Neutrophils actively swell to potentiate rapid migration

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Directed extension of the plasma membrane is needed for eukaryotic cell migration. While the role of actin polymerization in generating protrusive forces is well appreciated, we have a more limited understanding of the role of transmembrane water flow in cell motility. We investigate water influx-based migration in neutrophils, which undergo directed movement to sites of injury and infection. Chemoattractant exposure increases cell volume and potentiates neutrophil migration, but the causal link between these processes is not known. By measuring single cell volumes in primary human neutrophils, we find that chemoattractant induces a biphasic volume response with spreading-mediated volume loss followed by an increase in both cell volume and migratory speed. Using a genome-wide CRISPR screen, we identify the regulators of the chemoattractant-induced neutrophil swelling, including PI3K-gamma, CA2, NHE1 and AE2. Through NHE1 inhibition in primary human neutrophils, we show that cell swelling is both necessary and sufficient for rapid migration following chemoattractant stimulation. Our data demonstrate that cell swelling complements cytoskeletal inputs for chemoattractant-induced potentiation of migration.

Cell Migration | Cell Volume | Buoyant Density | NHE1 | AE2 | PI3K | CA2
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Introduction

Following chemoattractant exposure, neutrophils dramatically change their shape and movement. From a resting spherical shape, stimulated neutrophils polarize their actin assembly and actomyosin contractility to direct their movement to sites of injury and infection Weiner et al. (1999); Sengupta et al. (2006); Lämmermann et al. (2013). Actin cytoskeletal rearrangements are not the only modulators of cell shape and movement. Chemoattractant stimulation also initiates water influx, eliciting an approximately 15% increase in cell volume Grinstein et al. (1986). In contrast to the well-established role of the actin cytoskeleton in neutrophil movement, the role of water influx in chemoattractant-stimulated migration is poorly understood.

Directed water influx has previously been shown to participate in cell movement, particularly in the context of confined environments. In 1D confinement, directed water influx can power cell migration even in the absence of the actin cytoskeleton Stroka et al. (2014). Hypoosmotic shocks, which force water into the cytoplasm, have been shown to enhance neutrophil chemotaxis through nitrocellulose filters in vitro Rosengren et al. (1994). Here we investigated whether water influx is also relevant for unconfined 2D migration where actin polymerization is thought to dominate Keren et al. (2008); Mitchison et al. (2008). There is growing appreciation that cell volume is tightly coupled to cell morphogenesis and mechanics Venkova et al. (2022), but whether cells actively manipulate water fluxes to potentiate their motility is unknown.

Here we leverage recent advances in measuring the volume of single cells Zlotek-Zlotkiewicz et al. (2015); Cadart et al. (2017) to reveal the competing volume responses downstream of chemoattractant stimulation in human primary neutrophils. As the cells go from spherical to spread in response, they lose volume (as reported in other cell types by Venkova and colleagues Venkova et al. (2022)), but as they start migrating they then show a robust, sustained volume increase. We perform a genome-wide CRISPR screen to identify the mediators of this chemoattractant-induced cell swelling. By leveraging these regulators, we show that cell swelling is necessary and sufficient for the potentiation of cell migration following chemoattractant stimulation.

Results

Chemoattractant stimulation elicits competing volume responses in primary human neutrophils

Neutrophils are a powerful system to study the biophysical demands of cell motility, as they acutely initiate rapid migration following stimulation with chemoattractant. Neutrophils normally exist in a quiescent non-motile state Metzemaekers et al. (2020). Upon exposure to chemoattractants, neutrophils respond with large-scale morphological changes Sengupta et al. (2006); Denk et al. (2017) and a dramatic increase in motility Martin et al. (2015).

To probe the role of osmotics in chemoattractant-stimulated morphogenesis and movement (Fig 1A; Fig S1A-E), we adapted the single cell volume measurement technique, Fluorescence eXclusion Microscopy (FxM) Cadart et al. (2017) to primary human neutrophils. This assay enables us to accurately measure absolute cell volume in single primary human neutrophils during activa-

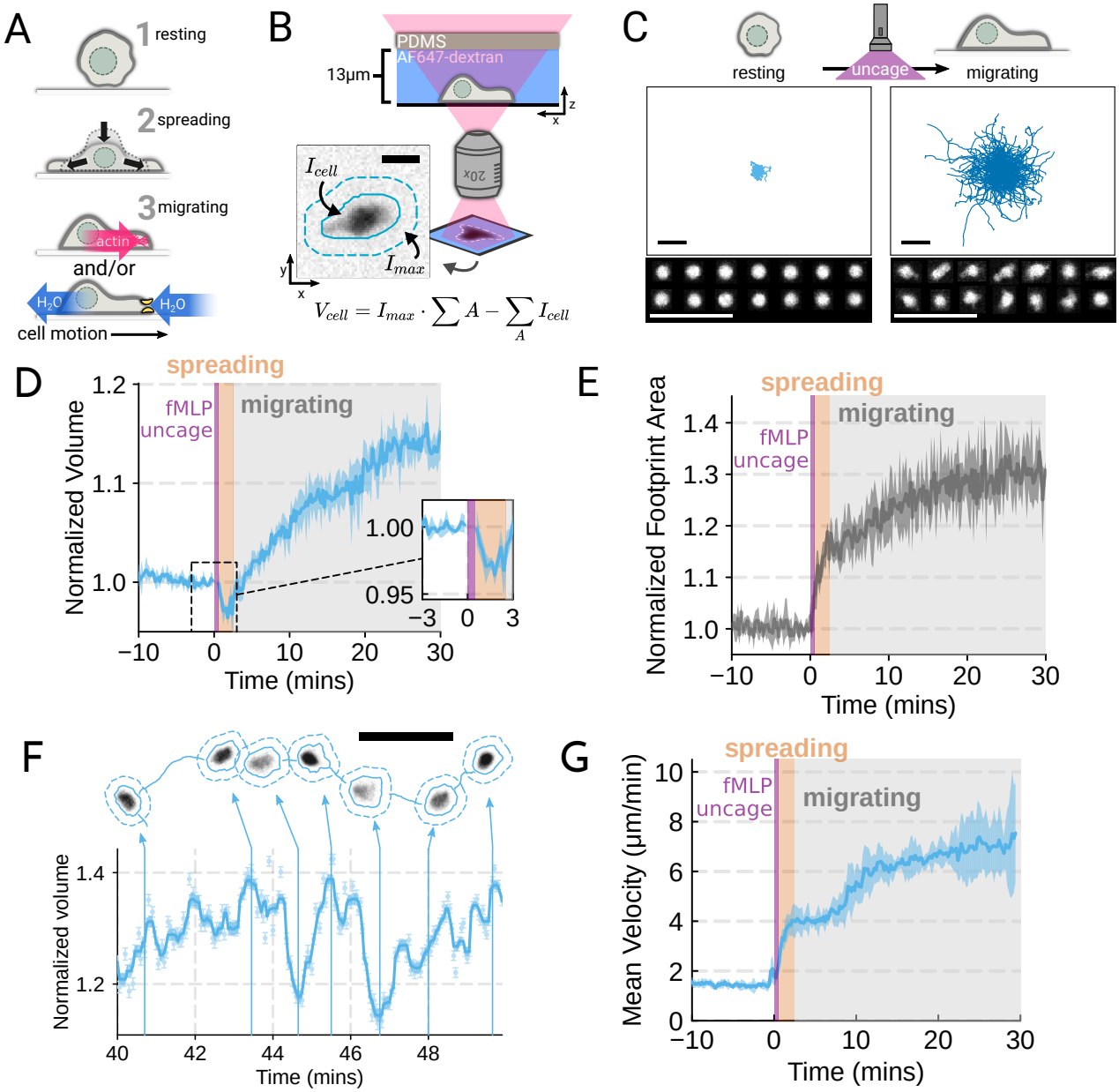

Figure 1. Chemoattractant stimulation elicits competing volume responses in primary human neutrophils

(**A**) Schematic detailing the neutrophil activation process. Resting cells first spread and then begin migrating using cytoskeletal and/or osmotic forces. (**B**) Schematic detailing the Fluorescence Exclusion Microscopy (FxM) approach for measuring single cell volumes. This technique relies on cells displacing an extracellular dye in a shallow microfluidic chamber. The presence of a cell reduces the signal and the cell volume is equal to the difference between the measured signal over the cell's area and the expected signal if the cell was not there. The inset shows an example cell with the inner solid teal line indicating the cell footprint and the outer dashed line indicating the local background. The scale bar is 10um. (**C**) Primary human neutrophil tracks over 15 minute time windows before (left) and after (right) the uncaging of the fMLP chemoattractant. Bottom panel has enlarged images of randomly selected example cells detailing neutrophil shape before and after activation. All scale bars are 50um. (**D**) Primary human neutrophil normalized volume responses following chemoattractant stimulation (Volunteer N = 4, Cells = 440 total). Inset details the volume loss due to spreading immediately after uncaging. Cells initially lose volume during the spreading phase following the chemoattractant stimulation and then significantly increase in volume. The line plotted is the average of the median cell response for each volunteer, and the shaded region is the 95% CI of the mean. For each volunteer, cell volumes are normalized to the volume in the two minute window prior to uncaging. See Video SV1 for an animated version of this data. (**E**) The normalized footprint area of primary human neutrophils responding to chemoattractant. The line is the average across biological replicates of median cell footprint area at each timepoint. Areas are normalized to the mean value in the two minute window prior to uncaging. The footprint area shows a monotonic increase in response to activation with cell spreading prior to initiation of movement. (**F**) Single representative cell trace imaged with high time resolution to highlight the cell motility-related volume fluctuations. Top section depicts the cell track with the FxM images overlaid at key time points that are linked with cyan arrows to the corresponding volumes in the bottom plot. Bottom half has faint cyan scatter points indicating the raw volume measurements with the thick cyan line depicting the rolling median volume. See Video SV2 for an animated version of this data. Scale bar is 50um. (**G**) Mean of the per-replicate median cell velocities computed at each time point. The shaded area is the standard deviation at each time point. Cell migration begins to increase in the early spreading phase following chemoattractant stimulation and then continues to increase over the next 20 minutes following stimulation.

tion by chemoattractant (Fig 1B-C). For stimulating cells in the FxM microfluidic chambers, we leveraged a UV-uncageable chemoattractant Collins et al. (2015). This enabled us to capture both the volume and motility response of cells before and after activation. Following chemoattractant-uncaging, the cells spread and transformed into a motile, amoeboid state with high persistence (Fig 1C). Simultaneously measuring the single cell volumes reveals a biphasic volume response (Fig 1D; Video SV1). Immediately following chemoattractant exposure, the cells lose ~5-8% of their cell volume (Fig 1D, inset), consistent with spreading-induced volume losses previously observed in other cells Venkova et al. (2022). Preventing cell spreading by depolymerizing the actin cytoskeleton with Latrunculin B abrogates this initial volume loss in neutrophil-like differentiated HL-60 (dHL-60) cells (Fig S1F). Following this spreading-mediated initial volume loss, the cells swelled significantly, reaching a median volume 15% larger than their resting volumes 20 minutes post-stimulation. The chemoattractant-induced spreading can be seen by the increased cell footprint area post-stimulation (Fig 1E).

The volume of the median cell increases significantly from 2-20 minutes following chemoattractant stimulation. However, this masks more complex behavior at the single cell level. Single-cell analyses reveal that even as the baseline volume has increased post-activation, individual cells exhibit large fluctuations in volume on the single-minute time scale as they move (Fig 1F; Video SV2). These appear correlated with the neutrophil motility cycle and require an intact actin polymerized cytoskeleton (Fig S1F). The increase in the volume set point (from 2 mins to 20-30 mins) is closely correlated with the increases in cell velocities over the same time frame (Fig 1G). To investigate whether there is a causal link between the chemoattractant-induced cell swelling and migration potentiation, we next sought to identify the molecular regulators of neutrophil swelling.

Genome-wide screen identifies regulators of chemoattractant-induced cell swelling

As an unbiased approach for identifying the regulators of chemoattractant-induced cell swelling, we turned to pooled genome-wide CRISPR/Cas9 screening Shalem et al. (2014). Our approach relies on creating a population of cells with single gene knockouts and then enriching for the cells that fail to swell following stimulation. The quality of this enrichment is the most critical step for success of these screens Nagy and Kampmann (2017). A key challenge in adapting pooled CRISPR screening to this context was the lack of highly scalable approaches for accurately separating the cells based on their volumes directly. Although volume is difficult to use as a separation approach, cells can be easily separated by buoyant density (mass over volume), and buoyant density is related to volume over short timescales. Because neutrophil swelling in suspension results from the uptake of water Grinstein et al. (1986), stimulated neutrophils exhibit a corresponding decrease in buoyant density Pember et al. (1983). Buoyant density has been successfully used in other genetic screens, including the identification of secretion-defective mutants in yeast Novick et al. (1980). Finally, buoyant density is a particularly homogenous parameter at the population-level, with 100-fold less variation than either mass or volume across multiple different cell types Grover et al. (2011).

To verify the chemoattractant-induced shifts in neutrophil buoyant density in our own hands, we deposited linear Percoll gradients (Fig S2A-B) in centrifuge tubes and carefully layered nutridoma-differentiated HL-60s (dHL-60s) onto the gradients in the absence or presence of the chemoattractant fMLP (Fig 2A). Stimulating dHL-60s with fMLP and using an optimized centrifugation protocol (Fig S2C) led to a robust, long-term decrease in buoyant density across millions of cells with a shift in population position clearly visible by eye (Fig 2B). The buoyant density change corresponded to a ~15% increase in cell volume (Fig 2C). This effect depends on chemoattractant-based cell stimulation, as knockout of the fMLP receptor FPR1 completely inhibits fMLP-induced swelling (Fig 2C, right).

To screen for the chemoattractant-induced regulators of cell volume, we transduced HL-60 cells with a commercial genome-wide CRISPR knockout library, differentiated them, and spun the cell population into Percoll density gradients with or without fMLP stimulation. We then fractionated the tubes and partitioned the samples into 3 different groups: low, medium, and high buoyant density (Fig S2D). We used next-generation sequencing to determine which CRISPR guides were over-represented in the high-density bin versus the other two bins, i.e. those that failed to swell and decrease in density following stimulation with fMLP (Fig 2D). To verify CRISPR knockout efficacy, we confirmed the systematic depletion of essential genes from the population (Fig S2E). Computing median log2-fold enrichment of the guides targeting each gene in the dense bin and plotting this value against the false discovery rate reveals the regulators of chemoattractant-induced cell swelling (Fig 2E). The top right corner is occupied by genes that are over-represented in the dense, i.e. non-swelling, bin. The top hit was FPR1, the high affinity GPCR that specifically binds to fMLP to initiate the chemoattractant signaling cascade.

Our screen revealed a potential transduction cascade from the chemoattractant receptor to the final effectors of cell swelling, including the sodium-proton antiporter NHE1 (SLC9A1), the gamma subunit of phophoinositide 3-kinase (PI3Kγ), carbonic anhydrase II (CA2), and the chloride-bicarbonate exchanger 2 (AE2, i.e. SLC4A2) (Fig 2F). These hits suggest that the cell swelling cascade begins with fMLP binding to the chemoattractant receptor FPR1, which activates PI3Kγ, which in turn activates NHE1 and AE2 which then work together to form the canonical regulatory volume increase (RVI) complex Hoffmann et al. (2009). NHE1 and AE2 would, in this model, eject cy-

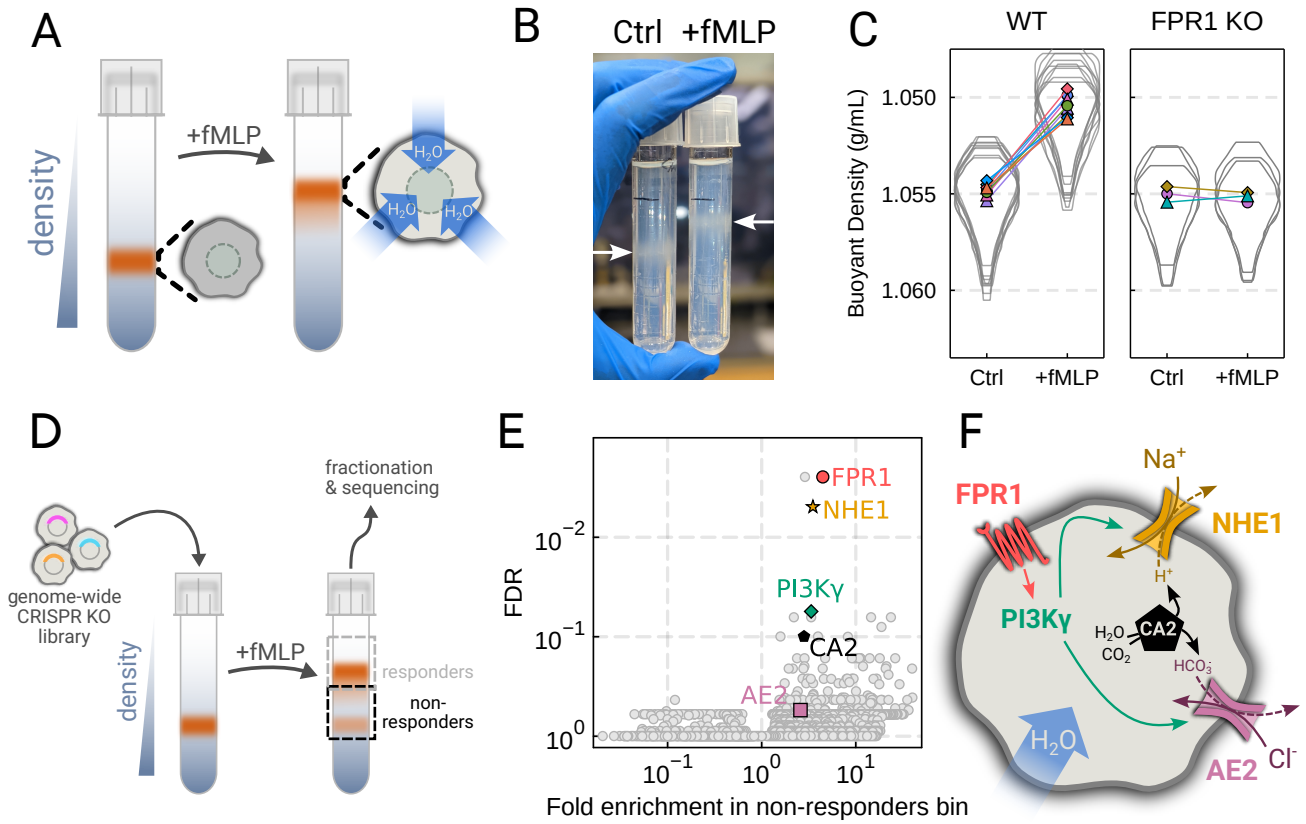

Figure 2. Genome-wide screen identifies regulators of chemoattractant-induced cell swelling
(**A**) Schematic detailing the buoyant density assay. The addition of fMLP causes cells to swell and decrease their density. As a result, the stimulated cells float higher in the Percoll density gradient. (**B**) Representative image of cell density shift following chemoattractant stimulation. Millions of cells appear as white fuzzy bands (indicated with the arrows). Cells in the right tube are stimulated with 20 nM chemoattractant (fMLP), causing them to swell and float higher in the gradient. (**C**) Violin plots quantifying the relative cell numbers as a function of density. Individual lines link replicate pairs. WT cells shift from 1.055g/mL to 1.050g/mL upon stimulation, while FPR1 KO cells do not shift following fMLP stimulation. (**D**) Schematic detailing the buoyant density-based genome-wide CRISPR knockout screen for identifying cells that are deficient at chemoattractant-induced cell swelling. (**E**) Volcano plot of the results of the chemoattractant-induced cell swelling screen. Genes that showed large inhibition of cell swelling and consistent behavior across their targeting guides appear in the upper right. The genes selected for further analysis are highlighted for a more complete list see Table S1. (**F**) Schematic outlining a potential pathway from chemoattractant stimulation to cell swelling.

toplasmic protons and bicarbonate ions in exchange for extracellular sodium and chloride, respectively. CA2 catalyzes the production of protons and bicarbonate from CO2 and water and directly binds the tail of NHE1 to enhance its activity Li et al. (2002, 2006). Thus, fMLP binding would lead to a net influx of sodium and chloride into the cell, mediating the influx of water and resulting in cell swelling.

Mechanistically separating chemoattractant versus motility-based volume changes

We next sought to individually validate our hits for chemoattractant-induced swelling. We created and verified single gene knockouts of the four components–NHE1, AE2, PI3Kγ, and CA2–using CRISPR/Cas9 in HL-60 cells. Using our buoyant density assay, we found that loss of either NHE1 or AE2 completely ablated the fMLP-induced volume increase in dHL-60s (Fig 3A). Our data indicate that both ion channels are needed for chemoattractant-induced swelling. Knockouts of PI3Kγ and CA2 partially inhibited chemoattractant-induced swelling (Fig S3A).

Since dHL-60 cells exhibit significant basal migration even in the absence of chemoattractant stimulation, they are a non-ideal model for chemoattractant-stimulated migration compared to primary human neutrophils, which are completely quiescent and non-motile prior to stimulation. We next sought to replicate our knockout results through pharmacological inhibition of our CRISPR hits in human primary neutrophils. We used BIX (iNHE1), a potent and selective inhibitor of NHE1 Huber et al. (2012), and Duvelisib (iPI3Kγ), a potent PI3Kδ/γ inhibitor Winkler et al. (2013). We compared chemoattractant-stimulated single cell volume responses in unperturbed, NHE1 inhibited (Fig 3B), or PI3Kδ/γ inhibited neutrophils (Fig S3B). Inhibition of either NHE1 or PI3Kδ/γ prevented chemoattractant-induced swelling in human primary neutrophils. At the single cell level, the NHE1 inhibited population brackets the initial cell volumes even 30 minutes post-stimulation, and this is consistent across days and replicates (Fig 3C). To orthogonally verify the volume defect, we used a Coulter counter, an electronic particle sizing method, to measure the single cell volume responses following stimula-

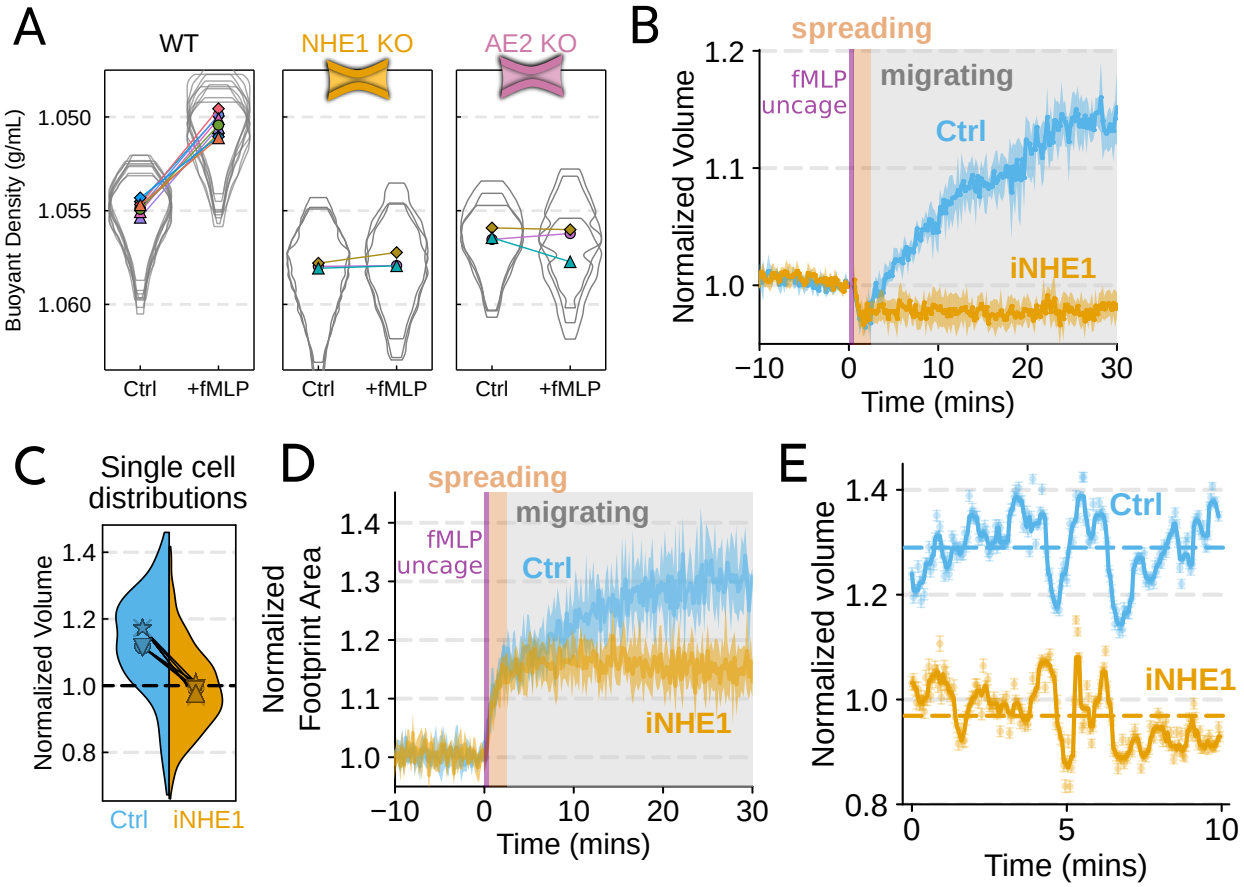

Figure 3. Mechanistically separating chemoattractant versus motility-based volume changes
(**A**) Knockout of NHE1 or AE2 is sufficient to completely inhibit the chemoattractant-induced swelling in neutrophil-like differentiated HL-60 cells (**B**) NHE1 inhibition in human primary neutrophils blocks fMLP-induced swelling but does not inhibit the spreading-induced volume loss. An animated version is available as Video SV4. (Ctrl: Volunteer N = 4, iNHE1: Volunteer N = 6). (**C**) The distributions of single cell volumes 30 minutes post-chemoattractant stimulation demonstrates that the NHE1 inhibited neutrophils remain close to the pre-stimulation volumes, i.e. 1.0 on the ordinate (**D**) NHE1 inhibited neutrophils have similar increases in their footprint area to control cells when they spread and begin moving following fMLP stimulation, but lag control cells at later time points (**E**) High temporal resolution imaging of the motility-induced volume fluctuations starting at 30 minutes post-stimulation demonstrate that both control and NHE1-inhibited neutrophils show similar short-term volume fluctuations around significantly different baselines (dashed lines). For an animated version, see Video SV2 and Video SV3.

tion in suspension. These experiments confirmed that inhibition of NHE1 blocked cell swelling in suspension as well (Fig S3C). NHE1-inhibited cells maintained their ability to change shape and spread in response to chemoattractant, though they lagged behind control cells at later time points (Fig 3D). In contrast, PI3Kδ/γ inhibition blocked chemoattractant-induced shape change (Fig S3D).

Blocking NHE1 activity did not interfere with the spreading-induced volume loss of primary human neutrophils but it prevented the subsequent chemoattractant-induced volume gain. We next sought to determine whether the oscillatory volume fluctuations associated with the motility-cycle were affected by NHE1 inhibition. Performing high temporal resolution imaging of single cells at later time points (30-50 minutes) following uncaging revealed that the iNHE1 cells exhibit similar motility-coupled volume changes but at vastly different baselines (Fig 3E). So despite the motility-cycle-associated volume fluctuations being similar (Fig S3E; Video SV3), the baselines are approximately 20% decreased in NHE1 inhibited versus unperturbed cells following chemoattractant stimulation.

The chemoattractant-driven volume gain is necessary and sufficient for rapid migration

We next sought to leverage our identified volume regulators to probe the relation between cell swelling and motility. Turning again to the FxM assay, we activated primary human neutrophils by uncaging fMLP and measured the average cell velocity over the population (Fig 4A). In the first 10 minutes following uncaging, both WT and NHE1-inhibited cells both exhibited a similar potentiation of migration. However, after 10 minutes the unperturbed neutrophils continued increasing in speed, while the iNHE1 cells plateaued. The WT speed potentiation is closely correlated with the kinetics of swelling. To visualize the volume-velocity relationship, we plotted the average volume versus average speed of single WT cells in the first 10 minutes following uncaging versus 20-30 minutes post-uncaging (Fig 4B). In the early time points following chemoattractant stimulation, control cells operate in a low-

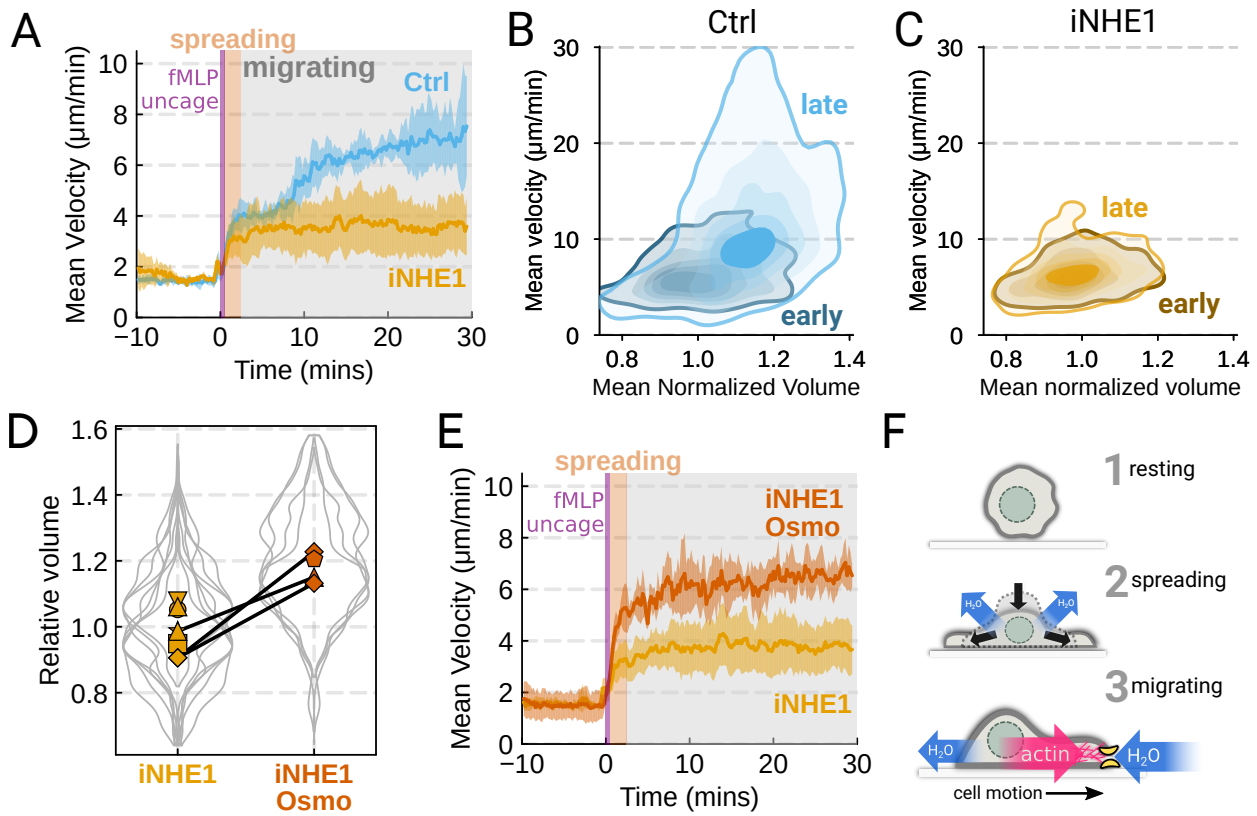

Figure 4. The chemoattractant-driven volume gain is necessary and sufficient for rapid cell migration following stimulation
(**A**) Comparison of control (cyan) or NHE1-inhibited (gold) primary human neutrophil migration following chemoattractant stimulation. Mean of the per-replicate median cell velocities is shown, with the shaded area indicating standard deviation at each time point. (Ctrl: Volunteer N = 4, iNHE1: Volunteer N = 6). (**B**) Contour plots of the average velocity versus average normalized volume for single unperturbed neutrophils for the initial 10 minute window following stimulation (early) and from 20-30 minutes following stimulation (late) (**C**) Contour plots of the average velocity versus average normalized volume for single NHE1-inhibited neutrophils for the initial 10 minute window following stimulation (early) and from 20-30 minutes following stimulation (late) (**D**) Dilution of imaging media with 20% water led to a ~15% increase in the median cell volumes of iNHE1 cells (iNHE1 Osmo; red) versus iNHE1 cells in normal media (gold). Volumes are normalized relative to the median iNHE1 cell volume. This is similar to the magnitude of chemoattractant-induced swelling in control cells. The black lines connect conditions where both conditions were measured for the same volunteer. (iNHE1 Osmo: Volunteer N = 3, 4 total replicates; iNHE1: Volunteer N = 6) (**E**) Exogeneous cell swelling via hypoosmotic shock is sufficient to rescue the migration defect in NHE1-inhibited neutrophils. Mean of the pre-replicate median cell velocities computed at each time point for NHE1 inhibited cells (yellow) versus mildly hypoosmotically swollen NHE1 inhibited cells (red). Shaded area is the standard deviation at each time point. (iNHE1 Osmo: Volunteer N = 3, 4 total replicates; iNHE1: Volunteer N = 6). See Video SV5 for representative chemokinetic behavior. (**F**) Summary schematic. Cell swelling collaborates with actin polymerization to potentiate chemoattractant-induced cell migration.

volume, low-velocity regime. At later time points following stimulation, control cells operate in a higher-volume high-velocity state. The iNHE1 cells persist in the low-volume, low-velocity state even 20-30 minutes post stimulation (Fig 4C). To test whether other aspects of chemokinesis are affected in the iNHE1 cells, we also computed the angular persistence of single cells over 10 micron distance windows and found no difference in between WT and iNHE1 cells (Fig S4A). This is in contrast to the PI3Kδ/γ-inhibited cells, which failed to increase their velocity following chemoattractant uncaging (Fig S4B).

NHE1-inhibited cells are defective in both chemoattractant-induced swelling and rapid migration. To determine if the lack of cell swelling is the basis of their migration defect, we sought to rescue cell swelling for iNHE1 cells through a mild hypoosmotic shock. Diluting the media 20% (v/v) with water led to a ~15% increase in volume of the iNHE1 cells, approximating the magnitude of swelling elicited by fMLP in control cells (Fig 4D). Uncaging fMLP initiated chemokinesis for both iNHE1 and iNHE1-Osmo cells, but the hypoosmotically shocked cells continued accelerating for longer and reached higher sustained speeds (Fig 4E; Video SV5). Intriguingly, the hypoosmotically shocked cells are precocious in their rapid motility. This might be expected, since these cells are pre-swollen prior to stimulation, whereas control cells take longer to reach the high-volume high-velocity state following chemoattractant stimulation. Our data suggest that the water influx following chemoattractant stimulation plays an important role in the potentiation of neutrophil migration (Fig 4F).

Discussion

Neutrophils are remarkable for the rapid migration that is key to their innate immune function Lämmermann et al. (2013). Here we show that human primary neutrophils actively increase their cell volumes when stimulated with

chemoattractant, and this correlates with their rapid movement (Fig 1). We then perform an unbiased genome-wide screen to identify the molecular components of chemoattractant-induced cell swelling (Fig 2D-F). While one of the hits, NHE1, has been investigated in previous studies Ritter et al. (1998); Denker and Barber (2002); Frantz et al. (2007); Zhang et al. (2022), our work systematically identifies the dominant players in a larger network that contribute to the swelling response. Buoyant density screening was used with great success by Schekman and colleagues to elucidate the secretory pathway in yeast Novick et al. (1980); Novick and Schekman (1979). Here, we use the sensitivity of this assay combined with the power of modern forward genetics to uncover the mechanistic basis of how cells actively manipulate their volume to enhance migration.

Our work implicates both NHE1 and AE2 in cell swelling, as knockout of either completely ablates chemoattractant-induced swelling in dHL-60 cells (Fig 3A). PI3Kδ/γ inhibition was sufficient to prevent swelling in primary human neutrophils while also blocking chemokinesis (Fig S3B,S4B). This agrees with earlier work demonstrating an essential role for PI3Kγ activity in neutrophil chemokinesis Ferguson et al. (2007). Finally, knockout of CA2 also reduced swelling in dHL-60s (Fig S3A), supporting the previously reported role of CA2 in enhancing the activity of NHE1 Li et al. (2006); Vargas et al. (2013). We then confirmed our dHL-60 results via pharmacological inhibition of NHE1 in human primary neutrophils and verified the necessity of NHE1 in the chemoattractant-induced swelling response (Fig 3). NHE1-inhibited cells showed a defect in both motility and chemoattractant-induced swelling (Fig 4A-C). This agrees with previous work mostly in slow-moving immortalized cell lines where NHE1 is critical for optimal motility Denker and Barber (2002); Stroka et al. (2014); Zhang et al. (2022); Klein et al. (2000). In contrast, previous work in chemotaxing primary human neutrophils suggested only a housekeeping role for NHE1 in preventing the acidification of the cytoplasm Hayashi et al. (2008). Consistent with previous results, we observe only minor defects for NHE1-inhibition in the first 10 minutes following chemoattractant stimulation. At longer time points, NHE1-inhibited cells fail to continue their migration acceleration compared to uninhibited cells. This lack of migration potentiation in NHE-1 inhibited cells can be explained by their defective cell swelling, as exogenous swelling via hypoosmotic shock rescues the velocity defect (Fig 4D-E; Video SV5).

How might swelling contribute to rapid neutrophil migration? Given that neutrophils are approximately 65% water (Fig S2F), the 15% increase in cell volume corresponds to almost a ~25% increase in the water content of the cell after 20 minutes. This change could affect global biophysical parameters such as a decrease in cytoplasmic viscosity or an increase in the diffusion of biochemical or cytoskeletal regulators of movement. Alternatively or in addition, local water influx could collaborate with the actin polymerization machinery in facilitating the extension of the plasma membrane Mitchison et al. (2008); García-Arcos et al. (2022). The regulatory volume components identified here are ubiquitously expressed, so it is possible that they also facilitate chemoattractant-induced migration in other contexts. NHE1-dependent swelling has been observed in dendritic cells responding to LPS Rotte et al. (2010), and NHE1 inhibition slows microglial chemotaxis Shi et al. (2013). NHE1's role in migration and metastasis is well-established Stroka et al. (2014); Zhang et al. (2022), and several other constituents of our chemoattractant-induced cell swelling program have been implicated in cell migration responses as well. AE2 plays a role in murine osteoclast spreading and migration Coury et al. (2013). Similarly, carbonic anhydrases have been implicated in facilitating migration Svastova et al. (2012), and PI3K isoforms have a well-appreciated role in migration Ferguson et al. (2007); Devreotes and Horwitz (2015). Systematic investigation of this chemoattractant-induced cell swelling network could reveal a general role for water influx in potentiating cell migration.

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Methods

Medias and Inhibitors

For all imaging experiments, imaging media was made with Phenol Red-free Leibovitz's L-15 media (Gibco #21083027) supplemented with 10% (v/v) heat-inactivated fetal bovine serum (Gibco) and filtered with a 0.22 um Steriflip filter (MilliporeSigma #SCGP00525). Imaging media was always prepared fresh on the same day of imaging. For FxM coating, 0.2% endotoxin and fatty acid-free Bovine Serum Albumin (BSA) (Sigma #A8806) was dissolved in L15 via pulse centrifugation. The mix was then filtered with a Steriflip filter before further use. For all density experiments, divalent-free mHBSS media was prepared as

in Houk et al Houk et al. (2012). In short, 150 mM NaCl, 4 mM KCl, 10 mg/mL glucose and 20 mM HEPES were dissolved in Milli-Q (Millipore) water and the pH adjusted to 7.2 with 1M NaOH. The osmolarity was verified to be 315 mOsm/kg on a micro-osmometer (Fiske Model 210). Culturing media (R10) was made from RPMI 1640 media (Gibco #11875093) supplemented with 25mM HEPES and L-glutamine supplemented with 10% (v/v) heat inactivated fetal bovine serum (Gibco). The NHE1 inhibitor, BIX (Tocris #5512), was dissolved in dry DMSO to a final concentration of 25 mM and stored at -20℃ in single use aliquots that were diluted in imaging media the day of the experiment. All iNHE1 experiments used BIX at a 5 uM final concentration. Similarly, Latrunculin-B (Sigma #428020) was stored at 10 mM in DMSO and used at 1 uM final. For PI3Kδ/γ inhibition, Duvelisib (MedChemExpress #HY-17044) was stored at 10 mM in DMSO and used at a final concentration of 1 uM.

Human primary neutrophil isolation and drug treatment

All blood specimens from patients were obtained with informed consent according to the institutional review board-approved study protocol at the University of California - San Francisco (Study #21-35147), see Table S2 for demographic information. Fresh samples of peripheral blood from healthy adult volunteers were collected via a 23-gauge butterfly needle collection set (BD #23-021-022) into 10 ml Vacutainer EDTA tubes (BD #366643). Blood was kept on a shaker at minimum setting and utilized within 2 hours of the draw. Neutrophils were isolated using the EasySep Direct Human Neutrophil Isolation Kit (STEMCELL Tech #19666) with the BigEasy magnet (STEMCELL Tech #18001) according to the manufacturer's protocol.

Isolated neutrophils were spun down at 200g for 5 min and resuspended in a dye media consisting of imaging media containing 5ug/ml Hoechst 3334 (Invitrogen #H3570) and 0.25 uM Calcein Red-Orange AM (Invitrogen #C34851). This cell suspension was incubated at room temperature in the dark for 15 min, and then the cells were spun down at 200g for 5 min. The dye medium was aspirated and replaced with R10 to achieve a final cell density at or below $1x10^6$ cells/mL. Purified neutrophils were then kept in polystyrene T25 flasks (Corning) at 37℃ in a 5% CO2 environment until imaging. Cells were used ~5-8 hours post-isolation.

Cell culture

Short tandem repeat authenticated HL-60 cells Saha et al. (2023) were maintained in R10 media at 5% CO2 and 37℃ and at a concentration of 0.2-1 million/mL by passaging every 2-3 days. 5 days prior to experiments, HL-60s were differentiated into a neutrophil-like state by taking an aliquot of cells in their culturing medium and supplementing with an equal volume of Nutridoma-CS (Roche #11363743001) and DMSO diluted in RPMI such that that the final concentrations were 0.2 million/mL HL-60 cells, 2% (v/v) Nutridoma-CS, 1.3% (v/v) DMSO, 5% (v/v) FBS in RPMI. After 5 days at 37℃/5% CO2, we observed robust expression of terminal differentiation markers like FPR1 as reported previously Rincón et al. (2018).

Lenti-X HEK-293Ts (Takara) were used for lentivirus production and maintained at below 80% confluency in DMEM supplemented with 10% (v/v) heat-inactivated fetal bovine serum. These cells were also maintained at 5% CO2 and 37℃. All cell lines were routinely monitored for mycoplasma contamination using standard mycoplasma monitoring kits (Lonza).

FxM single cell volume measurements

FxM microfluidic chips were prepared as previously described Zlotek-Zlotkiewicz et al. (2015); Cadart et al. (2017) using a custom mold generously provided by the Piel lab. Briefly, 10:1 (w/w) PDMS elastomer base and crosslinker (Momentive #RTV615-1P) were thoroughly mixed, poured into the FxM mold, and degassed under a vacuum for one hour. The PDMS was then baked at 80℃ for 2 hours and removed from the mold. The day prior to experiments, the molded PDMS was cut with a scalpel to form 3 lane "chips" and the inlet and outlet holes were created using a 0.5mm punch. The chips and 35mm glass-bottomed dishes (Willco Wells #HBST-3522) were then plasma cleaned for 30 s, and chips were gently pressed down onto the glass to form a watertight seal. A good seal was verified visually by the refractive index change upon glass/PDMS contact. The chips were then baked at 80℃ for 10 minutes to ensure thorough bonding. The chips were then quickly coated with 100 ug/mL human fibronectin (Sigma #SLCL0793) diluted in PBS and injected using a pipette tip. Coating was allowed to proceed for 30 minutes at RT before the chamber was flushed with imaging media. The chips were then submerged in PBS and allowed to incubate with L15 + 0.2% BSA overnight at 4℃.

On the day of the experiment, pre-prepared microfluidic chips were allowed to warm up at RT. Human primary neutrophils were gently pipetted up and down to resuspend if they had settled and spun down at 200xg for 4 minutes. The cell pellet was very slowly resuspended in imaging media to achieve a cellular concentration of 60 million per mL. The cells were allowed to equilibrate for 30 minutes at RT. The lanes of the chip were flushed with the corresponding final media. The cells were gently mixed with a 2x solution such that the final concentrations were 0.5mg/mL Alexa Fluor 647-tagged 10,000 MW dextran (Invitrogen #D22914), 200nM caged fMLP (NEP), and 30 million per mL cells in imaging media. This mixture was then slowly pulled into the chamber using a partially depressed pipette tip to minimize the shear forces on the cells, as these are known to affect neutrophil response to fMLP Mitchell and King (2012). Once loading was complete, the entire chamber was submerged in imaging media to stop all flows and allowed to warm up to 37℃. Experiments were started promptly 20 minutes post-submersion.

Suspension cell volume measurements

Suspension cell volume measurements were performed as in Graziano et al Graziano et al. (2019). Briefly, human primary neutrophils were spun out of culture media at 200xg for 4 minutes and gently resuspended in mHBSS. They were then diluted to 20,000 cells/mL in warm 15mL of mHBSS in Accuvettes (Beckman-Coulter). The cells were incubated at 37℃ for 5 minutes, and then either a DMSO blank or the indicated amount of drug was added to the correct final concentration. The cells were again incubated for 5 minutes at 37℃. They were then quickly transported to the Multisizer Z2 instrument (Beckman-Coulter) at RT. Three time points were taken to set a baseline, and then fMLP (Sigma) was added to a final concentration of 20 nM, and the Accuvette was inverted to mix. Then 0.5 mL samples were taken continuously every minute using a 100 um diameter aperture with a current of 0.707 mA, a gain of 64, a pre-amp gain of 179.20, a calibration factor (Kd) of 59.41 and a resolution of 256 bits. 5000-10,000 cells were sampled per time point and the medians of the population was extracted using our software available at `https://github.com/tlnagy/Coulter.jl`

Buoyant Density Measurements

Buoyant density measurements were done by pre-pouring gradients, layering dHL-60s on top, centrifuging, fractionating, and then imaging to count cells. First, solutions were made with either 32.6% or 57% (v/v) Percoll (Sigma) with 10% (v/v) 10x divalent-free mHBSS and diluted with ultrapure water, making a low density solution (LDS) and high density solution (HDS), respectively. The refractive index of both solutions was determined with a MA871 refractometer (Milwaukee Instruments) as 1.3419 and 1.3467, respectively. Given that the density is linearly related to the refractive index (Fig S2A) the solutions have densities of 1.045 g/mL and 1.074 g/mL, respectively. For the chemoattractant-condition, 20 nM fMLP (Sigma) was added. A linear gradient mixer was attached to an Auto Densi-Flow (Labconco) gradient fractionator and used to dispense gradients into 14 mL round bottom tubes (Falcon #352041).

For each gradient, approximately 5 million dHL-60s were spun down at 200xg for 4 minutes and resuspended in 1mL of 1x mHBSS. The cells were then labeled with 0.5 µM Calcein-AM (Invitrogen) for 5 minutes then spun down and resuspended in LDS. For mixed populations, the two cell types were spun down and labeled separately with either Calcein-AM or Calcein Red-Orange-AM and then mixed together. The cells were layered gently on top of the gradient and spun at 250xg for 1 hour. Neutrophils display homotypic aggregation when activated during centrifugation Simon et al. (1990) so we used a divalent-free media and very long centrifugation times optimized for separation at low centrifugation speeds (Fig S2C).

After centrifugation, the cells were fractionated into a 96-well using the Auto Densi-Flow in "remove" modality and a homemade fractionator. 6-7 wells were taken, and their refractive index was measured using the refractometer to align the gradients and verify linearity (Fig S2B). A 2x volume of blank media was added to each well to reduce the density, and then the plates were spun in the centrifuge at 250xg to assist the settling of the cells on the glass. The plates were then imaged using confocal microscopy to determine the number of cells in each well. For mixed population experiments, dual color imaging was done to determine the cell count of each sample.

CRISPR Genome Wide Screen on Buoyant Density

Lenti-X 293Ts (Takara) were transfected with the Guide-it library (Takara) according to the manufacturer's instructions and concentrated ~100x using the Lenti-X concentrator kit (Takara) and stored at -80℃ until needed. Human codon-optimized S. pyogenes Cas9-tagBFP expressing HL-60 cells Graziano et al. (2019) were transduced by spinoculating the cells on Retronectin-coated (Takara) non-TC treated 6-well plates (Falcon #351146). Briefly, each well was coated with 20ug/mL Retronectin stock solution diluted in DPBS for 2 hours and then blocked with 2% BSA (w/v) in PBS for 30 minutes and washed with PBS. 2mL of 1 million/mL Cas9-BFP HL-60s were added to each well of 4 plates (48 million cells total) and 30uL of concentrated Guide-it library lentivirus was added to each well. Using Lenti GoStix (Takara), we estimated that this corresponds to $8x10^6$ IFUs per well. The plates were spun at 1000xg for 30 mins, and then 1mL of R10 was added gently. This was followed by another dilution with 2 mL of the same media after 24 hours. 48 hours post spinoculation, the cells were spun down at 200xg and resuspended in R10. The cells were then sorted for mCherry-positive cells (cutoff set at 99.9th percentile of the untransduced cell population's mCherry signal) using a FACSAria 3 cell sorter (BD). We observed 4% of cells with a mCherry positive signal, equivalent to a MOI of 0.04. This gives a minimum coverage of 6-24x of the library at transduction; post-sequencing Monte Carlo simulations suggest a minimum coverage of 12x. After sorting, the cells were selected using 175 ug/mL hygromycin and kept in log-phase growth with regular supplementation with fresh media for 7 days, after which ~95% of the population were mCherry positive.

5 days prior to screening day, the cells were differentiated into neutrophil-like cells as described in the "Cell Culture" section. The buoyant density assay was performed as described in the "Buoyant Density Measurements" section with 6 million cells per tube split across 6 tubes, corresponding to 36 million cells or ~450x coverage of the library. The cells were layered on top of the gradients containing 20 nM fMLP with or without 1 uM Latrunculin-B, and then each tube was fractionated into 48 wells, which were combined into 3 separate bins such that they each contained approximately one third of the population (Fig S2B). The bins from each tube belonging to the same sample were combined, and then the cells were spun down, and the pellets were flash frozen to store for further processing. The genomic DNA was extracted using the QIAamp gDNA

kit (Qiagen) according to the manufacturer's instructions. The guides were then PCR amplified for 26 cycles using the Ex Taq polymerase (Takara) protocol with the P5 forward primer mix (Takara) and a unique reverse P7 primer for each condition. The specificity and quality of amplification for each sample was validated using a TapeStation 4200 (Agilent), and the precise DNA concentration was determined using a Qubit fluorometer (Invitrogen) according to manufacturers' instructions. The amplified DNA was then pooled to a 10 nM final concentration followed by a 5% PhiX (Illumina) spike and sequenced in a PE100 run on a HiSeq 4000 sequencer (Illumina) at the UCSF sequencing core.

To verify that we can detect the functioning of Cas9, we assayed for the depletion of guides targeting previously published essential genes Wang et al. (2015); Evers et al. (2016). We used MAGeCK Li et al. (2014) to compute the log fold change between the known frequencies of the guides in the library (Takara) and the actual observed frequencies of the guides (computed by pooling all bins together). The cumulative distribution of the essential gene ranks were compared to a randomly shuffling of those same genes to demonstrate that the essential genes were highly depleted from the population, as expected (Fig S2E).

Similarly, to determine which genes were involved in the chemoattractant-induced density change, we used MAGeCK to compute the false discovery rate and log fold change between the first and second bins vs the third bin (Fig S2D). The third bin was the most dense bin, so genes over-represented in this bin versus the other two were likely interfering with the swelling process. We pooled the samples with and without 1 uM Latrunculin-B together to improve our sensitivity as the swelling is not dependent on a polymerized cytoskeleton (Fig S1F). The combined fold change for each gene was then computed by taking the MAGeCK "alphamedian" log fold change (either positive or negative) that was most divergent. Using this fold change and the false discovery rate, we identified the genes that are most likely involved with the chemoattractant-induced swelling (Fig 2E, Table S1).

Single gene knockout line generation with CRISPR/Cas9

Single gene knockouts were generated and validated using wildtype HL-60s expressing human codon-optimized S. pyogenes Cas9-tagBFP cells as the base line as previously described Graziano et al. (2019). The two best performing guides from the genome-wide screen (Table S3) were selected and synthesized (IDT) and then cloned into the pLVXS-sgRNA-mCherry-hyg Vector (Takara) following the manufacturer's instructions. Lentivirus was then produced as previously described Graziano et al. (2019). Briefly, LX-293T cells (Takara) were seeded into 6-well plates and grown till 80% confluence was reached. 1.5 µg of the guide vector (from above) was mixed with 0.167 µg vesicular stomatitis virus-G vector and 1.2 µg cytomegalovirus 8.91 vector. This mixture was incubated with the TransIT-293 Transfection Reagent (Mirus Bio) and used to transfect the 293T cells following the manufacturer's instructions. The cells were grown for 72 hours post-transfection and the virus was concentrated ~40-fold from the supernatant using the Lenti-X concentrator kit (Takara) per the manufacturer's protocol. Concentrated virus stocks were stored at -80℃ until needed. For transduction, virus stocks were thawed and added to 300,000 cells in R10 in the presence of polybrene (8ug/mL) and incubated for 24 hours. Afterwards, the cells were washed twice with R10 to remove any remaining viral particles and sorted for mCherry-positivity on a FACSAria 3 cell sorter (BD). The heterogeneous population was then assayed for successful editing by sequencing the genomic DNA flanking the Cas9 cut site. Clonal populations were then isolated by seeding dual BFP and mCherry-positive cells into a 96-well plate such that only one cell was deposited in each well using a FACSAria Fusion (BD). The cells were then allowed to grow up and clonality was verified by genomic DNA sequencing of the cut site as previously described Graziano et al. (2017).

Microscopy Hardware

FxM and buoyant density experiments were performed on an inverted Eclipse TI microscope (Nikon) with a Borealis beam conditioning unit (Andor), and light was collected on an air-cooled iXon 888 Ultra EM-CCD (Andor). A 20x Plan Apochromat NA 0.75 objective (Nikon) was used for FxM, and a 10x Plan Apochromat (Nikon) was used for density experiments. Light sources include a Stradus Versalace 405, 488, 561, 647-nm laser line system (Vortran Laser Technologies) and a Sutter Lambda LS xenon-arc lamp used for FxM. Microscopy hardware was controlled with a TriggerScope 4 (Advanced Research Consulting) via MicroManager Edelstein et al. (2014).

UV light for uncaging was delivered via a 365nm Lambda FLED (Sutter) launched into a Lambda OBC and delivered via the condenser with all mobile optical elements removed and all apertures wide open. Before every experiment, the wattage was measured using a light meter (Thor Labs). The LED was controlled via a custom MicroManager script.

Data Analysis

FxM images were analyzed using a custom pipeline (Fig S1A) implemented in the Julia language Bezanson et al. (2017) available at `https://github.com/tlnagy/FluorescenceExclusion.jl`. Briefly, the raw images were denoised with a patch-based algorithm Boulanger et al. (2010) and then the edges were enhanced using a Scharr kernel. The magnitude of the edge values is log normally distributed, and we empirically determined that calling the edge of the cell at 1 standard deviation above the mean gave low noise and the maximum signal (Fig S1C). Flood-filling the areas encapsulated by these edges

gave a binary mask of the foreground, i.e. space occupied by the cells.

Independently, instance segmentation was performed using a custom Cellpose model trained using the human-in-the-loop feature Pachitariu and Stringer (2022) on the raw nuclear and cytoplasmic channels. Trackpy was used to link the Cellpose segmented instances together in time Allan et al. (2021) and these were then used to nucleate a watershed algorithm on the binary mask of the foreground and separate the foreground into the individual tracked cells. Next, the raw image was flatfield corrected by fitting a multiquadratic function at sinusoidally placed locations (avoiding the locations of cells or pillars) in the raw image which gave the densest sampling at the edges. Given that the chambers have flat ceilings supported by pillars Zlotek-Zlotkiewicz et al. (2015), the background signal can be used to compute the per-time point flatfield. After subtracting the darkfield image from both the raw FxM signal and the interpolant, the raw signal was divided by the interpolant giving extremely uniform homogeneous signal across the FOV.

Next, the local background was computed for each cell which we defined as the region 2 to 10 pixels away (1.3 to 6.5 microns) from the cell borders while avoiding other cells. The median of this local background was used to compute the counterfactual of what the signal would have been if the cell was not there by multiplying by the pixel area of the cell A (Fig 1B, inset). The measured signal over the area of the cell was then subtracted from that value to give the volume excluded by the cell according to equation 2 from Cadart et al. (2017):

$$V_{cell} = \sum_{x,y \in A} \frac{I_{max} - I_{cell}(x,y)}{\alpha} \quad \textbf{(1)}$$

where I_{max} is the median signal of the locality, i.e. the maximum signal if the cell was not there. A is the cell footprint area and I_{cell} is the signal at each point $x, y \in A$. To convert this to absolute volume measurements we divide by α which is the fluorescence as a function of object height:

$$\alpha = (I_{max} - I_{min})/h_{chamber} \quad \textbf{(2)}$$

Where the minimum signal I_{min} is the signal at the pillars that support the chamber's roof and $h_{chamber}$ is the height of the chamber in microns. As discussed in Cadart et al. (2017), while the per-pixel heights might not be accurate due light scatter, segmenting a slightly larger area than the cell footprint (S1C) captures any scattered signal and yields accurate whole cell volumes.

For velocity measurements, cell tracks were analyzed using the following equation to compute the velocity at frame i over a window τ given the x and y coordinates in microns and time t in seconds:

$$\nu_i = \frac{\sqrt{(x_{i+\tau} - x_{i-\tau})^2 + (y_{i+\tau} - y_{t-\tau})^2}}{t_{i+\tau} - t_{i-\tau}} \quad \textbf{(3)}$$

For all plots in this paper a τ of 3 corresponding to approximately a one minute window was used, but similar results were obtained at other values of τ.

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Supplementary Information

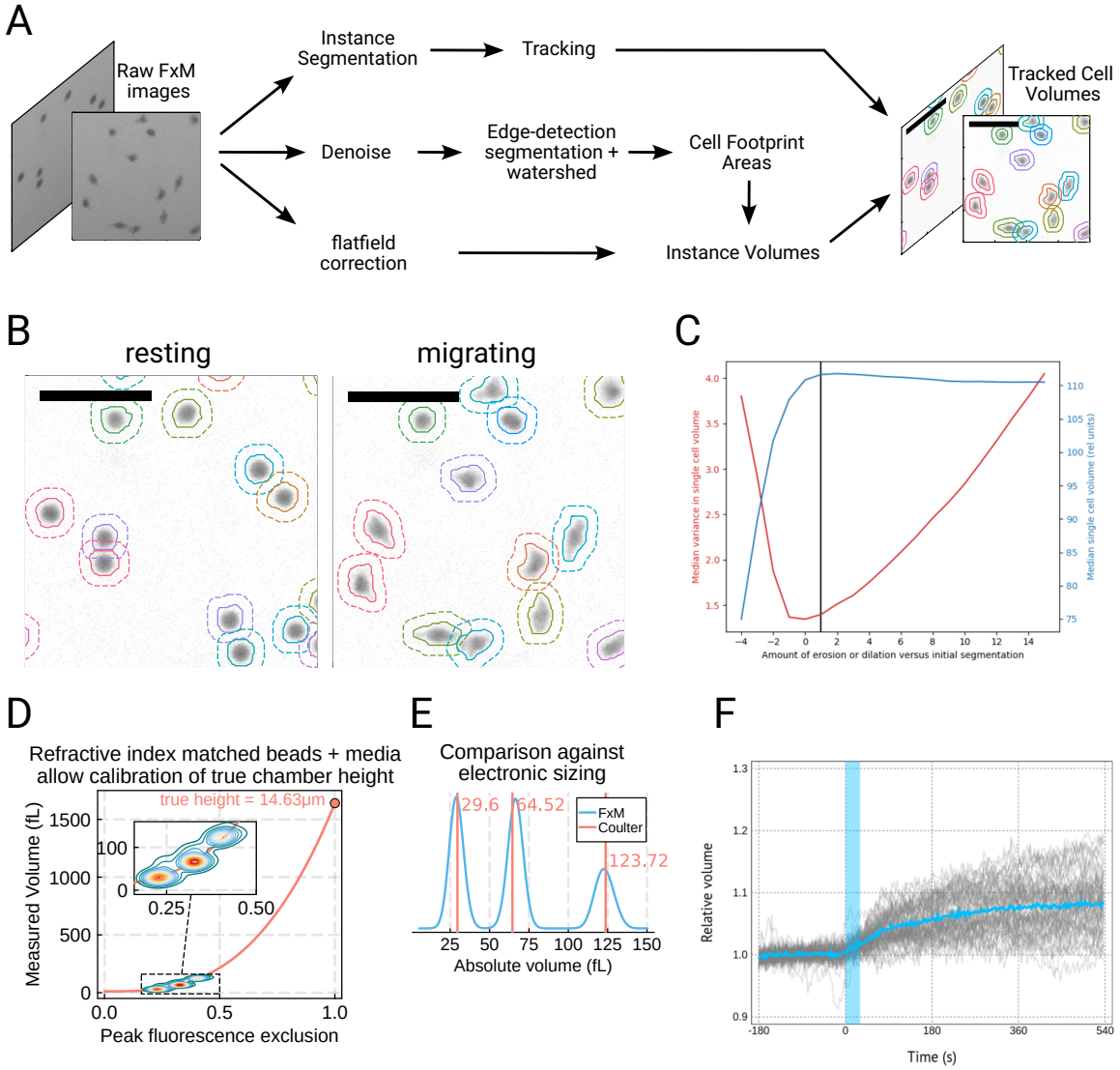


Figure S1. Details and validation of the Fluorescence eXclusion Microscopy pipeline
(**A**) Overview of the modified FxM pipeline used in this work. Raw FxM images are segmented into "seeds," which are then tracked. To identify cell boundaries, we use a custom algorithm that involves denoising the raw FxM followed by edge detection and watershedding that was nucleated at the seeds. Finally, to extract the volumes we apply minimal processing with a custom flatfield correction algorithm followed by extraction using the previously-determined cell boundaries. (**B**) Examples of resting (left) and migrating (right) cells segmented and tracked using the pipeline above (S1A). (**C**) Quantifying the signal-to-noise tradeoff with the edge detection. Overly conservative or overly liberal segmentation leads to non-optimal volume measurement. The chosen cutoff (black line) balances the noise (red) and measured volume (blue). This was computed on unstimulated cells. (**D**) Injecting beads into the FxM chambers in refractive-index media to minimize distortions allows for true calibration of chamber height. The contour plot of the per-bead max signal depth (i.e. height of the beads from FxM) vs the measured volume using FxM is well fit by the spherical volume formula (salmon line). The intersection of this line with 1.0 on the abscissa is equivalent to a sphere that completely fills the chambers and indicates the true height of the chamber. (**E**) Comparing calibrated FxM volumes of the beads (cyan) against the gold standard Coulter counter (salmon) shows good agreement. (**F**) dHL-60 cells treated with 1uM Latruculin-B swell in response to chemoattractant stimulation but lack cell spreading and spreading-related volume loss.

Ranking	HUGO ID	Fold Change	FDR	# Good sgRNAs	Common Name
1	**FPR1**	**4.4617**	**0.00248**	**3**	**FPR1**
2	STAT3	2.8815	0.00248	4	
3	**SLC9A1**	**3.5013**	**0.00495**	**4**	**NHE1**
4	**PIK3CG**	**3.3557**	**0.05569**	**4**	**PI3Kγ**
5	MARS2	23.6178	0.06374	3	
6	NUP35	14.5253	0.06374	3	
7	SKA1	3.3554	0.06374	4	
8	**CA2**	**2.8157**	**0.09942**	**4**	**CA2**
9	CANX	3.966	0.09942	4	
10	COPS3	8.2426	0.10015	4	
11	RPS2	18.7498	0.07976	3	
12	TPR	9.6024	0.16455	4	
13	RFT1	26.2401	0.16455	2	
14	SETD1A	11.1409	0.16455	2	
15	TP53TG3C	11.2083	0.16455	3	
16	UHRF1	4.7194	0.16455	3	
17	THG1L	10.4411	0.16455	3	
18	MRPL20	10.8506	0.16455	4	
19	UTP11L	9.0882	0.16455	3	
20	TPI1	17.976	0.16455	3	
21	CT47A6	2.8505	0.16455	3	
22	ESCO2	11.9249	0.1982	4	
23	GRXCR2	2.8457	0.1982	4	
24	PARP12	21.181	0.1982	2	
25	NR1H2	39.6651	0.20894	2	
26	PPP2R2A	4.4472	0.20894	4	
27	SLC25A26	20.7941	0.20894	2	
28	GANAB	2.7762	0.20894	3	
29	MMGT1	22.231	0.24088	2	
30	TCEB2	9.1192	0.26382	4	
31	MRPL17	9.465	0.26382	3	
32	C1QB	2.7157	0.26382	4	
33	TMX3	3.0917	0.26382	4	
34	TOPBP1	14.0471	0.16455	3	
35	AP3M1	7.9696	0.26528	2	
36	MSMB	4.5751	0.26528	4	
37	WDR83	5.4812	0.26528	4	
38	MARCH7	6.5514	0.2937	2	
39	RNF111	2.9736	0.2937	4	
40	MOGS	3.5169	0.2937	3	
100	**SLC4A2**	**2.582**	**0.54636**	**2**	**AE2**

Table S1. Chemoattractant-induced swelling genome-wide CRISPR KO screen hits
Rankings determined using MAGeCK Li et al. (2014). Fold change is the median fold enrichment in the dense bin versus the other two bins of the functional guides. FDR is the false discovery rate of each gene given the distribution of negative control guides in the library. See Methods section for details.

Volunteer	Age	Sex
4	27	M
5	30	M
6	37	F
8	31	M
14	24	M
17	29	F
18	28	M
19	30	M

Table S2. Volunteer Demographic Information
Demographic information collected for the volunteer donors according to the Institutional Review Board-approved study protocol at the University of California - San Francisco (Study #21-35147)

HUGO gene name	Takara sgRNA ID	Guide Sequence (5' -> 3')	Internal ID
FPR1	sgFPR1_2	CTACAGTACCTGGTAAAACG	11
FPR1	sgFPR1_3	CTGACAGCAACGATGGACAT	12
SLC9A1	sgSLC9A1_2	TTTGCCAACTACGAACACGT	13
SLC9A1	sgSLC9A1_4	TGAGGAACAGGTCACACATG	15
PIK3CG	sgPIK3CG_1	ACTTAACCCTCTCACAGCAG	16
PIK3CG	sgPIK3CG_3	GAGAATACGTCCTCCACATG	18
CA2	sgCA2_2	TATGAGTGTCGATGTCAACA	19
CA2	sgCA2_4	TCACTGGAACACCAAATATG	20
SLC4A2	sgSLC4A2_2	ACCTGCCCCACATACCCACA	21
SLC4A2	sgSLC4A2_3	GAAGACGCAGGACCTGATAG	22
NegCtrl	Neg_Control_Human_0067	GGTAGGACCTCACGGCGCGC	23
NegCtrl	Neg_Control_Human_0084	GCTGTCGTGTGGAGGCTATG	24

Table S3. Guides used to make single gene knockouts in HL-60s
The two highest performing guides from the genome-wide screen were chosen to make single gene knockouts in the HL-60 cell line. See Methods for details.

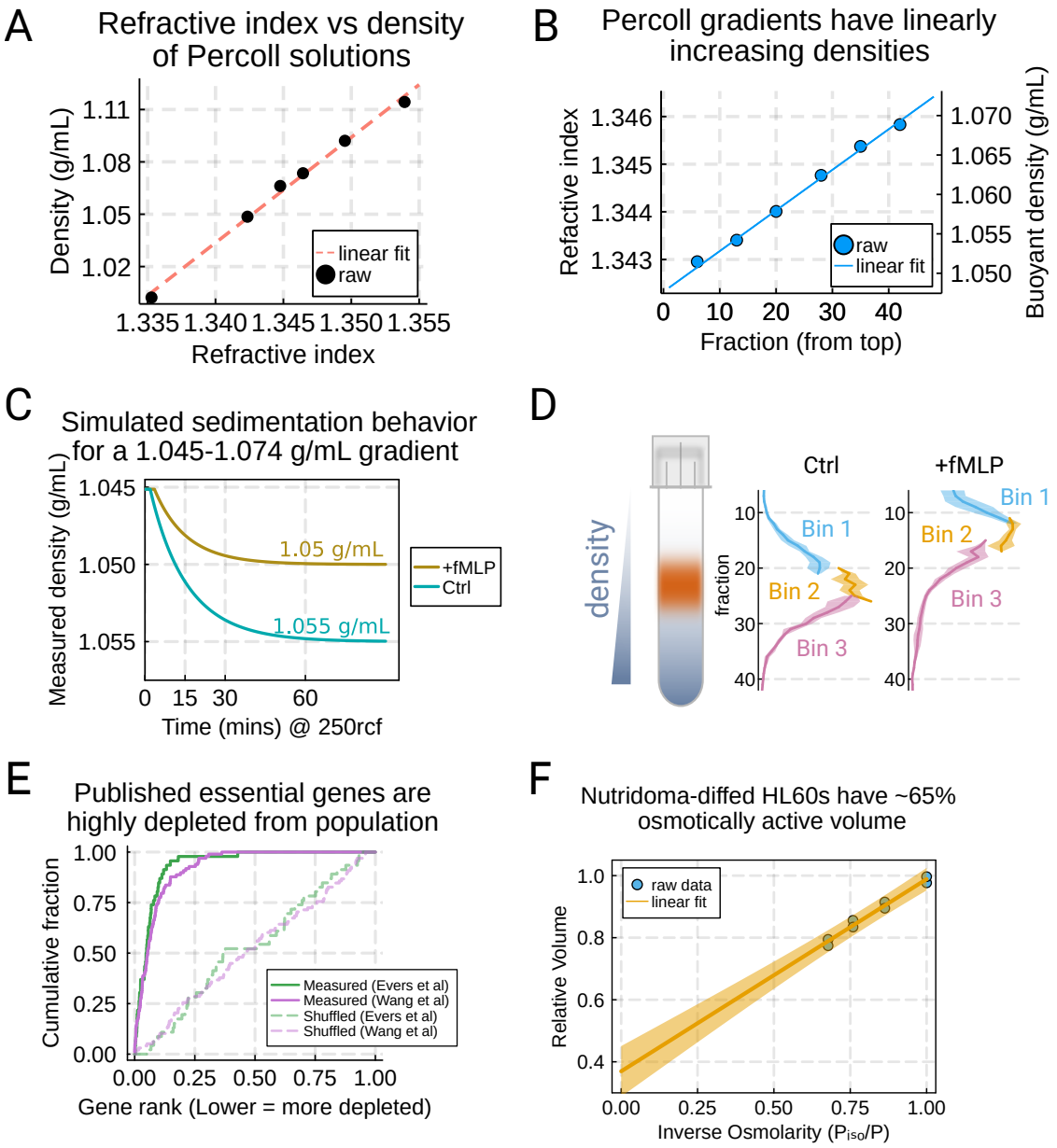


Figure S2. Validation of buoyant density assay and its use in CRISPR KO genome-wide screen for swelling regulators
(**A**) Varying the amount of Percoll shows the linear relationship between the refractive index (as measured by a refractometer) and the density as determined by weighing solutions in a volumetric flask on an analytical balance. (**B**) Measuring the refractive index of different fractions from the gradient shows a high degree of linearity in buoyant density. (**C**) Simulation of the settling behavior of the control (teal) and stimulated cells (gold) in the Percoll gradients under a centrifugal force of 250xg. The cells are predicted to arrive at their isopycnic point after approximately one hour. (**D**) The binning strategy for the screen for the control (left) and stimulated (right) conditions. For each replicate of each condition, the cells were split across 6 different tubes and these were combined into 3 bins to balance the minimum number of cells per bin with the resolution gained from multiple bins. (**E**) Previously published essential genes from Evers et al. (2016) and Wang et al. (2015), in green and purple, respectively, were highly depleted from the population, validating functionality of our CRISPR-based knockout library. (**F**) Ponder's relation for dHL-60s in suspension. Increasing amounts of hyperosmolarity drives the osmotically active fraction of the volume out of the cell, and projecting out to infinite osmolarity gives 65% of the cell volume as osmotically active.

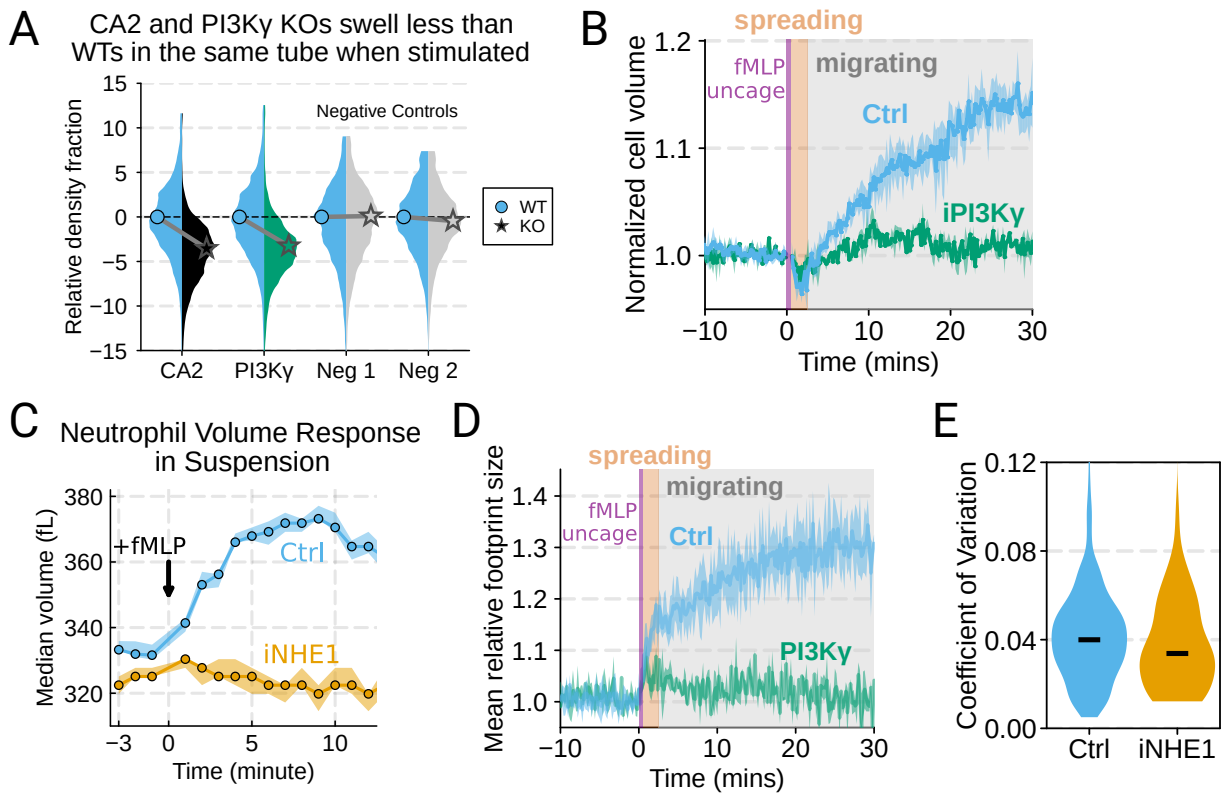


Figure S3. Additional validation of swelling screen hits

(**A**) Mixed WT and CRISPR KO dHL-60 populations post-stimulation show that CA2 (black) and PI3Ky (green) KO both fail to decrease their densities as much as the WT (cyan) population following chemoattractant stimulation. Cells with negative control guides (light grey) have normal volume responses. (**B**) PI3Kδ/γ inhibition completely blocks the chemoattractant-induced volume change in primary human neutrophils. (**C**) To validate the FxM results, primary human neutrophils were stimulated in suspension, and their volumes were measured using a Coulter counter (WT replicates = 4, NHE1 = 2). 20 nM fMLP was added at the 0 minute marker. (**D**) PI3Kδ/γ inhibition blocked the chemoattractant-drive shape change in human primary neutrophils, as measured by the change in footprint area in FxM (**E**) The coefficient of variation in volume for control (cyan) and iNHE1 (gold) human primary neutrophils undergoing chemokinesis are comparable, suggesting that the volume fluctuations are unchanged upon NHE1 inhibition despite the different baseline volumes.

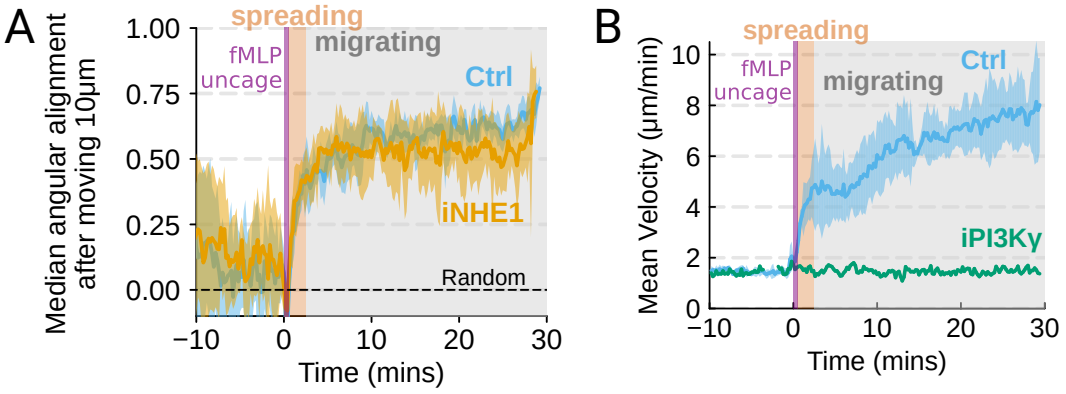
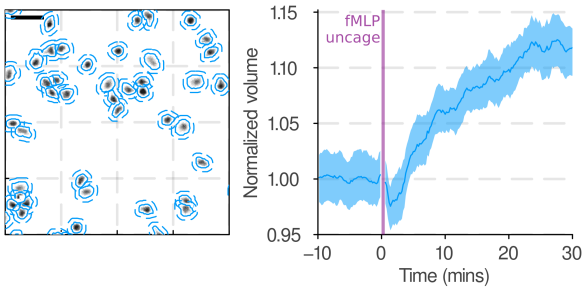


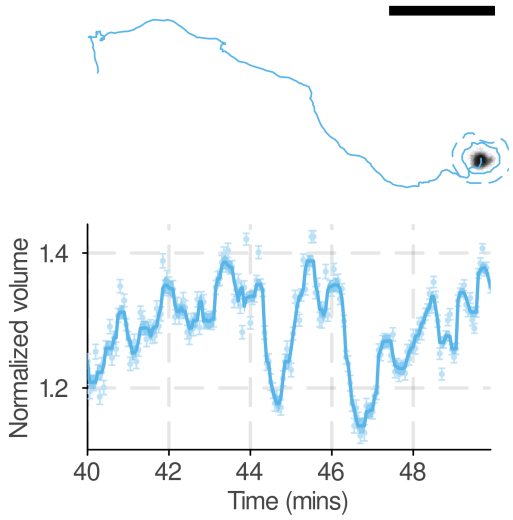
Figure S4. Additional validation of motility phenotypes

(**A**) Control neutrophils show an increased angular alignment upon stimulation as their motility becomes directional. NHE1-inhibition has very little effect on this process. (**B**) PI3Kδ/γ completely blocked the chemoattractant-induced motility increase in primary human neutrophils

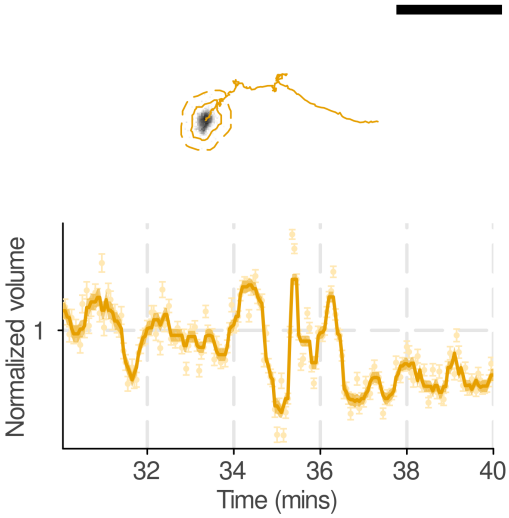
Supplementary Videos



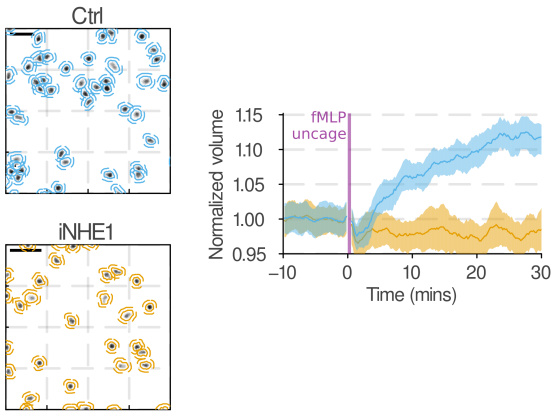
Video SV1. Primary human neutrophils show a biphasic volume response to chemoattractant stimulation
Left panel shows the individual cells (cyan solid lines) with their individual localities (dashed lines). The actual FxM signal is visible within the cell footprints. The movie is 40 minutes long with chemoattractant uncaging after the first 10 minutes. The scale bar is 50 um. The right panel shows the corresponding median volume of the population (cyan) with the 95% confidence interval (light cyan). The volume is relative to the average over the two minute window prior to uncaging.



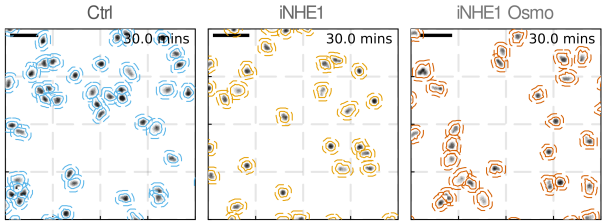
Video SV2. Single cell volume tracking reveals motility-associated volume changes in migrating primary human neutrophils
Top panel shows a representative cell migrating starting at 40 minutes following chemoattractant stimulation. The solid cyan line is the cell track. The cell's footprint is denoted with a solid cyan line while its local background is encapsulated by the dashed cyan line. The scale bar is 50 um. The bottom panel shows the concurrent volume changes with the raw FxM measurements displayed in light cyan and the rolling median is shown in cyan. The volume is normalized to the median cell volume in the two minute window prior to stimulation.



Video SV3. NHE1-inhibited primary human neutrophils retain the motility-related volume fluctuations but at much lower baseline volumes
Top panel shows a representative cell migrating starting at 30 minutes following chemoattractant stimulation. The solid gold line is the cell track and the cell's footprint is denoted with a solid gold line while its local background is encapsulated by the dashed gold line. The scale bar is 50 um. The bottom panel shows the concurrent volume changes with the raw FxM measurements displayed in light gold and the rolling median is shown in gold. The volume is normalized to the median cell volume in the two minute window prior to stimulation.



Video SV4. NHE1 inhibition blocks chemoattractant-induced cell swelling and impairs chemokinesis
Left panel shows the individual cells (cyan or gold solid lines) with their individual localities (dashed lines). The top left panel are control cells (cyan) and the bottom left are NHE1 inhibited (gold). The actual FxM signal is visible within the cell footprints. The movie is 40 minutes long with chemoattractant uncaging after the first 10 minutes. The scale bars are 50 um. The right panel shows the corresponding median volume of the population in cyan and gold for control and iNHE1, respectively. The corresponding 95% confidence interval is in light cyan or gold. The volume is relative to the average over the two minute window prior to uncaging.



Video SV5. NHE1-inhibition leads to impaired motility versus control, which is rescued by mild hypoosmotic shock
Each panel is a representative video of control, NHE1-inhibited, and hypoosmotically shocked NHE1-inhibited cells, respectively. Each video is 40 minutes long and chemoattractant uncaging occurs after 10 minutes. Scale bars are 50 um.