Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 00:35:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714223.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_ERR9714223 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714223.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 00:35:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714223.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	213,536
Mapped reads	29,680 / 13.9%
Unmapped reads	183,856 / 86.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	729 / 0.34%
Read min/max/mean length	30 / 151 / 65.08
Duplicated reads (estimated)	26,504 / 12.41%
Duplication rate	41.28%
Clipped reads	19,494 / 9.13%

2.2. ACGT Content

Number/percentage of A's	322,534 / 10.46%
Number/percentage of C's	227,660 / 7.38%
Number/percentage of T's	276,732 / 8.97%
Number/percentage of G's	2,257,411 / 73.19%
Number/percentage of N's	97 / 0%
GC Percentage	80.57%

2.3. Coverage

Mean	0.001

Standard Deviation	2.5589

2.4. Mapping Quality

Mean Mapping Quality	33.01

2.5. Mismatches and indels

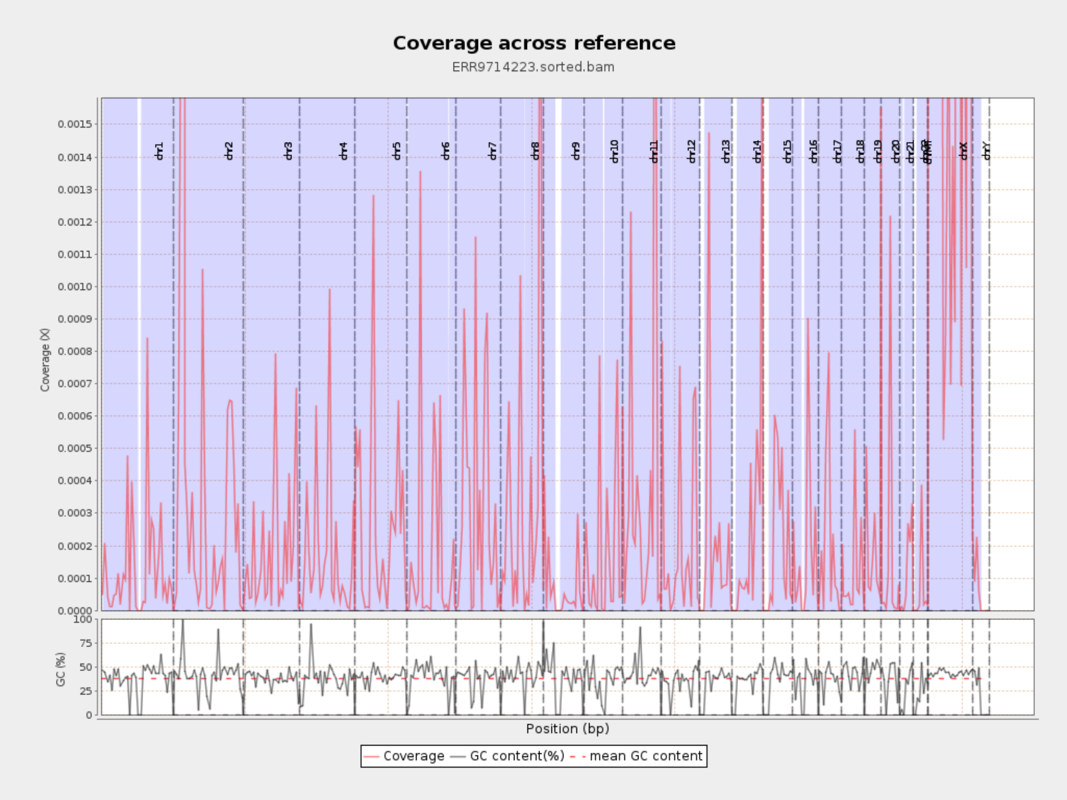
General error rate	3.4%
Mismatches	88,110
Insertions	2,840
Mapped reads with at least one insertion	7.36%
Deletions	4,269
Mapped reads with at least one deletion	13.84%
Homopolymer indels	41.58%

2.6. Chromosome stats

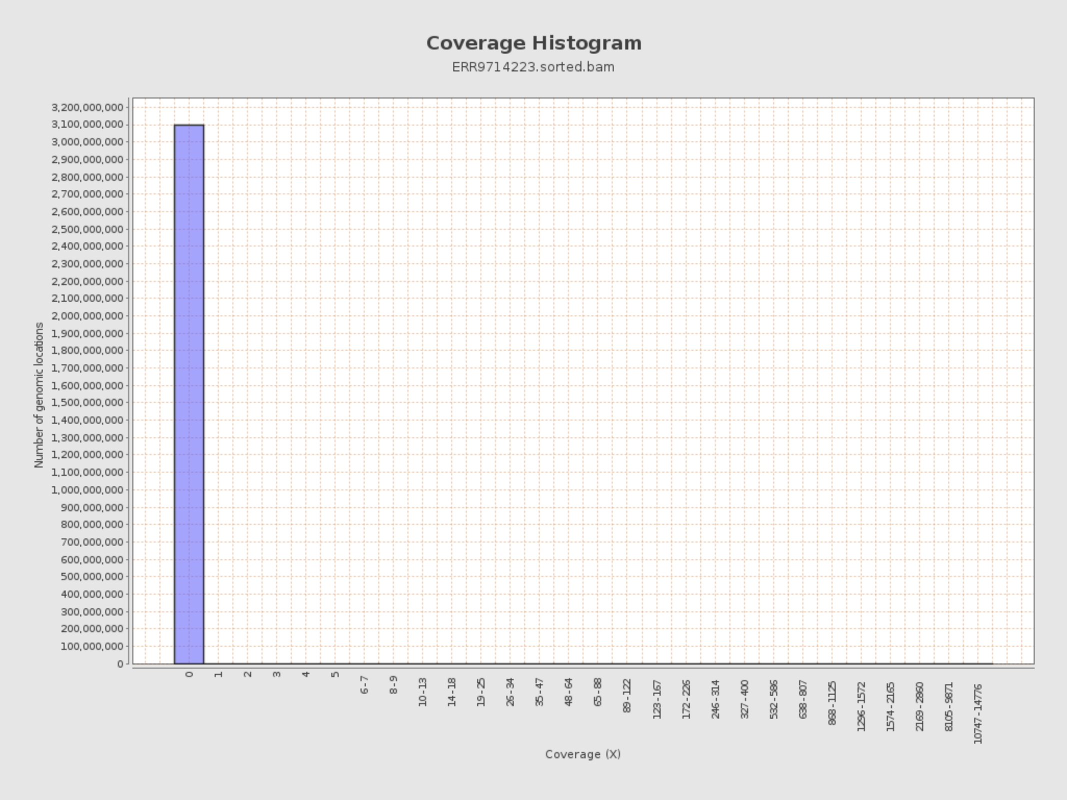
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	33147	0.0001	0.0447
chr2	243199373	2116856	0.0087	9.1229
chr3	198022430	35232	0.0002	0.0526
chr4	191154276	33030	0.0002	0.0441
chr5	180915260	51305	0.0003	0.0721
chr6	171115067	30737	0.0002	0.0559
chr7	159138663	49703	0.0003	0.1237

chr8	146364022	54810	0.0004	0.14
chr9	141213431	10272	0.0001	0.0211
chr10	135534747	25833	0.0002	0.059
chr11	135006516	53232	0.0004	0.1348
chr12	133851895	29777	0.0002	0.0713
chr13	115169878	22858	0.0002	0.0645
chr14	107349540	29865	0.0003	0.0837
chr15	102531392	20041	0.0002	0.0528
chr16	90354753	15253	0.0002	0.053
chr17	81195210	14978	0.0002	0.0707
chr18	78077248	9914	0.0001	0.0356
chr19	59128983	12848	0.0002	0.0565
chr20	63025520	11193	0.0002	0.0736
chr21	48129895	5756	0.0001	0.0308
chr22	51304566	3570	0.0001	0.0359
chrMT	16571	1631	0.0984	0.6845
chrX	155270560	436161	0.0028	0.3163
chrY	59373566	4085	0.0001	0.0219

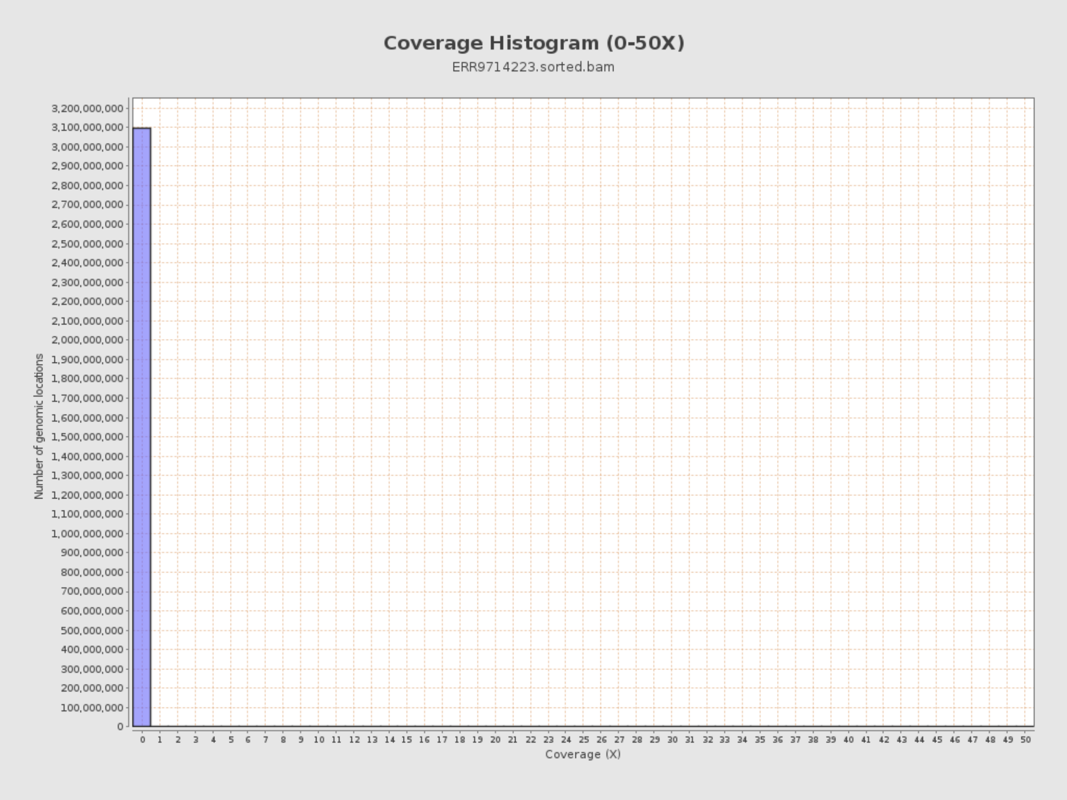
3. Results : Coverage across reference



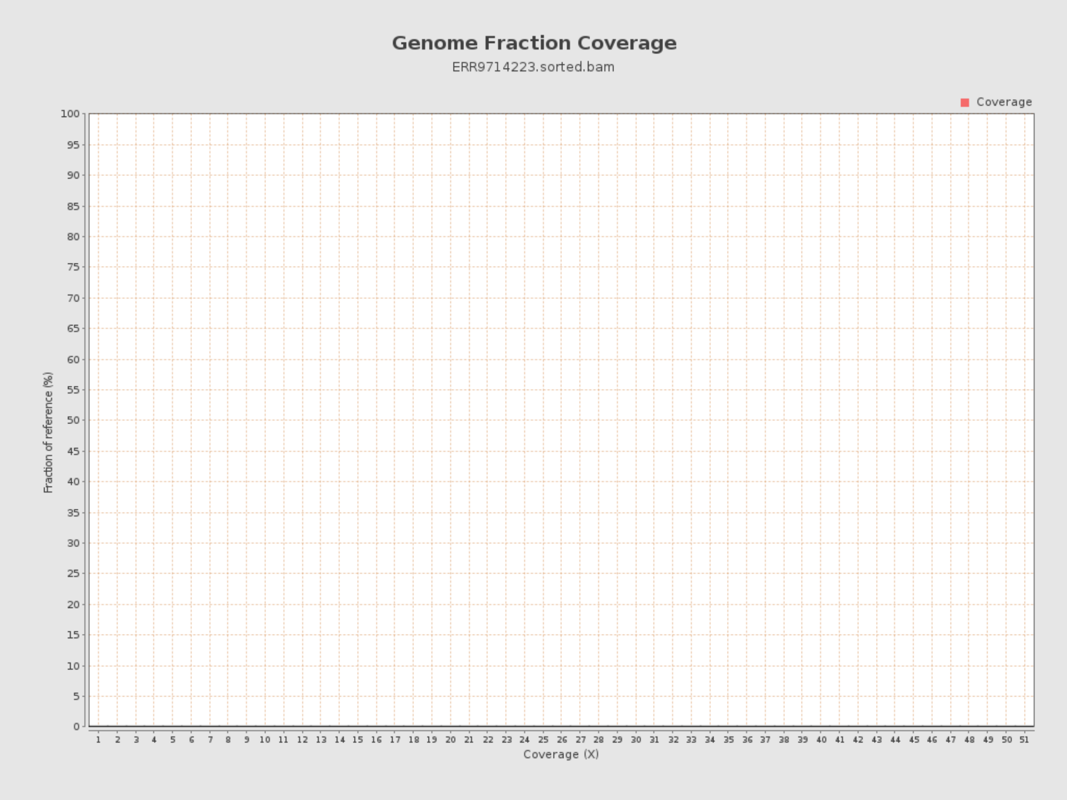
4. Results : Coverage Histogram



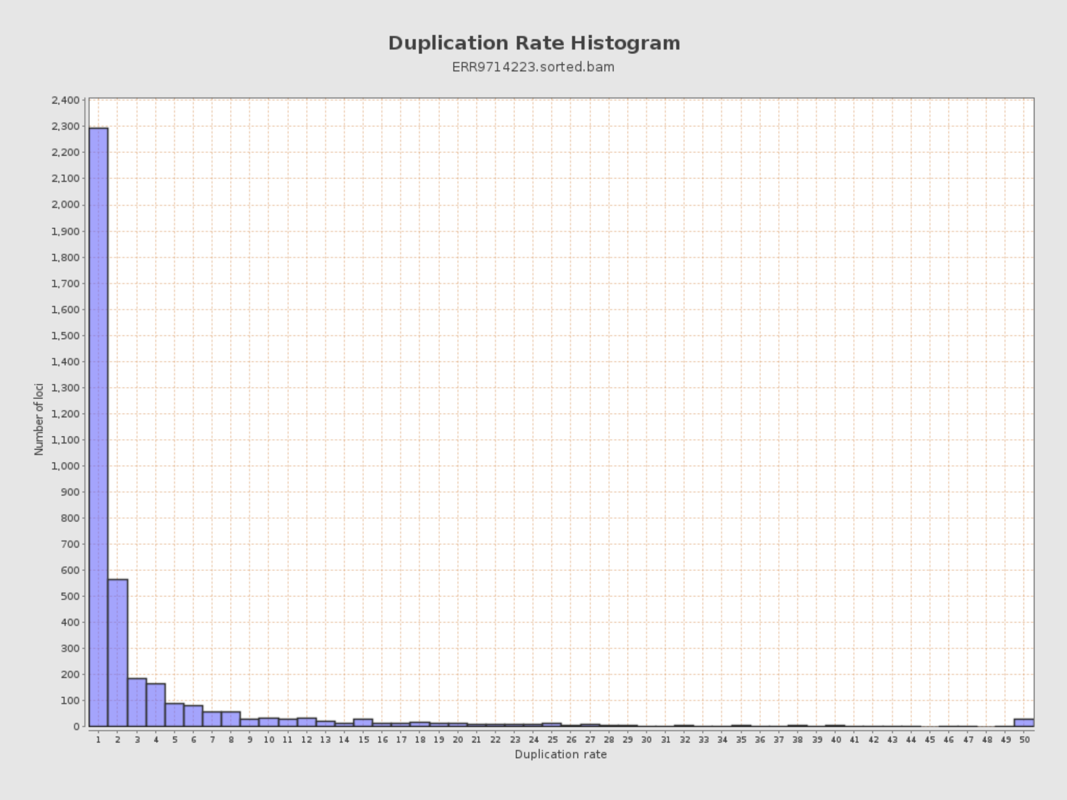
5. Results : Coverage Histogram (0-50X)



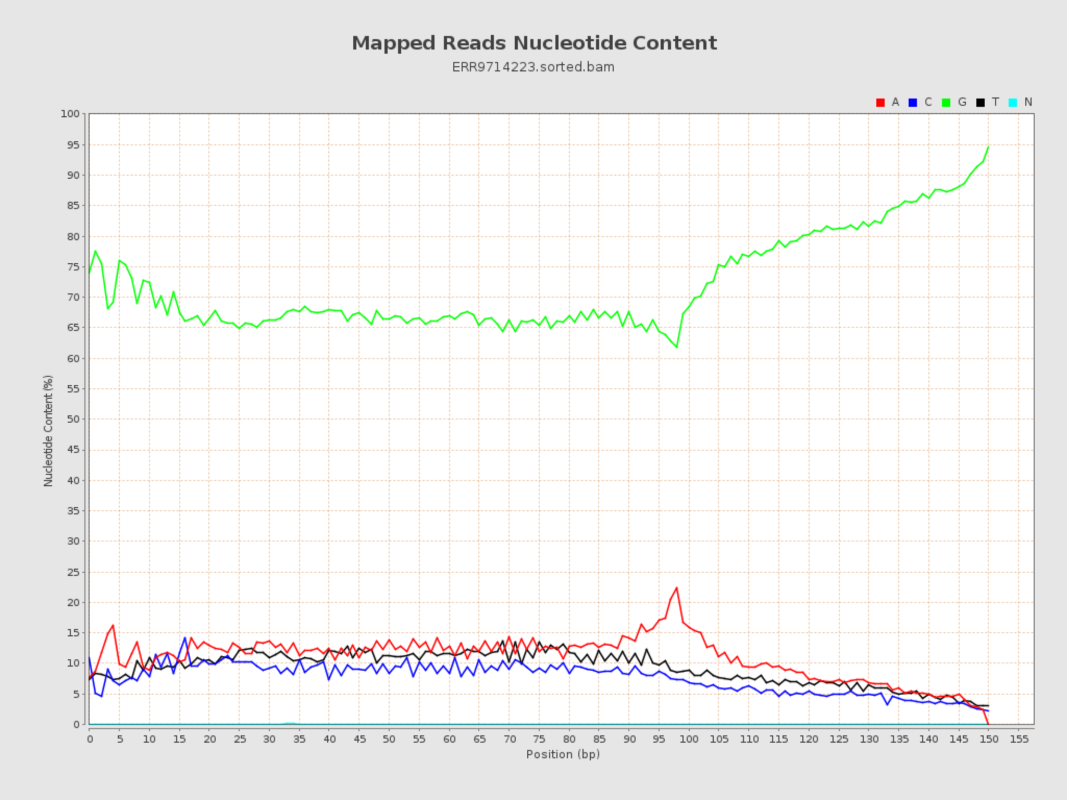
6. Results : Genome Fraction Coverage



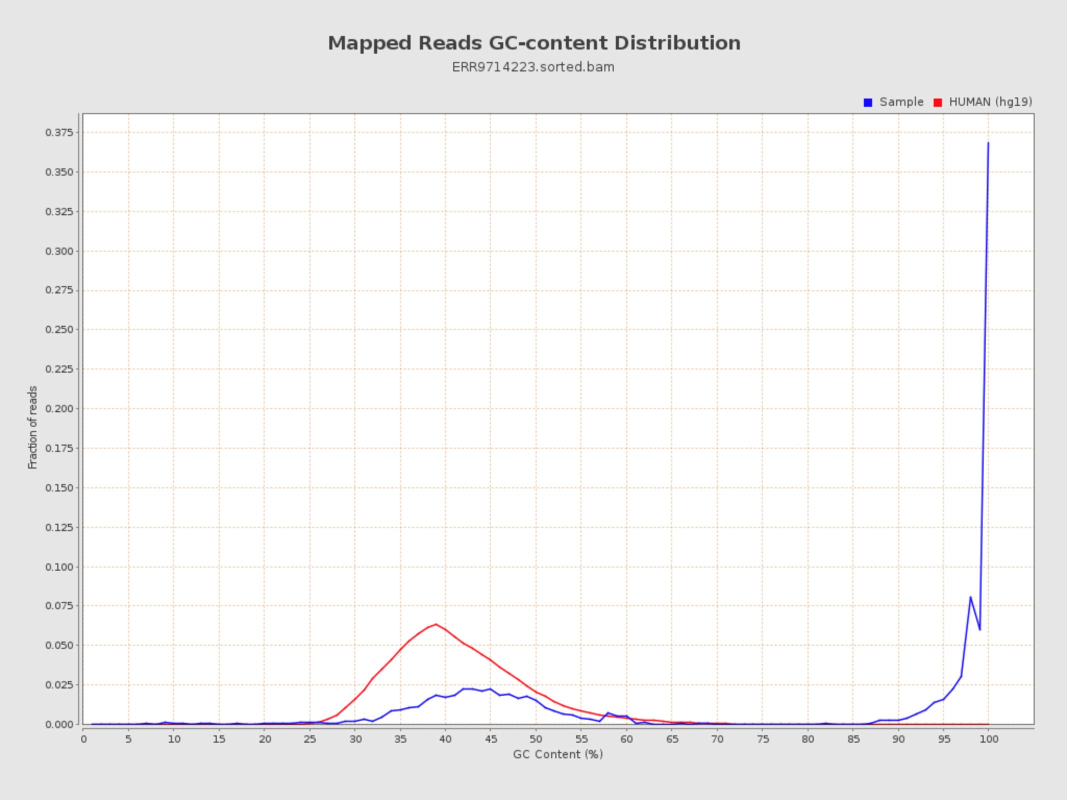
7. Results : Duplication Rate Histogram



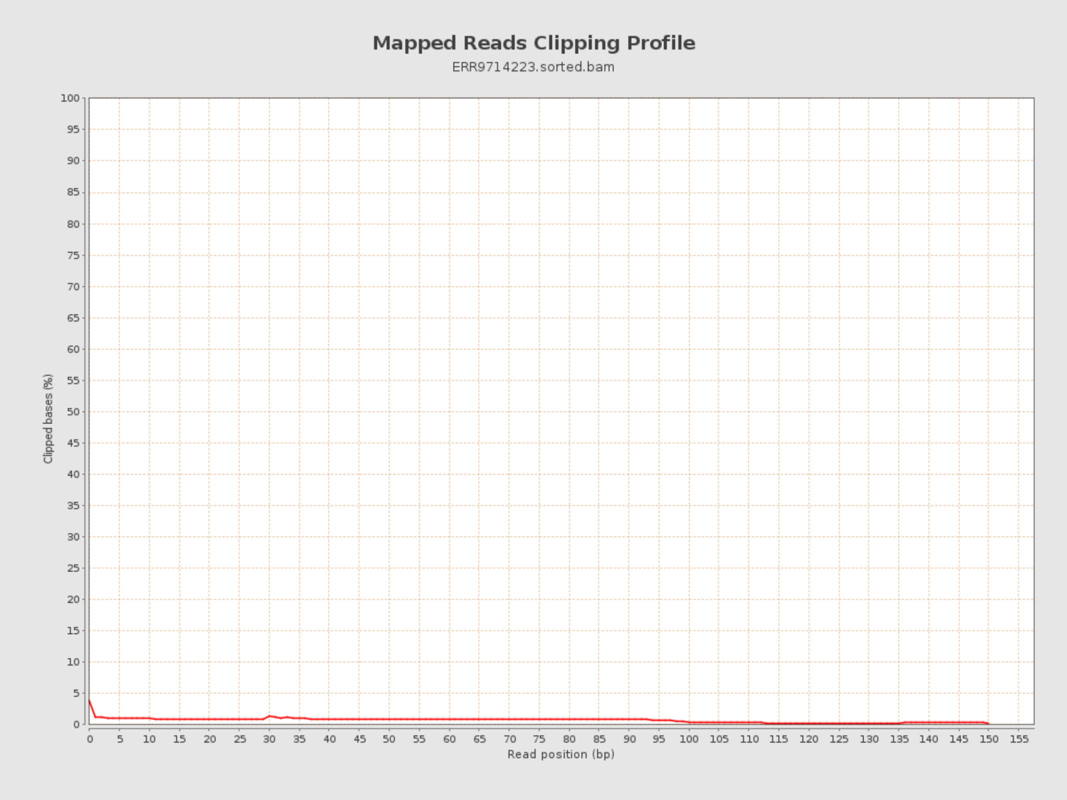
8. Results : Mapped Reads Nucleotide Content



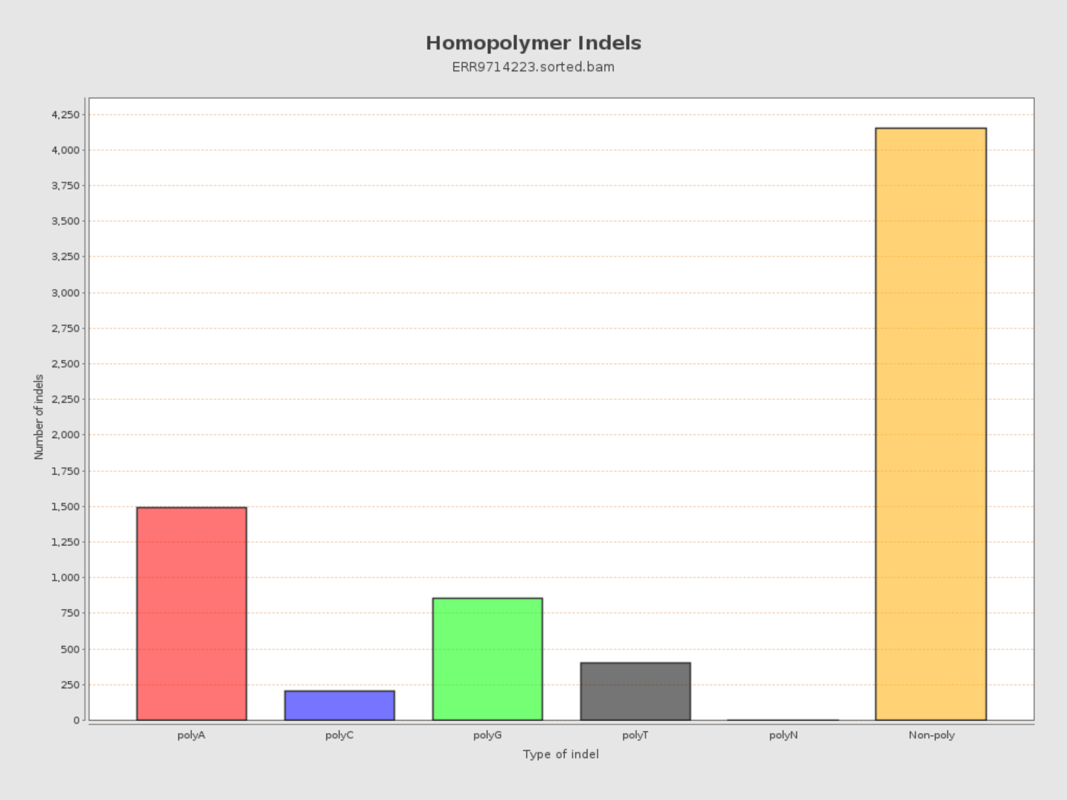
9. Results : Mapped Reads GC-content Distribution



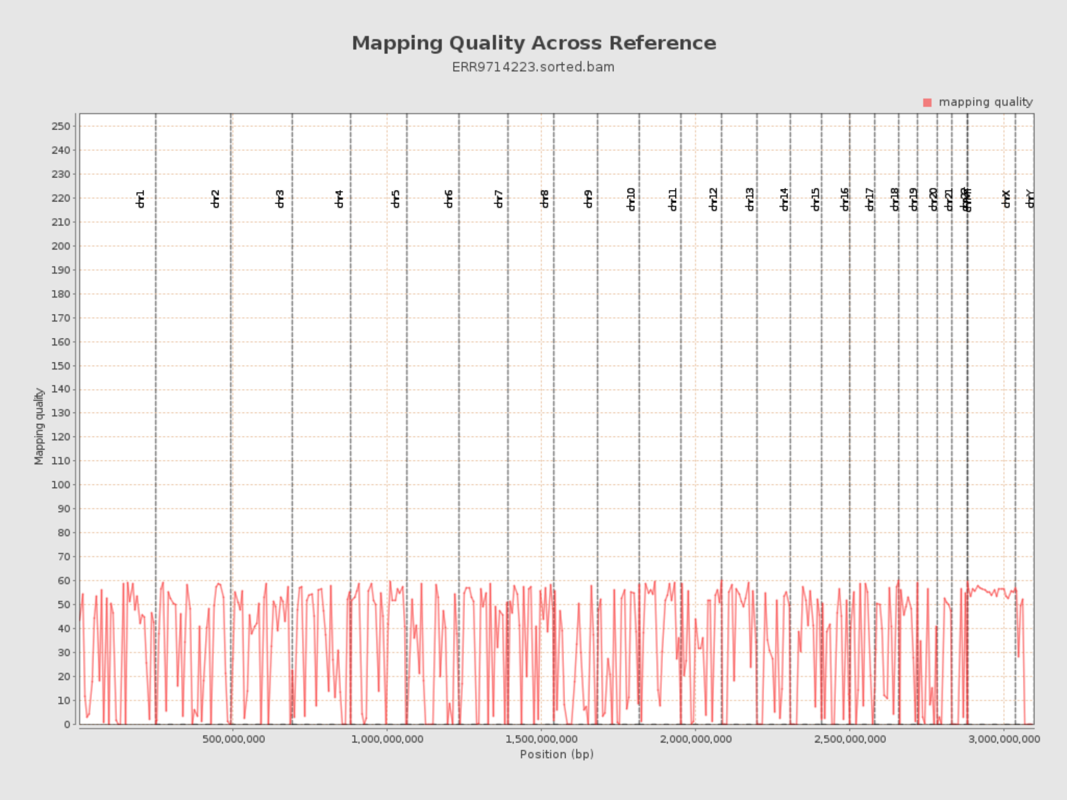
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram