Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 20:39:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714128.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_ERR9714128 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714128.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 20:39:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714128.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,199,008
Mapped reads	76,256 / 6.36%
Unmapped reads	1,122,752 / 93.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,916 / 0.16%
Read min/max/mean length	30 / 151 / 54.17
Duplicated reads (estimated)	70,874 / 5.91%
Duplication rate	33.19%
Clipped reads	60,794 / 5.07%

2.2. ACGT Content

Number/percentage of A's	748,235 / 11.48%
Number/percentage of C's	471,492 / 7.23%
Number/percentage of T's	623,113 / 9.56%
Number/percentage of G's	4,676,468 / 71.73%
Number/percentage of N's	196 / 0%
GC Percentage	78.96%

2.3. Coverage

Mean	0.0021

Standard Deviation	4.9189

2.4. Mapping Quality

Mean Mapping Quality	29.4

2.5. Mismatches and indels

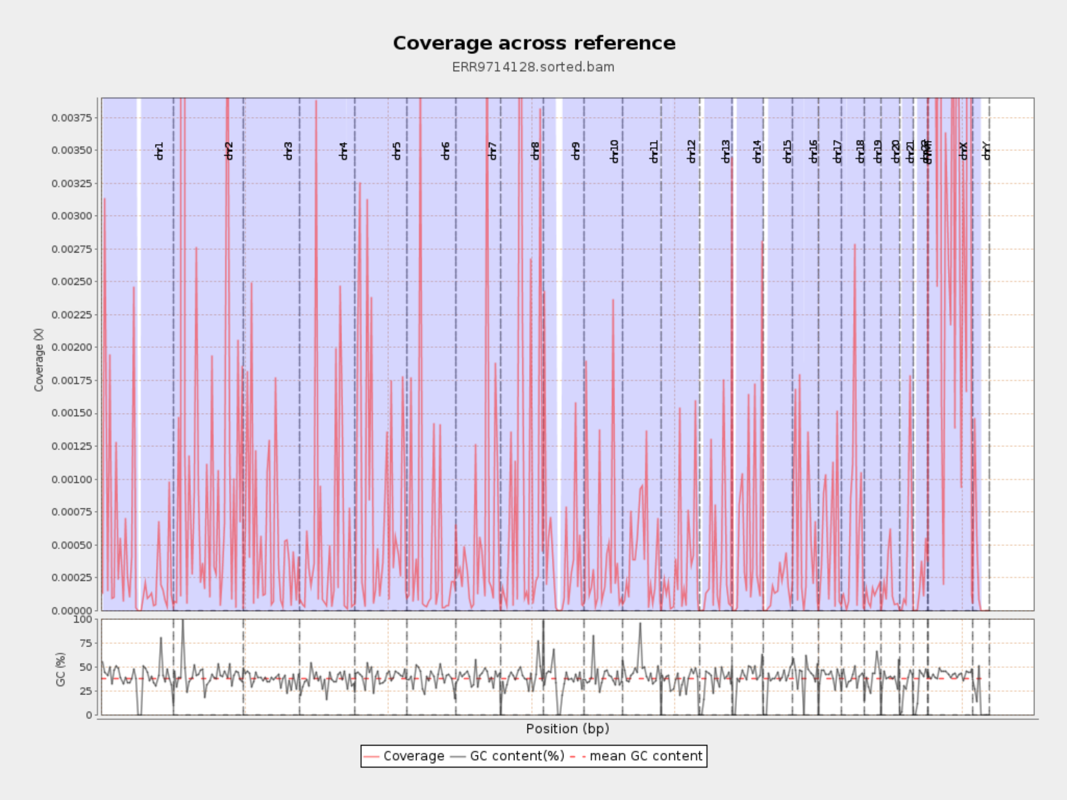
General error rate	3.36%
Mismatches	181,664
Insertions	7,026
Mapped reads with at least one insertion	7.08%
Deletions	9,096
Mapped reads with at least one deletion	11.49%
Homopolymer indels	39.22%

2.6. Chromosome stats

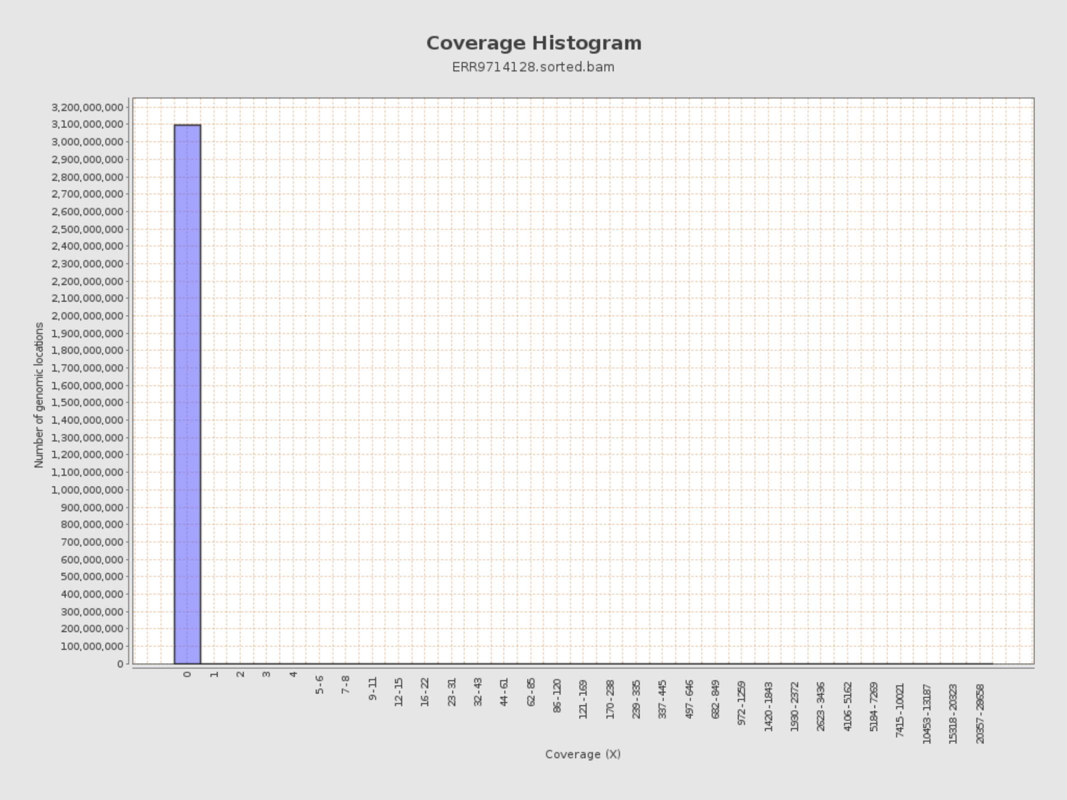
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	113155	0.0005	0.1646
chr2	243199373	4444293	0.0183	17.5286
chr3	198022430	113063	0.0006	0.1869
chr4	191154276	111584	0.0006	0.1918
chr5	180915260	169264	0.0009	0.2295
chr6	171115067	82624	0.0005	0.178
chr7	159138663	100697	0.0006	0.4983

chr8	146364022	151610	0.001	0.3289
chr9	141213431	63892	0.0005	0.146
chr10	135534747	65284	0.0005	0.1696
chr11	135006516	56661	0.0004	0.1261
chr12	133851895	48359	0.0004	0.1108
chr13	115169878	45479	0.0004	0.1237
chr14	107349540	71920	0.0007	0.21
chr15	102531392	17062	0.0002	0.0395
chr16	90354753	56690	0.0006	0.1502
chr17	81195210	45105	0.0006	0.1878
chr18	78077248	52247	0.0007	0.1616
chr19	59128983	7101	0.0001	0.0264
chr20	63025520	12562	0.0002	0.0473
chr21	48129895	23236	0.0005	0.1064
chr22	51304566	10088	0.0002	0.0489
chrMT	16571	14272	0.8613	7.8744
chrX	155270560	690703	0.0044	0.6222
chrY	59373566	16479	0.0003	0.1263

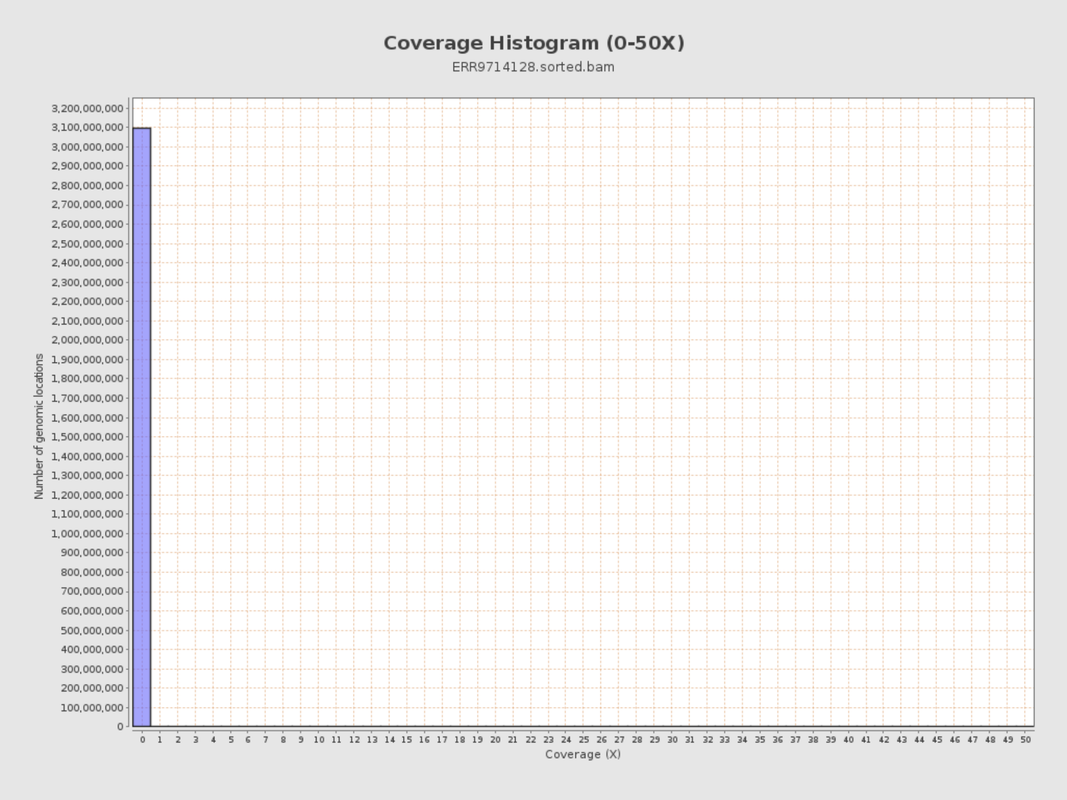
3. Results : Coverage across reference



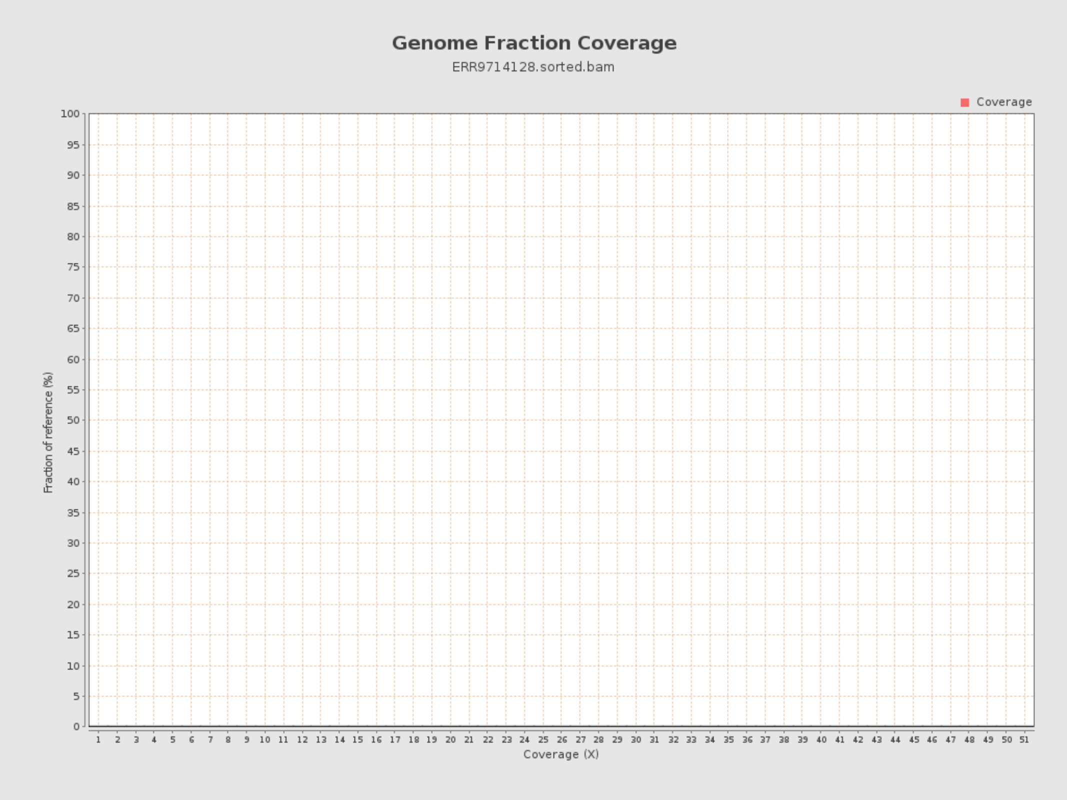
4. Results : Coverage Histogram



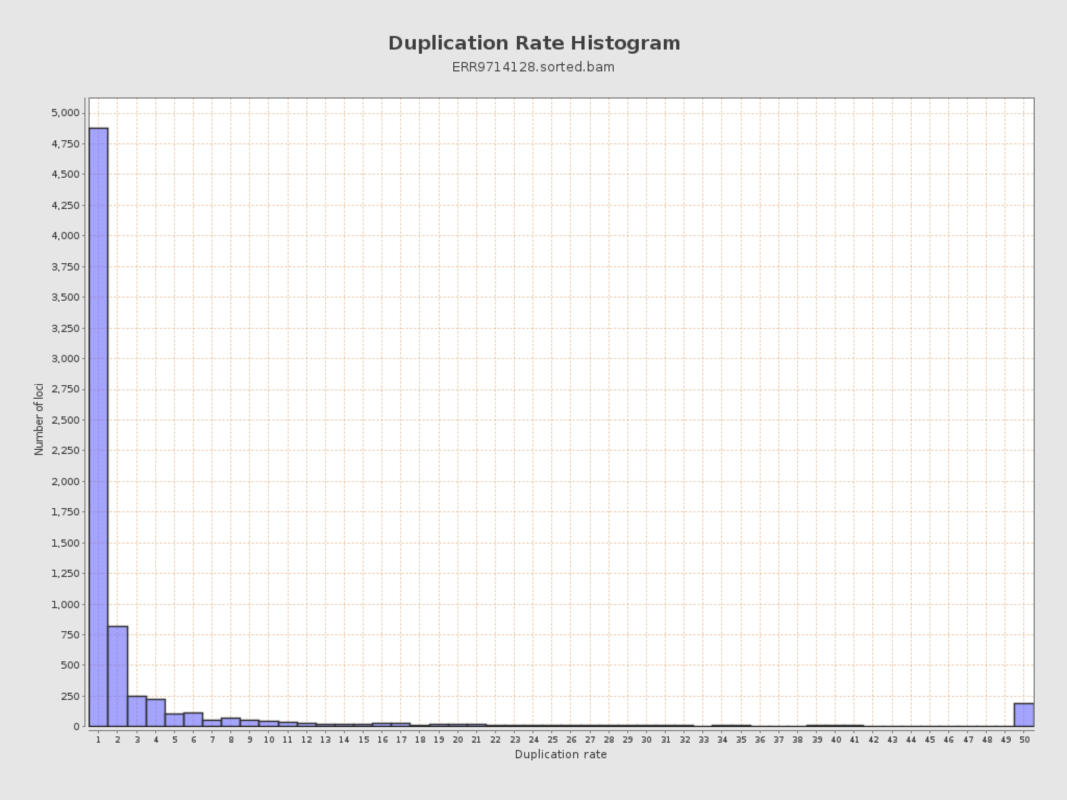
5. Results : Coverage Histogram (0-50X)



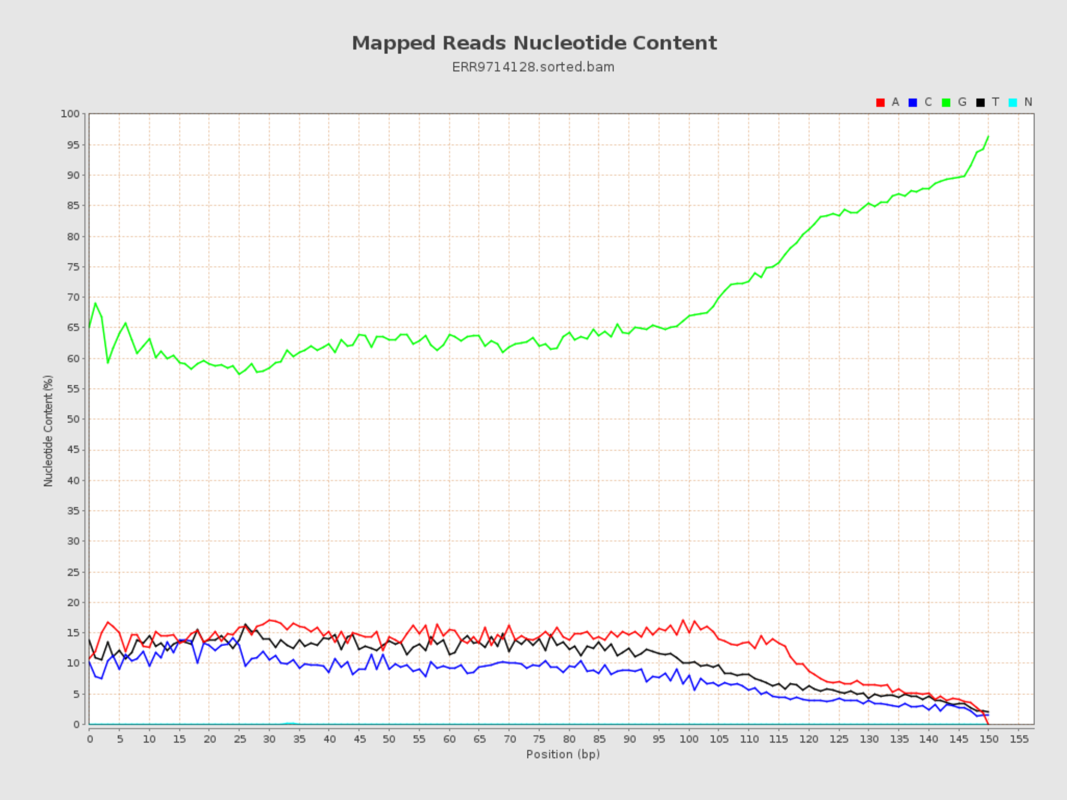
6. Results : Genome Fraction Coverage



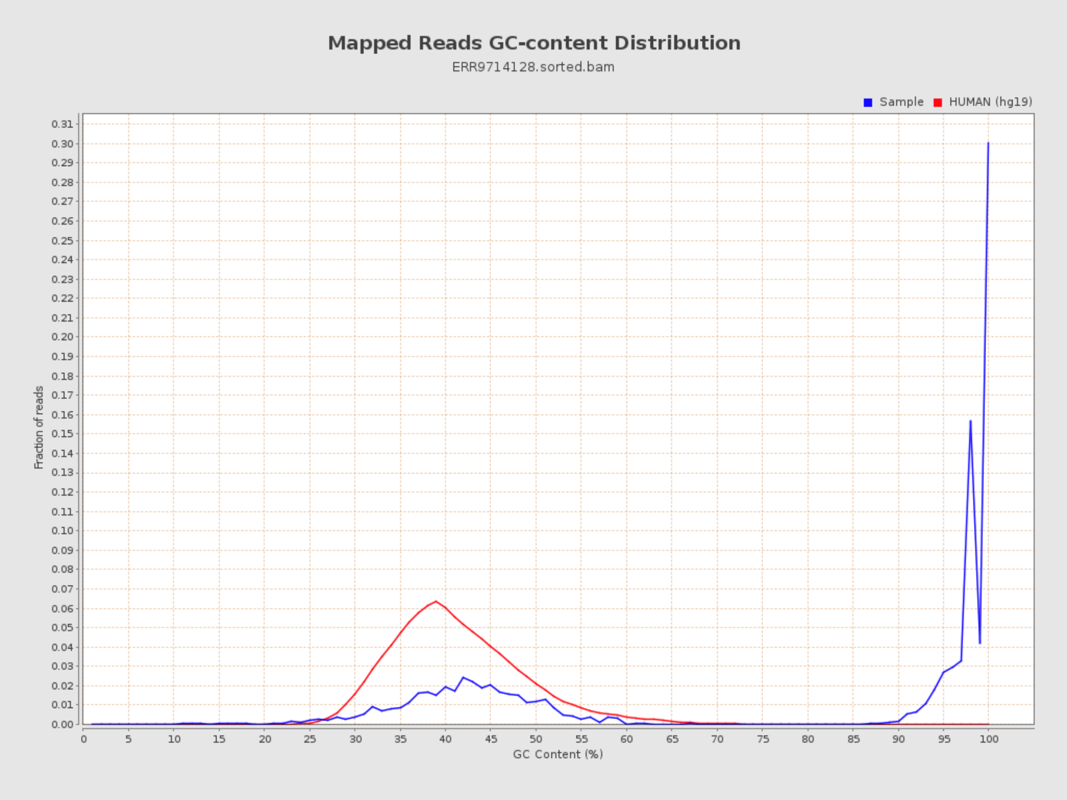
7. Results : Duplication Rate Histogram



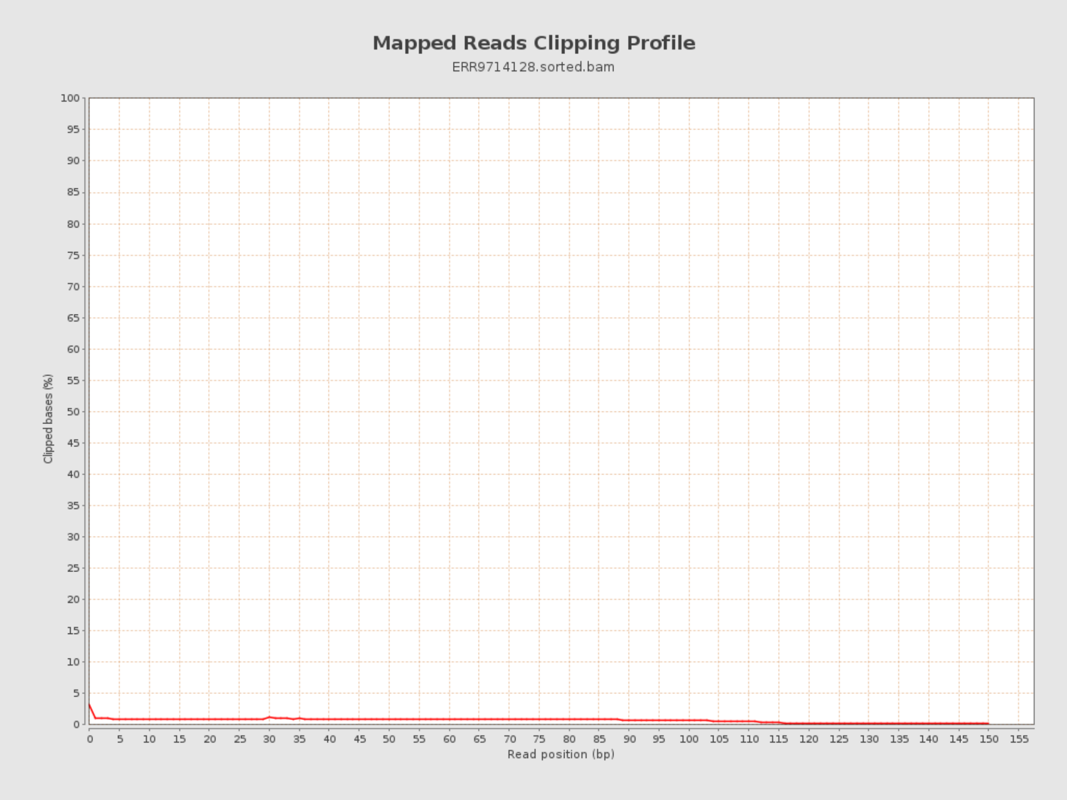
8. Results : Mapped Reads Nucleotide Content



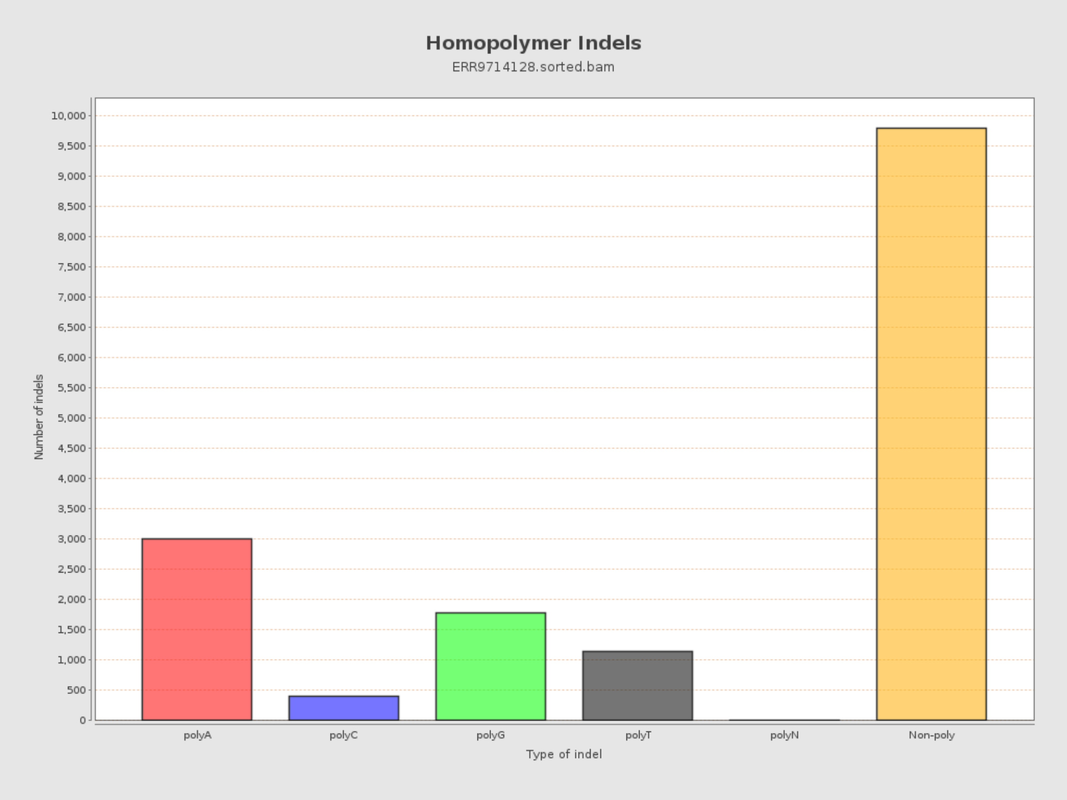
9. Results : Mapped Reads GC-content Distribution



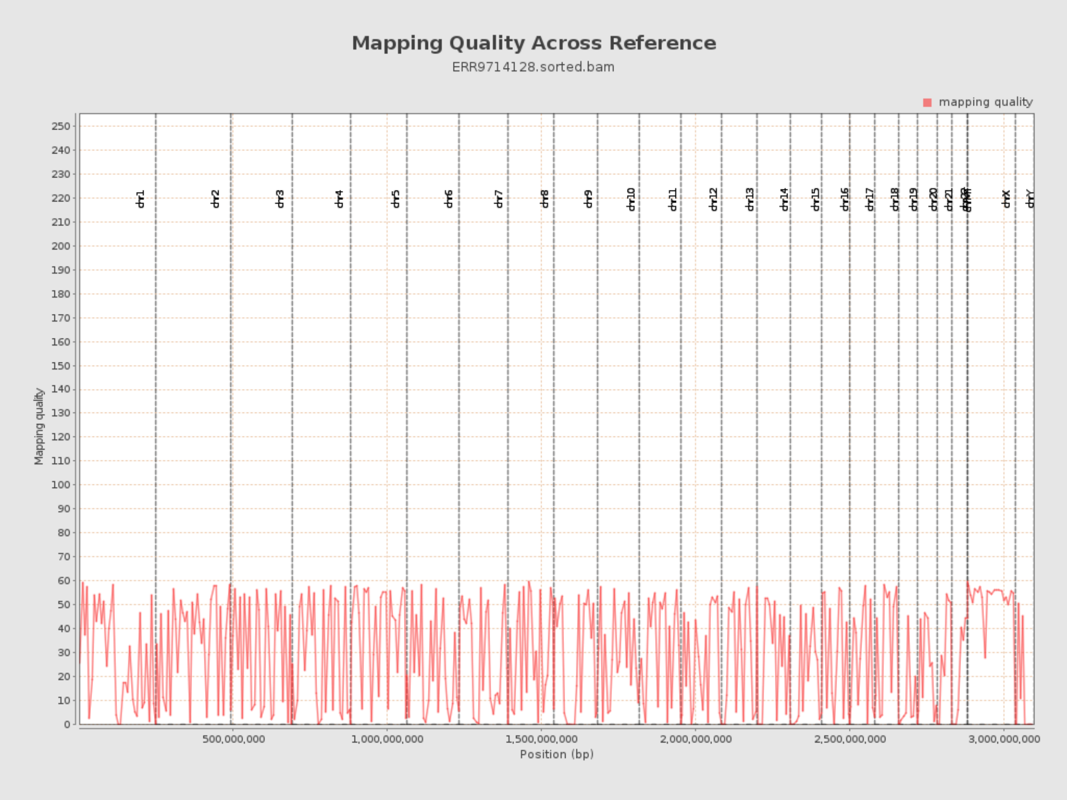
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram