VAMP8 function reveals tight linkage between endocytic recycling and endocytosis

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Significance Statement

This study reveals that the SNARE protein VAMP8 regulates clathrin-mediated endocytosis (CME) by controlling endocytic recycling of cargo, rather than through its direct recruitment to clathrin-coated vesicles. By demonstrating that VAMP8 depletion reroutes transferrin receptors toward lysosomal degradation—thereby impairing endocytic vesicle formation—the work uncovers a critical link between endocytic recycling and endocytosis, emphasizing how cargo fate dictates CME efficiency. These findings reshape our understanding of cellular trafficking mechanisms and highlight the importance of recycling pathways in maintaining membrane dynamics.

Abstract

Clathrin-mediated endocytosis (CME) is a multistage process that involves the initiation and stabilization of clathrin-coated pits (CCPs), which invaginate and finally detach from the plasma membrane to form clathrin-coated vesicles (CCVs). Given that SNARE proteins are essential for downstream vesicle targeting and fusion events, their recruitment into nascent CCVs has been suggested to play a role in regulating CME progression. However, which and how SNARE proteins regulate CME remains to be explored. Here, we showed that siRNA-mediated knockdown of the R-SNARE, VAMP8 impairs CCP initiation, stabilization and invagination and strongly inhibits CME. Mechanistically, recruitment of VAMP8 to CCVs is not required for CME regulation. Instead, VAMP8 regulates CME indirectly by mediating endocytic recycling. Depletion of VAMP8 skews endosomal recycling of CME cargo, exemplified here by transferrin receptor, toward lysosomal degradation, thereby inhibiting CCV formation. Overall, our study provides new insights into the crosstalk between endocytosis and VAMP8-mediated endocytic recycling of CME cargo and demonstrates the significance of cargo recruitment in CME regulation.

Introduction

Clathrin-mediated endocytosis (CME) is a major endocytic pathway that regulates the uptake of receptor proteins from the plasma membrane (PM), and is thus essential for signaling, cell-cell communication, and cellular homeostasis (McMahon and Boucrot, 2011; Mettlen et al., 2018). Productive CME events involve a multistage process that includes the initiation and stabilization of nascent clathrin-coated pits (CCPs). These pits invaginate, mature and eventually detach from the PM to form clathrin-coated vesicles (CCVs) that are loaded with cargo (Kaksonen and Roux, 2018; Mettlen et al., 2018). Not all CME initiation events complete this multistage process: many

nascent clathrin assemblies rapidly disassemble as early abortive coats (ACs); those that are stabilized are designated as *bona fide* CCPs. A second point of failure occurs when *bona fide* CCPs fail to grow and invaginate. These are turned over as late abortive pits (Aguet et al., 2013; Ehrlich et al., 2004; He et al., 2025; Loerke et al., 2011; Wang et al., 2020; Yang et al., 2025). The early stages of CME, including the initiation, stabilization and invagination of CCPs, are key steps in determining the fate of nascent CCPs. However, the underlying mechanisms determining their fates, and thereby the efficiency of CME, remain incompletely understood.

Soluble N-ethylmaleimide-sensitive factor attachment receptors (SNAREs) are small membrane-anchored proteins that function in complexes consisting of one R-SNARE and three Q-SNAREs, to provide the energy and specificity for intracellular vesicle-vesicle/targeting membrane fusion (Chen and Scheller, 2001; Dingjan et al., 2018; Fasshauer et al., 1998; Hong, 2005). SNARE proteins participate in almost all membrane fusion processes (Hong, 2005; Jahn and Scheller, 2006), including the targeting and fusion of nascent CCVs required for delivery of their cargo to early endosomes (Maxfield and McGraw, 2004). Indeed, the incorporation of SNARE proteins into nascent vesicles has been shown to be required for COPI (Rein et al., 2002) and COPII (Mossessova et al., 2003; Springer and Schekman, 1998), but this has not been shown for CME. However, the existence of SNARE-specific adaptor proteins (CALM for VAMPs 2, 3,7 and 8 (Miller et al., 2011; Sahlender et al., 2013) and Hrb for VAMP 7 (Chaineau et al., 2008)) has been suggested as a mechanism to ensure incorporation of SNARE proteins into CCVs without competition from other cargo. While depletion of either Hrb or CALM inhibits CME, these proteins have other partners and are likely to play additional critical roles in CME. Indeed, point mutations in CALM that selectively inhibit SNARE uptake, uncouple their effects on SNARE uptake from CALM's other roles in CME (Sahlender et al., 2013). A more recent study has shown that knockdown of several SNARE proteins alters early CCP dynamics (Bhave et al., 2020), but their effects on CME were not measured.

Vesicle-associated membrane protein 8 (VAMP8, also known as endobrevin) is an R-SNARE protein that is widely distributed on the PM, early/recycling/late endosomes, and lysosomes (Antonin et al., 2000b; Bagshaw et al., 2005; Bilan et al., 2008; Itakura et al., 2012). Best described are its involvement in regulated exocytosis (Puri and Roche, 2008; Tiwari et al., 2008; Wang et al., 2004; Wang et al., 2007), fusion of recycling endosomes with the PM (Marshall et al., 2015), lysosome-autophagosome fusion (Chen et al., 2021; Diao et al., 2015; Itakura et al., 2012; Jian et al., 2024) and homotypic fusion of early and late endosomes (Antonin et al., 2000a; Antonin et al., 2000b; Pryor et al., 2004). This latter function, together with its localization to CCPs and early endosomes (Antonin et al., 2000b) and an earlier finding that VAMP8

knockdown, in the context of a CRISPRi-based screen impairs CCP initiation and stabilization (Bhave et al., 2020), led us to further characterize the role of the R-SNARE, VAMP8 in CME.

In this study, we reveal that VAMP8 not only regulates CCP initiation and stabilization, but also CCP invagination. However, the regulation of CME by VAMP8 is not determined by its direct recruitment to CCVs. Instead, VAMP8 regulates CME, indirectly, by mediating endocytic recycling of cargo from early and recycling endosomes to the PM. Knocking down VAMP8 skews the sorting of endosomal CME cargo, shown here for transferrin receptor (TfnR), from recycling towards lysosomal degradation. We show that the resulting reduction in CME cargo at the plasma membrane inhibits CCV formation. Overall, our study provides new insights into the crosstalk between endocytosis and exocytosis intersected by VAMP8-mediated cargo recycling and demonstrates the significance of cargo recruitment in regulating CME.

Results

VAMP8 knockdown inhibits CCP maturation and TfnR uptake

To determine whether VAMP8 regulates CME, we first performed siRNA-mediated knockdown of VAMP8 in ARPE-HPV cells that stably express eGFP-tagged clathrin light chain a (referred to as ARPE-HPV eGFP-CLCa) and examined its effects on CCP initiation and maturation. Two sets of siRNA were used separately and both efficiently knocked down VAMP8 (Fig. 1A and B). Cells were time-lapse imaged using Total Internal Reflection Fluorescence Microscopy (TIRFM) (Chen et al., 2020; Mettlen and Danuser, 2014). Strikingly, the number of clathrin-coated structures (CCSs) on cell surface was strongly reduced after VAMP8 knockdown (Fig. 1C-E and Movie 1). To better quantify CCP dynamics and further determine which stage(s) of CME were regulated by VAMP8, we analyzed the acquired imaging data with cmeAnalysis (Aguet et al., 2013; Jaqaman et al., 2008; Loerke et al., 2011) and disassembly asymmetry score classification (DASC) , which together provide a comprehensive and unbiased characterization of CCP intermediates and CME progression (He et al., 2025). Software analysis revealed that VAMP8 knockdown not only significantly inhibited the initiation rate of CCSs (Fig. 1F), but also the initiation rate (Fig. 1G) and percentage of *bona fide* CCPs (CCP%, Fig. 1H). These findings confirm a role for VAMP8 in regulating CCP initiation and stabilization (Bhave et al., 2020). In addition, VAMP8 knockdown extends the lifetime of CCPs (Fig. 1I) while leading to a shift toward dimmer (i.e. smaller or flatter) structures (Fig. 1J), indicating that CCP maturation was also inhibited in the absence of VAMP8.

During CCP maturation, invagination of the clathrin-coat and its underlying membrane is a crucial determinant as to whether the nascent CCP will be either ‘productive’ or abortive (Aguet

et al., 2013; He et al., 2025; Wang et al., 2020). To determine whether VAMP8 knockdown affects CCP invagination, we conducted Epifluorescence (Epi)-TIRF microscopy imaging to measure CCP invagination depth in live ARPE-HPV eGFP-CLCa cells (He et al., 2025; Wang et al., 2020; Yang et al., 2025). In this approach, Epi and TIRF channel signals are near-simultaneously imaged. As CCPs invaginate, the TIRF channel signal becomes dimmer due to the exponential-decay of the evanescent wave energy, while the Epi channel signal is still proportional to the number of eGFP-tagged clathrin, resulting in an increased ratio of Epi/TIRF that allows us to measure the invagination depth of CCPs (Fig. 1K). To yield the average time course of the invagination depth (Δz) of the center-of-mass of CCPs, cmeAnalysis tracked CCSs using a primary (TIRF-channel)/subordinate (Epi-channel) algorithm. DASC was used to distinguish *bona fide* CCPs from ACs. The Epi and TIRF fluorescence intensity traces of CCPs were then temporally aligned, averaged and logarithmically transformed to measure the acquisition of curvature over time (Wang et al., 2020). Here, we present the cohort of CCPs with lifetime average of ~30s because they represent the invagination behavior of the most frequent tracks (Fig. 1I). Surprisingly, VAMP8 knockdown strongly inhibited CCP invagination (Fig. 1L), suggesting an unexpected role for VAMP8 in regulating the crucial invagination process of CME.

Next, we examined the effects of VAMP8 knockdown on the cellular uptake of a prototypical CME cargo protein, TfnR. Consistent with TIRFM analysis results, VAMP8 knockdown significantly reduced the uptake efficiency of TfnR (Fig. 1M). Interestingly, the level of TfnR on the cell surface was also significantly reduced (Fig. 1N). Typically, a reduction in the rate of TfnR endocytosis leads to an increase in surface TfnR, since the larger pool of intracellular TfnR are recycled to and accumulate on the PM. These results suggested an imbalance between the endocytosis and endocytic recycling of TfnR.

In parallel, we examined the effects of siRNA-mediated knockdown of VAMP2 (aka synaptobrevin 2, as closely related R-SNARE) on CME in ARPE-HPV eGFP-CLCa cells. VAMP2 is a neuron-abundant protein that plays a crucial role in neuronal synaptic transmission but is also expressed in ARPE-HPV and other nonneuronal cell types. Interestingly, depletion of VAMP2 in ARPE-HPV cells did not affect CCP initiation, maturation or TfnR uptake (Figure S1 and Movie 2), which further strengthens the specificity of VAMP8's role in CME in non-neuron cells.

Together these observations establish VAMP8 as a key regulator of CME; however, the mechanism by which VAMP8 regulates CME remains unknown. Next, we explore the mechanism behind CME regulation by VAMP8.

Abolishing VAMP8 recruitment to CCVs does not affect CME

Given that incorporation of a sufficient number of SNARE proteins into nascent CCVs has been suggested to be critical for CCP maturation (Bhave et al., 2020), we first tested whether the direct recruitment of VAMP8 is required for CME regulation.

Clathrin assembly lymphoid myeloid leukemia (CALM) has been identified as a VAMP8 adaptor protein (Miller et al., 2011). L219S/M244K mutations in the VAMP8 binding site on CALM prevent the recruitment of VAMP8 to CCPs (Miller et al., 2011). To examine the effect of abolishing VAMP8 recruitment to CME, we introduced these mutations into CALM and generated two cell lines: 1) ARPE-HPV eGFP-CLCa cells that stably express RFP-VAMP8 and siRNA-resistant, myc-tagged CALM (referred to as: CALM(WT)); 2) ARPE-HPV eGFP-CLCa cells that stably express RFP-VAMP8 and siRNA-resistant, myc-tagged CALM(L219S/M244K) (referred to as: CALM(SNARE*)) (Fig. S2A and B). Endogenous CALM was depleted with specifically targeted siRNA (Fig. S2C) and the distribution of VAMP8 was assessed by immunofluorescence. In cells expressing CALM(WT), VAMP8 appears in small clusters on the PM, many of which colocalize with CCPs (Fig. 2A). In contrast, and consistent with a previous report (Miller et al., 2011), VAMP8 is diffusely distributed on the PM of cells expressing CALM(SNARE*) (Fig. 2B). Moreover, dual-channel time-lapse TIRFM imaging (Aguet et al., 2013; Chen et al., 2020; He et al., 2025; Jaqaman et al., 2008) confirmed that VAMP8 can be recruited to CCPs in cells expressing CALM(WT) (Fig. 2C) but not in cells expressing CALM(SNARE*) (Fig. 2D).

Next, we compared CCP dynamics and CME efficiency in cells expressing CALM(WT) and CALM(SNARE*) after siRNA-mediated knockdown of endogenous CALM (Fig. S2C). As previously reported (Bhave et al., 2020; Wang et al., 2020), depletion of CALM in ARPE-HPV eGFP-CLCa cells significantly reduced CCS initiation rate (Fig. 2E), CCP initiation rate (Fig. 2F), CCP% (Fig. 2G), CCP invagination depth (Fig. 2H), and TfnR uptake efficiency (Fig. 2I), and as expected these defects were rescued in cells exogenously expressing siRNA-resistant CALM(WT). Surprisingly, the CALM knockdown phenotypes were also fully rescued by CALM(SNARE*) (Fig. 2E-I), indicating that abolishing VAMP8 recruitment to CCVs does not affect CME.

Together, these unexpected observations suggest that direct recruitment of VAMP8 to CCVs is not required for its role in regulating CME. Therefore, we next explored other possible mechanisms to explain the requirement for VAMP8 in CME.

VAMP8 knockdown downregulates CME cargo resulting in CME inhibition

Cargo loading has been proposed to be another key factor that determines the fate of CCPs (Ehrlich et al., 2004; Kadlecova et al., 2016; Loerke et al., 2009; Maib et al., 2018). We next examined whether VAMP8 knockdown affects the amount of CME cargo.

Differential proteomic analysis of ARPE-HPV cells treated with control or VAMP8 siRNA revealed that VAMP8 knockdown significantly down-regulates several cell surface receptors that are prototypical cargo of CME (Fig. 3A and Table S1), including TfnR (gene: TFRC), EGFR, VLDLR, and MET. Note that the extent of reduction of surface-expressed receptors is likely attenuated by the inhibition of CME that accompanies VAMP8 knockdown.

To determine whether VAMP8 knockdown inhibits CME by reducing the amount of cargo, we selected TfnR for validation and further functional study because: 1) it is an abundant cell surface protein that is primarily internalized via CME; 2) its clustering was observed to promote CCP initiation and increase TfnR uptake (Liu et al., 2010); and 3) its overexpression led to an increased ratio of CCPs/ACs without affecting their lifetimes, suggesting that its concentration may contribute to the stabilization and maturation of CCPs (Loerke et al., 2009). Western blotting results confirmed that TfnR was down-regulated upon VAMP8 knockdown (Fig. 3B and C).

Next, we directly knocked down TfnR in ARPE-HPV eGFP-CLCa cells (Fig. 3D) and strikingly observed that TfnR depletion phenocopies VAMP8 knockdown that led to: i) a strong reduction in the amount of clathrin on the PM (Fig. 3E and F and Movie 3); ii) a significant reduction in CCS initiation rate (Fig. 3G), CCP initiation rate (Fig. 3H) and CCP% (Fig. 3I); iii) extension of CCP lifetimes (Fig. 3J), iv) reduction in the size of CCPs (Fig. 3K); and iv) strong inhibition of CCP invagination depth (Fig. 3L).

Together these results demonstrate that VAMP8 knockdown down-regulates prototypical CME cargo, e.g. TfnR, which results in the inhibition of CCP initiation, stabilization and maturation. We next aimed to understand how does VAMP8 knockdown down-regulates CME cargo.

VAMP8 knockdown inhibits endocytic recycling and accumulates lysosomes where TfnR is degraded

To test whether the down-regulation of TfnR is a result of transcriptional inhibition, we conducted RT-qPCR and observed that VAMP8 knockdown did not significantly affect the mRNA level of TfnR (Fig. 4A), suggesting that TfnR was degraded upon VAMP8 knockdown.

In normal cells, the bulk of internalized Tfn/TfnR complexes are recycled back to the PM for reutilization (Hentze et al., 2004; Kawabata, 2019), while only a very small portion of TfnR is

retained in late endosomes and delivered to lysosomes for degradation (Matsui et al., 2011; Sirohi et al., 2013). In vitro studies have demonstrated that VAMP8 mediates homotypic fusion of both early and late endosomes (Antonin et al., 2000a; Antonin et al., 2000b; Pryor et al., 2004), while another study established a role for VAMP8 in the fusion of Rab11-positive recycling endosomes at immunological synapses in activated CD8-positive T cells (Marshall et al., 2015). Although a role for VAMP8 in TfnR recycling has not been reported, based on these finding, we reasonably hypothesized that VAMP8 knockdown could skew endocytic recycling of TfnR towards lysosomal degradation.

To test this hypothesis, we first examined whether the endocytic recycling of Tfn/TfnR was affected by VAMP8 knockdown via measuring the rate of intracellular recycling of internalized Tfn following well-established protocols (Chen et al., 2017; Chen et al., 2020). Internalized Tfn/TfnR can be recycled to the PM through two pathways: i) a fast recycling pathway, measured following a brief pulse of Tfn uptake, where Tfn/TfnR is recycled to the PM from early endosomes; and ii) a slow recycling pathway, measured following a prolonged pulse of Tfn uptake, where Tfn/TfnR is first transported to the recycling endosomes before being recycled to the PM (Kawabata, 2019; Lakadamyali et al., 2006; Mayle et al., 2012; Navaroli et al., 2012). Upon siRNA-mediated knockdown of VAMP8, we found that both the fast recycling from the early endosome (Fig. 4B) and the slow recycling from the recycling endosomes (Fig. 4C) of Tfn were significantly inhibited, implying that VAMP8 plays a key role in regulating Tfn/TfnR recycling.

We next examined whether more TfnR was delivered to lysosomes for degradation upon VAMP8 knockdown. Firstly, we conducted electron microscopy imaging and revealed a significant increase in the number of lysosomes when VAMP8 was knocked down in ARPE-HPV cells (Fig. 4D and E), which is an indication of enhanced lysosome activities. Secondly, we treated cells with leupeptin, a well-established inhibitor of lysosomal proteases, and observed by Western blotting that leupeptin treatment rescued the reduction of TfnR levels caused by VAMP8 knockdown (Fig. 4F-H). Furthermore, we conducted immunofluorescence and observed that VAMP8 knockdown not only increased the amount of LAMP1, a marker of late endosomes/lysosomes (Fig. 5A, quantified in B), and decreased the amount of TfnR (Fig. 5A, quantified in C), but also significantly enhanced the colocalization of TfnR with LAMP1 (Fig. 5A, quantified in D). In control cells, leupeptin treatment enhanced LAMP1 expression (Fig. 5B), but did not affect TfnR levels (Fig. 5C). Comparing VAMP8 knockdown cells to control cells, leupeptin treatment successfully restored TfnR level and significantly enhanced the colocalization of LAMP1 and TfnR (Fig. 5C and D). Interestingly, upon leupeptin treatment in VAMP8

knockdown cells, TfnR and LAMP1 primarily colocalized in tightly clustered lysosomes in the perinuclear regions (Fig. 5A), rendering the depletion of peripherally located TfnR was apparent. As a result, although leupeptin treatment restored the cellular level of TfnR in VAMP8 knockdown cells, the lysosome-trapped, non-degraded TfnR was unable to rescue either the levels of surface TfnR (Fig. 5E) or the CME uptake efficiency (Fig. 5F).

Together these observations demonstrate that VAMP8 knockdown impairs Tfn/TfnR recycling from the early and recycling endosomes to the PM, resulting in the mis-sorting of TfnR to late endosomes/lysosomes and its degradation therein (Fig. 5G). We conclude that VAMP8 knockdown deregulates early and late stages of CME indirectly by depleting cargo molecules from the cell surface (Fig. 5G).

Discussion

VAMP8 is a ubiquitously expressed R-SNARE protein best studied for its role in regulated exocytosis, exemplified by the defective secretion phenotypes observed in VAMP8 knockout mice (Puri and Roche, 2008; Tiwari et al., 2008; Wang et al., 2004; Wang et al., 2007). VAMP8 is also involved in lysosome-autophagosome fusion (Diao et al., 2015; Itakura et al., 2012; van Tol et al., 2020) and the homotypic fusion of early and late endosomes (Antonin et al., 2000a; Antonin et al., 2000b; Pryor et al., 2004). Few studies, however, have explored the role of VAMP8 in CME. Here we show that VAMP8 regulates CME indirectly through defects in endocytic recycling, diverting endocytic cargo towards lysosomal degradation and leading to a reduction of transmembrane cargo essential for CCP assembly, stabilization, curvature generation and productive CCP formation. These studies reveal that VAMP8 mediates a tight coupling between endocytic recycling and endocytosis, which impacts every stage of CME.

Re-evaluating the role of SNARE Proteins in CME

Previous studies proposed that SNARE incorporation into nascent CCVs might be essential for CME progression, given their essential role in priming vesicles for downstream fusion events (Bhave et al., 2020). This hypothesis is consistent with evidence for direct roles for SNARE proteins in stabilizing nascent COPI (Rein et al., 2002) and COPII (Mossessova et al., 2003; Springer and Schekman, 1998). However, we show that abolishing VAMP8 recruitment to CCVs—via expression of the CALM (SNARE*) mutant—does not impair CME (Fig. 2). This result appears to challenge the dogma that SNARE loading directly regulates vesicle formation.

We focused our studies on VAMP8 given its localization to CCPs, that it binds to CALM with the highest affinity relative to other R-SNAREs, VAMP2 and VAMP3 (Miller et al., 2011),

and its established role in the earliest endosomal fusion events (Antonin et al., 2000b). However, it is possible that other R-SNAREs either naturally or in compensation for the loss of CCP-associated VAMP8, might suffice to stabilize CCPs in VAMP8's absence. Other post-Golgi R-SNAREs include VAMP2, VAMP3, VAMP4 and VAMP7. Notably, VAMP2 and 3 bind, albeit with lower affinity, to the same site on CALM as VAMP8, so that the CALM(SNARE*) would also prevent their recruitment to CCPs. VAMP4 bears a dileucine motif, shown to interact with AP1 (Peden et al., 2001), but can also be recognized by AP2 (Kelly et al., 2008) and CALM (Sahlender et al., 2013); however, unlike VAMP3 and VAMP8, VAMP4 is primarily localized intracellularly (Steegmaier et al., 1999). VAMP7 is recognized by the clathrin adaptor Hrb (Pryor et al., 2008); however, unlike VAMP3, knockdown of VAMP7 did not phenocopy knockdown of VAMP8 (Bhave et al., 2020). Thus, while we cannot rule out the possibility that the incorporation of SNARE proteins is essential for CCP formation, current data do not support this. Given the multiple functions of SNARE proteins and their adaptors, resolving this question will involve knockdown and reconstitution studies with discriminating point mutations, as illustrated by (Sahlender et al., 2013).

VAMP8 links endocytic recycling to CME efficiency

Our data establish that VAMP8 knockdown down-regulates surface TfnR and other CME cargo receptors by disrupting their recycling from early/recycling endosomes to the PM. Instead, cargo is rerouted to lysosomes for degradation.

The consequent reduction in cargo availability inhibits CCP dynamics through two primary mechanisms. First, initiation/stabilization of nascent CCPs is impaired. These results are consistent with previous studies showing that cargo clustering promotes CCP assembly (Liu et al., 2010; Loerke et al., 2009) and are supported by our finding that siRNA-mediated depletion of TfnR depletion recapitulated the VAMP8 knockdown phenotype (Fig. 3). Second, and unexpectedly, the ability of CCPs to invaginate is severely impaired when cargo loading is insufficient. This finding is consistent with previous suggestions that cargo enrichment may induce crowding effect that provides energy for membrane curvature (Chen et al., 2016; Snead et al., 2017; Stachowiak et al., 2012). It is also possible that defects in the cargo-dependent recruitment of peripheral membrane proteins such as AP2 complexes and their associated membrane curvature-generating endocytic accessory factors contribute to the defect in invagination.

Importantly, our findings provide direct evidence for the essential role of cargo in CCP formation and the essential role of endocytic recycling in maintaining CME. Our work positions VAMP8-dependent cargo recycling as a critical checkpoint for CME. By controlling cargo fate, VAMP8 integrates endocytic uptake with post-endocytic sorting, ensuring a steady supply of receptors to the PM and sustaining CME in non-neuronal cells, with potential implications for tissue homeostasis, nutrient uptake, and receptor signaling.

Materials and Methods

Plasmids

The VAMP8 (full-length, human) cDNA was purchased from Addgene (cat# 92424) and mutated to be siRNA resistant while retaining the amino acid sequence. RFP and VAMP8 were then subcloned into pLVX-IRES-puro vector employing NEBuilder® HiFi DNA Assembly Master Mix (Vazyme, Cat# E2621) to generate the RFP-VAMP8 construct. The LAMP1-mCherry (full-length, human) plasmid was purchased from Addgene (cat# 45147). eGFP-CLCa in pLVX-IRES-puro vector was generated in our previous study (Chen et al., 2020). The siRNA resistant and myc-tagged CALM (full-length, human) cDNA was a kind gift from David J. Owen (Cambridge, UK) in pBMN vector and then mutated (SNARE*: L219S/M244K) to abolish CALM-VAMP8 interactions. Primers used for cloning and mutagenesis are listed in Table S2.

Antibodies

Primary antibodies used in this study include rabbit polyclonal antibody to VAMP8 (Cell Signaling Technology, 13060S), rabbit polyclonal antibody to CALM (Proteintech, 28554-1-AP), rabbit polyclonal antibody to TfnR (AiFang biological, AF301044) and rabbit polyclonal antibody to GAPDH (Abclonal, AC1001). Secondary antibody used in Electrochemiluminescence (ECL) is HRP-conjugated Goat-anti-rabbit (ABclonal, AS014). Secondary antibodies used in the immunofluorescence assay include Alexa Fluor 488-anti-mouse (Jackson, 170970), and Alexa Fluor 647-anti-mouse (Cell Signaling Technology, 4410S).

Cell culture and siRNA transfection

HEK 293T and ARPE19-HPV16 (referred to as ARPE-HPV) cells were purchased from ATCC and cultured in DMEM (Gibco, Cat# 8122070) and DMEM/F12 (Gibco, Cat# 8122502), respectively. Culture medium was supplemented with 10% FBS.

For siRNA transfection, cells were seeded on 6-well plates overnight to reach ~50% confluence before siRNA treatment. Two rounds of siRNA treatment were performed through

three days. For each round of siRNA treatment, 0.11 nmol siRNA was added and the siRNA transfection was mediated by Opti-MEM and Lipofectamine RNAi-MAX (Invitrogen, cat# 13778150). Negative Control siRNA was purchased from ThermoFisher (Silencer Select Negative Control #1 siRNA, cat# 4390843). The siRNAs targeting VAMP2, VAMP8 and transferrin receptor (TfnR) were reported in previous studies and synthesized by GenePharma. siVAMP2: 5'-CAAGCGCAGCCA AGCUC-3'; siVAMP8 #1: 5'-CGCAACAAGACAGAGGATCTGGAAG-3'; siVAMP8 #2: mixture of 5'-AGGAAAUGAUCGUGUGCGGAACCU-3' and 5'-GGCUCGAAAAUUCUGGU GGAAGAA-3'; siCALM: 5'-ACAGUUGGCAGACAGUUU A-3'; siTfnR: 5'-AACUUCAAGG UUUCUGCCAGC-3' (Huang et al., 2021; Miller et al., 2011; Nakase et al., 2009). For cells treated with leupeptin, 100 µM leupeptin (MCE, cat# HY-18234A) was added at the beginning of the first round of siRNA treatment and maintained for three days.

Virus production and transfection

Lentiviruses were generated following standard protocol (Kutner et al., 2009). Briefly, HEK293T packaging cells were seeded on 10 cm plate and incubated overnight to reach approximately 60-70% confluency. Next day, the culture medium was replaced with 7 ml fresh culture medium supplemented with pre-mixed NaCl (120 µL from 150 mM filter sterilized stock), RFP-VAMP8 (WT) or LAMP1-mCherry plasmid (5 µg), pSPAX2 packaging vector (3 µg), pMD2G packaging vector (3 µg), and PEI (33 µL from 1 mg/ml stock). Lentiviruses encoding RFP-VAMP8 (WT) or LAMP1-mCherry were harvested after 48-72h and subsequently used to transfect ARPE-HPV eGFP-CLCa cells and ARPE-HPV cells with the assistance of polybrene (Merck, cat# TR-1003-G), respectively. The resulting ARPE-HPV eGFP-CLCa RFP-VAMP8 cells and ARPE-HPV LAMP1-mCherry cells were sorted by Fluorescence-activated Cell Sorting (FACS).

Retroviruses encoding CALM (WT) and CALM (SNARE*) were generated following standard protocol (Mann et al., 1983). The procedure was the same as described for lentivirus production except that retroviruses were packaged with GAG/POL and VSVG envelopes. The harvested retroviruses were used to transfect ARPE-HPV eGFP-CLCa RFP-VAMP8 cells, ultimately generating ARPE-HPV eGFP-CLCa RFP-VAMP8 CALM(WT) or ARPE-HPV eGFP-CLCa RFP-VAMP8 CALM(SNARE*) cells.

Transferrin receptor (TfnR) uptake assay

Internalization of TfnR was assessed using in-cell enzyme-linked immunosorbent assay (ELISA) following established protocols (Chen et al., 2020; Conner and Schmid, 2003; Srinivasan et al.,

2018). Briefly, cells were seeded on 96-well Strip plate (Costar, cat# 11621042) overnight to reach 60%-70% confluency. Before assay, cells were starved for 30 min in 37 °C incubator with pre-warmed PBS^{4+} (1× PBS buffer plus 1 mM $CaCl_2$, 1 mM $MgCl_2$, 0.2% BSA, and 5 mM D-glucose) and then moved to 4 °C fridge before adding ice-cold PBS^{4+} that contained 5 ug/ml HTR-D65 (a polyclonal antibody to TfnR) (Schmid and Smythe, 1991). Next, cells were divided into three groups: Surface-bound, Blank, and 10 min uptake. Surface bound group cells were kept in 4 °C fridge to measure the amount of surface-bound TfnR. Blank group cells were kept in 4 °C fridge for 10min and then acid-washed (0.2 M acetic acid and 0.2 M NaCl, pH 2.3, 4 °C) to remove surface-bound HTR-D65 that indicates the background signal. 10 min uptake group cells were incubated at 37 °C water bath for 10 min to measure the internalization of TfnR and then acid-washed to remove surface-bound HTR-D65. Subsequently, all groups were washed with cold PBS and fixed with 4% PFA before being permeabilized with 0.1% Triton X-100. Permeabilized cells were blocked with Q-PBS (1×PBS plus 2% BSA, 0.1% lysine, and 0.01% saponin, pH 7.4) and then probed with HRP-conjugated Goat anti-Mouse IgG (BioRad). Finally, O-phenylenediamine dihydrochloride (OPD, Sigma-Aldrich) was added to detect the amount of surface and internalized HTR-D65 while BCA assays were used to account for well-to-well cell number variations.

Transferrin (Tfn) recycle assay

Recycling of Tfn was assessed following established protocol (Chen et al., 2017; Chen et al., 2020). Before assays, cells were cultured in biotin-free medium for at least 48 h and then seeded on 96-well strip plate overnight to reach a confluency of 60-70%. Next day, cells were starved in PBS^{4+} for 30 min at 37 °C and then cooled down to 4 °C before adding ice-cold PBS^{4+} that contained 5 ug/ml Biotin-Tfn (Sigma-Aldrich). Cells were then incubated at 37 °C water bath for 10 or 30 min pulse to load Biotin-Tfn into cells. Excess Biotin-Tfn were removed by washing with ice-cold PBS^{4+}. Some cells were kept at 4 °C as loading control whose surface-bound Biotin-Tfn was masked with avidin and biocytin. The other cells were incubated at 37 °C for indicated time points to measure the remaining amount of Biotin-Tfn in cells. Subsequently, all cells were acid-washed, fixed, permeabilized, and blocked as stated in TfnR uptake assay. Finally, the amount of Biotin-Tfn was probed with streptavidin-HRP (ThermoFisher) and O-phenylenediamine dihydrochloride (OPD, Sigma-Aldrich).

TIRF and Epi-TIRF microscopy

Prior to imaging, cells were seeded on gelatin-coated coverslips (Merck, cat# 2850-22) or glass-bottom dishes (Ibidi, cat# 81218-800) overnight. For live cell imaging, a Nikon Eclipse Ti2 inverted microscope was equipped with: i) a 100x 1.49 Oil immersion lens; ii) a Prime Back Illuminated sCMOS Camera (Prime BSI, 6.5 x 6.5μm pixel size and 95% peak quantum efficiency); iii) a H-TIRF module for TIRF imaging with a penetration depth fixed at 80 nm; iv) a M-TIRF module for Epifluorescence (Epi) imaging; and v) an Oko-lab Cage Incubator to maintain 37 °C and 5% CO2.

Time-lapse movies (451 frames) were acquired at a rate of 1 frame/s for single-channel TIRF imaging, a rate of 0.5 frame/s for dual-channel TIRF imaging, and a rate of 0.67 frame/s for Epi-TIRF imaging. cmeAanalysis (Aguet et al., 2013; Jaqaman et al., 2008) and DASC were applied to analyze the imaging data. Detailed information is available on the website: https://github.com/DanuserLab/cmeAnalysis.

Immunofluorescence

Cells were seeded on gelatin-coated coverslips overnight to reach a confluency of ~70% and then washed with PBS before fixing with 4% PFA for 30min at room temperature. The fixed cells were permeabilized with 0.1% Triton X-100 for 10 min and then blocked with culture medium for 2 h at room temperature. After immunostaining with primary and secondary antibodies. The cells were imaged with Nikon Eclipse Ti2 inverted microscope and Zeiss LSM980 confocal laser scanning microscope.

RNA extraction and quantitative reverse transcription polymerase chain reaction (RT-qPCR) assay

Cells were lysed using TransZol UP (Transgen) at room temperature for 5 min and then moved to 1.5 ml centrifuge tube, followed by adding chloroform and shaking vigorously for 30 s before centrifuging at 10,000 × g for 15 min. Isopropanol was added to the supernatant and gelatinous precipitate was obtained after centrifugation at 10,000 × g for 10 min. Next, 75% alcohol was used to wash the gelatinous precipitate by violently shaking. RNA was collected after centrifugation at 7,500 × g for 5 min finally dissolved in RNase-free water. 2 ug RNA was reverse transcribed to the first chain of cDNA in 20 uL reaction system using FsstKing-RT Super Mix kit (TIANGEN, cat# Y1629) according to manufacturer's instructions. The primers used in qPCR were: 5'-CAGGAGGCATTGCTGATGAT-3' and 5'-GAAGGCTGGGGCTCATTT-3' for GAPDH; 5'-AGGTCAAAGACAGCGCTCAA-3' and 5'-GCCACATAACCCCCAGGATT-3' for TfnR.

Electron microscope

Cell precipitation was fixed overnight in 2.5% glutaraldehyde and 2% PFA in 0.1 M phosphate buffer (pH 7.2–7.4), then replaced by 1% osmium tetroxide (Ted Pella, Cat# 20816-12-0) at 0°C for 1h. After fixation, samples were stained with 1% aqueous uranyl acetate (Electron Microscopy Sciences, Cat# 22400, USA) for 1 h, then dehydrated in ethanol (Sinopharm, Cat# 64-17-5) and embedded by EMbed 812 (Electron Microscopy Sciences, Cat# 14900, 13710, 19000 and 13600). Ultrathin sections were stained with Sato's lead citrate and imagined with a HT7800 electron microscope (Hitachi Hi-tech, Hitachinaka-shi, Japan).

Proteomic Analysis

Sample preparation. Cells were seeded on 15 cm plates overnight to reach ~50% confluency before siRNA treatment. Two rounds of siRNA transfection were performed over three days. After siRNA treatment, the cells lysates were collected and lysed in ten volumes of modified SDT buffer (0.1 M Tris-HCL, pH 7.6, 0.1 M DTT, 1% SDS, 1% SDC) and incubated at 95 °C for 5 min. The lysate was sonicated to shear genomic DNA, and clarified by centrifugation at 20,000 × g for 15 min at 20 °C. The supernatant was transferred to ultrafiltration units (Millipore, Amicon Ultra 4 Ultracel 10 KD) and centrifuged at 4000 × g for 40 min. After centrifugation, the concentrates were mixed with 2 mL of 50 mM iodoacetamide in UA solution (8 M urea, 100 mM Tris-HCl pH 8.5) and incubated in darkness at room temperature (RT) for 30 min followed by centrifugation for 30 min. After alkylation, the filter units were washed four times with 4 ml UA buffer and two times 4 mL of 50 mM ammonium bicarbonate by centrifugation at 4,000 × g. Proteins were then digested with Lys-C (1:100, w/w, Wako) for 6 h at 37 °C and trypsin (1:50, w/w, Promega) overnight at 37 °C. The resulting peptide mixture was acidified (pH 2.0) with formic acid, loaded onto SepPak tC18 cartridges (Waters), desalted and eluted with 70% acetonitrile. The eluted peptides were lyophilized and stored at -80 °C before analysis.

LC-MS/MS analysis. MS experiments were performed on a nanoscale Vanquish Neo UHPLC system (Thermo Fisher Scientific) connected to an Orbitrap Exploris 480 MS equipped with a nanoelectrospray source (Thermo Fisher Scientific). Mobile phase A contained 0.1% formic acid (v/v) in water; mobile phase B contained 0.1% formic acid in 80% acetonitrile (ACN). The peptides were dissolved in 0.1% formic acid (FA) with 2% acetonitrile and separated on a RP-HPLC analytical column (75 μm × 25 cm) packed with 2 μm C18 beads (Thermo Fisher Scientific) using a linear gradient ranging from 8% to 28% ACN in 70 min and followed by a linear increase to 44% B in 15 min at a flow rate of 300 nL/min. The Orbitrap Exploris 480 MS

acquired data in a data independent manner alternating between full scan MS and MS2 scans. The spray voltage was set at 2.2 kV and the temperature of ion transfer capillary was 300 °C. The MS spectra (380–980 m/z) were collected with 120,000 resolutions, AGC of 3 × 106, and 25 ms maximal injection time. Ions were sequentially fragmented by HCD with 30% normalized collision energy, specified isolated windows 6.0 m/z, 30,000 resolutions. and 54 ms maximal injection time were used.

Mass spectrometry data analysis. Raw data were processed using DIA-NN (version 2.0), and MS/MS spectra were searched against the SwissProt human database (downloaded in April 2024), and the total number of entries is 20,354. All searches were carried out with precursor mass tolerance of 10 ppm,, oxidation (Met) (+15.9949 Da), carbamidomethylation (Cys) (+57.0215 Da), and acetylation (protein N-terminus) (+42.0106 Da) as modifications, two trypsin missed cleavages allowed when searching for proteins. The peptide and protein identifications were filtered by DIA-NN to control the false discovery rate (FDR) < 1%.

Statistical analysis

Statistical analysis of the parameters from TIRF and Epi-TIRF microscopy, such as the initiation rates of all CCSs and *bona fide* CCPs and the CCP%, is the Wilcoxon Rank Sum test by Matlab. Statistical analysis of the data obtained from western blotting, TfnR uptake assay, immunofluorescence, RT-qPCR and EM are student's t-test using GraphPad Prism 8. The data from immunofluorescence are presented as means ± SD, while the data from western blotting, TfnR uptake assay, immunofluorescence, RT-qPCR and EM are presented as means ± SEM. Statistical significance levels: ns: $P > 0.05$ *, $P \leq 0.05$, ** $P \leq 0.01$, *** $P \leq 0.001$.

Data availability

The data supporting the findings of this work are available within the paper and the Supplementary Information files.

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Author contributions

Z.C., S.L.S., A.L., Y.L., X.L., Y.H., X.W. and D.W. designed the experiments; A.L., Y.L., Z.H., W.C., Y.H. and P.X. performed the experiments; Z.C., A.L., G.H., D.W. and Y.L. analyzed and interpreted the data; Z.C., S.L.S., A.L. and Y.L. wrote the manuscript with contributions from other co-authors; Z.H. drew the cartoon illustrations.

Competing interests

The authors declare no competing interests.

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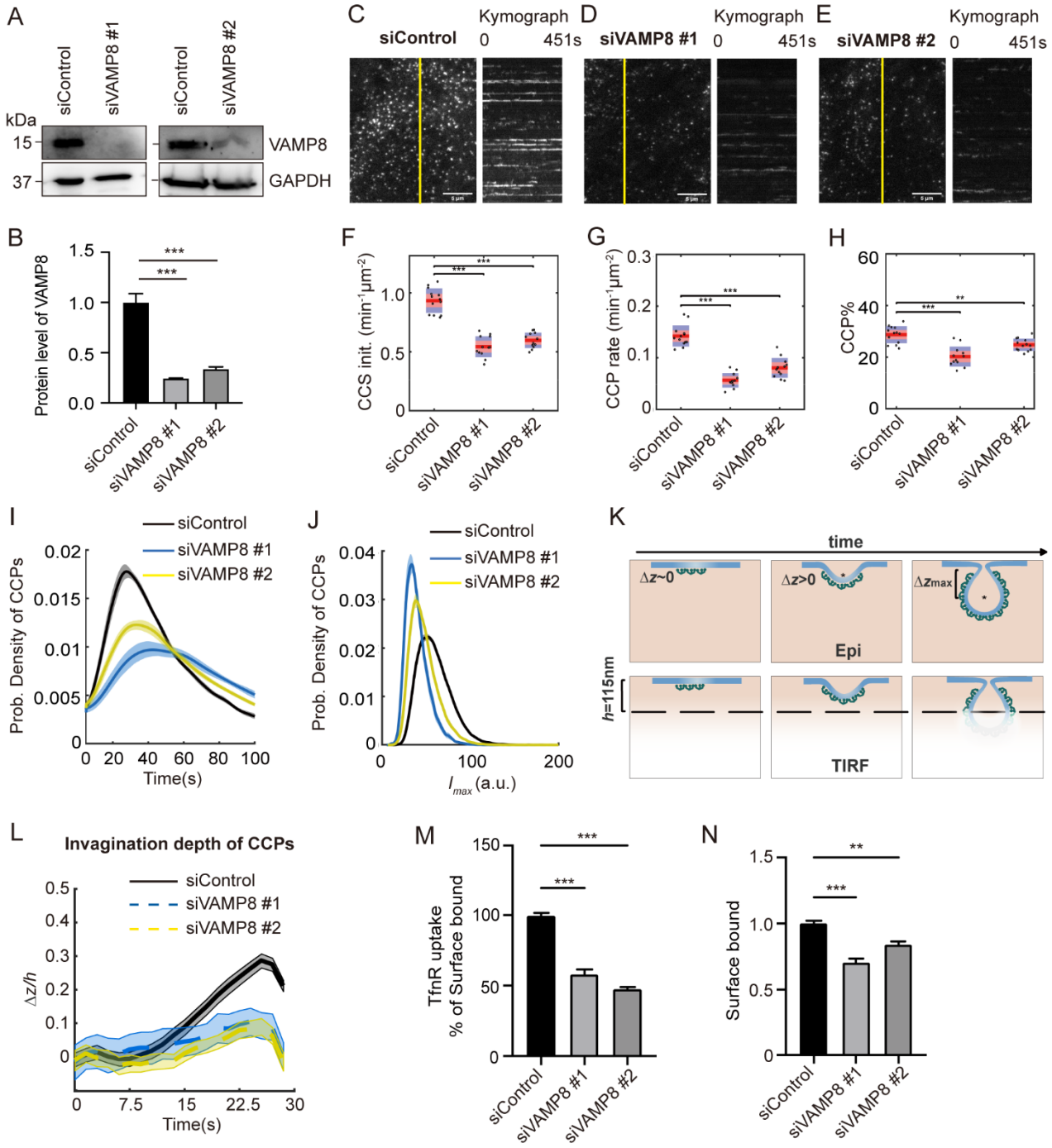

Figure 1. VAMP8 knockdown inhibits CCP maturation and TfnR uptake. (A) ARPE-HPV eGFP-CLCa cells were transfected with control or VAMP8 siRNA. Two sets of siRNAs were used to knock down VAMP8. Western blotting was used to determine the knockdown efficiency of VAMP8. **(B)** Quantification of the VAMP8 knockdown efficiency. Error bars indicate SEM of three independent experiments. **(C-E)** Representative single frame images and corresponding kymographs (for region indicated by yellow lines) from TIRFM movies (1 frame/s, 7.5 min/movie, see Movie 1) that were captured in ARPE-HPV eGFP-CLCa cells treated with (C) control siRNA or (D and E) VAMP8 siRNA. Scale bars = 5 μm. **(F-H)** Effect of VAMP8

knockdown on the initiation rates of (F) all CCSs and (G) *bona fide* CCPs, as well as (H) CCP%. Each dot represents a movie, and N = 12 movies for each condition. **(I and J)** Effect of VAMP8 knockdown on the (I) lifetime distribution and (J) Maximum fluorescence intensity (I_{max}) distribution of *bona fide* CCPs. The data presented was acquired from a single experiment that represents three independent biological repeats. Number of dynamic tracks analyzed: 16,7117 for siControl, 11,0803 for siVAMP8 #1, and 10,6918 for siVAMP8 #2. Shadow area indicates 95% confidential interval. **(K)** Scheme of Epi-TIRF microscopy for measuring the invagination of CCPs using primary/subordinate tracking. Δz denotes the invagination depth of CCPs. □=115 nm is the evanescent depth of TIRF field. See Methods for more details. **(L)** Epi-TIRF microscopy analysis showed that VAMP8 knockdown significantly inhibited CCP invagination. Curves are the mean invagination traces of *bona fide* CCPs represented by $\Delta z(t)/h$. Shadowed area indicates 95% confidence interval. The presented data was acquired from a single experiment that represents three independent repeats. N = 15 movies for each condition. Number of CCP tracks analyzed to obtain the $\Delta z(t)/h$ curves: 18,625 for siControl, 2,715 for siVAMP8 #1 and 3,911 for siVAMP8 #2. **(M and N)** Evaluation of the (M) Surface bound and (N) uptake efficiency of TfnR (Internalized/Surface-bound) by in-cell ELISA. Error bars indicate SEM of N = 16 samples. Statistical analysis of the data in (B, K and L) was performed using GraphPad Prism 8 by unpaired t-test. Statistical analysis of the data in (F-H) is the Wilcoxon Rank Sum test, $^{**}P \leq 0.01$, $^{***}P \leq 0.001$.

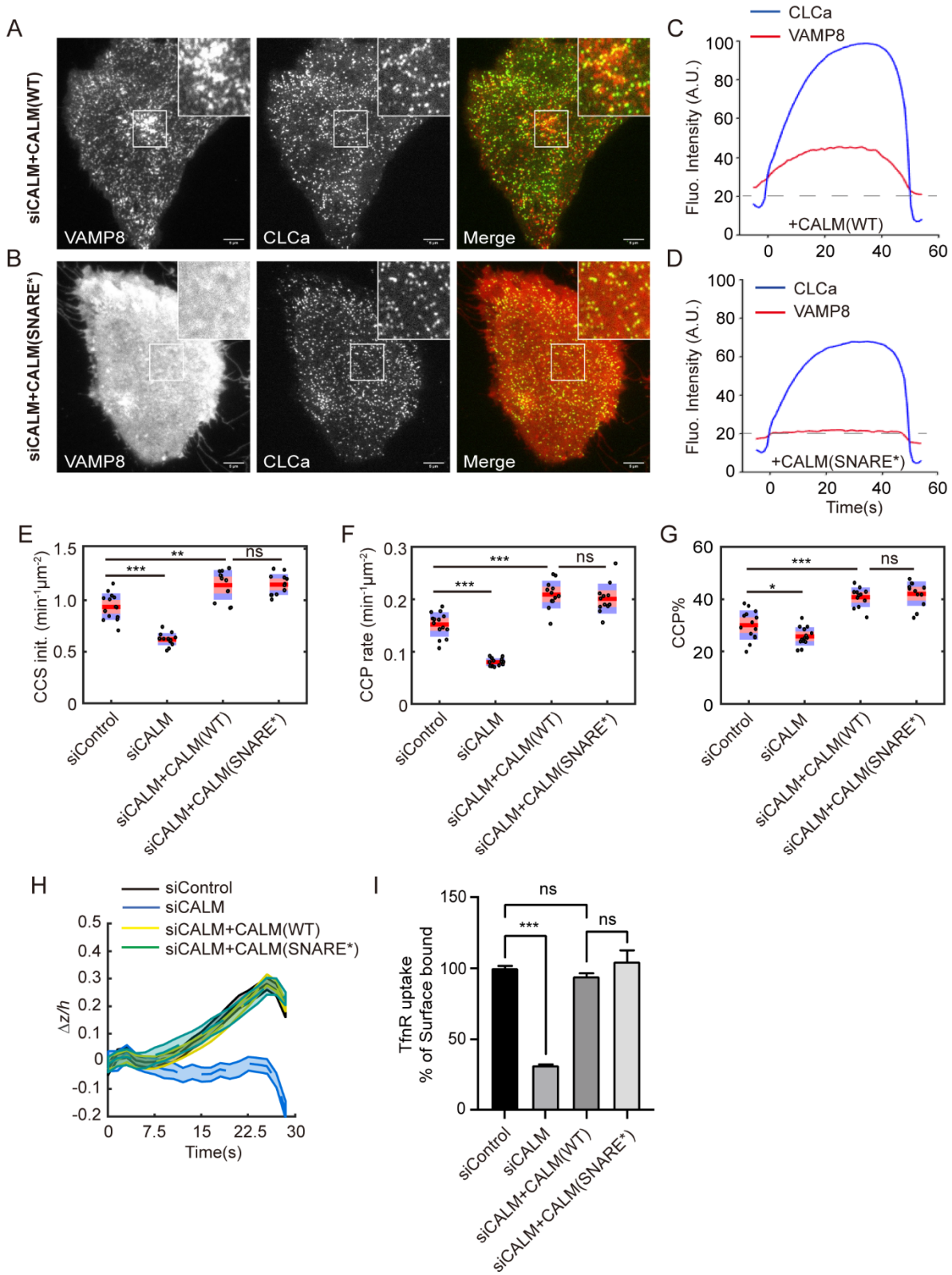

Figure 2. Abolishing VAMP8 recruitment to CCVs does not affect CME. (A and B) Representative TIRFM images of ARPE-HPV eGFP-CLCa + RFP-VAMP8 cells that stably express myc-tagged (A) CALM(WT) or (B) CALM(SNARE*) and treated with CALM siRNA to specifically knock down endogenous CALM but not exogenous CALM. White ROI is magnified on the top-right corner. VAMP8 formed clusters on the PM of cells expressing CALM(WT) and

was abundant but diffusive on the PM of cells expressing CALM(SNARE*). Scale bars = 5 μm. **(C and D)** The cohort-averaged fluorescence intensity traces for CCPs (tagged with eGFP-CLCa) and CCP-enriched RFP-VAMP8 in cells expressing (C) CALM(WT) or (D) CALM(SNARE*). CALM(SNARE*) failed to recruit VAMP8 to CCPs. Number of dynamic tracks analyzed: 27,028 for (C) and 25,052 for (D). **(E-G)** TIRF microscopy analysis showed that, unlike CALM knockdown, abolishing VAMP8 recruitment to CCVs by rescue with CALM(SNARE*) does not affect (E) CCSs initiation rate, (F) *bona fide* CCPs initiation rate, and (G) % of *bona fide* CCPs. The data presented was acquired from a single experiment that represents three independent repeats. Each dot in (E-G) represents a movie. N = 12 movies for each condition. Number of dynamic tracks analyzed: 200,143 for siControl, 112,579 for siCALM, 140,451 for siCALM+CALM(WT) and 113,132 for siCALM+CALM(SNARE*). **(H)** Epi-TIRF microscopy analysis showed that abolishing VAMP8 recruitment to CCVs does not affect CCP invagination. The data provided were acquired from a single experiment that represents three independent repeats. N = 15 movies for each condition. Shadowed area indicates 95% confidence interval. Number of CCP tracks analyzed to obtain the $\Delta z(t)/h$ curves: 14,562 for siControl, 2,482 for siCALM, 22,402 for siCALM+CALM(WT) and 16,572 for siCALM+CALM(SNARE*). **(I)** Measurements of the TfnR uptake efficiency. Error bars: SEM of N = 24 samples. Statistical analysis of the data in (E-G) is the Wilcoxon Rank Sum test. Statistical analysis of the data in (I) was performed using GraphPad Prism by unpaired *t*-test. ***$P \leq 0.001$, **$P \leq 0.01$, ns, $P > 0.05$.

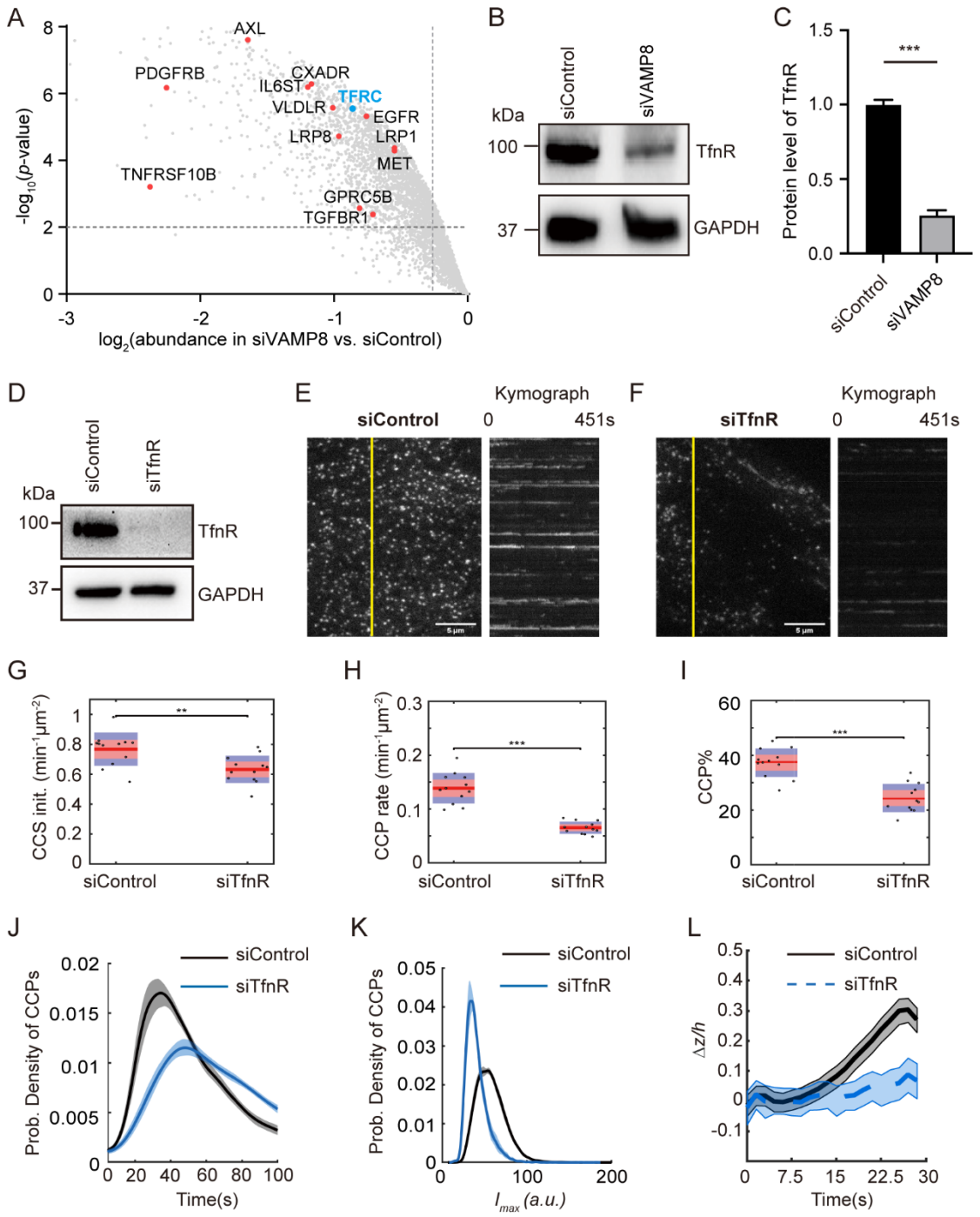

Figure 3. VAMP8 knockdown downregulates CME cargos that results in the inhibition of CME. (A) MassSpec analysis revealed that VAMP8 knockdown downregulates the expression levels of several surface receptors (see also in Table S1). Two dashed lines indicate *p*-value = 0.01 and FC = 1.2. **(B)** Western blotting confirmed that VAMP8 knockdown downregulates the level of TfnR in ARPE-HPV eGFP-CLCa cells. **(C)** Quantification of the protein levels of TfnR from the western blotting results. Error bars: SEM of N = 3 biological repeats. **(D)** siRNA treatment efficiently depleted TfnR in ARPE-HPV eGFP-CLCa cells. **(E and F)** Representative single frame images and corresponding kymographs (for region indicated by yellow lines) from

TIRFM movies (1 frame/s, 7.5 min/movie) that were captured in ARPE-HPV eGFP-CLCa cells treated with (E) control siRNA or (F**)** TfnR siRNA (see Movie 3**)**. Scale bars = 5 µm. **(G-I)** Effect of TfnR knockdown on the initiation rates of (G) all CCSs and (H) *bona fide* CCPs, as well as (I) % of *bona fide* CCPs. Each dot represents a movie. **(J and K)** Effect of TfnR knockdown on the (J) lifetime distribution and (K) maximum fluorescence intensity (I_{max}) distribution of *bona fide* CCPs. The data presented was acquired from a single experiment that represents three independent repeats. N = 12 movies for each condition. Number of dynamic tracks analyzed: 58,038 for siControl and 45,988 for siTfnR. Shadowed area indicates 95% confidence interval. **(L)** Effect of TfnR knockdown on CCP invagination. The data presented was acquired from a single experiment that represents three independent repeats. N = 15 movies for each condition. Number of CCP tracks analyzed to obtain the $\Delta z(t)/h$ curves: 7,777 for siControl and 741 for siTfnR. 95% confidence interval was indicated by shadow area. Statistical analysis of the data in (C) was performed using GraphPad Prism by unpaired t-test. Statistical analysis of the data in (G-I) is the Wilcoxon Rank Sum test. $^{**}P \leq 0.01$, $^{***}P \leq 0.001$.

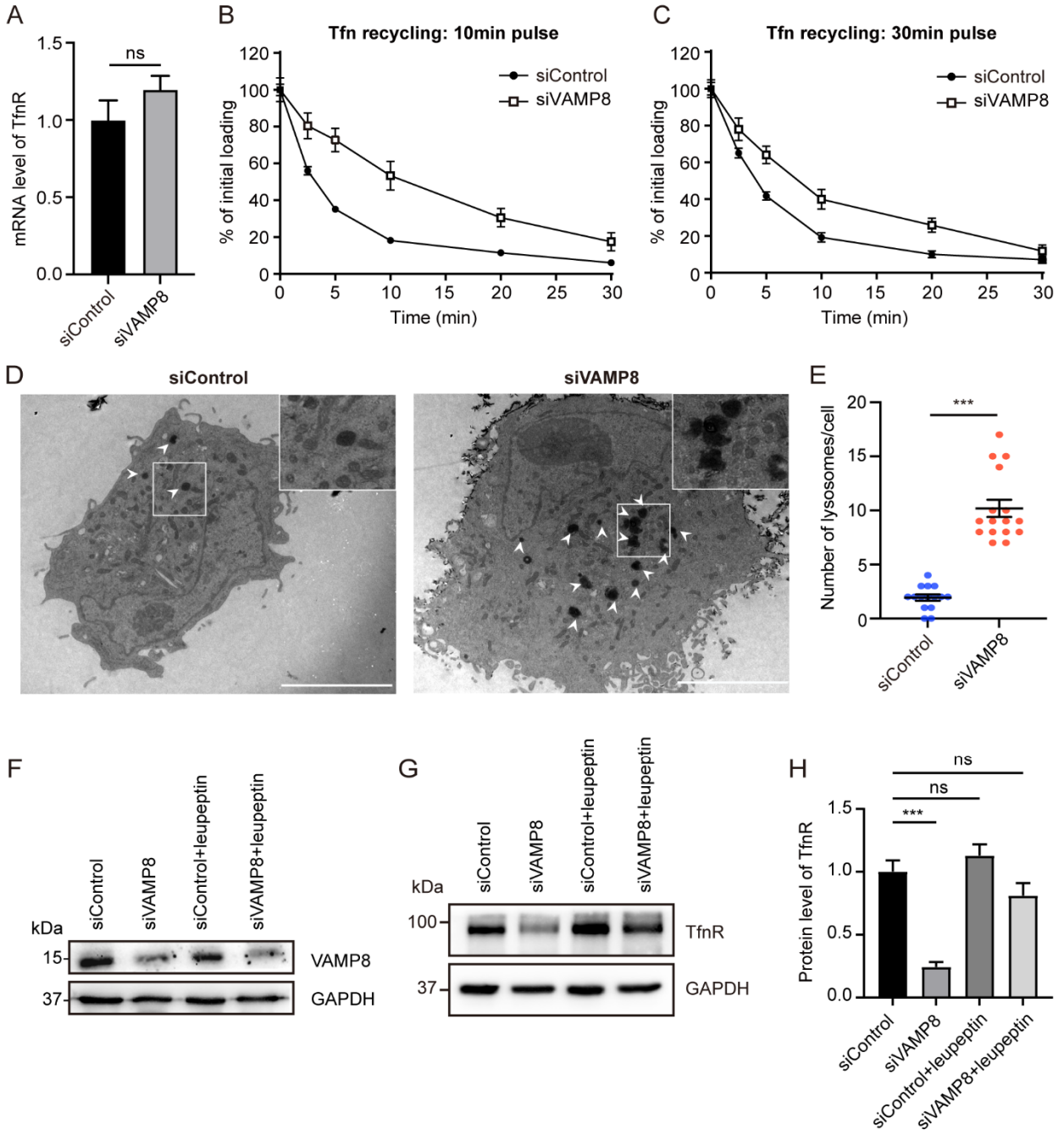

Figure 4. VAMP8 knockdown inhibits endocytic recycling and accumulates lysosomes. (A) Quantification of the mRNA level of TfnR. GAPDH mRNA was used as an internal standard for normalization. Error bars: SEM of N = 9 samples. **(B and C)** In-cell ELISA assay revealed that VAMP8 knockdown inhibits Biotin-Tfn recycling. Biotin-Tfn was initially loaded into cells for (B) 10min pulse to measure fast recycling or (C) 30min pulse to measure slow recycling. Error bars: SEM of N = 12 samples. **(D)** Representative transmission electron microscope images of ARPE-HPV eGFP-CLCa cells treated with control (left) or VAMP8 (right) siRNA. Lysosomes accumulated upon VAMP8 knockdown. White ROI is magnified on the top-right corner. White arrowheads point to lysosomes. Scale bars = 5μm. **(E)** Quantification of the number of lysosomes

per cell. Each dot represents a cell. Error bars in (E) indicate SEM of N = 15 for siControl and N = 16 for siVAMP8. **(F-H)** ARPE-HPV eGFP-CLCa cells were treated with 100 μM leupeptin and transfected with indicated siRNAs for 72 h. (F) Western blotting indicates the knockdown efficiency of VAMP8. (G) Western blotting indicates the protein levels of TfnR. (H) Quantification of TfnR levels from western blotting results. Error bars indicate SEM of N = 3 biological repeats. Statistical analysis of the data in (A and H) was performed using GraphPad Prism by unpaired t-test. ***$P \leq 0.001$, ns, $P > 0.05$.

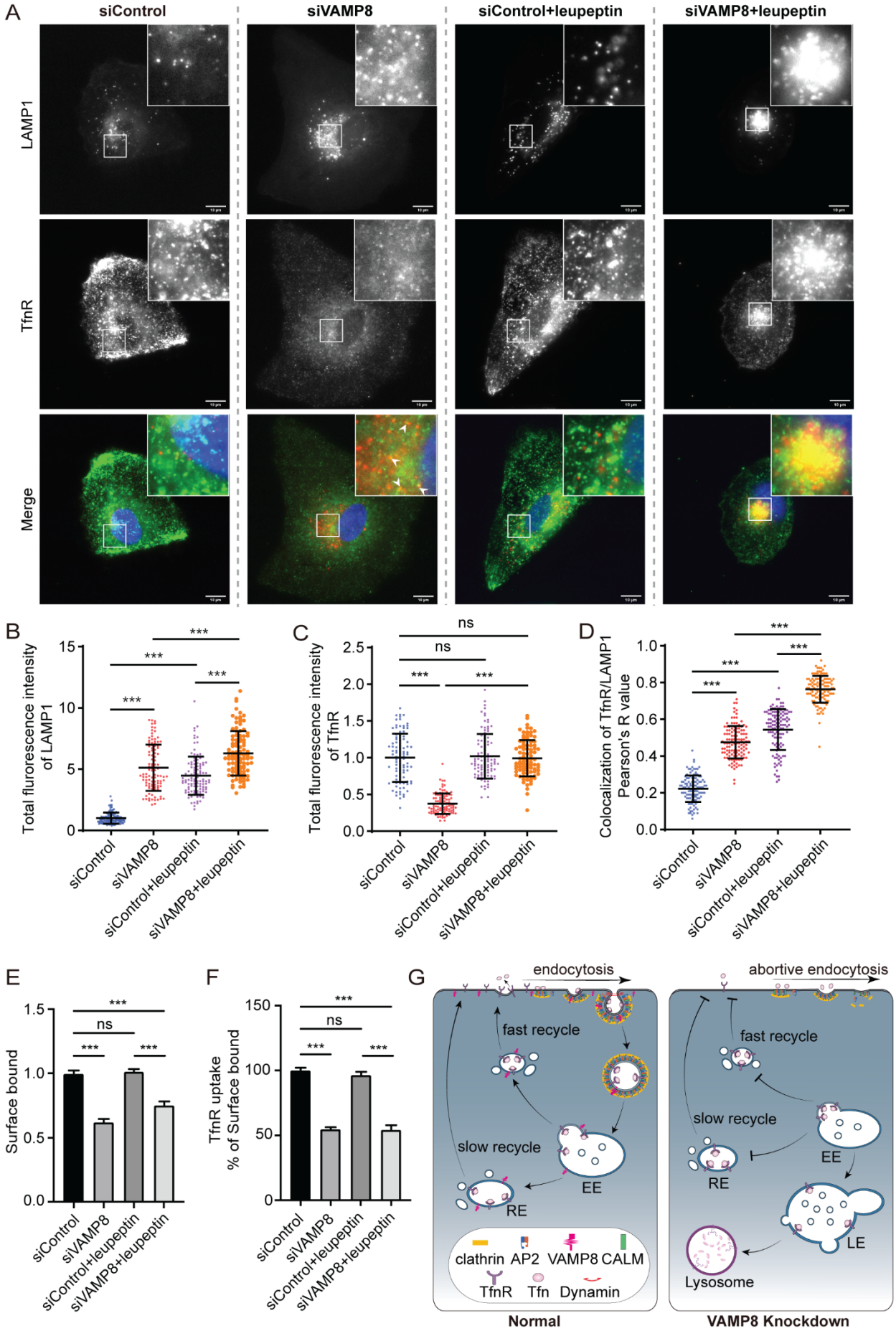
A
siControl
siVAMP8
siControl+leupeptin
siVAMP8+leupeptin
LAMP1
TfnR
Merge
B
Total fluorescence intensity of LAMP1
C
Total fluorescence intensity of TfnR
D
Colocalization of TfnR/LAMP1 Pearson's R value
E
Surface bound
F
TfnR uptake % of Surface bound
G
endocytosis
abortive endocytosis
fast recycle
slow recycle
EE
RE
LE
Lysosome
clathrin
AP2
VAMP8
CALM
TfnR
Tfn
Dynamin
Normal
VAMP8 Knockdown

Figure 5. VAMP8 knockdown skews endosomal recycling of TfnR towards lysosomal degradation. (A) Representative Epi-fluorescence images of ARPE-HPV cells that stably express LAMP1-mCherry (red) and were stained with anti-TfnR antibody (green) and DAPI (blue). White ROI is magnified on the top-right corner. White arrowheads point to the colocalized LAMP1 and TfnR. Scale bars = 10 μm. **(B)** The total fluorescence intensities of LAMP1-mCherry. **(C)** The total fluorescence intensities of TfnR. **(D)** Pearson's correlation coefficients of TfnR and LAMP1. Each dot shown in (B-D) represents a cell. N = 93 for siControl, N = 100 for siVAMP8, N = 101 for siControl+leupeptin, and N = 93 for siVAMP8+leupeptin. Error bars in (B-D) indicate SD. **(E and F)** Measurements of (E) the surface bound and (F) the uptake efficiency of TfnR. Error bars indicate SEM of N = 16 samples. **(G)** Illustration of intracellular trafficking of Tfn/TfnR complex in the presence (left) and in the absence of VAMP8 (right). EE: early endosome; RE: recycling endosome; LE: late endosome. In normal cells, internalized Tfn/TfnR can be recycled to the PM to maintain CME. Nonetheless, VAMP8 knockdown reroutes Tfn/TfnR to the lysosome for degradation, resulting in the inhibition of CME. Statistical analysis of the data in (B-F) was performed using GraphPad Prism by unpaired t-test, ***, $P \leq 0.001$, ns, $P > 0.05$.

Supplementary Information:

Movie 1: Time-lapse TIRFM imaging was performed on ARPE-HPV eGFP-CLCa cells treated with siControl, siVAMP8 #1, and siVAMP8 #2. Images were captured at a rate of 1 frame per second over a period of 7.5 min. The movie is displayed at 25 times the actual speed.

Movie 2: Time-lapse TIRFM imaging was performed on ARPE-HPV eGFP-CLCa cells treated with siControl and siVAMP2. Images were captured at a rate of 1 frame per second over a period of 7.5 min. The movie is displayed at 25 times the actual speed.

Movie 3: Time-lapse TIRFM imaging was performed on ARPE-HPV eGFP-CLCa cells treated with siControl and siTfnR. Images were captured at a rate of 1 frame per second over a period of 7.5 min. The movie is displayed at 25 times the actual speed.

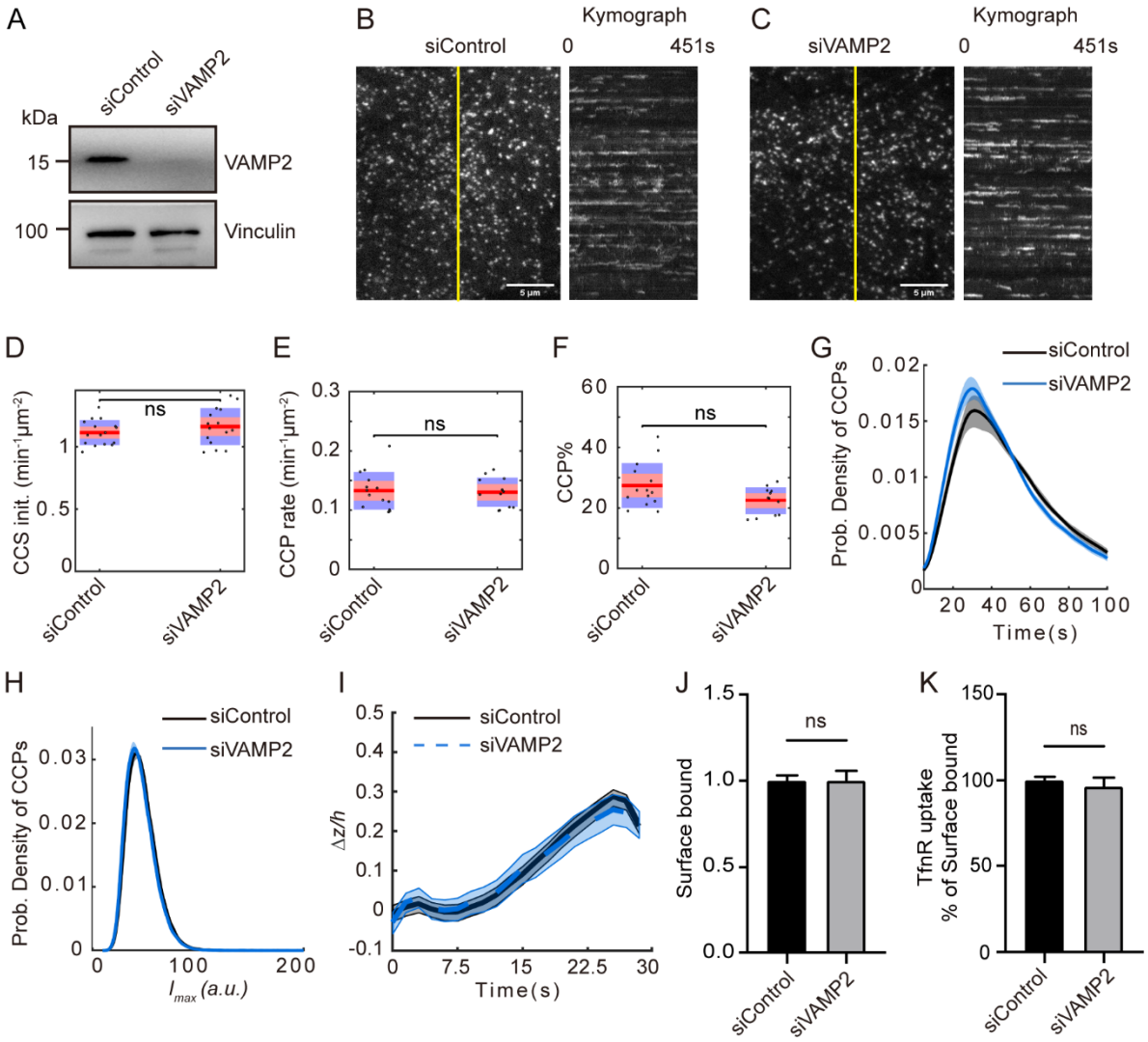

Figure S1. VAMP2 knockdown does not inhibits CME. (A) ARPE-HPV eGFP-CLCa cells were transfected with control or VAMP2 siRNA. Western blotting indicates good knockdown efficiency of VAMP2. **(B and C)** Representative single frame images and corresponding kymographs (for region indicated by yellow lines) from TIRFM movies (1 frame/s, 7.5 min/movie, see Movie 2) that were captured in ARPE-HPV eGFP-CLCa cells treated with (B) control or (C) VAMP2 siRNA. Scale bars = 5 µm. **(D-F)** Effect of VAMP2 knockdown on the initiation rates of (D) all CCSs and (E) *bona fide* CCPs, as well as (F) % of *bona fide* CCPs. Each dot represents a movie, and N = 15 movies for each condition. **(G and H)** Effect of VAMP2 knockdown on the (G) lifetime distribution and (H) Maximum fluorescence intensity (I_{max}) distribution of *bona fide* CCPs. The data presented was acquired from a single experiment that represents three independent biological repeats. Number of dynamic tracks analyzed: 189,191 for siControl, and 134,710 for siVAMP2. **(I)** Epi-TIRF microscopy analysis showed that VAMP2 knockdown did not affect CCP invagination. The presented data was acquired from a single experiment that represents three independent repeats. N = 15 movies for each condition. Number

of CCP tracks analyzed to obtain the $\Delta z(t)/h$ curves: 18,625 for siControl and 9,947 for siVAMP2. Shadowed area in (G-I) indicates 95% confidence interval. **(J and K)** Evaluation of the (J) surface bound and (K) uptake efficiency of TfnR (Internalized/Surface-bound). Error bars in (J and K) indicate SEM of N = 12 samples. Statistical analysis of the data in (J and K) was performed using GraphPad Prism 8 by unpaired t-test: ns, $P > 0.05$. Statistical analysis of the data in (D-F) is the Wilcoxon Rank Sum test, ns, $P > 0.05$.

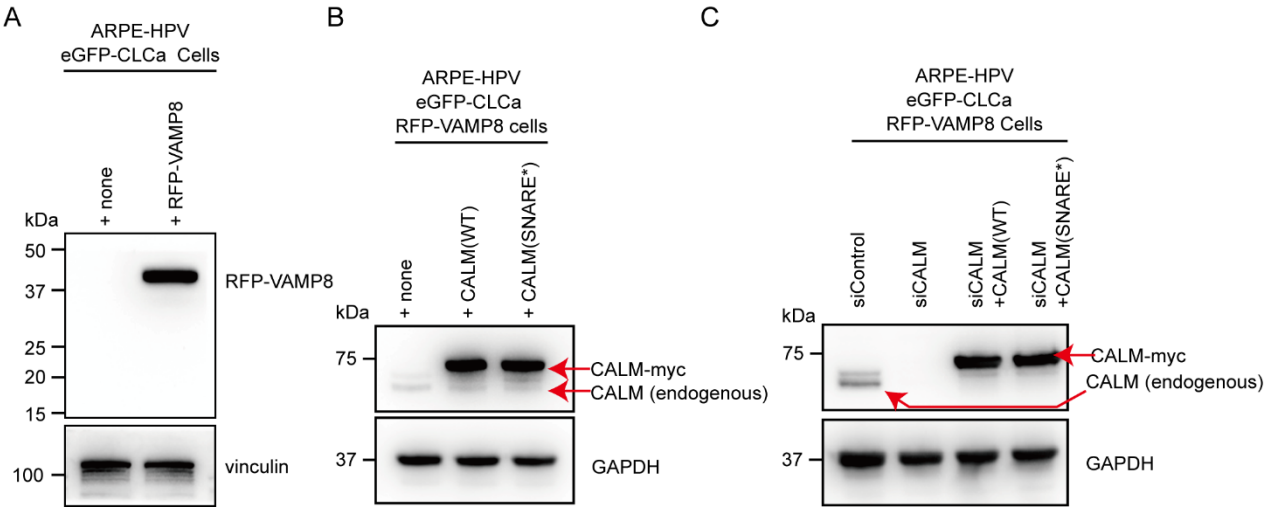

Figure S2. Western blotting of engineered cell lines. (A) Western blotting indicates the expression of exogenous RFP-VAMP8 in ARPE-HPV eGFP-CLCa cells. Cells were FACS sorted to have homogenous expression of RFP-VAMP8. **(B)** Western blotting indicates the expression of exogenous, myc-tagged CALM(WT) and CALM(SNARE*) in ARPE-HPV eGFP-CLCa + RFP-VAMP8 cells. **(C)** CALM siRNA knocks down endogenous but not exogenous CALM in ARPE-HPV eGFP-CLCa + RFP-VAMP8 cells.

Table S1. List of down-regulated genes after VAMP8 knockdown.

Gene	Protein description	Fold Change	p-value
TNFRSF10B	Tumor necrosis factor receptor superfamily member 10B	-5.2	6.2E-04
PDGFRB	Platelet-derived growth factor receptor beta	-4.8	6.6E-07
AXL	Tyrosine-protein kinase receptor UFO	-3.1	2.4E-08
IL6ST	Interleukin-6 receptor subunit beta	-2.3	6.4E-07
CXADR	Coxsackievirus and adenovirus receptor	-2.2	5.1E-07
VLDLR	Very low-density lipoprotein receptor	-2.0	2.7E-06
LRP8	Low-density lipoprotein receptor-related protein 8	-1.9	1.9E-05

TFRC	Transferrin receptor protein 1	-1.8	2.8E-06
GPRC5B	G-protein coupled receptor family C group 5 member B	-1.8	2.7E-03
EGFR	Epidermal growth factor receptor	-1.7	4.8E-06
TGFBR1	TGF-beta receptor type-1	-1.6	4.2E-03
MET	Hepatocyte growth factor receptor	-1.5	5.1E-05
LRP1	Prolow-density lipoprotein receptor-related protein 1	-1.5	4.3E-05

Table S2. List of primers.

Mutagenesis	**Forward primer**	**Reverse primer**
VAMP8_siRNA Resistant	*GGGGGGAAAACTTGGAACATCTCCGAAATAAAACCGAAGACCTAGAGGCCACATCTGAGCACTTCAAGA*	*TCTTGAAGTGCTCAGATGTGGCCTCTAGGTCTTCGGTTTTATTTCGGAGATGTTCCAAGTTTTCCCCCC*
SNARE: L219S*	*GTTTGCAGCATACAATGAAGGAATTATTAATTTGTCGGAAAAATATTTTGATATGAAAA*	*TTTTCATATCAAAATATTTTTCCGACAAATTAATAATTCCTTCATTGTATGCTGCAAAC*
SNARE:M244K*	*TAAGAAGTTCCTAACTAGGAAGACAAGAATCTCAGAGTTCC*	*GGAACTCTGAGATTCTTGTCTTCCTAGTTAGGAACTTCTTA*
Cloning	**Forward primer**	**Reverse primer**
Backbone: pLVX-IRES-puro *insert gene: RFP-VAMP8*	*RFP* fragment: *TAGAGGATCTATTTCCGGTGCCACCATGGTAGCAGG* *VAMP8* fragment: *GGATCACCGCGCTTGAGAGCATGGAGGAAGCCAGTGAAGG*	*RFP* fragment: *CTTCACTGGCTTCCTCCATGCTCTCAAGCGCGGTG* *VAMP8* fragment: *CGGCCGCTCTAGAACTAGTTTATGAGAAGGCACCAGTGGC*
Backbone: pLVX-IRES-puro *insert gene: LAMP1-mCherry*	*TAGAGGATCTATTTCCGGTCCATGGGCGGCCCCC*	*CGGCCGCTCTAGAACTAGTCTACTTGTACAGCTCGTCCATGCC*