Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 01:42:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714259.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_ERR9714259 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714259.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 01:42:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714259.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	432,796
Mapped reads	63,525 / 14.68%
Unmapped reads	369,271 / 85.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,151 / 0.27%
Read min/max/mean length	30 / 151 / 58.99
Duplicated reads (estimated)	62,558 / 14.45%
Duplication rate	32.91%
Clipped reads	34,876 / 8.06%

2.2. ACGT Content

Number/percentage of A's	156,681 / 2.45%
Number/percentage of C's	64,001 / 1%
Number/percentage of T's	79,223 / 1.24%
Number/percentage of G's	6,082,292 / 95.3%
Number/percentage of N's	131 / 0%
GC Percentage	96.3%

2.3. Coverage

Mean	0.0021

Standard Deviation	7.8782

2.4. Mapping Quality

Mean Mapping Quality	7.67

2.5. Mismatches and indels

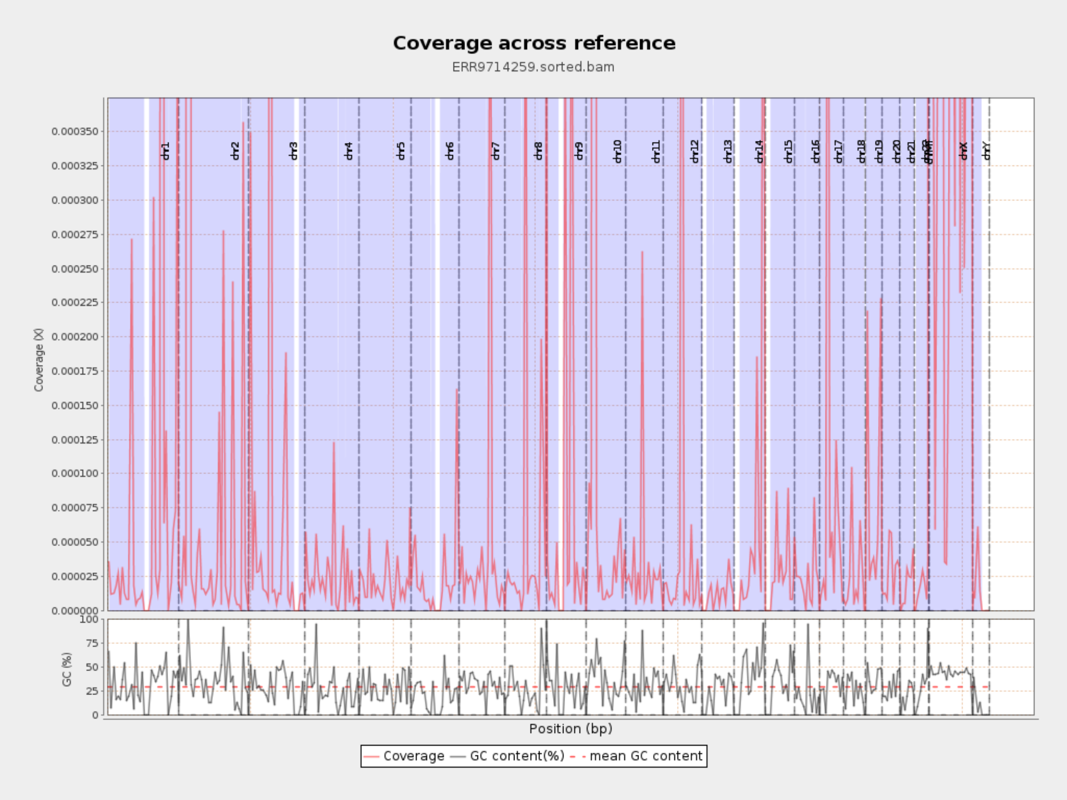
General error rate	3.15%
Mismatches	154,731
Insertions	6,553
Mapped reads with at least one insertion	7.25%
Deletions	3,008
Mapped reads with at least one deletion	4.55%
Homopolymer indels	63.88%

2.6. Chromosome stats

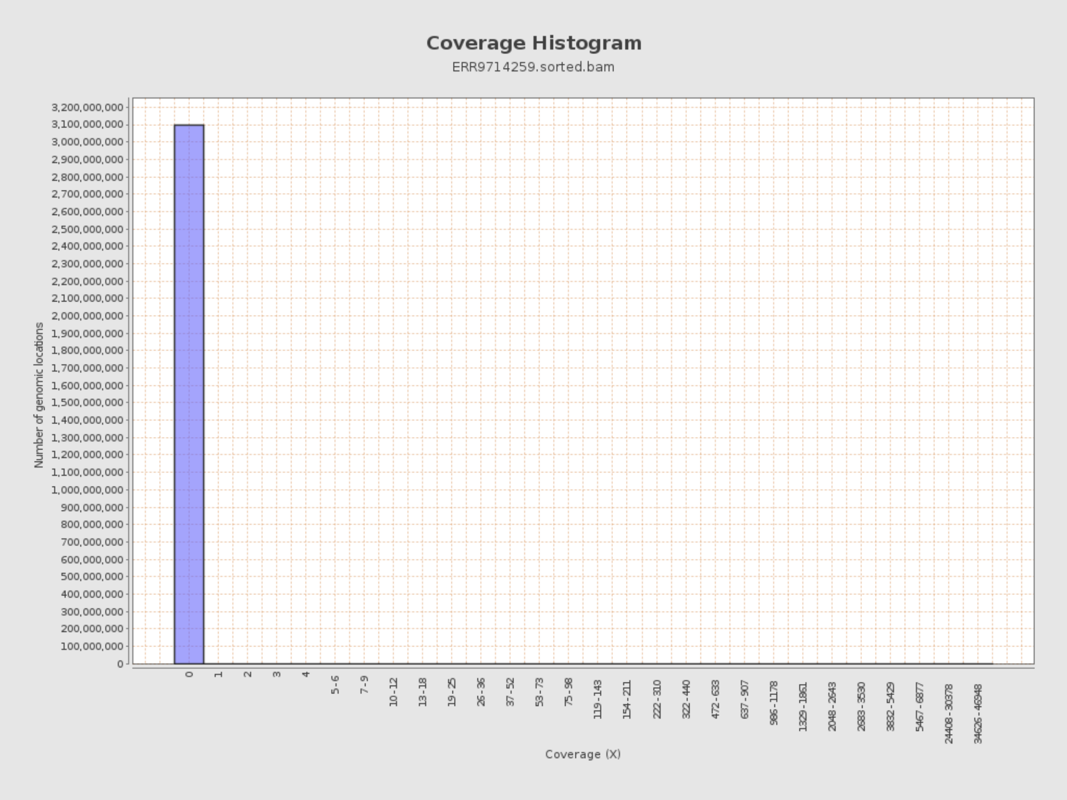
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	55026	0.0002	0.4849
chr2	243199373	6087751	0.025	28.0988
chr3	198022430	16973	0.0001	0.0568
chr4	191154276	4862	0	0.0102
chr5	180915260	3760	0	0.006
chr6	171115067	4078	0	0.0122
chr7	159138663	8160	0.0001	0.057

chr8	146364022	8808	0.0001	0.0363
chr9	141213431	10321	0.0001	0.0396
chr10	135534747	45768	0.0003	0.6395
chr11	135006516	4658	0	0.0251
chr12	133851895	8772	0.0001	0.0594
chr13	115169878	1350	0	0.0058
chr14	107349540	8563	0.0001	0.0889
chr15	102531392	2734	0	0.0127
chr16	90354753	2329	0	0.0076
chr17	81195210	9011	0.0001	0.1046
chr18	78077248	1996	0	0.015
chr19	59128983	4804	0.0001	0.022
chr20	63025520	1790	0	0.0112
chr21	48129895	920	0	0.0049
chr22	51304566	745	0	0.0048
chrMT	16571	4182	0.2524	1.8982
chrX	155270560	97651	0.0006	0.1194
chrY	59373566	734	0	0.0055

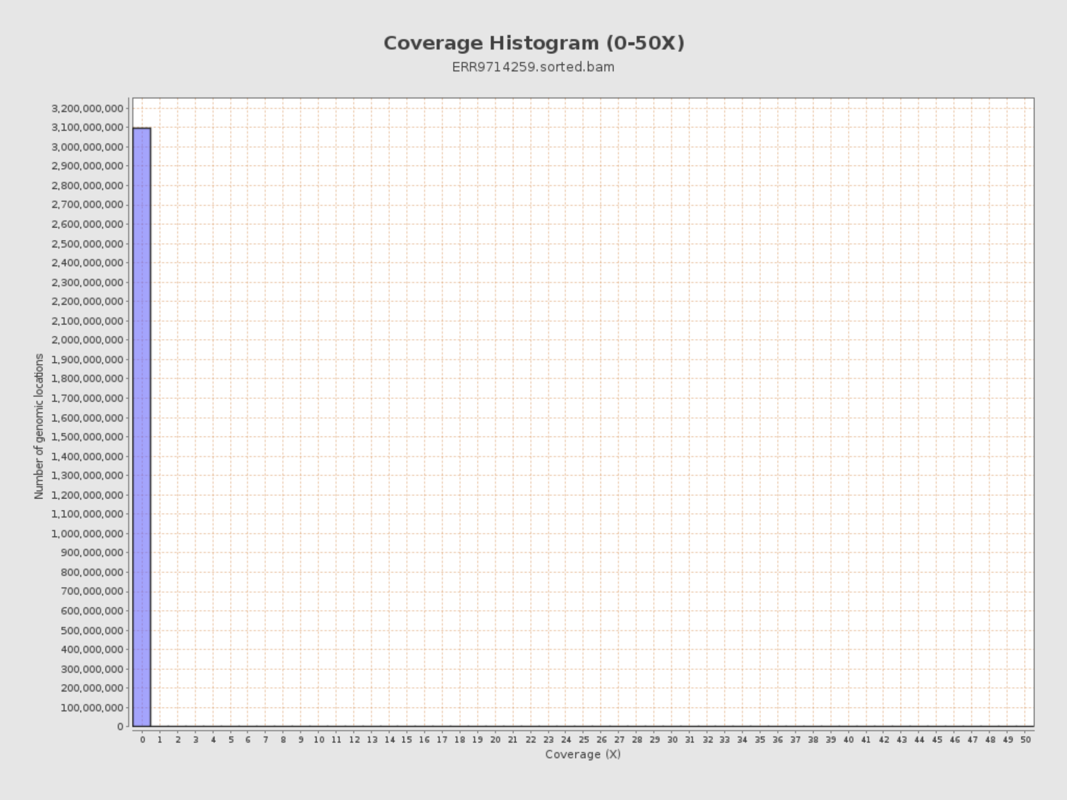
3. Results : Coverage across reference



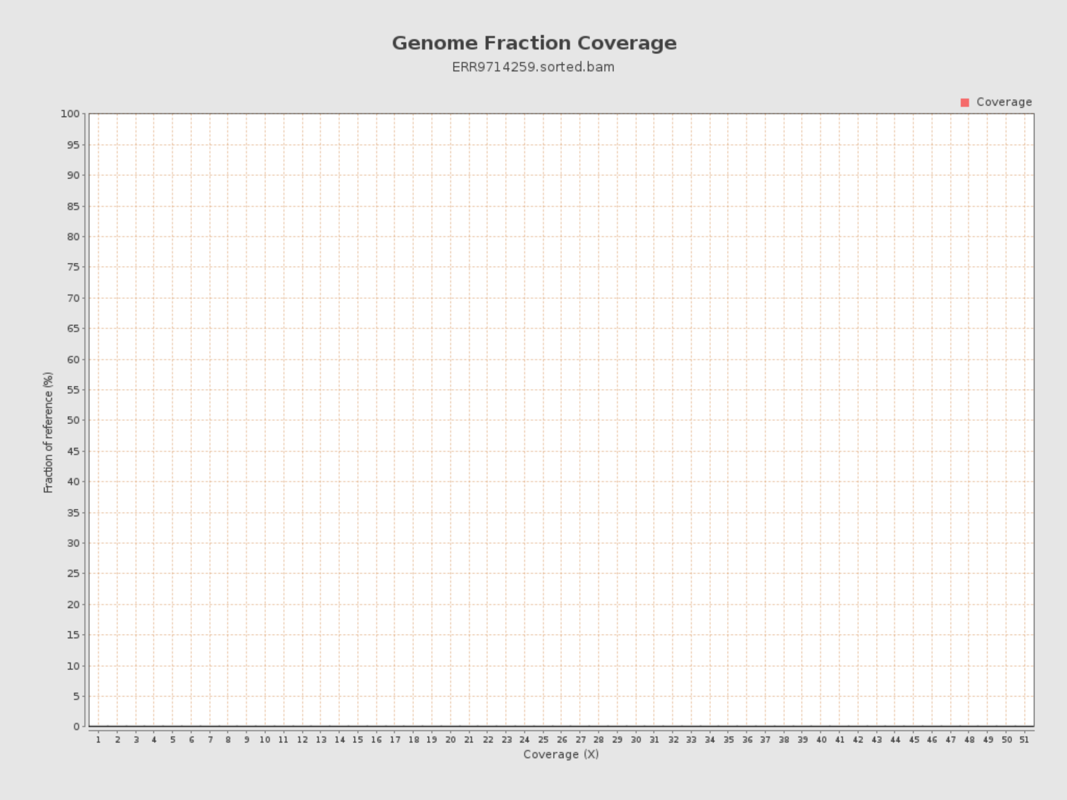
4. Results : Coverage Histogram



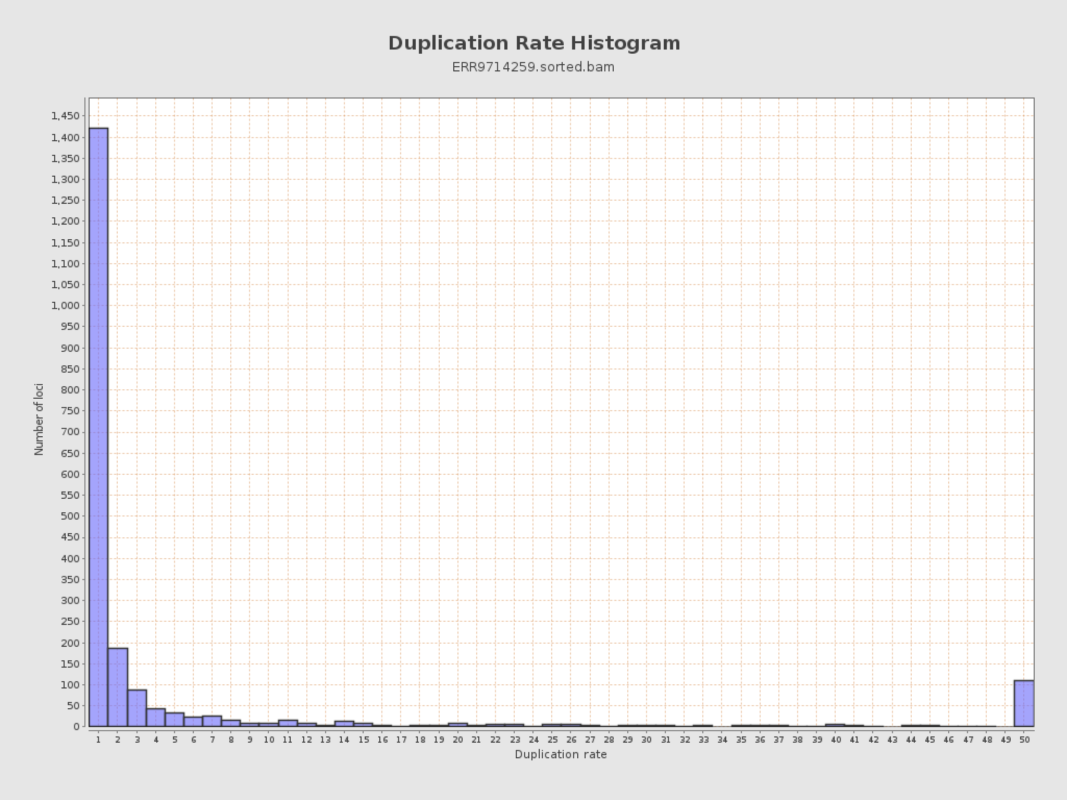
5. Results : Coverage Histogram (0-50X)



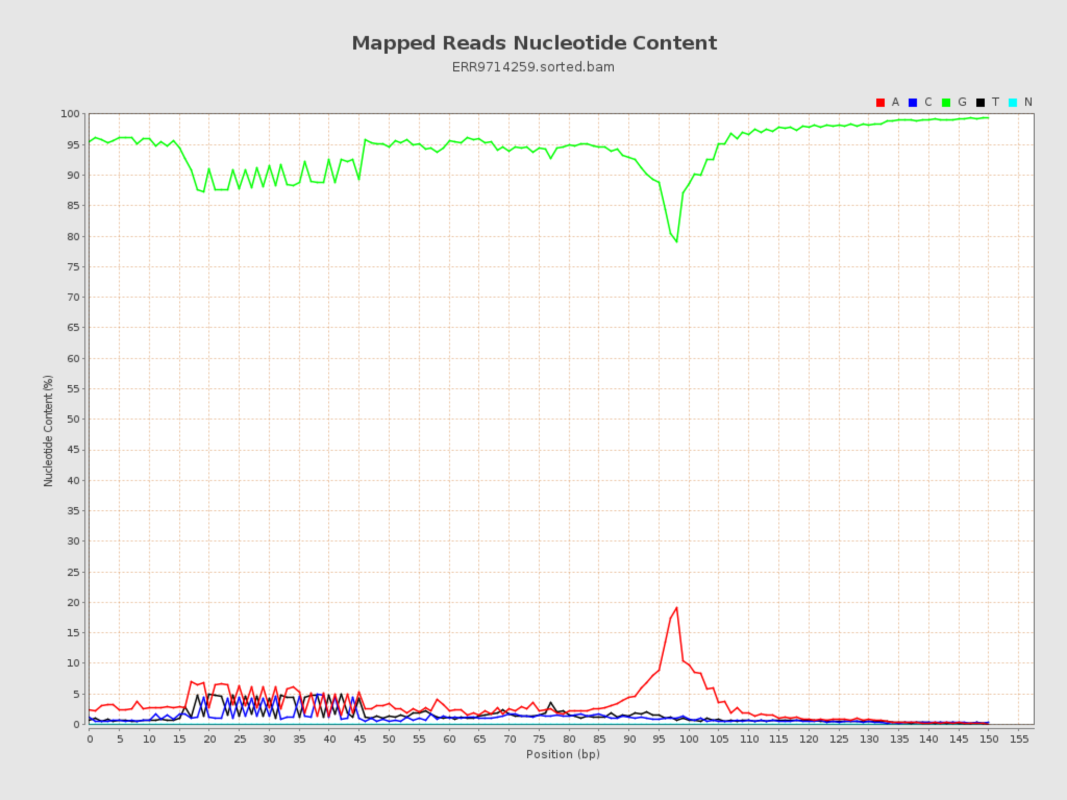
6. Results : Genome Fraction Coverage



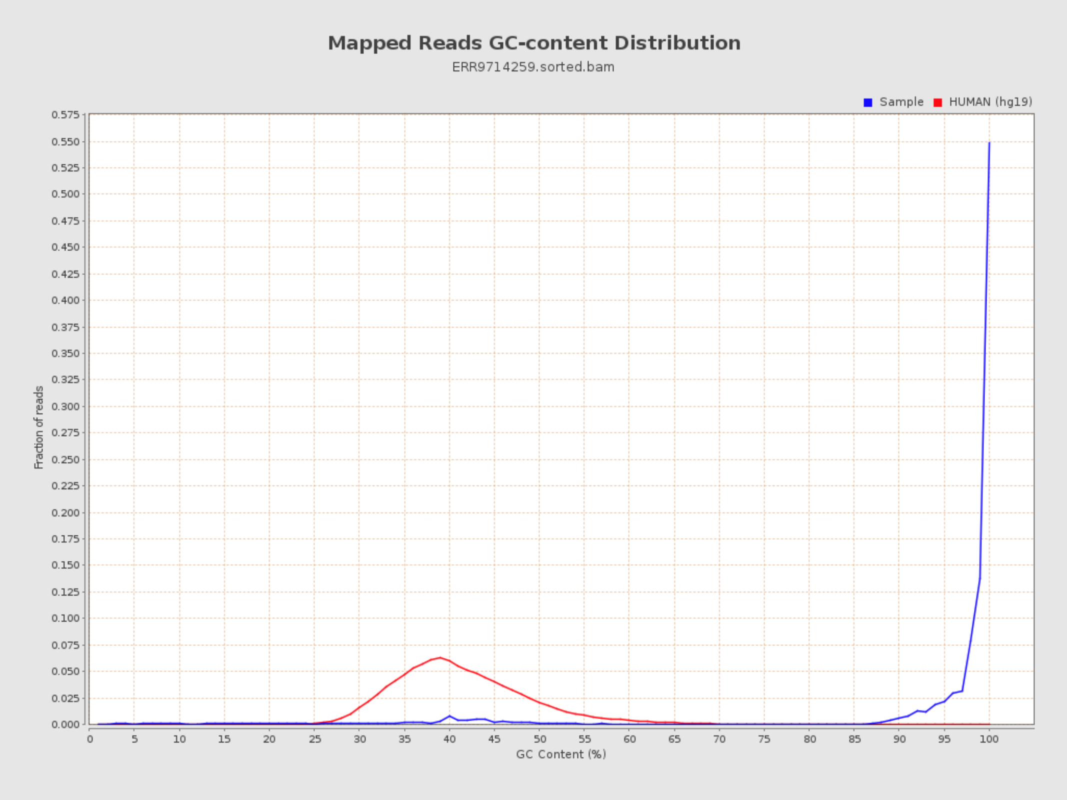
7. Results : Duplication Rate Histogram



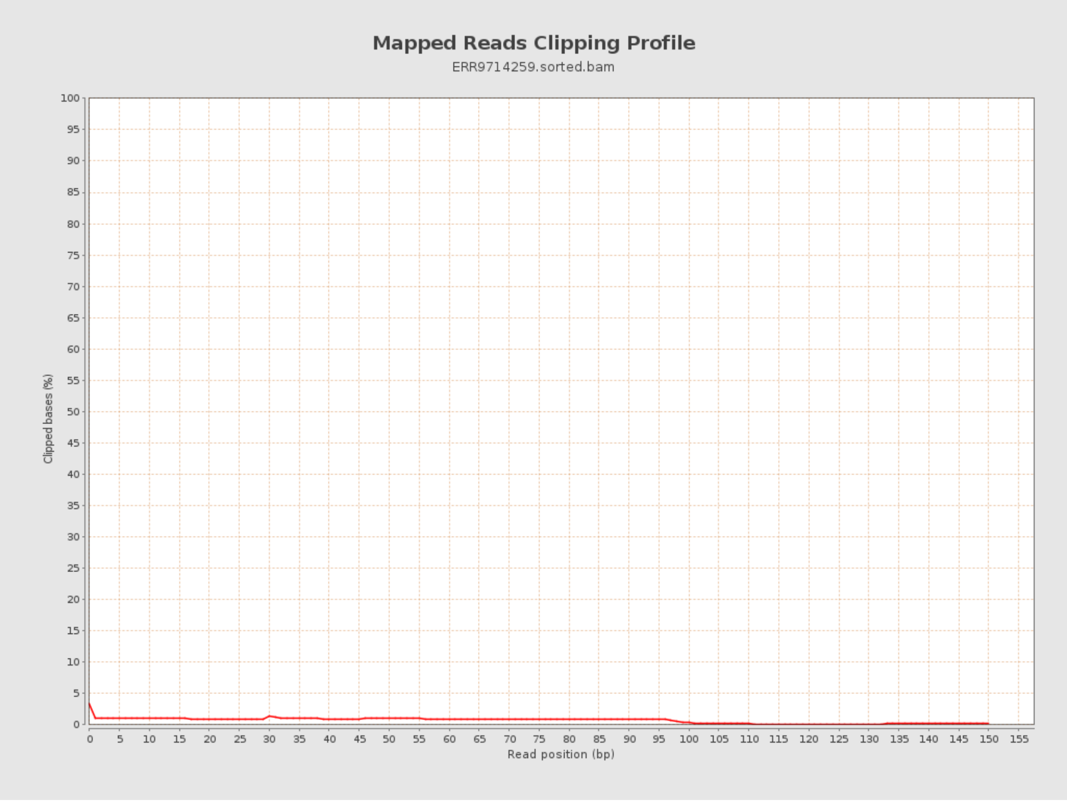
8. Results : Mapped Reads Nucleotide Content



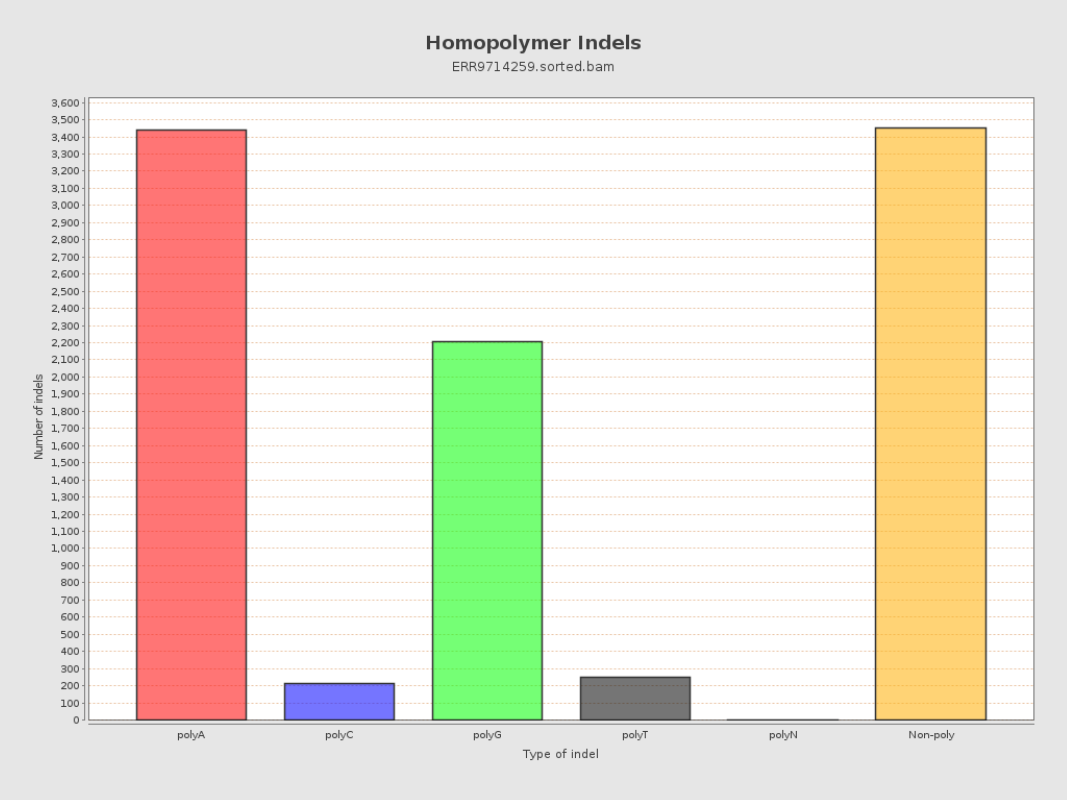
9. Results : Mapped Reads GC-content Distribution



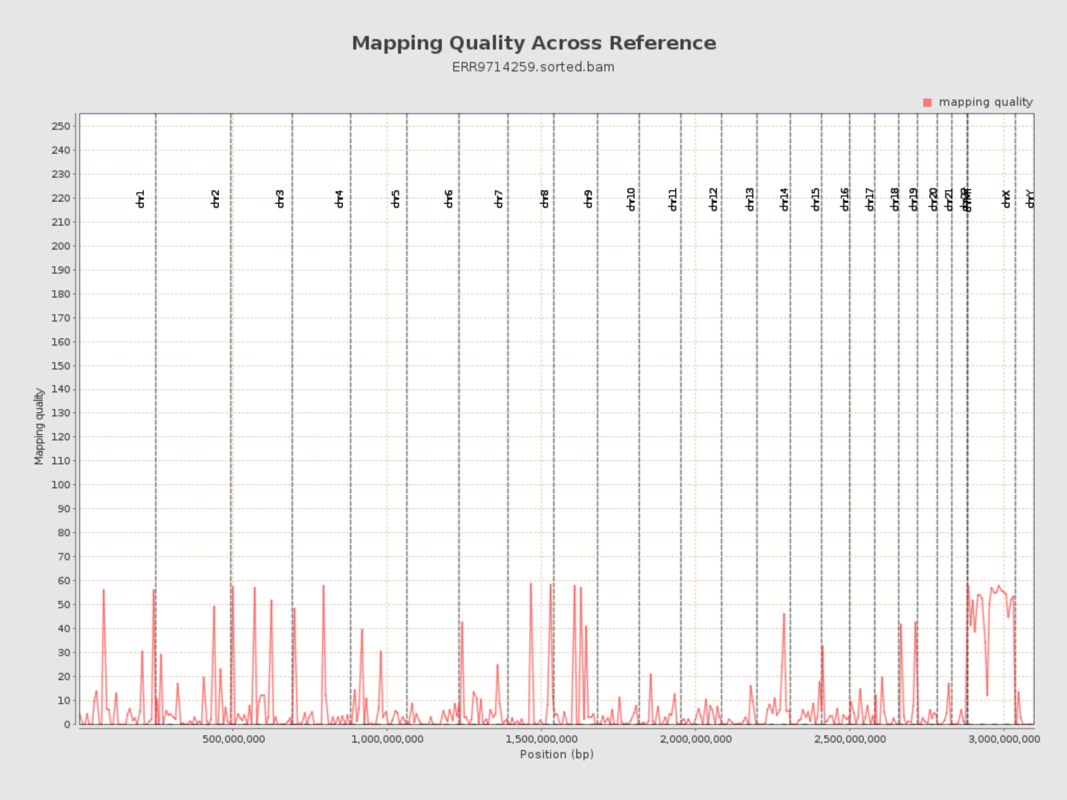
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram