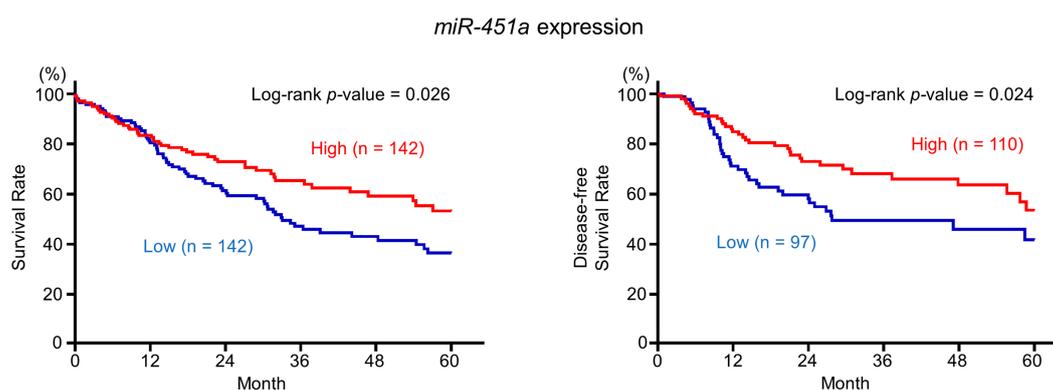
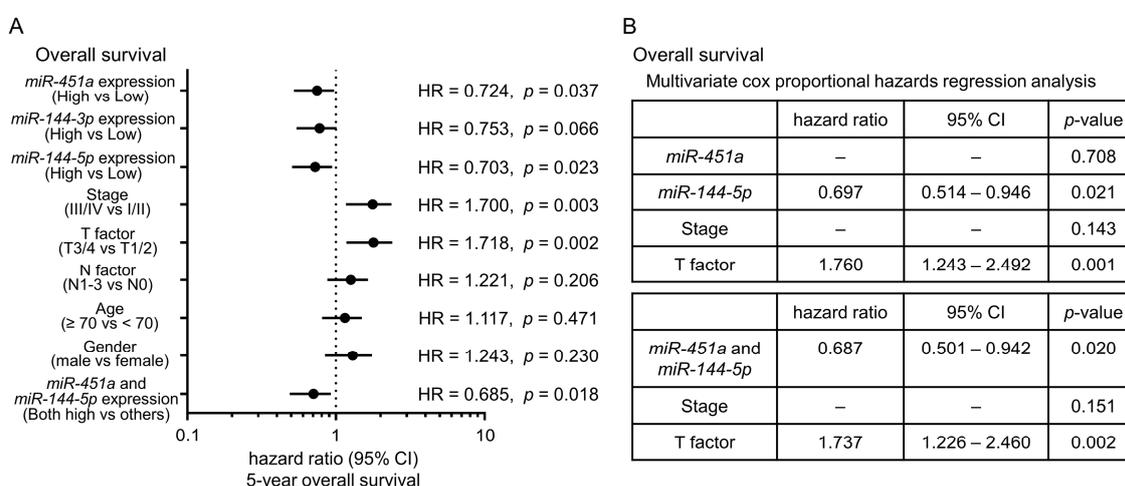


# Supplementary Materials: Regulation of *KIF2A* by Antitumor *miR-451a* Inhibits Cancer Cell Aggressiveness Features in Lung Squamous Cell Carcinoma

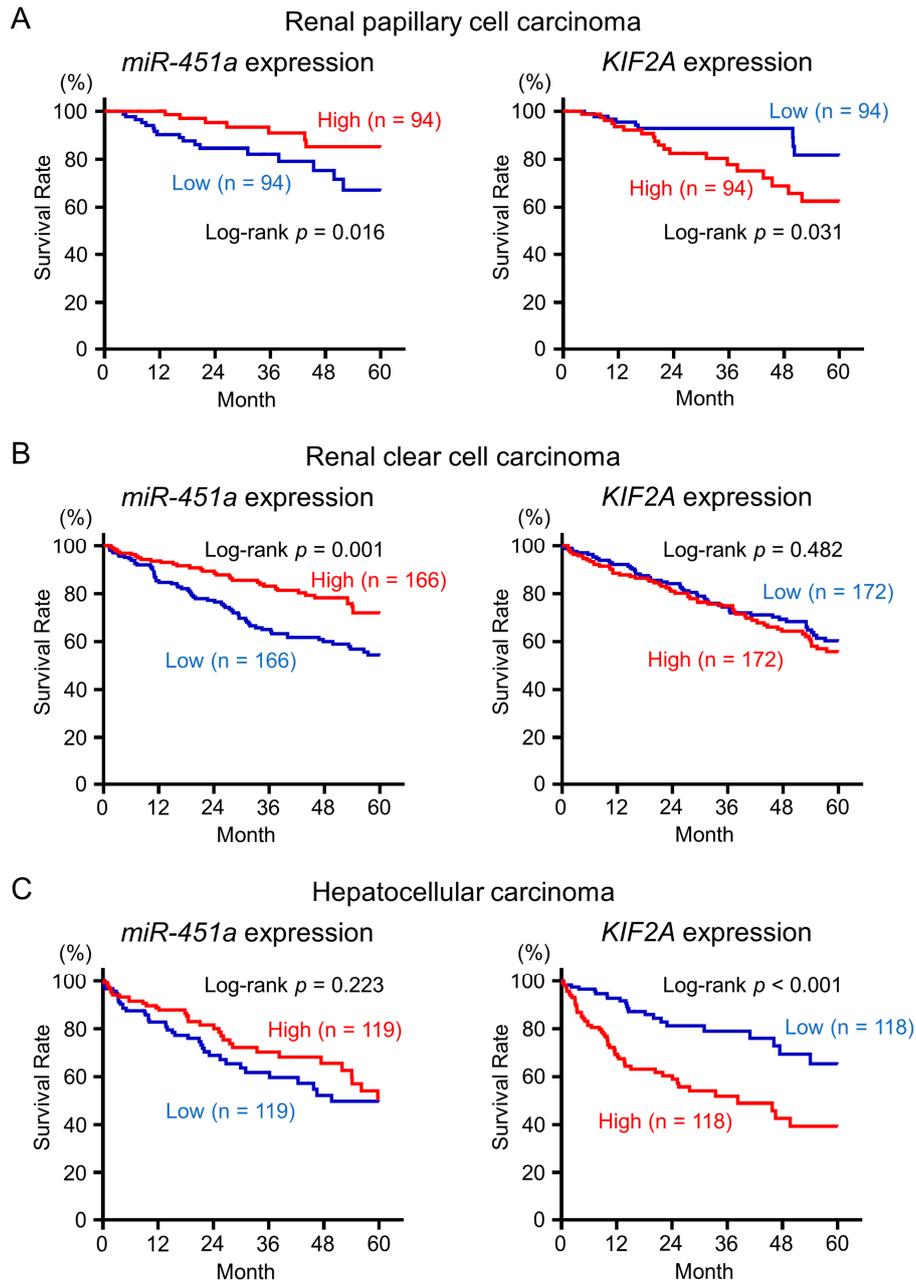
Akifumi Uchida, Naohiko Seki, Keiko Mizuno, Yasutaka Yamada, Shunsuke Misono, Hiroki Sanada, Naoko Kikkawa, Tomohiro Kumamoto, Takayuki Suetsugu and Hiromasa Inoue



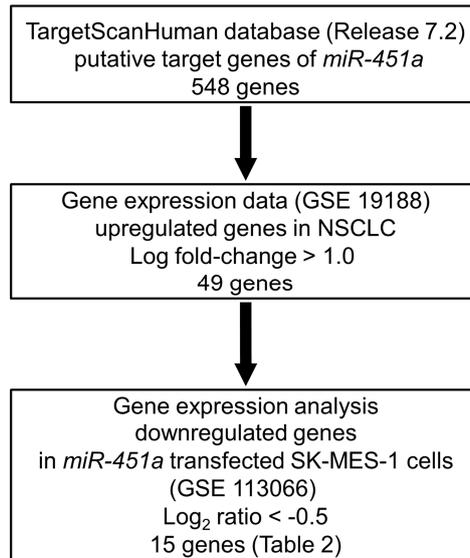
**Figure S1.** Kaplan-Meier analysis of *miR-451a* expression among LUSQ patients with adjusting clinical stage and age distribution. Kaplan-Meier curve of 5-year overall survival and 5-year disease-free survival according to *miR-451a* expression among patients with LUSQ in TCGA database ( $p = 0.026$  and  $p = 0.024$ , respectively). Clinical stage and patient’s age were adjusted and analyzed. Patients were divided into high (red) and low (blue) expression groups.



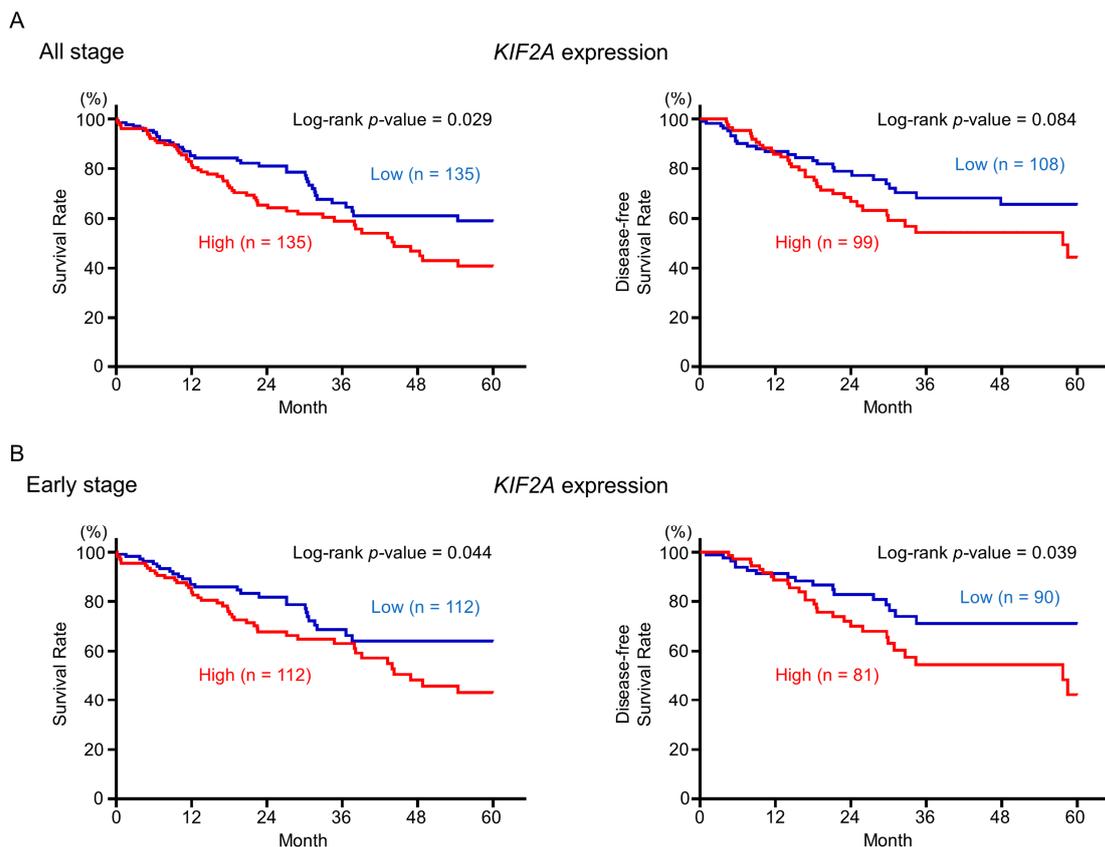
**Figure S2.** Clinical significance of expression of *miR-451a*, *miR-144-3p* and *miR-144-5p* in the patients with LUSQ. (A) Forest plot of univariate Cox proportional hazards regression analysis of 5-year overall survival. (B) Multivariate Cox proportional hazards regression analysis of 5-year overall survival using TCGA database. High expression of 2 miRNAs (*miR-451a* and *miR-144-5p*) was an independent predictive factor for survival of the patients. For this analysis, patients were divided in half by expression levels of miRNA among TCGA database and were merged by patients ID.



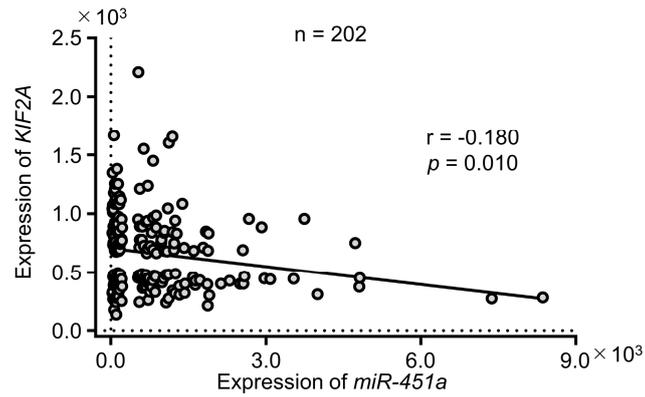
**Figure S3.** Kaplan-Meier analyses of *miR-451a* and *KIF2A* expression among other types of cancers. Kaplan-Meier curve of 5-year overall survival according to *miR-451a* and *KIF2A* expression among patients with renal papillary cell carcinoma (A), renal clear cell carcinoma (B), and hepatocellular carcinoma (C). Patients were divided into high (red) and low (blue) expression groups.



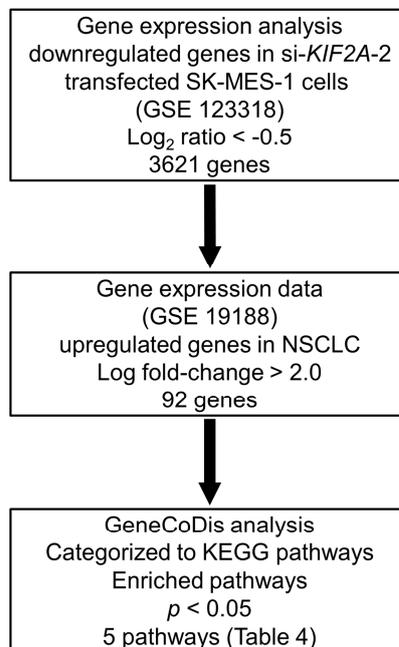
**Figure S4.** Flowchart illustration of the strategy for identification of target genes of *miR-451a*. By combination of *in silico* database exploration and gene expression analysis using *miR-451a*-transfected SK-MES-1 cells, we identified 15 candidate target genes.



**Figure S5.** Kaplan-Meier analyses of *KIF2A* expression among LUSQ patients with adjusting clinical stage and age distribution. (A) Kaplan-Meier curve of 5-year overall survival and 5-year disease-free survival according to *miR-451a* expression among patients with LUSQ in TCGA database ( $p = 0.029$  and  $p = 0.084$ , respectively). Clinical stage and patient's age were adjusted and analyzed. Patients were divided into high (red) and low (blue) expression groups. (B) Kaplan-Meier curve analyses using early stage patients of LUSQ (stage I and II). Patients were divided into high (red) and low (blue) expression groups.



**Figure S6.** Correlation between *miR-451a* and *KIF2A* expression in LUSQ patients. TCGA database analyses showed that a negative correlation was detected between *miR-451a* and *KIF2A* expression in LUSQ patients ( $r = -0.180$  and  $p = 0.010$ ).



**Figure S7.** Flowchart illustration of the strategy for identification of *KIF2A*-mediated downstream pathways. By combination of genome-wide gene expression analyses and *in silico* analyses using si-*KIF2A*-transfected SK-MES-1 cells, we identified 5 pathways as significantly enriched pathways.

