Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 00:41:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714227.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_ERR9714227 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714227.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 00:41:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714227.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	234,302
Mapped reads	35,812 / 15.28%
Unmapped reads	198,490 / 84.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	808 / 0.34%
Read min/max/mean length	30 / 151 / 61.17
Duplicated reads (estimated)	34,881 / 14.89%
Duplication rate	34.16%
Clipped reads	19,796 / 8.45%

2.2. ACGT Content

Number/percentage of A's	113,672 / 3.17%
Number/percentage of C's	47,572 / 1.33%
Number/percentage of T's	67,198 / 1.87%
Number/percentage of G's	3,359,010 / 93.63%
Number/percentage of N's	54 / 0%
GC Percentage	94.96%

2.3. Coverage

Mean	0.0012

Standard Deviation	4.2438

2.4. Mapping Quality

Mean Mapping Quality	7.42

2.5. Mismatches and indels

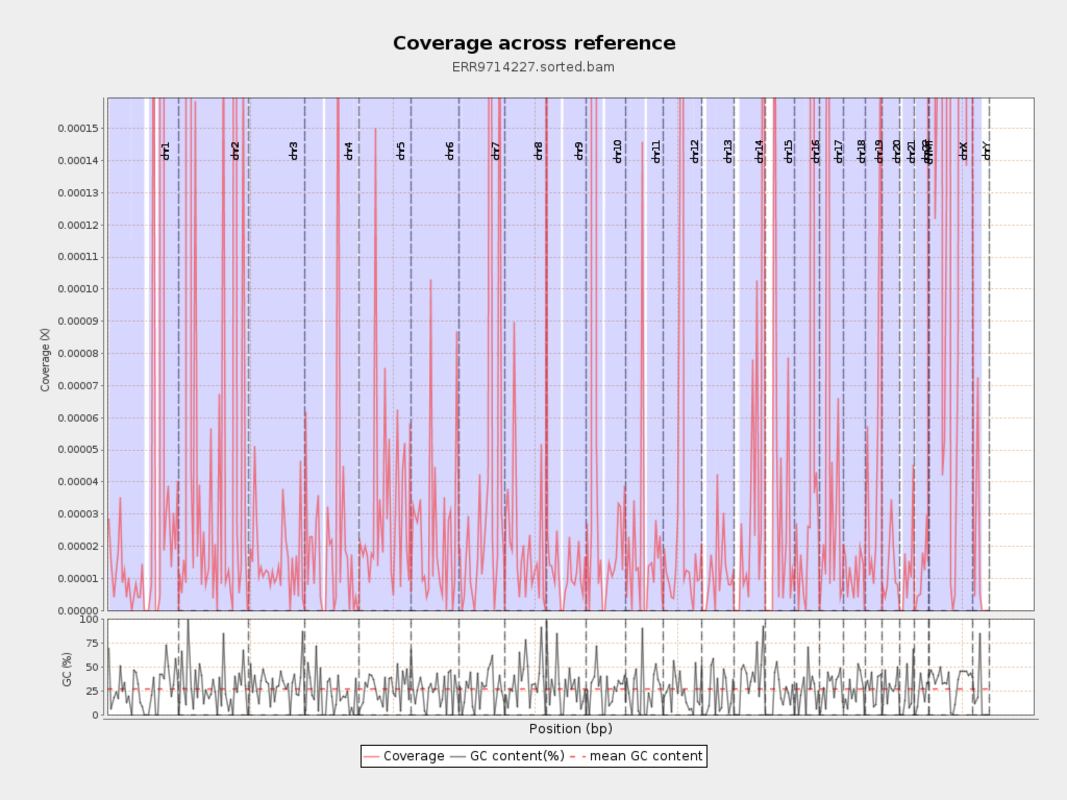
General error rate	3.33%
Mismatches	90,548
Insertions	4,156
Mapped reads with at least one insertion	7.9%
Deletions	2,004
Mapped reads with at least one deletion	5.33%
Homopolymer indels	62.45%

2.6. Chromosome stats

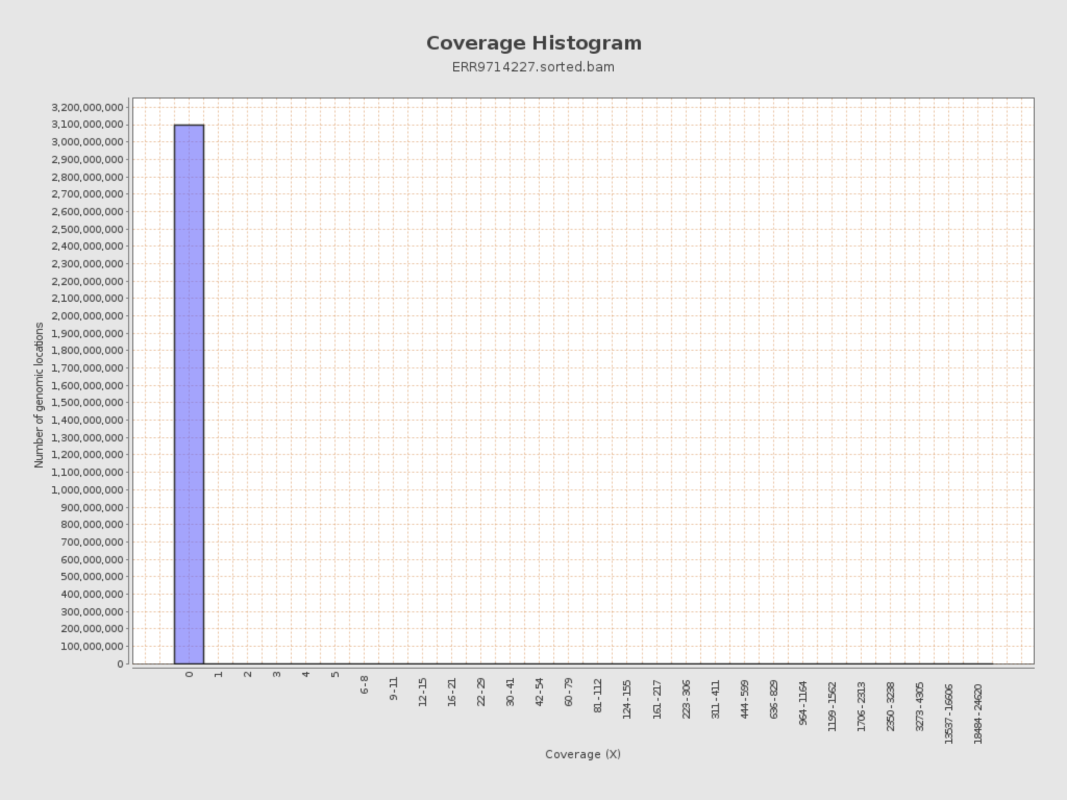
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	46154	0.0002	0.4779
chr2	243199373	3354727	0.0138	15.1258
chr3	198022430	3100	0	0.0054
chr4	191154276	4527	0	0.011
chr5	180915260	5788	0	0.0097
chr6	171115067	4201	0	0.0102
chr7	159138663	7507	0	0.043

chr8	146364022	3013	0	0.008
chr9	141213431	1921	0	0.006
chr10	135534747	41699	0.0003	0.6117
chr11	135006516	2713	0	0.0151
chr12	133851895	5690	0	0.0302
chr13	115169878	1316	0	0.0049
chr14	107349540	4895	0	0.0399
chr15	102531392	3620	0	0.015
chr16	90354753	12592	0.0001	0.0961
chr17	81195210	5217	0.0001	0.0646
chr18	78077248	861	0	0.0035
chr19	59128983	2912	0	0.0211
chr20	63025520	838	0	0.0046
chr21	48129895	589	0	0.0046
chr22	51304566	573	0	0.0043
chrMT	16571	1829	0.1104	0.6832
chrX	155270560	80372	0.0005	0.0987
chrY	59373566	740	0	0.0053

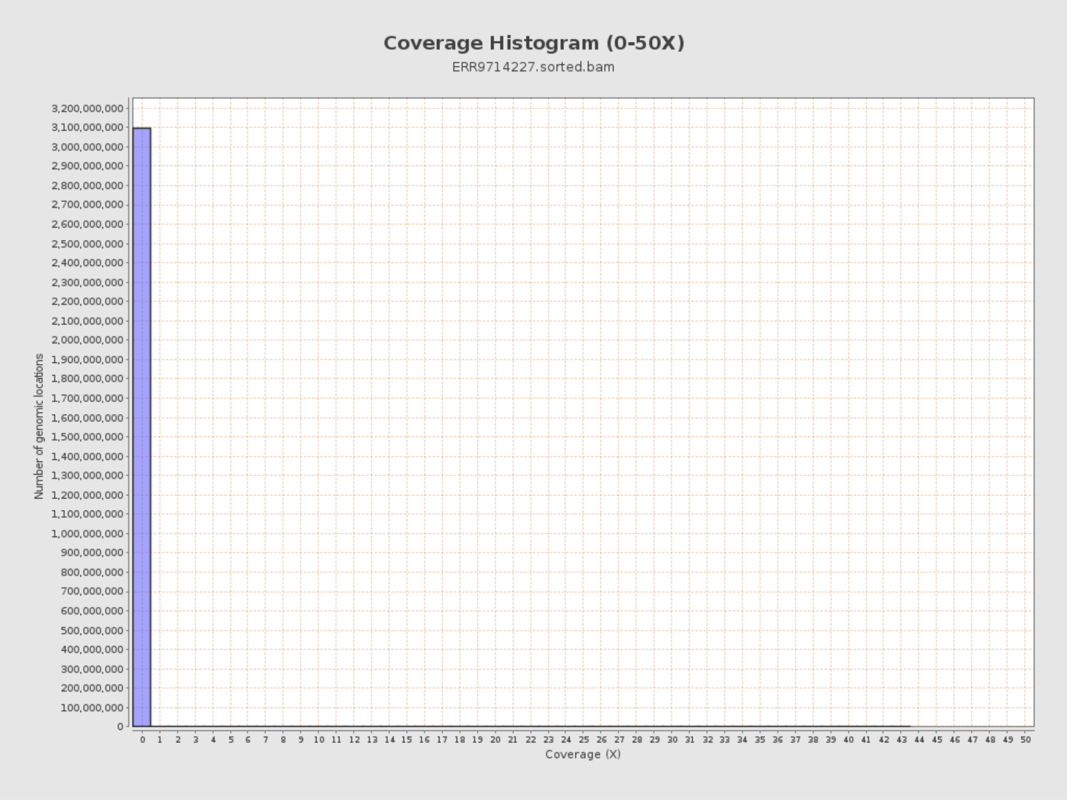
3. Results : Coverage across reference



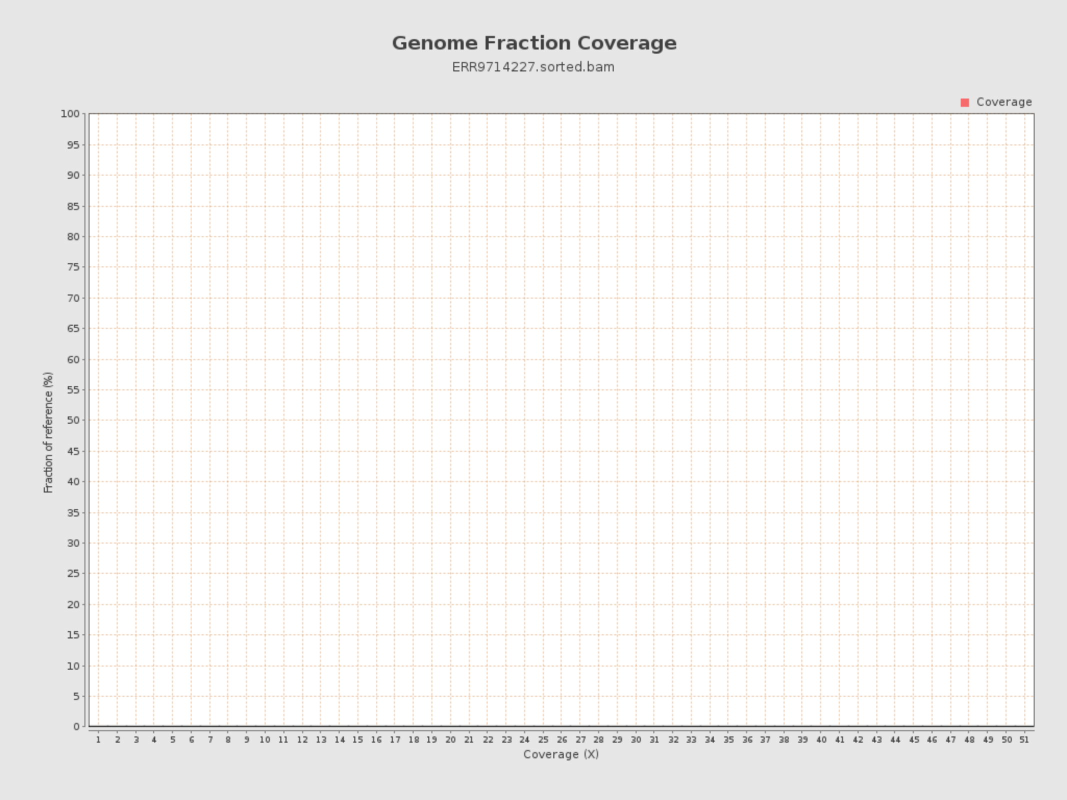
4. Results : Coverage Histogram



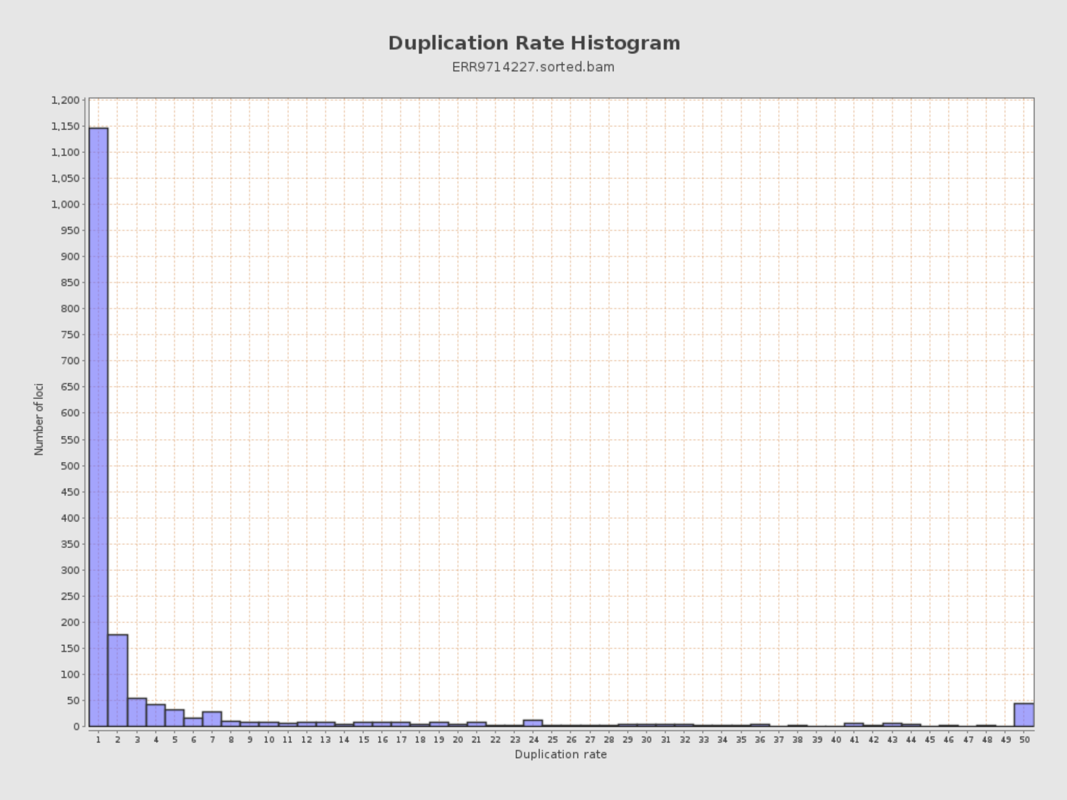
5. Results : Coverage Histogram (0-50X)



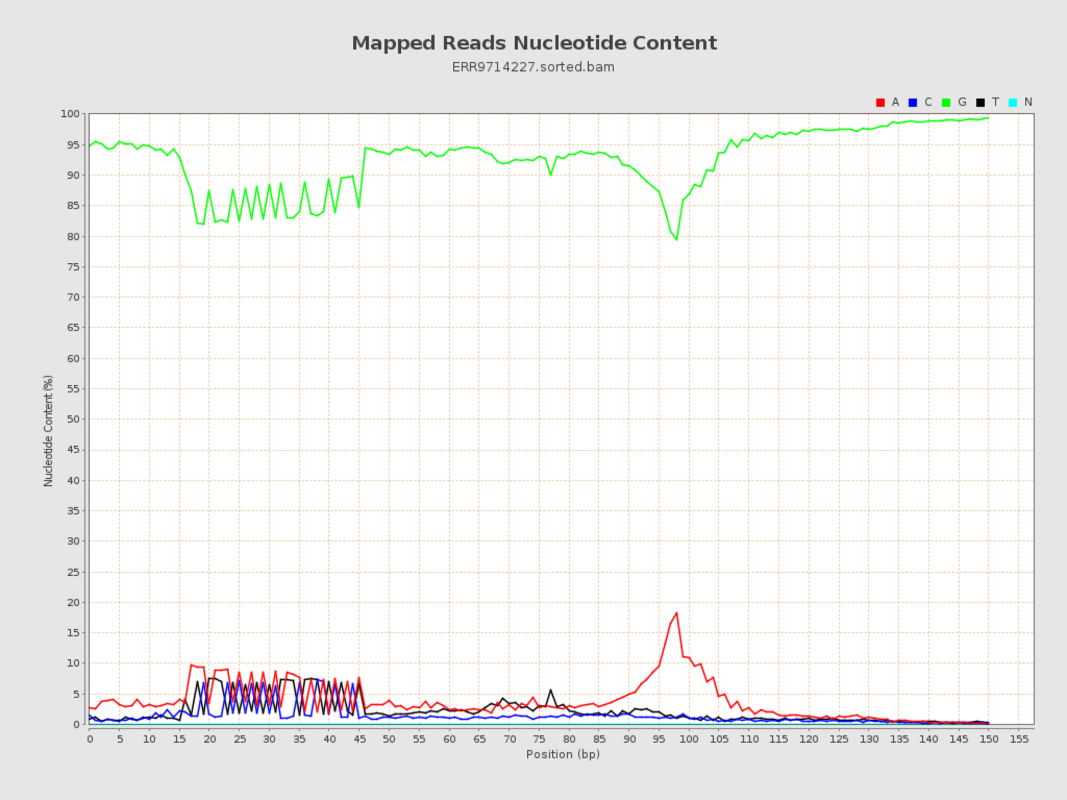
6. Results : Genome Fraction Coverage



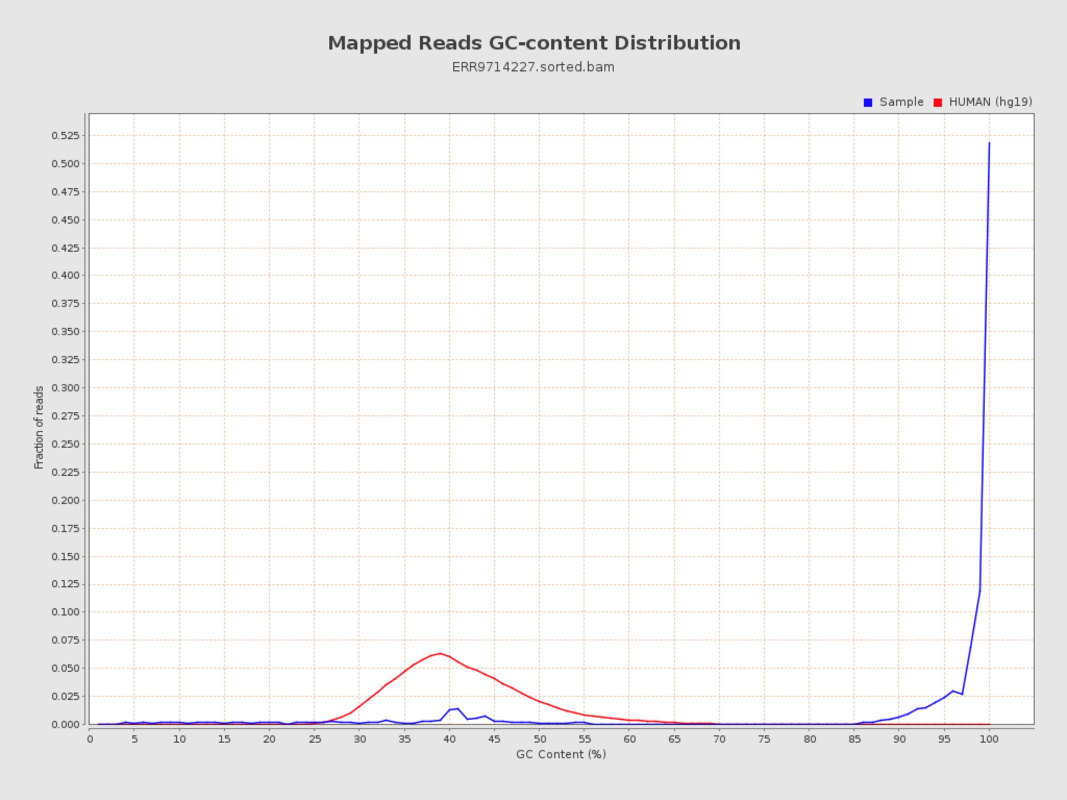
7. Results : Duplication Rate Histogram



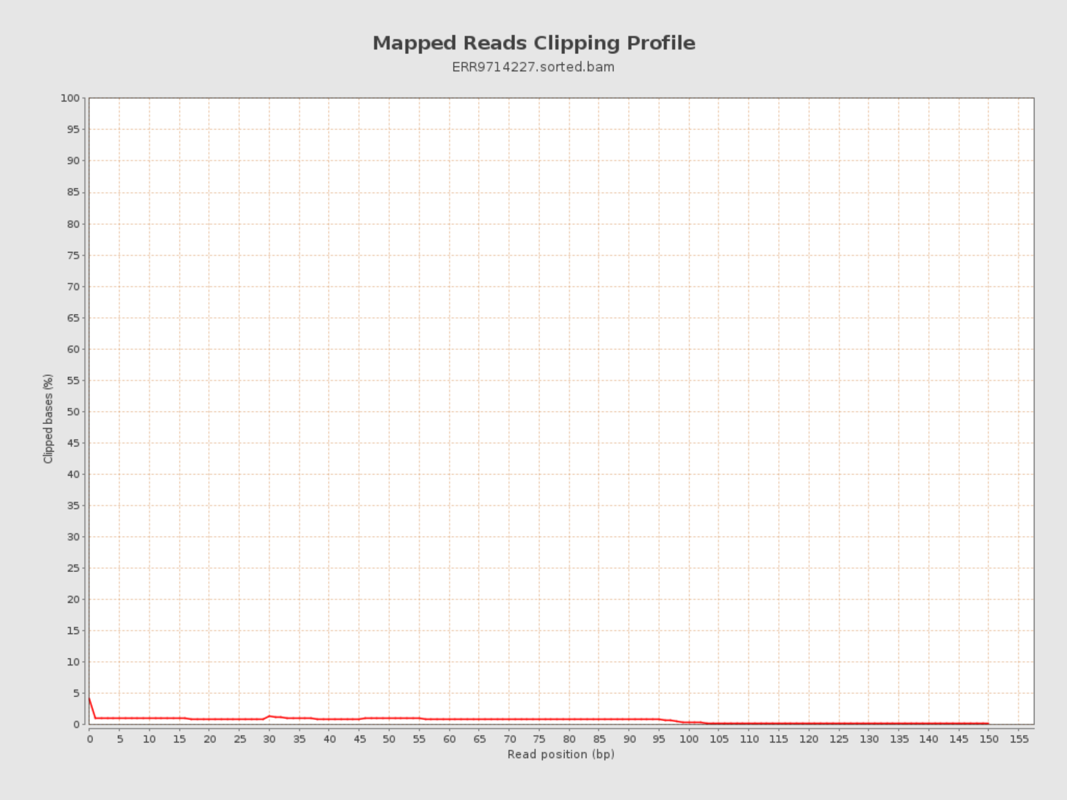
8. Results : Mapped Reads Nucleotide Content



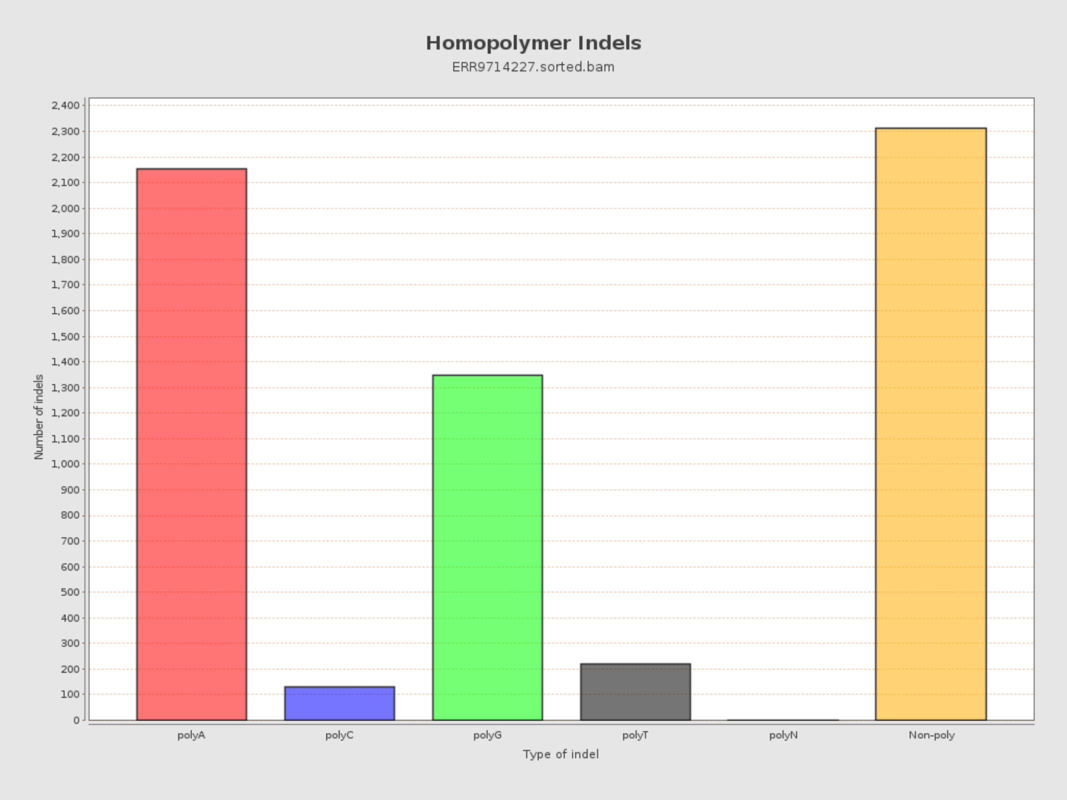
9. Results : Mapped Reads GC-content Distribution



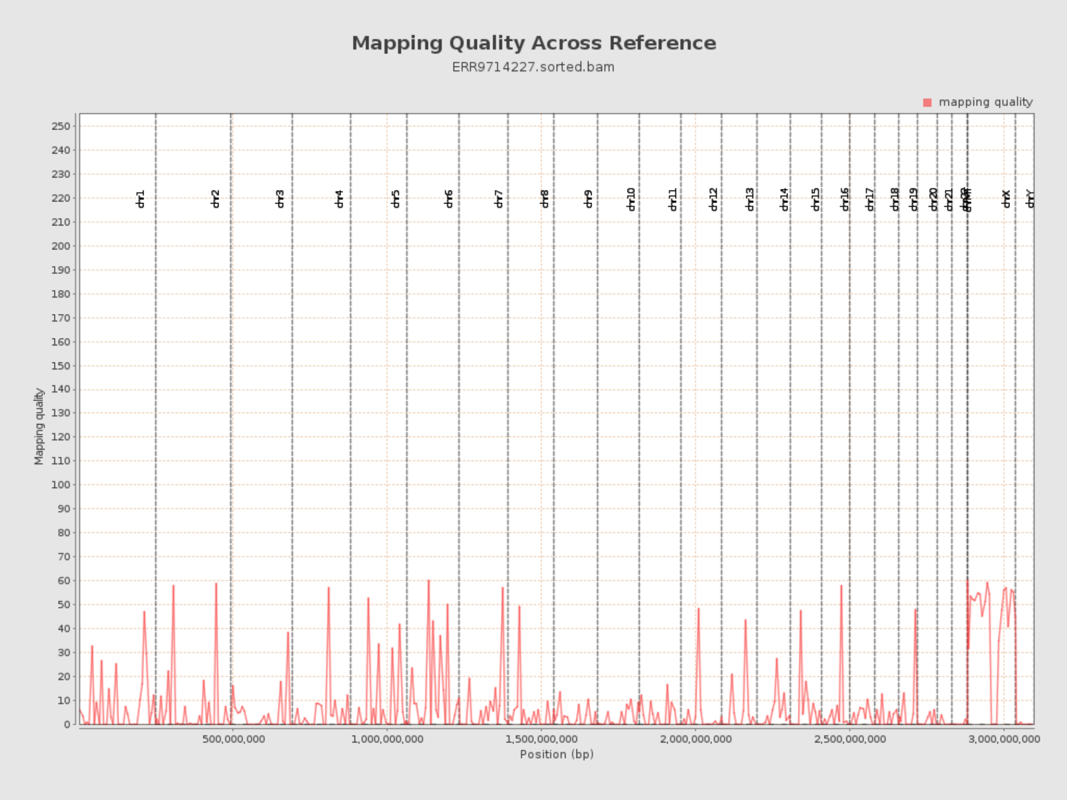
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram