Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 00:22:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714214.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_ERR9714214 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714214.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 00:22:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714214.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,274
Mapped reads	834 / 13.29%
Unmapped reads	5,440 / 86.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21 / 0.33%
Read min/max/mean length	30 / 151 / 60.72
Duplicated reads (estimated)	569 / 9.07%
Duplication rate	27.27%
Clipped reads	629 / 10.03%

2.2. ACGT Content

Number/percentage of A's	7,036 / 9.51%
Number/percentage of C's	4,258 / 5.76%
Number/percentage of T's	4,915 / 6.64%
Number/percentage of G's	57,762 / 78.09%
Number/percentage of N's	0 / 0%
GC Percentage	83.84%

2.3. Coverage

Mean	0

Standard Deviation	0.0668

2.4. Mapping Quality

Mean Mapping Quality	5.41

2.5. Mismatches and indels

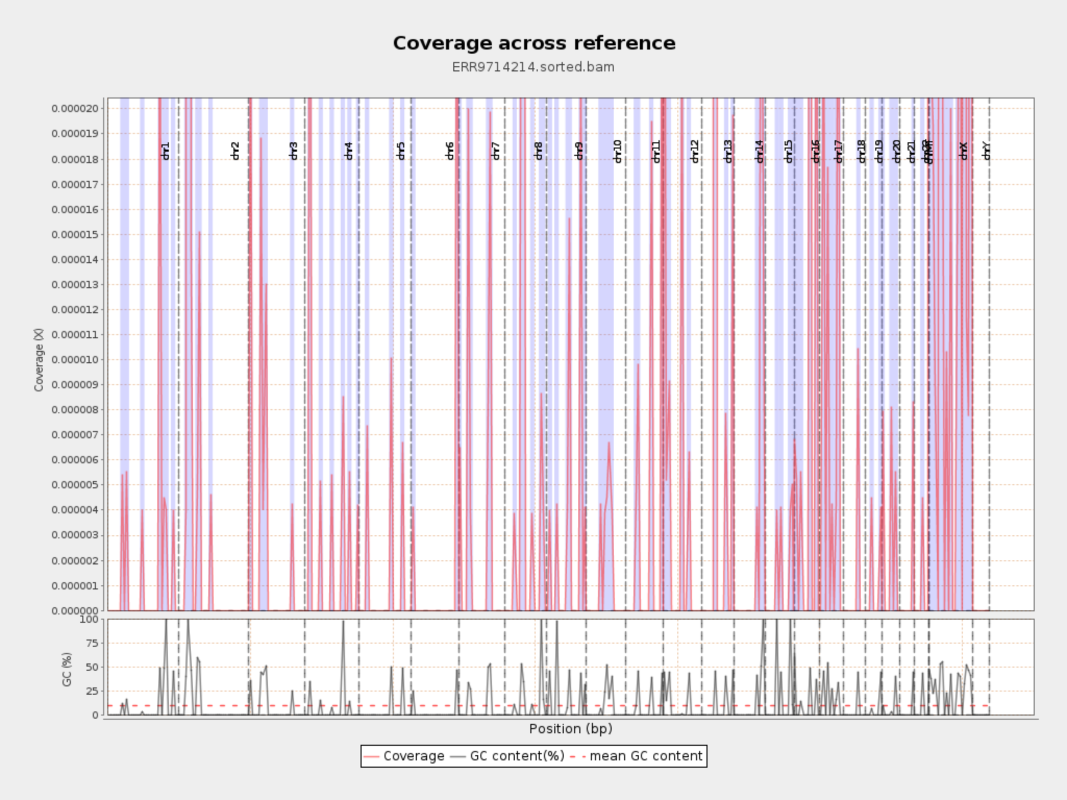
General error rate	3.65%
Mismatches	2,003
Insertions	128
Mapped reads with at least one insertion	10.79%
Deletions	59
Mapped reads with at least one deletion	6.95%
Homopolymer indels	44.92%

2.6. Chromosome stats

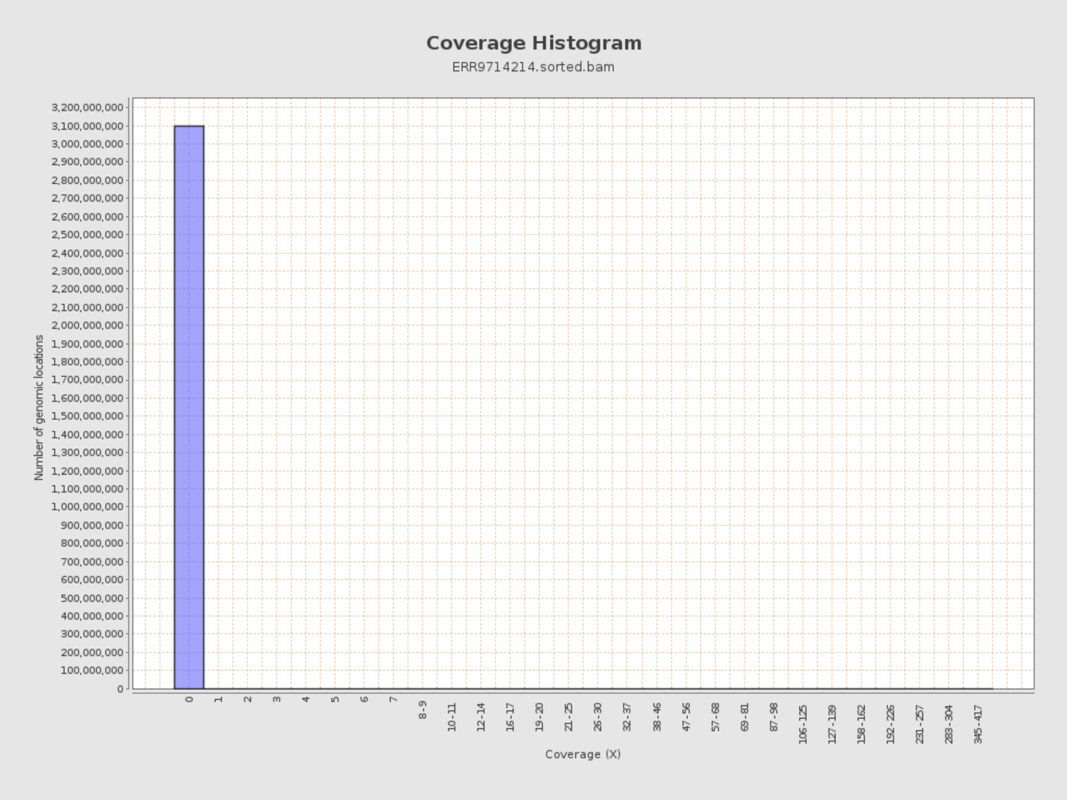
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	425	0	0.0015
chr2	243199373	54779	0.0002	0.2367
chr3	198022430	507	0	0.0017
chr4	191154276	502	0	0.0018
chr5	180915260	187	0	0.001
chr6	171115067	295	0	0.0015
chr7	159138663	433	0	0.0026

chr8	146364022	1003	0	0.0046
chr9	141213431	417	0	0.0017
chr10	135534747	180	0	0.0012
chr11	135006516	493	0	0.0022
chr12	133851895	630	0	0.0028
chr13	115169878	3899	0	0.0283
chr14	107349540	428	0	0.003
chr15	102531392	133	0	0.0011
chr16	90354753	828	0	0.0037
chr17	81195210	675	0	0.0041
chr18	78077248	81	0	0.001
chr19	59128983	67	0	0.0011
chr20	63025520	151	0	0.0015
chr21	48129895	41	0	0.0009
chr22	51304566	35	0	0.0008
chrMT	16571	302	0.0182	0.1489
chrX	155270560	7887	0.0001	0.0192
chrY	59373566	0	0	0

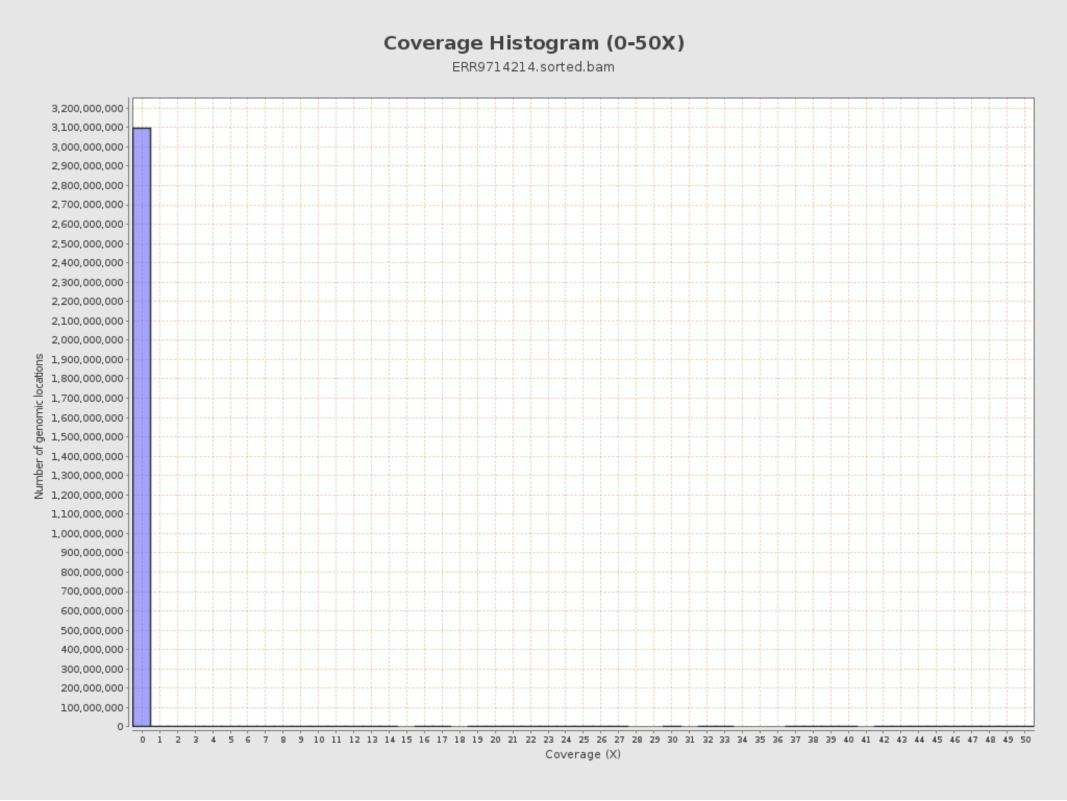
3. Results : Coverage across reference



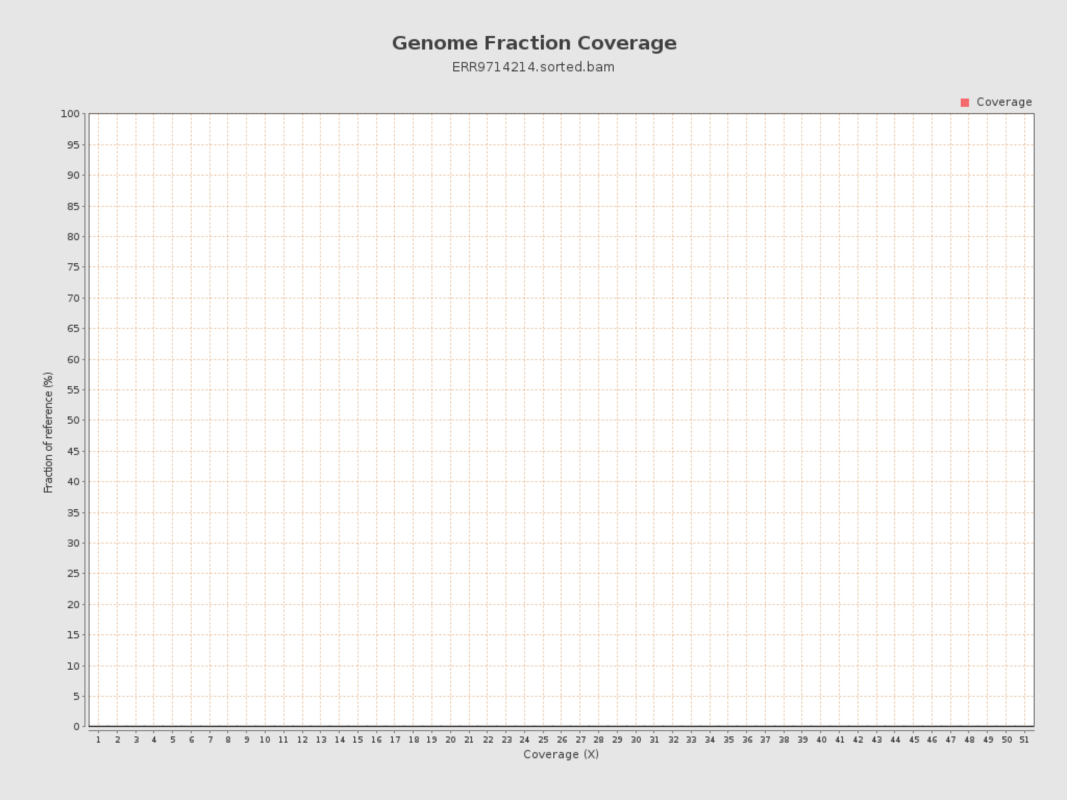
4. Results : Coverage Histogram



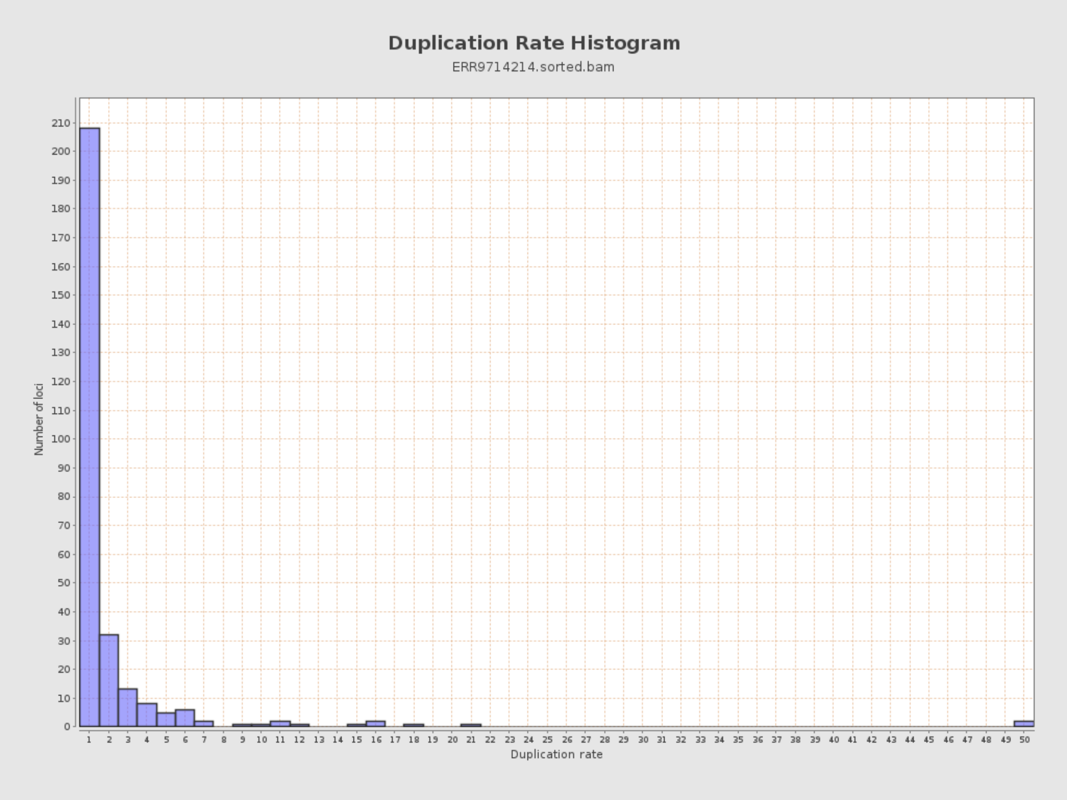
5. Results : Coverage Histogram (0-50X)



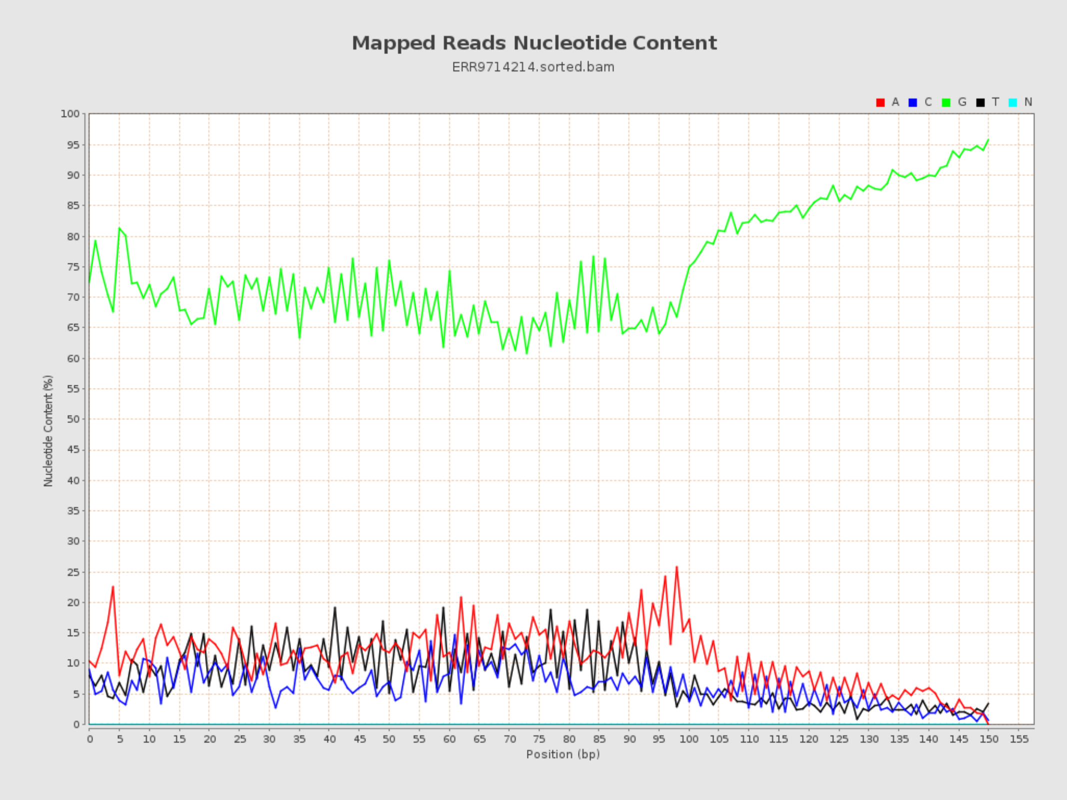
6. Results : Genome Fraction Coverage



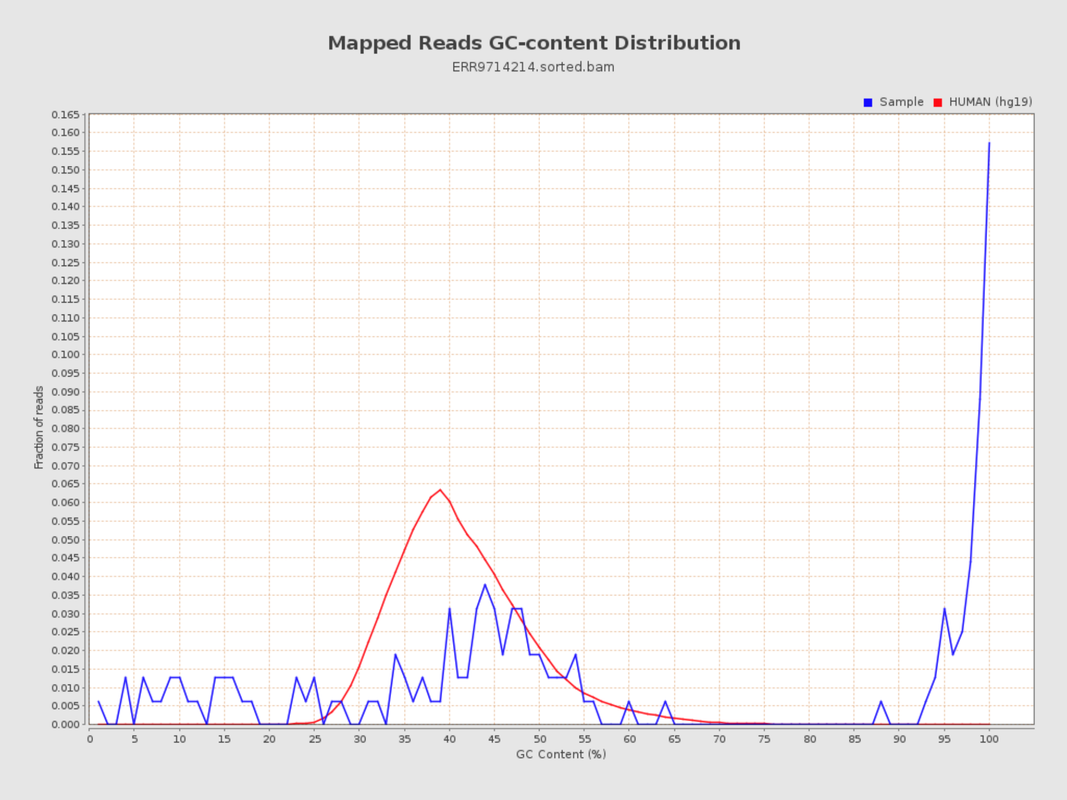
7. Results : Duplication Rate Histogram



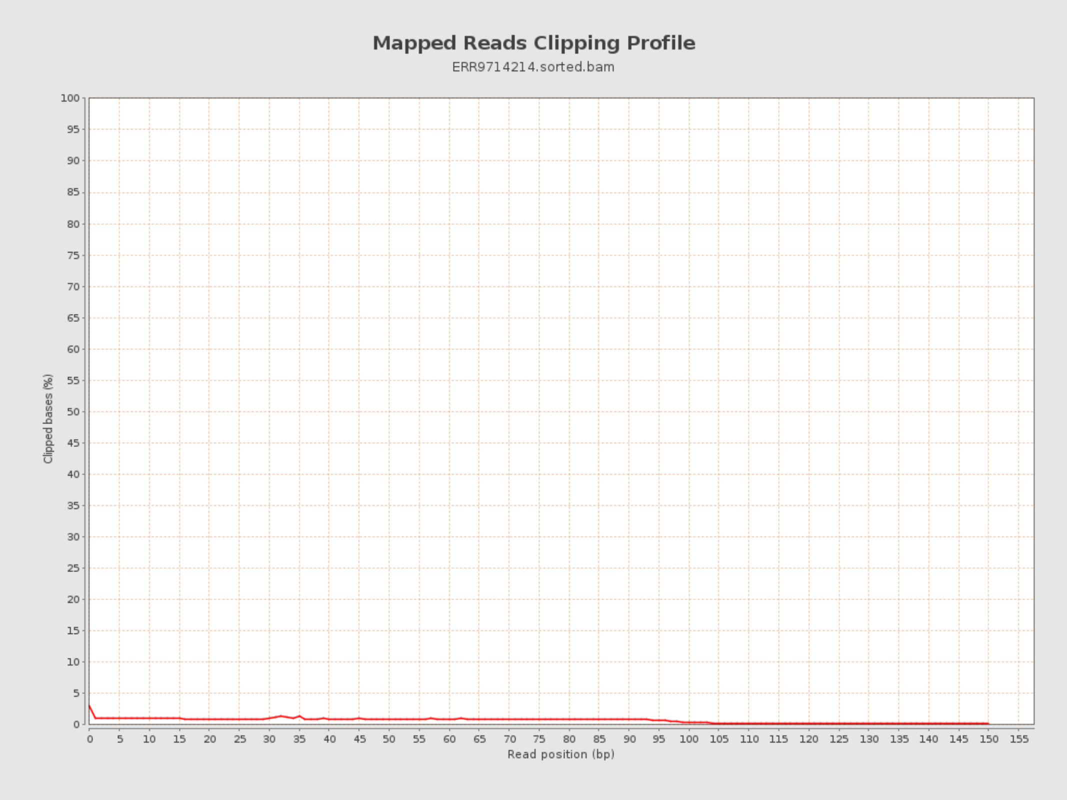
8. Results : Mapped Reads Nucleotide Content



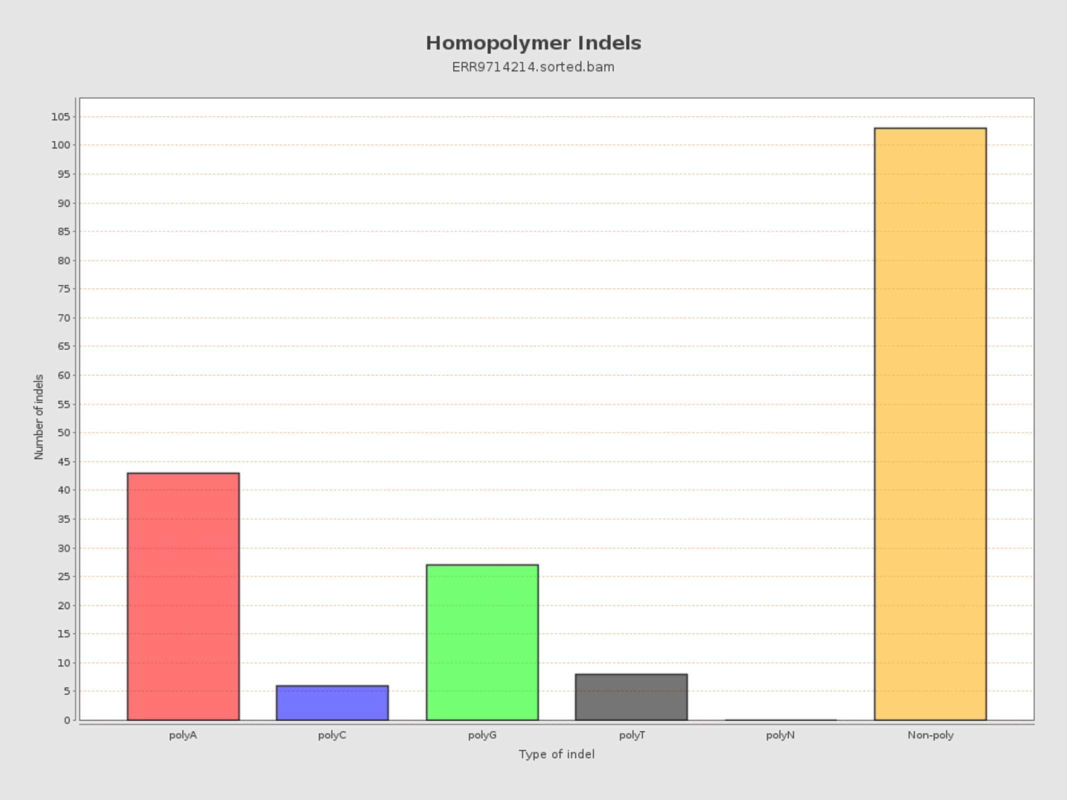
9. Results : Mapped Reads GC-content Distribution



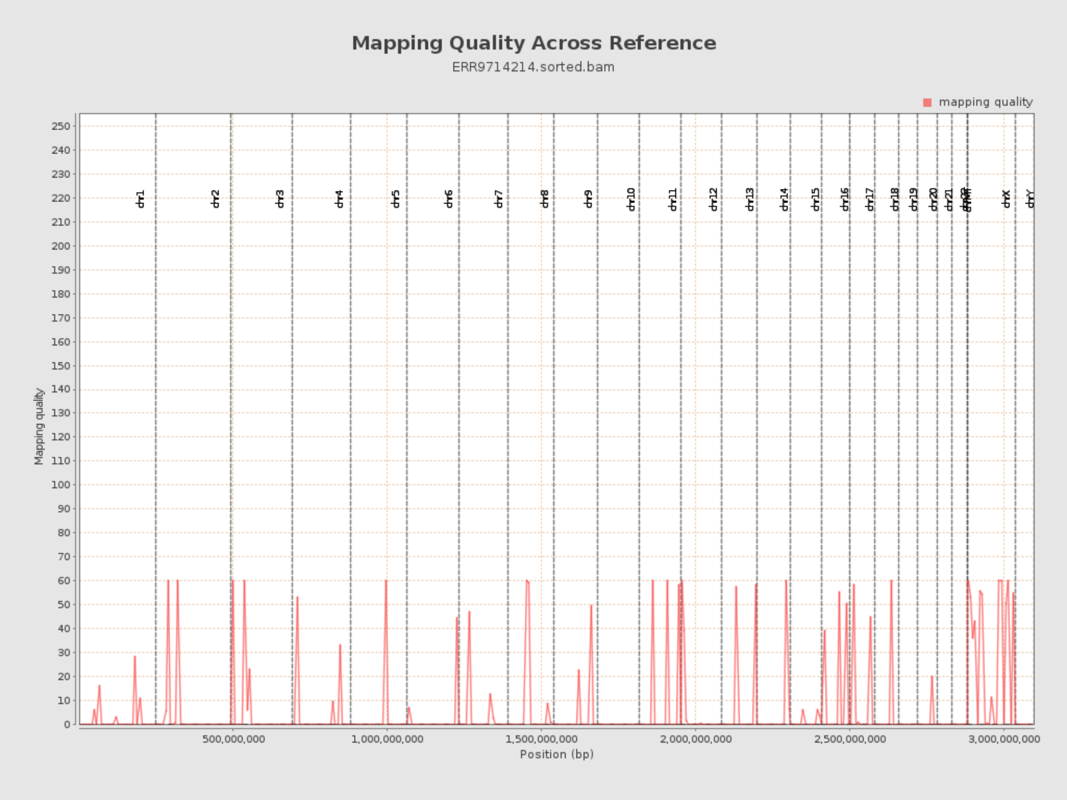
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram