NHX-type $Na^+(K^+)/H^+$ antiporter activity is required for endomembrane trafficking and ion homeostasis in *Arabidopsis thaliana*

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Abstract

The regulation of ion and pH homeostasis of endomembrane organelles is critical for functional protein trafficking, sorting and modification in eukaryotic cells. pH homeostasis is maintained through the activity of vacuolar H^+-ATPases (V-ATPases) pumping protons (H^+) into the endomembrane lumen, and counter-action by cation/proton exchangers such as the NHX family of $Na^+(K^+)/H^+$ exchangers. In plants, disturbing V-ATPase activity at the *trans*-Golgi network/early endosome (TGN/EE) results in impairment of secretory and endocytic trafficking. However, it is not clear if knock out of endosomal NHX type antiporters cause similar trafficking defects, and whether this is due to a disruption of ion or pH homeostasis. Here we show through genetic, pharmacological, and live-cell imaging approaches that *nhx5 nhx6* double knockouts have defects in Golgi and TGN/EE motility, protein recycling at the TGN/EE, but not the secretion of transmembrane proteins. Furthermore, we report that NHX5 and NHX6 are required for a novel mechanism of osmotic swelling of late endosomes induced by treatment with the phosphatidylinositol 3/4-kinase inhibitor wortmannin. This wortmannin swelling-insensitive phenotype appears linked to the insensitivity of *nhx5 nhx6* TGN/EE to swelling induced with the monovalent cation ionophore monensin, and suggests that NHX5 and NHX6 are required for maintaining endosomal cation homeostasis. Lastly, we report that the distal region of the cytosolic tail of NHX6 is required for mediating NHX6 localisation to late endosomes, but does not appear to be essential for NHX6 function.

Introduction

The endomembrane system of eukaryotic cells is composed of a complex series of interconnected compartments which function in the synthesis, sorting, transport and degradation of proteins. Regulation of pH homeostasis in endomembrane organelles is critical for functional protein sorting, trafficking and modification (Casey et al., 2010). In plants, vacuolar type H^+-ATPases (V-ATPases) on the TGN/EE and tonoplast pump H^+ ions into the lumen to generate proton gradients and drive luminal acidification (Schumacher, 2014). Conversely, cation/proton exchangers such as the NHX family of $Na^+(K^+)/H^+$ antiporters, act as a proton leak to alkalinise the lumen of endosomal compartments and the vacuole and assist in fine tuning organelle pH. Recent work has shown the pH gradient in the endomembrane system in plants differs from animals, with the TGN/EE as the most acidic endomembrane compartment (Martinière et al., 2013; Shen et al., 2013), and this has functional consequences for the site of receptor ligand binding and release (Früholz et al., 2018; Künzl et al., 2016).

Arabidopsis thaliana contains eight NHX isoforms; four tonoplast localised isoforms (AtNHX1-

AtNHX4), two endosomal isoforms (AtNHX5-AtNHX6), and two plasma membrane isoforms (AtNHX7/SOS1 and AtNHX8) (Brett et al., 2005b). Intracellular NHX-type antiporters are evolutionarily conserved transporters which function in ion and pH homeostasis, and in plants play roles in development and vacuolar trafficking (Bassil et al., 2012; Chanroj et al., 2012; Dragwidge et al., 2018; Rodríguez-Rosales et al., 2009). Double knockouts of the *A.thaliana* endosomal NHX isoforms *nhx5 nhx6* have delayed trafficking of the endocytic tracer dye FM4-64 to the vacuole, and disruptions to sorting of a vacuolar targeted yeast carboxypeptidase-Y fragment (Bassil et al., 2011a). NHX5 and NHX6 have also recently been implicated in processing and transport of seed storage proteins to the vacuole in embryos (Ashnest et al., 2015; Reguera et al., 2015). Similar vacuolar trafficking defects have been described in yeast, with the knockout of the single endosomal *nhx1* gene causing altered CPY secretion, delayed vacuolar trafficking, and defects in multi-vesicular body (MVB) formation and sorting (Bowers et al., 2000; Brett et al., 2005a; Kallay et al., 2011; Mitsui et al., 2011). Furthermore, RNAi silencing of mammalian endosomal orthologs *NHE6* and *NHE8* leads to disruptions in endosome trafficking and recycling (Lawrence et al., 2010; Ohgaki et al., 2010), demonstrating the conserved role of eukaryotic endosomal NHXs in subcellular protein trafficking and recycling.

Unlike animal cells, in plant cells the *trans*-Golgi network also acts as an early endosome where the endocytic and secretory pathways converge (Viotti et al., 2010). Soluble proteins destined for vacuolar degradation can be recycled at the TGN/EE by vacuolar sorting receptors (VSRs) (Künzl et al., 2016), or are otherwise transported by budding and maturation of the TGN/EE into the MVB/LE, which then ultimately fuse with the vacuole (Scheuring et al., 2011). In *A. thaliana* the *nhx5 nhx6* T-DNA double knockouts endomembrane compartments are hyper-acidified (Reguera et al., 2015), and this is believed to underlie defects in receptor mediated recycling of VSRs, processing of seed storage proteins, and vacuolar trafficking in these mutants (Ashnest et al., 2015; Reguera et al., 2015). Conversely, reduction of V-ATPase activity at the TGN/EE through Concanamycin-A treatment or in the *det3* mutant results in alkalisation of the TGN/EE, and leads to defects in recycling and secretion pathways, including delayed trafficking to the vacuole and reduced Golgi and TGN/EE motility (Dettmer et al., 2006; Luo et al., 2015; Viotti et al., 2010). This data demonstrates that the functional acidification of the TGN/EE is essential for not just vacuolar trafficking, but also protein secretion and recycling. While it is clear that NHX5 and NHX6 play roles in vacuolar trafficking of soluble cargo proteins, it has not been shown whether the disrupted pH and ion balance of endosomal compartments in *nhx5 nhx6* results in defects in protein secretion, sorting and recycling pathways of transmembrane proteins.

Here we investigated the effects of disrupted endomembrane pH and ion balance through dissection of the secretory and endocytic transport pathways in the double knockout *nhx5 nhx6*. Through live cell-imaging we reveal that *nhx5 nhx6* mutants have reduced Golgi and TGN/EE motility and defects in the recycling of transmembrane receptors from the TGN/EE. Furthermore, our results reveal that *nhx5 nhx6* endosomes are insensitive to osmotic swelling induced by the ionophore monensin, or with the late endosome inhibitor wortmannin. Furthermore, we identified that the cytosolic tail of NHX6 is required for mediating NHX6 localisation to the late endosome, but is not essential for ion regulation.

Results

NHX5 and NHX6 are involved in endomembrane compartment motility

In plant cells the movement of endomembrane organelles through the secretory and endocytic pathways is essential for functional protein delivery, and is highly dependent on the cytoskeleton network of actin filaments and microtubules (Brandizzi and Wasteneys, 2013). As alkalinisation of the TGN/EE has been shown to reduce Golgi and TGN/EE motility (Luo et al., 2015), we questioned whether the acidification of endomembrane organelles in *nhx5 nhx6* could also negatively affect their motility. We generated stable *nhx5 nhx6* lines in Arabidopsis expressing the endosomal markers YFP-Got1p (Golgi), and YFP-VTI12 (TGN/EE) and examined endosomal motility through live cell spinning disk confocal microscopy. Quantitative analysis revealed that the movement of Golgi and TGN/EE vesicles were significantly reduced in *nhx5 nhx6* cells compared to wild type (Fig. 1A-E, S1A-B). Additionally, the proportion of slower moving bodies (< 10 µm min^{-1}) was more than two-fold higher in *nhx5 nhx6* compared to wild type, demonstrating that a high proportion of vesicles exhibited minimal movement in *nhx5 nhx6* (Fig. S1C). We also assessed the straightness of particle tracks to determine whether organelle behaviour, or their potential association with the cytoskeleton may be altered. Quantification revealed a significant reduction in TGN/EE track straightness in *nhx5 nhx6* cells, indicating that these vesicles displayed increased disordered, non-continuous movement which is typical of cytoskeletal independent endosome movement (Fig. 1E) (Akkerman et al., 2011).

BRI1 recycling, but not secretion is reduced in *nhx5 nhx6*

Next, we investigated whether the transport or recycling of transmembrane receptors at the TGN/EE may be inhibited in *nhx5 nhx6* cells. We employed the well characterised receptor kinase BRASSINOSTEROID-INSENSITVE 1 (BRI1) which is constitutively endocytosed from the plasma membrane to the TGN/EE, where it is sorted between recycling to the plasma membrane or degradation at the vacuole (Dettmer et al., 2006; Geldner et al., 2007; Irani et

al., 2012). We treated root cells expressing BRI1-GFP with the fungal toxin Brefeldin-A (BFA) to reversibly inhibit TGN/EE and Golgi trafficking (Geldner et al., 2001; Richter et al., 2007), and assessed the recycling of BRI1-GFP out of BFA bodies after washout (Fig. 2A). Quantification revealed that *nhx5 nhx6* cells had larger BFA bodies and a higher proportion of cells containing BFA bodies after washout (Fig. 2B - C). These results indicate that BRI1 recycling from the TGN/EE is impaired in *nhx5 nhx6,* and together with similar BRI1 recycling defects in *det3* mutants (Luo et al., 2015), suggests pH sensitive trafficking machinery are required for efficient BRI1 recycling. We also assessed growth response of *nhx5 nhx6* treated with the V-ATPase inhibitor Concanamycin A (ConcA) which disrupts TGN/EE structure and endocytic and secretory trafficking (Dettmer et al., 2006; Viotti et al., 2010). *nhx5 nhx6* seedlings showed similar hypersensitivy to ConcA as *det3*, demonstrating that maintaining pH homeostasis at the TGN/EE is important for TGN/EE function (Fig. S2).

Dysregulation of TGN/EE V-ATPase activity has been implicated in defects in protein secretion and delivery of proteins to the plasma membrane (Dettmer et al., 2006; Luo et al., 2015), suggesting that these pathways may be sensitive to general pH disruptions. We first assessed whether steady state levels of BRI1-GFP at the plasma membrane may be reduced in *nhx5 nhx6*, but found no difference in BRI1-GFP fluorescence at the plasma membrane compared to wild type (Fig. 3A-B). Furthermore, fluorescence recovery after photobleaching (FRAP) experiments revealed no difference BRI1-GFP recovery to the plasma membrane in *nhx5 nhx6*, suggesting that the delivery of newly synthesised BRI1-GFP to the plasma membrane was not significantly reduced (Fig. 3C-D). We also assessed whether endocytosis may be disrupted in *nhx5 nhx6* using the endocytic tracer dye FM5-95 (FM4-64 analogue), but found no clear difference in endocytic uptake of FM (Fig. S3). Taken together, these findings indicate that the reduced recycling of BRI1 from the TGN/EE in *nhx5 nhx6* is insufficient to significantly affect steady state BRI1-GFP levels at the plasma membrane, and suggests that NHX5 and NHX6 are not required for functional BRI1 delivery to the plasma membrane.

NHX5 and NHX6 antiporter activity is required for wortmannin induced swelling of MVBs

As NHX5 and NHX6 have been reported to localise to the late endosome / multi-vesicular body (LE/MVB) (Reguera et al., 2015), we questioned whether trafficking or function at the LE/MVB could be affected in *nhx5 nhx6* mutants. Wortmannin inhibits phosphatidylinositol 3-kinases (PI3K) and PI4K at high concentrations (>30 µM) and has been used extensively to investigate late endosome trafficking in plants (Jaillais et al., 2006; Vermeer et al., 2006). In wild type root cells expressing the Rab5-like GTPase YFP-ARA7 (RABF2b) as a LE/MVB marker, wortmannin induced enlarged ring-like structures (Fig 4A). These wortmannin bodies were associated, but not completely fused with TGN/EE labelled with the SNARE VTI12 (Fig S4). While similar number of wortmannin bodies were present in *nhx5 nhx6* root cells compared to wild type, they were significantly smaller and denser, and did not exhibit the characteristic ring-like shape (Fig. 4A-B). To test if these wortmannin induced fusion defects were dependent on pH regulation by the antiporter activity of NHX6, we generated an antiporter inactive NHX6 by mutating the highly conserved acidic Asp194 residue which is critical for Na^+ and H^+ ion binding (Lee et al., 2013; Wang et al., 2015), and fused it to EGFP (Fig. S5A). This mutated $NHX6_{D194N}$-EGFP reporter did not rescue growth impairment in *nhx5 nhx6* (Fig. S5B), but localised correctly to core and peripheral BFA compartments as previously reported with functional NHX5/6 (Fig. S5C) (Bassil et al., 2011a). Additionally, $NHX6_{D194N}$-EGFP could not rescue the wortmannin induced LE/MVB swelling insensitivity in *nhx5 nhx6* (Fig. 4A-B).

To determine if the wortmannin induced bodies in *nhx5 nhx6* were structurally similar to those in wild type, we exploited the fact that reducing the confocal pinhole size increases resolution in x, y and z dimensions. Using a reduced pinhole, we resolved the structure of wortmannin bodies using *nhx5 nhx6* root cap cells and identified ring-like structures similar to wild type (Fig. 4C). Moreover, since wortmannin inhibits both PI3K and PI4K at high concentrations, we also assessed whether *nhx5 nhx6* swelling insensitivity was present during PI3K specific inhibition. Specifically targeting PI3K pathways by using the inhibitor LY294002 or with low concentrations of wortmannin (Fujimoto et al., 2015; Simon et al., 2016; Takáč et al., 2013), also caused similar fusion of MVBs into smaller, more densely labelled bodies in *nhx5 nhx6* cells (Fig. 4D). This suggests that swelling is induced by inhibition of PI(3)P on the LE/MVB (Fig 4E). Taken together, this data shows that along with inducing LE/MVB fusion, wortmannin induces rapid osmotic swelling of fused MVB bodies, consistent with data showing wortmannin causes alkalinisation of LE/MVBs (Martinière et al., 2013). Thus, the insensitivity to swelling in *nhx5 nhx6* are a consequence of the lack of normal ion or pH regulation mediated by NHX5

and NHX6 antiporter activity.

NHX5 and NHX6 do not regulate root vacuole morphology

In plants, the primary vacuolar transport pathway is marked by the co-ordinated sequential activity of the Rab GTPases Rab5 (RabF) and Rab7 (RabG) (Cui et al., 2014; Cui et al., 2016). This pathway is also implicated in the transport of storage proteins to the protein storage vacuole (PSV) in seeds (Ebine et al., 2014; Singh et al., 2014), which has shown to be disrupted in *nhx5 nhx6* (Ashnest et al., 2015; Reguera et al., 2015). However, it is not clear whether vacuolar transport pathways could be affected in root tissue of *nhx5 nhx6*. To investigate Rab5 mediated vacuolar transport, we examined the localisation of ARA7QL (RabF2bQL), a constitutively active GTP-bound mutant of ARA7 which localises to the LE/MVB and tonoplast (Ebine et al., 2011). While we observed no clear difference in ARA7QL localisation between wild type and *nhx5 nhx6* in root cells, we observed a similar insensitivity to swelling induced by wortmannin in *nhx5 nhx6* (Fig S6A). Furthermore, as endosomal NHX type antiporter activity has been previously reported to be implicated in vacuolar trafficking and fusion in the yeast *nhx1* mutant (Qiu and Fratti, 2010), we also examined vacuole morphology in *nhx5 nhx6* root cells, but found no clear abnormalities in vacuolar structure or response to wortmannin (Fig S5B-C). Together these results suggest NHX5 and NHX6 are not directly required for vacuole function in the root.

***nhx5 nhx6* endosomes have reduced sensitivity to monensin**

Since NHXs regulate Na^+ and K^+ accumulation in the endosomal lumen, we questioned whether the reduced swelling of LE/MVB induced by wortmannin in *nhx5 nhx6* could be due to an altered ionic composition in the LE/MVB lumen. The monovalent cation ionophore monensin induces rapid osmotic swelling of *trans*-Golgi stacks and TGN/EE through transport of Na^+/K^+ for H^+ across the endomembrane (Zhang et al., 1993). Consistent with this data, we observed rapid swelling TGN/EE, but not of LE/MVB in root cells (Fig 5A). Next, we assessed the pH of TGN/EE after monensin treatment using the TGN/EE localised ratiometric pH sensor SYP61-pHusion (Luo et al., 2015). TGN/EE of monensin treated root cells were less acidic than untreated cells, indicating a reduction in H^+, consistent with monensin induced luminal import of Na^+/K^+ (Fig 5B). We also assessed the pH of TGN/EE of *nhx5 nhx6* root cells and found a ~0.5 pH reduction (acidification) of TGN/EE (Fig 5C), similar to previous reports in Arabidopsis protoplasts (Reguera et al., 2015).

Given the increased acidity of *nhx5 nhx6* TGN/EE, we questioned whether *nhx5 nhx6* root cells could be hypersensitive to swelling induced by monensin, given they produce a stronger

proton gradient for monensin to act upon. We therefore assessed the response to monensin using established Golgi and TGN/EE markers in *nhx5 nhx6*. We could not detect any significant swelling of Golgi in either wild type or *nhx5 nhx6* monensin treated root cells, likely as the *trans* Golgi stack only swells slightly (Fig. 5D) (Zhang et al., 1993). TGN/EE in monensin treated roots showed clear clustering and swelling in wild type, however in *nhx5 nhx6* only minor swelling was seen despite clustering of TGN/EE, suggesting these TGN/EE had reduced capacity to swell (Fig. 5D). Furthermore, similar results were obtained using $NHX6_{D194N}$-EGFP as a marker for NHX6 activity in wild type and *nhx5 nhx6* (Fig. 5D). Together, these results suggest that *nhx5 nhx6* have reduced or slowed osmotic swelling induced by monensin, likely originating from a disruption to intraluminal ion (K^+) balance in these endosomes.

The C-terminal cytosolic tail of NHX6 mediates its localisation to the MVB

We previously reported that the cytosolic tail of NHX6 interacts with the retromer component SNX1 (Ashnest et al., 2015), however it is unclear what functional significance this interaction has, and whether the cytosolic tail mediates other functions. To investigate this, we generated a partial tail truncation of NHX6 lacking a short 28 amino acid region of the C-terminus fused to YFP (Fig. 6A), as a previous truncation lacking the entire C-terminal tail did not show stable expression (Ashnest et al., 2015). This $NHX6_{1\text{-}507}$-YFP construct completely complemented the dwarf phenotype of *nhx5 nhx6* plants (Fig. 6B), suggesting that this distal region of tail was not essential for NHX6 antiporter activity.

We inferred the localisation of this tail truncated, but antiporter active protein through pharmacological inhibitor experiments. $NHX6_{1\text{-}507}$-YFP was BFA sensitive, localising to core and peripheral BFA compartments, correspond to the TGN/EE and Golgi respectively (Fig 6C) (Naramoto et al., 2014; Richter et al., 2007), similar to full length NHX6 (Fig. S5). Moreover, $NHX6_{1\text{-}507}$-YFP was able to restore monensin insensitivity of *nhx5 nhx6*, confirming antiporter function at the TGN/EE. However, in response to inhibition of late endosomal trafficking by wortmannin, $NHX6_{1\text{-}507}$-YFP was only partially associated with wortmannin bodies unlike the full length NHX6 (Fig. 6E-F), a response typical of slow fusion of TGN/EE markers with the wortmannin body (Fig. S4), and suggested $NHX6_{1\text{-}507}$-YFP may be absent from the MVB. Surprisingly, in these wortmannin treated seedlings, the enlarged wortmannin bodies were morphologically similar to wild type, indicating $NHX6_{1\text{-}507}$-YFP can also restore the wortmannin induced swelling insensitivity in *nhx5 nhx6* (Fig. 6E). As the LE/MVB matures from TGN/EE derived compartments (Scheuring et al., 2011), $NHX6_{1\text{-}507}$-YFP antiporter activity at the Golgi and TGN/EE may be sufficient to maintain relatively normal pH in LE/MVB compartments, and thus may restore normal MVB function (Fig. 6G). Taken together, this data indicates that the

distal cytosolic tail region of NHX6 mediates its localisation to the LE/MVB, but NHX6 activity at the MVB is not essential for wortmannin induced MVB swelling.

Discussion

Despite clear evidence showing NHX5 and NHX6 are involved in vacuolar trafficking of soluble proteins in *A. thaliana* seeds (Ashnest et al., 2015; Reguera et al., 2015), the importance of endosomal NHX activity in endocytic and secretory transport in roots is not well described. NHX5 and NHX6 localise to a large proportion of the secretory and endocytic pathways - specifically the Golgi, TGN/EE, and LE/MVB (Bassil et al., 2011a; Reguera et al., 2015). Both NHX5 and NHX6 activity through regulating endomembrane luminal alkalinisation (Reguera et al., 2015), and cytosolic tail mediated protein-protein interactions (Ashnest et al., 2015) could potentially effect endomembrane sorting and trafficking pathways. Consistently, disruption of V-ATPase mediated acidification of the TGN/EE is linked to defects in both secretory and endocytic trafficking (Dettmer et al., 2006; Luo et al., 2015). Weak V-ATPase *det3* mutants display defects in secretion and recycling of BRI1, Golgi and TGN/EE motility, as well as a similarly described delay of endocytic trafficking to the vacuole as observed in *nhx5 nhx6* (Bassil et al., 2011a; Luo et al., 2015). Here we provide new evidence that shows NHX5 and NHX6 activity is essential for functional endomembrane trafficking.

The NHX6 C-terminal cytosolic tail is important for localisation to the MVB

We previously reported that the cytosolic tail of NHX6 was essential for NHX6 activity, protein stability and interaction with SNX1 (Ashnest et al., 2015). Here, we generated a partial tail deletion construct ($NHX6_{1-507}$-YFP) which appeared to be fully functional as it could completely restore the growth of *nhx5 nhx6* mutants. Pharmacological inference of $NHX6_{1-507}$-YFP localisation revealed that this distal region (amino acids 508-535) of the cytosolic tail is required for mediating NHX6 localisation to the LE/MVB. While the cytosolic tail of the K^+ transporter CHX17 has also been reported to mediate its localisation to the MVB (Chanroj et al., 2013), lack of significant sequence similarity suggests there is unlikely to be a strict sequence based sorting mechanism mediating endosomal cation/proton exchanger localisation. It is still unclear whether a conserved amino acid motif in this region, and/or in combination with other signals in the transmembrane domain may mediate the sorting of NHX5 and NHX6 or other endosomal transporters to the LE/MVB.

NHX5 and NHX6 are required for endosome motility

The movement of endomembrane organelles through the endocytic and secretory pathways is essential for functional protein delivery, and depends on the cytoskeleton network of actin filaments and microtubules (Brandizzi and Wasteneys, 2013). The mechanisms behind endosome-cytoskeletal movement is therefore of great interest. Here we report that Golgi and TGN/EE motility is significantly reduced in *nhx5 nhx6* hypocotyl cells, and that the behaviour of TGN/EE is altered, suggestive of a reduction in the ability of these TGN/EE to association with the cytoskeleton. These findings are similar to Golgi and TGN/EE motility defects observed in *det3* mutants which have altered TGN/EE pH (Luo et al., 2015). Collectively, these data indicate a pH sensitive mechanism governs endosome-cytoskeleton association. As the Golgi and TGN/EE have been implicated in actin mediated movement (Akkerman et al., 2011; Asaoka et al., 2013), endomembrane pH dysregulation may impair the function of actin-myosin motor proteins.

NHX5 and NHX6 play roles in recycling at the TGN/EE

In plants the sorting and recycling of membrane proteins at the TGN/EE to and from the plasma membrane is vital for controlling their abundance and activity at the plasma membrane. Hyper-alkalinisation of the TGN/EE vesicles has been shown to impair recycling of BRI1-GFP from the TGN/EE, as well as impair general BRI1 secretion to the plasma membrane (Luo et al., 2015). We did not observe any clear defects in secretion of BRI1-GFP to the plasma membrane, indicating that trafficking of plasma membrane proteins does not require NHX mediated pH regulation. However, our BFA washout experiments revealed a significant impairment in recycling of BRI1-GFP out of BFA bodies in *nhx5 nhx6*, suggesting that functional BRI1 recycling occurs through a pH sensitive TGN/EE recycling pathway/mechanism. This idea is consistent with *nhx5 nhx6* double mutants showing similar hypersensitivity to Concanamycin A treatment as *det3*, implying a defect at the TGN/EE. Surprisingly, we previously reported that the transport of the auxin carrier proteins PIN1-GFP and PIN2-GFP from the TGN/EE was not significantly impaired in *nhx5 nhx6* root cells (Dragwidge et al., 2018). Since these proteins localise polarly to the basal or apical plasma membrane respectively through distinct TGN/EE to plasma membrane routes (Li et al., 2016), this suggests that NHX5 and NHX6 function in non-polar TGN/EE trafficking pathways.

How NHX5 and NHX6 affect trafficking at the TGN/EE is unclear. In animals and *Drosophila*, NHX and V-ATPase activity has been shown to effect electrostatics at the cytosolic surface of endomembranes which can affect membrane signalling or protein recruitment. Similarly, endosomal V-ATPase activity is required for recruitment of the small GTPase Arf6 In mammalian cells (Hurtado-Lorenzo et al., 2006), while pH- and charge-dependent Wnt signalling at the plasma membrane is regulated by Nhe2 activity in Drosophila (Simons et al.,

2009). Thus, potential disruptions to endomembrane electrostatics in *nhx5 nhx6* may influence the charge-dependent recruitment of small GTPases or Arfs involved in protein trafficking or recycling. Further investigation of endosomal trafficking pathways through selective trafficking inhibitors such as Endosidin compounds may uncover a clearer understanding of the specific trafficking pathways which require NHX5 and NHX6 activity (Doyle et al., 2015; Hicks and Raikhel, 2010; Li et al., 2016).

Regulation of endosomal ion composition by NHX5 and NHX6

Here we identified a novel mechanism of swelling of late endosomes induced by wortmannin which shares a striking resemblance to osmotic swelling of TGN/EE induced by the cation ionophore monensin. While wortmannin is well described to cause enlargement of LE/MVBs from homotypic membrane fusion of MVBs (Wang et al., 2009; Zheng et al., 2014), the typical size of these wortmannin bodies is much larger than can be achieved through membrane fusion alone. Our data suggests that wortmannin induces osmotic swelling likely through rapid influx of K^+ ions. Monensin induced TGN/EE swelling occurs through Na^+/K^+ transport into the endosomal lumen across a proton gradient (Zhang et al., 1993), resulting in lumenal alkalinisation of endosomes consistent with our reported pH measurements. This is consistent with evidence showing wortmannin treatment induces alkalinisation of the LE/MVB (Martinière et al., 2013), suggesting wortmannin swelling occurs through luminal cation import.

As plant NHXs have a clear function in intracellular internalisation of Na^+ and K^+ (Bassil et al., 2011a; Bassil et al., 2011b), the luminal cation composition of endosomes in *nhx5 nhx6* should have reduced K^+ concentrations. We postulate that *nhx5 nhx6* insensitivity to swelling by wortmannin and monensin have similar mechanisms, and originate from an imbalance in lumenal K^+ at the TGN/EE. Thus, the necessary lumenal K^+ import required to generate osmotic swelling is much higher in *nhx5 nhx6*. This is consistent with our monensin experiments which revealed aggregation of TGN/EE, but reduced swelling in *nhx5 nhx6* compared to lines containing functional NHX5 or NHX6 activity. Surprisingly, activity of the $NHX6_{1\text{-}507}$-YFP reporter restores both monensin and wortmannin insensitivity to swelling, despite localising to the Golgi and TGN/EE but not the LE/MVB. However, as the MVB matures from the TGN/EE by budding (Scheuring et al., 2011), the MVB will likely share a similar ion composition from its source membrane. Furthermore, while the pH of *nhx5 nhx6* endosomes is hyper-acidified and thus possess a greater proton gradient available for monensin cation transport, this does not result in more rapid swelling as previously proposed (Zhang et al., 1993), indicating that the initial ion composition of the endosomal lumen is the most important factor in propensity to swell. Thus, NHX activity at the MVB appears largely inconsequential for maintaining ion balance at the MVB.

It is currently unclear how the presumed ion import is induced by wortmannin in fused late endosomes. Since NHX6$^{1-507}$-YFP activity at the TGN/EE but not MVB could restore wortmannin swelling insensitivity, this suggests that potential K^+ influx occurs independently of endosomal NHX5 and NHX6 activity. This could involve ion import into the MVB lumen by the wortmannin sensitive K^+/H^+ transporter AtCHX17 (Chanroj et al., 2013), or could be a general consequence from rapid homotypic fusion of LE/MVB. We speculate that inhibition of PI3K through wortmannin or LY294002 and the resulting loss of LE/MVB membrane identity could lead to uninhibition of transporters therefore facilitating ion influx and inducing osmotic swelling. It would be interesting to investigate this directly by assessing endosomal K^+ concentrations *in vivo* using genetically encoded fluorescent K^+ probes recently established (Bischof et al., 2017).

Here we show that endosomal pH and ion regulation by plant NHXs is important for functional endosomal behaviour. We demonstrate that NHX5 and NHX6 activity is involved in Golgi and TGN/EE motility, protein recycling at the TGN/EE, and for regulation of endomembrane ion balance. This work sheds light on the complex nature of the plant endomembrane system, and demonstrates the importance of regulation of endomembrane ion and pH homeostasis by NHX5 and NHX6.

Materials and Methods

Plant material and growth conditions

Arabidopsis thaliana lines were all in the Columbia-0 (Col-0) accession background. Plant lines used have been previously described, *nhx5-1 nhx6-1* (Bassil et al., 2011a)*, nhx5-2 nhx6-3* (Ashnest et al., 2015), *det3* (Schumacher et al., 1999), pBRI1::BRI1–GFP (Geldner et al., 2007), GFP-ARA7Q69L (Ebine et al., 2011), pUBQ10::xFP-RabF2b (Wave2Y/R), pUBQ10::YFP-Got1p (Wave18Y), pUBQ10::xFP-VAMP711 (Wave 9Y/R), pUBQ10::YFP-VTI12 (Wave13Y) (Geldner et al., 2009), VHA-a1-GFP x mRFP-ARA7 and 2xFYVE-GFP x VHA-a1-mRFP (Singh et al., 2014). The *nhx5-2 nhx6-3* allele combination was used for all experiments except for the SYP61-pHusion pH measurements and ConcA hypocotyl assay where *nhx5-1 nhx6-1* was used. BRI1-GFP in *nhx5 nhx6* was generated by crossing BRI1-GFP into NHX5 / *nhx5 nhx6* plants, and *nhx5 nhx6* plants homozygous for BRI-GFP were identified in the following generations. The *nhx5 nhx6* lines expressing other fluorescent markers were obtained by floral dripping (Martinez-Trujillo et al., 2004) using Agrobacterium *tumefaciens* GV3101 strain cultures containing the given constructs.

Seeds were surface sterilized with 70% ethanol for 5 minutes, 10% bleach for 5 minutes, and washed three times in ddH_2O and grown on ½ strength Murashige and Skoog (½ MS) medium containing 1.0% (w/v) agar, pH 5.8 without sucrose unless indicated. Seedlings were stratified for 48 hours at 4°C in the dark, and grown in a 16hr light /8hr dark photoperiod at 22°C at 100 umol m-2s-1 under cool-white fluorescent lights.

For live cell microscopy and chemical treatments, seedlings were grown vertically on ½ MS plates without sucrose. For time lapse motility assays, etiolated seedlings were grown at 22 °C in the dark for 4 days.

Construct Generation

For all cloning procedures, the Gateway recombination system (Thermo-Fisher) was used. $NHX6_{1\text{-}507}$-YFP was generated by amplifying amino acids 1-507 of NHX6 from a cloned NHX6 ORF plasmid template using NHX6FS and NHX6 507R primers with iProof polymerase. This fragment was cloned into pENTR-D-TOPO, sequenced, and recombined into pEarlyGate 101 (Earley et al., 2006) to generate 35S:$NHX6_{1\text{-}507}$-YFP. $NHX6_{D194N}$-EGFP was generated through site directed mutagenesis using partially overlapping primers. D194N-F1 and D194N-R1 primers were used to amplify from a NHX6-EGFP pENTR-D-TOPO template using PfuUltra high-fidelity DNA polymerase, then LR recombined into pEarlyGate 100 to generate 35S:$NHX6_{D194N}$-EGFP.

Confocal microscopy and drug treatments

Images were obtained on a Leica SP5 or Zeiss LSM 780 laser scanning confocal microscope using a C-Apochromat 40x/1.3 water objective with 2x digital zoom at 1024x1024x pixels per image. Excitation and emission detection settings are as follows: mCerulean, 458 nm, 460-520 nm, GFP/YFP, 488 nm/ 490-560 nm, mRFP/mCherry, 561 nm / 565-630 nm, FM5-95, 561 nm / 565-650 nm. For all quantification experiments, identical settings were used to acquire each image. Chemical stock solutions were made in DMSO at the following concentrations - BFA 50 mM (Sigma-Aldrich), CHX 50 mM (Sigma-Aldrich), FM5-95 4 mM (FM4-64 analogue, ThermoFisher), Wortmannin 33 mM (LC Laboratories), LY294002 50 mM (Sigma-Aldrich), 1 mM Concanamycin A (Santa Cruz Biotechnology). Monensin stock was made in Ethanol at 10mM (Santa Cruz Biotechnology). An equal concentration of DMSO or ethanol was used in control treatments. For drug treatments, 6-7 day old seedlings were incubated in 6 well plates for 60 minutes for BFA treatments, 90 minutes for wortmannin and LY294002 treatments, or 30 minutes for monensin treatments.

For quantification of BRI1-GFP BFA bodies, images were acquired of 3-4 slice Z-stacks with 2 µm spacing, from which maximum intensity projections were generated. BFA body size was quantified using Fiji (Schindelin et al., 2012) based on ImageJ v1.48g, with automated thresholding and the Analyse Particles tool, using a minimum size of 0.7 μm^2, and circularity of ≥ 0.3. At least 15 epidermal cells were counted from each root. For quantification of wortmannin bodies, circular regions of interest (ROIs) were manually drawn and body area was measured using ImageJ. For analysis of bodies in $NHX6_{1\text{-}507}$-YFP and YFP-VTI-12 lines only clearly fused bodies ≥ 1 μm^2 were used for analysis. For quantification of BRI1-GFP plasma membrane fluorescence, plasma membrane regions from ≥ 6 cells per root were quantified using fixed ROIs, and mean fluorescence was calculated after subtracting background fluorescence. For FM internalisation, 7 day old seedlings were incubated in 2 µM FM5-95 in 6 well plates on ice for 5 minutes, washed in ½ MS twice, and incubated at room temperature for 5 minutes before confocal imaging. For ConcA hypocotyl length measurements, etiolated seedlings were scanned and measured using the “segmented line” tool in ImageJ. For monensin images and low pinhole images, a gaussian blur filter was applied with 0.6 sigma.

Fluorescence recovery after photobleaching (FRAP)

FRAP analysis was performed on a Zeiss LSM 780 laser confocal microscope using a 40x water objective. 7 day old seedlings were transferred from plates onto single well Lab-Tek™ Chambered Coverglass slides, and a thin agar slice was placed on top. *Arabidopsis* root

epidermal cells were bleached using a 488 nm argon laser at 100% power for 60 seconds with a circular 30 µm diameter ROI. Images were acquired using 512 x 512 pixel resolution pre-bleach and 0 min, 10 min, 20 min, 30 min, 40 min, and 50 min after bleaching.

Image series were aligned using Stackreg and Linear Stack Alignment with SIFT in ImageJ. For analysis, a fixed ROI was used to select plasma membrane from completely bleached cells. Fluorescence values from bleached cells were normalised to fluorescence from ROIs from two unbleached cells in the same image to account for minor photobleaching during image acquisition. Plasma membrane fluorescence before bleaching was set to 100%, and directly after bleaching as 0%. Percent of fluorescence recovery after photobleaching was calculated by dividing the normalised bleached fluorescence value minus background (t = 0 min) from the pre-bleached value minus background (t = 0 min). The experiment was repeated, and similar results were obtained.

Endosome motility imaging and analysis

Time lapse motility experiments were performed on a Zeiss Cell Observer spinning disk confocal microscope equipped with a Yokogawa CSU-X1 spinning disk and Photometrics EMCCD camera, using a 63x oil immersion objective. Four day old dark grown seedlings were placed onto single well Lab-Tek™ Chambered Coverglass (ThermoFisher) and a thin agar slice was placed on top. Epidermal cells from the upper hypocotyl were imaged at the cortical focal plane just below the plasma membrane over a 2 min period with 1 s scanning intervals. Only similarly sized cells (~900 - 1200 μm^2) were selected for analysis to minimise variation in particle speeds due to cell size. Cytoplasmic streaming was observed to verify cell viability.

Image drift was corrected using the ImageJ plugin StackReg. Postprocessing and analysis was performed in IMARIS software v7.0 (Bitplane). Particle tracking was performed using the 'spots' feature with the autoregressive motion algorithm, with a max distance parameter of 10 pixels, and a gap parameter of 0. Particle tracks less than 10 seconds long were filtered and excluded from analysis. Tracks were verified manually, and misaligned tracks were realigned. Mean track speed and track straightness was calculated in IMARIS from pooled particle tracks from ≥ 5 individual seedlings. Kymographs were created in ImageJ using the MultipleKymograph plugins (http://www.embl.de/eamnet/html/body_kymograph.html).

Vacuolar morphology

For vacuolar morphology analysis 7 day old seedlings expressing YFP-VAMP711 or RFP-VAMP711 were imaged on a Zeiss spinning disk confocal microscope using a 63x oil immersion objective. Z-stacks from Atrichoblast epidermal cells were obtained from 30-45

slices with 200 nm step size and stacked as a maximal intensity projection. Vacuolar morphology index was calculated by measuring the maximal luminal length and width in each cell in ImageJ (Löfke et al., 2015). For quantification ≥ 5 cells from ≥ 5 individual seedlings were analysed.

TGN/EE pH measurements

pH measurements of TGN/EE using the SYP61-pHusion line was performed as previously described (Luo et al., 2015). Briefly, 6-7 day old seedlings expressing SYP61-pHusion were imaged on a Leica SP5 scanning confocal microscope with a HCX PL APO 63× 1.20 water immersion objective with GFP (ex 488, em 490-545), and mRFP (ex 561, em 600-670) settings. Ratios were calculated by dividing the average intensity of GFP/mRFP signals after background subtraction. pH was calibrated *in vivo* from buffers between pH 4.8 and 8.0 using free cytosolic pHusion, from which a sigmoidal calibration curve was obtained through the Boltzmann fit function in Origin Pro 9.1G and mapped to the corresponding measured values.

Statistics and Software

Statistics were performed in Microsoft Excel or R v3.3.2 using R Studio. Boxplots and stripcharts were generated in R v3.3.2. Images were prepared in Illustrator (Adobe).

Table S1 – List of primers used in this study

Primer	Sequence 5′-3′
D194N F1	TAAATAATGCAATGGCGATATCTCTGTACAGGACAATGTCC
D194N R1	CGCCATTGCATTATTTAAAACTGATTCTCCAAACACCAGGG
NHX6FS	CACCATGTCGTCGGAG
NHX6 507R	TCCGTTGTTACTTGTGAAGAACG

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Author Contributions

J.M.D. conducted the experiments and analysed the data. S.S. performed the pH measurements and Concanamycin A experiment. J.M.D., K.S., and A.R.G. designed the experiments. J.M.D and A.R.G wrote the manuscript.

Competing interests

No competing interests declared.

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Figure Legends

Figure 1. Golgi and TGN/EE motility are reduced in *nhx5 nhx6*.

(A-B) Time-lapse spinning disk imaging of Golgi localised YFP-Got1p (A), and TGN/EE localised YFP-VTI12 (B) in hypocotyl cells from 4 day old dark grown seedlings. The trajectory of particles visible from the initial frame of the time lapse are shown, coloured by mean particle speed.

(C and D) Kymograph of a representative continuously moving Golgi (C) and TGN/EE (D) particle over 20 seconds.

(E) Box plot of mean Golgi and TGN/EE particle speeds. ** $p < 0.01$, from Kolmogorov-Smirnov and Mann-Whitney tests. n = number of particle tracks analysed from ≥ 6 cells.

(F) Box plot of Golgi and TGN/EE particle straightness, where 1 indicates a perfectly straight line. ** $p < 0.01$ from Kolmogorov-Smirnov and Mann–Whitney U tests. Scale bars = 5 µm (A,

B), 2 µm (C and D). See also Movie S1 and Figure S1.

Figure 2. BRI1 recycling from the TGN/EE is reduced in *nhx5 nhx6*

(A) BFA washout experiment. Root epidermal cells expressing BRI1-GFP were pre-treated with Cycloheximide (CHX) for 1hr to inhibit protein synthesis, then incubated with Brefeldin A (BFA) + CHX for 1 hr, and then washed in CHX for the indicated times. BFA bodies are still present in *nhx5 nhx6* after 90 and 120 minutes (arrowheads).

(B and C) Quantification of BRI1-GFP BFA body size after washout (B), and proportion of cells containing BFA bodies after washout (C). ≥ 15 cells from ≥ 3 individual plants were analysed for each time point. Data is means ± S.D.

Figure 3. BRI1 secretion to the plasma membrane is unaffected in *nhx5 nhx6*

(A) BRI1-GFP fluorescence in wild type and *nhx5 nhx6* root epidermal cells. (B) Quantification of relative plasma membrane fluorescence. Data is means ± s.e.m., n.s.; not significant. ≥ 5 cells from ≥ 6 roots were analysed for each genotype. Scale bars = 10 µm. (C) Fluorescence recovery after photobleaching (FRAP) was performed on root epidermal cells from 7 day old wild type and *nhx5 nhx6* plants expressing BRI1-GFP. Roots were imaged pre-bleaching, directly after bleaching, and at time intervals as indicated. (D) Quantification of BRI1-GFP plasma membrane fluorescence after bleaching. Data is means ± SE, n ≥ 4 cells per time point. No significant difference was observed between wild type and *nhx5 nhx6*. Scale bar = 10 µm.

Figure 4. Endosomal NHX antiporter activity is required for Wortmannin induced LE/MVB swelling.

(A) Response of YFP-ARA7 (LE/MVB marker), and the antiporter inactive $NHX6_{D194N}$-EGFP in control and 33 µM wortmannin (Wm) treated root epidermal cells. Wortmannin induces homotypic fusion of MVBs into large wortmannin bodies. Note the large dilated wortmannin bodies in wild type, compared to much smaller, dense bodies in *nhx5 nhx6* cells (arrowheads), which lacked clear ring-like morphology as in wild type (arrows). Plasma membrane is counterstained in magenta.

(B) Quantification of wortmannin bodies from (A). Data is means ± SD, ** $p < 0.01$; t-test. ≥ 9 cells from ≥ 4 independent roots were analysed for each genotype.

(C) Wortmannin induced bodies in *nhx5 nhx6* are resolvable through confocal imaging with a reduced pinhole. Root cap cells treated with 33 µM wortmannin and imaged with 0.6 Airy Unit pinhole (PH) show a clear ring formation.

(D) Response of YFP-ARA7 root cap cells to 50 µM LY294002 or 1 µM wortmannin treatment. Inset shows an enlarged MVB/LE body.

(E) Schematic of drugs used to interrupt phosphoinositide conversion. LY294002 and 1 µM wortmannin specifically inhibit PI3K conversion of PI to PI(3)P, while concentrations above 30 µM Wm also inhibit PI4K conversion of PI to PI(4)P.
Scale bars = 5 µm (A, C), 2 µm (D).

Figure 5. *nhx5 nhx6* TGN/EE are partially insensitive to monensin induced swelling.
(A) Confocal images of Arabidopsis root cap cells treated with 10 µM monensin for 30 minutes. The ionophore monensin induces swelling of TGN/EE (VHA-a1-GFP), but not of MVB/LEs (mRFP-ARA7); see inset enlarged view showing swelling of TGN/EE.
(B) pH of TGN/EE in 6 days old *Arabidopsis thaliana* seedlings expressing the ratiometric pH sensor SYP61-pHusion after treatment with 5 µM monensin for 30 minutes.
(C) pH of TGN/EE in wild type and *nhx5-1 nhx6-1* seedlings expressing SYP61-pHusion.
Data from B-C represent means ± SD of three individual experiments from n = 15 seedlings.
* $p < 0.05$; Student´s t-test.
(D) Arabidopsis root cap cells following 30 minutes 10 µM monensin treatment, or mock control (0.1% EtOH). Swelling of Golgi (YFP-Got1p) was not detected. TGN/EE (YFP-VTI12) showed aggregation and enlargement of individual endosomes (arrowheads) which was less apparent in *nhx5 nhx6*. Similar results were obtained with the NHX6 antiporter inactive marker $NHX6_{D194N}$-EGFP. Scale bars, 5 µm.

Figure 6. The distal tail of NHX6 is required for localisation to the MVB.
(A) Cartoon showing structure of the $NHX6_{1-507}$ construct.
(B) Complementation of the *nhx5 nhx6* dwarf phenotype by $NHX6_{1-507}$-YFP in 28 day old Arabidopsis plants.
(C) Response of $NHX6_{1-507}$-YFP to 60 minute BFA treatment in root epidermal cells. Note the localisation of $NHX6_{1-507}$-YFP to core and peripheral (arrowheads) BFA regions, corresponding to TGN/EE and Golgi respectively.
(D) $NHX6_{1-507}$-YFP following 30 minute 10 µM monensin treatment in root cap cells. Note the enlargement of TGN/EE (arrowheads).
(E-F) Response of $NHX6_{1-507}$-YFP and $NHX6_{D194N}$-EGFP (Wild type) to 33 µM wortmannin treatment in root epidermal cells. Arrowheads indicate lack of $NHX6_{1-507}$-YFP labelling in Wm bodies. Partial labelling of $NHX6_{1-507}$-YFP to a Wm body (inset), compared to complete labelling in $NHX6_{D194N}$-EGFP. Counterstain FM5-95 (magenta) labels the plasma membrane and endocytic compartments.
(G) Schematic of monensin and wortmannin swelling phenotypes. In wild type cells the Golgi, TGN/EE, and MVB/LE in swell upon monensin and wortmannin/LY294002 treatment due to

Na^+/K^+ transport for H^+, resulting in alkalinisation. In *nhx5 nhx6* endosomal compartments are more acidic with lower lumenal Na^+/K^+, leading to only minor swelling with monensin, and fusion but no swelling with wortmannin. NHX6 activity at the Golgi and TGN/EE, but not MVB in $NHX6_{1\text{-}507}$-YFP/*nhx5 nhx6* is sufficient to restore both monensin and wortmannin insensitivity phenotypes.

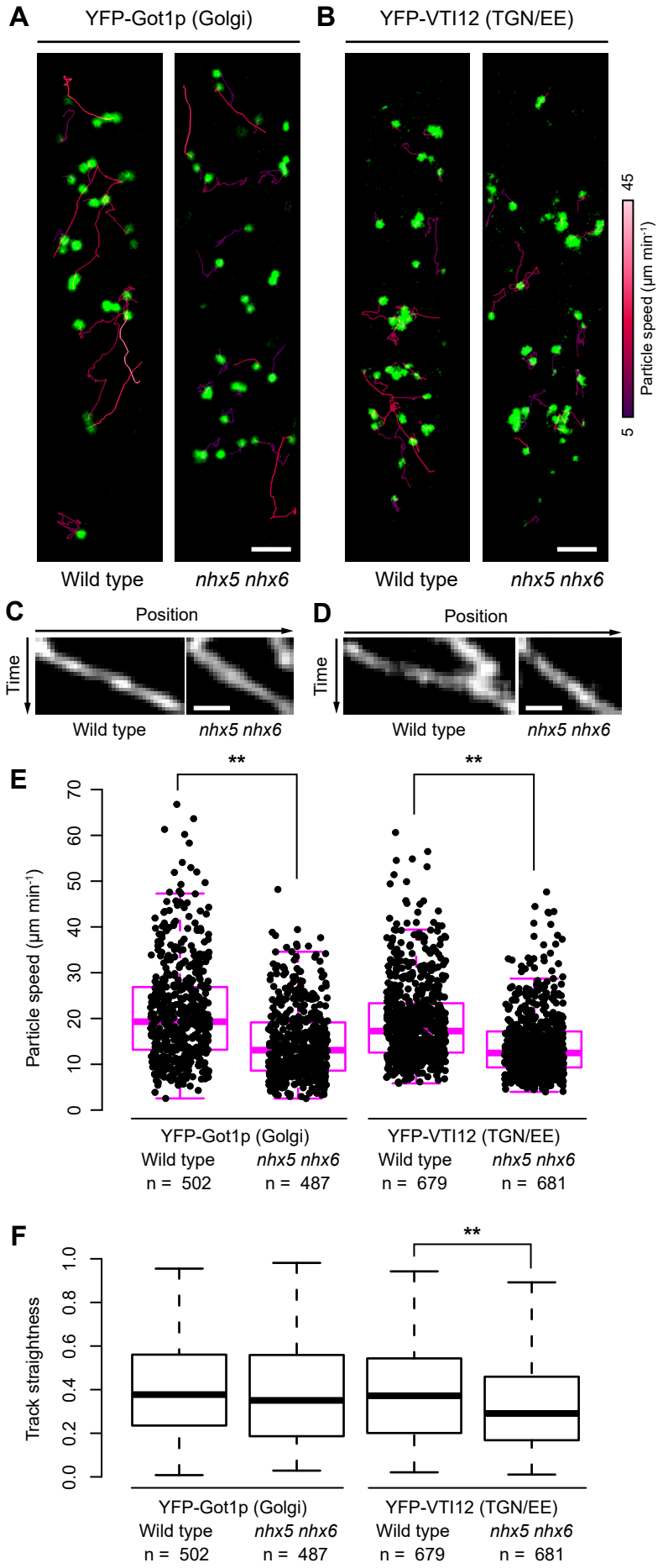
A
YFP-Got1p (Golgi)
B
YFP-VTI12 (TGN/EE)
Wild type
nhx5 nhx6
Wild type
nhx5 nhx6
45
5
Particle speed (µm min⁻¹)
C
Position
Time
Wild type
nhx5 nhx6
D
Position
Time
Wild type
nhx5 nhx6
E
Particle speed (µm min⁻¹)
0
10
20
30
40
50
60
70
**
**
YFP-Got1p (Golgi)
Wild type
n = 502
nhx5 nhx6
n = 487
YFP-VTI12 (TGN/EE)
Wild type
n = 679
nhx5 nhx6
n = 681
F
Track straightness
0.0
0.2
0.4
0.6
0.8
1.0
**
YFP-Got1p (Golgi)
Wild type
n = 502
nhx5 nhx6
n = 487
YFP-VTI12 (TGN/EE)
Wild type
n = 679
nhx5 nhx6
n = 681

Fig. 1

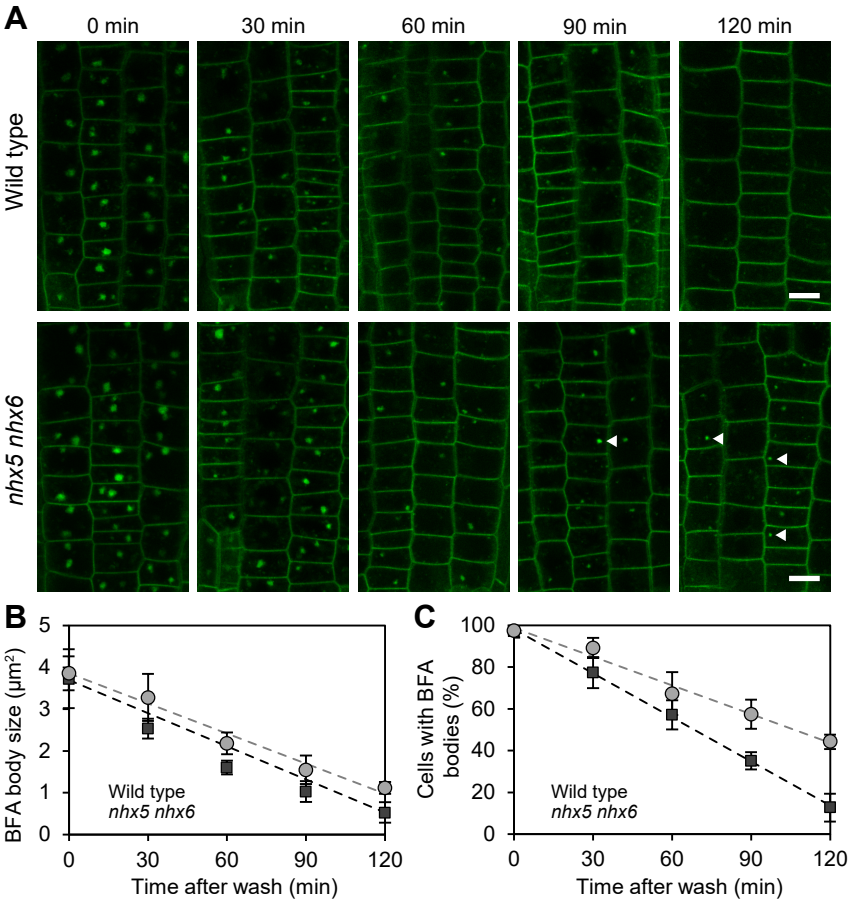
A
0 min
30 min
60 min
90 min
120 min
Wild type
nhx5 nhx6
B
BFA body size (μm²)
Wild type
nhx5 nhx6
Time after wash (min)
C
Cells with BFA bodies (%)
Wild type
nhx5 nhx6
Time after wash (min)

Fig. 2

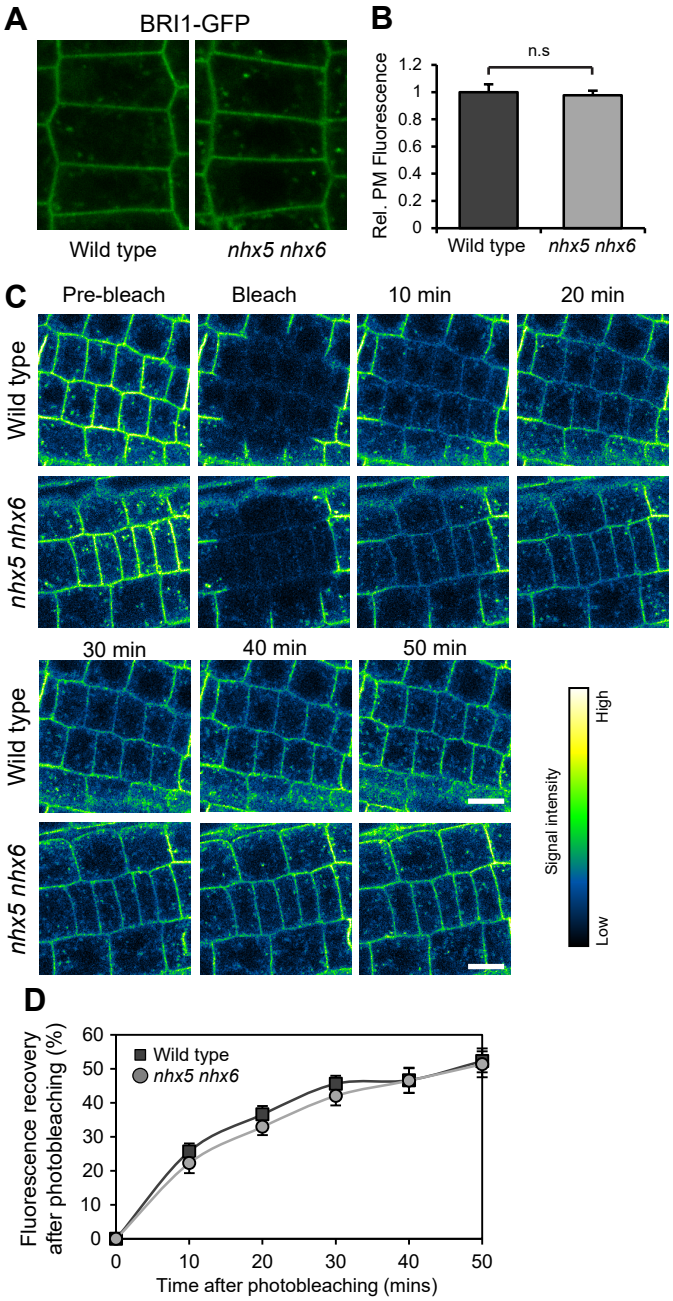
A
BRI1-GFP
Wild type
nhx5 nhx6
B
n.s
Rel. PM Fluorescence
1.2
1
0.8
0.6
0.4
0.2
0
Wild type
nhx5 nhx6
C
Pre-bleach
Bleach
10 min
20 min
Wild type
nhx5 nhx6
30 min
40 min
50 min
Wild type
nhx5 nhx6
Signal intensity
High
Low
D
Fluorescence recovery after photobleaching (%)
60
50
40
30
20
10
0
Wild type
nhx5 nhx6
0
10
20
30
40
50
Time after photobleaching (mins)

Fig. 3

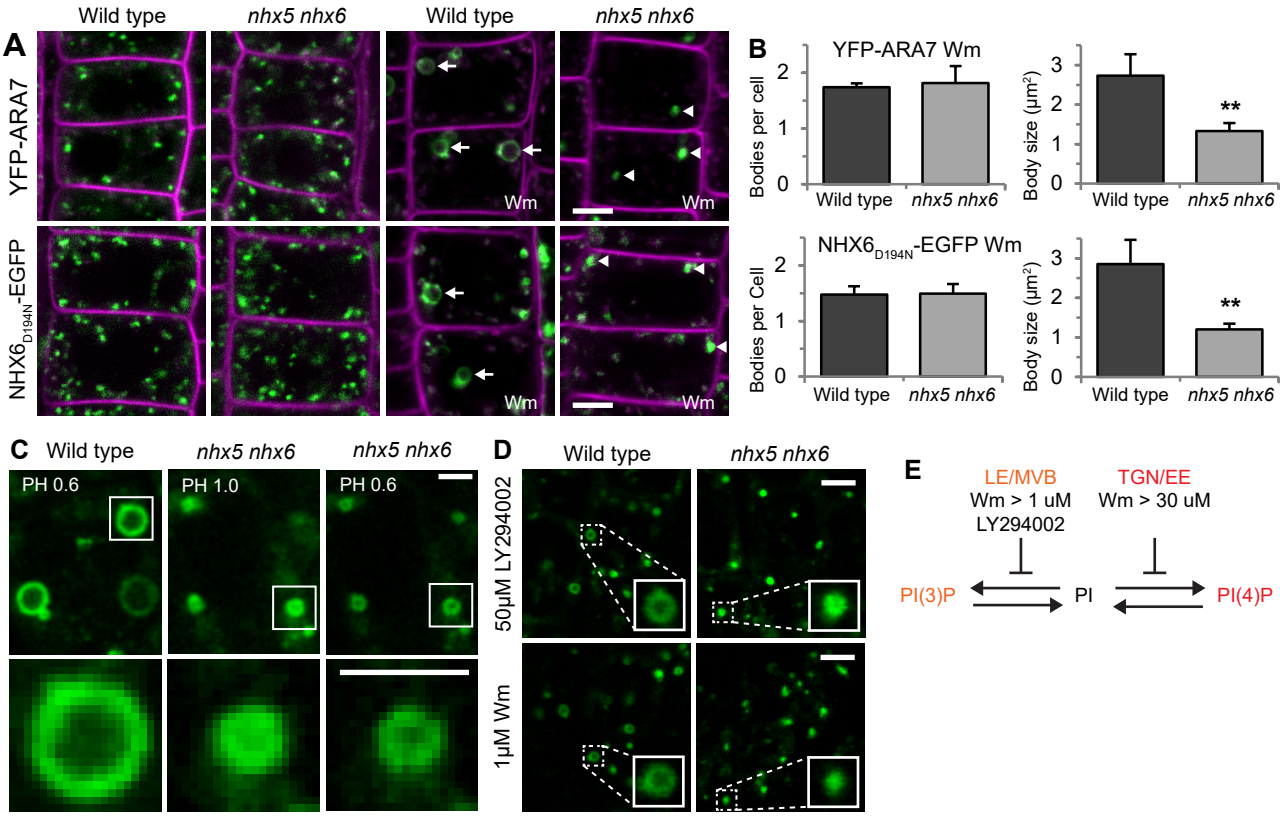
A
Wild type
nhx5 nhx6
Wild type
nhx5 nhx6
YFP-ARA7
NHX6D194N-EGFP
Wm
B
YFP-ARA7 Wm
NHX6D194N-EGFP Wm
Bodies per cell
Body size (μm²)
Wild type
nhx5 nhx6
**
C
PH 0.6
PH 1.0
D
50μM LY294002
1μM Wm
E
LE/MVB
Wm > 1 uM
LY294002
TGN/EE
Wm > 30 uM
PI(3)P
PI
PI(4)P

Fig. 4

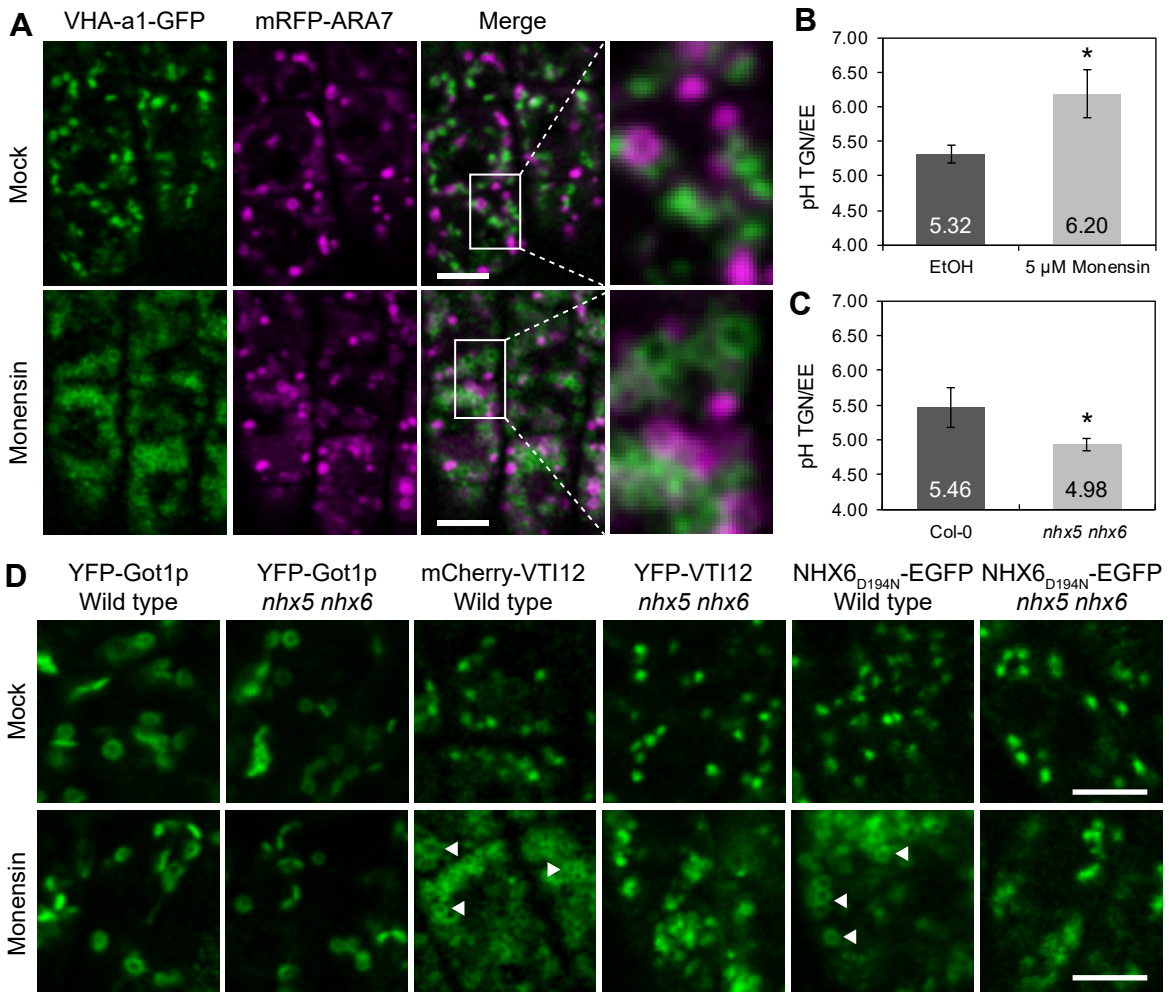
A
VHA-a1-GFP
mRFP-ARA7
Merge
Mock
Monensin
B
pH TGN/EE
7.00
6.50
6.00
5.50
5.00
4.50
4.00
5.32
6.20
*
EtOH
5 µM Monensin
C
pH TGN/EE
5.46
4.98
*
Col-0
nhx5 nhx6
D
YFP-Got1p
Wild type
YFP-Got1p
nhx5 nhx6
mCherry-VTI12
Wild type
YFP-VTI12
nhx5 nhx6
NHX6D194N-EGFP
Wild type
NHX6D194N-EGFP
nhx5 nhx6
Mock
Monensin

Fig. 5

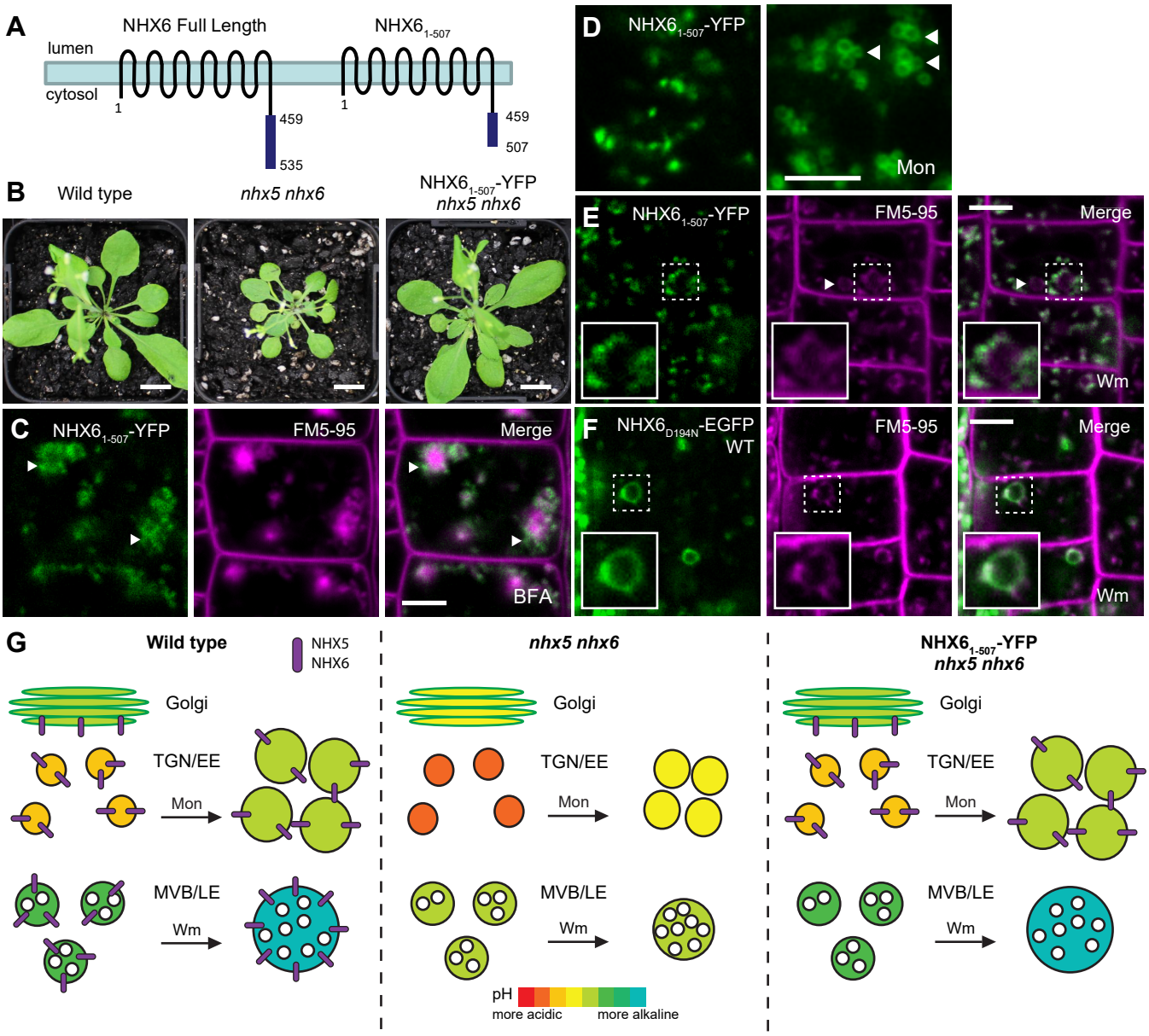
A
NHX6 Full Length
NHX6$_{1-507}$
lumen
cytosol
1
459
535
1
459
507
B
Wild type
nhx5 nhx6
NHX6$_{1-507}$-YFP
nhx5 nhx6
C
NHX6$_{1-507}$-YFP
FM5-95
Merge
BFA
D
NHX6$_{1-507}$-YFP
Mon
E
NHX6$_{1-507}$-YFP
FM5-95
Merge
Wm
F
NHX6$_{D194N}$-EGFP
WT
FM5-95
Merge
Wm
G
Wild type
NHX5
NHX6
Golgi
TGN/EE
Mon
MVB/LE
Wm
nhx5 nhx6
Golgi
TGN/EE
Mon
MVB/LE
Wm
pH
more acidic
more alkaline
NHX6$_{1-507}$-YFP
nhx5 nhx6
Golgi
TGN/EE
Mon
MVB/LE
Wm

Fig. 6