Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 21:45:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714150.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_ERR9714150 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714150.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 21:45:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714150.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	704,348
Mapped reads	615,467 / 87.38%
Unmapped reads	88,881 / 12.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,060 / 2.56%
Read min/max/mean length	30 / 151 / 139.27
Duplicated reads (estimated)	556,915 / 79.07%
Duplication rate	44.14%
Clipped reads	580,176 / 82.37%

2.2. ACGT Content

Number/percentage of A's	21,109,233 / 26.74%
Number/percentage of C's	17,721,737 / 22.45%
Number/percentage of T's	20,080,009 / 25.44%
Number/percentage of G's	20,017,005 / 25.36%
Number/percentage of N's	509 / 0%
GC Percentage	47.81%

2.3. Coverage

Mean	0.026

Standard Deviation	7.4035

2.4. Mapping Quality

Mean Mapping Quality	51.63

2.5. Mismatches and indels

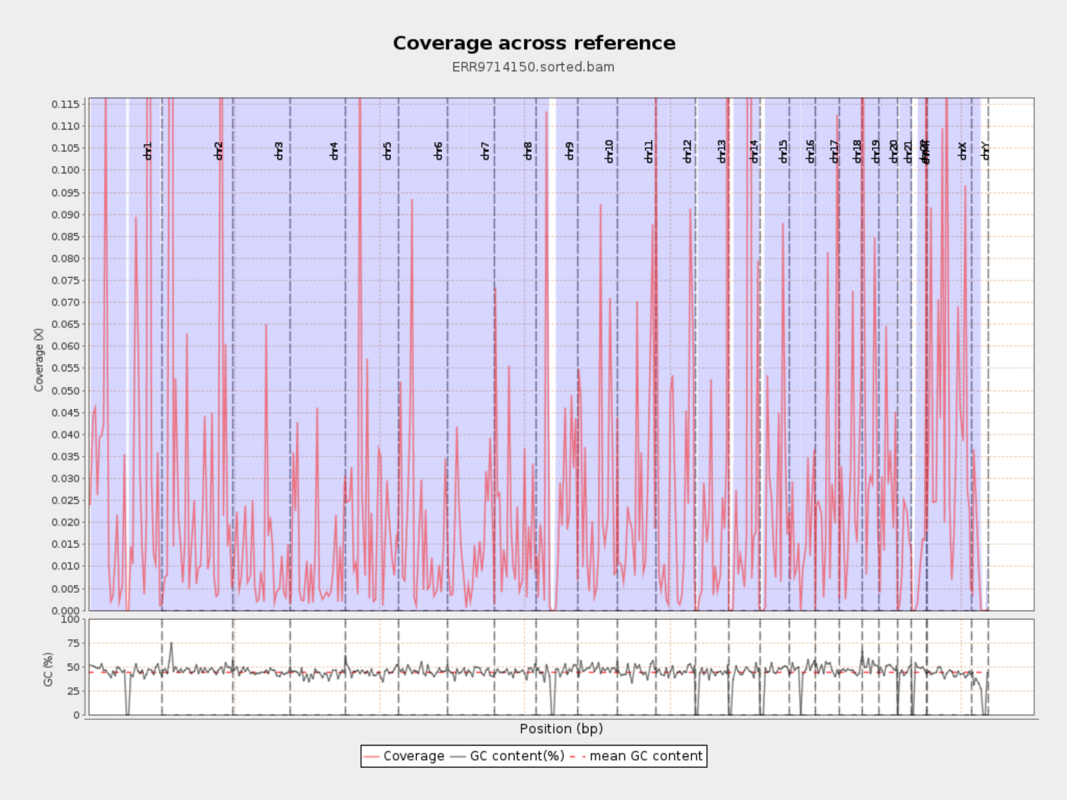
General error rate	4.31%
Mismatches	3,165,026
Insertions	85,169
Mapped reads with at least one insertion	13.38%
Deletions	274,711
Mapped reads with at least one deletion	42.46%
Homopolymer indels	30.32%

2.6. Chromosome stats

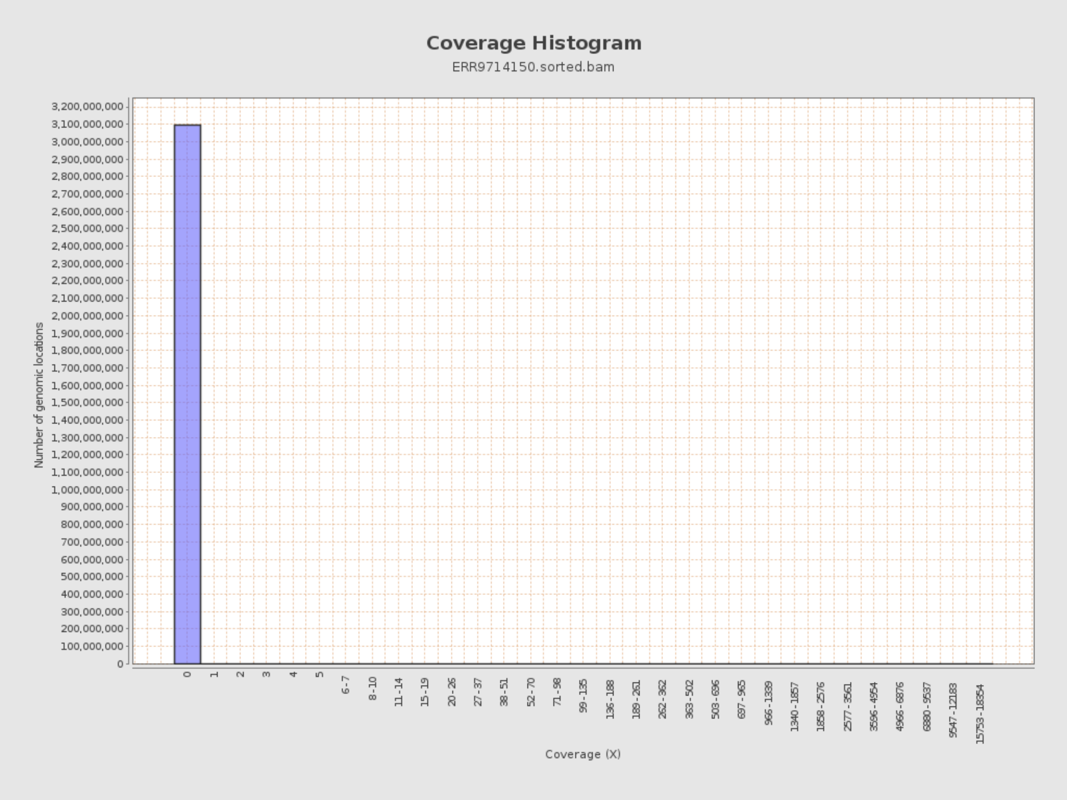
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8452598	0.0339	9.149
chr2	243199373	9574250	0.0394	12.5352
chr3	198022430	2412341	0.0122	2.0526
chr4	191154276	2282629	0.0119	2.4938
chr5	180915260	4204123	0.0232	6.5031
chr6	171115067	3237554	0.0189	4.0815
chr7	159138663	2344853	0.0147	2.6329

chr8	146364022	3014348	0.0206	4.7095
chr9	141213431	3303044	0.0234	5.7542
chr10	135534747	3685294	0.0272	4.9824
chr11	135006516	3658094	0.0271	4.6864
chr12	133851895	3666334	0.0274	4.9096
chr13	115169878	3121086	0.0271	10.8257
chr14	107349540	4367427	0.0407	20.9414
chr15	102531392	2591567	0.0253	4.2718
chr16	90354753	1549426	0.0171	2.4827
chr17	81195210	3003696	0.037	7.7811
chr18	78077248	2152895	0.0276	5.3593
chr19	59128983	2643573	0.0447	5.3453
chr20	63025520	1923952	0.0305	4.9772
chr21	48129895	630488	0.0131	2.0634
chr22	51304566	457386	0.0089	1.1391
chrMT	16571	386743	23.3385	203.8455
chrX	155270560	7393653	0.0476	5.5422
chrY	59373566	580725	0.0098	2.4162

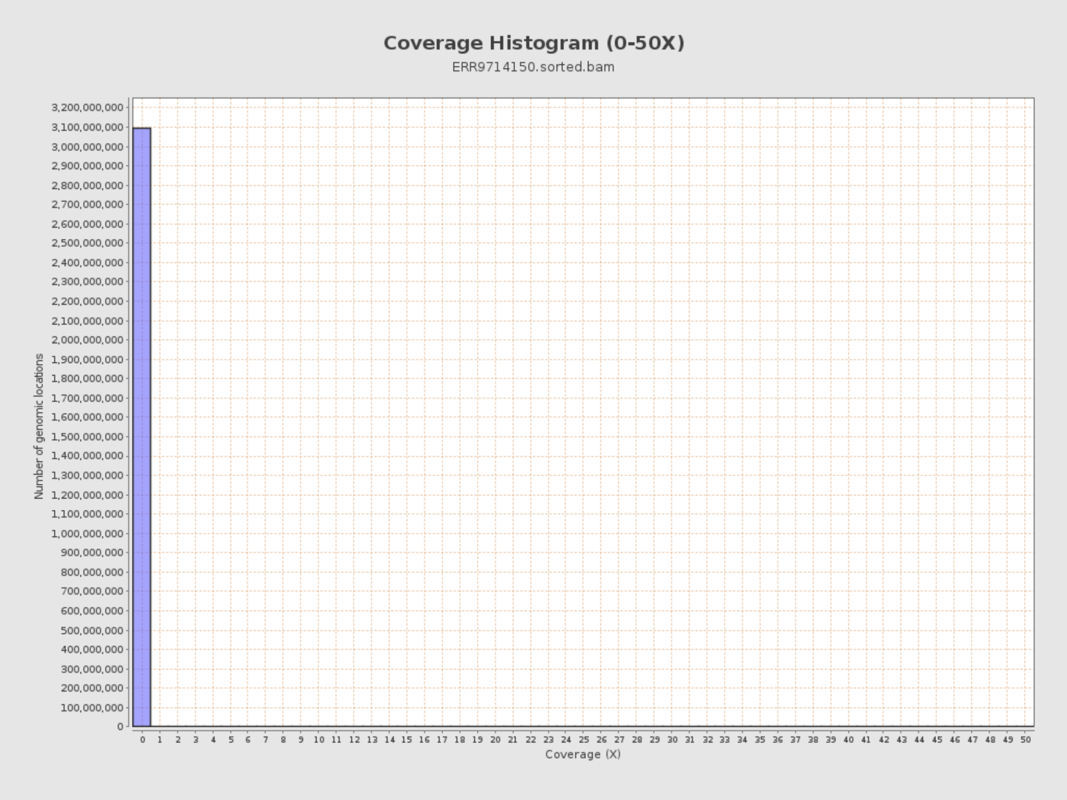
3. Results : Coverage across reference



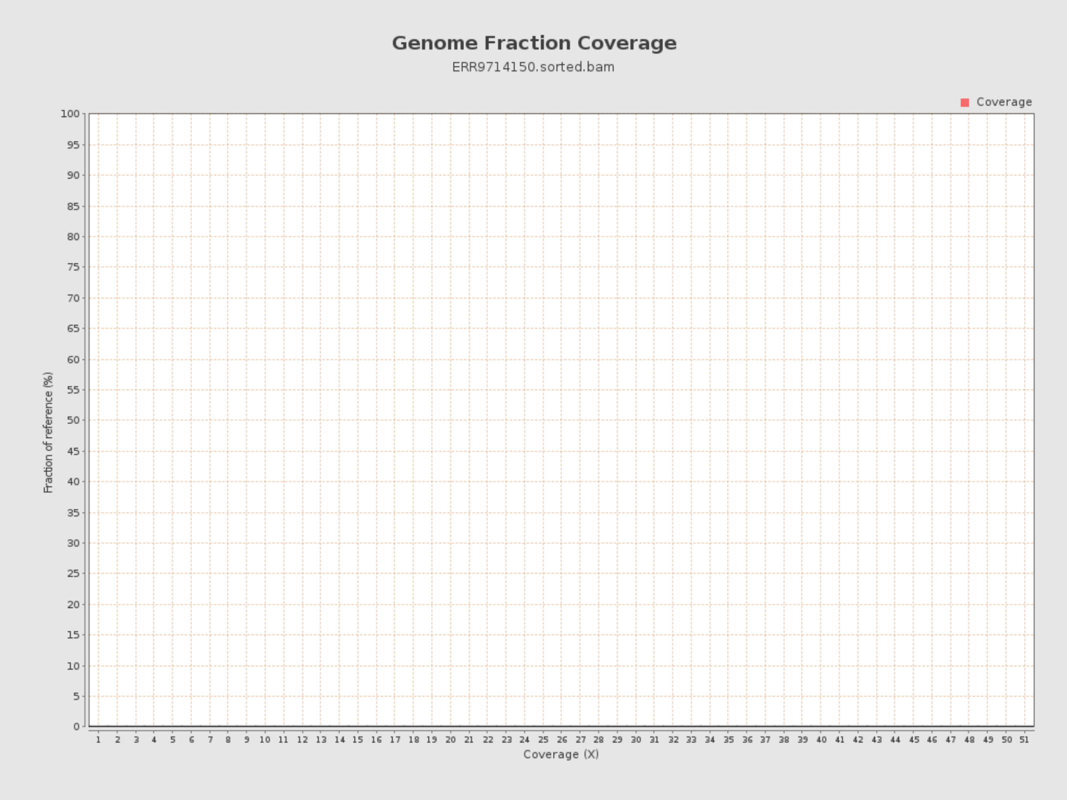
4. Results : Coverage Histogram



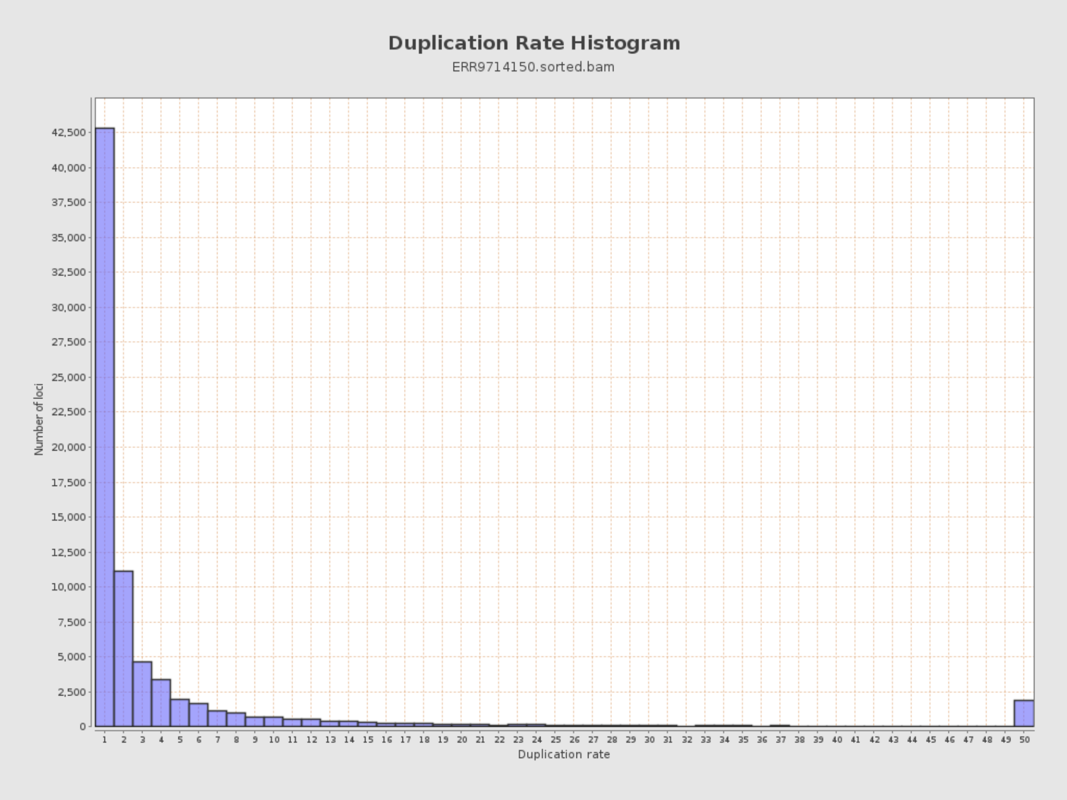
5. Results : Coverage Histogram (0-50X)



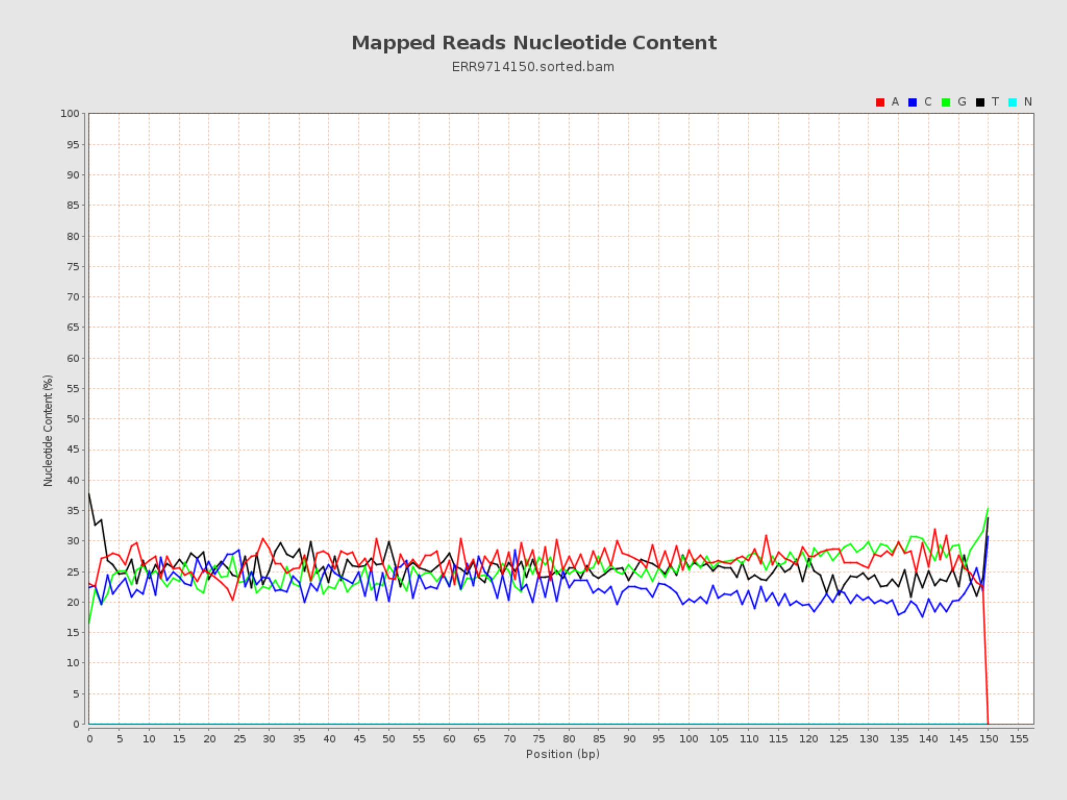
6. Results : Genome Fraction Coverage



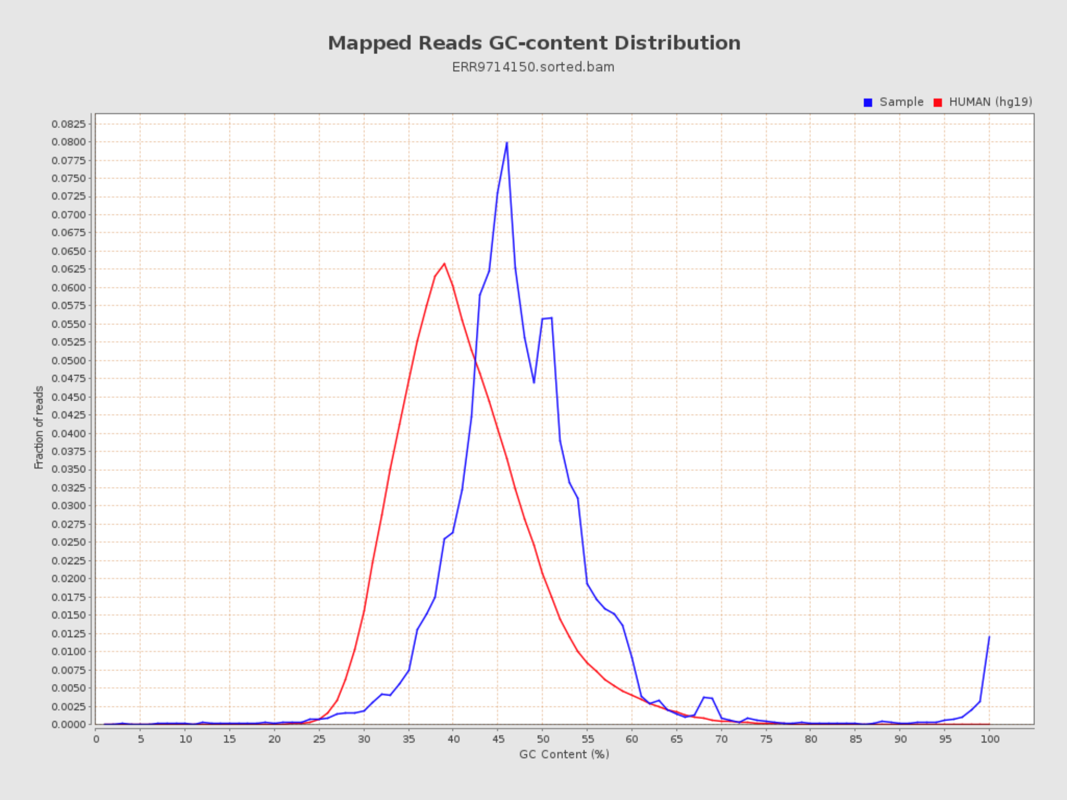
7. Results : Duplication Rate Histogram



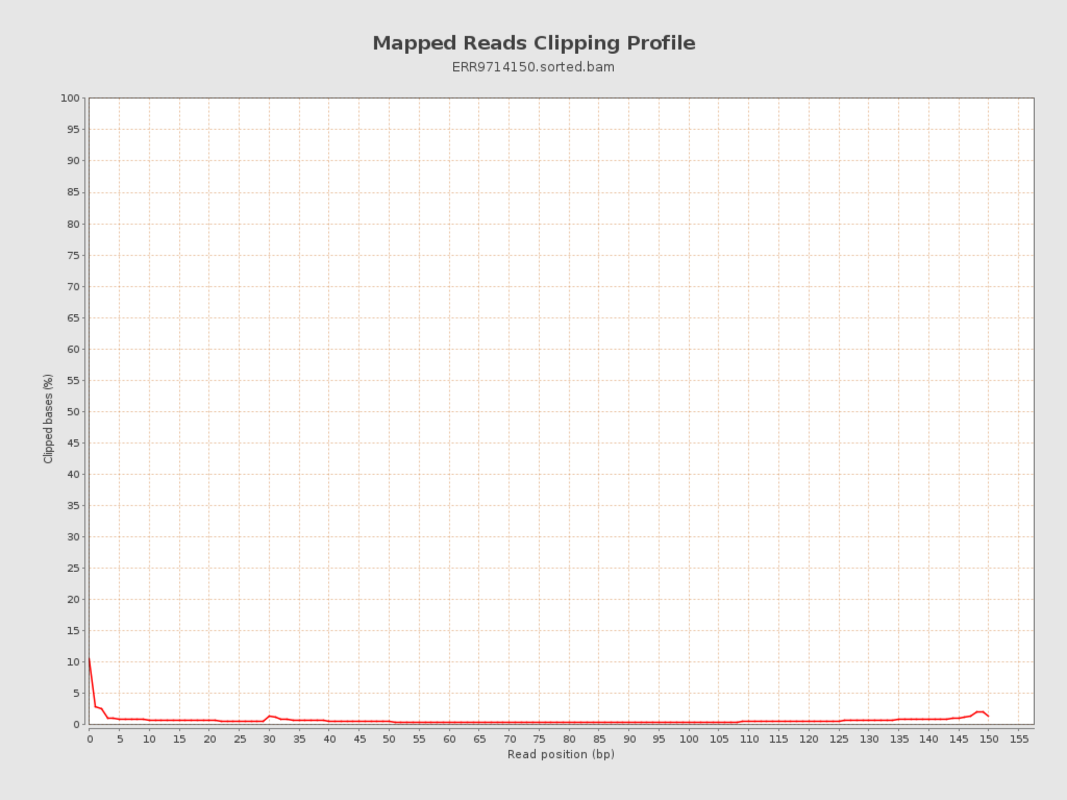
8. Results : Mapped Reads Nucleotide Content



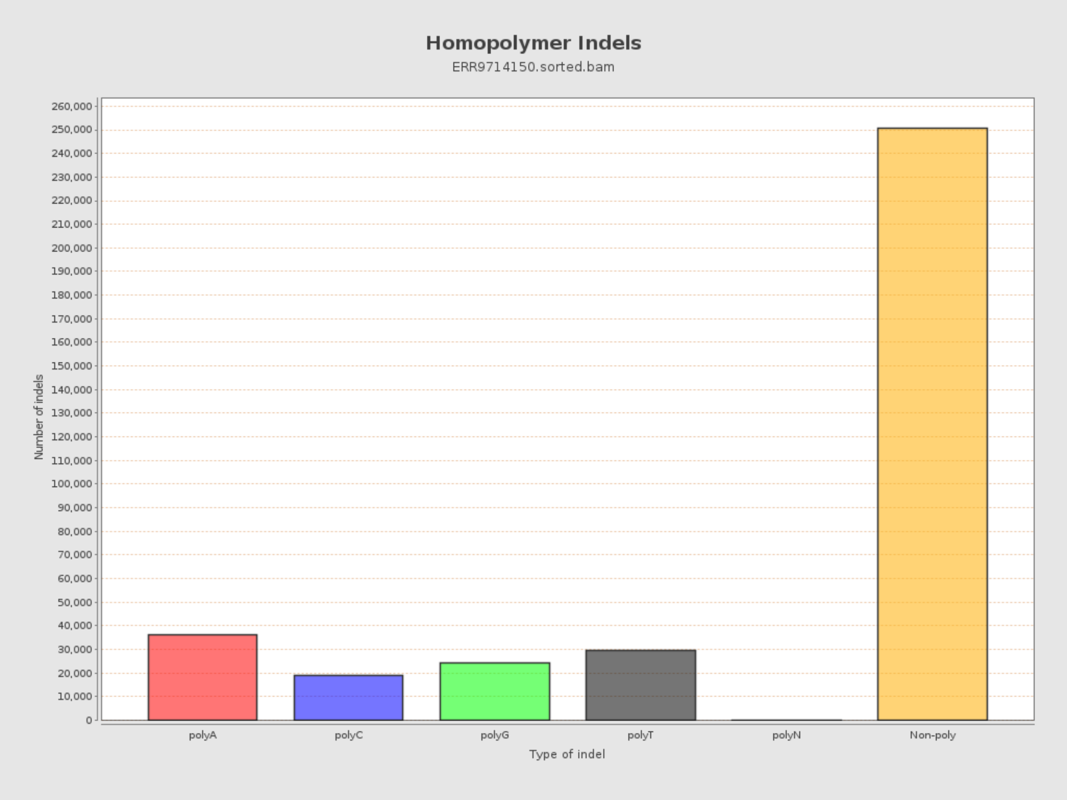
9. Results : Mapped Reads GC-content Distribution



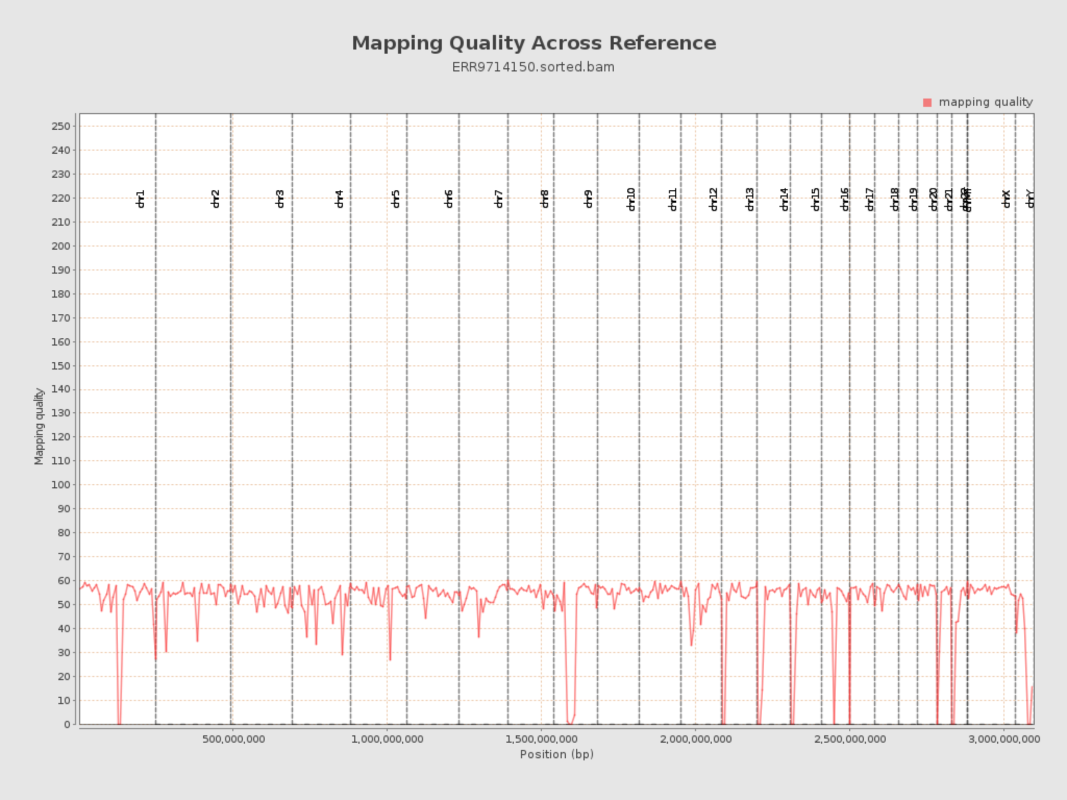
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram