Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 00:10:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714206.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_ERR9714206 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714206.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 00:10:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714206.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	122,072
Mapped reads	24,085 / 19.73%
Unmapped reads	97,987 / 80.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,044 / 0.86%
Read min/max/mean length	30 / 151 / 69.96
Duplicated reads (estimated)	21,060 / 17.25%
Duplication rate	46.38%
Clipped reads	17,681 / 14.48%

2.2. ACGT Content

Number/percentage of A's	424,935 / 15.99%
Number/percentage of C's	348,014 / 13.1%
Number/percentage of T's	383,209 / 14.42%
Number/percentage of G's	1,500,516 / 56.48%
Number/percentage of N's	89 / 0%
GC Percentage	69.58%

2.3. Coverage

Mean	0.0009

Standard Deviation	1.4241

2.4. Mapping Quality

Mean Mapping Quality	31.89

2.5. Mismatches and indels

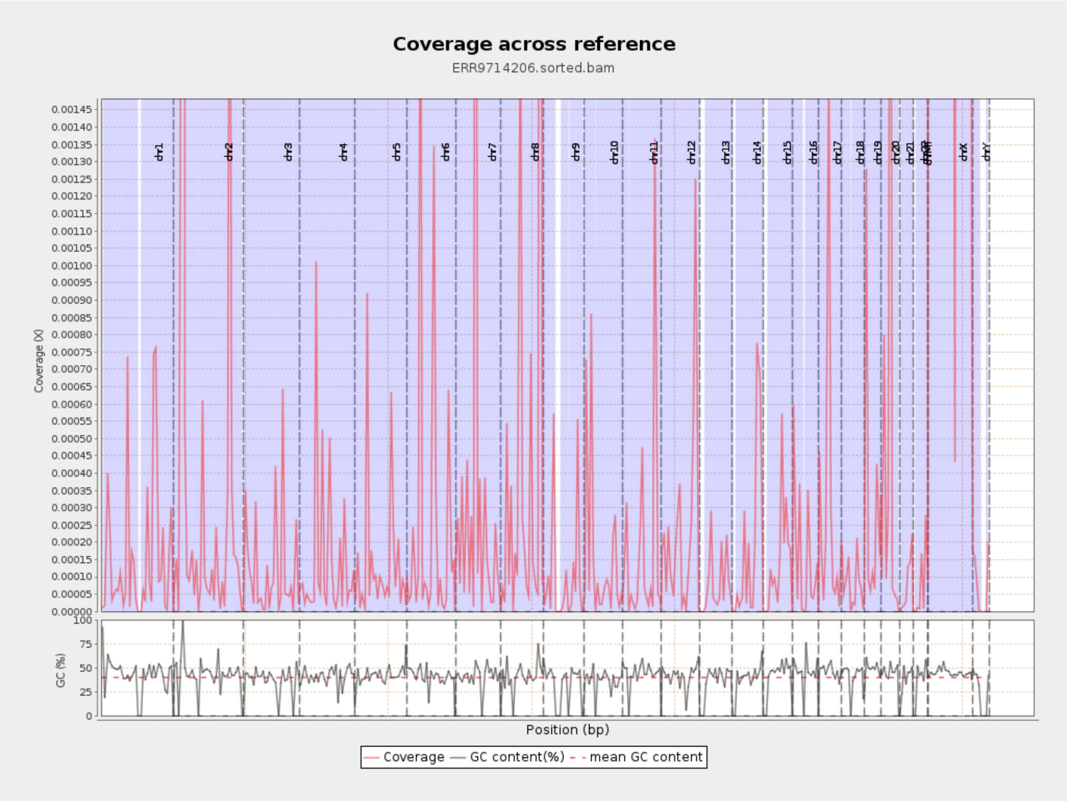
General error rate	3.74%
Mismatches	84,362
Insertions	2,498
Mapped reads with at least one insertion	7.07%
Deletions	5,038
Mapped reads with at least one deletion	20.42%
Homopolymer indels	40.46%

2.6. Chromosome stats

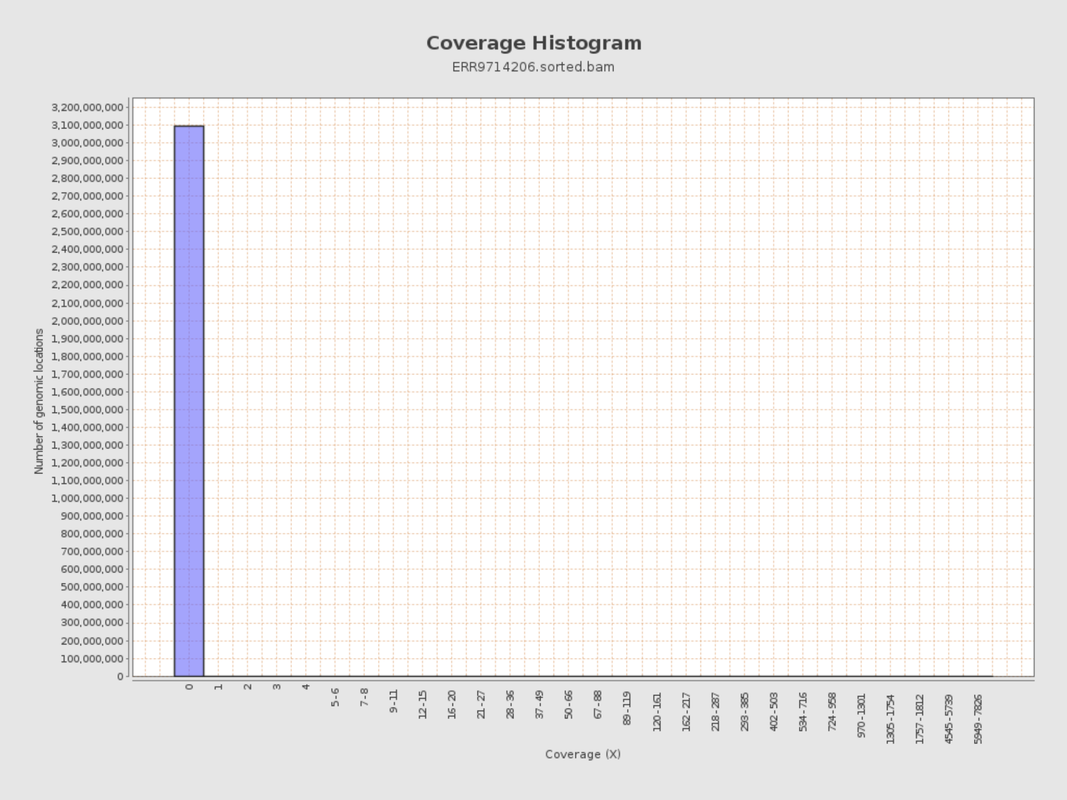
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	39984	0.0002	0.0821
chr2	243199373	1224858	0.005	5.0268
chr3	198022430	23888	0.0001	0.0361
chr4	191154276	27865	0.0001	0.0454
chr5	180915260	25903	0.0001	0.0403
chr6	171115067	44691	0.0003	0.1138
chr7	159138663	51373	0.0003	0.1691

chr8	146364022	92434	0.0006	0.3875
chr9	141213431	13854	0.0001	0.0387
chr10	135534747	21834	0.0002	0.1056
chr11	135006516	22933	0.0002	0.0728
chr12	133851895	34143	0.0003	0.0683
chr13	115169878	8788	0.0001	0.0213
chr14	107349540	19833	0.0002	0.0589
chr15	102531392	15229	0.0001	0.0411
chr16	90354753	13262	0.0001	0.039
chr17	81195210	24053	0.0003	0.0749
chr18	78077248	6280	0.0001	0.0188
chr19	59128983	17792	0.0003	0.1063
chr20	63025520	33679	0.0005	0.1892
chr21	48129895	3615	0.0001	0.0157
chr22	51304566	3895	0.0001	0.0256
chrMT	16571	1404	0.0847	0.406
chrX	155270560	917465	0.0059	0.7791
chrY	59373566	4421	0.0001	0.0149

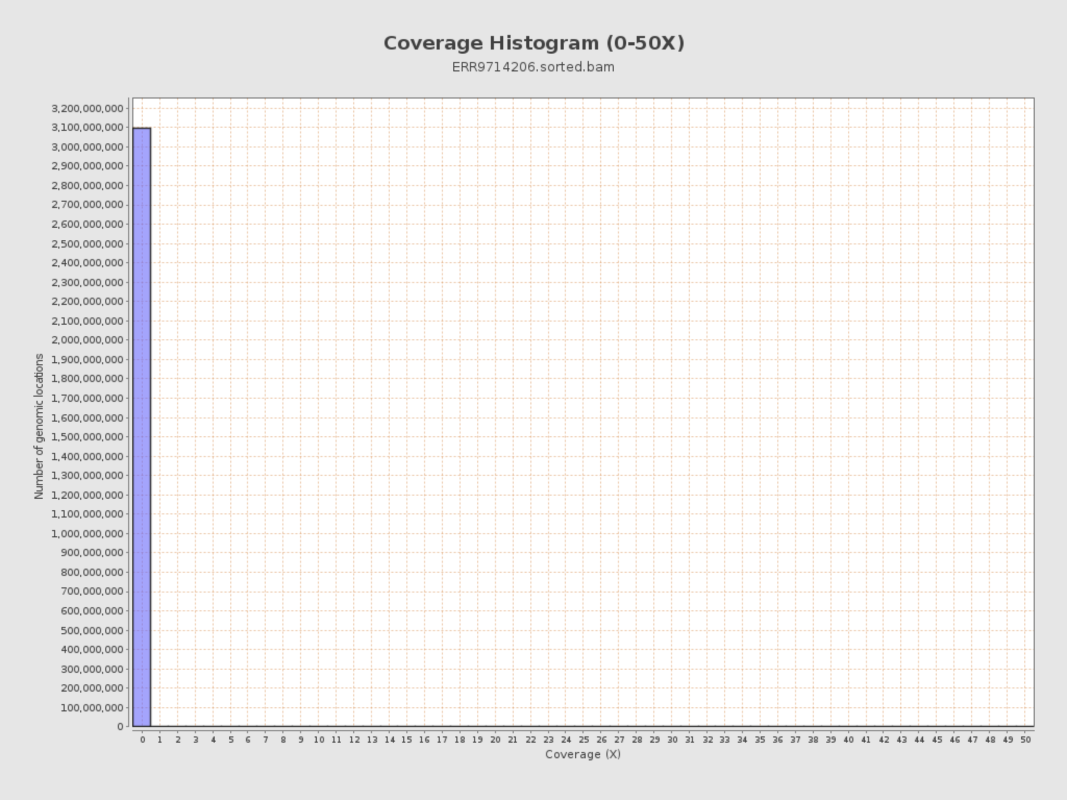
3. Results : Coverage across reference



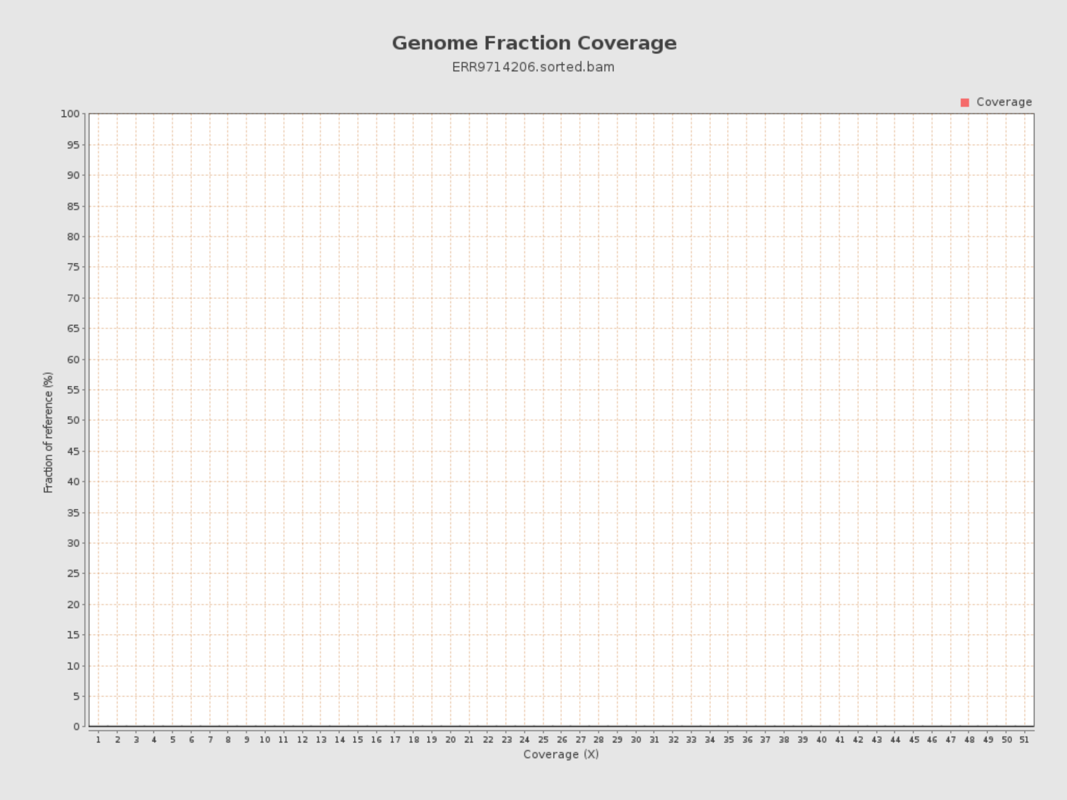
4. Results : Coverage Histogram



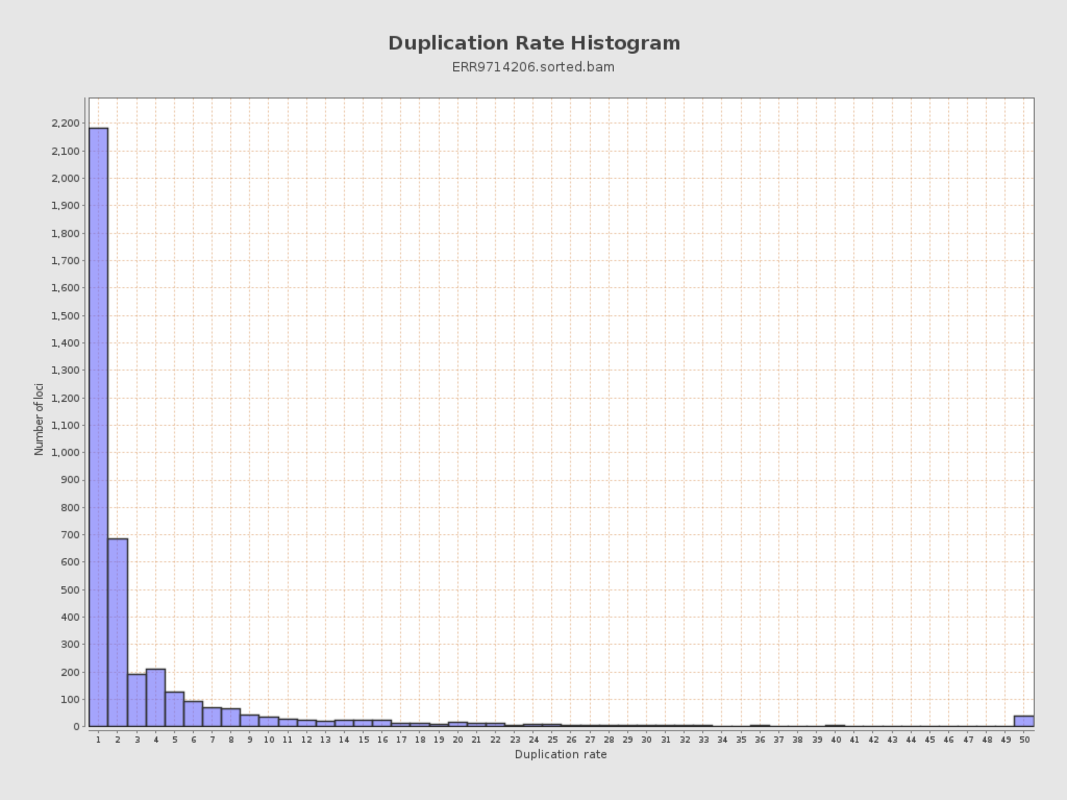
5. Results : Coverage Histogram (0-50X)



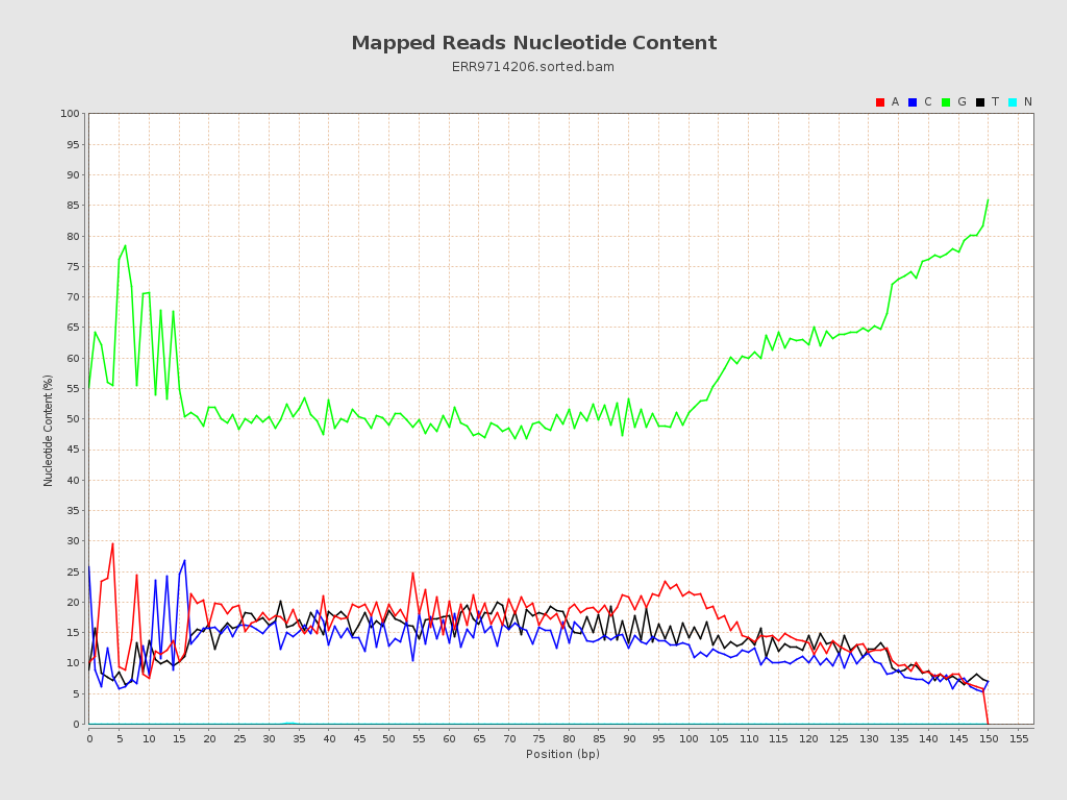
6. Results : Genome Fraction Coverage



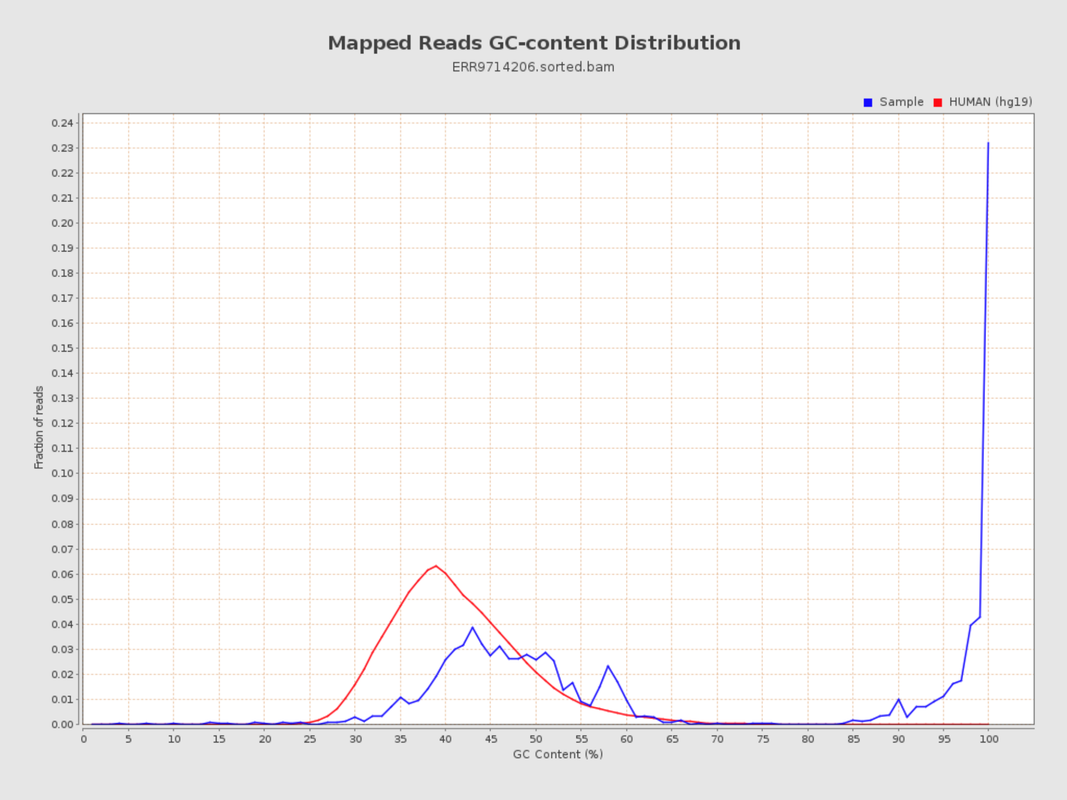
7. Results : Duplication Rate Histogram



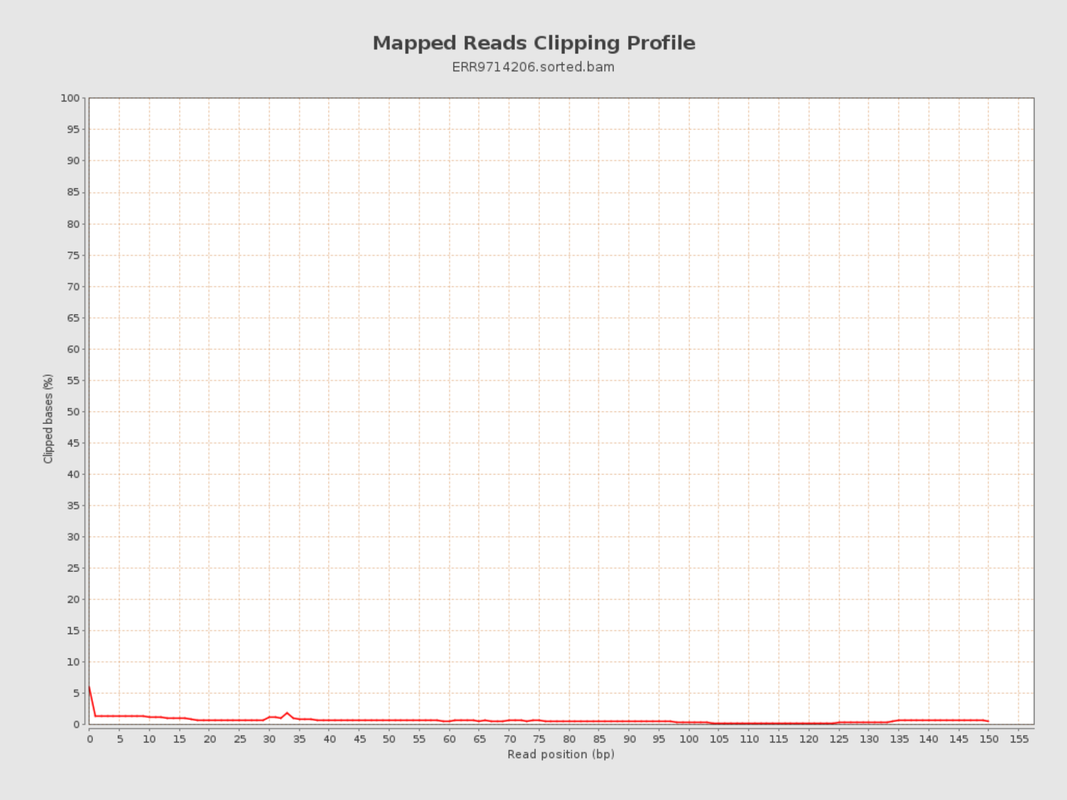
8. Results : Mapped Reads Nucleotide Content



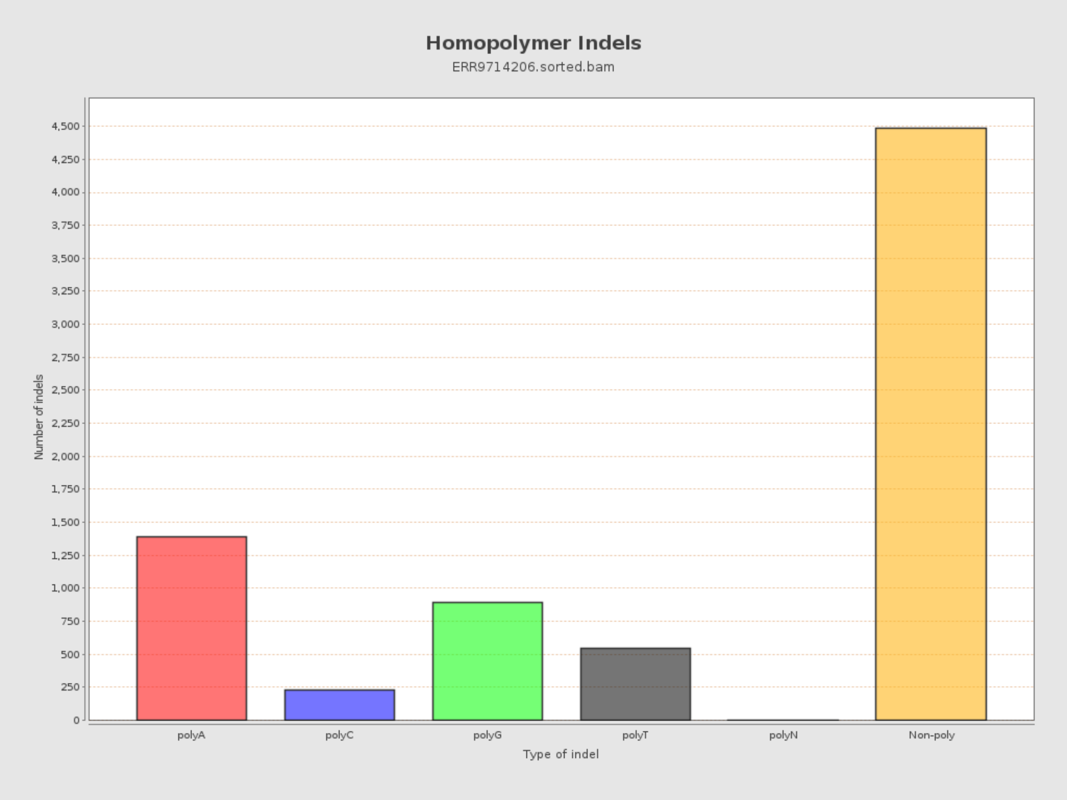
9. Results : Mapped Reads GC-content Distribution



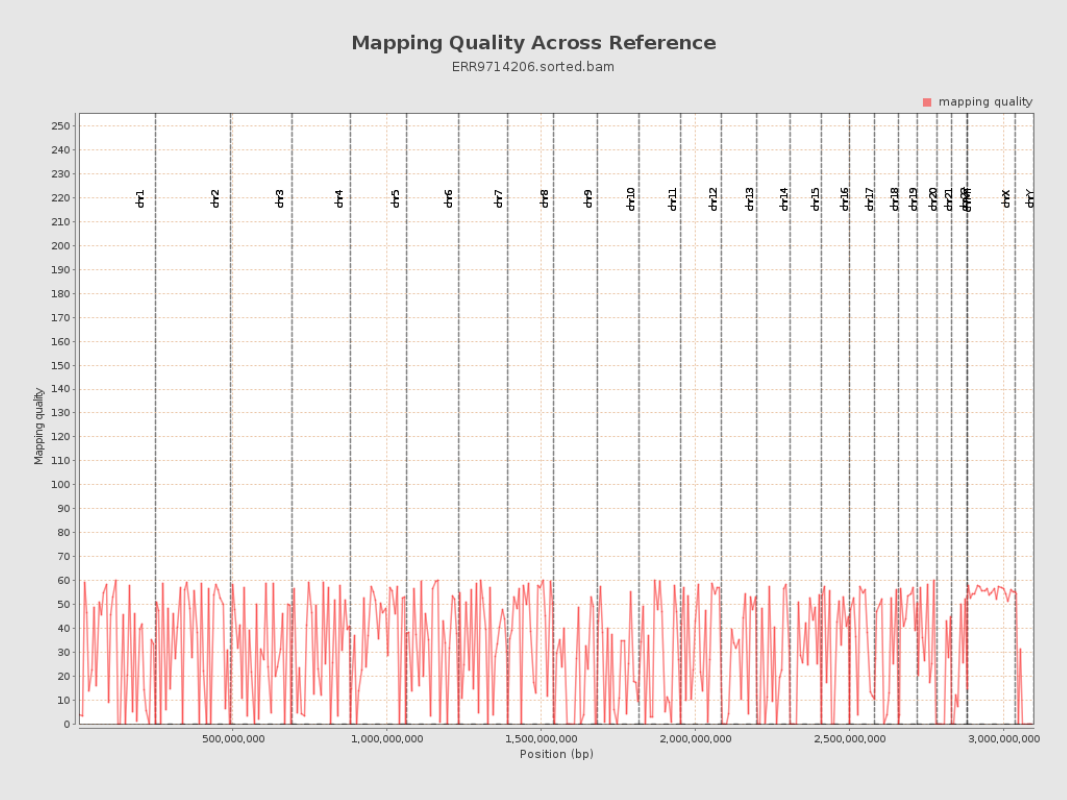
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram