

PI3K-AKT SIGNALING PATHWAY

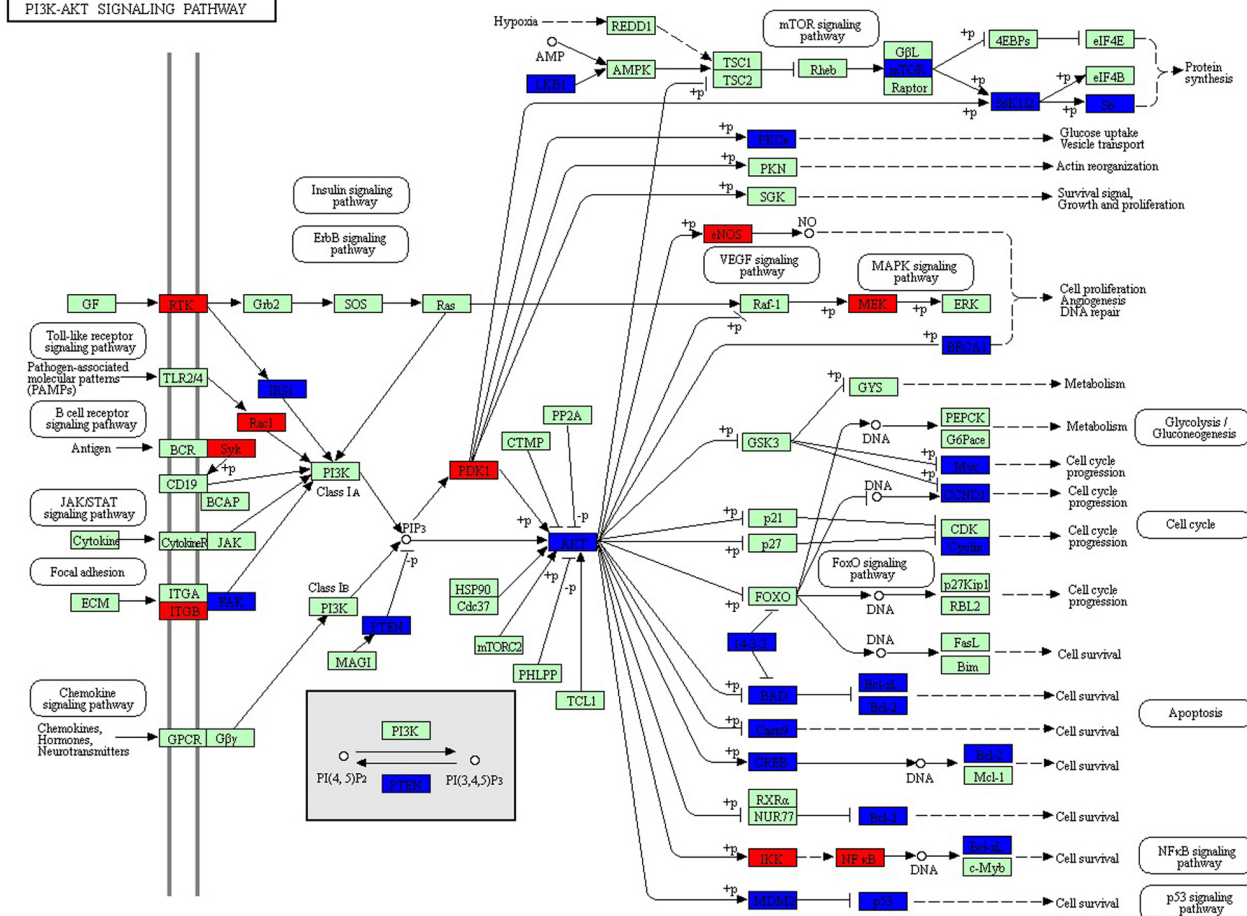


Figure S2. 'Pathways in cancer' is the second most enriched Kyoto Encyclopedia of Genes and Genomes pathway in VEN vs. CON group. Red represents the proteins with upregulated phosphorylation levels in the VEN group. Blue represents the proteins with downregulated phosphorylation levels in the VEN group. Green represents unaltered protein phosphorylation levels in the VEN group. CON, control; VEN, mechanically ventilated.

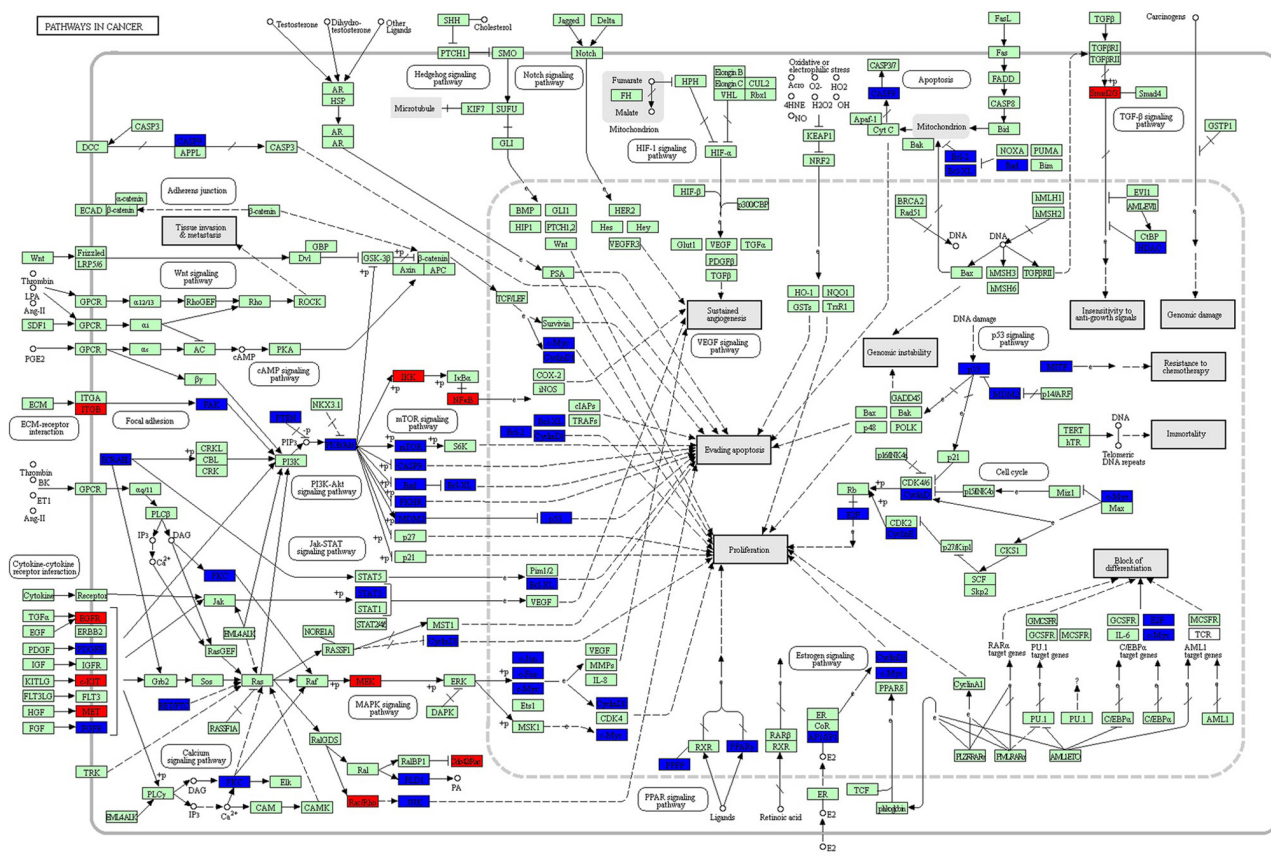


Figure S3. ‘Hepatitis B’ is the third most enriched Kyoto Encyclopedia of Genes and Genomes pathway in VEN vs. CON group. Red represents the proteins with upregulated phosphorylation levels in the VEN group. Blue represents the proteins with downregulated phosphorylation levels in the VEN group. Green represents unaltered protein phosphorylation levels in the VEN group. CON, control; VEN, mechanically ventilated.

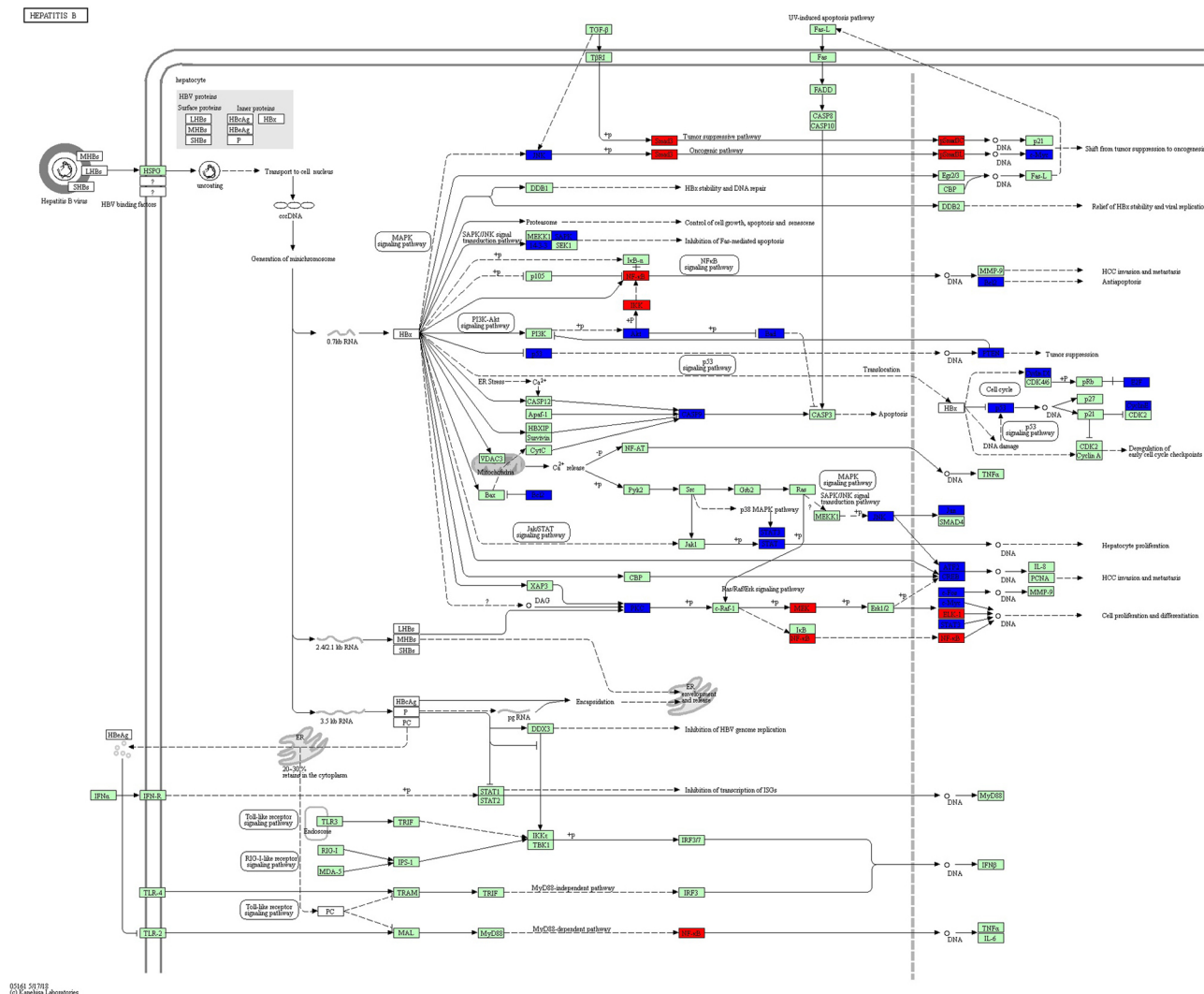


Figure S4. 'Prostate cancer' is the fourth most enriched Kyoto Encyclopedia of Genes and Genomes pathway in VEN vs. CON group. Red represents the proteins with upregulated phosphorylation levels in the VEN group. Blue represents the proteins with downregulated phosphorylation levels in the VEN group. Green represents unaltered protein phosphorylation levels in the VEN group. CON, control; VEN, mechanically ventilated.

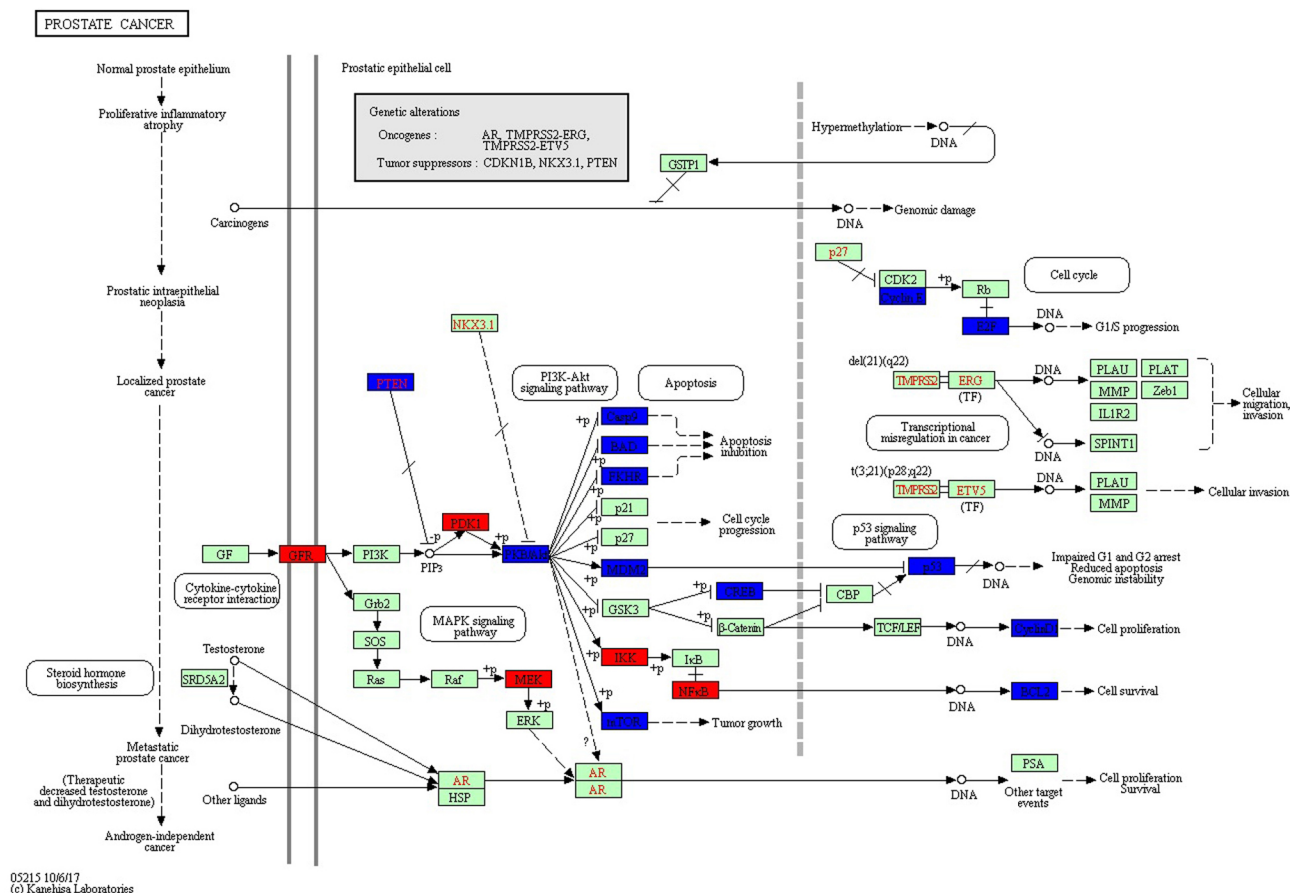


Figure S5. 'Focal adhesion' is the fifth most enriched Kyoto Encyclopedia of Genes and Genomes pathway in VEN vs. CON group. Red represents the proteins with upregulated phosphorylation levels in the VEN group. Blue represents the proteins with downregulated phosphorylation levels in the VEN group. Green represents unaltered protein phosphorylation levels in the VEN group. CON, control; VEN, mechanically ventilated.

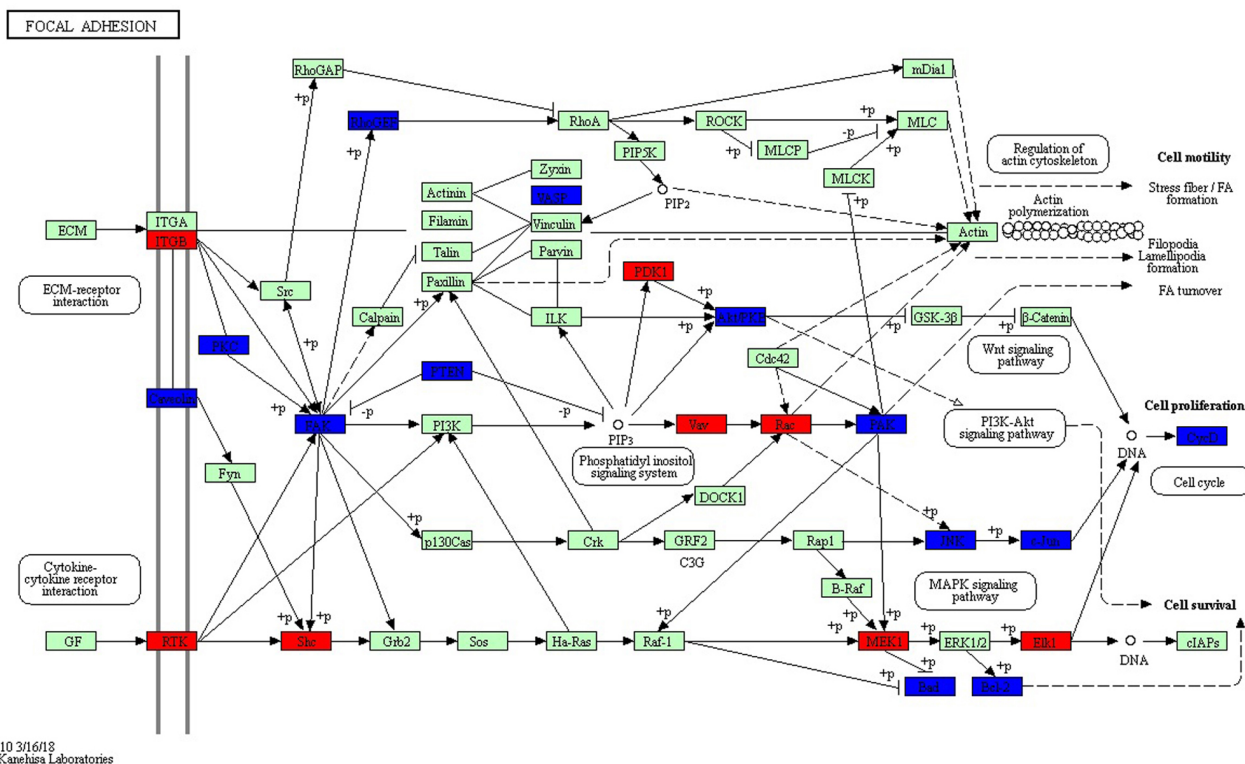


Table SI. Differentially phosphorylated protein UniProt IDs and fold changes between CON and VEN groups.

ID	Fold change	Log2 fold change
Q05513	2.998925702	1.58444578
Q13085	2.842539655	1.507180476
O15111	2.784558526	1.477448616
P43405	2.659710624	1.411269289
P10721	2.654814161	1.408610875
O15530	2.465149656	1.301675233
P15498	2.202811256	1.139345886
P11831	2.15522679	1.107839689
O75582	2.11104451	1.077956997
P63104	2.106859267	1.075093949
Q05469	2.067486744	1.047878079
P19419	2.037626587	1.026889689
Q05655	1.914921194	0.937285021
Q8IVT5	1.840850674	0.880372603
Q02750	1.820590574	0.864406516
P84022	1.811758692	0.857390816
P35968	1.784211388	0.835286552
P46734	1.770651427	0.824280229
P63000	1.766028144	0.820508334
Q15418	1.761512607	0.8168148
P05556	1.723158657	0.785055541
Q14012	1.690304742	0.757283371
Q04206	1.665008526	0.735529565
P06493	1.65837413	0.729769516
P29353	1.650309898	0.722736962
O14964	1.646496902	0.719399797
Q14683	1.609832181	0.686910301
P06127	1.597067981	0.675425724
P13639	1.594920975	0.673484943
P20963	1.593844683	0.672511048
Q04864	1.581180761	0.661002306
P29474	1.539286601	0.622261873
P56524	1.532692173	0.616067974
P00533	1.528264394	0.611894155
P30304	1.513537033	0.597923975
P15311	1.506311183	0.591019842
P08581	1.502353393	0.587224213
P45983	0.669584479	-0.578662008
P42345	0.658758794	-0.602177779
P05412	0.654304535	-0.611965825
P49840	0.653883568	-0.612894326
Q92934	0.653825884	-0.613021602
P23443	0.651043868	-0.619173338
O75030	0.649199215	-0.623266839
P17677	0.646579956	-0.62909931
P54762	0.643881705	-0.635132436
P35240	0.642363384	-0.638538436
P62753	0.639057883	-0.645981485
P43403	0.63855237	-0.647123149
Q13177	0.638441545	-0.64737356
Q06124	0.634709385	-0.65583192
Q13393	0.634517333	-0.65626852
P35568	0.633931127	-0.657601987
Q04637	0.631727685	-0.662625296
Q13972	0.630156023	-0.666219019

Table SI. Continued.

ID	Fold change	Log2 fold change
Q00987	0.628979528	-0.668915034
P16284	0.620320242	-0.688914892
O60825	0.618457881	-0.693252749
P00519	0.616987668	-0.696686441
P40763	0.616835664	-0.697041914
P01106	0.61527599	-0.7006944
P42575	0.614689551	-0.702070134
P10636	0.61428451	-0.703021091
P04637	0.61363911	-0.70453766
P10415	0.613602346	-0.704624096
P15336	0.610718188	-0.711421284
P27348	0.609161989	-0.715102173
P29966	0.603188634	-0.729318851
Q13094	0.600931669	-0.734727141
P31749	0.595660884	-0.747436872
P07949	0.592863276	-0.754228661
P05783	0.588831159	-0.764074079
O95471	0.58710524	-0.768308962
P09619	0.584270295	-0.775292152
P78552	0.583548346	-0.777075909
P11362	0.578481153	-0.789658138
P15941	0.576543511	-0.794498605
Q8WXE1	0.575896544	-0.796118431
Q9BY41	0.574090319	-0.800650368
P03372	0.573065961	-0.803226889
P02545	0.569157062	-0.813101268
Q01094	0.564909735	-0.823907732
P60484	0.5623979	-0.830336888
Q12778	0.55702078	-0.844196946
Q01201	0.550602934	-0.860915797
Q15831	0.540742099	-0.886987414
Q99683	0.539578168	-0.890096119
P24864	0.538703592	-0.89243641
Q13480	0.517867973	-0.949343756
P05106	0.507020552	-0.979883867
P24385	0.498667518	-1.003849863
P49137	0.495189515	-1.013947327
P19525	0.495061927	-1.014319093
O96017	0.489612903	-1.030286516
Q03135	0.4886801	-1.033037738
Q07817	0.486462352	-1.039599938
P18848	0.470375894	-1.088113969
O14757	0.470054732	-1.089099345
P55211	0.457456564	-1.12829333
P15976	0.447102225	-1.161323369
P37231	0.438930828	-1.187934494
Q05397	0.437286688	-1.193348665
P42261	0.434255489	-1.20338401
P01100	0.432335398	-1.209777131
Q02078	0.428194655	-1.223661308
P38398	0.420959409	-1.248246967
P14635	0.411376804	-1.281467647
O75914	0.400884851	-1.318740194
P17252	0.39749765	-1.330981764
O15551	0.397317266	-1.331636606
P50552	0.397039547	-1.332645381

Table SI. Continued.

ID	Fold change	Log2 fold change
Q13547	0.363405265	-1.460348773
P16104	0.330108594	-1.598987397
P17302	0.253190861	-1.981702764
P42262	0.207853852	-2.26635861

Table SII. Pathway summary of proteins differentially expressed in the VEN group compared with the CON group.

KEGG pathway name	Pathway ID	P-value	Gene lfold change	Count
PI3K-Akt signaling pathway	hsa04151	6.72E-23	CHUK12.784558526;SYK12.659710624;KIT12.654814161;PDK112.465149656;YWHAZ12.106859267;MAP2K111.820590574;KDR11.784211388;RAC111.766028144;ITGB111.723158657;RELA11.665008526;NOS311.539286601;EGFR11.528264394;MET11.502353393;MTOR10.658758794;BAD10.653825884;RPS6KB110.651043868;RPS610.639057883;IRS110.633931127;MDM210.628979528;MYC10.61527599;TP5310.61363911;BCL210.613602346;ATF210.610718188;YWHAQ10.609161989;AKT110.595660884;PDGFRB10.584270295;FGFR110.578481153;PTEN10.5623979;STK1110.540742099;CCNE110.538703592;ITGB310.507020552;CCND110.498667518;BCL2L110.486462352;ATF410.470375894;CASP910.457456564;PTK210.437286688;BRCA10.420959409;PRKCA10.39749765	38
Pathways in cancer	hsa05200	1.36E-19	CHUK12.784558526;KIT12.654814161;MAP2K111.820590574;SMAD311.811758692;RAC111.766028144;ITGB111.723158657;RELA11.665008526;EGFR11.528264394;MET11.502353393;MAPK810.669584479;MTOR10.658758794;JUN10.654304535;BAD10.653825884;MITF10.649199215;PLD110.634517333;MDM210.628979528;ABL110.616987668;STAT310.616835664;MYC10.61527599;TP5310.61363911;BCL210.613602346;AKT110.595660884;RET10.592863276;PDGFRB10.584270295;FGFR110.578481153;E2F110.564909735;PTEN10.5623979;FOXO110.55702078;CCNE110.538703592;CCND110.498667518;BCL2L110.486462352;CASP910.457456564;PPARG10.438930828;PTK210.437286688;FOS10.432335398;PRKCA10.39749765;HDAC110.363405265	37
Hepatitis B	hsa05161	2.07E-18	CHUK12.784558526;YWHAZ12.106859267;ELK112.037626587;MAP2K111.820590574;SMAD311.811758692;RELA11.665008526;MAPK810.669584479;JUN10.654304535;BAD10.653825884;STAT310.616835664;MYC10.61527599;TP5310.61363911;BCL210.613602346;ATF210.610718188;YWHAQ10.609161989;AKT110.595660884;E2F110.564909735;PTEN10.5623979;CCNE110.538703592;CCND110.498667518;ATF410.470375894;CASP910.457456564;FOS10.432335398;PRKCA10.39749765	24
Prostate cancer	hsa05215	2.89E-18	CHUK12.784558526;PDPK112.465149656;MAP2K111.820590574;RELA11.665008526;EGFR11.528264394;MTOR10.658758794;BAD10.653825884;MDM210.628979528;TP5310.61363911;BCL210.613602346;AKT110.595660884;PDGFRB10.584270295;FGFR110.578481153;E2F110.564909735;PTEN10.5623979;FOXO110.55702078;CCNE110.538703592;CCND110.498667518;ATF410.470375894;CASP910.457456564;MAP2K111.820590574;KDR11.784211388;RAC111.766028144;ITGB111.723158657;SHC111.650309898;EGFR11.528264394;MET11.502353393;MAPK810.669584479;JUN10.654304535;BAD10.653825884;PAK210.638441545;RASGRF110.630156023;BCL210.613602346;AKT110.595660884;PDGFRB10.584270295;PTEN10.5623979;ITGB310.507020552;CCND110.498667518;CAV110.48866801;PTK210.437286688;PAK310.400884851;PRKCA10.39749765;VASP10.397039547	20
Focal adhesion	hsa04510	4.07E-17	PDPK112.465149656;VAV112.202811256;ELK112.037626587;MAP2K111.820590574;KDR11.784211388;RAC111.766028144;ITGB111.723158657;SHC111.650309898;EGFR11.528264394;MET11.502353393;MAPK810.669584479;JUN10.654304535;BAD10.653825884;PAK210.638441545;RASGRF110.630156023;BCL210.613602346;AKT110.595660884;PDGFRB10.584270295;PTEN10.5623979;ITGB310.507020552;CCND110.498667518;CAV110.48866801;PTK210.437286688;PAK310.400884851;PRKCA10.39749765;VASP10.397039547	26
Proteoglycans in cancer	hsa05205	5.21E-17	PDPK112.465149656;ELK112.037626587;MAP2K111.820590574;KDR11.784211388;RAC111.766028144;ITGB111.723158657;EGFR11.528264394;EZR11.506311183;MET11.502353393;MTOR10.658758794;RPS6KB110.651043868;RPS610.639057883;PTPN1110.634709385;MDM210.628979528;STAT310.616835664;MYC10.61527599;TP5310.61363911;AKT110.595660884;FGFR110.578481153;ESR110.573065961;GAB110.517867973;ITGB310.507020552;CCND110.498667518;CAV110.48866801;PTK210.437286688;PRKCA10.39749765	26

Table SII. Continued.

KEGG pathway name	Pathway ID	P-value	Gene lfold change	Count
Ras signaling pathway	hsa04014	7.07E-17	CHUK12.784558526;KIT12.654814161;ELK112.037626587;KSR111.840850674;MAP2K111.820590574;KDR11.784211388;RAC111.766028144;RELA11.665008526;SHC111.650309898;REL11.581180761;EGFR11.528264394;MET11.502353393;MAPK810.669584479;BAD10.653825884;ZAP7010.63855237;PAK210.638441545;PTPN110.634709385;PLD110.634517333;RASGRF110.630156023;ABL10.616987668;AKT110.595660884;PDGFRB10.584270295;FGFR110.578481153;GAB110.517867973;BCL2L110.486462352;PAK310.400884851;PRKCA10.39749765	27
Neurotrophin signaling pathway	hsa04722	9.26E-17	PDPK112.465149656;RPS6KA512.11104451;PRKCD11.914921194;MAP2K111.820590574;RAC111.766028144;RPS6KA111.761512607;RELA11.665008526;SHC111.650309898;MAPK810.669584479;JUN10.654304535;BAD10.653825884;PTPN110.634709385;IRS110.633931127;ABL10.616987668;TP5310.61363911;BCL210.613602346;AKT110.595660884;MAP3K510.539578168;GAB110.517867973;MAPKAPK210.495189515;ATF410.470375894	21
MAPK signaling pathway	hsa04010	1.25E-15	CHUK12.784558526;SRF12.15522679;RPS6KA512.11104451;ELK112.037626587;MAP2K111.820590574;MAP2K311.770651427;RAC111.766028144;RPS6KA111.761512607;RELA11.665008526;EGFR11.528264394;MAPK810.669584479;JUN10.654304535;PAK210.638441545;RASGRF110.630156023;MYC10.61527599;MAPT10.61428451;TP5310.61363911;ATF210.610718188;AKT110.595660884;PDGFRB10.584270295;FGFR110.578481153;RELB10.550602934;MAP3K510.539578168;MAPKAPK210.495189515;ATF410.470375894;FOS10.432335398;PRKCA10.39749765	27
Pancreatic cancer	hsa05212	2.40E-15	CHUK12.784558526;MAP2K111.820590574;SMAD311.811758692;RAC111.766028144;RELA11.665008526;EGFR11.528264394;MAPK810.669584479;BAD10.653825884;PLD110.634517333;STAT310.616835664;TP5310.61363911;AKT110.595660884;E2F110.564909735;CCND110.498667518;BCL2L110.486462352;CASP910.457456564	16
Chronic myeloid leukemia	hsa05220	1.35E-14	CHUK12.784558526;MAP2K111.820590574;SMAD311.811758692;RELA11.665008526;SHC111.650309898;BAD10.653825884;PTPN110.634709385;MDM210.628979528;ABL110.616987668;MYC10.61527599;TP5310.61363911;AKT110.595660884;E2F110.564909735;CCND110.498667518;BCL2L110.486462352;HDAC110.363405265	16
ErbB signaling pathway	hsa04012	1.79E-14	ELK112.037626587;MAP2K111.820590574;SHC111.650309898;EGFR11.528264394;MAPK810.669584479;MTOR10.658758794;JUN10.654304535;BAD10.653825884;RPS6KB110.651043868;PAK210.638441545;ABL110.616987668;MYC10.61527599;AKT110.595660884;GAB110.517867973;PTK210.437286688;PAK310.400884851;PRKCA10.39749765	17
Viral carcinogenesis	hsa05203	6.34E-14	SYK12.659710624;SRF12.15522679;YWHAZ12.106859267;RAC111.766028144;RELA11.665008526;CDK111.65837413;REL11.581180761;HDAC411.532692173;JUN10.654304535;BAD10.653825884;MDM210.628979528;STAT310.616835664;TP5310.61363911;ATF210.610718188;YWHAQ10.609161989;HDAC810.574090319;CCNE110.538703592;CCND110.498667518;MAPKAPK210.495189515;EIF2AK210.495061927;ATF410.470375894;CHEK110.470054732;HDAC110.363405265	23
MicroRNAs in cancer	hsa05206	4.43E-13	RPS6KA512.11104451;MAP2K111.820590574;SHC111.650309898;HDAC411.532692173;EGFR11.528264394;CDC25A11.513537033;EZR11.506311183;MET11.502353393;MTOR10.658758794;IRS110.633931127;MDM210.628979528;ABL110.616987668;STAT310.616835664;MYC10.61527599;TP5310.61363911;BCL210.613602346;MARCKS10.603188634;PDGFRB10.584270295;E2F110.564909735;PTEN10.5623979;CCNE110.538703592;ITGB310.507020552;CCND110.498667518;BRCA110.420959409;PRKCA10.39749765;HDAC110.363405265	26

Table SII. Continued.

KEGG pathway name	Pathway ID	P-value	Gene lfold change	Count
Cell cycle	hsa04110	6.34E-12	YWHAZ12.106859267;SMAD311.811758692;CDK111.65837413;SMC1A11.609832181;CDC25A11.513537033;MDM210.628979528;ABL110.616987668;MYC10.61527599;TP5310.61363911;YWHAQ10.609161989;E2F110.564909735;CCNE110.538703592;CCND110.498667518;CHEK210.489612903;CHEK110.470054732;CCNB110.411376804;HDAC110.363405265	17
Colorectal cancer	hsa05210	8.66E-12	MAP2K111.820590574;SMAD311.811758692;RAC111.766028144;MAPK810.669584479;JUN10.654304535;BAD10.653825884;MYC10.61527599;TP5310.61363911;BCL210.613602346;AKT110.595660884;CCND110.498667518;CASP910.457456564;FOS10.432335398	13
Thyroid hormone signaling pathway	hsa04919	3.32E-11	PDPK112.465149656;MAP2K111.820590574;MTOR10.658758794;BAD10.653825884;MDM210.628979528;PFKFB210.618457881;MYC10.61527599;TP5310.61363911;AKT110.595660884;ESR110.573065961;FOXO110.55702078;ITGB310.507020552;CCND110.498667518;CASP910.457456564;PRKCA10.39749765;HDAC110.363405265	16
Epstein-Barr virus infection	hsa05169	4.14E-11	CHUK12.784558526;SYK12.659710624;YWHAZ12.106859267;MAP2K311.770651427;RELA11.665008526;CDK111.65837413;HDAC411.532692173;MAPK810.669584479;JUN10.654304535;MDM210.628979528;STAT310.616835664;MYC10.61527599;TP5310.61363911;BCL210.613602346;ATF210.610718188;YWHAQ10.609161989;AKT110.595660884;RELB10.550602934;EIF2AK210.495061927;HDAC110.363405265	20
Apoptosis	hsa04210	4.65E-11	CHUK12.784558526;PDPK112.465149656;MAP2K111.820590574;RELA11.665008526;MAPK810.669584479;JUN10.654304535;BAD10.653825884;CASP210.614689551;TP5310.61363911;BCL210.613602346;AKT110.595660884;LMNA10.569157062;MAP3K510.539578168;BCL2L110.486462352;ATF410.470375894;CASP910.457456564;FOS10.432335398	17
Small cell lung cancer	hsa05222	4.93E-11	CHUK12.784558526;ITGB111.723158657;RELA11.665008526;MYC10.61527599;TP5310.61363911;BCL210.613602346;AKT110.595660884;E2F110.564909735;PTEN10.5623979;CCNE110.538703592;CCND110.498667518;BCL2L110.486462352;CASP910.457456564;PTK210.437286688	14
Melanoma	hsa05218	5.38E-11	MAP2K111.820590574;EGFR11.528264394;MET11.502353393;BAD10.653825884;MITF10.649199215;MDM210.628979528;TP5310.61363911;AKT110.595660884;PDGFRB10.584270295;FGFR110.578481153;E2F110.564909735;PTEN10.5623979;CCND110.498667518	13
Insulin resistance	hsa04931	1.16E-10	PRKCZ12.998925702;PDPK112.465149656;PRKCD11.914921194;RPS6KA111.761512607;RELA11.665008526;NOS311.539286601;MAPK810.669584479;MTOR10.658758794;RPS6KB110.651043868;PTPN1110.634709385;IRS110.633931127;STAT310.616835664;AKT110.595660884;PTEN10.5623979;FOXO110.55702078	15
Glioma	hsa05214	2.80E-10	MAP2K111.820590574;SHC111.650309898;EGFR11.528264394;MTOR10.658758794;MDM210.628979528;TP5310.61363911;AKT110.595660884;PDGFRB10.584270295;E2F110.564909735;PTEN10.5623979;CCND110.498667518;PRKCA10.39749765	12
Endometrial cancer	hsa05213	3.43E-10	PDPK112.465149656;ELK112.037626587;MAP2K111.820590574;EGFR11.528264394;BAD10.653825884;MYC10.61527599;TP5310.61363911;AKT110.595660884;PTEN10.5623979;CCND110.498667518;CASP910.457456564	11
Central carbon metabolism in cancer	hsa05230	4.06E-10	KIT12.654814161;MAP2K111.820590574;EGFR11.528264394;MET11.502353393;MTOR10.658758794;MYC10.61527599;TP5310.61363911;AKT110.595660884;RET10.592863276;PDGFRB10.584270295;FGFR110.578481153;PTEN10.5623979	12

Table SII. Continued.

KEGG pathway name	Pathway ID	P-value	Gene lfold change	Count
AGE-RAGE signaling pathway in diabetic complications	hsa04933	4.58E-10	PRKCZ12.998925702;PRKCD11.914921194;SMAD311.811758692;RAC111.766028144;REL11.665008526; NOS311.539286601;MAPK810.669584479;JUN10.654304535;STAT310.616835664;BCL210.613602346; AKT110.595660884;FOXO110.55702078;CCND110.498667518;PRKCA10.39749765	14
Acute myeloid leukemia	hsa05221	9.80E-10	CHUK12.784558526;KIT112.654814161;MAP2K111.820590574;REL11.665008526;MTOR10.658758794; BAD10.653825884;RPS6KB110.651043868;STAT310.616835664;MYC10.61527599;AKT110.595660884; CCND110.498667518	11
FoxO signaling pathway	hsa04068	2.25E-09	CHUK12.784558526;PDPK112.465149656;MAP2K111.820590574;SMAD311.811758692;EGFR11.528264394; MAPK810.669584479;IRS110.633931127;MDM210.628979528;STAT310.616835664;AKT110.595660884; PTEN10.5623979;FOXO110.55702078;STK1110.540742099;CCND110.498667518;CCNB110.411376804	15
HTLV-I infection	hsa05166	2.99E-09	CHUK12.784558526;SRF12.15522679;ELK112.037626587;SMAD311.811758692;REL11.665008526; MAPK810.669584479;JUN10.654304535;MYC10.61527599;TP5310.61363911;ATF210.610718188; AKT110.595660884;PDGFRB10.584270295;E2F110.564909735;RELB10.550602934;CCND110.498667518; CHEK210.489612903;BCL2L110.486462352;ATF410.470375894;CHEK110.470054732;FOS10.432335398	20
Insulin signaling pathway	hsa04910	3.76E-09	PRKCZ12.998925702;ACACA12.842539655;PDPK112.465149656;L1PE12.067486744;ELK112.037626587; MAP2K111.820590574;SHC111.650309898;MAPK810.669584479;MTOR10.658758794;BAD10.653825884; RPS6KB110.651043868;RPS610.639057883;IRS110.633931127;AKT110.595660884;FOXO110.55702078	15
Amyotrophic lateral sclerosis (ALS)	hsa05014	5.01E-09	MAP2K311.770651427;RAC111.766028144;BAD10.653825884;TP5310.61363911;BCL210.613602346; MAP3K510.539578168;BCL2L110.486462352;CASP910.457456564;GRIA110.43255489;GRIA210.207853852	10
Choline metabolism in cancer	hsa05231	5.09E-09	PDPK112.465149656;MAP2K111.820590574;RAC111.766028144;EGFR11.528264394;MAPK810.669584479; MTOR10.658758794;JUN10.654304535;RPS6KB110.651043868;PLD110.634517333;AKT110.595660884; PDGFRB10.584270295;FOS10.432335398;PRKCA10.39749765	13
Sphingolipid signaling pathway	hsa04071	5.19E-09	PRKCZ12.998925702;PDPK112.465149656;MAP2K111.820590574;RAC111.766028144;REL11.665008526; NOS311.539286601;MAPK810.669584479;PLD110.634517333;TP5310.61363911;BCL210.613602346; AKT110.595660884;PTEN10.5623979;MAP3K510.539578168;PRKCA10.39749765	14
T cell receptor signaling pathway	hsa04660	8.26E-09	CHUK12.784558526;PDPK112.465149656;VAV112.202811256;MAP2K111.820590574;REL11.665008526; CD24711.593844683;JUN10.654304535;ZAP7010.63855237;PAK210.638441545;LCP210.600931669; AKT110.595660884;FOS10.432335398;PAK310.400884851	13
Non-small cell lung cancer	hsa05223	1.31E-08	PDPK112.465149656;MAP2K111.820590574;EGFR11.528264394;BAD10.653825884;TP5310.61363911; AKT110.595660884;E2F110.564909735;CCND110.498667518;CASP910.457456564;PRKCA10.39749765	10
Osteoclast differentiation	hsa04380	1.62E-08	CHUK12.784558526;SYK12.659710624;MAP2K111.820590574;RAC111.766028144;REL11.665008526; MAPK810.669584479;JUN10.654304535;MITF10.649199215;LCP210.600931669;AKT110.595660884; RELB10.550602934;ITGB310.507020552;PPARG10.438930828;FOS10.432335398	14
mTOR signaling pathway	hsa04150	2.62E-08	PDPK112.465149656;RPS6KA111.761512607;MTOR10.658758794;RPS6KB110.651043868;RPS610.639057883; IRS110.633931127;AKT110.595660884;PTEN10.5623979;STK1110.540742099;PRKCA10.39749765	10
VEGF signaling pathway	hsa04370	3.10E-08	MAP2K111.820590574;KDR11.784211388;RAC111.766028144;NOS311.539286601;BAD10.653825884; AKT110.595660884;MAPKAPK210.495189515;CASP910.457456564;PTK210.437286688;PRKCA10.39749765	10

Table SII. Continued.

KEGG pathway name	Pathway ID	P-value	Gene lfold change	Count
AMPK signaling pathway	hsa04152	6.95E-08	ACACA12.842539655;PDPK112.465149656;LIPE12.067486744;EEF211.594920975;MTOR10.658758794;RPS6KB110.651043868;IRS110.633931127;PFKFB210.618457881;AKT110.595660884;FOXO110.55702078;STK1110.540742099;CCND110.498667518;PPARG10.438930828	13
Fc epsilon RI signaling pathway	hsa04664	9.10E-08	SYK12.659710624;PDPK112.465149656;VAV112.202811256;MAP2K111.820590574;MAP2K311.770651427;RAC111.766028144;MAPK810.669584479;LCP210.600931669;AKT110.595660884;PRKCA10.39749765	10
p53 signaling pathway	hsa04115	1.05E-07	CDK111.65837413;MDM210.628979528;TP5310.61363911;PTEN10.5623979;CCNE110.538703592;CCND110.498667518;CHEK210.489612903;CHEK110.470054732;CASP910.457456564;CCNB110.411376804	10
TNF signaling pathway	hsa04668	1.35E-07	CHUK12.784558526;RPS6KA512.11104451;MAP2K111.820590574;MAP2K311.770651427;RELA11.665008526;MAPK810.669584479;JUN10.654304535;ATF210.610718188;AKT110.595660884;MAP3K510.539578168;ATF410.470375894;FOS10.432335398	12
Rap1 signaling pathway	hsa04015	1.74E-07	PRKCZ12.998925702;KIT12.654814161;MAP2K111.820590574;KDR11.784211388;MAP2K311.770651427;RAC111.766028144;ITGB111.723158657;EGFR11.528264394;MET11.502353393;LCP210.600931669;AKT110.595660884;PDGFRB10.584270295;FGFR110.578481153;ITGB310.507020552;PRKCA10.39749765;VASP10.397039547	16
Bladder cancer	hsa05219	1.93E-07	RPS6KA512.11104451;MAP2K111.820590574;EGFR11.528264394;MDM210.628979528;MYC10.615275599;TP5310.61363911;E2F110.564909735;CCND110.498667518	8
Fc gamma R-mediated phagocytosis	hsa04666	2.01E-07	SYK12.659710624;VAV112.202811256;PRKCD11.914921194;MAP2K111.820590574;RAC111.766028144;RPS6KB110.651043868;PLD110.634517333;MARCKS10.603188634;AKT110.595660884;PRKCA10.39749765;VASP10.397039547	11
Longevity regulating pathway	hsa04211	2.25E-07	RELA11.665008526;MTOR10.658758794;RPS6KB110.651043868;IRS110.633931127;TP5310.61363911;ATF210.610718188;AKT110.595660884;FOXO110.55702078;STK1110.540742099;ATF410.470375894;PPARG10.438930828	11
Toxoplasmosis	hsa05145	3.23E-07	CHUK12.784558526;PDPK112.465149656;MAP2K311.770651427;ITGB111.723158657;RELA11.665008526;MAPK810.669584479;BAD10.653825884;STAT310.616835664;BCL210.613602346;AKT110.595660884;BCL2L110.486462352;CASP910.457456564	12
Estrogen signaling pathway	hsa04915	3.84E-07	PRKCD11.914921194;MAP2K111.820590574;SHC111.650309898;NOS311.539286601;EGFR11.528264394;JUN10.654304535;ATF210.610718188;AKT110.595660884;ESR110.573065961;ATF410.470375894;FOS10.432335398	11
HIF-1 signaling pathway	hsa04066	5.76E-07	MAP2K111.820590574;RELA11.665008526;NOS311.539286601;EGFR11.528264394;MTOR10.658758794;RPS6KB110.651043868;RPS610.639057883;STAT310.616835664;BCL210.613602346;AKT110.595660884;PRKCA10.39749765	11
Renal cell carcinoma	hsa05211	9.16E-07	MAP2K111.820590574;RAC111.766028144;MET11.502353393;JUN10.654304535;PAK210.638441545;PTPN1110.634709385;AKT110.595660884;GAB110.517867973;PAK310.400884851	9
Hepatitis C	hsa05160	1.08E-06	CHUK12.784558526;PDPK112.465149656;RELA11.665008526;EGFR11.528264394;MAPK810.669584479;BAD10.653825884;STAT310.616835664;TP5310.61363911;AKT110.595660884;CLDN710.58710524;EIF2AK210.495061927;CLDN310.397317266	12

Table SII. Continued.

KEGG pathway name	Pathway ID	P-value	Gene lfold change	Count
Adipocytokine signaling pathway	hsa04920	1.34E-06	CHUK12.784558526;RELA11.665008526;MAPK810.669584479;MTOR10.658758794;PTPN1110.634709385;IRS110.633931127;STAT310.616835664;AKT110.595660884;STK1110.540742099	9
GnRH signaling pathway	hsa04912	1.48E-06	ELK112.037626587;PRKCD11.914921194;MAP2K111.820590574;MAP2K311.770651427;EGFR11.528264394;MAPK810.669584479;JUN10.654304535;PLD110.634517333;ATF410.470375894;PRKCA10.39749765	10
Prolactin signaling pathway	hsa04917	1.71E-06	MAP2K111.820590574;RELA11.665008526;SHC111.650309898;MAPK810.669584479;STAT310.616835664;AKT110.595660884;ESR110.573065961;CCND110.498667518;FOS10.432335398	9
B cell receptor signaling pathway	hsa04662	1.92E-06	CHUK12.784558526;SYK12.659710624;VAV112.202811256;MAP2K111.820590574;RAC111.766028144;REL11.665008526;JUN10.654304535;AKT110.595660884;FOS10.432335398	9
Leukocyte transendothelial migration	hsa04670	2.26E-06	VAV112.202811256;RAC111.766028144;ITGB111.723158657;EZR11.506311183;PTPN1110.634709385;PECAM110.620320242;CLDN710.58710524;PTK210.437286688;PRKCA10.39749765;CLDN310.397317266;VASP10.397039547	11
Phospholipase D signaling pathway	hsa04072	2.53E-06	SYK12.659710624;KIT12.654814161;MAP2K111.820590574;SHC111.650309898;EGFR11.528264394;MTOR10.658758794;PTPN1110.634709385;PLD110.634517333;AKT110.595660884;PDGFRB10.584270295;GAB110.517867973;PRKCA10.39749765	12
Thyroid cancer	hsa05216	4.93E-06	MAP2K111.820590574;MYC10.61527599;TP5310.61363911;RET10.592863276;CCND110.498667518;PPARG10.438930828	6
Amphetamine addiction	hsa05031	9.38E-06	JUN10.654304535;ATF210.610718188;ATF410.470375894;GRIA110.434255489;FOS10.432335398;PRKCA10.39749765;HDAC110.363405265;GRIA210.207853852	8
Epithelial cell signaling in Helicobacter pylori infection	hsa05120	1.05E-05	CHUK12.784558526;RAC111.766028144;REL11.665008526;EGFR11.528264394;MET11.502353393;MAPK810.669584479;JUN10.654304535;PTPN1110.634709385	8
cAMP signaling pathway	hsa04024	1.41E-05	VAV112.202811256;L1PE12.067486744;MAP2K111.820590574;RAC111.766028144;REL11.665008526;MAPK810.669584479;JUN10.654304535;BAD10.653825884;PLD110.634517333;AKT110.595660884;GRIA110.434255489;FOS10.432335398;GRIA210.207853852	13
Pathogenic Escherichia coli infection	hsa05130	2.27E-05	YWHAZ12.106859267;ITGB111.723158657;EZR11.506311183;ABL110.616987668;YWHAQ10.609161989;KRT11810.588831159;PRKCA10.39749765	7
Chemokine signaling pathway	hsa04062	3.67E-05	PRKCD12.998925702;CHUK12.784558526;VAV112.202811256;PRKCD11.914921194;MAP2K111.820590574;RAC111.766028144;REL11.665008526;SHC111.650309898;GSK3A10.653883568;STAT310.616835664;AKT110.595660884;PTK210.437286688	12
Toll-like receptor signaling pathway	hsa04620	4.20E-05	CHUK12.784558526;MAP2K111.820590574;MAP2K311.770651427;RAC111.766028144;REL11.665008526;MAPK810.669584479;JUN10.654304535;AKT110.595660884;FOS10.432335398	9
Natural killer cell mediated cytotoxicity	hsa04650	5.07E-05	SYK12.659710624;VAV112.202811256;MAP2K111.820590574;RAC111.766028144;SHC111.650309898;CD24711.593844683;ZAP7010.63855237;PTPN1110.634709385;LCP210.600931669;PRKCA10.39749765	10
Transcriptional misregulation in cancer	hsa05202	1.23E-04	REL11.665008526;REL11.581180761;MET11.502353393;MDM210.628979528;MYC10.61527599;TP5310.61363911;FOXO110.55702078;BCL2L110.486462352;PPARG10.438930828;PTK210.437286688;HDAC110.363405265	11
Regulation of actin cytoskeleton	hsa04810	1.42E-04	VAV112.202811256;MAP2K111.820590574;RAC111.766028144;ITGB111.723158657;EGFR11.528264394;EZR11.506311183;PAK210.638441545;PDGFRB10.584270295;FGFR110.578481153;ITGB310.507020552;PTK210.437286688;PAK310.400884851	12

Table SII. Continued.

KEGG pathway name	Pathway ID	P-value	Gene lfold change	Count
Oxytocin signaling pathway	hsa04921	1.90E-04	ELK112.037626587;MAP2K111.820590574;CAMK111.690304742;EEF211.594920975;NOS311.539286601;EGFR11.528264394;JUN10.654304535;CCND110.498667518;FOS10.432335398;PRKCA10.39749765	10
Dopaminergic synapse	hsa04728	2.05E-04	MAPK810.669584479;GSK3A10.653883568;ATF210.610718188;AKT110.595660884;ATF410.470375894;GRIA110.434255489;FOS10.432335398;PRKCA10.39749765;GRIA210.207853852	9
Bacterial invasion of epithelial cells	hsa05100	2.19E-04	RAC111.766028144;ITGB111.723158657;SHC111.650309898;MET11.502353393;GAB110.517867973;CAV110.4886801;PTK210.437286688	7
Chagas disease (American trypanosomiasis)	hsa05142	2.28E-04	CHUK12.784558526;SMAD311.811758692;REL11.665008526;CD24711.593844683;MAPK810.669584479;JUN10.654304535;AKT110.595660884;FOS10.432335398	8
cGMP-PKG signaling pathway	hsa04022	2.98E-04	SRF12.15522679;MAP2K111.820590574;NOS311.539286601;BAD10.653825884;IRS110.633931127;ATF210.610718188;AKT110.595660884;ATF410.470375894;MEF2A10.428194655;VASP10.397039547	10
Viral myocarditis	hsa05416	3.48E-04	RAC111.766028144;EIF4G110.631727685;ABL110.616987668;CCND110.498667518;CAV110.4886801;CASP910.457456564	6
Influenza A	hsa05164	4.53E-04	MAP2K111.820590574;MAP2K311.770651427;REL11.665008526;MAPK810.669584479;JUN10.654304535;ATF210.610718188;AKT110.595660884;EIF2AK210.495061927;CASP910.457456564;PRKCA10.39749765	10
Axon guidance	hsa04360	4.53E-04	RAC111.766028144;ITGB111.723158657;MET11.502353393;EPHB110.643881705;PAK210.638441545;PTPN1110.634709385;ABL110.616987668;PTK210.437286688;PAK310.400884851;PRKCA10.39749765	10
Longevity regulating pathway-multiple species	hsa04213	4.96E-04	MTOR10.658758794;RPS6KB110.651043868;IRS110.633931127;AKT110.595660884;FOXO110.557020278;HDAC110.363405265	6
Shigellosis	hsa05131	5.39E-04	CHUK12.784558526;RAC111.766028144;ITGB111.723158657;REL11.665008526;MAPK810.669584479;ABL110.616987668	6
Long-term potentiation	hsa04720	5.85E-04	MAP2K111.820590574;RPS6KA111.761512607;ATF410.470375894;GRIA110.434255489;PRKCA10.39749765;GRIA210.207853852	6
Non-alcoholic fatty liver disease	hsa04932	6.23E-04	RAC111.766028144;REL11.665008526;MAPK810.669584479;JUN10.654304535;GSK3A10.653883568;IRS110.633931127;AKT110.595660884;MAP3K510.539578168;ATF410.470375894	9
NF- KB signaling pathway	hsa04064	6.47E-04	CHUK12.784558526;SYK12.659710624;REL11.665008526;ZAP7010.63855237;BCL210.613602346;RELB10.550602934;BCL2L110.486462352	7
Platelet activation	hsa04611	6.72E-04	PRKCZ12.998925702;SYK12.659710624;ITGB111.723158657;NOS311.539286601;LCP210.600931669;AKT110.595660884;ITGB310.507020552;VASP10.397039547	8
Oocyte meiosis	hsa04114	7.10E-04	YWHAZ12.106859267;MAP2K111.820590574;RPS6KA111.761512607;CDK111.65837413;SMC1A11.609832181;YWHAQ10.609161989;CCNE110.538703592;CCNB110.411376804	8
Jak-STAT signaling pathway	hsa04630	8.64E-04	MTOR10.658758794;PTPN110.634709385;STAT310.616835664;MYC10.61527599;BCL210.613602346;AKT110.595660884;IL13RA110.583548346;CCND110.498667518;BCL2L110.486462352	9
Progesterone-mediated oocyte maturation	hsa04914	8.86E-04	MAP2K111.820590574;RPS6KA111.761512607;CDK111.65837413;CDC25A11.513537033;MAPK810.669584479;AKT110.595660884;CCNB110.411376804	7
Type II diabetes mellitus	hsa04930	9.15E-04	PRKCZ12.998925702;PRKCD11.914921194;MAPK810.669584479;MTOR10.658758794;IRS110.633931127	5
Cocaine addiction	hsa05030	1.01E-03	REL11.665008526;JUN10.654304535;ATF210.610718188;ATF410.470375894;GRIA210.207853852	5

Table SII. Continued.

KEGG pathway name	Pathway ID	P-value	Gene lfold change	Count
Measles	hsa05162	1.37E-03	CHUK12.784558526;RELA11.665008526;STAT310.616835664;TP5310.61363911;AKT110.595660884;CCNE110.538703592;CCND110.498667518;EIF2AK210.495061927	8
Apoptosis - multiple species	hsa04215	1.73E-03	MAPK810.669584479;BCL210.613602346;BCL2L110.486462352;CASP910.457456564	4
Wnt signaling pathway	hsa04310	1.88E-03	SMAD311.811758692;RAC111.766028144;MAPK810.669584479;JUN10.654304535;MYC10.61527599;TP5310.61363911;CCND110.498667518;PRKCA10.39749765	8
Gap junction	hsa04540	2.63E-03	MAP2K111.820590574;CDK111.65837413;EGFR11.528264394;PDGFRB10.584270295;PRKCA10.39749765;GJA110.253190861	6
Endocytosis	hsa04144	2.67E-03	PRKCZ12.998925702;KIT12.654814161;SMAD311.811758692;KDR11.784211388;HGS11.646496902;EGFR11.528264394;MET11.502353393;PLD110.634517333;MDM210.628979528;RET10.592863276;CAV110.4886801	11
Herpes simplex infection	hsa05168	2.69E-03	CHUK12.784558526;RELA11.665008526;CDK111.65837413;MAPK810.669584479;JUN10.654304535;PTPN1110.634709385;TP5310.61363911;EIF2AK210.495061927;FOS10.432335398	9
Adherens junction	hsa04520	6.22E-03	SMAD311.811758692;RAC111.766028144;EGFR11.528264394;MET11.502353393;FGFR110.578481153	5
Leishmaniasis	hsa05140	6.22E-03	ELK112.037626587;ITGB111.723158657;RELA11.665008526;JUN10.654304535;FOS10.432335398	5
Tight junction	hsa04530	6.43E-03	PRKCZ12.998925702;PRKCD11.914921194;AKT110.595660884;CLDN710.58710524;PTEN10.5623979;PRKCA10.39749765;CLDN310.397317266	7
Pertussis	hsa05133	6.58E-03	ITGB111.723158657;RELA11.665008526;MAPK810.669584479;JUN10.654304535;FOS10.432335398	5
Tuberculosis	hsa05152	7.40E-03	SYK12.659710624;KSR111.840850674;RELA11.665008526;MAPK810.669584479;BAD10.653825884;BCL210.613602346;AKT110.595660884;CASP910.457456564	8
Alcoholism	hsa05034	7.40E-03	MAP2K111.820590574;SHC111.650309898;HDAC411.532692173;ATF210.610718188;HDAC810.574090319;ATF410.470375894;HDAC110.363405265;H2AFX10.330108594	8
Cholinergic synapse	hsa04725	8.21E-03	MAP2K111.820590574;BCL210.613602346;AKT110.595660884;ATF410.470375894;FOS10.432335398;PRKCA10.39749765	6
Aldosterone synthesis and secretion	hsa04925	9.06E-03	LIPE12.067486744;CAMK111.690304742;ATF210.610718188;ATF410.470375894;PRKCA10.39749765	5
Hippo signaling pathway	hsa04390	1.10E-02	PRKCZ12.998925702;YWHAZ12.106859267;SMAD311.811758692;NF210.642363384;MYC10.61527599;YWHAQ10.609161989;CCND110.498667518	7
Salmonella infection	hsa05132	1.16E-02	RAC111.766028144;RELA11.665008526;MAPK810.669584479;JUN10.654304535;FOS10.432335398	5
Long-term depression	hsa04730	1.48E-02	MAP2K111.820590574;GRIA110.434255489;PRKCA10.39749765;GRIA210.207853852	4
Circadian entrainment	hsa04713	1.72E-02	RPS6KA512.111104451;GRIA110.434255489;FOS10.432335398;PRKCA10.39749765;GRIA210.207853852	5
Inflammatory bowel disease (IBD)	hsa05321	2.04E-02	SMAD311.811758692;RELA11.665008526;JUN10.654304535;STAT310.616835664	4
Glucagon signaling pathway	hsa04922	2.27E-02	ACACA12.842539655;ATF210.610718188;AKT110.595660884;FOXO110.55702078;ATF410.470375894	5
Aldosterone-regulated sodium reabsorption	hsa04960	2.35E-02	PDPK112.465149656;IRS110.633931127;PRKCA10.39749765	3
Signaling pathways regulating pluripotency of stem cells	hsa04550	2.51E-02	MAP2K111.820590574;SMAD311.811758692;STAT310.616835664;MYC10.61527599;AKT110.595660884;FGFR110.578481153	6

Table SII. Continued.

KEGG pathway name	Pathway ID	P-value	Gene lfold change	Count
Arrhythmogenic right ventricular cardiomyopathy (ARVC)	hsa05412	2.96E-02	ITGB111.723158657;LMNA10.569157062;ITGB310.507020552;GJA110.253190861	4
Adrenergic signaling in cardiomyocytes	hsa04261	3.08E-02	RPS6KA512.11104451;BCL210.613602346;ATF210.610718188;AKT110.595660884;ATF410.470375894;PRKCA10.39749765	6
Regulation of lipolysis in adipocytes	hsa04923	5.88E-02	LIPE12.067486744;IRS110.633931127;AKT110.595660884	3
NOD-like receptor signaling pathway	hsa04621	6.14E-02	CHUK12.784558526;RELA11.665008526;MAPK810.669584479	3
Inflammatory mediator regulation of TRP channels	hsa04750	6.99E-02	PRKCD11.914921194;MAP2K311.770651427;MAPK810.669584479;PRKCA10.39749765	4
Dorso-ventral axis formation	hsa04320	7.22E-02	MAP2K111.820590574;EGFR11.528264394	2
Melanogenesis	hsa04916	7.41E-02	KIT12.654814161;MAP2K111.820590574;MITF10.649199215;PRKCA10.39749765	4
Retrograde endocannabinoid signaling	hsa04723	7.63E-02	MAPK810.669584479;GRIA110.434255489;PRKCA10.39749765;GRIA210.207853852	4
RIG-I-like receptor signaling pathway	hsa04622	9.94E-02	CHUK12.784558526;RELA11.665008526;MAPK810.669584479	3
Thyroid hormone synthesis	hsa04918	1.03E-01	ATF210.610718188;ATF410.470375894;PRKCA10.39749765	3
Prion diseases	hsa05020	1.06E-01	ELK112.037626587;MAP2K111.820590574	2
Glutamatergic synapse	hsa04724	1.07E-01	PLD110.634517333;GRIA110.434255489;PRKCA10.39749765;GRIA210.207853852	4
Protein processing in endoplasmic reticulum	hsa04141	1.24E-01	MAPK810.669584479;BCL210.613602346;MAP3K510.539578168;EIF2AK210.495061927;ATF410.470375894	5
Nicotine addiction	hsa05033	1.32E-01	GRIA110.434255489;GRIA210.207853852	2
Hypertrophic cardiomyopathy (HCM)	hsa05410	1.45E-01	ITGB111.723158657;LMNA10.569157062;ITGB310.507020552	3
TGF-beta signaling pathway	hsa04350	1.48E-01	SMAD311.811758692;RPS6KB110.651043868;MYC10.61527599	3
Insulin secretion	hsa04911	1.52E-01	ATF210.610718188;ATF410.470375894;PRKCA10.39749765	3
Hematopoietic cell lineage	hsa04640	1.64E-01	KIT12.654814161;CD511.597067981;ITGB310.507020552	3
Hedgehog signaling pathway	hsa04340	1.71E-01	BCL210.613602346;CCND110.498667518	2
Endocrine and other factor-regulated calcium reabsorption	hsa04961	1.71E-01	ESR110.573065961;PRKCA10.39749765	2
Dilated cardiomyopathy	hsa05414	1.71E-01	ITGB111.723158657;LMNA10.569157062;ITGB310.507020552	3
Malaria	hsa05144	1.82E-01	MET11.502353393;PECAM110.620320242	2
Fatty acid biosynthesis	hsa00061	1.88E-01	ACACA12.842539655	1
Cell adhesion molecules (CAMs)	hsa04514	2.02E-01	ITGB111.723158657;PECAM110.620320242;CLDN710.58710524;CLDN310.397317266	4
Amoebiasis	hsa05146	2.12E-01	RELA11.665008526;PTK210.437286688;PRKCA10.39749765	3
Fanconi anemia pathway	hsa03460	2.17E-01	ATRIPO.575896544;BRCA110.420959409	2
Legionellosis	hsa05134	2.17E-01	RELA11.665008526;CASP910.457456564	2
Phagosome	hsa04145	2.32E-01	RAC111.766028144;ITGB111.723158657;HGS11.646496902;ITGB310.507020552	4
Cytokine-cytokine receptor interaction	hsa04060	2.44E-01	KIT12.654814161;KDR11.784211388;EGFR11.528264394;MET11.502353393;PDGFRB10.584270295;IL13RA110.583548346	6
Cytosolic DNA-sensing pathway	hsa04623	2.70E-01	CHUK12.784558526;RELA11.665008526	2
Arginine biosynthesis	hsa00220	2.86E-01	NOS311.539286601	1
Vascular smooth muscle contraction	hsa04270	2.97E-01	PRKCD11.914921194;MAP2K111.820590574;PRKCA10.39749765	3

Table SII. Continued.

KEGG pathway name	Pathway ID	P-value	Gene lfold change	Count
PPAR signaling pathway	hsa03320	3.17E-01	PDPK112.465149656;PPARG10.438930828	2
Calcium signaling pathway	hsa04020	3.20E-01	NOS311.539286601;EGFR11.528264394;PDGFRB10.584270295;PRKCA10.39749765	4
Gastric acid secretion	hsa04971	3.29E-01	EZR11.506311183;PRKCA10.39749765	2
Huntington's disease	hsa05016	3.67E-01	TP5310.61363911;CASP910.457456564;PPARG10.438930828;HDAC110.363405265	4
Hippo signaling pathway-multiple species	hsa04392	3.72E-01	NF210.642363384	1
ECM-receptor interaction	hsa04512	3.75E-01	ITGB111.723158657;ITGB310.507020552	2
Propanoate metabolism	hsa00640	4.01E-01	ACACA12.842539655	1
Fructose and mannose metabolism	hsa00051	4.11E-01	PFKFB210.618457881	1
Rheumatoid arthritis	hsa05323	4.26E-01	JUN10.654304535;FOS10.432335398	2
African trypanosomiasis	hsa05143	4.30E-01	PRKCA10.39749765	1
Primary immunodeficiency	hsa05340	4.48E-01	ZAP7010.63855237	1
Pancreatic secretion	hsa04972	4.53E-01	RAC111.766028144;PRKCA10.39749765	2
Phosphatidylinositol signaling system	hsa04070	4.63E-01	PTEN10.5623979;PRKCA10.39749765	2
Pyruvate metabolism	hsa00620	4.74E-01	ACACA12.842539655	1
Alzheimer's disease	hsa05010	5.01E-01	BAD10.653825884;MAPT10.61428451;CASP910.457456564	3
Ether lipid metabolism	hsa00565	5.14E-01	PLD110.634517333	1
Carbohydrate digestion and absorption	hsa04973	5.22E-01	AKT110.595660884	1
Serotonergic synapse	hsa04726	5.34E-01	MAP2K111.820590574;PRKCA10.39749765	2
Notch signaling pathway	hsa04330	5.37E-01	HDAC110.363405265	1
Fatty acid metabolism	hsa01212	5.37E-01	ACACA12.842539655	1
Arginine and proline metabolism	hsa00330	5.52E-01	NOS311.539286601	1
Vibrio cholerae infection	hsa05110	5.59E-01	PRKCA10.39749765	1
Basal cell carcinoma	hsa05217	5.87E-01	TP5310.61363911	1
Ubiquitin mediated proteolysis	hsa04120	6.44E-01	MDM210.628979528;BRCA110.420959409	2
Inositol phosphate metabolism	hsa00562	6.81E-01	PTEN10.5623979	1
GABAergic synapse	hsa04727	7.57E-01	PRKCA10.39749765	1
Salivary secretion	hsa04970	7.61E-01	PRKCA10.39749765	1
Morphine addiction	hsa05032	7.69E-01	PRKCA10.39749765	1
Glycerophospholipid metabolism	hsa00564	7.83E-01	PLD110.634517333	1
Systemic lupus erythematosus	hsa05322	8.89E-01	H2AFX10.330108594	1
Ribosome	hsa03010	8.92E-01	RPS610.639057883	1
Parkinson's disease	hsa05012	8.99E-01	CASP910.457456564	1
RNA transport	hsa03013	9.38E-01	EIF4G110.631727685	1
Neuroactive ligand-receptor interaction	hsa04080	9.39E-01	GRIA110.434255489;GRIA210.207853852	2
Metabolic pathways	hsa01100	1.00E+00	ACACA12.842539655;NOS311.539286601;PLD110.634517333	3