Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 18:03:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714067.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_ERR9714067 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714067.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 18:03:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714067.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	621,540
Mapped reads	37,789 / 6.08%
Unmapped reads	583,751 / 93.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	864 / 0.14%
Read min/max/mean length	30 / 151 / 55.46
Duplicated reads (estimated)	34,074 / 5.48%
Duplication rate	32.15%
Clipped reads	30,844 / 4.96%

2.2. ACGT Content

Number/percentage of A's	370,465 / 11.86%
Number/percentage of C's	241,269 / 7.72%
Number/percentage of T's	297,424 / 9.52%
Number/percentage of G's	2,214,436 / 70.89%
Number/percentage of N's	84 / 0%
GC Percentage	78.62%

2.3. Coverage

Mean	0.001

Standard Deviation	2.2946

2.4. Mapping Quality

Mean Mapping Quality	27.61

2.5. Mismatches and indels

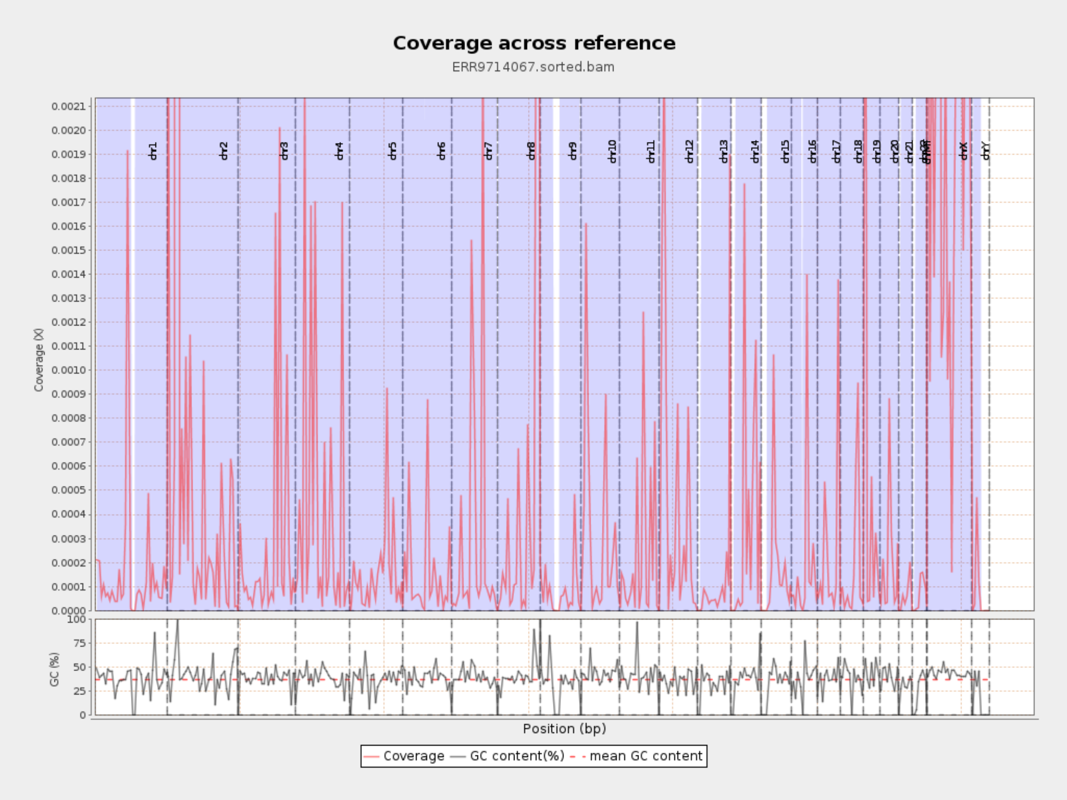
General error rate	3.12%
Mismatches	81,216
Insertions	3,163
Mapped reads with at least one insertion	6.33%
Deletions	4,344
Mapped reads with at least one deletion	11.07%
Homopolymer indels	40.87%

2.6. Chromosome stats

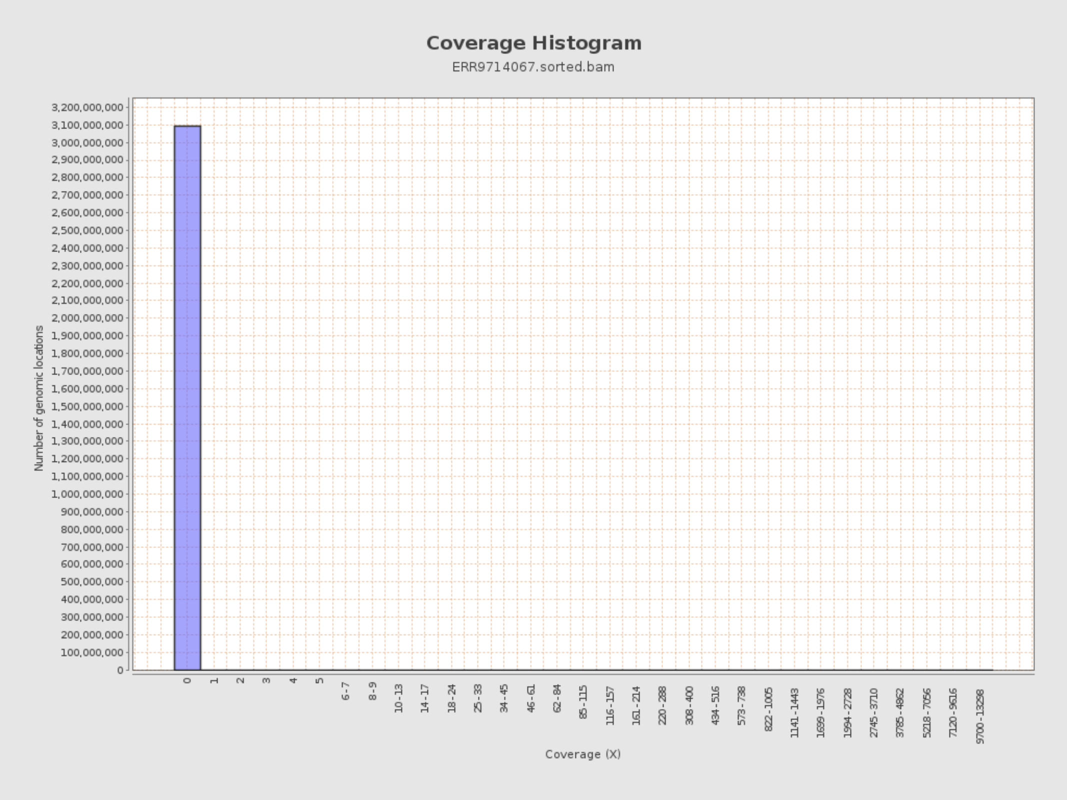
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	40187	0.0002	0.0732
chr2	243199373	2076230	0.0085	8.1711
chr3	198022430	55119	0.0003	0.1209
chr4	191154276	85189	0.0004	0.1691
chr5	180915260	29447	0.0002	0.046
chr6	171115067	25139	0.0001	0.0549
chr7	159138663	49040	0.0003	0.2708

chr8	146364022	76045	0.0005	0.2123
chr9	141213431	11571	0.0001	0.0213
chr10	135534747	44720	0.0003	0.1068
chr11	135006516	32230	0.0002	0.1003
chr12	133851895	60773	0.0005	0.1531
chr13	115169878	10417	0.0001	0.0327
chr14	107349540	40295	0.0004	0.1532
chr15	102531392	18193	0.0002	0.0639
chr16	90354753	17707	0.0002	0.0719
chr17	81195210	20740	0.0003	0.119
chr18	78077248	15558	0.0002	0.0734
chr19	59128983	36708	0.0006	0.2532
chr20	63025520	13242	0.0002	0.0604
chr21	48129895	3215	0.0001	0.0122
chr22	51304566	3294	0.0001	0.0135
chrMT	16571	2323	0.1402	1.0348
chrX	155270560	377610	0.0024	0.3402
chrY	59373566	4715	0.0001	0.0247

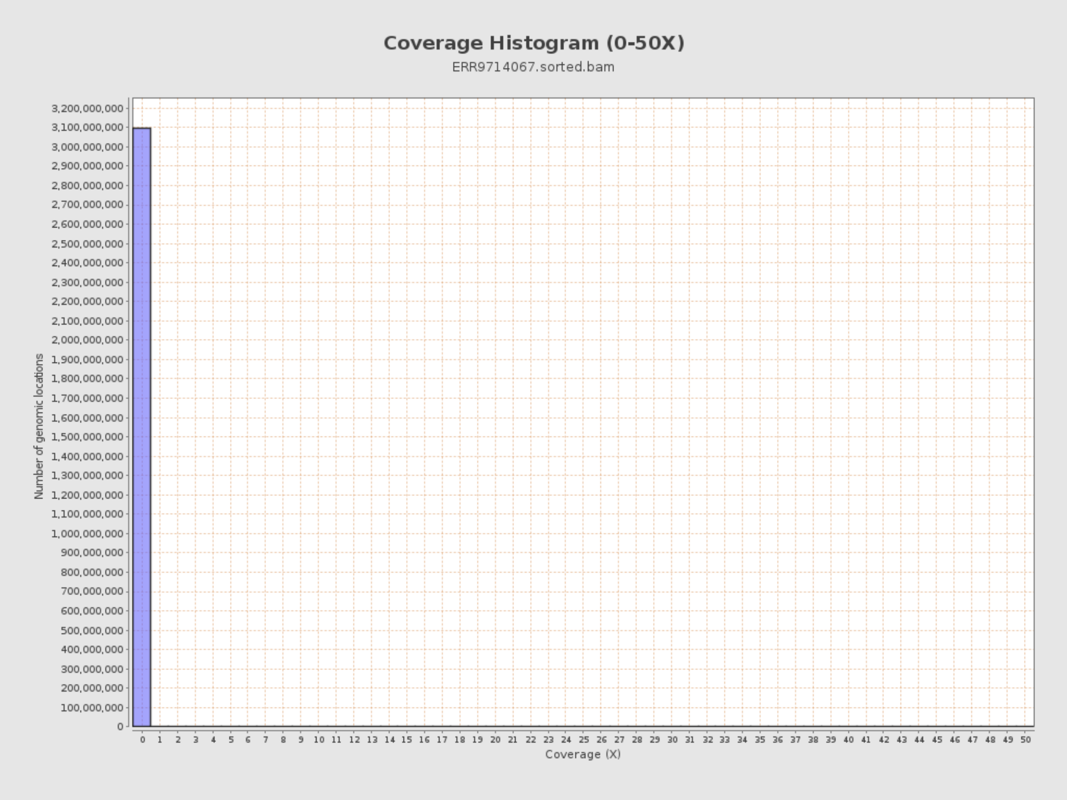
3. Results : Coverage across reference



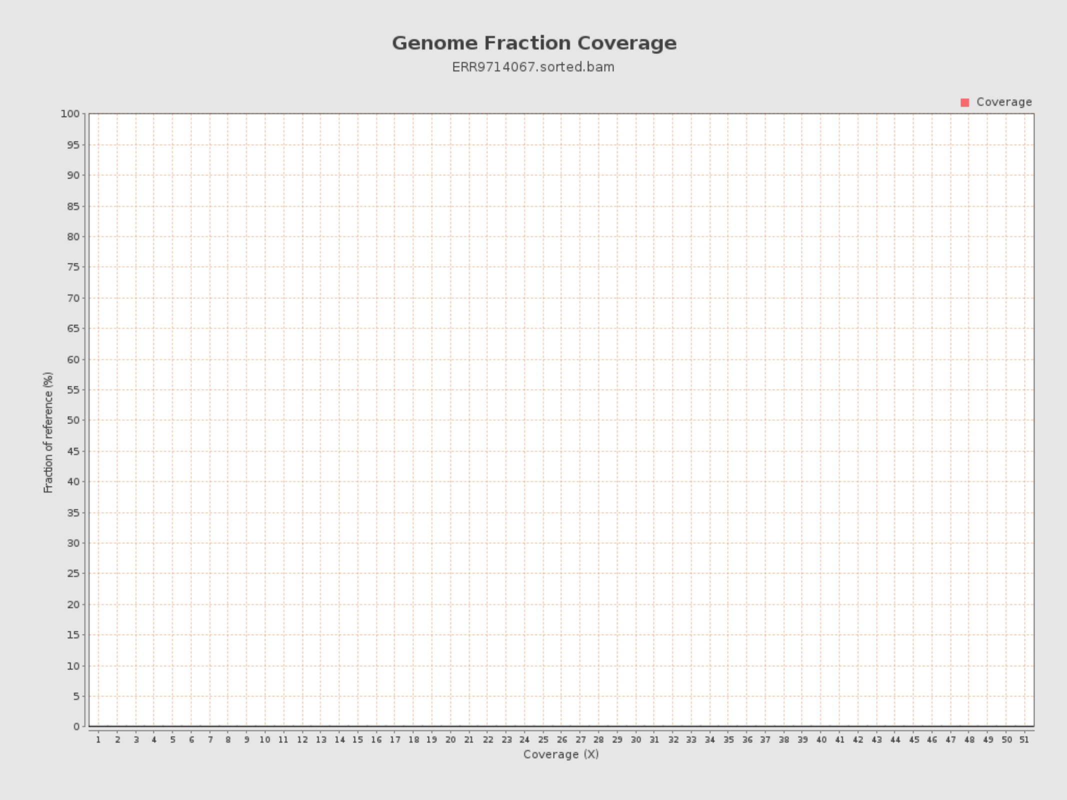
4. Results : Coverage Histogram



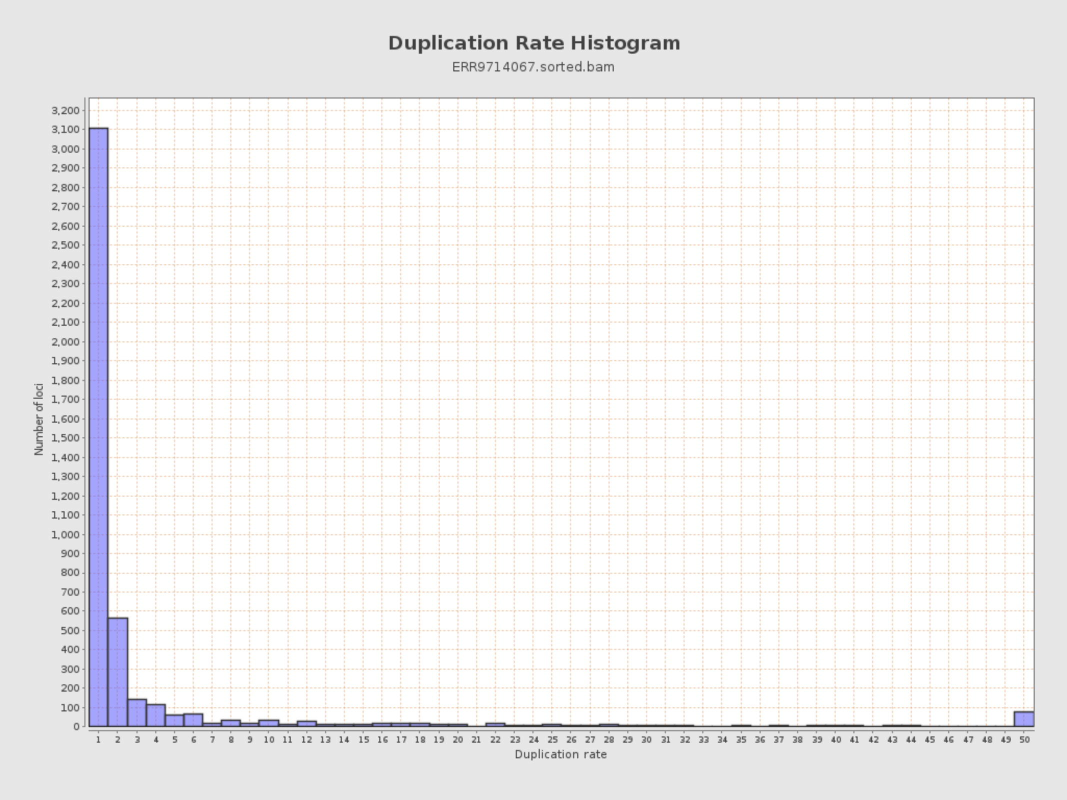
5. Results : Coverage Histogram (0-50X)



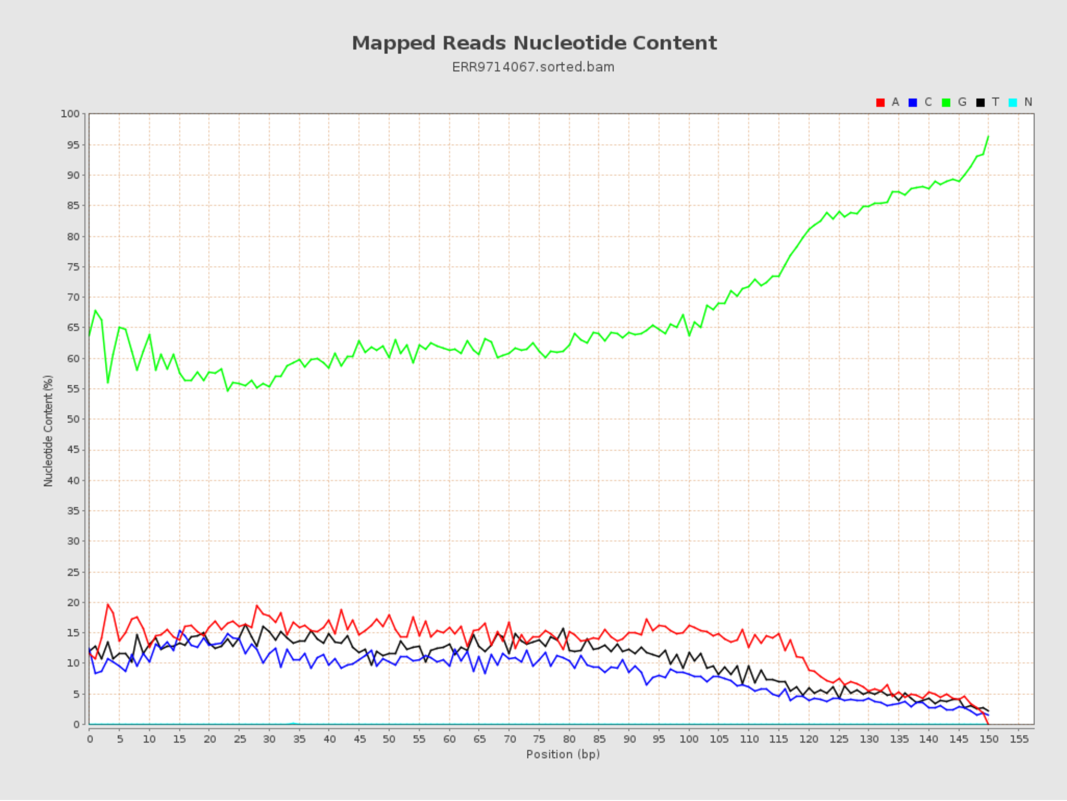
6. Results : Genome Fraction Coverage



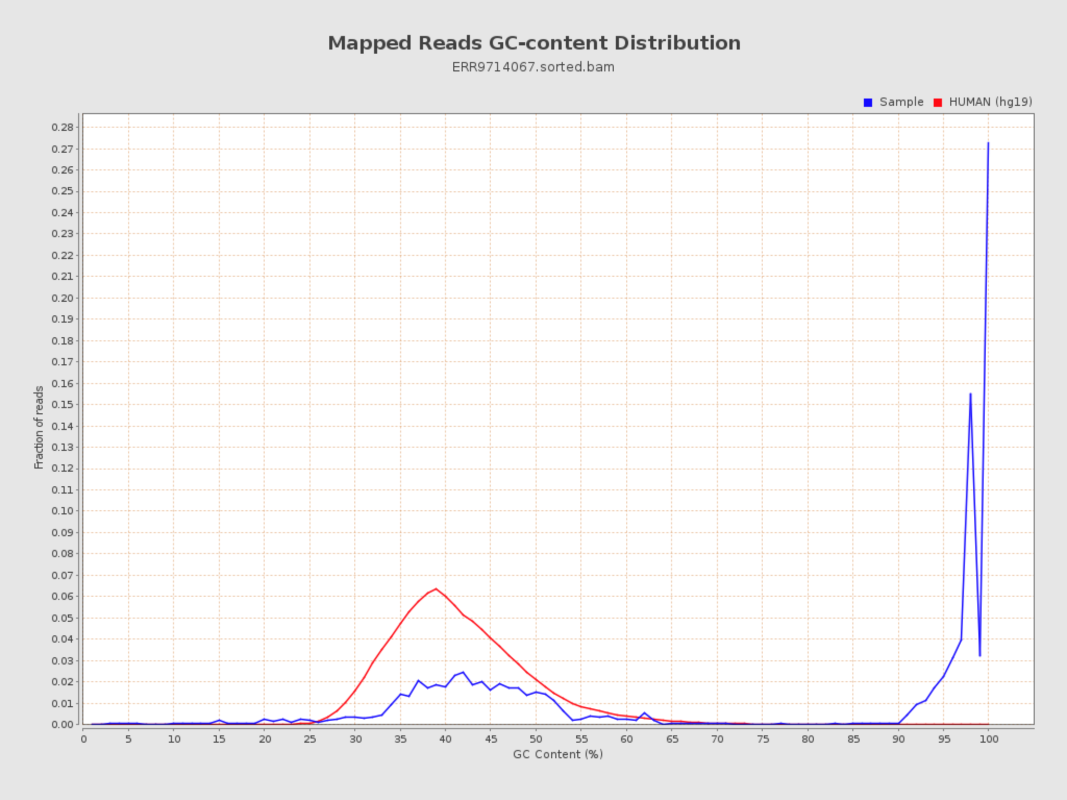
7. Results : Duplication Rate Histogram



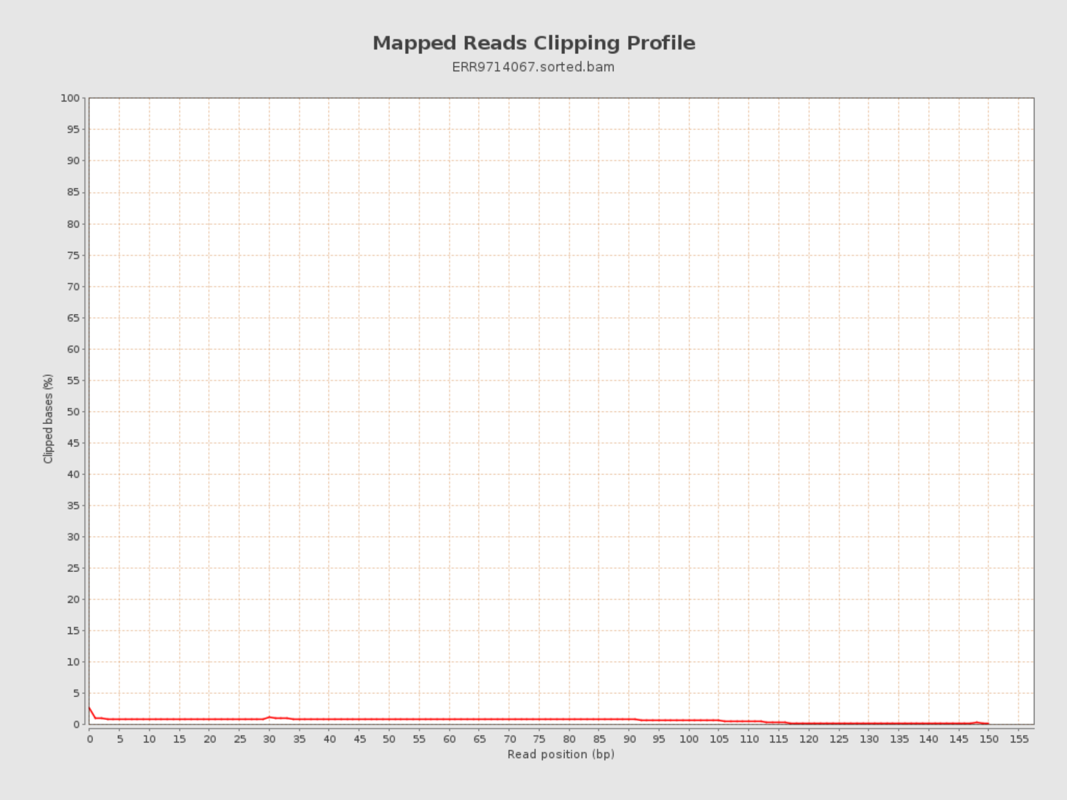
8. Results : Mapped Reads Nucleotide Content



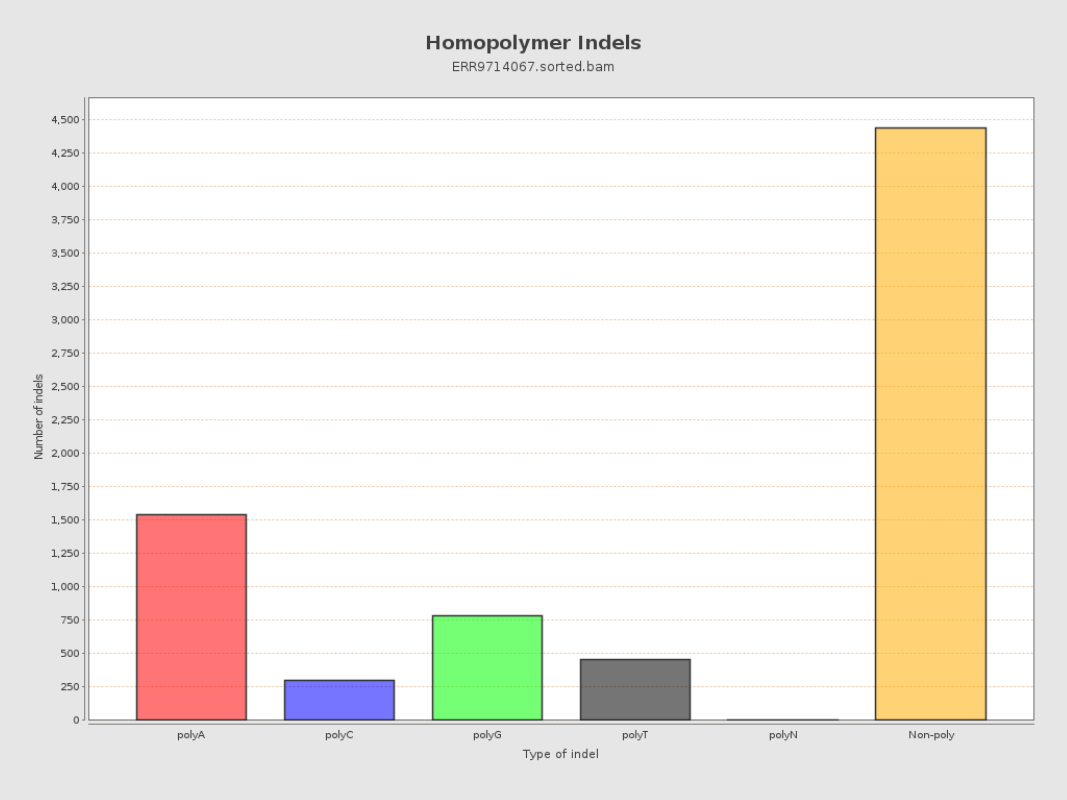
9. Results : Mapped Reads GC-content Distribution



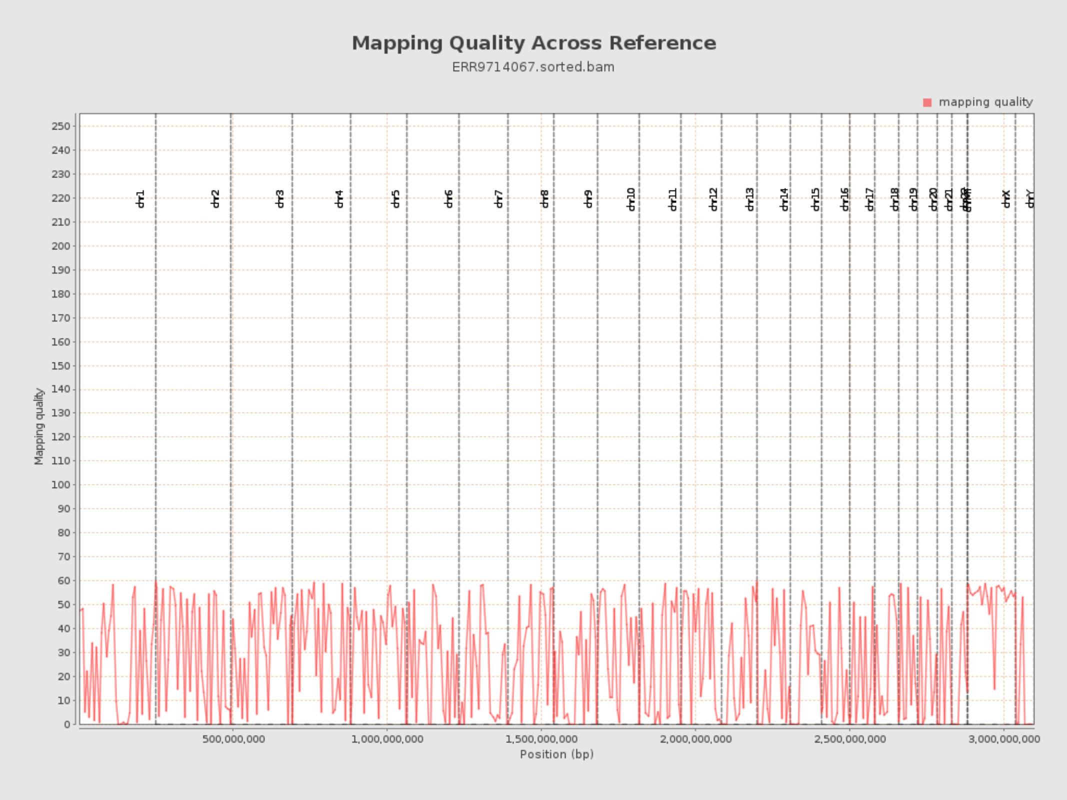
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram