Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 22:27:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714163.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_ERR9714163 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714163.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 22:27:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714163.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	810,002
Mapped reads	674,125 / 83.23%
Unmapped reads	135,877 / 16.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,114 / 2.36%
Read min/max/mean length	30 / 151 / 134.03
Duplicated reads (estimated)	611,191 / 75.46%
Duplication rate	44.61%
Clipped reads	634,946 / 78.39%

2.2. ACGT Content

Number/percentage of A's	22,643,616 / 26.41%
Number/percentage of C's	19,258,790 / 22.46%
Number/percentage of T's	21,481,608 / 25.05%
Number/percentage of G's	22,358,309 / 26.08%
Number/percentage of N's	585 / 0%
GC Percentage	48.54%

2.3. Coverage

Mean	0.0283

Standard Deviation	8.0988

2.4. Mapping Quality

Mean Mapping Quality	51.4

2.5. Mismatches and indels

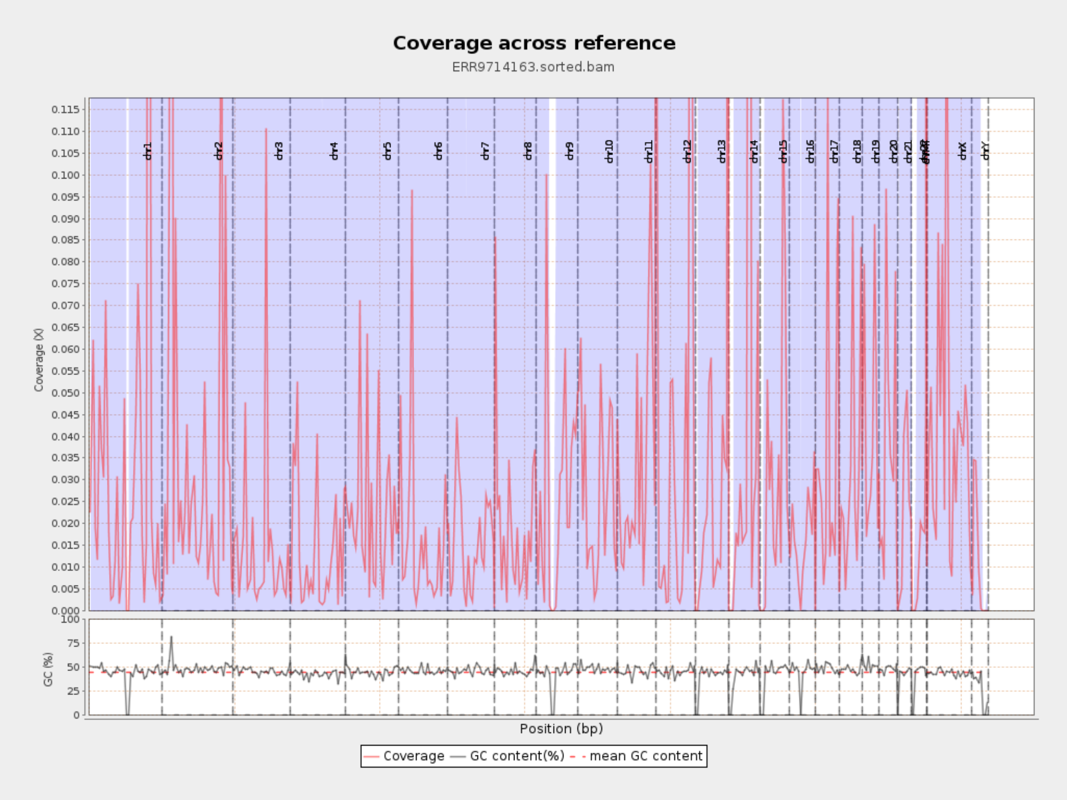
General error rate	4.37%
Mismatches	3,495,084
Insertions	89,473
Mapped reads with at least one insertion	12.75%
Deletions	303,022
Mapped reads with at least one deletion	42.68%
Homopolymer indels	30.1%

2.6. Chromosome stats

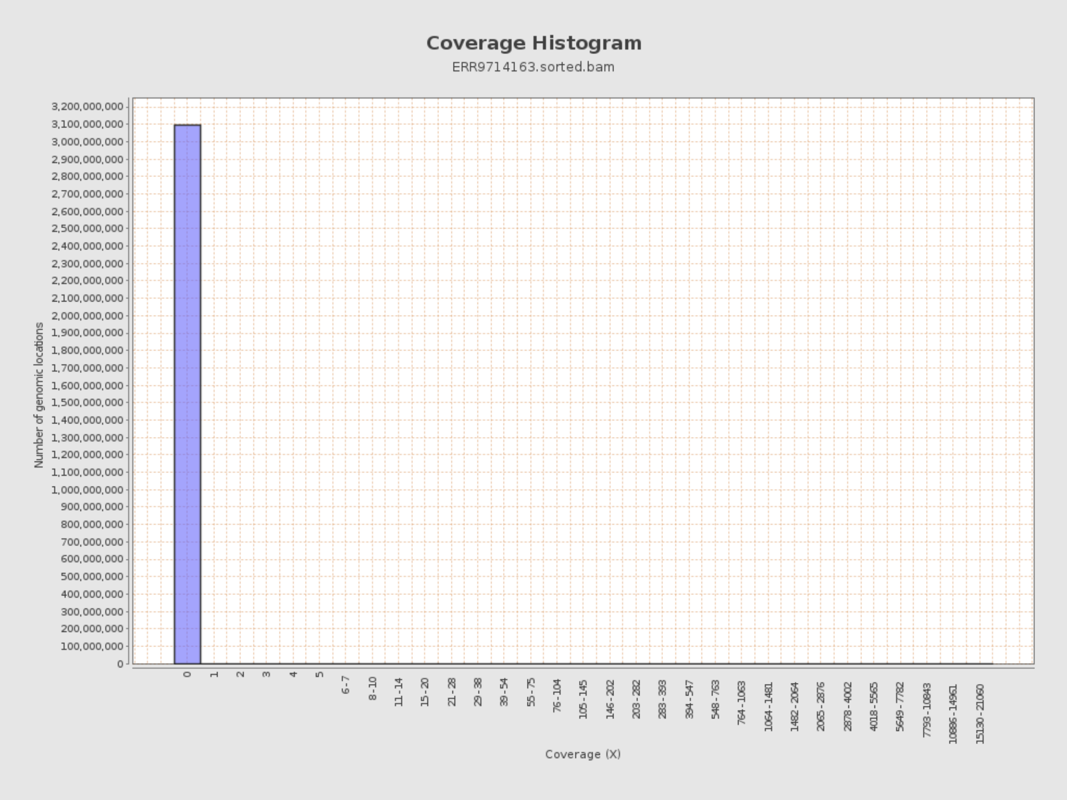
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8145576	0.0327	8.991
chr2	243199373	10929528	0.0449	13.9491
chr3	198022430	2948764	0.0149	3.5301
chr4	191154276	2699546	0.0141	2.7803
chr5	180915260	4203388	0.0232	4.7771
chr6	171115067	2975332	0.0174	3.7412
chr7	159138663	2551580	0.016	2.684

chr8	146364022	2907168	0.0199	4.2032
chr9	141213431	3493195	0.0247	5.3006
chr10	135534747	3786487	0.0279	4.1092
chr11	135006516	4468803	0.0331	5.3506
chr12	133851895	5522677	0.0413	12.3451
chr13	115169878	3392167	0.0295	9.0944
chr14	107349540	5265598	0.0491	24.0158
chr15	102531392	3275757	0.0319	5.6951
chr16	90354753	1528016	0.0169	2.2879
chr17	81195210	3134349	0.0386	6.4732
chr18	78077248	2412116	0.0309	6.3877
chr19	59128983	2398390	0.0406	4.7175
chr20	63025520	2576755	0.0409	6.2525
chr21	48129895	1065594	0.0221	4.2555
chr22	51304566	554318	0.0108	1.1669
chrMT	16571	109121	6.5851	51.6748
chrX	155270560	6692482	0.0431	5.1075
chrY	59373566	620104	0.0104	1.8922

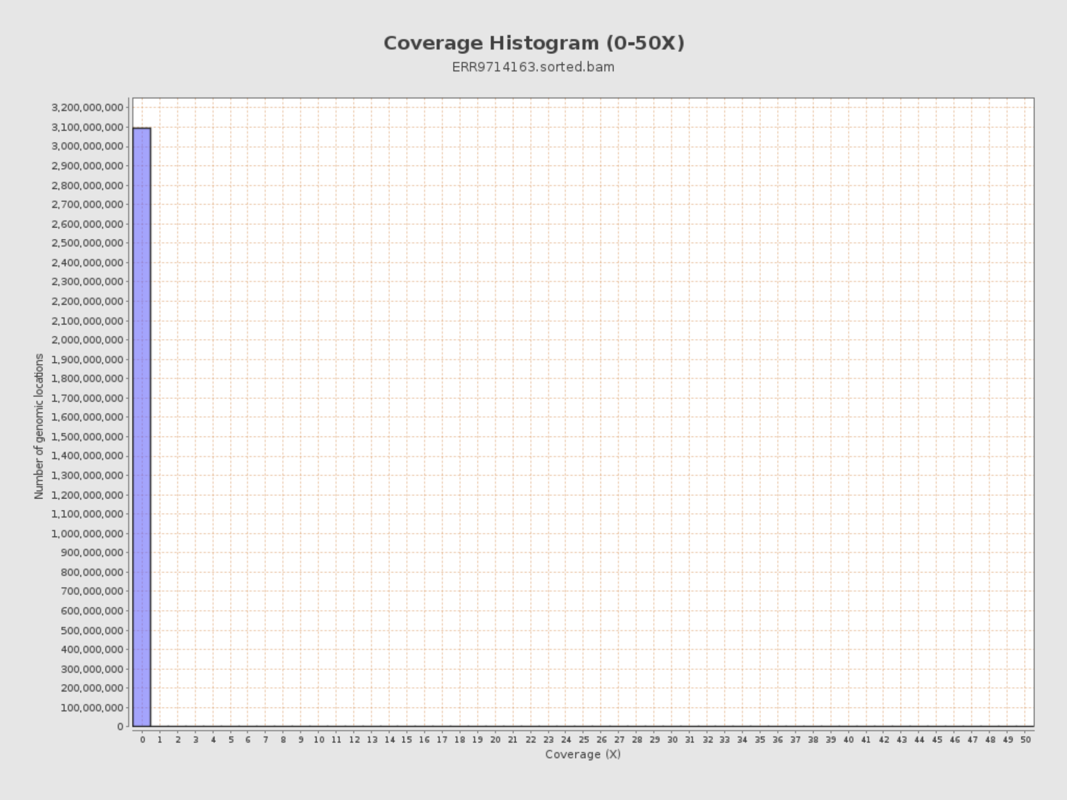
3. Results : Coverage across reference



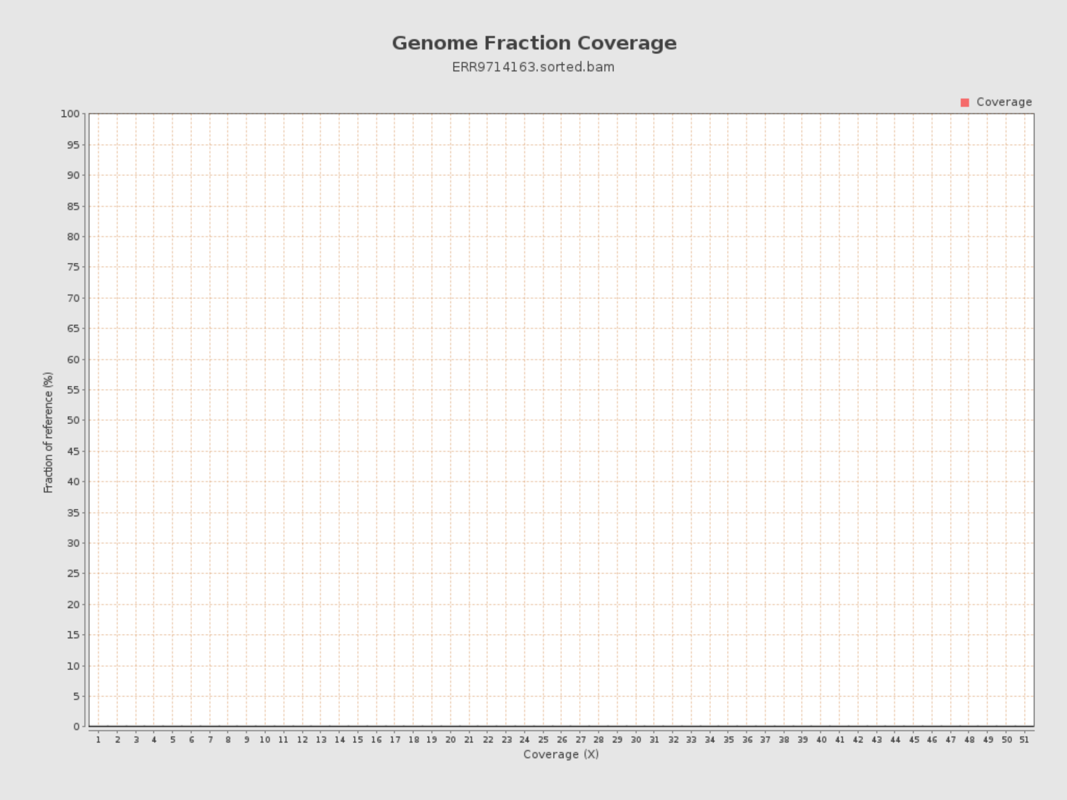
4. Results : Coverage Histogram



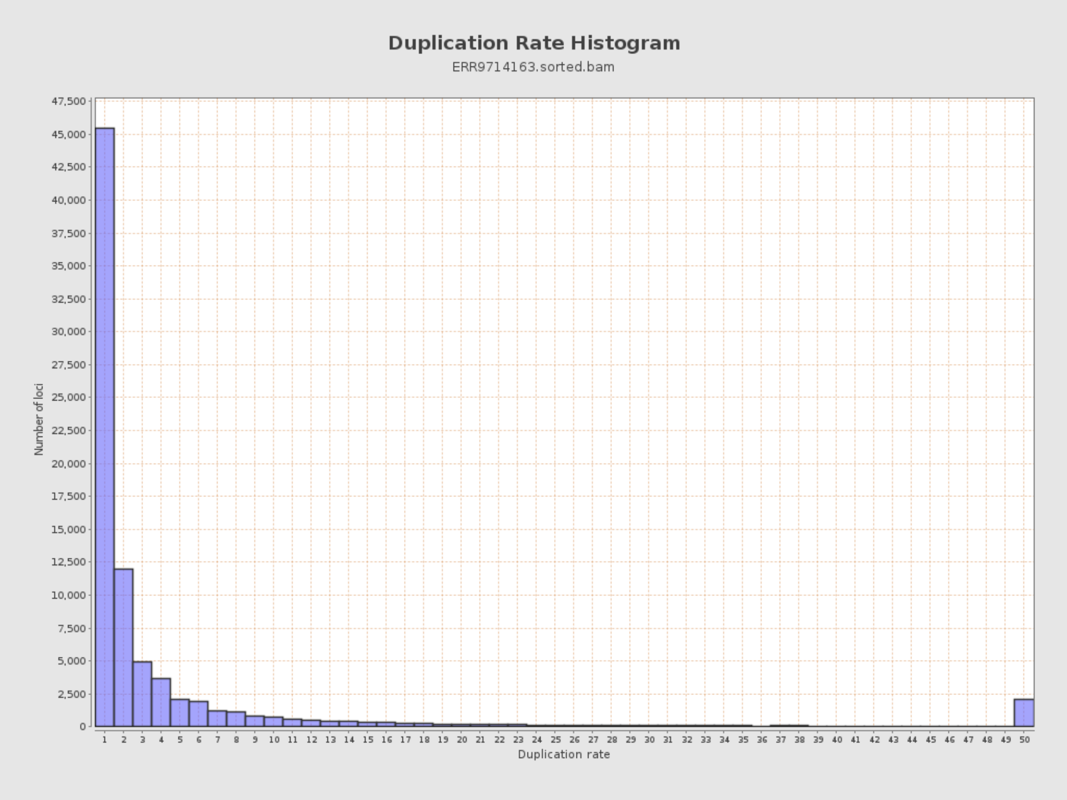
5. Results : Coverage Histogram (0-50X)



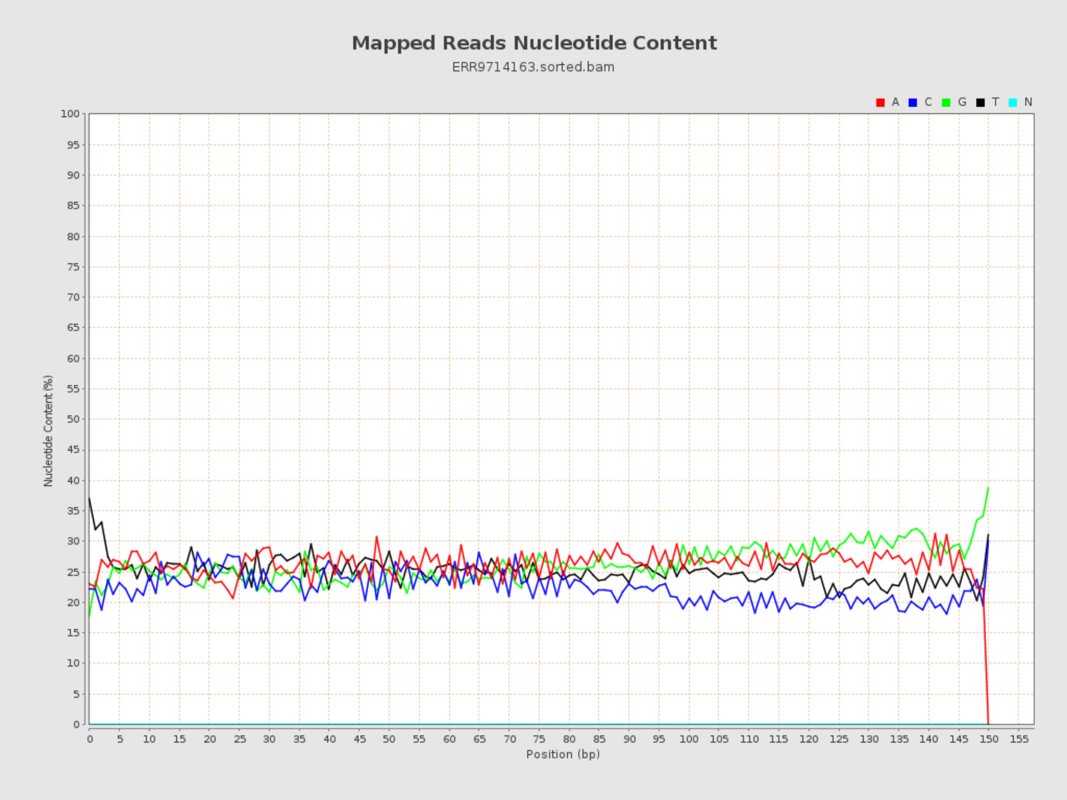
6. Results : Genome Fraction Coverage



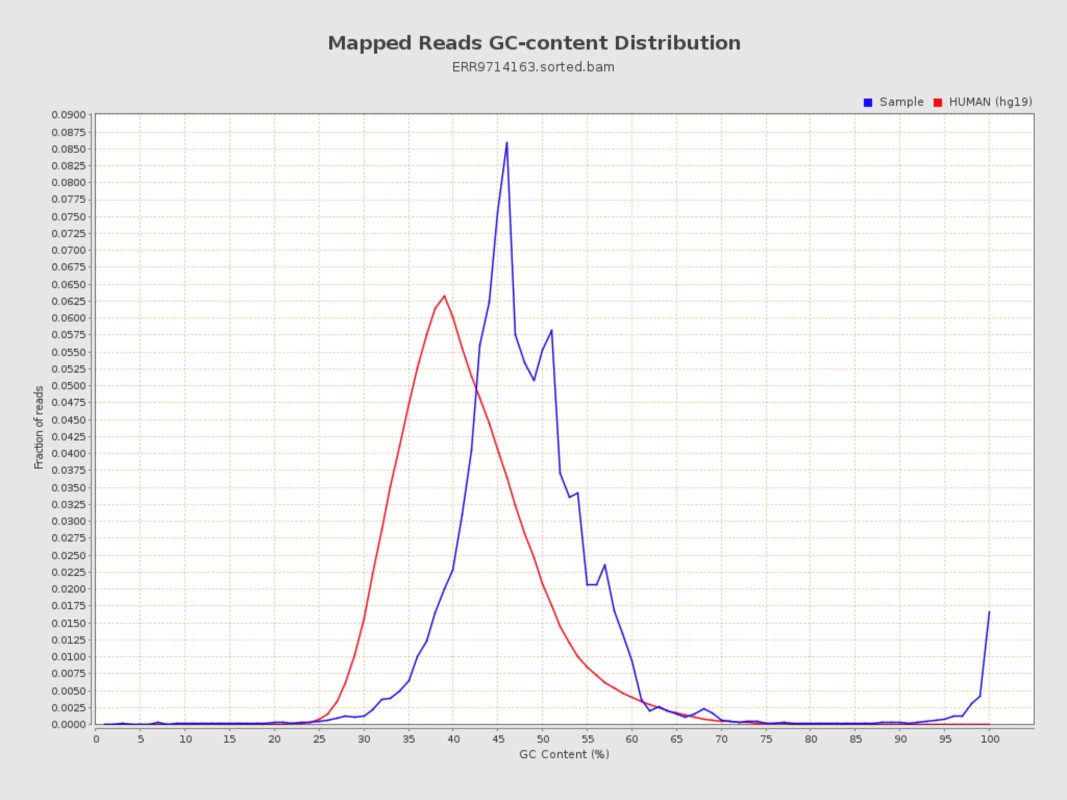
7. Results : Duplication Rate Histogram



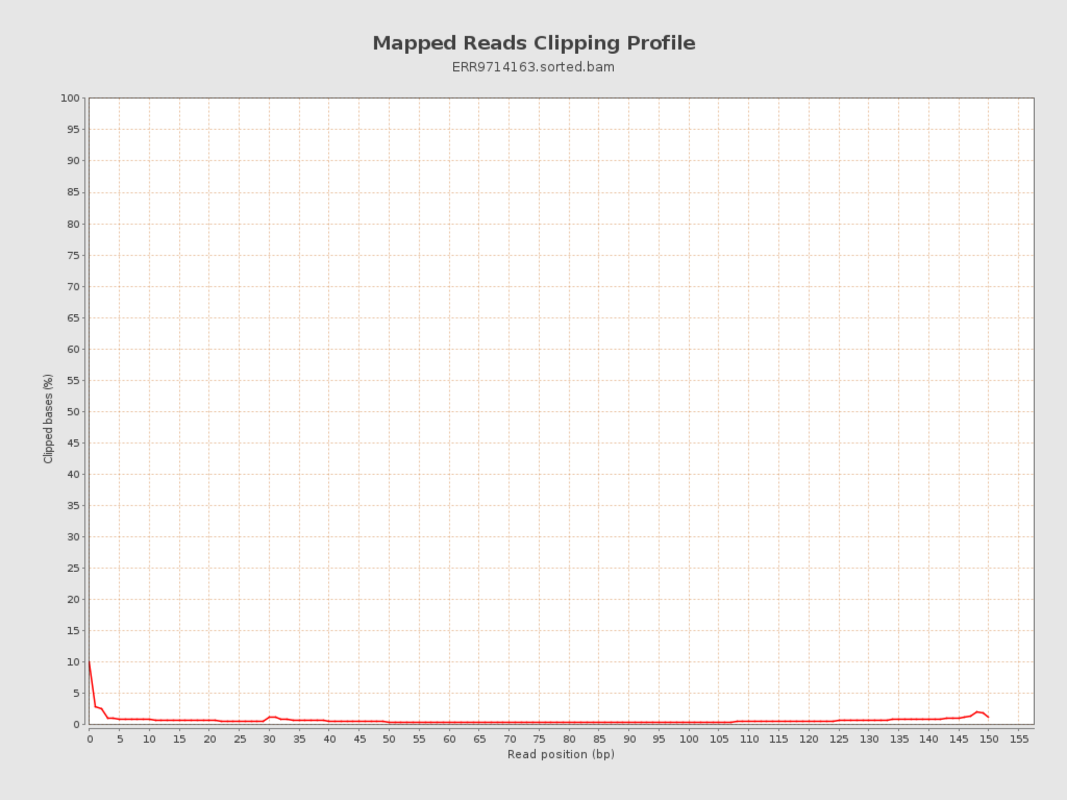
8. Results : Mapped Reads Nucleotide Content



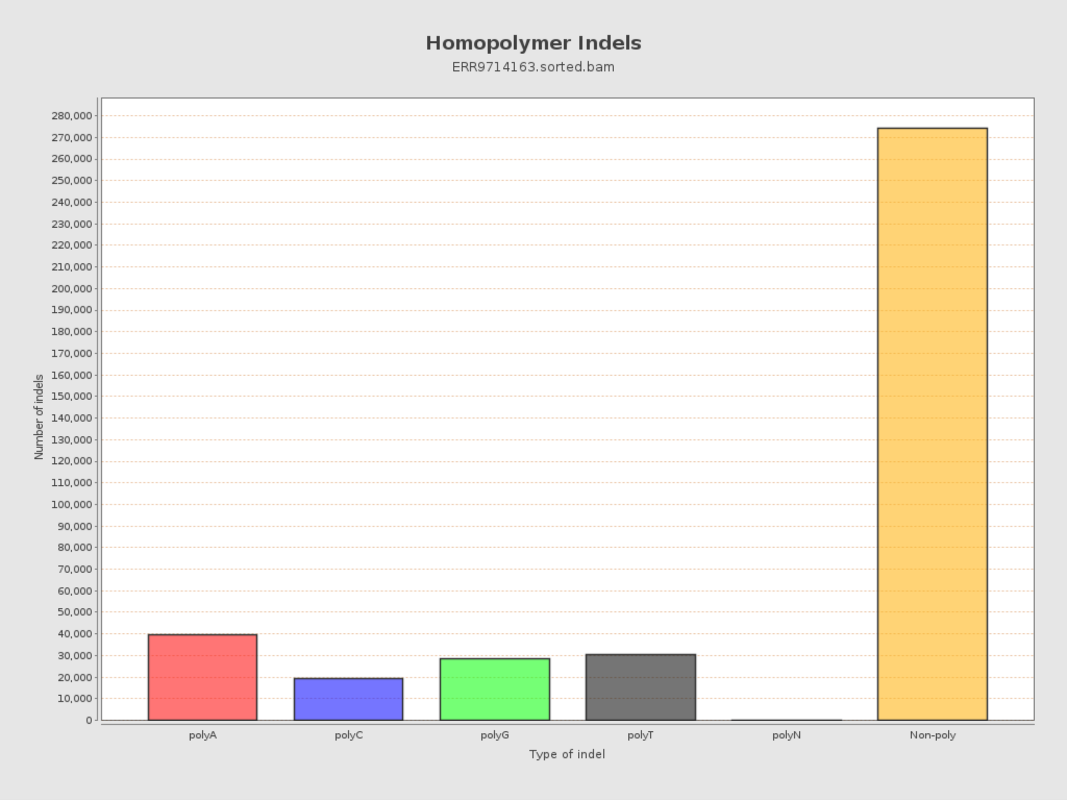
9. Results : Mapped Reads GC-content Distribution



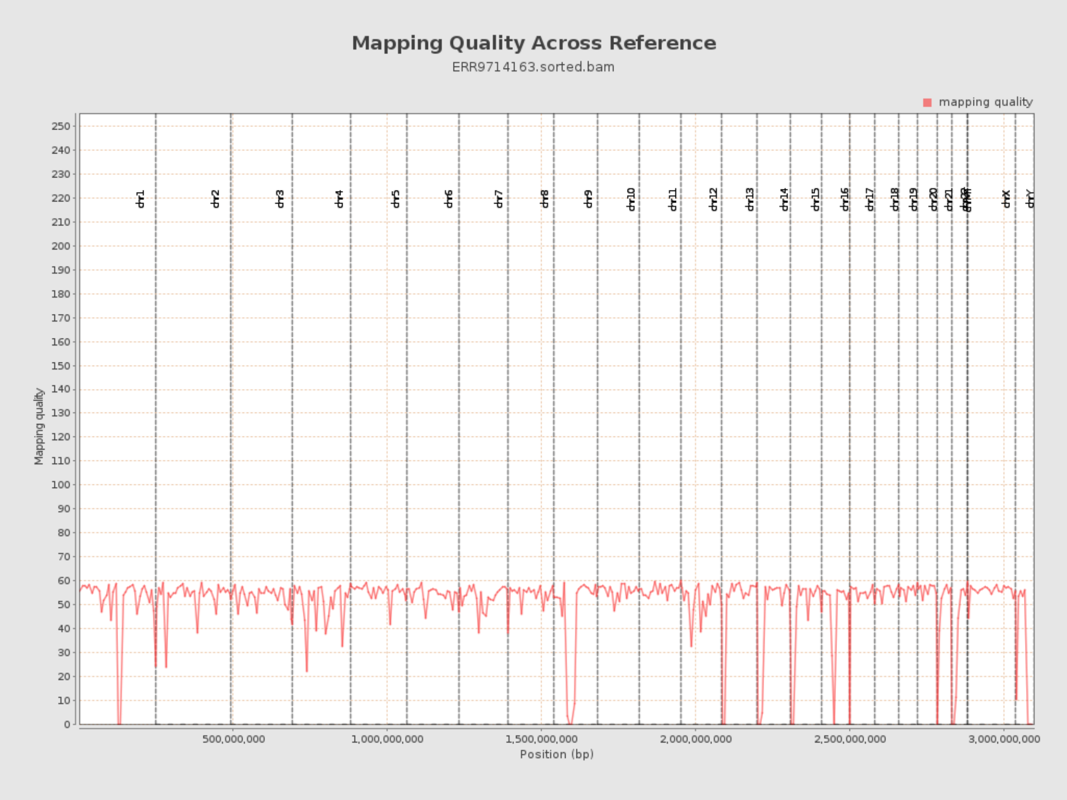
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram