Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 00:49:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714231.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_ERR9714231 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714231.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 00:49:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714231.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	248,334
Mapped reads	50,379 / 20.29%
Unmapped reads	197,955 / 79.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,923 / 0.77%
Read min/max/mean length	30 / 151 / 69.14
Duplicated reads (estimated)	45,792 / 18.44%
Duplication rate	50.26%
Clipped reads	35,811 / 14.42%

2.2. ACGT Content

Number/percentage of A's	781,651 / 14.28%
Number/percentage of C's	639,981 / 11.69%
Number/percentage of T's	714,158 / 13.05%
Number/percentage of G's	3,336,577 / 60.97%
Number/percentage of N's	85 / 0%
GC Percentage	72.67%

2.3. Coverage

Mean	0.0018

Standard Deviation	3.3449

2.4. Mapping Quality

Mean Mapping Quality	37.14

2.5. Mismatches and indels

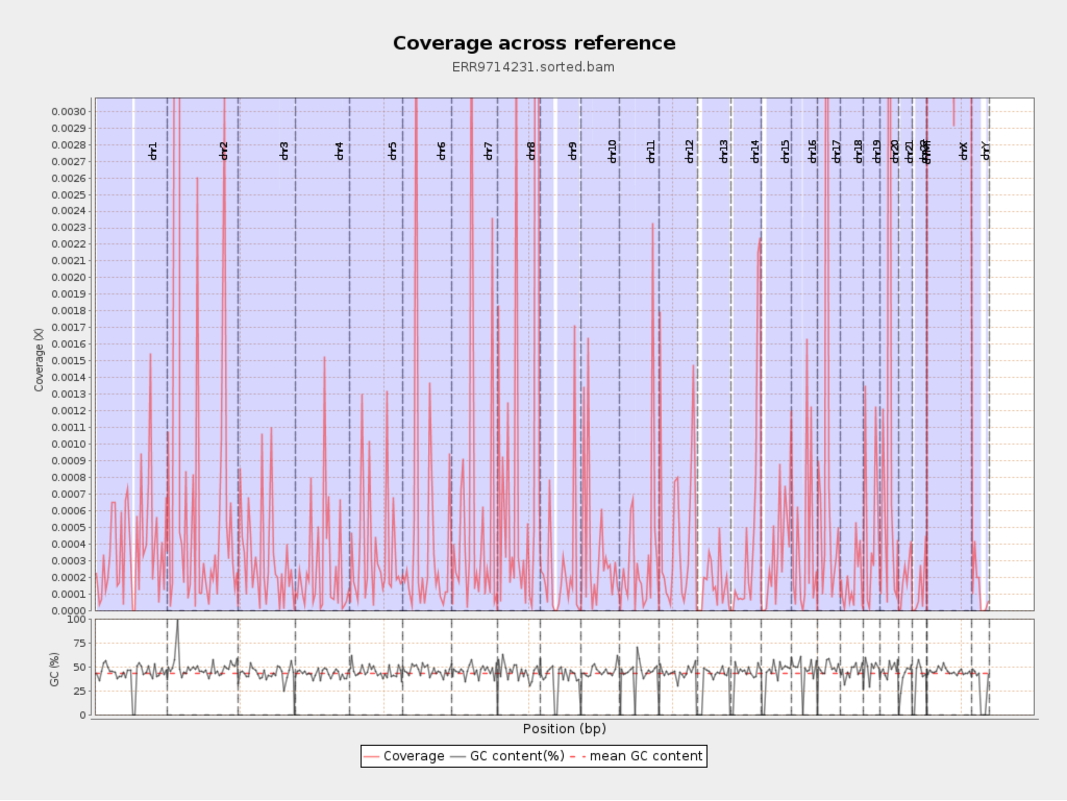
General error rate	3.51%
Mismatches	165,613
Insertions	4,340
Mapped reads with at least one insertion	6.18%
Deletions	9,011
Mapped reads with at least one deletion	17.21%
Homopolymer indels	39.83%

2.6. Chromosome stats

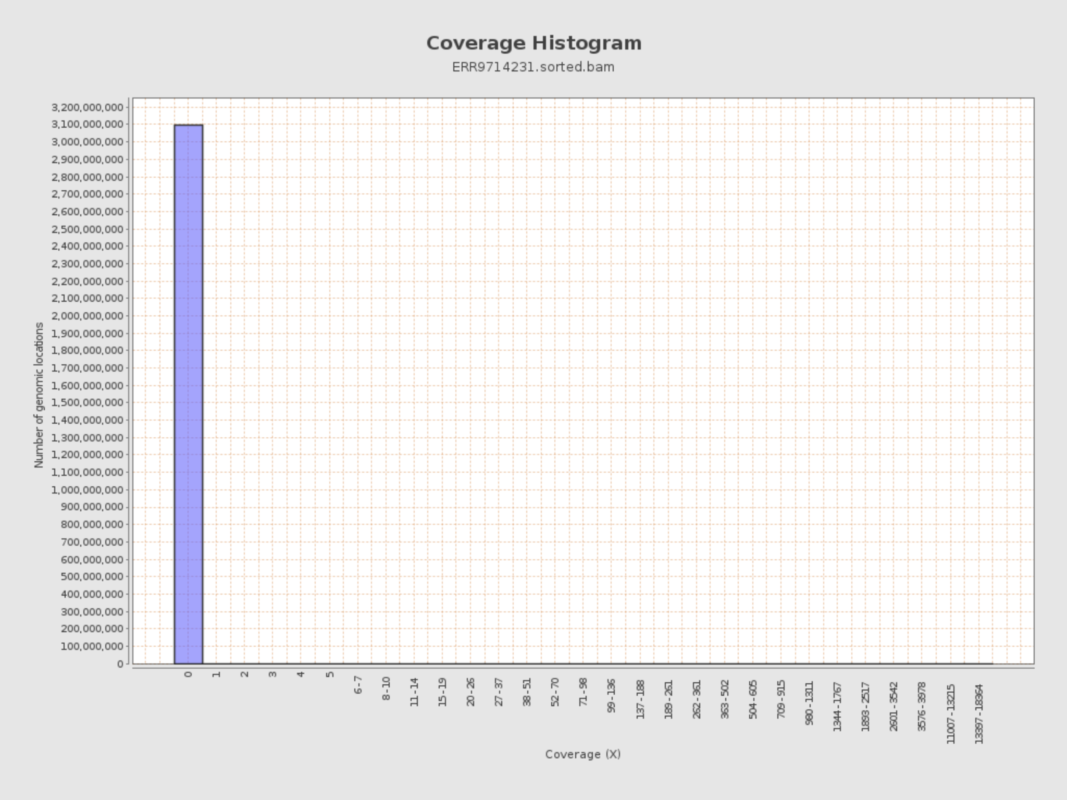
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	95950	0.0004	0.1518
chr2	243199373	2855183	0.0117	11.8817
chr3	198022430	62217	0.0003	0.0701
chr4	191154276	49644	0.0003	0.0718
chr5	180915260	64649	0.0004	0.0898
chr6	171115067	78524	0.0005	0.1598
chr7	159138663	87864	0.0006	0.2097

chr8	146364022	160052	0.0011	0.5112
chr9	141213431	34126	0.0002	0.0909
chr10	135534747	48944	0.0004	0.2038
chr11	135006516	47372	0.0004	0.0827
chr12	133851895	62611	0.0005	0.1171
chr13	115169878	17360	0.0002	0.0357
chr14	107349540	52778	0.0005	0.1611
chr15	102531392	34318	0.0003	0.0699
chr16	90354753	39133	0.0004	0.1147
chr17	81195210	77978	0.001	0.2495
chr18	78077248	13942	0.0002	0.038
chr19	59128983	28640	0.0005	0.1181
chr20	63025520	71334	0.0011	0.4038
chr21	48129895	9648	0.0002	0.0332
chr22	51304566	6298	0.0001	0.0346
chrMT	16571	392	0.0237	0.4282
chrX	155270560	1534029	0.0099	1.1694
chrY	59373566	7217	0.0001	0.0291

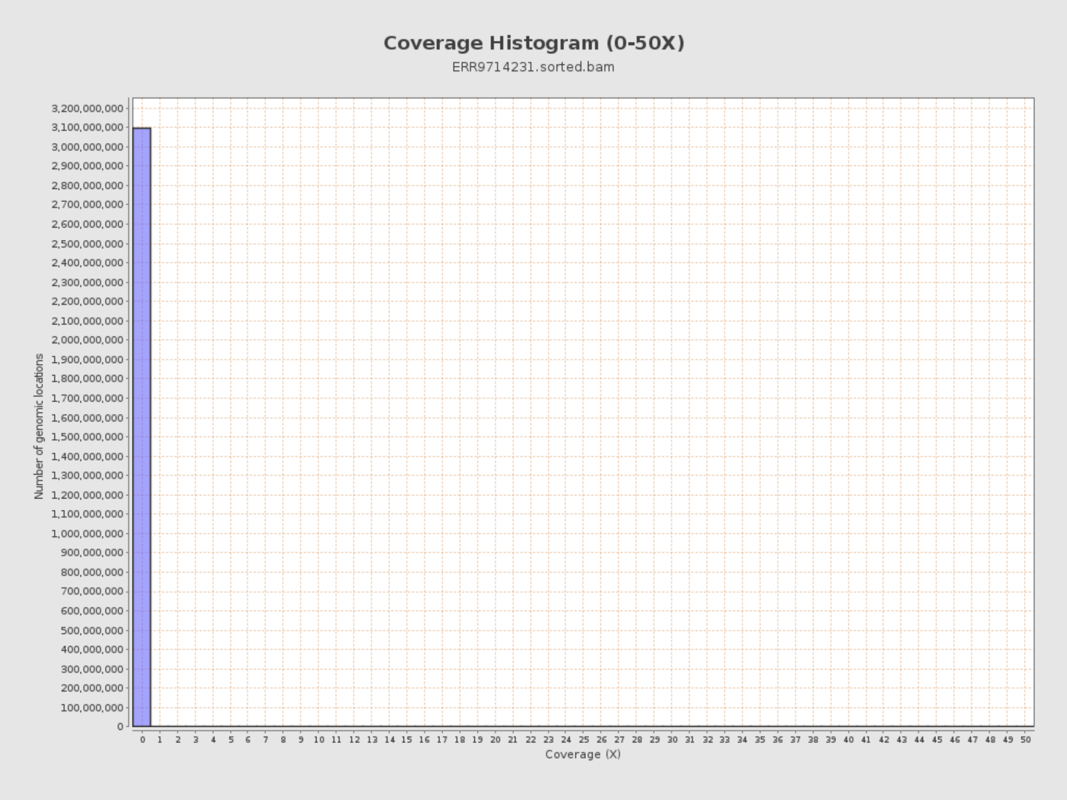
3. Results : Coverage across reference



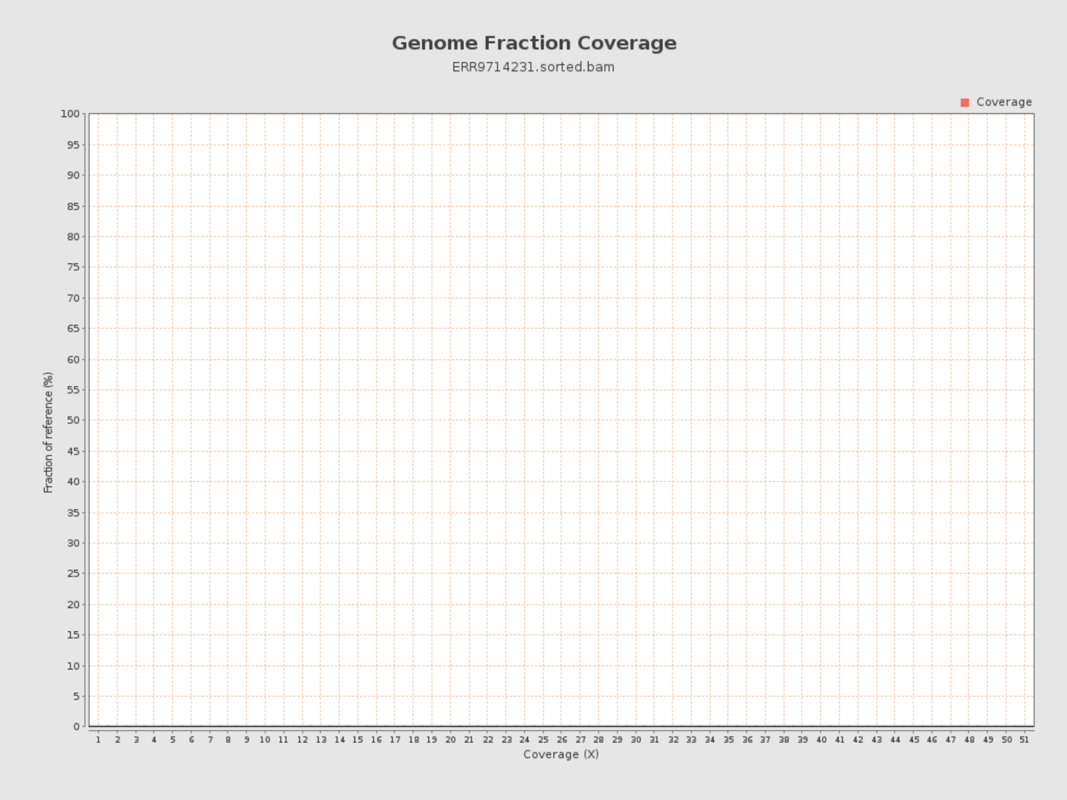
4. Results : Coverage Histogram



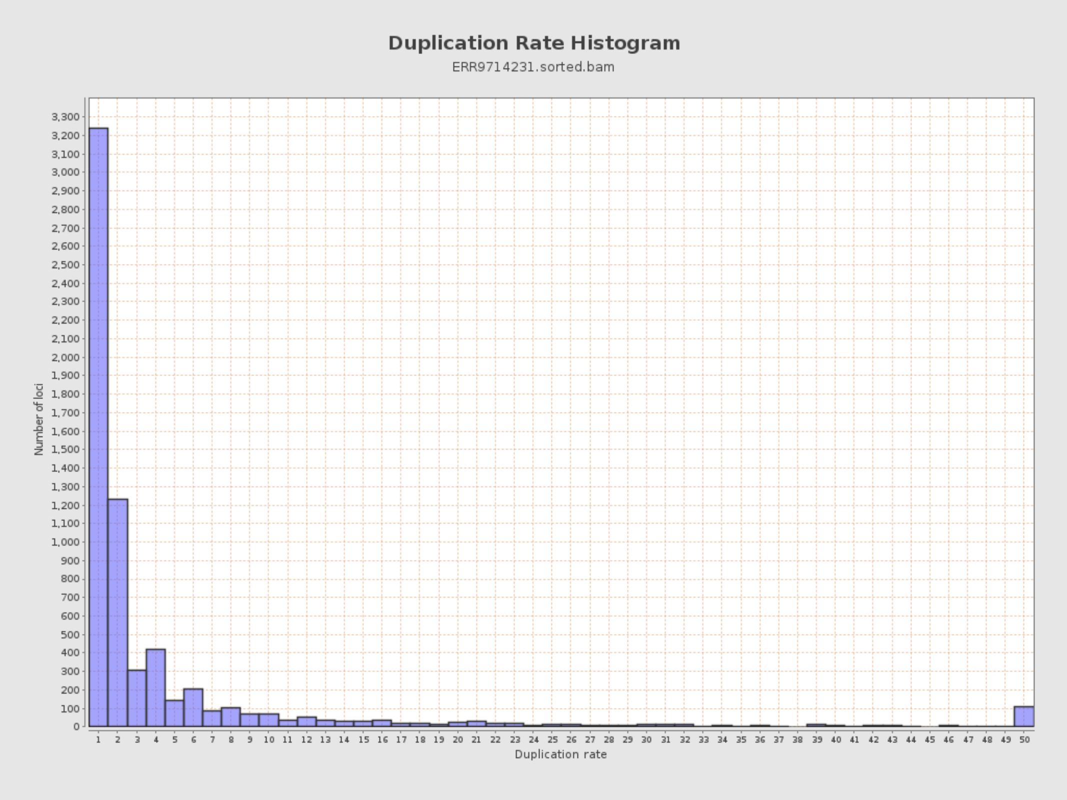
5. Results : Coverage Histogram (0-50X)



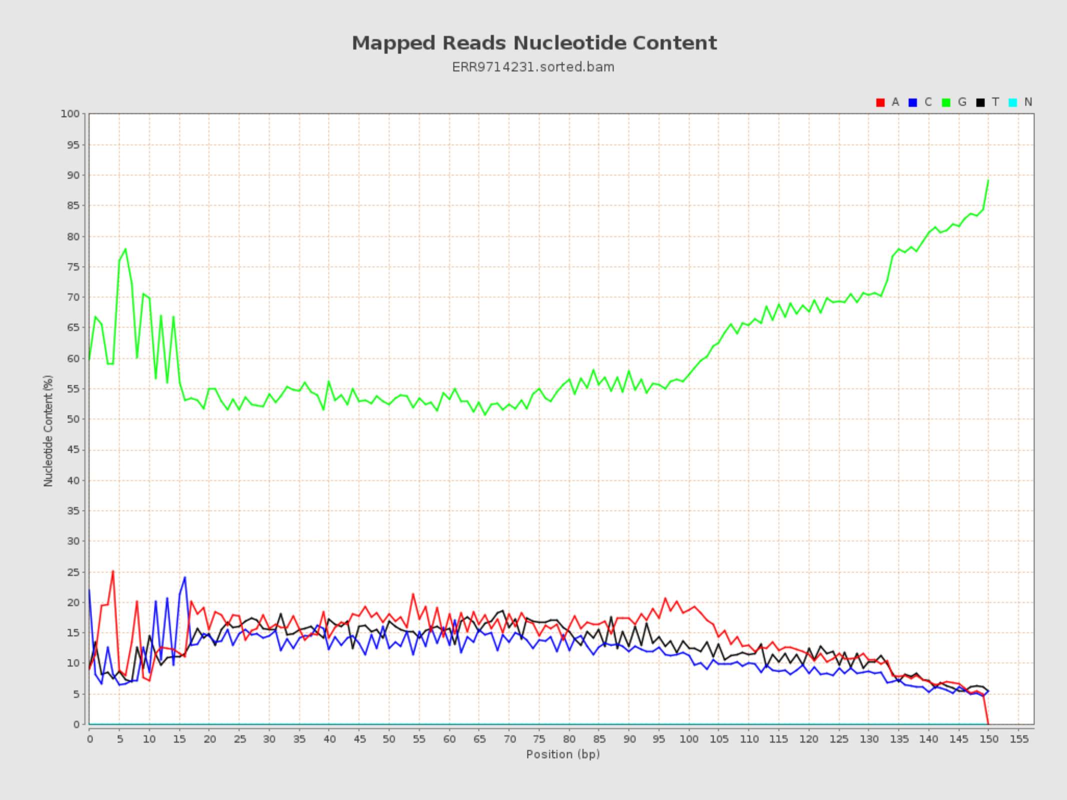
6. Results : Genome Fraction Coverage



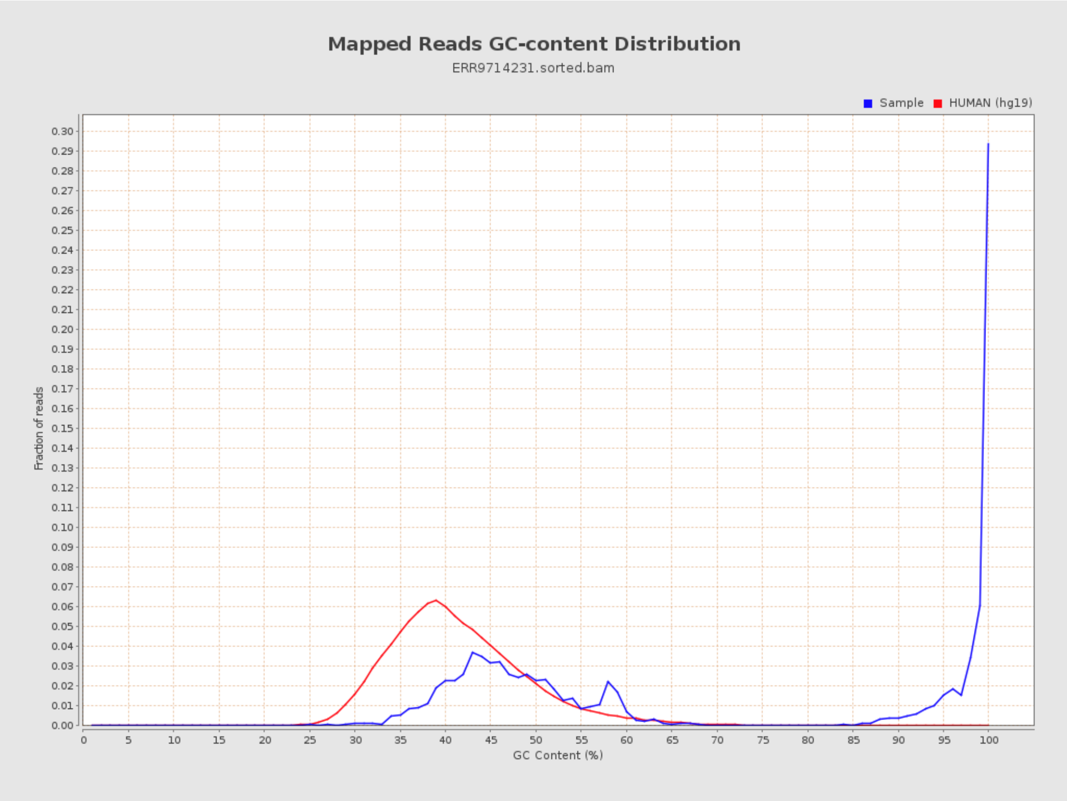
7. Results : Duplication Rate Histogram



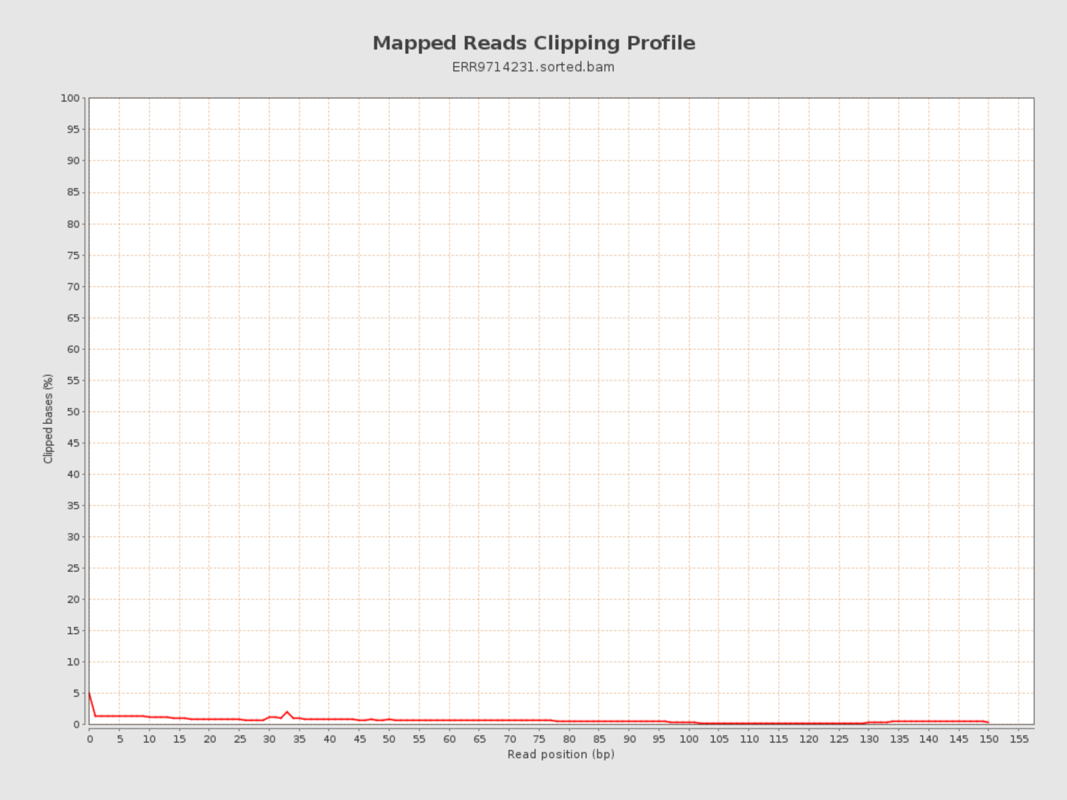
8. Results : Mapped Reads Nucleotide Content



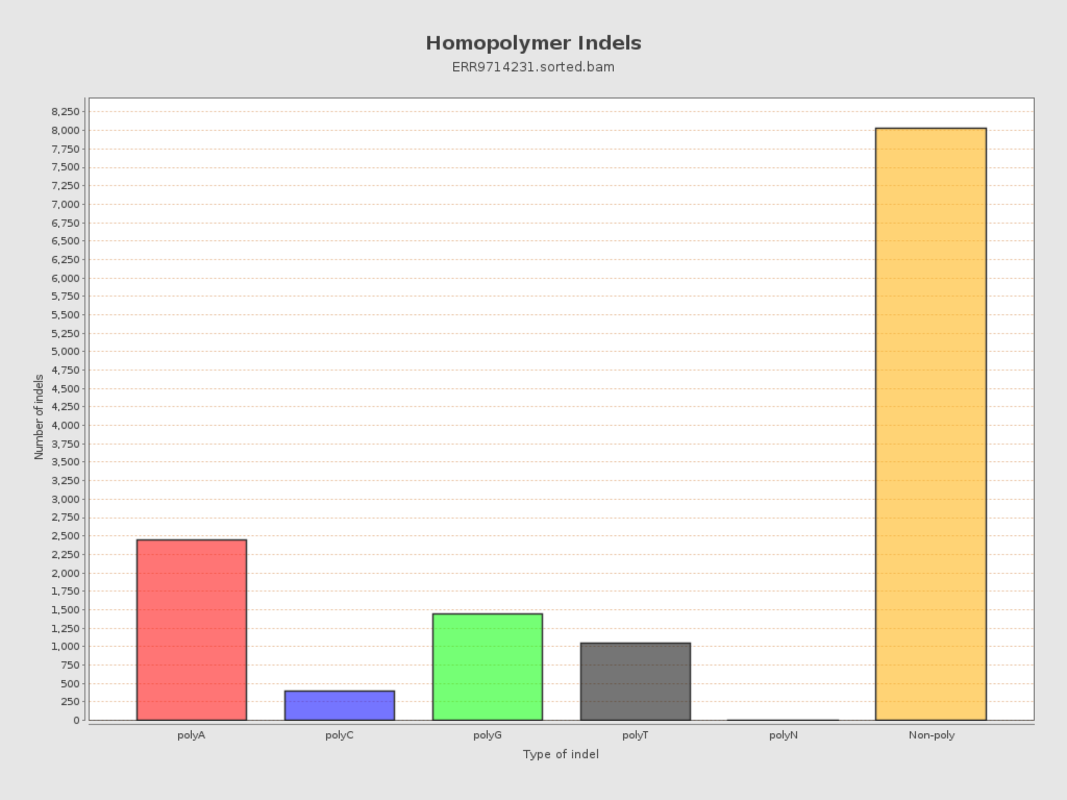
9. Results : Mapped Reads GC-content Distribution



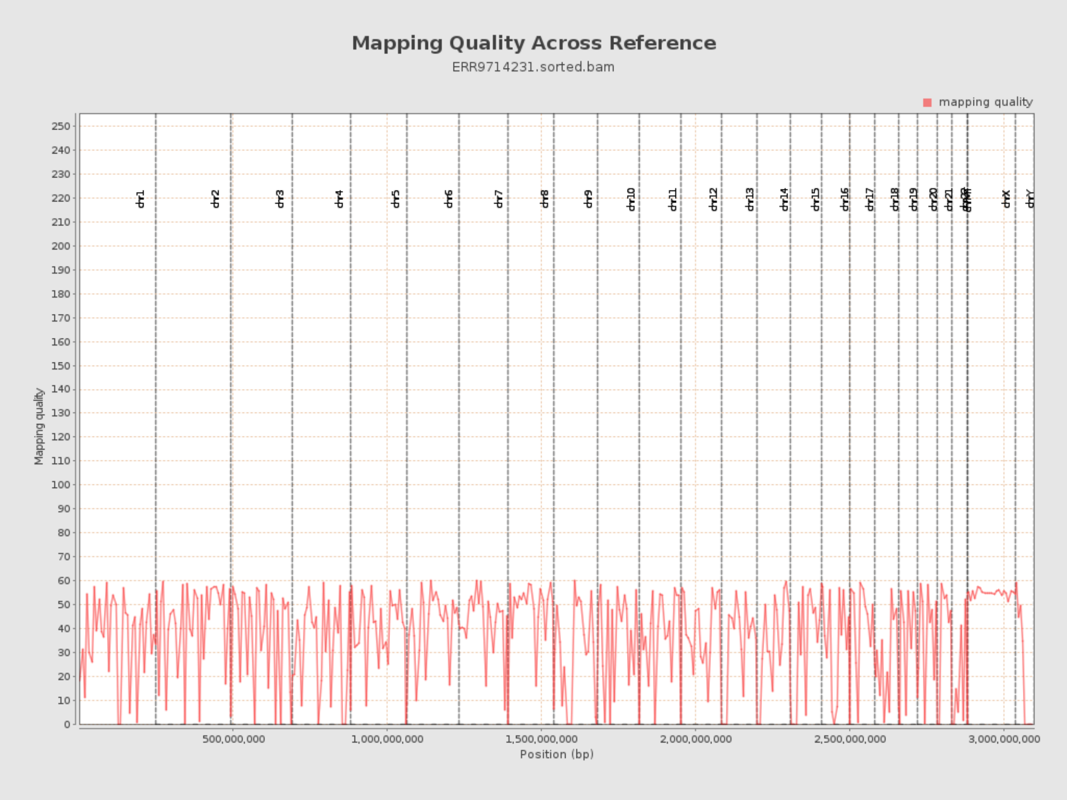
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram