Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 18:52:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714089.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_ERR9714089 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714089.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 18:52:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714089.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	528,416
Mapped reads	311,288 / 58.91%
Unmapped reads	217,128 / 41.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,722 / 2.22%
Read min/max/mean length	30 / 151 / 113.96
Duplicated reads (estimated)	274,183 / 51.89%
Duplication rate	43.3%
Clipped reads	283,931 / 53.73%

2.2. ACGT Content

Number/percentage of A's	10,448,319 / 26.49%
Number/percentage of C's	7,826,339 / 19.84%
Number/percentage of T's	9,889,000 / 25.07%
Number/percentage of G's	11,277,021 / 28.59%
Number/percentage of N's	384 / 0%
GC Percentage	48.44%

2.3. Coverage

Mean	0.013

Standard Deviation	4.7839

2.4. Mapping Quality

Mean Mapping Quality	50.02

2.5. Mismatches and indels

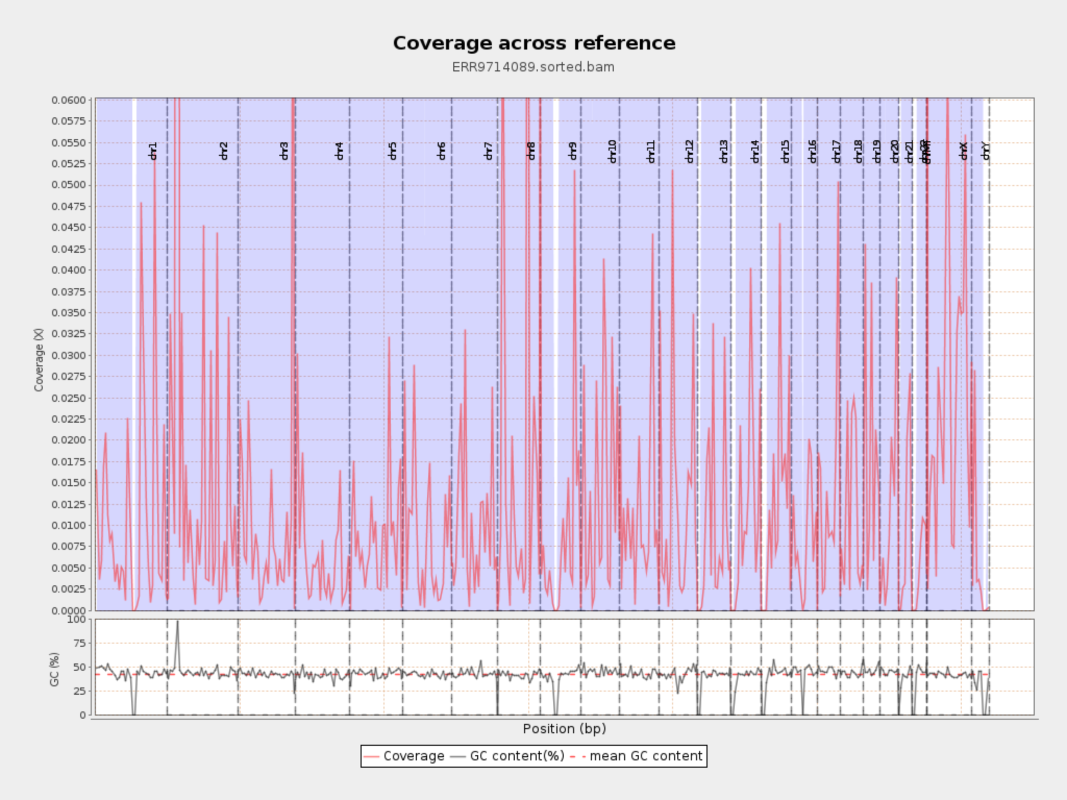
General error rate	4.41%
Mismatches	1,600,238
Insertions	48,449
Mapped reads with at least one insertion	14.78%
Deletions	138,039
Mapped reads with at least one deletion	41.14%
Homopolymer indels	31.06%

2.6. Chromosome stats

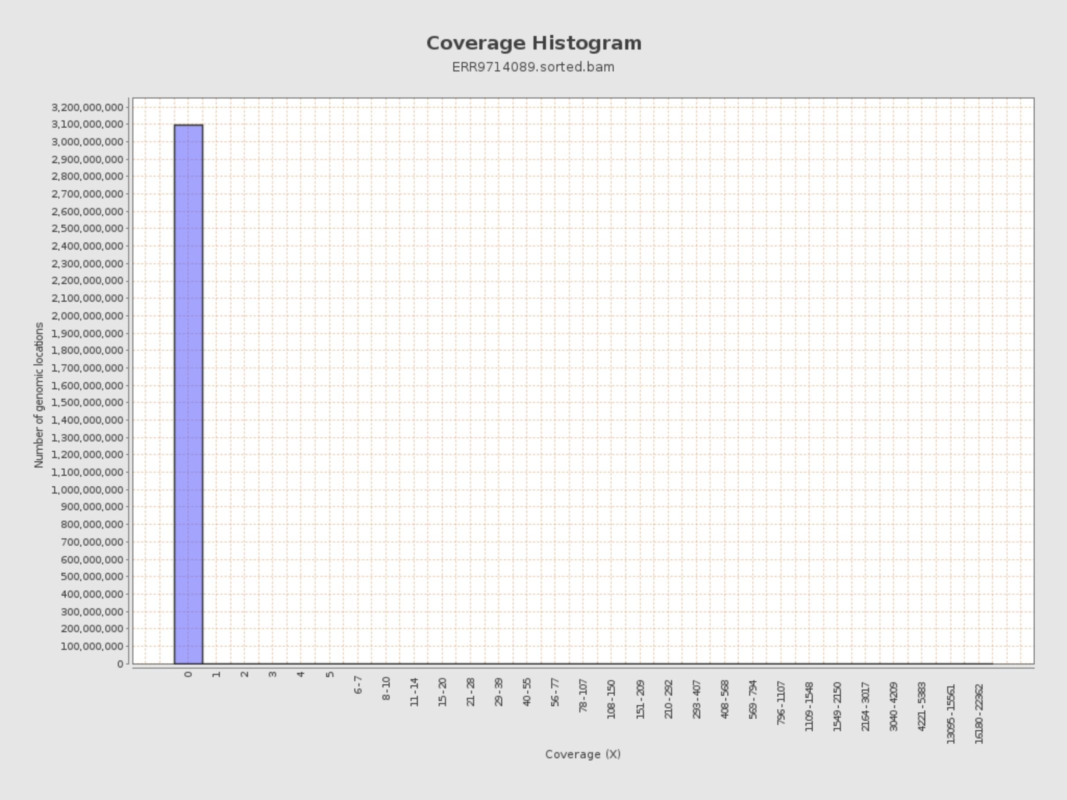
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2774506	0.0111	2.561
chr2	243199373	6282230	0.0258	14.2955
chr3	198022430	2396525	0.0121	4.5566
chr4	191154276	1236090	0.0065	1.4766
chr5	180915260	1677699	0.0093	1.3763
chr6	171115067	1473362	0.0086	1.4264
chr7	159138663	1621593	0.0102	1.873

chr8	146364022	2704278	0.0185	5.396
chr9	141213431	1253762	0.0089	2.3786
chr10	135534747	1916373	0.0141	2.728
chr11	135006516	1601944	0.0119	2.0103
chr12	133851895	1777263	0.0133	2.9684
chr13	115169878	1127755	0.0098	2.3437
chr14	107349540	1240541	0.0116	2.113
chr15	102531392	1332615	0.013	2.1992
chr16	90354753	770101	0.0085	1.4709
chr17	81195210	1173883	0.0145	3.2422
chr18	78077248	933938	0.012	2.077
chr19	59128983	1060910	0.0179	3.3138
chr20	63025520	824299	0.0131	1.7723
chr21	48129895	441162	0.0092	2.3623
chr22	51304566	255479	0.005	0.702
chrMT	16571	85093	5.1351	35.8805
chrX	155270560	3998632	0.0258	3.2583
chrY	59373566	307564	0.0052	1.5105

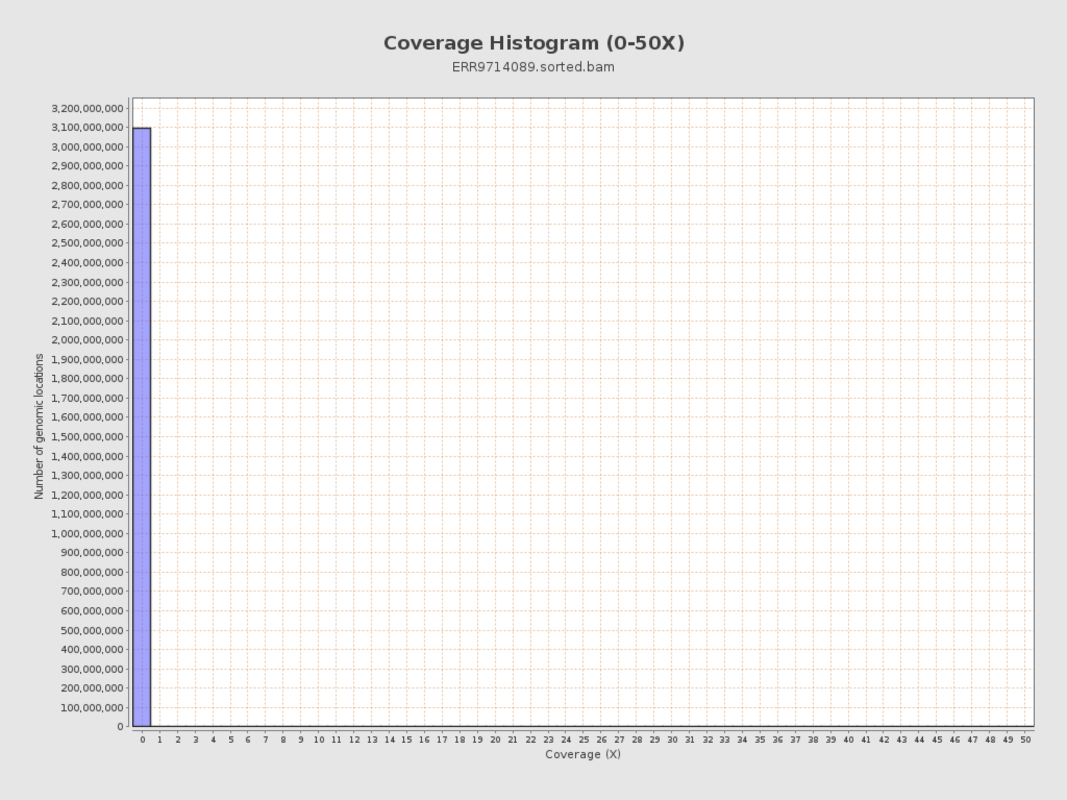
3. Results : Coverage across reference



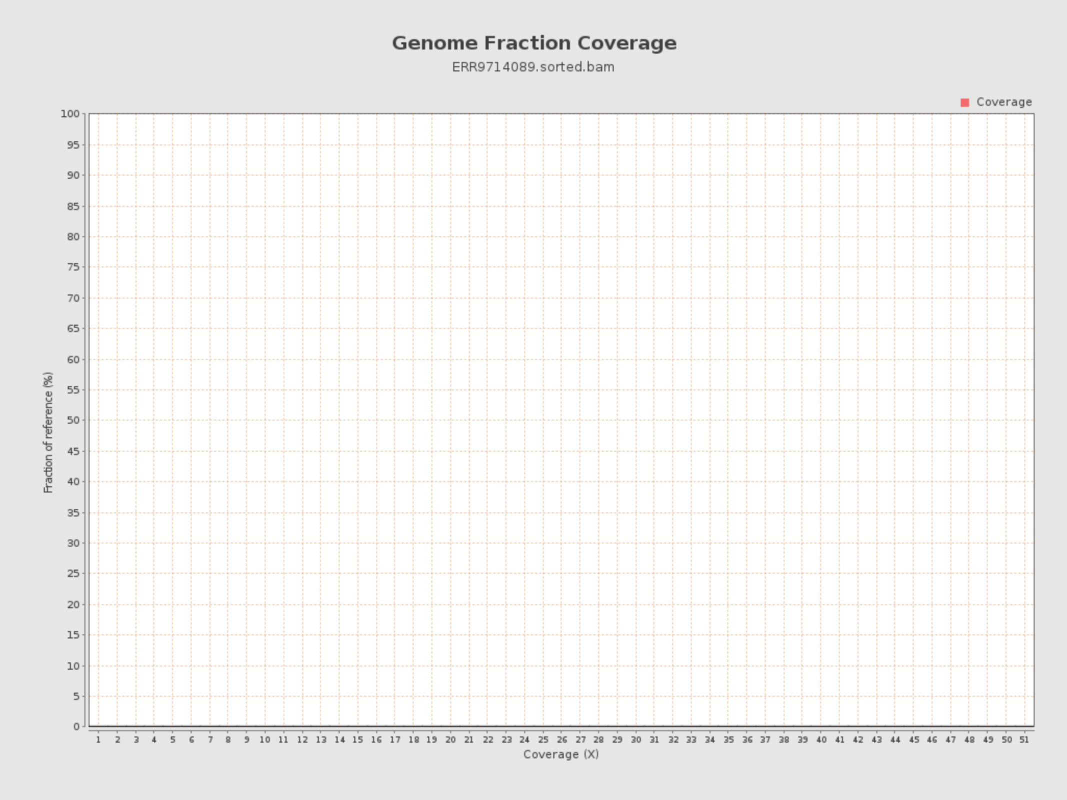
4. Results : Coverage Histogram



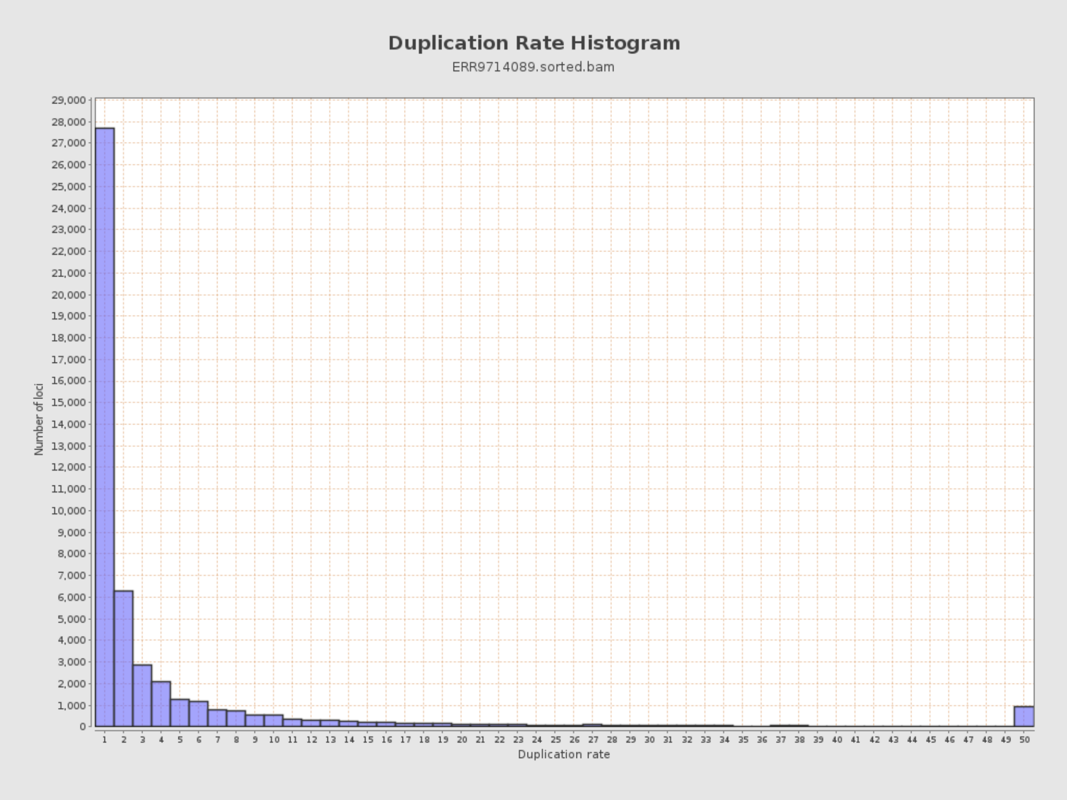
5. Results : Coverage Histogram (0-50X)



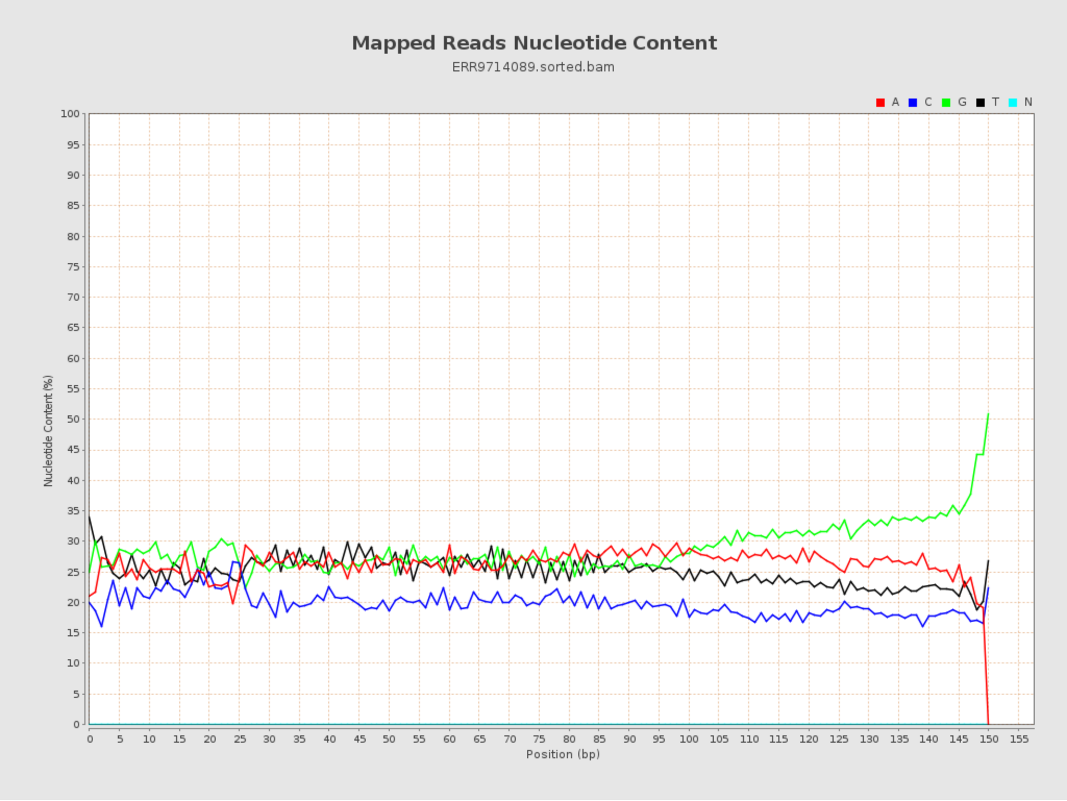
6. Results : Genome Fraction Coverage



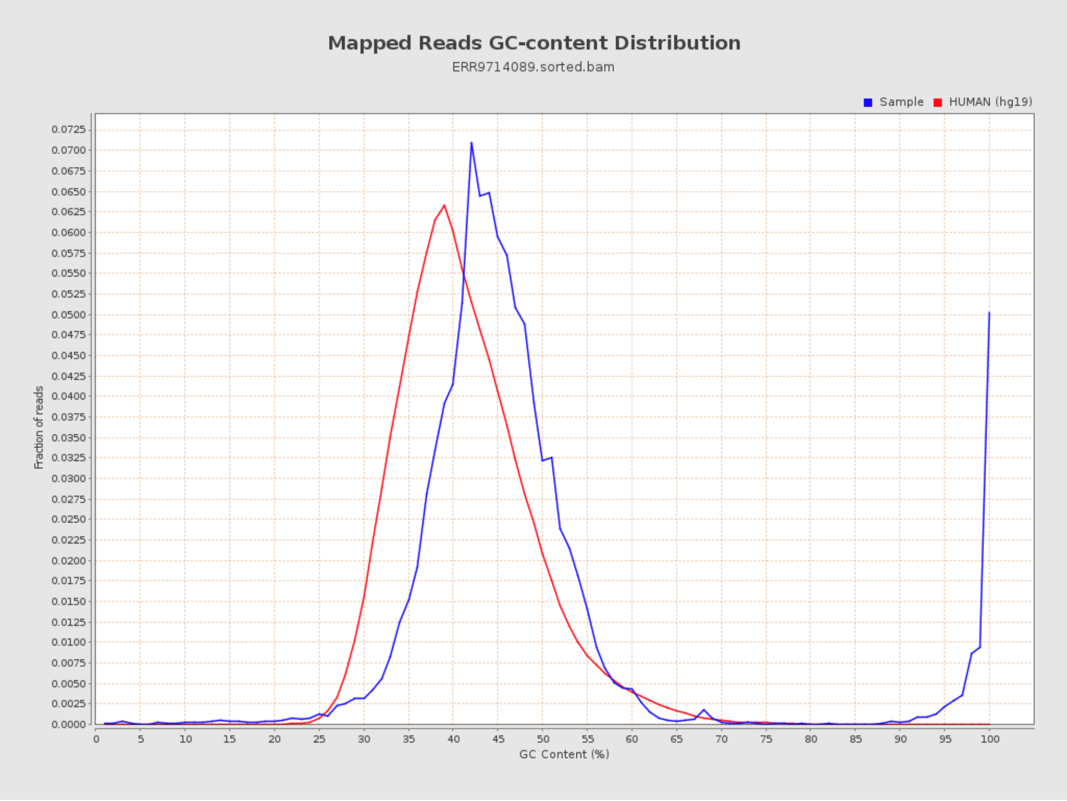
7. Results : Duplication Rate Histogram



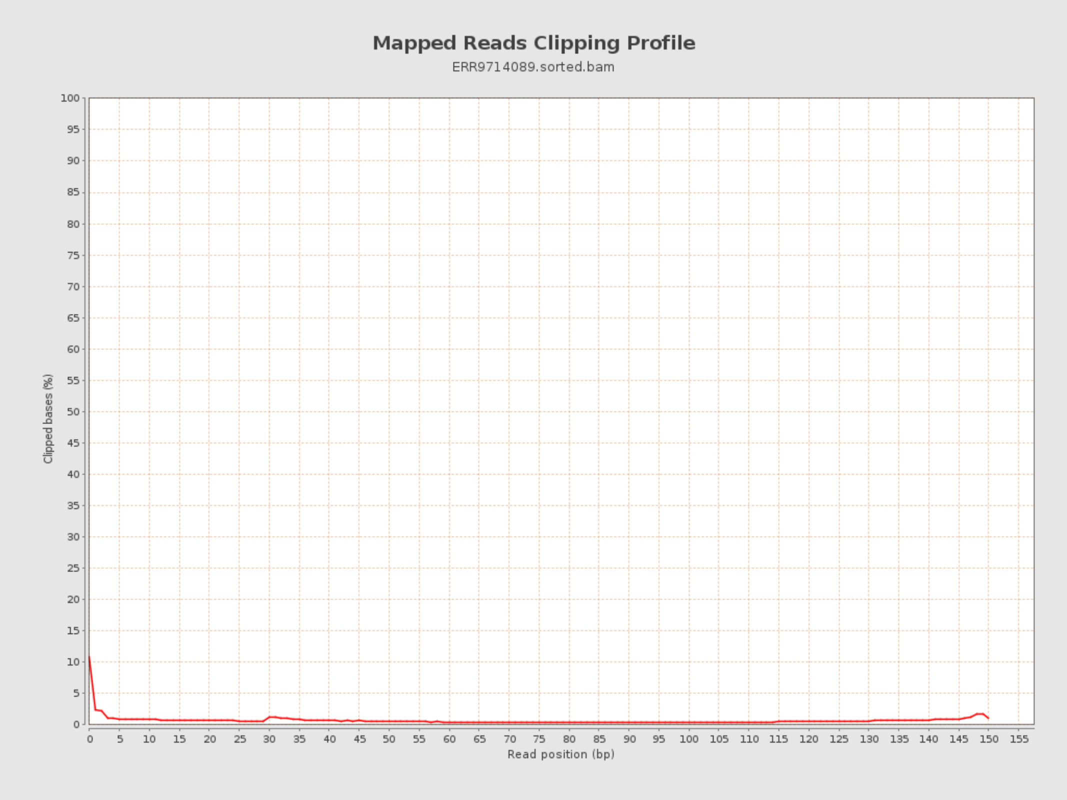
8. Results : Mapped Reads Nucleotide Content



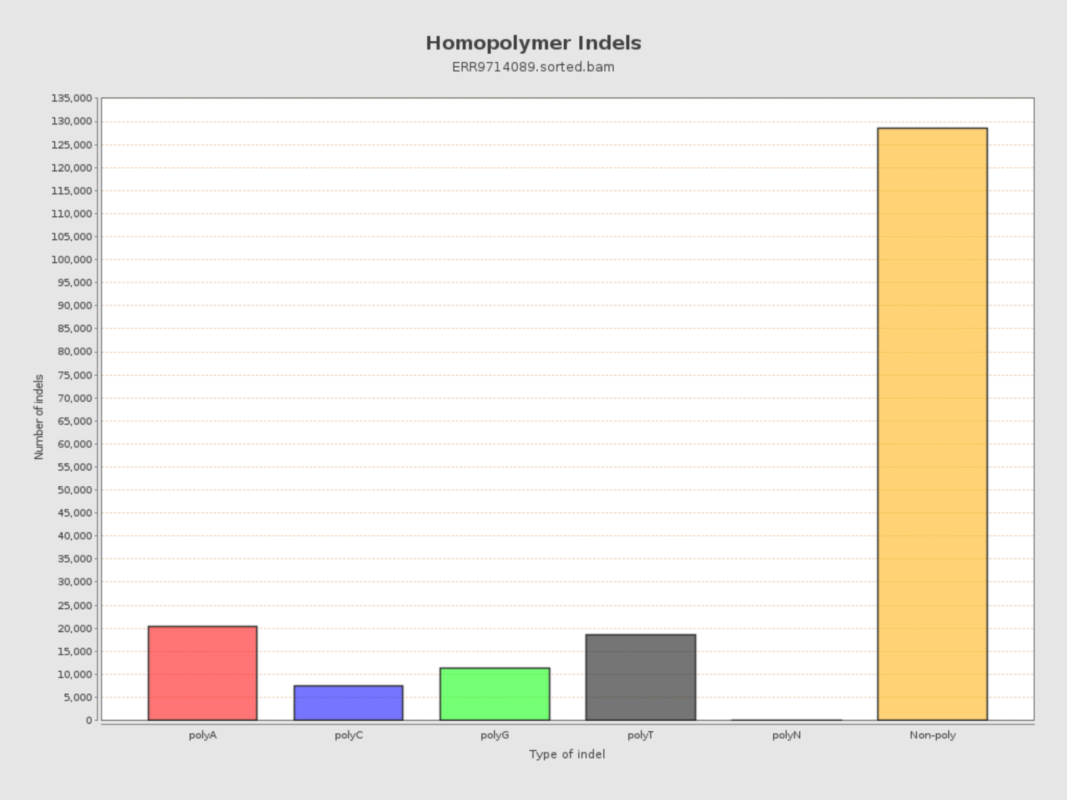
9. Results : Mapped Reads GC-content Distribution



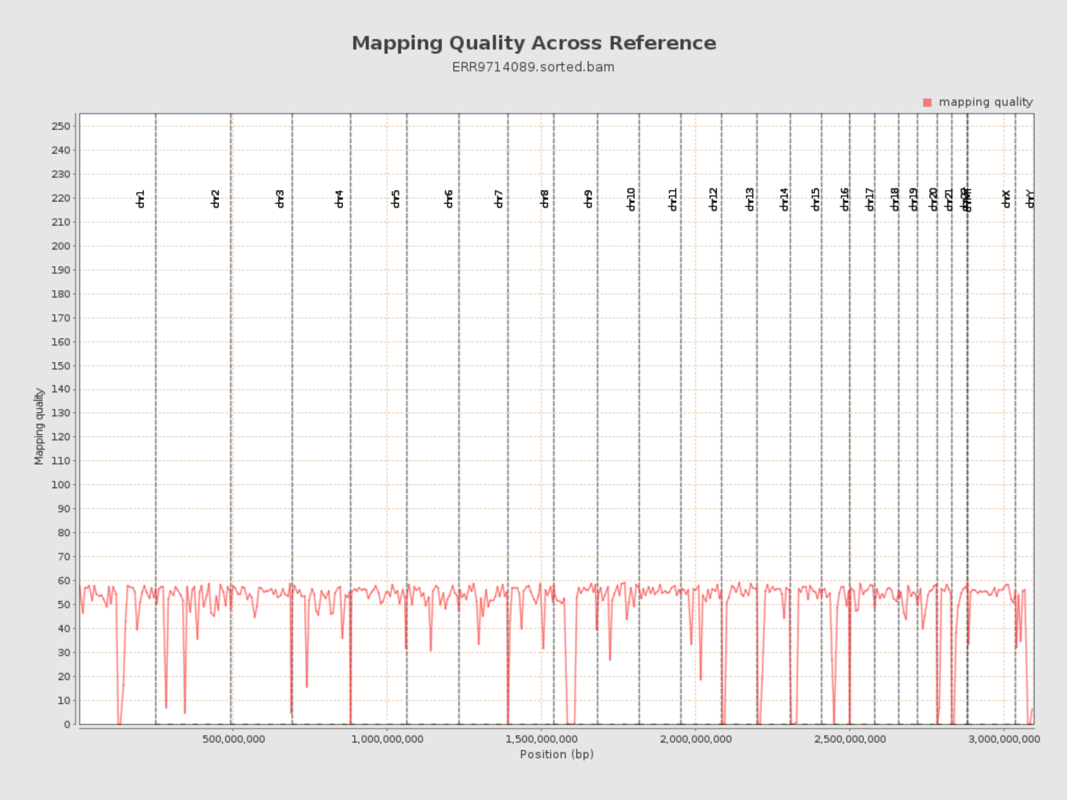
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram