Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 22:05:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714156.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_ERR9714156 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714156.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 22:05:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714156.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,118
Mapped reads	793 / 19.26%
Unmapped reads	3,325 / 80.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	47 / 1.14%
Read min/max/mean length	30 / 151 / 66.4
Duplicated reads (estimated)	486 / 11.8%
Duplication rate	39.27%
Clipped reads	497 / 12.07%

2.2. ACGT Content

Number/percentage of A's	10,209 / 11.58%
Number/percentage of C's	8,212 / 9.32%
Number/percentage of T's	9,179 / 10.41%
Number/percentage of G's	60,538 / 68.68%
Number/percentage of N's	9 / 0.01%
GC Percentage	77.99%

2.3. Coverage

Mean	0

Standard Deviation	0.0626

2.4. Mapping Quality

Mean Mapping Quality	7.99

2.5. Mismatches and indels

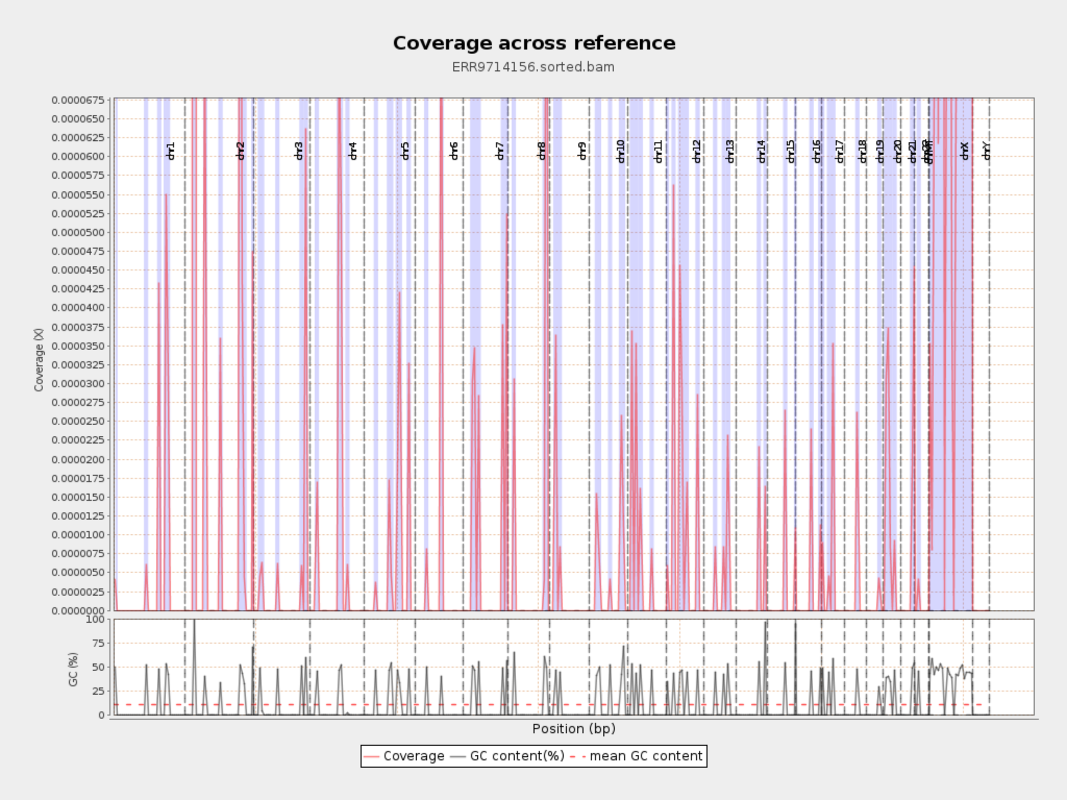
General error rate	4.6%
Mismatches	2,786
Insertions	159
Mapped reads with at least one insertion	14.38%
Deletions	135
Mapped reads with at least one deletion	16.77%
Homopolymer indels	59.18%

2.6. Chromosome stats

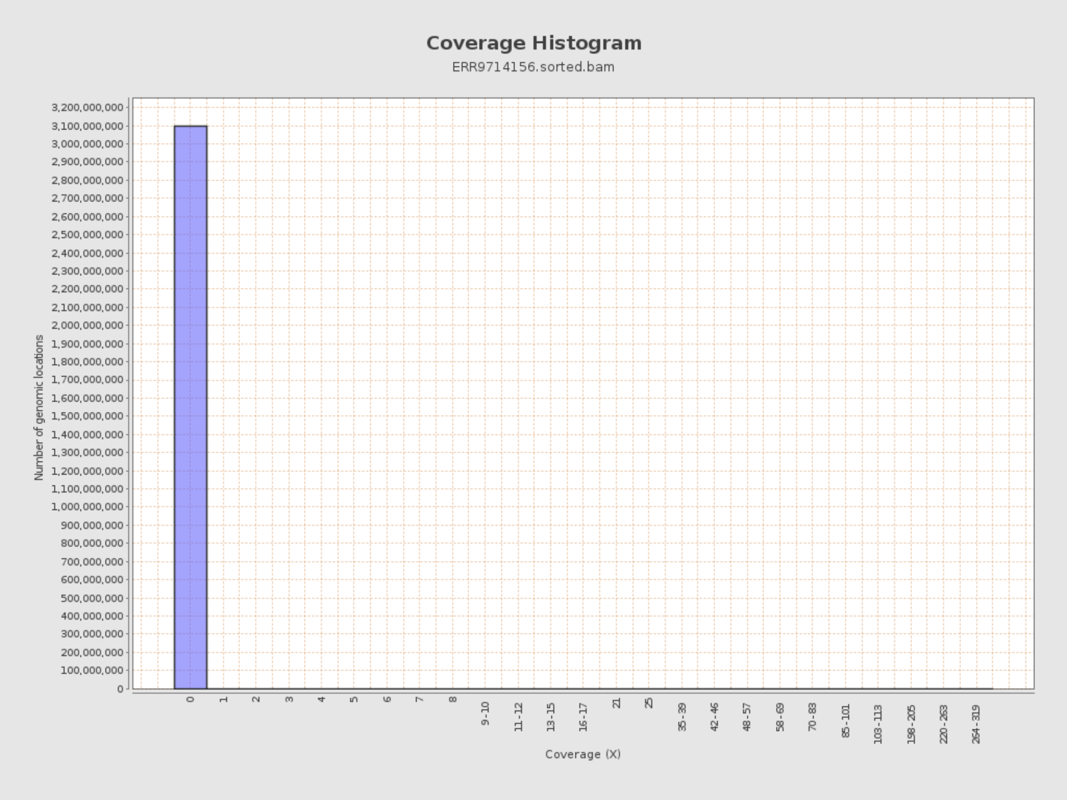
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1082	0	0.0039
chr2	243199373	55758	0.0002	0.2226
chr3	198022430	675	0	0.0032
chr4	191154276	1184	0	0.0044
chr5	180915260	918	0	0.003
chr6	171115067	815	0	0.0038
chr7	159138663	1410	0	0.0047

chr8	146364022	1273	0	0.0064
chr9	141213431	348	0	0.0021
chr10	135534747	484	0	0.0028
chr11	135006516	751	0	0.0029
chr12	133851895	1415	0	0.0054
chr13	115169878	312	0	0.0023
chr14	107349540	296	0	0.0031
chr15	102531392	238	0	0.0019
chr16	90354753	274	0	0.002
chr17	81195210	376	0	0.003
chr18	78077248	203	0	0.0016
chr19	59128983	34	0	0.0008
chr20	63025520	664	0	0.0044
chr21	48129895	363	0	0.0032
chr22	51304566	33	0	0.0008
chrMT	16571	0	0	0
chrX	155270560	20088	0.0001	0.0199
chrY	59373566	0	0	0

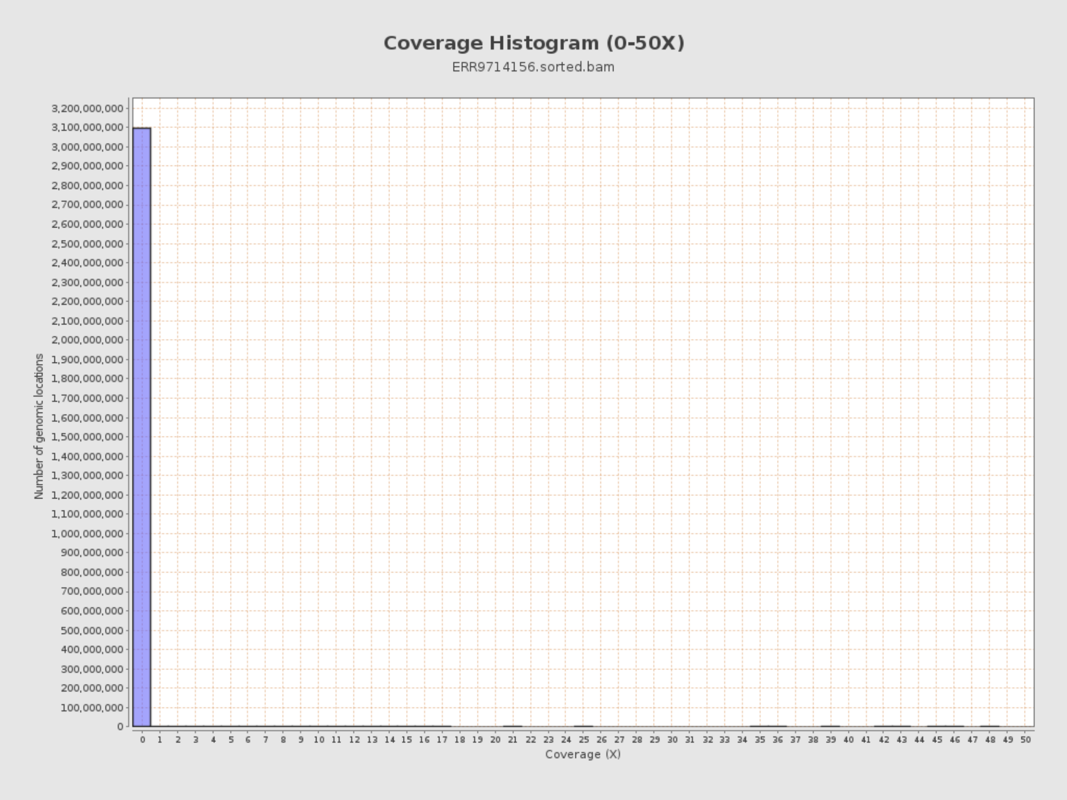
3. Results : Coverage across reference



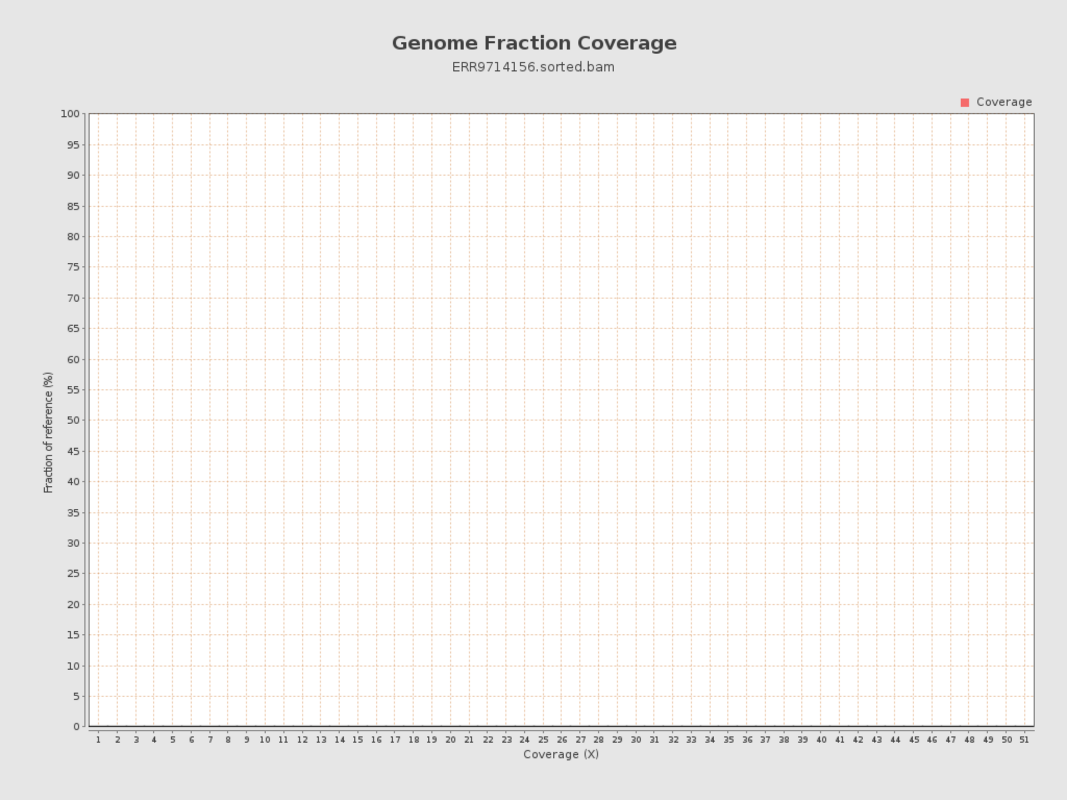
4. Results : Coverage Histogram



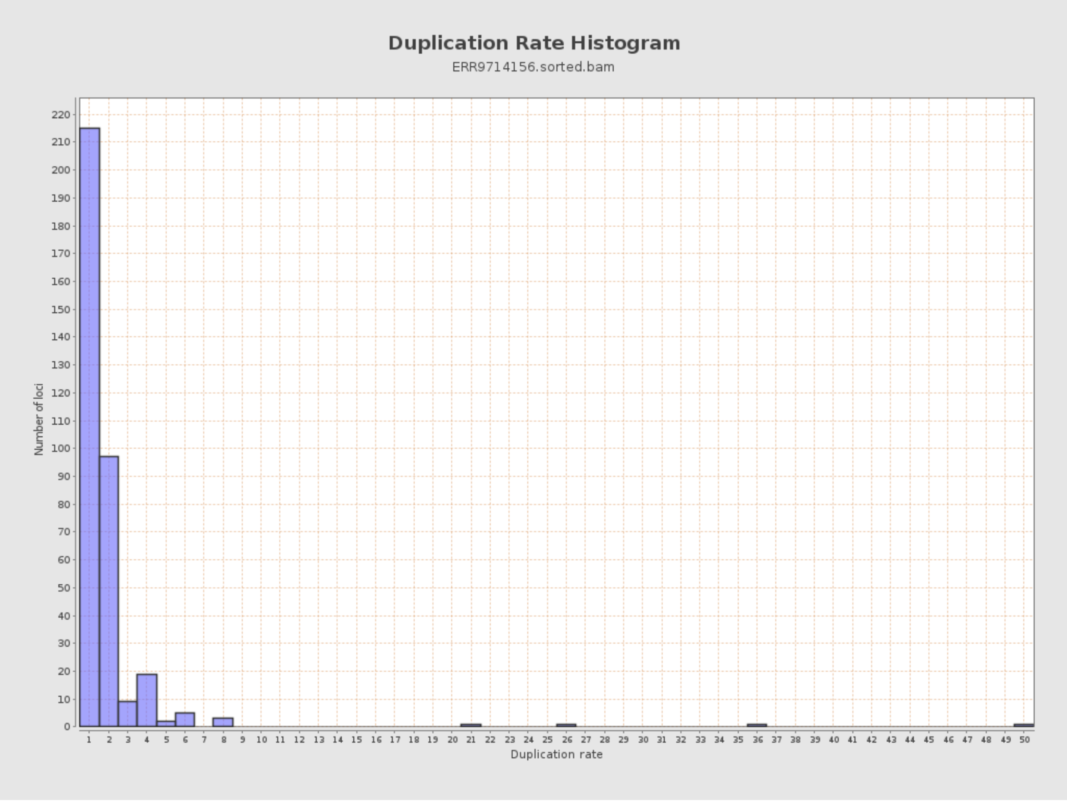
5. Results : Coverage Histogram (0-50X)



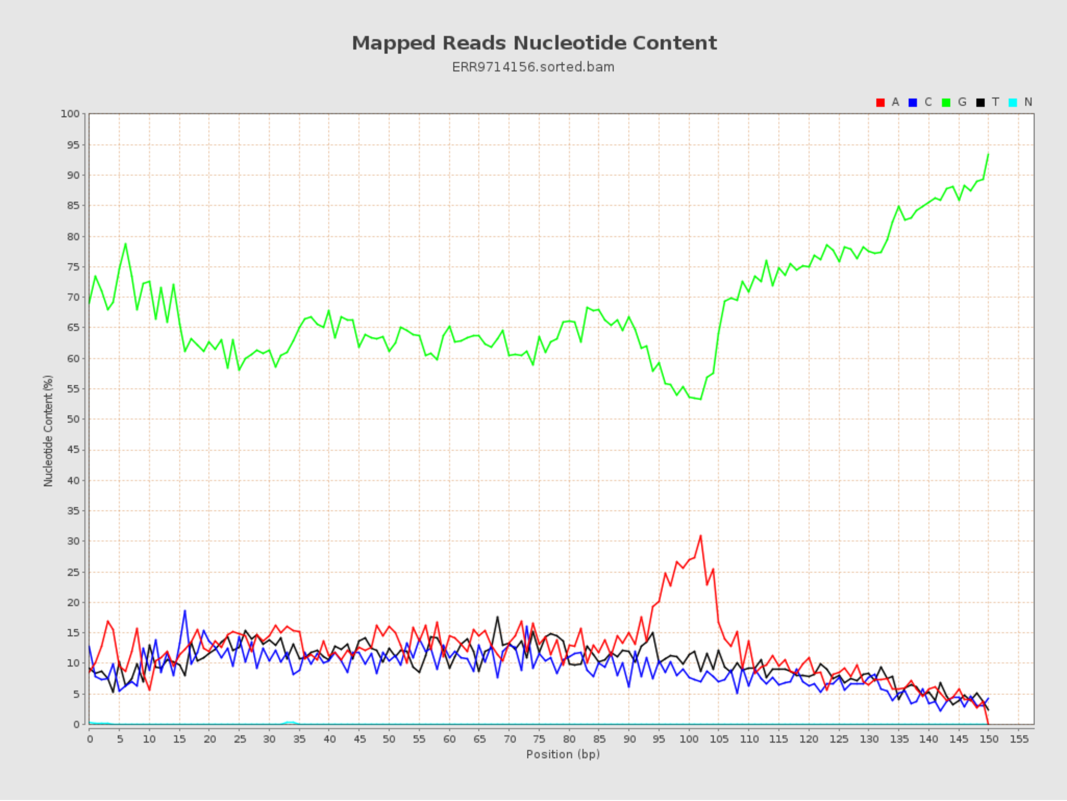
6. Results : Genome Fraction Coverage



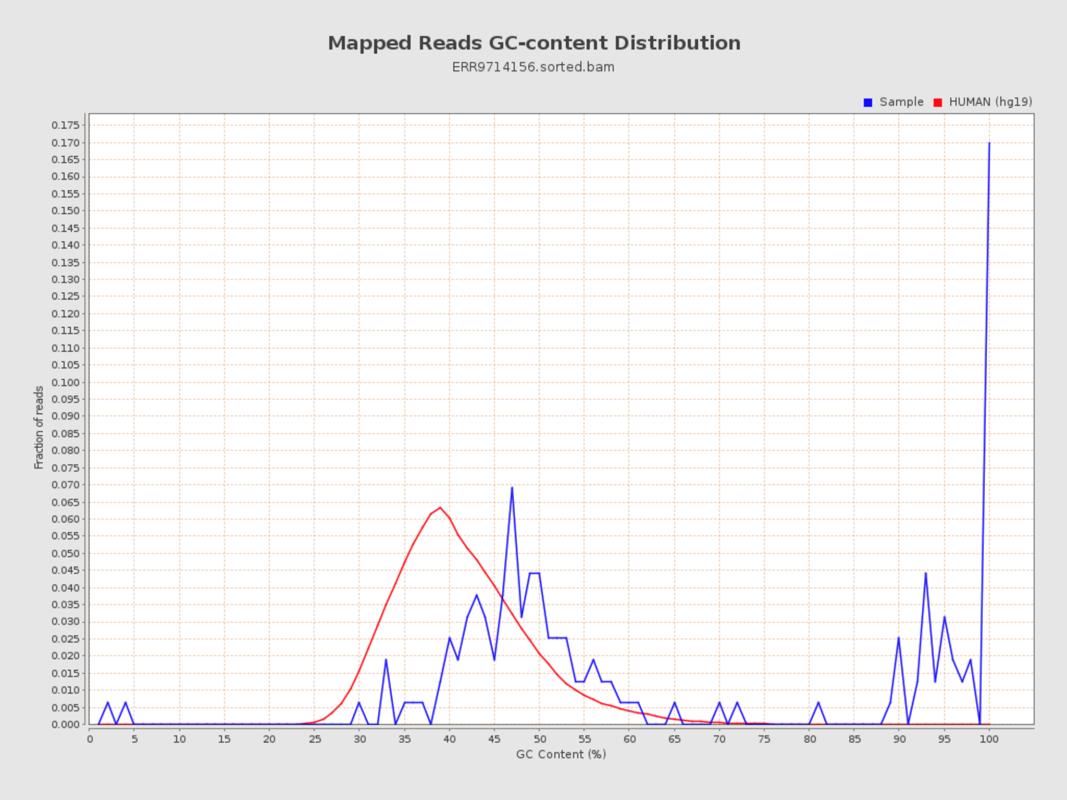
7. Results : Duplication Rate Histogram



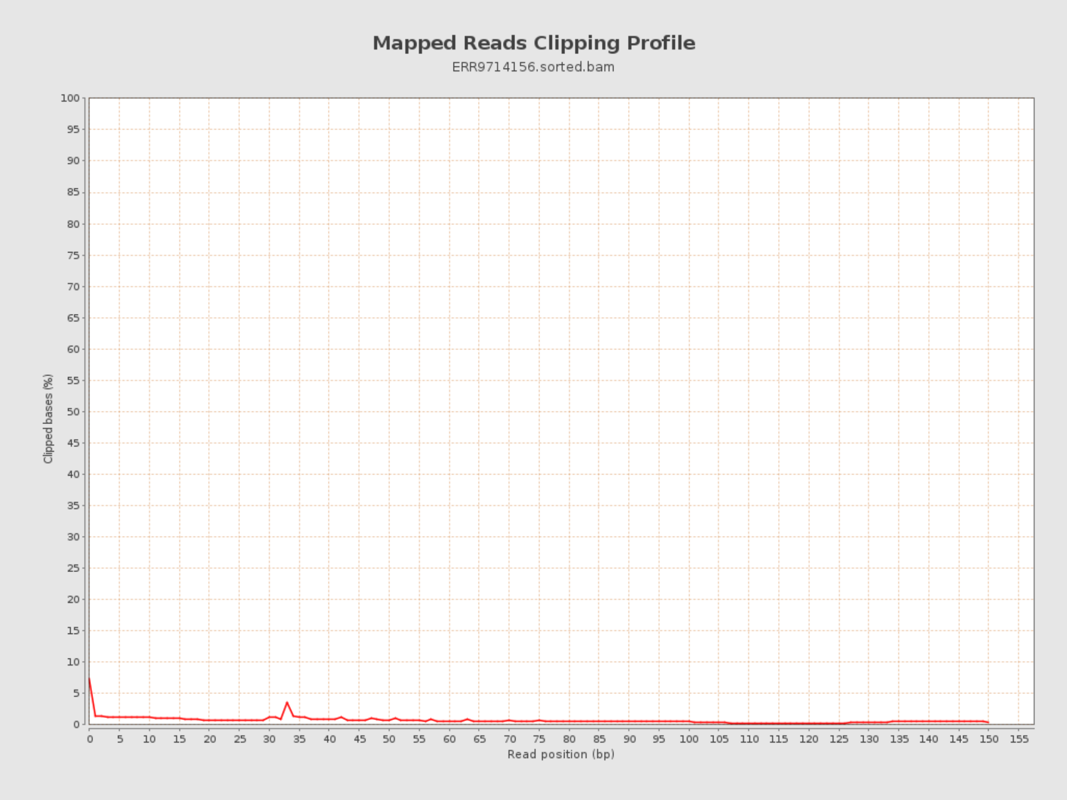
8. Results : Mapped Reads Nucleotide Content



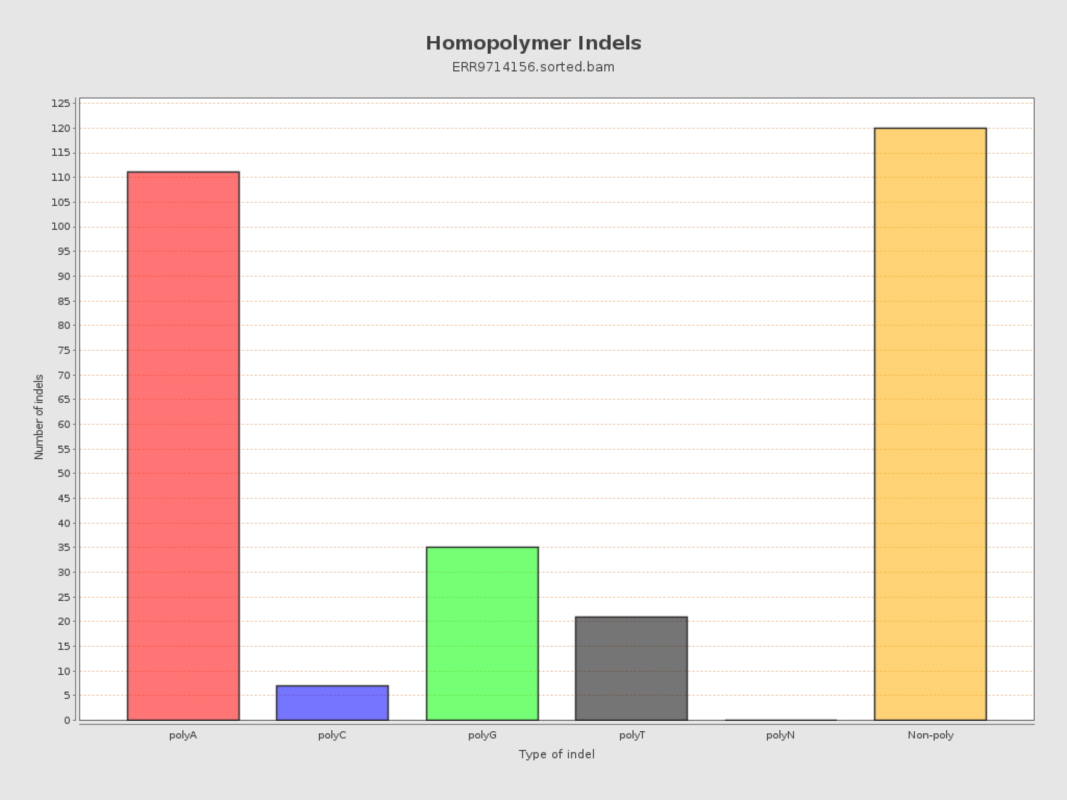
9. Results : Mapped Reads GC-content Distribution



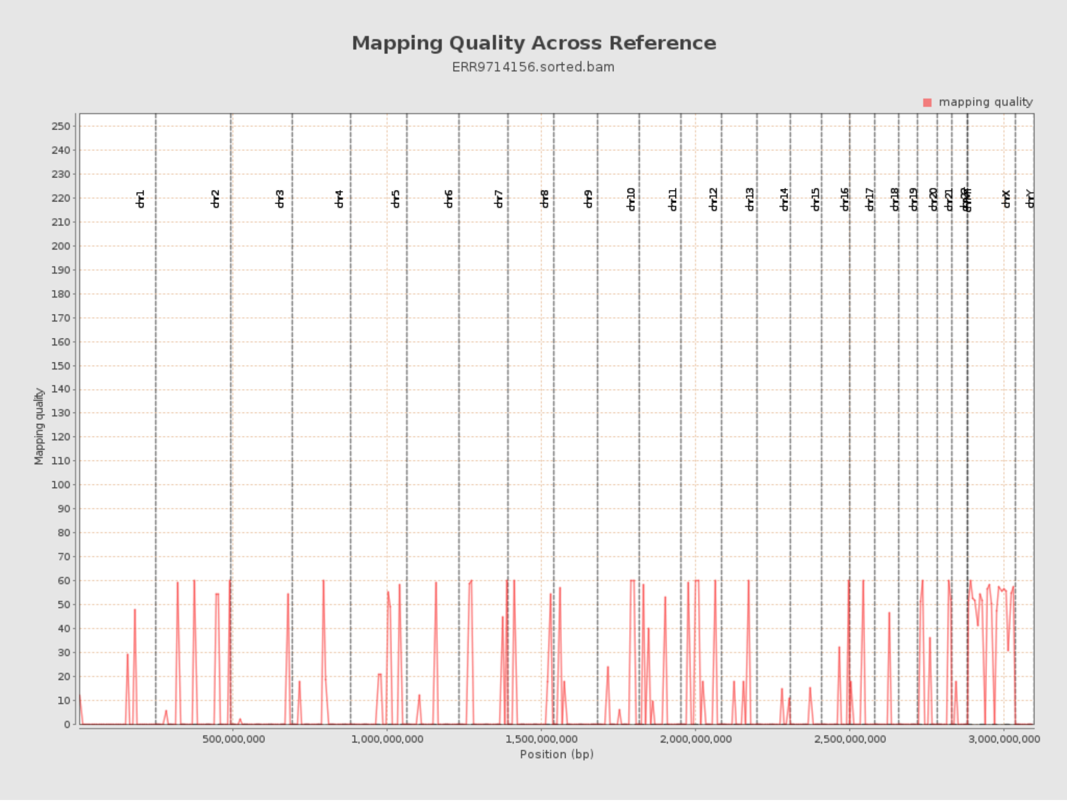
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram