Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 17:45:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714059.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_ERR9714059 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714059.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 17:45:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714059.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	517,250
Mapped reads	91,073 / 17.61%
Unmapped reads	426,177 / 82.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,637 / 0.32%
Read min/max/mean length	30 / 151 / 64.98
Duplicated reads (estimated)	89,609 / 17.32%
Duplication rate	29.15%
Clipped reads	48,753 / 9.43%

2.2. ACGT Content

Number/percentage of A's	243,015 / 2.63%
Number/percentage of C's	95,330 / 1.03%
Number/percentage of T's	130,090 / 1.41%
Number/percentage of G's	8,781,222 / 94.93%
Number/percentage of N's	210 / 0%
GC Percentage	95.96%

2.3. Coverage

Mean	0.003

Standard Deviation	11.3794

2.4. Mapping Quality

Mean Mapping Quality	12.85

2.5. Mismatches and indels

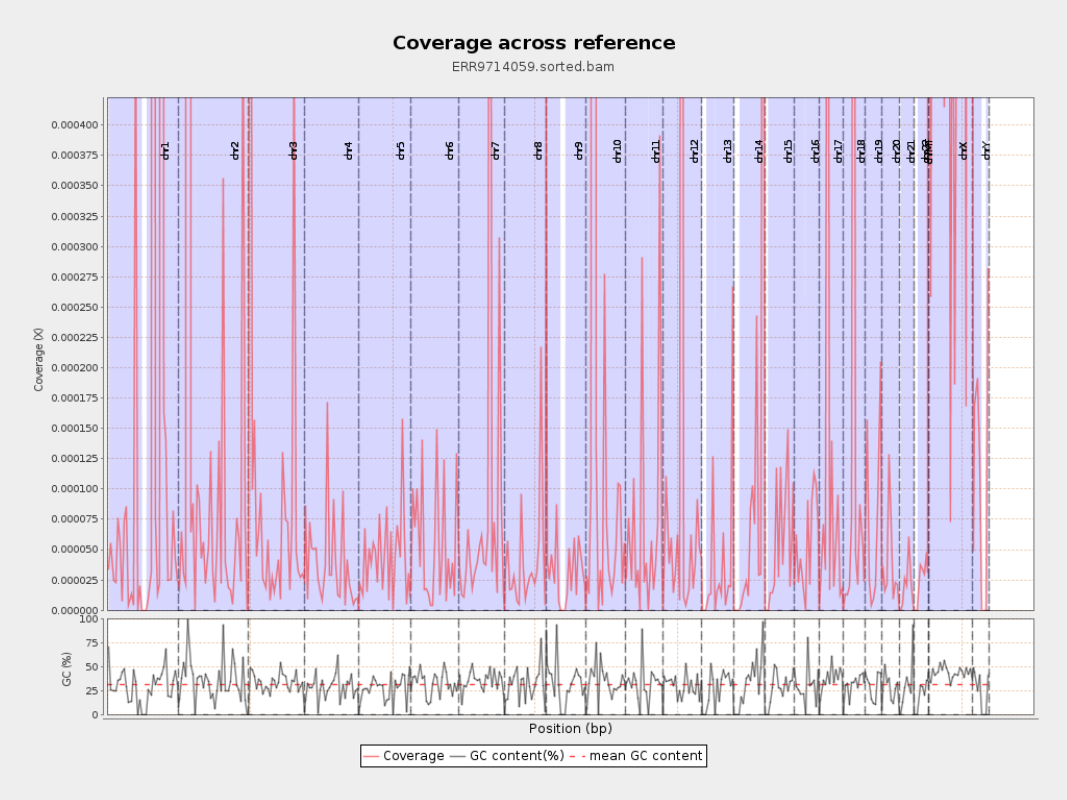
General error rate	3.13%
Mismatches	225,031
Insertions	9,539
Mapped reads with at least one insertion	7.13%
Deletions	4,099
Mapped reads with at least one deletion	4.34%
Homopolymer indels	63.57%

2.6. Chromosome stats

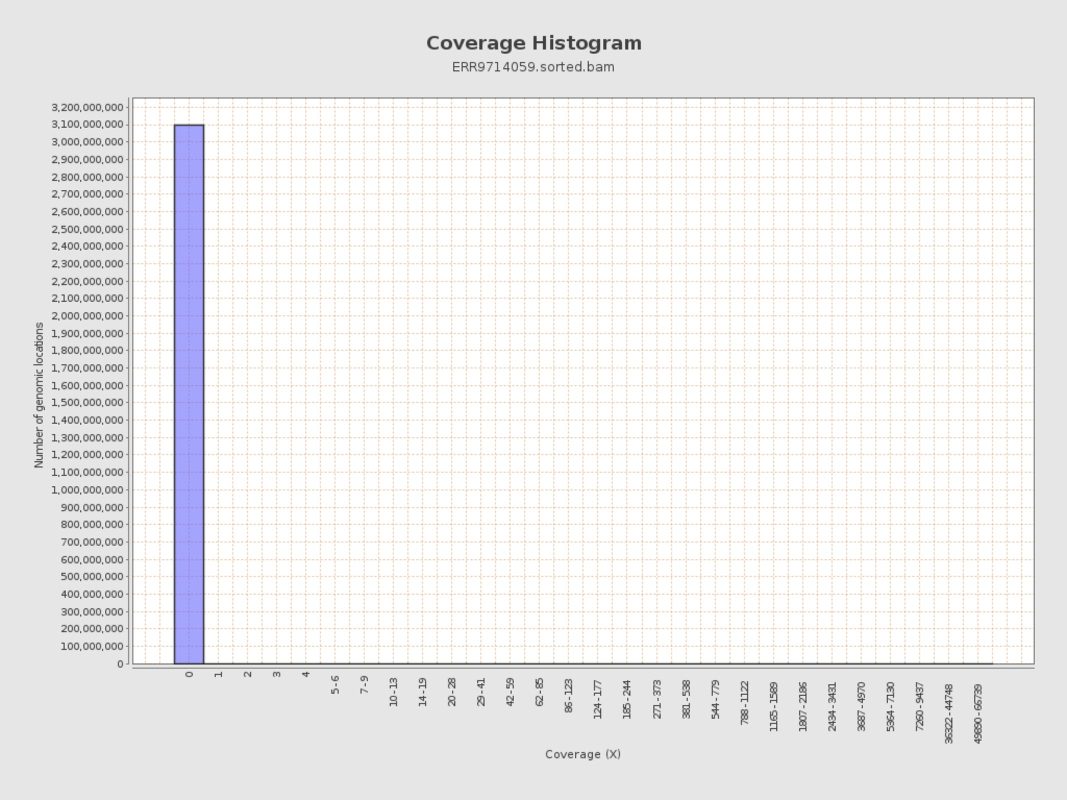
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	110949	0.0004	0.8006
chr2	243199373	8775621	0.0361	40.5834
chr3	198022430	20971	0.0001	0.0566
chr4	191154276	7558	0	0.0112
chr5	180915260	8202	0	0.0103
chr6	171115067	9041	0.0001	0.0161
chr7	159138663	16208	0.0001	0.1048

chr8	146364022	6033	0	0.0171
chr9	141213431	4644	0	0.0128
chr10	135534747	72870	0.0005	1.0117
chr11	135006516	9797	0.0001	0.036
chr12	133851895	17398	0.0001	0.1063
chr13	115169878	4469	0	0.0158
chr14	107349540	12013	0.0001	0.1226
chr15	102531392	5649	0.0001	0.0199
chr16	90354753	5037	0.0001	0.0152
chr17	81195210	11079	0.0001	0.1337
chr18	78077248	11646	0.0001	0.0691
chr19	59128983	4093	0.0001	0.0196
chr20	63025520	2463	0	0.0184
chr21	48129895	1096	0	0.0059
chr22	51304566	1228	0	0.0057
chrMT	16571	2074	0.1252	0.9972
chrX	155270560	141056	0.0009	0.1532
chrY	59373566	6202	0.0001	0.0246

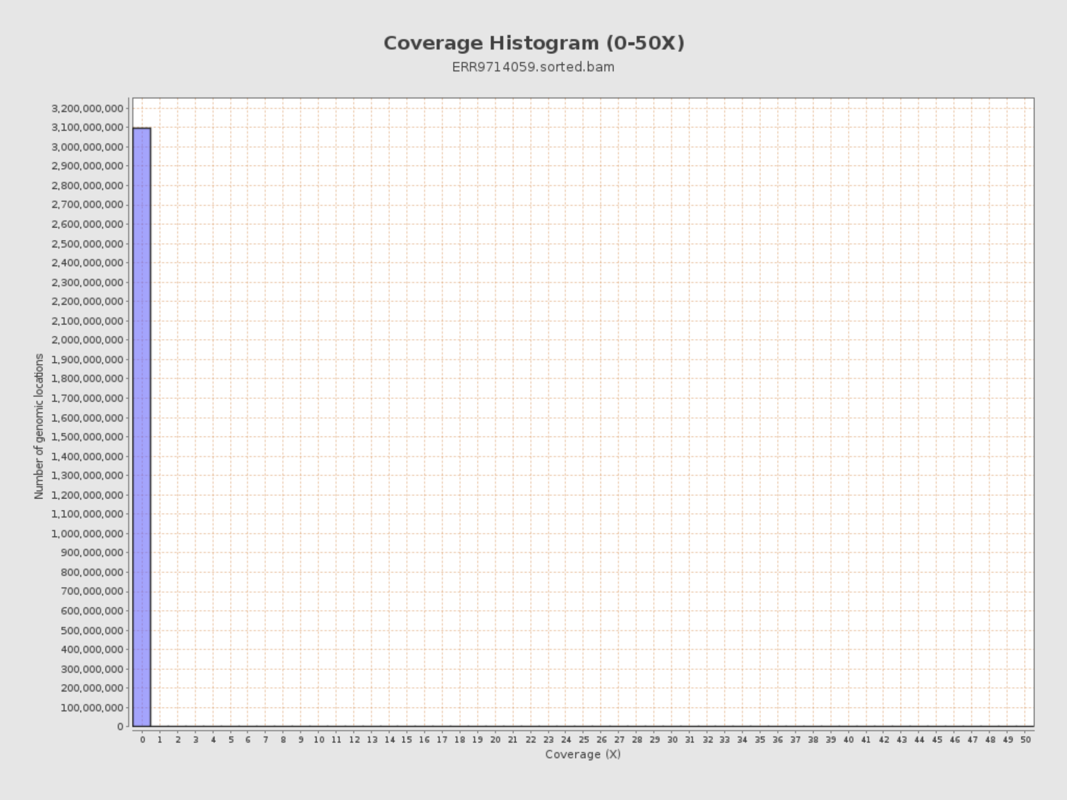
3. Results : Coverage across reference



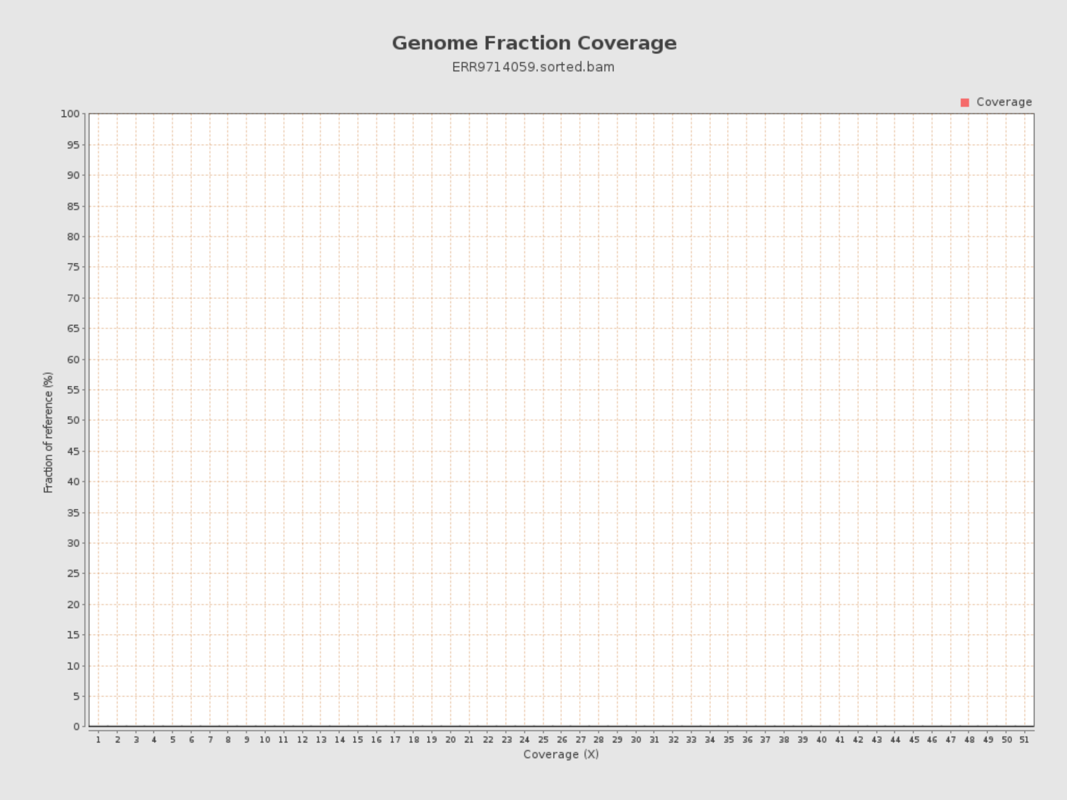
4. Results : Coverage Histogram



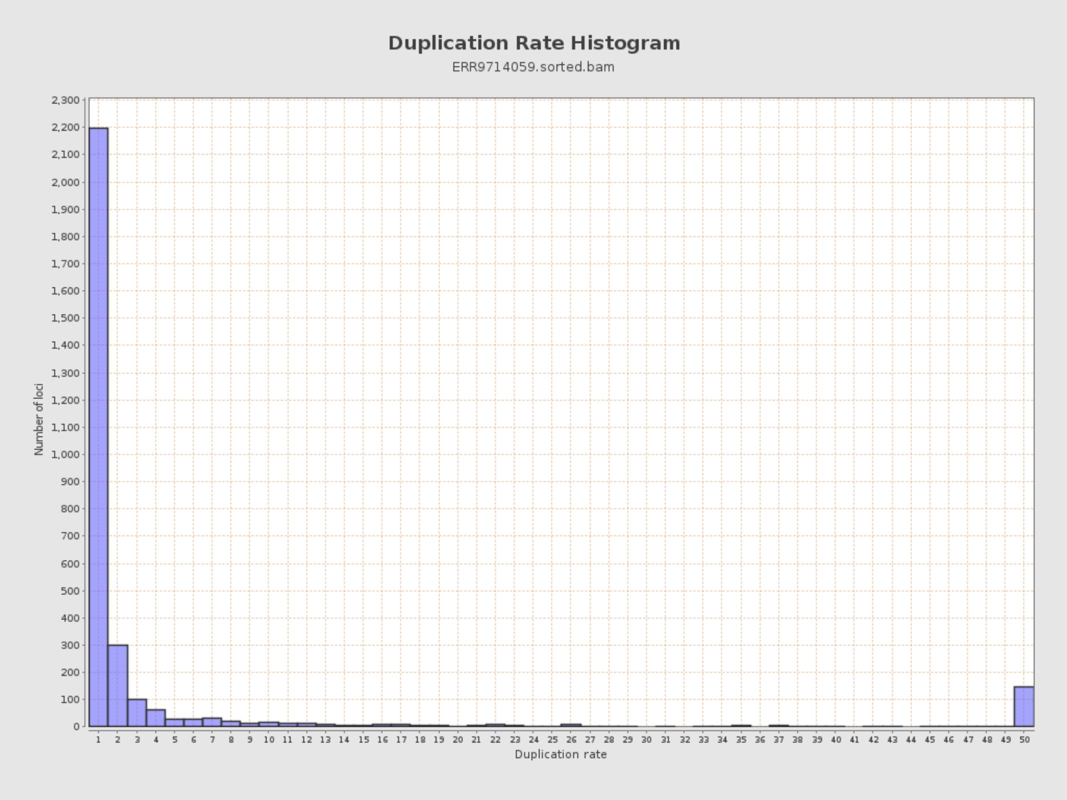
5. Results : Coverage Histogram (0-50X)



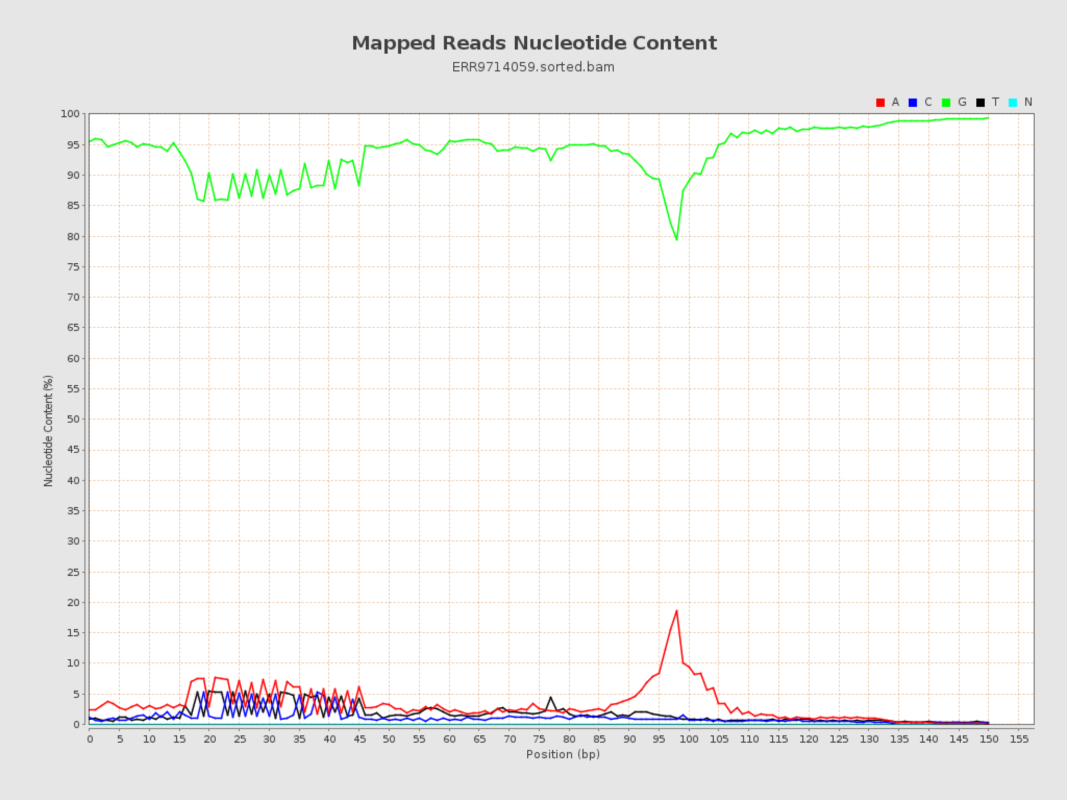
6. Results : Genome Fraction Coverage



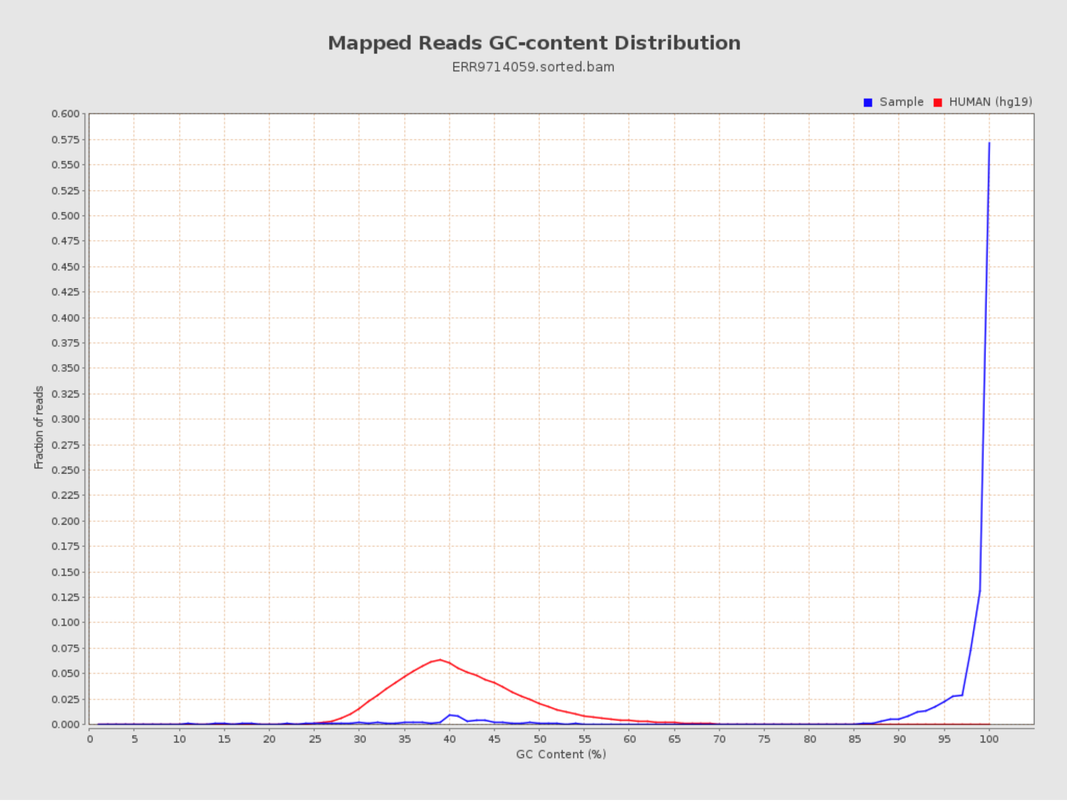
7. Results : Duplication Rate Histogram



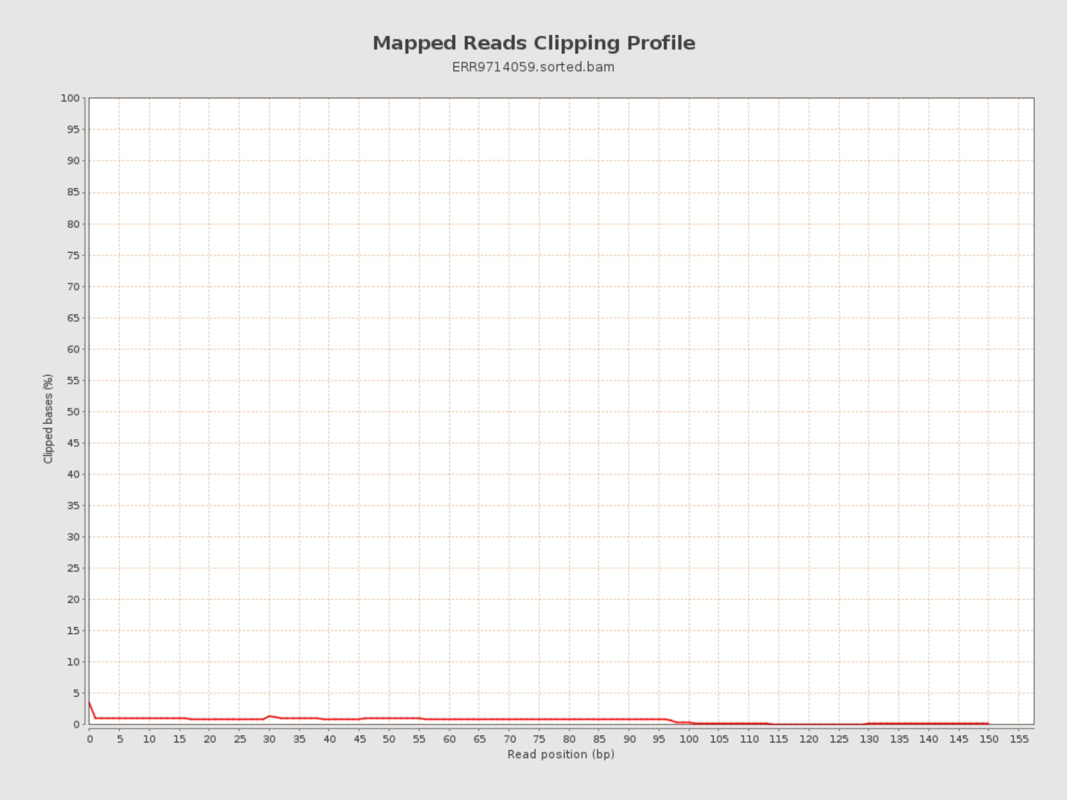
8. Results : Mapped Reads Nucleotide Content



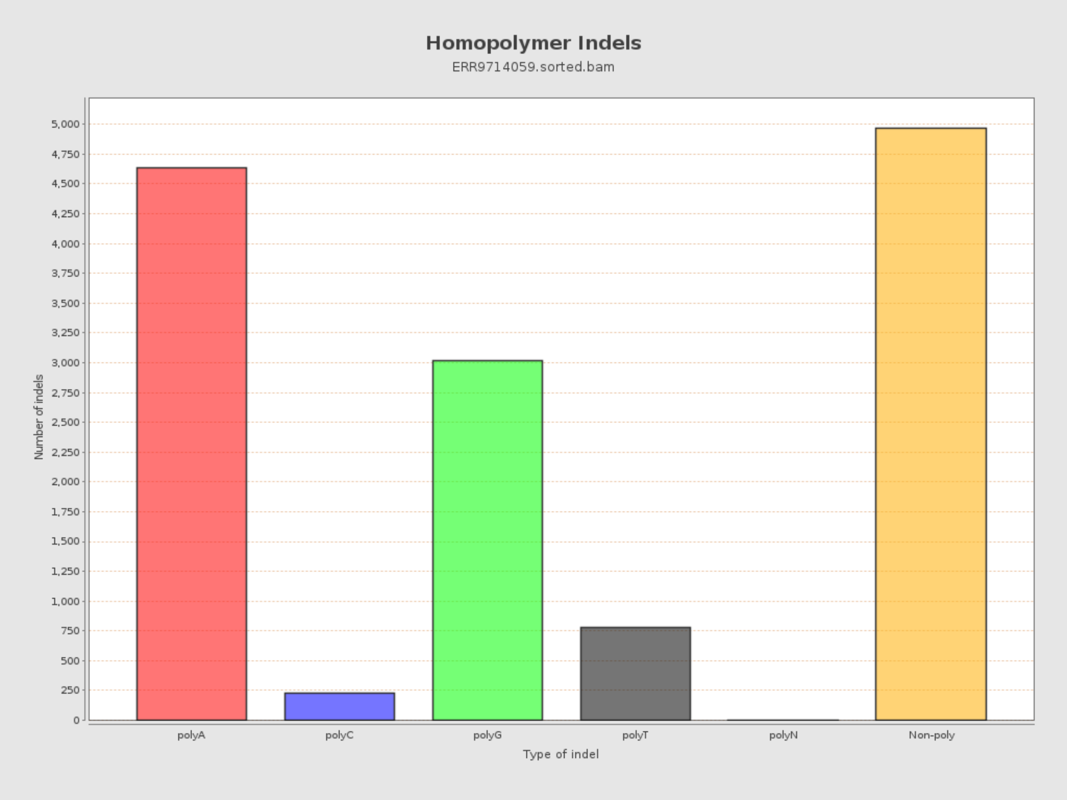
9. Results : Mapped Reads GC-content Distribution



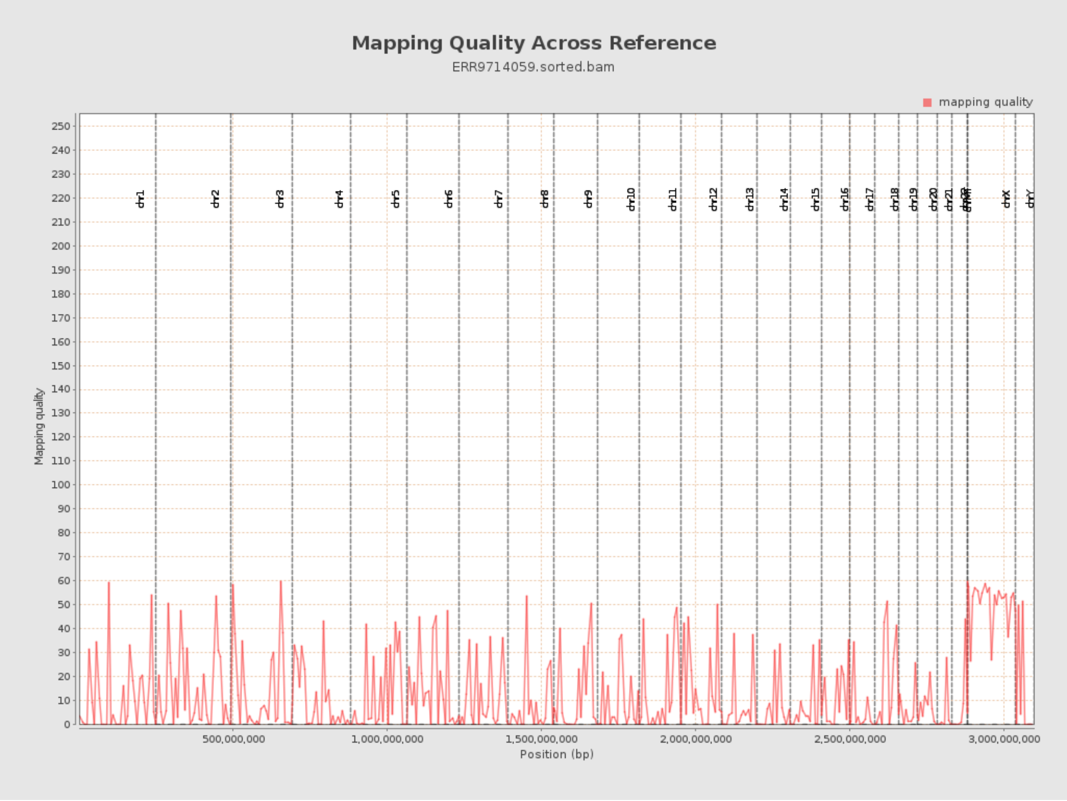
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram