



HAL
open science

Epigenetic Regulation by lncRNAs: An Overview Focused on UCA1 in Colorectal Cancer

Bernadette Neve, Nicolas Jonckheere, Audrey Vincent, Isabelle van Seuningen

► **To cite this version:**

Bernadette Neve, Nicolas Jonckheere, Audrey Vincent, Isabelle van Seuningen. Epigenetic Regulation by lncRNAs: An Overview Focused on UCA1 in Colorectal Cancer. *Cancers*, 2018, 10 (11), pp.440. 10.3390/cancers10110440 . inserm-02341333

HAL Id: inserm-02341333

<https://inserm.hal.science/inserm-02341333>

Submitted on 31 Oct 2019

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Review

Epigenetic Regulation by lncRNAs: An Overview Focused on UCA1 in Colorectal Cancer

Bernadette Neve , Nicolas Jonckheere , Audrey Vincent  and Isabelle Van Seuning 

Inserm UMR-S 1172, Centre de Recherche Jean-Pierre AUBERT Neurosciences et Cancer (JPArC), Team “Mucins, Epithelial Differentiation and Carcinogenesis”; University Lille; CHU Lille, 59045, Lille CEDEX, France; nicolas.jonckheere@inserm.fr (N.J.); audrey.vincent@inserm.fr (A.V.); isabelle.vanseuning@inserm.fr (I.V.S.)

* Correspondence: bernadette.neve@inserm.fr; Tel.: +33-320-29-88-64

Received: 19 October 2018; Accepted: 8 November 2018; Published: 14 November 2018



Abstract: Colorectal cancers have become the second leading cause of cancer-related deaths. In particular, acquired chemoresistance and metastatic lesions occurring in colorectal cancer are a major challenge for chemotherapy treatment. Accumulating evidence shows that long non-coding (lncRNAs) are involved in the initiation, progression, and metastasis of cancer. We here discuss the epigenetic mechanisms through which lncRNAs regulate gene expression in cancer cells. In the second part of this review, we focus on the role of lncRNA Urothelial Cancer Associated 1 (UCA1) to integrate research in different types of cancer in order to decipher its putative function and mechanism of regulation in colorectal cancer cells. UCA1 is highly expressed in cancer cells and mediates transcriptional regulation on an epigenetic level through the interaction with chromatin modifiers, by direct regulation via chromatin looping and/or by sponging the action of a diversity of miRNAs. Furthermore, we discuss the role of UCA1 in the regulation of cell cycle progression and its relation to chemoresistance in colorectal cancer cells.

Keywords: long non-coding RNA (lncRNA); lncRNA Urothelial Cancer Associated 1 (UCA1); colorectal cancer (CRC); competing endogenous RNAs (ceRNA)

1. Colorectal Cancer

Colon and rectal cancers (together nominated colorectal cancer (CRC)) have become the second leading cause of cancer deaths both in the United States and in Europe ([1,2], respectively). CRC occurrence has been correlated to an unhealthy lifestyle (tobacco, alcohol, red meat, sedentariness, obesity), whereas physical activity and dietary fibers protect against CRC [3]. In addition, early diagnosis by stool-based CRC screening has decreased disease mortality [4]. However, most patients are only diagnosed after they have symptoms and frequently present metastatic lesions (e.g., 14% in the German DACHS study [5], 19–24% in US SEER study [6]). An additional 20% of the CRC patients develop metastases during their disease evolution [5,7]. Distant metastases occur mainly in the liver, peritoneum and lung tissues. Non-metastatic colon cancer is generally treated by surgical colectomy combined with chemotherapy (e.g., inhibitors of DNA synthesis, FOLFOX (FOLinic acid, 5-Fluorouracil (5-FU) and OXaliplatin) or CAPEOX (CAPEcitabine and OXaliplatin), ±anti-VEGF antibodies such as bevacizumab [8]). Isolated and local metastases of colon cancer are also surgically resected. For unresectable metastatic CRC, a continuum of systemic chemotherapy is provided (e.g., combined therapy with reduced folate leucovorin, topoisomerase I inhibitor irinotecan, anti-EGFR antibodies cetuximab, or panitumumab; described in the National Comprehensive Cancer Network Clinical Practice Guidelines [8]).

Several tumor tissue alterations are important for the diagnosis and prognosis of CRC [8,9]. For example, CRC patients present 5–20% tumors with microsatellite instability (MSI) related to

mismatch repair (MMR) defaults, while 15% of the tumors have a CpG island methylation phenotype. CRC patients with a primary right-sided tumor have significantly greater rates of MSI and may have no benefit of 5FU chemotherapy at stage II of CRC [10]. In addition, the tumor tissue of metastatic CRC patients may present RAS (KRAS and NRAS) or B-RAF mutations that result in a constitutively active MAPK signaling pathway, which increases cellular proliferation. KRAS mutated tumors lack a response to EGFR inhibitors (e.g., cetuximab), whereas inhibitors of mutated B-RAF (e.g., vemurafenib) may be used in combination with chemotherapy [8]. In addition, classifying tumors according to gene expression-based molecular subtypes prognoses the response to therapy, and may innovate towards personalized therapy [11,12]. Actually, colon and rectal cancers are frequently analyzed in epidemiological studies as one entity, although differences in clinical and molecular characteristics of primary colon cancers were recently re-highlighted between tumors from the right side, including the caecum, ascending colon, hepatic flexure and two-thirds of the transverse colon (~27% of patients), and one from the left-sided colon, including the distal third of the transverse colon, splenic flexure, descending colon, sigmoid and rectum [13–15]. In these studies, the tumor location was found to be an independent prognostic factor for overall survival, which may be worse for patients with right-sided tumors [13]. The reported 5-year survival rate for patients with non-metastatic CRC is 70–90%, whereas for patients with metastatic CRC this was a poor 14% [16]. This bad prognosis could be due to the acquired cellular chemoresistance and the presence of residual colon cancer cells.

2. Mechanisms of Regulation by Long Non-Coding RNAs in Cancer Cells

Long non-coding RNAs (lncRNAs) are a heterogeneous class of RNAs that are arbitrarily defined as transcripts over 200 nucleotides long and lacking sequences encoding functional and/or conserved proteins. According to the current human GENCODE Release, 27% of all genes are lncRNA transcripts (15,779 transcripts, Release v28, <https://www.genencodegenes.org>). These lncRNAs are implicated in a diversity of physiological processes and a large range is implicated in CRC [17–19]. Moreover, differential lncRNA expression was related to different clinical CRC characteristics and molecular phenotypes [19,20]. lncRNA-mediated regulation has crucial roles in gene expression control, which implicates mechanisms based on both base-pair interactions (DNA/RNA) and protein interactions (Figure 1).

2.1. Interaction of lncRNAs with DNA

The lncRNAs-DNA interactions affect both DNA organization and transcription.

2.1.1. DNA Organization

Genomic DNA is packed in the nucleus into a higher order genome organization, which has a dynamic and spatial architecture. Within the nucleus, the nucleoli and paraspeckles display a unique morphology, positioning, and are related to transcriptional activity (review by References [21,22]). The lncRNAs, NEAT1 and MALAT1, were shown to play a role in the forming and organization of these nuclear speckle bodies. Both these lncRNAs are related to active chromatin sites in the nucleus, are overexpressed in CRC, and are correlated with a poor disease prognosis (References [23–27], respectively).

The packaging of genomic DNA also depends on histone and DNA modifications, which are regulated by epigenetic complexes, and that may bind lncRNAs. A common feature is the potential of lncRNAs to interact with the polycomb repressive complex-2 (PRC2), in which the principal subunits are subunit SUZ12, embryonic ectoderm development (EED) and the enhancer of zeste homolog 2 (EZH2). RNA-Immunoprecipitation experiments with SUZ12 and EZH2 showed that 20–30% of the intergenic lncRNAs interact with PRC2 [28]. In CRC cells, EZH2 has been shown to bind to at least 12 lncRNAs, including UCA1 (Table 1). lncRNAs recruit PRC2 towards gene promoters/enhancers and thus stimulate epigenetic silencing by trimethylation lysine 27 of histone H3 (H3K27me3) (reviewed by Reference [29]). Interestingly, the tumor suppressor KLF2 gene is reported to be silenced in CRC cells

by several lncRNAs through this mechanism (e.g., LINC00460, SH3PXD2A-AS1, HOXA-AS2 [30–32]), whereas for most genes, only a unique lncRNA/EZH2 combination is known. In addition, other CRC-related lncRNAs interact with adaptor protein WDR5 from the histone H3 lysine 4 (H3K4) methyltransferase-complex (Table 1). Inversely, lncRNAs may also affect histone demethylation. The interaction with histone lysine-specific demethylase 1 (LSD1) was shown for four different CRC-associated lncRNAs (Table 1). DNA methylation is affected by lncRNAs through several mechanisms. On the one hand, expression of DNA-methyl transferases is frequently regulated by lncRNAs through interference with miRNA-mediated transcript decay. On the other hand, some studies showed a physical interaction with DNMTs, including NEAT1 [33]. lncRNAs also affect chromatin configuration and DNA methylation via interaction with switching defective/sucrose non-fermenting (SWI/SNF) complexes (Reference [34]). lncRNAs, including UCA1, were shown to bind to Brahma related gene 1 (BRG1) in a variety of cancer cells (Table 1), while others bind to SNF5 and BAF200a of these SWI/SNF complexes [35,36].

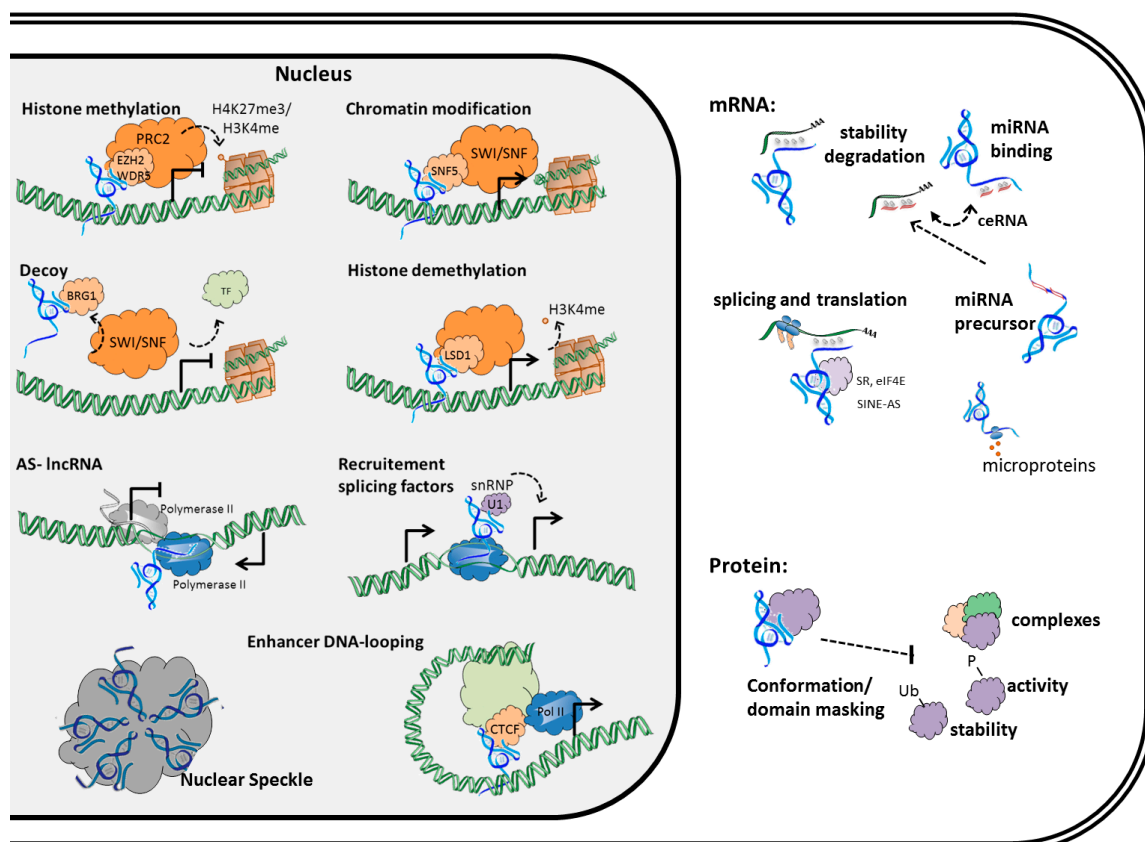


Figure 1. The function of lncRNAs in the cell. lncRNAs exert different functions in the nucleus, ranging from genomic DNA organization in speckle bodies, histone, and DNA methylation and direct transcriptional regulation (Section 2.1). Through their interaction with mRNA and function in miRNA regulation, they affect protein translation (Section 2.2). In addition, they interact with proteins, affecting stability, activity, and/or complex recruitment (Section 2.3).

Table 1. The examples of long non-coding RNAs in cancer cells.

	lncRNA	References
DNA organization		
Speckle formation		
	NEAT1	[23–25]
	MALAT1	[25,27]
Histone modification		
EZH2	AFAP1-AS1	[37]
	ANCR	[38]
	BLACAT1	[39]
	CRNDE	[40]
	HOTAIR	[41]
	HOXA-AS2	[32]
	HULC	[42]
	PINT	[43]
	LINC00460	[30]
	SH3PXD2A-AS1	[31]
	SNHG17	[44]
	UCA1	[45–47]
WDR5	HOTTIP	[48]
	CASC15	[49]
	GClnc1	[50]
	HOXD-AS	[51]
LSD1	HOTTAIR	[52]
	FOXP4-AS1	[53]
	HOXA11-AS	[54]
	HOXA-AS2	[32]
SWI/SNF chromatin modulation		
BRG1	lncTCF7	[55]
	lncFDZ6	[56]
	NEAT1	[21]
	UCA1	[57]
SNF5	SChLAP1	[35]
BAF200a	MVIH	[36]
RNA interaction		
miRNA-precursors		
miR-675	H19	[58,59]
miR-545/374a	Ftx	[60]
miR-143, -145	NCR143/145	[61]
miR-31	LOC554202	[62]
miR-125b-2, miR-99a and let-7c	MONC	[63]
miR-100, miR-125b-1 and let-7a-2	MIR100HG	[63]
Let-7c, miR99a and miR125b	LINC00478	[64]
Protein interaction		
Protein stability		
P53	PANDA	[65]
SREBP-1c	MALAT1	[66]
DNMT1	LUCAT1	[67]
SLUG	SNHG15	[68]

2.1.2. DNA Transcription

Many lncRNAs are antisense to coding mRNA transcripts. Our text-mining using the UCSC genome table browser shows that there are at least 991 genes with a known antisense transcript

(curated RefSeq track, GRCh38/hg38). The transcription of antisense lncRNA can directly inhibit transcription of sense coding genes [69–71], which may be mediated by Polymerase II collisions [26]. Both SPINT-AS1 and UTX-AS1 expression are negatively correlated with sense gene expression, and their overexpression is correlated with poor prognosis for CRC [72,73]. Transcripts of lncRNA may also bind to splicing machinery factors and activate proximal promoter regions, as shown for U1 snRNP/linc1319 that activated the malignant brain tumor (MBT) domain-containing protein Sfmbt2 [74]. In addition, long-range chromatin looping through lncRNA-DNA interaction may regulate protein-coding gene transcription [75,76]. Amaral et al. reported the association with chromatin looping for several lncRNAs differentially expressed in CRC cells (GAS5, H19, HAGLR, NEAT1, PINT, and CRNDE (in Supplementary Table S6 of Amaral et al. [76])). The lncRNA CCAT1-L that is upregulated in human CRC also regulates such chromatin looping at the MYC locus [77]. UCA1/CUDR promotes chromatin looping at the promoter of lncRNA HULC in liver cancer cells [78]. First reported for tumor suppressor lncRNA MEG3, one of the mechanisms that guide lncRNAs to target DNA sequences is the formation of the triplex RNA-DNA helices of GA-rich regions [76,79]

2.2. Interaction of lncRNAs with RNA

Evidence of direct physical lncRNA-mRNA interaction enhancing the stability of mRNA is sparse, but was shown for lncRNA MACC1-AS1 in gastric cancer cells and MAPT AS1 in breast cancer cells [80,81]. Similarly, the transforming growth factor- β (TGF β)-induced antisense RNA Zeb2/Sip1 in bladder carcinoma cells binds to the 5'UTR-splicing site of the ZEB2 transcript and prevents its degradation [82,83]. Nonetheless, the stability of mRNA is modified via the binding of miRNAs frequently, which recruits a miRNA-induced silencing complex (miRISC) triggering mRNA deadenylation and decay [84]. On one hand, lncRNAs can be processed to generate miRNAs changing the miRNome of cells. Several tumor-related lncRNAs have been shown to be miRNA-precursors (Table 1). On the other hand, lncRNAs are frequently reported to function as competing endogenous RNAs (ceRNAs) to relieve the miRNA-mediated degradation of mRNAs [85]. Besides lncRNA, ceRNAs may also include mRNAs, circle RNAs, and pseudogenes [86]. Despite the fact that the stoichiometric relationship between miRNAs/regulated genes and the affinity of ceRNAs to miRNAs may question the feasibility of gene regulation through changes in ceRNA levels [87], several dedicated databases list lncRNA-miRNA interactions [86,88] and the number of original reports on their interactions still increases every year (at least 130 articles on lnc-ceRNAs January–June 2018). Recently, an lncRNA/miRNA/mRNA interactome was reported based on CRC expression data from the TCGA database. These analyses illustrated a ceRNA network of 25 principal miRNAs and 64 lncRNAs, including CRNDE, H19, HULC and UCA1 [17,89]. As discussed below, UCA1 was reported to interact with 29 miRNAs in several types of cancers. Five of these miRNAs were reported as differentially expressed and in the ceRNA network (miR-143, -144, -145, -182, and -206; [89]). It remains unclear whether the binding of miRNAs to lncRNAs also triggers lncRNA decay, since this decay may be very slow.

Direct interaction of lncRNA-mRNA affects mRNA splicing, but may also interfere with protein translation. Antisense transcripts that overlap a gene translation start site and encode an inverted retrotransposon short interspersed nuclear element (SINE) may stimulate protein translation [90]. In addition, the interaction of lncRNA GAS5 in a complex with Eukaryotic Translation Initiation Factor 4E (eIF4E) inhibited the cMYC translation [91].

2.3. Interaction of lncRNAs with Proteins

The interaction of lncRNAs with proteins can evoke the recruitment of effector complexes: as discussed above, the interaction with protein complexes affect epigenetic modifications and the interaction with heterogeneous nuclear ribonucleoproteins (hnRNPs) can regulate gene transcription in the nucleus (respectively reviewed by References [29,92]). The binding of lncRNAs to proteins can also function as a scaffold to increase protein stability (Table 1), e.g., the binding of the lncRNA

Small Nucleolar RNA Host Gene (SNHG) 15 to SLUG blocks its ubiquitin-mediated degradation in colon cancer cells [68]. LncRNA binding to proteins can also decoy the protein function such as LINC01133 that titrates the splicing factor SRSF6 away from its targets, thereby preventing epithelial to mesenchymal transition in CRC cells [93]. Other lncRNAs also bind proteins of the splicing machinery (reviewed by Reference [94]), for example, lncRNA FAS-AS1 (SAF) interacts with SP45 resulting in alternatively spliced and anti-apoptotic FAS in cancer cells [95] and MALAT1 was shown to interact with serine/arginine (SR) splicing factors in nuclear speckle bodies [96]. Furthermore, interaction with signaling proteins may alter the activation of signaling pathways. For example, the binding of lncRNA NKILA to the NF- κ B/I κ B complex in breast cancer cells prevents I κ B phosphorylation, thereby preventing NF- κ B activation [97]. The cytoplasmic lncRNA LINK-A binding activates a protein tyrosine kinase complex (BRK/LRRK2), which results in the increased HIF1 α signaling in breast cancer cells [98].

Although defined as long “non-coding” RNA, recent findings suggest that the presence of ribosomes on lncRNAs may indicate that the short open reading frames are a source of small peptide synthesis [99,100]. The detection of microproteins is challenging, but some evidence was reported; the lncRNA LINC00961 encodes a polypeptide (SPAR) that negatively regulates mTORC1 activation [101]; the LINC01420-derived microprotein was identified as a novel component of the mRNA decapping complex regulating mRNA decay [102] and a HOXB-AS3-derived peptide was shown to regulate pyruvate kinase M splicing and to affect the metabolic reprogramming of CRC cells [103]. The number of lncRNAs that are actually a source of small regulatory peptides remains to be investigated. Alternatively, the interaction of lncRNAs with ribosome complexes may trigger lncRNA degradation [104].

Accumulating evidence shows that lncRNAs are involved in the initiation, progression, and metastasis of cancer [105,106]. We have discussed how lncRNAs may regulate cancer-associated expression profiles on diverse levels. We have briefly cited several well-known lncRNAs that are implicated in CRC (Table 1), such as GAS5, H19, HOTAIR, CCAT1-L, CRNDE, and MALAT1. It has been shown that the gene desert of Chr8q24, which is a CRC risk locus, harbors 7 lncRNAs including CCAT1 (CARLo-5), and CASC19 (CARLo-6). In addition, numerous colorectal cancer associated lncRNAs, such as CCAT6 (MYCLo-2), CASC8 (CARLo-1), CASC21 (CARLo-2), PRNCR1 (CARLo-3), PCAT2 (CARLo-4), and CASC11 (CARLo-7), have been identified [107]. Recently, the analysis of lncRNA expression in different CRC molecular phenotypes highlighted the decreased expression of UCA1 in tumors with Mismatch Repair (MMR) defaults compared to tumors without such defaults [19]. The following sections focus on the role of UCA1 to integrate research on different cancer cells in order to decipher its putative functions and mechanisms of regulation in CRC cells.

3. UCA1 Expression in Colorectal Cancer

3.1. Association of UCA1 Transcript Expression with Colorectal Cancer

Urothelial Cancer Associated 1 (UCA1) was first discovered in bladder cancer [108] and its long transcript is also the nominated Cancer Upregulated Drug-Resistant transcript (CUDR) [109]. Actually, three UCA1 transcript isoforms of 1.4 kb, 2.2 kb, and 2.7 kb have been described, but, in general, the most abundant 1.4 kb isoform is studied [110]. Analysis of UCA1 expression and patient survival data from the TCGA dataset shows that its expression was correlated with increased hazard ratio in different types of cancers, in particular with pancreatic adenocarcinoma (Table 2, [111–113]). Although several patient studies reported that a high expression of UCA1 is correlated with bad disease prognosis in CRC (the number of patient of these studies N = 80 [114], N = 54 [115], N = 90 [116] and the N = 530 for the Asian meta-analysis [117]), no such evidence was observed in the TCGA COAD-READ study (Table 2). Since separated analyses of colon (COAD) and rectal (READ) adenocarcinoma patients showed different Kaplan Meier survival curves, this discrepancy may originate from mixed colon and rectal adenocarcinoma patients in several studies (e.g., known mixed COAD:READ patient groups

in [114,116]). Recently, a genome-wide analysis of lncRNA expression in different CRC phenotypes was realized, highlighting the decreased expression of UCA1 in tumors with Mismatch Repair (MMR) defaults compared to tumors without such defaults [19]. These differences are in line with the notion that different primary tumor locations (COAD vs. READ) and, therefore, carcinogenesis pathways define the molecular characteristics and epigenetic signature of the tumor [118].

Table 2. The association of Urothelial Cancer Associated 1 (UCA1) transcript expression with cancer in The Cancer Genome Atlas (TCGA) datasets.

TCGA Cancer Classification	Total Patients Number (N); N in Low vs. High Risk Group	Log Rank Equal Curves	Hazard Ratio (95% CI)	p Value
Acute Myeloid Leukemia	N = 149; 138 vs. 11	$p = 0.77$	1.12 (CI 0.52; 2.43)	$p = 0.77$
Bile Duct Cholangiocarcinoma	N = 35; 16 vs. 19	$p = 0.15$	2.06 (CI 0.75; 5.64)	$p = 0.16$
Bladder—Urothelial Carcinoma	N = 389; 112 vs. 277	$p = 0.0034$	1.75 (CI 1.2; 2.56)	$p = 0.0038$
Breast invasive carcinoma—July 2016	N = 962; 844 vs. 118	$p = 0.29$	1.31 (CI 0.79; 2.15)	$p = 0.29$
Cervical squamous cell carcinoma and endocervical adenocarcinoma	N = 191; 121 vs. 70	$p = 0.051$	1.82 (CI 0.99; 3.35)	$p = 0.054$
Colon and Rectum adenocarcinoma:	N = 422; 151 vs. 371	$p = 0.66$	1.1 (CI 0.72; 1.69)	$p = 0.66$
Colon	N = 350; 197 vs. 153	$p = 0.51$	0.86 (CI 0.54; 1.36)	$p = 0.51$
Rectum	N = 57; 39 vs. 18	$p = 0.0075$	4.54 (CI 1.35; 15.27)	$p = 0.014$
Esophageal carcinoma	N = 184; 148 vs. 36	$p = 0.29$	0.72 (CI 0.38; 1.33)	$p = 0.29$
Head and Neck squamous cell carcinoma	N = 506; 304 vs. 198	$p = 0.45$	1.11 (CI 0.85; 1.46)	$p = 0.45$
Kidney PAN cancer	N = 892; 715 vs. 77	$p = 0.67$	1.11 (CI 0.68; 1.83)	$p = 0.67$
Liver hepatocellular carcinoma	N = 361; 318 vs. 43	$p = 0.025$	1.68 (CI 1.06; 2.66)	$p = 0.027$
Lung adenocarcinoma	N = 475; 384 vs. 91	$p = 0.0041$	1.69 (CI 1.18; 2.44)	$p = 0.0046$
Lung squamous cell carcinoma	N = 175; 123 vs. 52	$p = 0.93$	0.98 (CI 0.61; 1.58)	$p = 0.93$
Ovarian serous cystadenocarcinoma	N = 247; 25 vs. 222	$p = 0.21$	0.72 (CI 0.43; 1.21)	$p = 0.21$
Pancreatic adenocarcinoma	N = 176; 154 vs. 22	$p = 1.766 \times 10^{-0.5}$	2.94 (CI 1.75; 4.92)	$p = 4.249 \times 10^{-0.5}$
Stomach and Esophagous adenocarcinoma	N = 440; 220 vs. 220	$p = 0.90$	0.98 (CI 0.72; 1.33)	$p = 0.90$
Stomach adenocarcinoma	N = 352; 135 vs. 217	$p = 0.70$	1.07 (CI 0.75; 1.52)	$p = 0.70$
Testicular Germ Cell Tumors	N = 133; 105 vs. 28	$p = 0.19$	3.39 (CI 0.48; 24.1)	$p = 0.22$
Uterine Corpus Endometrial Carcinoma	N = 247; 130 vs. 117	$p = 0.084$	1.85 (CI 0.91; 3.75)	$p = 0.089$

Kaplan-Meier survival curve statistics are reported from the TCGA cohort data using the SurvExpress portal [119].

3.2. Regulation of UCA1 Transcript Expression

The UCA1 gene encodes 3 exons located on chromosome 19 and it is highly expressed in cancer cells. Indeed, its transcription is up-regulated by diverse oncogenic pathways. The Ras-responsive transcription factor Ets-2 was shown to regulate UCA1 transcription in both bladder and colorectal cells [115,120], UCA1 is upregulated by the major inducer of epithelial-mesenchymal transition (EMT) TGF β in gastric and breast cancer cells [121,122] and by mediators of chemoresistance like Hippo (TAZ/YAP/TEAD) signaling in bladder and breast cancer cells [123,124]. BMP9 has an ambiguous role in tumor progression, but it was recently shown that BMP9 stimulated UCA1 expression in bladder cancer cells [124]. Interestingly, in these cells, UCA1 expression was also stimulated during hypoxia

via Hypoxia-Inducible Factor-1 α (HIF1 α) and the secretion of UCA1-enriched exosomes was increased under those conditions [125,126].

Several chromatin remodeling factors inhibit UCA1 transcription. Although the transcription factor CCAAT/enhancer binding protein α (C/EBP α) upregulated the UCA1 expression [127], this activation was inhibited by the tumor repressor and part of an SWI/SNF chromatin remodeling complex, ARID1A [128]. Epigenetic inhibition of UCA1 in breast cancer cells was mediated by the Special AT-rich sequence Binding-protein 1 (SATB1) [129]. The Coactivator of AP1 and Estrogen Receptor (CAPER α)/ T-box3 (TBX3) repressor complex that mediates an arrest of cell growth also downregulated UCA1 in embryonic kidney cells [130].

Levels of UCA1 transcripts are also regulated post-transcriptionally; the RNA stability of UCA1 was downregulated by the interaction with insulin-like growth factor 2 messenger RNA binding protein (IMP1) [131] and by the interaction with miR-1 [132], whereas binding of UCA1 to heterogeneous nuclear ribonucleoprotein I (hnRNPI) increased its stability [133]. It remains to be explored if the described regulation of transcript levels in diverse cancer cells also regulates UCA1 in colorectal cells.

4. UCA1-Mechanism of Regulation

4.1. UCA1-Regulated Transcription

In common with a lot of other lncRNAs, UCA1 can regulate the transcription of genes via epigenetic modifications (Table 3). Recent studies showed that UCA1 can physically associate with EZH2 and suppress transcription via histone methylation (H3K27me3) on the promoter of cell cycle genes p21cip and p27Kip1 [45–47] and stimulate cyclin D1 expression [46]. The UCA1 interaction with SET1A in liver cancer cells enhanced the histone methylation (H3K4me3) loading onto the telomeric repeat binding factor 2 (TRF2) promoter region, increasing TRF2 expression and telomere length [134]. The binding of UCA1 to transcription regulating complexes can also function as a decoy. In gallbladder cancer cells, UCA1 interacted with Brahma related gene 1 (BRG1) of the chromatin SWI/SNF remodeling complex and prevented its binding to the p21 promoter locus [57]. Binding of UCA1 to heterogeneous nuclear ribonucleoprotein I (hnRNPI) in breast cancer cells resulted in the decreased stimulation of the p27 promoter by hnRNPI [133]. Another mechanism of transcriptional regulation by UCA1 occurs in hepatocytes where the UCA1/CUDR-induced chromatin loop recruits the transcription insulator CTCF and β -catenin enhancer resulting in the upregulation of β -catenin transcription [78]. Zhang et al. performed RNA immuno-precipitation assays showing a direct interaction of UCA1 with the mediators MOB1, Lats1, and YAP of the Hippo pathway, and demonstrated a major role of UCA1 for nuclear translocation of YAP and pancreatic cancer cell migration and invasion [113]. This pathway is also important in 5FU-chemoresistance CRC [135].

Table 3. The interaction of UCA1 with transcription regulating complexes.

Interaction	Complex	Target	Cells	Ref.
Enhancer of zeste homolog 2 (EZH2)	polycomb repressive complex-2	p21, E-cadherin Cycline D1 p27Kip1	gallbladder cancer gastric cancer hepatocarcinoma	[45] [46] [47]
CCCTC-binding factor (CTCF)	chromatin looping with RNA polIII and P300	HULC	Embryonic hepatocyte-like	[78]
Brahma related gene 1 (BRG1)	SWI/SNF chromatin remodeling	p21	bladder cancer	[57]
SET domain containing 1A (SET1A)	histone methyltransferase complex	TRF2	hepatocytes	[134]
MOB1, Lats1, and YAP	YAP-TEAD transcription complex	Hippo pathway	Pancreatic cancer	[113]

4.2. UCA1 and miRNA-Mediated Decay

With the exploring of the miRNA pathways, it has become clear that lncRNAs play an important role to fine-tune miRNA-mediated decay. In the last lustrum, over 40 articles have described the indirect regulation by UCA1 through sequestering of miRNAs and interfering with the degradation of downstream gene transcripts. At least 29 miRNAs were shown to interact with UCA1 (Table 4) and overall 32 different genes were reported with an altered expression mediated by the UCA1/miRNA interaction. In addition, our analysis of putative miRNA binding with miRCore [136], showed that another 9 miRNAs not previously described, may bind to the UCA1 transcript (highlighted in Table 4). These miRNAs also play a role in CRC (Table 4; references in “CRC” column). Focusing on CRC cells, the interaction of UCA1 with miR-143, first reported in bladder cancer cells [137], was confirmed and implicated UCA1 as an upstream effector of mTOR activation and as a regulator of K-Ras expression ([138], Figure 2). Furthermore, UCA1 could sponge endogenous miR-204-5p and inhibit the degradation of its targets CREB1, BCL-2 and RAB22A indicating UCA1 promotes proliferation, inhibits apoptosis and plays a role in the acquired chemoresistance of these CRC cells [116]. Overall, gene clustering analysis of the 29 UCA1-related miRNA targets with mirPath v.3 [139] showed a significant implication in cancer signaling pathways such as TGF β , mTOR and WNT signaling. We confirmed the UCA1/miRNA-regulated genes in these pathways with the miRNA network analysis tool ONCO.IO (Figure 2). These analyses indicate that UCA1 regulates genes that play a central role in CRC.

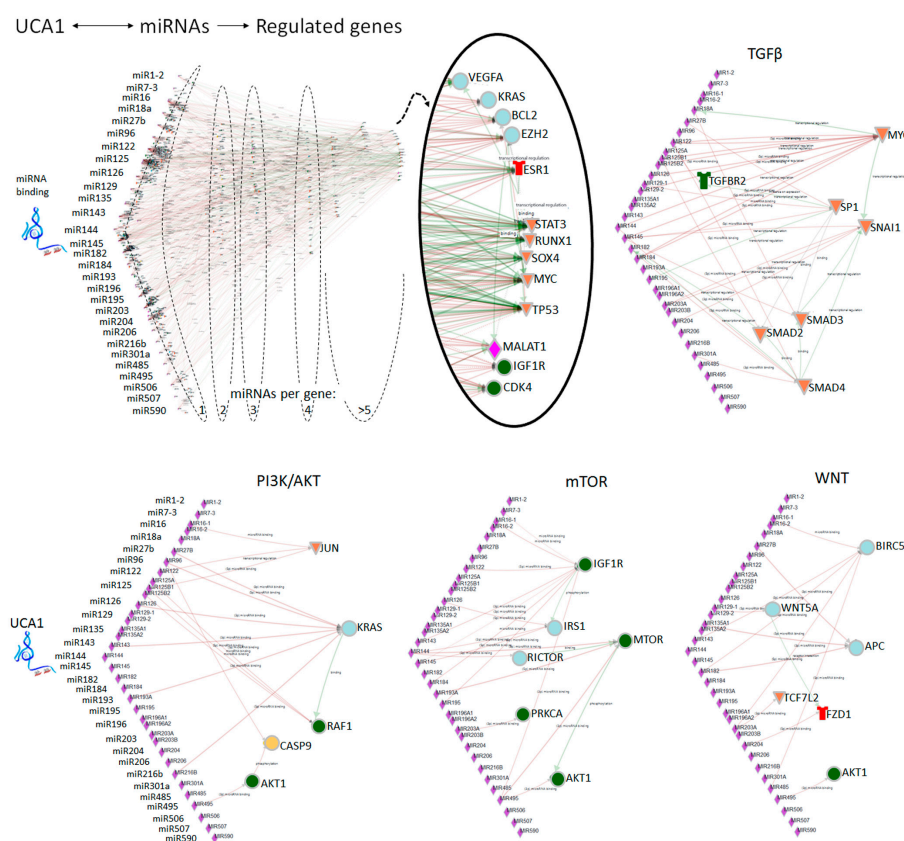


Figure 2. The regulation by Urothelial Cancer Associated 1 (UCA1)-associated miRNAs. All 29 miRNAs published to interact with UCA1 (Table 4) were submitted to the miRNA network analysis tool ONCO.IO and the downstream-regulated genes are visualized (<https://onco.io/main.php>). In the overall UCA1/miRNA image, genes were sorted based on the number of miRNAs bound per gene. The genes associated with over 5 miRNAs (circled) include VEGF, KRAS, BCL2, EZH2, receptor ESR1; transcription factors: STAT3, RUNX, SOX4, MYC, TP53; lncRNA MALAT1; and the kinases IGF1R and CDK4. Genes that were associated with the indicated signaling pathways are also represented in individual images.

Table 4. The UCA1-mediated regulation of miRNA targets.

UCA1-Mediated miR Regulation (Sponges/Competing Endogenous RNA)				miR-Mediated Regulation		
miRNA *	miR-Target	Type of Cells	Targets **	Biological Process ***	CRC	
miR-1	Hes1	neural stem cell	[140]	915	chromatin assembly, muscle contraction, nuclear transport	[141]
		bladder cancer cells	[132]			
	Slug	Breast cancer	[122]			
miR-7 miR-16	EGFR	gastric cancer	[142]	884 1646	transmembrane receptor protein tyrosine kinase signaling pathway protein folding, rRNA metabolic process, tRNA aminoacylation for protein translation, protein acetylation, regulation of sequence-specific DNA binding transcription factor activity, nuclear transport, nucleobase-containing compound transport, tRNA metabolic process, RNA localization, protein targeting, cellular component biogenesis	[143–151] [153]
	MDR1	chronic myeloid leukemia	[152]			
	GLS2	bladder cancer	[154]			
miR-18a	YAP	breast cancer	[155]	N.A.	N.A.	[156]
	HIF1 α	breast cancer	[157]			
miR-27b		gastric cancer	[158]	447	regulation of cell cycle, intracellular protein transport	[159]
miR-96	FOXO3	pancreatic cancer	[160]	237	regulation of cell cycle, regulation of phosphate metabolic process, regulation of catalytic activity, MAPK cascade, regulation of nucleobase-containing compound metabolic process, the catabolic process	[161,162]
miR-122		glioma	[163]	580	N.S.	[164]
		breast cancer	[131]			
miR-125	HK2	acute myeloid leukemia	[165]	899	negative regulation of apoptotic process, nuclear transport, glycolysis	[166]
miR-126	RAC1	human myelogenous leukemia	[167]	152	N.S.	-
miR-129	SOX4	renal cell carcinoma	[168]	499	N.S.	[169–174]
	ABCB1	ovarian cancer	[175]			
miR-135a	cMYC	pancreatic cancer thyroid cancer	[112] [177]	121	N.S.	[176]
miR-143	mTOR (cyclin D1, p27)	colorectal cancer	[138]	478	N.S.	[138,178]
	ERBB3 BCL-2	breast cancer	[179]			
	FOXO1	cardiomyocyte	[180]			
	HMGB1	bladder cancer	[181]			
	HK2	bladder cancer	[137]			
miR-144	PBX3	lung cancer	[182]	214	N.S.	[183]
miR-145	FSCN1 ZEB1/2	bladder cancer	[184]	263	cell proliferation, cytokinesis, negative regulation of apoptotic process, anatomical structure morphogenesis, regulation of cell cycle, MAPK cascade	[185–188]
miR-182	p53 (iASPP)	Glioma	[189]	189	N.S.	[190]
	PFKFB2	glioblastoma-associated stromal cells	[191]			
	TIMP2	gastric carcinoma	[192]			

Table 4. Cont.

UCA1-Mediated miR Regulation (Sponges/Competing Endogenous RNA)				miR-Mediated Regulation		
miRNA *	miR-Target	Type of Cells	Targets **	Biological Process ***	CRC	
miR-184	SF1	oral squamous cell carcinoma	[193]	29	N.S.	[194]
	BCL-2	prostate cancer	[195]			
miR-193a	HMGB1	lung cancer	[196]	144	N.S.	[197–201]
	ERBB4	non-small cell lung cancer	[202]			
miR-195	ARL2	bladder Cancer	[203]	692	angiogenesis, cell proliferation, cytokinesis, anatomical structure morphogenesis, mitosis, regulation of transcription from RNA polymerase II promoter	[204–210]
miR-196a	CREB	bladder cancer	[211]	450	RNA splicing, via transesterification reactions, response to stress, organelle organization	[212–215]
miR-203	Snail2	hepatocellular carcinoma	[216]	528	N.S.	[217–222]
	Slug	Breast cancer	[122]			
miR-204	CREB1, BCL2, RAB22A	colorectal cancer chondrocytes prostate cancer esophageal cancer thyroid cancer	[116]	488	N.S.	[116,223–226]
	MMP-13		[227]			
	Sirt1		[228]			
	Sox4		[229]			
	BRD4		[230]			
miR-206	VEGF	cervical cancer	[231]	95	pentose-phosphate shunt, chromatin assembly, chromatin remodeling, negative regulation of apoptotic process, chromatin organization, regulation of phosphate, metabolic process	-
miR-216b	FGFR1	hepatocellular carcinoma	[232]	235	protein targeting	[233–236]
miR-301a	CXCR4	osteosarcoma	[237]	430	N.S.	[238–240]
miR-485	MMP14	epithelial ovarian	[241]	505	N.S.	-
miR-495	p21	renal cell carcinoma	[242]	241	N.S.	[243–245]
miR-506	COTL1	non-small cell lung cancer	[246]	180	N.S.	[247–253]
miR-507	FOXM1	melanoma	[254]	169	N.S.	-
miR-590	CREB	gastric cancer	[255]	419	N.S.	[256–259]
miR-22	-	-	-	221	negative regulation of apoptotic process, regulation of transcription from RNA polymerase II promoter	[260–271]
miR-23a	-	-	-	353	N.S.	[272–278]
miR-26a	-	-	-	531	Mitosis, regulation of cell cycle, phosphate-containing compound, metabolic process	[279–287]

Table 4. Cont.

UCA1-Mediated miR Regulation (Sponges/Competing Endogenous RNA)				miR-Mediated Regulation		
miRNA *	miR-Target	Type of Cells	Targets **	Biological Process ***	CRC	
miR-103a/107/107ab	-	-	-	857	cytoskeleton organization, cell cycle	[288–291]
miR-124	-	-	-	1520	regulation of binding, cytokinesis, transmembrane receptor, protein tyrosine kinase signaling pathway, regulation of cell cycle	[247,286,292–308]
miR-138	-	-	-	239	N.S.	[309–314]
miR-190	-	-	-	770	RNA splicing, via transesterification reactions	-
miR-214	-	-	-	352	N.S.	[315–319]
miR-455	-	-	-	557	N.S.	[320–324]

* **in bold** = miRNA target site predicted at UCA1 gene by miRcode [136]; ** = number of miRNA-validated targets (identified in ChEMIRs/mirTAR database for 3p and 5p mature miRNA [325]) *** = Panther Go-Slim biological processes that present a ≥ 2 -fold enrichment for miRNA-validated targets (PANTHER [326]; Overrepresentation Test (version 20171205/version 13.1)). N.A. = miRNA data not available in ChEMIRs database. N.S. = No statistically significant results (FDR > 0.05). "CRC"-column: references of reports implicating miRNAs in CRC.

5. Role of UCA1-Mediated Regulation in Colorectal Cancer

Reciprocal to the regulation of UCA1 transcript expression by oncogenic pathways, UCA1 may regulate oncogenic pathways. UCA1 expression has been shown to stimulate factors of the WNT signaling pathway in diverse cancer cell types [78,327–330]. In CRC, WNT signaling is correlated to 5-FU chemoresistance [331] and UCA1 is induced by 5-FU treatment [332], but no direct correlation is described for UCA1 and WNT signaling in these cells. This also holds true for UCA1 regulating mediators of AKT signaling and its downstream targets in diverse cancer cells [46,108,120,333,334]. In CRC cells UCA1 was implicated in the induction of KRAS expression through the regulation of miR143 [138]. Although no direct evidence of UCA1 regulation for the TGF β pathway in colorectal cells was shown, UCA1 acts as a competitor RNA for several miRNAs that affect this pathway. Recently Li et al. showed that the interaction of UCA1 with miR-1 and miR203a stabilized the expression of SNAI2, mediating the effects of TGF β signaling in breast cancer cells [122]. In addition, UCA1 was shown to stimulate the ERK-MMP9 signaling in gastric cancer cells by interacting with G protein-coupled receptor kinase 2 (GRK2), stimulating its ubiquitination and degradation [335].

5.1. UCA1-Mediated Regulation of the Cell Cycle

UCA1 stimulates cell proliferation, and silencing its expression in cancer cells has been shown to arrest the cell cycle in the G0/G1 phase (in CRC [114,115] and other cancer cells [46,47,254,336–338]). Several key players in cell cycle progression are regulated by UCA1 (Figure 3A). Cell cycle progression from the G1 to S phase relies on the activation of E2F transcriptional regulation. Activation is mediated by dissociation of E2F from the Rb-complex after the phosphorylation of Rb by CDK-cyclin. From this phosphorylation complex, UCA1 increases cyclin D1 expression [46,337] and maintains CDK phosphorylation activity through the repression of its inhibitors p21CIP and p27Kip [45,47,57,133,138,211]. Moreover, during the G1-phase, the cyclin D1 expression and its binding to the CDK inhibitors increased, resulting in less binding of these inhibitors to cyclin E/Cdk2 complexes and acceleration of the cell cycle progression. This mechanism is further stimulated by the fact that UCA1 can upregulate cMYC, either by binding to cyclin D1 [339] or by sequestering miR-135 [177], respectively, in the liver and in thyroid cancer cells. This evidence was obtained in different types of cancer cells, but overall these studies show that UCA1 interferes at different levels with cell cycle regulation.

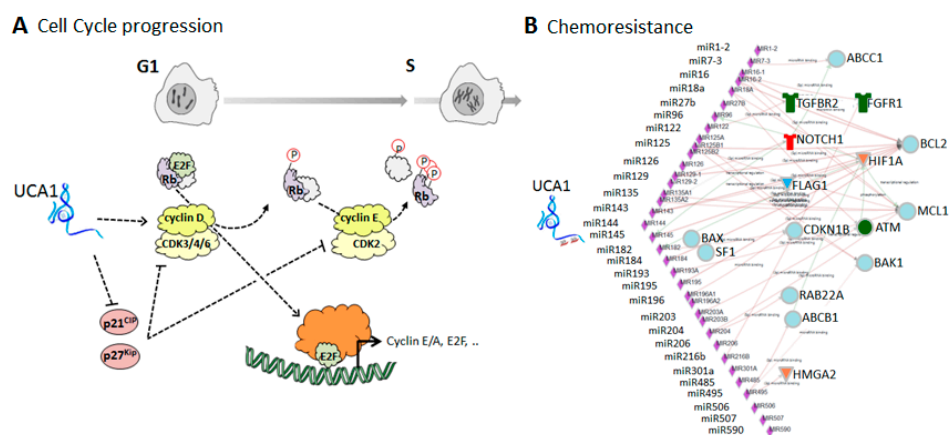


Figure 3. The UCA1-mediated regulation in colorectal cancer cells. (A) Schematically representation of UCA1 regulating key actors for cell cycle progression during G1 and S-phase in diverse cancer cell types. (B) All 29 miRNAs published to interact with UCA1 in diverse cancer cell types (Table 4) were submitted to the miRNA network analysis tool ONCO.IO and their interaction with chemoresistance-related genes were visualized (Receptors: TGFBR2, NOTCH1, FGFR1; Transcriptional regulating factors: HMGA2 and HIF1A; cell cycle kinase ATM, CDKN1 (p27); FLAG1, RAB22A, BAK1, BAX, ABCB1 (MDR1), ABCC1 (MRP1), MCL1, and BCL2).

5.2. Association of UCA1 with Chemoresistance

The high expression of UCA1 is correlated with a bad cancer prognosis, which is probably related to the induction of chemotherapy drug resistance. In fact, UCA1 levels are further increased upon the development of chemoresistance to cisplatin in oral squamous cell carcinoma, bladder cancer and gastric cancer cells [158,193,211,327], to tamoxifen in breast cancer cells [157], to paclitaxel in ovarian cancer cells [175], to doxorubicin in gastric cancer cells [158], and to 5-fluorouracil in gastric cancer and CRC cells [116,158]. The effects UCA1 has on cell cycle progression and on cell proliferation is probably an important aspect of chemoresistance in these cancers. Furthermore, UCA1 affects chemoresistance by sequestering miRNAs implicated in oncogenic pathways (miR-18a, [157]; miR-27b [158]; miR-129, [175]; miR-184, [193]; miR-196a-5p [211]). In particular, in CRC cells, UCA1/miR-204-5p interaction affects the chemoresistance-related genes CREB, Bcl2, and Rab22a [116]. Chemoresistance is also modulated via miR-204 by regulation of HMGA2 in CRC cells [224] and by TGF β -R2 in gastric cancer cells [340]. In addition, other UCA1-binding miRNAs affect these chemoresistance-related genes (Figure 3B). Although for several UCA1-binding miRNAs no direct relation between chemoresistance and UCA1 interference was studied, these miRNAs were shown to be associated to chemoresistance in CRC (miR-96 [341]; miR-129 [173]; miR-135a [342]; miR-182 [343]; miR-143, miR-145 [344]; miR-195-5p [345,346]; miR-203 [347–349]; miR-204-5p [116]; miR-206 [350]; miR-506 [252]). In addition, miR-27b, miR145, miR216, and miR125a-5p are related to FOLFOX resistance in CRC [351].

5.3. UCA1 in Colorectal Cancer Diagnosis and Therapy

Initially, UCA1 was proposed as a predictive biomarker for the prognosis and survival of CRC patients [114–117]. Since UCA1 expression in CRC may depend on primary tumor localization and molecular subtypes, its prognostic value may be restrictive to different CRC subclasses. Interestingly, a recent evaluation of tumor-derived exosomes in cancer diagnosis showed that UCA1 is not only expressed in gallbladder cancer exosomes [125], but also in exosomes isolated from the serum of CRC patients [352]. Whether the implication of UCA1 in several oncogenic pathways makes it a good target for therapy remains to be investigated. Inactivating an lncRNA, like UCA1 in CRC, may have the advantage of both inhibiting epigenetic silencing through chromatin remodeling for several tumor suppressor genes and stimulating the miRNA-mediated mRNA degradation of oncogenes due to a decreased ceRNA level. In that aspect, a recent innovation was the use of an artificial lncRNA targeting multiple miRNAs in hepatocellular carcinoma cells [353].

6. Conclusions

The lncRNA UCA1 has, like other lncRNAs, diverse functions and can affect both epigenetic and transcriptional gene regulation, as well as posttranscriptional regulation by acting as a ceRNA for diverse miRNAs. UCA1 has been studied in a wide range of cancer cells, including colorectal cancer. Extrapolating the role of UCA1 in different cancer cells to CRC cells suggests a role for UCA1 in cell cycle progression and cell proliferation, which is highly relevant to tumor growth. In addition, UCA1 plays a role in CRC chemoresistance, although the implicated mechanisms remain to be studied. It will also be worthwhile to identify more UCA1/EZH2-silenced target genes, to assess whether UCA1 is a driver of carcinogenesis by silencing key tumor repressor genes. UCA1 is probably not a strong general prognostic marker for CRC as its overexpression is dependent on the primary tumor site (colon vs. rectal) and molecular characteristics, such as the microsatellite stability profile. Nevertheless, studying the UCA1-regulated genes and miRNA decoy function in CRC cells may reveal novel pathways and potential new therapeutic targets for managing CRC.

Author Contributions: B.N.: data acquisition, analysis and interpretation, manuscript preparation and obtaining funding. N.J.: data acquisition, editing and critical reading of the manuscript. A.V.: editing and critical reading of the manuscript. I.V.S.: critical reading of the manuscript and obtaining funding. All authors approved the final version of the manuscript.

Funding: This research was funded by “Institut National de la Santé et de la Recherche Médicale” (Inserm), “Centre National de la Recherche Scientifique” (CNRS) and “la Ligue Nationale contre le Cancer” (Committees 59 (R17037EE - RAB17005EEA), 62 and 80).

Conflicts of Interest: The authors declare no conflict of interest.

References

1. American Cancer Society. Cancer Facts and Figures. 2018. Available online: <https://www.cancer.org> (accessed on 1 June 2018).
2. Malvezzi, M.; Carioli, G.; Bertuccio, P.; Boffetta, P.; Levi, F.; La Vecchia, C.; Negri, E. European cancer mortality predictions for the year 2018 with focus on colorectal cancer. *Ann. Oncol.* **2018**, *29*, 1016–1022. [[CrossRef](#)] [[PubMed](#)]
3. WCRF/AICR. Continuous Update Project Report: Food, Nutrition, Physical Activity, and the Prevention of Colorectal Cancer. 2011. Available online: <https://www.wcrf.org/sites/default/files/Colorectal-Cancer-2011-Report.pdf> (accessed on 1 June 2018).
4. Rank, K.M.; Shaikat, A. Stool Based Testing for Colorectal Cancer: An Overview of Available Evidence. *Curr. Gastroenterol. Rep.* **2017**, *19*. [[CrossRef](#)] [[PubMed](#)]
5. Rahbari, N.N.; Carr, P.R.; Jansen, L.; Chang-Claude, J.; Weitz, J.; Hoffmeister, M.; Brenner, H. Time of Metastasis and Outcome in Colorectal Cancer. *Ann. Surg.* **2017**, *1*. [[CrossRef](#)] [[PubMed](#)]
6. Akinyemiju, T.; Sakhuja, S.; Waterbor, J.; Pisu, M.; Altekruse, S.F. Racial/ethnic disparities in de novo metastases sites and survival outcomes for patients with primary breast, colorectal, and prostate cancer. *Cancer Med.* **2018**, *7*, 1183–1193. [[CrossRef](#)] [[PubMed](#)]
7. Luo, Q.; O’Connell, D.L.; Kahn, C.; Yu, X.Q. Colorectal cancer metastatic disease progression in Australia: A population-based analysis. *Cancer Epidemiol.* **2017**, *49*, 92–100. [[CrossRef](#)] [[PubMed](#)]
8. Benson, A.R.; Venook, A.; Cederquist, L.; Chan, E.; Chen, Y.; Cooper, H.; Deming, D.; Engstrom, P.; Enzinger, P.; Fichera, A.; et al. Clinical Practice Guidelines in Oncology. *Natl. Compr. Cancer Netw.* **2017**, *3*, 370–398. [[CrossRef](#)]
9. Puccini, A.; Berger, M.D.; Naseem, M.; Tokunaga, R.; Battaglin, F.; Cao, S.; Hanna, D.L.; McSkane, M.; Soni, S.; Zhang, W.; et al. Colorectal cancer: Epigenetic alterations and their clinical implications. *Biochim. Biophys. Acta Rev. Cancer* **2017**, *1868*, 439–448. [[CrossRef](#)] [[PubMed](#)]
10. Gupta, R.; Sinha, S.; Paul, R.N. The impact of microsatellite stability status in colorectal cancer. *Curr. Probl. Cancer* **2018**. [[CrossRef](#)] [[PubMed](#)]
11. Sadanandam, A.; Lyssiotis, C.A.; Homicsko, K.; Collisson, E.A.; Gibb, W.J.; Wullschlegel, S.; Ostos, L.C.G.; Lannon, W.A.; Grotzinger, C.; Del Rio, M.; et al. A colorectal cancer classification system that associates cellular phenotype and responses to therapy. *Nat. Med.* **2013**, *19*, 619–625. [[CrossRef](#)] [[PubMed](#)]
12. Guinney, J.; Dienstmann, R.; Wang, X.; de Reyniès, A.; Schlicker, A.; Sonesson, C.; Marisa, L.; Roepman, P.; Nyamundanda, G.; Angelino, P.; et al. The consensus molecular subtypes of colorectal cancer. *Nat. Med.* **2015**, *21*, 1350–1356. [[CrossRef](#)] [[PubMed](#)]
13. Merkel, S.; Schellerer, V.S.; Wein, A.; Semrau, S.; Geppert, C.; Göhl, J.; Hohenberger, W.; Weber, K.; Grützmann, R. The influence of tumour site on prognosis in metastatic colorectal carcinomas with primary tumour resection. *Int. J. Color. Dis.* **2018**, *33*, 1215–1223. [[CrossRef](#)] [[PubMed](#)]
14. Cremolini, C.; Antoniotti, C.; Lonardi, S.; Bergamo, F.; Cortesi, E.; Tomasello, G.; Moretto, R.; Ronzoni, M.; Racca, P.; Loupakis, F.; et al. Primary Tumor Sidedness and Benefit from FOLFOXIRI plus Bevacizumab as Initial Therapy for Metastatic Colorectal Cancer. *Ann. Oncol.* **2018**. [[CrossRef](#)] [[PubMed](#)]
15. Narayanan, S.; Gabriel, E.; Attwood, K.; Boland, P.; Nurkin, S. Association of Clinicopathologic and Molecular Markers on Stage-specific Survival of Right Versus Left Colon Cancer. *Clin. Color. Cancer* **2018**, *5*. [[CrossRef](#)] [[PubMed](#)]
16. Siegel, R.L.; Miller, K.D.; Jemal, A. Cancer statistics, 2018. *CA Cancer J. Clin.* **2018**, *68*, 7–30. [[CrossRef](#)] [[PubMed](#)]
17. Zhang, Y.; Tao, Y.; Li, Y.; Zhao, J.; Zhang, L.; Zhang, X.; Dong, C.; Xie, Y.; Dai, X.; Zhang, X.; et al. The regulatory network analysis of long noncoding RNAs in human colorectal cancer. *Funct. Integr. Genom.* **2018**, *18*, 261–275. [[CrossRef](#)] [[PubMed](#)]

18. Chen, D.; Sun, Q.; Cheng, X.; Zhang, L.; Song, W.; Zhou, D.; Lin, J.; Wang, W. Genome-wide analysis of long noncoding RNA (lncRNA) expression in colorectal cancer tissues from patients with liver metastasis. *Cancer Med.* **2016**, *5*, 1629–1639. [[CrossRef](#)] [[PubMed](#)]
19. De Bony, E.J.; Bizet, M.; Van Grembergen, O.; Hassabi, B.; Calonne, E.; Putmans, P.; Bontempi, G.; Fuks, F. Comprehensive identification of long noncoding RNAs in colorectal cancer. *Oncotarget* **2018**, *9*, 27605–27629. [[CrossRef](#)] [[PubMed](#)]
20. Li, Q.; Li, N.; Lao, Y.; Lin, W.; Jiang, G.; Wei, N.; Wang, C.; Liu, K.; Wu, J. Variable Levels of Long Noncoding RNA Expression in DNA Mismatch Repair-Proficient Early-Stage Colon Cancer. *Dig. Dis. Sci.* **2017**, *62*, 1235–1245. [[CrossRef](#)] [[PubMed](#)]
21. Kawaguchi, T.; Hirose, T. Chromatin remodeling complexes in the assembly of long noncoding RNA-dependent nuclear bodies. *Nucleus* **2015**, *6*, 462–467. [[CrossRef](#)] [[PubMed](#)]
22. Sawyer, I.A.; Dundr, M. Chromatin loops and causality loops: The influence of RNA upon spatial nuclear architecture. *Chromosoma* **2017**, *126*, 541–557. [[CrossRef](#)] [[PubMed](#)]
23. Clemson, C.M.; Hutchinson, J.N.; Sara, S.A.; Ensminger, A.W.; Fox, A.H.; Chess, A.; Lawrence, J.B. An architectural role for a nuclear noncoding RNA: NEAT1 RNA is essential for the structure of paraspeckles. *Mol. Cell.* **2009**, *33*, 717–726. [[CrossRef](#)] [[PubMed](#)]
24. Naganuma, T.; Hirose, T. Paraspeckle formation during the biogenesis of long non-coding RNAs. *RNA Biol.* **2013**, *10*, 456–461. [[CrossRef](#)] [[PubMed](#)]
25. Li, Y.; Chen, W.; He, F.; Tan, Z.; Zheng, J.; Wang, W.; Zhao, Q.; Li, J. NEAT expression is associated with tumor recurrence and unfavorable prognosis in colorectal cancer. *Oncotarget* **2015**, *6*, 27641–27650. [[CrossRef](#)] [[PubMed](#)]
26. Quinn, J.J.; Chang, H.Y. Unique features of long non-coding RNA biogenesis and function. *Nat. Rev. Genet.* **2016**, *17*, 47–62. [[CrossRef](#)] [[PubMed](#)]
27. Li, Y.; Bao, C.; Gu, S.; Ye, D.; Jing, F.; Fan, C.; Jin, M.; Chen, K. Associations between novel genetic variants in the promoter region of MALAT1 and risk of colorectal cancer. *Oncotarget* **2017**, *8*, 92604–92614. [[CrossRef](#)] [[PubMed](#)]
28. Khalil, A.M.; Guttman, M.; Huarte, M.; Garber, M.; Raj, A.; Rivea Morales, D.; Thomas, K.; Presser, A.; Bernstein, B.E.; van Oudenaarden, A.; et al. Many human large intergenic noncoding RNAs associate with chromatin-modifying complexes and affect gene expression. *Proc. Natl. Acad. Sci. USA* **2009**, *106*, 11667–11672. [[CrossRef](#)] [[PubMed](#)]
29. Davidovich, C.; Cech, T.R. The recruitment of chromatin modifiers by long noncoding RNAs: Lessons from PRC2. *RNA* **2015**, *21*, 2007–2022. [[CrossRef](#)] [[PubMed](#)]
30. Lian, Y.; Yan, C.; Xu, H.; Yang, J.; Yu, Y.; Jing, Z.; Shi, Y.; Ren, J.; Ji, G.; Wang, K. A novel lncRNA, LINC00460 affects cell proliferation and apoptosis by regulating KLF2 and CUL4A expression in colorectal cancer. *Mol. Ther. Nucleic Acids* **2018**. [[CrossRef](#)] [[PubMed](#)]
31. Ma, Z.; Peng, P.; Zhou, J.; Hui, B.; Ji, H.; Wang, J.; Wang, K. Long Non-Coding RNA SH3PXD2A-AS1 Promotes Cell Progression Partly Through Epigenetic Silencing P57 and KLF2 in Colorectal Cancer. *Cell Physiol. Biochem.* **2018**, *46*, 2197–2214. [[CrossRef](#)] [[PubMed](#)]
32. Ding, J.; Xie, M.; Lian, Y.; Zhu, Y.; Peng, P.; Wang, J.; Wang, L.; Wang, K. Long noncoding RNA HOXA-AS2 represses P21 and KLF2 expression transcription by binding with EZH2, LSD1 in colorectal cancer. *Oncogenesis* **2017**, *6*, e288. [[CrossRef](#)] [[PubMed](#)]
33. Li, Y.; Cheng, C. Long noncoding RNA NEAT1 promotes the metastasis of osteosarcoma via interaction with the G9a-DNMT1-Snail complex. *Am. J. Cancer Res.* **2018**, *8*, 81–90. [[PubMed](#)]
34. Tang, Y.; Wang, J.; Lian, Y.; Fan, C.; Zhang, P.; Wu, Y.; Li, X.; Xiong, F.; Li, X.; Li, G.; et al. Linking long non-coding RNAs and SWI/SNF complexes to chromatin remodeling in cancer. *Mol. Cancer* **2017**, *16*. [[CrossRef](#)] [[PubMed](#)]
35. Prensner, J.R.; Iyer, M.K.; Sahu, A.; Asangani, I.A.; Cao, Q.; Patel, L.; Vergara, I.A.; Davicioni, E.; Erho, N.; Ghadessi, M.; et al. The long noncoding RNA SchLAP1 promotes aggressive prostate cancer and antagonizes the SWI/SNF complex. *Nat. Genet.* **2013**, *45*, 1392–1398. [[CrossRef](#)] [[PubMed](#)]
36. Cheng, S.; Wang, L.; Deng, C.H.; Du, S.C.; Han, Z.G. ARID1A represses hepatocellular carcinoma cell proliferation and migration through lncRNA MVIH. *Biochem. Biophys. Res. Commun.* **2017**, *491*, 178–182. [[CrossRef](#)] [[PubMed](#)]

37. Tang, J.; Zhong, G.; Wu, J.; Chen, H.; Jia, Y. Long noncoding RNA AFAP1-AS1 facilitates tumor growth through enhancer of zeste homolog 2 in colorectal cancer. *Am. J. Cancer Res.* **2018**, *8*, 892–902. [[PubMed](#)]
38. Yang, Z.Y.; Yang, F.; Zhang, Y.L.; Liu, B.; Wang, M.; Hong, X.; Yu, Y.; Zhou, Y.H.; Zeng, H. LncRNA-ANCR down-regulation suppresses invasion and migration of colorectal cancer cells by regulating EZH2 expression. *Cancer Biomarkers* **2017**, *18*, 95–104. [[CrossRef](#)] [[PubMed](#)]
39. Su, J.; Zhang, E.; Han, L.; Yin, D.; Liu, Z.; He, X.; Zhang, Y.; Lin, F.; Lin, Q.; Mao, P.; et al. Long noncoding RNA BLACAT1 indicates a poor prognosis of colorectal cancer and affects cell proliferation by epigenetically silencing of p15. *Cell Death Dis.* **2017**, *8*, e2665. [[CrossRef](#)] [[PubMed](#)]
40. Ding, J.; Li, J.; Wang, H.; Tian, Y.; Xie, M.; He, X.; Ji, H.; Ma, Z.; Hui, B.; Wang, K.; et al. Long noncoding RNA CRNDE promotes colorectal cancer cell proliferation via epigenetically silencing DUSP5/CDKN1A expression. *Cell Death Dis.* **2017**, *8*, e2997. [[CrossRef](#)] [[PubMed](#)]
41. Kogo, R.; Shimamura, T.; Mimori, K.; Kawahara, K.; Imoto, S.; Sudo, T.; Tanaka, F.; Shibata, K.; Suzuki, A.; Komune, S.; et al. Long noncoding RNA HOTAIR regulates polycomb-dependent chromatin modification and is associated with poor prognosis in colorectal cancers. *Cancer Res.* **2011**, *71*, 6320–6326. [[CrossRef](#)] [[PubMed](#)]
42. Yang, X.J.; Huang, C.Q.; Peng, C.W.; Hou, J.X.; Liu, J.Y. Long noncoding RNA HULC promotes colorectal carcinoma progression through epigenetically repressing NKD2 expression. *Gene* **2016**, *592*, 172–178. [[CrossRef](#)] [[PubMed](#)]
43. Marin-Bejar, O.; Marchese, F.P.; Athie, A.; Sanchez, Y.; Gonzalez, J.; Segura, V.; Huang, L.; Moreno, I.; Navarro, A.; Monzo, M.; et al. Pint lincRNA connects the p53 pathway with epigenetic silencing by the Polycomb repressive complex 2. *Genome Biol.* **2013**, *14*, R104. [[CrossRef](#)] [[PubMed](#)]
44. Ma, Z.; Gu, S.; Song, M.; Yan, C.; Hui, B.; Ji, H.; Wang, J.; Zhang, J.; Wang, K.; Zhao, Q. Long non-coding RNA SNHG17 is an unfavourable prognostic factor and promotes cell proliferation by epigenetically silencing P57 in colorectal cancer. *Mol. Biosyst.* **2017**, *13*, 2350–2361. [[CrossRef](#)] [[PubMed](#)]
45. Cai, Q.; Jin, L.; Wang, S.; Zhou, D.; Wang, J.; Tang, Z.; Quan, Z. Long non-coding RNA UCA1 promotes gallbladder cancer progression by epigenetically repressing p21 and E-cadherin expression. *Oncotarget* **2017**, *8*, 47957–47968. [[CrossRef](#)] [[PubMed](#)]
46. Wang, Z.-Q.; Cai, Q.; Hu, L.; He, C.-Y.; Li, J.-F.; Quan, Z.-W.; Liu, B.-Y.; Li, C.; Zhu, Z.-G. Long noncoding RNA UCA1 induced by SP1 promotes cell proliferation via recruiting EZH2 and activating AKT pathway in gastric cancer. *Cell Death Dis.* **2017**, *8*, e2839. [[CrossRef](#)] [[PubMed](#)]
47. Hu, J.-J.; Song, W.; Zhang, S.-D.; Shen, X.-H.; Qiu, X.-M.; Wu, H.-Z.; Gong, P.-H.; Lu, S.; Zhao, Z.-J.; He, M.-L.; et al. HBx-upregulated lncRNA UCA1 promotes cell growth and tumorigenesis by recruiting EZH2 and repressing p27Kip1/CDK2 signaling. *Sci. Rep.* **2016**, *6*, 23521. [[CrossRef](#)] [[PubMed](#)]
48. Wang, K.C.; Yang, Y.W.; Liu, B.; Sanyal, A.; Corces-Zimmerman, R.; Chen, Y.; Lajoie, B.R.; Protacio, A.; Flynn, R.A.; Gupta, R.A.; et al. A long noncoding RNA maintains active chromatin to coordinate homeotic gene expression. *Nature* **2011**, *472*, 120–124. [[CrossRef](#)] [[PubMed](#)]
49. Wu, Q.; Xiang, S.; Ma, J.; Hui, P.; Wang, T.; Meng, W.; Shi, M.; Wang, Y. Long non-coding RNA CASC15 regulates gastric cancer cell proliferation, migration and epithelial mesenchymal transition by targeting CDKN1A and ZEB1. *Mol. Oncol.* **2018**, *12*, 799–813. [[CrossRef](#)] [[PubMed](#)]
50. Sun, T.T.; He, J.; Liang, Q.; Ren, L.L.; Yan, T.T.; Yu, T.C.; Tang, J.Y.; Bao, Y.J.; Hu, Y.; Lin, Y.; et al. LncRNA GCIncl1 Promotes Gastric Carcinogenesis and May Act as a Modular Scaffold of WDR5 and KAT2A Complexes to Specify the Histone Modification Pattern. *Cancer Discov.* **2016**, *6*, 784–801. [[CrossRef](#)] [[PubMed](#)]
51. Gu, P.; Chen, X.; Xie, R.; Han, J.; Xie, W.; Wang, B.; Dong, W.; Chen, C.; Yang, M.; Jiang, J.; et al. lncRNA HOXD-AS1 Regulates Proliferation and Chemo-Resistance of Castration-Resistant Prostate Cancer via Recruiting WDR5. *Mol. Ther.* **2017**. [[CrossRef](#)] [[PubMed](#)]
52. Xia, M.; Yao, L.; Zhang, Q.; Wang, F.; Mei, H.; Guo, X.; Huang, W. Long noncoding RNA HOTAIR promotes metastasis of renal cell carcinoma by up-regulating histone H3K27 demethylase JMJD3. *Oncotarget* **2017**, *8*, 19795–19802. [[CrossRef](#)] [[PubMed](#)]
53. Yang, L.; Ge, D.; Chen, X.; Qiu, J.; Yin, Z.; Zheng, S.; Jiang, C. FOXP4-AS1 participates in the development and progression of osteosarcoma by downregulating LATS1 via binding to LSD1 and EZH2. *Biochem. Biophys. Res. Commun.* **2018**, *502*, 493–500. [[CrossRef](#)] [[PubMed](#)]

54. Sun, M.; Nie, F.; Wang, Y.; Zhang, Z.; Hou, J.; He, D.; Xie, M.; Xu, L.; De, W.; Wang, Z.; et al. LncRNA HOXA11-AS Promotes Proliferation and Invasion of Gastric Cancer by Scaffolding the Chromatin Modification Factors PRC2, LSD1, and DNMT1. *Cancer Res.* **2016**, *76*, 6299–6310. [[CrossRef](#)] [[PubMed](#)]
55. Wang, Y.; He, L.; Du, Y.; Zhu, P.; Huang, G.; Luo, J.; Yan, X.; Ye, B.; Li, C.; Xia, P.; et al. The long noncoding RNA lncTCF7 promotes self-renewal of human liver cancer stem cells through activation of Wnt signaling. *Cell Stem Cell* **2015**, *16*, 413–425. [[CrossRef](#)] [[PubMed](#)]
56. Chen, Z.; Gao, Y.; Yao, L.; Liu, Y.; Huang, L.; Yan, Z.; Zhao, W.; Zhu, P.; Weng, H. LncFZD6 initiates Wnt/beta-catenin and liver TIC self-renewal through BRG1-mediated FZD6 transcriptional activation. *Oncogene* **2018**, *37*, 3098–3112. [[CrossRef](#)] [[PubMed](#)]
57. Wang, X.; Gong, Y.; Jin, B.O.; Wu, C.; Yang, J.; Wang, L.E.; Zhang, Z.; Mao, Z. Long non-coding RNA urothelial carcinoma associated 1 induces cell replication by inhibiting BRG1 in 5637 cells. *Oncol. Rep.* **2014**, *32*, 1281–1290. [[CrossRef](#)] [[PubMed](#)]
58. Tsang, W.P.; Ng, E.K.; Ng, S.S.; Jin, H.; Yu, J.; Sung, J.J.; Kwok, T.T. Oncofetal H19-derived miR-675 regulates tumor suppressor RB in human colorectal cancer. *Carcinogenesis* **2010**, *31*, 350–358. [[CrossRef](#)] [[PubMed](#)]
59. Matouk, I.J.; Raveh, E.; Abu-lail, R.; Mezan, S.; Gilon, M.; Gershtain, E.; Birman, T.; Gallula, J.; Schneider, T.; Barkali, M.; et al. Oncofetal H19 RNA promotes tumor metastasis. *Biochim. Biophys. Acta* **2014**, *7*, 1414–1426. [[CrossRef](#)] [[PubMed](#)]
60. Zhao, Q.; Li, T.; Qi, J.; Liu, J.; Qin, C. The miR-545/374a cluster encoded in the Ftx lncRNA is overexpressed in HBV-related hepatocellular carcinoma and promotes tumorigenesis and tumor progression. *PLoS ONE* **2014**, *9*, e109782. [[CrossRef](#)] [[PubMed](#)]
61. Iio, A.; Takagi, T.; Miki, K.; Naoe, T.; Nakayama, A.; Akao, Y. DDX6 post-transcriptionally down-regulates miR-143/145 expression through host gene NCR143/145 in cancer cells. *Biochim. Biophys. Acta* **2013**, *10*, 1102–1110. [[CrossRef](#)] [[PubMed](#)]
62. Augoff, K.; McCue, B.; Plow, E.F.; Sossey-Alaoui, K. miR-31 and its host gene lncRNA LOC554202 are regulated by promoter hypermethylation in triple-negative breast cancer. *Mol. Cancer* **2012**, *11*, 5. [[CrossRef](#)] [[PubMed](#)]
63. Emmrich, S.; Streltsov, A.; Schmidt, F.; Thangapandi, V.R.; Reinhardt, D.; Klusmann, J.H. LincRNAs MONC and MIR100HG act as oncogenes in acute megakaryoblastic leukemia. *Mol. Cancer* **2014**, *13*, 1476–4598. [[CrossRef](#)] [[PubMed](#)]
64. Sun, D.; Layer, R.; Mueller, A.C.; Cichewicz, M.A.; Negishi, M.; Paschal, B.M.; Dutta, A. Regulation of several androgen-induced genes through the repression of the miR-99a/let-7c/miR-125b-2 miRNA cluster in prostate cancer cells. *Oncogene* **2014**, *33*, 1448–1457. [[CrossRef](#)] [[PubMed](#)]
65. Kotake, Y.; Kitagawa, K.; Ohhata, T.; Sakai, S.; Uchida, C.; Niida, H.; Naemura, M.; Kitagawa, M. Long Non-coding RNA, PANDA, Contributes to the Stabilization of p53 Tumor Suppressor Protein. *Anticancer Res.* **2016**, *36*, 1605–1611. [[PubMed](#)]
66. Yan, C.; Chen, J.; Chen, N. Long noncoding RNA MALAT1 promotes hepatic steatosis and insulin resistance by increasing nuclear SREBP-1c protein stability. *Sci. Rep.* **2016**, *6*, 22640. [[CrossRef](#)] [[PubMed](#)]
67. Yoon, J.H.; You, B.H.; Park, C.H.; Kim, Y.J.; Nam, J.W.; Lee, S.K. The long noncoding RNA LUCAT1 promotes tumorigenesis by controlling ubiquitination and stability of DNA methyltransferase 1 in esophageal squamous cell carcinoma. *Cancer Lett.* **2018**, *417*, 47–57. [[CrossRef](#)] [[PubMed](#)]
68. Jiang, H.; Li, T.; Qu, Y.; Wang, X.; Li, B.; Song, J.; Sun, X.; Tang, Y.; Wan, J.; Yu, Y.; et al. Long non-coding RNA SNHG15 interacts with and stabilizes transcription factor Slug and promotes colon cancer progression. *Cancer Lett.* **2018**, *425*, 78–87. [[CrossRef](#)] [[PubMed](#)]
69. Nevers, A.; Doyen, A.; Malabat, C.; Neron, B.; Kergrohen, T.; Jacquier, A.; Badis, G. Antisense transcriptional interference mediates condition-specific gene repression in budding yeast. *Nucleic Acids Res.* **2018**. [[CrossRef](#)] [[PubMed](#)]
70. Muniz, L.; Deb, M.K.; Aguirrebengoa, M.; Lazorthes, S.; Trouche, D.; Nicolas, E. Control of Gene Expression in Senescence through Transcriptional Read-Through of Convergent Protein-Coding Genes. *Cell Rep.* **2017**, *21*, 2433–2446. [[CrossRef](#)] [[PubMed](#)]
71. Pelechano, V.; Steinmetz, L.M. Gene regulation by antisense transcription. *Nat. Rev. Genet.* **2013**, *14*, 880–893. [[CrossRef](#)] [[PubMed](#)]

72. Li, C.; Li, W.; Zhang, Y.; Zhang, X.; Liu, T.; Zhang, Y.; Yang, Y.; Wang, L.; Pan, H.; Ji, J.; et al. Increased expression of antisense lncRNA *SPINT1-AS1* predicts a poor prognosis in colorectal cancer and is negatively correlated with its sense transcript. *Oncotargets Ther.* **2018**, *11*, 3969–3978. [[CrossRef](#)] [[PubMed](#)]
73. Yin, J.; Luo, W.; Zeng, X.; Zeng, L.; Li, Z.; Deng, X.; Tan, X.; Hu, W. UXT-AS1-induced alternative splicing of UXT is associated with tumor progression in colorectal cancer. *Am. J. Cancer Res.* **2017**, *7*, 462–472. [[PubMed](#)]
74. Engreitz, J.M.; Haines, J.E.; Perez, E.M.; Munson, G.; Chen, J.; Kane, M.; McDonel, P.E.; Guttman, M.; Lander, E.S. Local regulation of gene expression by lncRNA promoters, transcription and splicing. *Nature* **2016**, *539*, 452–455. [[CrossRef](#)] [[PubMed](#)]
75. Jalali, S.; Singh, A.; Maiti, S.; Scaria, V. Genome-wide computational analysis of potential long noncoding RNA mediated DNA:DNA:RNA triplexes in the human genome. *J. Transl. Med.* **2017**, *15*, 186. [[CrossRef](#)] [[PubMed](#)]
76. Amaral, P.P.; Leonardi, T.; Han, N.; Viré, E.; Gascoigne, D.K.; Arias-Carrasco, R.; Büscher, M.; Pandolfini, L.; Zhang, A.; Pluchino, S.; et al. Genomic positional conservation identifies topological anchor point RNAs linked to developmental loci. *Genome Biol.* **2018**, *19*, 32. [[CrossRef](#)] [[PubMed](#)]
77. Xiang, J.-F.; Yin, Q.-F.; Chen, T.; Zhang, Y.; Zhang, X.-O.; Wu, Z.; Zhang, S.; Wang, H.-B.; Ge, J.; Lu, X.; et al. Human colorectal cancer-specific CCAT1-L lncRNA regulates long-range chromatin interactions at the MYC locus. *Cell Res.* **2014**, *24*, 513–531. [[CrossRef](#)] [[PubMed](#)]
78. Gui, X.; Li, H.; Li, T.; Pu, H.; Lu, D. Long Noncoding RNA CUDR Regulates HULC and β -Catenin to Govern Human Liver Stem Cell Malignant Differentiation. *Mol. Ther.* **2015**, *23*, 1843–1853. [[CrossRef](#)] [[PubMed](#)]
79. Mondal, T.; Subhash, S.; Vaid, R.; Enroth, S.; Uday, S.; Reinius, B.; Mitra, S.; Mohammed, A.; James, A.R.; Hoberg, E.; et al. MEG3 long noncoding RNA regulates the TGF- β pathway genes through formation of RNA–DNA triplex structures. *Nat. Commun.* **2015**, *6*, 7743. [[CrossRef](#)] [[PubMed](#)]
80. Zhao, Y.; Liu, Y.; Lin, L.; Huang, Q.; He, W.; Zhang, S.; Dong, S.; Wen, Z.; Rao, J.; Liao, W.; et al. The lncRNA MACC1-AS1 promotes gastric cancer cell metabolic plasticity via AMPK/Lin28 mediated mRNA stability of MACC1. *Mol. Cancer* **2018**, *17*, 69. [[CrossRef](#)] [[PubMed](#)]
81. Pan, Y.; Cheng, Y.; Yang, F.; Yao, Z.; Wang, O. Knockdown of lncRNA MAPT-AS1 inhibites proliferation and migration and sensitizes cancer cells to paclitaxel by regulating MAPT expression in ER-negative breast cancers. *Cell Biosci.* **2018**, *8*, 7. [[CrossRef](#)] [[PubMed](#)]
82. Beltran, M.; Puig, I.; Pena, C.; Garcia, J.M.; Alvarez, A.B.; Pena, R.; Bonilla, F.; de Herreros, A.G. A natural antisense transcript regulates Zeb2/Sip1 gene expression during Snail1-induced epithelial-mesenchymal transition. *Genes Dev.* **2008**, *22*, 756–769. [[CrossRef](#)] [[PubMed](#)]
83. Zhuang, J.; Lu, Q.; Shen, B.; Huang, X.; Shen, L.; Zheng, X.; Huang, R.; Yan, J.; Guo, H. TGFbeta1 secreted by cancer-associated fibroblasts induces epithelial-mesenchymal transition of bladder cancer cells through lncRNA-ZEB2NAT. *Sci. Rep.* **2015**, *5*, 11924. [[CrossRef](#)] [[PubMed](#)]
84. Fabian, M.R.; Sonenberg, N. The mechanics of miRNA-mediated gene silencing: A look under the hood of miRISC. *Nat. Struct. Mol. Biol.* **2012**, *19*, 586–593. [[CrossRef](#)] [[PubMed](#)]
85. Tay, Y.; Rinn, J.; Pandolfi, P.P. The multilayered complexity of ceRNA crosstalk and competition. *Nature* **2014**, *505*, 344–352. [[CrossRef](#)] [[PubMed](#)]
86. Yamamura, S.; Imai-Sumida, M.; Tanaka, Y.; Dahiya, R. Interaction and cross-talk between non-coding RNAs. *Cell Mol. Life Sci.* **2017**, *75*, 467–484. [[CrossRef](#)] [[PubMed](#)]
87. Denzler, R.; McGeary, S.E.; Title, A.C.; Agarwal, V.; Bartel, D.P.; Stoffel, M. Impact of MicroRNA Levels, Target-Site Complementarity, and Cooperativity on Competing Endogenous RNA-Regulated Gene Expression. *Mol. Cell* **2016**, *64*, 565–579. [[CrossRef](#)] [[PubMed](#)]
88. Li, J.-H.; Liu, S.; Zhou, H.; Qu, L.-H.; Yang, J.-H. starBase v2.0: Decoding miRNA-ceRNA, miRNA-ncRNA and protein–RNA interaction networks from large-scale CLIP-Seq data. *Nucleic Acids Res.* **2014**, *42*, D92–D97. [[CrossRef](#)] [[PubMed](#)]
89. Fan, Q.; Liu, B. Comprehensive analysis of a long noncoding RNA-associated competing endogenous RNA network in colorectal cancer. *Oncotargets Ther.* **2018**, *11*, 2453–2466. [[CrossRef](#)] [[PubMed](#)]
90. Schein, A.; Zucchelli, S.; Kauppinen, S.; Gustincich, S.; Carninci, P. Identification of antisense long noncoding RNAs that function as SINEUPs in human cells. *Sci. Rep.* **2016**, *6*. [[CrossRef](#)] [[PubMed](#)]
91. Hu, G.; Lou, Z.; Gupta, M. The Long Non-Coding RNA GAS5 Cooperates with the Eukaryotic Translation Initiation Factor 4E to Regulate c-Myc Translation. *PLoS ONE* **2014**, *9*, e107016. [[CrossRef](#)] [[PubMed](#)]

92. Sun, X.; Haider Ali, M.S.S.; Moran, M. The role of interactions of long non-coding RNAs and heterogeneous nuclear ribonucleoproteins in regulating cellular functions. *Biochem. J.* **2017**, *474*, 2925–2935. [[CrossRef](#)] [[PubMed](#)]
93. Kong, J.; Sun, W.; Li, C.; Wan, L.; Wang, S.; Wu, Y.; Xu, E.; Zhang, H.; Lai, M. Long non-coding RNA LINC01133 inhibits epithelial–mesenchymal transition and metastasis in colorectal cancer by interacting with SRSF6. *Cancer Lett.* **2016**, *380*, 476–484. [[CrossRef](#)] [[PubMed](#)]
94. Romero-Barrios, N.; Legascue, M.F.; Benhamed, M.; Ariel, F.; Crespi, M. Splicing regulation by long noncoding RNAs. *Nucleic Acids Res.* **2018**, *46*, 2169–2184. [[CrossRef](#)] [[PubMed](#)]
95. Villamizar, O.; Chambers, C.B.; Riberdy, J.M.; Persons, D.A.; Wilber, A. Long noncoding RNA Saf and splicing factor 45 increase soluble Fas and resistance to apoptosis. *Oncotarget* **2016**, *7*, 13810–13826. [[CrossRef](#)] [[PubMed](#)]
96. Tripathi, V.; Ellis, J.D.; Shen, Z.; Song, D.Y.; Pan, Q.; Watt, A.T.; Freier, S.M.; Bennett, C.F.; Sharma, A.; Bubulya, P.A.; et al. The Nuclear-Retained Noncoding RNA MALAT1 Regulates Alternative Splicing by Modulating SR Splicing Factor Phosphorylation. *Mol. Cell* **2010**, *39*, 925–938. [[CrossRef](#)] [[PubMed](#)]
97. Liu, B.; Sun, L.; Liu, Q.; Gong, C.; Yao, Y.; Lv, X.; Lin, L.; Yao, H.; Su, F.; Li, D.; et al. A Cytoplasmic NF- κ B Interacting Long Noncoding RNA Blocks I κ B Phosphorylation and Suppresses Breast Cancer Metastasis. *Cancer Cell* **2015**, *27*, 370–381. [[CrossRef](#)] [[PubMed](#)]
98. Lin, A.; Li, C.; Xing, Z.; Hu, Q.; Liang, K.; Han, L.; Wang, C.; Hawke, D.H.; Wang, S.; Zhang, Y.; et al. The LINK-A lncRNA activates normoxic HIF1 α signalling in triple-negative breast cancer. *Nat. Cell Biol.* **2016**, *18*, 213–224. [[CrossRef](#)] [[PubMed](#)]
99. Ruiz-Orera, J.; Messeguer, X.; Subirana, J.A.; Alba, M.M. Long non-coding RNAs as a source of new peptides. *Elife* **2014**, *3*, e03523. [[CrossRef](#)] [[PubMed](#)]
100. Matsumoto, A.; Nakayama, K.I. Hidden Peptides Encoded by Putative Noncoding RNAs. *Cell. Struct. Funct.* **2018**, *43*, 75–83. [[CrossRef](#)] [[PubMed](#)]
101. Matsumoto, A.; Pasut, A.; Matsumoto, M.; Yamashita, R.; Fung, J.; Monteleone, E.; Saghatelian, A.; Nakayama, K.I.; Clohessy, J.G.; Pandolfi, P.P. mTORC1 and muscle regeneration are regulated by the LINC00961-encoded SPAR polypeptide. *Nature* **2016**, *541*, 228–232. [[CrossRef](#)] [[PubMed](#)]
102. D’Lima, N.G.; Ma, J.; Winkler, L.; Chu, Q.; Loh, K.H.; Corpuz, E.O.; Budnik, B.A.; Lykke-Andersen, J.; Saghatelian, A.; Slavoff, S.A. A human microprotein that interacts with the mRNA decapping complex. *Nat. Chem. Biol.* **2016**, *13*, 174–180. [[CrossRef](#)] [[PubMed](#)]
103. Huang, J.-Z.; Chen, M.; Chen, D.; Gao, X.-C.; Zhu, S.; Huang, H.; Hu, M.; Zhu, H.; Yan, G.-R. A Peptide Encoded by a Putative lncRNA HOXB-AS3 Suppresses Colon Cancer Growth. *Mol. Cell* **2017**, *68*, 171–184. [[CrossRef](#)] [[PubMed](#)]
104. Carlevaro-Fita, J.; Rahim, A.; Guigó, R.; Vardy, L.A.; Johnson, R. Cytoplasmic long noncoding RNAs are frequently bound to and degraded at ribosomes in human cells. *RNA* **2016**, *22*, 867–882. [[CrossRef](#)] [[PubMed](#)]
105. Yan, X.; Hu, Z.; Feng, Y.; Hu, X.; Yuan, J.; Zhao, S.D.; Zhang, Y.; Yang, L.; Shan, W.; He, Q.; et al. Comprehensive Genomic Characterization of Long Non-coding RNAs across Human Cancers. *Cancer Cell* **2015**, *28*, 529–540. [[CrossRef](#)] [[PubMed](#)]
106. Li, J.; Meng, H.; Bai, Y.; Wang, K. Regulation of lncRNA and Its Role in Cancer Metastasis. *Oncol. Res.* **2016**, *23*, 205–217. [[CrossRef](#)] [[PubMed](#)]
107. Kim, T.; Croce, C.M. Long noncoding RNAs: Undeciphered cellular codes encrypting keys of colorectal cancer pathogenesis. *Cancer Lett.* **2018**, *417*, 89–95. [[CrossRef](#)] [[PubMed](#)]
108. Yang, C.; Li, X.; Wang, Y.; Zhao, L.; Chen, W. Long non-coding RNA UCA1 regulated cell cycle distribution via CREB through PI3-K dependent pathway in bladder carcinoma cells. *Gene* **2012**, *496*, 8–16. [[CrossRef](#)] [[PubMed](#)]
109. Tsang, W.P.; Wong, T.W.L.; Cheung, A.H.H.; Co, C.N.N.; Kwok, T.T. Induction of drug resistance and transformation in human cancer cells by the noncoding RNA CUDR. *RNA* **2007**, *13*, 890–898. [[CrossRef](#)] [[PubMed](#)]
110. Xue, M.; Chen, W.; Li, X. Urothelial cancer associated 1: A long noncoding RNA with a crucial role in cancer. *J. Cancer Res. Clin. Oncol.* **2016**, *142*, 1407–1419. [[CrossRef](#)] [[PubMed](#)]
111. Chen, P.; Wan, D.; Zheng, D.; Zheng, Q.; Wu, F.; Zhi, Q. Long non-coding RNA UCA1 promotes the tumorigenesis in pancreatic cancer. *Biomed. Pharmacother.* **2016**, *83*, 1220–1226. [[CrossRef](#)] [[PubMed](#)]

112. Zhang, X.; Gao, F.; Zhou, L.; Wang, H.; Shi, G.; Tan, X. UCA1 Regulates the Growth and Metastasis of Pancreatic Cancer by Sponging miR-135a. *Oncol. Res.* **2017**, *25*, 1529–1541. [[CrossRef](#)] [[PubMed](#)]
113. Zhang, M.; Zhao, Y.; Zhang, Y.; Wang, D.; Gu, S.; Feng, W.; Peng, W.; Gong, A.; Xu, M. LncRNA UCA1 promotes migration and invasion in pancreatic cancer cells via the Hippo pathway. *Biochim. Biophys. Acta Mol. Basis Dis.* **2018**, *1864*, 1770–1782. [[CrossRef](#)] [[PubMed](#)]
114. Han, Y.; Yang, Y.-N.; Yuan, H.-H.; Zhang, T.-T.; Sui, H.; Wei, X.-L.; Liu, L.; Huang, P.; Zhang, W.-J.; Bai, Y.-X. UCA1, a long non-coding RNA up-regulated in colorectal cancer influences cell proliferation, apoptosis and cell cycle distribution. *Pathology* **2014**, *46*, 396–401. [[CrossRef](#)] [[PubMed](#)]
115. Ni, B.; Yu, X.; Guo, X.; Fan, X.; Yang, Z.; Wu, P.; Yuan, Z.; Deng, Y.; Wang, J.; Chen, D.; et al. Increased urothelial cancer associated 1 is associated with tumor proliferation and metastasis and predicts poor prognosis in colorectal cancer. *Int. J. Oncol.* **2015**, *47*, 1329–1338. [[CrossRef](#)] [[PubMed](#)]
116. Bian, Z.; Jin, L.; Zhang, J.; Yin, Y.; Quan, C.; Hu, Y.; Feng, Y.; Liu, H.; Fei, B.; Mao, Y.; et al. LncRNA—UCA1 enhances cell proliferation and 5-fluorouracil resistance in colorectal cancer by inhibiting miR-204-5p. *Sci. Rep.* **2016**, *6*, 23892. [[CrossRef](#)] [[PubMed](#)]
117. Liu, F.; Dong, Q.; Gao, H.; Zhu, Z. The prognostic significance of UCA1 for predicting clinical outcome in patients with digestive system malignancies. *Oncotarget* **2017**, *8*, 40620. [[CrossRef](#)] [[PubMed](#)]
118. Renaud, F.; Vincent, A.; Mariette, C.; Crépin, M.; Stechly, L.; Truant, S.; Copin, M.-C.; Porchet, N.; Leteurtre, E.; Van Seuningen, I.; et al. MUC5AC hypomethylation is a predictor of microsatellite instability independently of clinical factors associated with colorectal cancer. *Int. J. Cancer* **2015**, *136*, 2811–2821. [[CrossRef](#)] [[PubMed](#)]
119. Aguirre-Gamboa, R.; Gomez-Rueda, H.; Martinez-Ledesma, E.; Martinez-Torteya, A.; Chacolla-Huaranga, R.; Rodriguez-Barrientos, A.; Tamez-Pena, J.G.; Trevino, V. SurvExpress: An online biomarker validation tool and database for cancer gene expression data using survival analysis. *PLoS ONE* **2013**, *8*, e74250. [[CrossRef](#)] [[PubMed](#)]
120. Wu, W.; Zhang, S.; Li, X.; Xue, M.; Cao, S.; Chen, W. Ets-2 regulates cell apoptosis via the Akt pathway, through the regulation of urothelial cancer associated 1, a long non-coding RNA, in bladder cancer cells. *PLoS ONE* **2013**, *8*, e73920. [[CrossRef](#)] [[PubMed](#)]
121. Zuo, Z.K.; Gong, Y.; Chen, X.H.; Ye, F.; Yin, Z.M.; Gong, Q.N.; Huang, J.S. TGFbeta1-Induced LncRNA UCA1 Upregulation Promotes Gastric Cancer Invasion and Migration. *DNA Cell Biol.* **2017**, *36*, 159–167. [[CrossRef](#)] [[PubMed](#)]
122. Li, G.Y.; Wang, W.; Sun, J.Y.; Xin, B.; Zhang, X.; Wang, T.; Zhang, Q.F.; Yao, L.B.; Han, H.; Fan, D.M.; et al. Long non-coding RNAs AC026904.1 and UCA1: A “one-two punch” for TGF-beta-induced SNAI2 activation and epithelial-mesenchymal transition in breast cancer. *Theranostics* **2018**, *8*, 2846–2861. [[CrossRef](#)] [[PubMed](#)]
123. Hiemer, S.E.; Szymaniak, A.D.; Varelas, X. The Transcriptional Regulators TAZ and YAP Direct Transforming Growth Factor-induced Tumorigenic Phenotypes in Breast Cancer Cells. *J. Biol. Chem.* **2014**, *289*, 13461–13474. [[CrossRef](#)] [[PubMed](#)]
124. Gou, L.; Liu, M.; Xia, J.; Wan, Q.; Jiang, Y.; Sun, S.; Tang, M.; Zhou, L.; He, T.; Zhang, Y. BMP9 Promotes the Proliferation and Migration of Bladder Cancer Cells through Up-Regulating lncRNA UCA1. *Int. J. Mol. Sci.* **2018**, *19*, 1116. [[CrossRef](#)] [[PubMed](#)]
125. Xue, M.; Chen, W.; Xiang, A.; Wang, R.; Chen, H.; Pan, J.; Pang, H.; An, H.; Wang, X.; Hou, H.; et al. Hypoxic exosomes facilitate bladder tumor growth and development through transferring long non-coding RNA-UCA1. *Mol. Cancer* **2017**, *16*. [[CrossRef](#)] [[PubMed](#)]
126. Xue, M.; Li, X.; Li, Z.; Chen, W. Urothelial carcinoma associated 1 is a hypoxia-inducible factor-1 α -targeted long noncoding RNA that enhances hypoxic bladder cancer cell proliferation, migration, and invasion. *Tumor Biol.* **2014**, *35*, 6901–6912. [[CrossRef](#)] [[PubMed](#)]
127. Xue, M.E.I.; Li, X.U.; Wu, W.; Zhang, S.; Wu, S.; Li, Z.; Chen, W.E.I. Upregulation of long non-coding RNA urothelial carcinoma associated 1 by CCAAT/enhancer binding protein α contributes to bladder cancer cell growth and reduced apoptosis. *Oncol. Rep.* **2014**, *31*, 1993–2000. [[CrossRef](#)] [[PubMed](#)]
128. Guo, X.; Zhang, Y.; Mayakonda, A.; Madan, V.; Ding, L.W.; Lin, L.H.; Zia, S.; Gery, S.; Tyner, J.W.; Zhou, W.; et al. ARID1A and CEBPalpha cooperatively inhibit UCA1 transcription in breast cancer. *Oncogene* **2018**. [[CrossRef](#)] [[PubMed](#)]
129. Lee, J.-J.; Kim, M.; Kim, H.-P. Epigenetic regulation of long noncoding RNA UCA1 by SATB1 in breast cancer. *BMB Rep.* **2016**, *49*, 578–583. [[CrossRef](#)] [[PubMed](#)]

130. Kumar, P.P.; Emechebe, U.; Smith, R.; Franklin, S.; Moore, B.; Yandell, M.; Lessnick, S.L.; Moon, A.M. Coordinated control of senescence by lncRNA and a novel T-box3 co-repressor complex. *Elife* **2014**, *29*, 02805. [[CrossRef](#)] [[PubMed](#)]
131. Zhou, Y.; Meng, X.; Chen, S.; Li, W.; Li, D.; Singer, R.; Gu, W. IMP1 regulates UCA1-mediated cell invasion through facilitating UCA1 decay and decreasing the sponge effect of UCA1 for miR-122-5p. *Breast Cancer Res.* **2018**, *20*. [[CrossRef](#)] [[PubMed](#)]
132. Wang, T.; Yuan, J.; Feng, N.; Li, Y.; Lin, Z.; Jiang, Z.; Gui, Y. Hsa-miR-1 downregulates long non-coding RNA urothelial cancer associated 1 in bladder cancer. *Tumour Biol.* **2014**, *35*, 10075–10084. [[CrossRef](#)] [[PubMed](#)]
133. Huang, J.; Zhou, N.; Watabe, K.; Lu, Z.; Wu, F.; Xu, M.; Mo, Y.Y. Long non-coding RNA UCA1 promotes breast tumor growth by suppression of p27 (Kip1). *Cell Death Dis.* **2014**, *5*, e1008. [[CrossRef](#)] [[PubMed](#)]
134. Li, T.; Zheng, Q.; An, J.; Wu, M.; Li, H.; Gui, X.; Pu, H.; Lu, D. SET1A Cooperates With CUDR to Promote Liver Cancer Growth and Hepatocyte-like Stem Cell Malignant Transformation Epigenetically. *Mol. Ther.* **2016**, *24*, 261–275. [[CrossRef](#)] [[PubMed](#)]
135. Corvaisier, M.; Bauzone, M.; Corfiotti, F.; Renaud, F.; Amrani, M.E.; Monté, D.; Truant, S.; Leteurtre, E.; Formstecher, P.; Seuningen, I.V.; et al. Regulation of cellular quiescence by YAP/TAZ and Cyclin E1 in colon cancer cells: Implication in chemoresistance and cancer relapse. *Oncotarget* **2016**, *7*, 56699. [[CrossRef](#)] [[PubMed](#)]
136. Jeggari, A.; Marks, D.S.; Larsson, E. miRcode: A map of putative microRNA target sites in the long non-coding transcriptome. *Bioinformatics* **2012**, *28*, 2062–2063. [[CrossRef](#)] [[PubMed](#)]
137. Li, Z.; Li, X.; Wu, S.; Xue, M.; Chen, W. Long non-coding RNA UCA1 promotes glycolysis by upregulating hexokinase 2 through the mTOR-STAT3/microRNA143 pathway. *Cancer Sci.* **2014**, *105*, 951–955. [[CrossRef](#)] [[PubMed](#)]
138. Jahangiri, B.; Khalaj-kondori, M.; Asadollahi, E.; Sadeghizadeh, M. Cancer-associated fibroblasts enhance cell proliferation and metastasis of colorectal cancer SW480 cells by provoking long noncoding RNA UCA1. *Cell Commun. Signal.* **2018**. [[CrossRef](#)] [[PubMed](#)]
139. Vlachos, I.S.; Zagganas, K.; Paraskevopoulou, M.D.; Georgakilas, G.; Karagkouni, D.; Vergoulis, T.; Dalamagas, T.; Hatzigeorgiou, A.G. DIANA-miRPath v3.0: Deciphering microRNA function with experimental support. *Nucleic Acids Res.* **2015**, *43*, 14. [[CrossRef](#)] [[PubMed](#)]
140. Zheng, J.; Yi, D.; Liu, Y.; Wang, M.; Zhu, Y.; Shi, H. Long noncoding RNA UCA1 regulates neural stem cell differentiation by controlling miR-1/Hes1 expression. *Am. J. Transl. Res.* **2017**, *9*, 3696–3704. [[PubMed](#)]
141. Xu, W.; Zhang, Z.; Zou, K.; Cheng, Y.; Yang, M.; Chen, H.; Wang, H.; Zhao, J.; Chen, P.; He, L.; et al. MiR-1 suppresses tumor cell proliferation in colorectal cancer by inhibition of Smad3-mediated tumor glycolysis. *Cell Death Dis.* **2017**, *8*, e2761. [[CrossRef](#)] [[PubMed](#)]
142. Yang, Z.; Shi, X.; Li, C.; Wang, X.; Hou, K.; Li, Z.; Zhang, X.; Fan, Y.; Qu, X.; Che, X.; et al. Long non-coding RNA UCA1 upregulation promotes the migration of hypoxia-resistant gastric cancer cells through the miR-7-5p/EGFR axis. *Exp. Cell Res.* **2018**, *368*, 194–201. [[CrossRef](#)] [[PubMed](#)]
143. Li, Y.; Liu, Y.; Xie, P.; Li, F.; Li, G. PAX6, a novel target of microRNA-7, promotes cellular proliferation and invasion in human colorectal cancer cells. *Dig. Dis. Sci.* **2014**, *59*, 598–606. [[CrossRef](#)] [[PubMed](#)]
144. Liu, M.L.; Zhang, Q.; Yuan, X.; Jin, L.; Wang, L.L.; Fang, T.T.; Wang, W.B. Long noncoding RNA RP4 functions as a competing endogenous RNA through miR-7-5p sponge activity in colorectal cancer. *World J. Gastroenterol.* **2018**, *24*, 1004–1012. [[CrossRef](#)] [[PubMed](#)]
145. Nagano, Y.; Toiyama, Y.; Okugawa, Y.; Imaoka, H.; Fujikawa, H.; Yasuda, H.; Yoshiyama, S.; Hiro, J.; Kobayashi, M.; Ohi, M.; et al. MicroRNA-7 Is Associated with Malignant Potential and Poor Prognosis in Human Colorectal Cancer. *Anticancer Res.* **2016**, *36*, 6521–6526. [[CrossRef](#)] [[PubMed](#)]
146. Pothoulakis, C.; Torre-Rojas, M.; Duran-Padilla, M.A.; Gevorgian, J.; Zoras, O.; Chrysos, E.; Chalkiadakis, G.; Baritaki, S. CRHR2/Ucn2 signaling is a novel regulator of miR-7/YY1/Fas circuitry contributing to reversal of colorectal cancer cell resistance to Fas-mediated apoptosis. *Int. J. Cancer* **2018**, *142*, 334–346. [[CrossRef](#)] [[PubMed](#)]
147. Suto, T.; Yokobori, T.; Yajima, R.; Morita, H.; Fujii, T.; Yamaguchi, S.; Altan, B.; Tsutsumi, S.; Asao, T.; Kuwano, H. MicroRNA-7 expression in colorectal cancer is associated with poor prognosis and regulates cetuximab sensitivity via EGFR regulation. *Carcinogenesis* **2015**, *36*, 338–345. [[CrossRef](#)] [[PubMed](#)]
148. Xu, K.; Chen, Z.; Qin, C.; Song, X. miR-7 inhibits colorectal cancer cell proliferation and induces apoptosis by targeting XRCC2. *OncoTargets Ther.* **2014**, *7*, 325–332. [[CrossRef](#)] [[PubMed](#)]

149. Zeng, C.Y.; Zhan, Y.S.; Huang, J.; Chen, Y.X. MicroRNA7 suppresses human colon cancer invasion and proliferation by targeting the expression of focal adhesion kinase. *Mol. Med. Rep.* **2016**, *13*, 1297–1303. [[CrossRef](#)] [[PubMed](#)]
150. Zeng, K.; Chen, X.; Xu, M.; Liu, X.; Hu, X.; Xu, T.; Sun, H.; Pan, Y.; He, B.; Wang, S. CircHIPK3 promotes colorectal cancer growth and metastasis by sponging miR-7. *Cell Death Dis.* **2018**, *9*, 417. [[CrossRef](#)] [[PubMed](#)]
151. Zhang, N.; Li, X.; Wu, C.W.; Dong, Y.; Cai, M.; Mok, M.T.; Wang, H.; Chen, J.; Ng, S.S.; Chen, M.; et al. microRNA-7 is a novel inhibitor of YY1 contributing to colorectal tumorigenesis. *Oncogene* **2013**, *32*, 5078–5088. [[CrossRef](#)] [[PubMed](#)]
152. Xiao, Y.; Jiao, C.; Lin, Y.; Chen, M.; Zhang, J.; Wang, J.; Zhang, Z. lncRNA UCA1 Contributes to Imatinib Resistance by Acting as a ceRNA Against miR-16 in Chronic Myeloid Leukemia Cells. *DNA Cell Biol.* **2017**, *36*, 18–25. [[CrossRef](#)] [[PubMed](#)]
153. Hasakova, K.; Bezakova, J.; Vician, M.; Reis, R.; Zeman, M.; Herichova, I. Gender-dependent expression of leading and passenger strand of miR-21 and miR-16 in human colorectal cancer and adjacent colonic tissues. *Physiol. Res.* **2017**, *66*, S575–S582. [[PubMed](#)]
154. Li, H.J.; Li, X.; Pang, H.; Pan, J.J.; Xie, X.J.; Chen, W. Long non-coding RNA UCA1 promotes glutamine metabolism by targeting miR-16 in human bladder cancer. *Jpn. J. Clin. Oncol.* **2015**, *45*, 1055–1063. [[CrossRef](#)] [[PubMed](#)]
155. Zhu, H.-Y.; Bai, W.-D.; Ye, X.-M.; Yang, A.-G.; Jia, L.-T. Long non-coding RNA UCA1 desensitizes breast cancer cells to trastuzumab by impeding miR-18a repression of Yes-associated protein 1. *Biochem. Biophys. Res. Commun.* **2018**, *496*, 1308–1313. [[CrossRef](#)] [[PubMed](#)]
156. Yue, J.; Humphreys, K.J.; McKinnon, R.A.; Michael, M.Z. miR-18a Inhibits CDC42 and Plays a Tumour Suppressor Role in Colorectal Cancer Cells. *PLoS ONE* **2014**, *9*, e112288. [[CrossRef](#)]
157. Li, X.; Wu, Y.; Liu, A.; Tang, X. Long non-coding RNA UCA1 enhances tamoxifen resistance in breast cancer cells through a miR-18a-HIF1alpha feedback regulatory loop. *Tumour Biol.* **2016**, *37*, 14733–14743. [[CrossRef](#)] [[PubMed](#)]
158. Fang, Q.; Chen, X.; Zhi, X. Long Non-Coding RNA (LncRNA) Urothelial Carcinoma Associated 1 (UCA1) Increases Multi-Drug Resistance of Gastric Cancer via Downregulating miR-27b. *Med. Sci. Monit.* **2016**, *22*, 3506–3513. [[CrossRef](#)] [[PubMed](#)]
159. Luo, Y.; Yu, S.Y.; Chen, J.J.; Qin, J.; Qiu, Y.E.; Zhong, M.; Chen, M. MiR-27b directly targets Rab3D to inhibit the malignant phenotype in colorectal cancer. *Oncotarget* **2018**, *9*, 3830–3841. [[CrossRef](#)] [[PubMed](#)]
160. Zhou, Y.; Chen, Y.; Ding, W.; Hua, Z.; Wang, L.; Zhu, Y.; Qian, H.; Dai, T. LncRNA UCA1 impacts cell proliferation, invasion, and migration of pancreatic cancer through regulating miR-96/FOXO3. *IUBMB Life* **2018**. [[CrossRef](#)] [[PubMed](#)]
161. Iseki, Y.; Shibutani, M.; Maeda, K.; Nagahara, H.; Fukuoka, T.; Matsutani, S.; Hirakawa, K.; Ohira, M. MicroRNA-96 Promotes Tumor Invasion in Colorectal Cancer via RECK. *Anticancer Res.* **2018**, *38*, 2031–2035. [[CrossRef](#)] [[PubMed](#)]
162. Rapti, S.-M.; Kontos, C.K.; Papadopoulos, I.N.; Scorilas, A. High miR-96 levels in colorectal adenocarcinoma predict poor prognosis, particularly in patients without distant metastasis at the time of initial diagnosis. *Tumor Biol.* **2016**, *37*, 11815–11824. [[CrossRef](#)] [[PubMed](#)]
163. Sun, Y.; Jin, J.G.; Mi, W.Y.; Zhang, S.R.; Meng, Q.; Zhang, S.T. Long Noncoding RNA UCA1 Targets miR-122 to Promote Proliferation, Migration, and Invasion of Glioma Cells. *Oncol. Res.* **2018**, *26*, 103–110. [[CrossRef](#)] [[PubMed](#)]
164. Iino, I.; Kikuchi, H.; Miyazaki, S.; Hiramatsu, Y.; Ohta, M.; Kamiya, K.; Kusama, Y.; Baba, S.; Setou, M.; Konno, H. Effect of miR-122 and its target gene cationic amino acid transporter 1 on colorectal liver metastasis. *Cancer Sci.* **2013**, *104*, 624–630. [[CrossRef](#)] [[PubMed](#)]
165. Zhang, Y.; Liu, Y.; Xu, X. Knockdown of LncRNA-UCA1 suppresses chemoresistance of pediatric AML by inhibiting glycolysis through the microRNA-125a/hexokinase 2 pathway. *J. Cell. Biochem.* **2018**, *119*, 6296–6308. [[CrossRef](#)] [[PubMed](#)]
166. Tong, Z.; Liu, N.; Lin, L.; Guo, X.; Yang, D.; Zhang, Q. miR-125a-5p inhibits cell proliferation and induces apoptosis in colon cancer via targeting BCL2, BCL2L12 and MCL1. *Biomed. Pharmacother.* **2015**, *75*, 129–136. [[CrossRef](#)] [[PubMed](#)]

167. Sun, M.D.; Zheng, Y.Q.; Wang, L.P.; Zhao, H.T.; Yang, S. Long noncoding RNA UCA1 promotes cell proliferation, migration and invasion of human leukemia cells via sponging miR-126. *Eur. Rev. Med. Pharmacol. Sci.* **2018**, *22*, 2233–2245. [[PubMed](#)]
168. Liu, Q.; Li, Y.; Lv, W.; Zhang, G.; Tian, X.; Li, X.; Cheng, H.; Zhu, C. UCA1 promotes cell proliferation and invasion and inhibits apoptosis through regulation of the miR129-SOX4 pathway in renal cell carcinoma. *OncoTargets Ther.* **2018**, *11*, 2475–2487. [[CrossRef](#)] [[PubMed](#)]
169. Fesler, A.; Zhai, H.; Ju, J. miR-129 as a novel therapeutic target and biomarker in gastrointestinal cancer. *OncoTargets Ther.* **2014**, *7*, 1481–1485.
170. Karaayvaz, M.; Zhai, H.; Ju, J. miR-129 promotes apoptosis and enhances chemosensitivity to 5-fluorouracil in colorectal cancer. *Cell Death Dis.* **2013**, *6*, 193. [[CrossRef](#)] [[PubMed](#)]
171. Lin, J.; Shi, Z.; Yu, Z.; He, Z. LncRNA HIF1A-AS2 positively affects the progression and EMT formation of colorectal cancer through regulating miR-129-5p and DNMT3A. *Biomed. Pharmacother.* **2018**, *98*, 433–439. [[CrossRef](#)] [[PubMed](#)]
172. Wu, J.; Qian, J.; Li, C.; Kwok, L.; Cheng, F.; Liu, P.; Perdomo, C.; Kotton, D.; Vaziri, C.; Anderlind, C.; et al. miR-129 regulates cell proliferation by downregulating Cdk6 expression. *Cell Cycle* **2010**, *9*, 1809–1818. [[CrossRef](#)] [[PubMed](#)]
173. Wu, N.; Fesler, A.; Liu, H.; Ju, J. Development of novel miR-129 mimics with enhanced efficacy to eliminate chemoresistant colon cancer stem cells. *Oncotarget* **2017**, *9*, 8887–8897. [[CrossRef](#)] [[PubMed](#)]
174. Ya, G.; Wang, H.; Ma, Y.; Hu, A.; Hu, J.; Yu, Y. Serum miR-129 functions as a biomarker for colorectal cancer by targeting estrogen receptor (ER) beta. *Pharmazie* **2017**, *72*, 107–112. [[PubMed](#)]
175. Wang, J.; Ye, C.; Liu, J.; Hu, Y. UCA1 confers paclitaxel resistance to ovarian cancer through miR-129/ABC1 axis. *Biochem. Biophys. Res. Commun.* **2018**, *501*, 1034–1040. [[CrossRef](#)] [[PubMed](#)]
176. Nagel, R.; le Sage, C.; Diosdado, B.; van der Waal, M.; Oude Vrielink, J.A.F.; Bolijn, A.; Meijer, G.A.; Agami, R. Regulation of the Adenomatous Polyposis Coli Gene by the miR-135 Family in Colorectal Cancer. *Cancer Res.* **2008**, *68*, 5795–5802. [[CrossRef](#)] [[PubMed](#)]
177. Wang, Y.; Hou, Z.; Li, D. Long noncoding RNA UCA1 promotes anaplastic thyroid cancer cell proliferation via miR-135a mediated cMYC activation. *Mol. Med. Rep.* **2018**, *18*, 3068–3076. [[CrossRef](#)] [[PubMed](#)]
178. Ahmad, A.; Gomes, S.E.; Pereira, D.M.; Roma-Rodrigues, C.; Fernandes, A.R.; Borralho, P.M.; Rodrigues, C.M.P. Convergence of miR-143 overexpression, oxidative stress and cell death in HCT116 human colon cancer cells. *PLoS ONE* **2018**, *13*, e0191607. [[CrossRef](#)]
179. Tuo, Y.-L.; Li, X.-M.; Luo, J. Long noncoding RNA UCA1 modulates breast cancer cell growth and apoptosis through decreasing tumor suppressive miR-143. *Eur. Rev. Med. Pharm. Sci.* **2015**, *19*, 3403–3411.
180. Tian, S.; Zhao, W.; Yang, D.; Yu, Y.; Zou, J.; Liu, Z.; Du, Z. Atorvastatin inhibits miR-143 expression: A protective mechanism against oxidative stress in cardiomyocytes. *Int. J. Cardiol.* **2016**, *211*, 115–118. [[CrossRef](#)] [[PubMed](#)]
181. Luo, J.; Chen, J.; Li, H.; Yang, Y.; Yun, H.; Yang, S.; Mao, X. LncRNA UCA1 promotes the invasion and EMT of bladder cancer cells by regulating the miR-143/HMGB1 pathway. *Oncol. Lett.* **2017**, *14*, 5556–5562. [[CrossRef](#)] [[PubMed](#)]
182. Li, D.; Li, H.; Yang, Y.; Kang, L. Long Noncoding RNA Urothelial Carcinoma Associated 1 Promotes the Proliferation and Metastasis of Human Lung Tumor Cells by Regulating MicroRNA-144. *Oncol. Res.* **2018**, *26*, 537–546. [[CrossRef](#)] [[PubMed](#)]
183. Iwaya, T.; Yokobori, T.; Nishida, N.; Kogo, R.; Sudo, T.; Tanaka, F.; Shibata, K.; Sawada, G.; Takahashi, Y.; Ishibashi, M.; et al. Downregulation of miR-144 is associated with colorectal cancer progression via activation of mTOR signaling pathway. *Carcinogenesis* **2012**, *33*, 2391–2397. [[CrossRef](#)] [[PubMed](#)]
184. Xue, M.; Pang, H.; Li, X.; Li, H.; Pan, J.; Chen, W. Long non-coding RNA urothelial cancer-associated 1 promotes bladder cancer cell migration and invasion by way of the hsa-miR-145-ZEB1/2-FSCN1 pathway. *Cancer Sci.* **2016**, *107*, 18–27. [[CrossRef](#)] [[PubMed](#)]
185. Sheng, N.; Tan, G.; You, W.; Chen, H.; Gong, J.; Chen, D.; Zhang, H.; Wang, Z. MiR-145 inhibits human colorectal cancer cell migration and invasion via PAK4-dependent pathway. *Cancer Med.* **2017**, *6*, 1331–1340. [[CrossRef](#)] [[PubMed](#)]
186. Yuan, F.; Sun, R.; Li, L.; Jin, B.; Wang, Y.; Liang, Y.; Che, G.; Gao, L.; Zhang, L. A functional variant rs353292 in the flanking region of miR-143/145 contributes to the risk of colorectal cancer. *Sci. Rep.* **2016**, *6*, 30195. [[CrossRef](#)] [[PubMed](#)]

187. Wang, W.; Ji, G.; Xiao, X.; Chen, X.; Qin, W.W.; Yang, F.; Li, Y.F.; Fan, L.N.; Xi, W.J.; Huo, Y.; et al. Epigenetically regulated miR-145 suppresses colon cancer invasion and metastasis by targeting LASP1. *Oncotarget* **2016**, *7*, 68674–68687. [[CrossRef](#)] [[PubMed](#)]
188. Li, S.; Wu, X.; Xu, Y.; Wu, S.; Li, Z.; Chen, R.; Huang, N.; Zhu, Z.; Xu, X. miR-145 suppresses colorectal cancer cell migration and invasion by targeting an ETS-related gene. *Oncol. Rep.* **2016**, *36*, 1917–1926. [[CrossRef](#)] [[PubMed](#)]
189. He, Z.; Wang, Y.; Huang, G.; Wang, Q.; Zhao, D.; Chen, L. The lncRNA UCA1 interacts with miR-182 to modulate glioma proliferation and migration by targeting iASPP. *Arch. Biochem. Biophys.* **2017**, *623–624*, 1–8. [[CrossRef](#)] [[PubMed](#)]
190. Zhang, Y.U.; Wang, X.; Wang, Z.; Tang, H.U.I.; Fan, H.; Guo, Q. miR-182 promotes cell growth and invasion by targeting forkhead box F2 transcription factor in colorectal cancer. *Oncol. Rep.* **2015**, *33*, 2592–2598. [[CrossRef](#)] [[PubMed](#)]
191. He, Z.; You, C.; Zhao, D. Long non-coding RNA UCA1/miR-182/PFKFB2 axis modulates glioblastoma-associated stromal cells-mediated glycolysis and invasion of glioma cells. *Biochem. Biophys. Res. Commun.* **2018**, *500*, 569–576. [[CrossRef](#)] [[PubMed](#)]
192. Qin, L.; Jia, Z.; Xie, D.; Liu, Z. Knockdown of long noncoding RNA urothelial carcinoma-associated 1 inhibits cell viability, migration, and invasion by regulating microRNA-182 in gastric carcinoma. *J. Cell Biochem.* **2018**. [[CrossRef](#)] [[PubMed](#)]
193. Fang, Z.; Zhao, J.; Xie, W.; Sun, Q.; Wang, H.; Qiao, B. LncRNA UCA1 promotes proliferation and cisplatin resistance of oral squamous cell carcinoma by suppressing miR-184 expression. *Cancer Med.* **2017**, *6*, 2897–2908. [[CrossRef](#)] [[PubMed](#)]
194. Wu, G.; Liu, J.; Wu, Z.; Wu, X.; Yao, X. MicroRNA-184 inhibits cell proliferation and metastasis in human colorectal cancer by directly targeting IGF-1R. *Oncol. Lett.* **2017**, *14*, 3215–3222. [[CrossRef](#)] [[PubMed](#)]
195. Zhou, Y.; Wang, X.; Zhang, J.; He, A.; Wang, Y.L.; Han, K.; Su, Y.; Yin, J.; Lv, X.; Hu, H. Artesunate suppresses the viability and mobility of prostate cancer cells through UCA1, the sponge of miR-184. *Oncotarget* **2017**, *8*, 18260–18270. [[CrossRef](#)] [[PubMed](#)]
196. Wu, H.; Zhou, C. Long non-coding RNA UCA1 promotes lung cancer cell proliferation and migration via microRNA-193a/HMGB1 axis. *Biochem. Biophys. Res. Commun.* **2018**, *496*, 738–745. [[CrossRef](#)] [[PubMed](#)]
197. Zhang, P.; Ji, D.B.; Han, H.B.; Shi, Y.F.; Du, C.Z.; Gu, J. Downregulation of miR-193a-5p correlates with lymph node metastasis and poor prognosis in colorectal cancer. *World J. Gastroenterol.* **2014**, *20*, 12241–12248. [[CrossRef](#)] [[PubMed](#)]
198. Takahashi, H.; Takahashi, M.; Ohnuma, S.; Unno, M.; Yoshino, Y.; Ouchi, K.; Takahashi, S.; Yamada, Y.; Shimodaira, H.; Ishioka, C. microRNA-193a-3p is specifically down-regulated and acts as a tumor suppressor in BRAF-mutated colorectal cancer. *BMC Cancer* **2017**, *17*, 723. [[CrossRef](#)] [[PubMed](#)]
199. Pekow, J.; Meckel, K.; Dougherty, U.; Huang, Y.; Chen, X.; Almoghrabi, A.; Mustafi, R.; Ayaloglu-Butun, F.; Deng, Z.; Haider, H.I.; et al. miR-193a-3p is a Key Tumor Suppressor in Ulcerative Colitis-Associated Colon Cancer and Promotes Carcinogenesis through Upregulation of IL17RD. *Clin. Cancer Res.* **2017**, *23*, 5281–5291. [[CrossRef](#)] [[PubMed](#)]
200. Mamoori, A.; Wahab, R.; Islam, F.; Lee, K.; Vider, J.; Lu, C.T.; Gopalan, V.; Lam, A.K. Clinical and biological significance of miR-193a-3p targeted KRAS in colorectal cancer pathogenesis. *Hum. Pathol.* **2018**, *71*, 145–156. [[CrossRef](#)] [[PubMed](#)]
201. Lin, M.; Duan, B.; Hu, J.; Yu, H.; Sheng, H.; Gao, H.; Huang, J. Decreased expression of miR-193a-3p is associated with poor prognosis in colorectal cancer. *Oncol. Lett.* **2017**, *14*, 1061–1067. [[CrossRef](#)] [[PubMed](#)]
202. Nie, W.; Ge, H.J.; Yang, X.Q.; Sun, X.; Huang, H.; Tao, X.; Chen, W.S.; Li, B. LncRNA-UCA1 exerts oncogenic functions in non-small cell lung cancer by targeting miR-193a-3p. *Cancer Lett.* **2016**, *371*, 99–106. [[CrossRef](#)] [[PubMed](#)]
203. Li, H.-J.; Sun, X.-M.; Li, Z.-K.; Yin, Q.-W.; Pang, H.; Pan, J.-J.; Li, X.; Chen, W. LncRNA UCA1 Promotes Mitochondrial Function of Bladder Cancer via the MiR-195/ARL2 Signaling Pathway. *Cell. Physiol. Biochem.* **2017**, *43*, 2548–2561. [[CrossRef](#)] [[PubMed](#)]
204. Zheng, L.; Chen, J.; Zhou, Z.; He, Z. miR-195 enhances the radiosensitivity of colorectal cancer cells by suppressing CARM1. *OncoTargets Ther.* **2017**, *10*, 1027–1038. [[CrossRef](#)] [[PubMed](#)]

205. Zhang, X.; Xu, J.; Jiang, T.; Liu, G.; Wang, D.; Lu, Y. MicroRNA-195 suppresses colorectal cancer cells proliferation via targeting FGF2 and regulating Wnt/beta-catenin pathway. *Am. J. Cancer Res.* **2016**, *6*, 2631–2640. [[PubMed](#)]
206. Ye, S.; Song, W.; Xu, X.; Zhao, X.; Yang, L. IGF2BP2 promotes colorectal cancer cell proliferation and survival through interfering with RAF-1 degradation by miR-195. *FEBS Lett.* **2016**, *590*, 1641–1650. [[CrossRef](#)] [[PubMed](#)]
207. Yang, I.P.; Tsai, H.L.; Miao, Z.F.; Huang, C.W.; Kuo, C.H.; Wu, J.Y.; Wang, W.M.; Juo, S.H.; Wang, J.Y. Development of a deregulating microRNA panel for the detection of early relapse in postoperative colorectal cancer patients. *J. Transl. Med.* **2016**, *14*, 108. [[CrossRef](#)] [[PubMed](#)]
208. Yang, B.; Tan, Z.; Song, Y. Study on the molecular regulatory mechanism of MicroRNA-195 in the invasion and metastasis of colorectal carcinoma. *Int. J. Clin. Exp. Med.* **2015**, *8*, 3793–3800. [[PubMed](#)]
209. Sun, M.; Song, H.; Wang, S.; Zhang, C.; Zheng, L.; Chen, F.; Shi, D.; Chen, Y.; Yang, C.; Xiang, Z.; et al. Integrated analysis identifies microRNA-195 as a suppressor of Hippo-YAP pathway in colorectal cancer. *J. Hematol. Oncol.* **2017**, *10*, 79. [[CrossRef](#)] [[PubMed](#)]
210. Kim, C.; Hong, Y.; Lee, H.; Kang, H.; Lee, E.K. MicroRNA-195 desensitizes HCT116 human colon cancer cells to 5-fluorouracil. *Cancer Lett.* **2018**, *412*, 264–271. [[CrossRef](#)] [[PubMed](#)]
211. Pan, J.; Li, X.; Wu, W.; Xue, M.; Hou, H.; Zhai, W.; Chen, W. Long non-coding RNA UCA1 promotes cisplatin/gemcitabine resistance through CREB modulating miR-196a-5p in bladder cancer cells. *Cancer Lett.* **2016**, *382*, 64–76. [[CrossRef](#)] [[PubMed](#)]
212. Zhang, H.; Su, Y.L.; Yu, H.; Qian, B.Y. Meta-Analysis of the Association between Mir-196a-2 Polymorphism and Cancer Susceptibility. *Cancer Biol. Med.* **2012**, *9*, 63–72. [[CrossRef](#)] [[PubMed](#)]
213. Shi, L.; Zhang, C.; Zhao, D.; Liu, K.; Li, T.; Tian, H. Mir-196a-2 C>T polymorphism as a susceptibility factor for colorectal cancer. *Int. J. Clin. Exp. Med.* **2015**, *8*, 2600–2606. [[PubMed](#)]
214. Ge, J.; Chen, Z.; Li, R.; Lu, T.; Xiao, G. Upregulation of microRNA-196a and microRNA-196b cooperatively correlate with aggressive progression and unfavorable prognosis in patients with colorectal cancer. *Cancer Cell Int.* **2014**, *14*, 128. [[CrossRef](#)] [[PubMed](#)]
215. Chen, X.; Du, P.; She, J.; Cao, L.; Li, Y.; Xia, H. Loss of ZG16 is regulated by miR-196a and contributes to stemness and progression of colorectal cancer. *Oncotarget* **2016**, *7*, 86695–86703. [[CrossRef](#)] [[PubMed](#)]
216. Xiao, J.N.; Yan, T.H.; Yu, R.M.; Gao, Y.; Zeng, W.L.; Lu, S.W.; Que, H.X.; Liu, Z.P.; Jiang, J.H. Long non-coding RNA UCA1 regulates the expression of Snail2 by miR-203 to promote hepatocellular carcinoma progression. *J. Cancer Res. Clin. Oncol.* **2017**, *143*, 981–990. [[CrossRef](#)] [[PubMed](#)]
217. Ye, H.; Hao, H.; Wang, J.; Chen, R.; Huang, Z. miR-203 as a novel biomarker for the diagnosis and prognosis of colorectal cancer: A systematic review and meta-analysis. *OncoTargets Ther.* **2017**, *10*, 3685–3696. [[CrossRef](#)] [[PubMed](#)]
218. Xu, Q.; Liu, M.; Zhang, J.; Xue, L.; Zhang, G.; Hu, C.; Wang, Z.; He, S.; Chen, L.; Ma, K.; et al. Overexpression of KLF4 promotes cell senescence through microRNA-203-survivin-p21 pathway. *Oncotarget* **2016**, *7*, 60290–60302. [[CrossRef](#)] [[PubMed](#)]
219. Takano, Y.; Masuda, T.; Iinuma, H.; Yamaguchi, R.; Sato, K.; Tobo, T.; Hirata, H.; Kuroda, Y.; Nambara, S.; Hayashi, N.; et al. Circulating exosomal microRNA-203 is associated with metastasis possibly via inducing tumor-associated macrophages in colorectal cancer. *Oncotarget* **2017**, *8*, 78598–78613. [[CrossRef](#)] [[PubMed](#)]
220. Shen, B.; Yuan, Y.; Zhang, Y.; Yu, S.; Peng, W.; Huang, X.; Feng, J. Long non-coding RNA FBXL19-AS1 plays oncogenic role in colorectal cancer by sponging miR-203. *Biochem. Biophys. Res. Commun.* **2017**, *488*, 67–73. [[CrossRef](#)] [[PubMed](#)]
221. Kingham, T.P.; Nguyen, H.C.B.; Zheng, J.; Konstantinidis, I.T.; Sadot, E.; Shia, J.; Kuk, D.; Zhang, S.; Saltz, L.; D'Angelica, M.I.; et al. MicroRNA-203 predicts human survival after resection of colorectal liver metastasis. *Oncotarget* **2017**, *8*, 18821–18831. [[CrossRef](#)] [[PubMed](#)]
222. Fu, Q.; Zhang, J.; Xu, X.; Qian, F.; Feng, K.; Ma, J. miR-203 is a predictive biomarker for colorectal cancer and its expression is associated with BIRC5. *Tumour Biol.* **2016**. [[CrossRef](#)] [[PubMed](#)]
223. Yin, Y.; Zhang, B.; Wang, W.; Fei, B.; Quan, C.; Zhang, J.; Song, M.; Bian, Z.; Wang, Q.; Ni, S.; et al. miR-204-5p inhibits proliferation and invasion and enhances chemotherapeutic sensitivity of colorectal cancer cells by downregulating RAB22A. *Clin. Cancer Res.* **2014**, *20*, 6187–6199. [[CrossRef](#)] [[PubMed](#)]

224. Wu, H.; Liang, Y.; Shen, L. MicroRNA-204 modulates colorectal cancer cell sensitivity in response to 5-fluorouracil-based treatment by targeting high mobility group protein A2. *Biol. Open* **2016**, *5*, 563–570. [[CrossRef](#)] [[PubMed](#)]
225. Sumbul, A.T.; Gogebakan, B.; Ergun, S.; Yengil, E.; Batmaci, C.Y.; Tonyali, O.; Yaldiz, M. miR-204-5p expression in colorectal cancer: An autophagy-associated gene. *Tumour Biol.* **2014**, *35*, 12713–12719. [[CrossRef](#)] [[PubMed](#)]
226. Shuai, F.; Wang, B.; Dong, S. microRNA-204 inhibits the growth and motility of colorectal cancer cells by downregulation of CXCL8. *Oncol. Res.* **2018**, *5*, 1295–1305. [[CrossRef](#)] [[PubMed](#)]
227. Wang, G.; Bu, X.; Zhang, Y.; Zhao, X.; Kong, Y.; Ma, L.; Niu, S.; Wu, B.; Meng, C. LncRNA-UCA1 enhances MMP-13 expression by inhibiting miR-204-5p in human chondrocytes. *Oncotarget* **2017**, *8*, 91281–91290. [[CrossRef](#)] [[PubMed](#)]
228. Wang, X.; Yang, B.; Ma, B. The UCA1/miR-204/Sirt1 axis modulates docetaxel sensitivity of prostate cancer cells. *Cancer Chemother. Pharmacol.* **2016**, *78*, 1025–1031. [[CrossRef](#)] [[PubMed](#)]
229. Jiao, C.; Song, Z.; Chen, J.; Zhong, J.; Cai, W.; Tian, S.; Chen, S.; Yi, Y.; Xiao, Y. lncRNA-UCA1 enhances cell proliferation through functioning as a ceRNA of Sox4 in esophageal cancer. *Oncol. Rep.* **2016**, *36*, 2960–2966. [[CrossRef](#)] [[PubMed](#)]
230. Li, D.; Cui, C.; Chen, J.; Hu, Z.; Wang, Y.; Hu, D. Long noncoding RNA UCA1 promotes papillary thyroid cancer cell proliferation via miR204mediated BRD4 activation. *Mol. Med. Rep.* **2018**, *18*, 3059–3067. [[CrossRef](#)] [[PubMed](#)]
231. Yan, Q.; Tian, Y.; Hao, F. Downregulation of lncRNA UCA1 inhibits proliferation and invasion of cervical cancer cells through miR-206 expression. *Oncol. Res.* **2018**. [[CrossRef](#)] [[PubMed](#)]
232. Wang, F.; Ying, H.Q.; He, B.S.; Pan, Y.Q.; Deng, Q.W.; Sun, H.L.; Chen, J.; Liu, X.; Wang, S.K. Upregulated lncRNA-UCA1 contributes to progression of hepatocellular carcinoma through inhibition of miR-216b and activation of FGFR1/ERK signaling pathway. *Oncotarget* **2015**, *6*, 7899–7917. [[CrossRef](#)] [[PubMed](#)]
233. Chen, X.; Liu, X.; He, B.; Pan, Y.; Sun, H.; Xu, T.; Hu, X.; Wang, S. MiR-216b functions as a tumor suppressor by targeting HMGB1-mediated JAK2/STAT3 signaling way in colorectal cancer. *Am. J. Cancer Res.* **2017**, *7*, 2051–2069. [[PubMed](#)]
234. Kim, S.Y.; Lee, Y.H.; Bae, Y.S. MiR-186, miR-216b, miR-337-3p, and miR-760 cooperatively induce cellular senescence by targeting alpha subunit of protein kinase CKII in human colorectal cancer cells. *Biochem. Biophys. Res. Commun.* **2012**, *429*, 173–179. [[CrossRef](#)] [[PubMed](#)]
235. Yao, Y.; Li, Q.; Wang, H. MiR-216b suppresses colorectal cancer proliferation, migration, and invasion by targeting SRPK1. *OncoTargets Ther.* **2018**, *11*, 1671–1681. [[CrossRef](#)] [[PubMed](#)]
236. Zou, J.; Kuang, W.; Hu, J.; Rao, H. miR-216b promotes cell growth and enhances chemosensitivity of colorectal cancer by suppressing PDZ-binding kinase. *Biochem. Biophys. Res. Commun.* **2017**, *488*, 247–252. [[CrossRef](#)] [[PubMed](#)]
237. Zhu, G.; Liu, X.; Su, Y.; Kong, F.; Hong, X.; Lin, Z. Knockdown of urothelial carcinoma associated 1 suppressed cell growth and migration through regulating miR-301a and CXCR4 in osteosarcoma MHCC97 cells. *Oncol. Res.* **2018**. [[CrossRef](#)] [[PubMed](#)]
238. Fang, Y.; Sun, B.; Xiang, J.; Chen, Z. MiR-301a promotes colorectal cancer cell growth and invasion by directly targeting SOCS6. *Cell Physiol. Biochem.* **2015**, *35*, 227–236. [[CrossRef](#)] [[PubMed](#)]
239. Ma, X.; Yan, F.; Deng, Q.; Li, F.; Lu, Z.; Liu, M.; Wang, L.; Conklin, D.J.; McCracken, J.; Srivastava, S.; et al. Modulation of tumorigenesis by the pro-inflammatory microRNA miR-301a in mouse models of lung cancer and colorectal cancer. *Cell Discov.* **2015**, *1*, 15005. [[CrossRef](#)] [[PubMed](#)]
240. Zhang, W.; Zhang, T.; Jin, R.; Zhao, H.; Hu, J.; Feng, B.; Zang, L.; Zheng, M.; Wang, M. MicroRNA-301a promotes migration and invasion by targeting TGFBR2 in human colorectal cancer. *J. Exp. Clin. Cancer Res.* **2014**, *33*, 113. [[CrossRef](#)] [[PubMed](#)]
241. Yang, Y.; Jiang, Y.; Wan, Y.; Zhang, L.; Qiu, J.; Zhou, S.; Cheng, W. UCA1 functions as a competing endogenous RNA to suppress epithelial ovarian cancer metastasis. *Tumour Biol.* **2016**, *37*, 10633–10641. [[CrossRef](#)] [[PubMed](#)]
242. Lu, Y.; Liu, W.-G.; Lu, J.-H.; Liu, Z.J.; Li, H.-B.; Liu, G.-J.; She, H.-Y.; Li, G.-Y.; Shi, X.-H. LncRNA UCA1 promotes renal cell carcinoma proliferation through epigenetically repressing p21 expression and negatively regulating miR-495. *Tumor Biol.* **2017**, *39*, 101042831770163. [[CrossRef](#)] [[PubMed](#)]

243. Bai, Z.; Wang, J.; Wang, T.; Li, Y.; Zhao, X.; Wu, G.; Yang, Y.; Deng, W.; Zhang, Z. The MiR-495/Annexin A3/P53 Axis Inhibits the Invasion and EMT of Colorectal Cancer Cells. *Cell Physiol. Biochem.* **2017**, *44*, 1882–1895. [[CrossRef](#)] [[PubMed](#)]
244. Chuang, A.Y.; Chuang, J.C.; Zhai, Z.; Wu, F.; Kwon, J.H. NOD2 expression is regulated by microRNAs in colonic epithelial HCT116 cells. *Inflamm. Bowel Dis.* **2014**, *20*, 126–135. [[CrossRef](#)] [[PubMed](#)]
245. Yan, L.; Yao, J.; Qiu, J. miRNA-495 suppresses proliferation and migration of colorectal cancer cells by targeting FAM83D. *Biomed. Pharmacother.* **2017**, *96*, 974–981. [[CrossRef](#)] [[PubMed](#)]
246. Guo, S.; Yang, P.; Jiang, X.; Li, X.; Wang, Y.; Zhang, X.; Sun, B.; Zhang, Y.; Jia, Y. Genetic and epigenetic silencing of mircoRNA-506-3p enhances COTL1 oncogene expression to foster non-small lung cancer progression. *Oncotarget* **2017**, *8*, 644–657. [[CrossRef](#)] [[PubMed](#)]
247. Chen, Z.; Liu, S.; Tian, L.; Wu, M.; Ai, F.; Tang, W.; Zhao, L.; Ding, J.; Zhang, L.; Tang, A. miR-124 and miR-506 inhibit colorectal cancer progression by targeting DNMT3B and DNMT1. *Oncotarget* **2015**, *6*, 38139–38150. [[CrossRef](#)] [[PubMed](#)]
248. Krawczyk, P.; Powrozek, T.; Olesinski, T.; Dmitruk, A.; Dziwota, J.; Kowalski, D.; Milanowski, J. Evaluation of miR-506 and miR-4316 expression in early and non-invasive diagnosis of colorectal cancer. *Int. J. Colorectal Dis.* **2017**, *32*, 1057–1060. [[CrossRef](#)] [[PubMed](#)]
249. Tong, J.L.; Zhang, C.P.; Nie, F.; Xu, X.T.; Zhu, M.M.; Xiao, S.D.; Ran, Z.H. MicroRNA 506 regulates expression of PPAR alpha in hydroxycamptothecin-resistant human colon cancer cells. *FEBS Lett.* **2011**, *585*, 3560–3568. [[CrossRef](#)] [[PubMed](#)]
250. Wu, M.; Zhang, Y.; Tang, A.; Tian, L. miR-506 inhibits cell proliferation and invasion by targeting TET family in colorectal cancer. *Iran J. Basic Med. Sci.* **2016**, *19*, 316–322. [[PubMed](#)]
251. Zhang, Y.; Lin, C.; Liao, G.; Liu, S.; Ding, J.; Tang, F.; Wang, Z.; Liang, X.; Li, B.; Wei, Y.; et al. MicroRNA-506 suppresses tumor proliferation and metastasis in colon cancer by directly targeting the oncogene EZH2. *Oncotarget* **2015**, *6*, 32586–32601. [[CrossRef](#)] [[PubMed](#)]
252. Zhou, H.; Lin, C.; Zhang, Y.; Zhang, X.; Zhang, C.; Zhang, P.; Xie, X.; Ren, Z. miR-506 enhances the sensitivity of human colorectal cancer cells to oxaliplatin by suppressing MDR1/P-gp expression. *Cell Prolif.* **2017**, *50*, e12341. [[CrossRef](#)] [[PubMed](#)]
253. Zu, C.; Liu, T.; Zhang, G. MicroRNA-506 Inhibits Malignancy of Colorectal Carcinoma Cells by Targeting LAMC1. *Ann. Clin. Lab. Sci.* **2016**, *46*, 666–674. [[PubMed](#)]
254. Wei, Y.; Sun, Q.; Zhao, L.; Wu, J.; Chen, X.; Wang, Y.; Zang, W.; Zhao, G. LncRNA UCA1-miR-507-FOXM1 axis is involved in cell proliferation, invasion and G0/G1 cell cycle arrest in melanoma. *Med. Oncol.* **2016**, *33*. [[CrossRef](#)] [[PubMed](#)]
255. Gu, L.; Lu, L.-S.; Zhou, D.-L.; Liu, Z.-C. UCA1 promotes cell proliferation and invasion of gastric cancer by targeting CREB1 sponging to miR-590-3p. *Cancer Med.* **2018**. [[CrossRef](#)] [[PubMed](#)]
256. Kim, C.W.; Oh, E.T.; Kim, J.M.; Park, J.S.; Lee, D.H.; Lee, J.S.; Kim, K.K.; Park, H.J. Hypoxia-induced microRNA-590-5p promotes colorectal cancer progression by modulating matrix metalloproteinase activity. *Cancer Lett.* **2018**, *416*, 31–41. [[CrossRef](#)] [[PubMed](#)]
257. Ou, C.; Sun, Z.; Li, X.; Ren, W.; Qin, Z.; Zhang, X.; Yuan, W.; Wang, J.; Yu, W.; Zhang, S.; et al. MiR-590-5p, a density-sensitive microRNA, inhibits tumorigenesis by targeting YAP1 in colorectal cancer. *Cancer Lett.* **2017**, *399*, 53–63. [[CrossRef](#)] [[PubMed](#)]
258. Sun, Z.Q.; Shi, K.; Zhou, Q.B.; Zeng, X.Y.; Liu, J.; Yang, S.X.; Wang, Q.S.; Li, Z.; Wang, G.X.; Song, J.M.; et al. MiR-590-3p promotes proliferation and metastasis of colorectal cancer via Hippo pathway. *Oncotarget* **2017**, *8*, 58061–58071. [[CrossRef](#)] [[PubMed](#)]
259. Zhou, Q.; Zhu, Y.; Wei, X.; Zhou, J.; Chang, L.; Sui, H.; Han, Y.; Piao, D.; Sha, R.; Bai, Y. MiR-590-5p inhibits colorectal cancer angiogenesis and metastasis by regulating nuclear factor 90/vascular endothelial growth factor A axis. *Cell Death Dis.* **2016**, *7*, e2413. [[CrossRef](#)] [[PubMed](#)]
260. Alvarez-Diaz, S.; Valle, N.; Ferrer-Mayorga, G.; Lombardia, L.; Herrera, M.; Dominguez, O.; Segura, M.F.; Bonilla, F.; Hernando, E.; Munoz, A. MicroRNA-22 is induced by vitamin D and contributes to its antiproliferative, antimigratory and gene regulatory effects in colon cancer cells. *Hum. Mol. Genet.* **2012**, *21*, 2157–2165. [[CrossRef](#)] [[PubMed](#)]
261. Li, B.; Song, Y.; Liu, T.J.; Cui, Y.B.; Jiang, Y.; Xie, Z.S.; Xie, S.L. miRNA-22 suppresses colon cancer cell migration and invasion by inhibiting the expression of T-cell lymphoma invasion and metastasis 1 and matrix metalloproteinases 2 and 9. *Oncol. Rep.* **2013**, *29*, 1932–1938. [[CrossRef](#)] [[PubMed](#)]

262. Li, B.; Sun, H.; Zhang, H. The predicted target gene validation, function, and prognosis studies of miRNA-22 in colorectal cancer tissue. *Tumour Biol.* **2017**, *39*, 1010428317692257. [[CrossRef](#)] [[PubMed](#)]
263. Li, J.; Zhang, Y.; Zhao, J.; Kong, F.; Chen, Y. Overexpression of miR-22 reverses paclitaxel-induced chemoresistance through activation of PTEN signaling in p53-mutated colon cancer cells. *Mol. Cell. Biochem.* **2011**, *357*, 31–38. [[CrossRef](#)] [[PubMed](#)]
264. Liu, Y.; Chen, X.; Cheng, R.; Yang, F.; Yu, M.; Wang, C.; Cui, S.; Hong, Y.; Liang, H.; Liu, M.; et al. The Jun/miR-22/HuR regulatory axis contributes to tumorigenesis in colorectal cancer. *Mol. Cancer* **2018**, *17*, 11. [[CrossRef](#)] [[PubMed](#)]
265. Tang, Y.; Liu, X.; Su, B.; Zhang, Z.; Zeng, X.; Lei, Y.; Shan, J.; Wu, Y.; Tang, H.; Su, Q. microRNA-22 acts as a metastasis suppressor by targeting metadherin in gastric cancer. *Mol. Med. Rep.* **2015**, *11*, 454–460. [[CrossRef](#)] [[PubMed](#)]
266. Tsuchiya, N.; Izumiya, M.; Ogata-Kawata, H.; Okamoto, K.; Fujiwara, Y.; Nakai, M.; Okabe, A.; Schetter, A.J.; Bowman, E.D.; Midorikawa, Y.; et al. Tumor suppressor miR-22 determines p53-dependent cellular fate through post-transcriptional regulation of p21. *Cancer Res.* **2011**, *71*, 4628–4639. [[CrossRef](#)] [[PubMed](#)]
267. Xia, S.S.; Zhang, G.J.; Liu, Z.L.; Tian, H.P.; He, Y.; Meng, C.Y.; Li, L.F.; Wang, Z.W.; Zhou, T. MicroRNA-22 suppresses the growth, migration and invasion of colorectal cancer cells through a Sp1 negative feedback loop. *Oncotarget* **2017**, *8*, 36266–36278. [[CrossRef](#)] [[PubMed](#)]
268. Yamakuchi, M.; Yagi, S.; Ito, T.; Lowenstein, C.J. MicroRNA-22 regulates hypoxia signaling in colon cancer cells. *PLoS ONE* **2011**, *6*, e20291. [[CrossRef](#)] [[PubMed](#)]
269. Yang, F.; Hu, Y.; Liu, H.X.; Wan, Y.J. MiR-22-silenced cyclin A expression in colon and liver cancer cells is regulated by bile acid receptor. *J. Biol. Chem.* **2015**, *290*, 6507–6515. [[CrossRef](#)] [[PubMed](#)]
270. Zhang, G.; Xia, S.; Tian, H.; Liu, Z.; Zhou, T. Clinical significance of miR-22 expression in patients with colorectal cancer. *Med. Oncol.* **2012**, *29*, 3108–3112. [[CrossRef](#)] [[PubMed](#)]
271. Zhang, H.; Tang, J.; Li, C.; Kong, J.; Wang, J.; Wu, Y.; Xu, E.; Lai, M. MiR-22 regulates 5-FU sensitivity by inhibiting autophagy and promoting apoptosis in colorectal cancer cells. *Cancer Lett.* **2015**, *356*, 781–790. [[CrossRef](#)] [[PubMed](#)]
272. Jahid, S.; Sun, J.; Edwards, R.A.; Dizon, D.; Panarelli, N.C.; Milsom, J.W.; Sikandar, S.S.; Gumus, Z.H.; Lipkin, S.M. miR-23a promotes the transition from indolent to invasive colorectal cancer. *Cancer Discov.* **2012**, *2*, 540–553. [[CrossRef](#)] [[PubMed](#)]
273. Li, X.; Liao, D.; Wang, X.; Wu, Z.; Nie, J.; Bai, M.; Fu, X.; Mei, Q.; Han, W. Elevated microRNA-23a Expression Enhances the Chemoresistance of Colorectal Cancer Cells with Microsatellite Instability to 5-Fluorouracil by Directly Targeting ABCF1. *Curr. Protein Pept. Sci.* **2015**, *16*, 301–309. [[CrossRef](#)] [[PubMed](#)]
274. Shang, J.; Yang, F.; Wang, Y.; Xue, G.; Mei, Q.; Wang, F.; Sun, S. MicroRNA-23a antisense enhances 5-fluorouracil chemosensitivity through APAF-1/caspase-9 apoptotic pathway in colorectal cancer cells. *J. Cell. Biochem.* **2014**, *115*, 772–784. [[CrossRef](#)] [[PubMed](#)]
275. Tang, H.L.; Deng, M.; Liao, Q.J.; Zeng, X.; Zhou, X.T.; Su, Q. Expression and clinical significance of miR-23a and metastasis suppressor 1 in colon carcinoma. *Zhonghua Bing Li Xue Za Zhi* **2012**, *41*, 28–32. [[PubMed](#)]
276. Wang, Z.; Wei, W.; Sarkar, F.H. miR-23a, a critical regulator of “migR”ation and metastasis in colorectal cancer. *Cancer Discov.* **2012**, *2*, 489–491. [[CrossRef](#)] [[PubMed](#)]
277. Yong, F.L.; Law, C.W.; Wang, C.W. Potentiality of a triple microRNA classifier: miR-193a-3p, miR-23a and miR-338-5p for early detection of colorectal cancer. *BMC Cancer* **2013**, *13*, 280. [[CrossRef](#)] [[PubMed](#)]
278. Yong, F.L.; Wang, C.W.; Roslani, A.C.; Law, C.W. The involvement of miR-23a/APAF1 regulation axis in colorectal cancer. *Int. J. Mol. Sci.* **2014**, *15*, 11713–11729. [[CrossRef](#)] [[PubMed](#)]
279. Chen, B.; Liu, Y.; Jin, X.; Lu, W.; Liu, J.; Xia, Z.; Yuan, Q.; Zhao, X.; Xu, N.; Liang, S. MicroRNA-26a regulates glucose metabolism by direct targeting PDHX in colorectal cancer cells. *BMC Cancer* **2014**, *14*, 1471–2407. [[CrossRef](#)] [[PubMed](#)]
280. Fu, X.; Meng, Z.; Liang, W.; Tian, Y.; Wang, X.; Han, W.; Lou, G.; Lou, F.; Yen, Y.; Yu, H.; et al. miR-26a enhances miRNA biogenesis by targeting Lin28B and Zcchc11 to suppress tumor growth and metastasis. *Oncogene* **2014**, *33*, 4296–4306. [[CrossRef](#)] [[PubMed](#)]
281. Ghanbari, R.; Mosakhani, N.; Asadi, J.; Nouraei, N.; Mowla, S.J.; Yazdani, Y.; Mohamadkhani, A.; Poustchi, H.; Knuutila, S.; Malekzadeh, R. Downregulation of Plasma MiR-142-3p and MiR-26a-5p in Patients With Colorectal Carcinoma. *Iran J. Cancer Prev.* **2015**, *8*, 22. [[CrossRef](#)] [[PubMed](#)]

282. Ghanbari, R.; Rezasoltani, S.; Hashemi, J.; Mohamadkhani, A.; Tahmasebifar, A.; Arefian, E.; Mobarra, N.; Asadi, J.; Nazemalhosseini Mojarad, E.; Yazdani, Y.; et al. Expression Analysis of Previously Verified Fecal and Plasma Down-regulated MicroRNAs (miR-4478, 1295-3p, 142-3p and 26a-5p), in FFPE Tissue Samples of CRC Patients. *Arch. Iran Med.* **2017**, *20*, 92–95. [[PubMed](#)]
283. Konishi, H.; Fujiya, M.; Ueno, N.; Moriichi, K.; Sasajima, J.; Ikuta, K.; Tanabe, H.; Tanaka, H.; Kohgo, Y. microRNA-26a and -584 inhibit the colorectal cancer progression through inhibition of the binding of hnRNP A1-CDK6 mRNA. *Biochem. Biophys. Res. Commun.* **2015**, *467*, 847–852. [[CrossRef](#)] [[PubMed](#)]
284. Li, Y.; Sun, Z.; Liu, B.; Shan, Y.; Zhao, L.; Jia, L. Tumor-suppressive miR-26a and miR-26b inhibit cell aggressiveness by regulating FUT4 in colorectal cancer. *Cell Death Dis.* **2017**, *8*, 281. [[CrossRef](#)] [[PubMed](#)]
285. Lopez-Urrutia, E.; Coronel-Hernandez, J.; Garcia-Castillo, V.; Contreras-Romero, C.; Martinez-Gutierrez, A.; Estrada-Galicia, D.; Terrazas, L.I.; Lopez-Camarillo, C.; Maldonado-Martinez, H.; Jacobo-Herrera, N.; et al. MiR-26a downregulates retinoblastoma in colorectal cancer. *Tumour Biol.* **2017**, *39*, 1010428317695945. [[CrossRef](#)] [[PubMed](#)]
286. Ying, H.Q.; Peng, H.X.; He, B.S.; Pan, Y.Q.; Wang, F.; Sun, H.L.; Liu, X.; Chen, J.; Lin, K.; Wang, S.K. MiR-608, pre-miR-124-1 and pre-miR26a-1 polymorphisms modify susceptibility and recurrence-free survival in surgically resected CRC individuals. *Oncotarget* **2016**, *7*, 75865–75873. [[CrossRef](#)] [[PubMed](#)]
287. Zeitels, L.R.; Acharya, A.; Shi, G.; Chivukula, D.; Chivukula, R.R.; Anandam, J.L.; Abdelnaby, A.A.; Balch, G.C.; Mansour, J.C.; Yopp, A.C.; et al. Tumor suppression by miR-26 overrides potential oncogenic activity in intestinal tumorigenesis. *Genes Dev.* **2014**, *28*, 2585–2590. [[CrossRef](#)] [[PubMed](#)]
288. Fasihi, A.; Soltani, B.; Atashi, A.; Nasiri, S. Introduction of hsa-miR-103a and hsa-miR-1827 and hsa-miR-137 as new regulators of Wnt signaling pathway and their relation to colorectal carcinoma. *J. Cell. Biochem.* **2017**, *119*, 5104–5117. [[CrossRef](#)] [[PubMed](#)]
289. Chen, H.Y.; Lin, Y.M.; Chung, H.C.; Lang, Y.D.; Lin, C.J.; Huang, J.; Wang, W.C.; Lin, F.M.; Chen, Z.; Huang, H.D.; et al. miR-103/107 promote metastasis of colorectal cancer by targeting the metastasis suppressors DAPK and KLF4. *Cancer Res.* **2012**, *72*, 3631–3641. [[CrossRef](#)] [[PubMed](#)]
290. Liu, F.; Liu, S.; Ai, F.; Zhang, D.; Xiao, Z.; Nie, X.; Fu, Y. miR-107 Promotes Proliferation and Inhibits Apoptosis of Colon Cancer Cells by Targeting Prostate Apoptosis Response-4 (Par4). *Oncol. Res.* **2017**, *25*, 967–974. [[CrossRef](#)] [[PubMed](#)]
291. Molina-Pinelo, S.; Carnero, A.; Rivera, F.; Estevez-Garcia, P.; Bozada, J.M.; Limon, M.L.; Benavent, M.; Gomez, J.; Pastor, M.D.; Chaves, M.; et al. MiR-107 and miR-99a-3p predict chemotherapy response in patients with advanced colorectal cancer. *BMC Cancer* **2014**, *14*, 1471–2407. [[CrossRef](#)] [[PubMed](#)]
292. Deng, G.; Kakar, S.; Kim, Y.S. MicroRNA-124a and microRNA-34b/c are frequently methylated in all histological types of colorectal cancer and polyps, and in the adjacent normal mucosa. *Oncol. Lett.* **2011**, *2*, 175–180. [[CrossRef](#)] [[PubMed](#)]
293. Gao, X.R.; Wang, H.P.; Zhang, S.L.; Wang, M.X.; Zhu, Z.S. Pri-miR-124 rs531564 polymorphism and colorectal cancer risk. *Sci. Rep.* **2015**, *5*, 14818. [[CrossRef](#)] [[PubMed](#)]
294. Jinushi, T.; Shibayama, Y.; Kinoshita, I.; Oizumi, S.; Jinushi, M.; Aota, T.; Takahashi, T.; Horita, S.; Dosaka-Akita, H.; Iseki, K. Low expression levels of microRNA-124-5p correlated with poor prognosis in colorectal cancer via targeting of SMC4. *Cancer Med.* **2014**, *3*, 1544–1552. [[CrossRef](#)] [[PubMed](#)]
295. Lin, S.M.; Xia, Q.; Zhang, Y.Q.; Sun, A.M.; Shi, Y.S.; Zheng, L.; Chen, L.H. miR-124 regulates radiosensitivity of colorectal cancer cells by targeting PRRX1. *Nan Fang Yi Ke Da Xue Xue Bao* **2016**, *36*, 1110–1116. [[PubMed](#)]
296. Liu, K.; Chen, W.; Lei, S.; Xiong, L.; Zhao, H.; Liang, D.; Lei, Z.; Zhou, N.; Yao, H.; Liang, Y. Wild-type and mutant p53 differentially modulate miR-124/iASPP feedback following photodynamic therapy in human colon cancer cell line. *Cell Death Dis.* **2017**, *8*, e3096. [[CrossRef](#)] [[PubMed](#)]
297. Liu, K.; Yao, H.; Lei, S.; Xiong, L.; Qi, H.; Qian, K.; Liu, J.; Wang, P.; Zhao, H. The miR-124-p63 feedback loop modulates colorectal cancer growth. *Oncotarget* **2017**, *8*, 29101–29115. [[CrossRef](#)] [[PubMed](#)]
298. Liu, K.; Zhao, H.; Yao, H.; Lei, S.; Lei, Z.; Li, T.; Qi, H. MicroRNA-124 regulates the proliferation of colorectal cancer cells by targeting iASPP. *Biomed. Res. Int.* **2013**, *2013*, 867537. [[PubMed](#)]
299. Park, S.Y.; Kim, H.; Yoon, S.; Bae, J.A.; Choi, S.Y.; Jung, Y.D.; Kim, K.K. KITENIN-targeting microRNA-124 suppresses colorectal cancer cell motility and tumorigenesis. *Mol. Ther.* **2014**, *22*, 1653–1664. [[CrossRef](#)] [[PubMed](#)]

300. Sun, Y.; Zhao, X.; Luo, M.; Zhou, Y.; Ren, W.; Wu, K.; Li, X.; Shen, J.; Hu, Y. The pro-apoptotic role of the regulatory feedback loop between miR-124 and PKM1/HNF4alpha in colorectal cancer cells. *Int. J. Mol. Sci.* **2014**, *15*, 4318–4332. [[CrossRef](#)] [[PubMed](#)]
301. Sun, Y.; Zhao, X.; Zhou, Y.; Hu, Y. miR-124, miR-137 and miR-340 regulate colorectal cancer growth via inhibition of the Warburg effect. *Oncol. Rep.* **2012**, *28*, 1346–1352. [[CrossRef](#)] [[PubMed](#)]
302. Taniguchi, K.; Sugito, N.; Kumazaki, M.; Shinohara, H.; Yamada, N.; Matsushashi, N.; Futamura, M.; Ito, Y.; Otsuki, Y.; Yoshida, K.; et al. Positive feedback of DDX6/c-Myc/PTB1 regulated by miR-124 contributes to maintenance of the Warburg effect in colon cancer cells. *Biochim. Biophys. Acta* **2015**, *1852*, 1971–1980. [[CrossRef](#)] [[PubMed](#)]
303. Taniguchi, K.; Sugito, N.; Kumazaki, M.; Shinohara, H.; Yamada, N.; Nakagawa, Y.; Ito, Y.; Otsuki, Y.; Uno, B.; Uchiyama, K.; et al. MicroRNA-124 inhibits cancer cell growth through PTB1/PKM1/PKM2 feedback cascade in colorectal cancer. *Cancer Lett.* **2015**, *363*, 17–27. [[CrossRef](#)] [[PubMed](#)]
304. Ueda, Y.; Ando, T.; Nanjo, S.; Ushijima, T.; Sugiyama, T. DNA methylation of microRNA-124a is a potential risk marker of colitis-associated cancer in patients with ulcerative colitis. *Dig. Dis. Sci.* **2014**, *59*, 2444–2451. [[CrossRef](#)] [[PubMed](#)]
305. Wang, M.J.; Li, Y.; Wang, R.; Wang, C.; Yu, Y.Y.; Yang, L.; Zhang, Y.; Zhou, B.; Zhou, Z.G.; Sun, X.F. Downregulation of microRNA-124 is an independent prognostic factor in patients with colorectal cancer. *Int. J. Color. Dis.* **2013**, *28*, 183–189. [[CrossRef](#)] [[PubMed](#)]
306. Xi, Z.W.; Xin, S.Y.; Zhou, L.Q.; Yuan, H.X.; Wang, Q.; Chen, K.X. Downregulation of rho-associated protein kinase 1 by miR-124 in colorectal cancer. *World J. Gastroenterol.* **2015**, *21*, 5454–5464. [[CrossRef](#)] [[PubMed](#)]
307. Zhang, J.; Lu, Y.; Yue, X.; Li, H.; Luo, X.; Wang, Y.; Wang, K.; Wan, J. MiR-124 suppresses growth of human colorectal cancer by inhibiting STAT3. *PLoS ONE* **2013**, *8*, e70300. [[CrossRef](#)] [[PubMed](#)]
308. Zhou, L.; Xu, Z.; Ren, X.; Chen, K.; Xin, S. MicroRNA-124 (MiR-124) Inhibits Cell Proliferation, Metastasis and Invasion in Colorectal Cancer by Downregulating Rho-Associated Protein Kinase 1(ROCK1). *Cell Physiol. Biochem.* **2016**, *38*, 1785–1795. [[CrossRef](#)] [[PubMed](#)]
309. Cristobal, I.; Torrejon, B.; Gonzalez-Alonso, P.; Manso, R.; Rojo, F.; Garcia-Foncillas, J. Downregulation of miR-138 as a Contributing Mechanism to Lcn-2 Overexpression in Colorectal Cancer with Liver Metastasis. *World J. Surg.* **2016**, *40*, 1021–1022. [[CrossRef](#)] [[PubMed](#)]
310. Long, L.; Huang, G.; Zhu, H.; Guo, Y.; Liu, Y.; Huo, J. Down-regulation of miR-138 promotes colorectal cancer metastasis via directly targeting TWIST2. *J. Transl. Med.* **2013**, *11*, 1479–5876. [[CrossRef](#)] [[PubMed](#)]
311. Pang, L.; Li, B.; Zheng, B.; Niu, L.; Ge, L. miR-138 inhibits gastric cancer growth by suppressing SOX4. *Oncol. Rep.* **2017**, *38*, 1295–1302. [[CrossRef](#)] [[PubMed](#)]
312. Yang, Q.; Wang, X.; Tang, C.; Chen, X.; He, J. H19 promotes the migration and invasion of colon cancer by sponging miR-138 to upregulate the expression of HMGA1. *Int. J. Oncol.* **2017**. [[CrossRef](#)] [[PubMed](#)]
313. Zhang, X.L.; Xu, L.L.; Wang, F. Hsa_circ_0020397 regulates colorectal cancer cell viability, apoptosis and invasion by promoting the expression of the miR-138 targets TERT and PD-L1. *Cell Biol. Int.* **2017**, *41*, 1056–1064. [[CrossRef](#)] [[PubMed](#)]
314. Zhao, L.; Yu, H.; Yi, S.; Peng, X.; Su, P.; Xiao, Z.; Liu, R.; Tang, A.; Li, X.; Liu, F.; et al. The tumor suppressor miR-138-5p targets PD-L1 in colorectal cancer. *Oncotarget* **2016**, *7*, 45370–45384. [[CrossRef](#)] [[PubMed](#)]
315. Chandrasekaran, K.S.; Sathyanarayanan, A.; Karunagar, D. MicroRNA-214 suppresses growth, migration and invasion through a novel target, high mobility group AT-hook 1, in human cervical and colorectal cancer cells. *Br. J. Cancer* **2016**, *115*, 741–751. [[CrossRef](#)] [[PubMed](#)]
316. Cristobal, I.; Carames, C.; Madoz-Gurpide, J.; Rojo, F.; Aguilera, O.; Garcia-Foncillas, J. Downregulation of miR-214 is specific of liver metastasis in colorectal cancer and could play a role determining the metastatic niche. *Int. J. Color. Dis.* **2014**, *29*, 885. [[CrossRef](#)] [[PubMed](#)]
317. He, G.Y.; Hu, J.L.; Zhou, L.; Zhu, X.H.; Xin, S.N.; Zhang, D.; Lu, G.F.; Liao, W.T.; Ding, Y.Q.; Liang, L. The FOXD3/miR-214/MED19 axis suppresses tumour growth and metastasis in human colorectal cancer. *Br. J. Cancer* **2016**, *115*, 1367–1378. [[CrossRef](#)] [[PubMed](#)]
318. Hu, J.L.; He, G.Y.; Lan, X.L.; Zeng, Z.C.; Guan, J.; Ding, Y.; Qian, X.L.; Liao, W.T.; Ding, Y.Q.; Liang, L. Inhibition of ATG12-mediated autophagy by miR-214 enhances radiosensitivity in colorectal cancer. *Oncogenesis* **2018**, *7*, 16. [[CrossRef](#)] [[PubMed](#)]
319. Zhou, Y.; Hong, L. Prediction value of miR-483 and miR-214 in prognosis and multidrug resistance of esophageal squamous cell carcinoma. *Genet. Test. Mol. Biomarkers* **2013**, *17*, 470–474. [[CrossRef](#)] [[PubMed](#)]

320. Chai, J.; Guo, D.; Ma, W.; Han, D.; Dong, W.; Guo, H.; Zhang, Y. A feedback loop consisting of RUNX2/LncRNA-PVT1/miR-455 is involved in the progression of colorectal cancer. *Am. J. Cancer Res.* **2018**, *8*, 538–550. [[PubMed](#)]
321. Chai, J.; Wang, S.; Han, D.; Dong, W.; Xie, C.; Guo, H. MicroRNA-455 inhibits proliferation and invasion of colorectal cancer by targeting RAF proto-oncogene serine/threonine-protein kinase. *Tumour Biol.* **2015**, *36*, 1313–1321. [[CrossRef](#)] [[PubMed](#)]
322. Mao, Q.D.; Zhang, W.; Zhao, K.; Cao, B.; Yuan, H.; Wei, L.Z.; Song, M.Q.; Liu, X.S. MicroRNA-455 suppresses the oncogenic function of HDAC2 in human colorectal cancer. *Braz. J. Med. Biol. Res.* **2017**, *50*. [[CrossRef](#)] [[PubMed](#)]
323. Yunqi, H.; Fangrui, Y.; Yongyan, Y.; Yunjian, J.; Wenhui, Z.; Kun, C.; Min, L.; Xianfeng, L.; Caixia, B. MiR-455 functions as a tumor suppressor through targeting GATA6 in colorectal cancer. *Oncol. Res.* **2018**, *3*. [[CrossRef](#)] [[PubMed](#)]
324. Zheng, J.; Lin, Z.; Zhang, L.; Chen, H. MicroRNA-455-3p Inhibits Tumor Cell Proliferation and Induces Apoptosis in HCT116 Human Colon Cancer Cells. *Med. Sci. Monit.* **2016**, *22*, 4431–4437. [[CrossRef](#)] [[PubMed](#)]
325. Su, E.C.-Y.; Chen, Y.-S.; Tien, Y.-C.; Liu, J.; Ho, B.-C.; Yu, S.-L.; Singh, S. ChemiRs: A web application for microRNAs and chemicals. *BMC Bioinform.* **2016**, *17*. [[CrossRef](#)] [[PubMed](#)]
326. Mi, H.; Huang, X.; Muruganujan, A.; Tang, H.; Mills, C.; Kang, D.; Thomas, P.D. PANTHER version 11: Expanded annotation data from Gene Ontology and Reactome pathways, and data analysis tool enhancements. *Nucleic Acids Res.* **2017**, *45*, D183–D189. [[CrossRef](#)] [[PubMed](#)]
327. Fan, Y.; Shen, B.; Tan, M.; Mu, X.; Qin, Y.; Zhang, F.; Liu, Y. Long non-coding RNA UCA1 increases chemoresistance of bladder cancer cells by regulating Wnt signaling. *FEBS J.* **2014**, *281*, 1750–1758. [[CrossRef](#)] [[PubMed](#)]
328. Liu, H.; Wang, G.; Yang, L.; Qu, J.; Yang, Z.; Zhou, X. Knockdown of Long Non-Coding RNA UCA1 Increases the Tamoxifen Sensitivity of Breast Cancer Cells through Inhibition of Wnt/beta-Catenin Pathway. *PLoS ONE* **2016**, *11*, e0168406. [[CrossRef](#)] [[PubMed](#)]
329. Yang, Y.T.; Wang, Y.F.; Lai, J.Y.; Shen, S.Y.; Wang, F.; Kong, J.; Zhang, W.; Yang, H.Y. Long non-coding RNA UCA1 contributes to the progression of oral squamous cell carcinoma by regulating the WNT/beta-catenin signaling pathway. *Cancer Sci.* **2016**, *107*, 1581–1589. [[CrossRef](#)] [[PubMed](#)]
330. Xiao, C.; Wu, C.H.; Hu, H.Z. LncRNA UCA1 promotes epithelial-mesenchymal transition (EMT) of breast cancer cells via enhancing Wnt/beta-catenin signaling pathway. *Eur. Rev. Med. Pharmacol. Sci.* **2016**, *20*, 2819–2824. [[PubMed](#)]
331. He, L.; Zhu, H.; Zhou, S.; Wu, T.; Wu, H.; Yang, H.; Mao, H.; SekharKathera, C.; Janardhan, A.; Edick, A.M.; et al. Wnt pathway is involved in 5-FU drug resistance of colorectal cancer cells. *Exp. Mol. Med.* **2018**, *50*. [[CrossRef](#)] [[PubMed](#)]
332. Bian, Z.; Zhang, J.; Li, M.; Feng, Y.; Yao, S.; Song, M.; Qi, X.; Fei, B.; Yin, Y.; Hua, D.; et al. Long non-coding RNA LINC00152 promotes cell proliferation, metastasis, and confers 5-FU resistance in colorectal cancer by inhibiting miR-139-5p. *Oncogenesis* **2017**, *6*. [[CrossRef](#)] [[PubMed](#)]
333. Li, C.; Liang, G.; Yang, S.; Sui, J.; Yao, W.; Shen, X.; Zhang, Y.; Peng, H.; Hong, W.; Xu, S.; et al. Dysregulated lncRNA-UCA1 contributes to the progression of gastric cancer through regulation of the PI3K-Akt-mTOR signaling pathway. *Oncotarget* **2017**, *8*, 93476. [[PubMed](#)]
334. Xu, Y.; Yao, Y.; Leng, K.; Li, Z.; Qin, W.; Zhong, X.; Kang, P.; Wan, M.; Jiang, X.; Cui, Y. Long non-coding RNA UCA1 indicates an unfavorable prognosis and promotes tumorigenesis via regulating AKT/GSK-3beta signaling pathway in cholangiocarcinoma. *Oncotarget* **2017**, *8*, 96203–96214. [[PubMed](#)]
335. Wang, Z.-Q.; He, C.-Y.; Hu, L.; Shi, H.-P.; Li, J.-F.; Gu, Q.-L.; Su, L.-P.; Liu, B.-Y.; Li, C.; Zhu, Z. Long noncoding RNA UCA1 promotes tumour metastasis by inducing GRK2 degradation in gastric cancer. *Cancer Lett.* **2017**, *408*, 10–21. [[CrossRef](#)] [[PubMed](#)]
336. Zhen, S.; Hua, L.; Liu, Y.-H.; Sun, X.-M.; Jiang, M.-M.; Chen, W.; Zhao, L.; Li, X. Inhibition of long non-coding RNA UCA1 by CRISPR/Cas9 attenuated malignant phenotypes of bladder cancer. *Oncotarget* **2017**, *8*, 9634–9646. [[CrossRef](#)] [[PubMed](#)]
337. Zhao, W.; Sun, C.; Cui, Z. A long noncoding RNA UCA1 promotes proliferation and predicts poor prognosis in glioma. *Clin. Transl. Oncol.* **2017**, *19*, 735–741. [[CrossRef](#)] [[PubMed](#)]

338. Zhengyuan, X.; Hu, X.; Qiang, W.; Nanxiang, L.; Junbin, C.; Wangming, Z. Silencing of Urothelial Carcinoma Associated 1 Inhibits the Proliferation and Migration of Medulloblastoma Cells. *Med. Sci. Monit.* **2017**, *23*, 4454–4461. [[CrossRef](#)] [[PubMed](#)]
339. Pu, H.; Zheng, Q.; Li, H.; Wu, M.; An, J.; Gui, X.; Li, T.; Lu, D. CUDR promotes liver cancer stem cell growth through upregulating TERT and C-Myc. *Oncotarget* **2015**, *6*, 40775–40798. [[CrossRef](#)] [[PubMed](#)]
340. Li, L.Q.; Pan, D.; Chen, Q.; Zhang, S.W.; Xie, D.Y.; Zheng, X.L.; Chen, H. Sensitization of Gastric Cancer Cells to 5-FU by MicroRNA-204 Through Targeting the TGFBR2-Mediated Epithelial to Mesenchymal Transition. *Cell. Physiol. Biochem.* **2018**, *47*, 1533–1545. [[CrossRef](#)] [[PubMed](#)]
341. Kim, S.A.; Kim, I.; Yoon, S.K.; Lee, E.K.; Kuh, H.J. Indirect modulation of sensitivity to 5-fluorouracil by microRNA-96 in human colorectal cancer cells. *Arch. Pharm. Res.* **2015**, *38*, 239–248. [[CrossRef](#)] [[PubMed](#)]
342. Shi, L.; Li, X.; Wu, Z.; Nie, J.; Guo, M.; Mei, Q.; Han, W. DNA methylation-mediated repression of miR-181a/135a/302c expression promotes the microsatellite-unstable colorectal cancer development and 5-FU resistance via targeting PLAG1. *J. Genet. Genom.* **2018**, *45*, 205–214. [[CrossRef](#)] [[PubMed](#)]
343. Liu, B.; Liu, Y.; Zhao, L.; Pan, Y.; Shan, Y.; Li, Y.; Jia, L. Upregulation of microRNA-135b and microRNA-182 promotes chemoresistance of colorectal cancer by targeting ST6GALNAC2 via PI3K/AKT pathway. *Mol. Carcinog.* **2017**, *56*, 2669–2680. [[CrossRef](#)] [[PubMed](#)]
344. Pagliuca, A.; Valvo, C.; Fabrizi, E.; di Martino, S.; Biffoni, M.; Runci, D.; Forte, S.; De Maria, R.; Ricci-Vitiani, L. Analysis of the combined action of miR-143 and miR-145 on oncogenic pathways in colorectal cancer cells reveals a coordinate program of gene repression. *Oncogene* **2013**, *32*, 4806–4813. [[CrossRef](#)] [[PubMed](#)]
345. Feng, C.; Zhang, L.; Sun, Y.; Li, X.; Zhan, L.; Lou, Y.; Wang, Y.; Liu, L.; Zhang, Y. GDPD5, a target of miR-195-5p, is associated with metastasis and chemoresistance in colorectal cancer. *Biomed. Pharmacother.* **2018**, *101*, 945–952. [[CrossRef](#)] [[PubMed](#)]
346. Jin, Y.; Wang, M.; Hu, H.; Huang, Q.; Chen, Y.; Wang, G. Overcoming stemness and chemoresistance in colorectal cancer through miR-195-5p-modulated inhibition of notch signaling. *Int. J. Biol. Macromol.* **2018**, *117*, 445–453. [[CrossRef](#)] [[PubMed](#)]
347. Zhou, Y.; Wan, G.; Spizzo, R.; Ivan, C.; Mathur, R.; Hu, X.; Ye, X.; Lu, J.; Fan, F.; Xia, L.; et al. miR-203 induces oxaliplatin resistance in colorectal cancer cells by negatively regulating ATM kinase. *Mol. Oncol.* **2014**, *8*, 83–92. [[CrossRef](#)] [[PubMed](#)]
348. Li, T.; Gao, F.; Zhang, X.P. miR-203 enhances chemosensitivity to 5-fluorouracil by targeting thymidylate synthase in colorectal cancer. *Oncol. Rep.* **2015**, *33*, 607–614. [[CrossRef](#)] [[PubMed](#)]
349. Liu, Y.; Gao, S.; Chen, X.; Liu, M.; Mao, C.; Fang, X. Overexpression of miR-203 sensitizes paclitaxel (Taxol)-resistant colorectal cancer cells through targeting the salt-inducible kinase 2 (SIK2). *Tumour Biol.* **2016**, *37*, 12231–12239. [[CrossRef](#)] [[PubMed](#)]
350. Meng, X.; Fu, R. miR-206 regulates 5-FU resistance by targeting Bcl-2 in colon cancer cells. *OncoTargets Ther.* **2018**, *11*, 1757–1765. [[CrossRef](#)] [[PubMed](#)]
351. Hon, K.W.; Abu, N.; Ab Mutalib, N.-S.; Jamal, R. miRNAs and lncRNAs as Predictive Biomarkers of Response to FOLFOX Therapy in Colorectal Cancer. *Front. Pharmacol.* **2018**, *9*. [[CrossRef](#)] [[PubMed](#)]
352. Dong, L.; Lin, W.; Qi, P.; Xu, M.D.; Wu, X.; Ni, S.; Huang, D.; Weng, W.W.; Tan, C.; Sheng, W.; et al. Circulating Long RNAs in Serum Extracellular Vesicles: Their Characterization and Potential Application as Biomarkers for Diagnosis of Colorectal Cancer. *Cancer Epidemiol. Biomarkers Prev.* **2016**, *25*, 1158–1166. [[CrossRef](#)] [[PubMed](#)]
353. Tang, S.; Tan, G.; Jiang, X.; Han, P.; Zhai, B.; Dong, X.; Qiao, H.; Jiang, H.; Sun, X. An artificial lncRNA targeting multiple miRNAs overcomes sorafenib resistance in hepatocellular carcinoma cells. *Oncotarget* **2016**, *7*, 73257–73269. [[CrossRef](#)] [[PubMed](#)]

