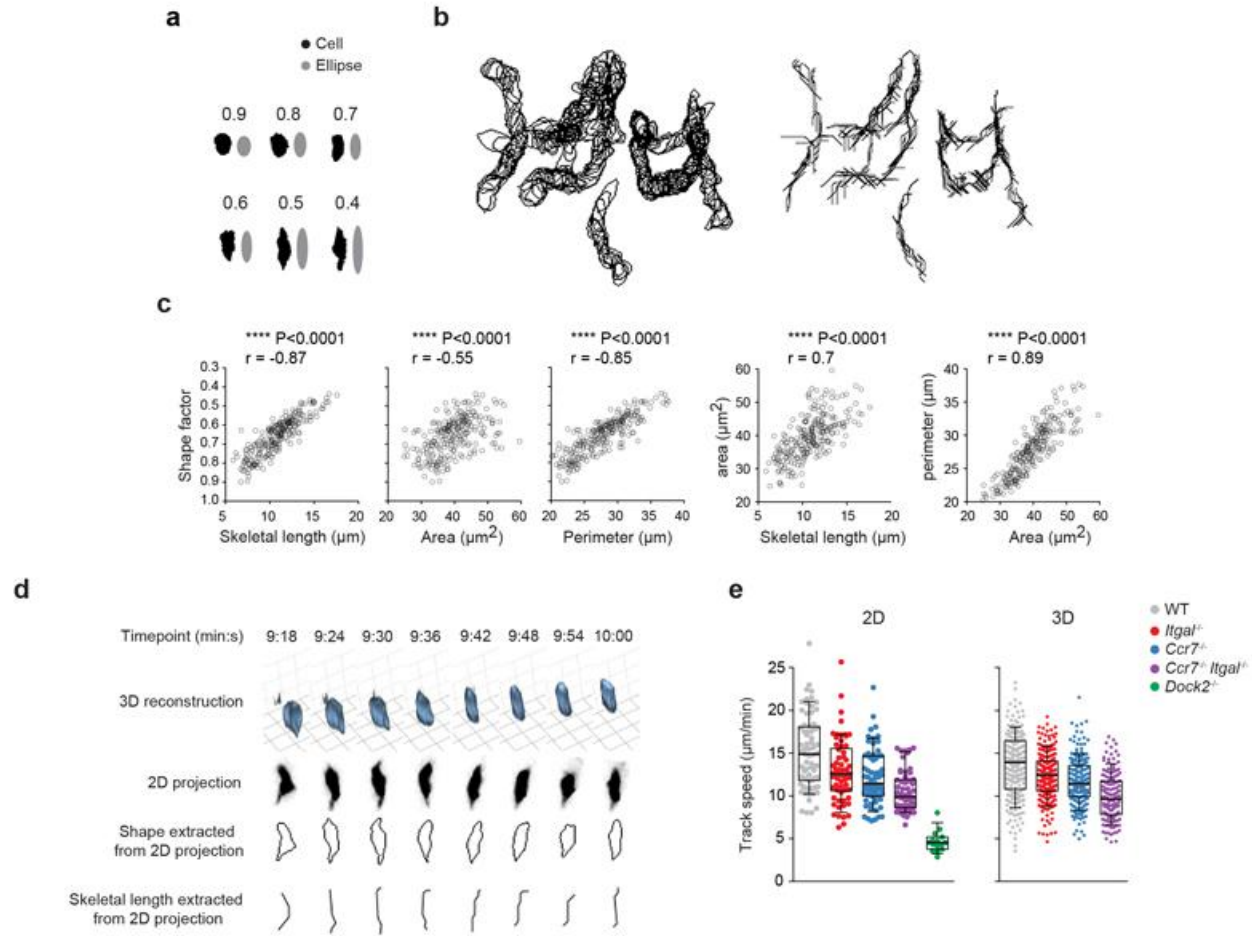


In the format provided by the authors and unedited.

Chemokines and integrins independently tune actin flow and substrate friction during intranodal migration of T cells

Miroslav Hons ^{1,2,3*}, Aglaja Kopf¹, Robert Hauschild ¹, Alexander Leithner¹, Florian Gaertner¹, Jun Abe ², Jörg Renkawitz¹, Jens V. Stein ^{2,3*} and Michael Sixt ^{1,3*}

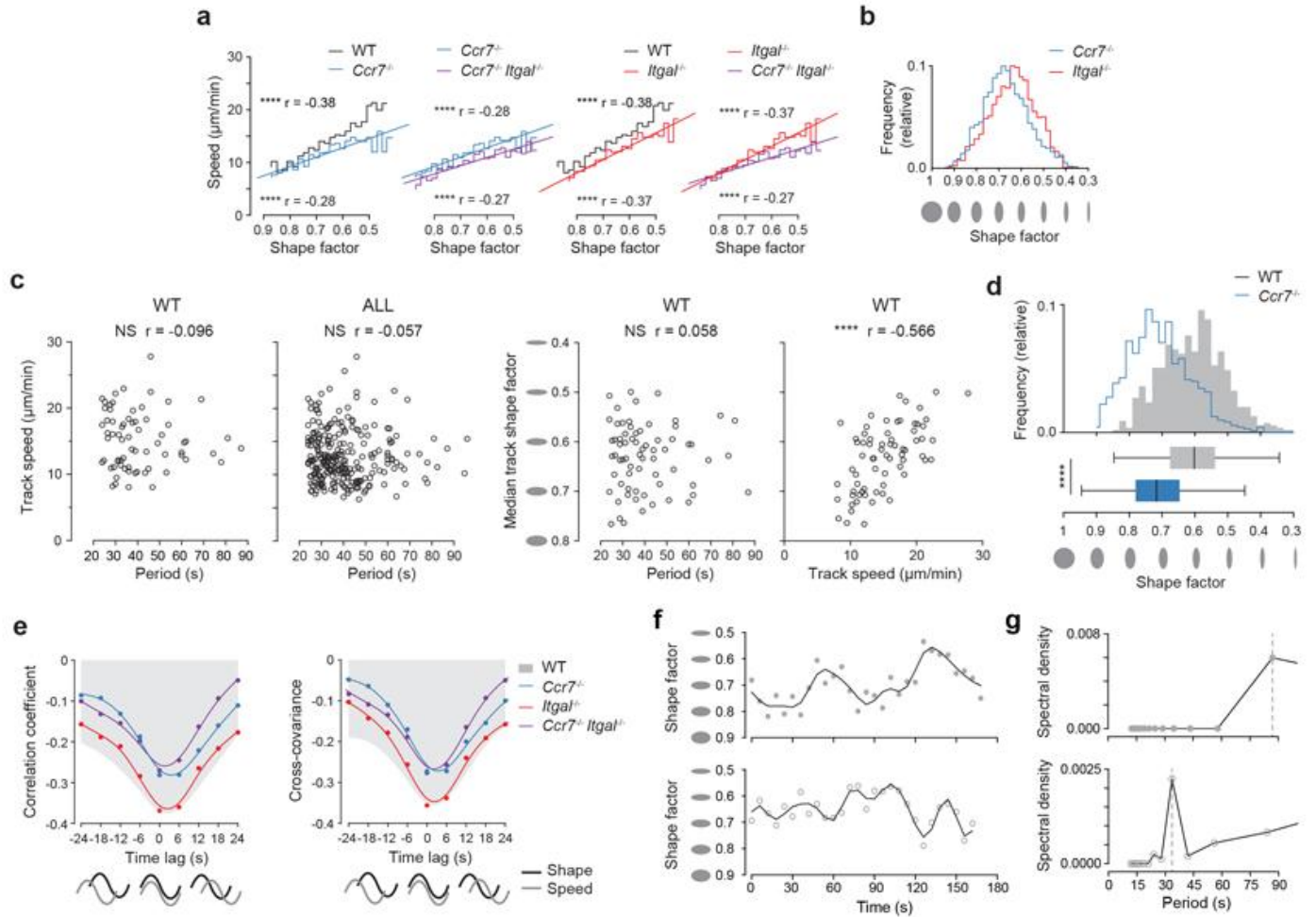
¹Institute of Science and Technology Austria, Klosterneuburg, Austria. ²Theodor Kocher Institute, University of Bern, Bern, Switzerland. ³These authors contributed equally: Miroslav Hons, Jens V. Stein, Michael Sixt. *e-mail: miroslav.hons@ist.ac.at; jens.stein@tki.unibe.ch; sixt@ist.ac.at



Supplementary Figure 1

Two-photon intravital microscopy and analysis showing morphodynamical parameters of T cells migrating in LN parenchyma after transfer into wild-type mice.

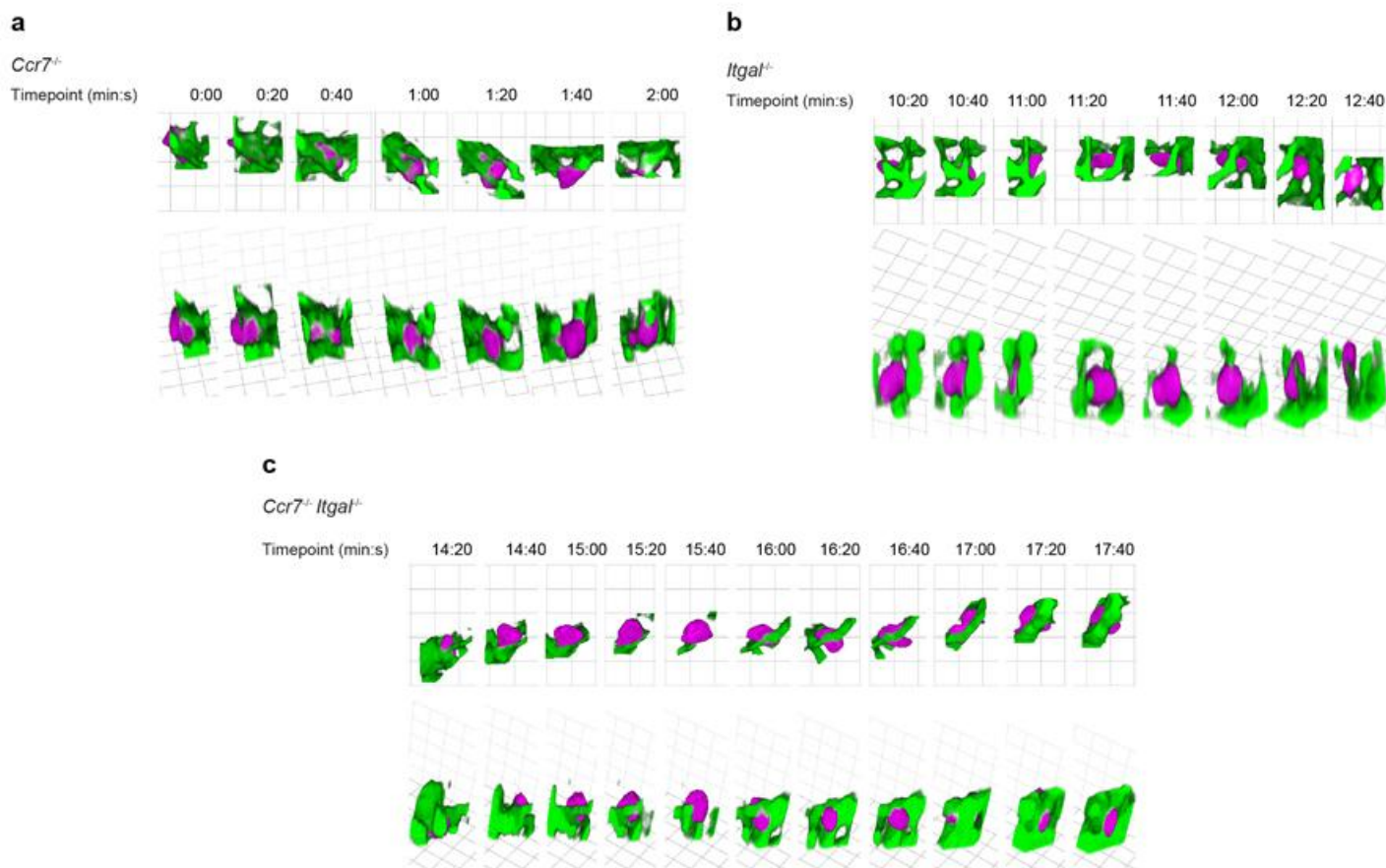
(a) Examples of actual cell shapes and idealized ellipses of a given shape factor. **(b)** Comparison of cell shape (left) and skeletal length (right) of WT T cells on an example dataset. **(c)** 2D morphometrical parameters of WT T cells from sample dataset as in **b**, Spearman correlation coefficient (r) as indicated, **** $P < 0.0001$, $n = 226$ shapes. **(d)** Example 3D reconstruction, 2D projection and morphometrical parameters from a track as in **Fig. 1b**. **(e)** Speed of primary naive T cells migrating in LN parenchyma as determined by 2D versus 3D tracking. Left, T cells tracked from 2D videos as in **Fig. 1** and **Fig. 2**, 6 s intervals, minimum track span 2 min. Dots represent individual cell tracks. WT $n=69$ cells, *Ccr7*^{-/-} $n=66$ cells, *Itgal*^{-/-} $n=61$ cells, *Ccr7*^{-/-} *Itgal*^{-/-} $n=55$ cells, *Dock2*^{-/-} $n=15$ cells. Right, tracks from independent experiments analyzed in 3D, tracked at 20 s intervals, minimum track span 7 min. Dots show individual cell tracks. WT $n=227$ cells, *CCR7*^{-/-} $n=217$ cells, LFA-1^{-/-} $n=245$ cells, *CCR7*^{-/-} LFA-1^{-/-} $n=155$ cells, whiskers represent Tukey fences.



Supplementary Figure 2

Two-photon intravital microscopy showing morphodynamical parameters of wild-type, $Ccr7^{-/-}$, $Itgal^{-/-}$ and $Ccr7^{-/-}; Itgal^{-/-}$ T cells migrating in LN parenchyma after transfer into wild-type mice.

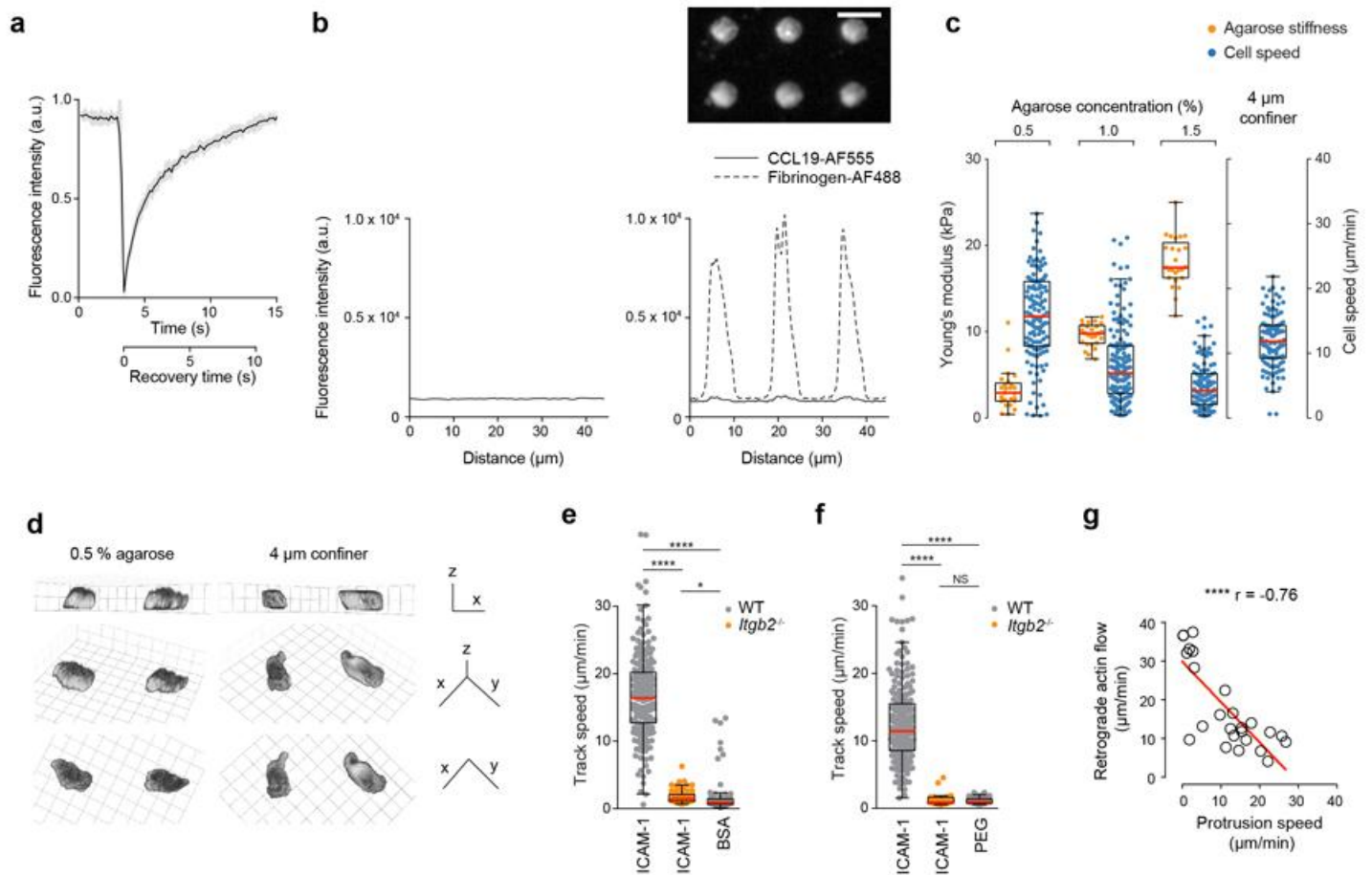
(a) Cell speed – shape correlation as in **Fig. 2a, e** and **f**. Lines show linear correlation fit, stairs show median values in respective bins. Spearman correlation coefficients (r) as indicated. **** $P < 0.0001$. **(b)** Cell shape frequency distribution of $Ccr7^{-/-}$ and $Itgal^{-/-}$ T cells as in **Fig. 2b**. **(c)** Relationship between periodicity of cell shape, track mean speed and track median cell shape of WT and all (WT, $Ccr7^{-/-}$, $Itgal^{-/-}$ and $Ccr7^{-/-} Itgal^{-/-}$) T cells analyzed. Dots show individual tracks. WT $n=69$ tracks, all $n=251$ tracks. Spearman correlation coefficient (r) as indicated, NS = not significant, **** $P < 0.0001$. **(d)** Shape frequency distribution of WT and $Ccr7^{-/-}$ T cells co-transferred in WT mice and analyzed from movies where both cell phenotypes were present. WT $n=553$ shapes, $Ccr7^{-/-}$ $n=726$ shapes. Box plots correspond to distribution plots, whiskers represent Tukey fences. Mann-Whitney test, **** $P < 0.0001$. **(e)** Temporal shift of speed - shape correlation and cross-covariance of speed and shape factor of WT, $Ccr7^{-/-}$, $Itgal^{-/-}$ and $Ccr7^{-/-} Itgal^{-/-}$ T cells. Dots indicate correlation coefficient or cross-covariance values. Curves show spline interpolation. **(f)** Evolution of cell shape in time illustrated on two example cell tracks. Dots and circles show actual measurements, curves show Fourier smoothing. **(g)** Spectral analysis of respective cell tracks from **f**.



Supplementary Figure 3

Two-photon intravital microscopy showing interactions of T cells with LN stroma after transfer of fluorescently labeled T cells into bone marrow chimeric mice expressing GFP in the LN stroma.

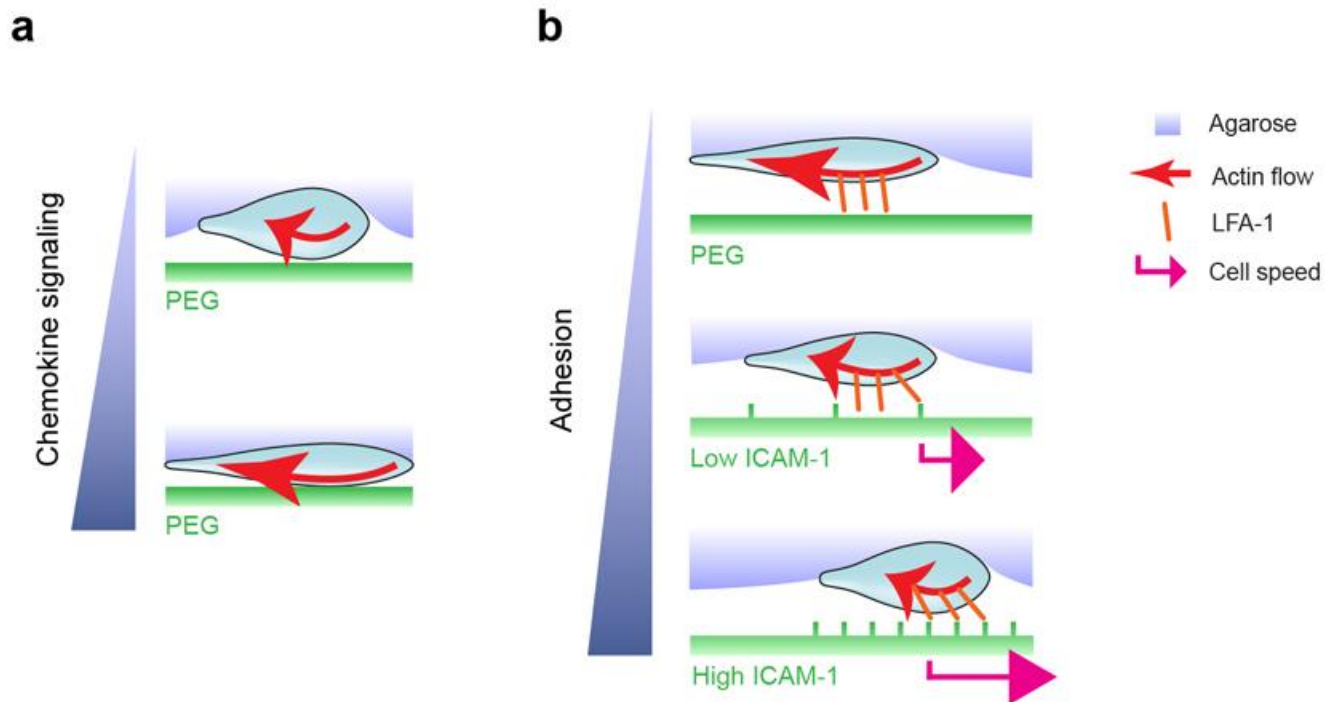
(a) Example *Ccr7*^{-/-} T cell interacting with local areas of LN stroma. Top view and upper left view (below) on a time-lapse sequence of a 3D reconstitution. (b) *Itgal*^{-/-} T cell interacting with local areas of LN stroma. Top view and bottom up view (below) on a time-lapse sequence of a 3D reconstitution. (c) *Ccr7*^{-/-} *Itgal*^{-/-} T cell interacting with local areas of LN stroma (green). Top view and upper right view (below) on a time-lapse sequence of a 3D reconstitution. a-c represent examples of data as described in Fig. 3. In a-c, side of one square is equivalent to 6.3 μ m.



Supplementary Figure 4

Characterization of the under-agarose assay.

(a) FRAP recovery of CCL19-AF555 in the agarose block. Grey areas indicate SD, n=11 bleaches. Data show one experiment. **(b)** CCL19 immobilization on surfaces. Fluorescent signal from UV-ablated areas on PEG-coated slides incubated with 100nM CCL19-AF555 (left). Subsequently, slides were incubated with 5μg/mL fibrinogen-AF488 (Right). Image on top shows UV-ablated pattern highlighted with fibrinogen-AF488, bar indicates 10 μm. Data show one experiment. **(c)** Agarose stiffness interpolated with cell speed as a function of agarose concentration. Agarose Young's modulus was determined by atomic force microscopy, 25 measurements per condition were taken in a 5 x 5 array. Primary WT T cells were migrating on dishes coated with 2 μg/mL ICAM-1 under agarose supplemented with 10 nM CCL19. 0.5% n=126 cells, 1% n=159 cells, 1.5% n=111 cells. Right, tracks speeds of cells migrating under 4 μm high PDMS confiner, n=112 cells. Dots indicate individual cell tracks or individual AFM measurement, whiskers represent Tukey fences. Data show one experiment. **(d)** Representative 3D reconstructions of cells under 0.5% agarose or 4 μm high PDMS confiner. Cells were placed on PEG coated surfaces in the presence of 10 nM CCL19. Side of one square is equivalent to 5.2 μm. **(e)** Speeds of WT and integrin β2-deficient T cells on 10% BSA or ICAM-1 (2 μg/mL) blocked with 10% BSA. Cells were placed under agarose supplemented with 5% BSA and 10 nM CCL19. WT on ICAM-1 n=210 cells, *Itgb2*^{-/-} on ICAM-1 n=108 cells, WT on BSA n=95 cells. **(f)** Speed of WT and integrin β2-deficient T cells on ICAM-1 immobilized on biotinylated PEG or on biotinylated PEG only. Cells were placed under agarose supplemented with 5% BSA and 10 nM CCL19. WT on ICAM-1 n=229 cells, *Itgb2*^{-/-} on ICAM-1 n=25 cells, WT on PEG n=88 cells. In **e** and **f** dots indicate individual cell tracks, whiskers represent Tukey fences. Kruskal-Wallis test, NS = not significant, * P<0.05, **** P<0.0001. Data represent pool of two experiments. **(g)** Correlation of retrograde actin flow and cell protrusion speed of T cells migrating on 10 ng/mL ICAM-1 blocked with BSA as in **Fig. 7c**. Cells were confined under agarose supplemented with 5% BSA with 10 nM CCL19. Data represent pool of three experiments. n=26 cells, r = spearman correlation coefficient, **** P<0.0001.



Supplementary Figure 5

Scheme of T cell shape and speed determination.

(a) T cell elongation is given by speed of cortical actin flow. High actin flow speed correlates with increase in cell elongation (below). **(b)** In absence of integrin engagement T cells can not migrate and actin flow speed and cell elongation are at maximum. Force transmission of actin flow through LFA-1 engagement with ICAM-1 leads to actin flow deceleration, cell speed increase and cell rounding (below).