1 **Multi-tier mechanics control stromal adaptations in swelling lymph nodes**
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3 Frank P. Assen[1,2,*], Miroslav Hons[1,3], Robert Hauschild[1], Shayan Shamipour[1], Jun Abe[4], Walter A.
4 Kaufmann[1], Tommaso Costanzo[1], Gabriel Krens[1], Markus Brown[1], Burkhard Ludewig[5], Simon
5 Hippenmeyer[1], Jens V. Stein[4], Carl-Philipp Heisenberg[1], Edouard Hannezo[1], Sanjiv A. Luther[6], Michael
6 Sixt[1,*]
7
[1]Institute of Science and Technology Austria (IST Austria), Klosterneuburg, Austria

[2]Department of Dermatology, Medical University Vienna, Vienna, Austria

[3]BIOCEV, First Faculty of Medicine, Charles University, Vestec, Czech Republic

[4]Department of Oncology, Microbiology and Immunology, University of Fribourg, Fribourg,

Switzerland

[5]Institute of Immunobiology, Kantonsspital St Gallen, St Gallen, Switzerland

[6]Department of Biochemistry, University of Lausanne, Epalinges, Switzerland

15
16 [*]Correspondence to: Sixt@ist.ac.at; frank.assen@meduniwien.ac.at
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Abstract

Lymph nodes (LNs) comprise two main structural elements: Fibroblastic reticular cells (FRCs)

that form dedicated niches for immune cell interaction and capsular fibroblasts that build a

shell around the organ. While LNs are fairly stable in size during homeostatic conditions,

immunological challenge causes more than 10-fold increase in size within only a few days.

How a solid organ can accommodate such extreme volumetric changes is poorly

understood. Here, we characterize the biomechanics of LN swelling on the cellular and

organ scale. We identify lymphocyte trapping by influx and proliferation as drivers of an

outward pressure force, causing FRCs and their associated conduits to stretch. After an

initial phase of relaxation, FRCs sense the resulting strain via cell matrix adhesions, which

coordinates local growth and remodeling of the stromal network. While the expanded FRC

network adopts its typical configuration, a massive fibrotic reaction of the organ capsule

sets in and counters further organ expansion. Thus, different fibroblast populations

mechanically control LN swelling in a multi-tier fashion.

Introduction

Lymph nodes (LNs) are the macroscopic organs of the adaptive immune system. As opposed to other organs, the LN parenchyma only contains few resident cells, while the bulk of lymphocytes is in transit. Lymphocytes circulate through the bodies' vascular systems, and from there they enter LNs via high endothelial venules (HEVs). Within the LN parenchyma, lymphocytes actively migrate to scan large numbers of potentially antigen-bearing dendritic cells (DCs). After several hours of unsuccessful search, lymphocytes exit the organ again via efferent lymphatic vessels that eventually drain back into the blood circulation and the cycle starts again[1,2]. Lymphocytes are densely packed within LNs and make up about 95% of its total cellularity. Despite dynamic cellular exchange, homeostatic LN size remains relatively stable. Known modulators of homeostatic LN cellularity (e.g., during circadian rhythms[3,4]) are mainly chemoattractants and adhesion molecules[2,5–8], which serve as entry and exit signals for lymphocytes, as well as stromal cell-derived survival factors[9–12] and adrenergic signals[13,14]. The main stromal cells found in LNs are FRCs. These form the non-hematopoietic backbone of the organ and deposit bundled fibers of extracellular matrix (ECM) that assemble an intricate 3D network termed conduits. FRCs enwrap these ECM conduits and form an interface with the immune cells[15,16]. They provide a multitude of signals that serve to compartmentalize the organ and support migration, cellular interactions and expansion of immune cell subsets[17–19].

Upon immunological challenge, reactive LNs swell rapidly by recruiting large numbers of naïve lymphocytes via HEVs, while lymphocyte egress via efferent lymphatics is initially blocked[20,21]. LNs can swell up to 10-fold in size in the order of days, imposing an internal structural problem on the FRC network that has to cope with this volumetric challenge. It has been demonstrated that FRCs are able to relax and expand upon interaction with activated DCs[22,23]. This has been proposed as one mechanism that allows the LN to create additional space during the swelling phase. In addition, FRC numbers expand during inflammation and various redundant mechanisms that drive this expansion in the early and late phase of LN swelling have been described[20,22–26]. The ratio of FRC- to lymphocyte numbers remains fairly constant in the swelling LN and trapping of naïve lymphocytes in the absence of inflammatory stimuli has been demonstrated as a sufficient stimulus for the FRC network to expand[20]. How network expansion is coordinated to prevent under- or

overgrowth of the FRC network is unknown, and although mechanical forces are obvious

feedback parameters, these aspects of LN swelling have not been measured until to date.

We measure the cellular and mechanical changes accompanying LN swelling and show that

mechanical load on the conduit network and subsequent FRC mechanosensing are central

to expansion of the FRC network and LN growth.

Results

The reactive lymph node resists swelling

To understand the global mechanical behavior of LNs while expanding, we started out with

a quantitative characterization of bulk tissue properties of the reactive organ. Upon

immunization with keyhole limpet hemocyanin in complete Freund's adjuvant (KLH/CFA) in

footpads of wild-type (wt) mice, we observed a more than 10-fold increase in volume of

draining popliteal LNs after 14 days, when the organ reached its maximum size. The volume

was calculated from 2D side-view images, which correlated well with the weight of the

organ and showed that LNs swell on average about 0.75 mm^3 per day (Figure 1A,B & Figure

S1A,B). We measured tissue mechanics by compressing explanted popliteal LNs between

two parallel plates at 75% of their original height (25% strain), while the resisting force

exerted by the LN on the top plate was measured over a time period of 20-60 minutes

(Figure 1C). During this time the LN underwent a viscoelastic relaxation behavior and

reached a new force-equilibrium, which is described by the stress-relaxation curve (Figure

1D & Figure S1C,D). Together with the geometrical parameters of LNs measured before

compression and at the new force-equilibrium, the *effective resistance* (σ, *surface tension*),

the *viscosity* (μ$_2$, fluidic resistance to deformation by an applied force), and the *elastic*

modulus (Young's Modulus, or elastic resistance to deformation by an applied force) of the

tissue were derived by modelling the parameters to a generalized Kelvin model (Figure

S1E)[27]. At equilibrium (long time scale), the LN resisted the external force exerted by the

plate, which sets the *effective resistance* (given in Newton/m). This parameter describes the

collective forces resisting organ expansion and is a measure of how much force is necessary

to drive the swelling of the LN by a certain length scale.

During the course of organ expansion (D0-D14), we observed a ~4-fold increase of effective

resistance and values remained elevated until the endpoint at D14 (Figure 1E). Viscosity –

the resistance to deformation on the medium time scale – only increased in the last phase

of swelling, while elasticity – the resistance to deformation on the short time scale – was

selectively increased from the homeostatic condition at D2 and D14 of inflammation (Figure

1F,G).

These data demonstrate that tissue properties of LNs show complex adaptive dynamics

upon swelling, and suggest that the mechanical features of the organ resist the forces

driving expansion.

Lymphocyte numbers generate pressure and drive lymph node swelling

Having defined that mechanical properties of the LN resist swelling, we next asked what are

the internal forces driving organ expansion. Lymphocytes constantly recirculate through LNs

where they are densely packed within the FRC scaffold (Figure S1F). Entry via HEVs,

blocking of exit in the early inflammation phase, and proliferation upon activation are the

main factors that increase cellularity of the node, making these potential factors driving

expansion[28–30]. Hence, we manipulated entry and activation and tested the impact on LN

bulk tissue properties.

We first perturbed lymphocyte entry under homeostatic conditions using an L-selecting

antagonizing antibody; anti-CD62L (α-CD62L). L-selectin is expressed on naïve lymphocytes

and rate-limiting for transmigration via HEVs[31]. After 24h of either α-CD62L or PBS

intravenous (i.v.) injection, popliteal LNs from wt mice were harvested and used for parallel

plate compression experiments. We found that blocking of lymphocyte entry significantly

reduced LN volume, effective resistance and viscosity, while the Young's Modulus remained

unchanged (Figure 2A-E). These data suggest that lymphocyte influx represents an internal

force, balancing the effective resistance of the homeostatic LN.

Next, we asked how lymphocyte cellularity affects bulk tissue properties of LNs during

inflammatory swelling. In order to distinguish between contribution of recirculating and

locally proliferating lymphocytes, we treated wt or OT-II mice with either α-CD62L or PBS,

immunized with KLH/CFA and measured tissue properties after four days (Figure 2F-J). Mice

carrying the OT-II TCR transgene suppress their natural TCRs [31], thereby creating a situation

where lymphocyte homing is maintained but the majority of B and T cell responses against

the mismatched KLH antigen eliminated. Homing, and to a lesser extent proliferation,

contributed significantly to LN swelling, while elimination of both parameters reduced LN

volumes even further (Figure 2G). In agreement with the findings under homeostatic

conditions, α-CD62L administration reduced the effective resistance in both wt and OT-II

mice, with blockade of homing showing the dominant effect (Figure 2H). While the viscosity

in the tested conditions did not show a clear trend with lymphocyte cellularity, the Young's

Modulus was reduced when lymphocyte trafficking was blocked in inflammation (Figure
2I,J).

Thus, lymphocyte trapping is not a consequence of LN swelling but drives the process as it
generates an outward pressure force which is countered by the organ's effective resistance.

The FRC network stretches upon lymph node swelling

Next, we investigated which mechanical features of the LN are resisting it's expansion. The
two candidate structures mediating the LNs effective resistance to swelling are the organ
capsule, and the FRC- and conduit network. To understand how the FRC network adapts to
volumetric changes upon swelling we quantified FRC spacing (gaps) within the T zone over
the time course of inflammation in Ccl19-Cre; mTmG (FRC-mGFP) (membrane Tomato,
membrane Green Fluorescent Protein (GFP)) mice that selectively express membrane GFP
(mGFP) in FRCs[32,33]. To this end, a circle-fitting algorithm was used to quantify the
distribution of gaps in FRC networks from two-dimensional (2D) tissue sections (Figure
3A,B). While we found no obvious disruptions of network integrity, the FRC network
dynamically adapted over time. In the first four days of inflammation the FRC network
widened, as indicated by larger gaps, and in the following days returned to homeostatic
levels (Figure 3C,D).

These results suggest that the intact FRC network initially stretches upon swelling and
subsequently remodels to accommodate the increased numbers of proliferating and
immigrating lymphocytes.

Conduits are stretched in the swelling lymph node

The FRC network comprises two principal structural components: the FRC itself and the ECM
conduit, a complex fibrillar structure, which the myofibroblastic FRC both produces and
ensheathes (Figure 4A). Both components have the potential to bear load and confer
mechanical resistance to swelling. In the following, we devised strategies to quantitatively
measure if and to what extent the two structures experience mechanical forces. We started
out with the ECM component and as a proxy for mechanical strain, we chose to investigate
the structural organization of the conduit's fibrillar collagen. Like in tendons and other
elastic ECM structures, fibrillar alignment should increase with strain.

We fixed homeostatic and reactive LNs and removed all cellular components by alkali-

maceration (Figure S2A,B). To resolve the 3-dimensional (3D) organization of individual

collagen fibrils, scanning transmission electron microscopy (STEM) tomograms of T zone

conduits were acquired at 2 degrees differential tilting angles (Figure 4A). 3D images were

reconstructed using computed weight back projection (Figure S2C,D). We quantified the

extent of conduit stretching by 3D manual tracking of individual collagen fibril segments and

by computationally calculating the centerline of each conduit based on the average

direction of its collagen fibrils. This allowed us to determine the angle of misalignment of

individual fibril segments relative to the centerline (Figure 4C,D). We found that compared

to homeostasis (D0), early in inflammation (D2, D4) conduit collagen fibrils become

progressively aligned, whereas later in inflammation (D14) they again adopted a misaligned

configuration (Figure 4D).

These results suggest that conduits stretch and bear an increased mechanical load early

upon LN swelling. At later time points they revert to the homeostatic state. Initial stretching

and later adaptation are well in line with our previous findings on network configuration.

FRC network tension increases upon lymph node swelling

We next addressed the cellular component of the FRC stretching-response. To study if the

previously observed change in conduit conformation is mirrored by the tension-state of the

FRC network, we directly measured FRC network tension by intravital laser ablation and

recoil analysis[34,35]. To this end, inguinal LNs of FRC-mGFP mice were surgically exposed and

the FRC network was imaged around 20 μm below the capsule. Individual strands of the 3D

network were cut using a high-power ultra-violet (UV)-laser (Figure 5A). FRC network

tension was subsequently determined in kymographs by calculating local recoil velocities of

the region around the site of ablation (Figure 5B,C and Supplemental Movie 1). We found

that at D4 and D8 of inflammation the tension on the FRC network almost doubled and was

restored again to homeostatic levels at D14 of inflammation.

As a proxy for the cellular mechano-response, we next measured the nuclear vs. cytoplasmic

intensity of the transcription factors Yes-associated protein (YAP), and transcriptional co-

activator with PDZ binding motif (TAZ), which are well-established downstream responses of

cytoskeletal tension[36]. FRCs and endothelial cells stained positive for YAP/TAZ, while no

signal could be observed in leukocytes (Figure 5D,E). The nuclear:cytoplasmic ratio of

YAP/TAZ (N:C YAP/TAZ ratio) in FRCs remained stable from D0 to D2 of inflammation but
increased at D4 and D8 of inflammation, confirming that FRCs experience increased
cytoskeletal tension during LN swelling. The N:C ratio decreased after FRC tension peaked
(Figure 5C,F), thereby faithfully recapitulating the tension as measured by laser cutting.
Interestingly, after two weeks of inflammation we observed a large population of FRCs that
had a negative N:C ratio, suggesting that those cells were completely shielded from active
tension.
Together, these data demonstrate that FRC tension increases upon LN swelling. However,
compared with the ECM conduit (Figure 4), tension at the cellular level increases with a two
day time delay. This kinetic is well in line with previous observations, suggesting that early in
inflammation FRCs experience a relaxation of actomyosin contractility[22,23]. This relaxation is
transient and followed by an increase in cytoskeletal tension. At later time points when
network geometry adopts its homeostatic configuration, tension drops again.
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FRCs in the swelling lymph node undergo distributed clonal expansion
The above data suggest that lymphocyte influx drives LN expansion, which initially stretches
the FRC network and elicits a mechanosensitive response by the cells, once their initial
relaxation[22,23] ceases. We next wanted to understand how the FRC network expands,
remodels and re-establishes its typical configuration and mechanical state, while
maintaining structural integrity.
To this end, we devised an approach to map the spatio-temporal expansion of the FRC
network in the swelling LN *in situ*. We used a sparse clonal labeling approach named Mosaic
Analysis with Double Markers (MADM)[37–39]. MADM labeling depends on rare
interchromosomal mitotic recombination driven by Cre-loxP sites (Figure S3A,B). Two
reciprocally split GFP and tdTomato genes (GT and TG) on identical loci of homologous
chromosomes are used to create transheterozygous offspring (GT/TG). Interchromosomal
recombination can take place in G_2 phase and restores functional GFP and tdTomato
expression. To trigger rare recombination specifically in FRCs we used the Ccl19-*Cre*
transgene[32]. When followed by X-segregation of chromosomes in mitosis, two daughter
cells are formed in which one expresses GFP (green lineage) and the other tdTomato (red
lineage). Recombination is irreversible and all subsequent progeny cells become part of the
lineage.

Homeostatic and reactive LNs were cleared and imaged by 3D light-sheet fluorescence
microscopy (LSFM). In reactive nodes, prominent clusters of FRCs emerged at D4 and D8 of
inflammation, while such clusters were rarely observed in homeostasis (Figure 6A,B & Figure
S3C). This suggested that individual FRC clones expanded following immunization and that
daughter-FRCs stay close to their precursor. No substantial bias in red vs. green lineage was
apparent, justifying combined analyses (Figure S3D). FRC clusters were quantitatively
analyzed using a density-based spatial clustering of applications with noise (DBSCAN)[40] for
which FRC bodies were semi-automatically mapped in 3D as spheres with a 12 µm diameter
(Figure S3E). A cluster was defined as at least three FRCs from the same lineage within a
radius of 20 µm. We found that both the number of labeled FRCs, number of clusters and
number of FRCs in clusters were significantly increased in reactive nodes (Figure 6C-F). Since
clusters can arise by chance, the cluster results were compared to the average of 10
simulated distributions in which the same number of FRCs were randomly distributed in the
same volume. Although clusters arise by chance in random distributions, FRCs in
inflammation were less uniformly distributed and formed more and larger clusters with FRC
numbers ranging from 3-14 (Figure 6G, Figure S3F). Clone size distribution was exponential
as is expected from an equipotent population of precursors that are dividing
stochastically[41]. To quantify the extent of FRC clustering within LNs, we defined a cluster
factor (CF) as the ratio of the number of FRCs found in clusters between the observed and
simulated distributions (Figure S3G). Hence, a CF of 100 indicates that 100x more cells are
found in clusters as by chance alone. We found an average CF of 5 in homeostatic conditions
and 117 in inflammation (respectively, 70 and 165 for D4 and D8), confirming that FRCs
form clusters in the swelling LN (Figure 6H).
We next investigated if FRC clusters are found at the vicinity of HEVs in the swelling LN as it
has been shown that *de novo* FRCs can derive from perivascular fibroblasts in the
developing spleen[42,43]. To this end, the CF was plotted as a function of the distance from
HEVs. No enrichment of clusters was found at these specific perivascular areas (Figure 6I).
To better understand the relationships between the measured parameters a correlation-
matrix was created (Figure 6J). As expected, the number of labeled FRCs correlated with the
number of observed clusters and the number of FRCs found in clusters, while the number of
clusters correlated well with the number of FRCs found in clusters. In the reactive LN *de*
novo MADM-events can occur, but our data indicate that these do not affect the CF as the

CF is independent of the number of labeled FRCs, and the relative numbers of FRC in
clusters remains unchanged in inflammation (Figure 6J, Figure S3H). LN volume was the best
determinant for the CF and also correlated well with the number of labeled FRCs, number of
clusters and FRCs in clusters (Figure 6J,K).
Together, these data show that FRCs expand in randomly distributed clusters and that FRC
growth correlates with LN volume (Figure 6K). This suggests that FRCs can expand in
response to local signals independent of their localization.
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Talin1 is required for FRC mechanosensing.
Given our previous observations, mechanical forces appeared as an attractive feedback
parameter regulating FRC network growth. Mechano-coupling of fibroblasts to their
underlying matrix is mediated by integrins and their associated intracellular force-sensitive
adaptor molecule talin. FRCs express both Talin1 and Talin2 isoforms which play non-
redundant roles in integrin activation and force transduction[44]. We selectively deleted
Talin1 in FRCs by generating Ccl19-*Cre; Talin1fl* (FRC$^{\Delta TLN1}$) mice.
Peripheral LNs of FRC$^{\Delta TLN1}$ mice were reduced in size and had lowered levels of the T-zone
chemokine CCL21 in the paracortex and the T cell zone was significantly reduced in size in
FRC$^{\Delta TLN1}$ LNs (FigureS4A-C). Within the T cell zone podoplanin (PDPN)+ FRCs$^{\Delta TLN1}$ still formed
a regularly interconnected network and expressed intercellular adhesion molecule 1 (ICAM-
1) and vascular cell adhesion molecule 1 (VCAM-1), arguing for regular differentiation
(Figure S4D). Within HEVs, CCL21 levels were unaffected (Figure S4B). Hence, despite the
reduced size, the basic organization and differentiation of the Talin1 deficient FRC network
was maintained. When FRC$^{\Delta TLN1}$ mice were immunized with KLH, LN swelling was substantial
(Figure7A) and during the initial four days after immunization, relative weight gain was
comparable to control mice. A mild reduction was only seen at D14. This demonstrates that
lymphocyte influx and proliferation were still occurring within the Talin deficient FRC
network, emphasizing the suitability of the genetic model to ask the principal question, if
FRC mechanosensing is required for network adaptation.
When we analyzed N:C YAP/TAZ ratio almost no FRCs$^{\Delta TLN1}$ showed a nuclear localization
both under homeostatic and reactive conditions (Figure 7B,C). This finding demonstrates
that Talin1 dependent mechanotransduction in FRCs is rate-limiting for YAP/TAZ nuclear
translocation and strongly indicate that FRCs$^{\Delta TLN1}$ lose their mechanosensitivity. To assess

the functional consequences for FRC network integrity we performed *in situ* network

analysis. To this end, 3D volumes of FRC networks were acquired from cleared thick

vibratome slices and network spacing was quantified using a 3D sphere-filling algorithm

(Figure 7D,E). In agreement with the previous 2D GAP analysis (Figure 2) the network of

control mice widened and remained intact at D4 of inflammation. The FRC$^{\Delta TLN1}$ network

under homeostatic conditions was widened compared to controls, but structurally intact.

Upon immunization the FRC$^{\Delta TLN1}$ network integrity became severely compromised, showing

large FRC-free gaps (Figure 7D,E & S4E). These defects were most apparent at D4 and partly

recovered by D14 of inflammation.

These data suggest that the FRC network in FRC$^{\Delta TLN1}$ mice failed to adapt to organ swelling

and partly disintegrated or ruptured. To investigate the fate of FRCs under these conditions

thick vibratome sections were stained for cleaved caspase 3 (cC3) and Ki67, to identify

apoptotic and proliferating FRCs, respectively (Figure 7F,G). These analyses showed little

apoptotic and proliferating FRCs in FRC$^{\Delta TLN1}$ and control mice under homeostatic conditions.

At D4 after immunization, the number of apoptotic FRCs per volume increased significantly

in FRC$^{\Delta TLN1}$ mice as compared to controls, while proliferation was similar in both control and

knockout. At D8, apoptotic FRCs per volume unit were still larger in FRC$^{\Delta TLN1}$ compared to

controls and proliferating FRCs were increased (Figure 7F,G).

These data indicate that compromised mechanosensing causes a severe dysregulation in

survival and proliferation of the FRC compartment, which leads to a loss of network

integrity. This finding is line with the idea that FRC remodeling is locally controlled by

mechanical feedback.

Capsule fibrosis constrains lymph nodes at late time points

Network analysis and tension measurements indicated that the FRC network reached a

"new equilibrium" two weeks after immunization, because it adopted its homeostatic

configuration. Nevertheless, effective resistance remained high at these late time points,

raising the question if another structure contributes to the force balance.

The LN capsule can be divided into two components: a floor that includes floor lymphatic

endothelial cells (fLECs) along with a basement membrane that connects to conduits, and a

roof that consists of ECM with embedded lymphoid fibroblasts to which ceiling lymphatic

endothelial cells (cLECs) adhere. We investigated the structural and mechanical properties of the two capsule components in homeostatic and inflammatory conditions.

fLECs are sparsely labeled in FRC-mTmG mice, as is demonstrated by their double positivity for mGFP and LYVE-1, and their location in the floor of the subcapsular sinus (SCS) (Figure S5A). Since the SCS floor is densely populated by fLECs, we used this sparse labeling to our advantage as it enabled the measurement of active tension on single fLECs *in vivo* using UV-laser ablation (Figure 8A). We found that fLECs had high levels of basal tension that exceeded those of FRCs (Figure 8B). Interestingly, after two days of inflammation fLECs showed reduced tension that was reverted to homeostatic levels in the further swelling phase. Likewise, no rise in active tension on the long time scale (D8-D14) was found on the capsule ECM following UV laser ablation of explanted popliteal LNs (Figure S5B,C).

The absence of a continuous rise in active tension on the capsule floor and roof entails that these components are being remodeled to keep up with the volumetric increase of the swelling LN. The capsule was therefore assessed by histology in Prospero homeobox protein 1 (Prox1)- GFP mice in which the cytoplasm of all LECs is labeled with GFP. Additional 4⊠,6-diamidino-2-phenylindole (DAPI) and platelet-derived growth factor receptor- β (PDGFR-β) staining allowed the measurement of capsule thickness and mesenchymal cell layers of the capsule above the SCS in homeostasis and inflammation. We found that the capsule thickness remained unchanged in the first four days of inflammation. Strikingly, the capsule thickness increased ~14-fold from D8 to D14 of inflammation, forming a dense fibrotic layer between the parenchyma and surrounding adipose and muscle tissue, while the SCS remained intact (Figure 8C,D & Figure S5D).

We asked if such significant remodeling of the capsule resulted in changes in its mechanical properties. To this end a micro-pipette with a small diameter was used to locally aspirate ERTR7 labeled capsules of popliteal LN explants. Using Laplace's law, an effective Young's modulus of the capsule was derived (Figure 8E). We found that the elastic modulus of the capsule remained stable over the first eight days of inflammation but was doubled at D14 (Figure 8F). By multiplying the capsule thickness and Young's modulus of the capsule, we derived the passive capsule tension; a measure of the amount of force necessary to enlarge the whole thickness of the capsule by a certain length, i.e. the force needed to swell the LN. The passive tension showed a substantive increase from D0 to D8 of inflammation and kept rising to a massive 150-fold increase at D14 of inflammation (Figure 8G).

These data indicate that during a sustained immune response, tension dissipates from the

remodeling FRC network at the intermediary time scale (D4-D14), while the capsule

remodels and becomes thicker, stiffer and more resistant to swelling at the long time scale

(D8-D14), establishing a new force-equilibrium within the organ that resists further swelling

(Figure 8H).

Discussion

Like glia cells of the nervous system, lymphatic stroma cells were long considered the
passive structural elements of the immune system. Only the last two decades revealed that
the stromal compartment decisively orchestrates immune cell encounters by providing
trophic and tactic cues and that in turn stromal cells dynamically respond to signals
provided by the immune cells[18,19]. Despite palpation of reactive LNs being part of every
physical exam and LNs being unmatched in their ability to change volume, the mechanical
aspects of LN swelling have never been directly addressed. By measuring organ mechanics
across different time and size scales we establish that reactive swelling of the LN is a multi-
tier process controlled by mechanical feedback. This allows the organ to expand in a step-
wise controlled fashion, without compromising its delicate architecture.

We demonstrate that upon inflammation, accumulating lymphocytes inflate the node and
initially stretch the FRC network. This is in line with previous findings that FRCs show an
early and transient increase in cell size[20]. Stretching puts tension on the ECM conduit as
revealed by a straightened configuration of its ECM fibrils. Although our ultrastructural
analysis did not show obvious ruptures of fibrillar collagen, Martinez et al.[45] detected gaps
in the ECM (but not the cellular) compartment of swelling LNs, raising the possibility that in
some areas of the LN, flexibility of the ECM cannot keep up with cellular deformation.
Interestingly, both our laser cutting experiments and the kinetics of nuclear shuttling of
YAP/TAZ revealed that compared to their ECM conduit, FRCs experience cytoskeletal
tension only with a time delay of two days. This is well in line with findings of the labs of
Turley and Reis e Sousa, who showed that early LN swelling is accompanied by a relaxation
of the FRC system, allowing the network to stretch[22,23]. Mechanistically, they demonstrated
that CLEC-2 ligand expressed on activated DCs binds podoplanin on FRCs and that this
interaction relaxes actomyosin contractility within the FRC myofibroblastic network. Such a
transient FRC relaxation explains why tension-increase of the ECM conduit precedes
tension-increase of FRCs and implies that the FRC cytoskeleton only experiences significant
tension once the DC-mediated relaxation signals fade after three to four days. Accordingly,
FRCs show increased αSMA expression only after the initial days of inflammation[20].

While the FRC network uses its intrinsic pliability to accommodate short-term volumetric
changes, sustained strain on the FRC cytoskeleton triggers the next stage of LN swelling,
which is characterized by actual growth and structural remodeling of the network. Our

results on genetic ablation of Talin1 in FRCs strongly support the idea that adhesion-
dependent mechanosensing is a critical feedback parameter that locally controls growth and
survival of the network, so that it reverts to its typical geometry, while being increased in
size. In line with these results, mice with a gain of function mutation in the
mechanosensitive YAP/TAZ pathway show fibrotic LNs with impaired FRC differentiation[46]
and blockade of β1 integrin triggered FRC apoptosis in swelling (but not in homeostatic)
LNs[47]. A critical prerequisite of a model where FRC mechanosensing locally controls network
remodeling is that the FRC responsiveness is not restricted to specific niches but rather
distributed throughout the organ. Our clonal analyses show that this is indeed the case and
match results in follicular dendritic cells and marginal reticular cells that were also shown to
undergo clonal expansion[48].

Beyond a week of structural adaptation the FRC network of the now massively enlarged LN
seemed to reach a new "mechanical equilibrium" as indicated by gap analysis, ECM
alignment, tension measurements and YAP/TAZ translocation. Nevertheless, bulk
mechanical properties of the LN did not return to homeostatic levels. They rather showed
an elevated effective resistance, indicating that another structure now countered the
internal pressure generated by the trapped lymphocytes. We thus turned to the capsule as
the second major stromal element and found that during these late stages, thickness and
mechanical strength of the capsule were massively increased, explaining resistance to
further organ expansion. Although capsule fibrosis is a characteristic histopathological
descriptor of reactive LNs[49], its mechanistic contributions are completely unexplored and
future studies will hopefully show how it contributes to sustained or chronic immune
responses.

As the multi-tier model of LN swelling moves through a succession of check-points, it has
the advantage of being adaptable to very different types of swelling-scenarios. Transient
swelling, as it occurs e.g. during circadian fluctuations, might stretch the network, but is
unlikely to cause structural remodeling. In contrary, sustained immune responses with
massive lymphocyte trapping and germinal center reactions, might rely on a fibrotic
strengthening of the capsule in order to limit excessive expansion of the organ.

Methods

Animals

All animal experiments are in accordance with the Austrian law for animal experiments.

Permission was granted by the Austrian Federal Ministry of Science, Research and Economy

(identification code: BMWFW 66.018/0010-WF/V/3b/2016). Mice were bred and

maintained at the local animal facility in accordance IST Austria Ethical Committee or

purchased from Charles River and maintained at the local animal facility in accordance with

IST Austria Ethical Committee. OT-II (Stock No: 004194) was bought from JAX. Ccl19-Cre

mice have been described previously[32]. MADM-7[39] and Talin1floxed[50] mice were provided

by Simon Hippenmeyer and David Critchley, respectively. All mice are on a C57BL/6J

background, with exception of MADM-7 which have a CD-1 background. Mice of both sexes

between the age of 6 to 20 weeks were used for experiments. For immunization, KLH

protein was dissolved in PBS to 5 mg/mL of and then mixed 1:1 with CFA (both Sigma-

Aldrich) upon which 40 µL of the immunization mixture was injected in footpads and flanks

of draining popliteal and inguinal LNS. LNs were harvested after various timepoint up to

two weeks of induction of immunization to be used for histology or explant experiments, or

used for *in vivo* imaging experiments. For LN cellularity manipulation experiments, mice

were i.v. injected with 100 µg α-CD62L (MEL14) (BioXCell), and control mice with PBS alone.

For steady-state evaluation, LNs were harvested 24h after injections were given, and for

inflammation conditions injections were given at onset of inflammation. Mice were

anesthetized by isoflurane inhalation (IsoFlo, Abbott) for all injection-based experiments, or

anaesthetized with a ketamine/xylazine/acepromazine mixture for *in vivo* imaging

experiments.

Histology and Imaging

LNs were fixed in 4% paraformaldehyde (Electron Microscopy Sciences) in PB (0.1 M, pH 7.4)

at 4°C overnight. For cryosections, tissues were additionally embedded for 24h in a solution

of 30% glucose in PB (0.1 M, pH 7.4) before embedding and freezing in Tissue-Tek optimum

cutting temperature (OCT) compound (Sakura). Cryostat section (10-12 µm) were collected

on Superfrost/Plus glass slides (Thermo Fisher Scientific). Alternatively fixed tissues were

embedded in 4% low melting temperature agarose (Invitrogen) after fixation and 100-400
μm sections were cut using a vibratome (VT1200S, Leica Microsystems).

Cryostat sections were air-dried for 2h at room temperature (RT) and washed in PBS.
Sections were blocked in SEABLOCK blocking buffer (Thermo Fisher Scientific) or in 5%
bovine serum albumin (BSA) (Thermo Fisher Scientific) in PBS for 1h, followed by incubation
of primary antibody solution diluted in 1% BSA/PBS for 1.5h at RT, 3 washing steps in PBS
and subsequent incubation of secondary antibody solution diluted in 1%BSA/PBS for 30 min
at RT. Finally, sections were washed three times in PBS, air-dried and mounted using
Fluoromount-G with DAPI (Thermo Fisher Scientific). Vibratome sections were blocked in 5%
BSA/0.3%Triton- x/PBS for 2h at RT under agitation followed by primary antibody incubation
in 1% BSA/0.3%Triton-x/PBS overnight at 4°C under agitation or for 2 days at RT in some
cases. The following day sections were washed three times in PBS. In case primary
antibodies were not conjugated with a fluorescent dye, samples were incubated with a
secondary antibody in 1% BSA/0.3%Triton-x/PBS for 4h at RT under mild agitation and
subsequently washed three times in PBS. All samples were then incubated in DAPI solution
for 15 min and mounted on a glass slide using Fluoromount-G (Thermo Fisher Scientific).
The following primary antibodies were used: α-CD3ε AF488 (17A2)(eBioscience), α-B220-
Biotin (RA3-6B2) (eBioscience), α-Collagen IV-Biotin (Abcam), α-CCL21-Biotin (R&D Systems),
α-PDPN-Biotin (8.1.1) (eBioscience), α-PDGFR-β (R&D Systems), α-YAP/TAZ (D24E4) (Cell
Signal), α-cleaved Caspase 3-AF647 (Asp175) (Cell Signal), α-Ki67-APC (SolA15)
(eBioscience), α-ICAM-1 (YN1/1.7.4) (BioXCell), α-VCAM-1 (Phe25-Glu698) (R&D Systems),
α-Fibroblast Marker-AF647 (ERTR7) (Santacruz Biotech). α-PNAd (MECA-79) was derived
from a concentrated hybridoma supernatant (kind gift from Christine Moussion). The
following secondary antibodies were used: Streptavidin-Cy3 (Sigma-Aldrich), Streptavidin-
AF647 (Jackson ImmunoResearch), chicken α-goat AF488 (Invitrogen), donkey α-rat AF647
(Jackson ImmunoResearch), donkey α-rabbit AF647 (Jackson ImmunoResearch), goat α-
mouse IgM AF647 (Invitrogen). Images were acquired on a Zeiss LSM800 inverted confocal
laser scanning microscope (CLSM) with the following objectives: 10x/NA0.45, 20x/NA0.8,
40x/NA1.2 Water and 63x/NA1.4 Oil Plan-APOCHROMAT.

Thick vibratome sections were in some cases cleared using the Ce3D protocol as described

previously[51]. Briefly, following antibody-staining samples were washed at RT on a shaker for

8h in washing buffer (PBS/0.3% Triton X-100, 0.5% 1-thioglycerol) which was refreshed after

4h. Next samples were cleared in freshly prepared Ce3D solution for 2x 1h, mounted in a μ-

dishes (Ibidi) and submerged in Ce3D solution. A cover-glass was placed on top to mount

cleared samples to the bottom of the well and the dish sealed with parafilm. Large 3D

volumes (xy:306x306 μm, z: 50-300 μm) were acquired from Ce3D cleared thick vibratome

sections using a spinning-disc microscope (Dragonfly, Andor) with a Apochromat LWD λS

40x/1.15 Water 0.60 mm WD objective.

3D LSFM Sample Preparation and Imaging

Terminally anesthetized Ccl19-cre hem; MADM-7$^{GT/TG}$ mice (mix C57BL/6J and CD1

background) were *in vivo* stained by retro-orbital injection of 40 μg/PBS mouse α-peripheral

node addressin (PNAd) concentrated hybridoma supernatant labeled with Atto-647N-NHS

(Atto-Tec). After 10 min, popliteal LNs were harvested and fixed in 4% paraformaldehyde

(Electron Microscopy Sciences) overnight at 4°C. Samples were washed in PBS, cleaned

under a stereomicroscope and cleared with the CUBIC protocol[52]. Briefly, samples were

incubated in CUBIC reagent 1 for 3 days at 37°C, which was replaced every 24h. Samples

were then washed with PBS, embedded in 2% low-meting temperature agarose (Sigma-

Aldrich), and sequentially dehydrated in 30% sucrose (Sigma-Aldrich) (1 day at 4°C) and 50%

sucrose (2 days at 4°C). Finally, samples were incubated in CUBIC reagent 2 for 2 days at RT.

Cleared samples were imaged using a custom LSFM setup[53]. Acquired images were stitched

using the FIJI Grid/Collection-stitching plugin (Preibitsch Laboratory), despeckled and

manually registered using a custom-alignment-tool in Matlab (developed by Ekaterina

Papusheva).

FRC Cluster Analysis

MADM-labeled cells were detected in 3D by employing a spot detection algorithm (Bitplane

Imaris) for each channel (tdTomato & GFP) separately. Chromatic aberrations and the

sequential nature of the image acquisition led to a channel misalignment which was

corrected for in the following way: the spot coordinates were exported from Imaris and

treated as a point cloud for each channel. These point clouds were then registered onto

each other using the Iterative closest point algorithm which corrected the shift and the
rotation of the spectral channels. Cells were then sorted into color classes (green (GFP), red
(tdTomato) or yellow (double positive) lineage). Red or green, if the spot existed solely in
one of the point clouds, or yellow if there were two corresponding spots in both channels
that are closer than the typical cell radius.

For the cluster analysis the LN outline and the HEVs were segmented in Imaris using the
surface detection feature. To correct errors in the cell detection, falsely detected spots from
autofluorescent structures outside of the LN volume were excluded from further analysis. In
order to avoid edge effects cells in a region 100 µm from the surface of the analyzed LNs
were excluded. FRC clusters were analyzed using a custom Matlab script utilizing a density-
based spatial clustering of applications with noise (DBSCAN) algorithm[40] in which FRCs were
represented as 3D spheres with a 12 µm diameter. An FRC cluster was defined as a
minimum of three FRCs of the same lineage (green or red) within a search-radius of 20 µm
from each FRC-sphere's surface.

To generate a random distribution (simulated FRCs), FRC-spheres were placed into the same
volume occupied by the real cells and excluded from HEV volumes. For each timepoint the
average of 10 distributions was used. The *cluster factor (CF)* was defined as *FRCs in*
clusters/Total number of FRCs divided by *Simulated FRCs in clusters/Total number of*
simulated FRCs.

FRC Network GAP Analysis
2D: A confocal laser scanning microscope with a 40x 1.2 water-objective (LSM800, Zeiss)
was used to acquire image stacks (range 10-30 µm and spaced at 1µm) with a field of view
of 240x240 µm and a pixel size of 0.5 µm from T zones in which FRCs were labeled by mGFP
(Ccl19-Cre; mTmG mice). These were subsequently segmented using Ilastik software, the
result was then transformed into a binary image and noise was removed using a custom FIJI
script that utilized the particle detection algorithm. Binarized 3D image-stacks were then
used to measure the spacing (gaps) in the network by analyzing the pore-size distribution on
individual z-sections. The pore-size distribution was obtained analogously to the pore-size
analysis described in *Acton et al.*[22]. Starting with a circle size which corresponded to the

maximum gap of the network, circles were consecutively positioned into fitting

corresponding gaps of the network. The maximum circle size was determined from a

distance transform of the segmented network. Once no more circles of the maximum size

could be placed into gaps of the network, the disk size was reduced by one unit and the

placement of the disks of reduced sized commenced. This way, the gaps in the network

were consecutively filled with circles of decreasing size until the entirety of the gap area was

filled. The results were then averaged over the

3D: Large 3D volumes (xy:306x306 μm, z:50-500 μm) were acquired from Ce3D[51] cleared

thick vibratome sections using a Apochromat LWD λS 40x/1.15 Water 0.60 mm WD

objective on a spinning disc microscope (Dragonfly, Andor). Acquired 3D stacks were

corrected for fluorescent intensity in z-axis using 'bleach correction (histogram matching)'

function in Fiji. Imaris was then used to generate a 3D binary image of the FRC network by

utilizing a surface detection feature from the FRC-network fluorescent channel. A custom

Matlab script was subsequently used to fit 3D spheres in the 3D gaps of the network analog

to the 2D approach.

Parallel Plate Compression Experiments

Explanted popliteal LNs were cleaned from adipose tissue under a stereomicroscope and

placed on a glass plate within the 37°C, RPMI 1640 (Invitrogen) filled incubation chamber of

a MicroSquisher device (CellScale). LNs were oriented to have their long axis along the field

of view of the camera. Compression was performed with a glass plate glued onto either a

0.304 or 0.408 mm diameter 40 GPa tungsten filament with a length of 60 mm. The glass

slide on the compression probe was coated with Poly-HEMA (Sigma-Aldrich) to reduce

sticking of the samples. LNs were then compressed by 25% of the initial height by lowering

the upper plate down in a timespan of 30 seconds. Lateral side-views of LNs were recorded

up to 20-60 min after onset of the experiment, while resistant forces were measured on the

upper plate. Compression protocols, images and force acquisition were realized with the

SquisherJoy software (CellScale). Length, height, contact area and curvature of LNs were

manually measured before compression, and at the equilibrium timepoints using Fiji

software. The recorded compression force together with the measured geometrical

parameters were used to calculate volumes, Young's modulus, effective resistance and

viscosity using a generalized Kelvin model[27]. This was done as following:

The force required to maintain a constant strain of 25% on a LN was measured over time

(F(t)). The force initially peaks and then follows a relaxation curve which is fitted by a double

exponential decay curve. The simplest way to describe this bimodal dynamic is to

incorporate two dashpots with constants μ_1 and μ_2, and two springs with k1 and k2

constants. After 20-60 min, the system reaches an equilibrium where the exerted force by

the plate equals the effective resistance of the LN (σ). Therefore, we have:

$$\sigma = \frac{F_{eq}/\pi R_3{}^2}{(1/R1 + 1/R2)}$$

582   where F_{eq} is the equilibrium force at steady state and R1, R2 and R3 are derived from the

583   geometry of the LN.

584   To obtain the elastic modulus, the stress and strain need to be acquired:

585   Stress (s) is calculated from the force at equilibrium divided by plate contact area:

$$s = F_{eq}/\pi R_3{}^2$$

586   and the strain (ε) from:

$$\varepsilon = 1 - \frac{h_{eq}}{h_0}$$

587   where h_0 and h_{eq} correspond to the initial and equilibrium height of the compressed LN.

588   From here the elastic modulus (E) can be derived:

$$E = s/\varepsilon$$

589   Next, by fitting a double exponential decay to the force curve we obtain two time-scales, τ_1

590   and τ_2, where:

$$\tau_i = \mu_i/k_i \quad , i = 1, 2$$

Following up on the derivations of the equations as in *Forgacs et al.*[27], μ_1 and μ_2 can be

acquired readily, where μ_1 corresponds to the initial fast response in the order of seconds

and μ_2 to the slower response in the order of minutes, of which the latter one becomes

relevant for the rearrangements of the cells within LNs. Hence, we use μ_2 as our viscosity.

Measurements in which the LN was damaged during preparation (lymphocytes leaking out)

or moved/rolled during compression were excluded. In a few cases the viscosity could not

be determined (infinitely small) and were also excluded.

LN volumes were calculated from side-view images at *t=0* with the following formula:

$$V = \frac{4}{3} \pi R1 \left(\frac{h_0}{2}\right)^2$$

Micropipette Assay

Popliteal LN explants were cleared from fat and incubated for 10 min in a 2 μg/mL ERTR7-

AF647 (Santa-Cruz) in RPMI 1640 (Invitrogen) to label the capsule. LNs were subsequently

placed on 3% methylcellulose coated glass bottom Petri dishes (MatTek) in RPMI and kept

at 37°C, while imaged on an inverted Leica SP5 microscope using a 20x, 0.7NA objective

(Leica Microsystems). The local Young's Modulus of the capsule was measured with a glass

micropipette connected to a Microfluidic Flow Control System (Fluigent, Fluiwell), with

negative pressure ranging from 7-750 Pa, a pressure accuracy of 7 Pa and change rate of

200 Pa*s^{-1}. The micropipette equipment was mounted on a motorized micromanipulator

(Eppendorf, Transferman Nk2). Both systems were controlled by Dikeria software, Labview

(National Instruments). A fire polished micropipette with an inner diameter of 15 μm and

flat end (BioMedical instruments) was used for aspiration. The chosen diameter ensured

that mainly the capsule was probed and not the underlying parenchyma. While localizing

the LN capsule with the micropipette, the pressure inside the micropipette was kept at 0 Pa.

For measurements, a negative pressure of 750 Pa was applied, which resulted in the

instantaneous aspiration of the capsule. This pressure was chosen as lower pressure

regimes did not result in proper aspiration of the capsule. The tongue length of the capsule

in the micropipette upon aspiration was manually measured in Fiji from acquired movies.

The elasticity was subsequently calculated using the Laplace law:

$$E = \frac{\Delta P}{\left(\frac{h}{d}\right)^2}$$

618 With ΔP being the pressure difference between micropipette and atmosphere, h the height

619 of the measured tongue, and d the micropipette diameter.

SEM Sample Preparation and Imaging

Terminally ketamine/xylazine/acepromazine anesthetized mice were transcardially perfused

with PB (0.1 M, pH 7.4) and subsequently fixed with 2.5% glutaraldehyde and 2%

paraformaldehyde (Science Services) in PB (0.1 M, pH 7.4). LN samples were then dissected

and post-fixed in the same buffer for another hour at RT. They were dehydrated in a graded

ethanol series of 50%, 70%, 90%, 96%, 100% in H$_2$O for a minimum of 10 min per step and

subsequently kept overnight in fresh 100% ethanol at 4°C. Once in 100% ethanol, samples

were dried with a critical point dryer (EM-CPD300, Leica Microsystems), cut in half and

coated with a 4nm layer of platinum using a sputter coater (EM-ACE600, Leica

Microsystems). The samples were imaged with a field emission scanning electron

microscope Merlin compact VP (Carl Zeiss) at 3 kV. The signal was detected by an Everhart-

Thornley type secondary electron detector.

STEM Tomography Sample Preparation

Alkali maceration of LNs was performed as previously described[54,55]. Briefly, popliteal LNs

were isolated from 8–12 weeks old wt C57BL/6 mice and directly fixed in a 2.5%

glutaraldehyde and 2% paraformaldehyde in PB (0.1 M, pH 7.4) for a minimum of two weeks

at 4°C. Samples were then macerated in aqueous 2.5 M (10% w/v) NaOH solution for 5 days

at RT under mild agitation. Next sections were rinsed in H_2O under mild agitation for one to

two days until samples became pale. If results were not sufficient, the maceration step was

repeated.

Samples were then treated with 0.5% tannic acid (w/v) in PB (0.1 M, pH 7.4) two times 1h

each with freshly prepared solutions, washed in PB and treated with aqueous 1% osmium

tetroxide (w/v) for 30 min at 4°C. Samples were contrast enhanced with aqueous 1% uranyl

acetate (w/v) overnight at 4°C and Walton´s lead aspartate for 30 min at 60°C. Samples

were then dehydrated in graded ethanol, infiltrated with anhydrous propylene oxide and

embedded in hard-grade epoxy resin (Durcupan® ACM, Fluca). Samples were consecutively

infiltrated with a 3:1 mixture of anhydrous acetone and Durcupan® for 1h at 4°C, 1:1

aceton/Durcupan® for 1.5h at 4°C, 1:3 aceton/Durcupan® for 2h at 4°C and mere Durcupan®

overnight at RT. Samples were transferred to BEEM capsules (Electron Microscopy

Sciences), filled with freshly prepared Durcupan® and cured for 48h at 60°C.

STEM Tomography Imaging

Semi-thin sections were cut at 450 nm using an UC7 ultramicrotome (Leica Microsystems)

and collected onto formvar-coated 200-line bar grids + 1C/bar (Science Services, G200PB)

and coated with evaporated carbon to a thickness of 8nm. Grids were cut in half, mounted

on a Half-Mesh High Tilt holder (Jeol, EM-21010/Z09291THTR) and observed under a JEM

2800 scanning transmission electron microscope (Jeol) operated at 200 kV in STEM mode.

To compensate for focus, contrast and brightness, and stage shift during image tilt series

recording, an automated system was used comprising the STEM Recorder V3 Vers. 3.2.8.0

and the STEM Magica Controller Vers. 0.9.8.1 (both System In Frontier Inc.). Images were

collected at 2° intervals between +/-76° of single tilt axis. Magnification was x80k – x600k,

image size 512x512 pixels giving a pixel sizes from 6.749463 nm/px to 0.899928 nm/px.

Conduit Stretching Quantification

STEM Tomography images were aligned by cross-correlation and 3D structure of area of

interest computed by weighted back-projection using Composer software Vers. 3.0 (System

In Frontier Inc.). A 3D Gaussian blur filter and background subtraction (rolling ball algorithm)

pre-processing step were performed on the images using FIJI. The 3D image stacks were

subsequently loaded into Imaris, and fibrils of conduits were manually traced using the

Filament Tracer tool and exported to Matlab format using the Object Exporter (exported

from Imaris as filaments). The overall orientation and curvature of the centerline of the

entire conduit was approximated by fitting a cubic spline curve with four support points

which minimized a hand-crafted cost function through all fibril track data. This cost function

penalizes the distance of the desired centerline to the tracks, the total curvature of the

centerline and the difference in length between it and the fibril bundles, and ensures that

the support points are spaced evenly. In a few cases this spline curve was corrected by hand

if it was found to not adequately represent the center line of the bundle. The alignment of

the individual fibrils with respect to the centerline of the conduit was calculated as follows:

The spline centerline was interpolated in a continuous fashion and the 3D orientation was

calculated. Likewise, the tracks of individual fibrils were first smoothed to reduce tracing

errors and the 3D orientation of each segment of the trace was calculated. The alignment

angle A between the fibril is then given by the angle between the orientation of the

segment and the orientation of the centerline at the point that is closest to the segment:

$$A = \text{acos}\left(abs\left(\frac{\vec{v}_{fibril} \cdot \vec{v}_{centerline}}{\left|\vec{v}_{fibril}\right| \times \left|\vec{v}_{centerline}\right|} \right) \right)$$

UV-Laser Cutter Setup

The UV-laser cutter setup is based on a previously described layout[35,56]. In brief, a passively Q-switched solid-state 355 nm UV-A laser (Powerchip, Teem Photonics) with a repetition rate of 1 kHz, pulse energy of 15 µJ, pulse-length of <350 ps and peak-power of 40 kW was used in conjugation with a spinning disc microscope (Axio Observer Z1, Zeiss). The system is controlled using custom-built software (LabView, National Instruments) enabling cutting in 3D. Typically 5% of the power is used to cut tissues.

UV-Laser Ablation Experiments

Tension on FRCs, fLECs and capsule ECM was measured by conducting laser ablations on an inverted UV-laser ablation setup with a manufacturer 40x 1.2NA water immersion lens in homeostatic and inflamed LNs. For all experiments 25 UV pulses at 1000 Hz to 40 equidistant sites using 200 ms exposure time and frame rate were used to ablate and capture tissue recoil. For FRC and LEC ablation, we established an intravital setup where Ccl19-Cre hem; mTmG hom mice were anesthetized and intact inguinal LNs exposed using a skin flap surgery. The paracortical site of the LN was mounted on a custom-made stage which allowed the LN temperature to be regulated at 37°C. For capsule ECM ablation, popliteal LNs were harvested and incubated in 100 µM TAMRA in RPMI 1640 solution (both Invitrogen) for 15 min at RT and directly used for experiments. Explanted LNs were mounted at room temperature in a glass bottom Petri dish (MatTek) in RPMI and prevented from floating using a 22x22 mm cover glass topping.

Cuts were performed in either three z-planes spaced 1 µm apart along a length of either 10 µm for FRCs, or in one z-plane along 20 µm for fLECs and capsule ECM. FRC cuts were typically performed at 10-20 µm depth underneath the capsule. Recoil of FRCs and LECs was quantified from kymographs made in FIJI, while capsule ECM recoil was quantified using PIVlab in Matlab. In the latter case, temporal recoil velocities were measured between bandpass filtered pre- and consecutive post-cut frames by averaging the component of the calculated velocity in the perpendicular direction to the cut, within an area of the surrounding cut site.

YAP/TAZ Quantification

The nuclear to cytoplasmic ration of stained YAP/TAZ in FRCs were measured from 3D

sections of peripheral LNs. In FIJI, FRCs were identified by the mGFP labeling and for each

FRC the average YAP/TAZ fluorescent intensity of the nucleus (identified by DAPI) was

divided by the average intensity of the adjacent cytoplasm of the cell body. In other cases,

YAP/TAZ localization was qualitatively assessed to contain to either contain a higher nuclear

or cytoplasmic YAP/TAZ intensity.

CCL21 Quantification

Cryosections containing both a control and FRC$^{\Delta TLN1}$ peripheral LN in a single section were

stained for CCL21 and pair-wise imaged using similar settings. The average fluorescent

intensities of CCL21 were then measured from paracortical areas and normalized to the

control.

Proliferation and Apoptosis Measurements of FRCs

Large 3D volumes (xy:306x306 µm, z: 50-150 µm) stained for either cleaved Caspase 3 or

Ki67 were acquired from Ce3D cleared thick vibratome sections were corrected for

fluorescent intensity in z-axis using 'bleach correction (histogram matching)' function in Fiji.

Imaris was then used to generate a 3D isosurface of the FRC network by utilizing a surface

detection feature from the FRC-network fluorescent channel. The isosurface was then used

to mask the cleaved Caspase 3 and Ki67 channels so only the fluorescent signal within the

FRC network remained. Positive nuclei were then manually counted from 2D slice views and

normalized for per volume unit.

Capsule Thickness Measurements

The thickness of capsules was measured in vibratome sections of PROX1-GFP or wt mice,

stained for PDGFR-β and DAPI. The size of the capsule was then manually measured in FIJI

from the SCS to the surrounding adipose or muscular tissue from at least 3 locations and

were averaged per LN.

Statistical Analysis

All statistical analyses were performed in GraphPad Prism 8. P-values <0.05 were considered

significant.

Software

FIJI	Schindelin et al., 2012	https://fiji.sc/
Imaris	Bitplane	https://imaris.oxinst.com/packages
Excel	Microsoft	https://products.office.com/en-us/?rtc=1
Prism	GraphPad Software	https://www.graphpad.com/scientific-software/prism/
MATLAB	MATLAB Software	https://www.mathworks.com/products/matlab.html
Ilastik	Sommer et al., 2011	https://www.ilastik.org/
SquisherJoy	Cell Scale	https://www.cellscale.com/products/microtester/
Composer software	System Frontier Inc.	In https://temography.com/en/composer-en/
PIVlab	Thielicke and Stamhuis 2014	https://pivlab.blogspot.com/

Data availability

Data supporting the findings of this study are available from the corresponding authors upon.

Code availability

Code used for various analyses in this study are available from the corresponding authors upon request.

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Acknowledgements

This research was supported by the Scientific Service Units of IST Austria through resources provided by the Bio Imaging, Electron Microscopy, Preclinical and Life Science Facilities. We thank Christine Moussion for providing anti-PNAd antibody, Simon Hippenmeyer and David Critchley for respectively donating transgenic MADM-7 and Talin1floxed mice, and Ekaterina Papusheva for providing a custom 3D channel alignment script. This work was supported by European Research Council grant ERC-CoG-72437.

Contributions

F.P.A. designed experiments, and performed all *in vivo* and *ex vivo* experiments with assistance of M.H., M.B., S.S and G.K.; J.A. cleared samples and did light-sheet imaging, F.P.A. did all other fluorescent imaging. W.A.K. processed samples for electron tomography, and W.A.K., T.C. and F.P.A. acquired tomograms. F.P.A. did all data processing and analysis with help of R.H., S.S. and G.K; R.H. wrote all custom analysis scripts. S.H. and E.H. aided in the interpretation of MADM and mechanical data, respectively. S.L discussed data. M.S. directed the study, F.P.A. and M.S. wrote the manuscript, and all authors critically reviewed the manuscript.

Ethics declarations

The authors declare no competing interests.

Figure 1. The reactive lymph node resists swelling. (**a**) Side-view focus-stack of popliteal LNs
in homeostasis (D0) and inflammation (D14). Scale bar = 500 µm. (**b**) Volumes of swelling
LNs calculated from 2D-side views over the course of two-week following onset of
immunization. Means±SEM are connected (blue line) and a linear regression line (dashed)
has been fitted to the data. (**c-d**) Overview of the stress-relaxation experiment on explanted
popliteal LNs (D2 of inflammation depicted). (**c**) Measured geometrical parameters are
annotated on 2D-side images acquired during a measurement. Scale bar = 300 µm. (**d**) The
stress relaxation curve is given by the measured force over time from which the equilibrium
force (long timescale) parameter), viscosity (medium timescale) and Young's Modulus (short
timescale) relaxation parameters are derived. (**e-g**) Quantification of tissue properties in
homeostasis (D0) and inflammation (D2, D4, D8, D14) derived from the stress relaxation
curve and geometrical properties. Each datapoint represents a single measured LN.
Measurements are pooled from LNs harvested from at least 5 mice and multiple
experiments. Mean±SEM. (**e**) Quantification of the effective resistance. (**f**) Quantification of
the viscosity. (**g**) Quantification of the Young's Modulus. For statistical analysis see
Supplementary Information, table 1. *$P<0.05$, **$P<0.01$, ****$P<0.0001$.

Figure 2. Lymphocyte numbers generate pressure and drive lymph node swelling. (**a-j**)
Analysis of stress-relaxation experiments on explanted LNs. Each datapoint represents a
single measured LN. Measurements are pooled from LNs harvested from at least 5 mice and
multiple experiments. Mean±SEM are given. (**a**) Side-view of explanted homeostatic LNs
from mice treated with anti-CD62L or PBS. Scale bars = 300 µm. Dashed lines depict the
outline of LNs. (**b**) Quantification of LN volume. (**c**) Quantification of the effective resistance.
(**d**) Quantification of the viscosity. (**e**) Quantification of the Young's Modulus. (**f**) Side-view of
explanted D4 inflamed LNs from wt and OTII mice treated with anti-CD62L or PBS. Scale bars
= 400 µm. Dashed lines depict the outline of LNs. (**g**) Quantification of LN volumes. (**h**)
Quantification of the effective resistance. (**i**) Quantification of the tissue viscosity. (**j**)
Quantification of the Young's Modulus. For statistical analysis see Supplementary
Information, table 1. ns, not significant. ns, not significant. *$P<0.05$, **$P<0.01$, ***$P<0.001$,
****$P<0.0001$.

Figure 3. The FRC network stretches upon lymph node swelling. (**a**) Overview of the FRC
network gap analysis. Left: mGFP labeled FRCs (green), middle: segmented FRC network
(white), right: gaps (randomly colored circles) in the FRC network. Scale bar = 20 μm. (**b**)
Representative images of FRC networks gaps in homeostasis (D0) and inflammation (D2, D4,
D8 and D14). (**c**) Averaged and smoothed distribution of FRC network fitted circle
distribution plotted as the Weighted Area Fraction as a function of the fitted circle diameter.
(**d**) Quantification of the mean fitted-circle diameter. Each datapoint represents the average
value of 10-30 analyzed consecutive sections of an acquired 3D volume. Means for each
timepoint are depicted as a black line. Data are for each timepoint pooled from 5 popliteal
or inguinal LNs from at least 3 mice and 2 separate experiments. For statistical analysis see
Supplementary Information, table 1. ***P<0.001, ****P<0.0001.

Figure 4. Conduits are stretched in the swelling lymph node. (**a**) Overview of STEM
tomography acquisition of macerated LN samples. Images show the fibrillar collagen of T
zone conduits at a single tilt angle, and a maximum intensity projection crop of a 3D conduit
reconstructed from multiple tilting angles. (**b**) Representative 3D reconstructions of fibrillar
collagen (blue) from macerated conduits at homeostasis (day 0) and inflammation (D2, D4
and D14) in which the conduit center line (yellow) and tracked fibril segments (grey) are
annotated. (**c**) Visual representation of the conduit fibril alignment analysis of an imaged 3D
conduit volume. Angles of individual fibril segments (thick colored lines) with the center line
of the conduit (dashed black line) are measured at multiple points along the fibril segment
(thin colored lines) and averaged per fibril segment. (**d**) Quantification of conduit fibril
alignment with center line. Each datapoint represents an individual fibril segment. Means
are depicted as black lines. For statistical analysis see Supplementary Information, table 1.
ns, not significant. ***P<0.001, ****P<0.0001.

Figure 5. FRC network tension increases upon lymph node swelling. (**a**) Overview of *in vivo*
UV-laser cut experiment of the FRC network. Inguinal LNs from FRC-mGFP mice are
surgically exposed and kept hydrated at 37°C. A high UV-laser cuts the FRC network along 10
μm at 3 different planes after which the local recoil of the FRC network is imaged. Scissor
and line indicate cutting location and arrows the recoiling FRC network. Scale bars = 20 μm.
(**b**) Representative example of FRC network recoil. Images depict stills from before (t=-1s),

directly after (t=0s) and late after (t=6.2s) cutting (scale bars = 5 µm), with corresponding
kymograph along the recoil axis (scale bar x-axis = 1s, y-axis = 2 µm). Scissor and line
indicate cutting location and arrows the recoiling FRC network. Dashed lines in kymograph
indicate slopes used to calculate the recoil velocity, and vertical white line the cut. (**c**)
Quantification of recoil velocity from kymographs. Each datapoint represents a single FRC
network cut. Data is pooled from 3-4 animals and at least 2 experiments per analyzed
timepoint. Means±SEM are depicted and connected with a line. (**d**) 3D view of the FRC
network and stained for YAP/TAZ. Stack size 20 µm. Scale bar = 20 µm. (**e**) Representative
examples of YAP/TAZ nuclear and cytoplasmic localization. N:C = nuclear to cytoplasmic
fluorescent intensity ratio. (**f**) Quantification of YAP/TAZ N:C ratio. Dashed line indicates an
equal ratio. Each datapoint corresponds to a single measured FRC. Measurements are taken
from a total of 3 LNs per analyzed timepoint from at least two separate experiments.
Means±SEM are depicted and connected with a line. For statistical analysis see
Supplementary Information, table 1. ns, not significant. *P<0.05, **P<0.001, ****P<0.0001.
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Figure 6. FRCs in the swelling lymph node undergo distributed clonal expansion. (**a**)
Schematic overview of the sparse mosaic analysis with double markers (MADM) labeling
approach for FRC cluster imaging. (**b-k**) Quantification of light sheet images from cleared
LNs in homeostasis (D0) and inflammation (D4 and D8). All graphs depict the mean±SD. Each
datapoint represents a single popliteal LN. LNs are retrieved from at least 3 mice and 2
separate experiments for each condition. (**b**) LN volumes. (**c**) Numbers of MADM labeled
FRCs. (**d**) Numbers of FRCs found in clusters. (**e**) Number of clusters. (**f**) 3D view of HEVs
(grey) and smoothed convex-hull of cluster volumes (randomly colored) in a homeostatic
(D0) and inflamed (D4) LN, scale bar = 200 µm (**g**) Frequency distribution of FRC cluster sizes
found in observed and simulated data in homeostasis (D0) and inflammation (D4 and D8).
(**h**) Quantification of the cluster factor (CF) between homeostatic (D0) and inflamed LNs (D4
and D8). (**i**) Number of FRC clusters in homeostatic (D0) and inflamed LNs (D4 and D8)
plotted as a function of the distance from the nearest HEV. (**j**) Correlation-matrix of paired
variables assessed in the cluster analysis. Spearman correlation: *p*-values are given and the
correlation-coefficients are color-coded. (**k**) CF plotted as a function of the LN volume. A
spline-fit is plotted through the data-points. For statistical analysis see Supplementary
Information, table 1. ns, not significant. **P<0.01, ***P<0.001, ****P<0.0001.

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Figure 7. Talin1 is required for FRC mechanosensing. (**a**) Quantification of LN weights in

homeostasis and following inflammation (D4 and D14) in control and $FRC^{\Delta Talin1}$ mice. Each

datapoint represents a single LN. Data is pooled from at least 5 mice from multiple

experiments per condition. Insert depicts the grow curves of the plotted data fitted with a

non-linear regression function. Mean±SEM. (**b**) T zone FRC network of FRC-mGFP (control)

and $FRC^{\Delta Talin1}$-GFP mice stained for YAP/TAZ. Enlargements depict representative examples

of the N:C of YAP/TAZ. Scale bars = 10 μm. (**c**) Quantification of YAP/TAZ localization in FRCs

of control and $FRC^{\Delta Talin1}$ mice in homeostasis (D0) and at inflammation (D4). Mean±SEM. (**d**)

Representative 3D images of 3D network analysis of control and $FRC^{\Delta Talin1}$ mice in

homeostasis (D0) and following inflammation (D4 and D14). Imaged stack size: 100-300 μm.

Scale bars = 50 μm. (**e**) Quantification of FRC network analysis as shown in **d**. Left: average

weighted volume fraction plotted as function of the sphere diameter. Right: average sphere

diameter for all conditions. Each datapoint represents an individual LN from at least 3 mice

and 2 experiments per condition. Means are depicted by black lines. (**f**) Quantification of

cleaved Caspase3+ FRCs from FRC-mGFP (control) and $FRC^{\Delta Talin1}$-GFP mice in homeostasis

(D0) and inflammation (D4 and D8). Each datapoint represents a single LN. Data pooled

from 3 mice per timepoint. Images depict the identification of an apoptotic FRC. Scale bar =

3 μm. (**g**) Quantification of Ki67+ FRCs from FRC-mGFP (control) and $FRC^{\Delta Talin1}$-GFP mice in

homeostasis (D0) and inflammation (D4 and D8). Each datapoint represents a single LN.

Images depict the identification of a proliferating FRC. Scale bar = 3 μm. Data pooled from 3

mice per timepoint. Mean±SD. For statistical analysis see Supplementary Information, table

1. ns, not significant. *P<0.05, **P<0.01, ***P<0.001, ****P<0.0001.

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Figure 8. Capsule fibrosis constrains lymph nodes at late timepoints. (**a**) Overview of

intravital UV-laser cut experiments of the SCS fLECs. Inguinal LNs from FRC-mGFP mice, in

which SCS fLECs are sparsely labeled with a mGFP are surgically exposed. A high UV-laser

cuts the cell along 20 μm in one plane after which the local recoil is imaged. Images depict

stills from before (t=-1s), directly after (t=0s) and late after (t=10.2s) cutting (scale bars = 5

μm), with corresponding kymograph along the recoil axis (scale bar x-axis = 1s, y-axis = 2

μm). Scissor and line indicate location of cut and arrows the recoiling cell. Dashed lines in

kymograph indicate slopes used to calculate the recoil velocity, and vertical white line the

cut. (**b**) Quantification of experiments as described in **a** for homeostatic (D0) and inflamed

(D2, D4, D8, D14) LNs. Each datapoint represents a recoil-measurement of a single fLEC.

Data pooled from 3 mice and at least two experiments. Mean±SEM are depicted and

connected with a line. (**c**) Representative confocal images of LN capsules from PROX1-GFP

mice in homeostasis (D0) and inflammation (D4, D8 and D14), in which LECs are labeled by a

cytoplasmic GFP. Mesenchymal cells are stained for PDGFR-β, and nuclei are counterstained

with DAPI. Scale bars = 20 μm. (**d**) Quantification of the capsule thickness measured from

the SCS as depicted in **c.** Each datapoint represents the average of 3 measurements per LN.

Mean±SEM are connected with a line. Data pooled from 5 LNs derived from 3 mice per

timepoint. (**e**) Overview of micro-pipette assay for capsule stiffness measurements.

Capsules of explanted popliteal LNs are labeled by brief incubation with Alexa Fluor 647-

conjugated anti-ERTR7 antibody, upon which a small diameter glass pipette is placed on the

capsule and a defined negative pressure applied. The ECM 'tongue' entering the pipette is

subsequently measured. The local effective Young's Modulus of the capsule is derived using

Laplace's law. Scale bar = 50 μm. (**f**) Quantification of measurements as described in **e** for

homeostatic (D0) and inflamed (D2, D4, D8 and D14) LNs. Each datapoint represents the

average of 3 measurements per LN. Mean±SEM are connected with a line. Data pooled from

5 LNs derived from 3 mice per timepoint. (**g**) Quantification of the Capsule swelling

resistance as measured by the Passive Tension, given by multiplying the capsule thickness

and Young's modulus from **d** and **f**, respectively. Each datapoint represents a single LN.

Mean±SEM are connected with a line. (**h**) Schematic of the mechanical dynamics of the

swelling LN. For statistical analysis see Supplementary Information, table 1. ns, not

significant. **P<0.01, ***P<0.001.

Supplementary Figure 1. (**a**) Quantification of popliteal LN volumes calculated from 2D side

views in homeostasis (D0) and inflammation (D2, D4, D8, D14) acquired from parallel plate

compression experiments. Mean±SEM. (**b**) Relation between calculated volumes and

measured weights of popliteal LNs in homeostasis and inflammation. A regression line is

fitted. (**c**) Example of a double-exponential force fit (red line) on a stress-relaxation

measurement. Arrow indicates the force at equilibrium (F_{eq}). (**d**) Average of stress-relaxation

curves for all measured conditions. Mean±SEM. (**e**) Schematic representation of the

generalized Kelvin model and formulas used to calculate tissue properties from parallel
plate stress-relaxation experiments. Adapted from *Forgacs et al.*. (**f**) SEM image of packed
lymphocytes in the LN paracortex. Scale bar = 2 μm. For statistical analysis see
Supplementary Information, table 1. **P<0.01, ****P<0.0001.

Supplementary Figure 2. (**a**) Schematic of LN processing for STEM tomography of T zone
conduits. (**b**) Example of a macerated conduit imaged by STEM in which the characteristic D-
period of collagen fibrils can be observed. Scale bar = 500 μm. (**c**) Examples of a T zone
conduit at different tilting angles acquired by STEM tomography. (**d**) Schematic of a
computed weight back projection to reconstruct a 3D volume of a conduit from differential
tilting angles.

Supplementary Figure 3. (**a**) Schematic of the MADM labeling principle. Rare
interchromosomal recombination in the G2 cell cycle phase following x-segregation of
chromosomes labels FRCs with either a cytoplasmic tdTomato or GFP. (**b**) Sparse labeling of
FRCs. Scale bar = 200 μm. (**c**) 3D fluorescent intensity images of GFP labeled FRCs and *in situ*
labeled HEVs by anti-PNAd-ATTO647n antibody. (**d**) Quantification of the MADM labeling
distribution in homeostasis (D0) and inflammation (D4 and D8). Each datapoint represents a
single LN. Mean±SD. (**e**) Overview of the labeling of HEVs and mapping of labeled FRCs (only
tdTomato+FRCs are shown) at D4 of inflammation. The enlarged image depicts the mapping
of individual FRCs by a grey sphere at the center of each cell. Scale bars = 200 μm. (**f**)
Formula for the calculation of the cluster factor (CF) per LN. (**g**) Quantification of the
average distance to the nearest neighbor (NN) of both mapped FRCs and randomly localized
FRCs from simulations in homeostasis (D0) and inflammation (D4 and D8). Means are
depicted by black lines. (**h**) Quantification of relative numbers of MADM-labeled FRCs found
in clusters in both homeostasis (D0) and inflammation (D4 and D8). Mean±SD. For statistical
analysis see Supplementary Information, table 1. ns, not significant. **P<0.01, ***P<0.001.

Supplementary Figure 4. (**a**) Quantification of steady-state popliteal and inguinal LN weights
from control and FRC$^{\Delta Talin1}$ mice. Each datapoint represents a measured LN. Images show a
representative inguinal LN for each condition. Scale bars = 1 mm. (**b**) Quantification of
steady-state T zone CCL21 protein as measured *in situ* by fluorescent intensity following
staining for CCL21. Measurements are taken from histological sections from 5 LNs of 3 mice

for each condition. Mean±SEM. Scale bars = 20 μm. (**c**) T zone and B-cell follicles in steady-

state popliteal LNs from control and FRC$^{\Delta Talin1}$ mice stained for CD3 (T cells) and B220 (B

cells). Scale bars = 200 μm. (**d**) ICAM-1, PDPN, VCAM and merged staining from steady-state

popliteal LN T zones from control and FRC$^{\Delta Talin1}$ mice. Scale bars = 20 μm. (**e**) Overview of

the T zone FRC network in homeostasis (D0) and inflammation (D4 and D14) between FRC-

mGFP (control) and FRC$^{\Delta Talin1}$-mGFP mice stained for collagen IV. Scale bar = 50 μm. For

statistical analysis see Supplementary Information, table 1. *P<0.05, ****P<0.0001.

Supplementary Figure 5. (**a**) Ccl19-Cre; mTmG mice sparsely label fLECs of the SCS. Zoomed

window depict the SCS with LECs brightly labeled with tdTomato (mTdT) and the sparsely

labeled fLEC (mGFP), given by the double positive labeling with the fLEC-marker LYVE-1

(gray). (**b**) Overview of the UV-laser cut experiment on TAMRA labeled capsule ECM of

explanted LNs in homeostasis (D0) and inflammation (D2, D4, D8, D14), which faithfully

represents capsule ECM as observed in alkali macerated LNs imaged by STEM and SEM.

Particle imaging velocimetry (PIV) was used to measure displacement of structures above

and below the cut site from band-pass filtered images. Recoil displacement is depicted by

orange vectors. Scale bar STEM image = 5 μm, SEM image = 1 μm, fluorescent TAMRA-

labeled image = 20 μm. (**c**) Quantification of recoil velocities of capsule cuts from

experiments on homeostatic (D0) and inflamed (D2, D4, D8, D14) LNs as described in **b**. Each

datapoint represents a single cut. Between 14 and 24 cuts were taken per measured

timepoint from at least 5 LNs from two animals and at least two separate experiments.

Mean+SEM connected by a line. (**d**) Representative histological examples of LN capsules

from PROX1-GFP mice in homeostasis and D14 of inflammation, stained for PDGFR-β and

counterstained with DAPI. Scale bars = 200 μm. For statistical analysis see Supplementary

Information, table 1. *P<0.05, **P<0.01.

Supplementary Movie 1. Example of low (homeostasis; D0) and high tension (Inflammation;

D4) of the FRC network as given by the recoil speed following *in vivo* UV-laser cutting in

surgically exposed inguinal LNs of FRC-mGFP mice.

A FRC Network Analysis

FRC-mGFP

Binary representatation

Circle fitting of gaps

B

| D0 | D2 | D4 | D8 | D14 |

C

Weighted Area Fraction
(Area Fraction x Circle diameter)

- D0
- D2
- D4
- D8
- D14

Circle Diameter (µm)

D

Mean Circle Diameter (µm)

D0 D2 D4 D8 D14

Figure 6

A Lymph Node Weights

B Control / FRC^ΔTalin1

C FRC YAP/TAZ Localization

D Control / FRC^ΔTalin1

Spheres FRC network (FRC-mGFP)

E FRC Network Analysis

F FRC Apoptosis

FRC-mGFP
Cleaved Caspase 3
Apoptotic FRC

G FRC Proliferation

FRC-mGFP
Ki67
Proliferating FRC

Figure 8

A t= -1.0s | t= 0.0s | t= 10.2s | Kymograph
fLEC-mGFP
Skin flap
Inguinal Lymph Node
Glass
40X

B fLEC Tension
ns
**
Recoil Velocity (μm/min)
300
200
100
0
D0 D2 D4 D8 D14

C D0 | D4 | D8 | D14
PROX1-GFP PDGFR-β DAPI

D Capsule Thickness
***
**
Capsule Thickness (μm)
150
100
50
0
D0 D2 D4 D8 D14

E Capsule Stiffness Measurement
micro-pipette φ: 15 μm
Lymph node
P= 0 mBar | P = -750 mBar
P_{atm} $P_{pipette}$
d
h
Lymph Node
$$E\ (Pa) = \frac{\Delta P}{\left(\frac{h}{d}\right)^2}$$
ERTR7

F Capsule Stiffness
**
Young's Modulus (kPa)
D0 D2 D4 D8 D14

G Capsule Resistance
***
**
Passive Tension (kPa*μm)
D0 D2 D4 D8 D14

H Mechanical Dynamics of the Swelling Lymph Node

LN Volume
Capsule Thickness

FRC Network Configuration

Conduit Allignment

FRC Tension & Mechanosensing

FRC Clonal Expansion

Capsule Resistance

Effective Resistance

Day 0 | Day 2 | Day 4 | Day 8 | Day 14

Phase I FRC relaxation and stretching

Phase II Increasing FRC tension and proliferation

Phase III Decreasing FRC tension, and growth

Phase IV Growth with capsule thickening and further strong resistance to growth

A Lymph Node Volumes

B Volume-Weight Correlation

$R^2 = 0.9779$

C Force Fit

$$Force\ (t) = A_1 * e^{-t/\tau 1} + A_2 * e^{-t/\tau 2}$$

F_{eq}

D Stress Relaxation Curves

D0
D2
D4
D8
D14

E

Generalized Kelvin Model

Viscous Components

Elastic Components

μ_1 k1

μ_2 k2

Effective Resistance

σ

μ_0

1) **Volume** = $(4/3)\,\pi\,R1\,(H_0/2)^2$
2) **Contact Area** = $\pi\,R3^2$
3) **Effective Resistance** = σ
   is derived from
   $$\frac{F_{eq}}{\pi\,R3^2} = \sigma\left(\frac{1}{R1} + \frac{1}{R2}\right)$$
4) **Strain** = $1 - (H_{eq}/H_0)$
5) **Stress** = F_{eq} / Contact Area
6) **Elastic Modulus** = Stress / Strain
7) $\mu_0 = F_{eq}/\sigma$
8) $K_1 = A_1/\mu_0$ $K_2 = A_2/\mu_0$
9) **Viscosity** = $\mu_2 = \tau_2\,K_2$

F

A

Lymph Node Decellarization

10% NaOH
5 days

H₂O
3 days

Contrasting

0.5% tannic acid
1% OsO₄

Sample trimming

450nm

B

Decellularized Conduit

C

| Tilt angle -76° | Tilt angle -38° | Tilt angle 0° | Tilt angle +38° | Tilt angle +76° |

D

Computed weight back projection

A Mosaic Analysis with Double Markers (MADM) Principle

B Sparse Labeling of FRCs

C Homeostasis   Inflammation

FRCs-GFP+ HEVs

D ● tdTomato+GFP- ● tdTomato-GFP+

E 3D: HEV network   3D: tdTomato+FRCs   Slice view FRCs   Mapping of FRCs

F Cluster Factor Calculation

$$CF = \dfrac{\dfrac{\#\ FRCs\ Clustered}{\#\ FRCs\ Total}}{\dfrac{\#\ Simulated\ FRCs\ Clustered}{\#\ Simulated\ FRCs\ Total}}$$

G ● FRCs ● Simulated FRCs

H ● D0 ● D4 ● D8

A Lymph Node Weights

Control FRCΔTalin1

Control FRC^{ΔTalin1}

B CCL21 Protein

Control FRC^{ΔTalin1}

PNAd CCL21

C Control FRC^{ΔTalin1}

CD3 B220

D VCAM-1 PDPN ICAM-1 Merge

Control

FRC^{ΔTalin1}

E FRC-mGFP Collagen IV Merge

D0 Control

D0 FRCΔ^{Talin1}

D4 Control

D4 FRCΔ^{Talin1}

D14 Control

D14 FRCΔ^{Talin1}

A Ccl19-Cre; mTmG

SCS | mTdT | mGFP | LYVE-1 | MERGE

B

Capsule ECM (STEM)

Capsule ECM (SEM)

Explant

popliteal Lymph Node

Glass

40X

561nm imaging laser
High Power UV-laser

Capsule ECM (TAMRA labeled)

Pre Cut | Post Cut

bandpass filtered

Vectors only

PIV

C

Capsule ECM Tension

Recoil Velocity (um/s)

D0 D2 D4 D8 D14

D

Homeostasis | D14

Muscle
Capsule
Parenchyma

PROX1-GFP PDGFR-β DAPI