Review Article

Expression and crucial role of long non-coding RNA FGD5-AS1 in human cancers

Lixu Zhu 1,2,3,4* , Xiaoyi Shi 1,2,3,4* , Xiao Yu 1,2,3,4* , Zhihui Wang 1,2,3,4 , Menggang Zhang 1,2,3,4 , Yuting He 1,2,3,4 , Wenzhi Guo 1,2,3,4

¹Department of Hepatobiliary and Pancreatic Surgery, The First Affiliated Hospital of Zhengzhou University, Zhengzhou 450052, Henan, China; ²Key Laboratory of Hepatobiliary and Pancreatic Surgery and Digestive Organ Transplantation of Henan Province, The First Affiliated Hospital of Zhengzhou University, Zhengzhou 450052, Henan, China; ³Open and Key Laboratory of Hepatobiliary & Pancreatic Surgery and Digestive Organ Transplantation at Henan Universities, Zhengzhou 450052, Henan, China; ⁴Henan Key Laboratory of Digestive Organ Transplantation, Zhengzhou 450052, Henan, China. *Equal contributors.

Received April 6, 2021; Accepted August 23, 2021; Epub October 15, 2021; Published October 30, 2021

Abstract: Long non-coding RNAs (IncRNAs) are transcribed by RNA polymerase II and are longer than 200 nucleotides. Several studies have revealed that IncRNAs are important regulators of cancer progression. The IncRNA FGD5-AS1, first identified in 2018, has emerged as a crucial regulator of processes related to carcinogenesis. The expression levels of FGD5-AS1 are known to be significantly up-regulated in a variety of human cancers. Moreover, FGD5-AS1 expression closely correlates with clinical features and poor prognosis and its expression has been shown to attenuate cell proliferation, cell migration, cell invasiveness, drug resistance, and the epithelial-mesenchymal transition through several pathways. Here, we provide an overview of the role of FGD5-AS1 in various cancers and discuss its potential clinical utility in tumor progression. In addition, we used a gene expression profiling interactive analysis dataset to explore associations between FGD5-AS1 pan-cancer expressions and prognoses.

Keywords: LncRNA, FGD5-AS1, mechanism, prognosis, clinical utility

Introduction

Cancers are complex diseases that are driven by many factors [1, 2], including changes in the transcriptome [3, 4], proteome [5, 6], and the metabolome [7, 8]. In addition, cancers still have high rates of morbidity and mortality [9-11], making them important public-health problems. Although cancer treatments have improved greatly in past years [12, 13], effective treatments for many cancers are still elusive. Therefore, further studies exploring cancer pathogenesis remain highly relevant.

Long non-coding RNAs (IncRNAs) have more than 200 nucleotides [14, 15], and are transcribed by RNA polymerase II [16]. When first identified, IncRNAs were considered to be transcriptional noise without biological functions [17-19]. However, a large literature has emerged recently supporting the idea that IncRNAs are important regulators of cancer progression

for many solid tumors [20-24]. LncRNAs have been shown to affect cell proliferation, migration, and apoptosis by regulating gene expression at all levels: transcriptional, posttranscriptional, epigenetic, and by protein translation [25-27]. Several studies have also revealed that IncRNAs represent potential diagnostic biomarkers and targets for tumor treatments [28-30].

FGD5 antisense RNA 1 (FGD5-AS1), a novel lncRNA, was first identified in 2018 [31, 32]. Accumulating evidence has suggested that FGD5-AS1 is a functional factor in cancer, with up-regulated expression levels in several types of solid tumors. FGD5-AS1 expression has also been shown to be closely associated with several clinicopathologic features, indicating its possible use as a prognostic biomarker. Moreover, FGD5-AS1 has been shown to affect biological functions both by acting as a competing endogenous RNA (ceRNA) and by regulating other pathways. Here, we have summa-

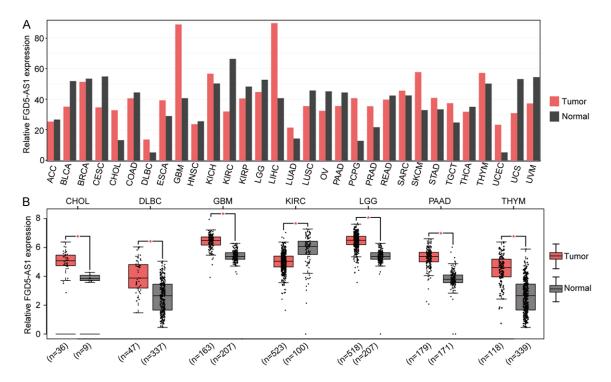


Figure 1. Pan-cancer expression patterns for IncRNA FGD5-AS1. A. FGD5-AS1 expression levels among 33 types of cancer and their paired normal tissues based on the gene expression profiling interactive analysis (GEPIA) dataset. B. High FGD5-AS1 expression levels were observed in CHOL, DLBC, GBM, LGG, PAAD, and THYM samples. However, decreased FGD5-AS1 expression was observed in KIRC samples.

Table 1. Clinical characters associated with FGD5-AS1 in different cancers

Туре	Expression	Clinical characters	Refs
non-small cell lung cancer	upregulated	TNM stage, metastasis, and tumor sizes	[40, 41]
hepatocellular carcinoma	upregulated	overall survival	[65]
osteosarcoma	upregulated	tumor size, clinical stage, and 5-year survival rate	[64]
melanoma	upregulated	tumor thickness and tumor stage, overall survival, and disease-free survival	[66]
esophageal squamous cell carcinoma	upregulated	tumor size, TNM stage, lymph node metastasis, and overall survival	[61]

rized the literature related to the oncogenic roles and regulatory mechanisms of FGD5-AS1 in solid tumors and discuss its use for novel diagnostic and therapeutic strategies related to cancer.

Expression levels of FGD5-AS1 in different cancers

To systematically identify the expression of FGD5-AS1 in different cancers, we used the Gene Expression Profiling Interactive Analysis (GEPIA, http://gepia.cancer-pku.cn/) tool [32]. The results showed that FGD5-AS1 expression levels were dysregulated in many solid tumors (Figure 1A) and that it was significantly up-regulated in cholangiocarcinoma (CHOL) (Figure 1B). Similarly, significant increases in its expression were observed in lymphoma (DLBC),

glioblastoma multiforme (GBM), brain low-grade glioma (LGG), pancreatic adenocarcinoma (PAAD), and thymoma (THYM). Interestingly, FGD5-AS1 expression was significantly down-regulated in kidney renal clear cell carcinoma (KIRC) (Figure 1B).

Clinical significance and functions of FGD5-AS1

Increasing evidence indicates that FGD5-AS1 plays crucial roles in cancer progression through demonstrated relationships between FGD5-AS1 expression and clinical significance (**Table 1**). Several studies have reported that FGD5-AS1 may be a prognostic biomarker for a variety of cancers. Below, we discuss the clinical significance and functions of FGD5-AS1 in different tumors (**Table 2**).

LncRNA FGD5-AS1 in human cancers

Table 2. Roles and functions of FGD5-AS1 in different cancers

Туре	Role	Function	Refs
non-small cell lung cancer	oncogene	proliferation, viability, migration, invasion, autophagy, and EMT	[39-42]
hepatocellular carcinoma	oncogene	/	[65]
osteosarcoma	oncogene	viability, invasion, and apoptosis	[64]
melanoma	oncogene	/	[66]
glioma	oncogene	proliferation, migration, and invasion	[47]
glioblastoma	oncogene	proliferation, viability, migration, invasion, and tumor growth	[48, 49]
colorectal cancer	oncogene	proliferation, migration, invasion, and apoptosis	[67]
oral cancer	oncogene	proliferation, cell growth, migration, invasion, and apoptosis	[56, 57]
renal cell carcinoma	oncogene	proliferation, migration, EMT, and invasion	[68, 69]
esophageal squamous cell carcinoma	oncogene	proliferation, migration, invasion, apoptosis, and tumor growth	[61]
gastric cancer	oncogene	cancer proliferation, 5-FU chemoresistance, and tumorigenicity	[70]

Lung cancer

Lung cancer is a leading cause of cancer-related deaths in the world [33-35]. Many risk factors have been shown to contribute to it, including age, gender, race, environmental pollution, cigarette smoking, and pre-existing lung diseases [35, 36]. Non-small cell lung cancer (NSCLC) is the most prevalent type of lung cancer, accounting for approximately 85% of all lung cancer cases [37, 38].

FGD5-AS1 expression levels were found to be up-regulated in both NSCLC tissues and cells [39-41]. The levels of FGD5-AS1 have also been reported to be significantly correlated with many clinicopathologicfeatures (e.g., TNM staging, tumor size, and metastasis) [40, 41]. Elevated expression of FGD5-AS1 was correlated with a higher TNM stage, larger tumor size, and NSCLC metastasis. Furthermore, the up-regulation of FGD5-AS1 has been shown not only to accelerate cell proliferation, migration, invasiveness, and epithelial-mesenchymal transitions (EMTs) in NSCLC but also to increase cell viability in patients with NSCLC. Intriguingly, Fu et al. [42] reported that the expression of FGD5-AS1 was also increased in patients with cisplatin-resistant NSCLC. In addition, cell proliferation and motility were also found to be promoted by FGD5-AS1 expression, and FGD5-AS1 was reported to enhance cell autophagy in NSCLC by increasing the levels of both LC3-II/LC3-I and Beclin-1 protein, and by decreasing p62 expression. In contrast, the knockdown of FGD5-AS1 expression has been shown to inhibit tumor growth in patients with cisplatin-resistant NSCLC [42].

Glioma

Glioma is the most common type of primary intracranial tumor in the central nervous system [43, 44], and glioblastoma (GBM) represents the most common type of aggressive malignant glioma [45, 46]. FGD5-AS1 levels have been shown to be significantly up-regulated in both glioma tissue and cells [47], with similar findings in GBM tissue and cells [48, 49]. The down-regulation of FGD5-AS1 levels has been shown to attenuate proliferation capacity, invasiveness, and cell migration in both glioma and GBM, and both cell viability and colony-forming capacity were impaired as a result of FGD5-AS1 silencing [49]. In addition, FGD5-AS1 expression was positively correlated with tumor weights using in vivo studies for both glioma and GBM. Overall, these findings indicate that FGD5-AS1 functions as an oncogene and facilitates tumor progression in both glioma and GBM [47-49].

Oral cancer

Oral cancer (OC) continues to have a high mortality rate in head-and-neck cancer patients [50, 51], with oral squamous cell carcinoma (OSCC) being the most common type of oral cancer [52, 53]. Despite advances in clinical treatment, the prognosis of patients with OSCC remains poor [54, 55]. Several research groups have reported that FGD5-AS1 expression levels were markedly up-regulated in both OC tissues and cells [56, 57], and, FGD5-AS1 levels have been shown to be positively correlated with smoking, clinical staging, tumor staging, and tumor sizes in patients with OC [56]. Increased FGD5-AS1 expression has been re-

ported to significantly promote cell growth, migration, and invasiveness, while negatively inhibiting apoptosis in OC cells. In addition, xenograft studies using a nude-mouse model showed that FGD5-AS1 expression contributed OC tumor growth [56, 57].

Esophageal cancer

Esophageal cancer is the sixth most common cause of cancer-related death worldwide [58, 591, with esophageal squamous cell carcinoma (ESCC) being its most common type [60]. The search for effective treatments for esophageal cancer needs to continue. Gao et al. [61] observed that the expression of FGD5-AS1 was significantly increased in both ESCC tissues and cell lines. Moreover, FGD5-AS1 expression has been shown to be positively associated with tumor size, TNM staging, and lymph node metastasis, while being negatively associated with ESCC patient overall survival. Importantly, the silencing of FGD5-AS1 expression was shown to suppress cell proliferation, migration, and invasiveness in ESCC but promote cell apoptosis. Furthermore, in vivo experiments have demonstrated that FGD5-AS1 expression functioned to promote ESCC tumor growth [61].

Osteosarcoma

Osteosarcoma is the most frequent type of primary bone tumor, often occurring in children, adolescents, and young adults [62, 63]. Studies have reported that FGD5-AS1 levels in both serum and tissue were significantly elevated in patients with osteosarcoma [64], and that FGD5-AS1 might be used as a diagnostic biomarker for this type of cancer. In addition, FGD5-AS1 expression has been positively associated with both osteosarcoma tumor size and clinical staging, with increased serum and tissue expression levels being a poor predictor of prognosis. Biological functions, represented by measures of cell viability, invasiveness, and EMT capacity, have been reported to be enhanced by the up-regulation of FGD5-AS1 expression [64]. Therefore, FGD5-AS1 is also considered an oncogene for osteosarcoma tumorigenesis and progression.

Other cancer types

In addition to the above tumor types, studies have also found FGD5-AS1 expression levels to be significantly up-regulated in hepatocellu-

lar carcinoma [65], melanoma [66], colorectal cancer [67], renal cell carcinoma [68, 69], and gastric cancer [70]. Levels of FGD5-AS1 have been reported to be negatively associated with prognoses for both hepatocellular carcinoma [65] and melanoma [66], and FGD5-AS1 expression was found to be significantly correlated with both tumor thickness and advancedtumor staging in melanoma [66]. Patients with lower FGD5-AS1 expression had higher overall survival and disease-free survival than patients with higher FGD5-AS1 expression in melanoma. Functionally, FGD5-AS1 has been shown to contribute to cell proliferation in colorectal cancer, renal cell carcinoma, and gastric cancer. Expression of FGD5-AS1 promoted cell proliferation and motility, and accelerated cell apoptosis in colorectal cancer [67], whereas knockdown of FGD5-AS1 inhibited cell proliferation, motility, and the EMT process in renal cell carcinoma [68]. Moreover, decreased FGD5-AS1 expression was shown to restrain chemoresistance to 5-FU in gastric cancer cells, and the up-regulation of FGD5-AS1 has been reported to promote the EMT process [70].

FGD5-AS1 regulatory mechanisms

FGD5-AS1 has been revealed to have important roles in both tumorigenesis and tumor development. It has been shown to affect tumor progression by regulating several pathways (Figure 2). In this section, we will summarize FGD5-AS1 regulatory mechanisms according to cell-biology functions in different cancers.

Cell proliferation

Cell proliferation is a fundamental characteristic of all organisms [71, 72], and this process becomes abnormal in many cancers [73, 74]. Growing evidence suggests that IncRNAs have fundamental roles in cellular proliferation related to cancer [22, 75, 76], and FGD5-AS1 has been shown to function as a ceRNA-type controller of this process. FGD5-AS1 has been reported to act as a ceRNA for hsa-miR-107 in NSCLC, resulting in accelerated cell proliferation through the increased expression of FGFRL1 [39] (Figure 3). Similarly, FGD5-AS1 has also been shown to promote NSCLC cell proliferation by regulating the miR-493-5p/ DDX5 pathway [41], and its regulation of the miR-140-5p/WEE1 axis promoted cisplatin-resistant NSCLC cell proliferation but inhibited

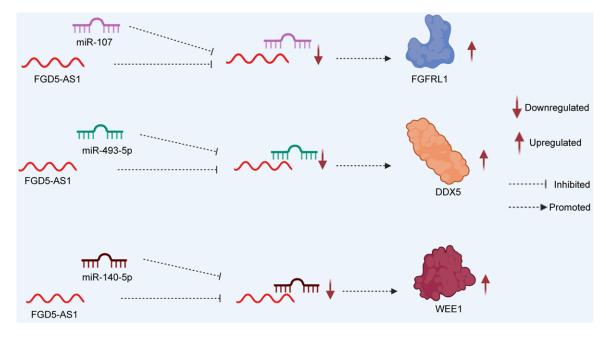


Figure 2. The regulatory mechanisms of FGD5-AS1 in lung cancer. FGD5-AS1 promoted NSCLC cell proliferation through a series of pathways, including the FGD5-AS1/miR-107/FGFRL1 pathway, the FGD5-AS1/miR-493-5p/DDX5 pathway, and the FGD5-AS1/miR-140-5p/WEE1 pathway. FGD5-AS1 increased the level of FGFRL1 by sponging miR-107. FGD5-AS1 also significantly downregulated miR-493-5p levels to promote the expression of DDX5 and enhanced the expression of WEE1 by sponging miR-140-5p.

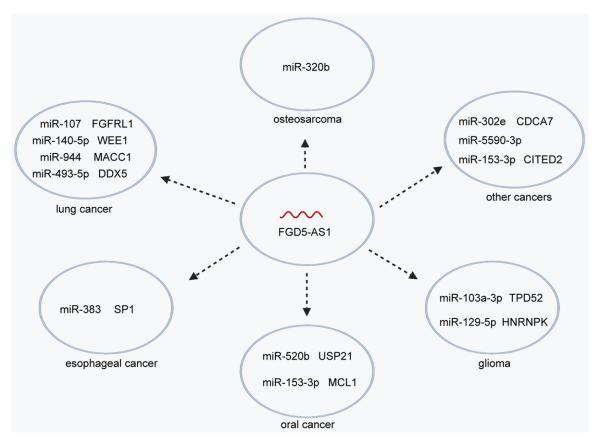


Figure 3. FGD5-AS1 interactions with target molecules in different cancers. FGD5-AS1 often acts as a competing endogenous RNA (ceRNA), contributing to cancer progression.

apoptosis [42] (Figure 3). In addition, FGD5-AS1 expression was reported to contribute to GBM cancer-cell proliferation through the down-regulation of HNRNPK by miR-129-5p sponging [49], and to promote GBM cell proliferation by regulating the Wnt/β-catenin pathway [47]. In colorectal cancer, FGD5-AS1 expression was shown to facilitate cancer-cell proliferation through the sponging of miR-302e to up-regulate CDCA7 expression [67], and in oral cancer [57], FGD5-AS1 was reported to attenuate the expression of miR-153-3p and up-regulate MCL1 to enhance cellular proliferation. Furthermore, cell proliferation in renal cancer was reportedly reduced by FGD5-AS1-inhibition of miR-5590-3p levels [68], although it was shown to promote cellular proliferation in ESCC by targeting miR-383 [61]. Similarly, cell proliferation in gastric cancer has been shown to be facilitated through the FGD5-AS1/miR-153-3p/CITED2 pathway [70].

Cell migration and invasiveness

A leading cause for the failure of cancer treatments is cancer metastasis [77]. The ability of cells to migrate and to invade other tissues has a direct effect on cancer metastasis [78, 79], and IncRNAs have been found to be significantly associated with cancer-cell capacities for both migration and invasiveness [80-82]. FGD5-AS1 has been shown to promote cell migration and cell invasion using several molecular pathways. In NSCLC, the down-regulation of FGD5-AS1 reduced migration and invasiveness by its action as a ceRNA for miR-944 [40], thereby increasing MACC1 expression. FGD5-AS1 was also shown to promote NSCLC cell migration and invasiveness by lowering the expression of miR-493-5p and upregulating the level of DDX5 [41]. In cisplatinresistant NSCLC cells, FGD5-AS1 was also reported to promote migration and invasiveness through the modulation of the miR-140-5p/WEE1 axis [42]. In osteosarcoma cells, FGD5-AS1 expression was shown to downregulate the expression levels of miR-320b, which facilitated both cell migration and invasiveness [64]. In addition, FGD5-AS1 expression was reported to accelerate cell migration and invasiveness by activating the Wnt/βcatenin pathway in both glioma and GBM [47, 49]. In the case of GBM, FGD5-AS1 expression reduced miR-130-3p levels, resulting in increased TPD52 levels and the promotion of cell migration and invasiveness [48]. In colorectal cancer, FGD5-AS1 was shown to act as a ceRNA for miR-302e, thereby enhancing cell migration and invasiveness by up-regulating CDCA7 [67]. Cell invasiveness was also reported to be enhanced through the FGD5-AS1/miR-520b/USP21 and FGD5-AS1/miR-153-3p/MCL1 pathways in oral cancer [56, 57]. In renal cell carcinoma, FGD5-AS1 expression accelerated cell migration and invasiveness by activating ERK/AKT signaling via the sponging of miR-5590-3p [68], and in ESCC, FGD5-AS1 expression promoted tumor metastasis by inhibiting miR-383 levels and thereby up-regulating the expression of SP1 [61].

Chemoresistance and the epithelial-mesenchymal transition (EMT)

Although chemotherapy treatments are wellestablished for tumors [83, 84], drug resistance has reduced chemotherapy efficacy [85-87]. Therefore, determining the mechanisms responsible for tumor resistance will be very important for the future of clinical tumor treatment. In gastric cancer, Gao et al. found that elevated levels of FGD5-AS1 increased cell chemoresistance to 5-FU [70], and in NSCLC, the expression of FGD5-AS1 increased cisplatin resistance through by modulating the miR-140-5p/WEE1 pathway [42]. This not only provides guidance for potential clinical therapies, but also provides new insight into potential therapeutic targets for both gastric cancer and NSCLC.

EMT, the transdifferentiation process whereby epithelial cells become motile mesenchymal cells [88, 89], is known to be crucial for many biological processes, including embryonic development, fibrosis, and tumor progression [90-92]. In NSCLC, FGD5-AS1 expression was found to promote the EMT process by increasing the expression level of DDX5 through miR-493-5p sponging [41], and in renal cancer, FGD5-AS1 was reported to inhibit the expression of miR-5590-3p, thereby activating the ERK/AKT pathway to facilitate the EMT process [68].

The potential clinical utility of FGD5-AS1

Above, we have summarized the regulatory mechanisms, clinical significance, and func-

tions of FGD5-AS1 for different tumors, highlighting its potential for clinical use. Below, we discuss the potential clinical utility of FGD5-AS1 for cancer diagnosis, prognosis, and therapy.

FGD5-AS1 as a diagnostic biomarker

Diagnostic biomarkers have become important and gained attention because they offer the promise of early diagnosis for tumors and may improve patient prognoses [93-95], FGD5-AS1 is such a promising biomarker for cancer diagnosis. FGD5-AS1 has been shown to be significantly up-regulated in NSCLC [39-42], hepatocellular carcinoma (HCC) [65], osteosarcoma [64], melanoma [66], glioma [47], GBM [48, 49], colorectal cancer [67], oral cancer [56, 57], renal cell carcinoma [68, 69], ESCC [61], and gastric cancer [70]. This was especially true for the significantly elevated serum levels of FGD5-AS1 from patients with osteosarcoma compared to serum levels from normal controls [64]. In addition, FGD5-AS1 expression has been shown to be significantly correlated with both TNM and clinical staging [40, 61, 64, 66], which may help to assess clinical severity in patients with tumors. However, the clinical application of FGD5-AS1 levels for diagnostic use still requires more basic and clinical research support.

FGD5-AS1 as a prognosis predictor

Current evidence suggests that IncRNAs significantly correlated with tumor-patient prognoses could be used as biomarkers for prognosis [76, 96]. Up-regulated FGD5-AS1 expression has been positively associated with poor prognoses (e.g., in HCC [65], osteosarcoma [64], melanoma [66], and ESCC [61]) and predicted shorter patient overall survival for HCC [65], melanoma [66], and ESCC [61]. FGD5-AS1 expression levels were also negatively correlated with 5-year survival rates in patients with osteosarcoma [64]. Using a multivariate analysis of melanoma data, the FGD5-AS1 expression level was determined to be an independent risk factor for both overall survival prognosis and disease-free survival [66].

Using the GEPIA online tool, we explored other associations between FGD5-AS1 expression levels and patient prognoses in several cancers [97]. The expression of FGD5-AS1 was significantly associated with prognoses for

KIRC, liver hepatocellular carcinoma (LIHC), GBM, and for mesothelioma (MESO). For KIRC, decreased levels of FGD5-AS1 predicted shorter overall patient survival (Figure 4A), while high FGD5-AS1 expression was positively correlated with overall survival in LIHC patients (Figure 4B). In addition, its expression level was negatively correlated with disease-free survival in both GBM and KIRC (Figure 4C and 4D). In contrast, up-regulated FGD5-AS1 expression was associated with shorter disease-free survival in both ACC and MESO [97] (Figure 4E and 4F).

FGD5-AS1 as a therapeutic target

As FGD5-AS1 expression has been shown to affect carcinogenesis by regulating a variety of molecular pathways, this suggests that it may also be a therapeutic target for cancer treatments. FGD5-AS1-mediated regulation of biological functions is known to occur via many pathways in different cancers, including the hsa-miR-107/FGFRL1 [39], miR-493-5p/DDX5 [41], miR-140-5p/WEE1 [42], miR-129-5p/ HNRNPK [49], Wnt/β-catenin [47], miR-302e/ CDCA7 [67], and the miR-153-3p/MCL1 pathways [57]. In addition, the observation that upregulated FGD5-AS1 expression also promoted cellular chemoresistance to 5-FU in gastric cancer may guide its future treatment [70]. Furthermore, as FGD5-AS1 has been shown to function as an oncogene in NSCLC [39, 42], HCC [65], osteosarcoma [64], melanoma [66], glioma [47], GBM [48, 49], colorectal cancer [67], oral cancer [56], renal cell carcinoma [68, 69], ESCC [61], and gastric cancer [70], its down-regulation could be used to block tumor progression for these cancers. For NSCLC, in vivo studies found that FGD5-AS1 knockdown attenuated tumor growth in cisplatin-resistant NSCLC [42], and in osteosarcoma [64], decreased both FGD5-AS1 expression and cell viability and invasiveness. For GBM, FGD5-AS1 silencing resulted in reduced cell viability, colony-forming capacity, cell proliferation, invasiveness, and promoted apoptosis [49].

Conclusions and future perspectives

FGD5-AS1, first identified in 2018, has emerged as a crucial factor in both tumorigenesis and tumor development. The expression levels of FGD5-AS1 have been shown to be significantly up-regulated in NSCLC, HCC, osteosar-

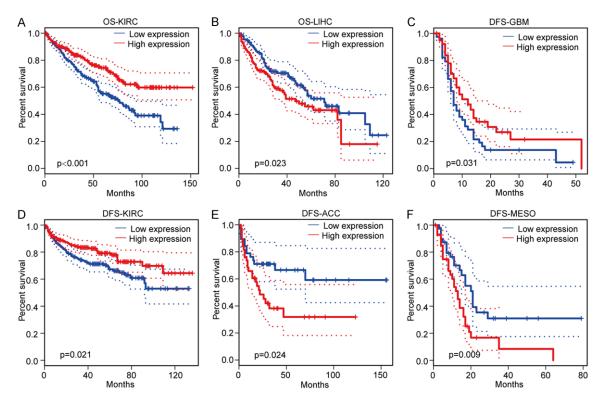


Figure 4. Pan-cancer prognostic predictions using FGD5-AS1 levels. A. KIRC patients with high FGD5-AS1 expressions had better overall survival (OS) times (P<0.001). B. LIHC patients with low FGD5-AS1 expressions had better OS times (P=0.023). C and D. Both GBM and KIRC patients with high FGD5-AS1 expressions had better disease-free survival (DFS) times (GBM, P=0.031; KIRC, P=0.021). E and F. Both ACC and MESO patients with low FGD5-AS1 expressions had better DFS times (ACC, P=0.024; MESO, P=0.009).

coma, melanoma, glioma, GBM, colorectal cancer, oral cancer, renal cell carcinoma, ES-CC, and gastric cancer. In addition, FGD5-AS1 expression has been closely correlated with clinical features, including tumor size, tumor thickness, clinical staging, TNM staging, and metastasis. Moreover, FGD5-AS1 levels have been positively correlated with poor prognosis in HCC, osteosarcoma, melanoma, and ESCC. FGD5-AS1 expression is known to regulate cell proliferation, migration, invasiveness, drug resistance, and EMT by modifying different pathways, including the hsa-miR-107/FGFRL1 pathway, the Wnt/β-catenin pathway, the miR-302e/CDCA7 pathway, and miR-520b/USP21 pathway in different cancers. However, the specific regulatory mechanisms underlying the functions of FGD5-AS1 remain to be elucidated. FGD5-AS1 has also been shown to have an oncogenic role in tumor progression, and its down-regulation could be used to block the processes that promote carcinogenesis in these tumors. As a promising biomarker, FGD5-AS1 levels may also be used for cancer diagnosis and for predicting their prognoses, especially for the early diagnosis of tumors. However, these FGD5-AS1 clinical applications will require further systematic studies.

Acknowledgements

This work was supported by the National Natural Science Foundation of China (81671-958), the Youth Talent Lifting Project of Henan Province (2021HYTP059), and Key Scientific Research Project of Henan Higher Education Institutions of China (21A320026).

Disclosure of conflict of interest

None.

Address correspondence to: Drs. Yuting He and Wenzhi Guo, The First Affiliated Hospital of Zhengzhou University, Zhengzhou 450052, Henan, China. Tel: +86-371-67967126; E-mail: fccheyt1@zzu.edu.cn (YTH); Tel: +86-371-67967128; E-mail: fccguowz@zzu.edu.cn (WZG)

References

- [1] Bugter JM, Fenderico N and Maurice MM. Mutations and mechanisms of WNT pathway tumour suppressors in cancer. Nat Rev Cancer 2021; 21: 5-21.
- [2] Doherty GJ, Petruzzelli M, Beddowes E, Ahmad SS, Caldas C and Gilbertson RJ. Cancer treatment in the genomic era. Annu Rev Biochem 2019; 88: 247-280.
- [3] Xiang Y, Ye Y, Zhang Z and Han L. Maximizing the utility of cancer transcriptomic data. Trends Cancer 2018; 4: 823-837.
- [4] Chang WH and Lai AG. An immunoevasive strategy through clinically-relevant pan-cancer genomic and transcriptomic alterations of JAK-STAT signaling components. Mol Med 2019; 25: 46.
- [5] Ellis MJ, Gillette M, Carr SA, Paulovich AG, Smith RD, Rodland KK, Townsend RR, Kinsinger C, Mesri M, Rodriguez H and Liebler DC; Clinical Proteomic Tumor Analysis Consortium (CPTAC). Connecting genomic alterations to cancer biology with proteomics: the NCI Clinical Proteomic Tumor Analysis Consortium. Cancer Discov 2013; 3: 1108-1112.
- [6] Peng X, Xu X, Wang Y, Hawke DH, Yu S, Han L, Zhou Z, Mojumdar K, Jeong KJ, Labrie M, Tsang YH, Zhang M, Lu Y, Hwu P, Scott KL, Liang H and Mills GB. A-to-I RNA editing contributes to proteomic diversity in cancer. Cancer Cell 2018; 33: 817-828, e817.
- Wang LB, Karpova A, Gritsenko MA, Kyle JE, Cao S, Li Y, Rykunov D, Colaprico A, Rothstein JH, Hong R, Stathias V, Cornwell M, Petralia F, Wu Y, Reva B, Krug K, Pugliese P, Kawaler E, Olsen LK, Liang WW, Song X, Dou Y, Wendl MC, Caravan W, Liu W, Cui Zhou D, Ji J, Tsai CF, Petyuk VA, Moon J, Ma W, Chu RK, Weitz KK, Moore RJ, Monroe ME, Zhao R, Yang X, Yoo S, Krek A, Demopoulos A, Zhu H, Wyczalkowski MA, McMichael JF, Henderson BL, Lindgren CM, Boekweg H, Lu S, Baral J, Yao L, Stratton KG, Bramer LM, Zink E, Couvillion SP, Bloodsworth KJ, Satpathy S, Sieh W, Boca SM, Schürer S, Chen F, Wiznerowicz M, Ketchum KA, Boja ES, Kinsinger CR, Robles AI, Hiltke T, Thiagarajan M, Nesvizhskii Al, Zhang B, Mani DR, Ceccarelli M, Chen XS, Cottingham SL, Li QK, Kim AH, Fenyö D, Ruggles KV, Rodriguez H, Mesri M, Payne SH, Resnick AC, Wang P, Smith RD, lavarone A, Chheda MG, Barnholtz-Sloan JS, Rodland KD, Liu T and Ding L; Clinical Proteomic Tumor Analysis Consortium (CPTAC). Proteogenomic and metabolomic characterization of human glioblastoma. Cancer Cell 2021; 39: 509-528, e20.
- [8] Sreekumar A, Poisson LM, Rajendiran TM, Khan AP, Cao Q, Yu J, Laxman B, Mehra R, Lonigro RJ, Li Y, Nyati MK, Ahsan A, Kalyana-Sun-

- daram S, Han B, Cao X, Byun J, Omenn GS, Ghosh D, Pennathur S, Alexander DC, Berger A, Shuster JR, Wei JT, Varambally S, Beecher C and Chinnaiyan AM. Metabolomic profiles delineate potential role for sarcosine in prostate cancer progression. Nature 2009; 457: 910-914.
- [9] Moukayed M and Grant WB. The roles of UVB and vitamin D in reducing risk of cancer incidence and mortality: a review of the epidemiology, clinical trials, and mechanisms. Rev Endocr Metab Disord 2017; 18: 167-182.
- [10] Arnold M, Karim-Kos HE, Coebergh JW, Byrnes G, Antilla A, Ferlay J, Renehan AG, Forman D and Soerjomataram I. Recent trends in incidence of five common cancers in 26 European countries since 1988: analysis of the European cancer observatory. Eur J Cancer 2015; 51: 1164-1187.
- [11] Rao S, Mondragón L, Pranjic B, Hanada T, Stoll G, Köcher T, Zhang P, Jais A, Lercher A, Bergthaler A, Schramek D, Haigh K, Sica V, Leduc M, Modjtahedi N, Pai TP, Onji M, Uribesalgo I, Hanada R, Kozieradzki I, Koglgruber R, Cronin SJ, She Z, Quehenberger F, Popper H, Kenner L, Haigh JJ, Kepp O, Rak M, Cai K, Kroemer G and Penninger JM. AIF-regulated oxidative phosphorylation supports lung cancer development. Cell Res 2019; 29: 579-591.
- [12] Topper MJ, Vaz M, Marrone KA, Brahmer JR and Baylin SB. The emerging role of epigenetic therapeutics in immuno-oncology. Nat Rev Clin Oncol 2020; 17: 75-90.
- [13] Herrmann J. Adverse cardiac effects of cancer therapies: cardiotoxicity and arrhythmia. Nat Rev Cardiol 2020; 17: 474-502.
- [14] Li J, Li Z, Zheng W, Li X, Wang Z, Cui Y and Jiang X. LncRNA-ATB: an indispensable cancer-related long noncoding RNA. Cell Prolif 2017; 50: e12381.
- [15] Liu SJ, Horlbeck MA, Cho SW, Birk HS, Malatesta M, He D, Attenello FJ, Villalta JE, Cho MY, Chen Y, Mandegar MA, Olvera MP, Gilbert LA, Conklin BR, Chang HY, Weissman JS and Lim DA. CRISPRi-based genome-scale identification of functional long noncoding RNA loci in human cells. Science 2017; 355: aah7111.
- [16] Bunch H, Lawney BP, Burkholder A, Ma D, Zheng X, Motola S, Fargo DC, Levine SS, Wang YE and Hu G. RNA polymerase II promoter-proximal pausing in mammalian long non-coding genes. Genomics 2016; 108: 64-77.
- [17] Ponting CP, Oliver PL and Reik W. Evolution and functions of long noncoding RNAs. Cell 2009; 136: 629-641.
- [18] Wu SC, Kallin EM and Zhang Y. Role of H3K27 methylation in the regulation of IncRNA expression. Cell Res 2010; 20: 1109-1116.
- [19] Cloutier SC, Wang S, Ma WK, Al Husini N, Dhoondia Z, Ansari A, Pascuzzi PE and Tran EJ.

- Regulated formation of IncRNA-DNA hybrids enables faster transcriptional induction and environmental adaptation. Mol Cell 2016; 61: 393-404.
- [20] Kim J, Piao HL, Kim BJ, Yao F, Han Z, Wang Y, Xiao Z, Siverly AN, Lawhon SE, Ton BN, Lee H, Zhou Z, Gan B, Nakagawa S, Ellis MJ, Liang H, Hung MC, You MJ, Sun Y and Ma L. Long noncoding RNA MALAT1 suppresses breast cancer metastasis. Nat Genet 2018; 50: 1705-1715.
- [21] Huang D, Chen J, Yang L, Ouyang Q, Li J, Lao L, Zhao J, Liu J, Lu Y, Xing Y, Chen F, Su F, Yao H, Liu Q, Su S and Song E. NKILA IncRNA promotes tumor immune evasion by sensitizing T cells to activation-induced cell death. Nat Immunol 2018; 19: 1112-1125.
- [22] Pandey GK, Mitra S, Subhash S, Hertwig F, Kanduri M, Mishra K, Fransson S, Ganeshram A, Mondal T, Bandaru S, Ostensson M, Akyürek LM, Abrahamsson J, Pfeifer S, Larsson E, Shi L, Peng Z, Fischer M, Martinsson T, Hedborg F, Kogner P and Kanduri C. The risk-associated long noncoding RNA NBAT-1 controls neuroblastoma progression by regulating cell proliferation and neuronal differentiation. Cancer Cell 2014; 26: 722-737.
- [23] Schmitt AM and Chang HY. Long noncoding RNAs in cancer pathways. Cancer Cell 2016; 29: 452-463.
- [24] Sun TT, He J, Liang Q, Ren LL, Yan TT, Yu TC, Tang JY, Bao YJ, Hu Y, Lin Y, Sun D, Chen YX, Hong J, Chen H, Zou W and Fang JY. LncRNA GCInc1 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.
- [25] Ma Y, Zhang J, Wen L and Lin A. Membranelipid associated IncRNA: a new regulator in cancer signaling. Cancer Lett 2018; 419: 27-29.
- [26] Zhu J, Fu H, Wu Y and Zheng X. Function of IncRNAs and approaches to IncRNA-protein interactions. Sci China Life Sci 2013; 56: 876-885.
- [27] Vance KW and Ponting CP. Transcriptional regulatory functions of nuclear long noncoding RNAs. Trends Genet 2014; 30: 348-355.
- [28] Silva AM, Moura SR, Teixeira JH, Barbosa MA, Santos SG and Almeida MI. Long noncoding RNAs: a missing link in osteoporosis. Bone Res 2019: 7: 10.
- [29] Ni W, Zhang Y, Zhan Z, Ye F, Liang Y, Huang J, Chen K, Chen L and Ding Y. A novel IncRNA uc.134 represses hepatocellular carcinoma progression by inhibiting CUL4A-mediated ubiquitination of LATS1. J Hematol Oncol 2017; 10: 91.

- [30] Tang F, Xu Y, Wang H, Bian E and Zhao B. Ln-cRNA-ATB in cancers: what do we know so far? Mol Biol Rep 2020; 47: 4077-4086.
- [31] Li S, Liu X, Li H, Pan H, Acharya A, Deng Y, Yu Y, Haak R, Schmidt J, Schmalz G and Ziebolz D. Integrated analysis of long noncoding RNA-associated competing endogenous RNA network in periodontitis. J Periodontal Res 2018; 53: 495-505.
- [32] Zhu H, Lu J, Zhao H, Chen Z, Cui Q, Lin Z, Wang X, Wang J, Dong H, Wang S and Tan J. Functional long noncoding RNAs (IncRNAs) in clear cell kidney carcinoma revealed by reconstruction and comprehensive analysis of the IncRNA-miRNA-mRNA regulatory network. Med Sci Monit 2018; 24: 8250-8263.
- [33] Chen J, Yang H, Teo ASM, Amer LB, Sherbaf FG, Tan CQ, Alvarez JJS, Lu B, Lim JQ, Takano A, Nahar R, Lee YY, Phua CZJ, Chua KP, Suteja L, Chen PJ, Chang MM, Koh TPT, Ong BH, Anantham D, Hsu AAL, Gogna A, Too CW, Aung ZW, Lee YF, Wang L, Lim TKH, Wilm A, Choi PS, Ng PY, Toh CK, Lim WT, Ma S, Lim B, Liu J, Tam WL, Skanderup AJ, Yeong JPS, Tan EH, Creasy CL, Tan DSW, Hillmer AM and Zhai W. Genomic landscape of lung adenocarcinoma in East Asians. Nat Genet 2020; 52: 177-186.
- [34] Duruisseaux M and Esteller M. Lung cancer epigenetics: from knowledge to applications. Semin Cancer Biol 2018; 51: 116-128.
- [35] Yu T, Chen X, Zhang W, Liu J, Avdiushko R, Napier DL, Liu AX, Neltner JM, Wang C, Cohen D and Liu C. KLF4 regulates adult lung tumor-initiating cells and represses K-Ras-mediated lung cancer. Cell Death Differ 2016; 23: 207-215.
- [36] de Groot P and Munden RF. Lung cancer epidemiology, risk factors, and prevention. Radiol Clin North Am 2012; 50: 863-876.
- [37] Liu G, Pei F, Yang F, Li L, Amin AD, Liu S, Buchan JR and Cho WC. Role of autophagy and apoptosis in non-small-cell lung cancer. Int J Mol Sci 2017; 18: 367.
- [38] Gelatti ACZ, Drilon A and Santini FC. Optimizing the sequencing of tyrosine kinase inhibitors (TKIs) in epidermal growth factor receptor (EGFR) mutation-positive non-small cell lung cancer (NSCLC). Lung Cancer 2019; 137: 113-122.
- [39] Fan Y, Li H, Yu Z, Dong W, Cui X, Ma J and Li S. Long non-coding RNA FGD5-AS1 promotes non-small cell lung cancer cell proliferation through sponging hsa-miR-107 to up-regulate FGFRL1. Biosci Rep 2020; 40: BSR20193309.
- [40] Lv J, Li Q, Ma R, Wang Z, Yu Y, Liu H, Miao Y and Jiang S. Long noncoding RNA FGD5-AS1 knockdown decrease viability, migration, and invasion of non-small cell lung cancer (NSCLC)

- cells by regulating the MicroRNA-944/MACC1 axis. Technol Cancer Res Treat 2021; 20: 1533033821990090.
- [41] Cui F, Luo P, Bai Y and Meng J. Silencing of long non-coding RNA FGD5-AS1 inhibits the progression of non-small cell lung cancer by regulating the miR-493-5p/DDX5 axis. Technol Cancer Res Treat 2021; 20: 1533033821990007.
- [42] Fu J, Cai H, Wu Y, Fang S and Wang D. Elevation of FGD5-AS1 contributes to cell progression by improving cisplatin resistance against nonsmall cell lung cancer cells through regulating miR-140-5p/WEE1 axis. Gene 2020; 755: 144886.
- [43] Ostrom QT, Bauchet L, Davis FG, Deltour I, Fisher JL, Langer CE, Pekmezci M, Schwartzbaum JA, Turner MC, Walsh KM, Wrensch MR and Barnholtz-Sloan JS. The epidemiology of glioma in adults: a "state of the science" review. Neuro Oncol 2014; 16: 896-913.
- [44] Saxena S and Jha S. Role of NOD- like receptors in glioma angiogenesis: insights into future therapeutic interventions. Cytokine Growth Factor Rev 2017; 34: 15-26.
- [45] Liao W, Fan S, Zheng Y, Liao S, Xiong Y, Li Y and Liu J. Recent advances on glioblastoma multiforme and nano-drug carriers: a review. Curr Med Chem 2019; 26: 5862-5874.
- [46] Pang B, Xu J, Hu J, Guo F, Wan L, Cheng M and Pang L. Single-cell RNA-seq reveals the invasive trajectory and molecular cascades underlying glioblastoma progression. Mol Oncol 2019; 13: 2588-2603.
- [47] Margo CE. Surgical enucleation in community hospitals. Am J Ophthalmol 1989; 108: 452-453.
- [48] Su D, Ji Z, Xue P, Guo S, Jia Q and Sun H. Longnoncoding RNA FGD5-AS1 enhances the viability, migration, and invasion of glioblastoma cells by regulating the miR-103a-3p/TPD52 axis. Cancer Manag Res 2020; 12: 6317-6329.
- [49] Wu L, Zhu X, Song Z, Guo M, Liang J and Yan D. FGD5-AS1 facilitates glioblastoma progression by activation of Wnt/β-catenin signaling via regulating miR-129-5p/HNRNPK axis. Life Sci 2020; 256: 117998.
- [50] Chang CF, Kuo YL, Pu C and Chou YJ. Neck dissection and stroke in patients with oral cavity cancer: a population-based cohort study. Head Neck 2017; 39: 63-70.
- [51] Cheraghlou S, Schettino A, Zogg CK and Judson BL. Changing prognosis of oral cancer: an analysis of survival and treatment between 1973 and 2014. Laryngoscope 2018; 128: 2762-2769.
- [52] Bagan J, Sarrion G and Jimenez Y. Oral cancer: clinical features. Oral Oncol 2010; 46: 414-417.

- [53] Islami F, Kamangar F, Nasrollahzadeh D, Møller H, Boffetta P and Malekzadeh R. Oesophageal cancer in Golestan Province, a highincidence area in northern Iran-a review. Eur J Cancer 2009: 45: 3156-3165.
- [54] Sun L, Xu Y, Zhang X, Gao Y, Chen J, Zhou A, Lu Q, Wang Z, Shao K, Wu H and Ning X. Mesenchymal stem cells functionalized sonodynamic treatment for improving therapeutic efficacy and compliance of orthotopic oral cancer. Adv Mater 2020; 32: e2005295.
- [55] Pickering CR, Zhang J, Yoo SY, Bengtsson L, Moorthy S, Neskey DM, Zhao M, Ortega Alves MV, Chang K, Drummond J, Cortez E, Xie TX, Zhang D, Chung W, Issa JP, Zweidler-McKay PA, Wu X, El-Naggar AK, Weinstein JN, Wang J, Muzny DM, Gibbs RA, Wheeler DA, Myers JN and Frederick MJ. Integrative genomic characterization of oral squamous cell carcinoma identifies frequent somatic drivers. Cancer Discov 2013; 3: 770-781.
- [56] Liu L, Zhan Y, Huang Y and Huang L. LncRNA FGD5-AS1 can be predicted as therapeutic target in oral cancer. J Oral Pathol Med 2020; 49: 243-252.
- [57] Ge C, Dong J, Chu Y, Cao S, Zhang J and Wei J. LncRNA FGD5-AS1 promotes tumor growth by regulating MCL1 via sponging miR-153-3p in oral cancer. Aging (Albany NY) 2020; 12: 14355-14364.
- [58] Smyth EC, Lagergren J, Fitzgerald RC, Lordick F, Shah MA, Lagergren P and Cunningham D. Oesophageal cancer. Nat Rev Dis Primers 2017; 3: 17048.
- [59] Song Y, Li L, Ou Y, Gao Z, Li E, Li X, Zhang W, Wang J, Xu L, Zhou Y, Ma X, Liu L, Zhao Z, Huang X, Fan J, Dong L, Chen G, Ma L, Yang J, Chen L, He M, Li M, Zhuang X, Huang K, Qiu K, Yin G, Guo G, Feng Q, Chen P, Wu Z, Wu J, Ma L, Zhao J, Luo L, Fu M, Xu B, Chen B, Li Y, Tong T, Wang M, Liu Z, Lin D, Zhang X, Yang H, Wang J and Zhan Q. Identification of genomic alterations in oesophageal squamous cell cancer. Nature 2014; 509: 91-95.
- [60] Codipilly DC, Qin Y, Dawsey SM, Kisiel J, Topazian M, Ahlquist D and Iyer PG. Screening for esophageal squamous cell carcinoma: recent advances. Gastrointest Endosc 2018; 88: 413-426.
- [61] Gao J, Zhang Z, Su H, Zong L and Li Y. Long noncoding RNA FGD5-AS1 acts as a competing endogenous RNA on microRNA-383 to enhance the malignant characteristics of esophageal squamous cell carcinoma by increasing SP1 expression. Cancer Manag Res 2020; 12: 2265-2278.
- [62] Zhou Y, Yang D, Yang Q, Lv X, Huang W, Zhou Z, Wang Y, Zhang Z, Yuan T, Ding X, Tang L, Zhang J, Yin J, Huang Y, Yu W, Wang Y, Zhou C, Su Y, He A, Sun Y, Shen Z, Qian B, Meng W, Fei J, Yao

- Y, Pan X, Chen P and Hu H. Single-cell RNA landscape of intratumoral heterogeneity and immunosuppressive microenvironment in advanced osteosarcoma. Nat Commun 2020; 11: 6322.
- [63] Brown HK, Tellez-Gabriel M and Heymann D. Cancer stem cells in osteosarcoma. Cancer Lett 2017; 386: 189-195.
- [64] Song QH, Guo MJ, Zheng JS, Zheng XH, Ye ZH and Wei P. Study on targeting relationship between miR-320b and FGD5-AS1 and its effect on biological function of osteosarcoma cells. Cancer Manag Res 2020; 12: 13589-13598.
- [65] Zhang J and Lou W. A key mRNA-miRNA-IncRNA competing endogenous RNA triple subnetwork linked to diagnosis and prognosis of hepatocellular carcinoma. Front Oncol 2020; 10: 340.
- [66] Gao Y, Zhu H and Mao Q. Expression of IncRNA FGD5-AS1 correlates with poor prognosis in melanoma patients. J Gene Med 2020; 22: e3278.
- [67] Li D, Jiang X, Zhang X, Cao G, Wang D and Chen Z. Long noncoding RNA FGD5-AS1 promotes colorectal cancer cell proliferation, migration, and invasion through upregulating CDCA7 via sponging miR-302e. In Vitro Cell Dev Biol Anim 2019; 55: 577-585.
- [68] Yang Y, Dong MH, Hu HM, Min QH and Xiao L. LncRNA FGD5-AS1/miR-5590-3p axis facilitates the proliferation and metastasis of renal cell carcinoma through ERK/AKT signalling. Eur Rev Med Pharmacol Sci 2020; 24: 8756-8766.
- [69] Hamilton MJ, Girke T and Martinez E. Global isoform-specific transcript alterations and deregulated networks in clear cell renal cell carcinoma. Oncotarget 2018; 9: 23670-23680.
- [70] Gao Y, Xie M, Guo Y, Yang Q, Hu S and Li Z. Long non-coding RNA FGD5-AS1 regulates cancer cell proliferation and chemoresistance in gastric cancer through miR-153-3p/CITED2 axis. Front Genet 2020; 11: 715.
- [71] Chung S, Kim SH, Seo Y, Kim SK and Lee JY. Quantitative analysis of cell proliferation by a dye dilution assay: application to cell lines and cocultures. Cytometry A 2017; 91: 704-712.
- [72] Lai De Oliveira A and Binder BJ. Modeling uniaxial nonuniform cell proliferation. Bull Math Biol 2019; 81: 2220-2238.
- [73] Sancho P, Barneda D and Heeschen C. Hallmarks of cancer stem cell metabolism. Br J Cancer 2016; 114: 1305-1312.
- [74] Currie E, Schulze A, Zechner R, Walther TC and Farese RV Jr. Cellular fatty acid metabolism and cancer. Cell Metab 2013; 18: 153-161.
- [75] Tan DSW, Chong FT, Leong HS, Toh SY, Lau DP, Kwang XL, Zhang X, Sundaram GM, Tan GS, Chang MM, Chua BT, Lim WT, Tan EH, Ang MK,

- Lim TKH, Sampath P, Chowbay B, Skanderup AJ, DasGupta R and Iyer NG. Long noncoding RNA EGFR-AS1 mediates epidermal growth factor receptor addiction and modulates treatment response in squamous cell carcinoma. Nat Med 2017; 23: 1167-1175.
- [76] Yin D, Lu X, Su J, He X, De W, Yang J, Li W, Han L and Zhang E. Long noncoding RNA AFAP1-AS1 predicts a poor prognosis and regulates non-small cell lung cancer cell proliferation by epigenetically repressing p21 expression. Mol Cancer 2018; 17: 92.
- [77] Gao G, Jiang YW, Jia HR, Sun W, Guo Y, Yu XW, Liu X and Wu FG. From perinuclear to intranuclear localization: a cell-penetrating peptide modification strategy to modulate cancer cell migration under mild laser irradiation and improve photothermal therapeutic performance. Biomaterials 2019; 223: 119443.
- [78] Duff D and Long A. Roles for RACK1 in cancer cell migration and invasion. Cell Signal 2017; 35: 250-255.
- [79] Yoon YJ, Han YM, Choi J, Lee YJ, Yun J, Lee SK, Lee CW, Kang JS, Chi SW, Moon JH, Lee S, Han DC and Kwon BM. Benproperine, an ARPC2 inhibitor, suppresses cancer cell migration and tumor metastasis. Biochem Pharmacol 2019; 163: 46-59.
- [80] Lingadahalli S, Jadhao S, Sung YY, Chen M, Hu L, Chen X and Cheung E. Novel IncRNA LINCO0844 regulates prostate cancer cell migration and invasion through AR signaling. Mol Cancer Res 2018; 16: 1865-1878.
- [81] Zheng S, Jiang F, Ge D, Tang J, Chen H, Yang J, Yao Y, Yan J, Qiu J, Yin Z, Ni Y, Zhao L, Chen X, Li H and Yang L. LncRNA SNHG3/miRNA-151a-3p/RAB22A axis regulates invasion and migration of osteosarcoma. Biomed Pharmacother 2019; 112: 108695.
- [82] Zhuang C, Ma Q, Zhuang C, Ye J, Zhang F and Gui Y. LncRNA GCInc1 promotes proliferation and invasion of bladder cancer through activation of MYC. FASEB J 2019; 33: 11045-11059.
- [83] Weingart SN, Zhang L, Sweeney M and Hassett M. Chemotherapy medication errors. Lancet Oncol 2018; 19: e191-e199.
- [84] Zhou J, Yu G and Huang F. Supramolecular chemotherapy based on host-guest molecular recognition: a novel strategy in the battle against cancer with a bright future. Chem Soc Rev 2017; 46: 7021-7053.
- [85] Vasan N, Baselga J and Hyman DM. A view on drug resistance in cancer. Nature 2019; 575: 299-309.
- [86] Wu Q, Yang Z, Nie Y, Shi Y and Fan D. Multidrug resistance in cancer chemotherapeutics: mechanisms and lab approaches. Cancer Lett 2014; 347; 159-166.

LncRNA FGD5-AS1 in human cancers

- [87] Hughes D and Andersson DI. Evolutionary consequences of drug resistance: shared principles across diverse targets and organisms. Nat Rev Genet 2015; 16: 459-471.
- [88] Lamouille S, Xu J and Derynck R. Molecular mechanisms of epithelial-mesenchymal transition. Nat Rev Mol Cell Biol 2014; 15: 178-196.
- [89] Dongre A and Weinberg RA. New insights into the mechanisms of epithelial-mesenchymal transition and implications for cancer. Nat Rev Mol Cell Biol 2019; 20: 69-84.
- [90] Marcucci F, Stassi G and De Maria R. Epithelial-mesenchymal transition: a new target in anticancer drug discovery. Nat Rev Drug Discov 2016; 15: 311-325.
- [91] Ye X and Weinberg RA. Epithelial-mesenchymal plasticity: a central regulator of cancer progression. Trends Cell Biol 2015; 25: 675-686.
- [92] Li L and Li W. Epithelial-mesenchymal transition in human cancer: comprehensive reprogramming of metabolism, epigenetics, and differentiation. Pharmacol Ther 2015; 150: 33-46.

- [93] Sears CR and Mazzone PJ. Biomarkers in lung cancer. Clin Chest Med 2020; 41: 115-127.
- [94] Pan Y, Liu G, Zhou F, Su B and Li Y. DNA methylation profiles in cancer diagnosis and therapeutics. Clin Exp Med 2018; 18: 1-14.
- [95] Crowley E, Di Nicolantonio F, Loupakis F and Bardelli A. Liquid biopsy: monitoring cancergenetics in the blood. Nat Rev Clin Oncol 2013; 10: 472-484.
- [96] Ramnarine VR, Kobelev M, Gibb EA, Nouri M, Lin D, Wang Y, Buttyan R, Davicioni E, Zoubeidi A and Collins CC. The evolution of long noncoding RNA acceptance in prostate cancer initiation, progression, and its clinical utility in disease management. Eur Urol 2019; 76: 546-559.
- [97] Tang Z, Li C, Kang B, Gao G, Li C and Zhang Z. GEPIA: a web server for cancer and normal gene expression profiling and interactive analyses. Nucleic Acids Res 2017; 45: W98-W102.