10/ATF2/MEN1/G	66

							NAS/RB1/KCNK2/CREB3L1/GNAQ/ADCY2/ITPR2/WNT5A/AHR/HSD3B2/CACNA1S/WNT8A/WNT5B/AGT/ADCY4/ADCY9/FZD5/FZD8/CREB3L3	
hsa04977	Vitamin digestion and absorption	15/2512	24/8105	0.001406741	0.019284079	0.014375909	BTD/PLB1/CUBN/SLC19A3/ABCC1/SLC46A1/FOLH1/SLC5A6/APOB/SLC52A3/PNLIP/AWAT2/TCN2/SLC19A2/LMBRD1	15
hsa04917	Prolactin signaling pathway	34/2512	70/8105	0.001500995	0.019535184	0.014563103	SOCS2/ESR2/TNFSF11/TNFRSF11A/MAPK8/SOCS4/ESR1/GCK/TH/SOS2/SOCS7/MAPK3/PIK3CD/KRAS/MAPK14/CGA/FOXO3/STAT3/RAF1/GSK3B/ELF5/SOCS5/SOCS6/PIK3R3/STAT5B/SRRC/MAPK9/PIK3CA/AKT2/PIK3R1/SHC4/STAT1/MAPK10/LHCGR	34
hsa04927	Cortisol synthesis and secretion	32/2512	65/8105	0.001543814	0.019535184	0.014563103	CACNA1C/ITPR1/CACNA1G/PRKACB/CACNA1F/LDLR/PDE8B/CREB5/CACNA1D/ATF4/ADCY7/ADCY3/PLCB1/CREB1/ADCY8/KCNK3/ITPR3/CACNA1H/KCNA4/ATF2/GNAS/KCNK2/CREB3L1/GNAQ/ADCY2/ITPR2/HSD3B2/CACNA1S/AGT/ADCY4/ADCY9/CRE	32

							B3L3	
hsa040 22	cGMP-PKG signaling pathway	70/2512	167/81 05	0.00167 607	0.01998 1074	0.01489 5506	CACNA1C/ITPR1/NFATC4/ATP2B1/K CNMA1/SLC8A1/NFATC1/PDE5A/MR VI1/CACNA1F/ATP2A1/KNG1/GUCY1 A1/CREB5/GTF2I/EDNRB/PPP3CB/AT P2A2/MEF2D/MAPK3/PRKG2/ATP1A1 /CACNA1D/PPP3CA/NFATC2/PDE3A/ IRS2/ATF4/ADCY7/ADCY3/PLCB1/R AF1/CREB1/ADCY8/ATP1B1/CALM1/ ATP2B4/EDNRA/ITPR3/PIK3R5/ATP1 B4/GNA13/PRKG1/GNAI3/MYLK3/PP P3R1/ATP2A3/ATF2/MYH7/CREB3L1/ GNAQ/ADCY2/ITPR2/KCNMB4/PIK3 R6/MEF2C/KCNMB3/SLC8A2/ADRA2 B/AKT2/MYLK4/NPR2/CACNA1S/SL C25A5/PDE3B/ADCY4/ADCY9/ROCK 1/CREB3L3/MYH6	70
hsa052 10	Colorectal cancer	40/2512	86/810 5	0.00172 5219	0.01998 1074	0.01489 5506	CTNNB1/TCF7/SMAD2/MAPK8/MLH1 /EGF/SOS2/MAPK3/EGFR/PIK3CD/KR AS/RALA/BRAF/RAF1/GSK3B/MSH6/ SMAD3/TGFBR1/APC/BCL2L11/CYCS /PIK3R3/TP53/RAC2/AXIN2/RALB/M	40

							APK9/TGFA/BCL2/BAK1/PIK3CA/AKT2/PIK3R1/GADD45B/TGFB3/MSH3/JUN/MAPK10/MSH2/DCC	
hsa05135	Yersinia infection	59/2512	137/8105	0.001766416	0.019981074	0.014895506	ARHGEF7/NFATC1/PTK2/RPS6KA3/FN1/ARHGEF12/MAPK8/RPS6KA6/IRAK1/CASP1/MAP3K7/PKN2/ITGB1/MAPK3/PIK3CD/MAPK14/NFATC2/NLRP3/ARHGEF1/MAP2K4/CRKL/RPS6KA2/IL6/ITGA5/ACTR3/GSK3B/MEFV/PIP5K1C/MAP2K6/NLRC4/VAV3/PIK3R3/RAC2/RHOG/ARPC3/IFNB1/TAB2/SRC/SKAP2/MAPK9/GNAQ/FYB1/ARF6/CDC42/ELMO1/PIP5K1B/PXN/PIK3CA/AKT2/PIK3R1/CD4/TRAF6/ZAP70/FCGR2A/ROCK1/WIPF3/JUN/MAPK10/ITGA4	59
hsa04725	Cholinergic synapse	50/2512	113/8105	0.001927318	0.019981074	0.014895506	CACNA1C/ITPR1/PRKACB/CAMK2B/CACNA1F/FYN/KCNQ3/KCNJ3/CREB5/CAMK2G/MAPK3/PIK3CD/KRAS/CAMK4/CACNA1D/GNG4/ATF4/ADCY7/ADCY3/PLCB1/CREB1/ADCY8/SLC5A7/ITPR3/KCNJ2/PIK3R5/PIK3R3/GN	50

							AI3/GNG2/CREB3L1/GNAQ/ADCY2/KCNJ14/ITPR2/GNG12/PIK3R6/PRKCB/BCL2/CHRM5/PIK3CA/CHRNA2/AKT2/CHRNA4/PIK3R1/CACNA1S/KCNQ5/ADCY4/ADCY9/CHRM1/CREB3L3	
hsa05212	Pancreatic cancer	36/2512	76/8105	0.001938134	0.019981074	0.014895506	JAK1/SMAD2/MAPK8/E2F3/ERBB2/EGF/MAPK3/EGFR/PIK3CD/KRAS/RALA/CDK6/BRAF/STAT3/RAF1/BRCA2/SMAD3/TGFBR1/PLD1/PIK3R3/TP53/RAC2/RALB/RB1/MAPK9/CDC42/TGFA/BAK1/PIK3CA/AKT2/PIK3R1/GADD45B/TGFB3/STAT1/MAPK10/RALBP1	36
hsa04070	Phosphatidylinositol signaling system	44/2512	97/8105	0.001943448	0.019981074	0.014895506	ITPR1/PIP5K1/INPP4B/SYNJ1/INPP5B/IP6K1/CDIPT/PIP4K2C/DGKH/DGKK/DGKA/MTMR8/PIK3CD/SYNJ2/DGKZ/OCRL/DGKI/MTMR2/PLCB1/DGKB/IPMK/CALM1/ITPR3/PIP5K1C/PI4K2B/PIK3R3/PIP4K2B/ITPR2/PRKCB/MTMR3/IP6K3/PIP5K1B/CDS1/MTMR7/CDS2/PIK3CA/INPP5F/PIK3R1/DGKQ/ITPKC/PI4KB/MTMR6/PLCD4/MTM1	44
hsa046	Platelet activation	54/2512	124/81	0.00201	0.02005	0.01494	ITPR1/PRKACB/ARHGEF12/FYN/GU	54

11			05	1361	2664	8875	CY1A1/ITGB1/MAPK3/PIK3CD/MAPK14/PRKG2/MYL12B/ARHGEF1/F2R/ADCY7/ADCY3/PLCB1/ITGA2/ADCY8/ITPR3/COL3A1/PIK3R5/JMJD7-PLA2G4B/RASGRP1/GNA13/PIK3R3/PRKG1/GNAI3/MYLK3/GP1BA/PLA2G4F/SRC/GNAS/GNAQ/ADCY2/ARHGAP35/ITPR2/PIK3R6/PIK3CA/AKT2/PIK3R1/MYLK4/FCER1G/SNAP23/PRKCI/MYL12A/P2RX1/ADCY4/ADCY9/FCGR2A/PLA2G4B/TLN2/ROCK1/PLA2G4E/ITGB3	
hsa04915	Estrogen signaling pathway	59/2512	138/8105	0.002169481	0.020992919	0.015649817	ITPR1/OPRM1/PRKACB/ESR2/KCNJ3/CREB5/GRM1/ESR1/SOS2/NCOA1/MAPK3/EGFR/PIK3CD/KRAS/GABBR1/ATF4/ADCY7/ADCY3/KRT20/PLCB1/RAF1/CREB1/ADCY8/CALM1/ITPR3/PGR/FKBP5/PIK3R3/GNAI3/ATF2/KRT27/KRT12/SRC/MMP9/GNAS/CREB3L1/GNAQ/ADCY2/ITPR2/EBAG9/KRT10/KRT38/TGFA/BCL2/GPER1/NCOA2/PIK3CA/AKT2/PIK3R1/SHC4/KRT25/	59

							ADCY4/KRT23/KRT13/ADCY9/JUN/H BEGF/KRT14/CREB3L3	
hsa049 24	Renin secretion	33/2512	69/810 5	0.00241 542	0.02270 4948	0.01692 6101	CACNA1C/ITPR1/PRKACB/KCNMA1/ ADCYAP1R1/CACNA1F/GUCY1A1/C TSB/PDE1C/PPP3CB/PRKG2/CACNA1 D/PPP3CA/PDE3A/CLCA4/PLCB1/AD CYAP1/CREB1/CALM1/EDNRA/ITPR 3/KCNJ2/GNAI3/PPP3R1/ACE/GNAS/ GNAQ/ITPR2/CACNA1S/CLCA1/PTG ER4/AGT/PDE3B	33
hsa049 29	GnRH secretion	31/2512	64/810 5	0.00251 808	0.02301 2449	0.01715 5337	CACNA1C/ITPR1/CACNA1G/TRPC4/C ACNA1F/ESR2/KCNJ3/ARRB1/MAPK 3/PIK3CD/KRAS/CACNA1D/GABBR1/ CGA/PLCB1/RAF1/ITPR3/KCNJ11/HC N1/CACNA1H/PIK3R3/GNAQ/ITPR2/P RKCB/GPER1/GNRH1/PIK3CA/AKT2/ PIK3R1/CACNA1S/TRPC5	31
hsa046 25	C-type lectin receptor signaling pathway	46/2512	104/81 05	0.00289 0684	0.02570 3649	0.01916 1575	ITPR1/NFATC4/NFATC1/ARHGEF12/ CYLD/MAPK8/MDM2/PPP3CB/CASP1 /MAPK3/KSR1/PIK3CD/KRAS/MAPK1 4/NFKB2/PPP3CA/NFATC2/NLRP3/CL EC7A/PAK1/IL6/RAF1/CALM1/ITPR3/	46

							CLEC1B/BCL10/PIK3R3/PPP3R1/MAL T1/SRC/MAPK9/MRAS/ITPR2/CBLB/S TAT2/PIK3CA/CLEC4D/AKT2/PIK3R1 /FCER1G/CASP8/STAT1/MAP3K14/IR F9/JUN/MAPK10	
hsa049 19	Thyroid hormone signaling pathway	52/2512	121/81 05	0.00338 2877	0.02928 8596	0.02183 4084	CTNNB1/PRKACB/ATP2A1/MDM2/HI F1A/PFKM/ESR1/ATP2A2/MED12L/N COA1/MED13L/MAPK3/PIK3CD/KRA S/ATP1A1/TSC2/TBC1D4/RCAN2/SLC 16A2/DIO2/PLCB1/RAF1/GSK3B/ATP 1B1/ATP1B4/PIK3R3/TP53/SLC9A1/A TP2A3/MYH7/MED12/SRC/RCAN1/PR KCB/THRB/NCOA2/HDAC1/MED1/M ED24/PIK3CA/AKT2/PIK3R1/KAT2B/P FKP/FOXO1/NCOR1/PLCD4/STAT1/P FKL/SLC16A10/ITGB3/MYH6	52
hsa052 15	Prostate cancer	43/2512	97/810 5	0.00370 2594	0.03071 8503	0.02290 0051	CTNNB1/FGFR2/TCF7/CREB5/MDM2/ CDK2/AR/ZEB1/E2F3/ERBB2/CCNE2/ EGF/FGFR1/IGF1/SOS2/MAPK3/EGFR /PIK3CD/KRAS/KLK3/BRAF/ATF4/PD GFD/RAF1/GSK3B/CREB1/PIK3R3/TP 53/MMP9/RB1/PDGFRB/CREB3L1/PD	43

							GFC/TGFA/BCL2/SPINT1/PIK3CA/AKT2/PIK3R1/FOXO1/TMPRSS2/ETV5/CREB3L3	
hsa04211	Longevity regulating pathway	40/2512	89/8105	0.003734772	0.030718503	0.022900051	PRKAG2/PRKACB/EHMT1/SOD2/SEN3/SEN1/CREB5/RB1CC1/IGF1/PIK3CD/KRAS/CAMK4/TSC2/IRS2/FOXO3/ATF4/ADCY7/ADCY3/ADIPOQ/CREB1/PRKAA1/ADCY8/PIK3R3/TP53/ADIPOR2/ATF2/CREB3L1/ADCY2/EIF4E/PIK3CA/AKT2/PIK3R1/PRKAG3/ULK1/FOXO1/PRKAB2/PPARGC1A/ADCY4/ADCY9/CREB3L3	40
hsa0420	Calcium signaling pathway	94/2512	240/8105	0.003870084	0.031055062	0.02315095	CACNA1C/ITPR1/CACNA1G/PRKACB/FGFR2/FGF1/ATP2B1/SLC8A1/CAMK2B/CACNA1F/ATP2A1/FLT1/RET/EDNRB/ERBB2/PHKB/PDE1C/PHKA1/PPP3CB/CAMK2G/ADORA2A/EGF/GRM1/ATP2A2/FGFR1/CACNA1E/SPHK2/CCKAR/PTGER3/EGFR/CAMK4/RYR3/CACNA1D/ORAI2/ASPH/PPP3CA/PTAFR/TRDN/CCKBR/TACR1/F2R/ADCY7/ADCY3/PDGFD/PTGFR/MET/GRI	94

							N2A/PLCB1/ADCY8/DRD5/CALM1/A TP2B4/EDNRA/ITPR3/CXCR4/NTRK2/ CACNA1H/HRH1/MYLK3/PPP3R1/ER BB3/ATP2A3/GNAS/PDGFRB/GNAQ/ ADCY2/FGF21/NOS1/ITPR2/PRKCB/P DGFC/TACR2/HTR2B/SLC8A2/CHRM 5/FGF17/CAMK1D/MYLK4/GRPR/CA CNA1S/ITPKC/SLC25A5/PLCD4/P2RX 1/P2RX7/AVPR1A/ADCY4/TPCN2/STI M2/ADCY9/CASQ1/CHRM1/CASQ2/L HCGR	
hsa049 14	Progesterone- mediated oocyte maturation	44/2512	100/81 05	0.00397 1896	0.03111 3182	0.02319 4278	PRKACB/RPS6KA3/CPEB2/MAPK8/C DC16/CDK2/RPS6KA6/KIF22/IGF1/CP EB1/MAPK3/PIK3CD/KRAS/MAPK14/ BUB1/CPEB4/BRAF/RPS6KA2/CDC27/ ADCY7/ANAPC13/ADCY3/RAF1/ADC Y8/ANAPC4/CDC25A/MAD1L1/ANAP C1/PGR/PIK3R3/GNAI3/CCNA2/CCNB 3/MAPK9/ADCY2/PIK3CA/AKT2/PIK3 R1/PDE3B/CDC25C/ADCY4/ADCY9/A NAPC2/MAPK10	44
hsa015	EGFR tyrosine	36/2512	79/810	0.00437	0.03349	0.02497	NRG1/FGFR2/JAK1/ERBB2/GAB1/EG	36

21	kinase inhibitor resistance		5	7899	6014	0633	F/IGF1/SOS2/MAPK3/EGFR/PIK3CD/KRAS/BRAF/FOXO3/IL6/PDGFD/STAT3/MET/RAF1/GSK3B/BCL2L11/PIK3R3/ERBB3/SRC/NRG2/PDGFRB/PRKCB/PDGFC/TGFA/BCL2/EIF4E/PIK3CA/AKT2/PIK3R1/SHC4/RPS6	
hsa04928	Parathyroid hormone synthesis, secretion and action	46/2512	106/8105	0.004515566	0.033764116	0.025170498	ITPR1/PRKACB/PDE4A/PDE4D/AKAP13/TNFSF11/PDE4C/CREB5/ARRB1/RUNX2/FGFR1/MEF2D/MAPK3/EGFR/ARHGEF11/ARHGEF1/BRAF/MMP16/ATF4/ADCY7/ADCY3/PLCB1/RAF1/CREB1/ADCY8/ITPR3/PLD1/GNA13/GNAI3/MMP14/ATF2/GNAS/LRP6/CREB3L1/GNAQ/ADCY2/ITPR2/PRKCB/BCL2/MEF2C/JUND/ADCY4/ADCY9/HBEGF/PDE4B/CREB3L3	46
hsa04750	Inflammatory mediator regulation of TRP channels	43/2512	98/8105	0.004653889	0.034025098	0.025365055	ITPR1/PRKACB/TRPV1/CAMK2B/KNAG1/MAPK8/CAMK2G/IGF1/PIK3CD/MAPK14/IL1R1/ASIC3/ADCY7/ADCY3/PLCB1/ADCY8/TRPM8/CALM1/ITPR3/MAP2K6/JMJD7-PLA2G4B/HRH1/PIK3R3/PLA2G4F/SR	43

							C/GNAS/MAPK9/GNAQ/ADCY2/ITPR2/PRKCB/HTR2B/ALOX12/ASIC5/PIK3CA/IL1RAP/PIK3R1/PTGER4/ADCY4/ADCY9/PLA2G4B/MAPK10/PLA2G4E	
hsa04911	Insulin secretion	38/2512	86/8105	0.006549388	0.046842365	0.03492008	CACNA1C/PRKACB/KCNMA1/ADCYAP1R1/CAMK2B/CACNA1F/RIMS2/CREB5/CAMK2G/GCK/CCKAR/ATP1A1/CACNA1D/ATF4/ADCY7/ADCY3/PLCB1/ADCYAP1/CREB1/ADCY8/ATP1B1/ITPR3/KCNJ11/ATP1B4/PCLO/TRPM4/ATF2/GNAS/CREB3L1/GNAQ/ADCY2/KCNMB4/PRKCB/KCNMB3/CACNA1S/ADCY4/ADCY9/CREB3L3	38
hsa00564	Glycerophospholipid metabolism	42/2512	98/8105	0.008386468	0.05850884	0.043617212	LPGAT1/AGPAT3/PLB1/CDIPT/DGKH/DGKK/DGKA/PNPLA6/GPD2/GPAT2/DGKZ/PLA2G15/LYPLA1/ETNK2/DGKI/LPCAT2/MBOAT1/DGKB/GPAT3/JMJD7-PLA2G4B/CRLS1/PLD1/SELENOI/PLA2G2D/GPAM/PLA2G5/PLA2G4F/GPAT4/CDS1/CHKA/CDS2/PLA2G12A/DGKQ/PCYT1A/PGS1/PLA2G3/AGPAT5/PL	42

							A2G4B/PLPP5/CHPT1/PLA2G4E/LYPLA2	
hsa04976	Bile secretion	39/2512	90/8105	0.008744308	0.05850884	0.043617212	PRKACB/LDLR/ABCC3/ABCC4/ATP1A1/SLC4A5/SLCO1A2/UGT2B28/UGT2A1/UGT2A2/ADCY7/CFTR/ADCY3/B AAT/ADCY8/ABCB11/ATP1B1/UGT2B4/SLC22A1/EPHX1/ABCB4/SLC22A7/ATP1B4/SLC4A4/SLC9A1/GNAS/AD CY2/SLCO1B1/CYP3A4/UGT1A10/AB CC2/HMGCR/UGT2B10/UGT2B11/SL C4A2/ABCB1/ADCY4/ADCY9/SLC51 B	39
hsa04668	TNF signaling pathway	47/2512	112/8105	0.008763342	0.05850884	0.043617212	DAB2IP/CFLAR/TNFAIP3/MAPK8/CR EB5/CSF1/NOD2/BIRC3/MAP3K7/MA PK3/PIK3CD/TRAF1/MAPK14/IL15/V CAM1/RPS6KA4/MAP3K8/MAP2K4/A TF4/IL6/CXCL10/CCL20/BAG4/CREB1 /RIPK3/MAP2K6/TNFRSF1A/PIK3R3/ MMP14/ATF2/IFNB1/TAB2/MMP9/MA PK9/CREB3L1/ICAM1/CX3CL1/SELE/ LIF/PIK3CA/AKT2/PIK3R1/CASP8/MA P3K14/JUN/MAPK10/CREB3L3	47

hsa020 10	ABC transporters	22/2512	45/810 5	0.00889 1921	0.05850 884	0.04361 7212	ABCC3/ABCC4/ABCB7/ABCA2/ABCC11/ABCC1/ABCA8/ABCA10/ABCA13/ABCA12/CFTR/ABCA5/ABCB11/ABCB4/ABCD4/ABCD1/ABCG1/ABCA9/ABCC2/ABCC5/ABCB8/ABCB1	22
hsa043 10	Wnt signaling pathway	66/2512	166/810 05	0.00958 2008	0.06133 9309	0.04572 7273	CTNNB1/PRKACB/NFATC4/NFATC1/FZD3/CAMK2B/BTRC/TCF7/FBXW11/MAPK8/TBL1X/PPP3CB/CAMK2G/CSNK2A1/MAP3K7/RSP01/WNT2B/LGR5/PPP3CA/CCND3/NFATC2/TLE3/SIAH1/NKD1/DVL3/CTNNBIP1/PLCB1/GSK3B/RYK/ROR1/FZD4/DAAM1/SMA D3/APC/LGR6/CSNK1E/ZNRF3/WNT10B/WNT9B/TP53/RAC2/PPP3R1/AXIN2/LGR4/FZD10/LRP6/MAPK9/RNF43/PKCB/WNT5A/PRICKLE2/SEN2/DAAM2/FRAT2/WNT8A/CHD8/WNT5B/CSNK1A1/CTBP2/CSNK2A3/FZD5/JUN/MAPK10/TBL1XR1/INVS/FZD8	66
hsa049 22	Glucagon signaling pathway	45/2512	107/810 05	0.00972 4292	0.06133 9309	0.04572 7273	ITPR1/PRKAG2/PRKACB/CAMK2B/CREB5/G6PC/PFKFB1/PHKB/PHKA1/PPP3CB/CAMK2G/ACACA/CPT1C/PFK	45

							M/GCK/PPP3CA/ATF4/SIK1B/PLCB1/CREB1/PRKAA1/CALM1/ITPR3/PPARA/PPP3R1/PDHA2/ATF2/GNAS/CREB3L1/GNAQ/ADCY2/ITPR2/CPT1A/GYS1/AKT2/PRKAG3/PFKP/FOXO1/PRKAB2/PPARGC1A/LDHA/PDE3B/PFKL/CREB3L3/PPP4R3B	
hsa04010	MAPK signaling pathway	110/2512	294/8105	0.009881408	0.061339309	0.045727273	CACNA1C/CACNA1G/CACNB4/CACNB2/PRKACB/FGFR2/FGF1/NFATC1/RPS6KA3/MAP4K4/CACNA1F/MAP3K13/MAPK8/PTPRR/FLT1/RPS6KA6/IRAK1/MAP3K20/CSF1/ARRB1/CACNA2D2/ERBB2/RASGRF1/PPP3CB/EGF/MAP3K7/FGFR1/IGF1/SOS2/CACNA1E/MAPK3/EGFR/KRAS/MAPK14/NFKB2/CACNA1D/TEK/MAP3K3/PPP3CA/RPS6KA4/IL1R1/MAP3K8/PAK1/BRAF/MAP2K4/CRKL/RPS6KA2/ATF4/DUSP9/PDGFD/MET/RAF1/TAOK1/TGFBP1/FLNC/MAP2K6/JMJD7-PLA2G4B/RASA1/DUSP6/CD14/NTRK2/RASGRP1/MAP4K3/TNFRSF1A/CAC	110

							NA1H/ELK4/TP53/MAPKAPK3/MAP3K1/RAC2/ANGPT4/PPP3R1/ERBB3/DUSP16/ATF2/TAB2/MAP3K4/PLA2G4F/RASGRP3/CACNG8/PDGFRB/MAPK9/MRAS/BDNF/FGF21/DUSP8/GNG12/CDC42/PRKCB/PDGFC/TGFA/MEF2C/IL1A/JUND/FGF17/IL1RAP/AKT2/CACNA1S/DUSP2/TRAF6/CACNA2D1/GADD45B/TGFB3/MAP3K14/MAP3K6/PLA2G4B/JUN/MAPK10/PLA2G4E/DDIT3	
hsa04110	Cell cycle	51/2512	124/8105	0.010261228	0.06251748	0.046605576	CDC14A/ORC4/PRKDC/TFDP2/SMAD2/CDC16/MDM2/CDK2/ATM/SMC1A/E2F3/CDC14B/CCNE2/STAG1/ORC1/ATR/BUB1/CCND3/YWHAB/SKP2/CDK6/CDC27/ANAPC13/GSK3B/ZBTB17/ANAPC4/CDC7/SMAD3/CDC25A/MAD1L1/ANAPC1/CDKN2B/TP53/CCNA2/RBL2/RAD21/RB1/CCNB3/ORC5/E2F5/HDAC1/RBL1/ESPL1/BUB1B/GADD45B/MCM2/TGFB3/CDC25C/ANAPC2/YWHAB/STAG2	51

hsa043 40	Hedgehog signaling pathway	26/2512	56/810 5	0.01072 89	0.06368 7764	0.04747 8	CSNK1G3/PRKACB/PTCH1/BTRC/FB XW11/GPR161/IQCE/ARRB1/GLI3/CU L3/SPOPL/SCUBE2/KIF3A/CSNK1G1/ GSK3B/EVC/CDON/MEGF8/CSNK1E/ CSNK1G2/IHH/BCL2/LRP2/MOSMO/C SNK1A1/PTCH2	26
hsa040 15	Rap1 signaling pathway	81/2512	210/81 05	0.01084 047	0.06368 7764	0.04747 8	CTNND1/CTNNB1/FGFR2/FGF1/SIPA 1L1/KRIT1/RASSF5/FLT1/CSF1/RAPG EF6/ADORA2A/EGF/FGFR1/IGF1/LPA R4/MAGI2/ITGB1/LPAR3/MAPK3/EG FR/PIK3CD/KRAS/MAPK14/ITGAM/T EK/ENAH/RALA/BRAF/CRKL/DOCK4 /F2R/ADCY7/GRIN2B/ADCY3/CNR1/P DGFD/MET/GRIN2A/PLCB1/RAF1/M AGI1/TIAM1/ARAP3/ADCY8/EVL/CD H1/CALM1/MAP2K6/RAPGEF5/VAV3 /PIK3R3/GNAI3/RAC2/ANGPT4/SIPA1 L2/SKAP1/RASGRP3/SRC/RALB/GNA S/PDGFRB/MRAS/GNAQ/ADCY2/FYB 1/FGF21/RAPGEF3/CDC42/PRKCB/PD GFC/FGF17/SIPA1/PIK3CA/AKT2/PIK 3R1/PRKCI/ADCY4/ITGAL/ADCY9/T	81

							LN2/ITGB3	
hsa051 66	Human T-cell leukemia virus 1 infection	84/2512	219/81 05	0.01126 7519	0.06421 1786	0.04786 8649	PRKACB/JAK1/NFATC4/NFATC1/SM AD2/MAPK8/RAN/TCF3/CDC16/CREB 5/CDK2/ATM/E2F3/CCNE2/PPP3CB/M APK3/PIK3CD/KRAS/NFYB/NFKB2/A TR/XIAP/IL15/MAP3K3/PPP3CA/CCN D3/NFATC2/IL1R1/CRTC3/MAP2K4/A TF4/IL6/CDC27/ADCY7/ADCY3/CREB 1/ADCY8/ANAPC4/SMAD3/TGFBR1/T BPL1/MAD1L1/ANAPC1/CDKN2B/TN FRSF1A/ELK4/PIK3R3/ETS1/STAT5B/ TP53/MAP3K1/PPP3R1/CCNA2/ATF2/ RB1/MAPK9/CREB3L1/ADCY2/POLB/ ICAM1/XPO1/IL15RA/HLA- DRB5/PIK3CA/AKT2/PIK3R1/KAT2B/ ESPL1/SLC25A5/BUB1B/CD4/TGFB3/ MAP3K14/ADCY4/ITGAL/ADCY9/TL N2/ANAPC2/JUN/MAPK10/ZFP36/ETS 2/HLA-DPB1/CREB3L3	84
hsa042 70	Vascular smooth muscle contraction	54/2512	133/81 05	0.01132 0011	0.06421 1786	0.04786 8649	CACNA1C/ITPR1/PRKACB/KCNMA1/ MRVI1/PPP1R12B/ARHGEF12/CACN A1F/GUCY1A1/CALD1/ADORA2A/M	54

							APK3/MYH10/CACNA1D/ARHGEF11/ ARHGEF1/BRAF/CALCRL/ADCY7/A DCY3/PLCB1/RAF1/ADCY8/CALM1/E DNRA/ITPR3/JMJD7- PLA2G4B/GNA13/ADM/PRKG1/MYL K3/PLA2G2D/PLA2G5/PLA2G4F/GNA S/GNAQ/ADCY2/ITPR2/KCNMB4/PR KCB/KCNMB3/PLA2G12A/MYLK4/N PR2/CACNA1S/PLA2G3/AGT/AVPR1 A/ADCY4/ADCY9/PLA2G4B/ROCK1/ PPP1R12C/PLA2G4E	
hsa047 13	Circadian entrainment	41/2512	97/810 5	0.01197 1013	0.06675 3617	0.04976 3535	CACNA1C/ITPR1/CACNA1G/PRKAC B/ADCYAP1R1/CAMK2B/GUCY1A1/ KCNJ3/CAMK2G/MAPK3/ADCY10/PR KG2/RYR3/CACNA1D/GNG4/ADCY7/ GRIN2B/ADCY3/GRIN2A/PLCB1/ADC YAP1/CREB1/GRIA3/ADCY8/CALM1/ ITPR3/CACNA1H/PRKG1/GNAI3/GNG 2/GNAS/GNAQ/ADCY2/NOS1/GNG12/ PRKCB/PER2/GRIA2/ADCY4/ADCY9/ PER3	41
hsa049	AGE-RAGE	42/2512	100/81	0.01253	0.06872	0.05123	NFATC1/FN1/F3/DIAPH1/SMAD2/MA	42

33	signaling pathway in diabetic complications		05	3161	3501	2045	PK8/NOX4/MAPK3/PIK3CD/KRAS/M APK14/VCAM1/IL6/STAT3/PLCB1/SM AD3/TGFBR1/COL3A1/COL4A3/PIK3 R3/STAT5B/MAPK9/ICAM1/CDC42/P RKCB/BCL2/IL1A/SELE/PIK3CA/AKT 2/PIK3R1/FOXO1/THBD/PIM1/PLCD4/ TGFB3/AGT/STAT1/JUN/MAPK10/CO L4A1/COL4A2	
hsa047 10	Circadian rhythm	16/2512	31/810 5	0.01313 8357	0.07086 0977	0.05282 5492	PRKAG2/BTRC/FBXW11/RORA/ROR C/CLOCK/CREB1/PRKAA1/CSNK1E/ RORB/BHLHE40/PER2/PRKAG3/PRK AB2/PER3/NPAS2	16
hsa049 25	Aldosterone synthesis and secretion	41/2512	98/810 5	0.01454 937	0.07527 1965	0.05611 3799	CACNA1C/ITPR1/CACNA1G/PRKAC B/ATP2B1/CAMK2B/CACNA1F/LDLR /CREB5/CAMK2G/CAMK4/ATP1A1/C ACNA1D/ATF4/ADCY7/ADCY3/PLCB 1/CREB1/ADCY8/ATP1B1/KCNK3/CA LM1/ATP2B4/ITPR3/ATP1B4/CACNA 1H/ATF2/GNAS/CREB3L1/GNAQ/AD CY2/ITPR2/PRKCB/HSD3B2/CAMK1D /CACNA1S/AGT/ADCY4/ADCY9/KCN K9/CREB3L3	41

hsa049 71	Gastric acid secretion	33/2512	76/810 5	0.01459 0324	0.07527 1965	0.05611 3799	ITPR1/PRKACB/CAMK2B/KCNK10/CAMK2G/ATP1A1/CCKBR/ADCY7/CFT R/ADCY3/PLCB1/ADCY8/ATP1B1/EZ R/CALM1/ITPR3/KCNJ2/ATP1B4/GNA I3/MYLK3/SLC9A1/GNAS/KCNK2/GN AQ/ADCY2/ITPR2/PRKCB/KCNJ1/MY LK4/SLC4A2/ADCY4/SLC9A4/ADCY9	33
hsa041 14	Oocyte meiosis	52/2512	129/81 05	0.01490 217	0.07527 1965	0.05611 3799	ITPR1/PRKACB/RPS6KA3/CAMK2B/CPEB2/BTRC/FBXW11/FBXO5/CDC16/SLK/CDK2/AR/RPS6KA6/PPP2R1B/REC8/SMC1A/CCNE2/PPP3CB/CAMK2G/IGF1/CPEB1/SGO1/MAPK3/MAPK14/PPP2R5D/BUB1/PPP3CA/YWHAB/CPEB4/RPS6KA2/CDC27/ADCY7/ANAPC13/ADCY3/ADCY8/ANAPC4/CALM1/ITPR3/MAD1L1/ANAPC1/PGR/PPP3R1/ADCY2/ITPR2/FBXO43/ESPL1/PPP2R5E/CDC25C/ADCY4/ADCY9/ANAPC2/YWHAH	52
hsa049 26	Relaxin signaling pathway	52/2512	129/81 05	0.01490 217	0.07527 1965	0.05611 3799	PRKACB/SMAD2/MAPK8/CREB5/ARRB1/EDNRB/RXFP1/SOS2/MAPK3/EGFR/PIK3CD/KRAS/MAPK14/GNG4/M	52

							AP2K4/ATF4/ADCY7/ADCY3/PLCB1/RAF1/CREB1/MMP1/ADCY8/TGFBR1/COL3A1/COL4A3/PIK3R3/GNAI3/GNG2/RXFP4/ATF2/SRC/MMP9/GNAS/RXFP2/MAPK9/CREB3L1/ADCY2/NOS1/GNG12/PIK3CA/AKT2/PIK3R1/SHC4/RXFP3/ADCY4/ADCY9/JUN/MAPK10/COL4A1/COL4A2/CREB3L3	
hsa052 26	Gastric cancer	59/2512	149/81 05	0.01510 0151	0.07527 1965	0.05611 3799	CTNNB1/FGFR2/FGF1/FZD3/CTNNA2/TCF7/SMAD2/CDK2/E2F3/ERBB2/MLH1/GAB1/CCNE2/EGF/SOS2/MAPK3/EGFR/PIK3CD/KRAS/WNT2B/BRAF/DVL3/MET/RAF1/GSK3B/CDH1/FZD4/SMAD3/TGFBR1/APC/CDKN2B/WNT10B/PIK3R3/WNT9B/TP53/AXIN2/FZD10/RB1/LRP6/FGF21/BCL2/WNT5A/B AK1/FGF17/PIK3CA/AKT2/PIK3R1/SHC4/FRAT2/WNT8A/WNT5B/CDX2/GADD45B/CSNK1A1/TGFB3/ABCB1/JUP/FZD5/FZD8	59
hsa042 61	Adrenergic signaling in	59/2512	150/81 05	0.01753 9143	0.08612 5046	0.06420 4562	CACNA1C/CACNB4/CACNB2/PRKACB/ATP2B1/TNNT2/SLC8A1/SCN5A/C	59

	cardiomyocytes						AMK2B/CACNA1F/ATP2A1/CREB5/PP2R1B/CACNA2D2/PPP2R2C/CAMK2G/ATP2A2/MAPK3/MAPK14/PPP2R5D/ATP1A1/CACNA1D/KCNE1/ATF4/ADCY7/ADCY3/TPM3/PLCB1/CREB1/ADCY8/ATP1B1/CALM1/ATP2B4/PIK3R5/ATP1B4/GNAI3/SLC9A1/ATP2A3/ATF2/MYH7/CACNG8/GNAS/CREB3L1/GNAQ/ADCY2/RAPGEF3/PIK3R6/BCL2/SLC8A2/AKT2/CACNA1S/PPP2R5E/CACNA2D1/TPM1/AGT/ADCY4/ADCY9/CREB3L3/MYH6	
hsa04512	ECM-receptor interaction	37/2512	88/8105	0.017993332	0.087055974	0.06489855	NPNT/FN1/ITGB6/LAMA3/LAMA2/FREM2/ITGB1/ITGA6/HSPG2/ITGA5/FREM1/ITGA3/ITGA2/RELN/COL6A6/LAMC2/ITGA10/COL4A3/COL9A1/SV2B/GP1BA/SV2C/LAMA1/DAG1/TNC/DSP/FRAS1/ITGA11/COL6A3/ITGB5/CHAD/COL9A2/COL4A1/COL4A2/ITGA4/ITGB3/COL6A5	37
hsa05032	Morphine addiction	38/2512	91/8105	0.018792165	0.08848113	0.065960977	OPRM1/PRKACB/PDE4A/PDE4D/PDE4C/KCNJ3/PDE8B/ARRB1/GRK4/PDE1	38

							C/PDE11A/GABRA2/GNG4/GABBR1/P DE3A/GABRG1/PDE7B/ADCY7/ADC Y3/GABRG3/ADCY8/GABRR2/GNAI3 /PDE7A/GNG2/GABRQ/GNAS/ADCY2 /GNG12/GABRA3/PRKCB/PDE10A/PD E3B/GABRE/ADCY4/ADCY9/GABRB 2/PDE4B	
hsa051 61	Hepatitis B	63/2512	162/81 05	0.01882 5772	0.08848 113	0.06596 0977	APAF1/JAK1/NFATC4/NFATC1/STAT 6/MAPK8/MAVS/CREB5/CDK2/IRAK1 /E2F3/CCNE2/MAP3K7/SOS2/MAPK3/ PIK3CD/KRAS/MAPK14/HSPG2/NFAT C2/YWHAB/BRAF/MAP2K4/ATF4/IL6 /STAT3/RAF1/CREB1/SMAD3/TGFBR 1/MAP2K6/TYK2/CYCS/PIK3R3/STAT 5B/TP53/MAP3K1/DDX3X/CCNA2/AT F2/TICAM2/IFNB1/TAB2/SRC/MMP9/ RB1/MAPK9/CREB3L1/PRKCB/BCL2/ STAT2/PIK3CA/AKT2/PIK3R1/TRAF6/ CASP8/TGFB3/ATP6AP1/IFIH1/STAT1 /JUN/MAPK10/CREB3L3	63
hsa043 80	Osteoclast differentiation	51/2512	128/81 05	0.02003 4426	0.09165 1259	0.06832 4247	JAK1/NFATC1/SIRPB1/SIRPG/TNFSF1 1/CYLD/FYN/TNFRSF11A/MAPK8/CS	51

							F1/PPP3CB/MAP3K7/CALCR/MAPK3/PIK3CD/CAMK4/MAPK14/NFKB2/PPP3CA/NFATC2/IL1R1/FHL2/NCF2/CREB1/TGFBR1/MAP2K6/TYK2/TNFRSF1A/PIK3R3/PPP3R1/IFNB1/TAB2/MAPK9/IFNGR2/IFNGR1/IL1A/JUND/FOSB/STAT2/PIK3CA/AKT2/PIK3R1/FOSL2/TRAF6/STAT1/MAP3K14/IRF9/FCGR2A/JUN/MAPK10/ITGB3	
hsa052 23	Non-small cell lung cancer	31/2512	72/810 5	0.02005 7418	0.09165 1259	0.06832 4247	RASSF5/RET/E2F3/ERBB2/EGF/SOS2/MAPK3/EGFR/PIK3CD/KRAS/CDK6/BRAF/FOXO3/STAT3/MET/RAF1/KIF5A/KIF5B/PIK3R3/STAT5B/TP53/RB1/PRKCB/TGFA/BAK1/PIK3CA/AKT2/PIK3R1/GADD45B/FHIT/EML4	31
hsa047 27	GABAergic synapse	37/2512	89/810 5	0.02181 2538	0.09705 2563	0.07235 0815	CACNA1C/PRKACB/CACNA1F/SLC38A2/ABAT/SLC38A1/GLUL/GABRA2/SLC6A11/CACNA1D/GNG4/GABBR1/GLS/GABRG1/ADCY7/ADCY3/GABRG3/ADCY8/GABRR2/GNAI3/GNG2/GABRQ/SRC/GAD1/TRAK2/ADCY2/GNG12/GABRA3/PRKCB/PLCL1/CACNA	37

							1S/GABRE/ADCY4/GABARAP/ADCY9/GABRB2/SLC6A12	
hsa04152	AMPK signaling pathway	48/2512	120/8105	0.021829452	0.097052563	0.072350815	PRKAG2/LEPR/HNF4A/CREB5/G6PC/PPP2R1B/PFKFB1/PPP2R2C/ACACA/CPT1C/PFKM/MAP3K7/IGF1/PIK3CD/PPP2R5D/TSC2/IRS2/PFKFB4/FOXO3/CFTR/ADIPOQ/CREB1/PRKAA1/SCD/RAB14/PIK3R3/SLC2A4/EEF2K/ADIPOR2/CCNA2/CREB3L1/CAB39L/CPT1A/LEP/GYS1/PIK3CA/AKT2/PIK3R1/HMGCR/PRKAG3/ULK1/PFKP/PPP2R5E/FOXO1/PRKAB2/PPARGC1A/PFKL/CREB3L3	48
hsa04720	Long-term potentiation	29/2512	67/8105	0.022209127	0.097424038	0.072627742	CACNA1C/ITPR1/PRKACB/RPS6KA3/CAMK2B/RPS6KA6/PPP3CB/CAMK2G/GRM1/MAPK3/KRAS/CAMK4/PPP3CA/BRAF/RPS6KA2/ATF4/GRIN2B/GRIN2A/PLCB1/RAF1/ADCY8/CALM1/ITPR3/PPP3R1/GNAQ/ITPR2/RAPGEF3/PRKCB/GRIA2	29
hsa04930	Type II diabetes mellitus	21/2512	46/8105	0.025518668	0.110468969	0.082352487	CACNA1C/CACNA1G/HK1/SOCS2/MAPK8/SOCS4/GCK/CACNA1E/MAPK3	21

							/PIK3CD/CACNA1D/IRS2/ADIPOQ/PKLR/KCNJ11/PIK3R3/SLC2A4/MAPK9/PIK3CA/PIK3R1/MAPK10	
hsa052 24	Breast cancer	57/2512	147/81 05	0.02606 3555	0.11136 2462	0.08301 8569	CTNNB1/FGF1/FZD3/ESR2/TNFSF11/TCF7/E2F3/BRCA1/ERBB2/EGF/ESR1/FGFR1/IGF1/SOS2/NCOA1/MAPK3/EGFR/PIK3CD/KRAS/NFKB2/WNT2B/CDK6/BRAF/DVL3/RAF1/GSK3B/BRCA2/FZD4/APC/JAG2/WNT10B/PGR/PIK3R3/WNT9B/TP53/AXIN2/FZD10/RB1/LRP6/FGF21/WNT5A/BAK1/FGF17/PIK3CA/AKT2/PIK3R1/SHC4/FRAT2/WNT8A/WNT5B/HEY1/GADD45B/HEY2/CSNK1A1/FZD5/JUN/FZD8	57
hsa049 23	Regulation of lipolysis in adipocytes	25/2512	57/810 5	0.02715 3391	0.11426 5896	0.08518 3023	PRKACB/ABHD5/TSHR/PTGER3/PIK3CD/MGLL/PRKG2/CGA/IRS2/ADCY7/ADCY3/PLIN1/ADCY8/PIK3R3/PRKG1/GNAI3/GNAS/ADCY2/PIK3CA/AKT2/PIK3R1/PDE3B/ADCY4/ADCY9/NPY1R	25
hsa005 65	Ether lipid metabolism	22/2512	49/810 5	0.02778 502	0.11426 5896	0.08518 3023	PLB1/TMEM189/PLA2G7/ENPP2/LPCAT2/PAFAH1B3/GDPD1/JMJD7-	22

							PLA2G4B/PLD1/SELENOI/PLA2G2D/P LA2G5/PLA2G4F/TMEM189- UBE2V1/AGPS/PAFAH1B2/PAFAH2/P LA2G12A/PLA2G3/PLA2G4B/CHPT1/ PLA2G4E	
hsa050 30	Cocaine addiction	22/2512	49/810 5	0.02778 502	0.11426 5896	0.08518 3023	PRKACB/CREB5/TH/PPP1R1B/RGS9/ MAOA/ATF4/GRIN2B/GRIN2A/DLG4/ CREB1/DDC/GNAI3/ATF2/GNAS/BDN F/CREB3L1/FOSB/GRIA2/JUN/CREB3 L3/GRM2	22
hsa047 30	Long-term depression	26/2512	60/810 5	0.02891 8378	0.11745 8597	0.08756 312	ITPR1/GUCY1A1/PPP2R1B/GRM1/IGF 1/MAPK3/KRAS/PRKG2/BRAF/PLCB1 /RAF1/GRIA3/ITPR3/JMJD7- PLA2G4B/GNA13/PRKG1/GNAI3/PLA 2G4F/GNAS/GNAQ/NOS1/ITPR2/PRK CB/GRIA2/PLA2G4B/PLA2G4E	26
hsa046 70	Leukocyte transendothelial migration	45/2512	114/81 05	0.03262 7377	0.13090 7403	0.09758 8945	CTNND1/CTNNB1/PTK2/CTNNA2/RA SSF5/OCLN/ITGB1/PIK3CD/MAPK14/I TGAM/MYL12B/VCAM1/CXCL12/NC F2/CLDN1/EZR/ARHGAP5/CXCR4/VA V3/CD99/PIK3R3/GNAI3/RAC2/CD99L 2/MMP9/ARHGAP35/RAPGEF3/ICAM	45

							1/CDC42/PRKCB/PXN/MSN/F11R/SIP A1/CLDN20/PIK3CA/PECAM1/PIK3R1 /MYL12A/ESAM/CLDN17/ITGAL/RO CK1/JAM2/ITGA4	
hsa050 31	Amphetamine addiction	29/2512	69/810 5	0.03378 1596	0.13326 8169	0.09934 8851	CACNA1C/PRKACB/CAMK2B/CREB5 /PPP3CB/CAMK2G/TH/CAMK4/CACN A1D/PPP3CA/PPP1R1B/MAOA/ATF4/ GRIN2B/GRIN2A/CREB1/DDC/GRIA3/ CALM1/PPP3R1/ATF2/GNAS/CREB3L 1/PRKCB/FOSB/HDAC1/GRIA2/JUN/C REB3L3	29
hsa052 13	Endometrial cancer	25/2512	58/810 5	0.03402 5916	0.13326 8169	0.09934 8851	CTNNB1/CTNNA2/TCF7/ERBB2/MLH 1/EGF/SOS2/MAPK3/EGFR/PIK3CD/K RAS/BRAF/FOXO3/RAF1/GSK3B/CD H1/APC/PIK3R3/TP53/AXIN2/BAK1/PI K3CA/AKT2/PIK3R1/GADD45B	25
hsa047 28	Dopaminergic synapse	51/2512	132/81 05	0.03619 5766	0.14009 8908	0.10444 1035	CACNA1C/ITPR1/PRKACB/SCN1A/C AMK2B/MAPK8/KCNJ3/CREB5/PPP2 R1B/ARRB1/PPP2R2C/PPP3CB/CAMK 2G/TH/MAPK14/PPP2R5D/CLOCK/CA CNA1D/PPP3CA/GNG4/PPP1R1B/MA OA/ATF4/GRIN2B/GRIN2A/PLCB1/GS	51

							K3B/CREB1/DDC/GRIA3/KIF5A/DRD5/CALM1/ITPR3/KIF5B/GNAI3/GNG2/ATF2/GNAS/MAPK9/CREB3L1/GNAQ/ITPR2/GNG12/PRKCB/COMT/AKT2/GRIA2/PPP2R5E/MAPK10/CREB3L3	
hsa05222	Small cell lung cancer	37/2512	92/8105	0.037193098	0.142285223	0.106070891	APAF1/PTK2/FN1/LAMA3/CDK2/E2F3/BIRC3/LAMA2/CCNE2/ITGB1/PIK3CD/TRAF1/XIAP/ITGA6/SKP2/CDK6/ITGA3/ZBTB17/ITGA2/LAMC2/CDKN2B/COL4A3/CYCS/PIK3R3/TP53/LAMA1/RB1/BCL2/BAK1/PIK3CA/AKT2/PIK3R1/TRAF6/GADD45B/COL4A1/COL4A2/FHIT	37
hsa05230	Central carbon metabolism in cancer	29/2512	70/8105	0.041051391	0.155240317	0.115728664	HK1/FGFR2/HIF1A/RET/ERBB2/SCO2/PFKM/GCK/FGFR1/MAPK3/EGFR/PIK3CD/KRAS/GLS/MET/RAF1/G6PD/PIK3R3/TP53/PDHA2/PDGFRB/SLC1A5/IDH2/PIK3CA/AKT2/PIK3R1/PFKP/LDHA/PFKL	29
hsa04370	VEGF signaling pathway	25/2512	59/8105	0.042126311	0.156393137	0.116588069	PTK2/PPP3CB/SPHK2/MAPK3/PIK3CD/KRAS/MAPK14/PPP3CA/NFATC2/RAFI/JMJD7-	25

							PLA2G4B/PIK3R3/MAPKAPK3/RAC2/ PPP3R1/PLA2G4F/SRC/CDC42/PRKCB /PXN/PIK3CA/AKT2/PIK3R1/PLA2G4 B/PLA2G4E	
hsa015 24	Platinum drug resistance	30/2512	73/810 5	0.04259 1064	0.15639 3137	0.11658 8069	APAF1/MDM2/ATM/BRCA1/ERBB2/ MLH1/BIRC3/MAPK3/PIK3CD/XIAP/R EV3L/ATP7B/MSH6/GSTO1/CYCS/PI K3R3/GSTA4/TP53/BCL2/BAK1/ABCC 2/PIK3CA/SLC31A1/AKT2/PIK3R1/TO P2A/GSTM3/CASP8/MSH3/MSH2	30
hsa052 02	Transcriptional misregulation in cancer	71/2512	192/81 05	0.04278 2317	0.15639 3137	0.11658 8069	CDK14/PTK2/SUPT3H/HMGA2/KDM6 A/HPGD/CD86/ETV1/PAX5/PML/TCF3 /FLT1/MDM2/MLLT3/ATM/ZEB1/PBX 3/BIRC3/NFKBIZ/EYA1/RUNX1/RUN X2/IGF1/FUT8/TRAF1/ITGAM/WT1/M YCN/IL6/JMJD1C/SSX2/SSX2B/MET/ GRIA3/ZBTB17/REL/FUS/DUSP6/CD1 4/PROM1/CCNT2/ELK4/TP53/NSD2/C CNA2/MEN1/MMP9/SSX1/LMO2/BAK 1/BMI1/MEF2C/SIX1/HDAC1/DOT1L/ BMP2K/SPINT1/HOXA10/PER2/SS18/ CCNT1/FOXO1/ZBTB16/GADD45B/N	71

							COR1/JUP/RUNX1T1/TMPRSS2/MAF/ETV5/DDIT3	
hsa04213	Longevity regulating pathway - multiple species	26/2512	62/8105	0.044112752	0.157508283	0.117419389	PRKAG2/PRKACB/CLPB/SOD2/IGF1/PIK3CD/KRAS/CRYAB/IRS2/FOXO3/ADCY7/ADCY3/PRKAA1/ADCY8/PIK3R3/ADCY2/HDAC1/PIK3CA/AKT2/PIK3R1/PRKAG3/FOXA2/FOXO1/PRKAB2/ADCY4/ADCY9	26
hsa05163	Human cytomegalovirus infection	82/2512	225/8105	0.044113798	0.157508283	0.117419389	ITPR1/CTNNB1/PRKACB/JAK1/NFATC4/NFATC1/PTK2/ARHGEF12/AKAP13/CREB5/MDM2/E2F3/PPP3CB/SOS2/MAPK3/PTGER3/EGFR/PIK3CD/KRAS/MAPK14/PPP3CA/NFATC2/TSC2/ARHGEF11/ARHGEF1/GNG4/IL1R1/CDK6/CXCL12/CRKL/ATF4/IL6/ADCY7/ADCY3/STAT3/PLCB1/RAF1/GSK3B/CREB1/ADCY8/CALM1/ITPR3/MAP2K6/CXCR4/TNFRSF1A/GNA13/CYCS/PIK3R3/GNAI3/TP53/RAC2/PPP3R1/GNG2/ATF2/IFNB1/SRC/GNAS/RB1/CREB3L1/GNAQ/ADCY2/ITPR2/GNG12/CCR1/IL10RB/PRKCB/BAK1/PXN/CX	82

							3CL1/PIK3CA/AKT2/PIK3R1/PTGER4/ CASP8/CCR3/ADCY4/CCL3/CCL3L3/ ADCY9/ROCK1/ITGB3/CREB3L3	
hsa040 71	Sphingolipid signaling pathway	46/2512	119/81 05	0.04452 3618	0.15750 8283	0.11741 9389	KNG1/FYN/MAPK8/CERS5/PPP2R1B/ PPP2R2C/ASAH2/SPHK2/MAPK3/PIK 3CD/KRAS/MAPK14/PPP2R5D/CERS2 /ABCC1/MS4A2/S1PR1/CERS3/CERS6/ PLCB1/RAF1/PLD1/TNFRSF1A/SGPP1 /GNA13/PIK3R3/GNAI3/TP53/RAC2/S PTLC3/ASAH1/MAPK9/GNAQ/PRKCB /BCL2/PIK3CA/AKT2/PIK3R1/FCER1 G/SGPP2/PPP2R5E/SPTLC1/ROCK1/N SMAF/S1PR3/MAPK10	46
hsa053 21	Inflammatory bowel disease	27/2512	65/810 5	0.04598 7806	0.16095 732	0.11999 0579	NFATC1/STAT6/SMAD2/NOD2/FOXP 3/RORA/RORC/IL4R/IL12RB2/IL6/IL4/ IL18RAP/STAT3/IL21R/SMAD3/TLR5/ IFNGR2/IFNGR1/IL1A/HLA- DRB5/TGFB3/STAT1/JUN/IL5/IL13/M AF/HLA-DPB1	27
hsa012 12	Fatty acid metabolism	24/2512	57/810 5	0.04938 4131	0.16969 8508	0.12650 6967	ACSL6/ELOVL5/ACADM/ACACA/CP T1C/HACD4/SCP2/HADH/ACSBG2/HT D2/FADS1/ACSL5/FADS2/ELOVL2/E	24

							HHADH/ACSL1/SCD/ACADVL/CPT1 A/HADHA/PPT1/ELOVL4/CBR4/ACA DL	
hsa045 14	Cell adhesion molecules	56/2512	149/81 05	0.04951 689	0.16969 8508	0.12650 6967	NRCAM/VTCN1/CD86/OCLN/NRXN1/ LRRC4C/ALCAM/CD276/SPN/ITGB1/ CD274/ITGA6/ITGAM/VCAN/NFASC/I COSLG/VCAM1/NEO1/L1CAM/PTPR M/SELPLG/CLDN1/NLGN4X/NRXN3/ CDH1/NRXN2/CDH3/IGSF11/ICOS/CD 99/CD99L2/NCAM2/NTNG1/CNTNAP 1/CD226/ICAM1/CDH4/F11R/SELE/CL DN20/HLA- DRB5/PECAM1/CNTN2/NLGN1/CD4/ LRRC4/ESAM/CLDN17/ITGAL/JAM2/ NECTIN3/HLA- DPB1/CDH15/MAG/ITGA4/SELP	56
hsa049 74	Protein digestion and absorption	40/2512	103/81 05	0.05409 9886	0.18349 3428	0.13679 0814	COL25A1/SLC8A1/COL12A1/COL24A 1/MME/SLC38A2/COL19A1/PRSS3/CO L17A1/ATP1A1/COL21A1/COL8A2/SL C7A7/SLC36A3/MEP1A/COL16A1/AT P1B1/COL6A6/COL3A1/COL8A1/ATP 1B4/PRCP/COL4A3/COL9A1/PGA3/PG	40

							A4/PGA5/COL11A2/SLC1A5/COL15A1/SLC8A2/PRSS1/COL20A1/COL6A3/COL10A1/COL9A2/SLC16A10/COL4A1/COL4A2/COL6A5	
hsa05235	PD-L1 expression and PD-1 checkpoint pathway in cancer	35/2512	89/8105	0.057565116	0.193254316	0.144067368	JAK1/NFATC1/HIF1A/PPP3CB/EGF/C SNK2A1/MAPK3/EGFR/PIK3CD/KRAS/CD274/MAPK14/MAP3K3/PPP3CA/NFATC2/STAT3/RAF1/MAP2K6/RAS GRP1/PIK3R3/PPP3R1/TICAM2/IFNGR2/IFNGR1/NFKBIE/PIK3CA/AKT2/PIK3R1/CD4/TRAF6/ZAP70/CSNK2A3/S TAT1/JUN/EML4	35
hsa00532	Glycosaminoglycan biosynthesis - chondroitin sulfate / dermatan sulfate	10/2512	20/8105	0.058752193	0.193339682	0.144131006	CHST15/CHST11/DSE/CHST3/CSGAL NACT2/CHPF2/UST/XYLT1/CHSY1/CHSY3	10
hsa04962	Vasopressin-regulated water reabsorption	19/2512	44/8105	0.058765861	0.193339682	0.144131006	PRKACB/RAB5A/CREB5/DYNC1I2/D YNC1I1/RAB5B/DCTN2/ARHGDIB/ADCY3/CREB1/DCTN1/DYNC1LI2/GNAS/CREB3L1/STX4/DCTN6/ADCY9/D YNC2LI1/CREB3L3	19
hsa002	Purine metabolism	49/2512	130/81	0.06002	0.19551	0.14575	AK4/ENTPD1/PDE4A/PDE4D/PDE5A/	49

30			05	0477	2247	0612	PRUNE1/GDA/AK9/PDE4C/GUCY1A1/PDE8B/PDE1C/PDE11A/ADCY10/GMPR2/RRM2B/CANT1/RRM2/PDE3A/AK2/AK3/PDE7B/ADCY7/ADCY3/ADCY8/PKLR/PDE7A/HDDC3/NT5C1A/ENPP3/ENTPD5/ADCY2/NME6/NT5C/HPRT1/AK7/NT5M/NPR2/PGM1/PNP/PDE10A/PDE3B/PAPSS1/ADCY4/ADCY9/NTPCR/NT5E/FHIT/PDE4B	
hsa04722	Neurotrophin signaling pathway	45/2512	119/8105	0.065857154	0.212421604	0.158356211	RPS6KA3/CAMK2B/IRAK3/MAPK8/RPS6KA6/IRAK1/GAB1/CAMK2G/SOS2/MAPK3/PIK3CD/KRAS/CAMK4/MAPK14/KIDINS220/ARHGDIB/MAP3K3/BRAF/CRKL/RPS6KA2/FOXO3/ATF4/RAF1/GSK3B/PSEN2/CALM1/NTRK2/PIK3R3/TP53/MAP3K1/SORT1/MAPK9/BDNF/CDC42/BCL2/NFKBIE/RIPK2/PIK3CA/AKT2/PIK3R1/SHC4/TRAF6/JUN/MAPK10/IRAK2	45
hsa04115	p53 signaling pathway	29/2512	73/8105	0.069773207	0.222867816	0.16614366	APAF1/MDM4/SESN3/SESN1/RCHY1/CCNG1/MDM2/CDK2/ATM/CCNE2/IGF1/ATR/CCND3/TSC2/RRM2B/RRM2/	29

							CDK6/CCNG2/SIAH1/COP1/SERPINB 5/PPM1D/SHISA5/CYCS/TP53/ZMAT3 /BCL2/GADD45B/CASP8	
hsa034 50	Non-homologous end-joining	7/2512	13/810 5	0.07303 4772	0.23104 2692	0.17223 7873	POLL/PRKDC/DCLRE1C/XRCC4/LIG4 /MRE11/XRCC5	7
hsa041 46	Peroxisome	32/2512	82/810 5	0.07402 6539	0.23194 9823	0.17291 4122	ACSL6/SOD2/EPHX2/SCP2/HMGCLL1 /ACSL5/MPV17L/NUDT7/PEX1/EHHA DH/BAAT/ACSL1/PEX11G/FAR2/ABC D4/PEX2/AMACR/PEX19/PXMP4/PEX 14/ABCD1/HACL1/AGPS/PIPOX/DDO/ IDH2/DAO/PXMP2/PEX5/ECH1/MPV1 7/HAO1	32
hsa045 40	Gap junction	34/2512	88/810 5	0.07637 6698	0.23705 5979	0.17672 0662	ITPR1/PRKACB/TUBB/GUCY1A1/EG F/GRM1/SOS2/MAPK3/EGFR/KRAS/P RKG2/ADCY7/ADCY3/PDGFD/PLCB1 /RAF1/ADCY8/TJP1/ITPR3/PRKG1/GN AI3/SRC/GNAS/PDGFRB/GNAQ/ADC Y2/ITPR2/PRKCB/PDGFC/HTR2B/TU BB8/TUBB4B/ADCY4/ADCY9	34
hsa046 64	Fc epsilon RI signaling pathway	27/2512	68/810 5	0.07862 2859	0.24151 4212	0.18004 4189	FYN/MAPK8/SOS2/MAPK3/PIK3CD/K RAS/MAPK14/MAP2K4/MS4A2/IL4/R AF1/MAP2K6/JMJD7-	27

							PLA2G4B/VAV3/PIK3R3/RAC2/PLA2G4F/MAPK9/PIK3CA/AKT2/PIK3R1/FER1G/PLA2G4B/MAPK10/IL5/IL13/PLA2G4E	
hsa04913	Ovarian steroidogenesis	21/2512	51/8105	0.079281261	0.241514212	0.180044189	PRKACB/CYP1A1/LDLR/IGF1/CGA/CYP19A1/ADCY7/ADCY3/ADCY8/JMD7-PLA2G4B/CYP1B1/PLA2G4F/GNAS/ADCY2/BMP6/HSD3B2/ADCY4/ADCY9/PLA2G4B/PLA2G4E/LHCGR	21
hsa04520	Adherens junction	28/2512	71/8105	0.08031535	0.242419727	0.180719234	CTNND1/CTNNB1/LMO7/PTPRB/CTNNA2/TCF7/FYN/ERBB2/WASF1/CSNK2A1/MAP3K7/FGFR1/MAPK3/EGFR/TPRM/IQGAP1/MET/TJP1/CDH1/SMA D3/TGFBR1/NECTIN4/RAC2/SRC/CD C42/YES1/CSNK2A3/NECTIN3	28
hsa00770	Pantothenate and CoA biosynthesis	10/2512	21/8105	0.081919773	0.242976027	0.181133944	BCAT1/PPCDC/PANK2/PANK1/DPYD/VNN1/AASDHPPT/ENPP3/PANK3/VNN2	10
hsa03460	Fanconi anemia pathway	22/2512	54/8105	0.081976714	0.242976027	0.181133944	FANCI/BRCA1/MLH1/CENPS-CORT/POLI/ATR/EME1/REV1/FANCD2/REV3L/BLM/BRCA2/POLN/FAAP24/	22

							PALB2/FANCA/USP1/TOP3A/CENPS/ EME2/FANCC/FANCF	
hsa043 90	Hippo signaling pathway	57/2512	157/81 05	0.08718 8167	0.25611 5239	0.19092 8974	CTNNB1/YAP1/DLG2/FGF1/FZD3/CT NNA2/BTRC/TCF7/SMAD2/FBXW11/P PP2R1B/WWC1/BMPR1B/BIRC3/PPP2 R2C/CRB1/WNT2B/CCND3/YWHAB/ NKD1/DVL3/AMOT/LATS1/GSK3B/D LG4/SCRIB/CDH1/FZD4/LIMD1/SMA D3/TGFBR1/APC/MPP5/CSNK1E/WNT 10B/BMP8A/WNT9B/AXIN2/FZD10/B MPR2/WNT5A/BMP6/TP53BP2/BMP7/ WNT8A/WNT5B/PRKCI/TGFB3/AMH/ MOB1A/FZD5/TEAD1/GDF6/YWHAH/ FZD8/AFP/TEAD3	57
hsa046 60	T cell receptor signaling pathway	39/2512	104/81 05	0.09199 8201	0.26723 9649	0.19922 2007	NFATC1/FYN/MAPK8/PPP3CB/MAP3 K7/SOS2/MAPK3/PIK3CD/KRAS/MAP K14/PPP3CA/NFATC2/MAP3K8/PAK1/ IL4/RAF1/GSK3B/PAK4/BCL10/RASG RP1/VAV3/ICOS/PIK3R3/PPP3R1/MA LT1/MAPK9/CDC42/PAK5/CBLB/NFK BIE/PIK3CA/AKT2/PIK3R1/CD4/ZAP7 0/MAP3K14/JUN/MAPK10/IL5	39

hsa046 59	Th17 differentiation cell	40/2512	107/81 05	0.09259 9757	0.26723 9649	0.19922 2007	JAK1/NFATC1/STAT6/SMAD2/MAPK 8/HIF1A/FOXP3/PPP3CB/RORA/RUN X1/RORC/MAPK3/IL6ST/MAPK14/PP P3CA/NFATC2/IL4R/IL1R1/IL6/IL4/ST AT3/IL21R/SMAD3/TGFBR1/TYK2/ST AT5B/PPP3R1/MAPK9/IFNGR2/IFNGR 1/AHR/NFKBIE/HLA- DRB5/IL1RAP/CD4/ZAP70/STAT1/JU N/MAPK10/HLA-DPB1	40
hsa052 18	Melanoma	28/2512	72/810 5	0.09389 5687	0.26862 3313	0.20025 3502	FGF1/MDM2/E2F3/EGF/FGFR1/IGF1/ MAPK3/EGFR/PIK3CD/KRAS/CDK6/B RAF/PDGFD/MET/RAF1/CDH1/PIK3R 3/TP53/RB1/PDGFRB/FGF21/PDGFC/B AK1/FGF17/PIK3CA/AKT2/PIK3R1/G ADD45B	28
hsa052 14	Glioma	29/2512	75/810 5	0.09532 463	0.27008 222	0.20134 1089	CAMK2B/MDM2/E2F3/CAMK2G/EGF/ IGF1/SOS2/MAPK3/EGFR/PIK3CD/KR AS/CAMK4/CDK6/BRAF/RAF1/CALM 1/PIK3R3/TP53/RB1/PDGFRB/PRKCB/ TGFA/BAK1/PIK3CA/CAMK1D/AKT2 /PIK3R1/SHC4/GADD45B	29
hsa043	Apelin signaling	50/2512	137/81	0.09604	0.27008	0.20134	ITPR1/PRKAG2/PRKACB/SLC8A1/SM	50

71	pathway		05	7476	222	1089	AD2/MEF2D/SPHK2/MAPK3/ADCY10 /KRAS/CAMK4/RYR3/GNG4/ADCY7/ ADCY3/PLCB1/RAF1/PLIN1/PRKAA1/ ADCY8/CDH1/CALM1/SMAD3/ITPR3/ TGFB1/PIK3R5/GNA13/GNAI3/MYL K3/SLC9A1/GNG2/MRAS/GNAQ/ADC Y2/NOS1/ITPR2/GNG12/PIK3R6/MEF2 C/SLC8A2/AKT2/MYLK4/PRKAG3/PR KAB2/PPARGC1A/PDE3B/ADCY4/RP S6/GABARAP/ADCY9	
hsa052 19	Bladder cancer	17/2512	41/810 5	0.10144 4317	0.28284 0512	0.21085 215	MDM2/E2F3/ERBB2/EGF/MAPK3/EGF R/KRAS/BRAF/RAF1/MMP1/CDH1/TP 53/SRC/MMP9/RB1/DAPK3/HBEGF	17
hsa049 72	Pancreatic secretion	38/2512	102/81 05	0.10356 2193	0.28631 9004	0.21344 5298	ITPR1/ATP2B1/KCNMA1/ATP2A1/PR SS3/ATP2A2/CCKAR/ATP1A1/ADCY7 /CLCA4/CFTR/ADCY3/PLCB1/ADCY8 /ATP1B1/ATP2B4/ITPR3/SLC12A2/AT P1B4/SLC4A4/PLA2G2D/SLC9A1/ATP 2A3/PLA2G5/GNAS/GNAQ/ADCY2/IT PR2/PRKCB/PNLIP/PRSS1/PLA2G12A/ CLCA1/PLA2G3/SLC4A2/ADCY4/TPC N2/ADCY9	38

hsa049 31	Insulin resistance	40/2512	108/81 05	0.10456 0427	0.28666 9837	0.21370 6837	PRKAG2/RPS6KA3/PPARGC1B/MAP K8/CREB5/G6PC/RPS6KA6/NR1H3/PI K3CD/TBC1D4/IRS2/RPS6KA2/IL6/ST AT3/GSK3B/CREB1/PRKAA1/OGT/PP ARA/TNFRSF1A/PIK3R3/SLC2A4/MA PK9/CREB3L1/CPT1A/PRKCB/SLC27 A3/PPP1R3A/GFPT2/GYS1/PIK3CA/A KT2/PIK3R1/PRKAG3/FOXO1/PRKAB 2/PPARGC1A/AGT/MAPK10/CREB3L 3	40
hsa040 14	Ras signaling pathway	81/2512	232/81 05	0.10859 9026	0.29528 1649	0.22012 6777	PRKACB/FGFR2/FGF1/RAB5A/RASSF 5/MAPK8/FLT1/ABL2/CSF1/RASAL1/ GAB1/RASGRF1/EGF/FGFR1/IGF1/RA B5B/SOS2/MAPK3/EGFR/KSR1/PIK3C D/KRAS/TEK/GNG4/RALA/RGL1/PA K1/KSR2/GRIN2B/PDGFD/MET/GRIN 2A/RAF1/TIAM1/CALM1/REL/SHOC2/ JMJD7- PLA2G4B/RASA1/PAK4/RIN1/PLD1/N TRK2/RASGRP1/RAPGEF5/PIK3R3/ET S1/PLA2G2D/RAC2/ANGPT4/GNG2/P LA2G5/PLA2G4F/RASGRP3/RALB/PD	81

							GFRB/MAPK9/MRAS/BDNF/FGF21/G NG12/ARF6/CDC42/PRKCB/PAK5/PD GFC/TGFA/FGF17/PIK3CA/PLA2G12A /AKT2/PIK3R1/SHC4/PLA2G3/ZAP70/ PLA2G4B/MAPK10/ETS2/PLA2G4E/R ASAL2/RALBP1	
hsa051 65	Human papillomavirus infection	113/251 2	331/81 05	0.11505 8724	0.31028 1313	0.23130 8737	CTNNB1/PRKACB/UBE3A/JAK1/DLG 2/FZD3/PTK2/FN1/ATP6V0A4/TCF7/EI F2AK2/ITGB6/LAMA3/CREB5/MDM2/ CDK2/ATM/PPP2R1B/PPP2R2C/LAM A2/CCNE2/RBPJ/EGF/MAML2/SOS2/I TGB1/MAPK3/EGFR/PIK3CD/KRAS/P PP2R5D/WNT2B/ATR/ITGA6/CCND3/ TSC2/CDK6/DVL3/ITGA5/ITGA3/RAF 1/GSK3B/MAGI1/CREB1/ITGA2/RELN /SCRIB/COL6A6/FZD4/LAMC2/APC/ MPP5/TBPL1/ITGA10/TYK2/TNFRSF1 A/WNT10B/COL4A3/PIK3R3/COL9A1/ WNT9B/TP53/ATP6V1D/AXIN2/FZD1 0/CCNA2/IFNB1/RBL2/LAMA1/MAM L3/GNAS/RB1/PDGFRB/CREB3L1/CD C42/WNT5A/BAK1/TNC/PXN/STAT2/	113

							HDAC1/ITGA11/COL6A3/ITGB5/RBL1 /PIK3CA/AKT2/PIK3R1/WNT8A/CHA D/WNT5B/PRKCI/PPP2R5E/PTGER4/F OXO1/HEYL/COL9A2/HEY2/CSNK1A 1/CASP8/ATP6AP1/STAT1/IRF9/FZD5/ ATP6V1G1/MX1/COL4A1/COL4A2/FZ D8/ITGA4/ITGB3/CREB3L3/COL6A5	
hsa051 62	Measles	50/2512	139/81 05	0.11828 9239	0.31639 967	0.23586 9855	APAF1/JAK1/ADAR/TNFAIP3/EIF2AK 2/MAPK8/MAVS/RCHY1/CDK2/EIF2A K1/IRAK1/OAS1/CCNE2/CSNK2A1/M AP3K7/PIK3CD/RAB9A/CCND3/CDK6 /IL6/STAT3/GSK3B/OAS2/TYK2/CYC S/PIK3R3/STAT5B/TP53/RAB9B/IFNB 1/TAB2/MAPK9/BCL2/CBLB/BAK1/IL 1A/STAT2/MSN/PIK3CA/AKT2/PIK3R 1/TRAF6/CASP8/CSNK2A3/IFIH1/STA T1/IRF9/JUN/MAPK10/MX1	50
hsa041 44	Endocytosis	87/2512	252/81 05	0.12313 9789	0.32570 2935	0.24280 526	NEDD4L/FGFR2/NEDD4/AGAP1/RAB 5A/RNF41/USP8/DNM3/IST1/SMAD2/ WASHC2A/SMAP2/PML/LDLR/MDM2 /ASAP2/SH3KBP1/ARRB1/RUFY2/GR K4/PDCD6IP/RAB5B/STAMBP/ARAP2	87

							/EGFR/VPS45/AGAP2/CAV1/RUFY1/A RFGAP1/ACAP2/IGF2R/ACTR3/RAB4 A/ARAP3/KIF5A/AP2M1/CBL/SMAD3 /TGFB1/GIT1/PIP5K1C/AP2B1/CXCR 4/AGAP4/ASAP3/PLD1/KIF5B/PSD2/E PS15L1/ARPC3/VPS26B/STAM2/SRC/ CHMP6/ACAP3/ARF6/CDC42/CBLB/A P2S1/ARF4/PIP5K1B/EEA1/RAB11FIP 5/CYTH3/ARF5/CHMP7/RAB11FIP2/S H3GL3/PSD3/PRKCI/TRAFF6/DNAJC6/ SPART/VPS4B/CYTH2/AGAP6/AGAP 5/SNX6/SH3GLB2/CHMP1A/WIPF3/V PS26A/VPS36/RAB31/CBLC/RAB22A	
hsa051 32	Salmonella infection	86/2512	249/81 05	0.12374 7316	0.32570 2935	0.24280 526	CTNNB1/ABI1/TUBB/RAB5A/NAIP/T CF7/MAPK8/IRAK1/CYFIP1/DYNC1I2 /STX10/BIRC3/CASP1/CYFIP2/DYNC1 I1/MAP3K7/RAB5B/MAPK3/PIK3CD/ MAPK14/RAB9A/DCTN2/MYL12B/NL RP3/RALA/PAK1/MAP2K4/ARL8B/TL R6/EXOC7/KPNA1/TNFSF10/IL6/ACT R3/RAF1/KIF5A/EXOC5/MYO6/FLNC/ RIPK3/M6PR/MAP2K6/ARL8A/CD14/	86

							NLRC4/TNFRSF1A/GCC2/KPNA4/CYCS/KIF5B/RAB7B/TLR5/RAB9B/RHOG/ARPC3/DCTN1/DYNC1LI2/TAB2/MAPK9/ARF6/CDC42/BCL2/BAK1/ELMO1/ACTR1A/NOD1/TUBB8/RIPK2/CYTH3/VPS39/TUBB4B/PIK3CA/AKT2/DCTN6/DYNLT1/DYNLT3/TRAF6/PLEKHM1/TXN2/MYL12A/CASP8/CYTH2/NCKAP1/DYNC2LI1/JUN/MAPK10	
hsa04658	Th1 and Th2 cell differentiation	34/2512	92/8105	0.129796937	0.336383833	0.250767663	JAK1/NFATC1/STAT6/MAPK8/PPP3CB/RBPJ/MAML2/MAPK3/MAPK14/PPP3CA/NFATC2/IL4R/IL12RB2/IL4/JAG2/TYK2/STAT5B/PPP3R1/MAML3/MAPK9/IFNGR2/IFNGR1/NFKBIE/HLA-DRB5/CD4/ZAP70/STAT1/JUN/MAPK10/IL5/IL13/MAF/HLA-DPB1/RUNX3	34
hsa04140	Autophagy animal	- 49/2512	137/8105	0.130784305	0.336383833	0.250767663	ITPR1/PRKACB/CFLAR/ATG12/MAPK8/CTSB/HIF1A/RB1CC1/STX17/MAP3K7/MAPK3/ATG7/PIK3CD/KRAS/ATG2A/TSC2/ATG10/IRS2/ATG4C/RUBCN/TANK/RAF1/PRKAA1/WDR41/C9orf72/WIP1/CTSL/RAB7B/PIK3R3/ULK	49

							2/ATG9B/ATG16L1/MAPK9/MRAS/H MGB1/DAPK3/MTMR3/BCL2/AMBRA 1/RRAGD/PIK3CA/AKT2/PIK3R1/ULK 1/TRAF6/DEPTOR/LAMP1/GABARAP /MAPK10	
hsa049 16	Melanogenesis	37/2512	101/81 05	0.13087 2738	0.33638 3833	0.25076 7663	CTNNB1/PRKACB/FZD3/CAMK2B/TC F7/EDNRB/CAMK2G/MAPK3/KRAS/ WNT2B/DVL3/ADCY7/ADCY3/PLCB1 /RAF1/GSK3B/CREB1/ADCY8/CALM1 /FZD4/WNT10B/GNAI3/WNT9B/FZD1 0/GNAS/CREB3L1/GNAQ/ADCY2/PR KCB/WNT5A/WNT8A/WNT5B/ADCY 4/ADCY9/FZD5/FZD8/CREB3L3	37
hsa006 70	One carbon pool by folate	9/2512	20/810 5	0.13358 6346	0.34069 6961	0.25398 3017	DHFR2/MTR/MTHFD2L/MTHFR/ALD H1L2/SHMT1/ST20- MTHFS/MTHFS/SHMT2	9
hsa049 20	Adipocytokine signaling pathway	26/2512	69/810 5	0.14144 4593	0.35523 1077	0.26481 792	PRKAG2/ACSL6/LEPR/MAPK8/G6PC/ CPT1C/ACSBG2/ACSL5/IRS2/STAT3/ ADIPOQ/ACSL1/PRKAA1/PPARA/TN FRSF1A/SLC2A4/ADIPOR2/MAPK9/C PT1A/LEP/NFKBIE/AKT2/PRKAG3/PR KAB2/PPARGC1A/MAPK10	26

hsa05211	Renal cell carcinoma	26/2512	69/8105	0.141444593	0.355231077	0.26481792	CUL2/HIF1A/GAB1/EGLN3/SOS2/MAK3/PIK3CD/KRAS/PAK1/BRAF/CRKL/MET/RAF1/PAK4/PIK3R3/ETS1/EGLN1/CDC42/PAK5/TGFA/PIK3CA/AKT2/PIK3R1/VHL/TGFB3/JUN	26
hsa00515	Mannose type O-glycan biosynthesis	10/2512	23/8105	0.14262643	0.355485573	0.265007642	ST3GAL3/B3GAT1/POMT2/FKTN/POMGNT1/LARGE1/POMK/CHST10/LARGE2/POMGNT2	10
hsa00563	Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	11/2512	26/8105	0.14998024	0.371003751	0.276576145	PIGN/PIGL/PIGW/PIGA/PIGM/PIGO/PIGV/PGAP1/PIGC/GPLD1/PIGH	11
hsa04210	Apoptosis	48/2512	136/8105	0.158541929	0.389255931	0.290182793	ITPR1/APAF1/DAB2IP/CFLAR/MAPK8/CTSV/CTSB/ATM/CAPN1/BIRC3/CASP2/PTPN13/MAPK3/SPTAN1/PIK3CD/TRAF1/KRAS/XIAP/HRK/TNFSF10/ATF4/RAF1/ITPR3/BCL2L11/DFFB/TNFRSF1A/CTSL/CYCS/PIK3R3/TP53/PARP4/MAPK9/ITPR2/BCL2/BAK1/CAPN2/PIK3CA/AKT2/PIK3R1/CTSC/GADD45B/CASP8/MAP3K14/JUN/MAPK10/CTSS/CTSZ/DDIT3	48
hsa052	Acute myeloid	25/2512	67/810	0.16075	0.38951	0.29037	TCF7/PML/RUNX1/SOS2/MAPK3/PIK	25

21	leukemia		5	6736	3167	4558	3CD/KRAS/ITGAM/BRAF/STAT3/RAF1/DUSP6/CD14/PIK3R3/STAT5B/CCNA2/PIK3CA/AKT2/PIK3R1/PER2/ZBTB16/PIM1/JUP/RUNX1T1/PIM2	
hsa04215	Apoptosis - multiple species	13/2512	32/8105	0.161014562	0.389513167	0.290374558	APAF1/MAPK8/BIRC3/XIAP/BIRC6/BCL2L11/TNFRSF1A/CYCS/MAPK9/BCL2/BAK1/CASP8/MAPK10	13
hsa05220	Chronic myeloid leukemia	28/2512	76/8105	0.162559252	0.390379518	0.291020405	MDM2/E2F3/RUNX1/SOS2/MAPK3/PIK3CD/KRAS/CDK6/BRAF/CRKL/RAF1/BCR/CBL/SMAD3/TGFBR1/PIK3R3/STAT5B/TP53/RB1/BAK1/HDAC1/PIK3CA/AKT2/PIK3R1/SHC4/GADD45B/TGFB3/CTBP2	28
hsa03440	Homologous recombination	16/2512	41/8105	0.17152818	0.408933126	0.304851762	RBBP8/ATM/BRCA1/POLD3/EME1/TOPBP1/RAD52/BABAM1/BLM/BRCA2/MRE11/PALB2/TOP3A/RAD51D/BABAM2/RAD51B	16
hsa04910	Insulin signaling pathway	48/2512	137/8105	0.173512333	0.41058424	0.306082636	PRKAG2/HK1/PRKACB/SOCS2/MAPK8/G6PC/PRKAR1A/SOCS4/PHKB/PHKA1/ACACA/GCK/SOS2/MAPK3/PIK3CD/KRAS/PRKAR2A/TSC2/BRAF/IRS2/CRKL/EXOC7/RAF1/GSK3B/PRKAA1/	48

							CALM1/CBL/PKLR/PIK3R3/SLC2A4/RHOQ/MAPK9/CBLB/PPP1R3A/GYS1/EIF4E/PIK3CA/AKT2/PIK3R1/SHC4/PRKAG3/PRKCI/FOXO1/PRKAB2/PPARGC1A/PDE3B/RPS6/MAPK10	
hsa05152	Tuberculosis	62/2512	180/8105	0.175561943	0.41058424	0.306082636	APAF1/JAK1/NFYC/CAMK2B/RAB5A/ARHGEF12/ATP6V0A4/MAPK8/CEBP G/IRAK1/NOD2/PLA2R1/PPP3CB/CAMK2G/RAB5B/SPHK2/MAPK3/KSR1/NFYB/MAPK14/ITGAM/PPP3CA/CLEC7A/TLR6/IL6/MRC1/RAF1/CREB1/CALM1/NFYA/CD14/BCL10/RFX5/TNFRSF1A/CYCS/PPP3R1/IFNB1/MALT1/SRC/MAPK9/IL10RB/BCL2/IFNGR2/IFNGR1/IL1A/RIPK2/EEA1/HLA-DRB5/AKT2/FCER1G/TRAFF6/CASP8/TGFB3/ATP6AP1/STAT1/LAMP1/FCGR2A/MAPK10/CTSS/HLA-DPB1/TLR1/IRAK2	62
hsa04973	Carbohydrate digestion and absorption	18/2512	47/8105	0.175964674	0.41058424	0.306082636	HK1/G6PC/PIK3CD/ATP1A1/CACNA1D/PLCB1/ATP1B1/ATP1B4/PIK3R3/MGAM/TAS1R2/LCT/PRKCB/PIK3CA/A	18

							KT2/PIK3R1/SLC37A4/GNAT3	
hsa049 61	Endocrine and other factor- regulated calcium reabsorption	20/2512	53/810 5	0.17902 2984	0.41477 8603	0.30920 9453	PRKACB/ATP2B1/SLC8A1/DNM3/ES R1/ATP1A1/PLCB1/ATP1B1/AP2M1/A TP2B4/AP2B1/ATP1B4/CALB1/GNAS/ GNAQ/PRKCB/AP2S1/SLC8A2/KLK1/ ADCY9	20
hsa043 30	Notch signaling pathway	22/2512	59/810 5	0.18106 4537	0.41657 5053	0.31054 8671	NUMB/DTX3/ATXN1/RBPJ/DTX2/MA ML2/TLE3/DVL3/DTX3L/ATXN1L/PS EN2/NCSTN/JAG2/DTX4/DTX1/MAM L3/NUMBL/HDAC1/KAT2B/HEYL/HE Y2/CTBP2	22
hsa000 30	Pentose phosphate pathway	12/2512	30/810 5	0.19024 1699	0.43165 1856	0.32178 8138	RPE/PFKM/GLYCTK/ALDOB/G6PD/H 6PD/RPIA/TKT/RBKS/PFKP/PGM1/PF KL	12
hsa006 30	Glyoxylate and dicarboxylate metabolism	12/2512	30/810 5	0.19024 1699	0.43165 1856	0.32178 8138	PCCA/GLUL/PCCB/GLYCTK/HOGA1/ SHMT1/ACSS1/ACO2/MDH1/GCSH/S HMT2/HAO1	12
hsa051 42	Chagas disease	36/2512	102/81 05	0.20005 9183	0.44974 0287	0.33527 2714	CFLAR/KNG1/SMAD2/MAPK8/PPP2R 1B/IRAK1/PPP2R2C/MAPK3/PIK3CD/ MAPK14/MAP2K4/TLR6/IL6/C1QB/PL CB1/TGFBR1/TNFRSF1A/PIK3R3/GN AI3/ACE/IFNB1/GNAS/MAPK9/GNAQ	36

							/IFNGR2/IFNGR1/PIK3CA/AKT2/PIK3R1/TRAF6/CASP8/TGFB3/CCL3/CCL3L3/JUN/MAPK10	
hsa00380	Tryptophan metabolism	16/2512	42/8105	0.201307404	0.449740287	0.335272714	CYP1A1/HADH/IL4I1/ALDH8A1/MAOA/EHHADH/DDC/AADAT/CYP1B1/KYAT1/HADHA/IDO1/TDO2/TPH2/KYAT3/AANAT	16
hsa04970	Salivary secretion	33/2512	93/8105	0.20231478	0.449740287	0.335272714	ITPR1/PRKACB/ATP2B1/KCNMA1/GUCY1A1/DMBT1/PRKG2/RYR3/ATP1A1/ADCY7/ADCY3/PLCB1/ADCY8/ATP1B1/CALM1/ATP2B4/ITPR3/SLC12A2/ATP1B4/PRKG1/SLC9A1/GNAS/GNAQ/ADCY2/NOS1/ITPR2/TRPV6/PRKCB/CST1/CST3/SLC4A2/ADCY4/ADCY9	33
hsa05416	Viral myocarditis	22/2512	60/8105	0.206254486	0.452632617	0.33742889	EIF4G1/CD86/FYN/CXADR/ABL2/CD55/LAMA2/CAV1/SGCD/CYCS/RAC2/MYH7/LAMA1/DAG1/ICAM1/EIF4G3/HLA-DRB5/CASP8/ITGAL/SGCB/HLA-DPB1/MYH6	22
hsa052	Basal cell	23/2512	63/810	0.20636	0.45263	0.33742	CTNNB1/PTCH1/FZD3/TCF7/GLI3/W	23

17	carcinoma		5	7454	2617	889	NT2B/DVL3/GSK3B/FZD4/APC/WNT1 0B/WNT9B/TP53/AXIN2/FZD10/WNT5 A/BAK1/WNT8A/WNT5B/GADD45B/P TCH2/FZD5/FZD8	
hsa041 51	PI3K-Akt signaling pathway	117/251 2	354/81 05	0.21193 9791	0.46177 6101	0.34424 5181	MYB/FGFR2/JAK1/FGF1/PTK2/FN1/IT GB6/LAMA3/CREB5/FLT1/MDM2/CD K2/G6PC/PPP2R1B/LPAR6/CSF1/PHLP P2/BRCA1/TCL1A/ERBB2/PPP2R2C/L AMA2/CCNE2/EGF/FGFR1/IGF1/PKN 2/SOS2/LPAR4/MAGI2/ITGB1/LPAR3/ MAPK3/EGFR/PIK3CD/KRAS/PPP2R5 D/ITGA6/CSF3R/TEK/CCND3/TSC2/G NG4/EIF4B/IL4R/YWHAB/CDK6/FOX O3/ATF4/IL6/IL4/ITGA5/F2R/PDGFD/I TGA3/MET/RAF1/GSK3B/MAGI1/C8orf44- SGK3/CREB1/PRKAA1/ITGA2/RELN/ CD19/COL6A6/OSM/LAMC2/PIK3R5/ BCL2L11/ITGA10/NTRK2/COL4A3/PI K3R3/COL9A1/TP53/THEM4/ANGPT4/ ERBB3/GNG2/ATF2/IFNB1/RBL2/LA MA1/PDGFRB/BDNF/CREB3L1/FGF21	117

							/GNG12/PIK3R6/PDGFC/TGFA/BCL2/TNC/GYS1/EIF4E/ITGA11/COL6A3/FGF17/ITGB5/PIK3CA/AKT2/PIK3R1/CHAD/PPP2R5E/COL9A2/PIK3AP1/RPS6/CHRM1/COL4A1/COL4A2/YWHAH/IL7R/ITGA4/ITGB3/CREB3L3/COL6A5	
hsa00592	alpha-Linolenic acid metabolism	10/2512	25/8105	0.220715275	0.470315823	0.35061138	PLB1/FADS2/JMJD7-PLA2G4B/PLA2G2D/PLA2G5/PLA2G4F/PLA2G12A/PLA2G3/PLA2G4B/PLA2G4E	10
hsa04350	TGF-beta signaling pathway	33/2512	94/8105	0.223332908	0.470315823	0.35061138	SMAD2/LTBP1/PPP2R1B/BMPR1B/MAPK3/ACVR2A/NEO1/GREM1/SMAD3/ACVR1C/TGFBR1/CDKN2B/NODAL/BMP8A/INHBC/BMPR2/FMOD/INHB/B/BMP6/INHBA/E2F5/PITX2/RBL1/BMP7/FBN1/THSD4/ID4/TGIF1/TGFB3/AMH/ACVR2B/ROCK1/GDF6	33
hsa04141	Protein processing in endoplasmic reticulum	58/2512	171/8105	0.224628473	0.470315823	0.35061138	SEC31A/NGLY1/PRKCSH/UBE2D3/DNAJC5G/DNAJC10/GANAB/YOD1/EIF2AK2/MAPK8/HSPH1/EIF2AK1/CAPN1/ATXN3/SAR1B/UBXN8/CRYAB/STT	58

							3A/SEC61A2/DERL2/ATF4/EDEM2/SEC63/SSR1/PDIA4/NSFL1C/SEC24A/DERL1/UBQLN1/SEC24D/SEC24C/SEC62/UBE2J1/MAN1A2/DERL3/PREB/ERP29/UGGT1/MAPK9/UBXN2A/UBE2D1/BCL2/BAK1/CAPN2/PPP1R15A/DNAJC3/SELENOS/PDIA6/UBE2D4/SEC23A/FBXO6/UBQLN3/PLAA/ERLEC1/UBE2J2/MAPK10/ERO1A/DDIT3	
hsa01523	Antifolate resistance	12/2512	31/8105	0.227547827	0.470315823	0.35061138	ABCC3/ABCC4/DHFR2/ABCC1/IL6/SLC46A1/MTHFR/SHMT1/ALOX12/ABC2/ABCC5/SHMT2	12
hsa04630	JAK-STAT signaling pathway	55/2512	162/8105	0.229331327	0.470315823	0.35061138	JAK1/SOCS2/THPO/STAT6/LEPR/SOC4/EGF/SOS2/SOCS7/EGFR/PIK3CD/IL6ST/IL15/CSF3R/CCND3/IL4R/IL22RA2/IL5RA/PIAS2/IL12RB2/IL6/IL4/STAT3/RAF1/PIAS3/IL21R/OSM/LIFR/SOCS5/TYK2/SOCS6/PIK3R3/STAT5B/IFNB1/STAM2/PDGFRB/IL10RB/BCL2/IL15RA/LEP/IFNGR2/IFNGR1/STAT2/LIF/PIK3CA/AKT2/PIK3R1/PIM1/IL22RA1/STAT1/IRF9/IL5/IL13/IL7R/GFAP	55

hsa051 33	Pertussis	27/2512	76/810 5	0.22938 513	0.47031 5823	0.35061 138	CFL2/MAPK8/IRAK1/CASP1/ITGB1/MAPK3/MAPK14/ITGAM/NLRP3/IL6/ITGA5/C1QB/CALM1/CD14/C4A/GNAI3/SFTPA2/C5/TICAM2/MAPK9/IL1A/NO D1/C4BPA/TRAF6/C1R/JUN/MAPK10	27
hsa005 62	Inositol phosphate metabolism	26/2512	73/810 5	0.23025 0164	0.47031 5823	0.35061 138	PLCH1/INPP4B/SYNJ1/INPP5B/CDIPT/PIP4K2C/MTMR8/PIK3CD/SYNJ2/OCRL/MTMR2/PLCB1/IPMK/PIP5K1C/PI4K2B/PIP4K2B/MTMR3/PIP5K1B/MTMR7/PIK3CA/INPP5F/ITPKC/PI4KB/MTMR6/PLCD4/MTM1	26
hsa049 60	Aldosterone-regulated sodium reabsorption	14/2512	37/810 5	0.23136 277	0.47031 5823	0.35061 138	NEDD4L/IGF1/MAPK3/PIK3CD/KRAS/ATP1A1/NR3C2/ATP1B1/ATP1B4/PIK3R3/PRKCB/KCNJ1/PIK3CA/PIK3R1	14
hsa054 17	Lipid and atherosclerosis	72/2512	215/810 05	0.23232 1824	0.47031 5823	0.35061 138	ITPR1/APAF1/NFATC1/PTK2/SOD2/CAMK2B/CYP1A1/MAPK8/LDLR/POU2F1/IRAK1/PPP3CB/CAMK2G/CASP1/MAP3K7/MIB1/MAPK3/PIK3CD/KRAS/MAPK14/PPP3CA/NFATC2/NLRP3/ARHGEF1/VCAM1/MAP2K4/TLR6/TNFSF10/ATF4/IL6/NCF2/TANK/POU2F2/STAT3/PLCB1/GSK3B/MMP1/CALM1	72

							/MAP2K6/CD14/TNFRSF1A/VAV3/CYCS/PIK3R3/TP53/PPP3R1/APOB/TICAM2/IFNB1/TAB2/SRC/MMP9/ABCG1/MAPK9/ICAM1/CDC42/BCL2/SELE/PIK3CA/AKT2/PIK3R1/HSPA4/TRAF6/CASP8/CCL3/CCL3L3/JUN/MAPK10/CYP2B6/ERO1A/DDIT3/SELP	
hsa05033	Nicotine addiction	15/2512	40/8105	0.23251484	0.470315823	0.35061138	GABRA2/GABRG1/GRIN2B/GABRG3/GRIN2A/GRIA3/GABRR2/GABRQ/GABRA3/CHRNA2/CHRNA4/SLC17A6/GRIA2/GABRE/GABRB2	15
hsa00430	Taurine and hypotaurine metabolism	5/2512	11/8105	0.232544955	0.470315823	0.35061138	BAAT/ADO/GAD1/CDO1/GGT7	5
hsa00561	Glycerolipid metabolism	22/2512	61/8105	0.233013614	0.470315823	0.35061138	AGPAT3/DGKH/DGKK/DGKA/PNPLA3/MGLL/GPAT2/DGKZ/DGKI/GLYCTK/MBOAT1/DGKB/GPAT3/GK2/GPAM/LIPC/GPAT4/PNLIP/MOGAT2/DGKQ/AGPAT5/PLPP5	22
hsa04621	NOD-like receptor signaling pathway	61/2512	181/8105	0.235677174	0.472791404	0.352456877	ITPR1/ERBIN/JAK1/NLRX1/TNFAIP3/ATG12/NAIP/MAPK8/MAVS/CTSB/NLRP1/TXNIP/NOD2/OAS1/BIRC3/CAS	61

							P1/MAP3K7/PKN2/MAPK3/MAPK14/XIAP/NLRP3/IL6/TANK/CARD16/PLCB1/OAS2/ITPR3/RIPK3/MEFV/TYK2/NLRC4/GPRC6A/TRPM7/ANTXR2/IFNB1/ATG16L1/TAB2/NLRP12/MFN1/MAPK9/ITPR2/PANX1/TRPM2/BCL2/NOD1/CARD17/RIPK2/STAT2/RNF31/TRAFF6/TXN2/CASP8/P2RX7/STAT1/IRF9/GABARAP/RNASEL/JUN/MAPK10/TP53BP1	
hsa04064	NF-kappa B signaling pathway	36/2512	104/8105	0.240784729	0.480110157	0.357912867	UBE2I/CFLAR/TNFAIP3/EDA2R/TNFSF11/CYLD/TNFRSF11A/ATM/IRAK1/BIRC3/CARD14/CSNK2A1/MAP3K7/EDA/TRAFF1/NFKB2/XIAP/ERC1/VCAM1/IL1R1/CXCL12/CD14/BCL10/TNFRSF1A/TICAM2/TAB2/MALT1/CCL21/ICAM1/PRKCB/BCL2/TRAFF6/GADD45B/ZAP70/CSNK2A3/MAP3K14	36
hsa00450	Selenocompound metabolism	7/2512	17/8105	0.253202306	0.500990927	0.373479079	PSTK/MTR/SEPSECS/KYAT1/SCLY/PAPSS1/KYAT3	7
hsa05100	Bacterial invasion of epithelial cells	27/2512	77/8105	0.254302386	0.500990927	0.373479079	CTNNB1/PTK2/CTNNA2/FN1/DNM3/GAB1/WASF1/ITGB1/PIK3CD/CAV1/	27

							CTTN/CRKL/ITGA5/ACTR3/MET/CDH1/CBL/PIK3R3/RHOG/ARPC3/SRC/CDC42/ELMO1/PXN/PIK3CA/PIK3R1/SHC4	
hsa04137	Mitophagy - animal	24/2512	68/8105	0.258546412	0.506320058	0.377451843	RHOT1/NBR1/USP8/MAPK8/HIF1A/CNK2A1/KRAS/FOXO3/ATF4/BNIP3L/RAB7B/TP53/ATG9B/SRC/MFN1/MAPK9/MRAS/AMBRA1/ULK1/CITED2/CNK2A3/GABARAP/JUN/MAPK10	24
hsa04062	Chemokine signaling pathway	64/2512	192/8105	0.262309677	0.5106502	0.38067988	PRKACB/PTK2/ARRB1/GRK4/SOS2/MAPK3/PIK3CD/KRAS/CCR9/GNG4/CXCR5/PAK1/CXCL12/BRAF/CRKL/FOXO3/CXCL10/ADCY7/CCL20/ADCY3/STAT3/PLCB1/RAF1/GSK3B/TIAM1/ADCY8/PIK3R5/CCR6/CXCR4/VAV3/CXCR3/PIK3R3/GNAI3/STAT5B/CCL16/CCR7/RAC2/GNG2/CCL18/SRC/CCL21/GNAQ/ADCY2/GNG12/PIK3R6/CCR1/CDC42/CCL11/PRKCB/ELMO1/PXN/STAT2/CX3CL1/PIK3CA/AKT2/PIK3R1/SHC4/STAT1/CCR3/ADCY4/CCL3/CCL3L3/ADCY9/ROCK1	64

hsa005 91	Linoleic acid metabolism	11/2512	29/810 5	0.26652 7087	0.51279 1881	0.38227 6462	PLB1/JMJD7- PLA2G4B/PLA2G2D/CYP2C19/PLA2G 5/PLA2G4F/CYP3A4/PLA2G12A/PLA2 G3/PLA2G4B/PLA2G4E	11
hsa043 92	Hippo signaling pathway - multiple species	11/2512	29/810 5	0.26652 7087	0.51279 1881	0.38227 6462	YAP1/FAT4/WWC1/PAK1/LATS1/LIM D1/CSNK1E/DCHS2/MOB1A/TEAD1/T EAD3	11
hsa051 31	Shigellosis	81/2512	246/81 05	0.27384 6061	0.52145 0067	0.38873 0973	ITPR1/HK1/CAST/UBE2V1/TNIP1/PT K2/UBE2D3/ATG12/NAIP/DIAPH1/BT RC/FNBP1L/FBXW11/MAPK8/MDM2/ ATM/CAPN1/WASF1/CASP1/MAP3K7 /ITGB1/MAPK3/EGFR/PIK3CD/MAPK 14/MYL12B/NLRP3/CTTN/FNBP1/IL1 R1/CRKL/FOXO3/ITGA5/ACTR3/PLC B1/GSK3B/ITPR3/WIPI1/CD14/NLRC4 /BCL10/TNFRSF1A/CYCS/PIK3R3/TP5 3/TLR5/ARPC3/IFNB1/ATG16L1/TAB2 /MALT1/SRC/MAPK9/ITPR2/UBE2D1/ ARF6/CDC42/BCL2/ELMO1/CAPN2/N OD1/PXN/RRAGD/RIPK2/RNF31/CYT H3/PIK3CA/UBE2D4/AKT2/PIK3R1/T RAF6/FOXO1/MYL12A/PLCD4/CYTH	81

							2/GABARAP/PPID/TLN2/ROCK1/JUN/ MAPK10	
hsa042 60	Cardiac muscle contraction	30/2512	87/810 5	0.27419 7148	0.52145 0067	0.38873 0973	CACNA1C/CACNB4/CACNB2/TNNT2/ SLC8A1/CACNA1F/ATP2A1/CACNA2 D2/ATP2A2/ATP1A1/CACNA1D/ASPH /TRDN/TPM3/ATP1B1/ATP1B4/SLC9A 1/COX6B2/ATP2A3/MYH7/COX7A2L/ CACNG8/SLC8A2/COX4I2/CACNA1S/ CACNA2D1/TPM1/UQCRC1/MYH6/C ASQ2	30
hsa050 17	Spinocerebellar ataxia	48/2512	143/81 05	0.27849 8194	0.52495 6865	0.39134 5223	ITPR1/ATP2A1/MAPK8/SPTBN2/TWN K/RB1CC1/ATXN3/ATXN1/RBPJ/GR M1/RORA/ATP2A2/PIK3CD/ATG2A/A TXN2/GRIN2B/GRIN2A/ATXN1L/PLC B1/GRIA3/RELN/ITPR3/TBPL1/NFYA/ WIPI1/CYCS/PIK3R3/PSMB2/ULK2/A TP2A3/OMA1/MAPK9/GNAQ/ITPR2/P RKCB/PSMD4/AMBRA1/PSMC3/PSM A1/PIK3CA/AKT2/PIK3R1/ULK1/BEA N1/GRIA2/SLC25A5/MAPK10/NOP56	48
hsa052 25	Hepatocellular carcinoma	56/2512	168/81 05	0.27923 2375	0.52495 6865	0.39134 5223	CTNNB1/SMARCA4/FZD3/TCF7/SMA D2/E2F3/GAB1/NQO1/SMARCC2/SOS	56

							2/ARID2/MAPK3/EGFR/PIK3CD/KRAS/WNT2B/CDK6/BRAF/DVL3/SMARD1/MET/RAF1/GSK3B/GSTO1/PBRM1/FZD4/SMAD3/TGFBR1/APC/WNT10B/PIK3R3/GSTA4/WNT9B/TP53/AXIN2/FZD10/RB1/LRP6/PRKCB/TGFA/WNT5A/BAK1/PIK3CA/AKT2/PIK3R1/ARID1B/SHC4/FRAT2/WNT8A/WNT5B/GSTM3/GADD45B/CSNK1A1/TGFB3/FZD5/FZD8	
hsa04066	HIF-1 signaling pathway	37/2512	109/8105	0.282608787	0.528285744	0.393826838	HK1/CAMK2B/CUL2/FLT1/HIF1A/ERBB2/CAMK2G/PFKM/EGF/IGF1/EGLN3/MAPK3/EGFR/PIK3CD/TEK/ALDOB/IL6/STAT3/PIK3R3/ANGPT4/PDHA2/EGLN1/PRKCB/BCL2/IFNGR2/IFNGR1/EIF4E/PIK3CA/AKT2/PIK3R1/VHL/PFKP/ENO2/TF/LDHA/RPS6/PFKL	37
hsa04142	Lysosome	43/2512	128/8105	0.290117185	0.539193325	0.40195823	ATP6V0A4/CD63/CTSV/AP4S1/CTSB/MFSD8/AP4E1/AP3M1/ABCA2/PLA2G15/IGF2R/HYAL4/ACP2/LITAF/MAN2B1/HEXB/GAA/CTSE/M6PR/AP3D1/LGMN/CTSL/AP1G1/GGA2/HYAL1/SO	43

							RT1/ASAH1/GNS/PPT1/FUCA2/GALC/ CTSC/AP1S3/SLC17A5/ATP6AP1/LA MP1/AP4B1/NPC2/AP1S1/CTSS/CTSZ/ TPP1/LIPA	
hsa049 78	Mineral absorption	21/2512	60/810 5	0.29267 648	0.53919 3325	0.40195 823	TRPM6/ATP2B1/SLC8A1/STEAP2/HE PH/ATP1A1/SLC26A6/CYBRD1/ATP7 B/SLC46A1/HMOX2/ATP1B1/ATP2B4/ SLC26A9/ATP1B4/TRPM7/TRPV6/SLC 8A2/HEPHL1/SLC31A1/TF	21
hsa051 30	Pathogenic Escherichia coli infection	65/2512	197/81 05	0.29336 0502	0.53919 3325	0.40195 823	ABI1/TUBB/ARHGEF12/NAIP/FYN/M YO5A/MYO1C/MAPK8/OCLN/IRAK1/ CYFIP1/WASF1/CASP1/CYFIP2/MAP3 K7/LPAR4/ITGB1/MAPK3/MYH10/MA PK14/NLRP3/ARHGEF11/ARHGEF1/C TTN/IL1R1/PAK1/TNFSF10/IL6/MYO1 0/F2R/ACTR3/CLDN1/TJP1/EZR/SEC2 4A/MYO6/SEC24D/MYO1D/SEC24C/T NFRSF1A/GNA13/CYCS/TLR5/ARPC3 /TAB2/SRC/MAPK9/ARF6/CDC42/BA K1/TUBB8/MYO1F/CLDN20/CYTH3/T UBB4B/TRAF6/CASP8/CYTH2/NCKA P1/CLDN17/FCGR2A/ROCK1/WIPF3/J	65

							UN/MAPK10	
hsa045 30	Tight junction	56/2512	169/81 05	0.29738 7776	0.54355 8768	0.40521 2584	PRKAG2/PRKACB/NEDD4L/DLG2/NE DD4/RDX/BVES/MAPK8/OCLN/PPP2 R1B/ERBB2/RAPGEF6/PPP2R2C/RUN X1/ITGB1/MYH10/CACNA1D/MYL12 B/CTTN/AMOT/ACTR3/CFTR/MAGI1/ CLDN1/TIAM1/PRKAA1/TJP1/SCRIB/ MPDZ/ARHGAP17/EZR/CGNL1/YBX3 /SYNPO/MPP5/AMOTL1/MAP3K1/AR PC3/SRC/MAPK9/CDC42/MSN/F11R/C LDN20/PRKAG3/HSPA4/PRKCI/PRKA B2/MYL12A/RAB13/CLDN17/ROCK1/ JUN/MAPK10/JAM2/IGSF5	56
hsa005 20	Amino sugar and nucleotide sugar metabolism	17/2512	48/810 5	0.30078 7458	0.54673 5213	0.40758 0562	HK1/UAP1/CYB5R3/GNE/PGM3/GCK/ CHIT1/FPGT/HEXB/GNPNAT1/UGDH/ CYB5RL/PMM1/GFPT2/GMDS/GNPD A1/PGM1	17
hsa051 60	Hepatitis C	52/2512	157/81 05	0.30752 8533	0.55591 6964	0.41442 538	CTNNB1/APAF1/JAK1/CFLAR/EIF2A K2/LDLR/MAVS/OCLN/CDK2/EIF2A K1/PPP2R1B/E2F3/OAS1/PPP2R2C/NR 1H3/EGF/SOS2/MAPK3/EGFR/PIK3CD /KRAS/YWHAB/CDK6/BRAF/CXCL10	52

							/STAT3/RAF1/GSK3B/CLDN1/OAS2/TYK2/PPARA/TNFRSF1A/CYCS/PIK3R3/TP53/IFNB1/RB1/BAK1/STAT2/CLDN20/PIK3CA/AKT2/PIK3R1/TRAF6/CASP8/STAT1/IRF9/CLDN17/RNASEL/MX1/YWHAH	
hsa00061	Fatty acid biosynthesis	7/2512	18/8105	0.310687157	0.558557785	0.416394062	ACSL6/ACACA/ACSBG2/HTD2/ACSL5/ACSL1/CBR4	7
hsa05120	Epithelial cell signaling in Helicobacter pylori infection	24/2512	70/8105	0.315364926	0.563886199	0.420366291	ATP6V0A4/MAPK8/PTPRZ1/EGFR/MAPK14/PAK1/MAP2K4/MET/TJP1/GIT1/ATP6V1D/SRC/MAPK9/CDC42/NOD1/F11R/ATP6AP1/MAP3K14/ATP6V1G1/JUN/MAPK10/HBEGF/JAM2/IGSF5	24
hsa04150	mTOR signaling pathway	51/2512	155/8105	0.329963134	0.586799303	0.437447569	FZD3/CLIP1/RPS6KA3/GRB10/FNIP1/RPS6KA6/IGF1/SOS2/MAPK3/WDR59/PIK3CD/KRAS/WNT2B/TSC2/EIF4B/SKP2/BRAF/RPS6KA2/DVL3/RAF1/GSK3B/PRKAA1/FZD4/TNFRSF1A/WNT10B/PIK3R3/WNT9B/ULK2/ATP6V1D/RICTOR/FZD10/LRP6/CAB39L/PRKCB/RNF152/WNT5A/MAPKAP1/RRAGD/EIF4E/PIK3CA/AKT2/PIK3R1/ULK1	51

							/WNT8A/WNT5B/DEPTOR/RPS6/MIO S/FZD5/ATP6V1G1/FZD8	
hsa051 67	Kaposi sarcoma- associated herpesvirus infection	63/2512	193/81 05	0.33347 17	0.58985 048	0.43972 2162	ITPR1/CTNNB1/JAK1/NFATC4/NFAT C1/TCF7/CD86/EIF2AK2/MAPK8/HIF1 A/E2F3/PPP3CB/MAPK3/PIK3CD/KRA S/IL6ST/MAPK14/PPP3CA/NFATC2/G NG4/CDK6/MAP2K4/IL6/STAT3/RAF1 /GSK3B/CREB1/CALM1/ITPR3/PIK3R 5/MAP2K6/TYK2/TNFRSF1A/CYCS/PI K3R3/TP53/PPP3R1/GNG2/IFNB1/SRC /RB1/MAPK9/ITPR2/GNG12/PIK3R6/C CR1/ICAM1/RCAN1/BAK1/IFNGR1/S TAT2/PIK3CA/AKT2/PIK3R1/CASP8/S TAT1/CCR3/IRF9/GABARAP/JUN/MA PK10/ZFP36/CD200R1	63
hsa046 72	Intestinal immune network for IgA production	17/2512	49/810 5	0.33628 3234	0.59164 2695	0.44105 8224	CD86/IL15/ICOSLG/CCR9/PIGR/CXCL 12/IL6/IL4/CXCR4/ICOS/IL15RA/HLA- DRB5/MAP3K14/IL5/TNFRSF17/HLA- DPB1/ITGA4	17
hsa008 60	Porphyrin and chlorophyll metabolism	15/2512	43/810 5	0.34277 6707	0.59985 9238	0.44718 3499	HMBS/HEPH/UROS/UGT2B28/UGT2A 1/UGT2A2/HMOX2/UGT2B4/MMAB/B LVRB/HEPHL1/UGT1A10/UGT2B10/U	15

							GT2B11/FECH	
hsa052 16	Thyroid cancer	13/2512	37/810 5	0.34950 1243	0.60839 1053	0.45354 3802	CTNNB1/TCF7/RET/MAPK3/KRAS/TP R/BRAF/TPM3/CDH1/TP53/BAK1/CC DC6/GADD45B	13
hsa051 45	Toxoplasmosis	37/2512	112/81 05	0.35251 4816	0.61020 2459	0.45489 417	JAK1/LAMA3/MAPK8/LDLR/IRAK1/B IRC3/LAMA2/MAP3K7/ITGB1/MAPK3 /MAPK14/XIAP/ITGA6/STAT3/LAMC 2/PIK3R5/MAP2K6/TYK2/TNFRSF1A/ CYCS/GNAI3/LAMA1/TAB2/MAPK9/ PIK3R6/IL10RB/BCL2/IFNGR2/IFNGR 1/HLA- DRB5/AKT2/TRAF6/CASP8/TGFB3/ST AT1/MAPK10/HLA-DPB1	37
hsa051 64	Influenza A	56/2512	172/81 05	0.35425 1276	0.61020 2459	0.45489 417	APAF1/JAK1/ADAR/NLRX1/EIF2AK2/ PML/MAVS/OAS1/HNRNPUL1/PRSS3 /CASP1/MAPK3/PIK3CD/PABPN1/CC ND3/NLRP3/CDK6/KPNA1/TNFSF10/I L6/CXCL10/RAF1/KPNA2/OAS2/TYK 2/TNFRSF1A/CYCS/PIK3R3/IFNB1/PL G/NXF5/ICAM1/PRKCB/XPO1/BAK1/I FNGR2/IFNGR1/IL1A/PRSS1/STAT2/D NAJC3/HLA-	56

							DRB5/PIK3CA/AKT2/PIK3R1/SLC25A5/CASP8/IFIH1/STAT1/IRF9/RNASEL/KPNA5/MX1/TMPRSS2/HLA-DPB1/KPNA7	
hsa00650	Butanoate metabolism	10/2512	28/8105	0.359926694	0.616749387	0.459774779	ABAT/BDH1/HADH/HMGCLL1/ALDH5A1/EHHADH/ACSM1/GAD1/ACSM2A/HADHA	10
hsa04666	Fc gamma R-mediated phagocytosis	32/2512	97/8105	0.370935587	0.626528377	0.467064827	CFL2/ASAP2/WASF1/SPHK2/MAPK3/PIK3CD/PAK1/CRKL/MYO10/GSN/ACTR3/RAF1/PIP5K1C/JMJD7-PLA2G4B/ASAP3/PLD1/LIMK2/VAV3/PIK3R3/RAC2/ARPC3/PLA2G4F/ARF6/CDC42/PRKCB/PIP5K1B/PIK3CA/AKT2/PIK3R1/FCGR2A/PLA2G4B/PLA2G4E	32
hsa00270	Cysteine and methionine metabolism	17/2512	50/8105	0.37266571	0.626528377	0.467064827	BCAT1/AHCYL2/MAT2B/GCLC/IL4I1/MTR/AMD1/APIP/MRI1/DNMT1/GCLM/CDO1/KYAT1/MDH1/LDHA/SMS/KYAT3	17
hsa00510	N-Glycan biosynthesis	17/2512	50/8105	0.37266571	0.626528377	0.467064827	GANAB/ST6GAL2/FUT8/ALG8/MGAT4C/STT3A/MAN2A2/ALG10/ALG10B/MAN1A2/MGAT4A/ALG6/MGAT5/AL	17

							G14/ALG3/MAN2A1/DPAGT1	
hsa007 30	Thiamine metabolism	6/2512	16/810 5	0.37325 0948	0.62652 8377	0.46706 4827	AK4/AK2/TPK1/AK7/NFS1/NTPCR	6
hsa005 14	Other types of O- glycan biosynthesis	16/2512	47/810 5	0.37717 3533	0.62989 8946	0.46957 7522	ST3GAL3/ST6GAL2/POFUT1/POMT2/ GXYLT1/GALNT15/GALNT5/OGT/CO LGALT1/EOGT/GALNT8/COLGALT2/ B3GLCT/GALNTL5/GALNT3/POGLU T1	16
hsa046 10	Complement and coagulation cascades	28/2512	85/810 5	0.38750 1564	0.64387 8861	0.47999 9279	F3/KNG1/CD55/MASP1/PLAUR/CFH/I TGAM/F2R/C1QB/MBL2/F5/F9/C4A/C 5/A2M/F8/PLG/F13A1/C6/C4BPA/SER PINF2/PROS1/MASP2/F13B/CLU/THB D/C1R/F11	28
hsa054 18	Fluid shear stress and atherosclerosis	45/2512	139/81 05	0.39242 5426	0.64878 3744	0.48365 5775	CTNNB1/PTK2/MAPK8/BMPRI1/NQ O1/MAP3K7/PIK3CD/CAV1/MAPK14/ ACVR2A/VCAM1/IL1R1/MAP2K4/NC F2/SUMO2/GSTO1/PRKAA1/CALM1/ MAP2K6/TNFRSF1A/CTSL/PIK3R3/G STA4/TP53/RAC2/SRC/MMP9/BMPRI2/ MAPK9/ICAM1/BCL2/MEF2C/IL1A/S ELE/PIK3CA/PECAM1/AKT2/PIK3R1/ GSTM3/TXN2/THBD/ACVR2B/JUN/M	45

							APK10/ITGB3	
hsa030 22	Basal transcription factors	15/2512	45/810 5	0.42144 0914	0.69170 0052	0.51564 9055	TAF8/TAF5L/GTF2A1/GTF2I/TAF1/GT F2H5/TBPL1/TAF4B/GTF2H1/TAF1L/ TAF7/TAF12/TAF11/TAF3/GTF2A1L	15
hsa049 64	Proximal tubule bicarbonate reclamation	8/2512	23/810 5	0.42258 8785	0.69170 0052	0.51564 9055	ATP1A1/GLS/ATP1B1/SLC25A10/ATP 1B4/SLC4A4/MDH1/CA4	8
hsa005 90	Arachidonic acid metabolism	20/2512	61/810 5	0.42784 5305	0.69683 7155	0.51947 8666	CYP4F3/PLB1/EPHX2/GPX5/JMJD7- PLA2G4B/PLA2G2D/PTGIS/CYP2C19/ PLA2G5/PLA2G4F/ALOX12/CYP2U1/ CBR1/GPX7/PLA2G12A/HPGDS/PLA2 G3/PLA2G4B/CYP2B6/PLA2G4E	20
hsa001 20	Primary bile acid biosynthesis	6/2512	17/810 5	0.43873 2025	0.70756 2923	0.52747 452	HSD3B7/SCP2/BAAT/CYP39A1/AMA CR/CYP8B1	6
hsa009 10	Nitrogen metabolism	6/2512	17/810 5	0.43873 2025	0.70756 2923	0.52747 452	GLUL/CA12/CA7/CA13/CA14/CA4	6
hsa005 33	Glycosaminoglycan biosynthesis - keratan sulfate	5/2512	14/810 5	0.44834 5404	0.71836 1589	0.53552 4717	ST3GAL3/FUT8/ST3GAL1/CHST4/CH ST1	5
hsa000 51	Fructose and mannose metabolism	11/2512	33/810 5	0.44979 4794	0.71836 1589	0.53552 4717	HK1/PFKFB1/PFKM/FPGT/PFKFB4/A LDOB/PMM1/ENOSF1/GMDS/PFKP/P FKL	11

hsa001 30	Ubiquinone and other terpenoid-quinone biosynthesis	4/2512	11/810 5	0.45958 4908	0.73045 1375	0.54453 7419	NQO1/GGCX/HPD/VKORC1	4
hsa010 40	Biosynthesis of unsaturated fatty acids	9/2512	27/810 5	0.46756 7329	0.73818 3972	0.55030 1922	ELOVL5/HACD4/SCP2/FADS1/FADS2 /ELOVL2/BAAT/SCD/ELOVL4	9
hsa000 71	Fatty acid degradation	14/2512	43/810 5	0.46893 7539	0.73818 3972	0.55030 1922	ACSL6/ACADM/CPT1C/HADH/ACSB G2/ACSL5/EHHADH/ACSL1/ACADVL /ADH4/CPT1A/HADHA/CYP2U1/ACA DL	14
hsa046 62	B cell receptor signaling pathway	26/2512	82/810 5	0.48584 1267	0.75475 5764	0.56265 5873	NFATC1/PPP3CB/SOS2/MAPK3/PIK3 CD/KRAS/PPP3CA/NFATC2/CD72/RA F1/GSK3B/CD19/BCL10/VAV3/PIK3R 3/RAC2/PPP3R1/RASGRP3/MALT1/PR KCB/NFKBIE/PIK3CA/AKT2/PIK3R1/ PIK3AP1/JUN	26
hsa050 22	Pathways of neurodegeneration - multiple diseases	148/251 2	475/81 05	0.48620 916	0.75475 5764	0.56265 5873	CACNA1C/ITPR1/CTNNB1/APAF1/TU BB/FZD3/CAMK2B/RAB5A/CACNA1F /ATP2A1/MAPK8/SPTBN2/RB1CC1/C SF1/CAPN1/ATXN3/ATXN1/PPP3CB/ CAMK2G/CSNK2A1/GRM1/ATP2A2/H	148

							IP1/ATP5MC3/NOX4/MAPK3/SPG11/A LS2/KRAS/MAPK14/WNT2B/DCTN2/ RYS3/ATG2A/CACNA1D/SNCA/DNA H8/PPP3CA/TRAP1/ATXN2/ATP5F1C/ BRAF/DVL3/ATF4/IL6/TANK/GRIN2B /GRIN2A/ATXN1L/TOMM40L/PLCB1/ RAF1/GSK3B/DLG4/PSEN2/GRIA3/D NAH5/DNAH10/NDUFB9/KIF5A/GPX 5/DNAH9/DNAH6/WDR41/NEFL/CAL M1/FZD4/C9orf72/ITPR3/APC/UBA1/ MAP2K6/DERL1/FUS/WIP1/HSD17B1 0/CSNK1E/TNFRSF1A/WNT10B/CYCS /KIF5B/UBE2J1/PSMB2/WNT9B/ULK2 /UCHL1/PPP3R1/COX6B2/AXIN2/ATP 2A3/FZD10/DCTN1/HTT/COX7A2L/M FN1/LRP6/MAPK9/BDNF/GNAQ/NOS 1/ITPR2/PRKCB/DNAL4/BCL2/WNT5 A/BAK1/ACTR1A/PSMD4/NDUFS2/IL 1A/CAPN2/AMBRA1/PSMC3/PSMA1/ TUBB8/CHRM5/NDUFB6/NEFM/COX 4I2/DNAH1/TUBB4B/GPX7/DCTN6/F RAT2/ULK1/CACNA1S/WNT8A/GRIA	
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							2/SLC25A5/WNT5B/DNAH11/CSNK1A1/CASP8/PARK7/CSNK2A3/DNAH7/GPR37/GABARAP/DNAH3/PPID/ATP5F1A/CHRM1/FZD5/UBE2J2/MAPK10/DDIT3/FZD8/UQCRC1	
hsa00250	Alanine, aspartate and glutamate metabolism	12/2512	37/8105	0.486347179	0.754755764	0.562655873	ABAT/ASNS/GLUL/IL4I1/GLS/ALDH5A1/FOLH1/GAD1/DDO/GFPT2/GPT/RIMKLB	12
hsa05110	Vibrio cholerae infection	16/2512	50/8105	0.4918485	0.759172943	0.565948795	PRKACB/ATP6V0A4/SEC61A2/CFTR/ADCY3/KDELRL1/PDIA4/TJP1/SLC12A2/KDELRL3/ATP6V1D/GNAS/ATP6AP1/ADCY9/ATP6V1G1/ERO1A	16
hsa00040	Pentose and glucuronate interconversions	11/2512	34/8105	0.496116057	0.759172943	0.565948795	RPE/UGT2B28/UGT2A1/UGT2A2/UGT2B4/UGDH/CRYL1/UGT1A10/UGT2B10/UGT2B11/XYLB	11
hsa00640	Propanoate metabolism	11/2512	34/8105	0.496116057	0.759172943	0.565948795	ECHDC1/PCCA/ABAT/ACACA/PCCB/HIBCH/DBT/EHHADH/ACSS1/HADHA/LDHA	11
hsa05169	Epstein-Barr virus infection	63/2512	202/8105	0.502821168	0.764826197	0.570163186	ENTPD1/APAF1/JAK1/NEDD4/TNFAIP3/USP7/EIF2AK2/MAPK8/MAVS/MDM2/CDK2/IRAK1/E2F3/OAS1/CCNE2/RBPJ/MAP3K7/PIK3CD/MAPK14/NFK	63

							B2/CCND3/SKP2/CDK6/MAP2K4/IL6/ CXCL10/STAT3/OAS2/CD19/MAP2K6/ BCL2L11/TYK2/CYCS/PIK3R3/TP53/C CNA2/IFNB1/TAB2/RB1/MAPK9/ICA M1/BCL2/BAK1/PSMD4/PSMC3/NFK BIE/STAT2/HDAC1/HLA- DRB5/PIK3CA/AKT2/PIK3R1/TRAF6/ GADD45B/CASP8/STAT1/MAP3K14/I RF9/ITGAL/JUN/MAPK10/HLA- DPB1/RUNX3	
hsa047 26	Serotonergic synapse	36/2512	115/81 05	0.50650 3818	0.76482 6197	0.57016 3186	CACNA1C/ITPR1/PRKACB/CACNA1F /KCNJ3/MAPK3/KRAS/CACNA1D/GN G4/BRAF/MAOA/PLCB1/RAF1/DDC/I TPR3/JMJD7- PLA2G4B/GNAI3/CYP2C19/GNG2/PL A2G4F/HTR3C/GNAS/GNAQ/ITPR2/R APGEF3/GNG12/PRKCB/CYP2D7/HT R1F/HTR2B/ALOX12/CACNA1S/TPH2 /PLA2G4B/GABRB2/PLA2G4E	36
hsa000 52	Galactose metabolism	10/2512	31/810 5	0.50678 4532	0.76482 6197	0.57016 3186	HK1/G6PC/PFKM/GCK/GAA/MGAM/ LCT/PFKP/PGM1/PFKL	10
hsa006	Glycosphingolipid	5/2512	15/810	0.51850	0.77894	0.58068	ST3GAL1/HEXB/B4GALNT1/ST6GAL	5

04	biosynthesis - ganglio series		5	5256	1686	6011	NAC5/ST8SIA1	
hsa00760	Nicotinate and nicotinamide metabolism	11/2512	35/8105	0.541403304	0.809644031	0.603574018	SIRT5/NADK2/NNT/NMRK2/NT5C1A/ENPP3/NMNAT2/NT5C/NT5M/PNP/NT5E	11
hsa04657	IL-17 signaling pathway	29/2512	94/8105	0.551047477	0.818602878	0.610252665	TNFAIP3/MAPK8/MAP3K7/MAPK3/MAPK14/USP25/IL6/IL4/CXCL10/CCL20/IL17RA/GSK3B/TRAF3IP2/MMP1/S100A8/TAB2/MMP9/MAPK9/SRSF1/CCL11/JUND/FOSB/TRAF6/MAPK6/CASP8/JUN/MAPK10/IL5/IL13	29
hsa04136	Autophagy - other	10/2512	32/8105	0.553951716	0.818602878	0.610252665	ATG12/ATG7/ATG2A/ATG10/ATG4C/WIP1/ULK2/ATG9B/ATG16L1/GABARAP	10
hsa01240	Biosynthesis of cofactors	48/2512	156/8105	0.554858486	0.818602878	0.610252665	AK4/BCAT1/AK9/HMBS/PPCDC/PANK2/MAT2B/NADK2/NQO1/PANK1/URO5/GGCX/DHFR2/GCLC/AK2/AK3/PNP/UGT2B28/UGT2A1/UGT2A2/HPD/PDXK/PKLR/UGT2B4/UGDH/RDH13/MMAB/TPK1/MTHFD2L/VKORC1/PANK3/NMNAT2/GCLM/SHMT1/NME6/PMM1/DHRS3/IDO1/AK7/UGT1A10/T	48

							DO2/UMPS/UGT2B10/UGT2B11/DHO DH/NFS1/SHMT2/FECH	
hsa012 10	2-Oxocarboxylic acid metabolism	6/2512	19/810 5	0.56393 1141	0.82827 3863	0.61746 2198	BCAT1/AADAT/IDH2/ACO2/GPT/AB HD14A-ACY1	6
hsa005 13	Various types of N- glycan biosynthesis	12/2512	39/810 5	0.57227 1052	0.83080 5897	0.61934 978	ST3GAL3/FUT8/MGAT4C/STT3A/HE XB/MAN2A2/MAN1A2/MGAT4A/CHS T9/ALG14/ALG3/MAN2A1	12
hsa009 82	Drug metabolism - cytochrome P450	22/2512	72/810 5	0.57652 3073	0.83080 5897	0.61934 978	FMO1/FMO5/MAOA/FMO4/UGT2B28/ UGT2A1/UGT2A2/GSTO1/UGT2B4/A DH4/GSTA4/FMO2/CYP2C19/CYP2D7 /CYP3A4/UGT1A10/FMO3/UGT2B10/ UGT2B11/HPGDS/GSTM3/CYP2B6	22
hsa006 00	Sphingolipid metabolism	15/2512	49/810 5	0.57675 5141	0.83080 5897	0.61934 978	ACER3/KDSR/CERS5/ASAH2/SPHK2/ CERS2/CERS3/CERS6/SGPP1/SPTLC3/ ASAH1/GALC/SGPP2/SPTLC1/SMPD3	15
hsa049 50	Maturity onset diabetes of the young	8/2512	26/810 5	0.58331 8268	0.83080 5897	0.61934 978	HNF4A/NR5A2/GCK/PKLR/FOXA3/F OXA2/PAX6/ONECUT1	8
hsa003 50	Tyrosine metabolism	11/2512	36/810 5	0.58515 6283	0.83080 5897	0.61934 978	GSTZ1/TH/IL4I1/MAOA/HPD/DDC/A OC3/ADH4/HGD/COMT/FAH	11
hsa051 46	Amoebiasis	31/2512	102/81 05	0.58978 4181	0.83080 5897	0.61934 978	PRKACB/PTK2/FN1/RAB5A/LAMA3/ LAMA2/RAB5B/PIK3CD/ITGAM/IL1R	31

							1/IL6/PLCB1/LAMC2/COL3A1/CD14/COL4A3/RAB7B/PIK3R3/LAMA1/GNAS/GNAQ/PRKCB/PIK3CA/SERPINB9/PIK3R1/ARG2/SERPINB13/TGFB3/SERPINB3/COL4A1/COL4A2	
hsa00240	Pyrimidine metabolism	17/2512	56/8105	0.59120843	0.830805897	0.61934978	ENTPD1/AK9/RRM2B/CANT1/RRM2/DPYD/NT5C1A/TK1/ENPP3/ENTPD5/NME6/NT5C/NT5M/UMPS/DHODH/PNP/NT5E	17
hsa04723	Retrograde endocannabinoid signaling	45/2512	148/8105	0.592999963	0.830805897	0.61934978	CACNA1C/ITPR1/PRKACB/RIMS1/CACNA1F/MAPK8/KCNJ3/GRM1/MAPK3/GABRA2/MGLL/MAPK14/CACNA1D/GNG4/GABRG1/ADCY7/ADCY3/CNR1/GABRG3/PLCB1/GRIA3/NDUFB9/ADCY8/GABRR2/ITPR3/GNAI3/GNG2/GABRQ/MAPK9/GNAQ/ADCY2/ITPR2/GNG12/GABRA3/PRKCB/NDUFS2/NDUFB6/SLC17A6/CACNA1S/GRIA2/GABRE/ADCY4/ADCY9/GABRB2/MAPK10	45
hsa03320	PPAR signaling pathway	23/2512	76/8105	0.597937776	0.830805897	0.61934978	ACSL6/ACADM/NR1H3/CPT1C/SCP2/ACSBG2/ACSL5/FADS2/EHHADH/AD	23

							IPOQ/PLIN1/ACSL1/MMP1/GK2/SCD/ PPARA/FABP2/FABP7/CPT1A/FABP6/ CYP8B1/ACADL/ME1	
hsa034 10	Base excision repair	10/2512	33/810 5	0.59923 7334	0.83080 5897	0.61934 978	POLL/POLD3/SMUG1/POLE2/PARP4/ POLB/HMGB1/MBD4/MPG/TDG	10
hsa041 30	SNARE interactions in vesicular transport	10/2512	33/810 5	0.59923 7334	0.83080 5897	0.61934 978	GOSR2/STX16/STX17/STX3/VAMP1/V AMP7/VTI1B/STX4/SNAP23/GOSR1	10
hsa030 60	Protein export	7/2512	23/810 5	0.60090 3937	0.83080 5897	0.61934 978	SRPRA/SEC61A2/SEC63/SRP19/SRP72 /SEC62/OXA1L	7
hsa046 14	Renin-angiotensin system	7/2512	23/810 5	0.60090 3937	0.83080 5897	0.61934 978	MME/PRCP/ACE/LNPEP/KLK1/NLN/ AGT	7
hsa052 03	Viral carcinogenesis	62/2512	204/81 05	0.60100 8521	0.83080 5897	0.61934 978	PRKACB/UBE3A/JAK1/USP7/HDAC9/ EIF2AK2/HDAC8/CREB5/MDM2/CDK 2/GTF2A1/HPN/CCNE2/RBPJ/MAPK3/ PIK3CD/TRAF1/KRAS/IL6ST/NFKB2/ CCND3/YWHAB/SKP2/CDK6/ATF4/G SN/STAT3/CREB1/SCRIB/REL/MRPS1 8B/TBPL1/MAD1L1/CDKN2B/PIK3R3/ STAT5B/TP53/DDX3X/CCNA2/ATF2/ RBL2/SRC/RB1/CREB3L1/POLB/CDC 42/BAK1/PXN/HDAC1/RBL1/PIK3CA/	62

							GTF2H1/PIK3R1/KAT2B/HDAC7/CASP8/CCR3/IRF9/JUN/YWHAH/CREB3L3/GTF2A1L	
hsa05150	Staphylococcus aureus infection	29/2512	96/8105	0.604599273	0.83227264	0.620443209	FCAR/MASP1/CFH/ITGAM/PTAFR/C1QB/SELPLG/KRT20/MBL2/C4A/C5/KRT27/KRT12/PLG/FPR3/ICAM1/KRT10/KRT38/HLA-DRB5/MASP2/KRT25/C1R/ITGAL/KRT23/KRT13/FCGR2A/KRT14/HLA-DPB1/SELP	29
hsa04217	Necroptosis	48/2512	159/8105	0.617298428	0.846213262	0.630835674	JAK1/STAT6/CFLAR/TNFAIP3/CAMK2B/CYLD/EIF2AK2/MAPK8/CAPN1/BIRC3/CAMK2G/CASP1/GLUL/XIAP/NLRP3/TNFSF10/STAT3/SPATA2/RIPK3/JMJD7-PLA2G4B/TYK2/TRPM7/TNFRSF1A/STAT5B/TICAM2/IFNB1/PLA2G4F/CHMP6/MAPK9/HMGB1/BCL2/IFNGR2/IFNGR1/IL1A/CAPN2/STAT2/RNF31/CHMP7/SLC25A5/VPS4B/CASP8/STAT1/IRF9/PPID/PLA2G4B/CHMP1A/MAPK10/PLA2G4E	48

hsa051 40	Leishmaniasis	23/2512	77/810 5	0.62694 9038	0.85587 6487	0.63803 9423	JAK1/IRAK1/MAP3K7/ITGB1/MAPK3/ MAPK14/ITGAM/IL4/NCF2/TAB2/EEF 1A1/PRKCB/IFNGR2/IFNGR1/IL1A/H LA- DRB5/TRAF6/TGFB3/STAT1/FCGR2A /JUN/HLA-DPB1/ITGA4	23
hsa000 62	Fatty acid elongation	8/2512	27/810 5	0.63205 5505	0.85928 2071	0.64057 822	ELOVL5/HACD4/HADH/ELOVL2/THE M4/HADHA/PPT1/ELOVL4	8
hsa046 20	Toll-like receptor signaling pathway	31/2512	104/81 05	0.63985 7265	0.86630 8807	0.64581 6516	CD86/MAPK8/IRAK1/MAP3K7/MAPK 3/PIK3CD/MAPK14/MAP3K8/MAP2K4 /TLR6/IL6/CXCL10/MAP2K6/CD14/PI K3R3/TLR5/TICAM2/IFNB1/TAB2/MA PK9/PIK3CA/AKT2/PIK3R1/TRAF6/C ASP8/STAT1/CCL3/CCL3L3/JUN/MAP K10/TLR1	31
hsa003 60	Phenylalanine metabolism	5/2512	17/810 5	0.64527 9073	0.86932 1002	0.64806 2049	IL4I1/MAOA/HPD/DDC/AOC3	5
hsa005 34	Glycosaminoglyca n biosynthesis - heparan sulfate / heparin	7/2512	24/810 5	0.65157 0233	0.86932 1002	0.64806 2049	EXTL2/HS3ST5/EXTL3/NDST1/EXT2/ XYLT1/EXTL1	7
hsa042	Ferroptosis	12/2512	41/810	0.65168	0.86932	0.64806	ACSL6/ATG7/GCLC/ACSL5/SLC7A11/	12

16			5	885	1002	2049	ACSL1/TP53/FTMT/MAP1LC3A/GCLM/SLC39A14/TF	
hsa030 15	mRNA surveillance pathway	29/2512	98/810 5	0.65541 662	0.86932 1002	0.64806 2049	GSPT1/RNMT/HBS1L/CPSF7/PPP2R1B/PPP2R2C/RNPS1/ACIN1/SMG6/SMG1/PABPN1/PPP2R5D/CASC3/PAPOLB/FIP1L1/CSTF2T/GSPT2/PNN/FUS/NXF5/PAPOLA/CSTF3/PCF11/PAPOLG/PABPC1L2B/PABPC1L2A/PPP2R5E/WDR33/DDX19B	29
hsa008 30	Retinol metabolism	20/2512	68/810 5	0.65565 189	0.86932 1002	0.64806 2049	CYP1A1/ALDH1A2/UGT2B28/UGT2A1/UGT2A2/UGT2B4/ALDH1A3/RDH13/ADH4/RDH10/DHRS9/CYP27C1/DHRS3/CYP3A4/RDH8/AWAT2/UGT1A10/UGT2B10/UGT2B11/CYP2B6	20
hsa053 10	Asthma	9/2512	31/810 5	0.65893 3092	0.86932 1002	0.64806 2049	MS4A2/IL4/CCL11/EPX/HLA-DRB5/FCER1G/IL5/IL13/HLA-DPB1	9
hsa002 80	Valine, leucine and isoleucine degradation	14/2512	48/810 5	0.66057 8269	0.86932 1002	0.64806 2049	BCAT1/PCCA/ABAT/ACADM/HADH/PCCB/IL4I1/HMGCLL1/HIBCH/DBT/EHHADH/HSD17B10/HADHA/HIBADH	14
hsa030 13	RNA transport	55/2512	186/810 05	0.69054 7257	0.90513 9631	0.67476 4147	UBE2I/EIF2B4/EIF4G1/NUP214/RAN/NUP153/CYFIP1/THOC5/RNPS1/CYFIP2/RPP40/ACIN1/GEMIN4/EIF5/PAIP1	55

							/THOC6/NUP210L/EIF4B/TPR/CASC3/RPP30/NUP188/EIF5B/GEMIN5/SUMO2/KPNB1/PNN/FMR1/NUP107/FUS/RP P14/RANBP2/FXR1/NUP133/NXF5/ND C1/EEF1A1/XPO1/STRAP/NUP160/EIF 2B3/EIF4E/SNUPN/TACC3/EIF4G3/SE NP2/PABPC1L2B/PABPC1L2A/XPO5/ NUP35/EIF3F/NUP210/NUP58/DDX19 B/NUP205	
hsa00500	Starch and sucrose metabolism	10/2512	36/8105	0.719974541	0.934773465	0.696855598	HK1/G6PC/GCK/GAA/MGAM/ENPP3/PGM2L1/GYS1/TREH/PGM1	10
hsa00220	Arginine biosynthesis	6/2512	22/8105	0.72167921	0.934773465	0.696855598	GLUL/GLS/NOS1/GPT/ABHD14A-ACY1/ARG2	6
hsa00900	Terpenoid backbone biosynthesis	6/2512	22/8105	0.72167921	0.934773465	0.696855598	GGPS1/FNTA/IDI1/HMGCR/PCYOX1/PDSS1	6
hsa05134	Legionellosis	16/2512	57/8105	0.729339187	0.936407762	0.698073935	APAF1/NAIP/HBS1L/CASP1/SAR1B/NFKB2/ITGAM/IL6/CD14/NLRC4/CYCS/TLR5/EEF1A1/RAB1B/CLK4/CASP8	16
hsa04080	Neuroactive ligand-receptor interaction	101/2512	341/8105	0.731114223	0.936407762	0.698073935	OPRM1/TRPV1/LEPR/ADCYAP1R1/KNG1/P2RY6/P2RY10/LPAR6/EDNRB/RXFP1/PRSS3/ADORA2A/GRM1/LPAR	101

							4/TSHR/CALCR/LPAR3/CHRNA5/CC KAR/PTGER3/MCHR2/OPRK1/GABR A2/GRIK2/NR3C1/GABBR1/CGA/CAL CRL/GABRG1/PTAFR/GPR156/PYY/N MUR2/CCKBR/S1PR1/TACR1/OPRL1/ F2R/GRM7/GRIN2B/CNR1/PTGFR/GA BRG3/GRIN2A/ADCYAP1/NPY5R/GRI A3/VIPR1/DRD5/GIPR/GABRR2/EDN RA/TAAR6/GRIK1/HRH1/ADM/GALR 1/C5/RXFP4/GABRQ/NMUR1/PLG/FP R3/RXFP2/GABRA3/GRIK3/THRB/HT R1F/TACR2/LEP/HTR2B/PRSS1/CHR M5/ADRA2B/GNRH1/CORT/CHRNA2/ CHRNA4/GRPR/GRIA2/TAAR1/PTGE R4/MC5R/AGT/P2RX1/RXFP3/CHRNA 10/P2RX7/GABRE/AVPR1A/HCRTR1/ TAAR8/CHRM1/GABRB2/S1PR3/GLP 2R/BRS3/GPR50/GRM2/NPY1R/LHCG R	
hsa006 03	Glycosphingolipid biosynthesis - globo and isoglobo	4/2512	15/810 5	0.73147 9619	0.93640 7762	0.69807 3935	B3GALNT1/ST3GAL1/HEXB/ST8SIA1	4

	series							
hsa05170	Human immunodeficiency virus 1 infection	62/2512	212/8105	0.734774084	0.936979355	0.698500047	ITPR1/NFATC4/NFATC1/PTK2/CFL2/BTRC/FBXW11/MAPK8/CUL4B/ATM/IRAK1/PPP3CB/MAP3K7/MAPK3/PIK3CD/KRAS/MAPK14/ATR/PPP3CA/NFATC2/GNG4/PAK1/CRKL/RAF1/DCAF1/CALM1/ITPR3/MAP2K6/CXCR4/PAK4/LIMK2/TNFRSF1A/AP1G1/CYCS/PIK3R3/GNAI3/RAC2/PPP3R1/GNG2/IFNB1/TAB2/CCNB3/MAPK9/GNAQ/ITPR2/GNG12/PRKCB/PAK5/BCL2/BAK1/PXN/PIK3CA/AKT2/PIK3R1/CD4/TRAFF6/CASP8/AP1S3/CDC25C/JUN/MAPK10/AP1S1	62
hsa00531	Glycosaminoglycan degradation	5/2512	19/8105	0.748726621	0.947231153	0.706142565	HYAL4/HEXB/HYAL1/GNS/HPSE2	5
hsa01230	Biosynthesis of amino acids	21/2512	75/8105	0.751698251	0.947231153	0.706142565	RPE/BCAT1/MAT2B/ASNS/PFKM/GLUL/ALDOB/MTR/PKLR/RPIA/TKT/SHMT1/IDH2/ACO2/PFKP/GPT/ABHD14A-ACY1/ARG2/ENO2/SHMT2/PFKL	21
hsa04640	Hematopoietic cell lineage	28/2512	99/8105	0.754504757	0.947231153	0.706142565	THPO/MME/CSF1/CD55/CD33/ITGA6/ITGAM/CSF3R/IL4R/IL1R1/IL5RA/IL6	28

							/IL4/ITGA5/ITGA3/ITGA2/CD19/CD14/ GP1BA/CD37/IL1A/HLA- DRB5/CD4/IL5/HLA- DPB1/IL7R/ITGA4/ITGB3	
hsa000 53	Ascorbate and aldarate metabolism	8/2512	30/810 5	0.75720 9098	0.94723 1153	0.70614 2565	UGT2B28/UGT2A1/UGT2A2/UGT2B4/ UGDH/UGT1A10/UGT2B10/UGT2B11	8
hsa004 10	beta-Alanine metabolism	8/2512	30/810 5	0.75720 9098	0.94723 1153	0.70614 2565	ABAT/HIBCH/DPYD/EHHADH/AOC3/ SMOX/GAD1/HADHA	8
hsa034 30	Mismatch repair	6/2512	23/810 5	0.76430 5777	0.95248 7123	0.71006 0789	MLH1/POLD3/MSH6/RFC4/MSH3/MS H2	6
hsa050 10	Alzheimer disease	108/251 2	369/81 05	0.78478 022	0.97431 2047	0.72633 0849	CACNA1C/ITPR1/CTNNB1/RTN3/APA F1/RTN4/TUBB/FZD3/APBB1/CACNA 1F/ATP2A1/EIF2AK2/MME/MAPK8/ID E/RB1CC1/CSF1/CAPN1/NAE1/PPP3C B/CSNK2A1/ATP2A2/ATP5MC3/NOX 4/MAPK3/PIK3CD/KRAS/WNT2B/RY R3/ATG2A/CACNA1D/SNCA/PPP3CA/ ATP5F1C/BRAF/IRS2/DVL3/ATF4/IL6/ GRIN2B/GRIN2A/PLCB1/RAF1/GSK3 B/PSEN2/NDUFB9/KIF5A/NCSTN/CA LM1/FZD4/ITPR3/APC/WIP1/HSD17B	108

							10/CSNK1E/TNFRSF1A/WNT10B/CYC S/KIF5B/PIK3R3/PSMB2/WNT9B/ULK 2/PPP3R1/COX6B2/AXIN2/ATP2A3/FZ D10/COX7A2L/LRP6/MAPK9/GNAQ/ NOS1/ITPR2/LRP1/WNT5A/PSMD4/N DUFS2/IL1A/CAPN2/AMBRA1/PSMC3 /PSMA1/TUBB8/CHRM5/NDUFB6/CO X4I2/TUBB4B/PIK3CA/AKT2/PIK3R1/ FRAT2/ULK1/CACNA1S/WNT8A/SLC 25A5/WNT5B/CSNK1A1/CASP8/CSNK 2A3/PPID/ATP5F1A/CHRM1/FZD5/M APK10/DDIT3/FZD8/UQCRC1	
hsa047 21	Synaptic vesicle cycle	21/2512	78/810 5	0.81626 2018	1	0.74548 0723	SLC1A2/SLC6A2/RIMS1/SYT1/ATP6V 0A4/DNM3/UNC13C/STX3/SLC6A11/S LC1A3/SLC1A7/UNC13B/AP2M1/AP2 B1/ATP6V1D/AP2S1/UNC13A/SLC17A 6/NAPA/ATP6V1G1/SLC6A12	21
hsa004 80	Glutathione metabolism	15/2512	57/810 5	0.81775 4757	1	0.74548 0723	GCLC/RRM2B/RRM2/GSTO1/G6PD/G PX5/CHAC1/GSTA4/GCLM/IDH2/GGT 7/GPX7/HPGDS/GSTM3/SMS	15
hsa049 79	Cholesterol metabolism	13/2512	50/810 5	0.82020 822	1	0.74548 0723	LDLR/OSBPL5/ANGPTL3/ABCB11/LR PAP1/CETP/APOB/SORT1/LIPC/LRP1/	13

							LRP2/NPC2/LIPA	
hsa047 42	Taste transduction	23/2512	86/810 5	0.83477 8161	1	0.74548 0723	CACNA1C/PRKACB/SCN3A/SCN2A/P DE1C/GRM1/GABRA2/GABBR1/TAS1 R1/PLCB1/ADCY8/PKD2L1/ITPR3/TA S1R2/PKD1L3/HTR3C/GABRA3/HTR1 F/TRPM5/CALHM1/TAS2R3/ADCY4/ GNAT3	23
hsa053 23	Rheumatoid arthritis	25/2512	93/810 5	0.83510 9205	1	0.74548 0723	ATP6V0A4/TNFSF11/CD86/TNFRSF11 A/FLT1/CSF1/IL15/TEK/CXCL12/IL6/ CCL20/MMP1/CTSL/ATP6V1D/ICAM1 /IL1A/HLA- DRB5/TGFB3/ATP6AP1/ITGAL/CCL3/ CCL3L3/ATP6V1G1/JUN/HLA-DPB1	25
hsa040 61	Viral protein interaction with cytokine and cytokine receptor	27/2512	100/81 05	0.83576 3313	1	0.74548 0723	CSF1/IL6ST/CCR9/CXCR5/CXCL12/T NFSF10/IL6/CXCL10/IL18RAP/CCL20/ CCR6/CXCR4/TNFRSF1A/CXCR3/CC L16/CCR7/CCL18/CCL21/CCR1/IL10R B/CCL11/CX3CL1/IL22RA1/CCR3/AC KR3/CCL3/CCL3L3	27
hsa002 60	Glycine, serine and threonine metabolism	10/2512	40/810 5	0.83967 6346	1	0.74548 0723	GCAT/MAOA/GLYCTK/AOC3/SHMT1 /PIPOX/DAO/GCSH/SHMT2/DMGDH	10

hsa041 45	Phagosome	42/2512	152/81 05	0.83969 8906	1	0.74548 0723	TUBB/FCAR/RAB5A/ATP6V0A4/DYN C1I2/PLA2R1/DYNC1I1/RAB5B/ITGB 1/COLEC11/ITGAM/CLEC7A/SEC61A 2/TLR6/MRC1/ITGA5/NCF2/ITGA2/M BL2/M6PR/CD14/CTSL/RAB7B/SFTPA 2/ATP6V1D/DYNC1LI2/NOS1/TUBB8/ EEA1/ITGB5/TUBB4B/MARCO/HLA- DRB5/SFTPD/C1R/ATP6AP1/LAMP1/F CGR2A/ATP6V1G1/CTSS/HLA- DPB1/ITGB3	42
hsa052 04	Chemical carcinogenesis	22/2512	83/810 5	0.84335 437	1	0.74548 0723	CYP1A1/CYP3A43/UGT2B28/UGT2A1 /UGT2A2/GSTO1/UGT2B4/EPHX1/AD H4/GSTA4/CYP1B1/CYP2C19/KYAT1/ HSD11B1/CYP3A4/CBR1/UGT1A10/U GT2B10/UGT2B11/HPGDS/GSTM3/KY AT3	22
hsa040 60	Cytokine-cytokine receptor interaction	84/2512	295/81 05	0.84551 3954	1	0.74548 0723	THPO/LEPR/EDA2R/TNFSF11/TNFRS F11A/CSF1/BMPRI1B/EDA/IL6ST/IL15/ CSF3R/ACVR2A/CCR9/CXCR5/IL4R/I L1R1/CXCL12/IL5RA/TNFSF10/IL12R B2/IL6/IL4/CXCL10/IL18RAP/CCL20/ MSTN/IL17RA/IL21R/OSM/IL36G/AC	84

							VR1C/TGFB1/LIFR/CCR6/CXCR4/TNFRSF1A/CXCR3/NODAL/BMP8A/TNFSF9/CCL16/CCR7/IL1RN/TNFRSF21/INHBC/IFNB1/CCL18/BMP2/CCL21/CCR1/IL10RB/CCL11/INHBB/BMP6/INHBA/IL15RA/LEP/IFNGR2/IFNGR1/IL1A/INHA/CX3CL1/IL31RA/LIF/BMP7/IL1RAP/GDF9/CD4/IL22RA1/TGFB3/AMH/CCR3/IL27/ACKR3/CCL3/CCL3L3/TNFSF18/ACVR2B/GDF6/IL5/IL13/TNFRSF17/BMP10/IL7R	
hsa01200	Carbon metabolism	31/2512	115/8105	0.852162555	1	0.745480723	HK1/RPE/PCCA/PFKM/GCK/OGDH/MET/PCCB/HIBCH/GLYCTK/ALDOB/G6PD/PKLR/ESD/H6PD/RPIA/TKT/PDHA2/SHMT1/ACSS1/IDH2/ACO2/MDH1/GCSH/PFKP/GPT/ENO2/ME1/SHMT2/PFKL/HAO1	31
hsa05143	African trypanosomiasis	9/2512	37/8105	0.85565508	1	0.745480723	KNG1/VCAM1/IL6/PLCB1/GNAQ/ICAM1/PRKCB/IDO1/SELE	9
hsa00511	Other glycan degradation	4/2512	18/8105	0.85690403	1	0.745480723	MAN2C1/MAN2B1/HEXB/FUCA2	4
hsa046	RIG-I-like receptor	18/2512	70/810	0.86274	1	0.74548	NLRX1/ATG12/CYLD/MAPK8/MAVS/	18

22	signaling pathway		5	4623		0723	MAP3K7/MAPK14/CXCL10/TANK/MAP3K1/DDX3X/RNF125/IFNB1/MAPK9/TRAF6/CASP8/IFIH1/MAPK10	
hsa00072	Synthesis and degradation of ketone bodies	2/2512	10/8105	0.865697673	1	0.745480723	BDH1/HMGCLL1	2
hsa00920	Sulfur metabolism	2/2512	10/8105	0.865697673	1	0.745480723	BPNT1/PAPSS1	2
hsa00980	Metabolism of xenobiotics by cytochrome P450	20/2512	78/8105	0.876167532	1	0.745480723	CYP1A1/UGT2B28/UGT2A1/UGT2A2/GSTO1/UGT2B4/EPHX1/ADH4/GSTA4/CYP1B1/CYP2D7/HSD11B1/CYP3A4/CBR1/UGT1A10/UGT2B10/UGT2B11/HPGDS/GSTM3/CYP2B6	20
hsa05168	Herpes simplex virus 1 infection	143/2512	498/8105	0.882433546	1	0.745480723	APAF1/JAK1/ZFP90/EIF2B4/ZNF200/ZNF426/ZNF33A/EIF2AK2/ZNF331/PM L/POU2F1/MAVS/ZNF559/ZNF2/EIF2AK1/ZNF587/ZNF610/IRAK1/ZNF229/ZNF189/ZNF557/ZNF544/ZNF124/OAS1/BIRC3/ZNF805/ZNF621/ZNF135/MAP3K7/ZNF473/ZNF829/ZNF286A/ZNF432/ZNF30/ZNF566/ZNF195/ZNF300/PIK3CD/ZNF605/ZFP37/ZSCAN32/TSC2/	143

							ZNF540/ZNF253/ZNF431/ZNF208/ZNF 736/ZNF780B/ZNF597/ZNF470/ZNF334 /IL6/ITGA5/ZNF221/ZNF214/ZNF398/P OU2F2/ZNF233/ZNF3/RBAK/SRSF7/Z NF888/ZNF549/ZNF12/ZNF454/ZNF18 1/OAS2/ZNF383/ZNF793/ZNF766/ZNF 674/ZNF641/ZNF707/TYK2/ZNF282/Z NF382/ZNF546/TNFRSF1A/ZNF98/ZN F101/CYCS/ZNF727/PIK3R3/ZNF529/Z NF527/TP53/ZNF490/ZNF333/ZNF320/ ZNF677/C5/ZNF589/ZNF517/IFNB1/TA B2/SRC/ZNF33B/NXF5/ZNF737/SRSF1 /BCL2/ZNF468/BAK1/ZNF565/ZNF433 /IFNGR2/IFNGR1/ZNF583/ZNF175/EIF 2B3/ZNF26/ZNF585B/ZNF570/ZNF180/ STAT2/ZNF846/ZNF841/ZNF616/HLA- DRB5/PIK3CA/AKT2/ZNF250/PIK3R1/ ZNF667/ZNF91/TRAF6/ZNF84/PILRB/ ZNF343/ZNF136/CASP8/ZNF79/ZNF71 3/IFIH1/STAT1/IRF9/RNASEL/ZNF273 /ZNF772/HLA- DPB1/ZNF790/ZNF45/ITGB3	
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hsa00601	Glycosphingolipid biosynthesis - lacto and neolacto series	6/2512	27/8105	0.886987539	1	0.745480723	B3GALNT1/ST3GAL3/ST3GAL4/ST3GAL6/B3GALT1/ST8SIA1	6
hsa03020	RNA polymerase	7/2512	31/8105	0.889568561	1	0.745480723	POLR2E/POLR1A/POLR3G/POLR1D/POLR3D/POLR2J2/POLR2G	7
hsa03018	RNA degradation	20/2512	79/8105	0.890170147	1	0.745480723	CNOT4/PFKM/CNOT10/C1D/DDX6/LSM8/CNOT6L/XRN1/CNOT8/EXOSC10/EXOSC9/SKIV2L/PABPC1L2B/PABPC1L2A/PFKP/DCPS/ENO2/PFKL/PNPT1/PATL1	20
hsa05144	Malaria	12/2512	50/8105	0.892143332	1	0.745480723	VCAM1/GYPC/IL6/MET/ACKR1/LRP1/ICAM1/SELE/PECAM1/TGFB3/ITGAL/SELP	12
hsa00330	Arginine and proline metabolism	12/2512	51/8105	0.907407603	1	0.745480723	PRODH2/MAOA/HOGA1/AMD1/PRODH/SMOX/NOS1/DAO/AZIN2/ARG2/AGMAT/SMS	12
hsa00100	Steroid biosynthesis	4/2512	20/8105	0.909382427	1	0.745480723	LSS/LBR/DHCR24/LIPA	4
hsa05171	Coronavirus disease - COVID-19	62/2512	232/8105	0.934553037	1	0.745480723	JAK1/ADAR/RPS24/EIF2AK2/MAPK8/MAVS/RPL15/IRAK1/OAS1/CASP1/MAP3K7/MASP1/MAPK3/EGFR/PIK3CD/IL6ST/MAPK14/NLRP3/IL6/CXCL10/	62

							C1QB/STAT3/OAS2/MMP1/MBL2/RPL13A/TYK2/RPL35A/TNFRSF1A/C4A/PIK3R3/RPS28/C5/ACE/IFNB1/TAB2/MAPK9/RPS29/PRKCB/F13A1/C6/STAT2/PIK3CA/PIK3R1/MASP2/F13B/TRAF6/RPL37/RPS23/C1R/IFIH1/STAT1/IRF9/RPS6/FCGR2A/JUN/MAPK10/HBEGF/MX1/TMPRSS2/SELP/RPL3	
hsa00140	Steroid hormone biosynthesis	14/2512	61/8105	0.936923583	1	0.745480723	CYP1A1/CYP19A1/UGT2B28/UGT2A1/UGT2A2/UGT2B4/CYP1B1/COMT/HSDD11B1/CYP3A4/HSD3B2/UGT1A10/UGT2B10/UGT2B11	14
hsa05340	Primary immunodeficiency	8/2512	38/8105	0.938316746	1	0.745480723	DCLRE1C/CD19/RFX5/ICOS/RAG1/CD4/ZAP70/IL7R	8
hsa00983	Drug metabolism - other enzymes	19/2512	80/8105	0.93988433	1	0.745480723	RRM2B/CES1/RRM2/DPYD/UGT2B28/UGT2A1/UGT2A2/GSTO1/UGT2B4/GSTA4/TK1/NME6/HPRT1/CYP3A4/UGT1A10/UMPS/UGT2B10/UGT2B11/GSTM3	19
hsa05014	Amyotrophic lateral sclerosis	100/2512	364/8105	0.939942659	1	0.745480723	SLC1A2/NRG1/APAF1/TUBB/RAB5A/NUP214/ANXA7/RB1CC1/NUP153/PPP3CB/CASP1/ATP5MC3/SPG11/ALS2/H	100

							NRNPA3/MAPK14/NRG3/DCTN2/ATG2A/DNAH8/PPP3CA/NUP210L/ATXN2/ATP5F1C/TPR/ATF4/NUP188/SETX/TANK/GRIN2B/GRIN2A/TOMM40L/SRSF7/DNAH5/DNAH10/NDUFB9/KIF5A/GPX5/DNAH9/DNAH6/WDR41/NEFL/C9orf72/ITPR3/MAP2K6/DERL1/NUP107/FUS/WIP1/UBQLN1/TNFRSF1A/CYCS/KIF5B/PSMB2/TP53/ULK2/RANBP2/PPP3R1/COX6B2/NUP133/DCTN1/COX7A2L/NXF5/NRG2/NOS1/NDC1/DNAL4/BCL2/ACTR1A/PSMD4/NRG4/NDUFS2/AMBRA1/PSMC3/NUP160/PSMA1/TUBB8/NDUFB6/NEFM/COX4I2/DNAH1/TUBB4B/GPX7/DCTN6/ANG/ULK1/GRIA2/HNRNPA1L2/DNAH11/NUP35/UBQLN3/DNAH7/GABARAP/DNAH3/NUP210/ATP5F1A/NUP58/DDIT3/NUP205/UQCRC1	
hsa04975	Fat digestion and absorption	9/2512	43/8105	0.949311633	1	0.745480723	CLPS/FABP2/PLA2G2D/APOB/PLA2G5/PNLIP/MOGAT2/PLA2G12A/PLA2G3	9

hsa034 20	Nucleotide excision repair	10/2512	47/810 5	0.94983 1593	1	0.74548 0723	CUL4B/POLD3/GTF2H5/ERCC6/POLE 2/XPC/GTF2H1/CETN2/RFC4/ERCC8	10
hsa049 32	Non-alcoholic fatty liver disease	39/2512	155/81 05	0.95497 5639	1	0.74548 0723	PRKAG2/LEPR/MAPK8/NR1H3/PIK3C D/MAPK14/IRS2/ATF4/IL6/GSK3B/AD IPOQ/PRKAA1/NDUFB9/PKLR/BCL2L 11/PPARA/TNFRSF1A/CYCS/PIK3R3/ COX6B2/ADIPOR2/COX7A2L/MAPK9 /CDC42/LEP/NDUFS2/IL1A/NDUFB6/ COX4I2/PIK3CA/AKT2/PIK3R1/PRKA G3/PRKAB2/CASP8/JUN/MAPK10/DD IT3/UQCRC1	39
hsa047 14	Thermogenesis	60/2512	232/81 05	0.96470 1387	1	0.74548 0723	PRKAG2/ACSL6/PRKACB/SMARCA4/ RPS6KA3/CREB5/RPS6KA6/NDUFAF 7/SMARCC2/CPT1C/FGFR1/ATP5MC3 /SOS2/ADCY10/KRAS/MGLL/MAPK1 4/PRKG2/TSC2/ACSL5/ATP5F1C/ZNF 516/RPS6KA2/PRDM16/ADCY7/ADCY 3/SMARCD1/CNR1/PLIN1/CREB1/AC SL1/PRKAA1/NDUFB9/ADCY8/COA4/ PRKG1/BMP8A/COX6B2/ATF2/COX7 A2L/GNAS/CREB3L1/ADCY2/FGF21/ NDUFAF4/CPT1A/NDUFS2/NDUFB6/	60

							COX4I2/ARID1B/PRKAG3/PRKAB2/PARGC1A/ADCY4/RPS6/KLB/ADCY9/ATP5F1A/CREB3L3/UQCRC1	
hsa04612	Antigen processing and presentation	17/2512	78/8105	0.973664261	1	0.745480723	NFYC/KLRD1/CTSB/NFYB/CREB1/NFYA/RFX5/LGMN/CTSL/PSME1/HLA-DRB5/IFI30/HSPA4/CD4/KIR2DL4/CTSS/HLA-DPB1	17
hsa04650	Natural killer cell mediated cytotoxicity	31/2512	131/8105	0.97509939	1	0.745480723	NFATC1/KLRD1/FYN/SH3BP2/PPP3CB/SOS2/MAPK3/CD48/PIK3CD/KRAS/PPP3CA/NFATC2/PAK1/BRAF/TNFSF10/RAF1/VAV3/PIK3R3/RAC2/PPP3R1/IFNB1/ICAM1/PRKCB/IFNGR2/IFNGR1/PIK3CA/PIK3R1/SHC4/FCER1G/ZAP70/ITGAL	31
hsa00010	Glycolysis / Gluconeogenesis	14/2512	67/8105	0.976445112	1	0.745480723	HK1/G6PC/PFKM/GCK/ALDOB/PKLR/ADH4/PDHA2/ACSS1/PFKP/PGM1/ENO2/LDHA/PFKL	14
hsa00620	Pyruvate metabolism	9/2512	47/8105	0.976794441	1	0.745480723	ACACA/ME2/PKLR/ADH4/PDHA2/ACSS1/MDH1/LDHA/ME1	9
hsa00020	Citrate cycle (TCA cycle)	5/2512	30/8105	0.976917472	1	0.745480723	OGDH/PDHA2/IDH2/ACO2/MDH1	5
hsa049	Type I diabetes	8/2512	43/810	0.97749	1	0.74548	CD86/PTPRN/ICA1/GAD1/IL1A/CPE/H	8

40	mellitus		5	9852		0723	LA-DRB5/HLA-DPB1	
hsa03008	Ribosome biogenesis in eukaryotes	25/2512	110/8105	0.979210089	1	0.745480723	REXO5/RAN/UTP15/IMP4/CSNK2A1/RPP40/RBM28/RCL1/RPP30/XRN1/WDR75/WDR3/UTP14A/WDR36/EFL1/NOL6/RIOK1/NXF5/XPO1/MDN1/UTP14C/GNL3/HEATR1/CSNK2A3/NOP56	25
hsa00790	Folate biosynthesis	4/2512	26/8105	0.979833028	1	0.745480723	TH/DHFR2/CBR1/TPH2	4
hsa00512	Mucin type O-glycan biosynthesis	6/2512	36/8105	0.984200543	1	0.745480723	ST3GAL1/GALNT15/GALNT5/GALNT8/GALNTL5/GALNT3	6
hsa03030	DNA replication	6/2512	36/8105	0.984200543	1	0.745480723	POLD3/POLE2/RNASEH2B/RFC4/PRI-M2/MCM2	6
hsa05016	Huntington disease	78/2512	306/8105	0.98667554	1	0.745480723	ITPR1/SLC1A2/APAF1/TUBB/SOD2/MAPK8/CREB5/RB1CC1/HIP1/ATP5MC3/SLC1A3/DCTN2/ATG2A/DNAH8/ATP5F1C/GRIN2B/PLCB1/DLG4/CREB1/GRIA3/DNAH5/DNAH10/NDUFB9/KIF5A/GPX5/DNAH9/DNAH6/AP2M1/POLR2E/AP2B1/TBPL1/WIP1/TAF4B/CYC/CS/KIF5B/PSMB2/TP53/ULK2/COX6B2/DCTN1/HTT/COX7A2L/MAPK9/BDNF/CREB3L1/GNAQ/DNAL4/ACTR1A	78

							/AP2S1/PSMD4/NDUFS2/AMBRA1/PSMC3/PSMA1/TUBB8/HDAC1/NDUFB6/COX4I2/DNAH1/TUBB4B/TGM2/GPX7/DCTN6/ULK1/GRIA2/SLC25A5/DNAH11/PPARGC1A/CASP8/DNAH7/DNAH3/ATP5F1A/MAPK10/POLR2J2/RCOR1/POLR2G/CREB3L3/UQCRC1	
hsa04744	Phototransduction	4/2512	29/8105	0.991009061	1	0.745480723	RGS9/SLC24A1/CALM1/GUCA1B	4
hsa04623	Cytosolic DNA-sensing pathway	11/2512	63/8105	0.995212047	1	0.745480723	ADAR/MAVS/CASP1/IL6/CXCL10/POLR2E/RIPK3/IFNB1/POLR3G/POLR1D/POLR3D	11
hsa05020	Prion disease	66/2512	273/8105	0.995266171	1	0.745480723	CACNA1C/ITPR1/APAF1/PRKACB/TUBB/CACNA1F/FYN/MAPK8/CREB5/PPP3CB/CSNK2A1/ATP5MC3/MAPK3/PIK3CD/CAV1/MAPK14/RYR3/CACNA1D/PPP3CA/ATP5F1C/ATF4/IL6/C1QB/STIP1/NCF2/GRIN2B/GRIN2A/GSK3B/CREB1/NDUFB9/KIF5A/ITPR3/CYCS/KIF5B/PIK3R3/PSMB2/RAC2/PPP3R1/COX6B2/C5/ATF2/COX7A2L/NCAM2/MAPK9/CREB3L1/ITPR2/PSMD4/NDU	66

							FS2/IL1A/PSMC3/C6/PSMA1/TUBB8/ NDUFB6/COX4I2/TUBB4B/PIK3CA/PI K3R1/CACNA1S/SLC25A5/CSNK2A3/ ATP5F1A/MAPK10/DDIT3/CREB3L3/ UQCRC1	
hsa049 66	Collecting duct acid secretion	3/2512	27/810 5	0.99629 2991	1	0.74548 0723	ATP6V0A4/ATP6V1D/ATP6V1G1	3
hsa053 32	Graft-versus-host disease	6/2512	42/810 5	0.99641 5412	1	0.74548 0723	KLRD1/CD86/IL6/IL1A/HLA- DRB5/HLA-DPB1	6
hsa003 40	Histidine metabolism	2/2512	22/810 5	0.99692 2502	1	0.74548 0723	MAOA/HAL	2
hsa054 15	Diabetic cardiomyopathy	46/2512	203/81 05	0.99698 4735	1	0.74548 0723	CAMK2B/ATP2A1/SMAD2/MAPK8/C AMK2G/ATP2A2/ATP5MC3/PIK3CD/ MAPK14/TBC1D4/ATP5F1C/NCF2/PL CB1/GSK3B/G6PD/NDUFB9/SMAD3/T GFBR1/COL3A1/PPARA/PIK3R3/SLC2 A4/RAC2/COX6B2/ACE/ATP2A3/PDH A2/COX7A2L/MMP9/MAPK9/PRKCB/ NDUFS2/GFPT2/GYS1/NDUFB6/COX4 I2/PIK3CA/AKT2/PIK3R1/SLC25A5/T GFB3/AGT/ATP5F1A/PDK3/MAPK10/ UQCRC1	46

hsa053 30	Allograft rejection	5/2512	38/810 5	0.99708 6145	1	0.74548 0723	CD86/IL4/HLA-DRB5/IL5/HLA-DPB1	5
hsa053 20	Autoimmune thyroid disease	8/2512	53/810 5	0.99767 9278	1	0.74548 0723	CD86/TSHR/TG/CGA/IL4/HLA- DRB5/IL5/HLA-DPB1	8
hsa030 50	Proteasome	6/2512	46/810 5	0.99873 9142	1	0.74548 0723	PSMB2/PSMD4/PSMC3/PSMA1/PSME 1/PSMF1	6
hsa050 34	Alcoholism	38/2512	187/81 05	0.99965 4577	1	0.74548 0723	PRKACB/HDAC9/HDAC8/CREB5/PKI A/ADORA2A/TH/SOS2/MAPK3/KRAS /CAMK4/GNG4/PPP1R1B/BRAF/MAO A/ATF4/SLC29A2/GRIN2B/CAMKK1/ GRIN2A/RAF1/CREB1/DDC/CALM1/N TRK2/GNAI3/GNG2/ATF2/GNAS/BDN F/CREB3L1/GNG12/FOSB/HDAC1/SH C4/HDAC7/SLC29A1/CREB3L3	38
hsa052 06	MicroRNAs in cancer	68/2512	310/81 05	0.99988 5771	1	0.74548 0723	UBE2I/DICER1/FZD3/MDM4/RDX/HM GA2/EZH2/CCNG1/MDM2/ATM/ZEB1 /E2F3/BRCA1/ERBB2/CCNE2/SOS2/M APK3/EGFR/PIK3CD/KRAS/CDK6/M MP16/GLS/IRS2/CRKL/ABCC1/ITGA5/ STAT3/MET/RAF1/SERPINB5/TP63/KI F23/EZR/APC/CDC25A/BCL2L11/PAK 4/DNMT1/PIK3R3/TP53/CYP1B1/ERB	68

							B3/SOX4/MMP9/BMP2/ZEB2/ZFPM2 /PDGFRB/PRKCB/BCL2/FOXP1/BAK1 /BMI1/SPRY2/TNC/HDAC1/PIK3CA/PI K3R1/SHC4/BCL2L2/TPM1/PIM1/ABC B1/CDC25C/ROCK1/TRIM71/ITGB3	
hsa009 70	Aminoacyl-tRNA biosynthesis	8/2512	66/810 5	0.99991 5778	1	0.74548 0723	WARS2/PSTK/NARS2/FARS2/SARS2/ RARS2/SEPSECS/IARS2	8
hsa050 12	Parkinson disease	51/2512	249/81 05	0.99994 0289	1	0.74548 0723	ITPR1/APAF1/PRKACB/TUBB/CAMK 2B/MAPK8/CAMK2G/ADORA2A/TH/ ATP5MC3/RYR3/SNCA/TRAP1/ATP5F 1C/MAOA/ATF4/NDUFB9/KIF5A/CAL M1/ITPR3/UBA1/CYCS/KIF5B/UBE2J1 /GNAI3/PSMB2/TP53/UCHL1/COX6B2 /COX7A2L/MFN1/GNAS/MAPK9/ITPR 2/PSMD4/NDUFS2/PSMC3/PSMA1/TU BB8/NDUFB6/COX4I2/TUBB4B/SLC2 5A5/TXN2/PARK7/GPR37/ATP5F1A/U BE2J2/MAPK10/DDIT3/UQCRC1	51
hsa046 13	Neutrophil extracellular trap formation	36/2512	190/81 05	0.99994 6695	1	0.74548 0723	CLCN5/CLCN4/HDAC9/HDAC8/CLCN 3/CASP1/MAP3K7/MAPK3/ATG7/PIK3 CD/MAPK14/ITGAM/CLEC7A/NCF2/S ELPLG/PLCB1/RAF1/PIK3R3/RAC2/C	36

							5/GP1BA/FPR3/SRC/HMGB1/PRKCB/ HDAC1/PADI4/PIK3CA/AKT2/PIK3R1 /HDAC7/SLC25A5/ITGAL/FCGR2A/IT GB3/SELP	
hsa030 40	Spliceosome	26/2512	150/81 05	0.99995 8635	1	0.74548 0723	TCERG1/ACIN1/HNRNPA3/CRNKL1/ LSM8/RBM17/SF3B3/SRSF7/CDC5L/D DX46/U2SURP/FUS/DHX8/SRSF1/RB MXL1/CHERP/SLU7/WBP11/HNRNPU /PRPF38A/HNRNPA1L2/TRA2B/SNRP A1/SNRNP40/PRPF40A/SNRNP200	26
hsa001 90	Oxidative phosphorylation	14/2512	133/81 05	0.99999 9996	1	0.74548 0723	ATP6V0A4/ATP5MC3/ATP5F1C/NDU FB9/COX6B2/ATP6V1D/COX7A2L/ND UFS2/NDUFB6/COX4I2/ATP6AP1/ATP 5F1A/ATP6V1G1/UQCRC1	14
hsa030 10	Ribosome	17/2512	158/81 05	1	1	0.74548 0723	MRPL11/RPS24/RPL15/MRPS11/MRPS 5/RPL13A/RPL35A/RPS28/MRPL30/M RPL10/RPS29/MRPL20/RPL37/RPS23/ MRPL1/RPS6/RPL3	17
hsa053 22	Systemic lupus erythematosus	12/2512	136/81 05	1	1	0.74548 0723	CD86/SSB/C1QB/GRIN2B/GRIN2A/C4 A/C5/C6/HLA- DRB5/C1R/FCGR2A/HLA-DPB1	12
hsa047	Olfactory	51/2512	443/81	1	1	0.74548	PRKACB/SLC8A1/CAMK2B/SLC24A4	51

40	transduction		05			0723	/ARRB1/PDE1C/CAMK2G/PRKG2/OR6B2/OR9Q2/ADCY3/ANO2/OR10H1/CALM1/OR2C3/PRKG1/OR2T11/OR11L1/OR51E2/OR51F1/OR51T1/OR51G2/OR5P2/OR5P3/OR10G2/OR1E2/OR13A1/OR2B11/OR4X1/SLC8A2/OR2A42/OR2A1/OR8B12/OR8J3/OR8J1/OR10W1/OR1L8/OR4F6/OR4K5/OR4P4/OR2S2/OR10A5/OR8A1/OR1I1/OR1A1/OR5B3/OR2H1/OR1F1/CNGA4/OR6B1/OR9Q1	
C, Green								
ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	count
hsa04211	Longevity regulating pathway	28/1162	89/8105	2.76598E-05	0.009044766	0.007802985	ATG13/PPARG/ATF2/PIK3R3/ADCY5/FOXO3/TSC1/SOD2/EIF4E/PIK3CB/ATG5/NFKB1/IGF1/IGF1R/CREB1/ULK1/KRAS/SESN1/AKT1S1/PRKAG3/ADCY1/ADCY7/PIK3CA/PRKACG/PRKAA2/IRS1/ADCY6/SESN3	28
hsa04140	Autophagy animal	- 37/1162	137/8105	6.86806E-05	0.011229284	0.009687585	MAP3K7/MRAS/ATG13/MAPK9/DAPK1/PIK3R3/TSC1/PIK3CB/ITPR1/ATG5/IGF1R/ULK1/ATG16L1/KRAS/UVR	37

							AG/AKT1S1/RAB33B/PDPK1/EIF2S1/ATG9B/MAPK1/WDR41/BCL2L1/DAPK2/PIK3CA/PRKACG/PRKAA2/MAPK10/ATG14/RRAGA/HMGB1/MAP2K1/IRS1/MTMR4/CTSD/ATG2B/ATG2A	
hsa01522	Endocrine resistance	28/1162	98/8105	0.000182969	0.019943587	0.017205476	MAPK9/PIK3R3/ADCY5/PIK3CB/IGF1/IGF1R/JAG2/KRAS/ARAF/GNAS/ESR2/ADCY1/E2F3/NOTCH2/MAPK1/E2F1/MAPK13/CDKN2C/ADCY7/NOTCH1/PIK3CA/PRKACG/MAPK10/MAP2K1/ADCY6/ABCB11/SHC4/MMP9	28
hsa04550	Signaling pathways regulating pluripotency of stem cells	36/1162	143/8105	0.000389501	0.03184171	0.027470074	RIF1/TCF3/JAK1/BMPR1B/SKIL/SMARCAD1/ACVR1/PIK3R3/KAT6A/PIK3CB/IGF1/IGF1R/HOXA1/STAT3/ACVR2A/PAX6/FGFR2/KRAS/TBX3/ID1/INHBA/FZD4/JARID2/FZD2/MAPK1/LIF/MAPK13/AXIN2/FGFR1/PIK3CA/BMPR2/WNT10B/FGFR3/MAP2K1/LEFTY1/LEFTY2	36
hsa04213	Longevity regulating pathway - multiple species	19/1162	62/8105	0.000755499	0.048112193	0.041506737	PIK3R3/ADCY5/FOXO3/SOD2/PIK3CB/ATG5/IGF1/IGF1R/KRAS/AKT1S1/PRKAG3/ADCY1/HDAC1/ADCY7/PIK3	19

							CA/PRKACG/PRKAA2/IRS1/ADCY6	
hsa05205	Proteoglycans in cancer	46/1162	205/8105	0.001044403	0.048112193	0.041506737	MRAS/CDC42/PIK3R3/DDX5/EIF4B/PIK3CB/ITPR1/IGF1/IGF1R/PLAU/STAT3/FLNC/RHOA/FASLG/ACTG1/SDC4/TLR4/KRAS/GAB1/HPSE2/TLR2/ARHGEF1/ARAF/PDPK1/PRKCA/HGF/FZD4/FZD2/ITGB3/MAPK1/MAPK13/ARHGEF12/FGFR1/PIK3CA/PPP1CB/PRKACG/IGF2/WNT10B/MAP2K1/IHH/PLAUR/LUM/ITGA5/MSN/ROCK1/MMP9	46
hsa04722	Neurotrophin signaling pathway	30/1162	119/8105	0.001125996	0.048112193	0.041506737	MATK/MAPK9/CDC42/KIDINS220/PIK3R3/MAGED1/FOXO3/BDNF/PIK3CB/NTRK1/NFKB1/PSEN1/RPS6KA6/SORT1/RHOA/FASLG/KRAS/GAB1/RAPGEF1/PDPK1/MAPK1/MAPK13/NTRK3/NGF/PIK3CA/MAPK10/IRAK2/MAP2K1/IRS1/SHC4	30
hsa01521	EGFR tyrosine kinase inhibitor resistance	22/1162	79/8105	0.001264065	0.048112193	0.041506737	JAK1/NRG2/PIK3R3/FOXO3/EIF4E/PIK3CB/IGF1/IGF1R/STAT3/FGFR2/KRAS/GAB1/ARAF/PRKCA/HGF/PDGFR/AMAPK1/BCL2L1/PIK3CA/FGFR3/MAP2K1/SHC4	22

hsa049 14	Progesterone- mediated oocyte maturation	26/1162	100/81 05	0.00145 732	0.04811 2193	0.04150 6737	MAPK9/CPEB2/PIK3R3/ADCY5/SPDY E1/PIK3CB/IGF1/IGF1R/RPS6KA6/SP DYE5/SPDYE6/ANAPC1/KRAS/ARAF/ ADCY1/MAPK1/MAPK13/SPDYE2/SP DYE2B/ADCY7/ANAPC2/PIK3CA/PR KACG/MAPK10/MAP2K1/ADCY6	26
hsa041 51	PI3K-Akt signaling pathway	71/1162	354/81 05	0.00162 4563	0.04811 2193	0.04150 6737	JAK1/CHRM2/LAMB4/COL6A3/ATF2/ PIK3R3/PHLPP2/FOXO3/TSC1/BDNF/ FLT4/PPP2R2B/EIF4E/EIF4B/PIK3CB/ NTRK1/NFKB1/IGF1/MCL1/IGF1R/CR EB1/GYS1/EFNA5/FASLG/FGFR2/VW F/TLR4/ITGA2B/LAMB2/LAMA2/KRA S/TLR2/LPAR5/SYK/NR4A1/CHAD/C CND2/PDPK1/PRKCA/OSMR/LPAR1/ HGF/GNG12/IL3/ITGB3/PDGFRA/MA PK1/RBL2/BCL2L1/ITGA8/FGFR1/NG F/PPP2R2C/PIK3CA/IGF2/IL2RA/PRK AA2/YWHAZ/COL4A1/FGFR3/PPP2R2 A/MAP2K1/IRS1/COL4A3/FGF18/PPP2 R3B/NOS3/ITGA5/COL6A5/LAMA3/M AGI1	71
hsa040	Rap1 signaling	46/1162	210/81	0.00176	0.04811	0.04150	MRAS/CDC42/ENAH/PIK3R3/ADCY5/	46

15	pathway		05	4685	2193	6737	FLT4/PIK3CB/IGF1/IGF1R/EFNA5/RHOA/ACTG1/FGFR2/SIPA1L2/ITGA2B/KRAS/RAPGEF1/LPAR5/RAPGEF3/MAGI3/ITGAL/ITGAM/ID1/GNAS/PRKCA/ADCY1/LPAR1/HGF/ITGB3/EVL/PDGfra/MAPK1/MAPK13/PFN4/FGFR1/NGF/ADCY7/PIK3CA/GRIN2B/FGFR3/MAP2K1/FGF18/PRKD2/ADCY6/PRKD3/MAGI1	
hsa04360	Axon guidance	41/1162	182/8105	0.001765585	0.048112193	0.041506737	NTNG1/CDC42/SEMA4D/ENAH/BMPR1B/PIK3R3/L1CAM/SEMA6C/SEMA6D/PIK3CB/EFNA5/RHOA/SRGAP3/SEMA3A/KRAS/TRPC1/PLXNA4/SLIT2/PDPK1/PRKCA/CXCL12/MAPK1/ABLIM2/PPP3R1/NFATC2/BMP7/ARHGEF12/PLXNA1/SLIT1/PIK3CA/EPHB3/BMPR2/SRGAP2/SRGAP1/PLXNB1/ROBO2/TRPC5/LRRC4/SEMA6B/EPHA8/ROCK1	41
hsa04810	Regulation of actin cytoskeleton	47/1162	218/8105	0.002225041	0.055018083	0.047464498	MRAS/SPATA13/PIP4K2C/CDC42/GNA12/CHRM2/ABI2/ENAH/PIK3R3/PIK3CB/RHOA/ACTG1/FGFR2/PIP4K2A/I	47

							TGA2B/KRAS/LPAR5/ARHGEF1/ARAF/ITGAL/ITGAM/CHRM3/LPAR1/GNG12/CXCL12/ITGB3/BDKRB2/PDGFR/ARHGEF12/PIKFYVE/PFN4/F2/ITGA8/FGFR1/ITGAD/PIK3CA/PPP1CB/FGFR3/MAP2K1/FGF18/ARPC1B/ITGA5/MSN/BRK1/MYLK/ROCK1	
hsa04010	MAPK signaling pathway	60/1162	294/8105	0.002392747	0.055018083	0.047464498	CACNB4/CACNA1C/CACNA1E/MAP3K7/MRAS/MAP4K4/MAX/MAP3K20/MAPK9/CDC42/GNA12/MEF2C/MKNK1/ATF2/MAP3K13/BDNF/FLT4/NTRK1/NFKB1/IGF1/NFATC1/RPS6KA4/IGF1R/RPS6KA6/EFNA5/FLNC/FASLG/FGFR2/CACNA1D/KRAS/TAOK1/NR4A1/ARAF/MAP4K2/PRKCA/CACNG4/HGF/ELK4/GNG12/PDGFR/ARHGEF1/PLA2G4D/PPP3R1/MAPK13/MECOM/FGFR1/NGF/PRKACG/DUSP8/IGF2/MAPK10/LAMTOR3/FGFR3/MAP2K1/DUSP16/MAPK8IP3/FGF18/PTPN7/TAOK2/MYD88	60
hsa041	Mitophagy - animal	19/1162	68/810	0.00253	0.05501	0.04746	OPTN/MRAS/MAPK9/MFN2/TAX1BP	19

37			5	5269	8083	4498	1/FOXO3/NBR1/ATG5/ULK1/KRAS/UBA52/PGAM5/ATG9B/BCL2L1/E2F1/C SNK2A3/USP30/UBB/MAPK10	
hsa041 52	AMPK signaling pathway	29/1162	120/81 05	0.00269 2016	0.05501 8083	0.04746 4498	MAP3K7/PPARG/CPT1C/ACACA/PIK3 R3/CAB39/FOXO3/TSC1/PPP2R2B/PIK 3CB/IGF1/IGF1R/CREB1/GYS1/ULK1/ AKT1S1/PFKFB1/FASN/PDPK1/PRKA G3/EEF2K/PFKP/PPP2R2C/PIK3CA/PR KAA2/PPP2R2A/IRS1/PFKFB3/PPP2R3 B	29
hsa046 21	NOD-like receptor signaling pathway	40/1162	181/81 05	0.00288 6112	0.05551 5211	0.04789 3374	MAP3K7/CARD8/JAK1/MCU/MAPK9/ MFN2/ANTXR2/NAMPT/NLRP3/NLRP 1/ITPR1/ATG5/IKBKE/NFKB1/VDAC1 /RHOA/ATG16L1/MAVS/TLR4/BIRC3/ PSTPIP1/CASP4/CASP5/RNF31/STAT1 /MAPK1/BCL2L1/MAPK13/CARD6/BI RC2/TXNIP/NAIP/NLRP7/MAPK10/GB P5/RIPK1/CYBB/AIM2/NOD2/MYD88	40
hsa049 28	Parathyroid hormone synthesis, secretion and action	26/1162	106/81 05	0.00351 4012	0.06237 0729	0.05380 7679	MEF2A/MEF2D/PDE4D/GNA12/MEF2 C/ATF2/ADCY5/ITPR1/AKAP13/CREB 1/RHOA/CYP24A1/LRP5/ARHGEF1/A RAF/RXR/GB/GNAS/PRKCA/ADCY1/M	26

							APK1/FGFR1/ADCY7/PRKACG/MAP2K1/ADCY6/TRPV5	
hsa05230	Central carbon metabolism in cancer	19/1162	70/8105	0.003623987	0.062370729	0.053807679	HK1/LDHA/PIK3R3/PIK3CB/NTRK1/FGFR2/KRAS/SLC7A5/PDGFR/PAK1/NTRK3/PFKP/FGFR1/PIK3CA/HKDC1/FGFR3/SLC1A5/MAP2K1/PKM	19
hsa04930	Type II diabetes mellitus	14/1162	46/8105	0.003890353	0.063607278	0.054874459	CACNA1C/CACNA1E/HK1/MAPK9/PIK3R3/SOCS2/PIK3CB/CACNA1D/MAPK1/PIK3CA/HKDC1/MAPK10/IRS1/PKM	14
hsa04750	Inflammatory mediator regulation of TRP channels	24/1162	98/8105	0.005033404	0.07785234	0.067163776	MAPK9/PIK3R3/ADCY5/PIK3CB/ITPR1/NTRK1/IGF1/GNAS/PRKCA/ADCY1/BDKRB2/PLA2G4D/MAPK13/NGF/ADCY7/PIK3CA/PPP1CB/PRKACG/MAPK10/PRKCH/ADCY6/HTR2A/PTGER2/TRPM8	24
hsa04066	HIF-1 signaling pathway	26/1162	109/8105	0.005237772	0.07785234	0.067163776	HK1/LDHA/ALDOA/MKNK1/ARNT/PIK3R3/EIF4E/TFRC/PIK3CB/NFKB1/IGF1/IGF1R/STAT3/VHL/TLR4/ENO4/PRKCA/MAPK1/PFKP/PIK3CA/HKDC1/MAP2K1/TF/PFKFB3/CYBB/NOS3	26
hsa045	Focal adhesion	42/1162	201/81	0.00663	0.09426	0.08132	MAPK9/CDC42/LAMB4/COL6A3/PIK3	42

10			05	0411	7144	4946	R3/FLT4/PIK3CB/IGF1/ARHGAP5/IGF1R/FLNC/RHOA/ACTG1/VWF/BIRC3/ITGA2B/LAMB2/LAMA2/RAPGEF1/CHAD/CCND2/PDPK1/PRKCA/HGF/ITGB3/PDGfra/MAPK1/ITGA8/BIRC2/PIK3CA/PPP1CB/PARVA/MAPK10/COL4A1/MAP2K1/COL4A3/ITGA5/SHC4/MYLK/COL6A5/ROCK1/LAMA3	
hsa04924	Renin secretion	18/1162	69/8105	0.0071471	0.09737924	0.084009774	KCNMA1/CACNA1C/ADCY5/ITPR1/CREB1/PDE1A/CACNA1D/ACE/GNAS/ADRB1/PPP3R1/CLCA2/ADRB2/PRKACG/EDNRA/ADCY6/REN/PTGER2	18
hsa04917	Prolactin signaling pathway	18/1162	70/8105	0.008366639	0.105987281	0.091435994	MAPK9/PIK3R3/SOCS2/FOXO3/PIK3CB/NFKB1/STAT3/KRAS/SOCS7/CCND2/ESR2/STAT1/MAPK1/MAPK13/PIK3CA/MAPK10/MAP2K1/SHC4	18
hsa04611	Platelet activation	28/1162	124/8105	0.008532065	0.105987281	0.091435994	PIK3R3/ADCY5/PIK3CB/ITPR1/PRKG1/RHOA/ACTG1/VWF/ITGA2B/BTK/SYK/ARHGEF1/GNAS/ADCY1/ITGB3/MAPK1/PLA2G4D/MAPK13/ARHGEF12/F2/ADCY7/PIK3CA/PPP1CB/PRKACG/ADCY6/NOS3/MYLK/ROCK1	28

hsa052 15	Prostate cancer	23/1162	97/810 5	0.00897 2632	0.10598 7281	0.09143 5994	AR/PIK3R3/ZEB1/PIK3CB/IL1R2/NFKB1/IGF1/IGF1R/CREB1/PLAU/FGFR2/KRAS/ARAF/PDPK1/E2F3/PDGFR/MAPK1/E2F1/FGFR1/PIK3CA/NKX3-1/MAP2K1/MMP9	23
hsa049 35	Growth hormone synthesis, secretion and action	27/1162	119/810 05	0.00907 5364	0.10598 7281	0.09143 5994	CACNA1C/MAPK9/ATF2/PIK3R3/SOC2/ADCY5/PIK3CB/ITPR1/IGF1/CREB1/STAT3/CACNA1D/KRAS/GNAS/PRKCA/ADCY1/STAT1/MAPK1/MAPK13/ADCY7/PIK3CA/PRKACG/MAPK10/MAP2K1/IRS1/ADCY6/SHC4	27
hsa047 24	Glutamatergic synapse	26/1162	114/810 05	0.00964 5998	0.10876 6941	0.09383 4026	CACNA1C/DLGAP1/ADCY5/GLUL/ITPR1/DLG4/GRIA4/SLC1A7/CACNA1D/TRPC1/GRIK4/GNAS/PRKCA/ADCY1/GNG12/SLC1A1/MAPK1/PLA2G4D/PPP3R1/ADCY7/GRM1/GRIN2B/PRKACG/ADCY6/GRM8/GRIK1	26
hsa041 20	Ubiquitin mediated proteolysis	30/1162	140/810 05	0.01401 4487	0.15275 7909	0.13178 5352	UBOX5/UBE2D3/SIAH1/PIAS1/PPIL2/CUL4B/WWP2/VHL/FANCL/CBLB/BIRC3/UBA1/ANAPC1/UBE2I/UBA52/CUL4A/COP1/UBE2G1/FBXO4/PIAS2/UBB/UBE2J1/BIRC2/BIRC6/ANAPC2/C	30

							UL3/RHOBTB1/UBE2R2/SMURF1/CUL7	
hsa04071	Sphingolipid signaling pathway	26/1162	119/8105	0.016694072	0.176095531	0.151918887	MAPK9/GNA12/PIK3R3/PPP2R2B/PIK3CB/NFKB1/RHOA/KRAS/PDPK1/PRKCA/ASAH2/BDKRB2/MAPK1/ASAH1/MAPK13/PPP2R2C/PIK3CA/SPTLC1/MAPK10/PPP2R2A/MAP2K1/CTSD/PPP2R3B/NOS3/S1PR2/ROCK1	26
hsa04910	Insulin signaling pathway	29/1162	137/8105	0.018233177	0.185271452	0.15983502	HK1/MAPK9/MKNK1/ACACA/PIK3R3/SOCS2/TSC1/EIF4E/PIK3CB/GYS1/CBLB/KRAS/RAPGEF1/ARAF/FASN/PDPK1/PRKAG3/INPP5A/PRKAR2A/MAPK1/PIK3CA/PPP1CB/PRKACG/PRKAA2/HKDC1/MAPK10/MAP2K1/IRS1/SHC4	29
hsa04150	mTOR signaling pathway	32/1162	155/8105	0.019317842	0.185271452	0.15983502	PRR5/PIK3R3/CAB39/TSC1/EIF4E/EIF4B/PIK3CB/IGF1/IGF1R/RPS6KA6/ULK1/RHOA/ATP6V1H/LRP5/KRAS/AKT1S1/PDPK1/SLC7A5/PRKCA/FZD4/FZD2/MAPK1/PIK3CA/WNT10B/PRKAA2/LAMTOR3/TBC1D7/RRAGA/WDR59/MAP2K1/MIOS/IRS1	32

hsa052 12	Pancreatic cancer	18/1162	76/810 5	0.01959 8969	0.18527 1452	0.15983 502	JAK1/MAPK9/CDC42/PIK3R3/PIK3CB /NFKB1/STAT3/KRAS/ARAF/STAT1/E 2F3/MAPK1/BCL2L1/E2F1/PIK3CA/M APK10/MAP2K1/RAD51	18
hsa040 22	cGMP-PKG signaling pathway	34/1162	167/81 05	0.01983 0278	0.18527 1452	0.15983 502	KCNMA1/CACNA1C/MRVI1/MEF2A/ MEF2D/GNA12/MEF2C/ATF2/ADCY5/ ATP2B3/ITPR1/NFATC1/CREB1/PRK G1/VDAC1/RHOA/CACNA1D/ATP2B1 /ADCY1/ADRB1/BDKRB2/MAPK1/PP P3R1/NFATC2/ADCY7/ADRB2/PPP1C B/EDNRA/MAP2K1/IRS1/ADCY6/NOS 3/MYLK/ROCK1	34
hsa042 70	Vascular smooth muscle contraction	28/1162	133/81 05	0.02152 3767	0.19010 3228	0.16400 3428	KCNMA1/CACNA1C/MRVI1/GNA12/ ADCY5/ITPR1/PRKG1/RHOA/CACNA 1D/ARHGEF1/ARAF/GNAS/PRKCA/A DCY1/MAPK1/PLA2G4D/ARHGEF12/ ADCY7/PPP1CB/PRKACG/EDNRA/M AP2K1/PRKCH/RAMP3/ADCY6/CALC RL/MYLK/ROCK1	28
hsa054 18	Fluid shear stress and atherosclerosis	29/1162	139/81 05	0.02196 2979	0.19010 3228	0.16400 3428	MAP3K7/MEF2A/MAPK9/MEF2C/BM PR1B/ACVR1/NCF2/PIK3R3/SUMO3/P IK3CB/IL1R2/NFKB1/SUMO1/RHOA/	29

							ACTG1/ACVR2A/SDC4/ITGA2B/ITGB3/MAPK13/GSTO2/PIK3CA/BMP2R/P RKAA2/MAPK10/GSTT2B/PECAM1/N OS3/MMP9	
hsa052 02	Transcriptional misregulation in cancer	38/1162	192/81 05	0.02209 1507	0.19010 3228	0.16400 3428	PAX5/RUNX1/TCF3/MAX/WT1/PPAR G/MEF2C/NSD2/ASPSCR1/DDX5/ZEB 1/IL1R2/NTRK1/NFKB1/IGF1/IGF1R/P LAU/CCNT2/BIRC3/KMT2A/EWSR1/I TGAM/RXRB/CCND2/ELK4/IL3/HDA C1/SIN3A/BCL2L1/PTCRA/CDKN2C/ MYCN/BIRC2/HOXA11/MAF/CD86/JU P/MMP9	38
hsa041 42	Lysosome	27/1162	128/81 05	0.02313 1286	0.19394 6938	0.16731 9425	ARSA/ENTPD4/GGA1/AP1B1/HGSNA T/SORT1/M6PR/SLC11A2/ATP6V1H/H YAL2/AP4B1/ACP2/CTSC/LGMN/AP1 G1/ASA1/CLTA/AP4M1/CLTCL1/AG A/NPC1/TPP1/SLC11A1/ARSG/CTSD/ CTSZ/CTSF	27
hsa049 26	Relaxin signaling pathway	27/1162	129/81 05	0.02539 9149	0.20763 8044	0.17913 0841	MAPK9/ATF2/PIK3R3/ADCY5/NOS1/P IK3CB/RXFP1/NFKB1/CREB1/KRAS/ GNAS/PRKCA/ADCY1/GNG12/MAPK 1/MAPK13/ADCY7/PIK3CA/PRKACG/	27

							MAPK10/COL4A1/MAP2K1/COL4A3/ ADCY6/NOS3/SHC4/MMP9	
hsa052 19	Bladder cancer	11/1162	41/810 5	0.02606 7839	0.20790 6911	0.17936 2795	DAPK1/KRAS/ARAF/E2F3/MAPK1/E2 F1/DAPK2/RASSF1/FGFR3/MAP2K1/ MMP9	11
hsa046 64	Fc epsilon RI signaling pathway	16/1162	68/810 5	0.02838 6485	0.22022 6277	0.18999 08	MAPK9/PIK3R3/PIK3CB/KRAS/BTK/S YK/PDPK1/PRKCA/IL3/MAPK1/PLA2 G4D/MAPK13/PIK3CA/MAPK10/MAP 2K1/INPP5D	16
hsa040 72	Phospholipase D signaling pathway	30/1162	148/81 05	0.02895 9419	0.22022 6277	0.18999 08	MRAS/PTGFR/GNA12/PIK3R3/ADCY5 /TSC1/PIK3CB/RHOA/KRAS/GAB1/LP AR5/SYK/RAPGEF3/GNAS/PRKCA/A DCY1/LPAR1/PDGFR/MAPK1/PLA2 G4D/F2/ADCY7/GRM1/PIK3CA/AGPA T5/MAP2K1/PLPP1/ADCY6/GRM8/SH C4	30
hsa049 60	Aldosterone- regulated sodium reabsorption	10/1162	37/810 5	0.03152 4821	0.22857 6029	0.19719 4192	PIK3R3/PIK3CB/IGF1/SCNN1A/KRAS/ PDPK1/PRKCA/MAPK1/PIK3CA/IRS1	10
hsa054 17	Lipid and atherosclerosis	41/1162	215/81 05	0.03157 8307	0.22857 6029	0.19719 4192	MAP3K7/PPARG/MAPK9/POU2F2/CD C42/POU2F1/NCF2/PIK3R3/NLRP3/SO D2/PIK3CB/ITPR1/IKBKE/NFKB1/NF	41

							ATC1/STAT3/RHOA/FASLG/TLR4/KRAS/TLR2/ARHGEF1/RXRB/PDPK1/EIF2S1/PRKCA/ERO1A/MAPK1/BCL2L1/PPP3R1/MAPK13/NFATC2/PIK3CA/MAPK10/ABCA1/CYBB/NOS3/ATF6/SELP/MYD88/MMP9	
hsa04020	Calcium signaling pathway	45/1162	240/8105	0.032842156	0.228576029	0.197194192	CACNA1C/CACNA1E/ASPH/MCU/GDNF/PTGFR/CHRM2/CHRNA7/FLT4/NOS1/ATP2B3/P2RX4/ITPR1/NTRK1/MST1R/PDE1A/VDAC1/FGFR2/CACNA1D/ATP2B1/LTB4R2/PTAFR/GNAS/PRKCA/CHRM3/ADCY1/ADRB1/HGF/BDKRB2/PDGFR/PPP3R1/NTRK3/FGFR1/NGF/ADCY7/GRM1/ADRB2/PRKACG/FGFR3/EDNRA/FGF18/NOS3/HTR2A/CCKAR/MYLK	45
hsa04961	Endocrine and other factor-regulated calcium reabsorption	13/1162	53/8105	0.03334524	0.228576029	0.197194192	RAB11A/AP2B1/AP2A2/ATP2B3/ATP2B1/GNAS/PRKCA/BDKRB2/CLTA/CLTCL1/PRKACG/ADCY6/TRPV5	13
hsa04929	GnRH secretion	15/1162	64/8105	0.034223963	0.228576029	0.197194192	CACNA1C/PIK3R3/PIK3CB/ITPR1/CACNA1D/KRAS/TRPC1/ESR2/PRKCA/H	15

							CN3/MAPK1/KCNN4/PIK3CA/MAP2K1/TRPC5	
hsa00061	Fatty acid biosynthesis	6/1162	18/8105	0.034251454	0.228576029	0.197194192	ACSL4/ACSL1/ACACA/MCAT/FASN/ACSBG1	6
hsa04919	Thyroid hormone signaling pathway	25/1162	121/8105	0.035326726	0.231036786	0.199317105	PIK3R3/PIK3CB/MED13L/ACTG1/THRB/DIO2/KRAS/RXRB/PDPK1/PRKCA/STAT1/HDAC1/ITGB3/NOTCH2/SIN3A/MAPK1/PFKP/MED14/NOTCH1/PIK3CA/PRKACG/NCOA2/MAP2K1/NCOA1/MED12	25
hsa03460	Fanconi anemia pathway	13/1162	54/8105	0.038366428	0.245996508	0.212222965	FAN1/ATRIP/FANCD2/FANCL/FANCI/FANCA/BRIP1/EME1/CENPS/RPA2/USP1/EME2/RAD51	13
hsa04730	Long-term depression	14/1162	60/8105	0.041320429	0.259841926	0.224167507	GNA12/NOS1/ITPR1/IGF1/IGF1R/PRKG1/KRAS/ARAF/GNAS/PRKCA/MAPK1/PLA2G4D/GRM1/MAP2K1	14
hsa04114	Oocyte meiosis	26/1162	129/8105	0.042503655	0.262239534	0.226235941	AR/CPEB2/ADCY5/SPDYE1/ITPR1/IGF1/IGF1R/RPS6KA6/SPDYE5/SPDYE6/ANAPC1/ADCY1/MAPK1/PPP3R1/MAPK13/STAG3/SPDYE2/SPDYE2B/ADCY7/ANAPC2/PPP1CB/PRKACG/YWHAZ/MAP2K1/ADCY6/REC8	26

hsa052 35	PD-L1 expression and PD-1 checkpoint pathway in cancer	19/1162	89/810 5	0.04571 7155	0.26688 5134	0.23024 3734	JAK1/PIK3R3/PIK3CB/NFKB1/NFATC 1/STAT3/TLR4/KRAS/CD274/TLR2/ST AT1/MAPK1/PPP3R1/MAPK13/NFATC 2/CSNK2A3/PIK3CA/MAP2K1/MYD88	19
hsa052 23	Non-small cell lung cancer	16/1162	72/810 5	0.04595 8978	0.26688 5134	0.23024 3734	PIK3R3/FOXO3/PIK3CB/STAT3/KRAS /ARAF/RXRBP/PDPK1/PRKCA/HGF/E2 F3/MAPK1/E2F1/RASSF1/PIK3CA/MA P2K1	16
hsa042 10	Apoptosis	27/1162	136/81 05	0.04639 0286	0.26688 5134	0.23024 3734	MAPK9/PIK3R3/PIK3CB/ITPR1/NTRK 1/NFKB1/MCL1/FASLG/ACTG1/BIRC 3/KRAS/CTSC/PDPK1/EIF2S1/IL3/MA PK1/BCL2L1/BIRC2/NGF/PIK3CA/MA PK10/MAP2K1/RIPK1/CTSD/PRF1/CT SZ/CTSF	27
hsa002 70	Cysteine and methionine metabolism	12/1162	50/810 5	0.04652 1262	0.26688 5134	0.23024 3734	AHCYL2/LDHA/CBSL/MRI1/BCAT2/ GOT2/CBS/GCLC/IL4I1/CTH/DNMT1/ MDH1	12
hsa051 30	Pathogenic Escherichia coli infection	37/1162	197/81 05	0.04829 7039	0.26805 5172	0.23125 3134	MAP3K7/MAPK9/MYO1B/CDC42/GN A12/MYO1C/RPS3/NLRP3/MYO10/NF KB1/RHOA/FASLG/ACTG1/TLR4/LPA R5/CASP4/ARHGEF1/TMED10/LPAR1 /MYO1H/MAPK1/MYO5B/MAPK13/A	37

							RHGEF12/CLDN7/F2/MYO6/NAIP/MA PK10/RIPK1/MYO1G/CLDN4/ARPC1B /BRK1/MYD88/MYO5C/ROCK1	
hsa047 20	Long-term potentiation	15/1162	67/810 5	0.04929 2403	0.26805 5172	0.23125 3134	CACNA1C/ITPR1/RPS6KA6/KRAS/RA PGEF3/ARAF/PRKCA/ADCY1/MAPK1 /PPP3R1/GRM1/GRIN2B/PPP1CB/PRK ACG/MAP2K1	15
hsa040 68	FoxO signaling pathway	26/1162	131/81 05	0.05006 4221	0.26805 5172	0.23125 3134	MAPK9/PIK3R3/FOXO3/SOD2/PIK3C B/IGF1/PLK4/IGF1R/STAT3/USP7/FAS LG/KRAS/ARAF/CCND2/PDPK1/PRK AG3/CDKN2D/MAPK1/RBL2/MAPK13 /GRM1/PIK3CA/PRKAA2/MAPK10/M AP2K1/IRS1	26
hsa054 14	Dilated cardiomyopathy	20/1162	96/810 5	0.05149 3109	0.26805 5172	0.23125 3134	CACNB4/CACNA1C/ADCY5/IGF1/AC TG1/ITGA2B/LAMA2/CACNA1D/GNA S/CACNG4/ADCY1/ADRB1/ITGB3/M YBPC3/ITGA8/ADCY7/PRKACG/ADC Y6/ITGA5/MYL3	20
hsa051 46	Amoebiasis	21/1162	102/81 05	0.05230 9866	0.26805 5172	0.23125 3134	LAMB4/PIK3R3/C8B/PIK3CB/IL1R2/N FKB1/TLR4/LAMB2/LAMA2/TLR2/IT GAM/GNAS/PRKCA/ADCY1/PIK3CA/ PRKACG/COL4A1/COL4A3/C9/LAMA	21

							3/SERPINB4	
hsa03018	RNA degradation	17/1162	79/8105	0.053048675	0.268055172	0.231253134	CNOT4/PNLDC1/EXOSC1/ENO4/CNOT2/DCP1A/DCP2/BTG4/CNOT6L/TOB2/NUDT16/PFKP/DIS3L/DDX6/EXOSC3/TTC37/PABPC1	17
hsa05161	Hepatitis B	31/1162	162/8105	0.053713539	0.268055172	0.231253134	MAP3K7/JAK1/MAPK9/ATF2/PIK3R3/PIK3CB/IKBKE/NFKB1/NFATC1/CREB1/STAT3/FASLG/MAVS/TLR4/KRAS/TLR2/ARAF/PRKCA/STAT1/E2F3/MAPK1/E2F1/MAPK13/NFATC2/STAT4/PIK3CA/YWHAZ/MAPK10/MAP2K1/MYD88/MMP9	31
hsa04218	Cellular senescence	30/1162	156/8105	0.053936128	0.268055172	0.231253134	MRAS/MCU/PIK3R3/HIPK2/FOXO3/TSC1/PIK3CB/HIPK1/ITPR1/NFKB1/NFATC1/VDAC1/CACNA1D/KRAS/CCND2/ETS1/E2F3/MAPK1/RBL2/E2F1/PPP3R1/MAPK13/RBL1/NFATC2/CHEK1/PIK3CA/PPP1CB/MAP2K1/FOXO1/CHEK2	30
hsa04261	Adrenergic signaling in cardiomyocytes	29/1162	150/8105	0.054102879	0.268055172	0.231253134	CACNB4/CACNA1C/SCN5A/ATF2/KCNE1/ADCY5/CREM/PPP2R2B/ATP2B3/CREB1/CACNA1D/ATP2B1/RAPGEF3	29

							/GNAS/PRKCA/CACNG4/ADCY1/ADRB1/MAPK1/MAPK13/ADCY7/PPP2R2C/ADRB2/PPP1CB/PRKACG/PPP2R2A/PPP2R3B/ADCY6/MYL3	
hsa04923	Regulation of lipolysis in adipocytes	13/1162	57/8105	0.056590552	0.269283722	0.232313013	PIK3R3/ADCY5/PIK3CB/PRKG1/GNAS/ADCY1/ADRB1/ADCY7/PIK3CA/ADRB2/PRKACG/IRS1/ADCY6	13
hsa05162	Measles	27/1162	139/8105	0.058502935	0.269283722	0.232313013	CD46/MAP3K7/ADAR/JAK1/MAPK9/PIK3R3/PIK3CB/IKBKE/NFKB1/STAT3/FASLG/MAVS/CBLB/TLR4/SLAMF1/TLR2/CCND2/EIF2S1/STAT1/BCL2L1/CSNK2A3/PIK3CA/RAB9B/IL2RA/MAPK10/MSN/MYD88	27
hsa04623	Cytosolic DNA-sensing pathway	14/1162	63/8105	0.059350371	0.269283722	0.232313013	POLR3H/ADAR/CCL4L2/IKBKE/NFKB1/MAVS/TREX1/POLR3B/POLR3K/POLR1D/RIPK1/POLR3G/AIM2/POLR3A	14
hsa04216	Ferroptosis	10/1162	41/8105	0.05985968	0.269283722	0.232313013	ACSL4/STEAP3/ACSL1/TFRC/ATG5/SLC11A2/GCLC/SLC39A8/TF/CYBB	10
hsa04742	Taste transduction	18/1162	86/8105	0.060026733	0.269283722	0.232313013	CACNA1C/SCN3A/SCN2A/SCN9A/PDE1A/SCNN1A/TAS1R1/CHRM3/TAS2R7/TAS2R38/GRM1/PRKACG/HTR1E/	18

							GABRA4/CALHM1/ADCY6/TAS2R60/HTR1D	
hsa049 11	Insulin secretion	18/1162	86/810 5	0.06002 6733	0.26928 3722	0.23231 3013	KCNMA1/CACNA1C/ATF2/ADCY5/RIMS2/CREB1/CACNA1D/GNAS/PRKCA/CHRM3/ADCY1/KCNN4/ADCY7/PRKACG/RAB3A/GPR119/ADCY6/CCKAR	18
hsa001 30	Ubiquinone and other terpenoid-quinone biosynthesis	4/1162	11/810 5	0.06021 5932	0.26928 3722	0.23231 3013	VKORC1L1/GGCX/COQ7/COQ3	4
hsa030 15	mRNA surveillance pathway	20/1162	98/810 5	0.06182 3581	0.26928 3722	0.23231 3013	GSPT1/PPP2R2B/UPF2/NCBP2/NCBP1/PYM1/PABPN1/HBS1L/WDR33/PCF1/PPP2R2C/SMG1/PPP1CB/PPP2R2A/PPP2R3B/PABPC1/SMG6/EIF4A3/PAPOLG/CSTF1	20
hsa046 25	C-type lectin receptor signaling pathway	21/1162	104/810 05	0.06240 9069	0.26928 3722	0.23231 3013	MRAS/MAPK9/PIK3R3/NLRP3/PIK3CB/ITPR1/IKBKE/NFKB1/NFATC1/RHOA/CBLB/KRAS/SYK/STAT1/MAPK1/PPP3R1/MAPK13/NFATC2/ARHGEF12/PIK3CA/MAPK10	21
hsa005	Mucin type O-	9/1162	36/810	0.06305	0.26928	0.23231	ST6GALNAC4/GALNTL6/GALNT6/G	9

12	glycan biosynthesis		5	1641	3722	3013	ALNT2/GALNT1/B4GALT5/GCNT1/G ALNT14/ST6GALNAC2	
hsa049 18	Thyroid hormone synthesis	16/1162	75/810 5	0.06340 9317	0.26928 3722	0.23231 3013	ATF2/IYD/ADCY5/ITPR1/CREB1/GNA S/PRKCA/ADCY1/ASGR2/TG/ADCY7/ DUOX1/PRKACG/GPX7/ADCY6/DUO XA2	16
hsa051 33	Pertussis	16/1162	76/810 5	0.07010 7255	0.28803 3966	0.24848 8984	MAPK9/C4BPB/NLRP3/NFKB1/RHOA /TLR4/ITGAM/MAPK1/MAPK13/SFTP A1/C5/MAPK10/ITGA5/MYD88/C4A/C 4B	16
hsa052 20	Chronic myeloid leukemia	16/1162	76/810 5	0.07010 7255	0.28803 3966	0.24848 8984	RUNX1/PIK3R3/PIK3CB/NFKB1/KRA S/ARAF/E2F3/HDAC1/MAPK1/BCL2L 1/E2F1/MECOM/CTBP1/PIK3CA/MAP 2K1/SHC4	16
hsa043 70	VEGF signaling pathway	13/1162	59/810 5	0.07155 0398	0.28803 3966	0.24848 8984	CDC42/PIK3R3/PIK3CB/KRAS/PRKC A/MAPK1/PLA2G4D/PPP3R1/MAPK13 /NFATC2/PIK3CA/MAP2K1/NOS3	13
hsa049 21	Oxytocin signaling pathway	29/1162	154/81 05	0.07168 3671	0.28803 3966	0.24848 8984	CACNB4/CACNA1C/MEF2C/ADCY5/I TPR1/NFATC1/RHOA/ACTG1/CACNA 1D/KRAS/GNAS/PRKAG3/PRKCA/CA CNG4/ADCY1/MAPK1/EEF2K/PLA2G 4D/PPP3R1/NFATC2/ADCY7/PPP1CB/	29

							PRKACG/PRKAA2/MAP2K1/ADCY6/ NOS3/MYLK/ROCK1	
hsa040 24	cAMP signaling pathway	39/1162	216/81 05	0.07222 8701	0.28803 3966	0.24848 8984	CACNA1C/PDE4D/MAPK9/CHRM2/PI K3R3/ADCY5/BDNF/ATP2B3/PIK3CB/ NFKB1/NFATC1/CREB1/GRIA4/RHO A/SUCNR1/CACNA1D/ATP2B1/ACOX 3/RAPGEF3/GNAS/ADCY1/ADRB1/M APK1/ADCY7/PIK3CA/ADRB2/GRIN2 B/PPP1CB/PRKACG/HTR1E/MAPK10/ EDNRA/MAP2K1/GPR119/GIPR/ADC Y6/PTGER2/HTR1D/ROCK1	39
hsa051 35	Yersinia infection	26/1162	137/81 05	0.07850 9591	0.30426 2501	0.26248 9459	MAP3K7/MAPK9/CDC42/PIK3R3/ARH GEF28/NLRP3/PIK3CB/NFKB1/NFAT C1/RPS6KA6/RHOA/ACTG1/TLR4/GI T2/ARHGEF1/MAPK1/MAPK13/NFAT C2/ARHGEF12/PIK3CA/MAPK10/MAP 2K1/ARPC1B/ITGA5/MYD88/ROCK1	26
hsa000 71	Fatty acid degradation	10/1162	43/810 5	0.07878 5101	0.30426 2501	0.26248 9459	ACSL4/ACSL1/CPT1C/ACADS/ECI2/A COX3/CYP2U1/ALDH9A1/ADH4/ACS BG1	10
hsa047 27	GABAergic synapse	18/1162	89/810 5	0.07908 9641	0.30426 2501	0.26248 9459	CACNA1C/SLC6A1/ADCY5/GLUL/GA BRP/CACNA1D/PRKCA/ADCY1/GNG	18

							12/GABRE/NSF/SLC6A11/GABRG2/ADCY7/PRKACG/GABRR2/GABRA4/ADCY6	
hsa052 18	Melanoma	15/1162	72/810 5	0.08368 734	0.31531 6122	0.27202 5498	PIK3R3/PIK3CB/IGF1/IGF1R/KRAS/A RAF/HGF/E2F3/PDGFR/PAK1/E2F 1/FGFR1/PIK3CA/PAK2K1/FGF18	15
hsa051 63	Human cytomegalovirus infection	40/1162	225/81 05	0.08389 1445	0.31531 6122	0.27202 5498	CCL4L2/JAK1/GNA12/ATF2/PIK3R3/A DCY5/TSC1/PIK3CB/ITPR1/AKAP13/ NFKB1/NFATC1/CREB1/STAT3/RHO A/FASLG/KRAS/ARHGEF1/GNAS/PR KCA/ADCY1/GNG12/CXCL12/E2F3/IT GB3/PDGFR/PAK1/E2F1/PPP3R1/ PAK13/NFATC2/ARHGEF12/ADCY7 /PIK3CA/PRKACG/PAK2K1/RIPK1/A DCY6/PTGER2/ROCK1	40
hsa046 70	Leukocyte transendothelial migration	22/1162	114/81 05	0.08624 3785	0.31967 3855	0.27578 4945	CDC42/NCF2/PIK3R3/PIK3CB/ARHG AP5/RHOA/ACTG1/RAPGEF3/ITGAL/ ITGAM/PRKCA/CXCL12/F11R/PAK 13/CLDN7/PIK3CA/PECAM1/CLDN4/ CYBB/MSN/ROCK1/MMP9	22
hsa051 71	Coronavirus disease - COVID-	41/1162	232/81 05	0.08700 6034	0.31967 3855	0.27578 4945	MAP3K7/ADAR/JAK1/RPL10/RPL15/ PAK9/RPS3/PIK3R3/NLRP3/C8B/PIK	41

	19						3CB/IKBKE/NFKB1/RPL32/STAT3/M AVS/VWF/TLR4/TLR2/UBA52/ACE/S YK/TLR8/ADAM17/PRKCA/RPL37/ST AT1/MAPK1/MAPK13/F2/C5/PIK3CA/ MAPK10/RPS24/MASP1/C9/CYBB/SE LP/MYD88/C4A/C4B	
hsa000 51	Fructose and mannose metabolism	8/1162	33/810 5	0.08984 3808	0.32301 143	0.27866 4295	HK1/ALDOA/GMPPB/PFKFB1/PFKP/ HKDC1/PFKFB3/AKR1B10	8
hsa052 21	Acute myeloid leukemia	14/1162	67/810 5	0.09072 0095	0.32301 143	0.27866 4295	RUNX1/PIK3R3/PIK3CB/NFKB1/STAT 3/KRAS/ARAF/ITGAM/IL3/MAPK1/PI M2/PIK3CA/MAP2K1/JUP	14
hsa041 44	Endocytosis	44/1162	252/81 05	0.09147 8164	0.32301 143	0.27866 4295	AGAP3/SMAP2/RAB11A/CDC42/AP2B 1/WASHC2C/GRK4/AP2A2/SNX1/SNX 12/TFRC/AGAP1/ZFYVE27/IGF1R/RH OA/CBLB/FGFR2/ASAP1/SNX4/GIT2/ RABEP1/IST1/ARFGAP2/WASHC2A/R BSN/SPART/PDGFR/CHMP3/CHMP1 B/CLTA/IZUMO1R/CLTCL1/RAB11FI P2/IL2RA/PSD2/CAPZA2/IQSEC2/FGF R3/CHMP4C/SMURF1/ARPC1B/GRK1/ ARAP2/CHMP6	44

hsa040 12	ErbB signaling pathway	17/1162	85/810 5	0.09352 4275	0.32301 143	0.27866 4295	MAPK9/NRG2/PIK3R3/ABL2/PIK3CB/CBLB/KRAS/GAB1/ARAF/PRKCA/MAPK1/PIK3CA/MAPK10/MAP2K1/NRG4/NRG3/SHC4	17
hsa046 10	Complement and coagulation cascades	17/1162	85/810 5	0.09352 4275	0.32301 143	0.27866 4295	CD46/C4BPB/C8B/PLAU/VWF/ITGAM/SERPINB2/BDKRB2/F2/C5/MASP1/PROCR/A2M/C9/PLAUR/C4A/C4B	17
hsa047 13	Circadian entrainment	19/1162	97/810 5	0.09384 1241	0.32301 143	0.27866 4295	CACNA1C/NOS1AP/ADCY5/NOS1/ITPR1/CREB1/GRIA4/PRKG1/CACNA1D/RASD1/GNAS/PRKCA/ADCY1/GNG12/MAPK1/ADCY7/GRIN2B/PRKACG/ADCY6	19
hsa043 80	Osteoclast differentiation	24/1162	128/810 05	0.09818 8457	0.33278 9817	0.28710 018	MAP3K7/JAK1/PPARG/MAPK9/NCF2/PIK3R3/PIK3CB/NFKB1/NFATC1/CREB1/BTK/SYK/FOSL2/STAT1/ITGB3/MAPK1/PPP3R1/MAPK13/NFATC2/FHL2/PIK3CA/MAPK10/MAP2K1/SIRPB1	24
hsa046 20	Toll-like receptor signaling pathway	20/1162	104/810 05	0.10112 8967	0.33278 9817	0.28710 018	MAP3K7/CCL4L2/MAPK9/PIK3R3/PIK3CB/IKBKE/NFKB1/TLR4/TLR2/TLR8/STAT1/MAPK1/MAPK13/PIK3CA/MAPK10/CD80/MAP2K1/CD86/RIPK1/MYD88	20

hsa04660	T cell receptor signaling pathway	20/1162	104/8105	0.101128967	0.332789817	0.28710018	MAP3K7/MAPK9/CDC42/PIK3R3/PIK3CB/NFKB1/NFATC1/RHOA/CBLB/CTLA4/KRAS/PDPK1/MAPK1/PPP3R1/MAPK13/NFATC2/PIK3CA/MAPK10/MAP2K1/CARD11	20
hsa04658	Th1 and Th2 cell differentiation	18/1162	92/8105	0.101770586	0.332789817	0.28710018	JAK1/IL12RB2/MAPK9/NFKB1/NFATC1/JAG2/STAT1/NOTCH2/MAPK1/RBPJ/PPP3R1/MAPK13/NFATC2/STAT4/NOTCH1/IL2RA/MAPK10/MAF	18
hsa05222	Small cell lung cancer	18/1162	92/8105	0.101770586	0.332789817	0.28710018	MAX/LAMB4/PIK3R3/PIK3CB/NFKB1/BIRC3/ITGA2B/LAMB2/LAMA2/RXR/B/E2F3/BCL2L1/E2F1/BIRC2/PIK3CA/COL4A1/COL4A3/LAMA3	18
hsa03450	Non-homologous end-joining	4/1162	13/8105	0.103479479	0.334867064	0.288892236	PRKDC/DNTT/LIG4/POLL	4
hsa04913	Ovarian steroidogenesis	11/1162	51/8105	0.104453946	0.334867064	0.288892236	ADCY5/IGF1/IGF1R/GNAS/ADCY1/PLA2G4D/ADCY7/PRKACG/HSD17B7/ADCY6/CYP1B1	11
hsa05031	Amphetamine addiction	14/1162	69/8105	0.10968337	0.34303968	0.295942811	CACNA1C/ATF2/ADCY5/CREB1/GRIA4/CACNA1D/GNAS/PRKCA/HDAC1/PPP3R1/GRIN2B/PPP1CB/PRKACG/SLC18A2	14

hsa052 11	Renal carcinoma	14/1162	69/810 5	0.10968 337	0.34303 968	0.29594 2811	CDC42/ARNT/PIK3R3/PIK3CB/VHL/K RAS/GAB1/RAPGEF1/ARAF/HGF/ETS 1/MAPK1/PIK3CA/MAP2K1	14
hsa049 12	GnRH signaling pathway	18/1162	93/810 5	0.11015 0356	0.34303 968	0.29594 2811	CACNA1C/MAPK9/CDC42/ADCY5/IT PR1/CACNA1D/KRAS/GNAS/PRKCA/ ADCY1/MAPK1/PLA2G4D/MAPK13/A DCY7/PRKACG/MAPK10/MAP2K1/A DCY6	18
hsa040 14	Ras signaling pathway	40/1162	232/81 05	0.11927 5187	0.36211 7316	0.31240 1225	MRAS/MAPK9/CDC42/PIK3R3/BDNF/ FLT4/ABL2/PIK3CB/NTRK1/NFKB1/I GF1/IGF1R/KSR2/EFNA5/RHOA/FASL G/SYNGAP1/FGFR2/KRAS/GAB1/PRK CA/HGF/GNG12/ETS1/PDGFR/MA PK1/BCL2L1/PLA2G4D/FGFR1/RASSF1 /NGF/PIK3CA/GRIN2B/PRKACG/IGF2 /MAPK10/FGFR3/MAP2K1/FGF18/SH C4	40
hsa045 12	ECM-receptor interaction	17/1162	88/810 5	0.11959 8379	0.36211 7316	0.31240 1225	LAMB4/COL6A3/SDC4/VWF/ITGA2B/ LAMB2/LAMA2/CHAD/ITGB3/ITGA8/ COL4A1/COL4A3/FREM2/ITGA5/FRA S1/COL6A5/LAMA3	17
hsa045	Gap junction	17/1162	88/810	0.11959	0.36211	0.31240	ADCY5/ITPR1/PRKG1/KRAS/GNAS/P	17

40			5	8379	7316	1225	RKCA/ADCY1/ADRB1/LPAR1/PDGFR A/MAPK1/ADCY7/GRM1/PRKACG/M AP2K1/ADCY6/HTR2A	
hsa047 25	Cholinergic synapse	21/1162	113/81 05	0.12424 601	0.37102 0005	0.32008 1639	CACNA1C/CHRM2/CHRNA7/PIK3R3/ ADCY5/PIK3CB/ITPR1/CREB1/CACN A1D/KRAS/PRKCA/CHRM3/ADCY1/G NG12/MAPK1/ADCY7/PIK3CA/PRKA CG/MAP2K1/ADCY6/CHRNA3	21
hsa049 15	Estrogen signaling pathway	25/1162	138/81 05	0.12548 3183	0.37102 0005	0.32008 1639	ATF2/PIK3R3/ADCY5/PIK3CB/ITPR1/ CREB1/KRAS/GNAS/ESR2/ADCY1/M APK1/ADCY7/GRM1/PIK3CA/PRKAC G/NCOA2/MAP2K1/NCOA1/CTSD/AD CY6/NOS3/KRT10/KRT33B/SHC4/MM P9	25
hsa051 31	Shigellosis	42/1162	246/81 05	0.12594 257	0.37102 0005	0.32008 1639	CAST/MAP3K7/HK1/MAPK9/CDC42/ UBE2D3/PIK3R3/FOXO3/NLRP3/PIK3 CB/ITPR1/ATG5/NFKB1/VDAC1/RHO A/ATG16L1/ACTG1/TLR4/UBA52/AK T1S1/CASP4/RNF31/TIFA/MAPK1/BC L2L1/FNBP1/MAPK13/UBB/TNIP1/PF N4/NAIP/PIK3CA/HKDC1/MAPK10/A TG14/RRAGA/UBE2V1/RIPK1/ARPC1	42

							B/ITGA5/MYD88/ROCK1	
hsa047 28	Dopaminergic synapse	24/1162	132/81 05	0.12736 2102	0.37185 1852	0.32079 928	CACNA1C/SCN1A/MAPK9/ATF2/DRD 3/ADCY5/PPP2R2B/ITPR1/CREB1/GRI A4/CACNA1D/GNAS/PRKCA/GNG12/ MAPK13/PPP2R2C/GRIN2B/PPP1CB/P RKACG/MAPK10/PPP2R2A/LRTOMT/ SLC18A2/PPP2R3B	24
hsa051 65	Human papillomavirus infection	55/1162	331/81 05	0.13044 781	0.37490 1396	0.32343 0144	JAK1/CDC42/LAMB4/COL6A3/CHD4/ PIK3R3/DLG2/TSC1/PPP2R2B/PIK3CB /IKBKE/NFKB1/CREB1/PSEN1/FASLG /VWF/ATP6V1H/ITGA2B/LAMB2/LA MA2/KRAS/TUBG1/CHAD/GNAS/CC ND2/FZD4/STAT1/HDAC1/FZD2/ITGB 3/NOTCH2/MAPK1/RBL2/RBPJ/E2F1/ RBL1/AXIN2/TERT/ITGA8/PPP2R2C/ NOTCH1/PIK3CA/PRKACG/WNT10B/ COL4A1/PPP2R2A/MAP2K1/COL4A3/ PPP2R3B/ITGA5/TUBG2/PKM/COL6A 5/LAMA3/MAGI1	55
hsa053 21	Inflammatory bowel disease	13/1162	65/810 5	0.13069 9569	0.37490 1396	0.32343 0144	IL12RB2/NFKB1/NFATC1/STAT3/RO RC/TLR4/TLR2/STAT1/RORA/STAT4/ MAF/IL18RAP/NOD2	13

hsa051 42	Chagas disease	19/1162	102/81 05	0.13619 6174	0.38727 0861	0.33410 137	MAPK9/PIK3R3/PPP2R2B/PIK3CB/NF KB1/FASLG/TLR4/TLR2/ACE/GNAS/ ADCY1/BDKRB2/MAPK1/MAPK13/PP P2R2C/PIK3CA/MAPK10/PPP2R2A/M YD88	19
hsa002 80	Valine, leucine and isoleucine degradation	10/1162	48/810 5	0.14049 6775	0.39532 8897	0.34105 3096	ACADS/BCAT2/AOX1/MCCC1/DLD/A LDH9A1/MCEE/AUH/OXCT1/IL4I1	10
hsa047 21	Synaptic vesicle cycle	15/1162	78/810 5	0.14144 7954	0.39532 8897	0.34105 3096	SLC6A1/AP2B1/AP2A2/SLC1A7/ATP6 V1H/NSF/SLC1A1/CPLX3/STX1B/SLC 6A11/CLTA/CLTCL1/SLC6A4/RAB3A/ SLC18A2	15
hsa030 20	RNA polymerase	7/1162	31/810 5	0.14569 4107	0.40374 5534	0.34831 419	POLR3H/POLR2B/POLR3B/POLR3K/P OLR1D/POLR3G/POLR3A	7
hsa001 00	Steroid biosynthesis	5/1162	20/810 5	0.14786 3812	0.40631 4846	0.35053 0754	CYP51A1/MSMO1/CYP24A1/HSD17B 7/SQLE	5
hsa050 32	Morphine addiction	17/1162	91/810 5	0.14957 7992	0.40760 0029	0.35163 9491	PDE4D/GRK4/ADCY5/GABRP/PDE1A /GNAS/PRKCA/ADCY1/GNG12/GABR E/GABRG2/ADCY7/PRKACG/GABRR 2/GABRA4/ADCY6/PDE7B	17
hsa005 62	Inositol phosphate metabolism	14/1162	73/810 5	0.15411 7409	0.41603 1374	0.35891 3273	SYNJ1/PIP4K2C/PIK3CB/PLCH1/MTM R2/PIP4K2A/INPP1/INPP5A/ITPK1/PIK	14

							FYVE/PIK3CA/MTMR4/PIK3C2B/INP P5D	
hsa050 30	Cocaine addiction	10/1162	49/810 5	0.15521 6598	0.41603 1374	0.35891 3273	ATF2/ADCY5/BDNF/DLG4/NFKB1/CR EB1/GNAS/GRIN2B/PRKACG/SLC18A 2	10
hsa049 25	Aldosterone synthesis and secretion	18/1162	98/810 5	0.15813 9998	0.41951 6412	0.36191 984	CACNA1C/ATF2/ADCY5/ATP2B3/ITP R1/CREB1/KCNK9/CACNA1D/ATP2B 1/NR4A1/GNAS/PRKCA/ADCY1/ADC Y7/PRKACG/PRKD2/ADCY6/PRKD3	18
hsa051 66	Human T-cell leukemia virus 1 infection	37/1162	219/81 05	0.15908 2676	0.41951 6412	0.36191 984	TCF3/JAK1/MAPK9/ATF2/PIK3R3/AD CY5/PIK3CB/IL1R2/NFKB1/NFATC1/ CREB1/VDAC1/ANAPC1/KRAS/ITGA L/CCND2/ADCY1/ELK4/ETS1/E2F3/M APK1/BCL2L1/E2F1/PPP3R1/NFATC2/ CDKN2C/CHEK1/TERT/ADCY7/ANA PC2/PIK3CA/PRKACG/IL2RA/MAPK1 0/MAP2K1/ADCY6/CHEK2	37
hsa046 30	JAK-STAT signaling pathway	28/1162	162/81 05	0.16590 6069	0.43401 0277	0.37442 3802	JAK1/IL12RB2/PIK3R3/SOCS2/PIAS1/ PIK3CB/MCL1/STAT3/CRLF2/AOX1/S OCS7/CCND2/OSMR/STAT1/IL3/PDG FRA/IL5RA/LIF/BCL2L1/PTPN2/PIAS2 /CNTF/STAT4/PIK3CA/IL2RA/GFAP/I	28

							L19/IL9R	
hsa049 62	Vasopressin- regulated water reabsorption	9/1162	44/810 5	0.17011 7204	0.44023 367	0.37979 2769	DYNC1I2/RAB11A/CREB1/GNAS/NSF /PRKACG/DYNC1LI1/ADCY6/DYNC1 LI2	9
hsa049 70	Salivary secretion	17/1162	93/810 5	0.17165 7597	0.44023 367	0.37979 2769	KCNMA1/ADCY5/NOS1/ATP2B3/ITP R1/PRKG1/ATP2B1/GNAS/PRKCA/CH RM3/ADCY1/ADRB1/KCNN4/ADCY7/ ADRB2/PRKACG/ADCY6	17
hsa046 68	TNF signaling pathway	20/1162	112/81 05	0.17367 0163	0.44023 367	0.37979 2769	MAP3K7/MAPK9/ATF2/PIK3R3/PIK3C B/NFKB1/RPS6KA4/CREB1/BIRC3/PG AM5/MAPK1/LIF/MAPK13/BIRC2/PIK 3CA/MAPK10/MAP2K1/RIPK1/NOD2/ MMP9	20
hsa051 45	Toxoplasmosis	20/1162	112/81 05	0.17367 0163	0.44023 367	0.37979 2769	MAP3K7/JAK1/MAPK9/LAMB4/NFKB 1/STAT3/TLR4/BIRC3/LAMB2/LAMA 2/TLR2/PDPK1/STAT1/MAPK1/BCL2L 1/MAPK13/BIRC2/MAPK10/MYD88/L AMA3	20
hsa051 60	Hepatitis C	27/1162	157/81 05	0.17809 1443	0.44454 5063	0.38351 2239	JAK1/NR1H3/PSME3/PIK3R3/PPP2R2 B/PIAS1/PIK3CB/IKBKE/NFKB1/STA T3/FASLG/MAVS/KRAS/ARAF/EIF2S 1/STAT1/E2F3/MAPK1/E2F1/CLDN7/P	27

							PP2R2C/PIK3CA/YWHAZ/PPP2R2A/MAP2K1/RIPK1/CLDN4	
hsa052 14	Glioma	14/1162	75/810 5	0.17943 4548	0.44454 5063	0.38351 2239	PIK3R3/PIK3CB/IGF1/IGF1R/KRAS/ARAF/PRKCA/E2F3/PDGFR/ALPHA/PAK1/PIK3CA/PAK2/SHC4	14
hsa049 33	AGE-RAGE signaling pathway in diabetic complications	18/1162	100/8105	0.18007 5968	0.44454 5063	0.38351 2239	MAPK9/CDC42/PIK3R3/PIK3CB/NFkB1/NFATC1/STAT3/KRAS/PRKCA/STAT1/PAK1/PAK13/PIK3CA/PAK10/COL4A1/COL4A3/CYBB/NOS3	18
hsa046 13	Neutrophil extracellular trap formation	32/1162	190/8105	0.18467 3098	0.44454 5063	0.38351 2239	MAP3K7/CLCN3/HDAC7/NCF2/PIK3R3/PIK3CB/NFkB1/VDAC1/ACTG1/VWF/TLR4/HDAC10/ITGA2B/TLR2/SYK/TLR8/CASP4/ITGAL/ITGAM/PRKCA/HDAC1/ITGB3/PAK1/HDAC4/PAK13/C5/AQP9/PIK3CA/HMGB1/PAK2K1/CYBB/SELP	32
hsa012 12	Fatty acid metabolism	11/1162	57/8105	0.18556 2937	0.44454 5063	0.38351 2239	ACSL4/ACSL1/CPT1C/ACACA/SCP2/ACADS/ACOX3/HACD3/MCAT/FASN/ACSBG1	11
hsa005 13	Various types of N-glycan biosynthesis	8/1162	39/8105	0.18696 1553	0.44454 5063	0.38351 2239	ALG9/MAN2A1/ALG1/ALG3/RPN1/MAN2A2/MGAT2/TUSC3	8
hsa007	Thiamine	4/1162	16/810	0.18722	0.44454	0.38351	AK5/AK4/TPK1/ALPI	4

30	metabolism		5	7882	5063	2239		
hsa02010	ABC transporters	9/1162	45/8105	0.187391223	0.444545063	0.383512239	ABCC5/ABCG2/ABCB6/ABCC6/ABCB10/ABCA6/ABCA1/ABCB1/ABCB11	9
hsa05132	Salmonella infection	41/1162	249/8105	0.187606173	0.444545063	0.383512239	DYNC1I2/MAP3K7/MAPK9/CDC42/RPS3/NLRP3/PIK3CB/NFKB1/FLNC/RHOA/ACTG1/M6PR/TLR4/BIRC3/FBXO22/TLR2/CASP4/CASP5/KLC4/ACBD3/VPS41/MAPK1/ARL8B/MAPK13/PFN4/MYO6/BIRC2/NAIP/VPS39/PIK3CA/RAB9B/MAPK10/DYNC1LI1/MAP2K1/RIPK1/PLEKHM2/ARPC1B/PIK3C2B/DYNC1LI2/BRK1/MYD88	41
hsa04972	Pancreatic secretion	18/1162	102/8105	0.203466936	0.46895916	0.404574456	KCNMA1/RAB11A/ADCY5/ATP2B3/ITPR1/RHOA/ATP2B1/TRPC1/GNAS/PKCACA/CHRM3/ADCY1/PRSS1/CLCA2/ADCY7/ADCY6/CPA1/CCKAR	18
hsa05224	Breast cancer	25/1162	147/8105	0.20525565	0.46895916	0.404574456	PIK3R3/FLT4/PIK3CB/IGF1/IGF1R/JAG2/LRP5/KRAS/ARAF/ESR2/FZD4/E2F3/FZD2/NOTCH2/MAPK1/E2F1/AXIN2/FGFR1/NOTCH1/PIK3CA/WNT10B/MAP2K1/FGF18/NCOA1/SHC4	25
hsa000	Pentose and	7/1162	34/810	0.20617	0.46895	0.40457	UGP2/UGT1A6/UGDH/CRYL1/DHHDH/	7

40	glucuronate interconversions		5	5259	916	4456	UGT1A1/AKR1B10	
hsa006 40	Propanoate metabolism	7/1162	34/810 5	0.20617 5259	0.46895 916	0.40457 4456	LDHA/ACACA/ACADS/ACOX3/DLD/MCEE/SUCLG1	7
hsa050 33	Nicotine addiction	8/1162	40/810 5	0.20638 4875	0.46895 916	0.40457 4456	CHRNA7/GABRP/GRIA4/GABRE/GABRG2/GRIN2B/GABRR2/GABRA4	8
hsa047 26	Serotonergic synapse	20/1162	115/810 05	0.20651 4125	0.46895 916	0.40457 4456	CACNA1C/ADCY5/ITPR1/CACNA1D/KRAS/TRPC1/RAPGEF3/ARAF/GNAS/PRKCA/GNG12/MAPK1/PLA2G4D/PRKACG/HTR1E/SLC6A4/MAP2K1/SLC18A2/HTR2A/HTR1D	20
hsa049 76	Bile secretion	16/1162	90/810 5	0.21203 3023	0.47489 5881	0.40969 6109	NR1H4/ADCY5/SLC22A7/ABCG2/UGT1A6/GNAS/ADCY1/CYP7A1/ADCY7/UGT1A1/AQP9/PRKACG/SLC10A2/ABCB1/ADCY6/ABCB11	16
hsa054 10	Hypertrophic cardiomyopathy	16/1162	90/810 5	0.21203 3023	0.47489 5881	0.40969 6109	CACNB4/CACNA1C/IGF1/ACTG1/ITGA2B/LAMA2/CACNA1D/ACE/PRKAG3/CACNG4/ITGB3/MYBPC3/ITGA8/PRKAA2/ITGA5/MYL3	16
hsa049 27	Cortisol synthesis and secretion	12/1162	65/810 5	0.21410 294	0.47626 9805	0.41088 1402	CACNA1C/ATF2/ADCY5/ITPR1/CREB1/CACNA1D/NR4A1/GNAS/ADCY1/ADCY7/PRKACG/ADCY6	12

hsa043 30	Notch signaling pathway	11/1162	59/810 5	0.21767 6541	0.47784 7233	0.41224 2261	NCOR2/PSEN1/JAG2/ADAM17/HDAC1/NOTCH2/RBPJ/PTCRA/CTBP1/NOTCH1/DTX4	11
hsa040 70	Phosphatidylinositol signaling system	17/1162	97/810 5	0.22045 0088	0.47784 7233	0.41224 2261	SYNJ1/PIP4K2C/PIK3R3/PIK3CB/ITPR1/MTMR2/PIP4K2A/PIP4P1/INPP1/PRKCA/INPP5A/ITPK1/PIKFYVE/PIK3CA/MTMR4/PIK3C2B/INPP5D	17
hsa052 25	Hepatocellular carcinoma	28/1162	168/810 05	0.22052 7931	0.47784 7233	0.41224 2261	PIK3R3/PIK3CB/IGF1R/ACTG1/LRP5/PBRM1/KRAS/GAB1/ARAF/PRKCA/HGF/FZD4/E2F3/FZD2/MAPK1/BCL2L1/E2F1/AXIN2/GSTO2/TERT/PIK3CA/IGF2/WNT10B/GSTT2B/ARID2/MAP2K1/DPF3/SHC4	28
hsa049 34	Cushing syndrome	26/1162	155/810 05	0.22065 7285	0.47784 7233	0.41224 2261	CACNA1C/ATF2/ARNT/ADCY5/ARMC5/ITPR1/CREB1/KMT2A/CACNA1D/RASD1/NR4A1/GNAS/ADCY1/FZD4/E2F3/FZD2/MAPK1/E2F1/CDKN2C/AXIN2/ADCY7/PRKACG/WNT10B/MAP2K1/WDR5B/ADCY6	26
hsa005 14	Other types of O-glycan biosynthesis	9/1162	47/810 5	0.22407 055	0.47889 5882	0.41314 6938	GXYLT1/POMT1/GALNTL6/POFUT1/EOGT/GALNT6/GALNT2/GALNT1/GALNT14	9

hsa006 20	Pyruvate metabolism	9/1162	47/810 5	0.22407 055	0.47889 5882	0.41314 6938	LDHA/ACACA/ME2/DLD/ALDH9A1/ ADH4/ACYP2/PKM/MDH1	9
hsa045 14	Cell adhesion molecules	25/1162	149/810 05	0.22579 6996	0.47945 2063	0.41362 676	NRXN1/NTNG1/L1CAM/NRXN3/SDC 4/CTLA4/CD274/ITGAL/ITGAM/CNT N2/CADM1/F11R/NECTIN3/TIGIT/CL DN7/ITGA8/NLGN4Y/SPN/CD80/CD86 /PECAM1/CLDN4/LRRC4/SELP/NRXN 2	25
hsa012 40	Biosynthesis of cofactors	26/1162	156/810 05	0.23093 2601	0.48719 3294	0.42030 5175	CTPS2/PANK2/FECH/VKORC1L1/AK5 /GGCX/UGP2/BCAT2/GMPPB/UGT1A 6/UGDH/AK4/AK9/TPK1/DLD/COQ7/ GCLC/UGT1A1/UROS/MTHFD2/UMP S/COQ3/COX10/PKM/ALPI/PANK1	26
hsa052 31	Choline metabolism in cancer	17/1162	98/810 5	0.23352 7514	0.48950 9596	0.42230 3466	MAPK9/SLC44A3/SLC22A5/PIK3R3/T SC1/PIK3CB/KRAS/PDPK1/PRKCA/P DGFR/AMAPK1/PLA2G4D/PIK3CA/M APK10/CHPT1/MAP2K1/PLPP1	17
hsa041 15	p53 signaling pathway	13/1162	73/810 5	0.24088 3691	0.50171 3166	0.43283 1574	STEAP3/SHISA5/SIAH1/IGF1/SESN1/ COP1/CCND2/BCL2L1/CHEK1/PPM1D /ZMAT3/SESN3/CHEK2	13
hsa006 00	Sphingolipid metabolism	9/1162	49/810 5	0.26318 8353	0.54469 9945	0.46991 6579	ARSA/ACER3/UGCG/ASAH2/ASAH1/ SPTLC1/KDSR/PLPP1/UGT8	9

hsa049 22	Glucagon signaling pathway	18/1162	107/81 05	0.26757 5812	0.55029 7425	0.47474 5566	LDHA/CPT1C/ATF2/ACACA/ITPR1/C REB1/GYS1/PFKFB1/GNAS/PRKAG3/ PPP3R1/PFKP/PRKACG/PRKAA2/PPP 4R3A/PPP4R3C/PKM/PPP4R3B	18
hsa002 50	Alanine, aspartate and glutamate metabolism	7/1162	37/810 5	0.27433 0895	0.55511 1463	0.47889 8671	ASNS/GLUL/FOLH1/GOT2/ALDH4A1/ RIMKLA/IL4I1	7
hsa043 40	Hedgehog signaling pathway	10/1162	56/810 5	0.27644 4647	0.55511 1463	0.47889 8671	CDON/CCND2/CSNK1G1/HHATL/CU L3/PRKACG/EVC2/IHH/SMURF1/CSN K1G2	10
hsa000 52	Galactose metabolism	6/1162	31/810 5	0.27940 3199	0.55511 1463	0.47889 8671	HK1/UGP2/PFKP/MGAM2/HKDC1/AK R1B10	6
hsa049 20	Adipocytokine signaling pathway	12/1162	69/810 5	0.28018 3513	0.55511 1463	0.47889 8671	ACSL4/MAPK9/ACSL1/CPT1C/NFKB1 /STAT3/RXR/PRKAG3/ACSBG1/PRK AA2/MAPK10/IRS1	12
hsa049 31	Insulin resistance	18/1162	108/81 05	0.28122 82	0.55511 1463	0.47889 8671	MAPK9/NR1H3/PPARGC1B/PIK3R3/PI K3CB/NFKB1/CREB1/RPS6KA6/GYS1 /STAT3/PDPK1/PRKAG3/PIK3CA/PPP 1CB/PRKAA2/MAPK10/IRS1/NOS3	18
hsa046 62	B cell receptor signaling pathway	14/1162	82/810 5	0.28172 6487	0.55511 1463	0.47889 8671	PIK3R3/PIK3CB/NFKB1/NFATC1/KR AS/BTK/SYK/MAPK1/PPP3R1/NFATC 2/PIK3CA/MAP2K1/INPP5D/CARD11	14

hsa005 10	N-Glycan biosynthesis	9/1162	50/810 5	0.28349 7291	0.55511 1463	0.47889 8671	ALG9/MAN2A1/ALG1/ALG3/RPN1/M AN2A2/MGAT2/TUSC3/ALG6	9
hsa051 44	Malaria	9/1162	50/810 5	0.28349 7291	0.55511 1463	0.47889 8671	TLR4/TLR2/ITGAL/HGF/GYP A/GYPC/ PECAM1/SELP/MYD88	9
hsa047 23	Retrograde endocannabinoid signaling	24/1162	148/81 05	0.28803 9461	0.56064 8237	0.48367 5285	CACNA1C/MAPK9/NDUFS1/ADCY5/I TPR1/GABRP/GRIA4/NDUFB4/NDUF A5/CACNA1D/PRKCA/ADCY1/GNG1 2/GABRE/MAPK1/MAPK13/GABRG2/ ADCY7/GRM1/PRKACG/GABRR2/MA PK10/GABRA4/ADCY6	24
hsa052 26	Gastric cancer	24/1162	149/81 05	0.29999 0014	0.58045 4051	0.50076 1905	PIK3R3/PIK3CB/FGFR2/REG4/LRP5/K RAS/GAB1/ARAF/RXRB/HGF/FZD4/E 2F3/FZD2/MAPK1/E2F1/AXIN2/TERT/ PIK3CA/WNT10B/MAP2K1/FGF18/AB CB1/JUP/SHC4	24
hsa041 36	Autophagy - other	6/1162	32/810 5	0.30584 1324	0.58178 0315	0.50190 6083	ATG13/ATG5/ATG16L1/ATG9B/ATG2 B/ATG2A	6
hsa042 15	Apoptosis - multiple species	6/1162	32/810 5	0.30584 1324	0.58178 0315	0.50190 6083	MAPK9/BIRC3/BCL2L1/BIRC2/BIRC6/ MAPK10	6
hsa054 12	Arrhythmogenic right ventricular cardiomyopathy	13/1162	77/810 5	0.30629 3701	0.58178 0315	0.50190 6083	CACNB4/CACNA1C/ACTG1/DSP/PKP 2/ITGA2B/LAMA2/CACNA1D/CACNG 4/ITGB3/ITGA8/ITGA5/JUP	13

hsa05017	Spinocerebellar ataxia	23/1162	143/8105	0.307792032	0.581780315	0.501906083	ATG13/MCU/MAPK9/TWINK/PIK3R3/PIK3CB/ITPR1/PUM2/ULK1/VDAC1/GF14/PRKCA/ATXN2L/RBPJ/RORA/OMA1/GRM1/PIK3CA/GRIN2B/MAPK10/ATG14/ATG2B/ATG2A	23
hsa05213	Endometrial cancer	10/1162	58/8105	0.315456489	0.588136822	0.507389886	PIK3R3/FOXO3/PIK3CB/KRAS/ARAF/PDPK1/MAPK1/AXIN2/PIK3CA/MAP2K1	10
hsa04390	Hippo signaling pathway	25/1162	157/8105	0.316153479	0.588136822	0.507389886	BMPR1B/DLG2/PPP2R2B/DLG4/LATS2/ACTG1/BIRC3/MOB1B/ID1/CCND2/FZD4/FZD2/BMP7/TP53BP2/AXIN2/CRB1/BIRC2/RASSF1/PPP2R2C/BMPR2/PPP1CB/WNT10B/YWHAZ/PPP2R2A/AFP	25
hsa04064	NF-kappa B signaling pathway	17/1162	104/8105	0.317923989	0.588136822	0.507389886	MAP3K7/CCL4L2/EDA/NFKB1/PLAU/TLR4/BIRC3/UBE2I/BTK/SYK/CXCL12/BCL2L1/CSNK2A3/BIRC2/RIPK1/CARD11/MYD88	17
hsa00532	Glycosaminoglycan biosynthesis - chondroitin sulfate / dermatan sulfate	4/1162	20/8105	0.320147872	0.588136822	0.507389886	DSE/CHST11/CHST15/CHST7	4

hsa006 70	One carbon pool by folate	4/1162	20/810 5	0.32014 7872	0.58813 6822	0.50738 9886	GART/ST20-MTHFS/MTHFS/MTHFD2	4
hsa042 17	Necroptosis	25/1162	159/81 05	0.34035 4828	0.62176 5523	0.53640 161	JAK1/MAPK9/NLRP3/GLUL/USP21/V DAC1/STAT3/FASLG/SPATA2/TLR4/ BIRC3/PGAM5/RNF31/STAT1/CHMP3 /PLA2G4D/CHMP1B/BIRC2/STAT4/M APK10/CHMP4C/HMGB1/RIPK1/CYB B/CHMP6	25
hsa043 10	Wnt signaling pathway	26/1162	166/81 05	0.34375 2829	0.62448 4306	0.53874 7124	MAP3K7/RNF43/MAPK9/PRICKLE1/S IAH1/TBL1XR1/NFATC1/PSEN1/RHO A/LRP5/INVS/CCND2/PRKCA/FZD4/F ZD2/PPP3R1/DAAM2/NFATC2/CSNK2 A3/AXIN2/CTBP1/PRKACG/WNT10B/ MAPK10/ROR2/DKK1	26
hsa015 24	Platinum drug resistance	12/1162	73/810 5	0.35155 7393	0.63194 0303	0.54517 9466	PIK3R3/PIK3CB/FASLG/BIRC3/ATP7 B/PDPK1/MAPK1/BCL2L1/GSTO2/BIR C2/PIK3CA/GSTT2B	12
hsa007 70	Pantothenate and CoA biosynthesis	4/1162	21/810 5	0.35487 9196	0.63194 0303	0.54517 9466	PANK2/BCAT2/DPYD/PANK1	4
hsa049 78	Mineral absorption	10/1162	60/810 5	0.35558 7204	0.63194 0303	0.54517 9466	TRPM6/ATP2B3/SLC11A2/ATP2B1/AT P7B/SLC26A9/SLC30A1/TF/STEAP1/C YBRD1	10

hsa054 16	Viral myocarditis	10/1162	60/810 5	0.35558 7204	0.63194 0303	0.54517 9466	CXADR/ABL2/ACTG1/LAMA2/ITGAL /EIF4G1/CD80/CD86/PRF1/EIF4G3	10
hsa006 04	Glycosphingolipid biosynthesis - ganglio series	3/1162	15/810 5	0.36675 281	0.64826 0372	0.55925 8908	ST6GALNAC4/ST6GALNAC6/B3GAL T4	3
hsa043 50	TGF-beta signaling pathway	15/1162	94/810 5	0.36919 8874	0.64907 5439	0.55996 2072	LTBP1/BMPR1B/ACVR1/RHOA/ACV R2A/ID1/INHBA/MAPK1/RBL1/BMP7/ BMPR2/LEFTY1/LEFTY2/SMURF1/R OCK1	15
hsa034 40	Homologous recombination	7/1162	41/810 5	0.37210 781	0.65069 1197	0.56135 5998	BRIP1/EME1/RPA2/SSBP1/RAD51D/T OPBP1/RAD51	7
hsa002 20	Arginine biosynthesis	4/1162	22/810 5	0.38959 4766	0.67764 6215	0.58461 0287	NOS1/GLUL/GOT2/NOS3	4
hsa043 92	Hippo signaling pathway - multiple species	5/1162	29/810 5	0.40403 8547	0.68581 7658	0.59165 985	LATS2/DCHS1/FAT4/MOB1B/RASSF1	5
hsa005 65	Ether lipid metabolism	8/1162	49/810 5	0.40496 3751	0.68581 7658	0.59165 985	PAFAH1B2/PAFAH1B1/PLA2G4D/CH PT1/PAFAH2/PLPP1/UGT8/GDPD3	8
hsa049 74	Protein digestion and absorption	16/1162	103/81 05	0.40565 8436	0.68581 7658	0.59165 985	COL12A1/COL6A3/COL11A2/SLC36A 1/SLC36A2/SLC1A1/KCNN4/PRSS1/C OL5A3/COL24A1/COL4A1/SLC1A5/C OL4A3/CPA1/SLC7A8/COL6A5	16

hsa043 71	Apelin signaling pathway	21/1162	137/81 05	0.40594 4481	0.68581 7658	0.59165 985	MRAS/MEF2A/MEF2D/MEF2C/ADCY 5/NOS1/ITPR1/KRAS/PRKAG3/ADCY 1/GNG12/MAPK1/HDAC4/ADCY7/PR KACG/PRKAA2/MAP2K1/ADCY6/NO S3/MYL3/MYLK	21
hsa033 20	PPAR signaling pathway	12/1162	76/810 5	0.40692 856	0.68581 7658	0.59165 985	ACSL4/PPARG/NR1H3/ACSL1/CPT1C/ SCP2/ACOX3/RXRB/PDPK1/CYP7A1/ GK2/ACSBG1	12
hsa049 71	Gastric acid secretion	12/1162	76/810 5	0.40692 856	0.68581 7658	0.59165 985	SLC26A7/ADCY5/ITPR1/ACTG1/GNA S/PRKCA/CHRM3/ADCY1/ADCY7/PR KACG/ADCY6/MYLK	12
hsa003 50	Tyrosine metabolism	6/1162	36/810 5	0.41424 9642	0.68581 7658	0.59165 985	AOX1/GOT2/FAHD1/ADH4/LRTOMT/ IL4I1	6
hsa003 10	Lysine degradation	10/1162	63/810 5	0.41685 1395	0.68581 7658	0.59165 985	NSD2/KMT2A/SMYD1/DLD/ALDH9A 1/KMT2E/MECOM/BBOX1/ASH1L/T MLHE	10
hsa050 22	Pathways of neurodegeneration - multiple diseases	70/1162	475/81 05	0.41974 7377	0.68581 7658	0.59165 985	CACNA1C/OPTN/ATG13/MCU/MAPK 9/MFN2/CHRNA7/VAPB/NDUFS1/BD NF/NOS1/ITPR1/DLG4/NFKB1/PSEN1/ ULK1/GRIA4/VDAC1/FASLG/NDUFB 4/NDUFA5/LRP5/UBA1/CACNA1D/K RAS/UBA52/ARAF/HTT/DNAH1/KLC	70

							4/COX4I1/EIF2S1/PRKCA/CHRM3/UBE2G1/HIP1/FZD4/FZD2/GPR37/MAPK1/ATXN2L/WDR41/BCL2L1/PPP3R1/MAPK13/CSNK2A3/UBB/COX6B1/AXIN2/DNAH5/UBE2J1/DNAH9/GRM1/GRIN2B/WNT10B/GPX7/UQCRB/MAPK10/ATP5MC3/ATG14/NEFL/MAP2K1/DNAH11/CYBB/LRRK2/DKK1/ATG2B/DNAH6/ATF6/ATG2A	
hsa04622	RIG-I-like receptor signaling pathway	11/1162	70/8105	0.421484091	0.685817658	0.59165985	MAP3K7/MAPK9/OTUD5/ATG5/IKBKE/NFKB1/MAVS/MAPK13/RNF125/MAPK10/RIPK1	11
hsa03060	Protein export	4/1162	23/8105	0.424032977	0.685817658	0.59165985	SEC61A1/OXA1L/SRP54/SRP68	4
hsa04614	Renin-angiotensin system	4/1162	23/8105	0.424032977	0.685817658	0.59165985	ACE/LNPEP/REN/ENPEP	4
hsa05100	Bacterial invasion of epithelial cells	12/1162	77/8105	0.425507303	0.685817658	0.59165985	CDC42/PIK3R3/PIK3CB/RHOA/ACTG1/GAB1/CLTA/CLTCL1/PIK3CA/ARPC1B/ITGA5/SHC4	12
hsa05140	Leishmaniasis	12/1162	77/8105	0.425507303	0.685817658	0.59165985	MAP3K7/JAK1/NCF2/NFKB1/TLR4/TLR2/ITGAM/STAT1/MAPK1/MAPK13/CYBB/MYD88	12

hsa049 79	Cholesterol metabolism	8/1162	50/810 5	0.42810 0219	0.68581 7658	0.59165 985	STARD3/VAPB/VDAC1/SORT1/CYP7 A1/NPC1/ABCA1/ABCB11	8
hsa009 20	Sulfur metabolism	2/1162	10/810 5	0.43115 8493	0.68581 7658	0.59165 985	BPNT1/SELENBP1	2
hsa000 30	Pentose phosphate pathway	5/1162	30/810 5	0.43414 1453	0.68581 7658	0.59165 985	ALDOA/PFKP/DERA/PGLS/GLYCTK	5
hsa004 10	beta-Alanine metabolism	5/1162	30/810 5	0.43414 1453	0.68581 7658	0.59165 985	ACADS/ACOX3/CARNS1/ALDH9A1/ DPYD	5
hsa006 30	Glyoxylate and dicarboxylate metabolism	5/1162	30/810 5	0.43414 1453	0.68581 7658	0.59165 985	GLUL/DLD/MCEE/GLYCTK/MDH1	5
hsa052 16	Thyroid cancer	6/1162	37/810 5	0.44133 069	0.69382 2768	0.59856 5916	PPARG/NTRK1/KRAS/RXRB/MAPK1/ MAP2K1	6
hsa001 20	Primary bile acid biosynthesis	3/1162	17/810 5	0.44874 4914	0.70210 3286	0.60570 9579	SCP2/CYP7A1/HSD3B7	3
hsa049 77	Vitamin digestion and absorption	4/1162	24/810 5	0.45796 2412	0.71311 2899	0.61520 7652	SLC19A2/MMACHC/FOLH1/AWAT2	4
hsa015 23	Antifolate resistance	5/1162	31/810 5	0.46389 881	0.71554 2032	0.61730 3282	NFKB1/ABCC5/ABCG2/GART/IZUMO 1R	5
hsa047 10	Circadian rhythm	5/1162	31/810 5	0.46389 881	0.71554 2032	0.61730 3282	CREB1/RORC/PRKAG3/RORA/PRKA A2	5
hsa046	Th17 cell	16/1162	107/81	0.46947	0.72074	0.62178	RUNX1/JAK1/MAPK9/NFKB1/NFATC	16

59	differentiation		05	3815	1491	8893	1/STAT3/RORC/RXRB/STAT1/MAPK1/RORA/PPP3R1/MAPK13/NFATC2/IL2RA/MAPK10	
hsa04062	Chemokine signaling pathway	28/1162	192/8105	0.49275683	0.752950857	0.649576146	CCL4L2/CDC42/GRK4/PIK3R3/ADCY5/FOXO3/PIK3CB/NFKB1/CCR9/STAT3/RHOA/KRAS/CX3CR1/ADCY1/GNG12/CXCL12/STAT1/MAPK1/CXCL14/ADCY7/PIK3CA/PRKACG/CXCR6/MAP2K1/ADCY6/GRK1/SHC4/ROCK1	28
hsa00010	Glycolysis / Gluconeogenesis	10/1162	67/8105	0.498180084	0.75769715	0.653670807	HK1/LDHA/ALDOA/ENO4/DLD/ALDH9A1/PFKP/ADH4/HKDC1/PKM	10
hsa04110	Cell cycle	18/1162	124/8105	0.51665244	0.775623018	0.669135583	TFDP2/PRKDC/ANAPC1/CDC14B/ORC4/ORC1/CCND2/E2F3/HDAC1/CDKN2D/RBL2/E2F1/RBL1/CDKN2C/CHEK1/ANAPC2/YWHAZ/CHEK2	18
hsa04080	Neuroactive ligand-receptor interaction	49/1162	341/8105	0.517604656	0.775623018	0.669135583	PTGFR/CHRM2/CHRNA7/DRD3/P2RX4/RXFP1/GABRP/GRIA4/PTGDR/CHRNA2/THRB/HCRT2/GRIK4/LTB4R2/PTAFR/NPY5R/P2RY13/CHRM3/ADRB1/LPAR1/GABRE/BDKRB2/PTH2R/GABRG2/F2/C5/PRSS1/GRM1/TAAR9/ADRB2/GRIN2B/HTR1E/GABRR2/GAB	49

							RA4/EDNRA/P2RY6/GIPR/CALCRL/H TR2A/GRM8/GLP2R/LTB4R/PTGER2/ CHRNA3/S1PR2/GRIK1/CCKAR/HTR1 D/HRH4	
hsa012 30	Biosynthesis of amino acids	11/1162	75/810 5	0.51777 0019	0.77562 3018	0.66913 5583	ASNS/ALDOA/GLUL/CBSL/BCAT2/E NO4/GOT2/CBS/PFKP/CTH/PKM	11
hsa049 73	Carbohydrate digestion and absorption	7/1162	47/810 5	0.51973 7234	0.77562 3018	0.66913 5583	HK1/PIK3R3/PIK3CB/CACNA1D/MGA M2/PIK3CA/HKDC1	7
hsa034 10	Base excision repair	5/1162	33/810 5	0.52182 5884	0.77562 3018	0.66913 5583	MUTYH/LIG1/XRCC1/POLL/HMGB1	5
hsa005 31	Glycosaminoglyca n degradation	3/1162	19/810 5	0.52608 604	0.77841 6901	0.67154 5886	HGSNAT/HYAL2/HPSE2	3
hsa046 66	Fc gamma R- mediated phagocytosis	14/1162	97/810 5	0.53372 1752	0.78615 7715	0.67822 3942	CDC42/PIK3R3/PIK3CB/MYO10/ASAP 1/SYK/PRKCA/MAPK1/PLA2G4D/PIK 3CA/MAP2K1/PLPP1/ARPC1B/INPP5D	14
hsa054 15	Diabetic cardiomyopathy	29/1162	203/81 05	0.53969 922	0.79139 7511	0.68274 4352	MAPK9/NDUFS1/NCF2/PIK3R3/PIK3C B/NFKB1/GYS1/VDAC1/NDUFB4/ND UFA5/ACE/COX4I1/PRKCA/MAPK13/ PDK4/COX6B1/PIK3CA/PPP1CB/PDK 3/UQCRB/MAPK10/ATP5MC3/MPC1/I RS1/CTSD/CYBB/REN/NOS3/MMP9	29

hsa005 20	Amino sugar and nucleotide sugar metabolism	7/1162	48/810 5	0.54328 4634	0.79309 855	0.68421 1851	HK1/UXS1/UGP2/GMPPB/UGDH/CYB 5RL/HKDC1	7
hsa047 14	Thermogenesis	33/1162	232/81 05	0.54921 2299	0.79818 8541	0.68860 3023	ACSL4/PPARG/ACSL1/CPT1C/NDUFS 1/ATF2/SLC25A29/ADCY5/TSC1/CRE B1/RPS6KA6/PRKG1/ACTG1/NDUFB4 /NDUFA5/KRAS/AKT1S1/KDM3A/GN AS/PRKAG3/COX4I1/ADCY1/MAPK1 3/COX6B1/FGFR1/ADCY7/PRKACG/P RCAA2/UQCRB/ATP5MC3/DPF3/ADC Y6/COX10	33
hsa051 20	Epithelial cell signaling in Helicobacter pylori infection	10/1162	70/810 5	0.55716 6767	0.80616 6075	0.69548 5299	MAPK9/CDC42/NFKB1/ATP6V1H/AD AM17/F11R/MAPK13/MAPK10/IGSF5/ PTPRZ1	10
hsa045 20	Adherens junction	10/1162	71/810 5	0.57622 078	0.83006 2533	0.71610 0946	MAP3K7/CDC42/IGF1R/RHOA/ACTG 1/PTPRJ/MAPK1/NECTIN3/CSNK2A3/ FGFR1	10
hsa051 34	Legionellosis	8/1162	57/810 5	0.58383 0371	0.83216 7502	0.71791 6918	NFKB1/TLR4/TLR2/ITGAM/HBS1L/N AIP/CLK4/MYD88	8
hsa006 50	Butanoate metabolism	4/1162	28/810 5	0.58502 1712	0.83216 7502	0.71791 6918	ACADS/ACSM5/OXCT1/ACSM6	4

hsa051 67	Kaposi sarcoma-associated herpesvirus infection	27/1162	193/81 05	0.58735 9296	0.83216 7502	0.71791 6918	JAK1/MAPK9/PIK3R3/PIK3CB/ITPR1/I KBKE/NFKB1/NFATC1/CREB1/STAT 3/KRAS/UBA52/SYK/GNG12/STAT1/E 2F3/MAPK1/E2F1/PPP3R1/MAPK13/N FATC2/UBB/PIK3CA/MAPK10/ATG14 /MAP2K1/CD86	27
hsa051 10	Vibrio cholerae infection	7/1162	50/810 5	0.58884 1958	0.83216 7502	0.71791 6918	ACTG1/ATP6V1H/GNAS/PRKCA/ERO 1A/PRKACG/SEC61A1	7
hsa051 64	Influenza A	24/1162	172/81 05	0.59140 192	0.83216 7502	0.71791 6918	ADAR/JAK1/RAB11A/HNRNPUL1/PI K3R3/NLRP3/PIK3CB/IKBKE/NFKB1/ VDAC1/FASLG/MAVS/ACTG1/TLR4/ EIF2S1/PRKCA/STAT1/PABPN1/MAP K1/PRSS1/PIK3CA/MAP2K1/NUP98/M YD88	24
hsa012 00	Carbon metabolism	16/1162	115/81 05	0.59295 1156	0.83216 7502	0.71791 6918	HK1/ALDOA/ACADS/ME2/ENO4/AC OX3/GOT2/DLD/PFKP/MCEE/PGLS/H KDC1/GLYCTK/PKM/SUCLG1/MDH1	16
hsa049 16	Melanogenesis	14/1162	101/81 05	0.59821 2466	0.83567 1764	0.72094 007	ADCY5/CREB1/KRAS/GNAS/PRKCA/ ADCY1/FZD4/FZD2/MAPK1/ADCY7/P RKACG/WNT10B/MAP2K1/ADCY6	14
hsa002 30	Purine metabolism	18/1162	130/81 05	0.60250 7424	0.83567 1764	0.72094 007	PDE4D/PRUNE1/ENTPD4/ADCY5/PD E1A/AK5/GART/AK4/AK9/ADCY1/NU	18

							DT16/AMPD3/ADCY7/NT5C3A/PDE6 B/ADCY6/PKM/PDE7B	
hsa005 00	Starch and sucrose metabolism	5/1162	36/810 5	0.60311 479	0.83567 1764	0.72094 007	HK1/GYS1/UGP2/MGAM2/HKDC1	5
hsa003 30	Arginine and proline metabolism	7/1162	51/810 5	0.61074 768	0.84267 7178	0.72698 3692	NOS1/GOT2/CARNS1/P4HA2/ALDH4 A1/ALDH9A1/NOS3	7
hsa005 33	Glycosaminoglyca n biosynthesis - keratan sulfate	2/1162	14/810 5	0.61715 9131	0.84794 5529	0.73152 8736	CHST2/B3GNT2	2
hsa003 40	Histidine metabolism	3/1162	22/810 5	0.62977 0831	0.85548 0567	0.73802 9268	CARNS1/ALDH9A1/HNMT	3
hsa009 00	Terpenoid backbone biosynthesis	3/1162	22/810 5	0.62977 0831	0.85548 0567	0.73802 9268	PDSS2/RCE1/FNTA	3
hsa052 03	Viral carcinogenesis	28/1162	204/81 05	0.63049 1794	0.85548 0567	0.73802 9268	JAK1/CDC42/CHD4/ATF2/HDAC7/PIK 3R3/PIK3CB/NFKB1/CREB1/STAT3/R HOA/USP7/HDAC10/KRAS/SYK/CCN D2/HDAC1/MAPK1/RBL2/HDAC4/RB PJ/RBL1/CHEK1/PIK3CA/PRKACG/Y WHAZ/PKM/DNAJA3	28
hsa051 70	Human immunodeficiency	29/1162	212/81 05	0.63929 3603	0.86345 0008	0.74490 4562	MAP3K7/APOBEC3H/MAPK9/PIK3R3/ AP1B1/PIK3CB/ITPR1/CUL4B/NFKB1/	29

	virus 1 infection						NFATC1/FASLG/TLR4/KRAS/TLR2/C UL4A/AP1G1/PRKCA/GNG12/MAPK1/ BCL2L1/PPP3R1/MAPK13/NFATC2/C HEK1/PIK3CA/MAPK10/MAP2K1/RIP K1/MYD88	
hsa000 53	Ascorbate and aldarate metabolism	4/1162	30/810 5	0.64164 6336	0.86345 0008	0.74490 4562	UGT1A6/UGDH/ALDH9A1/UGT1A1	4
hsa049 32	Non-alcoholic fatty liver disease	21/1162	155/81 05	0.64643 9233	0.86633 4545	0.74739 3073	PPARG/MAPK9/NR1H3/CDC42/NDUF S1/PIK3R3/PIK3CB/NFKB1/FASLG/N DUFB4/NDUFA5/PRKAG3/COX4I1/EI F2S1/MAPK13/COX6B1/PIK3CA/PRK AA2/UQCRB/MAPK10/IRS1	21
hsa008 30	Retinol metabolism	9/1162	68/810 5	0.65525 682	0.87085 9052	0.75129 6398	DGAT1/UGT1A6/AOX1/ADH4/AWAT 2/UGT1A1/RDH10/CYP3A7/CYP26B1	9
hsa052 04	Chemical carcinogenesis	11/1162	83/810 5	0.65905 8835	0.87085 9052	0.75129 6398	CHRNA7/ARNT/CBR1/UGT1A6/GSTO 2/ADH4/UGT1A1/AKR1C2/CYP3A7/G STT2B/CYP1B1	11
hsa034 30	Mismatch repair	3/1162	23/810 5	0.66063 1509	0.87085 9052	0.75129 6398	LIG1/RPA2/SSBP1	3
hsa001 40	Steroid hormone biosynthesis	8/1162	61/810 5	0.66313 1205	0.87085 9052	0.75129 6398	UGT1A6/CYP7A1/UGT1A1/AKR1C2/C YP3A7/HSD17B7/LRTOMT/CYP1B1	8

hsa00561	Glycerolipid metabolism	8/1162	61/8105	0.663131205	0.870859052	0.751296398	DGAT1/ALDH9A1/AGK/GK2/AGPAT5/GLYCTK/PLPP1/AKR1B10	8
hsa05169	Epstein-Barr virus infection	27/1162	202/8105	0.685324193	0.896404045	0.773334248	MAP3K7/JAK1/MAPK9/PIK3R3/NCOR2/PIK3CB/IKBKE/NFKB1/STAT3/USP7/MAVS/BTK/TLR2/SYK/ITGAL/CCND2/STAT1/E2F3/HDAC1/SIN3A/RBPJ/E2F1/MAPK13/PIK3CA/MAPK10/RIPK1/MYD88	27
hsa00980	Metabolism of xenobiotics by cytochrome P450	10/1162	78/8105	0.697965337	0.905866399	0.781497489	CBR1/UGT1A6/AKR7A3/GSTO2/DHDH/ADH4/UGT1A1/GSTT2B/CBR3/CYP1B1	10
hsa00260	Glycine, serine and threonine metabolism	5/1162	40/8105	0.698098876	0.905866399	0.781497489	CBSL/CBS/DLD/GLYCTK/CTH	5
hsa05210	Colorectal cancer	11/1162	86/8105	0.7055771	0.91195143	0.786747089	MAPK9/PIK3R3/PIK3CB/RHOA/KRAS/ARAF/MAPK1/AXIN2/PIK3CA/MAPK10/MAP2K1	11
hsa00240	Pyrimidine metabolism	7/1162	56/8105	0.710088548	0.913260028	0.787876026	TK2/CTPS2/ENTPD4/AK9/NT5C3A/UMPS/DPYD	7
hsa04130	SNARE interactions in vesicular transport	4/1162	33/8105	0.71655588	0.913260028	0.787876026	STX5/STX1B/YKT6/BET1	4

hsa045 30	Tight junction	22/1162	169/81 05	0.72207 0626	0.91326 0028	0.78787 6026	RUNX1/MAPK9/CDC42/DLG2/PPP2R2 B/RHOA/ACTG1/CACNA1D/PRKAG3/ F11R/CLDN7/PPP2R2C/PRKACG/PRK AA2/MAPK10/PPP2R2A/CLDN4/ARPC 1B/IGSF5/MSN/ROCK1/MAGI1	22
hsa003 60	Phenylalanine metabolism	2/1162	17/810 5	0.72334 6628	0.91326 0028	0.78787 6026	GOT2/IL4I1	2
hsa004 50	Selenocompound metabolism	2/1162	17/810 5	0.72334 6628	0.91326 0028	0.78787 6026	CTH/MARS2	2
hsa009 10	Nitrogen metabolism	2/1162	17/810 5	0.72334 6628	0.91326 0028	0.78787 6026	GLUL/CA8	2
hsa003 80	Tryptophan metabolism	5/1162	42/810 5	0.73925 0488	0.92899 7687	0.80145 3018	AOX1/DLD/ALDH9A1/IL4I1/CYP1B1	5
hsa007 90	Folate biosynthesis	3/1162	26/810 5	0.74182 824	0.92899 7687	0.80145 3018	CBR1/AKR1B10/ALPI	3
hsa030 13	RNA transport	24/1162	186/81 05	0.74433 4538	0.92899 7687	0.80145 3018	SUMO3/GEMIN4/EIF4E/EIF4B/FXR1/S UMO1/UPF2/NUP58/EIF5B/NUP210L/ UBE2I/NCBP2/EIF2S1/NCBP1/XPO5/X POT/PYM1/NUP205/EIF4G1/EIF3A/NU P98/PABPC1/EIF4G3/EIF4A3	24
hsa008 60	Porphyrin and chlorophyll	5/1162	43/810 5	0.75822 0386	0.93390 0853	0.80568 3015	FECH/UGT1A6/UGT1A1/UROS/COX1 0	5

	metabolism							
hsa049 40	Type I diabetes mellitus	5/1162	43/810 5	0.75822 0386	0.93390 0853	0.80568 3015	PTPRN/FASLG/CD80/CD86/PRF1	5
hsa049 75	Fat digestion and absorption	5/1162	43/810 5	0.75822 0386	0.93390 0853	0.80568 3015	NPC1L1/DGAT1/GOT2/PLPP1/ABCA1	5
hsa007 60	Nicotinate and nicotinamide metabolism	4/1162	35/810 5	0.75968 6932	0.93390 0853	0.80568 3015	NAMPT/NNT/AOX1/NMRK1	4
hsa010 40	Biosynthesis of unsaturated fatty acids	3/1162	27/810 5	0.76520 1796	0.93715 7256	0.80849 2337	SCP2/ACOX3/HACD3	3
hsa046 40	Hematopoietic cell lineage	12/1162	99/810 5	0.77750 3641	0.94493 7808	0.81520 4675	TFRC/IL1R2/ITGA2B/DNTT/ITGAM/I L3/ITGB3/IL5RA/GYPA/IL2RA/IL9R/I TGA5	12
hsa012 10	2-Oxocarboxylic acid metabolism	2/1162	19/810 5	0.77941 505	0.94493 7808	0.81520 4675	BCAT2/GOT2	2
hsa051 68	Herpes simplex virus 1 infection	66/1162	498/81 05	0.78022 3878	0.94493 7808	0.81520 4675	ZNF84/MAP3K7/ZNF544/JAK1/POU2F 2/ZNF790/ZNF227/POU2F1/SRSF5/ZN F189/PIK3R3/TSC1/ZNF226/ZNF772/Z NF398/PIK3CB/IKBKE/NFKB1/ZNF37 A/ZNF605/ZNF234/ZNF597/FASLG/M AVS/ZNF667/BIRC3/ZNF573/ZNF45/Z	66

							NF641/ZNF561/ZNF81/ZNF141/TLR2/SYK/ZNF778/EIF2S1/ZNF714/ZNF680/ZNF248/STAT1/ITGB3/BCL2L1/ZNF836/ZNF570/ZNF684/ZNF136/C5/BIRC2/ZNF607/ZNF311/ZNF624/ZNF7/ZNF559-ZNF177/ZNF436/ZNF23/ZNF773/ZNF8/PIK3CA/PPP1CB/ZNF708/SRPK1/ZNF320/ZNF484/ITGA5/ZNF343/MYD88	
hsa00072	Synthesis and degradation of ketone bodies	1/1162	10/8105	0.787412579	0.945957292	0.816084192	OXCT1	1
hsa00590	Arachidonic acid metabolism	7/1162	61/8105	0.790924856	0.945957292	0.816084192	CBR1/CYP2U1/PLA2G4D/GPX7/CBR3/CYP4F3/PTGES2	7
hsa05320	Autoimmune thyroid disease	6/1162	53/8105	0.791147885	0.945957292	0.816084192	FASLG/CTLA4/TG/CD80/CD86/PRF1	6
hsa04650	Natural killer cell mediated cytotoxicity	16/1162	131/8105	0.792636997	0.945957292	0.816084192	PIK3R3/PIK3CB/NFATC1/FASLG/KRAS/SYK/ARAF/ITGAL/PRKCA/MAPK1/PPP3R1/NFATC2/PIK3CA/MAP2K1/PRF1/SHC4	16
hsa04744	Phototransduction	3/1162	29/8105	0.806766989	0.958167652	0.826618158	PDE6B/GRK1/SLC24A1	3
hsa041	Protein processing	21/1162	171/81	0.81074	0.95816	0.82661	MAPK9/UBE2D3/SEC31A/DNAJC10/S	21

41	in endoplasmic reticulum		05	6524	7652	8158	ELENOS/EIF2S1/UBE2G1/ERO1A/SEC23B/RPN1/UBE2J1/LMAN1L/TUSC3/DNAJB11/SVIP/TRAM1/MAPK10/SEC61A1/UBXN8/DNAJC5/ATF6	
hsa05016	Huntington disease	39/1162	306/8105	0.813162839	0.958167652	0.826618158	ATG13/PPARG/MAPK9/AP2B1/NDUF S1/BDNF/AP2A2/SOD2/ITPR1/DLG4/CREB1/ULK1/GRIA4/VDAC1/NDUFB4/NDUFA5/POLR2B/HTT/DNAH1/KLC4/COX4I1/HIP1/HDAC1/SIN3A/CLTA/C OX6B1/DNAH5/DNAH9/CLTCL1/GRI N2B/GPX7/UQCRB/MAPK10/ATP5MC 3/ATG14/DNAH11/ATG2B/DNAH6/AT G2A	39
hsa05330	Allograft rejection	4/1162	38/8105	0.814589013	0.958167652	0.826618158	FASLG/CD80/CD86/PRF1	4
hsa04260	Cardiac muscle contraction	10/1162	87/8105	0.818439883	0.959246745	0.827549099	CACNB4/CACNA1C/ASPH/CACNA1D /SLC9A7/COX4I1/CACNG4/COX6B1/ UQCRB/MYL3	10
hsa00020	Citrate cycle (TCA cycle)	3/1162	30/8105	0.825113728	0.961542173	0.829529382	DLD/SUCLG1/MDH1	3
hsa03040	Spliceosome	18/1162	150/8105	0.82627936	0.961542173	0.829529382	SRSF5/DDX5/PRPF40B/HNRNPM/PRP F38B/SRSF10/NCBP2/U2SURP/SNRPB	18

							/SART1/NCBP1/ISY1-RAB43/SF3B3/DHX38/SF3B2/WBP11/DHX16/EIF4A3	
hsa05010	Alzheimer disease	47/1162	369/8105	0.834729025	0.967109833	0.834332642	CACNA1C/ATG13/BACE1/MCU/MAPK9/CHRNA7/NDUFS1/PIK3R3/NOS1/PIK3CB/ITPR1/NFKB1/PSEN1/ULK1/VDAC1/NDUFB4/NDUFA5/LRP5/CACNA1D/KRAS/ARAF/KLC4/COX4I1/ADAM17/EIF2S1/CHRM3/FZD4/FZD2/MAPK1/PPP3R1/CSNK2A3/COX6B1/AXIN2/PIK3CA/GRIN2B/WNT10B/UQCRB/MAPK10/ATP5MC3/ATG14/MAP2K1/IRS1/CYBB/DKK1/ATG2B/ATF6/ATG2A	47
hsa05206	MicroRNAs in cancer	39/1162	310/8105	0.836978846	0.967109833	0.834332642	FOXP1/PIK3R3/ZEB1/PIK3CB/NFKB1/MCL1/PLAU/EFNA5/STAT3/RHOA/CYP24A1/UBE2I/KRAS/ZEB2/CCND2/PKCA/SLC7A1/E2F3/HDAC1/ITGB3/NOTCH2/PDGFR/ALPHA/MAPK1/HDAC4/E2F1/RASSF1/NOTCH1/PIK3CA/BMP2/FGFR3/MAP2K1/IRS1/ABCB1/ITGA5/DNMT1/SHC4/CYP1B1/ROCK1/MMP9	39
hsa041	Phagosome	18/1162	152/81	0.84231	0.96864	0.83565	DYNC1I2/NCF2/NOS1/TFRC/ACTG1/	18

45			05	4697	395	6135	M6PR/TLR4/ATP6V1H/TLR2/ITGAM/ITGB3/SFTPA1/PIKFYVE/DYNC1LI1/SEC61A1/CYBB/ITGA5/DYNC1LI2	
hsa00480	Glutathione metabolism	6/1162	57/8105	0.845563983	0.96864395	0.835656135	GGCT/GSTO2/GCLC/NAT8/GPX7/GSTT2B	6
hsa05014	Amyotrophic lateral sclerosis	46/1162	364/8105	0.847193179	0.96864395	0.835656135	OPTN/ATG13/MATR3/MCU/VAPB/NDUFS1/NRG2/NOS1/ULK1/NUP58/VDAC1/ACTG1/NDUFB4/SETX/NUP210L/NDUFA5/DNAH1/KLC4/COX4I1/EIF2S1/NCBP1/ATXN2L/WDR41/BCL2L1/PPP3R1/MAPK13/ANXA11/PFN4/COX6B1/DNAH5/NUP205/DNAH9/GRIN2B/GPX7/UQCRB/ATP5MC3/ATG14/NEFL/NRG4/NRG3/DNAH11/NUP98/ATG2B/DNAH6/ATF6/ATG2A	46
hsa00515	Mannose type O-glycan biosynthesis	2/1162	23/8105	0.862352153	0.982540607	0.847644882	POMT1/B3GALNT2	2
hsa05332	Graft-versus-host disease	4/1162	42/8105	0.871335361	0.989328691	0.853501012	FASLG/CD80/CD86/PRF1	4
hsa05020	Prion disease	33/1162	273/8105	0.87995401	0.995657306	0.858960753	CACNA1C/MCU/MAPK9/NDUFS1/ATF2/NCF2/PIK3R3/C8B/PIK3CB/ITPR1/CREB1/VDAC1/NDUFB4/NDUFA5/CA	33

							CNA1D/KLC4/COX4I1/EIF2S1/MAPK1 /PPP3R1/MAPK13/CSNK2A3/COX6B1/ C5/NOTCH1/PIK3CA/GRIN2B/PRKAC G/UQCRB/MAPK10/ATP5MC3/C9/CY BB	
hsa046 57	IL-17 signaling pathway	10/1162	94/810 5	0.88389 8116	0.99667 1324	0.85983 5554	MAP3K7/MAPK9/IKBKE/NFKB1/MAP K1/MAPK13/IL17RB/MAPK10/USP25/ MMP9	10
hsa005 92	alpha-Linolenic acid metabolism	2/1162	25/810 5	0.89209 4787	0.99988 5017	0.86260 803	ACOX3/PLA2G4D	2
hsa051 50	Staphylococcus aureus infection	10/1162	96/810 5	0.89858 867	0.99988 5017	0.86260 803	ITGAL/ITGAM/PTAFR/C5/MASP1/KR T10/KRT33B/SELP/C4A/C4B	10
hsa006 03	Glycosphingolipid biosynthesis - globo and isoglobo series	1/1162	15/810 5	0.90205 7915	0.99988 5017	0.86260 803	A3GALT2	1
hsa005 63	Glycosylphosphati dylinositol (GPI)- anchor biosynthesis	2/1162	26/810 5	0.90461 6999	0.99988 5017	0.86260 803	GPLD1/PIGN	2
hsa049 50	Maturity onset diabetes of the young	2/1162	26/810 5	0.90461 6999	0.99988 5017	0.86260 803	PAX6/MNX1	2

hsa03030	DNA replication	3/1162	36/8105	0.906570798	0.999885017	0.86260803	LIG1/RPA2/SSBP1	3
hsa00601	Glycosphingolipid biosynthesis - lacto and neolacto series	2/1162	27/8105	0.915770215	0.999885017	0.86260803	ST3GAL6/B3GNT2	2
hsa05143	African trypanosomiasis	3/1162	37/8105	0.916190712	0.999885017	0.86260803	FASLG/PRKCA/MYD88	3
hsa05152	Tuberculosis	20/1162	180/8105	0.916334706	0.999885017	0.86260803	JAK1/MAPK9/NFKB1/CREB1/RHOA/TLR4/ATP6V1H/TLR2/SYK/ITGAM/STAT1/MAPK1/PPP3R1/MAPK13/ARHGAP12/MAPK10/IRAK2/CTSD/NOD2/MYD88	20
hsa04146	Peroxisome	8/1162	82/8105	0.917325704	0.999885017	0.86260803	ACSL4/ACSL1/SCP2/SOD2/ECI2/ACOX3/MPV17/GNPAT	8
hsa03420	Nucleotide excision repair	4/1162	47/8105	0.920687184	1	0.862707227	CUL4B/LIG1/CUL4A/RPA2	4
hsa04672	Intestinal immune network for IgA production	4/1162	49/8105	0.935124503	1	0.862707227	CCR9/CXCL12/CD80/CD86	4
hsa05012	Parkinson disease	28/1162	249/8105	0.937730603	1	0.862707227	MCU/MAPK9/MFN2/NDUFS1/ADCY5/ITPR1/VDAC1/NDUFB4/NDUFA5/UBA1/UBA52/KLC4/GNAS/COX4I1/EIF2	28

							S1/UBE2G1/GPR37/BCL2L1/UBB/COX 6B1/UBE2J1/PRKACG/UQCRB/MAPK 10/ATP5MC3/SLC18A2/LRRK2/ATF6	
hsa005 11	Other glycan degradation	1/1162	18/810 5	0.93849 3587	1	0.86270 7227	AGA	1
hsa009 83	Drug metabolism - other enzymes	7/1162	80/810 5	0.95250 0409	1	0.86270 7227	TK2/UGT1A6/GSTO2/UGT1A1/GSTT2 B/UMPS/DPYD	7
hsa009 82	Drug metabolism - cytochrome P450	6/1162	72/810 5	0.95705 9205	1	0.86270 7227	UGT1A6/AOX1/GSTO2/ADH4/UGT1A 1/GSTT2B	6
hsa040 61	Viral protein interaction with cytokine and cytokine receptor	9/1162	100/81 05	0.96026 7114	1	0.86270 7227	CCL4L2/CCR9/CX3CR1/CXCL12/CXC L14/TNFRSF10D/IL2RA/IL19/IL18RAP	9
hsa050 34	Alcoholism	19/1162	187/81 05	0.96518 0808	1	0.86270 7227	ATF2/HDAC7/ADCY5/BDNF/CREB1/ HDAC10/KRAS/ARAF/GNAS/GNG12/ HDAC1/MAPK1/HDAC4/GRIN2B/PPP 1CB/PRKACG/MAP2K1/SLC18A2/SH C4	19
hsa030 22	Basal transcription factors	3/1162	45/810 5	0.96605 8342	1	0.86270 7227	TAF2/TAF7/GTF2F1	3
hsa053 23	Rheumatoid arthritis	8/1162	93/810 5	0.96620 2441	1	0.86270 7227	CTLA4/TLR4/ATP6V1H/TLR2/ITGAL/ CXCL12/CD80/CD86	8

hsa049 64	Proximal tubule bicarbonate reclamation	1/1162	23/810 5	0.97168 6607	1	0.86270 7227	MDH1	1
hsa005 34	Glycosaminoglycan biosynthesis - heparan sulfate / heparin	1/1162	24/810 5	0.97575 7401	1	0.86270 7227	HS6ST3	1
hsa040 60	Cytokine-cytokine receptor interaction	3D,1/1162	295/8105	0.98035 8594	1	0.86270 7227	CCL4L2/IL12RB2/EDA/BMPR1B/ACVR1/IL31RA/IL1R2/CCR9/FASLG/ACVR2A/CRLF2/CX3CR1/INHBA/OSMR/CXCL12/IL3/IL5RA/LIF/BMP7/CNTF/CXCL14/TNFRSF10D/NGF/IL17RB/BMPR2/IL2RA/CXCR6/IL19/TNFRSF21/IL9R/IL18RAP	31
hsa000 62	Fatty acid elongation	1/1162	27/810 5	0.98478 4481	1	0.86270 7227	HACD3	1
hsa052 17	Basal cell carcinoma	4/1162	63/810 5	0.98554 7752	1	0.86270 7227	FZD4/FZD2/AXIN2/WNT10B	4
hsa030 10	Ribosome	14/1162	158/8105	0.98648 647	1	0.86270 7227	RPL10/RPL15/MRPS18C/RPS3/RPL32/UBA52/MRPL1/MRPL32/RPL37/MRPL17/MRPL18/RPS24/MRPS9/MRPS6	14
hsa005	Linoleic acid	1/1162	29/810	0.98884	1	0.86270	PLA2G4D	1

91	metabolism		5	7301		7227		
hsa053 10	Asthma	1/1162	31/810 5	0.99182 5954	1	0.86270 7227	IL3	1
hsa030 50	Proteasome	2/1162	46/810 5	0.99306 3103	1	0.86270 7227	PSME3/PSMF1	2
hsa005 64	Glycerophospholipid metabolism	6/1162	98/810 5	0.99686 511	1	0.86270 7227	PCYT2/PLA2G4D/GNPAT/CHPT1/AGPAT5/PLPP1	6
hsa053 40	Primary immunodeficiency	1/1162	38/810 5	0.99724 671	1	0.86270 7227	BTK	1
hsa009 70	Aminoacyl-tRNA biosynthesis	3/1162	66/810 5	0.99742 8192	1	0.86270 7227	HARS2/DARS2/MARS2	3
hsa001 90	Oxidative phosphorylation	9/1162	133/810 05	0.99798 1036	1	0.86270 7227	NDUFS1/NDUFB4/ATP6V1H/NDUFA5/COX4I1/COX6B1/UQCRCB/ATP5MC3/COX10	9
hsa053 22	Systemic lupus erythematosus	9/1162	136/810 05	0.99850 0568	1	0.86270 7227	C8B/SNRPB/C5/GRIN2B/CD80/CD86/C9/C4A/C4B	9
hsa030 08	Ribosome biogenesis in eukaryotes	6/1162	110/810 05	0.99916 8619	1	0.86270 7227	UTP15/NOB1/CSNK2A3/MDN1/REXO1/UTP6	6
hsa046 12	Antigen processing and presentation	3/1162	78/810 5	0.99946 1267	1	0.86270 7227	PSME3/CREB1/LGMN	3
hsa047	Olfactory	24/1162	443/81	1	1	0.86270	PRKG1/PDE1A/OR13A1/OR1F1/OR4F	24

40	transduction		05			7227	3/OR4F29/OR4F16/OR52E2/OR2F1/OR 4F21/OR5B2/PRKACG/OR2T7/OR2T2/ OR2G6/OR2T11/OR2T35/OR52K1/OR5 1E1/OR4K14/OR4K13/OR4E1/OR5K4/ OR5B3	
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Table SII. Targeted genes for each factor associated with type 2 diabetes.

A, Red q<0.5												
Symb ol	d b S N P	Consequen ce	varID	Refere nce	Alt	Phenoty pe	Pvalue	Beta	n	stdErr	zScore	A l i g n e m e n t
ACS L1	r s 7 3 5 9 4 9	intron_vari ant	4:185716232:T: C	T	C	T2D	7.27E- 13	-0.056	842115	0.0046	-7.174	1
DGK B	r s 1	intergenic_ variant	7:15063833:T:G	T	G	T2D	1.56E- 44	0.0517	1076590	0.0027	14	1

	0 2 4 4 0 5 1											
MEF 2C	r s 1 1 2 8 6 2 6 3 4	intron_vari ant	5:87970352:G:C	G	C	T2D	2.61E- 08	0.0313	868950	0.0038	5.566	1
BDN F	r s 1 0	intron_vari ant	11:27686196:G: T	G	T	T2D	2.95E- 09	-0.0282	868949	0.0035	-5.94	1

	7 6 7 6 5 9											
NRX N3	r s 1 0 1 4 6 9 9 7	intron_vari ant	14:79945162:A: G	A	G	T2D	1.74E- 17	0.0464	741407	0.0038	8.51	1
LEP R	r s 1 1 2 0	intron_vari ant	1:65983626:C:T	C	T	T2D	7.78E- 11	0.0516	1179100	0.0048	6.505	1

	8 6 6 0											
GNA S	r s 3 7 4 6 7 0 9	upstream_g ene_variant	20:57393941:C: T	C	T	T2D	9.22E- 11	0.0339	884504	0.0034	6.479	1
NFA TC2	r s 3 7 8 7 1 8 6	intron_vari ant	20:50153344:T: C	T	C	T2D	1.54E- 08	-0.0254	1147420	0.0029	-5.657	1

VEG FA	r s 9 4 7 2 1 3 8	intergenic_ variant	6:43811762:C:T	C	T	T2D	1.07E- 17	0.0393	1337680	0.0029	8.566	1
NSD 1	r s 1 2 5 1 9 1 4 5	upstream_g ene_variant	5:17655523:G: A	G	A	T2D	8.79E- 13	-0.036	1174390	0.0032	-7.148	1
ATP 2A3	r s 1	missense_v ariant	17:3828086:C:G	C	G	T2D	1.12E- 16	0.0429	794957	0.0044	8.292	1

	0 4 3 2 4 6											
GRB 10	r s 3 4 0 6 1 1 0 3	intron_vari ant	7:50804205:G:C	G	C	T2D	2.50E- 08	-0.0367	864796	0.0048	-5.573	1
NFK B1	r s 2 8 6 6	missense_v ariant	4:103557077:G: A	G	A	T2D	1.74E- 09	-0.017	1292620	0.0026	-6.02	1

	4 1 3											
BMP R1B	r s 3 7 7 5 0 5 7	intron_vari ant	4:96117715:G:A	G	A	T2D	6.74E- 09	-0.024	918796	0.0033	-5.797	1
ADC Y5	r s 1 1 7 0 8 0 6 7	intron_vari ant	3:123065778:A: G	A	G	T2D	5.47E- 54	-0.0782	1011740	0.0034	-15.471	1

LDH B	r s 6 6 5 9 2 8 3 0	intron_vari ant	12:21834560:C: A	C	A	T2D	2.93E- 10	-0.0321	824965	0.004	-6.302	1
MRA S	r s 1 6 7 9 1 4 7	intron_vari ant	3:138097537:A: G	A	G	T2D	2.19E- 09	-0.0293	1089680	0.0032	-5.983	1
RAS GRP 1	r s 7	intron_vari ant	15:38843476:G: A	G	A	T2D	3.27E- 14	0.0349	868949	0.0032	7.587	1

	2 7 2 7 3 8 7											
PIK3 R3	r s 1 6 2 2 2 0 8	synonymou s_variant	1:46498375:A:G	A	G	T2D	1.36E- 11	0.0269	1178170	0.0028	6.762	1
INSR	r s 8 1 0 0	intron_vari ant	19:7241501:C:T	C	T	T2D	7.14E- 09	0.0343	868950	0.004	5.788	1

	5 6 2											
PTC H1	r s 1 0 5 1 2 2 4 8	intron_vari ant	9:98259703:T:G	T	G	T2D	1.77E- 08	-0.0255	1343780	0.0027	-5.634	1
ETS1	r s 6 7 2 3 2 5 4	non_coding _transcript_ exon_varia nt	11:128398938:C :T	C	T	T2D	6.48E- 17	0.0421	870912	0.0038	8.356	1

	6											
TCF7 L2	r s 7 0 7 4 4 4 0	intron_vari ant	10:114785424:G :A	G	A	T2D	1.07e- 321	0.2293	972227	0.0037	38.345	1
GTF 2I	r s 3 4 3 2 4 9 7 1	intron_vari ant	7:74107374:G:A	G	A	T2D	6.91E- 10	0.0301	735117	0.0046	6.168	1
SLC2 A2	r s	intron_vari ant	3:170733076:G: A	G	A	T2D	1.18E- 18	-0.0427	868949	0.0035	-8.817	1

	9 8 7 3 6 1 8											
CTS B	r s 6 9 8 7 6 9 2	non_coding _transcript_ exon_varia nt	8:11777849:C:T	C	T	T2D	8.69E- 09	0.0243	491761	0.0039	5.755	1
HNF 4A	r s 1 2 6 2	intron_vari ant	20:42994812:T: C	T	C	T2D	1.63E- 25	0.0593	870910	0.004	10.44	1

	5 6 7 1											
SDC 2		intron_vari ant	8:97538579:G:A	G	A	T2D	9.40E- 09	0.21	230864	0.0366	5.741	1
SOC S2	r s 3 8 2 5 1 9 9	3_prime_U TR_variant	12:93976954:A: G	A	G	T2D	7.66E- 09	0.0209	1333380	0.0027	5.776	1
HLA - DQB 1	r s 5 5 4 4 4	upstream_g ene_variant	6:32623943:C:T	C	T	T2D	7.05E- 10	0.0404	296583	0.0065	6.165	1

	8 1 1 7											
ABC B9	r s 4 2 7 5 6 5 9	intron_vari ant	12:123447928:T :C	T	C	T2D	4.13E- 16	0.0345	1338760	0.0027	8.135	1
FAD S1	r s 1 7 4 5 5 0	5_prime_U TR_variant	11:61571478:T C	T	C	T2D	1.38E- 10	-0.0259	1267810	0.0027	-6.418	1
DGA	r	intron_vari	8:145545949:T:	T	C	T2D	3.65E-	0.0334	848066	0.0033	8.15	1

T1	s 3 7 5 7 9 7 1	ant	C				16					
PDE 8B	r s 6 4 5 3 2 8 5	intron_vari ant	5:76445549:T:C	T	C	T2D	3.79E- 09	-0.04	514455	0.0068	-5.893	1
EHM T2	r s 1 1 5	missense_v ariant	6:31864538:G:A	G	A	T2D	3.76E- 08	0.1289	288701	0.0202	5.502	1

	8											
	8											
	4											
	6											
	5											
	8											
ANK 1	r s 5 1 6 9 4 6	non_coding _transcript_ exon_varia nt	8:41519248:T:C	T	C	T2D	2.34E- 95	0.0723	1433920	0.003	20.72	1
ARA P1	r s 1 1 6 0 3 3	5_prime_U TR_variant	11:72432985:G: A	G	A	T2D	1.46E- 57	-0.0827	1192070	0.0037	-15.992	1

	3											
	4											
PPIP 5K2	r s 1 5 2 1 2 3	intron_vari ant	5:102531919:C: T	C	T	T2D	7.74E- 11	0.0215	919794	0.0028	6.506	1
ANA PC1	r s 1 3 4 5 2 0 3	intron_vari ant	2:112253851:T: C	T	C	T2D	9.57E- 09	-0.0292	809084	0.0043	-5.738	1
ITGB 6	r s 7	intron_vari ant	2:161144079:T: C	T	C	T2D	1.12E- 08	-0.05	532655	0.0064	-5.712	1

	7 7 0 4 4 2 4											
GCK	r s 2 2 6 8 5 7 4	intron_vari ant	7:44189321:A:G	A	G	T2D	3.43E- 20	0.0358	1016870	0.003	9.205	1
CAM K2B	r s 1 1 6 9	non_coding _transcript_ exon_varia nt	7:44365549:C:T	C	T	T2D	2.74E- 09	-0.04	733069	0.0049	-5.946	1

	1 3 0 3 3											
IRS1	r s 2 6 7 3 1 4 1	intergenic_ variant	2:227159177:G: A	G	A	T2D	6.34E- 37	0.06	1159400	0.0032	12.695	1
CAL CR	r s 1 7 7 8 8 3	intron_vari ant	7:93111506:T:A	T	A	T2D	4.30E- 08	-0.0244	868948	0.0031	-5.478	1

	1											
	2											
ASA H1	r s 5 7 4 1 1 4	3_prime_U TR_variant	8:17914859:A:T	A	T	T2D	2.17E- 08	0.0723	431521	0.0099	5.598	1
CCN D2	r s 7 6 8 9 5 9 6 3	intron_vari ant	12:4384844:T:G	T	G	T2D	5.30E- 70	-0.48	231420	0.0271	-17.687	1
ALD OA	r s	intron_vari ant	16:30068354:C: T	C	T	T2D	1.64E- 09	0.0301	864280	0.0032	6.03	1

	9 9 3 9 7 7 4											
SIN3 A	r s 4 8 8 6 7 0 7	downstrea m_gene_va riant	15:75755467:C: T	C	T	T2D	1.84E- 15	-0.0349	1079450	0.0029	-7.952	1
LPL	r s 1 2 6 7	intergenic_ variant	8:19844222:A:G	A	G	T2D	4.91E- 13	-0.0467	1332050	0.0043	-7.228	1

	8 9 1 9											
HLA - DQA 1	r s 5 7 4 5 7 6 0 4 6	downstrea m_gene_va riant	6:32619099:A:T	A	T	T2D	7.58E- 15	0.0523	296583	0.0061	7.774	1
ATP 2A1	r s 1 1 6 4 2	intron_vari ant	16:28896015:C: T	C	T	T2D	3.66E- 08	0.0256	958651	0.0034	5.51	1

	4 4 9											
IGF1 R	r s 9 0 7 8 0 1	intron_vari ant	15:99321747:T: C	T	C	T2D	4.03E- 08	0.0336	1162050	0.0038	5.489	1
CAS R	r s 6 4 3 8 7 1 7	intron_vari ant	3:121971296:A: G	A	G	T2D	1.76E- 08	-0.0475	385000	0.0059	-5.634	1
NUD T12	r s	intergenic_ variant	5:102973337:A: G	A	G	T2D	3.58E- 10	0.10	240274	0.0159	6.271	1

	1 1 6 4 0 7 1 9 6											
GCD H	r s 2 2 4 2 5 1 7	non_coding _transcript_ exon_varia nt	19:13002563:T: G	T	G	T2D	1.31E- 11	-0.03	895673	0.0034	-6.767	1
TFR C	r s 9 8	intergenic_ variant	3:195831237:T: C	T	C	T2D	1.92E- 11	0.0313	866263	0.0034	6.712	1

	7 2 3 4 7											
ABC B10	r s 3 4 8 3 3 0	intron_vari ant	1:229672955:G: A	G	A	T2D	3.39E- 21	-0.0439	870157	0.0033	-9.45	1
REL N	r s 2 6 2 3 5 0	intron_vari ant	7:103420708:T: C	T	C	T2D	2.03E- 09	0.0226	868948	0.0029	5.995	1
GLP	r	missense_v	6:39033595:G:A	G	A	T2D	1.38E-	-0.0827	620922	0.0067	-8.799	1

1R	s 3 7 6 5 4 6 7	ariant					18					
KCN J11	r s 5 2 1 9	missense_v ariant	11:17409572:T: C	T	C	T2D	2.89E- 54	-0.0579	1342880	0.0026	-15.51	1
EML 4		intron_vari ant	2:42506923:TA: T	TA	T	T2D	2.43E- 08	0.3551	2656	0.0641	5.578	1
BCL 2	r s 1 2 4 5	intron_vari ant	18:60845884:T: C	T	C	T2D	2.16E- 19	-0.0397	1138370	0.0029	-9.005	1

	4 7 1 2											
LAM A1	r s 1 2 4 5 4 6 5 8	intron_vari ant	18:7076061:C:A	C	A	T2D	9.01E- 12	0.0326	868948	0.0032	6.822	1
KCN Q1	r s 2 2 8 3 1 6	intron_vari ant	11:2579163:A:G	A	G	T2D	1.34E- 12	-0.0733	878113	0.0072	-7.09	1

	4											
FOX A2	r s 6 0 3 6 1 2 6	intergenic_ variant	20:22445543:C: T	C	T	T2D	2.15E- 10	-0.0352	868947	0.0037	-6.35	1
ANA PC5		intron_vari ant	12:121822670:T :C	T	C	T2D	3.61E- 08	0.2716	183379	0.0493	5.509	1
VAV 2	r s 5 5 9 2 3 9 3 4	upstream_g ene_variant	9:136888233:C: G	C	G	T2D	2.25E- 08	0.024	813694	0.0033	5.591	1

CAM K1D	r s 2 0 9 6 3 9 6	intergenic_ variant	10:12343629:A: G	A	G	T2D	3.88E- 08	-0.0243	885381	0.0034	-5.496	1
MYB L2	r s 6 1 9 2 8 9	upstream_g ene_variant	20:42294613:T: C	T	C	T2D	1.11E- 08	0.03	1199890	0.0035	5.714	1
EP30 0	r s 4 8 2	intron_vari ant	22:41514155:G: A	G	A	T2D	6.45E- 10	0.0241	916933	0.0032	6.179	1

	2 0 0 5											
HSD 17B1 2	r s 7 1 1 0 4 3 7	intron_vari ant	11:43780553:C: A	C	A	T2D	3.16E- 09	-0.0246	924237	0.0034	-5.923	1
CCN D1	r s 3 9 1 8 2 9 8	intron_vari ant	11:69463273:G: A	G	A	T2D	2.69E- 15	-0.1086	466381	0.0147	-7.904	1

PLC D3	r s 1 2 9 4 6 4 5 4	intron_vari ant	17:43208121:A: T	A	T	T2D	7.67E- 09	0.0175	1291080	0.0029	5.775	1
EPH A3	r s 6 7 7 6 9 6 7	intergenic_ variant	3:90025022:C:T	C	T	T2D	7.80E- 11	0.03	896908	0.0036	6.504	1
ITG A1	r s 3	intergenic_ variant	5:51754635:A:G	A	G	T2D	4.51E- 09	-0.0245	868950	0.0031	-5.864	1

	5 8 3 3 9 4 5											
PDE 3B	r s 1 1 7 7 2 0 4 6 8	intron_vari ant	11:14731666:G: C	G	C	T2D	4.57E- 09	0.1247	240274	0.0216	5.862	1
NRB F2	r s 1 6	3_prime_U TR_variant	10:64914193:T: C	T	C	T2D	9.65E- 14	-0.0603	572498	0.0062	-7.446	1

	9 1 8 2 3 9											
PRK AG3	r s 7 8 0 5 8 1 9 0	upstream_g ene_variant	2:219699999:G: A	G	A	T2D	6.50E- 09	0.0645	514536	0.0088	5.803	1
GRM 8	r s 1 1 7 7	intron_vari ant	7:126526991:A: G	A	G	T2D	4.47E- 31	0.1631	330810	0.011	11.59	1

	37118											
PPARG	rs71304101	intron_variant	3:12396913:G:A	G	A	T2D	1.19E-39	-0.0841	738093	0.0052	-13.177	1
PGM1	rs111208	missense_variant	1:64114301:T:C	T	C	T2D	9.30E-16	-0.0348	1161630	0.0033	-8.036	1

	257											
FGFR3	rs61006	intergenic_variant	4:1784605:G:C	G	C	T2D	7.73E-34	-0.0484	801710	0.0034	-12.126	1
P2RY1	rs12629237	intergenic_variant	3:152380932:A:G	A	G	T2D	1.04E-09	-0.0281	868949	0.0033	-6.104	1

SH2 B3		intron_vari ant	12:111836771:A C:A	AC	A	T2D	1.22E- 09	0.0657	329507	0.0077	6.077	1
LEP	r s 7 2 6 0 7 7 4 6	downstrea m_gene_va riant	7:127899718:C: T	C	T	T2D	4.06E- 35	0.2288	334897	0.015	12.365	1
SGC G	r s 3 1 4 8 7 9	intergenic_ variant	13:23309382:C: T	C	T	T2D	3.86E- 09	-0.0345	895537	0.0041	-5.89	1
HLA -	r s	downstrea m_gene_va	6:32544901:T:C	T	C	T2D	3.71E- 11	0.06	217602	0.0075	6.615	1

DRB 1	5 5 7 6 7 3 7 6 8	riant										
KCN U1	r s 1 2 6 8 1 9 9 0	intergenic_ variant	8:36859186:T:C	T	C	T2D	1.90E- 13	0.0361	1179350	0.0033	7.356	1
DGK D	r s 3	intron_vari ant	2:234271522:C: T	C	T	T2D	1.94E- 09	0.0265	867068	0.0032	6.00	1

	4 3 3 9 0 0 6											
LRR C4	r s 1 1 6 9 4 4 3 5 4	intron_vari ant	7:127705515:A: G	A	G	T2D	5.43E- 29	0.3073	191553	0.0275	11.175	1
HLA - DRB 5	r s 5 2	upstream_g ene_variant	6:32500749:A:T	A	T	T2D	9.63E- 12	0.0578	262719	0.0072	6.812	1

	9 0 8 2 0 0 0											
KL	r s 5 7 6 6 7 4	intergenic_ variant	13:33554302:G: A	G	A	T2D	1.71E- 24	-0.053	1303950	0.0035	-10.214	1
ADR B1	r s 7 0 7 6 9	regulatory_ region_vari ant	10:115789375:C :T	C	T	T2D	1.19E- 10	-0.0222	1338300	0.0029	-6.44	1

	3											
	8											
MYO 5C	r s 1 4 9 3 3 6 3 2 9	intron_vari ant	15:52587740:G: T	G	T	T2D	6.73E- 13	-0.091	573933	0.0102	-7.185	1
PDE 3A	r s 7 1 3 4 1 5 0	intron_vari ant	12:20591332:G: A	G	A	T2D	2.10E- 08	0.0447	1023450	0.0059	5.604	1

HLA-A	r s 1 1 6 9 1 9 3 4 7	upstream_g ene_variant	6:29964462:A:G	A	G	T2D	3.17E-08	-0.0849	310710	0.0121	-5.532	1
PHLPP2	r s 6 1 7 3 3 1 2 5	synonymou s_variant	16:71682796:T:C	T	C	T2D	4.23E-10	-0.0285	967291	0.0037	-6.25	1
IL13	r	intergenic_	X:117847909:T:	T	C	T2D	4.37E-	0.0318	244515	0.005	6.93	1

RA1	s 7 8 7 8 6 7 7	variant	C				12					
GIPR	r s 8 1 0 7 3 7 6	intergenic_ variant	19:46163769:T: C	T	C	T2D	7.68E- 44	0.0617	862844	0.0033	13.886	1
CTR B1	r s 1 1 1	upstream_g ene_variant	16:75249170:T: A	T	A	T2D	1.59E- 25	-0.0934	749725	0.0066	-10.442	1

	8 5 2 1 2 7											
CRH R2	r s 9 1 7 1 9 5	non_coding _transcript_ exon_varia nt	7:30728452:C:T	C	T	T2D	8.07E- 17	-0.0387	920794	0.0037	-8.33	1
SUM O2	r s 5 6 7 3 9 2	intron_vari ant	17:73176835:T: G	T	G	T2D	3.64E- 09	-0.03	864280	0.0034	-5.9	1

	30											
ADR A2A	rs10885120	regulatory_region_variant	10:113038224:A:T	A	T	T2D	4.07E-08	-0.0472	1158550	0.0048	-5.488	1
ZNF43	rs77763540	intron_variant	19:22015113:T:C	T	C	T2D	7.41E-19	-0.243	211039	0.0274	-8.869	1

ZFP3 6L2	r s 7 6 8 5 7 2 9 3	intron_vari ant	2:43591676:C:T	C	T	T2D	5.84E- 32	-0.0976	713514	0.006	-11.766	1
P2R X7	r s 5 3 0 3 9 4 8 5 5	regulatory_ region_vari ant	12:121533667:G :A	G	A	T2D	2.34E- 08	-0.3971	200348	0.0711	-5.585	1
TPC	r	missense_v	11:68855363:G:	G	A	T2D	3.13E-	0.0255	1414160	0.0027	8.706	1

N2	s 3 8 2 9 2 4 1	ariant	A				18					
KIF5 C		3_prime_U TR_variant	2:149544648:G A:G	GA	G	T2D	1.79E- 08	0.0421	330261	0.0054	5.631	1
AGA P5	r s 2 8 9 4 0 4 0	intron_vari ant	10:75478159:A: C	A	C	T2D	3.84E- 08	0.026	908766	0.0033	5.498	1
CHM P4B	r s 1	intron_vari ant	20:32437142:C: T	C	T	T2D	1.49E- 08	0.0245	868947	0.0033	5.662	1

	8 1 0 5 3 4											
ZNF 251	r s 7 8 3 8 8 4 6	upstream_g ene_variant	8:145982179:G: T	G	T	T2D	4.04E- 11	0.0272	913987	0.0031	6.603	1
ZNF 799	r s 4 8 0 4 1	intron_vari ant	19:12509536:C: A	C	A	T2D	1.83E- 13	0.0357	862967	0.0036	7.361	1

	81											
ZNF429	rs188360789	intron_variant	19:21649675:C:T	C	T	T2D	2.04E-13	-0.2123	210775	0.0289	-7.346	1
B, Blue q<0.5												
Symbol	dbSNP	Consequence	variant ID	Reference	Alt	Phenotype	Pvalue	Beta	n	stdErr	zScore	Alignment
PT	rs105122	intron_variant	9:982	T	G	T2D	1.77E-08	-0.0255	1343780	0.0027	-5.634	1

C H 1	48		59 70 3: T: G									
S O C S 2	rs38 2519 9	3_prime_UTR_v ariant	12: 93 97 69 54: A: G	A	G	T2D	7.66E- 09	0.0209	1333380	0.0027	5.776	1
C A M K 2 B	rs11 6913 033	non_coding_trans cript_exon_varian t	7:4 43 65 54 9: C: T	C	T	T2D	2.74E- 09	-0.0414	733069	0.0049	-5.946	1
A T P	rs11 6424 49	intron_variant	16: 28 89	C	T	T2D	3.66E- 08	0.0256	958651	0.0034	5.507	1

2 A 1			60 15: C: T									
I T G B 6	rs77 7044 24	intron_variant	2:1 61 14 40 79: T: C	T	C	T2D	1.12E- 08	-0.0468	532655	0.0064	-5.712	1
N S D 1	rs12 5191 45	upstream_gene_va riant	5:1 76 55 55 23: G: A	G	A	T2D	8.79E- 13	-0.036	1174390	0.0032	-7.148	1
P D E 8	rs64 5328 5	intron_variant	5:7 64 45 54	T	C	T2D	3.79E- 09	-0.0402	514455	0.0068	-5.893	1

B			9: T: C									
G C K	rs22 6857 4	intron_variant	7:4 41 89 32 1: A: G	A	G	T2D	3.43E- 20	0.0358	1016870	0.003	9.205	1
C T S B	rs69 8769 2	non_coding_trans cript_exon_varian t	8:1 17 77 84 9: C: T	C	T	T2D	8.69E- 09	0.0243	491761	0.0039	5.755	1
B M P R 1	rs37 7505 7	intron_variant	4:9 61 17 71 5:	G	A	T2D	6.74E- 09	-0.024	918796	0.0033	-5.797	1

B			G: A									
T H	rs10 8404 95	upstream_gene_va riant	11: 21 95 83 7: A: G	A	G	T2D	1.95E- 46	-0.0584	827568	0.0036	-14.308	1
P D E 3 A	rs71 3415 0	intron_variant	12: 20 59 13 32: G: A	G	A	T2D	2.10E- 08	0.0447	1023450	0.0059	5.604	1
F B X W 7	rs68 1319 5	intergenic_variant	4:1 53 52 04 75: C:	C	T	T2D	2.10E- 33	-0.0534	1344110	0.0028	-12.043	1

			T									
G T F 2 I	rs34 3249 71	intron_variant	7:7 41 07 37 4: G: A	G	A	T2D	6.91E- 10	0.0301	735117	0.0046	6.168	1
N F A T C 2	rs37 8718 6	intron_variant	20: 50 15 33 44: T: C	T	C	T2D	1.54E- 08	-0.0254	1147420	0.0029	-6	1
K C N J 1 1	rs52 19	missense_variant	11: 17 40 95 72: T: C	T	C	T2D	2.89E- 54	-0.0579	1342880	0.0026	-15.512	1

D G K B	rs10 2440 51	intergenic_variant	7:1 50 63 83 3: T: G	T	G	T2D	1.56E- 44	0.0517	1076590	0.0027	14	1
H C N 1	rs81 8824 5	intergenic_variant	5:4 61 74 86 4: A: G	A	G	T2D	2.15E- 08	0.023	1047420	0.0029	5.6	1
P I K 3 R 3	rs16 2220 8	synonymous_vari ant	1:4 64 98 37 5: A: G	A	G	T2D	1.36E- 11	0.0269	1178170	0.0028	6.762	1
G	rs37	upstream_gene_va	20:	C	T	T2D	9.22E-	0.0339	884504	0.0034	6.479	1

N A S	4670 9	riant	57 39 39 41: C: T				11					
B C L 2	rs12 4547 12	intron_variant	18: 60 84 58 84: T: C	T	C	T2D	2.16E- 19	-0.0397	1138370	0.0029	-9.005	1
P C G F 3	rs73 2211 26	missense_variant	4:7 27 69 5: A: C	A	C	T2D	6.79E- 15	0.096	630860	0.0108	7.788	1
R A S	rs72 7273 87	intron_variant	15: 38 84	G	A	T2D	3.27E- 14	0.0349	868949	0.0032	7.587	1

G R P 1			34 76: G: A									
E P H A 3	rs67 7696 7	intergenic_variant	3:9 00 25 02 2: C: T	C	T	T2D	7.80E- 11	0.0276	896908	0.0036	6.504	1
A T P 2 A 3	rs10 4324 6	missense_variant	17: 38 28 08 6: C: G	C	G	T2D	1.12E- 16	0.0429	794957	0.0044	8.292	1
D U S P	rs48 9843 1	intergenic_variant	X: 15 28 96	T	G	T2D	2.98E- 70	-0.0724	165093	0.0048	-17.719	1

9			96									
			9:									
			T:									
			G									
L	rs12	intron_variant	18:	C	A	T2D	9.01E-	0.0326	868948	0.0032	6.822	1
A	4546		70				12					
M	58		76									
A			06									
1			1:									
			C:									
			A									
Z	rs64	downstream_gene	16:	C	T	T2D	1.26E-	-0.0253	862965	0.0033	-6.072	1
F	1674	_variant	73				09					
H	9		10									
X			03									
3			08:									
			C:									
			T									
B	rs93	upstream_gene_va	6:3	C	T	T2D	8.12E-	-0.0312	865832	0.0038	-5.766	1
A	5716	riant	35				09					
K	1		49									
1			40									

			3: C: T									
A N A P C 1	rs13 4520 3	intron_variant	2:1 12 25 38 51: T: C	T	C	T2D	9.57E- 09	-0.0292	809084	0.0043	-5.738	1
M R A S	rs16 7914 7	intron_variant	3:1 38 09 75 37: A: G	A	G	T2D	2.19E- 09	-0.0293	1089680	0.0032	-5.983	1
C D K N 2	rs23 8320 8	regulatory_region _variant	9:2 21 32 07 6:	A	G	T2D	1.09E- 176	-0.136	1319060	0.0032	-28.341	1

B			A: G									
P D E 3 B	rs11 7720 468	intron_variant	11: 14 73 16 66: G: C	G	C	T2D	4.57E- 09	0.1247	240274	0.0216	5.862	1
P R K A G 3	rs78 0581 90	upstream_gene_va riant	2:2 19 69 99 99: G: A	G	A	T2D	6.50E- 09	0.0645	514536	0.0088	5.803	1
R E L N	rs26 2350	intron_variant	7:1 03 42 07 08: T:	T	C	T2D	2.03E- 09	0.0226	868948	0.0029	5.995	1

			C									
Z N R F 3	rs17 5180 58	intron_variant	22: 29 37 86 10: T: C	T	C	T2D	3.27E- 10	0.0288	866759	0.0031	6.286	1
M E F 2 C	rs11 2862 634	intron_variant	5:8 79 70 35 2: G: C	G	C	T2D	2.61E- 08	0.0313	868950	0.0038	5.566	1
U B E 3 C	rs23 0191 4	synonymous_vari ant	7:1 57 00 01 76: T: C	T	C	T2D	9.72E- 29	-0.044	1024650	0.003	-11.123	1

EST1	rs67232546	non_coding_transcript	11:128398938:CT	C	T	T2D	6.48E-17	0.0421	870912	0.0038	8.356	1
GIPR	rs8107376	intergenic_variant	19:46163769:TC	T	C	T2D	7.68E-44	0.0617	862844	0.0033	13.886	1
CAMK1D	rs2096396	intergenic_variant	10:12343629:AG	A	G	T2D	3.88E-08	-0.0243	885381	0.0034	-5.50	1

Z F P 3 6 L 2	rs76 8572 93	intron_variant	2:4 35 91 67 6: C: T	C	T	T2D	5.84E- 32	-0.0976	713514	0.006	-11.766	1
U B E 2 Z	rs46 522	non_coding_trans cript_exon_varian t	17: 46 98 85 97: C: T	C	T	T2D	2.66E- 16	0.0334	1070740	0.0029	8.188	1
H E R C 1	rs99 7252 7	upstream_gene_va riant	15: 64 12 75 31: T: C	T	C	T2D	5.58E- 09	-0.0284	1195170	0.003	-5.829	1
H	rs52	upstream_gene_va	6:3	A	T	T2D	9.63E-	0.0578	262719	0.0072	6.812	1

L A - D R B 5	9082 000	riant	25 00 74 9: A: T				12					
O N E C U T 1	rs24 5652 6	downstream_gene _variant	15: 53 08 94 42: T: C	T	C	T2D	2.14E- 08	0.0336	1199880	0.0036	5.6	1
B D N F	rs10 7676 59	intron_variant	11: 27 68 61 96: G: T	G	T	T2D	2.95E- 09	-0.0282	868949	0.0035	-5.935	1
M	rs61	upstream_gene_va	20:	T	C	T2D	1.11E-	0.03	1199890	0.0035	5.714	1

Y B L 2	9289	riant	42 29 46 13: T: C				08					
L R R C 4	rs11 6944 354	intron_variant	7:1 27 70 55 15: A: G	A	G	T2D	5.43E- 29	0.3073	191553	0.0275	11.175	1
A N K 1	rs51 6946	non_coding_trans cript_exon_varian t	8:4 15 19 24 8: T: C	T	C	T2D	2.34E- 95	0.0723	1433920	0.003	20.719	1
P 2	rs53 0394	regulatory_region _variant	12: 12	G	A	T2D	2.34E- 08	-0.3971	200348	0.0711	-5.585	1

R X 7	855		15 33 66 7: G: A									
T P C N 2	rs38 2924 1	missense_variant	11: 68 85 53 63: G: A	G	A	T2D	3.13E- 18	0.0255	1414160	0.0027	8.706	1
C Green, q<0.5												
S y m b o l	dbSNP	C o n s e q u e n c e	varID	Referenc e	Alt	Phenoty pe	Pvalue	Beta	n	stdErr	zScore	Alignme nt
P	rs1622208	sy	1:464983	A	G	T2D	1.36E-	0.0269	1178170	0.0028	6.762	1

I K 3 R 3		n o n y m o u s - v a r i a n t	75:A:G				11					
M R A S	rs1679147	in tr o n - v a r i a n t	3:138097 537:A:G	A	G	T2D	2.19E- 09	-0.0293	1089680	0.0032	-5.983	1
P	rs71304101	in	3:123969	G	A	T2D	1.19E-	-0.0841	738093	0.0052	-13.177	1

P A R G		tr o n - va ri an t	13:G:A				39					
A D C Y 5	rs11708067	in tr o n - va ri an t	3:123065 778:A:G	A	G	T2D	5.47E- 54	-0.0782	1011740	0.0034	-15.471	1
B M P R 1	rs3775057	in tr o n -	4:961177 15:G:A	G	A	T2D	6.74E- 09	-0.024	918796	0.0033	-5.797	1

B		va ri an t										
I G F 1 R	rs907801	in tr o n – va ri an t	15:99321 747:T:C	T	C	T2D	4.03E- 08	0.0336	1162050	0.0038	5.489	1
P H L P P 2	rs61733125	sy n o n y m o u s –	16:71682 796:T:C	T	C	T2D	4.23E- 10	-0.0285	967291	0.0037	-6.245	1

		va ri an t										
B D N F	rs10767659	in tr o n — va ri an t	11:27686 196:G:T	G	T	T2D	2.95E- 09	-0.0282	868949	0.0035	-5.935	1
G N A S	rs3746709	u ps tr ea m — ge ne —	20:57393 941:C:T	C	T	T2D	9.22E- 11	0.0339	884504	0.0034	6.479	1

		va ri an t										
P R K A G 3	rs78058190	u ps tr ea m - ge ne - va ri an t	2:219699 999:G:A	G	A	T2D	6.50E- 09	0.0645	514536	0.0088	5.80	1
N F K B 1	rs2866413	m is se ns e_	4:103557 077:G:A	G	A	T2D	1.74E- 09	-0.017	1292620	0.0026	-6.02	1

		va ri an t										
A N A P C 1	rs1345203	in tr o n - va ri an t	2:112253 851:T:C	T	C	T2D	9.57E- 09	-0.0292	809084	0.0043	-5.738	1
M E F 2 C	rs11286263 4	in tr o n - va ri an t	5:879703 52:G:C	G	C	T2D	2.61E- 08	0.0313	868950	0.0038	5.566	1

I R S 1	rs2673141	in te rg en ic - va ri an t	2:227159 177:G:A	G	A	T2D	6.34E- 37	0.0646	1159400	0.0032	12.695	1
F G F R 3	rs6831006	in te rg en ic - va ri an t	4:178460 5:G:C	G	C	T2D	7.73E- 34	-0.0484	801710	0.0034	-12.126	1
N F	rs3787186	in tr	20:50153 344:T:C	T	C	T2D	1.54E- 08	-0.03	1147420	0.0029	-5.657	1

A T C 2		o n - va ri an t										
C C N D 2	rs76895963	in tr o n - va ri an t	12:43848 44:T:G	T	G	T2D	5.30E- 70	-0.48	231420	0.0271	-17.687	1
L R R C 4	rs11694435 4	in tr o n - va	7:127705 515:A:G	A	G	T2D	5.43E- 29	0.3073	191553	0.0275	11.175	1

		ri an t										
D, Red top 10												
Sy mb ol	dbSNP	Consequen ce	varID	Reference	Alt	Phenoty pe	Pvalue	Beta	n	stdE rr	zScore	Align ment
MEF2C	rs112862634	intron_variant	5:87970352:G:C	G	C	T2D	2.61E-08	0.0313	868950	0.0038	5.566	1
VEGFA	rs9472138	intergenic_variant	6:43811762:C:T	C	T	T2D	1.07E-17	0.0393	1337680	0.0029	8.566	1
NFATC2	rs3787186	intron_variant	20:50153344:T:C	T	C	T2D	1.54E-08	-0.0254	1147420	0.0029	-5.657	1
GNAS	rs3746709	upstream_gene_variant	20:57393941:C:T	C	T	T2D	9.22E-11	0.0339	884504	0.0034	6.479	1
ATP2A3	rs1043246	missense_variant	17:3828086:C:G	C	G	T2D	1.12E-16	0.0429	794957	0.0044	8.292	1
B	rs3775	intron_variant	4:961177	G	A	T2D	6.74E-	-0.024	918796	0.00	-5.797	1

MP R1 B	057	ant	15:G:A				09			33		
PT CH 1	rs1051 2248	intron_vari ant	9:982597 03:T:G	T	G	T2D	1.77E- 08	-0.0255	1343780	0.00 27	-5.634	1
ET S1	rs6723 2546	non_coding _transcript_ exon_varia nt	11:12839 8938:C:T	C	T	T2D	6.48E- 17	0.0421	870912	0.00 38	8.356	1
NF KB 1	rs2866 413	missense_v ariant	4:103557 077:G:A	G	A	T2D	1.74E- 09	-0.017	1292620	0.00 26	-6.02	1
AD CY 5	rs1170 8067	intron_vari ant	3:123065 778:A:G	A	G	T2D	5.47E- 54	-0.08	1011740	0.00 34	-15.471	1
PI K3 R3	rs1622 208	synonymou s_variant	1:464983 75:A:G	A	G	T2D	1.36E- 11	0.0269	1178170	0.00 28	6.76	1
IN SR	rs8100 562	intron_vari ant	19:72415 01:C:T	C	T	T2D	7.14E- 09	0.0343	868950	0.00 4	5.788	1
AR	rs1160	5_prime_U	11:72432	G	A	T2D	1.46E-	-0.0827	1192070	0.00	-15.992	1

AP 1	3334	TR_variant	985:G:A				57			37		
IT GB 6	rs7770 4424	intron_vari ant	2:161144 079:T:C	T	C	T2D	1.12E- 08	-0.0468	532655	0.00 64	-5.712	1
SL C2 A2	rs9873 618	intron_vari ant	3:170733 076:G:A	G	A	T2D	1.18E- 18	-0.0427	868949	0.00 35	-8.817	1
LD HB	rs6659 2830	intron_vari ant	12:21834 560:C:A	C	A	T2D	2.93E- 10	-0.0321	824965	0.00 4	-6.302	1
AT P2 A1	rs1164 2449	intron_vari ant	16:28896 015:C:T	C	T	T2D	3.66E- 08	0.0256	958651	0.00 34	5.507	1
CA M K2 B	rs1169 13033	non_coding _transcript_ exon_varia nt	7:443655 49:C:T	C	T	T2D	2.74E- 09	-0.0414	733069	0.00 49	-5.946	1
CA SR	rs6438 717	intron_vari ant	3:121971 296:A:G	A	G	T2D	1.76E- 08	-0.0475	385000	0.00 59	-5.634	1
TF RC	rs9872 347	intergenic_ variant	3:195831 237:T:C	T	C	T2D	1.92E- 11	0.0313	866263	0.00 34	6.712	1
AN	rs1345	intron_vari	2:112253	T	C	T2D	9.57E-	-0.0292	809084	0.00	-5.738	1

AP C1	203	ant	851:T:C				09			43		
LA M A1	rs1245 4658	intron_vari ant	18:70760 61:C:A	C	A	T2D	9.01E- 12	0.0326	868948	0.00 32	6.822	1
EP 30 0	rs4822 005	intron_vari ant	22:41514 155:G:A	G	A	T2D	6.45E- 10	0.0241	916933	0.00 32	6.179	1
EP HA 3	rs6776 967	intergenic_ variant	3:900250 22:C:T	C	T	T2D	7.80E- 11	0.0276	896908	0.00 36	6.504	1
BC L2	rs1245 4712	intron_vari ant	18:60845 884:T:C	T	C	T2D	2.16E- 19	-0.0397	1138370	0.00 29	-9.005	1
IT GA 1	rs3583 3945	intergenic_ variant	5:517546 35:A:G	A	G	T2D	4.51E- 09	-0.0245	868950	0.00 31	-5.864	1
HL A- DQ B1	rs5544 48117	upstream_g ene_variant	6:326239 43:C:T	C	T	T2D	7.05E- 10	0.0404	296583	0.00 65	6.165	1
GC K	rs2268 574	intron_vari ant	7:441893 21:A:G	A	G	T2D	3.43E- 20	0.0358	1016870	0.00 3	9.205	1

PD E3 B	rs1177 20468	intron_vari ant	11:14731 666:G:C	G	C	T2D	4.57E- 09	0.1247	240274	0.02 16	5.862	1
IR S1	rs2673 141	intergenic_ variant	2:227159 177:G:A	G	A	T2D	6.34E- 37	0.0646	1159400	0.00 32	12.695	1
CC ND 1	rs3918 298	intron_vari ant	11:69463 273:G:A	G	A	T2D	2.69E- 15	-0.1086	466381	0.01 47	-7.904	1
PL CD 3	rs1294 6454	intron_vari ant	17:43208 121:A:T	A	T	T2D	7.67E- 09	0.0175	1291080	0.00 29	5.775	1
CC ND 2	rs7689 5963	intron_vari ant	12:43848 44:T:G	T	G	T2D	5.30E- 70	-0.48	231420	0.02 71	-17.69	1
SG CG	rs3148 79	intergenic_ variant	13:23309 382:C:T	C	T	T2D	3.86E- 09	-0.0345	895537	0.00 41	-5.89	1
PR KA G3	rs7805 8190	upstream_g ene_variant	2:219699 999:G:A	G	A	T2D	6.50E- 09	0.0645	514536	0.00 88	5.803	1
KL	rs5766 74	intergenic_ variant	13:33554 302:G:A	G	A	T2D	1.71E- 24	-0.053	1303950	0.00 35	-10.214	1
AN		intron_vari	12:12182	T	C	T2D	3.61E-	0.2716	183379	0.04	5.509	1

AP C5		ant	2670:T:C				08			93		
KC NQ 1	rs2283 164	intron_vari ant	11:25791 63:A:G	A	G	T2D	1.34E- 12	-0.0733	878113	0.00 72	-7.09	1
HL A- DQ A1	rs5745 76046	downstrea m_gene_va riant	6:326190 99:A:T	A	T	T2D	7.58E- 15	0.05	296583	0.00 61	7.774	1
IG F1 R	rs9078 01	intron_vari ant	15:99321 747:T:C	T	C	T2D	4.03E- 08	0.0336	1162050	0.00 38	5.489	1
VA V2	rs5592 3934	upstream_g ene_variant	9:136888 233:C:G	C	G	T2D	2.25E- 08	0.024	813694	0.00 33	5.591	1
LR RC 4	rs1169 44354	intron_vari ant	7:127705 515:A:G	A	G	T2D	5.43E- 29	0.3073	191553	0.02 75	11.175	1
AD RB 1	rs7076 938	regulatory_ region_vari ant	10:11578 9375:C:T	C	T	T2D	1.19E- 10	-0.0222	1338300	0.00 29	-6.44	1
PP AR	rs7130 4101	intron_vari ant	3:123969 13:G:A	G	A	T2D	1.19E- 39	-0.0841	738093	0.00 52	-13.18	1

G												
HL A- A	rs1169 19347	upstream_g ene_variant	6:299644 62:A:G	A	G	T2D	3.17E- 08	-0.0849	310710	0.01 21	-5.532	1
HL A- DR B1	rs5576 73768	downstrea m_gene_va riant	6:325449 01:T:C	T	C	T2D	3.71E- 11	0.055	217602	0.00 75	6.615	1
KI F5 C		3_prime_U TR_variant	2:149544 648:GA: G	GA	G	T2D	1.79E- 08	0.0421	330261	0.00 54	5.631	1
FG FR 3	rs6831 006	intergenic_ variant	4:178460 5:G:C	G	C	T2D	7.73E- 34	-0.0484	801710	0.00 34	-12.13	1
HL A- DR B5	rs5290 82000	upstream_g ene_variant	6:325007 49:A:T	A	T	T2D	9.63E- 12	0.0578	262719	0.00 72	6.812	1
AG AP 5	rs2894 040	intron_vari ant	10:75478 159:A:C	A	C	T2D	3.84E- 08	0.026	908766	0.00 33	5.498	1
CH	rs1810	intron_vari	20:32437	C	T	T2D	1.49E-	0.0245	868947	0.00	5.662	1

MP 4B	534	ant	142:C:T				08			33		
E, Blue top 10												
Symb ol	db SN P	Consequen ce	varID	Referenc e	Alt	Phenotype	Pvalue	Beta	n	stdErr	zScore	A li g n m e nt
PTC H1	rs1 05 12 24 8	intron_vari ant	9:982597 03:T:G	T	G	T2D	1.77E- 08	-0.0255	13437 80	0.0027	-5.634	1
CAM K2B	rs1 16 91 30 33	non_coding _transcript_ exon_varia nt	7:443655 49:C:T	C	T	T2D	2.74E- 09	-0.0414	73306 9	0.0049	-5.946	1
ATP 2A1	rs1 16	intron_vari ant	16:28896 015:C:T	C	T	T2D	3.66E- 08	0.0256	95865 1	0.0034	5.507	1

	42 44 9											
BMP R1B	rs3 77 50 57	intron_vari ant	4:961177 15:G:A	G	A	T2D	6.74E- 09	-0.024	91879 6	0.0033	-5.797	1
ITGB 6	rs7 77 04 42 4	intron_vari ant	2:161144 079:T:C	T	C	T2D	1.12E- 08	-0.0468	53265 5	0.0064	-5.712	1
PCG F3	rs7 32 21 12 6	missense_v ariant	4:727695: A:C	A	C	T2D	6.79E- 15	0.096	63086 0	0.0108	7.788	1
GNA S	rs3 74 67 09	upstream_g ene_variant	20:57393 941:C:T	C	T	T2D	9.22E- 11	0.0339	88450 4	0.0034	6.479	1
EPH	rs6	intergenic_	3:900250	C	T	T2D	7.80E-	0.0276	89690	0.0036	6.504	1

A3	77 69 67	variant	22:C:T				11		8			
ATP 2A3	rs1 04 32 46	missense_v ariant	17:38280 86:C:G	C	G	T2D	1.12E- 16	0.0429	79495 7	0.0044	8.292	1
DUS P9	rs4 89 84 31	intergenic_ variant	X:152896 969:T:G	T	G	T2D	2.98E- 70	-0.0724	16509 3	0.0048	-17.719	1
LAM A1	rs1 24 54 65 8	intron_vari ant	18:70760 61:C:A	C	A	T2D	9.01E- 12	0.0326	86894 8	0.0032	6.822	1
NFA TC2	rs3 78 71 86	intron_vari ant	20:50153 344:T:C	T	C	T2D	1.54E- 08	-0.0254	11474 20	0.0029	-5.657	1
ZFH X3	rs6 41	downstrea m_gene_va	16:73100 308:C:T	C	T	T2D	1.26E- 09	-0.0253	86296 5	0.0033	-6.072	1

	67 49	riant										
PRK AG3	rs7 80 58 19 0	upstream_g ene_variant	2:219699 999:G:A	G	A	T2D	6.50E- 09	0.0645	51453 6	0.0088	5.803	1
PIK3 R3	rs1 62 22 08	synonymou s_variant	1:464983 75:A:G	A	G	T2D	1.36E- 11	0.0269	11781 70	0.0028	6.762	1
CDK N2B	rs2 38 32 08	regulatory_ region_vari ant	9:221320 76:A:G	A	G	T2D	1.09E- 176	-0.136	13190 60	0.0032	-28.341	1
ETS1	rs6 72 32 54 6	non_coding _transcript_ exon_varia nt	11:12839 8938:C:T	C	T	T2D	6.48E- 17	0.0421	87091 2	0.0038	8.356	1
MRA S	rs1 67	intron_vari ant	3:138097 537:A:G	A	G	T2D	2.19E- 09	-0.0293	10896 80	0.0032	-5.983	1

	91 47											
ZFP3 6L2	rs7 68 57 29 3	intron_vari ant	2:435916 76:C:T	C	T	T2D	5.84E- 32	-0.0976	71351 4	0.006	-11.766	1
ONE CUT 1	rs2 45 65 26	downstrea m_gene_va riant	15:53089 442:T:C	T	C	T2D	2.14E- 08	0.0336	11998 80	0.0036	5.6	1
MYB L2	rs6 19 28 9	upstream_g ene_variant	20:42294 613:T:C	T	C	T2D	1.11E- 08	0.03	11998 90	0.0035	5.71	1
LRR C4	rs1 16 94 43 54	intron_vari ant	7:127705 515:A:G	A	G	T2D	5.43E- 29	0.3073	19155 3	0.0275	11.175	1
ANK 1	rs5 16	non_coding _transcript_	8:415192 48:T:C	T	C	T2D	2.34E- 95	0.0723	14339 20	0.003	20.719	1

	94 6	exon_variant										
F, Green top 10												
Symbol	dbSNP	Consequence	varID	Reference	Alt	Phenotype	Pvalue	Beta	n	stdErr	zScore	Alignment
PIK3R3	rs1622208	synonymous_variant	1:46498375:A:G	A	G	T2D	1.36E-11	0.0269	1178170	0.0028	6.762	1
MRAS	rs1679147	intron_variant	3:138097537:A:G	A	G	T2D	2.19E-09	-0.0293	1089680	0.0032	-5.983	1
PPARG	rs71304101	intron_variant	3:12396913:G:A	G	A	T2D	1.19E-39	-0.0841	738093	0.0052	-13.177	1
ADCY5	rs11708067	intron_variant	3:123065778:A:G	A	G	T2D	5.47E-54	-0.0782	1011740	0.0034	-15.471	1
BMPR1B	rs3775057	intron_variant	4:96117715:G:A	G	A	T2D	6.74E-09	-0.024	918796	0.0033	-5.797	1
IGF1R	rs907801	intron_variant	15:99321747:T:C	T	C	T2D	4.03E-08	0.0336	1162050	0.0038	5.489	1
PHLPP2	rs61733125	synonymous_variant	16:71682796:T:C	T	C	T2D	4.23E-10	-0.028	967291	0.0037	-6.245	1

								5				
BDNF	rs10767659	intron_variant	11:27686196:G:T	G	T	T2D	2.95E-09	-0.0282	868949	0.0035	-5.935	1
GNAS	rs3746709	upstream_gene_variant	20:57393941:C:T	C	T	T2D	9.22E-11	0.0339	884504	0.0034	6.48	1
PRKAG3	rs78058190	upstream_gene_variant	2:219699999:G:A	G	A	T2D	6.50E-09	0.0645	514536	0.0088	5.803	1
NFKB1	rs2866413	missense_variant	4:103557077:G:A	G	A	T2D	1.74E-09	-0.017	1292620	0.0026	-6.02	1
ANAPC1	rs1345203	intron_variant	2:112253851:T:C	T	C	T2D	9.57E-09	-0.0292	809084	0.0043	-5.738	1
IRS1	rs2673141	intergenic_variant	2:227159177:G:A	G	A	T2D	6.34E-37	0.06	1159400	0.0032	12.695	1
FGFR3	rs6831006	intergenic_variant	4:1784605:G:C	G	C	T2D	7.73E-34	-0.0484	801710	0.0034	-12.126	1
CCND2	rs76895963	intron_variant	12:4384844:T:G	T	G	T2D	5.30E-70	-0.48	231420	0.0271	-17.687	1

