Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 00:09:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714205.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_ERR9714205 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714205.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 00:09:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714205.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	87,638
Mapped reads	45,458 / 51.87%
Unmapped reads	42,180 / 48.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,206 / 1.38%
Read min/max/mean length	30 / 151 / 102.8
Duplicated reads (estimated)	33,053 / 37.72%
Duplication rate	41.52%
Clipped reads	39,990 / 45.63%

2.2. ACGT Content

Number/percentage of A's	1,450,608 / 25.61%
Number/percentage of C's	1,106,594 / 19.54%
Number/percentage of T's	1,377,964 / 24.33%
Number/percentage of G's	1,728,512 / 30.52%
Number/percentage of N's	52 / 0%
GC Percentage	50.06%

2.3. Coverage

Mean	0.0019

Standard Deviation	0.77

2.4. Mapping Quality

Mean Mapping Quality	50.71

2.5. Mismatches and indels

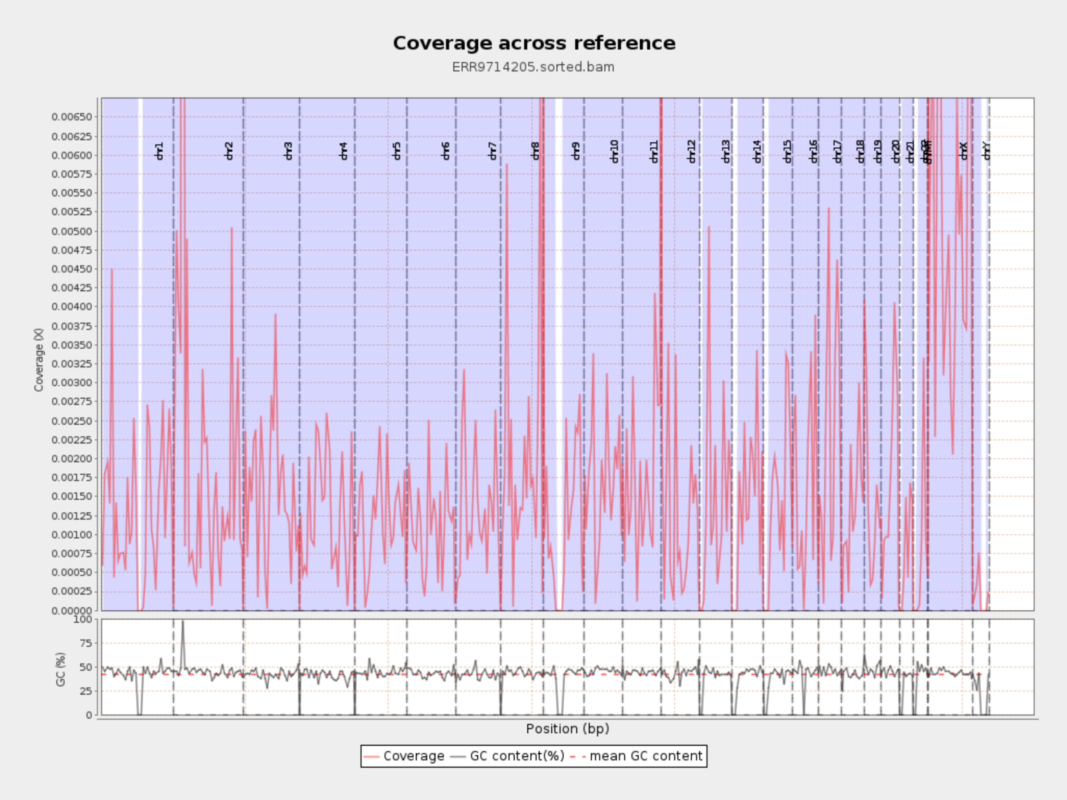
General error rate	4.06%
Mismatches	211,300
Insertions	5,542
Mapped reads with at least one insertion	11.44%
Deletions	17,249
Mapped reads with at least one deletion	36.58%
Homopolymer indels	30.73%

2.6. Chromosome stats

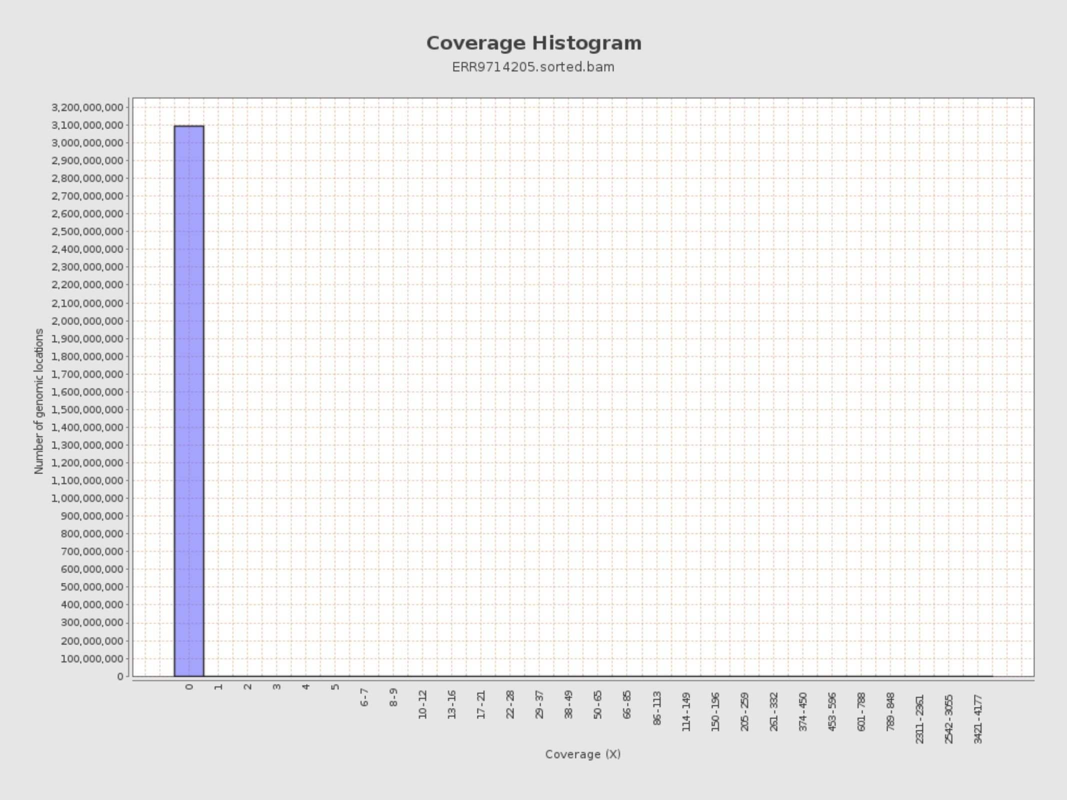
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	341701	0.0014	0.1789
chr2	243199373	1030734	0.0042	2.6151
chr3	198022430	308374	0.0016	0.1861
chr4	191154276	245407	0.0013	0.1779
chr5	180915260	221659	0.0012	0.1635
chr6	171115067	194903	0.0011	0.1576
chr7	159138663	212783	0.0013	0.184

chr8	146364022	299866	0.002	0.2911
chr9	141213431	164242	0.0012	0.1545
chr10	135534747	231548	0.0017	0.2118
chr11	135006516	246007	0.0018	0.2427
chr12	133851895	166205	0.0012	0.1838
chr13	115169878	158727	0.0014	0.1968
chr14	107349540	150851	0.0014	0.1962
chr15	102531392	143340	0.0014	0.175
chr16	90354753	143741	0.0016	0.1995
chr17	81195210	183442	0.0023	0.2795
chr18	78077248	108070	0.0014	0.1786
chr19	59128983	82422	0.0014	0.1926
chr20	63025520	109545	0.0017	0.2048
chr21	48129895	38491	0.0008	0.1229
chr22	51304566	41913	0.0008	0.1311
chrMT	16571	79227	4.7811	44.3006
chrX	155270560	853746	0.0055	0.4992
chrY	59373566	12320	0.0002	0.0524

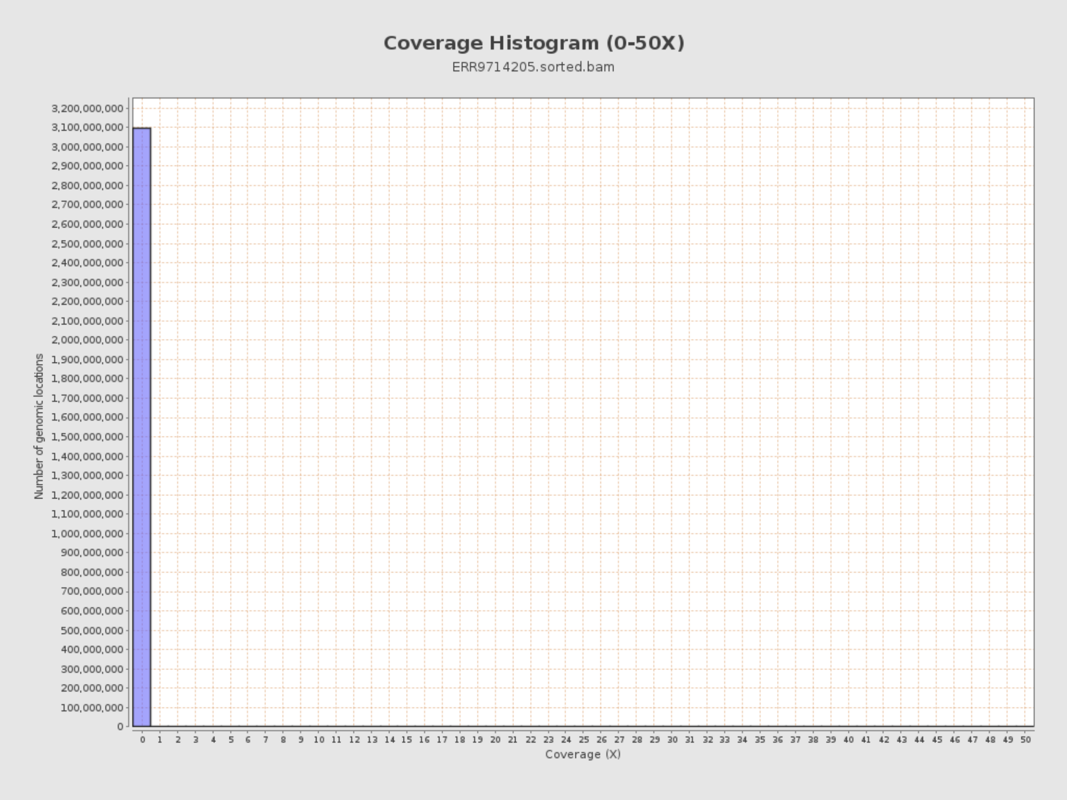
3. Results : Coverage across reference



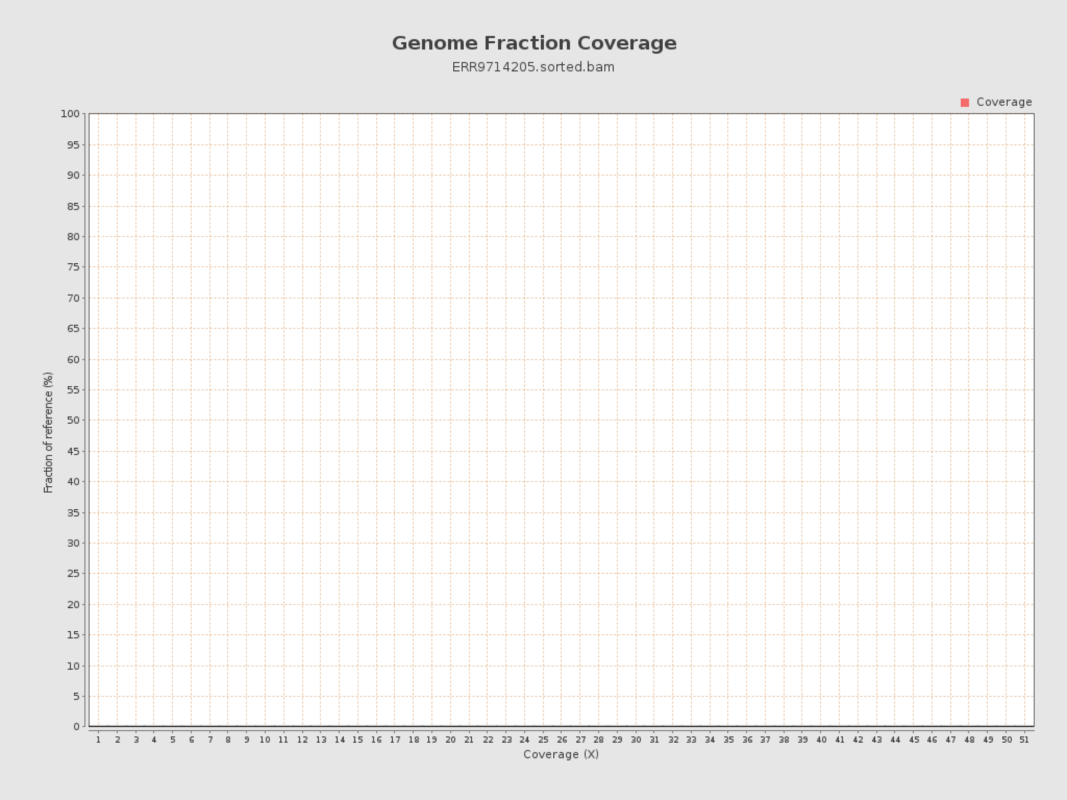
4. Results : Coverage Histogram



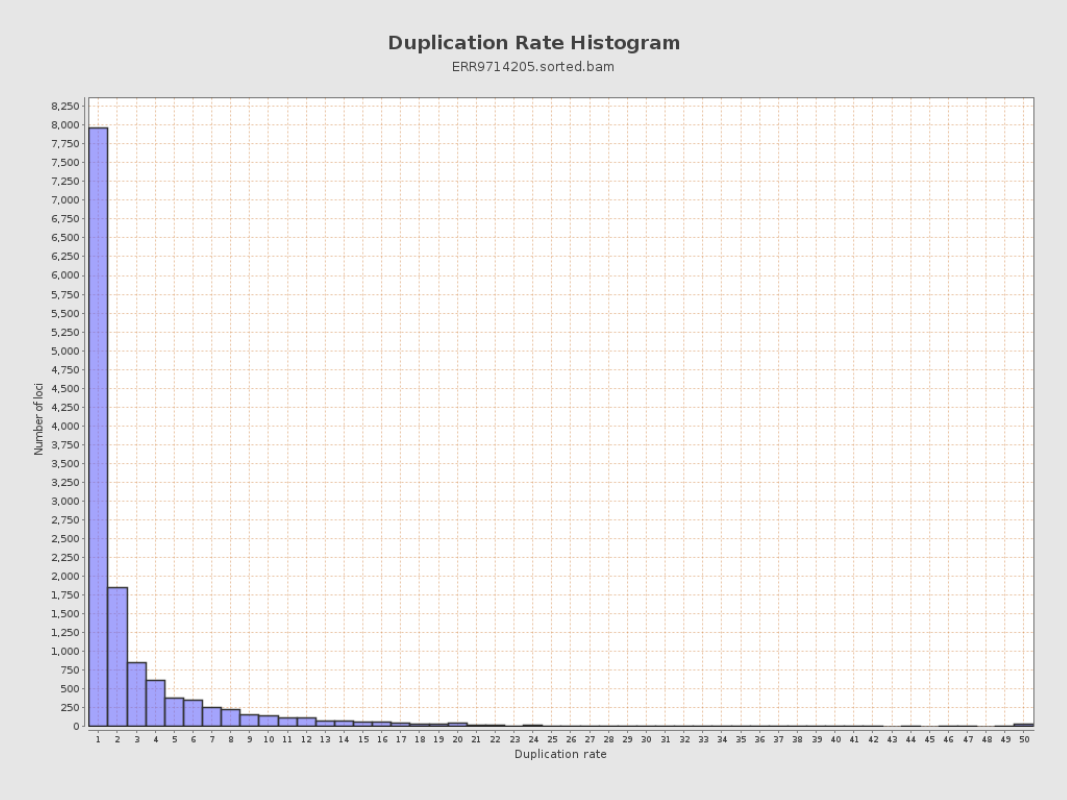
5. Results : Coverage Histogram (0-50X)



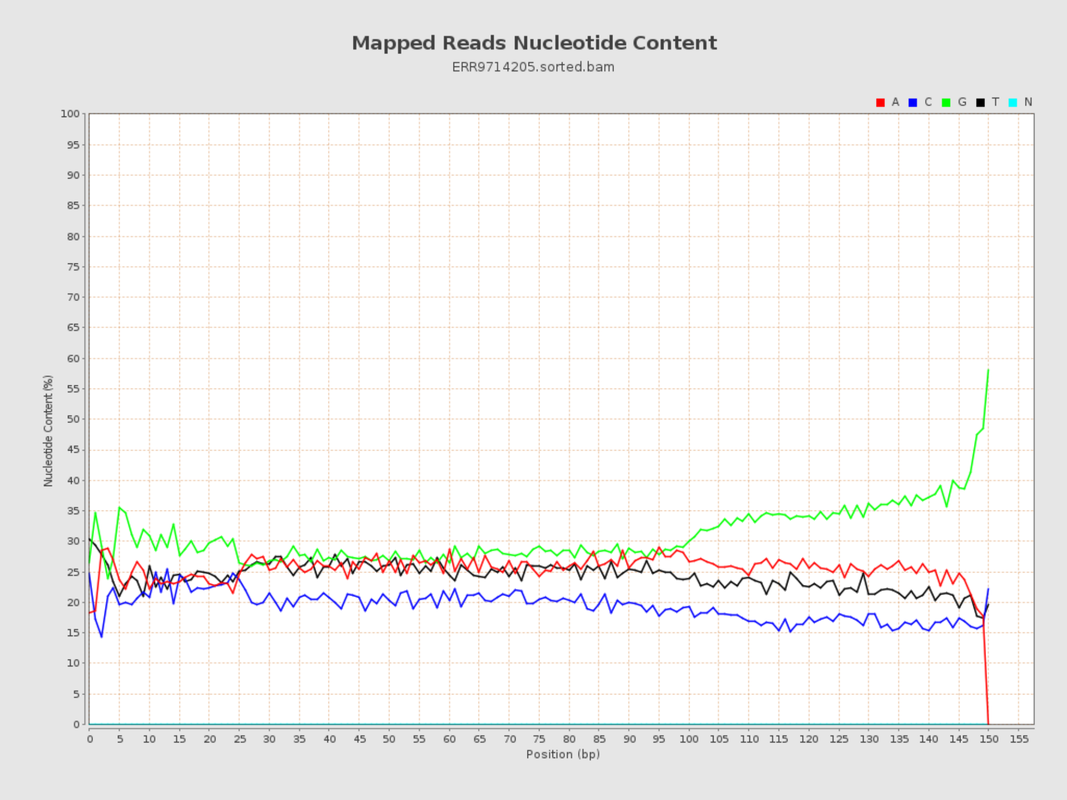
6. Results : Genome Fraction Coverage



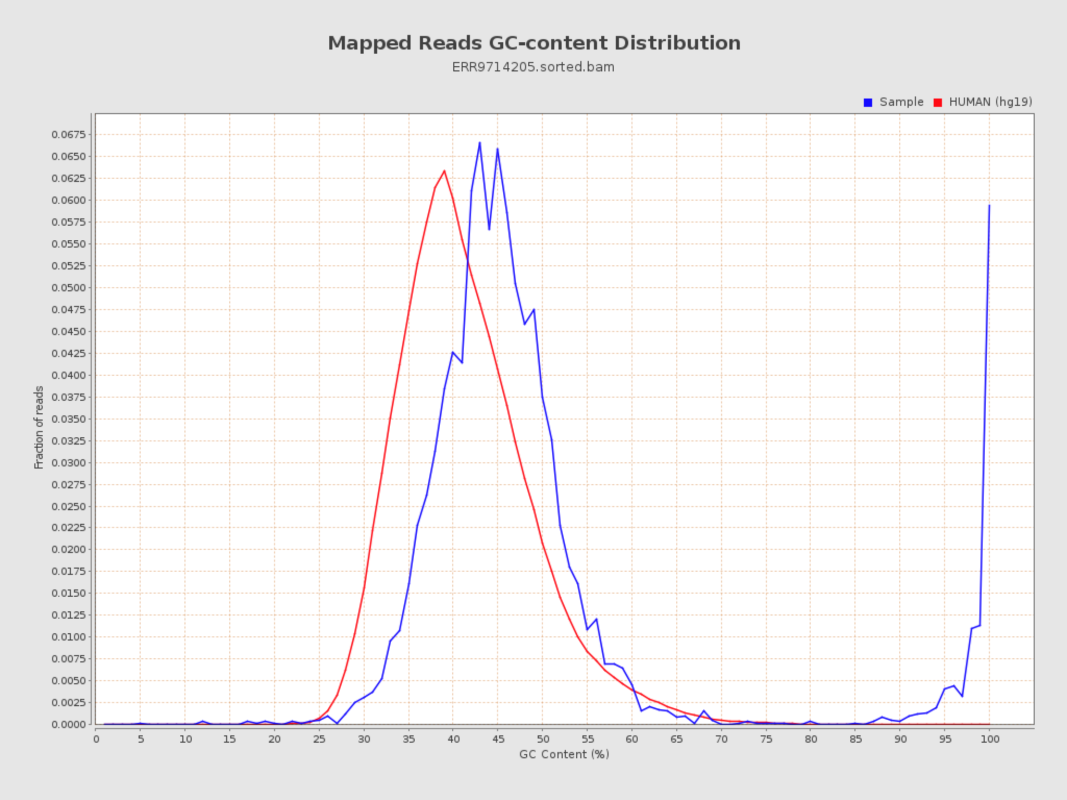
7. Results : Duplication Rate Histogram



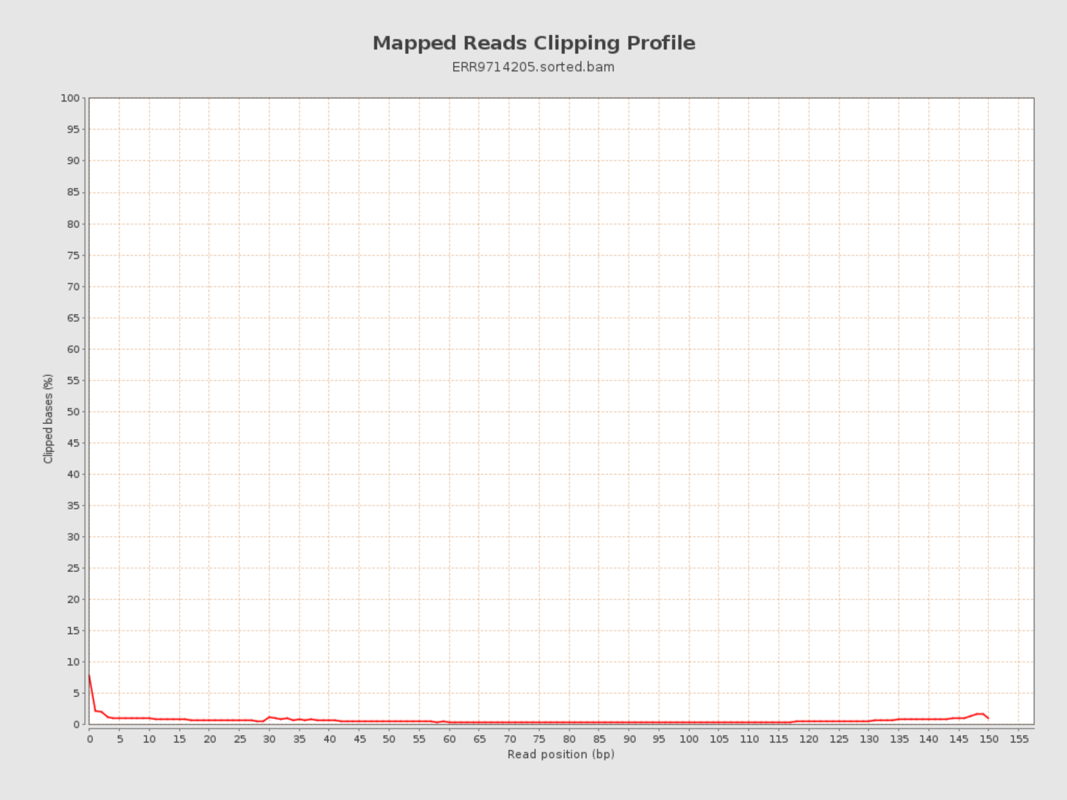
8. Results : Mapped Reads Nucleotide Content



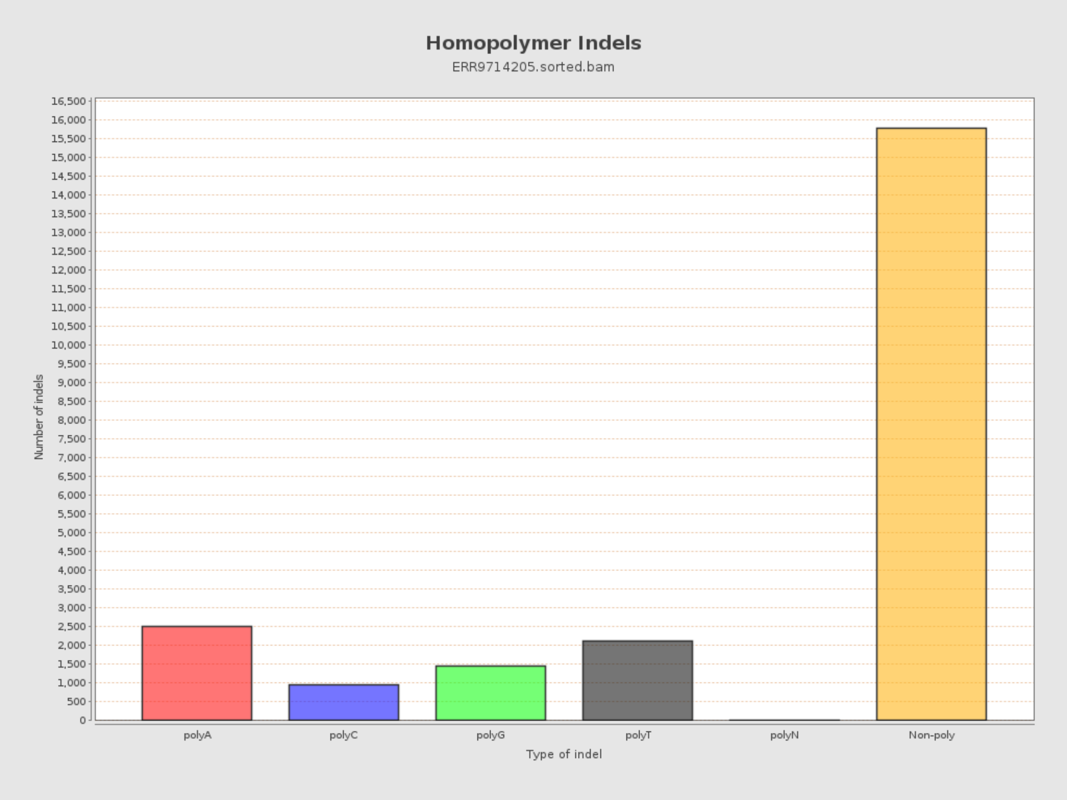
9. Results : Mapped Reads GC-content Distribution



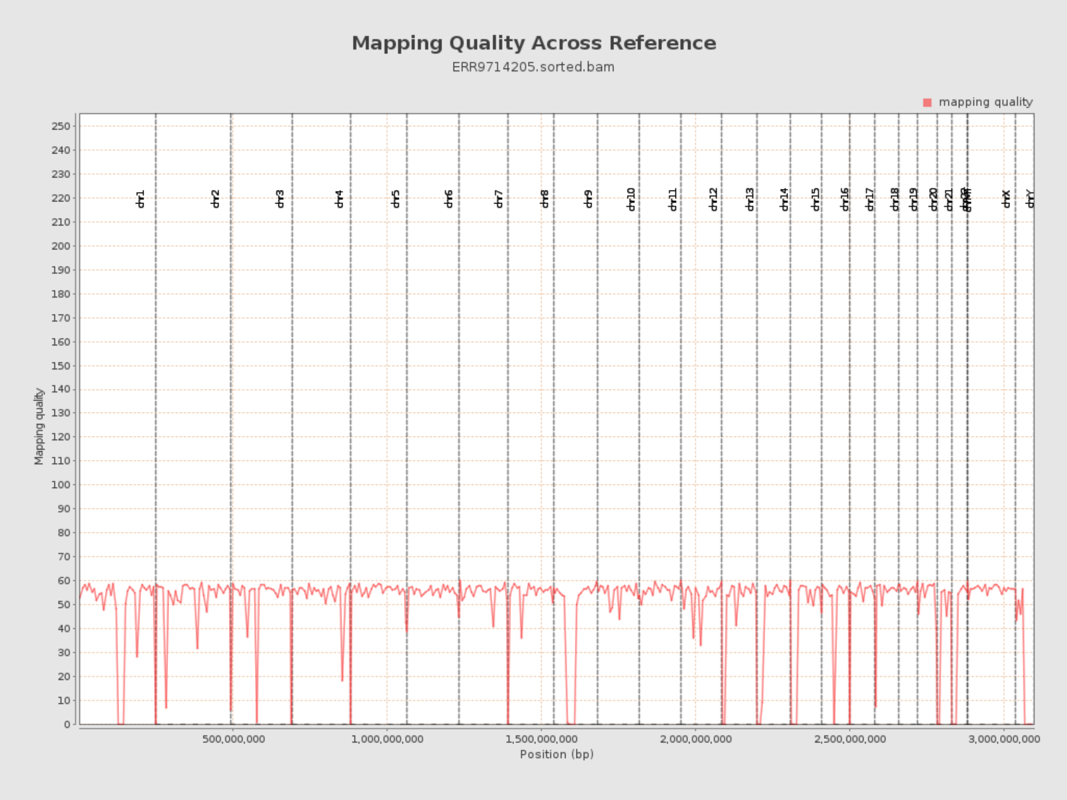
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram