Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 01:26:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714251.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_ERR9714251 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714251.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 01:26:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714251.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	382,698
Mapped reads	61,755 / 16.14%
Unmapped reads	320,943 / 83.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,052 / 0.27%
Read min/max/mean length	30 / 151 / 62.64
Duplicated reads (estimated)	60,795 / 15.89%
Duplication rate	29.92%
Clipped reads	31,647 / 8.27%

2.2. ACGT Content

Number/percentage of A's	127,034 / 1.96%
Number/percentage of C's	43,222 / 0.67%
Number/percentage of T's	56,311 / 0.87%
Number/percentage of G's	6,246,197 / 96.5%
Number/percentage of N's	141 / 0%
GC Percentage	97.17%

2.3. Coverage

Mean	0.0021

Standard Deviation	8.1152

2.4. Mapping Quality

Mean Mapping Quality	8.35

2.5. Mismatches and indels

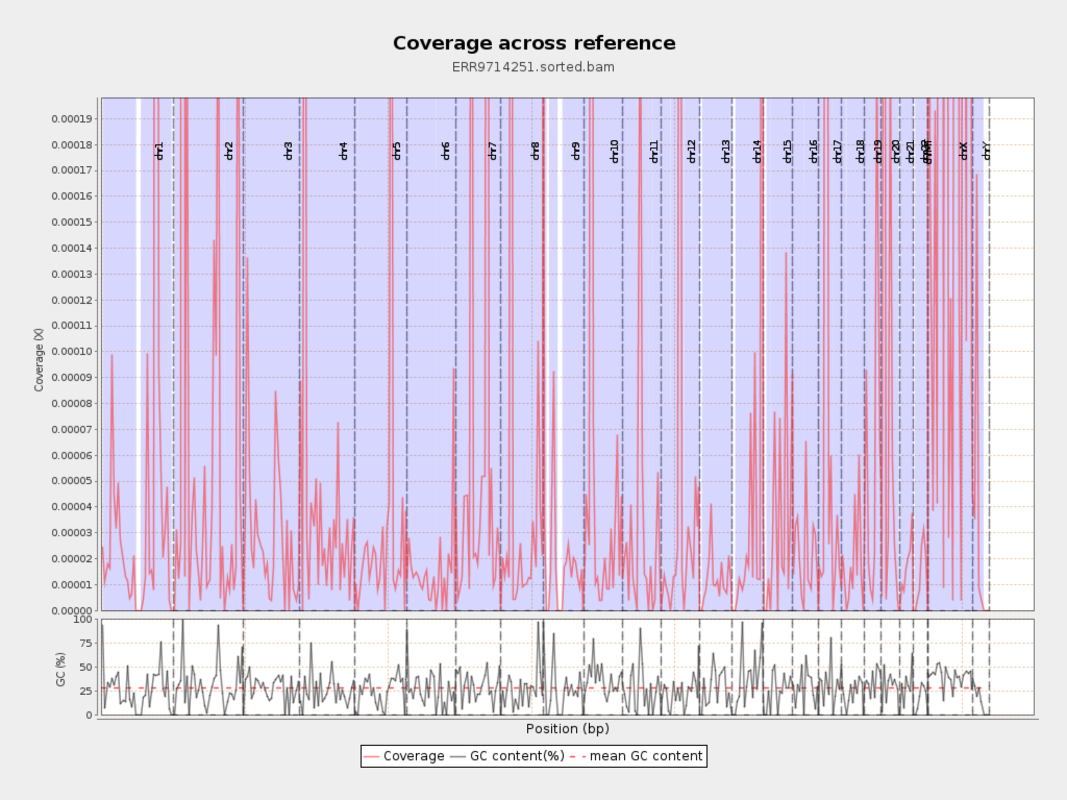
General error rate	3.21%
Mismatches	160,670
Insertions	6,916
Mapped reads with at least one insertion	7.57%
Deletions	2,925
Mapped reads with at least one deletion	4.55%
Homopolymer indels	63.67%

2.6. Chromosome stats

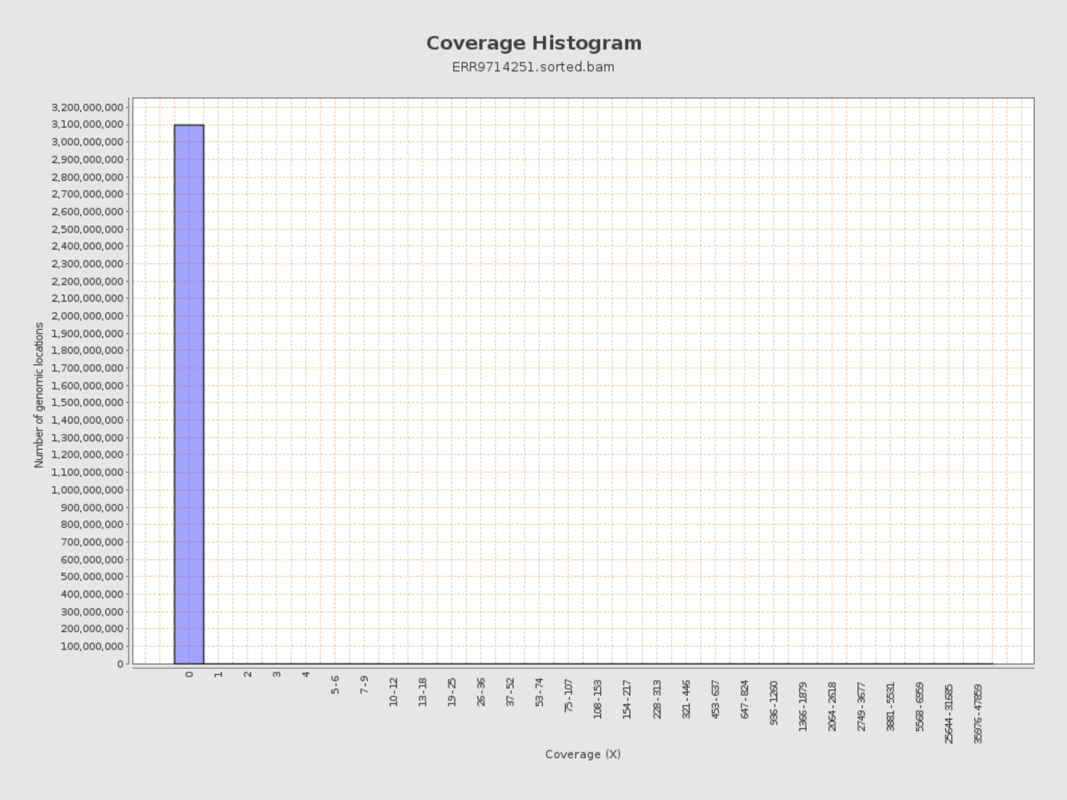
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13355	0.0001	0.0823
chr2	243199373	6276140	0.0258	28.9525
chr3	198022430	5809	0	0.0094
chr4	191154276	9033	0	0.0224
chr5	180915260	6200	0	0.0196
chr6	171115067	2649	0	0.0067
chr7	159138663	13063	0.0001	0.0773

chr8	146364022	7040	0	0.0311
chr9	141213431	2742	0	0.0112
chr10	135534747	9757	0.0001	0.1024
chr11	135006516	4193	0	0.0265
chr12	133851895	7231	0.0001	0.0455
chr13	115169878	1374	0	0.0039
chr14	107349540	7404	0.0001	0.0845
chr15	102531392	3393	0	0.0146
chr16	90354753	2033	0	0.007
chr17	81195210	6651	0.0001	0.0911
chr18	78077248	1475	0	0.0054
chr19	59128983	3452	0.0001	0.0197
chr20	63025520	6340	0.0001	0.0396
chr21	48129895	785	0	0.0057
chr22	51304566	698	0	0.0043
chrMT	16571	755	0.0456	0.2836
chrX	155270560	92357	0.0006	0.1679
chrY	59373566	1912	0	0.0105

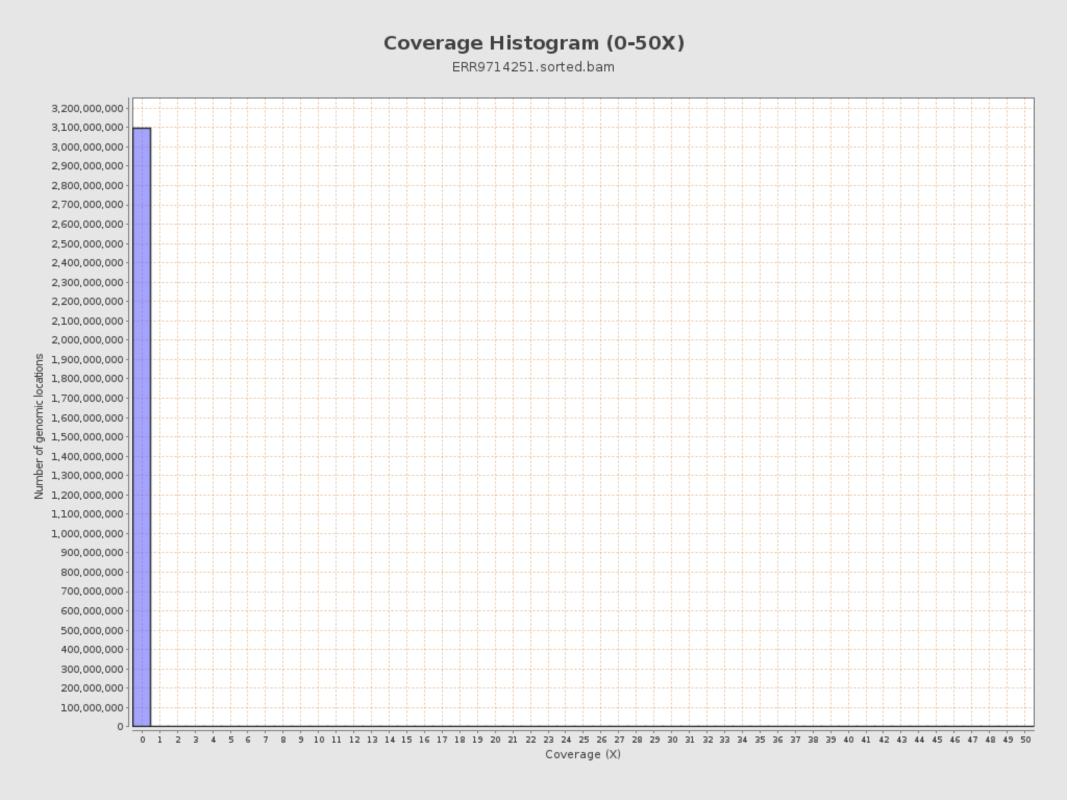
3. Results : Coverage across reference



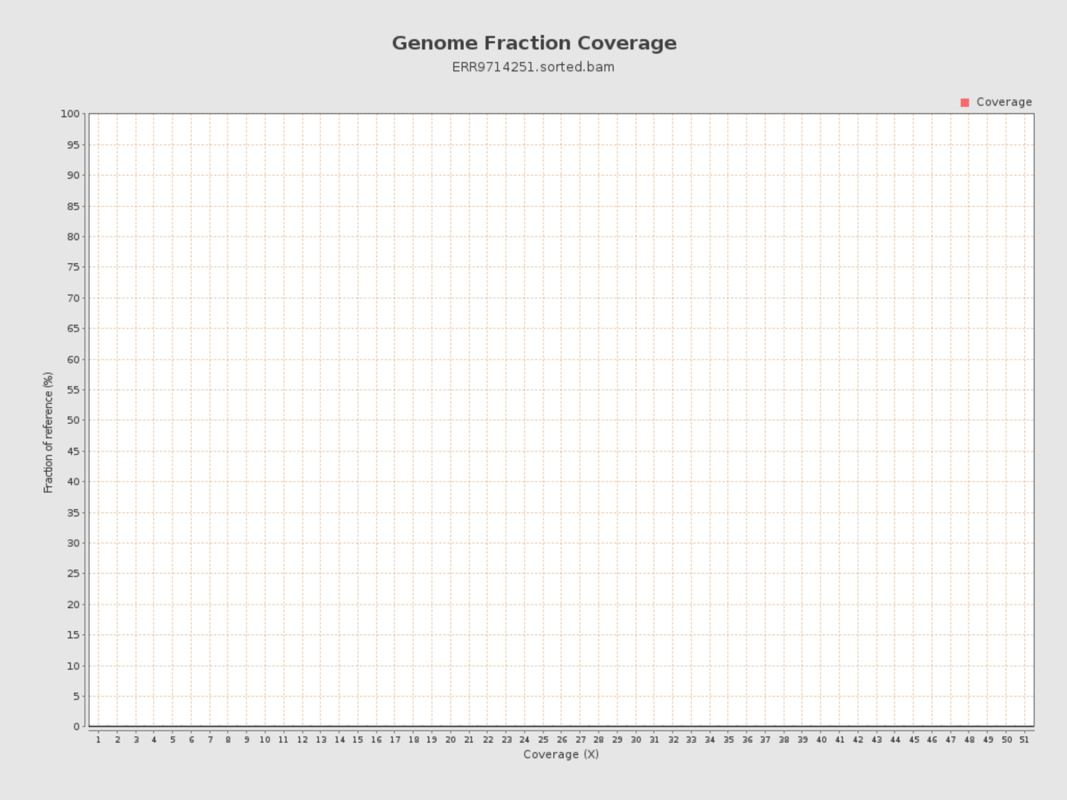
4. Results : Coverage Histogram



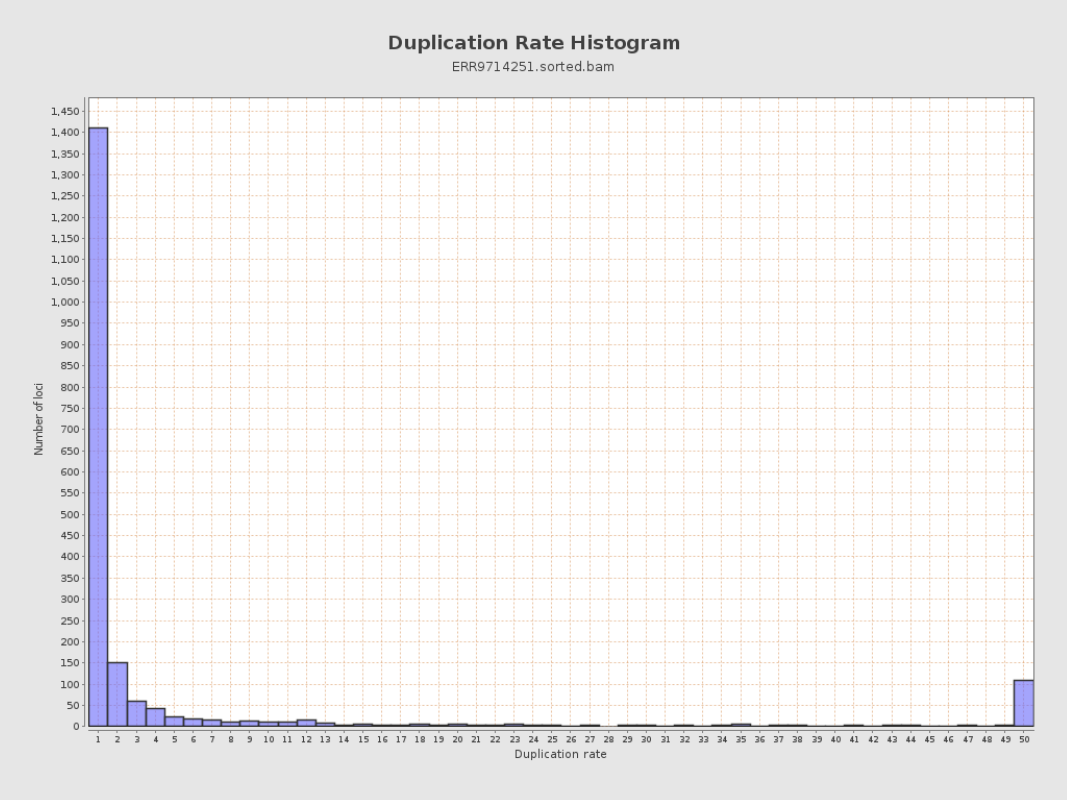
5. Results : Coverage Histogram (0-50X)



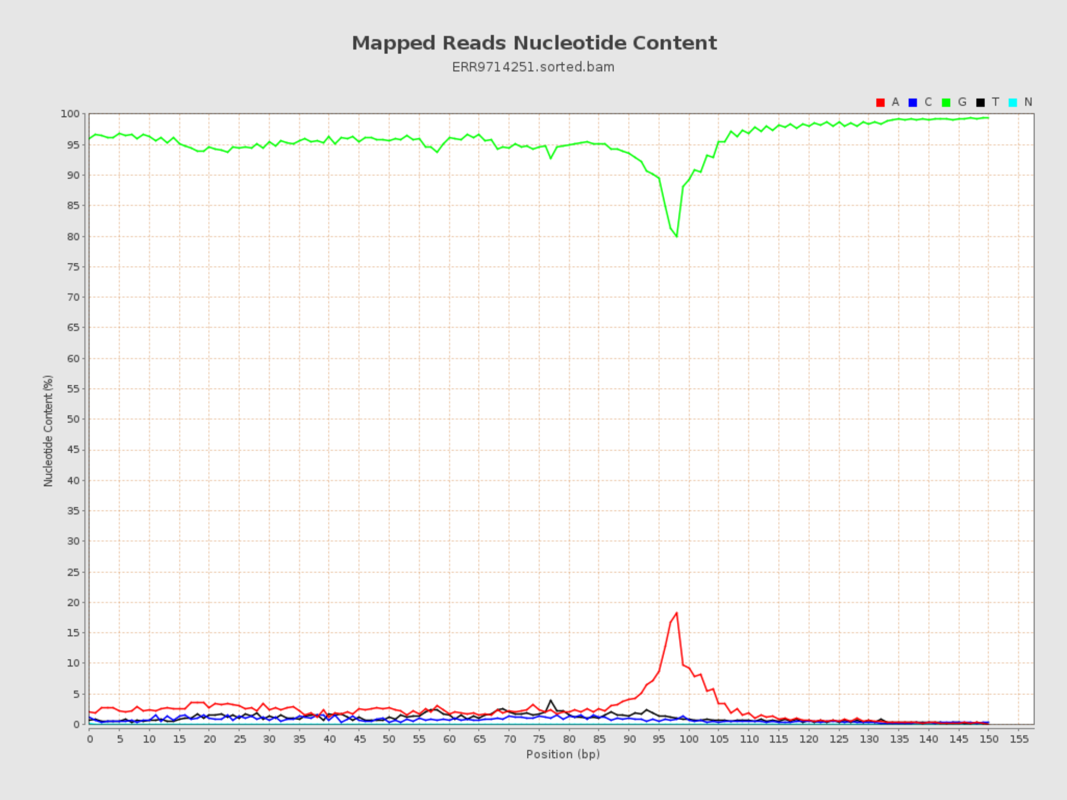
6. Results : Genome Fraction Coverage



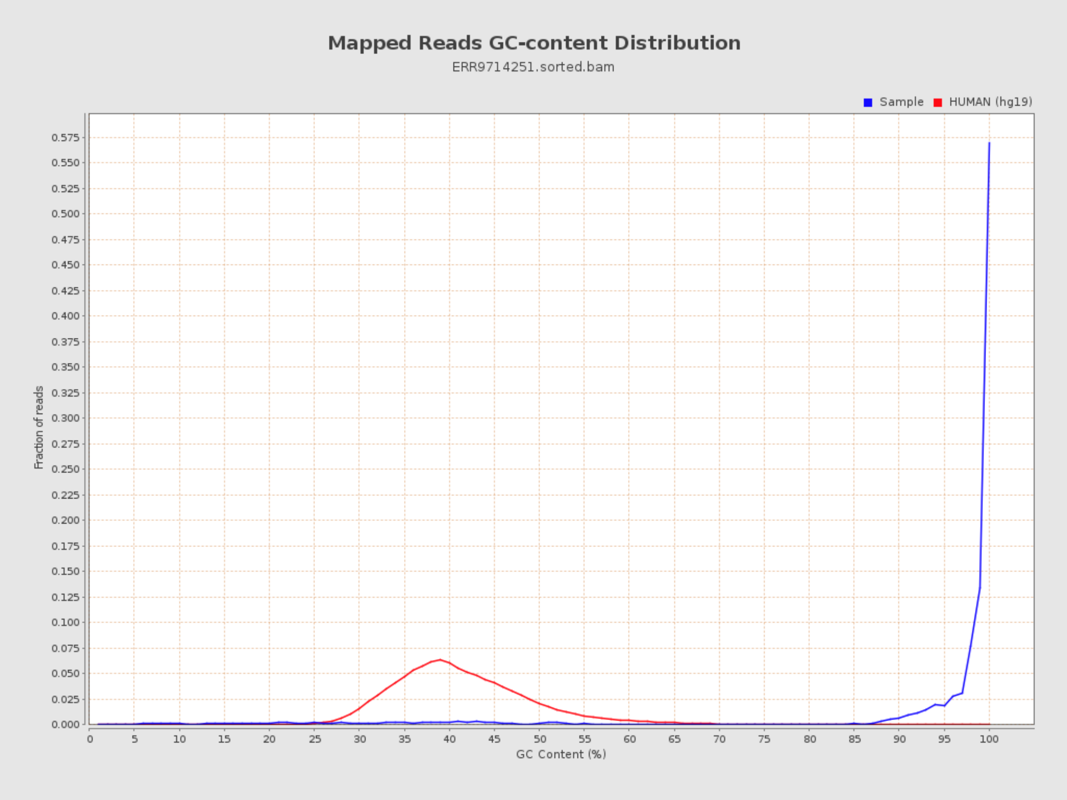
7. Results : Duplication Rate Histogram



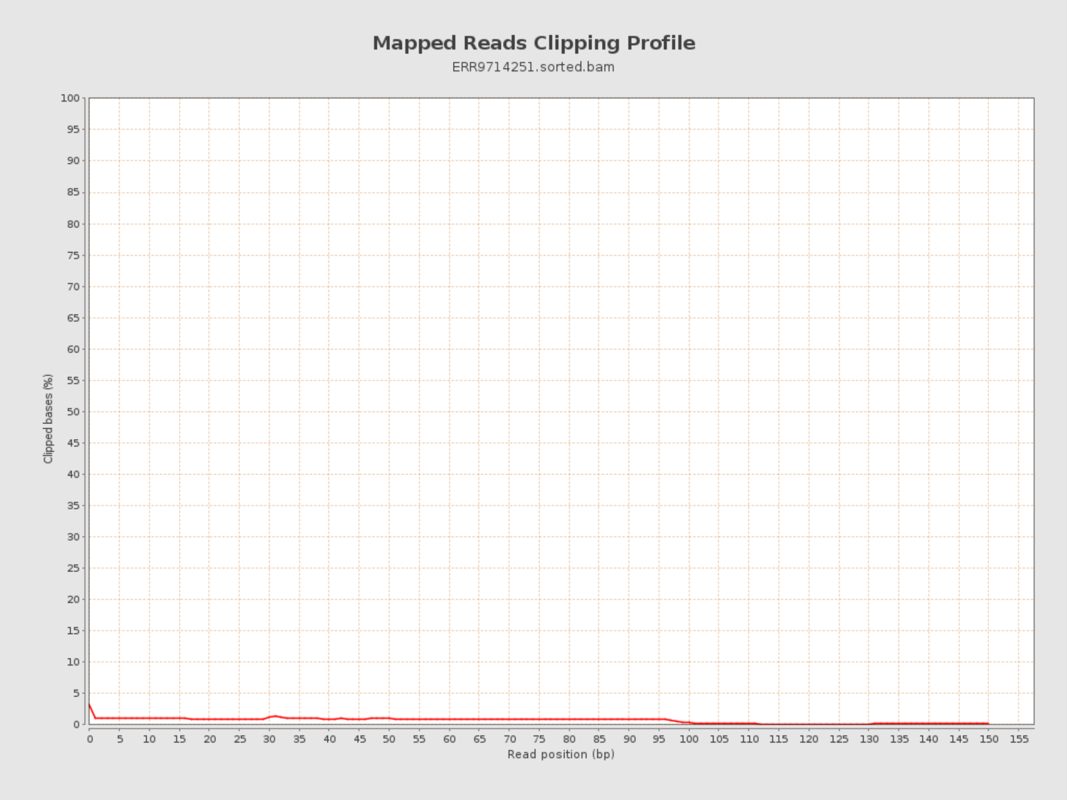
8. Results : Mapped Reads Nucleotide Content



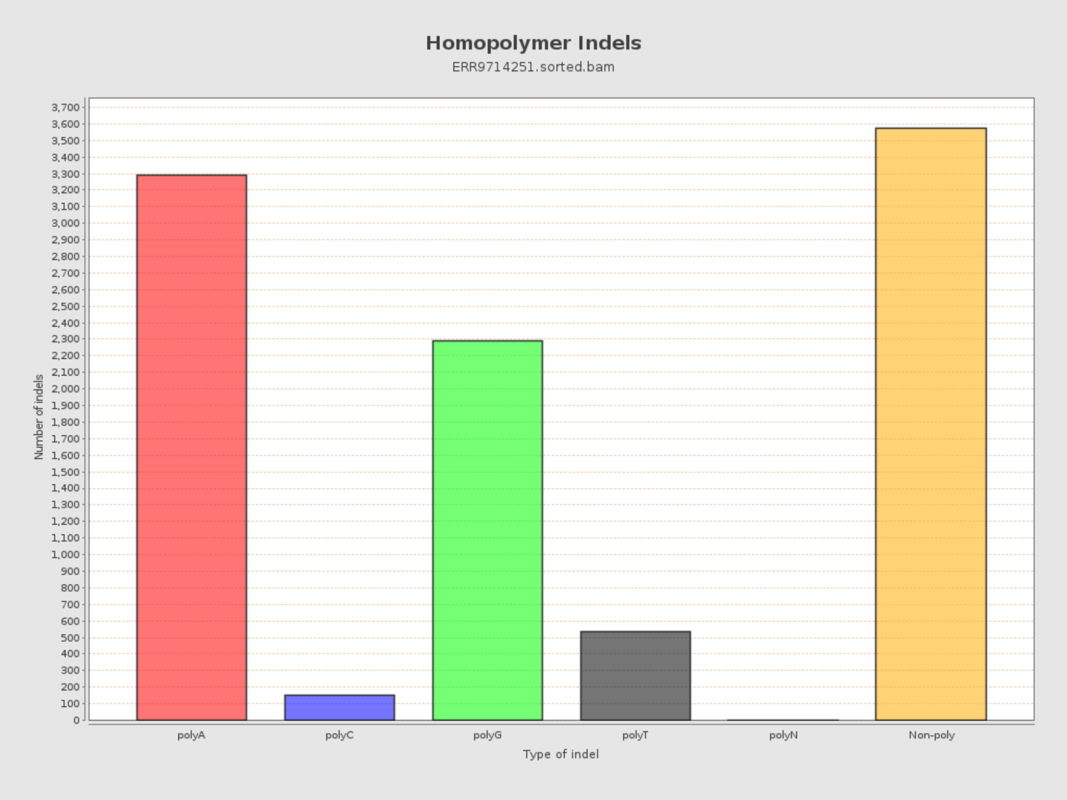
9. Results : Mapped Reads GC-content Distribution



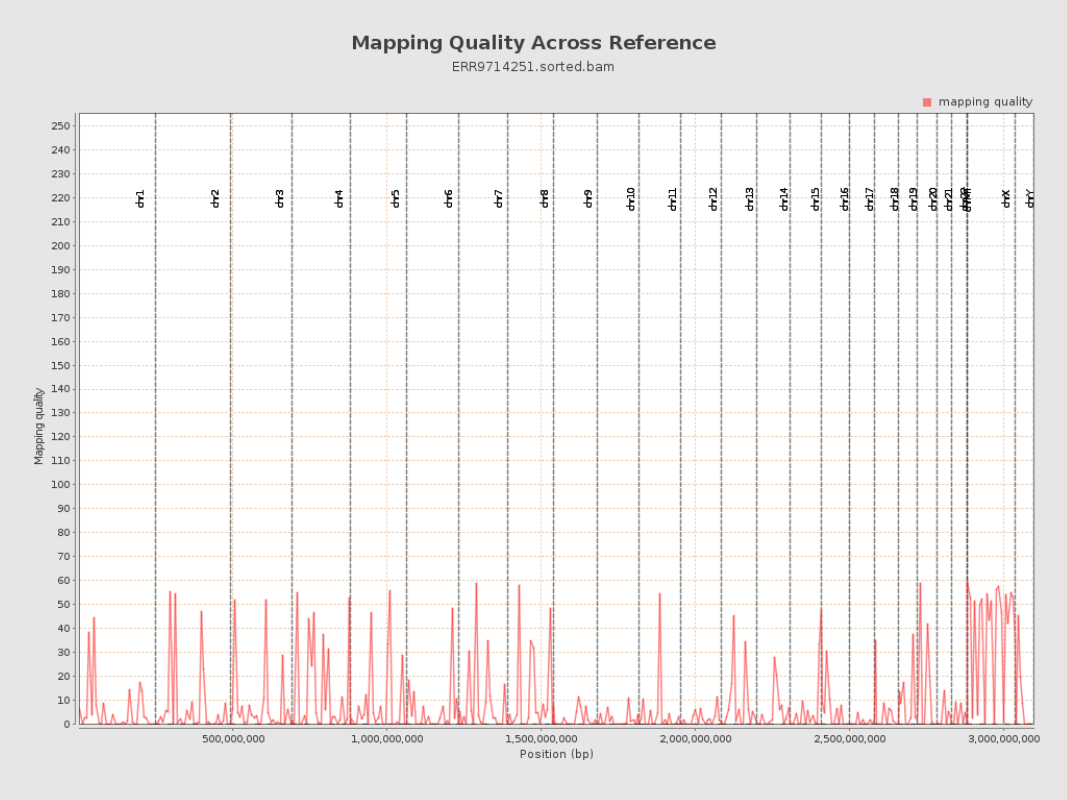
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram