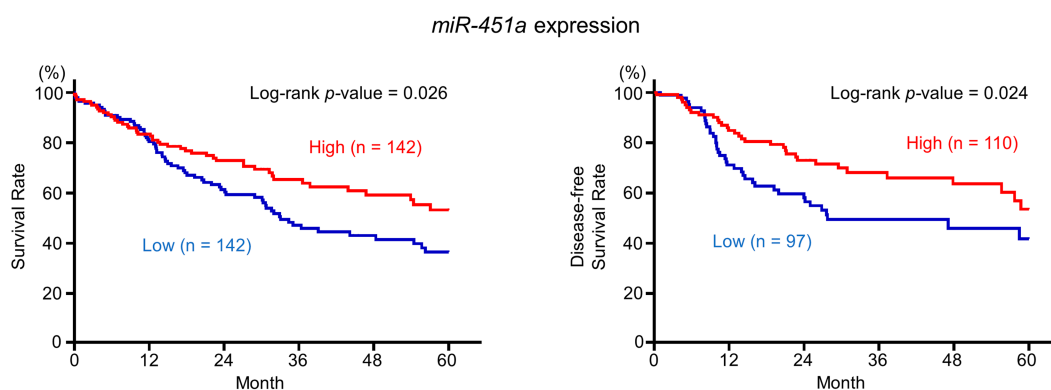
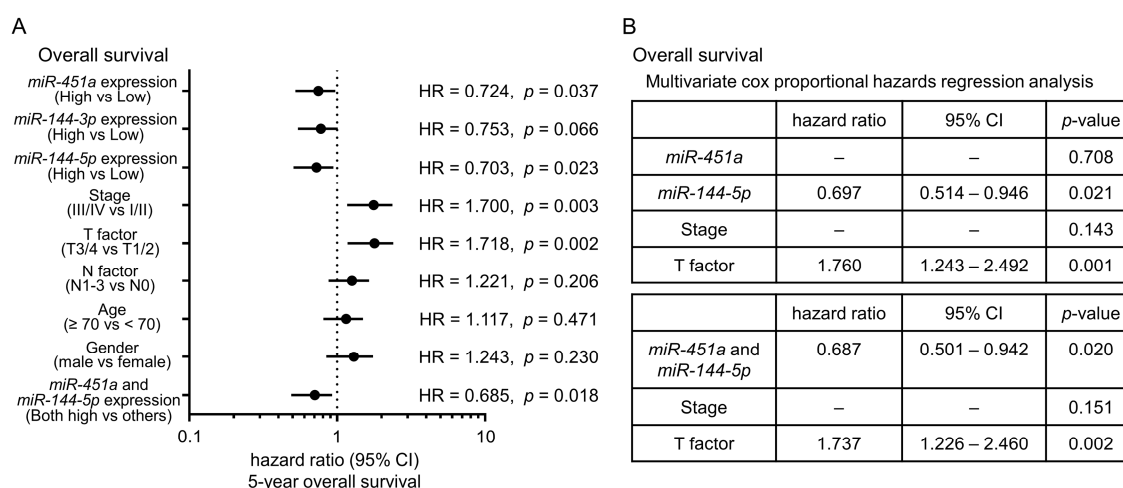


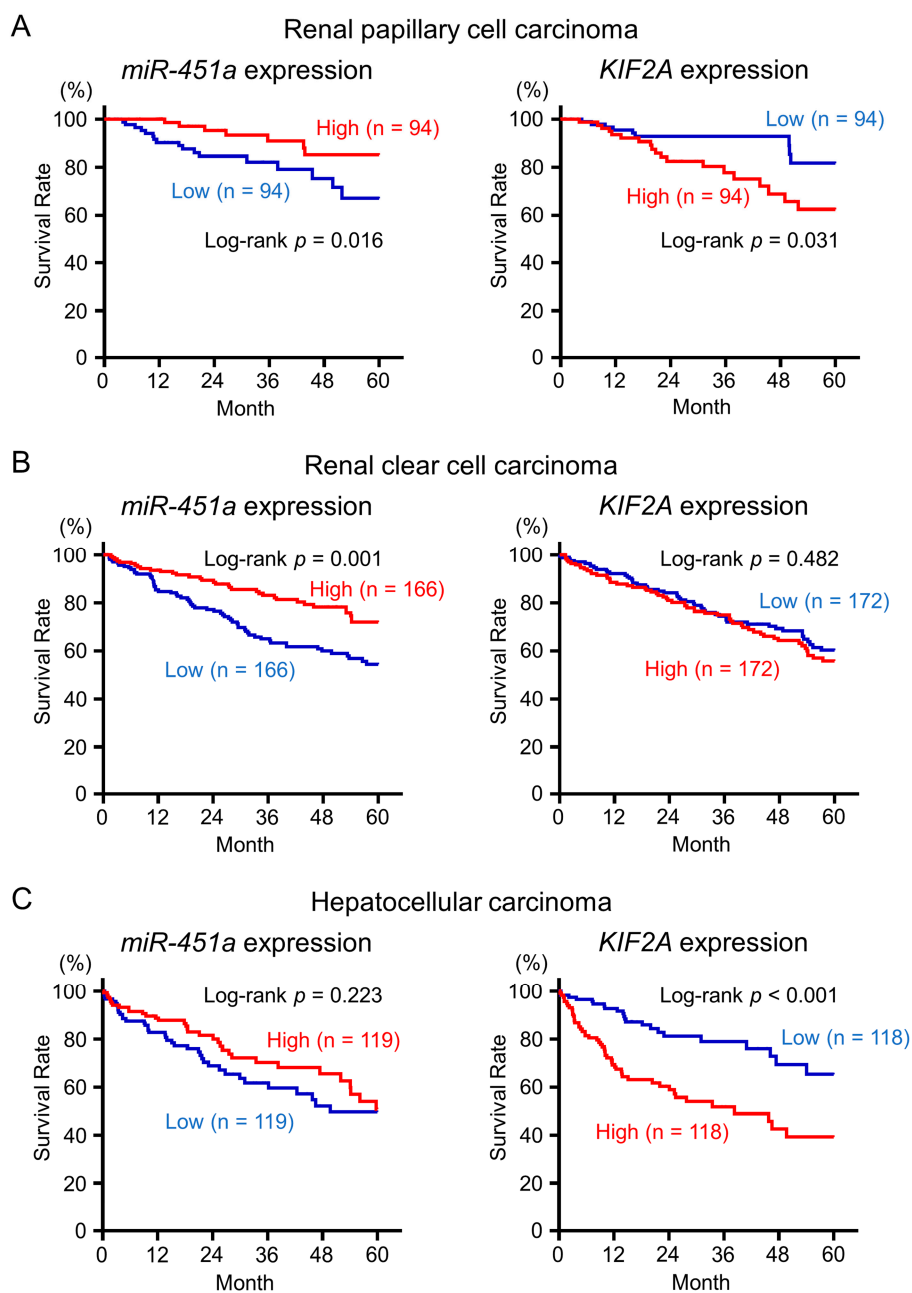
# Supplementary Materials: Regulation of *KIF2A* by Antitumor *miR-451a* Inhibits Cancer Cell Aggressiveness Features in Lung Squamous Cell Carcinoma

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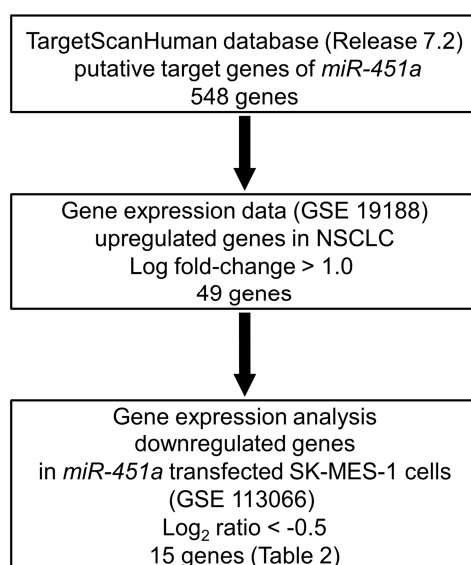


**Figure S1.** Kaplan-Meier analysis of *miR-451a* expression among LUSQ patients with adjusting clinical stage and age distribution. Kaplan-Meier curve of 5-year overall survival and 5-year disease-free survival according to *miR-451a* expression among patients with LUSQ in TCGA database ( $p = 0.026$  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.

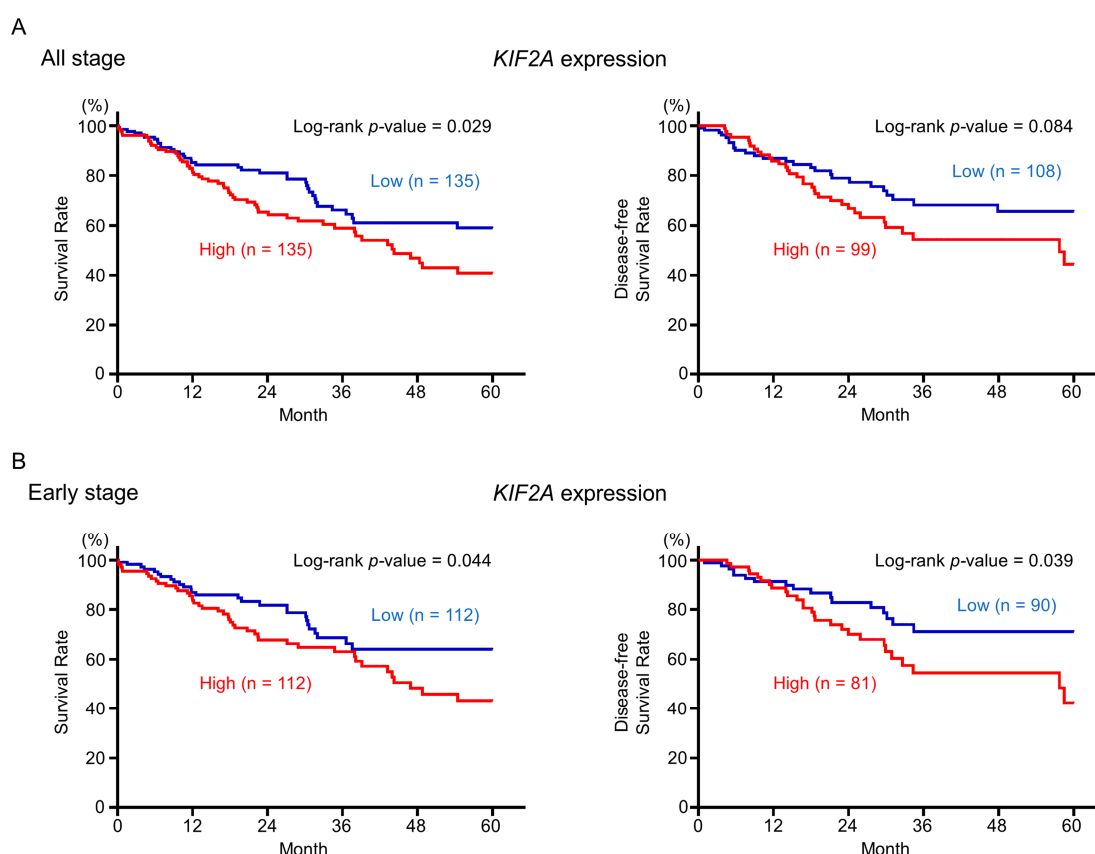




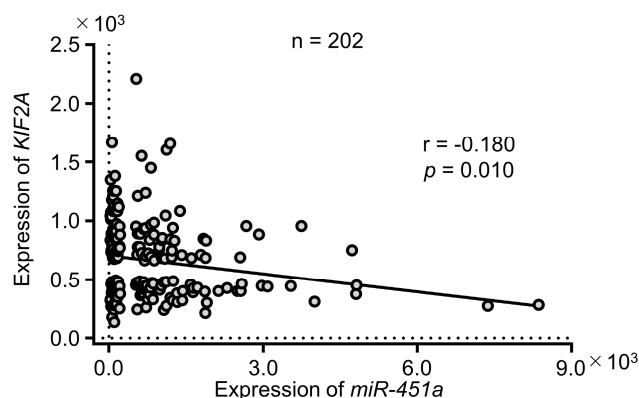
**Figure S3.** Kaplan-Meier analyses of *miR-451a* and *KIF2A* expression among other types of cancers. Kaplan-Meier curve of 5-year overall survival according to *miR-451a* and *KIF2A* expression among patients with renal papillary cell carcinoma (A), renal clear cell carcinoma (B), and hepatocellular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



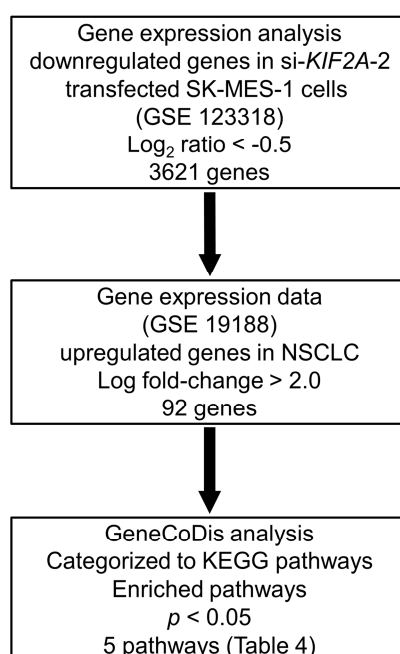
**Figure S4.** Flowchart illustration of the strategy for identification of target genes of *miR-451a*. By combination of *in silico* database exploration and gene expression analysis using *miR-451a*-transfected SK-MES-1 cells, we identified 15 candidate target genes.



**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.



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