Materials and methods

Statistical analysis. Receiver operating characteristic (ROC) curves were used to evaluate the diagnostic values of microRNA (miR)-130a, miR-25 and miR-191* in patients with non-small cell lung cancer (NSCLC). The χ^2 test was used to analyze the different frequencies of microRNAs in distinguishing between adenocarcinomas and squamous cell carcinomas, as well as between patients with or without radiotherapy.

Results

Relative expression of serum miR-130a, miR-25 and miR-191* in patients with NSCLC compared with that in healthy controls and its diagnostic value for lung cancer. The RT-qPCR results

demonstrated that the expression levels of miR-130a, miR-25 and miR-191* in the serum of patients with NSCLC were higher compared with those of healthy control subjects (P<0.001; Fig. S2A-a, B-a and C-a). ROC curve analysis was used to evaluate the efficacy of miR-130a, miR-25 and miR-191* in the diagnosis of lung cancer (Fig. S2A-b, B-b and C-b). The areas under the curves of miR-130a, miR-25 and miR-191* were 0.817 (95% CI, 0.745-0.889), 0.774 (95% CI, 0.694-0.853) and 0.817 (95% CI, 0.745-0.889), respectively. The best cut-off values were 1.4343, 1.2844 and 1.3551, the sensitivity values were 66.67, 66.67 and 59.52%, and the specificity values were 90.48, 90.48 and 95.24%, respectively (Fig. S2A-b, B-b and C-b).

Figure S1. Relative expression levels of serum miR-130a, miR-25 and miR-191* between patients with non-small cell lung cancer with different clinical features. Relative expression levels of (A) miR-130a, (B) miR-25 and (C) miR-191* in the serum of patients \geq 60 vs. <60 years old, with radiotherapy vs. without radiotherapy, with adenocarcinoma vs. squamous carcinoma type, and death vs. survivors at the time of the last follow-up. The data were presented as a dot plot of the raw data, overlaid by a box and whisker plot (median, first and third percentiles, range). miR, microRNA.

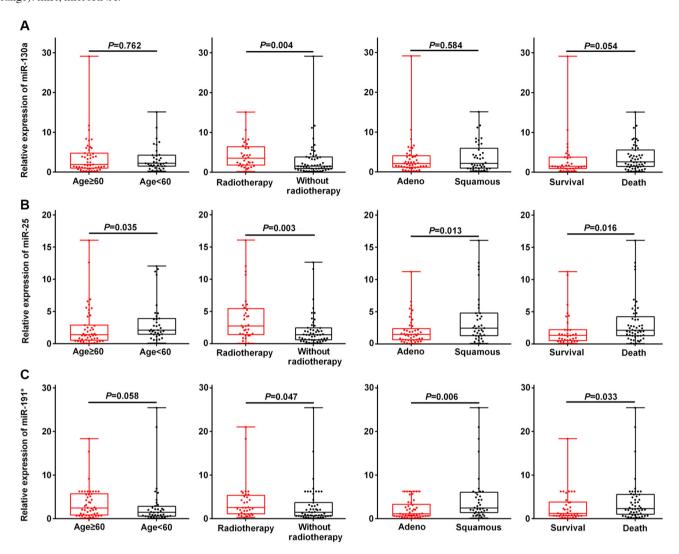


Figure S2. Relative expression levels of serum miR-130a, miR-25 and miR-191* in patients with non-small cell lung cancer versus HC, and their diagnostic value for lung cancer. The data was presented as a dot plot of the raw data, overlaid by a box and whisker plot (median, first and third percentiles, range). (A-a) miR-130a expression in the serum of patients versus HC and (A-b) ROC curve for miR-130a expression in predicting lung cancer. (B-a) miR-25 expression in the serum of patients versus HC and (B-b) ROC curve for miR-25 expression in predicting lung cancer. (C-a) miR-191* expression in the serum of patients versus HC and (C-b) ROC curve for miR-1191* expression in predicting lung cancer. ROC, receiver operating characteristic; HC, healthy control; miR, microRNA.

