STATUS OF THE WATER BUFFALO GENOME

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Water Buffalo dataset overview

Number of reads

Illumina GAII paired end reads: 571,334,795 * 2

Illumina GAII jump libraries: 167,677,444 * 2 (insert size 4-6 kb)

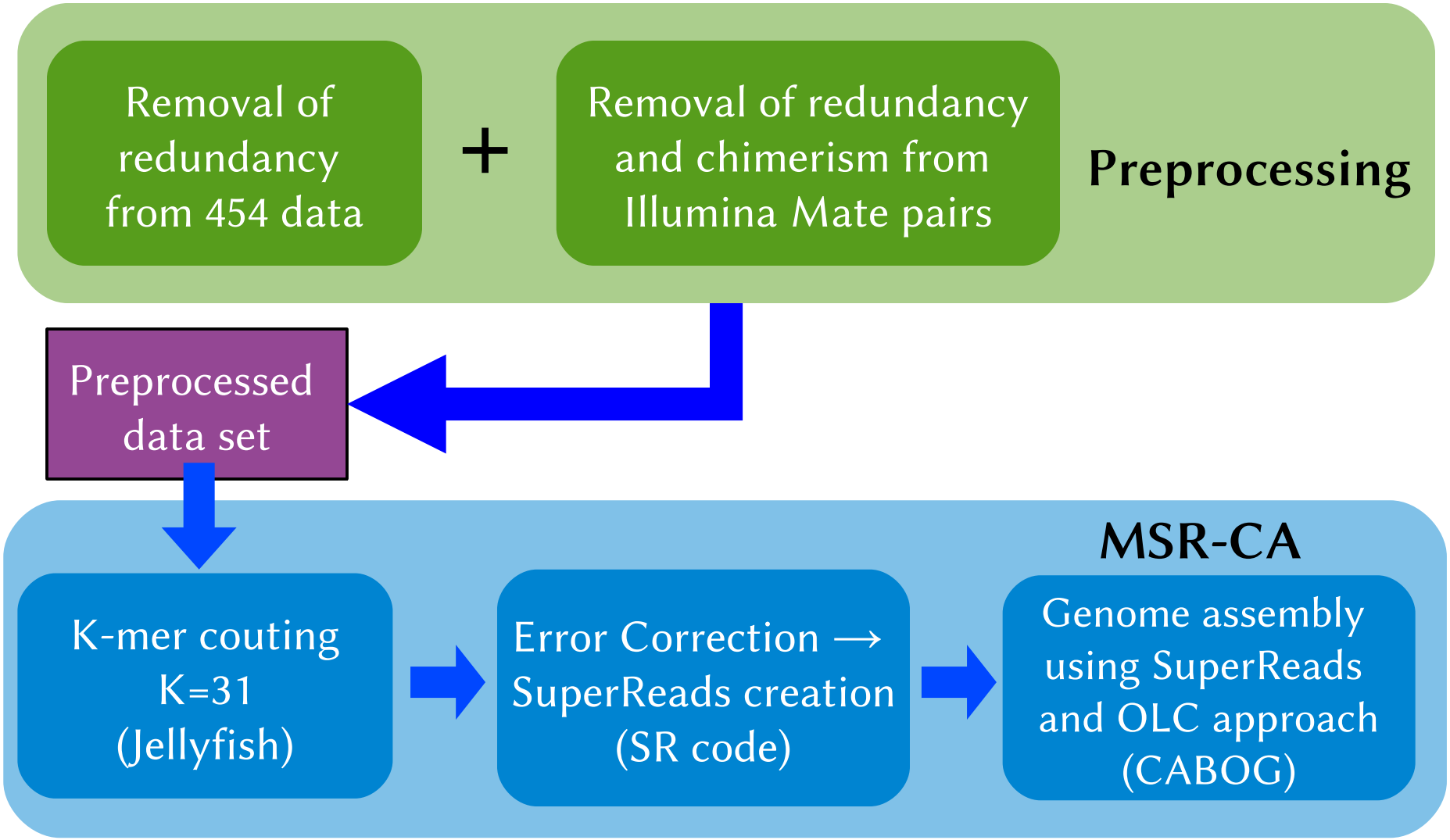
Roche 454 Unmated reads: 10,228,343

Roche 454 Mate pairs: 2,416,466 * 2 (insert size 15-35 kb)

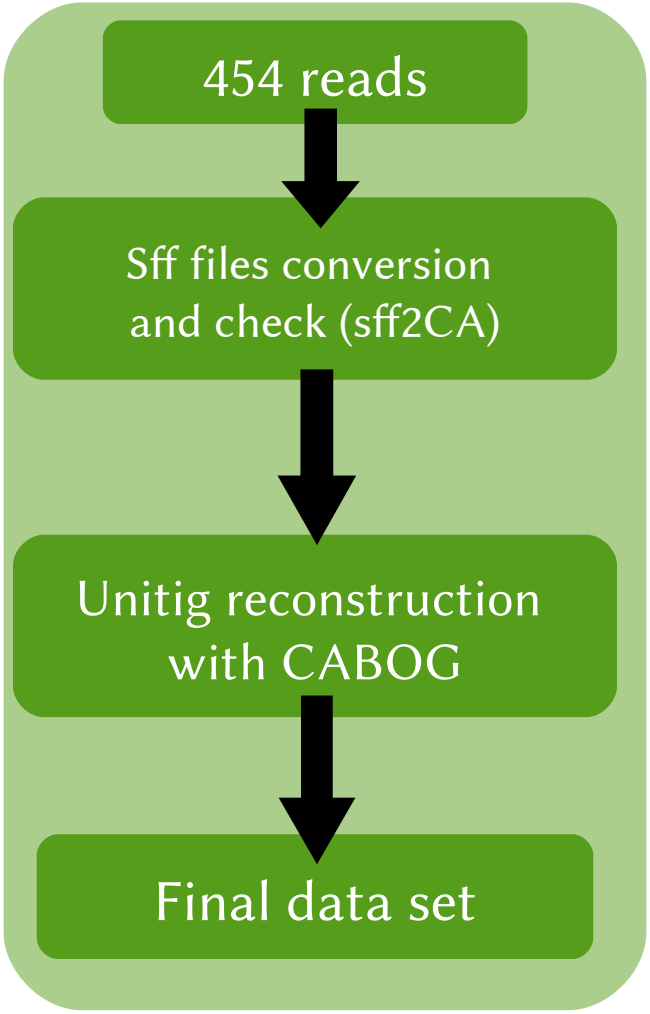
Total length of genomic DNA: ~300 Gbases

Clone Coverage: > 40 x

Outline of the assembly procedure

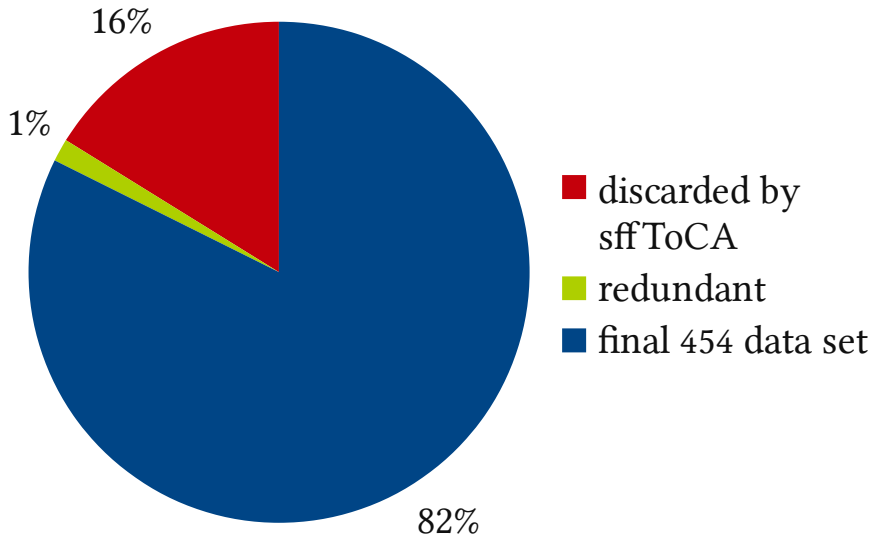


Preprocessing: Roche 454 Draft Assembly



Data is cleaned removing reads with the same coordinates in a given unitig.

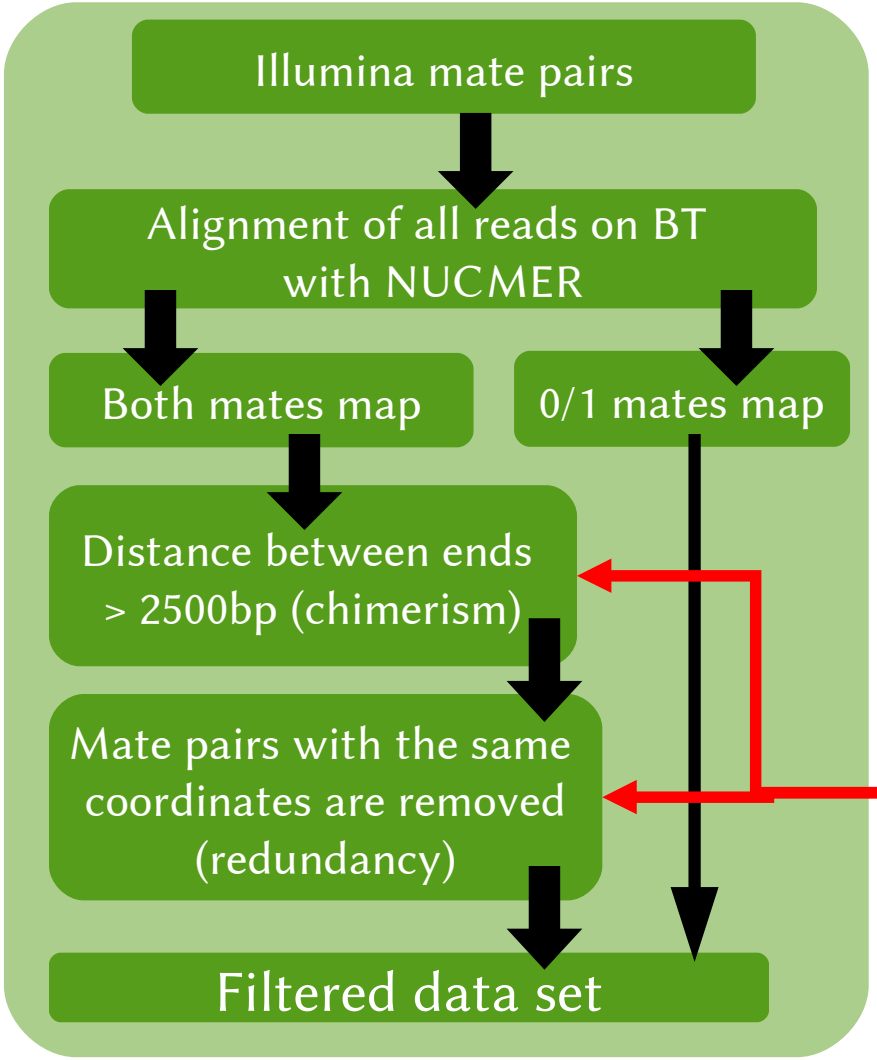
Results:



Computational resources:

Computation time: 10 days
Number of CPUs: 216 on 27 nodes
RAM (each node): 16/32 Gb
Disk space: 1.35 TB

Preprocessing: Illumina mate pairs alignment on *Bos taurus* genome



BT genome version: UMD 3.1

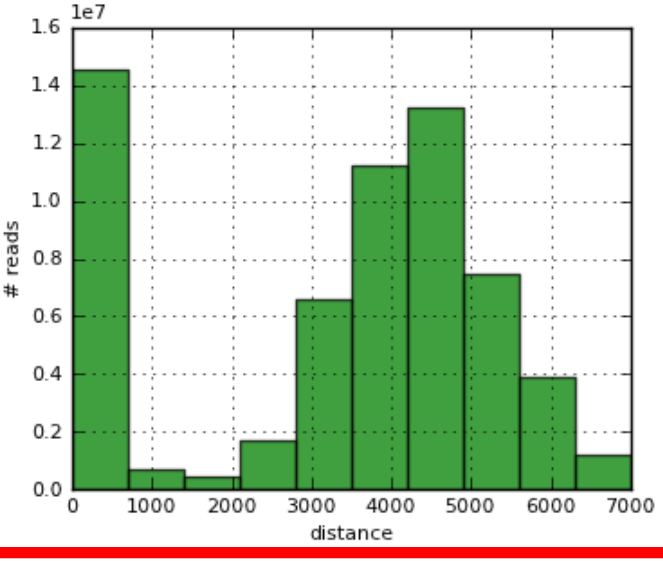
Starting mate pairs: 167,677,444

Mapping mate pairs (both mates): 63%

Chimeric reads: 10 %

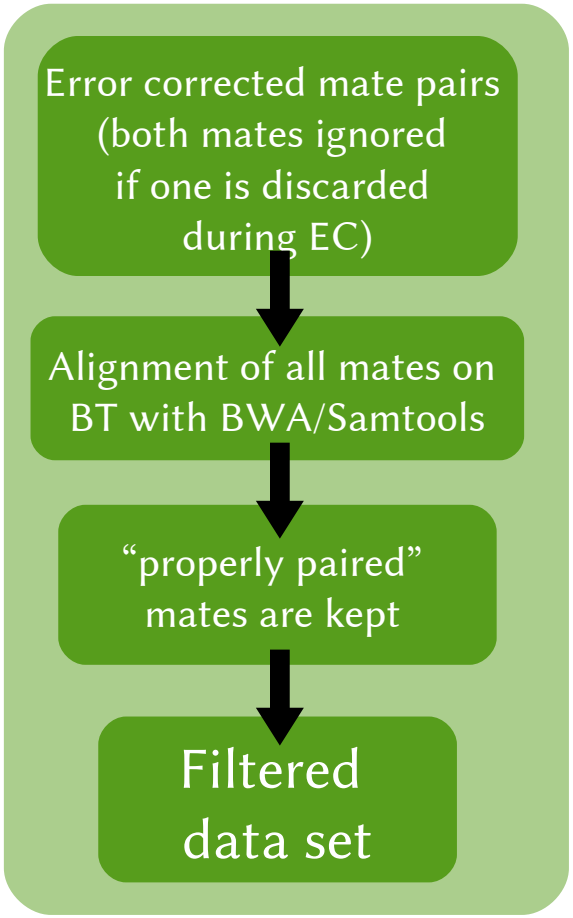
Redundant reads: 11 %

Refined data set mate pairs: 32 %

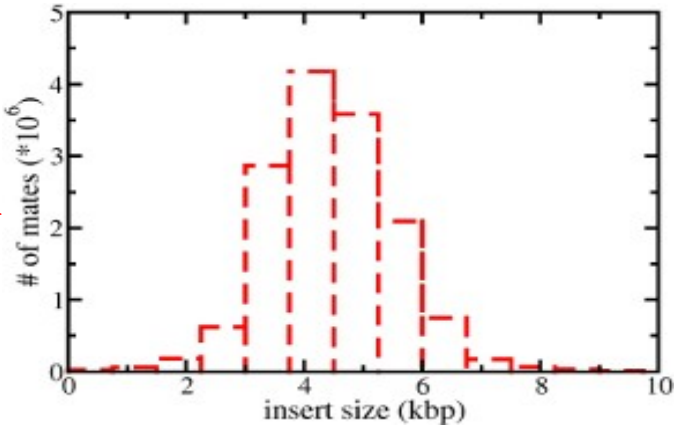


Alternative approach (assembly 2): alignment on *Bos taurus* after Error Correction

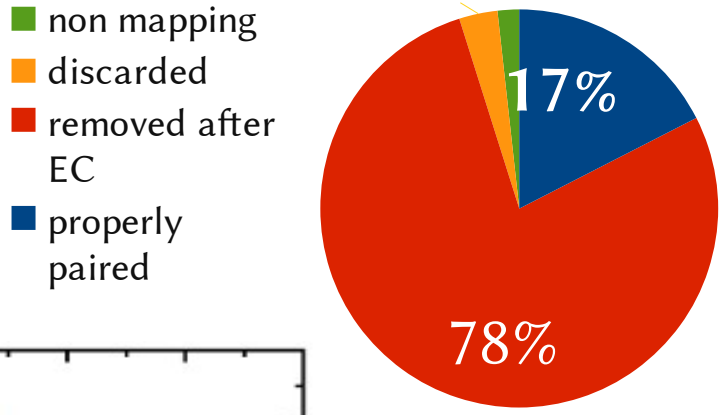
Illumina mate pairs are re-filtered and new genome assembly with CABOG is started



Insert size of properly paired reads

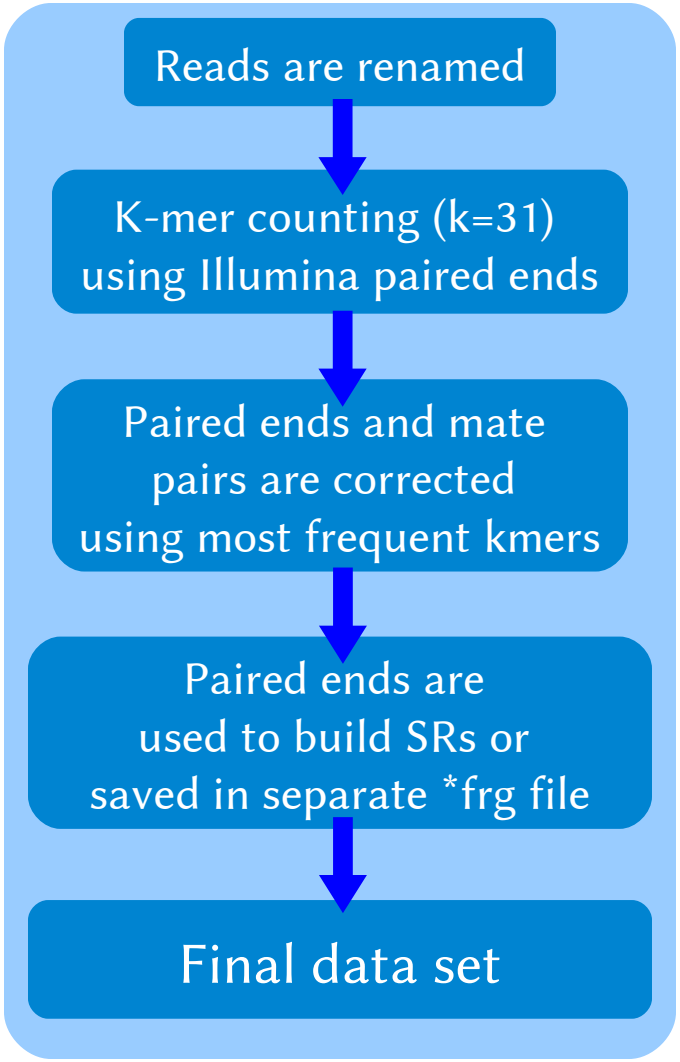


Results:

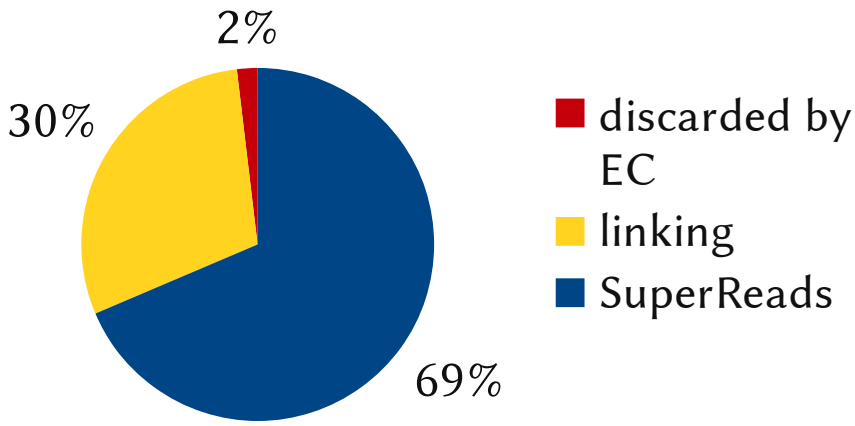


The final jump library data set contained 58,679,256 reads → 29,339,628 mate pairs → 17.5% of initial (uncorrected) data

MSR-CA: k-mer counting → Error correction → SuperReads creation



Paired ends after EC:

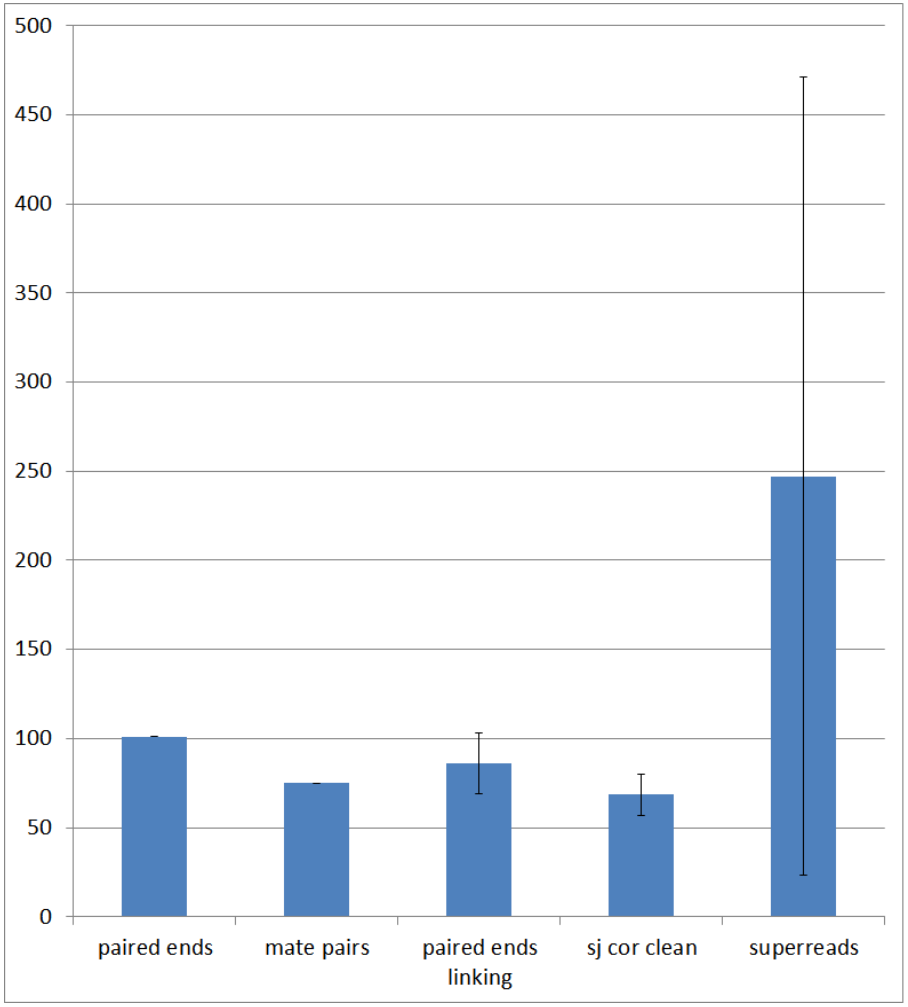


1.5B reads → 40M Super Reads

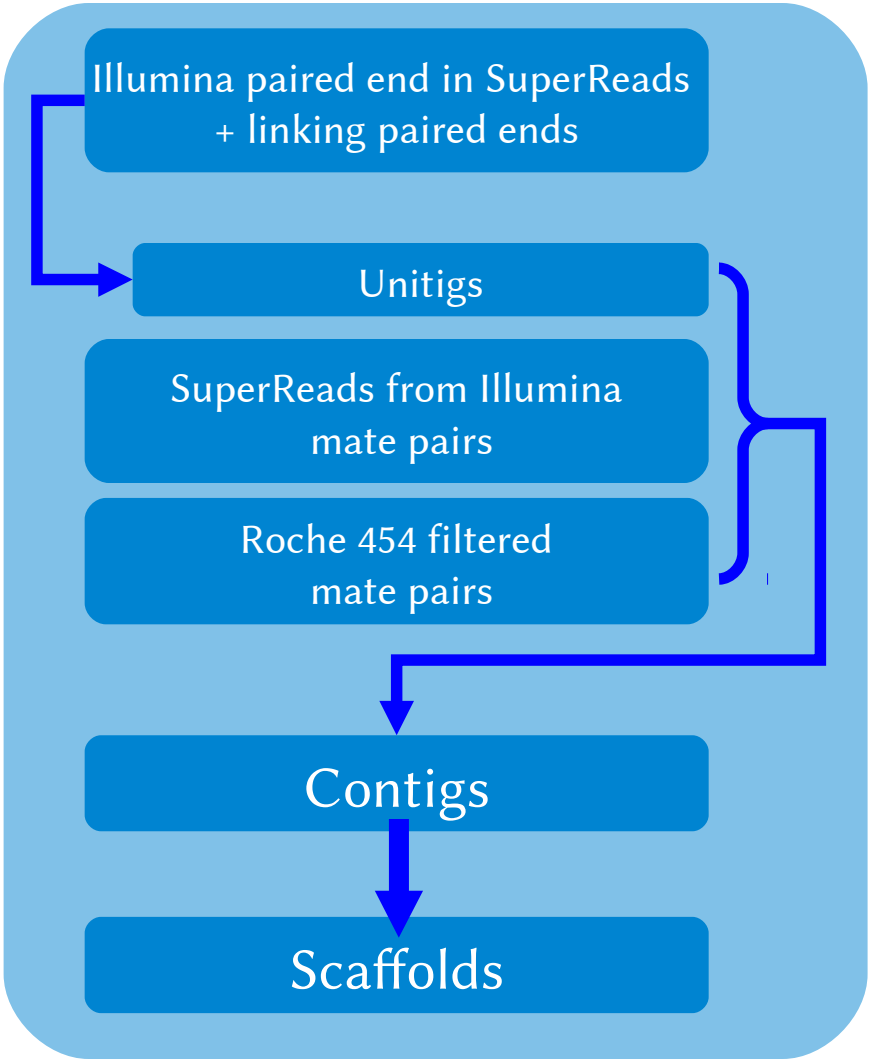
Computational resources:

Computation time: 8 days
Number of CPUs: 48 on 1 node with HyperThreading
RAM: ~400 GB (512 GB available)
Disk space: 1.5 TB

Starting and final average read length



Genome Assembly with SuperReads and CABOG (assembly 1)



Computational resources:

Computation time: 30* days
Number of CPUs: 48 on 1 node with HyperThreading
RAM: ~100 GB (512 GB available)
Disk space: 7.0 TB

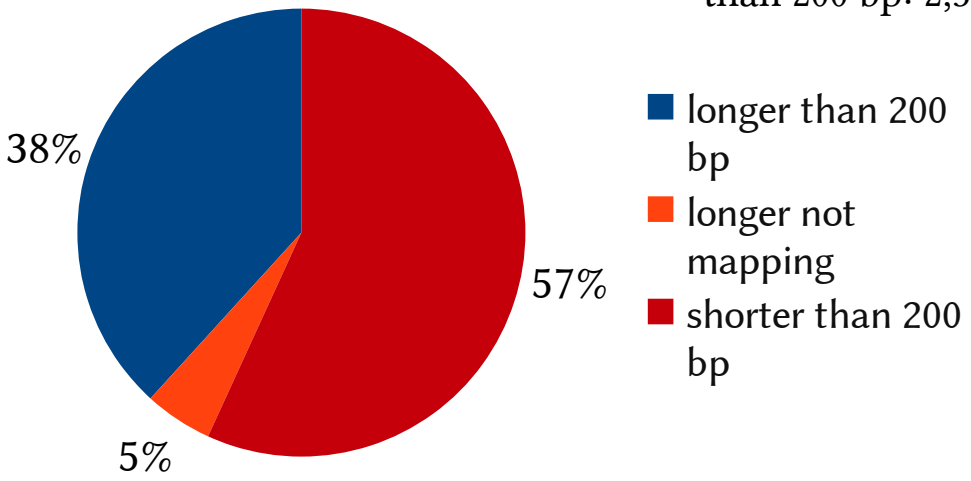
Currently we are in the scaffold merging phase of the OLC algorithm and we expect to obtain the final genome in a few days

Alignment of unitigs on *Bos taurus* genome

After the unitig-consensus step of CABOG a total of 11,214,882 unitigs have been obtained. Long unitigs (>200bp) have been aligned on Bos Taurus genome with NUCMER to estimate genome coverage and try a first reconstruction of scaffolds.

Bos taurus genome length (excluding gaps): ~2.63 Gb

Total length of BT genome covered joining unitigs longer than 200 bp: 2,379,273,793 ~ 90.5% of Bos Taurus genome



Conclusions

1) The first (draft) version of the water buffalo genome will be obtained in a few days, once the scaffolding still running terminates.

2) A second, better, version obtained including both significant improvements to the MSR-CA pipeline and better mate pair processing strategies (alignment after Error Correction) should be much quicker and we hope to obtain it in about a month.

3) Current data already allows to perform SNP discovery using Jellyfish and the Error Correction pipeline.

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