

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 00:56:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714235.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_ERR9714235 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714235.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 00:56:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714235.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	281,986
Mapped reads	21,963 / 7.79%
Unmapped reads	260,023 / 92.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	654 / 0.23%
Read min/max/mean length	30 / 151 / 57.59
Duplicated reads (estimated)	18,161 / 6.44%
Duplication rate	36.22%
Clipped reads	18,625 / 6.6%

2.2. ACGT Content

Number/percentage of A's	429,365 / 19.75%
Number/percentage of C's	297,497 / 13.69%
Number/percentage of T's	386,517 / 17.78%
Number/percentage of G's	1,059,961 / 48.77%
Number/percentage of N's	123 / 0.01%
GC Percentage	62.46%

2.3. Coverage

Mean	0.0007

Standard Deviation	0.8824
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2.4. Mapping Quality

Mean Mapping Quality	33.64
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2.5. Mismatches and indels

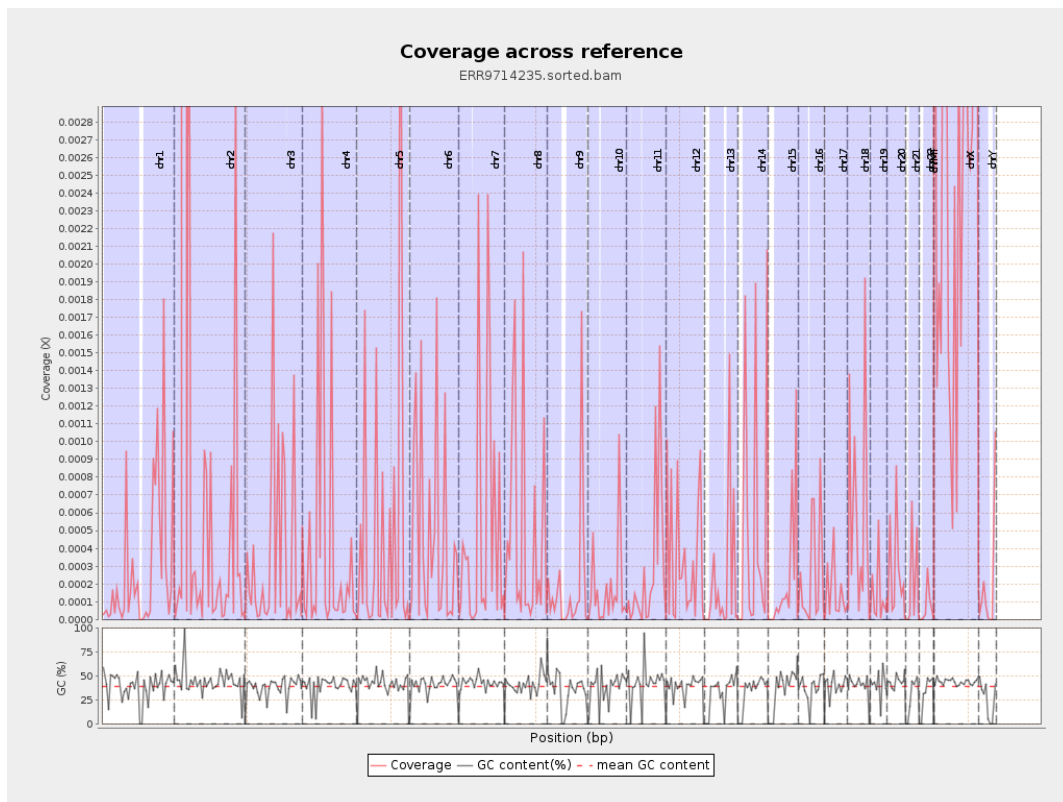
General error rate	3.58%
Mismatches	67,966
Insertions	2,149
Mapped reads with at least one insertion	8.2%
Deletions	4,916
Mapped reads with at least one deletion	20.72%
Homopolymer indels	34.39%

2.6. Chromosome stats

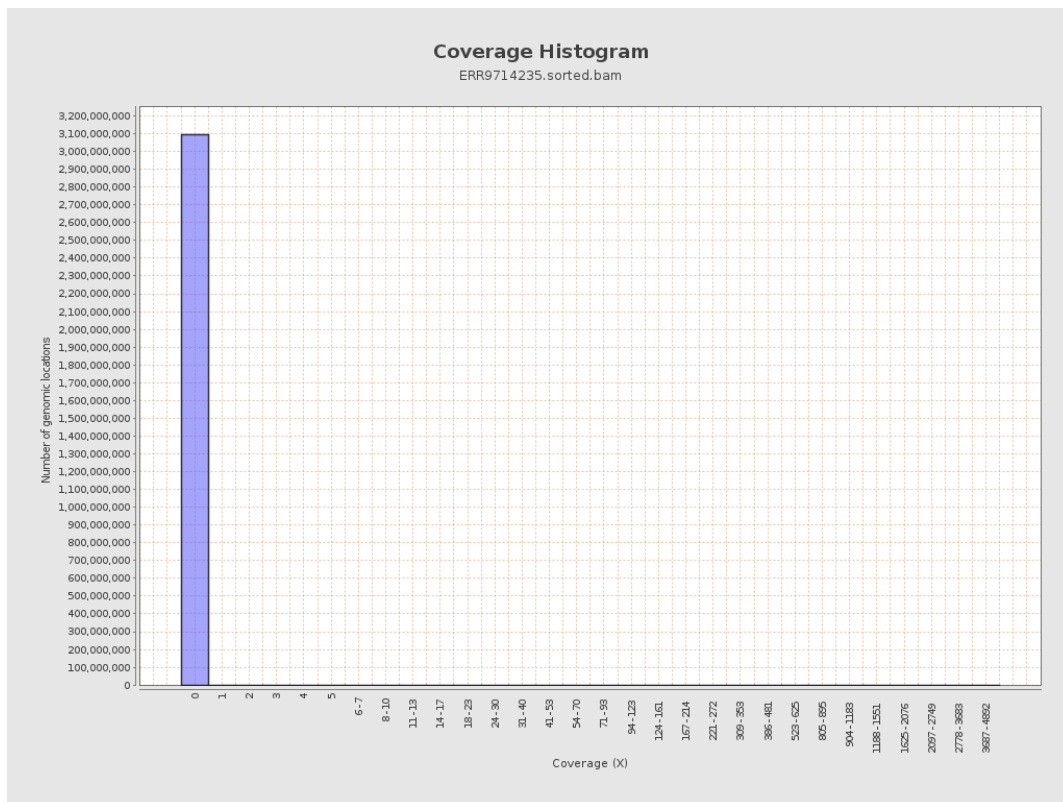
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	74289	0.0003	0.1047
chr2	243199373	874147	0.0036	3.1052
chr3	198022430	72283	0.0004	0.1339
chr4	191154276	77315	0.0004	0.1758
chr5	180915260	89513	0.0005	0.2357
chr6	171115067	81482	0.0005	0.1494
chr7	159138663	79678	0.0005	0.1983

chr8	146364022	70278	0.0005	0.1545
chr9	141213431	26998	0.0002	0.0692
chr10	135534747	21718	0.0002	0.0552
chr11	135006516	39334	0.0003	0.0787
chr12	133851895	46095	0.0003	0.0885
chr13	115169878	23576	0.0002	0.0962
chr14	107349540	55766	0.0005	0.1467
chr15	102531392	23187	0.0002	0.0766
chr16	90354753	22310	0.0002	0.0706
chr17	81195210	12739	0.0002	0.0498
chr18	78077248	47523	0.0006	0.1579
chr19	59128983	8347	0.0001	0.0392
chr20	63025520	17365	0.0003	0.0701
chr21	48129895	9766	0.0002	0.0726
chr22	51304566	3664	0.0001	0.0194
chrMT	16571	8502	0.5131	4.7581
chrX	155270560	406215	0.0026	0.3488
chrY	59373566	11498	0.0002	0.0303

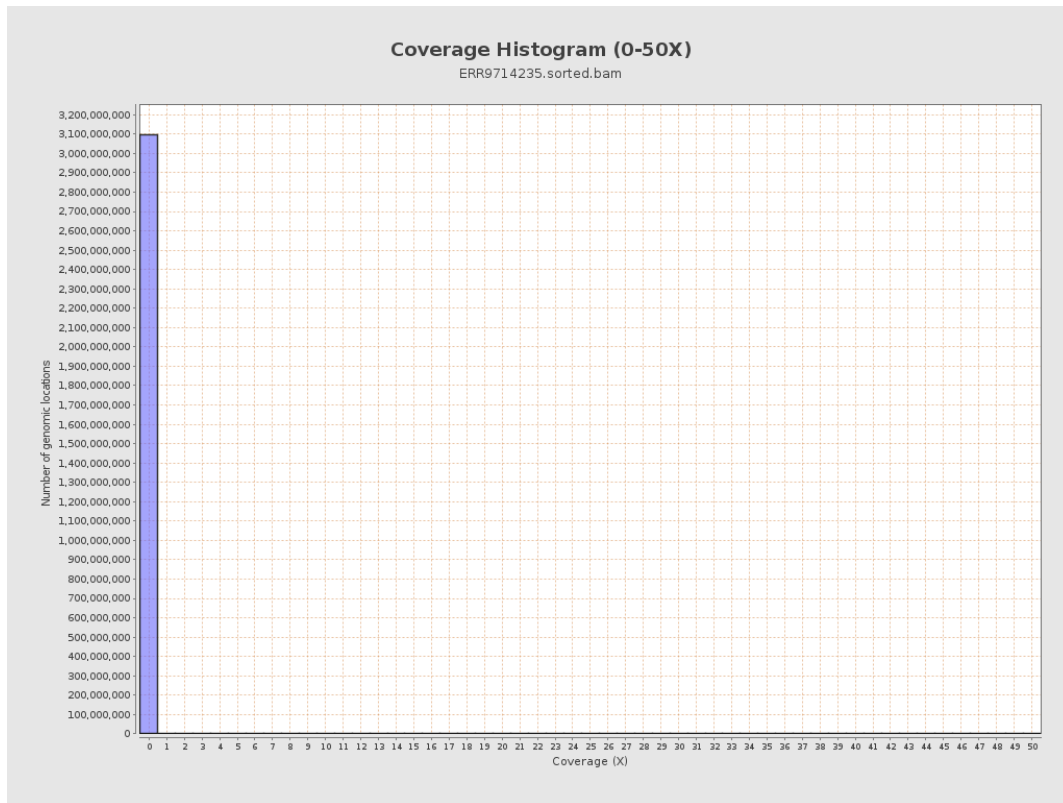
3. Results : Coverage across reference



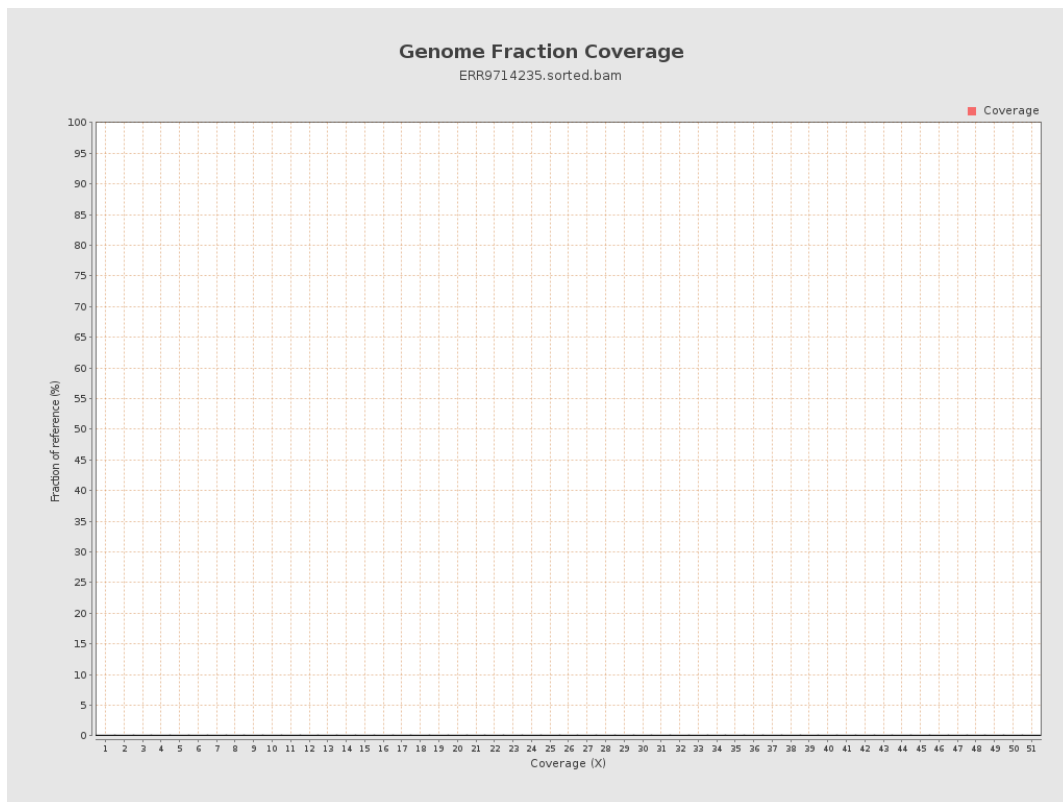
4. Results : Coverage Histogram



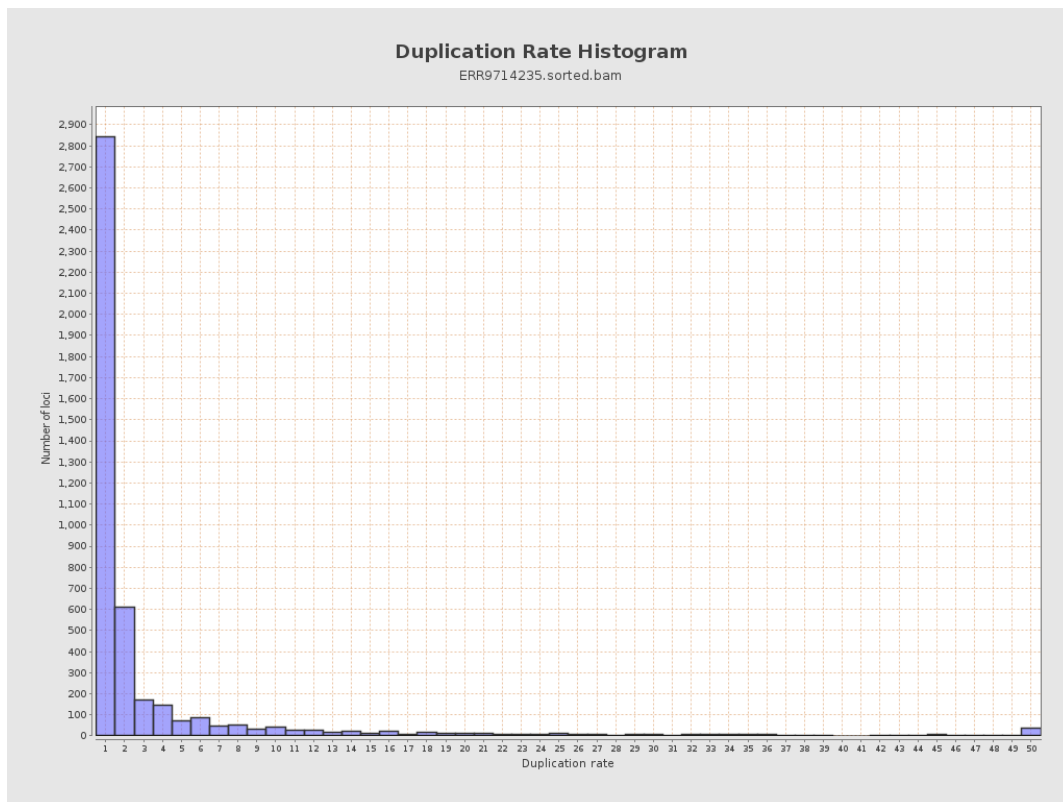
5. Results : Coverage Histogram (0-50X)



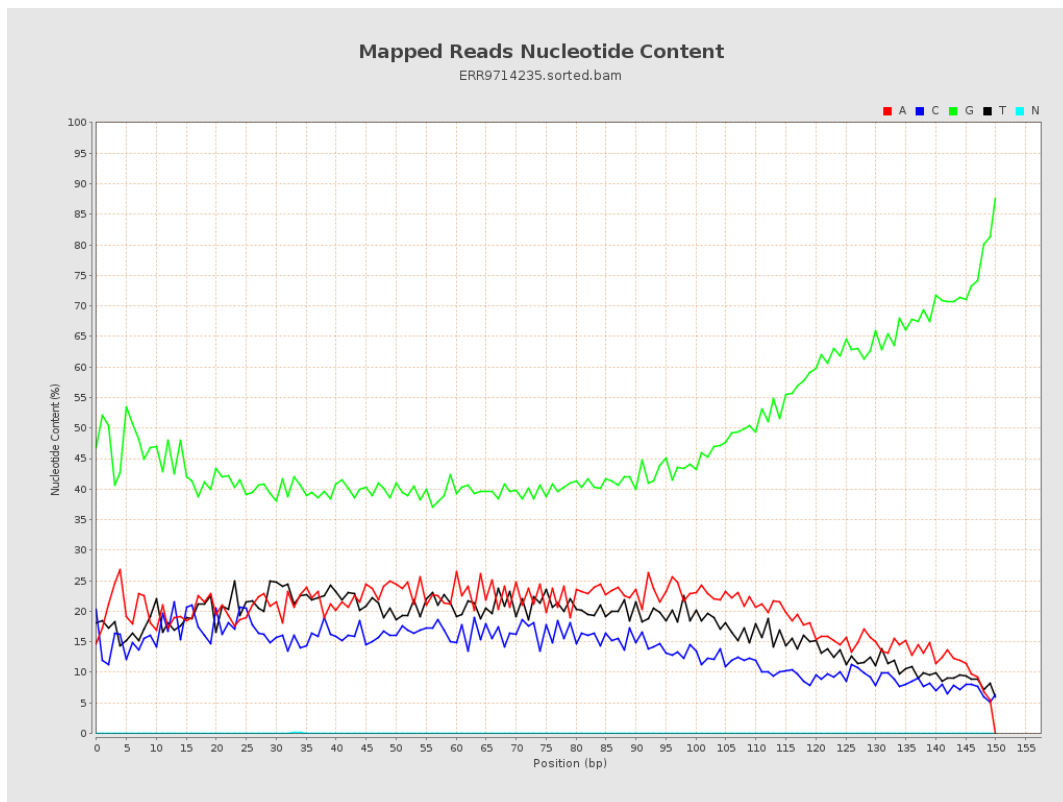
6. Results : Genome Fraction Coverage



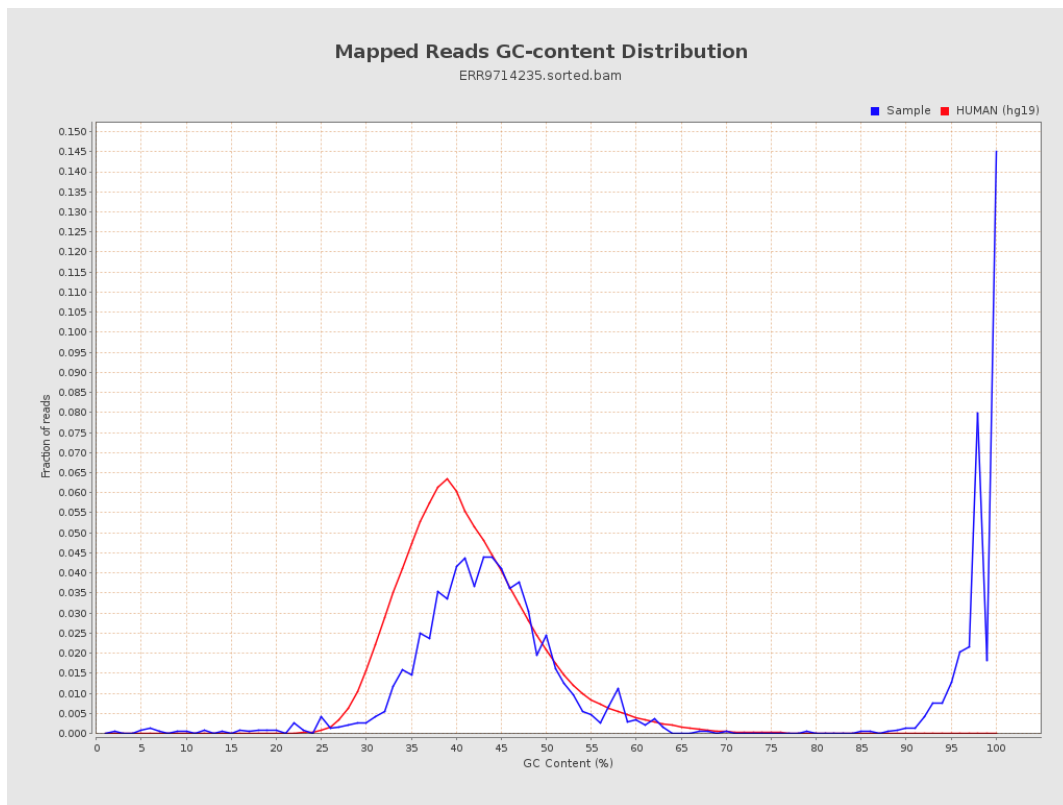
7. Results : Duplication Rate Histogram



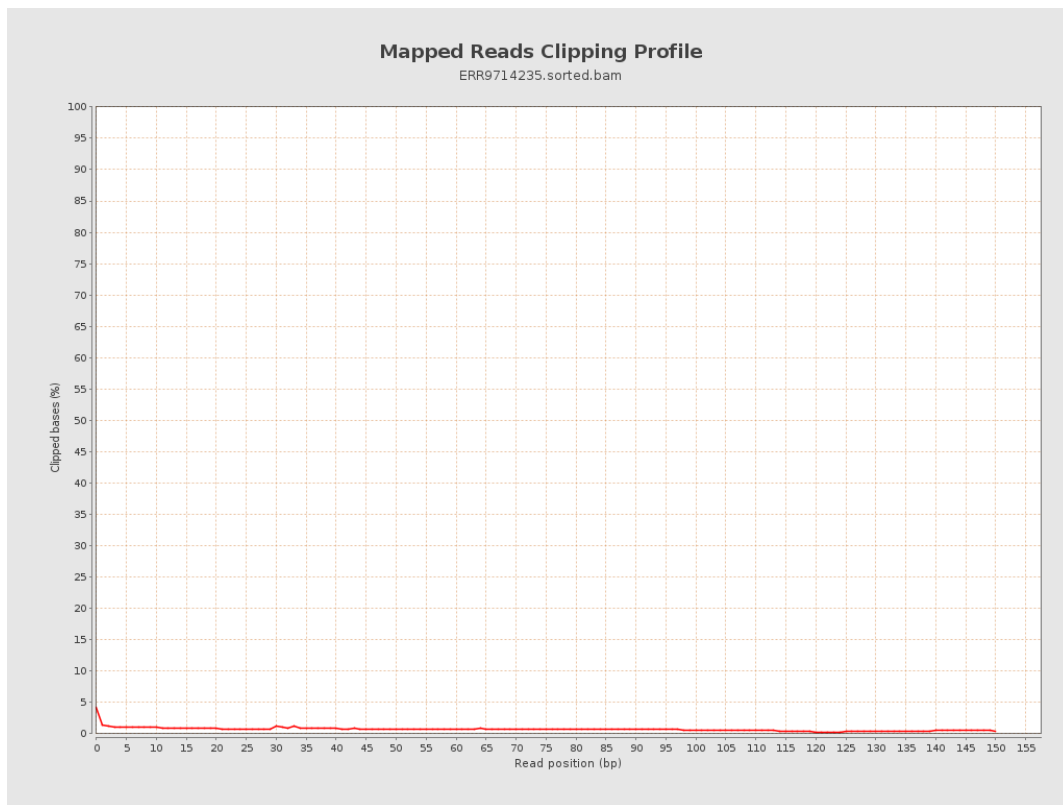
8. Results : Mapped Reads Nucleotide Content



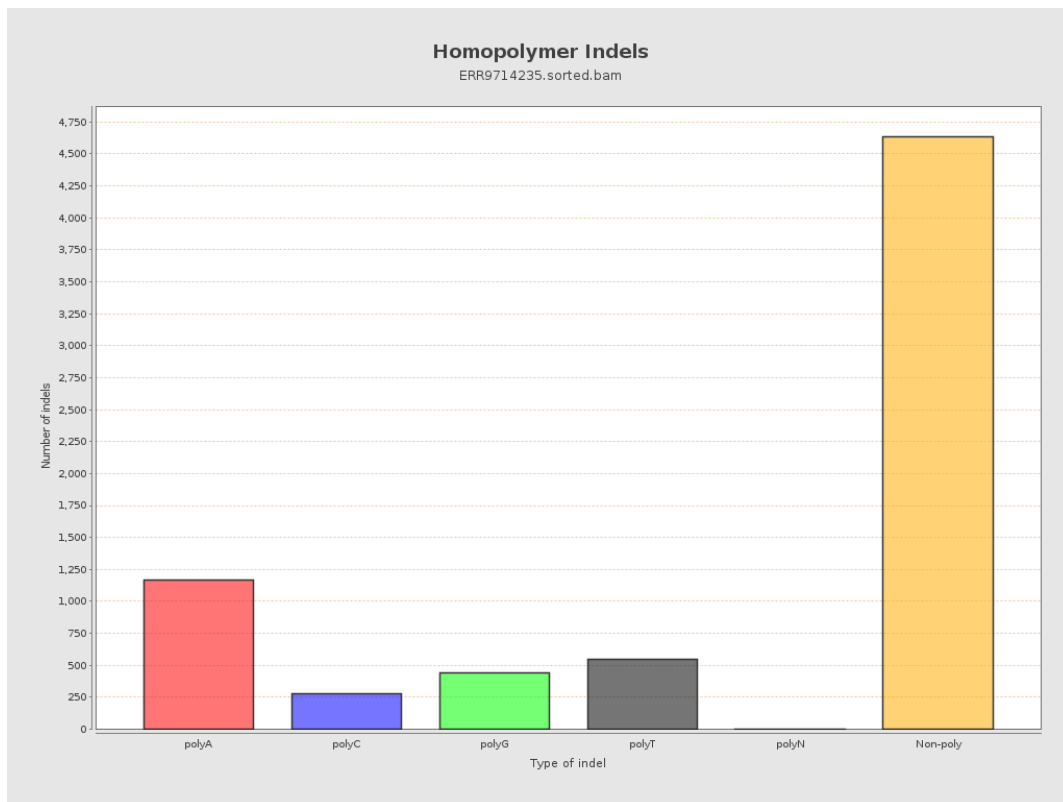
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

