Microarray expression data analysis
Groups: siA against hnRNP A2/B1(A549 siA), Empty Vector (A549 EV)
Repeats: 3 times each group
Total: 6 arrays (Affymetrix Human Genome U133 Plus 2.0)
Cell lines: Lung cancer cell lines A549 EV and A549 siA

Data preprocessing and normalization:
Data preprocessing and normalization were performed using the Bioconductor package affy and Affymetrix GeneChip software. Quality plots including RNA degradation plots and boxplots are displayed in:
Supplementary_Fig1

Data filtering:
There were 1060 (1.9%) probe sets with 95th percentile/5th percentile >= 2 folds. All (54675) spots based on RMA summary measure were used in further class comparison analysis.

Class comparison:
Two-sample t-test was performed on 54675 spots. Genes significantly up- or down-regulated between siA and EV were selected based on p-value <=0.001 and fold change >=1.5. 425 probe sets were identified as differentially expressed between siA vs EV at 0.001 level and 232 of them with fold change >= 1.5. False Discovery Rate (FDR) at 0.001 level was 12.8%. The analysis results were displayed by p-value plot shown in:
Supplementary_Fig2

Cluster analysis:
Average linkage hierarchical clustering of samples was performed with Pearson correlation as the similarity metric. Results are shown in:
Supplementary_Fig3

Gene list:
232 probe sets were identified as differentially expressed genes between siRNA and Empty Vector. These 232 probed sets were identified as 173 different genes. 111 were down-regulated after silencing hnRNP A2/B1 and 62 were up-regulated. Final list of 173 genes has been saved as:
Supplementary_Table1

Pathway Identification:
One of the challenging aspects of expression profiling is determining the biologic interactions and relevance of large numbers of differentially expressed genes. We used the newly developed Ingenuity Pathway Systems (www.ingenuity.com) to identify clusters of interacting genes that coordinately up- or downregulated, and thus identify several pathways.