m\textsuperscript{6}A methyltransferase METTL3 maintains colon cancer tumorigenicity by suppressing SOCS2 to promote cell proliferation

JIHAO XU\textsuperscript{1-3*}, QIKUI CHEN\textsuperscript{1,3*}, KUANGYI TIAN\textsuperscript{1,2}, RONGLONG LIANG\textsuperscript{3,4}, TING CHEN\textsuperscript{2,5}, AIXU GONG\textsuperscript{2}, NICHOLAS W. MATHY\textsuperscript{2}, TAO YU\textsuperscript{1,3*} and XIANMING CHEN\textsuperscript{2}

\textsuperscript{1}Department of Gastroenterology, Sun Yat-Sen Memorial Hospital, Sun Yat-Sen University, Guangzhou, Guangdong 510120, P.R. China; \textsuperscript{2}Department of Medical Microbiology and Immunology, Creighton University School of Medicine, Omaha, NE 68178, USA; \textsuperscript{3}Guangdong Provincial Key Laboratory of Malignant Tumor Epigenetics and Gene Regulation; \textsuperscript{4}Department of Pediatrics, Sun Yat-Sen Memorial Hospital, Sun Yat-Sen University, Guangzhou, Guangdong 510120; \textsuperscript{5}Department of Gastroenterology, College of Clinical Medicine, Hubei University of Science and Technology, Xianning, Hubei 437100, P.R. China

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Abstract. N\textsuperscript{6}-methyladenosine (m\textsuperscript{6}A) RNA modification maintained by N6-methyltransferases and demethylases is involved in multiple biological functions. Methyltransferase like 3 (METTL3) is a major N\textsuperscript{6}-methyltransferase. However, the role of METTL3 and its installed m\textsuperscript{6}A modification in colorectal tumorigenesis remains to be fully elucidated. METTL3 is highly expressed as indicated in colorectal cancer samples in the TCGA and Oncomine databases, implying its potential role in colon tumorigenesis. SW480 cell line with stable METTL3 knockout (METTL3-KO) was generated using CRISPR/Cas9 and were confirmed by the loss of METTL3 expression and suppression of m\textsuperscript{6}A modification. The proliferation of METTL3-KO cells was significantly inhibited compared with that of control cells. METTL3-KO decreased the decay rate of suppressor of cytokine signaling 2 (SOCS2) RNA, resulting in elevated SOCS2 protein expression. m\textsuperscript{6}A-RNA immunoprecipitation-qPCR (MeRIP-qPCR) revealed that SOCS2 mRNA was targeted by METTL3 for m\textsuperscript{6}A modification. Similar to METTL3-KO SW480 cells, SW480 cells treated with 3-deazaadenosine, an RNA methylation inhibitor, exhibited elevated SOCS2 protein expression. Increased levels of SOCS2 in METTL3-KO SW480 cells were associated with decreased expression of leucine-rich repeat-containing G protein-coupled receptor 5 (LGR5), contributing to the inhibition of cell proliferation. The underlying associations among METTL3, SOCS2, and LGR5 were further confirmed in SW480 cells transfected with si-METTL3 and in tumor samples from patients with colorectal cancer. Taken together, our data demonstrate that an increased level of METTL3 may maintain the tumorigenicity of colon cancer cells by suppressing SOCS2.

Introduction

Colorectal cancer (CRC) is the third most common cancer and the second leading cause of cancer-related death worldwide (1,2). The incidence of CRC continues to increase in developing countries and is also increasing in individuals younger than 50 years (3). A worldwide health burden, CRC exhibits molecular heterogeneity, which contributes to the variable clinical outcomes (4). The identification of prognostic and predictive biomarkers for early diagnosis, prevention, and targeted therapy is a major challenge in CRC treatment. Progress has been made in the discovery of key oncogenic
markers and transcriptional modifications for decades (5,6); for example, RAS mutation testing has shown beneficial effects in predicting the clinical outcome of anti-EGFR therapy in patients with CRC, and immunohistochemical analysis of DNA mismatch repair proteins (MLH1, MSH2, MSH6 and PMS2) has been shown to have predictive value in CRC and is recommended for clinical use. However, the molecular mechanisms of CRC pathogenesis remain unclear. More effective and sensitive biomarkers are still urgently needed for defining therapeutic targets and personalized therapeutic regimens in CRC.

N^6-methyladenosine (m^6A), a reversible posttranscriptional RNA modification, is installed by methyltransferase like 3 (METTL3) in cooperation with methyltransferase like 14 (METTL14) and Wilms tumor 1-associated protein (WTAP) (7). m^6A RNA modification is erased by fat mass and obesity-associated protein (FTO) and the RNA demethylase alkB homolog 5 (ALKBH5) (7). The YT521-B homology (YTH) domain family proteins (YTHDF1, YTHDF2, YTHDF3, and YTHDC1) have been identified as m^6A readers (7). The functional effects of m^6A RNA modification include RNA splicing, degradation, and translation and RNA-protein interaction (8-10). This type of RNA modification is critical for circadian clock regulation, self-renewal and cell fate transition (11,12). Accumulating studies have demonstrated that m^6A modification plays regulatory roles in various malignancies (13-15). METTL3 promotes glioblastoma progression and enhances cancer stem cell (CSC) self-renewal (15), and METTL3 upregulation appears to be critical for cancer cell growth, survival and invasion in lung cancer (16). Moreover, METTL3 dysfunction exerts critical effects in gastrointestinal tract cancers. Elevated METTL3 expression augments tumor proliferation and liver metastasis by increasing the RNA m^6A level in gastric cancer (17,18), and METTL3 is involved in cancer progression and therapeutic resistance in pancreatic cancer (19). However, the roles of m^6A and METTL3 in CRC still need to be demonstrated, and this knowledge may provide insight into the development of new therapeutic strategies.

Accumulating evidence indicates that the activity of suppressor of cytokine signaling (SOCS) family proteins correlates with progression and poor prognosis in various cancers (20,21). SOCS2, a member of the SOCS family, is well defined as a transcriptional repressor in multiple proliferation-related pathways and acts as a tumor suppressor in multiple malignancies. Previous studies have reported downregulation of SOCS2 in breast and ovarian cancers (22,23). In addition, SOCS2 has been reported to inhibit metastasis in prostate cancer and hepatocellular carcinoma (24,25). However, the molecular mechanisms underlying the role of SOCS2 in tumorigenesis, including CRC tumorigenesis, are still obscure. Leucine-rich repeat-containing G protein-coupled receptor 5 (LGR5) is characterized as a CSC biomarker and is essential for the maintenance of stemness properties (26,27). Previously, LGR5 upregulation was found in CRC and was found to be positively correlated with the pathological grade and invasiveness of CRC (28). Thus, LGR5 is considered a promising new therapeutic target for CRC. Although LGR5 has been revealed to be associated with the prognosis and progression of CRC, the upstream regulation of LGR5 in CRC is unclear.

Here, we report that METTL3 overexpression promotes tumor cell proliferation in CRC. Mechanistically, METTL3 induces SOCS2 mRNA instability via m^6A modification. Aberrant overexpression of LGR5 is caused by SOCS2 instability in CRC, and this effect maintains the high stemness and robust cell proliferation observed in CRC.

Materials and methods

Clinical sample collection. Fresh colon tumor tissues and matched adjacent normal colon tissues (>5 cm from the tumor border) (n=24 pairs) were collected from patients with CRC after surgical resection at the Department of Gastroenterological Surgery, Sun Yat-Sen Memorial Hospital, Sun Yat-Sen University, between June and August 2018. Samples were immediately frozen in liquid nitrogen and stored at -80°C until analysis. Tumor tissues and adjacent normal colon tissues were confirmed by postoperative pathological diagnosis. All patients recruited in the study were confirmed by pathological diagnosis. The exclusion criteria were as follows: i) Patients with a metastatic colon tumor originating in another organ; ii) CRC patients who had already received chemotherapy and/or radiotherapy; and iii) patients with CRC in situ or a benign tumor confirmed by pathological diagnosis. The clinicopathological features of the patients (sex, age, tumor size, pathological type and TNM stage) were collected. All enrolled patients and their respective guardians provided written consent, and the study strictly adhered to the guidelines of the Institutional Review Board Committee of Sun Yat-Sen Memorial Hospital, Sun Yat-Sen University (Guangzhou, Guangdong, China) (Approval no. 58, 2016 record for Ethics).

Cancer database analysis. CRC-related data with entries defined as colorectal adenocarcinoma were downloaded from The Cancer Genome Atlas (TCGA; http://www.cbiportal.org). Expression levels of METTL3, SOCS2 and LGR5 in normal colon tissues were compared with those in CRC tissues. To comprehensively identify the gene expression profile in CRC, we utilized the Oncomine database, an online public cancer database of DNA and RNA sequences, to collect transcriptional expression data for METTL3, SOCS2 and LGR5 in CRC using the ‘Gene summary view’ and ‘Dataset view’ (https://www.oncomine.org/resource/login.html). Transcriptional expression of METTL3, SOCS2 and LGR5 in CRC samples was compared with that in normal colorectal epithelium samples using Student’s t-test. A total of 12 datasets were found. Statistically significant differences and fold changes were defined as P<0.05 and ≥2, respectively.

Cytoscape literature mining was performed with the search term ‘METTL3’ to query the whole NCBI database (https://www.ncbi.nlm.nih.gov/pubmed) by default parameters. The software automatically retrieved all articles in PubMed mentioning METTL3. The reported correlations of METTL3 with other genes were assembled and visualized with Cytoscape (29).

Colon cancer cell line culture. SW480 cells (a colon cancer cell line) were obtained from the American Type Culture Collection (ATCC, USA) and cultured in the recommended medium [L-15 medium supplemented with 10% fetal bovine serum (FBS),...
100 µg/ml streptomycin, and 100 U/ml penicillin). Cells were maintained in a humidified incubator without CO₂ at 37°C.

**CRISPR-Cas9-mediated knockout of METTL3.** CRISPR/Cas9 was applied to stably knock out the METTL3 gene (NCBI GeneID 56339) to generate stable cell lines. In brief, SW480 cells were transfected with the METTL3 CRISPR/Cas9 and HDR plasmids (sc-404029, Santa Cruz Biotechnology, Inc.). Colonies were selected, and western blotting was used to detect METTL3 protein expression. The clones with the expected knockdown of METTL3 were further validated by qPCR and Sanger sequencing.

**Cell transfection.** To transiently knock down METTL3 expression, siRNA transfection was used. Two siRNAs targeting METTL3 (si-METTL3#1 and si-METTL3#2) were synthesized by GenPharma Corporation. The siRNA sequences were as follows: si-METTL3#1, 5’-GGUGACGUCUCUUC CUUATT-3’ and 3’-UAAGGAAAGAGCAUCACCTT-5’; si-METTL3#2, 5’-GCUACCUGGACUGCUAATT-3’ and 3’-AUCUGACGUCCAGGUACTT-3’. The negative control siRNA sequences were as follows: si-Ctrl, 5’-UUCUGGAA CGUGUCAGCUTT-3’ and 5’-AUCUGACGUCGUCCAGAGA ATT-3’. The siRNA targeting SOCS2 (si-SOCS2) was obtained from Santa Cruz Biotechnology, Inc. The pCMV6 plasmid containing the full-length SOCS2 sequence (FULL-SOCS2) was purchased from Origene (RC203163).

Cells were cultured in 6-well plates (1x10⁵ cells per well) overnight prior to the experiment. The following day, siRNA (80 µM) was transfected into cells with Lipofectamine RNAiMAX (5 µl per well) (Thermo Fisher Scientific, Inc.). For plasmid transfection, cells were seeded at a density of 1x10⁵ cells per well in 6-well plates. Twenty-four hours later, Lipofectamine 2000 (5 µl per well; Thermo Fisher Scientific, Inc.) was used to transfect cells with the plasmid (2.5 µg per well) following the manufacturer’s instructions. Cells were harvested 48 h after transfection for RNA and protein detection.

**Cell proliferation assays.** For the MTS assay, cells were seeded in 96-well plates at a density of 1x10⁴ cells per well and cultured for 4 days. The absorbance at 490 nm was measured every 24 h after incubation with 20 µl of MTS reagent (Promega, Corp.) for 2 h.

A cell counting assay was utilized to assess the cell proliferation ability. Cells (1x10⁵ cells per well) were plated in a 12-well plate. On days 1, 2, 3, and 4 after seeding, the plated cells were trypsinized and then stained by trypan blue staining. The total number of cells was counted by Olympus BX63 microscope and image software (cellSens Dimension; Olympus).

**m6A quantification.** Total RNA extracted from cells was purified and quantified. The isolated total RNA was subjected to mRNA purification using a Dynabeads mRNA Purification Kit (Thermo Fisher Scientific, Inc.) to deplete rRNA and noncoding RNAs. A total of 200 ng of mRNA from each sample was used, and m6A quantification was carried out by using an EpiQuik m6A Methylation Quantification kit (Colorimetric, Epigentek) according to the manufacturer’s instructions.

**m6A-RNA immunoprecipitation-qPCR (MeRIP-qPCR).** MeRIP-qPCR was performed as previously reported (31). In brief, mRNA was isolated, purified and chemically shredded into ~100-nt fragments using Ambion fragmentation reagent (Thermo Fisher Scientific, Inc.). mRNA fragments (200 ng) were denatured at 65°C for 5 min and incubated with 20 µl of Magna ChIP Protein A+G Magnetic Beads (2923270,
Millipore) conjugated to 1 µg of anti-m\textsuperscript{6}A polyclonal antibody (ab208577, Abcam) or mouse control IgG (sc-2025, Santa Cruz Biotechnology, Inc.) in 1X IPP buffer (15 mM NaCl, 10 mM Tris-HCl and 0.1% NP-40). mRNA was incubated with m\textsuperscript{6}A-bound beads with rotation at 4°C for 3 h in IPP buffer. The beads were washed twice with 1X IPP buffer, twice with low-salt buffer (50 mM NaCl, 10 mM Tris-HCl and 0.1% NP-40), twice with high-salt buffer (500 mM NaCl, 10 mM Tris-HCl and 0.1% NP-40) and once with 1X IPP buffer. RNA was eluted from the beads with 50 µl of RLT buffer and purified through Qiagen RNEasy columns (Qiagen) according to the manufacturer's recommendation. Total RNA was finally eluted in 100 µl of RNase-free water. The relative abundances of RNAs of interest were measured using qPCR and normalized to the input level.

RNA stability. Cells (2x10\textsuperscript{4} cells per well) were plated in 12-well plates. After overnight incubation, cells were treated with actinomycin D (ACD; A9415, Sigma-Aldrich; Merck KGaA) at a final concentration of 10 µg/ml and incubated in a humidified incubator without CO\textsubscript{2} at 37°C. Total RNA was extracted at different time points after actinomycin D treatment (0, 1, 2, 4 and 8 h). Following total RNA extraction and quantification, the expression levels of specific genes of interest were quantified using qPCR.

Demethylation treatment with 3-deazaadenosine (DAA). The global methylation inhibitor DAA (D8296, Sigma-Aldrich; Merck KGaA) was used to inhibit RNA methylation (11,32). After seeding, cells were treated with 10 µg/ml DAA for 48 h. Cells were then collected for mRNA and protein analysis.

Luciferase assay. The LGR5 promoter region sequence (-2 kb~+100 b) was obtained from National Center for Biotechnology Information (NCBI). The LGR5 promoter was cloned using specific primers and was then ligated into the pGL3 vector digested with Xho\textsubscript{I} and Sac\textsubscript{I}. The pGL3-LGR5 promoter and the FULL-SOCS2 plasmid were cotransfected into SW480 cells. Twenty-four hours after transfection, cells were collected with luciferase lysis buffer (E3971, Promega Corp.). Luciferase Assay Reagent (E1483, Promega Corp.) was used to measure luciferase activity after cotransfection. β-Gal activity was measured as an internal transfection control.

Statistical analysis. Each experiment was performed at least three independent times. All experimental data are presented as the mean ± SEM values. Student’s t-test or one-way ANOVA was conducted for evaluating intergroup differences. The correlation of protein expression and clinicopathological features was analyzed by Fisher's exact test or Chi-square test. Linear regression analysis was used to analyze the correlation between two genes. Statistical analysis was performed using GraphPad Prism 5 (GraphPad Software). P<0.05 was considered to indicate a statistically significant difference.

Results

**METTL3 expression is increased in CRC.** To determine the expression pattern of METTL3 in CRC, we queried the TCGA database. A total of 480 colon cancer samples and 41 normal colon tissues were found. Compared to normal colon tissues, colon cancer samples showed an elevated METTL3 RNA level (P<0.05; Fig. 1A).

To explore the potential role of METTL3 expression in CRC tumorigenesis, we conducted literature mining via Cytoscape network analysis and identified 52 candidate genes that may interact with METTL3 (Fig. 1B). Both METTL3 and METTL14 have been reported to act coordinately to maintain m\textsuperscript{6}A modification (7). Cytoscape analysis of METTL14 revealed the same group of genes found for METTL3, suggesting that METTL3 and METTL14 were considered a single complex in the Cytoscape analysis. Those candidate genes were further subjected to Gene Ontology analysis (Table SII) via the Database for Annotation, Visualization and Integrated Discovery (DAVID) tool (https://david.ncifcrf.gov/). Our analysis revealed that METTL3 is mainly involved in the following three bioprocesses: Cell proliferation, inflammatory response and RNA processing. Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analysis indicated that these candidate genes are closely associated with multiple diseases, including acute myeloid leukemia, CRC and prostate cancer (Table SIIB). These results imply a potential role for METTL3 in tumor progression and the regulation of inflammation, cell proliferation and RNA processing.

Establishment of stable METTL3-knockout (METTL3-KO) colon cancer cell lines. We used CRISPR-Cas9 to generate stable METTL3-KO colon cancer cell lines in SW480 cells. Two lines of METTL3-KO cells, SW480 A7 and SW480 A12, were finally obtained through antibiotic selection, and the absence of METTL3 expression in these cell lines was confirmed by qPCR and western blotting (Fig. 1C-E). No qPCR product was detected using the specific primer sets covering the targeted region of METTL3; in addition, the western blot results indicated the knockout of the METTL3 protein in METTL3-KO SW480 cells. Moreover, to verify METTL3 inhibition in METTL3-KO cells, global m\textsuperscript{6}A levels were measured using the EpiQuik m\textsuperscript{6}A Methylation Quantification kit. The overall m\textsuperscript{6}A level was evidently decreased in METTL3-KO SW480 cells when compared with the parental cells (Fig. 1F).

**METTL3-KO elicits an inhibitory effect on SW480 cell proliferation.** Given the potential function of METTL3 in regulating cell proliferation implied by the above bioinformatic analysis results, we screened the differential expression profiles of proliferation-related genes in METTL3-KO SW480 cells vs. the control SW480 (SW480 WT) cells to determine whether downregulation of METTL3 modulates cell proliferation in CRC. Ki67, LGR5, PCNA, SOX2 and Cyclin B1 have been reported to be positively correlated with cell proliferation (33-36). All five of these genes were significantly downregulated in the METTL3-KO SW480 cells. On the other hand, two antiproliferative genes, SOCS2 and P27, were upregulated (Fig. 2A).

We then examined the effects of METTL3 knockout on SW480 cell proliferation and stemness. Both METTL3-KO lines, SW480 A7 and SW480 A12, showed a decrease in cell proliferation in the MTS assay (Fig. 2B). In addition, the growth of METTL3-KO cells was markedly inhibited,
as measured by cell counting and colony formation assays (Fig. 2C and D). Moreover, we performed a tumorsphere formation assay to observe stemness properties arising from METTL3 knockout. Spheroid formation can be used to estimate the percentage of CSCs present in a population of tumor cells. Spheroid formation by METTL3-KO SW480 cell lines was significantly inhibited, suggesting the loss of stemness of these cells (Fig. 2E). Collectively, these data indicate that METTL3 may play an important role in regulating SW480 cell self-renewal.

Figure 1. High level of METTL3 expression in colon cancer and the establishment of METTL3-KO SW480 cells. (A) TCGA database analysis showed an elevated expression level of METTL3 in colon cancer (\(P<0.01\)). (B) Literature mining identified 52 candidate genes potentially associated with METTL3. (C-E) METTL3-KO SW480 cells showed diminished expression of METTL3 at both the (C) mRNA and (D and E) protein levels (\(P<0.05\), compared with the SW480 WT cells). (F) METTL3-KO abolished the maintenance of overall RNA methylation (\(P<0.05\), compared with the SW480 WT cells). METTL3, methyltransferase like 3; KO, knockout; TCGA, The Cancer Genome Atlas; SW480 A7 and SW480 A12, METTL3-KO SW480 cells.

Figure 2. Inhibition of cell proliferation in METTL3-KO SW480 cells. (A) METTL3-KO SW480 cells showed dysregulation of several proliferation-related genes (\(P<0.05\), compared with the SW480 WT cells). (B) MTS assay results validated the decreased proliferation of METTL3-KO cells (\(P<0.05\), compared with the SW480 WT cells). (C) METTL3-KO cells showed a reduced proliferation rate, as measured by cell counting (\(P<0.05\), compared with the SW480 WT cells). (D) METTL3-KO cells showed a lower colony formation rate than control cells at 7 days after seeding. (E) Tumorigenic ability of METTL3-KO SW480 cells was reduced (\(P<0.05\), compared with the SW480 WT cells). SOCS2, suppressor of cytokine signaling 2; METTL3, methyltransferase like 3; LGR5, leucine-rich repeat-containing G protein-coupled receptor 5; SOX2, SRY-box transcription factor 2; PCNA, proliferating cell nuclear antigen; KO, knockout; SW480 A7 and SW480 A12, METTL3-KO SW480 cells.
SOCS2 RNA levels are negatively correlated with METTL3 expression levels in CRC. To identify the downstream regulatory effectors controlling the inhibition of cell proliferation in METTL3-KO cells, we sought to determine whether METTL3 regulates the expression of SOCS2 to modulate the transcription of those proliferation-related genes. A previous study indicated a potential correlation between the expression levels of SOCS2 and METTL3 in hepatocellular cancer (37). We utilized the TCGA database to evaluate SOCS2 expression in CRC. In the same set of TCGA samples used for METTL3 analysis, we found a significant decrease in the SOCS2 RNA level in CRC (Fig. 3A). The correlation between the expression levels of METTL3 and SOCS2 was studied by linear regression analysis of data from the TCGA database. A significant inverse association between the expression levels of METTL3 and SOCS2 in CRC was identified (P<0.05; Fig. 3B), and the R² coefficient was small (0.018). We considered that the correlation between METTL3 and SOCS2 in these TCGA data might not be strong but was significant. The actual correlation still needs in-depth investigation.

The correlation between the levels of SOCS2 and METTL3 in CRC samples prompted us to investigate whether this association holds in SW480 cells. We measured the SOCS2 expression levels in METTL3-KO SW480 cells and compared them to those in control SW480 cells. Consistent with the pattern in the TCGA data, knockout of METTL3 was accompanied by SOCS2 upregulation (Fig. 3C-E). Our data thus imply that METTL3 may control SOCS2 expression in CRC.

METTL3 controls SOCS2 expression by modulating methylation-mediated SOCS2 RNA degradation. To explore the underlying molecular mechanisms by which METTL3 controls SOCS2 expression, we sought to determine whether SOCS2 is a direct substrate of METTL3 for methylation. We first verified whether METTL3 maintains the methylation status of SOCS2 mRNA in SW480 cells. The MeRIP-qPCR results revealed a significant decrease in SOCS2 RNA m⁶A methylation in METTL3-KO SW480 cells compared with the control SW480 WT cells (Fig. 4A). To evaluate the effect of m⁶A modification on SOCS2 expression, we used the global methylation inhibitor DAA to block RNA methylation and quantified SOCS2 mRNA and protein expression in SW480 cells. The abundance of SOCS2 mRNA was increased in the DAA-treated SW480 cells in a DAA dose-dependent manner (P<0.05; Fig. 4B). Consistent with the results from METTL3-KO cells, DAA treatment increased the SOCS2 protein content (P<0.05; Fig. 4C and D). Since DAA globally inhibits all methyltransferase reactions, we used MeRIP-qPCR to confirm its demethylation of SOCS2 mRNA. A significant decrease in m⁶A-modified SOCS2 mRNA was detected in SW480 cells after DAA intervention (P<0.05; Fig. 4E).

A previous study showed that RNA m⁶A methylation exerts its effects via modulation of RNA stability (8). To investigate this possibility, we carried out an RNA stability assay. New RNA synthesis was blocked with actinomycin D, and the decay rate of SOCS2 mRNA was observed to be lower in METTL3-KO SW480 cells than in control SW480 cells.
cells (P<0.05; Fig. 4F), suggesting that knockout of METTL3 significantly enhanced SOCS2 mRNA stability. Collectively, our findings revealed that METTL3 controls SOCS2 expression by modulating its mRNA stability.

**Changes in SOCS2 expression impact LGR5 expression and disrupt colon cancer cell proliferation.** To define whether SOCS2 is an effector regulating colon cancer cell proliferation, we monitored the effects of modulating SOCS2 expression on SW480 cell proliferation. Treatment of cells with a SOCS2-specific siRNA and transfection with the FULL-SOCS2 plasmid effectively downregulated and upregulated SOCS2 expression, respectively (Fig. 5A-C and E-G). Accordingly, a significant increase and a marked decrease in the cell number were detected in siRNA-treated SW480 cells and SOCS2-overexpressing SW480 cells, respectively (Fig. 5D and H).

Previous studies have demonstrated that SOCS2 acts as a negative feedback regulator in multiple signaling pathways. Dysregulation of SOCS2 crucially modulates the cell cycle progression and apoptosis of cancer cells (38-40). Recent research advances suggest that CSCs may be the origin of colon tumorigenesis and tumor growth maintenance (41). As an important CSC marker, LGR5 may enhance the stemness and chemoresistance development of tumor cells (26,27,42). Hence, we measured the abundance of LGR5 in SW480 cells with SOCS2 downregulation or overexpression. SOCS2 knockdown via siRNA significantly elevated both the mRNA and protein expression levels of LGR5 in the SW480 cells (P<0.05; Fig. 5A-C). Correspondingly, SOCS2 overexpression appreciably suppressed LGR5 expression (P<0.05; Fig. 5E-G).

Taken together, these results suggest that SOCS2 may regulate colon cancer cell proliferation via LGR5.

**SOCS2 suppresses LGR5 promoter activity.** First, we explored the association of LGR5 and SOCS2 in data from the TCGA database. In the same set of TCGA samples used in the present study, we found a distinct increase in the LGR5 RNA level in CRC (Fig. 6A). Although the R² coefficient was too small to be considered to indicate a strong correlation, linear regression analysis implied a potential negative correlation between the expression levels of SOCS2 and LGR5 in CRC (P<0.05; Fig. 6B). This finding prompted us to investigate the mechanism underlying the correlation between SOCS2 and LGR5.

To exclude direct regulatory effects of METTL3 on LGR5 expression, MeRIP-qPCR was applied. The m⁶A methylation level of LGR5 did not differ between METTL3-KO SW480 cells and control SW480 WT cells (P>0.05; Fig. 6C), nor did METTL3 knockout impact the stability of LGR5 mRNA in SW480 cells (P>0.05; Fig. 6D). Furthermore, DAA treatment had little impact on the stability of LGR5 mRNA in SW480 cells (P>0.05; Fig. 6E). These data did not support a direct modulatory effect of METTL3 on LGR5, indicating the necessity of SOCS2 for the regulation of LGR5 by METTL3.

SW480 cells were cotransfected with the FULL-SOCS2 plasmid or the empty vector (as the control) and the luciferase reporter vector containing the LGR5 promoter region, and luciferase activity was then measured. Our luciferase activity assay results showed that SOCS2 overexpression effectively repressed LGR5 promoter activity in SW480 cells, suggesting a suppressive role of SOCS2 in modulating LGR5 transcription (P<0.05; Fig. 6F).
Measurement of SOCS2 and METTL3 expression and their correlation in colon cancer tumorigenesis. To rule out the compensatory effect of other molecules on SOCS2 and LGR5 expression in stable METTL3-KO SW480 cells, we used two separate siRNAs (si-METTL3#1 and si-METTL3#2) to knockdown METTL3 expression in SW480 cells. Transient inhibition of METTL3 via either siRNA resulted in significantly increased SOCS2 expression but significantly decreased LGR5 expression at both the mRNA and protein levels (P<0.05; Fig. 7A-C).
Moreover, we collected 24 paired samples (i.e., tumor tissues and paired adjacent normal colon tissues) from patients with CRC in the Department of Gastroenterology Surgery, Sun Yat-Sen Memorial Hospital. The protein expression levels of METTL3, SOCS2, and LGR5 were upregulated in CRC datasets. In contrast, SOCS2 was downregulated in CRC datasets. CRC, colorectal cancer; SOCS2, suppressor of cytokine signaling 2; METTL3, methyltransferase like 3; LGR5, leucine-rich repeat-containing G protein-coupled receptor 5.

Figure 7. Correlations among METTL3, SOCS2 and LGR5 expression levels in CRC. (A-C) Knockdown of METTL3 using siRNA (si-METTL3#1 and si-METTL3#2) significantly upregulated SOCS2 expression but downregulated LGR5 expression in SW480 cells (*P<0.05, compared with the si-Ctrl group). (D and E) Western blotting analysis of 24 paired tissues collected from CRC patients showed high protein levels of METTL3 and LGR5 and a relatively low protein level of SOCS2 in colon cancer (T, colon tumor samples; N, adjacent normal colon tissues; *P<0.05, compared to Normal tissues). (F) Visualization of expression profiles of METTL3, SOCS2 and LGR5 in CRC through the Oncomine database. METTL3 and LGR5 were upregulated in CRC datasets. In contrast, SOCS2 was downregulated in CRC datasets.
METTL3, SOCS2 and LGR5 were measured in the 24 paired CRC samples and histologically normal adjacent tissues using western blotting. The expression levels of METTL3 and LGR5 were increased in colon tumor samples compared to the paired adjacent colon tissues (fold change ≥1.5) in 19 (79.2%) and 20 (83.3%) cases, respectively. In contrast, the level of SOCS2 was lower in the tumor samples (fold change ≤0.5) in 18 (75.0%) cases (Fig. 7D and Table I). Additionally, we analyzed the correlations between the expression levels of these three genes and clinicopathological features (sex, age, TNM stage). Upregulation of METTL3 or LGR5 was not correlated with sex, age, tumor size, or TNM stage (P>0.05; Table I). Consistent with this result, downregulation of SOCS2 was not associated with these clinical features (P>0.05; Table I). These results demonstrated that in general, the expression levels of METTL3 and LGR5 are increased in CRC, whereas that of SOCS2 is decreased.

To further evaluate the clinical value of our findings, we searched the expression profiles of METTL3, SOCS2 and LGR5 in CRC through the Oncomine database (43-52). Regarding METTL3, analysis confirmed that METTL3 was upregulated in CRC in 13/20 datasets (P<0.05; Fig. 7F and Table SIII). In contrast, analysis revealed that SOCS2 was downregulated in CRC in 13/19 datasets (P<0.05; Fig. 7 and Table SIII). Accordingly, LGR5 expression was significantly increased in all 13 CRC datasets (P<0.05; Fig. 7F and Table SIII).

**Discussion**

The present study indicates that methyltransferase like 3 (METTL3) is generally upregulated in colorectal cancer (CRC), contributing to the maintenance of m6A modification in cancer cells. As a major m6A writer, METTL3 accelerates suppressor of cytokine signaling 2 (SOCS2) mRNA decay to maintain a high leucine-rich repeat-containing G protein-coupled receptor 5 (LGR5) expression level in colon cancer cells, resulting in enhanced tumorigenicity. Thus, our results provide additional evidence that aberrant METTL3 expression may be involved in tumorigenesis. As the most prevalent internal modification of RNA, m6A modification regulates many biological processes of RNA, including decay, splicing, translation and transport (53). Maintenance of m6A RNA methylation is crucial for embryonic stem cell pluripotency (54,55). Emerging evidence indicates that the cellular status of m6A modification may impact the pathological processes of various types of cancers, including acute myeloid leukemia, glioblastoma, lung cancer and liver cancer (56). METTL3 is often upregulated in malignancies and elicits potentially oncogenic effects by epigenetically silencing the expression of specific genes, such as ADAM19 and SOCS2 (15,37). Previous studies demonstrated that the expression level of METTL3 can critically alter the cell cycle and apoptosis processes in hepatic cancer and acute myeloid leukemia (37,57). Knockdown of METTL3 increases chemosensitivity and radiosensitivity in pancreatic cancer (19).

Having confirmed an elevated expression level of METTL3 in CRC tissues from the TCGA database, we generated METTL3-KO colon cancer (SW480) cell lines. Our m6A quantification analysis results confirmed that CRISPR/Cas9-mediated METTL3 knockout resulted in inhibition of both METTL3 expression and m6A modification in the cells. Functionally, knockout of METTL3 significantly reduced the cell proliferation ability. METTL3 acts as a key m6A methyltransferase and thus may promote cell proliferation via the installation of m6A on key genes critical to cell growth (58-60). Indeed, our data suggest that elevated expression of METTL3 accelerates SOCS2 mRNA decay to maintain a high level of LGR5 and thus promotes the proliferation of colon cancer cells.

SOCS2, a member of the SOCS family, regulates multiple cytokine-induced intracellular signaling pathways essential to numerous biological processes, including immune responses (61,62). For example, SOCS2 can act as a downstream factor of the JAK/STAT pathway, regulating signaling activity via negative feedback (63). Accumulating evidence suggests a carcinostatic effect of SOCS2 in numerous cancers. Disruption of SOCS2 promotes colon tumorigenesis in Apc(Min/+) mice (64). On the other hand, overexpression of SOCS2 has an antiproliferative effect on Caco-2 colon cancer cells (65). A meta-analysis integrating more than 600 CRC patients and normal samples from different datasets revealed that SOCS2 expression is markedly reduced in CRC and may be a novel diagnostic biomarker for CRC (66). Indeed, the JAK/STAT signaling pathway is often dysregulated in CRC (67). Our TCGA database analysis results confirmed the downregulation of SOCS2 in CRC. Furthermore, our data supported the hypothesis that SOCS2 may play an antioncogenic role in colon malignancies. We observed a negative association between SOCS2 expression and the cell proliferation ability in colon cancer cells. Knockdown of SOCS2 increased the proliferation of colon cancer cells, while overexpression of SOCS2 effectively inhibited cell proliferation.

The molecular mechanisms underlying the dysregulation of SOCS2 and SOCS2-mediated cell proliferation in CRC are still unclear. Our data revealed a negative correlation between METTL3 and SOCS2 in clinical CRC tissues and colon cancer cells. Moreover, knockdown of METTL3 in colon cancer cells increased the expression of SOCS2. Given that METTL3 is the predominant m6A RNA methyltransferase and that mRNA stability is confirmed as a cellular biological processes regulated by m6A modification, we speculated that METTL3 may control SOCS2 expression through modulation of SOCS2 RNA stability. The results of our MeRIP-qPCR and RNA decay experiments revealed that METTL3 may directly install m6A on SOCS2 mRNA and decrease its stability. Inhibition of global demethylation with DAA, a global methylation inhibitor, further confirmed the effect of RNA methylation on SOCS2 expression. The effect of DAA on SOCS2 expression was dose-dependent and showed a positive correlation between m6A demethylation and SOCS2 expression.

One pathological hallmark of cancer cells is their potential for uncontrolled self-renewal (68). Targeting biomarkers of significance in self-renewal may be an effective strategy to reverse tumorigenesis. LGR5, which can maintain continuous self-renewal of the intestinal epithelium, is considered a cancer stem cell (CSC) marker in CRC (69). Cancer cells with LGR5 expression in CRC tissues possess an enhanced self-renewal capacity and have been referred to as colon...
Table I. Association between patient characteristics and gene expression in 24 paired CRC cases.

|                          | Expression of METTL3<sup>a</sup> | Fisher's exact test (P-value) | Expression of SOCS2<sup>b</sup> | Fisher's exact test (P-value) | Expression of LGR5<sup>a</sup> | Fisher's exact test (P-value) |
|--------------------------|----------------------------------|-----------------------------|---------------------------------|--------------------------------|--------------------------------|-------------------------------|
| Total, n (%)             | 24                               | 5 (20.8) 19 (79.2)          | 18 (75.0) 6 (25.0)              | 4 (16.7) 20 (83.3)              |                                |                               |
| Sex                      |                                  |                             |                                 |                                |                                |                               |
| Male                     | 12 (50.0)                        | 2                             | 8                               | 2                              | 2                              | 0.99                          |
| Female                   | 12 (50.0)                        | 4                             | 10                              | 4                              | 2                              |                               |
| Mean age (years)         | 61±11.64                         | 1                             | 9                               | 3                              | 1                             | 0.27                          |
| ≤60                      | 10 (41.7)                        | 1                             | 9                               | 3                              | 1                             |                               |
| >60                      | 14 (58.3)                        | 4                             | 10                              | 3                              | 1                             |                               |
| Tumor size (cm)          |                                  | 3                             | 7                               | >0.99                          | 2                              | >0.99                         |
| ≤5                       | 10 (41.7)                        | 3                             | 7                               | >0.99                          | 2                              | >0.99                         |
| >5                       | 14 (58.3)                        | 2                             | 12                              | >0.99                          | 2                              | >0.99                         |
| Pathologic type          |                                  | 18                            | 6                               | 4                              | 20                             |                               |
| Adenocarcinoma           | 24                               | 5                             | 19                              | 4                              | 20                             |                               |
| Other                    | 0                                | 0                             | 0                               | 0                              | 0                              |                               |
| pT grade                 |                                  |                              |                                 |                                |                                |                               |
| Ta, Tis, T1              | 2 (8.3)                          | 0                             | 2                               | 2                              | 0.99                          | 1                             |
| T2-T4                    | 22 (91.7)                        | 5                             | 17                              | 16                             | 6                              | 3                             |
| pN grade                 |                                  |                              |                                 |                                |                                |                               |
| N0                       | 13 (54.2)                        | 1                             | 12                              | >0.99                          | 1                              | 1                             |
| N1, N2                   | 11 (45.8)                        | 4                             | 7                               | >0.99                          | 1                              | 12                            |
| pM grade                 |                                  |                              |                                 |                                |                                |                               |
| M0                       | 18 (75.0)                        | 4                             | 14                              | 3                              | 3                              | 16                            |
| M1                       | 6 (25.0)                         | 1                             | 5                               | 3                              | 3                              | 4                             |
| TNM staging              |                                  |                              |                                 |                                |                                |                               |
| I                        | 5 (20.8)                         | 0                             | 5                               | >0.99                          | 1                              | 4                             |
| II                       | 7 (29.2)                         | 2                             | 5                               | 0.77<sup>b</sup>               | 1                              | 4                             |
| III                      | 7 (29.2)                         | 2                             | 5                               | 0.33<sup>b</sup>               | 2                              | 3                             |
| IV                       | 5 (20.8)                         | 1                             | 4                               | 1                              | 2                              |                               |

<sup>a</sup>Protein expression in tumor sample in contrast to adjacent (>5 cm) normal mucosa. <sup>b</sup>Chi-square test P-value. CRC, colorectal cancer; METTL3, methyltransferase like 3; SOCS2, suppressor of cytokine signaling 2; LGR5, leucine-rich repeat-containing G protein-coupled receptor 5.
CSCs (26,27). A meta-analysis revealed that tumor tissues from patients with CRC often show upregulated LGR5 expression and that an increased level of LGR5 could be a prognostic factor for CRC (70). Consistent with these results, the results of our TCGA database analysis showed a higher LGR5 expression level in CRC tissues than on their normal counterparts; this finding was further confirmed by our Oncomine database analysis in a larger clinical cohort. Moreover, we collected clinical CRC tissue samples from our hospital to assess the protein expression profiles of METTL3, SOCS2 and LGR5. METTL3 and LGR5 were highly expressed in our CRC samples. Although SOCS2 showed highly heterogeneous expression, the statistical analysis results supported the downregulation of SOCS2 in our CRC samples. Accordingly, the decreased SOCS2 expression level was negatively correlated with the elevated LGR5 expression level and increased tumor spheroid formation rate in colon cancer cell lines, consistent with a previous meta-analysis (55). Alteration of either METTL3 or SOCS2 expression can cause reciprocal alterations in the LGR5 expression level in SW480 cells. Interestingly, METTL3 does not appear to directly regulate LGR5 mRNA stability through m6A methylation but instead appears to maintain LGR5 expression through suppression of SOCS2. However, several limitations should be resolved to fully reveal the precise mechanisms of METTL3 facilitating CRC tumorigenesis. Notably, the expression of METTL3, SOCS2 and LGR5 in our CRC samples was not significantly correlated with the clinicopathological features of the patients (sex, age, tumor size, pathological type and TNM stage). This statistically insignificant correlation may be due to the small enrolled sample size. Moreover, the present study did not measure the gene expression of METTL3, SOCS2 and LGR5 in CRC samples. Both a comprehensive study with a larger sample size and a multicenter clinical study would be conducted to fully evaluate the therapeutic potential of METTL3 for CRC.

In conclusion, our study revealed elevated METTL3 expression in CRC. Uregulation of METTL3 was associated with decreased expression of SOCS2 and promoted tumor cell proliferation via induction of LGR5. To our knowledge, our finding provides the first characterization of the underlying mechanism of METTL3/m6A-mediated posttranscriptional modification in CRC tumorigenesis, suggesting the therapeutic potential of targeting this axis in CRC.

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Availability of data and materials

All data generated or analyzed in the present study (and its supplementary information files) are fully available without restrictions.

Authors’ contributions

JX, QC, TY and XC conceived the project. JX, TC, KT, AG and RL carried out the experiments. JX, AG, QC, TY and XC analyzed and interpreted the data. JX, NWM and XC wrote the study. NWM and RL participated in the bioinformatics research. All authors read and approved the manuscript and agree to be accountable for all aspects of the research in ensuring that the accuracy or integrity of any part of the work are appropriately investigated and resolved.

Ethics approval and consent to participate

All enrolled patients and their respective guardians provided written consent prior to the use of clinical samples and pathological features for research purposes. The overall protocol strictly adhered to the guidelines of the Institutional Review Board Committee of Sun Yat-Sen Memorial Hospital, Sun Yat-Sen University (approval no. 58, 2016 record for Ethics).

Patient consent for publication

Not applicable.

Competing interests

The authors have no conflicts of interest to declare.

References

1. Arnold M, Sierra MS, Laversanne M, Soerjomataram I, Jemal A and Bray F: Global patterns and trends in colorectal cancer incidence and mortality. Gut 66: 683-691, 2017.
2. Bray F, Ferlay J, Soerjomataram I, Siegel RL, Torre LA and Jemal A: Global cancer statistics 2018: GLOBOCAN estimates of incidence and mortality worldwide for 36 cancers in 185 countries. CA Cancer J Clin 68: 394-424, 2018.
3. Dekker E, Tanis PJ, Vleugels JLA, Kasi PM and Wallace MB: Colorectal cancer. Lancet 394: 1467-1480, 2019.
4. Prasetyanti PR, van Hooff SR, van Herwaarden T, de Vries N, Kalloe K, Rodermond H, van Leersum R, de Jong JH, Franitza M, Nürnberg P, et al: Capturing colorectal cancer inter-tumor heterogeneity in patient-derived xenograft (PDX) models. Int J Cancer 144: 366-371, 2019.
5. Mahasneh A, Al-Shaheri F and Jamal E: Molecular biomarkers for an early diagnosis, effective treatment and prognosis of colorectal cancer: Current updates. Exp Mol Pathol 102: 475-483, 2017.
6. Sepulveda AR, Hamilton SR, Allegra CJ, Grody W, Cushman-Vokoun AM, Funkhouser WK, Kopetz SE, Lieu C, Lindor NM, Minsky BD, et al: Molecular biomarkers for the evaluation of colorectal cancer: Guideline from the American society for clinical pathology, college of American Pathologists, Association for Molecular Pathology, and the American Society of Clinical Oncology. J Clin Oncol 35: 1453-1486, 2017.
7. Wang S, Sun C, Li J, Zhang E, Ma Z, Xu W, Li H, Qiu M, Xu Y, Xia W, et al: Roles of RNA methylation by means of N6-methyladenosine (m^6A) in human cancers. Cancer Lett 408: 112-120, 2017.
8. Wang X, Lu Z, Gomez A, Hon GC, Yue Y, Han D, Fu Y, Parisien M, Dai Q, Jia G, et al: N6-methyladenosine-dependent regulation of messenger RNA stability. Nature 505: 117-120, 2014.
Zheng G, Dahl JA, Niu Y, Fedorcsak P, Huang CM, Li CJ, Vágboi CB, Shi Y, Wang WL, Song SH, et al: ALKBH5 is a mammalian RNA demethylase that impacts RNA metabolism in cancer. Genes & Dev 34: 1298-304, 2020.

Zhao X, Yang Y, Sun BF, Shi Y, Yang X, Xiao W, Hao YJ, Ping XL, Chen YS, Wang WJ, et al: FTO-dependent demethylation of N6-methyladenosine regulates mRNA splicing and is required for adipo genesis. Cell Res 22: 1403-1419, 2014.

Fustin JM, Dori M, Yamaguchi Y, Hida H, Nishimura S, Yosada M, Makita M, Morika MS, Takahashi T, Maruhime M, et al: RNA methylation-dependent RNA processing controls the speed of the circadian clock. Cell 155: 793–806, 2013.

Wang Y, Li Y, Toth JI, Petroski MD, Zhang S and Zhao JC: N6-methyladenosine modification destabilizes developmental regulators in mouse stem cells. Nat Cell Biol 16: 191-198, 2014.

Zhang S, Zhao BS, Zhou A, Lin K, Zheng S, Lu C, Yang YJ, Su RH, et al: N6-methyladenosine demethylase ALKBH5 maintains tumorigenicity of glioblastoma stem-like cells by sustaining FOXM1 expression and cell proliferation program. Cancer Cell 31: 591-606.e6, 2017.

Li Z, Weng H, Su R, Weng X, Zuo Z, Li C, Huang H, Nachtgeraede S, Dong L, Hu C, et al: FTO plays an oncogenic role in acute myeloid leukemia as a N6-methyladenosine RNA demethylase. Cancer Cell 31: 127-141, 2017.

Cui Q, Shi H, Ye F, Li L, Qu Q, Sun G, Sun G, Lu Z, Zhang Y, Huang CY, et al: N6-methyladenosine demethylates the self-renewal and tumorigenesis of glioblastoma stem cells. Cell Rep 18: 2622-2634, 2017.

Lin S, Choi J, Du P, Triboulet R and Gregory RI: The m(6)A methyltransferase METTL3 promotes translation in human cancer cells. Cell 162: 335-345, 2015.

Wang Q, Chen C, Ding Q, Zhao Y, Wang Z, Chen J, Jiang Z, Zhang Y, Xu G, Zhang J, et al: METTL3-mediated m(6)A modification of HDGF mRNA promotes gastric cancer progression and has prognostic significance. Gut 69: 1193-1205, 2020.

Yue B, Song C, Yang L, Cui R, Cheng X, Zhang Z and Zhao G: METTL3-mediated N6-methyladenosine modification is critical for epithelial-mesenchymal transition and metastasis of gastric cancer. Mol Med 18: 14, 2019.

Taketo K, Konno M, Asai A, Koseki J, Toratani M, Satoh T, Doki Y, Mori M, Ishii H and Ogawa K: The epitranscriptome cation of HDGF mRNA promotes gastric cancer progression and tumorigenesis of glioblastoma stem-like cells. Cell Rep 18: 2622-2634, 2017.

Slattery ML, Lundgreen A, Hines LM, Torres-Mejia G, Wolfik RK, Stern MC and John EM: Genetic variation in the JAK/STAT/SOCS signaling pathway influences breast cancer-specific mortality through interaction with cigarette smoking and use of aspirin/NSAIDs: The Breast Cancer Health Disparities Study. Breast Cancer Res Treat 147: 145-158, 2014.

Das R, Gregory PA, Fernandez RC, Denis I, Wang Q, Townley SL, Zhang SG, Hanson AR, Pickering MA, Armstrong HK, et al: MicroRNA-29 promotes proliferation by inhibiting SOCS2. Cancer Res 77: 1021-1034, 2017.

Vitali C, Bassani C, Chiodoni C, Fellin S, Guarnotta C, Miotti S, Vitali C, Bassani C, Chiodoni C, Fellin S, Guarnotta C, Miotti S, et al: LncRNA CASC15 promotes colon cancer cell proliferation and metastasis by regulating the miR4310/LGR5/Wnt/β-catenin signaling pathway. Mol Med Rep 18: 2269-2276, 2018.

Gopalan V, Ebrahimi F, Islam F, Vider J, Qallandar OB, Pillaia S, Lu CT and Lam AK: Tumor suppressor properties of miR-15a and its regulatory effects on BCL2 and SOX2 proteins in colorectal carcinomas. Exp Cell Res 370: 245-253, 2018.

Alcantara-Flores E, Brechu-Franco AE, Garcia-Lopez P, Rocha-Zaavaleta L, Lopez-Marure R and Martinez-Vazquez M: Argentatia B inhibits proliferation of prostate and colon cancer cells by inducing cell senescence. Molecules 20: 21125-21137, 2015.

Gong S, Xu D, Zhu J, Zou F and Peng R: Efficacy of the MEK inhibitor cobimetinib and its potential application to colorectal cancer cells. Cell Physiol Biochem 47: 680-693, 2018.

Zhou M, Wei L, Law CT, Tsang FH, Shen J, Cheng CL, Tsang LH, Ho DW, Chiu DK, Lee JM, et al: RNA N6-methyladenosine methyltransferase-like 3 promotes liver cancer progression through YTHDF2-dependent posttranscriptional silencing of SOCS2. Hepatology 67: 2254-2270, 2018.

Zhao X, Zhang W and Ji W: miR-196b is a prognostic factor of human laryngeal squamous cell carcinoma and promotes tumor progression by targeting SOCS2. Biochem Biophys Res Commun 501: 584-592, 2018.

Zhou Y, Zhang Z, Wang N, Chen J, Zhang X, Guo M, John ZL and Wang Q: Suppressor of cytokine signaling-2 limits IFG/R-mediated regulation of epithelial-mesenchymal transition in lung adenocarcinoma. Cell Death Dis 9: 429, 2018.

Chinabara Y, Wang H, Holm J, Kroeljaisen LF, Steinocher H, Papadopoulos A, Tunny KA, Meunier FA, Smith AG, Krugelund BB, Brooks AJ, et al: A growth hormone receptor SNP promotes lung cancer by impairment of SOCS2-mediated degradation. Oncogene 37: 489-501, 2018.

Hwang Y, Fukuda S, Kitano K, Hirata A, Hara A and Tomita H: Multifaceted Interpretation of Colon Cancer Stem Cells. Int J Mol Sci 13: 1846, 2012.

Chen X, Wei B, Han X, Zheng Z, Huang J, Liu Y and Wei H: LGR5 is required for the maintenance of spheroid-derived colon cancer stem cells. Int J Mol Med 34: 35-42, 2014.

Skrzypczak M, Goryca K, Rubel T, Paziewska A, Mikula M, Jarosz D, Pachlewski J, Oledzikı J and Ostrowski J: Modeling oncogenic signaling in colon tumors by multidirectional analyses of microarray data directed for maximization of analytical reliability. PLoS One 5: e13091, 2010.

Grahnens E, Biottani V, Mollard C, Mariage-Samson R, Barlet X, Gremy G, Couilaut C, Lajemi M, Piatier-Tonneau D, Zaborski P, et al: Deciphering cellular states of innate tumor drug responses. Genome Biol 17: R99, 2016.

Sabates-Bellver J, Van der Flier LG, de Palo M, Cattaneo E, Maake C, Rehrauer H, Luczkó E, Kuroswi MA, Bunkic J, Menigatti M, et al: Transcription profile of human colorectal adenomas. Mol Cancer Res 5: 1263-1275, 2007.

Kaiser S, Park YK, Franklin JL, Halberg RB, Yu M, Jansen WJ, Freudenberg J, Chen X, Hages K, Jegga AG, et al: Transcriptional recapitulation of cancer from cancer to cancer development by mouse colon tumor models and human colon cancer. Genome Biol 8: R131, 2007.

Hong Y, Downey T, Eu KW, Koh PK and Cheah PY: A metastasis-prone signature for early-stage mismatch-repair proficient sporadic colorectal cancer patients and its implications for possible therapeutics. Clin Exp Metastasis 27: 83-90, 2010.
53. Dominissini D, Moshitch-Moshkovitz S, Schwartz S, Deng X, Su R, Weng H, Huang H, Li Z and Chen J: RNA
56. Notterman DA, Alon U, Sierk AJ and Levine AJ: Transcriptional
49. Alon U, Barkai N, Notterman DA, Gish K, Ybarra S, Mack D
48. Gaedcke J, Grade M, Jung K, Camps J, Boer JM, de Menezes RX and Fodde R: Cross-species comparison of human and mouse intestinal polyps reveals conserved mechanisms in adenomatous polyposis coli (APC)-driven tumorigenesis. Am J Pathol 172: 1363-1380, 2008.

50. Notterman DA, Alon U, Sierk AJ and Levine AJ: Transcriptional gene expression profiles of colorectal adenoma, adenocarcinoma, and normal tissue examined by oligonucleotide arrays. Proc Natl Acad Sci USA 96: 6745-6750, 1999.

51. Ki DH, Jeung HC, Park CH, Kang SH, Lee GY, Lee WS, Kim NK, Chang HC and Rha SY: Whole genome analysis for liver metastasis gene signatures in colorectal cancer. Int J Cancer 121: 2005-2012, 2007.

52. Gaspar C, Cardoso J, Franken P, Molenaar L, Morreau H, Moslein G, Sampson J, Boer JM, de Menezes RX and Fodde R: Cross-species comparison of human and mouse intestinal polyps reveals conserved mechanisms in adenomatous polyposis coli (APC)-driven tumorigenesis. Am J Pathol 172: 1363-1380, 2008.

53. Dominissini D, Moshitch-Moshkovitz S, Schwartz S, Salmon-Divon M, Ungar L, Olseneg S, Cesarkas K, Jacob-Hirsch J, Amargilio N, Kupiec M, et al: Topology of the human and mouse m6A RNA methylomes revealed by m6A-seq. Nature 485: 201-206, 2012.

54. Yang D, Qiao J, Wang G, Lan Y, Li G, Guo X, Xi J, Ye D, Zhu S, Chen W, et al: N6-methyladenosine modification of lincRNA 1281 is critically required for mESC differentiation potential. Nucleic Acids Res 46: 3906-3920, 2018.

55. Bertero A, Brown S, Madrigal P, Osnato A, Ortmann D, Sax U, Schirmer M, Becker H, et al: Mutated KRAS results in overexpression of DUSP4, a MAP kinase phosphatase, and SMYD3, a histone methyltransferase, in rectal carcinomas. Genes Chromosomes Cancer 49: 1024-1034, 2010.

56. Notterman DA, Alon U, Sierk AJ and Levine AJ: Broad patterns of gene expression revealed by oligonucleotide arrays. Proc Natl Acad Sci USA 96: 6745-6750, 1999.

57. Vu LP, Pickering BF, Cheng Y, Zaccara S, Nguyen D, Minuesa G, Chou T, Chow A, Salatore Y, MacKay M, et al: The N6-methyladenosine (m6A)-forming enzyme METTL3 controls myeloid differentiation of normal hematopoietic and leukemia cells. Nat Med 23: 1369-1376, 2017.

58. Visvanathan A, Patil V, Arora A, Hegde AS, Arivazhagan A, Santosh V and Somasundaram K: Essential role of METTL3-mediated m6A modification in glioma stem-like cells maintenance and radioresistance. Oncogene 37: 522-533, 2018.

59. Cai X, Wang X, Cao C, Gao Y, Zhang S, Yang Z, Liu Y, Zhang X, Zhang W and Ye L: HBXIP-elevated methyltransferase METTL3 promotes the progression of breast cancer via inhibiting tumor suppressor let-7g. Cancer Lett 415: 11-19, 2018.

60. Cai X, Wang X, Cao C, Gao Y, Zhang S, Yang Z, Liu Y, Zhang X, Zhang W and Ye L: METTL3 promotes the progression of breast cancer via inhibiting tumor suppressor let-7g. Cancer Lett 415: 11-19, 2018.

61. Dimitriou ID, Clemenza L, Scotti AJ, Chen G, Guerra FM and Rottapel R: Putting out the fire: Coordinated suppression of the innate and adaptive immune systems by SOCS1 and SOCS3 proteins. Immunol Rev 224: 265-283, 2008.

62. Palmer DC and Restifo NP: Suppressors of cytokine signaling (SOCS) in T cell differentiation, maturation, and function. Trends Immunol 30: 592-602, 2009.

63. Letellier E and Haan S: SOCS2: Physiological and pathological functions. Front Biosci (Elite Ed) 8: 189-204, 2016.

64. Newton VA, Ramocki NM, Scull BP, Simmons JG, McNaughton K and Lund PK: Suppressor of cytokine signaling-2 gene disruption promotes Apc(Min/+) tumorigenesis and activator protein-l activation. Am J Pathol 176: 2320-2332, 2010.

65. Miller ME, Michaylira CZ, Simmons JG, Nye DM, Dahly EM, Heath JK and Lund PK: Suppressor of cytokine signaling-2: A growth hormone-inducible inhibitor of intestinal epithelial cell proliferation. Gastroenterology 127: 570-581, 2004.

66. Letellier E, Schmitz M, Baig K, Beaune N, Schwartz C, Frasquilho S, Antunes L, Marcon N, Nazarow PV, Vallar L, et al: Identification of SOCS2 and SOCS6 as biomarkers in human colorectal cancer. Br J Cancer 111: 726-735, 2014.

67. Slattery ML, Lundgreen A, Kaldalbar SA, Bondurant KL and Wolff RK: JAK/STAT/SOCS-signaling pathway and colon and rectal cancer. Mol Carcinog 52: 155-166, 2013.

68. Hanahan D and Weinberg RA: Hallmarks of cancer: The next generation. Cell 144: 646-674, 2011.

69. Barker N, van Es JH, Kuipers J, Kujala P, van den Born M, Crotjinse M, Haegebarth A, Korving J, Begthel H, Peters PJ, et al: The SMAD2/3 interactome reveals that TGF-β controls m 6A-dependent translation control. Nature 555: 256-259, 2018.

70. Jiang Y, Li W, He X, Zhang H, Jiang F and Chen Z: Lgr5 expression is a valuable prognostic factor for colorectal cancer: Evidence from a meta-analysis. BMC Cancer 16: 12, 2016.

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