

Supplementary Information

Automated tracking of label-free cells with enhanced recognition of whole tracks

Naim Al-Zaben^{1,2,†}, Anna Medyukhina^{1,†}, Stefanie Dietrich^{1,2}, Alessandra Marolda^{2,3}, Kerstin Hünninger^{3,4}, Oliver Kurzai^{3,4,5}, Marc Thilo Figge^{1,2,5,*}

¹Applied Systems Biology, Leibniz Institute for Natural Product Research and Infection Biology – Hans Knöll Institute (HKI), Jena, Germany.

²Faculty of Biological Sciences, Friedrich Schiller University Jena, Jena, Germany.

³Fungal Septomics, Leibniz Institute for Natural Product Research and Infection Biology – Hans Knöll Institute (HKI), Jena, Germany.

⁴Institute of Hygiene and Microbiology, University of Würzburg, Würzburg, Germany.

⁵Center for Sepsis Control and Care (CSCC), Jena University Hospital, Jena, Germany.

† These authors contributed equally to this work.

* Correspondence should be addressed to M.T.F.: thilo.figge@leibniz-hki.de

FIGURE S1:

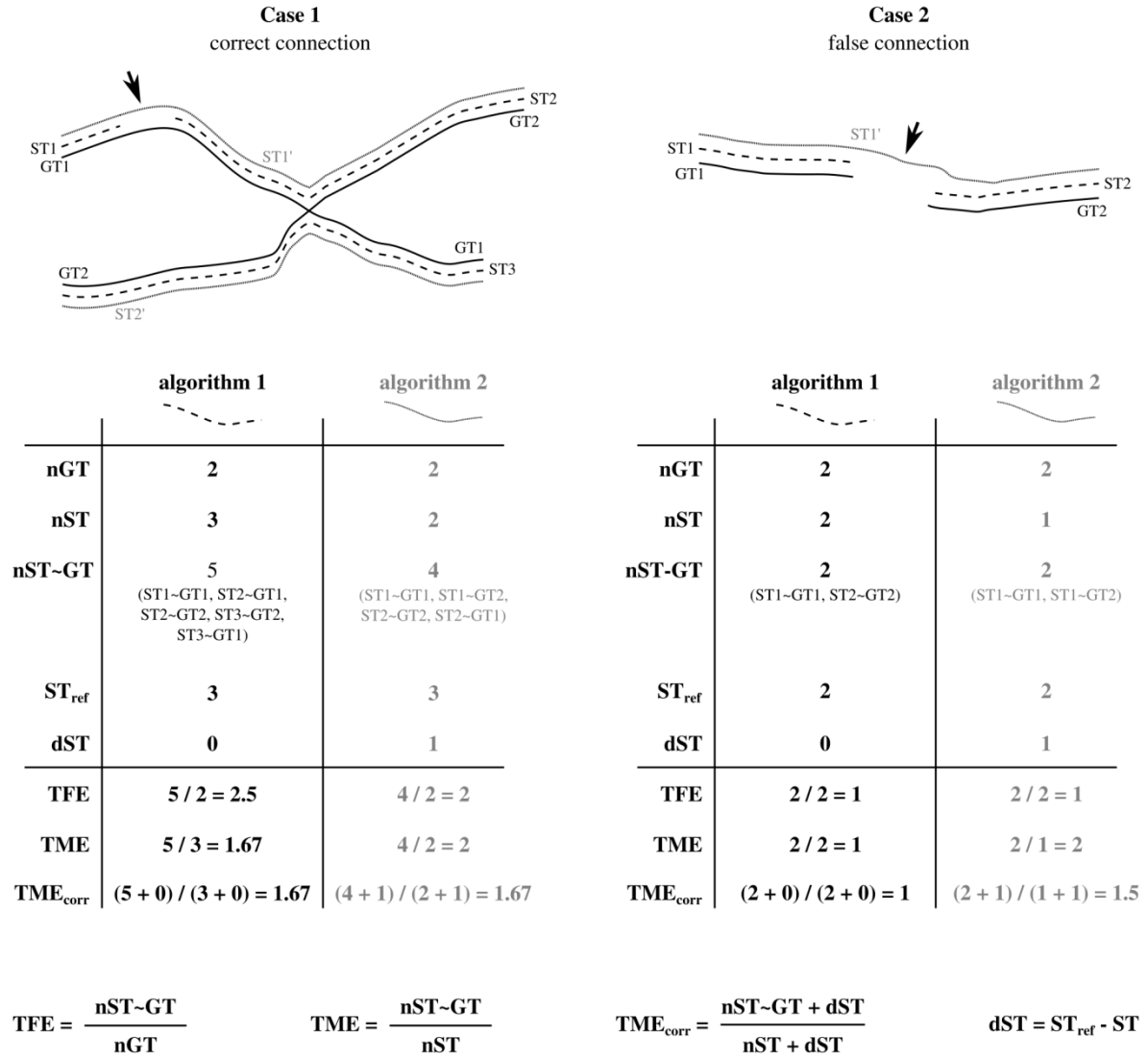


Figure S1. Exemplary computation of track fragmentation error (TFE), track merging error (TME) and corrected track merging error (TME_{corr}) for two arbitrary algorithms, where the second algorithm generates an additional track connection (arrow) that is either correct or wrong.

FIGURE S2:

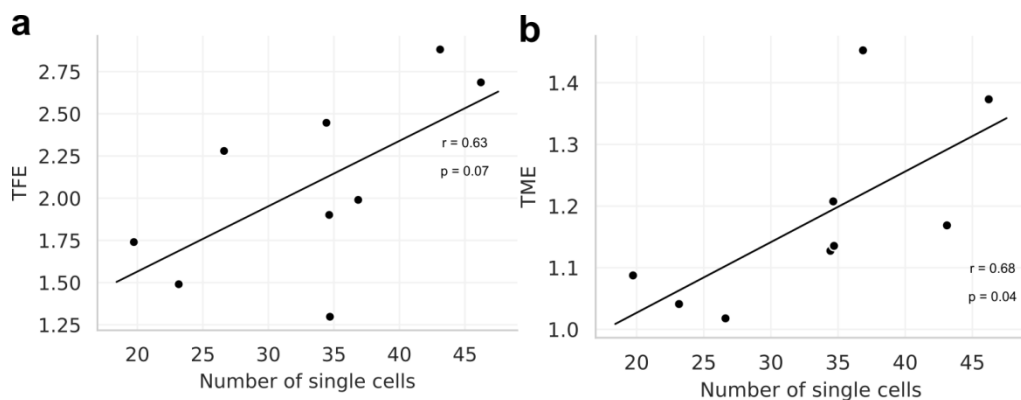
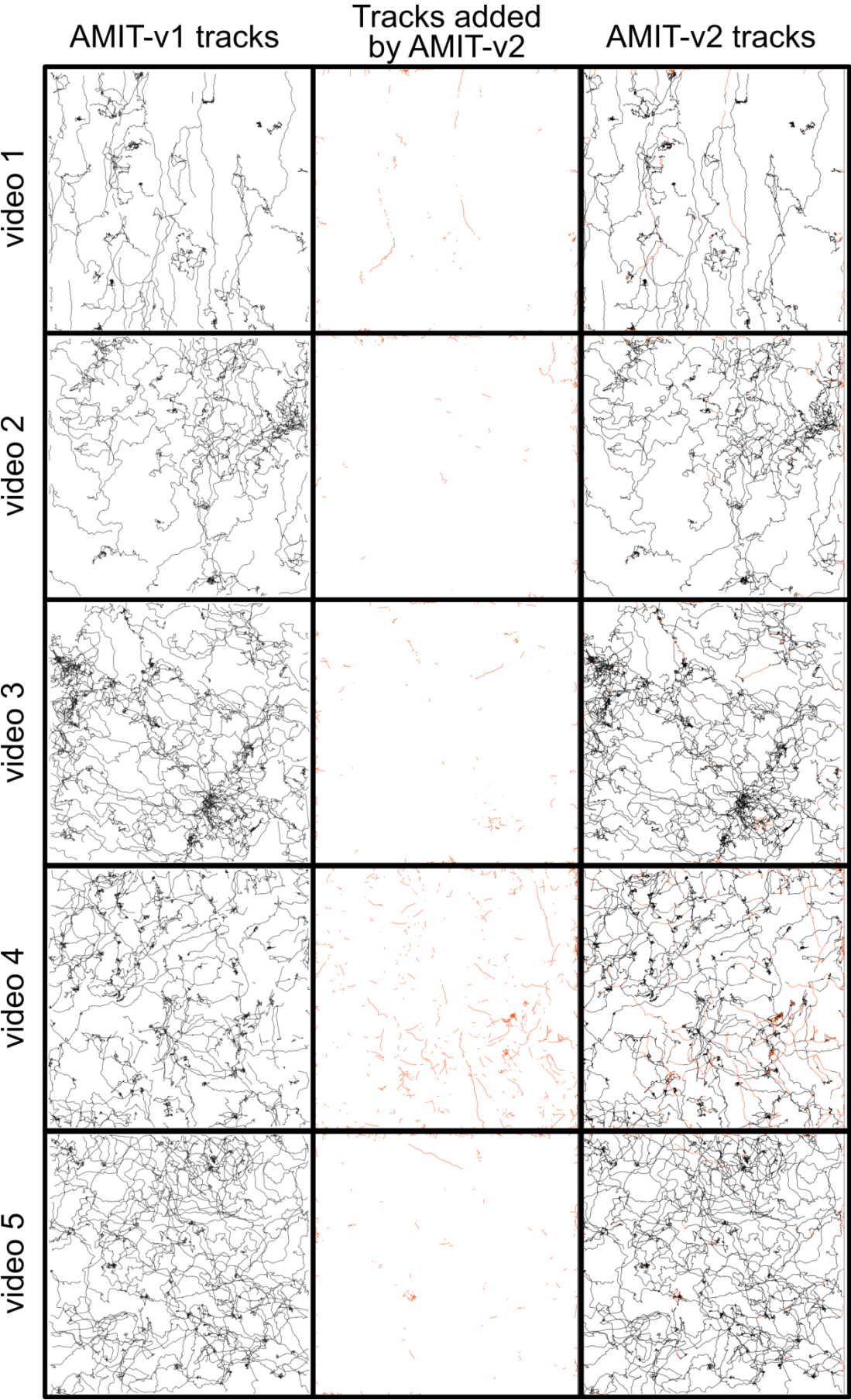


Figure S2. The track fragmentation error (TFE) (a) and the track merging error (TME) (b) of AMIT-v1 increase with the average number of single cells in the field of view. The parameters r and p denote the Pearson correlation coefficient and the p -value for the Pearson correlation coefficient, respectively.

FIGURE S3:



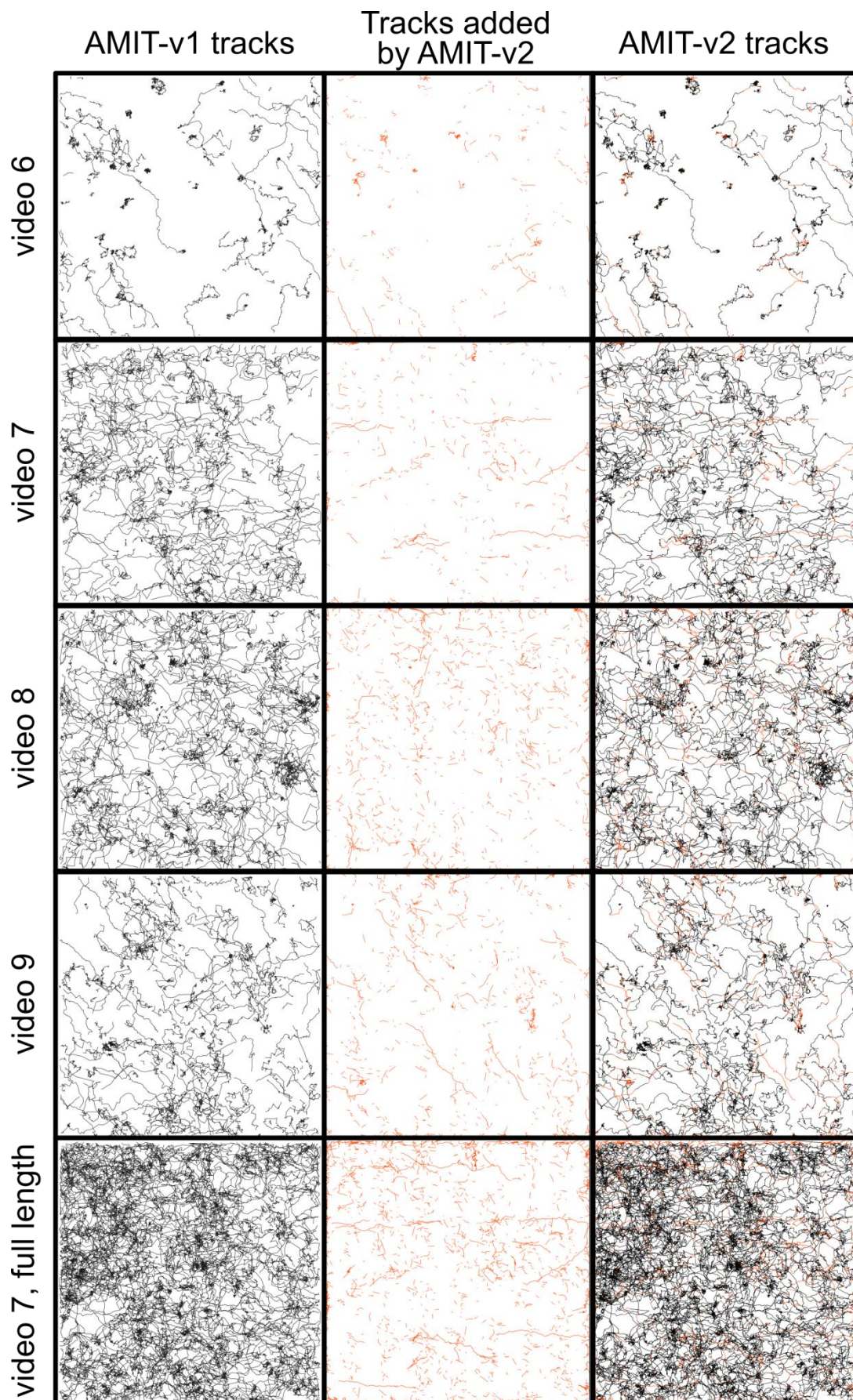


Figure S3. Final tracks generated by AMIT-v1 and AMIT-v2. The size of the field of view is $425 \times 425 \mu\text{m}$.

FIGURE S4:

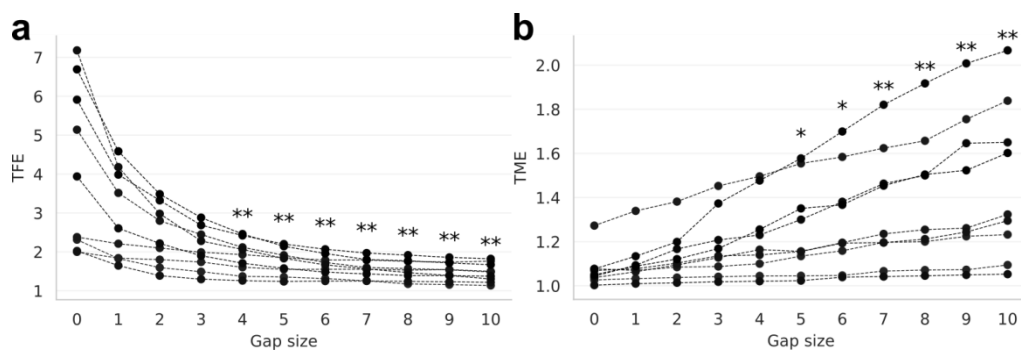


Figure S4. Tracking errors of AMIT-v1 for different values of the gap size parameter. (a) Track fragmentation errors (TFE); (b) track merging errors (TME). Stars indicate significant difference with respect to gap size 3: * $p < 0.05$, ** $p < 0.01$ (Wilcoxon signed-rank test, $n=9$, two-tailed).

FIGURE S5:

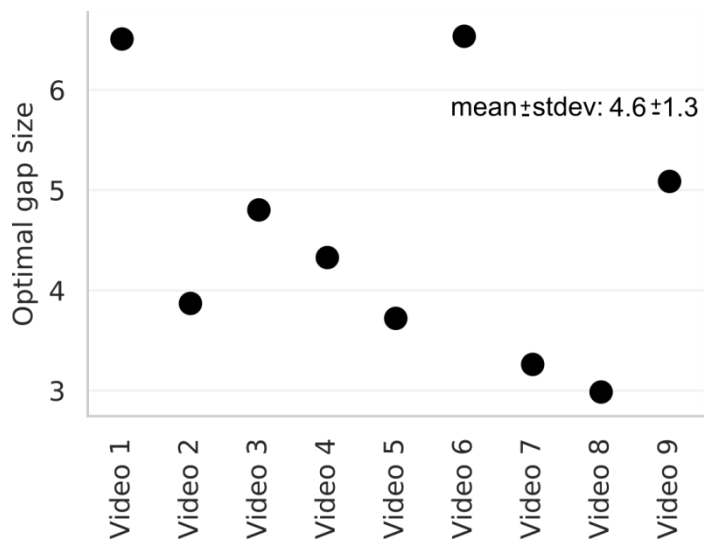


Figure S5. Optimal gap size computed according to equation (4) for videos 1-9.

FIGURE S6:

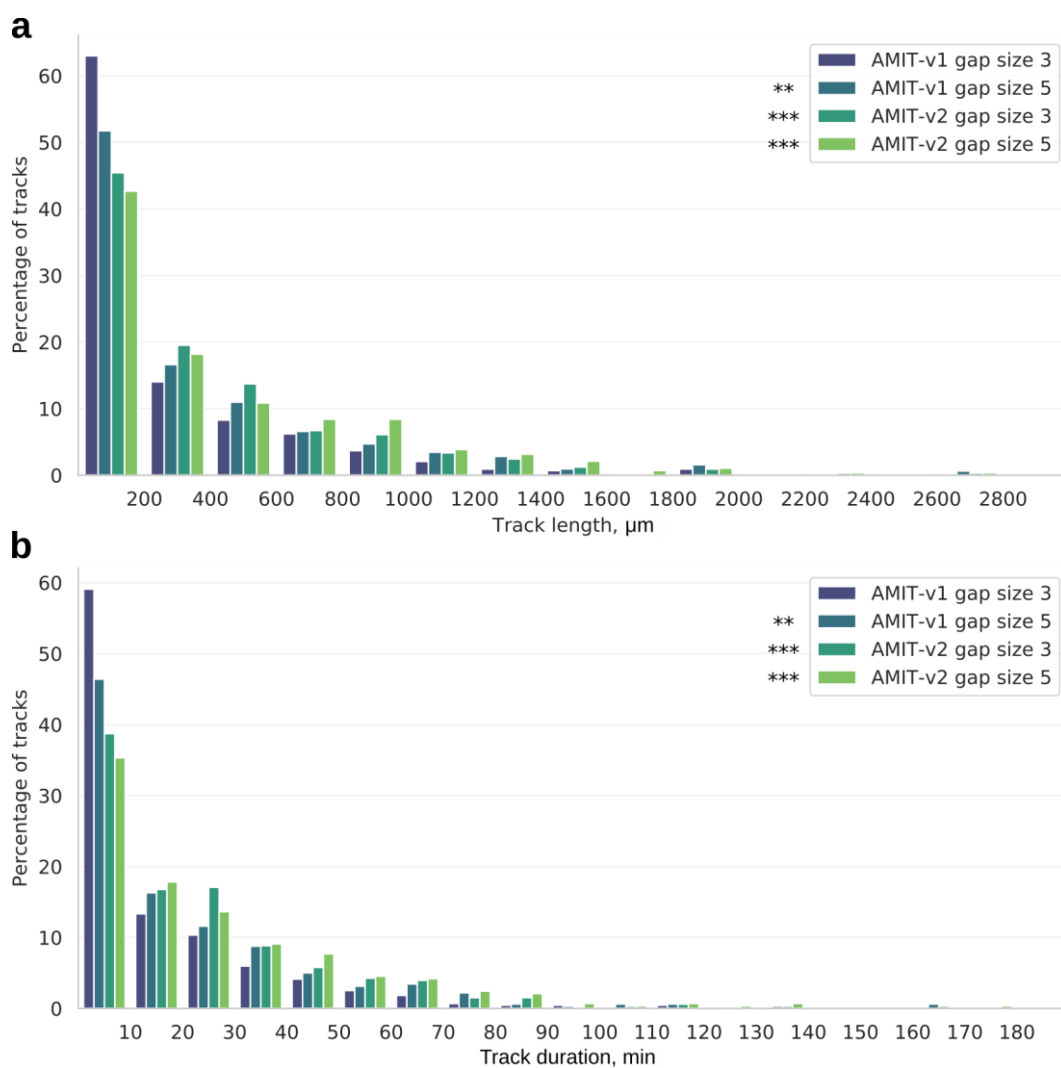


Figure S6. Distribution of tracks with different (a) track lengths and (b) track durations in a full-length video of three hours for AMIT-v1 and AMIT-v2 with gap sizes three and five time frames, stars indicate significant difference with respect to AMIT-v1 with gap size 3: ** $p < 0.01$, *** $p < 10^{-5}$ (Kolmogorov–Smirnov test, two-tailed).

FIGURE S7:

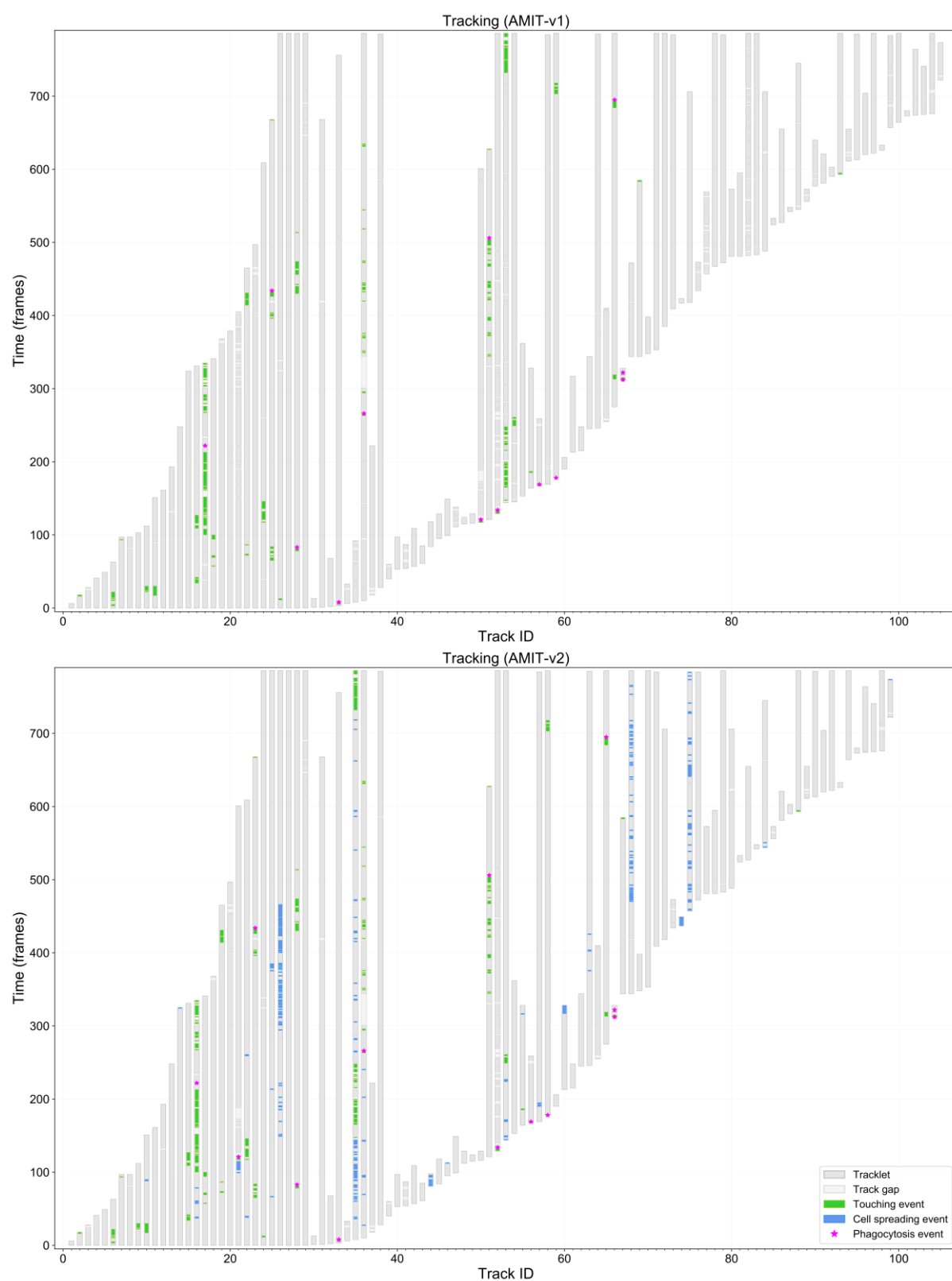


Figure S7. Tracks of polymorphonuclear neutrophils (PMN) confronted with *Candida glabrata* generated by AMIT-v1 (top) and AMIT-v2 (bottom) arranged by their starting time point in the video; touching events are highlighted in green, phagocytosis events are indicated by stars. Frame rate is six frames per minute.