Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 00:13:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714208.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_ERR9714208 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714208.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 00:13:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714208.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	150,524
Mapped reads	6,743 / 4.48%
Unmapped reads	143,781 / 95.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	209 / 0.14%
Read min/max/mean length	30 / 151 / 50.35
Duplicated reads (estimated)	5,800 / 3.85%
Duplication rate	40.1%
Clipped reads	5,414 / 3.6%

2.2. ACGT Content

Number/percentage of A's	59,652 / 10.71%
Number/percentage of C's	40,504 / 7.27%
Number/percentage of T's	46,863 / 8.41%
Number/percentage of G's	410,029 / 73.6%
Number/percentage of N's	55 / 0.01%
GC Percentage	80.87%

2.3. Coverage

Mean	0.0002

Standard Deviation	0.427

2.4. Mapping Quality

Mean Mapping Quality	11.85

2.5. Mismatches and indels

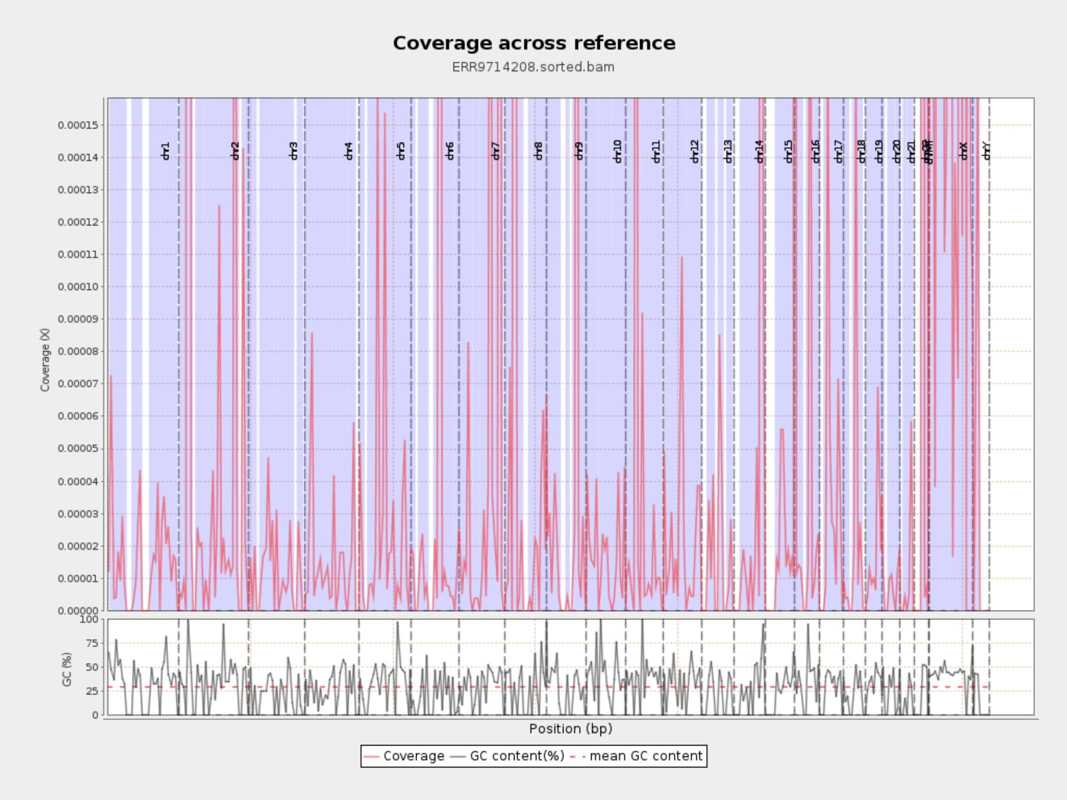
General error rate	3%
Mismatches	13,376
Insertions	536
Mapped reads with at least one insertion	6.1%
Deletions	895
Mapped reads with at least one deletion	11.03%
Homopolymer indels	44.3%

2.6. Chromosome stats

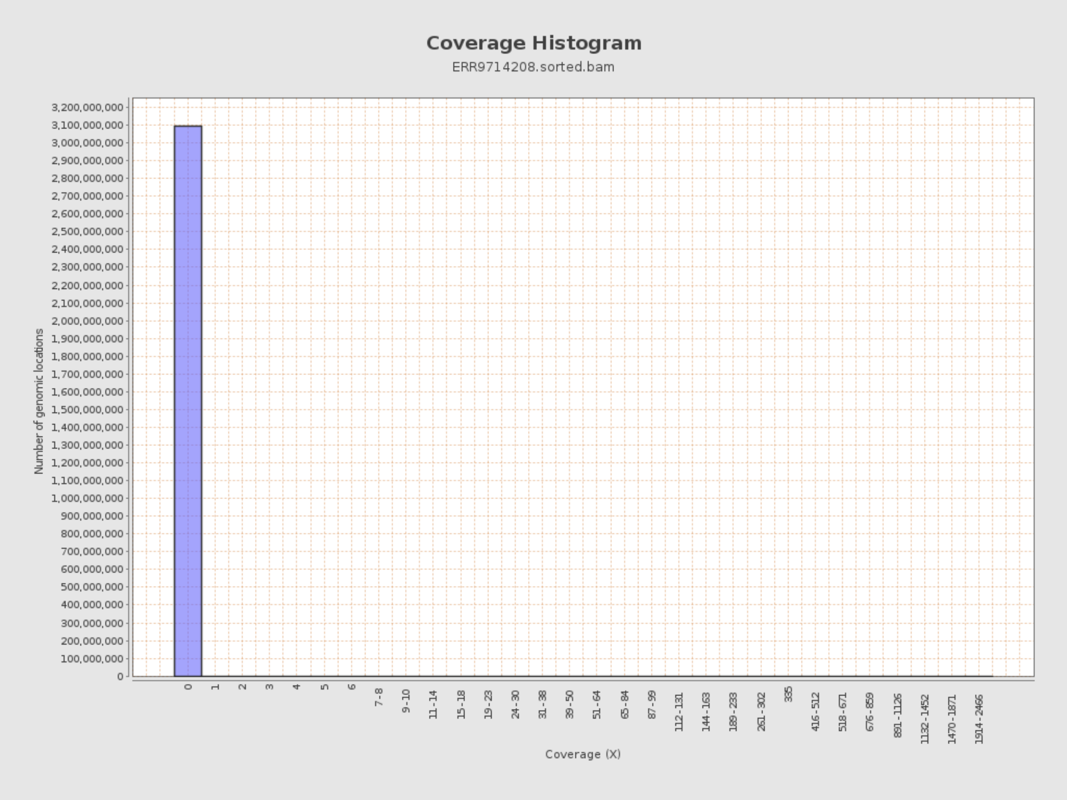
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3695	0	0.006
chr2	243199373	379064	0.0016	1.5138
chr3	198022430	2344	0	0.0047
chr4	191154276	3030	0	0.0098
chr5	180915260	4954	0	0.0115
chr6	171115067	5245	0	0.0276
chr7	159138663	13844	0.0001	0.065

chr8	146364022	7391	0.0001	0.037
chr9	141213431	6039	0	0.0273
chr10	135534747	2388	0	0.0065
chr11	135006516	5037	0	0.0231
chr12	133851895	3284	0	0.01
chr13	115169878	1988	0	0.0129
chr14	107349540	8746	0.0001	0.0564
chr15	102531392	1590	0	0.0067
chr16	90354753	9693	0.0001	0.0607
chr17	81195210	3155	0	0.0207
chr18	78077248	1846	0	0.0142
chr19	59128983	1072	0	0.0114
chr20	63025520	417	0	0.0028
chr21	48129895	526	0	0.0041
chr22	51304566	7230	0.0001	0.0871
chrMT	16571	667	0.0403	0.2884
chrX	155270560	85861	0.0006	0.1725
chrY	59373566	1517	0	0.0132

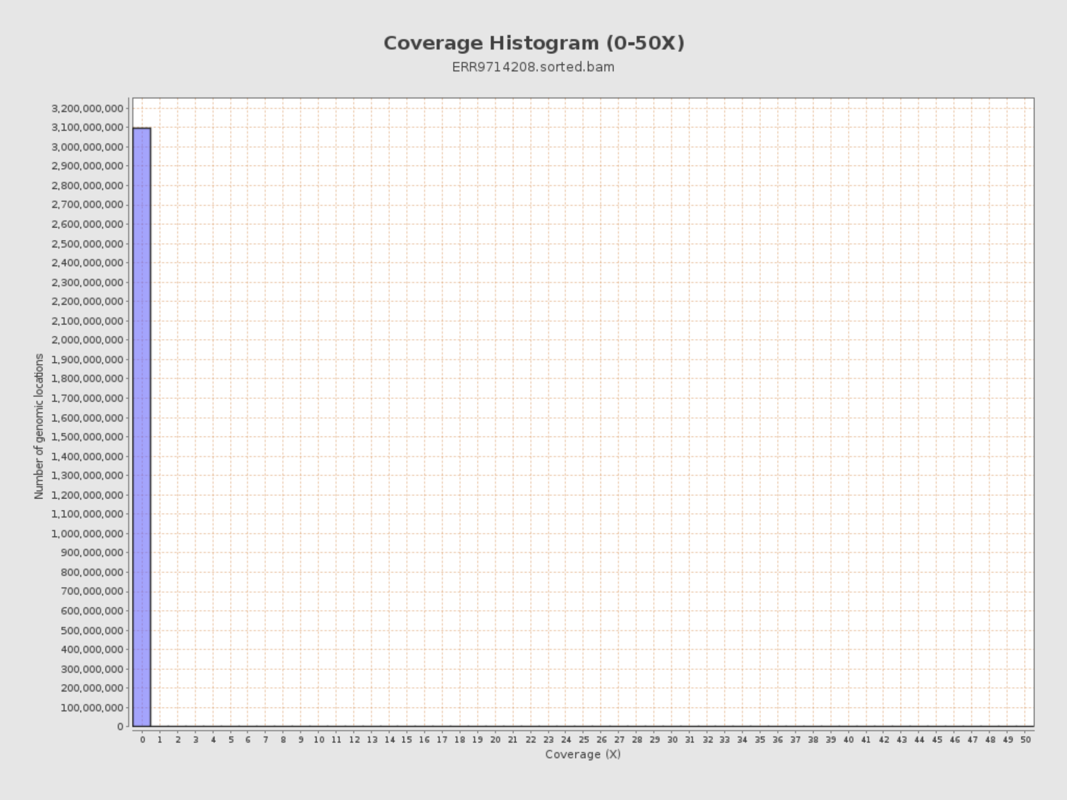
3. Results : Coverage across reference



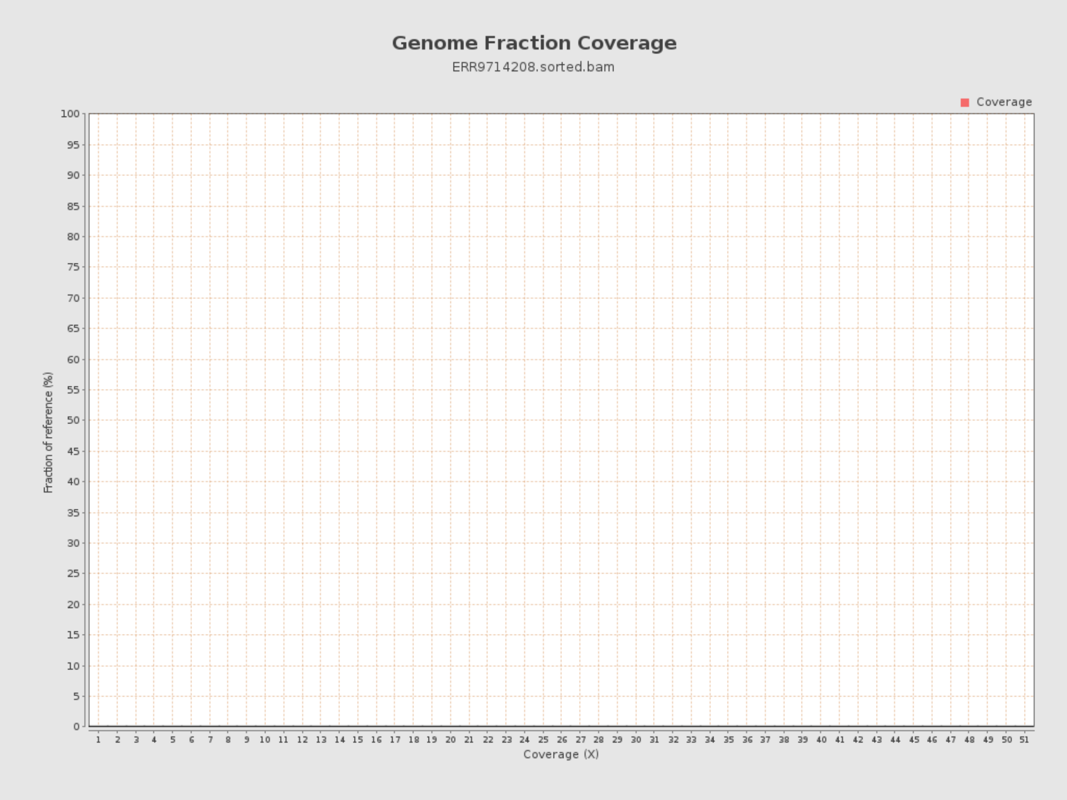
4. Results : Coverage Histogram



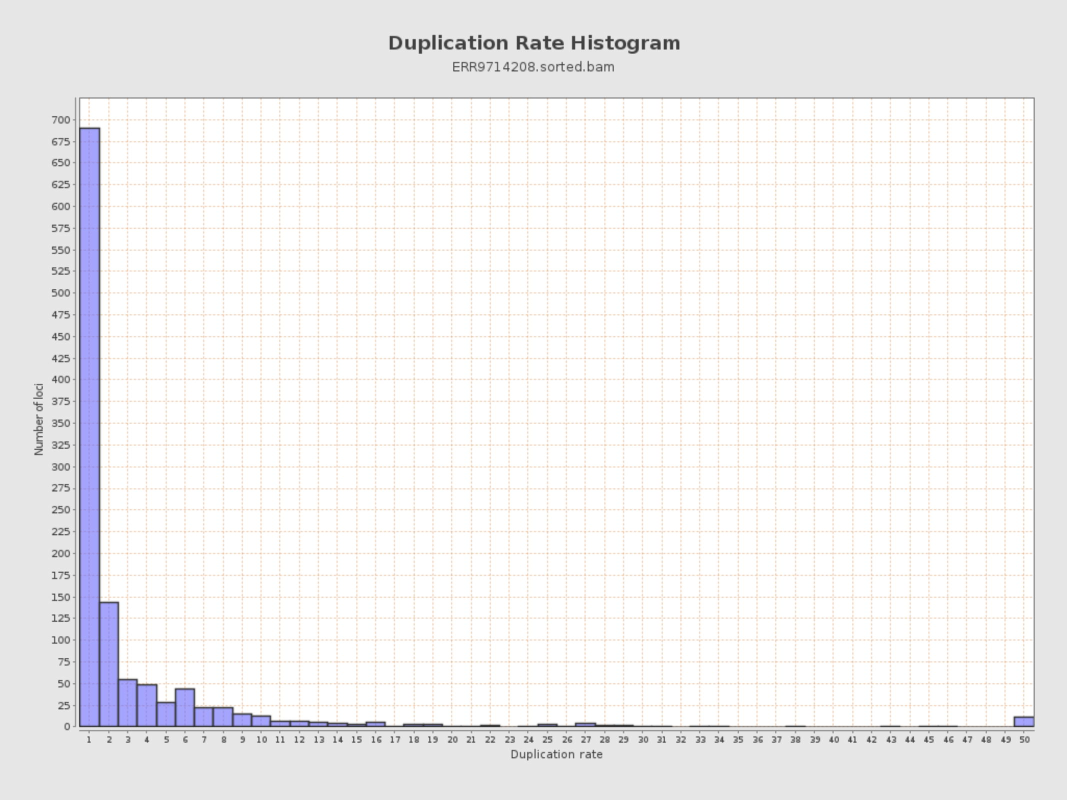
5. Results : Coverage Histogram (0-50X)



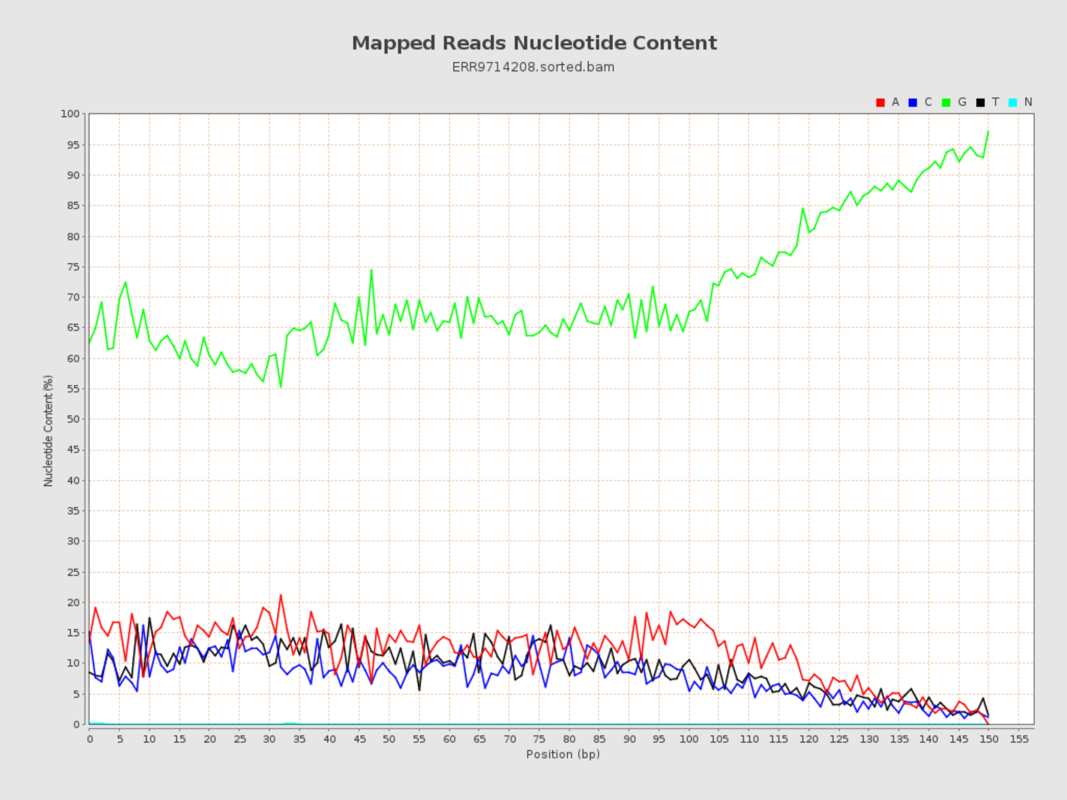
6. Results : Genome Fraction Coverage



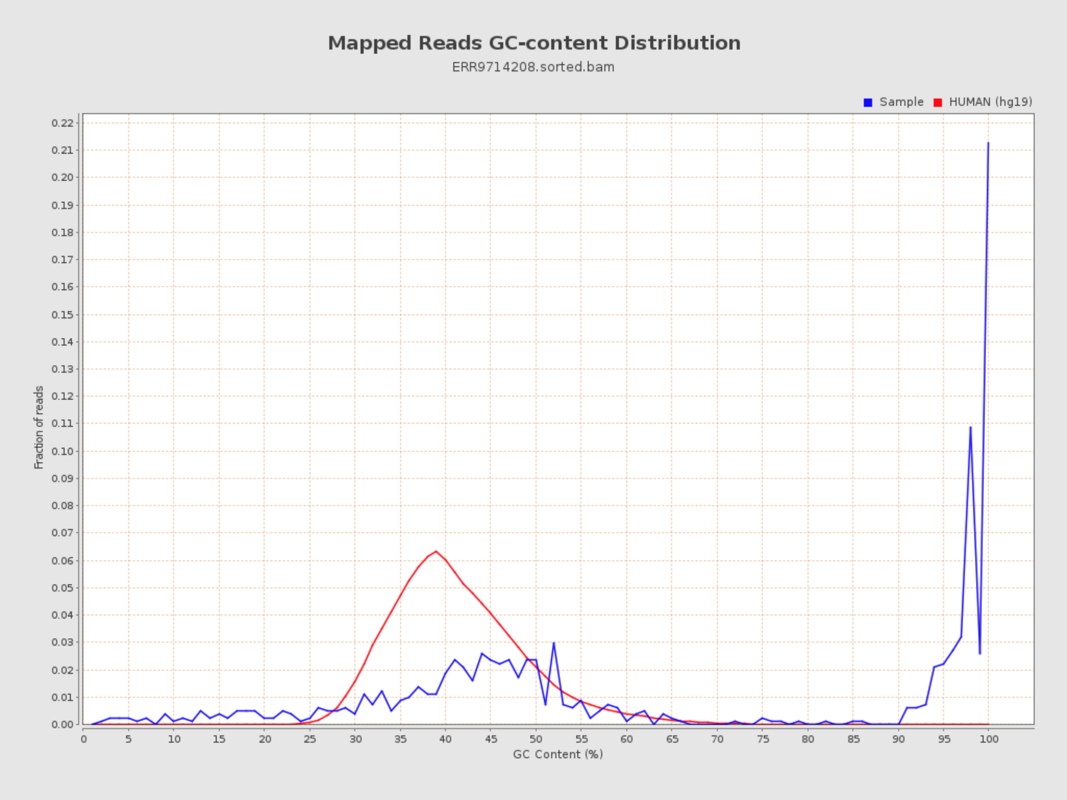
7. Results : Duplication Rate Histogram



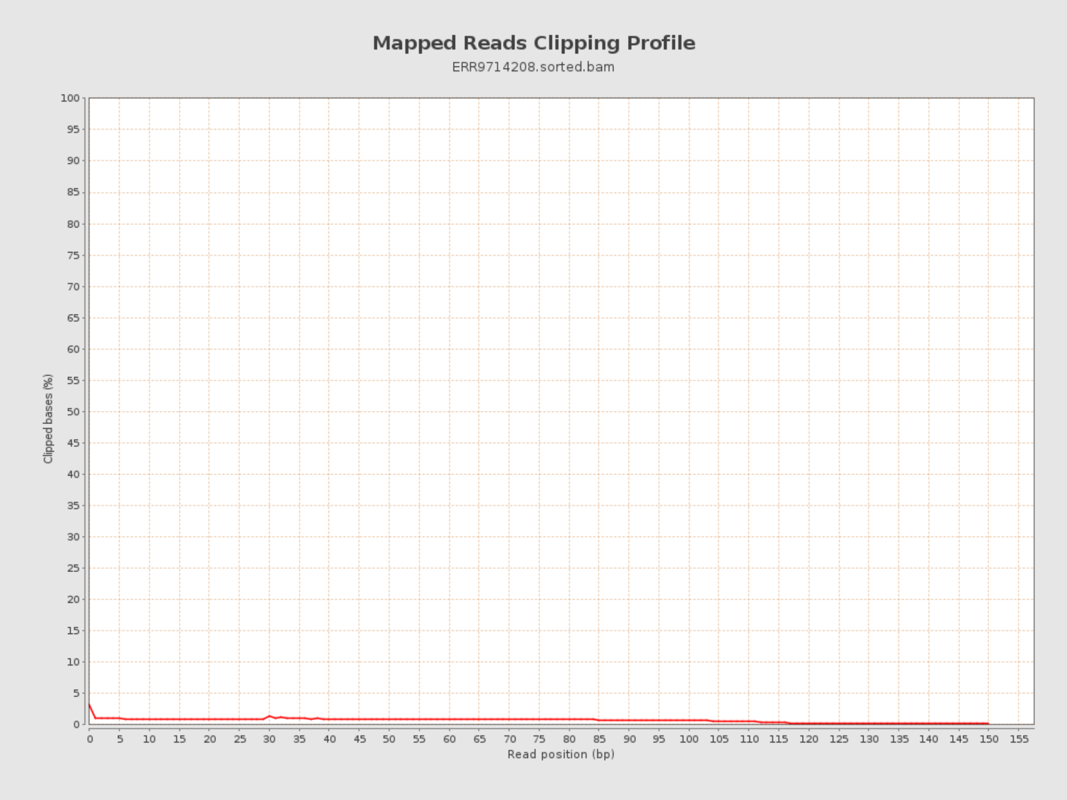
8. Results : Mapped Reads Nucleotide Content



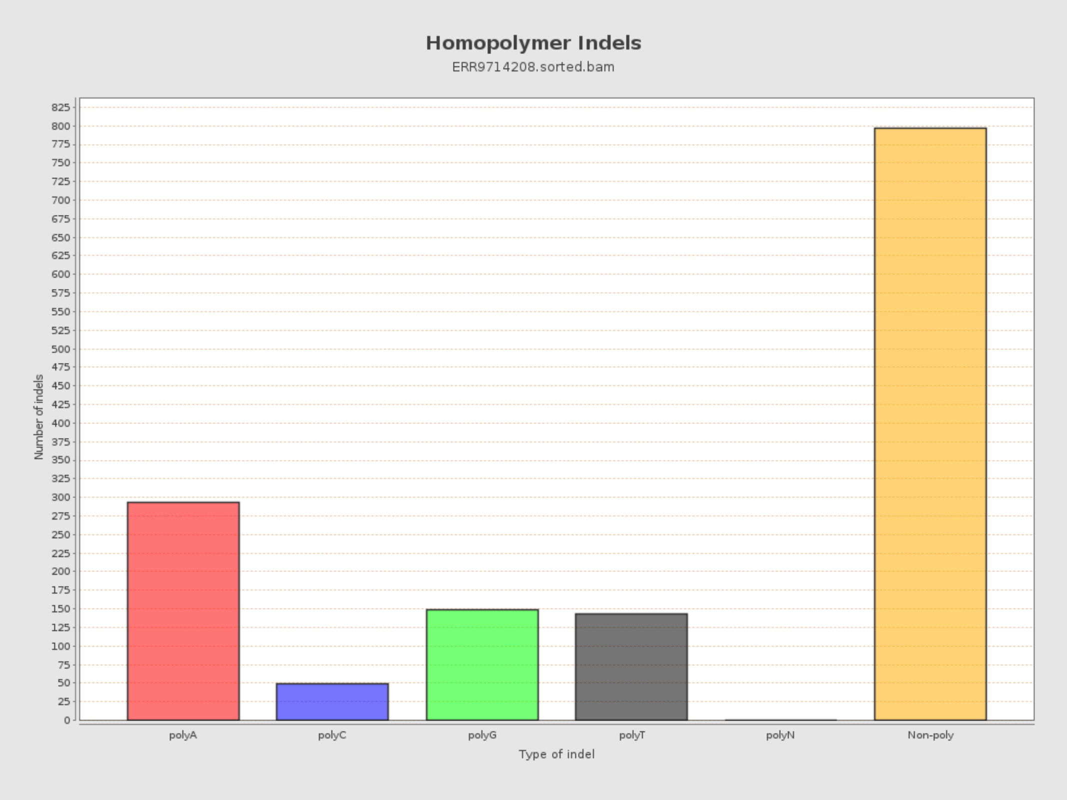
9. Results : Mapped Reads GC-content Distribution



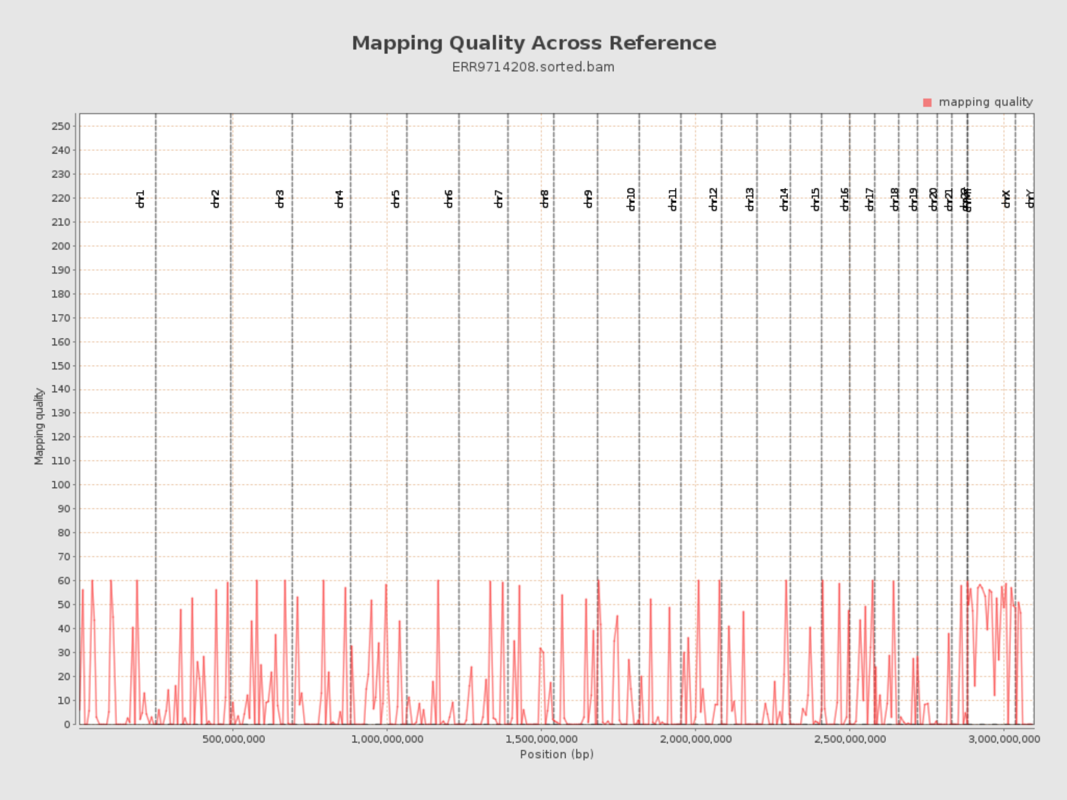
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram