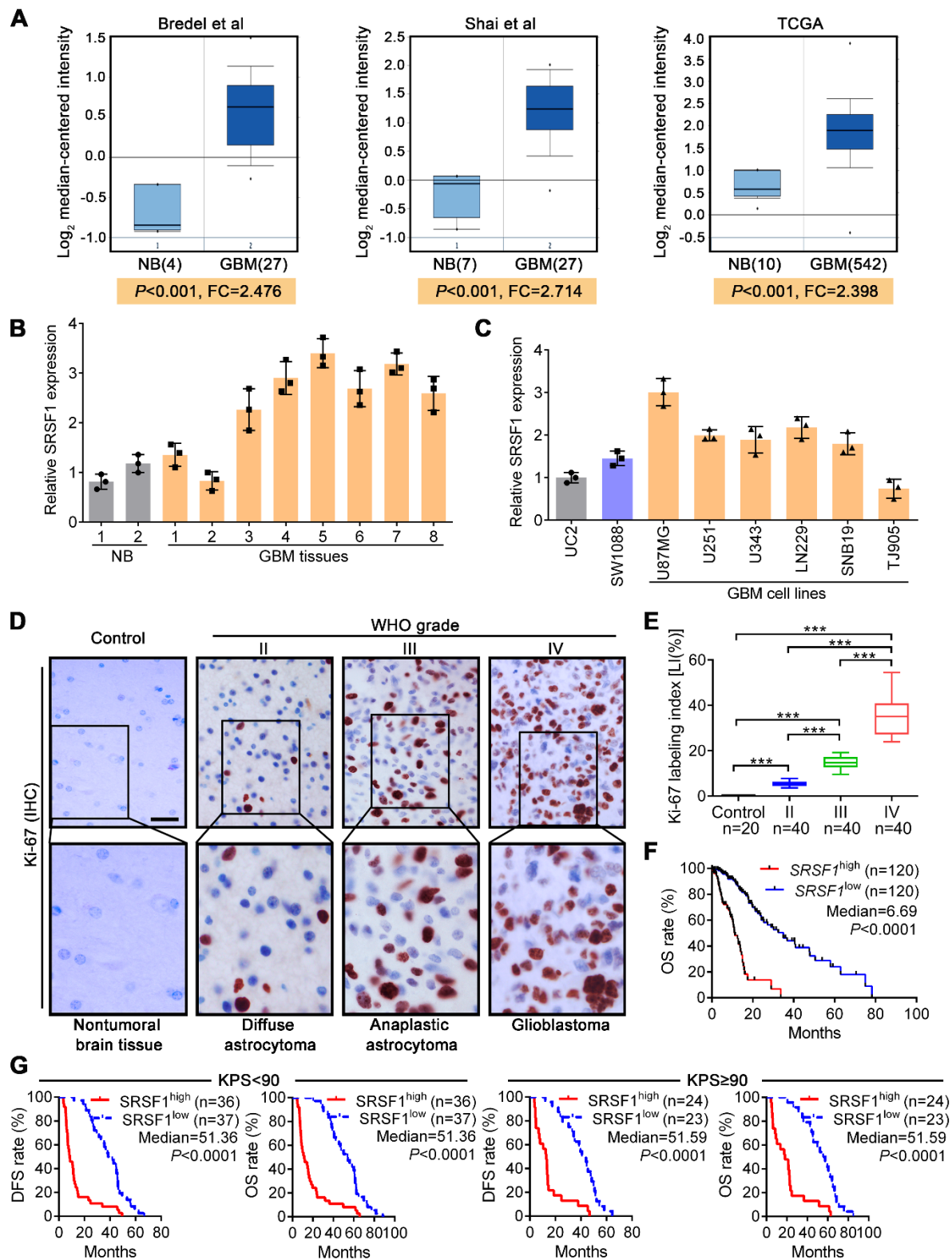


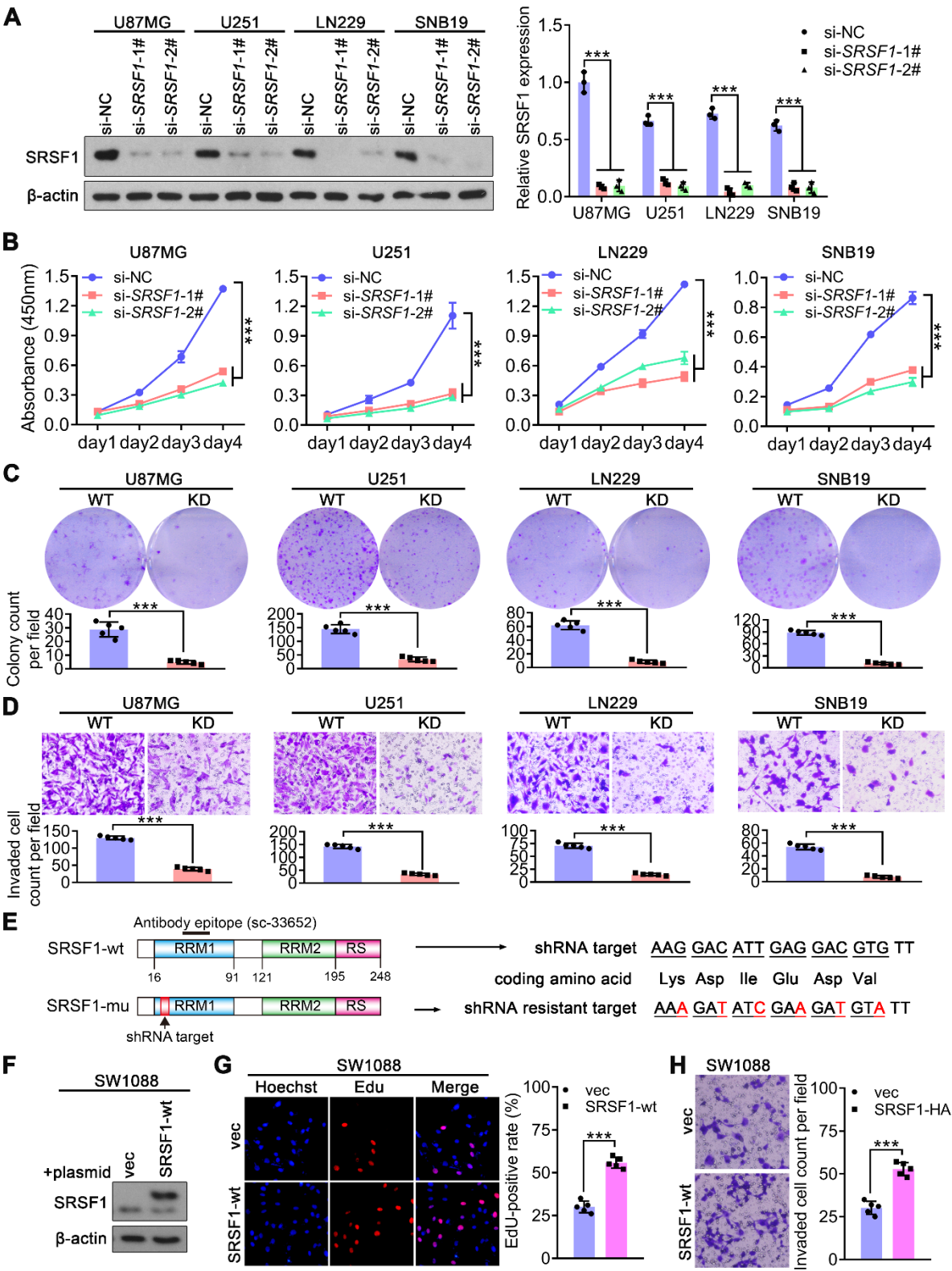
1 Supplemental Figure 1



Supplemental Figure 1. High SRSF1 levels correlate with poor prognoses of glioma

(A) Box plots comparing *SRSF1* mRNA levels between NB and GBM tissues using the data from three published microarray datasets. Boxes represent the 25th and 75th percentiles, lines represent the median, and whiskers show the minimum and maximum points. Oncomine™ (Compendia Bioscience, Ann Arbor, MI) was used for data analysis and visualization. Bredel et al: NB (n=4), GBM (n=27). Shai et al: NB (n=7), GBM (n=27). TCGA: NB (n=10), GBM (n=542). Data are expressed as normalized expression units. $P < 0.001$ by 2-tailed Student's *t* test. FC, fold change. **(B, C)** *SRSF1* protein levels from Figure 1B and 1C were quantified and normalized against those of β -actin. Data are presented as mean $\pm$ SD, n=3. **(D)** IHC staining of Ki-67 in control (nontumoral) and glioma tissues. Scale bar, 20 μ m. **(E)** Comparison of Ki-67 LIs (%) among 20 normal brain tissues and 120 gliomas of various grades. Data are presented as box plots. *** $P < 0.001$ by 1-way ANOVA with Tukey's post-test. **(F)** Kaplan-Meier analysis of the TCGA data. Patients with gliomas (including 120 LGGs and 120 GBMs) were stratified into high and low *SRSF1* expression subgroups using the median of relative *SRSF1* levels. $P < 0.0001$ by log-rank (Mantel-Cox) test. **(G)** Kaplan-Meier analyses of the DFS and OS of our glioma patients with similar KPS (<90 or ≥ 90). Patients were stratified into high and low *SRSF1* expression subgroups using the median of *SRSF1* LIs. $P < 0.0001$ by log-rank (Mantel-Cox) test.

22 **Supplemental Figure 2**

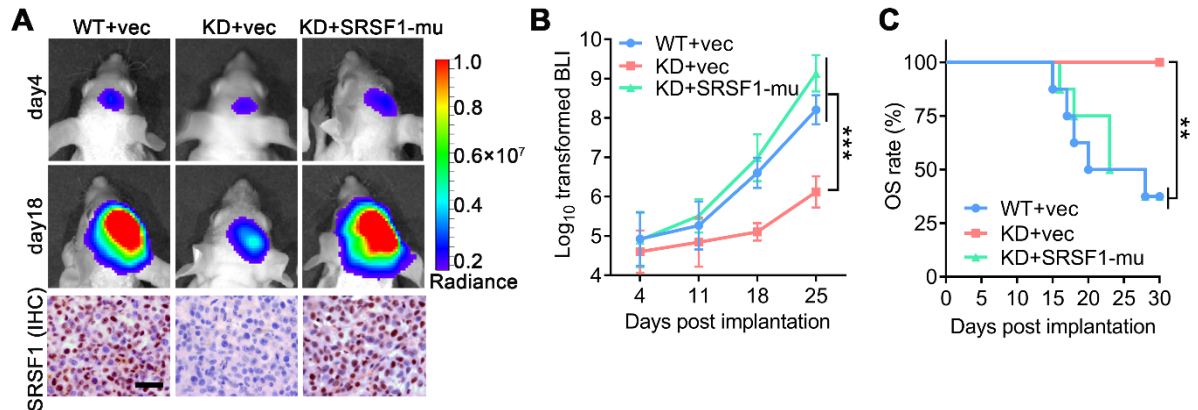


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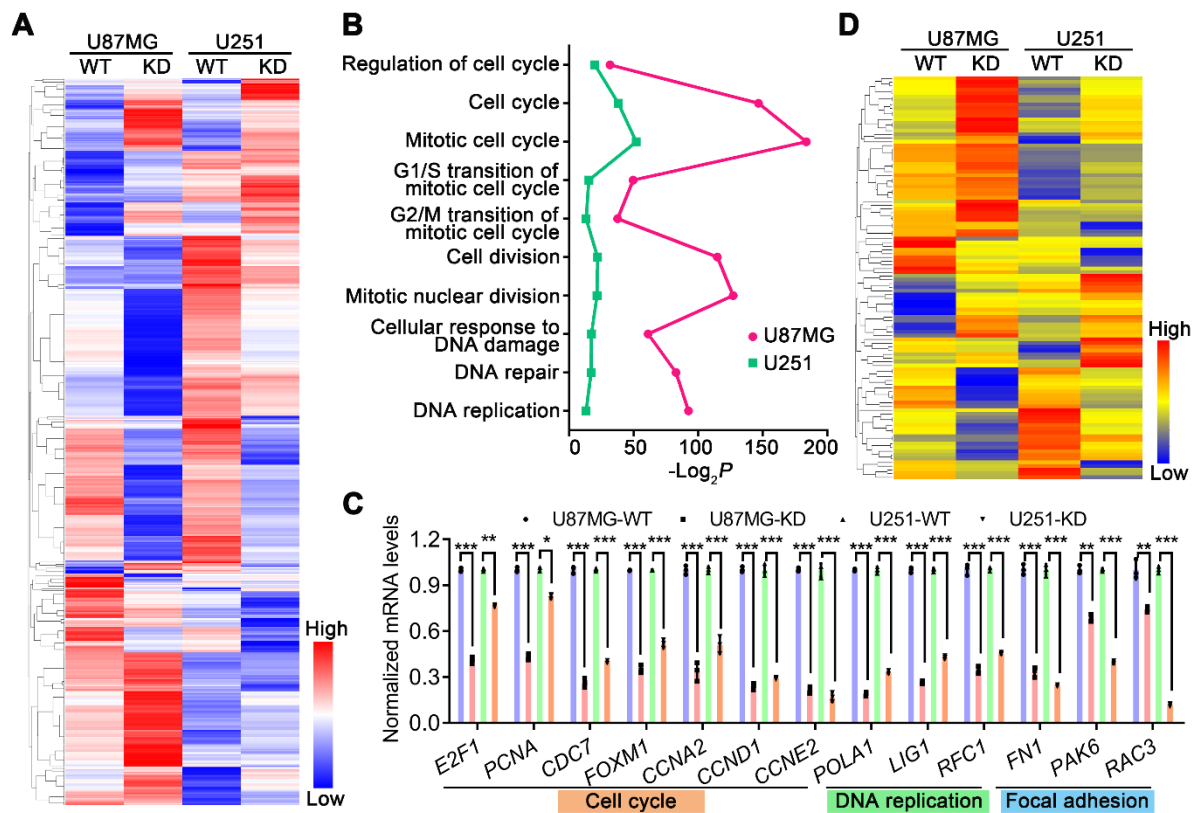
Supplemental Figure 2. The oncogenic roles of SRSF1 in glioma cells. **(A)** Confirmation of SRSF1 knockdown efficiencies by Western blot in U87MG, U251, LN229 and SNB19 cells transiently transfected with *SRSF1* siRNAs (si-*SRSF1*-1#, si-*SRSF1*-2#) or control siRNA (si-NC). Loading control: β -actin. **(B)** Growth curves of U87MG, U251, LN229 and SNB19 cells transfected with the siRNAs as indicated. **(C)** Colony formation assay results. **(D)** Transwell invasion assay results. **(E)** Schematic of SRSF1 domains, antibody epitope and SRSF1-mu, the shRNA resistant synonymous mutant of SRSF1. **(F)** Confirmation of SRSF1 overexpression efficiency by Western blot in SW1088 cells stably transfected by empty vector (vec) or HA tagged SRSF1 (SRSF1-wt) plasmid. Loading control: β -actin. **(G)** EdU staining results. **(H)** Transwell invasion assay results. Data in **(A-D, G, H)** are presented as mean $\pm$ SD, n=3 for **(A)**, n=5 for **(B-D, G, H)**. *** P <0.001 by 1-way ANOVA with Dunnett's post-test for **(A, B)**, 2-tailed Student's t test for **(C, D, G, H)**. Representative images from biological triplicate experiments are shown for **(C, D, G, H)**.

Supplemental Figure 3



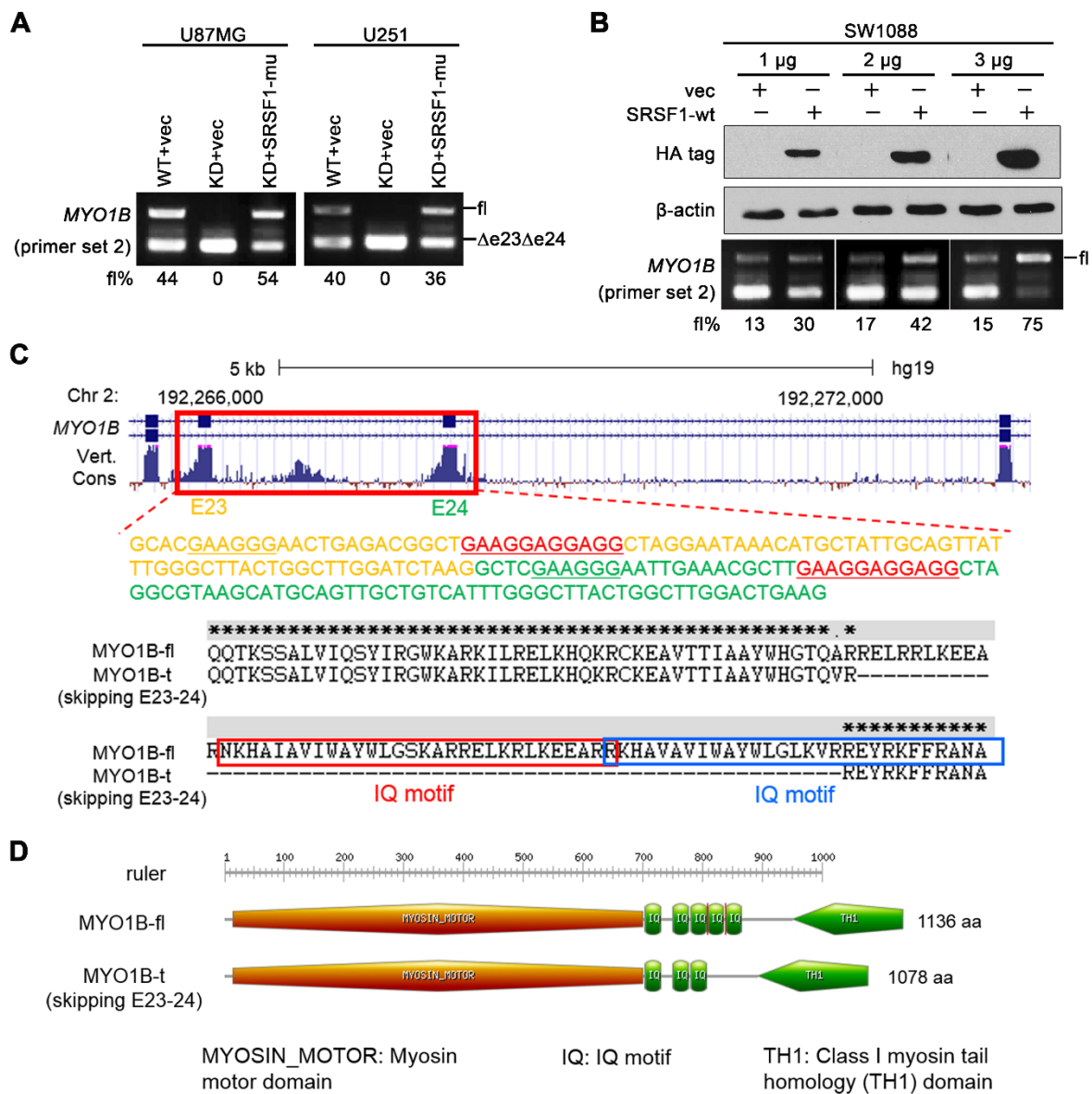
Supplemental Figure 3. In vivo study of SRSF1 knockdown on the intracranial xenograft formation using U87MG cells. (A) Upper: Bioluminescence images. Bottom: IHC of SRSF1 in outgrowing tumor slices. Scale bar, 20 μ m. Images of representative mice and tumors are shown. **(B)** Bioluminescence was quantified at day 4, 11, 18 and 25 after implantation. Data are presented as mean $\pm$ SD, n=8 for each group. *** P <0.001 by 1-way ANOVA with Dunnett's post-test. **(H)** The OS of the nude mice were analyzed by the Kaplan-Meier method. ** P <0.01 for the difference of WT+vec vs. KD+vec and KD+SRSF1-mu vs. KD+vec by log-rank (Mantel-Cox) test.

Supplemental Figure 4



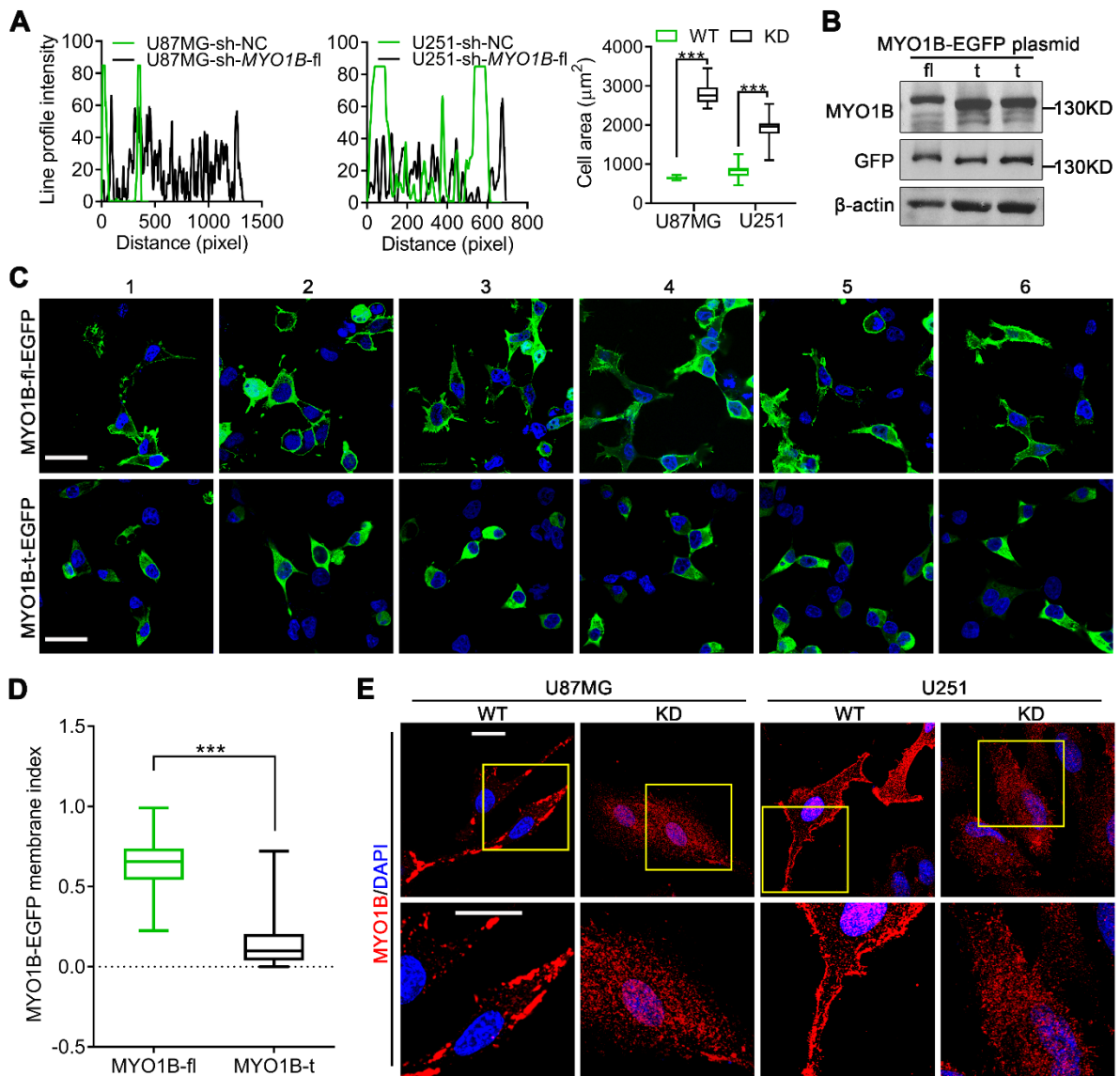
Supplemental Figure 4. Differential expression of coding and non-coding RNAs affected by SRSF1 in GBM cells. (A) Heatmap of the coding genes differentially expressed among the WT and KD groups of U87MG and U251 cells. The raw signal values from RNA-seq were arranged by unsupervised complete linkage clustering. Red stands for upregulation while blue stands for downregulation. (B) Gene ontology of SRSF1-regulated common coding genes in U87MG and U251 cells. $-\log_2$ transformed fisher exact P values were plotted for each enriched functional category. (C) Validation of gene expression changes by qRT-PCR, with the genes sorted by their functions. Data are presented as mean $\pm$ SD, $n=3$. $*P<0.05$, $**P<0.01$, $***P<0.001$ by 2-tailed Student's t test. (D) Heatmap of the differentially expressed non-coding RNAs among the WT and KD groups of U87MG and U251 cells.

Supplemental Figure 5



Supplemental Figure 5. SRSF1 regulates *MYO1B* splicing to induce the full-length *MYO1B* isoform. (A) Inclusion of exon 23 and 24 was examined by RT-PCR (primer set 2). (B) *MYO1B*-fl% in SW1088 cells increases with exogenous SRSF1 expression in a dose dependent manner. The dosage of plasmid for transfection are presented. The expression of HA tagged SRSF1-wt was monitored by Western blot. The inclusion of exon 23 and 24 was examined by RT-PCR (primer set 2). The lanes for *MYO1B* RT-PCR were on the same gel but noncontiguous. (C) Upper: Structure and conservation of the human *MYO1B* exon 22-25. Sequences of exon 23 (orange) and exon 24 (green) with potential SRSF1 binding site (red) are presented. Bottom: Partial aligned sequence of *MYO1B* protein isoforms. Two IQ motifs predicted by Prosite are indicated. (D) Schematic of *MYO1B* domains predicted by Prosite. The percentages of *MYO1B*-fl to total *MYO1B* transcripts are presented using fl% in (A, B).

77 **Supplemental Figure 6**

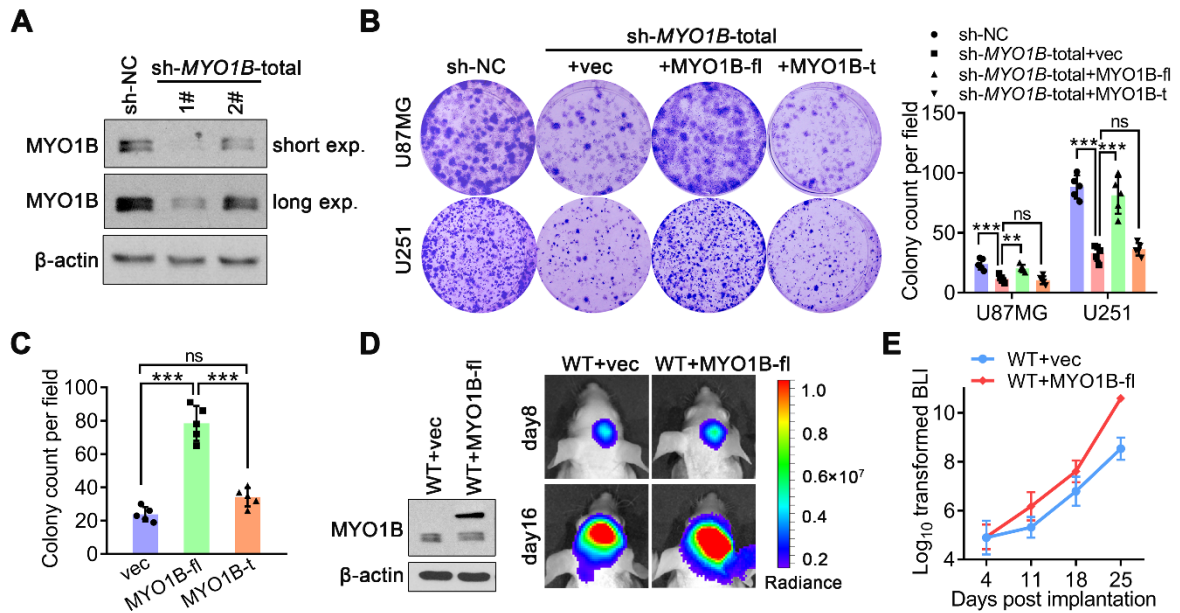


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Supplemental Figure 6. MYO1B-fl remodels cytoskeleton and shows distinct localization with MYO1B-t. (A) Line profile intensities of green fluorescence (Phalloidin) along the red lines indicated in Figure 6D (left and middle panels), and cell area comparison of the indicated cells (right panel). Data are presented as box plots, $n=300$. $***P<0.001$ by 2-tailed Student's t test. **(B)** Western blot of EGFP fused MYO1B-fl and MYO1B-t expressed in U251 cells using MYO1B and GFP antibodies. **(C)** Fluorescence images of the U251 cells expressing EGFP fused MYO1B isoforms (green). Cell nuclei were counter-stained with DAPI (blue). Representative images from six biological repeated experiments are shown. Scale bar, 30 μm . **(D)** Comparison of the membrane indexes of EGFP fused MYO1B-fl and -t. Data are presented as box plots, $n=300$. $***P<0.001$ by Mann-Whitney test. **(E)** Immunofluorescence of MYO1B in the sub-cell lines as indicated. Cell nuclei were counter-stained with DAPI (blue). Representative images from biological triplicate experiments are shown. Scale bar, 20 μm .

Supplemental Figure 7



Supplemental Figure 7. MYO1B-fl promotes survival and tumorigenic abilities of GBM

cells. **(A)** Western blot confirmation of total MYO1B knockdown efficiencies in U87MG cells.

Loading control: β-actin. **(B)** Colony formation assays of the indicated cells. Representative

images from biological triplicate experiments are shown. **(C)** Colony formation efficiencies of

the U251 cells infected with empty lentivirus (vec), lentivirus expressing MYO1B-fl or

lentivirus expressing MYO1B-t. **(D)** Left: Confirmation of MYO1B-fl overexpression

efficiency by Western blot in U87MG cells. Loading control: β-actin. Right: Bioluminescence

images of mice bearing intracranially glioma xenografts formed by the indicated U87MG

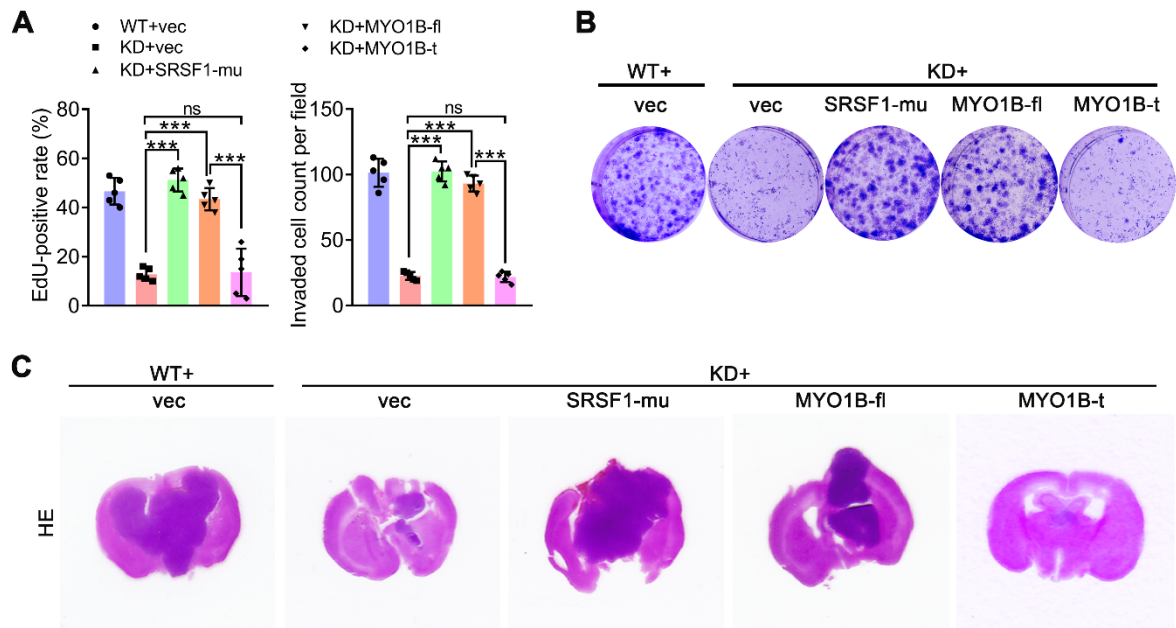
cells. Images of representative mice are shown. **(E)** Bioluminescence quantification of the

xenografts at day 4, 11, 18 and 25 after implantation (n=5 for each group). Data in **(B, C, E)**

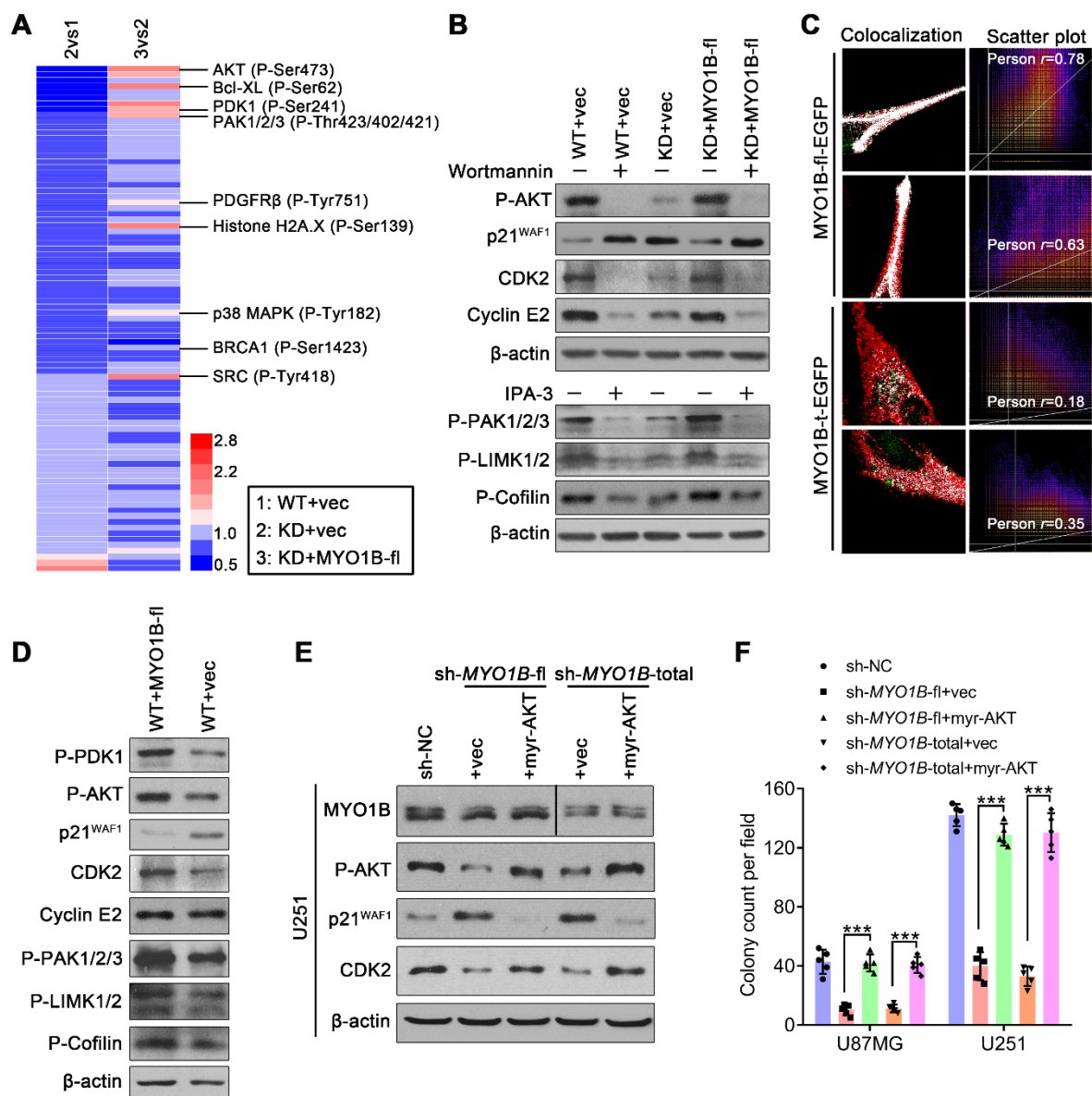
are presented as mean ± SD, n=5. ***P*<0.01, ****P*<0.001 by 1-way ANOVA with Dunnett's

post-test for **(B)**, ****P*<0.001 by 1-way ANOVA with Tukey's post-test for **(C)**.

Supplemental Figure 8



Supplemental Figure 8. MYO1B-fl isoform restores tumorigenesis defects caused by SRSF1 disruption in GBM cells. (A) Quantitation and data analysis of **Figure 8B**. Data are presented as mean $\pm$ SD, n=5. *** P <0.001 by 1-way ANOVA with Tukey's post-test. **(B)** Colony formation assay results in U87MG cells. Representative images from biological triplicate experiments are shown. **(C)** H&E staining brain slices of the nude mice with glioma xenografts. Images of representative tumors are shown.



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Supplemental Figure 9. MYO1B-fl promotes gliomagenesis through PDK1/AKT and PAK/LIMK pathways. (A) Heatmap of the phosphoproteins with altered ratios compared between the groups as indicated. The data presented are non-biased adjusting results of the raw signal values from Fullmoon phospho explorer antibody array. (B) Western blot of the indicated proteins in U87MG sub-cell lines. (C) Subcellular colocalization images (left) and scatter plots (right) of exogenous MYO1B and endogenous p85 signals indicated in Figure 8E. Pearson correlation test, r values are calculated by Image J. (D) Western blot of the indicated proteins in U87MG sub-cell lines. (E) Western blot of the indicated proteins in U251 cells. The lanes for MYO1B were run on the same gel but were noncontiguous. (F) Colony formation assay results of the indicated cells. Data are presented as mean $\pm$ SD, $n=5$. *** $P<0.001$ by 1-way ANOVA with Tukey's post-test.

Supplemental Table 1. Multivariate analysis for DFS and OS in patients with gliomas

Factors	DFS		OS	
	HR (95%CI)	<i>P</i>	HR (95%CI)	<i>P</i>
Gender	0.863 (0.582-1.280)	0.464	0.889 (0.600-1.318)	0.557
Age	1.000 (0.985-1.015)	0.990	0.998 (0.983-1.041)	0.833
Predominant side	1.354 (0.967-1.895)	0.077	1.272 (0.910-1.777)	0.159
Predominant location	1.292 (0.999-1.671)	0.051	1.287 (0.996-1.663)	0.054
<i>IDH1/2</i> status	0.085 (0.048-0.151)	<0.0001	0.078 (0.044-0.139)	<0.0001
KPS	0.997 (0.972-1.022)	0.805	0.997 (0.973-1.023)	0.842
SRSF1 LI	1.043 (1.029-1.058)	<0.0001	1.045 (1.030-1.059)	<0.0001

Supplemental Table 2. Univariate analysis for DFS and OS in patients with gliomas

Factors	DFS		OS	
	HR (95%CI)	<i>P</i>	HR (95%CI)	<i>P</i>
Gender	0.920 (0.637-1.329)	0.656	0.925 (0.640-1.336)	0.677
Age	1.022 (1.008-1.036)	0.002	1.021 (1.007-1.035)	0.003
Predominant side	0.963 (0.713-1.301)	0.806	0.953 (0.705-1.289)	0.756
Predominant location	1.291 (1.022-1.630)	0.032	1.283 (1.016-1.620)	0.037
Grade	5.557 (3.915-7.889)	<0.0001	5.622 (3.932-8.038)	<0.0001
<i>IDH1/2</i> status	0.089 (0.055-0.146)	<0.0001	0.086 (0.052-0.141)	<0.0001
KPS	0.994 (0.972-1.016)	0.585	0.994 (0.972-1.016)	0.582
SRSF1 LI	1.050 (1.038-1.063)	<0.0001	1.049 (1.037-1.062)	<0.0001
Ki-67 LI	1.249 (1.206-1.293)	<0.0001	1.252 (1.209-1.297)	<0.0001

Supplemental Table 3. Summary of the different AS events identified in U87MG and U251 cells affected by SRSF1

AS type	Total events		U87MG		U251		Shared events	
	U87MG	U251	activation	repression	activation	repression	activation	repression
SE	918	912	568	350	513	399	196	133
RI	103	106	44	59	60	46	17	15
A5SS	138	127	84	54	63	64	19	15
A3SS	110	112	55	55	48	64	11	7
MXE	79	75	38	41	38	37	11	12
sum	1348	1332	789	559	722	610	254	182

Abbreviations: AS: alternative splicing; SE: skipped exon; RI: retained intron; A5SS: alternative 5' splice site; A3SS: alternative 3' splice site; MXE: mutually exclusive exon; sum: summary.

Supplemental Table 4. List of top 50 AS events shared by U87MG and U251 cell lines affected by SRSF1

Gene	Exon location	Reads coverage (Ex::In)		<i>P</i>	Reads coverage (Ex::In)		<i>P</i>	AS type
		U87MG-WT	U87MG-KD		U251-WT	U251-KD		
<i>HNRNPM</i>	chr19:8530246-8530364	1397::1932	3232::2476	2.55E-41	2036::3836	2804::3454	4.13E-30	RI
<i>CD46</i>	chr1:207941124-207941168	394::565	821::162	6.25E-34	103::844	192::601	3.58E-06	SE
<i>P4HA1</i>	chr10:74776653-74776657	1::456	91::205	2.543E-32	500::921	0::993	2.28E-41	A3SS
<i>P4HA1</i>	chr10:74790025-74790029	0::456	91::207	2.17E-27	502::915	3::990	4.59E-34	A5SS
<i>LOC220729</i>	chr3:197349058-197349201	57::0	14::240	8.67E-32	151::76	38:187	1.75E-20	SE
<i>CTTN</i>	chr11:70267576-70267686	2701::1081	613::1834	1.66E-31	854::1092	128::713	1.90E-14	SE
<i>ATP2C1</i>	chr3:130698093-130698263	363::349	38::574	7.28E-31	188::428	24::485	1.40E-14	SE
<i>MYO1B</i>	chr2:192265475-192265561	144::31	89::247	3.55E-28	115::55	49::284	1.35E-23	SE
<i>MYO1B</i>	chr2:192267358-192267444	97::88	49::217	9.16E-11	77::92	26::174	2.19E-09	SE
<i>C11orf24</i>	chr11:68029193-68030199	115::242	322::136	1.19E-27	7::217	28::188	1.46E-04	RI
<i>PSMD11</i>	chr17:30807649-30807771	846::227	1104::69	2.31E-27	722::342	827::118	2.54E-26	RI
<i>DLG1</i>	chr3:196802708-196802741	591::36	255::150	1.09E-26	908::41	545::95	2.45E-06	SE
<i>PKD1P1</i>	chr16:16443086-16443155	58::168	63::0	2.78E-26	125::321	146::108	2.25E-11	SE
<i>PPM1A</i>	chr14:60743723-60743809	77::187	138::28	2.41E-25	100::105	74::13	3.15E-09	SE
<i>FAM122B</i>	chrX:133923610-133923666	103::390	339::240	1.07E-24	158::735	439::436	1.26E-19	SE
<i>CCDC107</i>	chr9:35660855-35660937	343::2074	445::1185	1.43E-24	103::1772	193::830	1.38E-10	RI
<i>OS9</i>	chr12:58113882-58114046	533::146	227::407	2.10E-24	404::300	217::402	6.52E-08	SE
<i>DBF4B</i>	chr17:42809546-42809633	39::5	60::54	5.28E-05	186::30	99::110	6.75E-15	SE
<i>USP53</i>	chr4:120135225-120135377	85::284	199::83	6.57E-23	40::25	43::3	1.32E-04	SE
<i>TMED5</i>	chr1:93621593-93621641	408::170	445::17	1.09E-22	755::194	639::6	2.51E-21	SE
<i>USP8</i>	chr15:50776472-50776558	137::61	84::281	4.95E-22	212::84	85::249	1.21E-26	SE
<i>MYEF2</i>	chr15:48454874-48455090	154::228	256::67	8.91E-22	130::282	285::67	9.89E-30	SE
<i>YPEL5</i>	chr2:30371111-30371171	226::20	56::67	2.70E-20	78::0	49::13	4.56E-05	SE
<i>GOLGA4</i>	chr3:37402734-37402796	83::318	181::143	1.83E-19	56::278	97::147	2.20E-08	SE
<i>CD47</i>	chr3:107770786-107770817	98::1165	429::802	6.38E-19	33::1328	198::1235	1.76E-08	SE
<i>ENO2</i>	chr12:7028730-7028927	192::542	4::609	8.49E-18	37::205	1::256	2.09E-06	SE
<i>MORF4L2</i>	chrX:102939609-102939657	959::436	660::1104	2.75E-17	1376::221	1024::522	3.71E-10	SE
<i>PRRC2C</i>	chr1:171560291-171560343	89::50	54::216	5.63E-17	236::116	95::244	5.13E-22	SE
<i>EIF4H</i>	chr7:73604577-73604636	679::243	727::975	8.59E-17	1152::298	875::448	1.31E-04	SE

<i>CD97</i>	chr19:14507154-14507285	15::357	127::284	1.44E-16	47::239	119::106	1.78E-14	SE
<i>PYURF</i>	chr4:89444649-89444654	0::351	116::242	2.10E-16	242::151	121::204	6.35E-05	A5SS
<i>LSM14A</i>	chr19:34717313-34717369	324::85	237::226	6.96E-16	581::96	249::128	1.06E-09	SE
<i>HNRNPDL</i>	chr4:83347616-83347786	426::1552	21::2905	3.58E-15	683::2030	29::3052	3.18E-17	SE
<i>TNC</i>	chr9:117810539-117810811	952::27	759::147	5.82E-05	896::72	487::308	1.96E-16	SE
<i>PCGF3</i>	chr4:726189-726287	149::14	131::113	1.56E-14	247::16	191::83	1.14E-12	SE
<i>MPP5</i>	chr14:67745735-67745967	6::74	64::39	8.67E-11	0::84	59::42	1.01E-16	A3SS
<i>LRRFIP1</i>	chr2:238659843-238659914	376::4	327::73	2.08E-14	340::6	206::117	7.32E-31	SE
<i>UPF3A</i>	chr13:115064315-115064475	335::359	175::800	2.56E-14	263::284	101::424	2.21E-12	SE
<i>PRMT2</i>	chr21:48056351-48056459	77::13	64::128	4.22E-14	127::95	94::325	4.49E-15	SE
<i>GOLGA2</i>	chr9:131029473-131029553	107::533	208::269	5.13E-14	192::508	166::195	2.53E-06	SE
<i>MFF</i>	chr2:228217230-228217289	57::821	159::418	5.58E-14	20::746	96::544	6.21E-09	SE
<i>HMGNI</i>	chr21:40719305-40719409	34::78	171::49	2.40E-12	27::61	126::5	2.03E-19	MXE
<i>P4HA2</i>	chr5:131534014-131534073	102::84	40::194	7.48E-14	81::24	50::83	3.27E-08	MXE
<i>DNM1</i>	chr9:131002264-131002275	122::117	85::334	7.98E-14	217::61	146::134	1.23E-09	SE
<i>ESYT2</i>	chr7:158545472-158545534	385::230	357::68	8.60E-11	302::346	314::95	1.53E-16	SE
<i>RCOR3</i>	chr1:211485697-211485829	134::31	76::118	2.20E-13	165::12	70::51	4.91E-10	SE
<i>PPP3CC</i>	chr8:22396982-22397011	106::423	162::186	5.26E-13	99::278	101::114	3.86E-05	SE
<i>CHCHD7</i>	chr8:57129239-57129313	273::63	413::10	5.58E-13	209::37	282::10	1.05E-05	SE
<i>IRF3</i>	chr19:50167931-50168103	29::23	2::141	6.53E-13	20::34	1::94	9.87E-07	SE
<i>FLNA</i>	chrX:153585619-153585642	1390::1691	926::3697	1.14E-12	1925::5242	646::8082	2.81E-12	SE

Abbreviations: Ex: exclusion; In: inclusion; RI: retained intron; SE: skipped exon; A3SS: alternative 3' splice site; A5SS: alternative 5' splice site; MXE: mutually exclusive exon.

Supplemental Table 5. The clinicopathological characteristics of the 120 glioma patients enrolled in this study

Feature	WHO Grade		
	II (n=40)	III (n=40)	IV (n=40)
Gender			
Male	22	22	27
Female	18	18	13
Age (Year, Mean±SD)	42.73±11.88	47.68±15.24	55.68±13.05
Age < 50	29	22	10
Age ≥ 50	11	18	30
Predominant side			
Left	20	17	20
Right	17	21	18
Middle	3	2	2
Predominant location			
Frontal lobe	30	26	19
Temporal lobe	6	8	13
Parietal lobe	1	3	5
Occipital lobe	1	1	1
Others	2	2	2
IDH1/2 status			
Wild type (<i>IDH1/2</i>)	5	7	38
Mutant type (<i>IDH1</i> R132H)	35	33	2
KPS score			
< 90	23	24	26
≥ 90	17	16	14

Abbreviation: SD, Standard deviation; KPS, Karnofsky performance score.

Supplemental Table 6. Sequences of siRNAs

Name	Sequences
si-<i>SRSF1</i>-1#-Sense	5'-AGGACAUUGAGGACGUGUUdTdT-3'
si-<i>SRSF1</i>-1#-Antisense	5'-AACACGUCCUCA AUGUCCUdTdT-3'
si-<i>SRSF1</i>-2#-Sense	5'-GAAAGAAGAU AUGACCUAUdTdT-3'
si-<i>SRSF1</i>-2#-Antisense	5'-AUAGGUCAUAUCUUCUUUCdTdT-3'
si-<i>MYO1B</i>-fl-1#-Sense	5'-GGCUCGAAGGGAAUUGAAAdTdT-3'
si-<i>MYO1B</i>-fl-1#-Antisense	5'-UUUCAAUUCCCUUCGAGCCdTdT-3'
si-<i>MYO1B</i>-fl-2#-Sense	5'-GCUCGAAGGGAAUUGAAACdTdT-3'
si-<i>MYO1B</i>-fl-2#-Antisense	5'-GUUUCAAUUCCCUUCGAGCdTdT-3'
si-NC-Sense	5'-GGUGGAACAAUUGCUUUUAdTdT-3'
si-NC-Antisense	5'-UAAAAGCAAUUGUCCACCdTdT-3'

Supplemental Table 7. Sequences of cloning primers

Name	Sequences
SRSF1-BamHI-Forward	5'-CGCGGATCCATGTCGGGAGGTGGTGTG-3'
SRSF1-EcoRI-Reverse	5'-CCGGAATTCTTATGTACGAGAGCGAGAT-3'
mu-SRSF1-Forward	5'-GACATCCGAACCAAAGATATCGAAGATGTATTCTACAAATACGGC-3'
mu-SRSF1-Reverse	5'-GCCGTATTTGTAGAATACATCTTCGATATCTTTGGTTCGGATGTC-3'
SRSF1-ΔRRM1-Forward	5'-GGGAACAACGATTGCGGCCGTGGAACAGGC-3'
SRSF1-ΔRRM1-Reverse	5'-GCCTGTTCCACGGCCGCAATCGTTGTTCCC-3'
SRSF1-ΔRRM2-Forward	5'-CAGGCGGTCTGAAAACGGGCCCAGAAGTCC-3'
SRSF1-ΔRRM2-Reverse	5'-GGACTTCTGGGCCCCGTTTTTCAGACCGCCTG-3'
SRSF1-ΔRS-BamHI-Forward	5'-CGCGGATCCATGTCGGGAGGTGGTGTG-3'
SRSF1-ΔRS-EcoRI-Reverse	5'-CCGGAATTCTTAATCAACTTTAACCCGGATG-3'
MYO1B-EcoR1-Forward	5'-CCGGAATTCTATGGCCAAAATGGAGGTGAAAACC-3'
MYO1B-Sal1-Reverse	5'-ACGCGTCGACTTAAGGGACAGCAACTTCAAGG-3'
MYO1B-miniF1-BamH1-Forward	5'-CGCGGATCCGCTCGAAAAATTCTGCGGGAAC-3'
MYO1B-miniF1-Hind3-Reverse	5'-CCCAAGCTTATGTTTCCAGGTGTGTTAAATCTGGC-3'
MYO1B-miniF2-Hind3-Forward	5'-CCCAAGCTTTTTGGGTTTAAATTGTTATGCAC-3'
MYO1B-miniF2-EcoR1-Reverse	5'-CCGGAATTCTCTTCTGAAAAAGGTACAAAAT-3'
MYO1B-miniF3-EcoR1-Forward	5'-CCGGAATTCTATGAATGTGTTTCAATTATTTTAC-3'
MYO1B-miniF3-Xho1-Reverse	5'-CCGCTCGAGAATTCTCTGAAGCGTAAACTC-3'

Supplemental Table 8. Sequences of shRNAs

Name	Sequences
sh-NC-Sense	5'-ccggTTCCTGGAACAATTGCTTTTACTCGAGTAAAAGCAATTGTTCCAGGAATTTTTg-3'
sh-NC-Antisense	5'-aattcAAAAATTCCTGGAACAATTGCTTTTACTCGAGTAAAAGCAATTGTTCCAGGAA-3'
sh-SRSF1-Sense	5'-ccggAAAGGACATTGAGGACGTGTTCTCGAGAACACGTCCTCAATGTCCTTTTTTTTTg-3'
sh-SRSF1-Antisense	5'-aattcAAAAAAAAGGACATTGAGGACGTGTTCTCGAGAACACGTCCTCAATGTCCTTT-3'
sh-MYO1B-fl-Sense	5'-ccggAAGCTCGAAGGGAATTGAAACCTCGAGGTTTCAATTCCCTTCGAGCTTTTTTTg-3'
sh-MYO1B-fl-Antisense	5'-aattcAAAAAAAGCTCGAAGGGAATTGAAACCTCGAGGTTTCAATTCCCTTCGAGCTT-3'
sh-MYO1B-total1-Sense	5'-ccggAAGGTATTATGTAAATAATAAACTCGAGTTTATTATTTAACATAATACCTTTTTTTg-3'
sh-MYO1B-total1-Antisense	5'-aattcAAAAAAAGGTATTATGTAAATAATAAACTCGAGTTTATTATTTAACATAATACCTT-3'
sh-MYO1B-total2-Sense	5'-ccggAAGCATATTACTCATAAATCATTCTCGAG AATGATTTATGAGTAATATGCTTTTTTTg-3'
sh-MYO1B-total2-Antisense	5'-aattcAAAAAAAGCATATTACTCATAAATCATTCTCGAG AATGATTTATGAGTAATATGCTT-3'

Supplemental Table 9. Sequences of qRT-PCR primers

Name	Sequences
<i>SRSF1</i> -Forward	5'- GCCGCATCTACGTGGGTAAC-3'
<i>SRSF1</i> -Reverse	5'- GAGGTCGATGTCGCGGATAG-3'
<i>ACTB</i> -Forward	5'-GATCATTGCTCCTCCTGAGC-3'
<i>ACTB</i> -Reverse	5'-ACTCCTGCTTGCTGATCCAC-3'
<i>E2F1</i> -Forward	5'- GCAGAGCAGATGGTTATGGTGAT-3'
<i>E2F1</i> -Reverse	5'- GGGCACAGGAAAACATCGAT-3'
<i>PCNA</i> -Forward	5'- CAGGGCTCCATCCTCAAGAA-3'
<i>PCNA</i> -Reverse	5'- GTCCATGCTCTGCAGGTTTACA-3'
<i>CDC7</i> -Forward	5'- GGATCAGCAGTCCACCACAA-3'
<i>CDC7</i> -Reverse	5'- CCCTCCTTTCCGTCTTTTCC-3'
<i>FOXM1</i> -Forward	5'-GGGCGCACGGCGGAAGATGAA-3'
<i>FOXM1</i> -Reverse	5'-CCACTCTTCCAAGGGAGGGCTC-3'
<i>CCNA2</i> -Forward	5'- GCGCTGGCGGTACTGAAGT-3'
<i>CCNA2</i> -Reverse	5'- AGGAACGGTGACATGCTCATC-3'
<i>CCND1</i> -Forward	5'-CTGGAGGTCTGCGAGGAACA-3'
<i>CCND1</i> -Reverse	5'-CTGCAGGCGGCTCTTTTTC-3'
<i>CCNE2</i> -Forward	5'-TTGGCTATGCTGGAGGAAGTAAA-3'
<i>CCNE2</i> -Reverse	5'-TGGTGTCATAATGCCTCCATTG-3'
<i>POLA1</i> -Forward	5'-AGGCTTCACCTCTGACCTTTACA-3'
<i>POLA1</i> -Reverse	5'-TTGCGACAGGTTGGCTCTTC-3'
<i>LIG1</i> -Forward	5'-GGCCTGGTGGATAGTGACAAG-3'
<i>LIG1</i> -Reverse	5'-AATCTGACTTTGCTTCCGGTACA-3'
<i>RFC1</i> -Forward	5'-TAAGCCAACCTCGCTCAAGAC-3'
<i>RFC1</i> -Reverse	5'-TTCGGAGCCAGCGTAGGA-3'
<i>FN1</i> -Forward	5'-GAGGTGGACCCCGCTAAACT-3'
<i>FN1</i> -Reverse	5'-CCTGCCGCAACTACTGTGAT-3'
<i>PAK6</i> -Forward	5'-GTGGGAACCCCCTACTGGAT-3'
<i>PAK6</i> -Reverse	5'-GTACGGTGGCTCCCCATCTA-3'
<i>RAC3</i> -Forward	5'-GCCACTCTCCTACCCCCAAA-3'
<i>RAC3</i> -Reverse	5'-CTTGGCACGAACATTCTCGAA-3'

Supplemental Table 10. Sequences of RT-PCR primers

Name	Sequences
<i>USP8</i> -Forward	5'-ATCGTTCCACCAAGCCAGTA-3'
<i>USP8</i> -Reverse	5'-TTCGTGCTCTTGTCAAAGGTTCT-3'
<i>DBF4B</i> -Forward	5'-CAGAGAAGTAAAGGCAGAGAGCA-3'
<i>DBF4B</i> -Reverse	5'-CACACATAAAGACGCAAGAGACA-3'
<i>MYO1B</i> -e22-Forward-1	5'-AGGAAGCAGTCACGACCATT-3'
<i>MYO1B</i> -e24-Reverse	5'-AGCAACTGCATGCTTACGCC-3'
<i>MYO1B</i> -e22-Forward-2	5'-GCGCTGTAAGGAAGCAGTCA-3'
<i>MYO1B</i> -e25-Reverse	5'-CTTTCCAGCATTGGCTCTGAAG-3'
<i>PRRC2C</i> -Forward	5'-TCCTACACAGTTTGCACCCC-3'
<i>PRRC2C</i> -Reverse	5'-TCACTGTCCACTTTCTGGGC-3'
<i>OS9</i> -Forward	5'-CCAAAAAGCCTCCCCCATCA-3'
<i>OS9</i> -Reverse	5'-CGTGTCTCATCAGTCAGCC-3'
<i>HNRNPDL</i> -Forward	5'-AGTTGCACAACCCAAAGAGGT-3'
<i>HNRNPDL</i> -Reverse	5'-TTGTTTTGGTGATTGCCACCC-3'
<i>HNRNPM</i> -Forward	5'-AGCTGCGGAAGTCCTAAACA-3'
<i>HNRNPM</i> -Reverse	5'-CCACCACACCAGCCATACTA-3'
<i>PRMT2</i> -Forward	5'-AGCGGAGAAACGCGATTGA-3'
<i>PRMT2</i> -Reverse	5'-TGCGATTCACTTCTGGGACA-3'
<i>GOLGA4</i> -Forward	5'-AGAGAAGATGCTCGGCTGAT-3'
<i>GOLGA4</i> -Reverse	5'-TTTCCAAGCAGCAGTCACCC-3'
<i>MYO1B</i> -minigene-Forward	5'-GATAAGAGCCCGGGCGGATCCGCTCGAAAA-3'
<i>MYO1B</i> -minigene-Reverse	5'-TACCGGGCCCCCCTCGAGAATTCTCTGAA-3'

Supplemental Table 11. Primary antibodies for Western blot

Name	Catlog No.	Company
Mouse anti-human SRSF1	sc-33652	Santa Cruz Biotechnology
Mouse anti-human β -actin	sc-47778	Santa Cruz Biotechnology
Mouse anti-human CDK2	sc-6248	Santa Cruz Biotechnology
Rabbit anti-human P-PDK1	3438	Cell Signaling Technology
Rabbit anti-human P-AKT	4060	Cell Signaling Technology
Rabbit anti-human p21 ^{WAF1}	2947	Cell Signaling Technology
Rabbit anti-human Cyclin E2	4132	Cell Signaling Technology
Rabbit anti-human P-LIMK1/2	3841	Cell Signaling Technology
Rabbit anti-human p85 PI3K	4292	Cell Signaling Technology
Rabbit anti-human P-PAK1/2/3	ab118537	Abcam
Rabbit anti-HA tag	ab9110	Abcam
Mouse anti-GFP tag	T0005	Affinity Biosciences
Rabbit anti-human MYO1B	HPA013607	Sigma-Aldrich
Rabbit anti-human P-Cofilin	YP0070	Immunoway