

Figure S1 Identification report of cell lines and lentiviral vector. (A,B) Electrophoretogram of Hep3b and Huh7 cell line authentication, respectively. (C,D) Diagram of kinesin family member 2C and short hairpin RNA lentivirus vectors.

Table S1 The primer sequence

| Gene | forward | reverse |
|-------------------|-----------------------------|-----------------------------|
| <i>KIF2C</i> | 5'-TGGGTCTAGGCAGGGTCTGA-3' | 5'-TGAGGGCGACAACCTGAGGA-3' |
| <i>GAPDH</i> | 5'-AGGCCGGTGCTGAGTATGTC-3' | 5'-TGCCTGCTTCACCACCTTCT-3' |
| <i>E-cadherin</i> | 5'-TTAACAGGAACACAGGAGTC-3' | 5'-GGATTGAAGATCGGAGGATT-3' |
| <i>N-cadherin</i> | 5'-CATCATCCTGCTTATCCTT-3' | 5'-AGTCATAGTCCTGGTCTTCT-3' |
| <i>Slug</i> | 5'-CAAGGACACATTAGAACTCAC-3' | 5'-GAGACATTCTGGAGAAGGTT-3' |
| <i>Snail</i> | 5'-CCAATCGGAAGCCTAACTAC-3' | 5'-CAGAGTCCCAGATGAGCATT-3' |
| <i>Vimentin</i> | 5'-TACATCGACAAGGTGCGCTT-3' | 5'-CTCCTCCTGCAATTTCTCCCG-3' |

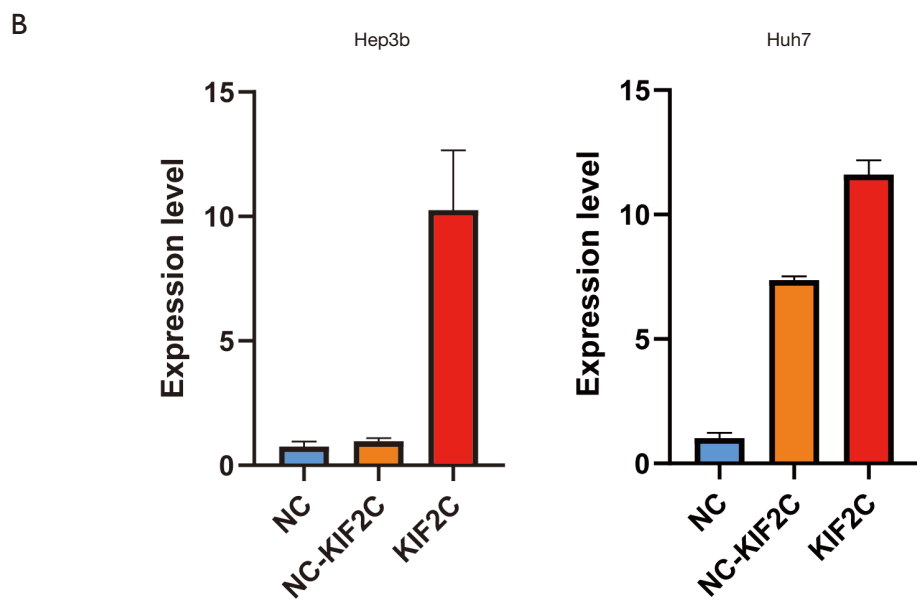
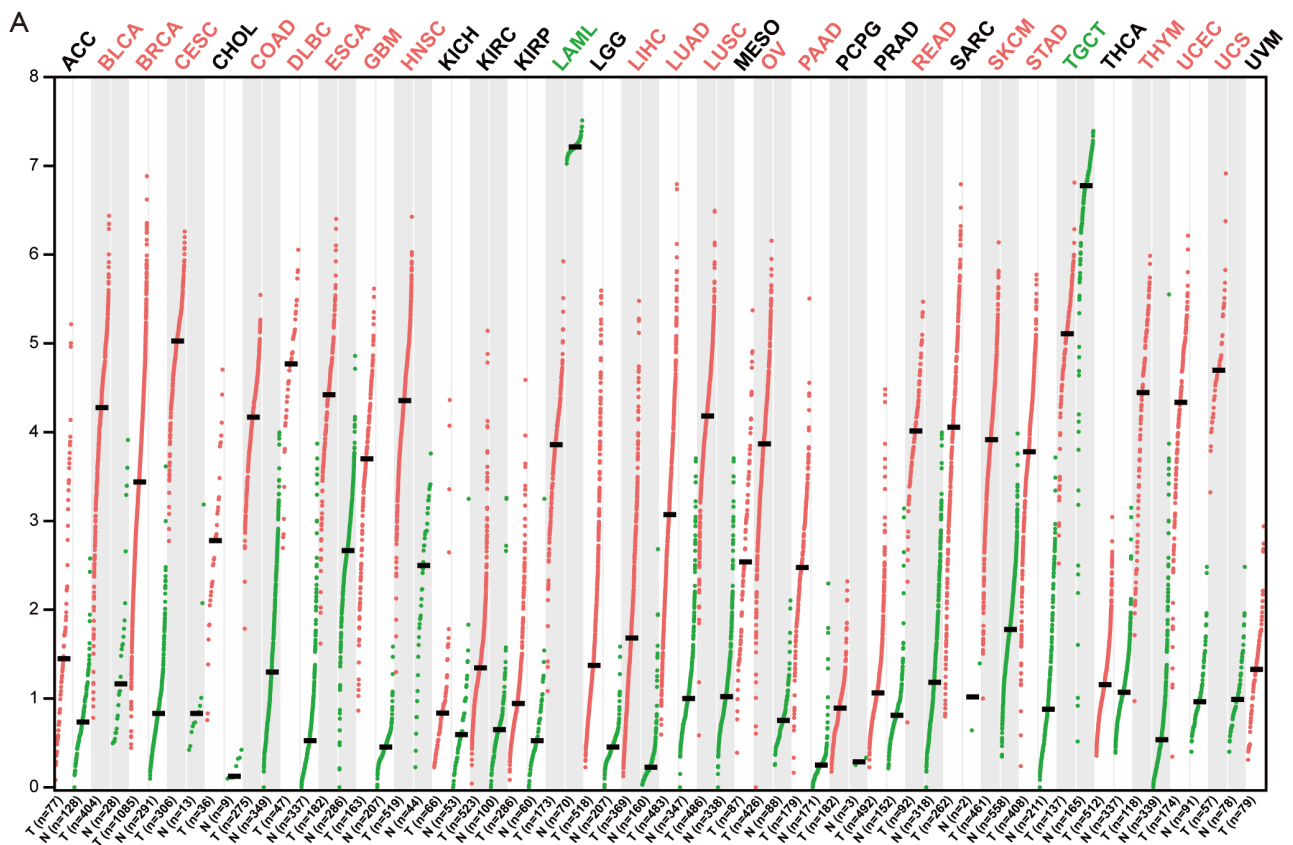


Figure S2 *KIF2C* expression level in pan-cancer and lentivirus overexpression efficiency (A) Expression level of *KIF2C* in different tumors. (B) Real-time polymerase chain reaction results for expression of *KIF2C* in overexpressed Hep3b and Huh7 cell lines. *KIF2C*, kinesin family member 2C; NC, negative control.

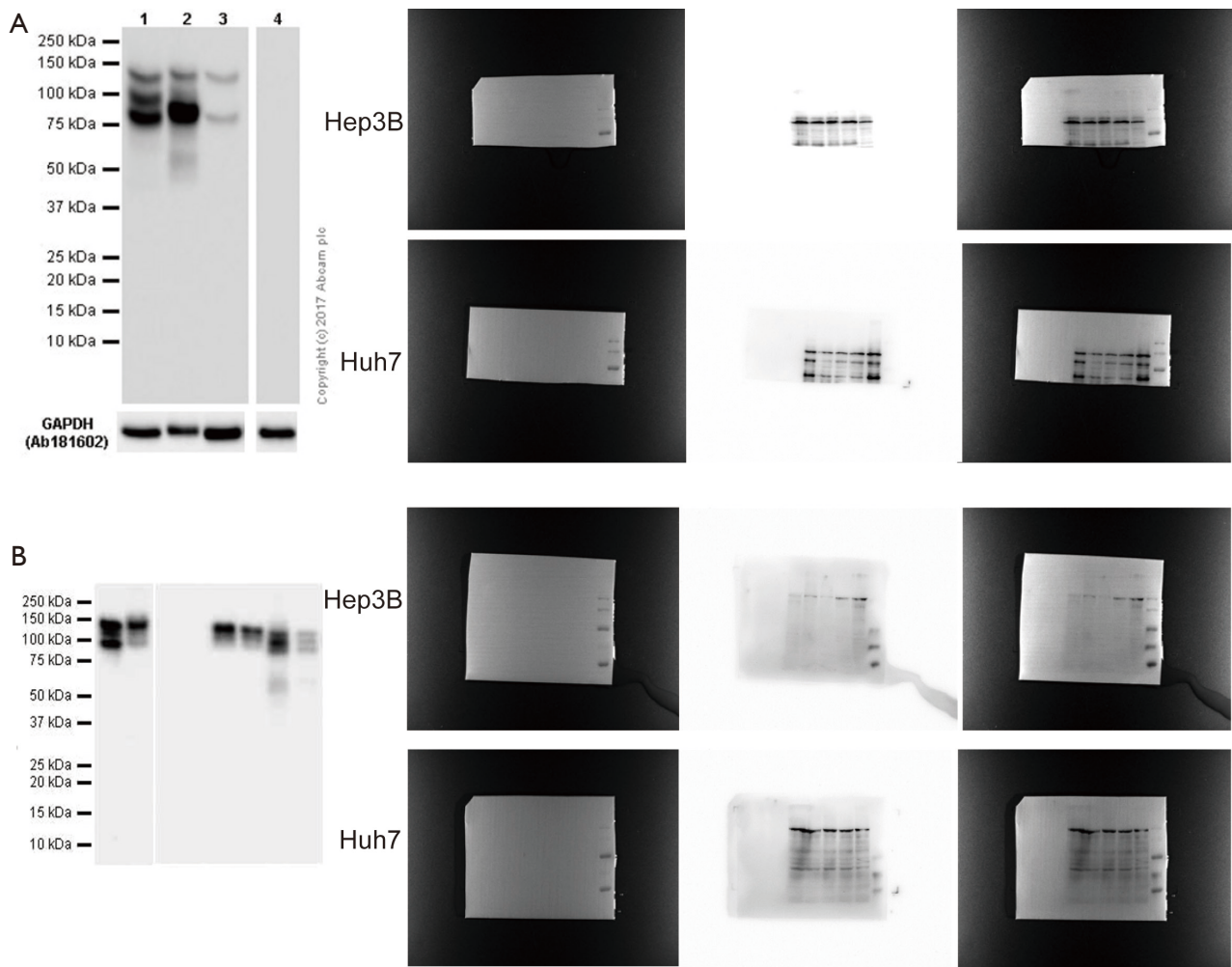


Figure S3 Official and original images of western blot. (A) Official and original E-cadherin bands of Western blot and was found in the range of 80–125 kDa; (B) official and original N-cadherin bands of Western blot and was found in 125 and 170 kDa, respectively.

Table S2 Results of KEGG pathway analysis of mRNA

| KEGG pathway term ID | KEGG pathway term description | Rich ratio | P value |
|----------------------|--|------------|----------|
| 4512 | ECM-receptor interaction | 0.039683 | <0.001 |
| 4151 | PI3K-Akt signaling pathway | 0.019011 | 0.001095 |
| 4010 | MAPK signaling pathway | 0.019048 | 0.003447 |
| 4974 | Protein digestion and absorption | 0.038095 | 0.003497 |
| 4510 | Focal adhesion | 0.021053 | 0.00693 |
| 4928 | Parathyroid hormone synthesis, secretion, and action | 0.028169 | 0.010067 |
| 4014 | Ras signaling pathway | 0.019169 | 0.010718 |
| 5200 | Pathways in cancer | 0.013643 | 0.011387 |
| 140 | Steroid hormone biosynthesis | 0.036585 | 0.012721 |
| 590 | Arachidonic acid metabolism | 0.036585 | 0.012721 |
| 5031 | Amphetamine addiction | 0.034884 | 0.014454 |
| 3320 | PPAR signaling pathway | 0.029703 | 0.022096 |
| 4060 | Cytokine-cytokine receptor interaction | 0.016173 | 0.022854 |
| 4015 | Rap1 signaling pathway | 0.018315 | 0.023082 |
| 5418 | Fluid shear stress and atherosclerosis | 0.020202 | 0.030058 |
| 4662 | B-cell receptor signaling pathway | 0.025641 | 0.032251 |
| 4380 | Osteoclast differentiation | 0.019048 | 0.036141 |
| 4657 | IL-17 signaling pathway | 0.023256 | 0.041214 |
| 4933 | AGE-RAGE signaling pathway in diabetic complications | 0.022901 | 0.042817 |
| 5224 | Breast cancer | 0.018018 | 0.042888 |
| 600 | Sphingolipid metabolism | 0.033898 | 0.04776 |
| 5146 | Amoebiasis | 0.021898 | 0.047814 |
| 5030 | Cocaine addiction | 0.032787 | 0.050698 |
| 4913 | Ovarian steroidogenesis | 0.031746 | 0.053699 |
| 5202 | Transcriptional misregulation in cancer | 0.015326 | 0.069385 |
| 460 | Cyanoamino acid metabolism | 0.076923 | 0.07435 |
| 480 | Glutathione metabolism | 0.025316 | 0.079779 |
| 5221 | Acute myeloid leukemia | 0.022727 | 0.09585 |
| 430 | Taurine and hypotaurine metabolism | 0.058824 | 0.096106 |
| 4927 | Cortisol synthesis and secretion | 0.022472 | 0.097689 |
| 4810 | Regulation of actin cytoskeleton | 0.013514 | 0.098895 |
| 4917 | Prolactin signaling pathway | 0.022222 | 0.099539 |
| 5165 | Human papillomavirus infection | 0.010969 | 0.105775 |
| 4260 | Cardiac muscle contraction | 0.020619 | 0.112751 |
| 5226 | Gastric cancer | 0.014778 | 0.119386 |
| 1230 | Biosynthesis of amino acids | 0.019231 | 0.126388 |
| 4145 | Phagosome | 0.012232 | 0.129157 |
| 5218 | Melanoma | 0.018868 | 0.130355 |
| 5133 | Pertussis | 0.018692 | 0.132349 |
| 4012 | ErbB signaling pathway | 0.018349 | 0.136358 |
| 1521 | EGFR tyrosine kinase inhibitor resistance | 0.018018 | 0.140395 |
| 4630 | Jak-STAT signaling pathway | 0.013699 | 0.140612 |
| 5210 | Colorectal cancer | 0.017857 | 0.142423 |
| 4360 | Axon guidance | 0.013453 | 0.146108 |
| 5410 | Hypertrophic cardiomyopathy | 0.017544 | 0.146498 |

KEGG, Kyoto Encyclopedia of Genes and Genomes; ECM, extracellular matrix; PI3K, phosphoinositide 3-kinase; MAPK, mitogen-activated protein kinase; PPAR, peroxisome proliferator-activated receptor- γ ; IL, interleukin; AGE, advanced glycation end products; RAGE, receptor for advanced glycation end products; EGFR, epidermal growth factor receptor.

Table S3 Results of KEGG pathway analysis of long non-coding RNA

| KEGG pathway term ID | KEGG pathway term description | Rich ratio | P value |
|----------------------|--|-------------|-------------|
| 3060 | Protein export | 0.066666667 | <0.001 |
| 4974 | Protein digestion and absorption | 0.019047619 | 0.009187952 |
| 72 | Synthesis and degradation of ketone bodies | 0.071428571 | 0.01924159 |
| 4614 | Renin-angiotensin system | 0.033333333 | 0.04079921 |
| 650 | Butanoate metabolism | 0.02173913 | 0.06190407 |
| 4014 | Ras signaling pathway | 0.006389776 | 0.0691404 |
| 565 | Ether lipid metabolism | 0.019230769 | 0.06970352 |
| 5230 | Central carbon metabolism in cancer | 0.012345679 | 0.1065363 |
| 140 | Steroid hormone biosynthesis | 0.012195122 | 0.1077813 |
| 5217 | Basal cell carcinoma | 0.011764706 | 0.1115061 |
| 4111 | Yeast cell cycle | 0.00990099 | 0.1311227 |
| 310 | Lysine degradation | 0.009803922 | 0.1323349 |
| 562 | Inositol phosphate metabolism | 0.009803922 | 0.1323349 |
| 5212 | Pancreatic cancer | 0.009090909 | 0.1419746 |
| 4972 | Pancreatic secretion | 0.009090909 | 0.1431724 |
| 5210 | Colorectal cancer | 0.008928571 | 0.1443685 |
| 3008 | Ribosome biogenesis in eukaryotes | 0.007874016 | 0.1621207 |
| 4916 | Melanogenesis | 0.007874016 | 0.1621207 |
| 4666 | Fc gamma R-mediated phagocytosis | 0.007633588 | 0.1667949 |
| 4070 | Phosphatidylinositol signaling system | 0.007407407 | 0.1714442 |
| 4114 | Oocyte meiosis | 0.005882353 | 0.2110827 |
| 4919 | Thyroid hormone signaling pathway | 0.005681818 | 0.2176935 |
| 4310 | Wnt signaling pathway | 0.005263158 | 0.2329137 |
| 4550 | Signaling pathways regulating pluripotency of stem cells | 0.005235602 | 0.23399 |
| 4390 | Hippo signaling pathway | 0.005208333 | 0.2350648 |
| 4072 | Phospholipase D signaling pathway | 0.005076142 | 0.2404174 |
| 5226 | Gastric cancer | 0.004926108 | 0.2467933 |
| 4150 | mTOR signaling pathway | 0.004830918 | 0.2510155 |
| 4934 | Cushing's syndrome | 0.004807692 | 0.2520675 |
| 5224 | Breast cancer | 0.004504505 | 0.2666484 |
| 4360 | Axon guidance | 0.004484305 | 0.2676794 |
| 5200 | Pathways in cancer | 0.002728513 | 0.2702418 |
| 5225 | Hepatocellular carcinoma | 0.004385965 | 0.2728139 |
| 3013 | RNA transport | 0.004048583 | 0.2920133 |
| 4141 | Protein processing in endoplasmic reticulum | 0.004048583 | 0.2920133 |
| 4020 | Calcium signaling pathway | 0.00390625 | 0.300938 |
| 4015 | Rap1 signaling pathway | 0.003663004 | 0.3175035 |
| 5205 | Proteoglycans in cancer | 0.003571429 | 0.3242151 |
| 5164 | Influenza A | 0.003546099 | 0.3261211 |
| 5016 | Huntington's disease | 0.003533569 | 0.3270721 |
| 4080 | Neuroactive ligand-receptor interaction | 0.00295858 | 0.3774527 |
| 4010 | MAPK signaling pathway | 0.002380952 | 0.445933 |
| 4144 | Endocytosis | 0.002314815 | 0.4553301 |
| 5166 | HTLV-I infection | 0.002237136 | 0.4668626 |
| 5165 | Human papillomavirus infection | 0.001828154 | 0.5379964 |

KEGG, Kyoto Encyclopedia of Genes and Genomes; MAPK, mitogen-activated protein kinase; mTOR, mammalian target of rapamycin.

Table S4 Results of KEGG pathway analysis of miRNA

| KEGG pathway term ID | KEGG pathway term description | Rich ratio | P value |
|----------------------|--|-------------|-------------|
| 4011 | MAPK signaling pathway—yeast | 0.069767442 | 0.004472886 |
| 4714 | Thermogenesis | 0.022012579 | 0.01195188 |
| 4723 | Retrograde endocannabinoid signaling | 0.027777778 | 0.0131002 |
| 4070 | Phosphatidylinositol signaling system | 0.02962963 | 0.02090116 |
| 592 | Alpha-linolenic acid metabolism | 0.064516129 | 0.02392995 |
| 4660 | T-cell receptor signaling pathway | 0.027586207 | 0.02632254 |
| 5213 | Endometrial cancer | 0.035294118 | 0.02833318 |
| 4391 | Hippo signaling pathway—fly | 0.034883721 | 0.02919557 |
| 591 | Linoleic acid metabolism | 0.057142857 | 0.03001341 |
| 4071 | Sphingolipid signaling pathway | 0.024539877 | 0.03803573 |
| 4926 | Relaxin signaling pathway | 0.024390244 | 0.03876129 |
| 4664 | Fc epsilon RI signaling pathway | 0.030612245 | 0.04061433 |
| 5223 | Non-small cell lung cancer | 0.03030303 | 0.04165402 |
| 1524 | Platinum drug resistance | 0.02970297 | 0.04377343 |
| 4138 | Autophagy—yeast | 0.02970297 | 0.04377343 |
| 4919 | Thyroid hormone signaling pathway | 0.022727273 | 0.04808599 |
| 4624 | Toll and IMD signaling pathway | 0.041666667 | 0.05333537 |
| 5210 | Colorectal cancer | 0.026785714 | 0.05636666 |
| 4960 | Aldosterone-regulated sodium reabsorption | 0.04 | 0.05735102 |
| 4068 | FoxO signaling pathway | 0.020942408 | 0.06133822 |
| 565 | Ether lipid metabolism | 0.038461538 | 0.06146856 |
| 1100 | Metabolic pathways | 0.010920437 | 0.06518307 |
| 5132 | Salmonella infection | 0.025 | 0.06648798 |
| 5205 | Proteoglycans in cancer | 0.017857143 | 0.06683517 |
| 740 | Riboflavin metabolism | 0.1 | 0.0748772 |
| 5034 | Alcoholism | 0.019230769 | 0.07845541 |
| 564 | Glycerophospholipid metabolism | 0.022900763 | 0.08165378 |
| 5231 | Choline metabolism in cancer | 0.022222222 | 0.08750878 |
| 4724 | Glutamatergic synapse | 0.02189781 | 0.09050143 |
| 4978 | Mineral absorption | 0.03030303 | 0.09281642 |
| 4014 | Ras signaling pathway | 0.015974441 | 0.09634893 |
| 5215 | Prostate cancer | 0.021126761 | 0.09816741 |
| 4010 | MAPK signaling pathway | 0.014285714 | 0.1082272 |
| 4530 | Tight junction | 0.016736402 | 0.1150601 |
| 4270 | Vascular smooth muscle contraction | 0.019607843 | 0.1159115 |
| 510 | N-glycan biosynthesis | 0.025974026 | 0.1199953 |
| 4370 | VEGF signaling pathway | 0.025641026 | 0.1225561 |
| 1522 | Endocrine resistance | 0.01910828 | 0.1226449 |
| 4722 | Neurotrophin signaling pathway | 0.01875 | 0.1277874 |
| 561 | Glycerolipid metabolism | 0.024691358 | 0.1303174 |
| 4062 | Chemokine signaling pathway | 0.015873016 | 0.132303 |
| 590 | Arachidonic acid metabolism | 0.024390244 | 0.1329296 |
| 4976 | Bile secretion | 0.024096386 | 0.1355538 |
| 603 | Glycosphingolipid biosynthesis—globo and isoglobo series | 0.052631579 | 0.1374972 |
| 4140 | Autophagy—animal | 0.008728943 | 0.1394996 |

KEGG, Kyoto Encyclopedia of Genes and Genomes; MAPK, mitogen-activated protein kinase; VEGF, vascular endothelial growth factor.