

Computational efficiency of software for the analysis of Next Generation Sequencing data

Magda Mielczarek¹, [Joanna Szyda](mailto:joanna.szyda@up.wroc.pl)¹, Artur Gurgul², Kacper Żukowski², Monika Bugno-Poniewierska²

joanna.szyda@up.wroc.pl

¹ Biostatistics Group, Department of Genetics, Wrocław University of Environmental and Life Sciences, Wrocław, Poland

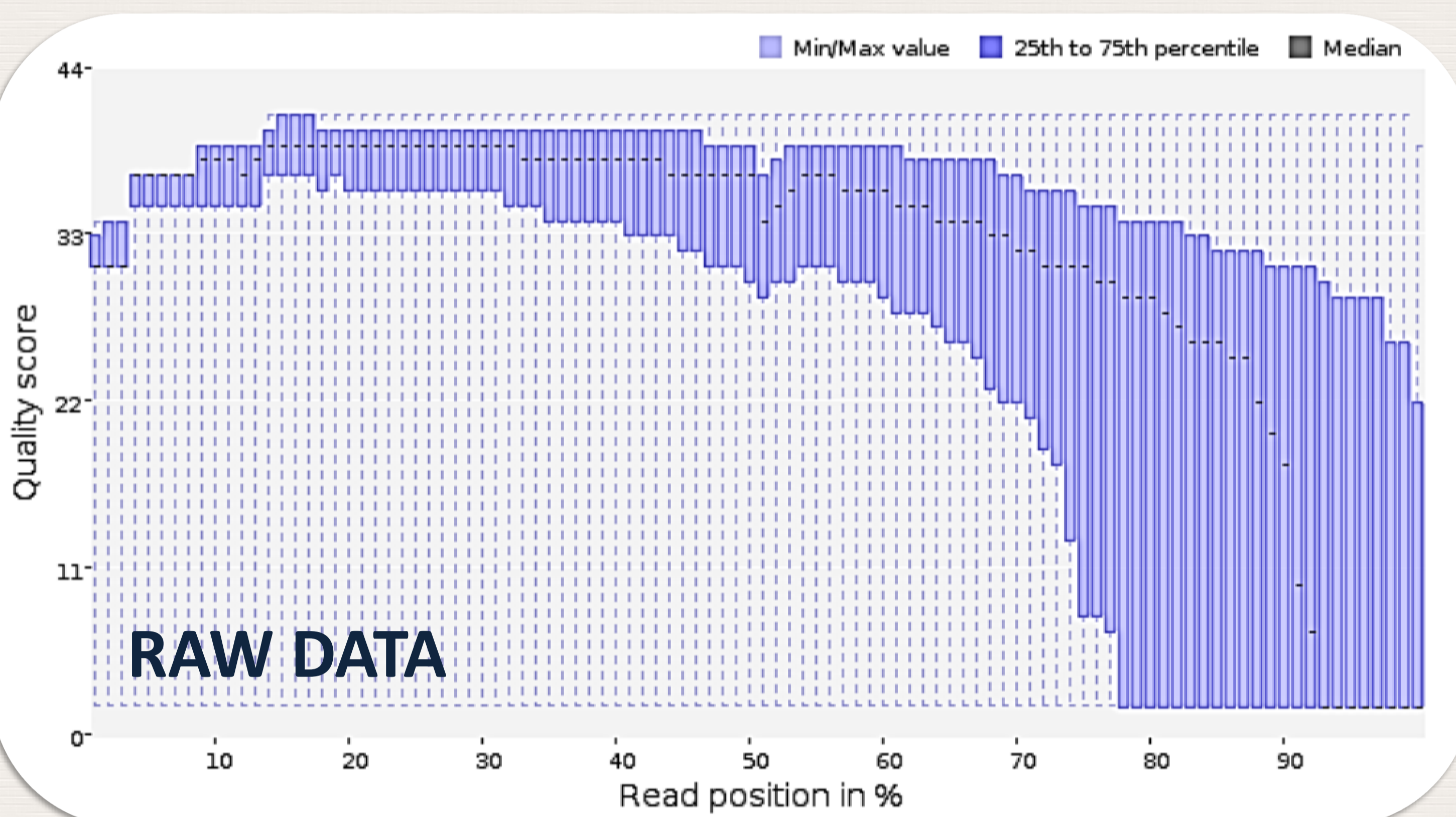
² National Research Institute of Animal Production, Cracow, Poland

CONCLUSIONS

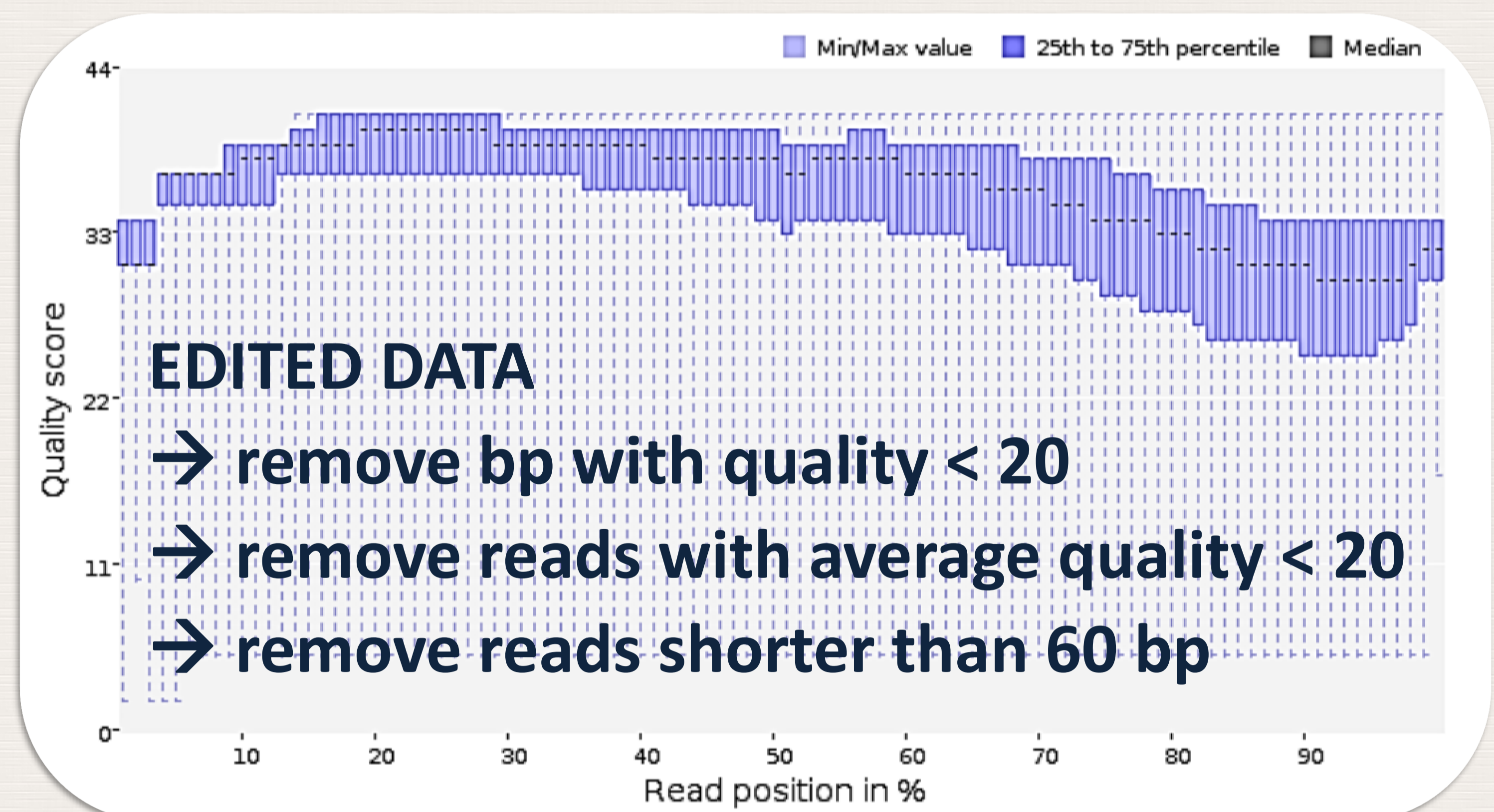
whole genome NGS data editing & alignment are possible on a small server
BOWTIE2 software showed the best performance

MATERIAL & METHODS

whole genome NGS of a dog generated by Illumina



- # reads: 44 926 270
- # base pairs: 4 537 553 270
- read length: 101 bp ± 0 (101 – 101)



- # reads: 34 176 710
- # base pairs: 3 103 884 408
- read length: 91 bp ± 11 (60 – 101)

RESULTS

BOWTIE2

Langmead & Salzberg (2012)

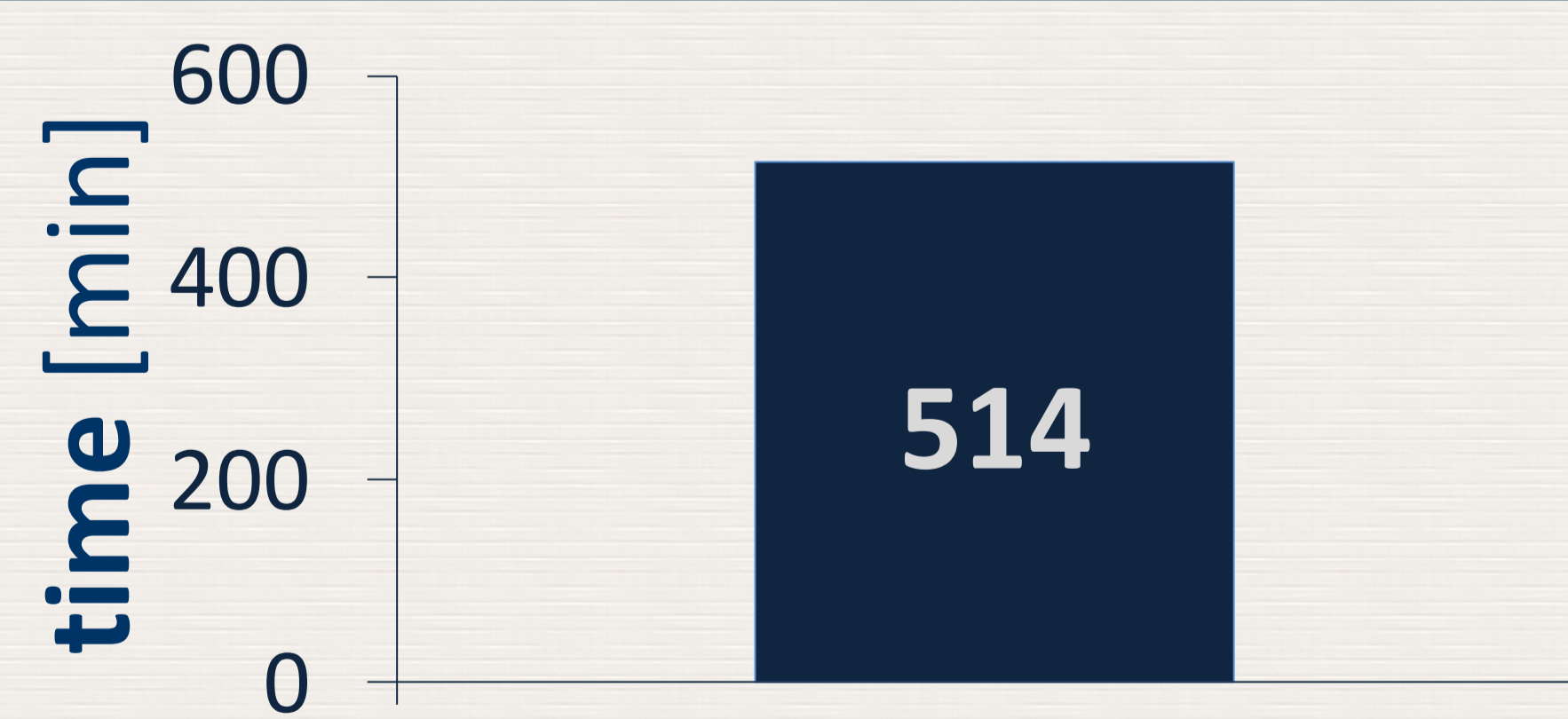
SOAP2

Luo et al. (2012)

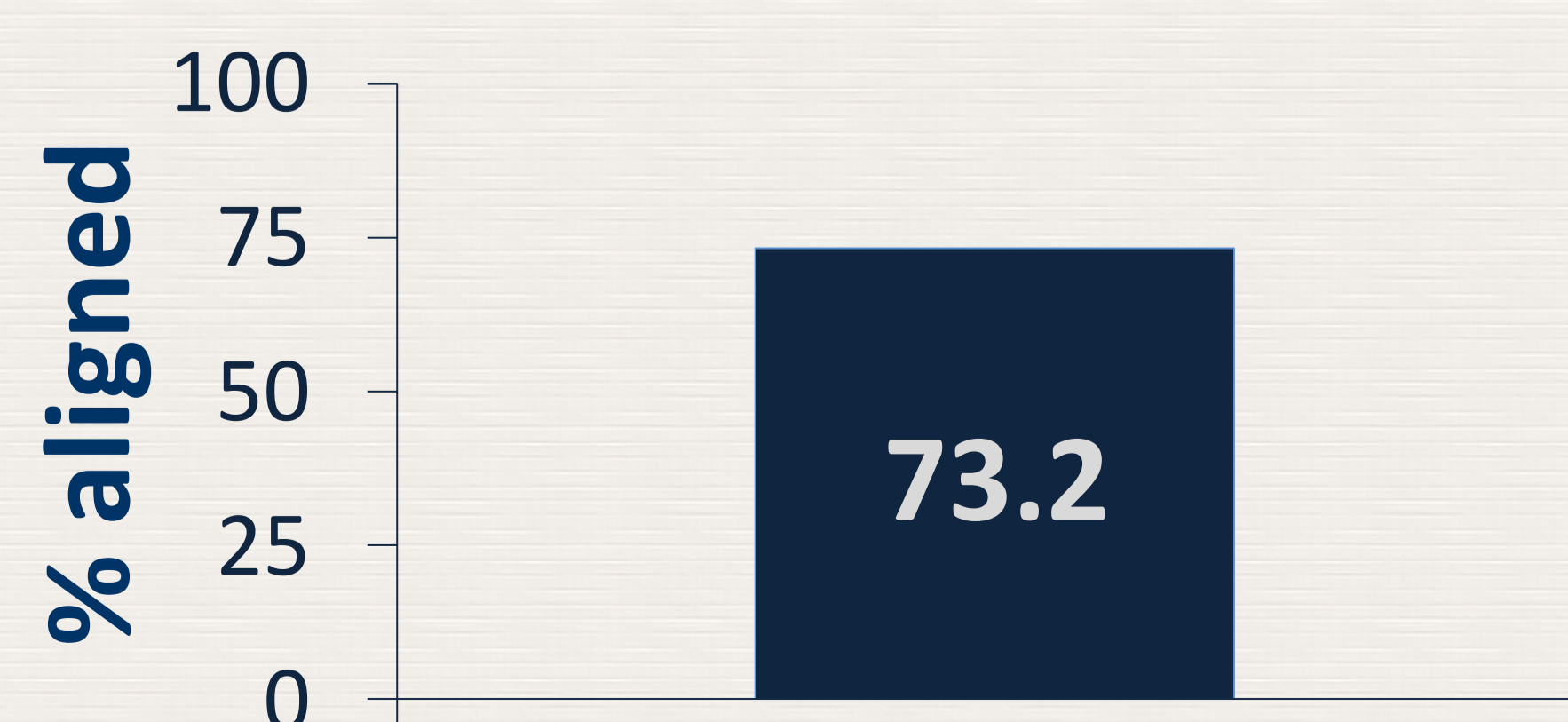
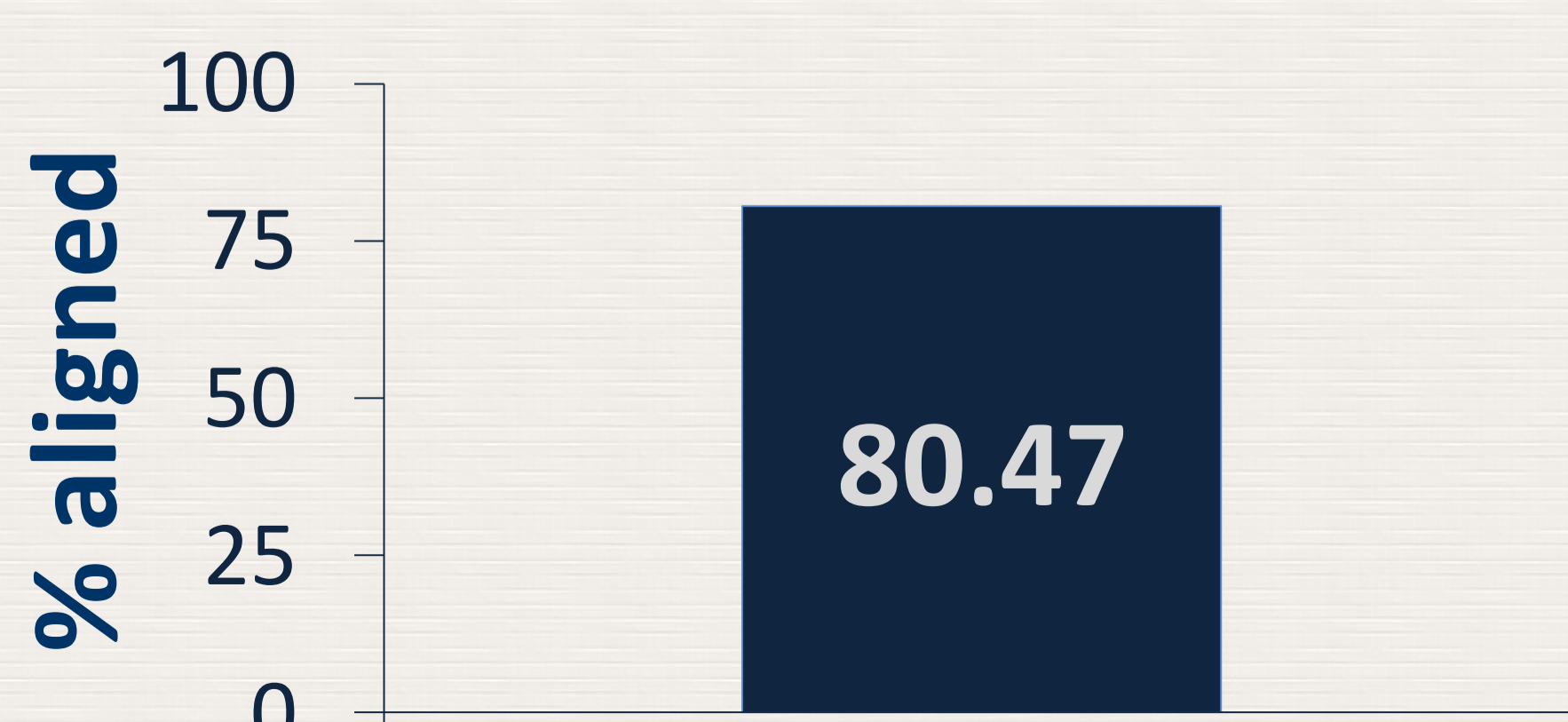
BFAST

Homer et al. (2009)

DATA EDITING



READ ALIGNMENT



not enough memory