Table S8. Targets of the retro-miRs

KEGG URL	KEGG.pathway	n.genes	total.genes	perc.genes	fold.enrichment	FDR	genes
http://www.genome.jp/kegg-bin/show_pathway?hsa04712	Circadian rhythm	18	31	48.39%	2.26915	1.12E-02	FBXL3 CRY1 PER2 RORA FBXW11 PRKAB1 SIK1 CREB1 CRY2 PER3 CLOCK PRKAA2 BTRC PER1 CSNK1E
http://www.genome.jp/kegg-bin/show_pathway?hsa05219	Bladder cancer	17	41	41.46%	1.94446	2.41E-02	DAPK2 ARAF MAPK1 E2F1 E2F3 CDKN1A MAP2K2 KRAS MYC EGF TP53 EGFR CDKN2A BRAF CXCL8 DAPK1 NRAS
http://www.genome.jp/kegg-bin/show_pathway?hsa04520	Adherens junction	29	71	40.85%	1.91546	4.34E-03	VCL CTNNA1 RHOA SORBS1 MAPK1 CSNK2A1 MET WASL TGFBR1 SSX2IP PTPRB RAC2 WASF3 MAPK3K7 IQGAP1 SMAD4 MAPK1 ACP1 EGFR PARD3 TCF7L2 ITGB1B2 INSR NECTIN3 CTNNA3 CTNND1
http://www.genome.jp/kegg-bin/show_pathway?hsa04730	Long-term depression	24	60	40.00%	1.87583	1.12E-02	IGF1 GNAQ ARAF GNAS NOS1 MAPK1 PPP2R1A PPP2CA GRIA2 ITPR2 MAP2K2 KRAS PPP3R1B IGF1R GNAI2 PLCB3 GUCY1A2 GRM1 BRAF GUCY1A1 PLCB1 PLA2G4E NRAS LYN
http://www.genome.jp/kegg-bin/show_pathway?hsa05210	Colorectal cancer	34	86	39.53%	1.83402	2.91E-03	BAK1 MAPK9 PIK3CB RHOA ARAF GSK3B MAPK1 TGFBR1 MSH3 MSH6 PIK3CA CDKN1A MAP2K2 RAC2 CASP9 KRAS MYC EGF TP53 SMAD4 PIAS4*1 EGFR TCF7L2 TCF7L1 AFAP1 BRAF TGFA TGFBR2 FOS BCL2 CYCS SMAD2 JUN NRAS
http://www.genome.jp/kegg-bin/show_pathway?hsa05218	Melanoma	28	72	38.89%	1.82372	1.03E-02	IGF1 BAK1 PIK3CB FGF10 ARAF MAPK1 E2F1 FGF9 CDK6 MET E2F3 PIK3CA CDKN1A MAP2K2 KRAS FGF5 EGF FGF7 IGF1R TP53 PDGFC EGFR CDKN2A BRAF PDGFD FGF3 MITF NRAS
http://www.genome.jp/kegg-bin/show_pathway?hsa04917	Prolactin signaling pathway	26	70	37.14%	1.74184	1.72E-02	MAPK9 PIK3CB GSK3B ESR1 JAK2 MAPK1 MAPK14 PRLR CSN1 SOCS2 PIK3CA STAT5A MAP2K2 KRAS ELF5 LHCGR ESR2 TNFRSF11A SHC3 MAPK13 SLC2A2 STAT3 FOS SOCS6 SOCS4 NRAS
http://www.genome.jp/kegg-bin/show_pathway?hsa01524	Platinum drug resistance	27	73	36.99%	1.73493	1.58E-02	ERCC1 BID FAS BAK1 PIK3CB MSH2 MAPK1 XIAP MSH3 MSH6 PIK3CA ATP7B CDKN1A CASP9 GSTM5 GSTM3 PDHA1 TP53 PIAK3*1 MSH73 CDKN2A ATM ATP7A POLH BCL2L1 BCL2 CYCS
http://www.genome.jp/kegg-bin/show_pathway?hsa04150	PI3 signaling pathway	27	73	36.99%	1.73450	1.58E-02	BID IGF1 FAS RRAS2B TP73 CD82 TNFRSF10A CDK6 SERPINE1 CCND3 CDKN1A CASP9 CCNG2 TP53 PIAK3*1 IGF2P3 CDKN2A SESN3 ATM CHEK1 PPM1D BCL2L1 BCL2 RRAS CYCS CCNE2 MDM4
http://www.genome.jp/kegg-bin/show_pathway?hsa05220	Chronic myeloid leukemia	28	76	36.84%	1.72774	1.52E-02	BAK1 PIK3CB ARAF ABL1 CRKL MAPK1 E2F1 CDK6 TGFBR1 CBL E2F3 PIK3CA CDKN1A STAT5A MAP2K2 KRAS MYC TP53 SMAD4 CDKN2A SHC3 BRAF CTBP1 TGFBR2 BCL2L1 CTBP2 HDAC2 NRAS
http://www.genome.jp/kegg-bin/show_pathway?hsa04141	Protein processing in endoplasmic reticulum	62	169	36.69%	1.72043	3.19E-04	BAK1 HSPA5 MAPK9 EIF2AK2 SEC61A1 SEC61A2 ATXN3 DNAJA2 UBE2D1 DERL2 UMAH1 DNAJC10 UBE2D4 SARA HSPA8AH EIF2AK1 ERO1B PPP5R1A NSFL1C ERP29 XBP1 SEC23A TUSC1 USE2D3 MANH1A1 BAG2 SKP1 SEC24A SSR2 FBXO2 ATF6 RPN2 HSPH1 ATXN3L SSR1 HSPA2 TRAF2 EDEM1 UBQLN1 CHAP4 UGGT1 FLAA SEC24B RNF185 MSTP51 MARCH6 DNAJB12 HSPH4L HSPA5B1 PDIA3 UBAN2 BCL2 HSPA5 UBXN2A ERN1 CALR YOD1 NPLOC4 UBQLN2 ERO1A MANK1A2 SVIP
http://www.genome.jp/kegg-bin/show_pathway?hsa04512	Endometrial cancer	21	58	36.21%	1.69766	4.07E-02	BAK1 CTNNA1 PIK3CB ARAF GSK3B MAPK1 PIK3CA CDKN1A MAP2K2 CASP9 KRAS MYC EGF PDPK1 TP53 EGFR TCF7L2 TCF7L1 BRAF CTNNA3 NRAS
http://www.genome.jp/kegg-bin/show_pathway?hsa05221	Acute myeloid leukemia	24	67	35.82%	1.67965	3.25E-02	PIK3CB ARAF RUNX1T1 MAPK1 PIM2 ZBTB16 PPARD PIK3CA STAT5A MAP2K2 FER2 KRAS MYC DUSP6 PML CCNA2 TCF7L2 TCF7L1 KIT BRAF STAT3 JUP EIF4EBP1 NRAS
http://www.genome.jp/kegg-bin/show_pathway?hsa01522	Endocrine resistance	34	95	35.79%	1.67837	1.13E-02	IGF1 MAPK9 PIK3CB ARAF ADCY2 GNAS ESR1 MAPK1 JAG1 E2F1 MAPK14 E2F3 ADCY7 PIK3CA CDKN2C CDKN1A MAP3K2 KRAS NOTCH2 ESR2 IGF1R TP53 EGFR CDKN2A SHC3 MAPK13 BRAF ADCY1 FOS BCL2 JUN JAG2 SP1 NRAS
http://www.genome.jp/kegg-bin/show_pathway?hsa05212	Pancreatic cancer	27	76	35.53%	1.66603	2.51E-02	BAK1 MAPK9 PIK3CB PLD1 ARAF MAPK1 E2F1 CDK6 TGFBR1 E2F3 PIK3CA CDKN1A RAC2 ARHGEF6 CASP9 KRAS EGF TP53 SMAD4 EGFR CDKN2A BRAF TGFA TGFBR2 STAT3 BCL2L1 SMAD2
http://www.genome.jp/kegg-bin/show_pathway?hsa05206	MicroRNAs in cancer	57	161	35.40%	1.66028	1.29E-03	CD44 BAK1 PIK3CB RHOA ROCK1 HDAC4 TP63 ABCB1 E2F6 ABL1 CRKL MAPK1 DICER1 E2F1 UBE2I BMF FZD3 CDK6 MET E2F3 FOXP1 TNR DNMT3A TNN PIK3CA CDKN1A MAP2K2 BCL2L2 PAK4 KRAS NOTCH2 MYC RDX SLC7A1 TP53 MCL1 EPAS1 EGFR CDC42 CDKN2A ATM HMGA2 WNT3A MMP16 IGF2BP1 STAT3 IRS1 ZEB2 ZFPM2 BCL2 CCND2 EPAS1 HDAC2 MDM4 TRIM71 NRAS ITGB3
http://www.genome.jp/kegg-bin/show_pathway?hsa05414	Arrhythmogenic right ventricular cardiomyopathy	27	77	35.06%	1.64439	2.98E-02	ITGA3 CACNG3 CTNNA1 DSG2 PKP2 CACNB1 ATP2A1 ITGB5 SLC8A3 ITGB8 SGCA ITGA4 CACNG8 ITGA9 TCF7L2 TCF7L1 CACNA1D CACNB2 CACNG2 SGCD JUP ATP2A2 CACNB4 SLC9A1 CTNNA3 LAMA2 ITGB3
http://www.genome.jp/kegg-bin/show_pathway?hsa05215	Prostate cancer	34	97	35.05%	1.64377	1.48E-02	IGF1 PIK3CB ARAF HSP90AA1 GSK3B MAPK1 E2F1 E2F3 CREB1 PIK3CA CDK2 CDKN1A MAP2K2 CASP9 KRAS EGF IGF1R PDPK1 TP53 PDGFC EGFR TCF7L2 MMP9 TCF7L1 BRAF TGFA SPINT1 HSPA8B1 AR PDGFD BCL2 CCND2 CREB3L2 NRAS
http://www.genome.jp/kegg-bin/show_pathway?hsa05223	Non-small cell lung cancer	25	72	34.72%	1.62832	3.92E-02	BAK1 PIK3CB ARAF MAPK1 STK4 E2F1 CDK6 MET E2F3 PIK3CA CDKN1A STAT3A MAP2K2 CASP9 KRAS EGF PDPK1 TP53 EGFR CDKN2A BRAF TGFA STAT3 KIF5B NRAS
http://www.genome.jp/kegg-bin/show_pathway?hsa05202	Transcriptional misregulation in cancer	66	192	34.38%	1.61204	1.09E-03	ETV1 PAX7 IGF1 BAK1 TRAF1 CDK14 HOXA9 RUNX1T1 MEF2C CCNT2 SIX4 FLT1 EVI1 DOT1L MET DDX5 NSD2 KLF3 ZBTB16 NRIP3 CDKN2C ATF1 CDKN1A RUNX2 MAX BCL11B CCNT1 PER2 HG-3B MEN1 LMO2 CDK9 MYC BMP2K ETV6 DUSP6 IGF1R PML NCOR1 SIX6 TP53 MEIS1 CCNA2 IGFBP3 ATM HMGA2 MMP3 ELK4 REL TGFBR2 HPGD SPINT1 SIN3A CXCL8 BCL2L1 MLLT3 AFF1 JUP MLF1 MAF SP1 PDX1 MITF SUPT3H HDAC2 HDC10
http://www.genome.jp/kegg-bin/show_pathway?hsa04211	Rap1 signaling pathway	72	210	34.29%	1.60765	6.22E-04	IGF1 MAPK9 FLT4 PIK3CB GNAI3 RHOA FGF10 ARB2HYP ADCY2 WASL GNAS ANGPT2 CSNL MAPK1 ANGPT4 FGF9 FLT1 PRKD2 MET MAP2K6 RAPGEF3 MAPK14 PIK3CI RAP1A CNR1 ADCY7 PIK3CA VASP MAP2K2 RAP1B RAC2 KRAS RAPGEF5 FGF5 EGF FGF7 IGF1R EPHA3 PDGFC EGFR LPAR4 PARD3 PLCB3 RASGRP3 ANGPT1 EPHA1 MAPK13 KIT BRAF VAV2 PRKCI ADCY1 FGFR1 PDGFD INSR LPAR3 TLN2 F2R PLCB1 GRIN2A PRKD1 EPHA3 LPAR5 FGF3 MAGI2 SVIL SIPA1L1 CTNND1 CALM1 NRAS ITGB3 GRIN2B
http://www.genome.jp/kegg-bin/show_pathway?hsa01521	EGFR tyrosine kinase inhibitor resistance	27	79	34.18%	1.60276	3.82E-02	IGF1 PIK3CB ARAF GSK3B JAK2 MAPK1 MET GAB1 PIK3CA MAP3K2 KRAS EIF4E2 EGF IGF1R PDGFC EGFR SHC3 EIF4E BRAF TGFA STAT3 PDGFD BCL2L1 BCL2 EIF4EBP2 EIF4EBP1 NRAS
http://www.genome.jp/kegg-bin/show_pathway?hsa04110	Cell cycle	43	126	34.13%	1.60041	1.06E-02	CCNT2 CBFA CABC1A MCM6 CDC14B GSK3B CDC6 CDC20 ABL1 CDC7 E2F1 E2F3 CDK6 CCNE3 CDKN1A PKMYT1 PCNA MYC TP53 ANAPC11 SMAD4 CCNA2 CDKN2A ATM CHEK1 BUB3 RAD21 ORC5 ANAPC16 WEE1 YWHAB BUB1 YWHAG CDK1 CCNE2 SMAD2 HDAC2
http://www.genome.jp/kegg-bin/show_pathway?hsa04140	Autophagy	48	141	34.04%	1.59645	6.74E-03	CFLAR LAMP3 SRA1D DAPK2 MAPK9 PIK3CB VMP1 ATG2B PIK3C3 SH3GLB1 SNAP29 MAPK1 MTMR3 PPP2CA RRAGC PIK3CA ATG4C ATG14 MAP3K2 RB1 KRAS MAP3K7 TAB1 IGF1R MAP1LC3B PDPK1 ATG3 ISL BCN ATG12 CSnrf2 DEPTOR RRAGA PRKAA2 WDR41 TSC1 ZFYVE1 RAB8A ATG16L2 IRS1 BCL2L1 BCL2 TRAF6 BNIP3 ERN1 HMGB1 PIK3R4 DAPK1 NRAS
http://www.genome.jp/kegg-bin/show_pathway?hsa05224	Breast cancer	50	147	34.01%	1.59509	6.45E-03	IGF1 BAK1 FLT4 PIK3CB FGF10 ARAF PGR GSK3B WNT1 ESR1 MAPK1 JAG1 E2F1 FGF9 FZD3 CDK6 E2F3 CSNK1A1 PIK3CA CDKN1A MAP2K2 KRAS WNT3B NOTCH2 HEY2 MYC FGF5 EGF ISG2 FGF7 IGF1R TP53 EGFR SHC3 TCF7L2 TCF7L1 WNT3A WNT7A KIT BRAF WNT4 HEY1 FZD6 ROS FZD8 JUN JAG2 SP1 FGF3 NRAS
http://www.genome.jp/kegg-bin/show_pathway?hsa05226	Gastric cancer	50	148	33.78%	1.58401	8.72E-03	BAK1 CTNNA1 PIK3CB FGF10 ARAF GSK3B ABCB1 WNT1 MAPK1 E2F1 FGF9 FZD3 MET TGFBR1 GAB1 E2F3 CSNK1A1 PIK3CA CDK2 CDKN1A MAP2K2 KRAS RECQL WNT3B MYC FGF5 EGF FGF7 TP53 SMAD4 EGFR SHC3 TCF7L2 TCF7L1 WNT3A WNT7A BRAF WNT4 TGFBR2 SHH FZD6 CDH2 BCL2 JUP CCND2 SMAD2 FZD8 CTNNA3 FGF3 NRAS
http://www.genome.jp/kegg-bin/show_pathway?hsa04360	Axon guidance	61	181	33.70%	1.58048	2.54E-03	SEMA3F PIK3CB GNAI3 RHOA ROCK1 EPHA8 TRPC5 SEMA3C PLXNA2 PAK3 SEMA3B GSK3B SEMA4G ABL1 NRP1 MAPK1 MAPK7 BMP7 FZD3 MET CXCL12 UNC5B SEMA5A PIK3CA CXCR4 RAC2 PAK4 TRPC4 KRAS EPHA7 ROS3 EPHA3 DCF7 SLIT2 EPHA5 RASA1 PARD3 ENAH UNC5D WNT4 NTNG1 PLXNB1 SHH CFL2 SEMA6C ROBO1 SSH3 ABLIM3 SLIT3 EFNA5 ROBO2 PTCH1 PPP3R2 SRGAP3 ARHGEF12 SRGAP1 LRG2 NRAS PPP3R1 PLXNA4
http://www.genome.jp/kegg-bin/show_pathway?hsa04975	Choline metabolism in cancer	33	98	33.67%	1.57914	2.01E-02	MAPK9 PIK3CB DGKG SLC44A1 PLD1 MAPK1 DGKA SLC22A2 LYPLA1 PIK2CA MAP2K2 RAC2 SLC44A2 WASF3 KRAS DGKB EGF PDPK1 DGKQ PDGFC EGFR DGKE DGKI PCYT1A TSC1 FOS PIGF2I SLCO2A1 JUN SP1 EIF4EBP1 PLA2G4E NRAS
http://www.genome.jp/kegg-bin/show_pathway?hsa04934	Cushing syndrome	52	155	33.55%	1.57328	6.70E-03	GNAI3 ADCY2 GSK3B WNT1 GNAS MAPK1 CACNA1I E2F1 FZD3 CDK6 CSHR2 AHR E2F3 ATF2 RAP1A CREB1 ADCY7 CDKN2C ITPR2 CDKN1A MAP3K2 RAP1B PDE1A ARL1 ASIG5L MEN1 WNT3B ARMC5 NCSH1 EGFR CDKN2A TCF7L2 PLCB3 TCF7L1 WNT3A WNT7A CACNA1D BRAF WNT4 ADCY1 FZD6 KMT2D CCND2 FZD8 CREB3L2 PLCB1 SP1 PDX1 CACNA1H WDR5B HSD3B1 CRAI1
http://www.genome.jp/kegg-bin/show_pathway?hsa04014	Ras signaling pathway	28	84	33.33%	1.56319	4.34E-02	MAPK9 PIK3CB PAK3 ARAF GSK3B ABL1 CRKL MAPK1 GAB1 CBL PIK3CA CDKN1A STAT5A MAP2K2 PAK4 KRAS MYC EGF ABL2 EGFR SHC3 BRAF TGFA NRG4 JUN ERBB4 EIF4EBP1 NRAS
http://www.genome.jp/kegg-bin/show_pathway?hsa00230	Purine metabolism	42	126	33.33%	1.56319	1.42E-02	ENPP4 AK2 RRM2B ADCY2 ADA2 PDE4D PDE1A NT5C1A ADCY7 PNCS PPAT PDE7A NTPCR ENTPD1 ATIC AK3 PDE3B GUCY1A2 PDE1C AK9 DCK PDE8D AK4 GMPS GUCY1A1 ADCY1 NUDT2 NUDT5 RRM1 ENTPD3 ADPRM NUDT9 PDE7B RRM2 NME6 PDE3A PRA5 ENTPD5 ENPP1 PNP PDE7A ADSL
http://www.genome.jp/kegg-bin/show_pathway?hsa04350	TGF-beta signaling pathway	31	93	33.33%	1.56319	3.41E-02	DCN RHOA ROCK1 BAMBI MAPK1 BMP7 SMAD7 PPP2R1A TGFBR1 SMURF2 SKP1 PPP2CA SMAD5 ACVR2B SMPB6 TGIF2 SMAD9 ACVR2A PMCD BMP2 MYC PPP2R1B SMAD6 SMAD4 GDF7 TGFBR2 PITX2 FBN1 RHAB2 SMAD2 SP1
http://www.genome.jp/kegg-bin/show_pathway?hsa04611	Platelet activation	41	124	33.06%	1.55058	1.58E-02	BTK PIK3CB PPP1R12A GNAI3 RHOA ROCK1 ARB6HYP ADCY2 GNAS SNAP23 PTGS1 MAPK1 MAPK14 RAP1A ADCY7 PIK3CA ITPR2 VASP RAP1B PIK3R3 FCGR2A PLCB3 GUCY1A2 MAPK13 ARHGAP35 PRKCI GUCY1A1 COL1A2 ADCY1 NOS3 PSTP1 TLN2 RASGRP1 F2R PLCB1 PPP1CC PLA2G4E ARHGEF12 LYN ITGB3 ORAI1
http://www.genome.jp/kegg-bin/show_pathway?hsa04071	Sphingolipid signaling pathway	39	119	32.77%	1.53692	2.22E-02	BID MAP3K9 PIK3CB GNAI3 TNFRSF1A RHOA ROCK1 PPP3CA PLD1 PPP2R5C SPTLC1 MAPK1 SPTLC2 PPP2R1A MAPK14 PPP3CA PIK3CA MAP3K2 TRAF2 RAC2 KRAS PPP2R5B PDPK1 TP53 CERS2 GNAI2 PLCB3 PPP2R5E CERS3 MAPK13 SGPP2 NOS3 SPHK2 CERS6 SPTLC3 ACER2 PLCB1 NRAS S1PR3
http://www.genome.jp/kegg-bin/show_pathway?hsa05168	Herpes simplex virus 1 infection	162	466	32.73%	1.53477	5.98E-07	ZNF195 ZNF200 BID ZNF382 CD74 FAS BAK1 PIK3CB EIF2AK2 SP100 TNFRSF1A ZNF316 TRAF3 ZNF324 EIF2AK1 SIRPA1 JAK2 SRSF5 ZNF175 OAS3 OAS2 EIF2B1 HDAC2 SRSF3 SRSF7 EIF2B2 ZNF846 PIL5B PIK3CA SRSF6 TNFSF14 TRAF2 ZNF426 ZNF331 ZNF227 ZNF141 TRAF3 ZNF34A OASPB MAP3K7 SRSF1 ZFP37 ZNF189 PML ZSCAN32 TP53 IFNAR1 ZNFX14 POU2F1 RBAK ZNF167 IFNAR6 ZNF547 ZNF773 ZNF886 ZNF19 ZNF230 ZNF222 ZNF208 ZNF333 SRSF2 ZNF577 ZNF589 TLR3 CGAS ZNF12 TSC1 PDIA3 ZNF91 ZNF23 ZNF226 ZNF561 ZNF328 ZNF283 ZNF597 ZNF77
http://www.genome.jp/kegg-bin/show_pathway?hsa04218	Cellular senescence	51	156	32.69%	1.53313	1.06E-02	MRE11 MAPK9 PIK3CB HIPK2 FBXW11 TRP67 MAPK1 E2F1 CDK6 SERPINE1 TGFBR1 MAP2K6 HIPK3 MAPK14 E2F3 CCND3 RAD1 PIK3CA ITPR2 CDK2 CDKN1A MAP3K2 KRAS MYC TP53 CCNA2 IGFBP3 CDKN2A ATM CHEK1 SLC35A4 ZFP36L2 MAPK13 CACNA1D RBBP4 MAPKAPK2 TGFBR2 TSC1 BTRC CXCL8 CDK1 CCNE2 SMAD2 LIN9 PPP1CC EIF4EBP1 PPP3R2 LIN54 CALM1 NRAS PPP3R1
http://www.genome.jp/kegg-bin/show_pathway?hsa04370	MAPK signaling pathway	96	294	32.65%	1.53129	3.19E-04	CACNG3 PPP5C MAPK9 IGF1 FAS MAP3K3 FLT4 MAPK9 RASGRF1 TNFRSF1A CACNB1 FGF10 MAPK14 RPS6KA2 RPS6KA6 ARAF MECP2C MAP3K9 ANGPT2 MKNK2 CSNL MAPK1 CACNA1I PTK7A STK4 ANGPT4 FGF9 FLT1 MET TGFBR1 DUSP3 MAP2K6 RAPGEF2 MAPK14 RASGRF2 MAPK3K3 ATF2 RAP1A MAX HSPA2 MAP3K2 TRAF2 RAF1B RAC2 KRAS MAP3K7 MYC ARRB1 PTK61B FGF5 EGF DUSP8 FGF7 IGF1R TP53 CACNG8 EFNA3 PDGFC RASA1 GNA12 EGFR NTRK3 TAOK2 RASGRP3 PTPRR ANGPT1 MAPK13 CACNA1D KIT BRAF ELK4 TAOK1 MAPKAPK2 TGFA TGF1
http://www.genome.jp/kegg-bin/show_pathway?hsa05160	Ubiquitin mediated proteolysis	46	141	32.62%	1.52960	1.42E-02	CDC27 PIAS1 NEDD4 UBE2I 3KO8TB3 FBXW11 UBE2K UBE2D4 CDC23 CDC16 XIAP MGRN1 UBE2I ELOB UBE2M FZR1 UBE2R2 UBE2S TRIM37 SMURF2 UBE2D3 FBXW7 UBE4A CUL SKP1 FBXO3 YHL UBE2Q2 PML ANAPC11 HERC4 UBC TBP12 ELOC UBE3A CUL4B BTRC ANAPC16 UBE2E3 FBXW8 TRAF6 UBE2N UBE2E2 UBE2F UBE3L3 UBE2H
http://www.genome.jp/kegg-bin/show_pathway?hsa05160	Hepatitis C	51	157	32.48%	1.52336	1.13E-02	CFLAR BID NEFH3 FAS BAK1 PAK1 PIK3CB EIF2AK2 TNFRSF1A ARAF GSK3B EIF2AK1 MAPK1 E2F1 PPP2R1A CDK6 OAS3 OAS2 E2F3 PPP2CA PIK3CA CDK2 CDKN1A MAP2K2 TRAF2 TRAF3 CASP9 KRAS MYC PPP2R1B EGF TP53 IFNAR1 EGFR IFNAR CLDN6 BRAF CLDN1 CLDN19 TLR3 YWHAB STAT3 YWHAG CYCS TRAF6 CLDN22 CLDN5 CLDN8 IFIT1 PPARA NRAS
http://www.genome.jp/kegg-bin/show_pathway?hsa04144	Endocytosis	81	252	32.14%	1.50736	1.60E-03	CYTH3 VTA1 EHD3 EHD2 SNX1 EPN1 RHOA VPS35 NEDD4 TFRC PLD1 CAP2B AMPH CHMP3B SMAP2 RAB10 SNX6 SH3GL3 GRK3 CHMP4B EEA1 RAB11A CAV1 WASL TGFBR1 RAB11FIP3 CYTH1 RABGC SMURF2 CBL ARPC3 RAB35 ACAP2 CHMP3 CAP2A1 DNAJC6 CXCR4 WIPF3 VPS26A ARRGEF2 STAM2P PSD4 HSPA2 EPS15L1 RBSN SPART ILR3A VPS45 STAM ARRB1 ACTR2 GIT2 VPS37B IGF1R PML IGSEC1 EGFR SH3KBP1 SNX12 PARD3 ASAP1 VPS37A PSD3 RAB11FIP1 LDLRAP1 AGAP1 CORS AP2M1 TGFBR2 PRKCI RABBA RABA KIF5B HSPA8 TRAF6 SMAD2 IGF2R