METTL3 promotes non-small cell lung cancer (NSCLC) cell proliferation and colony formation in a m6A-YTHDF1 dependent way

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Abstract

Background: N6-methyladenosine (m6A) is the most common RNA modification, which plays a pivotal role in tumor development and progression. In this study, we assessed the role of m6A methyltransferase METTL3 in FRAS1-involved cell proliferation and colony formation of non-small cell lung cancer (NSCLC) cell lines.

Methods: Cell viability was analyzed by Cell Counting Kit (CCK-8) and colony formation. M6A RNA immunoprecipitation (IP), Ribosomal immunoprecipitation, RNA immunoprecipitation (RIP) were performed to verify the relationship between METTL3, FRAS1 and YTHDF1. Rescue experiments to confirm the regulatory mechanism of METTL3-FRAS1 promoted NSCLC cell proliferation through CDON by cooperating YTHDF1.

Results: We found that FRAS1 was correlated with poor prognosis in NSCLC patients, of which the transcript undergoes m6A modification regulated by METTL3. METTL3 silence reduced cell viability of NSCLC cells HCC827 and NCI-H1975, which could be restored by FRAS1 overexpression. The m6A modification of FRAS1 could be recognized by YTHDF1. FRAS1 silence or YTHDF1 silence could rescue the elevated NSCLC cell proliferation, colony formation, and tumor growth induced by METTL3 overexpression in vitro and in vivo.

Conclusions: Our study reveals that METTL3-FRAS1 plays a crucial role in NSCLC cell proliferation, colony formation, and tumor growth through the regulation of CDON by cooperating YTHDF1.

Keywords: METTL3, Non-small cell lung cancer (NSCLC), Cell proliferation, Colony formation, YTHDF1, FRAS1, CDON

Introduction

N6-methyladenosine (m6A) modification has been identified to play a vital role in tumorigenesis [1–3]. Abnormal m6A modifications have been reported to be associated with glioblastoma (GBM), ovarian cancer, bladder cancer, gastric cancer, pancreatic cancer and so on [4–6]. Existing studies showed that m6A modification acts the dual roles in cancers. Nonetheless, there are still largely unknown about the role, the mechanism and the clinical value of m6A in lung cancer.

M6A modification is regulated by specific methyltransferases (referred to as “writers”), m6A recognition proteins (referred to as “readers”) and demethylases (referred to as “erasers”). METTL3 is the first identified methyltransferase which is responsible for m6A modification. Emerging evidence have shown that METTL3 plays multiple functions in tumorigenesis [7, 8]. For instance, METTL3 promotes liver cancer progression via regulating SOCS2 expression in an m6A-dependent manner [9]. In gastric cancer (GC), METTL3 promotes cell proliferation and liver metastasis in GC by enhancing m6A modification and stability of HDGF [10]. It is reported
that METTL3 accelerates colorectal cancer progression by inducing m6A modification of GLUT1 and activating mTORC1 signaling [11]. METTL3 is also found to facilitate breast cancer tumorigenesis by regulating Bcl-2 [12]. Recent research reveals that METTL3 is upregulated in lung cancer [13]. METTL3-induced m6A methylation of IncRNA ABHD11-AS1 could promote cell proliferation and Warburg effect of NSCLC [14]. These studies indicate that METTL3-modulated m6A mRNA methylation plays vital roles in human tumors including lung cancer.

YT521-B homology (YTH) domain-containing proteins (YTHDFs) YTH could recognize and regulate the effects of RNA m6A modification. YTHDF2 is the first reported m6A reader and studies have shown that YTHDF2 promotes tumorogenesis in multiple cancers [2]. For example, YTHDF2 could promote glioblastoma growth by remaining the stability of MYC and VEGFA transcripts in an m6A-dependent way [15]. In hepatocellular carcinoma (HCC), one research shows that YTHDF2 expression has a positive correlation with HCC progression [16] whereas another research reports that YTHDF2 suppressed HCC tumor growth through accelerating EGFR mRNA degradation [17]. Except for YTHDF2, the YTHDFs family contains YTHDF1, YTHDF3, YTHDC1. It is reported that YTHDF1 functions as a tumor promoter in various cancers such as gastric cancer [18], HCC [19, 20], NSCLC [21]. Up to now, little is known about the role of YTHDF1 in NSCLC.

Fraser extracellular matrix complex subunit 1 (FRAS1) has been reported to be essential for embryonic epithelial-mesenchymal integrity [22]. Recent studies show that FRAS1 contributes to the malignant phenotype of NSCLC [23], gastric cancer [24], colorectal cancer [25].

In this study, we explored the role and the potential molecular mechanism of FRAS1 in NSCLC. Our data demonstrates that m6A methyltransferase METTL3 induced FRAS1 m6A modification and protein stability, thus accelerating NSCLC cell proliferation.

Methods

Data analysis

The overall survival analysis of FRAS1 in non-small-cell lung cancer (NSCLC) was assessed by using the online survival analysis tool Kaplan–Meier plotter (https://kmplot.com/analysis/index.php?p=background) [26], containing the clinical information of NSCLC patients (https://kmplot.com/analysis/index.php?p=service&cancer=lung) [27]. The NSCLC patients were divided into two groups by the medium expression of FRAS1. The hazard ratio (HR) with 95% confidence intervals (CIs) and log rank p value were labeled in the curve. The JetSet probe set for FRAS1 (220910_at) was used for analysis. Pearson correlation analysis was performed to identify co-expressed genes related to METTL3 and YTHDF1 with a cut-off of the |Pearson R| > 0.3 and P < 0.05 in TCGA-LUAD&LUSC dataset. According to the correlation coefficient for METTL3 greater than 0.6, correlation coefficient for YTHDF1 greater than 0.45, and P value less than 0.001, the intersection genes were screened out and listed in the Additional file 1: Table S1.

Human tissues and cell lines

This study includes five pairs of lung adenocarcinoma (LUAD) tissues from Space Central Hospital. The ethical approval for this study was from Space Central Hospital (20,200,511-JJHZ-01). Written informed consents were obtained from each patient. Four NSCLC cell lines (A549, NCI-H1299, HCC827, and NCI-H1975) and human bronchial epithelial cell line HBEC were obtained from Procell Life Science&Technology Co.,Ltd (Wuhan, China). A549 cells were cultured in DMEM (High glucose, Gibco, Grand Island, NY, USA, 11,965–092) with 10% FBS (Gibco) and 1% penicillin/streptomycin (P/S, Procell). NCI-H1299, HCC827, and NCI-H1975 cells were cultured in RPMI-1640 medium (Gibco) with 10% FBS (Gibco) and 1% penicillin/streptomycin (P/S, Procell). HBEC cells were cultured in the bronchial epithelial growth medium (BEGM, Lonza, CC-3170). All the cells were cultured at 37 °C in a 5% CO2 incubator.

Stable cell lines

shMETTL3, shYTHDF1, shFRAS1 and shScramble were synthesized from RiboBio (Guangzhou, China), which were cloned into the vector pLKO.1 puro. The stable cell lines such as shMETTL3, shYTHDF1, shFRAS1 and shscramble were generated by infecting these corresponding lentivirus. Two days after infection, the puromycin (1 μg/mL) was added. The shRNA sequences were shown in Table 1.

Quantitative Reverse Transcription-Polymerase chain reaction (qRT-PCR)

Total RNA was isolated using Trizol (Beyotime, Shanghai, China) and reverse transcription was performed with the EasyScript® First-Strand cDNA Synthesis SuperMix (Transgen, Beijing, China). Quantitative real-time PCR analysis was performed with the TransStart® Green qPCR SuperMix (Transgen). The relative expression of each gene was analyzed by the standard 2−ΔΔCt method [28] and normalized to GAPDH. The sequences of qPCR Primers were listed in Table 2.

Western blot

Cells were lysed and proteins were extracted using the ice-cold lysis buffer. The equal amount of proteins were separated by 6% or 10% SDS-PAGE and transferred to
nitrocellulose membrane. After blocked with 5% non-fat milk for 1 h at room temperature, membranes were incubated with corresponding primary antibodies at 4 °C overnight. Then the membranes were incubated with horseradish peroxidase (HRP)-conjugated secondary antibodies and sensed by the enhanced chemiluminescence (ECL) substrates (Beyotime, Shanghai, China). Primary antibodies were as follows: anti-FRAS1 (#ab240583; Abcam, Cambridge, UK), anti-METTL3 (#ab195352; Abcam), anti-YTHDF1 (#ab252346; Abcam), anti-RPL-22 (#ab77720; Abcam), anti-CCND1 (#ab227056; Abcam), anti-β-actin (#ab8226; Abcam), anti-α-tubulin (#ab7291, Abcam) and anti-GAPDH (#ab8245; Abcam).

CCK-8 and colony formation
Cell viability was analyzed using the cell counting kit-8 (CCK-8, Beyotime). Cells were seeded in the 96-well plate (2 × 10³/well) and cultured for different time (0, 1, 2, 3, 4 or 5 days). Cells were incubated with 10 μL CCK-8 solution for 1 h. The absorbance at 450 nm was detected using a multimode plate reader.

For colony formation assay, cells were plated at a density of 4 × 10³/well in the 6-well plate with complete medium. After 2 weeks, cells were fixed with paraformaldehyde and then stained with 0.1% crystal violet. The colonies images were determined by using a camera.

EDU incorporation
The chamber slides were coated with poly-D-lysine and matrigel. HCC827 and NCI-H1975 cells were seeded on the coated slides. The next day, cells were transfected with si-CDON or si-NC plasmids. After transfection for 48 h, EDU was added for 4 h before fixation. Cells were incubated with fixative solution for 15 min and permeabilized for 20 min. Then the reaction mix was used to fluorescently label EDU for 30 min. Cells were stained for DAPI for 30 min. After that, the EDU positive cells were analyzed using fluorescence microscope, ImageJ software and GraphPad Prism 8.0. The EDU incorporation was performed using Edu staining proliferation kit (Abcam, ab222421).

RNA immunoprecipitation (RIP)
RIP was performed with EZ-Magna RIP RNA-Binding Protein Immunoprecipitation Kit (Millipore, Billerica, MA). Cells were lysed with specially formulated RIP lysis buffer. Cell lysates were incubated with the indicated antibodies together with the mixed protein A/G-beads at 4 °C overnight. The precipitated RNA was examined by qRT-PCR.

RNA stability assays
HCC827 or NCI-H1975 cells were treated with actinomycin D (5 μg/mL, Sigma) for 0, 2, 4, 6 h. Total RNA was extracted by TRizol and analyzed by qRT-PCR.

m6A RNA immunoprecipitation assay (MeRIP)
Total RNA was isolated using TRizol (Beyotime) and then sonicated into RNA fragments. Then, the RNA fragments were incubated with the antibody against m6A (ab208577, Abcam) together with protein A beads at 4 °C for 10 h. The protein-RNA complex was washed...
and treated with proteinase K. The immunoprecipitated RNA was detected by qRT-PCR.

**Ribosomal immunoprecipitation**

HCC827 or NCI-H1975 cells with stable shYTHDF1 or shscr were transfected with RPL22-Myc (Origene, Beijing, China). For 48 h later, cells were lysed using RIPA buffer and then incubated with anti-Myc antibody (Abcam) mixed with protein A beads at 4 °C for 8 h. The normal mouse immunoglobulin G (IgG) was used as control. The protein-RNA complex was washed and treated with proteinase K. The immunoprecipitated RNA was detected by qRT-PCR.

**Xenograft tumor models**

Twenty BALB/c nude mice (6–8 weeks old) were purchased from Beijing Viewsolid Biotechnology Co. LTD (Beijing, China). Mice were randomly divided into four groups (five mice/group). The stable cells of NCI-H1975/Vector + sh-NC, NCI-H1975/METTL3 + sh-NC, NCI-H1975/METTL3 + sh-YTHDF1, and NCI-H1975/METTL3 + sh-FRAS1 were infected and constructed by using lentivirus (Gene Pharma, Shanghai, China). The xenografts in each group were established by using subcutaneous injection with approximately 1 × 10⁶ cells in each mouse. Tumor volume was measured every 7 days. The tumor volume was calculated as 1/2 × length × width². The tumor weight was recorded 28 days after inoculation.

**Statistical analysis**

All experiments were independently repeated at least three times. Data was analyzed using GraphPad Prism 8.0 (GraphPad Software, La Jolla, CA). Group differences were analyzed using Student’s t-test. The correlation between FRAS1 and CDON expression was tested via starbase RNA-RNA module (https://starbase.sysu.edu.cn/index.php). P < 0.05 was considered to be statistical significance.

**Results**

**N6-methyladenosine (m6A) modification and protein level of FRAS1 is upregulated in NSCLC**

We used TCGA-LUAD/LUSC database to analyze the correlated genes with METTL3 and YTHDF1, respectively. FRAS1 was identified to be the gene most associated both with METTL3 and YTHDF1 in non-small cell lung cancer (NSCLC) as shown in Fig. 1A (R_{METTL3} = 0.730, R_{YTHDF1} = 0.452, P < 0.001, Additional file 1: Table S1). Next, we found an interesting phenotype that the mRNA level of FRAS1 was significantly lower in 106 paired of NSCLC tumor tissues than that in the corresponding normal tissues (Fig. 1B) whereas the Kaplan–Meier plotter analysis indicated that high FRAS1 expression was associated with shorter overall survival of NSCLC patients (log rank P = 7e-04, https://kmplot.com/analysis/, Fig. 1C), suggesting that FRAS1 might be a risk prognosis biomarker in NSCLC. We wondered whether there was m6A modification of FRAS1 mRNA in lung cancer. Then, we evaluated the expression of FRAS1 and its m6A level in our collected LUAD samples. Consistent with the public database analysis, FRAS1 mRNA level was decreased in tumor tissues compared to normal tissues (Fig. 1D). However, the m6A level and the protein level of FRAS1 was significantly increased in 3 cases of tumor tissues compared to the paired corresponding normal tissues (Fig. 1E, F). A similar result was also observed in NSCLC cell lines. FRAS1 mRNA level was decreased in NSCLC cell lines A549, HCC827, NCI-H1975 and NCI-H1299 compared to the human bronchial epithelial cells HBEC (Fig. 1G). The m6A level and protein level of FRAS1 in NSCLC cell lines were higher than in HBEC (Fig. 1H, I). These results suggest that m6A modification of FRAS1 mRNA and its protein level was obviously increased in NSCLC tumor tissues.

**METTL3 induces FRAS1 mRNA m6A modification**

Emerging studies show that m6A plays a critical role in messenger RNA (mRNA) by regulating mRNA process, translation or decay [3]. For example, m6A may accelerate the processing time of mRNA precursors and promote mRNA transport and nucleation speed in cells [29, 30]. To investigate the regulatory mechanism of the m6A modification on FRAS1 mRNA, we focused on the m6A “writer” METTL3. We observed that METTL3 was highly expressed in NSCLC tumor tissues compared to normal tissues (Fig. 2A). The m6A modification sites of FRAS1 mRNA were predicted by SRAMP (http://www.cuilab.cn/sramp/) [31], of which the consensus motif were near the terminator (Fig. 2B). To verify the presence of FRAS1 mRNA m6A methylation, we performed the m6A immunoprecipitation using m6A antibody. The immunoprecipitated RNA fragments were detected by qRT-PCR as shown in Fig. 2C and 2D. The m6A modification of FRAS1 mRNA was both detected in HCC827 and NCI-H1975 cells (Fig. 2C). Moreover, the m6A methylation level in shMETTL3 cells (HCC827 and NCI-H1975) was remarkably reduced than the shscr group (Fig. 2D). There was 80% knockdown efficiency of shMETTL3 which was validated by qPCR and western blot (Fig. 2E). Above
all, these results suggest that METTL3 could promote FRAS1 transcript m6A modification.

**METTL3 silence led to the decreased FRAS1 protein expression and cell proliferation**

To explore the biological function of METTL3-regulated FRAS1 m6A modification, we generated the two stabilized METTL3-silenced cells (HCC827 and NCI-H1975). METTL3 was effectively decreased at protein level in shMETTL3 cells compared to shscr cells together with the reduced FRAS1 expression at protein level (Fig. 3A). There was no effect on the alteration of FRAS1 mRNA upon METTL3 knockdown (Fig. 3B). Additionally, the protein level of FRAS1 was no longer reduced with the extension time of actinomycin D (ActD) treatment, suggesting that METTL3 regulated FRAS1 expression dependent on the m6A manner but had no direct effect on FRAS1 protein (Fig. 3C). CCK-8 analysis showed
that cell proliferation was decreased in stable METTL3-silenced HCC827 and NCI-H1975 cells (Fig. 3D), which was consistent with the colony formation results (Fig. 3E). These results suggest that METTL3 alters FRAS1 protein level but not mRNA level and has an inhibiting action on cell proliferation.

**YTHDF1 plays a role in m6A-modified FRAS1 expression**

M6A-modified RNAs could be recognized and transmitted to the downstream pathway by the m6A reader proteins. YTHDF1 has been identified to be critical for NSCLC proliferation [21]. In this study, we found that YTHDF1 was highly expressed in NSCLC tumor tissues compared to normal tissues via UALCAN (Fig. 4A), indicating that YTHDF1 may play a critical role in m6A-regulated FRAS1 expression. The RIP assay validated that YTHDF1 could bind to FRAS1 mRNA (Fig. 4B). To investigate the role of YTHDF1 in the regulation of m6A-modified FRAS1, we constructed stable YTHDF1-silenced HCC827 and NCI-H1975 cells. qRT-PCR analysis showed that YTHDF1 was significantly knockdown in shYTHDF1 cells, while FRAS1 mRNA has no obvious change, but a remarkable decrease at protein level (Fig. 4D). Furthermore, we performed ribosome immunoprecipitation to analyze the YTHDF1-silence effects on the ribosome occupancy on m6A-modified FRAS1 mRNAs. Results indicated that the ribosome occupancy on FRAS1 mRNA was reduced in YTHDF1-silenced cells compared to control cells (Fig. 4D). As expected, FRAS1 mRNA stability was not changed when treated with ActD upon loss of YTHDF1, suggesting that YTHDF1 was not involved in FRAS1 RNA synthesis. Next, to investigate whether YTHDF1 was involved in the regulation of FRAS1 protein stability, we treated cells with the proteasome inhibitor MG132. We observed that FRAS1 protein was still decreased in YTHDF1-silenced cells even with MG132 treatment (Fig. 4E), indicating that YTHDF1 could modulate FRAS1 protein stability not dependent on the protein degradation pathway. These results further suggest that m6A reader protein YTHDF1 may recognize...
Fig. 3 (See legend on previous page.)
the m6A modification of FRAS1, which was increased by METTL3.

**METTL3 induced FRAS1 m6A modification modulates CDON expression**

We found that cell adhesion associated, oncogene regulated (CDON) had a strong positive correlation with FRAS1 by the online bioinformatics analysis. The Pearson analysis showed that CDON was the strongest correlated factor with FRAS1 in NSCLC (R = 0.61, Fig. 5A). Starbase online database revealed that there was a strong associated between FRAS1 and CDON in 526 pairs of NSCLC samples (r = 0.505, P < 0.001, Fig. 5B). In addition, FRAS1 overexpression could rescue the CDON protein level in shMETTL3 cells (Fig. 5C). CCK-8 analysis and colony formation analysis revealed that the decreased proliferation caused by METTL3 knockdown could be reversed by FRAS1 overexpression (Fig. 5D, E). These data suggest that METTL3 regulates cell proliferation via FRAS1.

In addition, we also preliminarily explored the biological role of CDON in HCC827 and NCI-H1975 cells by performing loss-of-function by introducing siRNA targeting CDON. CDON expression at mRNA and protein level was significantly decreased in si-CDON-transfected cells as shown in Additional file 1: Figs. S1A and 1B. CCK-8 assay results showed that CDON downregulation led to reduced cell proliferation (Additional file 1: Fig. S1C). Consistently, we also observed that EDU positive cells were decreased when CDON was knockdown by performing EDU incorporation (Additional file 1: Fig. S1D). These results suggest that CDON may act as an oncogene in HCC827 and NCI-H1975 cells.

**FRAS1 is a target of N6-methyladenosine METTL3 in NSCLC**

To further explore METTL3-induced FRAS1 m6A modification in NSCLC cell proliferation, rescue experiments were performed in stable YTHDF1-silence, FRAS1-silence cells by overexpressing METTL3. qRT-PCR results showed that there was no obvious alteration on the mRNA level of FRAS1 in METTL3-overexpression group compared to sh-YTHDF1 + METTL3-overexpression group (Fig. 6A). The upregulated FRAS1 and CDON protein levels induced by METTL3-overexpression could be restored by YTHDF1 silence or FRAS1 silence (Fig. 6B). Moreover, we also found that the elevated expression of cyclin D1 (CCND1) induced by METTL3 overexpression could be reversed by YTHDF1 knockdown or FRAS1 knockdown. CCND1 which belongs to the highly conserved cyclin family, regulates cell cycle G1/S transition and promotes cell proliferation in multiple tumors [32–34]. Consistently, we also detected CDON, METTL3 and YTHDF1 protein expressions in five collected tumor samples as shown in Additional file 1: Fig. S2. The result showed that CDON expression was upregulated in T1, T2, T3 and T5 tumor tissues compared to their corresponding normal tissues but T4 sample. YTHDF1 and METTL3 expression at protein levels were all upregulated in five tumor tissues compared to their paired normal tissues. Functional studies showed that the METTL3-overexpression induced elevated cell proliferation could also be rescued by YTHDF1 silence or FRAS1 silence analyzed by CCK-8 and colony formation assay (Fig. 6C and D). Moreover, we also validated the expression of CDON, YTHDF1, and METTL3 in collected NSCLC tumor samples. It was observed that CDON, YTHDF1 and METTL3 were highly expressed in cancer tissues compared to that of in corresponding normal tissues (Additional file 1: Fig. S2), suggesting that there was a positive relationship between FRAS1, CDON, and METTL3/YTHDF1. Above all, our data indicate that FRAS1 was a major target of METTL3 regulating NSCLC cell proliferation.

**METTL3-induced FRAS1 promotes NSCLC tumor growth in vivo**

To confirm the role of METTL3/FRAS1 axis in vivo, we verified its effects on tumor growth using xenograft tumor model. As shown in Fig. 7, the excessive tumor growth induced by METTL3 upregulation was blocked by FRAS1 or YTHDF1 knockdown, including tumor volume and tumor weight (Fig. 7A–C). Consistently, the increased expression of FRAS1 caused by METTL3 overexpression was reduced when FRAS1 or YTHDF1 silence (Fig. 7D). Taken together, METTL3-induced FRAS1 promotes NSCLC tumor growth in vivo.
Fig. 4 (See legend on previous page.)
Discussion

Lung cancer is considered to be the leading cause of cancer-related death in the world. The dysregulation of m6A modification is strongly associated with various tumor progression. The role of m6A regulators has been extensively reported in multiple tumors. However, not enough is known about the impact of m6A modification in lung cancer. This study addresses the role and functions of METTL3/YTHDF1/FRAS1 m6A in NSCLC cell proliferation.

In this study, we found an interesting phenomenon that there was an obvious difference between mRNA and protein level of FRAS1 in collected LUAD tissues, which was consistent in NSCLC cell lines. That is, there was no significant difference at mRNA level of FRAS1 between NSCLC tumors and normal tissues whereas FRAS1 at protein level was upregulated in LUAD tumors compared to normal tissues. However, our results were not consistent with the TCGA analysis, of which the mRNA is lower in lung cancer tumor tissues than normal tissues. There

| Genes | Pearson CC |
|-------|------------|
| CDON  | 0.81       |
| REEP1 | 0.58       |
| EFNB3 | 0.57       |
| ARHGAP28 | 0.57 |
| BGHE  | 0.56       |
| PTGIS | 0.52       |
| PRG4  | 0.52       |
| UPK3B | 0.52       |
| SYDE2 | 0.51       |
| OGN   | 0.51       |
| CLDN15| 0.51       |
| TGM1  | 0.51       |

Fig. 5 FRAS1 overexpression rescues the phenotype induced by METTL3 silence and CDON expression. A The positively associated genes with FRAS1 in NSCLC (pearson correlation r > 0.5). B The relationship between CDON and FRAS1 in NSCLC was analyzed using starbase (http://starbase.sysu.edu.cn/index.php). r = 0.505, P < 0.001. C The protein level of FRAS1 and CDON was analyzed by western blot in shMETTL3 HCC827 and NCI-H1975 cells with or without FRAS1 overexpression, or Ctrl cells. D CCK-8 assay was performed in shMETTL3 HCC827 and NCI-H1975 cells with or without FRAS1 overexpression, or Ctrl cells. * P < 0.05, ** P < 0.01, *** P < 0.001. E Colony formation was analyzed in shMETTL3 HCC827 and NCI-H1975 cells with or without FRAS1 overexpression, or Ctrl cells.
were three possible reasons. The first reason is that the size of our collected sample was small, just five pairs of samples. We would collected more samples to identify the expression of FRAS1 mRNA level between tumor tissues and normal tissues. Second, the tumor samples and normal samples were not paired in TCGA database. The
The m6A modification is dynamic and reversible, which could be removed by “eraser” m6A demethylase enzymes, such as FTO, ALKBH5 and demethylases et al. It is reported that FTO could promote hepatocellular carcinoma tumorigenesis via triggering PKM2 demethylation [42]. A study reported that ALKBH5 could maintains tumorigenicity of glioblastoma stem-like cells by sustaining FOXM1 expression [43]. In this study, we mainly focused on FRAS1 m6A modification by “Writers” and “Readers.” It would be interesting to investigate the possible regulatory mechanisms of FRAS1 modification by erasers enzymes such as FTO, which will be performed in our further project and enrich the regulatory mechanism mediated by FRAS1 in NSCLC.

**Fig. 7** METTL3 induced FRAS1 promotes tumor growth in vivo. A Representative images of tumors originated from xenografted NCI-H1975 cells stably expressing Vector + sh-NC, METTL3 + sh-NC, METTL3 + sh-YTHDF1, and METTL3 + sh-FRAS1 by subcutaneous injection. B The xenograft tumor model was constructed by using H1975 cells stably expressing Vector + sh-NC, METTL3 + sh-NC, METTL3 + sh-YTHDF1, and METTL3 + sh-FRAS1 and the tumor volumen was measured at the indicated time points 7, 14, 21, 28 days after subcutaneous injection. C The tumor tissues were weighed after mice were sacrificed after 28 days. D The protein expression of METTL3, YTHDF1, and METTL3 was detected by western blot. *P<0.05 or **P<0.01 indicates a significant difference between the indicated groups.
Fig. 7 (See legend on previous page.)
CDON (cell adhesion associated, oncogene regulated) is a cell surface protein that activates SHH signaling, which plays an important role in endothelium integrity [44, 45]. Nowadays, CDON was identified to participate in tumor progression. It was reported that CDON was involved in tumor cell growth and invasion in prostate cancer [41]. In this study, METTL3/YTHDF1 elevated FRAS1 protein expression, thus accelerating cell proliferation and tumor growth (colony formation). Meanwhile, we observed that FRAS1 modulated CDON expression. The increased expression of CDON in METTL3-overexpression cells was reversed by FRAS1 silence or YTHDF1 silence. These findings were consistent with the previous reports, that is, CDON was crucial for NSCLC cancer cell proliferation and tumorigenesis [41].

To sum up, our study first demonstrates the tumor-promoter role of FRAS1 in NSCLC and provides an m6A-dependent regulatory mechanism by METTL3. The m6A methyltransferase METTL3 promotes FRAS1 protein levels by enhancing FRAS1 mRNA m6A modification and FRAS1 transcript stability. The regulatory network of “writer” METTL3, “reader” YTHDF1, and “target” FRAS1 inspires the understanding of m6A-dependent gene regulatory mechanism in cancer biology, which offers a possibility of m6A regulators as promising biomarkers in NSCLC.

Abbreviations
m6A: N6-methyladenosine; NSCLC: Non-small cell lung cancer; LUAD: Lung adenocarcinoma; FRAS1: Fraser extracellular matrix complex subunit 1; CDON: Cell adhesion associated, oncogene regulated; METTL3: Methyltransferase 3, N6-adenosine-methyltransferase complex catalytic subunit; YTHDF1: YTH N6-methyladenosine RNA binding protein 1; IP: Immunoprecipitation; RIP: RNA immunoprecipitation; qRT-PCR: Quantitative Reverse Transcription-Polymerase chain reaction; CDS: Coding sequence; HR: Hazard ratio; CI: Confidence Interval; PCR: Polymerase chain reaction; CCK-8: Cell Counting Kit; EDU: 5-Ethynyl-2’-deoxyuridine.

Supplementary Information
The online version contains supplementary material available at https://doi.org/10.1186/s12890-022-02119-3.

Additional file 1: Supplementary figures and tables.

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Author contributions
XD and ZW: project design, literature research, clinical study, data analysis, manuscript writing and revise. WL, LM and YZ: literature research, clinical study, data analysis, and manuscript draft. All authors have read and approved the manuscript.

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Availability of data and materials
The datasets generated during the current study are available from the corresponding author on reasonable request.

Declarations

Competing interests
The authors declare no competing interests.

Ethics approval and consent to participate
The research was carried out in accordance with relevant guidelines and regulations. Ethics approval of the Ethics Committee of Space Central Hospital (20200511-JJHZ-01). Written informed consents were obtained from each patient.

Consent for publication
Not applicable.

Competing interest
The authors declare that they have no competing interests.

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