Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 20:51:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714132.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_ERR9714132 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714132.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 20:51:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714132.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	649,660
Mapped reads	519,341 / 79.94%
Unmapped reads	130,319 / 20.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,571 / 2.7%
Read min/max/mean length	30 / 151 / 133.52
Duplicated reads (estimated)	457,972 / 70.49%
Duplication rate	43.71%
Clipped reads	481,589 / 74.13%

2.2. ACGT Content

Number/percentage of A's	18,565,904 / 27.91%
Number/percentage of C's	13,625,571 / 20.49%
Number/percentage of T's	17,650,943 / 26.54%
Number/percentage of G's	16,666,837 / 25.06%
Number/percentage of N's	530 / 0%
GC Percentage	45.55%

2.3. Coverage

Mean	0.022

Standard Deviation	5.231

2.4. Mapping Quality

Mean Mapping Quality	50.65

2.5. Mismatches and indels

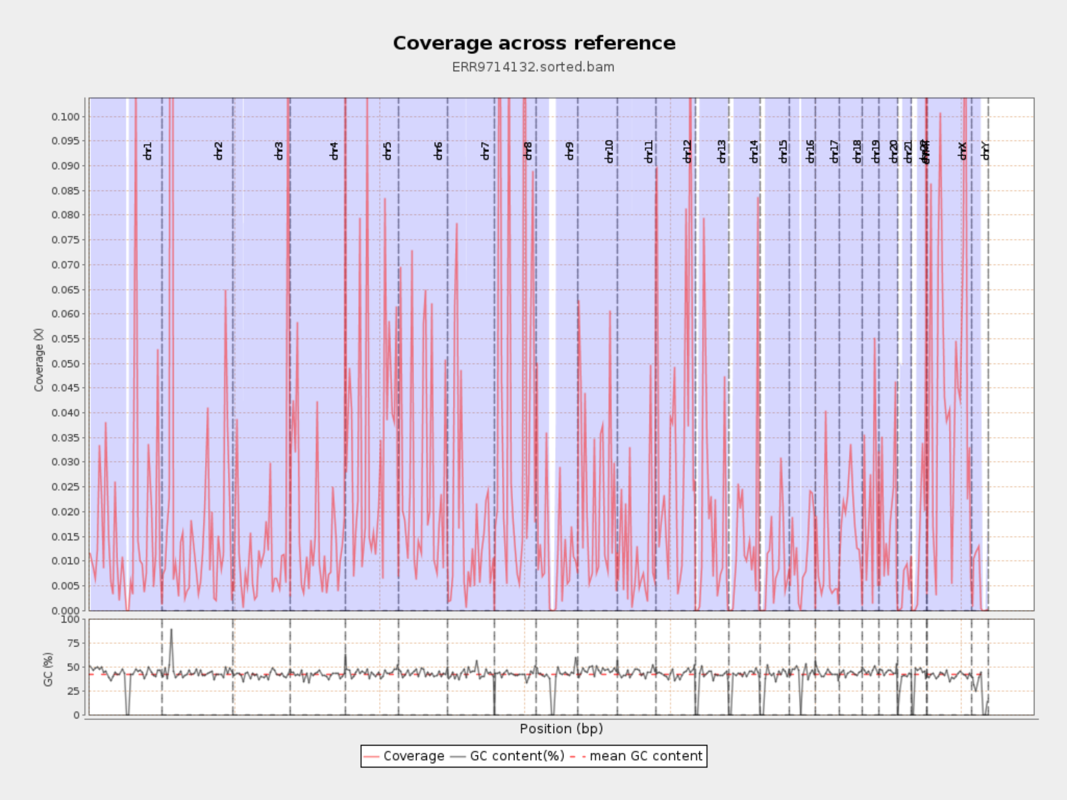
General error rate	4.65%
Mismatches	2,893,983
Insertions	74,151
Mapped reads with at least one insertion	13.68%
Deletions	258,968
Mapped reads with at least one deletion	46.29%
Homopolymer indels	30.04%

2.6. Chromosome stats

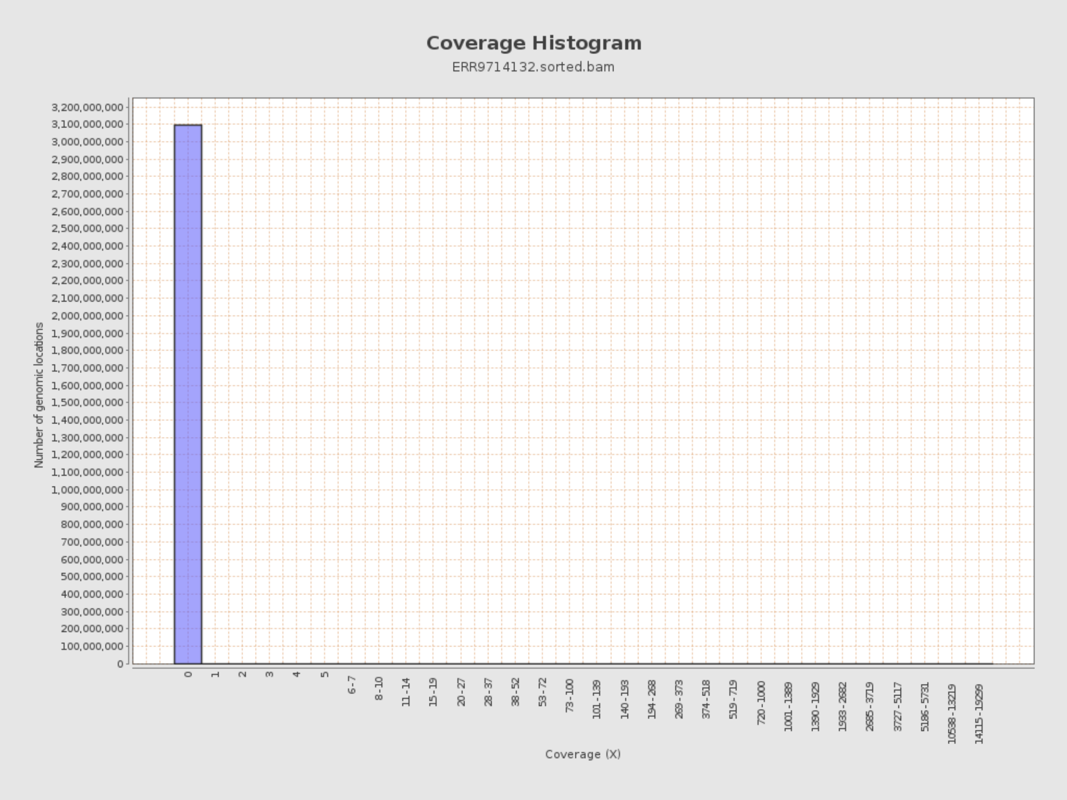
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3994471	0.016	3.131
chr2	243199373	6541018	0.0269	12.0637
chr3	198022430	2828911	0.0143	4.7766
chr4	191154276	3121114	0.0163	2.49
chr5	180915260	6397624	0.0354	6.2466
chr6	171115067	4693361	0.0274	4.2986
chr7	159138663	2853943	0.0179	3.3682

chr8	146364022	6724375	0.0459	9.2806
chr9	141213431	1442318	0.0102	1.6116
chr10	135534747	3393248	0.025	3.6563
chr11	135006516	1624597	0.012	1.8454
chr12	133851895	4690993	0.035	4.6521
chr13	115169878	2065412	0.0179	2.9543
chr14	107349540	1742963	0.0162	4.356
chr15	102531392	965643	0.0094	1.7838
chr16	90354753	1081042	0.012	1.5157
chr17	81195210	852268	0.0105	2.4819
chr18	78077248	1477784	0.0189	2.4308
chr19	59128983	1204088	0.0204	2.8107
chr20	63025520	1221523	0.0194	3.4521
chr21	48129895	229894	0.0048	0.5828
chr22	51304566	704972	0.0137	1.9886
chrMT	16571	501675	30.2743	243.5043
chrX	155270560	7456960	0.048	5.0411
chrY	59373566	279230	0.0047	1.1678

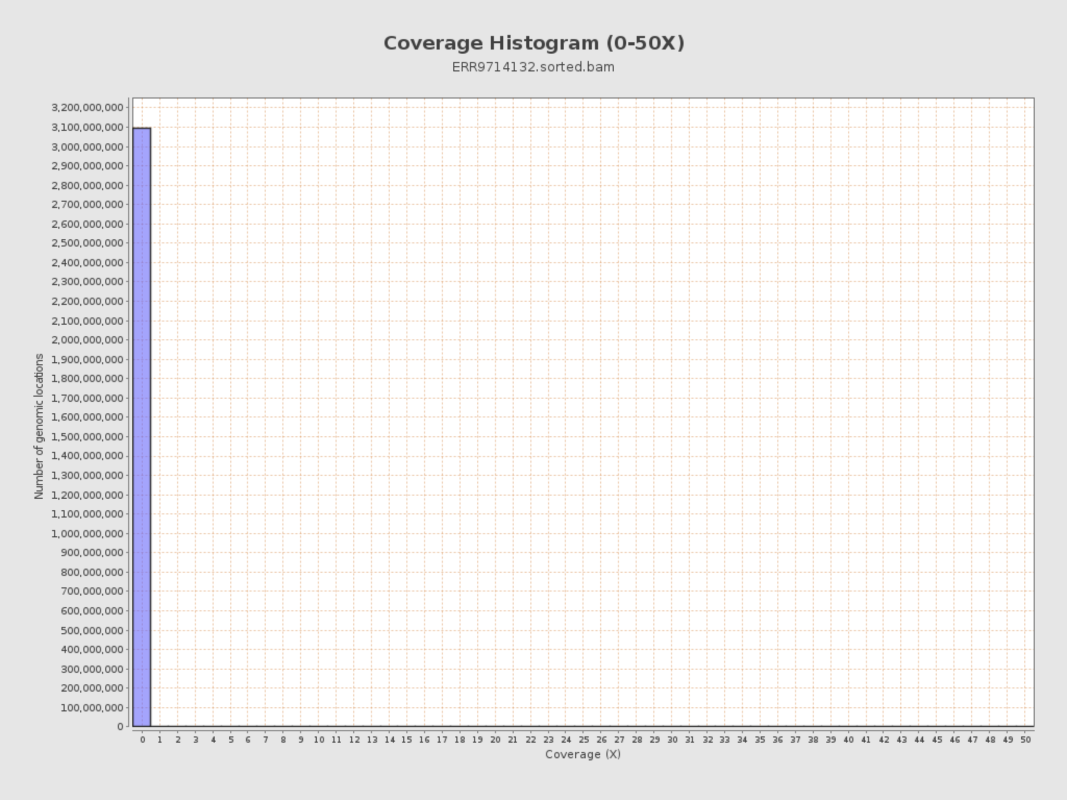
3. Results : Coverage across reference



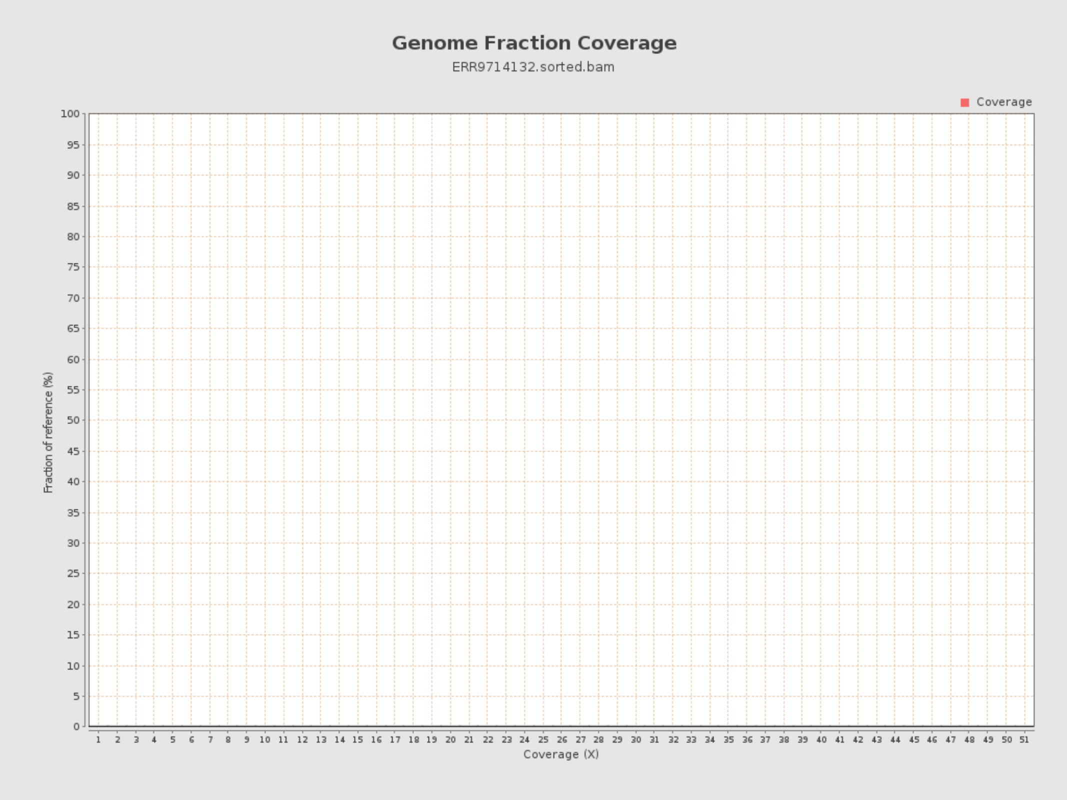
4. Results : Coverage Histogram



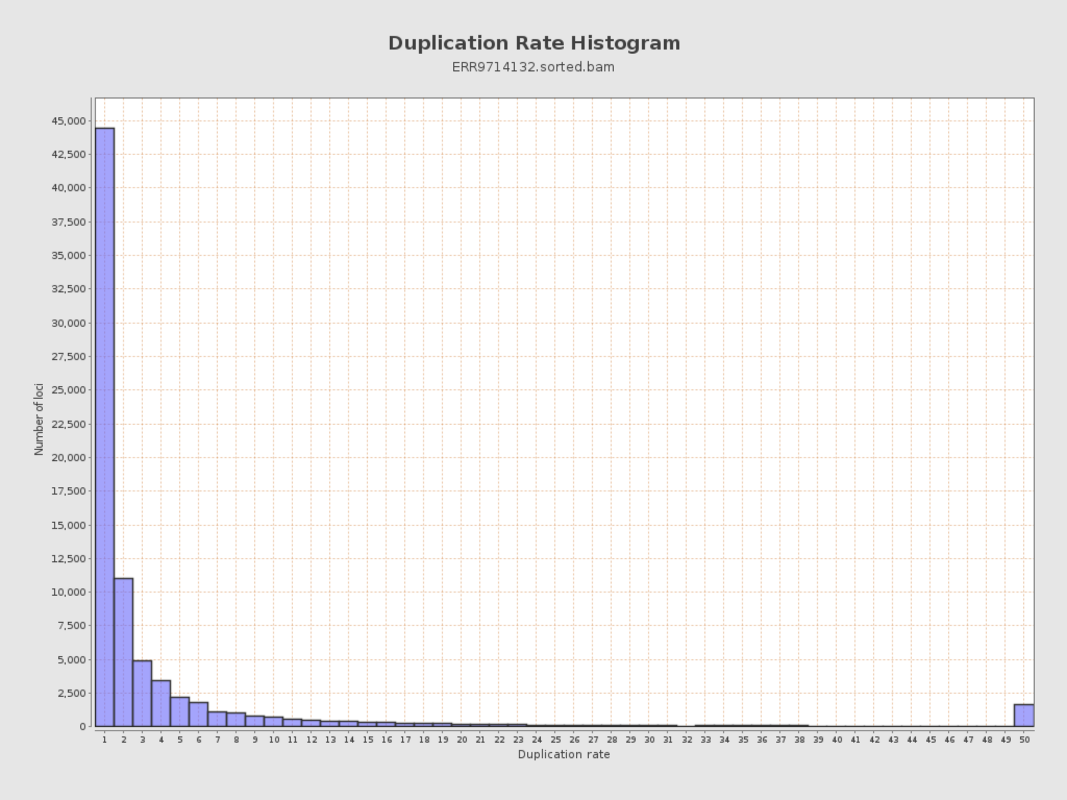
5. Results : Coverage Histogram (0-50X)



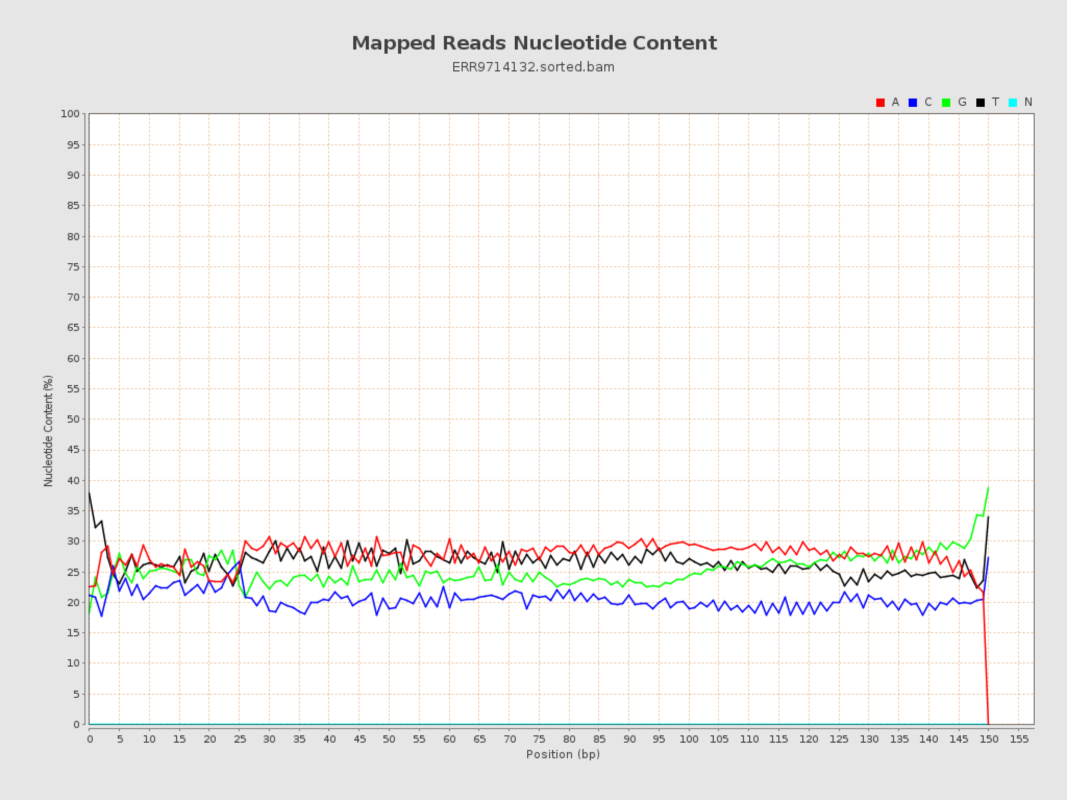
6. Results : Genome Fraction Coverage



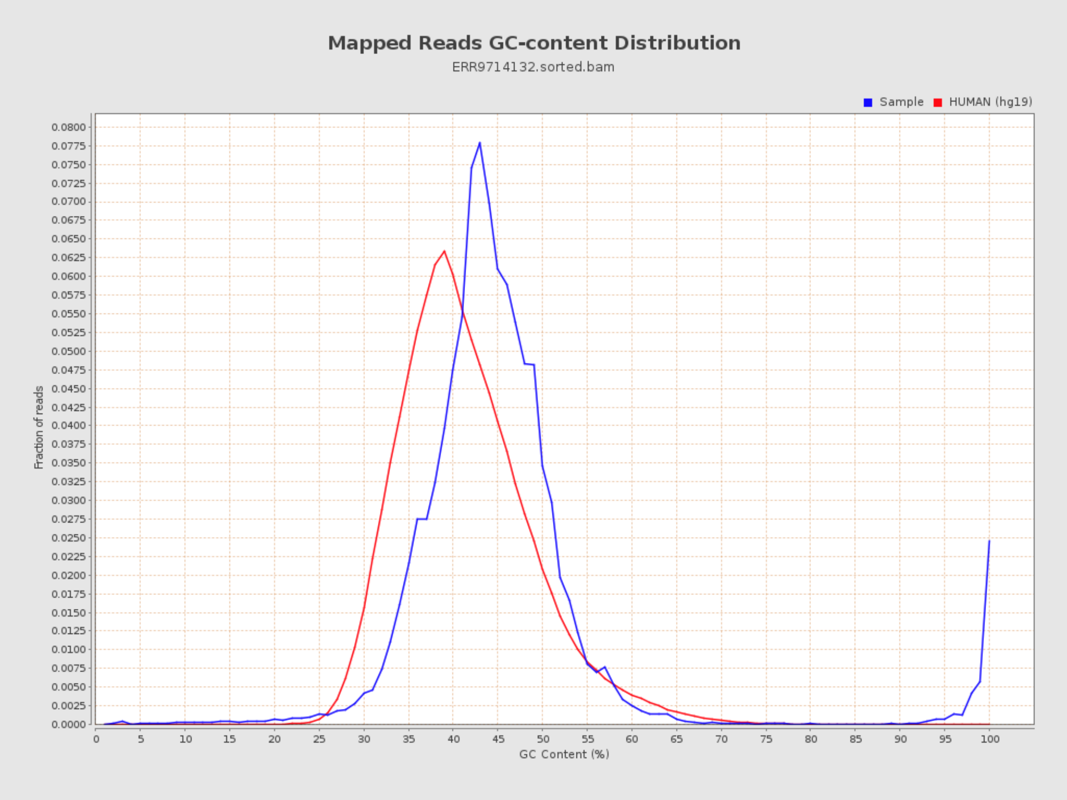
7. Results : Duplication Rate Histogram



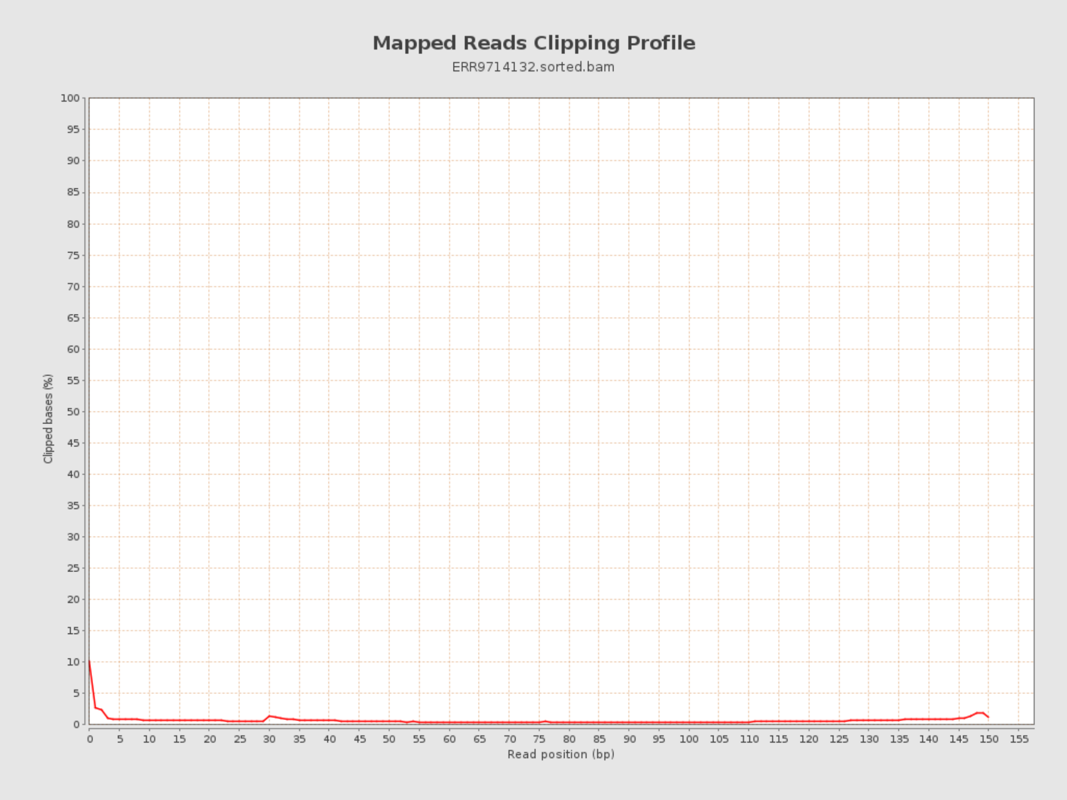
8. Results : Mapped Reads Nucleotide Content



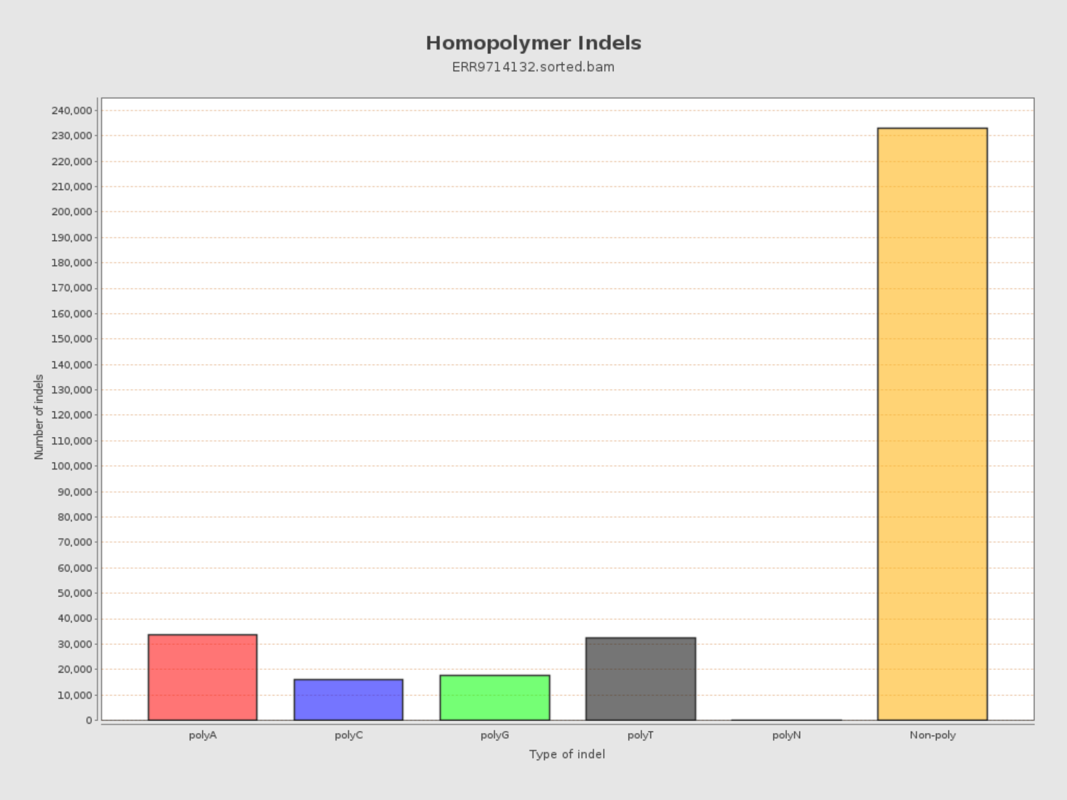
9. Results : Mapped Reads GC-content Distribution



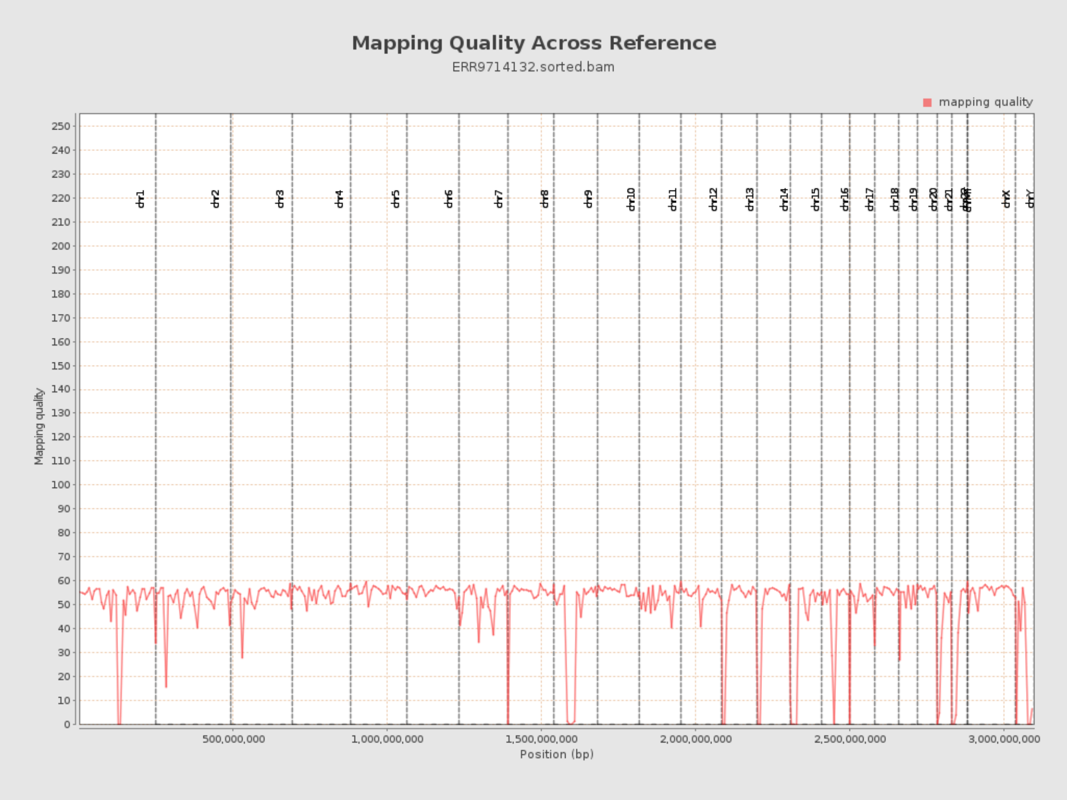
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram