Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 00:12:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714207.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_ERR9714207 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714207.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 00:12:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714207.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	92,190
Mapped reads	26,639 / 28.9%
Unmapped reads	65,551 / 71.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	923 / 1%
Read min/max/mean length	30 / 151 / 99.3
Duplicated reads (estimated)	21,402 / 23.22%
Duplication rate	37.61%
Clipped reads	24,059 / 26.1%

2.2. ACGT Content

Number/percentage of A's	867,085 / 26.81%
Number/percentage of C's	588,385 / 18.19%
Number/percentage of T's	810,661 / 25.06%
Number/percentage of G's	968,335 / 29.94%
Number/percentage of N's	29 / 0%
GC Percentage	48.13%

2.3. Coverage

Mean	0.0011

Standard Deviation	0.4895

2.4. Mapping Quality

Mean Mapping Quality	42.54

2.5. Mismatches and indels

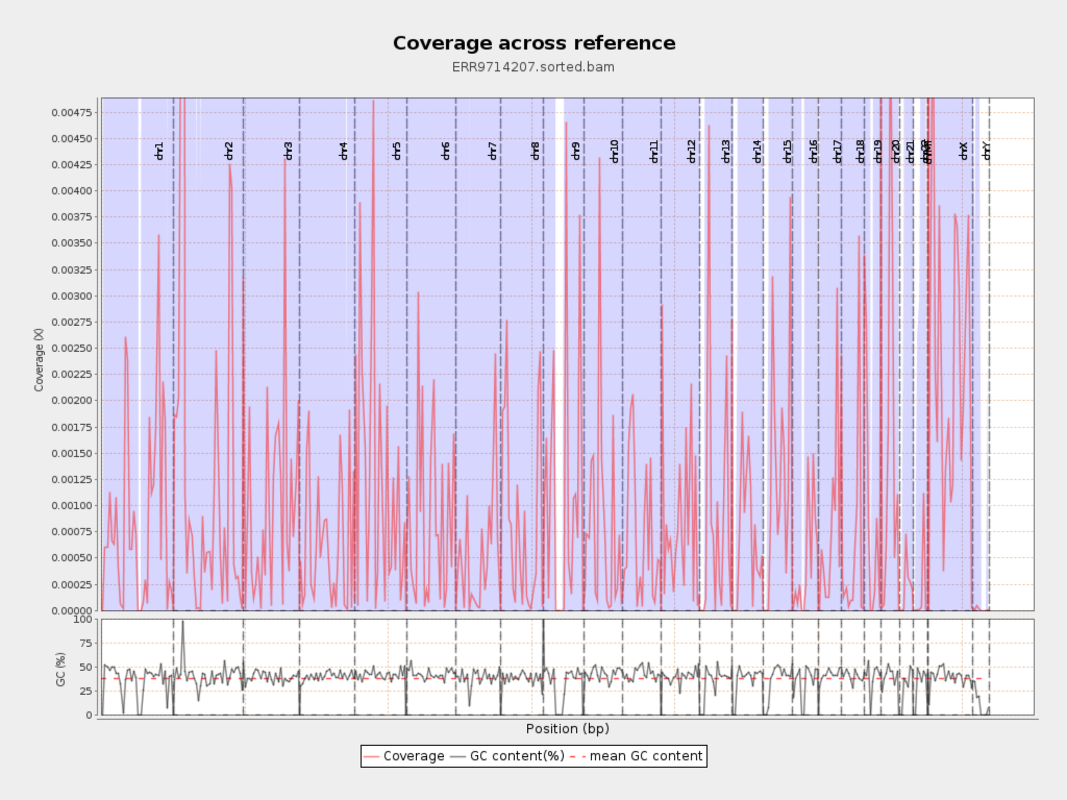
General error rate	4.08%
Mismatches	121,435
Insertions	3,441
Mapped reads with at least one insertion	12.38%
Deletions	10,293
Mapped reads with at least one deletion	36.69%
Homopolymer indels	26.16%

2.6. Chromosome stats

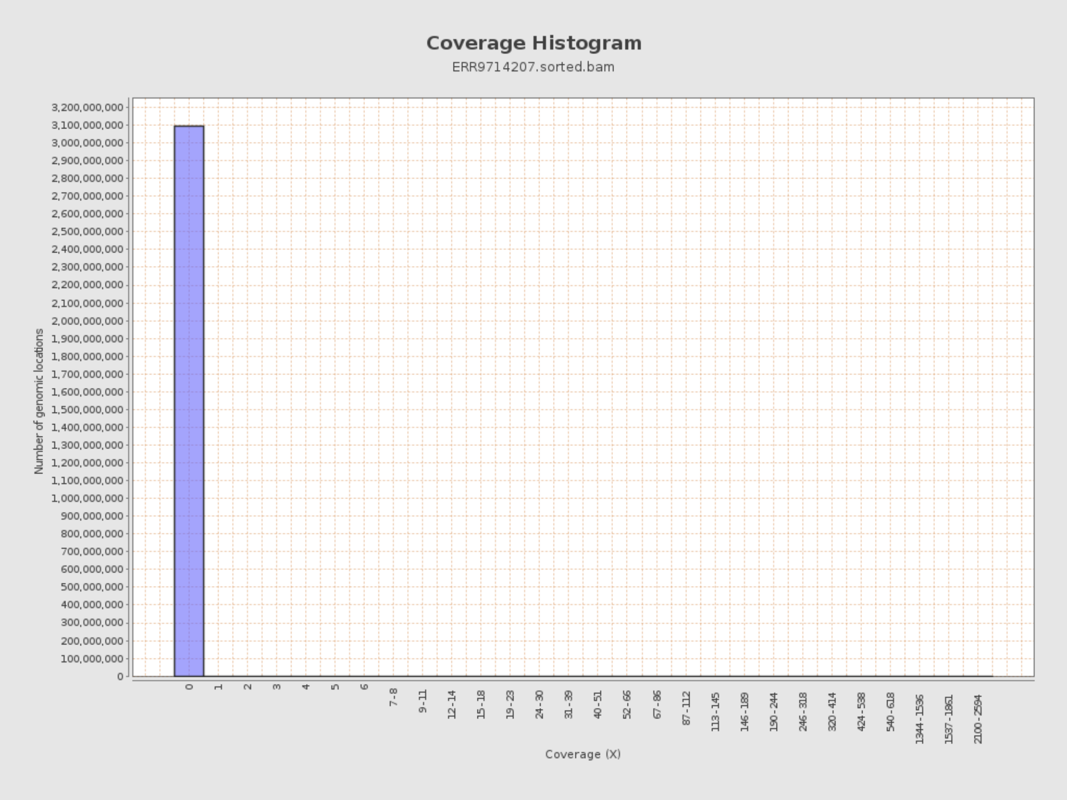
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	216101	0.0009	0.1912
chr2	243199373	622461	0.0026	1.5816
chr3	198022430	202845	0.001	0.2528
chr4	191154276	127112	0.0007	0.1408
chr5	180915260	229894	0.0013	0.2425
chr6	171115067	153347	0.0009	0.1831
chr7	159138663	84053	0.0005	0.1337

chr8	146364022	127720	0.0009	0.2053
chr9	141213431	154785	0.0011	0.2286
chr10	135534747	111735	0.0008	0.1881
chr11	135006516	103570	0.0008	0.1485
chr12	133851895	114665	0.0009	0.1548
chr13	115169878	95792	0.0008	0.2306
chr14	107349540	75518	0.0007	0.1606
chr15	102531392	127795	0.0012	0.2587
chr16	90354753	42830	0.0005	0.1341
chr17	81195210	68798	0.0008	0.1986
chr18	78077248	46100	0.0006	0.1599
chr19	59128983	57494	0.001	0.2234
chr20	63025520	104294	0.0017	0.4783
chr21	48129895	11351	0.0002	0.0804
chr22	51304566	9244	0.0002	0.0691
chrMT	16571	43566	2.6291	22.4422
chrX	155270560	365108	0.0024	0.312
chrY	59373566	756	0	0.0041

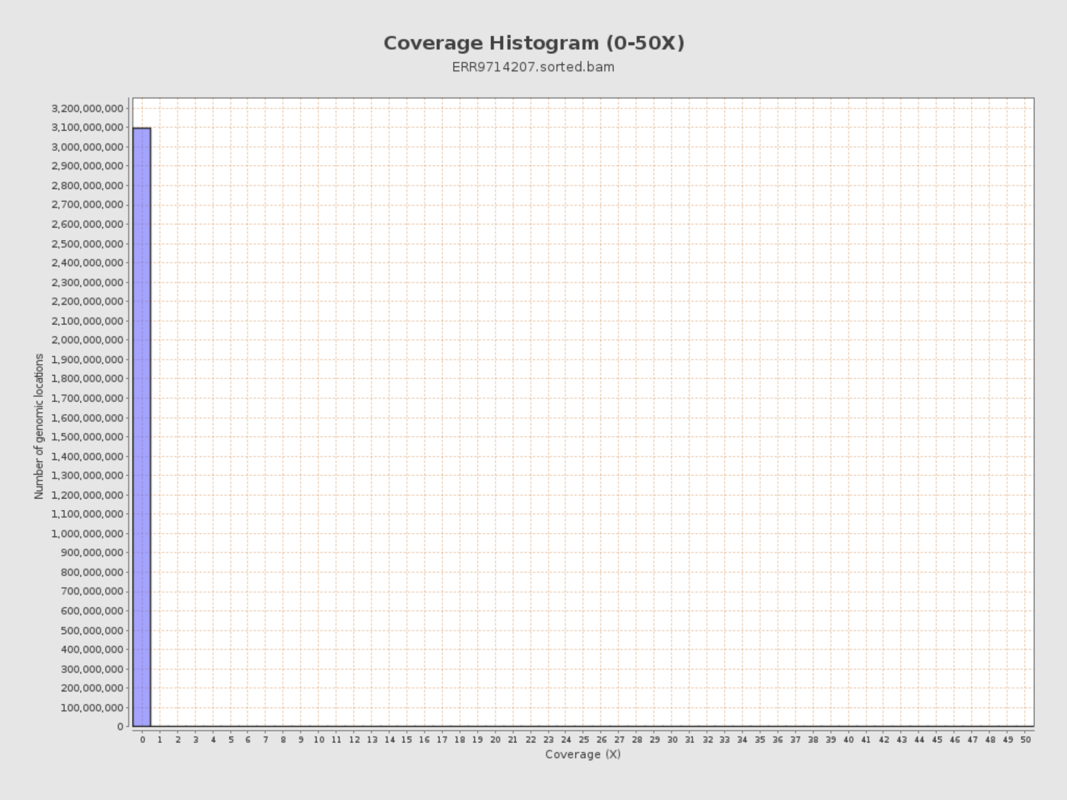
3. Results : Coverage across reference



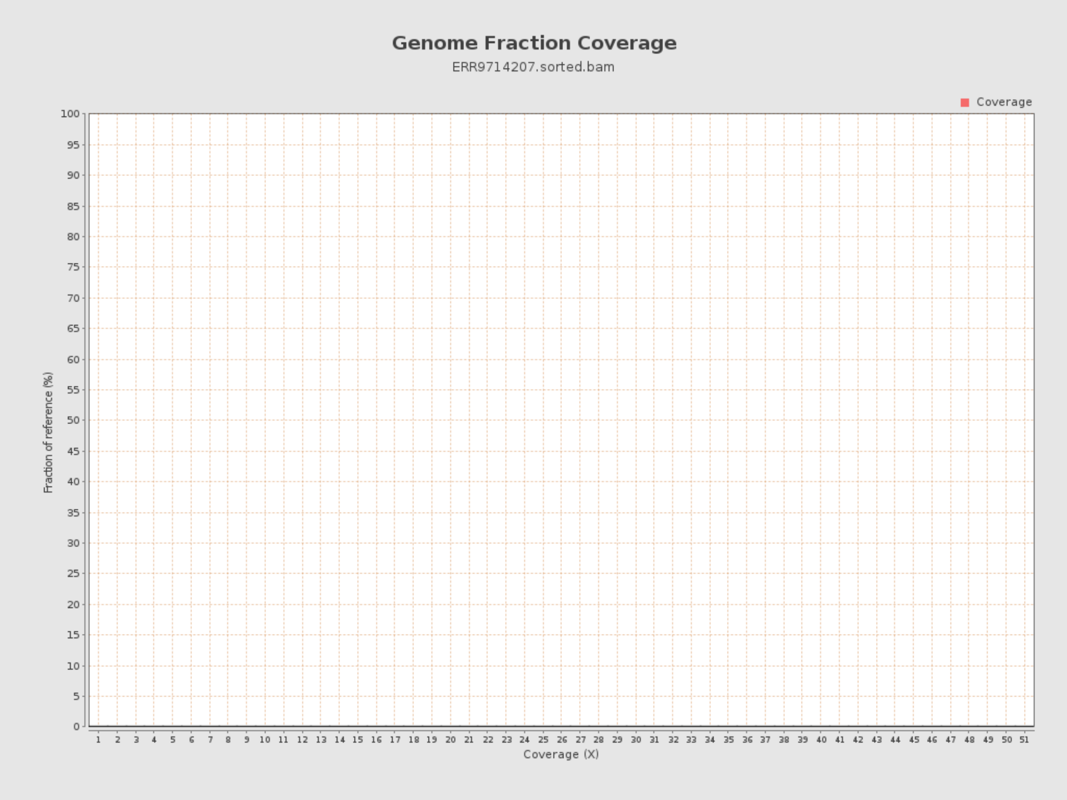
4. Results : Coverage Histogram



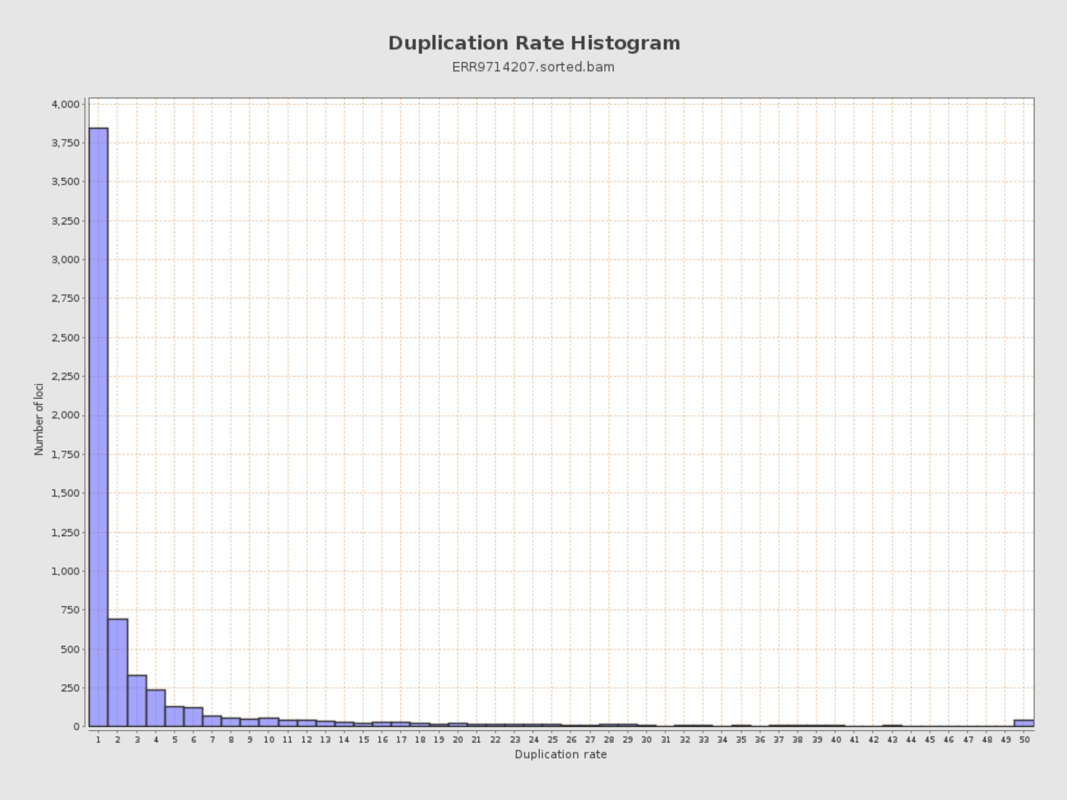
5. Results : Coverage Histogram (0-50X)



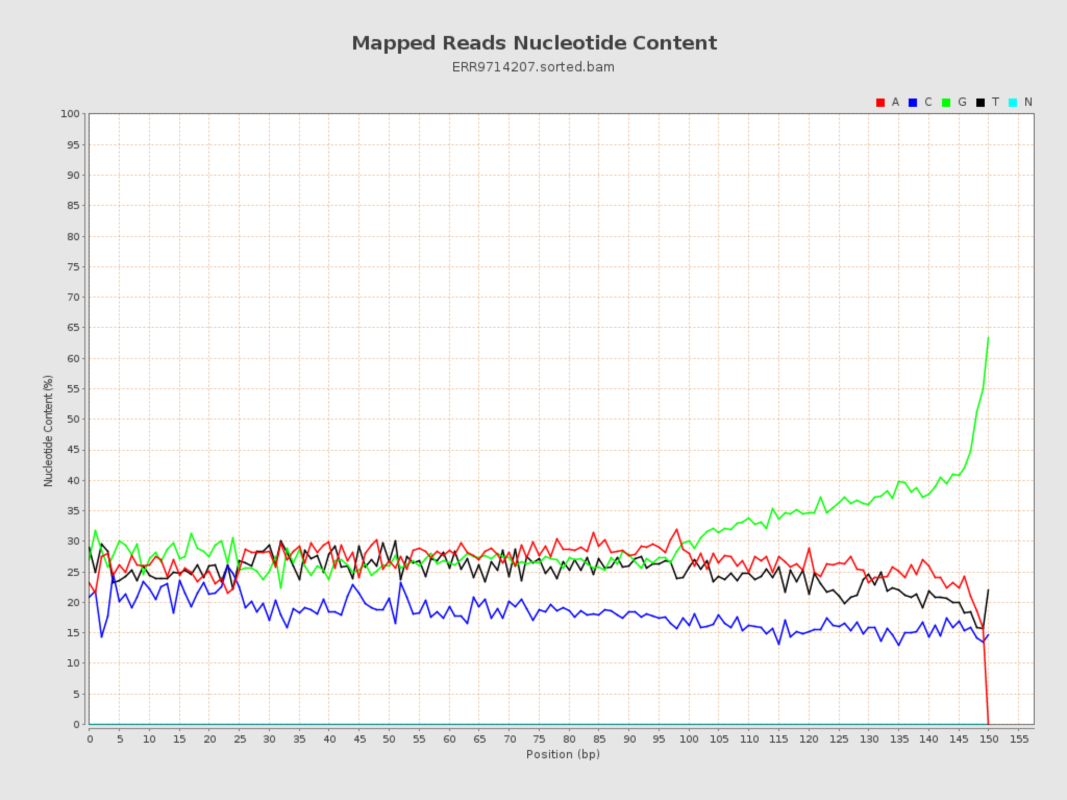
6. Results : Genome Fraction Coverage



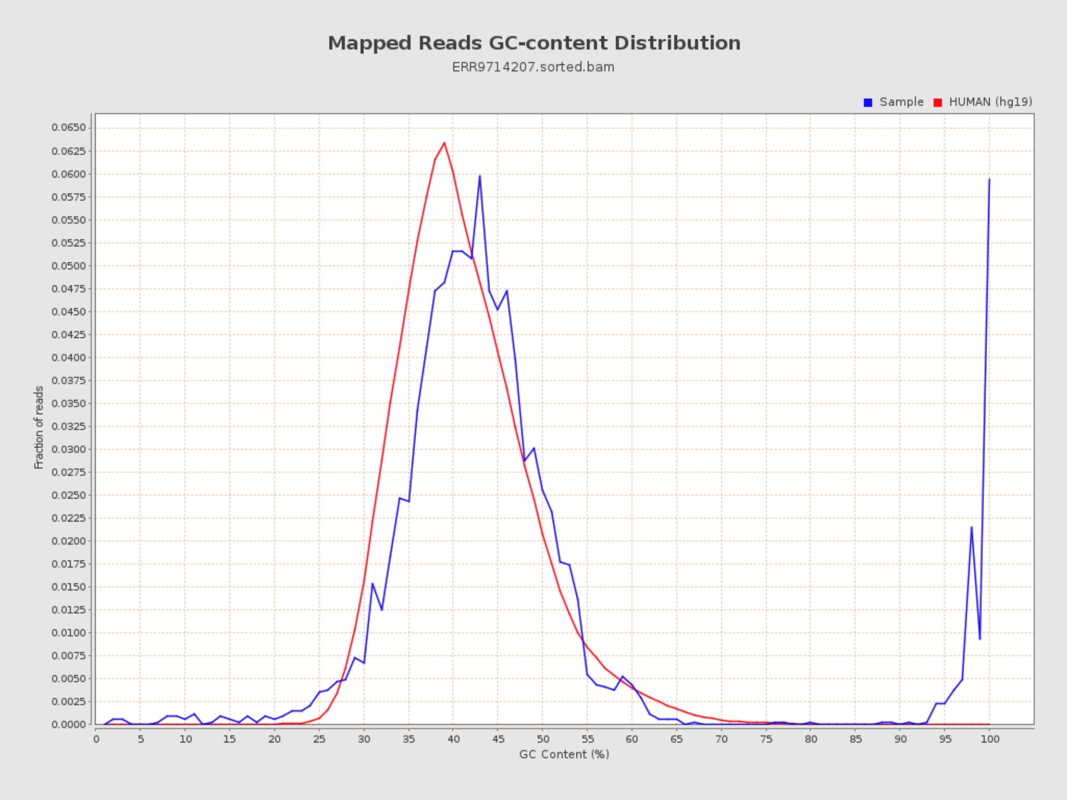
7. Results : Duplication Rate Histogram



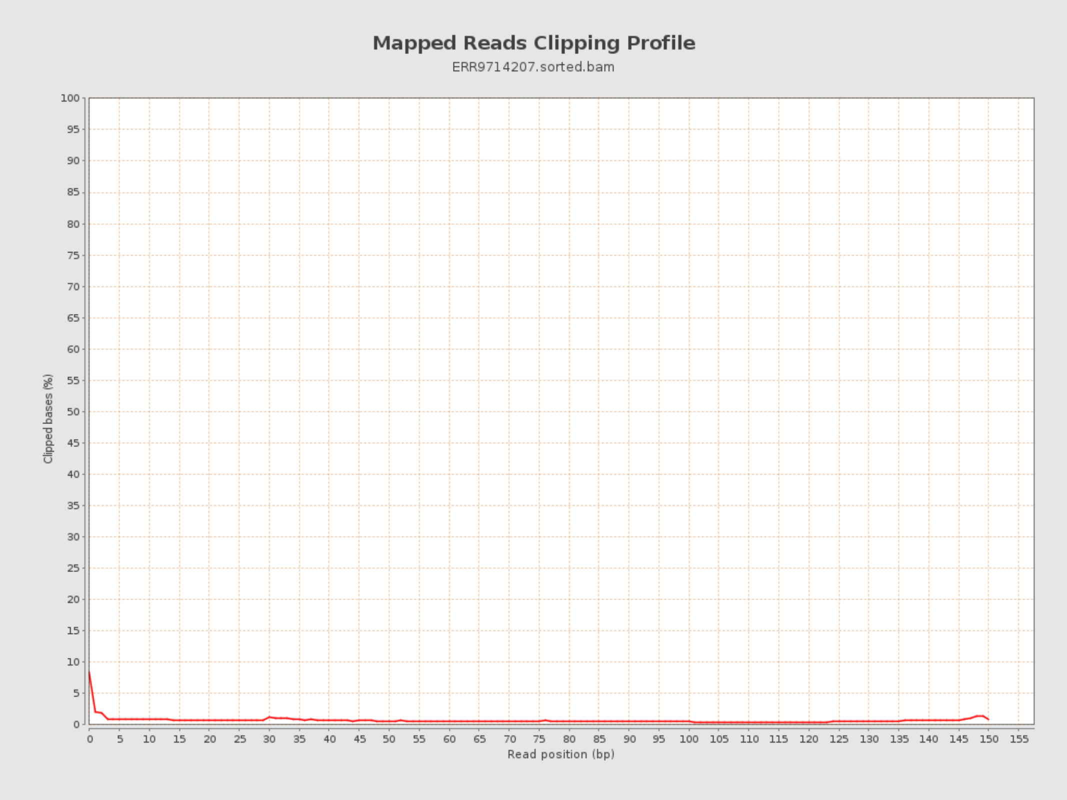
8. Results : Mapped Reads Nucleotide Content



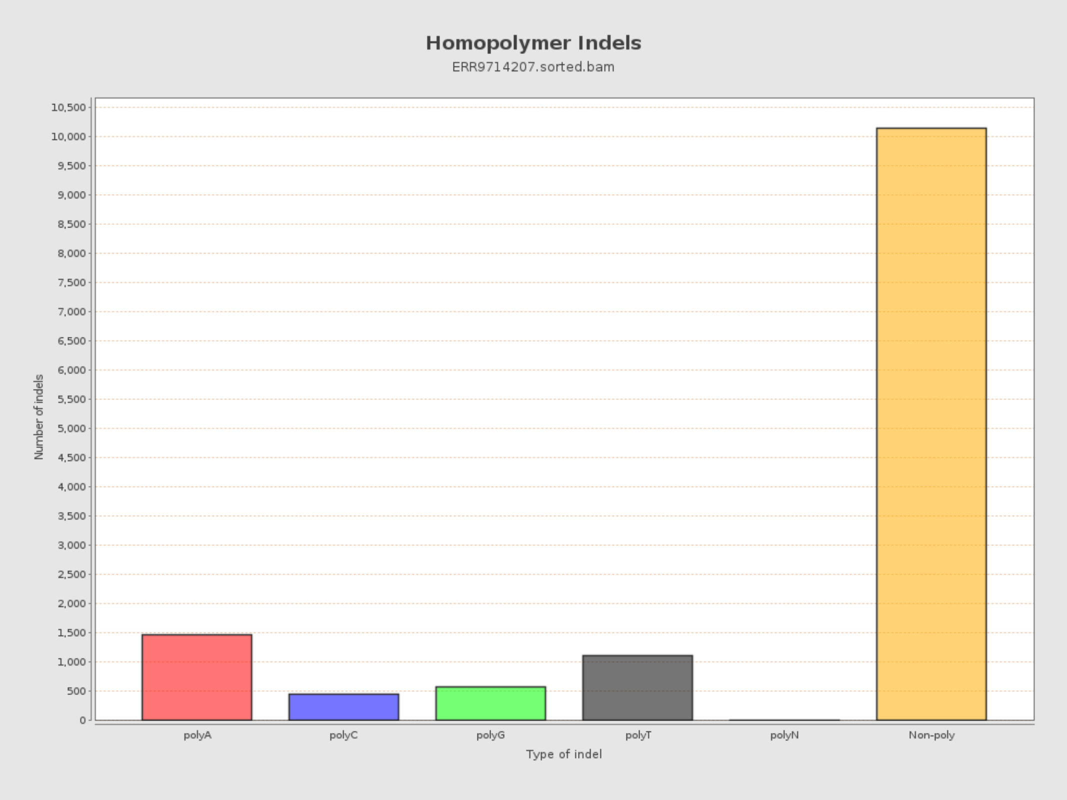
9. Results : Mapped Reads GC-content Distribution



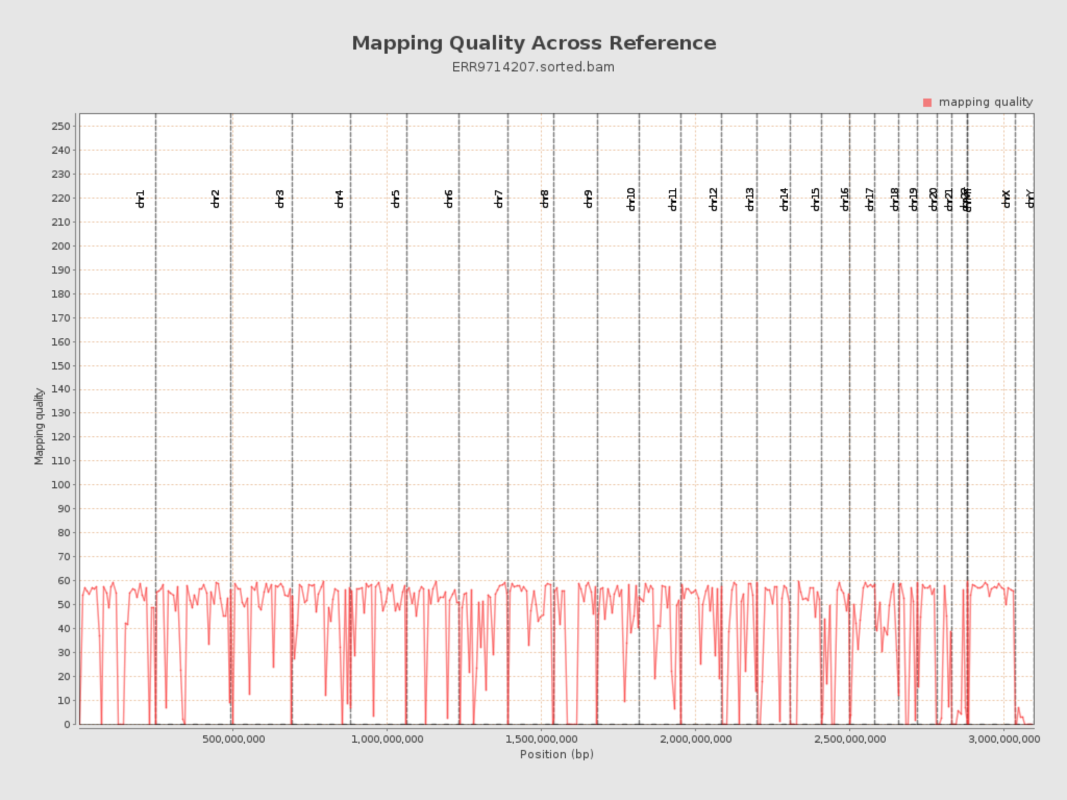
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram