Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 00:53:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714233.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_ERR9714233 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714233.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 00:53:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714233.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	269,230
Mapped reads	38,665 / 14.36%
Unmapped reads	230,565 / 85.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	962 / 0.36%
Read min/max/mean length	30 / 151 / 60.36
Duplicated reads (estimated)	37,573 / 13.96%
Duplication rate	35.25%
Clipped reads	21,178 / 7.87%

2.2. ACGT Content

Number/percentage of A's	117,515 / 3.01%
Number/percentage of C's	56,868 / 1.46%
Number/percentage of T's	74,286 / 1.9%
Number/percentage of G's	3,652,766 / 93.62%
Number/percentage of N's	86 / 0%
GC Percentage	95.08%

2.3. Coverage

Mean	0.0013

Standard Deviation	4.5874

2.4. Mapping Quality

Mean Mapping Quality	13.35

2.5. Mismatches and indels

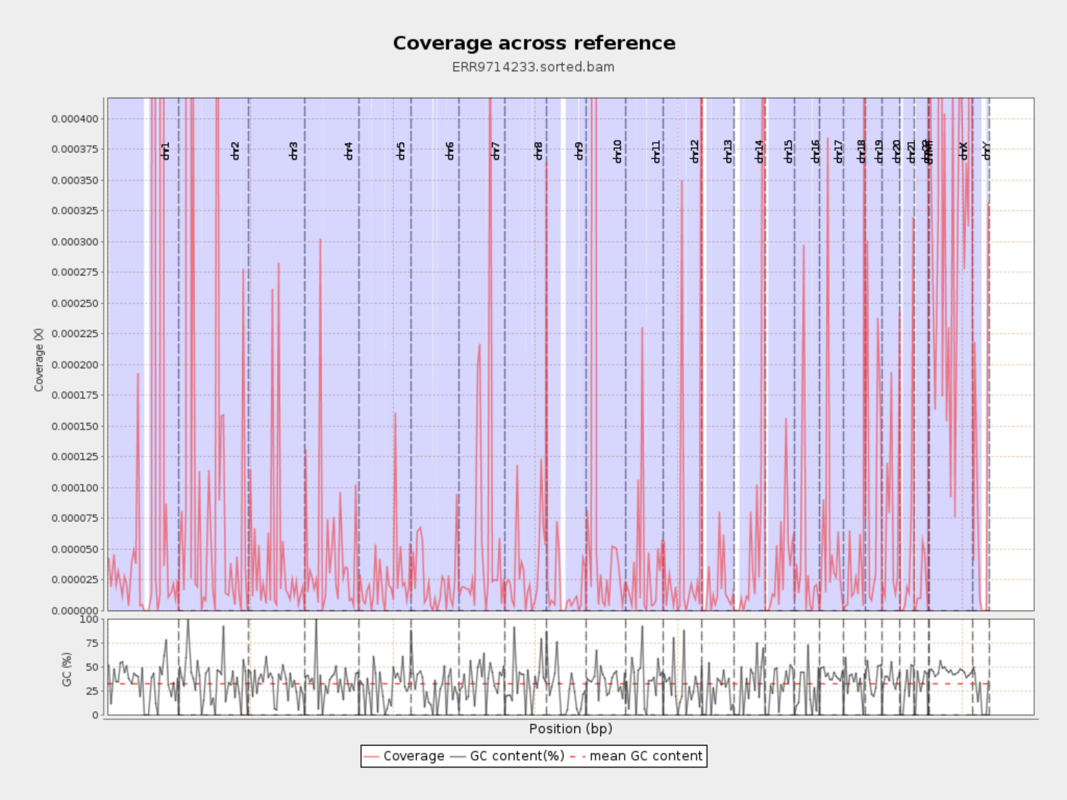
General error rate	3.34%
Mismatches	98,364
Insertions	4,686
Mapped reads with at least one insertion	8.34%
Deletions	2,022
Mapped reads with at least one deletion	5.01%
Homopolymer indels	60.49%

2.6. Chromosome stats

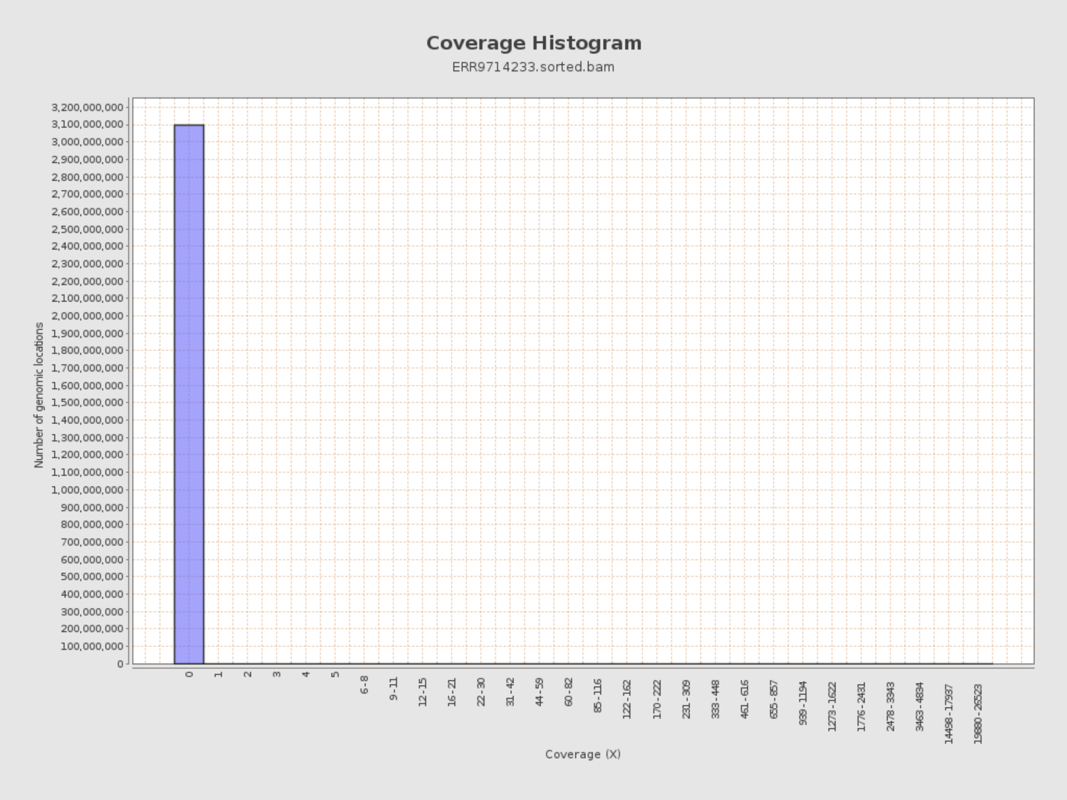
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	53325	0.0002	0.3513
chr2	243199373	3649984	0.015	16.3603
chr3	198022430	8850	0	0.0234
chr4	191154276	8731	0	0.0168
chr5	180915260	4690	0	0.0087
chr6	171115067	4196	0	0.0082
chr7	159138663	10344	0.0001	0.0573

chr8	146364022	5018	0	0.0136
chr9	141213431	2591	0	0.0087
chr10	135534747	28655	0.0002	0.3873
chr11	135006516	4947	0	0.0248
chr12	133851895	6481	0	0.0261
chr13	115169878	2036	0	0.0069
chr14	107349540	8470	0.0001	0.0503
chr15	102531392	3905	0	0.0117
chr16	90354753	3632	0	0.0131
chr17	81195210	5554	0.0001	0.0512
chr18	78077248	5047	0.0001	0.0305
chr19	59128983	6092	0.0001	0.0299
chr20	63025520	4508	0.0001	0.0211
chr21	48129895	2451	0.0001	0.0136
chr22	51304566	1061	0	0.0059
chrMT	16571	10675	0.6442	2.5653
chrX	155270560	64311	0.0004	0.0672
chrY	59373566	5139	0.0001	0.0198

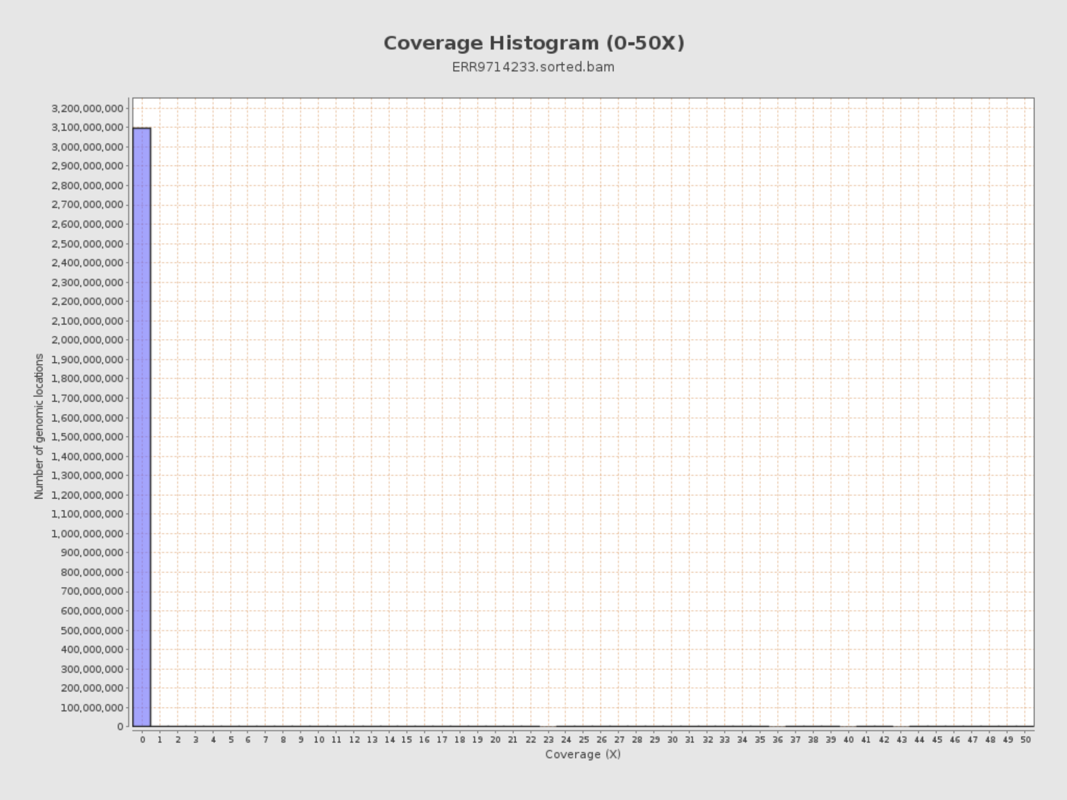
3. Results : Coverage across reference



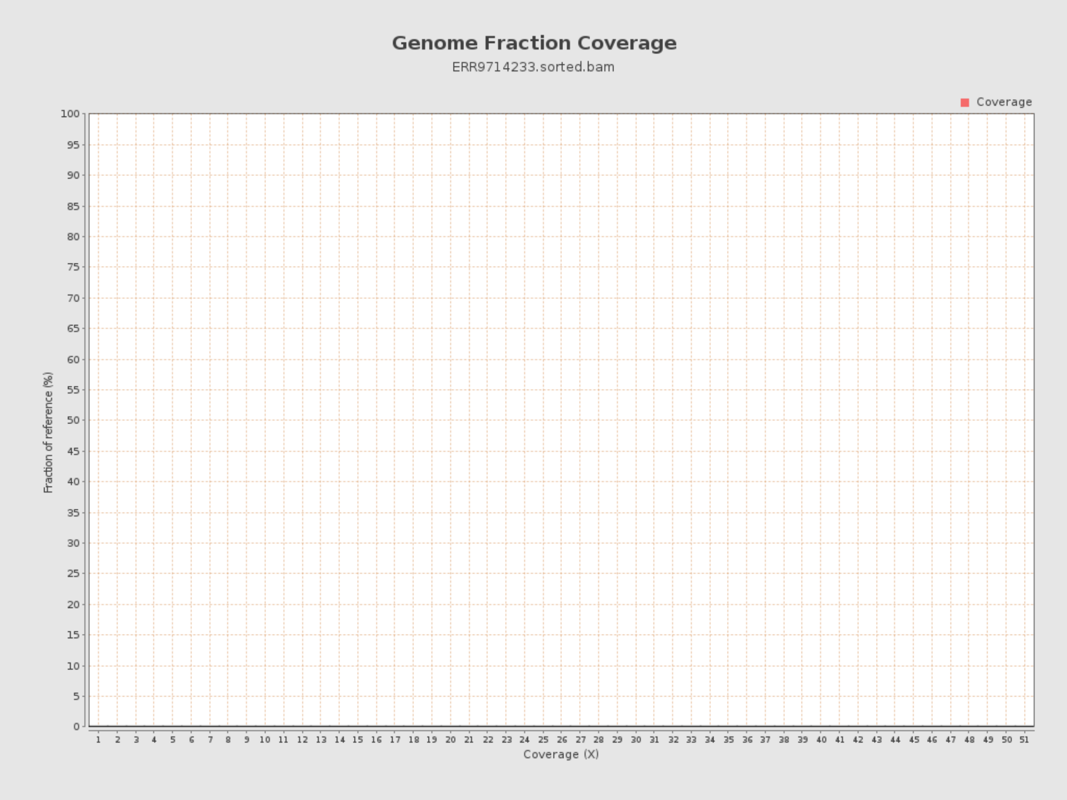
4. Results : Coverage Histogram



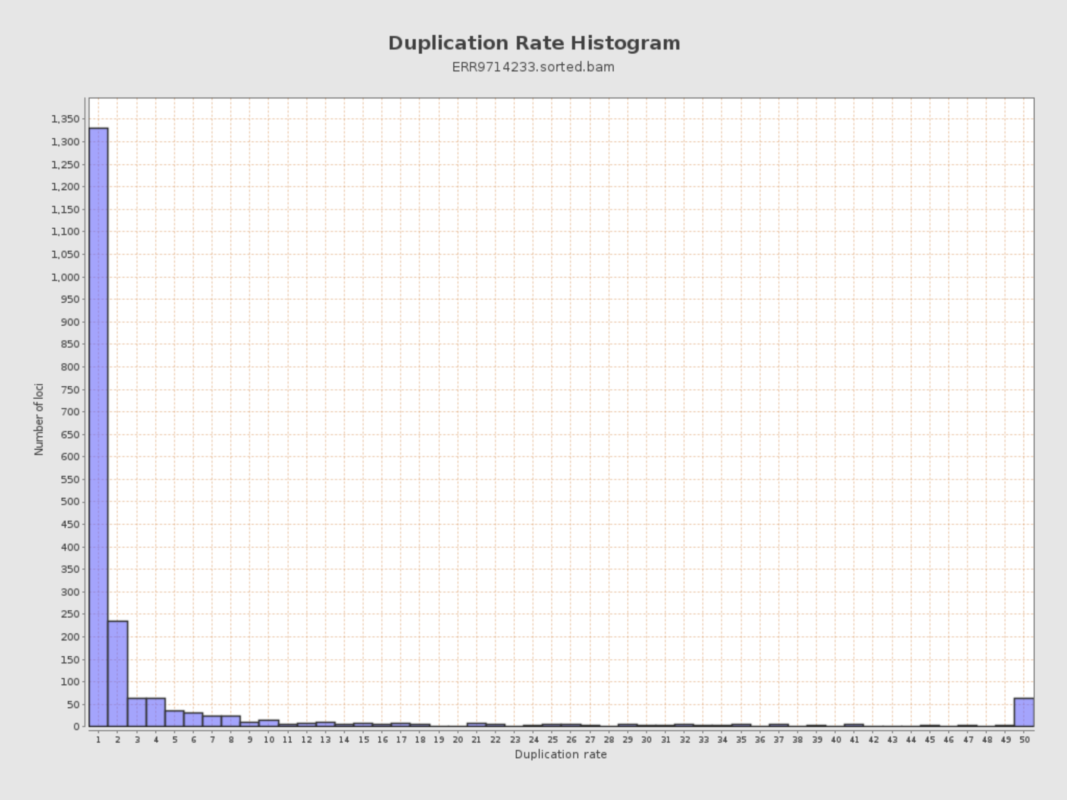
5. Results : Coverage Histogram (0-50X)



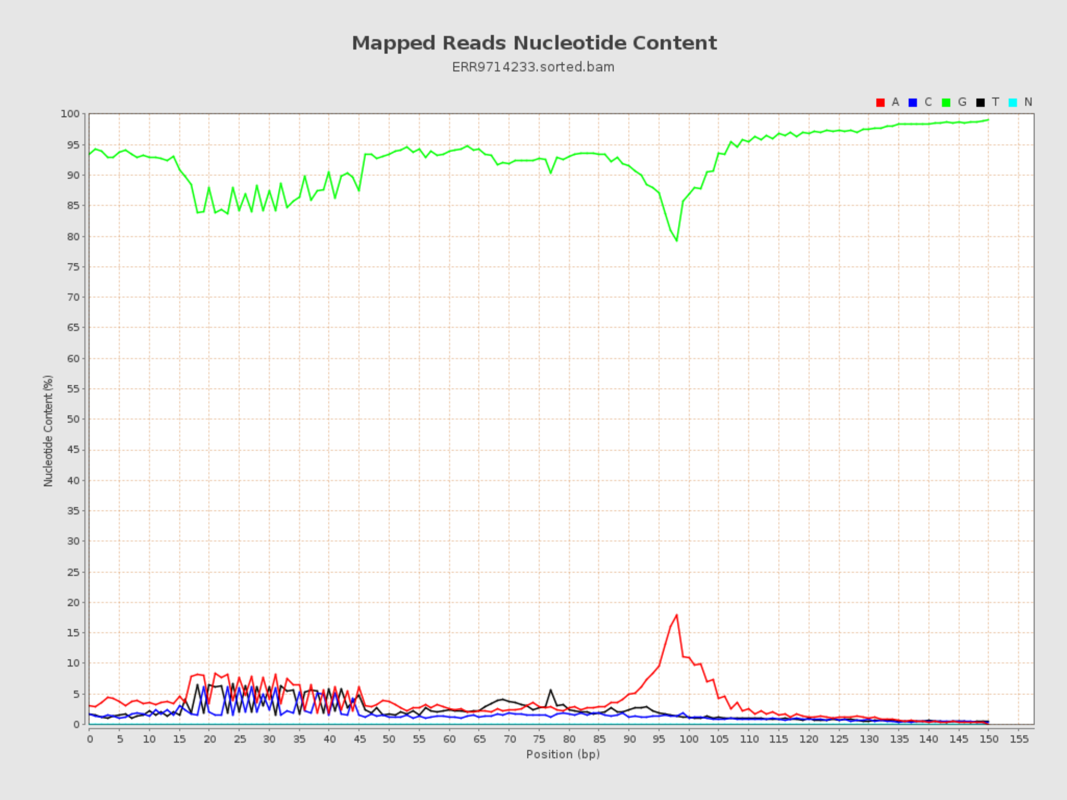
6. Results : Genome Fraction Coverage



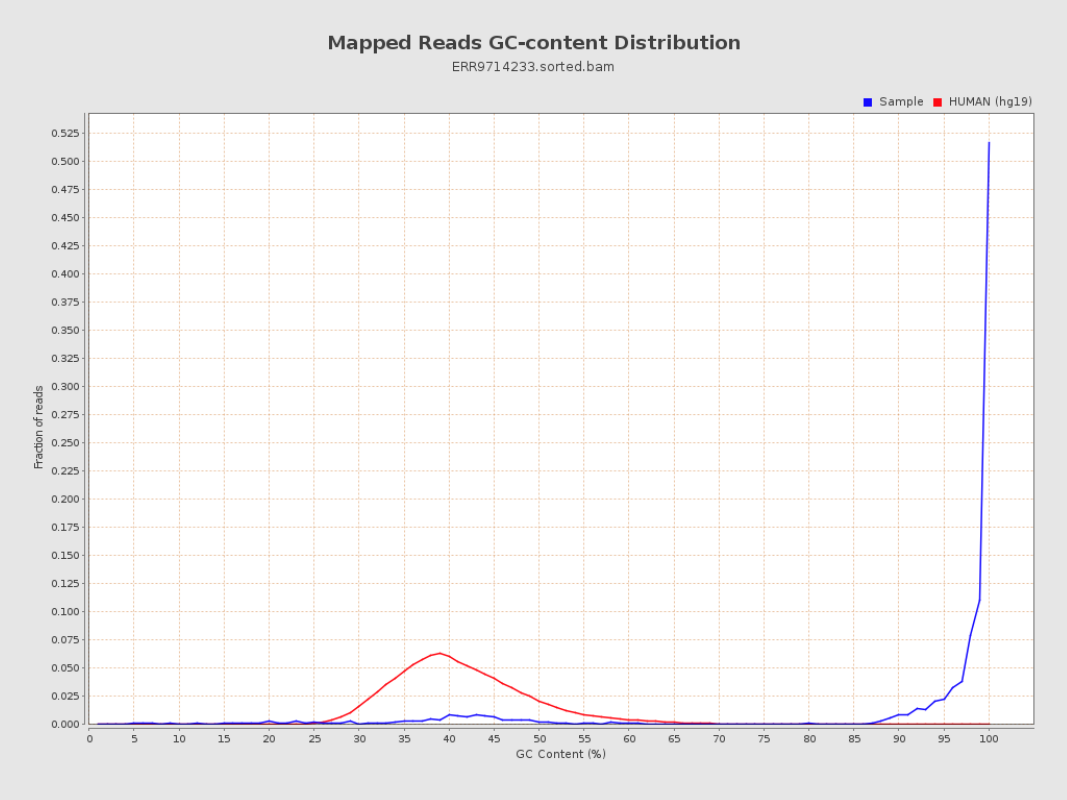
7. Results : Duplication Rate Histogram



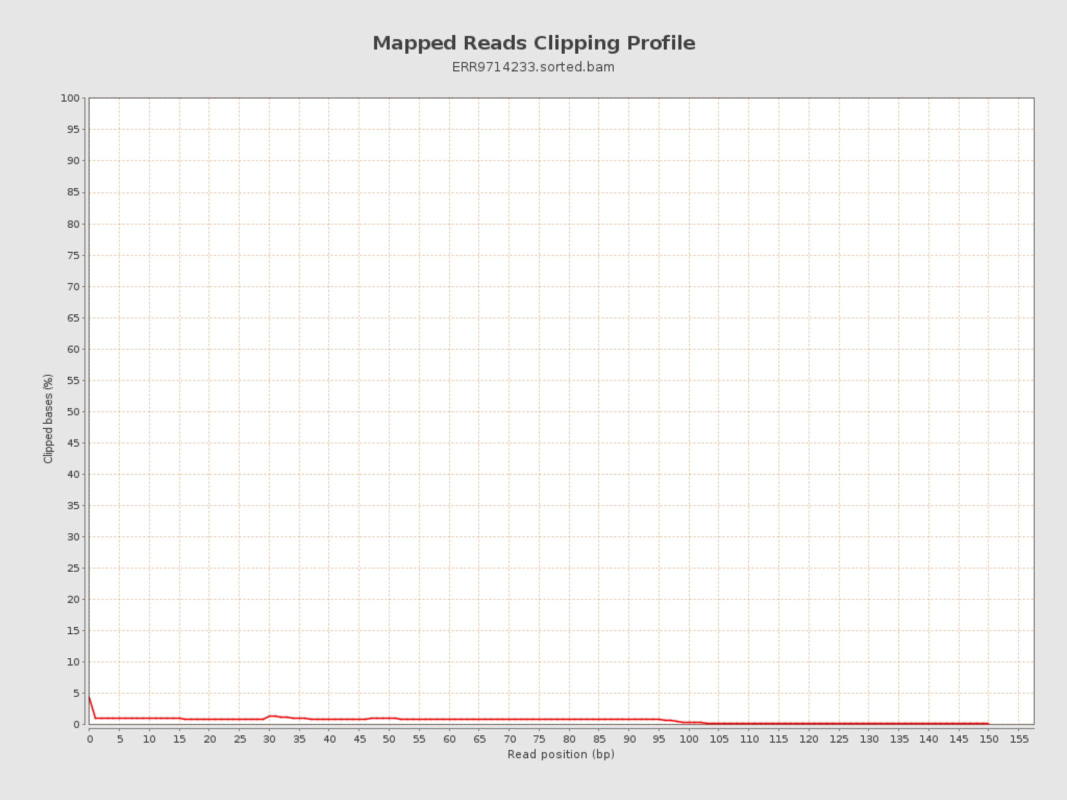
8. Results : Mapped Reads Nucleotide Content



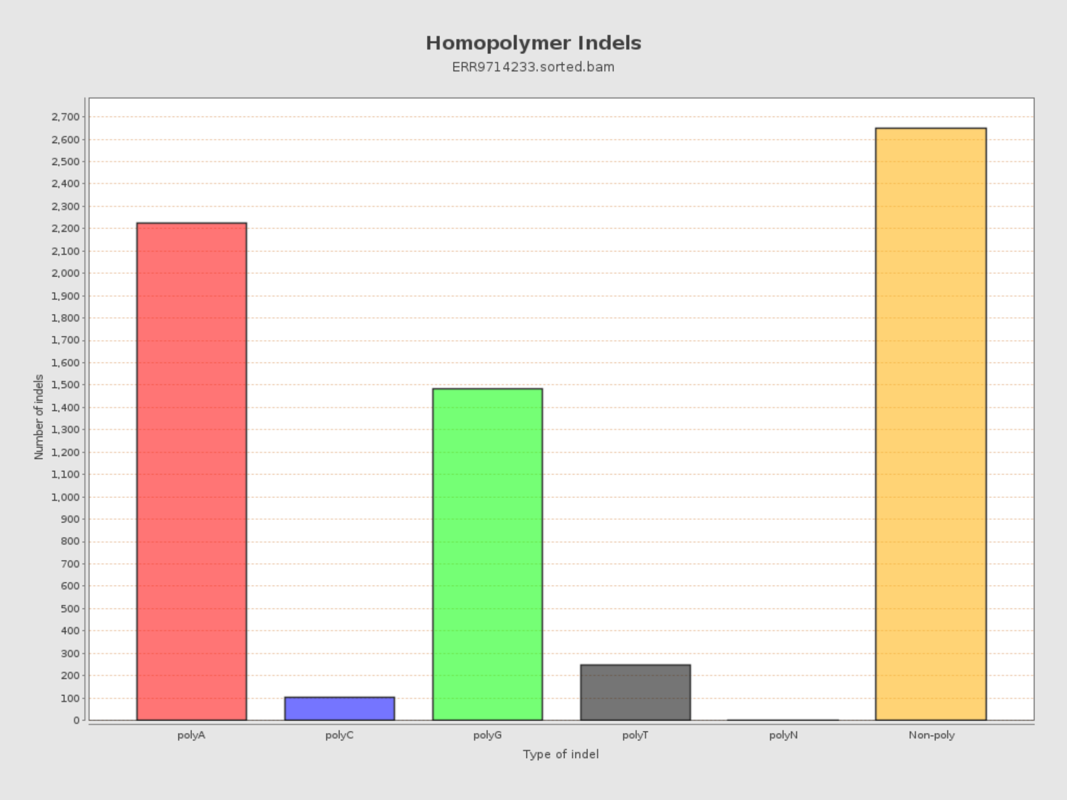
9. Results : Mapped Reads GC-content Distribution



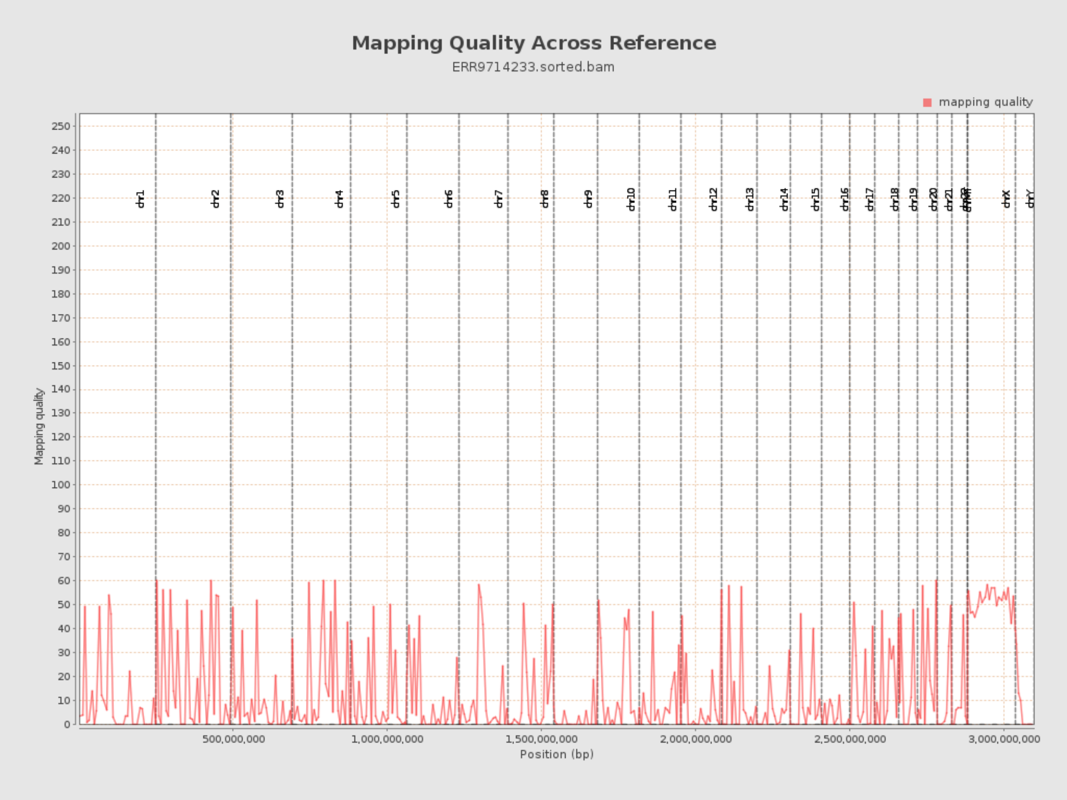
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram