Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 00:47:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714230.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_ERR9714230 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714230.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 00:47:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714230.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	259,020
Mapped reads	41,058 / 15.85%
Unmapped reads	217,962 / 84.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	705 / 0.27%
Read min/max/mean length	30 / 151 / 62.43
Duplicated reads (estimated)	40,182 / 15.51%
Duplication rate	34.09%
Clipped reads	20,965 / 8.09%

2.2. ACGT Content

Number/percentage of A's	84,310 / 1.95%
Number/percentage of C's	30,915 / 0.72%
Number/percentage of T's	38,267 / 0.89%
Number/percentage of G's	4,169,684 / 96.45%
Number/percentage of N's	86 / 0%
GC Percentage	97.16%

2.3. Coverage

Mean	0.0014

Standard Deviation	5.3831

2.4. Mapping Quality

Mean Mapping Quality	7.81

2.5. Mismatches and indels

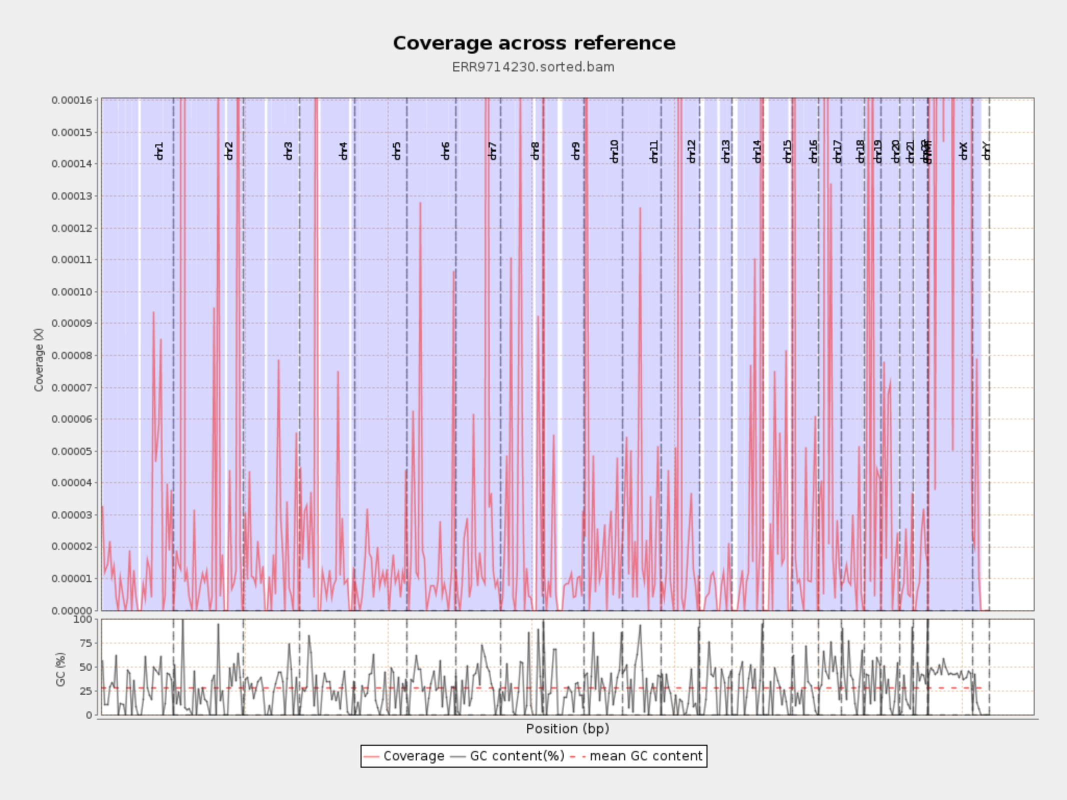
General error rate	3.29%
Mismatches	108,507
Insertions	4,908
Mapped reads with at least one insertion	8.22%
Deletions	2,138
Mapped reads with at least one deletion	4.99%
Homopolymer indels	63.01%

2.6. Chromosome stats

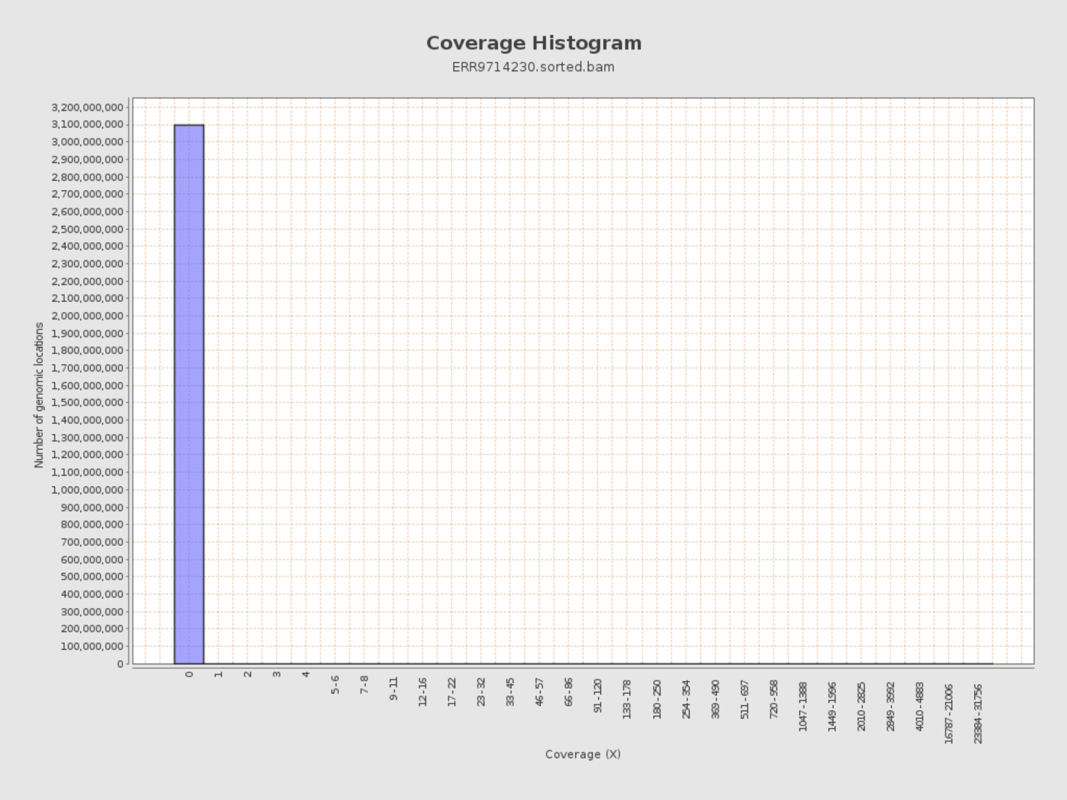
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4594	0	0.0075
chr2	243199373	4188076	0.0172	19.2053
chr3	198022430	3237	0	0.0082
chr4	191154276	5288	0	0.0153
chr5	180915260	2023	0	0.0039
chr6	171115067	3719	0	0.0097
chr7	159138663	6127	0	0.0465

chr8	146364022	4472	0	0.0136
chr9	141213431	1420	0	0.0054
chr10	135534747	4115	0	0.0139
chr11	135006516	3672	0	0.0154
chr12	133851895	6241	0	0.0413
chr13	115169878	673	0	0.0025
chr14	107349540	5750	0.0001	0.0608
chr15	102531392	2295	0	0.0113
chr16	90354753	4696	0.0001	0.0245
chr17	81195210	5859	0.0001	0.0649
chr18	78077248	1088	0	0.006
chr19	59128983	3836	0.0001	0.0203
chr20	63025520	2185	0	0.0145
chr21	48129895	557	0	0.0056
chr22	51304566	726	0	0.0043
chrMT	16571	0	0	0
chrX	155270560	71037	0.0005	0.0831
chrY	59373566	975	0	0.0054

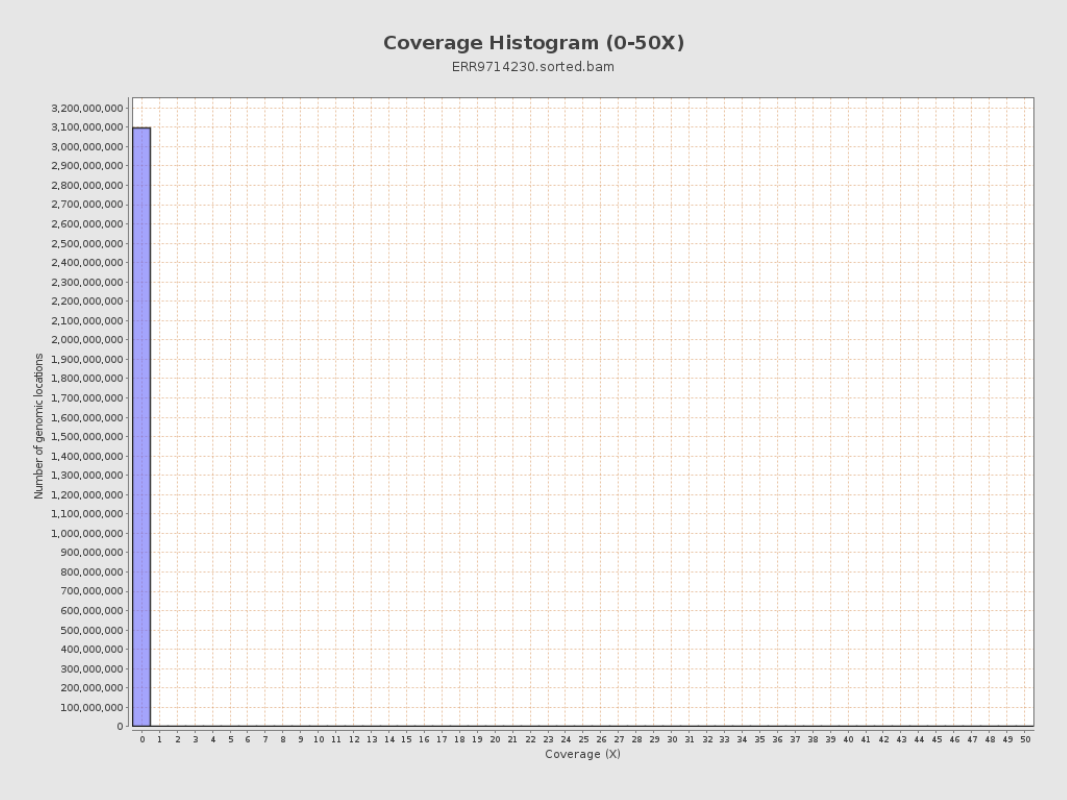
3. Results : Coverage across reference



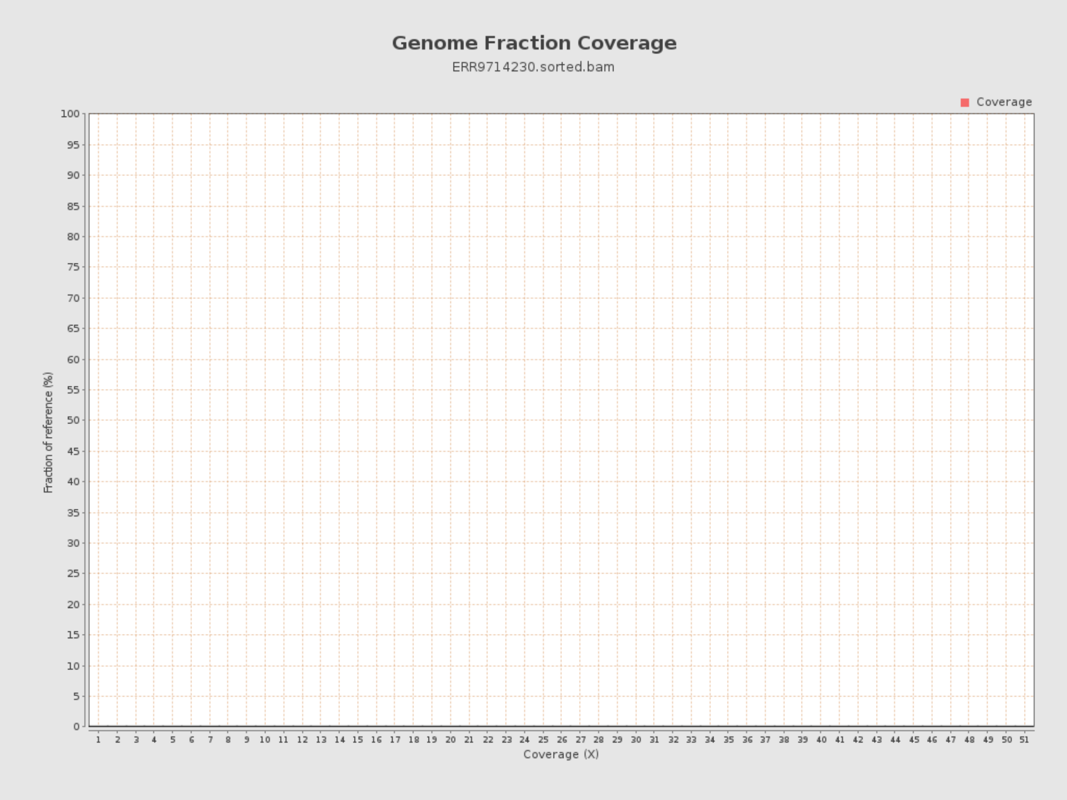
4. Results : Coverage Histogram



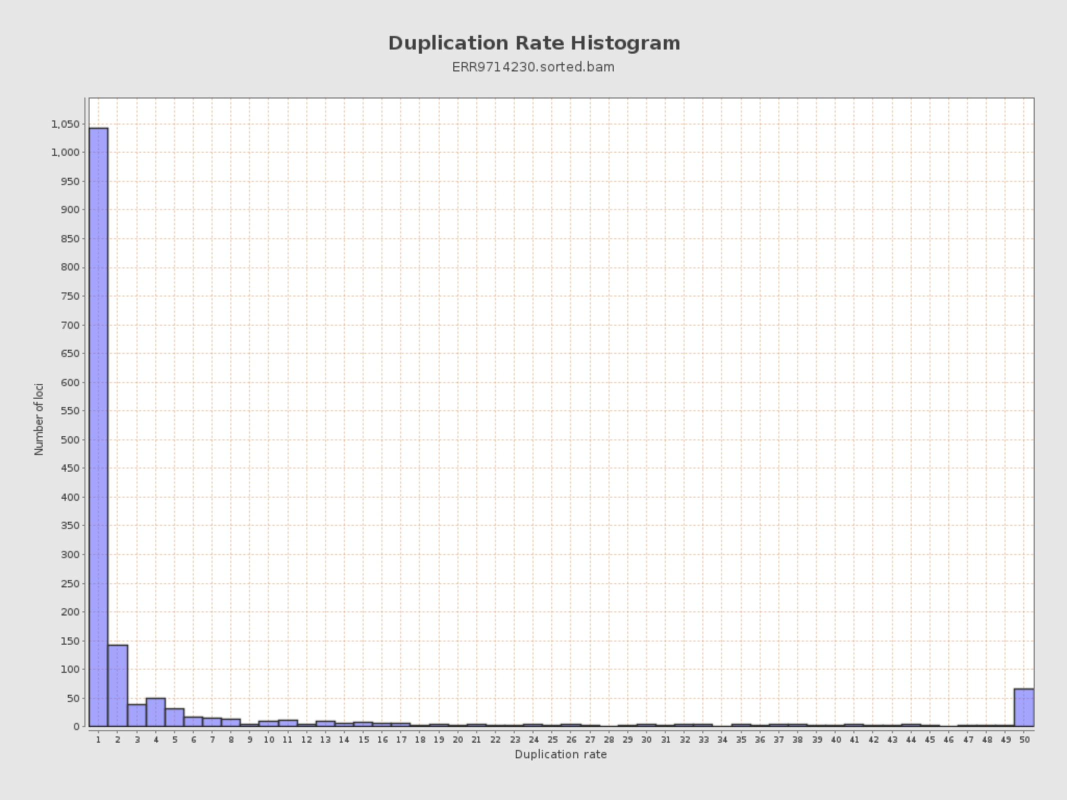
5. Results : Coverage Histogram (0-50X)



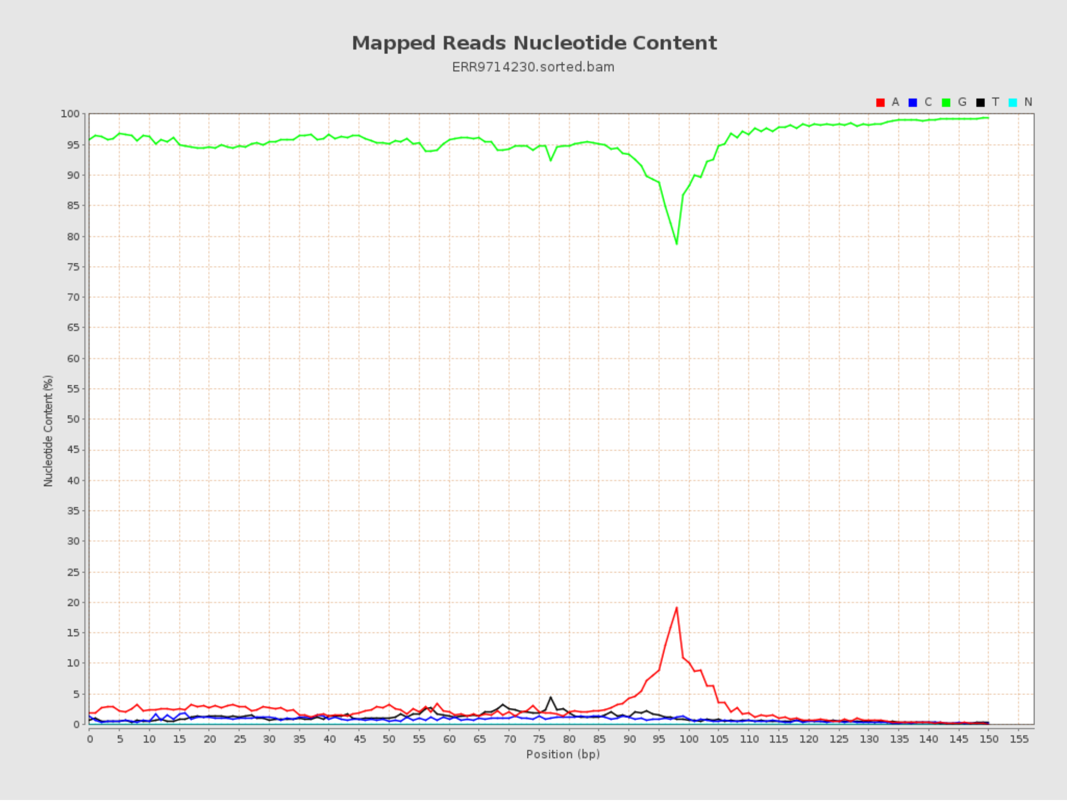
6. Results : Genome Fraction Coverage



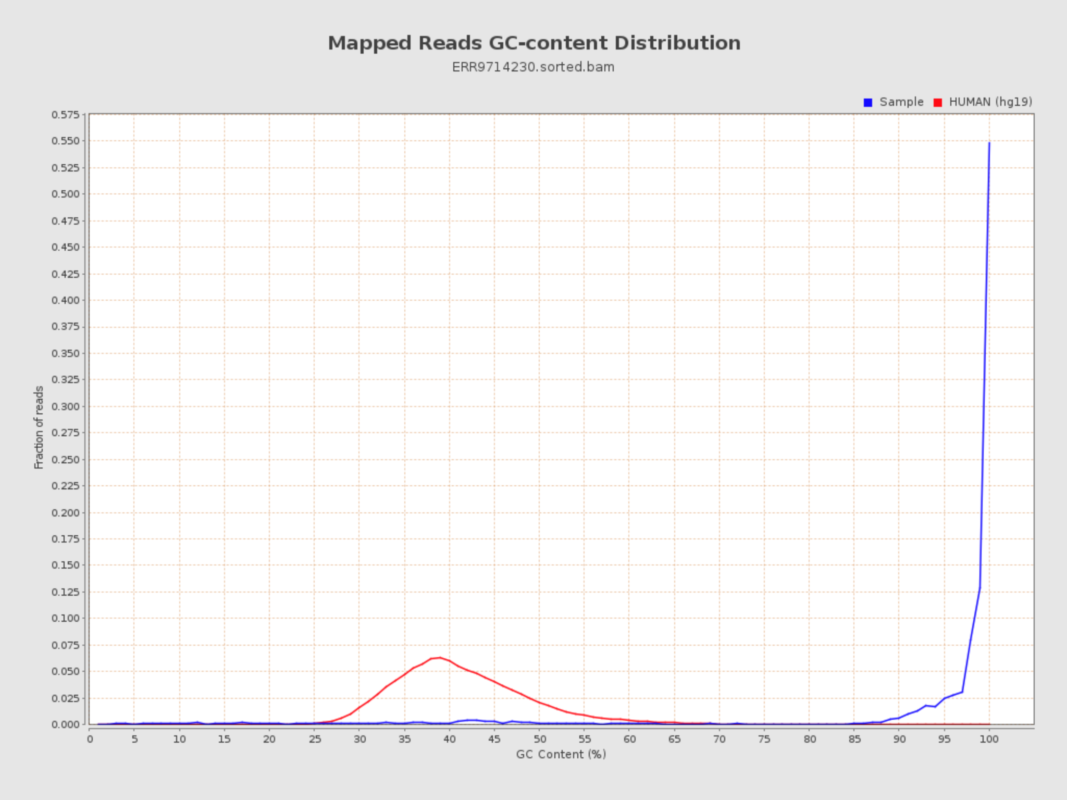
7. Results : Duplication Rate Histogram



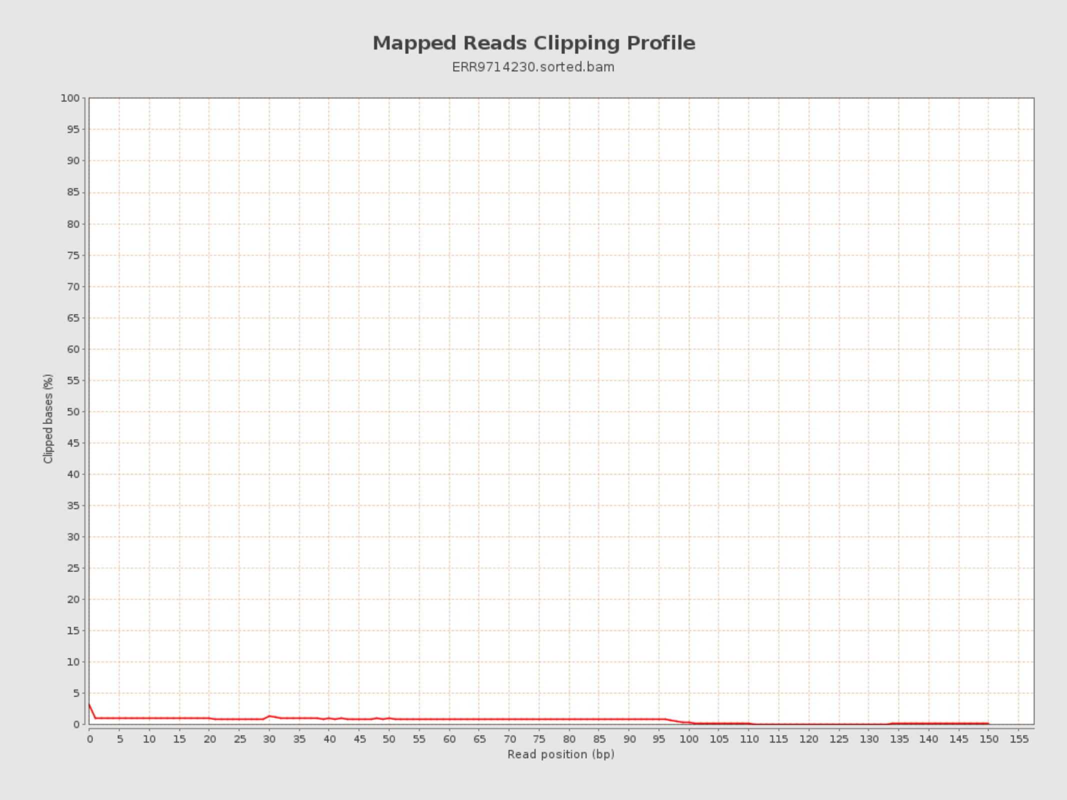
8. Results : Mapped Reads Nucleotide Content



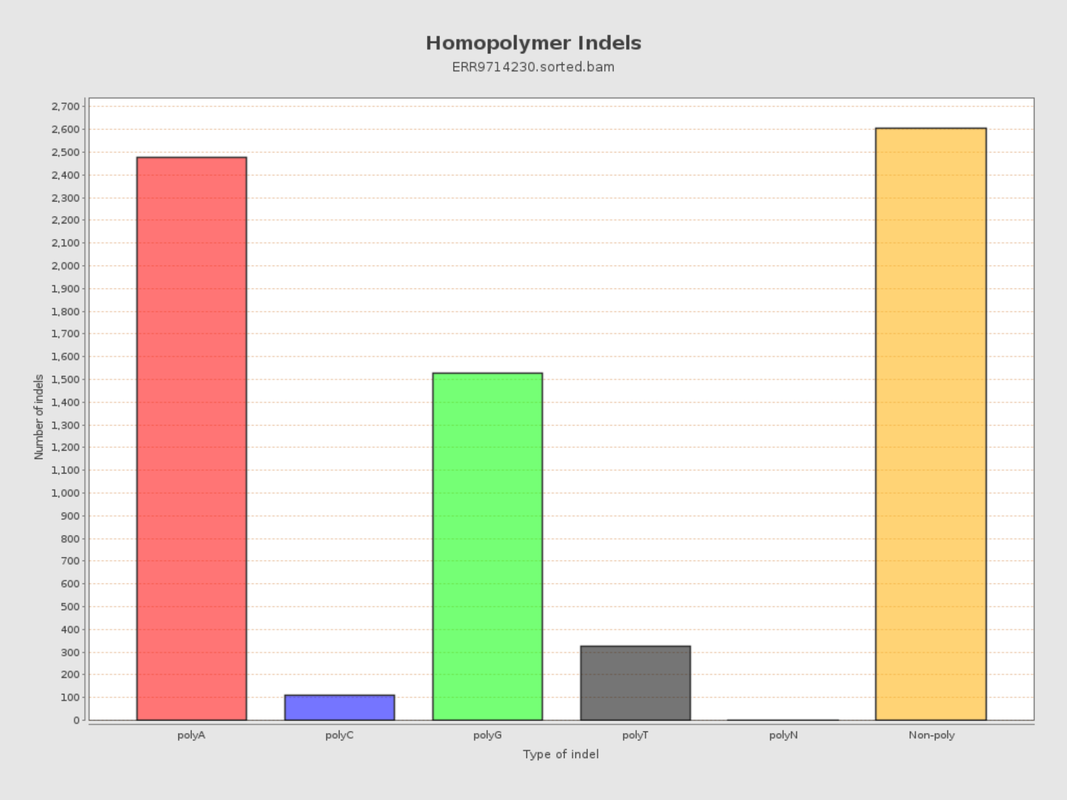
9. Results : Mapped Reads GC-content Distribution



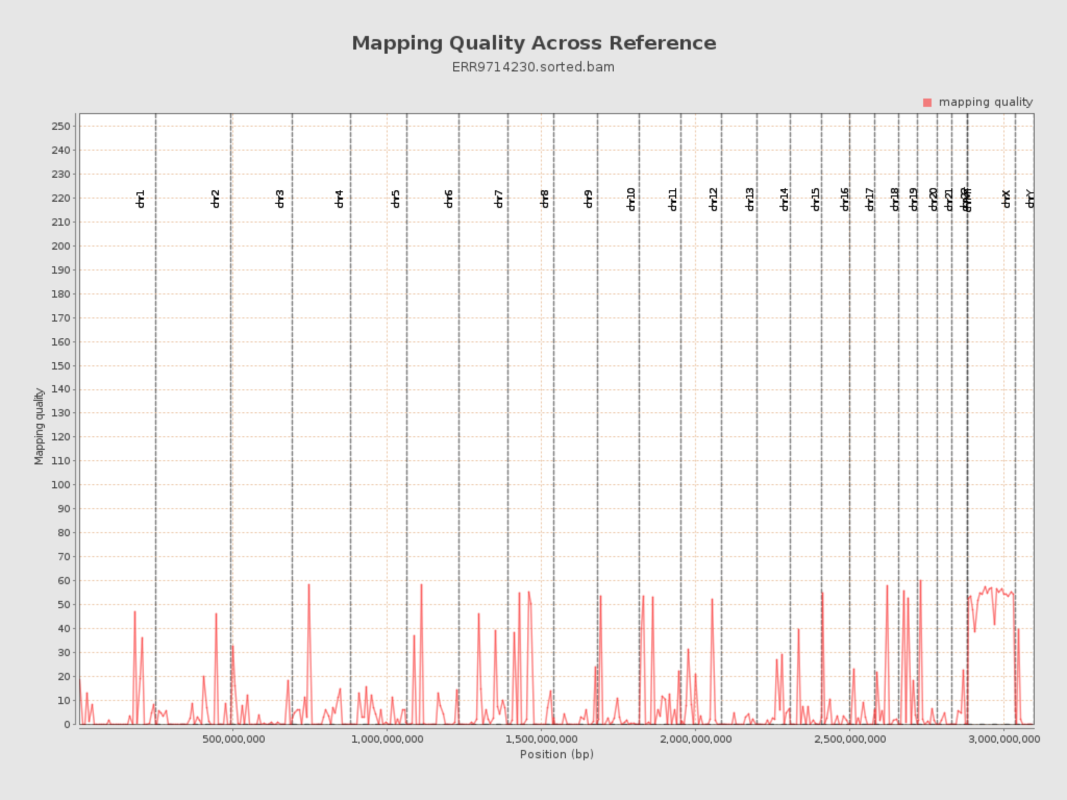
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram