Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 18:04:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714068.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_ERR9714068 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714068.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 18:04:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714068.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,786
Mapped reads	8,159 / 69.23%
Unmapped reads	3,627 / 30.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	149 / 1.26%
Read min/max/mean length	30 / 151 / 123.56
Duplicated reads (estimated)	6,422 / 54.49%
Duplication rate	37.27%
Clipped reads	7,504 / 63.67%

2.2. ACGT Content

Number/percentage of A's	281,558 / 27.55%
Number/percentage of C's	201,853 / 19.75%
Number/percentage of T's	266,906 / 26.12%
Number/percentage of G's	271,692 / 26.58%
Number/percentage of N's	8 / 0%
GC Percentage	46.33%

2.3. Coverage

Mean	0.0003

Standard Deviation	0.157

2.4. Mapping Quality

Mean Mapping Quality	27.54

2.5. Mismatches and indels

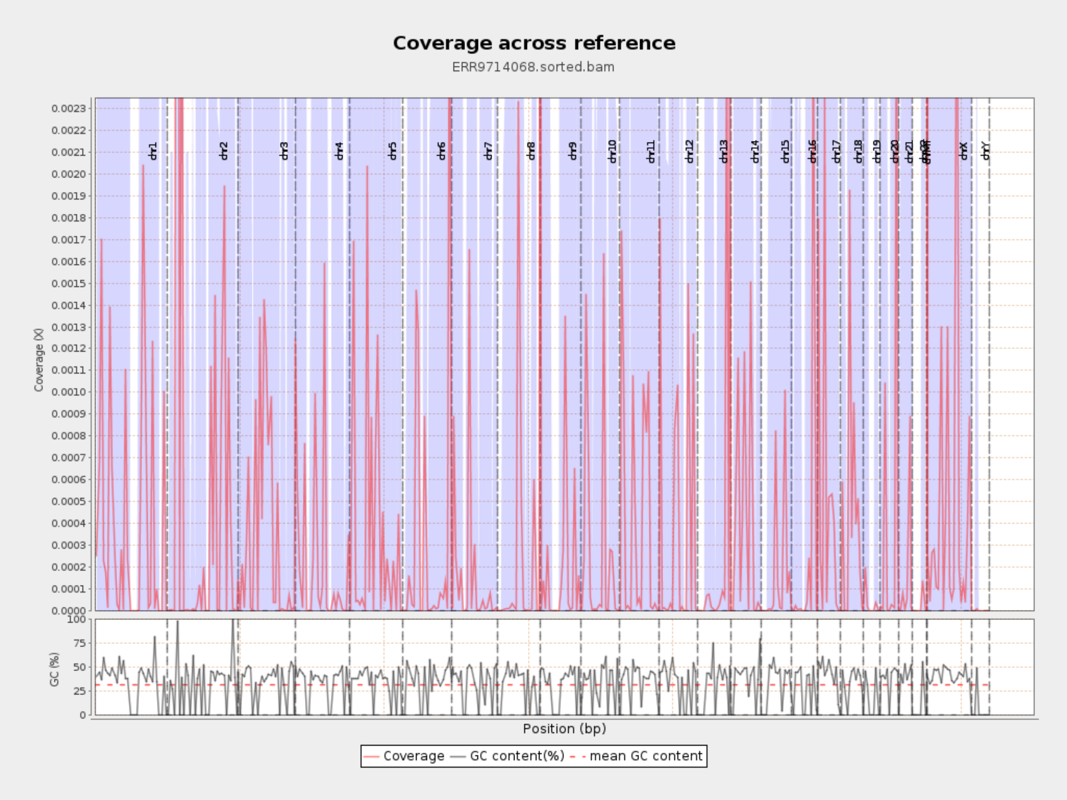
General error rate	4.59%
Mismatches	42,996
Insertions	1,251
Mapped reads with at least one insertion	14.95%
Deletions	3,930
Mapped reads with at least one deletion	44.98%
Homopolymer indels	30.13%

2.6. Chromosome stats

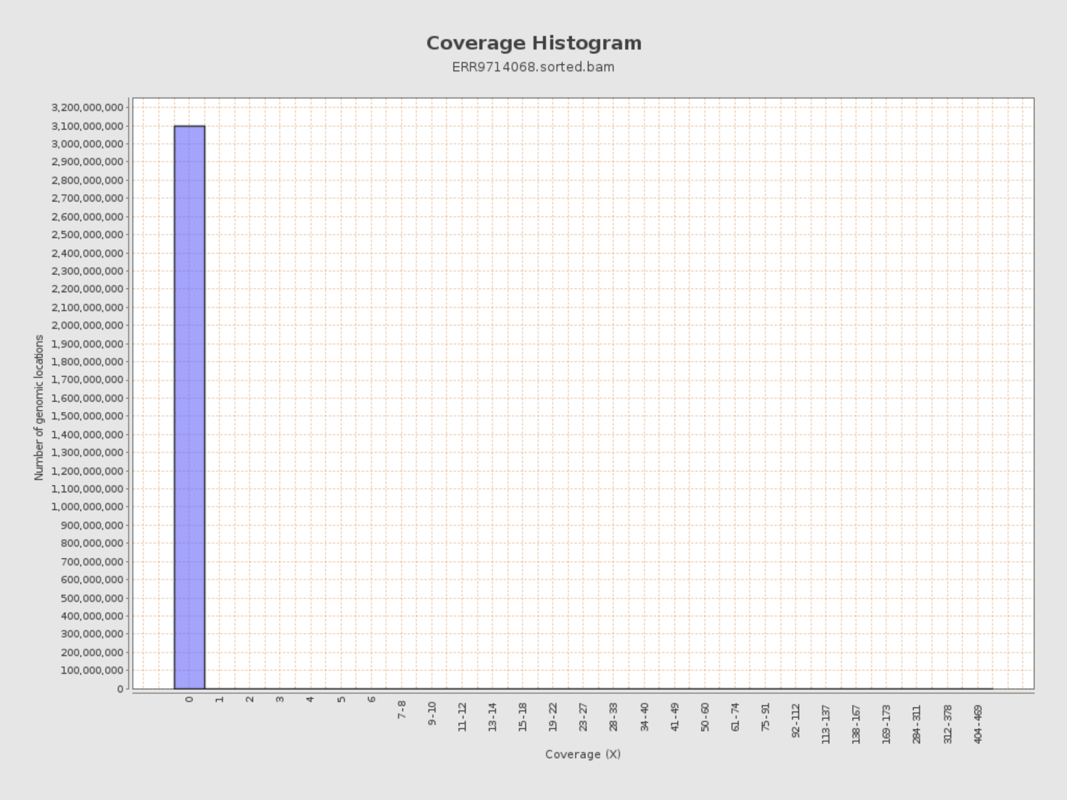
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	100093	0.0004	0.1401
chr2	243199373	151908	0.0006	0.3358
chr3	198022430	70916	0.0004	0.121
chr4	191154276	47089	0.0002	0.1019
chr5	180915260	70089	0.0004	0.131
chr6	171115067	58353	0.0003	0.1822
chr7	159138663	27456	0.0002	0.0935

chr8	146364022	27223	0.0002	0.1203
chr9	141213431	29389	0.0002	0.0837
chr10	135534747	37462	0.0003	0.1069
chr11	135006516	58595	0.0004	0.1405
chr12	133851895	49423	0.0004	0.1389
chr13	115169878	29724	0.0003	0.1634
chr14	107349540	40009	0.0004	0.139
chr15	102531392	17828	0.0002	0.0809
chr16	90354753	23517	0.0003	0.1312
chr17	81195210	45095	0.0006	0.2005
chr18	78077248	37935	0.0005	0.167
chr19	59128983	1968	0	0.0145
chr20	63025520	33942	0.0005	0.1978
chr21	48129895	8038	0.0002	0.0766
chr22	51304566	1063	0	0.0116
chrMT	16571	5243	0.3164	1.8019
chrX	155270560	72610	0.0005	0.1471
chrY	59373566	64	0	0.001

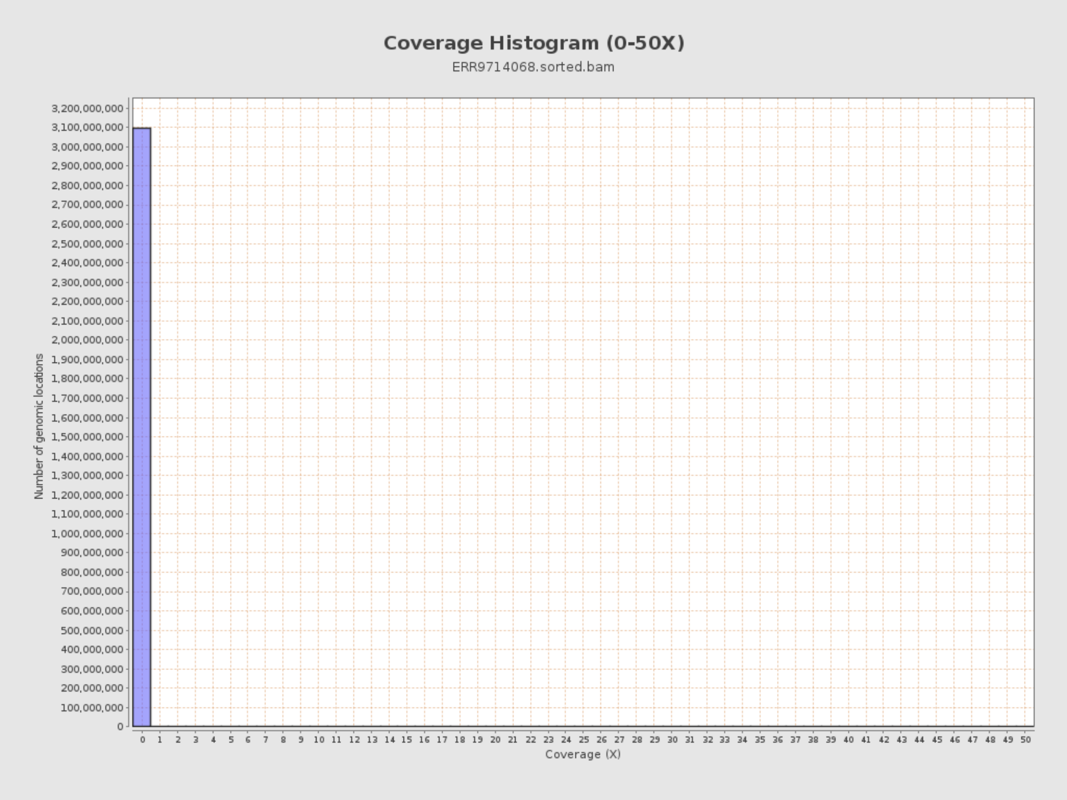
3. Results : Coverage across reference



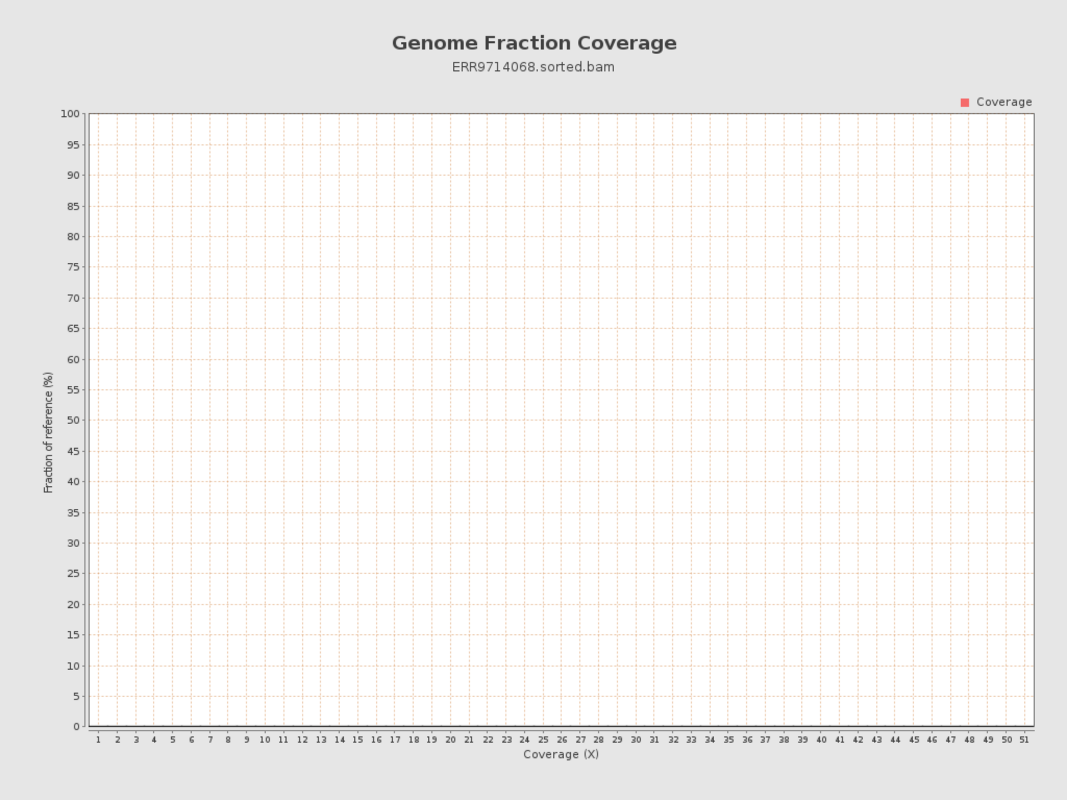
4. Results : Coverage Histogram



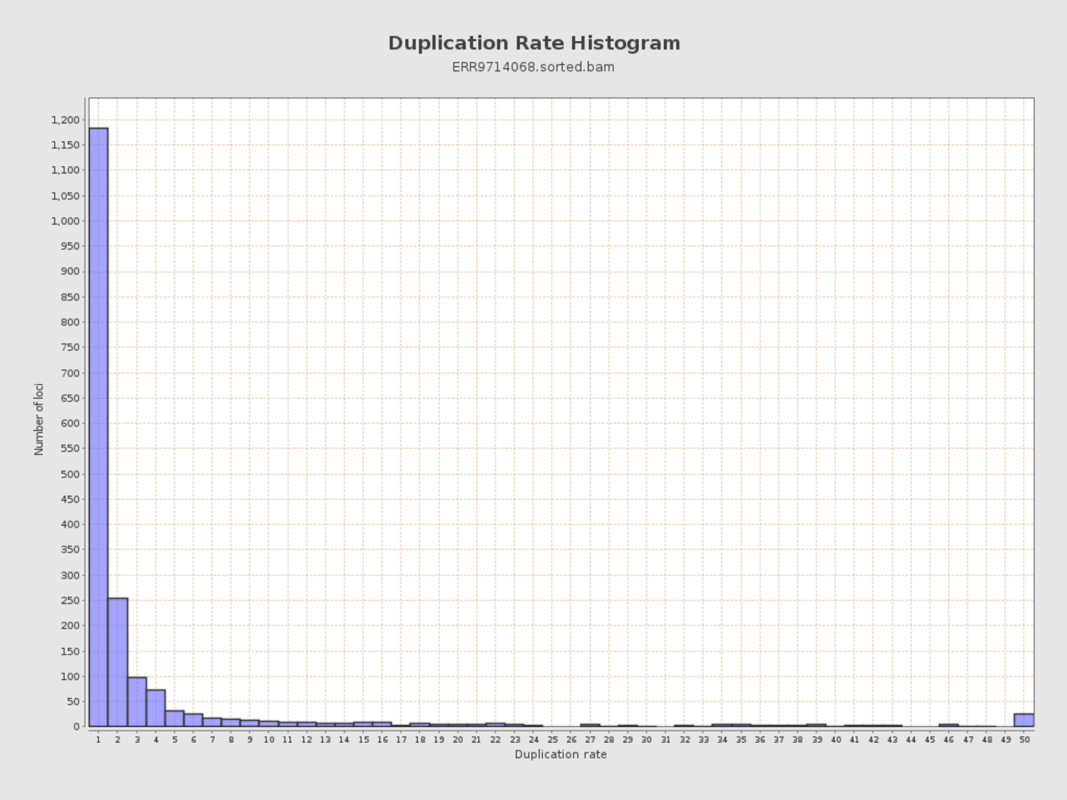
5. Results : Coverage Histogram (0-50X)



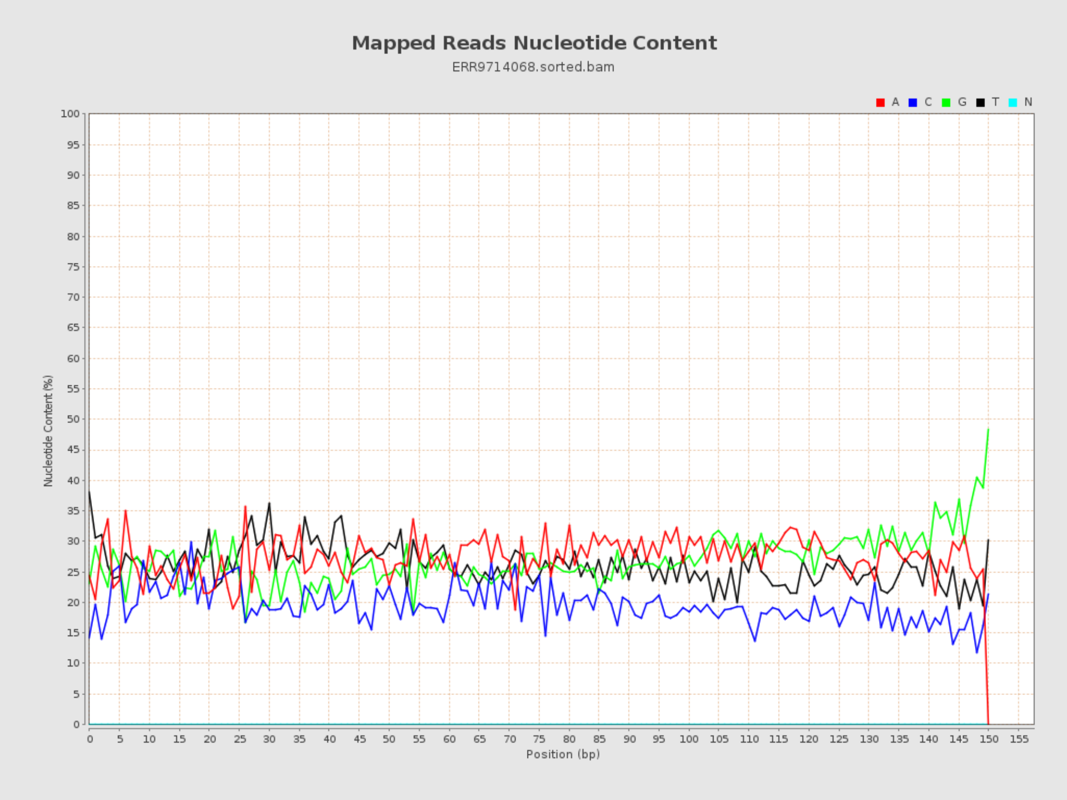
6. Results : Genome Fraction Coverage



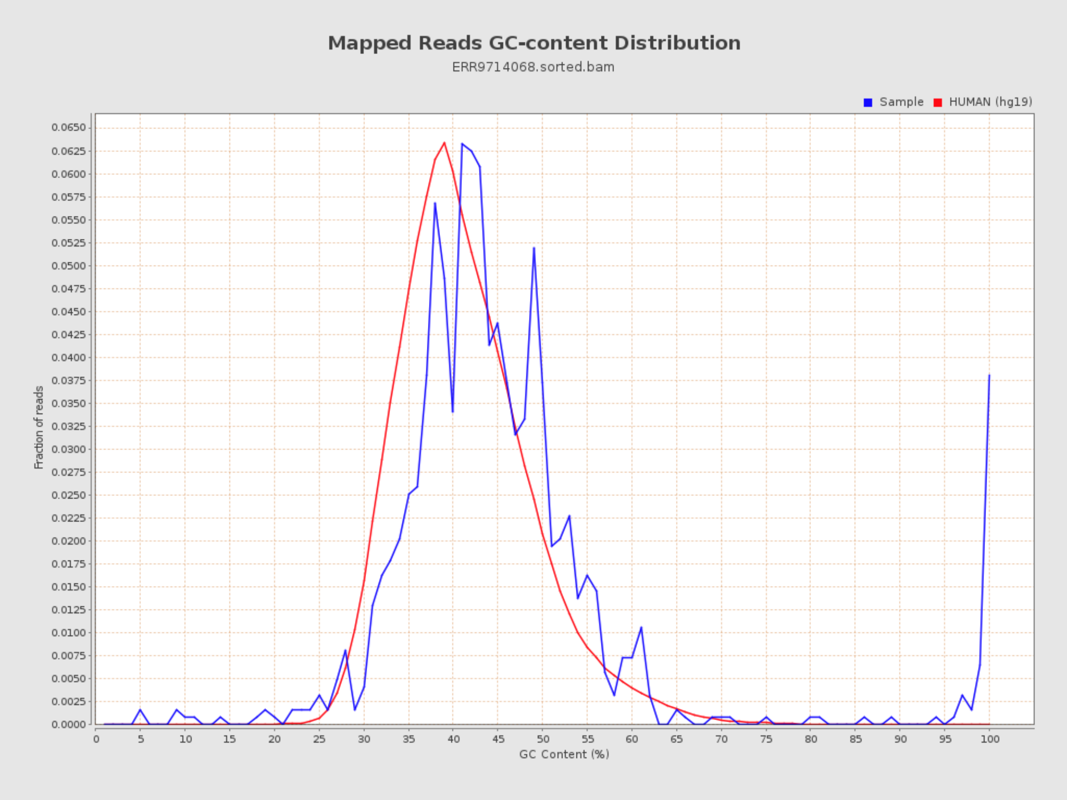
7. Results : Duplication Rate Histogram



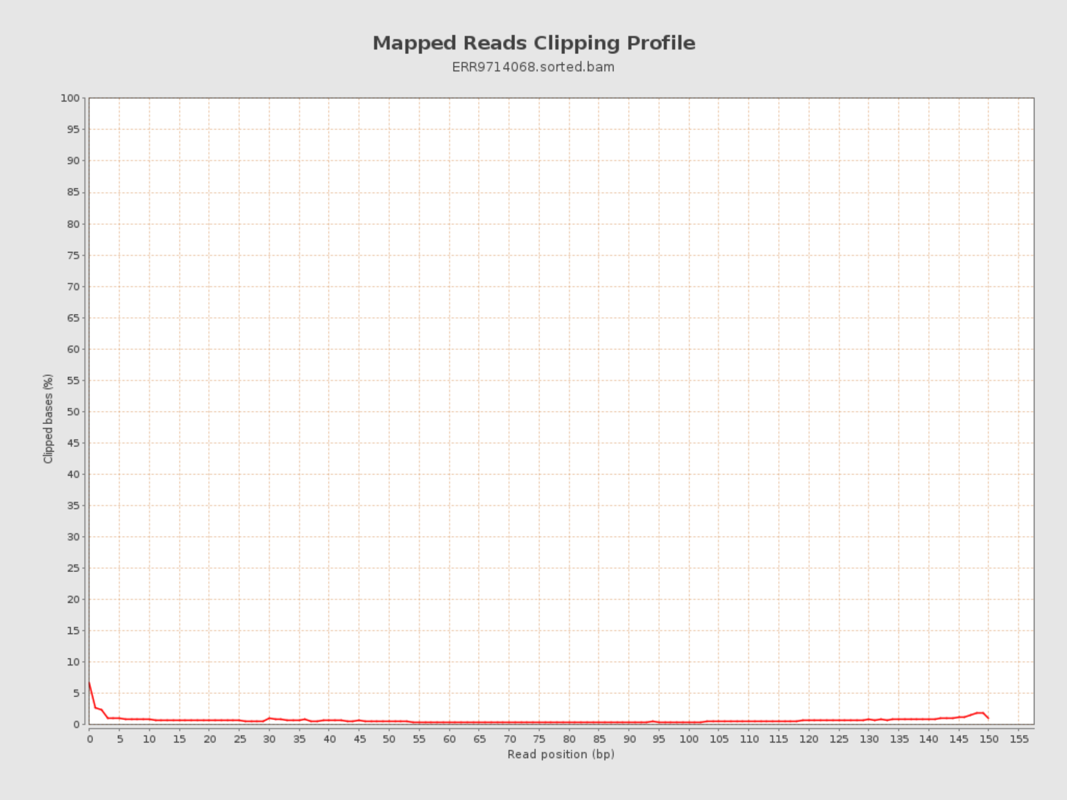
8. Results : Mapped Reads Nucleotide Content



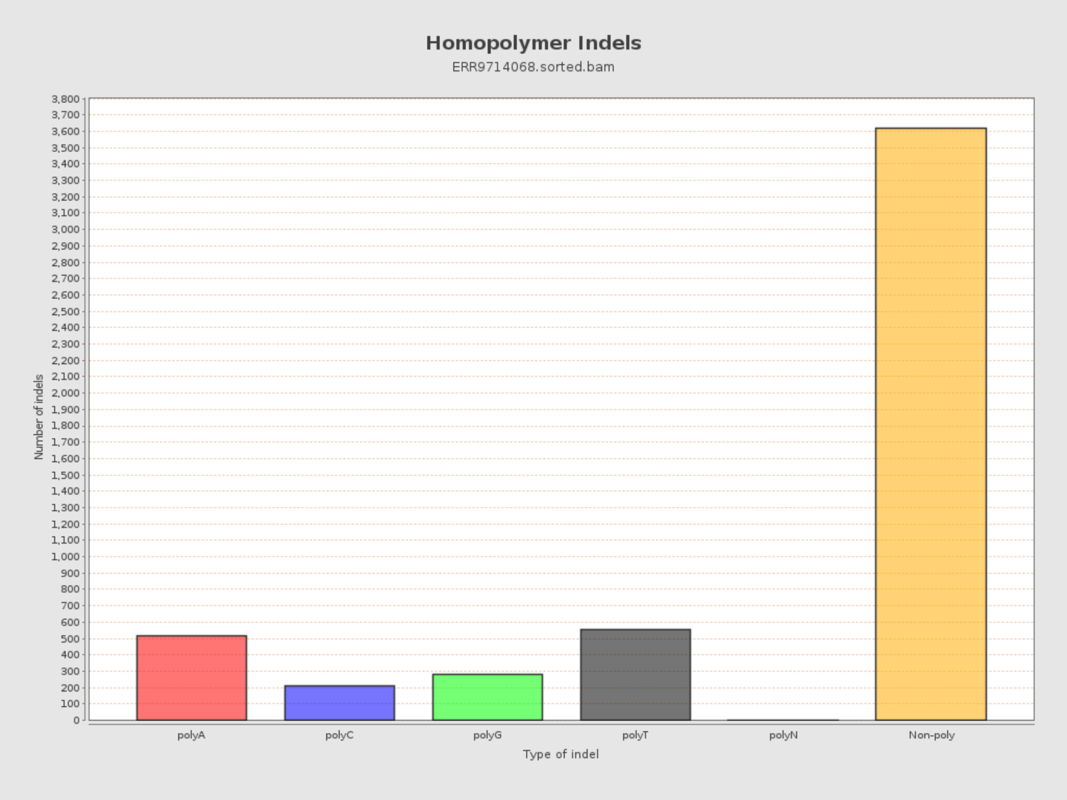
9. Results : Mapped Reads GC-content Distribution



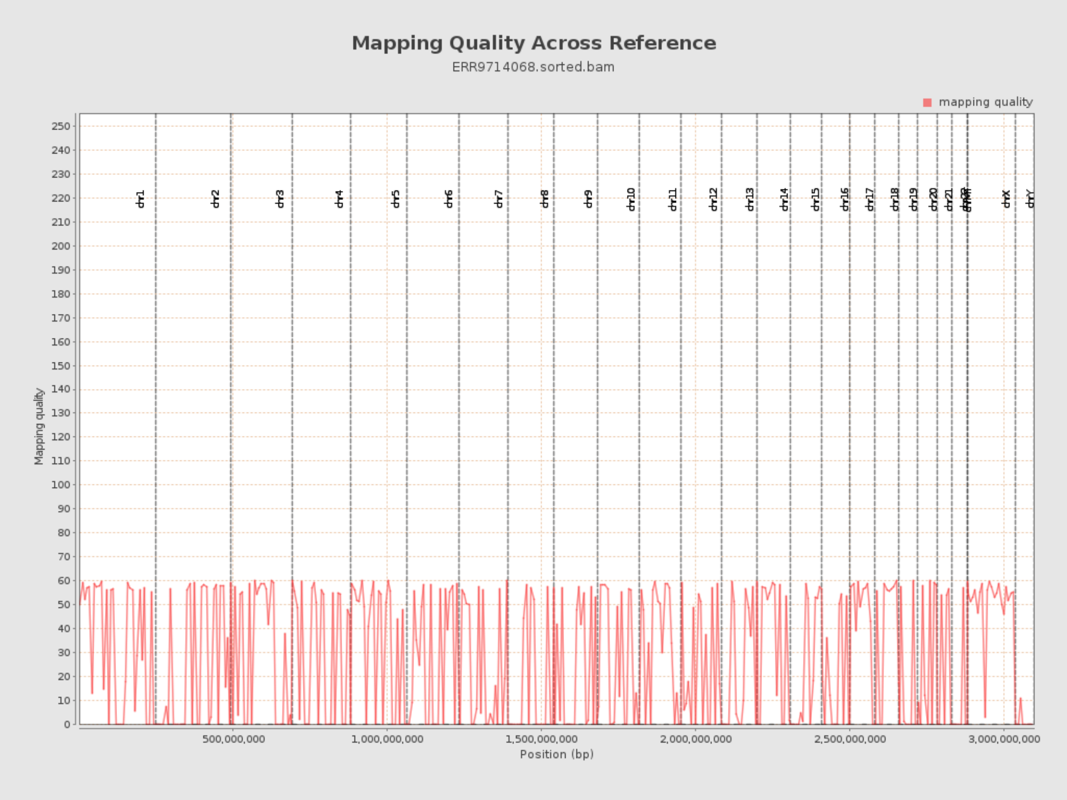
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram