1 Proper migration of lymphatic endothelial cells requires survival and guidance cues 2 from arterial mural cells 3 Di Peng¹, Koji Ando^{2#}, Marleen Gloger¹, Renae Skoczylas¹, Naoki Mochizuki³, Christer 4 Betsholtz^{4,5}, Shigetomo Fukuhara², Katarzyna Koltowska^{1#} 5 6 ¹ Uppsala University, Immunology Genetics and Pathology, 752 37 Uppsala Sweden 7 8 ² Department of Molecular Pathophysiology, Institute of Advanced Medical Sciences, Nippon 9 Medical School, Sendagi Bunkyo-ku, Tokyo 113 8602, JAPAN 10 ³ Department of Cell Biology, National Cerebral and Cardiovascular Center Research Institute, 11 Suita, Osaka 564 8565, Japan 12 ⁴ Department of Immunology, Genetics and Pathology, Rudbeck Laboratory, Uppsala 13 University, Dag Hammarskjölds väg 20, SE-751 85 Uppsala, Sweden 14 ⁵ Department of Medicine Huddinge (MedH), Karolinska Institutet, Campus Flemingsberg, 15 Neo, Blickagången 16, Hiss S, plan 7, SE-141 57 Huddinge, Sweden 16 17 18 19 [#]Author for Correspondence: 20 Koji Ando, koji-ando@nms.ac.jp 21 Katarzyna Koltowska, kaska.koltowska@igp.uu.se 22 23 **Keywords:** Lymphatics, Lymphangiogenesis, mural cells, Pdgfrß, cell migration, Vegfc, 24 Cxcl12b 25

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27 ABSTRACT

28 The migration of lymphatic endothelial cells (LECs) is key for the development of the complex 29 and vast lymphatic vascular network that pervades most of the tissues in an organism. In 30 zebrafish, arterial intersegmental vessels together with chemokines have been shown to 31 promote lymphatic cell migration from the horizontal myoseptum (HM). Here we found that 32 LECs departure from HM coincides with the emergence of mural cells around the 33 intersegmental arteries, raising the possibility that arterial mural cells promote LEC migration. 34 Our live imaging and cell ablation experiments revealed that LECs migrate slower and fail to 35 establish the lymphatic vascular network in the absence of arterial mural cells. We determined 36 that mural cells are a source for the C-X-C motif chemokine 12 (Cxcl12a and Cxcl12b) and 37 vascular endothelial growth factor C (Vegfc). We showed that ERK, a downstream component 38 of Vegfc-Vegfr3 singling cascade, is activated in migrating LECs and that both chemokine and 39 growth factor signalling is required for the robust migration. Furthermore, Vegfc-Vegfr3 has a 40 pro-survival role in LECs during the migration. Together, the identification of mural cells a 41 source for signals that guide LEC migration and survival will be important in the future design 42 for rebuilding lymphatic vessels in the disease contexts.

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44 INTRODUCTION

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46 The lymphatic vessel network spans across the whole body to balance the tissue fluid 47 homeostasis, coordinate the immune responses, and enable dietary fat absorption in the 48 intestine. The robustness of the formation and reproducibility of the vascular tree is dependent 49 on molecular dynamics and tissue-tissue interaction required for the precision and fine-tuning 50 of lymphatic endothelial cell (LEC) migration. Although multiple previous studies have 51 uncovered important signals and cells guiding lymphatic vessel formation (Bussmann et al., 52 2010; Cha et al., 2012; Jafree et al., 2021), the recent technological developments and new 53 transgenic lines (Ando et al., 2016; Wang et al., 2020) have opened up opportunities to identify 54 further regulators of LEC migration.

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56 In zebrafish trunk, lymphatic vessel specification is marked by the expression of transcription 57 factor Prox1 in ECs around 32 hours post fertilization (hpf) in response to Vegfc-Vegfr3 58 signalling (Koltowska et al., 2015a). Around 34 hpf, venous-derived Prox1 positive cells sprout from the posterior cardinal vein (PCV) and migrate to the horizontal myoseptum (HM), 59 60 establishing parachordal lymphatic endothelial cells (PL) (Hogan and Schulte-Merker, 2017). 61 After about 10 hours the PLs move out from HM and migrate dorsally or ventrally and by 5 62 days post fertilization (dpf) give raise to the main trunk lymphatic vessels, including dorsal 63 longitude lymphatic vessel (DLLV), intersegmental lymphatic vessel (ISLV) and thoracic duct 64 (TD), by 5 days post fertilization (dpf) (Kuchler et al., 2006; Yaniv et al., 2006). During this later 65 migration, vast majority of the LECs are associated with the arterial intersegmental vessels 66 (alSV) al.. 2010). In mutant embryos alSV (Bussmann et lacking (plcv^{t26480} and kdrl^{hu5088} mutants), PLs remain in HM, and subsequent the lymphatic network 67 formation is compromised (Bussmann et al., 2010). On molecular level, Cxcl12b secreted from 68 69 arterial ECs (aECs) in ISV guides this LECs migration via Cxcr4 receptor expressed in LECs 70 (Cha et al., 2012). Yet, if other tissues or cells cooperate with arterial ECs to support this 71 migration remains unknown.

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Simultaneous with LEC development described above, vascular mural cells (MC) are formed *de novo* along alSVs and beneath the dorsal aorta. alSVs play a critical role in this process,
and MC-emergence is completely abolished in the absence of arterial ECs (Ando *et al.*, 2016).
The spatio-temporal similarity of MC and lymphatic vessel development around alSV raises
the question about possible interaction between MCs and LECs in this region.

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79 VEGFC-mediated signalling through the VEGFR3 receptor is essential for multiple steps of 80 lymphatic vessels formation, including LEC proliferation, differentiation, and migration. In vitro 81 cell culture experiments have demonstrated that VEGFC-VEGFR3 and β 1 integrin to promote 82 LEC migration (Makinen et al., 2001; Wang et al., 2001). Studies using vegfc reporter 83 zebrafish line has uncovered multiple sources of *veqfc*, including the fibroblasts and neurons, 84 which contributes to the initial sprouting and migration of lymphatic vessel into the HM (early 85 migration) (Wang et al., 2020). The requirement of VEGFC-VEGFR3 and its source(s) in the 86 LEC migration out of the HM (late migration) remains to be defined. Mechanistically, 87 transcription factor Mafba, which regulates LEC migration but not proliferation, has been 88 shown to act downstream of VEGFC-VEGFR3 signalling (Dieterich et al., 2015; Koltowska et 89 al., 2015b). A genome-wide analysis further indicted the presence of a transcriptional network 90 controlling LEC migration, through the induction of chemokine receptors that promote 91 chemotaxis in migrating LECs (Williams et al., 2017). Although the migratory regulators have 92 been identified, the upstream cellular source of the signals initiating the migration is unknown.

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Here, we took advantage of the transgenic zebrafish reporters which allow to visualize MC and LEC simultaneously at high spatio-temporal resolution *in vivo*, and to investigate their communication during lymphangiogenesis. We found that MCs emergence precedes LEC migration along alSV and that LECs interact with MCs residing at the alSVs. Moreover, in the absence of MCs, the LECs migration was inhibited, and lymphatic vessel formation was compromised. We further determined that MCs produce lymphangiogenic factors including

- 100 vegfc, cxcl12a, and cxcl12b. Thus, this study uncovers a close interaction between MC-LEC
- 101 of functional importance for lymphatic vessel formation in the zebrafish trunk.
- 102

103 **RESULTS AND DISUCSSION**

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105 $\,$ MCs and LECs interact during LEC migration $\,$

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107 To address a potential interaction between MCs and LECs around arteries, we examined their 108 distribution around alSVs, using the reporter lines 109 Tg(lyve1b:DsRed);Tg(flt1:YFP);Tg(pdgfrb:GFP) and found the spatial proximity, with MCs 110 being sandwiched between the aISV and the migrating LEC at 4 dpf (Figure 1A). Time lapse 111 imaging showed that LECs migrated out from HM immediately after the emergence of pdgfrb⁺ 112 MCs (Figure 1B and C, Supplemental Figure 1A). The number of MCs was not changed before and after the LEC migration along aISV (Figure 1D) and in approximately 90% of the 113 114 cases, LEC migrated towards and interacted with the MC residing on aISV (n=24 Figure 1E-115 F). When LEC migrated out from HM, we noticed that LEC dynamically extended and 116 regressed protrusions as if they sensed the environment and searched for the nearby located 117 MC (Figure 1E, Supplemental Figure 1A). To understand the biological significance of this 118 interaction, we quantified the velocity of LEC migration along aISV and found that the LECs in 119 contact with the MCs migrated two times faster than LECs migrating along aISV without MCs 120 (Figure 1G). These observations suggest that MCs might provide directional cues to promote 121 robust LEC migration.

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123 MCs promote lymphatic vessel formation

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125 We next asked if *pdgfrb* positive MCs are necessary for lymphatic vessels formation. PDGFRB 126 is known to be essential for MC development, especially their proliferation and migration (Ando et al., 2016; Gaengel et al., 2009). The pdgfrb^{um148} mutant zebrafish (Kok et al., 2015) showed 127 30% reduction of MC-number around aISVs (Figure 1H-I). Coincidently, trunk lymphatic 128 vasculature formation in *pdgfrb^{um148}* mutant zebrafish revealed slight reduction in the network 129 130 formation. The rendering of the area of *lyve:DsRed* labelled lymphatic vessels, as a measure of lymphatic vessels density, revealed on average an area of 100 mm² in the sibling vs. 70 131 mm² in the *pdgfrb^{um148}* mutants (**Figure 1H and 1J**). Treatment with a PDGFRβ inhibitor, 132 133 AG1296 from 48 hpf, led to a greater reduction in MC-coverage and LECs number 134 (Supplementary Figure 1B). Together, although it cannot be excluded that AG1296 inhibitor 135 directly affected lymphatic vessels development, these observations suggest a requirement of 136 *pdgfrb*⁺ MCs for lymphatic development.

137 As both mutant or AG1296-treated larvae retained a substantial proportion of their MCs, we 138 decided to eliminate pdgfrb⁺ MCs utilizing MC-selective Nitroreductaes (NTR) and 139 metorodinazole (Mtz) (NTR-system) system (Curado et al.. 2008), 140 TgBAC(pdgfrb:Gal4FF);Tg(14xUAS:3xFLAG-NTR, NLS-mCherry) to confirm the involvement 141 of MCs for lymphatic vessel formation. In this transgenic line, Mtz is converted to its cytotoxic 142 form by NTR expressed in $pdqfrb^+$ MCs leading to selective MC-death in the trunk 143 (Supplementary Figure 2A). When ablating MCs just prior to LEC migration out from HM by 144 utilizing this MC-selective NTR-MTZ ablation system, LEC migration along aISV and 145 subsequent TD formation were severely compromised (Figure 2 A-C). To further determine if 146 MCs are necessary for LEC migration, we ablated MCs locally by multi-photon laser after LEC 147 just migrated out of HM (Figure 2D). As a control we targeted the tissue adjacent to the MCs 148 in the same embryo (Figure 2E). We imaged the same embryos one day later and observed 149 that 40% of the LECs in the MC-ablated group fail to migrate to form DLLV (Figure 2E-H). 150 The time-lapse imaging over 5 hours post ablation (pa) confirmed that LEC migration was 151 dramatically inhibited in the MC-ablated group compared to the control non-MC ablated group 152 (Figure 2E-H).

Together, these data show the MC-LEC interaction at high spatio-temporal resolution during
 lymphatic development and demonstrate an important role of arterial associated MCs for the
 robust LEC migration.

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157 Chemokines are expressed in *pdgfrb*⁺-mural cells during LEC migration

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159 The importance of MCs for LEC migration might represent a direct interaction between the 160 two cells or an indirect effect mediated via aISV ECs, which were previously shown to be 161 necessary for LEC guidance (Bussmann et al., 2010). The absence of MCs does not affect 162 arterial identity at early stages in zebrafish (Ando et al., 2019), arguing that the importance of 163 MC in LEC development is not simply to regulate aEC presence or abundance. However, in 164 order to directly test aEC function is critical for MC-dependent LEC migration in aISV, we also 165 ablated ECs in aISV after the emergence of MCs using the multi-photon laser system. We 166 observed that even in the absence of aEC, but remaining presence of MCs, LEC migration 167 progressed (Figure 3A), suggesting that signals from MCs are sufficient to promote LEC 168 migration. Thus, the previously reported strong inhibition of LEC development in alSV-169 depleted mutants (Bussmann et al., 2010) might include the effects of MC-loss as aISVs ECs 170 are essential for MC-formation (Ando et al., 2016). However, as the aISV rapidly regrow 171 following laser ablation system (Figure 3A-C), the long-term effects cannot be assessed, and 172 it remains to be determined to what extend the molecular signals from MC act in synergy with 173 aECs to promote LEC migration.

174 Based on the above observations, we hypothesise that MC may also secrete chemoattractant 175 molecules to guide the LECs (Figure 3A). It has been shown that the LEC migration is driven 176 by the chemokines Cxcl12a and Cxcl12b (Cha et al., 2012), which are expressed in ECs. To 177 test if Cxcl12a and Cxcl12b are also expressed in MCs we collected cells by fluorescent 178 activated cell sorting (FACS) from Tg(flt1:YFP); TgBAC(abcc9:Gal4FF); Tg(UAS:GFP); 179 *Tg(lyve1b:DsRED); Tg(kdrl:mCherry)* larvae at 3 dpf and analysed candidate genes 180 expression in aECs (double positive for green (YFP) and red (mCherry) fluorescence), MCs 181 (single positive for green (GFP) fluorescence), and venous ECs and LECs (single positive for 182 red (DsRED/mCherry) fluorescence) (Figure 3D, Supplementary Figure 3A). Although 183 abcc9 reporter is highly selective for ISV-MCs in the trunk, posterior notochord is also labelled 184 (Ando et al., 2019). Therefore, to avoid the possible contamination of other cell types than 185 abcc9 positive MCs, we used micro-dissection to isolate the trunk region containing abcc9-186 positive ISV-MCs for FACS. We confirmed the identity of sorted MCs by expression of abcc9 187 and *pdqfrb* (Supplementary Figure 3B). In line with published data, that *cxcr4a* and *cxcr4b* 188 are expressed by LECs and cxcl12b by aECs (Cha et al., 2012). In addition, we found that 189 cxcl12a and cxcl12b are expressed in the abcc9-positive MC population (Figure 3E). To 190 further understand if signalling by these ligands is essential for LEC migration, we have treated 191 embryos with a Cxcr4 inhibitor, AMD3100 (Figure 3F, Supplementary Figure 3C), and found 192 LECs migrated less and their migration velocity is decreased (Figure 3G-J). This coincided 193 with an increased number of filopodia formation on LEC (Figure 3 K), indicating loss of 194 guidance (Meyen et al., 2015). Together our data show that MCs produce the LEC chemo-195 attractants driving LEC migration.

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197 MC and arterial derived *vegfc* promotes LEC migration and survival

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199 Vegfc-Vegfr3 initiates a signalling cascade driving lymphangiogenesis in zebrafish and is 200 required for sprouting and LEC migration towards the HM (Hogan et al., 2009a; Yaniv et al., 201 2006). As Vegfc has been shown to be expressed in vascular smooth muscle cells (VSMCs) 202 in mice (Antila et al., 2017), we hypothesised that it might be expressed also in zebrafish MC. 203 Firstly, we checked *vegfc* expression in FAC-sorted cells by RT-gPCR and found that *vegfc* 204 expression in aISV-MCs as well as aECs (Figure 4A). We also found that phospho(p)-ERK 205 staining of LEC, which is known to be activated downstream of Vegfc-Vegfr3 or Cxcl12-Cxcr4 206 (Spinosa et al., 2019; Xing et al., 2017), during LEC migration along aISV (Figure 4B). To 207 assess if ERK activation is required for the LEC migration from HM we have used the MEK 208 inhibitor, SL327 (Supplementary Figure 4A). We treated embryos at 51 hpf just prior to their 209 migration and assessed the phenotypes by time-lapse imaging (Figure 4C-D). We traced the 210 migration distance and observed a reduced number of migrating cells and increased number 211 of cells that stalled or regressed their migration in SL327-treated embryos (n=5) (Figure 4E). 212 In addition, we found a dramatic decrease of LEC cell division from 25% controls to 1.5 % 213 precent in SL327-treated embryos (Figure 4G), which is in agreement with the known 214 necessary role of Vegfc-Vegfr3 in cell proliferation (Cao et al., 1998). SL327-treatment induced 215 cell death in 7 out of 12 cells, which was further confirmed by TUNEL staining (Figure 4 H-I), 216 suggesting that during this lymphatic developmental window ERK activation acts as a LEC 217 pro-survival factor. These effects were not observed in AMD3100 treated embryos, indicating 218 that ERK activation may be induced mainly via Vegfc-Vegfr3 signalling rather than Cxcl12-219 Cxcr4 signalling. Together, these results indicate that in addition to LEC specification and 220 sprouting from the PCV (Karkkainen et al., 2004; Koltowska et al., 2015a), Vegfc-Vegfr3 221 signalling also instructs LEC in the subsequent migratory events to establish the lymphatic 222 vessel network in the trunk.

223

224 In summary, we demonstrated MC-LEC interaction at high spatio-temporal resolution during 225 lymphatic development. We further uncovered an important role for artery-associated MCs in 226 guidance of LECs, which is mediated by their secretion of chemoattractants including Cxcl12 227 and Vegfc. Since other sources of Cxcl12 and Vegfc have already been demonstrated in the 228 zebrafish embryonic trunk (Cha et al., 2012; Wang et al., 2020), we propose that colonisation 229 of the aISV by MC may provide a signalling threshold needed for LECs to depart from the HM 230 and begin migrating along the aISVs. Our study underscores the importance of spatial and 231 temporal control of the guidance cues and mitogens in order to promote and refine the 232 migratory path and survival of LECs. Our finding of MC as molecular source for 233 lymphangiogenic factors should have relevance to future designs aiming at re-establishing 234 lymphatic vessels in disease contexts.

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237 Material and methods

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239 Zebrafish

240 Zebrafish were maintained in Genome Engineering Zebrafish National Facility, Uppsala 241 University using standard husbandry conditions (Alestrom et al., 2020). Animal experiments 242 were carried out under ethical approval from the Swedish Board of Agriculture (5.2.18-7558/14). Previously published transgenic lines used were Tg(fli1a:nEGFP)^{y7}, Tg(-243 244 5.2lyve1b:DsRed2)^{nz101} (Okuda et al., 2012), Tg(1xUAS:GFP) (Asakawa et al., 2008), 245 TgBAC(pdgfrb:Gal4FF), (Ando et al., 2016) TgBAC(pdgfrb:GFP) (Ando et al., 2016), TqBAC(abcc9:GAL4FF) (Ando et al., 2019), Tq(flt1:YFP)^{hu4881} (Hogan et al., 2009b), 246 247 Tg(fli1a:GFP)^{y1} (Nathan and Weinstein, 2002), Tg(-7kdrl:DsRed2)^{pd27} (Kikuchi et al., 2011), 248 pdgfrb^{um148} (Kok et al., 2015), Tg(kdrl:TagBFP)^{mu293Tg} (Matsuoka et al., 2016), Tg(fli1a:Myr-

- 249 GFP)^{*ncv2Tg*} (Fukuhara et al., 2014), $Tg(dab2:GFP)^{ncv67Tg}$ (Shin et al., 2019).
- 250 $Tg(lyve1:mCherry)^{ncv87Tg}$ and $Tg(14xUAS:3xFLAG-NTR,NLS-mCherry)^{ncv514Tg}$ were generated
- in this study.
- 252

253 Genotyping

- 254 For *pdgfrb^{um148}* the following primers were used for PCR
- 255 pdfgrb Forward 5'- ATGCGCTAAAGGTGAATTGG- 3'
- 256 pdgfrb Reverse 5'- GCGTCTGCCATAGTTGAACA- 3'

The PCR product was digested with Mbo1 restriction enzyme at 37 °C for 1 h. The digested product was run on 2% agarose gel. The wild type fragment is cut resulting in two bands of 200 bp and 300 bp long; $pdgfrb^{um148}$ mutant is not cut and the band is 500 bp long; heterozygous $pdgfrb^{um148}$ is a combination of three fragments with bands sizes of 200 bp, 300 bp and 500 bp.

262

263 Immunohistochemistry

264 Immunohistochemistry was performed according to a previously published protocol (Le Guen 265 et al., 2014; Shin et al., 2016) with the following modifications. After acetone treatment 266 embryos were treated with Proteinase K at 10 mg/ml diluted in PBST for 35 mins. Antibodies used were chicken α -GFP (1:400, ab13970 Abcam), rabbit α -DsRed (1:400, Living colors, 267 268 632496 Takara Bio), rabbit α -Phospho-p44/42 MAPK (1:250, #4370 Cell Signaling 269 Technology), and α -rabbit IgG-HRP (1:1000, #7074 Cell Signaling Technology). TUNEL 270 staining was performed with In Situ Cell Death Detection Kit, Fluorescein (Merck, 271 11684795910) with the instruction provided by manufacture.

272

273 Image acquisition

274 Embryos were anesthetized and mounted in 1% low-melting agarose on a 35-mm-diameter 275 glass-base dish (627870 or 627861 Greiner). Confocal images were obtained using a Leica 276 TCS SP8 confocal microscope (Leica Microsystems) equipped with water-immersion 25X 277 (Fluotar VISR, 0.95 NA) objective, water-immersion 40X (HC PL APO CS2, 1.1 NA) objective 278 and glycerol-immersion 63X (HC PL APO CS2, 1.3 NA) objective or FluoView 279 FV1000/FV1200/FV3000 confocal upright microscope (Olympus) equipped with a waterimmersion 20x (XLUMPlanFL, 1.0 NA) lens. The 473 nm (for GFP), 559 nm (for mCherry), 280 281 and 633 nm (for Qdot 655) laser lines in FluoView FV1000/FV1200/FV3000 confocal 282 microscope and the 488 nm (for GFP) and 587 nm (for mCherry) in Leica TCS SP8 confocal 283 microscope were employed, and 488 nm and 651 nm on the Zeiss NLO710, respectively.

284

285 Image analysis

Image quantification was performed using z-stacks in ImageJ 2.0.0 (Schindelin et al., 2012), Olympus Fluoview (FV10-ASW, FV31S-SW), or IMARISx64 9.5.1 software (Bitplane). Total LEC number was counted manually using the overlay of DsRed and GFP channels over five somites in the trunk. Lymphatic vessel area was calculated by rendering the surface using DsRed channel, the non- lymphatic structures were manually removed. Measurements of surface area were exported directly from Imaris (Bitplane).

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- 293 Cell tracking

To quantify the migrating distance the centre of PL nuclei in figure 3G and figure 4D was manually tracked until either cell dying or disappearing from the view in Imaris (Bitplane). The individual cell track was generated by "spot" and "cell track" function and then manually edited

297 if needed. The data was exported to GraphPad for plotting and statistical analysis.

298

299 Distance measurement

The migrating distance in all figures were measured in three-dimension using spot function in Imaris (Bitplane), see cell tracking. In figure 3B-C, the sprouting front of PL just migrating out of HM was chosen as start point (T0) and the migrating front at the end of the time lapse video was chosen as end point (T1). A direct line was used to connect the dots and the length of line segment is measured. In figure 2H, the perpendicular distance between point T1 and HM was also measured in addition to the measurement above.

306

307 Chemical treatment

To inhibit Cxcr4 signalling, the embryos were treated in 20 μ M antagonist ADM3100 (Merk) from 51 hpf to 72 hpf. To block phosphorylation and activation of ERK1/2, embryos were treated in 10 μ M SL327 (EMD Millipore) from 51 hpf to 72 hpf. Embryos were anesthetized and mounted in 1% low-melting agarose in a 2-well slide with separate chambers which allows . The prepared chemical solution (3 ml) was added on top of the agarose layer in one chamber and the E3 water or DMSO (3 ml) to the other.

314

315 Fluorescence Activated Cell Sorting (FACS) and qPCR analysis

316 Embryos of *Tg(flt1:YFP);Tg(-5.2lyve1b:DsRed2)* and *Tg(flt1:YFP);Tg(-5.2lyve1b:DsRed2)*

- 317 were collected at 3 dpf and screened as described in figure 3D, dissociation was performed
- as previously described (Kartopawiro et al., 2014). The dissociated cells were sorted using a
- 319 FACS Aria III (BD Biosciences) into 300µl TRIzol[™] LS Reagent (Thermo Fisher). Total RNA
- 320 was extracted using the Quick-RNA Microprep kit (Cambridge Bioscience) following the

321 manufacturer's instructions. RNA guality and concentration were determined using 2100 322 Bioanalyser Instrument (Agilent) together with Bioanalyser High Sensitivity RNA Anlysis Kit (Agilent). 1 ng of RNA template was subjected to cDNA synthesis using SuperScript[™] VILO[™] 323 cDNA Synthesis Kit (Thermo Fisher). qPCR analysis was performed using the primers in Table 324 325 S1 on CFX384 Touch Real-Time PCR Detection System (BioRad). Data were analysed using 326 the CFX Maestro Software (BioRad). The geometric average of *rpl13* and β -actin expression 327 was used as reference to calculate relative gene expression of target genes with the ddCT 328 method. Primer sequences listed below in Table 1.

329

Target	Forward primer Sequence 5'-	Forward primer Sequence 5'-3'	Referenc
gene	3'		е
β-actin	CGAGCTGTCTTCCCATCCA	TCACCAACGTAGCTGTCTTT	Designed for this study
rpl13	CATCTCTGTTGACTCACGTC G	CATCTTGAGCTCCTCCTCAGTA C	Designed for this study
cxcr4a	CATGACAGACAAGTACCGT CT	TGCTGTACAAGTTTACCGTGTA	qPrimerD B
cxcr4b	TGCTAACATTCCTGATAAGA CC	GTACTTTTATTGCCAGACCTAAA GG	qPrimerD B
cxcl12 a	GCAAGTGCTTTGACACAAAA AG	TTTGTTTGGCAAAGTAACCCTG	qPrimerD B
cxcl12 b	GATCGTGATAGCTTTGTGAA CC	AATGTTAACAATGCTTGGCCTC	qPrimerD B
vegfc	TCTTAAAAGGGAGACGGTTT CA	TACATTTCCTTCTCTTGGGGTC	qPrimerD B
abcc9	AAAGTTATGGAAGTTTGCCG AG	AAAGTTATGGAAGTTTGCCGAG	qPrimerD B
pdgfrb	CGTTCCCAGGAGCCTTTTCT	TTGGGATCAGGGATGGGGAT	(Ando <i>et</i> <i>al.</i> , 2019)

330

331 Ablation experiments

332 Ablation with multi-photon microscopy

For mural cells ablation, embryos of *Tg(-5.2lyve1b:DsRed2);Tg(pdgfrb:GFP)* were laterally mounted in 1% low melting-point agarose at 57 hpf. An aISV with migrating LEC was chosen

100 medine 1 / 100 meding-point agaiose at 57 mpl. An alov with migrating EEC was chosen

randomly, a GFP-positive MC were identified using 488-nm laser. MC locating ahead of

336 migrating route were ablated using a two-photon laser at 790 nm (Mai Tai, Spectr-Physics

337 Millenia PRO). Control ablations were performed as above but the adjacent area to the pdgfrb+ 338 cell targeted with two-photon laser. For alSV the ablation. Tg(-339 5.2lyve1b:DsRed2);Tg(flt:YFP);Tg(pdqfrb:GFP) embryos were prepared as described above 340 and an aISV, with LEC migrating along, was ablated using the two-photon laser targeting the 341 nuclei of aEC. Larvae were imaged before and after ablation with a Zeiss LSM 710 FCS 342 confocal microscope, which was followed by either time-lapse imaging for around 5 h or follow-343 up z-stack imaging at 3 dpf.

344

345 Ablation with NTR-Mtz system

Embryos from *Tg(Pdgfrb:Gal4FF,UAS:NTR-mCherry);Tg(fli1a:GFP)* were collected and screened as described in figure 2A. Embryos both positive and negative for *mCherry* were treated with medium mixture of E3 water and either 5mM MTZ or DMSO from 48 hpf, and replaced daily with fresh medium mixture. The region above the yolk extension was imaged at 120 hpf. The formation of thoracic duct was analyzed by scoring the extend of the thoracic duct formation.

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353 Statistical analysis

Statistical analysis was performed using Prism software (GraphPad). Gaussian distribution of
 samples was tested with either D'Agostino–Pearson test or Shapiro-Wilk normality test.
 Student's t test was used for comparison of two means. One-way ANOVA with post hoc test

- 357 was used for multiple comparison as stated in corresponding figure legend.
- 358

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367 Author contribution

D.P, K.A. and K.K, conceptualised the project, performed, analysed experiments and co-wrote the
 manuscript. R.S. and M.G. performed and analysed experiments. N. M, C. B., and S.F unpublished
 reagents and resources contribution.

- 371
- 372
- 373 Figure Legends

Figure 1. *pdgfrb* ^{high} mural cells emerge around alSVs prior to LEC migration and provide
 guidance.

- 376 (A) Confocal stack image of trunk alSV in 4 dpf Tg(-5.2lyve1b:DsRed);Tg(flt1:YFP);
- 377 *TgBAC(pdgfrb:GFP)* of lymphatic endothelial cells (gray, LEC), arterial intersegments vessels
- 378 (magenta, alSV) and MCs (green, MC). Scale bar; 10 $\mu m.$
- 379 (B) Confocal stack images from time-lapse images in the trunk of 2 dpf Tg(lyve1b:
- 380 *mCherry*);*Tg(kdrl:TagBFP)*;*TgBAC(pdgfrb:GFP*) embryo. Boxed regions are enlarged in the
- 381 bottom.
- 382 Arrowheads indicate *pdgfrb*⁺ MCs (green) around aISV (magenta) prior to (bottom left) and
- during (bottom middle and right) LEC (gray) migration. Scale bars; 50 μm or 30 μm (enlarged
 image).
- 385 (C) Quantification of aISV with (n=10) or without (n=3) MCs presence when LECs left HM for
- time lapse videos as in (E).
- (D) Quantification of MC number around aISV (n=13) at the start and end of the migration for
 time lapse videos as in (E).
- 389 (E) Confocal stack images from time lapse of LEC migration.
 390 *TgBAC(pdgfrb:GAL4FF);(UAS:GFP)* in green and *Tg(-5.2lyve1b:DsRed2)* in grey. Scale bar;
 391 50 μm.
- 392 (F) Quantification of LEC and MC interaction during migration. Migrating following MC n=21,

393 migrating not following MC n=3.

- (G) Quantification of duration of LEC migration with (n=5) or without (n=3) contacting MCs.
- 395 Data are presented as mean \pm SEM. **p<0.005
- 396 (H) Confocal stack images of Tg(pdgfrb:GAL4FF); Tg(UAS:GFP) (green) and Tg(-397 5.2lyve1b:DsRed2) (grey) in the trunk of sibling (top) and $pdgfrb^{UM148}$ mutant (bottom) embryos
- at 5 dpf. Lymphatic structure is rendered with *lyve* channel in IMARIS (right panel). Scale bar;
 100 μm.
- 400 (I) Quantification of number of $pdgfrb^+$ mural cells around ISVs in siblings (n=20) and 401 $pdgfrb^{UM148}$ mutant (n=10). Data are presented as mean ± SEM, unpaired two-tailed Student's 402 t-test was used. ***p<0.0001.
- 403 (J) Quantification of surface area of lymphatic vasculature in siblings (n=20) and *pdgfrb*^{UM148}
 404 mutant (n=10). Data are presented as mean ± SEM, unpaired two-tailed Student's t-test was
 405 used. *p<0.05.
- 406
- 407 Figure 2. Mural cells are required for robust formation of lymphatic vascular bed.

- 408 (A) Work flow of cell ablation by NTR-MTZ system. *Tg(pdgfrb:Gal4FF);Tg(14xUAS:3xFLAG-*
- 409 *NTR,NLS-mCherry*) (red) and *Tg(fli1a:GFP*) (grey) were imaged at 120 hpf after treatment of
- 410 DMSO or 5mM MTZ from 48 hpf, and the formation of thoracic duct (TD) was analyzed.
- 411 (B) Confocal stack images of the trunk in 5 dpf embryos treated as described in (A). Arrows
- 412 indicates TD forming beneath dorsal aorta. Asterisks indicates the absence of TD. Scale bar;
- 413 100 μm.
- 414 (C) Quantification of (B). Embryos were scored as fully, partially and hardly formed based on
- 415 the TD development. Data were presented as ratio to total number of embryos analyzed.
- 416 (D) Work flow of cell ablation by multi-photon microscopy. Mural cells (MC, green) labelled by
- 417 *TgBAC(pdgfrb:GAL4FF);(UAS:GFP)* and PL by -5.2lyve1b:DsRed2 (grey) embryo. The MC
- 418 on intersegmental vessels in proximity to PL were ablated at 57 hpf. For analysis, ablation was
- 419 either followed by time-lapse imaging or confocal imaging at 3 dpf.
- 420 (E) Confocal stack images of before and after ablation (top two raw) and follow-up at 3 dpf
 421 (bottom two row). Control ablation (dashed box) at the adjacent region of GFP⁺ MCs and GFP+
 422 MC on aISV ablation (solid grey box) was performed in the same embryos. Arrowheads
 423 indicate ablated GFP-positive cells and development of targeted LEC at 3 dpf. Scale bar; 100
 424 μm. Middle and right panel, zoom-in images cropped in z-stacked.
- 425 (F) Live imaging of the lymphatic endothelial cells (LEC) migration in the context of control
- 426 (top images) and GFP+ MC on alSV (bottom images) ablation, confocal stack images from
 427 time lapse at selected timepoints from 0 hours post ablation (hpa) to 4.96 (hpa). Scale bar; 50
 428 μm.
- 429 (G) Quantification of ablated LEC forming DLLV at 3 dpf. DLLV forming (n=3), not forming430 (n=2).
- 431 (H) Quantification of migrating distance from time-lapse videos corresponding in (D). Distance 432 was calculated as both T0-T1 and the perpendicular distance between the T1 and HM for 433 embryos with (ablated, n=4) or without (control, n=3) ablation. T0, the sprouting front of LEC 434 at the start of video; T1, sprouting front of LEC at the end of video. Data are presented as 435 mean \pm SEM, unpaired two-tailed Student's t-test was used on two types of measurements 436 respectively. *p<0.05.
- 437

438 Figure 3. Chemokines are expressed in ISV-mural cells during LEC migration

439 (A) Confocal stack images from time lapse post multi-photon laser ablation in 2 dpf 440 Tg(flt1:YFP) (magenta); TgBAC(pdgfrb:GFP) (green) and Tg(-5.2lyve1b:DsRed2) (grey). 441 Arrowheads indicate remained GFP⁺ mural cells without alSV. White arrows indicate the 442 ablated site of alSV. Scale bar; 50 µm. 443 (B-C) Quantification of LEC (n=4) and aISV (n=4) migration distance post two-photon laser444 ablation.

- 445 (D) Illustration of FACS sorting and qPCR analysis on 3 dpf embryos.
- 446 (E) qRT-qPCR of *cxcr4a*, *cxcr4b*, *cxcl12a* and *cxcl12b* in FACS sorted population cells at 3
- 447 dpf. Graph represents gene expression relative to geometric average of *rpl13* and β -actin from
- 448 three biological repeats (mean ± SEM). Kruskal-Wallis test with Dunn's post hoc test was
- 449 used. No significance (ns), $p \ge 0.9999$.
- 450 (F) Work flow of Cxcr4 inhibitor treatment. Embryos of *Tg(fli1:GFP);Tg(lyve1b:mCherry)* was
- 451 grown in PTU from 24 hpf, then changed to 20 μM ADM3100 or E3 water at 51 hpf. Time-
- 452 lapse imaging was started then in a two-well slide that allows spontaneous imaging for both453 groups.
- 454 (G) Confocal stack images from time lapse imaging indicated in (F). Scale bar; 50 μ m.
- (H) Quantification of dorso-ventral migration showing individual tracks for sprouting front of
 PLs in E3 water (n=10) and AMD3100 (n=25) treated embryos as described in (G).
- 457 (I) Quantification of dorso-ventral migration showing average (mean) of tracks in DMSO and
- AMD3100 treated group. Data are presented as mean ± SEM, unpaired two-tailed Student's
 t-test was used. **p<0.005.
- 460 (J) Quantification of velocity of dorso-ventral migration from time lapse video described in (3F).
- 461 Nuclei of PLs in E3 water (n=10) and AMD3100 (n=25) treated embryos were tracked and the
- 462 distance between begin and end position of nuclei was measured then divided by duration.
- 463 Data are presented as mean ± SEM. unpaired two-tailed Student's t-test was used.
- 464 (K) Quantification of frequency of filopodia formation from time lapse video described in (3F).
- 465 (left) Number of protrusions other than the sprouting front was counted and divided by the 466 corresponding duration in E3 (n=12) and AMD3100 (n=20) treated embryos. Data are 467 presented as mean \pm SEM. unpaired two-tailed Student's t-test was used. (right) Number of 468 protrusions other than the sprouting front was counted and divided by the corresponding 469 duration in E3 (n=12) and AMD3100 (n=20) treated embryos. Data are presented as mean \pm
- 470 SEM. unpaired two-tailed Student's t-test was used.
- 471

472 Figure 4. Mural cell and arterial derived *vegfc* promotes LEC migration

- 473 (A) qRT-qPCR of *vegfc* expression in trunk ECs and MCs cells at 3 dpf as described in (3E).
- 474 Graph represents gene expression relative to geometric average of *rpl13* and β -actin from
- 475 three biological repeats (mean ± SEM). Kruskal-Wallis test with Dunn's post hoc test was
- 476 used. *p<0.05
- 477 (B) Endogenous pErk (cyan, right) in migrating LEC in trunk of *Tg(-5.2lyve1b:venus)* embryos
- 478 (α -GFP, grey, middle) at 3 dpf. Scale bar 100 μ m; 50 μ m in enlarged images.

479 (C) Work flow of vegfc inhibitor treatment. Embryos of Tg(fli1:GFP);Tg(lyve1b:mCherry) was 480 grown in PTU from 24 hpf, then changed to 10 μ M SI327 or DMSO at 51 hpf. Time-lapse

481 imaging was started at 57 hpf.

- 482 (D) Confocal stack images from time lapse of 57 hpf Tg(fli1a:nEGFP)^{y7} (green) and Tg(-
- 483 5.2*lyve1b:DsRed2*) (grey) treated with DMSO or 10 μ M SL327 from 51 hpf. Grey arrowheads
- 484 indicate cell death. Scale bar in 50 μ m.
- 485 (E) Quantification of dorso-ventral migration showing individual cell tracks for nuclei of PLs
- 486 (top panel) in DMSO (n=11) and SL327 (n=12) treated embryos as described in (4C). Red
- 487 cross indicates cell death at the end of tracking. Bottom panel, average (mean) of tracks in
 488 DMSO and SL327 treated group. Data are presented as mean ± SEM, unpaired two-tailed
- 489 Student's t-test was used. ****p<0.0001
- 490 (F) Quantification of cell proliferation in DMSO (n=14) and SL327 treated (n=17) embryos as
- 491 described in (4C). Nuclei marker in green was used to count the cell division event.
- 492 (G) Quantification of total LEC number at beginning (T0) and end (T1) of the time lapse in
- 493 DMSO (n=10) and SL327 (n=9) treated embryos as described in (C), data are presented as
- 494 mean ± SEM. T0 DMSO vs T1 SL327 p<0.0001, T0 SL327 vs T1 SL327, T1 DMSO vs T1
- 495 SL327 p<0.0001. Other comparisons were ns, p≥0.9999. One-way ANOVA with Tukey's post
- 496 hoc test for statistical analysis. ****p<0.0001
- 497 (H) Confocal stack image of embryos treated with DMSO or SL327 as described in (4C).
- 498 Embryos were fixed at 3 dpf and used for TUNEL (cyan) and α -DsRed staining (grey). Zoom-499 in single z stack images of TUNEL staining in merged and TUNEL channel showing the 500 colocalization of the signal. Scale bar; 100 μ m, 30 μ m (enlarged images).
- (I) Corresponding quantification of TUNEL signal from (I). In SL327 treated group (n=45) LEC
 showed a positive TUNEL staining rate of 15.56% while it was 0% in DMSO treated group
 (n=45).
- 504 (J) A model of LEC migration in zebrafish trunk. Signals promoting cell survival and migration
- 505 expressed in MCs include *vegfc*, *cxcl12a* and *cxcl12b*at 3 dpf (top). In absence of the arterial
- 506 mural cells, LECs fail to establish a robust lymphatic network at 5 dpf (bottom panel).
- 507

508 Supplementary Figure 1, related to Figure 1; *pdgfrb* ^{high} mural cells emerge around 509 alSVs prior to LEC migration and provide guidance.

- 510 (A) Confocal stack images from time-lapse images in the trunk of
- 511 *Tg(dab2:GALFF);Tg(UAS:GFP)* in grey and *Tg(pdgfrb:mCherry)* in green. White Arrow heads,
- 512 MCs appear around aISV. Arrow, sprouting front of migrating LEC. Scale bar; 50 μ m.

- 513 (B) Confocal stack images of 5 dpf *Tg(fli1a:nEGFP);(-5.2lyve1b:DsRed2)* treated with 20 μM
- 514 PDGFR inhibitor AG1296 (n=15) or DMSO (n=15) from 48 hpf. Data are presented as mean
- 515 ± SEM, unpaired two-tailed Student's t-test was used. ***p<0.0005.
- 516

517 Supplementary Figure 2, related to Figure 2; Mural cells are required for robust 518 formation of the lymphatic vascular bed.

- 519 (A) Representative stack images of 5 dpf confocal 520 TgBAC(pdgfrb:Gal4FF);Tg(14xUAS:3xFlag-NTR, NLS-mCherry);Tg(fli1:GFP) with high and 521 low NTR expression treated with 5 mM MTZ or vehicle for 16 h. NTR expression was highly 522 selective on MCs but not on pdgfrb-low population. MCs were ablated after 16 h of 5 mM MTZ 523 treatment. Arrows indicate floorplate and hyperchord were not ablated by the treatment 524 despite the expression of NTR. Scale bar; 100 μ m
- 525 (B) Confocal stack images from *Tg(fli1a:Myr-GFP)* in control and ablated embryos described
- 526 in Figure 2A post injection of Qtracker 705 vascular labels (shown in grey) into common
- 527 cardinal vein. Arrows indicate lymphatic vessels labeled by leaked dye when injected or during
- 528 $\,$ the circulation in the control but not in the MC-ablated larva. Scale bar; 100 μm
- 529

Supplementary Figure 3, related to Figure 3; Chemokines are expressed in ISV-mural cells during LEC migration.

- 532 (A) Gating strategy for FACS sort of *Tg(flt1:YFP);Tg(-5.2lyve1b:DsRed2)* and *Tg(abcc9:GFP);*
- 533 *Tg(kdrl:DsRed2)* as described in Figure 3D. Sorting was performed on all singlet, alive cells 534 according to their expression of DsRed (red, 561 nm) and GFP/ YFP (green, 488 nm).
- 535 (B) RT-qPCR of *abcc9* and *pdgfrb* expression in trunk ECs and MCs cells at 3 dpf as described
- 536 in (3E). Graph represents gene expression relative to gematric average of *rpl13* and β -actin
- 537 from three biological repeats (mean ± SEM). Kruskal-Wallis test with Dunn's post hoc test was
- 538 used. No significance (ns), $p \ge 0.9999$.
- 539 (C) Confocal stack images of embryos as described in Figure 3F treated with 20 μM ADM3100
- 540 $\,$ or E3 water from 51 hpf to 120 hpf. Scale bar; 100 $\mu m.$
- 541

542 Supplementary Figure 4, related to Figure 4; Mural cell and arterial derived *vegfc* 543 promotes lymphatic endothelial cell migration and survival

- 544 (A) Confocal stack images of embryos as described in Figure 4C treated with 4 μ M SL327 or
- 545 DMSO from 51 hpf to 120 hpf. Scale bar; 100 $\mu m.$
- 546
- 547 Supplementary Movies S1 related to Figure 1.

- 548 Confocal time lapse imaging in trunk in 2 dpf Tg(lyve1b: mCherry), Tg(kdrl:TagBFP),
- 549 *TgBAC(pdgfrb:GFP)* embryos corresponding in Figure 1B
- 550

551 Supplementary Movies S2 related to Figure 1.

- 552 Confocal time lapse imaging in trunk in 2 dpf TgBAC(pdgfrb:GAL4FF);(UAS:GFP), Tg(-
- 553 5.2lyve1b:DsRed2) embryos corresponding in Figure 1E
- 554

555 Supplementary Movies S3-4 related to Figure 1.

- 556 Representative confocal time lapse imaging of LEC migrating with or without contacting MCs
- 557 in trunk in 2 dpf embryos corresponding Figure 1G.
- 558

559 Supplementary Movies S5-6 related to Figure 2.

- 560 Representative confocal time lapse imaging of multi-photon ablation of MCs in
- 561 *TgBAC(pdgfrb:GAL4FF);(UAS:GFP), Tg(-5.2lyve1b:DsRed2),* corresponding Figure 2F.
- 562

563 Supplementary Movies S7 related to Figure 3.

- 564 Representative confocal time lapse imaging of multi-photon ablation of aISV in *Tg(flt1:YFP*);
- 565 *TgBAC(pdgfrb:GFP); Tg(-5.2lyve1b:DsRed2)*, corresponding Figure 3A.
- 566

567 **Supplementary Movies S8-11 related to Figure 3.**

- 568 Representative confocal time lapse imaging of *Tg(fli1:GFP);Tg(lyve1b:mCherry*) treated with
- 569 20 μ M ADM3100 or E3 water at from 51 hpf, corresponding Figure 3G.
- 570

571 Supplementary Movies S12-15 related to Figure 3.

- 572 Representative confocal time lapse imaging of *Tg(fli1a:nEGFP)*^{7y}; *Tg(-5.2lyve1b:DsRed2)*
- 573 treated with 10 μ M SL327 or DMSO from 51 hpf. Grey arrowheads indicate cell death.
- 574
- 575

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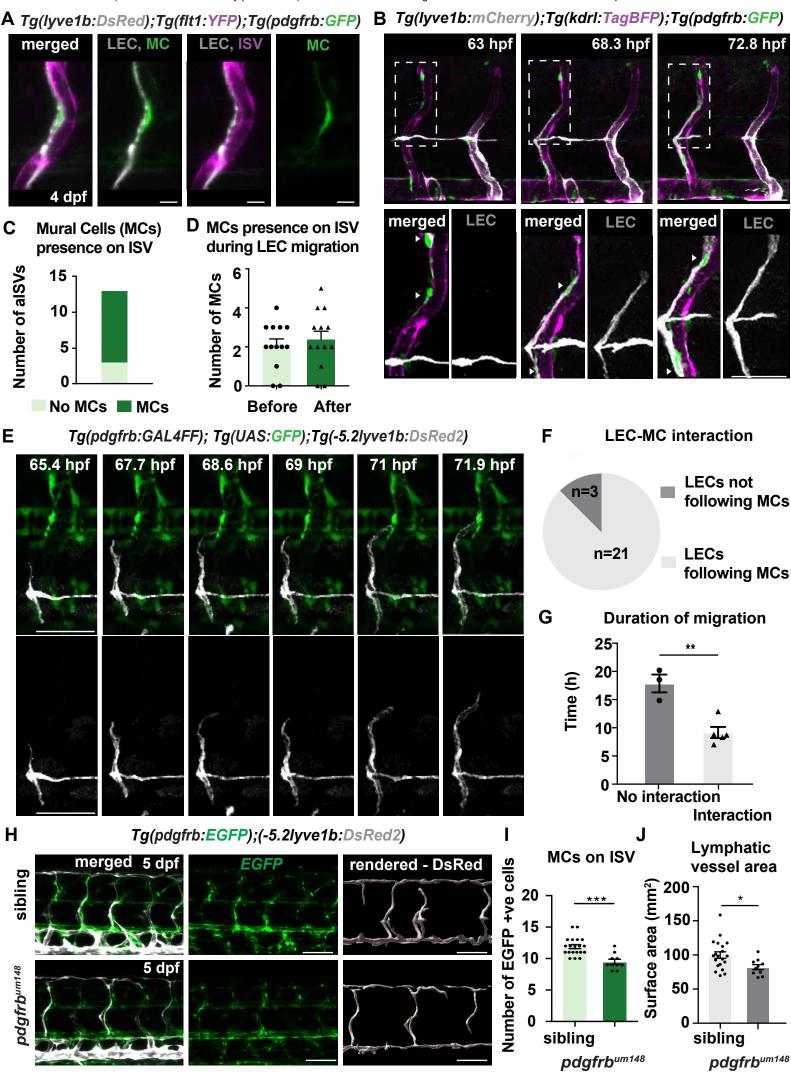
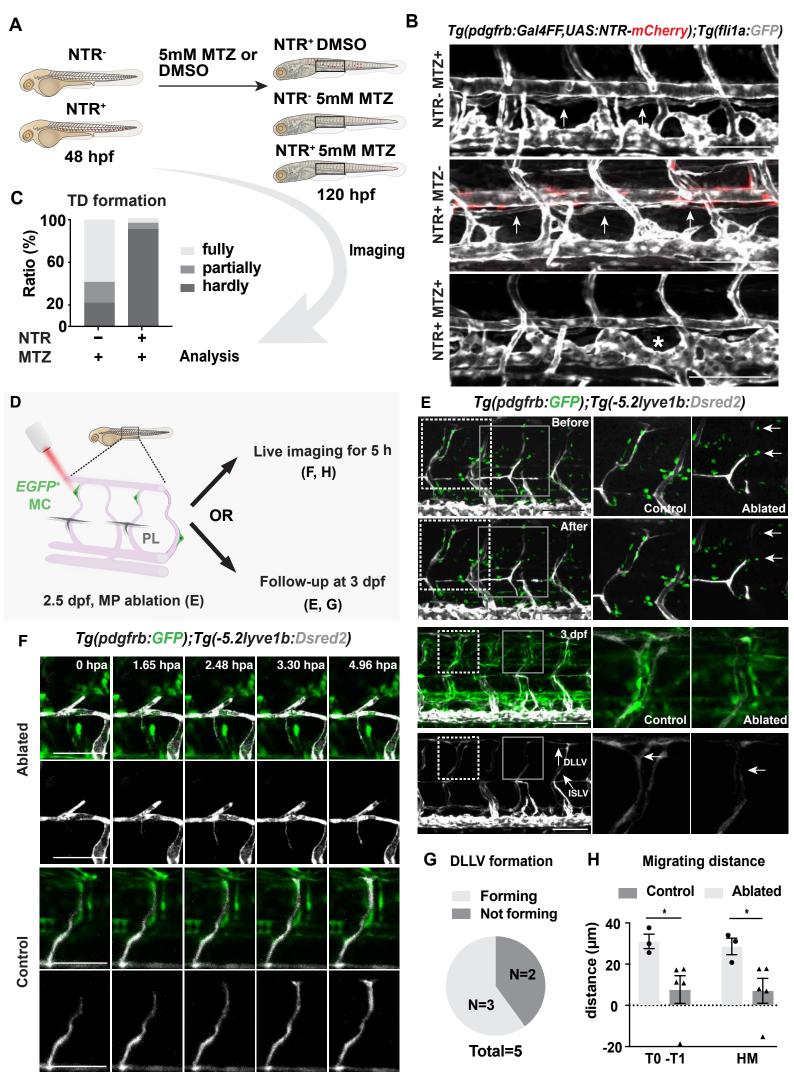
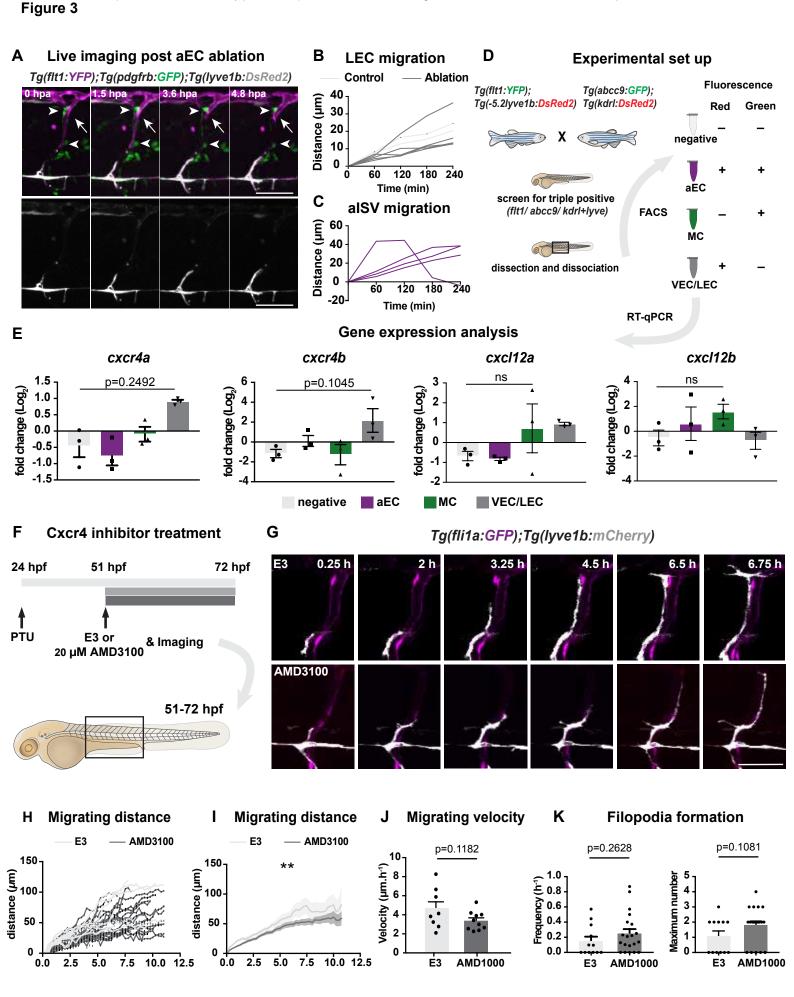
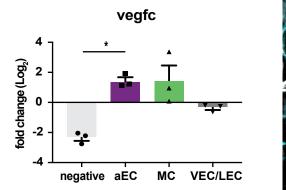


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Merged



51 hpf

DMSO or

DMSO

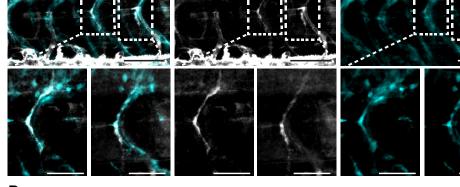
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С

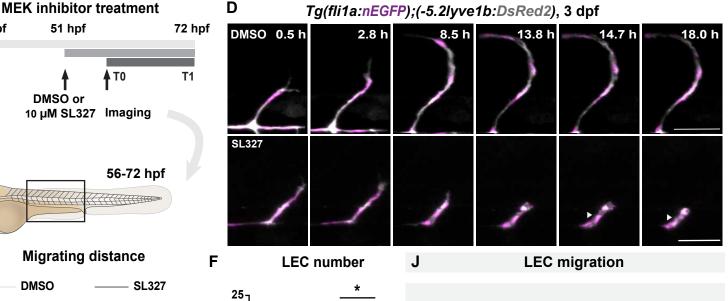
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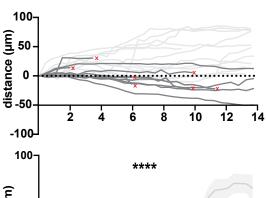
24 hpf

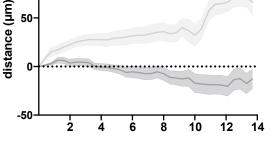
PTU

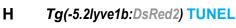


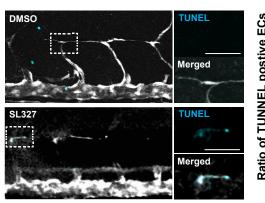
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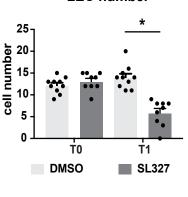


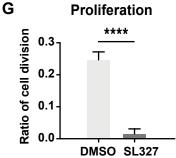


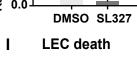


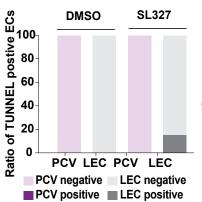


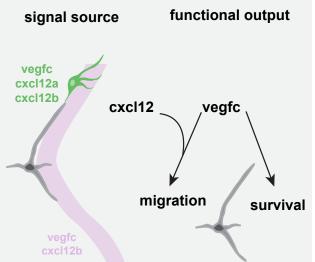




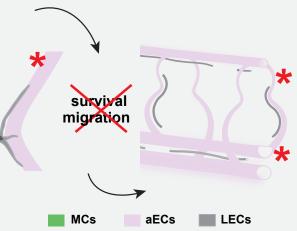




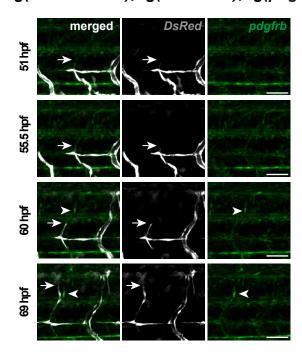




atrerial mural cell deficit

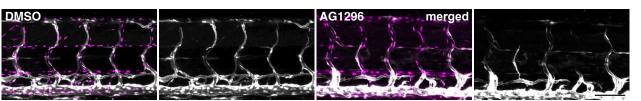


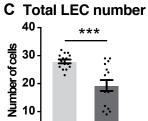
Sup. Figure preprint doi: https://doi.org/10.1101/2021.06.30.450504; this version posted June 30, 2021. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.
 A Tg(dab2:GALFF);Tg(UAS:GFP);Tg(pdgfrb:mCherry)





Tg(fli1a:nEGFP)^{y7};(-5.2lyve1b:DsRed2), 5 dpf



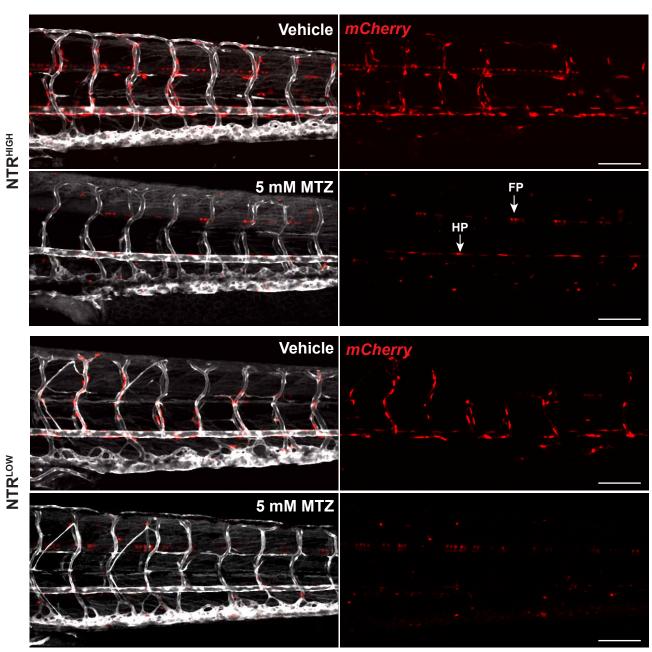


DMSO AG1296

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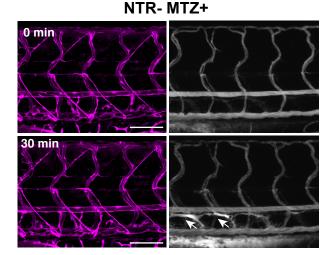
Sup. Figure 2 reprint doi: https://doi.org/10.1101/2021.06.30.450504; this version posted June 30, 2021. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

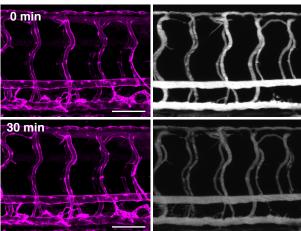
TgBAC(pdgfrb:Gal4FF);Tg(14xUAS:3xFlag-NTR, NLS-mCherry);Tg(fli1:GFP), 5 dpf Α



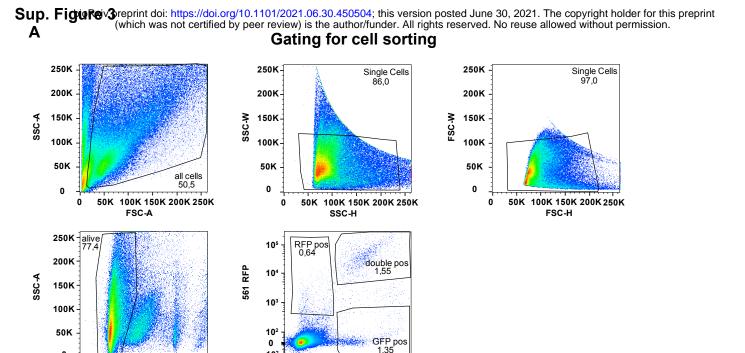


Tg(fli1a:Myr-GFP) Qtracker 705





NTR+ MTZ+



1**0**⁵

104



0

-103

0 10³

405 Sytox

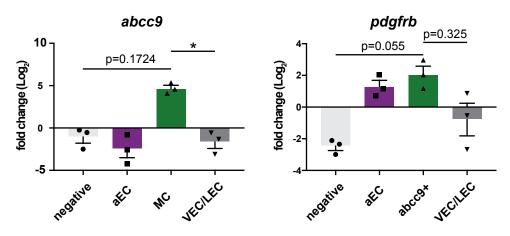
104

105

qPCR analysis on FACS sorted cells

103

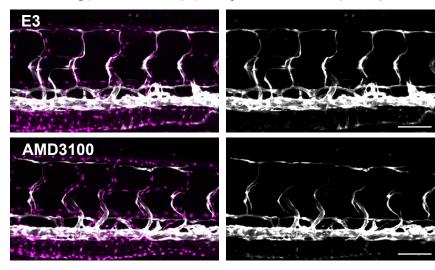
488 GFP



-10²

С

Tg(fli1a:nEGFP);(-5.2lyve1b:DsRed2), 5 dpf



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A Tg(fli1a:nEGFP);(-5.2lyve1b:DsRed2), 5 dpf

