Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 17:14:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714045.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_ERR9714045 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714045.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 17:14:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714045.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	492
Mapped reads	212 / 43.09%
Unmapped reads	280 / 56.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4 / 0.81%
Read min/max/mean length	31 / 151 / 90.23
Duplicated reads (estimated)	133 / 27.03%
Duplication rate	22.89%
Clipped reads	118 / 23.98%

2.2. ACGT Content

Number/percentage of A's	2,173 / 8.62%
Number/percentage of C's	1,721 / 6.83%
Number/percentage of T's	1,918 / 7.61%
Number/percentage of G's	19,383 / 76.93%
Number/percentage of N's	0 / 0%
GC Percentage	83.76%

2.3. Coverage

Mean	0

Standard Deviation	0.0218

2.4. Mapping Quality

Mean Mapping Quality	4.27

2.5. Mismatches and indels

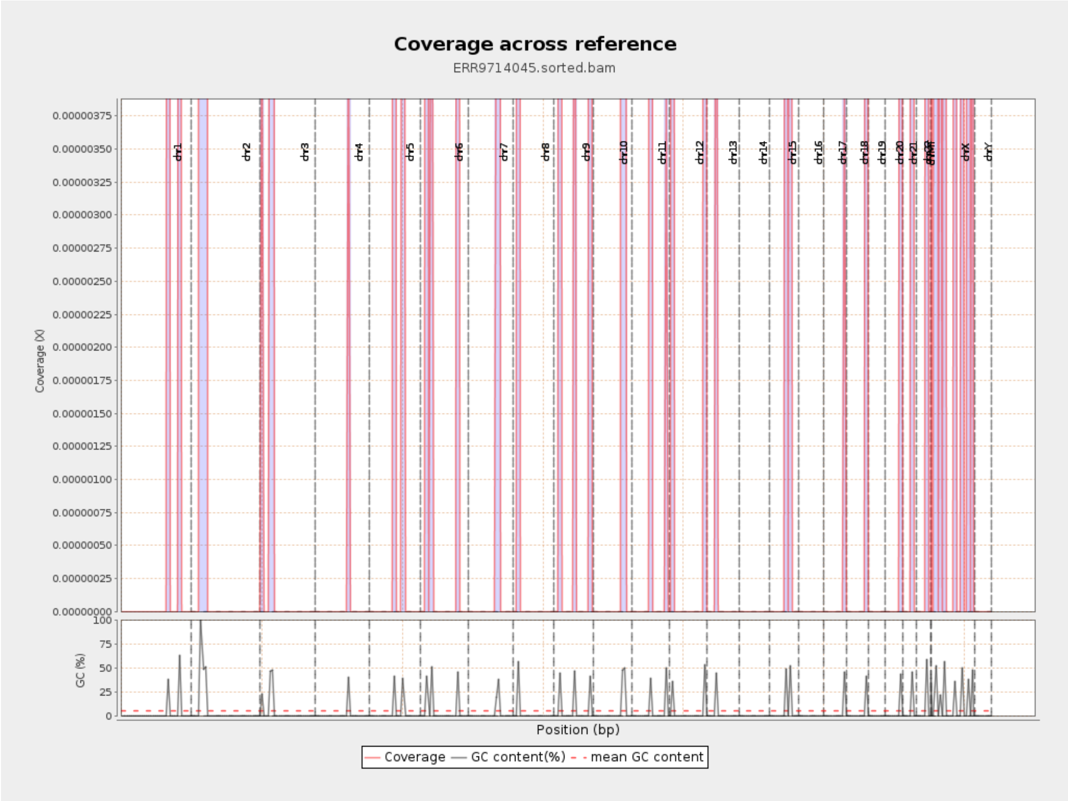
General error rate	2.73%
Mismatches	583
Insertions	18
Mapped reads with at least one insertion	7.08%
Deletions	21
Mapped reads with at least one deletion	9.91%
Homopolymer indels	43.59%

2.6. Chromosome stats

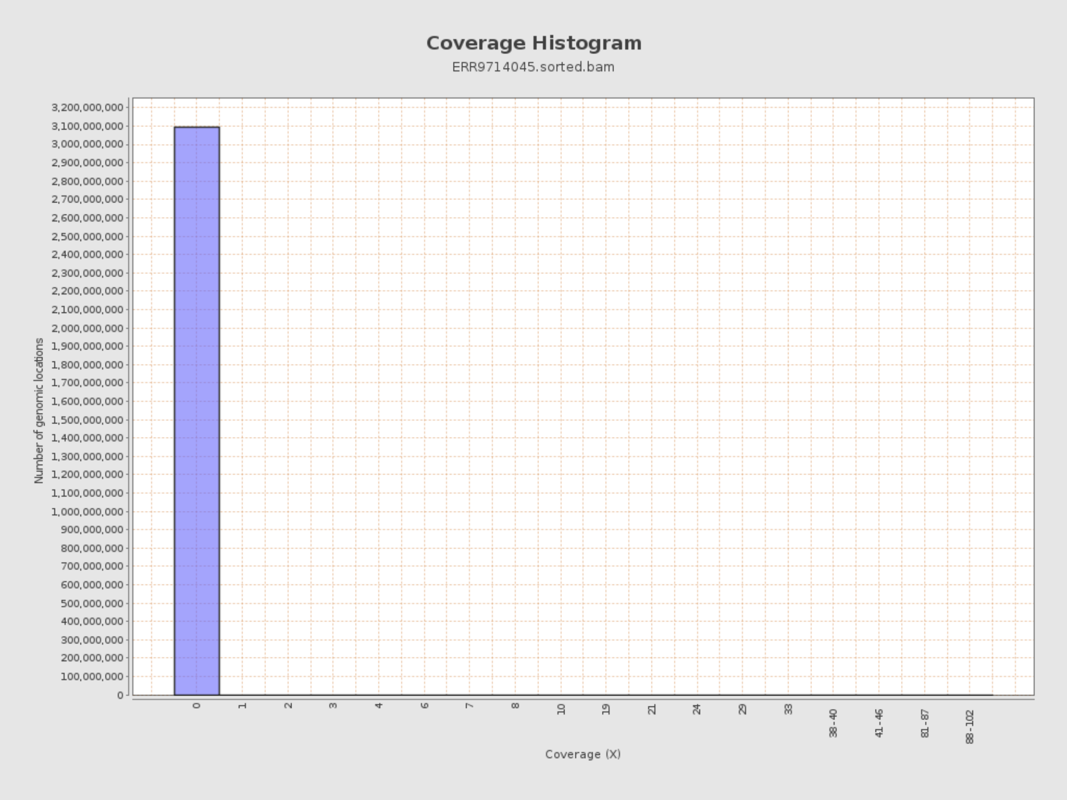
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	356	0	0.0014
chr2	243199373	18143	0.0001	0.0776
chr3	198022430	386	0	0.0018
chr4	191154276	35	0	0.0004
chr5	180915260	373	0	0.0019
chr6	171115067	579	0	0.0025
chr7	159138663	337	0	0.0019

chr8	146364022	293	0	0.0019
chr9	141213431	632	0	0.0028
chr10	135534747	745	0	0.0035
chr11	135006516	315	0	0.0021
chr12	133851895	573	0	0.003
chr13	115169878	56	0	0.0007
chr14	107349540	0	0	0
chr15	102531392	307	0	0.0019
chr16	90354753	0	0	0
chr17	81195210	31	0	0.0006
chr18	78077248	120	0	0.0012
chr19	59128983	0	0	0
chr20	63025520	140	0	0.0015
chr21	48129895	272	0	0.0033
chr22	51304566	210	0	0.0026
chrMT	16571	150	0.0091	0.0944
chrX	155270560	1216	0	0.0032
chrY	59373566	0	0	0

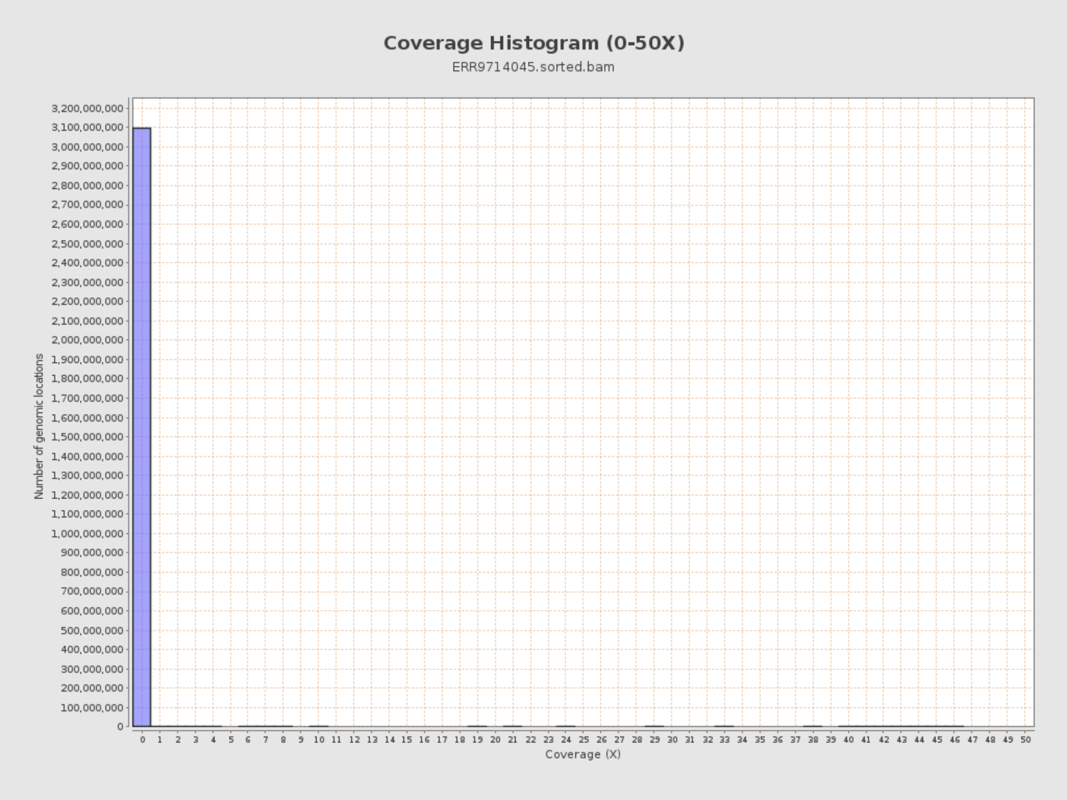
3. Results : Coverage across reference



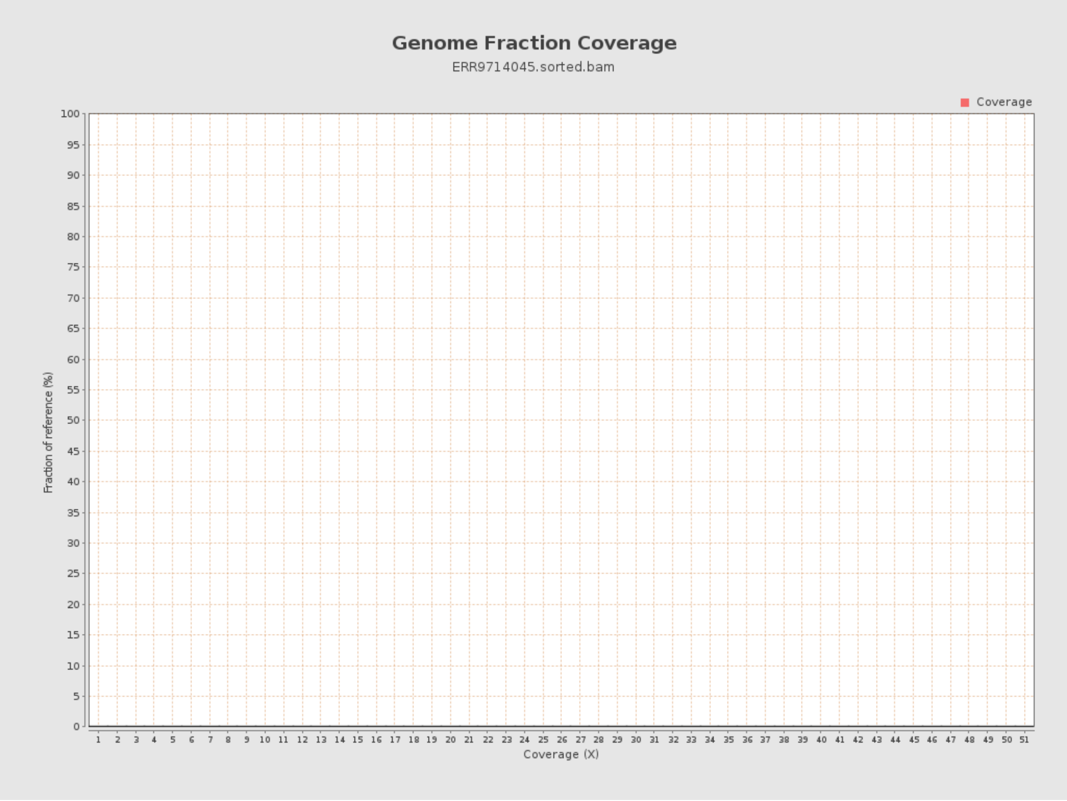
4. Results : Coverage Histogram



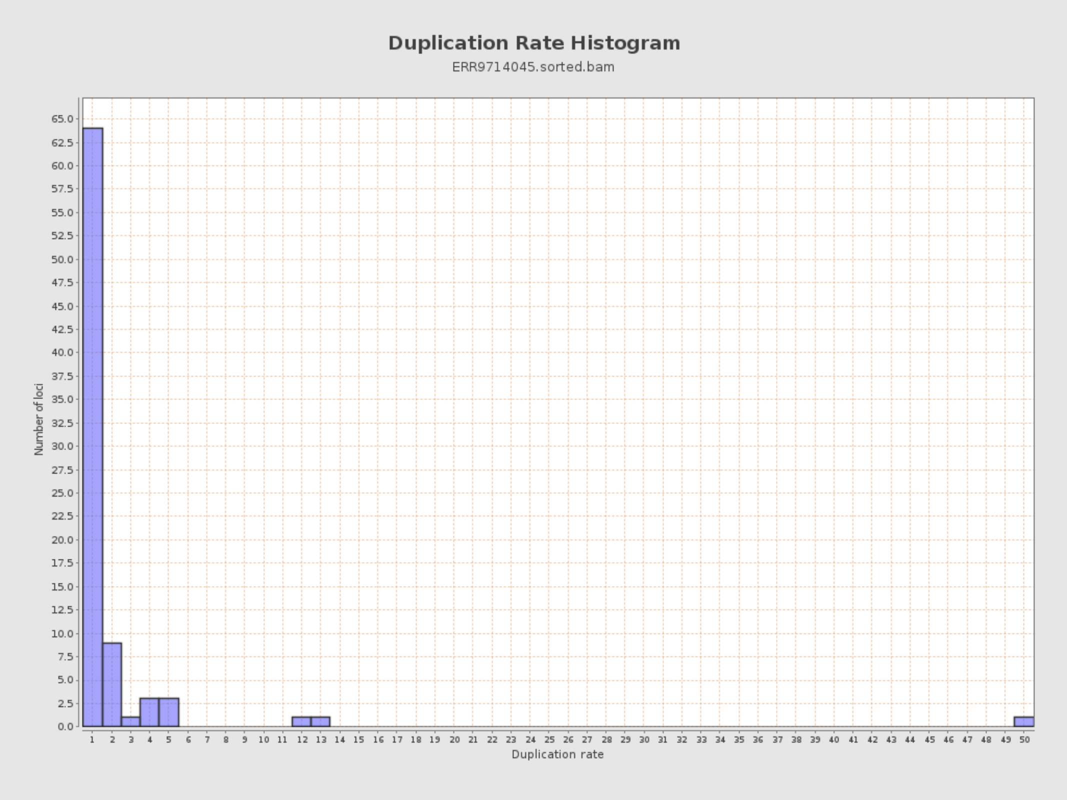
5. Results : Coverage Histogram (0-50X)



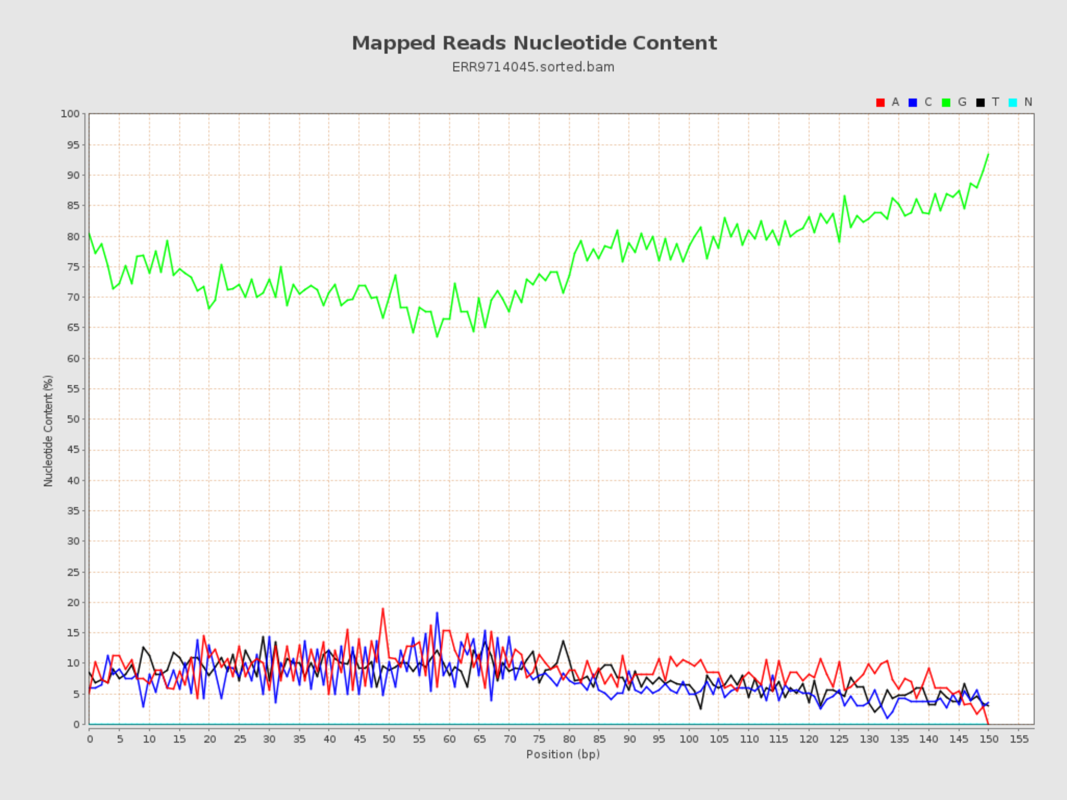
6. Results : Genome Fraction Coverage



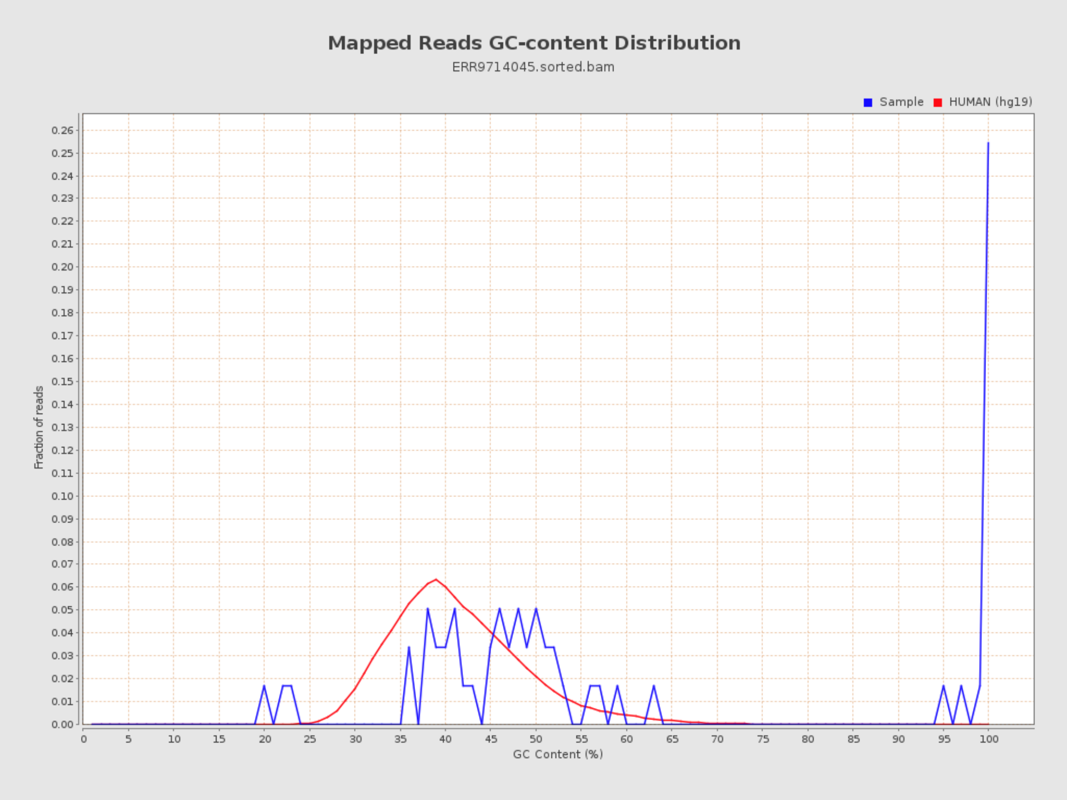
7. Results : Duplication Rate Histogram



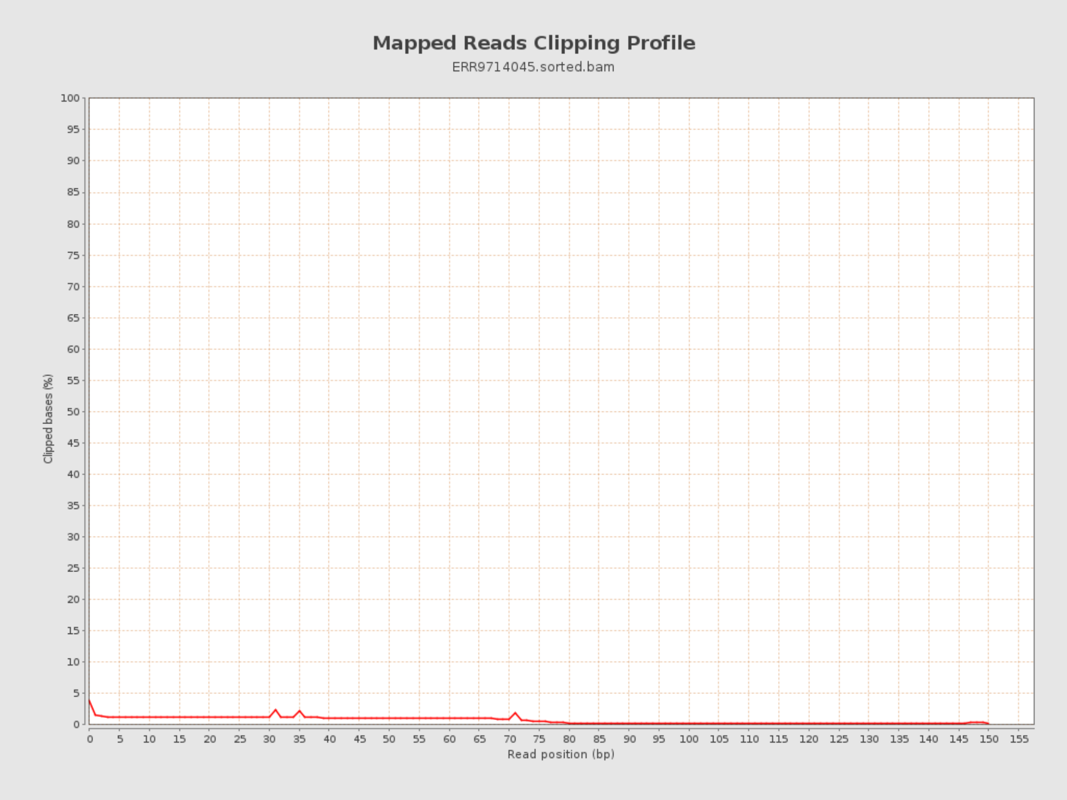
8. Results : Mapped Reads Nucleotide Content



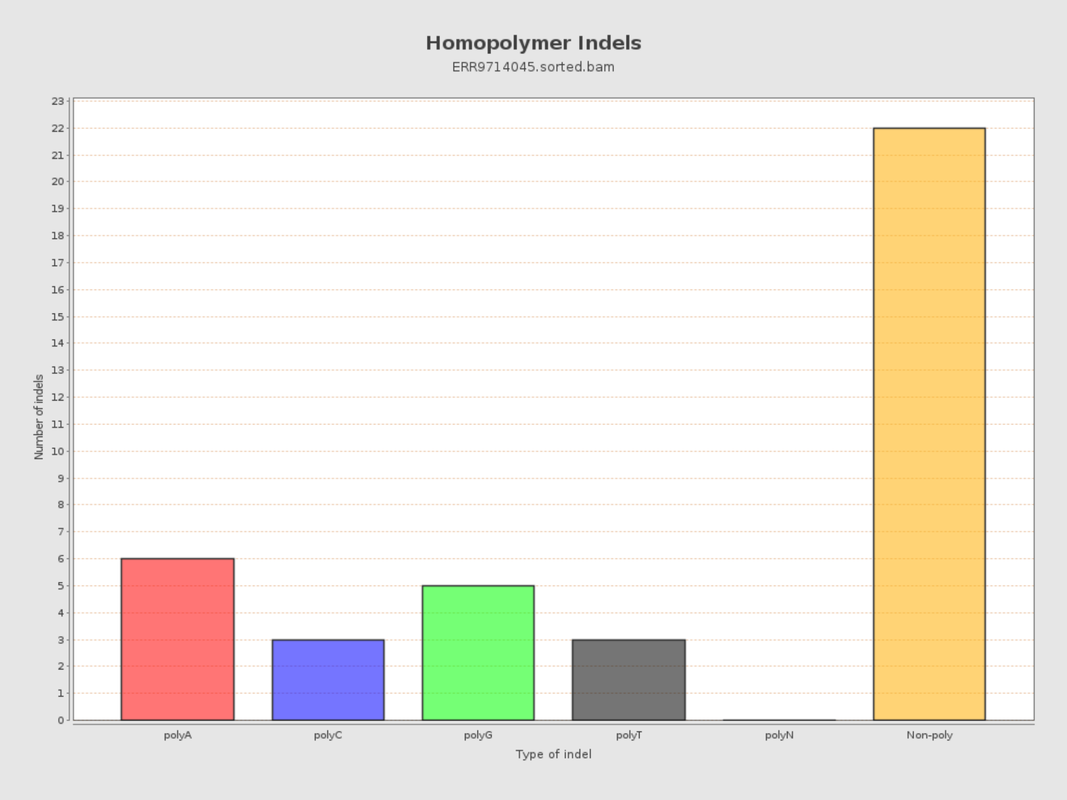
9. Results : Mapped Reads GC-content Distribution



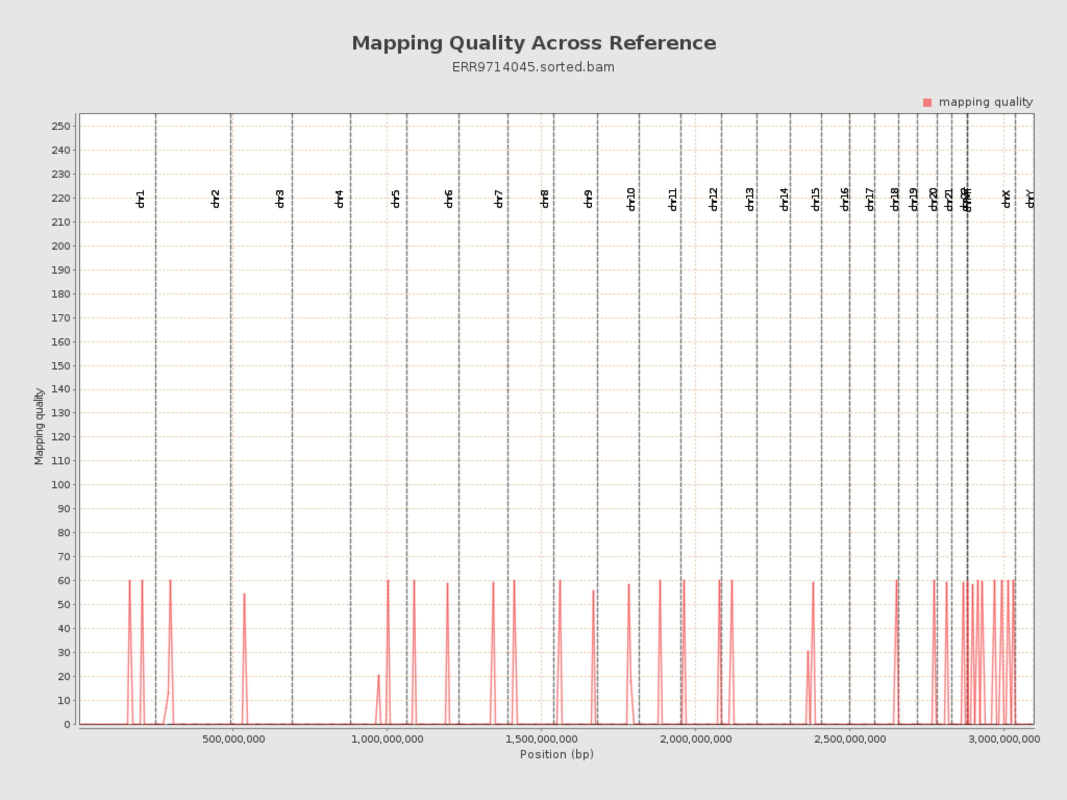
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram