The RNA-binding protein Musashi1 is a central regulator of adhesion pathways in glioblastoma – supplementary table captions

Table S1: Genomic locations of significant peaks in all three iCLIP replicates as determined by Piranha. The genes overlapping each location are also listed, as are their strand and the p-value (corrected for multiple hypothesis testing) of the peak. A cutoff of corrected p ¡ 0.05 was used to determine significance.

Table S2: Counts of the number of significant iCLIP sites falling within each gene per replicate are given. Also listed are counts for only 5 UTRs, 3 UTRs, coding sequence and introns for each gene. The final list of genes considered putative MSI1 targets, which is also provided, is those which contain at least one significant iCLIP site in either 5 or 3 UTR in two or more replicates.

Table S3: Exons showing significant changes in inclusion rate between MSI1 knockdown and control RNA-Seq. An odds-ratio of greater than 1.5 or less than 0.33 and an adjusted p-value of less than 0.01 in all three replicates was considered significant.

Table S4: KEGG pathways enriched for MSI1 iCLIP targets. A background of expressed genes, defined by RNA-Seq, was used when determining enrichment.

Table S5: Biological processes enriched for MSI1 iCLIP targets. A background of expressed genes, defined by RNA-Seq, was used when determining enrichment.