VHL Mutation Drives Human Clear Cell Renal Cell Carcinoma Progression Through PI3K/AKT-Dependent Cholesteryl Ester Accumulation

Authors

Shuo Zhang[1], Yexuan He[1], Weichen Feng[1], Yaoyao Zheng[2], Shuai Hu[2], Tinghe Fang[1], Zhuojun Liu[3], Jia Liu[3], Jian Yu[1,3], Anbang He[2], Yanqing Gong[2], Zhisong He[2], Kaiwei Yang[2], Zhijun Xi[2], Wei Yu[2], Liqun Zhou[2], Lin Yao[2*], Shuhua Yue[1*]

Affiliations

[1]Key Laboratory of Biomechanics and Mechanobiology (Beihang University), Ministry of Education, Institute of Medical Photonics, Beijing Advanced Innovation Center for Biomedical Engineering, School of Biological Science and Medical Engineering, Beihang University, Beijing, 100191, China

[2]Department of Urology, Peking University First Hospital, Beijing, 100034, China

[3]School of Engineering Medicine, Beihang University, Beijing, 100191, China

*Corresponding authors: yue_shuhua@buaa.edu.cn (S.Y.); poparies@163.com (L.Y.)

ABSTRACT

Cholesteryl ester (CE) accumulation is an essential signature of clear cell renal cell carcinoma (ccRCC), but its biological mechanism and pathological significance remain elusive. Here, enabled by label-free Raman spectromicroscopy, we confirmed aberrant CE accumulation in human ccRCC tissues but not in normal kidney tissues. To elucidate the underlying mechanism, commonly used ccRCC cell lines were quantitatively analyzed but unfortunately did not show detectable CEs. To overcome this problem, primary cancer cells were isolated from human tissues to retain the CE-rich phenotype. Our results further revealed that CE accumulation in ccRCC was induced by the mutation of tumor suppressor VHL and subsequent upregulation of the HIFα/PI3K/AKT/mTOR/SREBP pathway. Inspiringly, inhibition of cholesterol esterification remarkably suppressed ccRCC aggressiveness through the reduced membrane cholesterol-mediated downregulations of the integrin and MAPK signaling pathways. Collectively, our study improves current understanding of the role of CE accumulation in ccRCC and opens up new opportunities for treatment.

SIGNIFICANCE

Enabled by label-free Raman spectromicroscopy, our study elucidated the mechanism underlying CE accumulation, a key signature of ccRCC, which was induced by the mutation of tumor suppressor VHL and subsequent activation of the HIFα mediated PI3K/AKT/mTOR pathway. CE depletion remarkably impaired ccRCC aggressiveness, which opens a new avenue for treatment.

INTRODUCTION

As an essential hallmark of human cancers, dysregulated lipid metabolism promotes cancer development and progression through increased lipid biosynthesis, transport, oxidation, and hydrolysis (1,2). For accommodating vigorous lipid turnover, excessive lipids are esterified into neutral lipids, primarily triacylglycerols (TAGs) and cholesteryl esters (CEs), and subsequently stored in lipid droplets (LDs) (3). As a critical organelle to maintain intracellular lipid homeostasis, LD has been frequently found to accumulate in various cancers and play an important role in cancer development (4,5).

As the most common (>75%) and aggressive subtype of renal carcinoma, clear cell renal cell carcinoma (ccRCC) is known to be one of the most LD-rich cancers (6,7). A couple of studies have been conducted to elucidate the mechanism underlying the accumulation and function of LDs in ccRCC (8-10). Specifically, as the most prevalent molecular feature of ccRCC, constitutive stabilization of hypoxia inducible factors (HIFs) (11), induced by the mutation of tumor suppressor VHL (60~90% of ccRCC) (12), was found to drive LD accumulation via downregulation of the rate-limiting enzyme of mitochondrial fatty acid transport, carnitine palmitoyltransferase 1A (CPT1A) (8), and upregulation of the LD-associated protein perilipin 2 (PLIN2) (9). Such LD accumulation was shown to maintain endoplasmic reticulum (ER) integrity (9) and promote lipid homeostasis by suppressing fatty acid toxicity (10), particularly under hypoxic stress, thus further facilitate ccRCC cell survival.

It is well known that the major form of neutral lipid accumulated in ccRCC is CE but not TAG (7,13,14). Unfortunately, most of the previous studies in ccRCC focus on fatty acid metabolism instead of cholesterol metabolism. More recently, high-density lipoprotein (HDL) has been found to be the source of cholesterol, the driving force for ccRCC growth (15). Nevertheless, the biological mechanism and pathological significance of CEs accumulated in ccRCC remain unclear.

The reason why CE accumulation in ccRCC has not been well studied is partially due to a lack of proper analytical tools. For LD visualization in single cells, lipophilic dyes are commonly used but lack the compositional information. For lipid compositional analysis, analytical methods, such as mass spectrometry and nuclear magnetic resonance spectroscopy, are regularly performed but cannot provide the spatial distribution information. Recently developed mass spectrometry imaging has been applied to chemical imaging of tissues *in situ* (16), but the limited spatial resolution prohibited its application in the study of LD biology. As a chemical imaging method with submicron resolution, stimulated Raman scattering (SRS) microscopy has made significant contributions to the study of lipid metabolism at the single cell level in various type of diseases (17,18), including cancer (19-23).

In this study, we elucidated the role of CE accumulation in ccRCC by integrating SRS-based spectroscopic imaging with biochemical and molecular biology methods. Our chemical imaging data revealed an aberrant accumulation of CEs in human ccRCC tissues (n = 24), but not in normal kidney tissues (n = 24), collected from 41 patients undergone surgery. To unravel the underlying mechanism of CE accumulation, we firstly analyzed a panel of commonly used ccRCC cell lines, including 786-O, 769-P, OSRC, Caki-1, and RCC4, but unfortunately did not find any detectable CEs in LDs, suggesting that these cell lines may not be appropriate for the study of cholesterol metabolism. This finding partially explains why the role of CEs in ccRCC progression remains unclear. To develop an appropriate cell model, we then extracted primary cancer cells from human ccRCC tissues and verified that the CE levels of primary cells were close to their original ccRCC tissues. Notably, the CE level was significantly higher in those with VHL mutation than those without VHL mutation, suggesting the possible link between VHL mutation and CE accumulation. By integrating with biological methods, we unraveled that the aberrant CE accumulation in ccRCC was induced by the VHL mutation and subsequently upregulated PI3K/Akt/mTOR/SREBPs pathway in a HIFα-dependent manner. Besides, exogenous HDL uptake was the primary

source of cholesterol for CE accumulation. Importantly, we demonstrated that inhibition of cholesterol esterification effectively impaired ccRCC growth, migration, and invasion, likely due to the reduced membrane cholesterol mediated downregulations of the integrin and MAPK signaling pathways. These results collectively improve understanding of the role of CE accumulation in ccRCC and open up new opportunities for treatment.

RESULTS

Aberrant CE Accumulation in Human ccRCC Tissues but Not in Normal Kidney Tissues

By integrating SRS microscopy and confocal Raman spectroscopy, we performed *in situ* lipid imaging and analysis of 24 ccRCC tissues and 24 normal kidney tissues, collected from 41 patients undergone kidney cancer surgery. By tuning the laser beating frequency to be resonant with the C-H stretching vibration at 2,850 cm^{-1}, strong SRS signals arose from the lipid-rich structures, such as cell membranes and LDs, and in the meanwhile much weaker signals came from the lipid-poor structures, such as the nuclei. Such imaging contrast permit clear visualization of cellular morphology and intracellular LD accumulation in a label-free manner. As shown in Figure 1A-D and Supplementary Fig. S1A-D, the SRS images showed very similar morphological features compared to the hematoxylin and eosin (H&E) images of the adjacent tissue slices. It was found that the autofluorescent granules, known as the lipofuscins, were consistently present in all normal tissues but not in any of the ccRCC tissues (Fig. 1E and F; Supplementary Fig. S1E and F; Supplementary Table 1). More importantly, abundant LD accumulation was observed in the ccRCC tissues but not in any of the normal tissues (Fig. 1E and F; Supplementary Fig. S1E and F; Supplementary Table 1). Quantitatively, the LD amount calculated in the way of LD area fraction was 13.7% ± 2.1% in the ccRCC tissues (Fig. 1G; Supplementary Table 1).

For further compositional analysis by confocal Raman spectroscopy, the autofluorescent granules in normal tissues were found to show characteristic Raman peaks for lipid (1,200-1,800 cm^{-1}), phenylalanine (1,000 cm^{-1}), and prominent CH_3 stretching (2,930 cm^{-1}). In contrast, the LDs in ccRCC tissues exhibited a series of strong representative peaks for CEs, including cholesterol rings around 428 and 702 cm^{-1}, ester bond around 1,742 cm^{-1} (Fig. 1H). Since LDs are primarily composed of TAGs and CEs, we made emulsions mixed with different molar

ratios between cholesteryl oleate and glyceryl trioleate for Raman spectral analysis (Supplementary Fig. S2A) to get a calibration curve for quantification of CE percentage in LDs (21). As shown in Supplementary Fig. S2B, the height ratio between the most prominent band for cholesterol ring around 702 cm^{-1} and the CH_2 bending band around 1,442 cm^{-1} was linearly proportional to the molar percentage of CEs in LDs. Based on this calibration curve, CE percentage in LDs of ccRCC tissues were as high as 66.5% ± 5.7% (Fig. 1I; Supplementary Table 1). The detailed quantifications of LD amount and composition for each patient are shown in the Supplementary Table 1. Liquid chromatography-mass spectrometry analysis of lipids extracted from tissues confirmed that CE accumulation in ccRCC tissues was significantly higher than that in normal kidney tissues (Supplementary Fig. S2C).

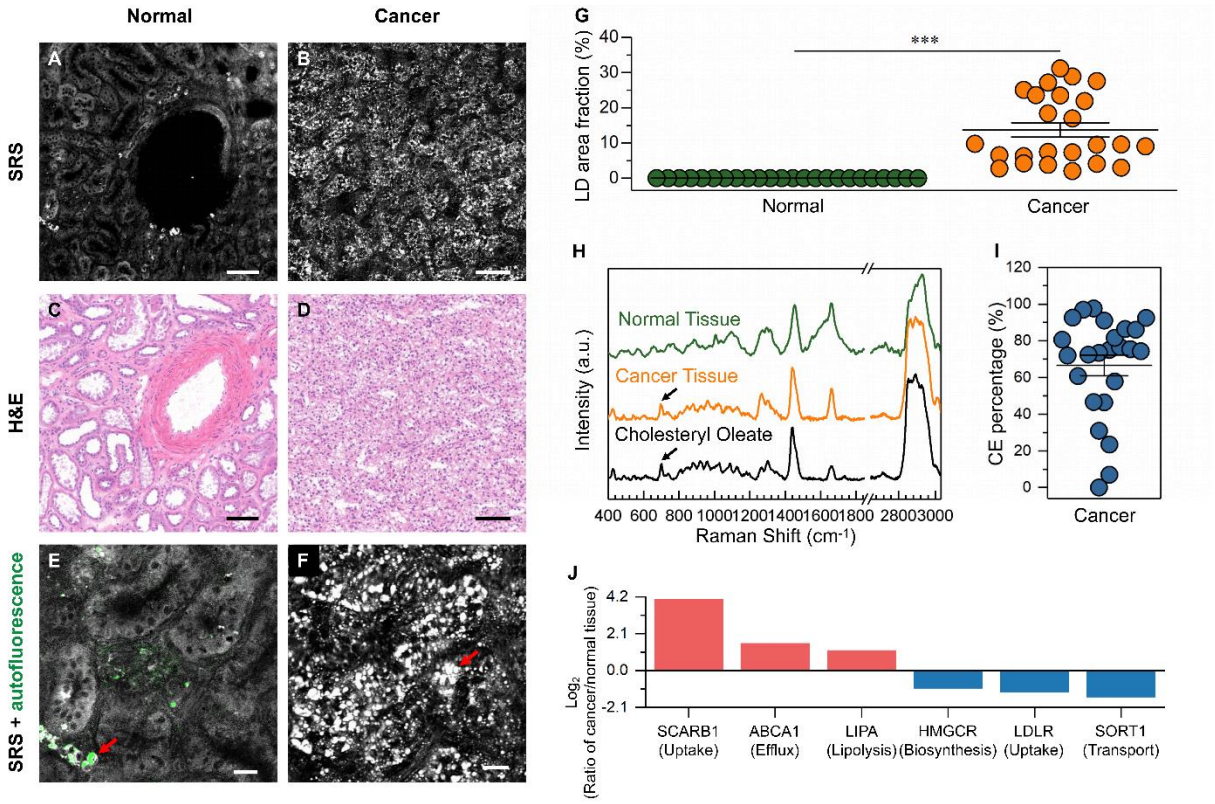

Figure 1. Aberrant CE accumulation in human ccRCC tissues. **A** and **B,** Representative SRS images of human normal kidney and ccRCC tissues. Scale bar, 100 µm. **C** and **D,** H&E images of the adjacent slices shown in **A** and **B**. Scale bar, 100 µm. **E** and **F,** Magnified SRS and autofluorescence images of the ones shown in **A** and **B**.

Autofluorescent granules and LDs are indicated by red arrows. Scale bar, 25 μm. **G,** Quantitation of LD area fraction for 24 normal kidney and ccRCC tissues. Error bars represent SEM. ***$p < 0.0005$. **H,** Representative Raman spectra of autofluorescence granule in normal kidney tissue, LD in ccRCC tissue, and pure cholesteryl oleate. Spectral intensity was normalized by CH_2 bending band at 1,442 cm^{-1}. Black arrows indicate the band of cholesterol ring at 702 cm^{-1}. **I,** Quantitation of CE percentage for 24 ccRCC tissues. Error bars represent SEM. **J,** Significantly differential expression of genes involved in the cholesterol metabolic pathway in ccRCC tissues compared to normal tissues based on TCGA dataset (p-value < 0.05 and |log2(cancer/normal tissues) |> 0.5).

Furthermore, based on The Cancer Genome Atlas (TCGA) dataset, we evaluated the mRNA expression levels of cholesterol metabolism-related genes in 72 normal kidney tissues and 538 ccRCC tissues. As shown in Figure 1J, the HDL uptake related gene SCARB1, the cholesterol efflux related gene ABCA1, and the CE hydrolysis related gene LIPA were significantly upregulated in ccRCC tissues relative to those in normal tissues. Meanwhile, the cholesterol biosynthesis related gene HMGCR, the low-density lipoprotein (LDL) uptake related gene LDLR, and the cholesterol transport related gene SORT1 were downregulated in ccRCC tissues relative to those in normal tissues. These findings together demonstrate elevated CE accumulation and possible reprogramming of cholesterol metabolism in human ccRCC.

Primary Cell as a Preferable Model for the Study of Cholesterol Metabolism in ccRCC

To investigate how CEs accumulate in human ccRCC, we employed SRS microscopy to quantitatively analyze lipid content in a panel of commonly used cell lines, including ccRCC cell lines (786-O, 769-P, Caki-1, OSRC, and RCC4), normal kidney epithelial HK-2 cell line and embryonic kidney 293 cell line. All the above ccRCC cell lines contained substantially fewer LDs than human cancer tissues and did not show significant differences compared to the normal kidney cell lines (Fig. 2A and B). Moreover, CEs were undetectable in any of the cell lines based on Raman spectral analysis (Fig. 2C). Our results suggest that these commonly used immortalized cell lines may not be suitable for the study of CE accumulation in ccRCC.

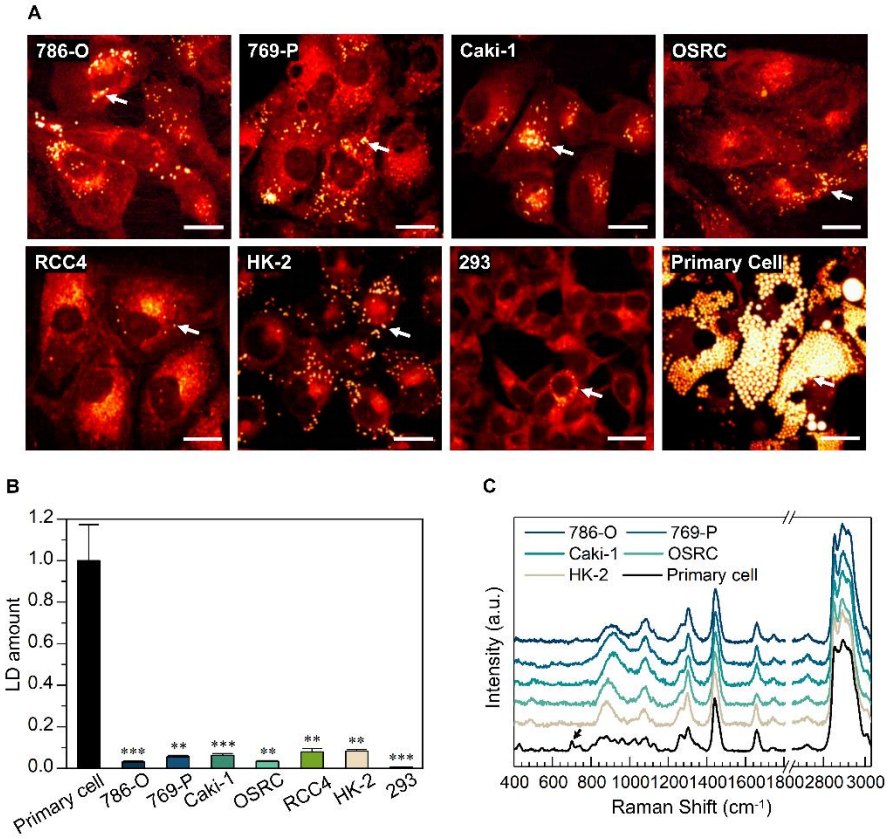

Figure 2. Primary cancer cell as an appropriate model for the study of cholesterol metabolism in ccRCC. **A,** Representative SRS images of ccRCC cell lines (786-O, 769-P, Caki-1, OSRC and RCC4), normal kidney cell lines (HK-2 and 293) and primary cancer cells isolated from human ccRCC tissues. LDs are indicated by white arrows. Scale bar, 20 μm. **B,** Quantitation of LD amount in primary cancer cells and cell lines, normalized by the LD amount in primary cancer cells. Error bars represent SEM. $^{**}p < 0.005$, $^{***}p < 0.0005$. **C,** Representative Raman spectra of LDs in cell lines (786-O, 769-P, Caki-1, OSRC and HK-2) and primary cancer cells. Spectral intensity was normalized by the peak at 1,442cm^{-1}. The black arrow indicates the band of cholesterol rings at 702 cm^{-1} in primary cancer cells.

In order to address this problem, primary cancer cells were isolated from human ccRCC tissues and confirmed by immunostaining of the epithelium marker (Supplementary Fig. S3A). The SRS images revealed numerous LDs in primary cancer cells (Fig. 2A), also confirmed by Bodipy labeling (Supplementary Fig. S3A), which represented the “clear cell” phenotype of ccRCC tissues. Quantitatively, LD amount in primary cancer cells was 10~30 times greater than the cell lines (Fig. 2B). Based on Raman spectral analysis, the LDs in primary cancer cells showed CE levels (Fig. 2C; details shown in Supplementary Table 2) that were as high as the original cancerous tissues

(Supplementary Fig. S3B).

Although cryopreservation is a routine procedure for cell culture, both LD amount and CE level were significantly reduced in primary cells after thawing from cryopreservation (Supplementary Fig. S4A-S4C). To further investigate the reason why cryopreservation reduced accumulation of LDs and CEs, whole-transcriptome RNA sequencing was performed. As shown in Supplementary Fig. S4D, the cholesterol transport related gene STARD3 and the cholesterol efflux related gene NR1H2 were upregulated, whereas the lipid regulation related genes PIK3CA and PIK3CB, the low-density lipoprotein (LDL) uptake related gene LRP2, and the CE hydrolysis related genes NCEH1 and LIPA were downregulated, after thawing from cryopreservation. Such alterations in gene expression imply that cryopreservation may reduce LD amount and CE level by enhancing cholesterol efflux and inhibiting cholesterol uptake.

In addition, our data showed a gradual reduction in both LD amount (Supplementary Fig. S5A and S5B) and CE level (Supplementary Fig. S5C) over time with prolonged culture *in vitro*. Particularly, the LD mount gradually decreased to around 70% (Supplementary Fig. S5B) and the average CE percentage gradually reduced around half (Supplementary Fig. S5C) on Day 7. As shown in Supplementary Figure S5C, the CE percentage for different LDs varied, that is, some of LDs contained high levels of CEs while the others might not have detectable CEs. Due to such variations, regarding the analysis of CE level in this study, we quantified not only the average CE percentage, but also the fraction of LDs with detectable CEs and the CE percentage of the LDs with detectable CEs. As shown in Supplementary Fig. S5D, the fraction of LDs with detectable CEs decreased gradually from 100% on Day 1 to 50% on Day 7. Within the LDs with detectable CEs, the CE percentage did not change significantly until Day 11 (Supplementary Fig. S5E).

Thus, to avoid the influence of cryopreservation and culture time, we only used primary cancer cells at the first

subculture and compare cells with or without treatment on the same day. Collectively, primary cancer cells retain the CE-rich phenotype of ccRCC and thus can be used as an appropriate model for the study of CE accumulation in ccRCC.

CE Accumulation in ccRCC is Induced by VHL Mutation and Subsequent Upregulation of HIFα

Given that VHL is a prevalently mutated tumor suppressor in ccRCC (24), we collected primary ccRCC cells from 17 patients and divided them into VHL mutation group (n = 11) and VHL non-mutation group (n = 6) (Supplementary Table 2). Although the LD amount was not significantly different between the primary cancer cells from patients with and without VHL mutation (Fig. 3A), the cells in VHL mutation group showed much stronger Raman peaks for CEs compared to those in VHL non-mutation group (Fig. 3B). Quantitatively, the CE level of primary cancer cells with VHL mutation was 68.4% ± 4.3%, which was significantly higher than that in cells without VHL mutation (21.7% ± 9.3%) (Fig. 3C). Particularly, primary cells from two out of the six patients without VHL mutation contained no detectable CEs (Fig. 3C). The detailed quantifications of LD amount and CE percentage for each patient with or without VHL mutation are shown in the Supplementary Table 2. These findings indicate a potential link between VHL mutation and CE accumulation in ccRCC.

To further determine whether VHL mutation was involved in CE accumulation, wild-type VHL was stably reintroduced into the primary cancer cells with VHL mutation, which resulted in significant reductions in both LD amount (Fig. 3D and E) and CE level (Fig. 3F-H). Specifically, there was a remarkable reduction in the Raman peaks for CEs upon VHL overexpression (Fig. 3F). Quantitatively, the average CE percentage was significantly reduced in VHL overexpression group compared to the control group (Fig. 3G). Furthermore, the fraction of LDs with detectable CEs was found to be significantly decreased upon VHL overexpression (Fig. 3H), while the CE

level of the LDs with detectable CEs remained unchanged (Supplementary Fig. S6C). Detailed information regarding LD amount and CE level for each patient is shown in Supplementary Fig. S6A and S6B, and Supplementary Table 3. Together, these results demonstrate that CE accumulation is likely driven by VHL mutation in ccRCC.

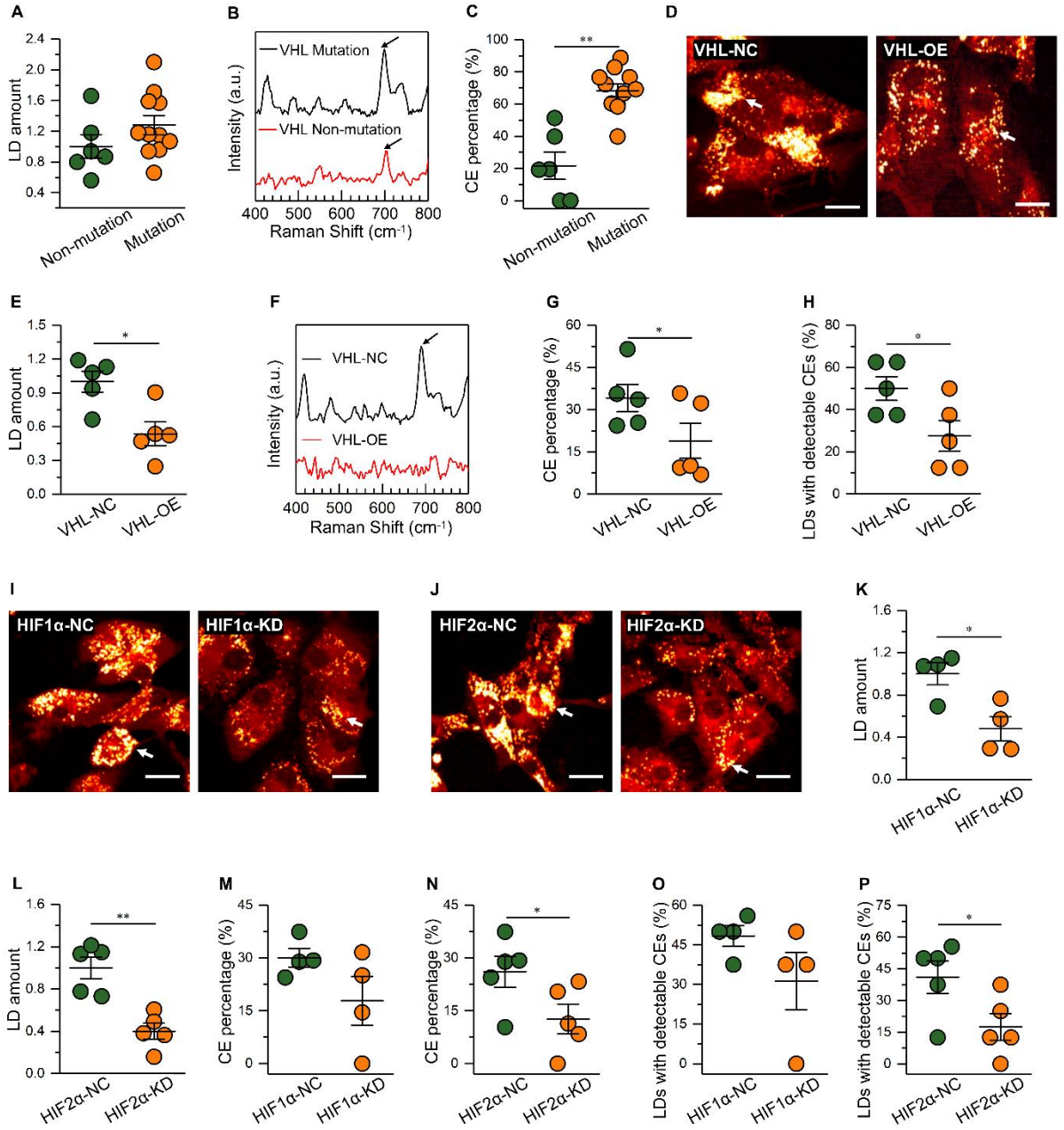

Figure 3. CE accumulation in ccRCC driven by VHL mutation and subsequent upregulation of HIFα. **A,** Quantitation of LD amount in primary cancer cells with and without VHL mutation, normalized by the non-mutation group. **B,**

Representative Raman spectra of LDs in primary cancer cells with and without VHL mutation. Spectral intensity was normalized by the peak at 1,442 cm^{-1}. The bands of cholesterol ring at 702 cm^{-1} are indicated by black arrows. **C,** Quantitation of CE percentage in primary cancer cells with and without VHL mutation. **D,** Representative SRS images of VHL-mutated primary cancer cells transfected with lentiviral negative control (VHL-NC) and VHL (VHL-OE). LDs are indicated by white arrows. Scale bar, 20 μm. **E,** Quantitation of LD amount in primary cancer cells of the VHL-NC and VHL-OE groups. LD amount was normalized by the VHL-NC group. **F,** Representative Raman spectra of LDs in primary cancer cells of the VHL-NC and VHL-OE groups. Spectral intensity was normalized by the peak at 1,442 cm^{-1}. The band of cholesterol ring at 702 cm^{-1} is indicated by black arrow. **G,** Quantitation of CE percentage in primary cancer cells of the VHL-NC and VHL-OE groups. **H,** The fraction of LDs with detectable CEs in primary cancer cells of the VHL-NC and VHL-OE groups. **I,** Representative SRS images of VHL-mutated primary cancer cells stably transfected with negative control (HIF1α-NC) and HIF1α shRNA (HIF1α-KD). LDs are indicated by white arrows. Scale bar, 20 μm. **J,** Representative SRS images of VHL-mutated primary cancer cells stably transfected with negative control (HIF2α-NC) and HIF2α shRNA (HIF2α-KD). LDs are indicated by white arrows. Scale bar, 20 μm. **K** and **L,** Quantitation of LD amount in primary cancer cells of the HIF1α-NC/HIF2α-NC and HIF1α-KD/HIF2α-KD groups. LD amount was normalized by the HIF1α-NC or HIF2α-NC group. **M** and **N,** Quantitation of CE percentage in primary cancer cells of the HIF1α-NC/HIF2α-NC and HIF1α-KD/HIF2α-KD groups. **O** and **P,** The fraction of LDs with detectable CEs in primary cancer cells of the HIF1α-NC/HIF2α-NC and HIF1α-KD/HIF2α-KD groups. Each circle represents average LD amount for one patient in **A**, **E**, **K**, and **L**. Each circle represents average CE percentage for one patient in **C**, **G**, **M** and **N**. Each circle represents the average fraction of LDs with detectable CEs for one patient in **H**, **O** and **P**. Error bars represent SEM. *$p < 0.05$, **$p < 0.005$.

VHL mutation leads to degradation failure and constitutive stabilization of HIFα, which is considered as the major driving force for ccRCC development (11,12). Our western blot data confirmed the reduction in HIFα expression upon VHL overexpression in primary cancer cells (Supplementary Fig. S6D). Although HIFα has been shown to regulate fatty acid metabolism (8,9), its role in CE accumulation remains elusive. To address this question, we tested if knockdown of HIFα by shRNA could reduce CE accumulation in primary cancer cells. As shown in Fig. 3I and J, LD accumulation in primary cancer cells was obviously decreased upon knockdown of either HIF1α or HIF2α. Quantitatively, the LD amount was reduced about half in the cells of both HIF1α knockdown group and HIF2α knockdown group (Fig. 3K and L). In terms of the CE level in primary cancer cells, the average CE percentage was not significantly changed upon HIF1α knockdown (Fig. 3M), but significantly reduced upon HIF2α knockdown (Fig. 3N). Consistently, the fraction of LDs with detectable CEs was not changed upon HIF1α

knockdown (Fig. 3O), but significantly reduced upon HIF2α knockdown (Fig. 3P). Notably, the CE level of the LDs with detectable CEs remained unchanged in both HIF1α knockdown group and HIF2α knockdown group (Supplementary Fig. S6E and S6F). Detailed information regarding LD amount and CE level for each patient is shown in Supplementary Fig. S6G and S6H, and Supplementary Table 4 and 5. Together, these results suggest that CE accumulation is probably induced by upregulation of HIFα.

CE Accumulation in ccRCC is Dependent on the Upregulation of PI3K/AKT/mTOR/SREBP Pathway

VHL and HIFα have been found to be closely related with PI3K/AKT/mTOR signaling pathway in ccRCC (25). Our western blot data confirmed that both VHL overexpression and HIFα knockdown induced significant reductions in the expression of p-AKT and p-S6 (Supplementary Fig. S6D, Supplementary Fig. S6I and S6J). As one of the interfaces of oncogenic signaling and cancer metabolism, PI3K/AKT/mTOR pathway is known to promote ccRCC (26), but its link with CE accumulation is not clear. To clarify this question, we inhibited the PI3K/AKT/mTOR pathway in primary cancer cells with LY294002 (a selective PI3K inhibitor), MK2206 (a selective AKT inhibitor), and rapamycin (a selective mTOR inhibitor), respectively. As shown in Fig. 4A and B, inhibition of PI3K/AKT/mTOR pathway significantly reduced LD amount in primary cancer cells. Regarding the CE level, although the average CE percentage was not significantly reduced due to big variations among patients (Fig. 4C), the fraction of LDs with detectable CEs was significantly decreased by PI3K/AKT inhibition in primary cancer cells (Fig. 4D). Detailed information regarding LD amount and CE level for each patient is shown in Supplementary Fig. S7A and S7B, and Supplementary Table 6.

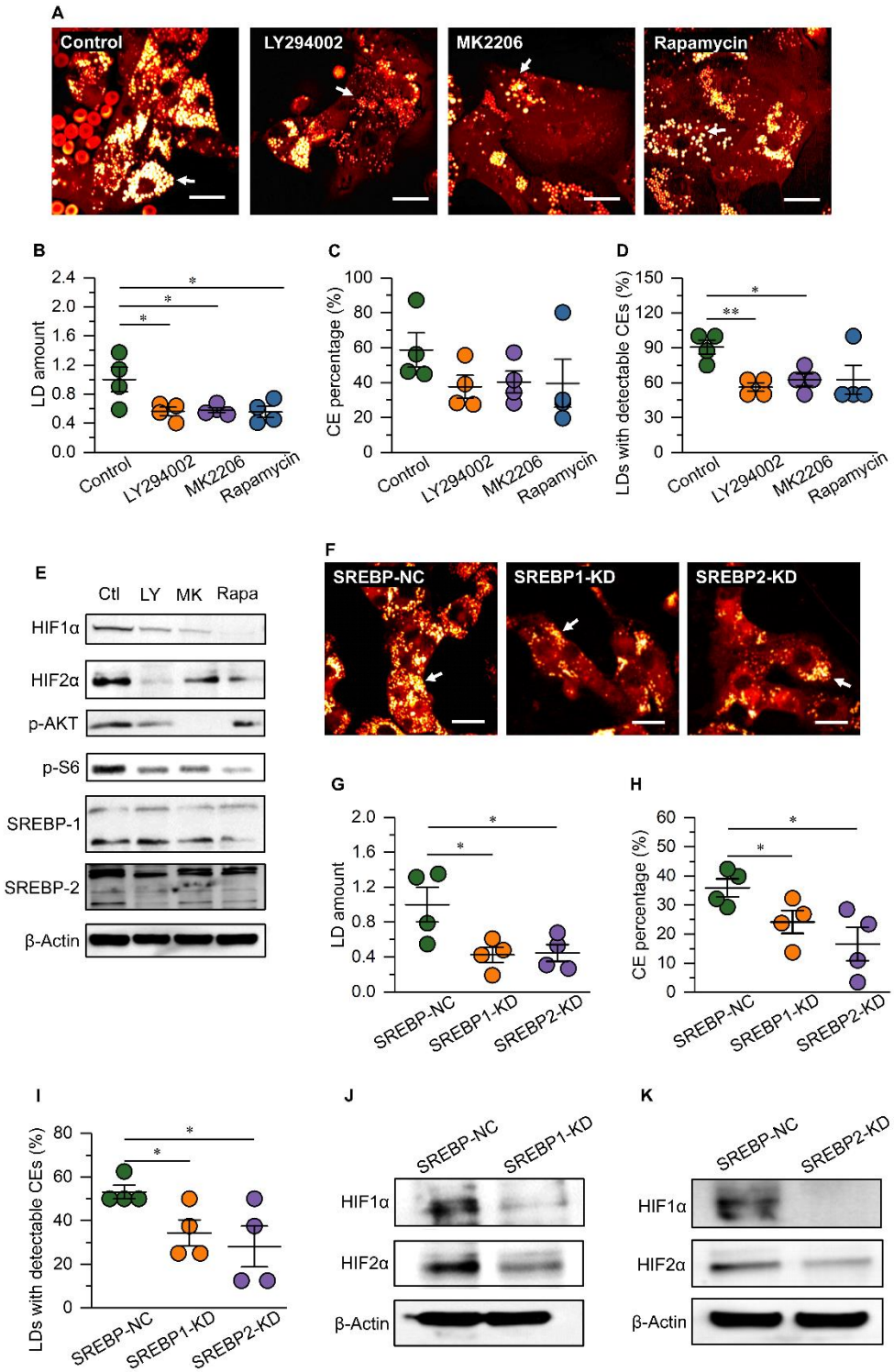

Figure 4. CE accumulation in ccRCC induced by the upregulation of PI3K/AKT/mTOR/SREBP pathway. **A,** Representative SRS images of primary cancer cells treated with DMSO as control, LY294002 (50 μM, 3 day), MK2206 (10 μM, 2 day), and rapamycin (100 nM, 2 day). LDs are indicated by white arrows. Scale bar, 20 μm. **B,** Quantitation of LD amount in primary cancer cells of control, LY294002, MK2206, and rapamycin groups. LD amount was normalized by the control group. **C,** Quantitation of CE percentage in primary cancer cells of control,

LY294002, MK2206, and rapamycin groups. **D,** The fraction of LDs with detectable CEs in primary cancer cells of control, LY294002, MK2206, and rapamycin groups. **E,** Immunoblot of antibodies against HIF1α, HIF2α, p-AKT, p-S6, SREBP-1, SREBP-2, and β-actin in primary cancer cells of control (Ctl), LY294002 (LY), MK2206 (MK), and rapamycin (Rapa) groups. **F,** Representative SRS images of primary cancer cells transfected with negative control (SREBP-NC), SREBP-1 shRNA (SREBP1-KD), and SREBP-2 shRNA (SREBP2-KD). LDs are indicated by white arrows. Scale bar, 20 μm. **G,** Quantitation of LD amount in primary cancer cells of the SREBP-NC, SREBP1-KD, or SREBP2-KD groups. LD amount was normalized by the SREBP-NC group. **H,** Quantitation of CE percentage in primary cancer cells of the SREBP-NC, SREBP1-KD, and SREBP2-KD groups. **I,** The fraction of LDs with detectable CEs in primary cancer cells of the SREBP-NC, SREBP1-KD, and SREBP2-KD groups. Each circle represents average LD amount for one patient in **B**, and **G**. Each circle represents average CE percentage for one patient in **C**, and **H**. Each circle represents the average fraction of LDs with detectable CEs for one patient in **D** and **I**. Error bars represent SEM. *$p < 0.05$, **$p < 0.005$. **J** and **K,** Immunoblot of antibodies against HIF1α, HIF2α, and β-actin in primary cancer cells of the SREBP-NC, SREBP1-KD, and SREBP2-KD groups.

Sterol regulatory element-binding proteins (SREBPs), which can be controlled by PI3K/AKT/mTOR, mainly regulate genes involved in intracellular lipid homeostasis (27). Our western blot data confirmed that the inhibition of PI3K/AKT/mTOR induced downregulation of SREBPs, in which SREBP-2 changed more prominently (Fig. 4E). Upon knockdown of SREBP-1 and SREBP-2, the LD amount, the average CE percentage, and the fraction of LDs with detectable CEs were all significantly decreased in primary cancer cells (Fig. 4F-I). Notably, the knockdown of SREBP-2, which is specifically responsible for regulating cholesterol synthesis and uptake, affected the CE level more evidently (Fig. 4H and I). Detailed information regarding LD amount and CE level for each patient is shown in Supplementary Fig. S7C and S7D, and Supplementary Table 7. In addition, the western blots revealed that inhibition of the PI3K/AKT/mTOR pathway and SREBPs in turn suppressed the HIFα expression (Fig. 4E, 4J and 4K). Together, these results reveal that CE accumulation in ccRCC is promoted by the PI3K/AKT/mTOR/SREBP pathway, which shows a positive feedback loop with HIFα.

Exogenous Lipoprotein Uptake is the Primary Source of Cholesterol for CE Accumulation in ccRCC

The cholesterol stored in LDs arise from either *de novo* biosynthesis or extracellular lipoprotein uptake (28).

To investigate the source of cholesterol for CE accumulation in ccRCC, we firstly evaluated the impact of exogenous lipoprotein uptake on CE accumulation in primary cancer cells. As shown in Fig. 5A-D, depriving serum from the culture medium led to substantial reductions in the LD amount, the average CE percentage, and the fraction of LDs with detectable CEs in primary cancer cells. As expected, such reductions were partly restored by adding back exogenous LDL or HDL. Detailed information regarding LD amount and CE level for each patient is shown in Supplementary Fig. S8A and S8B, and Supplementary Table 8. Moreover, inhibition of the PI3K/AKT/mTOR pathway effectively decreased the uptake of DiI-labeled LDL (Fig. 5E) and DiI-labeled HDL (Fig. 5F), which were consistent with the reduced expression levels of LDLR and SCARB1 (Fig. 5G). Notably, SCARB1 was greatly elevated, but LDLR was significantly reduced, in human ccRCC tissues compared with normal kidney tissues (Fig. 1J). Consistently, SCARB1 expression of primary cancer cells was significantly stronger than the commonly used cell lines, such as 786-O and RCC4 (Supplementary Fig. S8C and S8D). These findings suggest that although both LDL and HDL uptake contributes to CE accumulation in primary cancer cells, HDL is the primary exogenous source.

Secondly, besides exogenous lipoprotein uptake, we also assessed the contribution of *de novo* cholesterol biosynthesis to CE accumulation in ccRCC. As shown in Fig. 5H-K, inhibition of 3-hydroxy-3-methylglutaryl coenzyme A reductase (HMGCR), the rate-limiting enzyme for cholesterol synthesis, by simvastatin caused significant reductions in LD amount, the average CE percentage, and the fraction of LDs with detectable CEs in primary cancer cells. Detailed information regarding LD amount and CE level for each patient is shown in Supplementary Fig. S9 and Supplementary Table 9. Notably, the HMGCR expression was significantly lower in human ccRCC tissues than normal kidney tissues (Fig. 1J). Thus, although *de novo* cholesterol biosynthesis is also involved in CE accumulation, exogenous lipoprotein uptake makes much bigger contribution in ccRCC.

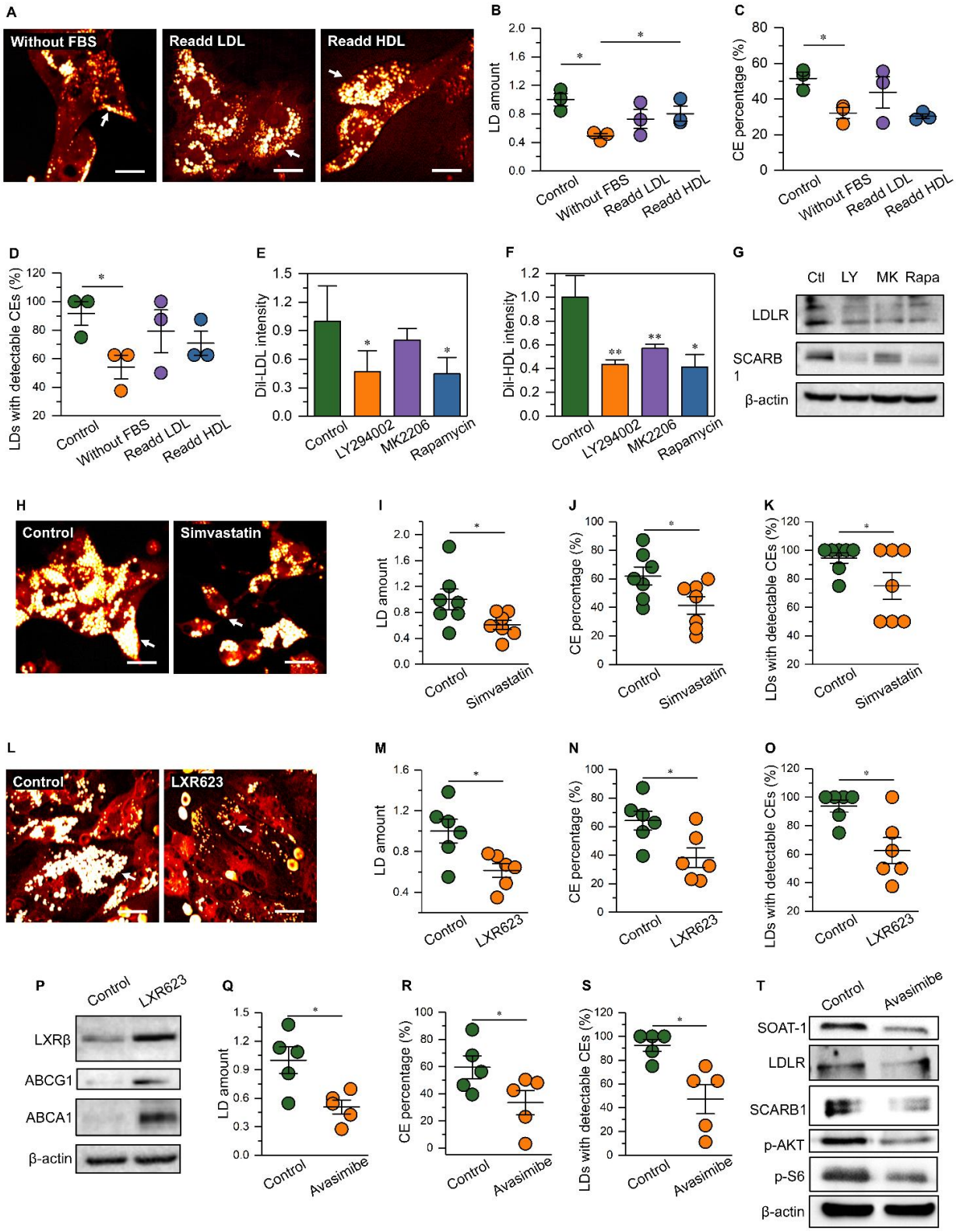

Figure 5. Source of cholesterol for CE accumulation in ccRCC. **A,** Representative SRS images of primary cancer cells cultured without FBS (1 day) and then with re-addition of LDL or HDL (45 mg/ml, 1 day). LDs are indicated

by white arrows. Scale bar, 20 μm. **B,** Quantitation of LD amount in primary cancer cells of control, without FBS, and then with re-addition of LDL or HDL. LD amount was normalized by the control group. **C,** Quantitation of CE percentage in primary cancer cells of control, without FBS, and then with re-addition of LDL or HDL. **D,** The fraction of LDs with detectable CEs in primary cancer cells of control, without FBS, and then with re-addition of LDL or HDL. **E** and **F,** Quantitation of DiI-LDL or Dil-HDL uptake in primary cancer cells treated with DMSO as control, LY294002 (50 μM, 3 day), MK2206 (10 μM, 2 day), and rapamycin (100 nM, 2 day) (n = 3 patients). DiI-LDL/HDL intensity was normalized by the control group. **G,** Immunoblot of antibodies against LDLR, SCARB1, and β-actin in primary cancer cells treated without (Ctl) or with LY294002 (LY), MK2206 (MK), and rapamycin (Rapa). **H,** Representative SRS images of primary cancer cells treated with DMSO as control and simvastatin (10 μM, 1 day). LDs are indicated by white arrows. Scale bar, 20 μm. **I,** Quantitation of LD amount in primary cancer cells of control and simvastatin groups. LD amount was normalized by the control group. **J,** Quantitation of CE percentage in primary cancer cells of control and simvastatin groups. **K,** The fraction of LDs with detectable CEs in primary cancer cells of control and simvastatin groups. **L,** Representative SRS images of primary cancer cells treated with DMSO as control and LXR623 (5 μM, 2 day). LDs are indicated by white arrows. Scale bar, 20 μm. **M,** Quantitation of LD amount in primary cancer cells of control and LXR623 groups. LD amount was normalized by the control group. **N,** Quantitation of CE percentage in primary cancer cells of control and LXR623 groups. **O,** The fraction of LDs with detectable CEs in primary cancer cells of control and LXR623 groups. **P,** Immunoblot of antibodies against LXRβ, ABCG1, ABCA1, and β-actin in ccRCC primary cells of control and LXR623 groups. **Q,** Quantitation of LD amount in ccRCC primary cells treated with DMSO as control and avasimibe (20 μM, 2 day). LD amount was normalized by the control group. **R,** Quantitation of CE percentage in primary cancer cells of control and avasimibe groups. **S,** The fraction of LDs with detectable CEs in primary cancer cells of control and avasimibe groups. Each circle represents average LD amount for one patient in **B**, **I**, **M**, and **Q**. Each circle represents average CE percentage for one patient in **C**, **J**, **N**, and **R**. Each circle represents the average fraction of LDs with detectable CEs for one patient in **D**, **K**, **O**, and **S**. Error bars represent SEM. *$p < 0.05$, **$p < 0.005$. **T,** Immunoblot of antibodies against SOAT-1, LDLR, SCARB1, p-AKT, p-S6, and β-actin in primary cancer cells of control and avasimibe groups.

Thirdly, the high expression of cholesterol efflux-related gene in ccRCC (Fig. 1J) made us to wonder how cholesterol efflux was involved in CE accumulation. As a cholesterol sensor, liver X receptor β (LXRβ) is known to promote ABCA1 and ABCG1-mediated cholesterol efflux for maintenance of cholesterol homeostasis (29). As shown in Fig. 5L-O, activation of cholesterol efflux by LXR623, a LXRβ agonist, led to significant decreases of LD amount, the average CE percentage, and the fraction of LDs with detectable CEs in primary cancer cells. Detailed information regarding LD amount and CE level for each patient is shown in Supplementary Fig. S10A and S10B, and Supplementary Table 10. Additionally, the western blot data confirmed that LXR623 effectively upregulated ABCA1 and ABCG1 (Fig. 5P). These findings imply that cholesterol efflux hinders CE accumulation,

but such repressive effect apparently could not counteract the substantial upregulation of HDL uptake in ccRCC. Taken together, these results reveal that cholesterol biosynthesis, uptake and efflux are all involved in CE accumulation, and exogenous HDL uptake is the dominant source of cholesterol for CE accumulation in ccRCC.

Inhibition of Cholesterol Esterification Significantly Suppressed CE Accumulation in ccRCC

Excess free cholesterol needs to be converted to CEs by sterol O-acyltransferase (SOAT) enzymes and then stored into LDs to avoid toxicity (30). As excepted, inhibition of SOAT enzymes with a potent SOAT inhibitor, avasimibe, induced significant reductions in LD amount, the average CE percentage, and the fraction of LDs with detectable CEs in primary cancer cells (Fig. 5Q-S). Detailed information regarding LD amount and CE level for each patient is shown in Supplementary Fig. S10C and S10D, and Supplementary Table 11. Interestingly, inhibition of SOAT effectively hindered the uptake of Dil-LDL and Dil-HDL (Supplementary Fig. S10E and S10F), also reduced the expression of the corresponding receptors LDLR and SCARB1, and even affected the upstream PI3K/AKT/mTOR pathway in primary cancer cells (Figure 5T). Collectively, these results demonstrate that CE accumulation in ccRCC relies on sufficient cholesterol esterification.

CE Depletion Impaired ccRCC Aggressiveness *in Vitro*

Considering that aberrant CE accumulation occurs in ccRCC but not normal kidney, here we explored whether cholesterol esterification affected ccRCC viability, migration, and invasion. Firstly, CE depletion by avasimibe significantly reduced viability of primary cancer cells with IC_{50} value of ~15 μM (Fig. 6A; Supplementary Fig. S11A and S11B), while the inhibitory effects by avasimibe were much more moderate in the commonly used ccRCC cell lines (786-O, 769-P, Caki-1, OSRC, and RCC4) and normal kidney cell line (HK-2) (Supplementary Fig. S11C).

Further flow cytometry analysis revealed that avasimibe treatment significantly prohibited the transition from G1 to S phase of primary cancer cells (Fig. 6B), which might explain why avasimibe reduced cell viability. Secondly, results of the Transwell experiments indicated that CE depletion by avasimibe significantly suppressed migration and invasion capabilities of primary cancer cells (Fig. 6C). These results suggest that CE depletion substantially suppresses ccRCC aggressiveness *in vitro*.

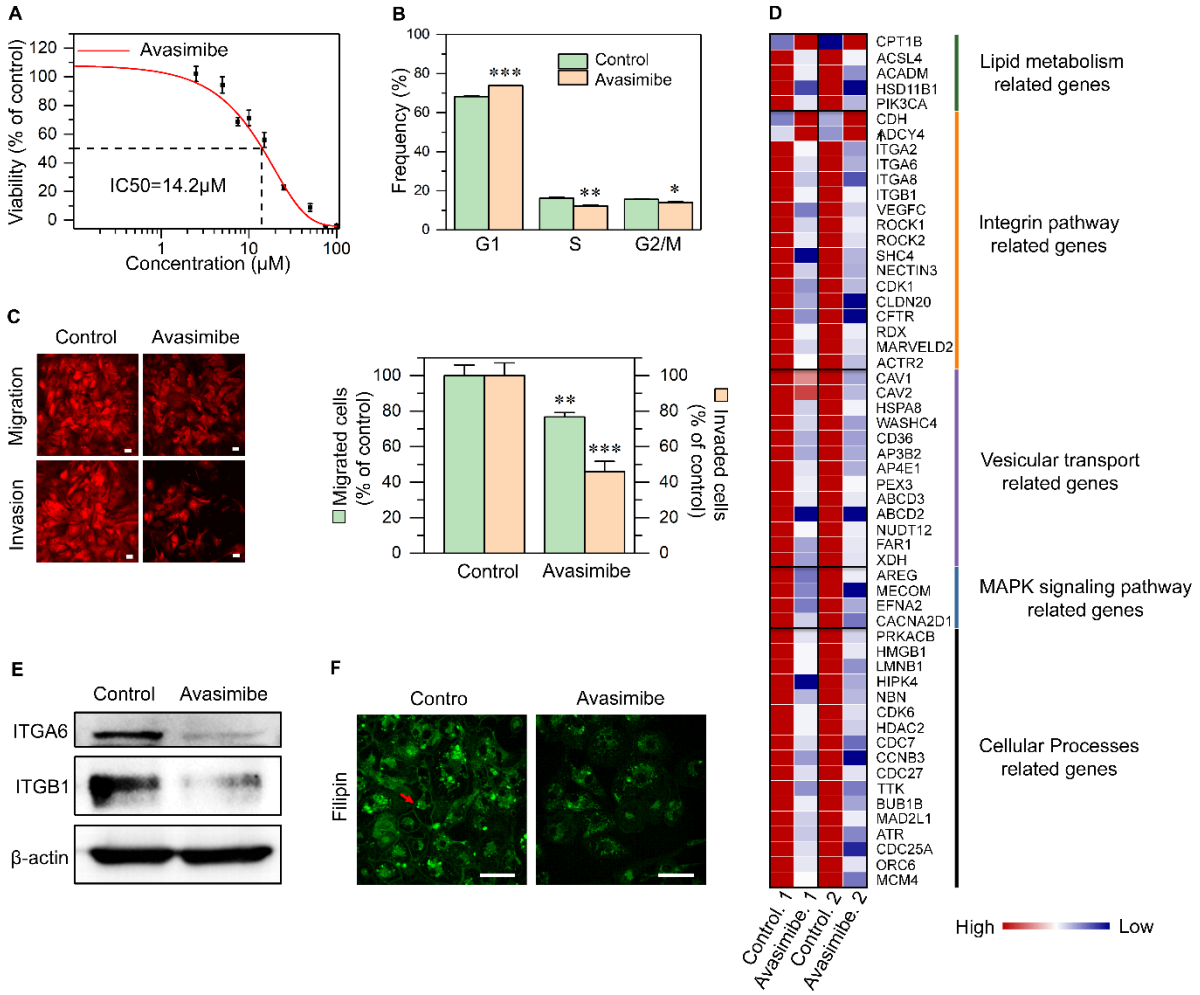

Figure 6. Inhibition of cholesterol esterification impaired ccRCC aggressiveness. **A,** IC50 curve of primary cancer cells upon avasimibe treatment (3 day) (IC50 ≈ 15 μM). **B,** Flow cytometry analysis of cell cycle in primary cancer cells treated with DMSO as control and avasimibe (15 μM, 2 day) (n = 3 patients). **C,** Representative images and quantitation of migration and invasion of primary cancer cells upon avasimibe treatment (15 μM, 3 day) (n = 7). The control group (DMSO) was used for normalization. Scale bar, 20 μm. Error bars represent SEM. **p < 0.005, ***p < 0.0005. **D,** Differential gene expression of primary cancer cells upon avasimibe treatment (20 μM, 2 day) for two

patients. **E,** Immunoblot of antibodies against ITGA6, ITGB1, and β-actin in primary cancer cells of control and avasimibe groups. **F,** Representative images of filipin staining for cellular cholesterol in primary cancer cells upon avasimibe treatment. Cholesterol staining on the membrane is indicated by the red arrow. Scale bars, 20 μm.

CE Depletion Impaired ccRCC Aggressiveness through Downregulation of the Integrin and MAPK Signaling Pathways

To elucidate the underlying mechanisms by which CE depletion impaired ccRCC aggressiveness, we firstly analyzed differentially expressed genes in primary cancer cells treated with avasimibe using whole-transcriptome RNA sequencing (Fig. 6D). In consistency with the inhibitory effects of avasimibe, various genes related to cellular processes were significantly downregulated in the avasimibe-treated group compared with the control group. Importantly, multiple genes related to the integrin pathway (e.g., ITGA6 and ITGB1), which plays a crucial role in cancer progression, were significantly downregulated upon avasimibe treatment. The western blot data also confirmed the reduced expression of ITGA6 and ITGB1 in the avasimibe-treated group (Fig. 6E). Given that integrins are located on the plasma membrane and regulated by the membrane cholesterol level (31), we further clarified how integrins were downregulated by avasimibe in primary cancer cells. As shown in Fig. 6F, the filipin fluorescence, which mapped intracellular free cholesterol, was remarkedly decreased on cell membranes of primary cancer cells treated with avasimibe. Besides the integrin pathway, caveolin-1 (CAV1) and several genes associated with MAP kinase (MAPK) signaling pathway were also markedly downregulated in primary cancer cells upon avasimibe treatment (Fig. 6D). As a regulator of intracellular cholesterol homeostasis, CAV1 has been shown to be widely upregulated in various cancers and promote tumor progression and drug resistance (32). CAV1-mediated MAPK pathway may contribute to cancer cell survival and metastasis (23,33). Taken together, these results suggest that CE depletion impaired ccRCC aggressiveness due to reduced cholesterol levels on cell membranes and

subsequent downregulation of integrin and MAPK signaling pathways.

DISCUSSION

Although CE accumulation has been recognized as a hallmark of ccRCC, its exact role in ccRCC progression remains elusive. As illustrated in Figure 7, our study unraveled that CE accumulation in LDs was induced by the mutation of tumor suppressor VHL and subsequent activation of the HIFα mediated PI3K/AKT/mTOR pathway. The esterified cholesterol accumulated in LDs predominantly arose from exogenous HDL uptake. Inspiringly, inhibition of cholesterol esterification effectively suppressed ccRCC progression via reduced membrane cholesterol levels and the subsequent downregulation of integrin and MAPK signaling pathways. As discussed below, these findings improve current understanding of the molecular mechanisms and pathological significance of CE accumulation in ccRCC progression, which may provide a potential metabolic target for ccRCC treatment.

Firstly, our study demonstrates the need for primary cancer cell, instead of cell lines, as the suitable model to study CE accumulation in ccRCC. Enabled by the label-free Raman spectromicroscopy platform, which integrated stimulated Raman scattering microscopy with confocal Raman spectroscopy, we could quantitatively analyze LD distribution and composition at the single cell level in intact cancer cell and tissue specimens *in situ* without any processing or exogenous labeling. Our results revealed that, in contrast with the high CE level in human ccRCC tissues, the commonly used ccRCC cell lines in literatures did not contain detectable CEs in LDs. Thus, it is not surprising that most previous mechanistic studies about LD accumulation in ccRCC focused on the altered metabolism of fatty acid but not cholesterol (8-10). This is very likely the culprit for current limited understanding of CE accumulation in ccRCC. In order to address this problem, we isolated primary cancer cells from human ccRCC tissues and showed that they could represent the signature of ccRCC with CE level as high as the original

tissue. Collectively, our study indicates that primary cancer cell is an appropriate cell model to elucidate the role of CE in ccRCC.

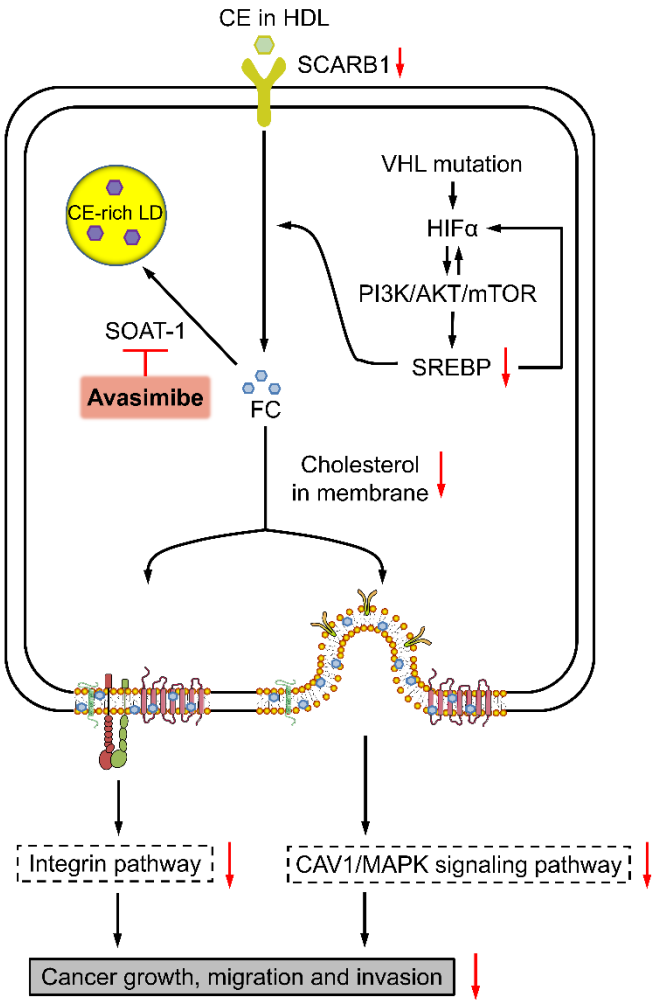

Figure 7. Molecular mechanism underlying CE accumulation in ccRCC and suppression of cancer progression upon CE depletion**.** The schematic shows that VHL mutation activates PI3K/AKT/mTOR/SREBPs pathway in a HIFα-dependent manner. Exogenous HDL uptake is the primary cholesterol source. The excess free cholesterol (FC) is then esterified into CEs by SOAT-1 and stored into LDs. The red arrows indicate the consequences of CE depletion by avasimibe treatment. Inhibition of cholesterol esterification disturbs the cholesterol homeostasis by downregulations of SREBPs and lipoprotein uptake. Consequently, the reduced cholesterol level on cell membrane leads to downregulations of integrin and MAPK signaling pathways that further impair ccRCC progression.

Secondly, our study extends the current understanding of cholesterol metabolism in ccRCC. As the most common mutation of ccRCC, tumor suppressor VHL mutation induces constitutive stabilization of HIFα (11,12),

which has been shown to promote the storage of fatty acids in the form of triacylglycerol in LDs (8). Nevertheless, the role of VHL and HIFα in the regulation of cholesterol metabolism in ccRCC has not been investigated. Our results unraveled that aberrant CE accumulation in ccRCC was a consequence of VHL mutation and subsequent activation of HIFα, which has not been documented before. Moreover, our study further elucidates how VHL/HIFα regulates CE accumulation in ccRCC. Upregulations of PI3K/AKT/mTOR signaling pathway and subsequent SREBPs have been shown to alter lipid metabolism in a variety of human cancers (1). Thus, it is intriguing to explore whether VHL/HIFα links to CE accumulation via the PI3K/AKT/mTOR/SREBP pathway. Our results uncovered that VHL mutation and subsequent stabilization of HIFα upregulated the PI3K/AKT/mTOR/SREBP pathway, which induced CE accumulation. Meanwhile, the PI3K/AKT/mTOR/SREBP pathway in turn regulated HIFα to create a vicious circle.

In addition, our study confirmed the source of cholesterol for CE accumulation in ccRCC. The source of cholesterol for CE accumulation varies for different types of human cancers. For example, pancreatic cancer and melanoma elevate de novo cholesterol synthesis (34,35), whereas glioblastoma, breast cancer, prostate cancer, and hepatocellular carcinoma rely on exogenous cholesterol uptake (21,36-38). In this study, we found that ccRCC could get cholesterol from both *de novo* synthesis and exogenous uptake via LDL and HDL, which were regulated by the PI3K/AKT/mTOR/SREBP pathway. By incorporating transcriptomic data, we further recognized that remarkably enhanced exogenous HDL uptake was the primary driving source of cholesterol, which could counteract the effects of reduced synthesis and increased efflux in ccRCC compared to normal tissue. This finding is consistent with the very recent work on the role of HDL uptake in ccRCC progression (15).

Finally, our study discovers cholesterol esterification as a vulnerable metabolic target for ccRCC treatment. Although surgery is considered as the first choice for ccRCC treatment, adjuvant therapies are still crucial to reduce

recurrence and prolong survival. Unfortunately, ccRCC lacks sensitivity to chemotherapy and often develops resistance to current targeted therapies against vascular endothelial growth factor (VEGF) and mTOR (6). Recently developed immunotherapy could extend survival, but only benefit a limited population of patients (6). Thus, there is an urgent need to discover new therapeutic target for ccRCC. Our results showed that inhibition of cholesterol esterification by avasimibe, the potent inhibitor of SOAT, significantly impaired growth, migration and invasion of primary ccRCC cells, but not normal cells. Moreover, it is worth to mention that avasimibe was previously used to treat atherosclerosis and showed minimal toxicity (39). Avasimibe has also been used to effectively suppressed development and progression of many other types of cancers, such as prostate cancer, pancreatic cancer, glioblastoma, and liver cancer (21,23,38,40), which suggests that cholesterol esterification could become an universal therapeutic target for human cancers. Notably, the mechanism by which CE depletion impairs cancer progression varies in different cancers. Our results unraveled that inhibition of cholesterol esterification disturbed intracellular cholesterol homeostasis and reduced membrane cholesterol levels. Such membrane cholesterol reduction further led to downregulation of integrin signaling pathway and caveolin mediated MAPK pathway, both of which have been shown to promote cancer progression (23,33). Taken together, our study sheds new light on the mechanism underlying CE accumulation in ccRCC and opens up a new avenue for ccRCC treatment.

METHODS

Human Tissue Specimens

All tissues specimens were obtained from ccRCC patients undergone nephrectomy at Peking University First Hospital. This study was approved by the Institutional Review Boards of both Beihang University and Peking University First Hospital. Pathological examination was performed by experienced pathologists. Details were described in the Supplementary Experimental Procedures.

Cell Cultures

All cell lines were obtained from the American Type Culture Collection. Primary cancer cells were isolated from fresh human ccRCC tissues according to the procedures in previous studies (41). Details were described in the Supplementary Experimental Procedures.

Label-free Raman Spectromicroscopy

Label-free Raman spectromicroscopy was performed on unstained frozen tissue slices (~20 μm) and live cells. SRS images were obtained on a picosecond SRS microscope, with the laser-beating frequency tuned to the C-H stretching vibration band at 2850 cm^{-1}, as described previously (18). Compositional analysis of individual LDs and autofluorescent granules was conducted by integration of SRS imaging and confocal Raman spectral analysis on a single platform (42). Two-photon fluorescence signals were acquired through a 520/40 nm bandpass filter for the images of autofluorescent granules in human tissues. Details were described in the Supplementary Experimental Procedures.

We quantitatively analyzed LD amount and CE percentage in individual LDs. By using ImageJ “Threshold” function, LDs can be extracted based on the significantly higher signal intensities compared to other cellular compartments. Then, by using ImageJ “Analyze Particles” function, fractions of LD area out of cell area and tissue

area were acquired respectively. For tissue specimen of each patient, 6 different locations were averaged for the final value of LD area fraction. For cultured cells, about 20 cells were averaged for the final value of LD amount. The percentage of CE in individual LDs was linearly correlated with the height ratio of the 702 cm^{-1} peak to the 1,442 cm^{-1} peak (I_{702}/I_{1442}). Specifically, $I_{702}/I_{1442} = 0.003 \times$ CE percentage (%) (Supplementary Fig. S2B). CE percentage for each tissue specimen or cell culture was obtained by averaging the CE percentage of LDs in 6-10 cells. Details were described in the Supplementary Experimental Procedures.

Fluorescence Imaging of Dil-LDL/HDL Uptake

After treated with indicated inhibitors for a given time period, cells were incubated with 20 μg/ml Dil-labeled LDL/HDL (Dil-LDL/HDL) (Yiyuan Biotechnologies, cat YB-0011; Solarbio, cat H8910) for 3 hr at 37 °C in culture medium without FBS and then imaged by two-photon fluorescence microscopy through a 600/60 nm bandpass filter. The Dil-LDL or HDL intensity was quantified with ImageJ and normalized by cell number for lipoprotein uptake capacity.

TCGA RNA-seq Analysis

The transcriptome dataset of renal clear cell carcinoma (TCGA-KIRC) including 538 tumor tissues and 72 normal tissues were obtained from TCGA in December 2021. The detailed analysis procedure was described in the Supplementary Experimental Procedure.

Lipid Extraction and Measurements

Lipids in tissues were extracted and measured as described in the Supplementary Experimental Procedures.

DNA Sequencing and RNA Sequencing

Genomic DNA was extracted and purified from primary cells according to manufacturer's instruction of DNAzol™ reagent (Thermo Fisher Scientific, 10503027). RNA was extracted from primary cells according to

manufacturer's instruction of TRIzol™ reagent (Thermo Fisher Scientific, 15596026). Details were described in the Supplementary Experimental Procedure.

RNA Interference and Immunoblotting

RNA interference and immunoblotting were performed as described in the Supplementary Experimental Procedure.

Cell Viability Assay, Cell Cycle Analysis, Migration/Invasion Assay

Cell viability assay was performed with the MTT colorimetric assay (Thermo Fisher Scientific, M6494). Cell cycle analysis used PI staining (Thermo Fisher Scientific, P3566) and then was performed by flow cytometer (Peking University Health Science Center). Migration and invasion assays were performed in Transwell chambers coated with and without Matrigel (Corning, 354234). Details were described in the Supplementary Experimental Procedures.

Statistical Analysis

One-way ANOVA and Student's t test were used for comparisons between groups. $p < 0.05$ was considered statistically significant. All data was presented as mean ± standard error of the mean (SEM). Details were described in the Supplementary Experimental Procedures.

Author Contributions

Conception and design: Shuhua Yue, Lin Yao

Development of methodology: Shuo Zhang, Shuhua Yue

Acquisition of data: Shuo Zhang, Yexuan He, Yaoyao Zheng, Zhuojun Liu, Jia Liu, Jian Yu, Anbang He, Shuai Hu, Yanqing Gong, Zhijun Xi, Wei Yu, Lin Yao, Shuhua Yue

Analysis and interpretation of data: Shuo Zhang, Weichen Feng, Tinghe Fang, Shuhua Yue, Liqun Zhou

Writing, review, and/or revision of the manuscript: Shuo Zhang, Shuhua Yue, Lin Yao

Study supervision: Shuhua Yue, Lin Yao

Disclosure of Potential Conflicts of Interest

The authors declare no potential conflicts of interest.

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