Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 17:48:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714060.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_ERR9714060 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714060.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 17:48:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714060.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	552,246
Mapped reads	82,966 / 15.02%
Unmapped reads	469,280 / 84.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,777 / 0.32%
Read min/max/mean length	30 / 151 / 59.07
Duplicated reads (estimated)	81,821 / 14.82%
Duplication rate	34.02%
Clipped reads	45,646 / 8.27%

2.2. ACGT Content

Number/percentage of A's	183,057 / 2.18%
Number/percentage of C's	73,510 / 0.87%
Number/percentage of T's	85,627 / 1.02%
Number/percentage of G's	8,070,644 / 95.93%
Number/percentage of N's	167 / 0%
GC Percentage	96.8%

2.3. Coverage

Mean	0.0027

Standard Deviation	10.3927

2.4. Mapping Quality

Mean Mapping Quality	13.21

2.5. Mismatches and indels

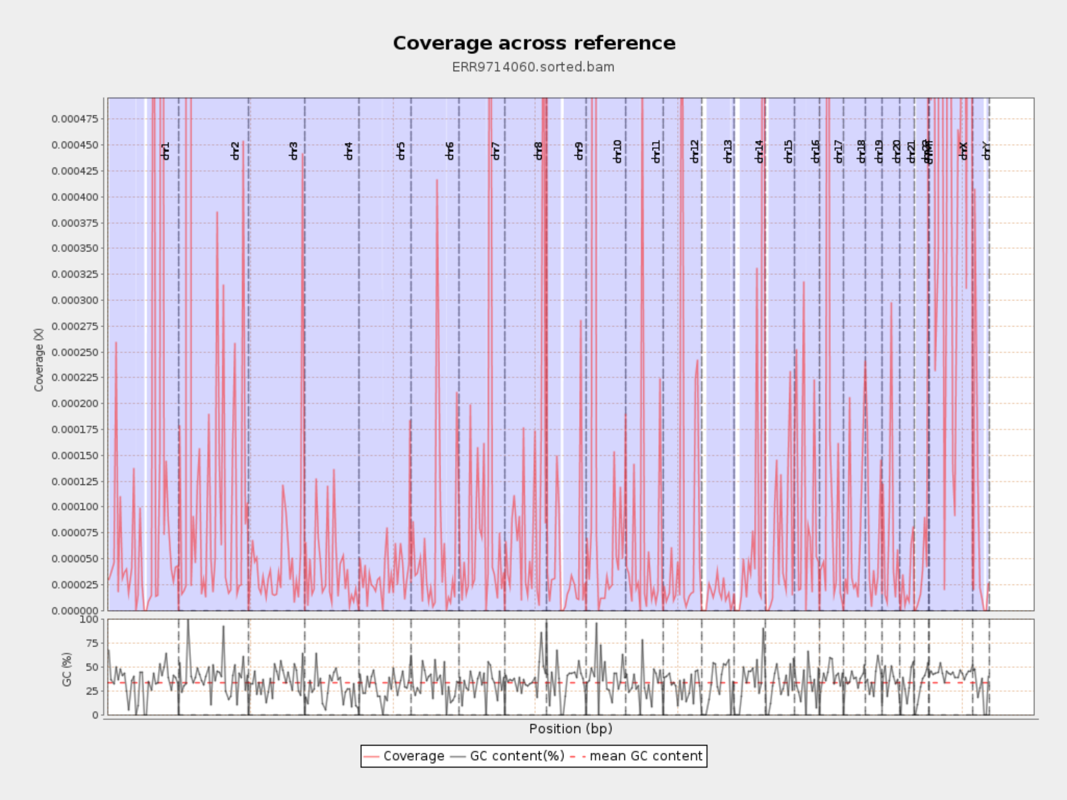
General error rate	3.2%
Mismatches	203,924
Insertions	9,179
Mapped reads with at least one insertion	7.91%
Deletions	3,926
Mapped reads with at least one deletion	4.56%
Homopolymer indels	64.3%

2.6. Chromosome stats

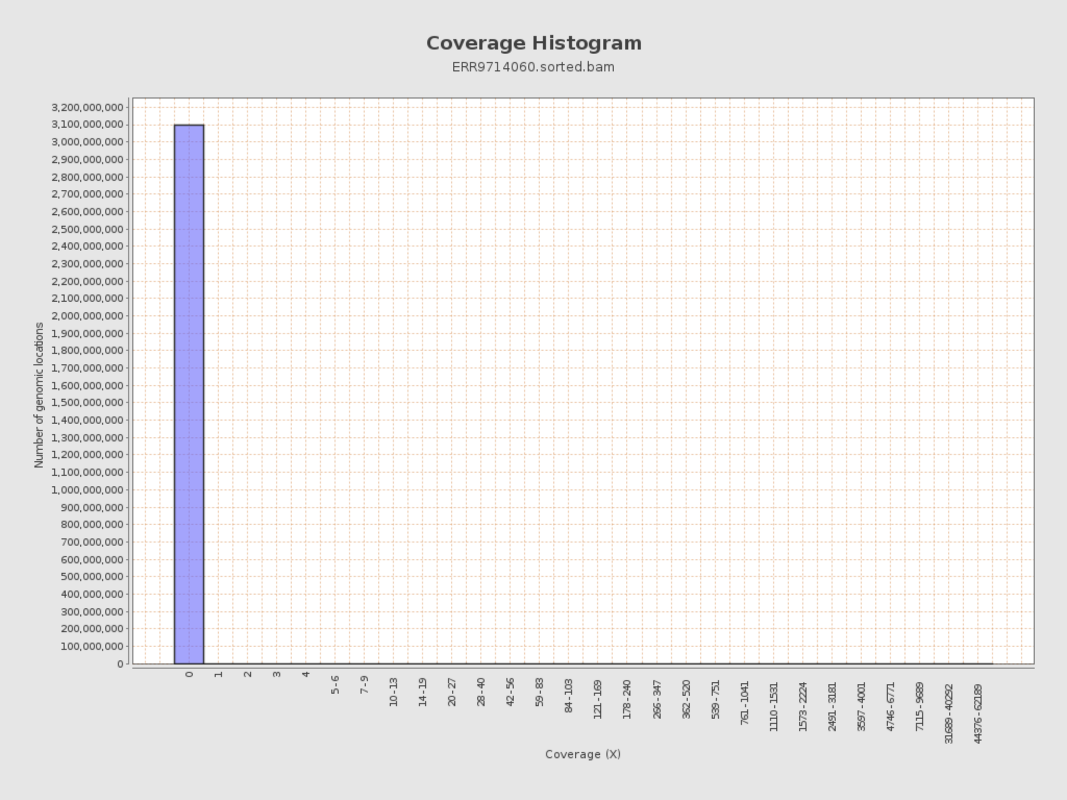
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	33373	0.0001	0.1682
chr2	243199373	8105725	0.0333	37.0777
chr3	198022430	10588	0.0001	0.0223
chr4	191154276	7747	0	0.0119
chr5	180915260	6383	0	0.009
chr6	171115067	10141	0.0001	0.0186
chr7	159138663	16388	0.0001	0.1051

chr8	146364022	14818	0.0001	0.0391
chr9	141213431	6798	0	0.0196
chr10	135534747	20931	0.0002	0.2247
chr11	135006516	9850	0.0001	0.0448
chr12	133851895	12588	0.0001	0.0589
chr13	115169878	1704	0	0.0054
chr14	107349540	13575	0.0001	0.1251
chr15	102531392	6878	0.0001	0.0266
chr16	90354753	9365	0.0001	0.0233
chr17	81195210	12915	0.0002	0.1494
chr18	78077248	5593	0.0001	0.0274
chr19	59128983	4128	0.0001	0.0207
chr20	63025520	4785	0.0001	0.0203
chr21	48129895	1379	0	0.0067
chr22	51304566	2180	0	0.0123
chrMT	16571	453	0.0273	0.1793
chrX	155270560	107665	0.0007	0.1028
chrY	59373566	4699	0.0001	0.0218

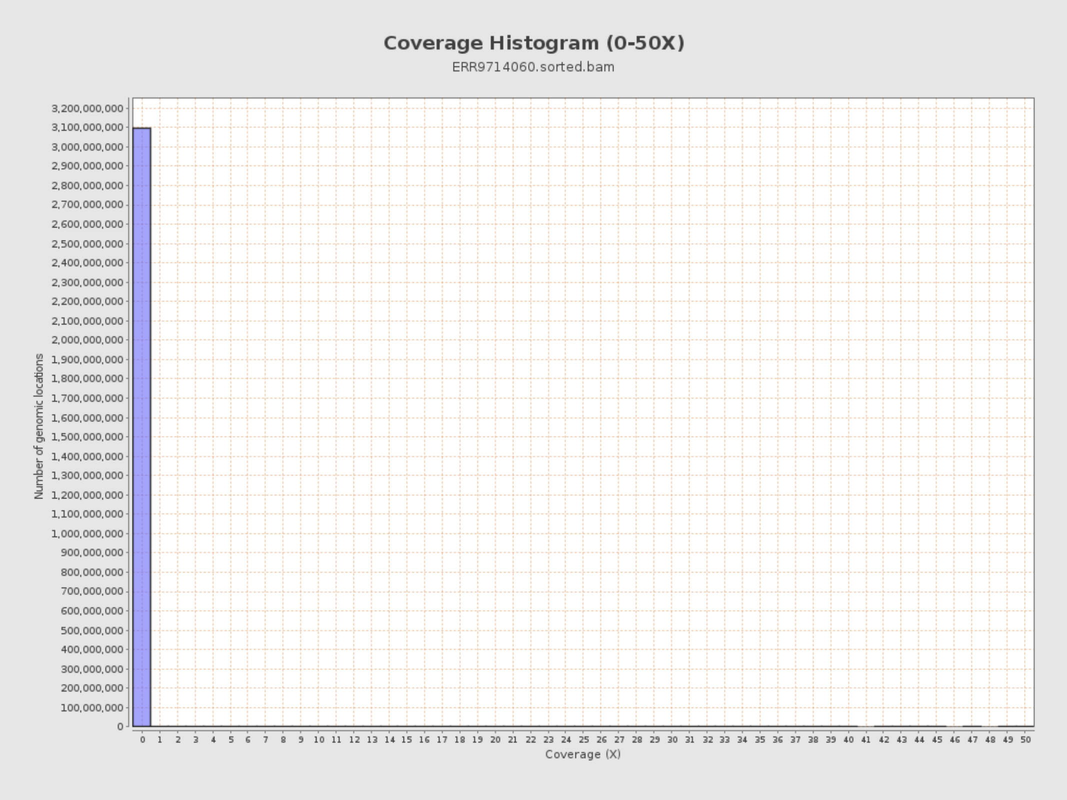
3. Results : Coverage across reference



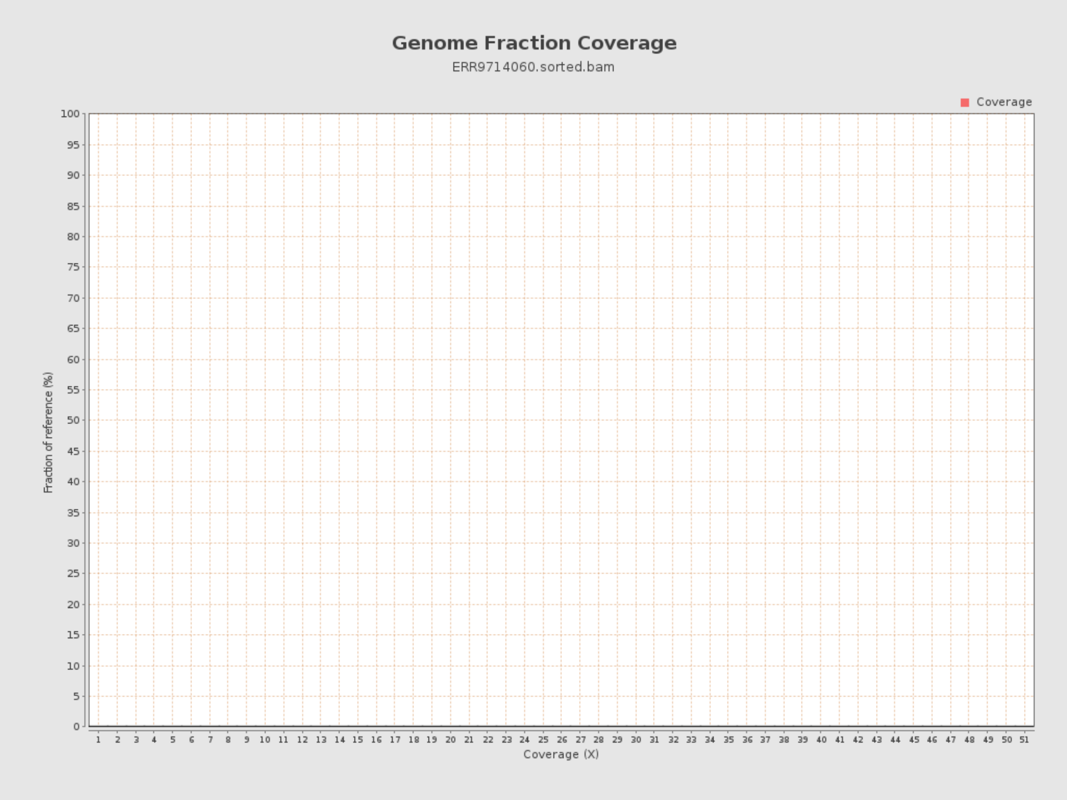
4. Results : Coverage Histogram



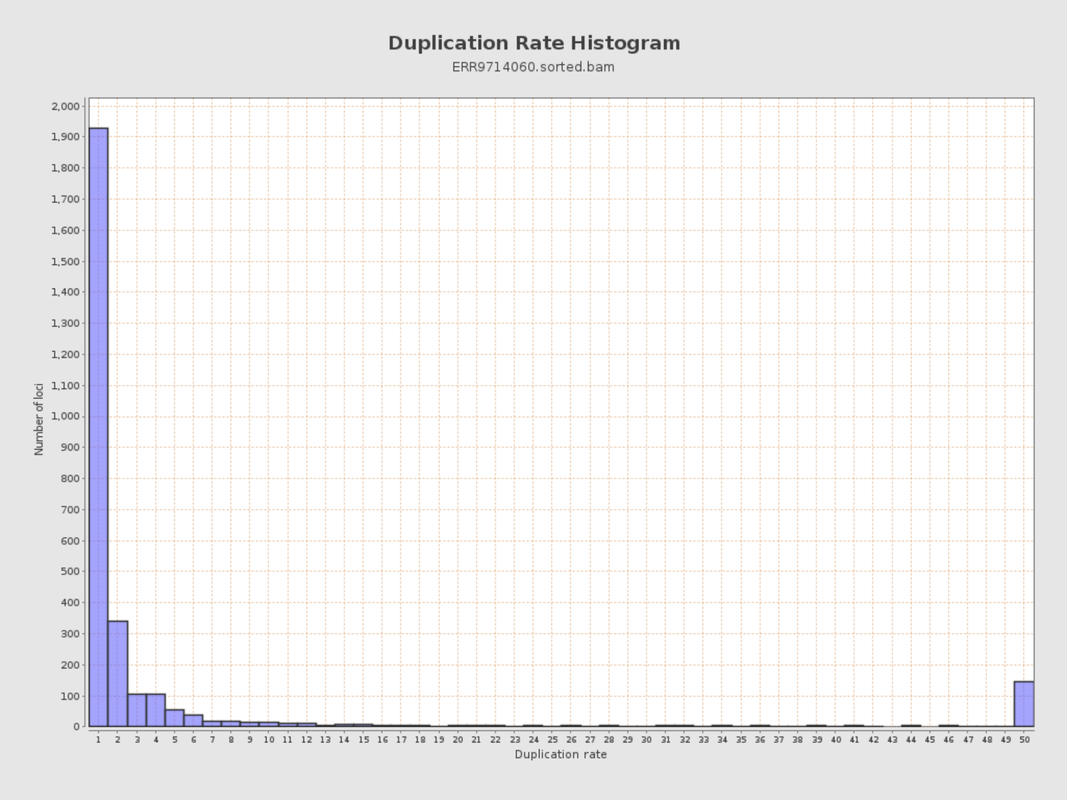
5. Results : Coverage Histogram (0-50X)



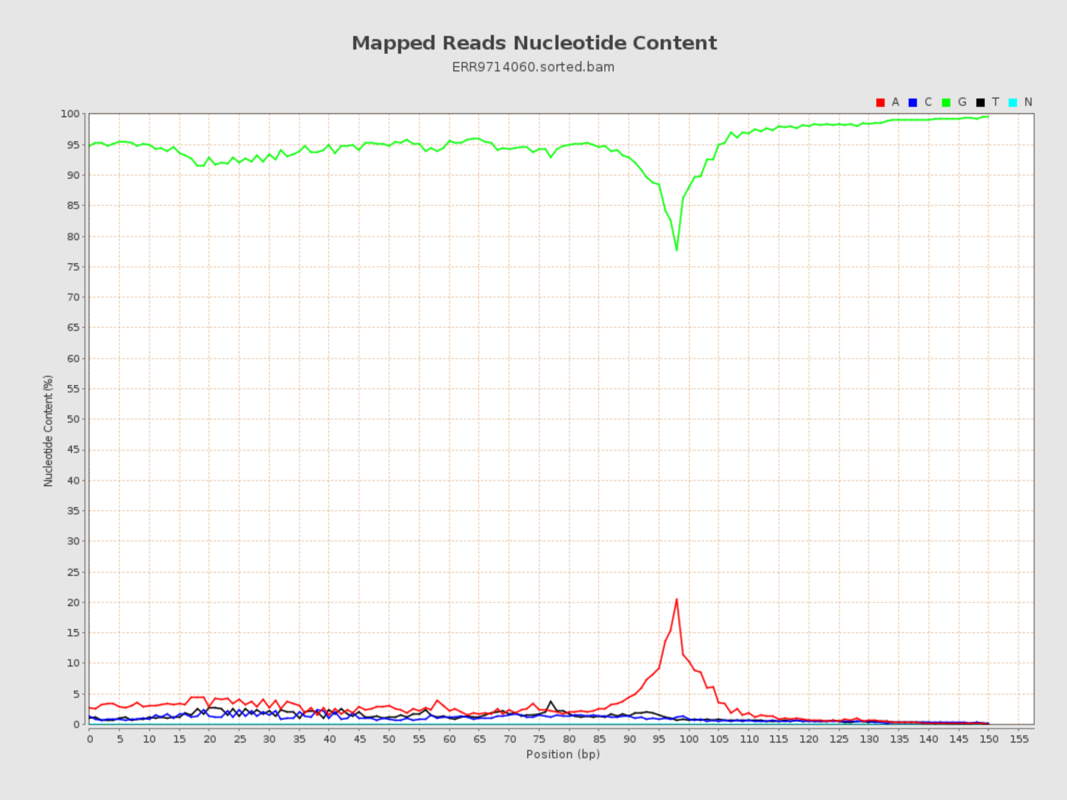
6. Results : Genome Fraction Coverage



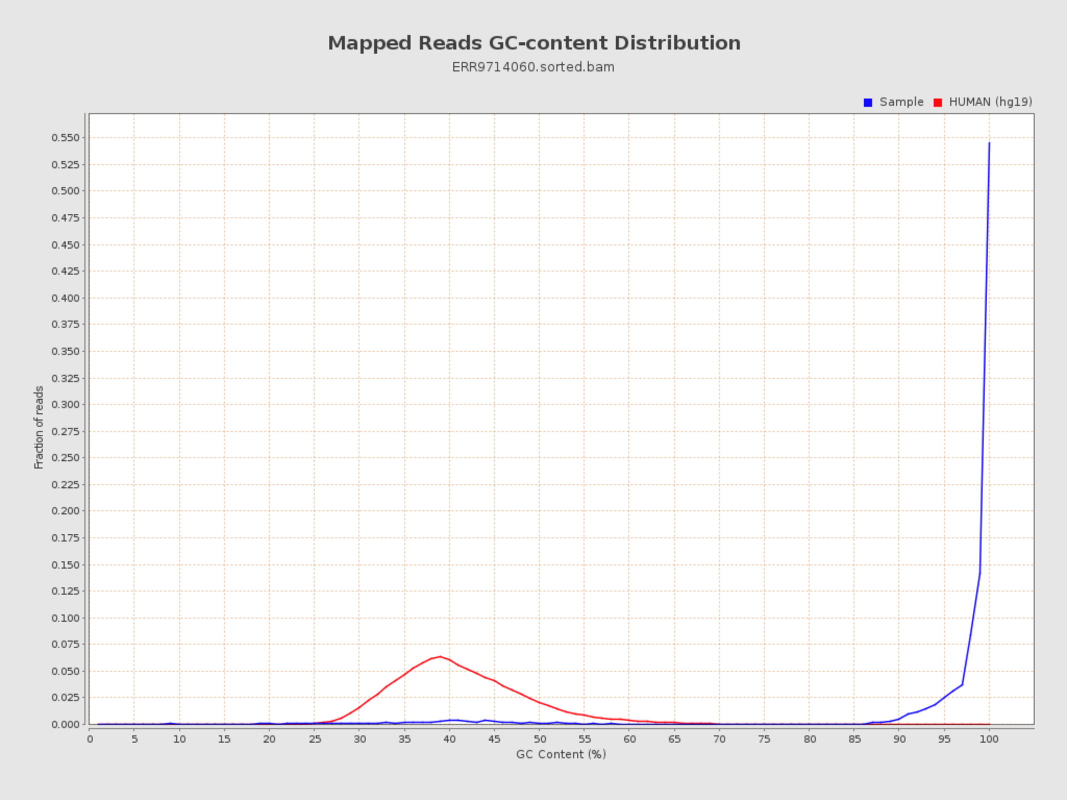
7. Results : Duplication Rate Histogram



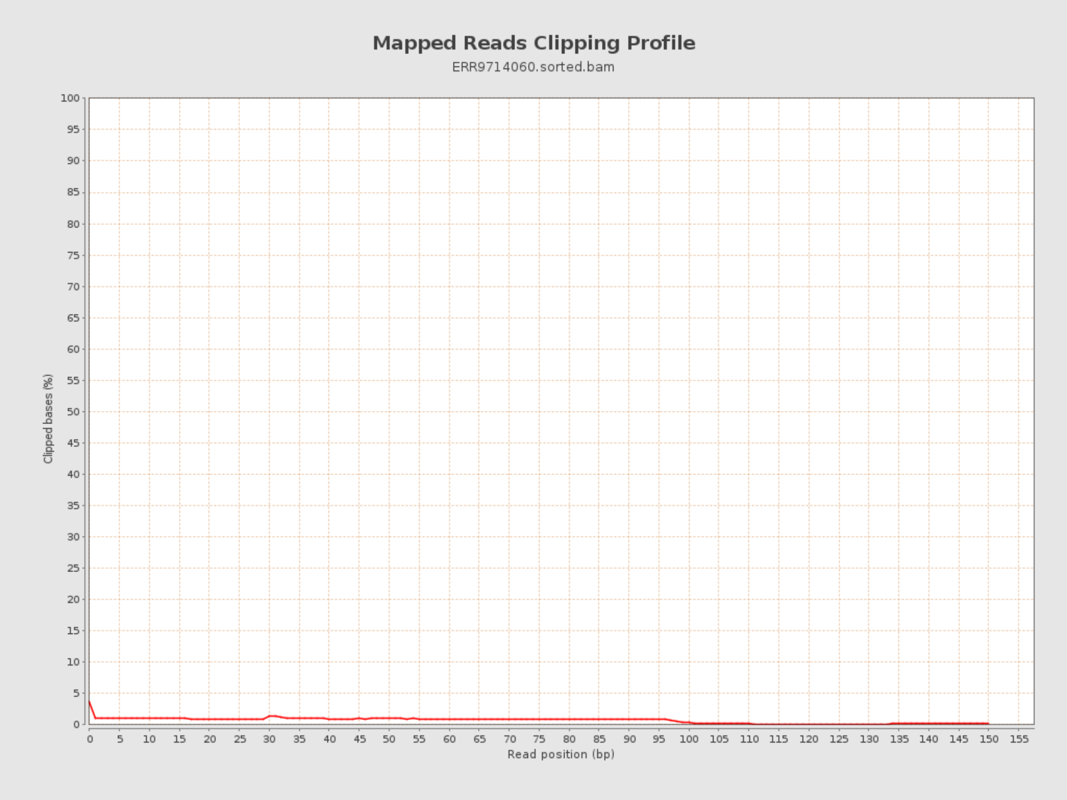
8. Results : Mapped Reads Nucleotide Content



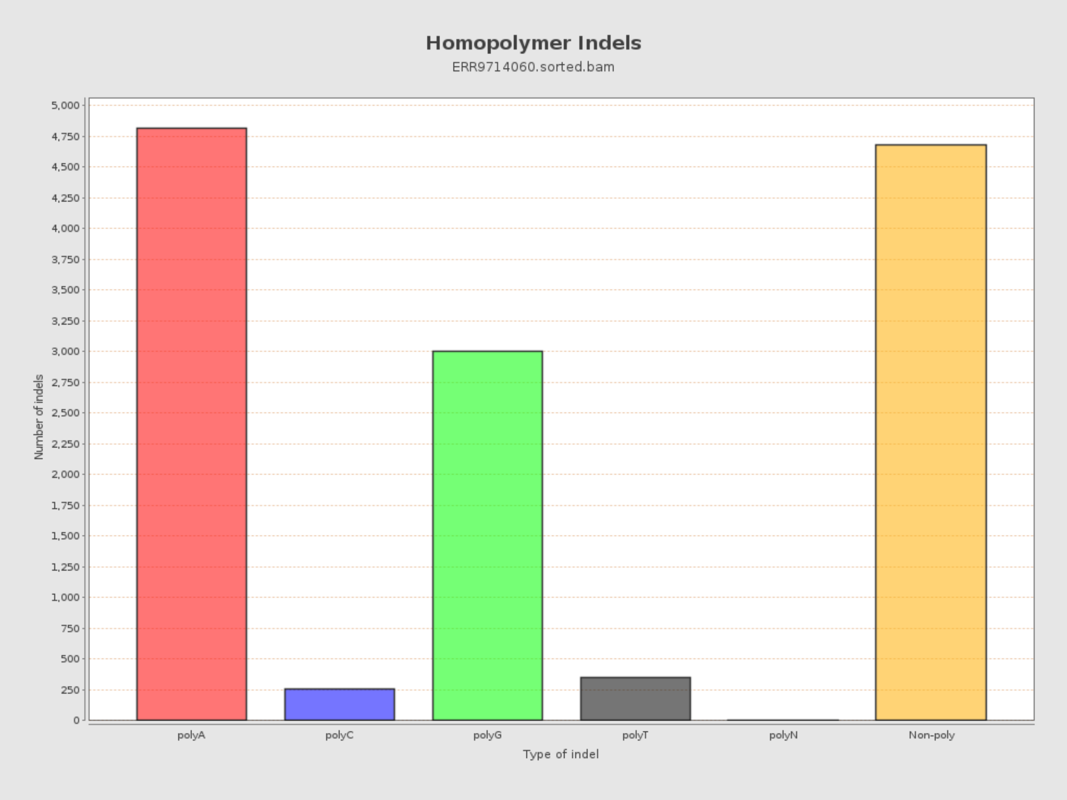
9. Results : Mapped Reads GC-content Distribution



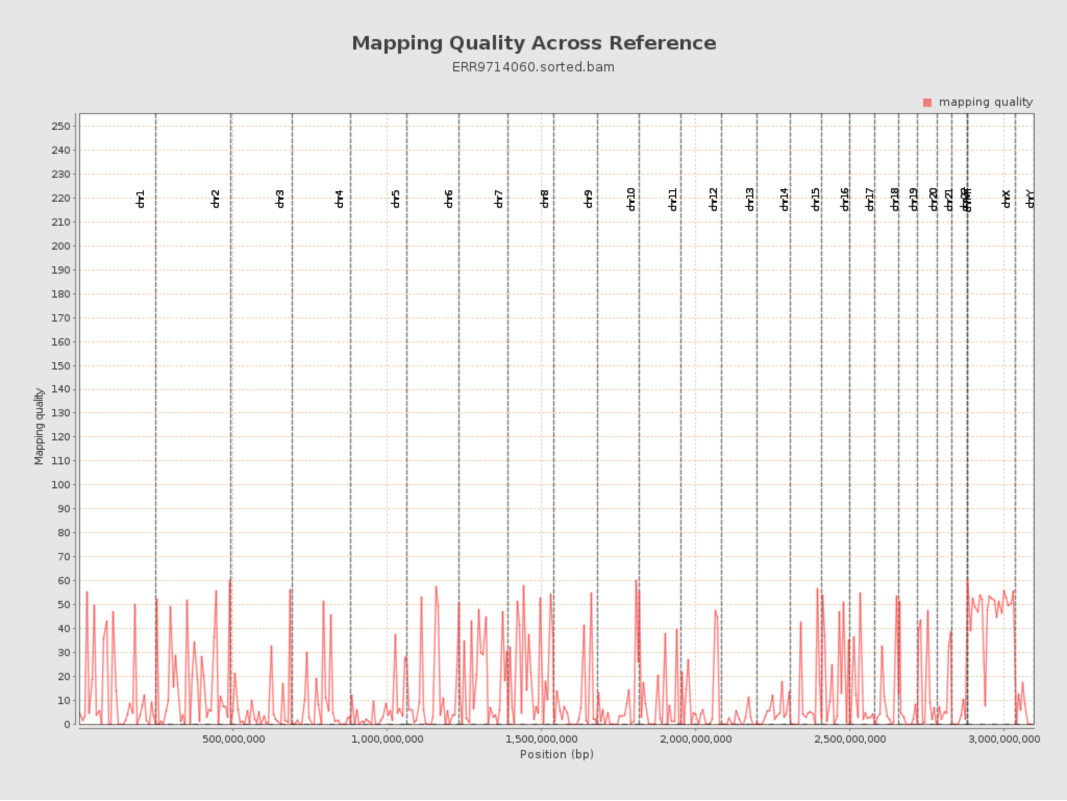
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram