***eLife’s* transparent reporting form**

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* You should state whether an appropriate sample size was computed when the study was being designed
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* If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

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All relevant information is mentioned in the second paragraph of subsection ‘Sample imaging’ in the ‘Materials and Methods’ section.

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* Statistical analysis methods should be described and justified
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* For each experiment, you should identify the statistical tests used, exact values of N, definitions of center, methods of multiple test correction, and dispersion and precision measures (e.g., mean, median, SD, SEM, confidence intervals; and, for the major substantive results, a measure of effect size (e.g., Pearson's r, Cohen's d)
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This information is mentioned in the ‘Results’ section of the manuscript (mean ± standard deviation due to heterogeneous population of cells).

(For large datasets, or papers with a very large number of statistical tests, you may upload a single table file with tests, Ns, etc., with reference to sections in the manuscript.)

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* Indicate how samples were allocated into experimental groups (in the case of clinical studies, please specify allocation to treatment method); if randomization was used, please also state if restricted randomization was applied
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This is not applicable for our study.

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* Include model definition files including the full list of parameters used
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We have uploaded the source data file for all Figures (except the raw image files and Figure 5, B and C) in separate excel files and each excel file is to linked to a subfigure as denoted in the Figure captions of the main manuscript. We have cited the standard plugins and MATLAB tracking functions that we use in the ‘Particle Tracking Velocimetry’ subsection in Methods. We have also provided the custom-written MATLAB codes and functions for fitting an ellipse to the edge of a Chlamydomonas cell and identifying its major axis vertex in a separate source code file ‘Source Code file.docx’. All data analysis methods are presented in the main text and in Materials and Methods. The numerical computation of Inverse Fourier Transform is detailed in Appendix 1, section 3.

The source movies are of large size (each movie about 10 GB) due to high-speed recording and are available upon request. Similarly, Figure 5, B and C contain trajectories of over 600 tracers, each and hence, the data file is very large for each one of them. They are available upon request.