Supplemental Table S1: All results of Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment analyses.

GO/KEGG	ID	Description	BgRatio	P value	Adjusted P value	q value	Count
BP	GO:0044843	cell cycle G1/S phase transition	310/18866	1,98E-20	1,11E-17	5,05E-18	11
BP	GO:0000082	G1/S transition of mitotic cell cycle	287/18866	6,16E-18	1,73E-15	7,88E-16	10
BP	GO:0000079	regulation of cyclin-dependent protein serine/threonine kinase activity	102/18866	3,55E-14	6,56E-12	2,99E-12	7
BP	GO:1904029	regulation of cyclin-dependent protein kinase activity	106/18866	4,68E-14	6,56E-12	2,99E-12	7
BP	GO:0000086	G2/M transition of mitotic cell cycle	254/18866	2,33E-11	2,61E-09	1,19E-09	7
BP	GO:2000134	negative regulation of G1/S transition of mitotic cell cycle	126/18866	3,54E-11	3,09E-09	1,41E-09	6
BP	GO:0044839	cell cycle G2/M phase transition	273/18866	3,86E-11	3,09E-09	1,41E-09	7
BP	GO:1902807	negative regulation of cell cycle G1/S phase transition	132/18866	4,70E-11	3,29E-09	1,50E-09	6
BP	GO:2000045	regulation of G1/S transition of mitotic cell cycle	185/18866	3,64E-10	2,20E-08	1,01E-08	6
BP	GO:0031100	animal organ regeneration	75/18866	3,93E-10	2,20E-08	1,01E-08	5
BP	GO:1902806	regulation of cell cycle G1/S phase transition	206/18866	6,96E-10	3,54E-08	1,62E-08	6
BP	GO:0007050	cell cycle arrest	234/18866	1,50E-09	6,99E-08	3,19E-08	6
BP	GO:1901991	negative regulation of mitotic cell cycle phase transition	251/18866	2,28E-09	9,16E-08	4,18E-08	6
BP	GO:0071156	regulation of cell cycle arrest	106/18866	2,29E-09	9,16E-08	4,18E-08	5
BP	GO:1901988	negative regulation of cell cycle phase transition	270/18866	3,54E-09	1,32E-07	6,03E-08	6
BP	GO:0045930	negative regulation of mitotic cell cycle	341/18866	1,43E-08	5,00E-07	2,28E-07	6
BP	GO:0048146	positive regulation of fibroblast proliferation	51/18866	1,54E-08	5,08E-07	2,32E-07	4
BP	GO:0010948	negative regulation of cell cycle process	359/18866	1,94E-08	6,04E-07	2,76E-07	6
BP	GO:0031571	mitotic G1 DNA damage checkpoint	63/18866	3,66E-08	1,04E-06	4,75E-07	4
BP	GO:0044783	G1 DNA damage checkpoint	64/18866	3,90E-08	1,04E-06	4,75E-07	4
BP	GO:0044819	mitotic G1/S transition checkpoint	64/18866	3,90E-08	1,04E-06	4,75E-07	4
BP	GO:0010389	regulation of G2/M transition of mitotic cell cycle	200/18866	5,59E-08	1,39E-06	6,37E-07	5
BP	GO:0031099	regeneration	201/18866	5,73E-08	1,39E-06	6,37E-07	5
BP	GO:1901990	regulation of mitotic cell cycle phase transition	448/18866	7,24E-08	1,69E-06	7,72E-07	6
BP	GO:1902749	regulation of cell cycle G2/M phase transition	217/18866	8,40E-08	1,88E-06	8,59E-07	5
BP	GO:0048145	regulation of fibroblast proliferation	83/18866	1,12E-07	2,36E-06	1,08E-06	4
BP	GO:1901987	regulation of cell cycle phase transition	486/18866	1,17E-07	2,36E-06	1,08E-06	6
BP	GO:0048144	fibroblast proliferation	84/18866	1,18E-07	2,36E-06	1,08E-06	4
BP	GO:0044773	mitotic DNA damage checkpoint	101/18866	2,48E-07	4,79E-06	2,19E-06	4
BP	GO:0006260	DNA replication	273/18866	2,63E-07	4,91E-06	2,24E-06	5
BP	GO:0044774	mitotic DNA integrity checkpoint	108/18866	3,25E-07	5,87E-06	2,68E-06	4
BP	GO:0010971	positive regulation of G2/M transition of mitotic cell cycle	27/18866	4,28E-07	7,37E-06	3,37E-06	3
BP	GO:0090068	positive regulation of cell cycle process	302/18866	4,34E-07	7,37E-06	3,37E-06	5
BP	GO:1902751	positive regulation of cell cycle G2/M phase transition	30/18866	5,94E-07	9,78E-06	4,47E-06	3
BP	GO:0000077	DNA damage checkpoint	151/18866	1,25E-06	1,99E-05	9,10E-06	4

Hoang T, Nguyen M, Chen W, Zhuang C, Wang Z, Wang H, Li J, Lin H. Elevated expression of SKP2 correlates with poor prognosis in osteosarcoma: a bioinformatics analysis. *Biomed. Res. Ther.*, 2021; 8(12):4782-4792.

BP	GO:0006270	DNA replication initiation	39/18866	1,33E-06	2,07E-05	9,47E-06	3
BP	GO:0016572	histone phosphorylation	40/18866	1,44E-06	2,18E-05	9,95E-06	3
BP	GO:0031570	DNA integrity checkpoint	161/18866	1,61E-06	2,37E-05	1,08E-05	4
BP	GO:0045787	positive regulation of cell cycle	396/18866	1,65E-06	2,38E-05	1,08E-05	5
BP	GO:0007093	mitotic cell cycle checkpoint	166/18866	1,82E-06	2,55E-05	1,16E-05	4
BP	GO:0006367	transcription initiation from RNA polymerase II promoter	189/18866	3,05E-06	4,16E-05	1,90E-05	4
BP	GO:0006977	DNA damage response, signal transduction by p53 class mediator resultin	56/18866	4,02E-06	5,36E-05	2,45E-05	3
BP	GO:0072431	signal transduction involved in mitotic G1 DNA damage checkpoint	57/18866	4,24E-06	5,40E-05	2,47E-05	3
BP	GO:1902400	intracellular signal transduction involved in G1 DNA damage checkpoint	57/18866	4,24E-06	5,40E-05	2,47E-05	3
BP	GO:0072413	signal transduction involved in mitotic cell cycle checkpoint	59/18866	4,71E-06	5,61E-05	2,56E-05	3
BP	GO:1902402	signal transduction involved in mitotic DNA damage checkpoint	59/18866	4,71E-06	5,61E-05	2,56E-05	3
BP	GO:1902403	signal transduction involved in mitotic DNA integrity checkpoint	59/18866	4,71E-06	5,61E-05	2,56E-05	3
BP	GO:0000075	cell cycle checkpoint	219/18866	5,47E-06	6,38E-05	2,91E-05	4
BP	GO:0097305	response to alcohol	234/18866	7,11E-06	8,13E-05	3,71E-05	4
BP	GO:0072401	signal transduction involved in DNA integrity checkpoint	73/18866	8,97E-06	9,79E-05	4,47E-05	3
BP	GO:0072422	signal transduction involved in DNA damage checkpoint	73/18866	8,97E-06	9,79E-05	4,47E-05	3
BP	GO:0006352	DNA-templated transcription, initiation	249/18866	9,09E-06	9,79E-05	4,47E-05	4
BP	GO:0072395	signal transduction involved in cell cycle checkpoint	74/18866	9,35E-06	9,87E-05	4,51E-05	3
BP	GO:0051321	meiotic cell cycle	254/18866	9,83E-06	0,00010195	4,66E-05	4
BP	GO:0071158	positive regulation of cell cycle arrest	81/18866	1,23E-05	0,000124956	5,71E-05	3
BP	GO:0016579	protein deubiquitination	283/18866	1,51E-05	0,000150555	6,88E-05	4
BP	GO:0070646	protein modification by small protein removal	300/18866	1,89E-05	0,00018539	8,47E-05	4
BP	GO:1901992	positive regulation of mitotic cell cycle phase transition	94/18866	1,92E-05	0,00018539	8,47E-05	3
BP	GO:0030330	DNA damage response, signal transduction by p53 class mediator	107/18866	2,83E-05	0,000268747	0,000122755	3
BP	GO:1901989	positive regulation of cell cycle phase transition	110/18866	3,08E-05	0,000287074	0,000131126	3
BP	GO:0006275	regulation of DNA replication	112/18866	3,25E-05	0,000298008	0,00013612	3
BP	GO:0071732	cellular response to nitric oxide	16/18866	3,69E-05	0,000333503	0,000152333	2
BP	GO:0007569	cell aging	118/18866	3,79E-05	0,000337271	0,000154054	3
BP	GO:0007127	meiosis I	119/18866	3,89E-05	0,000340479	0,000155519	3
BP	GO:0061982	meiosis I cell cycle process	124/18866	4,40E-05	0,000379084	0,000173153	3
BP	GO:1902170	cellular response to reactive nitrogen species	19/18866	5,26E-05	0,000446013	0,000203724	2
BP	GO:0042770	signal transduction in response to DNA damage	133/18866	5,42E-05	0,00045325	0,00020703	3
BP	GO:0042493	response to drug	397/18866	5,67E-05	0,000466868	0,00021325	4
BP	GO:0051412	response to corticosterone	20/18866	5,84E-05	0,000467103	0,000213357	2
BP	GO:0071731	response to nitric oxide	20/18866	5,84E-05	0,000467103	0,000213357	2
BP	GO:0055093	response to hyperoxia	22/18866	7,09E-05	0,000551773	0,000252032	2
BP	GO:0071157	negative regulation of cell cycle arrest	22/18866	7,09E-05	0,000551773	0,000252032	2
BP	GO:0000280	nuclear division	428/18866	7,60E-05	0,000582668	0,000266144	4

Hoang T, Nguyen M, Chen W, Zhuang C, Wang Z, Wang H, Li J, Lin H. Elevated expression of SKP2 correlates with poor prognosis in osteosarcoma: a bioinformatics analysis. *Biomed. Res. Ther.*, 2021; 8(12):4782-4792.

BP	GO:0006261	DNA-dependent DNA replication	151/18866	7,91E-05	0,000598748	0,000273488	3
BP	GO:0007095	mitotic G2 DNA damage checkpoint	24/18866	8,47E-05	0,000624166	0,000285098	2
BP	GO:0044321	response to leptin	24/18866	8,47E-05	0,000624166	0,000285098	2
BP	GO:0045931	positive regulation of mitotic cell cycle	168/18866	0,000108595	0,000789784	0,000360747	3
BP	GO:0034614	cellular response to reactive oxygen species	170/18866	0,000112472	0,000807492	0,000368836	3
BP	GO:0048285	organelle fission	476/18866	0,000114696	0,000813034	0,000371367	4
BP	GO:0036296	response to increased oxygen levels	29/18866	0,000124409	0,000870863	0,000397781	2
BP	GO:0140013	meiotic nuclear division	177/18866	0,000126752	0,000876307	0,000400268	3
BP	GO:0010165	response to X-ray	32/18866	0,000151842	0,001012283	0,000462377	2
BP	GO:0044818	mitotic G2/M transition checkpoint	32/18866	0,000151842	0,001012283	0,000462377	2
BP	GO:0051385	response to mineralocorticoid	32/18866	0,000151842	0,001012283	0,000462377	2
BP	GO:1903046	meiotic cell cycle process	193/18866	0,00016372	0,001078627	0,000492681	3
BP	GO:1901654	response to ketone	200/18866	0,000181881	0,001158028	0,000528949	3
BP	GO:0000083	regulation of transcription involved in G1/S transition of mitotic cell cycl	35/18866	0,000181976	0,001158028	0,000528949	2
BP	GO:1904031	positive regulation of cyclin-dependent protein kinase activity	35/18866	0,000181976	0,001158028	0,000528949	2
BP	GO:0031572	G2 DNA damage checkpoint	36/18866	0,000192619	0,001211985	0,000553595	2
BP	GO:0045740	positive regulation of DNA replication	40/18866	0,000238177	0,001481993	0,000676926	2
BP	GO:0000302	response to reactive oxygen species	235/18866	0,00029243	0,001799567	0,000821983	3
BP	GO:0033002	muscle cell proliferation	244/18866	0,000326545	0,001987668	0,000907901	3
BP	GO:0009636	response to toxic substance	250/18866	0,000350663	0,002111519	0,000964472	3
BP	GO:0007129	homologous chromosome pairing at meiosis	49/18866	0,000358072	0,002133193	0,000974372	2
BP	GO:0072331	signal transduction by p53 class mediator	267/18866	0,000425183	0,002506345	0,001144815	3
BP	GO:0045143	homologous chromosome segregation	62/18866	0,000573401	0,003344837	0,001527811	2
BP	GO:0002066	columnar/cuboidal epithelial cell development	64/18866	0,000610915	0,003526933	0,001610986	2
BP	GO:0034599	cellular response to oxidative stress	310/18866	0,000657404	0,003756592	0,001715887	3
BP	GO:0007568	aging	319/18866	0,000714475	0,004041472	0,001846011	3
BP	GO:0070192	chromosome organization involved in meiotic cell cycle	70/18866	0,00073043	0,004090408	0,001868363	2
BP	GO:0007265	Ras protein signal transduction	346/18866	0,000904497	0,004965869	0,002268244	3
BP	GO:0048545	response to steroid hormone	346/18866	0,000904497	0,004965869	0,002268244	3
BP	GO:0090398	cellular senescence	79/18866	0,000929201	0,005051968	0,002307572	2
BP	GO:0048638	regulation of developmental growth	353/18866	0,000958526	0,005161296	0,002357509	3
BP	GO:0062197	cellular response to chemical stress	360/18866	0,001014578	0,005411082	0,002471603	3
BP	GO:0031145	anaphase-promoting complex-dependent catabolic process	83/18866	0,001025008	0,005415139	0,002473456	2
BP	GO:0010038	response to metal ion	366/18866	0,001064255	0,005569931	0,00254416	3
BP	GO:0045132	meiotic chromosome segregation	93/18866	0,001284472	0,006660226	0,003042171	2
BP	GO:0070482	response to oxygen levels	396/18866	0,001335923	0,006863456	0,003135	3
BP	GO:0010972	negative regulation of G2/M transition of mitotic cell cycle	96/18866	0,001367837	0,006963533	0,003180712	2
BP	GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolic process	424/18866	0,001625962	0,008203051	0,003746882	3

Hoang T, Nguyen M, Chen W, Zhuang C, Wang Z, Wang H, Li J, Lin H. Elevated expression of SKP2 correlates with poor prognosis in osteosarcoma: a bioinformatics analysis. *Biomed. Res. Ther.*, 2021; 8(12):4782-4792.

BP	GO:1902750	negative regulation of cell cycle G2/M phase transition	108/18866	0,00172659	0,00863295	0,003943246	2
BP	GO:0006979	response to oxidative stress	458/18866	0,002028141	0,010050964	0,004590948	3
BP	GO:0016570	histone modification	468/18866	0,002157275	0,010520649	0,004805484	3
BP	GO:0002065	columnar/cuboidal epithelial cell differentiation	121/18866	0,00216049	0,010520649	0,004805484	2
BP	GO:0045471	response to ethanol	122/18866	0,0021958	0,010600414	0,004841918	2
BP	GO:0007098	centrosome cycle	125/18866	0,002303376	0,011024705	0,005035721	2
BP	GO:0016569	covalent chromatin modification	481/18866	0,002332733	0,011070599	0,005056684	3
BP	GO:0010498	proteasomal protein catabolic process	483/18866	0,002360497	0,011108222	0,005073868	3
BP	GO:0031023	microtubule organizing center organization	136/18866	0,002718856	0,012687993	0,005795456	2
BP	GO:0009411	response to UV	140/18866	0,002878086	0,013320066	0,006084166	2
BP	GO:0032355	response to estradiol	141/18866	0,002918569	0,013396708	0,006119173	2
BP	GO:0010212	response to ionizing radiation	144/18866	0,003041633	0,013848086	0,006325348	2
BP	GO:0051384	response to glucocorticoid	147/18866	0,003167117	0,014303108	0,006533186	2
BP	GO:0006606	protein import into nucleus	150/18866	0,003295012	0,014761652	0,006742634	2
BP	GO:0000723	telomere maintenance	161/18866	0,003784475	0,016819891	0,00768277	2
BP	GO:0031960	response to corticosteroid	164/18866	0,003923529	0,0173006	0,007902342	2
BP	GO:0051170	import into nucleus	171/18866	0,004257194	0,018625223	0,008507386	2
BP	GO:0048660	regulation of smooth muscle cell proliferation	173/18866	0,004354885	0,018904926	0,008635145	2
BP	GO:0032200	telomere organization	174/18866	0,004404122	0,018971602	0,0086656	2
BP	GO:0048659	smooth muscle cell proliferation	175/18866	0,00445362	0,019038374	0,0086961	2
BP	GO:0017038	protein import	200/18866	0,005775046	0,024308615	0,011103371	2
BP	GO:0045793	positive regulation of cell size	10/18866	0,005816704	0,024308615	0,011103371	1
BP	GO:1903862	positive regulation of oxidative phosphorylation	10/18866	0,005816704	0,024308615	0,011103371	1
BP	GO:0033148	positive regulation of intracellular estrogen receptor signaling pathway	11/18866	0,00639668	0,026147012	0,01194309	1
BP	GO:0033197	response to vitamin E	11/18866	0,00639668	0,026147012	0,01194309	1
BP	GO:0033327	Leydig cell differentiation	11/18866	0,00639668	0,026147012	0,01194309	1
BP	GO:0007623	circadian rhythm	218/18866	0,006824992	0,026879527	0,012277679	2
BP	GO:0007077	mitotic nuclear envelope disassembly	12/18866	0,006976347	0,026879527	0,012277679	1
BP	GO:0021670	lateral ventricle development	12/18866	0,006976347	0,026879527	0,012277679	1
BP	GO:0043696	dedifferentiation	12/18866	0,006976347	0,026879527	0,012277679	1
BP	GO:0043697	cell dedifferentiation	12/18866	0,006976347	0,026879527	0,012277679	1
BP	GO:0055015	ventricular cardiac muscle cell development	12/18866	0,006976347	0,026879527	0,012277679	1
BP	GO:2000105	positive regulation of DNA-dependent DNA replication	12/18866	0,006976347	0,026879527	0,012277679	1
BP	GO:0002064	epithelial cell development	221/18866	0,007007877	0,026879527	0,012277679	2
BP	GO:0071241	cellular response to inorganic substance	221/18866	0,007007877	0,026879527	0,012277679	2
BP	GO:0033145	positive regulation of intracellular steroid hormone receptor signaling pat	13/18866	0,007555708	0,028450728	0,012995351	1
BP	GO:1902916	positive regulation of protein polyubiquitination	13/18866	0,007555708	0,028450728	0,012995351	1
BP	GO:0010001	glial cell differentiation	230/18866	0,007569926	0,028450728	0,012995351	2

Hoang T, Nguyen M, Chen W, Zhuang C, Wang Z, Wang H, Li J, Lin H. Elevated expression of SKP2 correlates with poor prognosis in osteosarcoma: a bioinformatics analysis. *Biomed. Res. Ther.,* 2021; 8(12):4782-4792.

BP	GO:0045472	response to ether	14/18866	0,008134761	0,03016865	0,013780041	1
BP	GO:0090399	replicative senescence	14/18866	0,008134761	0,03016865	0,013780041	1
BP	GO:0048308	organelle inheritance	15/18866	0,008713507	0,031892574	0,014567473	1
BP	GO:0048313	Golgi inheritance	15/18866	0,008713507	0,031892574	0,014567473	1
BP	GO:0031668	cellular response to extracellular stimulus	253/18866	0,00909646	0,03272635	0,014948314	2
BP	GO:0002070	epithelial cell maturation	16/18866	0,009291946	0,03272635	0,014948314	1
BP	GO:0021542	dentate gyrus development	16/18866	0,009291946	0,03272635	0,014948314	1
BP	GO:0030397	membrane disassembly	16/18866	0,009291946	0,03272635	0,014948314	1
BP	GO:0051081	nuclear envelope disassembly	16/18866	0,009291946	0,03272635	0,014948314	1
BP	GO:0060576	intestinal epithelial cell development	16/18866	0,009291946	0,03272635	0,014948314	1
BP	GO:0006978	DNA damage response, signal transduction by p53 class mediator resultin	17/18866	0,009870078	0,033702704	0,01539428	1
BP	GO:0010224	response to UV-B	17/18866	0,009870078	0,033702704	0,01539428	1
BP	GO:0033599	regulation of mammary gland epithelial cell proliferation	17/18866	0,009870078	0,033702704	0,01539428	1
BP	GO:0055012	ventricular cardiac muscle cell differentiation	17/18866	0,009870078	0,033702704	0,01539428	1
BP	GO:0071850	mitotic cell cycle arrest	17/18866	0,009870078	0,033702704	0,01539428	1
BP	GO:0034501	protein localization to kinetochore	18/18866	0,010447903	0,034845278	0,01591617	1
BP	GO:0042772	DNA damage response, signal transduction resulting in transcription	18/18866	0,010447903	0,034845278	0,01591617	1
BP	GO:0071371	cellular response to gonadotropin stimulus	18/18866	0,010447903	0,034845278	0,01591617	1
BP	GO:0098813	nuclear chromosome segregation	272/18866	0,010453583	0,034845278	0,01591617	2
BP	GO:0034504	protein localization to nucleus	277/18866	0,010824933	0,035689226	0,016301658	2
BP	GO:0032026	response to magnesium ion	19/18866	0,011025422	0,035689226	0,016301658	1
BP	GO:0044320	cellular response to leptin stimulus	19/18866	0,011025422	0,035689226	0,016301658	1
BP	GO:0060749	mammary gland alveolus development	19/18866	0,011025422	0,035689226	0,016301658	1
BP	GO:0061377	mammary gland lobule development	19/18866	0,011025422	0,035689226	0,016301658	1
BP	GO:0003323	type B pancreatic cell development	20/18866	0,011602634	0,037341811	0,017056504	1
BP	GO:0036120	cellular response to platelet-derived growth factor stimulus	22/18866	0,01275614	0,040358409	0,018434386	1
BP	GO:0045655	regulation of monocyte differentiation	22/18866	0,01275614	0,040358409	0,018434386	1
BP	GO:0071459	protein localization to chromosome, centromeric region	22/18866	0,01275614	0,040358409	0,018434386	1
BP	GO:0048511	rhythmic process	305/18866	0,013011955	0,040936488	0,018698433	2
BP	GO:0042063	gliogenesis	307/18866	0,013175063	0,041022873	0,018737891	2
BP	GO:0010288	response to lead ion	23/18866	0,013332434	0,041022873	0,018737891	1
BP	GO:0036119	response to platelet-derived growth factor	23/18866	0,013332434	0,041022873	0,018737891	1
BP	GO:2000773	negative regulation of cellular senescence	23/18866	0,013332434	0,041022873	0,018737891	1
BP	GO:0018105	peptidyl-serine phosphorylation	310/18866	0,013421429	0,041071039	0,018759892	2
BP	GO:0007141	male meiosis I	24/18866	0,013908422	0,04232998	0,019334934	1
BP	GO:0009416	response to light stimulus	319/18866	0,014172726	0,042901225	0,01959586	2
BP	GO:0003309	type B pancreatic cell differentiation	25/18866	0,014484104	0,043374858	0,0198122	1
BP	GO:0060575	intestinal epithelial cell differentiation	25/18866	0,014484104	0,043374858	0,0198122	1

Hoang T, Nguyen M, Chen W, Zhuang C, Wang Z, Wang H, Li J, Lin H. Elevated expression of SKP2 correlates with poor prognosis in osteosarcoma: a bioinformatics analysis. *Biomed. Res. Ther.*, 2021; 8(12):4782-4792.

BP	GO:0071496	cellular response to external stimulus	326/18866	0,014769636	0,043994661	0,020095306	2
BP	GO:0002068	glandular epithelial cell development	26/18866	0,015059481	0,044318078	0,020243032	1
BP	GO:1902914	regulation of protein polyubiquitination	26/18866	0,015059481	0,044318078	0,020243032	1
BP	GO:0071375	cellular response to peptide hormone stimulus	330/18866	0,01511563	0,044318078	0,020243032	2
BP	GO:0018209	peptidyl-serine modification	333/18866	0,015377454	0,044850906	0,02048641	2
BP	GO:0007059	chromosome segregation	334/18866	0,01546517	0,044873033	0,020496517	2
BP	GO:0034698	response to gonadotropin	27/18866	0,015634553	0,045130667	0,020614196	1
BP	GO:0033598	mammary gland epithelial cell proliferation	28/18866	0,016209319	0,046312339	0,021153944	1
BP	GO:0035883	enteroendocrine cell differentiation	28/18866	0,016209319	0,046312339	0,021153944	1
BP	GO:0071902	positive regulation of protein serine/threonine kinase activity	345/18866	0,016444566	0,046745975	0,021352015	2
BP	GO:0090344	negative regulation of cell aging	29/18866	0,01678378	0,047296839	0,021603631	1
BP	GO:0009615	response to virus	349/18866	0,016807269	0,047296839	0,021603631	2
BP	GO:0006913	nucleocytoplasmic transport	354/18866	0,017265532	0,04812101	0,021980086	2
BP	GO:0043457	regulation of cellular respiration	30/18866	0,017357936	0,04812101	0,021980086	1
BP	GO:0071480	cellular response to gamma radiation	30/18866	0,017357936	0,04812101	0,021980086	1
BP	GO:0051169	nuclear transport	357/18866	0,017543084	0,048394713	0,022105104	2
BP	GO:0045737	positive regulation of cyclin-dependent protein serine/threonine kinase act	31/18866	0,017931787	0,049224514	0,022484129	1
BP	GO:0051052	regulation of DNA metabolic process	365/18866	0,018292675	0,04958367	0,02264818	2
BP	GO:0002082	regulation of oxidative phosphorylation	32/18866	0,018505334	0,04958367	0,02264818	1
BP	GO:0021591	ventricular system development	32/18866	0,018505334	0,04958367	0,02264818	1
BP	GO:0071353	cellular response to interleukin-4	32/18866	0,018505334	0,04958367	0,02264818	1
BP	GO:0097421	liver regeneration	32/18866	0,018505334	0,04958367	0,02264818	1
CC	GO:0000307	cyclin-dependent protein kinase holoenzyme complex	43/19559	9,35E-27	2,99E-25	1,08E-25	10
CC	GO:1902554	serine/threonine protein kinase complex	89/19559	2,47E-23	3,96E-22	1,43E-22	10
CC	GO:1902911	protein kinase complex	104/19559	1,27E-22	1,35E-21	4,90E-22	10
CC	GO:0061695	transferase complex, transferring phosphorus-containing groups	253/19559	1,19E-18	9,55E-18	3,46E-18	10
CC	GO:0016592	mediator complex	41/19559	0,000232991	0,00149114	0,000539557	2
CC	GO:0005667	transcription regulator complex	413/19559	0,001359362	0,007249931	0,00262333	3
CC	GO:0005923	bicellular tight junction	122/19559	0,002045718	0,009133296	0,003304811	2
CC	GO:0070160	tight junction	129/19559	0,002283324	0,009133296	0,003304811	2
CC	GO:0043296	apical junction complex	143/19559	0,002795933	0,009941094	0,003597106	2
CC	GO:0000781	chromosome, telomeric region	164/19559	0,003657089	0,011702685	0,004234524	2
CC	GO:0000805	X chromosome	10/19559	0,005611085	0,016323157	0,005906406	1
CC	GO:0045120	pronucleus	16/19559	0,008963982	0,023903953	0,008649457	1
CC	GO:0031965	nuclear membrane	301/19559	0,011845092	0,02915715	0,010550284	2
CC	GO:0098687	chromosomal region	350/19559	0,015783984	0,035727952	0,012927877	2
CC	GO:0000803	sex chromosome	30/19559	0,016747477	0,035727952	0,012927877	1
MF	GO:0016538	cyclin-dependent protein serine/threonine kinase regulator activity	50/18352	2,35E-16	7,29E-15	3,22E-15	7

Hoang T, Nguyen M, Chen W, Zhuang C, Wang Z, Wang H, Li J, Lin H. Elevated expression of SKP2 correlates with poor prognosis in osteosarcoma: a bioinformatics analysis. *Biomed. Res. Ther.*, 2021; 8(12):4782-4792.

MF	GO:0019887	protein kinase regulator activity	185/18352	3,01E-12	3,90E-11	1,72E-11	7
MF	GO:0030332	cyclin binding	30/18352	3,77E-12	3,90E-11	1,72E-11	5
MF	GO:0019207	kinase regulator activity	216/18352	9,00E-12	6,98E-11	3,08E-11	7
MF	GO:0004693	cyclin-dependent protein serine/threonine kinase activity	29/18352	1,65E-09	8,51E-09	3,75E-09	4
MF	GO:0097472	cyclin-dependent protein kinase activity	29/18352	1,65E-09	8,51E-09	3,75E-09	4
MF	GO:0008353	RNA polymerase II CTD heptapeptide repeat kinase activity	12/18352	3,51E-08	1,56E-07	6,87E-08	3
MF	GO:0035173	histone kinase activity	17/18352	4,42E-05	0,000171289	7,56E-05	2
MF	GO:0004674	protein serine/threonine kinase activity	435/18352	9,00E-05	0,000310064	0,00013687	4
MF	GO:0004861	cyclin-dependent protein serine/threonine kinase inhibitor activity	12/18352	0,007171155	0,022230579	0,009813159	1
MF	GO:0070064	proline-rich region binding	18/18352	0,010739172	0,030264938	0,013359735	1
MF	GO:0030291	protein serine/threonine kinase inhibitor activity	31/18352	0,018429918	0,047610622	0,021016574	1
KEGG	hsa04110	Cell cycle	126/8095	8,35E-21	5,18E-19	1,76E-19	11
KEGG	hsa05203	Viral carcinogenesis	204/8095	1,99E-18	6,18E-17	2,10E-17	11
KEGG	hsa04218	Cellular senescence	156/8095	5,73E-17	1,18E-15	4,02E-16	10
KEGG	hsa05169	Epstein-Barr virus infection	202/8095	8,08E-16	1,25E-14	4,25E-15	10
KEGG	hsa04115	p53 signaling pathway	73/8095	4,76E-15	5,91E-14	2,01E-14	8
KEGG	hsa05222	Small cell lung cancer	92/8095	3,28E-14	3,39E-13	1,15E-13	8
KEGG	hsa05165	Human papillomavirus infection	331/8095	1,47E-11	1,30E-10	4,42E-11	9
KEGG	hsa05166	Human T-cell leukemia virus 1 infection	222/8095	4,34E-11	3,36E-10	1,14E-10	8
KEGG	hsa04934	Cushing syndrome	155/8095	2,55E-10	1,76E-09	5,97E-10	7
KEGG	hsa05162	Measles	139/8095	9,91E-09	6,14E-08	2,09E-08	6
KEGG	hsa05161	Hepatitis B	162/8095	2,49E-08	1,40E-07	4,77E-08	6
KEGG	hsa04151	PI3K-Akt signaling pathway	354/8095	8,18E-08	4,23E-07	1,44E-07	7
KEGG	hsa05215	Prostate cancer	97/8095	9,72E-08	4,64E-07	1,57E-07	5
KEGG	hsa05226	Gastric cancer	149/8095	8,35E-07	3,70E-06	1,26E-06	5
KEGG	hsa05160	Hepatitis C	157/8095	1,08E-06	4,48E-06	1,52E-06	5
KEGG	hsa05218	Melanoma	72/8095	1,81E-06	6,61E-06	2,24E-06	4
KEGG	hsa05223	Non-small cell lung cancer	72/8095	1,81E-06	6,61E-06	2,24E-06	4
KEGG	hsa05214	Glioma	75/8095	2,14E-06	6,98E-06	2,37E-06	4
KEGG	hsa05212	Pancreatic cancer	76/8095	2,25E-06	6,98E-06	2,37E-06	4
KEGG	hsa05220	Chronic myeloid leukemia	76/8095	2,25E-06	6,98E-06	2,37E-06	4
KEGG	hsa04914	Progesterone-mediated oocyte maturation	102/8095	7,33E-06	2,16E-05	7,35E-06	4
KEGG	hsa05219	Bladder cancer	41/8095	1,93E-05	5,11E-05	1,74E-05	3
KEGG	hsa04068	FoxO signaling pathway	131/8095	1,98E-05	5,11E-05	1,74E-05	4
KEGG	hsa04114	Oocyte meiosis	131/8095	1,98E-05	5,11E-05	1,74E-05	4
KEGG	hsa05206	MicroRNAs in cancer	310/8095	3,05E-05	7,44E-05	2,53E-05	5
KEGG	hsa05224	Breast cancer	147/8095	3,12E-05	7,44E-05	2,53E-05	4
KEGG	hsa05225	Hepatocellular carcinoma	168/8095	5,27E-05	0,00012106	4,11E-05	4

Hoang T, Nguyen M, Chen W, Zhuang C, Wang Z, Wang H, Li J, Lin H. Elevated expression of SKP2 correlates with poor prognosis in osteosarcoma: a bioinformatics analysis. *Biomed. Res. Ther.*, 2021; 8(12):4782-4792.

KEGG	hsa05221	Acute myeloid leukemia	67/8095	8,53E-05	0,000188848	6,41E-05	3
KEGG	hsa05167	Kaposi sarcoma-associated herpesvirus infection	194/8095	9,25E-05	0,000197753	6,71E-05	4
KEGG	hsa05163	Human cytomegalovirus infection	225/8095	0,00016446	0,000339885	0,000115411	4
KEGG	hsa01522	Endocrine resistance	98/8095	0,0002646	0,0005292	0,000179694	3
KEGG	hsa04152	AMPK signaling pathway	120/8095	0,000480626	0,000931214	0,000316202	3
KEGG	hsa05216	Thyroid cancer	37/8095	0,001089466	0,002046875	0,000695034	2
KEGG	hsa05202	Transcriptional misregulation in cancer	192/8095	0,001883304	0,003434261	0,001166133	3
KEGG	hsa05213	Endometrial cancer	58/8095	0,002662247	0,004715981	0,001601352	2
KEGG	hsa05210	Colorectal cancer	86/8095	0,005765608	0,009929658	0,0033717	2
KEGG	hsa04933	AGE-RAGE signaling pathway in diabetic complications	100/8095	0,007727771	0,012949238	0,004397025	2
KEGG	hsa04921	Oxytocin signaling pathway	154/8095	0,017670273	0,028830445	0,009789625	2
KEGG	hsa04630	JAK-STAT signaling pathway	162/8095	0,019444484	0,030911743	0,010496347	2
KEGG	hsa04530	Tight junction	169/8095	0,021057072	0,032638462	0,01108267	2
KEGG	hsa05164	Influenza A	172/8095	0,021765106	0,032913088	0,011175921	2
KEGG	hsa05205	Proteoglycans in cancer	205/8095	0,03019939	0,044580052	0,015137539	2

Hoang T, Nguyen M, Chen W, Zhuang C, Wang Z, Wang H, Li J, Lin H. Elevated expression of SKP2 correlates with poor prognosis in osteosarcoma: a bioinformatics analysis. *Biomed. Res. Ther.*, 2021; 8(12):4782-4792.