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

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**Sample-size estimation**

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

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

Due to our experiments' exploratory nature, we did not compute appropriated sample sizes when the study was being designed. In sperm/cilia motility analyses, however, we designed two independent experimental methods to obtain reliable data sets: sperm, direct observations and CASA; and Kupffer’s vesicle cilia, direct observations and the analysis of left-right patterning. In structural analyses, we assessed Fourier shell correlation curves and estimated the effective resolutions of ~43 Å, which were enough to distinguish the localizations of each dynein subtype.

**Replicates**

* You should report how often each experiment was performed
* You should include a definition of biological versus technical replication
* The data obtained should be provided and sufficient information should be provided to indicate the number of independent biological and/or technical replicates
* If you encountered any outliers, you should describe how these were handled
* Criteria for exclusion/inclusion of data should be clearly stated
* High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)

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The information on the number of samples is described within each figure or figure legend. Other information regarding technical replicates can be found within the “Materials and Methods” section of the manuscript.

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* Statistical analysis methods should be described and justified
* Raw data should be presented in figures whenever informative to do so (typically when N per group is less than 10)
* 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)
* Report exact p-values wherever possible alongside the summary statistics and 95% confidence intervals. These should be reported for all key questions and not only when the p-value is less than 0.05.

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The statistical method used in this study is described in the “Materials and Methods” section of the manuscript. The raw data, means, SDs, and p-values are available in the source data files.

(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
* Indicate if masking was used during group allocation, data collection and/or data analysis

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Group allocation of samples was not relevant to our work.

**Additional data files (“source data”)**

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* Where provided, these should be in the most useful format, and they can be uploaded as “Source data” files linked to a main figure or table
* Include model definition files including the full list of parameters used
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Please indicate the figures or tables for which source data files have been provided:

Figure 2G (Figure 2-source data 1), Figure 2H (Figure 2-source data 2), Figure 2I (Figure 2-source data 3), Figure 2J (Figure 2-source data 4), Figure 2-figure supplement 1C (Figure 2-figure supplement 1-source data 1), and Figure 5E (Figure 5-source data 1).