Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 21:24:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714143.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_ERR9714143 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714143.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 21:24:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714143.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	714,372
Mapped reads	572,501 / 80.14%
Unmapped reads	141,871 / 19.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,846 / 2.22%
Read min/max/mean length	30 / 151 / 131.02
Duplicated reads (estimated)	515,827 / 72.21%
Duplication rate	44.04%
Clipped reads	535,816 / 75.01%

2.2. ACGT Content

Number/percentage of A's	19,471,071 / 26.71%
Number/percentage of C's	15,924,372 / 21.85%
Number/percentage of T's	18,456,085 / 25.32%
Number/percentage of G's	19,037,347 / 26.12%
Number/percentage of N's	538 / 0%
GC Percentage	47.97%

2.3. Coverage

Mean	0.0241

Standard Deviation	7.4442

2.4. Mapping Quality

Mean Mapping Quality	51.77

2.5. Mismatches and indels

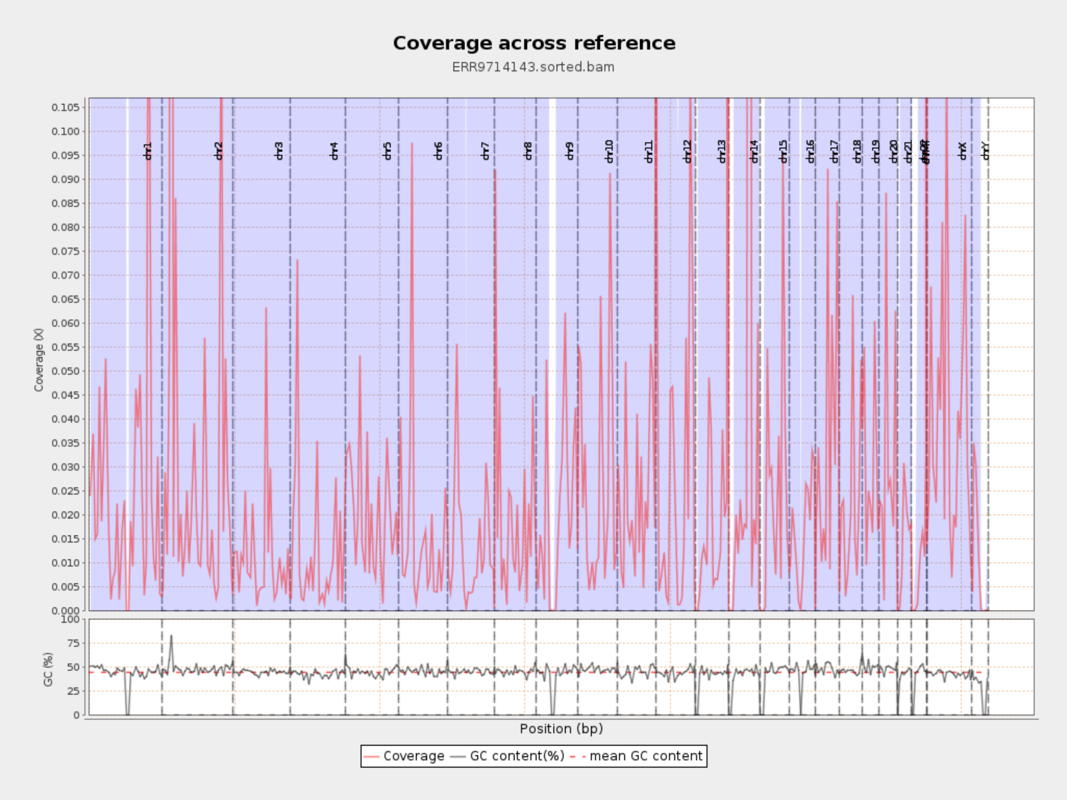
General error rate	4.54%
Mismatches	3,107,227
Insertions	75,556
Mapped reads with at least one insertion	12.7%
Deletions	270,363
Mapped reads with at least one deletion	44.72%
Homopolymer indels	29.06%

2.6. Chromosome stats

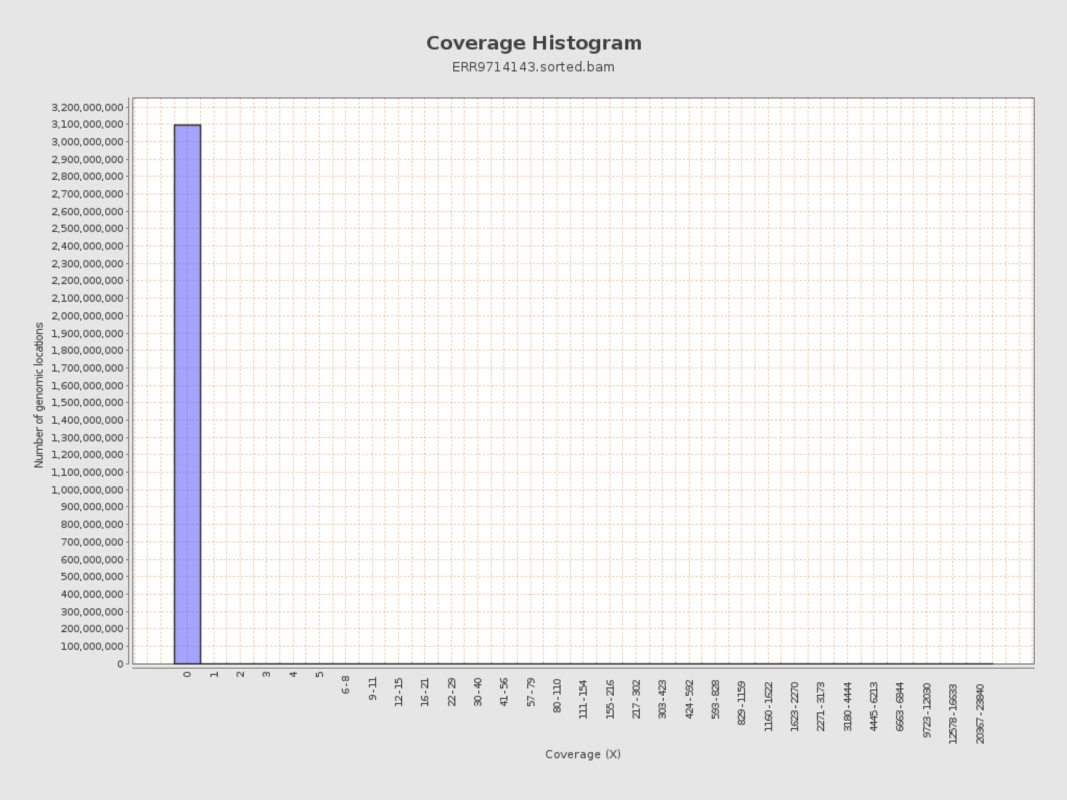
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6021260	0.0242	5.2514
chr2	243199373	9592159	0.0394	13.3963
chr3	198022430	2331542	0.0118	1.9647
chr4	191154276	2477816	0.013	2.6362
chr5	180915260	3713660	0.0205	3.5593
chr6	171115067	2829133	0.0165	3.6727
chr7	159138663	2215794	0.0139	2.2892

chr8	146364022	3084333	0.0211	4.993
chr9	141213431	2797297	0.0198	3.9038
chr10	135534747	3828704	0.0282	5.087
chr11	135006516	3369543	0.025	3.9098
chr12	133851895	3785583	0.0283	5.3887
chr13	115169878	2616402	0.0227	7.1138
chr14	107349540	5225181	0.0487	26.975
chr15	102531392	2585935	0.0252	4.5863
chr16	90354753	1526649	0.0169	2.4065
chr17	81195210	3103971	0.0382	6.7318
chr18	78077248	1710829	0.0219	4.7778
chr19	59128983	1729099	0.0292	3.6002
chr20	63025520	2072087	0.0329	5.2031
chr21	48129895	674221	0.014	2.334
chr22	51304566	389987	0.0076	0.8977
chrMT	16571	151104	9.1186	74.3418
chrX	155270560	6192909	0.0399	4.4526
chrY	59373566	609111	0.0103	1.9097

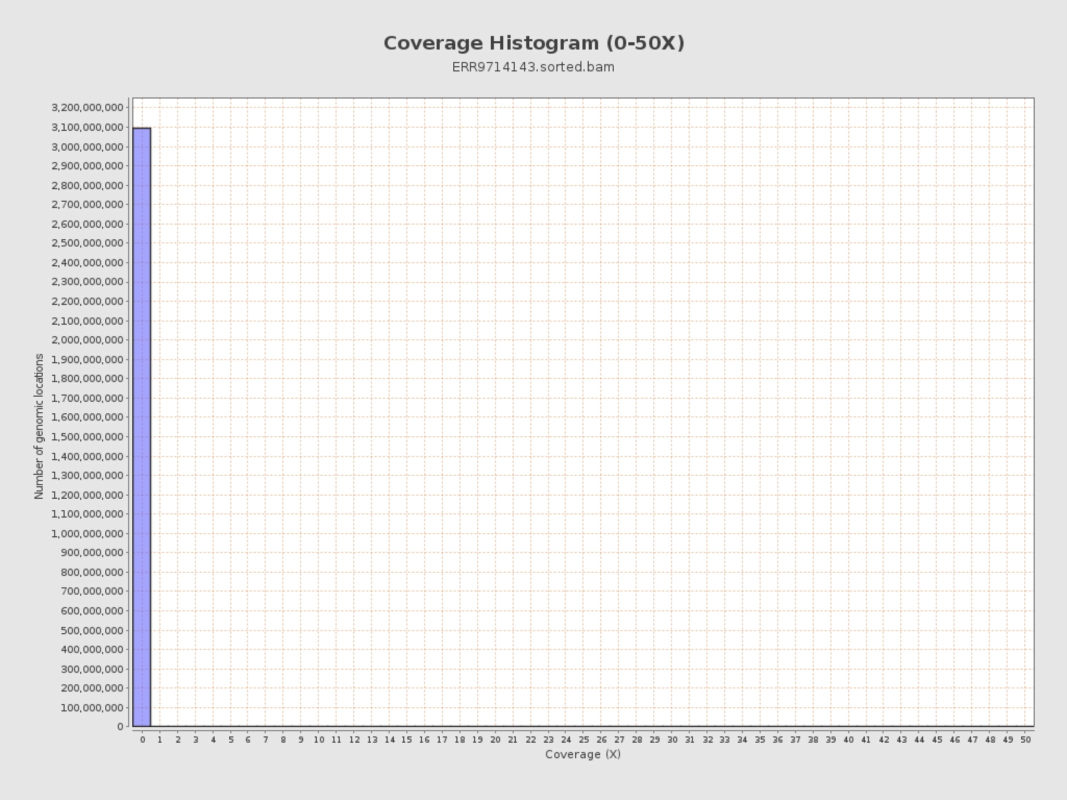
3. Results : Coverage across reference



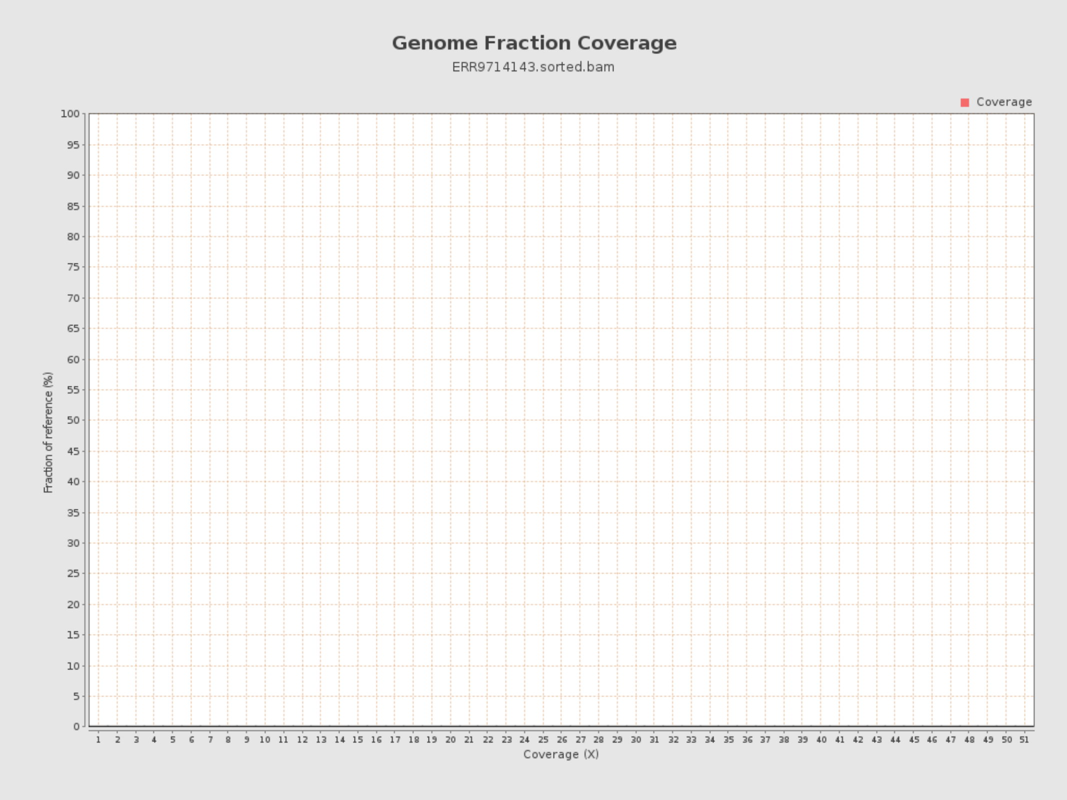
4. Results : Coverage Histogram



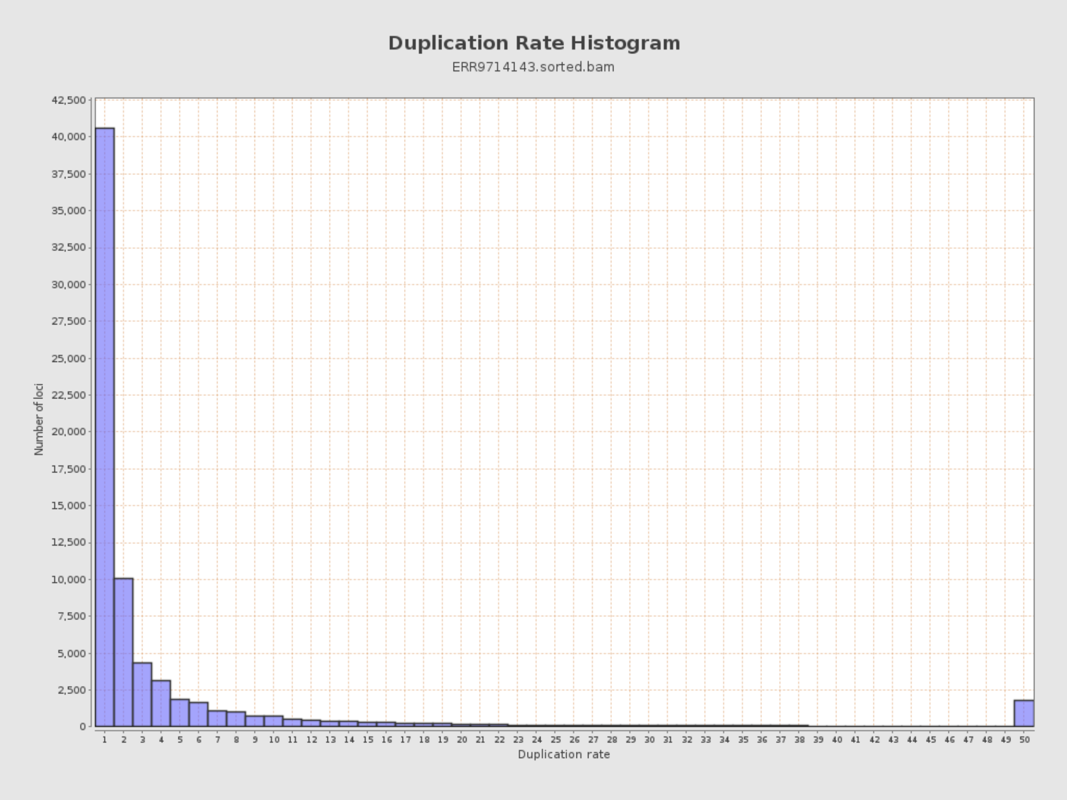
5. Results : Coverage Histogram (0-50X)



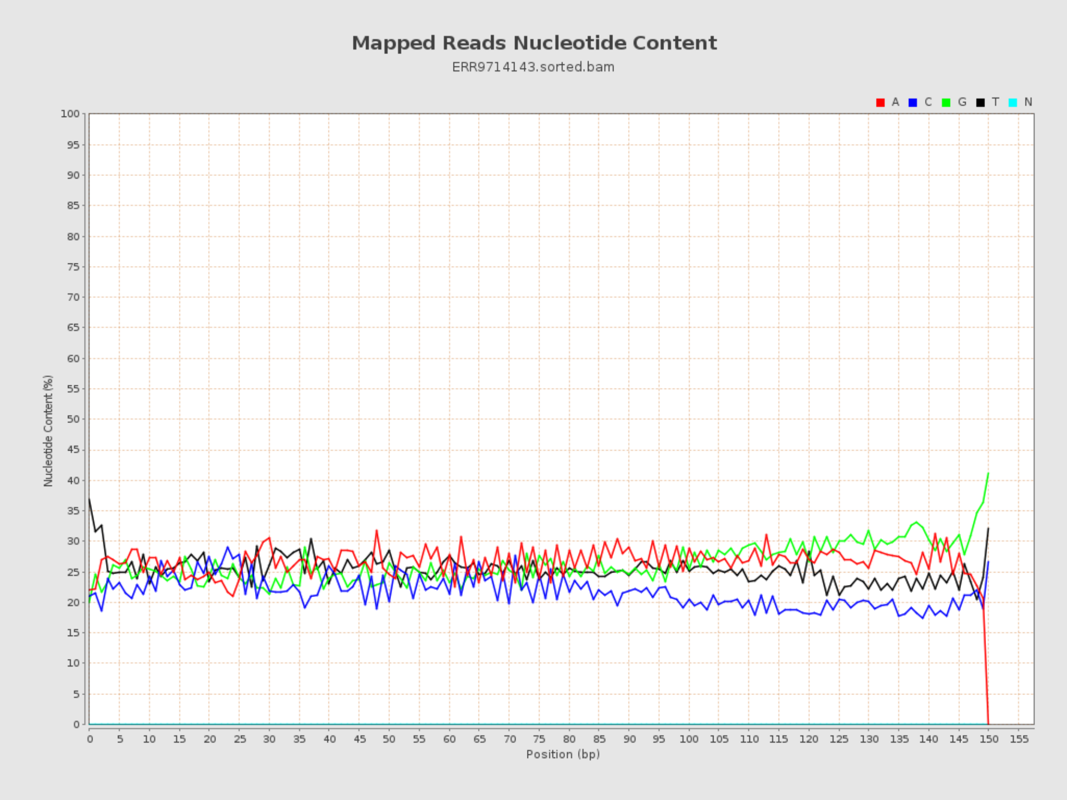
6. Results : Genome Fraction Coverage



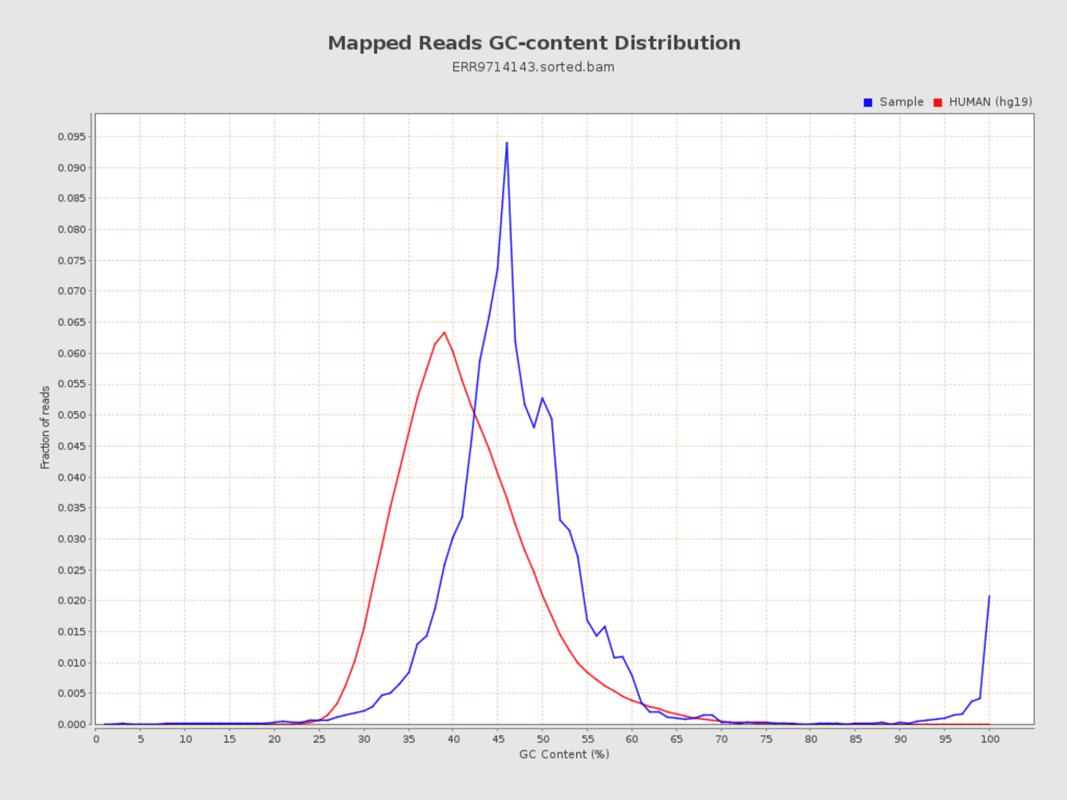
7. Results : Duplication Rate Histogram



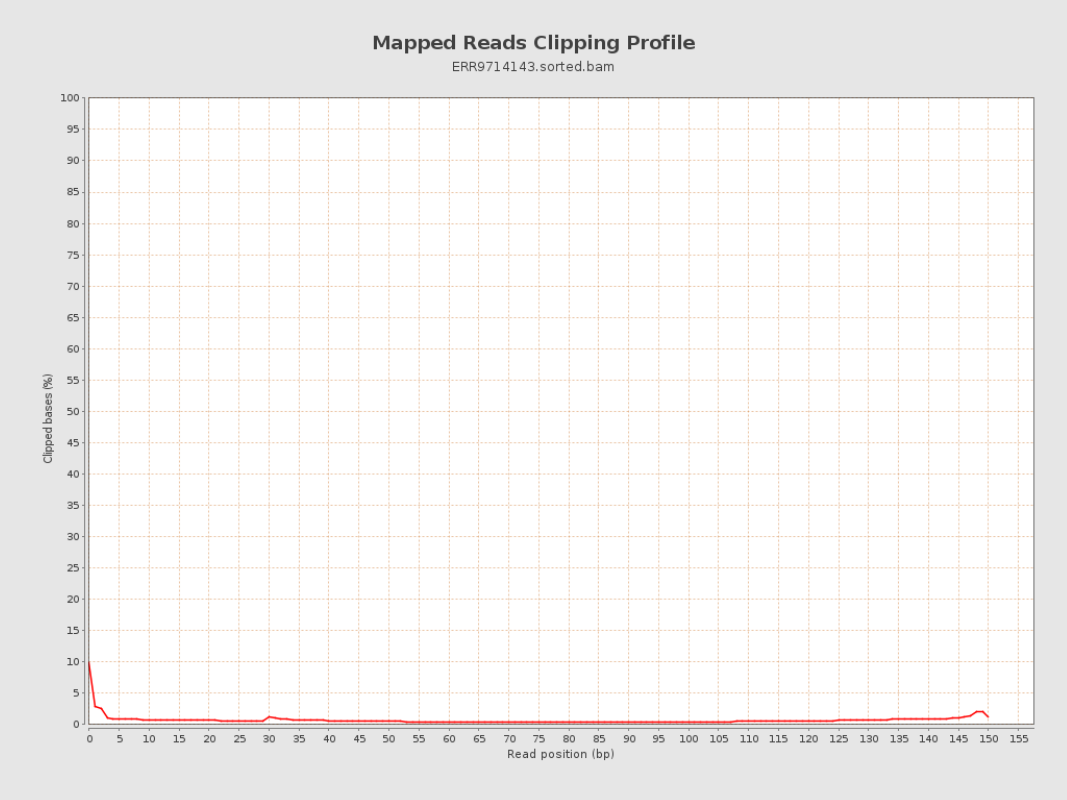
8. Results : Mapped Reads Nucleotide Content



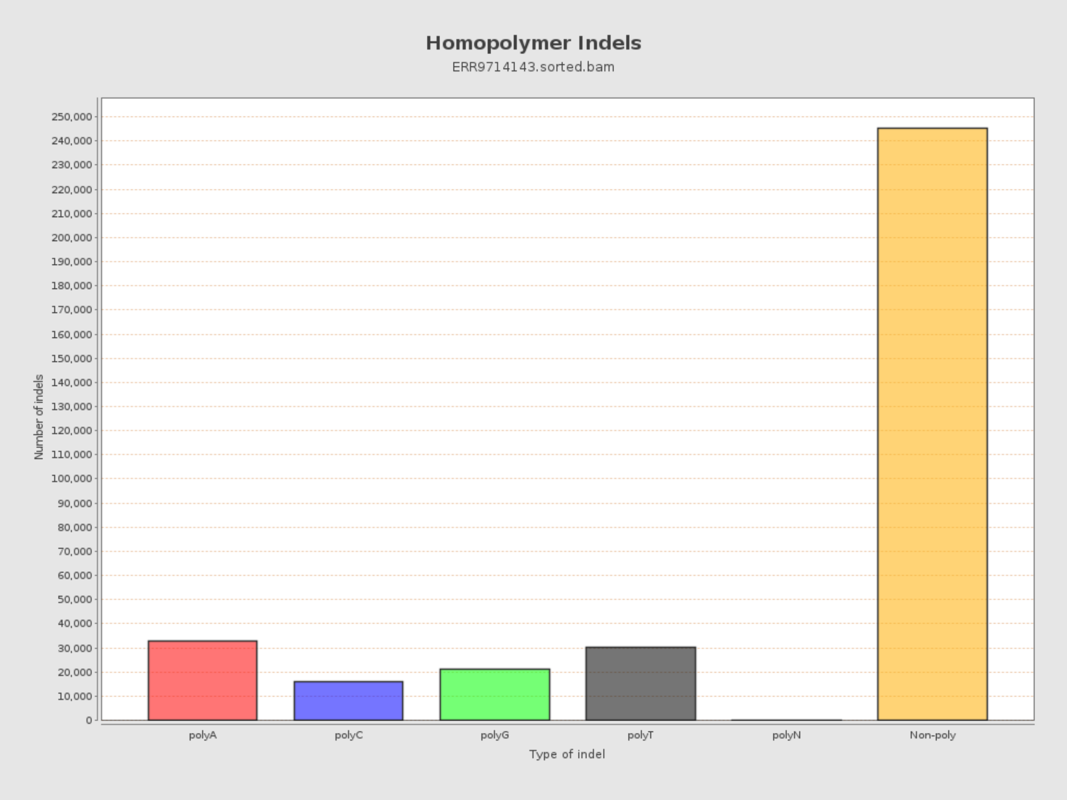
9. Results : Mapped Reads GC-content Distribution



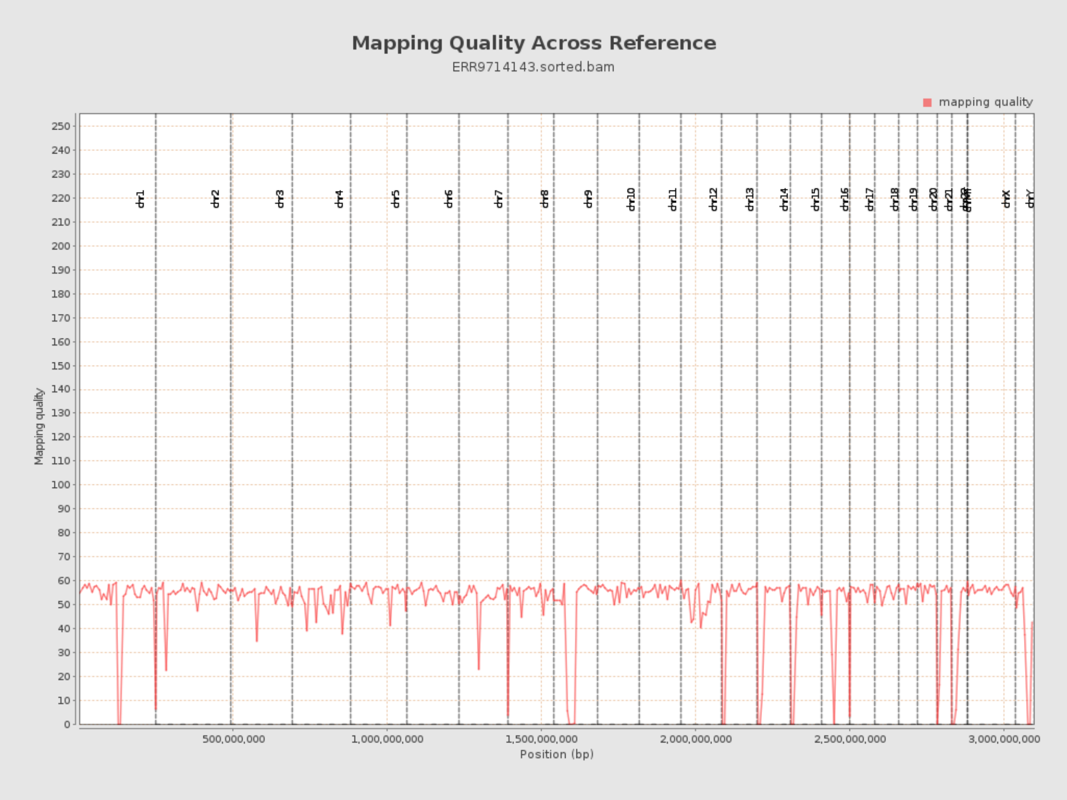
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram