Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 00:07:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714204.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_ERR9714204 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714204.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 00:07:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714204.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	113,396
Mapped reads	22,418 / 19.77%
Unmapped reads	90,978 / 80.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,111 / 0.98%
Read min/max/mean length	30 / 151 / 72.81
Duplicated reads (estimated)	19,549 / 17.24%
Duplication rate	52.31%
Clipped reads	17,837 / 15.73%

2.2. ACGT Content

Number/percentage of A's	437,494 / 18.01%
Number/percentage of C's	385,652 / 15.88%
Number/percentage of T's	406,194 / 16.72%
Number/percentage of G's	1,199,398 / 49.38%
Number/percentage of N's	55 / 0%
GC Percentage	65.26%

2.3. Coverage

Mean	0.0008

Standard Deviation	1.0189

2.4. Mapping Quality

Mean Mapping Quality	31.09

2.5. Mismatches and indels

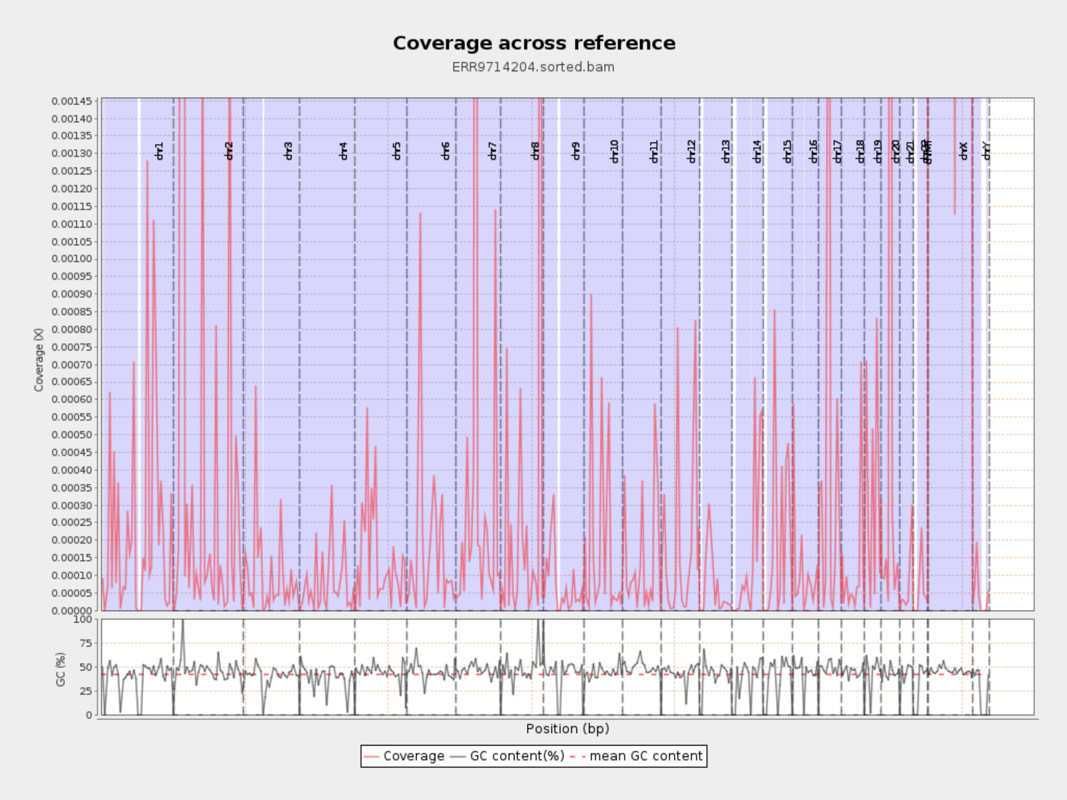
General error rate	3.85%
Mismatches	82,100
Insertions	1,951
Mapped reads with at least one insertion	6.4%
Deletions	5,155
Mapped reads with at least one deletion	22.23%
Homopolymer indels	37.39%

2.6. Chromosome stats

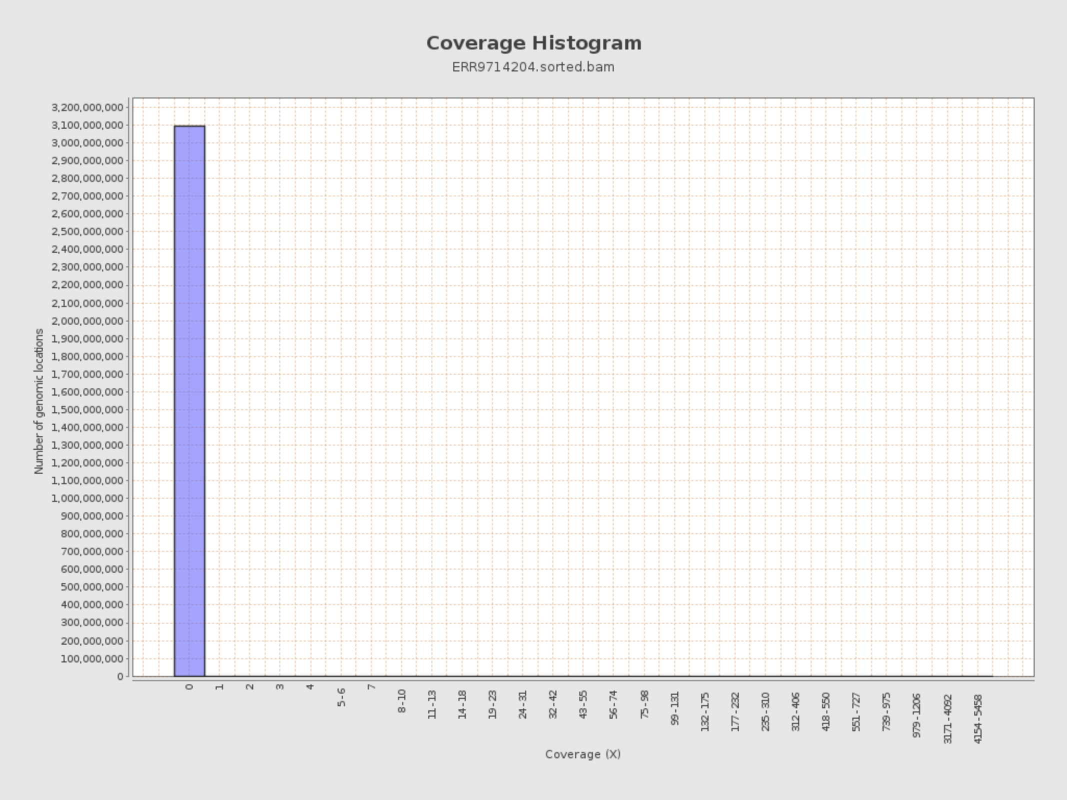
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	62779	0.0003	0.0947
chr2	243199373	905255	0.0037	3.5511
chr3	198022430	19787	0.0001	0.0291
chr4	191154276	15578	0.0001	0.0259
chr5	180915260	27259	0.0002	0.039
chr6	171115067	32319	0.0002	0.0454
chr7	159138663	73340	0.0005	0.2752

chr8	146364022	48084	0.0003	0.1914
chr9	141213431	10260	0.0001	0.0227
chr10	135534747	25167	0.0002	0.1201
chr11	135006516	19034	0.0001	0.0402
chr12	133851895	26850	0.0002	0.0596
chr13	115169878	7777	0.0001	0.0228
chr14	107349540	17851	0.0002	0.0492
chr15	102531392	20578	0.0002	0.0626
chr16	90354753	9276	0.0001	0.0323
chr17	81195210	36557	0.0005	0.1128
chr18	78077248	9432	0.0001	0.0336
chr19	59128983	19368	0.0003	0.0771
chr20	63025520	38136	0.0006	0.271
chr21	48129895	3571	0.0001	0.0153
chr22	51304566	3310	0.0001	0.0221
chrMT	16571	604	0.0364	0.2977
chrX	155270560	1033489	0.0067	0.8677
chrY	59373566	2847	0	0.0122

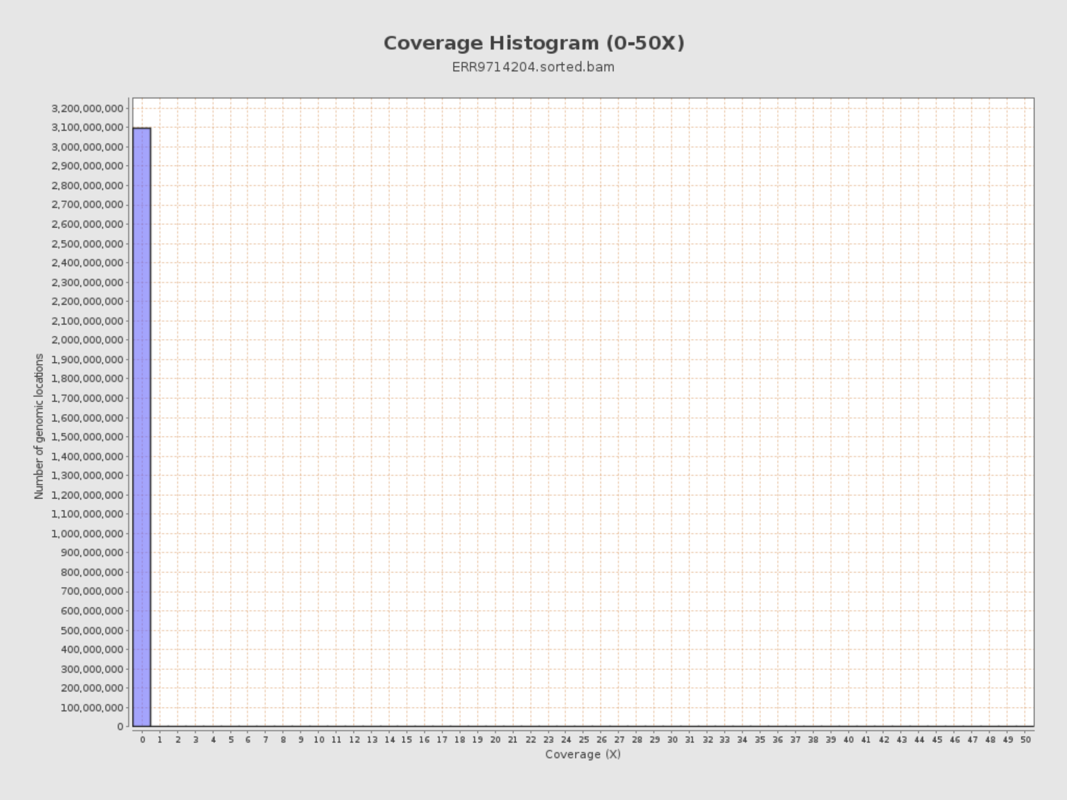
3. Results : Coverage across reference



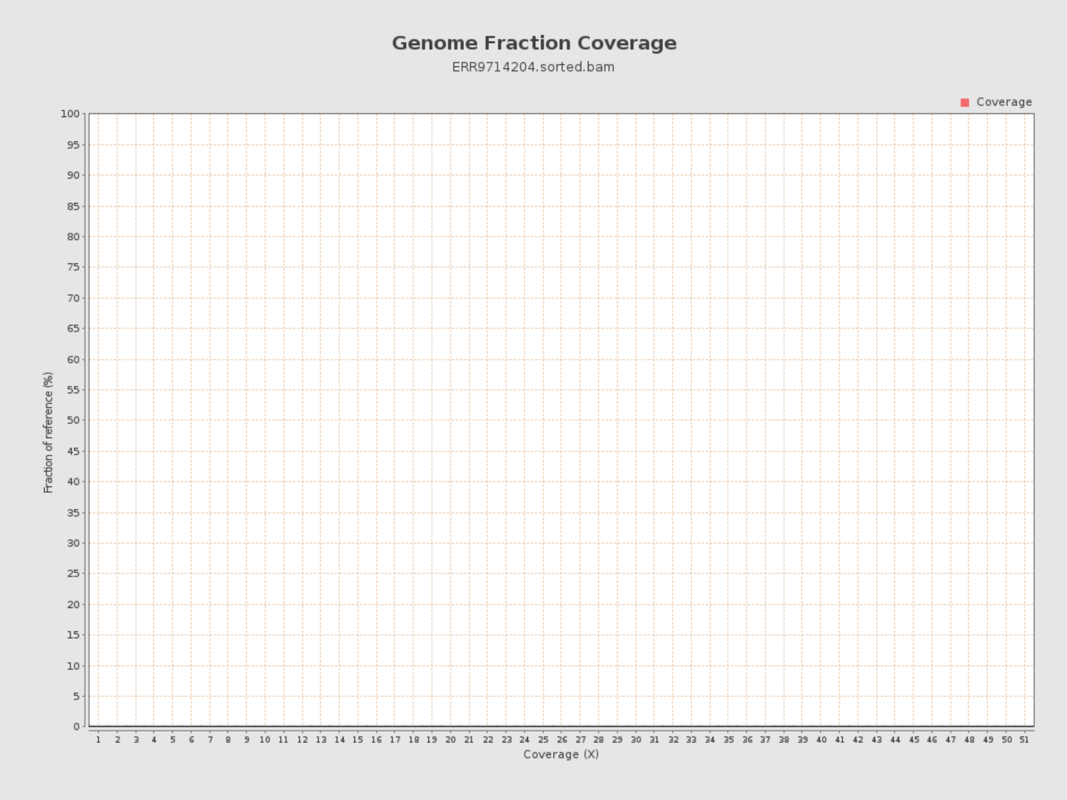
4. Results : Coverage Histogram



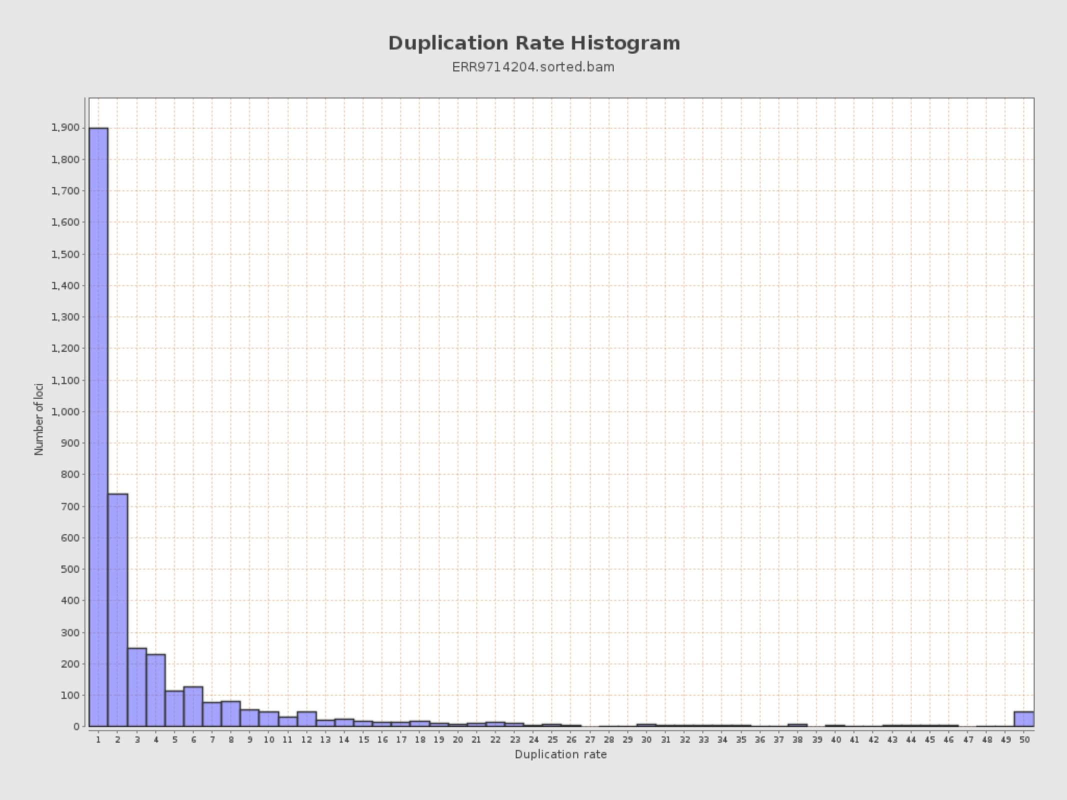
5. Results : Coverage Histogram (0-50X)



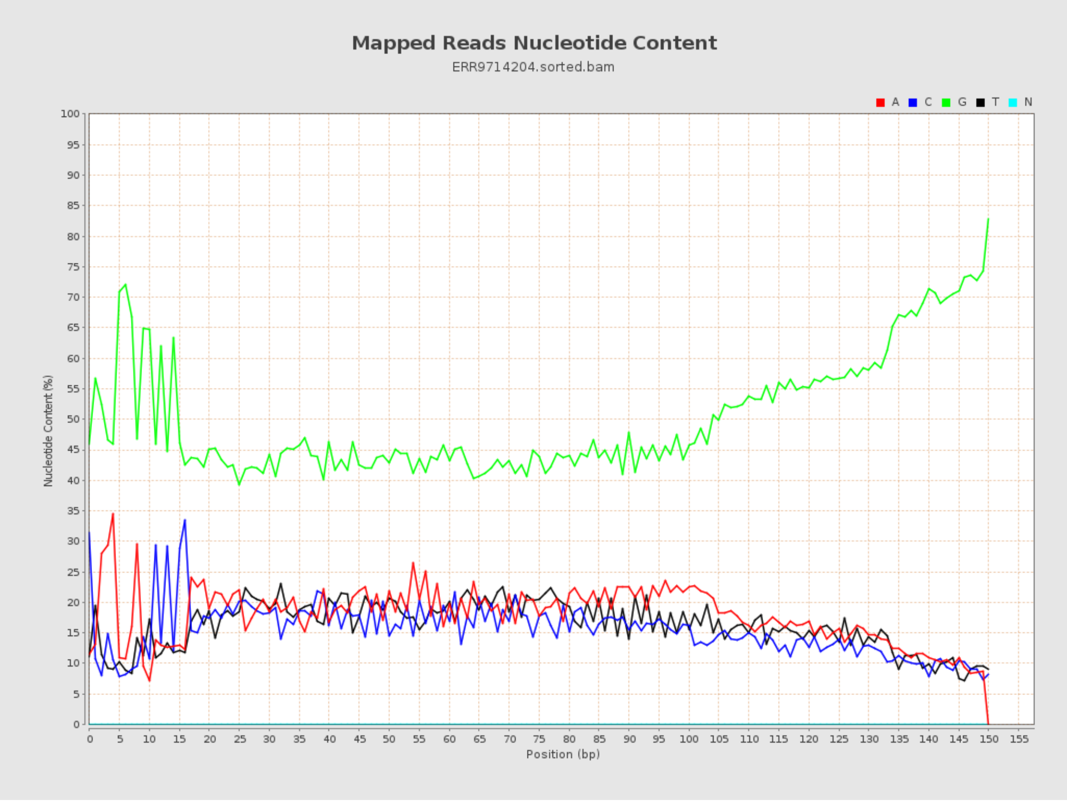
6. Results : Genome Fraction Coverage



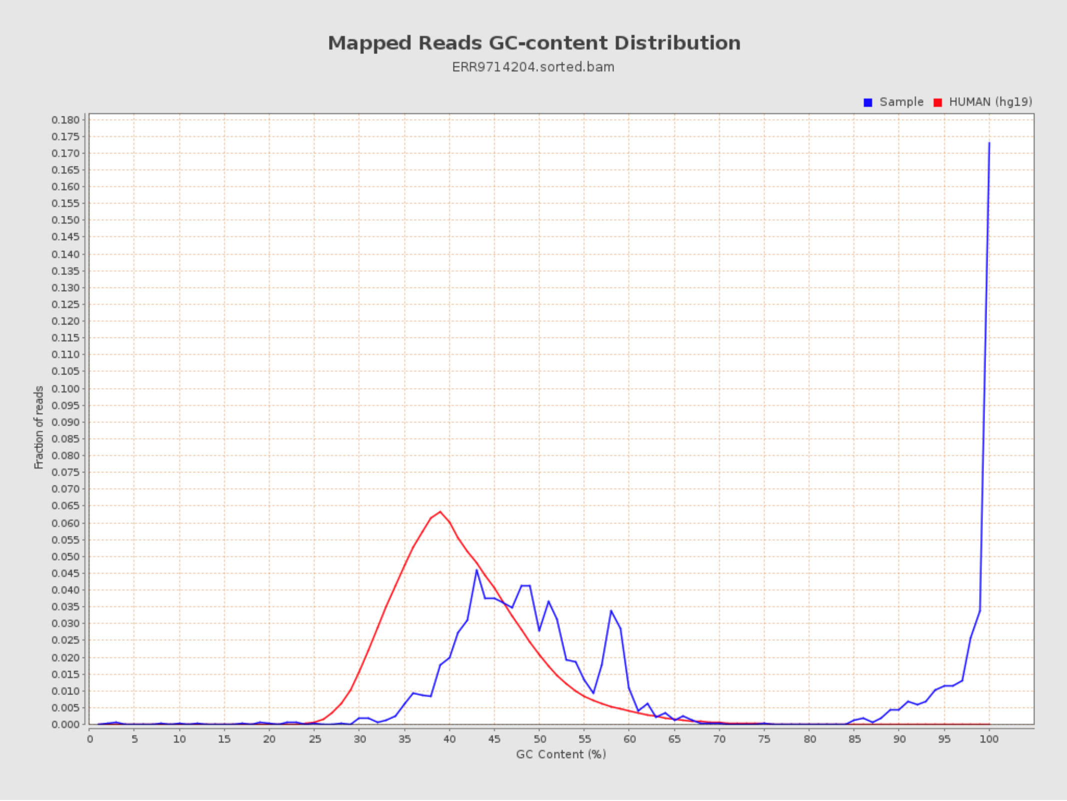
7. Results : Duplication Rate Histogram



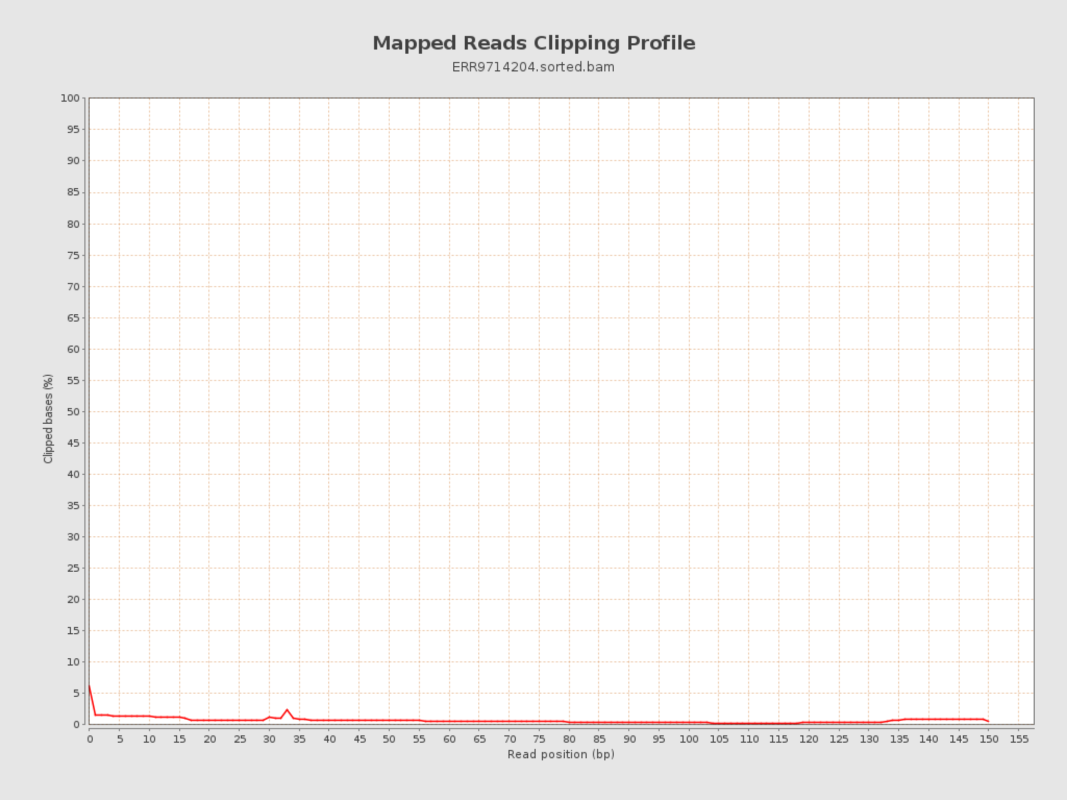
8. Results : Mapped Reads Nucleotide Content



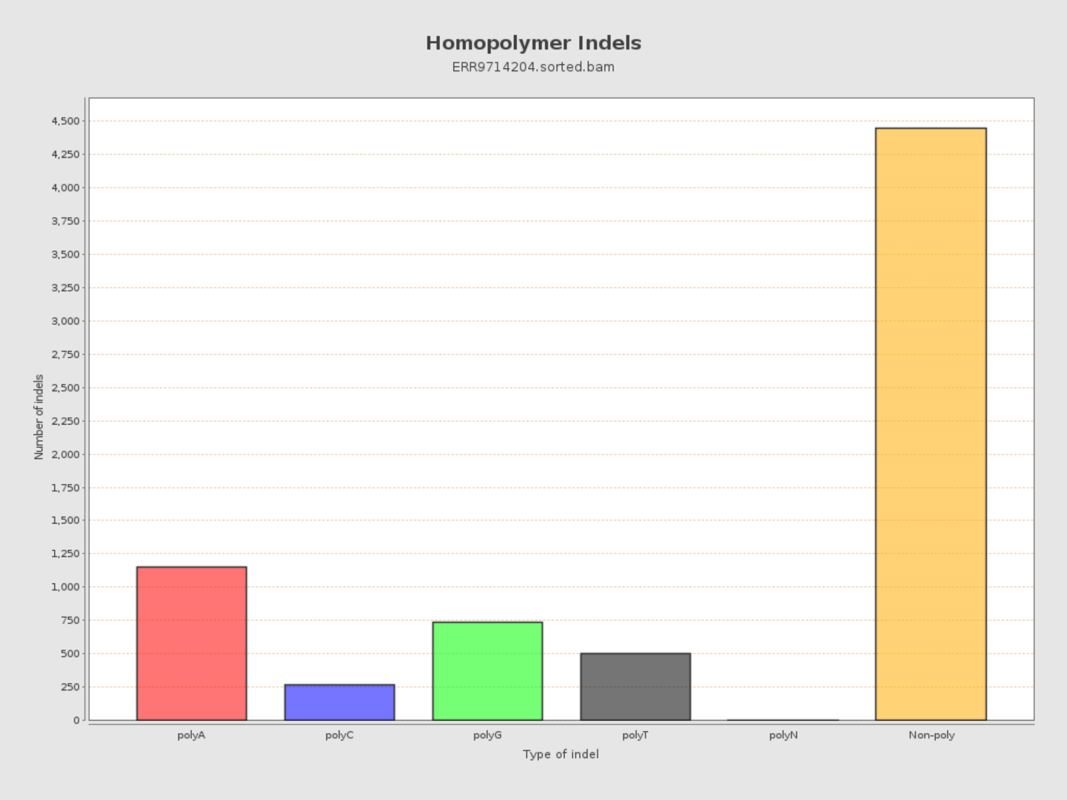
9. Results : Mapped Reads GC-content Distribution



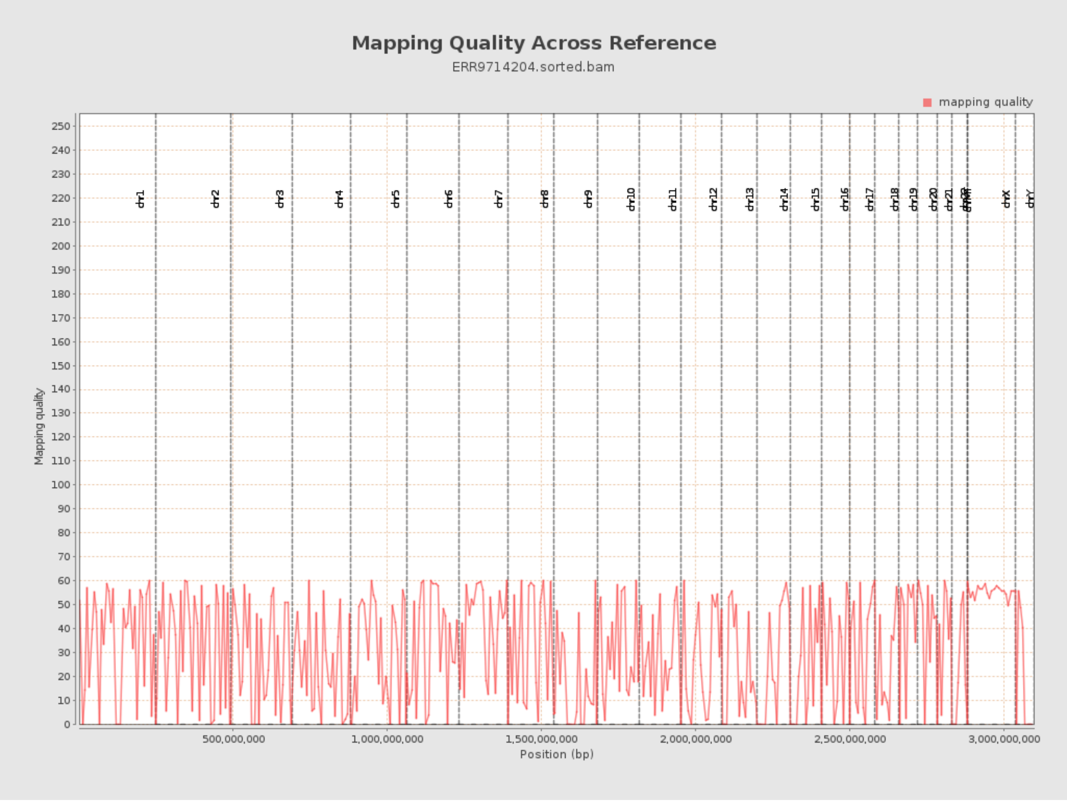
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram