Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 18:25:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714077.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_ERR9714077 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714077.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 18:25:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714077.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	680,552
Mapped reads	111,750 / 16.42%
Unmapped reads	568,802 / 83.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,016 / 0.59%
Read min/max/mean length	30 / 151 / 62.89
Duplicated reads (estimated)	110,248 / 16.2%
Duplication rate	22.04%
Clipped reads	62,620 / 9.2%

2.2. ACGT Content

Number/percentage of A's	330,168 / 2.87%
Number/percentage of C's	95,242 / 0.83%
Number/percentage of T's	128,123 / 1.12%
Number/percentage of G's	10,931,065 / 95.18%
Number/percentage of N's	438 / 0%
GC Percentage	96.01%

2.3. Coverage

Mean	0.0037

Standard Deviation	14.0617

2.4. Mapping Quality

Mean Mapping Quality	16.14

2.5. Mismatches and indels

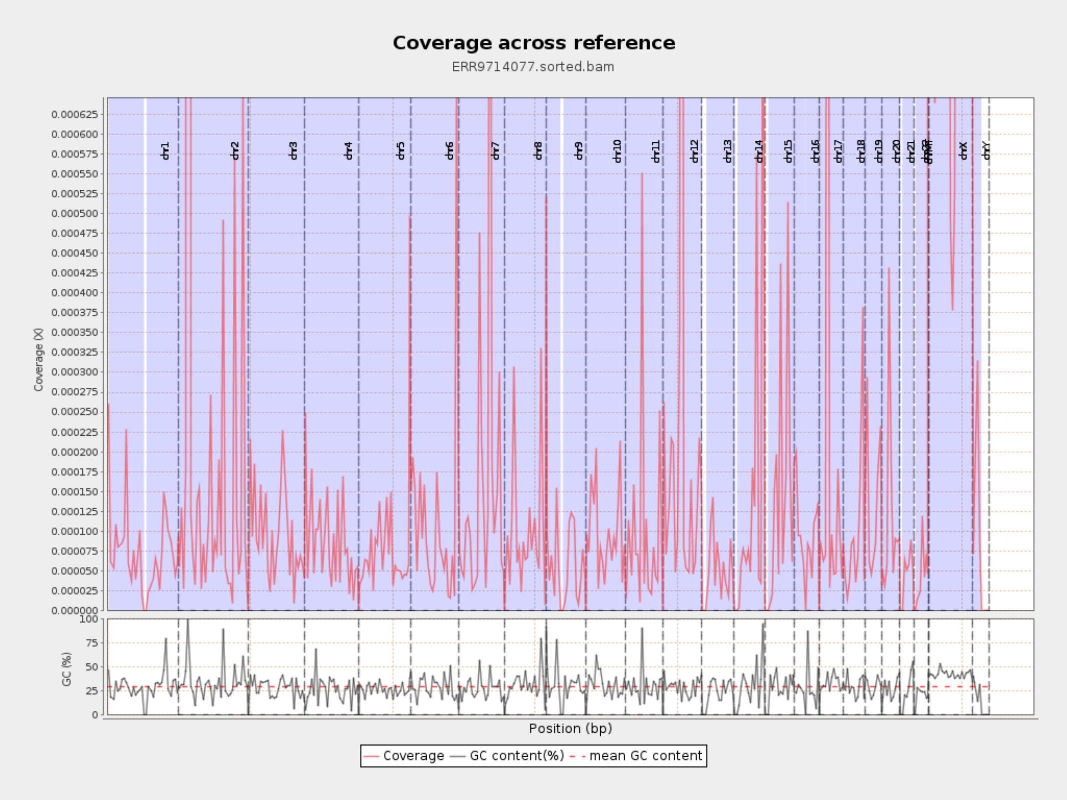
General error rate	3.27%
Mismatches	278,552
Insertions	13,431
Mapped reads with at least one insertion	7.72%
Deletions	5,663
Mapped reads with at least one deletion	4.86%
Homopolymer indels	66.89%

2.6. Chromosome stats

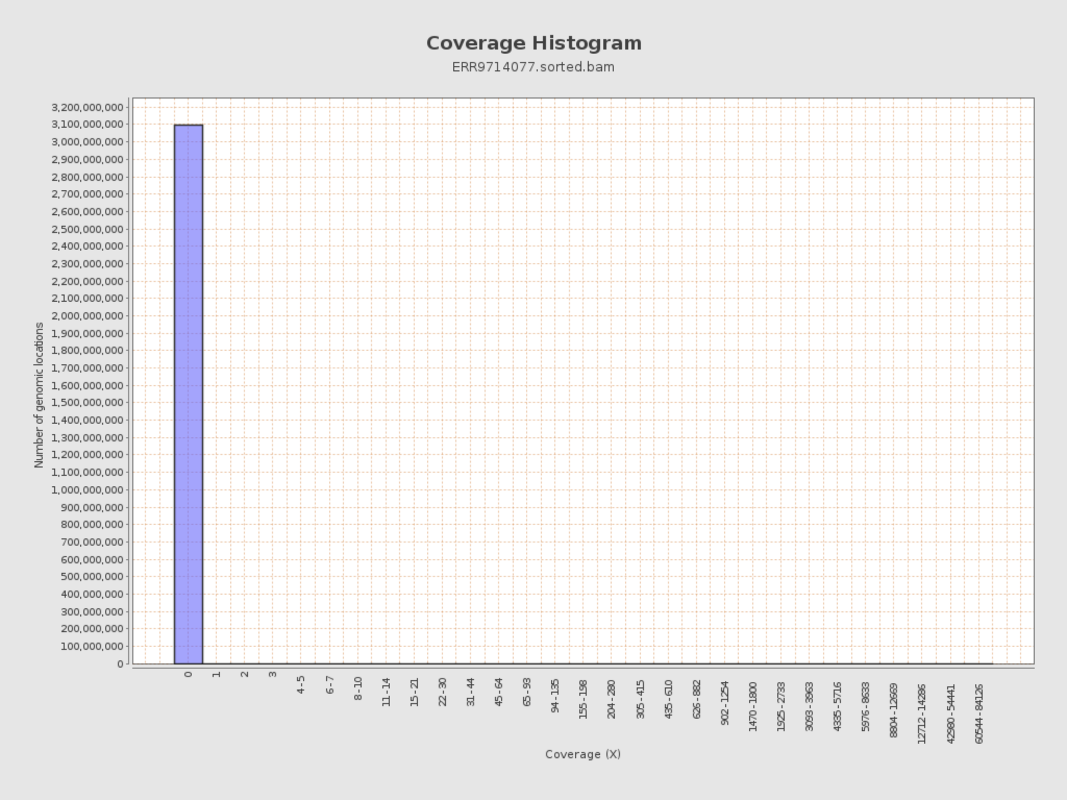
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18732	0.0001	0.0174
chr2	243199373	10972804	0.0451	50.1682
chr3	198022430	19094	0.0001	0.0244
chr4	191154276	16690	0.0001	0.0223
chr5	180915260	13266	0.0001	0.0131
chr6	171115067	19074	0.0001	0.0432
chr7	159138663	28067	0.0002	0.1246

chr8	146364022	14453	0.0001	0.0302
chr9	141213431	8259	0.0001	0.0172
chr10	135534747	13261	0.0001	0.0239
chr11	135006516	13361	0.0001	0.0562
chr12	133851895	38247	0.0003	0.1899
chr13	115169878	5804	0.0001	0.0099
chr14	107349540	17041	0.0002	0.1217
chr15	102531392	14659	0.0001	0.0508
chr16	90354753	8756	0.0001	0.0189
chr17	81195210	20135	0.0002	0.2456
chr18	78077248	7418	0.0001	0.0302
chr19	59128983	7811	0.0001	0.0426
chr20	63025520	7742	0.0001	0.0738
chr21	48129895	2287	0	0.0091
chr22	51304566	2178	0	0.0103
chrMT	16571	5032	0.3037	1.3868
chrX	155270560	232052	0.0015	0.1899
chrY	59373566	4650	0.0001	0.0237

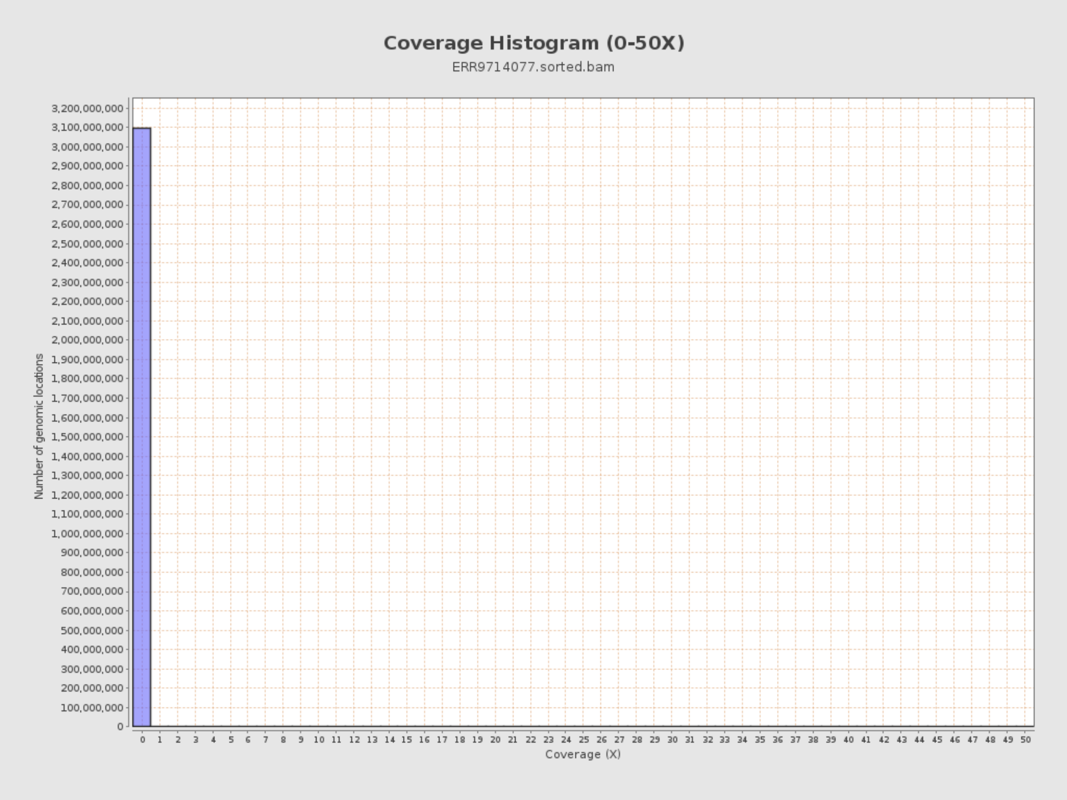
3. Results : Coverage across reference



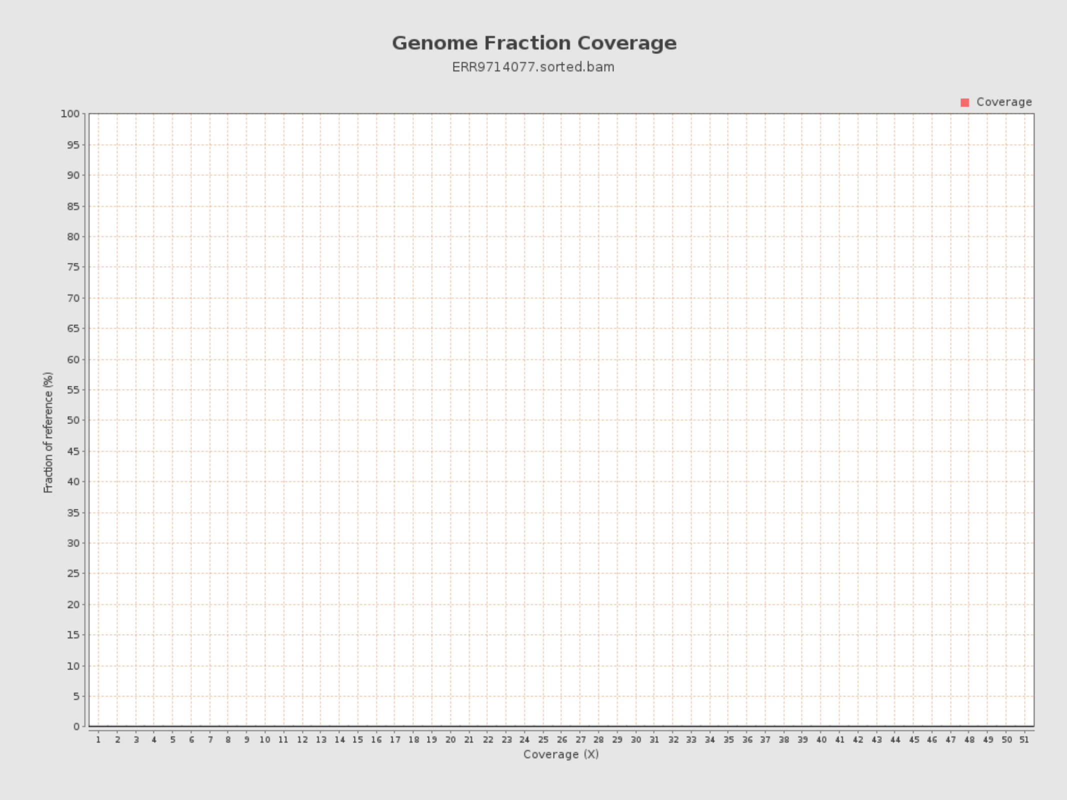
4. Results : Coverage Histogram



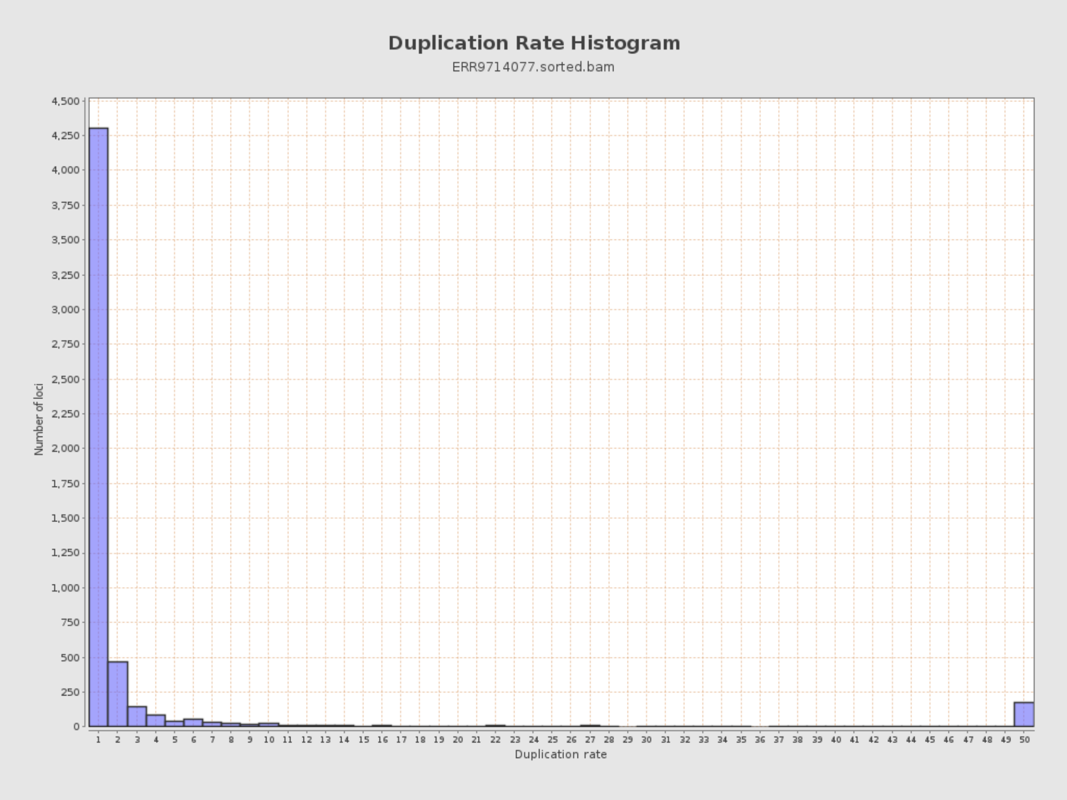
5. Results : Coverage Histogram (0-50X)



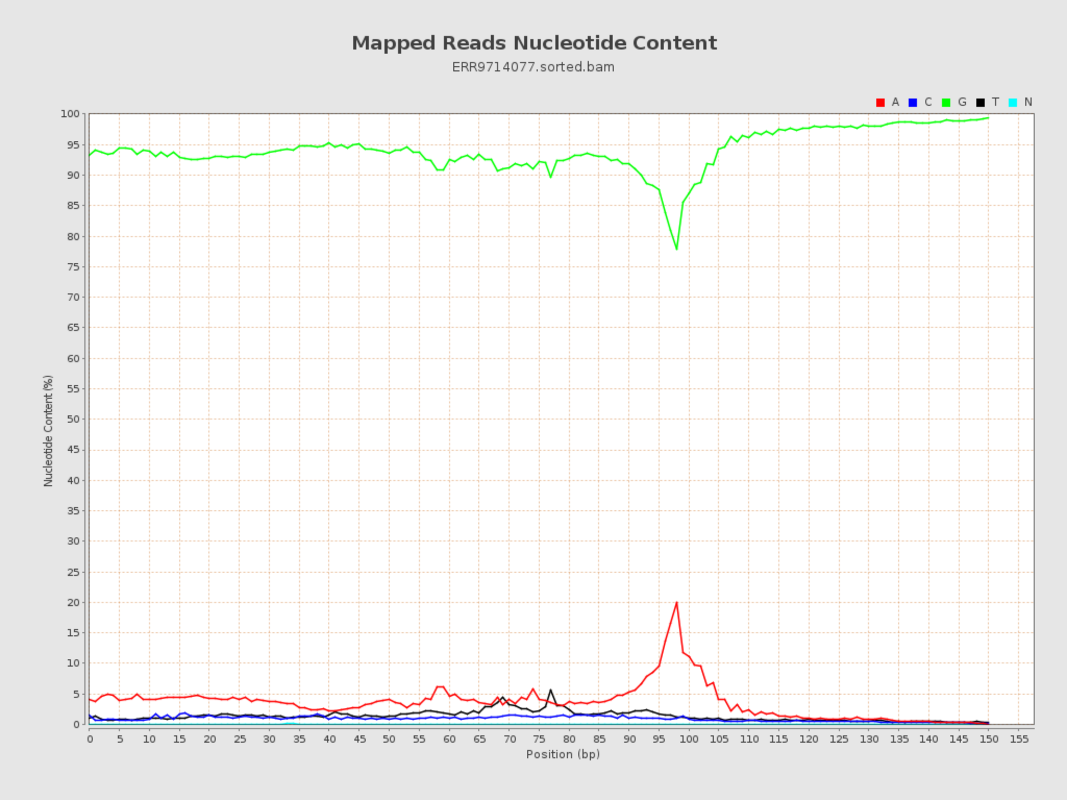
6. Results : Genome Fraction Coverage



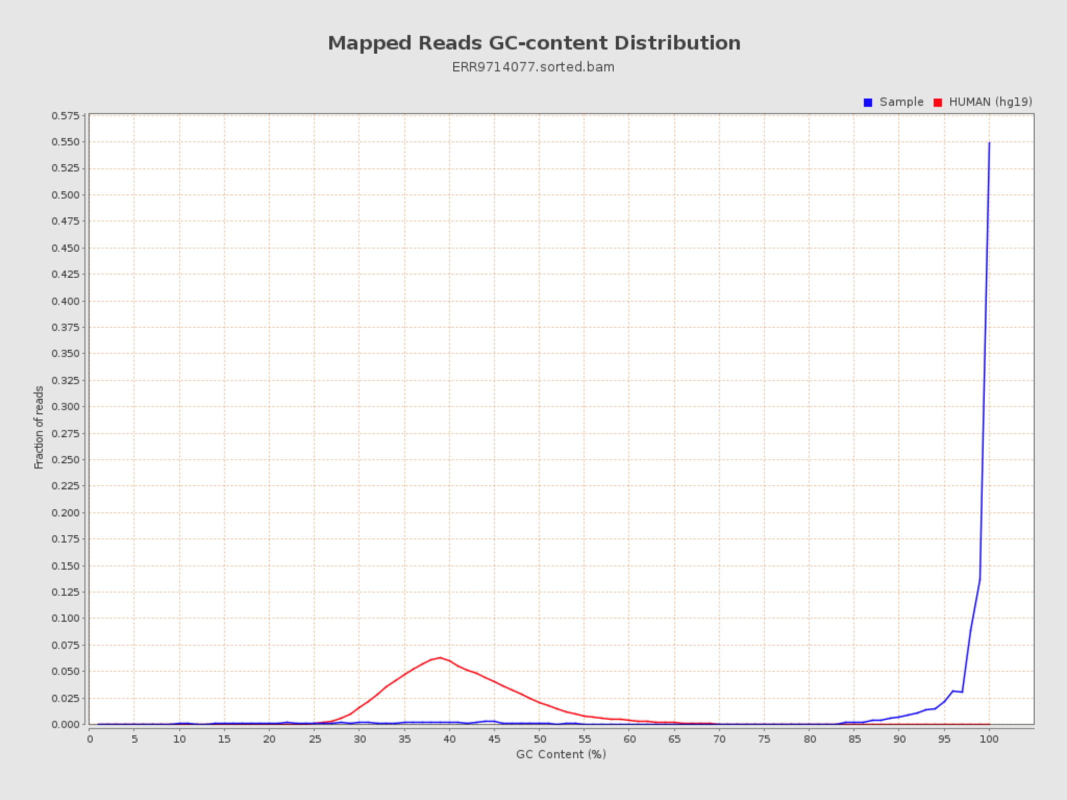
7. Results : Duplication Rate Histogram



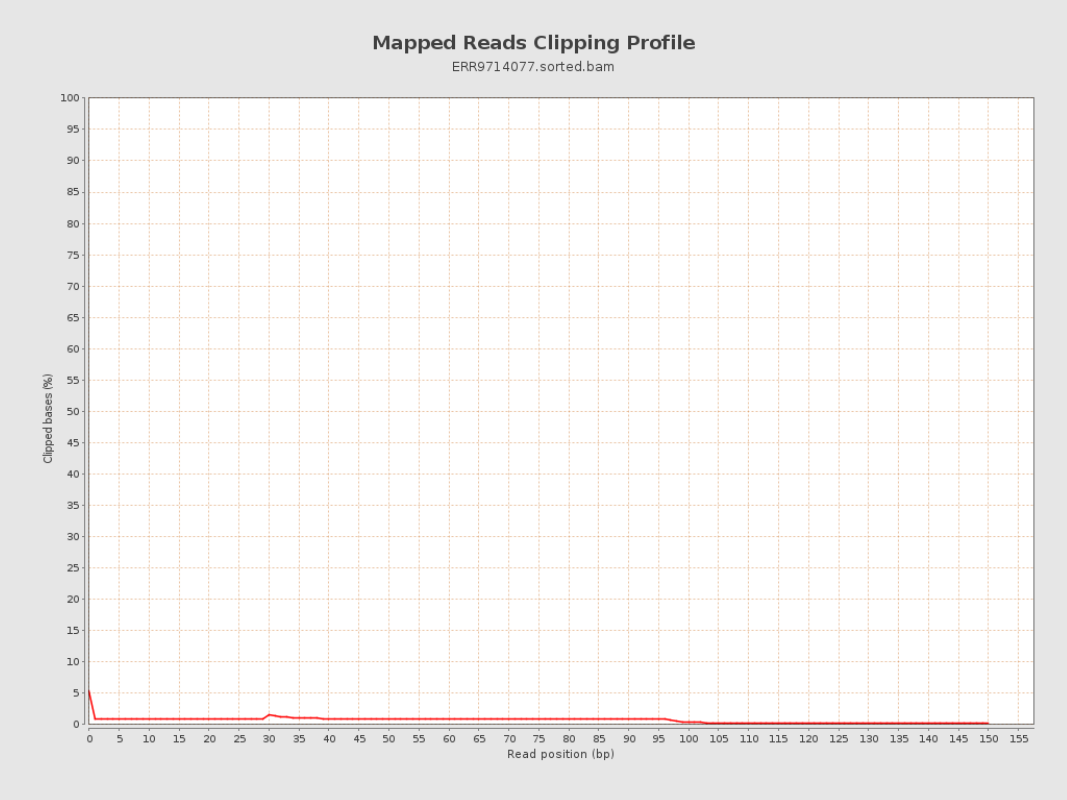
8. Results : Mapped Reads Nucleotide Content



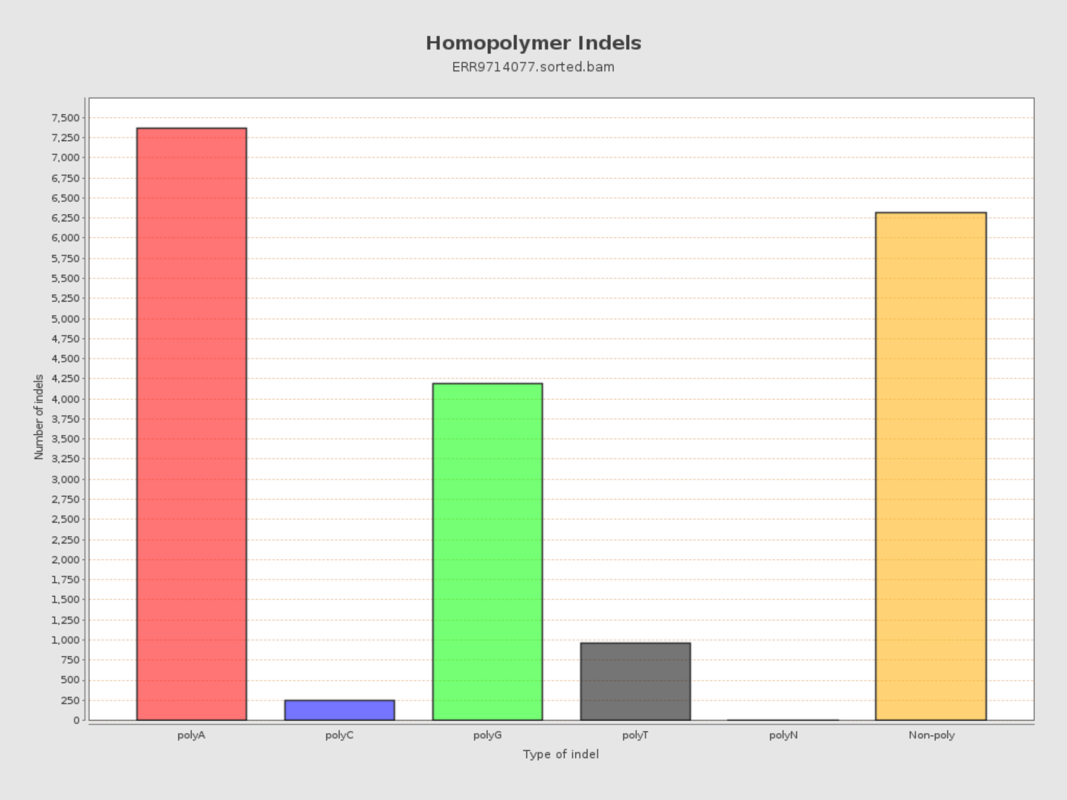
9. Results : Mapped Reads GC-content Distribution



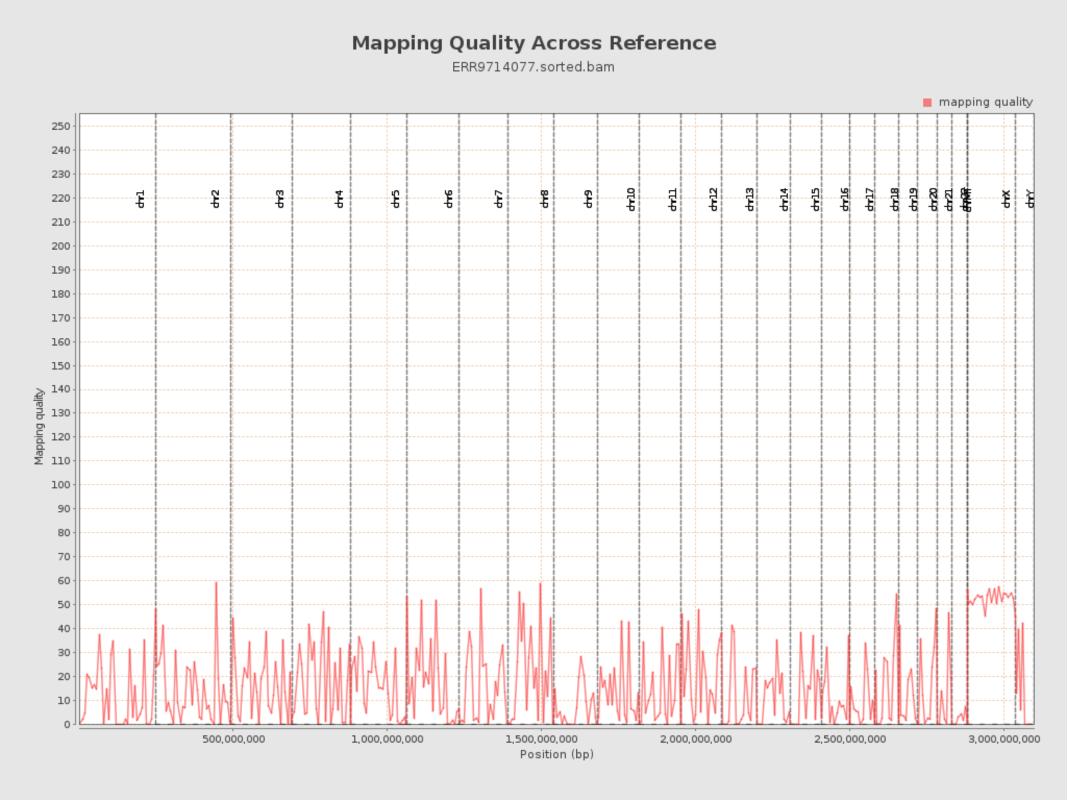
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram