Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 18:40:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714084.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_ERR9714084 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714084.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 18:40:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714084.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	762,832
Mapped reads	41,261 / 5.41%
Unmapped reads	721,571 / 94.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	918 / 0.12%
Read min/max/mean length	30 / 151 / 55.94
Duplicated reads (estimated)	37,757 / 4.95%
Duplication rate	31.64%
Clipped reads	34,085 / 4.47%

2.2. ACGT Content

Number/percentage of A's	342,275 / 10.62%
Number/percentage of C's	197,364 / 6.12%
Number/percentage of T's	266,167 / 8.26%
Number/percentage of G's	2,417,832 / 75%
Number/percentage of N's	58 / 0%
GC Percentage	81.12%

2.3. Coverage

Mean	0.001

Standard Deviation	2.561

2.4. Mapping Quality

Mean Mapping Quality	23.93

2.5. Mismatches and indels

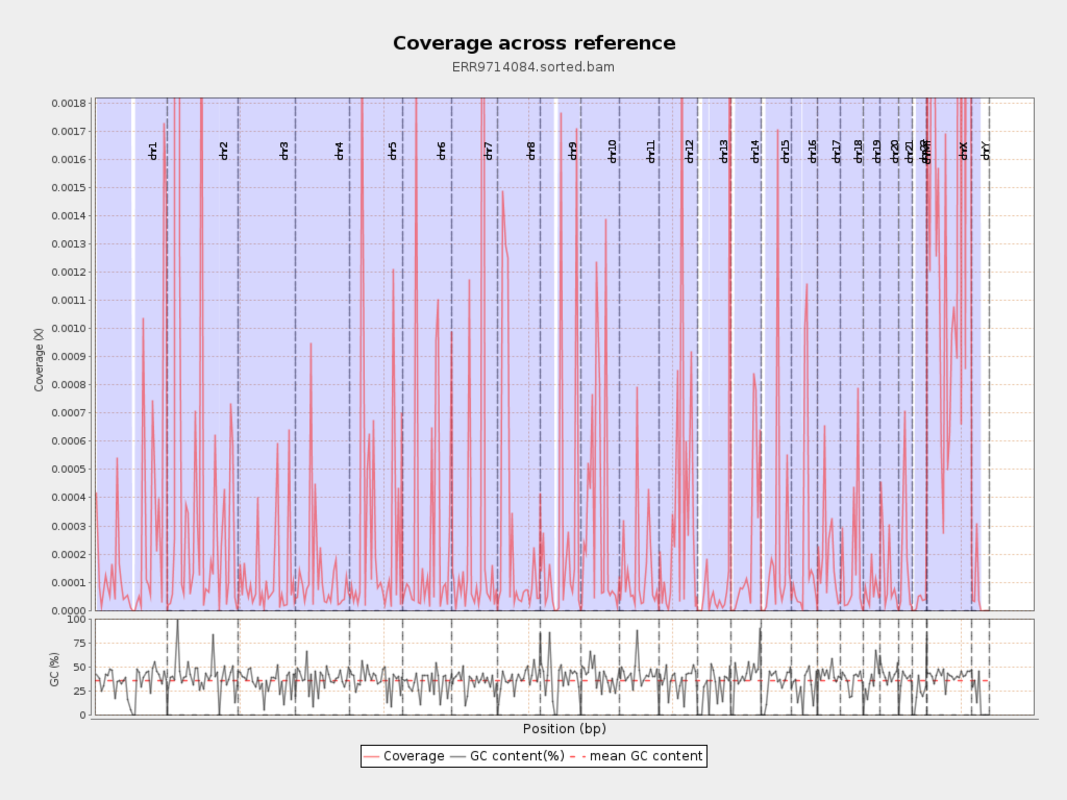
General error rate	3.28%
Mismatches	85,542
Insertions	3,873
Mapped reads with at least one insertion	7.15%
Deletions	4,337
Mapped reads with at least one deletion	10.07%
Homopolymer indels	43.58%

2.6. Chromosome stats

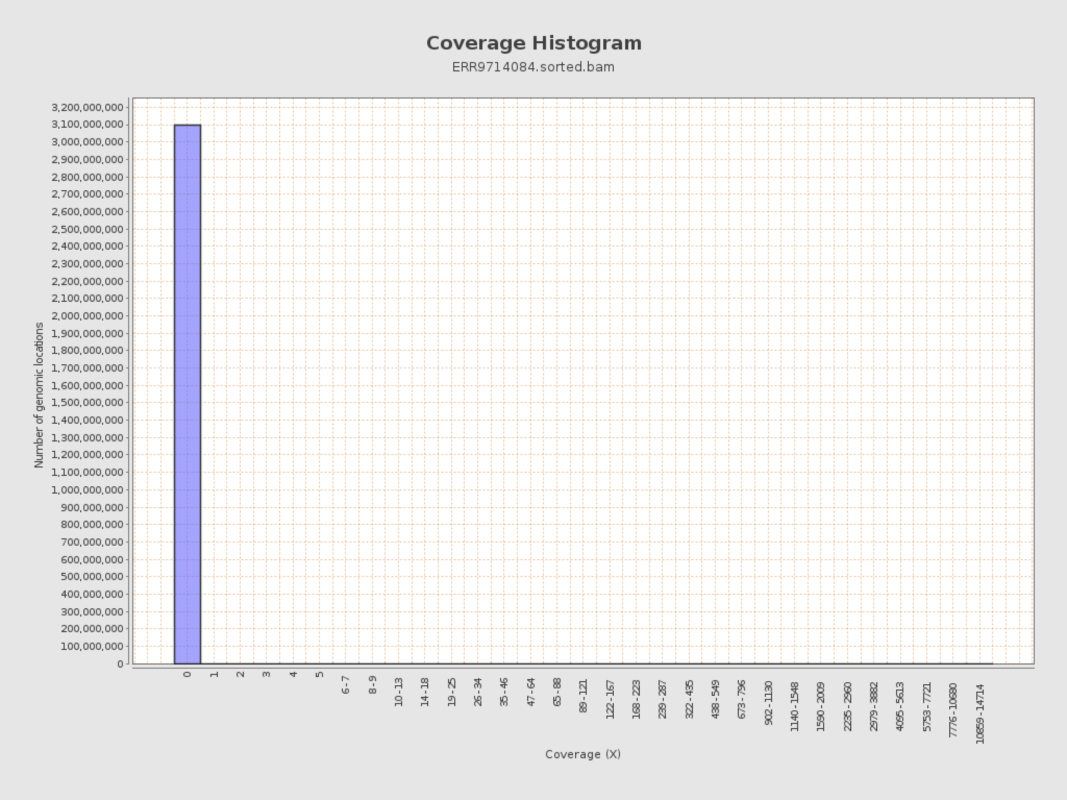
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	65591	0.0003	0.0944
chr2	243199373	2316487	0.0095	9.1241
chr3	198022430	25349	0.0001	0.0448
chr4	191154276	23969	0.0001	0.0455
chr5	180915260	53359	0.0003	0.1193
chr6	171115067	49176	0.0003	0.1113
chr7	159138663	54437	0.0003	0.3416

chr8	146364022	41200	0.0003	0.1025
chr9	141213431	38859	0.0003	0.1269
chr10	135534747	47481	0.0004	0.1109
chr11	135006516	20612	0.0002	0.0801
chr12	133851895	48309	0.0004	0.1474
chr13	115169878	13726	0.0001	0.0666
chr14	107349540	24148	0.0002	0.1121
chr15	102531392	24377	0.0002	0.097
chr16	90354753	21755	0.0002	0.0925
chr17	81195210	15871	0.0002	0.0972
chr18	78077248	14652	0.0002	0.0605
chr19	59128983	4371	0.0001	0.0222
chr20	63025520	8987	0.0001	0.0358
chr21	48129895	10161	0.0002	0.0646
chr22	51304566	2347	0	0.0119
chrMT	16571	9895	0.5971	5.5302
chrX	155270560	311346	0.002	0.3318
chrY	59373566	3115	0.0001	0.0267

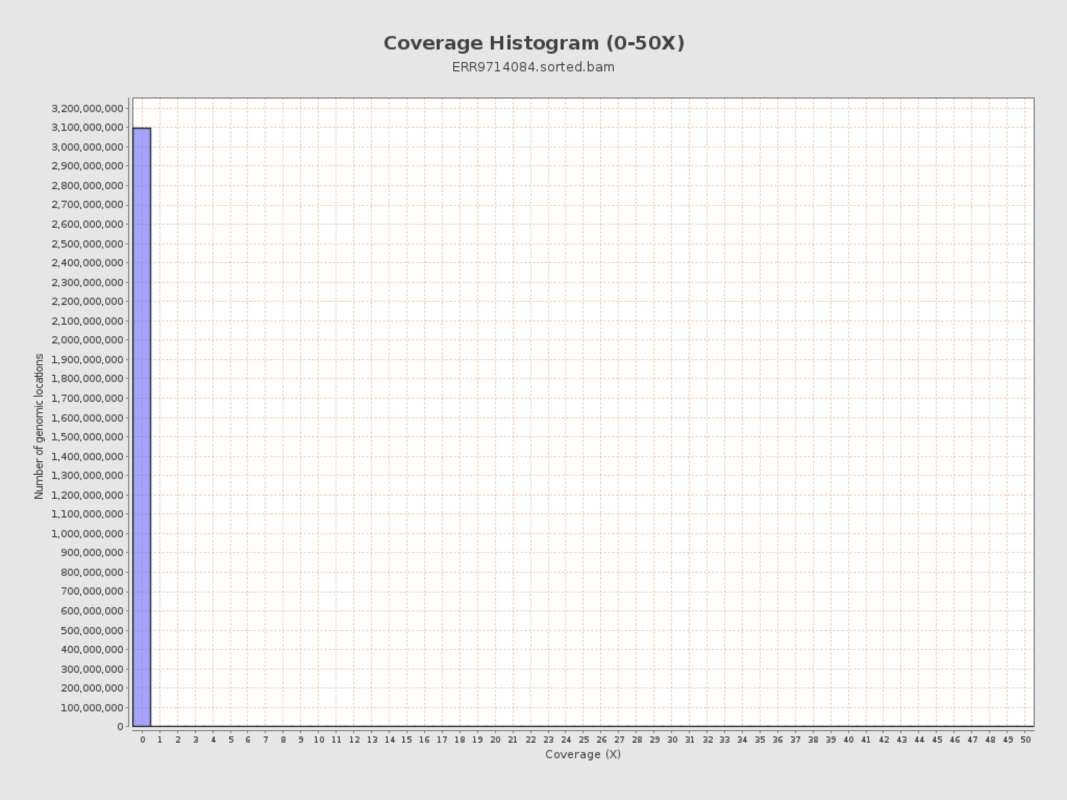
3. Results : Coverage across reference



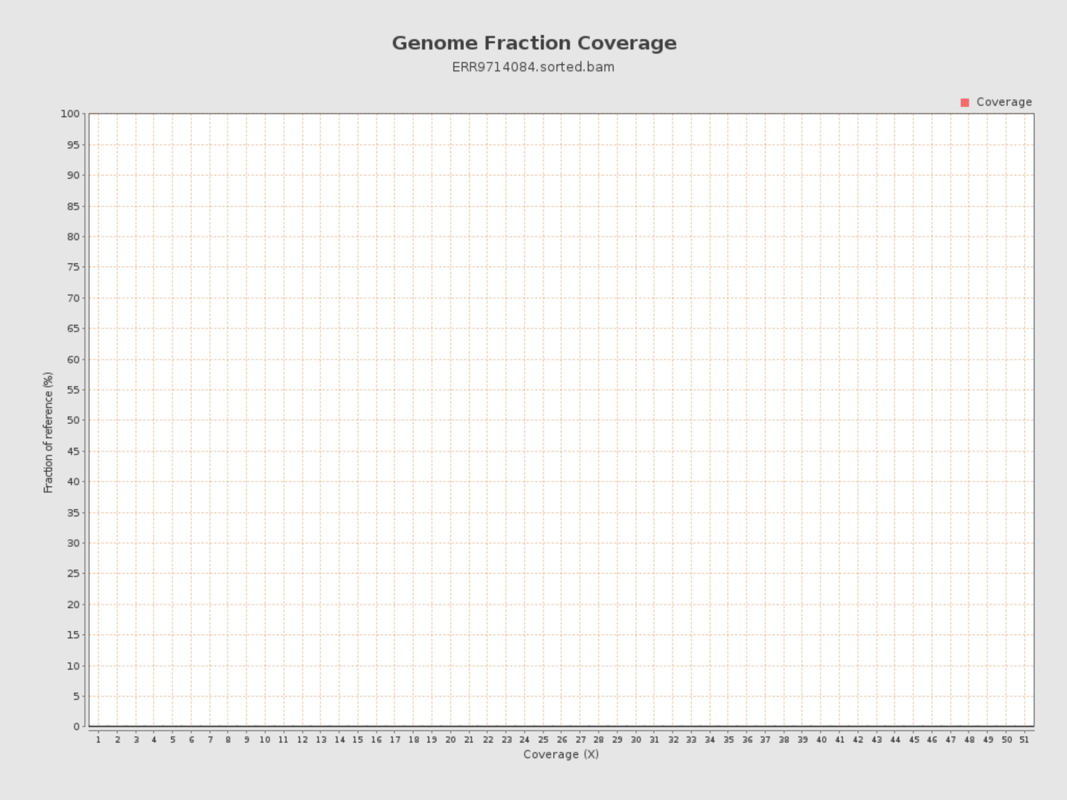
4. Results : Coverage Histogram



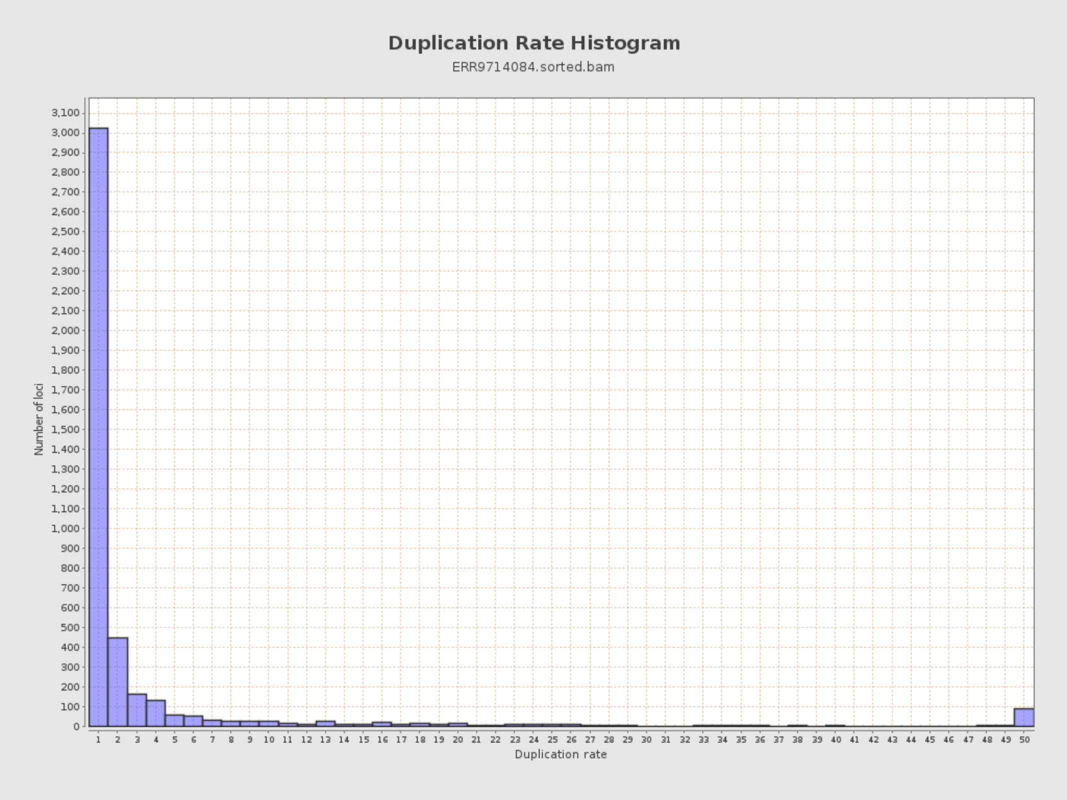
5. Results : Coverage Histogram (0-50X)



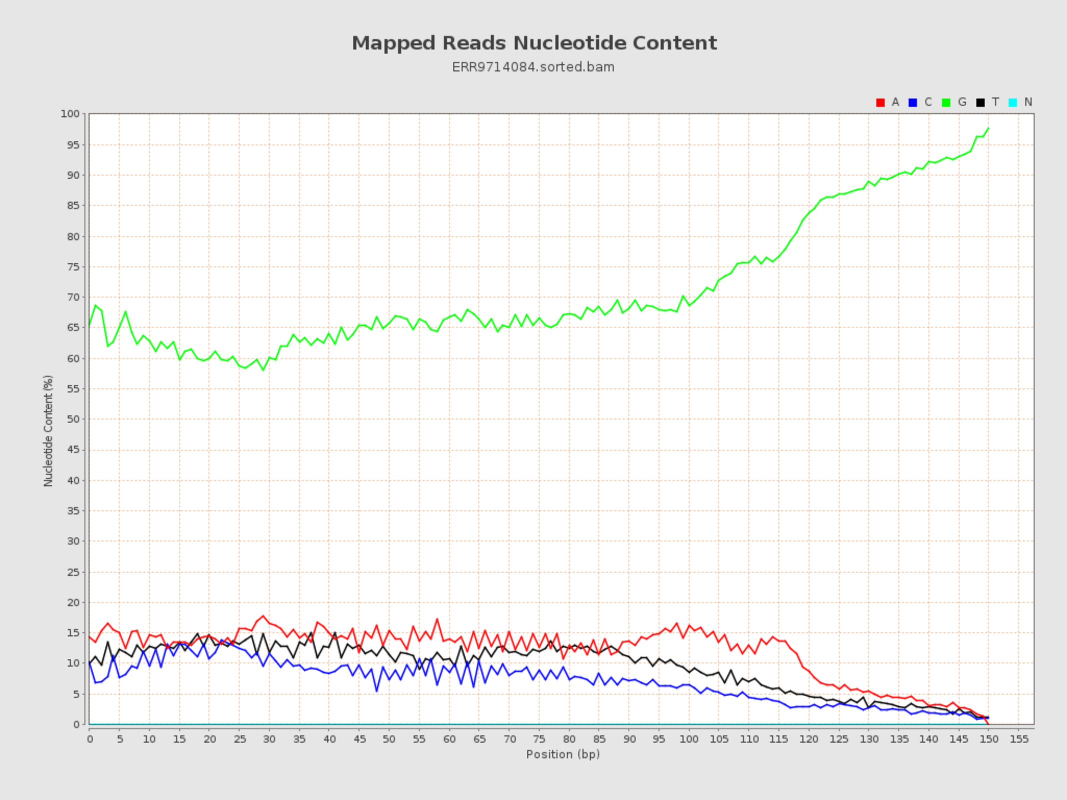
6. Results : Genome Fraction Coverage



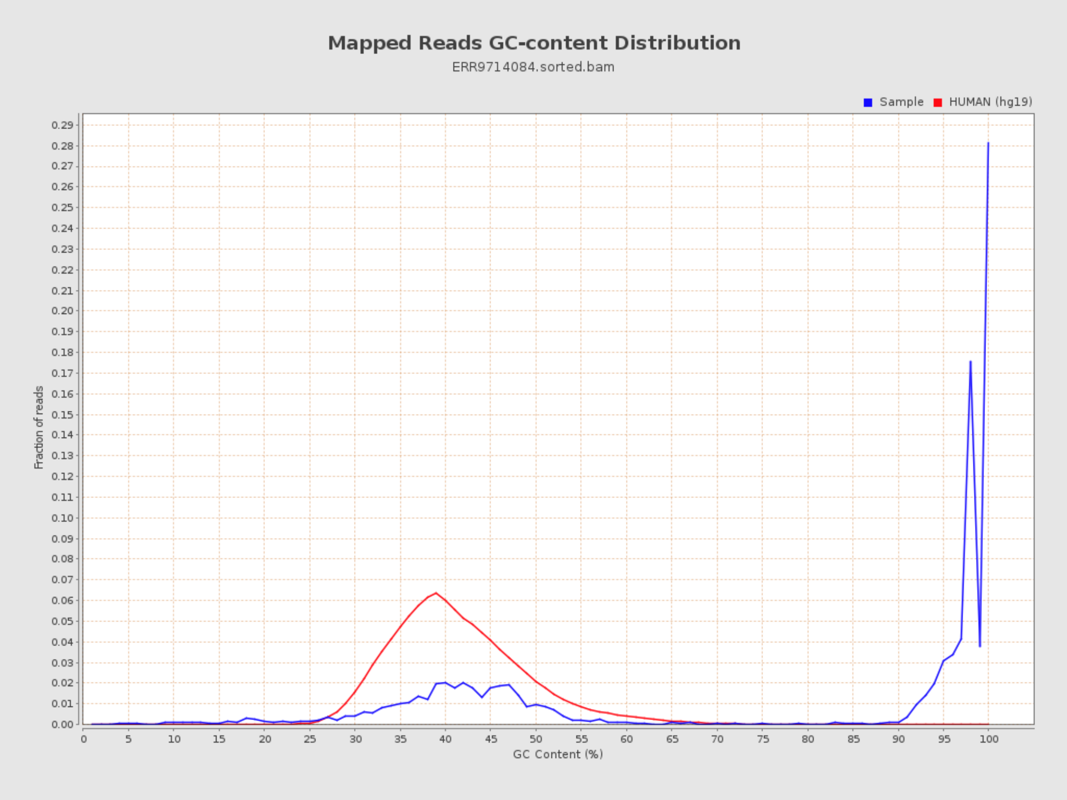
7. Results : Duplication Rate Histogram



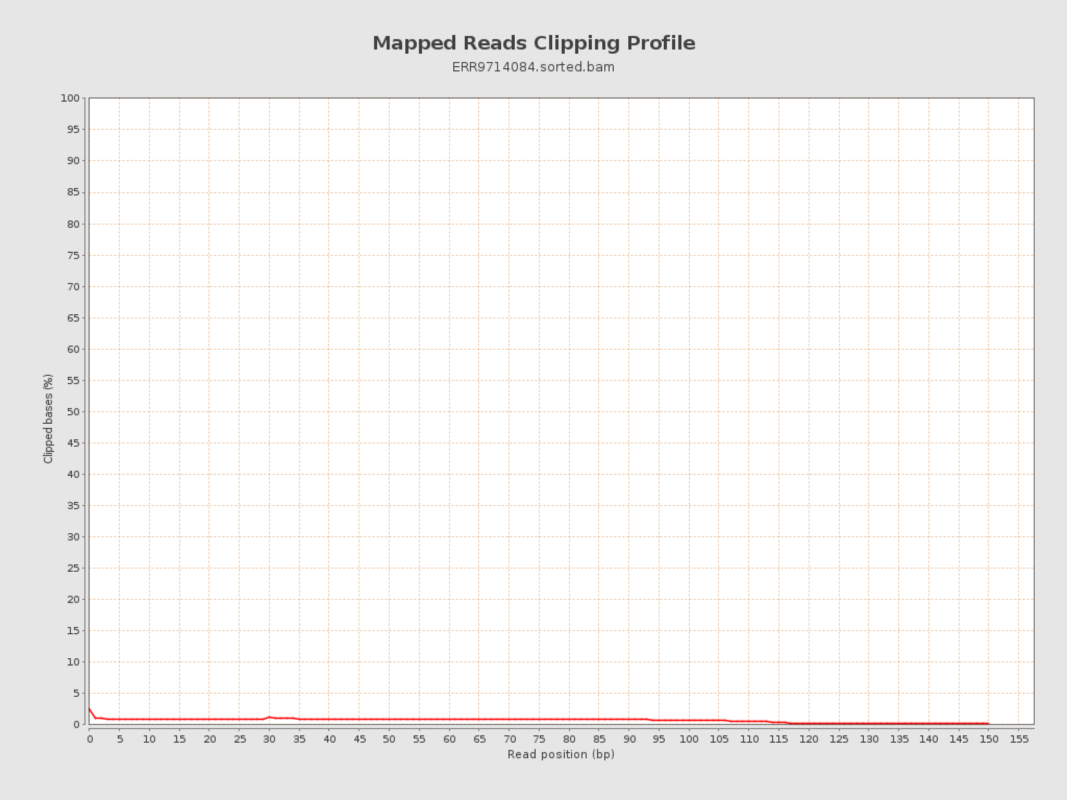
8. Results : Mapped Reads Nucleotide Content



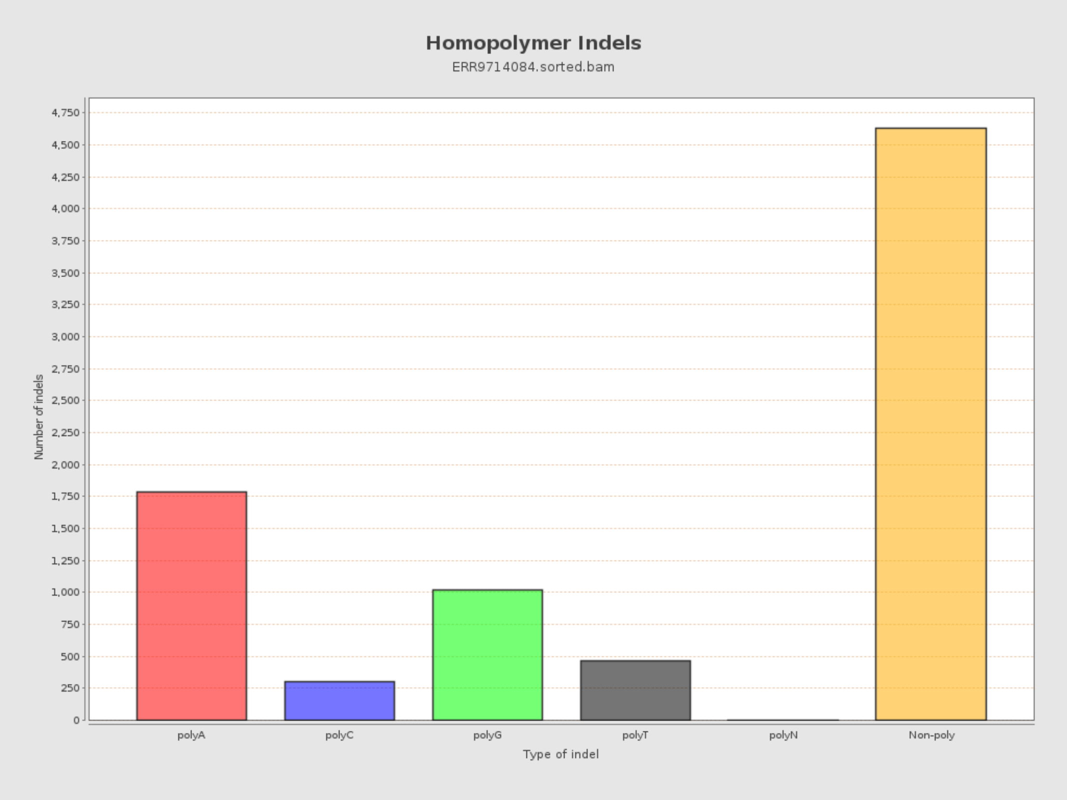
9. Results : Mapped Reads GC-content Distribution



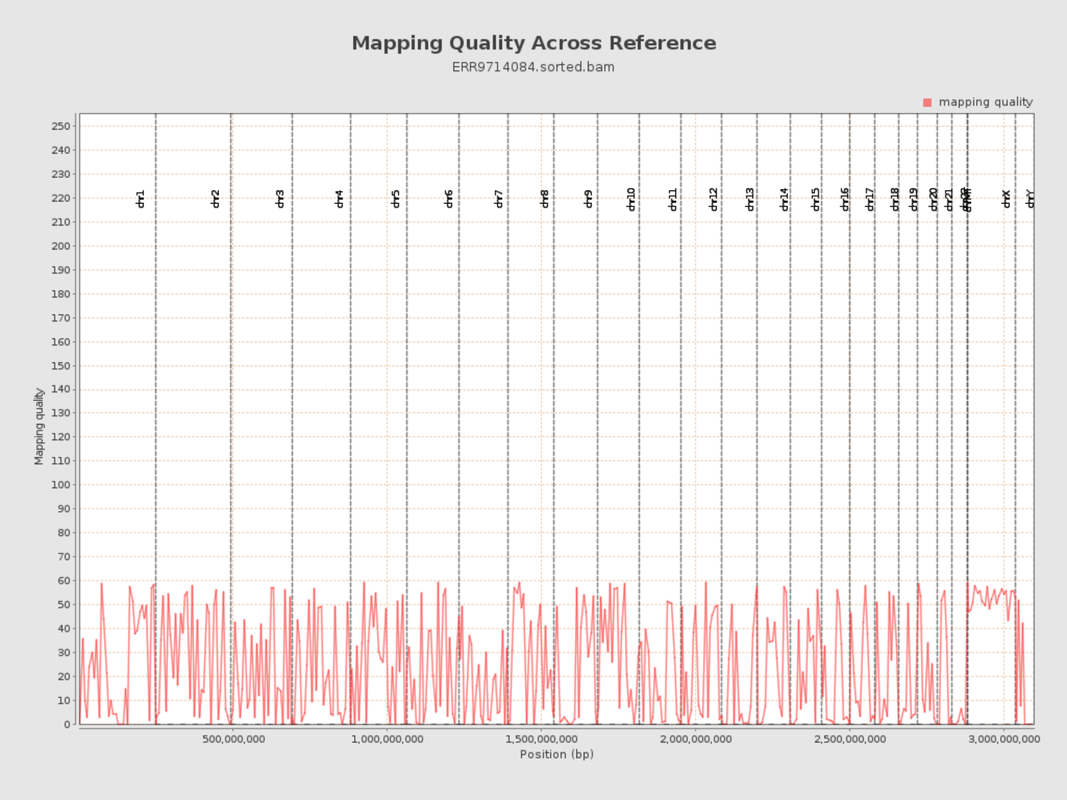
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram