Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 20:23:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714122.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_ERR9714122 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714122.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 20:23:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714122.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	617,818
Mapped reads	538,491 / 87.16%
Unmapped reads	79,327 / 12.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,507 / 2.67%
Read min/max/mean length	30 / 151 / 137.4
Duplicated reads (estimated)	486,698 / 78.78%
Duplication rate	43.68%
Clipped reads	509,785 / 82.51%

2.2. ACGT Content

Number/percentage of A's	18,441,580 / 26.84%
Number/percentage of C's	15,442,058 / 22.47%
Number/percentage of T's	17,410,771 / 25.34%
Number/percentage of G's	17,420,292 / 25.35%
Number/percentage of N's	416 / 0%
GC Percentage	47.82%

2.3. Coverage

Mean	0.0227

Standard Deviation	6.6679

2.4. Mapping Quality

Mean Mapping Quality	51.35

2.5. Mismatches and indels

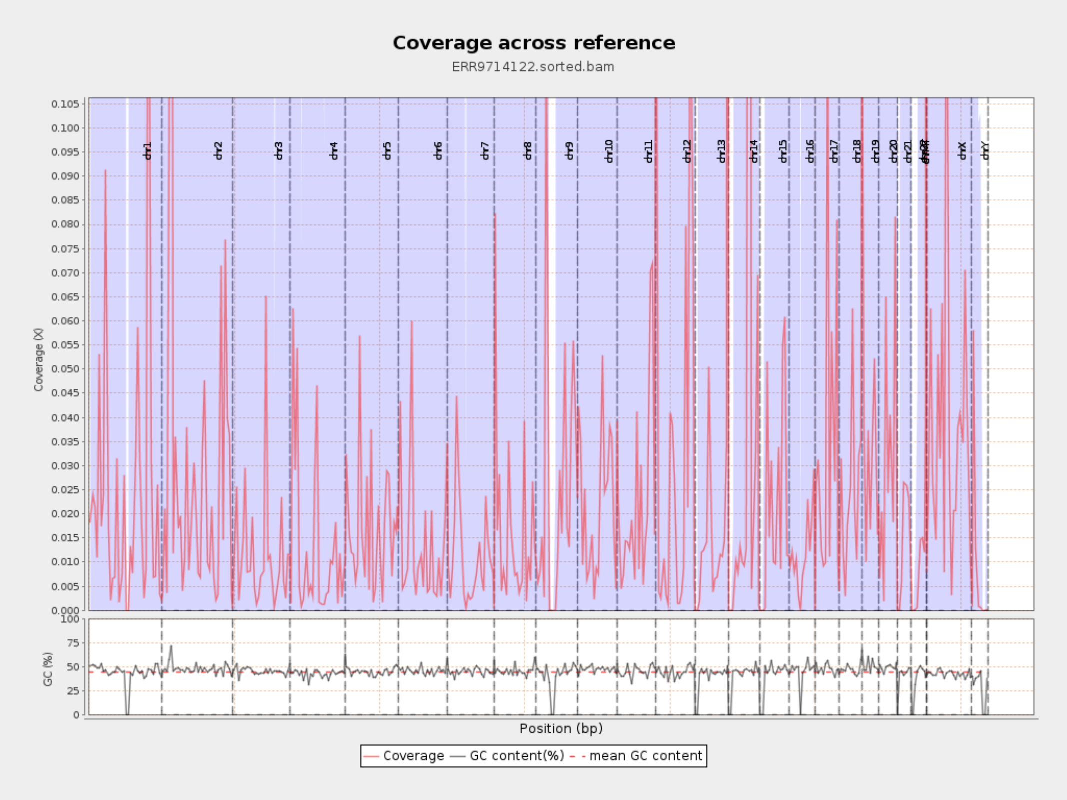
General error rate	4.48%
Mismatches	2,867,977
Insertions	76,790
Mapped reads with at least one insertion	13.8%
Deletions	251,940
Mapped reads with at least one deletion	44.43%
Homopolymer indels	29.07%

2.6. Chromosome stats

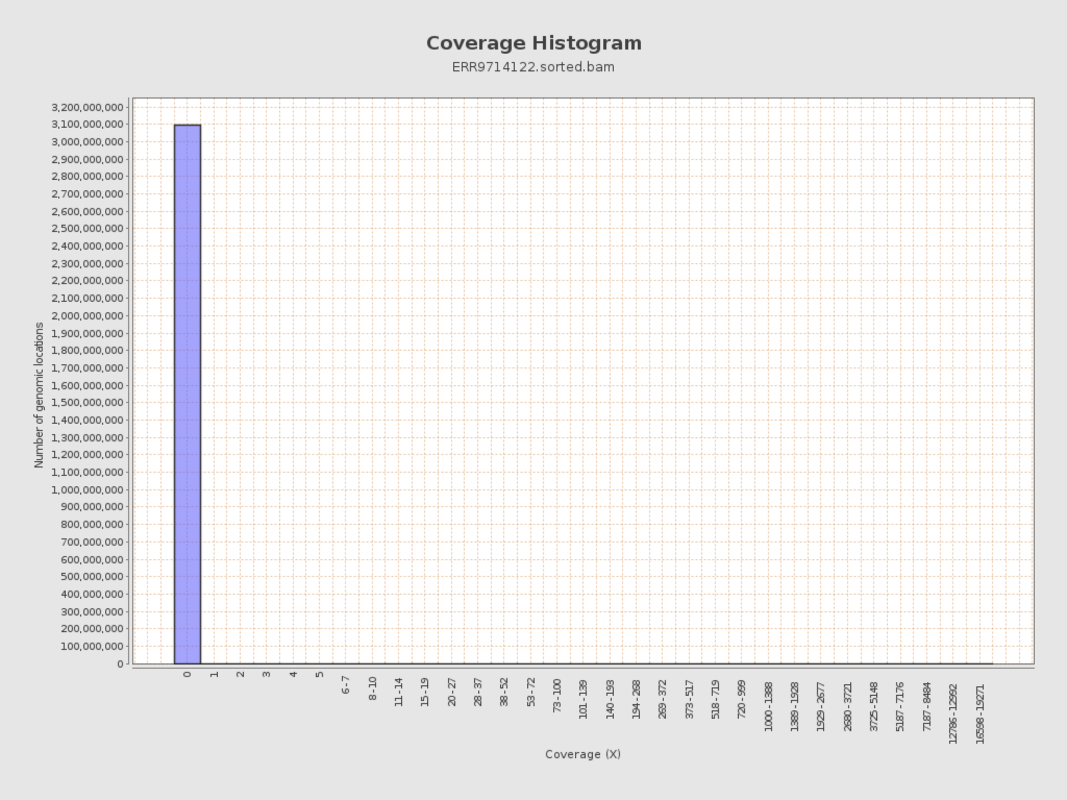
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6014449	0.0241	5.9604
chr2	243199373	8474783	0.0348	9.9193
chr3	198022430	2307478	0.0117	2.2274
chr4	191154276	2543805	0.0133	3.6685
chr5	180915260	3108928	0.0172	3.4028
chr6	171115067	2435081	0.0142	2.6539
chr7	159138663	1816363	0.0114	1.8388

chr8	146364022	2545674	0.0174	4.2576
chr9	141213431	3399228	0.0241	6.416
chr10	135534747	2968194	0.0219	3.4748
chr11	135006516	3118875	0.0231	3.6925
chr12	133851895	4371461	0.0327	7.795
chr13	115169878	2611351	0.0227	8.5825
chr14	107349540	4396739	0.041	21.916
chr15	102531392	2261860	0.0221	3.8757
chr16	90354753	1098762	0.0122	1.6353
chr17	81195210	3098892	0.0382	8.2058
chr18	78077248	1850972	0.0237	4.6525
chr19	59128983	2019184	0.0341	4.7299
chr20	63025520	2114754	0.0336	5.051
chr21	48129895	674362	0.014	2.4589
chr22	51304566	413433	0.0081	1.115
chrMT	16571	149035	8.9937	76.1944
chrX	155270560	5970775	0.0385	5.2794
chrY	59373566	565741	0.0095	3.405

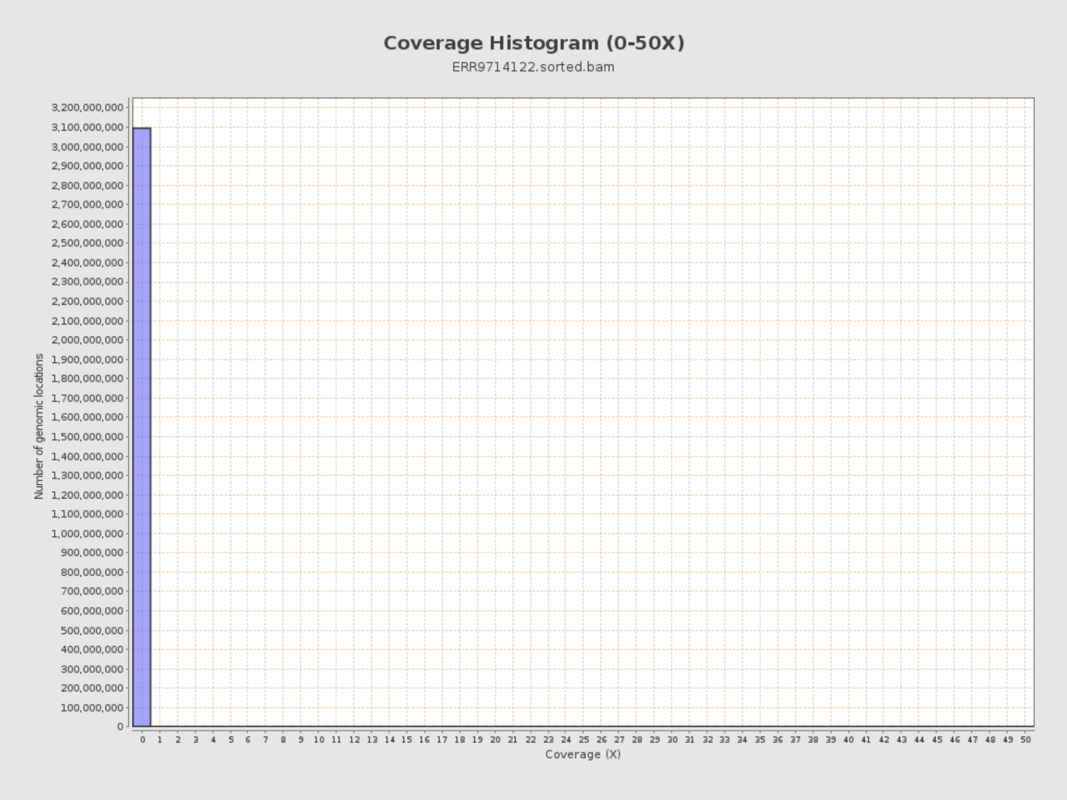
3. Results : Coverage across reference



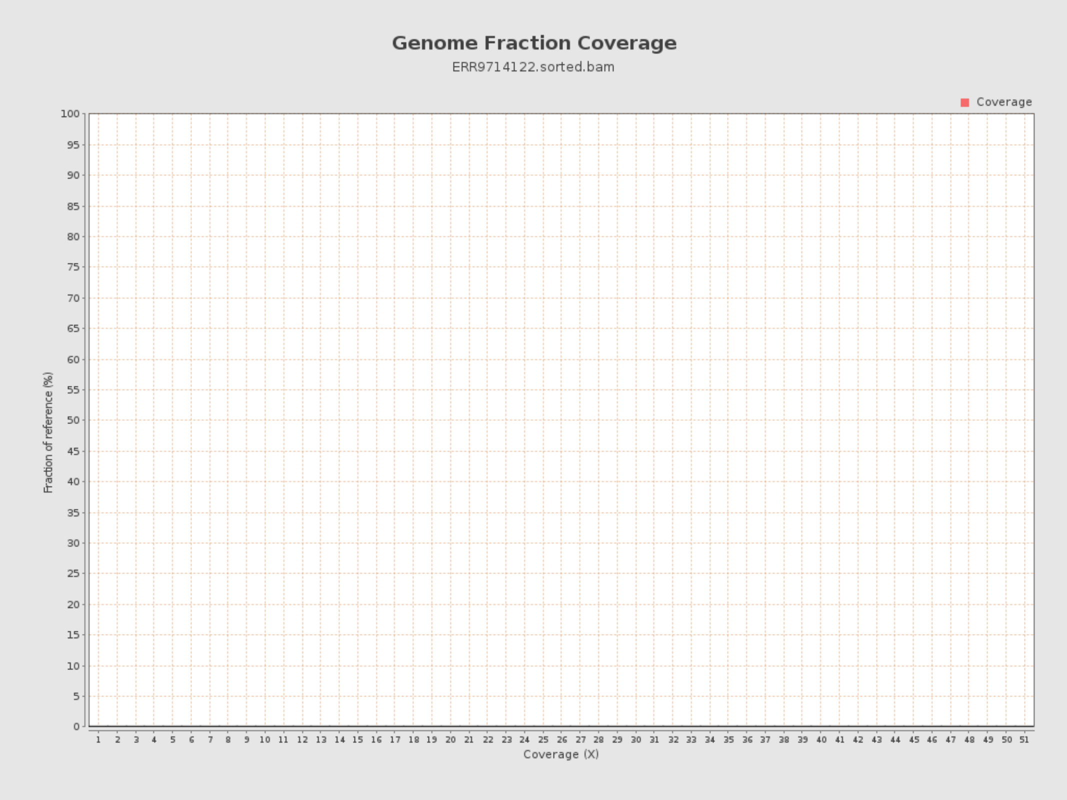
4. Results : Coverage Histogram



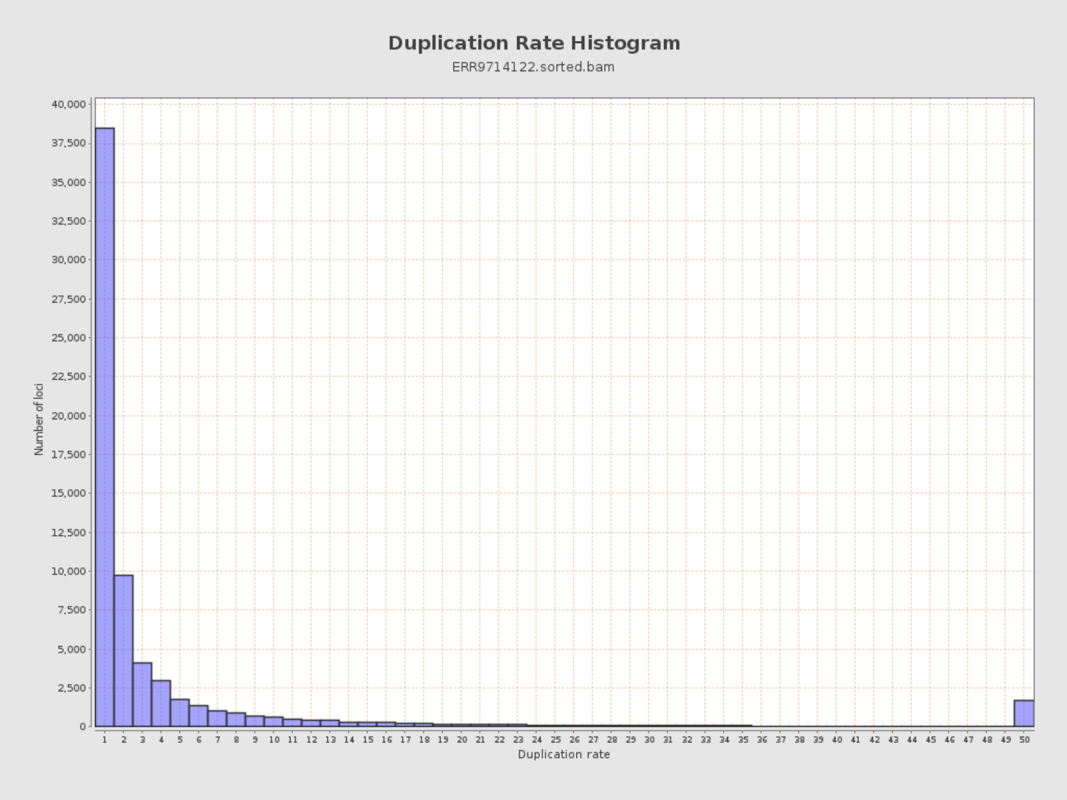
5. Results : Coverage Histogram (0-50X)



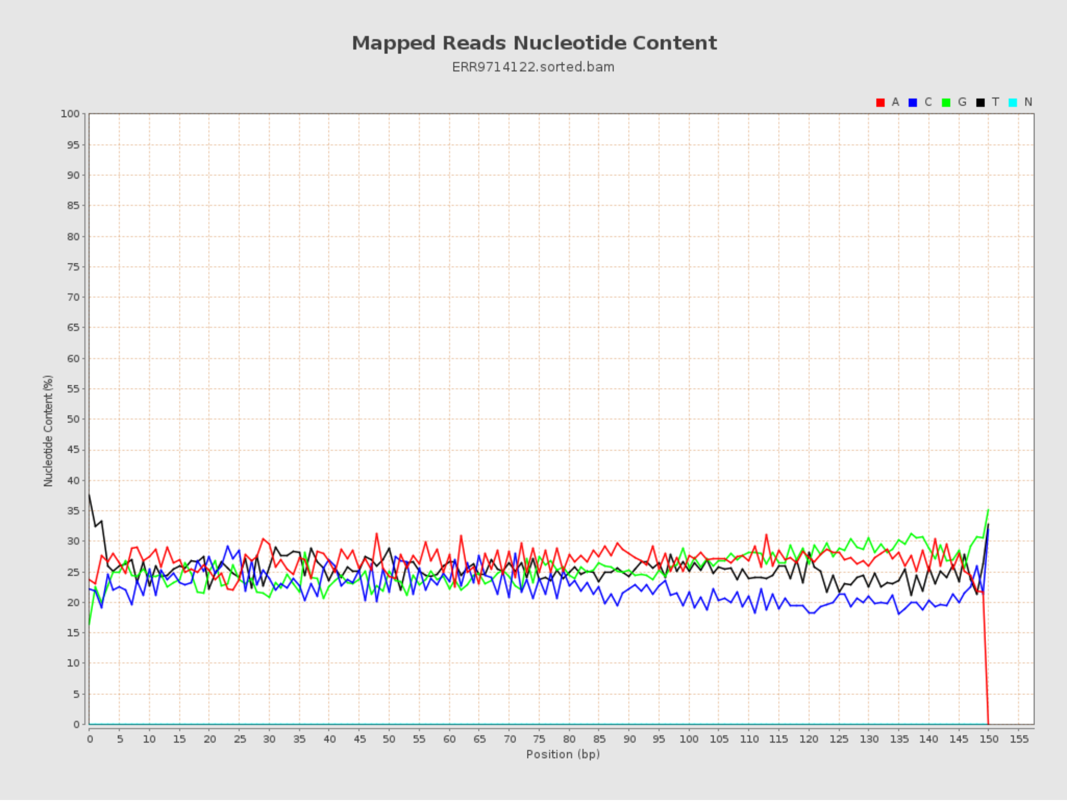
6. Results : Genome Fraction Coverage



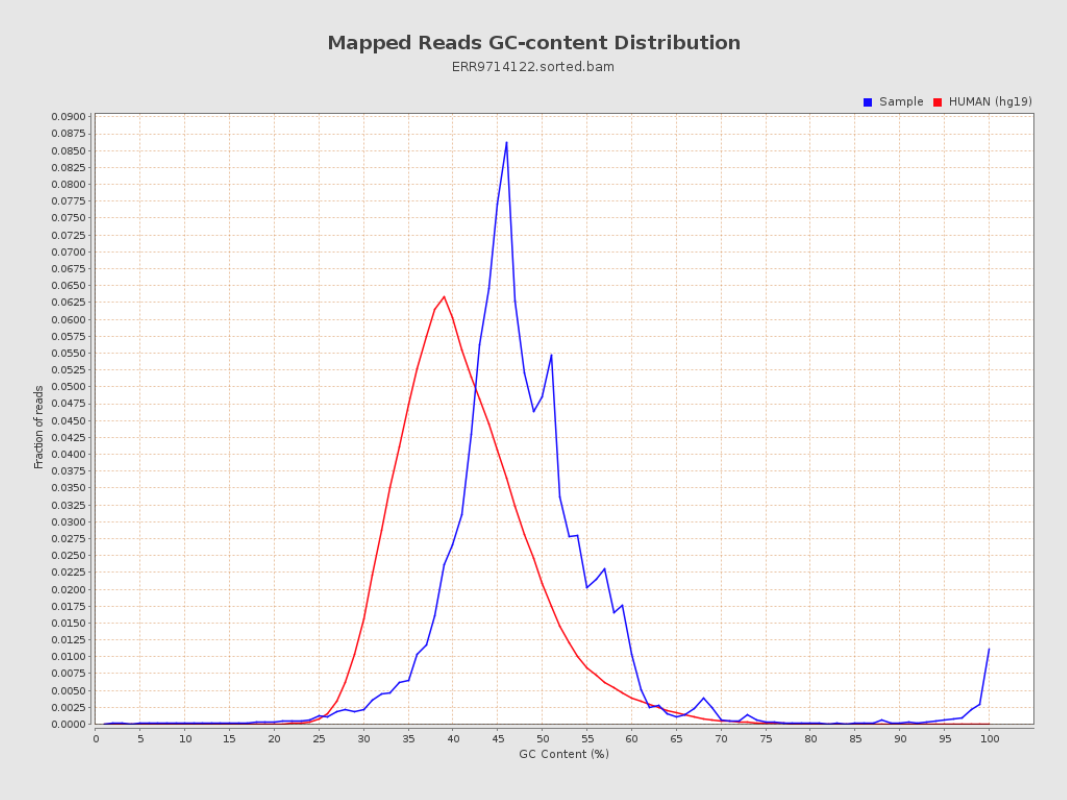
7. Results : Duplication Rate Histogram



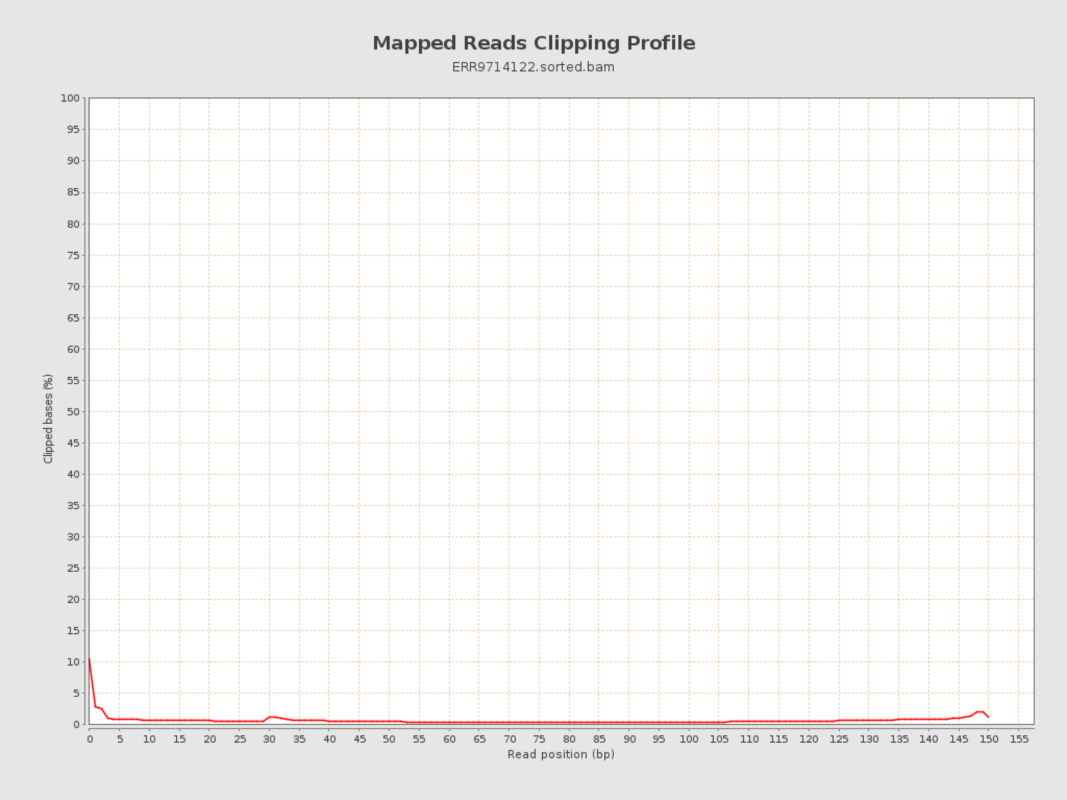
8. Results : Mapped Reads Nucleotide Content



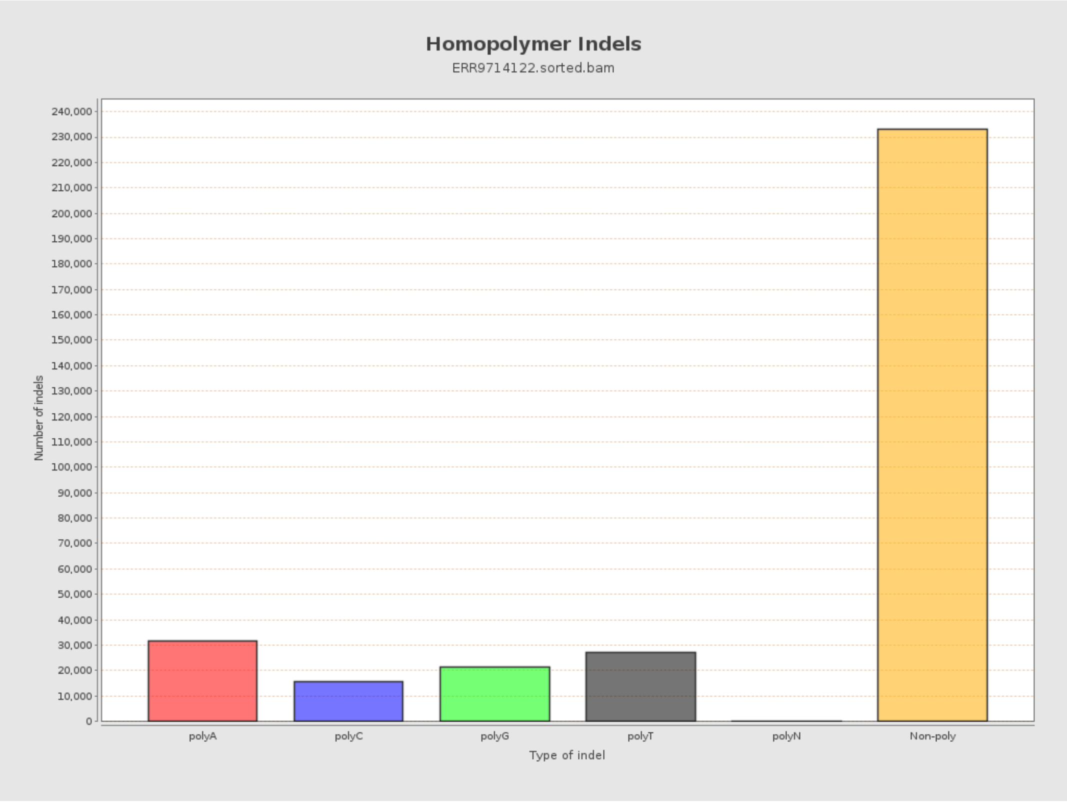
9. Results : Mapped Reads GC-content Distribution



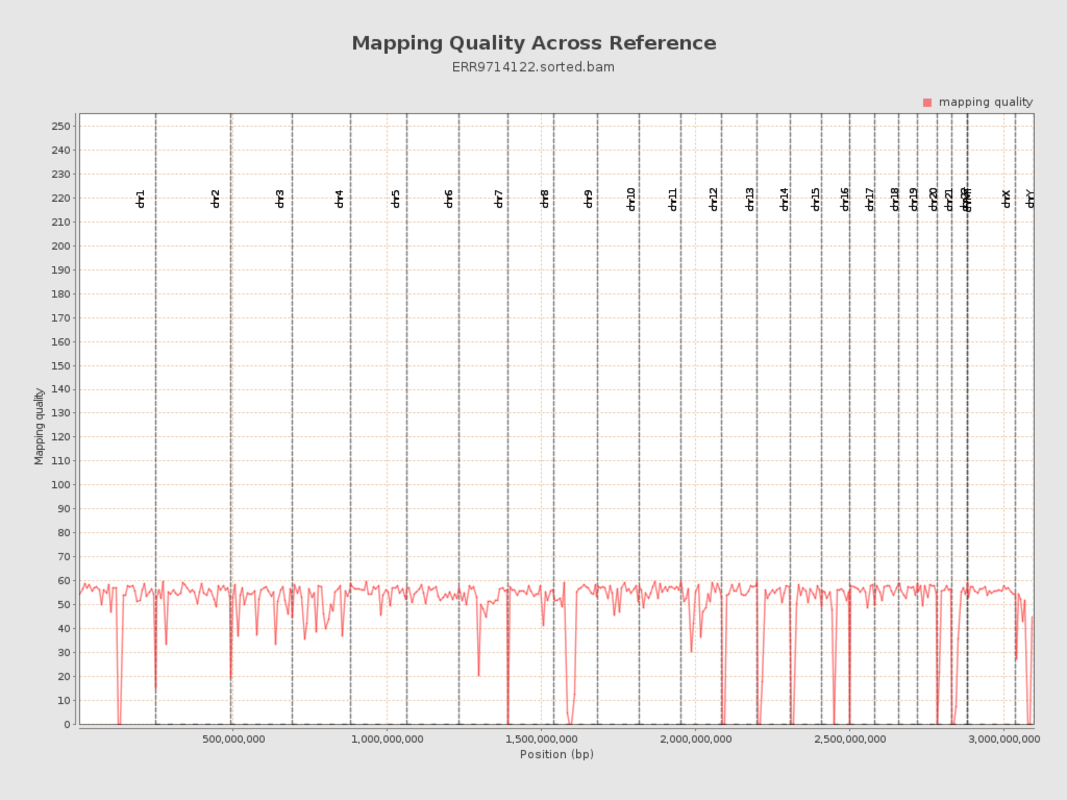
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram