LIX1 regulates YAP activity and controls gastrointestinal cancer cell plasticity
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INTRODUCTION

The digestive musculature arises from the differentiation of common mesenchymal progenitors into interstitial cells of Cajal (ICC) and smooth muscle cells (SMC). Unlike many other mature cell types in the adult body, smooth mesenchyme-derived cells do not terminally differentiate, but they can reversibly modulate their phenotype, switching between a differentiated functional quiescent state and a highly proliferative mesenchymal precursor state. This feature is often associated with high neoplastic risk. Gastrointestinal stromal tumours (GISTs) are the most common mesenchymal cancers of the gastrointestinal tract. GISTs result from deregulated proliferation of transformed KIT-positive interstitial cells of Cajal that share mesenchymal progenitors with smooth muscle cells. Despite the identification of selective KIT inhibitors, primary resistance and relapse remain a major concern. Moreover, most patients develop resistance partly through reactivation of KIT and its downstream signalling pathways. We previously identified the LIMB Expression 1 (LIX1) gene as a unique marker of digestive mesenchyme immaturity. We also demonstrated that LIX1 regulates mesenchymal progenitor proliferation and differentiation by controlling the Hippo effector YAP1, which is constitutively activated in many sarcomas. Therefore, we wanted to determine LIX1 role in GIST development. We found that LIX1 is strongly up-regulated in GIST samples and this is associated with unfavourable prognosis. Moreover, LIX1 controls GIST cell proliferation in vitro and in vivo. Upon LIX1 inactivation in GIST cells, YAP1/TAZ activity is reduced, KIT (the GIST signature) is down-regulated, and cells acquire smooth muscle lineage features. Our data highlight LIX1 role in digestive mesenchyme-derived cell-fate decisions and identify this novel regulator as a target for drug design for GIST treatment by influencing its differentiation status.

KEYWORDS
cancer, gastrointestinal, LIX1, sarcoma, signaling pathway, smooth muscle, YAP1

LIX1 regulates YAP activity and controls gastrointestinal cancer cell plasticity

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Abstract
Gastrointestinal stromal tumours (GISTs), the most common mesenchymal neoplasm of the gastrointestinal tract, result from deregulated proliferation of transformed KIT-positive interstitial cells of Cajal that share mesenchymal progenitors with smooth muscle cells. Despite the identification of selective KIT inhibitors, primary resistance and relapse remain a major concern. Moreover, most patients develop resistance partly through reactivation of KIT and its downstream signalling pathways. We previously identified the Limb Expression 1 (LIX1) gene as a unique marker of digestive mesenchyme immaturity. We also demonstrated that LIX1 regulates mesenchymal progenitor proliferation and differentiation by controlling the Hippo effector YAP1, which is constitutively activated in many sarcomas. Therefore, we wanted to determine LIX1 role in GIST development. We found that LIX1 is strongly up-regulated in GIST samples and this is associated with unfavourable prognosis. Moreover, LIX1 controls GIST cell proliferation in vitro and in vivo. Upon LIX1 inactivation in GIST cells, YAP1/TAZ activity is reduced, KIT (the GIST signature) is down-regulated, and cells acquire smooth muscle lineage features. Our data highlight LIX1 role in digestive mesenchyme-derived cell-fate decisions and identify this novel regulator as a target for drug design for GIST treatment by influencing its differentiation status.

1 | INTRODUCTION

The digestive musculature arises from the differentiation of common mesenchymal progenitors into interstitial cells of Cajal (ICC) and smooth muscle cells (SMC). Unlike many other mature cell types in the adult body, smooth mesenchyme-derived cells do not terminally differentiate, but they can reversibly modulate their phenotype, switching between a differentiated functional quiescent state and a highly proliferative mesenchymal precursor state. This feature is often associated with high neoplastic risk. Gastrointestinal stromal tumours (GISTs) are the most common mesenchymal cancers of the gastrointestinal tract. GISTs result from deregulated proliferation of KIT-positive cells, either ICCs or ICC/SMC mesenchymal progenitors. GISTs occur predominantly in...
the stomach (50%-60%) and small intestine (30%-35%). More than 80% of GISTs harbour KIT gain-of-function mutations that result in the constitutive activation of the KIT receptor and downstream signalling pathways, leading to spontaneous proliferation and uncontrolled tumour growth.7 Low-risk tumours can be managed by surgery alone; however, approximately 50% of GISTs relapse or metastasize after surgical resection. Imatinib mesylate, a small-molecular tyrosine kinase inhibitor against constitutively activated KIT, is efficient in adult patients with GIST.8 However, resistance to imatinib mesylate is increasing and complete remission is rare, highlighting the necessity to improve our molecular understanding of GIST pathophysiology.5

Cell dedifferentiation is a central mechanism in the initiation of neoplastic transformation and therapeutic resistance.9,11 It involves loss of lineage-specific gene expression and regression from a specialized tissue to a more primitive state of development through expression of genes that govern embryonic cell-fate specification. Accordingly, developmental biology studies are very useful for the identification of new tumour markers and therapeutic targets.12 In this context, we previously performed a screen to identify genes with high expression at the earliest stages of stomach development and found that Limb Expression 1 (LIX1) is a novel and unique marker of stomach mesenchymal progenitors. Moreover, we demonstrated that LIX1 stimulates the expression and activity of the Hippo effector YAP1 and that both LIX1 and YAP1 are key regulators of stomach mesenchymal progenitor development.13,14 Although LIX1 transcripts have been detected in human GIST cell lines,15 LIX1 role in GIST is unknown.

Here, we found that LIX1 is strongly up-regulated in GIST specimens and that its expression is associated with poor prognosis. LIX1 down-regulation reprogrammes KIT-positive GIST cells towards the SMC lineage, thereby limiting their tumorigenic and malignant potential. Therefore, our study reveals LIX1 key role in GIST pathophysiology as a rheostat for the control of cell identity.

2 | METHODS

2.1 | Cell culture and reagents

The GIST-T1 cell line was from Cosmo Bio. It was established from a metastatic human GIST sample with a heterozygous deletion of 57 bases in exon 11 of KIT.16 Human gastric SMCs, provided by Innoprot Innovative, were grown in Dulbecco’s modified Eagle medium (DMEM) supplemented with 10% foetal bovine serum (FBS) and 1% penicillin/streptomycin. GIST-T1 cells were resuspended in Accutase™ solution (Sigma-Aldrich) before electroporation of different constructs using the Neon Transfection System (Life Technologies), according to the manufacturer’s instructions. GIST-T1 stable cell lines were generated by selection in 500 ng/mL puromycin. All cell lines were routinely tested for the absence of mycoplasma contamination (VenorGeM OneStep Test, BioValley). Verteporfin (Sellekchem) was added to GIST-T1 cells at a final concentration of 2 μmol/L.

2.2 | Human GIST tissue microarrays (TMA) and GIST data set

The SuperBiochips GIST TMA (#DAA2) was purchased from Super BioChips laboratories. It contained 40 formalin-fixed, paraffin-embedded (FFPE) human GIST specimens and nine matched normal gut tissue specimens. The clinicopathological features of these patients are in Table S1. The second GIST TMA (#A225, BIOCAT, GmbH) contained 37 FFPE human GIST specimens and four non-neoplastic specimens. The clinicopathological features are in Table S2. For immunohistochemistry, TMAs were rehydrated through Histoclear (Fisher Scientific) and graded alcohol solutions, and then heated at 90°C in 0.01 mol/L citrate buffer (pH 6.0) for epitope unmasking. Spots were evaluated by three examiners blinded to the clinicopathological information. Immunoreactivity was considered positive when signal was above the background signal in the negative control. Staining intensity was scored as negative (−), intermediate (+) or high (++). A clinically annotated gene expression data set of localized, untreated GISTs (n = 60), quantified by microarray, was also used.17

2.3 | shRNAs and DNA plasmids

The human LIX1-specific short hairpin RNA (shRNA) constructs pGFP-C-LIX1-shRNA Lentil (TL303518A for shLIX1#1: 5′-AGTGGAGGCGAAGCTAGCCCTCCACCA-3′ and TL303518B forshLIX1#2: 5′-GCGGAAAGGCGGGACAAGCTACGCTG-3′) were obtained from Origene Technologies. The 29-mer Scrambled shRNA construct pGFP-C-Scr-shLenti (TR30021 for Scr absorbance: 5′-GCACTACAGGCAGTATACTAGTAC-3′) from Origene Technologies was used as control. SMARTpool ON-TARGETplus human YAP1 siRNA (L-016083-00-0010) and ON-TARGETplus WWTR1 siRNA (L-016083-00-0010) were from DHARMACON-GE.

2.4 | Cell proliferation and wound healing assays

BrdU incorporation was performed using the Cell Proliferation ELISA, BrdU (colorimetric) (ROCHE) following the manufacturer’s protocol. For wound healing experiments, 1.2 × 105 cells (Scrambled, GIST-T1-ShLIX1#1 and GIST-T1-ShLIX1#2) were plated in 6-well plates to reach 100% confluence 24 hours later. Then, a linear scratch in the cell monolayer was made using a 200 μL micropipette tip. Medium and cell debris were aspirated, followed by two washes with PBS. DMEM containing 2% SVF, penicillin and streptomycin, and 1 μmol/L aphidicolin (an inhibitor of cell growth) was carefully added to each well. The wound area was monitored by
video-microscopy from 0 to 48 hours post-wounding and measured with the ImageJ software.

2.5 | Reverse transcription and quantitative polymerase chain reaction (RT-qPCR)

Total RNA was extracted from cell cultures with the HighPure RNA Isolation kit (Roche). Reverse transcription was performed using the Verso cDNA synthesis kit (Thermo Scientific) and qPCR using the LightCycler technology (Roche Diagnostics). PCR primers (Table S3) were designed using the LightCycler Probe Design 2.0 software. Expression levels were determined with the LightCycler analysis software (version 3.5) relative to standard curves. Data are the mean level of gene expression relative to the expression of the reference genes GAPDH and RPLPO calculated using the $2^{-\Delta\Delta CT}$ method.

2.6 | Western blotting

Cells were resuspended in lysis buffer (20 mmol/L Tris pH8, 50 mmol/L NaCl, 1% NP40, complete EDTA-free Protease Inhibitor Cocktail [Roche]). For Western blot analysis, 10 µg of total protein lysates were boiled in SDS-PAGE sample buffer, separated by 10% SDS-PAGE and transferred to nitrocellulose membranes. Membranes were incubated with primary antibodies. Antibodies are listed in Table S4.

2.7 | Cell fixation, immunofluorescence microscopy, live cell imaging, quantification

Cells were seeded on fibronectin-coated (50 µg/mL per coverslips) coverslips, fixed with 4% paraformaldehyde in PBS containing 0.01% Triton X-100 for 10 minutes, blocked with 1% goat serum for 1 hour before incubation with primary and secondary antibodies (Alexa 350-, 488- and 555-conjugated secondary antibodies [Life Science]) in 0.1% goat serum (Table S4). Nuclei were labelled with Hoechst (Invitrogen).

2.8 | RNA sequencing, sequencing quality control and RNA-Seq data analysis

Libraries from GIST-T1-Scrambled, ShLIX1#1 and ShLIX1#2 cells were constructed using the TruSeq Stranded mRNA Library Prep Kit (Illumina, ref.RS-122-2101) according to the manufacturer’s instructions. Briefly, poly-A RNA was purified using oligo-d(T) magnetic beads, fragmented and reverse transcribed using random hexamers, Super Script II (Life Technologies, ref. 18064-014) and actinomycin D. During the second strand generation step, dUTP was added instead of dTTP to prevent the use of the second strand as template during the final PCR amplification. Double-stranded cDNA was adenyalted at the 3’ end before ligation using Illumina indexed adapters. Ligated cDNA was amplified by 15 cycles of PCR and PCR products were purified using AMPure XP Beads (Beckman Coulter Genomics, ref. A63881). Libraries were validated using a Fragment Analyzer (Agilent) and quantified using the KAPA Library quantification kit (Roche, ref. KK4824). Nine libraries were pooled in equimolar amounts and sequenced on an HiSeq2500 using the single read protocol (50 nt; 1.5 lane flowcell). Image analysis and base calling were performed using the Illumina HiSeq Control Software and the Real-Time Analysis component. Demultiplexing was performed using the Illumina conversion software (bcl2fastq 2.1.8). The raw data quality was assessed using FastQC from the Babraham Institute and the Illumina software SAV (Sequencing Analysis Viewer). Potential contaminants were monitored with the FastQ Screen software from the Babraham Institute.

RNA-seq reads were aligned to the human genome (UCSC Hg38) with the splice junction mapper TopHat 2.1.118 and Bowtie 2.2.9.19 Gene model annotations were downloaded from the UCSC database (14 January 2019). Final read alignments with more than three mismatches were discarded. Reads for each gene were counted using the union mode of HTSeq-count 0.9.0.20 Before statistical analysis, genes with fewer than 15 reads (cumulating all the analysed samples) were filtered out. Counts were normalized using the Relative Log Expression (RLE) method as implemented in the Bioconductor21 package EdgeR 3.20.1.22 Differentially expressed (DE) genes were identified using three different statistical methods: DESeq 1.30.0,23 EdgeR and DESeq 1.18.1.24 The P-values for multiple testing were corrected using the Benjamini-Hochberg FDR method.25 Genes with adjusted P-value < .001 were classified as ‘differentially expressed’. The final lists of DE genes (2767 genes) included the genes identified by all three tests and by the two comparisons (GIST-T1-Scrambled vs GIST-T1-ShLIX1#1 vs GIST-T1-ShLIX1#2 vs GIST-T1-Scrambled). DE genes were then divided in up-regulated genes (n = 1453) and down-regulated genes (n = 1314) in both the GIST-T1-Scrambled vs GIST-T1-ShLIX1#1 and GIST-T1-ShLIX1#2 vs GIST-T1-Scrambled comparisons. Genes with different directions of regulation in the two comparisons were removed. The functional analysis of the resulting DE genes was performed with the Gene Ontology (GO) annotations and the topGO26 package from Bioconductor. The IDs of the DE genes were retrieved from NCBI (24 January 2019). Overrepresented GO terms were identified using Fisher’s exact test with the weight method implemented in the topGO package. As confidence threshold, a P-value of .001 was used. To perform this analysis, DE genes were compared with all known genes present in the annotation. The GO categories were found in the Org.Hs.eg.db package based on the gene reporter EntrezGeneID. Plots were generated using GOplot v1.0.2 in R.

2.9 | Chorioallantoic membrane (CAM) assay

Fertilized White Leghorn eggs from Les Bruyeres Farm (France) were incubated at 38°C in humidified incubators. After 2 days of
incubation, 3 mL of albumin was removed with a sharp needle, and an approximately 10 mm opening was created at the top by carefully minimizing any contamination of the interior with shell fragments. The opening was sealed with scotch-tape and eggs incubated for 5 days. At day 7 of embryonic development (E7), the opening was enlarged to about 20 mm to allow grafting. For each condition, 1 × 10^6 GIST-T1 cells were resuspended in 25 μL serum-free medium and 25 μL Matrigel Matrix (BD Biosciences). After polymerization into a drop at 37°C for 5 minutes, cells were implanted at the top of the CAM. At day 5 post-graft, the GIST cell grafts were excised with the surrounding CAM, fixed in 4% paraformaldehyde, embedded in paraffin, cut in 10 μm sections, and processed for histological (haematoxylin-eosin solution) or immunohistochemistry analysis, as previously described.6,27 Images were acquired using a Nikon-AZ100 stereomicroscope.

2.10 | Statistical analysis

Data were analysed with the two-tailed or when appropriate, one-tailed Mann-Whitney test using the GraphPad Prism 6 software. Results were considered significant when \( P < .05 \) (*), \( P < .01 \) (**), \( P < .001 \) (***), or \( P < .0001 \) (****).

3 | RESULTS

3.1 | LIX1 expression is a negative prognostic factor in GIST

Gastrointestinal stromal tumours result from the deregulated proliferation of transformed KIT-positive ICCs that share mesenchymal
FIGURE 2 LIX1 down-regulation reduces the proliferative and invasive capacities of GIST cells. A, RT-qPCR analysis of LIX1 transcript level in GIST-T1 cells upon LIX1 silencing. Data were normalized to the mean GAPDH and RPLPO expression. Normalized expression levels were converted into fold changes. Values are presented as the mean ± SEM of n = 20 samples of GIST-T1-Scrambled, n = 15 for GIST-T1-ShLIX1#1 and n = 12 for ShLIX1#2 cells. *P < .05 and ****P < .0001 (one-tailed Mann–Whitney test). B, Cell proliferation analysis (BrdU incorporation) in GIST-T1-Scrambled, GIST-T1-ShLIX1#1 and -ShLIX1#2 cells. Cells were cultured for 2 d. Values are the mean ± standard deviation (SD) of n = 6 independent experiments. *P < .05 (two-tailed Mann–Whitney tests). C, Wound healing assays of GIST-T1-Scrambled, GIST-T1-ShLIX1#1 and -ShLIX1#2 cells cultured for 48 h after wounding. Graph represents the percentage of wound closure at 48 h post-scratch. ****P < .0001 (two-tailed Mann–Whitney test). D, Representative western blot showing phosphorylated KIT (pKIT), KIT and YAP1/TAZ levels in GIST-T1-Scrambled, GIST-T1-ShLIX1#1 and -ShLIX1#2 cells. Equal loading was verified by GAPDH expression. E, RT-qPCR analysis of CYR61 and CTGF expression. Data were normalized to the mean GAPDH and RPLPO expression, and converted to fold changes. Values are the mean ± SEM of n = 3 samples of GIST-T1-Scrambled, n = 3 for GIST-T1-ShLIX1#1, and n = 3 for ShLIX1#2 cells. *P < .05 (one-tailed Mann–Whitney test). F, Representative western blot showing YAP1/TAZ, phosphorylated KIT (pKIT) and KIT levels in GIST-T1-Scrambled, GIST-T1-SiYAP and GIST-T1-SiTAZ cells. Equal loading was verified by GAPDH expression. G, Representative western blot showing phosphorylated KIT and KIT expression in GIST-T1 cells untreated (T0) or incubated with 2 μmol/L verteporfin (VP) or DMSO (vehicle) for 2, 24 or 48 h. Equal loading was verified by GAPDH expression.
progenitors with SMCs. Neoplastic transformation requires changes in cell identity and acquisition of progenitor-like features. As LIX1 regulates the proliferation of muscle progenitors and cell-fate decisions within the digestive mesenchymal lineage, it could be implicated in GIST pathogenesis. In the course of this study, another group reported that LIX1 is expressed in two GIST cell lines. Here, analysis of LIX1 expression in another cell line (GIST-T1) that was derived from a metastatic human GIST with a heterozygous deletion of 57 bases in exon 11 of KIT confirmed LIX1 (mRNA and protein) expression (Figure 1A,B). Furthermore, immunohistochemical analysis of LIX1 expression in two GIST TMAs showed that LIX1 was expressed in 61 (79%) of all GIST specimens (n = 77), and in 34/43 high-grade GISTs (79%) (Figure 1C). To further understand LIX1 influence on the clinical outcome of patients with GIST, we analysed recurrence-free survival in function of LIX1 expression in a previously described clinical data set using Kaplan-Meier curves and the log-rank test. This data set included 60 patients with GIST and high (n = 16) or low (n = 44) LIX1 expression (median follow-up of 58 months). Recurrence-free survival was significantly reduced in the group with high LIX1 expression (relative risk = 17.669, 95% confidence interval 2.01-154.99, log-rank test, P = .0005) (Figure 1D). LIX1 expression was highest in patients with relapsed tumour (P = .015) (Figure 1E). These findings identify LIX1 expression as a novel prognostic factor in GIST.

3.2 | LIX1 down-regulation decreases YAP1/TAZ and KIT levels in GIST cells

As increased expression of LIX1 is associated with unfavourable prognosis in GISTs, we determined whether LIX1 regulates the growth of GIST cells in vitro. First, we established GIST cell lines that stably express GIST-T1-Scrambled (negative control shRNA) and shRNAs against LIX1 (GIST-T1-ShLIX1#1 and GIST-T1-ShLIX1#2). RT-qPCR analysis confirmed LIX1 down-regulation in GIST-T1-ShLIX1 cells (Figure 2A), particularly in cells transfected with ShLIX1#2. Proliferation assays (BrdU incorporation) in GIST-T1-Scrambled and GIST-T1-ShLIX1 cells showed that LIX1 silencing led to a significant reduction of cell proliferation compared with GIST-T1-Scrambled cells (Figure 2B). Then, to assess the effect of LIX1 silencing on GIST cell migration we performed wound healing assays. Scratch wound closure was slower in GIST-T1-ShLIX1#1 and GIST-T1-ShLIX1#2 cells than in GIST-T1-Scrambled (Figure 2C). Overall, these results suggest that LIX1 promotes GIST cell proliferation and migration in vitro.

In many GIST specimens (~85%), KIT harbours gain-of-function mutations that cause ligand-independent auto-activation of the receptor. Constitutive activation of the KIT receptor and of the downstream signalling pathways promotes tumour cell proliferation and uncontrolled growth. Therefore, we assessed KIT phosphorylation, a measure of KIT signalling activity. LIX1 silencing decreased KIT phosphorylation (TYR703) level compared with GIST-T1-Scrambled cells, and also KIT expression, a signature of GIST cell identity (Figure 2D), although KIT transcript level was not changed (Figure S1).

We next investigated the mechanisms by which LIX1 regulates KIT. We previously reported that LIX1 regulates mesenchymal progenitor proliferation and differentiation through the Hippo mediator YAP1, which is also involved in the control of GIST cell proliferation. Therefore, we investigated the effect of LIX1 silencing on the two Hippo effectors YAP1 and TAZ. LIX1 down-regulation resulted in a marked decrease of YAP1/TAZ expression (Figure 2D) and function, as indicated by the lower levels of CTGF and CYR61, their transcriptional targets (Figure 2E). Furthermore, reducing YAP1 or TAZ expression (by siRNA) (Figure 2F) and activity (using verteporfin, an inhibitor of YAP1-TEAD/TAZ-TEAD interactions) (Figure 2F) led to a marked decrease of KIT expression.

3.3 | LIX1 down-regulation induces a SMC-specific transcriptional programme in GIST cells

As LIX1 silencing was associated with loss of KIT expression, we wanted to thoroughly describe GIST-T1-ShLIX1 cell identity. To this aim, we determined the gene expression profile of GIST-T1 cells in function of LIX1 expression (GIST-T1-ShLIX1#1, GIST-T1-ShLIX1#2 and vs GIST-T1-Scrambled cells) using a high-throughput RNA-sequencing program.
approach. Transcriptomic analyses revealed the differential expression of several GIST-restricted genes (CD34, ENG) and genes involved in GIST aggressiveness (eg ETV4, SLITRK3) (Figure S2A,B; Tables S5 and S6). Unexpectedly, we observed the up-regulation of MYOCD, a master regulator of SMC-restricted gene expression, and of SMC-restricted contractile genes in GIST-T1-ShLIX1 cells (Figure 3A,B; Tables S7 and
A  cell grafting  graft dissection

Development day (E)  7  8  9  10  11  12

B  GIST-T1 Scrambled  GIST-T1 ShLIX1#1  GIST-T1 ShLIX1#2

C  GIST-T1 Scrambled  GIST-T1 ShLIX1#1  GIST-T1 ShLIX1#2

K67

enlargement

D  GIST-T1 Scrambled  GIST-T1 ShLIX1#1  GIST-T1 ShLIX1#2

KIT

CALPONIN

dry weight (mg)

Scrambled  ShLIX1#1  ShLIX1#2
We show that LIX1 is strongly expressed in GISTs and that its expression is associated with poor prognosis. We also demonstrated that LIX1 regulates YAP1/TAZ levels and activity, and controls the proliferative and invasive capacities of GIST cells. Lowfat, the arthropod homologue of LIX1, was characterized as a component of the Hippo pathway through its interaction with the atypical cadherins fat and dachsous. Over the past two decades, the Hippo pathway has been connected with developmental processes and with tissue repair that are intimately linked to the function of tissue-specific progenitor cells. Many studies have shown that the Hippo pathway controls cell proliferation by negatively regulating its downstream effectors YAP1 and TAZ. Constitutive activation of YAP1/TAZ has been observed in many human tumours. We found that reducing YAP1/TAZ protein level or activity results in a marked decrease of KIT expression. Although YAP1 regulates the proliferation of GIST cells, to our knowledge, our study is the first to reveal a control of YAP1/TAZ in KIT-mediated GIST development. We found that LIX1 silencing results in a marked decrease of YAP1/TAZ levels and function, and demonstrated that reducing YAP1 or TAZ expression or activity leads to a marked decrease of KIT expression. It is tempting to
hypothesize that LIX1 regulates KIT protein level upstream of YAP1/TAZ (Figure 5). Additional studies are now required to precisely determine how LIX1 regulates YAP1/TAZ levels. The human LIX1 gene encodes a 282-amino acid protein that includes a double-stranded RNA-binding domain. This suggests that LIX1 could be involved in mRNA or micro-RNA processing. Accordingly, miR-506 and miR-375 regulate YAP1 expression.\textsuperscript{22,43} We found that in response to LIX1 silencing, GIST cells lose KIT expression and subsequently acquire features of differentiated SMCs, a quality associated with reduced proliferative and invasive capacities. These findings provide the proof-of-concept that differentiation therapy could be a potential treatment strategy for GISTs.

In summary, our data demonstrate that LIX1 silencing in GIST cells results in their reprogramming to SMCs, thereby limiting their aggressive potential. These findings highlight LIX1 potential as a drug target in GISTs in the framework of a differentiation therapy strategy for this aggressive digestive mesenchymal malignancy.

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CONFLICT OF INTEREST

The authors disclose no potential conflicts of interest.

AUTHOR CONTRIBUTION

Amandine Guérin: Formal analysis (equal); Investigation (equal).
Delphine Martire: Formal analysis (equal); Investigation (equal).
Eva Trequier: Formal analysis (equal); Methodology (equal).
Tom Lesuyes: Formal analysis (equal); Methodology (equal).
Sébastien Sagnol: Conceptualization (equal); Formal analysis (equal).
Marie Pratlong: Conceptualization (equal); Investigation (equal).
Elise Lefebvre: Formal analysis (equal); Frédéric Chibon: Methodology (equal); Resources (equal).
Pascal de Santa Barbara: Funding acquisition (equal); Project administration (equal); Writing-original draft (equal); Writing-review & editing (equal).
Sandrine Faure: Conceptualization (equal); Funding acquisition (equal); Methodology (equal); Project administration (equal); Supervision (equal); Writing-original draft (equal); Writing-review & editing (equal).

DATA AVAILABILITY STATEMENT

The data that support the findings of this study are available from the corresponding author upon request.

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REFERENCES


**SUPPORTING INFORMATION**

Additional supporting information may be found online in the Supporting Information section.

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