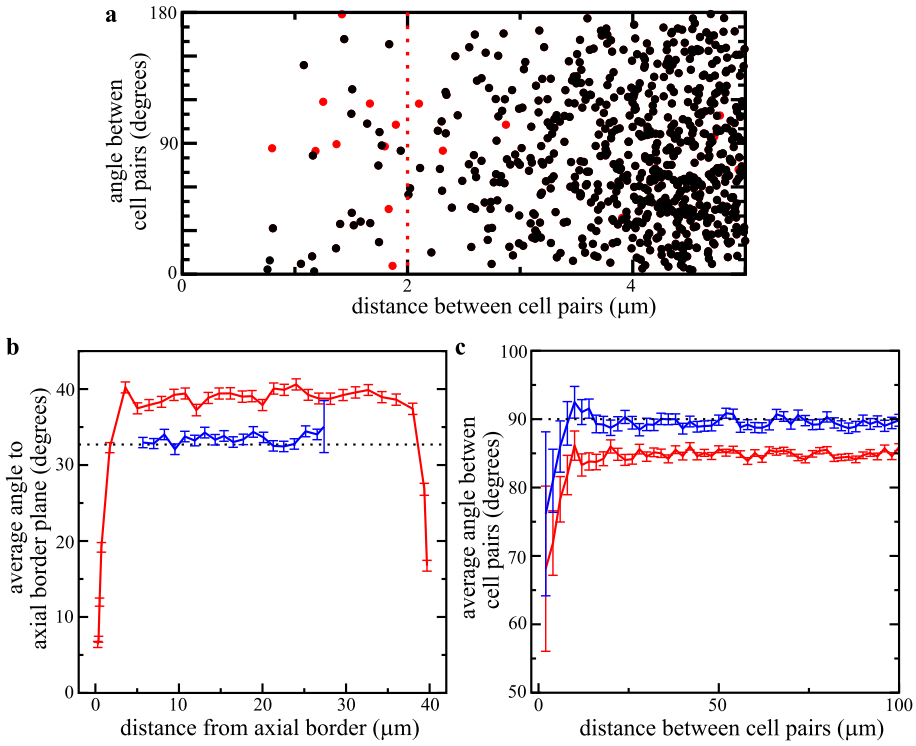
SUPPLEMENTARY INFORMATION S3 - FIGURE



Examples of artifact detection and correction in experimental data sets (compare to Figure 5 in main text).

a | Plot of angle between cell pairs and their distance for all possible cell pairs (each dot is one pair). In this data set all cells whose centres of mass approach another cell by less than 2 μm (the approximate cell radius of the cells in these experiments, denoted by the red dotted line) were manually checked for correctness. The red dots represent tracking errors (double tracking, or switching of tracks) and would be removed in subsequent analyses, while for the black dots such errors could not be detected. **b** | Plot of the average angle to the $z = 0$ border plane versus the distance to that border (bins consist of 1000 data points). **c** | Plot of the average angle between cell pairs versus the distance between the pairs (bin sizes are 2 μm). In **b** and **c** the raw data are shown in red, and the expectation for random migration as black dotted lines. The artifacts of tissue drift and imprecise z-calibration are visible as an overall average angle above (**b**) and below (**c**) that expectation, while the sharp drops in **b** near the borders of the image volume (around 0 μm and around 40 μm) are due to tracking errors near borders. The drop at small distances in **c** is due to the presence of small T cell streams (see Beltman *et al.* J. Exp. Med. **204**, 771–780 (2007)). The blue line shows results after correction for artifacts as explained in the main text. Note that the actual z-size of the image volume is smaller than the original z-calibration predicted (visible in **b**). Error bars are standard errors of the mean. All shown results are taken from experimental data published in Beltman *et al.* J. Exp. Med. **204**, 771–780 (2007).