Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 17:20:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714048.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_ERR9714048 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714048.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 17:20:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714048.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	470,956
Mapped reads	65,071 / 13.82%
Unmapped reads	405,885 / 86.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,276 / 0.27%
Read min/max/mean length	30 / 151 / 58.73
Duplicated reads (estimated)	64,002 / 13.59%
Duplication rate	27.97%
Clipped reads	33,013 / 7.01%

2.2. ACGT Content

Number/percentage of A's	126,500 / 1.85%
Number/percentage of C's	37,578 / 0.55%
Number/percentage of T's	42,978 / 0.63%
Number/percentage of G's	6,613,472 / 96.96%
Number/percentage of N's	158 / 0%
GC Percentage	97.51%

2.3. Coverage

Mean	0.0022

Standard Deviation	8.4527

2.4. Mapping Quality

Mean Mapping Quality	9.98

2.5. Mismatches and indels

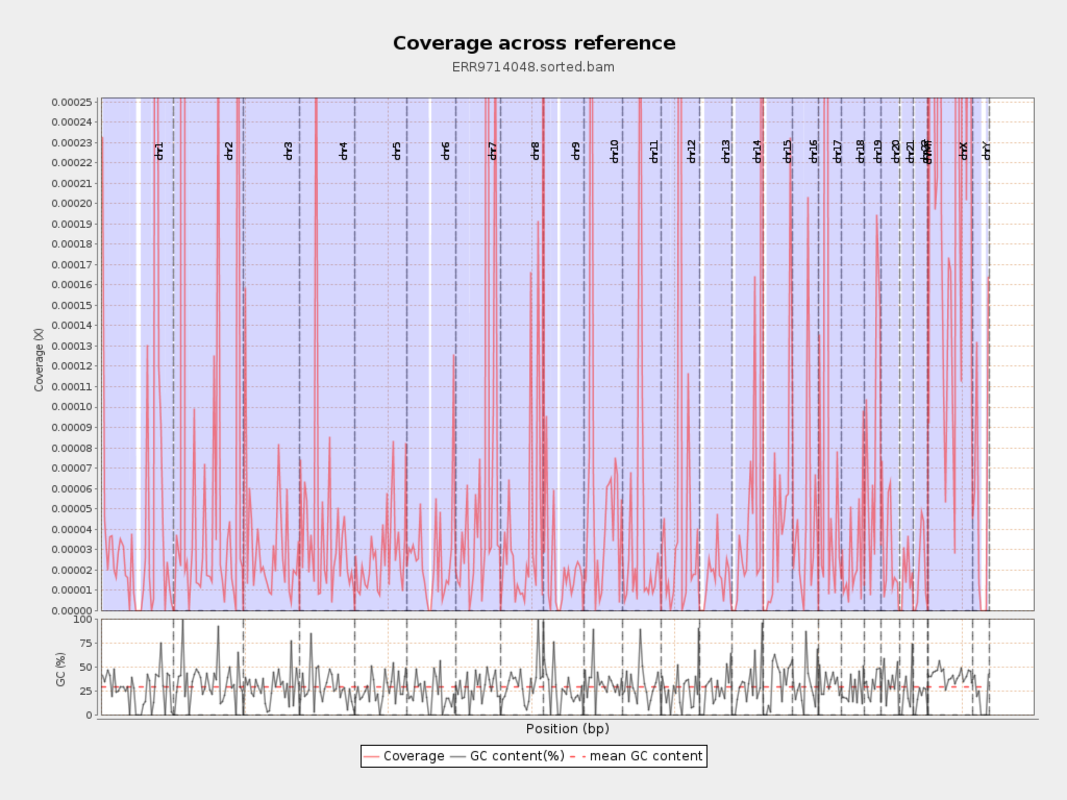
General error rate	3.4%
Mismatches	169,853
Insertions	8,373
Mapped reads with at least one insertion	9.11%
Deletions	3,235
Mapped reads with at least one deletion	4.8%
Homopolymer indels	67.63%

2.6. Chromosome stats

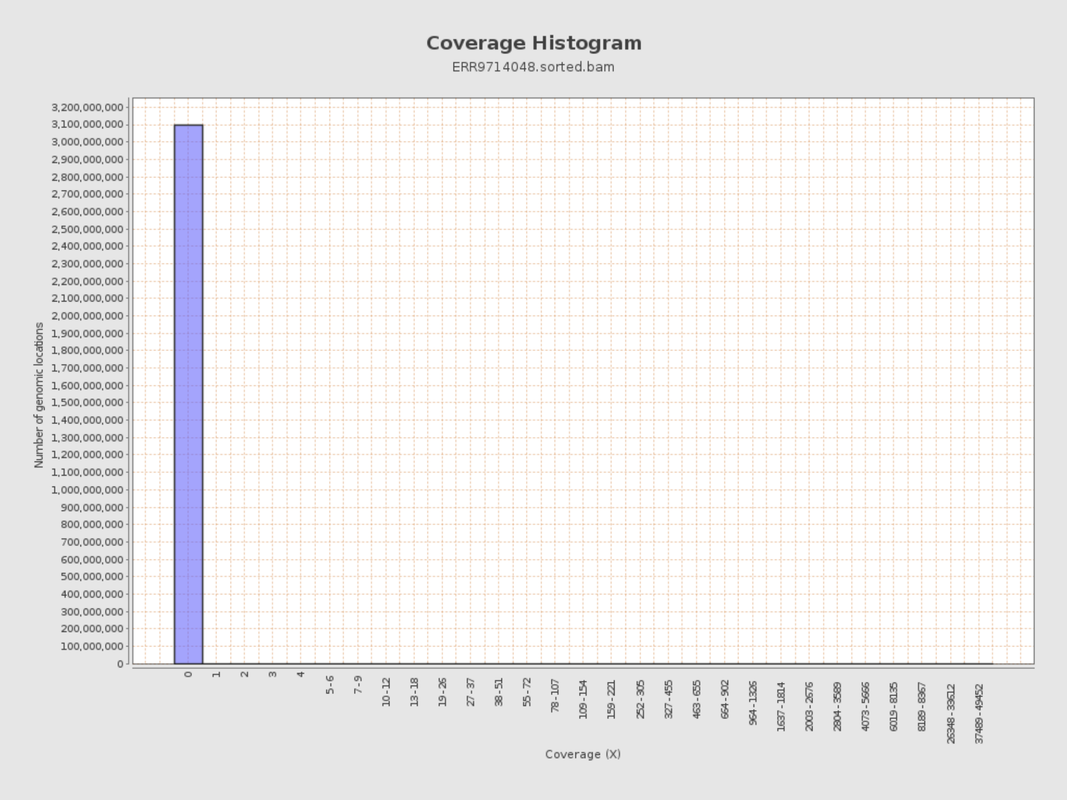
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12728	0.0001	0.0543
chr2	243199373	6660991	0.0274	30.1569
chr3	198022430	6275	0	0.0111
chr4	191154276	8179	0	0.0156
chr5	180915260	4961	0	0.0076
chr6	171115067	4632	0	0.0102
chr7	159138663	13329	0.0001	0.082

chr8	146364022	5695	0	0.0232
chr9	141213431	3307	0	0.011
chr10	135534747	8820	0.0001	0.0564
chr11	135006516	5599	0	0.0353
chr12	133851895	9474	0.0001	0.057
chr13	115169878	1722	0	0.0044
chr14	107349540	9460	0.0001	0.0947
chr15	102531392	4970	0	0.0201
chr16	90354753	3894	0	0.012
chr17	81195210	8696	0.0001	0.1041
chr18	78077248	2028	0	0.0105
chr19	59128983	4706	0.0001	0.0252
chr20	63025520	1835	0	0.012
chr21	48129895	809	0	0.0049
chr22	51304566	1021	0	0.0056
chrMT	16571	4978	0.3004	1.4282
chrX	155270560	43056	0.0003	0.0514
chrY	59373566	3083	0.0001	0.0131

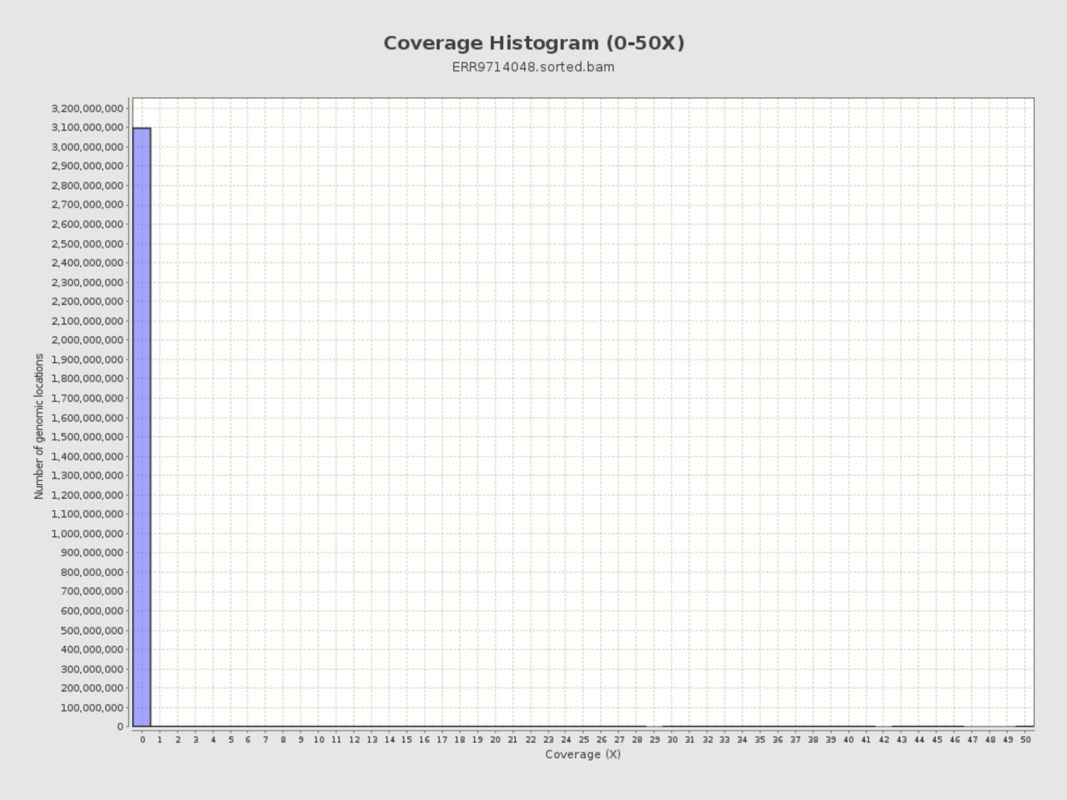
3. Results : Coverage across reference



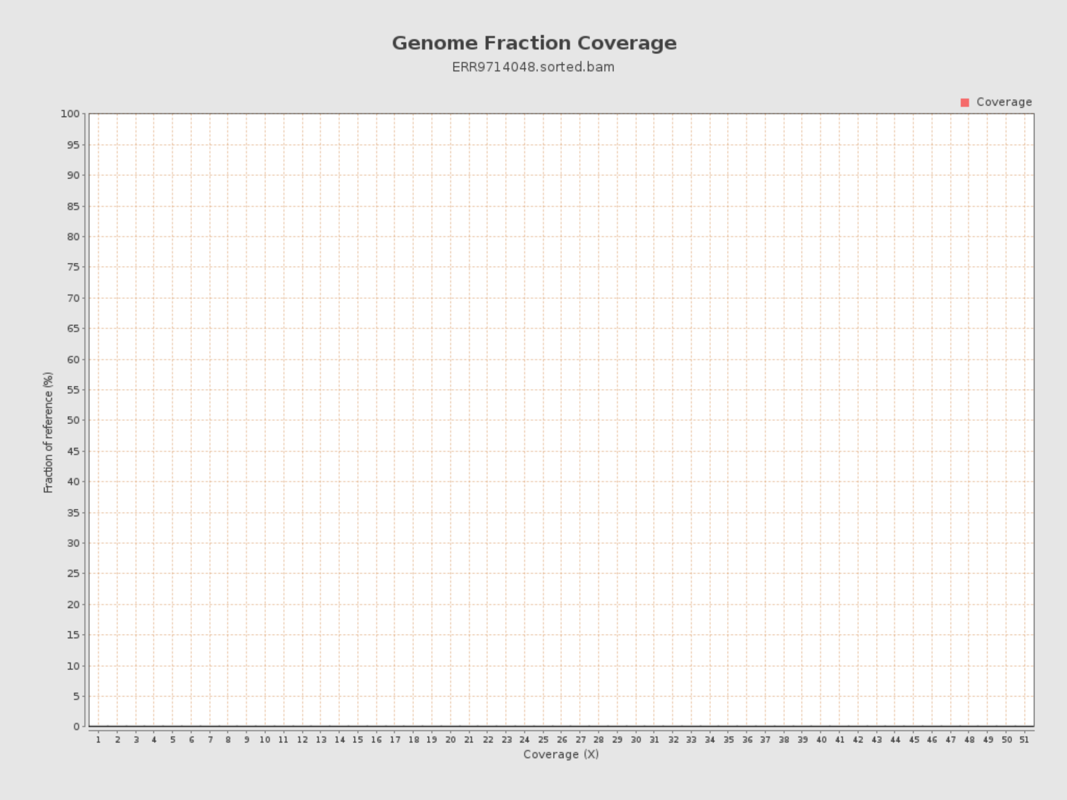
4. Results : Coverage Histogram



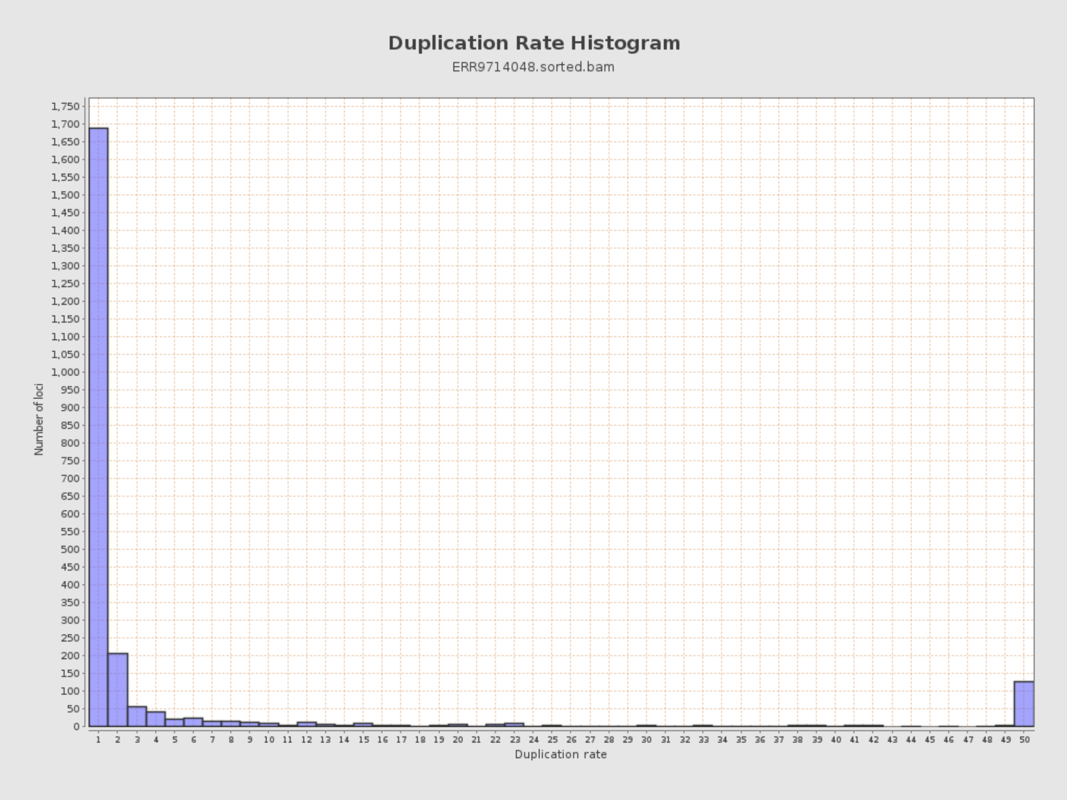
5. Results : Coverage Histogram (0-50X)



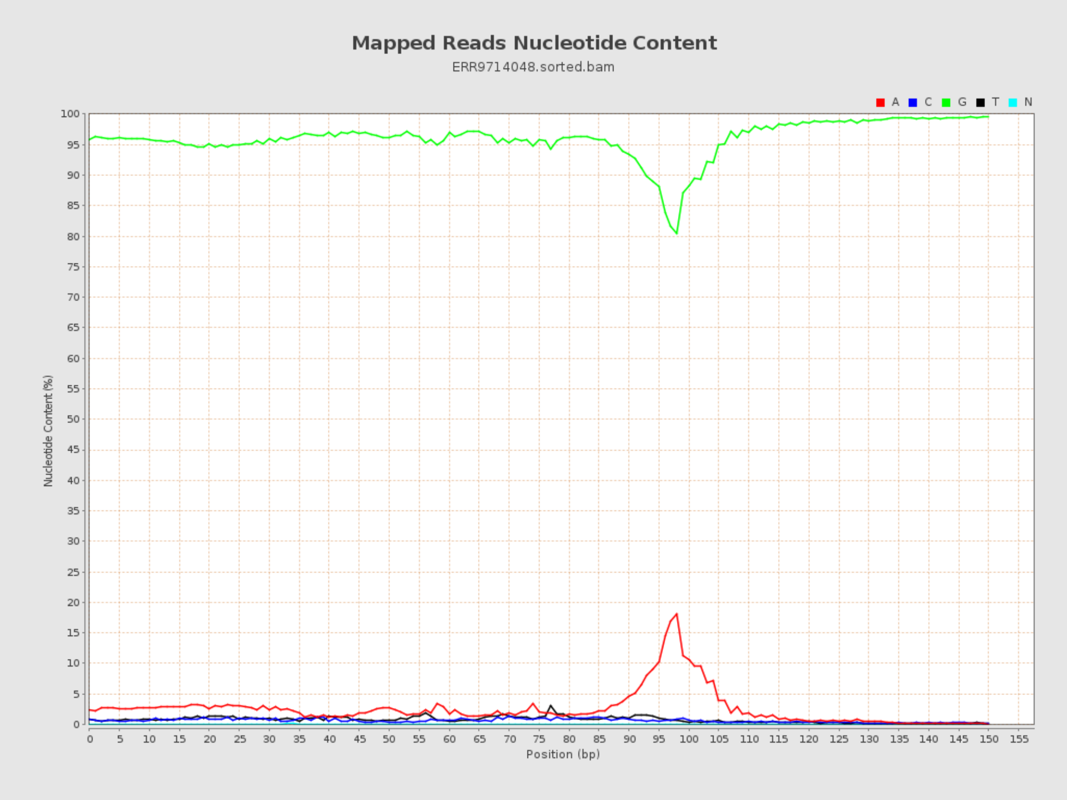
6. Results : Genome Fraction Coverage



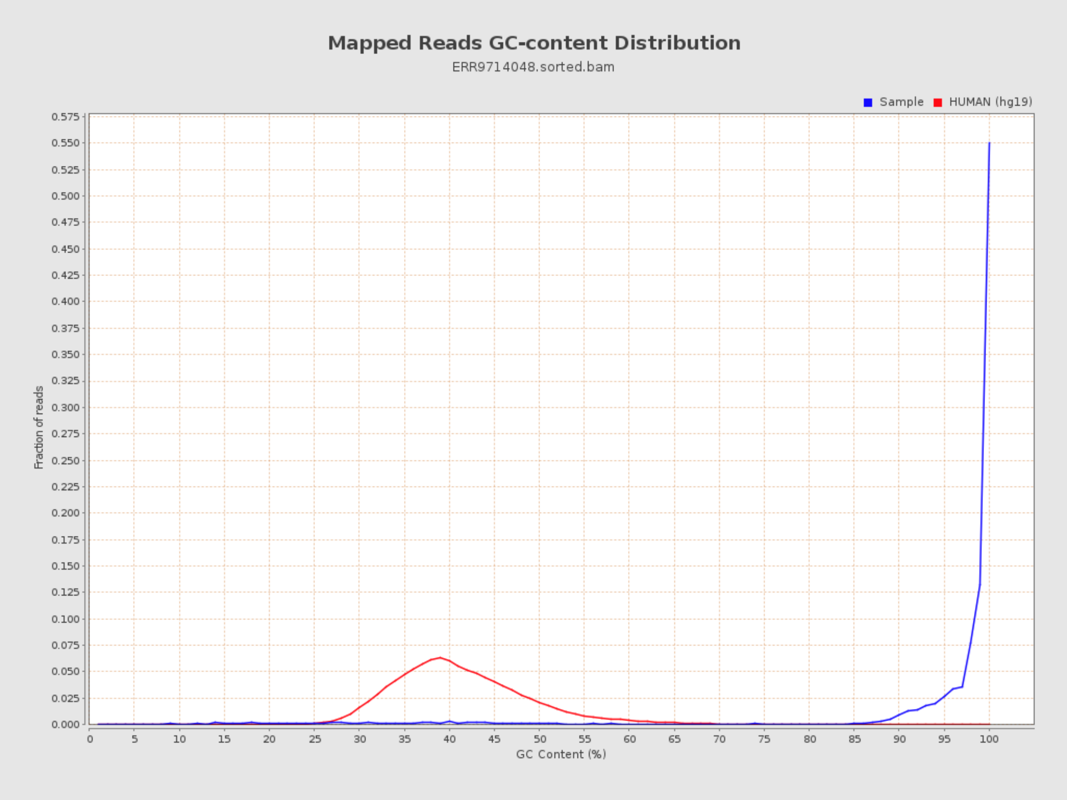
7. Results : Duplication Rate Histogram



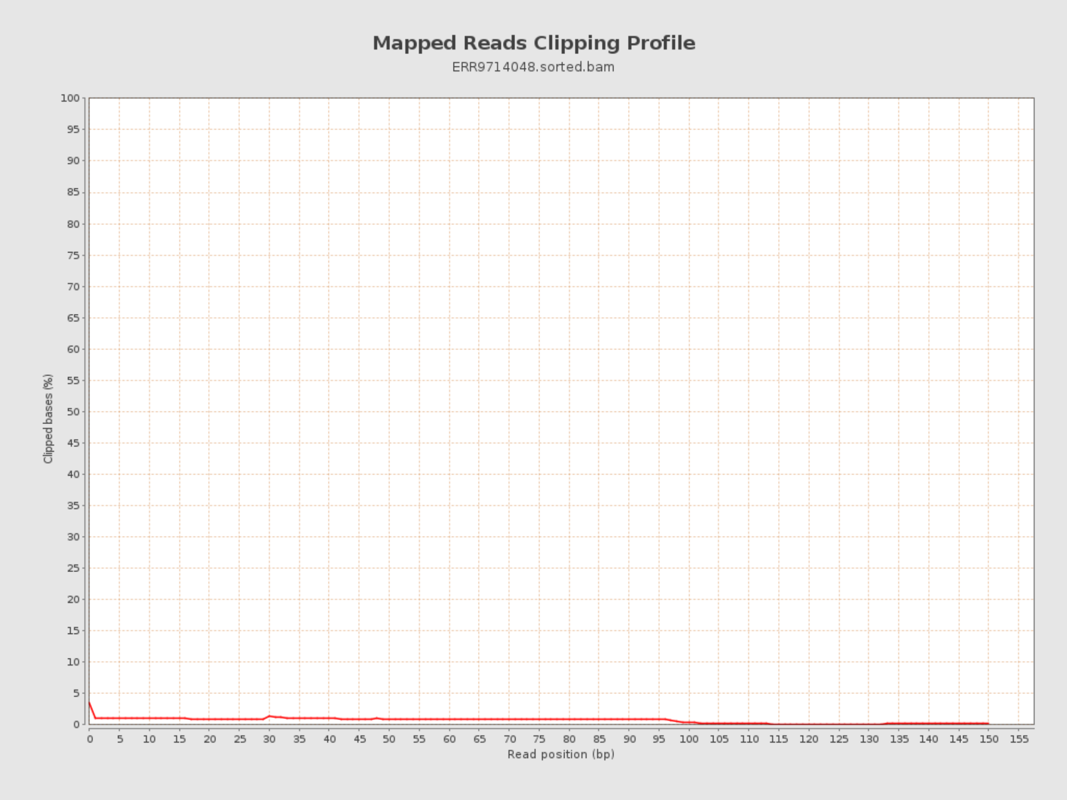
8. Results : Mapped Reads Nucleotide Content



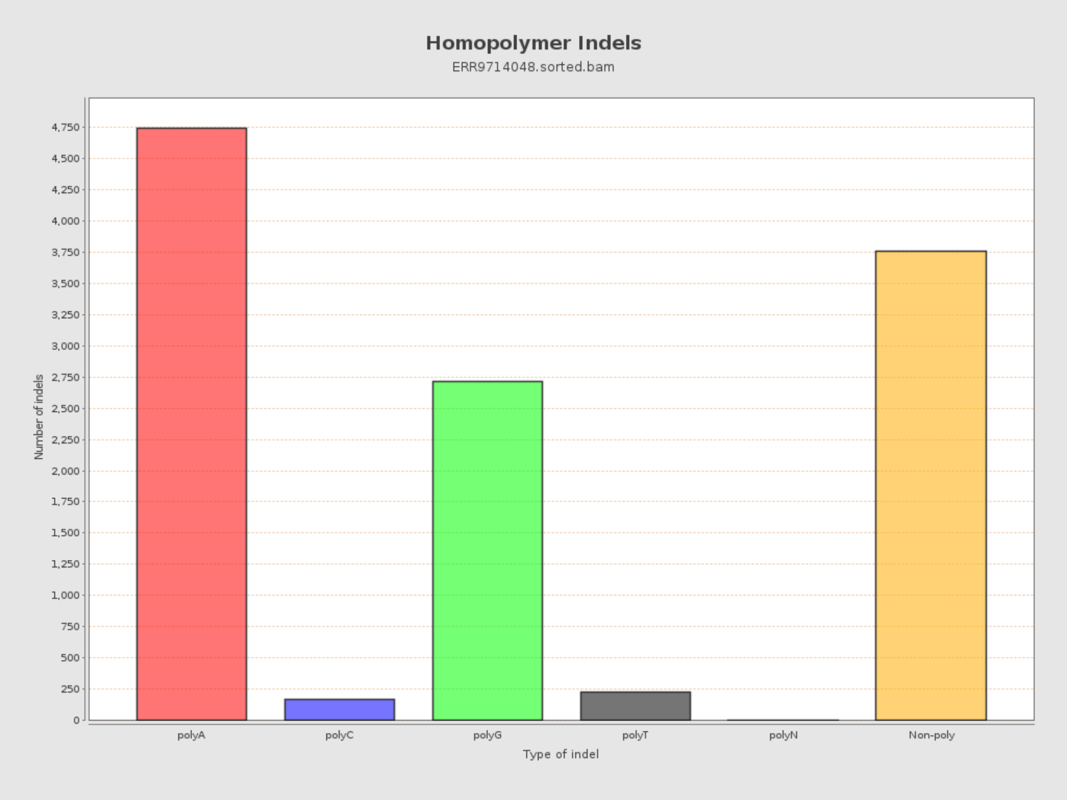
9. Results : Mapped Reads GC-content Distribution



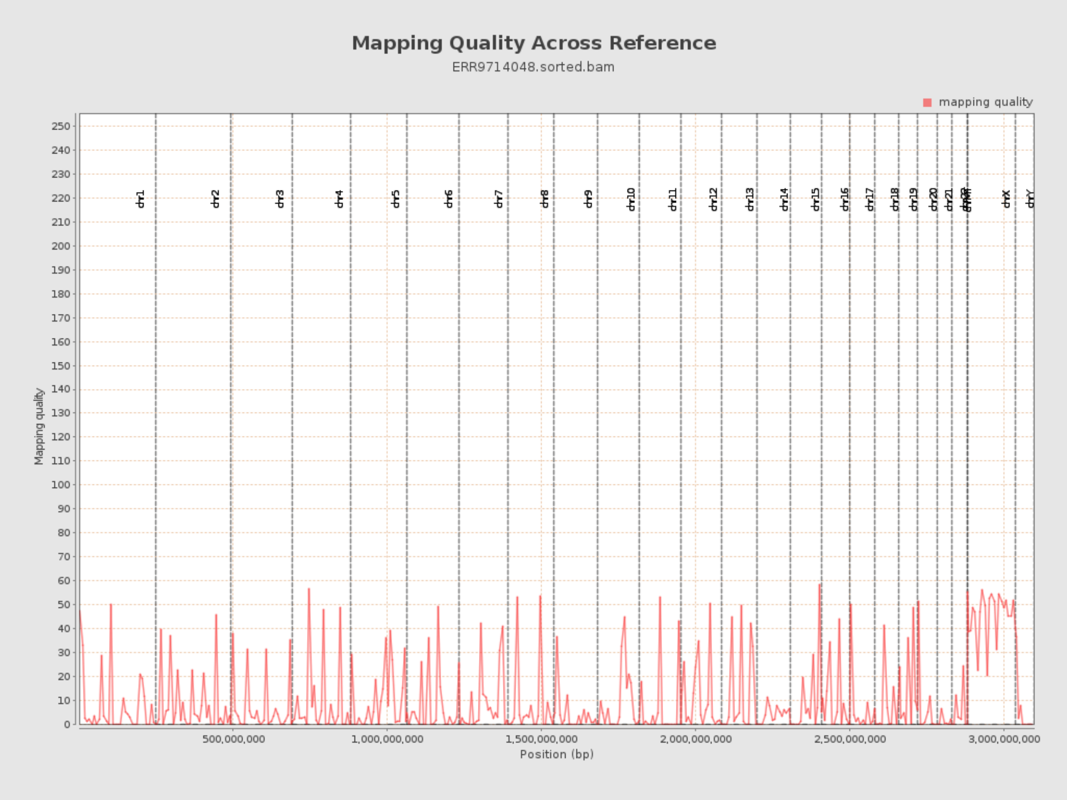
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram