Figure S1. The expression and gene copy number of EGFR and MYC do not correlate with glioma patient survival.

(*A*). Kaplan-Meier plots show the correlation between EGFR gene copy number and glioma patient survival. Samples with gene amplification (red line) n=325. Samples with gene deletion (green line) n=19. Blue line represents the survival of all glioma patients. Log-rank p-value (Amplified vs. deleted): 0.216. Data based on the National Cancer Institute REMBRANDT data set (http://rembrandt.mci.nih/gov).

(*B*). Kaplan-Meier survival plots show the survival of glioma patients with differential expression of EGFR: Samples with up-regulation (red line) Down-regulation (green line) Samples with intermediate expression (yellow). The blue line represents the survival of all glioma patients. Number of samples in group: Up-Regulated: 275 Down-Regulated: 12 Intermediate: 57 Log-rank p-value(for significance of difference of survival between group of samples) Up-Regulated vs. Intermediate: 0.663 Up-Regulated vs. Down-Regulated: 0.092 Down-Regulated vs. Intermediate: 0.038 Up-Regulated vs. all other samples: 0.660 Down-Regulated vs. all other samples: 0.078 Intermediate vs. all other samples: 0.550 Data based on the National Cancer Institute REMBRANDT data set (http://rembrandt.mci.nih/gov).

(*C*). Kaplan-Meier plots show the correlation between MYC gene copy number and glioma patient survival. Samples with gene amplification (red line) n=259. Samples with gene deletion (green line) n=71. Blue line represents the survival of all glioma patients. Log-rank p-value (Amplified vs deleted): 0.342. Data based on the National Cancer Institute REMBRANDT data set (http://rembrandt.mci.nih/gov).

(*D*). Kaplan-Meier survival plots show the survival of glioma patients with differential expression of MYC: Samples with up-regulation (red line) Down-regulation (green line) Samples with intermediate expression (yellow). The blue line represents survival of all glioma patients. Number of samples in group: Up-Regulated: 282 Down-Regulated: 5 Intermediate: 57 Log-rank p-value(for significance of difference of survival between group of samples) Up-Regulated vs. Intermediate: 0.088 Up-Regulated vs. Down-Regulated: 0.627 Down-Regulated vs. Intermediate: 0.931 Up-Regulated vs. all other samples: 0.078 Down-Regulated vs. all other samples: 0.687 Intermediate vs. all other samples: 0.090. Data based on the National Cancer Institute REMBRANDT data set (http://rembrandt.mci.nih/gov).

Figure S2. the expresion and gene copy number of TP73 and TP53 do not correlate with glioma patient survival.

(*A*). Kaplan-Meier plots show the correlation between TP73 gene copy number and glioma patient survival. Samples with gene amplification (red line) n=124. Samples with gene deletion (green line) n=48. Blue line represents the survival of all glioma patients. Log-rank p-value (Amplified vs. Deleted): 0.459. Data based on the National Cancer Institute REMBRANDT data set (http://rembrandt.mci.nih/gov).

(*B*). Kaplan-Meier survival plots show the survival of glioma patients with differential expression of TP73: Samples with up-regulation (red line) Down-regulation (green line) Samples with intermediate expression (yellow). The blue line represents the survival of all glioma patients. Number of samples in group: Up-Regulated: 18. Intermediate: 153 Log-rank p-value(for significance of difference of survival between group of samples) Up-Regulated vs. Intermediate: 0.742. Data based on the National Cancer Institute REMBRANDT data set (http://rembrandt.mci.nih/gov).

(*C*). Kaplan-Meier plots show the correlation between TP53 gene copy number and glioma patient survival. Samples with gene amplification (red line) n=158. Samples with gene deletion (green line) n=186. Blue line represents the survival of all glioma patients. Log-rank p-value (Amplified vs deleted): 0.064. Data based on the National Cancer Institute REMBRANDT data set (http://rembrandt.mci.nih/gov).

(*D*). Kaplan-Meier survival plots show the survival of glioma patients with differential expression of TP53: Samples with up-regulation (red line) Down-regulation (green line) Samples with intermediate expression (yellow). The blue line represents survival of all glioma patients. Number of samples in group: Up-Regulated: 276 Down-Regulated: 2 Intermediate: 66 Log-rank p-value(for significance of difference of survival between group of samples) Up-Regulated vs. Intermediate: 0.899Up-Regulated vs. Down-Regulated: 0.724. Down-Regulated vs. Intermediate: 0.662 Up-Regulated vs. all other samples: 0.942 Down-Regulated vs. all other samples: 0.710 Intermediate vs. all other samples: 0.887. Data based on the National Cancer Institute REMBRANDT data set (http://rembrandt.mci.nih/gov).

Figure S3. the expresion and gene copy number of PTEN correlates and AKT2 anti-correlates with glioma patient survival.

(*A*). Kaplan-Meier plots show the correlation between PTEN gene copy number and glioma patient survival. Samples with gene amplification (red line) n=118. Samples with gene deletion (green line) n=226. Blue line represents the survival of all glioma patients. Log-rank p-value (Amplified vs.

Deleted): 6.504E-6. Data based on the National Cancer Institute REMBRANDT data set (http://rembrandt.mci.nih/gov).

(*B*). Kaplan-Meier survival plots show the survival of glioma patients with differential expression of PTEN: Samples with Down-regulation (green line) n=44. Samples with intermediate expression (yellow) n=300. The blue line represents the survival of all glioma patients. Log-rank p-value (Down-regulated vs. Intermediate): 1.0E-10. Data based on the National Cancer Institute REMBRANDT data set (http://rembrandt.mci.nih/gov).

(*C*). Kaplan-Meier plots show the correlation between AKT2 gene copy number and glioma patient survival. Samples with gene amplification (red line) n=126. Samples with gene deletion (green line) n=205. Blue line represents the survival of all glioma patients. Log-rank p-value (Amplified vs. Deleted): 0.589. Data based on the National Cancer Institute REMBRANDT data set (http://rembrandt.mci.nih/gov).

(*D*). Kaplan-Meier survival plots show the survival of glioma patients with differential expression of AKT2: Samples with up-regulation (red line) n=157. Samples with down-regulation (green line) n=1. Samples with intermediate expression (yellow) n=186. The blue line represents the survival of all glioma patients. Log-rank p-value (Up-regulated vs. Intermediate): 9.0E-10. Up-Regulated vs. all other samples: 1.1E-9. Intermediate vs. All other samples: 7.0E-10. Data based on the National Cancer Institute REMBRANDT data set (http://rembrandt.mci.nih/gov).

Figure S4. Gene copy number of hnRNP A1 and SF2/ASF expression do not correlate with glioma patient survival.

(*A*). Kaplan-Meier survival plots show the survival of glioma patients with differential expression of hnRNP A1: Samples with intermediate expression (yellow) n=342. Up-Regulated (red) n=2. The blue line represents the survival of all glioma patients. Log-rank p-value(for significance of difference of survival between group of samples) Up-Regulated vs. Intermediate: 0.9660533414. Data based on the National Cancer Institute REMBRANDT data set (http://rembrandt.mci.nih/gov).

(*B*). Kaplan-Meier plots show the correlation between *HNRNPA1* gene copy number and glioma patient survival. Samples with gene amplification (red line) n=321. Samples with gene deletion (green line) n=23. Blue line represents the survival of all glioma patients. Log-rank p-value (Amplified vs. Deleted): 0.4227139388. Data based on the National Cancer Institute REMBRANDT data set (http://rembrandt.mci.nih/gov).

(*C*). Kaplan-Meier survival plots show the survival of glioma patients with differential expression of SF2/ASF: Samples with up-regulation (red line) n=72. Samples with intermediate expression (yellow) n=271. The blue line represents the survival of all glioma patients. Log-rank p-value (Up-

regulated vs. Intermediate): 0.1474297111. Data based on the National Cancer Institute REMBRANDT data set (http://rembrandt.mci.nih/gov).

Figure S5. hnRNP A2/B1 is required for of glioblsatoma transformation.

(*A*). T98G cells were transduced with retroviruses encoding hnRNP A2/B1-specific shRNAs or empty vector (MLP(-)) and after selection cells were analyzed by Western blotting for hnRNP A2/B1 protein expression. β-actin and β-catenin levels were used as loading control. (*B*). Quantification of colony formation in soft agar of cells described in (A). Error bars represents standard deviations (n=2). (*C*). Representative fields of colonies in soft agar described in (B).

Figure S6. hnRNP A2/B1 contributes to cell proliferation.

Cell proliferation of U87MG cells transduced with retroviruses encoding hnRNP A2/B1-specific shRNA or empty vector (MLP(-)), at different serum conditions was determinate by methylen blue staining (*A,B* and *C*). Error bars represents standard deviations (n=4). Cell proliferation of U87MG cells transduced with empty vector (pBABE) or hnRNP A2/B1 (A2) at different serum conditions was determinate by methylen blue staining (*D,E* and *F*). Error bars represents standard deviations (n=4). (*G*). During cell growth U87MG cells transduced with retroviruses encoding hnRNP A2/B1-specific shRNA or empty vector (MLP(-)) were analyzed by Western blotting for hnRNP A2/B1 protein expression at 24 , 48 and 72 hours of culturing. β-catenin was used as loading control.. (*H*). During cell growth U87MG cells transduced with empty vector (pBABE) or hnRNP A2/B1 (A2) were analyzed by Western blotting for hnRNP A2/B1 protein expression at 24 , 48 and 72 hours of culturing. β-catenin was used as loading control.

Figure S7. hnRNP A2/B1 down-regulation increased the inclusion of hnRNP A1 exon 7B and exon 7 of the SMN gene.

(*A*). U87MG glioblastoma cancer cells were transduced with retroviruses encoding shRNA empty vector (MLP), or hnRNP A2/B1 specific shRNA. After selection cells were lysed, RNA isolated and the alternative splicing pattern of *HNRPA1* and *SMN* genes was determined by RT-PCR.

(*B*).NIH-3T3 cells U87MG transduced with empty vector (pBABE) or hnRNP A2/B1 (A2). After selection cells were lysed, RNA isolated and the alternative splicing pattern of *BIN* was determined by RT-PCR. Beta actin was used as control.

Figure S8. hnRNP A2/B1 down-regulation did not change the protein levels of SRSF1 (SF2/ASF), SRSF6 (SRp55) and hnRNP A1.

Western blot using specific antibodies to SRSF1 (SF2/ASF), SRSF6 (SRp55) and hnRNP A1 in lysates from U87MG cells transduced with the indicated retroviruses.