Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 01:14:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714245.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_ERR9714245 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714245.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 01:14:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714245.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	348,262
Mapped reads	49,661 / 14.26%
Unmapped reads	298,601 / 85.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,484 / 0.43%
Read min/max/mean length	30 / 151 / 60.16
Duplicated reads (estimated)	48,579 / 13.95%
Duplication rate	34.37%
Clipped reads	29,268 / 8.4%

2.2. ACGT Content

Number/percentage of A's	179,663 / 3.68%
Number/percentage of C's	87,821 / 1.8%
Number/percentage of T's	116,500 / 2.38%
Number/percentage of G's	4,502,601 / 92.14%
Number/percentage of N's	149 / 0%
GC Percentage	93.94%

2.3. Coverage

Mean	0.0016

Standard Deviation	5.6327

2.4. Mapping Quality

Mean Mapping Quality	12.64

2.5. Mismatches and indels

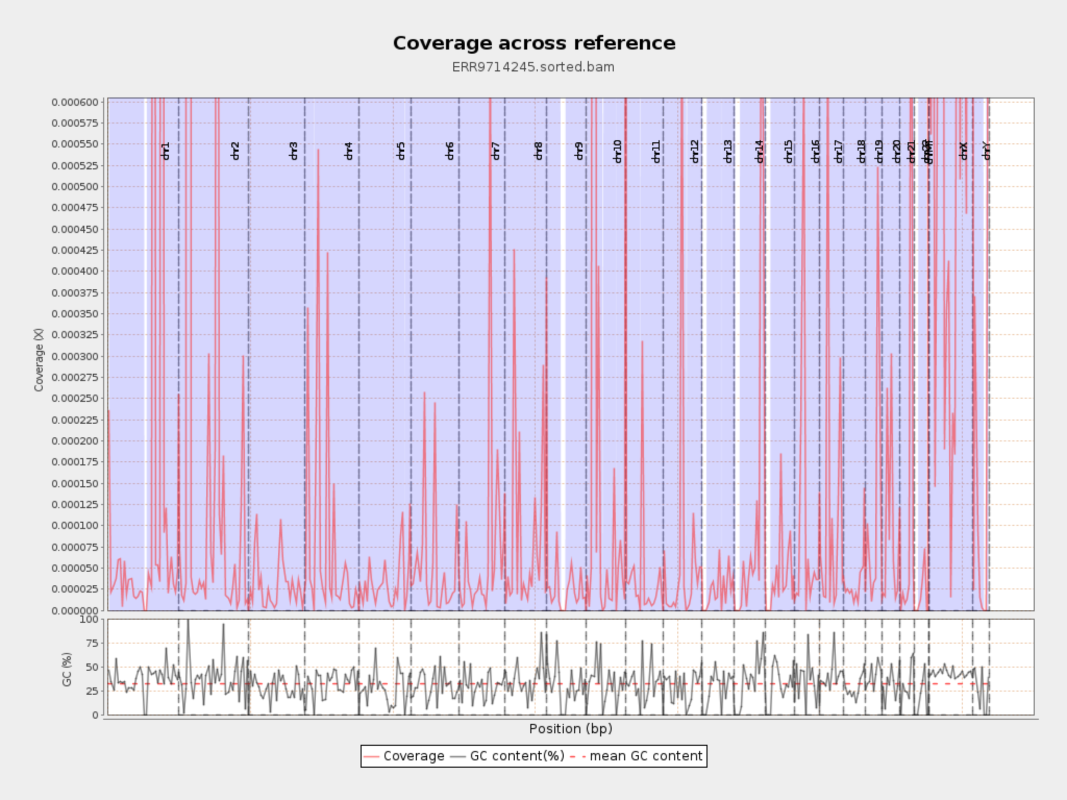
General error rate	3.37%
Mismatches	122,999
Insertions	5,981
Mapped reads with at least one insertion	8.1%
Deletions	2,902
Mapped reads with at least one deletion	5.49%
Homopolymer indels	60.36%

2.6. Chromosome stats

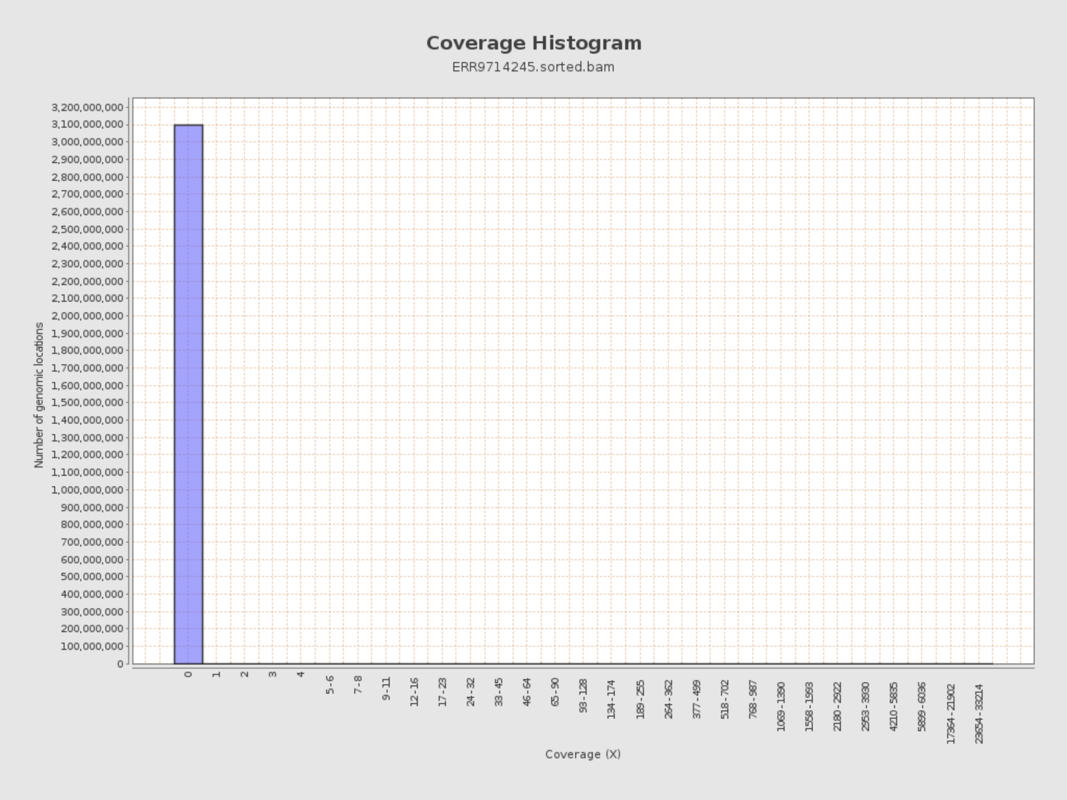
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	65872	0.0003	0.4311
chr2	243199373	4483799	0.0184	20.0871
chr3	198022430	6234	0	0.011
chr4	191154276	16635	0.0001	0.0351
chr5	180915260	5954	0	0.0124
chr6	171115067	9196	0.0001	0.0193
chr7	159138663	11932	0.0001	0.0683

chr8	146364022	12086	0.0001	0.0281
chr9	141213431	3700	0	0.0107
chr10	135534747	40105	0.0003	0.5034
chr11	135006516	8514	0.0001	0.0348
chr12	133851895	9474	0.0001	0.0501
chr13	115169878	2727	0	0.0072
chr14	107349540	13477	0.0001	0.0738
chr15	102531392	4274	0	0.0151
chr16	90354753	8773	0.0001	0.0324
chr17	81195210	10781	0.0001	0.0965
chr18	78077248	2630	0	0.0151
chr19	59128983	7009	0.0001	0.0395
chr20	63025520	6413	0.0001	0.0307
chr21	48129895	8518	0.0002	0.0814
chr22	51304566	968	0	0.0133
chrMT	16571	232	0.014	0.2201
chrX	155270560	151275	0.001	0.1653
chrY	59373566	10617	0.0002	0.0427

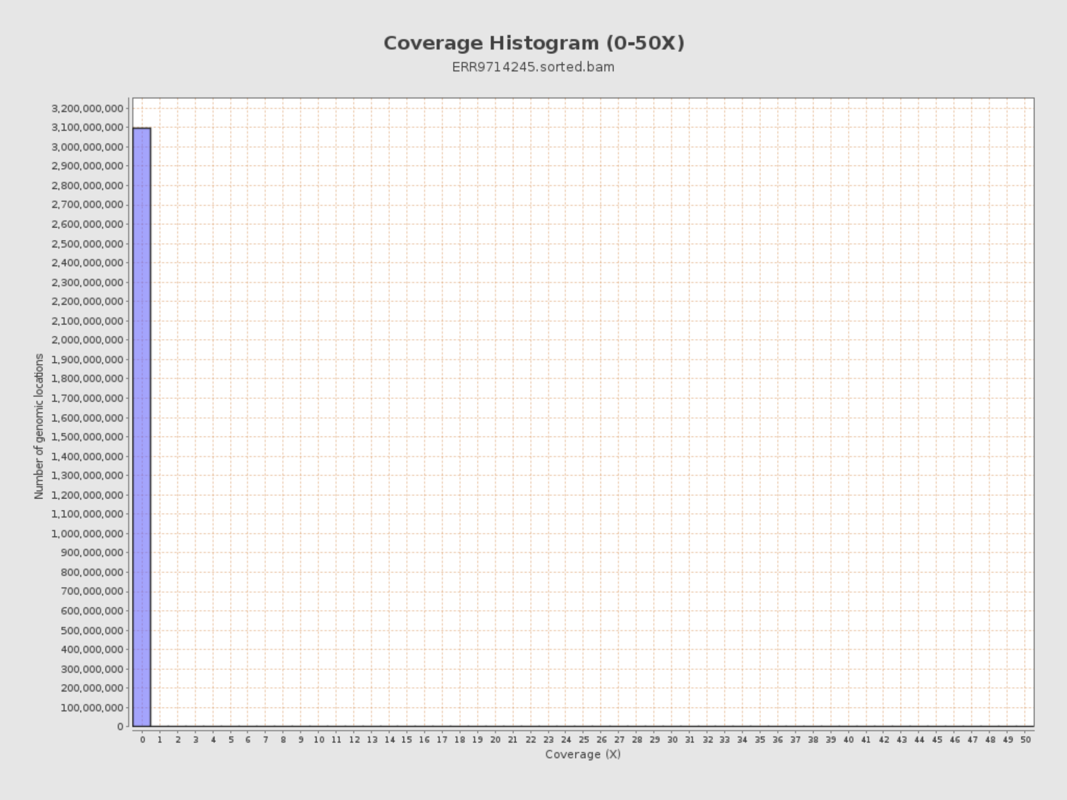
3. Results : Coverage across reference



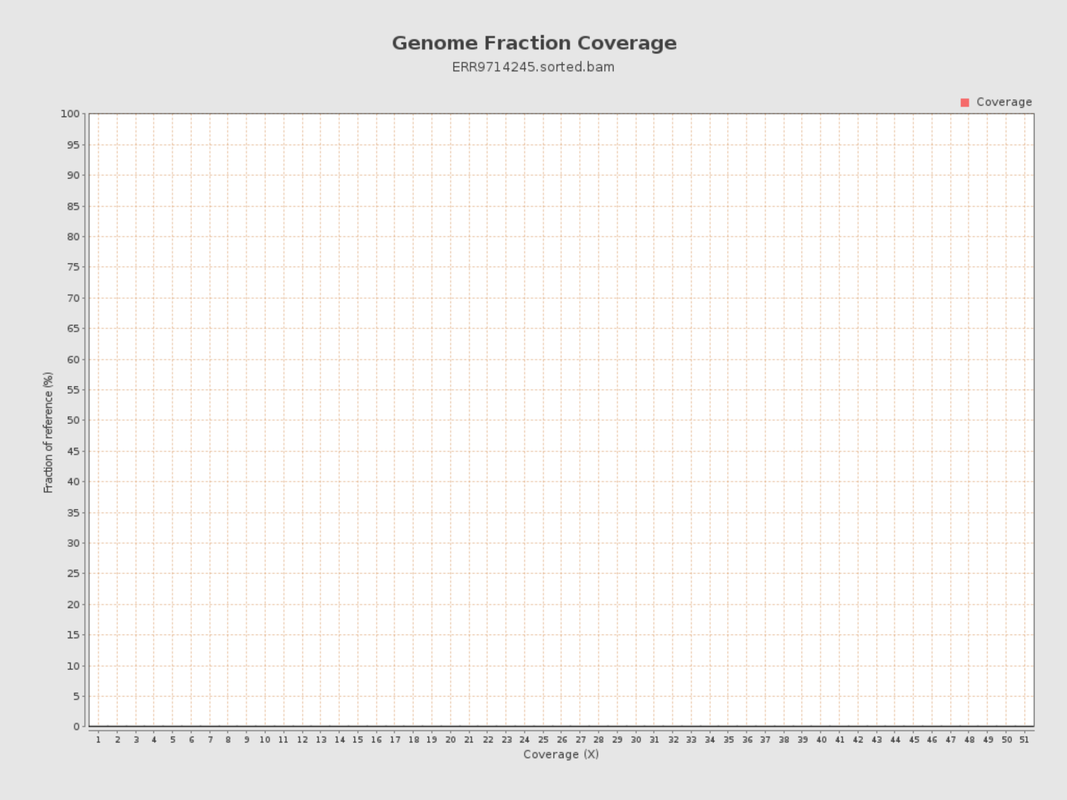
4. Results : Coverage Histogram



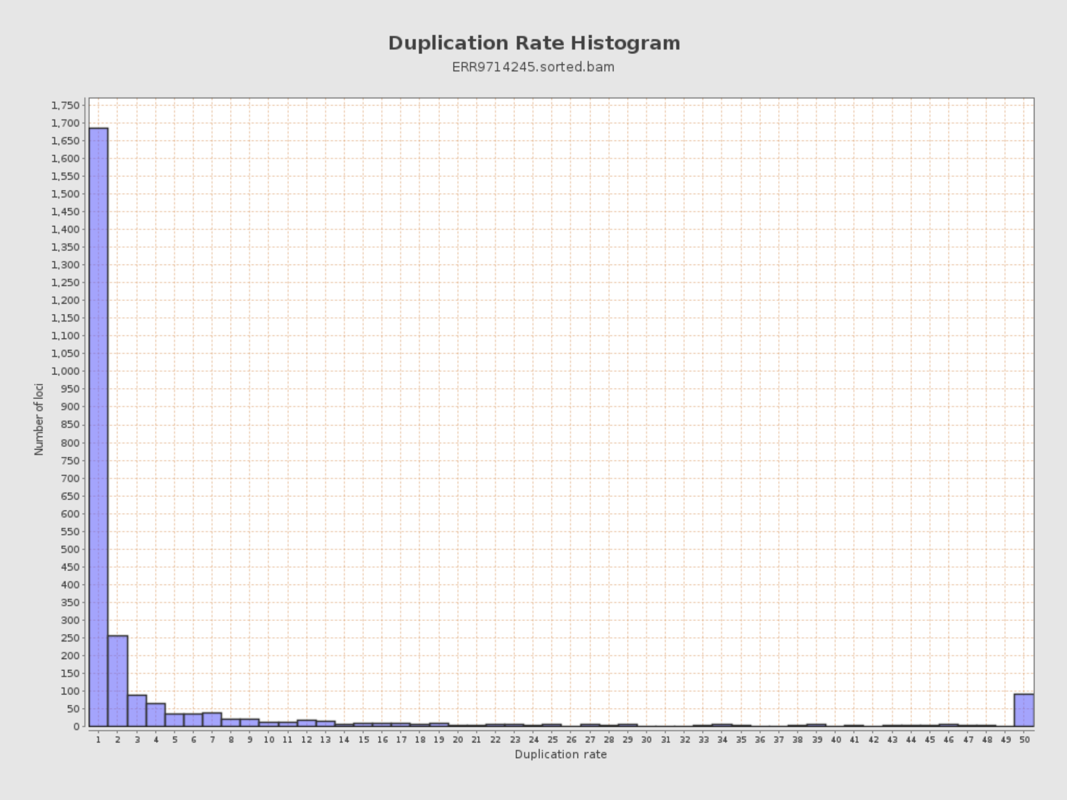
5. Results : Coverage Histogram (0-50X)



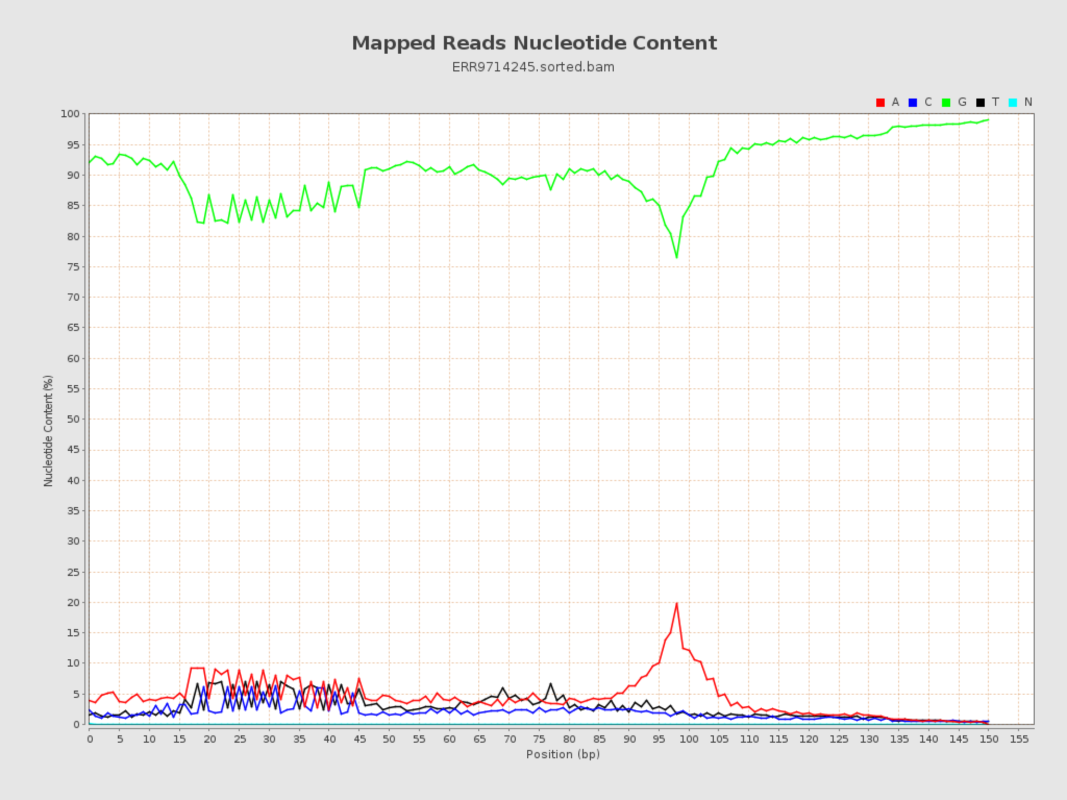
6. Results : Genome Fraction Coverage



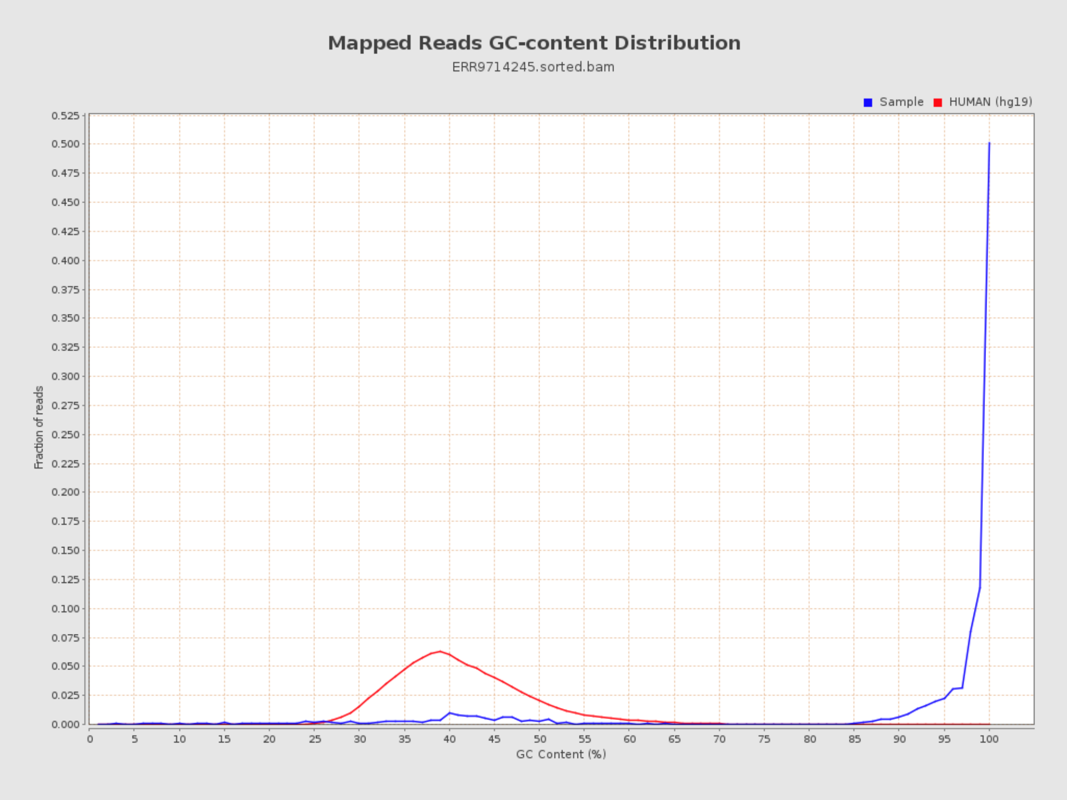
7. Results : Duplication Rate Histogram



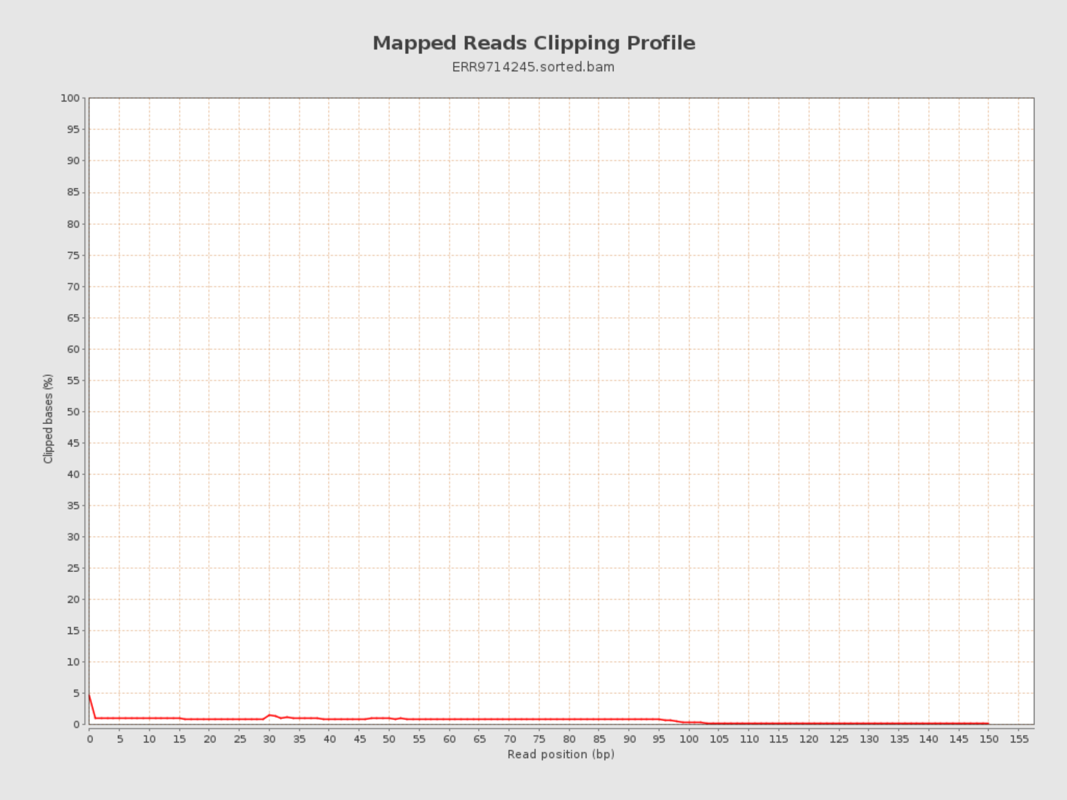
8. Results : Mapped Reads Nucleotide Content



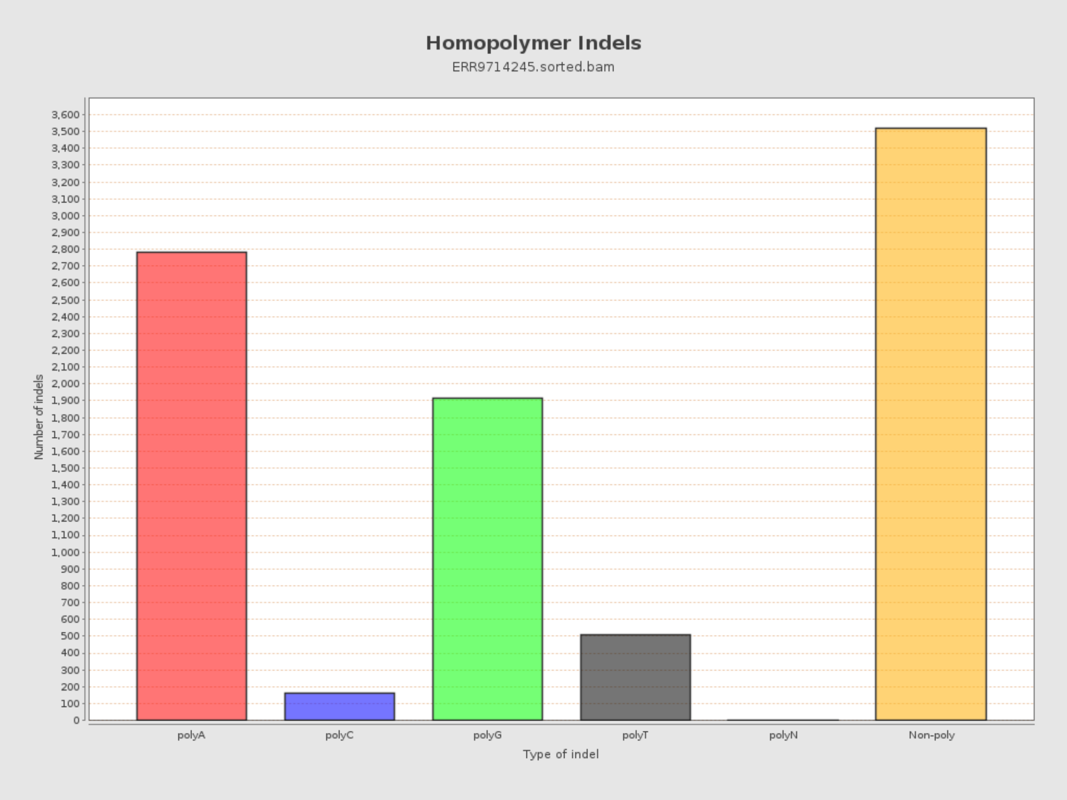
9. Results : Mapped Reads GC-content Distribution



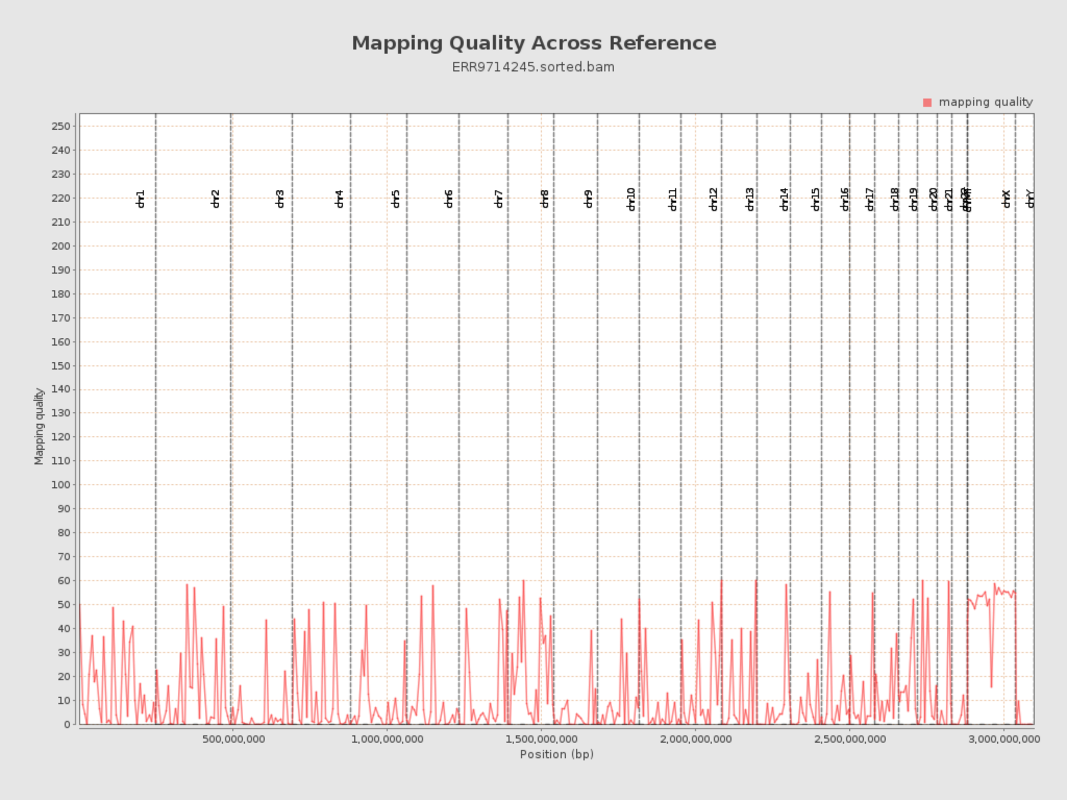
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram