Supplementary Text 1. Commands for maximum likelihood tree reconstruction with iqtree2.

For detailed description and references, see Material and Methods section in main text.

> Find best model and best-fit partitioning scheme

iqtree2 -s sperm_alignment_all.fas -p partition_DNA.txt -m MFP+MERGE -g constraints.txt -pre DAPH_DNA_ALL -nt AUTO -pers 0.2 -nstop 500

> constrained ML tree

iqtree2 -s sperm_alignment_all.fas -p best.nex -g constraints.txt -pre DAPH_DNA_ALL -nt AUTO -pers 0.2 -nstop 500

> unconstrained ML tree

iqtree2 -s sperm_alignment_all.fas -p best.nex -pre DAPH_DNA_UNC -nt AUTO -pers 0.2 -nstop 500

> compare unconstrained and constrained tree

iqtree2 -s sperm_alignment_all.fas -p best.nex -z both.treefiles -pre COMP_TREES -n 0 -zb 10000 –au

> final constrained ML tree with ultrafast bootstrap and SH-aLRT

iqtree2 -s sperm_alignment_all.fas -p best.nex -g constraints.txt -bb 10000 -alrt 10000 -pers 0.2 -nstop 500 -pre DAPH_ALL_FINAL -nt AUTO

> final constrained ML tree without ultrafast bootstrap and SH-aLRT

iqtree2 -s sperm_alignment_all.fas -p best.nex -g constraints.txt -pers 0.2 -nstop 500 -pre DAPH_ALL_FINAL_PURE -nt AUTO