Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 22:53:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714173.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_ERR9714173 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714173.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 22:53:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714173.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	921,010
Mapped reads	871,974 / 94.68%
Unmapped reads	49,036 / 5.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	37,288 / 4.05%
Read min/max/mean length	30 / 151 / 145.67
Duplicated reads (estimated)	824,018 / 89.47%
Duplication rate	40.98%
Clipped reads	845,454 / 91.8%

2.2. ACGT Content

Number/percentage of A's	32,866,976 / 29.94%
Number/percentage of C's	22,045,687 / 20.08%
Number/percentage of T's	30,853,258 / 28.1%
Number/percentage of G's	24,014,926 / 21.88%
Number/percentage of N's	635 / 0%
GC Percentage	41.96%

2.3. Coverage

Mean	0.0362

Standard Deviation	12.741

2.4. Mapping Quality

Mean Mapping Quality	47.86

2.5. Mismatches and indels

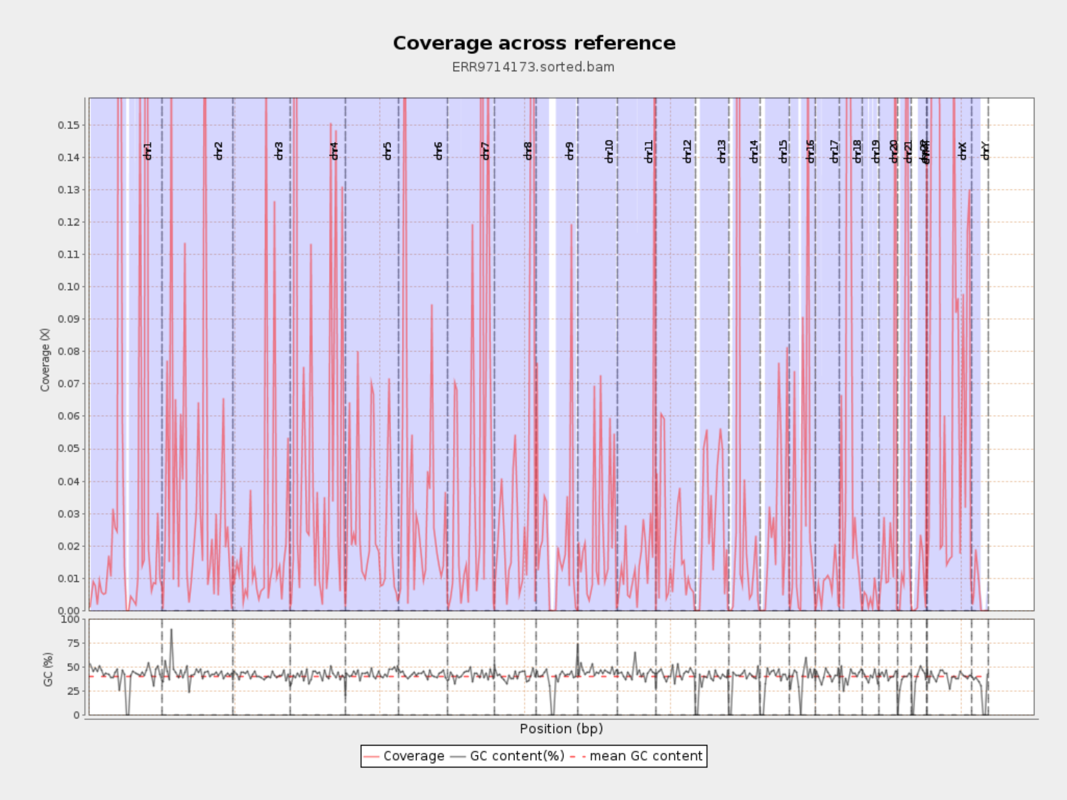
General error rate	4.49%
Mismatches	4,464,603
Insertions	135,479
Mapped reads with at least one insertion	15.09%
Deletions	378,034
Mapped reads with at least one deletion	41.33%
Homopolymer indels	25%

2.6. Chromosome stats

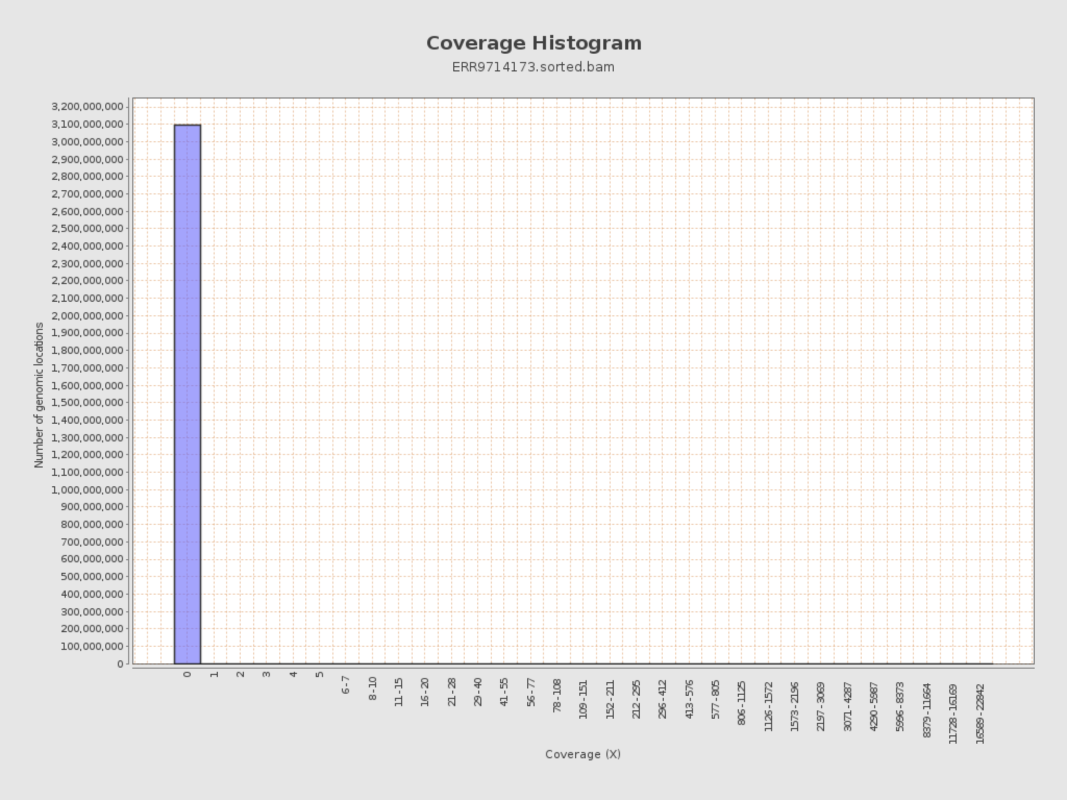
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10186593	0.0409	21.0114
chr2	243199373	9498068	0.0391	10.299
chr3	198022430	4655965	0.0235	6.9957
chr4	191154276	10935986	0.0572	15.6864
chr5	180915260	4926903	0.0272	6.459
chr6	171115067	5986284	0.035	8.3804
chr7	159138663	8228401	0.0517	17.2748

chr8	146364022	6500916	0.0444	12.4718
chr9	141213431	2865014	0.0203	4.1265
chr10	135534747	3343963	0.0247	3.8173
chr11	135006516	3290443	0.0244	8.3953
chr12	133851895	2608710	0.0195	4.2432
chr13	115169878	3083717	0.0268	4.9359
chr14	107349540	4341043	0.0404	22.9038
chr15	102531392	2698769	0.0263	6.9482
chr16	90354753	3294670	0.0365	10.7078
chr17	81195210	676551	0.0083	1.136
chr18	78077248	4658772	0.0597	19.7913
chr19	59128983	210245	0.0036	0.5698
chr20	63025520	2717684	0.0431	18.9187
chr21	48129895	2177140	0.0452	22.6399
chr22	51304566	371235	0.0072	1.3892
chrMT	16571	2379	0.1436	1.3389
chrX	155270560	14592221	0.094	18.1821
chrY	59373566	260168	0.0044	0.8834

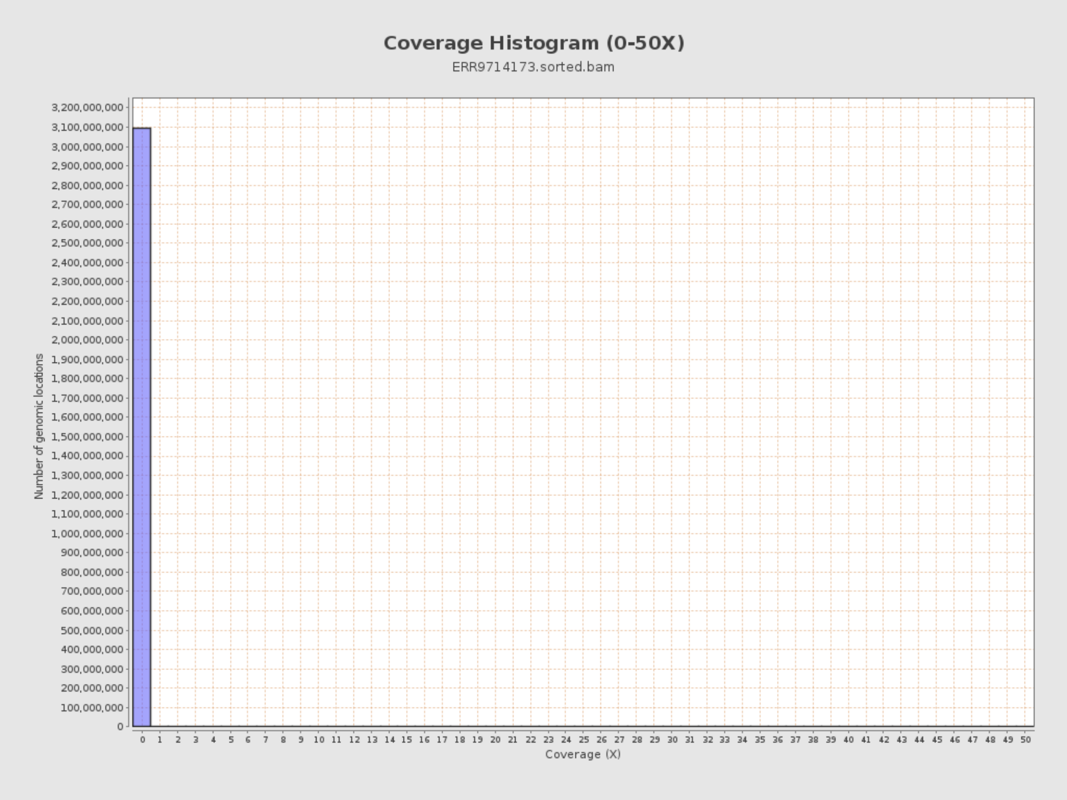
3. Results : Coverage across reference



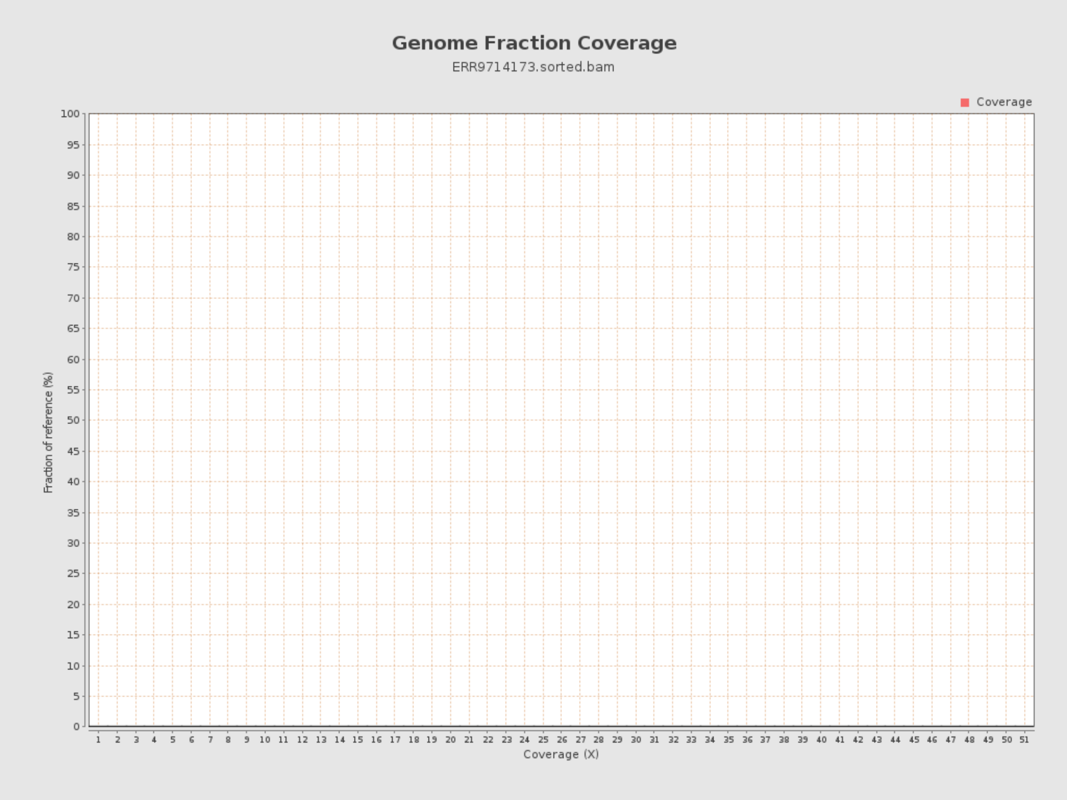
4. Results : Coverage Histogram



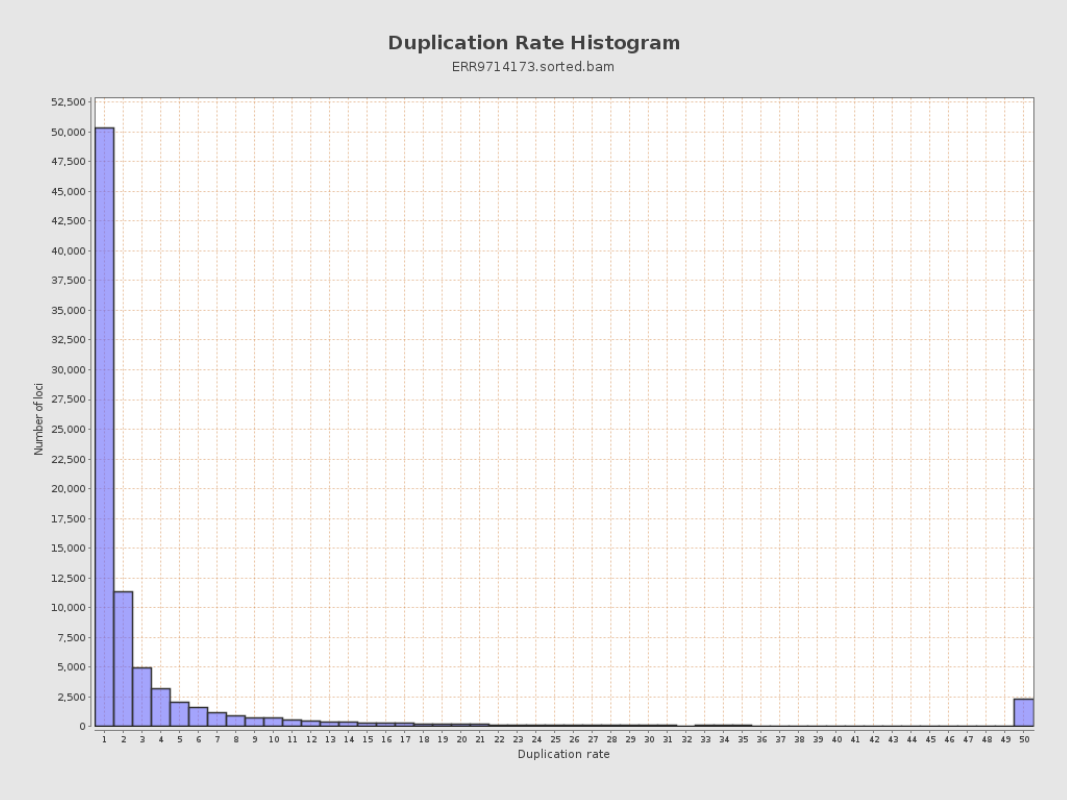
5. Results : Coverage Histogram (0-50X)



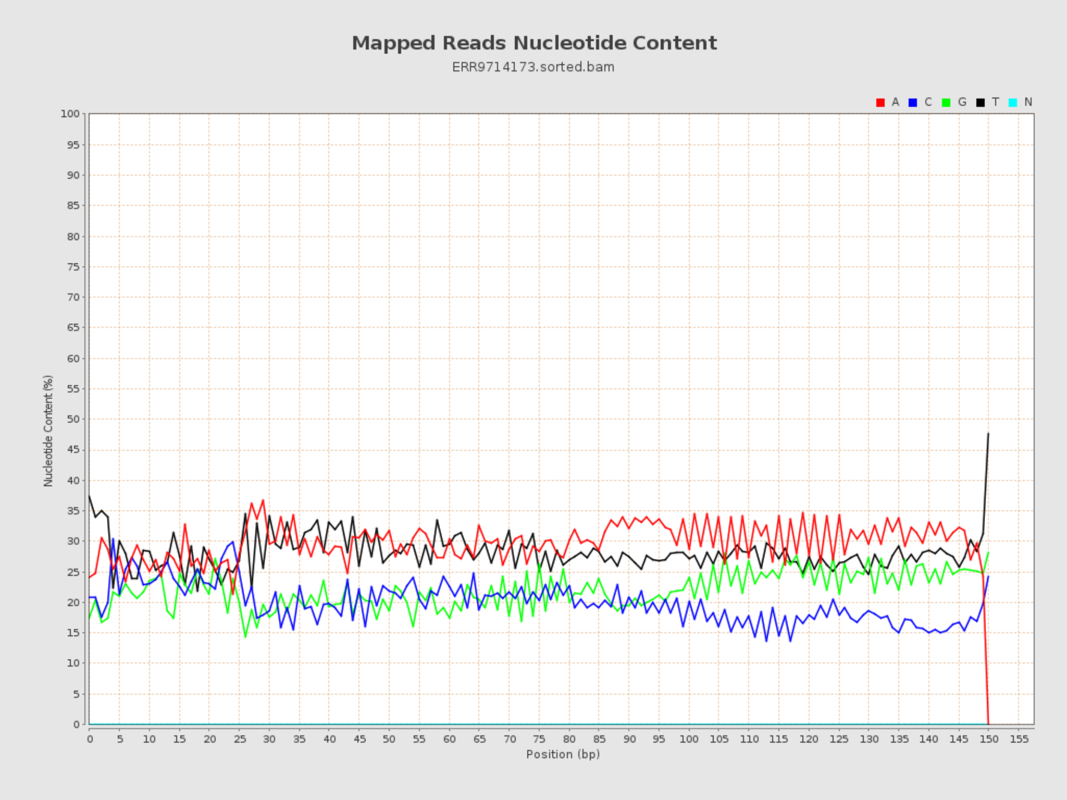
6. Results : Genome Fraction Coverage



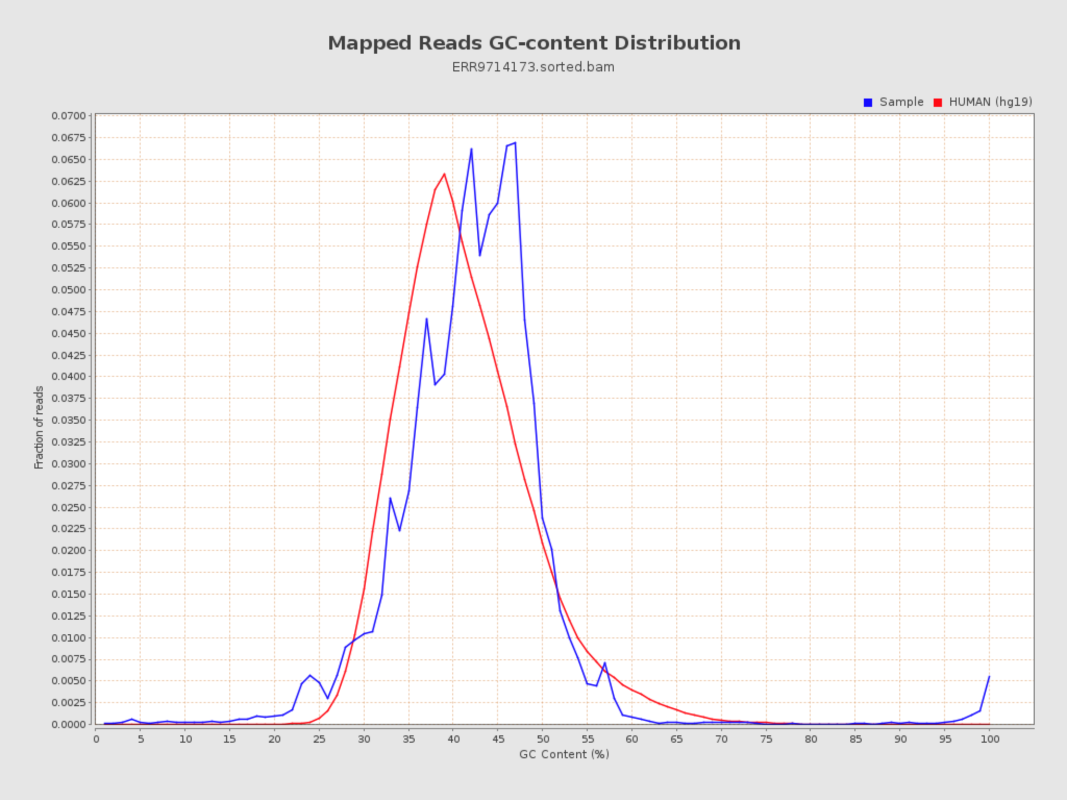
7. Results : Duplication Rate Histogram



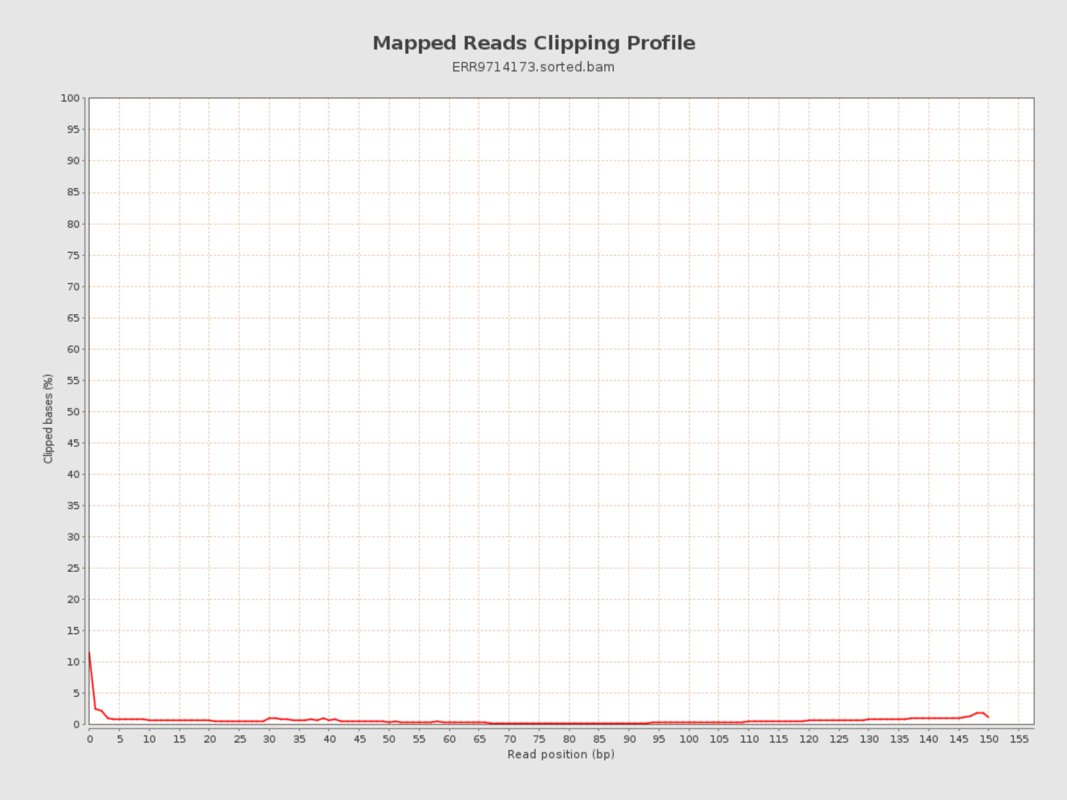
8. Results : Mapped Reads Nucleotide Content



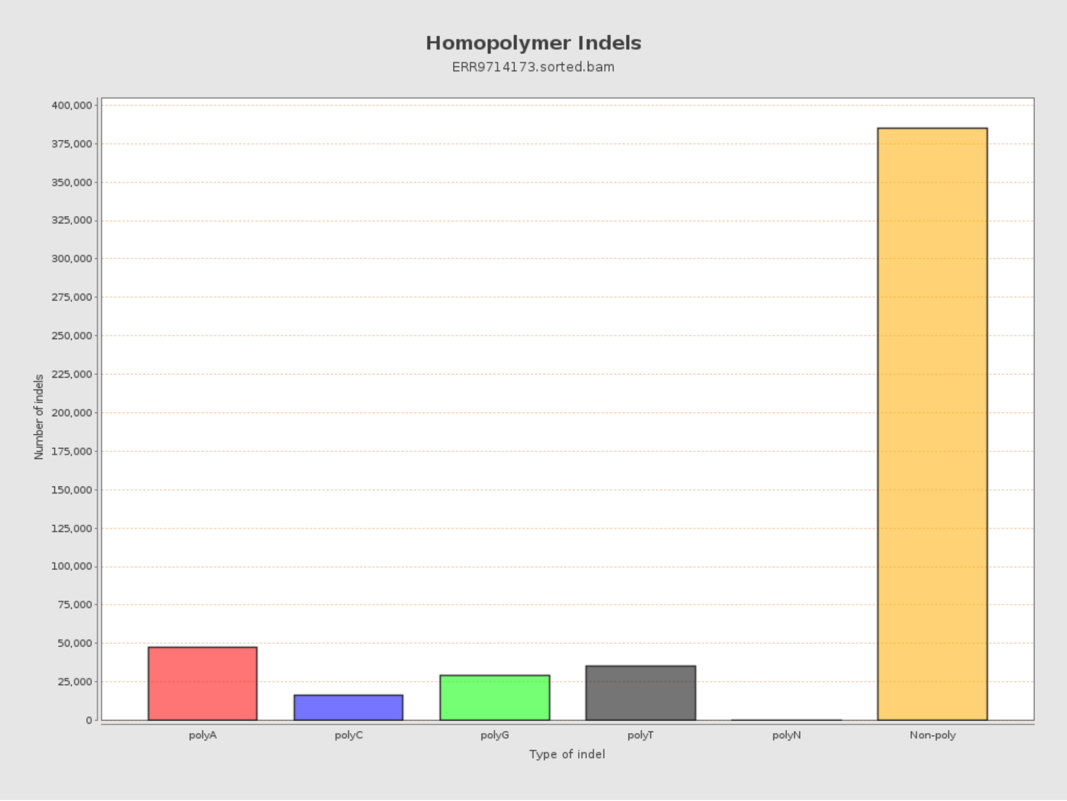
9. Results : Mapped Reads GC-content Distribution



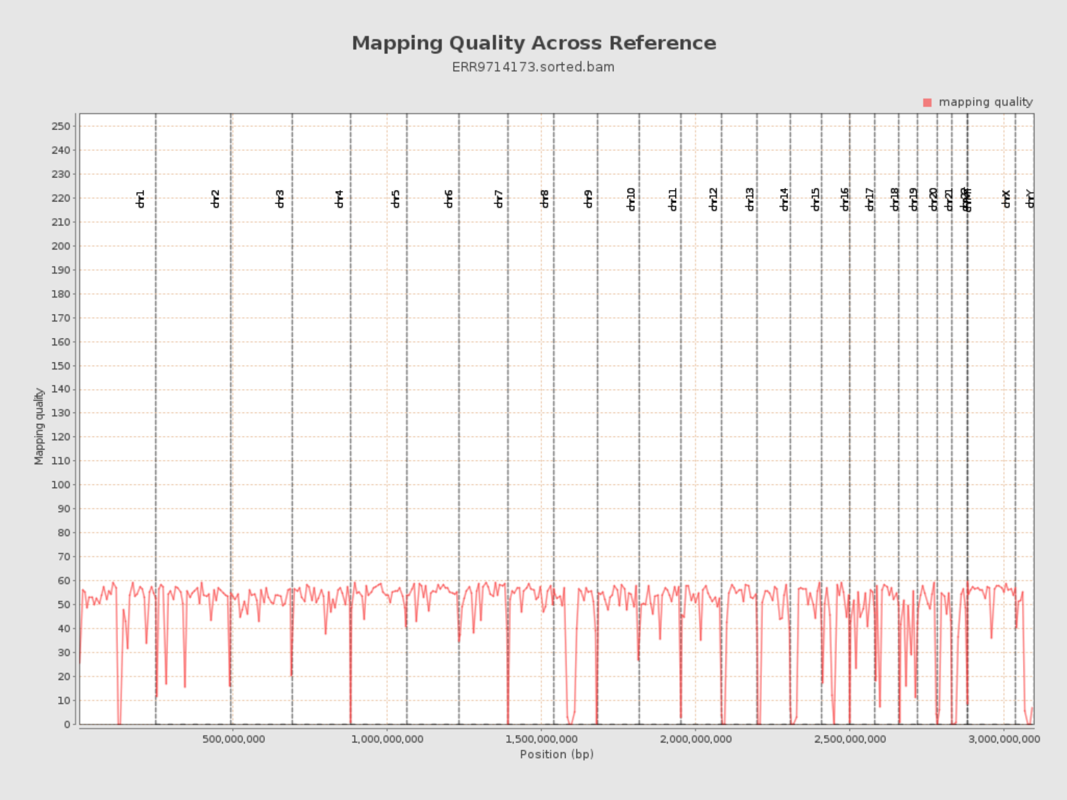
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram