

# READ UNTIL WITH BASECALL- AND REFERENCE-INFORMED CRITERIA (RUBRIC)

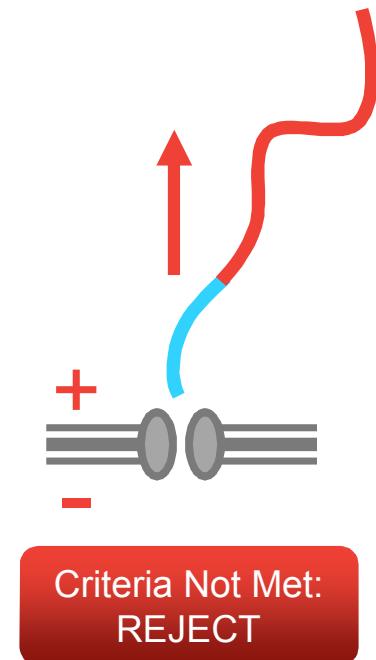
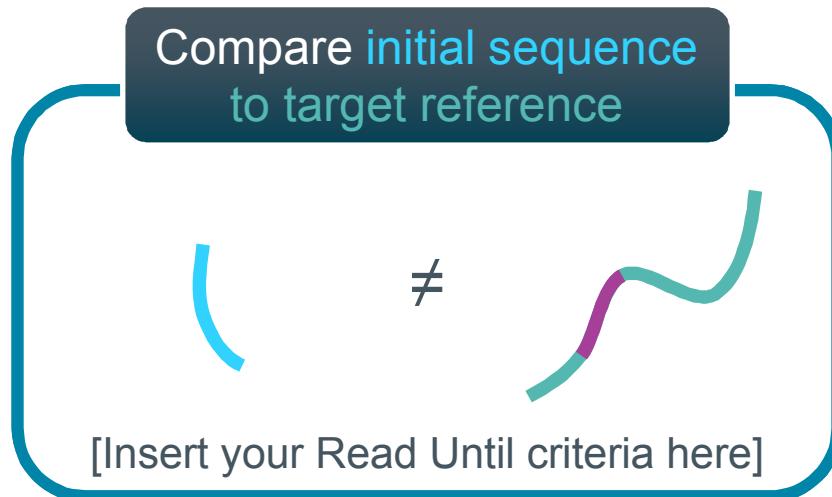
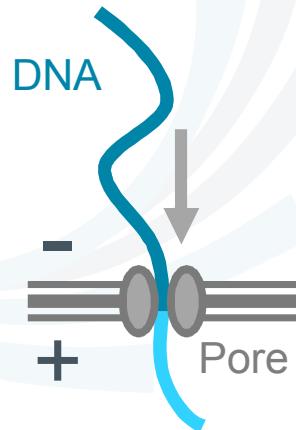
Michael S. Bartsch, Ph.D.

Sandia National Laboratories, Livermore, CA, USA

# “READ UNTIL” SELECTIVE SEQUENCING

An emerging nanopore sequencing capability

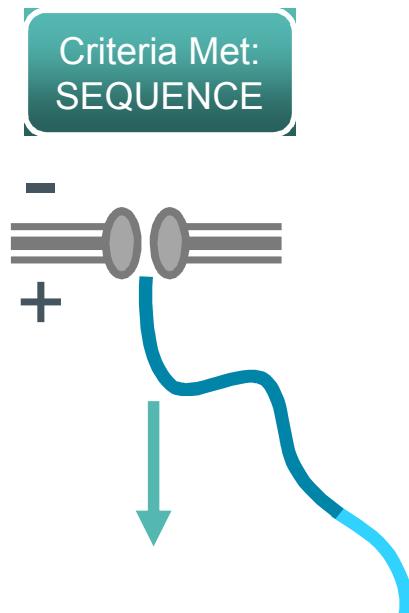
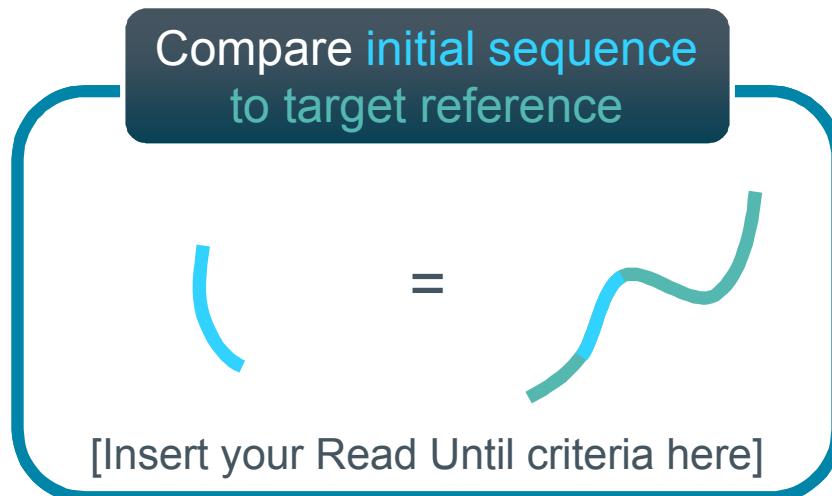
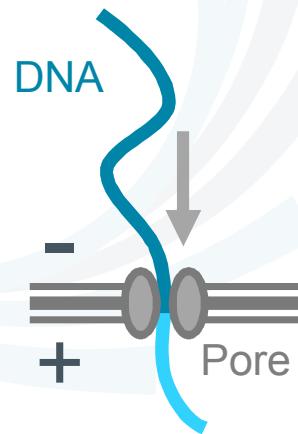
Access to real-time data enables real-time rejection of non-informative DNA



# “READ UNTIL” SELECTIVE SEQUENCING

An emerging nanopore sequencing capability

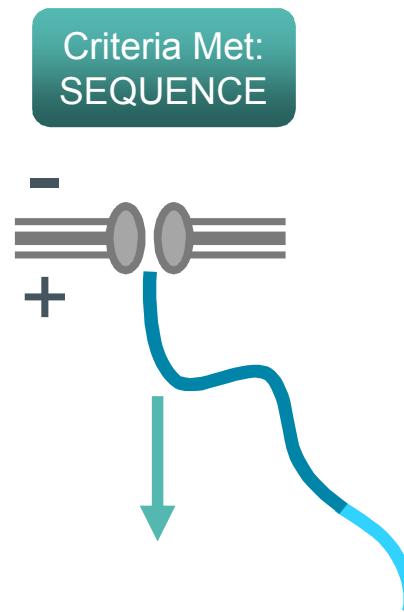
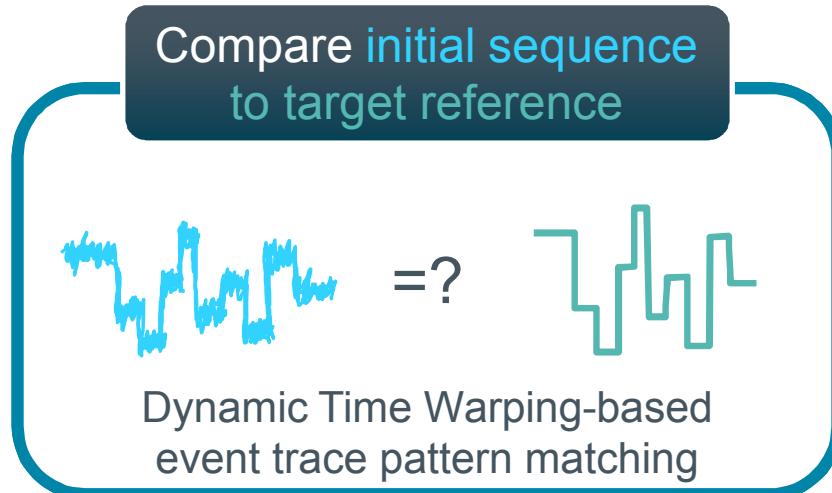
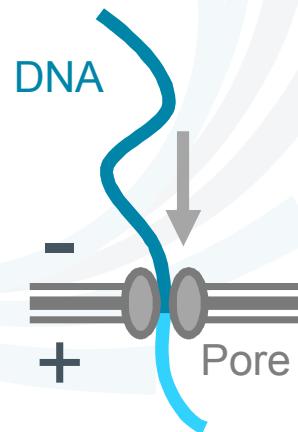
Access to real-time data enables real-time rejection of non-informative DNA



# “READ UNTIL” SELECTIVE SEQUENCING

Original pattern-matching approach

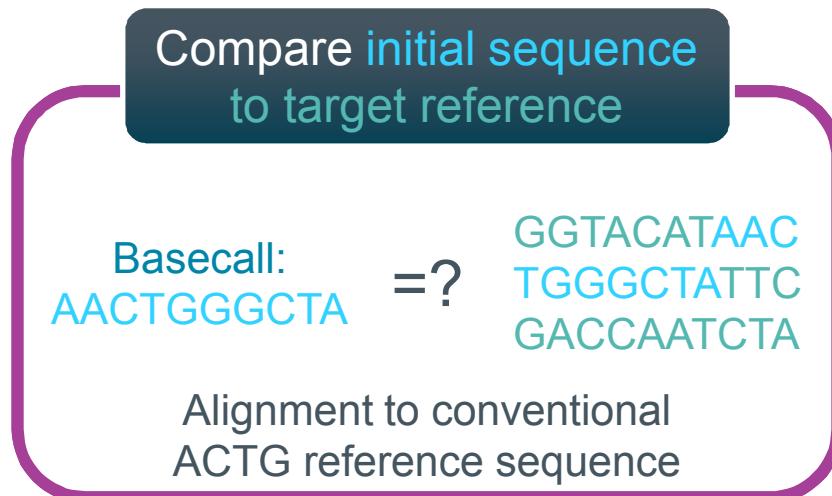
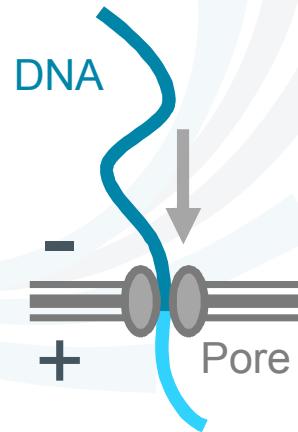
First published implementation of Read Until by Loose, Malla, and Stout, *Nature Methods*, 2016



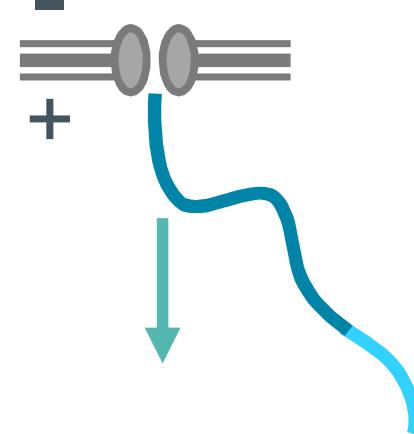
# “READ UNTIL” SELECTIVE SEQUENCING

Read Until with Basecall- and Reference-Informed Criteria (RUBRIC)

Sandia RUBRIC method by Edwards, Krishnakumar, Sinha, Patel, and Bartsch, 2017



Criteria Met:  
SEQUENCE



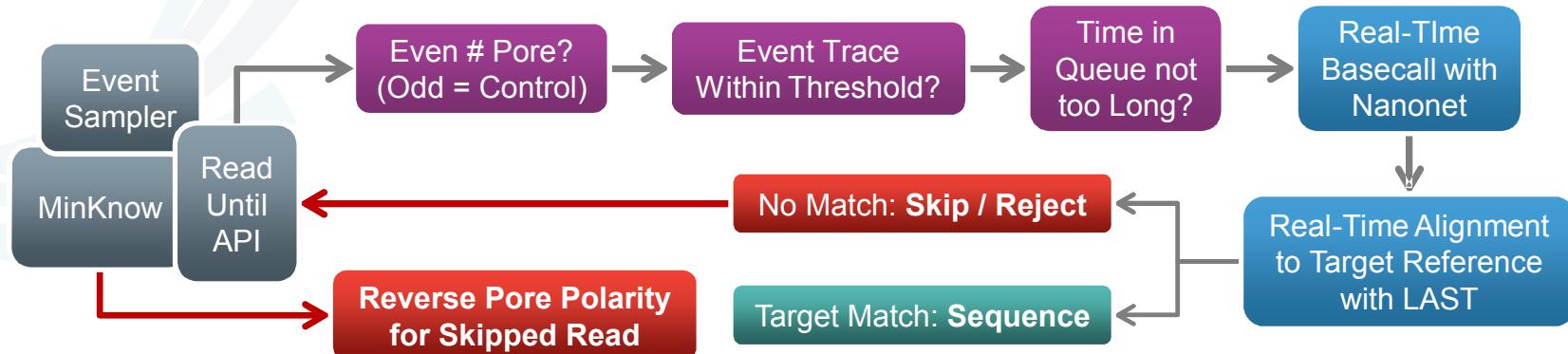
# THE RUBRIC WORKFLOW

An exercise in efficient use of limited computing resources

## Key Elements of the Method

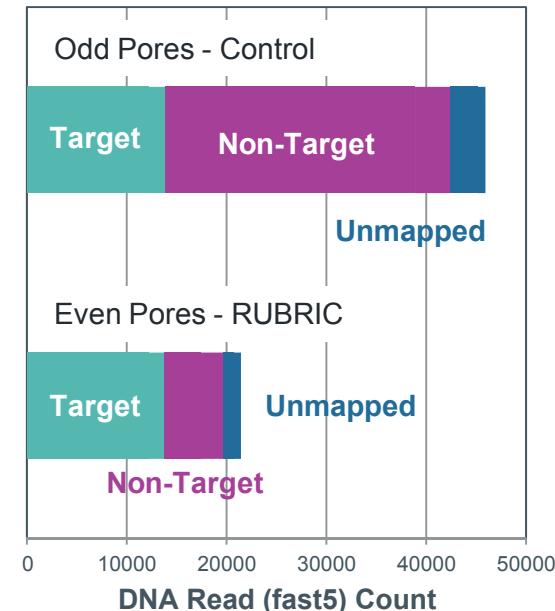
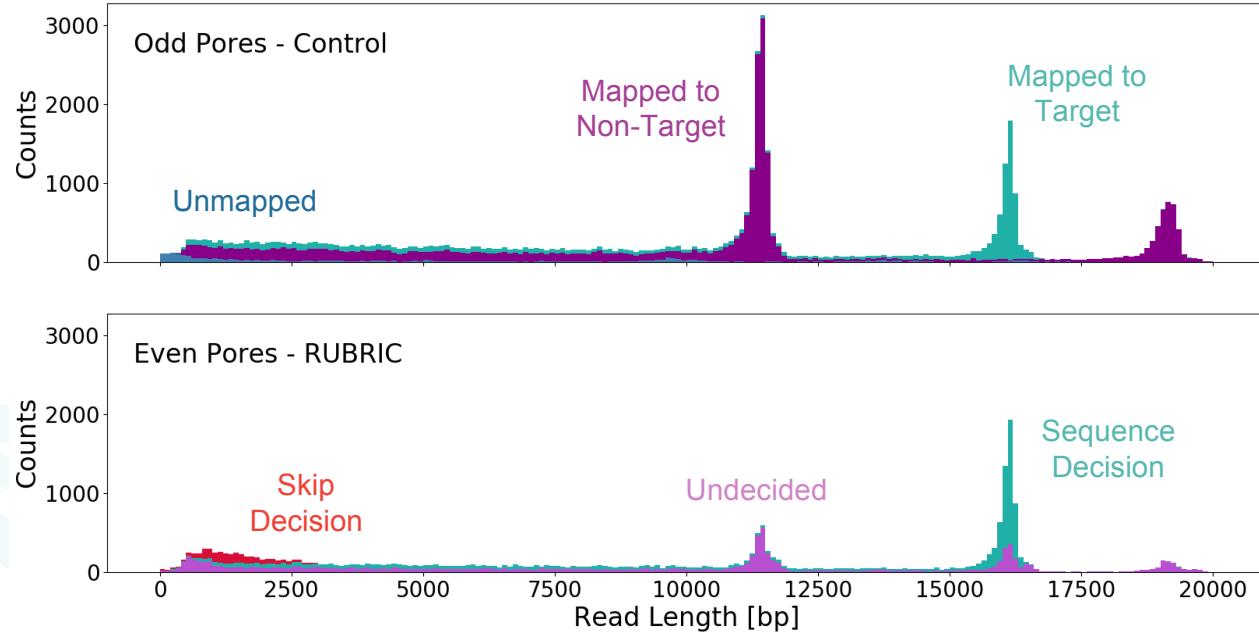
- Laptop runs MinKnow while ethernet-linked desktop runs RUBRIC
- Event trace threshold filters out reads unlikely to become mappable fast5s
- Decision queue screens out reads that are too “old” for a timely decision
- **IN REAL-TIME**: nanonet basecalls 300 events (~80 bases) and LAST aligns to reference

Average Decision  
Time: 0.65 sec



# SUCCESSFUL SELECTION WITH RUBRIC

Proof of concept: Eag1-digested Lambda DNA



# EVALUATING RUBRIC PERFORMANCE

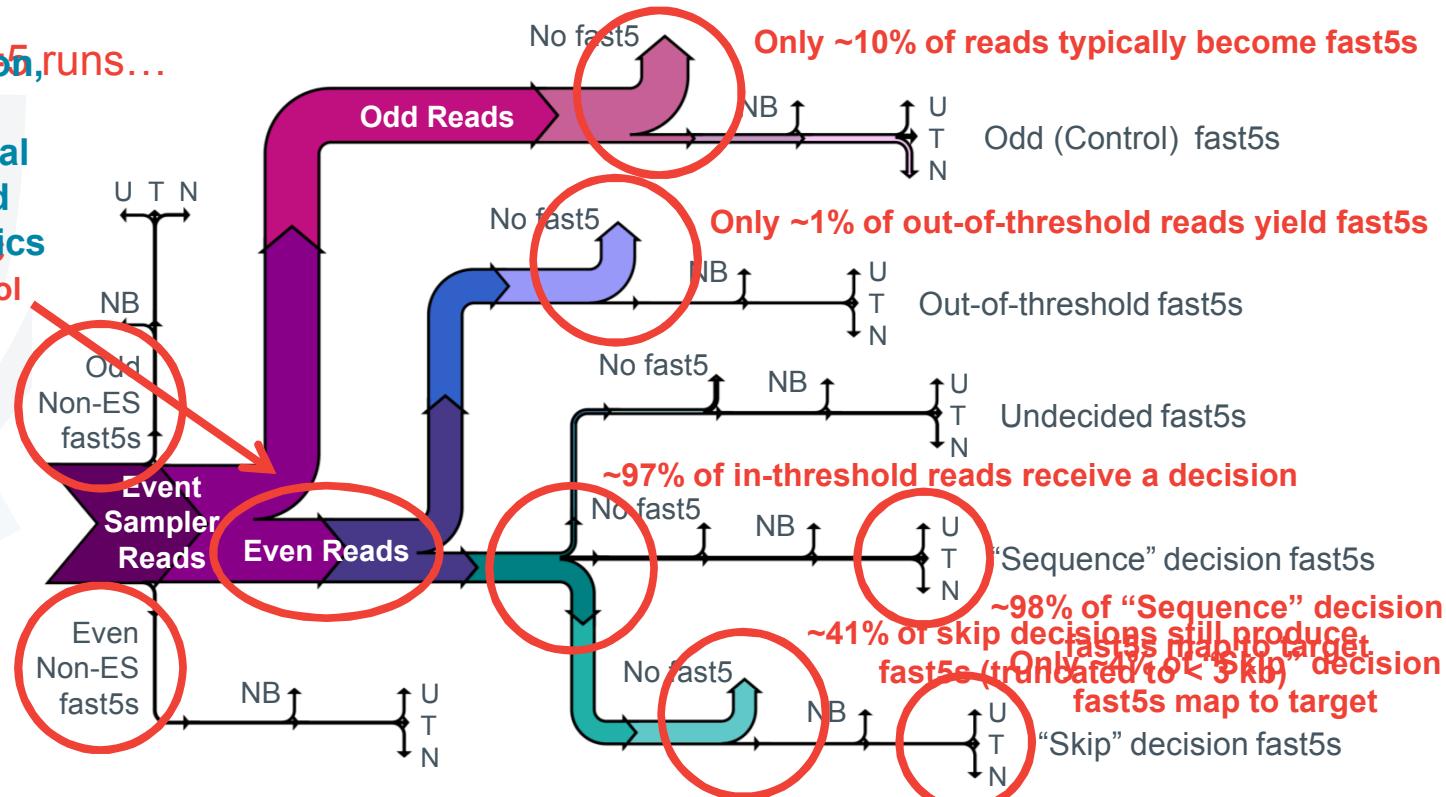
Detailed “data flow” analysis provides critical insights

## Testing, optimization, runs...

and analysis are ongoing with a goal of RUBRIC-based pathogen diagnostics. 10.9 more RUBRIC reads/pore vs. control

~16% of all fast5s are never reported by the Event Sampler

U – Unmapped  
T – Maps Target  
N – Maps Non-Target  
  
NB – No Basecall

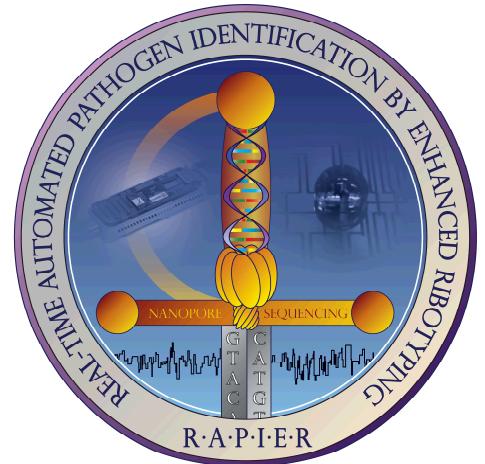


# ACKNOWLEDGEMENTS

Name	Division / Location
<b>Harrison S. Edwards</b>	Advanced Systems Engineering & Deployment Dept., Sandia National Labs (CA)...now University of Toronto
<b>Raga Krishnakumar, Ph.D.</b>	Systems Biology Dept., Sandia National Labs (CA)
<b>Anupama Sinha</b>	Systems Biology Dept., Sandia National Labs (CA)
<b>Kamlesh D. Patel, Ph.D.</b>	Advanced Systems Engineering & Deployment Dept., Sandia National Labs (CA)
<b>Michael S. Bartsch, Ph.D.</b> <i>(mbarts@sandia.gov)</i>	Advanced Systems Engineering & Deployment Dept., Sandia National Labs (CA)

**Special thanks to Matt Loose (U. Nottingham), and Julian Atienza & Richard Ronen (ONT)**

This work was supported by the Laboratory Directed Research and Development program at Sandia National Laboratories, a multi-mission laboratory managed and operated by National Technology and Engineering Solutions of Sandia, LLC, a wholly owned subsidiary of Honeywell International, Inc., for the U.S. Department of Energy's National Nuclear Security Administration under contract DE-NA0003525.



# THANK YOU

The content contained in this presentation should not be reproduced without permission of the speaker.

© Copyright 2017 Oxford Nanopore Technologies. The MinION, GridION, PromethION and VolTRAX are for research use only.



# ADDITIONAL OBSERVATIONS ON RUBRIC OPERATION

## Fugitives from RUBRIC selection

