Review Article

A narrative review of papillary thyroid carcinoma-related long non-coding RNAs and their relevance to malignant tumors

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Background and Objective: In recent years, research on the relationship between papillary thyroid carcinoma (PTC) and long non-coding RNAs (lncRNAs) has been burgeoning. However, there has not been an analysis of the regulatory mechanisms of these lncRNAs in all tumors, nor a comprehensive categorization and comparison of these mechanisms. This review aims to uncover whether PTC-related lncRNAs also play an important role in other tumors and to identify a common pattern of action.

Methods: We conducted a statistical analysis of lncRNAs related to PTC that have been reported during the period from Jan 2022 to May 2024 through searching in the Embase, Web of Science, and PubMed databases, focusing on those with greater research value. Using them as the focal points of our study, we compiled data on their different regulatory mechanisms across various malignant tumors, emphasizing key findings.

Key Content and Findings: This comprehensive analysis not only provides valuable insights into potential regulatory mechanisms of these lncRNAs in PTC but also serves as a reference for exploring their broader regulatory networks within cancer. The principal discovery is that lncRNAs associated with PTC can competitively interact with microRNAs (miRNAs). This interaction influences miRNA-targeted messenger RNA (mRNA) and the expression of cancer-related proteins, ultimately facilitating the progression of PTC as well as other malignant tumors.

Conclusions: The lncRNAs associated with PTC exert regulatory functions in other malignancies as well and possess similar regulatory mechanisms. This provides a molecular basis for the future development of relevant targeted therapies.

Keywords: Papillary thyroid carcinoma (PTC); long non-coding RNAs (lncRNAs); targeted therapy

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Introduction

Papillary thyroid carcinoma (PTC) represents the predominant histological subtype among thyroid cancer cases, constituting 89.1% of all instances (1). The incidence of thyroid cancer has witnessed a substantial rise in recent decades, primarily attributed to the heightened diagnosis of the PTC subtype (2). PTC, a well-differentiated subtype, has been reported to have the potential for progression towards a poorly differentiated state, resulting in a significant decrease in life expectancy (3,4). Due to our incomplete understanding of the molecular mechanisms underlying PTC progression, further research is imperative to uncover novel therapeutic targets.

Long non-coding RNAs (lncRNAs) are a class of transcripts exceeding 200 nucleotides in length with

Table 1 The search strategy summary

Items	Specification
Date of search	May 1st, 2024
Databases and other sources searched	PubMed, Web of Science, Embase
Search terms used	"Thyroid Cancer, Papillary", "RNA, Long Noncoding", Papillary Thyroid Carcinoma, Carcinoma, Cancer
Timeframe	From Jan 2022 to May 2024
Inclusion criteria	(I) The effects of lncRNA on PTC and other cancers have been experimentally validated
	(II) The methodology is rational and rigorous after undergoing a comprehensive evaluation
	(III) The reporting is accurate and comprehensive, with no selective reporting
	(IV) The article is written in English
Selection process	Y.S. and Y.J., independently conducted the literature search and assessment. Discrepancies were resolved through consultation

lncRNA, long non-coding RNA; PTC, papillary thyroid carcinoma.

minimal or virtually no protein-coding capacity (5). Recent studies have revealed a pivotal role of lncRNAs in modulating the growth, invasion, and metastasis of colorectal cancer (6-9), hepatic cancer (10-16), breast cancer (17-19), etc. It is evident that lncRNAs play a significant role in the initiation and progression of various types of cancer through diverse molecular interaction mechanisms. We identified lncRNAs related to PTC that have been reported in the past 2 years and provided an overview of the roles and mechanisms of these lncRNAs in PTC, along with their roles and mechanisms in other cancers. This comprehensive exploration serves as a valuable resource for researchers seeking a thorough understanding of the latest PTC-associated lncRNAs. We present this article in accordance with the Narrative Review reporting checklist (available at https://tcr.amegroups.com/article/view/10.21037/tcr-24-1038/rc).

Methods

We conducted a review of articles published during the period from Jan 2022 to May 2024 pertaining to the relationship between lncRNAs and PTC. This ensured the novelty of the research object. We conducted a search in large literature databases such as PubMed, Web of Science, and Embase. The search terms for PubMed are: (PTC[Title/Abstract] OR "papillary thyroid"[Title/Abstract]) AND (lncRNA[Title/Abstract] OR "long non-coding RNA"[Title/Abstract]). For Web of Science, the search terms are: "PTC" OR "Papillary thyroid" (Topic) and lncRNA OR "long non-coding RNA" (Topic). In Embase, the search terms are: (ptc:ti,ab,kw OR 'papillary thyroid':ti,ab,kw) AND (lncrna:ti,ab,kw OR 'long non-coding rna':ti,ab,kw). The summary of the search strategy can be found in *Table 1*. Subsequently, we filtered out studies with low quality and those lacking experimental validation, focusing our review on the high-confidence PTC-associated lncRNAs that remained. We centered our research around these latest PTC-related lncRNAs, conducted searches for relevant articles exploring their relationships with various types of tumors, and analyzed their modes of regulation on tumors. We provided summaries for the key aspects and analyzed the patterns present in these studies. And specific regulatory axes of each lncRNA regulating PTC are presented in *Figure 1*.

PTC-related lncRNAs

lncRNA HOXD antisense growth-associated lncRNA (HAGLROS)

HAGLR opposite strand lncRNA (HAGLROS) has only one transcript, a 699 bp lncRNA, according the National Center for Biotechnology Information (NCBI) tified (NR_110457.1). Studies have indicated that lncRNA HAGLROS may promote the malignant behavior of cancer cells, suggesting its potential involvement in cancer initiation and progression (20). All the currently retrieved studies consistently indicate that lncRNA HAGLROS plays a positive role in the development of malignant tumors.

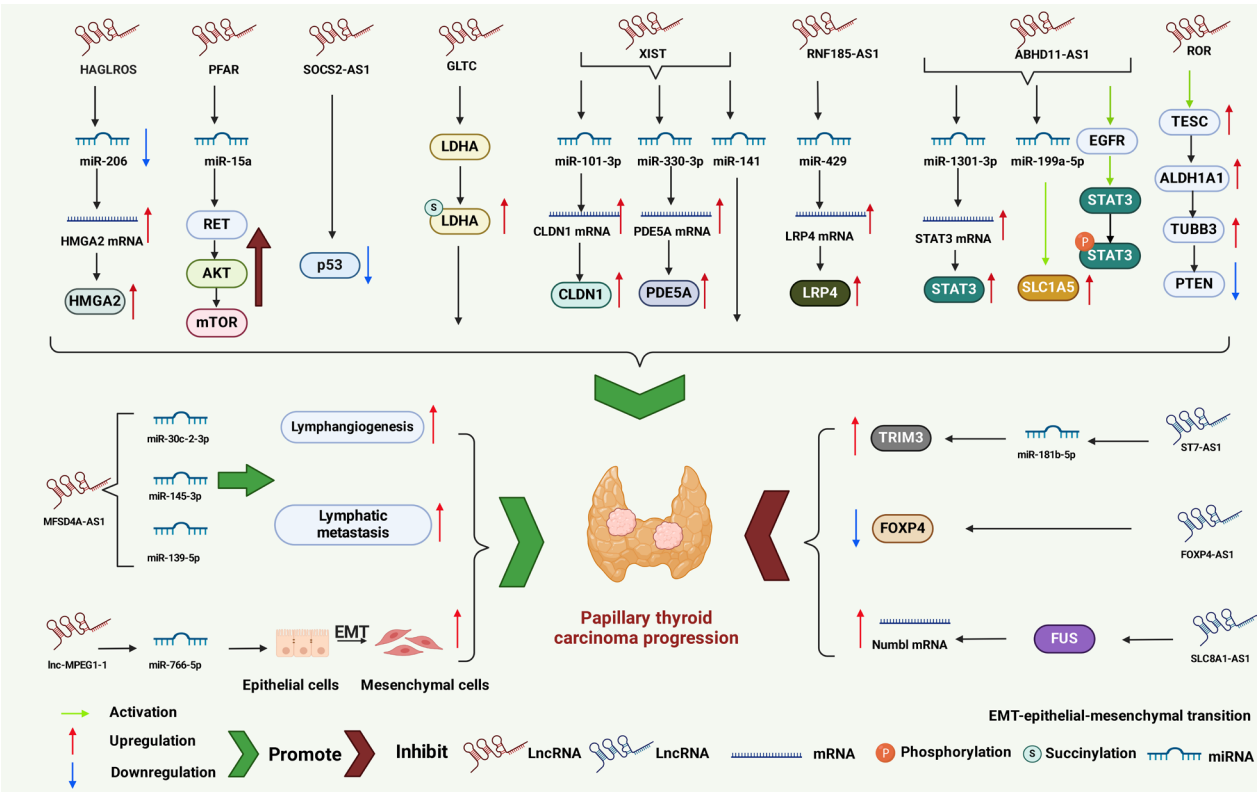

Figure 1 Regulatory network diagram of lncRNAs in papillary thyroid carcinoma. Created with BioRender.com. ABHD11-AS1, alpha/beta hydrolase domain containing 11 antisense RNA 1; EMT, epithelial-mesenchymal transition; FOXP4-AS1, forkhead box P4 antisense RNA 1; GLTC, gamma-glutamyltransferase containing; HAGLROS, HOXD antisense growth-associated lncRNA; lncRNA, long non-coding RNA; NA, not involved or not specified; PFAR, pancreatic functional islet-associated regulator; PTC, papillary thyroid carcinoma; RNF185-AS1, ring finger protein 185 antisense RNA 1; ROR, regulator of reprogramming; SLC8A1-AS1, solute carrier family 8 member A1 antisense RNA 1; SOCS2-AS1, suppressor of cytokine signaling 2-antisense transcript 1; ST7-AS1, suppressing tumorigenicity 7 antisense RNA 1; XIST, X inactivate-specific transcript.

This is achieved through its interactions with various microRNAs (miRNAs), utilizing miRNAs as downstream targets, and influencing the expression of tumor-related proteins via miRNA modulation. The regulatory axes of each lncRNA in regulating tumors other than PTC are displayed in *Table 2*. Among the downstream miRNAs affected by HAGLROS, notable ones include miR-138-5p, miR-330-5p, miR-26b-5p, miR-100, miR-206, miR-26b-5p, miRNA-152, miR-5095, and miR-100-5p (21-31). HAGLROS's regulatory impact extends to particular proteins or pathways, many of which are associated with apoptosis, such as Bcl-2, Bax, caspase-3, and NOTCH3. In the context of PTC, The study conducted by Mutlu Icduygu *et al.* indicates that HAGLROS exhibits higher expression levels in clinical samples of PTC (32). Specific regulatory axes of each lncRNA regulating PTC are presented in *Table 3*, Research conducted by Zeng and colleagues has revealed the existence of the HAGLROS/miR-206/HMGA2 pathway in PTC (33). Research on this type of lncRNA in the context of PTC is relatively limited. Existing studies generally suggest a positive role for it in the development of PTC. However, further research is needed to validate its credibility. The specific regulatory network can be seen in *Figure 2*.

In summary, we have observed that lncRNA HAGLROS primarily exerts its influence on cancer through interactions with downstream miRNAs, acting as a miRNA sponge to modulate the expression of miRNA target proteins, ultimately promoting cancer development. Notably, miRNA-330-5p and miR-100 are targeted by HAGLROS. This underscores the significance of these two classes of miRNAs in the context of HAGLROS-mediated oncogenic effects.

Table 2 The regulatory mechanisms of PTC-related lncRNAs in other cancers

LncRNA	Cancer type	Type of interaction	Target miRNA	Regulated protein(s)
HAGLROS	Hepatocellular carcinoma	pos	miR-26b-5p	KPNA2
	Hepatocellular carcinoma	pos	miR-5095	ATG12
	Esophageal cancer	pos	miR-206	NOTCH3
	Hepatocellular carcinoma	pos	miR-5095	ATG12
	Gastric cancer	pos	miR-100-5p	mTOR
	Lung carcinoma	pos	miR-100	SMARCA5
	Lung carcinoma	pos	miRNA-152	NA
	Laryngeal cance	pos	miR-138-5p	CLN5
	TNBC	pos	miR-330-5p	PAX5
	Ovarian cancer	pos	miR-26b-5p	Ki67/Bcl-2/Bax/caspase-3
	Bladder cancer	pos	miR-330-5p	SPRR1B
	LargeB-cell lymphoma	pos	miR-100	NA
SOCS2-AS1	Hepatocellular carcinoma	neg	miR-454-3p	CPEB1
	Endometrial cancer	neg	NA	AURKA
	Colorectal cancer	neg	miR-1264	SOCS2
	Prostate cancer	pos	NA	Proteins related to the apoptosis
	Glioma	pos	NA	ITGB1
XIST	Esophageal cancer	pos	miR-101	EZH2
	Gastric cancer	pos	miR-101	EZH2
	Colorectal cancer	pos	miR-137	EZH2
	Laryngeal cancer	pos	miR-124	EZH2
	Pancreatic cancer	pos	miR-140/124	iASPP/CDK1
	Lung cancer	pos	miR-140	iASPP
	Pancreatic cancer	pos	miR-137	Notch1
	Colorectal cancer	pos	miR-137	PKM2/PKM1
	Lung cancer	pos	miR-137	Notch1
	Glioma	pos	miR-137	Rac1
	Glioma	pos	miR-137	ZO-2/FOXC1
	Osteosarcoma	pos	miR-137	NA
ST7-AS1	Gastric cancer	pos	NA	EZH2
	Gastric cancer	pos	NA	PI3K-AKT/EMT
	Laryngeal carcinoma	pos	NA	CARM1/Sox-2
FOXP4-AS1	Hepatocellular carcinoma	pos	NA	EZH2/ZC3H12D
	Nasopharyngeal carcinoma	pos	miR-136-5p	MAPK1
	Ewing sarcoma	pos	NA	TME
	Colorectal cancer	pos	miR-423-5p	NACC1
	Cervical cancer	pos	miR-136-5p	CBX4
	Lung cancer	pos	miR-3184-5p	EIF5A
	Esophageal carcinoma	pos	NA	FOXP4/β-catenin

Table 2 *(continued)*

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LncRNA	Cancer type	Type of interaction	Target miRNA	Regulated protein(s)
	Prostate cancer	pos	miR-3184-5p	FOXP4
	Mantle cell lymphoma	pos	miR-423-5p	NACC1
	Osteosarcoma	pos	NA	LATS1
SLC8A1-AS1	Glioma	pos	NA	Wnt/β-catenin signaling pathway
RNF185-AS1	Hepatocellular carcinoma	pos	miR-221-5p	Integrin β5
ROR	Breast cancer	pos	miRNA-205	ZEB1/ZEB2/vimentin/E-cadherin
	Gastric cancer	pos	NA	MRP1
	Gastric cancer	pos	miR-519d-3p	HMGA2
	Gastric cancer	pos	NA	OCT4/SOX2/NANOG
	Colorectal cancer	pos	miR-6833-3p	SMC4
	Colorectal cancer	pos	NA	p53
	Colorectal cancer	pos	miR-223-3p	NF2
	Hepatocellular carcinoma	pos	miRNA-145	RAD18
	Endometrial cancer	pos	miR-34a	Notch1
	Renal cancer	pos	NA	p53/c-Myc
	Osteosarcoma	pos	miR-153-3p	ABCB1
	Ovarian cancer	pos	miR-145	FLNB-EMT
	Esophageal cancer	pos	miR-145	LMNB2
	Bladder cancer	pos	NA	ZEB1/EMT
	Prostate cancer	pos	miR-145	Oct4
	Gallbladder cancer	pos	NA	EMT
ABHD11-AS1	Cervical cancer	pos	NA	ABHD11/EGFR
	Cervical carcinoma	pos	miR-1254	NA
	Cervical cancer	pos	miR-330-5p	MARK2
	Ovarian cancer	pos	miR-133a-3p	NA
	Ovarian cancer	pos	NA	RhoC
	Endometrial carcinoma	pos	NA	cyclin D1
	Triple-negative breast cancer	pos	miR-199a-5p	NA
	Pancreatic cancer	pos	NA	EMT/PI3K-AKT pathway
	Pancreatic cancer	pos	miR-1231	cyclin E1
	Colorectal cancer	pos	miR-1254	WNT11
	Colorectal cancer	pos	miR-133a	SOX4
	Colorectal cancer	pos	NA	ITGA5/Fak/PI3K/Akt
	Gastric cancer	pos	miR-361-3p	PDPK1

neg: overexpression inhibits tumor progression. Decreased expression promotes tumor progression. pos: overexpression promotes tumor progression or increases resistance to radiotherapy and chemotherapy. Decreased expression inhibits tumor progression. ABHD11-AS1, alpha/beta hydrolase domain containing 11 antisense RNA 1; FOXP4-AS1, forkhead box P4 antisense RNA 1; HAGLROS, HOXD antisense growth-associated lncRNA; lncRNA, long non-coding RNA; NA, not involved or not specified; PTC, papillary thyroid carcinoma; RNF185-AS1, ring finger protein 185 antisense RNA 1; ROR, regulator of reprogramming; SLC8A1-AS1, solute carrier family 8 member A1 antisense RNA 1; SOCS2-AS1, suppressor of cytokine signaling 2-antisense transcript 1; ST7-AS1, suppressing tumorigenicity 7 antisense RNA 1; XIST, X inactivate-specific transcript.

Table 3 The regulatory mechanisms of lncRNAs in PTC

LncRNA	Type of interaction	Target miRNA	Regulated protein(s)
HAGLROS	pos	miR-206	HMGA2
PFAR	pos	miR-15a	RET-AKT-mTOR
SOCS2-AS1	pos	NA	p53
GLTC	pos	NA	LDHA
XIST	pos	miR-101-3p	CLDN1
	pos	miR-330-3p	PDE5A
	pos	miR-141	NA
MFSD4A-AS1	pos	miR-30c-2-3p/miR-145-3p/miR-139-5p	NA
ST7-AS1	neg	miR-181b-5p	TRIM3
FOXP4-AS1	neg	NA	AKT signaling pathway
SLC8A1-AS1	neg	NA	FUS/Numbl
lnc-MPEG1-1	pos	miR-766-5p	EMT
RNF185-AS1	pos	miR-429	LRP4
ROR	pos	NA	TESC/ALDH1A1/TUBB3/PTEN
ABHD11-AS1	pos	NA	EPS15L1/EGFR signaling pathway
	pos	miR-199a-5p	SLC1A5
	pos	miR-1301-3p	STAT3

neg: overexpression inhibits tumor progression. Decreased expression promotes tumor progression. pos: overexpression promotes tumor progression or increases resistance to radiotherapy and chemotherapy. Decreased expression inhibits tumor progression. ABHD11-AS1, alpha/beta hydrolase domain containing 11 antisense RNA 1; FOXP4-AS1, forkhead box P4 antisense RNA 1; HAGLROS, HOXD antisense growth-associated lncRNA; lncRNA, long non-coding RNA; NA, not involved or not specified; PTC, papillary thyroid carcinoma; RNF185-AS1, ring finger protein 185 antisense RNA 1; ROR, regulator of reprogramming; SLC8A1-AS1, solute carrier family 8 member A1 antisense RNA 1; SOCS2-AS1, suppressor of cytokine signaling 2-antisense transcript 1; ST7-AS1, suppressing tumorigenicity 7 antisense RNA 1; XIST, X inactivate-specific transcript.

lncRNA pancreatic functional islet-associated regulator (PFAR)

Pancreatic fibrosis-associated lncRNA (lnc-PFAR) facilitates autophagy and exacerbates pancreatic fibrosis (34). Fang's research proposed that lncRNA PFAR acts as a sponge for miR-15a, leading to the upregulation of RET and consequently promoting the activation of the AKT/mTOR signaling pathway, thereby facilitating the progression of PTC (35). Activation of RET was found closely related to thyroid cancer (36), found to be targeted by miR-15a (37), found to contribute to the progression of cancer by triggering the AKT/mTOR signaling pathway (38). Akt/mTOR pathway was reported to inhibit autophagy (39,40).

In summary, lncRNA PFAR orchestrates a regulatory axis by modulating miR-15a, which in turn targets RET. This interaction results in the activation of RET, subsequently triggering the AKT/mTOR signaling pathway. Ultimately, this cascade leads to the inhibition of apoptosis in PTC cells and promotes PTC progression. The establishment of this regulatory axis appears to be robust and reliable. However, there is currently no other research indicating the role of lncRNA PFAR in the development of PTC, nor is there evidence to suggest its specific involvement in the occurrence of other cancers. Therefore, there is significant room for exploration in this field.

lncRNA suppressor of cytokine signaling 2-antisense transcript 1 (SOCS2-AS1)

LncRNA SOCS2-AS1 is situated on the reverse strand of chromosome 12. In recent years, complex associations have

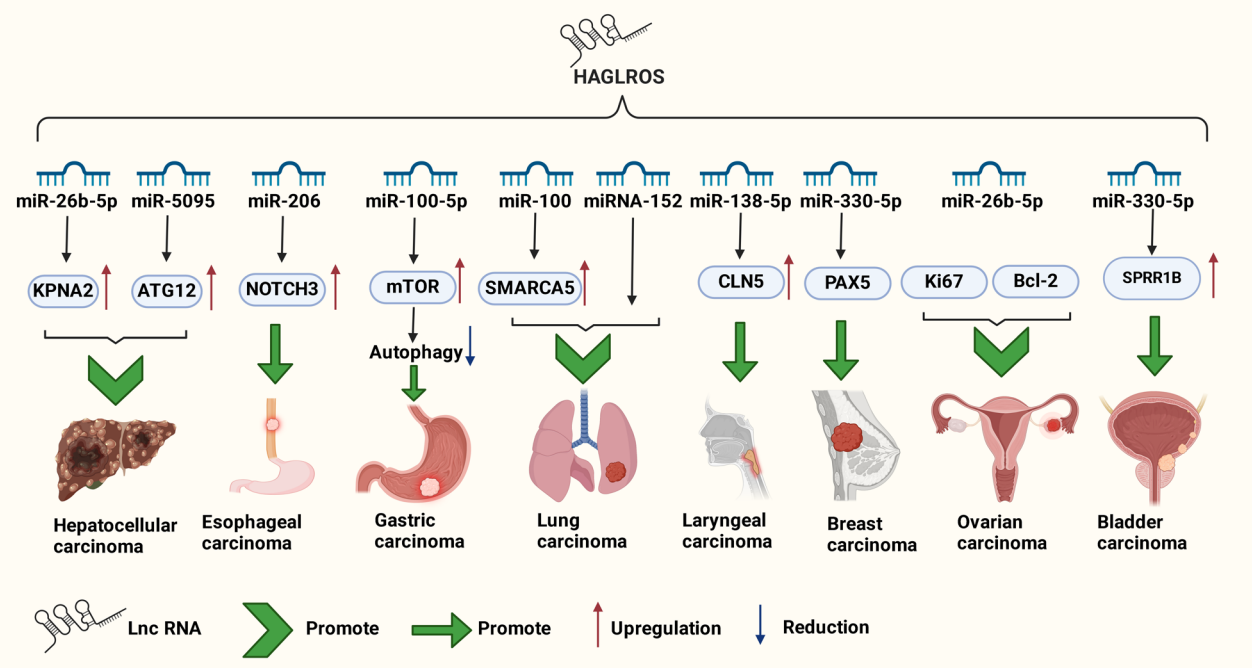

Figure 2 Regulatory network of lncRNA HAGLROS in various cancers. Created with BioRender.com. HAGLROS, HOXD antisense growth-associated lncRNA; lncRNA, long non-coding RNA.

been unveiled between SOCS2-AS1 and various types of cancer, exhibiting both promotive and inhibitory roles in cancer development and progression. SOCS2-AS1 promotes the progression of glioma by upregulating the expression of integrin subunit beta 1 (ITGB1), which plays an essential role in various cellular functions, including the regulation of cell proliferation, thereby influencing biological processes such as immune responses and carcinogenesis (41-43). It also plays a positive role in the development of castration-resistant prostate cancer by inhibiting apoptosis (44), Specifically, SOCS2-AS1 modulates the expression of genes associated with apoptosis, such as TNFSF10 (45). Additionally, the study revealed that silencing SOCS2-AS1 downregulates oncogenic genes, namely forkhead box protein M1 (FOXM1) and its downstream target, centromere protein F (CENPF). Co-expression of FOXM1 and CENPF has been linked to the activation of the PI3K and MAPK signaling pathways, thus playing a role in cell growth and migration processes (46,47). These findings lay the groundwork for further research in this area. In addition to its promoting role in cancer development mentioned above, SOCS2-AS1 exhibits inhibitory effects on several types of cancers, SOCS2-AS1 exerts its inhibitory effects on colorectal cancer progression and metastasis by stabilizing SOCS2 and acting as a sponge for miR-1264 (48), facilitating the expression of SOCS2, which is a tumor suppressor to inhibit proliferation and invasion of human cancer (49,50). In hepatocellular carcinoma (HCC), SOCS2-AS1 regulates miR-454-3p, which in turn affects the expression of CPEB1, which inhibits the proliferation of glioblastoma cells and regulates the differentiation of glioma stem cells (51,52), ultimately leading to the suppression of cancer stem cell properties and progression in liver cancer cells (53). LncRNA SOCS2-AS1 also promotes the degradation of AURKA by enhancing the interaction between FBXW7 and AURKA, which is frequently amplified in various tumors (54-56), associated with a poor prognosis, thereby inhibiting the growth and metastasis of endometrial cancer (57). In Glioma, the expression of SOCS2-AS1 is positively correlated with the expression levels of the core factor ITGB1 in the extracellular matrix (ECM)-receptor interaction signaling pathway, which plays an essential role in numerous cellular functions, including the control of cell proliferation (58). Regarding the role of this lncRNA in PTC, a study conducted by Zhang *et al.* proposed that the high expression of SOCS2-AS1 in PTC enhances the degradation of p53, and promotes PTC cell proliferation and the fatty acid oxidation rate (59).

In summary, lncRNA SOCS2-AS1 exhibits a promotive role in cancer development in glioma and prostate cancer, while it exerts inhibitory effects in HCC, endometrial cancer, and colorectal cancer. In HCC and colorectal cancer, its impact on cancer is mediated through post-regulation of downstream protein expression by interacting with miR-454-3p and miR-1264, respectively. Although other studies have suggested the regulation of specific proteins by lncRNA SOCS2-AS1, but whether a miRNA is involved in this process and which miRNA it is remains unclear. Therefore, this represents a subject worthy of further investigation in the future.

lncRNA gamma-glutamyltransferase containing (GLTC)

Previously, the role of the lncRNA GLTC in the development of cancer had not been established. However, a recent study has proposed that GLTC is an oncogenic lncRNA in PTC. This finding has been rigorously validated through experimental investigations. The study revealed that GLTC promotes cell growth and glycolysis in cultured PTC cells and in a mouse xenograft tumor model (60). LDHA is an oncogenic metabolic enzyme that initiates a phenotypic shift from mitochondrial respiration to glycolysis (61,62). Elevated levels of LDHA messenger RNA (mRNA) and protein significantly impact the progression of PTC (63). Data from the TCGA database confirm LDHA as a potential diagnostic and therapeutic target in PTC (64). The study by Shi *et al.* further demonstrated that GLTC increases the succinylation of LDHA at the K155 site, enhancing LDHA activity, thus promoting the progression of PTC (60,65). Furthermore, the enhanced LDHA activity mediated by GLTC contributes to the development of resistance to radioiodine therapy in PTC, a phenomenon observed both *in vitro* and *in vivo* (60). The role of LncRNA GLTC in PTC or cancer is still a relatively new field of study, and the research conducted by Shi and colleagues holds significant value. It can serve as a valuable reference for future studies in this area.

lncRNA X inactivate-specific transcript (XIST)

XIST is an identified lncRNA which has been found to be highly expressed in various types of cancers, including digestive system cancers; respiratory system cancers; nervous system tumors such as glioma and neuroblastoma; other system tumors such as sarcomas, bladder cancer, cervical cancer and melanoma. In these contexts, XIST exerts its influence by modulating specific miRNAs, which, in turn, regulate the expression of cancer-related target genes, ultimately contributing to tumor progression (66). In the regulatory networks, we have observed the recurrence of certain key genes. For instance, in esophageal cancer, gastric cancer, colorectal cancer, and laryngeal cancer, XIST consistently emerges as a pivotal factor influencing the expression of the *EZH2* gene (67-70), which plays a critical role in the regulation of cell proliferation, migration, invasion, tumorigenesis and metastasis, ultimately driving cancer progression (71,72). In both colorectal cancer and pancreatic cancer, XIST ultimately promotes tumor progression by regulating the expression of the *ZEB1* gene (73,74), which is an important regulator of epithelial-mesenchymal transition (EMT) and cell invasion in different tumor types (75,76), and in lung cancer, pancreatic cancer and osteosarcoma, XIST ultimately promotes tumor progression by regulating the expression of the *iASPP* gene (77-79), which has been discovered to function as an oncogene (80,81). The recurrent presence of these genes in the regulatory network of XIST underscores their significance. Furthermore, several key miRNAs have also been found to recur within the regulatory network governed by XIST. In colorectal cancer (69,82), pancreatic cancer (83), lung cancer (84), glioma (85,86), and osteosarcoma (87), XIST exerts its influence by targeting miR-137. In esophageal cancer, gastric cancer, retinoblastoma, XIST exerts its influence by targeting miR-101 (68,88,89). This also underscores the crucial role of these miRNAs in XIST-mediated regulation of malignant tumors. In addition to its promoting role, studies have also reported that XIST exhibits anti-tumorigenic properties in lymphoma (90) and contradictory effects within the same type of cancer (91,92). These studies indicate that lncRNA XIST has complex network mechanisms in the regulation of cancer, and the majority of research suggests its role in promoting cancer progression, while its role in PTC is less studied. Two studies currently demonstrate the involvement of lncRNA XIST in the occurrence and progression of PTC. Du *et al.* proposed in their study that XIST can upregulate CLDN1 by sequestering miR-101-3p, thereby promoting the migration and invasion of PTC cells (93). MiR-101-3p, known as a tumor-suppressive miRNA (94-96), and CLDN1, a tight junction protein associated with cancer proliferation, migration, and invasion, play key roles in this regulatory mechanism (97). In addition

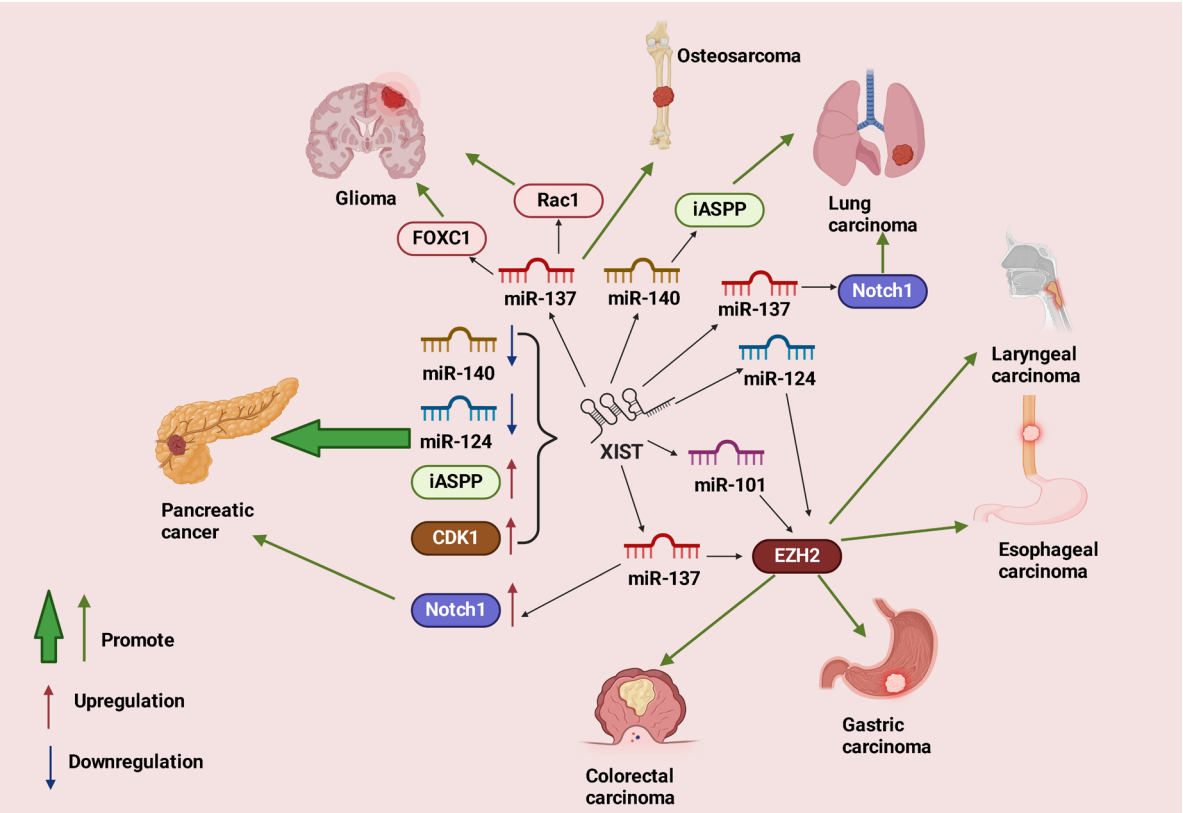

Figure 3 Regulatory network of lncRNA XIST in various cancers. Created with BioRender.com. lncRNA, long non-coding RNA; XIST, X inactivate-specific transcript.

to the aforementioned studies, Cai *et al.* proposed that XIST enhances the malignant behavior of PTC by inhibiting miR-330-3p, thereby increasing the expression of PDE5A (98), which was recently demonstrated as a downstream target of BRAF (99). Activated BRAF downregulates the expression of PDE5A, resulting in reduced degradation of cGMP, leading to an increase in intracellular calcium ion concentration, triggering the invasion and metastasis of tumor cells (100). Xu *et al.* suggested that XIST functions as an oncogene in PTC progression by regulating miR-141. However, they did not provide information about the downstream genes affected or whether specific genes need to be targeted, which is a gap that needs to be addressed (101). The specific regulatory network can be seen in *Figure 3*.

lncRNA MFSD4A antisense RNA 1 (MFSD4A-AS1)

MFSD4A-AS1 is a relatively novel lncRNA, and its precise functional mechanisms are yet to be fully elucidated. There is limited literature regarding its association with malignant tumors, with one study specifically highlighting its involvement in PTC. Liu *et al.*'s study proposed that MFSD4A-AS1 acts as a ceRNA by sequestering miR-30c-2-3p, miR-145-3p, and miR-139-5p (102). On one hand, it disrupts the miRNA-mediated inhibition of VEGFA and VEGFC, which are identified as the predominant tumor metastasis-driving factors in various human cancers types (103). On the other hand, MFSD4A-AS1 upregulates TGFBR2 and USP15 by sponging miR-30c-2-3p and activates the TGF-β signaling pathway. It has been demonstrated that the activation of the TGF-β signaling pathway promotes tumor lymphatic metastasis through various mechanisms (104-106). The synergistic effect of these two processes promotes lymphangiogenesis and lymphatic metastasis in PTC (102). However, the results of this study require further comprehensive clinical and experimental validation.

In conclusion, lncRNA MFSD4A-AS1, as an emerging lncRNA, presents significant potential for exploration in its

association with malignancies, particularly in the context of PTC. Existing research has indicated its relevance to lymphatic metastasis in PTC. However, its expression levels show no significant differences between normal thyroid tissues and PTC tissues without lymph node metastasis, while it exhibits a notable increase in PTC tissues with lymph node metastasis. This raises the question of whether similar expression patterns exist in other tumor types, where elevated expression may also be specific to tumors with lymph node metastasis. This intriguing possibility opens up new avenues for future research on this gene.

lncRNA suppressing tumorigenicity 7 antisense RNA 1 (ST7-AS1)

ST7-AS1 is a newly discovered lncRNA that has been associated with immune infiltrates in breast cancer (107), the EMT process, anti-apoptotic mechanisms in gastric cancer (108,109), and the promotion of laryngeal squamous cell carcinoma by stabilizing CARM1 (110) which were negatively correlated with gene expression signatures of key immune pathways, including the MHC class I antigen presentation, type 1 interferon and IFNγ pathways (111), indicating its immunosuppressive effects and favorable contribution to tumor development. Additionally, it has been shown to facilitate the malignant transformation of lung adenocarcinoma by regulating the miR-181b-5p/KPNA4 axis (112). Moreover, studies have indicated that miR-3619-5p inhibits cell proliferation in cutaneous squamous cell carcinoma by targeting KPNA4 (113), and increased miR-181 reverses EMT in glioblastoma by reducing KPNA4 (114). This indirectly underscores the potential positive role of KPNA4 in cancer progression. Regarding the relationship between ST7-AS1 and PTC, there is a singular study positing that increased levels of ST7-AS1 may enhance the expression of TRIM3 by harboring miR-181b-5p, thereby manifesting a tumor-suppressive function (115). TRIM3 also functions as a tumor suppressor gene across multiple cancer types (116-118).

Based on the above discussion, it becomes evident that the impact of lncRNA ST7-AS1 varies across different types of tumors. It exhibits a positive effect on gastric cancer and laryngeal squamous cell carcinoma, while its effect is negative in the case of PTC. This highlights the intricate regulatory network of ST7-AS1 in the development of tumors. Given its status as a novel lncRNA, there remains significant room for further exploration into its relationship with cancer.

lncRNA forkhead box P4 antisense RNA 1 (FOXP4-AS1)

The lncRNA FOXP4-AS1 has recently been identified as an emerging cancer-related biomarker, exhibiting variable roles across different cancer types. The following is an introduction to specific regulatory mechanisms for each type of malignant tumor. In HCC, FOXP4-AS1 has been implicated in promoting tumor progression (119,120) and the mechanism involves FOXP4-AS1 inhibiting the expression of ZC3H12D by mediating the deposition of H3K27me3 through the recruitment of EZH2 (121). In esophageal squamous cell carcinoma (ESCC), FOXP4-AS1 also exerts a promotive role, as its mechanism involves upregulating the expression of FOXP4, thereby promoting the transcription of β-catenin, which is a crucial factor in the WNT signaling pathway and regulates tumorigenesis development (122), and ultimately driving the malignant progression of ESCC (123,124). In prostate cancer, FOXP4-AS1 functions by sequestering miR-3184-5p to upregulate FOXP4, which is a member of the P subfamily of the forkhead box (FOX) family, a novel transcription factor (125) and can regulate tumor growth, progression and metastasis (126), thereby promoting the growth of prostate cancer cells (127), In non-small cell lung cancer (NSCLC), FOXP4-AS1 similarly promotes tumor cell growth by interacting with miR-3184-5p. However, in this context, miR-3184-5p ultimately targets the protein EIF5A (128), which exists complex relationships between tumor growth and cell signal transduction (129). In nasopharyngeal carcinoma, the knockdown of FOXP4-AS1 resulted in a reduction of metastasis and the inhibition of EMT through the miR-136-5p/MAPK1 pathway (130-132). In cervical cancer, FOXP4-AS1 also acts as competing endogenous RNA for miR-136-5p but ultimately regulating chromobox 4 (CBX4) expression (133). In Ewing sarcoma (ES), Xiong *et al.* proposed that FOXP4-AS1 may potentially modulate the expression of TMPO by sequestering miR-298, thereby regulating the malignant phenotype of ES. However, further validation is required to substantiate this hypothesis. They also uncovered that FOXP4-AS1 might modulate the tumor immune microenvironment through extracellular vesicle-mediated mechanisms. Notably, three immune cell types, namely Tregs, activated NK cells, and M1 macrophages, exhibited significant associations with FOXP4-AS1 expression (134). These findings could potentially provide valuable insights for future immunotherapeutic strategies. In both colorectal cancer and Mantle cell lymphoma (MCL), FOXP4-AS1 operates

as a competitive endogenous RNA by sequestering miR-423-5p, ultimately leading to an upregulation of nucleus accumbens-associated 1 (NACC1) expression, which has been reported to promote the progression of various cancers and studies have indicated its ability to transcriptionally activate HOXA9, thereby regulating apoptosis in colorectal cancer cells (135), then promoting tumor progression (136,137). This highlights the significance of this axis in oncogenesis. Furthermore, in osteosarcoma, upregulated FOXP4-AS1 promotes proliferation, migration, and cell cycle progression by downregulating LATS1, which has also been reported to be a tumor suppressor (138), through its interaction with LSD1 and EZH2 (139). Regarding its relationship with PTC, it exhibits a unique characteristic, as it exerts inhibitory effects on PTC through the modulation of the AKT signaling pathway. In contrast to previous findings, Luo *et al.* have suggested that FOXP4-AS1 also negatively regulates the expression of its host gene, FOXP4 (140).

In summary, FOXP4-AS1 appears to promote tumor progression in the majority of cancers, except for PTC, where it plays a suppressive role. The underlying reasons for its inhibitory role in PTC warrant further investigation. Additionally, the involvement of the FOXP4-AS1/miR-423-5p/NACC1 axis in two distinct classes of tumors underscores the significance of this regulatory pathway.

lncRNA solute carrier family 8 member A1 antisense RNA 1 (SLC8A1-AS1)

The lncRNA SLC8A1-AS1 is a recently discovered lncRNA in the past few years. Prior studies have suggested that lncRNA SLC8A1-AS1 may serve as an early diagnostic marker for oral squamous cell carcinoma (141). Study has also reported that the knockout of SLC8A1-AS1 inhibits the growth and migration of glioma cancer cells by suppressing the Wnt/β-catenin signaling pathway (142). Regarding its relationship with PTC, recent research has proposed a mechanism wherein SLC8A1-AS1 interacts with FUS within PTC cells, thereby preserving the stability of Numbl mRNA and subsequently modulating the notch signaling pathway. In a word, SLC8A1-AS1 suppresses PTC progression via the FUS/Numbl axis (143).

From the above content, it can be observed that there is currently a lack of comprehensive research on the relationship between SLC8A1-AS1 and cancer. Existing reports suggest that it can either promote the progression of certain tumors or inhibit the progression of others, indicating the existence of a complex regulatory network.

lncRNA long non-coding RNA-MPEG1-1 (lnc-MPEG1-1)

Research on the relationship between lnc-MPEG1-1 and cancer is very limited, with only one study suggesting its regulatory role in the progression of PTC. Huang *et al.* proposed that lnc-MPEG1-1 is overexpressed in the cytoplasm of PTC cells and functionally promotes cellular proliferation and migration in PTC cells by competitively occupying the shared binding sites of miR-766-5p (144), which is considered a tumor suppressor gene in many cancers (145,146). lnc-MPEG1-1 knockdown suppresses EMT by miR-766-5p in PTC cells. Additionally, it can serve as a predictor of lymph node metastasis in PTC (144).

lncRNA ring finger protein 185 antisense RNA 1 (RNF185-AS1)

LncRNA RNF185-AS1, situated on chromosome 22, represents a recently discovered lncRNA. Huang and colleagues have proposed that the lncRNA RNF185-AS1 can act as a "sponge" for miR-221-5p, binding to miR-221-5p and influencing its function. This interaction subsequently leads to the regulation of integrin β5, a substance known to promote tumorigenesis (147,148). Ultimately, these molecular mechanisms promotes the growth and metastasis of HCC (149). Regarding its relationship with PTC, Liu *et al.* suggested that the downregulation of RNF185-AS1 may potentially act as a "sponge" for miR-429, hindering the expression of LRP4 (150), a protein known to promote the development of various cancers (151,152). This inhibition of LRP4 expression could ultimately suppress the progression of PTC (150).

In summary, RNF185-AS1 has been found to target miRNAs, specifically miR-221-5p and miR-429, affecting HCC and PTC. Its mechanism of action involves competitive binding with these target miRNAs, ultimately regulating the expression of downstream cancer-related proteins, such as integrin β5 and LRP4, and thereby promoting cancer progression. Further research is needed to explore its associations with other types of cancer.

lncRNA regulator of reprogramming (ROR)

LncRNA ROR, known as a mediator of reprogramming, is recognized as an oncogene involved in cancer development (153). There is extensive research on the relationship between lncRNA ROR and cancers, with the majority suggesting its promotive role in cancer

progression. we have found a close relationship between ROR and miRNA-145 in various cancer types. Specifically, in liver cancer, ROR acts as a competing endogenous RNA for miR-145, thereby regulating RAD18 expression and ultimately promoting DNA repair (154). In ovarian cancer, ROR promotes the EMT process through the miR-145/FLNB regulatory axis (155). In esophageal cancer, ROR regulates the miR-145/LMNB2 axis, thereby promoting the proliferation and migration of esophageal cancer cells (156). Lastly, in prostate cancer, inhibition of ROR increases the available concentration of miR-145, which in turn prevents cell proliferation by decreasing oct4 expression (157). Additionally, by reviewing a substantial body of literature, we have found that ROR promotes the progression of various tumors by facilitating the EMT process. Here are some specific examples: In nasopharyngeal carcinoma, breast cancer, and bladder cancer, high expression of ROR is associated with enhanced EMT process (156,158-160). In ovarian cancer, ROR promotes EMT through the miR-145/FLNB regulatory axis (155). Furthermore, in gallbladder cancer, ROR promotes EMT mediated by TGF-β1 (161). We have also discovered a strong association between ROR and p53: ROR is capable of inhibiting the p53 signaling pathway, leading to the development of chemotherapy resistance in nasopharyngeal carcinoma cells (162). Through its regulation of p53, ROR promotes the proliferation and viability of colorectal cancer cells (163). Depletion of ROR, on the other hand, enhances p53 expression, thereby facilitating apoptosis in renal cancer cells (164). Key studies have indicated that lncRNA ROR enhances breast cancer development by recruiting histone methyltransferase MLL1 to up-regulate TIMP3 expression (165), facilitates endometrial cancer cell proliferation by modulating the Notch1 signaling pathway (166), contributes to human colorectal cancer tumorigenesis by targeting miR-6833-3p through SMC4 (167), inhibits the tumor suppressor gene NF2 through interaction with miR-223-3p, affecting colon cancer (168). Additionally, lncRNA ROR has been found to promote breast cancer by regulating the TGF-β pathway (169). Notably, one significant study suggests that lncRNA ROR acts as a decoy for gene-specific histone methylation, thereby promoting tumorigenesis (170). In gastric cancer, ROR knockdown downregulated HMGA2 to restrain cell proliferation, migration, invasion by targeting miR-519d-3p (171). ROR expression promotes MRP1 expression and multi-drug resistant of gastric cancer (172) and led to upregulation of several key stemness transcriptional factors, such as OCT4, SOX2, and NANOG, increasing the proliferation and invasion of gastric cancer stem cells (173). ROR contributed to cisplatin resistance in osteosarcoma via miR-153-3p/ABCB1 axis (174). These findings collectively underscore the diverse roles of lncRNA ROR in cancer biology. For the specific detailed regulatory pathways of ROR in various types of tumors, please refer to *Table 2*. In relation to its association with PTC, Fan *et al.* revealed that lncRNA ROR inhibits the recruitment of G9a to the TESC promoter, thereby upregulating TESC expression. TESC is likely to induce the upregulation of ALDH1, which in turn increases the expression of TUBB3, leading to reduced PTEN expression. Consequently, this cascade of events promotes the proliferation, migration, and invasion of PTC cells while suppressing apoptosis (175). The specific regulatory network can be seen in *Figure 4*.

In summary, lncRNA ROR exhibits a complex regulatory network in the development and progression of various types of tumors. It promotes cell growth and invasion in different tumor types and contributes to resistance to chemotherapy and radiotherapy. The mechanisms by which ROR exerts its effects are commonly through interactions with miR-145, further regulating the expression of downstream target genes. It can also promote the EMT process in cancer cells. The aforementioned key mechanisms are worthy of further investigation.

lncRNA alpha/beta hydrolase domain containing 11 antisense RNA 1 (ABHD11-AS1)

There is a substantial amount of research regarding the functional role of lncRNA ABHD11-AS1, located on human chromosome 7 q11.23. LncRNA ABHD11-AS1 plays a regulatory role in various cancer types by modulating different molecular pathways. In cervical cancer, it prevents FUS-mediated degradation of ABHD11 mRNA, leading to the activation of the EGFR signaling pathway (176). It also competitively binds to miR-330-5p and upregulates MARK2 expression, thereby promoting cervical cancer development (177). In addition, it accelerates the proliferation, invasion, and migration of cervical carcinoma cells by regulating miR-1254 (178). In epithelial ovarian cancer, three studies have demonstrated that ABHD11-AS1 promotes the progression of ovarian cancer through different mechanisms, namely, the EZH2/ABHD11-AS1/miR-133a-3p axis (179), the ABHD11-AS1/EZH2/TIMP2 axis (180), and by increasing the expression of RhoC (181). ABHD11-AS1 functions as an oncogene to promote cell proliferation and invasion in endometrial

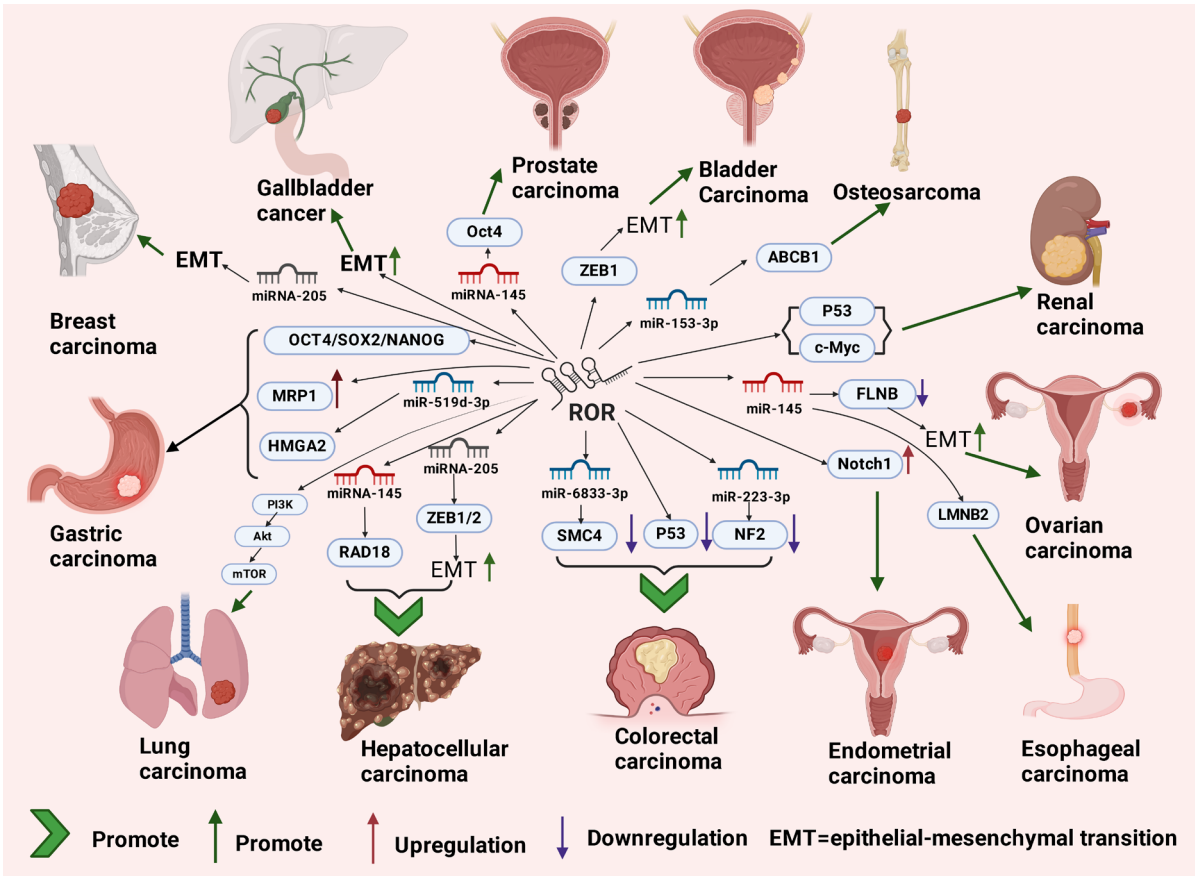

Figure 4 Regulatory network of lncRNA ROR in various cancers. Created with BioRender.com. EMT, epithelial-mesenchymal transition; lncRNA, long non-coding RNA; ROR, regulator of reprogramming.

carcinoma by positively targeting cyclin D1 (182). Knockdown of ABHD11-AS1 suppressed the progression of triple-negative breast cancer (TNBC) via upregulation of miR-199a-5p (183). In gastric cancer, boosts gastric cancer development by regulating miR-361-3p/PDPK1 signalling pathway (184). Furthermore, a study has suggested that the level of ABHD11-AS1 in gastric fluid is associated with tumor size, tumor stage, Lauren classification, and carcinoembryonic antigen levels in gastric cancer patients and ABHD11-AS1 in gastric fluid may serve as a potential biomarker for early gastric cancer screening (185). In pancreatic cancer, ABHD11-AS1 sponges miR-1231 (186), or activating the PI3K-AKT pathway (187), fostering cancer growth, and promoting lymphangiogenesis. In colorectal cancer, it advances cancer and invasion via ITGA5/FAK/PI3K/Akt pathway (188), miR-133a/SOX4 axis (189) or modulating the miR-1254-WNT11 pathway (190). In endometrial carcinoma, ABHD11-AS1 promotes tumor growth by targeting cyclin D1 (182). In epithelial ovarian cancer, it contributes to tumorigenesis and progression by regulating RhoC (181). Regarding its relationship with PTC, Lu *et al.* posit that ABHD11-AS1 promotes the progression of PTC by modulating the EPS15L1/EGFR pathway, leading to the activation of EGFR, EPS15L1, STAT3, and p-STAT3 (191). Zhuang *et al.* proposed that ABHD11-AS1 enhances cell proliferation, migration, and invasion *in vitro* by sequestering miR-199a-5p, leading to the activation of SLC1A5 and suppression of apoptosis, ultimately promoting tumorigenesis *in vivo* (192). Wen *et al.* proposed that ABHD11-AS1 positively regulates the PI3K/AKT signaling pathway, acting as a competitive endogenous RNA (ceRNA) by sequestering miR-1301-3p, thereby upregulating STAT3 expression, ultimately promoting the progression of PTC (193). The specific regulatory network can be seen in *Figure 5*.

Based on the above information, it can be observed that

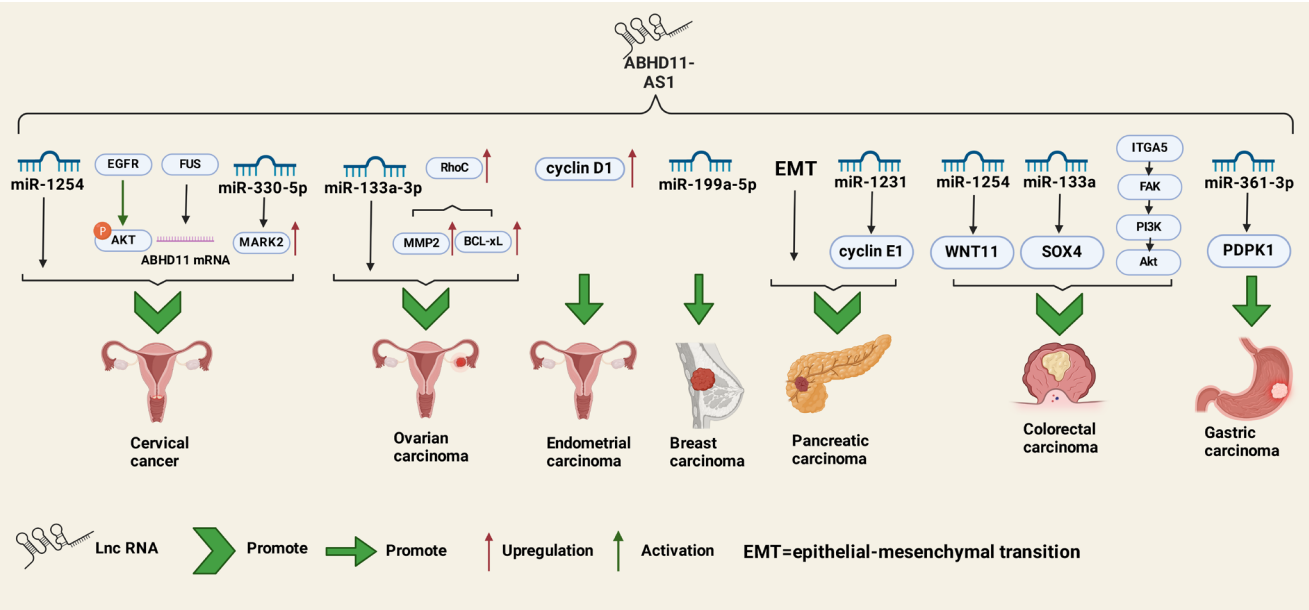

Figure 5 Regulatory network of lncRNA ABHD11-AS1 in various cancers. Created with BioRender.com. ABHD11-AS1, alpha/beta hydrolase domain containing 11 antisense RNA 1; EMT, epithelial-mesenchymal transition; lncRNA, long non-coding RNA.

lncRNA ABHD11-AS1 has been extensively studied in female reproductive system cancers such as cervical cancer and ovarian cancer, as well as digestive system cancers including pancreatic cancer, colorectal cancer, and gastric cancer. In all these cancers, ABHD11-AS1 has been found to play a role in promoting cancer progression. Additionally, in PTC, ABHD11-AS1 is also involved in tumor progression through different mechanisms. ABHD11-AS1 has the potential to serve as a novel target for cancer therapy. We have summarized the significant signaling pathways related to tumors other than PTC in *Table 2*. The regulation related to PTC has been compiled in *Table 3*.

Discussion

Cancer-related lncRNAs have gradually become a hot topic in the fields of RNA biology and oncology. In recent years, numerous studies have explored lncRNAs associated with PTC (194-196). Specifically, the biological and clinical relevance between lncRNAs and the occurrence and development of PTC is mainly manifested in the following aspects: (I) lncRNAs can competitively bind to targeted miRNAs that can mediate the degradation of mRNAs, thereby promoting the expression of specific PTC-related mRNAs and proteins. (II) Promote the modification of specific proteins and then affect their protein functions, such as enhancing the activity of metabolism-related enzymes. (III) Stimulate the degradation of tumor suppressor proteins such as P53. (IV) Activate specific oncogenic signaling pathways, such as the EPS15L1/EGFR signaling pathway, thereby promoting lymph node metastasis of PTC. All these pathways lead to the occurrence and development of PTC and poor clinical prognosis. However, current studies also show that a few lncRNAs can enhance the apoptosis of PTC cells and inhibit their proliferation (115,140,143). The mechanism is generally as follows: (I) competitively bind to targeted miRNAs to promote the expression of specific PTC inhibitory mRNAs and proteins. (II) Inhibit the progression of PTC by regulating tumor-related signaling pathways such as the AKT signaling pathway. Therefore, the role of lncRNAs in the occurrence and development of PTC is very complex and still has a very broad exploration prospect. It is worth noting that the most important mechanism by which lncRNAs affect PTC is through competitively binding to targeted miRNAs, thereby influencing the tumor-related mRNAs and proteins downstream of miRNAs and ultimately affecting the occurrence, development and prognosis of PTC.

According to the important role of lncRNAs in the pathogenesis of PTC as described above, we can propose corresponding possible treatment plans based on its carcinogenic pathogenesis: (I) since lncRNAs competitively

bind to miRNAs and prevent miRNAs from degrading targeted mRNAs, we can consider developing molecules that mimic miRNA activity to compensate for the role of miRNAs and play an antagonistic role against the carcinogenesis of lncRNAs. Existing studies have shown that this method can be used for the treatment of diseases (197,198). (II) Since carcinogenic lncRNAs related to PTC are overexpressed in PTC, specific drugs for treating PTC can be developed based on the principle that antisense oligonucleotides (ASOs) and siRNAs specifically bind to the target lncRNAs and then mediate the degradation of the target lncRNAs (199-202).

Radiotherapy has currently become an important means of treating patients with PTC (203). However, if patients have radiotherapy resistance, the therapeutic effect will be greatly reduced. A study has pointed out that radioiodine resistance is an important cause of death during PTC treatment, and the 10-year survival rate of affected patients is as low as 10% (204). Therefore, studying the influence of lncRNA on the sensitivity or resistance of radiotherapy in PTC patients is a very valuable topic. Existing studies have shown that lncRNA has a complex influence on the radioresistance and radiosensitivity of PTC. Among them, the study by Shi *et al.* found that LncRNA GLTC can enhance radioiodine resistance in papillary thyroid cancer (60). However, studies by some scholars have found that LncRNA-SLC6A9-5:2 and lncRNA CASC2 can increase the sensitivity of drug-resistant thyroid cancer cells to iodine-131 treatment (205,206). This clearly indicates that at present, there remain gaps in this field, and there is still extensive research space that merits further exploration.

Screening lncRNAs related to prognosis is of great significance for our future translational applications in clinical practice. Currently, the commonly used lncRNAs related to the prognosis of PTC patients are determined through statistical analysis and screening through The Cancer Genome Atlas (TCGA) database or other public databases. However, the lncRNAs identified by the above methods have not been verified by *in vivo* and *in vitro* experiments, so they do not have high credibility. Therefore, by searching relevant articles, we first determine high-quality PTC-related lncRNAs that have been experimentally verified, and then screen out lncRNAs related to the prognosis of PTC from them, which can effectively ensure their reliability. After careful screening, we found that in PTC patients, lncRNA SOCS2-AS1 and ABHD11-AS1 are significantly associated with poor prognosis (59,193). High expression of RNF185-AS1 is associated with larger tumor size, lymph node metastasis, and more advanced tumor-node-metastasis stage (150). High expression of lncRNA lnc-MPEG1-1 and MFSD4A-AS1 is significantly associated with lymph node metastasis in PTC patients, also indicating their association with worse prognosis (102,144). However, lncRNA FOXP4-AS1 is associated with a better prognosis in PTC patients (140). Based on this, we can construct a multi-lncRNA signature (SOCS2-AS1, ABHD11-AS1, RNF185-AS1, lnc-MPEG1-1, MFSD4A-AS1, FOXP4-AS1) to effectively predict the prognosis of PTC patients.

Moreover, it has been discovered that these lncRNAs also play regulatory roles in other malignant tumors. This indicates that they have complex regulatory networks involved in the growth processes of malignant tumors. Common mechanisms include the regulation of protein expression related to apoptosis, autophagy, and the cell cycle, as well as involvement in the EMT process of malignant tumor cells and the regulation of specific signaling pathways. Among these, the most common mechanism is the competitive binding of lncRNAs with specific miRNAs, ultimately affecting the expression of downstream proteins. The specific mechanisms are illustrated in *Figure 6*. However, for some recently discovered PTC-related lncRNAs, there is currently a lack of research reports on their association with other malignant tumors. Therefore, further research in this area is warranted. This review provides a valuable reference for future research.

Finally, although developing treatment regimens for malignant tumors based on lncRNAs is highly promising, it cannot be ignored that there are indeed some issues and challenges in the clinical application of lncRNAs that need to be overcome. (I) Specificity issues: undesired on-target effects due to uptake in cells other than the target cells, or off-target effects caused by sequence similarities or overdosing to levels much higher than the expected endogenous level. (II) Delivery issues: the "naked", unchemically modified RNA structure is unstable; there is inefficient intracellular delivery of RNA, and endosomal escape mechanisms need to be utilized for improvement; there is a lack of delivery vehicles suitable for targeting specific target organs and cell types. (III) Tolerability issues, such as the recognition of RNA structures by pathogen-associated molecular pattern receptors (such as Toll-like receptors), leading to adverse immune reactions (207,208). The above challenges also provide valuable directions for future research in this field.

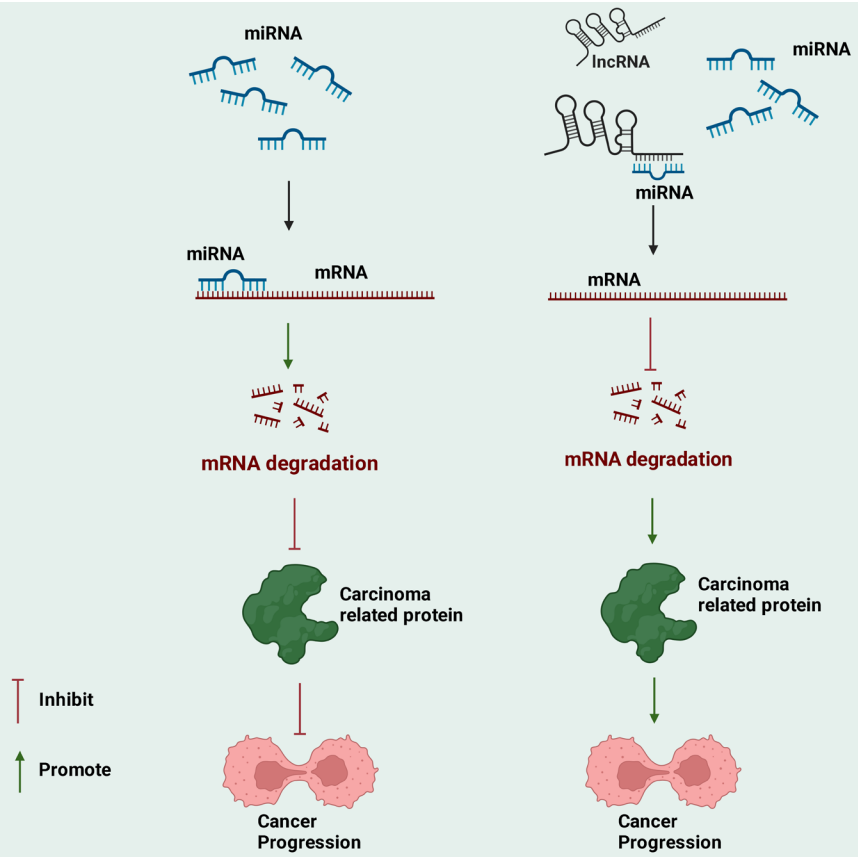

Figure 6 LncRNA competitively binds miRNAs, preventing mRNA degradation, leading to overexpression of cancer-related proteins, and promoting cancer onset, progression, invasion, and metastasis. Created with BioRender.com. lncRNA, long non-coding RNA; miRNAs, microRNAs; mRNA, messenger RNA.

Conclusions

The lncRNAs associated with PTC exert regulatory functions in other malignancies as well and possess similar regulatory mechanisms. The main mechanism is that PTC-related lncRNAs can competitively interact with miRNAs. This interaction affects miRNA-targeted mRNA and the expression of cancer-related proteins, ultimately promoting the progression of PTC and other malignant tumors. This provides a molecular basis for the future development of relevant targeted therapies.

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Footnote

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Ethical Statement: The authors are accountable for all aspects of the work in ensuring that questions related to the accuracy or integrity of any part of the work are appropriately investigated and resolved.

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