Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 18:34:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714081.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_ERR9714081 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714081.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 18:34:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714081.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	577,850
Mapped reads	187,488 / 32.45%
Unmapped reads	390,362 / 67.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,619 / 0.8%
Read min/max/mean length	30 / 151 / 81.42
Duplicated reads (estimated)	180,553 / 31.25%
Duplication rate	45.08%
Clipped reads	159,538 / 27.61%

2.2. ACGT Content

Number/percentage of A's	5,328,016 / 22.97%
Number/percentage of C's	4,022,792 / 17.34%
Number/percentage of T's	5,443,919 / 23.47%
Number/percentage of G's	8,399,414 / 36.21%
Number/percentage of N's	404 / 0%
GC Percentage	53.56%

2.3. Coverage

Mean	0.0076

Standard Deviation	12.5751

2.4. Mapping Quality

Mean Mapping Quality	34.07

2.5. Mismatches and indels

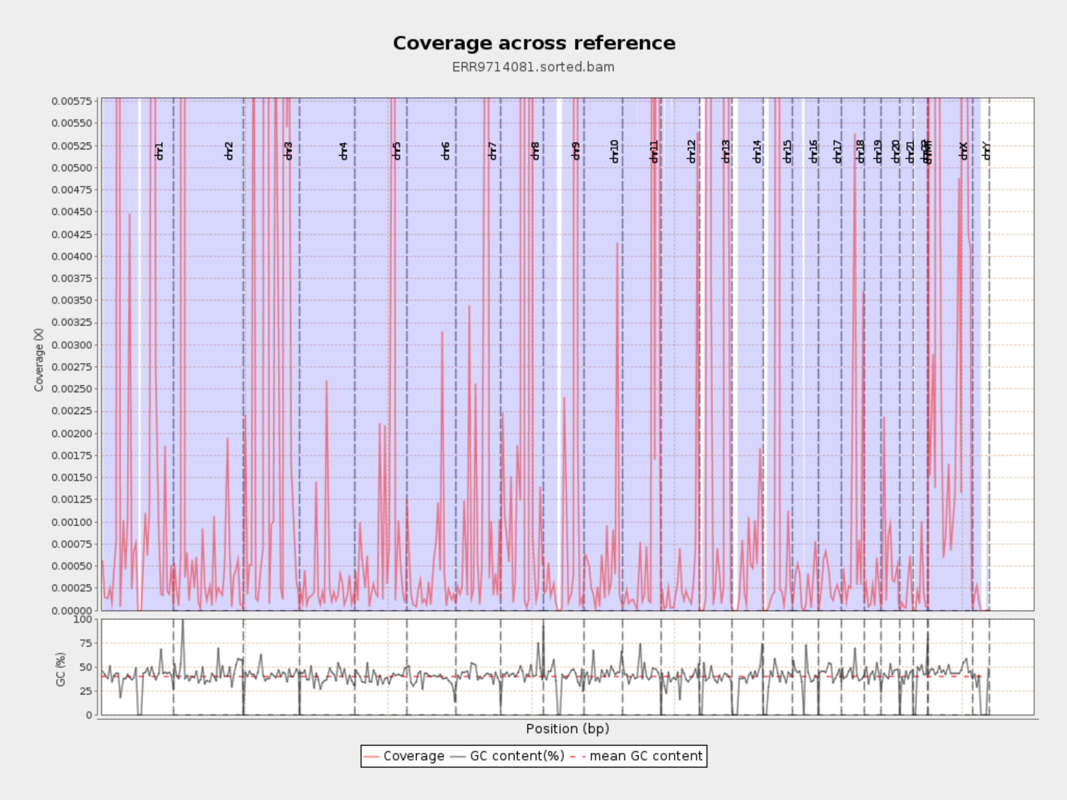
General error rate	4.15%
Mismatches	902,675
Insertions	18,994
Mapped reads with at least one insertion	9.18%
Deletions	59,086
Mapped reads with at least one deletion	30.07%
Homopolymer indels	59%

2.6. Chromosome stats

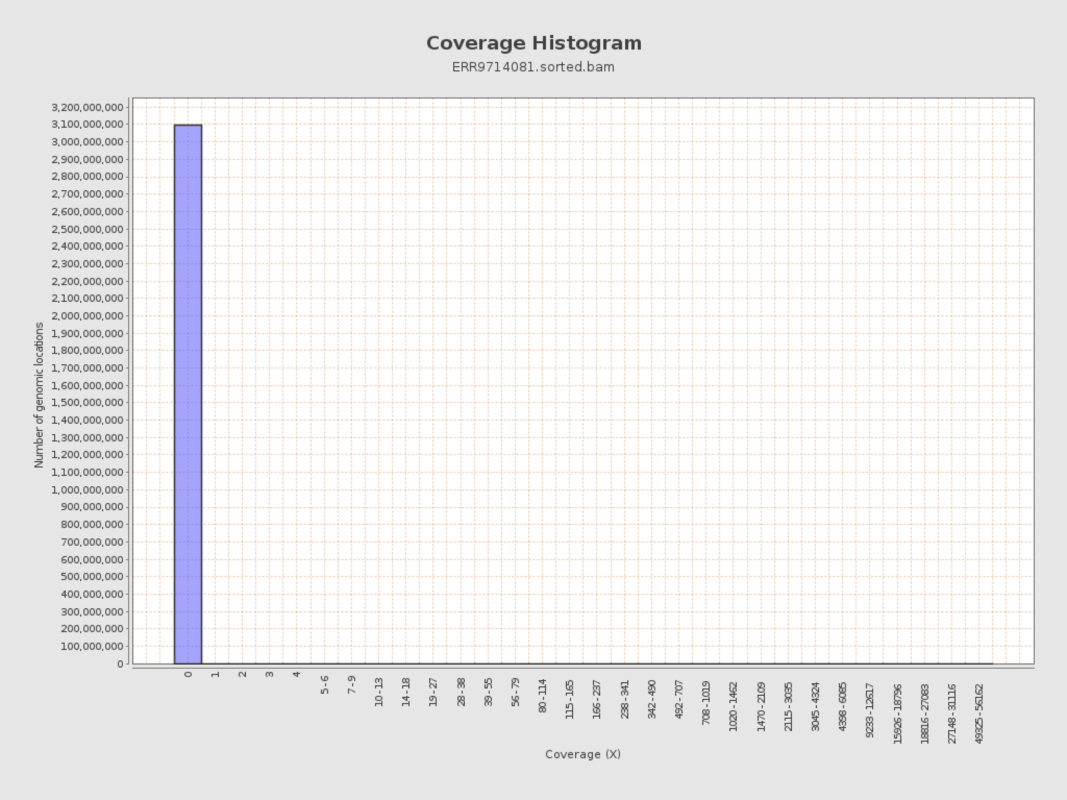
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	547303	0.0022	1.1189
chr2	243199373	4290603	0.0176	18.4574
chr3	198022430	955326	0.0048	2.0968
chr4	191154276	64552	0.0003	0.1008
chr5	180915260	326423	0.0018	0.8787
chr6	171115067	80813	0.0005	0.0683
chr7	159138663	310249	0.0019	1.1666

chr8	146364022	1127039	0.0077	5.1148
chr9	141213431	573158	0.0041	3.133
chr10	135534747	80311	0.0006	0.2509
chr11	135006516	304547	0.0023	0.9659
chr12	133851895	74369	0.0006	0.317
chr13	115169878	2903618	0.0252	14.7318
chr14	107349540	59633	0.0006	0.1329
chr15	102531392	246373	0.0024	1.6696
chr16	90354753	27268	0.0003	0.0534
chr17	81195210	23917	0.0003	0.1005
chr18	78077248	99945	0.0013	0.3676
chr19	59128983	11850	0.0002	0.0392
chr20	63025520	41802	0.0007	0.1104
chr21	48129895	9310	0.0002	0.0409
chr22	51304566	12080	0.0002	0.0565
chrMT	16571	9114191	550.0085	4,631.5224
chrX	155270560	2343871	0.0151	9.5093
chrY	59373566	4642	0.0001	0.018

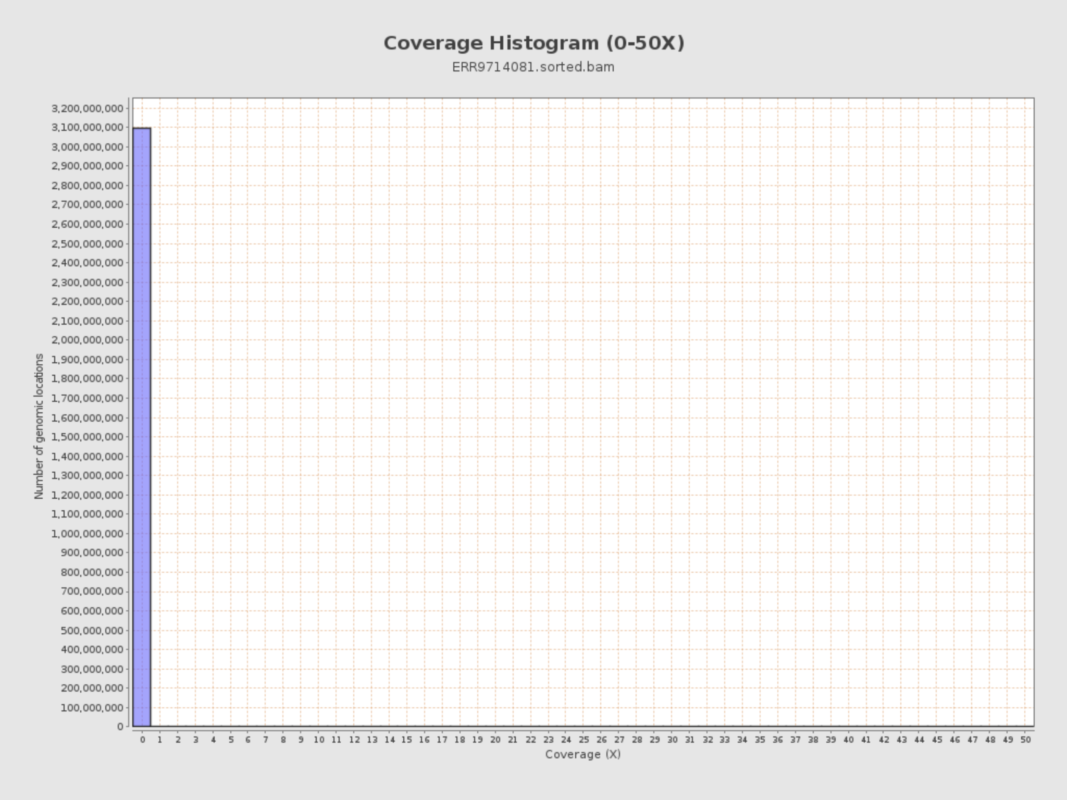
3. Results : Coverage across reference



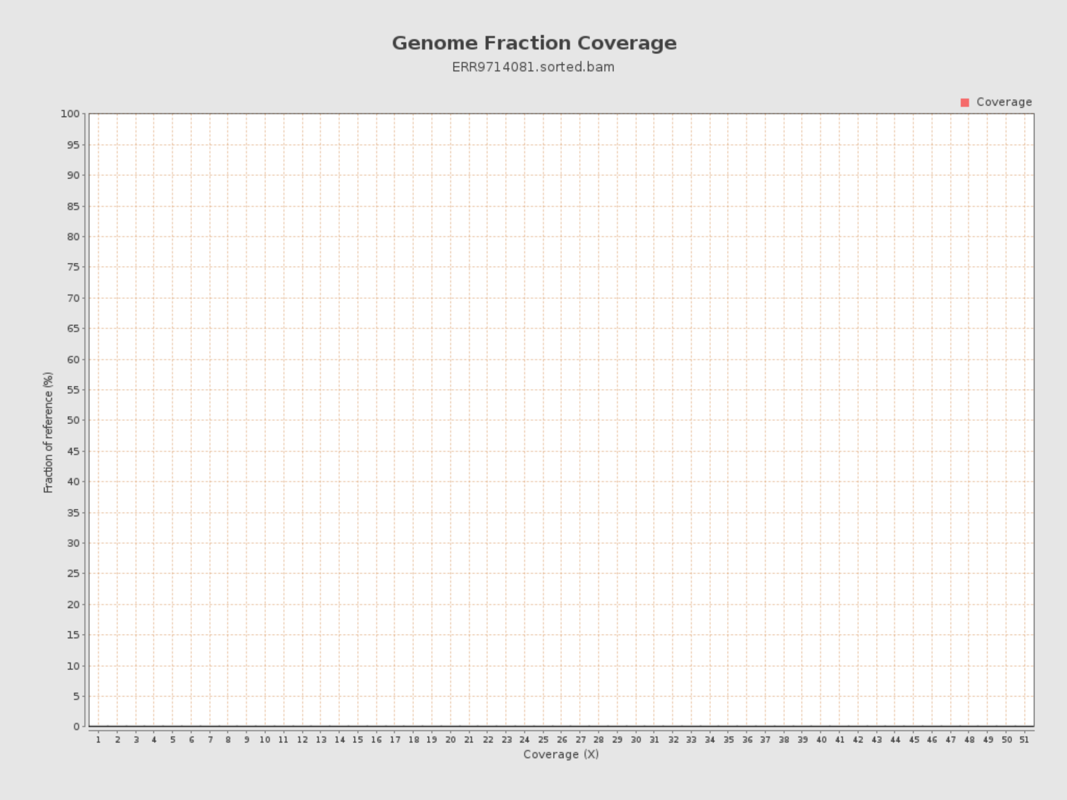
4. Results : Coverage Histogram



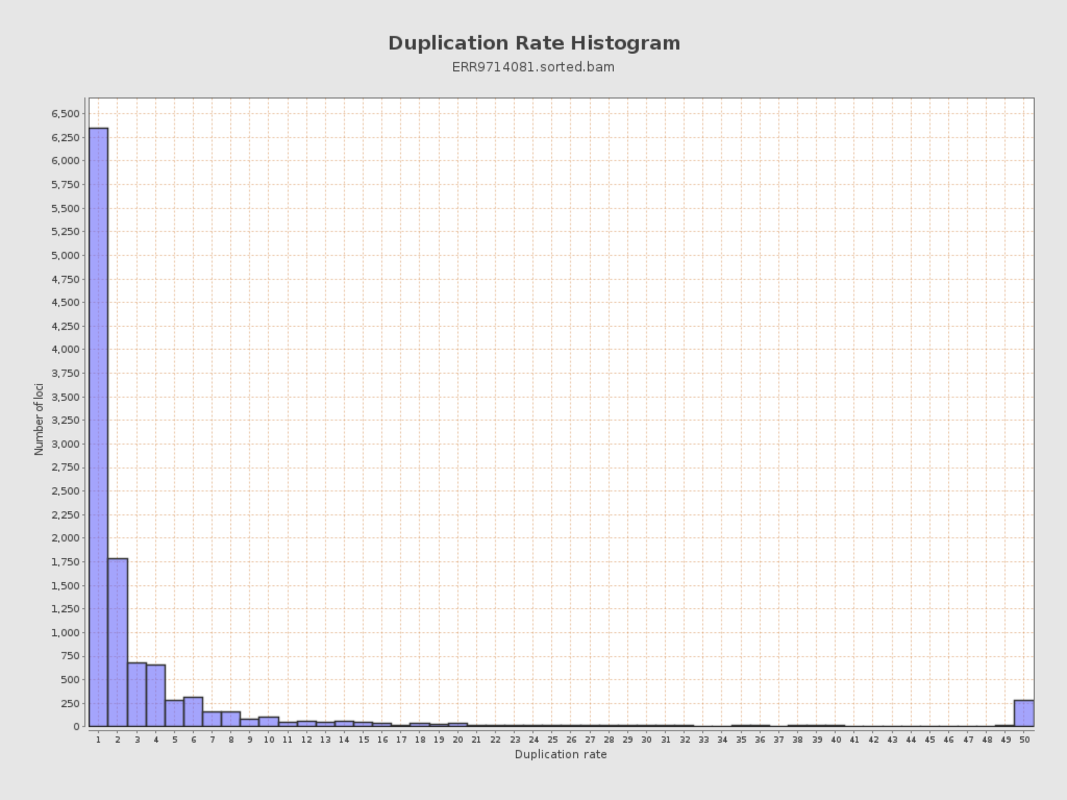
5. Results : Coverage Histogram (0-50X)



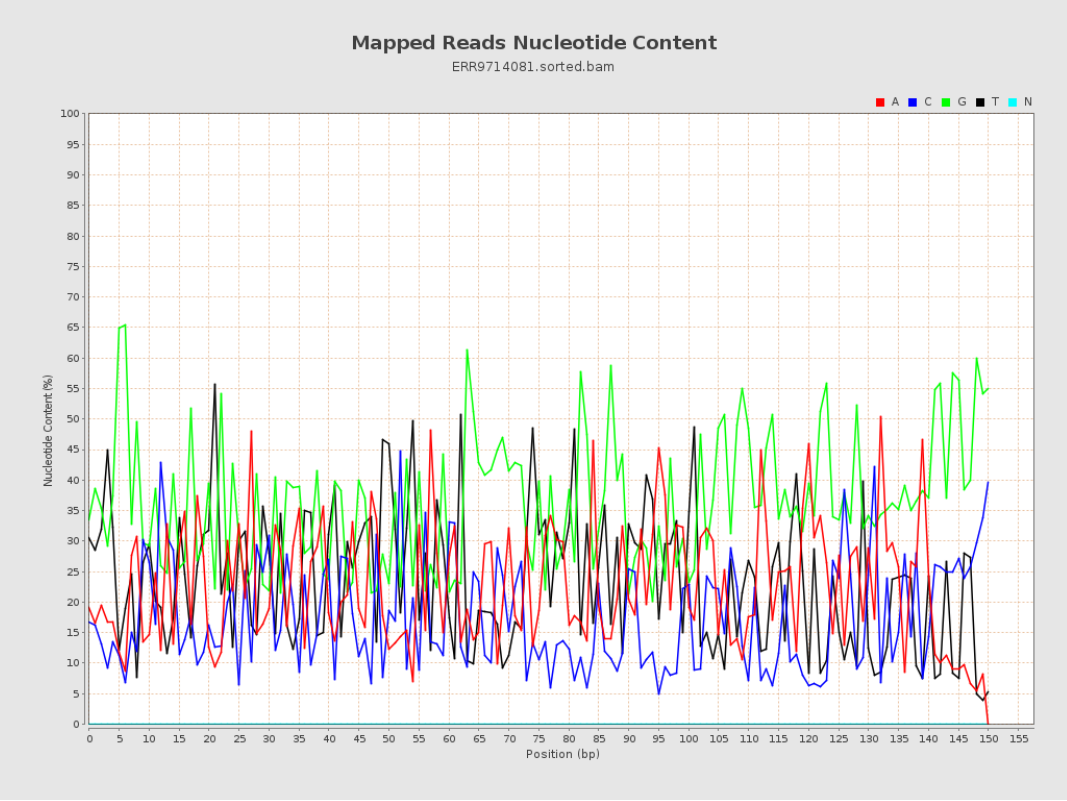
6. Results : Genome Fraction Coverage



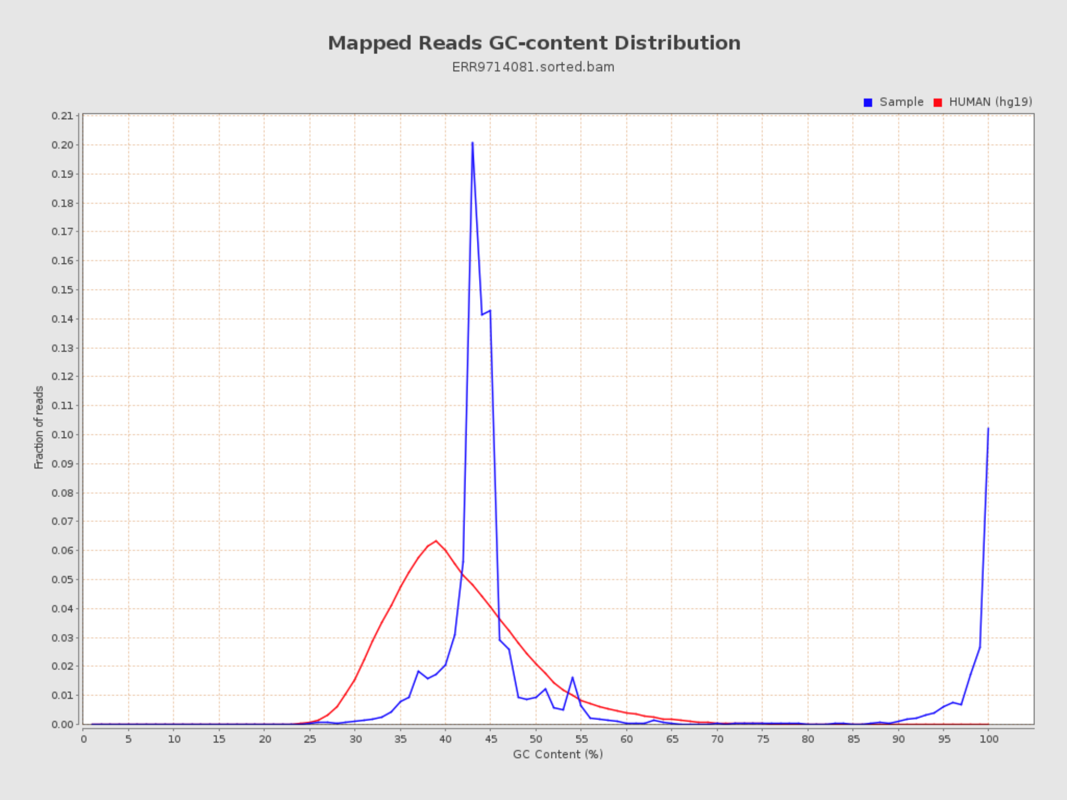
7. Results : Duplication Rate Histogram



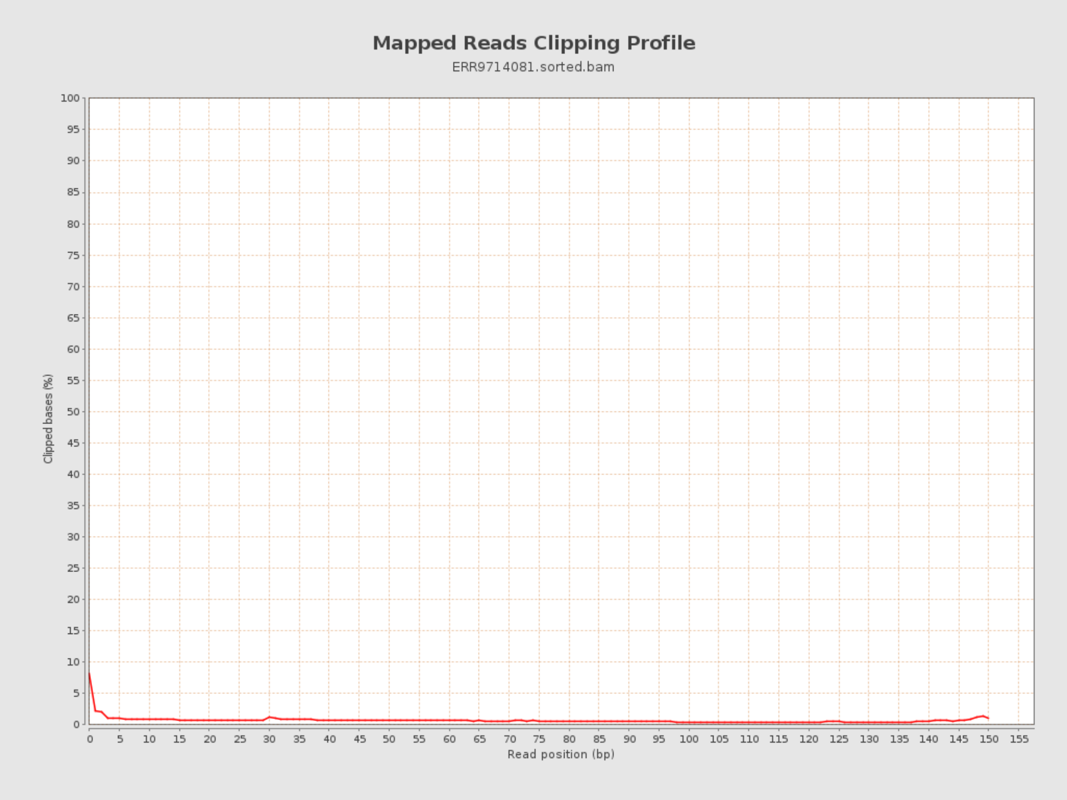
8. Results : Mapped Reads Nucleotide Content



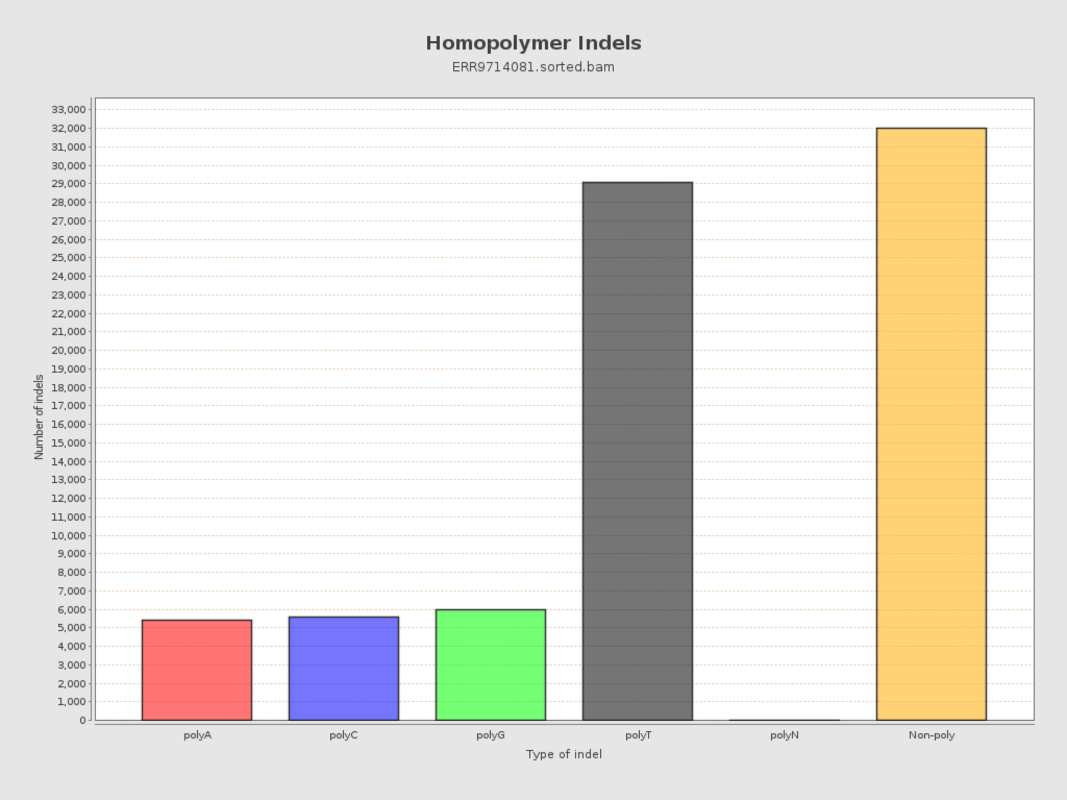
9. Results : Mapped Reads GC-content Distribution



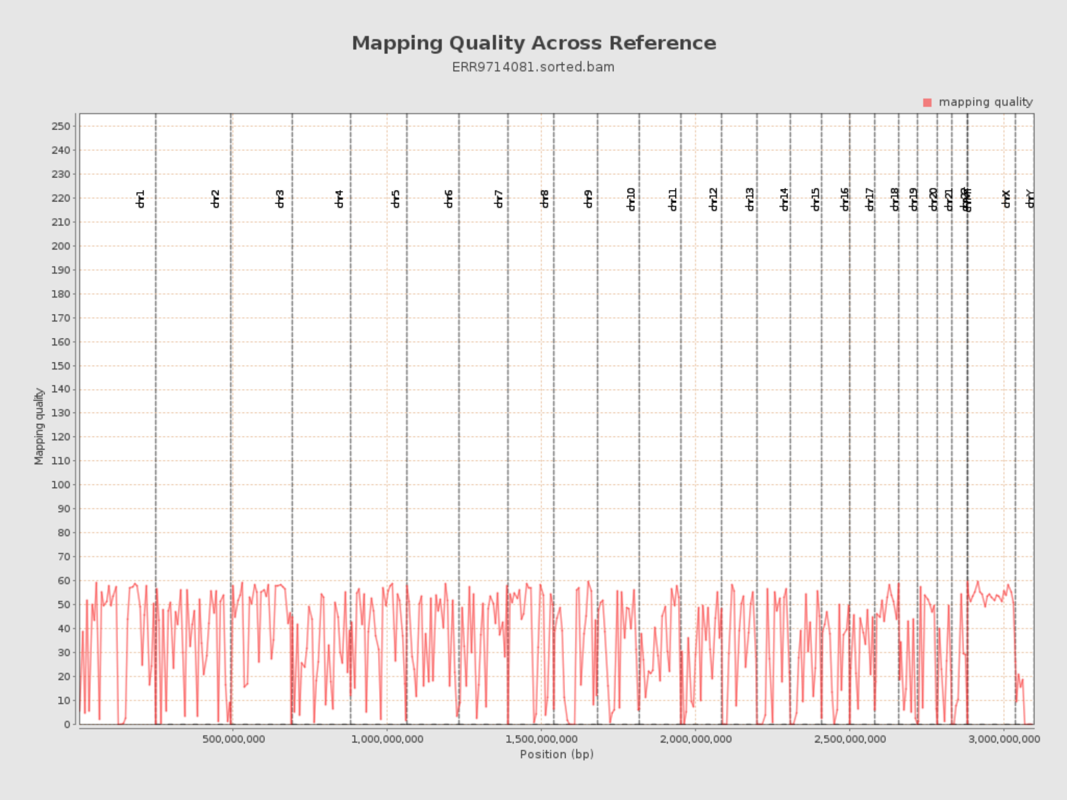
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram