## **1** Optogenetically Induced Microtubule Acetylation Unveils the Molecular Dynamics of

- Actin-Microtubule Crosstalk in Directed Cell Migration
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- 4 Abhijit Deb Roy<sup>1,3,4\*</sup>, Cristian Saez Gonzalez<sup>1</sup>, Farid Shahid<sup>2</sup>, Eesha Yadav<sup>2</sup>, Takanari Inoue<sup>1\*</sup>
- <sup>5</sup> <sup>1</sup> Department of Cell Biology and Center for Cell Dynamics, Johns Hopkins University School of
- 6 Medicine, 855 North Wolfe Street, Baltimore, MD 21205, USA
- 7 <sup>2</sup> The Johns Hopkins University, Baltimore, MD 21218, USA
- <sup>8</sup> <sup>3</sup> Center for Cell Analysis and Modeling, University of Connecticut School of Medicine, 400
- 9 Farmington Avenue, Farmington, CT 06030, USA
- <sup>4</sup> Department of Cell Biology, University of Connecticut School of Medicine, 263 Farmington
- 11 Avenue, Farmington, CT 06030, USA
- 12
- 13 \* Correspondence:
- 14 Abhijit Deb Roy: <u>abdebroy@uchc.edu</u>, Takanari Inoue: <u>jctinoue@jhmi.edu</u>
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#### 16 Abstract

Microtubule acetylation is implicated in regulating cell motility, yet its physiological role in 17 directional migration and the underlying molecular mechanisms have remained unclear. This 18 19 knowledge gap has persisted primarily due to a lack of tools capable of rapidly manipulating 20 microtubule acetylation in actively migrating cells. To overcome this limitation and elucidate the 21 causal relationship between microtubule acetylation and cell migration, we developed a novel optogenetic actuator, optoTAT, which enables precise and rapid induction of microtubule 22 23 acetylation within minutes in live cells. Using optoTAT, we observed striking and rapid responses 24 at both molecular and cellular level. First, microtubule acetylation triggers release of the RhoA 25 activator GEF-H1 from sequestration on microtubules. This release subsequently enhances 26 actomyosin contractility and drives focal adhesion maturation. These subcellular processes 27 collectively promote sustained directional cell migration. Our findings position GEF-H1 as a 28 critical molecular responder to microtubule acetylation in the regulation of directed cell migration, 29 revealing a dynamic crosstalk between the actin and microtubule cytoskeletal networks.

#### 30 Introduction:

Microtubules undergo at least nine different types of post-translational modifications, which 31 independently, or in concert, modulate microtubule properties including its dynamics as well as 32 their interaction with microtubule-associated proteins<sup>1</sup>. Acetylation of the lysine-40 residue of α-33 tubulin<sup>2-6</sup>, hereafter called microtubule acetylation for simplicity, is conserved throughout 34 eukaryotes<sup>7-9</sup>, and is one of the only few modifications known to take place inside microtubule 35 lumen<sup>9</sup>. Despite little significant structural changes<sup>10</sup>, microtubule acetylation provides structural 36 37 stability against bending forces<sup>11–16</sup>. Microtubule acetylation has been implicated in cellular processes, including mechanosensing<sup>12,17-21</sup>, adaptation to extracellular environment<sup>22-25</sup>. 38 intracellular transport via motor proteins<sup>26-31</sup>, DNA damage response<sup>32</sup>, autophagy<sup>33-35</sup>, and 39 40 regulation of cell motility<sup>22,23,36–39</sup>. Directionally persistent cell migration, a process critical for physiological functions as well as pathological events, heavily relies on microtubule dynamics. 41 While the involvement of microtubules in migration is well-established, the specific contributions 42 43 of microtubule post-translational modifications remain poorly understood<sup>40,41</sup>. Microtubule 44 acetylation, in particular, appears to exhibit differential roles in cell migration depending on cell type and environmental context. For example, it inhibits three-dimensional migration in human 45 46 foreskin fibroblasts<sup>23</sup> and transwell migration in NIH3T3 fibroblasts<sup>42</sup> while promoting motility in astrocytes<sup>22,24</sup> and breast cancer cells<sup>36–38</sup>. In contrast, acetylation is dispensable for the motility 47 48 of RPE1 epithelial cells<sup>43</sup>. These conclusions have largely been drawn from studies employing genetic engineering or pharmacological interventions to alter microtubule acetylation. 49

50 Genetic approaches are invaluable for identifying genes responsible for these effects; however, 51 they often lack the temporal precision required to investigate rapid cytoskeletal dynamics during 52 cell migration, which can occur within minutes. Similarly, pharmacological interventions to 53 modulate microtubule acetylation may have unintended non-specific effects<sup>42,44–47</sup>, complicating

the interpretation of results. The paucity of molecular tools capable of controlling microtubule 54 acetylation with rapid temporal resolution and high molecular specificity has presented a 55 56 significant challenge in elucidating its real-time roles in dynamic cell behavior such as directional cell migration. To address this, we developed a genetically encoded actuator, termed optoTAT, 57 that is designed to induce microtubule acetylation within minutes upon light illumination. By 58 59 leveraging this optogenetic actuator in combination with genetic knock-out models, migration assays, and live cell fluorescence imaging, we aimed to uncover the molecular interplay between 60 61 microtubule acetylation, actin cytoskeleton remodeling, and directional cell migration in real time.

#### 62 Results:

**Microtubule acetylation mediates directional migration:**  $\alpha$ -TAT1 is the only enzyme known 63 to acetylate microtubules in mammals<sup>12,48,49</sup>, whereas the deacetylation is catalyzed by HDAC6 64 and Sirt2<sup>42,50</sup>. Mouse Embryonic Fibroblasts (MEFs) obtained from α-TAT1 knockout (KO) mice 65 do not have detectable microtubule acetylation<sup>12,17,51</sup>. In a random migration assay,  $\alpha$ -TAT1 KO 66 67 MEFs showed significantly greater motility but reduced directional persistence compared to wildtype (WT) MEFs (Fig. 1a, b, c). In wound healing assays,  $\alpha$ -TAT1 KO MEFs closed the wound 68 69 more rapidly than WT MEFs (Fig.1d, e). To examine the effects of microtubule acetylation on 70 chemotaxis, we utilized an Ibidi chemotaxis chamber with 0-20% FBS gradient (Fig. 1f).  $\alpha$ -TAT1 71 KO MEFs failed to efficiently migrate towards the chemoattractant compared to WT MEFs (Fig. 72 1g, Supplementary Fig. S1a). Unlike the WT MEFs, the  $\alpha$ -TAT1 KO MEFs exhibited reduced 73 directional bias towards the chemoattractant gradient, as indicated by the reduced shift in the center of mass from the origin (Supplementary Fig. S1b). The α-TAT1 KO MEFs showed 74 75 significantly reduced directional persistence compared to WT MEFs, as shown by decreased 76 forward migration index (FMI) for the KO MEFs along the chemoattractant gradient (FMI<sup>II</sup>) (Fig. 77 1h), but not perpendicular to the gradient (FMI<sup>1</sup>) (Fig. 1i). These chemotaxis defects were 78 rescued by exogenous expression of mVenus-α-TAT1 in KO MEFs (Fig. 1g, h, supplementary Fig. S1a, b). 79

On examining the motility of WT and  $\alpha$ -TAT1 KO MEFs, we observed that in contrast to WT MEFs, the  $\alpha$ -TAT1 KO MEFs change their direction of motion repeatedly (Fig. 1j). The WT MEFs had two groups of protrusions, one short-lived and another long-lived, as indicated by the bimodal distribution of protrusion lifetimes.  $\alpha$ -TAT1 KO MEFs had very few such long-lived protrusions (Fig. 1k). The  $\alpha$ -TAT1 KO MEFs also produced new protrusions more frequently than WT MEFs, leading to changes in direction of movement (Fig. 1I). Directional persistence requires

a long-lasting front-back polarity<sup>52,53</sup>, and the frequent protrusion formation in  $\alpha$ -TAT1 KO MEFs suggest defects in maintenance of such front-back polarity. Consistent with this, morphological analyses showed that  $\alpha$ -TAT1 KO MEFs have higher circularity and higher convexity (Supplementary Fig. S1c, d), consistent with more protrusive phenotypes. The chemotaxis defects in  $\alpha$ -TAT1 KO MEFs were not due to defects in sensing the chemoattractant since serumstarved WT and  $\alpha$ -TAT1 KO MEFs showed comparable morphological changes: increased protrusions, on treatment with 10% FBS (Supplementary Fig. S1e).

93 Microtubule acetylation mediates focal adhesion maturation: In migrating cells, nascent 94 protrusions are stabilized by integrin mediated adhesion complexes which undergo maturation in response to actomyosin contractility<sup>54,55</sup>. On immunostaining for Vinculin, we observed fewer 95 96 adhesions in  $\alpha$ -TAT1 KO MEFs compared to WT MEFs (Fig. 2a, b). Consistent with decreased 97 adhesion, α-TAT1 KO MEFs also had smaller cell spread area (Supplementary Fig. S2a). α-98 TAT1 KO MEFs also had fewer larger mature adhesions (Fig. 2a, Supplementary Fig. S2b), 99 suggesting a defect in the adhesion maturation pathways. In WT MEFs, we observed a polarized 100 distribution of nascent and maturing adhesions in the front, and large mature adhesions at 101 retractions, whereas the  $\alpha$ -TAT1 KO MEFs lacked any such spatial polarization of adhesions 102 (Fig. 2a). We also observed lower levels of vinculin localization in the adhesions in the  $\alpha$ -TAT1 103 KO MEFs (Fig. 2a, Supplementary Fig. S2c, d), which is consistent with lower tensile forces 104 actin on these adhesions. Exogenous expression of mVenus- $\alpha$ -TAT1, but not a catalytically dead mVenus-a-TAT1(D157N)<sup>12</sup>, in a-TAT1 KO MEFs could rescue these adhesion defects 105 106 (Fig.2a, b, Supplementary Fig. S2b, c, d). These adhesion defects were not due to decreased 107 Vinculin expression since both WT and α-TAT1 KO MEFs showed comparable levels of Vinculin 108 expression (Fig. 2c, d). Adhesion maturation is mediated by tensile forces experienced by focal 109 adhesion components through the actin cytoskeleton. Using a Vin-TS FRET-based tension

sensor<sup>56</sup> we observed increased FRET in the α-TAT1 KO MEFs, indicating that focal adhesions
experienced significantly reduced forces compared to WT MEFs (Fig. 2e, f, Supplementary Fig.
S2e). Furthermore, the Vin-TS FRET signal also showed a polarized distribution in the WT
MEFs, indicating a polarized distribution of tensile forces, but not in the KO cells (Fig. 2e).

114 Microtubule acetylation mediates actomyosin contractility: Focal adhesions experience tensile forces through the actin cytoskeleton<sup>57</sup>. Phalloidin staining showed a significant reduction 115 116 in bundled actin in  $\alpha$ -TAT1 KO cells, suggesting that these cells have defects in actin contractility 117 (Fig. 2g, red arrowheads). Contractility in the actin cytoskeleton is generated through Myosin 118 motor proteins, which are activated through phosphorylation of the Myosin Regulatory Light 119 Chain (MRLC) at Serine19 by Myosin Light Chain Kinase (MLCK)<sup>58</sup>. Myosin activation is also 120 involved in directional persistence of migrating cells<sup>59</sup>. Immunostaining of WT or α-TAT1 KO 121 MEFs with an antibody against phospho-MRLC Serine 19 showed a significantly lower levels of 122 phospho-MRLC (Fig. 2g, h), indicating decreased activation levels of Myosin. The decrease in 123 phospho-MRLC levels was not due to a decrease in expression levels since WT and KO cells 124 showed comparable Myosin expression levels (Supplementary Fig. S2f, g). These defects in 125 MRLC phosphorylation could be rescued with exogenous expression of mVenus- $\alpha$ -TAT1 but not 126 mVenus-α-TAT1(D157N) mutant (Fig. 2h). Since MRLC phosphorylation leads to association 127 with the actin cytoskeleton, we measured optical flow of mCherry-MRLC to characterize myosin 128 activation dynamics. mCherry-MRLC flow was considerably lower in  $\alpha$ -TAT1 KO MEFs 129 compared to WT cells (Fig. 2i, j), indicating decreased association with the actin cytoskeleton. 130 Treatment of KO cells with Y-27632 led to a decrease in phospho-Myosin levels, suggesting a 131 residual amount of myosin activity, however diminutive (Supplementary Fig. S2h, i).

Inhibiting HDAC6 weakly promotes myosin activation: Our observations suggest that
 microtubule acetylation promotes myosin activation. Tubacin is a widely used pharmacological

inhibitor of HDAC6<sup>60</sup>. To test whether increase in microtubule acetylation levels could increase 134 135 myosin activation, we used TIRF microscopy to characterize changes in mCherry-MRLC 136 association with actin cytoskeleton in WT MEFs treated with 2 µM Tubacin. Over 5 hours post 137 Tubacin treatment, we observed a minor increase in mCherry-MRLC signal on the TIRF plane 138 (Supplementary Fig. S2i, k), indicating increased activation and association with the actin 139 cytoskeleton. However, this increase over the course of hours does not eliminate the possibility 140 of cell adaptation through transcriptional regulation or non-specific effects. HDAC6 has many 141 other substrates other than  $\alpha$ -Tubulin<sup>44,61,62</sup>, and it can also deacetylates additional acetylated lysine residues on α-Tubulin<sup>63</sup>. Thus, HDAC6 inhibition is not sufficiently specific to determine 142 143 causal relationships between acetylation of Lysine-40 in  $\alpha$ -Tubulin and cellular or molecular 144 responses.

145 Developing an optogenetic actuator to rapidly induce microtubule acetylation: To examine 146 a specific and causal relationship between microtubule acetylation and myosin activation, we 147 sought to develop an inducible molecular actuator to control microtubule acetylation. Initially we 148 tested Z-lock- $\alpha$ -TAT1 in HeLa cells<sup>64</sup>. However, we observed a significant increase in microtubule 149 acetylation in cells expressing mCherry-Z-lock- $\alpha$ -TAT1 even in dark (Supplementary Fig. 3a). 150 We have previously shown that cytoplasmic localization of  $\alpha$ -TAT1 through its C-terminal spatial 151 regulatory domain is critical for microtubule acetylation. Nuclear localization of α-TAT1 is 152 sufficient to sequester it from catalyzing microtubule acetylation<sup>51</sup>. Based on this, we reasoned 153 that inducing export of a nuclear-localized  $\alpha$ -TAT1 may induce acetylation of microtubules (Fig. 154 3a). We initially implemented the light-inducible nuclear export system (LEXY)<sup>65</sup> to sequester 155 full-length α-TAT1(M1-R323) in the nucleus in dark. We named this construct Optogenetic 156 Tubulin Acetyl-Transferase version 0 (optoTATv0) (Fig. 3b). On blue-light stimulation, we 157 observed a rapid nucleus-to-cytoplasm translocation of mCherry-optoTATv0 (Fig. 3c, d).

However, we also observed significant levels of cytoplasmic presence even in the absence of 158 159 blue-light stimulation (Fig. 3c, d), presumably due to the presence of nuclear export and 160 cytoplasmic retention machinery in  $\alpha$ -TAT1 C-terminus<sup>51</sup>. To improve upon this design, we tethered only the catalytic domain of  $\alpha$ -TAT1(M1-S236)<sup>12</sup> to LEXY (optoTATv1) or to LEXY with 161 162 two NLS (optoTATv2) (Fig. 3b). These versions showed increased nuclear sequestration (Fig. 163 3c, d), with rapid, robust and reversible cytoplasmic translocation on blue light stimulation (Fig. 3c, d, e, f,). To examine whether blue-light stimulation of these tools could acetylate 164 165 microtubules, we exposed HeLa cells expressing mCherry-optoTATv1 or mCherry-optoTATv2 to blue light for 2 hours and performed immunostaining for acetylated microtubules. We observed 166 167 that blue light stimulation of optoTATv1 or optoTATv2 significantly induced microtubule acetylation in HeLa cells (Fig. S3g, h). However, we observed that the cells expressing 168 169 optoTATv1, but not optoTATv2, showed increased levels of microtubule acetylation in dark when 170 compared to non-transfected cells (Fig. 3g, h). We used optoTATv2 for all further experiments, 171 and for simplicity, we will refer to it as optoTAT here onwards.

172 To assess the kinetics of microtubule acetylation by optoTAT, we used lentiviral transduction to generate a cell line of HeLa cells stably expressing mVenus-optoTAT. We used 173 174 flow cytometric cell sorting to select cells with comparable levels of mVenus expression. These 175 cells were incubated in dark for 24 hours and then exposed to blue-light for 0 min, 5 min, 10 min, 176 30 min, 60 min, 120 min and 240 min, followed by immunostaining for acetylated α-Tubulin and total α-Tubulin. We observed a rapid and significant increase in microtubule acetylation within 177 178 10 minutes of blue-light stimulation, which continued to increase and stabilize after an hour of 179 stimulation (Fig. 3i, Supplementary Fig. S3b,c,d). Our data demonstrate that we have developed 180 an optogenetic molecular actuator to rapidly induce microtubule acetylation in living cells, with a 181 tunable dynamic range.

OptoTAT stimulation rapidly induces myosin activation: Phosphorylation of MRLC at 182 Serine-19, leads to Myosin (and MRLC) activation, resulting in association with F-actin<sup>58</sup>. We 183 184 stimulated miRFP703-optoTAT in HeLa cells co-expressing mCherry-MRLC and visualized 185 changes in MRLC distribution using TIRF microscopy. We reasoned that Myosin activation will 186 coincide with an increased MRLC association with the actin cytoskeleton, leading to an increase 187 in mCherry-MRLC fluorescence in the TIRF plane<sup>66</sup>. On blue light stimulation, we observed a 188 rapid and persistent increase in mCherry intensity in the TIRF plane, indicating increased 189 association of mCherry-MRLC with actin cytoskeleton (Fig. 4a, b,). This increase was concurrent with increased coherence in mCherry-mRLC distribution (Fig. 4c, d), suggesting increased 190 191 isotropy in myosin distribution, consistent with higher levels of bundled actin and increased 192 actomyosin contractility. Catalytically dead miRFP-optoTAT(D157N) failed to elicit any increase 193 in mCherry-MRLC signal. Additionally, any increase in mCherry-MRLC intensity was abrogated 194 on treating the cells with ROCK inhibitor Y27632 for 10 minutes before optoTAT stimulation, or 195 by pre-saturating microtubule acetylation by treating the cells with HDAC6 inhibitor tubacin for 4 196 hours before optoTAT stimulation (Fig. 4e).

197 Consistent with an increase in myosin activity, miRFP703-optoTAT stimulation also led to 198 increased levels of bundled actin (Fig. 4f, g), and maturation of focal adhesions as indicated by 199 increased adhesion sizes and mCherry-Paxillin accumulation (Fig. 4h, i, j,). Taken together, 200 these data suggest that optoTAT stimulation rapidly induced Myosin activation through increased 201 microtubule acetylation and ROCK kinase activation.

Microtubule acetylation releases GEF-H1 from sequestration: Myosin activation on MRLC phosphorylation through MLCK is often downstream of RhoA-ROCK signaling. Our observation that inhibiting ROCK abrogated optoTAT mediated Myosin activation suggested that optoTAT stimulation leads to RhoA activation. GEF-H1 is an activator for RhoA, which is sequestered on

microtubules and is activated on disrupting microtubules using nocodazole<sup>67,68</sup>. GEF-H1 was 206 reported to mediate  $\alpha$ -TAT1 mediated cellular mechano-sensing<sup>22,69</sup>. Immunostaining revealed 207 208 significantly increased GEF-H1 sequestration on the microtubules in  $\alpha$ -TAT1 KO cells compared 209 to WT cells (Fig. 5a, b). This was not due to increased expression levels since both WT and  $\alpha$ -210 TAT1 KO MEFs had comparable GEF-H1 expression levels (Fig. 5c, d). Since acetylation has 211 been reported to stabilize microtubules, we speculated whether release of GEF-H1 was due to 212 increased stability of microtubules in WT MEFs. However, we did not detect any significant loss 213 of GEF-H1 sequestration in  $\alpha$ -TAT1 KO cells on treatment with Paclitaxel (Supplementary Fig. 214 S4a), suggesting that an increase in microtubule stability, or protection from disassembly, did 215 not significantly affect GEF-H1 sequestration. To examine if the acetyl moiety specifically was 216 responsible for GEF-H1 release, we co-immunostained for GEF-H1, acetylated microtubules 217 and  $\alpha$ -Tubulin in WT MEFs that were treated with Paclitaxel to eliminate any potential effects of 218 microtubule stability. We observed a negative correlation between the spatial distribution of 219 microtubule-bound GEF-H1 and acetylated microtubules (Fig. 5e, f, Supplementary Fig.S4b). To 220 test whether GEF-H1 specifically binds to non-acetylated microtubules, we exogenously 221 expressed mCherry- $\alpha$ -Tubulin or acetylation deficient mCherry- $\alpha$ -Tubulin(K40A) mutant in HeLa 222 cells and immunostained for GEF-H1. We observed increased microtubule-bound GEF-H1 in 223 the cells expressing mCherry- $\alpha$ -Tubulin(K40A), compared to non-transfected cells, or those 224 expressing WT mCherry-α-Tubulin (Supplementary Fig. S4c).

225 On stimulating α-TAT1 KO MEFs expressing mVenus-optoTAT with blue light and 226 immunostaining for GEF-H1, we observed reduced localization of endogenous GEF-H1 on 227 microtubules compared to those the cells kept in dark. (Fig. 5g, h). To examine the release 228 kinetics of GEF-H1 on microtubule acetylation, we exogenously expressed mCherry-GEF-H1, 229 EYFP-Map4m (Map4 microtubule binding domain) and miRFP703-optoTAT in HeLa cells and

characterized changes in mCherry-GEF-H1 distribution on blue light stimulation. Since YFP excitation was sufficient to activate optoTAT, we could not obtain any 'before' images except time zero. Nevertheless, we observed a persistent decrease in mCherry/EYFP signal, indicating a release of GEF-H1 from microtubules (Fig. 5i, j, Supplementary Fig. S4d,). Cross-correlation analysis of mCherry and EYFP signal in dark or after 20 min stimulation also showed a decrease, further confirming release of GEF-H1 (Fig. 5k). These data suggest that microtubule acetylation rapidly releases sequestered GEF-H1 to activate RhoA and actomyosin contractility.

237 GEF-H1 release mediates microtubule acetylation dependent myosin activation: To test whether GEF-H1 mediated optoTAT induced myosin activation, we used RNAi to deplete GEF-238 239 H1 in HeLa cells (Fig. 6a, b) and examined changes in mCherry-MRLC signal on miRFP703-240 optoTAT stimulation. Cells treated with siRNA against GEF-H1, but not the control siRNA, did 241 not show significant increase in mCherry-MRLC signal on optoTAT activation (Fig. 6c). To examine whether release of GEF-H1 from microtubules was critical for microtubule acetylation 242 243 mediated myosin activation, we used lentiviral transduction to stably express mCherry-GEF-244 H1(C53R) in α-TAT1 KO MEFs. GEF-H1(C53R) is a mutant that does not bind to microtubules (Fig. 6d) but retains its capability to activate RhoA<sup>70</sup>. mCherry-GEF-H1(C53R) expression was 245 246 sufficient to increase phospho-MRLC levels in α-TAT1 KO MEFs compared to non-transduced 247 ones in a ROCK kinase dependent manner (Fig. 6e, f). These data suggest that microtubule 248 acetylation dependent activation of Myosin was mediated by GEF-H1.

Microtubule binding deficient GEF-H1 rescues chemotaxis defects of  $\alpha$ -TAT1 KO MEFs: Based on our observations, we hypothesized that the defects in directional migration of  $\alpha$ -TAT1 KO MEFs is due to defects in release of GEF-H1 from microtubules, resulting in lower actomyosin contractility. If this were true, expressing GEF-H1(C53R) in  $\alpha$ -TAT1 KO MEFs should rescue their defects in chemotaxis. We performed chemotaxis assay with WT,  $\alpha$ -TAT1 KO MEFs

- 254 and α-TAT1 KO MEFs expressing mCherry-GEF-H1(C53R) in 0-20% FBS gradient. α-TAT1 KO-
- 255 GEF-H1(C53R) MEFs showed significantly improved chemotactic capability compared to α-
- 256 TAT1 KO MEFs, at levels comparable to WT MEFs (Fig. 6f, g, h, Supplementary Fig. S5a, b).
- 257 Altogether, these data demonstrate that microtubule acetylation drives directional migration by
- 258 modulating actomyosin contractility in migrating cells through dynamic release of sequestered
- 259 GEF-H1.

#### 260 Discussion:

Our data suggest that microtubule acetylation reduces overall motility in MEFs, but facilitates 261 directional motility by promoting a dominant protrusion, whilst inhibiting nascent ones (Fig. 1). 262 263 This coordination was achieved by modulation of actomyosin contractility and stabilizing 264 adhesions in the dominant protrusion (Fig. 2). While microtubules have been implicated in focal adhesion turnover and actomyosin contractility through Rac1 and RhoA<sup>71-77,68</sup>, the specific 265 266 effects of microtubule acetylation on myosin activation is unclear. In astrocytes and HUVEC cells, 267 microtubule acetylation promotes myosin activation through GEF-H1, whereas in human 268 foreskin fibroblasts microtubule acetylation inhibits myosin activity through MYPT1<sup>22,23</sup>. Our data 269 demonstrate that migration defects in  $\alpha$ -TAT1 KO MEFs arise from decreased actomyosin 270 contractility through sequestration of GEF-H1 in non-acetylated microtubules (Fig. 6). 271 Consistently, we observed rapid myosin activation on optoTAT stimulation through GEF-H1 272 release (Fig. 4, 5) in MEFs and HeLa cells. Intriguingly, microtubule acetylation mediated increased actomyosin contractility promoted astrocyte migration<sup>22</sup>, whereas decreased myosin 273 274 activation in human foreskin fibroblasts due to microtubule acetylation inhibited migration<sup>23</sup>. Our 275 data suggest an overall decrease in MEF motility due to increased actomyosin contractility (Fig. 276 1, 2). Although these variations in migratory phenotypes suggest a context dependent role of 277 actomyosin contractility in migrating cells, our findings using optoTAT provide evidence for a 278 specific molecular coupling between microtubule acetylation in GEF-H1 release and myosin activation. It should be noted that optoTAT lacks the C-terminus of  $\alpha$ -TAT1, which may prevent 279 280 it from fully recapitulating all signaling pathways involving α-TAT1. Additionally, the nuclear 281 sequestration of optoTAT may influence cell behavior. Nevertheless, the absence of myosin 282 activation upon stimulation with catalytically inactive optoTAT(D157N) (Fig. 4) and the increased 283 microtubule sequestration of GEF-H1 in cells expressing  $\alpha$ -Tubulin(K40A) (Supplementary Fig.

284 S4) strongly support a specific role for microtubule acetylation in facilitating GEF-H1 release and 285 myosin activation. We want to emphasize that our observations do not exclude the possibility 286 that MYPT1 plays a role in microtubule acetylation mediated regulation of myosin activity. Myosin 287 activation is spatiotemporally modulated in directionally migrating cells. It is tempting to speculate that microtubule acetylation may control GEF-H1 and MYPT1 activity in distinct 288 289 spatiotemporal manner to control myosin dynamics. Using optoTAT in these systems to test the 290 impact of microtubule acetylation on myosin activation may help resolve these contradictory 291 observations.

292 The critical role of GEF-H1 in optoTAT mediated myosin activation and rescue of chemotaxis 293 defects in α-TAT1 KO MEFs by microtubule non-binding GEF-H1(C53R) (Fig. 6) suggest that 294 GEF-H1 mediates crosstalk between actin and acetylated microtubules. Additionally, our data 295 also suggest that GEF-H1 release is not mediated solely by microtubule stability, but through the recognition of the acetyl moiety, directly or indirectly (Fig. 5, Supplementary Fig. S4). How GEF-296 297 H1 can detect acetylated versus non-acetylated microtubules is an intriguing question. Since acetylation occurs in the microtubule lumen<sup>6,9</sup>, one possibility is that GEF-H1 enters the lumen 298 299 to read the acetylation state of microtubules. Although GEF-H1 (~100 kDa) is not a small 300 molecule and its access to the narrow 15 nm diameter microtubule lumen appears difficult, larger 301 molecules such as CSPP1 (~138 kDa) have been reported to exist in the microtubule lumen<sup>78</sup>. 302 The rapid release of GEF-H1 from microtubules, in such a case, would imply a somewhat 303 permissive structure of a subset of microtubules, allowing for molecular exchange between the 304 lumen and cytoplasm. Another possibility is that while GEF-H1 binds to the microtubule surface, 305 it contains a domain which probes the lumen to detect the acetyl moiety, or the conformational 306 changes in α-tubulin due to acetylation. It is also possible that GEF-H1 localization on 307 microtubule is controlled by a third-party molecule that directly senses the acetylation state of

308 microtubules, and relays that information to GEF-H1<sup>70,79</sup>.

309 How, or even if, microtubule acetylation mediates spatiotemporal control of GEF-H1 activity is an intriguing question. In order to achieve directional persistence in migrating cells, RhoA and 310 myosin activation must be spatiotemporally regulated at sites of dynamic actin remodeling<sup>80</sup>, and 311 312 so it may be reasoned that GEF-H1 activation is also spatiotemporally regulated. One possibility 313 is that microtubule acetylation only releases GEF-H1 to increase the cytosolic pool, where GEF-314 H1 may be subcellularly activated through additional signaling pathways. Our data show 315 comparable kinetics of optoTAT mediated microtubule acetylation, GEF-H1 release, myosin 316 activation and adhesion maturation (Figs. 3, 4, 5), suggesting a direct and causal coupling of 317 these events. On the other hand, α-TAT1 KO MEFs expressing GEF-H1(C53R) are capable of 318 spatial regulation of myosin activation as well as directional migration (Fig. 6). This would 319 suggest that beyond release from sequestration, microtubule acetylation may not spatially 320 regulate GEF-H1 activation. Of course, we cannot rule out cellular adaptation in this instance. 321 OptoTAT design does not allow subcellular activation of microtubule acetylation, thus limiting our 322 capability of probing the effects of spatially restricted microtubule acetylation on cell behavior.  $\alpha$ -323 TAT1 localizes to focal adhesions through Talin binding<sup>22</sup>, which may provide localized 324 interaction with microtubules to facilitate spatially regulated GEF-H1 release and activation. 325 Spatial distribution of GEF-H1 may be fine-tuned by combination of microtubule assembly-326 disassembly and acetylation state. Further examination of the spatial regulation of microtubule 327 dynamics, microtubule acetylation and GEF-H1 activation may help us understand their interplay 328 in migrating cells.

329

#### 330 Materials and Methods

Cell culture and transfection: HeLa and HEK-293T cells were cultured in DMEM basal media 331 and passaged every third day of culture. For optimal growth, the media were supplemented with 332 333 10% (v/v) fetal bovine serum, L-Glutamine, Penicillin/Streptomycin, Non-essential amino acids 334 and 0.05 mM  $\beta$ -mercaptoethanol. WT and  $\alpha$ -TAT1 KO MEFs were a generous gift from Dr. Maxence Nachury and were cultured in DMEM basal media supplemented with 10% (v/v) fetal 335 bovine serum, L-Glutamine, Penicillin/Streptomycin, Non-essential amino acids and 0.05 mM β-336 337 mercaptoethanol. HeLa cells, WT MEFs and α-TAT1 KO MEFs stably transduced with mVenusα-TAT1, mVenus-α-TAT1(D157N), mCherry-MRLC, mVenus-optoTATV2 or mCherry-GEF-338 339 H1(C53R) were sorted using the Sony SH800 cell sorter using manufacturer's instructions to 340 select cell populations with similar mVenus or mCherry fluorescence thresholds to ensure similar 341 expression levels of the proteins of interest. The cells were maintained under standard cell 342 culture conditions (37 °C and 5% CO<sub>2</sub>) and were checked for mycoplasma contamination prior 343 to use in experiments. The stably transduced cells were cultured in medium containing 1 µg/ml 344 of puromycin. Effective puromycin dosage was ascertained by testing on WT and  $\alpha$ -TAT1 KO MEFs. FuGENE 6 reagent (Promega, Madison, WI) was used for transient transfection of HeLa 345 346 cells according to the manufacturer's instructions. For generation of lentiviral particles, HEK cells 347 were transfected using polyethyleneimine (PEI). Electroporation with Lonza electroporator was 348 performed for expression of VinTS in WT and α-TAT1 KO MEFs, according to the manufacturer's instructions. 349

DNA plasmids: α-TAT1 plasmid construct was a gift from Dr. Antonina Roll-Mecak. VinTS was
a gift from Dr. Martin Schwartz (Addgene plasmid # 26019). mCherry-MRLC and mCherryPaxillin were a gift from Dr. Yi I. Wu. NLS-mCherry-LEXY was a gift from Dr. Barbara Di Ventura
& Dr. Roland Eils (Addgene plasmid # 72655). Z-lock αTAT was a gift from Dr. Klaus Hahn

(Addgene plasmid # 175290). GFP-GEF-H1 was a gift from Dr. Hiroaki Miki. As indicated in the 354 results and figure legends, tags of compatible fluorescent proteins including Cerulean, mVenus. 355 356 mCherry and miRFP703 were appended to facilitate detection of the proteins of interest and the 357 plasmids were subcloned into C1 vector (Clontech) or pTriEx4 vector (Novagen). Unless 358 specified otherwise, the termini of tagging were positioned as in the orders they are written. 359 Lentiviral plasmids were generated based on a modified Puro-Cre vector (Addgene plasmid # 360 17408, mCMV promoter and no Cre encoding region). Point mutations or truncations of indicated 361 plasmid constructs were generated by PCR. The open reading frames of all DNA plasmids were verified by Sanger sequencing. 362

**Drug treatments:** Pharmacological drugs were purchased as indicated: Y-27632 (LC Laboratories, catalog # Y-5301), Tubacin (Selleck Chemicals, catalog # S2239), Taxol or Paclitaxel (Cell Signaling Technology, catalog # 9807S). Y-27632 was applied at 10  $\mu$ M final concentration 30 min before fixing cells or initiation of microscopy. Tubacin was applied at 2  $\mu$ M final concentration for 4 hours before initiation of microscopy. Taxol was applied at 100 nM final concentration overnight before fixing cells.

369 **Immunofluorescence assays:** For immunostaining of acetylated  $\alpha$ -Tubulin, total  $\alpha$ -Tubulin or GEF-H1, cells were fixed using ice-cold methanol for 10 minutes, washed thrice with cold PBS, 370 371 blocked with 2% BSA in PBS for one hour and then incubated overnight at 4°C with antibodies 372 against  $\alpha$ -tubulin (rat, MilliporeSigma, MAB1864), acetylated  $\alpha$ -Tubulin (mouse, MilliporeSigma, T7451) or GEF-H1 (rabbit, ThermoFisher, PA5-32213). Next day, the samples were washed 373 374 thrice with cold PBS and incubated with secondary antibodies (Invitrogen) for one hour at room 375 temperature, after which they were washed thrice with PBS and images were captured by 376 microscopy. For immunostaining of Vinculin, phospho-MRLC, and Myosin IIa, cells were fixed 377 using freshly prepared 4% paraformaldehyde at room temperature for 10 minutes, washed twice

with PBS, blocked and permeabilized in 1% BSA in PBS with 0.1% TritonX-100 at room 378 379 temperature for an hour and then incubated with antibody against Vinculin (mouse, Sigma 380 Aldrich, MAB3574), phospho-MRLC (rabbit, Cell Signaling Technology, 3671T), Myosin IIa 381 (rabbit, Cell Signaling Technology, 3403T) in the above blocking buffer at room temperature for 382 1 hour, washed three times in PBS and incubated with secondary antibody, Phalloidin 383 (ThermoFisher A22286) and DAPI (Cell Signaling Technology, 4083S). After that, they were 384 washed three times in PBS and the images were captured by microscopy. For HeLa cells 385 transiently transfected with mCherry-α-Tubulin or mCherry-α-Tubulin(K40A), fixing and immunostaining were performed 24 hours post-transfection. For Y-27632 treatment, HeLa cells 386 387 were treated with 10 µM Y-27632 or equal volume of vehicle (water), incubated for 4 hours, 388 followed by PFA fixation and immunostaining. For Taxol treatment, WT or  $\alpha$ -TAT1 KO MEFs were 389 treated with Taxol (100 nM) or vehicle (DMSO) overnight followed by methanol fixation and 390 immunostaining.

391 Western blot assays: Cell lysates were prepared by scraping cells using lysis buffer (RIPA 392 buffer, Cell Signalling # 9806S), mixed with protease/phosphatase inhibitor cocktail (Cell 393 Signaling # 5872S). Cell lysates were rotated on a wheel at 4°C for 15 min and centrifuged for 394 10 min at 15,000 g 4°C to pellet the cell debris, mixed with NuPAGE<sup>™</sup> LDS Sample Buffer 395 (Thermo Fisher # NP0007) with protease and phosphatase inhibitors and boiled 5 min at 95°C 396 before loading in polyacrylamide gels. Gels were transferred and membranes were blocked with TBST (0.1% Tween) and 5% BSA and incubated overnight with the primary antibody, and 1 h 397 398 with LiCOR IR-dye conjugated secondary antibodies after which bands were revealed using 399 Odyssey imaging system. Antibodies used: anti-α-Tubulin (rat, MilliporeSigma, MAB1864), anti-400 Vinculin (rabbit, Cell Signaling Technology, 13901S), anti-GEF-H1 (rabbit, ThermoFisher, PA5-401 32213). Secondary IR-dye conjugated antibodies were purchased from LiCOR.

Microscopy and image analyses: All epifluorescence imaging was performed with an Eclipse 402 403 Ti microscope (Nikon) with PCO.Edge sCMOS camera (Excelitas), driven by NIS Elements 404 software (Nikon). All TIRF imaging was performed with an Eclipse Ti microscope (Nikon) with 405 ORCA-FusionBT sCMOS camera (Hamamatsu), driven by NIS Elements software (Nikon). All 406 confocal images were captured using a laser scanning confocal Eclipse Ti2 microscope (Nikon) 407 equipped with a tunable GaAsp detector and 2k resonant scanner (AXR, Nikon) with camera, driven by NIS software (Nikon). All live cell imaging was conducted at 37°C, 5% CO2 and 90% 408 409 humidity with a stage top incubation system (Tokai Hit). Vitamin and phenol red-free media (US Biological) supplemented with 2% fetal bovine serum were used in imaging to reduce 410 411 background and photobleaching. Inhibitors and vehicles were present in the imaging media during imaging. All image processing and analyses were performed using Metamorph (Molecular 412 Devices, Sunnyvale, CA, USA) and FIJI software (NIH, Bethesda, MD, USA). OptoTAT 413 414 stimulation was provided by epifluorescent 440 nm excitation 20 s apart, or continual exposure 415 to blue LED light (Amazon, B08FQSFFJ60). Cells that were rounded up or showed a high degree 416 of blebbing were excluded from analysis to minimize artifacts from mitotic, apoptotic or dead 417 cells. For all ratiometric or intensity analyses, background subtraction based on a cell free area 418 on each image was performed prior to calculation of the ratio. For colocalization analysis, Coloc2 419 function in FIJI was used to calculate the Pearson's correlation coefficient (also called Pearson's R) value. Images containing any saturated pixels in any channel (65535 value) within the cell 420 421 area were excluded. The ratio of acetylated  $\alpha$ -Tubulin over  $\alpha$ -Tubulin (Ac.  $\alpha$ -Tub/ $\alpha$ -Tub) for 422 transiently transfected cells was normalized against that for non-transfected cells averaging over >20 non-transfected cells from the same dish. For mVenus-optoTAT mediated kinetics of 423 424 microtubule acetylation, only ratio of acetylated  $\alpha$ -Tubulin over  $\alpha$ -Tubulin (Ac.  $\alpha$ -Tub/ $\alpha$ -Tub) for 425 individual cells are shown. Changes in mCherry-MRLC distribution isotropy was analyzed by 426 OrientationJ plugin in FIJI<sup>81</sup>.

Cell migration assays: Random migration assays were performed in 24-well plates. 1.5 x 10<sup>4</sup> 427 WT MEFs or 1.2 x 10<sup>4</sup>  $\alpha$ -TAT1 KO MEFs were seeded and incubated for 4-5 hours. After 428 attachment, cells were imaged using phase contrast microscopy with 10X objective every 10 429 430 minutes for 15 hours. The wound healing assay was performed using Ibidi Culture-Insert 3 Well in 24-well plates (Ibidi, catalog # 80369). 3.5 x 10<sup>4</sup> WT and  $\alpha$ -TAT1 KO MEFs were seeded in 431 432 each insert well and incubated for 4-5 hours or until a full monolayer was created. After cells 433 were settled, the 3-well insert was removed, creating a 500 µm cell-free area between cell 434 monolayers. Cells were imaged using phase contrast microscopy with 10X objective every 5 435 minutes for 15 hours. The wound closure rate was calculated by determining the area of the cellfree area over time. Chemotaxis assay was performed using µ-slide chemotaxis chambers 436 437 coated with collagen IV (Ibidi, catalog # 80322) following the manufacturer's protocol. In short, 438 2.5 x 10<sup>6</sup> cells/mL aTAT1 KO MEFs, 3 x 10<sup>6</sup> cells/mL WT MEFs or 3 x 10<sup>6</sup> cells/mL KO MEFs 439 rescued with mVenus-α-TAT1 or mCherry-GEF-H1 (C53R), were seeded with serum-free DMEM and incubated at 37°C, 95% humidity, and 5% CO2 for 4-5 hours. After cells were settled, serum-440 441 free DMEM was added to the right and left reservoirs of the chamber. Half of the volume of the 442 left reservoir was replaced with DMEM supplemented with 20% FBS to generate the 443 chemoattractant gradient. Cells were imaged using phase contrast with 10X objective every 10 444 minutes for 15 hours at 37°C and 5% CO2. Tracking and analyses were performed using ImageJ 445 plug-ins, MTrackJ, and Chemotaxis tool, respectively.

Statistical analyses and reproducibility: Microsoft Excel (Microsoft, Redmond, WA, USA) and R (R Foundation for Statistical Computing, Vienna, Austria) were used for statistical analyses. The exact number of samples for each data set is specified in the respective figure legends. For live cell experiments, data were pooled from at least three independent experiments performed on different days. For immunocytochemistry data, compared data were collected from

experiments performed in parallel with cells plated on the same 8 well chambers (Cellvis, C8-1.5H-N) on the same day with the same reagents and imaging performed under the same conditions. Individual cells were identified based on Phalloidin or  $\alpha$ -Tubulin staining. Sample sizes were chosen based on the commonly used range in the field without performing any statistical power analysis and assumed to follow normal distribution. *P*-values were obtained from two-tailed Student's *t*-test assuming equal variance or paired *t*-test where applicable.

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458

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#### 471 Author contributions

472 ADR initiated the project. ADR and TI designed the experiments. ADR, CSG, FS, EY performed 473 the experiments and data analyses under guidance from TI. ADR wrote the manuscript in 474 consultation with CSG, FS and EY. TI edited the manuscript. All authors contributed to the final 475 version of the manuscript.

476

#### 477 Data availability

478 All data and plasmid constructs will be made available on reasonable requests.

479

#### 480 Competing Interests

481 The authors declare that there is a pending patent application related to optoTAT.

#### 482 Figure legends

**Figure 1.**  $\alpha$ -TAT1 modulates directional cell migration. a) Tracks, b) Speed ( $\mu$ m/hr) and c) 483 Directionality of WT and  $\alpha$ -TAT1 KO MEFs in a random migration assay, WT: 18, KO: 23 cells, 484 485 scale bar: 10 µm; d), e) Temporal changes in wound width in a wound healing assay with WT 486 and  $\alpha$ -TAT1 KO MEFs, n = 12 wound regions from 3 independent experiments, mean ± 95% C.I.; f) Schematic for chemotaxis assay (adapted from Ibidi); g) Rose plots of WT, α-TAT1 KO or 487 KO-rescue MEFs migrating in a chemotactic gradient, h) Forward migration indices along the 488 489 chemotactic gradient and i) Forward migration indices perpendicular to the chemotactic gradient 490 for WT,  $\alpha$ -TAT1 KO or KO-rescue MEFs, n = 120 cells (40 each from three independent experiments); j) Temporal changes in morphology of WT or  $\alpha$ -TAT1 KO MEFs undergoing 491 492 random migration, scale bar: 10 µm; k) Persistence of protrusions, I) Frequency of new protrusion formation in randomly migrating WT or α-TAT1 KO MEFs, WT: 23 and KO: 19 cells. 493 \*\*\*: p<0.001 494

#### 495 Figure 2. Microtubule acetylation promotes focal adhesion maturation and actomyosin

496 **contractility.** a) Vinculin distribution in WT,  $\alpha$ -TAT1 KO MEFs, and KO-rescue with mVenus- $\alpha$ -497 TAT1 or catalytic dead mVenus- $\alpha$ -TAT1(D157N) as indicated; b) Number of adhesions per cell (WT:20, KO: 17, rescue-WT: 16, rescue-D157N: 22 cells); c) Western blot showing Vinculin and 498 α-Tubulin expression in WT and α-TAT1 KO MEFs; d) Normalized Vinculin expression levels in 499 500 WT and α-TAT1 KO MEFs by Western blots (3 independent experiments, error bar: standard deviation); e) VinTS FRET index in WT and  $\alpha$ -TAT1 KO MEFs, f) Average VinTS FRET index in 501 502 WT and α-TAT1 KO MEFs (WT:: 18, KO: 16 cells); g) Phalloidin and phospho-MRLC distribution 503 in WT and  $\alpha$ -TAT1 KO MEFs, red arrowheads indicate bundled actin; h) Phospho-MRLC levels 504 in WT, α-TAT1 KO, rescue-WT and rescue-D157N MEFs (WT: 54, KO: 64, rescue-WT: 53 and rescue-D157N: 55 cells); i) mCherry-MRLC distribution and optical flow levels of mCherry-MRLC 505

506 in WT and α-TAT1 KO MEFs; j) Mean mCherry-MRLC optical flow levels in WT and α-TAT1 KO

507 MEFs (WT: 11, KO: 12 cells). Scale bar: 10 µm. \*\*\*: p<0.001

Figure 3. Developing an optogenetic actuator to induce microtubule acetylation. a) 508 509 OptoTAT design principle; b) OptoTAT versions; c) Ratio of cytoplasmic over nuclear signal for 510 different versions of optoTAT in dark and on 10 min blue light stimulation (V0: 14, V1: 17 and V2: 511 21 cells); d) Changes in intracellular distribution of mCherry-optoTAT V0, V1 and V2 in dark and 512 on blue light stimulation; e) Kymograph showing mCherry-optoTAT V2 response to blue light, 513 reference for kymograph is the red line in top panel of (d); f) Temporal changes in average 514 nuclear intensity of mCherry-optoTAT V2 on blue light stimulation indicated by blue lines, means 515  $\pm$  95% C.I. are shown, n= 21 cells; g) Microtubule acetylation levels in HeLa cells exogenously 516 expressing mCherry-optoTAT V2, kept in dark or exposed to blue light for 2 hours, red 517 arrowheads indicate transfected cells; h) Acetylated microtubule levels (normalized against total α-Tubulin) in HeLa cells expressing mCherry-optoTAT V1 or V2 in dark or exposed to 2 hours 518 519 blue light, values were normalized against non-transfected cells in the same dish (V1 dark: 30, 520 V1 light: 34, V2 dark: 27, V2 light: 33 cells); i) Temporal changes in levels of acetylated 521 microtubules (normalized against total  $\alpha$ -Tubulin) in HeLa cells stably expressing mVenus-522 optoTAT and continuously exposed to blue light stimulation for the duration indicated (0 min: 54, 523 5 min: 50, 10 min: 61, 30 min: 66, 60 min: 61, 120 min: 62, 180 min: 60 and 240 min: 61 cells), 524 means  $\pm$  95% C.I. are shown. Scale bar: 10  $\mu$ m.

Figure 4. OptoTAT stimulation rapidly induces actomyosin contractility. a) TIRF images
showing temporal changes in mCherry-MRLC distribution on miRFP703-optoTAT stimulation in
HeLa cells; b) Changes in mCherry-MRLC intensity on miRFP703-optoTAT stimulation, mean ±
95% C.I. are shown, n = 14 cells , c), d) Changes in MRLC distribution isotropy on miRFP703optoTAT stimulation, n = 14 cells; e) Changes in mCherry-MRLC intensity in TIRF plane on 30

min blue light stimulation of miRFP703-optoTAT (14 cells), catalytically dead miRFP703-530 531 optoTAT(D157N) (12 cells), miRFP703-optoTAT and pre-treatment with 2 µM Tubacin (12 cells) 532 or 10 µM Y27632 (12 cells); f) Changes in LifeAct-mCherry on miRFP703-optoTAT stimulation. 533 red arrowheads indicate bundled actin; g) Changes in LifeAct-mCherry intensity in TIRF plane 534 on 30 min blue light stimulation of miRFP703-optoTAT (12 cells), catalytically dead miRFP703-535 optoTAT(D157N) (12 cells), miRFP703-optoTAT and pre-treatment with 2 µM Tubacin (12 cells) 536 or 10 µM Y27632 (10 cells), h) Changes in mCherry-Paxillin on miRFP703-optoTAT stimulation, 537 i) Changes in average focal adhesion sizes and j) changes in average mCherry-Paxillin intensity on 30 min miRFP703-optoTAT stimulation, mean  $\pm$  95% C.I. are shown, n = 14 cells. Scale bar: 538 539 10 µm. \*\*\*: p<0.001. Blue line: Blue light stimulation.

540 Figure 5. Microtubule acetylation releases GEF-H1 sequestration . a) α-Tubulin and GEF-541 H1 localization in WT and  $\alpha$ -TAT1 KO MEFs, inset for GEF-H1 is magnified on right; b) linear 542 density of GEF-H1 along microtubules in WT and  $\alpha$ -TAT1 KO MEFs (5 microtubules from 30 543 cells each, total 150); c), d) GEF-H1 expression levels in WT and  $\alpha$ -TAT1 KO MEFs measured 544 using Western blots (3 independent experiments, error bar: standard deviation); e) Relative 545 distributions of acetylated microtubules (top panel) and microtubule-bound GEF-H1 (bottom 546 panel) in overnight 100 nM Taxol treated WT MEFs, inset magnified on the right panels; f) 547 Pearson's R value for spatial colocalization of acetylated microtubules and microtubule-bound 548 GEF-H1 in Taxol treated WT MEFs, n = 33 cells; g) GEF-H1 localization in  $\alpha$ -TAT1 KO MEFs stably expressing mVenus-optoTAT kept in dark or with 30 min blue light stimulation; h) linear 549 550 density of GEF-H1 along microtubules in α-TAT1 KO MEFs stably expressing mVenus-optoTAT 551 kept in dark or exposed to 30 min blue light stimulation (5 microtubules from 30 cells each, total 552 150); i) Changes in mCherry-GEF-H1/mVenus-MAP4m signal in HeLa cells expressing miRFP703-optoTAT on blue light stimulation, inset is magnified in the right panels; j) Temporal 553

554 changes in mCherry-GEF-H1/mVenus-MAP4m on miRFP703-optoTAT stimulation, mean  $\pm$  95% 555 C.I. are shown, n = 33 cells; k) Changes in colocalization of mCherry-GEF-H1 and mVenus-556 Map4m on miRFP703-optoTAT stimulation for 30 min, n = 33 cells. Scale bar: 10 µm. \*\*\*: 557 p<0.001

### 558 Figure 6. GEF-H1 mediates microtubule acetylation dependent actomyosin contractility .

559 a), b) GEF-H1 knock-down in HeLa cells by siRNA; c) Changes in mCherry-MRLC intensity on 560 miRFP703-optoTAT stimulation in HeLa cells with optoTAT (20 cells), scramble siRNA (21 cells), 561 siRNA1 (25 cells) and siRNA3 (22 cells) against GEF-H1; d) TIRF images of HeLa cells expressing GFP-GEF-H1 (top panel) and mCherry-GEF-H1(C53R); e) Phospho-MRLC levels in 562 WT (67 cells), a-TAT1 KO (69 cells), a-TAT1 KO MEFs expressing mCherry-GEF-H1(C53R) (67 563 564 cells) and same cells treated with 10 µM Y-27632 (60 cells); f) Phalloidin and phospho-MRLC 565 distribution in WT, a-TAT1 KO MEFs and a-TAT1 KO MEFs expressing mCherry-GEF-H1(C53R); g) Rose plots of WT, α-TAT1 KO and KO-GEF-H1(C53R) MEFs migrating in a chemotactic 566 567 gradient; g) Forward migration indices along the chemotactic gradient and h) Forward migration 568 indices perpendicular to the chemotactic gradient for WT,  $\alpha$ -TAT1 KO and KO-GEF-H1(C53R) 569 MEFs, n = 120 cells (40 each from three independent experiments). Scale bar: 10  $\mu$ m. \*\*\*: 570 p<0.001

#### 571 Supplementary information

**Supplementary Figure S1.** a) Tracks of WT,  $\alpha$ -TAT1 KO and KO-rescue with  $\alpha$ -TAT1 MEFs in chemotaxis assay, n = 120 cells (40 each from three independent experiments); b) Final location of individual cells (black dots) and the center of mass of all the cells (red circle) in chemotaxis assay, origin is indicated by "+", distance between origin and center of mass ( $\delta$ ) is shown above the inset; c) Circularity and d) Convexity of WT  $\alpha$ -TAT1 KO MEFs (WT: 40 and KO: 54 cells); e)

577 Morphological changes in serum-starved WT and α-TAT1 KO MEFs on addition of 10% FBS,

578 induced protrusions are indicated with red arrowheads, scale bar: 10 μm. \*\*\*: p<0.001

**Supplementary Figure S2.** a) Cell areas of WT and  $\alpha$ -TAT1 KO MEFs (WT: 40, KO: 54 cells); 579 580 b) adhesion sizes, c) average vinculin intensity per cell, d) average vinculin intensity per 581 adhesion in WT, α-TAT1 KO, rescue-WT and rescue-D157N MEFs (WT: 20, KO: 17, rescue-WT: 16, rescue-D157N: 22 cells); e) VinTS FRET index per adhesion in WT and α-TAT1 KO MEFs 582 (WT:: 18, KO: 16 cells); f), g) Myosin IIa levels in WT and α-TAT1 KO MEFs (WT: 69, KO: 65 583 584 cells); h), i) Phospho-MRLC levels in WT and α-TAT1 KO MEFs treated with vehicle or 10 μM Y-27632 (WT-vehicle: 88, WT-Y27632: 91, KO-vehicle: 89, KO-Y27632: 98 cells); j) TIRF images 585 of and k) changes in fluorescence intensity of mCherry-MRLC in WT MEFs on tubacin treatment, 586 587 12 cells, mean ± 95% C.I.; scale bar: 10 µm. \*\*\*: p<0.001

Supplementary Figure S3. a) Microtubule acetylation levels in HeLa cells exogenously 588 expressing mCherry-Z-Lock- $\alpha$ -TAT1, kept in dark or exposed to blue light for 2 hours, red 589 arrowheads indicate transfected cells; scale bar: 10 µm; b) Microtubule acetylation levels in Hela 590 591 cells expressing mCherry-Z-Lock- $\alpha$ -TAT1 in dark or after blue light exposure, normalized against 592 acetylation levels in non-transfected cells; c) Temporal changes in acetylated microtubules (normalized against total α-Tubulin) on blue light stimulation of HeLa cells stably expressing 593 594 mVenus-optoTAT V2 (0 min: 54, 5 min: 50, 10 min: 61, 30 min: 66, 60 min: 61, 120 min: 62, 180 595 min: 60 and 240 min: 61 cells), red dots indicate the mean values; note: time scale is not linear.

**Supplementary Figure S4.** a) Immunostaining against  $\alpha$ -Tubulin and GEF-H1  $\alpha$ -TAT1 KO MEFs treated with vehicle (DMSO) or 100 nM Taxol overnight; b) Immunostaining against  $\alpha$ -Tubulin, acetylated  $\alpha$ -Tubulin and GEF-H1 in WT MEFs treated with 100 nM Taxol overnight; c) Immunostaining against  $\alpha$ -Tubulin and GEF-H1 in HeLa cells expressing mCherry- $\alpha$ -Tubulin or mCherry- $\alpha$ -Tubulin(K40A) (lower panels), transfected cells are indicated with red arrowheads,

insets are magnified on the right panel; d) Changes in mCherry-GEF-H1/mVenus-MAP4m signal
in HeLa cells expressing miRFP703-optoTAT on blue light stimulation, inset is magnified in the
right panels; Scale bar: 10 µm or as indicated.

**Supplementary Figure S5.** a) Tracks of WT, α-TAT1 KO and KO-rescue with mCherry-GEF-

H1(C53R) MEFs in chemotaxis assay, n = 120 cells (40 each from three independent

606 experiments); b) Final location of individual cells (black dots) and the center of mass of all the

607 cells (red circle) in chemotaxis assay, origin is indicated by "+", distance between origin and

608 center of mass ( $\delta$ ) is shown above the inset.

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**Figure 1. α-TAT1 modulates directional cell migration.** a) Tracks, b) Speed (µm/hr) and c) Directionality of WT and α-TAT1 KO MEFs in a random migration assay, WT: 18, KO: 23 cells, scale bar: 10 µm; d), e) Temporal changes in wound width in a wound healing assay with WT and α-TAT1 KO MEFs, n = 12 wound regions from 3 independent experiments, mean  $\pm$  95% C.I.; f) Schematic for chemotaxis assay *(adapted from Ibidi);* g) Rose plots of WT, α-TAT1 KO or KO-rescue MEFs migrating in a chemotactic gradient, h) Forward migration indices along the chemotactic gradient and i) Forward migration indices perpendicular to the chemotactic gradient for WT, α-TAT1 KO or KO-rescue MEFs, n = 120 cells (40 each from three independent experiments); j) Temporal changes in morphology of WT or α-TAT1 KO MEFs undergoing random migration, scale bar: 10 µm; k) Persistence of protrusions, I) Frequency of new protrusion formations in randomly migrating WT or α-TAT1 KO MEFs, WT: 23 and KO: 19 cells. \*\*\*: p<0.001



## Figure 2. Microtubule acetylation promotes focal adhesion maturation and actomyosin

**contractility.** a) Vinculin distribution in WT,  $\alpha$ -TAT1 KO MEFs, and KO-rescue with mVenus- $\alpha$ -TAT1 or catalytic dead mVenus- $\alpha$ -TAT1(D157N) as indicated; b) Number of adhesions per cell (WT:20, KO: 17, rescue-WT: 16, rescue-D157N: 22 cells); c) Western blot showing Vinculin and  $\alpha$ -Tubulin expression in WT and  $\alpha$ -TAT1 KO MEFs; d) Normalized Vinculin expression levels in WT and  $\alpha$ -TAT1 KO MEFs by western blots (3 independent experiments, error bar: standard deviation); e) VinTS FRET index in WT and  $\alpha$ -TAT1 KO MEFs, f) Average VinTS FRET index in WT and  $\alpha$ -TAT1 KO MEFs (WT: 18, KO: 16 cells); g) Phalloidin and phospho-MRLC distribution in WT and  $\alpha$ -TAT1 KO MEFs, red arrowheads indicate bundled actin; h) Phospho-MRLC levels in WT,  $\alpha$ -TAT1 KO, rescue-WT and rescue-D157N MEFs (WT: 54, KO: 64, rescue-WT: 53 and rescue-D157N: 55 cells); i) mCherry-MRLC distribution and optical flow levels of mCherry-MRLC in WT and  $\alpha$ -TAT1 KO MEFs; j) Mean mCherry-MRLC optical flow levels in WT and  $\alpha$ -TAT1 KO MEFs (WT: 11, KO: 12 cells). Scale bar: 10 µm. \*\*\*: p<0.001



Figure 3. Developing an optogenetic actuator to induce microtubule acetylation. a) OptoTAT design principle; b) OptoTAT versions; c) Ratio of cytoplasmic over nuclear signal for different versions of optoTAT in dark and on 10 min blue light stimulation (V0: 14, V1: 17 and V2: 21 cells); d) Changes in intracellular distribution of mCherry-optoTAT V0, V1 and V2 in dark and on blue light stimulation; e) Kymograph showing mCherry-optoTAT V2 response to blue light, reference for kymograph is the red line in top panel of (d); f) Temporal changes in average nuclear intensity of mCherry-optoTAT V2 on blue light stimulation indicated by blue lines, means ± 95% C.I. are shown, n= 21 cells; g) Microtubule acetylation levels in HeLa cells exogenously expressing mCherry-optoTAT V2, kept in dark or exposed to blue light for 2 hours, red arrowheads indicate transfected cells; h) Acetylated microtubule levels (normalized against total α-Tubulin) in HeLa cells expressing mCherry-optoTAT V1 or V2 in dark or exposed to 2 hours blue light, values were normalized against non-transfected cells in the same dish (V1 dark: 30, V1 light: 34, V2 dark: 27, V2 light: 33 cells); i) Temporal changes in levels of acetylated microtubules (normalized against total α-Tubulin) in HeLa cells stably expressing mVenus-optoTAT and continuously exposed to blue light stimulation for the duration indicated (0 min: 54, 5 min: 50, 10 min: 61, 30 min: 66, 60 min: 61, 120 min: 62, 180 min: 60 and 240 min: 61 cells), means ± 95% C.I. are shown. Scale bar: 10 µm.



**Figure 4. OptoTAT stimulation rapidly induces actomyosin contractility.** a) TIRF images showing temporal changes in mCherry-MRLC distribution on miRFP703-optoTAT stimulation in HeLa cells; b) Changes in mCherry-MRLC intensity on miRFP703-optoTAT stimulation, mean  $\pm$  95% C.I. are shown, n = 14 cells; c), d) Changes in MRLC distribution isotropy on miRFP703-optoTAT stimulation, n = 14 cells; e) Changes in mCherry-MRLC intensity in TIRF plane on 30 min blue light stimulation of miRFP703-optoTAT (14 cells), catalytically dead miRFP703-optoTAT(D157N) (12 cells), miRFP703-optoTAT and pre-treatment with 2 µM Tubacin (12 cells) or 10 µM Y27632 (12 cells); f) Changes in LifeAct-mCherry on miRFP703-optoTAT stimulation, red arrowheads indicate bundled actin; g) Changes in LifeAct-mCherry intensity in TIRF plane on 30 min blue light stimulation of miRFP703-optoTAT (12 cells), catalytically dead miRFP703-optoTAT(D157N) (12 cells), miRFP703-optoTAT and pre-treatment with 2 µM Tubacin (12 cells) or 10 µM Y27632 (10 cells), miRFP703-optoTAT and pre-treatment with 2 µM Tubacin (12 cells) or 10 µM Y27632 (10 cells), miRFP703-optoTAT and pre-treatment with 2 µM Tubacin (12 cells) or 10 µM Y27632 (10 cells), h) Changes in mCherry-Paxillin on miRFP703-optoTAT stimulation, i) Changes in average focal adhesion sizes and j) changes in average mCherry-Paxillin intensity on 30 min miRFP703-optoTAT stimulation, mean  $\pm$  95% C.I. are shown, n = 14 cells. Scale bar: 10 µm. \*\*\*: p<0.001. Blue line: Blue light stimulation.



Figure 5. Microtubule acetylation releases GEF-H1 sequestration . a) α-Tubulin and GEF-H1 localization in WT and α-TAT1 KO MEFs, inset for GEF-H1 is magnified on right; b) linear density of GEF-H1 along microtubules in WT and  $\alpha$ -TAT1 KO MEFs (5 microtubules from 30 cells each, total 150); c), d) GEF-H1 expression levels in WT and α-TAT1 KO MEFs measured using western blots (3 independent experiments, error bar: standard deviation); e) Relative distributions of acetylated microtubules (top panel) and microtubule-bound GEF-H1 (bottom panel) in overnight 100 nM Taxol treated WT MEFs, inset magnified on the right panels; f) Pearson's R value for spatial colocalization of acetylated microtubules and microtubule-bound GEF-H1 in Taxol treated WT MEFs, n = 33 cells; g) GEF-H1 localization in α-TAT1 KO MEFs stably expressing mVenus-optoTAT kept in dark or with 30 min blue light stimulation; h) linear density of GEF-H1 along microtubules in α-TAT1 KO MEFs stably expressing mVenus-optoTAT kept in dark or exposed to 30 min blue light stimulation (5 microtubules from 30 cells each, total 150); i) Changes in mCherry-GEF-H1/mVenus-MAP4m signal in HeLa cells expressing miRFP703-optoTAT on blue light stimulation, inset is magnified in the right panels; j) Temporal changes in mCherry-GEF-H1/mVenus-MAP4m on miRFP703-optoTAT stimulation, mean ± 95% C.I. are shown, n = 33 cells; k) Changes in colocalization of mCherry-GEF-H1 and mVenus-Map4m on miRFP703-optoTAT stimulation for 30 min, n = 33 cells. Scale bar: 10 µm. \*\*\*: p<0.001



**Figure 6. GEF-H1 mediates microtubule acetylation dependent actomyosin contractility .** a), b) GEF-H1 knock-down in HeLa cells by siRNA; c) Changes in mCherry-MRLC intensity on miRFP703-optoTAT stimulation in HeLa cells with optoTAT (20 cells), scramble siRNA (21 cells), siRNA1 (25 cells) and siRNA3 (22 cells) against GEF-H1; d) TIRF images of HeLa cells expressing GFP-GEF-H1 (top panel) and mCherry-GEF-H1(C53R); e) Phospho-MRLC levels in WT (67 cells),  $\alpha$ -TAT1 KO (69 cells),  $\alpha$ -TAT1 KO MEFs expressing mCherry-GEF-H1(C53R) (67 cells) and same cells treated with 10  $\mu$ M Y-27632 (60 cells); f) Phalloidin and phospho-MRLC distribution in WT,  $\alpha$ -TAT1 KO MEFs and  $\alpha$ -TAT1 KO MEFs expressing mCherry-GEF-H1(C53R); g) Rose plots of WT,  $\alpha$ -TAT1 KO and KO-GEF-H1(C53R) MEFs migrating in a chemotactic gradient; g) Forward migration indices along the chemotactic gradient and h) Forward migration indices perpendicular to the chemotactic gradient for WT,  $\alpha$ -TAT1 KO and KO-GEF-H1(C53R) MEFs, n = 120 cells (40 each from three independent experiments). Scale bar: 10  $\mu$ m. \*\*\*: p<0.001

## Supplementary Figure 1



**Supplementary Figure S1.** a) Tracks of WT,  $\alpha$ -TAT1 KO and KO-rescue with  $\alpha$ -TAT1 MEFs in chemotaxis assay, n = 120 cells (40 each from three independent experiments); b) Final location of individual cells (black dots) and the center of mass of all the cells (red circle) in chemotaxis assay, origin is indicated by "+", distance between origin and center of mass ( $\delta$ ) is shown above the inset; c) Circularity and d) Convexity of WT  $\alpha$ -TAT1 KO MEFs (WT: 40 and KO: 54 cells); e) Morphological changes in serum-starved WT and  $\alpha$ -TAT1 KO MEFs on addition of 10% FBS, induced protrusions are indicated with red arrowheads, scale bar: 10 µm. \*\*\*: p<0.001

Supplementary Figure 2



**Supplementary Figure S2.** a) Cell areas of WT and  $\alpha$ -TAT1 KO MEFs (WT: 40, KO: 54 cells); b) adhesion sizes, c) average vinculin intensity per cell, d) average vinculin intensity per adhesion in WT,  $\alpha$ -TAT1 KO, rescue-WT and rescue-D157N MEFs (WT: 20, KO: 17, rescue-WT: 16, rescue-D157N: 22 cells); e) VinTS FRET index per adhesion in WT and  $\alpha$ -TAT1 KO MEFs (WT: 18, KO: 16 cells); f), g) Myosin IIa levels in WT and  $\alpha$ -TAT1 KO MEFs (WT: 69, KO: 65 cells); h), i) Phospho-MRLC levels in WT and  $\alpha$ -TAT1 KO MEFs (WT: 69, KO: 65 cells); h), i) Phospho-MRLC levels in WT and  $\alpha$ -TAT1 KO MEFs treated with vehicle or 10  $\mu$ M Y-27632 (WT-vehicle: 88, WT-Y27632: 91, KO-vehicle: 89, KO-Y27632: 98 cells); j) TIRF images of and k) changes in fluorescence intensity of mCherry-MRLC in WT MEFs on tubacin treatment, 12 cells, mean ± 95% C.I.; scale bar: 10  $\mu$ m. \*\*\*: p<0.001

# Supplementary Figure 3



**Supplementary Figure S3.** a) Microtubule acetylation levels in HeLa cells exogenously expressing mCherry-Z-Lock- $\alpha$ -TAT1, kept in dark or exposed to blue light for 2 hours, red arrowheads indicate transfected cells; scale bar: 10 µm; b) Microtubule acetylation levels in Hela cells expressing mCherry-Z-Lock- $\alpha$ -TAT1 in dark or after blue light exposure, normalized against acetylation levels in non-transfected cells; c) Temporal changes in acetylated microtubules (normalized against total  $\alpha$ -Tubulin) on blue light stimulation of HeLa cells stably expressing mVenus-optoTAT V2 (0 min: 54, 5 min: 50, 10 min: 61, 30 min: 66, 60 min: 61, 120 min: 62, 180 min: 60 and 240 min: 61 cells), red dots indicate the mean values; note: time scale is not linear.



**Supplementary Figure S4.** a) Immunostaining against  $\alpha$ -Tubulin and GEF-H1  $\alpha$ -TAT1 KO MEFs treated with vehicle (DMSO) or 100 nM Taxol overnight; b) Immunostaining against  $\alpha$ -Tubulin, acetylated  $\alpha$ -Tubulin and GEF-H1 in WT MEFs treated with 100 nM Taxol overnight; c) Immunostaining against  $\alpha$ -Tubulin and GEF-H1 in HeLa cells expressing mCherry- $\alpha$ -Tubulin or mCherry- $\alpha$ -Tubulin(K40A) (lower panels), transfected cells are indicated with red arrowheads, insets are magnified on the right panel; d) Changes in mCherry-GEF-H1/mVenus-MAP4m signal in HeLa cells expressing miRFP703-optoTAT on blue light stimulation, inset is magnified in the right panels; Scale bar: 10 µm or as indicated.

## **Supplementary Figure 5**



**Supplementary Figure S5.** a) Tracks of WT,  $\alpha$ -TAT1 KO and KO-rescue with mCherry-GEF-H1(C53R) MEFs in chemotaxis assay, n = 120 cells (40 each from three independent experiments); b) Final location of individual cells (black dots) and the center of mass of all the cells (red circle) in chemotaxis assay, origin is indicated by "+", distance between origin and center of mass ( $\delta$ ) is shown above the inset.