

Figure S1. DEGs identified between LPS and NF tissues. A total of 855 DEGs were extracted from the GSE21122 expression profile dataset, of which 334 were upregulated genes and 521 were downregulated genes. The grey points represent genes with an $FDR \geq 0.05$ or $|\log FC| < 1$. The red dots represent genes with an $FDR < 0.05$ and $|\log FC| > 1$. DEG, differentially expressed gene; FDR, false discovery rate; LPS, liposarcoma; NF, normal fatty; FC, fold change.

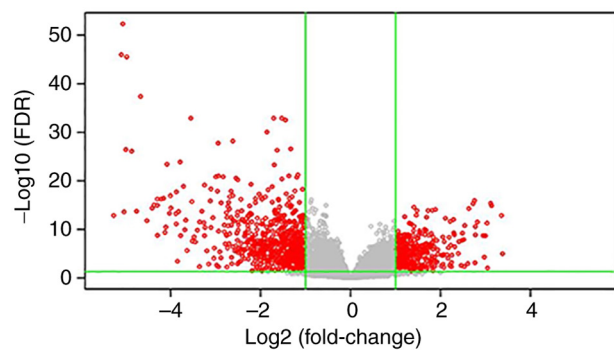


Figure S2. TYMS expression in RLPS tissues and its association with survival of patients with RLPS. (A) TYMS mRNA expression in 21 RLPS tissues and 10 NF tissues was assessed using reverse transcription-quantitative PCR. Relative mRNA expression of TYMS was notably higher in RLPS tissues compared NF tissues. *** $P < 0.001$. (B) Representative images of TYMS expression in RLPS tissues. TYMS protein was predominantly localized in the cytoplasm. Magnification: Left, $\times 100$; right, $\times 400$. Patients with RLPS with positive TYMS expression had (C) a low OS ($P = 0.024$) and (D) DFS ($P = 0.030$) time compared with those with negative TYMS expression. TYMS, thymidylate synthase; RLPS, retroperitoneal soft tissue sarcoma; NF, normal fatty; T, RLPS tissue; N, NF tissue; OS, overall survival; DFS, disease-free survival.

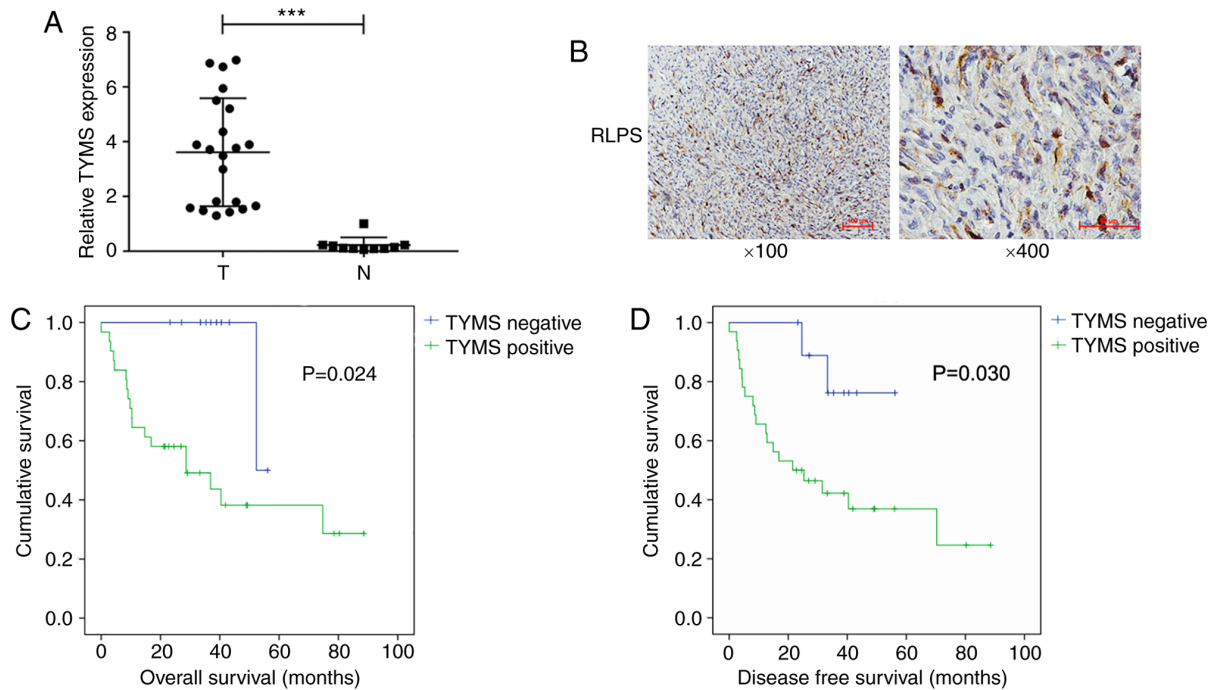


Figure S3. Association between TYMS expression and survival of patients with sarcoma from the GEPIA database. Survival curves of TYMS in the GEPIA database showed that sarcoma patients with TYMS-high expression had (A) low OS ($P=0.0065$) and (B) DFS ($P=0.019$) time compared with those with TYMS-low expression. TPM, Transcripts per million reads; TYMS, thymidylate synthase; OS, overall survival; DFS, disease free survival.

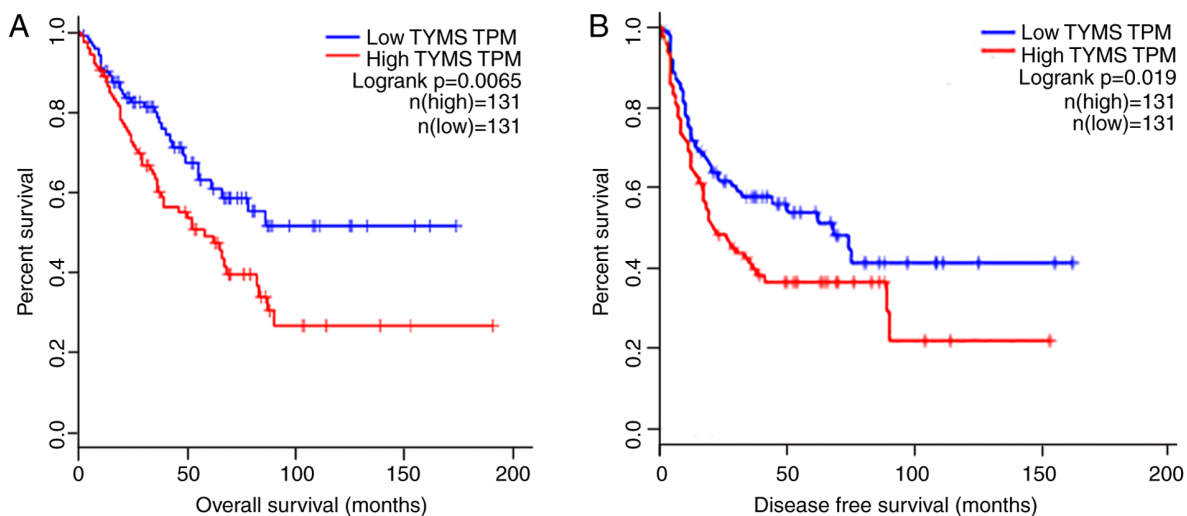


Figure S4. Expression of TYMS in RLPS cells before and after knockdown. (A) TYMS protein expression was evaluated using western blotting in three RLPS cell lines. The TYMS protein expression levels were considerably high in all three RLPS cell lines, particularly in 93T449 and SW872 cells. (B) Localization of TYMS protein was detected using immunofluorescence. It was predominantly located in the cytoplasm in all three human RLPS cell lines, consistent with the immunohistochemistry results. Scale bar, 20 μ m. Magnification, x630. (C) Control cells were transfected with lentiviral vectors containing Lenti-shCtrl and experimental cells were transfected with one of two different shTYMS shRNAs. TYMS mRNA expression levels in Lenti-shTYMS cells were significantly lower compared with Lenti-shCtrl cells in 93T449, 94T778 and SW872 infected cells. ***P<0.001. (D) Downregulation of TYMS protein expression was confirmed by western blotting. TYMS, thymidylate synthase; RLPS, retroperitoneal soft tissue sarcoma; sh, short hairpin.

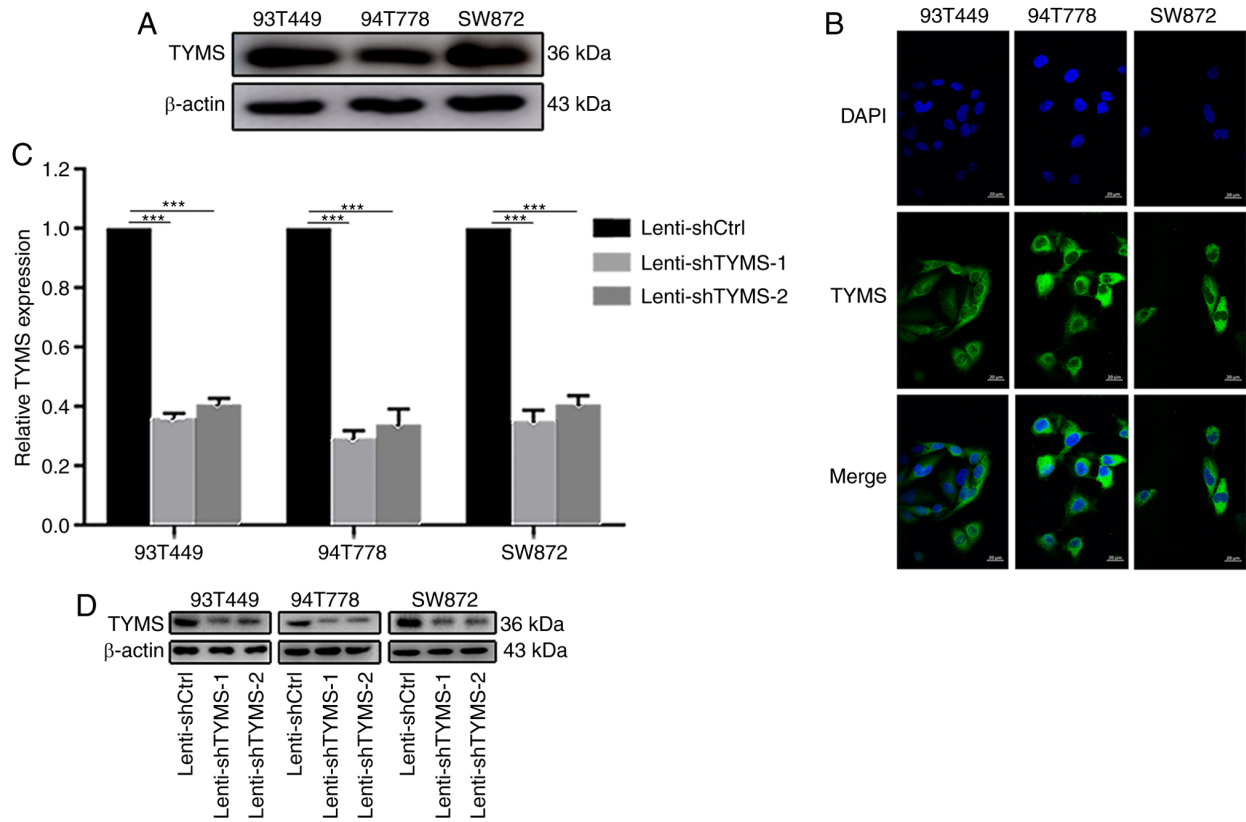


Figure S5. Knockdown of TYMS increases apoptosis of RLPS cells. (A) Apoptosis of cells was assessed by TUNEL assay. Nuclei were counterstained with DAPI. Representative images show apoptotic DNA staining (red) and the corresponding nuclei staining (blue). Scale bar, 100 μ m. (B) Lenti-shTYMS cells exhibit increased apoptosis compared with Lenti-shCtrl cells. ** $P < 0.01$. *** $P < 0.001$. TYMS, thymidylate synthase; RLPS, retroperitoneal soft tissue sarcoma; sh, short hairpin.

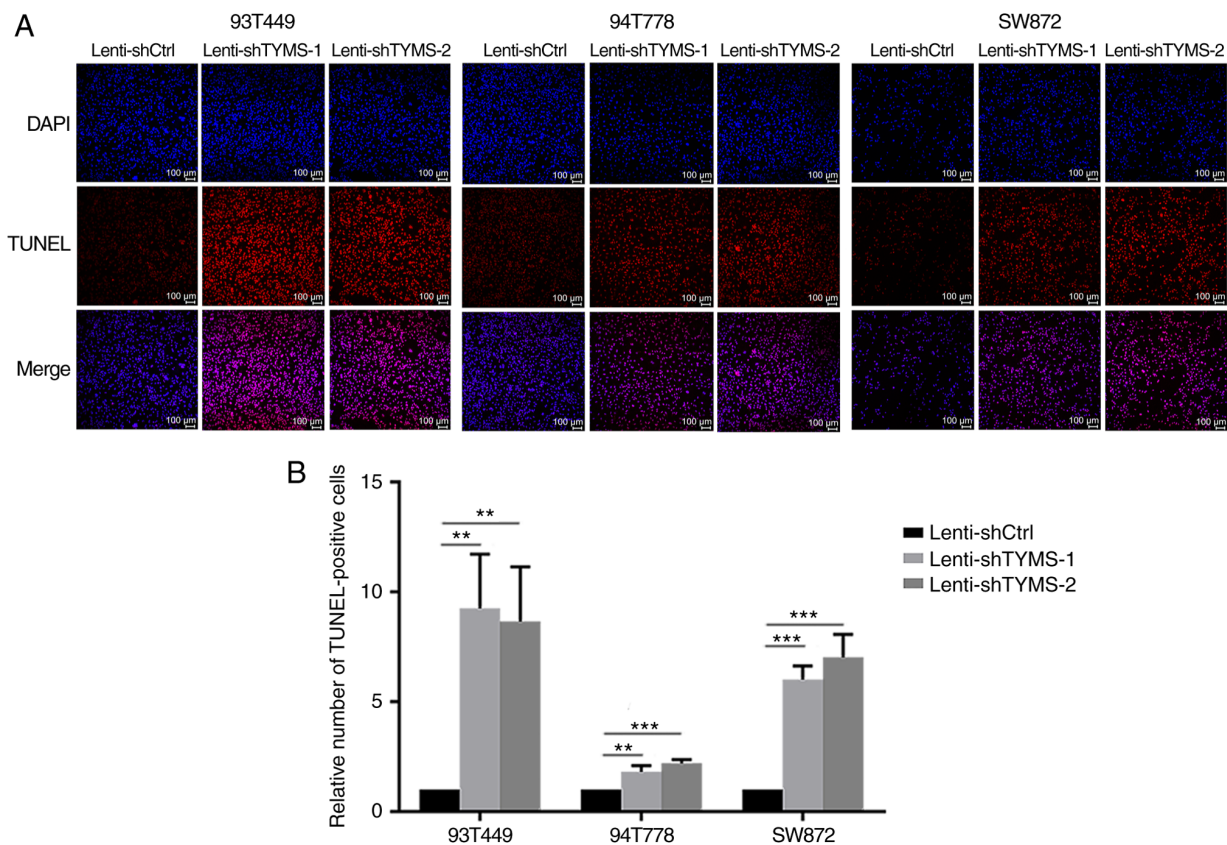


Figure S6. TYMS knockdown may reduce the activity of the JAK/STAT signaling pathway in RLPS cells. This assay was performed using protein microarray analysis. The results are shown for (A) 94T778 and (B) SW872 cells. Downregulation of phospho-STAT3 (Ser727), phospho-STAT5 (Y694), and phospho-STAT6 (Y641) in Lenti-shTYMS infected 94T778 and SW872 cells was observed (marked by the red frame). *P<0.05. **P<0.01. TYMS, thymidylate synthase; sh, short hairpin; RLPS, retroperitoneal soft tissue sarcoma; JAK/STAT, Janus kinase/signal transducers and activators of transcription.

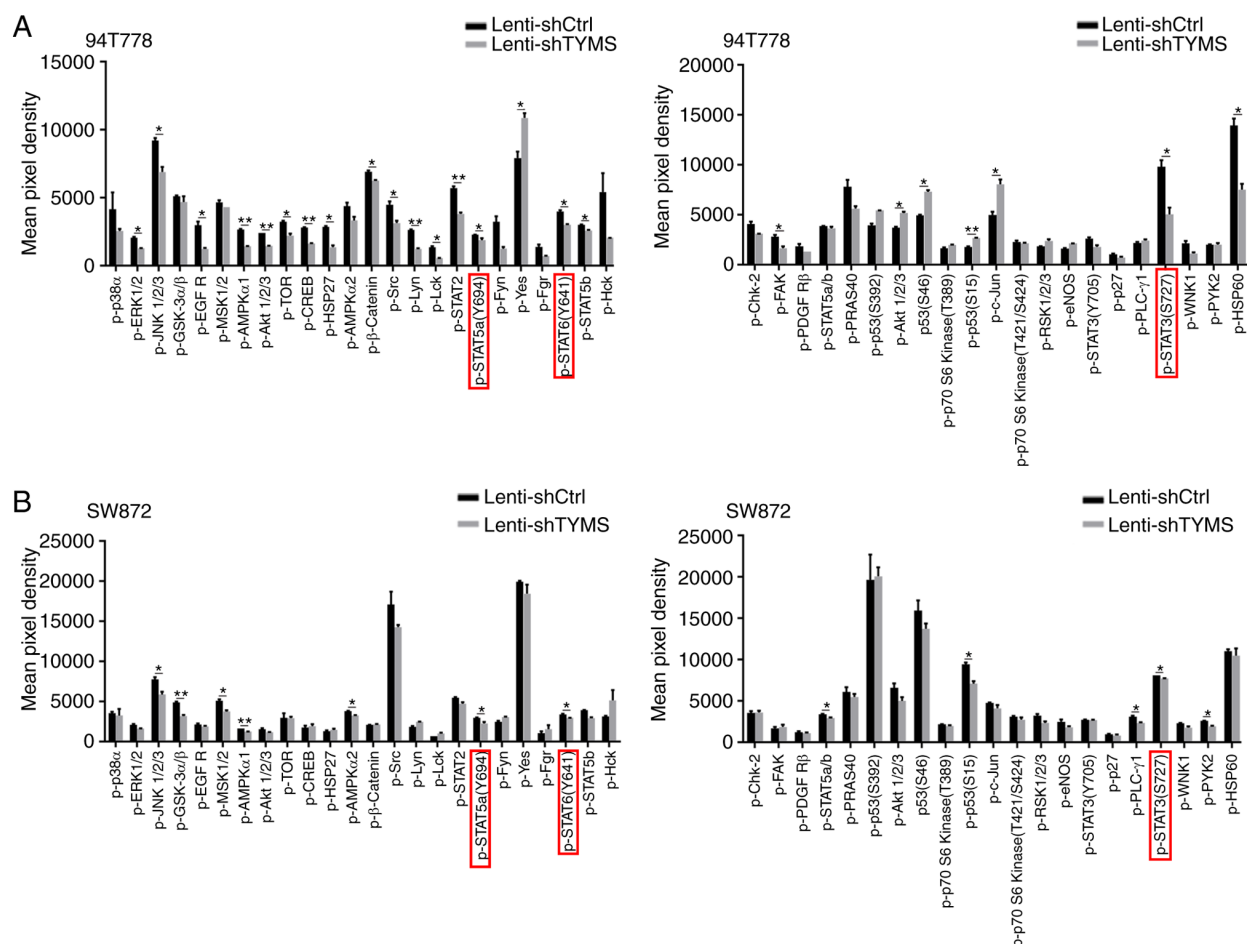


Figure S7. Quantitative data of phosphorylated bands in western blot analysis. The gray value of western blotting bands in Fig. 5 was analyzed. For each phosphorylated protein a normalization to its respective non-phosphorylated control is shown. * $P < 0.05$. ** $P < 0.01$. *** $P < 0.001$. TYMS, thymidylate synthase; p-, phosphorylated; sh, short hairpin.

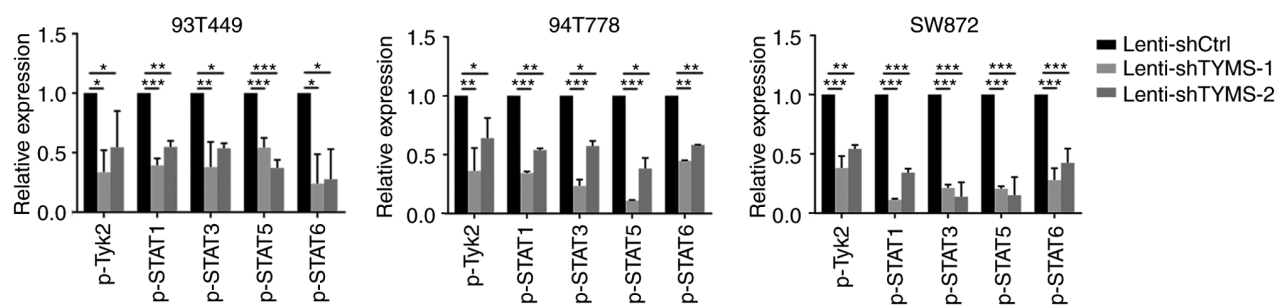


Table SI. Primer sequences used for quantitative-PCR.

Gene name	Sense	Antisense
GAPDH	F: 5'-TGA CTTCAACAGCGACACCCA-3'	R: 5'-CAC CCTGTTGCTGTAGCCAAA-3'
CKS2	F: 5'-TTCGACGAACACTACGAGTACC-3'	R: 5'-GGACACCAAGTCTCCTCCAC-3'
TYMS	F: 5'-CTGCTGACAACCAAACGTGTG-3	R: 5'-GCATCCCAGATTTTCACTCCCTT-3'
KIAA0101	F: 5'-CTCTGCCACTAATTCGACATCA-3'	R: 5'-TTCAGAATCTTTAGGGGACAAC-3'
SERPINE2	F: 5'-AACGCCGTGTTTGTGAAGAATG-3'	R: 5'-CGTGATTTCACAGACCCTTG-3'
RRM2	F: 5'-AAGAAACGAGGACTGATGC-3'	R: 5'-CTGTCTGCCACAACTCAA-3'
COL5A1	F: 5'-GATGGCAAGTGGCACAGAA-3'	R: 5'-CGGTGGTCCGAGACAAAGA-3'
RACGAP1	F: 5'-TCCTTGCCTCTGGAGTATTG-3'	R: 5'-AAGTTGCCTTGTCTGCTCTA-3'
ZWINT	F: 5'-CACGTAGAGGCCATCAAAATTGG-3'	R: 5'-CGGAGTTGTGTCCGTTTCCT-3'
COL3A1	F: 5'-TTGCTGTGGTGGTGTGG-3'	R: 5'-GCATCCTTGGTTAGGGTCA-3'
MXRA5	F: 5'-AGGGCCAAGAGAGCAAATCC-3'	R: 5'-GGCGTAATCTCCTTCTCCCG-3'
VCAN	F: 5'-TCACTCTAATCCCTGTCGTAATG-3'	R: 5'-ATGTCTCGGTATCTTGCTCAC-3'
DTL	F: 5'-TAAAAGCTGGTGAGCTGATTGG-3'	R: 5'-TCTTCCACCCGTACAGAATACA-3'
MFAP2	F: 5'-CGCCGTGTGTACGTCATTAAC-3'	R: 5'-CCATCACGCCACATTTGGA-3'
SNAI2	F: 5'-TGTGACAAGGAATATGTGAGCC-3'	R: 5'-ACCTGTCTGCAAATGCTCTG-3'
TRO	F: 5'-TGGTGGCAATCTCATTGGCAG-3'	R: 5'-TGTCAACCGGCCTAAGAAAAG-3'
COL5A2	F: 5'-CCACCAATCACCTAATACAGCC-3'	R: 5'-ATTTGCCCTTTGAGAACCAC-3'
PCOLCE	F: 5'-GCCGTGACTGTCAGTCTTATTG-3'	R: 5'-CTTCCTCTTGCTTAGGTTGGT-3'
SOX4	F: 5'-ACTTCGAGTTCCCGGACTACT-3'	R: 5'-TGAAAACCAAGGTTGGAGATGC-3'
CKAP2	F: 5'-GCAAGATGCTAACATGCCCAA-3'	R: 5'-TGGCTTTAGGTATAGTGGCTGA-3'
SEPT6	F: 5'-AACTGAAGATAGGCAACAAGA-3'	R: 5'-CGGCATACAGCTCATAGTG-3'
TIAM1	F: 5'-TAGTGCTCCTCGCTCTCC-3'	R: 5'-CTGTATTATGCTGACCGCTTC-3'
MELK	F: 5'-TATTCACCTCGATGATGATTGCG-3'	R: 5'-AGAAAGCCTTAAACGAACCTGGTT-3'
FSCN1	F: 5'-GGGCGGTTGATGAGCTTCA-3'	R: 5'-CTGCTACTTTGACATCGAGTGG-3'
RFC4	F: 5'-ATAATTGAACCCCTGACCTCTA-3'	R: 5'-TGTCTAGTAATCGCTGCTGTTG-3'
TIA1	F: 5'-GATGCCCCGAGTGGTAAAAGAC-3'	R: 5'-CCCATCTGTTGAATGGCGTTT-3'
MARCKS	F: 5'-GGGTGCCAGTTCTCCAA-3'	R: 5'-CTCCTGTCCGTTTCGCTTT-3'
ADAM12	F: 5'-GTTGGTAGGCGTGGAAGTGT-3'	R: 5'-GGGATTTGCGAGGTAGAAGC-3'
TMSB15A	F: 5'-GTTTCCTTTGAGGGAAGAG-3'	R: 5'-TTGTCGGAAGTGGAGAAGT-3'
HELLS	F: 5'-GAAGGCATGGAATGGCTTAG-3'	R: 5'-CCAGTTAGGAAGTGTAGACAAAGG-3'
TPX2	F: 5'-TCCTGCCCCGAGTGACTAAGG-3'	R: 5'-CTGTTAGGGGTTTCGTTTATGGAA-3'
MAGED1	F: 5'-GAAGACAGCGCCTTGCTTATG-3'	R: 5'-GTGGCCTGGTTAGTAGGTGG-3'
UBE2C	F: 5'-GATGTCTGGCGATAAAGGG-3'	R: 5'-TGATAGCAGGGCGTGAGGA-3'
KIF20A	F: 5'-TTGAGGGTTAGGCCCTTGTTA-3'	R: 5'-GTCCTTGGGTGCTTGTAGAAC-3'
BUB1B	F: 5'-AACTCTGTTGGCACTTGA-3'	R: 5'-GTCCTCTGTTCTGGCTTG-3'
GIN51	F: 5'-ACGAGGATGGACTCAGACAAG-3'	R: 5'-TGCAGCGTCGATTTCTTAACA-3'
PTTG1	F: 5'-AAATGGAGAACCAGGCACC-3'	R: 5'-GCATCATCTGAGGCAGGAA-3'
LMNB1	F: 5'-AATGGGAGGCTGGGAGATGAT-3'	R: 5'-TGGTTCTTCCAGATGAGGTCAGTT-3'
PKM	F: 5'-GCCATAATCGTCCTCACCAAGT-3'	R: 5'-GCACGTGGGCGGTATCTG-3'
CCNB2	F: 5'-CAACCCACCAAAAACAACA-3'	R: 5'-AGAGCAAGGCATCAGAAA-3'
GMNN	F: 5'-GGCAGAAGTAGCAGAACAT-3	R: 5'-GCATCCGTAGAGGAAGATA-3'

F, forward; R, reverse.

Table SII. Sequences of the short hairpin RNAs.

Target gene	Sequence (5' to 3')
Negative control	TTCTCCGAACGTGTACAGT
ADAM12	CTGAATCGTCAATGTCAAA TCGCAAATCCCATGACAA GAGATGAGAGATGCTAAAT
CKS2	ACATATTCTTCTCTTTAGA TGGTGTCCAACAGAGTCTA GCATGTTATGTTACCCAGA
RACGAP1	TTGATGAATCTGGTTCCAT AGGACGACAAGGCAACTTT CGCCTGCATGACTTTGTTT
RRM2	GAGGAGAGAGTAAGAGAAA TCAAGAAACGAGGACTGAT AGATGTATAAGAAGGCAGA
COL5A1	TCTATTGGATTCCCTGGAT GTATGATGACCTCACCTAT AGACCTATTACTACGAATA
TMSB15A	AACCTATCCAGCAAGAGAAA TGTCATAATCTCACCATT ACAGCAGATTTTCGACATTA
MAGED1	AGATGAAAGTGCTGAGATT GAATGTAAATCAGGCCAAA TCCAGAATGCCACCACAAA
LMNB1	CTTGAAGAACACTTCTGAA ATGAGAATTGAGAGCCTTT CAGATCAAGCTTCGAGAAT
CCNB2	CAAGAATGTGGTGAAAGTA AGTCCATAAACCCACATTT ACTATGATATGGTGCATTA
SERPINE2	TTGATTCATCAAAGGCCAAA ACACAAAGAAACGCACCTTT GCGTAAATGGAGTTGGTAA
KIF20A	CAGAAGAATATAAGGCTGT AGTGCAAAGCAGAGCTAAA GTTCCCTGCATGATTGTCAA
BUB1B	TCAGAAAGCATCACCTCAA AGTGTACCTTTCTCCATTT GACAACATAAAGTCAAATT
PTTG1	CTTCAATCCTCTAGACTTT TTACCTAAAGCTACTAGAA TTCAATCAAAGCCTTAGAT
SNAI2	CATTCTGATGTAAAGAAAT GCTGTAAATACTGTGACAA CGGATACTCCTCATCTTTG
FSCN1	ACTATAACAAGGTGGCCAT AGTTTGTGACCTCCAAGAA CGCCTTCCAGGACCAGCGCTA
TPX2	AGCCTATTGGCTTTGATTT TTTGAGAAAGGCTAATCTT CTGTAATCATCGATGAAAT
CKAP2	ACCTCCTATTAGAAGTCAT GCATTTGTTACTAACTGAA CAGCCCAAAGAAACCTCGGAA
RFC4	GAAGTCTATTATCACAGAA TGACCTCTAGATGTTCAAA ATCTGATGAACGTGGAATA
SEPT6	TGCTGATTTCGGGTCAACAT

Table SII. Continued.

Target gene	Sequence (5' to 3')
UBE2C	ATTTCTGAAGAGTGAGCTAA AATCCATGTCTGCTTGTAT CCCAACATTGATAGTCCCTTG
ZWINT	ACCTGCAAGAAACCTACTCAA CTGTATAGGACTCTTTATCTT CCAGAGGAAACGGACACAA
PCOLCE	CAGGAGAAGCATCTGCAGCAT GAGGCTGAGGCAGAGAATCTT AAGAAAGGAGTCAGTTATC
MFAP2	CCGTGACTGTCAGTCTTAT CTGACCTTCGAGAAGTTTG CACCCACTATAGCGACCAGAT
KIAA0101	CTCCATACACAGGCCTTGCAA GTTCTCCAAATGTGGCGTGAT TTTGTGTAACAGGCATTTA
GMNN	AACCTGATCACACAAATGA CATCAGTTTCATCGAGGAA GGATAATCAGGAATTTGAT
COL5A2	AGGAGTCATTTGATCTTAT GCAGAACATGTACAGTATA GTTGAAATTGGGCCAGTTT
MELK	GGCCACCTTACAGCTGCTCTT GGCCAGTAAATCTCCTGACAA GAGCATGGGCATACTGTTATA
TIA1	AACCAGTTCGTTTAAGGCTTT GTGGAATTGGATCTCAACCAA TATGAATGGACGGAAGATA
PKM	AGCCCAGAAATTACAACCTGAA AGGGATATGGCTTTGTCTCCT AGCAAGAAGGGTGTGAACCTT
TYMS	GTTCCGAGGTTTGATGAAATC GCCCCAGGCTTCTTCAAGAAG TGTCCTGACCTATCAGTTAT
	ATCCCACGTACTTATAAAGAA GAGGGAGCTGAGTAACACCAT

Table SIII. Information on antibodies used for western blotting.

Gene name	Catalog number	Company	Diluted concentration	Type	Species reactivity
β -actin	A4552	Sigma	1:20,000	Monoclonal	Mouse anti-human
TYMS	ab108995	Abcam	1:1,000	Monoclonal	Rabbit anti-human
Stat1	9172	Cell Signaling Technology, Inc.	1:1,000	Monoclonal	Rabbit anti-human
Stat3	4904	Cell Signaling Technology, Inc.	1:1,000	Monoclonal	Rabbit anti-human
Stat5	94205	Cell Signaling Technology, Inc.	1:1,000	Monoclonal	Rabbit anti-human
Stat6	5397	Cell Signaling Technology, Inc.	1:1,000	Monoclonal	Rabbit anti-human
Phospho-Stat1	7649	Cell Signaling Technology, Inc.	1:1,000	Monoclonal	Rabbit anti-human
Phospho-Stat3	9134	Cell Signaling Technology, Inc.	1:1,000	Monoclonal	Rabbit anti-human
Phospho-Stat5	4322	Cell Signaling Technology, Inc.	1:1,000	Monoclonal	Rabbit anti-human
Phospho-Stat6	9361	Cell Signaling Technology, Inc.	1:1,000	Monoclonal	Rabbit anti-human
Jak1	3344	Cell Signaling Technology, Inc.	1:1,000	Monoclonal	Rabbit anti-human
Tyk2	14193	Cell Signaling Technology, Inc.	1:1,000	Monoclonal	Rabbit anti-human
Phospho-Tyk2	68790	Cell Signaling Technology, Inc.	1:1,000	Monoclonal	Rabbit anti-human
Anti-mouse IgG	7076	Cell Signaling Technology, Inc.	1:5,000	Monoclonal	Goat anti-mouse
Anti-rabbit IgG	7074	Cell Signaling Technology, Inc.	1:5,000	Monoclonal	Goat anti-rabbit

Table SIV. List of 855 DEGs extracted from the expression profile dataset of GSE21122 (344 up-regulated genes and 521 down-regulated genes).

DEGs	Gene symbol
Upregulated	RACGAP1, KIAA0101, ZWINT, TYMS, QKI, COL3A1, CKAP2, RFC4, MAGED1, HMGN1, CKS2, DNAJC9, KIAA0907, DTL,RRM2, NREP,TUBB, CBX3,RSRP1, SMC4, ANP32E, NUSAP1, LUC7L3, SEPT8, CBX1, MCM5, DDOST, MCM2, CDK1, MARCKS, PCNA, SMARCC1, SUZ12P1, SUZ12, GINS1, SP3, ATP8B1, COL5A1, TIPRL, ZWILCH, BRD8, ZIC1, S100PBP, ZNF146, DCP2, CSE1L, COL5A2, BIRC5, CENPU, CEP170, POLE2, P3H1, MAGED2, EDRF1, EXTL2, PRC1, N4BP2L2, SPDL1, SUGP2, ST5, ZBED5, NUP43, XPO1, TOP2A, LIG1, SOX4, TMED3, CDK14, TRO, MELK, PHTF2, METTL3, FSCN1, CDC23, ITGB3BP, DR1, MCM6, MAGED4B, MAGED4, ACYP1, LOC100272216, ERBB2IP, RBM26, HELLS, TMF1, ORC5, FANCL, MFAP2, CCNB2, GMNN, HNRNPDL, TIA1, APP, CCNA2, TPX2, MCM4, MAD2L1, VCAN, EZH2, USP1, SNAI2, C5orf15, OGT, SMC1A, LMNB1, HMGB3, MBD4, BARD1, HSPB11, NT5DC2, GINS2, EVL, NACA, PTTG1, PRKDC, LOC105369253, CROCCP2, PCOLCE, KIF4A, FUBP1, DNMT1, PRPS2, NOTCH2NL, CENPE, MAST2, RMI1, UBE2C, BAX, HSPA13, GPX7, BUB1B, FMR1, GLT8D1, RRM1, SERPINH1, P3H4, KDELR2, MDK, HOMER3, PTK7, KIF20A, TMPO, PKM, WSB1, MARCKSL1, FKBP10, FZD2, CDC7, H2AFZ, PLOD1, GTF2H2B, CALU, GOLM1, MXRA5, SMARCA4, HMMR, WLS, COL1A1, PSME2, NEMP1, FEN1, ASPM, FANCI, PSRC1, KPNA2, LMNB2, ZBED8, COL6A1, STMN1, SLC2A10, IFI44, ANKRD36B, RFC3, KIF2C, PNISR, TTK, TRIP13, SQLE, HS2ST1, BMP1, UBE2SP1, UBE2S, PNN, ZNF302, C3orf14, HLTF, CKAP4, SERPINE2, CDKN3, WNT5A, DONSON, NPIPA2, NPIPB5, LOC101060275, NPIPB4, NPIPB3, NPIPA3, NPIPB11, LOC105376851, NPIPB1P, CALR, CCNB1, KNTC1, GGH, CDKN2A, KIF15, CDC20, MMP14, DLGAP5, KDELC1, TMEM97, CENPF, LAPTM4B, TMSB15B, CD47, HNRNPA3, LOC100506123, LOC100506076, GUCY1B3, CDC25B, RPL31, HMGB2, FAM46A, SAC3D1, TARDBP, TIAM1, SEPT6, GLYR1, PFN2, NINL, SDC1, SUCO, PSD3, ADAM12, EMILIN1, FOXM1, SHOX2, ARMCX2, SEC24D, EFS, H1FO, TSPYL4, TMSB15A, AURKA, CDK4, NID2, MEX3D, NUCB2, RBBP4, CEP55, THY1, SMC2, SKP2, PRRC2C, FKBP14, RAI14, GPSM2, RPS21, CD24, ADD3, PPP1R3C, MLLT11, SHMT2, TDO2, GPC4, BTBD3, ROBO1, PLK2, PNMAL1, CRABP2, PNMA2, PTPRD, SYNJ2, ADCY1, DYRK2, FAM3C, PEG10, PIEZO2, METTL21B, FOXD1, LBH, COL1A2, COL16A1, PTN, IFI6, TRIL, MMP2, OLFML2B, LRRC17, LOXL1, COL6A2, DLK1, CCT2, BGN, CXCL10, MDM1, METTL1, TMEM45A, TMEM158, FN1, SEMA5A, COL21A1, HOXA10-HOXA9, HOXA9, USP32P2, PLXDC1, CA12, SOX9, CNOT2, VASH2, DPYSL3, FGFR2, ISG15, ATP1B1, CDH11, LOX, DKK3, FZD1, ENO2, DDIT3, MEG3, FAP, SOX11, FZD7, TSFM, GDF15, AGT, MDM2, ALCAM, SLC35E3, DDX17, PLAGL1, P4HA2, EMX2
Downregulated	SLC19A3, SAA2-SAA4, SAA1, SAA2, CIDEA, CALB2, KCNIP2, GLYAT, APOB, PFKFB1, RDH5, BLOC1S1-RDH5, SNCG, PPP1R1A, CIDEA, C10orf10, GYG2, LOC101929726, CLSTN2, RETSAT, AGPAT2, NQO1, S100A1, PDE2A, HCAR3, MAOA, SLC7A6, AQP7, SAA4, COBLL1, DHRS12, TNS1, ALDH2, PGA4, PGA5, PGA3, NIPSNAP3B, TM7SF2, TIMP4, ARHGEF15, SOCS3, FADS3, MARC1, SIK2, C2CD2, C6, MOCS1, FAM47E-STBD1, STBD1, EIF5, LIPE, SYN2, HBG1, ALDH1L1, PRELP, ALDH4A1, MRAS, HSPB7, UVRAG, GPD5, HBB, ECHDC3, ADIRF, TF, HOOK2, FOSB, ALDOC, ABHD5, ADRBK2, STAT5B, SLC04A1, PLIN1, AZGP1, AZGP1P1, MMD, EMP1, CTIF, VTI1B, SELP, CYB5A, FASN, FGF2, SEMA3G, PISD, TMBIM1, ADRA2A, FAM107A, ADCK3, MAOB, LINC00312, MAPT, PFKFB3, EIF4EBP2, CX3CL1, BTG2, PRKAR2B, EIF1, ADIPOR2, PPP2R1B, HBG2, EMC3, SPTBN1, PDE3B, NMB, MT1M, GSN, PNPLA2, PPP2R5A, RASIP1, PLA2G16, BHMT2, TST, CXCL2, RBPMS, MMRN2, GPD1L, RNASE4, MTHFD1, ACOX1, BTD, ACKR1, KLF4, ADRB2, FAH, ETFDH, EPAS1, CLMN, HBA1, HBA2, PEX11A, SUCLG1, KIAA0040, SLC29A1, MCAM, GPD1, COX14, CRYAB, QDPR, ITSN1, UGP2, PCK2, PTEN, PTENP1, GABARAPL3, GABARAPL1, IL6, ADGRG1, BCL2L13, S100A8, S100P, TNIP1, SDPR, PTPRF, HRSP12, ACAT1, ECHS1, SCD, CD151, MIR22HG, ACOT2, ACOT1, TYRO3, ZBTB16, CAT, PYGL, GLUL, GOS2, ITPK1, SNN, CES1P1, CES1, AVPI1, BCAP31, PARVA, APOLD1, SYBU, PCBD1, AHNAK, PECR, GHR, PPP1R15A, TACC1, PRKCD, ACO2, POLR2L, CDV3, ANG, DGAT1, MYOC, ELOVL5, PDE8B, MAP7D1, CCNH, LMO3, RHOQ, ABLIM3, ITGA7, ZFAND5, CHP1, ADAMTS9, FHL1, CCL15-CCL14, CCL14, PHLDA3, ACSM5, ESYT1, MMP19, HSDL2, MAFF, RAPGEF3, NMT2, GPX3, S100A9, CDKN1C, TKT, PC, HEBP2, CRHBP, STON1, ZFP36, NDRG2, LYRM1, CCNL1, F8, PTRF, PALMD, MT1G, PPA1, MGLL, BMP2, AKR1C2, WASF3, RGCC, PDZD2, DHRS3, GCLM, CLDN5, CRIM1, EIF4A1, IL1R2, ME1, MARCH2, ARHGEF6, HADH, GPX4, DCXR, KLF11, ADGRF5, TXNIP, RRAS, BNIP3L, MCL1, DMD, LOC105372824, PDXK, CSF3R, OSBPL1A, PRDX6, SOCS2, POLR2E, SERPINB1, FERMT2, EPHX1, PNP, NPR1, CDC42EP4, CCL2, EPB41L4B, AOC3, PDK4, ITGB1BP1, ACSL1, AMOTL2, MT1F, VEGFB, TM4SF1, APMAP, MYC, TJP2, LMCD1, NR4A1, PICALM, MT1HL1, JUNB, SLC31A2, TRIB1, TUBB6, SLC7A10, HBEGF, CFD, LDLR, HSD11B1, MT1H, SLC35G2, TALDO1, LY75-CD302, CD302, TSPAN3, F3, APOD, PALM2-AKAP2, AKAP2, ICA1,

Table SIV. Continued.

DEGs	Gene symbol
	HACD2, IL6ST, ACSS3, MT1X, AKR1C1, PTPN11, LINC01140, RARRES2, KANK1, FCN1, NEDD9, FOS, FYCO1, ALDH6A1, ACO1, FXYP1, ICAM1, ASPH, CBX7, NFU1, MT1E, LINC00341, SYNE3, GADD45B, CA4, TNS2, ETFB, FOXO1, PIM1, PTGER3, TSPAN7, MCF2L, MARC2, IRS2, EGR3, C1orf115, ICAM2, COX7A1, ID4, TMEM140, MAP3K5, TSPAN4, AK4, KLF6, GCLC, MT2A, PPL, SIK1, LOC102724428, TNMD, BCL2, GPRC5A, HSPB2, IER2, MET, ATP9A, LMOD1, CPM, YBX3, SWAP70, ANGPTL4, KLF2, BAG3, CAV2, ATF3, EGR1, CDC37L1, ID1, ETS2, NFKBIA, TLN2, SVEP1, GLRX, SYNPO, VWF, FKBP5, ADM, CALM1, CALM2, GBE1, NPR3, ACACB, ERG, CAV1, STS, METTL7A, DLC1, ALDH1A1, MBD2, WISP2, CDO1, MME, GSTT1, JUND, RHOB, PMEPA1, GSE1, DNAJB1, SLC16A7, TIPARP, KLF9, CD59, LGALS3, GNAI1, CXCL8, CEBPB, AKAP12, TPD52L1, SLC19A2, NDRG1, CEBPA, SELENBP1, CDKN1A, FMO2, NR4A3, SORL1, ELL2, PLOD2, LPL, CCL4, RRAS2, INHBB, HLA-E, DSG2, FPR1, HSPA12A, CITED2, PRKCH, AKR1C3, ADAMTS1, TAGLN, SLC1A3, CHRDL1, CYP26B1, NQO2, NET1, FAM134B, RFTN1, AGTR1, SYNM, ANXA1, HK2, ABLIM1, LYVE1, NAMPT, DUSP1, TMEM135, SQRDL, RTN3, BCL6, ADGRL4, CEBPD, PER1, THBD, PECAM1, JUN, SOD2, LOC100129518, FBLN5, DPT, TIMP3, EDNRB, EGFR, HSPB8, TFPI2, CXCL14, CDH5, TNFRSF21, STEAP1, MYL9, LRRC32, SLC2A3, NFIL3, BNIP3, EMCN, FABP4, PTGDS, PPARG, THBS1, PLN, COPG2IT1, PCDH9, CLU, SRGN, LIMCH1, AMIGO2, TNFAIP3, FZD4, IL1R1, IGFBP6, CD44, RGS5, ITIH5, FGL2, GABRE, PLPP3, ANK2, SERPING1, AQP1, CCL8, ENPP1, EXOSC7, CLEC3B, AOX1, IGF1, NNMT, EFEMP1, IER3, SGK1, FBLN2, C7, FCGR2B, CYR61, CD36, CH25H, ASS1, C3, SLC2A3

DEGs, differentially expressed genes.

Table SV. Expression of 40 upregulated genes selected for study in RLPS cell line 94T778.

Gene	Fold change	P-value	FDR
CKS2	10.24	9.40x10 ¹⁶	1.34x10 ¹³
TYMS	8.78	5.36x10 ¹⁸	1.27x10 ¹⁵
KIAA0101	8.66	1.61x10 ¹⁸	4.17x10 ¹⁶
SERPINE2	7.86	4.13x10 ⁶	5.13x10 ⁵
RRM2	7.06	3.05x10 ¹⁴	2.98x10 ¹²
COL5A1	6.85	2.47x10 ¹¹	1.35x10 ⁹
RACGAP1	6.76	3.69x10 ¹⁹	1.13x10 ¹⁶
ZWINT	6.61	1.91x10 ¹⁸	4.87x10 ¹⁶
COL3A1	6.20	2.38x10 ¹⁷	4.97x10 ¹⁵
MXRA5	5.26	5.44x10 ⁷	8.88x10 ⁶
VCAN	4.99	1.37x10 ⁸	3.64x10 ⁷
DTL	4.89	7.94x10 ¹⁵	9.19x10 ¹³
MFAP2	4.69	5.61x10 ⁹	1.67x10 ⁷
SNAI2	4.52	2.26x10 ⁸	5.60x10 ⁷
TRO	4.24	7.86x10 ¹⁰	3.03x10 ⁸
COL5A2	4.15	7.01x10 ¹¹	3.42x10 ⁹
PCOLCE	3.83	6.96x10 ⁸	1.50x10 ⁶
SOX4	3.78	4.41x10 ¹⁰	1.81x10 ⁸
CKAP2	3.69	3.95x10 ¹⁷	8.07x10 ¹⁵
SEPT6	3.67	3.63x10 ⁵	3.18x10 ⁴
TIAM1	3.60	2.89x10 ⁵	2.63x10 ⁴
MELK	3.55	9.06x10 ¹⁰	3.42x10 ⁸
FSCN1	3.53	1.47x10 ⁹	5.18x10 ⁸
RFC4	3.52	5.72x10 ¹⁷	1.13x10 ¹⁴
TIA1	3.48	7.40x10 ⁹	2.11x10 ⁷
MARCKS	3.47	1.14x10 ¹¹	6.83x10 ¹⁰
ADAM12	3.44	5.58x10 ⁵	4.57x10 ⁴
TMSB15A	3.43	7.89x10 ⁵	6.11x10 ⁴
HELLS	3.38	3.96x10 ⁹	1.23x10 ⁷
TPX2	3.36	8.73x10 ⁹	2.45x10 ⁷
MAGED1	3.30	6.87x10 ¹⁷	1.31x10 ¹⁴
UBE2C	3.26	1.26x10 ⁷	2.49x10 ⁶
KIF20A	3.25	2.87x10 ⁷	5.13x10 ⁶
BUB1B	3.22	1.36x10 ⁷	2.67x10 ⁶
GINS1	3.15	2.03x10 ¹¹	1.15x10 ⁹
PTTG1	3.14	5.65x10 ⁸	1.25x10 ⁶
LMNB1	3.07	3.33x10 ⁸	7.89x10 ⁷
PKM	3.01	3.34x10 ⁷	5.82x10 ⁶
CCNB2	3.01	6.25x10 ⁹	1.84x10 ⁷
GMNN	3.00	6.77x10 ⁹	1.95x10 ⁷

RLPS, retroperitoneal liposarcoma; FDR, false discovery rate.

Table SVI. Thirty genes were detected having with higher gene expression abundance in RLPS cell line 94T778.

Gene	Ct value (GAPDH)	Ct value (target gene)	Δ Ct	Duplicate holes (GAPDH)	Duplicate holes (target gene)
KIAA0101	13.84	23.25	9.41	0.1	0.13
	13.74	23.12	9.38		
	13.78	23.21	9.43		
TIA1	13.84	24.05	10.21	0.1	0.05
	13.74	24.00	10.26		
	13.78	24.01	10.23		
TPX2	13.84	22.46	8.62	0.1	0.16
	13.74	22.62	8.88		
	13.78	22.53	8.75		
TYMS	13.84	22.03	8.19	0.1	0.14
	13.74	21.94	8.20		
	13.78	21.89	8.11		
ZWINT	13.84	23.12	9.28	0.1	0.07
	13.74	23.05	9.31		
	13.78	23.10	9.32		
LMNB1	13.84	25.22	11.38	0.1	0.38
	13.74	25.30	11.56		
	13.78	25.60	11.82		
KIF20A	13.84	24.87	11.03	0.1	0.55
	13.74	25.26	11.52		
	13.78	25.42	11.64		
CKS2	13.84	19.75	5.91	0.1	0.19
	13.74	19.87	6.13		
	13.78	19.94	6.16		
MFAP2	13.84	19.91	6.07	0.1	0.07
	13.74	19.97	6.23		
	13.78	19.98	6.20		
CKAP2	13.84	24.07	10.23	0.1	0.15
	13.74	24.12	10.38		
	13.78	23.97	10.19		
SERPINE2	13.84	22.45	8.61	0.1	0.01
	13.74	22.45	8.71		
	13.78	22.46	8.68		
COL5A2	13.84	19.24	5.40	0.1	0.14
	13.74	19.10	5.36		
	13.78	19.17	5.39		
PCOLCE	13.84	24.99	11.15	0.1	0.15
	13.74	24.85	11.11		
	13.78	24.84	11.06		
COL5A1	13.84	25.28	11.44	0.1	0.29
	13.74	25.19	11.45		
	13.78	25.48	11.70		
RFC4	13.84	23.02	9.18	0.1	0.16
	13.74	23.13	9.39		
	13.78	23.18	9.40		
ADAM12	13.84	24.94	11.10	0.1	0.09
	13.74	24.86	11.12		
	13.78	24.95	11.17		
UBE2C	13.84	20.76	6.92	0.1	0.09
	13.74	20.85	7.11		
	13.78	20.78	7.00		
PTTG1	13.84	18.77	4.93	0.1	0.16
	13.74	18.64	4.90		
	13.78	18.80	5.02		
BUB1B	13.84	25.74	11.90	0.1	0.19
	13.74	25.64	11.90		
	13.78	25.55	11.77		

Table SVI. Continued.

Gene	Ct value (GAPDH)	Ct value (target gene)	Δ Ct	Duplicate holes (GAPDH)	Duplicate holes (target gene)
GMNN	13.84	20.84	7.00	0.1	0.26
	13.74	20.97	7.23		
	13.78	21.10	7.32		
SNAI2	13.84	22.61	8.77	0.1	0.11
	13.74	22.58	8.84		
	13.78	22.69	8.91		
MELK	13.84	23.92	10.08	0.1	0.16
	13.74	24.03	10.29		
	13.78	23.87	10.09		
PKM	13.84	16.63	2.79	0.1	0
	13.74	16.63	2.89		
	13.78	16.63	2.85		
RACGAP1	13.84	21.51	7.67	0.1	0.06
	13.74	21.57	7.83		
	13.78	21.57	7.79		
SEPT6	13.84	22.63	8.79	0.1	0.16
	13.74	22.79	9.05		
	13.78	22.7	8.92		
CCNB2	13.84	21.81	7.97	0.1	0.18
	13.74	21.99	8.25		
	13.78	21.90	8.12		
RRM2	13.84	21.20	7.36	0.1	0.15
	13.74	21.06	7.32		
	13.78	21.21	7.43		
FSCN1	13.84	21.75	7.91	0.1	0.08
	13.74	21.71	7.97		
	13.78	21.67	7.89		
TMSB15A	13.84	24.06	10.22	0.1	0.06
	13.74	24.00	10.26		
	13.78	24.01	10.23		
MAGED1	13.84	20.92	7.08	0.1	0.19
	13.74	20.94	7.20		
	13.78	21.11	7.33		

RLPS, retroperitoneal liposarcoma; Δ Ct, Ct value (target gene)-Ct value (GAPDH).

Table SVII. Knockdown of 16 genes can significantly slow down the proliferation of 94T778 cells.

Group	Fold change (day 5 shCtrl/experimental group)	P-value (day 5 shCtrl vs. experimental group)
shCtrl	1.00	-
shTYMS	1.86	<0.001
shKIF20A	1.65	<0.001
shBUB1B	1.65	<0.001
shTMSB15A	1.58	<0.001
shKIAA0101	1.54	<0.001
shSNAI2	1.44	<0.001
shLMNB1	1.39	<0.001
shTIA1	1.37	<0.001
shTPX2	1.35	<0.001
shRRM2	1.33	<0.001
shPKM	1.32	<0.001
shPTTG1	1.28	<0.001
shCKS2	1.26	<0.001
shZWINT	1.25	<0.001
shMELK	1.18	0.019
shRACGAP1	1.15	0.032

Sh, short hairpin RNA; Ctrl, control.