Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 23:14:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714179.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_ERR9714179 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714179.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 23:14:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714179.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	42,286
Mapped reads	14,299 / 33.81%
Unmapped reads	27,987 / 66.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	607 / 1.44%
Read min/max/mean length	30 / 151 / 93.69
Duplicated reads (estimated)	11,275 / 26.66%
Duplication rate	50.43%
Clipped reads	12,132 / 28.69%

2.2. ACGT Content

Number/percentage of A's	368,266 / 22.61%
Number/percentage of C's	322,426 / 19.8%
Number/percentage of T's	346,056 / 21.25%
Number/percentage of G's	591,825 / 36.34%
Number/percentage of N's	25 / 0%
GC Percentage	56.14%

2.3. Coverage

Mean	0.0005

Standard Deviation	0.3744

2.4. Mapping Quality

Mean Mapping Quality	31.57

2.5. Mismatches and indels

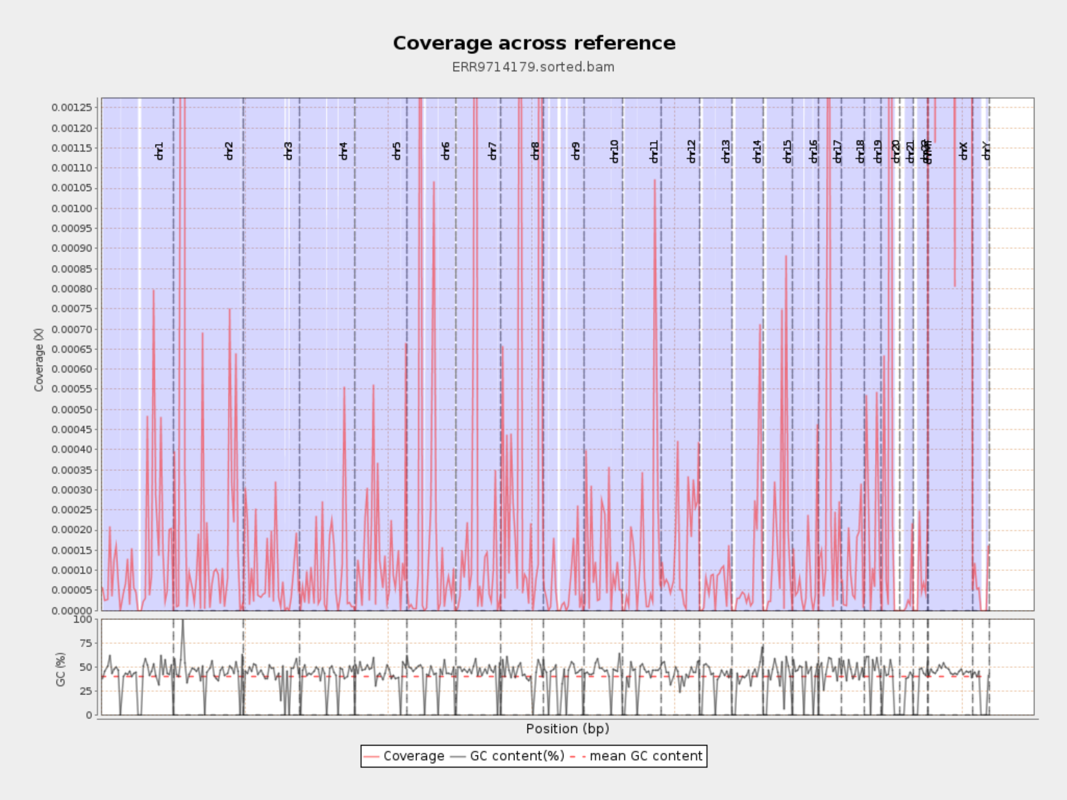
General error rate	3.85%
Mismatches	59,561
Insertions	906
Mapped reads with at least one insertion	5.25%
Deletions	4,350
Mapped reads with at least one deletion	29.39%
Homopolymer indels	30.38%

2.6. Chromosome stats

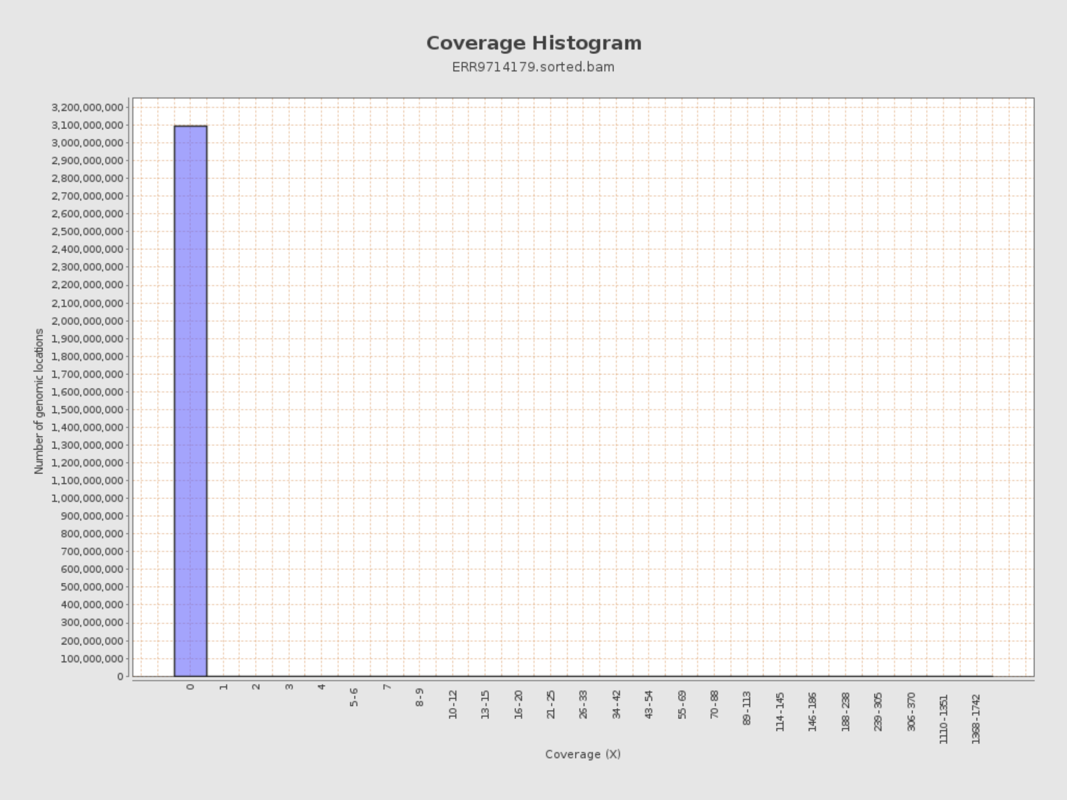
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	32524	0.0001	0.0472
chr2	243199373	317642	0.0013	1.1723
chr3	198022430	18107	0.0001	0.0227
chr4	191154276	17581	0.0001	0.0335
chr5	180915260	24953	0.0001	0.0381
chr6	171115067	35361	0.0002	0.0917
chr7	159138663	42709	0.0003	0.1638

chr8	146364022	79814	0.0005	0.2677
chr9	141213431	7784	0.0001	0.0191
chr10	135534747	17301	0.0001	0.0467
chr11	135006516	19948	0.0001	0.0356
chr12	133851895	20973	0.0002	0.0379
chr13	115169878	7085	0.0001	0.0156
chr14	107349540	11651	0.0001	0.0408
chr15	102531392	20156	0.0002	0.0566
chr16	90354753	8453	0.0001	0.0232
chr17	81195210	25337	0.0003	0.0741
chr18	78077248	8697	0.0001	0.0238
chr19	59128983	12631	0.0002	0.0523
chr20	63025520	38857	0.0006	0.2465
chr21	48129895	1444	0	0.0107
chr22	51304566	3639	0.0001	0.0224
chrMT	16571	395	0.0238	0.2268
chrX	155270560	886438	0.0057	0.7027
chrY	59373566	3270	0.0001	0.0109

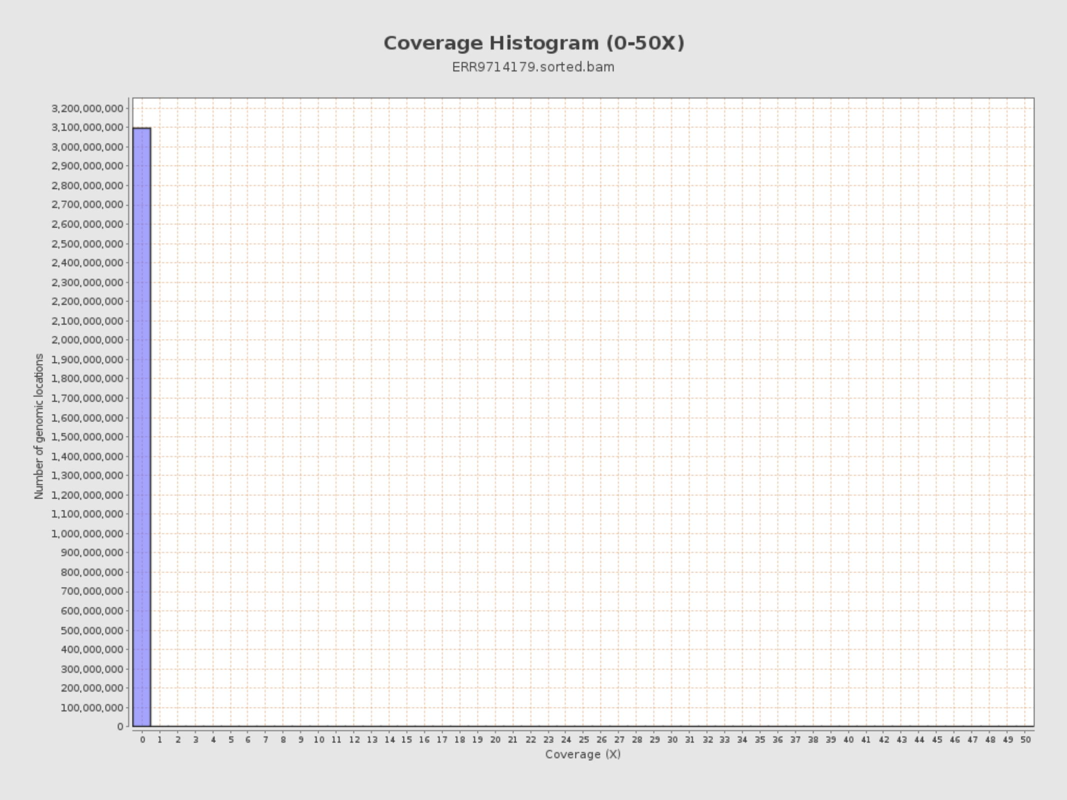
3. Results : Coverage across reference



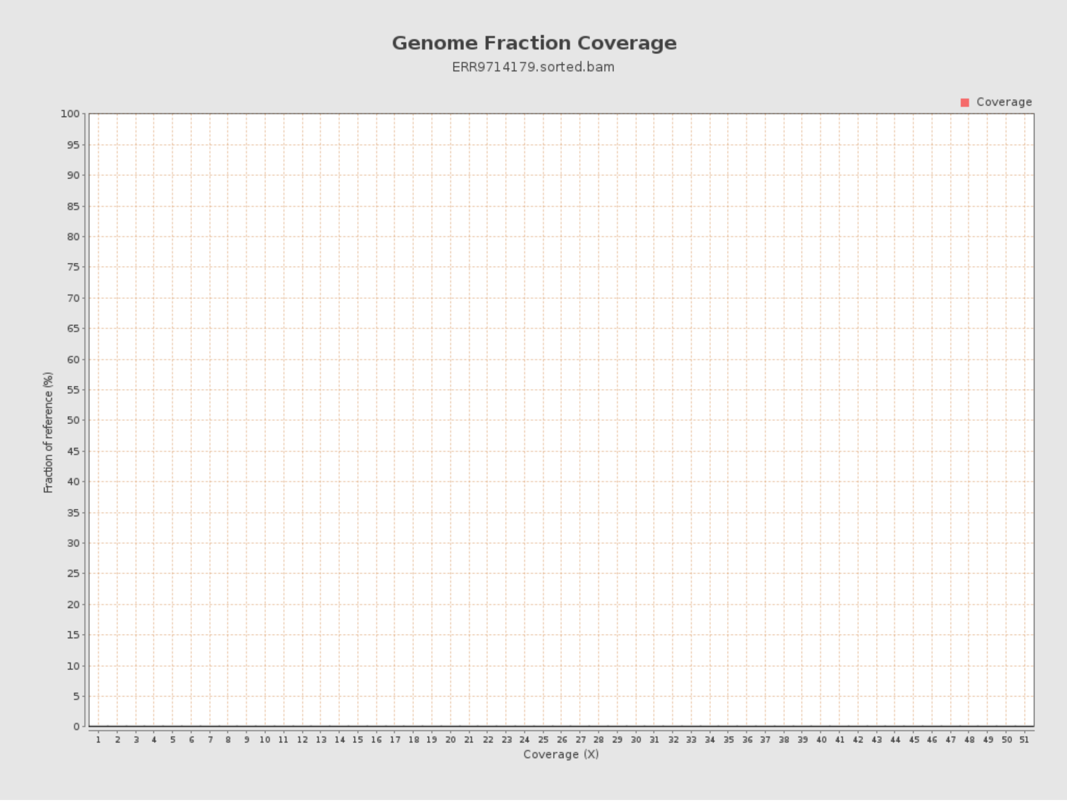
4. Results : Coverage Histogram



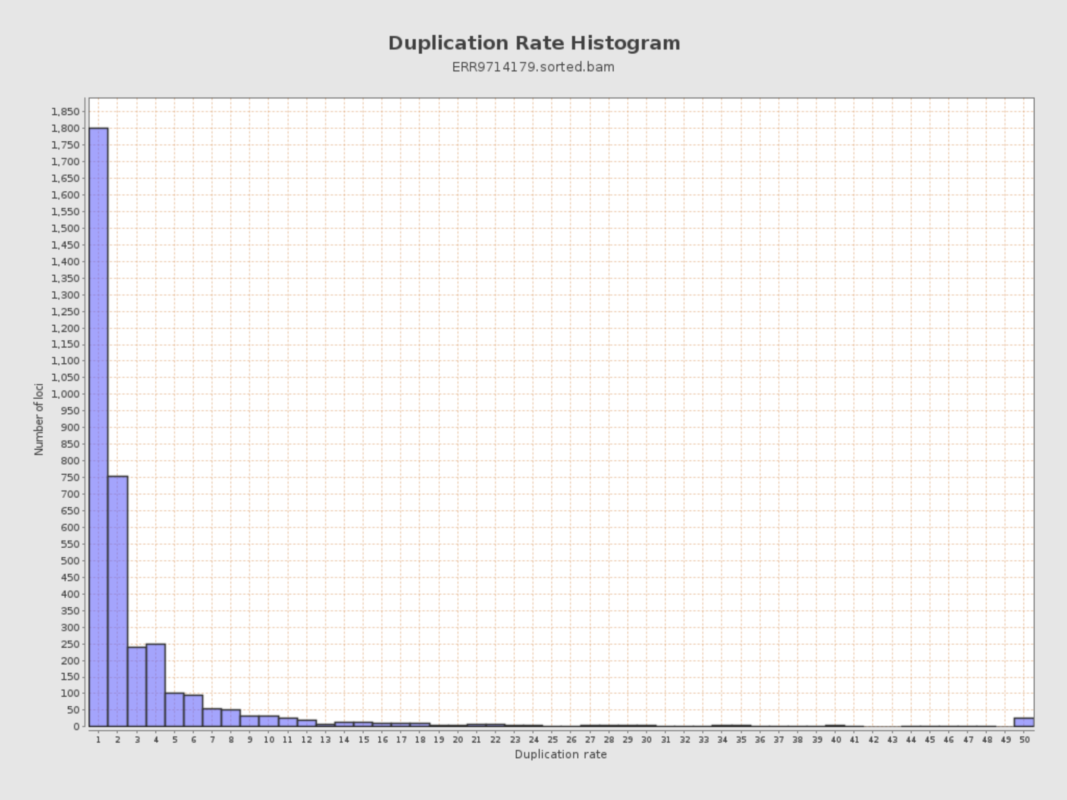
5. Results : Coverage Histogram (0-50X)



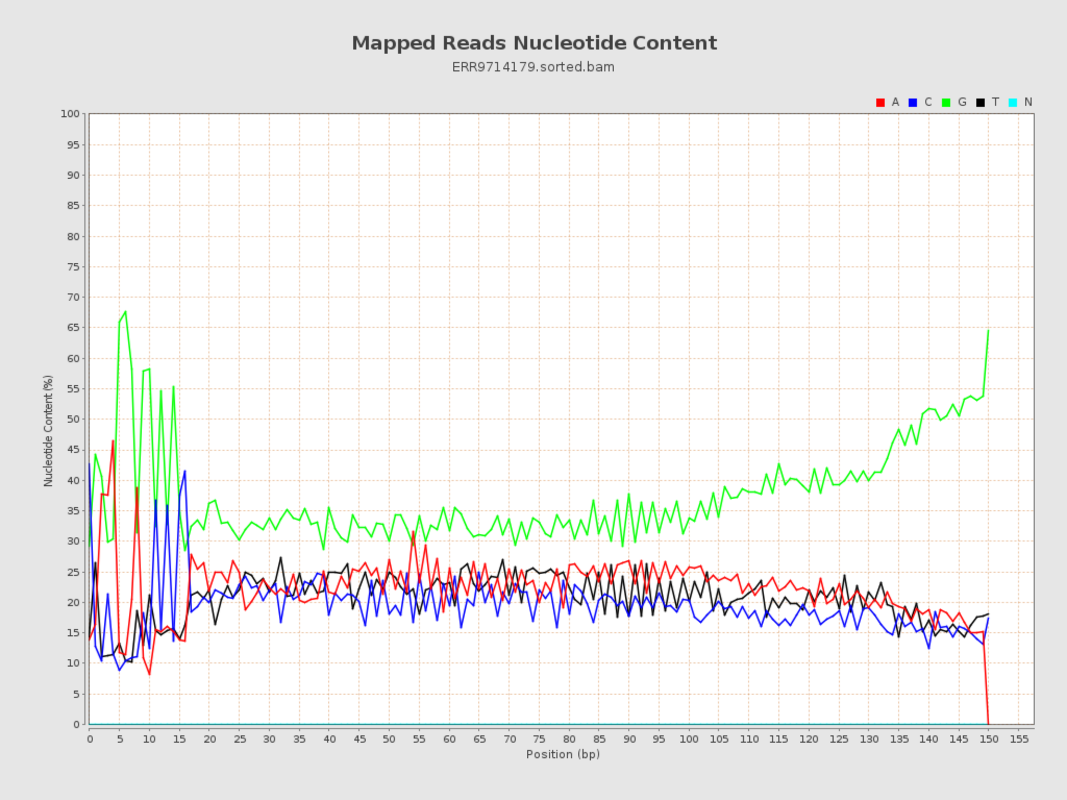
6. Results : Genome Fraction Coverage



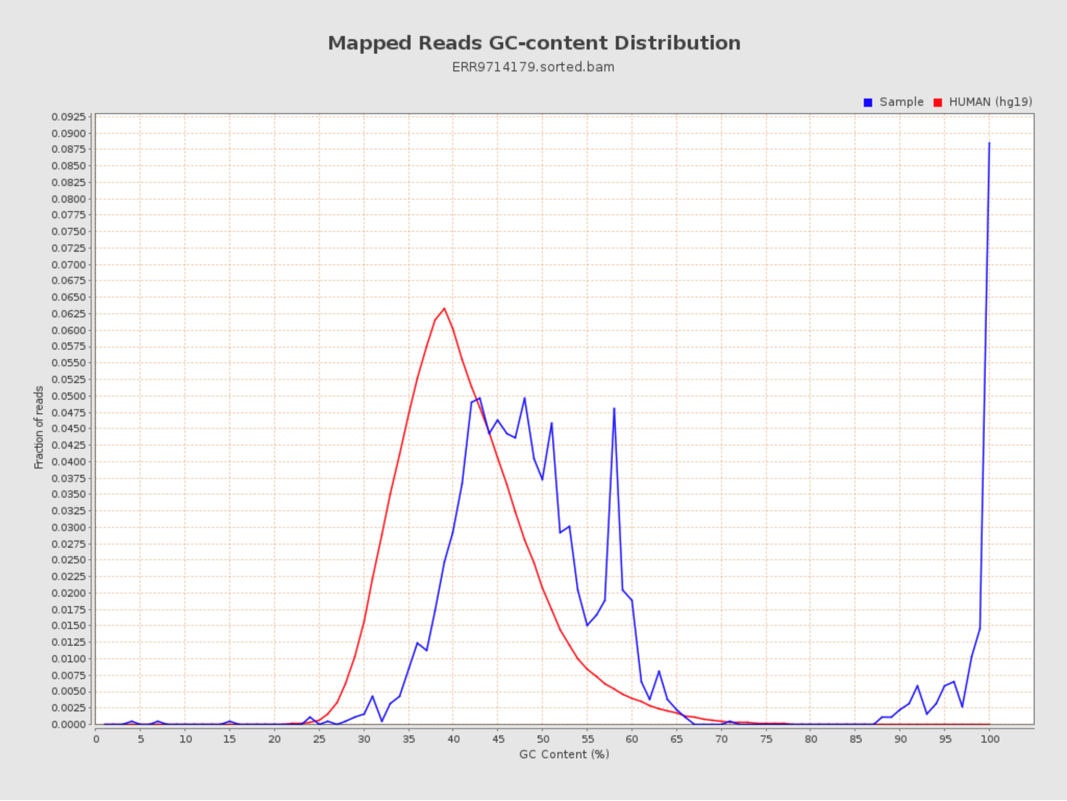
7. Results : Duplication Rate Histogram



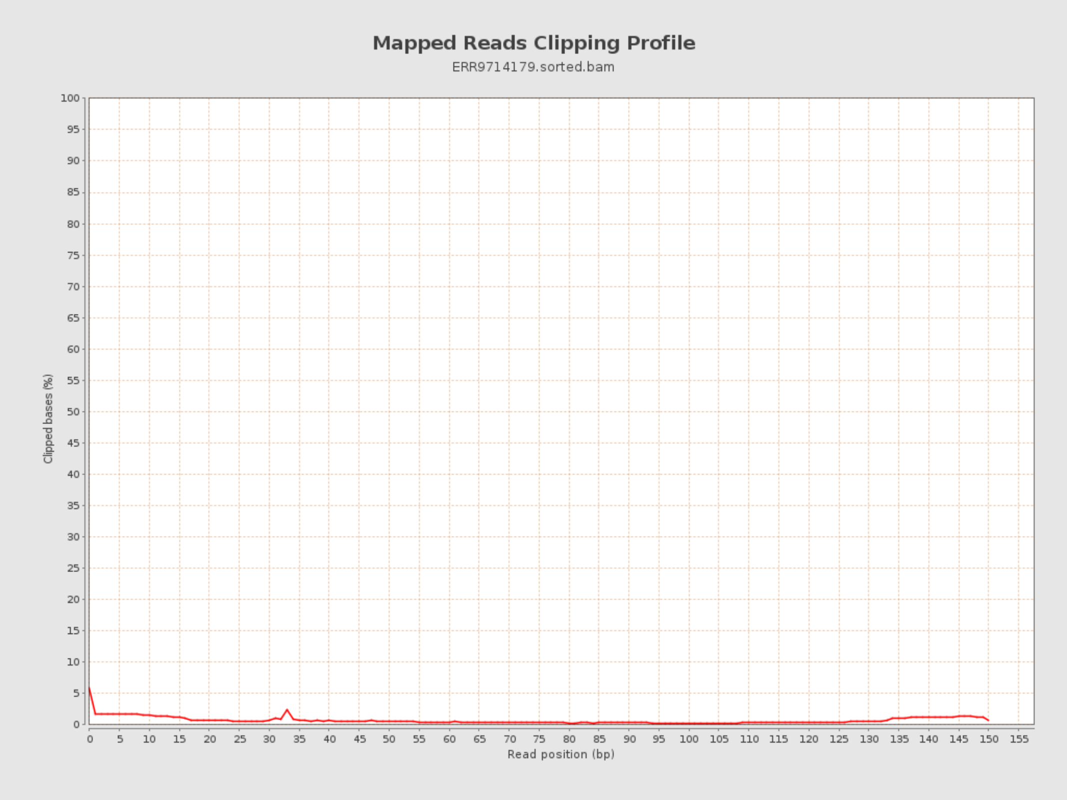
8. Results : Mapped Reads Nucleotide Content



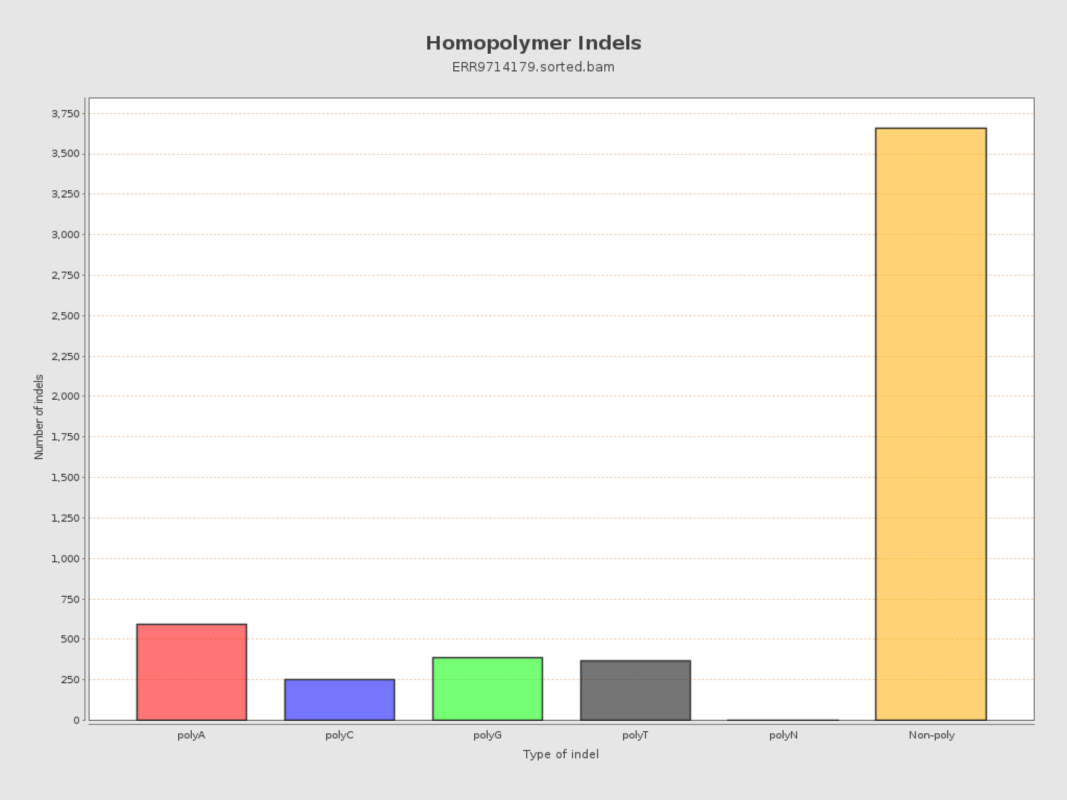
9. Results : Mapped Reads GC-content Distribution



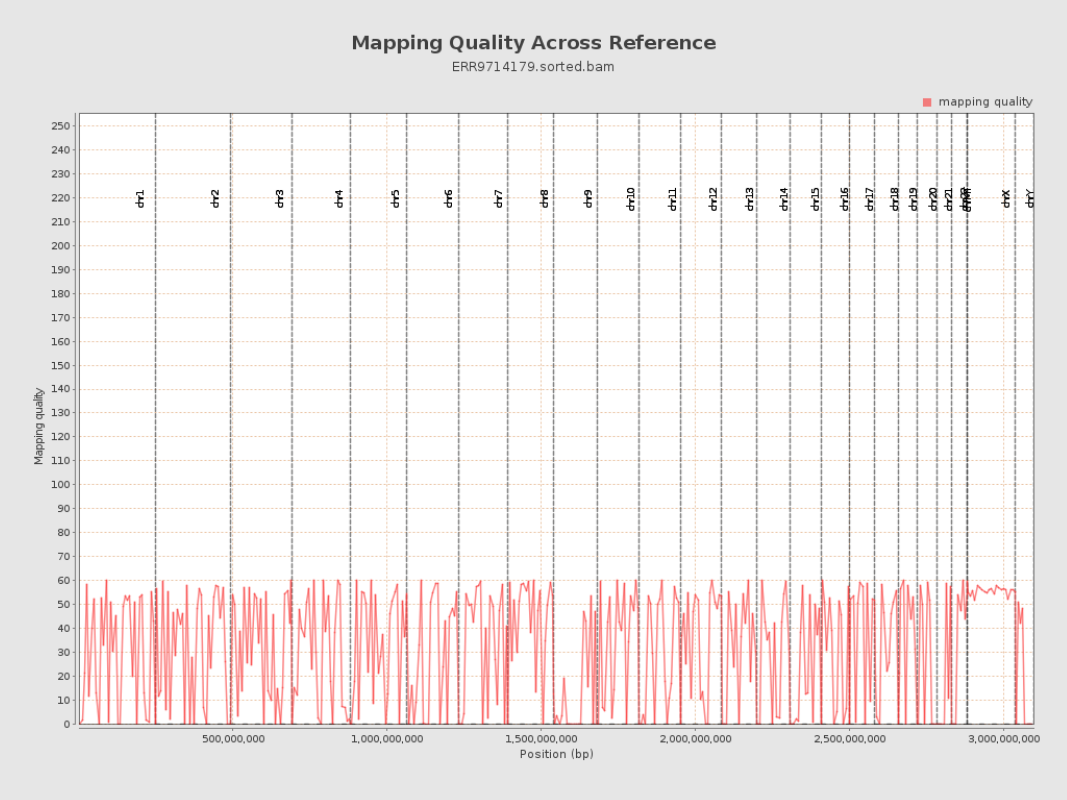
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram