Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 00:14:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714209.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_ERR9714209 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714209.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 00:14:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714209.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	141,638
Mapped reads	17,607 / 12.43%
Unmapped reads	124,031 / 87.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	867 / 0.61%
Read min/max/mean length	30 / 151 / 59.04
Duplicated reads (estimated)	15,328 / 10.82%
Duplication rate	19.99%
Clipped reads	11,032 / 7.79%

2.2. ACGT Content

Number/percentage of A's	137,403 / 7.78%
Number/percentage of C's	64,384 / 3.64%
Number/percentage of T's	81,517 / 4.61%
Number/percentage of G's	1,483,035 / 83.96%
Number/percentage of N's	36 / 0%
GC Percentage	87.6%

2.3. Coverage

Mean	0.0006

Standard Deviation	1.7342

2.4. Mapping Quality

Mean Mapping Quality	23.75

2.5. Mismatches and indels

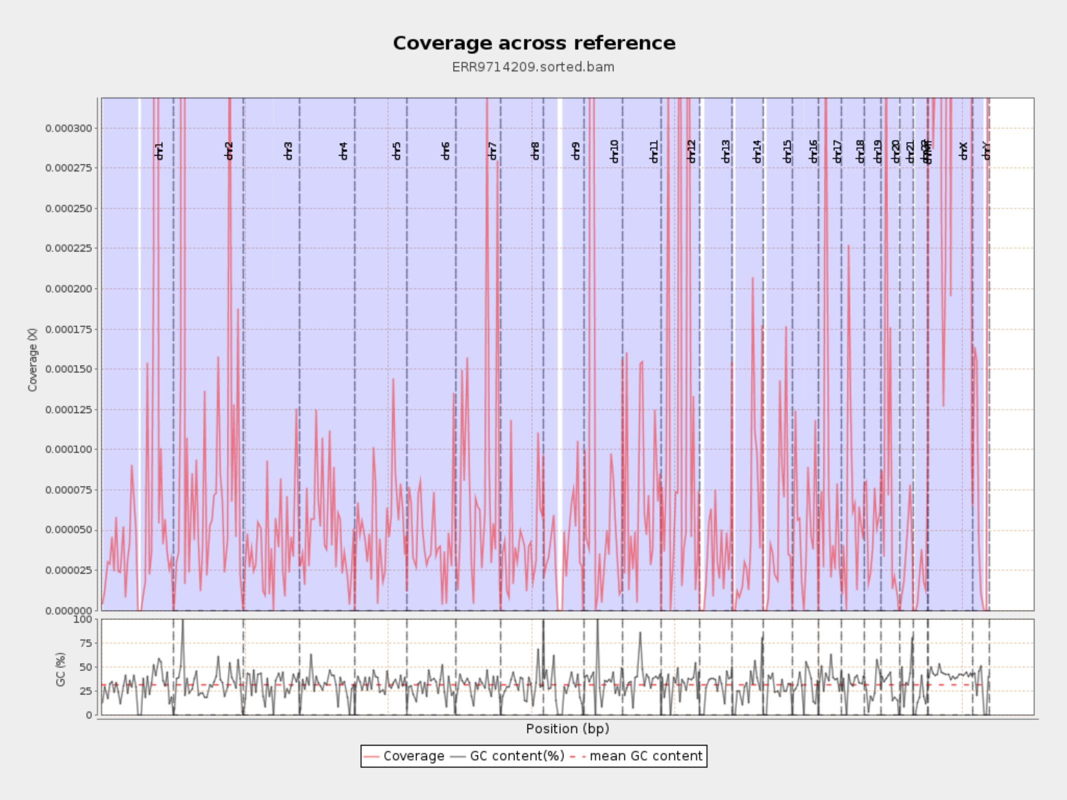
General error rate	3.94%
Mismatches	47,772
Insertions	2,916
Mapped reads with at least one insertion	10.74%
Deletions	1,521
Mapped reads with at least one deletion	8.27%
Homopolymer indels	65.68%

2.6. Chromosome stats

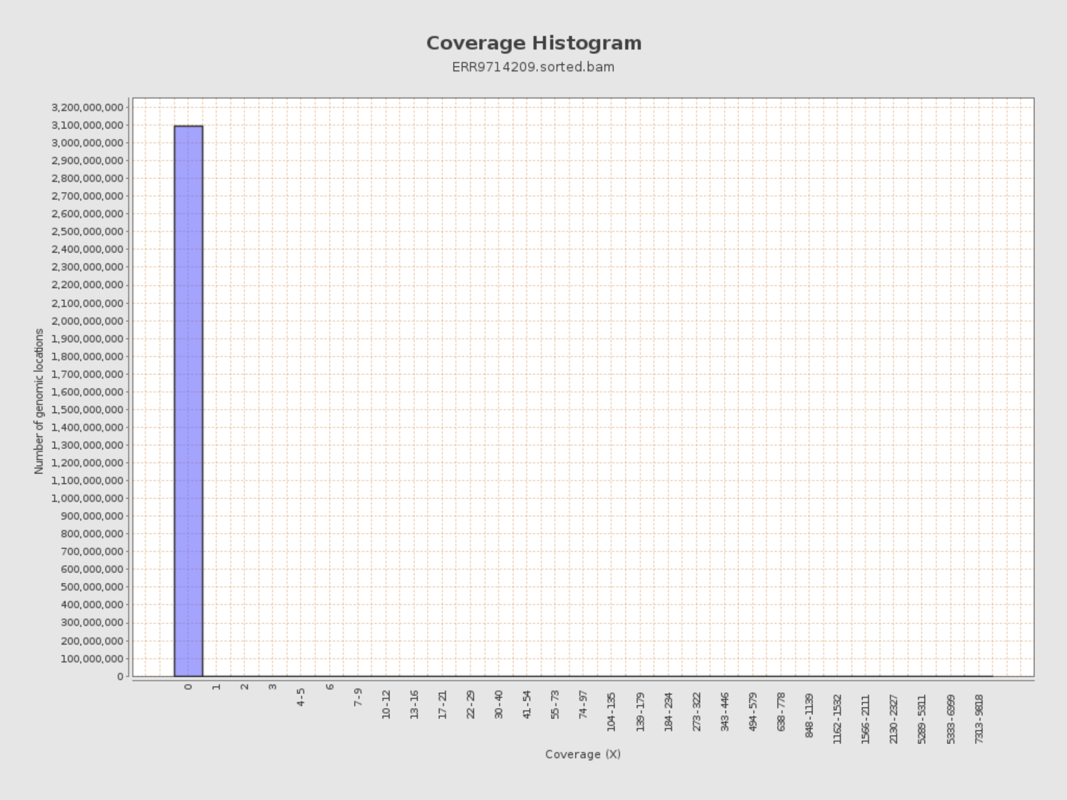
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21812	0.0001	0.1236
chr2	243199373	1456348	0.006	6.1836
chr3	198022430	8068	0	0.0083
chr4	191154276	9796	0.0001	0.0099
chr5	180915260	9763	0.0001	0.0083
chr6	171115067	7872	0	0.0086
chr7	159138663	13167	0.0001	0.0289

chr8	146364022	6244	0	0.0088
chr9	141213431	5345	0	0.0077
chr10	135534747	19111	0.0001	0.1638
chr11	135006516	9367	0.0001	0.018
chr12	133851895	17036	0.0001	0.0486
chr13	115169878	3825	0	0.0071
chr14	107349540	6020	0.0001	0.0221
chr15	102531392	5232	0.0001	0.0147
chr16	90354753	4904	0.0001	0.0102
chr17	81195210	6208	0.0001	0.05
chr18	78077248	5290	0.0001	0.0198
chr19	59128983	3079	0.0001	0.0108
chr20	63025520	5932	0.0001	0.031
chr21	48129895	1727	0	0.0073
chr22	51304566	918	0	0.0045
chrMT	16571	8766	0.529	2.5332
chrX	155270560	131893	0.0008	0.1311
chrY	59373566	6649	0.0001	0.025

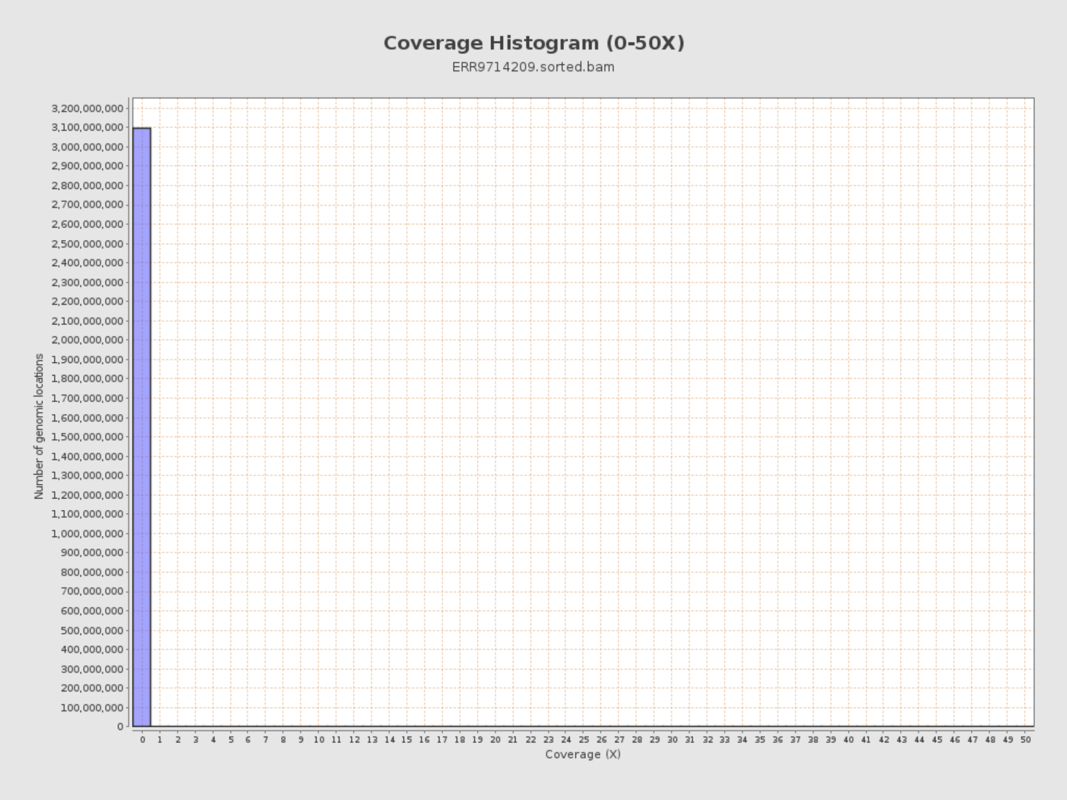
3. Results : Coverage across reference



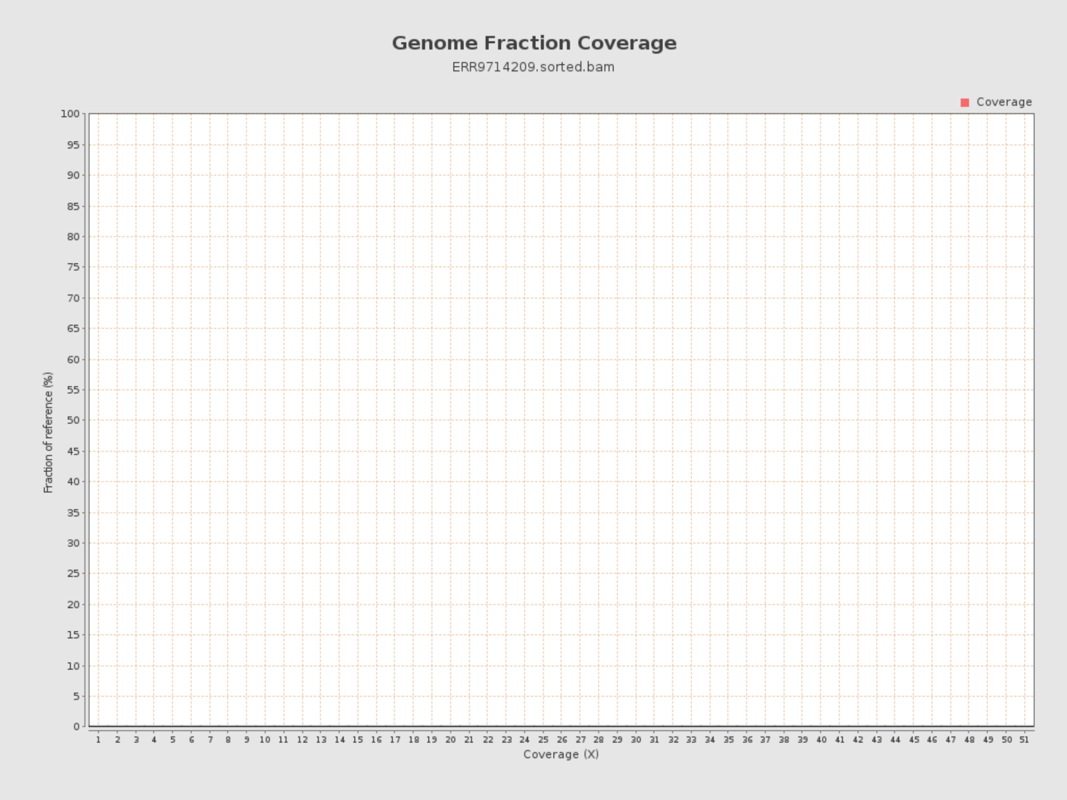
4. Results : Coverage Histogram



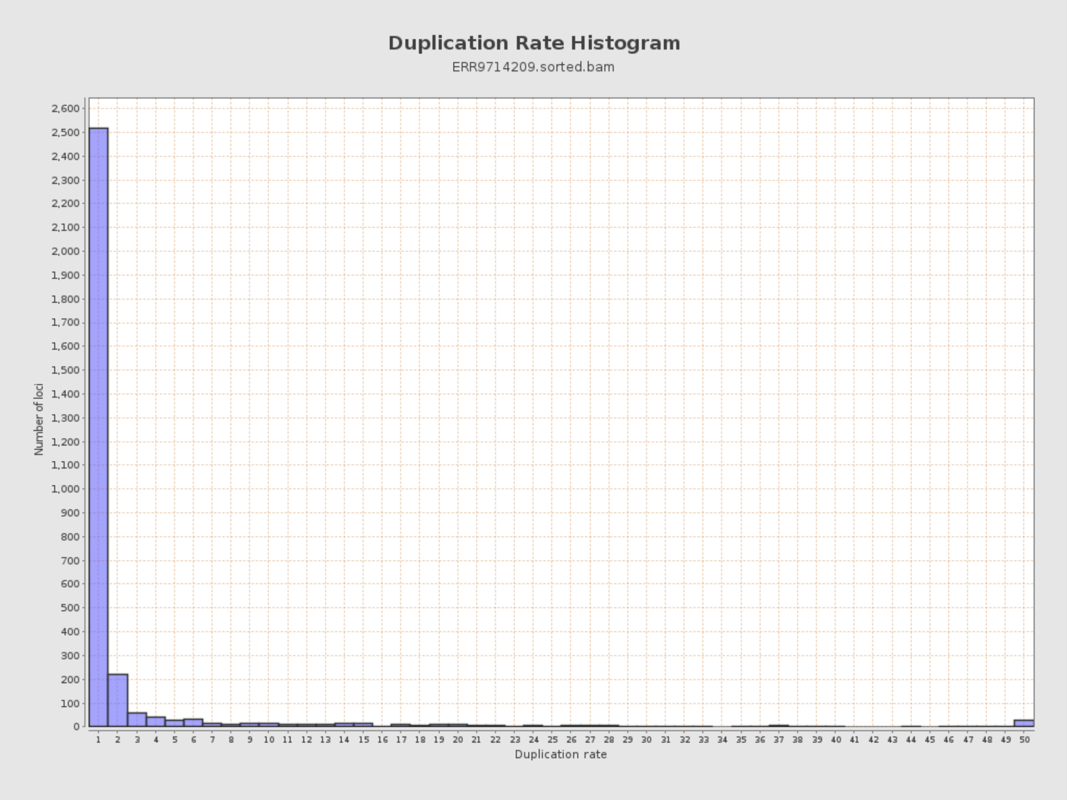
5. Results : Coverage Histogram (0-50X)



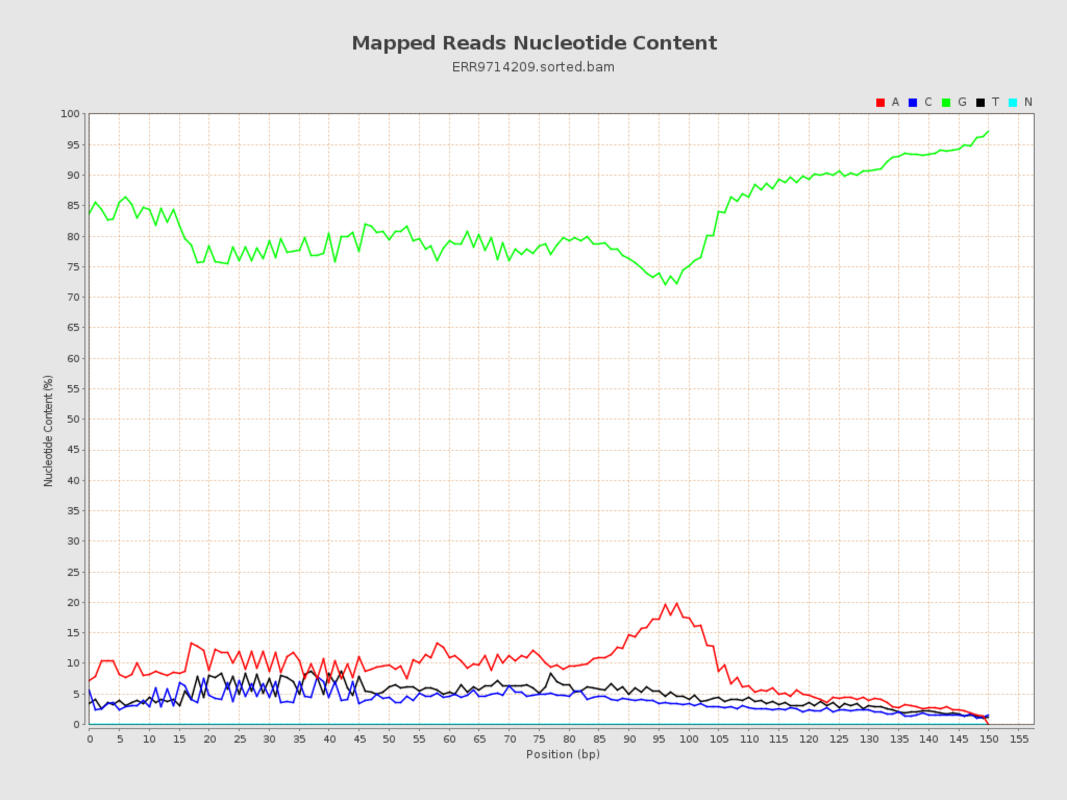
6. Results : Genome Fraction Coverage



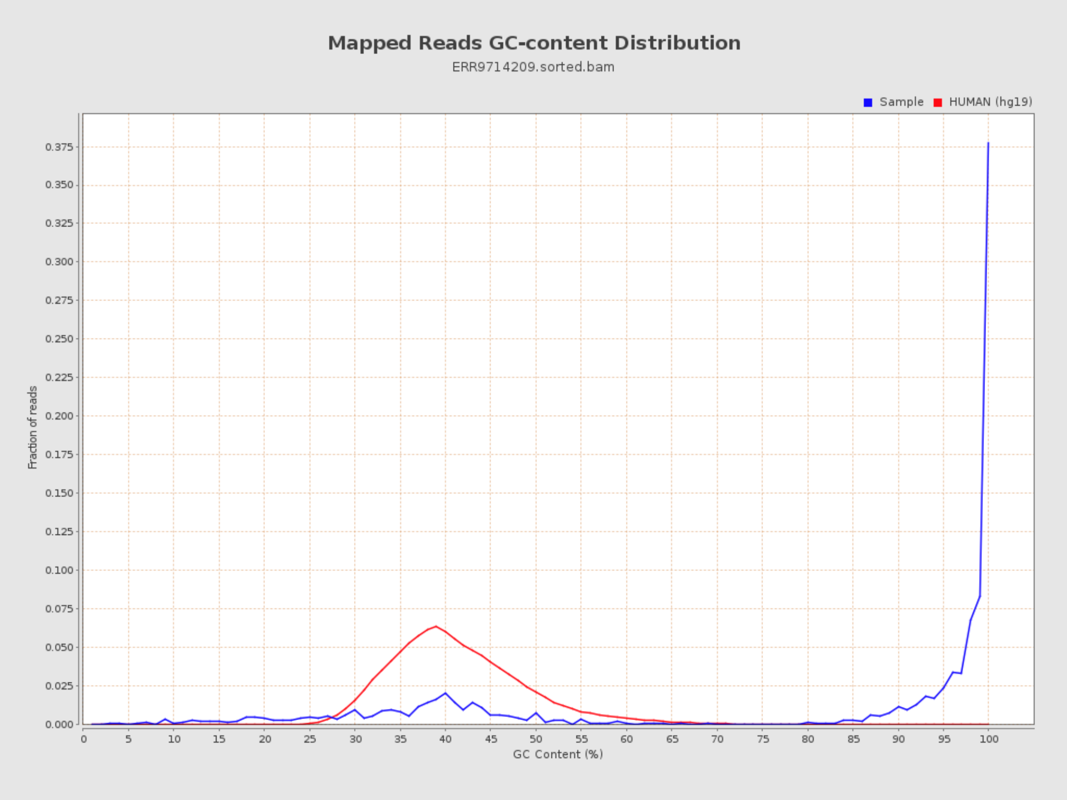
7. Results : Duplication Rate Histogram



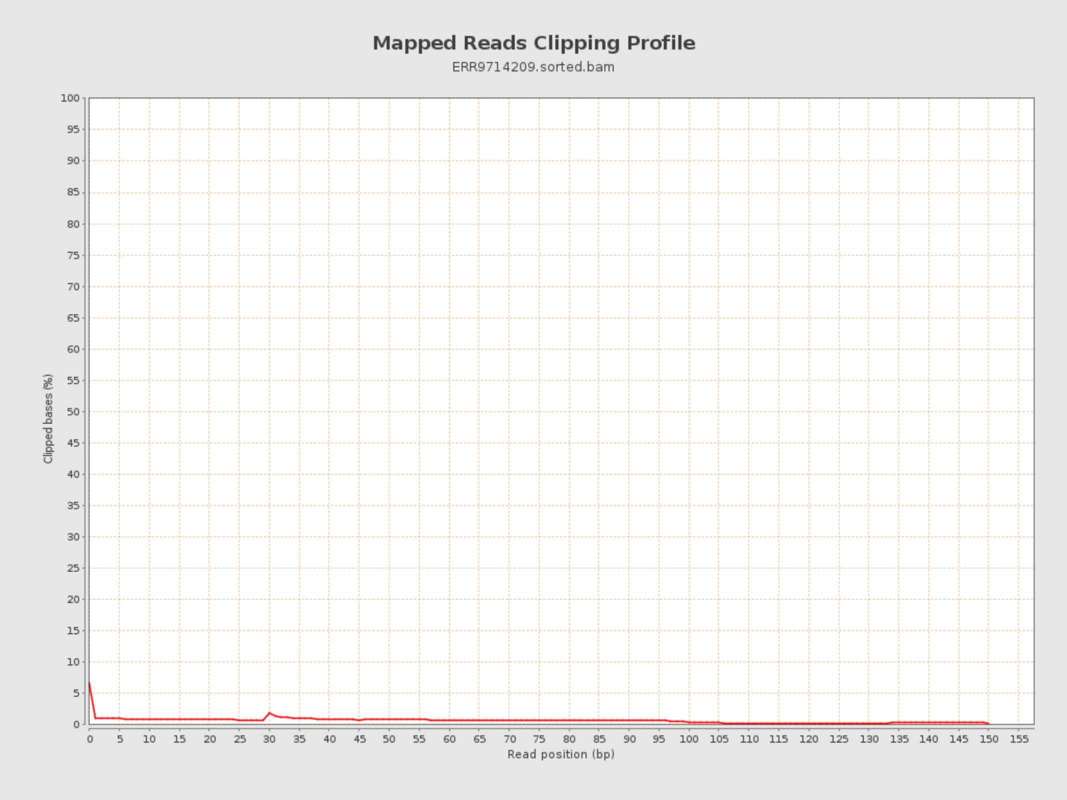
8. Results : Mapped Reads Nucleotide Content



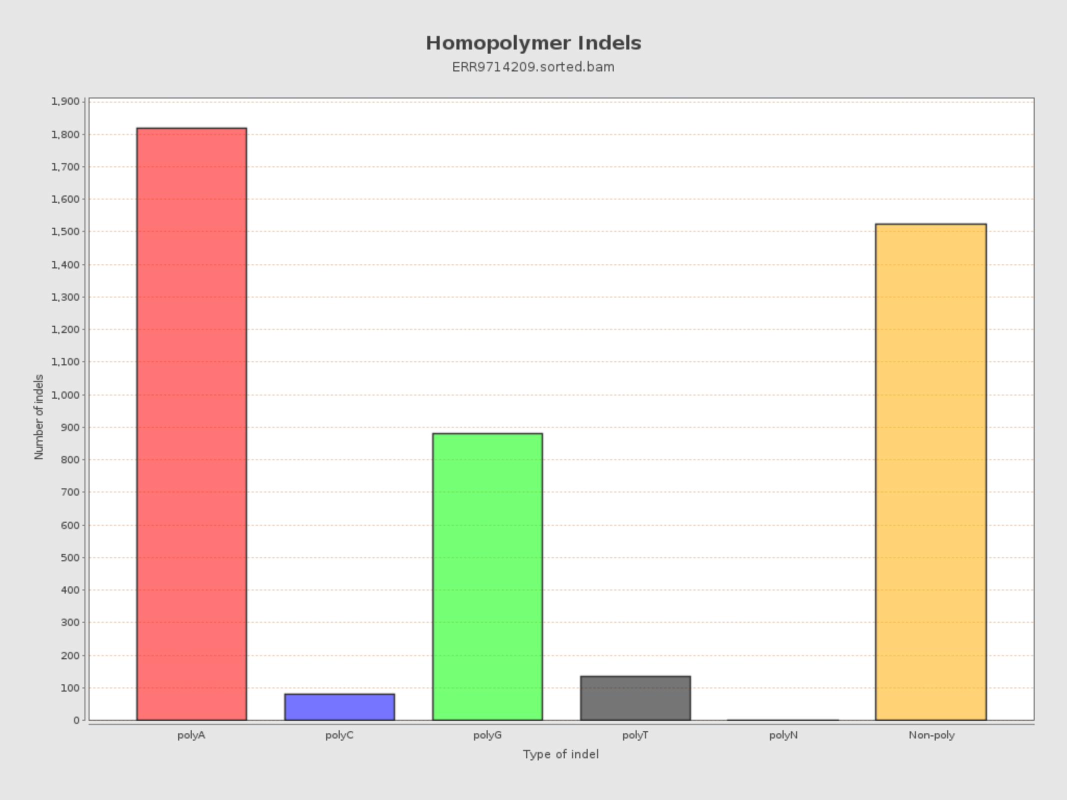
9. Results : Mapped Reads GC-content Distribution



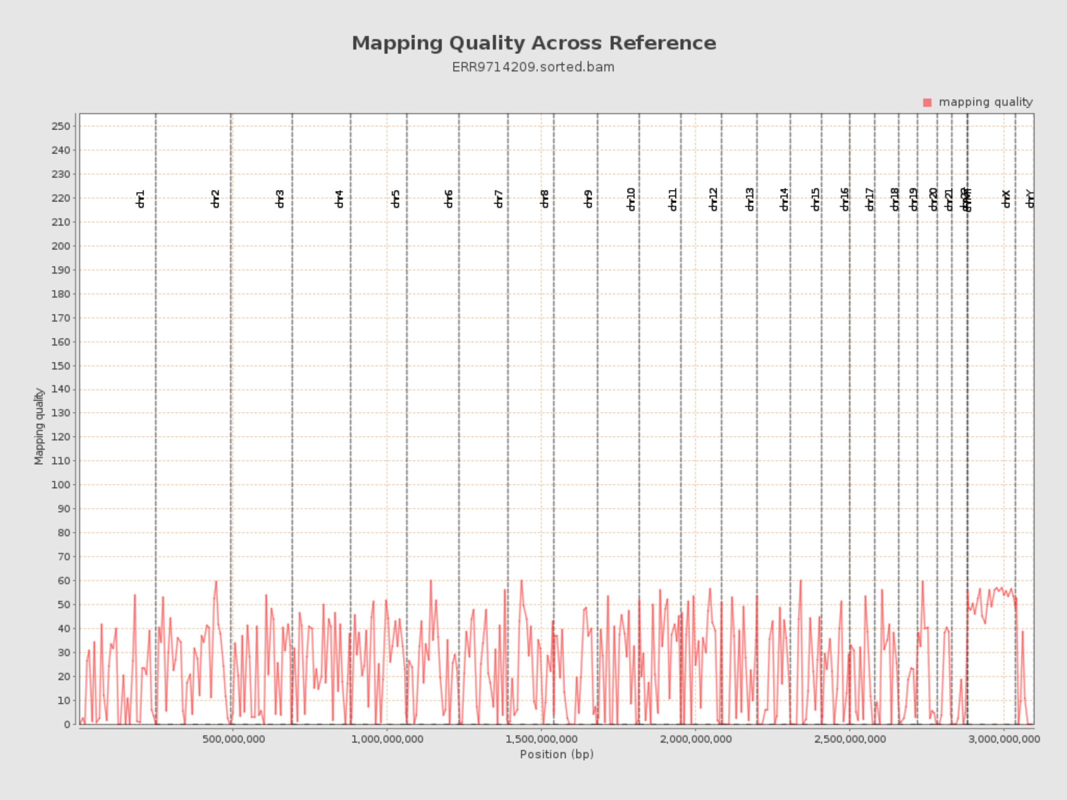
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram