Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 01:39:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714257.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_ERR9714257 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714257.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 01:39:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714257.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	436,616
Mapped reads	69,193 / 15.85%
Unmapped reads	367,423 / 84.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,494 / 0.34%
Read min/max/mean length	30 / 151 / 59.98
Duplicated reads (estimated)	67,961 / 15.57%
Duplication rate	32.94%
Clipped reads	36,733 / 8.41%

2.2. ACGT Content

Number/percentage of A's	166,560 / 2.33%
Number/percentage of C's	63,705 / 0.89%
Number/percentage of T's	73,791 / 1.03%
Number/percentage of G's	6,845,248 / 95.74%
Number/percentage of N's	186 / 0%
GC Percentage	96.64%

2.3. Coverage

Mean	0.0023

Standard Deviation	8.7849

2.4. Mapping Quality

Mean Mapping Quality	10.41

2.5. Mismatches and indels

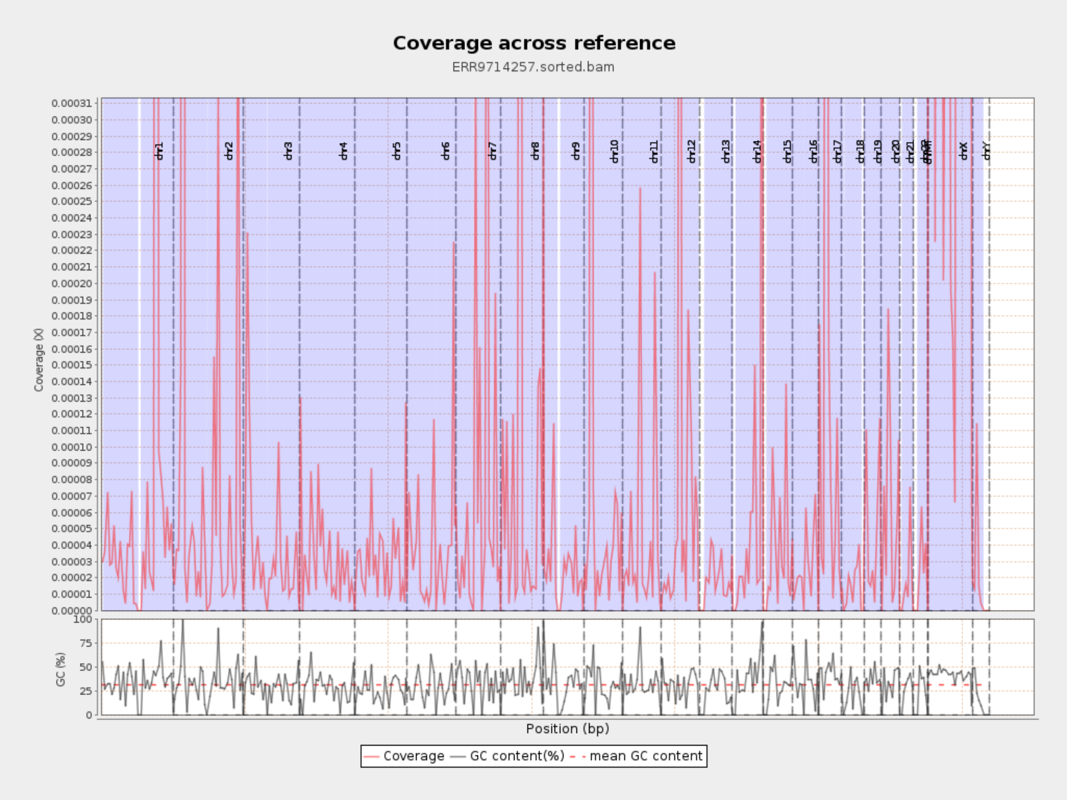
General error rate	3.32%
Mismatches	177,154
Insertions	8,338
Mapped reads with at least one insertion	8.47%
Deletions	3,613
Mapped reads with at least one deletion	5.03%
Homopolymer indels	65.74%

2.6. Chromosome stats

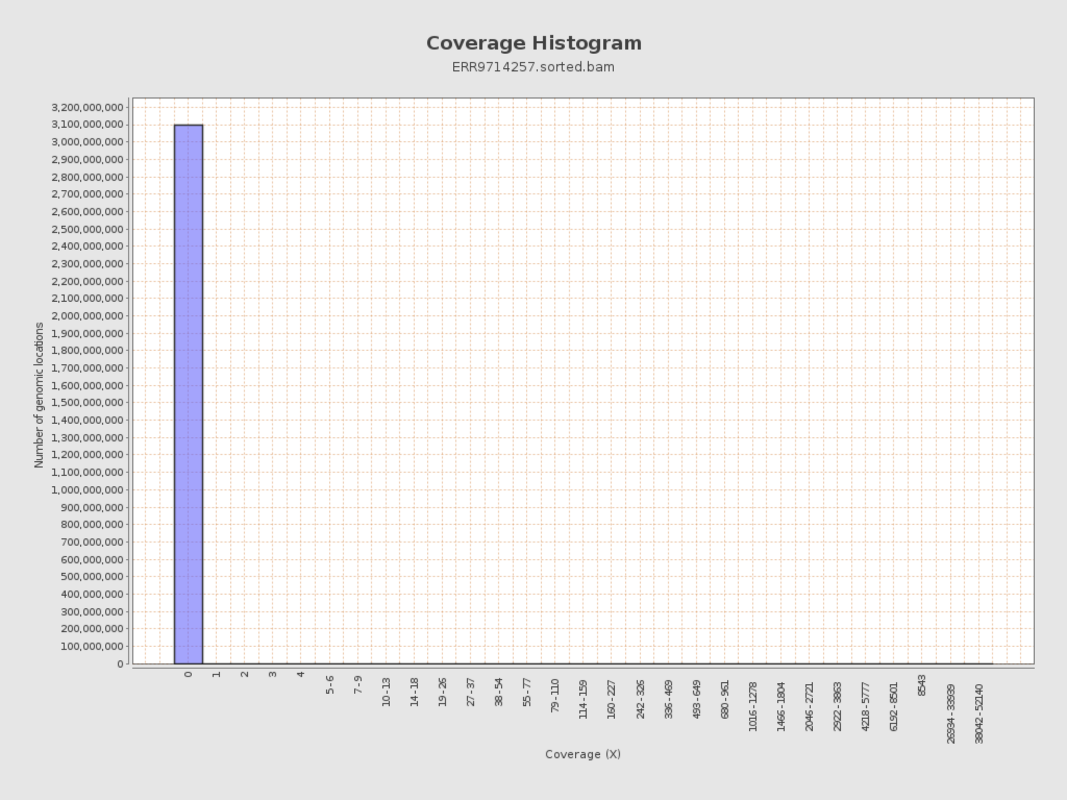
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	22982	0.0001	0.163
chr2	243199373	6868765	0.0282	31.3412
chr3	198022430	7676	0	0.0142
chr4	191154276	6072	0	0.0099
chr5	180915260	5415	0	0.0086
chr6	171115067	6810	0	0.0162
chr7	159138663	14450	0.0001	0.0741

chr8	146364022	15329	0.0001	0.0575
chr9	141213431	3851	0	0.0113
chr10	135534747	18683	0.0001	0.2181
chr11	135006516	6072	0	0.0287
chr12	133851895	13216	0.0001	0.0714
chr13	115169878	2092	0	0.0052
chr14	107349540	8381	0.0001	0.0857
chr15	102531392	3757	0	0.0127
chr16	90354753	2526	0	0.0098
chr17	81195210	11973	0.0001	0.1268
chr18	78077248	1112	0	0.005
chr19	59128983	2833	0	0.0169
chr20	63025520	4014	0.0001	0.031
chr21	48129895	900	0	0.0064
chr22	51304566	1173	0	0.0063
chrMT	16571	7180	0.4333	2.68
chrX	155270560	129283	0.0008	0.1126
chrY	59373566	1216	0	0.0092

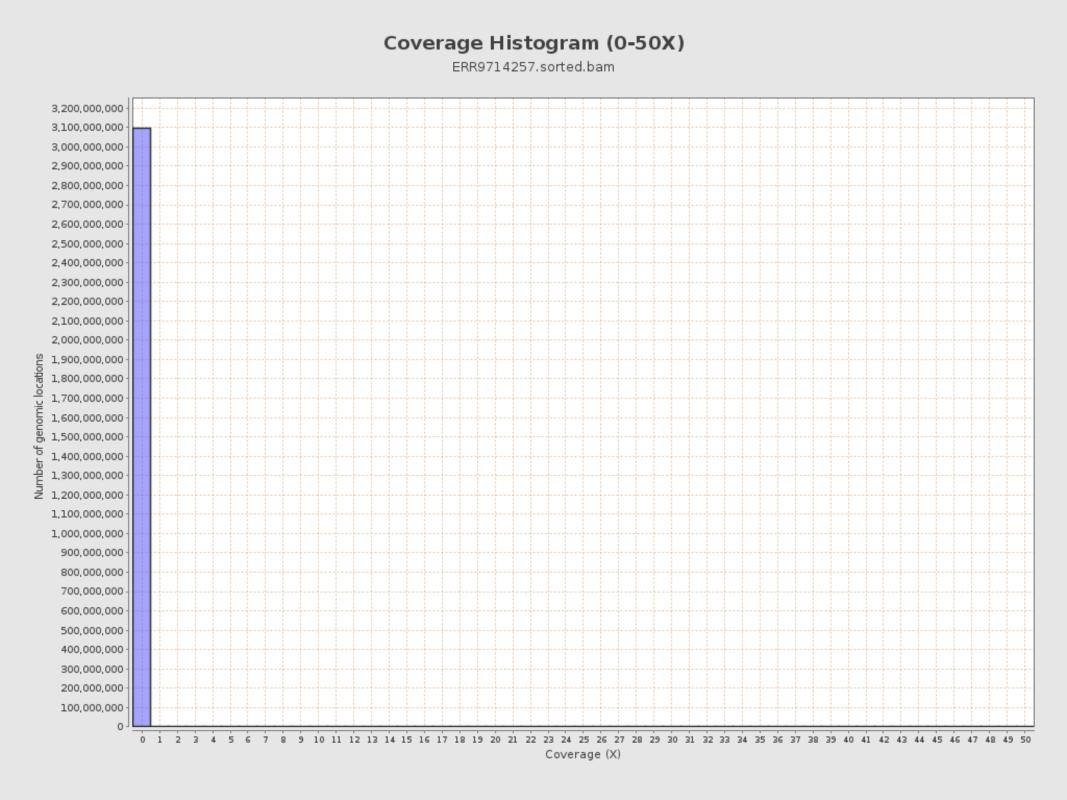
3. Results : Coverage across reference



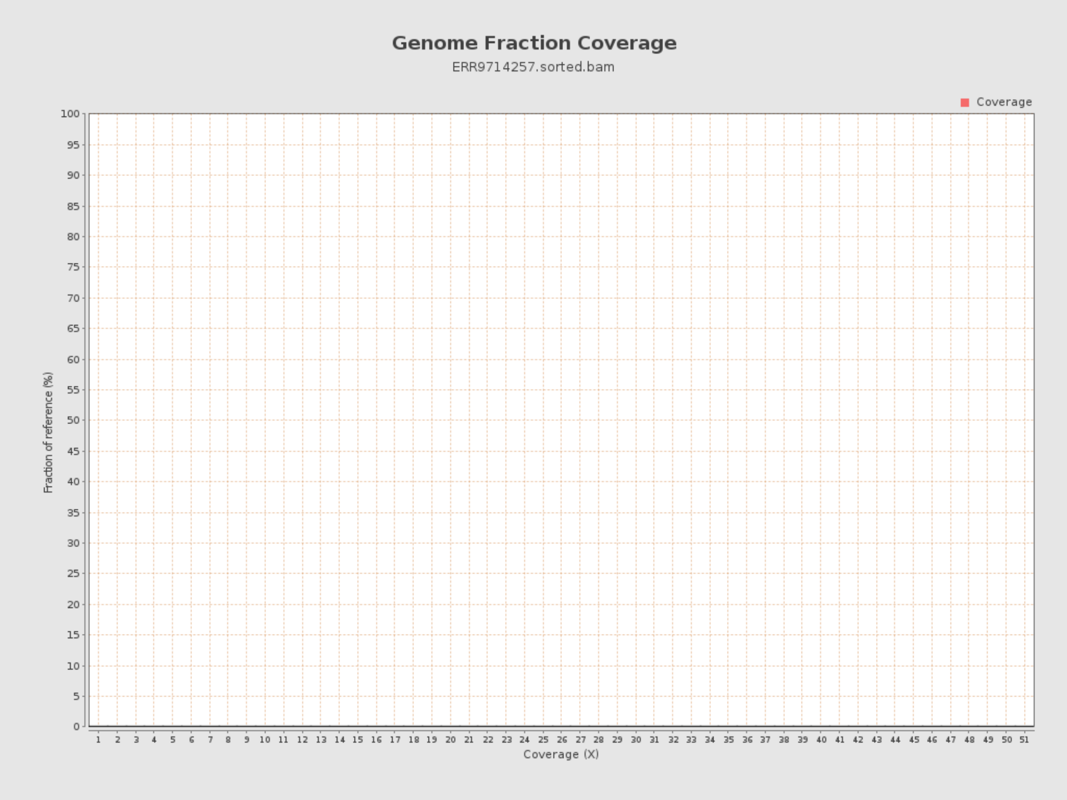
4. Results : Coverage Histogram



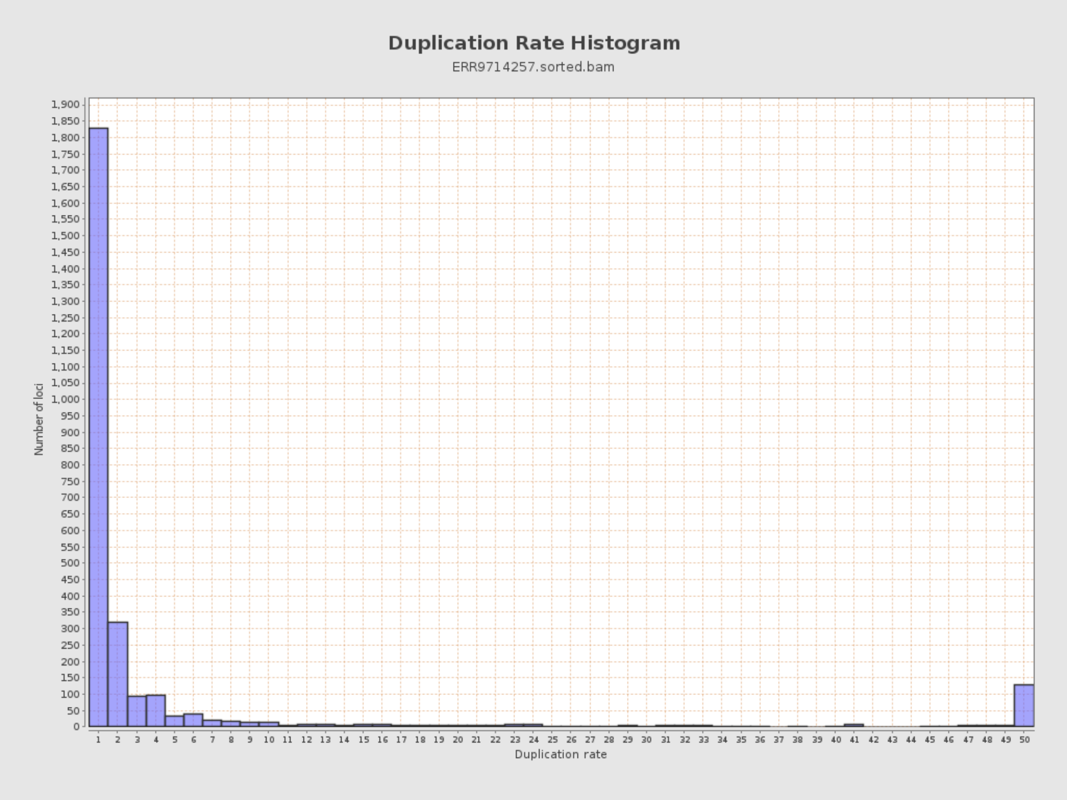
5. Results : Coverage Histogram (0-50X)



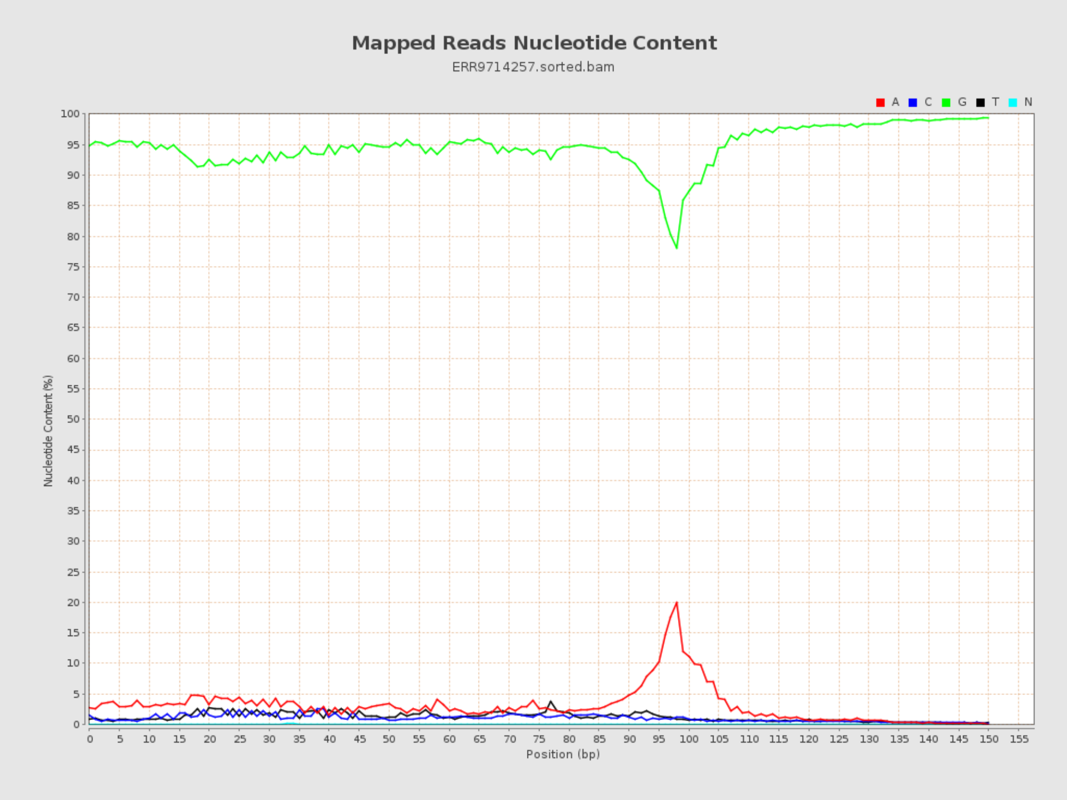
6. Results : Genome Fraction Coverage



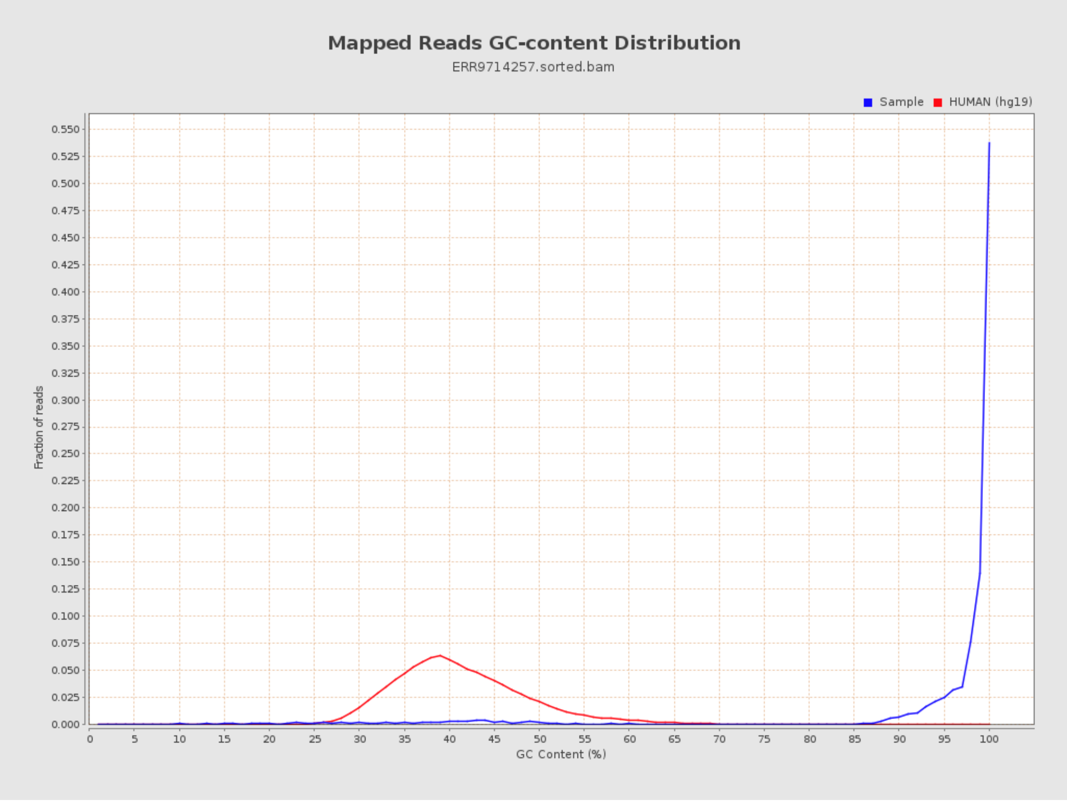
7. Results : Duplication Rate Histogram



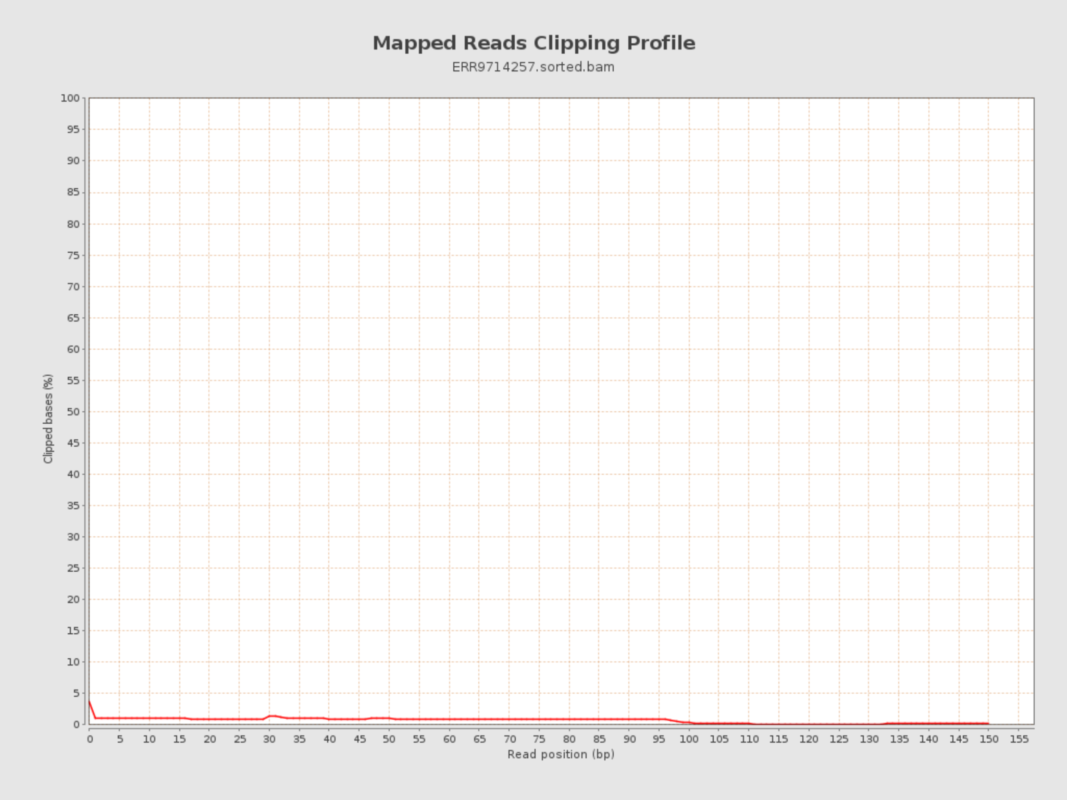
8. Results : Mapped Reads Nucleotide Content



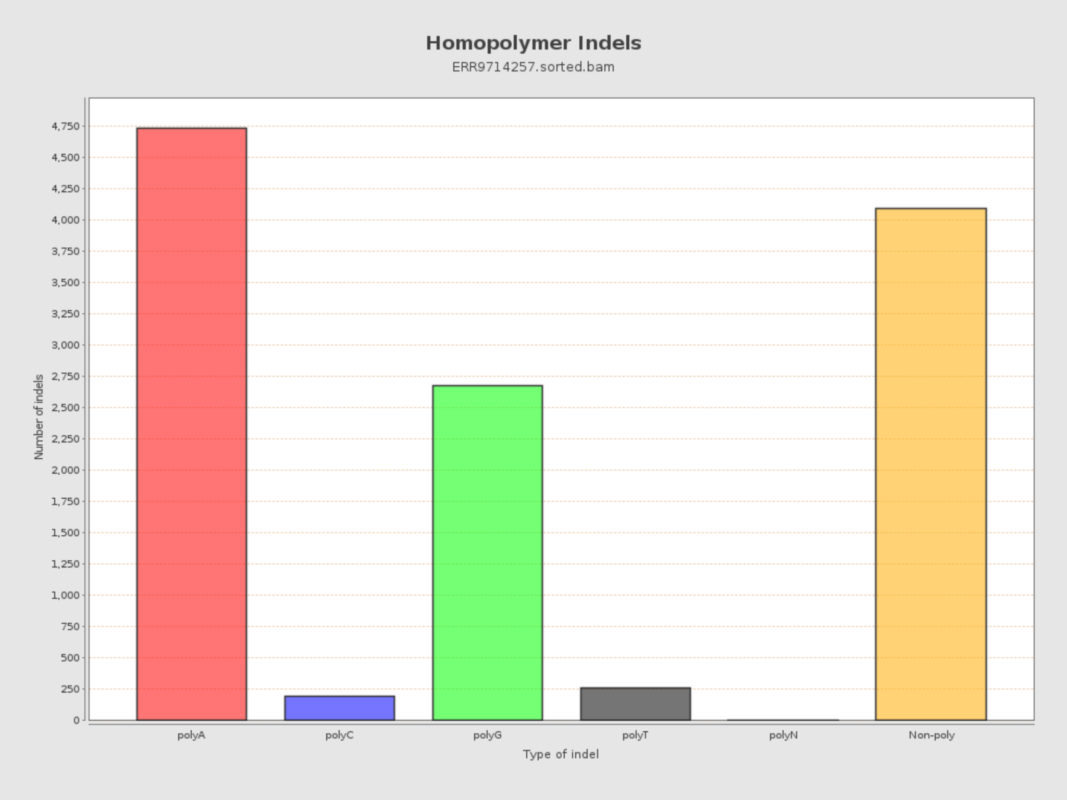
9. Results : Mapped Reads GC-content Distribution



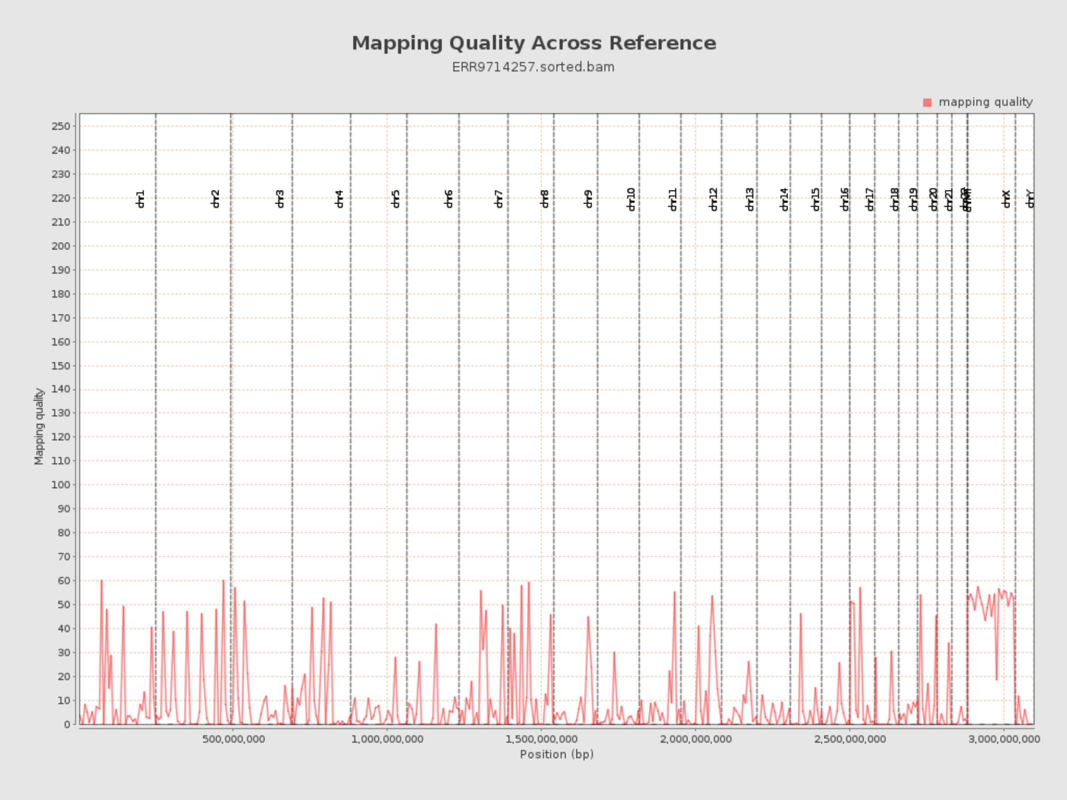
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram