Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 18:01:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714066.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_ERR9714066 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714066.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 18:01:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714066.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	577,282
Mapped reads	91,383 / 15.83%
Unmapped reads	485,899 / 84.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,590 / 0.28%
Read min/max/mean length	30 / 151 / 63.01
Duplicated reads (estimated)	90,126 / 15.61%
Duplication rate	27.61%
Clipped reads	47,093 / 8.16%

2.2. ACGT Content

Number/percentage of A's	183,986 / 1.93%
Number/percentage of C's	62,578 / 0.66%
Number/percentage of T's	80,609 / 0.84%
Number/percentage of G's	9,224,149 / 96.57%
Number/percentage of N's	199 / 0%
GC Percentage	97.23%

2.3. Coverage

Mean	0.0031

Standard Deviation	11.9056

2.4. Mapping Quality

Mean Mapping Quality	11.93

2.5. Mismatches and indels

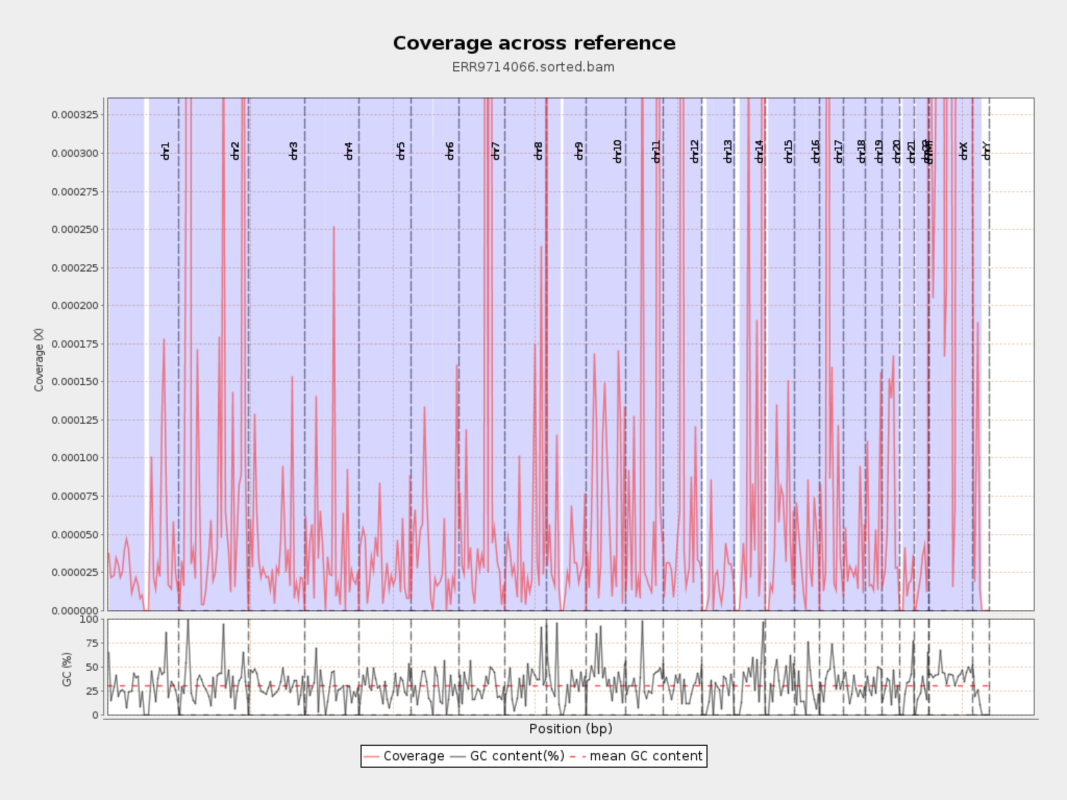
General error rate	3.23%
Mismatches	237,780
Insertions	10,746
Mapped reads with at least one insertion	7.88%
Deletions	4,365
Mapped reads with at least one deletion	4.62%
Homopolymer indels	62.56%

2.6. Chromosome stats

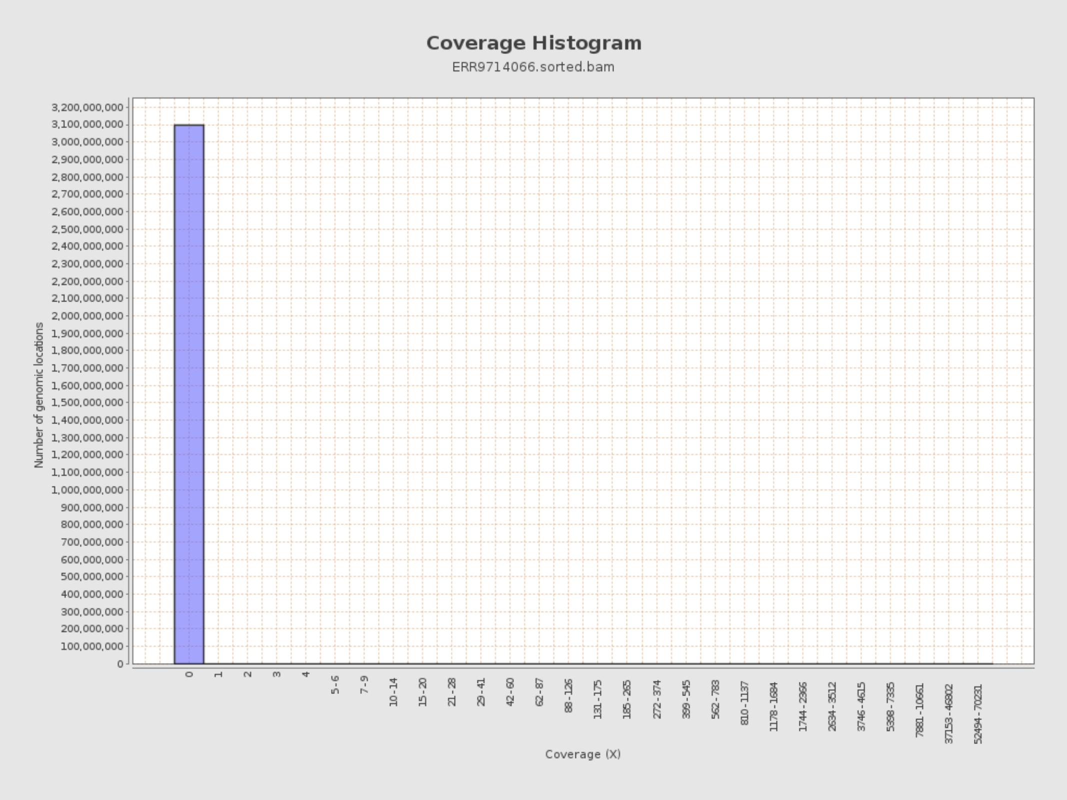
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8652	0	0.0144
chr2	243199373	9276619	0.0381	42.476
chr3	198022430	7444	0	0.0133
chr4	191154276	8398	0	0.0154
chr5	180915260	5407	0	0.0079
chr6	171115067	7018	0	0.0141
chr7	159138663	21777	0.0001	0.1343

chr8	146364022	7064	0	0.0248
chr9	141213431	5149	0	0.0166
chr10	135534747	10215	0.0001	0.0264
chr11	135006516	15030	0.0001	0.0681
chr12	133851895	13843	0.0001	0.0808
chr13	115169878	2390	0	0.0053
chr14	107349540	15560	0.0001	0.1552
chr15	102531392	5344	0.0001	0.0201
chr16	90354753	3607	0	0.0124
chr17	81195210	11921	0.0001	0.136
chr18	78077248	2627	0	0.0097
chr19	59128983	3113	0.0001	0.0165
chr20	63025520	4694	0.0001	0.0315
chr21	48129895	869	0	0.006
chr22	51304566	1008	0	0.0053
chrMT	16571	1500	0.0905	0.4205
chrX	155270560	129748	0.0008	0.1555
chrY	59373566	1915	0	0.013

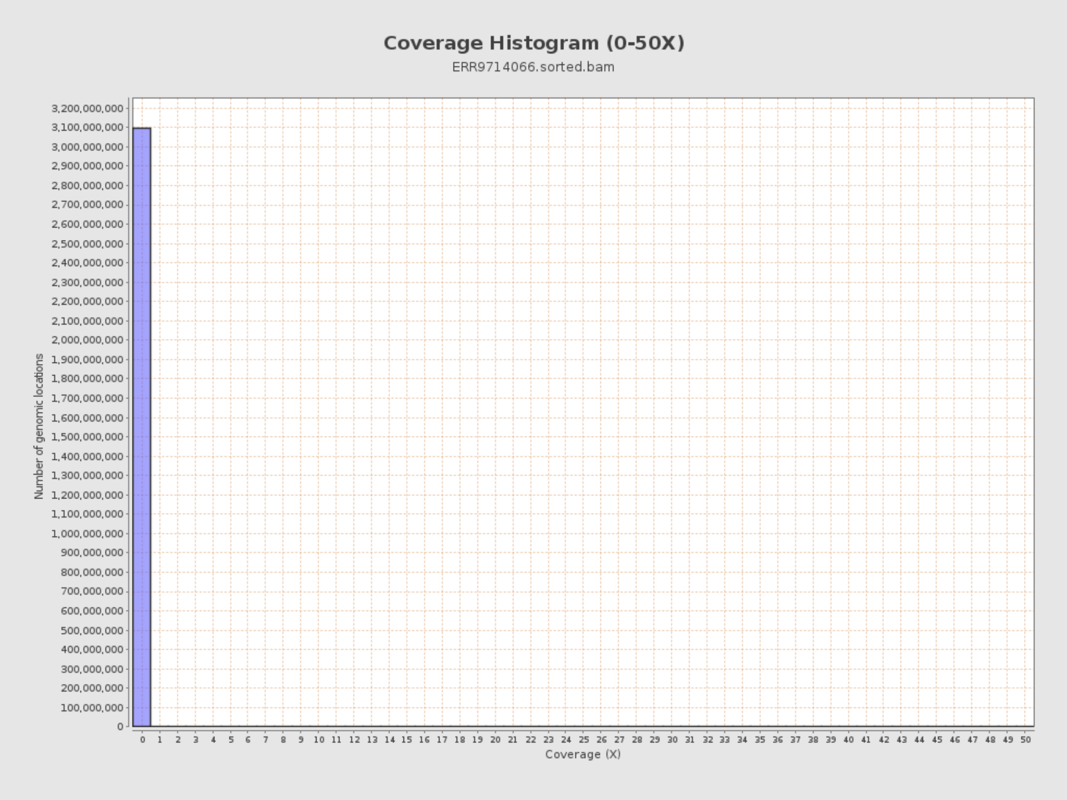
3. Results : Coverage across reference



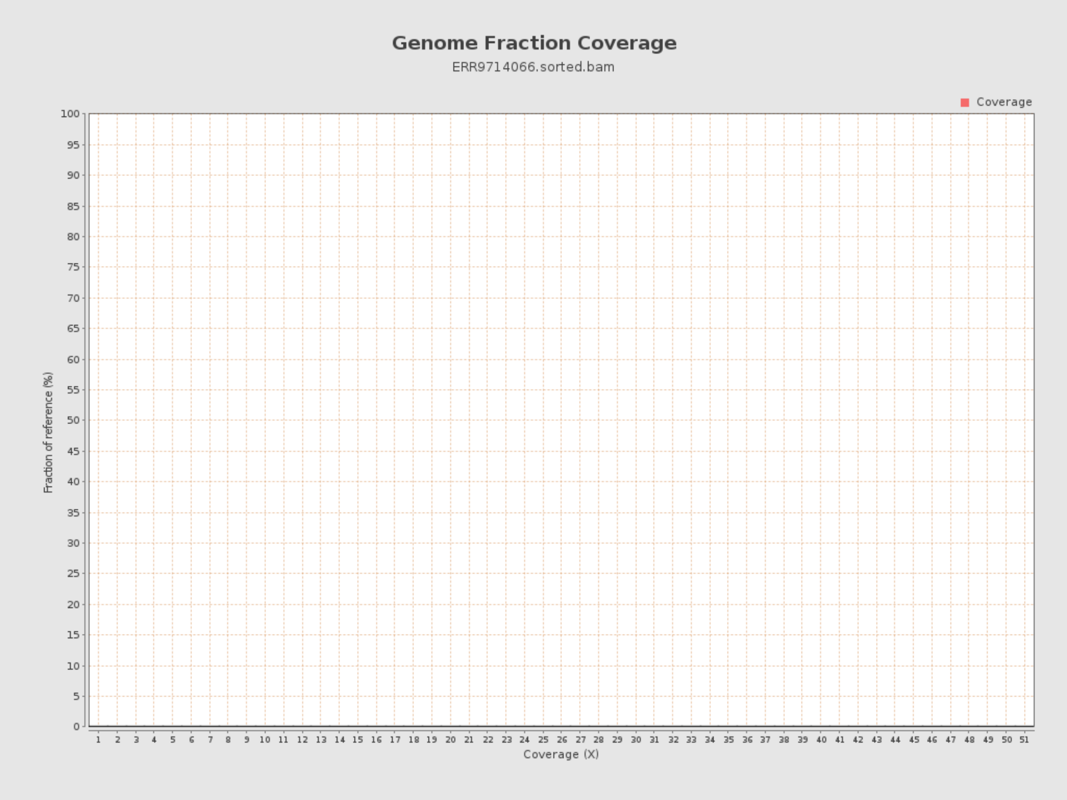
4. Results : Coverage Histogram



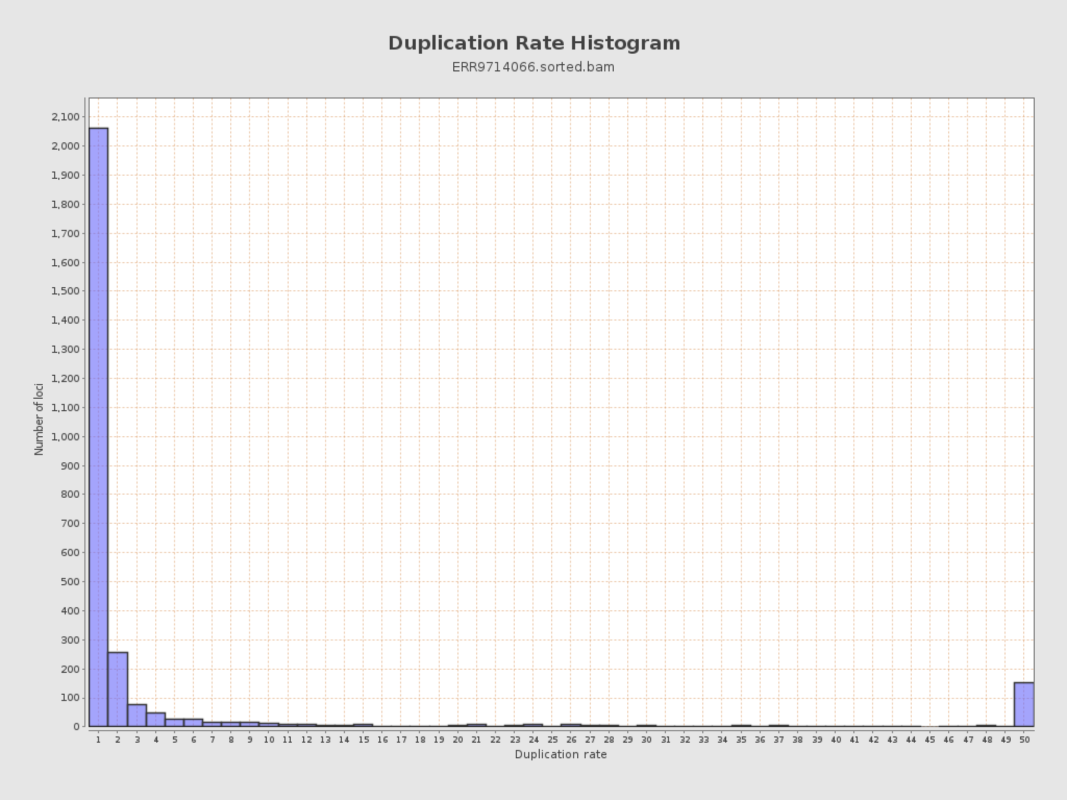
5. Results : Coverage Histogram (0-50X)



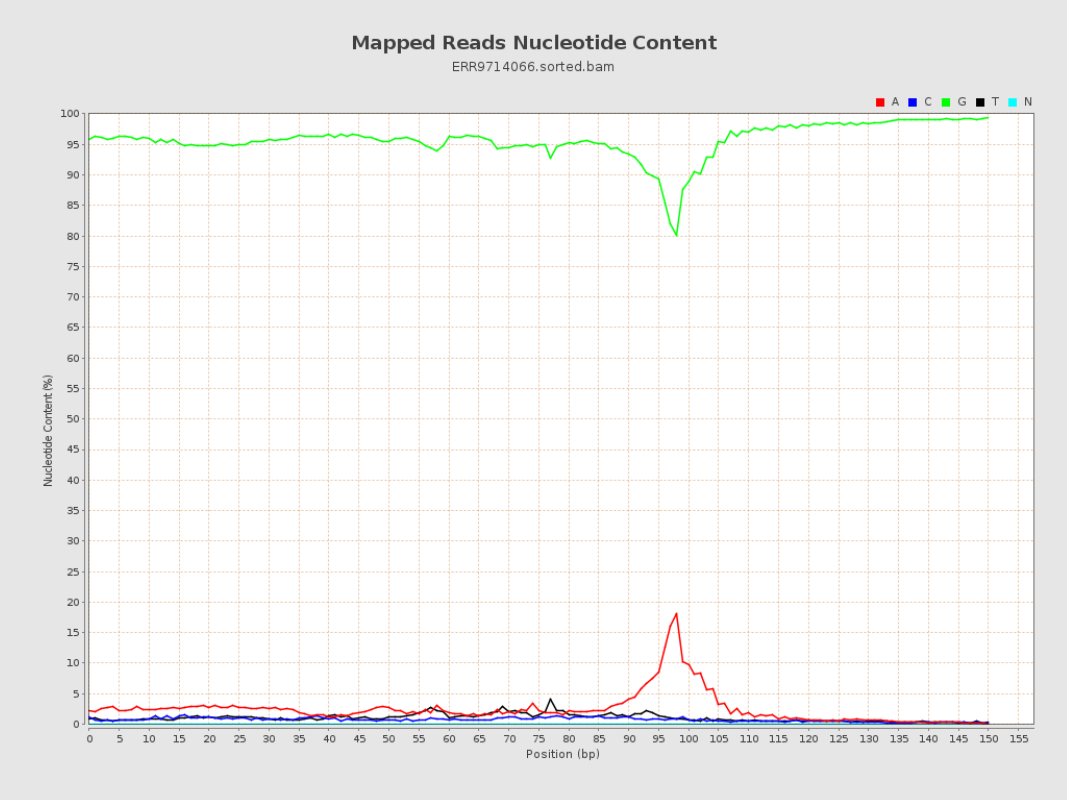
6. Results : Genome Fraction Coverage



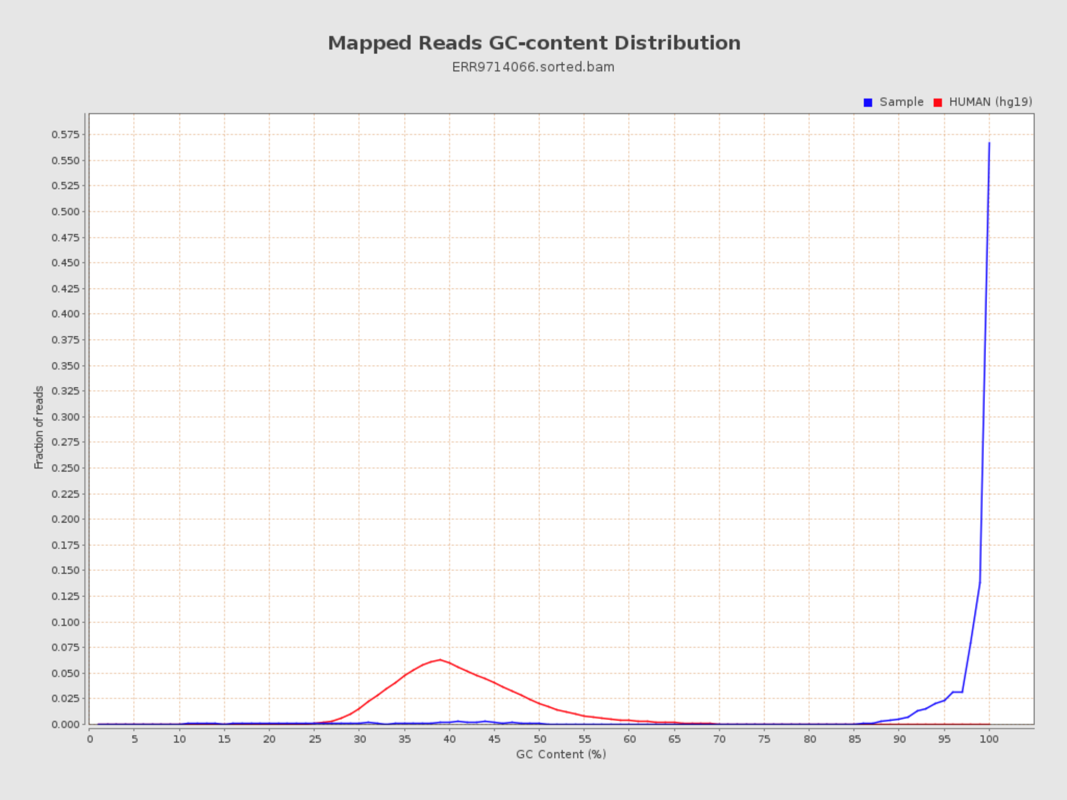
7. Results : Duplication Rate Histogram



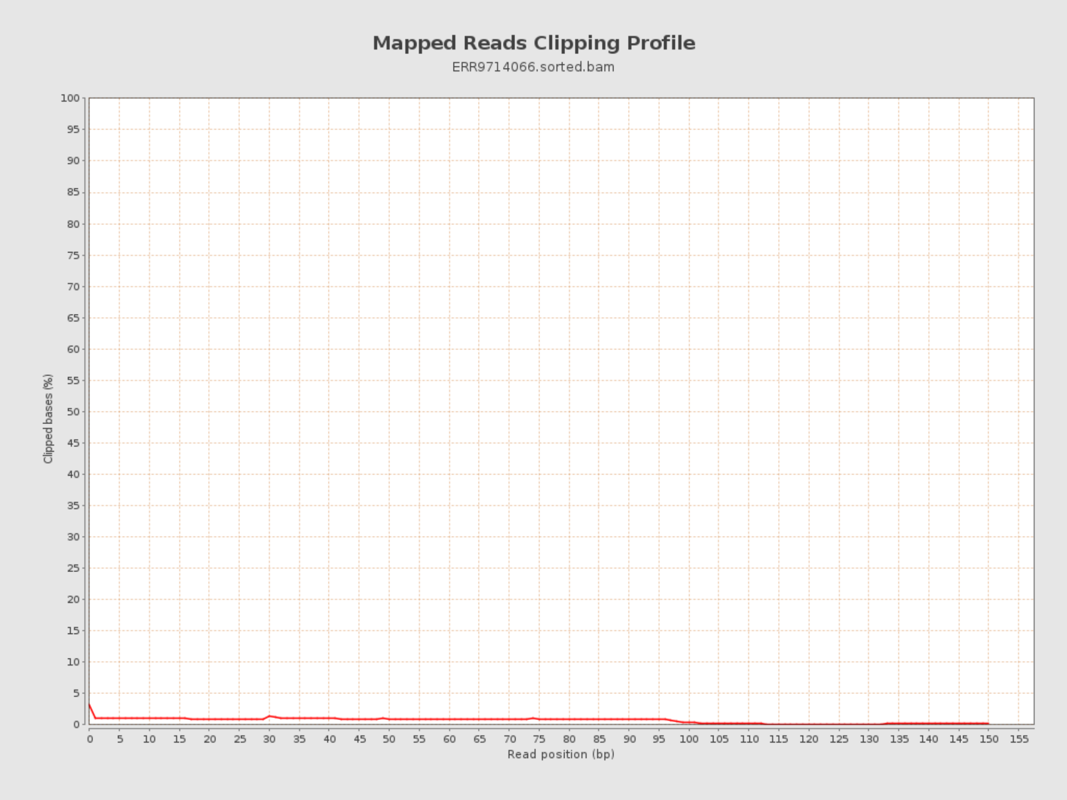
8. Results : Mapped Reads Nucleotide Content



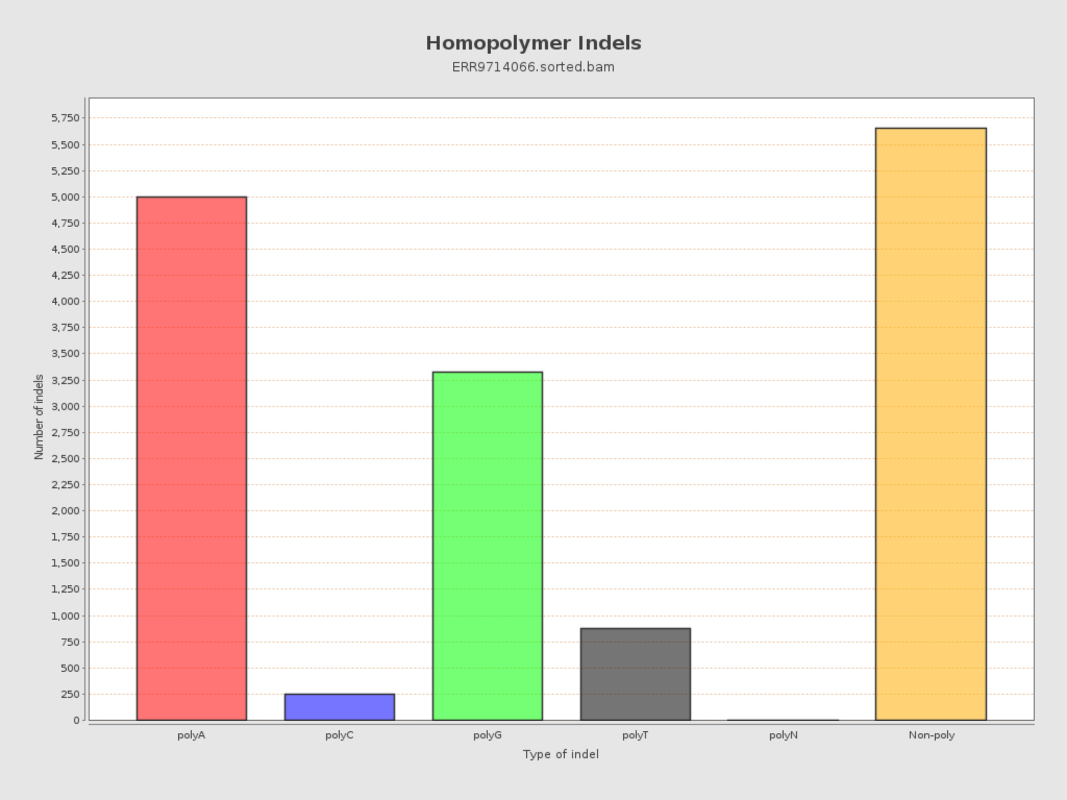
9. Results : Mapped Reads GC-content Distribution



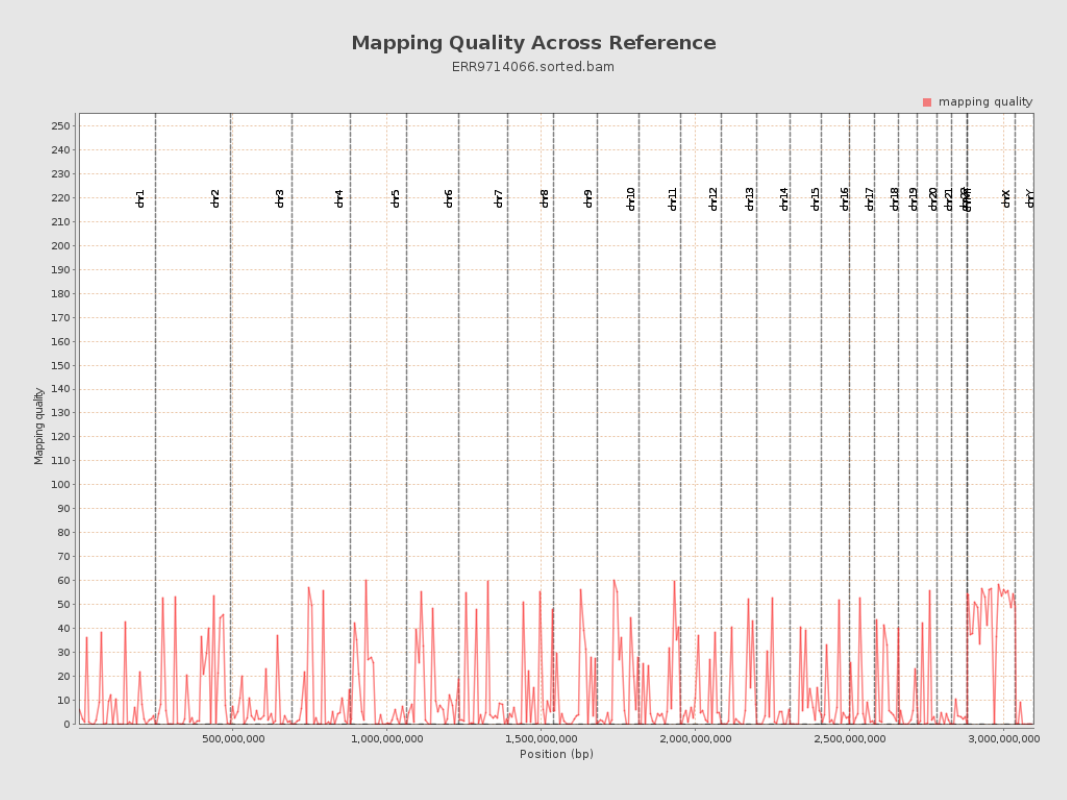
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram