

Introduction to genome assembly using Oxford Nanopore sequencing

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Resources for Oxford Nanopore Technology

The nanoporetech.com website features a prominent banner for "London Calling 2020 online". The Twitter post from @nanopore highlights the availability of all talks on-demand. The GitHub profile for Oxford Nanopore Technologies includes a repository for calling poly(A) tail lengths from nanopore direct RNA data.

Nanopore sequencing, the *only* technology for direct sequencing of native DNA/RNA, or

Direct sequencing of native DNA/RNA, or

London Calling 2020 online

Oxford Nanopore

10.2K Tweets

Breakout Rooms

London Calling 2020

all talks now available on-demand.

#nanoporeconf

Oxford Nanopore Technologies

Nanopores for single molecule (DNA/RNA, protein) analysis using the MinION, GridION and PromethION systems

Oxford, UK

Find a repository... Type: All Language: All

pipeline-poly-a-ng

Pipeline for calling poly(A) tail lengths from nanopore direct RNA data using nanopoli

rna direct-rna poly-a nanopoli

Python 1 stars 6 updated 9 hours ago

Top languages

Python C++ C TeX TypeScript

Most used topics

Oxford Nanopore Sequencing

MENU ▾

nature
biotechnology

Article | Open Access | Published: 04 May 2020

Nanopore sequencing and the Shasta toolkit enable efficient de novo assembly

MENU ▾

nature plants

Article | Open Access | Published: 10 February 2020

The hornwort genome and early land plant evolution

Science

RESEARCH ARTICLE SUMMARY

CANCER GENOMICS

Mechanisms generating cancer genome complexity from a single cell division error

Neil T. Umbreit*,†, Cheng-Zhong Zhang*,†, Luke D. Lynch‡, Logan J. Blaine‡, Anna M. Cheng, Richard Tourdot, Lili Sun, Hannah F. Almubarak, Kim Judge, Thomas J. Mitchell, Alexander Spektor, David Pellman†

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MENU ▾

nature
biotechnology

Letter | Open Access | Published: 10 February 2020

Complete, closed bacterial genomes from microbiomes using nanopore sequencing

Eli L. Moss, Dylan G. Maghini & Ami S. Bhatt✉

Nature Biotechnology 38, 701–707(2020) | Cite this article

22k Accesses | 3 Citations | 250 Altmetric | Metrics

Abstract

nature

Article | Published: 14 July 2020

This is an unedited manuscript that has been accepted for publication. Nature Research are providing this early version of the manuscript as a service to our authors and readers. The manuscript will undergo copyediting, typesetting and a proof review before it is published in its final form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers apply.

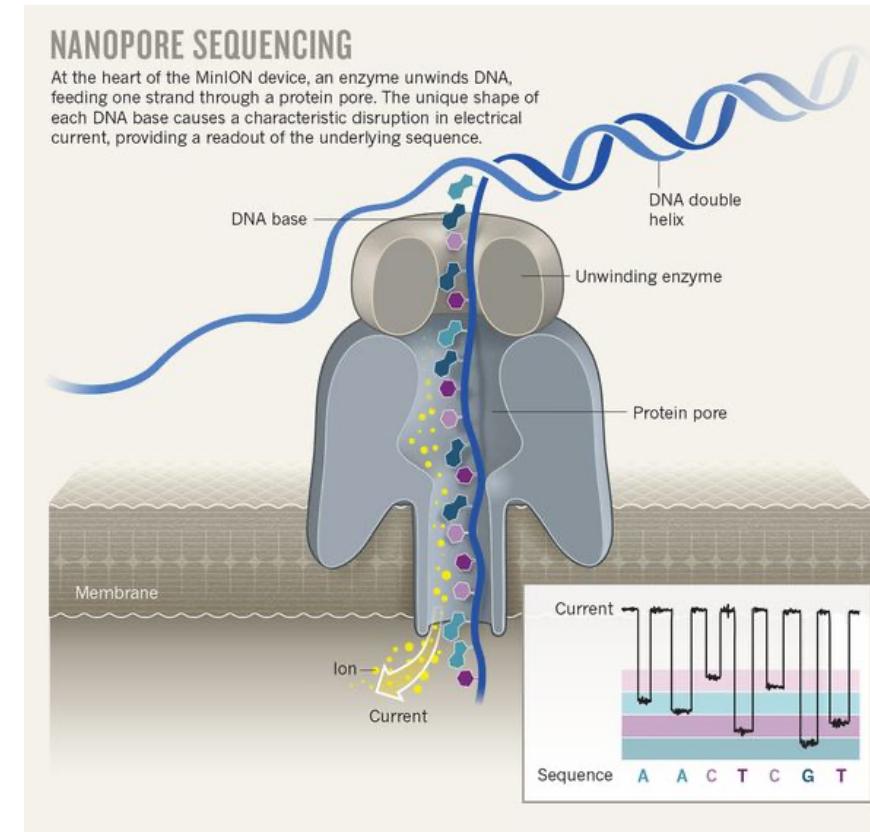
Telomere-to-telomere assembly of a complete human X chromosome

Karen H. Miga✉, Sergey Koren, Arang Rhee, Mitchell R. Vollger, Ariel Gershman,

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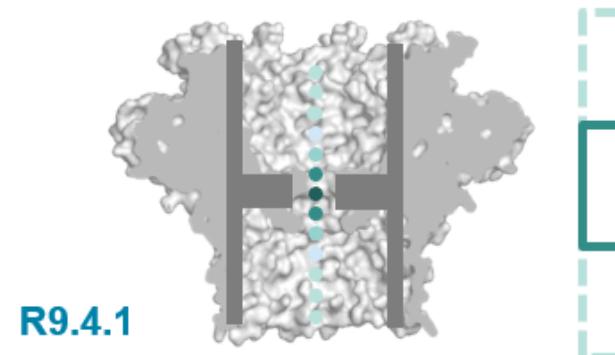
918

Oxford Nanopore Sequencing

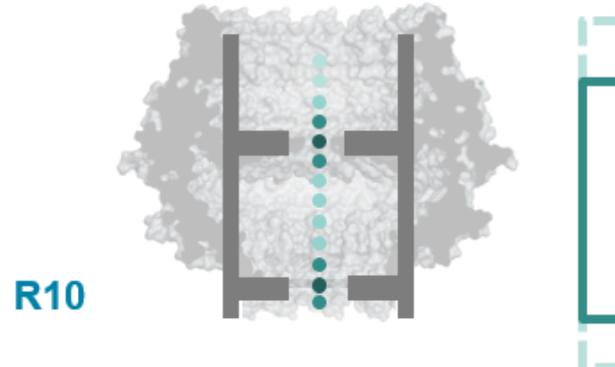


M. Eisenstein, An ace in the hole for DNA sequencing, Nature 550 (2017) 285

Oxford Nanopore Sequencing



R9.4.1



R10

ATCGGAAAAAAATCACGCCACGTCCAAA



<https://nanoporetech.com/about-us/news/r103-newest-nanopore-high-accuracy-nanopore-sequencing-now-available-store>

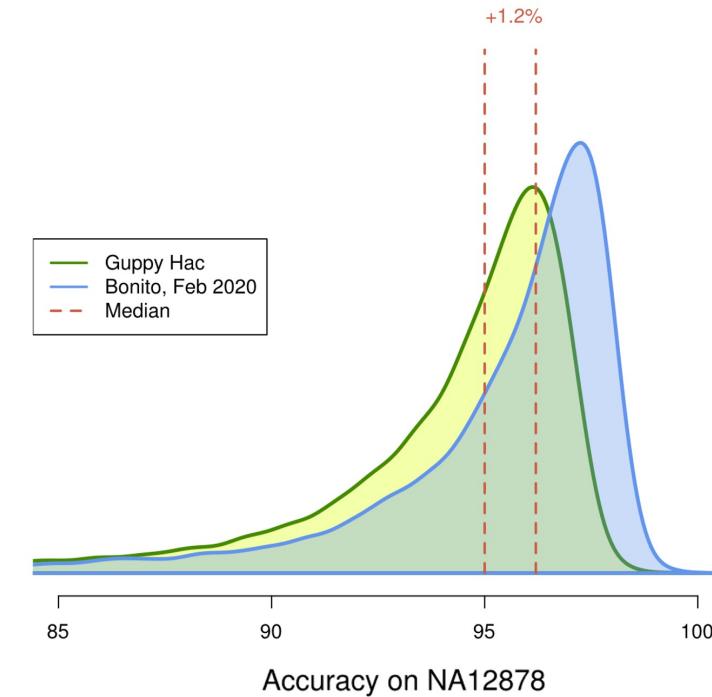
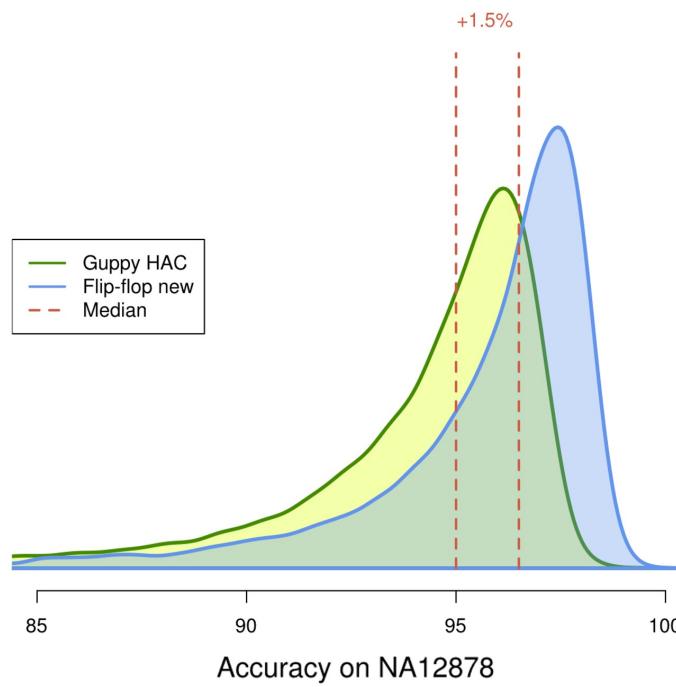
Oxford Nanopore Sequencing



Neural Networks

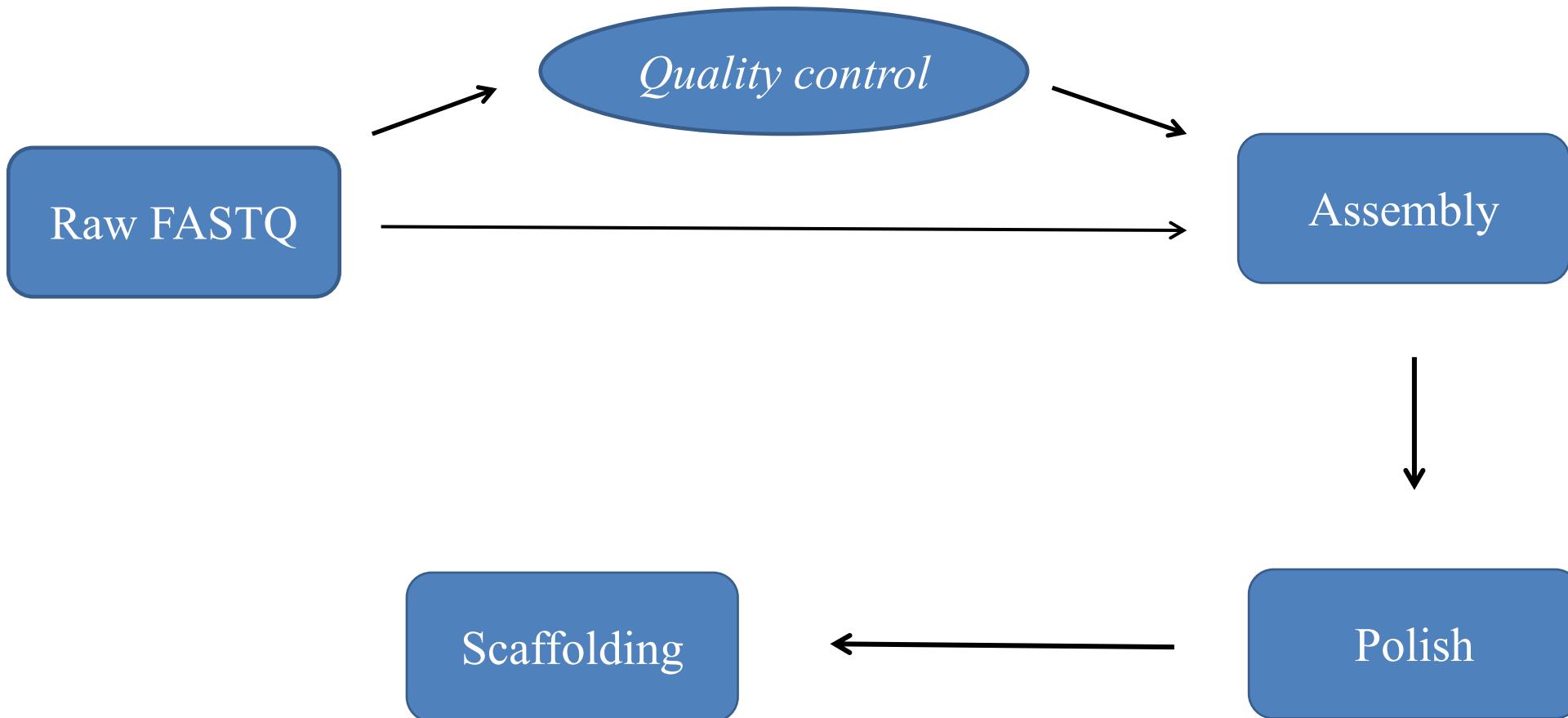
ATTACGGAAATTCCCGGAAG...

Comparison of Oxford Nanopore basecalling tools

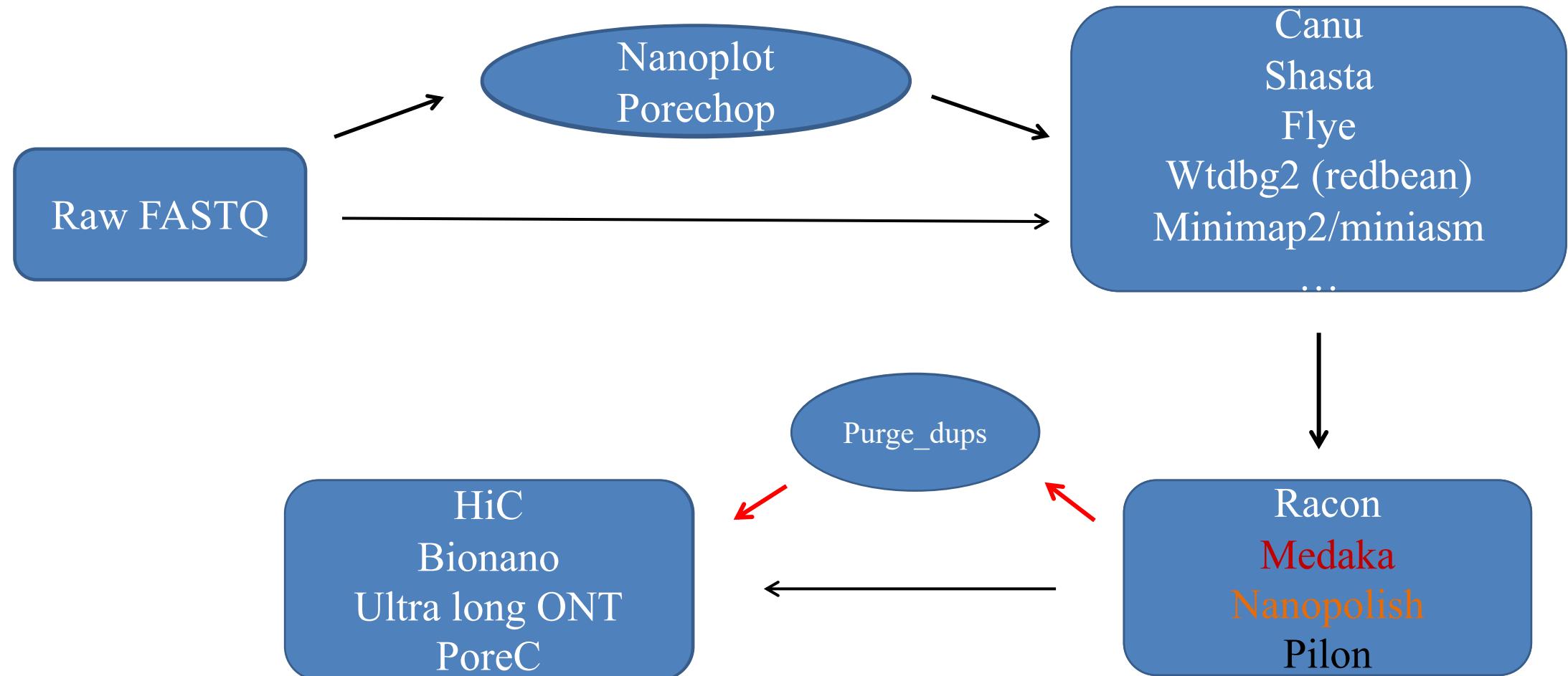


- <https://community.nanoporetech.com/posts/march-2020-accuracy-update>

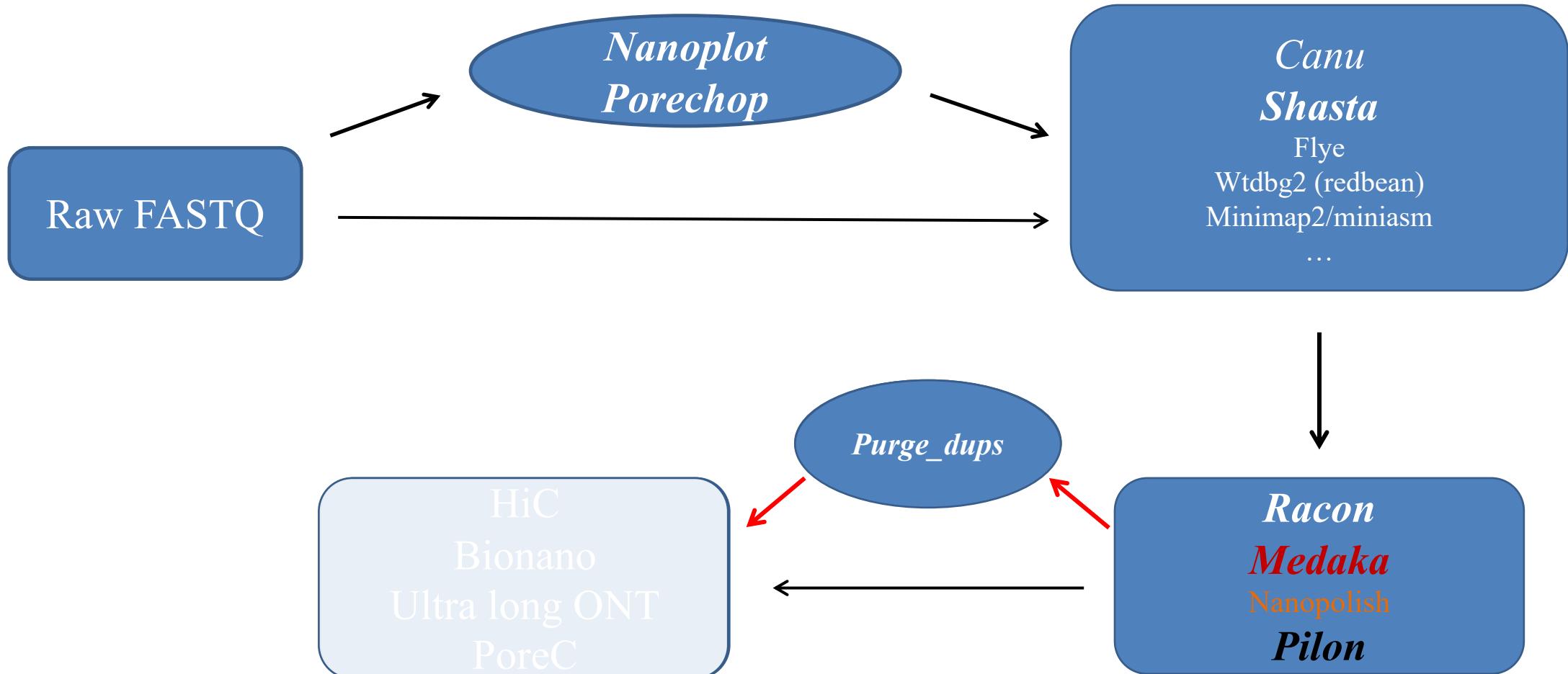
General workflow to create chromosome scale assemblies



Workflow to create chromosome scale assemblies



Genome assembly using ONT data



Thank you!

