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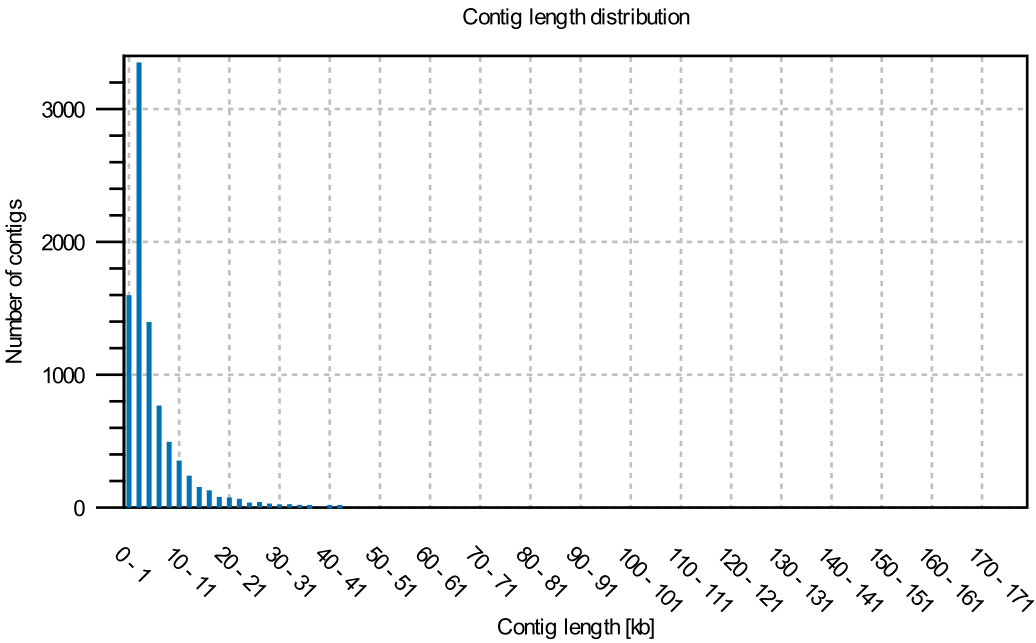
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# 1. Nucleotide distribution

Nucleotide	Count	Frequency (%)
Adenine (A)	12.344.973	23,70
Cytosine (C)	13.646.443	26,20
Guanine (G)	13.627.076	26,16
Thymine (T)	12.358.688	23,73
Any nucleotide (N)	106.657	0,20

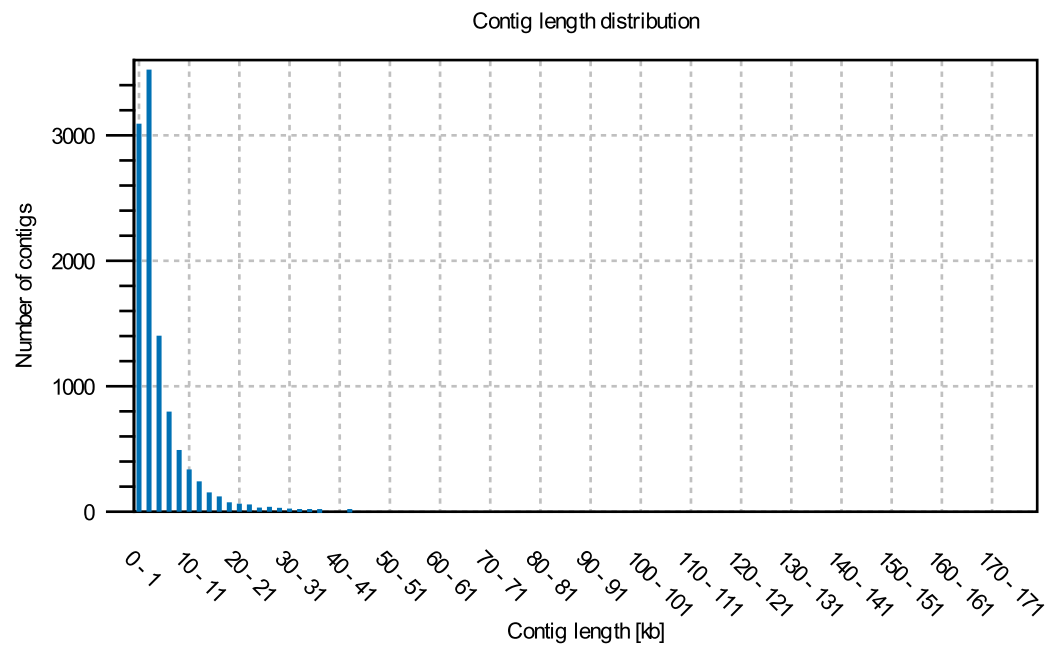
# 2. Contig measurements (including scaffolded regions)

	Length
N75	4.521
N50	10.097
N25	21.472
Minimum	1.000
Maximum	179.205
Average	5.789
Count	8.997
Total	52.083.837

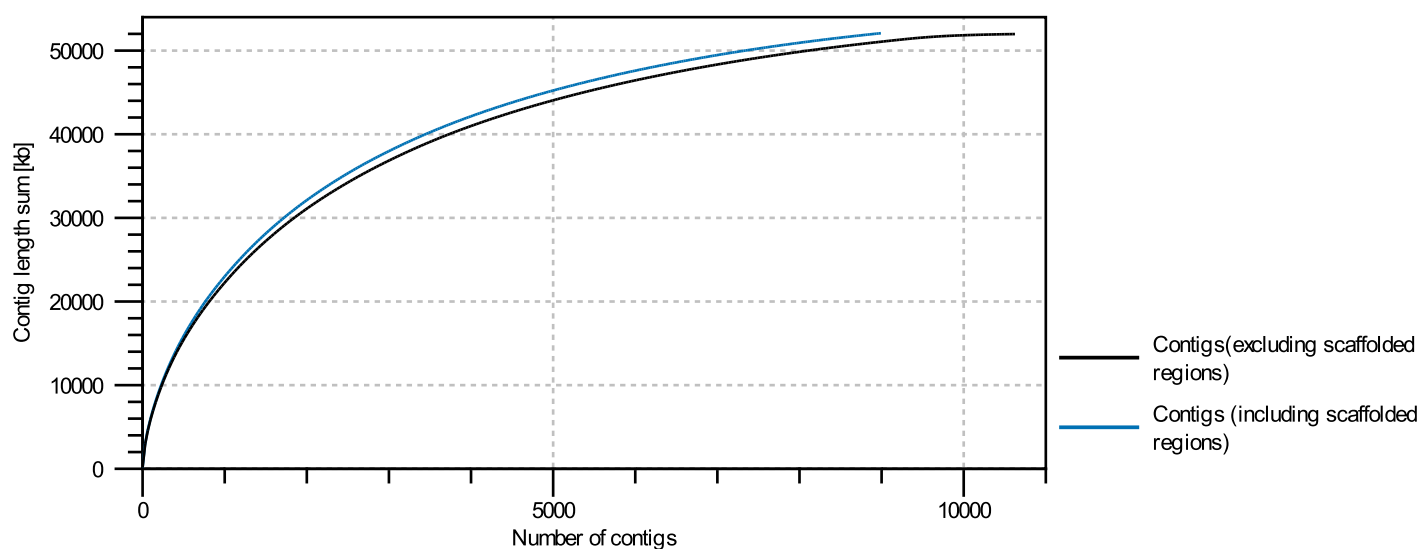


### 3. Contig measurements(excluding scaffolded regions)

	Length
N75	4.149
N50	9.327
N25	20.360
Minimum	115
Maximum	179.205
Average	4.889
Count	10.631
Total	51.976.409



### 4. Accumulated contig lengths



## 5. Summary statistics

	Count	Average length	Total bases
Reads	20.223.236	151,00	3.053.708.636
Matched	19.600.212	151,00	2.959.632.012
Not matched	623.024	151,00	94.076.624
Contigs	8.997	5.789,02	52.083.837
Reads in pairs	8.464.597	450,96	N/A
Broken paired reads	2.671.018	151,00	N/A

## 6. Distribution of read length

Length	Count
151	20.223.236

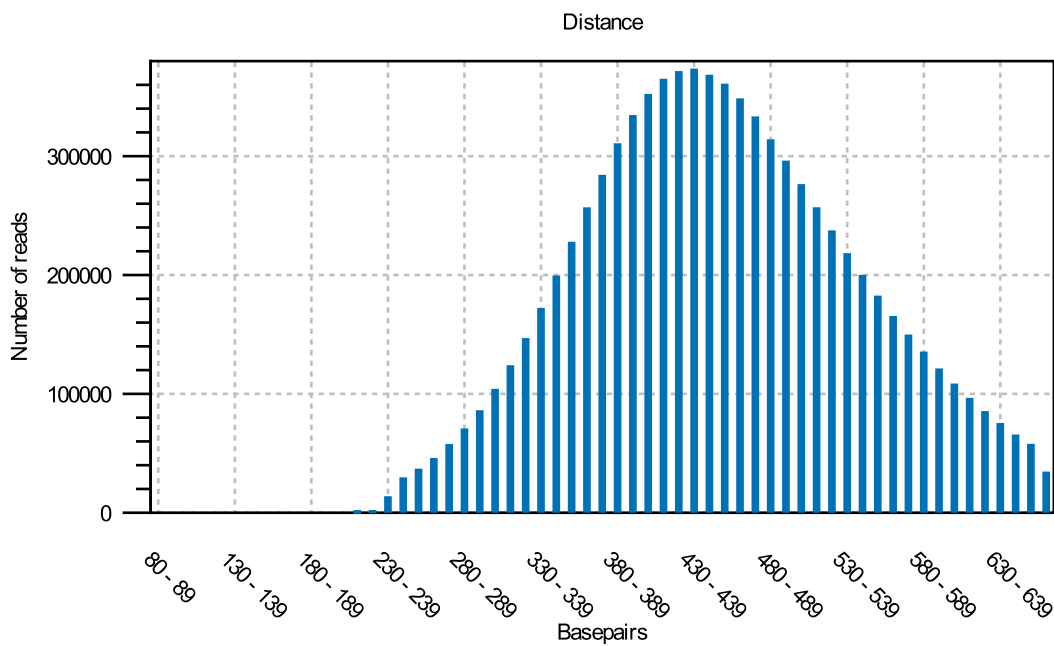
## 7. Distribution of matched read length

Length	Count
151	19.600.212

## 8. Distribution of non-matched read length

Length	Count
151	623.024

## 9. Paired reads distance distribution



## History for:

 ARA2\_1 (paired) assembly summary report

### De Novo Assembly 1.5

29 nov. 2022 22:07:17

Version:	CLC Genomics Workbench 22.0.2
Modified by:	Usuario
Mapping mode	Map reads back to contigs (slow)
Update contigs	Yes
Automatic bubble size	No
Bubble size	250
Minimum contig length	1.000
Automatic word size	No
Word size	40
Perform scaffolding	Yes
Auto-detect paired distances	Yes
Mismatch cost	3
Insertion cost	3
Deletion cost	3
Length fraction	0,5
Similarity fraction	0,75
Create list of un-mapped reads	No
input: ARA2_1 (paired)	
Guidance only reads	No
Min distance	1
Max distance	1000
Comments:	623.024 reads were not mapped Word size: 40 Bubble size: 250 Estimated paired distance range(s): ARA2_1 (paired): 235 to 666 bp
Originates from:	



ARA2\_1 (paired)