Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 01:00:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714238.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_ERR9714238 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714238.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 01:00:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714238.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	295,152
Mapped reads	26,859 / 9.1%
Unmapped reads	268,293 / 90.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	963 / 0.33%
Read min/max/mean length	30 / 151 / 60.97
Duplicated reads (estimated)	22,420 / 7.6%
Duplication rate	38.56%
Clipped reads	23,398 / 7.93%

2.2. ACGT Content

Number/percentage of A's	608,315 / 21.86%
Number/percentage of C's	428,945 / 15.41%
Number/percentage of T's	547,474 / 19.67%
Number/percentage of G's	1,198,351 / 43.06%
Number/percentage of N's	61 / 0%
GC Percentage	58.47%

2.3. Coverage

Mean	0.0009

Standard Deviation	0.8923

2.4. Mapping Quality

Mean Mapping Quality	38.07

2.5. Mismatches and indels

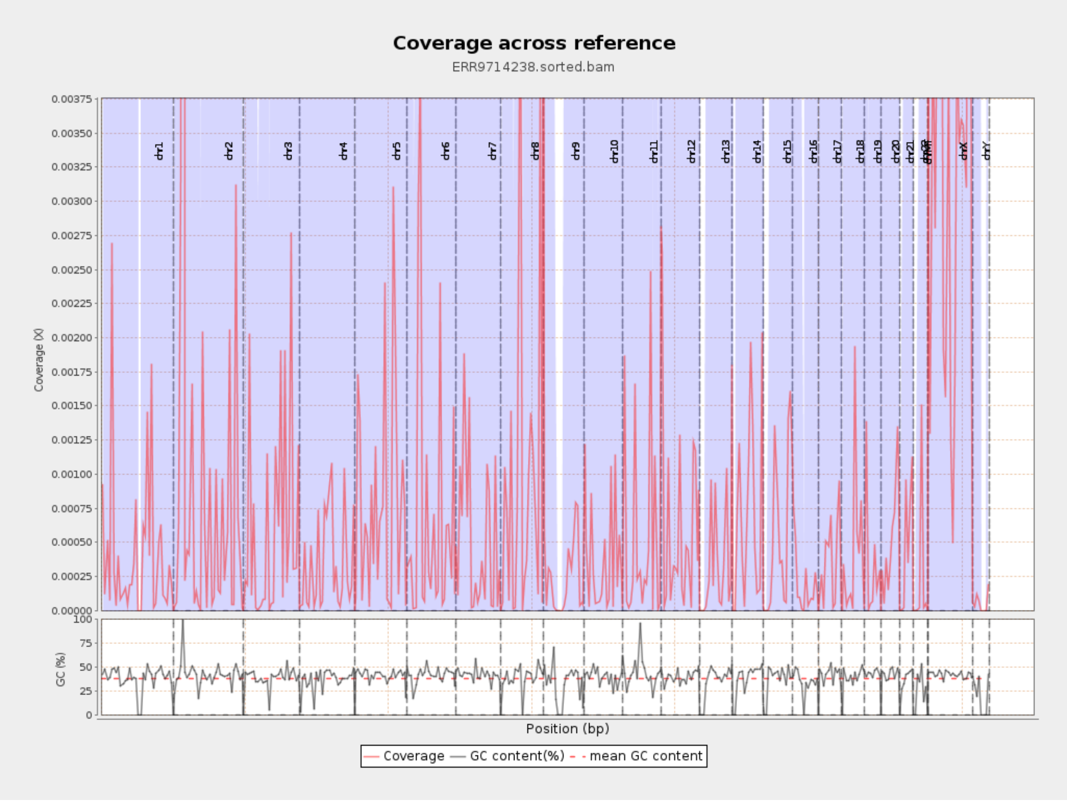
General error rate	3.96%
Mismatches	99,223
Insertions	2,857
Mapped reads with at least one insertion	9.11%
Deletions	7,926
Mapped reads with at least one deletion	27.73%
Homopolymer indels	31.59%

2.6. Chromosome stats

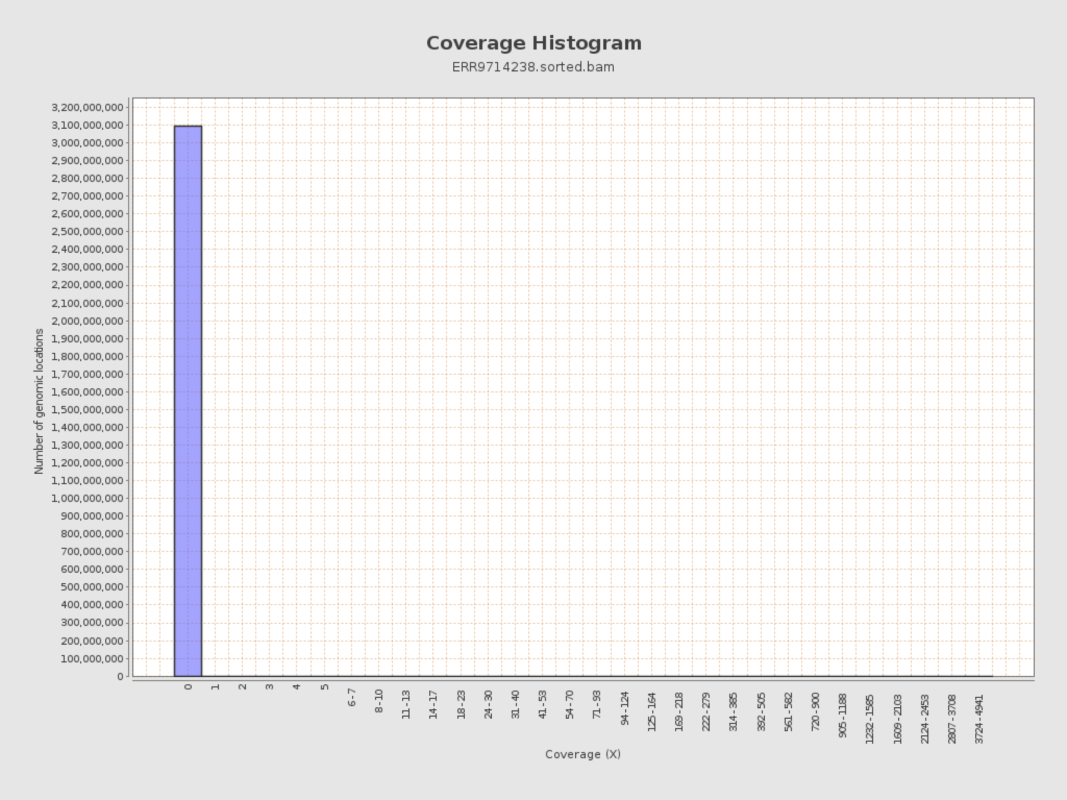
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	107032	0.0004	0.1266
chr2	243199373	920418	0.0038	3.1283
chr3	198022430	123511	0.0006	0.1899
chr4	191154276	66089	0.0003	0.0882
chr5	180915260	146877	0.0008	0.1904
chr6	171115067	126116	0.0007	0.1751
chr7	159138663	82288	0.0005	0.162

chr8	146364022	140982	0.001	0.2691
chr9	141213431	41553	0.0003	0.0911
chr10	135534747	52371	0.0004	0.0979
chr11	135006516	71566	0.0005	0.1491
chr12	133851895	78828	0.0006	0.1419
chr13	115169878	38116	0.0003	0.0846
chr14	107349540	77896	0.0007	0.1701
chr15	102531392	53436	0.0005	0.1329
chr16	90354753	16677	0.0002	0.0471
chr17	81195210	28905	0.0004	0.0994
chr18	78077248	34605	0.0004	0.1177
chr19	59128983	18994	0.0003	0.0943
chr20	63025520	33074	0.0005	0.1237
chr21	48129895	22043	0.0005	0.1133
chr22	51304566	12417	0.0002	0.0953
chrMT	16571	3340	0.2016	1.4823
chrX	155270560	532617	0.0034	0.4185
chrY	59373566	3534	0.0001	0.0123

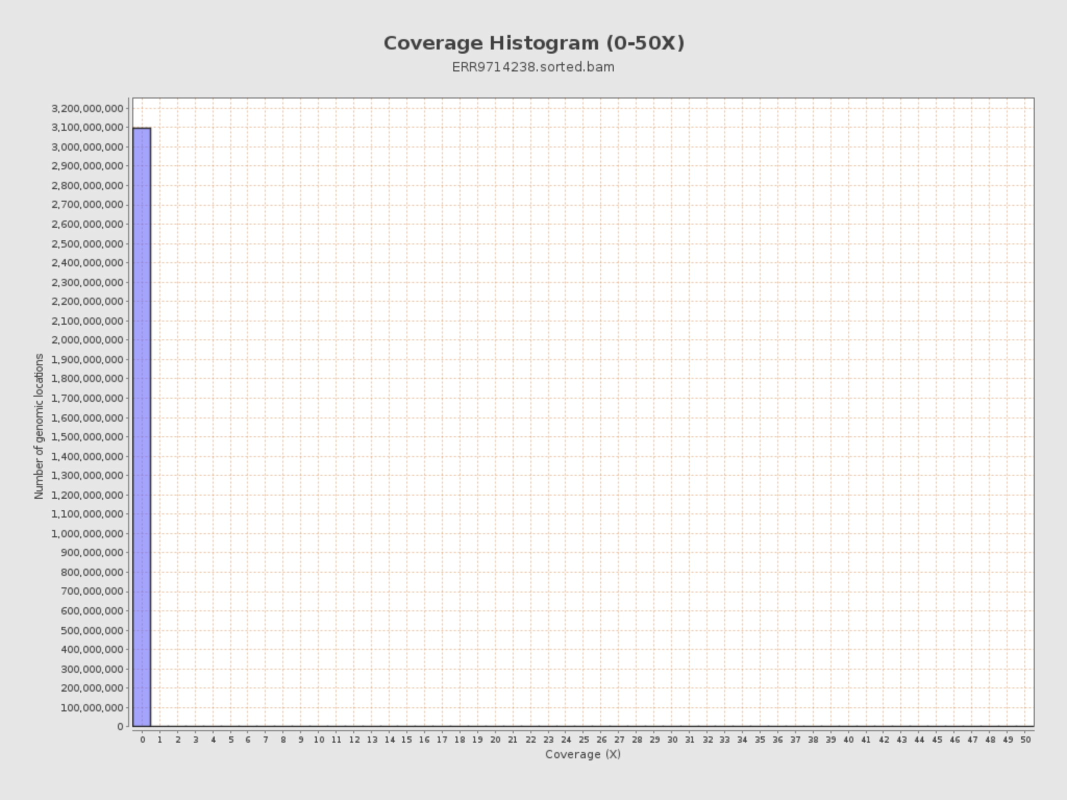
3. Results : Coverage across reference



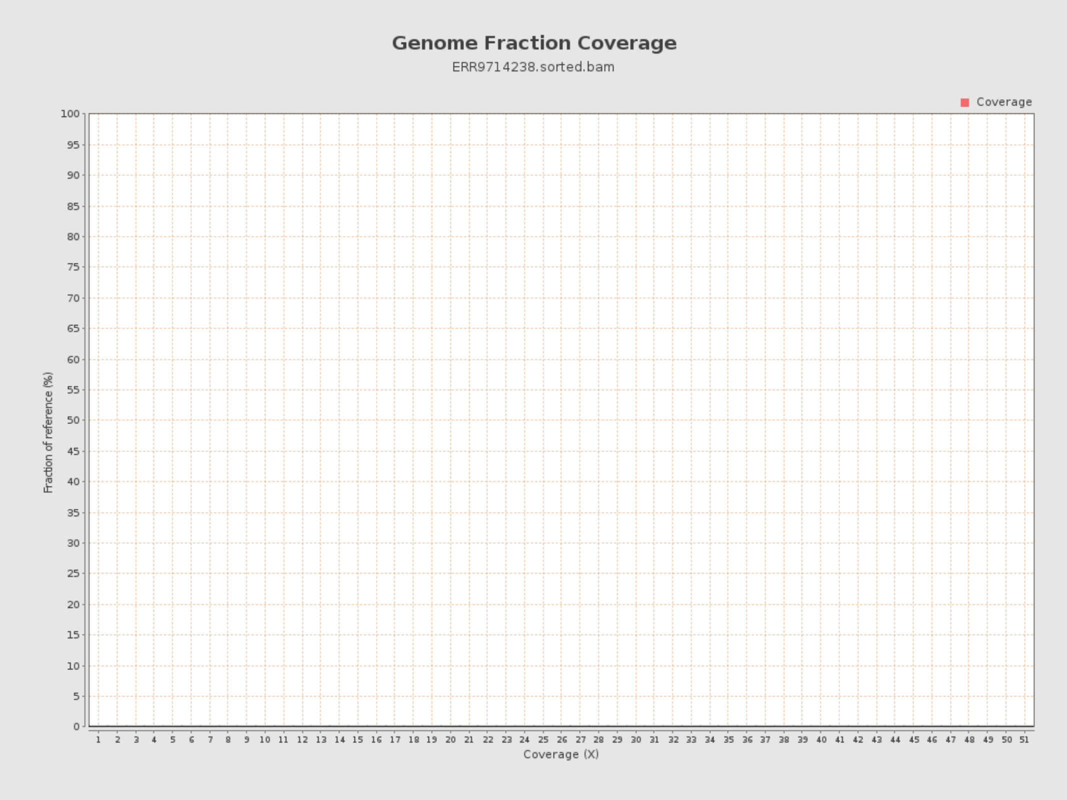
4. Results : Coverage Histogram



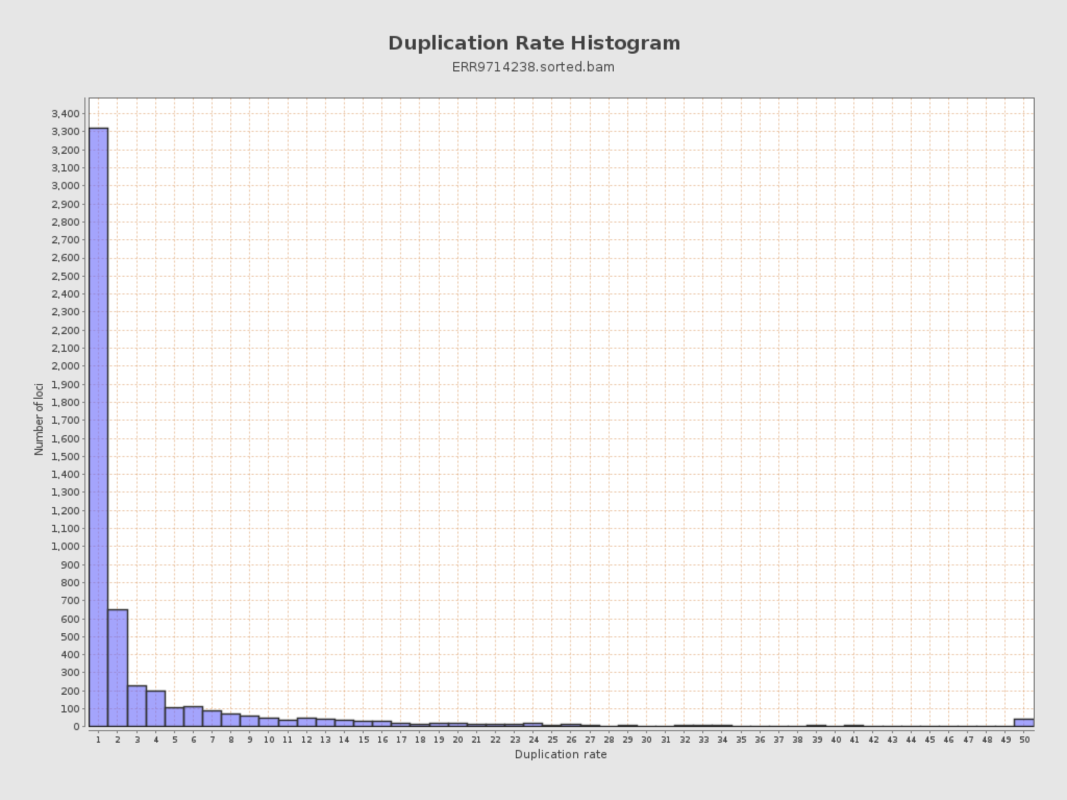
5. Results : Coverage Histogram (0-50X)



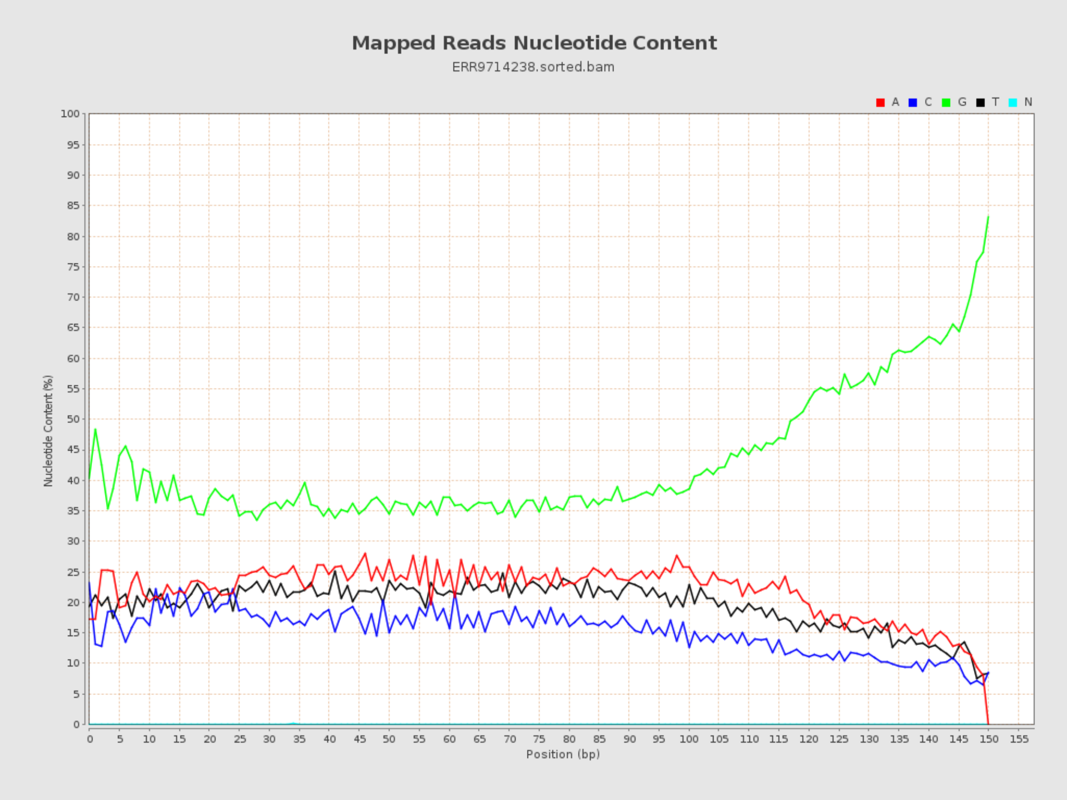
6. Results : Genome Fraction Coverage



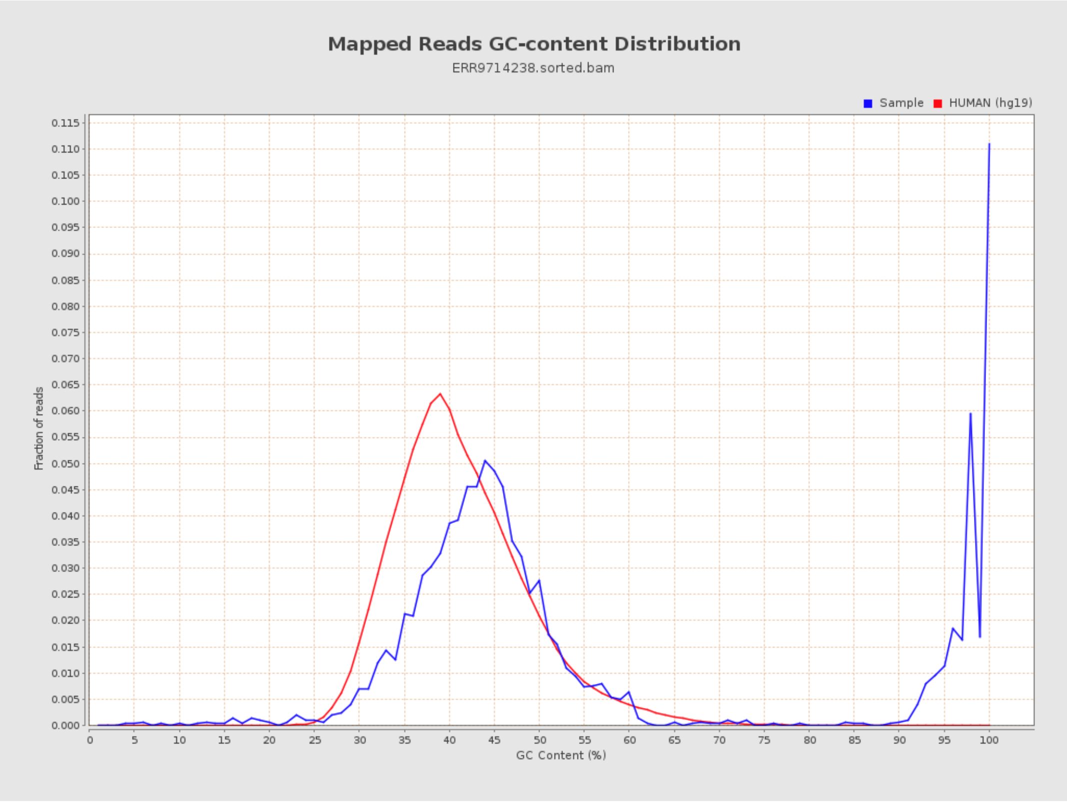
7. Results : Duplication Rate Histogram



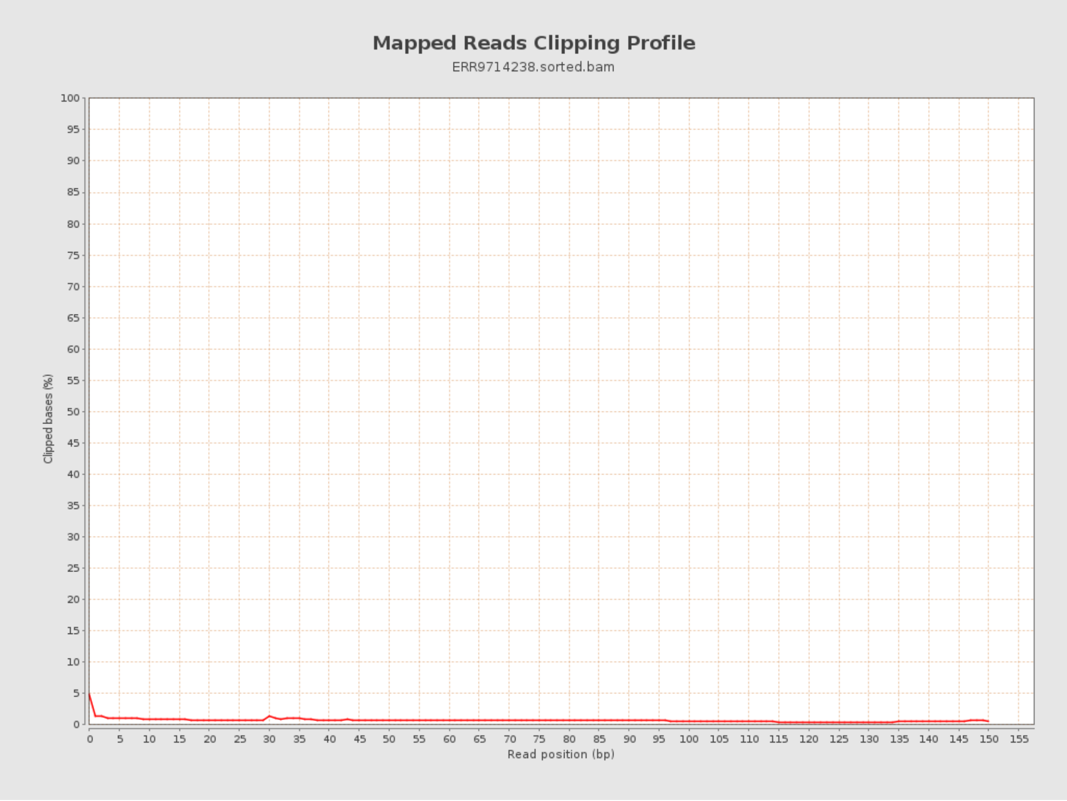
8. Results : Mapped Reads Nucleotide Content



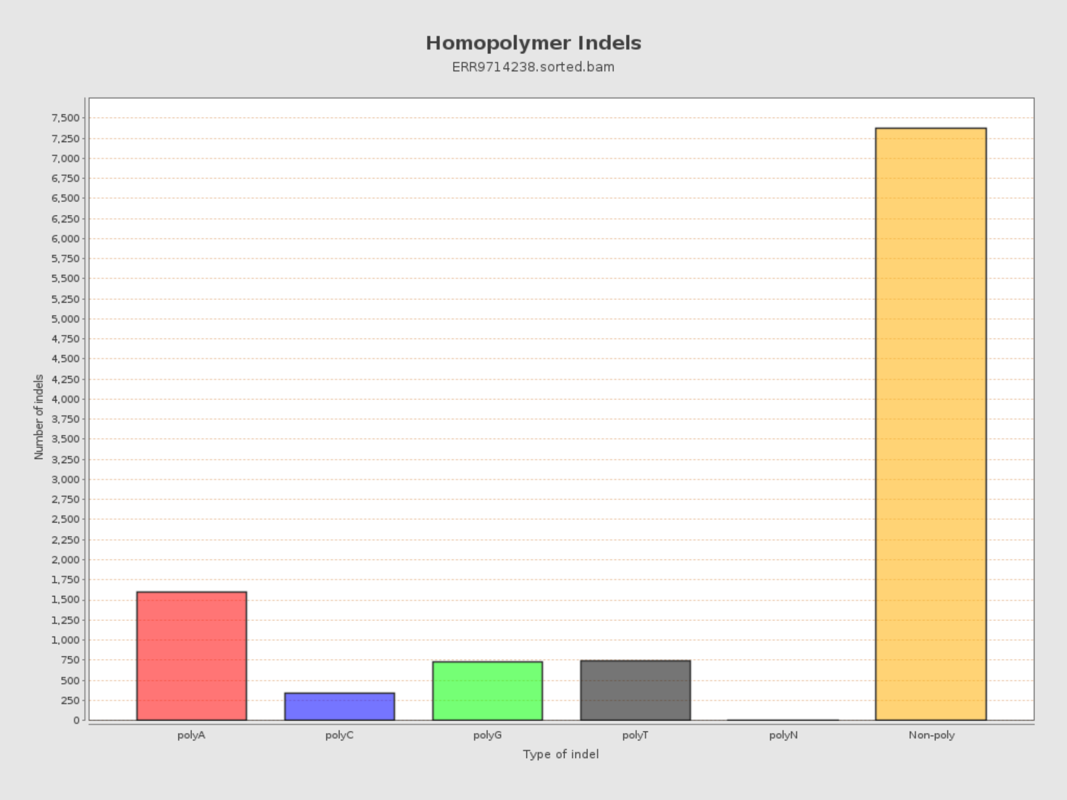
9. Results : Mapped Reads GC-content Distribution



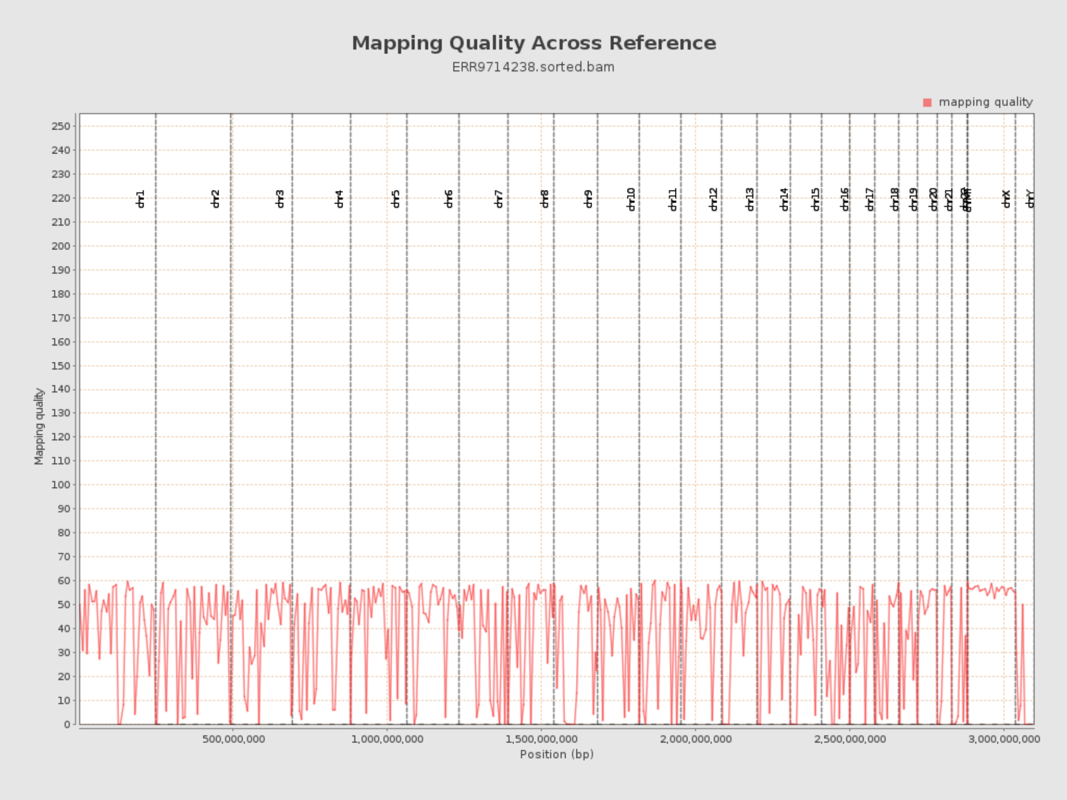
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram