



Genome assembly and structural variations across geographical isolates of *Meloidogyne enterolobii*

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Genome assembly and structural variations across geographical isolates of *Meloidogyne enterolobii*

Marine Poulet

Genomic and Adaptive Molecular Evolution team
Sophia Agrobiotech Institut

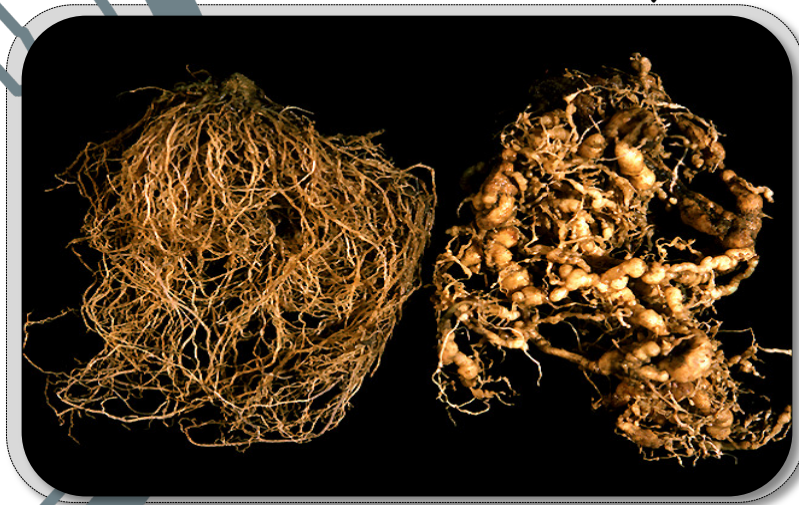
Root-knot nematode genus : *Meloidogyne*

M. floridensis
M. incognita
M. arenaria
M. javanica
M. lopezi
M. paranaensis
M. konaensis
M. luci
M. oryzae
M. ethiopica
M. inornata
M. enterolobii
M. graminicola
M. exigua
M. hapla

- Round worms
- Obligate parasites
- More than 100 described species



Root
galls



Root-knot nematode genus : *Meloidogyne*

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Root
galls



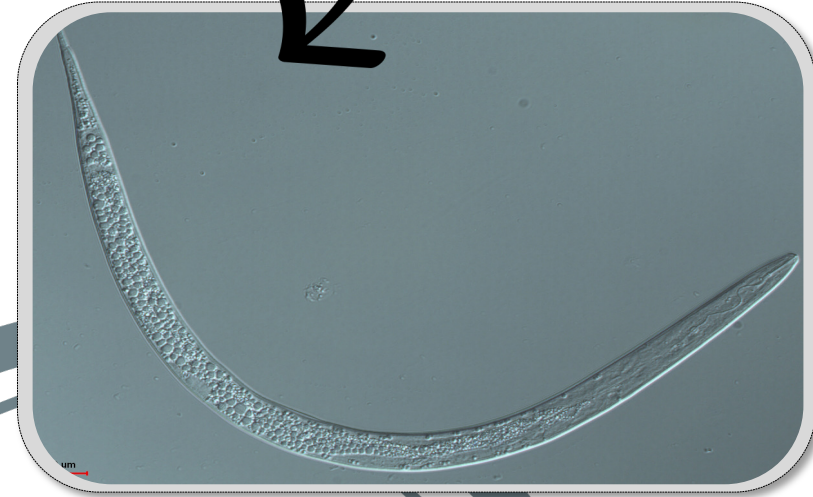
The nematode *Meloidogyne enterolobii*

- Polyphagous species
- Tropical/Subtropical species
- Insufficient control methods
- Reproduce in plant-resistant genes (containing the Mi-1 gene)

Impact the global food supply



European Quarantine pest

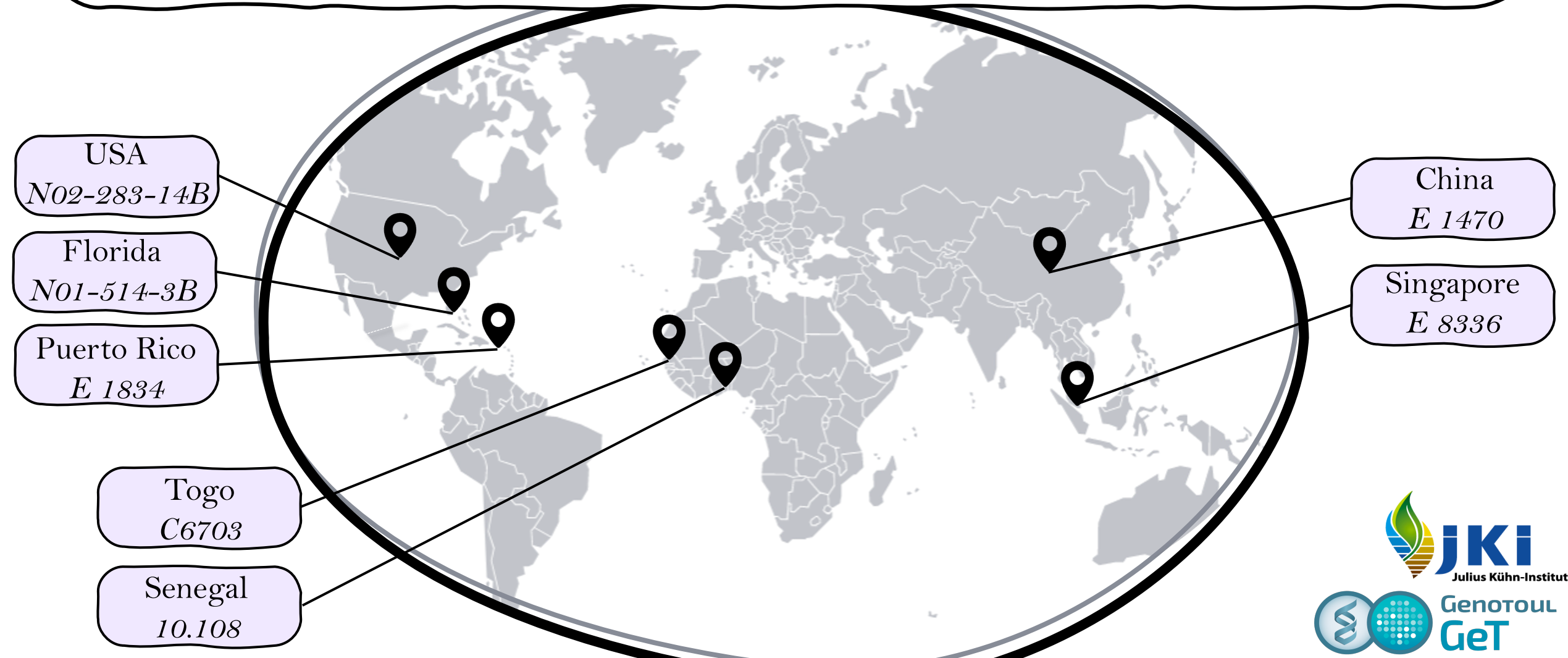


Root
galls



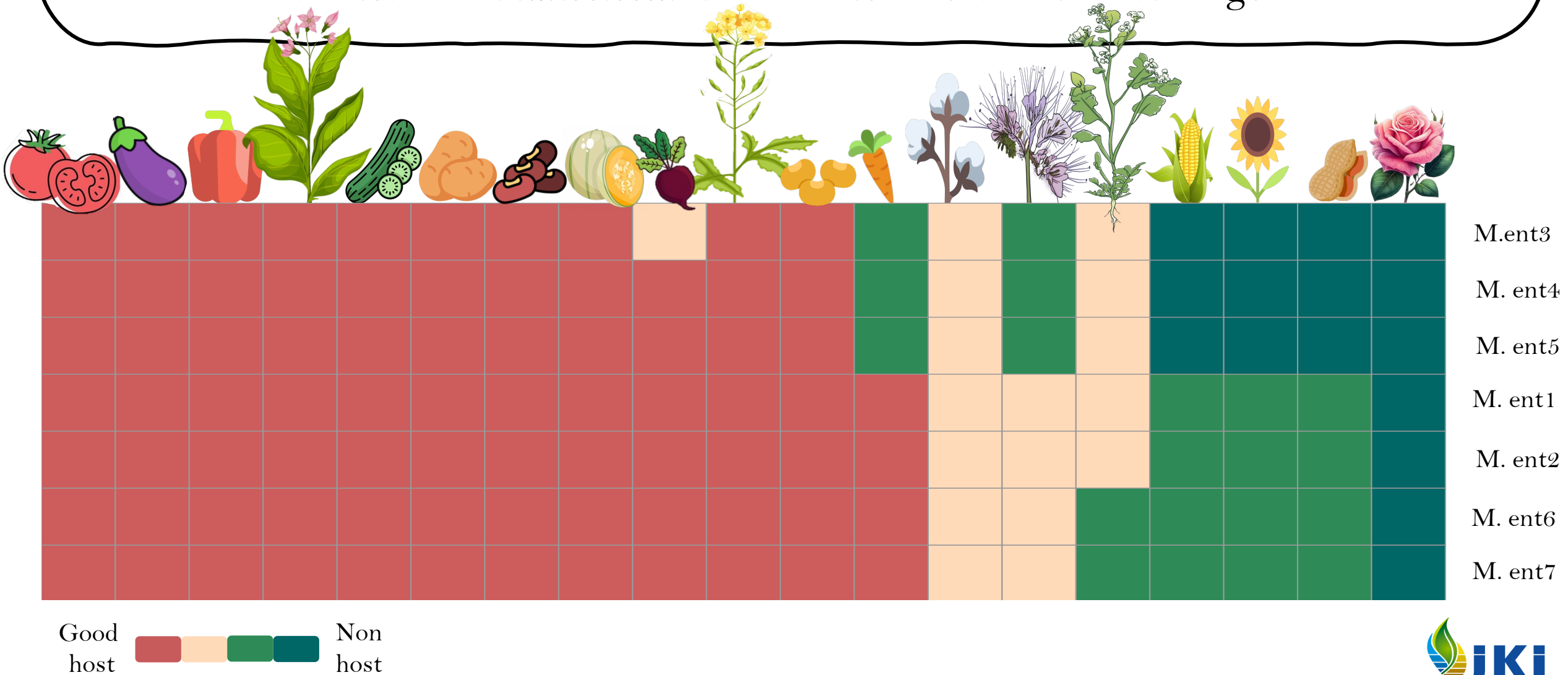
Exploration of the genomic plasticity of *M.enterolobii*

We have produced high-fidelity genome data (PacBio Hifi) for 7 different geographical isolates of *M. enterolobii*. Each isolate differs in its host range.



Exploration of the genomic plasticity of *M.enterolobii*

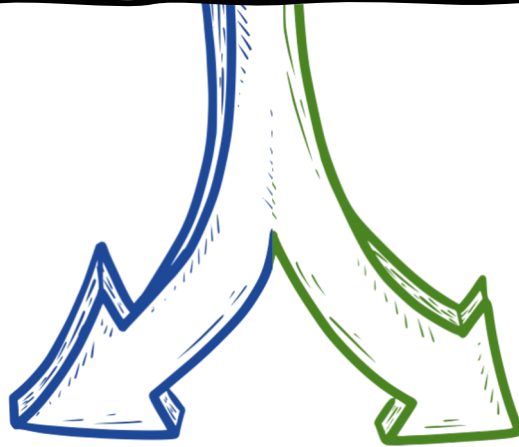
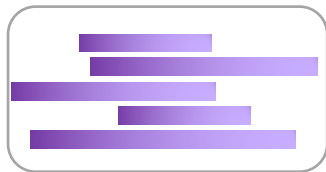
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Reference genome
assembly



Workflow strategies for
variant calling

Compatible
host



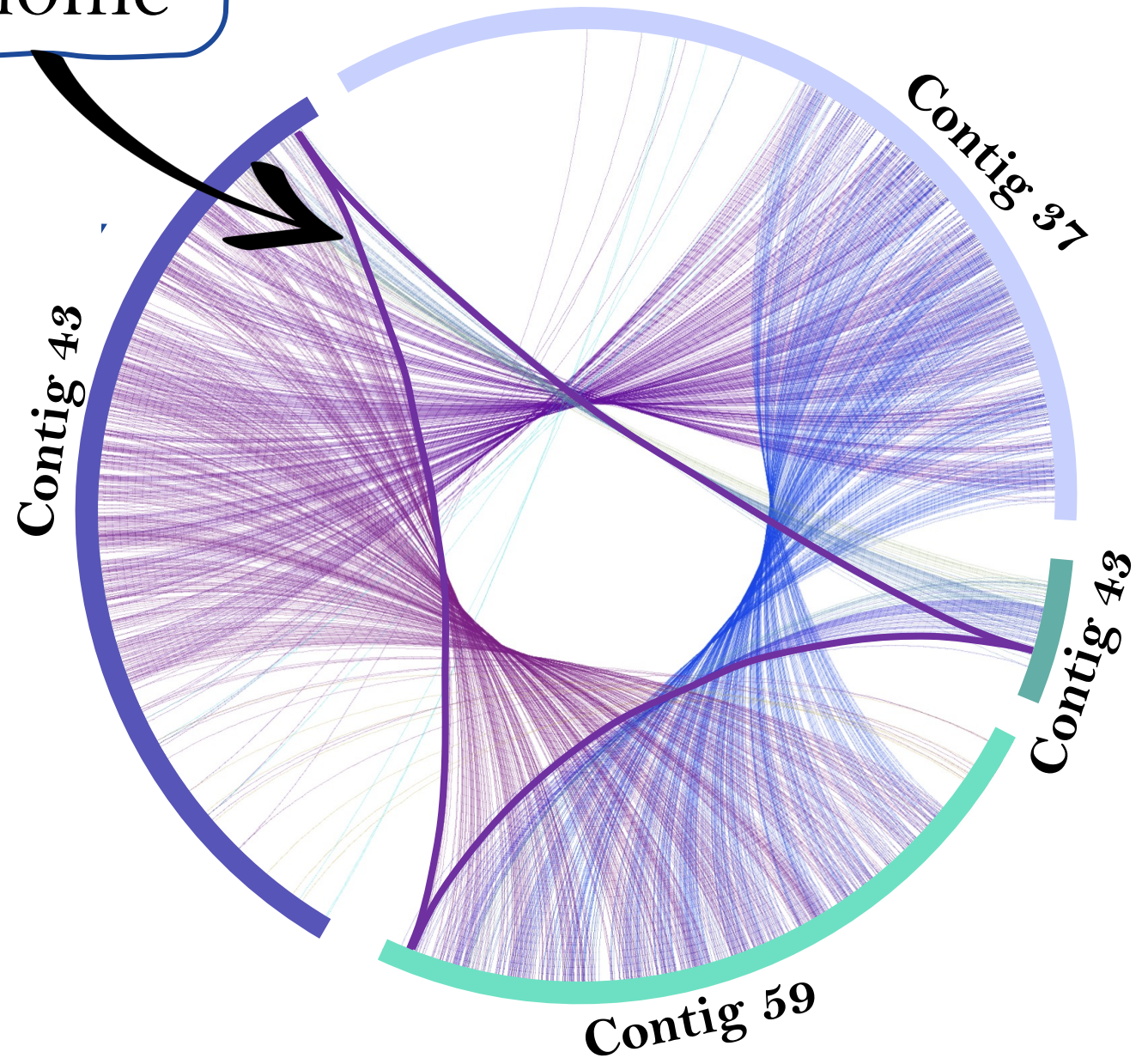
Geographical
distribution



M.ent has a triploid genome

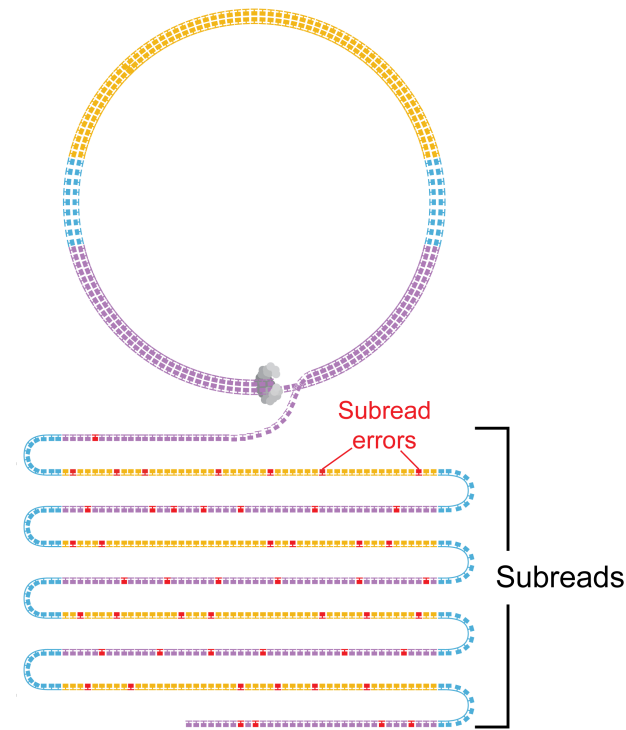
○ 39, 532 protein coding-genes predicted

○ 75.6% of the protein-coding genes are in three copies





PACBIO[®] Hifi Reads



DNA is sequenced
multiple times

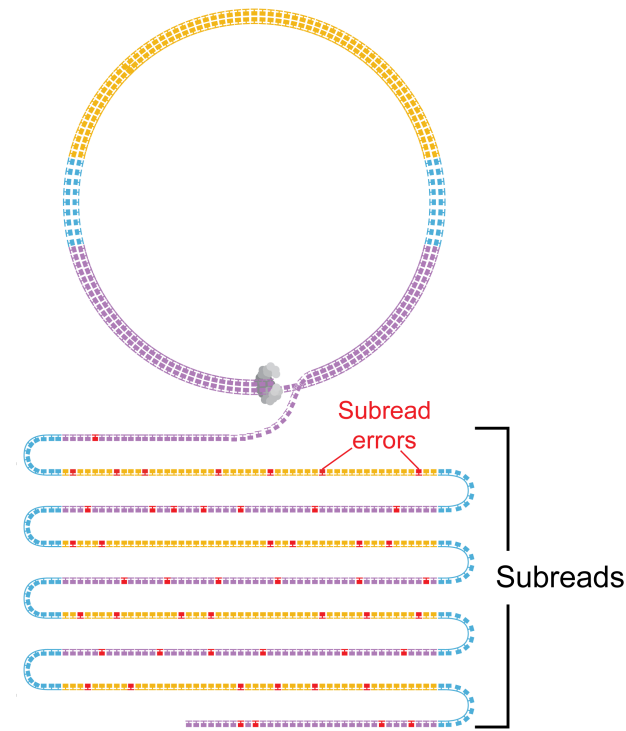
Trimmed of
adapters

pbccs method

Generate consensus read



HiFi read
ACTAG
99% accuracy



DNA is sequenced
multiple times

Trimmed of
adapters

pbccs method

Generate consensus read



..... HiFi read
ACTAG
99% accuracy



DeepConsensus

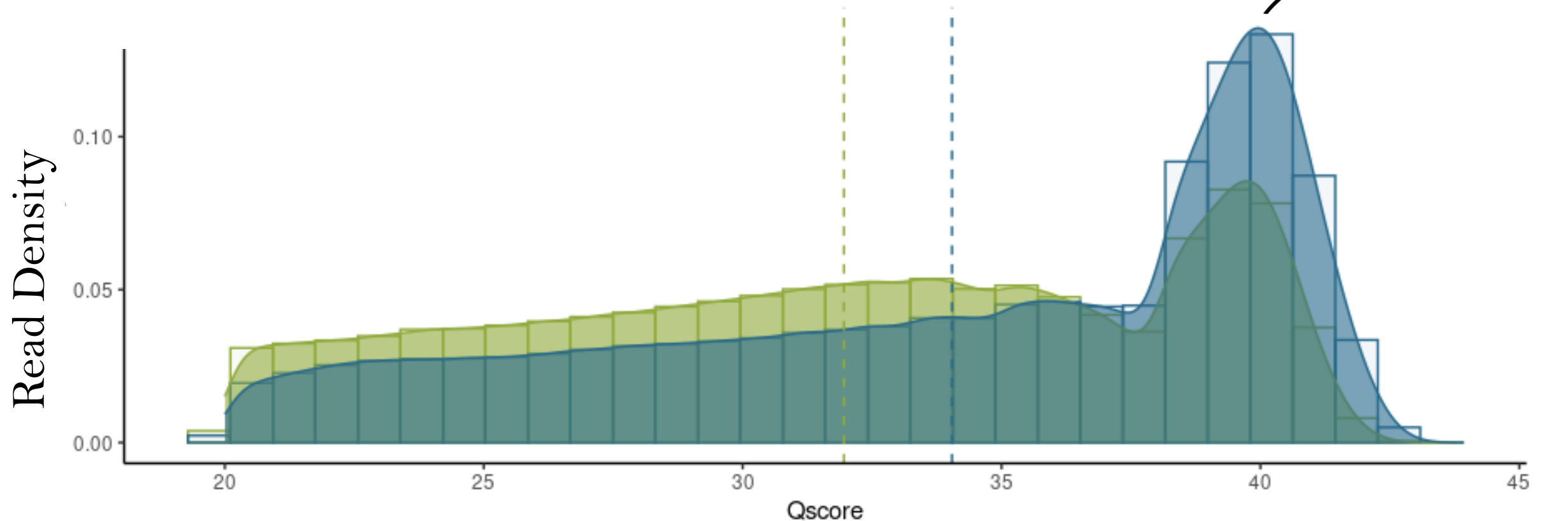
Encoder-only Transformer



New polished read

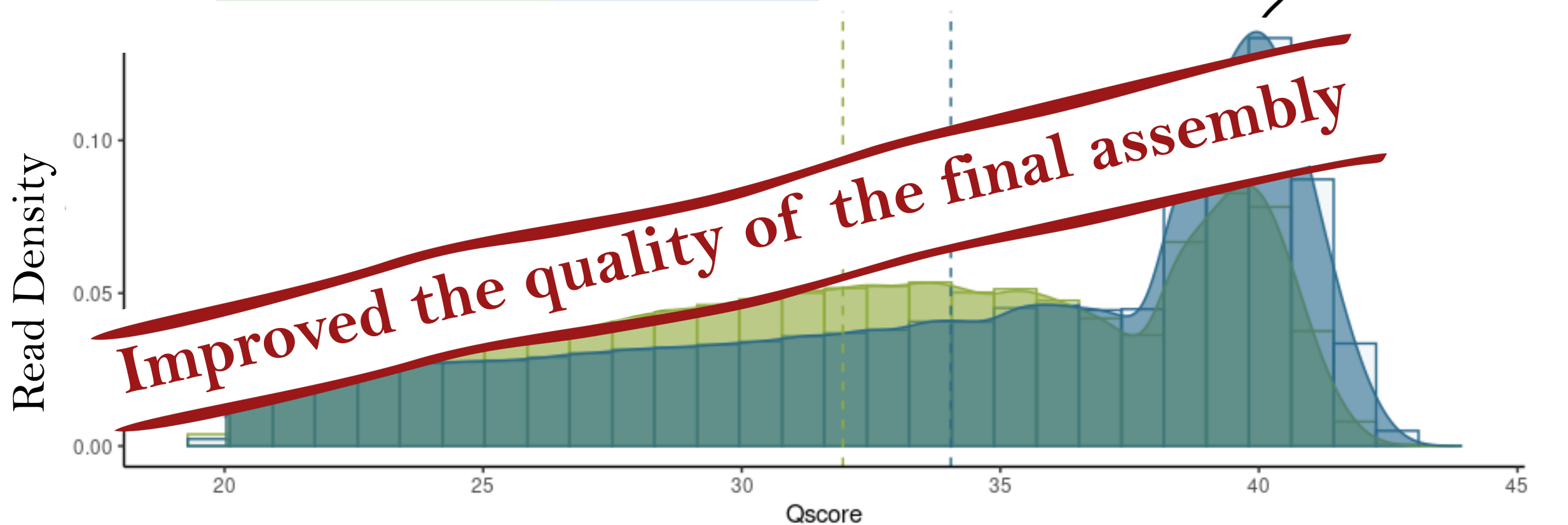
PACBIO® Improving Hifi Reads

	No DeepConsensus	DeepConsensus
No. of reads	2 250 199	2 449 079
Mean length	11 194 bp	11 187 bp
Mean Qscore	31.95	34.04

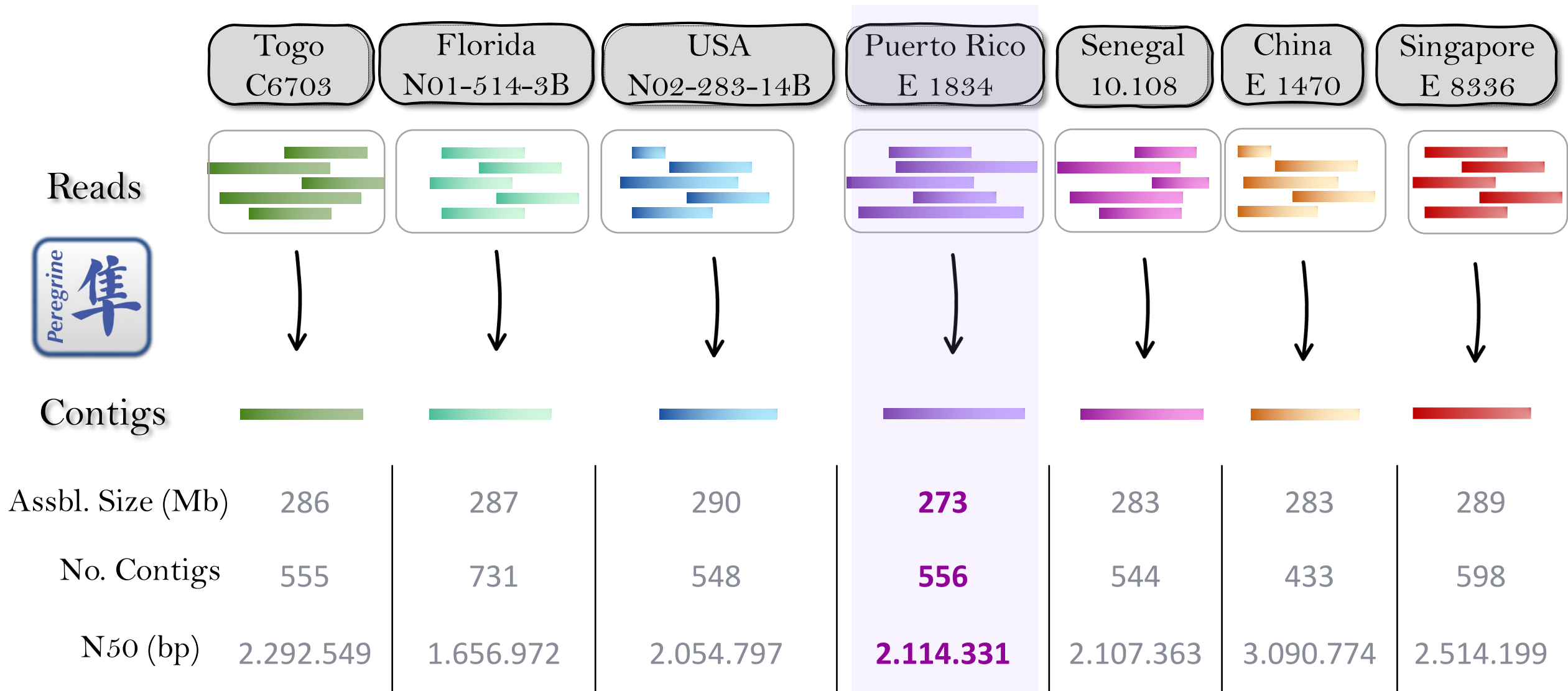


PACBIO® Improving Hifi Reads

	No DeepConsensus	DeepConsensus
No. of reads	2 250 199	2 449 079
Mean length	11 194 bp	11 187 bp
Mean Qscore	31.95	34.04



Assembly statistics



Estimated genome size via flow cytometry : **274.7 Mb \pm 18.5** (256.2 – 293.2)

Koutsovoulos, G.D., et al. (2020) Sci. Data.

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Workflow strategies for variant calling

Compatible
host



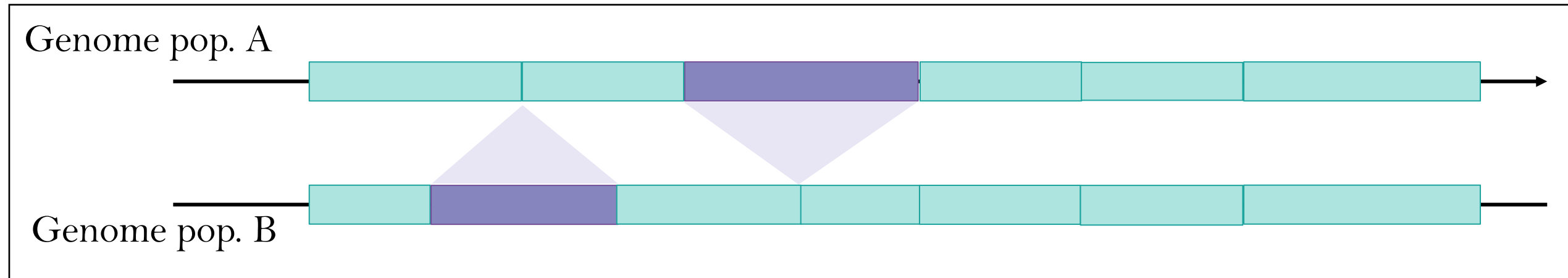
Geographical
distribution



Structural variations in a genome

Simple definition: Genome variation of size > 50 bp

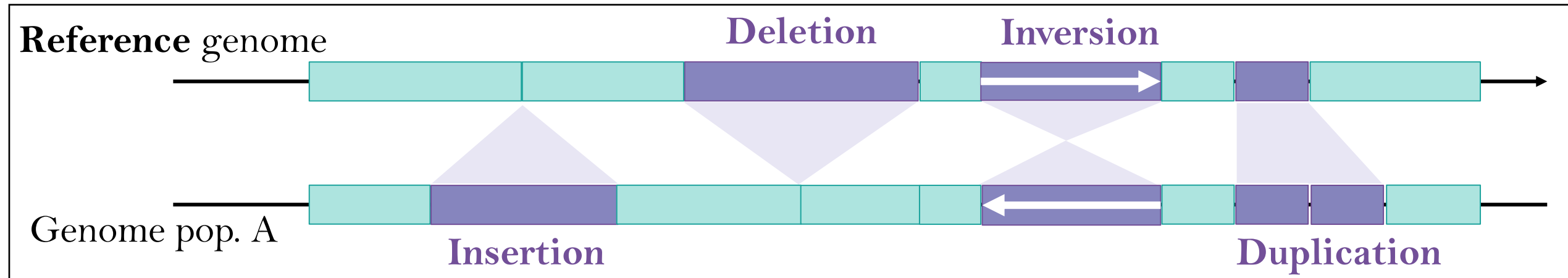
Gathers many different types



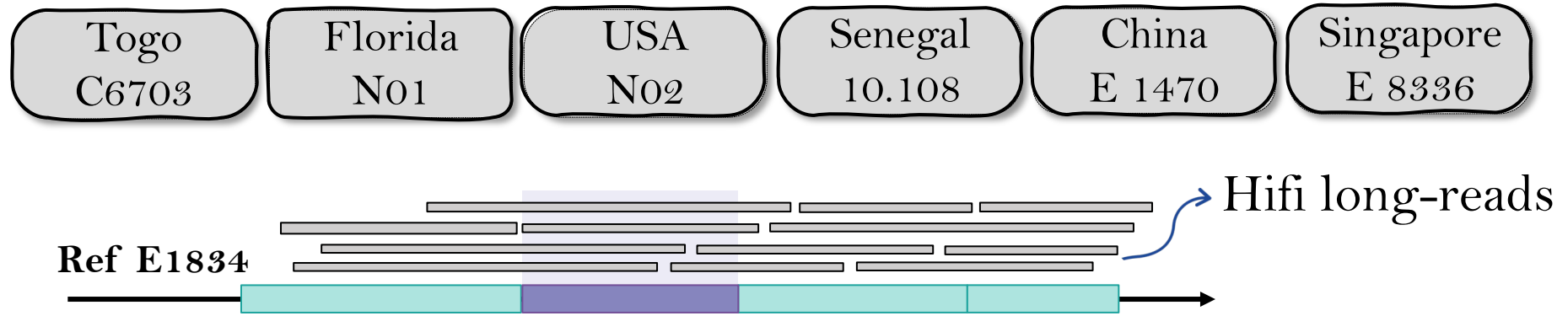
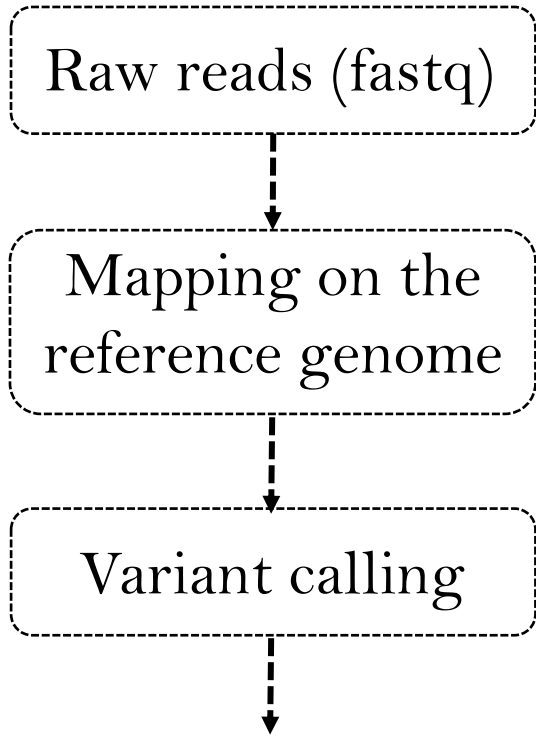
Structural variations in a genome

Simple definition: Genome variation of size $> 50\text{pb}$

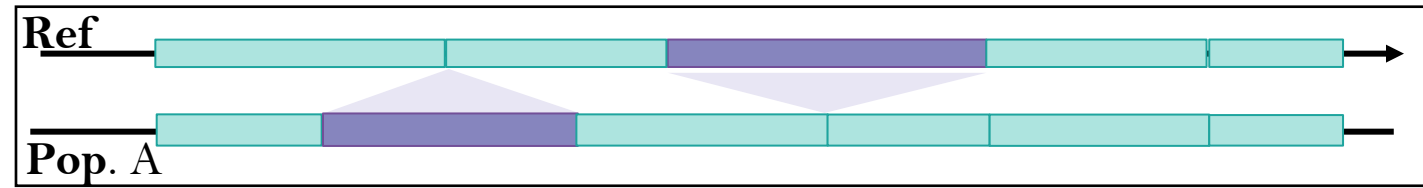
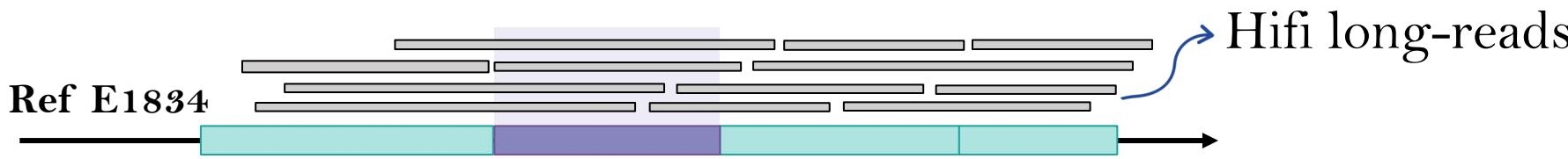
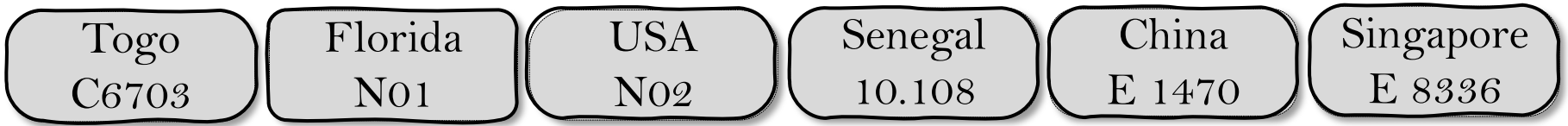
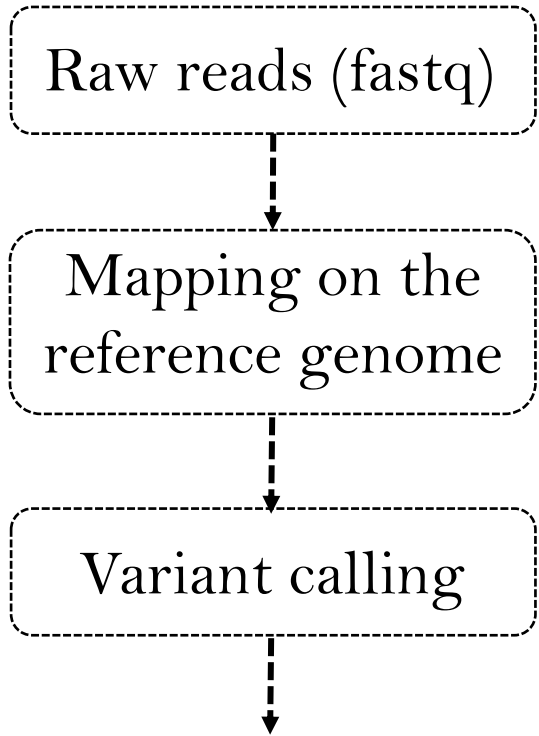
Gathers many different types



SVs Workflow

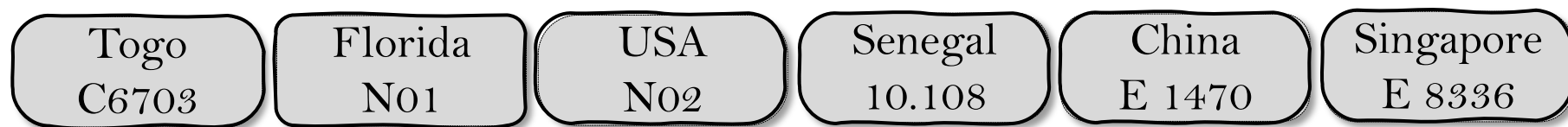
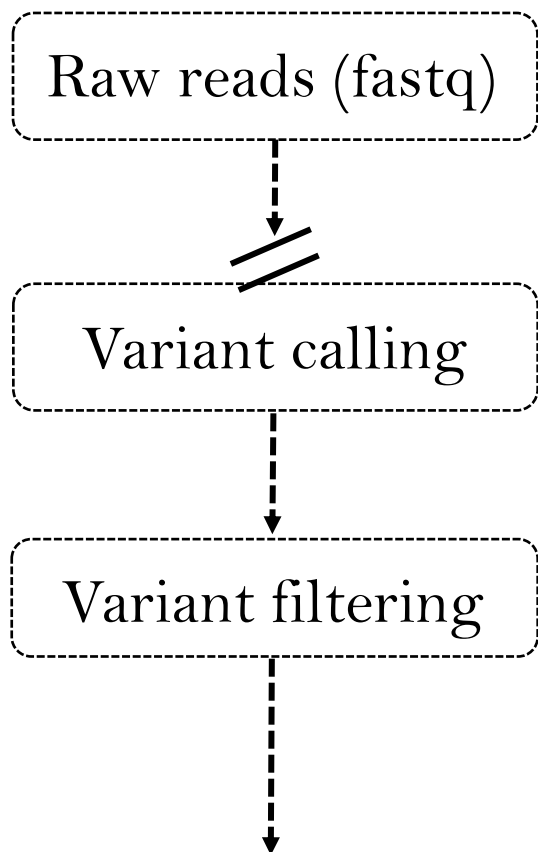


Variant calling



	Sniffles2	CuteSV	DeBreak
Average SV found per tool	11 142	16 232	5 593

Variant filtering



Sniffles2

11 142

CuteSV

16 232

DeBreak

5 593 SVs



50bp \ll SVs size \ll 1Mb

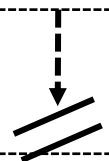
10 \ll SUPP reads \ll 200

Allele Frequency \gg 0.3

MAPQ \gg 10

Variant filtering

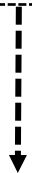
Raw reads (fastq)



Variant calling



Variant filtering



50bp \ll SVs size \ll 1Mb
10 \ll SUPP reads \ll 200
Allele Frequency \gg 0.3
MAPQ \gg 10

Togo
C6703

Florida
N01

USA
N02

Senegal
10.108

China
E 1470

Singapore
E 8336

Sniffles2

11 142

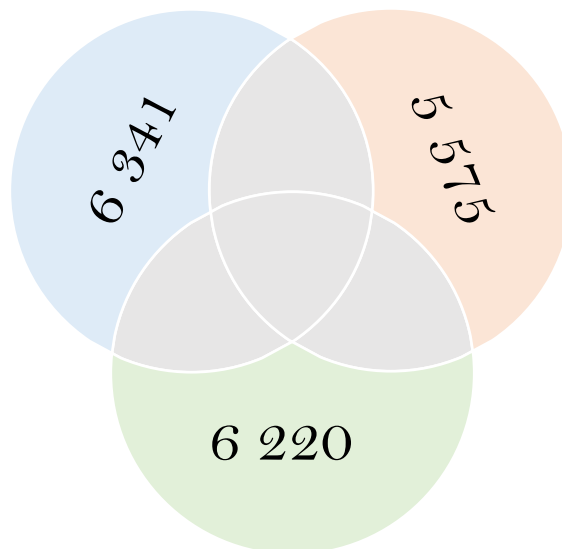
CuteSV

16 232

DeBreak

5 593 SVs

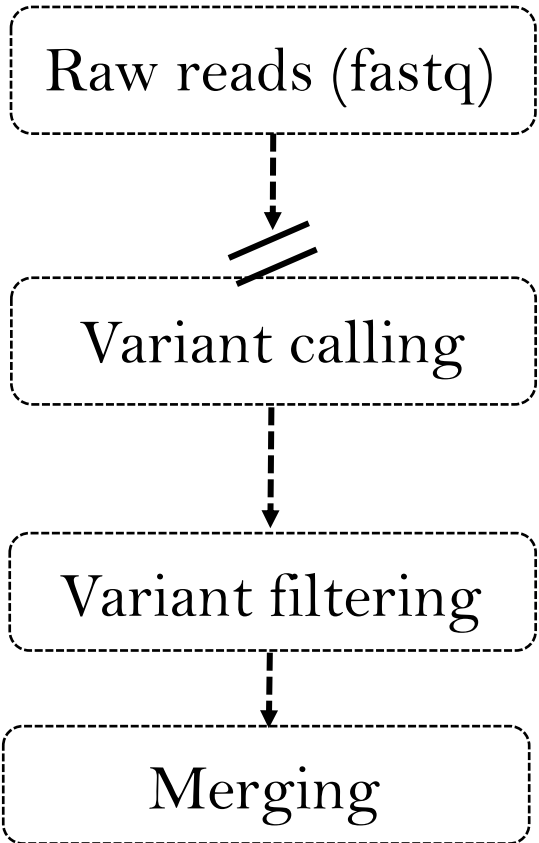
Sniffles2



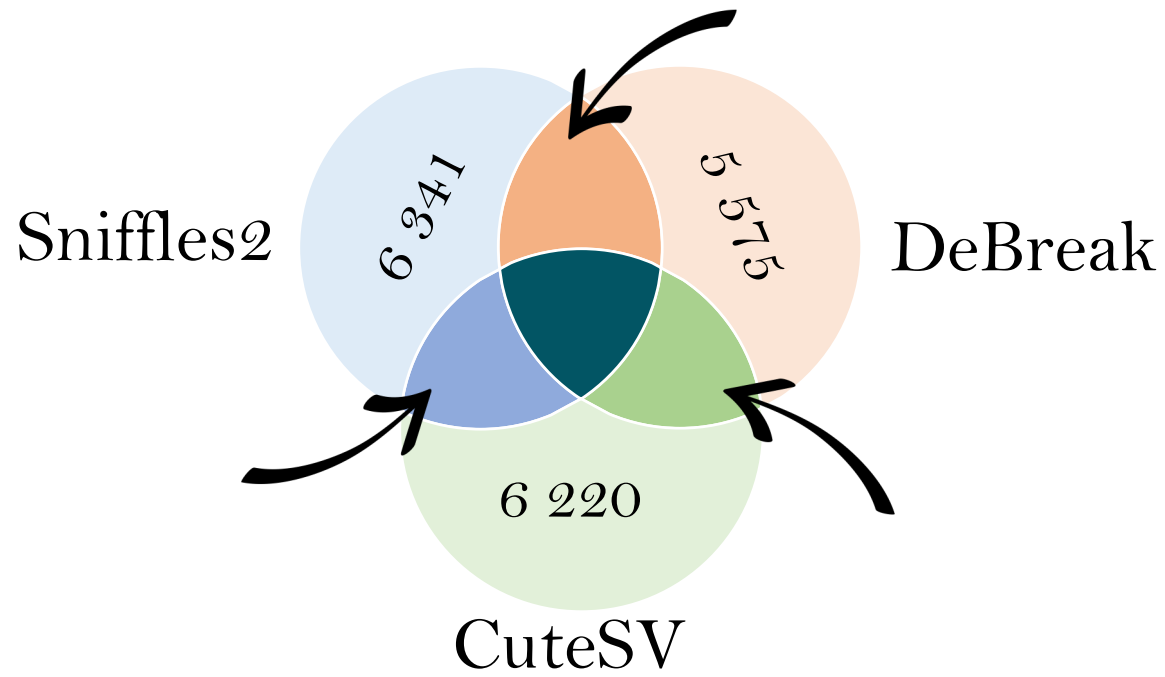
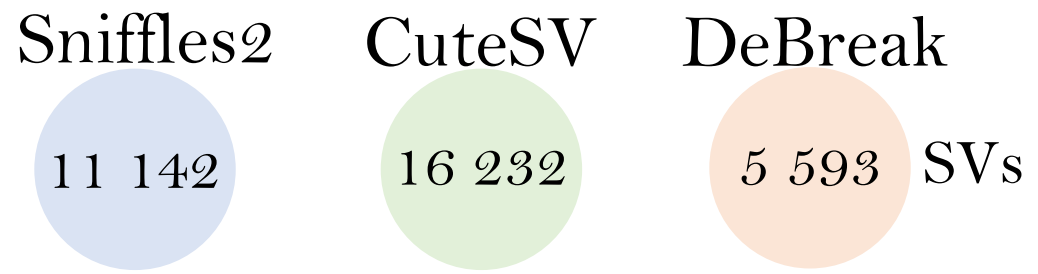
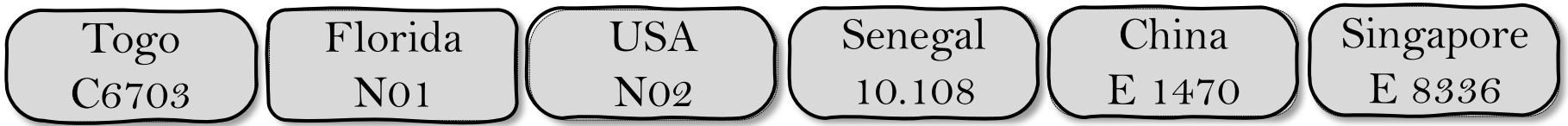
DeBreak

CuteSV

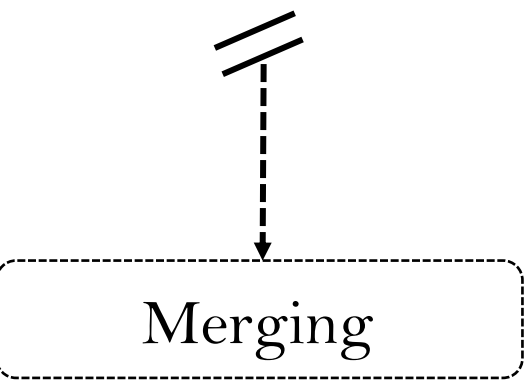
Merging all the SVs



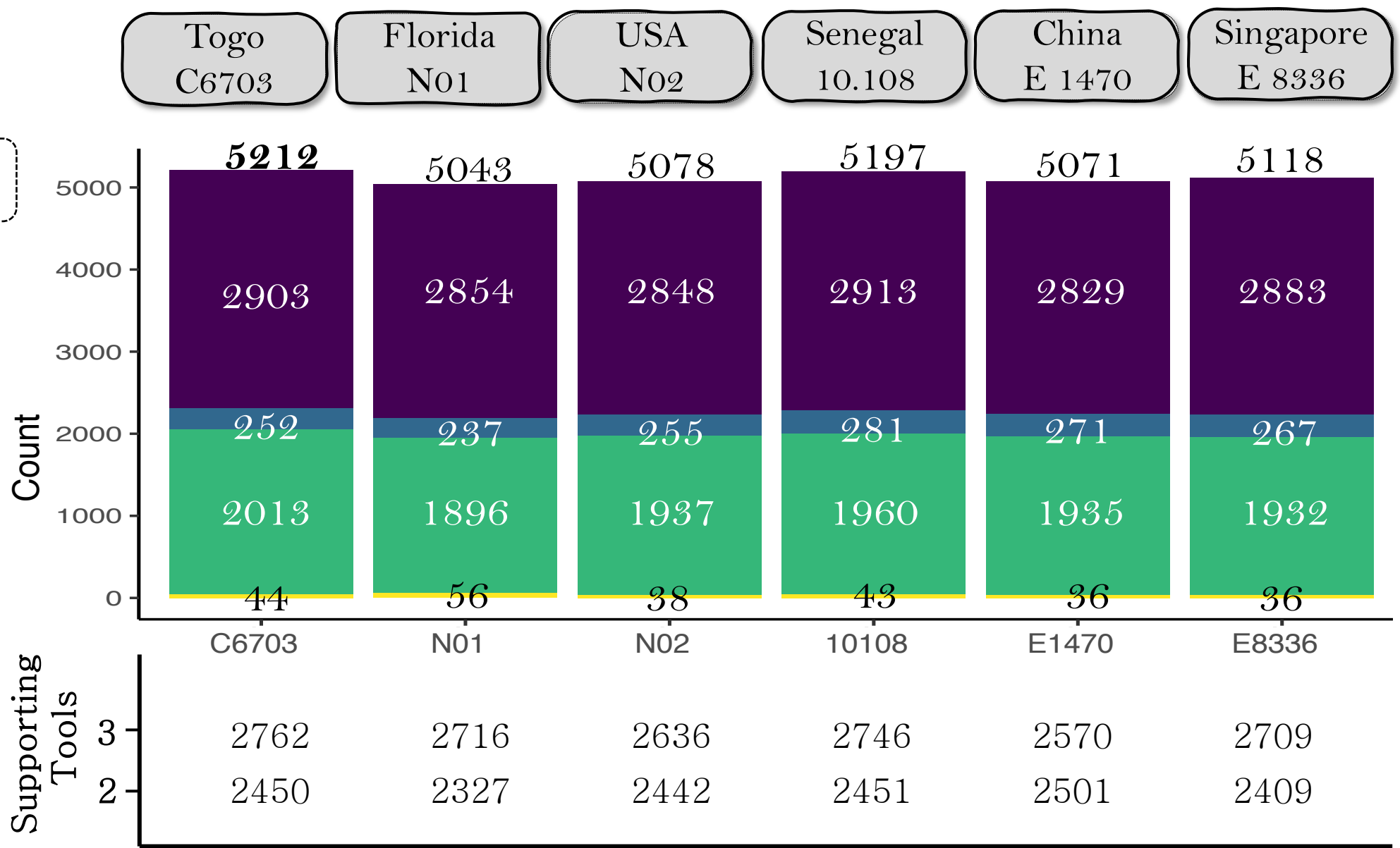
Jasmine
min_support=2
min_overlap=80%



Structural variants in *M. enterolobii*



Jasmine
min_support=2
min_overlap=80%



Structural variants in *M. enterolobii*



Merging

Jasmine

min_support=2
min_overlap=80%

Number of SVs

Togo
C6703

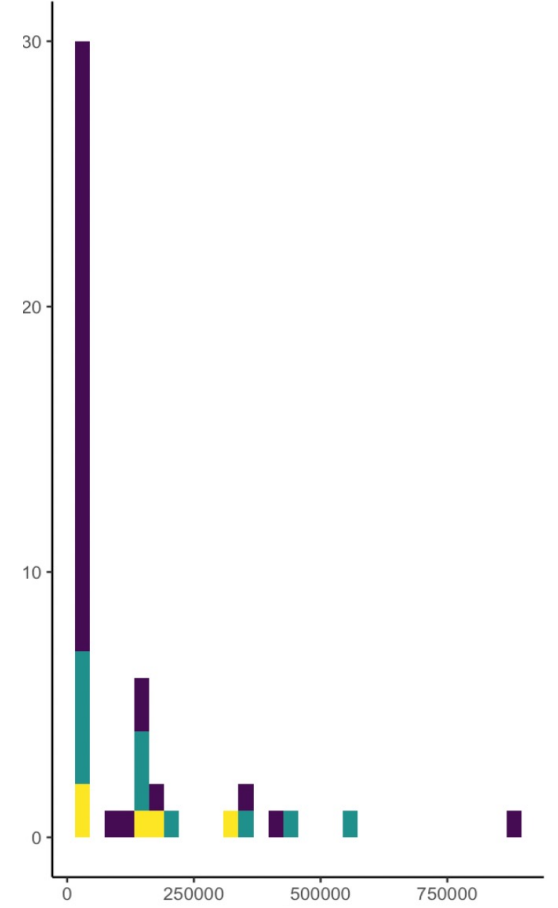
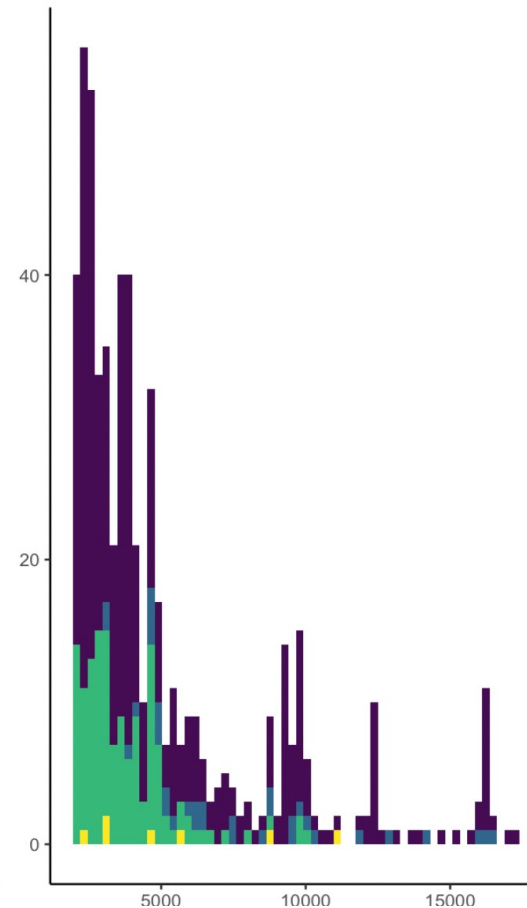
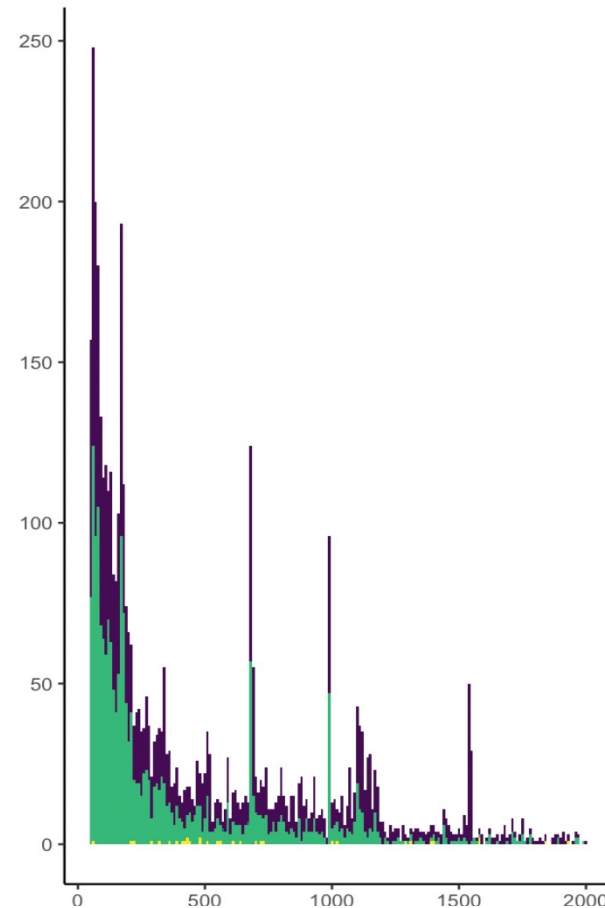
Florida
N01

USA
N02

Senegal
10.108

China
E 1470

Singapore
E 8336



SV length (bp)

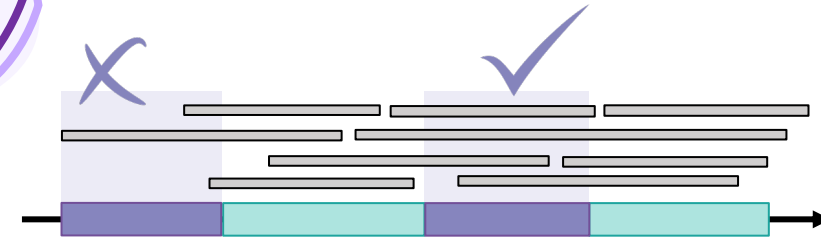
SV Type



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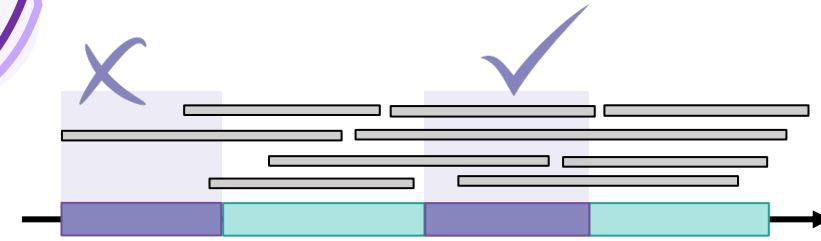
- Reference genome assembly
- Workflow strategies for variant calling



Exploration of the genomic plasticity of *M.enterolobii*

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- Reference genome assembly
- Workflow strategies for variant calling
- Correlate with phenotypes and snp



Compatible
host



Geographical
distribution



Thanks!

EAGS 2024



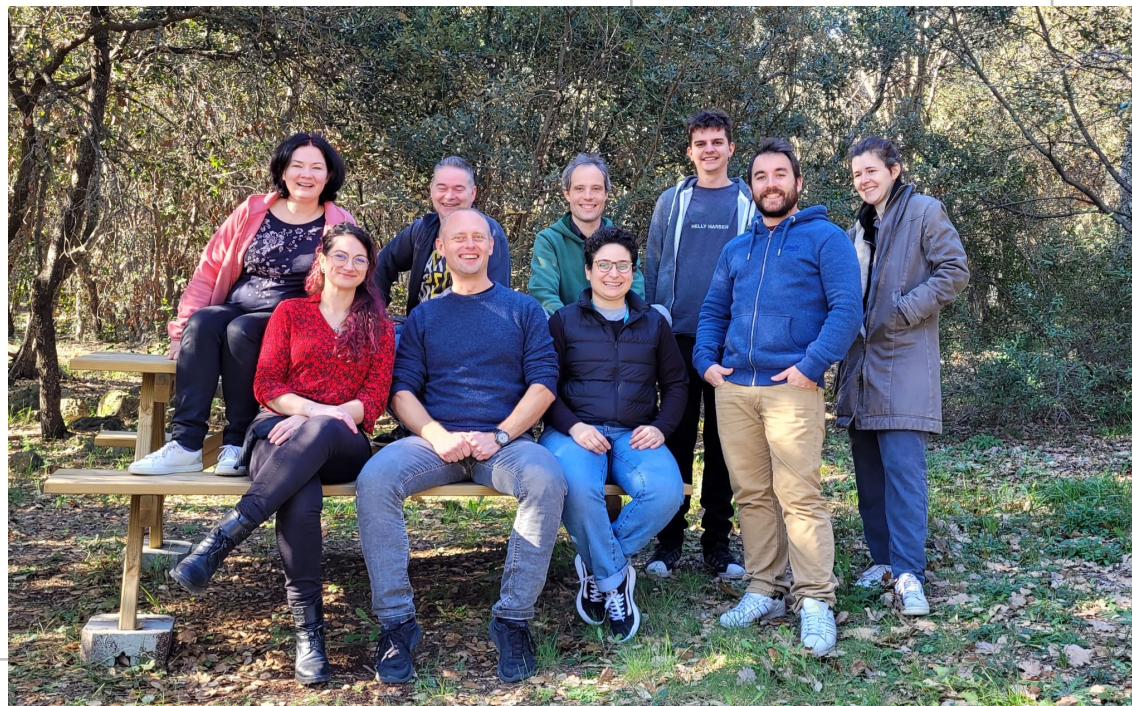
Corinne Rancurel
Martine Da-Rocha
Arthur Pere



Marine Sallaberry
Céline Lopez-Roques
Joanna Lledo



Sebastian Kiewnick
Hemanth Gopal



Etienne Danchin
Karine Robbe-Sermesant
Marc Bailly-Bechet
Dominique Colinet
Carole Belliardo
Ana Paula Zotta Mota
Djampa Kozlowski
Ercan Seckin

