Cluster	ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
Common	R-HSA-2262752	Cellular responses to stress	114/510	676/10856	2.52911E-35	2.65304E-32	1.24592E-32	TUBAL3/PSMA7/H2BC12/APOA1/CAT/APOB/TUBB4A/H2AC8/EIF2S1/RPLP1/RPLP2/H2BC11/GPX1/P4HB/HSP90A	114
Common	R-HSA-8953897	Cellular responses to external stimuli	114/510	690/10856	1.8787E-34	9.85379E-32	4.62754E-32	TUBAL3/PSMA7/H2BC12/APOA1/CAT/APOB/TUBB4A/H2AC8/EIF2S1/RPLP1/RPLP2/H2BC11/GPX1/P4HB/HSP90A	114
Common	R-HSA-422475	Axon guidance	100/510	552/10856	1.70831E-33	5.9734E-31	2.80523E-31	TUBAL3/AGRN/SDCBP/ADAM10/NRP1/PSMA7/MYL12A/NRP2/SEMA7A/COL2A1/COL3A1/TUBB4A/RPLP1/RPLP2/I	100
Common	R-HSA-114608	Platelet degranulation	50/510	129/10856	2.29404E-33	6.01613E-31	2.8253E-31	QSOX1/ACTN4/WDR1/F13A1/CFD/PLG/SERPINA3/A2M/TIMP1/KNG1/APOA1/FGB/APOH/FN1/AHSG/TF/ALDOA/AP	50
Common	R-HSA-76005	Response to elevated platelet cytosolic Ca2+	50/510	134/10856	2.00203E-32	4.20026E-30	1.97253E-30	QSOX1/ACTN4/WDR1/F13A1/CFD/PLG/SERPINA3/A2M/TIMP1/KNG1/APOA1/FGB/APOH/FN1/AHSG/TF/ALDOA/AP	50
Common	R-HSA-9675108	Nervous system development	100/510	577/10856	8.17013E-32	1.42841E-29	6.7081E-30	TUBAL3/AGRN/SDCBP/ADAM10/NRP1/PSMA7/MYL12A/NRP2/SEMA7A/COL2A1/COL3A1/TUBB4A/RPLP1/RPLP2/I	100
Common	R-HSA-8939236	RUNX1 regulates transcription of genes involved in differentiation of HSCs	46/510	130/10856	1.04593E-28	1.5674E-26	7.36081E-27	PSMA7/H2BC12/H2AC8/H2BC11/H2AZ1/UBB/UBC/H2AX/PSMB1/H2AC7/H2BC17/PSMA1/PSMA2/PSMA3/PSMA4	46
Common	R-HSA-5663205	Infectious disease	120/510	871/10856	1.38848E-28	1.79464E-26	8.428E-27	TUBAL3/PSMA7/H2BC12/PGK1/C3/LTF/TUBB4A/HLA-A/H2AC8/ATP1A1/APP/SLC25A5/ISG15/RPLP1/RPLP2/ITGB1	120
Common	R-HSA-5625740	RHO GTPases activate PKNs	40/510	95/10856	1.53973E-28	1.79464E-26	8.428E-27	MYL12A/H2BC12/H2AC8/H2BC11/H2AZ1/H2AX/H2AC7/H2BC17/YWHAQ/YWHAB/SFN/H2BC3/MYH9/MYH10/MY	40
Common	R-HSA-109582	Hemostasis	98/510	621/10856	8.93177E-28	8.59194E-26	4.03495E-26	TUBAL3/QSOX1/SLC16A3/ACTN4/WDR1/F13A1/F2/F10/CFD/PLG/PLAU/PLAT/SERPINC1/SERPINA3/A2M/TIMP1/K	98
Common	R-HSA-8852276	The role of GTSE1 in G2/M progression after G2 checkpoint	36/510	77/10856	9.00966E-28	8.59194E-26	4.03495E-26	TUBAL3/PSMA7/TUBB4A/HSP90AA1/HSP90AB1/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4	36
Common	R-HSA-1643685	Disease	171/510	1615/10856	1.9968E-27	1.74553E-25	8.19737E-26	TUBAL3/AGRN/ADAM10/PSMA7/B4GAT1/H2BC12/IDH1/CP/PGK1/F2/F10/C3/APOA1/FGB/FN1/RBP4/TTR/LTF/KLI	171
Common	R-HSA-977225	Amyloid fiber formation	40/510	111/10856	1.95613E-25	1.57844E-23	7.41269E-24	ADAM10/H2BC12/CST3/APOA1/APOE/TTR/LTF/H2AC8/APP/GSN/H2BC11/H2AZ1/UBB/UBC/H2AX/H2AC7/H2BC17	40
Common	R-HSA-381426	Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs)	42/510	125/10856	2.953E-25	2.08665E-23	9.79932E-24	QSOX1/ADAM10/PRSS23/CP/F2/PLG/SERPINC1/C3/TIMP1/CST3/KNG1/APOA1/APOE/FN1/AHSG/AFP/TF/APOB/AP	42
Common	R-HSA-392499	Metabolism of proteins	193/510	2036/10856	2.98377E-25	2.08665E-23	9.79932E-24	TUBAL3/QSOX1/GAPDHS/ADAM10/PSMA7/B4GAT1/H2BC12/PRSS23/VNN1/VNN2/CP/F2/F10/PLG/SERPINC1/C3/	193
Common	R-HSA-9609690	HCMV Early Events	43/510	135/10856	9.16691E-25	5.66189E-23	2.65894E-23	TUBAL3/H2BC12/TUBB4A/H2AC8/ITGB1/H2BC11/H2AC13/H2AC7/H2BC17/H2BC3/H2BC5/H4C9/TUBA1B/TUBA4	43
Common	R-HSA-389960	Formation of tubulin folding intermediates by CCT/TriC	21/510	25/10856	9.1756E-25	5.66189E-23	2.65894E-23	TUBAL3/TUBB4A/TCP1/CCT6A/CCT5/CCT8/CCT4/TUBA1B/TUBA4A/TUBB4B/CCT2/TUBB3/TUBB2A/TUBA3E/TUBA1	21
Common	R-HSA-195258	RHO GTPase Effectors	65/510	327/10856	5.03439E-24	2.93393E-22	1.37783E-22	TUBAL3/MYL12A/H2BC12/TUBB4A/H2AC8/ITGB1/H2BC11/PFN1/H2AZ1/CALM1/H2AX/H2AC7/FLNA/H2BC17/CFL	65
Common	R-HSA-6798695	Neutrophil degranulation	79/510	480/10856	1.60985E-23	8.88806E-22	4.17401E-22	QSOX1/SDCBP/MAN2B1/ADAM10/IDH1/VNN1/CFD/PLAU/SERPINA3/C3/CST3/AHSG/TTR/LTF/FTH1/CAT/ALDOA/H	79
Common	R-HSA-168249	Innate Immune System	125/510	1060/10856	1.9352E-23	1.01501E-21	4.76671E-22	QSOX1/SDCBP/MAN2B1/ADAM10/PSMA7/IDH1/VNN1/F2/CFD/PLAU/SERPINA3/C3/C5/CST3/FGB/C9/AHSG/TTR/L	125
Common	R-HSA-76002	Platelet activation, signaling and aggregation	57/510	263/10856	4.31846E-23	2.15717E-21	1.01305E-21	QSOX1/ACTN4/WDR1/F13A1/F2/CFD/PLG/SERPINA3/A2M/TIMP1/KNG1/COL1A1/APOA1/FGB/APOH/FN1/AHSG/T	57
Common	R-HSA-1266738	Developmental Biology	128/510	1127/10856	1.53747E-22	7.33095E-21	3.44276E-21	TUBAL3/AGRN/SDCBP/ADAM10/NRP1/PSMA7/MYL12A/NRP2/H2BC12/SEMA7A/COL2A1/COL3A1/TUBB4A/H2AC8	128
Common	R-HSA-389958	Cooperation of Prefoldin and TriC/CCT in actin and tubulin folding	22/510	32/10856	1.62142E-22	7.39507E-21	3.47288E-21	TUBAL3/TUBB4A/TCP1/CCT6A/CCT5/CCT8/CCT4/ACTB/TUBA1B/TUBA4A/TUBB4B/CCT2/TUBB3/TUBB2A/TUBA3E/T	22
Common	R-HSA-9609646	HCMV Infection	44/510	160/10856	2.05405E-22	8.9779E-21	4.2162E-21	TUBAL3/H2BC12/TUBB4A/H2AC8/ITGB1/H2BC11/H2AC13/H2AC7/H2BC17/H2BC3/H2BC5/HNRNPK/H4C9/TUBA1	44
Common	R-HSA-2559586	DNA Damage/Telomere Stress Induced Senescence	32/510	80/10856	3.28533E-22	1.37852E-20	6.47383E-21	H2BC12/H2AC8/H2BC11/H2AZ1/H1-4/H2AX/H1-5/H1-3/H1-2/HMGA1/H2AC7/H2BC17/H2BC3/HMGA2/LOC1027	32
Common	R-HSA-8957275	Post-translational protein phosphorylation	36/510	108/10856	1.15887E-21	4.67561E-20	2.19576E-20	QSOX1/ADAM10/PRSS23/CP/SERPINC1/C3/TIMP1/CST3/KNG1/APOA1/APOE/FN1/AHSG/AFP/TF/APOB/APP/SERPII	36
Common	R-HSA-68886	M Phase	70/510	418/10856	2.63283E-21	1.0229E-19	4.80377E-20	TUBAL3/PSMA7/H2BC12/TUBB4A/H2AC8/H2BC11/TUBB/HSP90AA1/H2AZ1/UBB/UBC/H2AX/PSMB1/H2AC7/H2B	70
Common	R-HSA-168256	Immune System	182/510	2012/10856	4.06037E-21	1.52119E-19	7.1438E-20	TUBAL3/QSOX1/SDCBP/MAN2B1/ADAM10/PSMA7/LAMA5/ICOSLG/FLNB/IDH1/TNFRSF6B/VNN1/F13A1/F2/CFD/P	182
Common	R-HSA-1474244	Extracellular matrix organization	58/510	301/10856	8.47005E-21	3.06382E-19	1.43883E-19	AGRN/ADAM10/LAMA5/PLOD3/PLG/A2M/TIMP1/COL1A1/COL2A1/COL3A1/FGB/FN1/TTR/KLKB1/VTN/APP/SERPII	58
Common	R-HSA-201681	TCF dependent signaling in response to WNT	50/510	233/10856	3.75443E-20	1.3128E-18	6.16517E-19	PSMA7/H2BC12/H2AC8/H2BC11/H2AZ1/UBB/UBC/H2AX/PSMB1/H2AC7/H2BC17/PSMA1/PSMA2/PSMA3/PSMA4	50
Common	R-HSA-171306	Packaging Of Telomere Ends	25/510	52/10856	5.16024E-20	1.74616E-18	8.20032E-19	H2BC12/H2AC8/H2BC11/H2AZ1/H2AX/H2AC7/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/H3-4/H2AC20/H2I	25
Common	R-HSA-2299718	Condensation of Prophase Chromosomes	29/510	74/10856	6.10448E-20	2.00112E-18	9.39769E-19	H2BC12/H2AC8/H2BC11/H2AZ1/H2AX/H2AC7/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/H3C1/H3-3A/SET/I	29
Common	R-HSA-157118	Signaling by NOTCH	50/510	236/10856	6.76002E-20	2.14887E-18	1.00915E-18	ADAM10/PSMA7/H2BC12/H2AC8/H2BC11/H2AZ1/UBB/UBC/B4GALT1/H2AX/PSMB1/H2AC7/H2BC17/PSMA1/PSI	50
Common	R-HSA-73728	RNA Polymerase I Promoter Opening	27/510	63/10856	7.13149E-20	2.20028E-18	1.03329E-18	H2BC12/H2AC8/H2BC11/H2AZ1/H2AX/H2AC7/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/H3C1/H3-3A/H2A	27
Common	R-HSA-69481	G2/M Checkpoints	42/510	168/10856	1.01592E-19	3.04484E-18	1.42992E-18	PSMA7/H2BC12/H2BC11/UBB/UBC/H2AX/PSMB1/H2BC17/PSMA1/PSMA2/PSMA3/PSMA4/YWHAQ/PSMA5/PSME	42
Common	R-HSA-5334118	DNA methylation	27/510	65/10856	1.93225E-19	5.63036E-18	2.64413E-18	H2BC12/H2AC8/H2BC11/H2AZ1/H2AX/H2AC7/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/H3C1/H3-3A/H2A	27
Common	R-HSA-5625886	Activated PKN1 stimulates transcription of AR (androgen receptor) regulated genes KLK2 and KLK3	27/510	67/10856	5.01569E-19	1.32455E-17	6.22038E-18	H2BC12/H2AC8/H2BC11/H2AZ1/H2AX/H2AC7/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/H3C1/H3-3A/H2A	27
Common	R-HSA-110330	Recognition and association of DNA glycosylase with site containing an affected purine	25/510	56/10856	5.05073E-19	1.32455E-17	6.22038E-18	H2BC12/H2AC8/H2BC11/H2AZ1/H2AX/H2AC7/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/H3-4/H2AC20/H2I	25
Common	R-HSA-110331	Cleavage of the damaged purine	25/510	56/10856	5.05073E-19	1.32455E-17	6.22038E-18	H2BC12/H2AC8/H2BC11/H2AZ1/H2AX/H2AC7/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/H3-4/H2AC20/H2I	25
Common	R-HSA-73927	Depurination	25/510	56/10856	5.05073E-19	1.32455E-17	6.22038E-18	H2BC12/H2AC8/H2BC11/H2AZ1/H2AX/H2AC7/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/H3-4/H2AC20/H2I	25
Common	R-HSA-427359	SIRT1 negatively regulates rRNA expression	27/510	68/10856	7.96052E-19	2.03673E-17	9.56489E-18	H2BC12/H2AC8/H2BC11/H2AZ1/H2AX/H2AC7/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/H3C1/H3-3A/H2A	27
Common	R-HSA-9646399	Aggrephagy	22/510	43/10856	1.6289E-18	4.06837E-17	1.91059E-17	TUBAL3/TUBB4A/HSP90AA1/VIM/UBB/UBC/VCP/RPS27A/UBA52/TUBA1B/TUBA4A/TUBB4B/TUBB3/TUBB2A/TUBB	22
Common	R-HSA-5689603	UCH proteinases	32/510	102/10856	1.74175E-18	4.24905E-17	1.99544E-17	PSMA7/H2AC8/H2AC13/UBB/UBC/PSMB1/H2AC7/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5	32
Common	R-HSA-110328	Recognition and association of DNA glycosylase with site containing an affected pyrimidine	25/510	61/10856	6.39513E-18	1.45837E-16	6.84879E-17	H2BC12/H2AC8/H2BC11/H2AZ1/H2AX/H2AC7/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/H3-4/H2AC20/H2I	25
Common	R-HSA-110329	Cleavage of the damaged pyrimidine	25/510	61/10856	6.39513E-18	1.45837E-16	6.84879E-17	H2BC12/H2AC8/H2BC11/H2AZ1/H2AX/H2AC7/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/H3-4/H2AC20/H2I	25
Common	R-HSA-73928	Depyrimidination	25/510	61/10856	6.39513E-18	1.45837E-16	6.84879E-17	H2BC12/H2AC8/H2BC11/H2AZ1/H2AX/H2AC7/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/H3-4/H2AC20/H2I	25
Common	R-HSA-212300	PRC2 methylates histones and DNA	27/510	73/10856	6.99977E-18	1.5056E-16	7.07059E-17	H2BC12/H2AC8/H2BC11/H2AZ1/H2AX/H2AC7/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/H3C1/H3-3A/H2A	27
Common	R-HSA-9710421	Defective pyroptosis	27/510	73/10856	6.99977E-18	1.5056E-16	7.07059E-17	H2BC12/H2AC8/H2BC11/H2AZ1/H2AX/H2AC7/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/H3C1/H3-3A/H2A	27
Common	R-HSA-190840	Microtubule-dependent trafficking of connexons from Golgi to the plasma membrane	15/510	18/10856	7.03282E-18	1.5056E-16	7.07059E-17	TUBAL3/TUBB4A/TUBA1B/TUBA4A/TUBB4B/TUBB3/TUBB2A/TUBB8/TUBA3E/TUBA1A/TUBA1C/TUBB6/TUBB2B/TU	15
Common	R-HSA-389957	Prefoldin mediated transfer of substrate to CCT/TriC	18/510	28/10856	7.86477E-18	1.65003E-16	7.74887E-17	TUBB4A/TCP1/CCT6A/CCT5/CCT8/CCT4/ACTB/TUBA4A/TUBB4B/CCT2/TUBB3/TUBB2A/TUBA1A/CCT6B/TUBA1C/TU	18
Common	R-HSA-5626467	RHO GTPases activate IQGAPs	19/510	32/10856	8.27913E-18	1.7029E-16	7.99717E-17	TUBAL3/TUBB4A/CALM1/ACTB/CDC42/ACTG1/TUBA1B/TUBA4A/TUBB4B/TUBB3/TUBB2A/TUBB8/TUBA3E/TUBA1A	19
Common	R-HSA-9670095	Inhibition of DNA recombination at telomere	26/510	68/10856	1.09474E-17	2.20842E-16	1.03712E-16	H2BC12/H2AC8/H2BC11/H2AZ1/H2AX/H2AC7/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/H3-3A/H3-4/H2AC	26
Common	R-HSA-73929	Base-Excision Repair, AP Site Formation	25/510	63/10856	1.62683E-17	3.2199E-16	1.51213E-16	H2BC12/H2AC8/H2BC11/H2AZ1/H2AX/H2AC7/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/H3-4/H2AC20/H2I	25
Common	R-HSA-9645723	Diseases of programmed cell death	31/510	102/10856	1.69292E-17	3.28866E-16	1.54442E-16	H2BC12/H2AC8/APP/H2BC11/H2AZ1/H2AX/H2AC7/H2BC17/PRDX2/H2BC3/LOC102724334/H2BC5/YWHAE/H4C	31
Common	R-HSA-8878171	Transcriptional regulation by RUNX1	47/510	239/10856	2.19792E-17	4.1906E-16	1.96799E-16	PSMA7/H2BC12/H2AC8/H2BC11/THBS1/H2AZ1/UBB/UBC/H2AX/PSMB1/H2AC7/H2BC17/PSMA1/PSMA2/PSMA3/	47
Common	R-HSA-5689880	Ub-specific processing proteases	45/510	220/10856	2.23712E-17	4.1906E-16	1.96799E-16	PSMA7/H2BC12/H2AC8/H2BC11/H2AC13/UBB/UBC/PSMB1/H2AC7/VDAC1/H2BC17/PSMA1/PSMA2/PSMA3/PSM	45
Common	R-HSA-3000178	ECM proteoglycans	27/510	76/10856	2.34047E-17	4.23303E-16	1.98791E-16	AGRN/LAMA5/COL1A1/COL2A1/COL3A1/FN1/VTN/APP/SERPINE1/ITGB1/COL5A2/LAMB1/COL1A2/COL4A2/LAMC	27
Common	R-HSA-427389	ERCC6 (CSB) and EHMT2 (G9a) positively regulate rRNA expression	27/510	76/10856	2.34047E-17	4.23303E-16	1.98791E-16	H2BC12/H2AC8/H2BC11/H2AZ1/H2AX/H2AC7/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/H3C1/H3-3A/H2A	27
Common	R-HSA-190872	Transport of connexons to the plasma membrane	15/510	19/10856	3.19763E-17	5.68527E-16	2.66992E-16	TUBAL3/TUBB4A/TUBA1B/TUBA4A/TUBB4B/TUBB3/TUBB2A/TUBB8/TUBA3E/TUBA1A/TUBA1C/TUBB6/TUBB2B/TU	15
Common	R-HSA-201722	Formation of the beta-catenin:TCF transactivating complex	29/510	91/10856	4.49055E-17	7.85097E-16	3.68698E-16	H2BC12/H2AC8/H2BC11/H2AZ1/H2AX/H2AC7/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/H3C1/H3-3A/H3-4	29
Common	R-HSA-1445148	Translocation of SLC2A4 (GLUT4) to the plasma membrane	26/510	72/10856	5.78713E-17	9.95197E-16	4.67365E-16	TUBAL3/TUBB4A/CALM1/YWHAQ/YWHAB/SFN/MYH9/ACTB/YWHAG/YWHAE/YWHAZ/ACTG1/TUBA1B/TUBA4A/TUE	26
Common	R-HSA-912446	Meiotic recombination	28/510	86/10856	8.35391E-17	1.41343E-15	6.63774E-16	H2BC12/H2AC8/H2BC11/H2AZ1/H2AX/H2AC7/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/H3C1/H3-3A/H3-4	28
Common	R-HSA-376176	Signaling by ROBO receptors	44/510	218/10856	8.76229E-17	1.45899E-15	6.85171E-16	NRP1/PSMA7/RPLP1/RPLP2/PFN1/RPSA/UBB/UBC/RPL7/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/I	44
Common	R-HSA-606279	Deposition of new CENPA-containing nucleosomes at the centromere	26/510	74/10856	1.26891E-16	2.04782E-15	9.61699E-16	H2BC12/H2AC8/NPM1/H2BC11/H2AZ1/H2AX/H2AC7/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/H2AC20/H:	26
Common	R-HSA-774815	Nucleosome assembly	26/510	74/10856	1.26891E-16	2.04782E-15	9.61699E-16	H2BC12/H2AC8/NPM1/H2BC11/H2AZ1/H2AX/H2AC7/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/H2AC20/H:	26
Common	R-HSA-450408	AUF1 (hnRNP D0) binds and destabilizes mRNA	23/510	56/10856	1.30206E-16	2.06949E-15	9.71874E-16	PSMA7/HSPB1/UBB/UBC/HSPA1A/HSPA8/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/	23
Common	R-HSA-2559582	Senescence-Associated Secretory Phenotype (SASP)	31/510	112/10856	3.28661E-16	5.14575E-15	2.41655E-15	H2BC12/H2AC8/H2BC11/H2AZ1/UBB/UBC/H2AX/H2AC7/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/RPS27A	31
Common	R-HSA-437239	Recycling pathway of L1	21/510	47/10856	3.45591E-16	5.33125E-15	2.50366E-15	TUBAL3/TUBB4A/EZR/MSN/RDX/ACTB/ACTG1/TUBA1B/TUBA4A/TUBB4B/CLTC/TUBB3/TUBB2A/TUBB8/TUBA3E/TU	21
Common	R-HSA-5250924	B-WICH complex positively regulates rRNA expression	28/510	91/10856	4.43536E-16	6.74303E-15	3.16666E-15	H2BC12/H2AC8/H2BC11/H2AZ1/H2AX/H2AC7/H2BC17/H2BC3/LOC102724334/H2BC5/ACTB/H4C9/H3C1/H3-3A	28
Common	R-HSA-1221632	Meiotic synapsis	26/510	79/10856	7.99604E-16	1.19826E-14	5.62729E-15	H2BC12/H2AC8/H2BC11/H2AZ1/H2AX/H2AC7/H2BC17/H2BC3/HSPA2/LOC102724334/H2BC5/H4C9/H3-4/H2A	26
Common	R-HSA-3371497	HSP90 chaperone cycle for steroid hormone receptors (SHR)	22/510	55/10856	1.18734E-15	1.75425E-14	8.23833E-15	TUBAL3/TUBB4A/HSP90AA1/HSP90AB1/HSPA1A/HSPA8/HSPA1L/CAPZA1/HSPA2/TUBA1B/TUBA4A/TUBB4B/TUBB	22
Common	R-HSA-71387	Metabolism of carbohydrates	50/510	295/10856	1.2112E-15	1.76466E-14	8.28718E-15	AGRN/MAN2B1/GAPDHS/HS3ST1/B4GAT1/ALDH1A1/GOT2/PGK1/ALDOA/GAPDH/ALDOB/ENO1/PYGL/GPI/PGK2/I	50
Common	R-HSA-69275	G2/M Transition	40/510	196/10856	1.57418E-15	2.26208E-14	1.06232E-14	TUBAL3/PSMA7/TUBB4A/TUBB/HSP90AA1/HSP90AB1/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/F	40
Common	R-HSA-195721	Signaling by WNT	53/510	332/10856	2.1936E-15	3.10958E-14	1.46032E-14	PSMA7/H2BC12/H2AC8/H2BC11/PFN1/H2AZ1/UBB/UBC/CALM1/H2AX/PSMB1/H2AC7/H2BC17/PSMA1/PSMA2/F	53
Common	R-HSA-453274	Mitotic G2-G2/M phases	40/510	198/10856	2.26803E-15	3.17222E-14	1.48974E-14	TUBAL3/PSMA7/TUBB4A/TUBB/HSP90AA1/HSP90AB1/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/F	40
Common	R-HSA-9010553	Regulation of expression of SLITs and ROBOs	37/510	171/10856	2.63134E-15	3.63194E-14	1.70563E-14	PSMA7/RPLP1/RPLP2/RPSA/UBB/UBC/RPL7/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSME	37
Common	R-HSA-8936459	RUNX1 regulates genes involved in megakaryocyte differentiation and platelet function	28/510	97/10856	2.80752E-15	3.82479E-14	1.7962E-14	H2BC12/H2AC8/H2BC11/THBS1/H2AZ1/H2AX/H2AC7/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/H3C1/H3-3	28
Common	R-HSA-9616222	Transcriptional regulation of granulopoiesis	27/510	90/10856	3.05486E-15	4.10839E-14	1.92938E-14	H2BC12/H2AC8/H2BC11/H2AZ1/H2AX/H2AC7/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/H3C1/H3-3A/H2A	27
Common	R-HSA-5610787	Hedgehog 'off' state	30/510	113/10856	3.48357E-15	4.62565E-14	2.1723E-14	PSMA7/TUBB4A/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2	30
Common	R-HSA-73772	RNA Polymerase I Promoter Escape	27/510	91/10856	4.15651E-15	5.45022E-14	2.55953E-14	H2BC12/H2AC8/H2BC11/H2AZ1/H2AX/H2AC7/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/H3C1/H3-3A/H2A	27
Common	R-HSA-597592	Post-translational protein modification	131/510	1434/10856	6.52426E-15	8.44931E-14	3.96797E-14	TUBAL3/QSOX1/ADAM10/PSMA7/B4GAT1/H2BC12/PRSS23/VNN1/VNN2/CP/F2/F10/SERPINC1/C3/TIMP1/CST3/K	131
Common	R-HSA-3000171	Non-integrin membrane-ECM interactions	22/510	59/10856	6.86069E-15	8.77666E-14	4.1217E-14	AGRN/LAMA5/COL1A1/COL2A1/COL3A1/FN1/TTR/VTN/ITGB1/COL5A2/LAMB1/THBS1/COL1A2/COL4A2/LAMC1/A	22
Common	R-HSA-1912408	Pre-NOTCH Transcription and Translation	27/510	93/10856	7.5909E-15	9.5938E-14	4.50544E-14	H2BC12/H2AC8/H2BC11/H2AZ1/H2AX/H2AC7/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/H3C1/H3-3A/H2A	27
Common	R-HSA-69278	Cell Cycle, Mitotic	71/510	561/10856	8.34126E-15	1.04166E-13	4.89187E-14	TUBAL3/PSMA7/H2BC12/TUBB4A/H2AC8/H2BC11/TUBB/HSP90AA1/HSP90AB1/H2AZ1/UBB/UBC/H2AX/PSMB1/H	71
Common	R-HSA-2559580	Oxidative Stress Induced Senescence	31/510	125/10856	9.43338E-15	1.16419E-13	5.46727E-14	H2BC12/H2AC8/H2BC11/H2AZ1/UBB/UBC/H2AX/H2AC7/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/RPS27A	31
Common	R-HSA-3214815	HDACs deacetylate histones	27/510	94/10856	1.01911E-14	1.24308E-13	5.83775E-14	H2BC12/H2AC8/H2BC11/H2AC13/H2AC7/H2BC17/H2BC3/H2BC5/H4C9/H3C1/H2AC20/H2BC21/H2BC18/H2AC1	27
Common	R-HSA-2559583	Cellular Senescence	39/510	197/10856	1.04291E-14	1.25748E-13	5.90538E-14	H2BC12/H2AC8/H2BC11/H2AZ1/UBB/UBC/H1-4/H2AX/H1-5/H1-3/H1-2/HMGA1/H2AC7/H2BC17/H2BC3/HMGA2	39
Common	R-HSA-450531	Regulation of mRNA stability by proteins that bind AU-rich elements	26/510	88/10856	1.51503E-14	1.80598E-13	8.48127E-14	PSMA7/HSPB1/UBB/UBC/HSPA1A/HSPA8/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/	26
Common	R-HSA-373760	L1CAM interactions	30/510	119/10856	1.59762E-14	1.88303E-13	8.8431E-14	TUBAL3/SDCBP/NRP1/NRP2/TUBB4A/ITGB1/LAMB1/LAMC1/HSPA8/NCAM1/EZR/MSN/RDX/ACTB/ACTG1/TUBA1B/	30
Common	R-HSA-9619483	Activation of AMPK downstream of NMDARs	16/510	29/10856	1.72272E-14	2.00792E-13	9.42962E-14	TUBAL3/TUBB4A/CALM1/TUBA1B/TUBA4A/TUBB4B/TUBB3/TUBB2A/TUBB8/TUBA3E/TUBA1A/TUBA1C/TUBB6/TUB	16
Common	R-HSA-194315	Signaling by Rho GTPases	81/510	703/10856	1.81381E-14	2.09087E-13	9.81913E-14	TUBAL3/MYL12A/H2BC12/TUBB4A/H2AC8/ITGB1/H2BC11/PFN1/HSP90AA1/HNRNPC/HSP90AB1/VIM/H2AZ1/CAI	81
Common	R-HSA-5250913	Positive epigenetic regulation of rRNA expression	28/510	106/10856	3.40163E-14	3.83689E-13	1.80188E-13	H2BC12/H2AC8/H2BC11/H2AZ1/H2AX/H2AC7/H2BC17/H2BC3/LOC102724334/H2BC5/ACTB/H4C9/H3C1/H3-3A	28
Common	R-HSA-5578749	Transcriptional regulation by small RNAs	28/510	106/10856	3.40163E-14	3.83689E-13	1.80188E-13	H2BC12/H2AC8/H2BC11/H2AZ1/H2AX/H2AC7/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/RAN/H3C1/H3-3A	28
Common	R-HSA-389977	Post-chaperonin tubulin folding pathway	14/510	22/10856	4.84566E-14	5.40756E-13	2.5395E-13	TUBAL3/TUBB4A/TUBA1B/TUBA4A/TUBB4B/TUBB3/TUBB2A/TUBA3E/TUBA1A/TUBA1C/TUBB6/TUBB2B/TUBB1/TU	14
Common	R-HSA-216083	Integrin cell surface interactions	25/510	85/10856	5.51333E-14	6.08788E-13	2.85899E-13	AGRN/COL1A1/COL2A1/COL3A1/FGB/FN1/VTN/ITGB1/COL5A2/THBS1/COL1A2/COL4A2/COL6A1/COL6A2/COL6A	25
Common	R-HSA-9716542	Signaling by Rho GTPases, Miro GTPases and RHOBTB3	81/510	719/10856	6.37006E-14	6.96061E-13	3.26884E-13	TUBAL3/MYL12A/H2BC12/TUBB4A/H2AC8/ITGB1/H2BC11/PFN1/HSP90AA1/HNRNPC/HSP90AB1/VIM/H2AZ1/CAI	81
Common	R-HSA-156842	Eukaryotic Translation Elongation	26/510	93/10856	6.54134E-14	7.07409E-13	3.32213E-13	RPLP1/RPLP2/RPSA/EEF2/RPL7/EEF1B2/EEF1G/EEF1D/RPS19/RPS10/RPL34/RPS3A/RPS7/RPS8/RPS15A/RPS18/RI	26
Common	R-HSA-1640170	Cell Cycle	79/510	692/10856	6.67454E-14	7.14448E-13	3.35519E-13	TUBAL3/PSMA7/H2BC12/TUBB4A/H2AC8/NPM1/H2BC11/TUBB/HSP90AA1/HSP90AB1/H2AZ1/UBB/UBC/H2AX/P	79
Common	R-HSA-1912422	Pre-NOTCH Expression and Processing	28/510	109/10856	7.33416E-14	7.77125E-13	3.64954E-13	H2BC12/H2AC8/H2BC11/H2AZ1/B4GALT1/H2AX/H2AC7/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/H3C1/H	28
Common	R-HSA-190828	Gap junction trafficking	19/510	47/10856	8.59382E-14	9.01492E-13	4.23359E-13	TUBAL3/TUBB4A/CLTCL1/ACTB/ACTG1/TUBA1B/TUBA4A/TUBB4B/CLTC/TUBB3/TUBB2A/TUBB8/TUBA3E/TUBA1A/T	19
Common	R-HSA-1500620	Meiosis	29/510	118/10856	9.04014E-14	9.38921E-13	4.40936E-13	H2BC12/H2AC8/H2BC11/H2AZ1/H2AX/H2AC7/H2BC17/H2BC3/HSPA2/LOC102724334/H2BC5/H4C9/H3C1/H3-3	29
Common	R-HSA-5688426	Deubiquitination	47/510	297/10856	1.30798E-13	1.34517E-12	6.3172E-13	PSMA7/H2BC12/H2AC8/H2BC11/H2AC13/UBB/UBC/PSMB1/H2AC7/VDAC1/H2BC17/PSMA1/PSMA2/PSMA3/PSM	47
Common	R-HSA-9663891	Selective autophagy	24/510	81/10856	1.48062E-13	1.50794E-12	7.08157E-13	TUBAL3/TUBB4A/HSP90AA1/VIM/UBB/UBC/HSPA8/VDAC1/VCP/RPS27A/UBA52/TUBA1B/TUBA4A/TUBB4B/TUBB3	24
Common	R-HSA-157858	Gap junction trafficking and regulation	19/510	49/10856	2.12777E-13	2.14619E-12	1.00789E-12	TUBAL3/TUBB4A/CLTCL1/ACTB/ACTG1/TUBA1B/TUBA4A/TUBB4B/CLTC/TUBB3/TUBB2A/TUBB8/TUBA3E/TUBA1A/T	19
Common	R-HSA-5358351	Signaling by Hedgehog	32/510	149/10856	2.6394E-13	2.63688E-12	1.23833E-12	PSMA7/TUBB4A/P4HB/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/I	32
Common	R-HSA-5362768	Hh mutants are degraded by ERAD	20/510	56/10856	3.08253E-13	3.05054E-12	1.4326E-12	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/VCP/PSI	20
Common	R-HSA-211733	Regulation of activated PAK-2p34 by proteasome mediated degradation	19/510	50/10856	3.28432E-13	3.20953E-12	1.50726E-12	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-427413	NoRC negatively regulates rRNA expression	27/510	107/10856	3.30438E-13	3.20953E-12	1.50726E-12	H2BC12/H2AC8/H2BC11/H2AZ1/H2AX/H2AC7/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/H3C1/H3-3A/H2A	27
Common	R-HSA-9610379	HCMV Late Events	28/510	116/10856	3.95787E-13	3.80899E-12	1.78878E-12	H2BC12/H2AC8/H2BC11/H2AC13/H2AC7/H2BC17/H2BC3/H2BC5/HNRNPK/H4C9/H3C1/H2AC20/H2BC21/H2BC	28
Common	R-HSA-73884	Base Excision Repair	25/510	92/10856	4.0802E-13	3.89103E-12	1.82731E-12	H2BC12/H2AC8/H2BC11/H2AZ1/H2AX/H2AC7/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/H3-4/H2AC20/H2I	25
Common	R-HSA-109581	Apoptosis	35/510	180/10856	4.44736E-13	4.20295E-12	1.97379E-12	PSMA7/GSN/VIM/HMGB1/UBB/UBC/H1-4/H1-5/H1-3/H1-2/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/YWHAQ/PSMA	35
Common	R-HSA-70263	Gluconeogenesis	16/510	34/10856	4.49463E-13	4.2097E-12	1.97696E-12	GAPDHS/GOT2/PGK1/ALDOA/GAPDH/ALDOB/ENO1/GPI/PGK2/ENO2/ALDOC/ENO3/PGAM2/PGAM1/MDH2/TPI1	16
Common	R-HSA-1474165	Reproduction	31/510	143/10856	4.81816E-13	4.47278E-12	2.10051E-12	H2BC12/H2AC8/H2BC11/H2AZ1/B4GALT1/H2AX/H2AC7/CD9/H2BC17/H2BC3/HSPA2/LOC102724334/H2BC5/H	31
Common	R-HSA-5250941	Negative epigenetic regulation of rRNA expression	27/510	110/10856	6.80093E-13	6.20363E-12	2.91335E-12	H2BC12/H2AC8/H2BC11/H2AZ1/H2AX/H2AC7/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/H3C1/H3-3A/H2A	27
Common	R-HSA-73854	RNA Polymerase I Promoter Clearance	27/510	110/10856	6.80093E-13	6.20363E-12	2.91335E-12	H2BC12/H2AC8/H2BC11/H2AZ1/H2AX/H2AC7/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/H3C1/H3-3A/H2A	27

Common	R-HSA-180534	Vpu mediated degradation of CD4	19/510	52/10856	7.55407E-13	6.50975E-12	3.05711E-12	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-349425	Autodegradation of the E3 ubiquitin ligase COP1	19/510	52/10856	7.55407E-13	6.50975E-12	3.05711E-12	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-69601	Ubiquitin Mediated Degradation of Phosphorylated Cdc25A	19/510	52/10856	7.55407E-13	6.50975E-12	3.05711E-12	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-69610	p53-Independent DNA Damage Response	19/510	52/10856	7.55407E-13	6.50975E-12	3.05711E-12	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-69613	p53-Independent G1/S DNA damage checkpoint	19/510	52/10856	7.55407E-13	6.50975E-12	3.05711E-12	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-75815	Ubiquitin-dependent degradation of Cyclin D	19/510	52/10856	7.55407E-13	6.50975E-12	3.05711E-12	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-5358346	Hedgehog ligand biogenesis	21/510	65/10856	7.57092E-13	6.50975E-12	3.05711E-12	PSMA7/P4HB/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/V	21
Common	R-HSA-5387390	Hh mutants abrogate ligand secretion	20/510	59/10856	9.60962E-13	8.19552E-12	3.84878E-12	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/VCP/PS	20
Common	R-HSA-9609736	Assembly and cell surface presentation of NMDA receptors	17/510	41/10856	1.08139E-12	9.09947E-12	4.2733E-12	TUBAL3/TUBB4A/NEFL/ACTN2/TUBA1B/TUBA4A/TUBB4B/TUBB3/TUBB2A/TUBB8/TUBA3E/TUBA1A/TUBA1C/TUBB	17
Common	R-HSA-73864	RNA Polymerase I Transcription	27/510	112/10856	1.0843E-12	9.09947E-12	4.2733E-12	H2BC12/H2AC8/H2BC11/H2AZ1/H2AX/H2AC7/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/H3C1/H3-3A/H2A	27
Common	R-HSA-169911	Regulation of Apoptosis	19/510	53/10856	1.12692E-12	9.38203E-12	4.40599E-12	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-71291	Metabolism of amino acids and derivatives	52/510	374/10856	1.19678E-12	9.88518E-12	4.64228E-12	PSMA7/PHGDH/GOT2/ASS1/RPLP1/RPLP2/SLC3A2/RPSA/CKB/NQO1/RPL7/PSMB1/AHCY/PSMA1/PSMA2/PSMA3/	52
Common	R-HSA-162909	Host Interactions of HIV factors	29/510	130/10856	1.2886E-12	1.05605E-11	4.95941E-12	PSMA7/HLA-A/SLC25A5/NPM1/UBB/UBC/SLC25A4/SLC25A6/HMGA1/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSM	29
Common	R-HSA-157579	Telomere Maintenance	27/510	113/10856	1.36333E-12	1.10863E-11	5.20634E-12	H2BC12/H2AC8/H2BC11/H2AZ1/H2AX/H2AC7/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/H3-3A/H3-4/H2AC	27
Common	R-HSA-9668328	Sealing of the nuclear envelope (NE) by ESCRT-III	15/510	31/10856	1.46741E-12	1.18409E-11	5.56071E-12	TUBAL3/TUBB4A/TUBA1B/TUBA4A/TUBB4B/TUBB3/TUBB2A/TUBB8/TUBA3E/TUBA1A/TUBA1C/TUBB6/TUBB2B/TU	15
Common	R-HSA-1474228	Degradation of the extracellular matrix	30/510	140/10856	1.59131E-12	1.27427E-11	5.98421E-12	ADAM10/LAMA5/PLG/A2M/TIMP1/COL1A1/COL2A1/COL3A1/FN1/KLKB1/COL5A2/CTSD/CTSB/LAMB1/COL1A2/M	30
Common	R-HSA-180585	Vif-mediated degradation of APOBEC3G	19/510	54/10856	1.66392E-12	1.30258E-11	6.11716E-12	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-8854050	FBXL7 down-regulates AURKA during mitotic entry and in early mitosis	19/510	54/10856	1.66392E-12	1.30258E-11	6.11716E-12	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-9604323	Negative regulation of NOTCH4 signaling	19/510	54/10856	1.66392E-12	1.30258E-11	6.11716E-12	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-1236974	ER-Phagosome pathway	24/510	90/10856	1.90047E-12	1.47674E-11	6.93506E-12	PSMA7/FGB/HLA-A/HMGB1/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/CALR/PSMA5/PSMB4/PSMB6/PSME	24
Common	R-HSA-5678895	Defective CFTR causes cystic fibrosis	20/510	61/10856	1.96401E-12	1.51488E-11	7.1142E-12	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/VCP/PS	20
Common	R-HSA-5357801	Programmed Cell Death	37/510	210/10856	2.18898E-12	1.67609E-11	7.87125E-12	SDCBP/PSMA7/GSN/HSP90AA1/VIM/HMGB1/UBB/UBC/H1-4/H1-5/H1-3/H1-2/PSMB1/PSMA1/PSMA2/PSMA3/PS	37
Common	R-HSA-68875	Mitotic Prophase	30/510	142/10856	2.34684E-12	1.78394E-11	8.37773E-12	H2BC12/H2AC8/H2BC11/H2AZ1/H2AX/H2AC7/H2BC17/PPP2R1A/H2BC3/LOC102724334/H2BC5/H4C9/H3C1/H	30
Common	R-HSA-174113	SCF-beta-TrCP mediated degradation of Emi1	19/510	55/10856	2.43281E-12	1.82287E-11	8.56057E-12	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-4641257	Degradation of AXIN	19/510	55/10856	2.43281E-12	1.82287E-11	8.56057E-12	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-2467813	Separation of Sister Chromatids	35/510	191/10856	2.71938E-12	2.02314E-11	9.5011E-12	TUBAL3/PSMA7/TUBB4A/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PPP2	35
Common	R-HSA-4641258	Degradation of DVL	19/510	57/10856	5.05848E-12	3.68496E-11	1.73053E-11	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-69541	Stabilization of p53	19/510	57/10856	5.05848E-12	3.68496E-11	1.73053E-11	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-8932339	ROS sensing by NFE2L2	19/510	57/10856	5.05848E-12	3.68496E-11	1.73053E-11	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-156827	L13a-mediated translational silencing of Ceruloplasmin expression	26/510	111/10856	5.84032E-12	4.22517E-11	1.98422E-11	EIF2S1/RPLP1/RPLP2/RPSA/RPL7/RPS19/RPS10/RPL34/EIF3B/EIF4A1/RPS3A/RPS7/RPS8/RPS15A/RPS18/RPS13/	26
Common	R-HSA-211000	Gene Silencing by RNA	29/510	138/10856	6.3269E-12	4.54583E-11	2.13481E-11	H2BC12/H2AC8/H2BC11/HSP90AA1/H2AZ1/H2AX/H2AC7/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/RAN/H	29
Common	R-HSA-72706	GTP hydrolysis and joining of the 60S ribosomal subunit	26/510	112/10856	7.27818E-12	5.19375E-11	2.43909E-11	EIF2S1/RPLP1/RPLP2/RPSA/RPL7/RPS19/RPS10/RPL34/EIF3B/EIF4A1/RPS3A/RPS7/RPS8/RPS15A/RPS18/RPS13/	26
Common	R-HSA-5617472	Activation of anterior HOX genes in hindbrain development during early embryogenesis	27/510	121/10856	7.74668E-12	5.45387E-11	2.56125E-11	H2BC12/H2AC8/H2BC11/H2AZ1/H2AX/H2AC7/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/H3C1/H3-3A/H2A	27
Common	R-HSA-5619507	Activation of HOX genes during differentiation	27/510	121/10856	7.74668E-12	5.45387E-11	2.56125E-11	H2BC12/H2AC8/H2BC11/H2AZ1/H2AX/H2AC7/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/H3C1/H3-3A/H2A	27
Common	R-HSA-5676590	NIK-->noncanonical NF-kB signaling	19/510	59/10856	1.01628E-11	7.03617E-11	3.30433E-11	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-68827	CDT1 association with the CDC6:ORC:origin complex	19/510	59/10856	1.01628E-11	7.03617E-11	3.30433E-11	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-1236975	Antigen processing-Cross presentation	25/510	105/10856	1.01954E-11	7.03617E-11	3.30433E-11	PSMA7/FGB/HLA-A/HMGB1/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/CALR/PSMA5/PSMB4/PSMB6/PSME	25
Common	R-HSA-9018519	Estrogen-dependent gene expression	30/510	150/10856	1.03241E-11	7.07839E-11	3.32415E-11	H2BC12/H2AC8/H2BC11/CTSD/HSP90AA1/HSP90AB1/H2AZ1/H2AX/H2AC7/H2BC17/H2BC3/LOC102724334/H2	30
Common	R-HSA-3214847	HATs acetylate histones	29/510	142/10856	1.33758E-11	9.11117E-11	4.27879E-11	H2BC12/H2AC8/H2BC11/H2AC13/H2AC7/H2BC17/H2BC3/H2BC5/ACTB/H4C9/H3C1/H2AC20/H2BC21/H2BC18/	29
Common	R-HSA-1650814	Collagen biosynthesis and modifying enzymes	20/510	67/10856	1.40204E-11	9.39029E-11	4.40987E-11	PLOD3/COL1A1/COL2A1/COL3A1/COL5A2/P4HB/COL1A2/COL4A2/COL6A1/COL6A2/COL6A3/COL5A1/PPIB/COL1	20
Common	R-HSA-5607761	Dectin-1 mediated noncanonical NF-kB signaling	19/510	60/10856	1.42331E-11	9.39029E-11	4.40987E-11	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-5610780	Degradation of GLI1 by the proteasome	19/510	60/10856	1.42331E-11	9.39029E-11	4.40987E-11	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-5610783	Degradation of GLI2 by the proteasome	19/510	60/10856	1.42331E-11	9.39029E-11	4.40987E-11	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-5610785	GLI3 is processed to GLI3R by the proteasome	19/510	60/10856	1.42331E-11	9.39029E-11	4.40987E-11	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-1474290	Collagen formation	23/510	90/10856	1.4491E-11	9.50067E-11	4.46171E-11	PLOD3/COL1A1/COL2A1/COL3A1/COL5A2/P4HB/CTSB/COL1A2/COL4A2/COL6A1/COL6A2/COL6A3/COL5A1/PPIB/	23
Common	R-HSA-8875878	MET promotes cell motility	16/510	41/10856	1.5474E-11	1.00696E-10	4.72888E-11	LAMA5/COL1A1/COL2A1/COL3A1/FN1/ITGB1/COL5A2/LAMB1/COL1A2/LAMC1/COL5A1/ITGA3/LAMB2/RAP1B/RA	16
Common	R-HSA-8874081	MET activates PTK2 signaling	14/510	30/10856	1.55507E-11	1.00696E-10	4.72888E-11	LAMA5/COL1A1/COL2A1/COL3A1/FN1/ITGB1/COL5A2/LAMB1/COL1A2/LAMC1/COL5A1/ITGA3/LAMB2/LAMB3	14
Common	R-HSA-390466	Chaperonin-mediated protein folding	23/510	91/10856	1.85569E-11	1.19425E-10	5.60843E-11	TUBAL3/GAPDHS/TUBB4A/TCP1/CCT6A/CCT5/CCT8/CCT4/ACTB/TUBA1B/TUBA4A/TUBB4B/CCT2/TUBB3/TUBB2A/	23
Common	R-HSA-190861	Gap junction assembly	15/510	36/10856	2.18529E-11	1.39778E-10	6.56428E-11	TUBAL3/TUBB4A/TUBA1B/TUBA4A/TUBB4B/TUBB3/TUBB2A/TUBB8/TUBA3E/TUBA1A/TUBA1C/TUBB6/TUBB2B/TU	15
Common	R-HSA-69620	Cell Cycle Checkpoints	43/510	294/10856	2.25051E-11	1.43078E-10	6.71921E-11	PSMA7/H2BC12/H2BC11/UBB/UBC/H2AX/PSMB1/H2BC17/PSMA1/PSMA2/PSMA3/PSMA4/YWHAQ/PSMA5/PSME	43
Common	R-HSA-8941858	Regulation of RUNX3 expression and activity	18/510	55/10856	2.63836E-11	1.66725E-10	7.82975E-11	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	18
Common	R-HSA-5619084	ABC transporter disorders	21/510	77/10856	2.93863E-11	1.84588E-10	8.66863E-11	PSMA7/APOA1/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/	21
Common	R-HSA-72613	Eukaryotic Translation Initiation	26/510	119/10856	3.16152E-11	1.96239E-10	9.21576E-11	EIF2S1/RPLP1/RPLP2/RPSA/RPL7/RPS19/RPS10/RPL34/EIF3B/EIF4A1/RPS3A/RPS7/RPS8/RPS15A/RPS18/RPS13/	26
Common	R-HSA-72737	Cap-dependent Translation Initiation	26/510	119/10856	3.16152E-11	1.96239E-10	9.21576E-11	EIF2S1/RPLP1/RPLP2/RPSA/RPL7/RPS19/RPS10/RPL34/EIF3B/EIF4A1/RPS3A/RPS7/RPS8/RPS15A/RPS18/RPS13/	26
Common	R-HSA-5689901	Metalloprotease DUBs	15/510	37/10856	3.51826E-11	2.17097E-10	1.01953E-10	H2AC8/H2AC13/UBB/UBC/H2AC7/RPS27A/UBA52/H2AC20/H2AC18/H2AW/H2AC21/H2AC6/H2AC12/H2AC1/H2	15
Common	R-HSA-69473	G2/M DNA damage checkpoint	23/510	95/10856	4.81497E-11	2.95375E-10	1.38714E-10	H2BC12/H2BC11/H2AX/H2BC17/YWHAQ/YWHAB/SFN/H2BC3/LOC102724334/H2BC5/YWHAG/YWHAE/H4C9/YW	23
Common	R-HSA-6806834	Signaling by MET	21/510	79/10856	5.01592E-11	3.05913E-10	1.43663E-10	LAMA5/COL1A1/COL2A1/COL3A1/FN1/ITGB1/COL5A2/LAMB1/COL1A2/UBB/UBC/LAMC1/COL5A1/ITGA3/LAMB2/	21
Common	R-HSA-1442490	Collagen degradation	19/510	64/10856	5.09154E-11	3.06956E-10	1.44153E-10	ADAM10/COL1A1/COL2A1/COL3A1/COL5A2/CTSD/CTSB/COL1A2/MMP2/COL4A2/MMP10/COL6A1/COL6A2/COL	19
Common	R-HSA-4608870	Asymmetric localization of PCP proteins	19/510	64/10856	5.09154E-11	3.06956E-10	1.44153E-10	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-73886	Chromosome Maintenance	28/510	141/10856	6.11947E-11	3.66818E-10	1.72265E-10	H2BC12/H2AC8/NPM1/H2BC11/H2AZ1/H2AX/H2AC7/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/H3-3A/H3-	28
Common	R-HSA-9707587	Regulation of HMOX1 expression and activity	19/510	65/10856	6.88541E-11	4.10386E-10	1.92726E-10	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-166658	Complement cascade	18/510	58/10856	7.22355E-11	4.28108E-10	2.01048E-10	F2/CFD/C3/C5/C9/C4BPA/VTN/SERPING1/CFH/C4A/C4B/C7/CLU/C6/CPN1/MASP1/CD81/CPB2	18
Common	R-HSA-391251	Protein folding	23/510	97/10856	7.60038E-11	4.4791E-10	2.10348E-10	TUBAL3/GAPDHS/TUBB4A/TCP1/CCT6A/CCT5/CCT8/CCT4/ACTB/TUBA1B/TUBA4A/TUBB4B/CCT2/TUBB3/TUBB2A/	23
Common	R-HSA-68882	Mitotic Anaphase	37/510	236/10856	7.77382E-11	4.55572E-10	2.13946E-10	TUBAL3/PSMA7/TUBB4A/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PPP2	37
Common	R-HSA-156902	Peptide chain elongation	22/510	89/10856	8.22646E-11	4.7942E-10	2.25145E-10	RPLP1/RPLP2/RPSA/EEF2/RPL7/RPS19/RPS10/RPL34/RPS3A/RPS7/RPS8/RPS15A/RPS18/RPS13/RPL7A/RPS26/RP	22
Common	R-HSA-2555396	Mitotic Metaphase and Anaphase	37/510	237/10856	8.81592E-11	5.10934E-10	2.39945E-10	TUBAL3/PSMA7/TUBB4A/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PPP2	37
Common	R-HSA-1234176	Oxygen-dependent proline hydroxylation of Hypoxia-inducible Factor Alpha	19/510	66/10856	9.25341E-11	5.27545E-10	2.47746E-10	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-69563	p53-Dependent G1 DNA Damage Response	19/510	66/10856	9.25341E-11	5.27545E-10	2.47746E-10	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-69580	p53-Dependent G1/S DNA damage checkpoint	19/510	66/10856	9.25341E-11	5.27545E-10	2.47746E-10	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-9013694	Signaling by NOTCH4	21/510	82/10856	1.08166E-10	6.13332E-10	2.88033E-10	ADAM10/PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB	21
Common	R-HSA-3000480	Scavenging by Class A Receptors	11/510	19/10856	1.18786E-10	6.69925E-10	3.14611E-10	COL1A1/COL3A1/APOA1/APOE/FTH1/APOB/COL1A2/COL4A2/HSP90B1/CALR/MASP1	11
Common	R-HSA-1169091	Activation of NF-kappaB in B cells	19/510	67/10856	1.23612E-10	6.93419E-10	3.25644E-10	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-449147	Signaling by Interleukins	55/510	462/10856	1.30359E-10	7.27376E-10	3.4159E-10	PSMA7/LAMA5/F13A1/TIMP1/FN1/ANXA1/APP/ITGB1/P4HB/ANXA2/HSP90AA1/COL1A2/MMP2/VIM/GSTA2/HM	55
Common	R-HSA-187577	SCF(Skp2)-mediated degradation of p27/p21	18/510	60/10856	1.36024E-10	7.54971E-10	3.5455E-10	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	18
Common	R-HSA-1168372	Downstream signaling events of B Cell Receptor (BCR)	21/510	83/10856	1.38572E-10	7.65061E-10	3.59288E-10	PSMA7/UBB/UBC/CALM1/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/	21
Common	R-HSA-174154	APC/C:Cdc20 mediated degradation of Securin	19/510	68/10856	1.64173E-10	8.87721E-10	4.16891E-10	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-5658442	Regulation of RAS by GAPs	19/510	68/10856	1.64173E-10	8.87721E-10	4.16891E-10	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-68867	Assembly of the pre-replicative complex	19/510	68/10856	1.64173E-10	8.87721E-10	4.16891E-10	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-69615	G1/S DNA Damage Checkpoints	19/510	68/10856	1.64173E-10	8.87721E-10	4.16891E-10	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-977606	Regulation of Complement cascade	16/510	47/10856	1.73575E-10	9.33743E-10	4.38505E-10	F2/C3/C5/C9/C4BPA/VTN/SERPING1/CFH/C4A/C4B/C7/CLU/C6/CPN1/CD81/CPB2	16
Common	R-HSA-72689	Formation of a pool of free 40S subunits	23/510	101/10856	1.82418E-10	9.7631E-10	4.58495E-10	RPLP1/RPLP2/RPSA/RPL7/RPS19/RPS10/RPL34/EIF3B/RPS3A/RPS7/RPS8/RPS15A/RPS18/RPS13/RPL7A/RPS26/R	23
Common	R-HSA-8948751	Regulation of PTEN stability and activity	19/510	69/10856	2.16825E-10	1.15457E-09	5.42209E-10	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-5693565	Recruitment and ATM-mediated phosphorylation of repair and signaling proteins at DNA double strand breaks	20/510	77/10856	2.29474E-10	1.21575E-09	5.70939E-10	H2BC12/H2BC11/UBB/UBC/H2AX/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/RPS27A/UBA52/H3-4/H2BC21/	20
Common	R-HSA-212165	Epigenetic regulation of gene expression	28/510	149/10856	2.37942E-10	1.25428E-09	5.89035E-10	H2BC12/H2AC8/H2BC11/H2AZ1/H2AX/H2AC7/H2BC17/H2BC3/LOC102724334/H2BC5/ACTB/H4C9/H3C1/H3-3	28
Common	R-HSA-3000157	Laminin interactions	13/510	30/10856	2.68187E-10	1.40664E-09	6.60587E-10	LAMA5/ITGB1/LAMB1/COL4A2/LAMC1/NID1/ITGA3/COL18A1/LAMB2/HSPG2/COL7A1/LAMB3/NID2	13
Common	R-HSA-9711123	Cellular response to chemical stress	29/510	160/10856	2.78851E-10	1.4553E-09	6.83436E-10	PSMA7/CAT/GPX1/P4HB/GSTP1/UBB/UBC/PSMB1/GPX3/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/	29
Common	R-HSA-5693606	DNA Double Strand Break Response	20/510	78/10856	2.95333E-10	1.5326E-09	7.19741E-10	H2BC12/H2BC11/UBB/UBC/H2AX/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/RPS27A/UBA52/H3-4/H2BC21/	20
Common	R-HSA-2173782	Binding and Uptake of Ligands by Scavenger Receptors	15/510	42/10856	2.98046E-10	1.5326E-09	7.19741E-10	COL1A1/COL3A1/APOA1/APOE/FTH1/APOB/HSP90AA1/COL1A2/COL4A2/HSP90B1/CALR/MASP1/HBB/HBA1/LRP1	15
Common	R-HSA-8955332	Carboxyterminal post-translational modifications of tubulin	15/510	42/10856	2.98046E-10	1.5326E-09	7.19741E-10	TUBAL3/TUBB4A/TUBA1B/TUBA4A/TUBB4B/TUBB3/TUBB2A/TUBB8/TUBA3E/TUBA1A/TUBA1C/TUBB6/TUBB2B/TU	15
Common	R-HSA-9612973	Autophagy	28/510	151/10856	3.28855E-10	1.68278E-09	7.90266E-10	TUBAL3/TUBB4A/HSP90AA1/HSP90AB1/VIM/UBB/UBC/HSPA8/GFAP/VDAC1/VCP/RPS27A/UBA52/EEF1A1/TUBA1	28
Common	R-HSA-1236978	Cross-presentation of soluble exogenous antigens (endosomes)	16/510	49/10856	3.54227E-10	1.80381E-09	8.47104E-10	PSMA7/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/PSMA8/P	16
Common	R-HSA-68949	Orc1 removal from chromatin	19/510	71/10856	3.72181E-10	1.88607E-09	8.85739E-10	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-174084	Autodegradation of Cdh1 by Cdh1:APC/C	18/510	64/10856	4.44399E-10	2.24122E-09	1.05252E-09	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	18
Common	R-HSA-5687128	MAPK6/MAPK4 signaling	21/510	89/10856	5.65057E-10	2.8361E-09	1.33189E-09	PSMA7/HSPB1/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/	21
Common	R-HSA-174184	Cdc20:Phospho-APC/C mediated degradation of Cyclin A	19/510	73/10856	6.26043E-10	3.09773E-09	1.45476E-09	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-69017	CDK-mediated phosphorylation and removal of Cdc6	19/510	73/10856	6.26043E-10	3.09773E-09	1.45476E-09	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-8939902	Regulation of RUNX2 expression and activity	19/510	73/10856	6.26043E-10	3.09773E-09	1.45476E-09	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-8948216	Collagen chain trimerization	15/510	44/10856	6.36439E-10	3.13439E-09	1.47197E-09	COL1A1/COL2A1/COL3A1/COL5A2/COL1A2/COL4A2/COL6A1/COL6A2/COL6A3/COL5A1/COL18A1/COL7A1/COL1	15
Common	R-HSA-72649	Translation initiation complex formation	17/510	58/10856	6.69114E-10	3.26465E-09	1.53315E-09	EIF2S1/RPSA/RPS19/RPS10/EIF3B/EIF4A1/RPS3A/RPS7/RPS8/RPS15A/RPS18/RPS13/RPS26/RPS27A/EIF3A/EIF4A	17
Common	R-HSA-72702	Ribosomal scanning and start codon recognition	17/510	58/10856	6.69114E-10	3.26465E-09	1.53315E-09	EIF2S1/RPSA/RPS19/RPS10/EIF3B/EIF4A1/RPS3A/RPS7/RPS8/RPS15A/RPS18/RPS13/RPS26/RPS27A/EIF3A/EIF4A	17
Common	R-HSA-350562	Regulation of ornithine decarboxylase (ODC)	16/510	51/10856	6.95511E-10	3.36217E-09	1.57894E-09	PSMA7/NQO1/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/PS	16
Common	R-HSA-6811436	COPI-independent Golgi-to-ER retrograde traffic	16/510	51/10856	6.95511E-10	3.36217E-09	1.57894E-09	TUBAL3/TUBB4A/CAPZA1/TUBA1B/TUBA4A/TUBB4B/TUBB3/TUBB2A/TUBB8/TUBA3E/TUBA1A/TUBA1C/TUBB6/TU	16
Common	R-HSA-168255	Influenza Infection	28/510	156/10856	7.19652E-10	3.46291E-09	1.62625E-09	ISG15/RPLP1/RPLP2/HSP90AA1/RPSA/HSPA1A/SLC25A6/RPL7/CALR/RPS19/RPS10/RPL34/RPS3A/RPS7/RPS8/RP	28
Common	R-HSA-8950505	Gene and protein expression by JAK-STAT signaling after Interleukin-12 stimulation	14/510	38/10856	7.29942E-10	3.49639E-09	1.64198E-09	ANXA2/GSTA2/LCP1/MIF/TCP1/HNRNPA2B1/CFL1/MSN/HSPA9/CAPZA1/CDC42/RAP1B/PPIA/ARF1	14
Common	R-HSA-174178	APC/C:Cdh1 mediated degradation of Cdc20 and other APC/C:Cdh1 targeted proteins in late mitosis/early G1	19/510	74/10856	8.06134E-10	3.8264E-09	1.79695E-09	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-179419	APC:Cdc20 mediated degradation of cell cycle proteins prior to satisfation of the cell cycle checkpoint	19/510	74/10856	8.06134E-10	3.8264E-09	1.79695E-09	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-72662	Activation of the mRNA upon binding of the cap-binding complex and eIFs, and subsequent binding to 43S	17/510	59/10856	8.99677E-10	4.25118E-09	1.99644E-09	EIF2S1/RPSA/RPS19/RPS10/EIF3B/EIF4A1/RPS3A/RPS7/RPS8/RPS15A/RPS18/RPS13/RPS26/RPS27A/EIF3A/EIF4A	17
Common	R-HSA-390450	Folding of actin by CCT/TriC	8/510	10/10856	9.31319E-10	4.38096E-09	2.05739E-09	TCP1/CCT6A/CCT5/CCT8/CCT4/ACTB/CCT2/CCT6B	8
Common	R-HSA-9613829	Chaperone Mediated Autophagy	11/510	22/10856	9.74484E-10	4.56354E-09	2.14313E-09	HSP90AA1/HSP90AB1/VIM/UBB/UBC/HSPA8/GFAP/RPS27A/UBA52/EEF1A1/HBB	11
Common	R-HSA-195253	Degradation of beta-catenin by the destruction complex	20/510	83/10856	9.79297E-10	4.5657E-09	2.14415E-09	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PPP2R1A/PSMB3/PSMB	20
Common	R-HSA-1234174	Cellular response to hypoxia	19/510	75/10856	1.03327E-09	4.79604E-09	2.25232E-09	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-4086400	PCP/CE pathway	21/510	92/10856	1.08809E-09	5.0282E-09	2.36134E-09	PSMA7/PFN1/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/P	21
Common	R-HSA-176409	APC/C:Cdc20 mediated degradation of mitotic proteins	19/510	76/10856	1.31853E-09	6.0664E-09	2.8489E-09	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-72764	Eukaryotic Translation Termination	21/510	93/10856	1.34498E-09	6.16107E-09	2.89336E-09	RPLP1/RPLP2/RPSA/APEH/RPL7/RPS19/RPS10/RPL34/RPS3A/RPS7/RPS8/RPS15A/RPS18/RPS13/RPL7A/RPS26/R	21
Common	R-HSA-2022090	Assembly of collagen fibrils and other multimeric structures	17/510	61/10856	1.59448E-09	7.27222E-09	3.41518E-09	COL1A1/COL2A1/COL3A1/COL5A2/CTSB/COL1A2/COL4A2/COL6A1/COL6A2/COL6A3/COL5A1/COL18A1/COL7A1/	17
Common	R-HSA-176814	Activation of APC/C and APC/C:Cdc20 mediated degradation of mitotic proteins	19/510	77/10856	1.67529E-09	7.54872E-09	3.54503E-09	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19

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Common	R-HSA-382556	ABC-family proteins mediated transport	22/510	103/10856	1.67669E-09	7.54872E-09	3.54503E-09	PSMA7/APOA1/EIF2S1/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/I	22
Common	R-HSA-9020702	Interleukin-1 signaling	22/510	103/10856	1.67669E-09	7.54872E-09	3.54503E-09	PSMA7/APP/HMGB1/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PS	22
Common	R-HSA-9020591	Interleukin-12 signaling	15/510	47/10856	1.82545E-09	8.18334E-09	3.84306E-09	P4HB/ANXA2/GSTA2/LCP1/MIF/TCP1/HNRNPA2B1/CFL1/MSN/HSPA9/CAPZA1/CDC42/RAP1B/PPIA/ARF1	15
Common	R-HSA-70171	Glycolysis	18/510	71/10856	2.82082E-09	1.25917E-08	5.9133E-09	GAPDHS/PGK1/ALDOA/GAPDH/ALDOB/ENO1/GPI/PGK2/ENO2/ALDOC/ENO3/PKM/PGAM2/PGAM1/PPP2R1A/PKL	18
Common	R-HSA-192823	Viral mRNA Translation	20/510	89/10856	3.64713E-09	1.62112E-08	7.6131E-09	RPLP1/RPLP2/RPSA/RPL7/RPS19/RPS10/RPL34/RPS3A/RPS7/RPS8/RPS15A/RPS18/RPS13/RPL7A/RPS26/RPL31/F	20
Common	R-HSA-8939211	ESR-mediated signaling	33/510	223/10856	3.84537E-09	1.70202E-08	7.99304E-09	H2BC12/HSPB1/H2AC8/H2BC11/CTSD/HSP90AA1/HSP90AB1/MMP2/H2AZ1/CALM1/H2AX/H2AC7/H2BC17/H2B	33
Common	R-HSA-176408	Regulation of APC/C activators between G1/S and early anaphase	19/510	81/10856	4.19201E-09	1.84765E-08	8.67696E-09	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-2871837	FCERI mediated NF-kB activation	19/510	82/10856	5.22202E-09	2.29201E-08	1.07637E-08	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-70326	Glucose metabolism	20/510	91/10856	5.5046E-09	2.40597E-08	1.12989E-08	GAPDHS/GOT2/PGK1/ALDOA/GAPDH/ALDOB/ENO1/GPI/PGK2/ENO2/ALDOC/ENO3/PKM/PGAM2/PGAM1/PPP2R1	20
Common	R-HSA-72695	Formation of the ternary complex, and subsequently, the 43S complex	15/510	51/10856	6.50512E-09	2.83148E-08	1.32972E-08	EIF2S1/RPSA/RPS19/RPS10/EIF3B/RPS3A/RPS7/RPS8/RPS15A/RPS18/RPS13/RPS26/RPS27A/EIF3A/EIF3C	15
Common	R-HSA-9633012	Response of EIF2AK4 (GCN2) to amino acid deficiency	21/510	101/10856	6.59647E-09	2.85938E-08	1.34282E-08	EIF2S1/RPLP1/RPLP2/RPSA/RPL7/RPS19/RPS10/RPL34/RPS3A/RPS7/RPS8/RPS15A/RPS18/RPS13/RPL7A/RPS26/I	21
Common	R-HSA-2995410	Nuclear Envelope (NE) Reassembly	18/510	75/10856	7.284E-09	3.14441E-08	1.47668E-08	TUBAL3/TUBB4A/PPP2R1A/RAN/TUBA1B/TUBA4A/TUBB4B/TUBB3/TUBB2A/KPNB1/TUBB8/TUBA3E/TUBA1A/TUBA	18
Common	R-HSA-351202	Metabolism of polyamines	16/510	59/10856	7.49829E-09	3.21049E-08	1.50771E-08	PSMA7/NQO1/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/PSI	16
Common	R-HSA-8866654	E3 ubiquitin ligases ubiquitinate target proteins	16/510	59/10856	7.49829E-09	3.21049E-08	1.50771E-08	H2BC12/HLA-A/H2BC11/UBB/UBC/H2BC17/H2BC3/VCP/H2BC5/RPS27A/UBA52/H2BC9/H2BC1/H2BC15/H2BC14	16
Common	R-HSA-2408557	Selenocysteine synthesis	20/510	93/10856	8.20714E-09	3.49971E-08	1.64354E-08	RPLP1/RPLP2/RPSA/RPL7/RPS19/RPS10/RPL34/RPS3A/RPS7/RPS8/RPS15A/RPS18/RPS13/RPL7A/RPS26/RPL31/F	20
Common	R-HSA-5632684	Hedgehog 'on' state	19/510	85/10856	9.88129E-09	4.17962E-08	1.96284E-08	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-69002	DNA Replication Pre-Initiation	19/510	85/10856	9.88129E-09	4.17962E-08	1.96284E-08	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-380320	Recruitment of NuMA to mitotic centrosomes	20/510	94/10856	9.97735E-09	4.20331E-08	1.97396E-08	TUBAL3/TUBB4A/TUBB/HSP90AA1/PPP2R1A/YWHAG/YWHAE/TUBA1B/TUBA4A/TUBB4B/TUBB3/TUBB2A/TUBB8/T	20
Common	R-HSA-2132295	MHC class II antigen presentation	23/510	123/10856	1.08295E-08	4.54405E-08	2.13398E-08	TUBAL3/TUBB4A/CTSD/CTSB/CTSH/RAB7A/CAPZA1/CTSC/TUBA1B/TUBA4A/TUBB4B/ARF1/CLTC/TUBB3/TUBB2A/TU	23
Common	R-HSA-975956	Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)	20/510	95/10856	1.2095E-08	5.05484E-08	2.37385E-08	RPLP1/RPLP2/RPSA/RPL7/RPS19/RPS10/RPL34/RPS3A/RPS7/RPS8/RPS15A/RPS18/RPS13/RPL7A/RPS26/RPL31/F	20
Common	R-HSA-5693571	Nonhomologous End-Joining (NHEJ)	17/510	69/10856	1.24833E-08	5.19642E-08	2.44034E-08	H2BC12/H2BC11/XRCC6/H2AX/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/H3-4/H2BC21/H2BU1/H2BC9/H2	17
Common	R-HSA-3000170	Syndecan interactions	11/510	27/10856	1.45293E-08	6.02419E-08	2.82908E-08	COL1A1/COL3A1/FN1/VTN/ITGB1/COL5A2/THBS1/COL1A2/ACTN1/COL5A1/TNC	11
Common	R-HSA-1632852	Macroautophagy	24/510	136/10856	1.70173E-08	7.028E-08	3.30049E-08	TUBAL3/TUBB4A/HSP90AA1/VIM/UBB/UBC/HSPA8/VDAC1/VCP/RPS27A/UBA52/TUBA1B/TUBA4A/TUBB4B/TUBB3	24
Common	R-HSA-983231	Factors involved in megakaryocyte development and platelet production	27/510	168/10856	1.74613E-08	7.18311E-08	3.37333E-08	TUBAL3/HBD/HBE1/TUBB4A/CAPZA1/ACTB/CDC42/TUBA1B/TUBA4A/TUBB4B/H3C1/HBB/HBG1/HBG2/H3-3A/TUB	27
Common	R-HSA-3214858	RMTs methylate histone arginines	18/510	79/10856	1.76004E-08	7.21204E-08	3.38692E-08	H2AC8/H2AZ1/H2AC13/H2AX/H2AC7/H4C9/H3C1/H2AC20/H2AC18/H3C14/H2AZ2/H2AW/H2AC21/H2AC6/H2A	18
Common	R-HSA-174143	APC/C-mediated degradation of cell cycle proteins	19/510	88/10856	1.81438E-08	7.37707E-08	3.46442E-08	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-453276	Regulation of mitotic cell cycle	19/510	88/10856	1.81438E-08	7.37707E-08	3.46442E-08	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-9006931	Signaling by Nuclear Receptors	38/510	299/10856	1.89406E-08	7.67131E-08	3.6026E-08	H2BC12/ALDH1A1/APOE/HSPB1/H2AC8/APOD/H2BC11/CTSD/HSP90AA1/HSP90AB1/MMP2/H2AZ1/CALM1/H2A	38
Common	R-HSA-5693607	Processing of DNA double-strand break ends	20/510	98/10856	2.11966E-08	8.552E-08	4.01619E-08	H2BC12/H2BC11/UBB/UBC/H2AX/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/RPS27A/UBA52/H3-4/H2BC21/	20
Common	R-HSA-438064	Post NMDA receptor activation events	18/510	80/10856	2.17368E-08	8.73638E-08	4.10278E-08	TUBAL3/TUBB4A/NEFL/CALM1/ACTN2/TUBA1B/TUBA4A/TUBB4B/TUBB3/TUBB2A/TUBB8/TUBA3E/TUBA1A/TUBA1	18
Common	R-HSA-2408522	Selenoamino acid metabolism	22/510	118/10856	2.39688E-08	9.59667E-08	4.50679E-08	RPLP1/RPLP2/RPSA/RPL7/AHCY/RPS19/RPS10/RPL34/RPS3A/RPS7/RPS8/RPS15A/RPS18/RPS13/RPL7A/RPS26/RI	22
Common	R-HSA-69052	Switching of origins to a post-replicative state	19/510	91/10856	3.2402E-08	1.29238E-07	6.06929E-08	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-446353	Cell-extracellular matrix interactions	9/510	18/10856	3.45799E-08	1.36642E-07	6.41697E-08	ITGB1/ACTN1/FLNA/VASP/ACTB/ACTG1/ILK/FLNC/RSU1	9
Common	R-HSA-1280218	Adaptive Immune System	70/510	763/10856	3.46364E-08	1.36642E-07	6.41697E-08	TUBAL3/PSMA7/ICOSLG/C3/COL1A1/COL2A1/COL3A1/FGB/TUBB4A/HLA-A/ITGB1/CTSD/CTSB/COL1A2/HMGB1/CT	70
Common	R-HSA-447115	Interleukin-12 family signaling	15/510	57/10856	3.46489E-08	1.36642E-07	6.41697E-08	P4HB/ANXA2/GSTA2/LCP1/MIF/TCP1/HNRNPA2B1/CFL1/MSN/HSPA9/CAPZA1/CDC42/RAP1B/PPIA/ARF1	15
Common	R-HSA-8982491	Glycogen metabolism	11/510	29/10856	3.53833E-08	1.39015E-07	6.52845E-08	PYGL/UBB/UBC/CALM1/PYGB/PYGM/PGM1/RPS27A/UBA52/GBE1/UGP2	11
Common	R-HSA-5607764	CLEC7A (Dectin-1) signaling	20/510	101/10856	3.62927E-08	1.42056E-07	6.67125E-08	PSMA7/UBB/UBC/CALM1/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/	20
Common	R-HSA-69202	Cyclin E associated events during G1/S transition	18/510	83/10856	4.00937E-08	1.5635E-07	7.34253E-08	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	18
Common	R-HSA-5668541	TNFR2 non-canonical NF-kB pathway	20/510	102/10856	4.32057E-08	1.67862E-07	7.88315E-08	PSMA7/TNFRSF6B/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMI	20
Common	R-HSA-983705	Signaling by the B Cell Receptor (BCR)	21/510	112/10856	4.51075E-08	1.74604E-07	8.19978E-08	PSMA7/UBB/UBC/CALM1/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/	21
Common	R-HSA-983189	Kinesins	15/510	59/10856	5.74417E-08	2.21531E-07	1.04035E-07	TUBAL3/TUBB4A/TUBA1B/TUBA4A/TUBB4B/TUBB3/TUBB2A/TUBB8/TUBA3E/TUBA1A/TUBA1C/TUBB6/TUBB2B/TU	15
Common	R-HSA-69656	Cyclin A:Cdk2-associated events at S phase entry	18/510	85/10856	5.9309E-08	2.27894E-07	1.07024E-07	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	18
Common	R-HSA-927802	Nonsense-Mediated Decay (NMD)	21/510	115/10856	7.2827E-08	2.77802E-07	1.30461E-07	RPLP1/RPLP2/RPSA/RPL7/PPP2R1A/RPS19/RPS10/RPL34/RPS3A/RPS7/RPS8/RPS15A/RPS18/RPS13/RPL7A/RPS2	21
Common	R-HSA-975957	Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC)	21/510	115/10856	7.2827E-08	2.77802E-07	1.30461E-07	RPLP1/RPLP2/RPSA/RPL7/PPP2R1A/RPS19/RPS10/RPL34/RPS3A/RPS7/RPS8/RPS15A/RPS18/RPS13/RPL7A/RPS2	21
Common	R-HSA-1430728	Metabolism	148/510	2119/10856	8.0983E-08	3.07794E-07	1.44546E-07	ACOT7/AGRN/MAN2B1/GAPDHS/HS3ST1/PSMA7/SLC16A3/PHGDH/B4GAT1/AOC2/IDH1/APOM/VNN1/VNN2/LDH	148
Common	R-HSA-5673001	RAF/MAP kinase cascade	35/510	280/10856	1.06451E-07	4.03129E-07	1.89317E-07	PSMA7/FGB/FN1/NEFL/UBB/UBC/CALM1/NCAM1/VCL/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSI	35
Common	R-HSA-8852135	Protein ubiquitination	17/510	79/10856	1.08023E-07	4.07613E-07	1.91423E-07	H2BC12/HLA-A/H2BC11/UBB/UBC/UBA1/H2BC17/H2BC3/VCP/H2BC5/RPS27A/UBA52/H2BC9/H2BC1/H2BC15/H	17
Common	R-HSA-202424	Downstream TCR signaling	19/510	98/10856	1.13772E-07	4.27768E-07	2.00888E-07	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-5684996	MAPK1/MAPK3 signaling	35/510	286/10856	1.80178E-07	6.75025E-07	3.17005E-07	PSMA7/FGB/FN1/NEFL/UBB/UBC/CALM1/NCAM1/VCL/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSI	35
Common	R-HSA-5653656	Vesicle-mediated transport	62/510	673/10856	1.99322E-07	7.4409E-07	3.4944E-07	TUBAL3/COL1A1/COL3A1/APOA1/APOE/TF/FTH1/APOB/TUBB4A/APP/HSP90AA1/COL1A2/COL4A2/UBB/UBC/CALM	62
Common	R-HSA-1799339	SRP-dependent cotranslational protein targeting to membrane	20/510	112/10856	2.18652E-07	8.13355E-07	3.81968E-07	RPLP1/RPLP2/RPSA/RPL7/RPS19/RPS10/RPL34/RPS3A/RPS7/RPS8/RPS15A/RPS18/RPS13/RPL7A/RPS26/RPL31/F	20
Common	R-HSA-442755	Activation of NMDA receptors and postsynaptic events	18/510	93/10856	2.52249E-07	9.35014E-07	4.39102E-07	TUBAL3/TUBB4A/NEFL/CALM1/ACTN2/TUBA1B/TUBA4A/TUBB4B/TUBB3/TUBB2A/TUBB8/TUBA3E/TUBA1A/TUBA1	18
Common	R-HSA-9707564	Cytoprotection by HMOX1	21/510	124/10856	2.77311E-07	1.02429E-06	4.81029E-07	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	21
Common	R-HSA-162582	Signal Transduction	169/510	2558/10856	3.10833E-07	1.14408E-06	5.37285E-07	TUBAL3/ADAM10/NRP1/PSMA7/MYL12A/LAMA5/NRP2/H2BC12/UTS2/ALDH1A1/F2/PLG/PLAT/C3/C5/KNG1/COL	169
Common	R-HSA-186797	Signaling by PDGF	14/510	58/10856	3.21171E-07	1.178E-06	5.53212E-07	PLG/PLAT/COL2A1/COL3A1/COL5A2/THBS1/COL4A2/COL6A1/COL6A2/COL6A3/COL5A1/THBS2/THBS4/THBS3	14
Common	R-HSA-1280215	Cytokine Signaling in Immune system	64/510	715/10856	3.52084E-07	1.28688E-06	6.04347E-07	PSMA7/LAMA5/FLNB/TNFRSF6B/F13A1/TIMP1/FN1/ANXA1/HLA-A/APP/ISG15/ITGB1/P4HB/ANXA2/HSP90AA1/CC	64
Common	R-HSA-8878159	Transcriptional regulation by RUNX3	18/510	96/10856	4.15483E-07	1.51334E-06	7.10695E-07	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	18
Common	R-HSA-5683057	MAPK family signaling cascades	37/510	325/10856	5.01568E-07	1.82057E-06	8.54977E-07	PSMA7/FGB/FN1/HSPB1/NEFL/UBB/UBC/CALM1/NCAM1/VCL/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSM	37
Common	R-HSA-162906	HIV Infection	30/510	234/10856	5.10322E-07	1.84596E-06	8.669E-07	PSMA7/HLA-A/SLC25A5/NPM1/UBB/UBC/SLC25A4/SLC25A6/XRCC6/HMGA1/PSMB1/PSMA1/PSMA2/PSMA3/PSM	30
Common	R-HSA-3247509	Chromatin modifying enzymes	33/510	274/10856	5.89889E-07	2.11915E-06	9.95198E-07	H2BC12/H2AC8/H2BC11/H2AZ1/H2AC13/H2AX/H2AC7/H2BC17/H2BC3/H2BC5/ACTB/H4C9/H3C1/H2AC20/H2B	33
Common	R-HSA-4839726	Chromatin organization	33/510	274/10856	5.89889E-07	2.11915E-06	9.95198E-07	H2BC12/H2AC8/H2BC11/H2AZ1/H2AC13/H2AX/H2AC7/H2BC17/H2BC3/H2BC5/ACTB/H4C9/H3C1/H2AC20/H2B	33
Common	R-HSA-446652	Interleukin-1 family signaling	22/510	141/10856	6.28657E-07	2.25072E-06	1.05698E-06	PSMA7/APP/HMGB1/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PS	22
Common	R-HSA-140342	Apoptosis induced DNA fragmentation	7/510	13/10856	6.50054E-07	2.31155E-06	1.08555E-06	HMGB1/H1-4/H1-5/H1-3/H1-2/H1-1/KPNB1	7
Common	R-HSA-75035	Chk1/Chk2(Cds1) mediated inactivation of Cyclin B:Cdk1 complex	7/510	13/10856	6.50054E-07	2.31155E-06	1.08555E-06	YWHAQ/YWHAB/SFN/YWHAG/YWHAE/YWHAZ/YWHAH	7
Common	R-HSA-202403	TCR signaling	20/510	120/10856	6.95141E-07	2.46352E-06	1.15692E-06	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/VASP/P	20
Common	R-HSA-5627123	RHO GTPases activate PAKs	9/510	24/10856	7.21604E-07	2.54869E-06	1.19692E-06	MYL12A/CALM1/FLNA/MYH9/MYH10/MYH11/MYL6/CDC42/MYH14	9
Common	R-HSA-8878166	Transcriptional regulation by RUNX2	20/510	121/10856	7.97069E-07	2.80579E-06	1.31766E-06	PSMA7/COL1A1/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2	20
Common	R-HSA-72766	Translation	34/510	291/10856	8.09123E-07	2.8387E-06	1.33311E-06	EIF2S1/RPLP1/RPLP2/RPSA/EEF2/APEH/RPL7/EEF1B2/EEF1G/EEF1D/RPS19/GARS1/RPS10/RPL34/EIF3B/EIF4A1/RI	34
Common	R-HSA-6807878	COPI-mediated anterograde transport	18/510	101/10856	9.10857E-07	3.18496E-06	1.49572E-06	TUBAL3/TUBB4A/CAPZA1/ARF3/TUBA1B/TUBA4A/TUBB4B/ARF1/TUBB3/TUBB2A/TUBB8/TUBA3E/TUBA1A/TUBA1	18
Common	R-HSA-140877	Formation of Fibrin Clot (Clotting Cascade)	11/510	39/10856	1.11673E-06	3.89186E-06	1.8277E-06	F13A1/F2/F10/SERPINC1/A2M/KNG1/FGB/KLKB1/SERPING1/SERPIND1/F5	11
Common	R-HSA-3858494	Beta-catenin independent WNT signaling	22/510	146/10856	1.15634E-06	4.01656E-06	1.88626E-06	PSMA7/PFN1/UBB/UBC/CALM1/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/P	22
Common	R-HSA-6802946	Signaling by moderate kinase activity BRAF mutants	12/510	47/10856	1.17689E-06	4.03451E-06	1.89469E-06	FGB/FN1/CALM1/VCL/PEBP1/YWHAB/PHB/ACTB/RAP1B/RAP1A/ACTG1/TLN1	12
Common	R-HSA-6802949	Signaling by RAS mutants	12/510	47/10856	1.17689E-06	4.03451E-06	1.89469E-06	FGB/FN1/CALM1/VCL/PEBP1/YWHAB/PHB/ACTB/RAP1B/RAP1A/ACTG1/TLN1	12
Common	R-HSA-6802955	Paradoxical activation of RAF signaling by kinase inactive BRAF	12/510	47/10856	1.17689E-06	4.03451E-06	1.89469E-06	FGB/FN1/CALM1/VCL/PEBP1/YWHAB/PHB/ACTB/RAP1B/RAP1A/ACTG1/TLN1	12
Common	R-HSA-9649948	Signaling downstream of RAS mutants	12/510	47/10856	1.17689E-06	4.03451E-06	1.89469E-06	FGB/FN1/CALM1/VCL/PEBP1/YWHAB/PHB/ACTB/RAP1B/RAP1A/ACTG1/TLN1	12
Common	R-HSA-168273	Influenza Viral RNA Transcription and Replication	21/510	135/10856	1.19003E-06	4.06626E-06	1.9096E-06	RPLP1/RPLP2/HSP90AA1/RPSA/RPL7/RPS19/RPS10/RPL34/RPS3A/RPS7/RPS8/RPS15A/RPS18/RPS13/RPL7A/RPS	21
Common	R-HSA-373755	Semaphorin interactions	14/510	65/10856	1.42588E-06	4.85631E-06	2.28062E-06	NRP1/MYL12A/SEMA7A/ITGB1/HSP90AA1/HSP90AB1/CFL1/MYH9/MYH10/MYH11/MYL6/SEMA3A/MYH14/TLN1	14
Common	R-HSA-445355	Smooth Muscle Contraction	11/510	40/10856	1.47581E-06	5.0101E-06	2.35285E-06	MYL12A/ANXA1/ANXA2/CALM1/MYL6B/VCL/MYH11/MYL6/ACTA2/ACTG2/TLN1	11
Common	R-HSA-8953854	Metabolism of RNA	59/510	673/10856	2.08605E-06	7.05893E-06	3.31502E-06	PSMA7/HSPB1/RPLP1/RPLP2/HNRNPC/RPSA/HNRNPA1/UBB/UBC/HSPA1A/HSPA8/RPL7/NCL/PSMB1/HNRNPA2B	59
Common	R-HSA-5663220	RHO GTPases Activate Formins	21/510	140/10856	2.18173E-06	7.35896E-06	3.45592E-06	TUBAL3/TUBB4A/ITGB1/PFN1/PPP2R1A/ACTB/CDC42/ACTG1/TUBA1B/TUBA4A/TUBB4B/TUBB3/TUBB2A/TUBB8/T	21
Common	R-HSA-111447	Activation of BAD and translocation to mitochondria	7/510	15/10856	2.24467E-06	7.547E-06	3.54422E-06	YWHAQ/YWHAB/SFN/YWHAG/YWHAE/YWHAZ/YWHAH	7
Common	R-HSA-9635486	Infection with Mycobacterium tuberculosis	9/510	27/10856	2.27907E-06	7.63818E-06	3.58704E-06	PGK1/LTF/ENO1/UBB/UBC/RAB7A/RPS27A/UBA52/KPNB1	9
Common	R-HSA-9006934	Signaling by Receptor Tyrosine Kinases	48/510	506/10856	2.34647E-06	7.839E-06	3.68135E-06	ADAM10/NRP1/LAMA5/NRP2/PLG/PLAT/COL1A1/COL2A1/COL3A1/APOE/FN1/HSPB1/ITGB1/COL5A2/HSP90AA1/	48
Common	R-HSA-199977	ER to Golgi Anterograde Transport	22/510	154/10856	2.88233E-06	9.59862E-06	4.5077E-06	TUBAL3/TUBB4A/F5/CAPZA1/CTSC/ARF3/TUBA1B/TUBA4A/TUBB4B/ARF1/COL7A1/TUBB3/TUBB2A/TUBB8/TUBA3I	22
Common	R-HSA-69239	Synthesis of DNA	19/510	120/10856	2.92385E-06	9.70607E-06	4.55817E-06	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-6811434	COPI-dependent Golgi-to-ER retrograde traffic	17/510	99/10856	3.11574E-06	1.03104E-05	4.84199E-06	TUBAL3/TUBB4A/ARF3/TUBA1B/TUBA4A/TUBB4B/ARF1/TUBB3/TUBB2A/TUBB8/TUBA3E/TUBA1A/TUBA1C/TUBB6/	17
Common	R-HSA-5693567	HDR through Homologous Recombination (HRR) or Single Strand Annealing (SSA)	20/510	132/10856	3.24611E-06	1.07081E-05	5.02872E-06	H2BC12/H2BC11/UBB/UBC/H2AX/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/RPS27A/UBA52/H3-4/H2BC21/	20
Common	R-HSA-2559584	Formation of Senescence-Associated Heterochromatin Foci (SAHF)	7/510	16/10856	3.82943E-06	1.25533E-05	5.89531E-06	H1-4/H1-5/H1-3/H1-2/HMGA1/HMGA2/H1-1	7
Common	R-HSA-3322077	Glycogen synthesis	7/510	16/10856	3.82943E-06	1.25533E-05	5.89531E-06	UBB/UBC/PGM1/RPS27A/UBA52/GBE1/UGP2	7
Common	R-HSA-6802948	Signaling by high-kinase activity BRAF mutants	10/510	36/10856	4.03482E-06	1.31855E-05	6.19216E-06	FGB/FN1/VCL/PEBP1/YWHAB/ACTB/RAP1B/RAP1A/ACTG1/TLN1	10
Common	R-HSA-2454202	Fc epsilon receptor (FCERI) signaling	20/510	134/10856	4.11424E-06	1.34011E-05	6.29343E-06	PSMA7/UBB/UBC/CALM1/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/	20
Common	R-HSA-975634	Retinoid metabolism and transport	11/510	44/10856	4.12636E-06	1.34011E-05	6.29343E-06	AGRN/APOM/APOA1/APOE/APOC3/RBP4/TTR/APOB/GPC1/HSPG2/LRP1	11
Common	R-HSA-2682334	EPH-Ephrin signaling	16/510	92/10856	5.11345E-06	1.65556E-05	7.77484E-06	SDCBP/ADAM10/MYL12A/MMP2/CFL1/MYH9/MYH10/MYH11/CLTCL1/MYL6/ACTB/CDC42/ACTR3/ACTG1/CLTC/M	16
Common	R-HSA-948021	Transport to the Golgi and subsequent modification	24/510	185/10856	5.7765E-06	1.86448E-05	8.75596E-06	TUBAL3/TUBB4A/F5/B4GALT1/MGAT1/CAPZA1/CTSC/ARF3/TUBA1B/TUBA4A/TUBB4B/ARF1/COL7A1/TUBB3/TUBB	24
Common	R-HSA-140837	Intrinsic Pathway of Fibrin Clot Formation	8/510	23/10856	5.89014E-06	1.88953E-05	8.8736E-06	F2/F10/SERPINC1/A2M/KNG1/KLKB1/SERPING1/SERPIND1	8
Common	R-HSA-9637690	Response of Mtb to phagocytosis	8/510	23/10856	5.89014E-06	1.88953E-05	8.8736E-06	PGK1/ENO1/UBB/UBC/RAB7A/RPS27A/UBA52/KPNB1	8
Common	R-HSA-5693538	Homology Directed Repair	20/510	138/10856	6.50827E-06	2.08146E-05	9.77494E-06	H2BC12/H2BC11/UBB/UBC/H2AX/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/RPS27A/UBA52/H3-4/H2BC21/	20
Common	R-HSA-5619115	Disorders of transmembrane transporters	23/510	175/10856	7.25234E-06	2.31237E-05	1.08594E-05	PSMA7/CP/APOA1/SLC3A2/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSM	23
Common	R-HSA-69306	DNA Replication	19/510	128/10856	7.75479E-06	2.46508E-05	1.15765E-05	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-5617833	Cilium Assembly	25/510	201/10856	7.89077E-06	2.50073E-05	1.17439E-05	TUBAL3/TUBB4A/TUBB/HSP90AA1/TCP1/PPP2R1A/CCT5/CCT8/CCT4/YWHAG/YWHAE/TUBA1B/TUBA4A/TUBB4B/	25
Common	R-HSA-5621481	C-type lectin receptors (CLRs)	20/510	142/10856	1.00971E-05	3.19031E-05	1.49824E-05	PSMA7/UBB/UBC/CALM1/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/	20
Common	R-HSA-6806667	Metabolism of fat-soluble vitamins	11/510	48/10856	1.02481E-05	3.22832E-05	1.51608E-05	AGRN/APOM/APOA1/APOE/APOC3/RBP4/TTR/APOB/GPC1/HSPG2/LRP1	11
Common	R-HSA-69206	G1/S Transition	19/510	131/10856	1.09267E-05	3.43177E-05	1.61163E-05	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PPP2R1A/PSMB3/PSME	19
Common	R-HSA-5674135	MAP2K and MAPK activation	10/510	40/10856	1.13547E-05	3.55555E-05	1.66976E-05	FGB/FN1/VCL/PEBP1/YWHAB/ACTB/RAP1B/RAP1A/ACTG1/TLN1	10
Common	R-HSA-9711097	Cellular response to starvation	21/510	156/10856	1.24402E-05	3.88386E-05	1.82394E-05	EIF2S1/RPLP1/RPLP2/RPSA/RPL7/RPS19/RPS10/RPL34/RPS3A/RPS7/RPS8/RPS15A/RPS18/RPS13/RPL7A/RPS26/I	21
Common	R-HSA-75205	Dissolution of Fibrin Clot	6/510	13/10856	1.35046E-05	4.19123E-05	1.96829E-05	PLG/PLAU/PLAT/SERPINE1/ANXA2/SERPINF2	6
Common	R-HSA-9637687	Suppression of phagosomal maturation	6/510	13/10856	1.35046E-05	4.19123E-05	1.96829E-05	UBB/UBC/RAB7A/RPS27A/UBA52/KPNB1	6
Common	R-HSA-3560782	Diseases associated with glycosaminoglycan metabolism	10/510	41/10856	1.43941E-05	4.45412E-05	2.09174E-05	AGRN/HEXB/VCAN/B4GALT1/OGN/GPC1/LUM/HSPG2/FMOD/EXT1	10
Common	R-HSA-446203	Asparagine N-linked glycosylation	32/510	304/10856	1.55441E-05	4.79582E-05	2.25222E-05	TUBAL3/TUBB4A/UBB/UBC/F5/B4GALT1/MGAT1/CALR/PDIA3/CAPZA1/CTSC/VCP/ARF3/RPS27A/UBA52/TUBA1B/T	32
Common	R-HSA-419037	NCAM1 interactions	10/510	42/10856	1.81084E-05	5.57058E-05	2.61606E-05	AGRN/COL2A1/COL3A1/COL5A2/COL4A2/COL6A1/COL6A2/COL6A3/NCAM1/COL5A1	10
Common	R-HSA-73894	DNA Repair	34/510	335/10856	1.83329E-05	5.62316E-05	2.64075E-05	H2BC12/H2AC8/ISG15/H2BC11/H2AZ1/UBB/UBC/XRCC6/H2AX/H2AC7/H2BC17/H2BC3/VCP/LOC102724334/H2	34
Common	R-HSA-5627117	RHO GTPases Activate ROCKs	7/510	20/10856	2.20116E-05	6.73184E-05	3.16141E-05	MYL12A/CFL1/MYH9/MYH10/MYH11/MYL6/MYH14	7
Common	R-HSA-9656223	Signaling by RAF1 mutants	10/510	43/10856	2.2617E-05	6.89687E-05	3.23891E-05	FGB/FN1/CALM1/VCL/YWHAB/ACTB/RAP1B/RAP1A/ACTG1/TLN1	10
Common	R-HSA-3371568	Attenuation phase	6/510	14/10856	2.26975E-05	6.90134E-05	3.24101E-05	HSP90AA1/HSP90AB1/HSPA1A/HSPA8/HSPA1L/HSPA2	6
Common	R-HSA-6807070	PTEN Regulation	19/510	140/10856	2.8587E-05	8.66698E-05	4.07019E-05	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-5620924	Intraflagellar transport	11/510	54/10856	3.36161E-05	0.000101623	4.77243E-05	TUBB4A/TUBA1B/TUBA4A/TUBB4B/TUBB3/TUBB2A/TUBA1A/TUBA1C/TUBB6/TUBB2B/TUBB1	11

Common	R-HSA-5693532	DNA Double-Strand Break Repair	21/510	167/10856	3.54129E-05	0.000106747	5.01307E-05	H2BC12/H2BC11/UBB/UBC/XRCC6/H2AX/H2BC17/H2BC3/LOC102724334/H2BC5/H4C9/RPS27A/UBA52/H3-4/H	21
Common	R-HSA-140875	Common Pathway of Fibrin Clot Formation	7/510	22/10856	4.46079E-05	0.000134079	6.29664E-05	F13A1/F2/F10/SERPINC1/FGB/SERPIND1/F5	7
Common	R-HSA-8963888	Chylomicron assembly	5/510	10/10856	4.64578E-05	0.000138844	6.5204E-05	APOA1/APOE/APOC3/APOB/P4HB	5
Common	R-HSA-8964058	HDL remodeling	5/510	10/10856	4.64578E-05	0.000138844	6.5204E-05	APOA1/APOE/APOC3/LCAT/PLTP	5
Common	R-HSA-8856688	Golgi-to-ER retrograde transport	18/510	133/10856	4.79641E-05	0.000142938	6.71268E-05	TUBAL3/TUBB4A/CAPZA1/ARF3/TUBA1B/TUBA4A/TUBB4B/ARF1/TUBB3/TUBB2A/TUBB8/TUBA3E/TUBA1A/TUBA1C	18
Common	R-HSA-9013418	RHOBTB2 GTPase cycle	7/510	23/10856	6.15469E-05	0.000182897	8.58923E-05	HSP90AA1/HNRNPC/HSP90AB1/ACTN1/CCT6A/ACTG1/CCT2	7
Common	R-HSA-453279	Mitotic G1 phase and G1/S transition	19/510	149/10856	6.83551E-05	0.000202555	9.5124E-05	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PPP2R1A/PSMB3/PSME	19
Common	R-HSA-446728	Cell junction organization	14/510	91/10856	8.12032E-05	0.00023995	0.000112685	ITGB1/ACTN1/FLNA/VASP/CDH6/CDH11/ACTB/ACTG1/ILK/LAMB3/FLNC/RSU1/CDH9/CDH10	14
Common	R-HSA-9614399	Regulation of localization of FOXO transcription factors	5/510	11/10856	8.18875E-05	0.000241292	0.000113316	YWHAQ/YWHAB/SFN/YWHAG/YWHAZ	5
Common	R-HSA-1500931	Cell-Cell communication	17/510	129/10856	0.000108363	0.000318411	0.000149532	ACTN4/ITGB1/ACTN1/FLNA/ACTN2/VASP/CDH6/CDH11/ACTB/ACTG1/ACTN3/ILK/LAMB3/FLNC/RSU1/CDH9/CDH1	17
Common	R-HSA-9648025	EML4 and NUDC in mitotic spindle formation	16/510	117/10856	0.000110283	0.000323149	0.000151757	TUBAL3/TUBB4A/PPP2R1A/TUBA1B/TUBA4A/TUBB4B/TUBB3/TUBB2A/TUBB8/TUBA3E/TUBA1A/TUBA1C/TUBB6/T	16
Common	R-HSA-3371511	HSF1 activation	5/510	12/10856	0.00013497	0.000393288	0.000184696	HSP90AA1/HSP90AB1/VCP/YWHAE/EEF1A1	5
Common	R-HSA-5689877	Josephin domain DUBs	5/510	12/10856	0.00013497	0.000393288	0.000184696	UBB/UBC/VCP/RPS27A/UBA52	5
Common	R-HSA-901042	Calnexin/calreticulin cycle	7/510	26/10856	0.000146046	0.000423853	0.00019905	UBB/UBC/CALR/PDIA3/RPS27A/UBA52/GANAB	7
Common	R-HSA-6791226	Major pathway of rRNA processing in the nucleolus and cytosol	21/510	184/10856	0.000146268	0.000423853	0.00019905	RPLP1/RPLP2/RPSA/RPL7/NCL/RPS19/RPS10/RPL34/RPS3A/RPS7/RPS8/RPS15A/RPS18/RPS13/RPL7A/RPS26/RPI	21
Common	R-HSA-8963898	Plasma lipoprotein assembly	6/510	19/10856	0.000167653	0.000484485	0.000227524	A2M/APOA1/APOE/APOC3/APOB/P4HB	6
Common	R-HSA-532668	N-glycan trimming in the ER and Calnexin/Calreticulin cycle	8/510	35/10856	0.000171689	0.000493429	0.000231724	UBB/UBC/CALR/PDIA3/VCP/RPS27A/UBA52/GANAB	8
Common	R-HSA-9706574	RHOBTB GTPase Cycle	8/510	35/10856	0.000171689	0.000493429	0.000231724	HSP90AA1/HNRNPC/HSP90AB1/VIM/ACTN1/CCT6A/ACTG1/CCT2	8
Common	R-HSA-69242	S Phase	19/510	162/10856	0.000210111	0.000602204	0.000282807	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	19
Common	R-HSA-5668914	Diseases of metabolism	25/510	245/10856	0.000215194	0.000615091	0.000288859	AGRN/B4GAT1/IDH1/ALDOB/HEXB/THBS1/UBB/UBC/VCAN/B4GALT1/OGN/AHCY/GPC1/THBS2/PGM1/GALK1/LUM	25
Common	R-HSA-2565942	Regulation of PLK1 Activity at G2/M Transition	13/510	88/10856	0.00022032	0.000628032	0.000294936	TUBB4A/TUBB/HSP90AA1/UBB/UBC/PPP2R1A/YWHAG/YWHAE/RPS27A/UBA52/TUBA4A/TUBB4B/TUBA1A	13
Common	R-HSA-5663202	Diseases of signal transduction by growth factor receptors and second messengers	35/510	395/10856	0.000221232	0.000628924	0.000295355	ADAM10/PSMA7/FGB/FN1/HSP90AA1/UBB/UBC/CALM1/VCL/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSM	35
Common	R-HSA-5625900	RHO GTPases activate CIT	6/510	20/10856	0.000230071	0.000652282	0.000306325	MYL12A/MYH9/MYH10/MYH11/MYL6/MYH14	6
Common	R-HSA-3371556	Cellular response to heat stress	13/510	89/10856	0.000247188	0.000698923	0.000328228	HSP90AA1/HSP90AB1/HSPA1A/HSPA5/HSPA8/HSPA6/HSPA1L/HSPA9/HSPA13/HSPA2/VCP/YWHAE/EEF1A1	13
Common	R-HSA-3299685	Detoxification of Reactive Oxygen Species	8/510	37/10856	0.000259255	0.000730416	0.000343018	CAT/GPX1/P4HB/GSTP1/GPX3/PRDX6/PRDX2/PRDX1	8
Common	R-HSA-6802952	Signaling by BRAF and RAF fusions	11/510	67/10856	0.000259719	0.000730416	0.000343018	FGB/FN1/CALM1/VCL/PEBP1/YWHAB/ACTB/RAP1B/RAP1A/ACTG1/TLN1	11
Common	R-HSA-2500257	Resolution of Sister Chromatid Cohesion	16/510	126/10856	0.00026491	0.000743023	0.000348938	TUBAL3/TUBB4A/PPP2R1A/TUBA1B/TUBA4A/TUBB4B/TUBB3/TUBB2A/TUBB8/TUBA3E/TUBA1A/TUBA1C/TUBB6/T	16
Common	R-HSA-8868773	rRNA processing in the nucleus and cytosol	21/510	194/10856	0.000305973	0.000855907	0.000401951	RPLP1/RPLP2/RPSA/RPL7/NCL/RPS19/RPS10/RPL34/RPS3A/RPS7/RPS8/RPS15A/RPS18/RPS13/RPL7A/RPS26/RPI	21
Common	R-HSA-416572	Sema4D induced cell migration and growth-cone collapse	6/510	21/10856	0.000309424	0.00086326	0.000405404	MYL12A/MYH9/MYH10/MYH11/MYL6/MYH14	6
Common	R-HSA-1852241	Organelle biogenesis and maintenance	28/510	296/10856	0.000328182	0.000913164	0.00042884	TUBAL3/TUBB4A/ATP5F1B/TUBB/HSP90AA1/CALM1/TCP1/PPP2R1A/HSPA9/CCT5/CCT8/CCT4/YWHAG/YWHAE/TU	28
Common	R-HSA-199991	Membrane Trafficking	49/510	634/10856	0.000371093	0.001029831	0.00048363	TUBAL3/TF/FTH1/APOB/TUBB4A/APP/UBB/UBC/CALM1/HSPA8/IGF2R/F5/YWHAQ/GDI1/YWHAB/SFN/MYH9/GDI2,	49
Common	R-HSA-390471	Association of TriC/CCT with target proteins during biosynthesis	8/510	39/10856	0.00038034	0.001049937	0.000493072	GAPDHS/TCP1/CCT6A/CCT5/CCT8/CCT4/CCT2/CCT6B	8
Common	R-HSA-76009	Platelet Aggregation (Plug Formation)	8/510	39/10856	0.00038034	0.001049937	0.000493072	F2/COL1A1/FGB/FN1/COL1A2/RAP1B/RAP1A/TLN1	8
Common	R-HSA-114452	Activation of BH3-only proteins	7/510	30/10856	0.000383844	0.001056831	0.000496309	YWHAQ/YWHAB/SFN/YWHAG/YWHAE/YWHAZ/YWHAH	7
Common	R-HSA-2979096	NOTCH2 Activation and Transmission of Signal to the Nucleus	6/510	22/10856	0.00040873	0.001122402	0.000527103	ADAM10/UBB/UBC/RPS27A/UBA52/CNTN1	6
Common	R-HSA-2214320	Anchoring fibril formation	5/510	15/10856	0.000454987	0.001233285	0.000579176	COL1A1/COL1A2/COL4A2/COL7A1/LAMB3	5
Common	R-HSA-2691230	Signaling by NOTCH1 HD Domain Mutants in Cancer	5/510	15/10856	0.000454987	0.001233285	0.000579176	ADAM10/UBB/UBC/RPS27A/UBA52	5
Common	R-HSA-2691232	Constitutive Signaling by NOTCH1 HD Domain Mutants	5/510	15/10856	0.000454987	0.001233285	0.000579176	ADAM10/UBB/UBC/RPS27A/UBA52	5
Common	R-HSA-354194	GRB2:SOS provides linkage to MAPK signaling for Integrins	5/510	15/10856	0.000454987	0.001233285	0.000579176	FGB/FN1/RAP1B/RAP1A/TLN1	5
Common	R-HSA-372708	p130Cas linkage to MAPK signaling for integrins	5/510	15/10856	0.000454987	0.001233285	0.000579176	FGB/FN1/RAP1B/RAP1A/TLN1	5
Common	R-HSA-8963899	Plasma lipoprotein remodeling	7/510	31/10856	0.000475985	0.001286878	0.000604344	APOA1/APOE/APOC3/APOB/LCAT/PLTP/MBTPS1	7
Common	R-HSA-6785807	Interleukin-4 and Interleukin-13 signaling	14/510	108/10856	0.000511368	0.001378985	0.000647599	LAMA5/F13A1/TIMP1/FN1/ANXA1/ITGB1/HSP90AA1/COL1A2/MMP2/VIM/HSPA8/HSP90B1/VCAM1/FSCN1	14
Common	R-HSA-6802957	Oncogenic MAPK signaling	12/510	84/10856	0.000522585	0.001405619	0.000660107	FGB/FN1/CALM1/VCL/PEBP1/YWHAB/PHB/ACTB/RAP1B/RAP1A/ACTG1/TLN1	12
Common	R-HSA-72312	rRNA processing	21/510	204/10856	0.000601681	0.00161423	0.000758075	RPLP1/RPLP2/RPSA/RPL7/NCL/RPS19/RPS10/RPL34/RPS3A/RPS7/RPS8/RPS15A/RPS18/RPS13/RPL7A/RPS26/RPI	21
Common	R-HSA-75153	Apoptotic execution phase	9/510	52/10856	0.000627123	0.001678194	0.000788114	GSN/VIM/HMGB1/H1-4/H1-5/H1-3/H1-2/H1-1/KPNB1	9
Common	R-HSA-1295596	Spry regulation of FGF signaling	5/510	16/10856	0.00063642	0.00168587	0.000791718	UBB/UBC/PPP2R1A/RPS27A/UBA52	5
Common	R-HSA-175474	Assembly Of The HIV Virion	5/510	16/10856	0.00063642	0.00168587	0.000791718	UBB/UBC/PPIA/RPS27A/UBA52	5
Common	R-HSA-3229121	Glycogen storage diseases	5/510	16/10856	0.00063642	0.00168587	0.000791718	UBB/UBC/RPS27A/UBA52/GBE1	5
Common	R-HSA-399954	Sema3A PAK dependent Axon repulsion	5/510	16/10856	0.00063642	0.00168587	0.000791718	NRP1/HSP90AA1/HSP90AB1/CFL1/SEMA3A	5
Common	R-HSA-375165	NCAM signaling for neurite out-growth	10/510	63/10856	0.000648401	0.00171328	0.000804591	AGRN/COL2A1/COL3A1/COL5A2/COL4A2/COL6A1/COL6A2/COL6A3/NCAM1/COL5A1	10
Common	R-HSA-3371571	HSF1-dependent transactivation	6/510	24/10856	0.000680553	0.001793719	0.000842367	HSP90AA1/HSP90AB1/HSPA1A/HSPA8/HSPA1L/HSPA2	6
Common	R-HSA-8963901	Chylomicron remodeling	4/510	10/10856	0.000805885	0.002113435	0.000992512	APOA1/APOE/APOC3/APOB	4
Common	R-HSA-937042	IRAK2 mediated activation of TAK1 complex	4/510	10/10856	0.000805885	0.002113435	0.000992512	UBB/UBC/RPS27A/UBA52	4
Common	R-HSA-210991	Basigin interactions	6/510	25/10856	0.000860353	0.002245052	0.001054322	SLC16A3/ITGB1/SLC3A2/ITGA3/PPIA/SLC7A5	6
Common	R-HSA-400685	Sema4D in semaphorin signaling	6/510	25/10856	0.000860353	0.002245052	0.001054322	MYL12A/MYH9/MYH10/MYH11/MYL6/MYH14	6
Common	R-HSA-382551	Transport of small molecules	53/510	729/10856	0.000915049	0.002381852	0.001118566	PSMA7/SLC16A3/CP/A2M/APOA1/APOE/APOC3/TF/FTH1/APOB/LCAT/ATP1A1/APOD/SLC25A5/EIF2S1/P4HB/SLC3	53
Common	R-HSA-397014	Muscle contraction	20/510	197/10856	0.000958575	0.002488974	0.001168873	MYL12A/ANXA1/ATP1A1/ANXA2/VIM/CALM1/ATP1A3/MYL6B/DES/VCL/ACTN2/MYH11/ATP1A2/MYL6/ACTA2/ACT	20
Common	R-HSA-9615710	Late endosomal microautophagy	7/510	35/10856	0.00103432	0.002679017	0.00125812	VIM/UBB/UBC/HSPA8/RPS27A/UBA52/HBB	7
Common	R-HSA-2173788	Downregulation of TGF-beta receptor signaling	6/510	26/10856	0.001074646	0.002776609	0.001303952	UBB/UBC/PPP1CA/RPS27A/UBA52/STRAP	6
Common	R-HSA-3781865	Diseases of glycosylation	16/510	143/10856	0.00108924	0.002807402	0.001318413	AGRN/B4GAT1/HEXB/THBS1/VCAN/B4GALT1/OGN/GPC1/THBS2/PGM1/GALK1/LUM/HSPG2/FMOD/EXT1/ADAMTS	16
Common	R-HSA-196025	Formation of annular gap junctions	4/510	11/10856	0.001219599	0.00310524	0.001458283	CLTCL1/ACTB/ACTG1/CLTC	4
Common	R-HSA-9014325	TICAM1,TRAF6-dependent induction of TAK1 complex	4/510	11/10856	0.001219599	0.00310524	0.001458283	UBB/UBC/RPS27A/UBA52	4
Common	R-HSA-9645460	Alpha-protein kinase 1 signaling pathway	4/510	11/10856	0.001219599	0.00310524	0.001458283	UBB/UBC/RPS27A/UBA52	4
Common	R-HSA-9664873	Pexophagy	4/510	11/10856	0.001219599	0.00310524	0.001458283	UBB/UBC/RPS27A/UBA52	4
Common	R-HSA-9708530	Regulation of BACH1 activity	4/510	11/10856	0.001219599	0.00310524	0.001458283	UBB/UBC/RPS27A/UBA52	4
Common	R-HSA-156590	Glutathione conjugation	7/510	36/10856	0.001232863	0.003131411	0.001470574	GSTA1/GSTA2/GSTP1/AKR1A1/GSTM2/GSTA3/GSTA5	7
Common	R-HSA-917937	Iron uptake and transport	9/510	58/10856	0.001414132	0.00358315	0.00168272	CP/TF/FTH1/UBB/UBC/ACO1/RPS27A/UBA52/CAND1	9
Common	R-HSA-68877	Mitotic Prometaphase	20/510	204/10856	0.001472784	0.003722771	0.001748288	TUBAL3/TUBB4A/TUBB/HSP90AA1/PPP2R1A/YWHAG/YWHAE/TUBA1B/TUBA4A/TUBB4B/TUBB3/TUBB2A/TUBB8/T	20
Common	R-HSA-174824	Plasma lipoprotein assembly, remodeling, and clearance	10/510	70/10856	0.00150055	0.003764167	0.001767729	A2M/APOA1/APOE/APOC3/APOB/LCAT/P4HB/PLTP/CLTC/MBTPS1	10
Common	R-HSA-110320	Translesion Synthesis by POLH	5/510	19/10856	0.001507102	0.003764167	0.001767729	UBB/UBC/VCP/RPS27A/UBA52	5
Common	R-HSA-1236382	Constitutive Signaling by Ligand-Responsive EGFR Cancer Variants	5/510	19/10856	0.001507102	0.003764167	0.001767729	HSP90AA1/UBB/UBC/RPS27A/UBA52	5
Common	R-HSA-5637815	Signaling by Ligand-Responsive EGFR Variants in Cancer	5/510	19/10856	0.001507102	0.003764167	0.001767729	HSP90AA1/UBB/UBC/RPS27A/UBA52	5
Common	R-HSA-8876725	Protein methylation	5/510	19/10856	0.001507102	0.003764167	0.001767729	CALM1/HSPA8/EEF2/VCP/EEF1A1	5
Common	R-HSA-196854	Metabolism of vitamins and cofactors	19/510	190/10856	0.001521527	0.003791168	0.001780409	AGRN/IDH1/APOM/VNN1/VNN2/APOA1/APOE/APOC3/RBP4/TTR/APOB/HSP90AA1/CALM1/SHMT1/SHMT2/GPC1/	19
Common	R-HSA-9683701	Translation of structural proteins	6/510	28/10856	0.001623623	0.004035973	0.001895374	UBB/UBC/MGAT1/RPS27A/UBA52/GANAB	6
Common	R-HSA-6814122	Cooperation of PDCL (PhLP1) and TRiC/CCT in G-protein beta folding	7/510	38/10856	0.001718576	0.004261906	0.002001477	TCP1/CCT6A/CCT5/CCT8/CCT4/CCT2/CCT6B	7
Common	R-HSA-190873	Gap junction degradation	4/510	12/10856	0.001761913	0.004328446	0.002032726	CLTCL1/ACTB/ACTG1/CLTC	4
Common	R-HSA-381033	ATF6 (ATF6-alpha) activates chaperones	4/510	12/10856	0.001761913	0.004328446	0.002032726	HSPA5/HSP90B1/CALR/MBTPS1	4
Common	R-HSA-430116	GP1b-IX-V activation signalling	4/510	12/10856	0.001761913	0.004328446	0.002032726	COL1A1/COL1A2/FLNA/YWHAZ	4
Common	R-HSA-9013973	TICAM1-dependent activation of IRF3/IRF7	4/510	12/10856	0.001761913	0.004328446	0.002032726	UBB/UBC/RPS27A/UBA52	4
Common	R-HSA-5213460	RIPK1-mediated regulated necrosis	6/510	29/10856	0.00196721	0.004810264	0.002258997	SDCBP/HSP90AA1/UBB/UBC/RPS27A/UBA52	6
Common	R-HSA-5675482	Regulation of necroptotic cell death	6/510	29/10856	0.00196721	0.004810264	0.002258997	SDCBP/HSP90AA1/UBB/UBC/RPS27A/UBA52	6
Common	R-HSA-3928663	EPHA-mediated growth cone collapse	6/510	30/10856	0.002363051	0.005764747	0.002707241	MYL12A/MYH9/MYH10/MYH11/MYL6/MYH14	6
Common	R-HSA-1358803	Downregulation of ERBB2:ERBB3 signaling	4/510	13/10856	0.002451258	0.005911195	0.002776016	UBB/UBC/RPS27A/UBA52	4
Common	R-HSA-2022857	Keratan sulfate degradation	4/510	13/10856	0.002451258	0.005911195	0.002776016	HEXB/OGN/LUM/FMOD	4
Common	R-HSA-209543	p75NTR recruits signalling complexes	4/510	13/10856	0.002451258	0.005911195	0.002776016	UBB/UBC/RPS27A/UBA52	4
Common	R-HSA-209560	NF-kB is activated and signals survival	4/510	13/10856	0.002451258	0.005911195	0.002776016	UBB/UBC/RPS27A/UBA52	4
Common	R-HSA-2168880	Scavenging of heme from plasma	4/510	13/10856	0.002451258	0.005911195	0.002776016	APOA1/HBB/HBA1/LRP1	4
Common	R-HSA-2122948	Activated NOTCH1 Transmits Signal to the Nucleus	6/510	31/10856	0.002815947	0.006775066	0.003181708	ADAM10/UBB/UBC/RPS27A/UBA52/CNTN1	6
Common	R-HSA-5205685	PINK1-PRKN Mediated Mitophagy	5/510	22/10856	0.003037533	0.007291469	0.003424221	UBB/UBC/VDAC1/RPS27A/UBA52	5
Common	R-HSA-6811442	Intra-Golgi and retrograde Golgi-to-ER traffic	19/510	202/10856	0.003066886	0.007345122	0.003449417	TUBAL3/TUBB4A/IGF2R/CAPZA1/ARF3/TUBA1B/TUBA4A/TUBB4B/ARF1/TUBB3/TUBB2A/TUBB8/TUBA3E/TUBA1A/T	19
Common	R-HSA-174490	Membrane binding and targetting of GAG proteins	4/510	14/10856	0.003305587	0.007827451	0.003675929	UBB/UBC/RPS27A/UBA52	4
Common	R-HSA-174495	Synthesis And Processing Of GAG, GAGPOL Polyproteins	4/510	14/10856	0.003305587	0.007827451	0.003675929	UBB/UBC/RPS27A/UBA52	4
Common	R-HSA-3656237	Defective EXT2 causes exostoses 2	4/510	14/10856	0.003305587	0.007827451	0.003675929	AGRN/GPC1/HSPG2/EXT1	4
Common	R-HSA-3656253	Defective EXT1 causes exostoses 1, TRPS2 and CHDS	4/510	14/10856	0.003305587	0.007827451	0.003675929	AGRN/GPC1/HSPG2/EXT1	4
Common	R-HSA-975110	TRAF6 mediated IRF7 activation in TLR7/8 or 9 signaling	4/510	14/10856	0.003305587	0.007827451	0.003675929	UBB/UBC/RPS27A/UBA52	4
Common	R-HSA-2173789	TGF-beta receptor signaling activates SMADs	6/510	32/10856	0.003330797	0.007869384	0.003695621	UBB/UBC/PPP1CA/RPS27A/UBA52/STRAP	6
Common	R-HSA-5675221	Negative regulation of MAPK pathway	7/510	43/10856	0.003584326	0.008449344	0.003967983	UBB/UBC/PEBP1/PPP2R1A/YWHAB/RPS27A/UBA52	7
Common	R-HSA-2187338	Visual phototransduction	12/510	105/10856	0.003705774	0.008716048	0.004093232	AGRN/APOM/APOA1/APOE/APOC3/RBP4/TTR/APOB/CALM1/GPC1/HSPG2/LRP1	12
Common	R-HSA-166663	Initial triggering of complement	5/510	23/10856	0.003733718	0.008742568	0.004105686	CFD/C3/C4A/C4B/MASP1	5
Common	R-HSA-5620922	BBSome-mediated cargo-targeting to cilium	5/510	23/10856	0.003733718	0.008742568	0.004105686	TCP1/CCT5/CCT8/CCT4/CCT2	5
Common	R-HSA-9679506	SARS-CoV Infections	15/510	147/10856	0.003799143	0.008875949	0.004168325	ATP1A1/ITGB1/TUBB/HSP90AA1/HSP90AB1/UBB/UBC/IMPDH2/ATP1A3/MGAT1/ATP1A2/VCP/RPS27A/UBA52/GA	15
Common	R-HSA-1592389	Activation of Matrix Metalloproteinases	6/510	33/10856	0.003912577	0.00906025	0.004254876	PLG/TIMP1/KLKB1/MMP2/MMP10/COL18A1	6
Common	R-HSA-1980145	Signaling by NOTCH2	6/510	33/10856	0.003912577	0.00906025	0.004254876	ADAM10/UBB/UBC/RPS27A/UBA52/CNTN1	6
Common	R-HSA-418990	Adherens junctions interactions	6/510	33/10856	0.003912577	0.00906025	0.004254876	CDH6/CDH11/ACTB/ACTG1/CDH9/CDH10	6
Common	R-HSA-445989	TAK1 activates NFkB by phosphorylation and activation of IKKs complex	6/510	33/10856	0.003912577	0.00906025	0.004254876	APP/HMGB1/UBB/UBC/RPS27A/UBA52	6
Common	R-HSA-1169410	Antiviral mechanism by IFN-stimulated genes	10/510	80/10856	0.004101327	0.009476414	0.004450315	FLNB/ISG15/UBB/UBC/FLNA/EIF4A1/RPS27A/UBA52/EIF4A2/KPNB1	10
Common	R-HSA-3134975	Regulation of innate immune responses to cytosolic DNA	4/510	15/10856	0.004342169	0.009923606	0.004660326	UBB/UBC/RPS27A/UBA52	4
Common	R-HSA-8875360	InlB-mediated entry of Listeria monocytogenes into host cell	4/510	15/10856	0.004342169	0.009923606	0.004660326	UBB/UBC/RPS27A/UBA52	4
Common	R-HSA-937039	IRAK1 recruits IKK complex	4/510	15/10856	0.004342169	0.009923606	0.004660326	UBB/UBC/RPS27A/UBA52	4
Common	R-HSA-9706369	Negative regulation of FLT3	4/510	15/10856	0.004342169	0.009923606	0.004660326	UBB/UBC/RPS27A/UBA52	4
Common	R-HSA-975144	IRAK1 recruits IKK complex upon TLR7/8 or 9 stimulation	4/510	15/10856	0.004342169	0.009923606	0.004660326	UBB/UBC/RPS27A/UBA52	4
Common	R-HSA-1638074	Keratan sulfate/keratin metabolism	6/510	34/10856	0.004566316	0.010390598	0.004879635	B4GAT1/HEXB/B4GALT1/OGN/LUM/FMOD	6
Common	R-HSA-5663084	Diseases of carbohydrate metabolism	6/510	34/10856	0.004566316	0.010390598	0.004879635	ALDOB/UBB/UBC/RPS27A/UBA52/GBE1	6
Common	R-HSA-3371453	Regulation of HSF1-mediated heat shock response	9/510	69/10856	0.00477212	0.010835398	0.005088522	HSPA1A/HSPA5/HSPA8/HSPA6/HSPA1L/HSPA9/HSPA13/HSPA2/YWHAE	9
Common	R-HSA-380259	Loss of Nlp from mitotic centrosomes	9/510	70/10856	0.005254811	0.011879949	0.005579064	TUBB4A/TUBB/HSP90AA1/PPP2R1A/YWHAG/YWHAE/TUBA4A/TUBB4B/TUBA1A	9

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Common	R-HSA-380284	Loss of proteins required for interphase microtubule organization from the centrosome	9/510	70/10856	0.005254811	0.011879949	0.005579064	TUBB4A/TUB8/HSP90AA1/PPP2R1A/YWHAG/YWHAE/TUBA4A/TUBB4B/TUBA1A	9
Common	R-HSA-1643713	Signaling by EGFR in Cancer	5/510	25/10856	0.00545639	0.012282732	0.005768219	HSP90AA1/UBB/UBC/RPS27A/UBAS2	5
Common	R-HSA-9013507	NOTCH3 Activation and Transmission of Signal to the Nucleus	5/510	25/10856	0.00545639	0.012282732	0.005768219	ADAM10/UBB/UBC/RPS27A/UBAS2	5
Common	R-HSA-110312	Translesion synthesis by REV1	4/510	16/10856	0.005577418	0.012317288	0.005784447	UBB/UBC/RPS27A/UBAS2	4
Common	R-HSA-193639	p75NTR signals via NF-kB	4/510	16/10856	0.005577418	0.012317288	0.005784447	UBB/UBC/RPS27A/UBAS2	4
Common	R-HSA-205043	NRIF signals cell death from the nucleus	4/510	16/10856	0.005577418	0.012317288	0.005784447	UBB/UBC/RPS27A/UBAS2	4
Common	R-HSA-2173791	TGF-beta receptor signaling in EMT (epithelial to mesenchymal transition)	4/510	16/10856	0.005577418	0.012317288	0.005784447	UBB/UBC/RPS27A/UBAS2	4
Common	R-HSA-392517	Rap1 signalling	4/510	16/10856	0.005577418	0.012317288	0.005784447	YWHAB/RAP1B/RAP1A/YWHAZ	4
Common	R-HSA-5684264	MAP3K8 (TPL2)-dependent MAPK1/3 activation	4/510	16/10856	0.005577418	0.012317288	0.005784447	UBB/UBC/RPS27A/UBAS2	4
Common	R-HSA-9651496	Defects of contact activation system (CAS) and kallikrein/kinin system (KKS)	4/510	16/10856	0.005577418	0.012317288	0.005784447	F2/F10/KLKB1/SERPING1	4
Common	R-HSA-9671793	Diseases of hemostasis	4/510	16/10856	0.005577418	0.012317288	0.005784447	F2/F10/KLKB1/SERPING1	4
Common	R-HSA-975163	IRAK2 mediated activation of TAK1 complex upon TLR7/8 or 9 stimulation	4/510	16/10856	0.005577418	0.012317288	0.005784447	UBB/UBC/RPS27A/UBAS2	4
Common	R-HSA-390522	Striated Muscle Contraction	6/510	36/10856	0.006109917	0.013464921	0.006323399	VIM/DES/ACTN2/ACTC1/ACTA1/ACTN3	6
Common	R-HSA-983169	Class I MHC mediated antigen processing & presentation	29/510	377/10856	0.00611182	0.013484861	0.006332763	PSMA7/FGB/HLA-A/HMGB1/UBB/UBC/HSPA5/PSMB1/UBA1/PSMA1/PSMA2/PSMA3/PSMA4/CALR/PSMA5/PSMB4,	29
Common	R-HSA-1169408	ISG15 antiviral mechanism	9/510	72/10856	0.006332913	0.013897962	0.006526764	FLNB/ISG15/UBB/UBC/EIF4A1/RPS27A/UBAS2/EIF4A2/KPNB1	9
Common	R-HSA-8854518	AURKA Activation by TPX2	9/510	73/10856	0.006931975	0.01518088	0.007129248	TUBB4A/TUB8/HSP90AA1/PPP2R1A/YWHAG/YWHAE/TUBA4A/TUBB4B/TUBA1A	9
Common	R-HSA-5655862	Translesion synthesis by POLK	4/510	17/10856	0.007026759	0.015261016	0.007166881	UBB/UBC/RPS27A/UBAS2	4
Common	R-HSA-5656121	Translesion synthesis by POLI	4/510	17/10856	0.007026759	0.015261016	0.007166881	UBB/UBC/RPS27A/UBAS2	4
Common	R-HSA-70221	Glycogen breakdown (glycogenolysis)	4/510	17/10856	0.007026759	0.015261016	0.007166881	PYGL/CALM1/PYGB/PYGM	4
Common	R-HSA-937072	TRAF6-mediated induction of TAK1 complex within TLR4 complex	4/510	17/10856	0.007026759	0.015261016	0.007166881	UBB/UBC/RPS27A/UBAS2	4
Common	R-HSA-8951664	Neddylation	20/510	234/10856	0.007086203	0.01535832	0.007212577	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PSMB3/PSMB2/PSMA6/	20
Common	R-HSA-2029482	Regulation of actin dynamics for phagocytic cup formation	8/510	61/10856	0.007380705	0.015963628	0.007496842	HSP90AA1/HSP90AB1/CFL1/MYH9/ACTB/CDC42/ACTR3/ACTG1	8
Common	R-HSA-5628897	TP53 Regulates Metabolic Genes	10/510	87/10856	0.00744842	0.016076939	0.007550055	GPI/YWHAQ/YWHAB/SFN/PRDX2/YWHAG/YWHAE/YWHAZ/YWHAH/PRDX1	10
Common	R-HSA-354192	Integrin signaling	5/510	27/10856	0.007675128	0.01649838	0.007747972	FGB/FN1/RAP1B/RAP1A/TLN1	5
Common	R-HSA-9648002	RAS processing	5/510	27/10856	0.007675128	0.01649838	0.007747972	UBB/UBC/CALM1/RPS27A/UBAS2	5
Common	R-HSA-112314	Neurotransmitter receptors and postsynaptic signal transmission	18/510	205/10856	0.007911203	0.016971067	0.007969956	TUBAL3/TUBB4A/NEFL/CALM1/ACTN2/TUBA1B/TUBA4A/TUBB4B/TUBB3/TUBB2A/TUBB8/TUBA3E/TUBA1A/TUBA1	18
Common	R-HSA-5696394	DNA Damage Recognition in GG-NER	6/510	38/10856	0.008002015	0.017130844	0.00804499	UBB/UBC/ACTB/RPS27A/UBAS2/RUVBL1	6
Common	R-HSA-2022377	Metabolism of Angiotensinogen to Angiotensins	4/510	18/10856	0.008704515	0.018521371	0.00869801	CTSD/ACE/CPB2/CTSZ	4
Common	R-HSA-2243919	Crosslinking of collagen fibrils	4/510	18/10856	0.008704515	0.018521371	0.00869801	COL1A1/COL3A2/COL4A2/LOXL2	4
Common	R-HSA-936964	Activation of IRF3/IRF7 mediated by TBK1/IKK epsilon	4/510	18/10856	0.008704515	0.018521371	0.00869801	UBB/UBC/RPS27A/UBAS2	4
Common	R-HSA-1614635	Sulfur amino acid metabolism	5/510	28/10856	0.008990673	0.019052961	0.008947655	GOT2/AHCY/MAT1A/BHMT/BHMT2	5
Common	R-HSA-2022854	Keratan sulfate biosynthesis	5/510	28/10856	0.008990673	0.019052961	0.008947655	B4GAT1/B4GALT1/OGN/LUM/FMOD	5
Common	R-HSA-110313	Translesion synthesis by Y family DNA polymerases bypasses lesions on DNA template	6/510	39/10856	0.009091233	0.019227225	0.009029493	ISG15/UBB/UBC/VCP/RPS27A/UBAS2	6
Common	R-HSA-9678108	SARS-CoV-1 Infection	7/510	51/10856	0.009332693	0.019698179	0.009250663	UBB/UBC/MGAT1/VCP/RPS27A/UBAS2/GANAB	7
Common	R-HSA-381183	ATF6 (ATF6-alpha) activates chaperone genes	3/510	10/10856	0.009656246	0.020340164	0.009552152	HSPA5/HSP90B1/CALR	3
Common	R-HSA-162588	Budding and maturation of HIV virion	5/510	29/10856	0.010453894	0.021844891	0.010258802	UBB/UBC/PPIA/RPS27A/UBAS2	5
Common	R-HSA-5205647	Mitophagy	5/510	29/10856	0.010453894	0.021844891	0.010258802	UBB/UBC/VDAC1/RPS27A/UBAS2	5
Common	R-HSA-5654732	Negative regulation of FGFR3 signaling	5/510	29/10856	0.010453894	0.021844891	0.010258802	UBB/UBC/PPP2R1A/RPS27A/UBAS2	5
Common	R-HSA-8863795	Downregulation of ERBB2 signaling	5/510	29/10856	0.010453894	0.021844891	0.010258802	HSP90AA1/UBB/UBC/RPS27A/UBAS2	5
Common	R-HSA-6804760	Regulation of TP53 Activity through Methylation	4/510	19/10856	0.010623825	0.022155849	0.010404834	UBB/UBC/RPS27A/UBAS2	4
Common	R-HSA-5357956	TNFR1-induced NFkappaB signaling pathway	5/510	30/10856	0.012072063	0.025076424	0.011776395	UBB/UBC/RPS27A/UBAS2/RACK1	5
Common	R-HSA-8866652	Synthesis of active ubiquitin: roles of E1 and E2 enzymes	5/510	30/10856	0.012072063	0.025076424	0.011776395	UBB/UBC/UBA1/RPS27A/UBAS2	5
Common	R-HSA-202733	Cell surface interactions at the vascular wall	13/510	137/10856	0.012214756	0.025322685	0.011892044	SLC16A3/F2/COL1A1/FN1/APOB/ITGB1/COL1A2/SLC3A2/MIF/ITGA3/GPC1/PPIA/SLC7A5	13
Common	R-HSA-9662361	Sensory processing of sound by outer hair cells of the cochlea	7/510	54/10856	0.012659803	0.026193557	0.012301023	GSN/EZR/MSN/RDX/MYH9/ACTB/ACTG1	7
Common	R-HSA-168927	TICAM1, RIP1-mediated IKK complex recruitment	4/510	20/10856	0.012796586	0.026214751	0.012310977	UBB/UBC/RPS27A/UBAS2	4
Common	R-HSA-3560783	Defective B4GALT7 causes EDS, progeroid type	4/510	20/10856	0.012796586	0.026214751	0.012310977	AGRN/VCAN/GPC1/HSPG2	4
Common	R-HSA-3560801	Defective B3GAT3 causes JDSSDHD	4/510	20/10856	0.012796586	0.026214751	0.012310977	AGRN/VCAN/GPC1/HSPG2	4
Common	R-HSA-4420332	Defective B3GALT6 causes EDSP2 and SEMDJL1	4/510	20/10856	0.012796586	0.026214751	0.012310977	AGRN/VCAN/GPC1/HSPG2	4
Common	R-HSA-8876384	Listeria monocytogenes entry into host cells	4/510	20/10856	0.012796586	0.026214751	0.012310977	UBB/UBC/RPS27A/UBAS2	4
Common	R-HSA-189085	Digestion of dietary carbohydrate	3/510	11/10856	0.012819988	0.026214751	0.012310977	AMY1A/AMY2A/AMY2B	3
Common	R-HSA-168928	DDX58/IFIH1-mediated induction of interferon-alpha/beta	9/510	81/10856	0.013411164	0.027370254	0.012853624	APP/ISG15/HSP90AA1/HSP90AB1/HMGB1/UBB/UBC/RPS27A/UBAS2	9
Common	R-HSA-1630316	Glycosaminoglycan metabolism	12/510	124/10856	0.013598154	0.027697987	0.013007534	AGRN/HS3ST1/B4GAT1/HEXB/VCAN/B4GALT1/OGN/GPC1/LUM/HSPG2/FMOD/EXT1	12
Common	R-HSA-182971	EGFR downregulation	5/510	31/10856	0.013852085	0.02799776	0.013148313	UBB/UBC/CDC42/RPS27A/UBAS2	5
Common	R-HSA-2022928	HS-GAG biosynthesis	5/510	31/10856	0.013852085	0.02799776	0.013148313	AGRN/HS3ST1/GPC1/HSPG2/EXT1	5
Common	R-HSA-5339562	Uptake and actions of bacterial toxins	5/510	31/10856	0.013852085	0.02799776	0.013148313	HSP90AA1/HSP90AB1/CALM1/EEF2/CD9	5
Common	R-HSA-5654733	Negative regulation of FGFR4 signaling	5/510	31/10856	0.013852085	0.02799776	0.013148313	UBB/UBC/PPP2R1A/RPS27A/UBAS2	5
Common	R-HSA-109606	Intrinsic Pathway for Apoptosis	7/510	55/10856	0.013937509	0.028116245	0.013203956	PSMA2/YWHAQ/YWHAB/SFN/YWHAG/YWHAE/YWHAZ/YWHAH	7
Common	R-HSA-1257604	PIP3 activates AKT signaling	21/510	267/10856	0.014409528	0.029003186	0.013620482	PSMA7/UBB/UBC/PSMB1/PSMA1/PSMA2/PSMA3/PSMA4/PSMA5/PSMB4/PSMB6/PSMB5/PPP2R1A/PSMB3/PSMB	21
Common	R-HSA-380270	Recruitment of mitotic centrosome proteins and complexes	9/510	82/10856	0.01446012	0.029003186	0.013620482	TUBB4A/TUB8/HSP90AA1/PPP2R1A/YWHAG/YWHAE/TUBA4A/TUBB4B/TUBA1A	9
Common	R-HSA-380287	Centrosome maturation	9/510	82/10856	0.01446012	0.029003186	0.013620482	TUBB4A/TUB8/HSP90AA1/PPP2R1A/YWHAG/YWHAE/TUBA4A/TUBB4B/TUBA1A	9
Common	R-HSA-4641263	Regulation of FZD by ubiquitination	4/510	21/10856	0.015233412	0.030379941	0.014267034	UBB/UBC/RPS27A/UBAS2	4
Common	R-HSA-6807004	Negative regulation of MET activity	4/510	21/10856	0.015233412	0.030379941	0.014267034	UBB/UBC/RPS27A/UBAS2	4
Common	R-HSA-901032	ER Quality Control Compartment (ERQC)	4/510	21/10856	0.015233412	0.030379941	0.014267034	UBB/UBC/RPS27A/UBAS2	4
Common	R-HSA-2173796	SMAD2/SMAD3:SMAD4 heterotrimer regulates transcription	5/510	32/10856	0.015800472	0.031391468	0.014742067	SERPINE1/UBB/UBC/RPS27A/UBAS2	5
Common	R-HSA-5656169	Termination of translesion DNA synthesis	5/510	32/10856	0.015800472	0.031391468	0.014742067	ISG15/UBB/UBC/RPS27A/UBAS2	5
Common	R-HSA-112315	Transmission across Chemical Synapses	21/510	270/10856	0.016156281	0.031985076	0.015020837	TUBAL3/TUBB4A/NEFL/CALM1/HSPA8/ACHE/ACTN2/CACNA2D1/TUBA1B/TUBA4A/TUBB4B/TUBB3/TUBB2A/TUBB8	21
Common	R-HSA-9694635	Translation of structural proteins	6/510	44/10856	0.016160238	0.031985076	0.015020837	UBB/UBC/MGAT1/RPS27A/UBAS2/GANAB	6
Common	R-HSA-83936	Transport of nucleosides and free purine and pyrimidine bases across the plasma membrane	3/510	12/10856	0.016506013	0.032607924	0.01531334	SLC25A5/SLC25A4/SLC25A6	3
Common	R-HSA-5218859	Regulated Necrosis	7/510	57/10856	0.016765011	0.033057324	0.015524387	SDCBP/HSP90AA1/HMGB1/UBB/UBC/RPS27A/UBAS2	7
Common	R-HSA-5654726	Negative regulation of FGFR1 signaling	5/510	33/10856	0.01792331	0.035051851	0.016461057	UBB/UBC/PPP2R1A/RPS27A/UBAS2	5
Common	R-HSA-1566948	Elastic fibre formation	6/510	45/10856	0.017930079	0.035051851	0.016461057	FN1/VTN/TIGB1/FBLN1/EFEMP1/LOXL2	6
Common	R-HSA-8862803	Deregulated CDK5 triggers multiple neurodegenerative pathways in Alzheimer's disease models	4/510	22/10856	0.017943607	0.035051851	0.016461057	APP/PRDX2/YWHAE/PRDX1	4
Common	R-HSA-8863678	Neurodegenerative Diseases	4/510	22/10856	0.017943607	0.035051851	0.016461057	APP/PRDX2/YWHAE/PRDX1	4
Common	R-HSA-912631	Regulation of signaling by CBL	4/510	22/10856	0.017943607	0.035051851	0.016461057	UBB/UBC/RPS27A/UBAS2	4
Common	R-HSA-8856828	Clathrin-mediated endocytosis	13/510	146/10856	0.019856343	0.038716179	0.018181899	TF/APOB/UBB/UBC/HSPA8/IGF2R/CLTCL1/ACTB/ACTR3/RPS27A/UBAS2/ACTG1/CLTC	13
Common	R-HSA-5654727	Negative regulation of FGFR2 signaling	5/510	34/10856	0.02022624	0.039291344	0.018452008	UBB/UBC/PPP2R1A/RPS27A/UBAS2	5
Common	R-HSA-936440	Negative regulators of DDX58/IFIH1 signaling	5/510	34/10856	0.02022624	0.039291344	0.018452008	ISG15/UBB/UBC/RPS27A/UBAS2	5
Common	R-HSA-879415	Advanced glycosylation endproduct receptor signaling	3/510	13/10856	0.02072244	0.040180849	0.018869738	APP/HMGB1/CAPZA1	3
Common	R-HSA-2173795	Downregulation of SMAD2/3:SMAD4 transcriptional activity	4/510	23/10856	0.020935163	0.040369459	0.018958313	UBB/UBC/RPS27A/UBAS2	4
Common	R-HSA-373753	Nephrin family interactions	4/510	23/10856	0.020935163	0.040369459	0.018958313	ACTN4/ACTN1/ACTN2/ACTN3	4
Common	R-HSA-450321	JNK (c-Jun kinases) phosphorylation and activation mediated by activated human TAK1	4/510	23/10856	0.020935163	0.040369459	0.018958313	UBB/UBC/RPS27A/UBAS2	4
Common	R-HSA-432720	Lysosome Vesicle Biogenesis	5/510	35/10856	0.022714434	0.043640003	0.020494226	APP/HSPA8/ARF1/CLTC/CTSZ	5
Common	R-HSA-5357905	Regulation of TNFR1 signaling	5/510	35/10856	0.022714434	0.043640003	0.020494226	UBB/UBC/RPS27A/UBAS2/RACK1	5
Common	R-HSA-73893	DNA Damage Bypass	6/510	48/10856	0.024024992	0.046073521	0.021637056	ISG15/UBB/UBC/VCP/RPS27A/UBAS2	6
Common	R-HSA-174048	APC/C:Cdc20 mediated degradation of Cyclin B	4/510	24/10856	0.024214759	0.046268273	0.021728515	UBB/UBC/RPS27A/UBAS2	4
Common	R-HSA-450302	activated TAK1 mediates p38 MAPK activation	4/510	24/10856	0.024214759	0.046268273	0.021728515	UBB/UBC/RPS27A/UBAS2	4
Common	R-HSA-6804757	Regulation of TP53 Degradation	5/510	36/10856	0.025392582	0.048406961	0.022732886	UBB/UBC/PPP2R1A/RPS27A/UBAS2	5
Common	R-HSA-162594	Early Phase of HIV Life Cycle	3/510	14/10856	0.025472491	0.048406961	0.022732886	XRCC6/HMGA1/PPIA	3
Common	R-HSA-399955	SEMA3A-Plexin repulsion signaling by inhibiting Integrin adhesion	3/510	14/10856	0.025472491	0.048406961	0.022732886	NRP1/SEMA3A/TLN1	3
Common	R-HSA-9659379	Sensory processing of sound	8/510	76/10856	0.025745328	0.048836979	0.022934831	GSN/EZR/MSN/RDX/MYH9/CAPZA1/ACTB/ACTG1	8
CSC	R-HSA-1799339	SRP-dependent cotranslational protein targeting to membrane	51/435	112/10856	8.44951E-42	9.3705E-39	6.16369E-39	SRP72/RPN1/RPN2/RPL10P/RPS11/SRP19/RPS2/RPL17/RPS4Y1/RPS3/RPL13/RPL10/RPL12/RPL22/RPL4/RPL3/DC	51
CSC	R-HSA-9010553	Regulation of expression of SLITs and ROBOs	59/435	171/10856	6.28323E-40	3.48405E-37	2.29173E-37	PSMD12/PSMD3/RPL10/RPS11/PABPC1/RPS2/PSMC3/RPL17/RPS4Y1/RPS3/RPL13/RPL10/RPL12/RPL4/EI	59
CSC	R-HSA-156827	L13a-mediated translational silencing of Ceruloplasmin expression	49/435	111/10856	2.33085E-39	8.61636E-37	5.66764E-37	EIF3F/RPLP0/RPS17/PABPC1/RPS2/RPL17/RPS4Y1/RPS3/RPL13/RPL10/RPL12/RPL22/RPL4/RPL3/RPL13A/EIF2S3	49
CSC	R-HSA-72706	GTP hydrolysis and joining of the 60S ribosomal subunit	49/435	112/10856	3.998E-39	1.009666E-36	6.64129E-37	EIF3F/RPLP0/RPS17/RPS2/RPL17/RPS4Y1/RPS3/RPL13/RPL10/RPL12/RPL22/RPL4/RPL3/RPL13A/EIF2S3/RPS27/l	49
CSC	R-HSA-2408522	Selenoamino acid metabolism	50/435	118/10856	4.55211E-39	1.009666E-36	6.64129E-37	EEF1E1/RPLP0/EPRS1/PABPC1/DARS1/RPS2/RPL17/RPS4Y1/RPS3/RPL13/RPL10/RPL12/RPL22/RPL4/RPL3/RPL13A	50
CSC	R-HSA-72613	Eukaryotic Translation Initiation	50/435	119/10856	7.57509E-39	1.200111E-36	7.89404E-37	EIF3F/RPLP0/RPS17/PABPC1/RPS2/RPL17/RPS4Y1/RPS3/RPL13/RPL10/RPL12/RPL22/RPL4/RPL3/RPL13A/EIF2S3	50
CSC	R-HSA-72737	Cap-dependent Translation Initiation	50/435	119/10856	7.57509E-39	1.200111E-36	7.89404E-37	EIF3F/RPLP0/RPS17/PABPC1/RPS2/RPL17/RPS4Y1/RPS3/RPL13/RPL10/RPL12/RPL22/RPL4/RPL3/RPL13A/EIF2S3	50
CSC	R-HSA-975956	Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)	45/435	95/10856	6.51971E-38	9.03795E-36	5.94495E-36	RPLP0/RPS17/PABPC1/RPS2/RPL17/RPS4Y1/RPS3/RPL13/RPL10/RPL12/RPL22/RPL4/RPL3/RPL13A/RPS27/RPL2	45
CSC	R-HSA-72689	Formation of a pool of free 40S subunits	46/435	101/10856	9.36922E-38	1.1545E-35	7.594E-36	EIF3F/RPLP0/RPS17/RPS2/RPL17/RPS4Y1/RPS3/RPL13/RPL10/RPL12/RPL22/RPL4/RPL3/RPL13A/RPS27/RPL27A,	46
CSC	R-HSA-156902	Peptide chain elongation	43/435	89/10856	9.98091E-37	1.006266E-34	6.61892E-35	RPLP0/RPS17/RPS2/RPL17/RPS4Y1/RPS3/RPL13/RPL10/RPL12/RPL22/RPL4/RPL3/RPL13A/RPS27/RPL27A/RPL5,	43
CSC	R-HSA-192823	Viral mRNA Translation	43/435	89/10856	9.98091E-37	1.006266E-34	6.61892E-35	RPLP0/RPS17/RPS2/RPL17/RPS4Y1/RPS3/RPL13/RPL10/RPL12/RPL22/RPL4/RPL3/RPL13A/RPS27/RPL27A/RPL5,	43
CSC	R-HSA-9633012	Response of EIF2AK4 (GCN2) to amino acid deficiency	45/435	101/10856	2.04964E-36	1.894211E-34	1.24596E-34	RPLP0/ASNS/RPS17/RPS2/RPL17/RPS4Y1/RPS3/RPL13/RPL10/RPL12/RPL22/RPL4/RPL3/RPL13A/EIF2S3/RPS27/l	45
CSC	R-HSA-376176	Signaling by ROBO receptors	62/435	218/10856	2.58228E-36	2.20289E-34	1.44901E-34	PSMD12/PSMD3/RPL10/RPS11/PABPC1/RPS2/PSMC3/RPL17/RPS4Y1/RPS3/RPL13/RPL10/RPL12/PFN2/RPL22/R	62
CSC	R-HSA-72766	Translation	70/435	291/10856	8.28677E-36	6.564314E-34	4.31785E-34	EIF3EF1E1/SRP72/RPN1/RPN2/RPL10P/EPRS1/RPS11/SRP19/PABPC1/DARS1/RPS2/RPL17/RPS4Y1/RPS3/RPL13	70
CSC	R-HSA-156842	Eukaryotic Translation Elongation	43/435	93/10856	1.09482E-35	7.142096E-34	4.69789E-34	RPLP0/RPS17/RPS2/RPL17/RPS4Y1/RPS3/RPL13/RPL10/RPL12/RPL22/RPL4/RPL3/RPL13A/RPS27/RPL27A/RPL5,	43
CSC	R-HSA-2408557	Selenocysteine synthesis	43/435	93/10856	1.09482E-35	7.142096E-34	4.69789E-34	RPLP0/RPS17/RPS2/RPL17/RPS4Y1/RPS3/RPL13/RPL10/RPL12/RPL22/RPL4/RPL3/RPL13A/RPS27/RPL27A/RPL5,	43
CSC	R-HSA-72764	Eukaryotic Translation Termination	43/435	93/10856	1.09482E-35	7.142096E-34	4.69789E-34	RPLP0/RPS17/RPS2/RPL17/RPS4Y1/RPS3/RPL13/RPL10/RPL12/RPL22/RPL4/RPL3/RPL13A/RPS27/RPL27A/RPL5,	43
CSC	R-HSA-927802	Nonsense-Mediated Decay (NMD)	46/435	115/10856	1.30283E-34	7.60443E-33	5.00201E-33	RPLP0/RPS17/PABPC1/RPS2/RPL17/RPS4Y1/RPS3/RPL13/RPL10/RPL12/RPL22/RPL4/EIF4A3/RPL3/RPL13A/RPS2	46
CSC	R-HSA-975957	Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC)	46/435	115/10856	1.30283E-34	7.60443E-33	5.00201E-33	RPLP0/RPS17/PABPC1/RPS2/RPL17/RPS4Y1/RPS3/RPL13/RPL10/RPL12/RPL22/RPL4/EIF4A3/RPL3/RPL13A/RPS2	46
CSC	R-HSA-71291	Metabolism of amino acids and derivatives	76/435	374/10856	1.60889E-33	9.32055E-32	6.13083E-32	PSMD12/PSMD3/EEF1E1/SLC25A12/FTCD/GLUD1/OAT/ASS/RPLP0/EPRS1/ASNS/PDHA1/RPS17/QDPR/DARS1/RPS	76
CSC	R-HSA-8953854	Metabolism of RNA	101/435	673/10856	7.26003E-33	3.83398E-31	2.52191E-31	PSMD12/NOP56/XPO1/PSMD3/HNRNPR/SRSF10/SNRNP200/NUP155/RPLP0/EPRS1/SNRNP70/RPS17/PABPC1/SF	101
CSC	R-HSA-168255	Influenza Infection	50/435	156/10856	4.03082E-32	2.0139E-30	1.33654E-30	IPO5/XPO1/NUP155/RPLP0/RPS17/RPS2/RPL17/RPS4Y1/RPS3/RPL13/RPL10/CANX/RPL12/RPL22/RPL4/RPL3/RP	50
CSC	R-HSA-168273	Influenza Viral RNA Transcription and Replication	47/435	135/10856	4.29352E-32	2.07023E-30	1.36174E-30	IPO5/NUP155/RPLP0/RPS17/RPS2/RPL17/RPS4Y1/RPS3/RPL13/RPL10/RPL12/RPL22/RPL4/RPL3/RPL13A/RPS27	47
CSC	R-HSA-5663205	Infectious disease	108/435	871/10856	8.0782E-28	3.7328E-26	2.45535E-26	GNAT3/PSMD12/IPO5/XPO1/ARPC1B/ARPC3/PSMD3/CTNND1/BANF1/NUP155/EGFR/RPN1/RPN2/GNAI2/RPLP0/	108
CSC	R-HSA-422475	Axon guidance	84/435	552/10856	1.46815E-27	6.51271E-26	4.2839E-26	PSMD12/ARPC1B/ARPC3/PSMD3/LYPLA2/EGFR/NRAS/HRAS/KRAS/RPLP0/FYN/YES1/LYN/RPS17/RRAS/FGFR1/PABI	84
CSC	R-HSA-9675108	Nervous system development	85/435	577/10856	7.14168E-27	3.0462E-25	2.00372E-25	PSMD12/ARPC1B/ARPC3/PSMD3/LYPLA2/EGFR/NRAS/HRAS/KRAS/RPLP0/FYN/YES1/LYN/RPS17/RRAS/FGFR1/PABI	85

CSC	R-HSA-9711097	Cellular response to starvation	45/435	156/10856	8.97306E-27	3.6856E-25	2.4243E-25	RPLP0/ASNS/RPS17/RPS2/RPL17/RPS4Y1/RPS3/RPL13/RPL10/RPL12/RPL22/RPL4/RPL3/RPL13A/EIF2S3/RPS27/I	45
CSC	R-HSA-6791226	Major pathway of rRNA processing in the nucleolus and cytosol	48/435	184/10856	2.40935E-26	9.54276E-25	6.277E-25	NOP56/RPLP0/RPS17/RPS2/RPL17/FBL/RPS4Y1/RPS3/RPL13/RPL10/RPL12/RPL22/RPL4/RPL3/RPL13A/RPS27/RI	48
CSC	R-HSA-8868773	rRNA processing in the nucleus and cytosol	49/435	194/10856	3.48786E-26	1.3338E-24	8.77344E-25	NOP56/RPLP0/RPS17/RPS2/RPL17/FBL/RPS4Y1/RPS3/RPL13/RPL10/RPL12/RPL22/RPL4/RPL3/RPL13A/RPS27/N	49
CSC	R-HSA-72312	rRNA processing	49/435	204/10856	4.07806E-25	1.50752E-23	9.91613E-24	NOP56/RPLP0/RPS17/RPS2/RPL17/FBL/RPS4Y1/RPS3/RPL13/RPL10/RPL12/RPL22/RPL4/RPL3/RPL13A/RPS27/N	49
CSC	R-HSA-2262752	Cellular responses to stress	86/435	676/10856	1.11144E-22	3.9761E-21	2.61538E-21	PSMD12/XPO1/PSMD3/DNAJB6/NUP155/HSPA4L/COX2/RPLP0/FABP1/H1-0/ASNS/RPS17/TXN/COX5B/CDK4/CO)	86
CSC	R-HSA-8953897	Cellular responses to external stimuli	86/435	690/10856	4.51572E-22	1.56498E-20	1.02941E-20	PSMD12/XPO1/PSMD3/DNAJB6/NUP155/HSPA4L/COX2/RPLP0/FABP1/H1-0/ASNS/RPS17/TXN/COX5B/CDK4/CO)	86
CSC	R-HSA-1643685	Disease	140/435	1615/10856	1.17205E-20	3.93878E-19	2.59084E-19	GNAT3/PSMD12/IPO5/XPO1/ARPC1B/ARPC3/PSMD3/CTNND1/ERLIN1/BANF1/NUP155/ERLIN2/EGFR/NRAS/HRAS	140
CSC	R-HSA-72649	Translation initiation complex formation	24/435	58/10856	5.73093E-19	1.81589E-17	1.19445E-17	EIF3F/RPS17/PABPC1/RPS2/RPS4Y1/RPS3/EIF2S3/RPS27/RPS9/EIF3E/RPS20/RPS16/RPS14/RPS23/RPS11/RPS4X/	24
CSC	R-HSA-72702	Ribosomal scanning and start codon recognition	24/435	58/10856	5.73093E-19	1.81589E-17	1.19445E-17	EIF3F/RPS17/RPS2/RPS4Y1/RPS3/EIF2S3/RPS27/RPS9/EIF5/EIF3E/RPS20/RPS16/RPS14/RPS23/RPS11/RPS4X/RPS	24
CSC	R-HSA-72662	Activation of the mRNA upon binding of the cap-binding complex and eIFs, and subsequent binding to 43S	24/435	59/10856	9.30852E-19	2.86754E-17	1.8862E-17	EIF3F/RPS17/PABPC1/RPS2/RPS4Y1/RPS3/EIF2S3/RPS27/RPS9/EIF3E/RPS20/RPS16/RPS14/RPS23/RPS11/RPS4X/	24
CSC	R-HSA-1430728	Metabolism	161/435	2119/10856	2.9877E-18	8.95503E-17	5.8904E-17	PSMD12/FBP2/CYB5B/PSMD3/EEF1E1/IDH3B/CS/NUP155/SLC25A12/ATP5MG/FTCD/NDUFB10/GLUD1/CYB5R3/(	161
CSC	R-HSA-72695	Formation of the ternary complex, and subsequently, the 43S complex	22/435	51/10856	5.78329E-18	1.68781E-16	1.1102E-16	EIF3F/RPS17/RPS2/RPS4Y1/RPS3/EIF2S3/RPS27/RPS9/EIF3E/RPS20/RPS16/RPS14/RPS23/RPS11/RPS4X/RPS6/RP	22
CSC	R-HSA-392499	Metabolism of proteins	153/435	2036/10856	9.98826E-17	2.84025E-15	1.86825E-15	GNAT3/PSMD12/EIF3F/NOP56/PSMD3/EEF1E1/NUP155/SRP72/LMNA/MMP1/RPN1/RPN2/RPLP0/CDK1/POLB/EP	153
CSC	R-HSA-72163	mRNA Splicing - Major Pathway	33/435	183/10856	2.28779E-13	6.3429E-12	4.17221E-12	HNRNPR/SRSF10/SNRNP200/SNRNP70/SNRPB/HNRNPL/DDX5/PTBP1/FUS/EIF4A3/HNRNPM/POLR2H/HNRNPF/SN	33
CSC	R-HSA-1266738	Developmental Biology	96/435	1127/10856	2.70998E-13	7.33016E-12	4.8216E-12	PSMD12/ARPC1B/ARPC3/PSMD3/LYPLA2/CER1/EGFR/NRAS/HRAS/KRAS/RPLP0/FYN/YES1/LYN/RPS17/RRAS/FGFR	96
CSC	R-HSA-72172	mRNA Splicing	33/435	191/10856	8.00823E-13	2.11455E-11	1.3909E-11	HNRNPR/SRSF10/SNRNP200/SNRNP70/SNRPB/HNRNPL/DDX5/PTBP1/FUS/EIF4A3/HNRNPM/POLR2H/HNRNPF/SN	33
CSC	R-HSA-72203	Processing of Capped Intron-Containing Pre-mRNA	35/435	244/10856	3.99726E-11	1.03092E-09	6.78115E-10	HNRNPR/SRSF10/SNRNP200/NUP155/SNRNP70/SNRPB/HNRNPL/DDX5/PTBP1/FUS/EIF4A3/HNRNPM/POLR2H/HI	35
CSC	R-HSA-379716	Cytosolic tRNA aminoacylation	11/435	24/10856	5.87897E-10	1.48177E-08	9.74672E-09	EEF1E1/EPRS1/DARS1/TARS1/VARS1/AARS1/RARS1/YARS1/MARS1/KARS1/LARS1	11
CSC	R-HSA-72165	mRNA Splicing - Minor Pathway	14/435	52/10856	9.79176E-09	2.41313E-07	1.5873E-07	SNRNP200/SNRPB/POLR2H/SNU13/SNRPE/SNRPD1/SNRPD2/SNRPD3/YBX1/SRSF1/SRSF6/SRSF7/PRPF8/SF3B6	14
CSC	R-HSA-162909	Host Interactions of HIV factors	21/435	130/10856	4.35173E-08	1.04914E-06	6.90102E-07	PSMD12/XPO1/PSMD3/BANF1/NUP155/LCK/FYN/HCK/PSMC3/RCC1/PSMC4/PSMD8/CDK9/PSMD7/NUP107/PSN	21
CSC	R-HSA-9707564	Cytoprotection by HMOX1	20/435	124/10856	9.39645E-08	2.21716E-06	1.4584E-06	PSMD12/PSMD3/COX2/FABP1/COX5B/COX4I1/PSMC3/BLVRB/LRPPRC/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/C	20
CSC	R-HSA-9707587	Regulation of HMOX1 expression and activity	14/435	65/10856	2.09379E-07	4.83752E-06	3.182E-06	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/CSNK2B/CSNK2A1/PSMD2/HM13/PSMD1/PSMI	14
CSC	R-HSA-450408	AUF1 (hnRNP D0) binds and destabilizes mRNA	13/435	56/10856	2.24885E-07	5.08975E-06	3.34791E-06	PSMD12/PSMD3/PABPC1/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/EIF4G1/PSMD2/PSMD1/PSMD13	13
CSC	R-HSA-8932339	ROS sensing by NFE2L2	13/435	57/10856	2.80858E-07	6.22942E-06	4.09756E-06	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/CSNK2B/CSNK2A1/PSMD2/PSMD1/PSMD13	13
CSC	R-HSA-3858494	Beta-catenin independent WNT signaling	21/435	146/10856	3.3484E-07	7.28112E-06	4.78935E-06	PSMD12/PSMD3/KRAS/GNAO1/RAC2/PSMC3/GNAT2/CTNNB1/PSMC4/PSMD8/PSMD7/RAC3/PSME3/PSMC5/GNB	21
CSC	R-HSA-5658442	Regulation of RAS by GAPs	14/435	68/10856	3.78925E-07	8.08131E-06	5.31569E-06	PSMD12/PSMD3/NRAS/HRAS/KRAS/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	14
CSC	R-HSA-9711123	Cellular response to chemical stress	22/435	160/10856	3.91385E-07	8.18955E-06	5.38689E-06	PSMD12/PSMD3/COX2/FABP1/TXN/COX5B/COX4I1/PSMC3/BLVRB/LRPPRC/PSMC4/PSMD8/PSMD7/PSME3/PSM(	22
CSC	R-HSA-983705	Signaling by the B Cell Receptor (BCR)	18/435	112/10856	4.37692E-07	8.98891E-06	5.91269E-06	PSMD12/PSMD3/NRAS/HRAS/KRAS/FYN/LYN/PSMC3/PSMC4/PSMD8/BLK/PSMD7/PSME3/PSMC5/FKBP1A/PSMD2	18
CSC	R-HSA-453279	Mitotic G1 phase and G1/S transition	21/435	149/10856	4.74104E-07	9.55966E-06	6.28812E-06	PSMD12/PSMD3/CDK1/LYN/CDK4/CCNB1/PSMC3/CDK2/MCM3/PPP2R1B/MCM7/PSMC4/PSMD8/PSMD7/PSME3	21
CSC	R-HSA-379724	tRNA Aminoacylation	11/435	42/10856	5.24108E-07	1.03331E-05	6.79687E-06	EEF1E1/EPRS1/DARS1/TARS1/VARS1/AARS1/RARS1/YARS1/MARS1/KARS1/LARS1	11
CSC	R-HSA-187577	SCF(Skp2)-mediated degradation of p27/p21	13/435	60/10856	5.31097E-07	1.03331E-05	6.79687E-06	PSMD12/PSMD3/CDK4/PSMC3/CDK2/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	13
CSC	R-HSA-5678895	Defective CFTR causes cystic fibrosis	13/435	61/10856	6.50693E-07	1.22546E-05	8.06078E-06	PSMD12/PSMD3/ERLIN1/ERLIN2/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	13
CSC	R-HSA-1428517	The citric acid (TCA) cycle and respiratory electron transport	23/435	178/10856	6.58677E-07	1.22546E-05	8.06078E-06	IDH3B/CS/ATP5MG/NDUFB10/COX2/FH/PDHA1/CYC1/COX5B/COX4I1/UQCRB/ATP5PB/ATP5F1A/UQCRC1/BSG/DI	23
CSC	R-HSA-68949	Orc1 removal from chromatin	14/435	71/10856	6.63008E-07	1.22546E-05	8.06078E-06	PSMD12/PSMD3/PSMC3/CDK2/MCM3/MCM7/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	14
CSC	R-HSA-75815	Ubiquitin-dependent degradation of Cyclin D	12/435	52/10856	7.07184E-07	1.28568E-05	8.45692E-06	PSMD12/PSMD3/CDK4/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	12
CSC	R-HSA-1168372	Downstream signaling events of B Cell Receptor (BCR)	15/435	83/10856	8.62779E-07	1.54326E-05	1.01512E-05	PSMD12/PSMD3/NRAS/HRAS/KRAS/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/FKBP1A/PSMD2/PSMD1/PSM	15
CSC	R-HSA-69206	G1/S Transition	19/435	131/10856	1.07117E-06	1.8856E-05	1.2403E-05	PSMD12/PSMD3/CDK1/CDK4/CCNB1/PSMC3/CDK2/MCM3/PPP2R1B/MCM7/PSMC4/PSMD8/PSMD7/PSME3/PSN	19
CSC	R-HSA-6798695	Neutrophil degranulation	42/435	480/10856	1.42365E-06	2.46691E-05	1.62267E-05	PSMD12/DDX3X/SURF4/PSMD3/CYB5R3/NRAS/APRT/FGR/XRCC5/JUP/ANPEP/DSP/TIMP2/PSMC3/STOM/DDOST/I	42
CSC	R-HSA-9009391	Extra-nuclear estrogen signaling	14/435	77/10856	1.85655E-06	3.14617E-05	2.06947E-05	GNAT3/XPO1/EGFR/NRAS/HRAS/KRAS/GNAI2/GNAI3/GNB1/GNB2/GNAI1/CAV1/PRMT1/GNB4	14
CSC	R-HSA-450531	Regulation of mRNA stability by proteins that bind AU-rich elements	15/435	88/10856	1.87238E-06	3.14617E-05	2.06947E-05	PSMD12/XPO1/PSMD3/PABPC1/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/EIF4G1/PSMD2/ELAVL1/PSMD1/	15
CSC	R-HSA-68867	Assembly of the pre-replicative complex	13/435	68/10856	2.4067E-06	3.98363E-05	2.62034E-05	PSMD12/PSMD3/PSMC3/MCM3/MCM7/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	13
CSC	R-HSA-68882	Mitotic Anaphase	26/435	236/10856	2.73615E-06	4.44883E-05	2.92633E-05	PSMD12/XPO1/PSMD3/BANF1/NUP155/LMNA/CDK1/CCNB1/PSMC3/RCC1/LMNB1/PPP2R1B/PPP1CC/RPS27/PSI	26
CSC	R-HSA-1236978	Cross-presentation of soluble exogenous antigens (endosomes)	11/435	49/10856	2.76798E-06	4.44883E-05	2.92633E-05	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	11
CSC	R-HSA-8948751	Regulation of PTEN stability and activity	13/435	69/10856	2.85902E-06	4.51651E-05	2.97085E-05	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/CSNK2B/CSNK2A1/PSMD2/PSMD1/PSMD13	13
CSC	R-HSA-2555396	Mitotic Metaphase and Anaphase	26/435	237/10856	2.96115E-06	4.51651E-05	2.97085E-05	PSMD12/XPO1/PSMD3/BANF1/NUP155/LMNA/CDK1/CCNB1/PSMC3/RCC1/LMNB1/PPP2R1B/PPP1CC/RPS27/PSI	26
CSC	R-HSA-109581	Apoptosis	22/435	180/10856	2.96304E-06	4.51651E-05	2.97085E-05	PSMD12/DNM1L/PSMD3/LMNA/H1-0/DSP/PSMC3/LMNB1/CTNNB1/PSMC4/PSMD8/BCAP31/PSMD7/PSME3/PSN	22
CSC	R-HSA-351202	Metabolism of polyamines	12/435	59/10856	2.97299E-06	4.51651E-05	2.97085E-05	PSMD12/PSMD3/PSMC3/SRM/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	12
CSC	R-HSA-211733	Regulation of activated PAK-2p34 by proteasome mediated degradation	11/435	50/10856	3.42249E-06	5.12911E-05	3.37381E-05	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	11
CSC	R-HSA-176408	Regulation of APC/C activators between G1/S and early anaphase	14/435	81/10856	3.48035E-06	5.14627E-05	3.38509E-05	PSMD12/PSMD3/CDK1/CCNB1/PSMC3/CDK2/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	14
CSC	R-HSA-210991	Basigin interactions	8/435	25/10856	3.69396E-06	5.39026E-05	3.54559E-05	MMP1/ITGA6/BSG/SLC16A1/ATP1B3/CAV1/SLC7A6/SLC7A7	8
CSC	R-HSA-350562	Regulation of ornithine decarboxylase (ODC)	11/435	51/10856	4.20853E-06	6.06137E-05	3.98703E-05	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	11
CSC	R-HSA-69202	Cyclin E associated events during G1/S transition	14/435	83/10856	4.69176E-06	6.67072E-05	4.38784E-05	PSMD12/PSMD3/CDK4/PSMC3/CDK2/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/RBBP4/PSMD2/PSMD1/PSMD13	14
CSC	R-HSA-180534	Vpu mediated degradation of CD4	11/435	52/10856	5.14791E-06	6.87836E-05	4.52442E-05	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	11
CSC	R-HSA-349425	Autodegradation of the E3 ubiquitin ligase COP1	11/435	52/10856	5.14791E-06	6.87836E-05	4.52442E-05	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	11
CSC	R-HSA-69601	Ubiquitin Mediated Degradation of Phosphorylated Cdc25A	11/435	52/10856	5.14791E-06	6.87836E-05	4.52442E-05	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	11
CSC	R-HSA-69610	p53-Independent DNA Damage Response	11/435	52/10856	5.14791E-06	6.87836E-05	4.52442E-05	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	11
CSC	R-HSA-69613	p53-Independent G1/S DNA damage checkpoint	11/435	52/10856	5.14791E-06	6.87836E-05	4.52442E-05	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	11
CSC	R-HSA-69002	DNA Replication Pre-Initiation	14/435	85/10856	6.26421E-06	8.00238E-05	5.26377E-05	PSMD12/PSMD3/PSMC3/CDK2/MCM3/MCM7/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	14
CSC	R-HSA-69656	Cyclin A:Cdk2-associated events at S phase entry	14/435	85/10856	6.26421E-06	8.00238E-05	5.26377E-05	PSMD12/PSMD3/CDK4/PSMC3/CDK2/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/RBBP4/PSMD2/PSMD1/PSMD13	14
CSC	R-HSA-169911	Regulation of Apoptosis	11/435	53/10856	6.26532E-06	8.00238E-05	5.26377E-05	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	11
CSC	R-HSA-2454202	Fc epsilon receptor (FCERI) signaling	18/435	134/10856	6.27779E-06	8.00238E-05	5.26377E-05	PSMD12/PSMD3/NRAS/HRAS/KRAS/FYN/LYN/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/RAC1/PSMD2/UBE2'	18
CSC	R-HSA-162906	HIV Infection	25/435	234/10856	7.37016E-06	9.248E-05	6.08311E-05	PSMD12/XPO1/PSMD3/BANF1/NUP155/LCK/FYN/HCK/XRCC5/PSMC3/RCC1/PSMC4/PSMD8/CDK9/PSMD7/POLR:	25
CSC	R-HSA-180585	Vif-mediated degradation of APOBEC3G	11/435	54/10856	7.58853E-06	9.248E-05	6.08311E-05	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	11
CSC	R-HSA-8854050	FBXL7 down-regulates AURKA during mitotic entry and in early mitosis	11/435	54/10856	7.58853E-06	9.248E-05	6.08311E-05	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	11
CSC	R-HSA-9604323	Negative regulation of NOTCH4 signaling	11/435	54/10856	7.58853E-06	9.248E-05	6.08311E-05	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	11
CSC	R-HSA-9669938	Signaling by KIT in disease	7/435	20/10856	7.78378E-06	9.28195E-05	6.10545E-05	NRAS/HRAS/KRAS/LCK/FYN/YES1/LYN	7
CSC	R-HSA-9670439	Signaling by phosphorylated juxtamembrane, extracellular and kinase domain KIT mutants	7/435	20/10856	7.78378E-06	9.28195E-05	6.10545E-05	NRAS/HRAS/KRAS/LCK/FYN/YES1/LYN	7
CSC	R-HSA-8873719	RAB geranylgeranylation	12/435	65/10856	8.59982E-06	0.00010146	6.67377E-05	RAB5A/RAB5C/RAB13/RAB15/RAB8A/RAB2A/RAB5B/RAB10/RAB1A/RAB35/RAB8B/RAB1B	12
CSC	R-HSA-176409	APC/C:Cdc20 mediated degradation of mitotic proteins	13/435	76/10856	8.7495E-06	0.000102139	6.71845E-05	PSMD12/PSMD3/CDK1/CCNB1/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	13
CSC	R-HSA-174113	SCF-beta-TrCP mediated degradation of Emi1	11/435	55/10856	9.14873E-06	0.00010353	6.80995E-05	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	11
CSC	R-HSA-4641257	Degradation of AXIN	11/435	55/10856	9.14873E-06	0.00010353	6.80995E-05	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	11
CSC	R-HSA-8941858	Regulation of RUNX3 expression and activity	11/435	55/10856	9.14873E-06	0.00010353	6.80995E-05	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	11
CSC	R-HSA-174143	APC/C-mediated degradation of cell cycle proteins	14/435	88/10856	9.50124E-06	0.000105369	6.9309E-05	PSMD12/PSMD3/CDK1/CCNB1/PSMC3/CDK2/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	14
CSC	R-HSA-453276	Regulation of mitotic cell cycle	14/435	88/10856	9.50124E-06	0.000105369	6.9309E-05	PSMD12/PSMD3/CDK1/CCNB1/PSMC3/CDK2/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	14
CSC	R-HSA-69563	p53-Dependent G1 DNA Damage Response	12/435	66/10856	1.01358E-05	0.000107199	7.05132E-05	PSMD12/PSMD3/PSMC3/CDK2/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	12
CSC	R-HSA-69580	p53-Dependent G1/S DNA damage checkpoint	12/435	66/10856	1.01358E-05	0.000107199	7.05132E-05	PSMD12/PSMD3/PSMC3/CDK2/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	12
CSC	R-HSA-176814	Activation of APC/C and APC/C:Cdc20 mediated degradation of mitotic proteins	13/435	77/10856	1.01496E-05	0.000107199	7.05132E-05	PSMD12/PSMD3/CDK1/CCNB1/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	13
CSC	R-HSA-5619084	ABC transporter disorders	13/435	77/10856	1.01496E-05	0.000107199	7.05132E-05	PSMD12/PSMD3/ERLIN1/ERLIN2/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	13
CSC	R-HSA-8852276	The role of GTSE1 in G2/M progression after G2 checkpoint	13/435	77/10856	1.01496E-05	0.000107199	7.05132E-05	PSMD12/PSMD3/CDK1/CCNB1/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	13
CSC	R-HSA-5687128	MAPK6/MAPK4 signaling	14/435	89/10856	1.08696E-05	0.000113721	7.48028E-05	PSMD12/XPO1/PSMD3/CDK1/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/RAC1/PSMD2/PSMD1/PSMD13	14
CSC	R-HSA-5362768	Hh mutants are degraded by ERAD	11/435	56/10856	1.09808E-05	0.00011381	7.48616E-05	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	11
CSC	R-HSA-5357801	Programmed Cell Death	23/435	210/10856	1.13802E-05	0.000116858	7.68665E-05	PSMD12/DNM1L/PSMD3/LMNA/H1-0/DSP/PSMC3/LMNB1/CTNNB1/PSMC4/PSMD8/BCAP31/PSMD7/PSME3/PSN	23
CSC	R-HSA-4641258	Degradation of DVL	11/435	57/10856	1.31235E-05	0.000132309	8.70298E-05	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	11
CSC	R-HSA-69541	Stabilization of p53	11/435	57/10856	1.31235E-05	0.000132309	8.70298E-05	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	11
CSC	R-HSA-69615	G1/S DNA Damage Checkpoints	12/435	68/10856	1.39425E-05	0.000139299	9.16276E-05	PSMD12/PSMD3/PSMC3/CDK2/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	12
CSC	R-HSA-69052	Switching of origins to a post-replicative state	14/435	91/10856	1.41388E-05	0.000139999	9.2088E-05	PSMD12/PSMD3/PSMC3/CDK2/MCM3/MCM7/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	14
CSC	R-HSA-392170	ADP signalling through P2Y purinoceptor 12	7/435	22/10856	1.59703E-05	0.000156403	0.000102878	GNAT3/GNAI2/GNAI3/GNB1/GNB2/GNAI1/GNB4	7
CSC	R-HSA-4086400	PCP/CE pathway	14/435	92/10856	1.60775E-05	0.000156403	0.000102878	PSMD12/PSMD3/RAC2/PSMC3/PSMC4/PSMD8/PSMD7/RAC3/PSME3/PSMC5/RAC1/PSMD2/PSMD1/PSMD13	14
CSC	R-HSA-5387390	Hh mutants abrogate ligand secretion	11/435	59/10856	1.85185E-05	0.00017553	0.000115459	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	11
CSC	R-HSA-5676590	NIK-->noncanonical NF-kB signaling	11/435	59/10856	1.85185E-05	0.00017553	0.000115459	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	11
CSC	R-HSA-68827	CDT1 association with the CDC6:ORC:origin complex	11/435	59/10856	1.85185E-05	0.00017553	0.000115459	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	11
CSC	R-HSA-2871837	FCERI mediated NF-kB activation	13/435	82/10856	2.0535E-05	0.000192994	0.000126947	PSMD12/PSMD3/LYN/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/UBE2V1/PSMD1/PSMD13	13
CSC	R-HSA-5663202	Diseases of signal transduction by growth factor receptors and second messengers	34/435	395/10856	2.10704E-05	0.000196362	0.000129162	PSMD12/PSMD3/ERLIN2/EGFR/NRAS/HRAS/KRAS/LMNA/LCK/FYN/YES1/LYN/FGFR1/RAC2/PSMC3/FGFR2/FGFR4/F	34
CSC	R-HSA-5607761	Dectin-1 mediated noncanonical NF-kB signaling	11/435	60/10856	2.18713E-05	0.000196994	0.000129578	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	11
CSC	R-HSA-5610780	Degradation of GLI1 by the proteasome	11/435	60/10856	2.18713E-05	0.000196994	0.000129578	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	11
CSC	R-HSA-5610783	Degradation of GLI2 by the proteasome	11/435	60/10856	2.18713E-05	0.000196994	0.000129578	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	11
CSC	R-HSA-5610785	GLI3 is processed to GLI3R by the proteasome	11/435	60/10856	2.18713E-05	0.000196994	0.000129578	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	11
CSC	R-HSA-8856688	Golgi-to-ER retrograde transport	17/435	133/10856	2.20264E-05	0.000196994	0.000129578	SURF4/ARF4/KIF5B/COPB2/CAPZB/TMED10/COPB1/RAB1A/DYNLL1/ARF5/KIF23/DYNC1H1/DYNLL2/RACGAP1/RAI	17
CSC	R-HSA-5619115	Disorders of transmembrane transporters	20/435	175/10856	2.28035E-05	0.000202313	0.000133076	PSMD12/PSMD3/ERLIN1/NUP155/ERLIN2/SLC2A1/PSMC3/HK1/BSG/PSMC4/PSMD8/PSMD7/SLC16A1/NUP107/F	20
CSC	R-HSA-195253	Degradation of beta-catenin by the destruction complex	13/435	83/10856	2.34773E-05	0.000206638	0.000135921	PSMD12/PSMD3/PSMC3/PPP2R1B/CTNNB1/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	13
CSC	R-HSA-194315	Signaling by Rho GTPases	51/435	703/10856	2.39133E-05	0.000208818	0.000137356	XPO1/ARPC1B/ARPC3/TFRC/LCK/TPM3/JUP/RAC2/DSP/LMNB1/MYL9/STOM/EPHA2/PPP2R1B/STIP1/KIF5B/PFN2/	51
CSC	R-HSA-8878166	Transcriptional regulation by RUNX2	16/435	121/10856	2.50169E-05	0.000216748	0.000142572	PSMD12/PSMD3/CDK1/YES1/CDK4/CCNB1/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/RBM14/PSMI	16
CSC	R-HSA-174184	Cdc20:Phospho-APC/C mediated degradation of Cyclin A	12/435	73/10856	2.93592E-05	0.000250457	0.000164745	PSMD12/PSMD3/CDK1/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	12
CSC	R-HSA-69017	CDK-mediated phosphorylation and removal of Cdc6	12/435	73/10856	2.93592E-05	0.000250457	0.000164745	PSMD12/PSMD3/PSMC3/CDK2/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	12
CSC	R-HSA-179419	APC:Cdc20 mediated degradation of cell cycle proteins prior to satisfation of the cell cycle checkpoint	12/435	74/10856	3.37933E-05	0.000286083	0.000188178	PSMD12/PSMD3/CDK1/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	12
CSC	R-HSA-392518	Signal amplification	8/435	33/10856	3.57475E-05	0.000300333	0.000197552	GNAT3/GNAI2/GNAI3/GNB1/GNB2/GNAI1/GNA13/GNB4	8
CSC	R-HSA-69275	G2/M Transition	21/435	196/10856	3.79838E-05	0.000316722	0.000208332	PSMD12/XPO1/PSMD3/CDK1/CCNB1/PSMC3/CDK2/PPP2R1B/PSMC4/PSMD8/PSMD7/RAB8A/PSME3/PPP1CB/PS	21
CSC	R-HSA-174084	Autodegradation of Cdh1 by Cdh1:APC/C	11/435	64/10856	4.1076E-05	0.000337432	0.000221955	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	11
CSC	R-HSA-4608870	Asymmetric localization of PCP proteins	11/435	64/10856	4.1076E-05	0.000337432	0.000221955	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	11
CSC	R-HSA-9716542	Signaling by Rho GTPases, Miro GTPases and RHOBTB3	51/435	719/10856	4.34273E-05	0.000354124	0.000232934	XPO1/ARPC1B/ARPC3/TFRC/LCK/TPM3/JUP/RAC2/DSP/LMNB1/MYL9/STOM/EPHA2/PPP2R1B/STIP1/KIF5B/PFN2/	51
CSC	R-HSA-453274	Mitotic G2-G2/M phases	21/435	198/10856	4.41663E-05	0.000357522	0.000235169	PSMD12/XPO1/PSMD3/CDK1/CCNB1/PSMC3/CDK2/PPP2R1B/PSMC4/PSMD8/PSMD7/RAB8A/PSME3/PPP1CB/PS	21
CSC	R-HSA-163200	Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins.	16/435	127/10856	4.58165E-05	0.000368192	0.000242188	ATP5MG/NDUFB10/COX2/CYC1/COX5B/COX4I1/UQCRB/ATP5PB/ATP5F1A/UQCRC1/LRPPRC/UQCRFS1/ATP5PO/N	16
CSC	R-HSA-5358346	Hedgehog ligand biogenesis	11/435	65/10856	4.76916E-05	0.000380503	0.000250286	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	11
CSC	R-HSA-5621481	C-type lectin receptors (CLRs)	17/435	142/10856	5.16543E-05	0.000409176	0.000269146	PSMD12/PSMD3/NRAS/HRAS/KRAS/FYN/LYN/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/UBE2V1/PSI	17
CSC	R-HSA-1234176	Oxygen-dependent proline hydroxylation of Hypoxia-inducible Factor Alpha	11/435	66/10856	5.52027E-05	0.000434183	0.000285595	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	11
CSC	R-HSA-382556	ABC-family proteins mediated transport	14/435	103/10856	5.87412E-05	0.00045876	0.000301762	PSMD12/PSMD3/ERLIN1/ERLIN2/PSMC3/EIF2S3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	14

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CSC	R-HSA-2029481	FCGR activation	5/435	12/10856	6.32994E-05	0.000490635	0.000322728	FYN/YES1/LYN/HCK/FGR	5
CSC	R-HSA-1169091	Activation of NF-kappaB in B cells	11/435	67/10856	6.37073E-05	0.000490635	0.000322728	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	11
CSC	R-HSA-1257604	PIP3 activates AKT signaling	25/435	267/10856	6.93837E-05	0.000530666	0.000349059	PSMD12/PSMD3/EGFR/LCK/FYN/FGFR1/RAC2/PSMC3/FGFR2/FGFR4/FGFR3/PPP2R1B/PSMC4/PSMD8/PSMD7/PS	25
CSC	R-HSA-174154	APC/C:Cdc20 mediated degradation of Securin	11/435	68/10856	7.3311E-05	0.000556862	0.000366291	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	11
CSC	R-HSA-168249	Innate Immune System	67/435	1060/10856	9.93532E-05	0.000749542	0.000493031	PSMD12/DDX3X/ARPC1B/ARPC3/SURF4/PSMD3/CYBSR3/NRAS/HRAS/KRAS/LCK/FYN/APRT/YES1/LYN/HCK/FGR/TD	67
CSC	R-HSA-8878159	Transcriptional regulation by RUNX3	13/435	96/10856	0.000111623	0.000836418	0.000550176	PSMD12/PSMD3/KRAS/PSMC3/CTNNB1/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	13
CSC	R-HSA-9006925	Intracellular signaling by second messengers	27/435	309/10856	0.000116926	0.000870277	0.000572447	PSMD12/PSMD3/EGFR/LCK/FYN/PRKAR1A/FGFR1/RAC2/PSMC3/FGFR2/FGFR4/FGFR3/PPP2R1B/PSMC4/PSMD8/F	27
CSC	R-HSA-69278	Cell Cycle, Mitotic	41/435	561/10856	0.000134145	0.000991779	0.000652368	PSMD12/XPO1/PSMD3/BANF1/NUP155/LMNA/CDK1/LYN/CDK4/CCNB1/PSMC3/RCC1/LMNB1/CDK2/MCM3/PPP.	41
CSC	R-HSA-202424	Downstream TCR signaling	13/435	98/10856	0.000138195	0.001014954	0.000667613	PSMD12/PSMD3/LCK/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/UBE2V1/PSMD1/PSMD13	13
CSC	R-HSA-8939902	Regulation of RUNX2 expression and activity	11/435	73/10856	0.000142126	0.001043957	0.000682086	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	11
CSC	R-HSA-162658	Golgi Cisternae Pericentriolar Stack Reorganization	5/435	14/10856	0.000149684	0.00107792	0.00070903	CDK1/CCNB1/RAB2A/RAB1A/RAB1B	5
CSC	R-HSA-170670	Adenylate cyclase inhibitory pathway	5/435	14/10856	0.000149684	0.00107792	0.00070903	GNAT3/GNAI2/GNAI3/GNAL/GNAI1	5
CSC	R-HSA-6811434	COPI-dependent Golgi-to-ER retrograde traffic	13/435	99/10856	0.00015341	0.001092844	0.000718847	SURF4/ARF4/KIF5B/COPB2/TMED10/COPB1/RAB1A/ARF5/KIF23/RACGAP1/RAB18/COPG2/COPG1	13
CSC	R-HSA-109582	Hemostasis	44/435	621/10856	0.000153727	0.001092844	0.000718847	GNAT3/ATP2A1/NRAS/HRAS/KRAS/MMP1/GNAI2/LCK/FYN/YES1/LYN/GNAI3/FGR/PRKAR1A/RAC2/ATP2A2/RAB5A/	44
CSC	R-HSA-174178	APC/C:Cdh1 mediated degradation of Cdc20 and other APC/C:Cdh1 targeted proteins in late mitosis/early G1	11/435	74/10856	0.000161041	0.001137544	0.000748249	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	11
CSC	R-HSA-8949613	Cristae formation	7/435	31/10856	0.000180069	0.001263904	0.000831366	ATP5MG/ATP5PB/ATP5F1A/ATP5PO/ATP5MF/IMMT/CHCHD3	7
CSC	R-HSA-1234174	Cellular response to hypoxia	11/435	75/10856	0.000182052	0.001269781	0.000835232	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	11
CSC	R-HSA-6807878	COPI-mediated anterograde transport	13/435	101/10856	0.000188205	0.001304496	0.000858066	ARF4/COPB2/CAP2B/TMED10/COPB1/RAB1A/DYNLL1/ARF5/DYNC1H1/DYNLL2/RAB18/COPG2/COPG1	13
CSC	R-HSA-9012999	RHO GTPase cycle	34/435	443/10856	0.00020507	0.001412562	0.000929149	TFRC/LCK/TPM3/IUP/RAC2/DSP/LMNB1/STOM/EPHA2/STIP1/IQGAP1/CAP2B/BCAP31/ARHGDIA/RAC3/RRAS2/TRA	34
CSC	R-HSA-5684996	MAPK1/MAPK3 signaling	25/435	286/10856	0.000206967	0.001416827	0.000931955	PSMD12/PSMD3/EGFR/NRAS/HRAS/KRAS/FYN/CDK1/FGFR1/PSMC3/FGFR2/FGFR4/FGFR3/PPP2R1B/PPP1CC/PSM	25
CSC	R-HSA-1268020	Mitochondrial protein import	10/435	64/10856	0.000209064	0.001422403	0.000935622	TIMM44/CS/SLC25A12/TOMM40/CYC1/ATP5F1A/CMC2/TOMM22/CHCHD3/SLC25A13	10
CSC	R-HSA-3928662	EPHB-mediated forward signaling	8/435	42/10856	0.000221415	0.001497252	0.000984857	ARPC1B/ARPC3/HRAS/FYN/YES1/LYN/ARPC4/RAC1	8
CSC	R-HSA-2467813	Separation of Sister Chromatids	19/435	191/10856	0.000235687	0.0015841	0.001041983	PSMD12/XPO1/PSMD3/PSMC3/PPP2R1B/PPP1CC/RPS27/PSMC4/PSMD8/PSMD7/NUP107/PSME3/PSMC5/DYNLI	19
CSC	R-HSA-1433557	Signaling by SCF-KIT	8/435	43/10856	0.000262643	0.001733754	0.001140422	NRAS/HRAS/KRAS/LCK/FYN/YES1/LYN/RAC1	8
CSC	R-HSA-977444	GABA B receptor activation	8/435	43/10856	0.000262643	0.001733754	0.001140422	GNAT3/GNAI2/GNAI3/GNAL/GNB1/GNB2/GNAI1/GNB4	8
CSC	R-HSA-991365	Activation of GABAB receptors	8/435	43/10856	0.000262643	0.001733754	0.001140422	GNAT3/GNAI2/GNAI3/GNAL/GNB1/GNB2/GNAI1/GNB4	8
CSC	R-HSA-5683057	MAPK family signaling cascades	27/435	325/10856	0.000267628	0.001756208	0.001155192	PSMD12/XPO1/PSMD3/EGFR/NRAS/HRAS/KRAS/FYN/CDK1/FGFR1/PSMC3/FGFR2/FGFR4/FGFR3/PPP2R1B/PPP1C	27
CSC	R-HSA-111885	Opioid Signalling	12/435	92/10856	0.00029126	0.001900046	0.001249805	GNAT3/GNAI2/GNAI3/PRKAR1A/PPP2R1B/GNAL/KPNA2/GNB1/GNB2/GNAI1/CDK5/GNB4	12
CSC	R-HSA-69239	Synthesis of DNA	14/435	120/10856	0.000307481	0.001982702	0.001304174	PSMD12/PSMD3/PSMC3/CDK2/MCM5/MCM7/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	14
CSC	R-HSA-73856	RNA Polymerase II Transcription Termination	10/435	67/10856	0.000307507	0.001982702	0.001304174	SNRPB/EIF4A3/SNRPE/SNRPD3/SRSF3/SRSF1/SRSF4/SRSF9/SRSF6/SRSF7	10
CSC	R-HSA-69620	Cell Cycle Checkpoints	25/435	294/10856	0.000316027	0.002025864	0.001332565	PSMD12/XPO1/PSMD3/CDK1/CCNB1/PSMC3/CDK2/MCM3/PPP2R1B/MCM7/PPP1CC/RPS27/PSMC4/PSMD8/PSM	25
CSC	R-HSA-68886	M Phase	32/435	418/10856	0.000329379	0.002099316	0.00138088	PSMD12/XPO1/PSMD3/BANF1/NUP155/LMNA/CDK1/CCNB1/PSMC3/RCC1/LMNB1/PPP2R1B/PPP1CC/RPS27/PSI	32
CSC	R-HSA-5673001	RAF/MAP kinase cascade	24/435	280/10856	0.000369136	0.002330154	0.001532172	PSMD12/PSMD3/EGFR/NRAS/HRAS/KRAS/FYN/FGFR1/PSMC3/FGFR2/FGFR4/FGFR3/PPP2R1B/PPP1CC/PSMC4/IQ	24
CSC	R-HSA-9006115	Signaling by NTRK2 (TRKB)	6/435	25/10856	0.000369799	0.002330154	0.00153272	NRAS/HRAS/KRAS/FYN/RAC1/CDK5	6
CSC	R-HSA-202733	Cell surface interactions at the vascular wall	15/435	137/10856	0.000380503	0.002384055	0.001568175	NRAS/HRAS/KRAS/MMP1/LCK/FYN/YES1/LYN/ITGA6/BSG/SLC16A1/ATP1B3/CAV1/SLC7A6/SLC7A7	15
CSC	R-HSA-9013694	Signaling by NOTCH4	11/435	82/10856	0.000404696	0.002518312	0.001656486	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	11
CSC	R-HSA-69481	G2/M Checkpoints	17/435	168/10856	0.000406472	0.002518312	0.001656486	PSMD12/PSMD3/CDK1/CCNB1/PSMC3/CDK2/MCM3/MCM7/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/UBE	17
CSC	R-HSA-8853334	Signaling by FGFR3 fusions in cancer	4/435	10/10856	0.000440426	0.002713513	0.001784884	NRAS/HRAS/KRAS/FGFR3	4
CSC	R-HSA-6807070	PTEN Regulation	15/435	140/10856	0.000480405	0.002943477	0.001936149	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/CSNK2B/CSNK2A1/RBBP4/PSMD2/RBBP7/PSMD	15
CSC	R-HSA-9664407	Parasite infection	9/435	59/10856	0.000518457	0.00312483	0.002055439	ARPC1B/ARPC3/FYN/YES1/LYN/HCK/FGR/ARPC4/RAC1	9
CSC	R-HSA-9664417	Leishmania phagocytosis	9/435	59/10856	0.000518457	0.00312483	0.002055439	ARPC1B/ARPC3/FYN/YES1/LYN/HCK/FGR/ARPC4/RAC1	9
CSC	R-HSA-9664422	FCGR3A-mediated phagocytosis	9/435	59/10856	0.000518457	0.00312483	0.002055439	ARPC1B/ARPC3/FYN/YES1/LYN/HCK/FGR/ARPC4/RAC1	9
CSC	R-HSA-5632684	Hedgehog 'on' state	11/435	85/10856	0.000553699	0.003319204	0.002183293	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	11
CSC	R-HSA-163210	Formation of ATP by chemiosmotic coupling	5/435	18/10856	0.000560836	0.003343908	0.002199543	ATP5MG/ATP5PB/ATP5F1A/ATP5PO/ATP5MF	5
CSC	R-HSA-5610787	Hedgehog 'off' state	11/435	113/10856	0.000573044	0.003383678	0.002225703	PSMD12/PSMD3/PPP2R1A/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/GNAS/PSMD1/PSMD13	13
CSC	R-HSA-418597	G alpha (z) signalling events	8/435	48/10856	0.000573608	0.003383678	0.002225703	GNAT3/GNAI2/GNAI3/GNB1/GNB2/GNAI1/GNAS/GNB4	8
CSC	R-HSA-69306	DNA Replication	14/435	128/10856	0.000597139	0.003503849	0.002304748	PSMD12/PSMD3/PSMC3/CDK2/MCM3/MCM7/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	14
CSC	R-HSA-6790901	rRNA modification in the nucleus and cytosol	9/435	61/10856	0.000666683	0.003857451	0.002537339	NOP56/RPS2/FBL/NOP2/RPS9/SNU13/RPS14/RPS6/NOL6	9
CSC	R-HSA-2514853	Condensation of Prometaphase Chromosomes	4/435	11/10856	0.000670281	0.003857451	0.002537339	CDK1/CCNB1/CSNK2B/CSNK2A1	4
CSC	R-HSA-5655291	Signaling by FGFR4 in disease	4/435	11/10856	0.000670281	0.003857451	0.002537339	NRAS/HRAS/KRAS/FGFR4	4
CSC	R-HSA-190236	Signaling by FGFR	11/435	87/10856	0.000676517	0.003857451	0.002537339	NRAS/HRAS/KRAS/FGFR1/FGFR2/FGFR4/FGFR3/PTBP1/HNRNPM/POLR2H/HNRNPF	11
CSC	R-HSA-6814122	Cooperation of PDCL (PhLP1) and TRiC/CCT in G-protein beta folding	7/435	38/10856	0.000678271	0.003857451	0.002537339	CCT3/GNB1/GNB2/CSNK2B/CSNK2A1/CCT7/GNB4	7
CSC	R-HSA-9013407	RHOH GTPase cycle	7/435	38/10856	0.000678271	0.003857451	0.002537339	TFRC/LCK/IUP/CTOM/ARHGDIA/CAV1/DBN1	7
CSC	R-HSA-5607764	CLEC7A (Dectin-1) signaling	12/435	101/10856	0.000691655	0.003913495	0.002574203	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/UBE2V1/PSMD1/PSMD13	12
CSC	R-HSA-2995383	Initiation of Nuclear Envelope (NE) Reformation	5/435	19/10856	0.000736307	0.004144995	0.002726479	BANF1/LMNA/CDK1/CCNB1/LMNB1	5
CSC	R-HSA-69242	S Phase	16/435	162/10856	0.000778493	0.004360349	0.002868133	PSMD12/PSMD3/CDK4/PSMC3/CDK2/MCM3/MCM7/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/RBBP4/PSMD2/PSM	16
CSC	R-HSA-9020702	Interleukin-1 signaling	12/435	103/10856	0.00082558	0.004600843	0.003026324	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/UBE2V1/PSMD1/PSMD13	12
CSC	R-HSA-1640170	Cell Cycle	45/435	692/10856	0.000842713	0.004654662	0.003061725	PSMD12/XPO1/PSMD3/BANF1/NUP155/LMNA/CDK1/LYN/CDK4/CCNB1/PSMC3/RCC1/LMNB1/CDK2/MCM3/PPP.	45
CSC	R-HSA-195721	Signaling by WNT	26/435	332/10856	0.000845626	0.004654662	0.003061725	PSMD12/XPO1/PSMD3/KRAS/GNAO1/RAC2/PSMC3/GNAT2/PPP2R1B/CTNNB1/PSMC4/PSMD8/PSMD7/RAC3/PSA	26
CSC	R-HSA-1226099	Signaling by FGFR in disease	9/435	63/10856	0.000847828	0.004654662	0.003061725	ERLIN2/NRAS/HRAS/KRAS/FGFR1/FGFR2/FGFR4/FGFR3/POLR2H	9
CSC	R-HSA-5218920	VEGFR2 mediated vascular permeability	6/435	29/10856	0.000865846	0.004730162	0.003111388	PSMD12/IUP/CTNNB1/RAC1/CAV1	6
CSC	R-HSA-1236974	ER-Phagosome pathway	11/435	90/10856	0.000902631	0.004906951	0.003227675	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	11
CSC	R-HSA-210990	PECAM1 interactions	4/435	12/10856	0.000973772	0.005267871	0.00346508	LCK/FYN/YES1/LYN	4
CSC	R-HSA-75153	Apoptotic execution phase	8/435	52/10856	0.000994628	0.005354578	0.003522113	DNM1L/LMNA/H1-0/DSP/LMNB1/CTNNB1/BCAP31/PLEC	8
CSC	R-HSA-202403	TCR signaling	13/435	120/10856	0.001014834	0.005436961	0.003576303	PSMD12/PSMD3/LCK/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/UBE2V1/PSMD1/PSMD13	13
CSC	R-HSA-2424491	DAP12 signaling	6/435	30/10856	0.001046225	0.005578188	0.003669199	NRAS/HRAS/KRAS/LCK/FYN/RAC1	6
CSC	R-HSA-422356	Regulation of insulin secretion	10/435	78/10856	0.001054421	0.005594989	0.00368025	GNAI2/PRKAR1A/SLC2A1/MARCKS/IQGAP1/GNB1/GNB2/GNAI1/GNAS/GNB4	10
CSC	R-HSA-191859	snRNP Assembly	8/435	53/10856	0.001131252	0.005945772	0.003910987	NUP155/SNRPB/CLNS1A/NUP107/SNRPE/SNRPD1/SNRPD2/SNRPD3	8
CSC	R-HSA-194441	Metabolism of non-coding RNA	8/435	53/10856	0.001131252	0.005945772	0.003910987	NUP155/SNRPB/CLNS1A/NUP107/SNRPE/SNRPD1/SNRPD2/SNRPD3	8
CSC	R-HSA-389513	CTLA4 inhibitory signaling	5/435	21/10856	0.001205968	0.006249617	0.004110849	LCK/FYN/YES1/LYN/PPP2R1B	5
CSC	R-HSA-445144	Signal transduction by L1	5/435	21/10856	0.001205968	0.006249617	0.004110849	EGFR/FGFR1/RAC1/CSNK2B/CSNK2A1	5
CSC	R-HSA-5621575	CD209 (DC-SIGN) signaling	5/435	21/10856	0.001205968	0.006249617	0.004110849	NRAS/HRAS/RAC/FYN/LYN	5
CSC	R-HSA-8848021	Signaling by PTK6	8/435	54/10856	0.001282443	0.006584395	0.004331058	EGFR/NRAS/HRAS/KRAS/CDK4/SFPQ/CDK2/RAC1	8
CSC	R-HSA-9006927	Signaling by Non-Receptor Tyrosine Kinases	8/435	54/10856	0.001282443	0.006584395	0.004331058	EGFR/NRAS/HRAS/KRAS/CDK4/SFPQ/CDK2/RAC1	8
CSC	R-HSA-179812	GRB2 events in EGFR signaling	4/435	13/10856	0.001362344	0.006962393	0.004579696	EGFR/NRAS/HRAS/KRAS	4
CSC	R-HSA-9663891	Selective autophagy	10/435	81/10856	0.00141487	0.007197663	0.004734451	TOMM40/DYNLL1/CSNK2B/CSNK2A1/UBE2V1/DYNC1H1/DYNLL2/PGAM5/PARK7/TOMM22	10
CSC	R-HSA-8939211	ESR-mediated signaling	19/435	223/10856	0.001580231	0.008002174	0.005263639	GNAT3/XPO1/EGFR/NRAS/HRAS/KRAS/GNAI2/GNAI3/DDX5/CDK9/KPNA2/POLR2H/GNB1/GNB2/GNAI1/CAV1/PTG	19
CSC	R-HSA-180336	SHC1 events in EGFR signaling	4/435	14/10856	0.001847408	0.009146318	0.006016229	EGFR/NRAS/HRAS/KRAS	4
CSC	R-HSA-418359	Reduction of cytosolic Ca++ levels	4/435	14/10856	0.001847408	0.009146318	0.006016229	ATP2A1/ATP2A2/SRI/ATP2A3	4
CSC	R-HSA-8849471	PTK6 Regulates RHO GTPases, RAS GTPase and MAP kinases	4/435	14/10856	0.001847408	0.009146318	0.006016229	NRAS/HRAS/KRAS/RAC1	4
CSC	R-HSA-8964539	Glutamate and glutamine metabolism	4/435	14/10856	0.001847408	0.009146318	0.006016229	GLUD1/OAT/GLUD2/PYCR3	4
CSC	R-HSA-9027284	Erythropoietin activates RAS	4/435	14/10856	0.001847408	0.009146318	0.006016229	NRAS/HRAS/KRAS/LYN	4
CSC	R-HSA-70263	Gluconeogenesis	6/435	34/10856	0.002069716	0.0102014	0.006710237	FBP2/SLC25A12/FBP1/MDH1/SLC25A1/SLC25A13	6
CSC	R-HSA-4419969	Depolymerisation of the Nuclear Lamina	4/435	15/10856	0.00244022	0.011817486	0.00777326	LMNA/CDK1/CCNB1/LMNB1	4
CSC	R-HSA-5637810	Constitutive Signaling by EGFRvIII	4/435	15/10856	0.00244022	0.011817486	0.00777326	EGFR/NRAS/HRAS/KRAS	4
CSC	R-HSA-5637812	Signaling by EGFRvIII in Cancer	4/435	15/10856	0.00244022	0.011817486	0.00777326	EGFR/NRAS/HRAS/KRAS	4
CSC	R-HSA-71336	Pentose phosphate pathway	4/435	15/10856	0.00244022	0.011817486	0.00777326	G6PD/PRPS2/PRPS1L1/PRPS1	4
CSC	R-HSA-5668541	TNFR2 non-canonical NF-kB pathway	11/435	102/10856	0.002517322	0.012085327	0.007949439	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	11
CSC	R-HSA-5689603	UCH proteinases	11/435	102/10856	0.002517322	0.012085327	0.007949439	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	11
CSC	R-HSA-977443	GABA receptor activation	8/435	60/10856	0.002558862	0.012231803	0.008045788	GNAT3/GNAI2/GNAI3/GNAL/GNB1/GNB2/GNAI1/GNB4	8
CSC	R-HSA-418346	Platelet homeostasis	10/435	88/10856	0.002652475	0.01262487	0.008304338	ATP2A1/FGR/ATP2A2/PPP2R1B/SRI/GNB1/GNB2/GNAS/ATP2A3/GNB4	10
CSC	R-HSA-9013106	RHOC GTPase cycle	9/435	74/10856	0.002687771	0.012738197	0.008378881	TFRC/IUP/STOM/IQGAP1/ARHGDIA/CAV1/C1QBP/CAVIN1/RACGAP1	9
CSC	R-HSA-611105	Respiratory electron transport	11/435	103/10856	0.002719596	0.012834179	0.008442016	NDUFB10/COX2/CYC1/COXSB/COX4I1/UQCRB/UQCRC1/LRPPRC/UQCRFS1/NDUFAB/NDUFA5	11
CSC	R-HSA-69273	Cyclin A/B1/B2 associated events during G2/M transition	5/435	25/10856	0.002759245	0.012966111	0.008528798	XPO1/CDK1/CCNB1/CDK2/PPP2R1B	5
CSC	R-HSA-5673000	RAF activation	6/435	36/10856	0.002801837	0.01306878	0.008596331	NRAS/HRAS/KRAS/PPP2R1B/PPP1CC/PPP1CB	6
CSC	R-HSA-112399	IRS-mediated signalling	7/435	48/10856	0.002804662	0.01306878	0.008596331	NRAS/HRAS/RAS/FGFR1/FGFR2/FGFR3	7
CSC	R-HSA-159236	Transport of Mature mRNA derived from an Intron-Containing Transcript	9/435	75/10856	0.002948898	0.01368338	0.0090006	NUP155/EIF4A3/NUP107/SRSF3/SRSF1/SRSF4/SRSF9/SRSF6/SRSF7	9
CSC	R-HSA-9658195	Leishmania infection	20/435	254/10856	0.003059236	0.014136219	0.009298467	GNAT3/ARPC1B/ARPC3/GNAI2/FYN/YES1/LYN/HCK/GNAI3/FGR/TXN/PRKAR1A/NT5E/ARPC4/GNB1/GNB2/RAC1/GI	20
CSC	R-HSA-6811442	Intra-Golgi and retrograde Golgi-to-ER traffic	17/435	202/10856	0.00310882	0.014203641	0.009342815	SURF4/ARF4/KIF5B/COPB2/CAP2B/TMED10/COPB1/RAB1A/DYNLL1/ARF5/KIF23/DYNC1H1/DYNLL2/RACGAP1/RAI	17
CSC	R-HSA-8876198	RAB GEFs exchange GTP for GDP on RABs	10/435	90/10856	0.003131989	0.014203641	0.009342815	RABSA/RABSC/RAB13/RABBA/RAB5B/RAB10/RAB1A/RAB15/RABBB/RAB1B	10
CSC	R-HSA-1433559	Regulation of KIT signaling	4/435	16/10856	0.003151776	0.014203641	0.009342815	LCK/FYN/YES1/LYN	4
CSC	R-HSA-1963640	GRB2 events in ERBB2 signaling	4/435	16/10856	0.003151776	0.014203641	0.009342815	EGFR/NRAS/HRAS/KRAS	4
CSC	R-HSA-399956	CRMPs in Sema3A signaling	4/435	16/10856	0.003151776	0.014203641	0.009342815	FYN/CDK5/CRMP1/DPYSL2	4
CSC	R-HSA-9665348	Signaling by ERBB2 ECD mutants	4/435	16/10856	0.003151776	0.014203641	0.009342815	EGFR/NRAS/HRAS/KRAS	4
CSC	R-HSA-1236975	Antigen processing-Cross presentation	11/435	105/10856	0.00316348	0.014203641	0.009342815	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	11
CSC	R-HSA-70326	Glucose metabolism	10/435	91/10856	0.003396353	0.015187725	0.009990122	FBP2/NUP155/SLC25A12/FBP1/HK1/PPP2R1B/MDH1/SLC25A1/NUP107/SLC25A13	10
CSC	R-HSA-2682334	EPH-Ephrin signaling	10/435	92/10856	0.003678151	0.016381803	0.010775559	ARPC1B/ARPC3/HRAS/FYN/YES1/LYN/MYL9/EPHA2/ARPC4/RAC1	10
CSC	R-HSA-111465	Apoptotic cleavage of cellular proteins	6/435	38/10856	0.003712329	0.016402284	0.01078903	LMNA/DSP/LMNB1/CTNNB1/BCAP31/PLEC	6
CSC	R-HSA-9607240	FLT3 Signaling	6/435	38/10856	0.003712329	0.016402284	0.01078903	NRAS/HRAS/KRAS/LCK/FYN/HCK	6
CSC	R-HSA-2219530	Constitutive Signaling by Aberrant PI3K in Cancer	9/435	78/10856	0.003854078	0.016961	0.01115654	EGFR/LCK/FYN/FGFR1/RAC2/FGFR2/FGFR4/FGFR3/RAC1	9
CSC	R-HSA-163685	Integration of energy metabolism	11/435	108/10856	0.003936653	0.017255921	0.011350532	GNAI2/PRKAR1A/SLC2A1/MARCKS/PPP2R1B/IQGAP1/GNB1/GNB2/GNAI1/GNAS/GNB4	11
CSC	R-HSA-2428928	IRS-related events triggered by IGF1R	7/435	52/10856	0.004443403	0.019324445	0.012711158	NRAS/HRAS/KRAS/FGFR1/FGFR2/FGFR4/FGFR3	7
CSC	R-HSA-2980766	Nuclear Envelope Breakdown	7/435	52/10856	0.004443403	0.019324445	0.012711158	BANF1/NUP155/LMNA/CDK1/CCNB1/LMNB1/NUP107	7
CSC	R-HSA-400042	Adrenaline,noradrenaline inhibits insulin secretion	5/435	28/10856	0.004624554	0.020005666	0.013159248	GNAI2/GNB1/GNB2/GNAI1/GNB4	5
CSC	R-HSA-1592230	Mitochondrial biogenesis	10/435	95/10856	0.004636119	0.020005666	0.013159248	ATP5MG/GLUD1/ATP5PB/ATP5F1A/ATP5PO/GLUD2/ATP5MF/SSBP1/IMMT/CHCHD3	10
CSC	R-HSA-9664323	FCGR3A-mediated IL10 synthesis	6/435	40/10856	0.004825678	0.020742933	0.013644206	FYN/YES1/LYN/HCK/FGR/PRKAR1A	6

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CSC	R-HSA-2428924	IGF1R signaling cascade	7/435	53/10856	0.004947426	0.021131562	0.013899836	NRAS/HRAS/KRAS/FGFR1/FGFR2/FGFR4/FGFR3	7
CSC	R-HSA-5654704	SHC-mediated cascade:FGFR3	4/435	18/10856	0.004973253	0.021131562	0.013899836	NRAS/HRAS/KRAS/FGFR3	4
CSC	R-HSA-881907	Gastrin-CREB signalling pathway via PKC and MAPK	4/435	18/10856	0.004973253	0.021131562	0.013899836	EGFR/NRAS/HRAS/KRAS	4
CSC	R-HSA-5205647	Mitophagy	5/435	29/10856	0.005407619	0.022802469	0.014998919	TOMM40/CSNK2B/CSNK2A1/PGAM5/TOMM22	5
CSC	R-HSA-9694548	Maturation of spike protein	5/435	29/10856	0.005407619	0.022802469	0.014998919	RPN1/RPN2/PRKCSH/CANX/DDOST	5
CSC	R-HSA-2404192	Signaling by Type 1 Insulin-like Growth Factor 1 Receptor (IGF1R)	7/435	54/10856	0.005493274	0.022988834	0.015121505	NRAS/HRAS/KRAS/FGFR1/FGFR2/FGFR4/FGFR3	7
CSC	R-HSA-74751	Insulin receptor signalling cascade	7/435	54/10856	0.005493274	0.022988834	0.015121505	NRAS/HRAS/KRAS/FGFR1/FGFR2/FGFR4/FGFR3	7
CSC	R-HSA-71406	Pyruvate metabolism and Citric Acid (TCA) cycle	7/435	55/10856	0.006083022	0.024867589	0.016357305	IDH3B/CS/FH/PDHA1/BSG/DLST/SLC16A1	7
CSC	R-HSA-1236382	Constitutive Signaling by Ligand-Responsive EGFR Cancer Variants	4/435	19/10856	0.006103106	0.024867589	0.016357305	EGFR/NRAS/HRAS/KRAS	4
CSC	R-HSA-392851	Prostacyclin signalling through prostacyclin receptor	4/435	19/10856	0.006103106	0.024867589	0.016357305	GNB1/GNB2/GNAS/GNB4	4
CSC	R-HSA-5637815	Signaling by Ligand-Responsive EGFR Variants in Cancer	4/435	19/10856	0.006103106	0.024867589	0.016357305	EGFR/NRAS/HRAS/KRAS	4
CSC	R-HSA-381676	Glucagon-like Peptide-1 (GLP1) regulates insulin secretion	6/435	42/10856	0.006166685	0.024867589	0.016357305	PRKAR1A/IQGAP1/GNB1/GNB2/GNAS/GNB4	6
CSC	R-HSA-9035034	RHOF GTPase cycle	6/435	42/10856	0.006166685	0.024867589	0.016357305	LMNB1/CAP2B/BASP1/CAV1/ESYT1/RHOF	6
CSC	R-HSA-9696264	RND3 GTPase cycle	6/435	42/10856	0.006166685	0.024867589	0.016357305	DSP/EPHA2/CAV1/CKAP4/TMOD3/NISCH	6
CSC	R-HSA-9696273	RND1 GTPase cycle	6/435	42/10856	0.006166685	0.024867589	0.016357305	TFRC/DSP/EPHA2/STIP1/RRAS2/CAV1	6
CSC	R-HSA-4420097	VEGFA-VEGFR2 Pathway	10/435	99/10856	0.006207027	0.024867589	0.016357305	CTNND1/NRAS/HRAS/KRAS/FYN/JUP/CTNNA1/CTNNB1/RAC1/CAV1	10
CSC	R-HSA-111367	SLBP independent Processing of Histone Pre-mRNAs	3/435	10/10856	0.006211291	0.024867589	0.016357305	SNRPB/SNRPE/SNRPD3	3
CSC	R-HSA-2465910	MASTL Facilitates Mitotic Progression	3/435	10/10856	0.006211291	0.024867589	0.016357305	CDK1/CCNB1/PPP2R1B	3
CSC	R-HSA-428542	Regulation of commissural axon pathfinding by SLIT and ROBO	3/435	10/10856	0.006211291	0.024867589	0.016357305	NELL2/ROBO2/ROBO1	3
CSC	R-HSA-3928663	EPHA-mediated growth cone collapse	5/435	30/10856	0.006279898	0.025051822	0.016478489	FYN/YES1/LYN/MYL9/EPHA2	5
CSC	R-HSA-72202	Transport of Mature Transcript to Cytoplasm	9/435	84/10856	0.0063064	0.025067376	0.01648872	NUP155/EIF4A3/NUP107/SRSF3/SRSF1/SRSF4/SRSF9/SRSF6/SRSF7	9
CSC	R-HSA-112040	G-protein mediated events	7/435	56/10856	0.006718754	0.026611064	0.017504122	GNAT3/GNAI2/GNAI3/PRKAR1A/GNAL/KPNA2/GNAI1	7
CSC	R-HSA-5358351	Signaling by Hedgehog	13/435	149/10856	0.0068176	0.02690647	0.017698433	PSMD12/PSMD3/PRKAR1A/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/GNAS/PSMD1/PSMD13	13
CSC	R-HSA-2029480	Fcgamma receptor (FCGR) dependent phagocytosis	9/435	86/10856	0.00734605	0.028805034	0.018947263	ARPC1B/ARPC3/FYN/YES1/LYN/HCK/FGR/ARPC4/RAC1	9
CSC	R-HSA-5654706	FRS-mediated FGFR3 signaling	4/435	20/10856	0.007391444	0.028805034	0.018947263	NRAS/HRAS/KRAS/FGFR3	4
CSC	R-HSA-5654719	SHC-mediated cascade:FGFR4	4/435	20/10856	0.007391444	0.028805034	0.018947263	NRAS/HRAS/KRAS/FGFR4	4
CSC	R-HSA-936837	Ion transport by P-type ATPases	7/435	57/10856	0.007402556	0.028805034	0.018947263	ATP2A1/ATP2A2/SRI/ATP12A/ATP1B3/ATP1A4/ATP2A3	7
CSC	R-HSA-8878171	Transcriptional regulation by RUNX1	18/435	239/10856	0.007596369	0.029455849	0.019375353	PSMD12/PSMD3/PSMC3/MYL9/PSMC4/PSMD8/BLK/PSMD7/PSME3/PSMC5/CSNK2B/CSNK2A1/CDK6/PSMD2/PSI	18
CSC	R-HSA-9662851	Anti-inflammatory response favouring Leishmania parasite infection	14/435	169/10856	0.007969451	0.030687919	0.02018578	GNAT3/GNAI2/PYN/YES1/LYN/HCK/GNAI3/FGR/PRKAR1A/GNB1/GNB2/GNAI1/GNAS/GNB4	14
CSC	R-HSA-9664433	Leishmania parasite growth and survival	14/435	169/10856	0.007969451	0.030687919	0.02018578	GNAT3/GNAI2/FYN/YES1/LYN/HCK/GNAI3/FGR/PRKAR1A/GNB1/GNB2/GNAI1/GNAS/GNB4	14
CSC	R-HSA-72187	mRNA 3'-end processing	7/435	58/10856	0.008136516	0.031037069	0.020415442	EIF4A3/SRSF3/SRSF1/SRSF4/SRSF9/SRSF6/SRSF7	7
CSC	R-HSA-446107	Type I hemidesmosome assembly	3/435	11/10856	0.00828917	0.031037069	0.020415442	ITGA6/PLEC/COL17A1	3
CSC	R-HSA-77588	SLBP Dependent Processing of Replication-Dependent Histone Pre-mRNAs	3/435	11/10856	0.00828917	0.031037069	0.020415442	SNRPB/SNRPE/SNRPD3	3
CSC	R-HSA-8851805	MET activates RAS signaling	3/435	11/10856	0.00828917	0.031037069	0.020415442	NRAS/HRAS/KRAS	3
CSC	R-HSA-8934903	Receptor Mediated Mitophagy	3/435	11/10856	0.00828917	0.031037069	0.020415442	CSNK2B/CSNK2A1/PGAM5	3
CSC	R-HSA-9028731	Activated NTRK2 signals through FRS2 and FRS3	3/435	11/10856	0.00828917	0.031037069	0.020415442	NRAS/HRAS/KRAS	3
CSC	R-HSA-9634285	Constitutive Signaling by Overexpressed ERBB2	3/435	11/10856	0.00828917	0.031037069	0.020415442	NRAS/HRAS/KRAS	3
CSC	R-HSA-2871796	FCERI mediated MAPK activation	5/435	32/10856	0.008312001	0.031037069	0.020415442	NRAS/HRAS/KRAS/LYN/RAC1	5
CSC	R-HSA-456926	Thrombin signalling through proteinase activated receptors (PARs)	5/435	32/10856	0.008312001	0.031037069	0.020415442	GNB1/GNB2/GNA12/GNA13/GNB4	5
CSC	R-HSA-5654738	Signaling by FGFR2	8/435	73/10856	0.008568557	0.031887683	0.020974956	NRAS/HRAS/KRAS/FGFR2/PTBP1/HNRNPM/PCLR2H/HNRNPF	8
CSC	R-HSA-2172127	DAP12 interactions	6/435	45/10856	0.008659217	0.032010238	0.021055569	NRAS/HRAS/KRAS/LCK/FYN/RAC1	6
CSC	R-HSA-3899300	SUMOylation of transcription cofactors	6/435	45/10856	0.008659217	0.032010238	0.021055569	DDX5/SUMO3/SUMO2/TRIM28/DDX17/PARK7	6
CSC	R-HSA-5654688	SHC-mediated cascade:FGFR1	4/435	21/10856	0.008846851	0.032595207	0.021440348	NRAS/HRAS/KRAS/FGFR1	4
CSC	R-HSA-199977	ER to Golgi Anterograde Transport	13/435	154/10856	0.008912351	0.032727804	0.021527567	ARF4/COPB2/CAP2B/TMED10/COPB1/RAB1A/DYNLL1/ARF5/DYNC1H1/DYNLL2/RAB1B/COPG2/COPG1	13
CSC	R-HSA-163359	Glucagon signaling in metabolic regulation	5/435	33/10856	0.009481455	0.03447519	0.022676956	PRKAR1A/GNB1/GNB2/GNAS/GNB4	5
CSC	R-HSA-389356	CD28 co-stimulation	5/435	33/10856	0.009481455	0.03447519	0.022676956	LCK/FYN/YES1/LYN/RAC1	5
CSC	R-HSA-418990	Adherens junctions interactions	5/435	33/10856	0.009481455	0.03447519	0.022676956	CTNND1/JUP/CTNNA1/CTNNB1/CDH12	5
CSC	R-HSA-8854214	TBC/RABGAPs	6/435	46/10856	0.009630534	0.034902816	0.022958238	RABSA/RABSC/RABBA/RABSB/RAB35/RABBB	6
CSC	R-HSA-6811558	PIP, PP2A and IER3 Regulate PI3K/AKT Signaling	10/435	106/10856	0.009919913	0.035834474	0.023571061	EGFR/LCK/FYN/FGFR1/RAC1/FGFR2/FGFR4/FGFR3/PPP2R1B/RAC1	10
CSC	R-HSA-2995410	Nuclear Envelope (NE) Reassembly	8/435	75/10856	0.010037497	0.036141506	0.023773019	BANF1/NUP155/LMNA/CDK1/CCNB1/RCC1/LMNB1/NUP107	8
CSC	R-HSA-1250196	SHC1 events in ERBB2 signaling	4/435	22/10856	0.010477282	0.036886684	0.024263179	EGFR/NRAS/HRAS/KRAS	4
CSC	R-HSA-5654712	FRS-mediated FGFR4 signaling	4/435	22/10856	0.010477282	0.036886684	0.024263179	NRAS/HRAS/KRAS/FGFR4	4
CSC	R-HSA-5655332	Signaling by FGFR3 in disease	4/435	22/10856	0.010477282	0.036886684	0.024263179	NRAS/HRAS/KRAS/FGFR3	4
CSC	R-HSA-71403	Citric acid cycle (TCA cycle)	4/435	22/10856	0.010477282	0.036886684	0.024263179	IDH3B/CS/FH/DLST	4
CSC	R-HSA-8853338	Signaling by FGFR3 point mutants in cancer	4/435	22/10856	0.010477282	0.036886684	0.024263179	NRAS/HRAS/KRAS/FGFR3	4
CSC	R-HSA-912631	Regulation of signaling by CBL	4/435	22/10856	0.010477282	0.036886684	0.024263179	FYN/YES1/LYN/HCK	4
CSC	R-HSA-9665686	Signaling by ERBB2 TMD/JMD mutants	4/435	22/10856	0.010477282	0.036886684	0.024263179	EGFR/NRAS/HRAS/KRAS	4
CSC	R-HSA-446728	Cell junction organization	9/435	91/10856	0.010517359	0.036910606	0.024278914	CTNND1/JUP/ITGA6/CTNNA1/CTNNB1/CDH12/PLEC/PARVB/COL17A1	9
CSC	R-HSA-446203	Asparagine N-linked glycosylation	21/435	304/10856	0.010713224	0.037062144	0.024378592	RPN1/RPN2/PRKCSH/ARF4/CANX/COPB2/DDOST/CAP2B/TMED10/COPB1/RAB1A/DYNLL1/ARF5/UBXN1/GFPT1/M	21
CSC	R-HSA-389359	CD28 dependent Vav1 pathway	3/435	12/10856	0.010727636	0.037062144	0.024378592	LCK/FYN/RAC1	3
CSC	R-HSA-8963693	Aspartate and asparagine metabolism	3/435	12/10856	0.010727636	0.037062144	0.024378592	SLC25A12/ASNS/SLC25A13	3
CSC	R-HSA-9673767	Signaling by PDGFRA transmembrane, juxtamembrane and kinase domain mutants	3/435	12/10856	0.010727636	0.037062144	0.024378592	NRAS/HRAS/KRAS	3
CSC	R-HSA-9673770	Signaling by PDGFRA extracellular domain mutants	3/435	12/10856	0.010727636	0.037062144	0.024378592	NRAS/HRAS/KRAS	3
CSC	R-HSA-446652	Interleukin-1 family signaling	12/435	141/10856	0.01103491	0.038005327	0.024998996	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/UBE2V1/PSMD1/PSMD13	12
CSC	R-HSA-194138	Signaling by VEGF	10/435	108/10856	0.011241223	0.038596026	0.025387543	CTNND1/NRAS/HRAS/KRAS/FYN/JUP/CTNNA1/CTNNB1/RAC1/CAV1	10
CSC	R-HSA-162582	Signal Transduction	123/435	2558/10856	0.011607125	0.039635235	0.02607111	GNAT3/PSMD12/XPO1/ATP2A1/ARPC1B/ARPC3/PSMD3/CTNND1/CER1/EGFR/NRAS/HRAS/KRAS/TFRC/GNAI2/LCK,	123
CSC	R-HSA-4086398	Ca2+ pathway	7/435	62/10856	0.011615375	0.039635235	0.02607111	KRAS/GNAO1/GNAT2/CTNNB1/GNB1/GNB2/GNB4	7
CSC	R-HSA-114604	GPVI-mediated activation cascade	5/435	35/10856	0.012150066	0.041302003	0.02716747	LCK/FYN/LYN/RAC2/RAC1	5
CSC	R-HSA-5654693	FRS-mediated FGFR1 signaling	4/435	23/10856	0.012290046	0.041302003	0.02716747	NRAS/HRAS/KRAS/FGFR1	4
CSC	R-HSA-5654699	SHC-mediated cascade:FGFR2	4/435	23/10856	0.012290046	0.041302003	0.02716747	NRAS/HRAS/KRAS/FGFR2	4
CSC	R-HSA-8949215	Mitochondrial calcium ion transport	4/435	23/10856	0.012290046	0.041302003	0.02716747	VDAC2/PHB2/STOML2/VDAC3	4
CSC	R-HSA-9013418	RHOBTB2 GTPase cycle	4/435	23/10856	0.012290046	0.041302003	0.02716747	TRA2B/DBN1/CCT7/TMOD3	4
CSC	R-HSA-201681	TCF dependent signaling in response to WNT	17/435	233/10856	0.012532754	0.041990404	0.027620284	PSMD12/XPO1/PSMD3/PSMC3/PPP2R1B/CTNNB1/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/CSNK2B/CSNK2A1/CA	17
CSC	R-HSA-171007	p38MAPK events	3/435	13/10856	0.013537223	0.045219219	0.029744121	NRAS/HRAS/KRAS	3
CSC	R-HSA-163560	Triglyceride catabolism	4/435	24/10856	0.014291784	0.047327885	0.031131151	FABP1/PPP1CC/PPP1CB/CAV1	4
CSC	R-HSA-428930	Thromboxane signalling through TP receptor	4/435	24/10856	0.014291784	0.047327885	0.031131151	GNB1/GNB2/GNA13/GNB4	4
CSC	R-HSA-1227986	Signaling by ERBB2	6/435	50/10856	0.014296521	0.047327885	0.031131151	EGFR/NRAS/HRAS/KRAS/FYN/YES1	6
CSC	R-HSA-1500931	Cell-Cell communication	11/435	129/10856	0.014423067	0.047604707	0.031313238	CTNND1/FYN/JUP/ITGA6/CTNNA1/CTNNB1/IQGAP1/CDH12/PLEC/PARVB/COL17A1	11
CSC	R-HSA-373755	Semaphorin interactions	7/435	65/10856	0.014851593	0.048873641	0.032147912	FYN/RRAS/MYL9/RAC1/CDK5/CRMP1/DPYSL2	7
CSC	R-HSA-9679506	SARS-CoV Infections	12/435	147/10856	0.015001338	0.049220366	0.03237598	RPN1/RPN2/PRKCSH/DDX5/CANX/DDOST/ATP1B3/FKBP14/RBBP4/ATP1A4/PTGES3/RBBP7	12
CSC	R-HSA-199418	Negative regulation of the PI3K/AKT network	10/435	113/10856	0.015126038	0.049483117	0.032548811	EGFR/LCK/FYN/FGFR1/RAC2/FGFR2/FGFR4/FGFR3/PPP2R1B/RAC1	10
CSC	R-HSA-8939236	RUNX1 regulates transcription of genes involved in differentiation of HSCs	11/435	130/10856	0.015210124	0.049611847	0.032633487	PSMD12/PSMD3/PSMC3/PSMC4/PSMD8/PSMD7/PSME3/PSMC5/PSMD2/PSMD1/PSMD13	11
NSCC	R-HSA-2022090	Assembly of collagen fibrils and other multimeric structures	6/67	61/10856	1.8715SE-06	0.000303956	0.000285241	CTSL/MMP3/COL15A1/LAMC2/PCOLCE/LAMA3	6
NSCC	R-HSA-1474244	Extracellular matrix organization	11/67	301/10856	1.99918E-06	0.000303956	0.000285241	CTSL/MMP3/CDH1/CD44/COL15A1/MMP12/LAMC2/DAG1/PCOLCE/LAMA3/LTBP4	11
NSCC	R-HSA-1474228	Degradation of the extracellular matrix	8/67	140/10856	2.15063E-06	0.000303956	0.000285241	CTSL/MMP3/CDH1/CD44/COL15A1/MMP12/LAMC2/LAMA3	8
NSCC	R-HSA-1474290	Collagen formation	6/67	90/10856	1.82471E-05	0.001934194	0.001815108	CTSL/MMP3/COL15A1/LAMC2/PCOLCE/LAMA3	6
NSCC	R-HSA-2168880	Scavenging of heme from plasma	3/67	13/10856	6.14862E-05	0.005214031	0.004893008	HP/HPR/HPX	3
NSCC	R-HSA-1442490	Collagen degradation	4/67	64/10856	0.000637444	0.045046073	0.042272631	CTSL/MMP3/COL15A1/MMP12	4
NSCC	R-HSA-8874081	MET activates PTK2 signaling	3/67	30/10856	0.00080974	0.049047121	0.046027338	MET/LAMC2/LAMA3	3