Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 23:49:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714191.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_ERR9714191 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714191.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 23:49:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714191.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	66,126
Mapped reads	17,361 / 26.25%
Unmapped reads	48,765 / 73.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	742 / 1.12%
Read min/max/mean length	30 / 151 / 80.15
Duplicated reads (estimated)	14,153 / 21.4%
Duplication rate	49.16%
Clipped reads	14,280 / 21.6%

2.2. ACGT Content

Number/percentage of A's	392,415 / 20.9%
Number/percentage of C's	336,684 / 17.93%
Number/percentage of T's	364,343 / 19.41%
Number/percentage of G's	784,033 / 41.76%
Number/percentage of N's	34 / 0%
GC Percentage	59.69%

2.3. Coverage

Mean	0.0006

Standard Deviation	0.5704

2.4. Mapping Quality

Mean Mapping Quality	33.82

2.5. Mismatches and indels

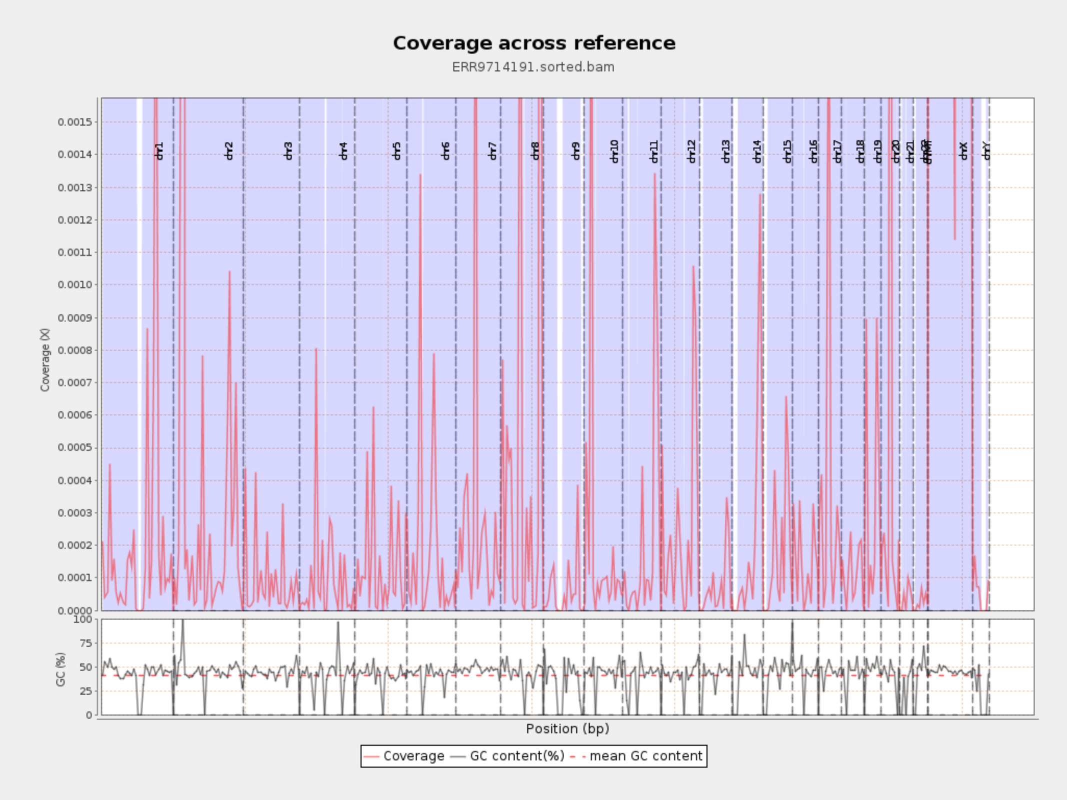
General error rate	3.6%
Mismatches	62,052
Insertions	1,163
Mapped reads with at least one insertion	5.29%
Deletions	4,257
Mapped reads with at least one deletion	23.74%
Homopolymer indels	32.82%

2.6. Chromosome stats

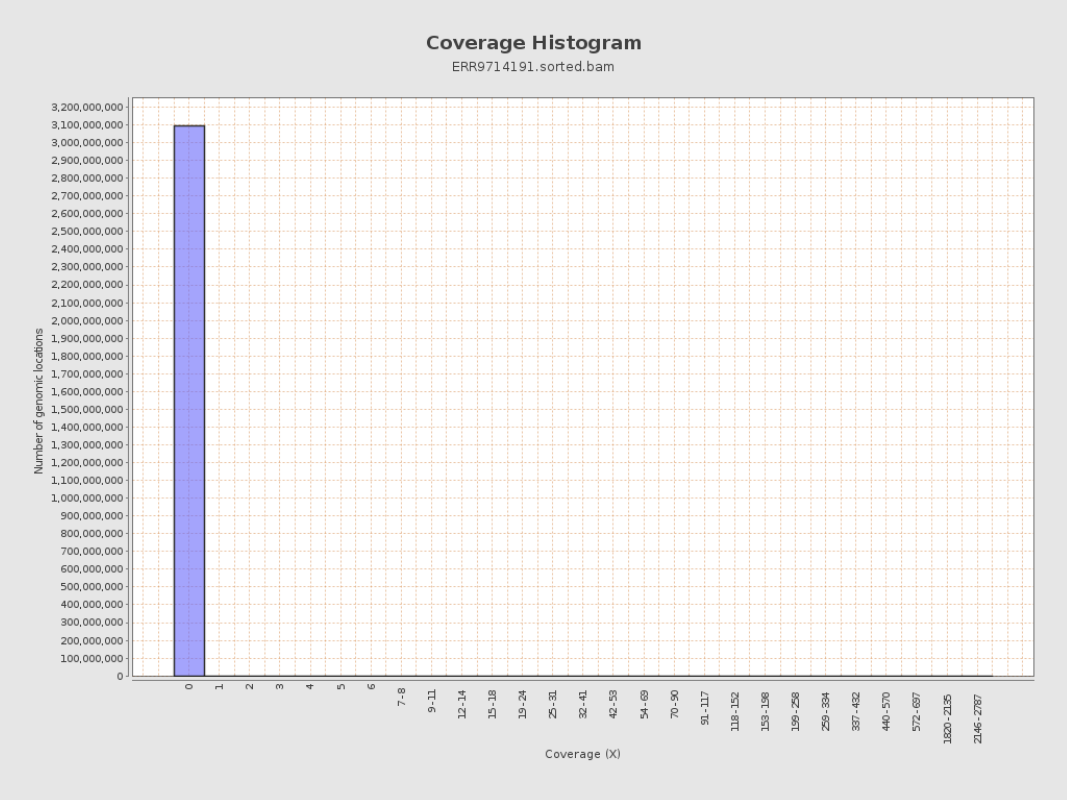
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	54651	0.0002	0.2105
chr2	243199373	507923	0.0021	1.9107
chr3	198022430	18781	0.0001	0.0278
chr4	191154276	19119	0.0001	0.0303
chr5	180915260	24055	0.0001	0.0415
chr6	171115067	32392	0.0002	0.055
chr7	159138663	44618	0.0003	0.1326

chr8	146364022	85856	0.0006	0.2787
chr9	141213431	8020	0.0001	0.021
chr10	135534747	31963	0.0002	0.2974
chr11	135006516	26290	0.0002	0.0587
chr12	133851895	34785	0.0003	0.0726
chr13	115169878	8213	0.0001	0.0225
chr14	107349540	23008	0.0002	0.0848
chr15	102531392	18215	0.0002	0.0429
chr16	90354753	13288	0.0001	0.0263
chr17	81195210	29855	0.0004	0.073
chr18	78077248	9248	0.0001	0.0233
chr19	59128983	18803	0.0003	0.0787
chr20	63025520	37817	0.0006	0.2569
chr21	48129895	1905	0	0.009
chr22	51304566	1350	0	0.0073
chrMT	16571	92	0.0056	0.1052
chrX	155270560	856437	0.0055	0.6895
chrY	59373566	3463	0.0001	0.0155

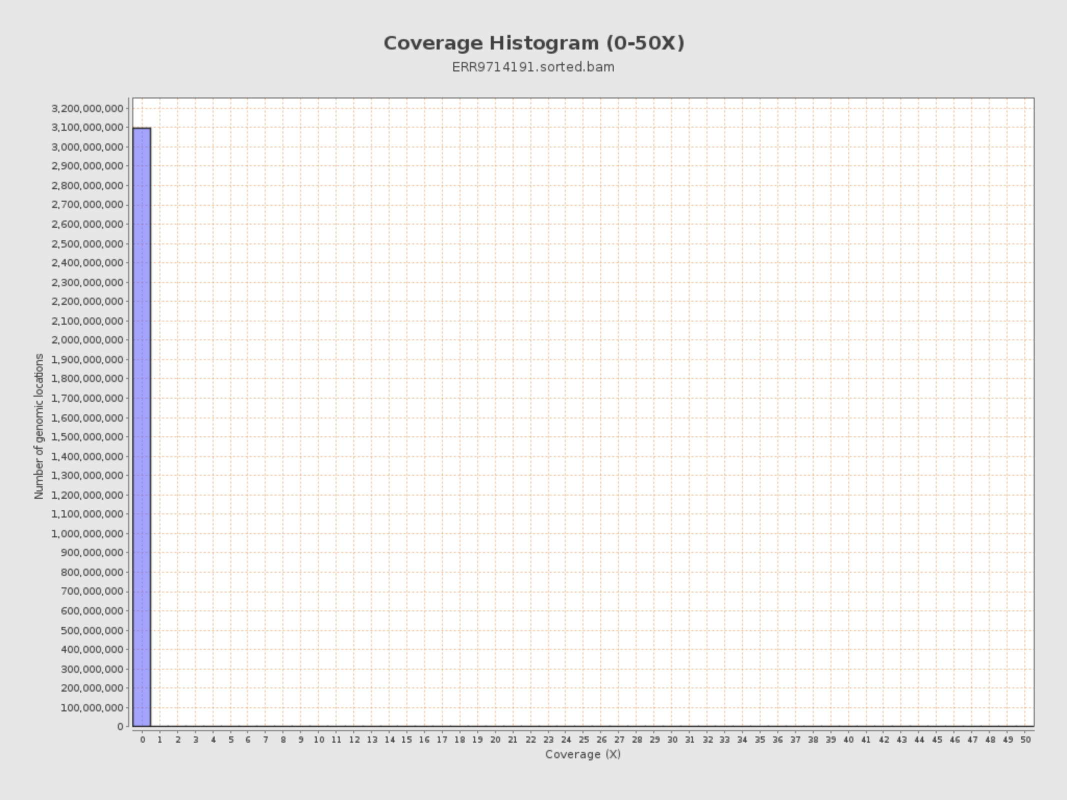
3. Results : Coverage across reference



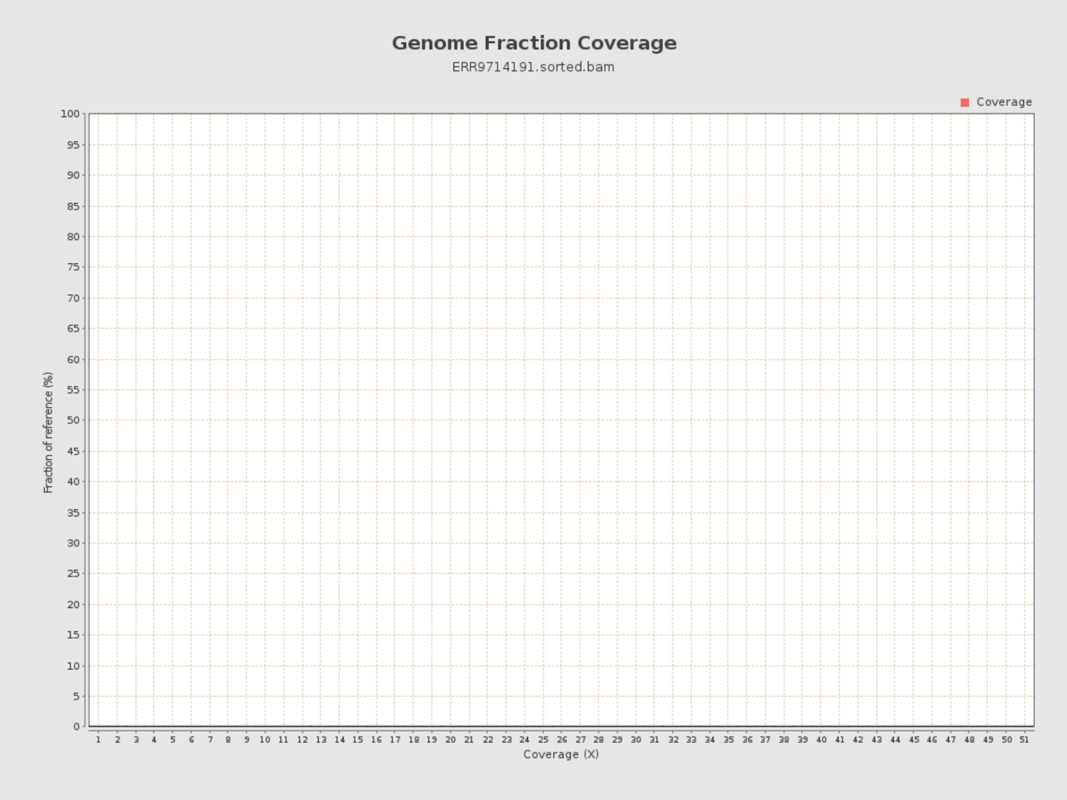
4. Results : Coverage Histogram



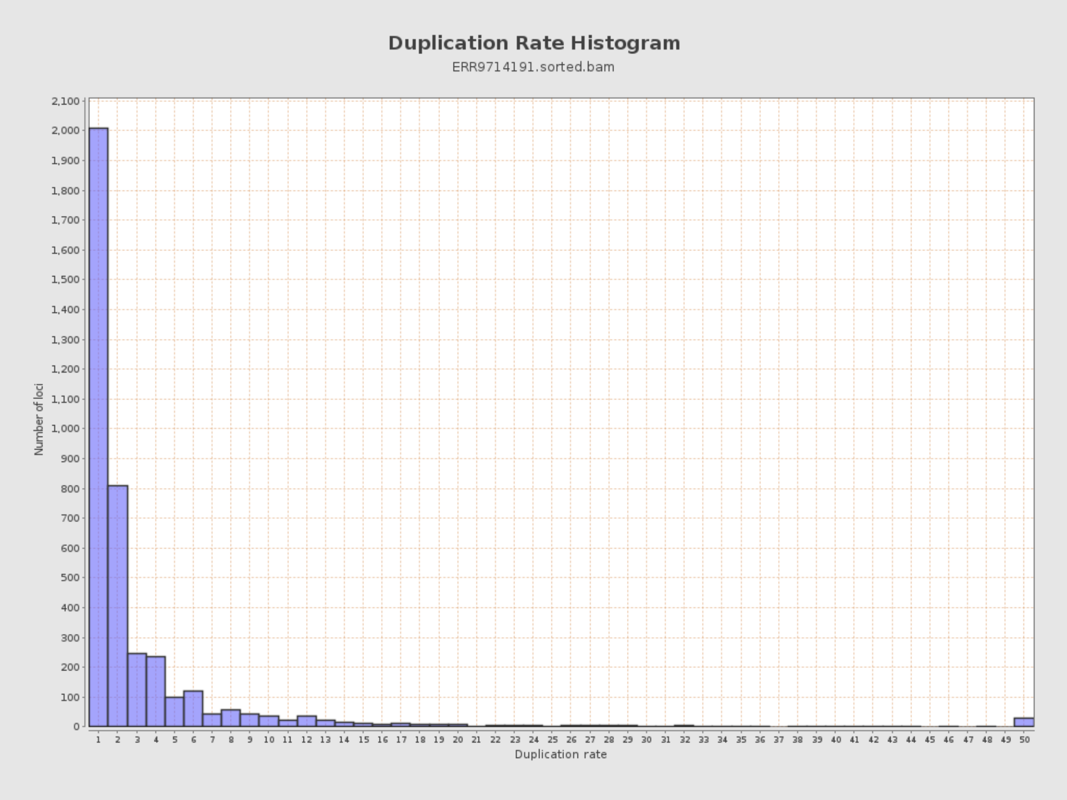
5. Results : Coverage Histogram (0-50X)



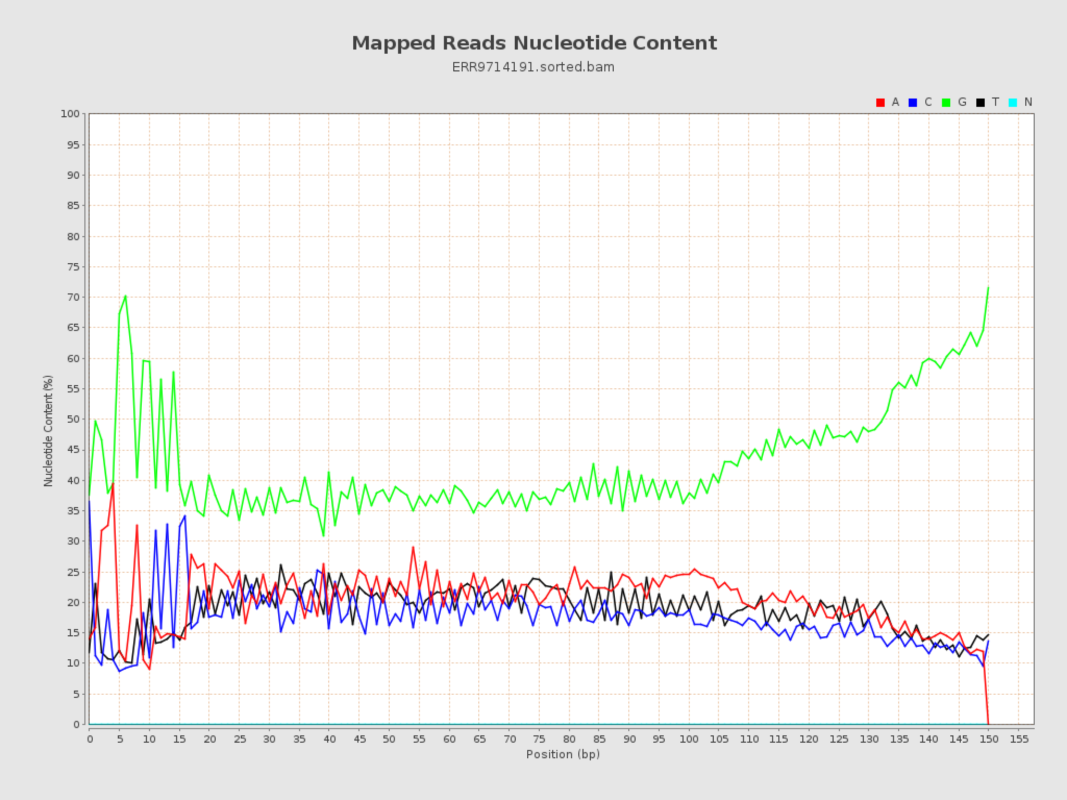
6. Results : Genome Fraction Coverage



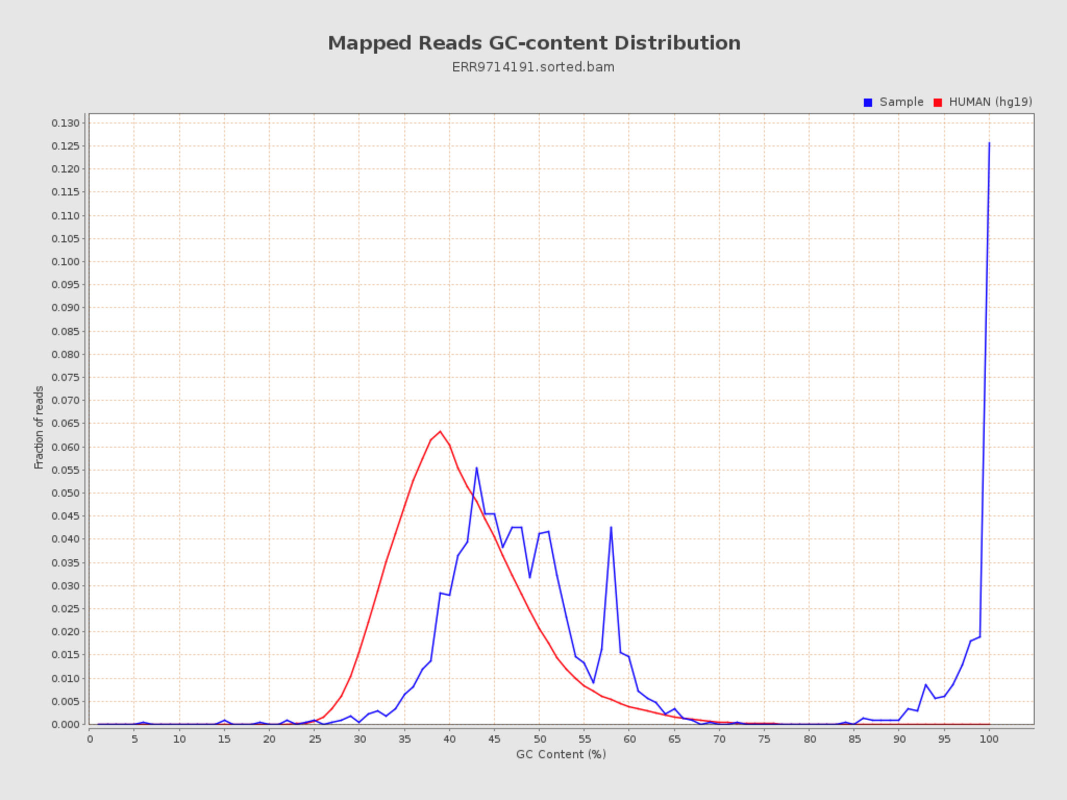
7. Results : Duplication Rate Histogram



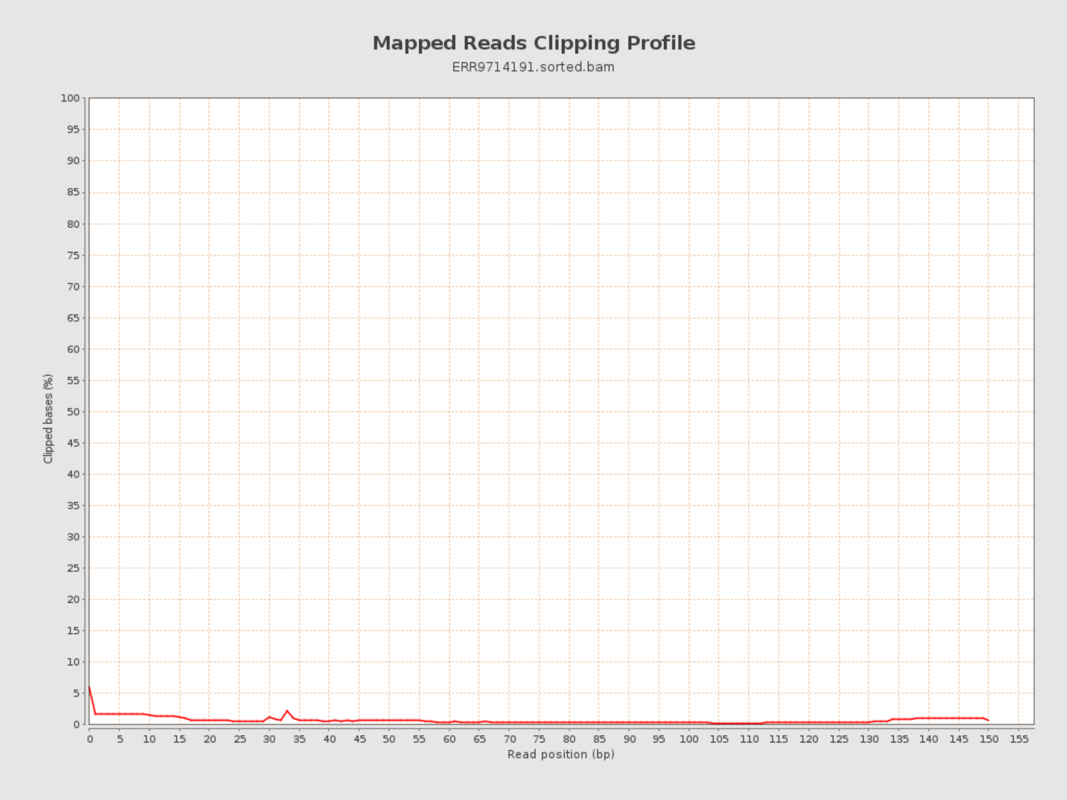
8. Results : Mapped Reads Nucleotide Content



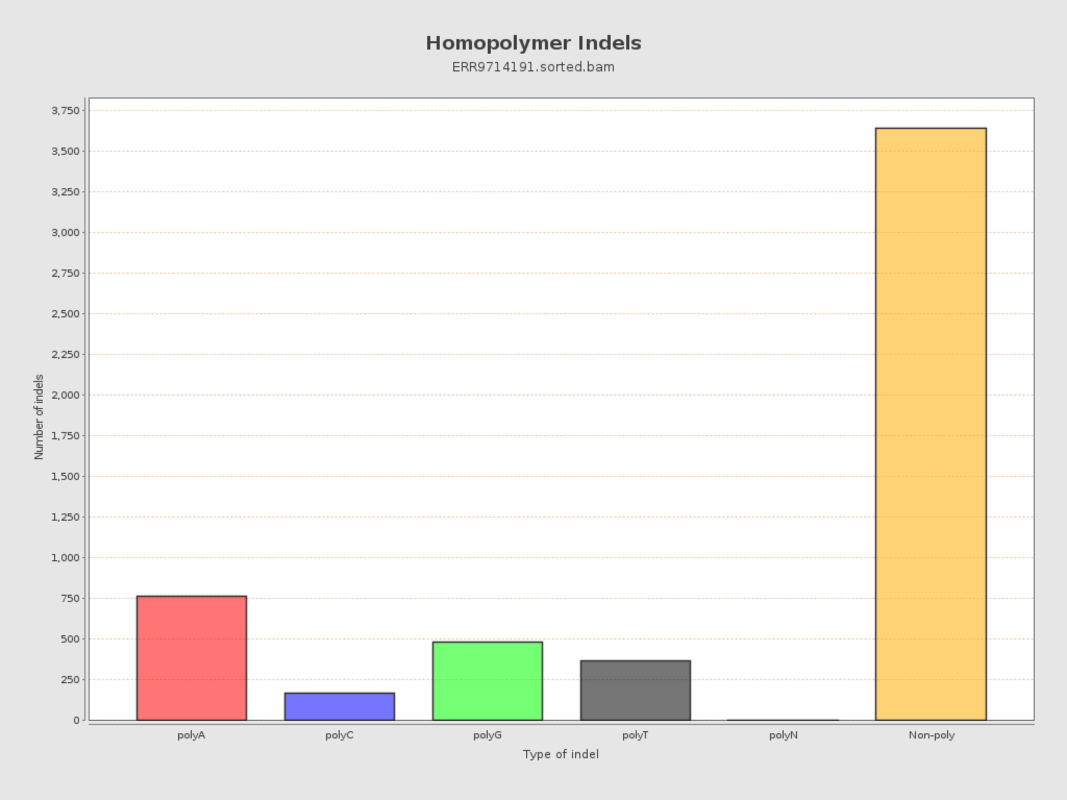
9. Results : Mapped Reads GC-content Distribution



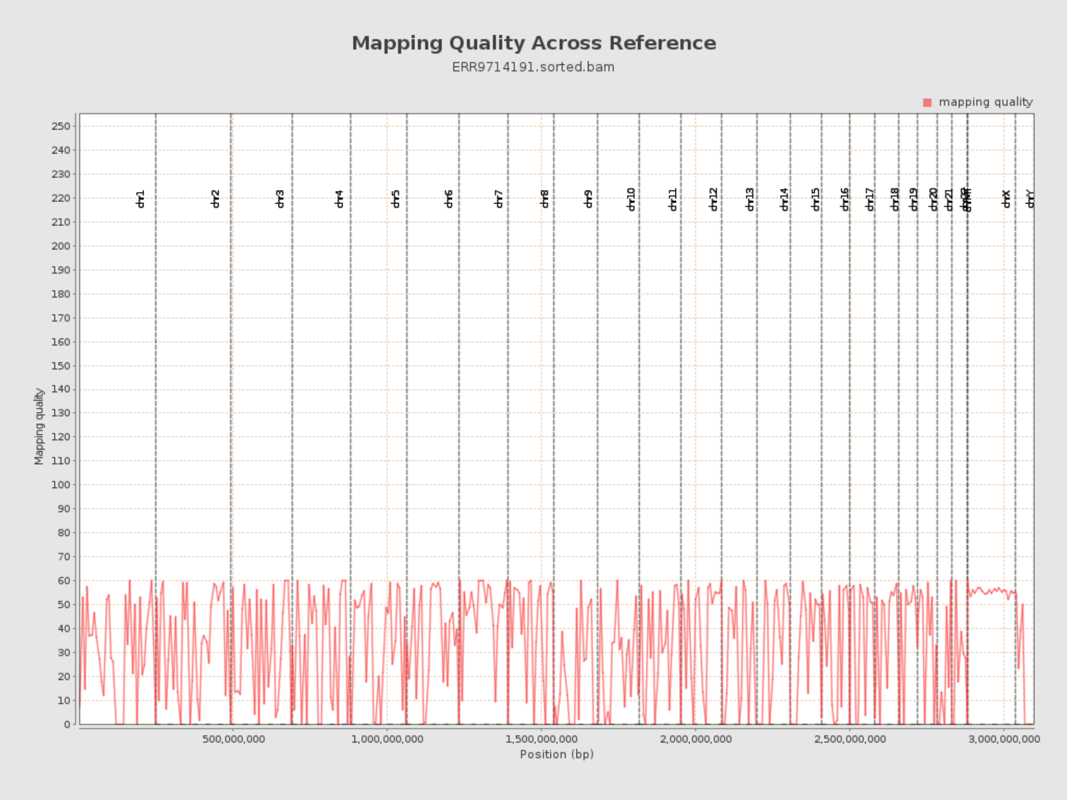
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram