

EXPANDING THE TRANSCRIPTOMIC TOOLBOX IN PROKARYOTES BY NANOPORE SEQUENCING OF RNA + CDNA MOLECULES

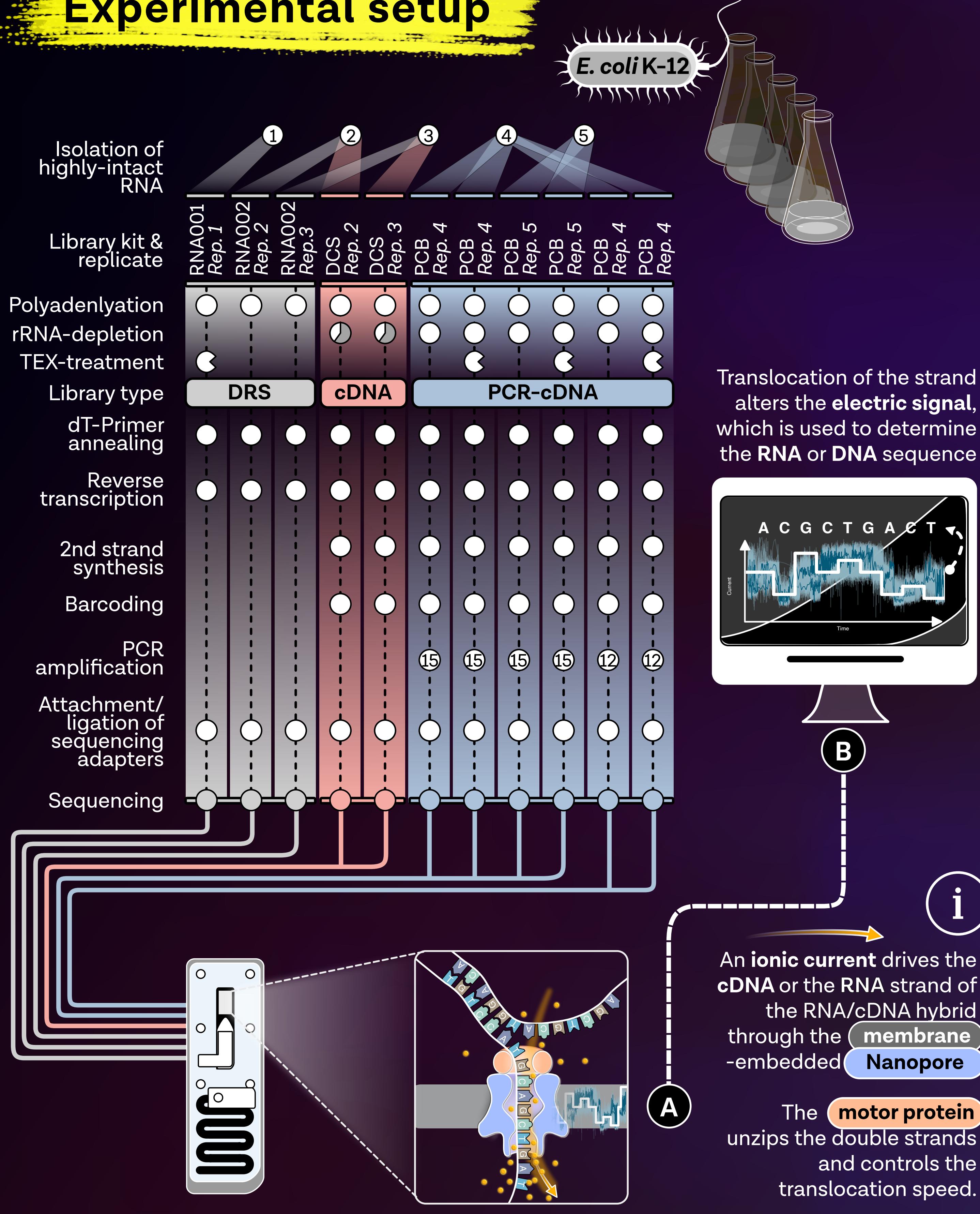
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Research aims

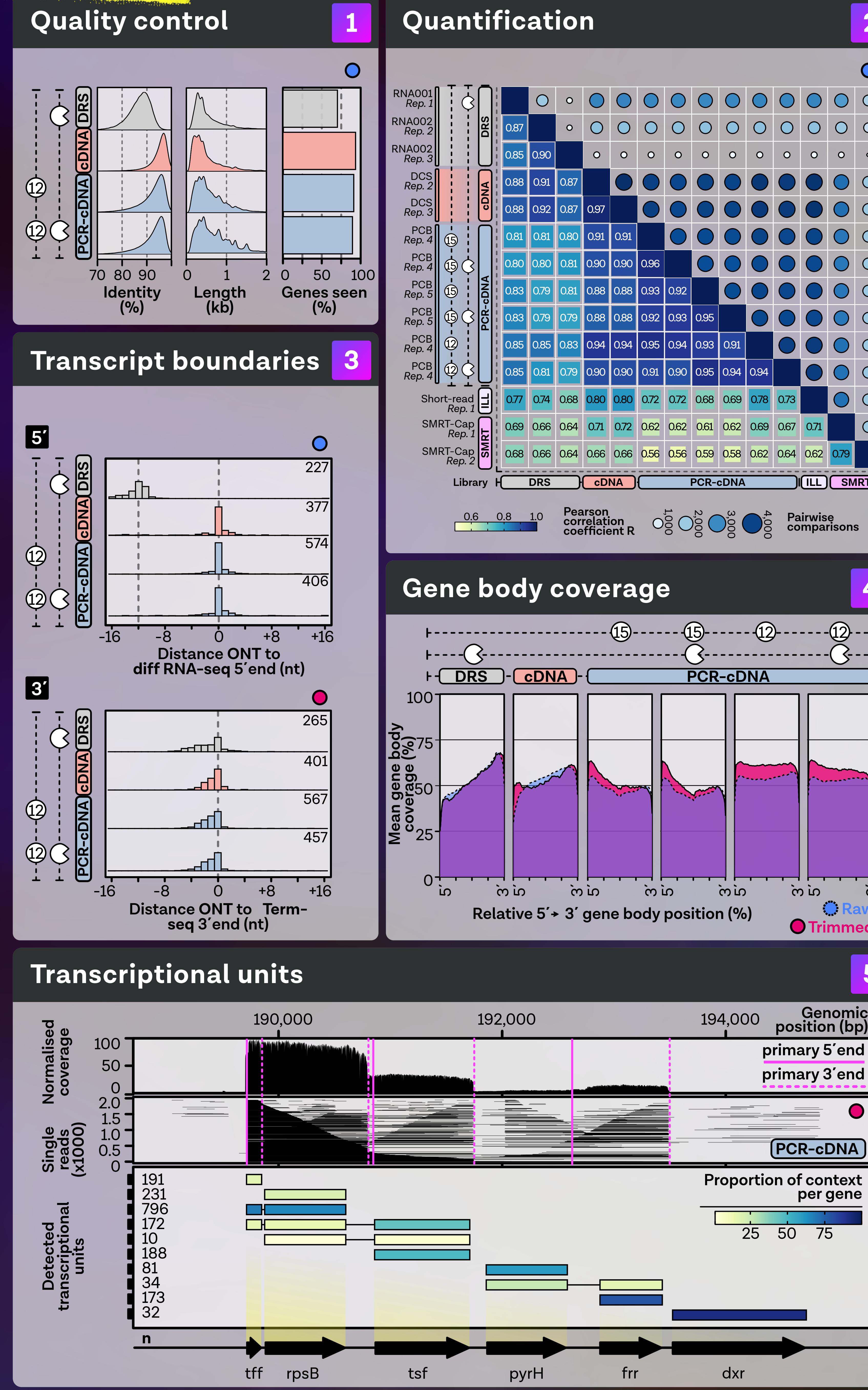
Benchmark Nanopore RNA-seq protocols in prokaryotes

Develop bioinformatical workflow for simultaneous detection of multiple transcriptomic features

Experimental setup

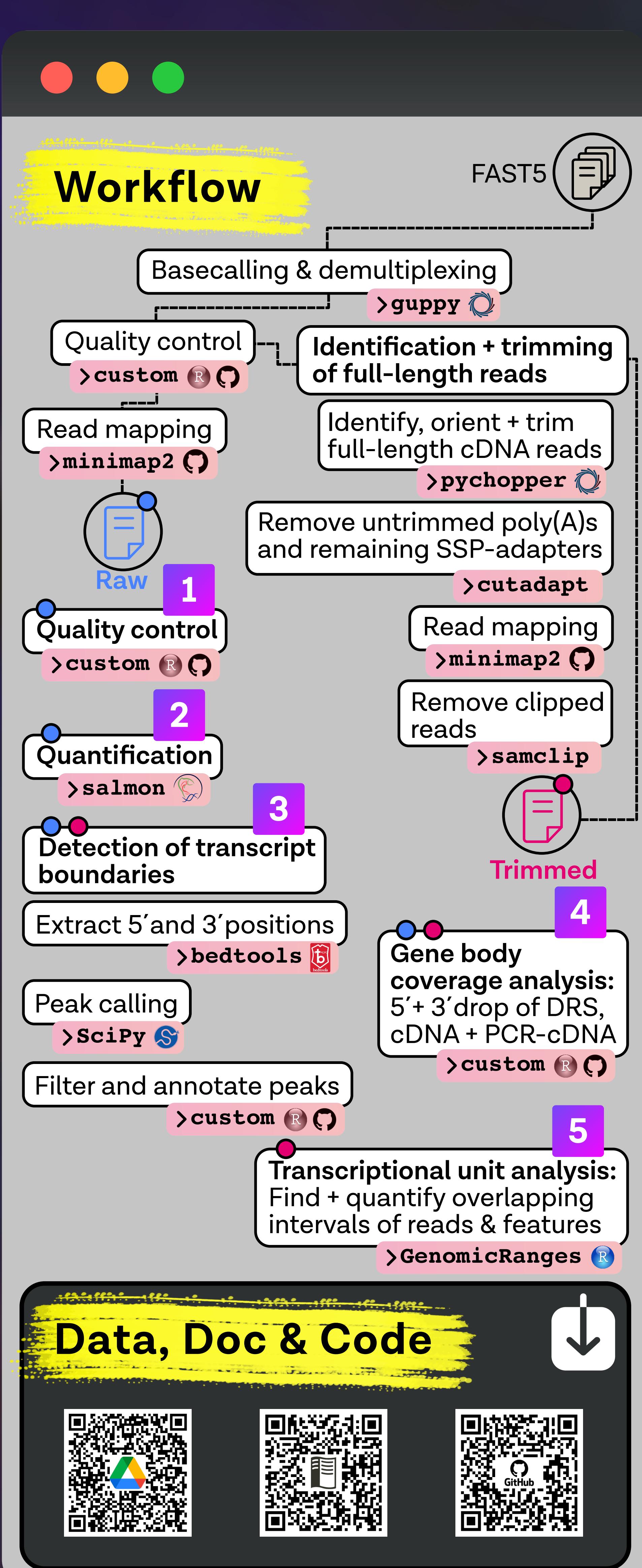


Results



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Conclusion

Not interested in RNA modifications, but in other transcriptomic features?

Use Nanopore (PCR)-cDNA-seq!

- ★ Highly reproducible
- ★ More cost-efficient
- ★ Improved yield
- ★ Higher accuracy
- ★ No bias in quantification
- Q High efficiency of polyadenylation required!
- Q Efficiency of RT critical!
- Q Mean identity only 95%!
- Q Number of PCR cycles critical!