Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 23:59:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714198.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_ERR9714198 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714198.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 23:59:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714198.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	102,590
Mapped reads	24,141 / 23.53%
Unmapped reads	78,449 / 76.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,037 / 1.01%
Read min/max/mean length	30 / 151 / 73.59
Duplicated reads (estimated)	21,242 / 20.71%
Duplication rate	50.28%
Clipped reads	17,232 / 16.8%

2.2. ACGT Content

Number/percentage of A's	379,483 / 14.53%
Number/percentage of C's	310,284 / 11.88%
Number/percentage of T's	345,366 / 13.23%
Number/percentage of G's	1,575,760 / 60.35%
Number/percentage of N's	58 / 0%
GC Percentage	72.24%

2.3. Coverage

Mean	0.0009

Standard Deviation	1.5752

2.4. Mapping Quality

Mean Mapping Quality	32.02

2.5. Mismatches and indels

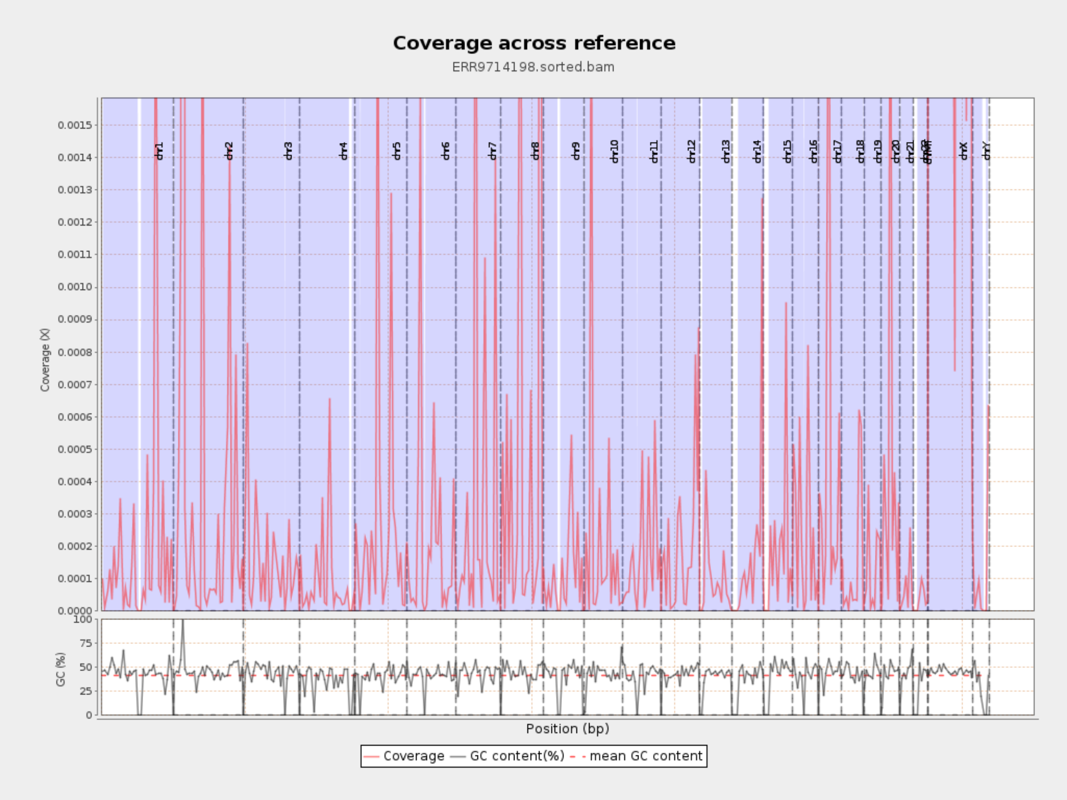
General error rate	3.44%
Mismatches	77,473
Insertions	2,007
Mapped reads with at least one insertion	5.87%
Deletions	4,219
Mapped reads with at least one deletion	16.93%
Homopolymer indels	41.1%

2.6. Chromosome stats

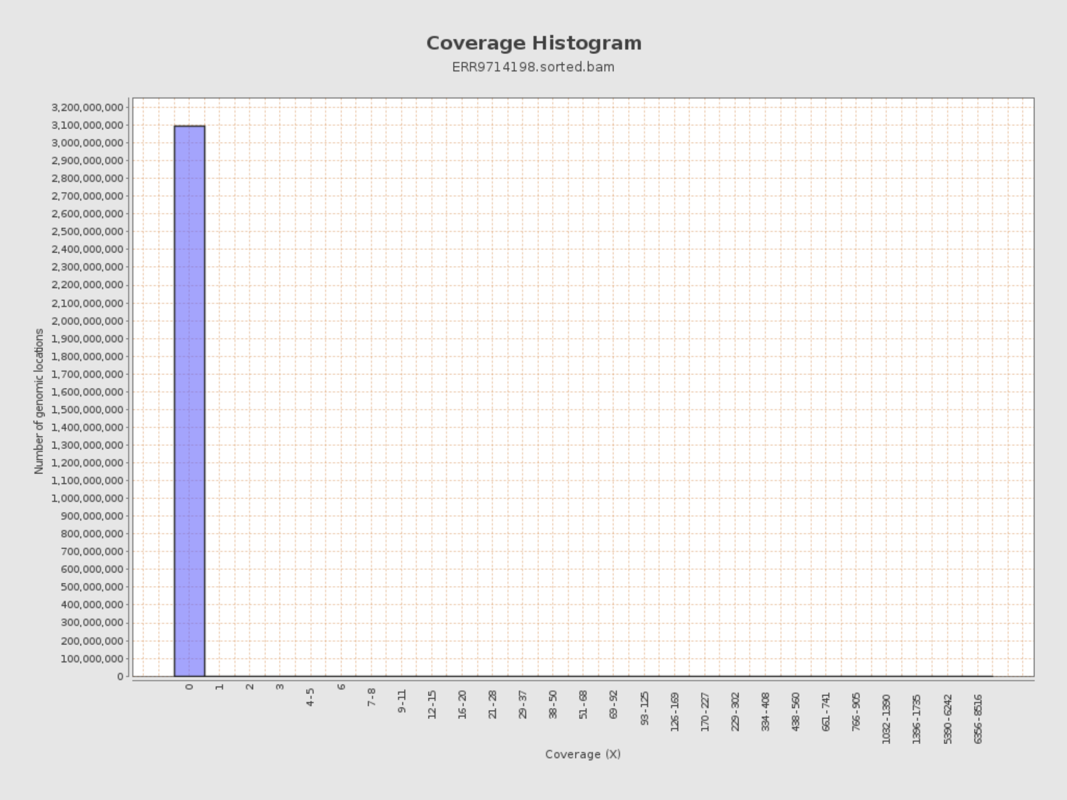
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	46133	0.0002	0.1856
chr2	243199373	1344594	0.0055	5.5877
chr3	198022430	31196	0.0002	0.0385
chr4	191154276	16736	0.0001	0.0268
chr5	180915260	51100	0.0003	0.1101
chr6	171115067	38550	0.0002	0.0611
chr7	159138663	53946	0.0003	0.1555

chr8	146364022	82091	0.0006	0.2598
chr9	141213431	16401	0.0001	0.0321
chr10	135534747	31790	0.0002	0.2521
chr11	135006516	22555	0.0002	0.0431
chr12	133851895	27644	0.0002	0.0448
chr13	115169878	9797	0.0001	0.0226
chr14	107349540	19287	0.0002	0.0697
chr15	102531392	18217	0.0002	0.0422
chr16	90354753	21376	0.0002	0.0684
chr17	81195210	34771	0.0004	0.107
chr18	78077248	11728	0.0002	0.0456
chr19	59128983	7543	0.0001	0.0384
chr20	63025520	30988	0.0005	0.1468
chr21	48129895	3495	0.0001	0.0269
chr22	51304566	1840	0	0.0102
chrMT	16571	337	0.0203	0.3719
chrX	155270560	711289	0.0046	0.5646
chrY	59373566	7223	0.0001	0.0212

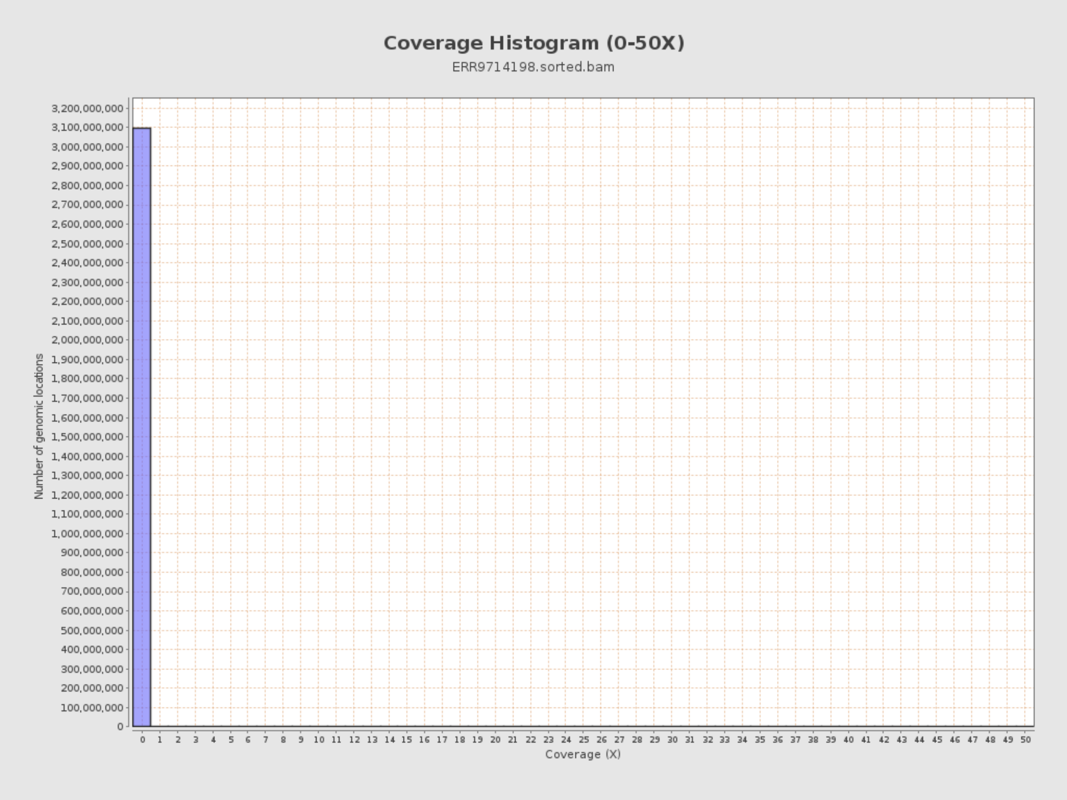
3. Results : Coverage across reference



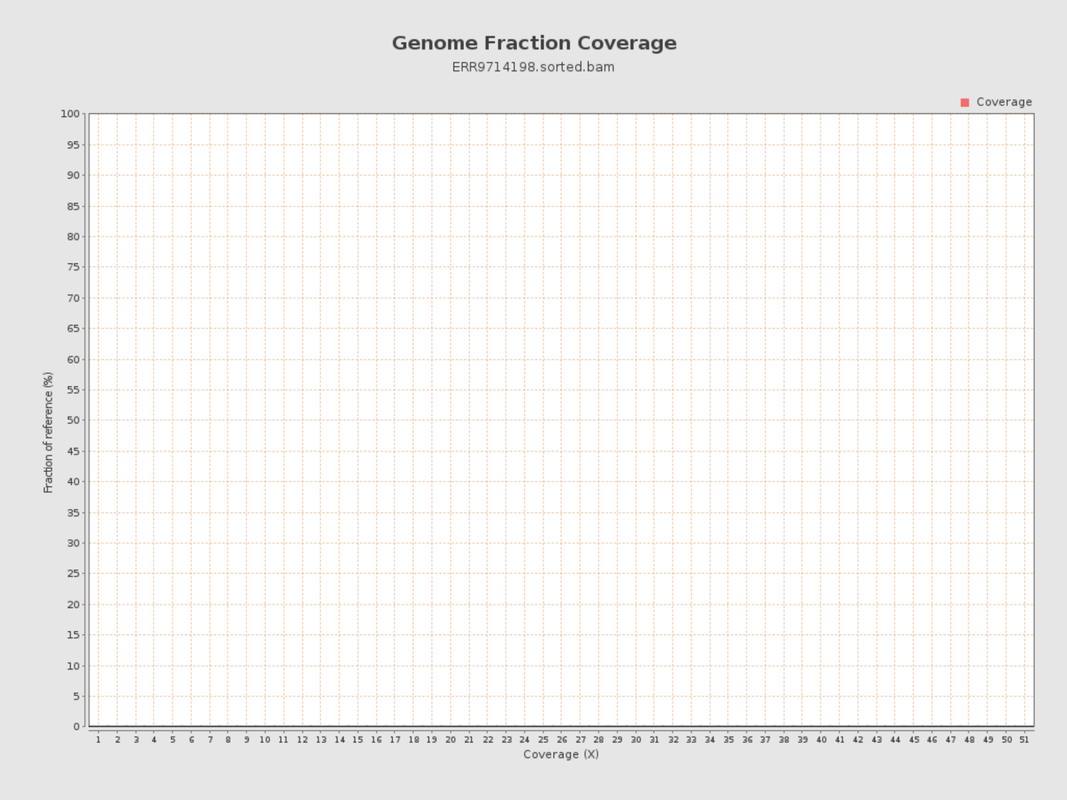
4. Results : Coverage Histogram



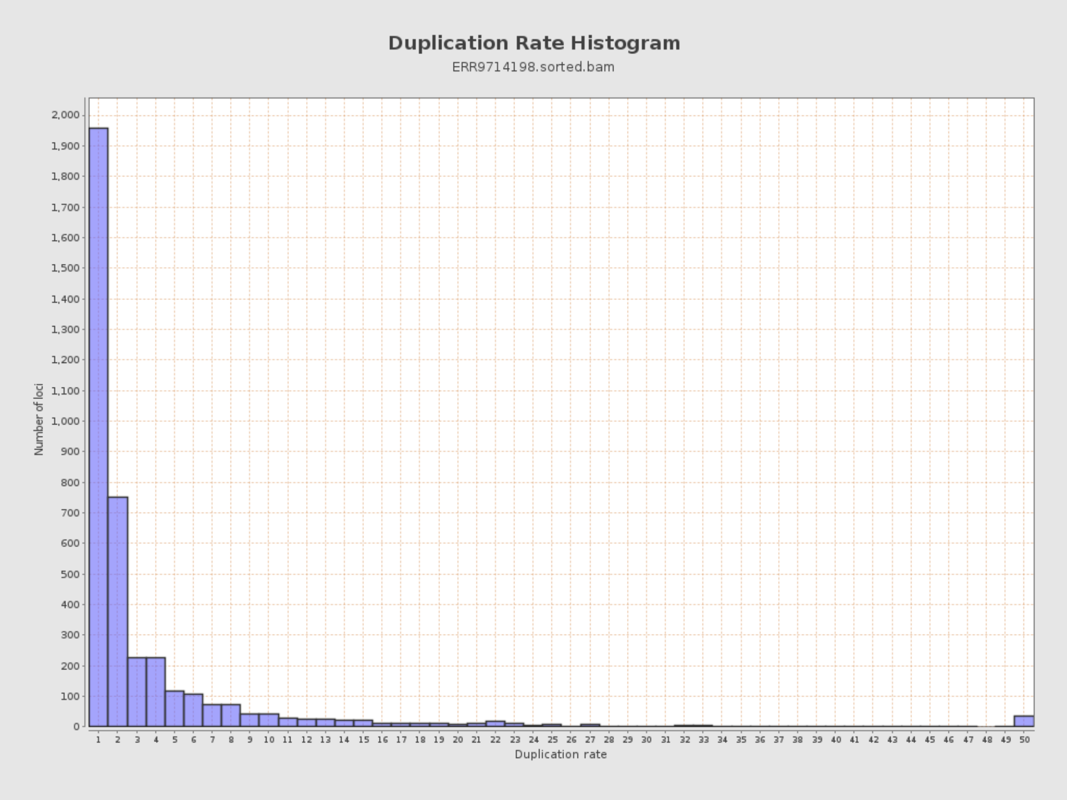
5. Results : Coverage Histogram (0-50X)



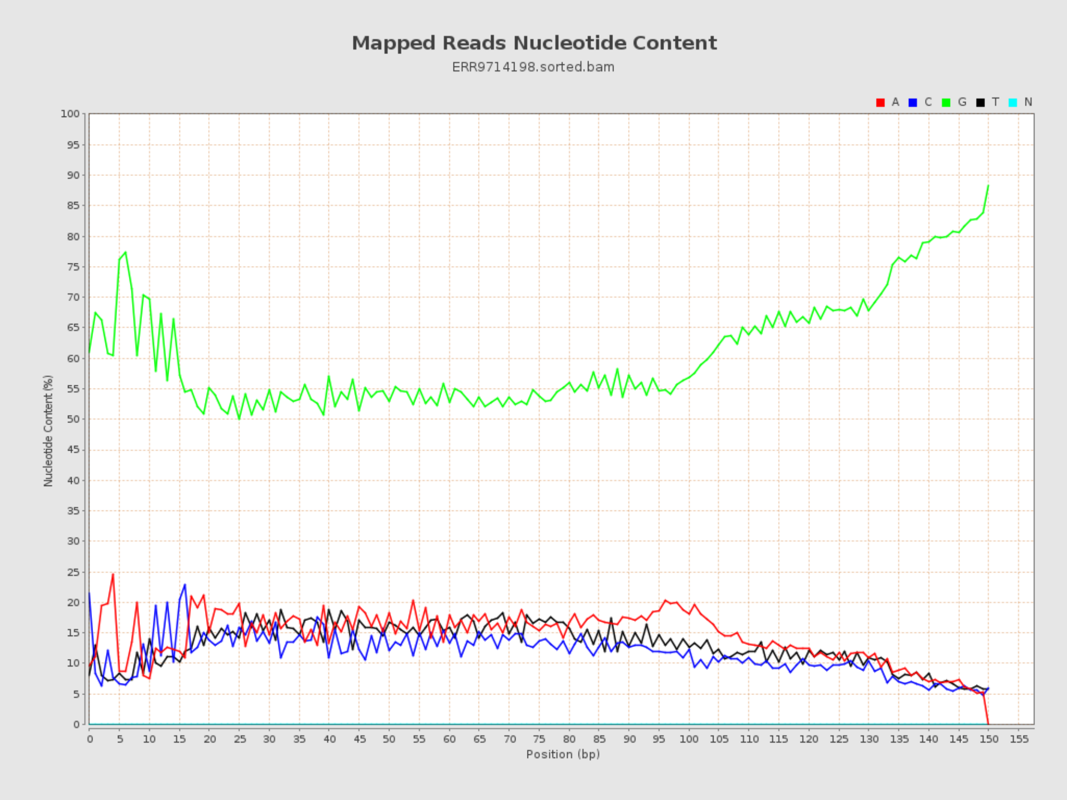
6. Results : Genome Fraction Coverage



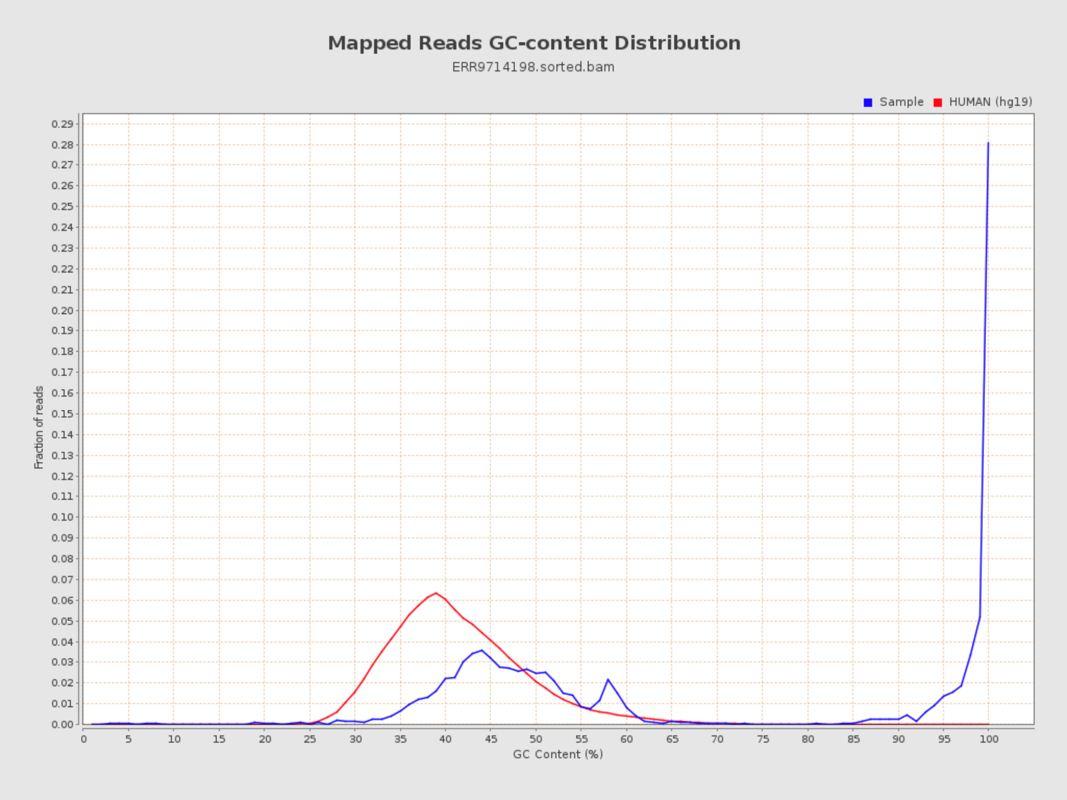
7. Results : Duplication Rate Histogram



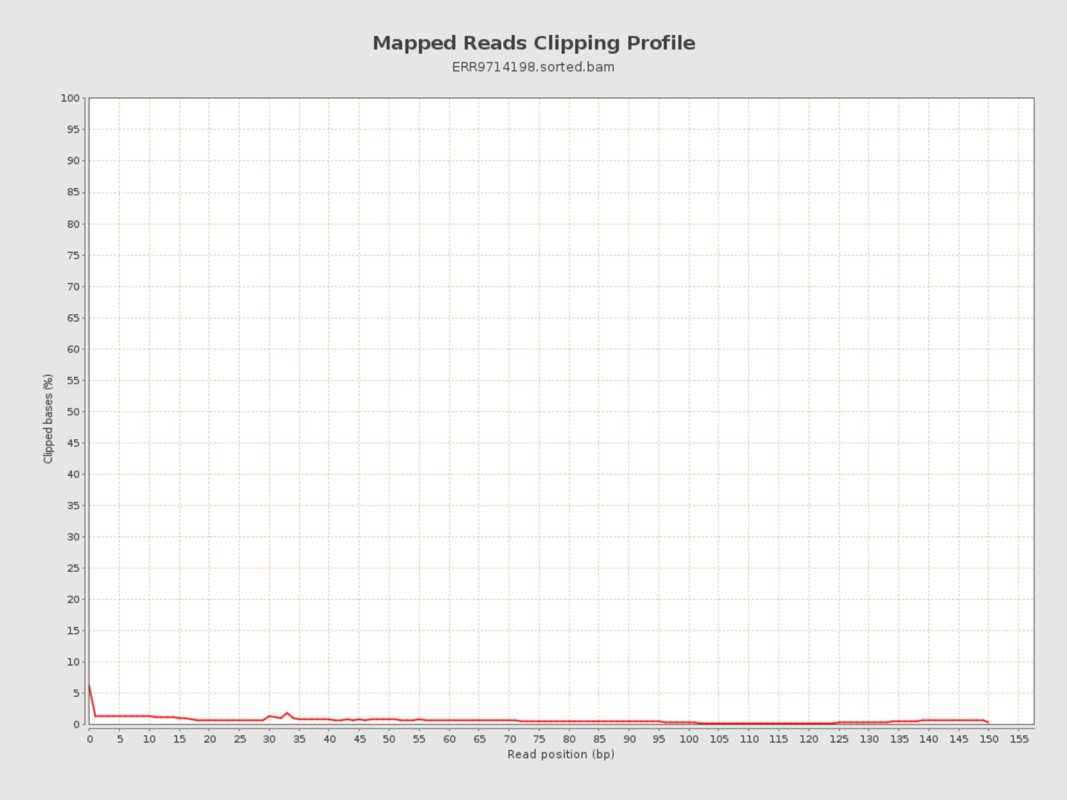
8. Results : Mapped Reads Nucleotide Content



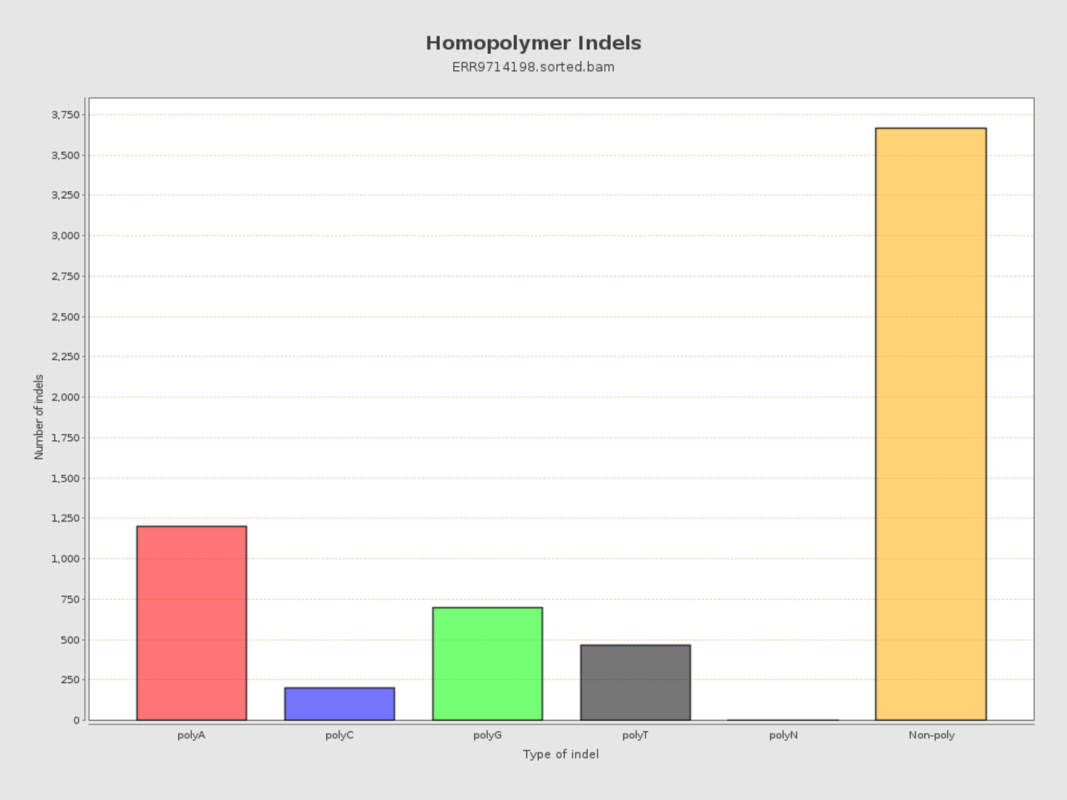
9. Results : Mapped Reads GC-content Distribution



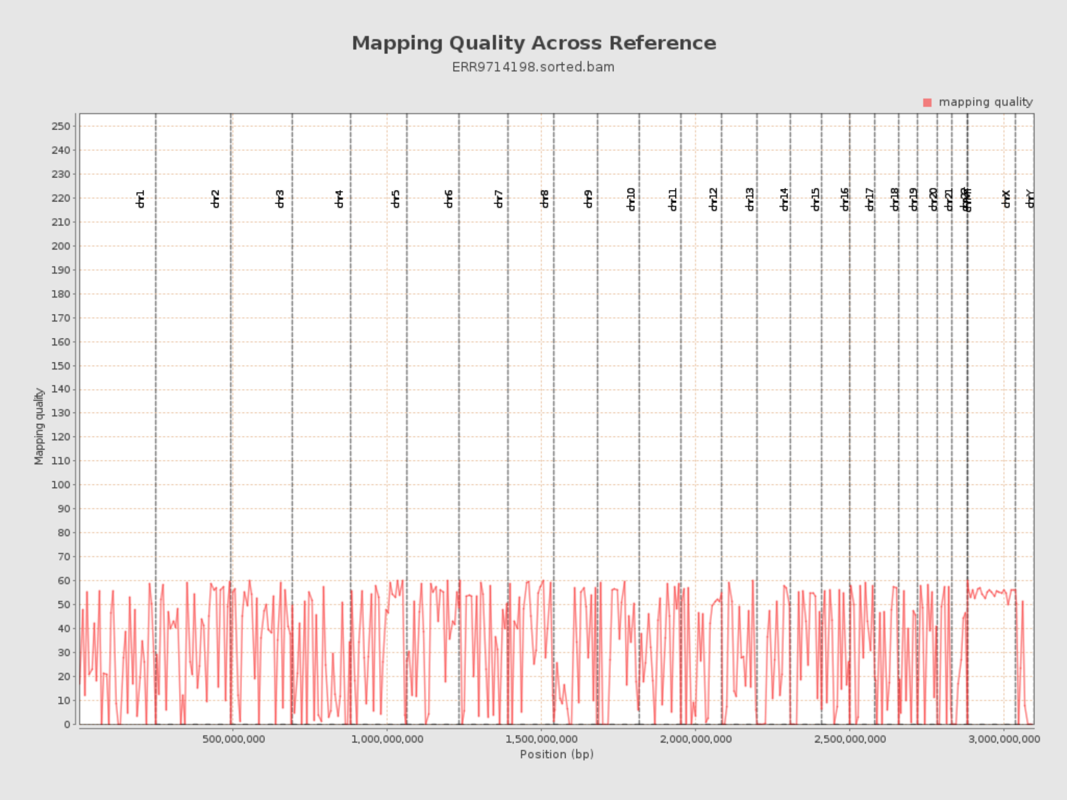
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram