Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 21:02:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714136.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_ERR9714136 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714136.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 21:02:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714136.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	664,782
Mapped reads	578,799 / 87.07%
Unmapped reads	85,983 / 12.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,971 / 2.55%
Read min/max/mean length	30 / 151 / 137.16
Duplicated reads (estimated)	517,767 / 77.89%
Duplication rate	44.13%
Clipped reads	545,760 / 82.1%

2.2. ACGT Content

Number/percentage of A's	19,679,685 / 26.66%
Number/percentage of C's	16,682,673 / 22.6%
Number/percentage of T's	18,676,484 / 25.3%
Number/percentage of G's	18,766,499 / 25.43%
Number/percentage of N's	598 / 0%
GC Percentage	48.03%

2.3. Coverage

Mean	0.0244

Standard Deviation	6.3381

2.4. Mapping Quality

Mean Mapping Quality	51.69

2.5. Mismatches and indels

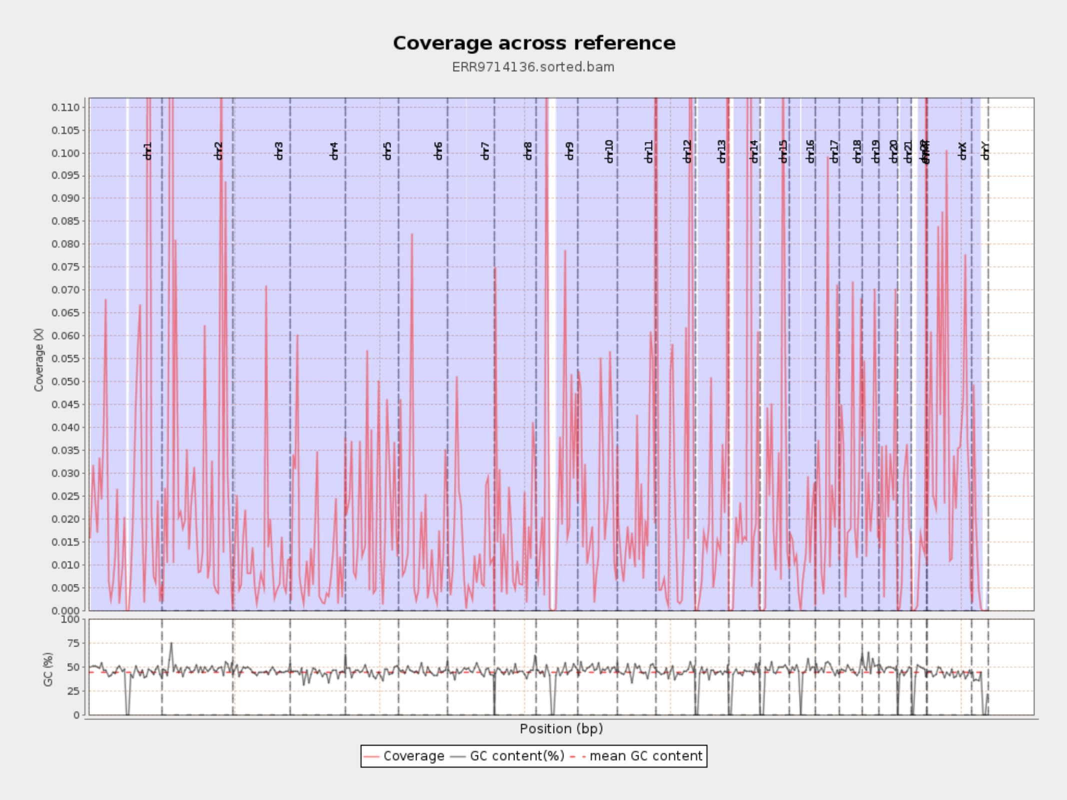
General error rate	4.38%
Mismatches	3,022,549
Insertions	78,577
Mapped reads with at least one insertion	13.07%
Deletions	266,983
Mapped reads with at least one deletion	43.88%
Homopolymer indels	29.92%

2.6. Chromosome stats

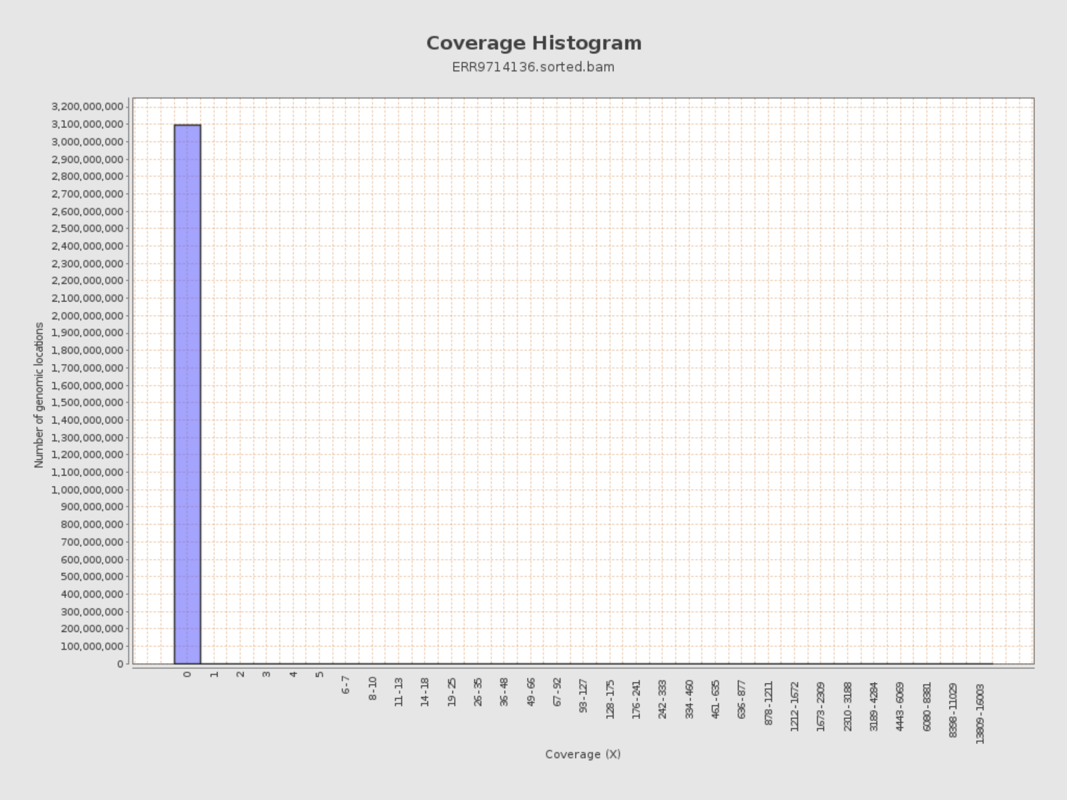
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6660432	0.0267	6.8282
chr2	243199373	9370810	0.0385	10.5847
chr3	198022430	2353035	0.0119	2.2501
chr4	191154276	2436252	0.0127	2.5861
chr5	180915260	3996384	0.0221	3.944
chr6	171115067	2929930	0.0171	3.2488
chr7	159138663	2159815	0.0136	2.2306

chr8	146364022	2725939	0.0186	3.8548
chr9	141213431	3749780	0.0266	6.781
chr10	135534747	3469386	0.0256	3.9395
chr11	135006516	3355238	0.0249	4.4628
chr12	133851895	4178011	0.0312	8.0204
chr13	115169878	2700857	0.0235	7.0423
chr14	107349540	4119647	0.0384	18.1773
chr15	102531392	2950415	0.0288	5.4842
chr16	90354753	1245618	0.0138	1.8304
chr17	81195210	2676243	0.033	5.7151
chr18	78077248	2285280	0.0293	6.3123
chr19	59128983	1884495	0.0319	3.3082
chr20	63025520	1856987	0.0295	3.6794
chr21	48129895	766953	0.0159	3.0137
chr22	51304566	446700	0.0087	1.0003
chrMT	16571	173077	10.4446	86.6667
chrX	155270560	6405218	0.0413	4.3547
chrY	59373566	582318	0.0098	2.3864

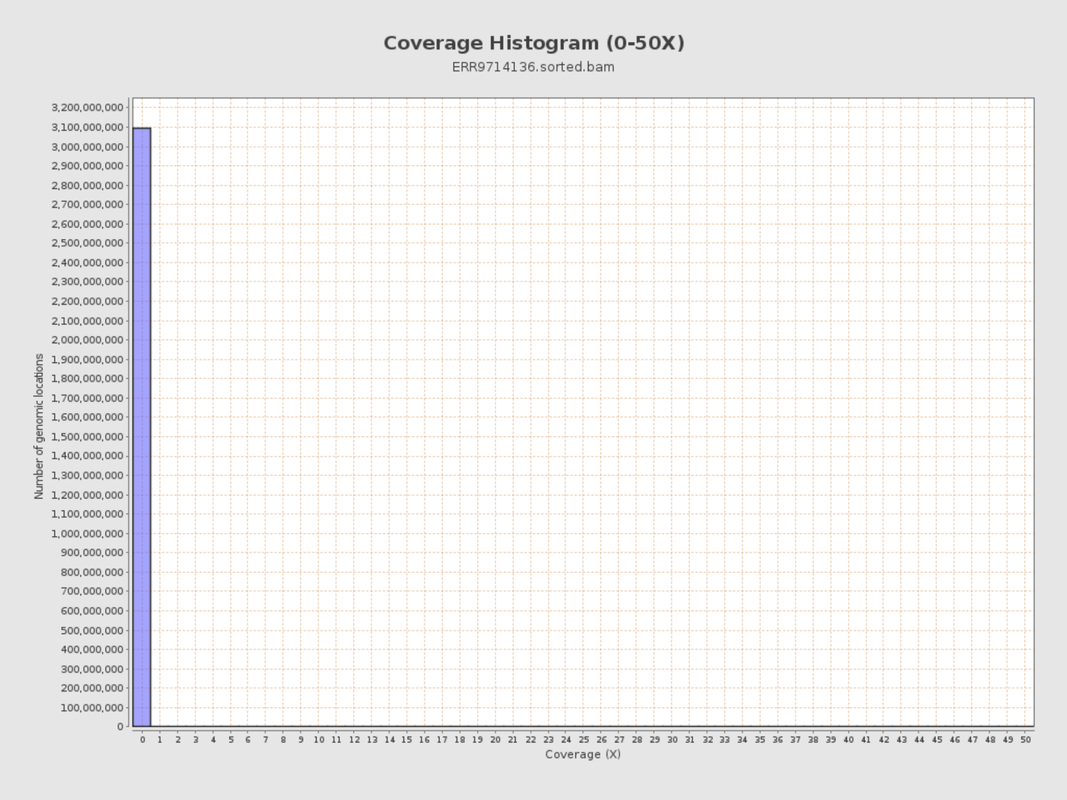
3. Results : Coverage across reference



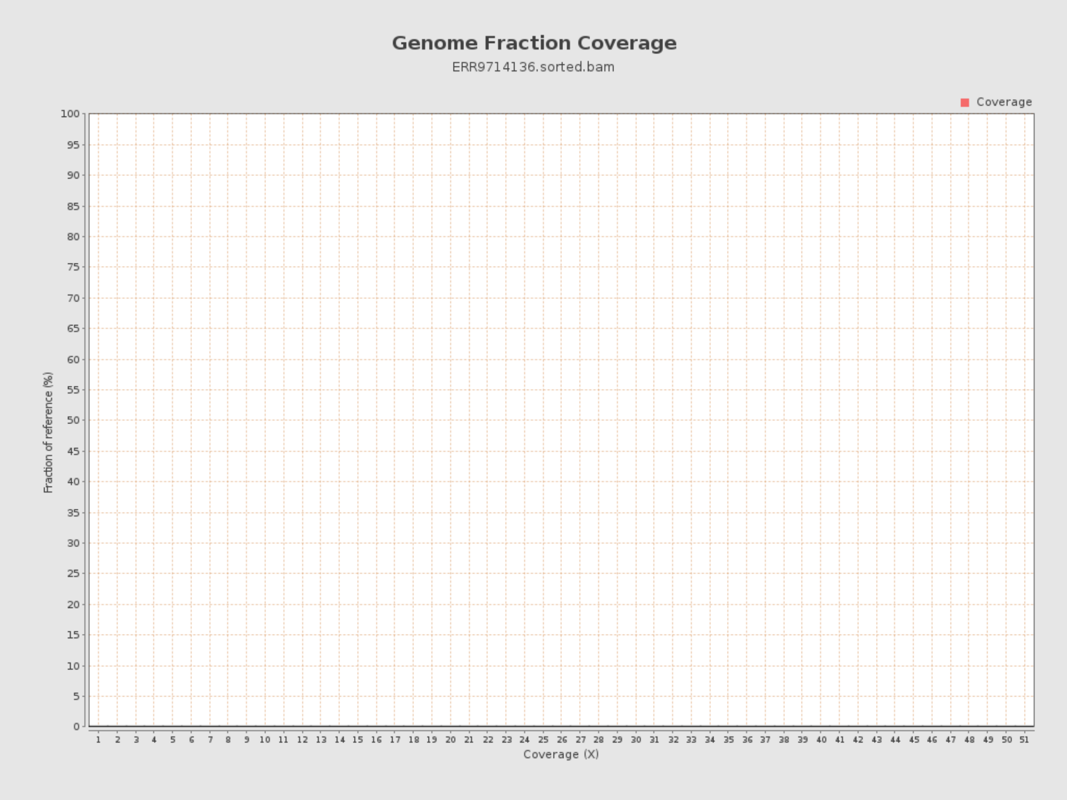
4. Results : Coverage Histogram



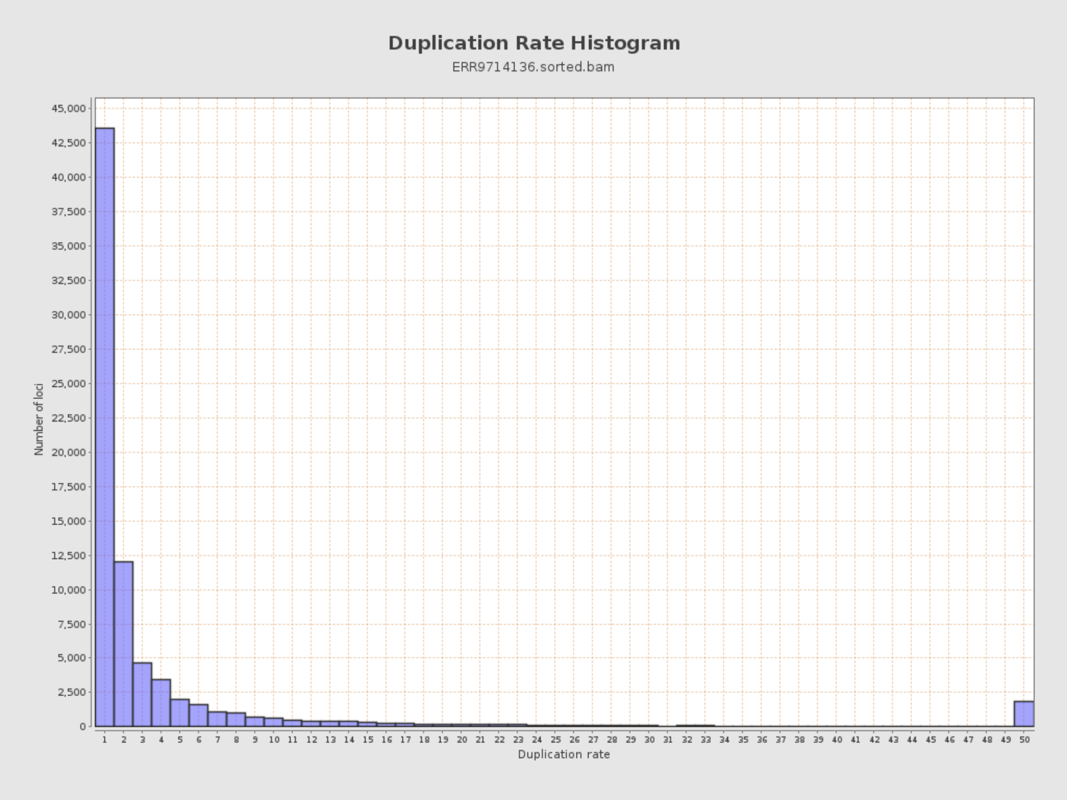
5. Results : Coverage Histogram (0-50X)



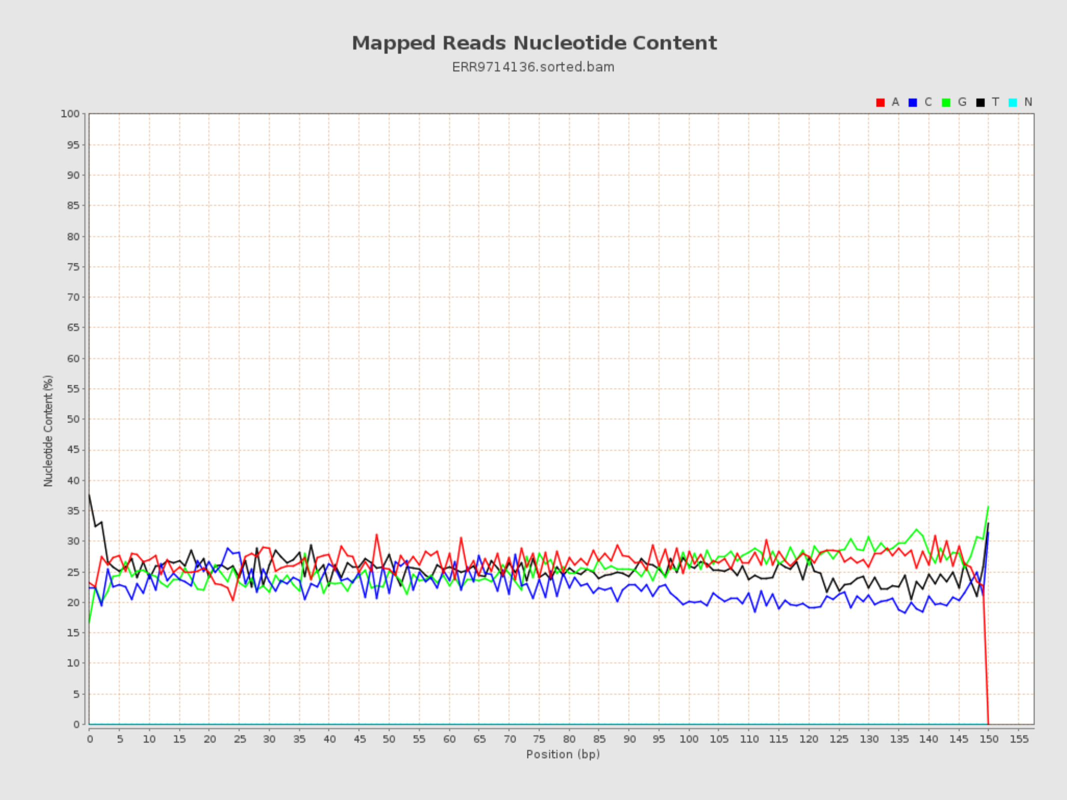
6. Results : Genome Fraction Coverage



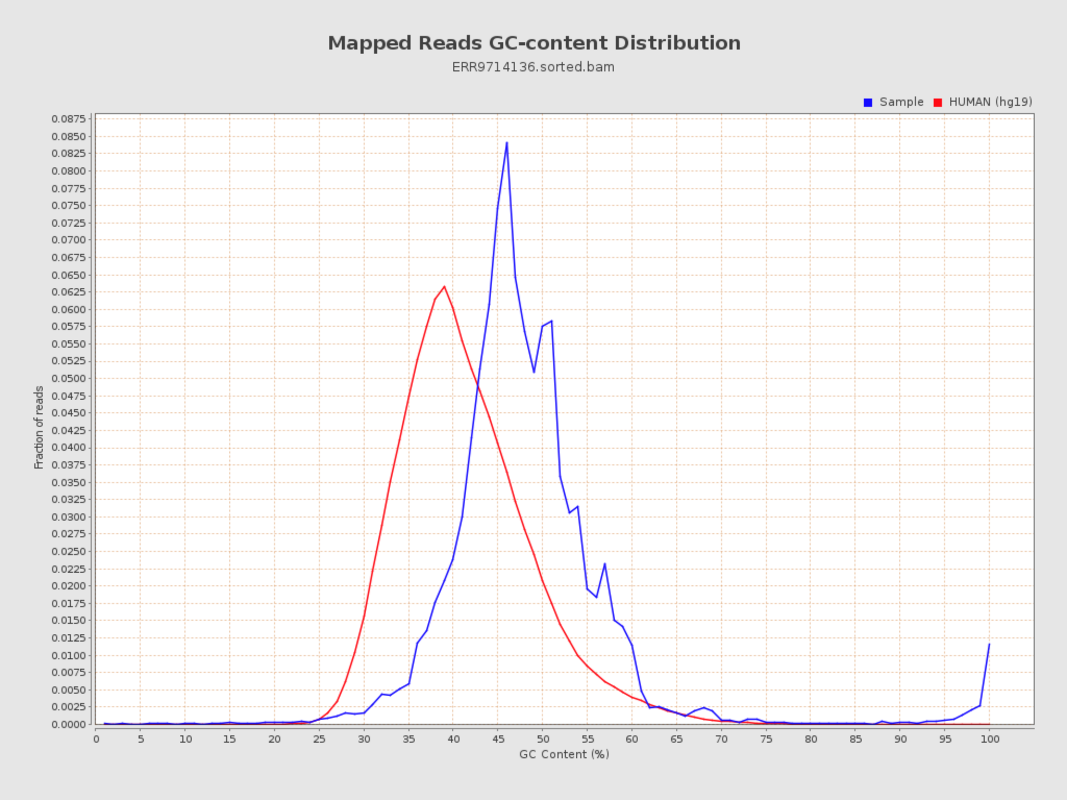
7. Results : Duplication Rate Histogram



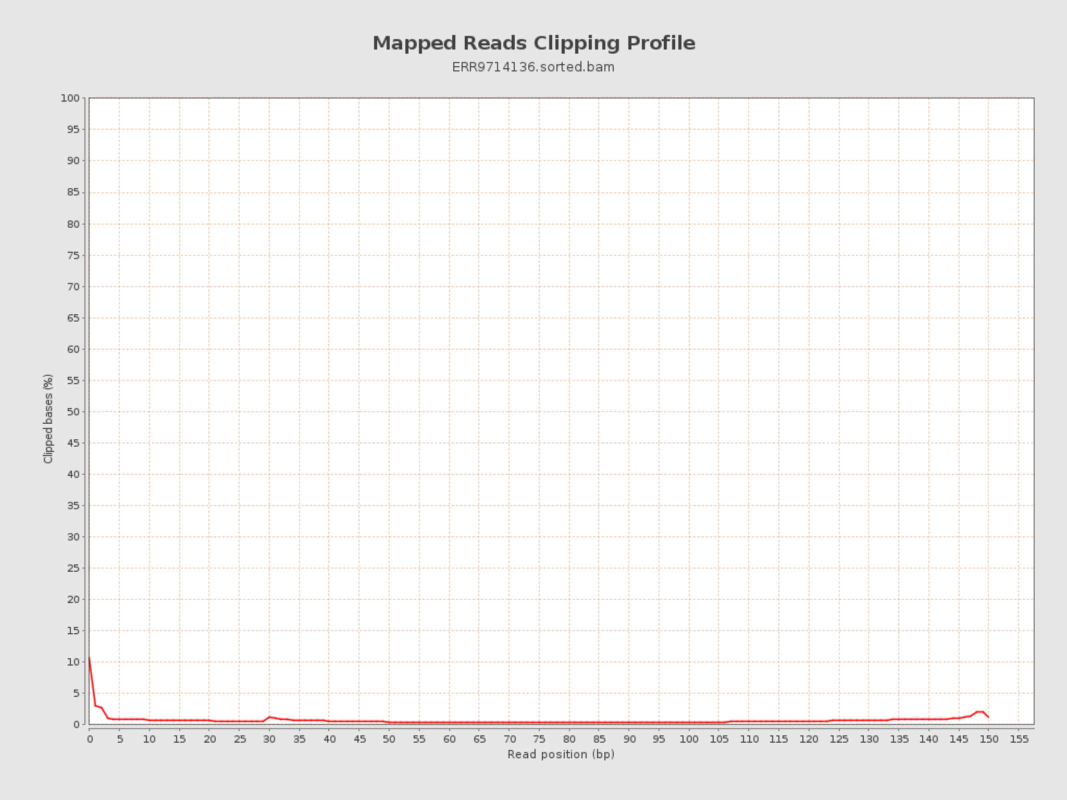
8. Results : Mapped Reads Nucleotide Content



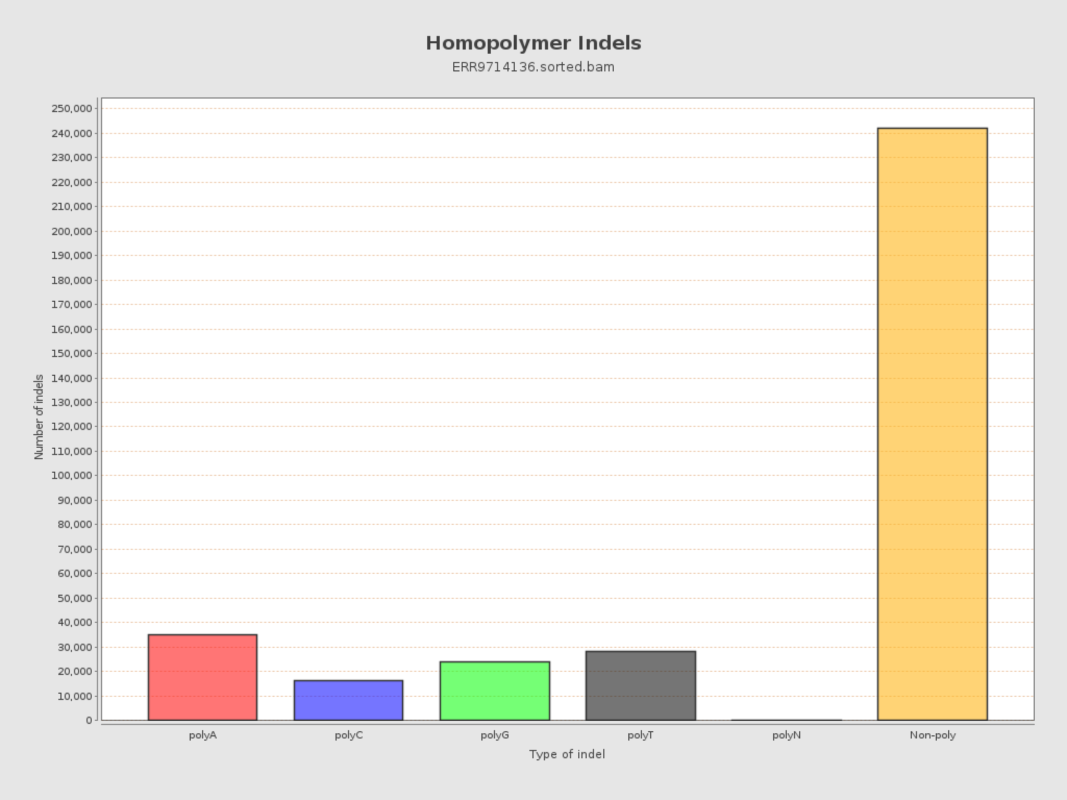
9. Results : Mapped Reads GC-content Distribution



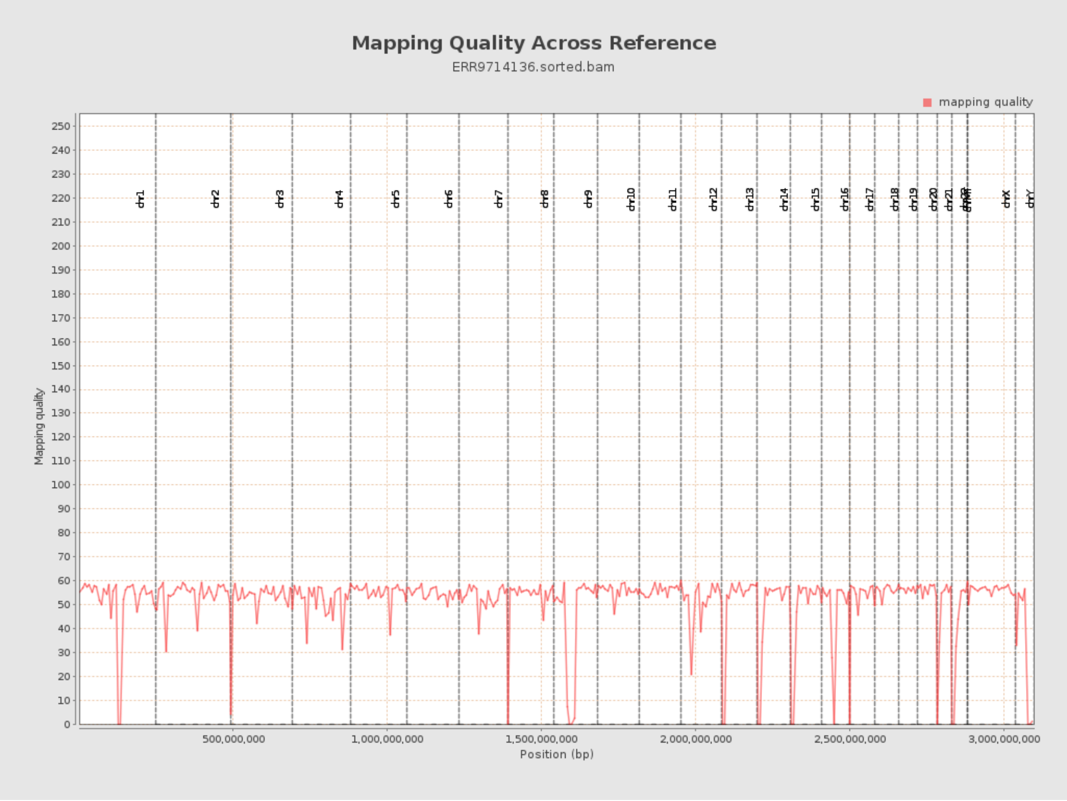
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram