Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 17:54:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714063.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_ERR9714063 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714063.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 17:54:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714063.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	570,468
Mapped reads	83,216 / 14.59%
Unmapped reads	487,252 / 85.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,541 / 0.27%
Read min/max/mean length	30 / 151 / 60.13
Duplicated reads (estimated)	82,232 / 14.41%
Duplication rate	28.16%
Clipped reads	43,744 / 7.67%

2.2. ACGT Content

Number/percentage of A's	153,040 / 1.78%
Number/percentage of C's	47,792 / 0.56%
Number/percentage of T's	52,389 / 0.61%
Number/percentage of G's	8,337,991 / 97.05%
Number/percentage of N's	200 / 0%
GC Percentage	97.61%

2.3. Coverage

Mean	0.0028

Standard Deviation	10.661

2.4. Mapping Quality

Mean Mapping Quality	7.41

2.5. Mismatches and indels

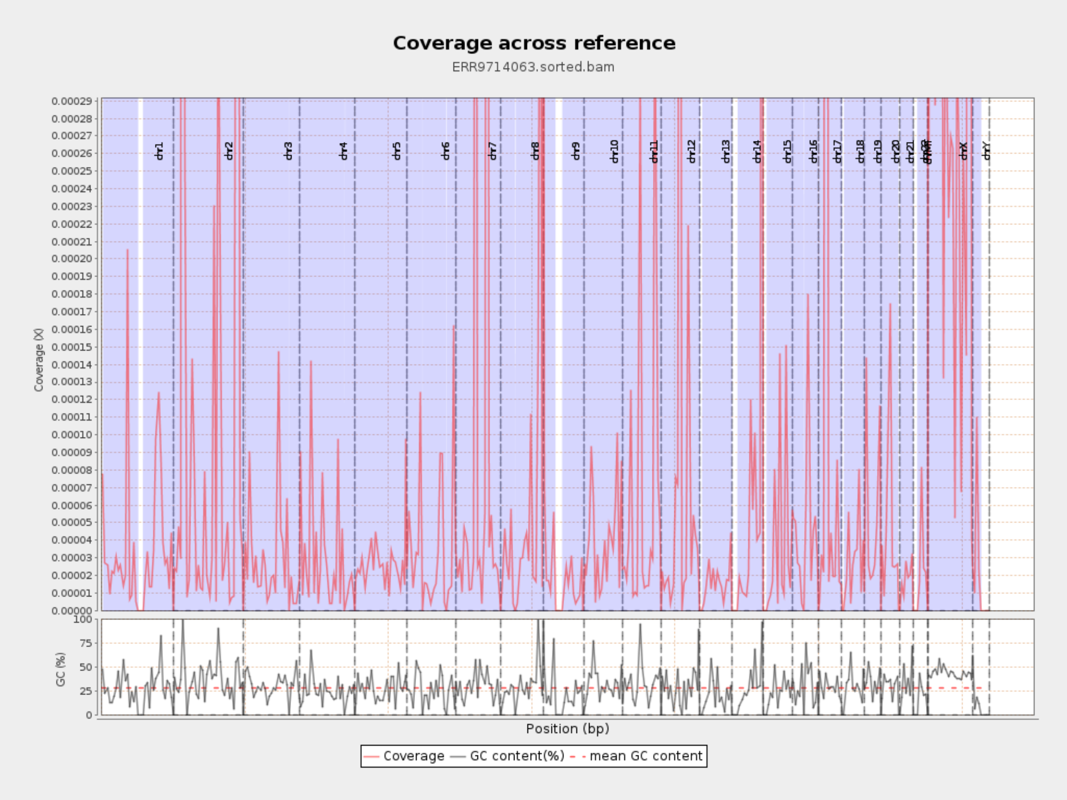
General error rate	3.27%
Mismatches	212,134
Insertions	9,880
Mapped reads with at least one insertion	8.4%
Deletions	4,031
Mapped reads with at least one deletion	4.66%
Homopolymer indels	63.76%

2.6. Chromosome stats

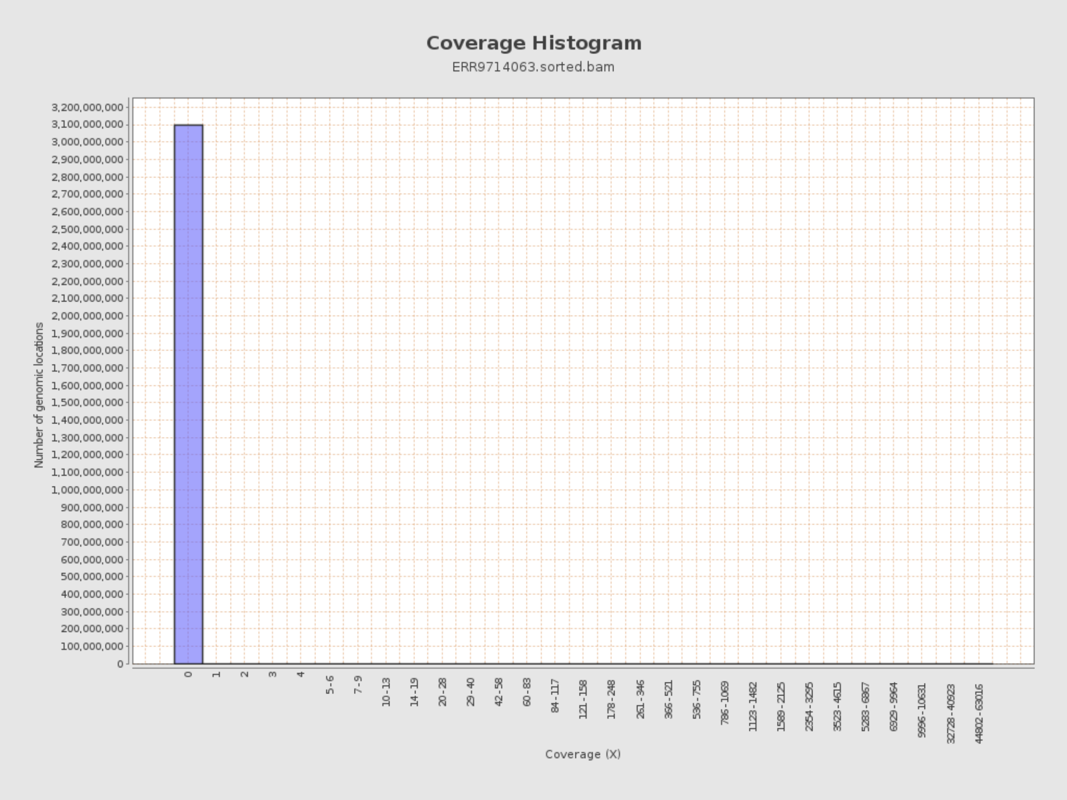
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8792	0	0.0146
chr2	243199373	8409000	0.0346	38.0358
chr3	198022430	5706	0	0.0131
chr4	191154276	5812	0	0.0114
chr5	180915260	4634	0	0.0067
chr6	171115067	6330	0	0.0139
chr7	159138663	18272	0.0001	0.1246

chr8	146364022	8858	0.0001	0.0309
chr9	141213431	3122	0	0.0124
chr10	135534747	5510	0	0.0171
chr11	135006516	8996	0.0001	0.0382
chr12	133851895	11622	0.0001	0.0605
chr13	115169878	1770	0	0.0043
chr14	107349540	10314	0.0001	0.1142
chr15	102531392	3846	0	0.0178
chr16	90354753	4068	0	0.0133
chr17	81195210	10532	0.0001	0.1521
chr18	78077248	2224	0	0.0079
chr19	59128983	3117	0.0001	0.0215
chr20	63025520	3384	0.0001	0.0193
chr21	48129895	864	0	0.0057
chr22	51304566	1109	0	0.0065
chrMT	16571	301	0.0182	0.1672
chrX	155270560	68050	0.0004	0.0707
chrY	59373566	1239	0	0.0106

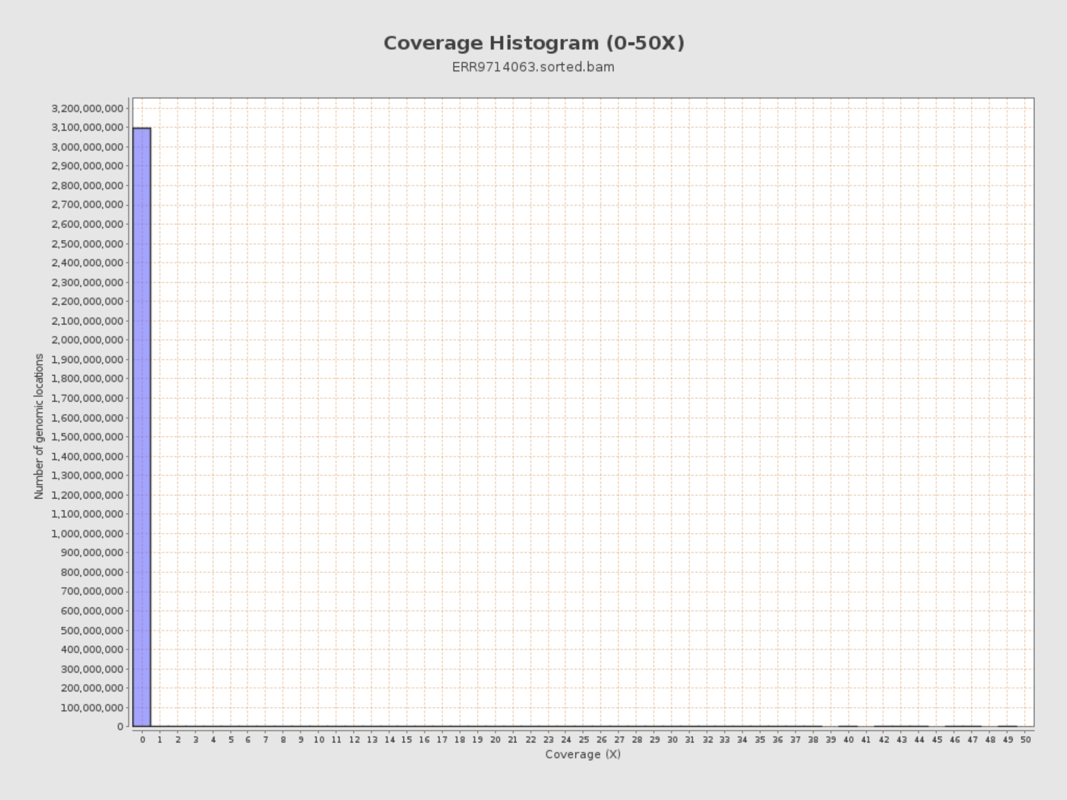
3. Results : Coverage across reference



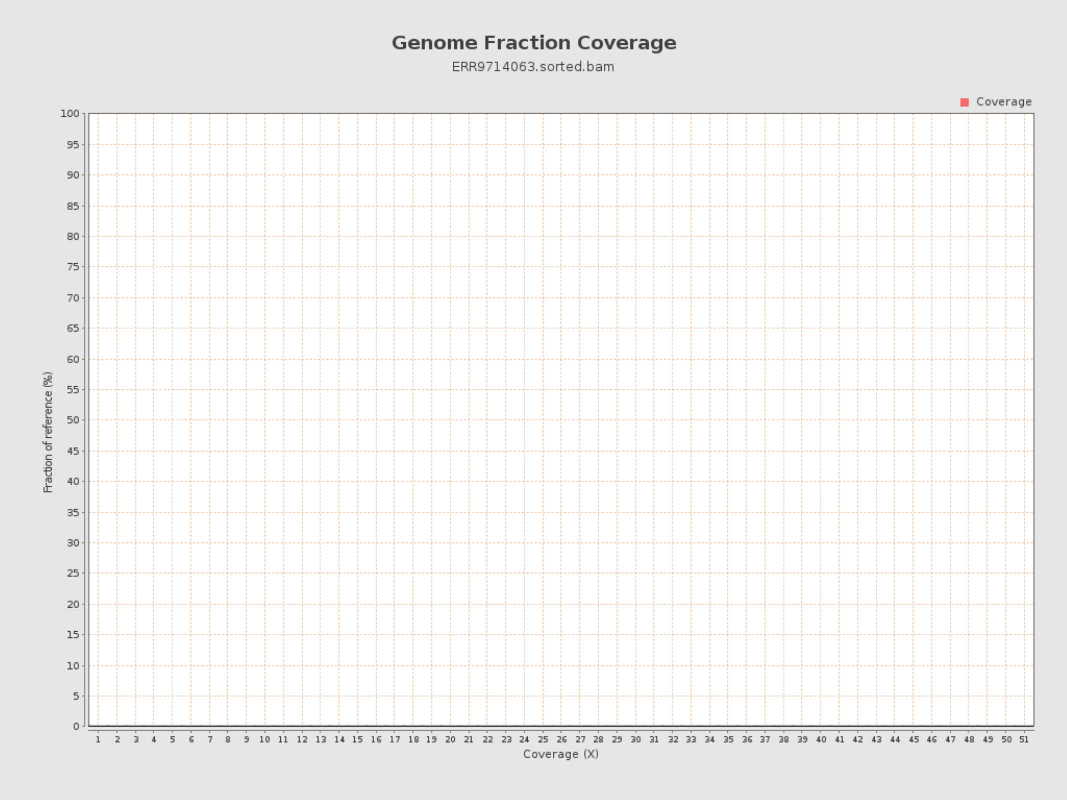
4. Results : Coverage Histogram



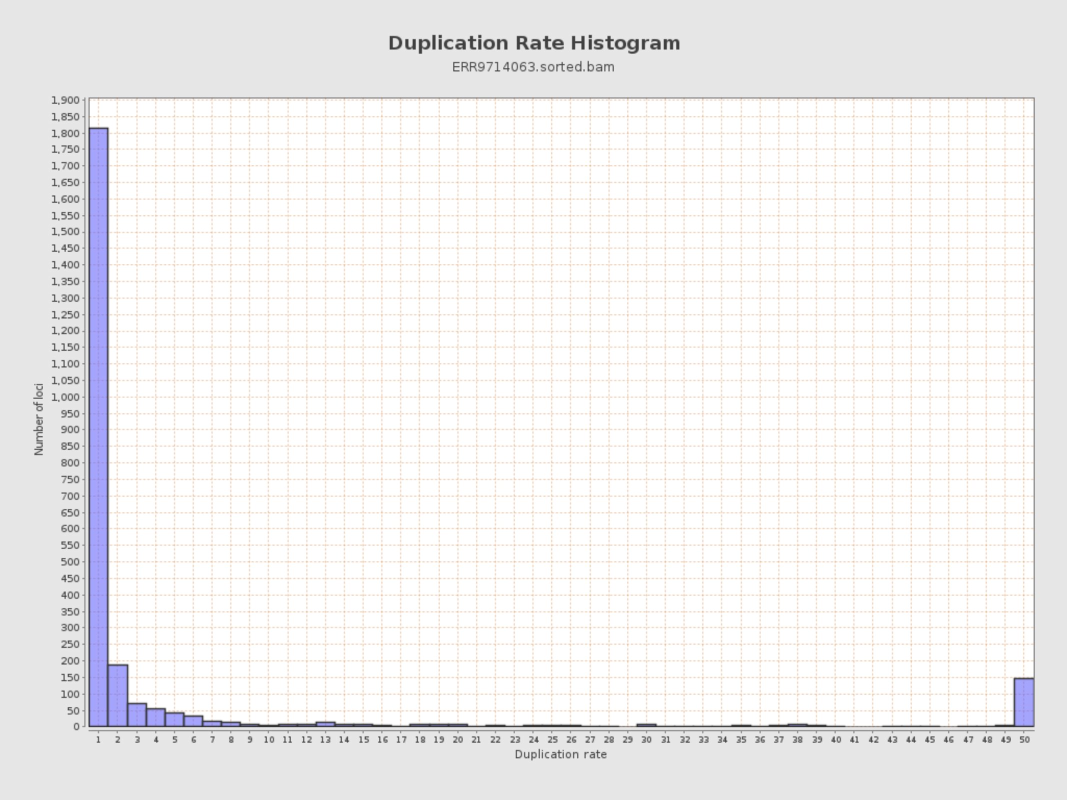
5. Results : Coverage Histogram (0-50X)



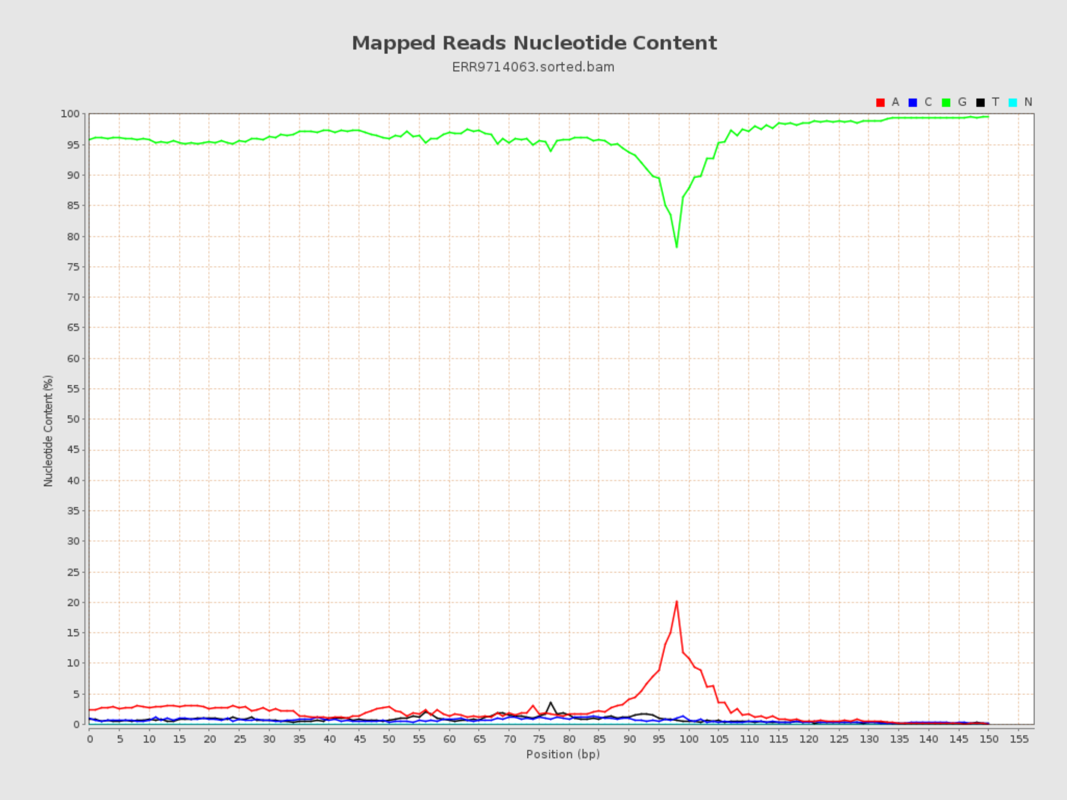
6. Results : Genome Fraction Coverage



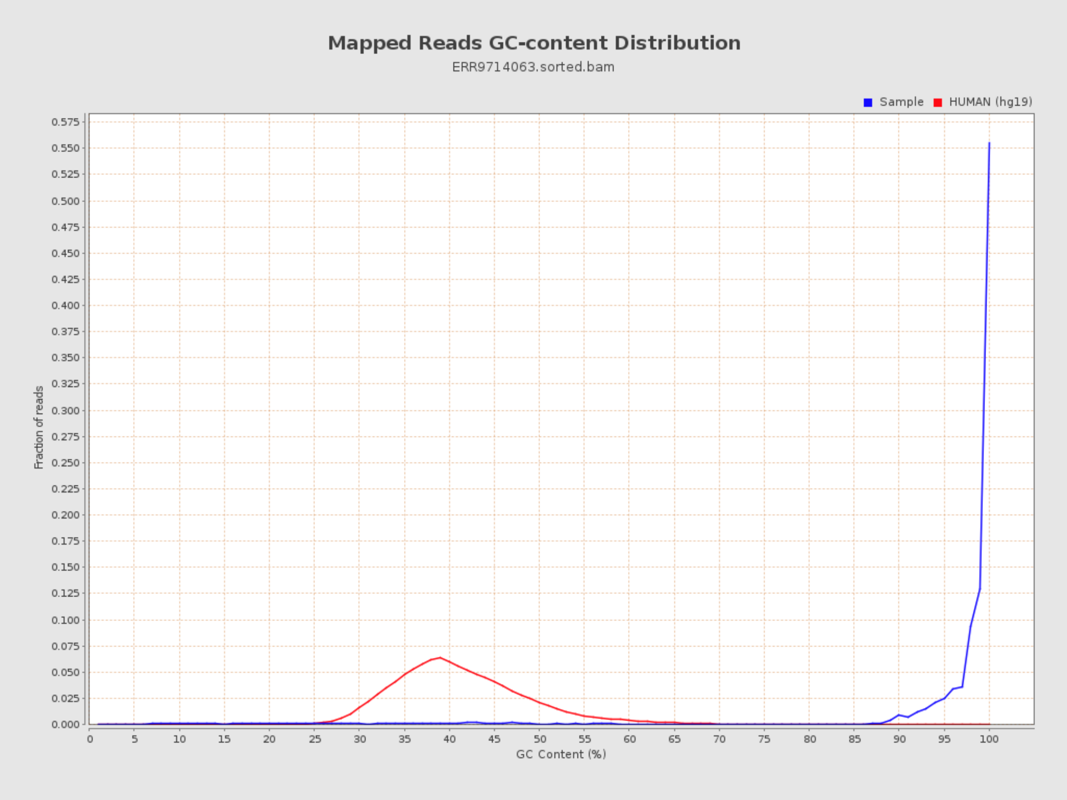
7. Results : Duplication Rate Histogram



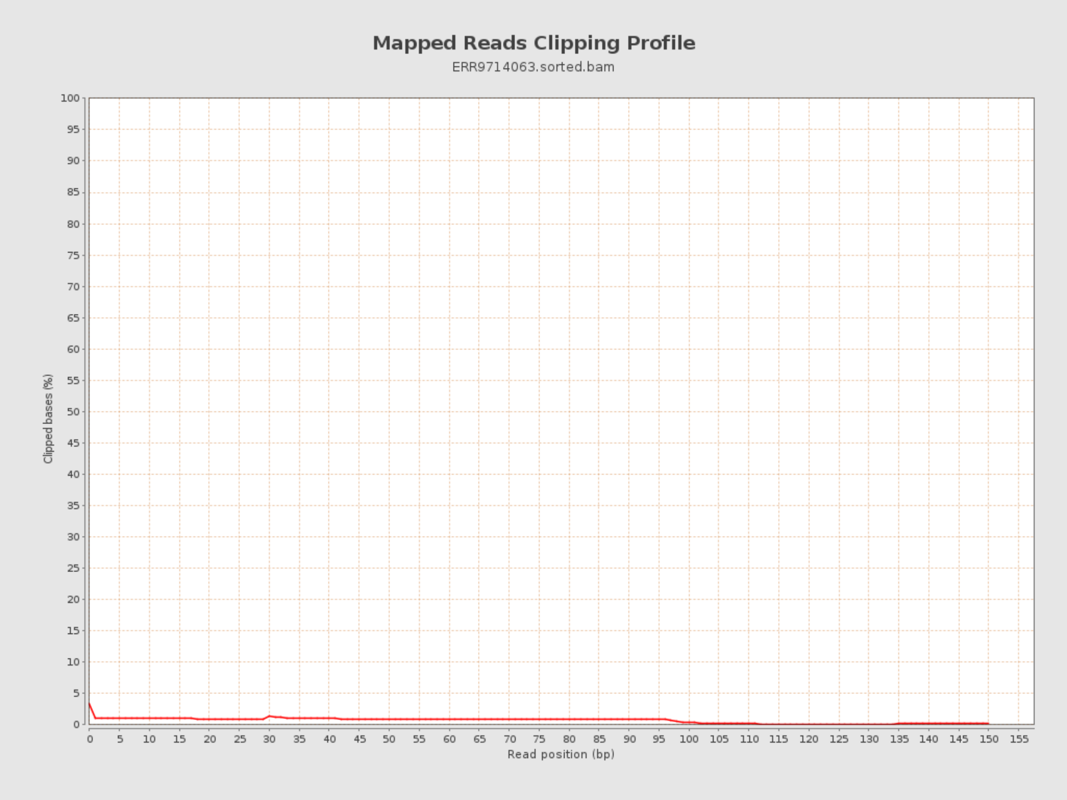
8. Results : Mapped Reads Nucleotide Content



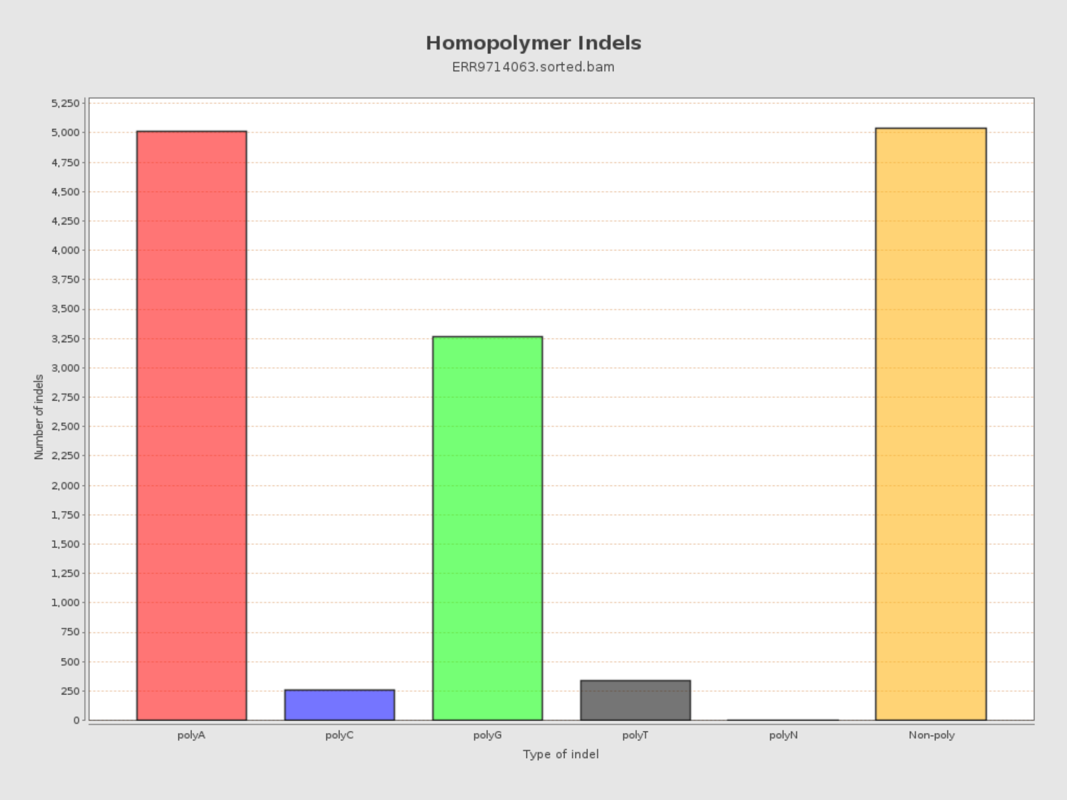
9. Results : Mapped Reads GC-content Distribution



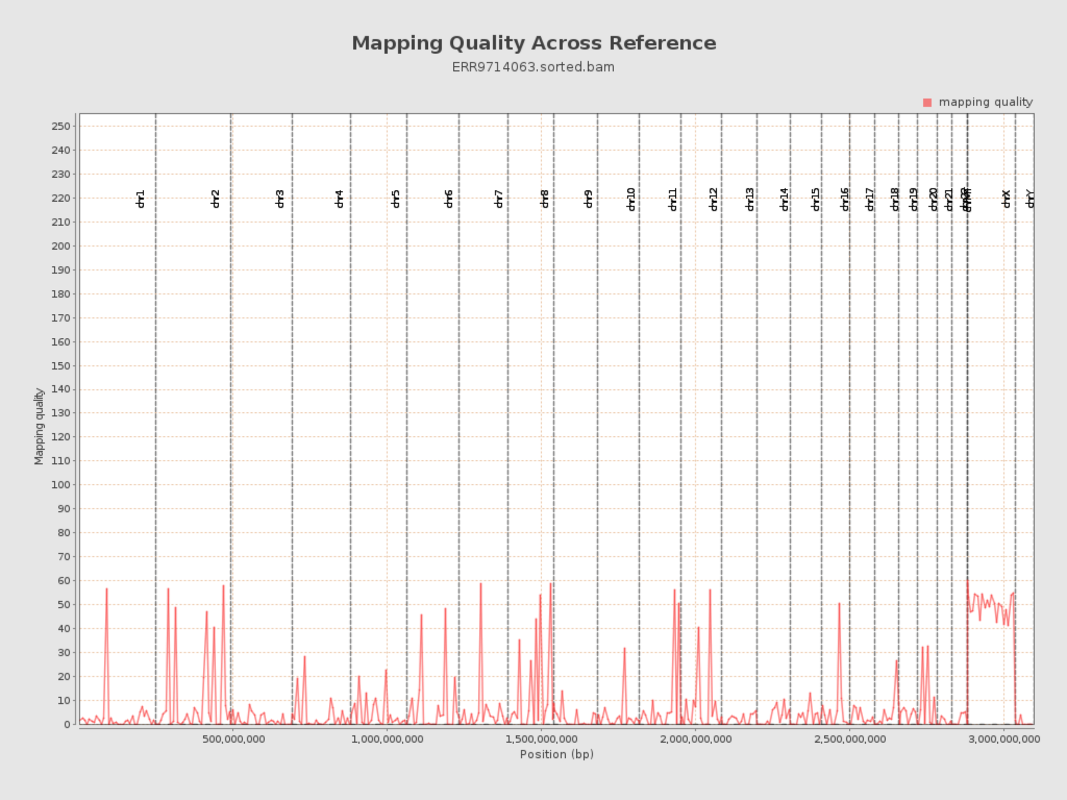
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram