Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 19:21:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714100.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_ERR9714100 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714100.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 19:21:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714100.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	549,398
Mapped reads	441,074 / 80.28%
Unmapped reads	108,324 / 19.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,709 / 2.5%
Read min/max/mean length	30 / 151 / 131.21
Duplicated reads (estimated)	377,672 / 68.74%
Duplication rate	43.94%
Clipped reads	409,770 / 74.59%

2.2. ACGT Content

Number/percentage of A's	15,760,166 / 28.02%
Number/percentage of C's	11,647,550 / 20.71%
Number/percentage of T's	15,060,506 / 26.78%
Number/percentage of G's	13,771,874 / 24.49%
Number/percentage of N's	494 / 0%
GC Percentage	45.2%

2.3. Coverage

Mean	0.0186

Standard Deviation	3.8697

2.4. Mapping Quality

Mean Mapping Quality	51.5

2.5. Mismatches and indels

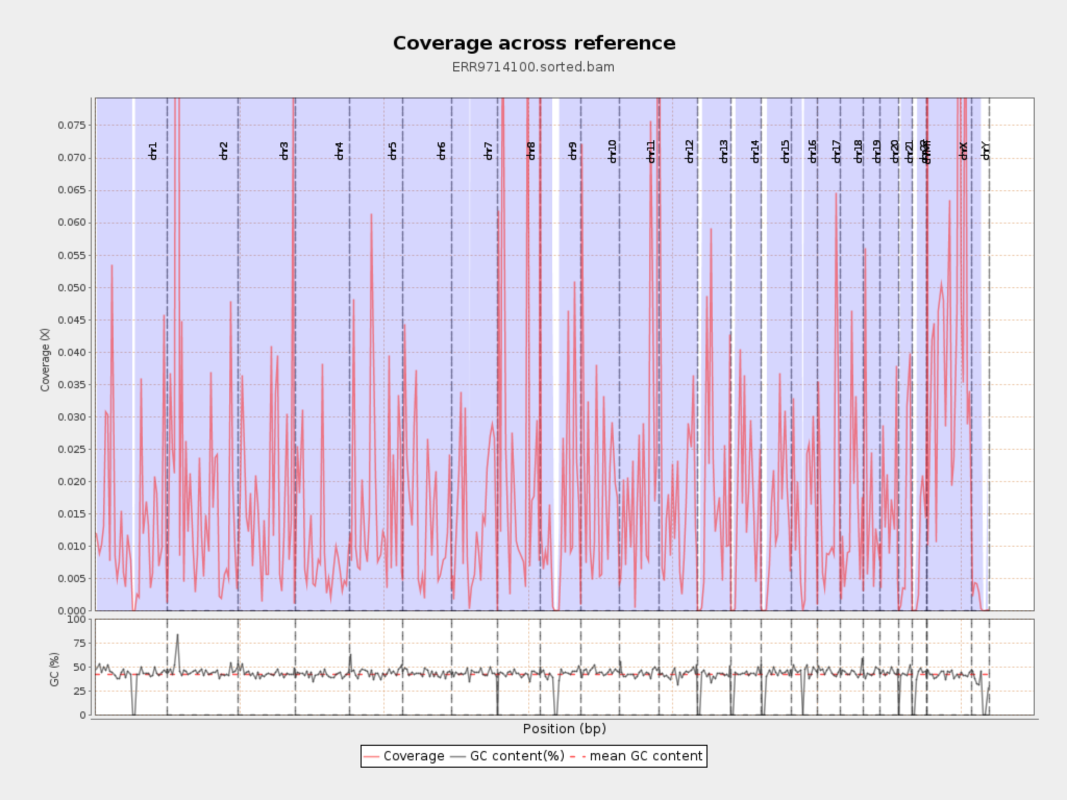
General error rate	4.76%
Mismatches	2,491,600
Insertions	66,189
Mapped reads with at least one insertion	14.34%
Deletions	222,997
Mapped reads with at least one deletion	46.54%
Homopolymer indels	29.57%

2.6. Chromosome stats

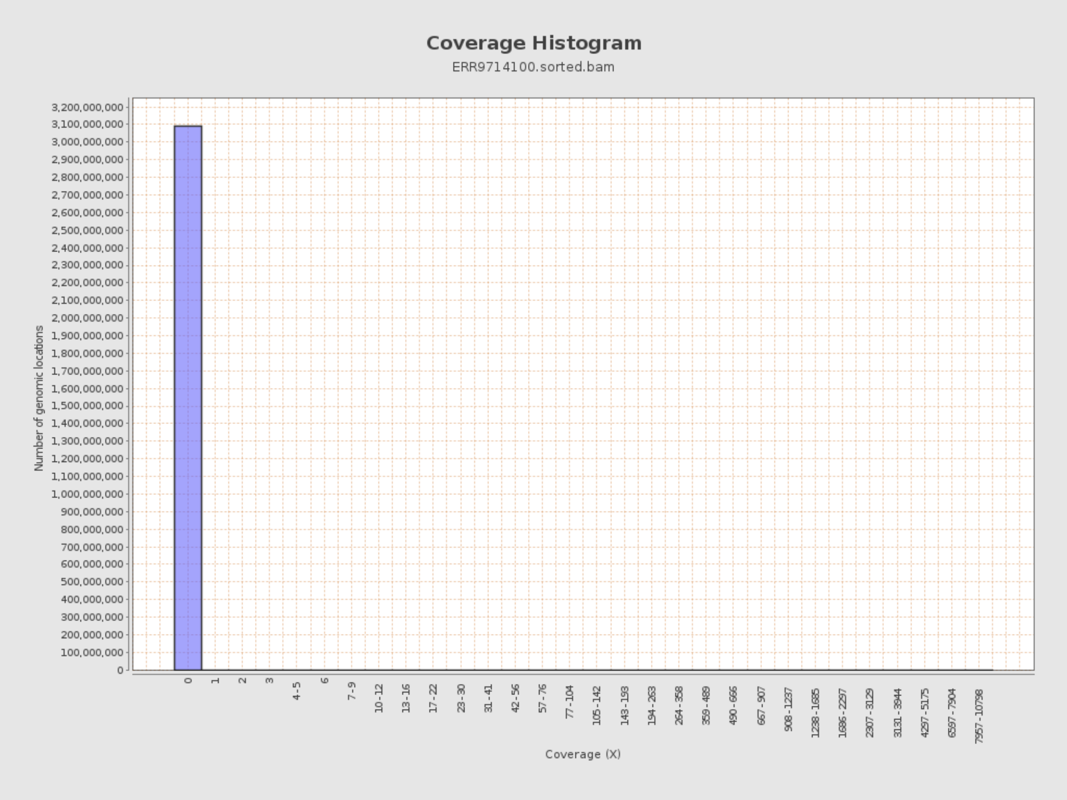
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3341552	0.0134	2.0545
chr2	243199373	6242997	0.0257	8.0061
chr3	198022430	3747906	0.0189	3.7854
chr4	191154276	1896610	0.0099	1.5876
chr5	180915260	3362173	0.0186	3.15
chr6	171115067	2634856	0.0154	2.2994
chr7	159138663	2270859	0.0143	2.1791

chr8	146364022	3713119	0.0254	5.5398
chr9	141213431	2049011	0.0145	2.5192
chr10	135534747	2722848	0.0201	3.2026
chr11	135006516	2980133	0.0221	4.6247
chr12	133851895	2430698	0.0182	2.6623
chr13	115169878	2049207	0.0178	3.653
chr14	107349540	1826558	0.017	2.6956
chr15	102531392	1441737	0.0141	1.734
chr16	90354753	1409685	0.0156	1.8999
chr17	81195210	1548164	0.0191	3.3355
chr18	78077248	1279675	0.0164	2.5349
chr19	59128983	997296	0.0169	3.4966
chr20	63025520	1110396	0.0176	2.7423
chr21	48129895	658777	0.0137	3.3641
chr22	51304566	494574	0.0096	1.1941
chrMT	16571	294318	17.761	135.9273
chrX	155270560	7023930	0.0452	6.1326
chrY	59373566	102648	0.0017	0.2779

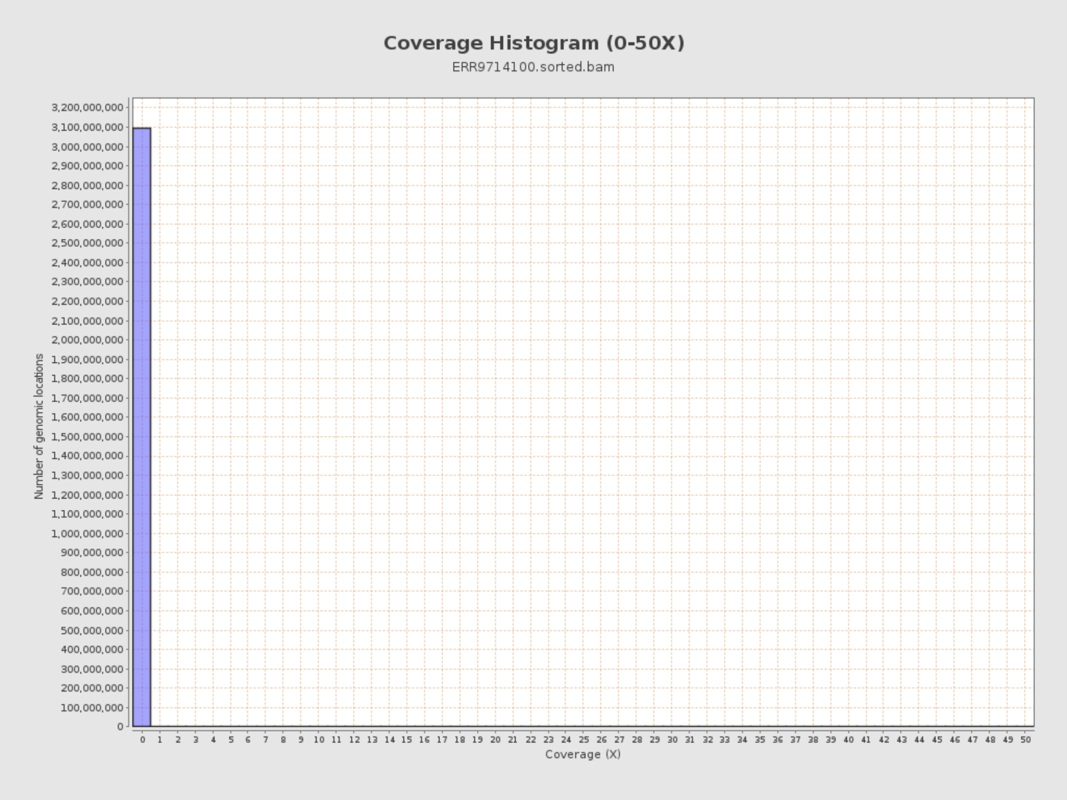
3. Results : Coverage across reference



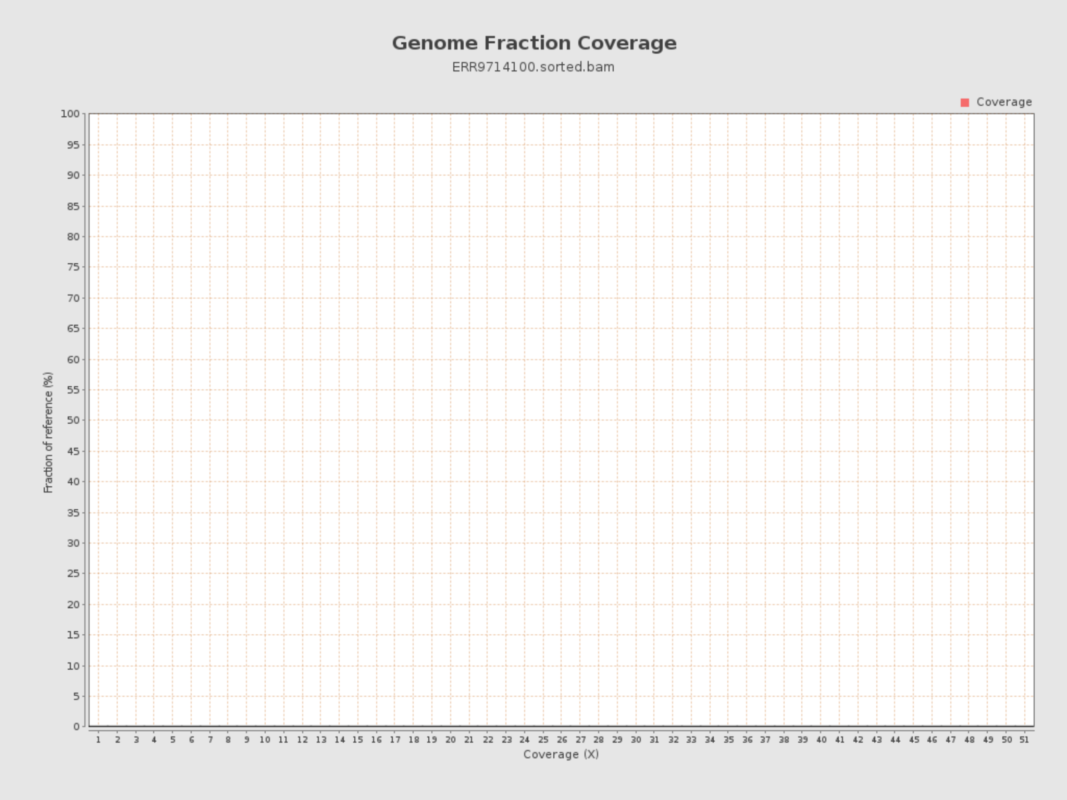
4. Results : Coverage Histogram



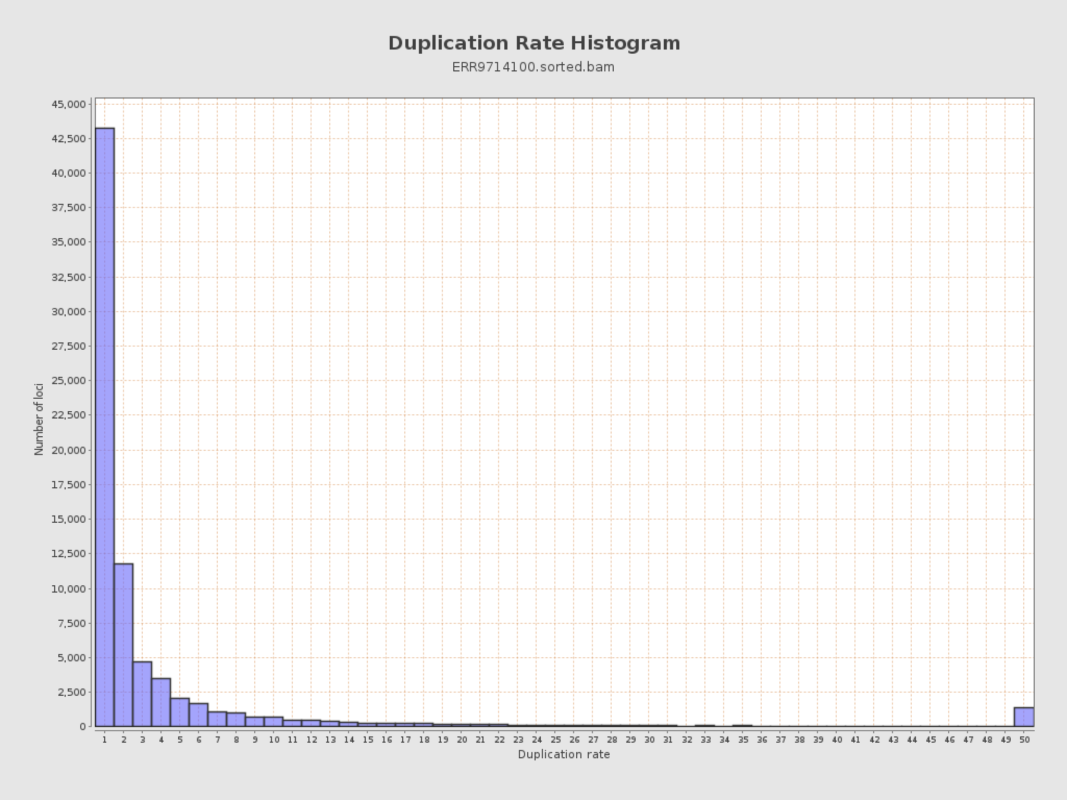
5. Results : Coverage Histogram (0-50X)



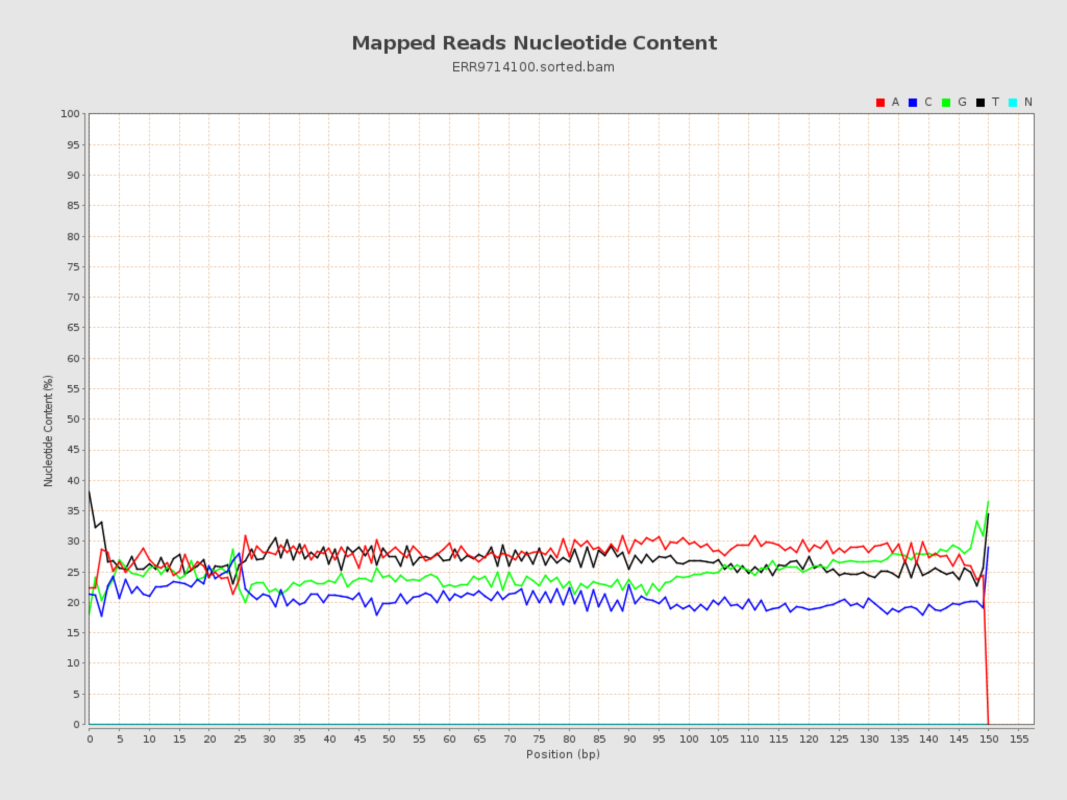
6. Results : Genome Fraction Coverage



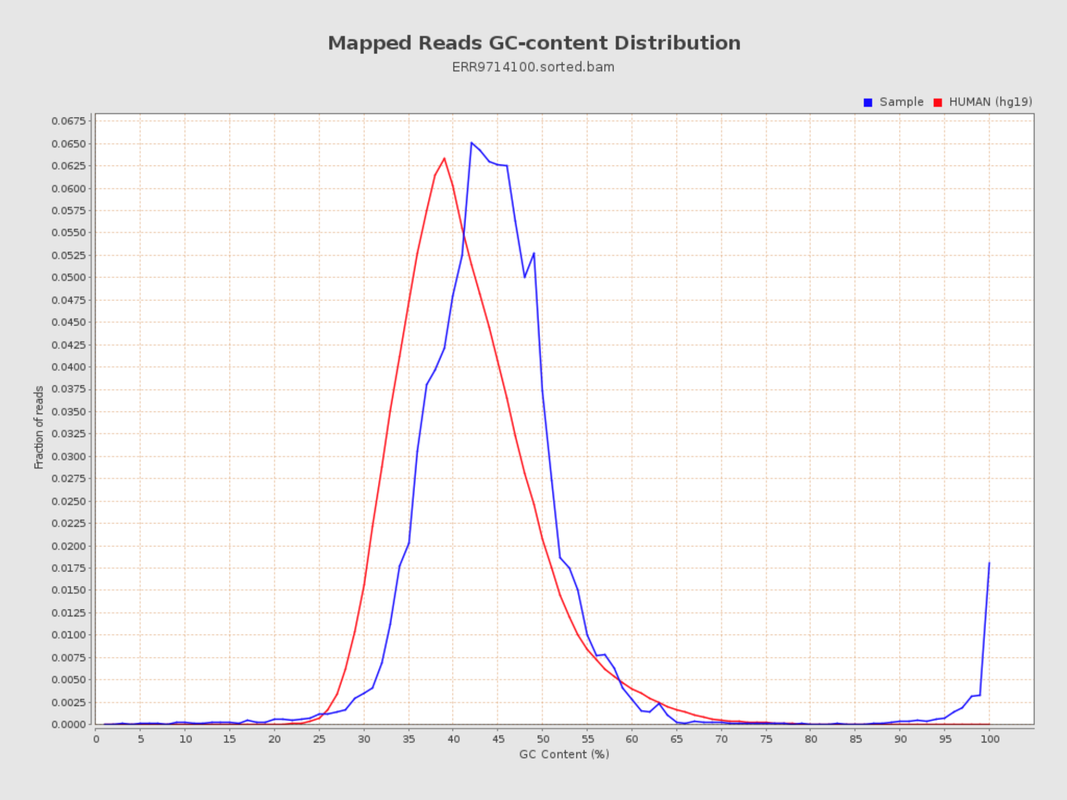
7. Results : Duplication Rate Histogram



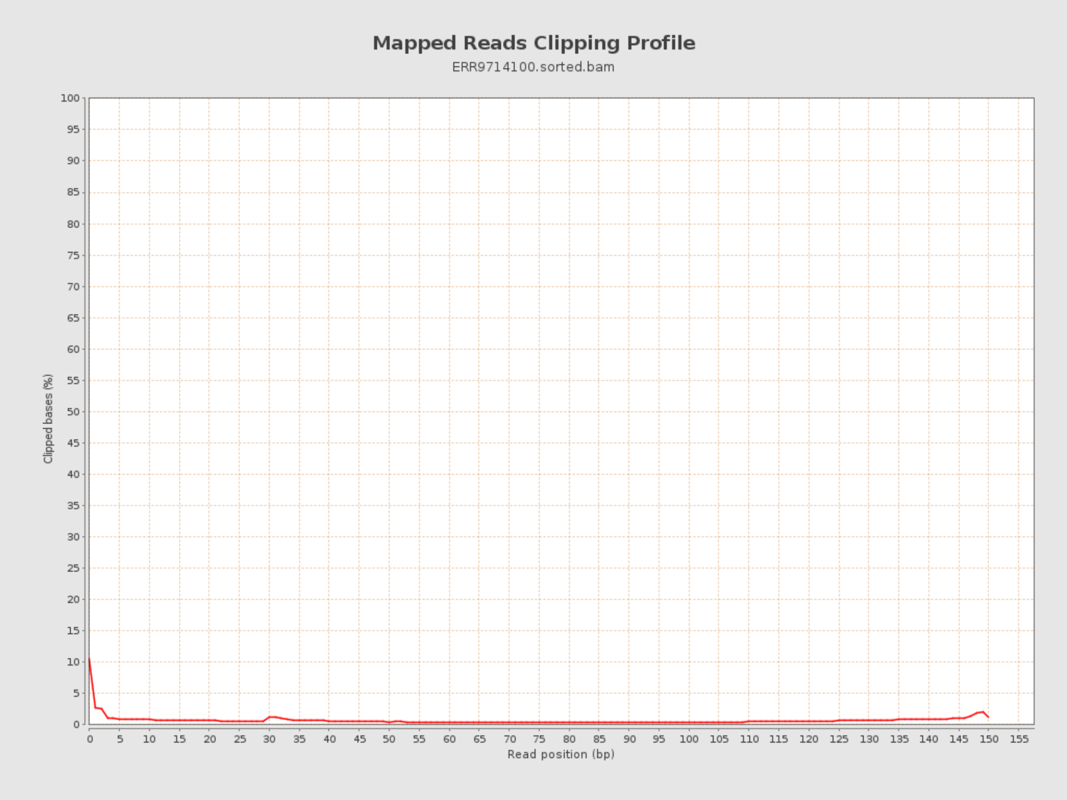
8. Results : Mapped Reads Nucleotide Content



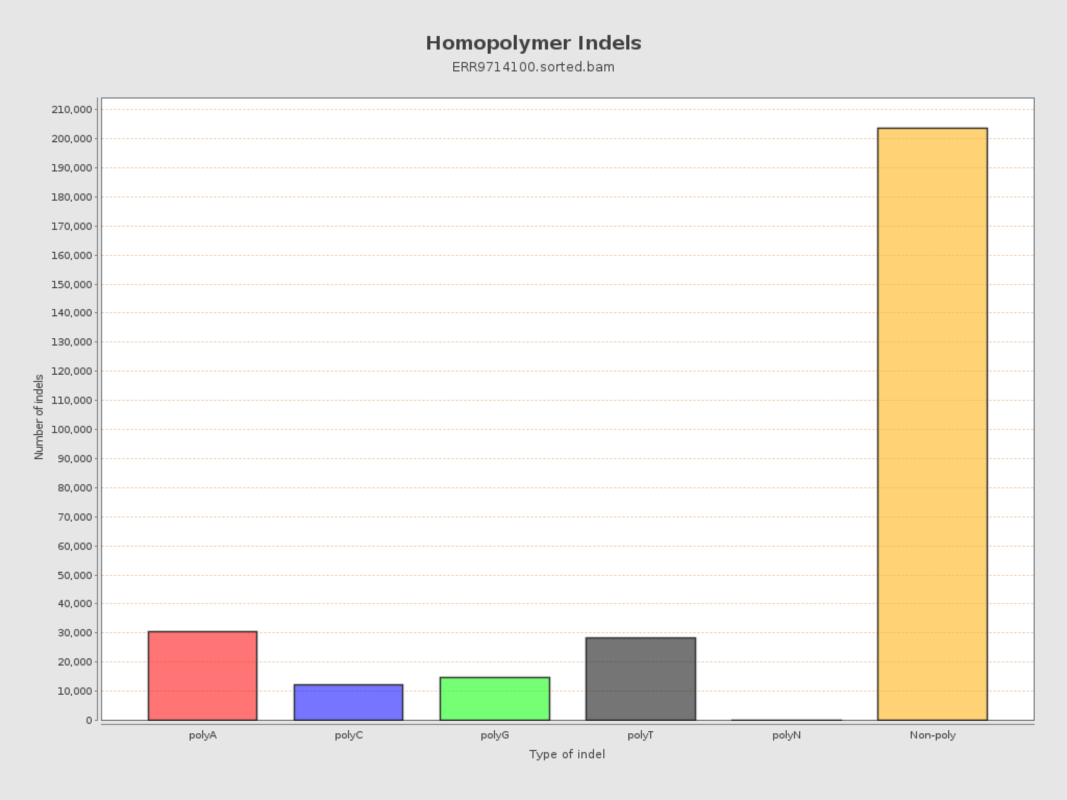
9. Results : Mapped Reads GC-content Distribution



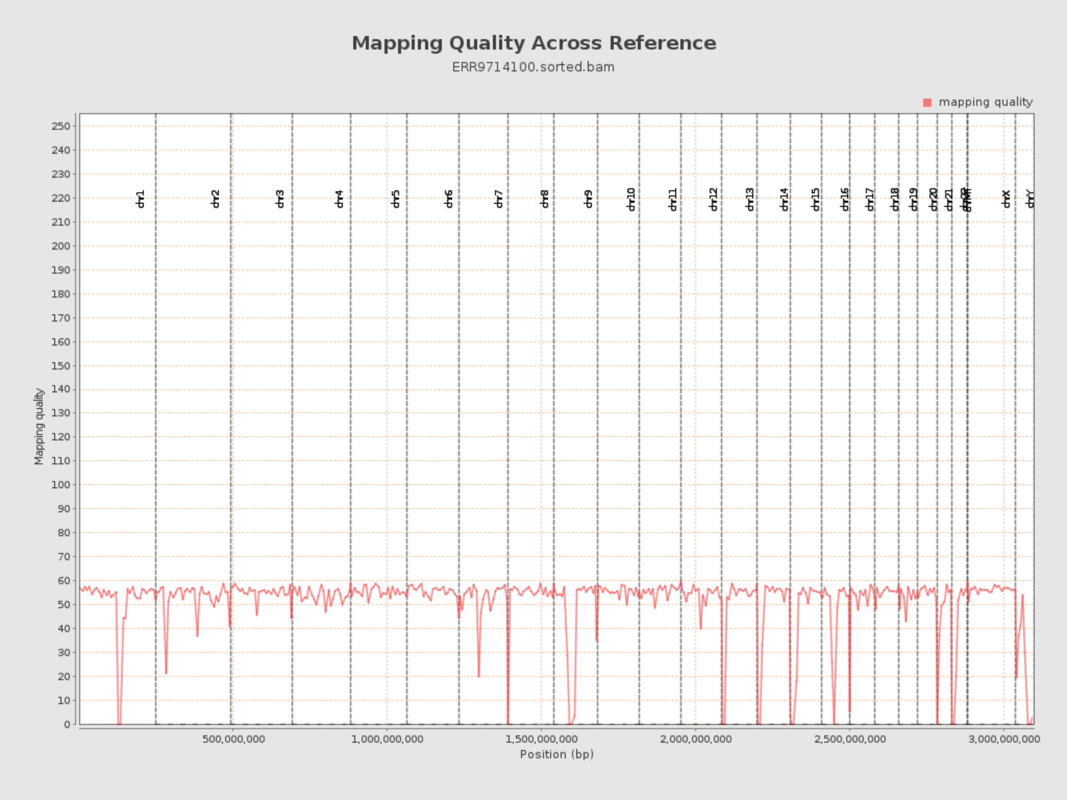
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram