Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 19:02:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714093.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_ERR9714093 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714093.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 19:02:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714093.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	641,920
Mapped reads	292,189 / 45.52%
Unmapped reads	349,731 / 54.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,831 / 0.91%
Read min/max/mean length	30 / 151 / 94.67
Duplicated reads (estimated)	278,808 / 43.43%
Duplication rate	38.02%
Clipped reads	263,753 / 41.09%

2.2. ACGT Content

Number/percentage of A's	9,388,000 / 25.82%
Number/percentage of C's	6,706,678 / 18.45%
Number/percentage of T's	9,410,243 / 25.88%
Number/percentage of G's	10,853,184 / 29.85%
Number/percentage of N's	388 / 0%
GC Percentage	48.3%

2.3. Coverage

Mean	0.012

Standard Deviation	16.4943

2.4. Mapping Quality

Mean Mapping Quality	41.38

2.5. Mismatches and indels

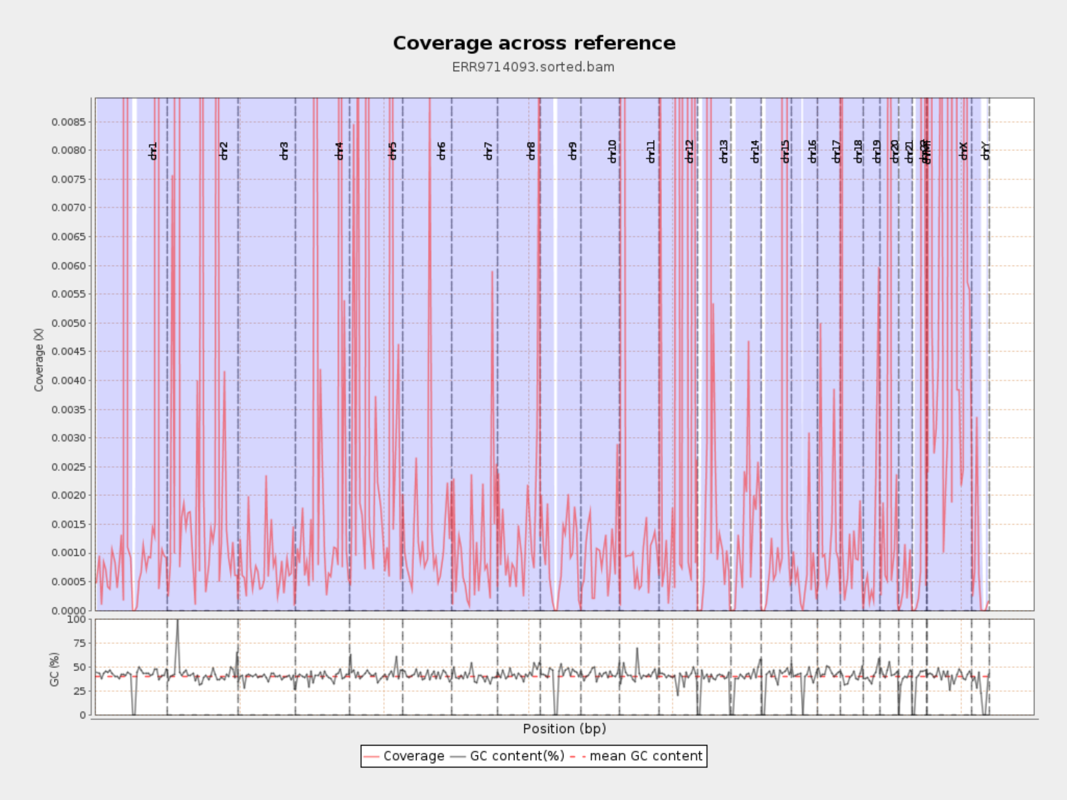
General error rate	4.18%
Mismatches	1,477,703
Insertions	19,929
Mapped reads with at least one insertion	6.15%
Deletions	97,354
Mapped reads with at least one deletion	31.78%
Homopolymer indels	45.62%

2.6. Chromosome stats

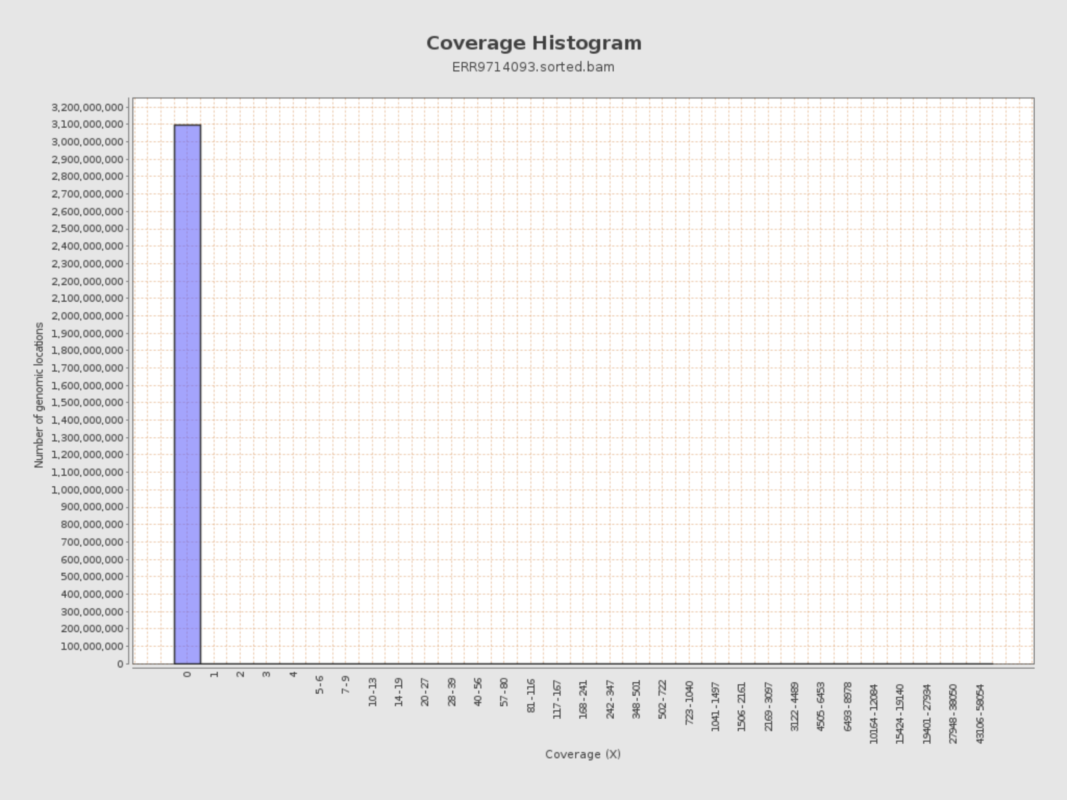
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12294210	0.0493	45.7105
chr2	243199373	4746726	0.0195	17.7924
chr3	198022430	157932	0.0008	0.101
chr4	191154276	579866	0.003	1.4611
chr5	180915260	831255	0.0046	1.7726
chr6	171115067	260318	0.0015	0.3504
chr7	159138663	195262	0.0012	0.4869

chr8	146364022	236136	0.0016	0.5145
chr9	141213431	137286	0.001	0.1249
chr10	135534747	132744	0.001	0.1492
chr11	135006516	793962	0.0059	3.6675
chr12	133851895	1271015	0.0095	4.4485
chr13	115169878	2977875	0.0259	18.9009
chr14	107349540	158350	0.0015	0.323
chr15	102531392	1830690	0.0179	13.7603
chr16	90354753	64131	0.0007	0.2774
chr17	81195210	122829	0.0015	0.4298
chr18	78077248	431014	0.0055	3.3687
chr19	59128983	78870	0.0013	0.4562
chr20	63025520	315104	0.005	2.3837
chr21	48129895	23464	0.0005	0.0943
chr22	51304566	252769	0.0049	2.6594
chrMT	16571	6212819	374.9212	3,137.6098
chrX	155270560	3020264	0.0195	8.5037
chrY	59373566	38526	0.0006	0.2401

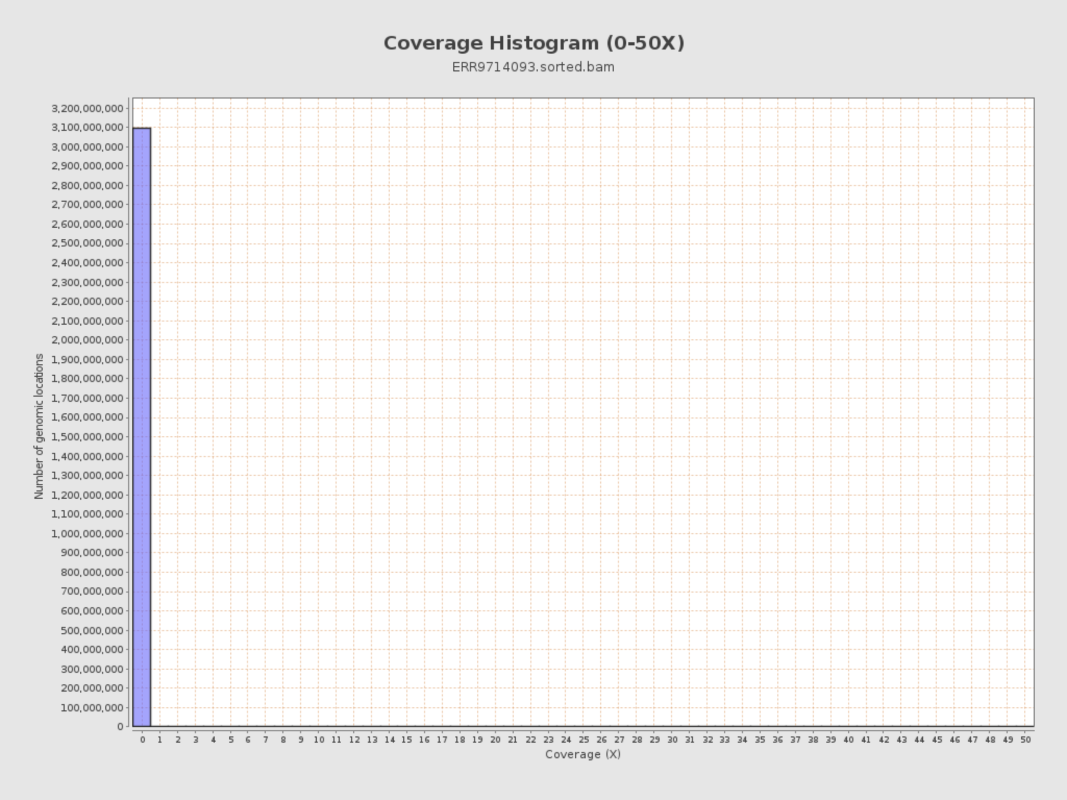
3. Results : Coverage across reference



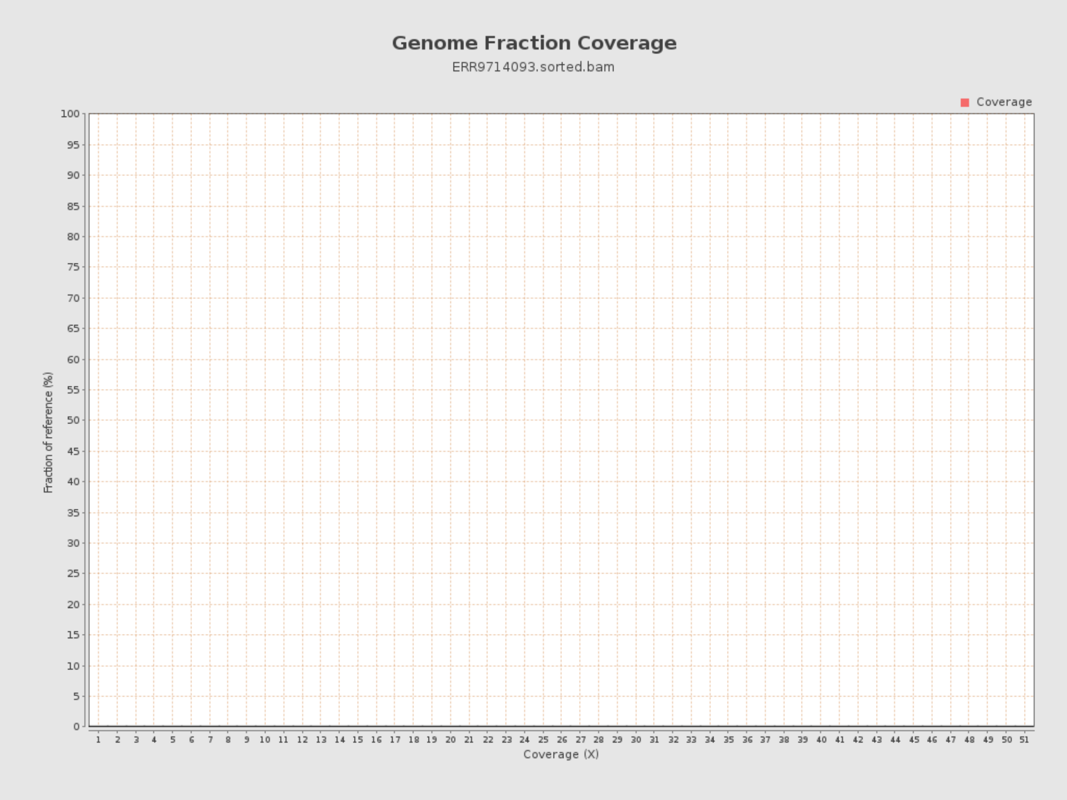
4. Results : Coverage Histogram



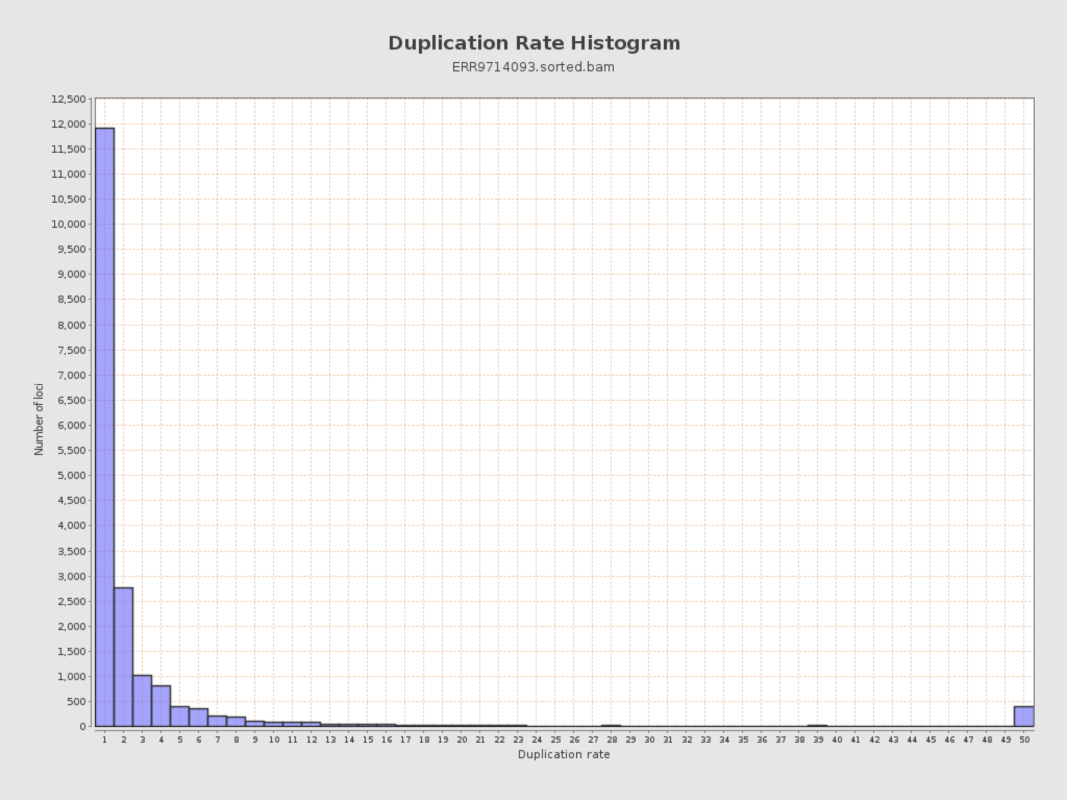
5. Results : Coverage Histogram (0-50X)



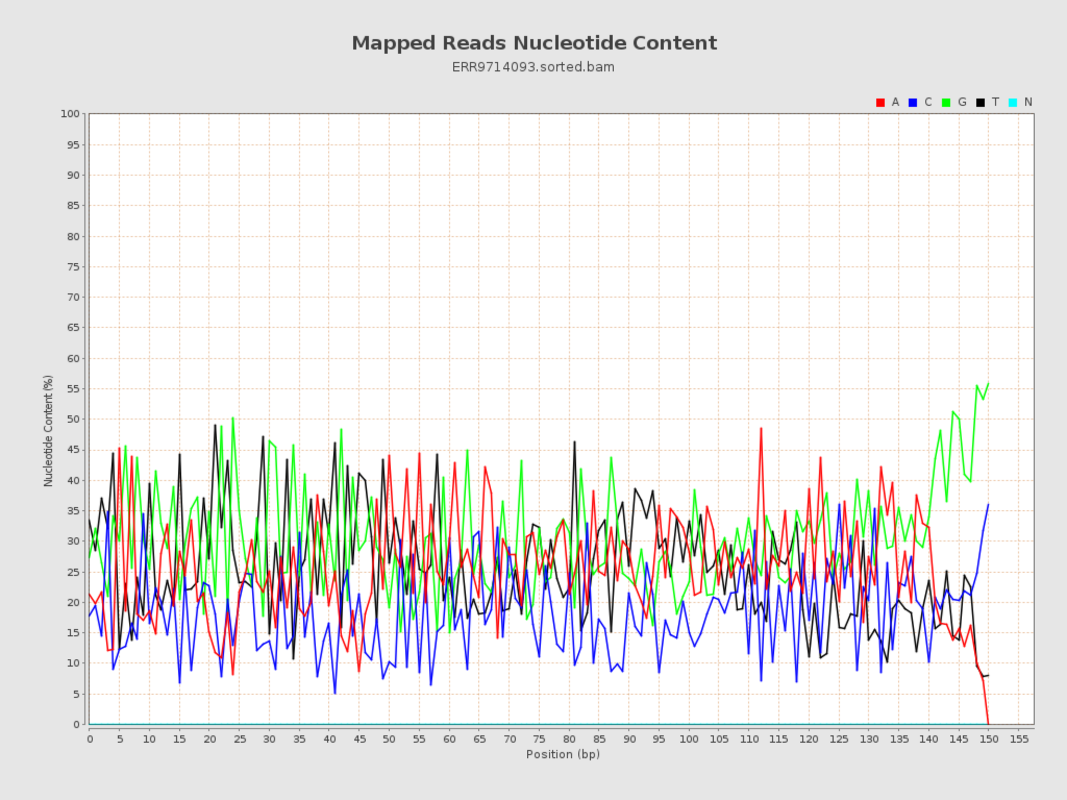
6. Results : Genome Fraction Coverage



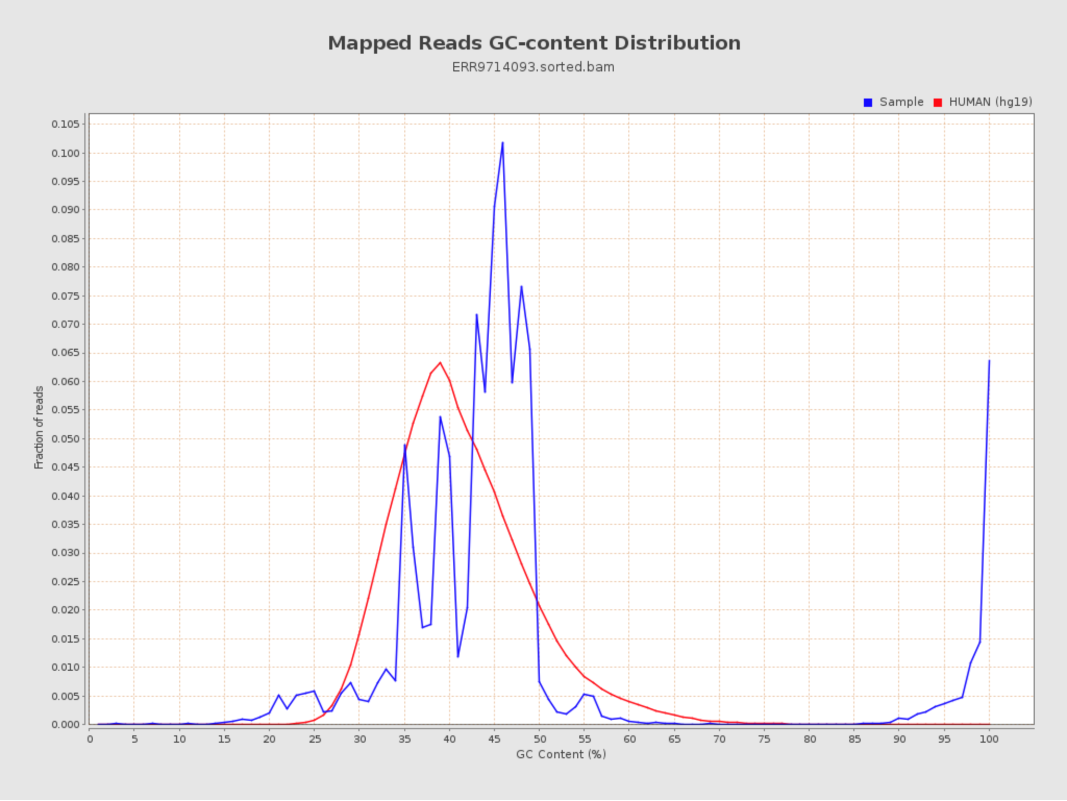
7. Results : Duplication Rate Histogram



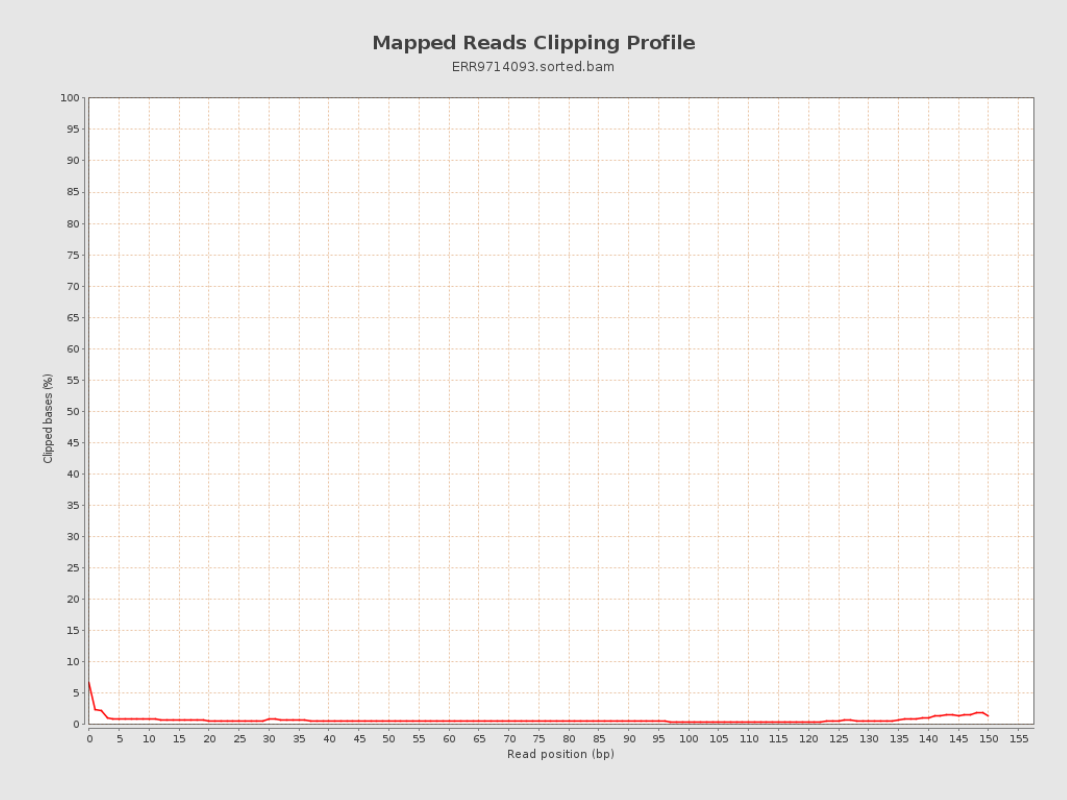
8. Results : Mapped Reads Nucleotide Content



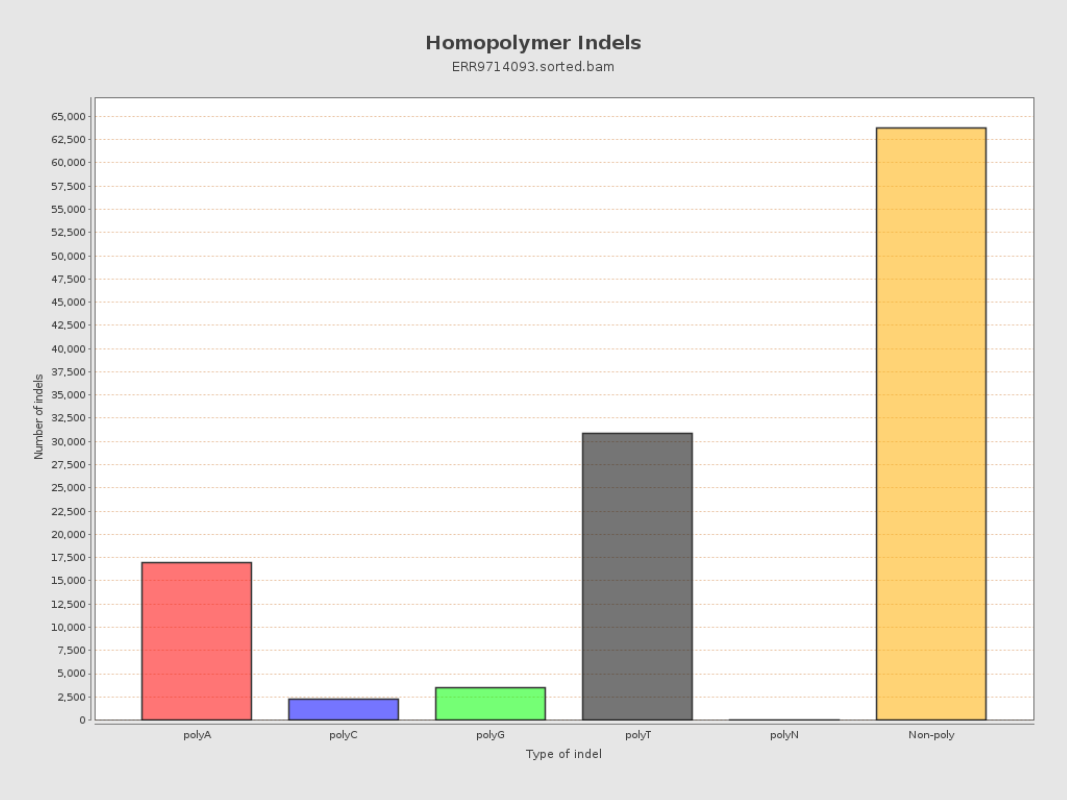
9. Results : Mapped Reads GC-content Distribution



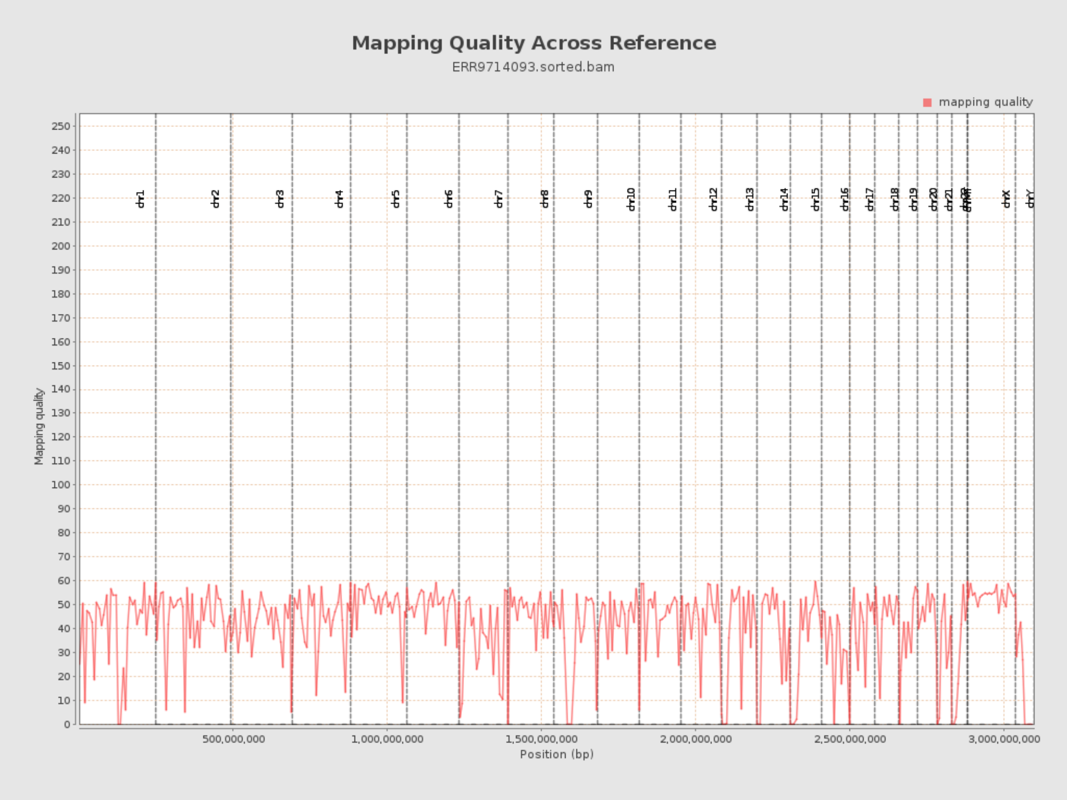
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram