Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 17:42:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714058.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_ERR9714058 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714058.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 17:42:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714058.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	513,986
Mapped reads	95,685 / 18.62%
Unmapped reads	418,301 / 81.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,083 / 0.6%
Read min/max/mean length	30 / 151 / 65.34
Duplicated reads (estimated)	91,487 / 17.8%
Duplication rate	23.18%
Clipped reads	56,170 / 10.93%

2.2. ACGT Content

Number/percentage of A's	446,285 / 4.65%
Number/percentage of C's	205,384 / 2.14%
Number/percentage of T's	264,047 / 2.75%
Number/percentage of G's	8,688,145 / 90.46%
Number/percentage of N's	296 / 0%
GC Percentage	92.6%

2.3. Coverage

Mean	0.0031

Standard Deviation	11

2.4. Mapping Quality

Mean Mapping Quality	23.88

2.5. Mismatches and indels

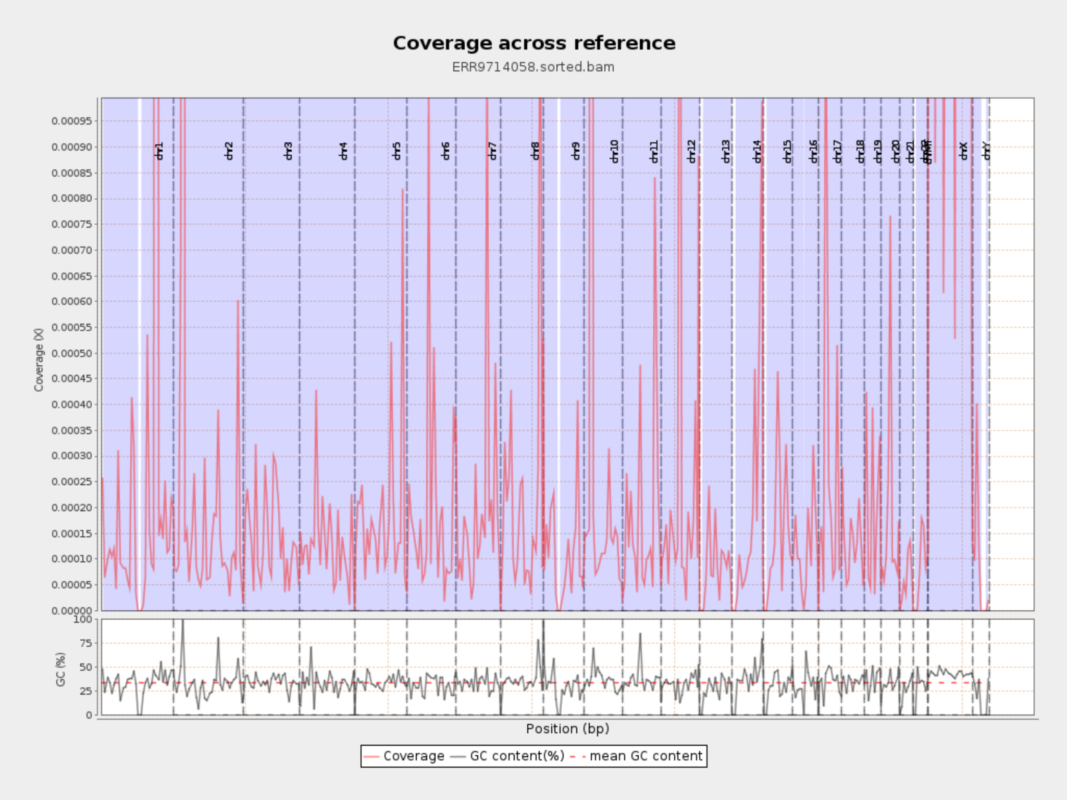
General error rate	3.27%
Mismatches	239,505
Insertions	10,476
Mapped reads with at least one insertion	7.07%
Deletions	5,938
Mapped reads with at least one deletion	5.97%
Homopolymer indels	62.93%

2.6. Chromosome stats

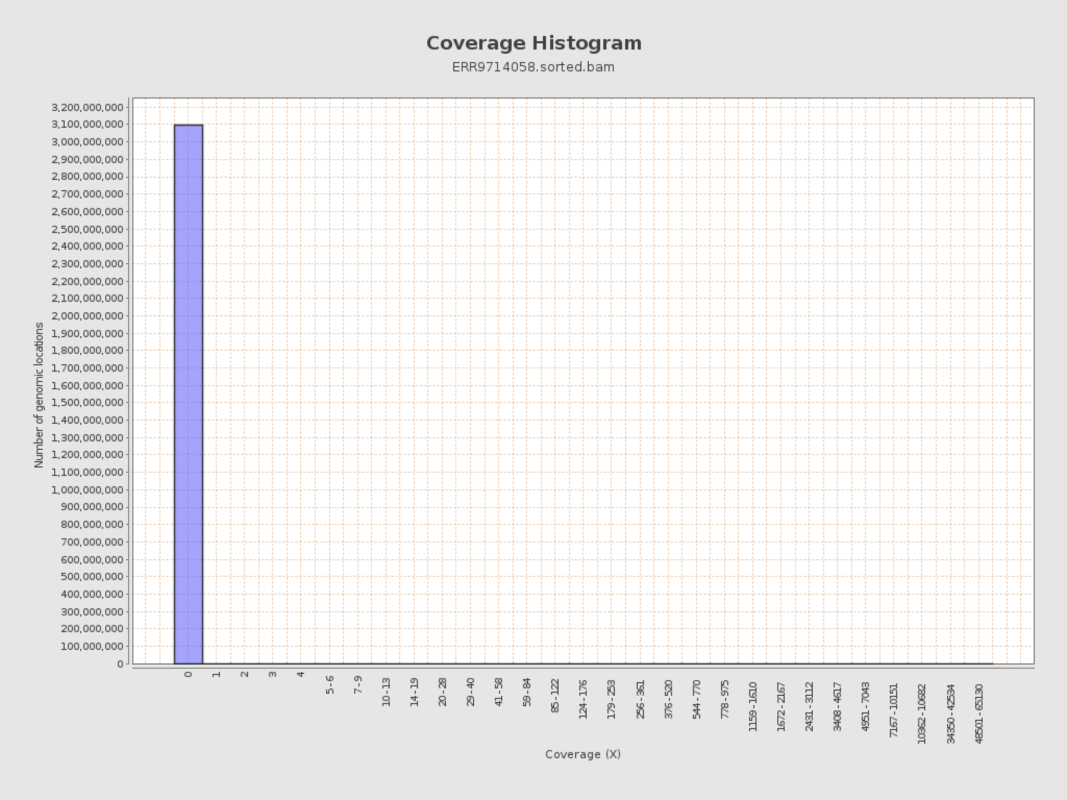
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	93681	0.0004	0.6862
chr2	243199373	8601573	0.0354	39.2316
chr3	198022430	28039	0.0001	0.0302
chr4	191154276	25074	0.0001	0.026
chr5	180915260	34149	0.0002	0.038
chr6	171115067	33253	0.0002	0.0584
chr7	159138663	32034	0.0002	0.1002

chr8	146364022	33822	0.0002	0.0599
chr9	141213431	15615	0.0001	0.0231
chr10	135534747	78802	0.0006	0.9393
chr11	135006516	24181	0.0002	0.053
chr12	133851895	34355	0.0003	0.1373
chr13	115169878	9485	0.0001	0.0122
chr14	107349540	23317	0.0002	0.0956
chr15	102531392	15157	0.0001	0.0395
chr16	90354753	11329	0.0001	0.0225
chr17	81195210	21565	0.0003	0.1692
chr18	78077248	10402	0.0001	0.0165
chr19	59128983	11767	0.0002	0.0401
chr20	63025520	12235	0.0002	0.0459
chr21	48129895	3058	0.0001	0.0103
chr22	51304566	4096	0.0001	0.0133
chrMT	16571	23255	1.4034	6.0939
chrX	155270560	449232	0.0029	0.3601
chrY	59373566	5621	0.0001	0.0248

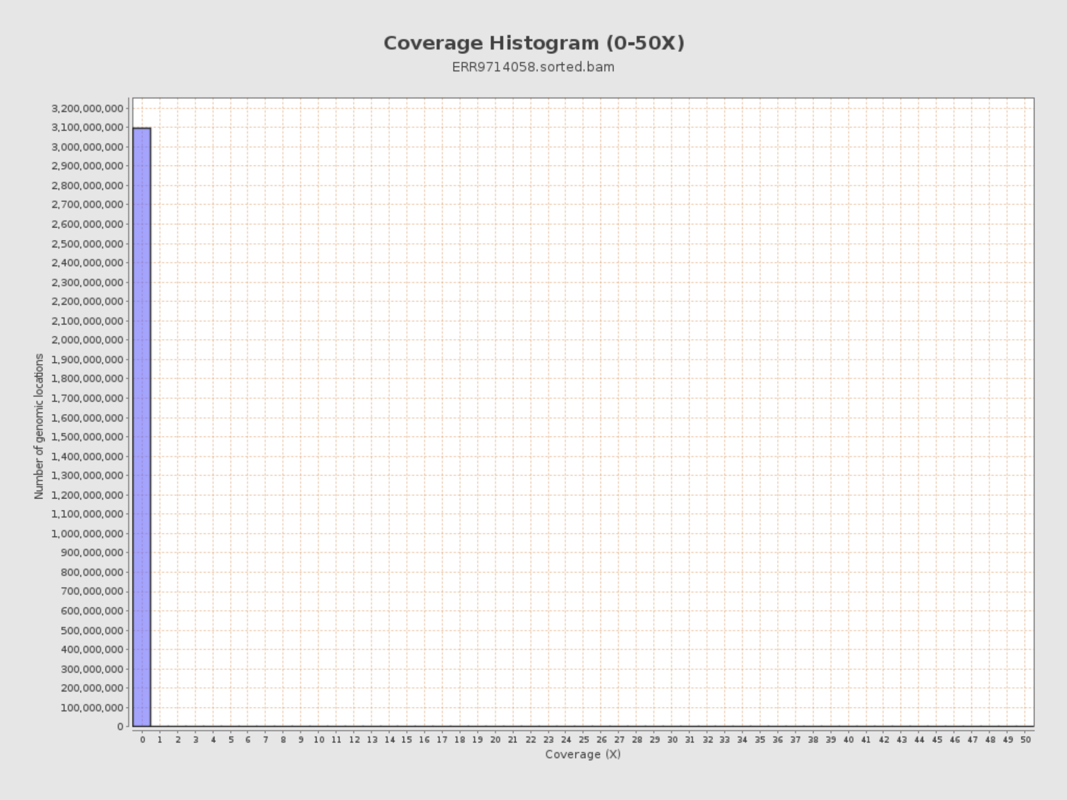
3. Results : Coverage across reference



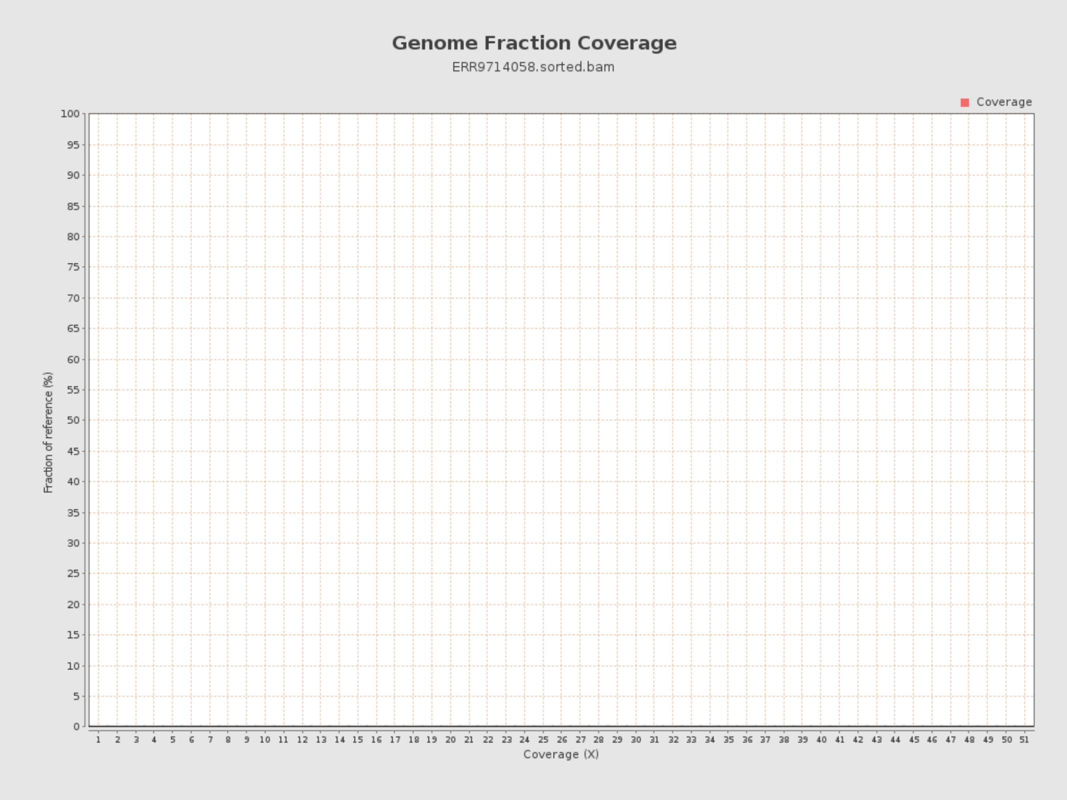
4. Results : Coverage Histogram



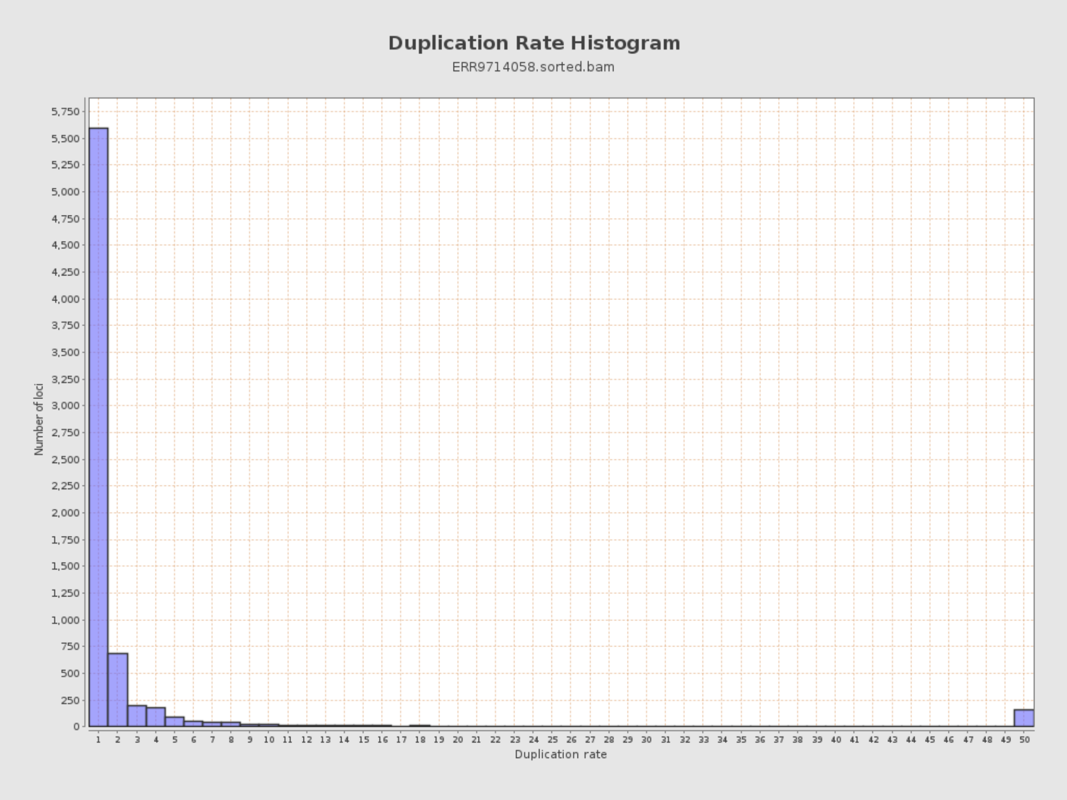
5. Results : Coverage Histogram (0-50X)



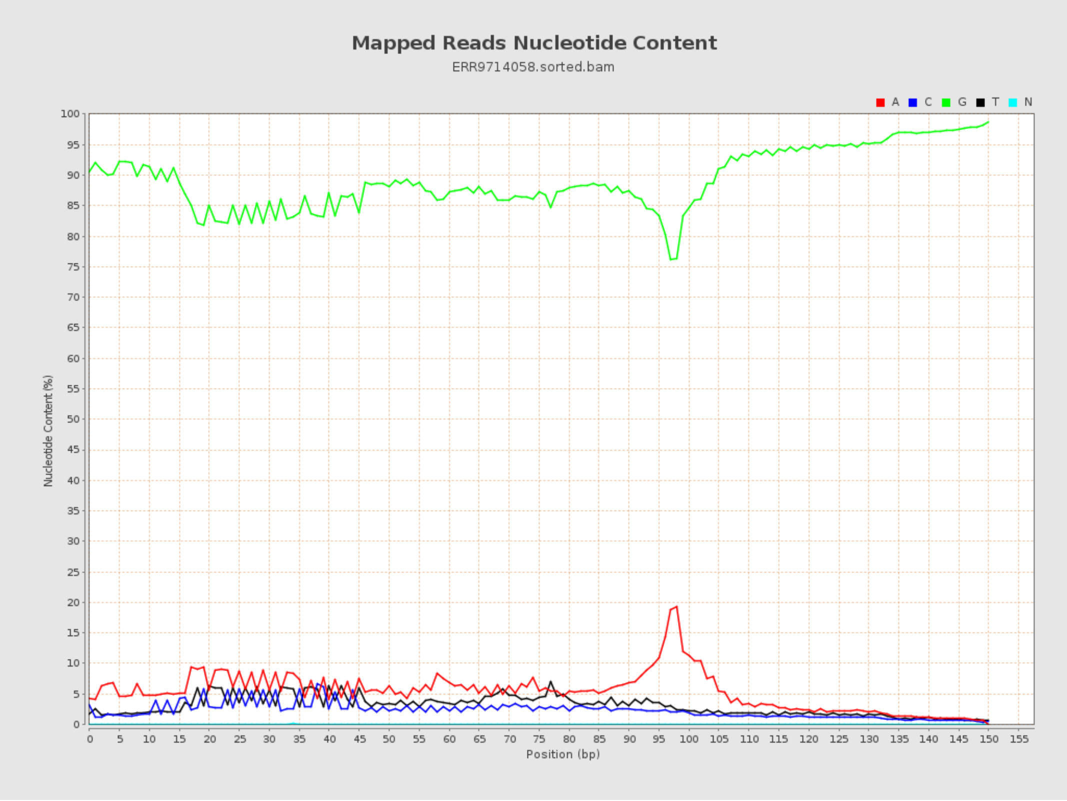
6. Results : Genome Fraction Coverage



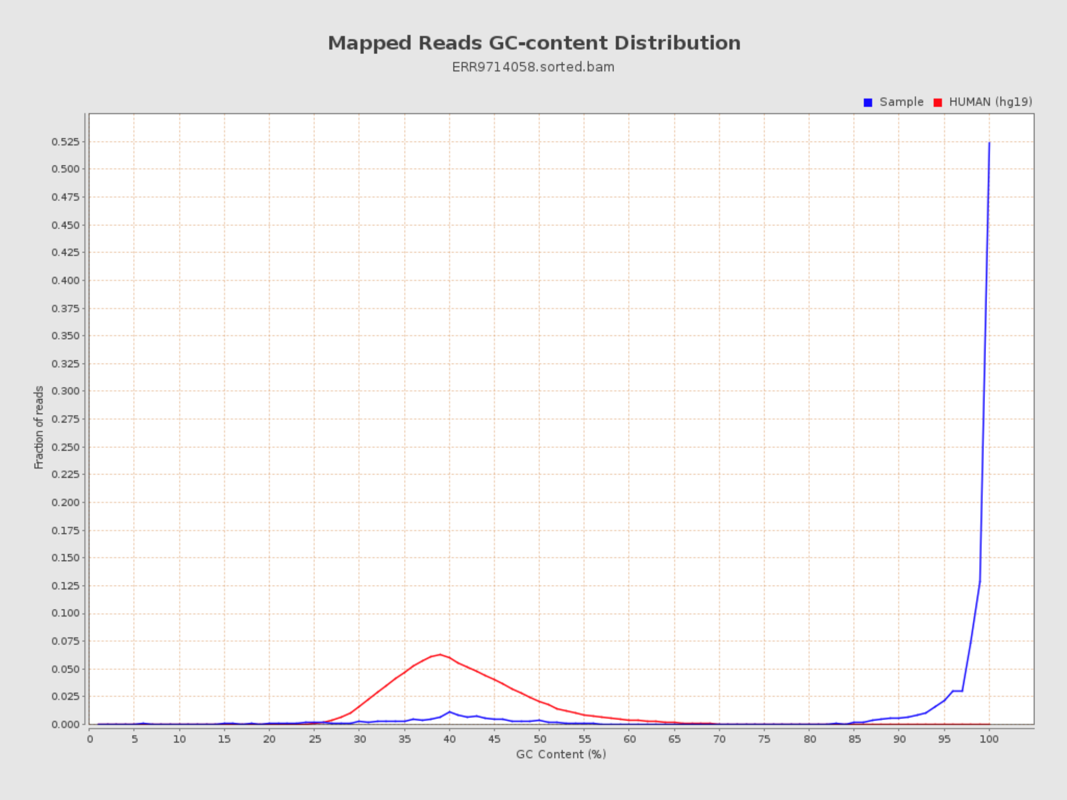
7. Results : Duplication Rate Histogram



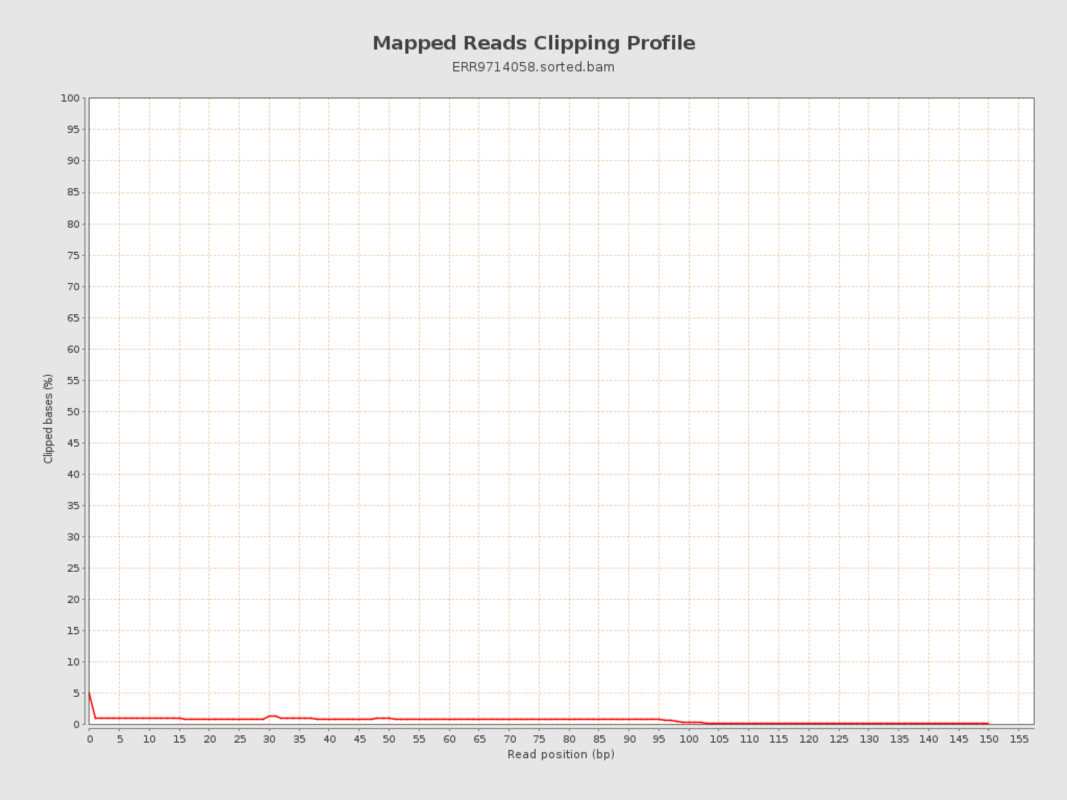
8. Results : Mapped Reads Nucleotide Content



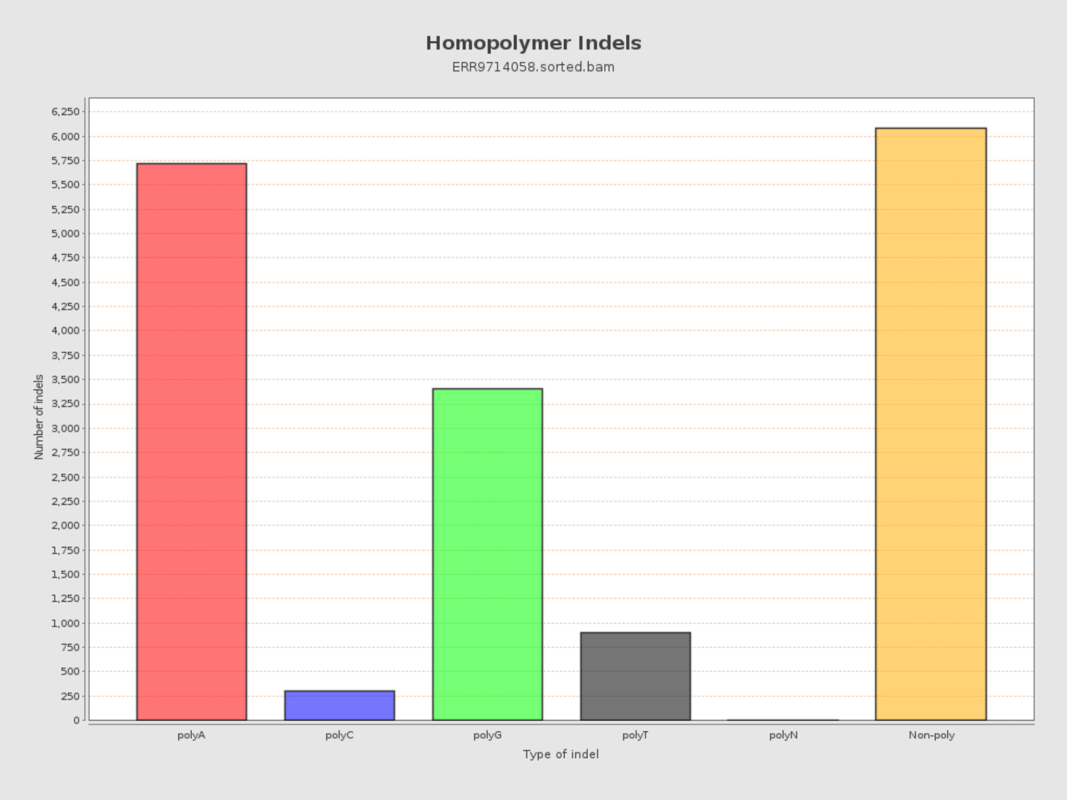
9. Results : Mapped Reads GC-content Distribution



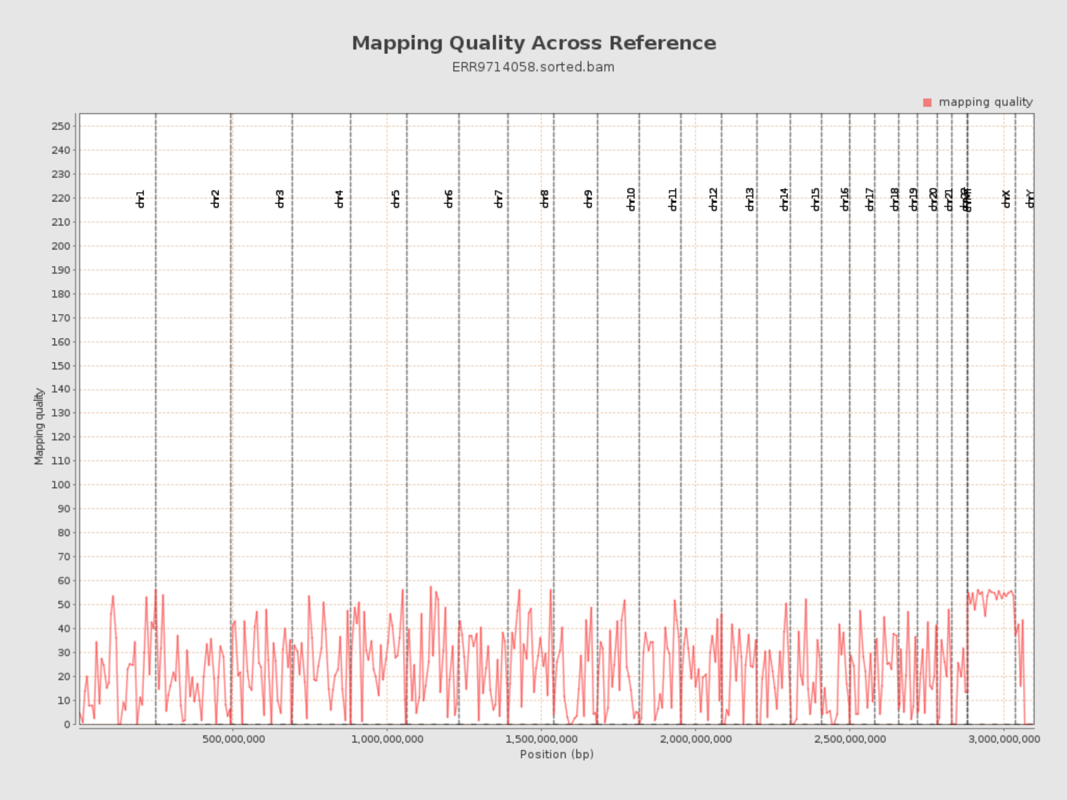
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram