Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 00:19:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714212.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_ERR9714212 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714212.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 00:19:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714212.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	146,024
Mapped reads	10,429 / 7.14%
Unmapped reads	135,595 / 92.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	279 / 0.19%
Read min/max/mean length	30 / 151 / 58.01
Duplicated reads (estimated)	8,687 / 5.95%
Duplication rate	38.5%
Clipped reads	8,699 / 5.96%

2.2. ACGT Content

Number/percentage of A's	168,936 / 17.71%
Number/percentage of C's	114,678 / 12.02%
Number/percentage of T's	149,380 / 15.66%
Number/percentage of G's	521,052 / 54.61%
Number/percentage of N's	17 / 0%
GC Percentage	66.63%

2.3. Coverage

Mean	0.0003

Standard Deviation	0.4712

2.4. Mapping Quality

Mean Mapping Quality	22.44

2.5. Mismatches and indels

General error rate	3.74%
Mismatches	31,077
Insertions	962
Mapped reads with at least one insertion	7.55%
Deletions	1,738
Mapped reads with at least one deletion	16.19%
Homopolymer indels	33.44%

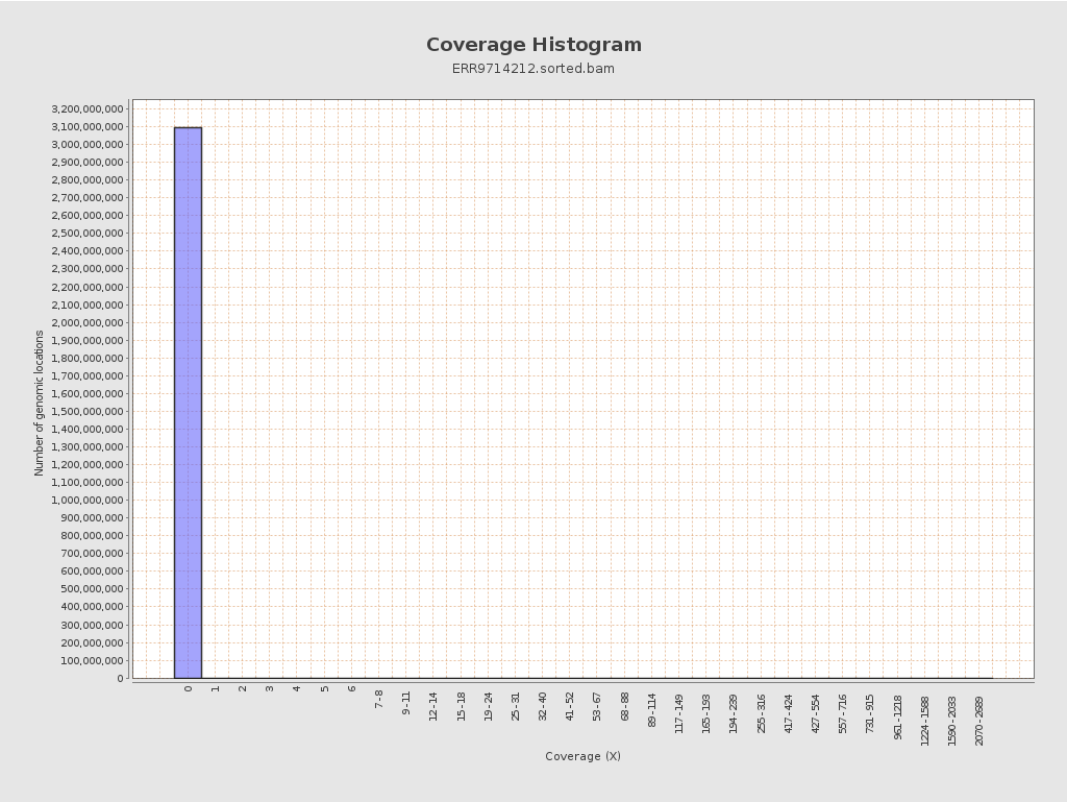
2.6. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	19553	0.0001	0.0337
chr2	243199373	438017	0.0018	1.6546
chr3	198022430	28883	0.0001	0.0562
chr4	191154276	9331	0	0.017
chr5	180915260	23876	0.0001	0.0999
chr6	171115067	35458	0.0002	0.1185
chr7	159138663	49866	0.0003	0.1274

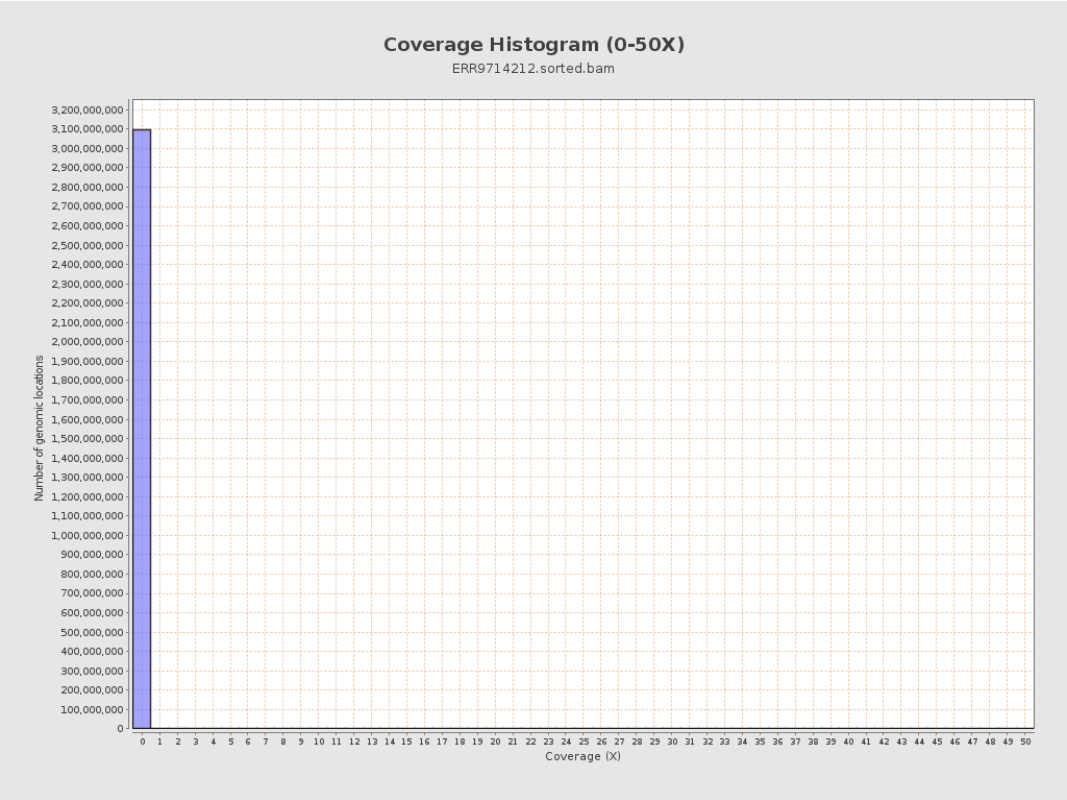
chr8	146364022	25420	0.0002	0.0619
chr9	141213431	15800	0.0001	0.0514
chr10	135534747	22214	0.0002	0.0936
chr11	135006516	25490	0.0002	0.082
chr12	133851895	40824	0.0003	0.1213
chr13	115169878	4045	0	0.014
chr14	107349540	3745	0	0.0201
chr15	102531392	7445	0.0001	0.0215
chr16	90354753	9457	0.0001	0.0728
chr17	81195210	9059	0.0001	0.0433
chr18	78077248	6939	0.0001	0.0434
chr19	59128983	1317	0	0.0056
chr20	63025520	18256	0.0003	0.1107
chr21	48129895	899	0	0.0055
chr22	51304566	3311	0.0001	0.0216
chrMT	16571	592	0.0357	0.3029
chrX	155270560	163161	0.0011	0.2101
chrY	59373566	6255	0.0001	0.0433

3. Results : Coverage across reference

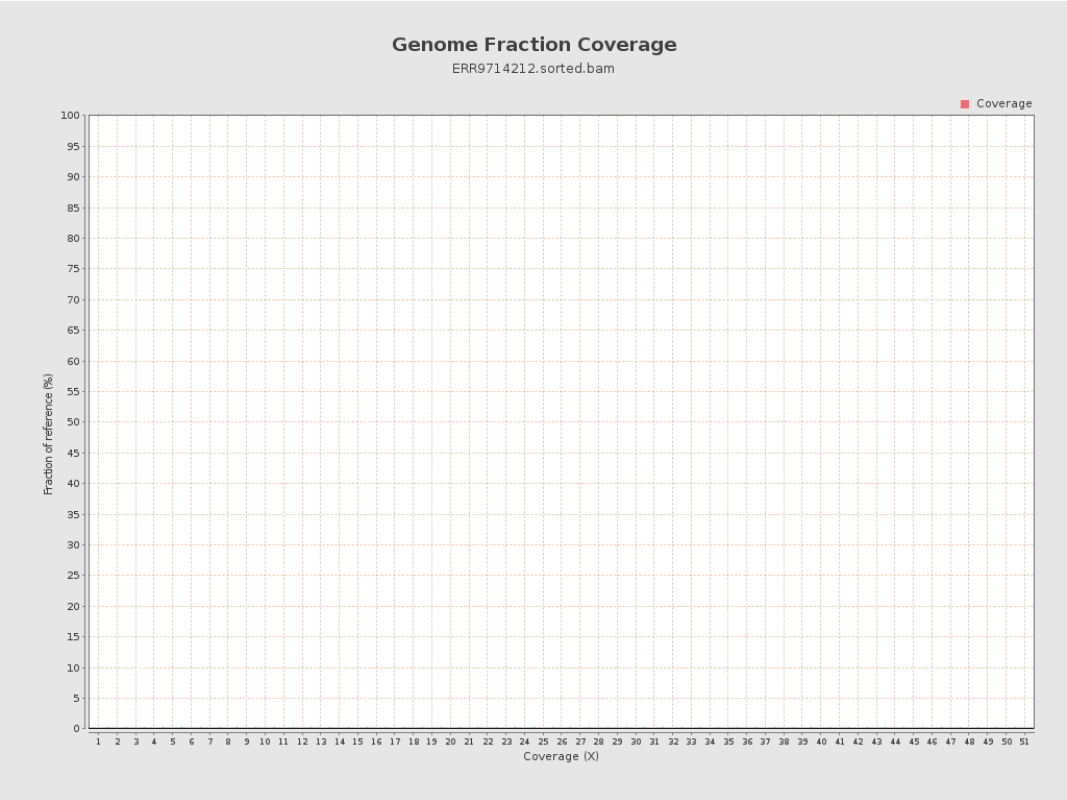
4. Results : Coverage Histogram



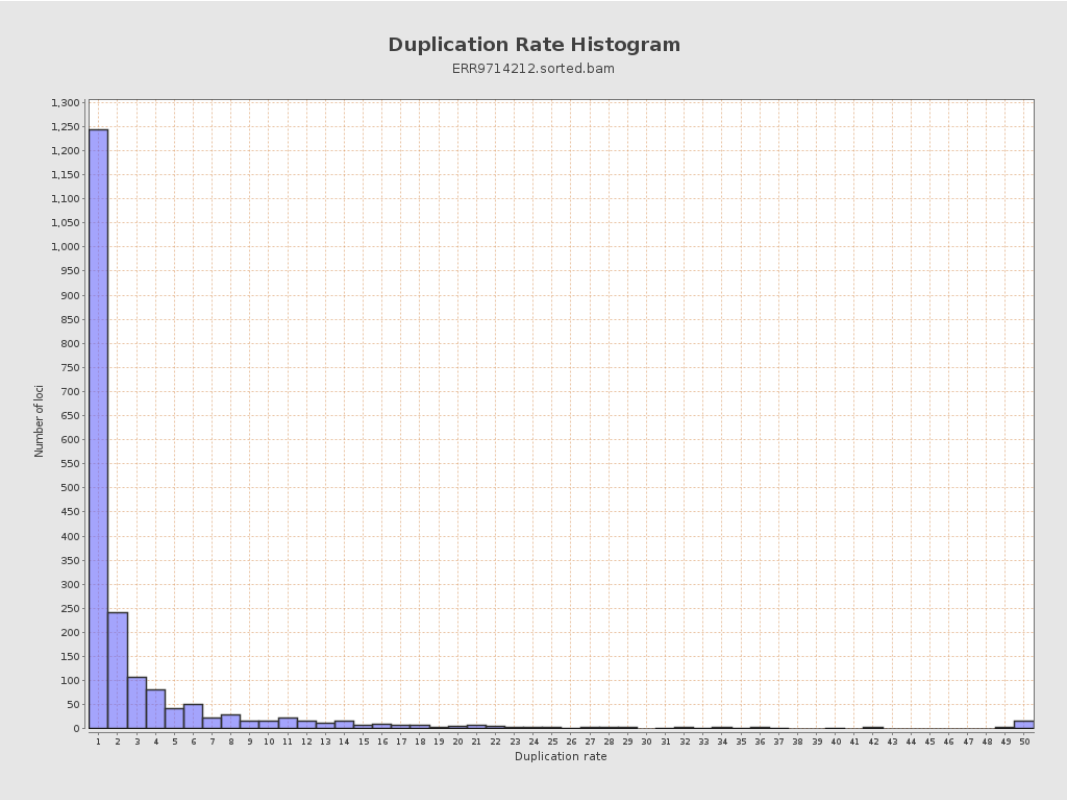
5. Results : Coverage Histogram (0-50X)



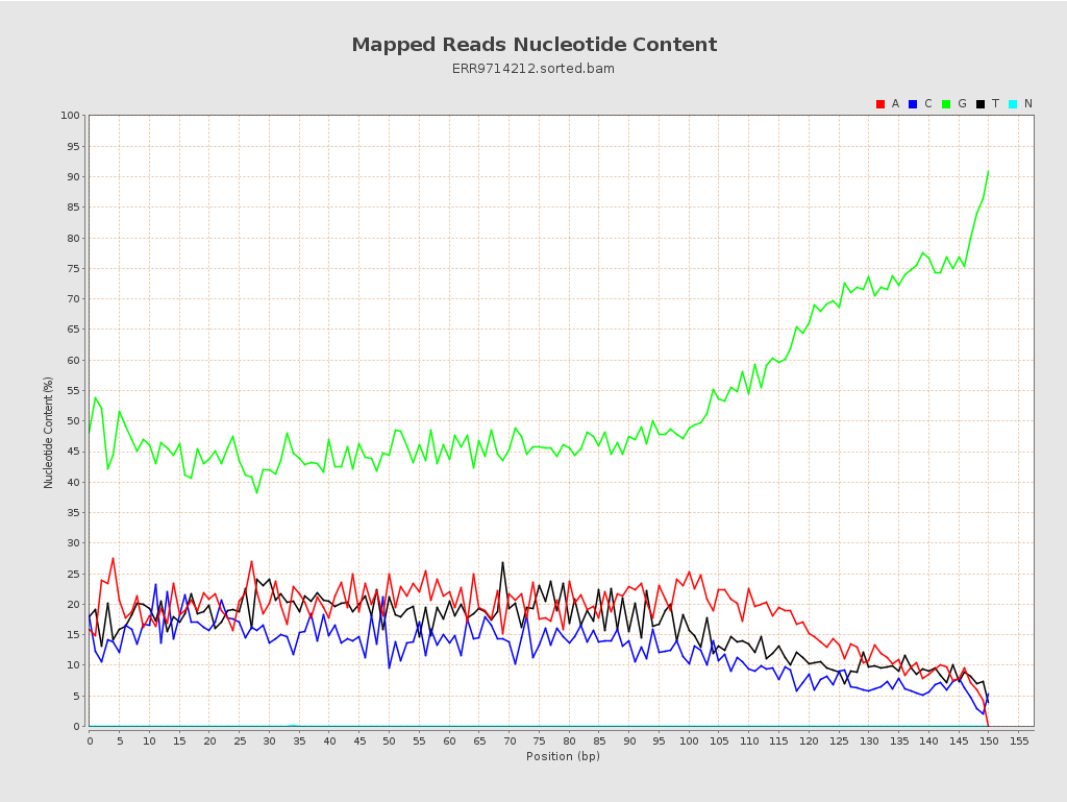
6. Results : Genome Fraction Coverage



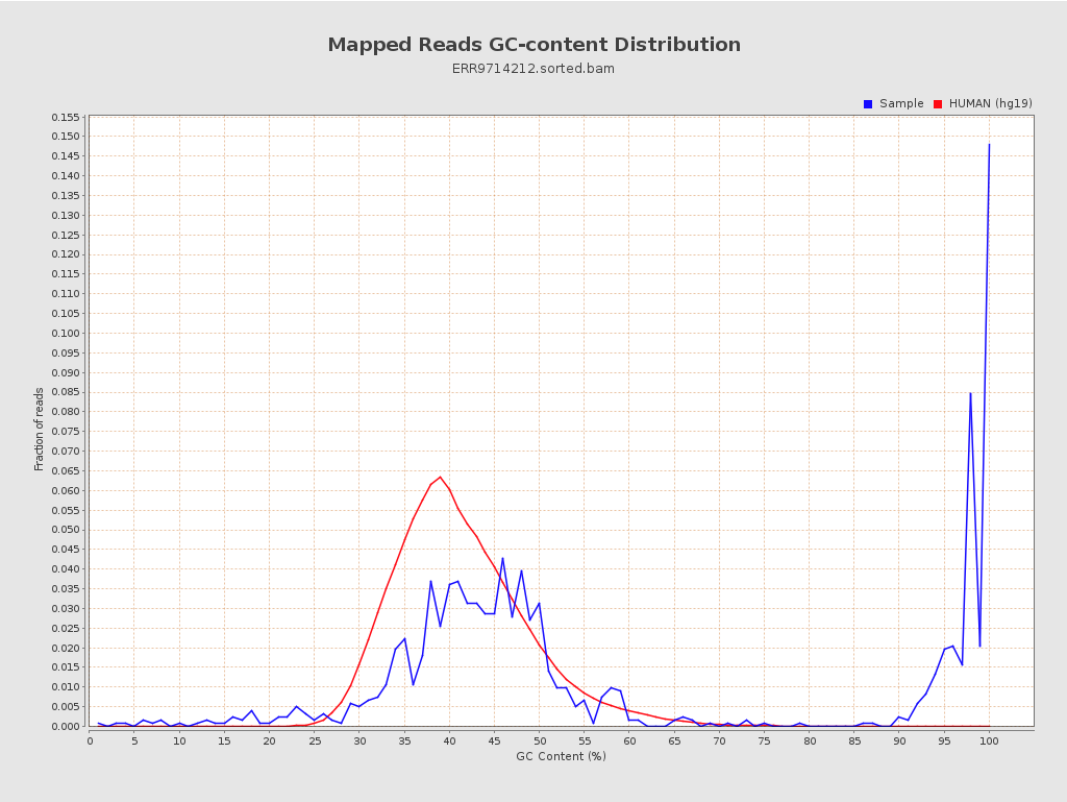
7. Results : Duplication Rate Histogram



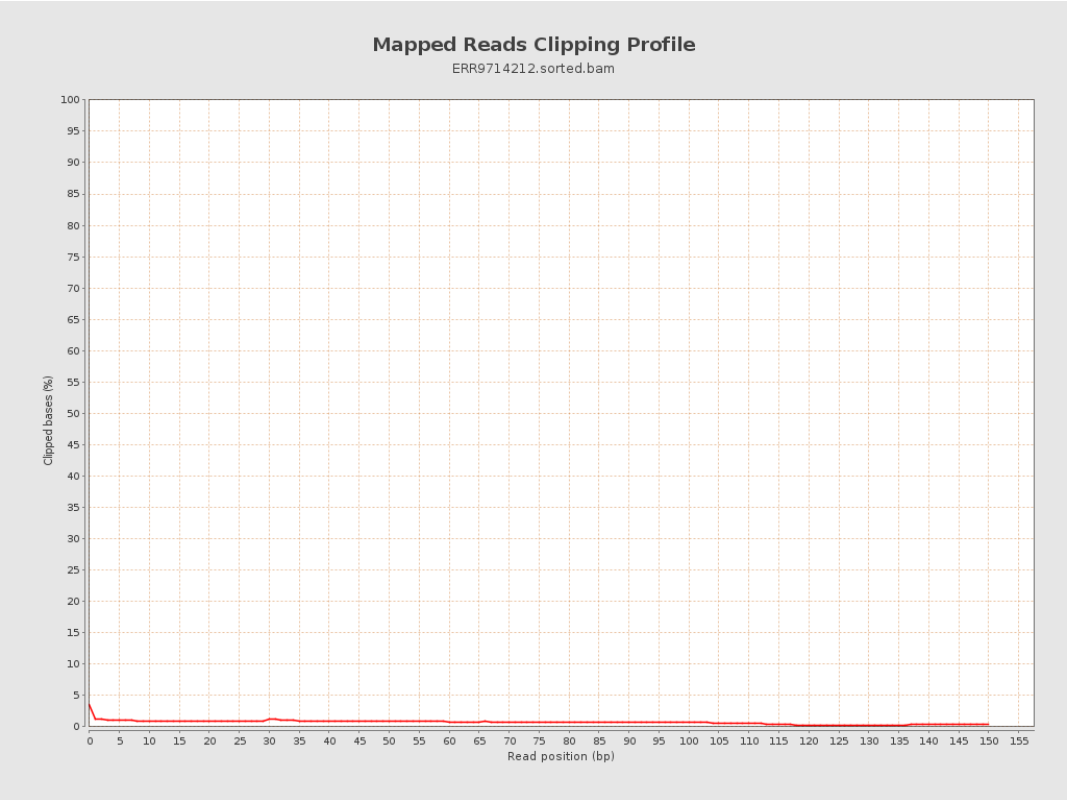
8. Results : Mapped Reads Nucleotide Content



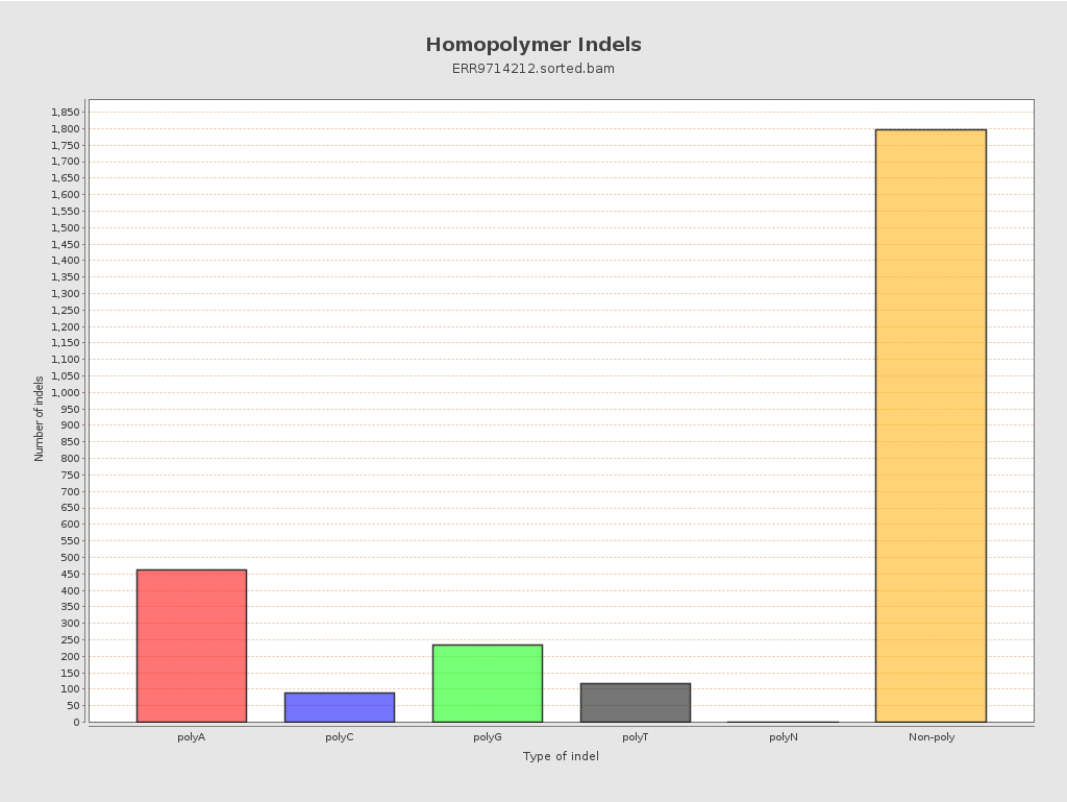
9. Results : Mapped Reads GC-content Distribution



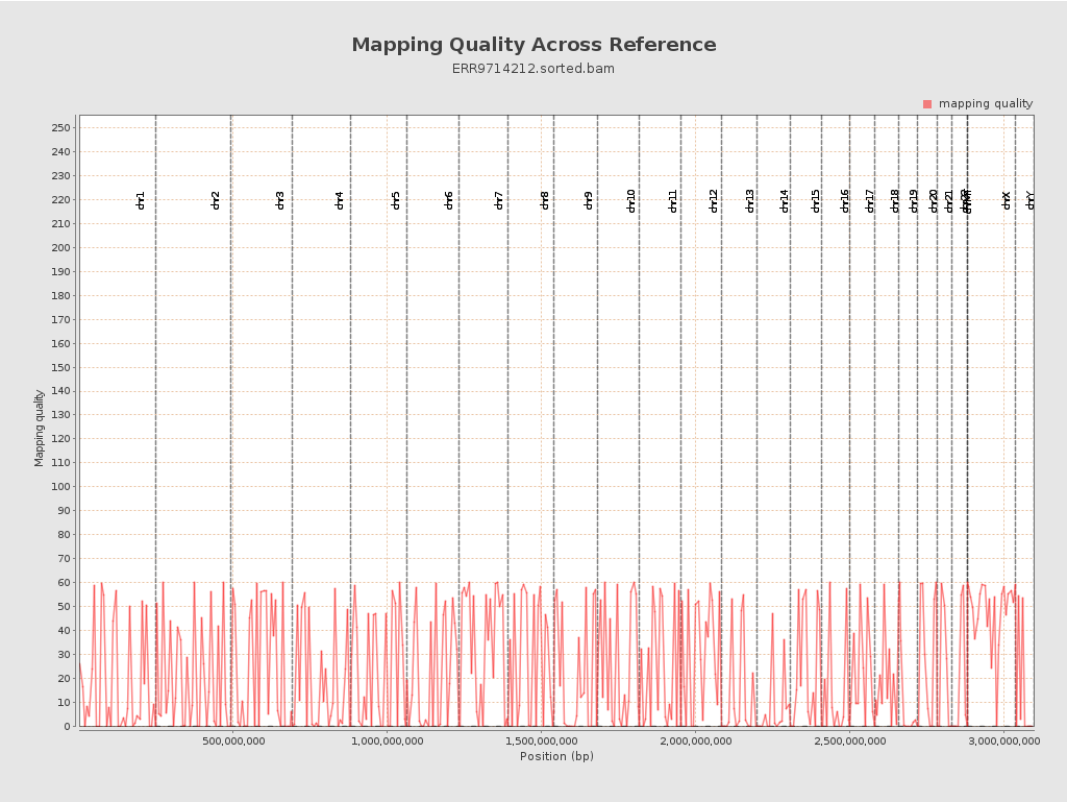
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram