Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 01:02:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714239.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_ERR9714239 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714239.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 01:02:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714239.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	319,976
Mapped reads	48,825 / 15.26%
Unmapped reads	271,151 / 84.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,186 / 0.37%
Read min/max/mean length	30 / 151 / 60.48
Duplicated reads (estimated)	47,944 / 14.98%
Duplication rate	35.66%
Clipped reads	25,369 / 7.93%

2.2. ACGT Content

Number/percentage of A's	115,485 / 2.26%
Number/percentage of C's	44,513 / 0.87%
Number/percentage of T's	56,456 / 1.1%
Number/percentage of G's	4,898,457 / 95.77%
Number/percentage of N's	90 / 0%
GC Percentage	96.64%

2.3. Coverage

Mean	0.0017

Standard Deviation	6.164

2.4. Mapping Quality

Mean Mapping Quality	12.57

2.5. Mismatches and indels

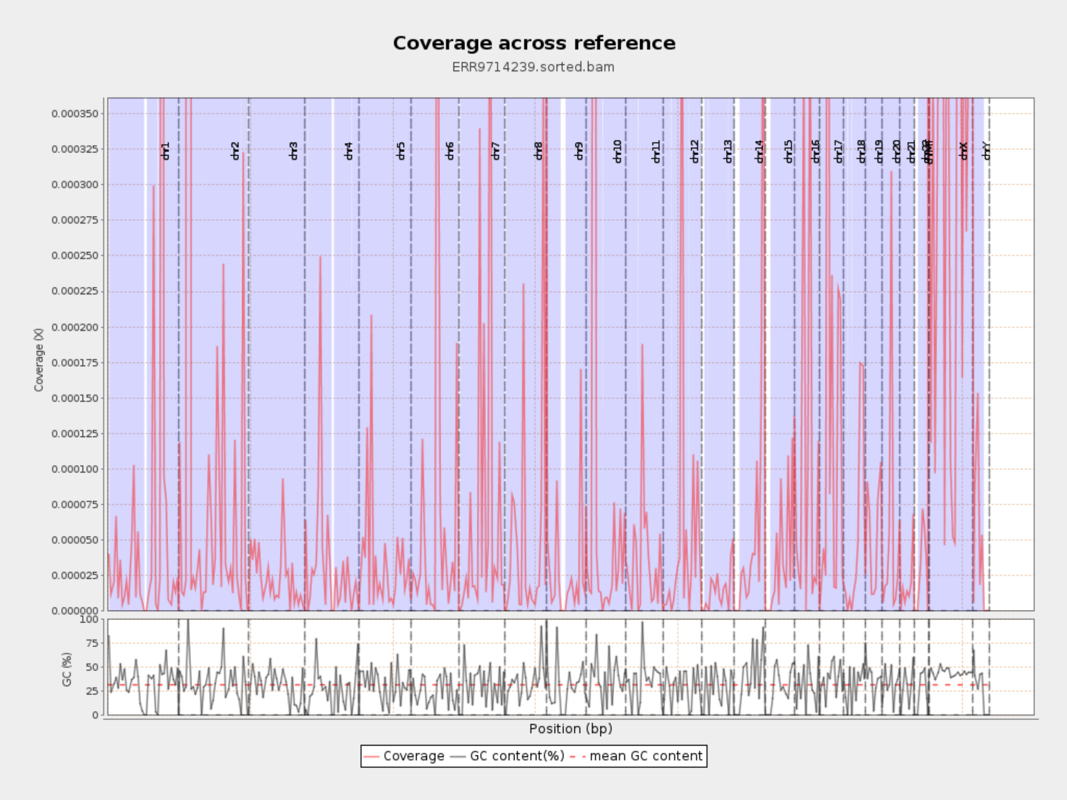
General error rate	3.41%
Mismatches	128,571
Insertions	6,469
Mapped reads with at least one insertion	9.01%
Deletions	2,669
Mapped reads with at least one deletion	5.21%
Homopolymer indels	63.45%

2.6. Chromosome stats

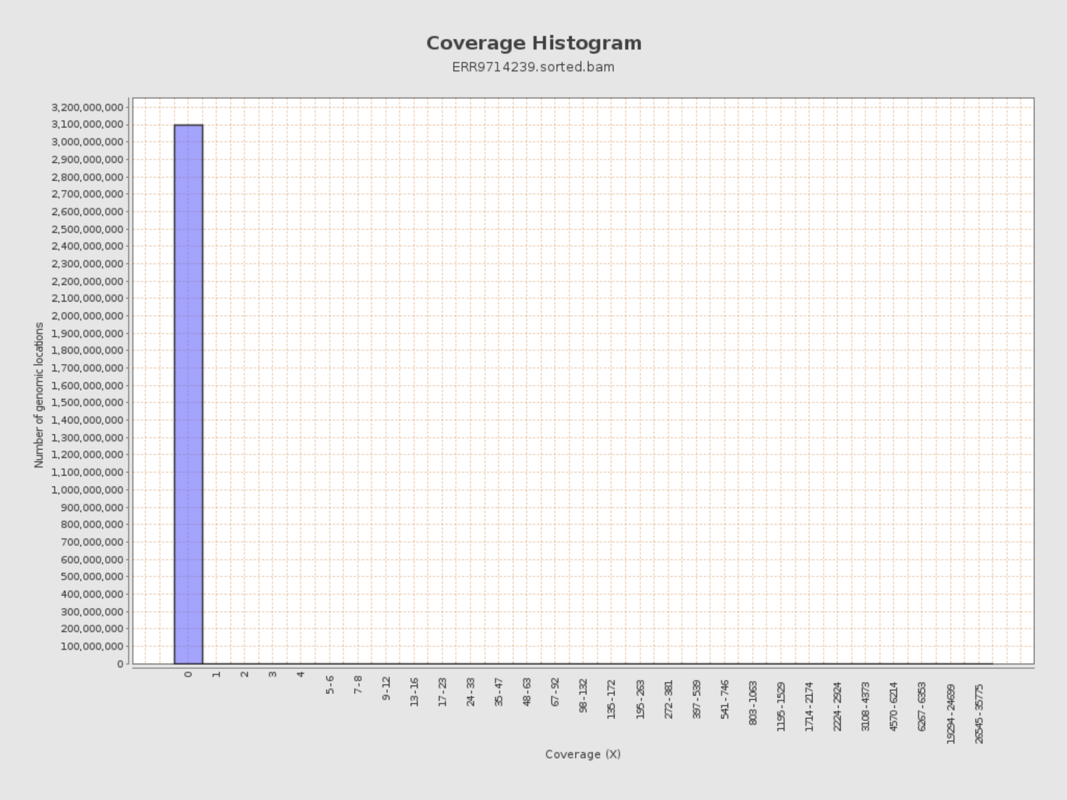
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17417	0.0001	0.1081
chr2	243199373	4918464	0.0202	21.9911
chr3	198022430	4672	0	0.0102
chr4	191154276	6285	0	0.0133
chr5	180915260	6533	0	0.013
chr6	171115067	10716	0.0001	0.026
chr7	159138663	12647	0.0001	0.0649

chr8	146364022	7857	0.0001	0.0214
chr9	141213431	4236	0	0.0153
chr10	135534747	11926	0.0001	0.1339
chr11	135006516	4954	0	0.0222
chr12	133851895	8150	0.0001	0.0403
chr13	115169878	1734	0	0.0047
chr14	107349540	7523	0.0001	0.061
chr15	102531392	3749	0	0.0131
chr16	90354753	10098	0.0001	0.0374
chr17	81195210	13174	0.0002	0.1026
chr18	78077248	3916	0.0001	0.015
chr19	59128983	3120	0.0001	0.0153
chr20	63025520	3614	0.0001	0.0225
chr21	48129895	836	0	0.0096
chr22	51304566	1475	0	0.0067
chrMT	16571	1185	0.0715	0.3909
chrX	155270560	59313	0.0004	0.0629
chrY	59373566	2419	0	0.0116

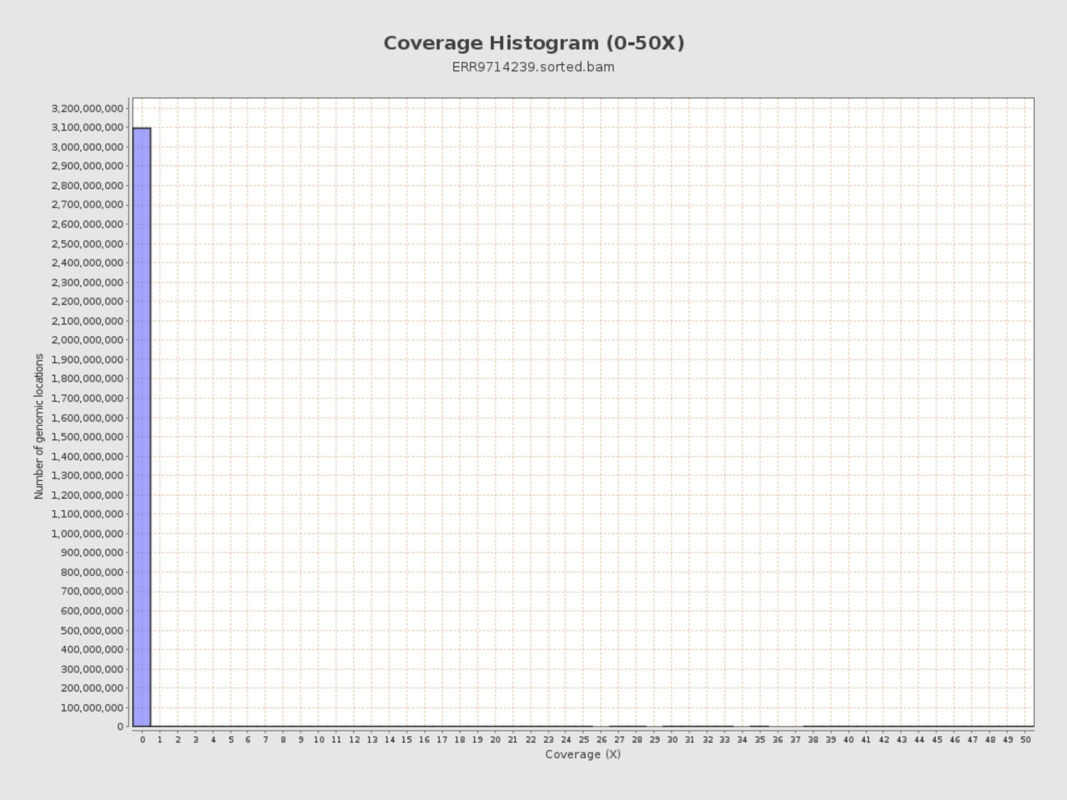
3. Results : Coverage across reference



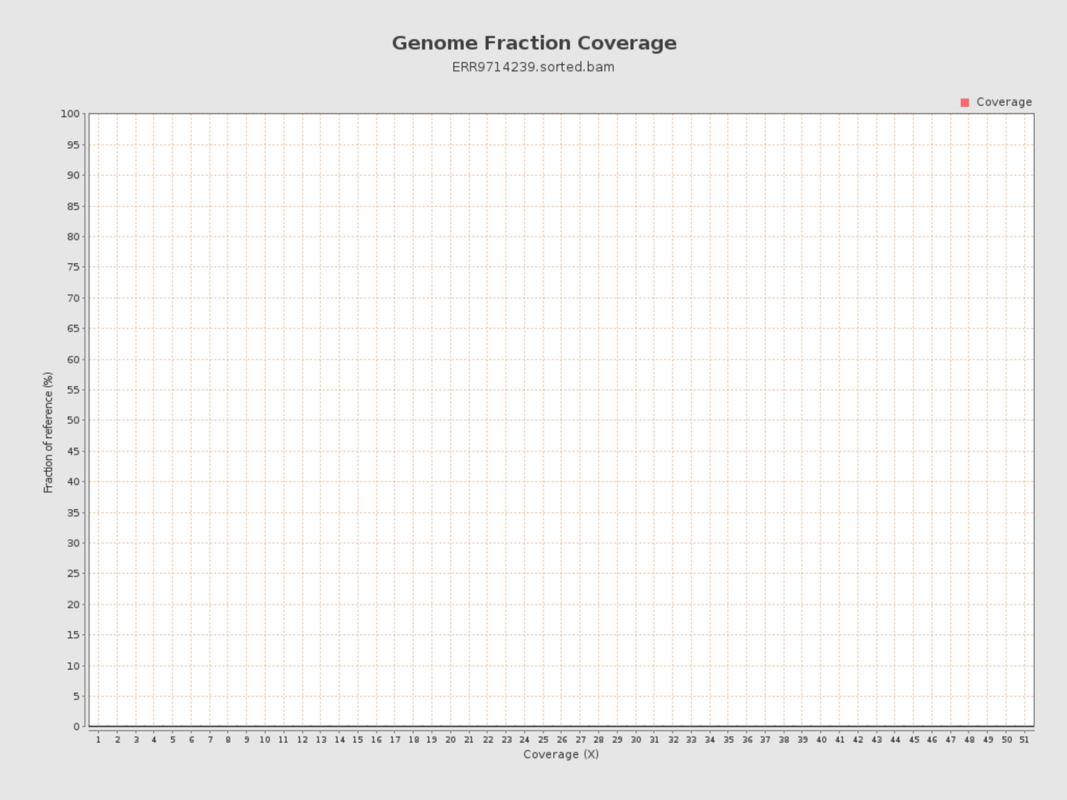
4. Results : Coverage Histogram



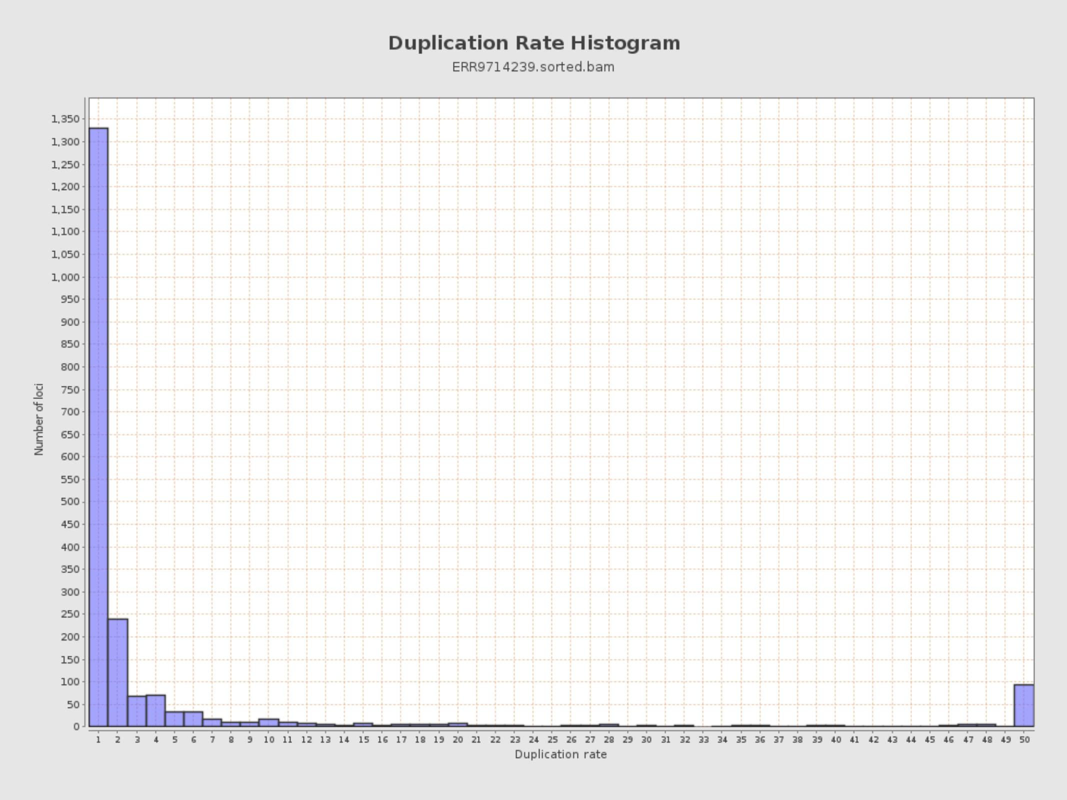
5. Results : Coverage Histogram (0-50X)



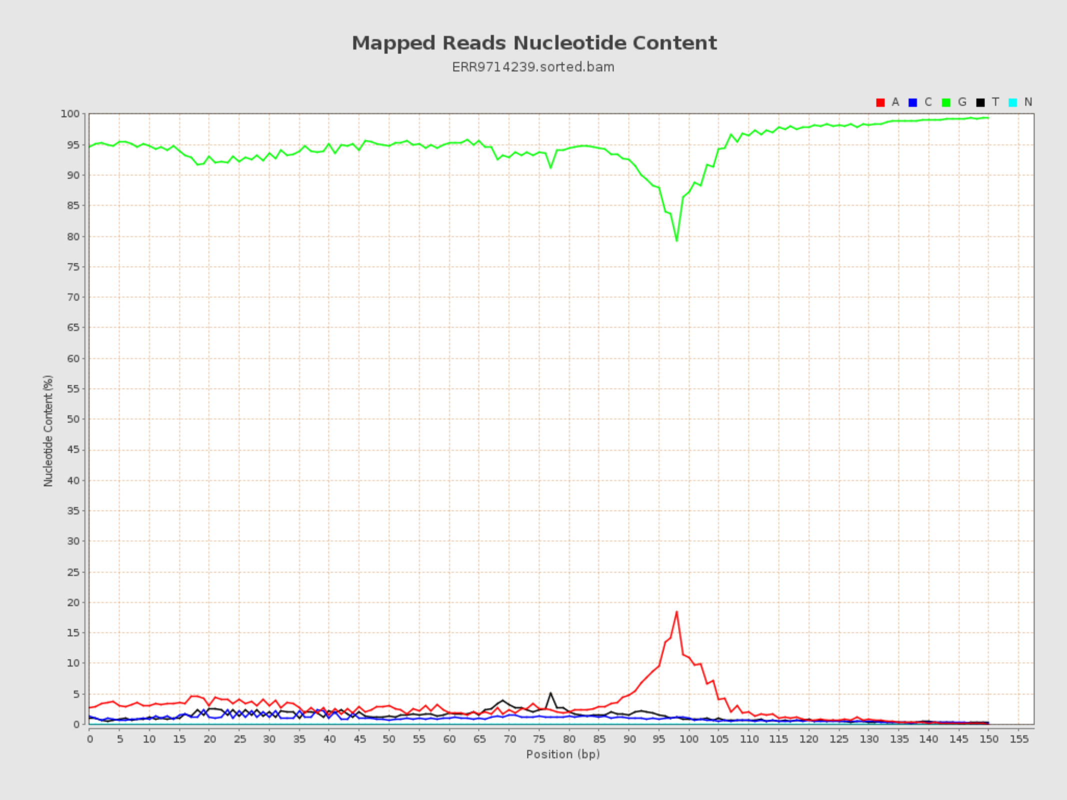
6. Results : Genome Fraction Coverage



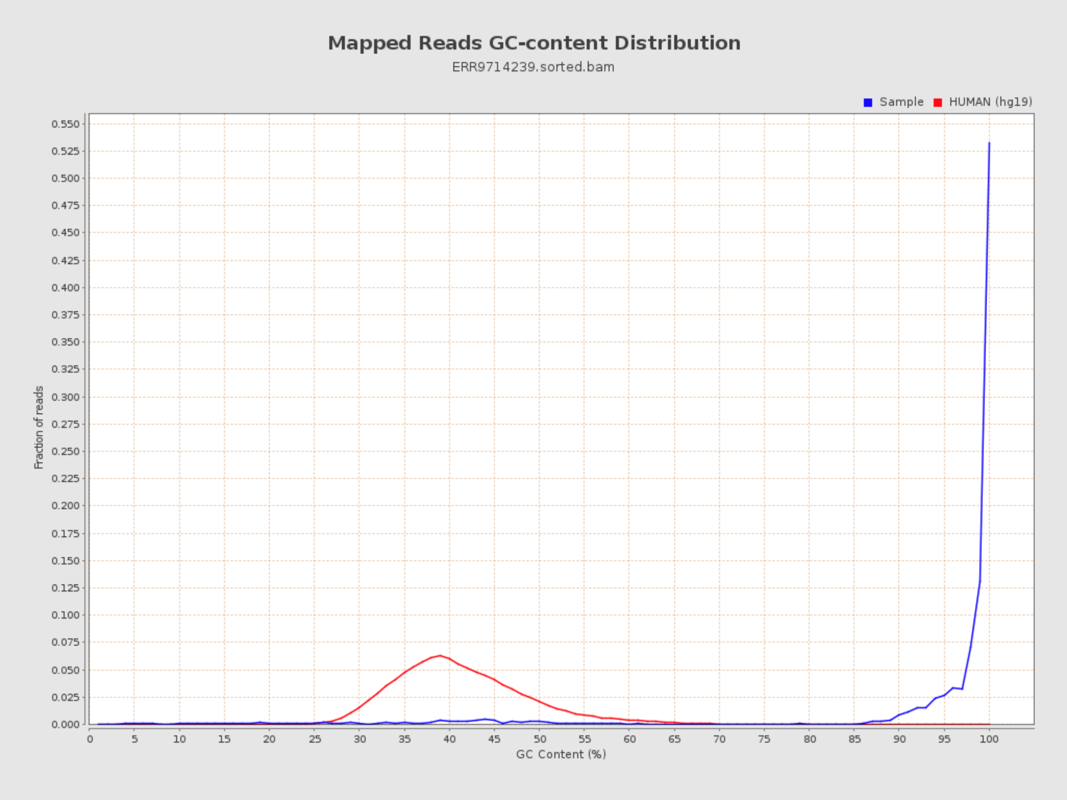
7. Results : Duplication Rate Histogram



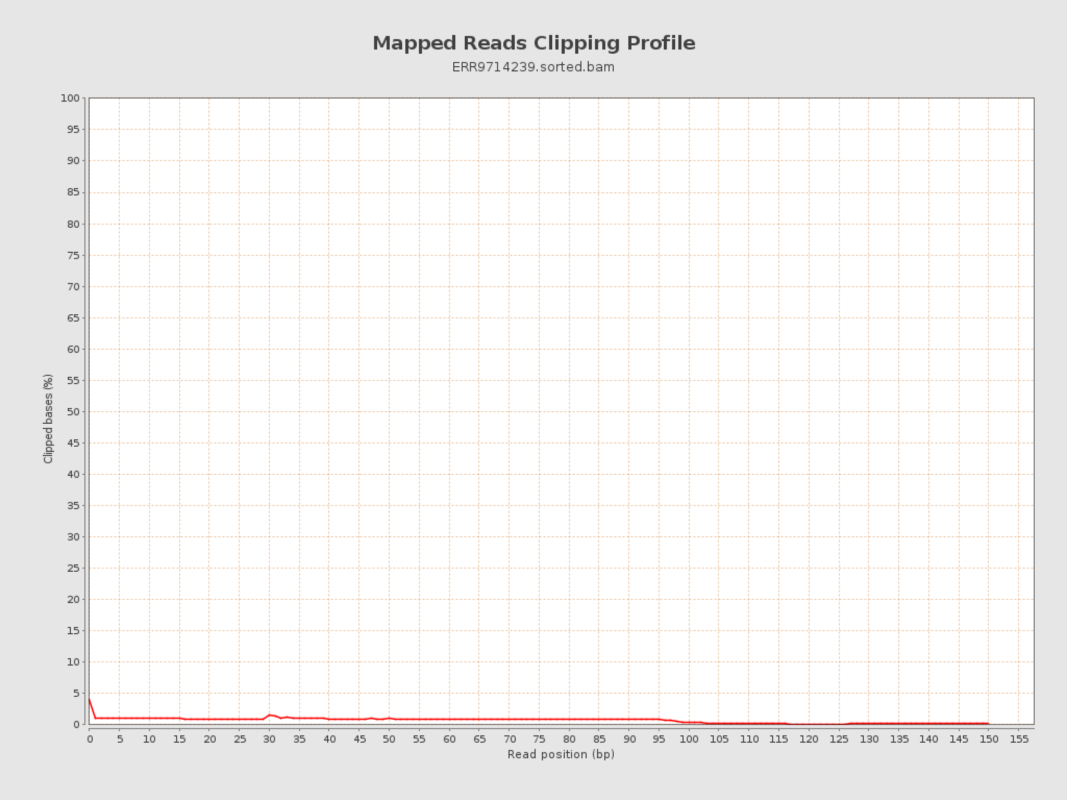
8. Results : Mapped Reads Nucleotide Content



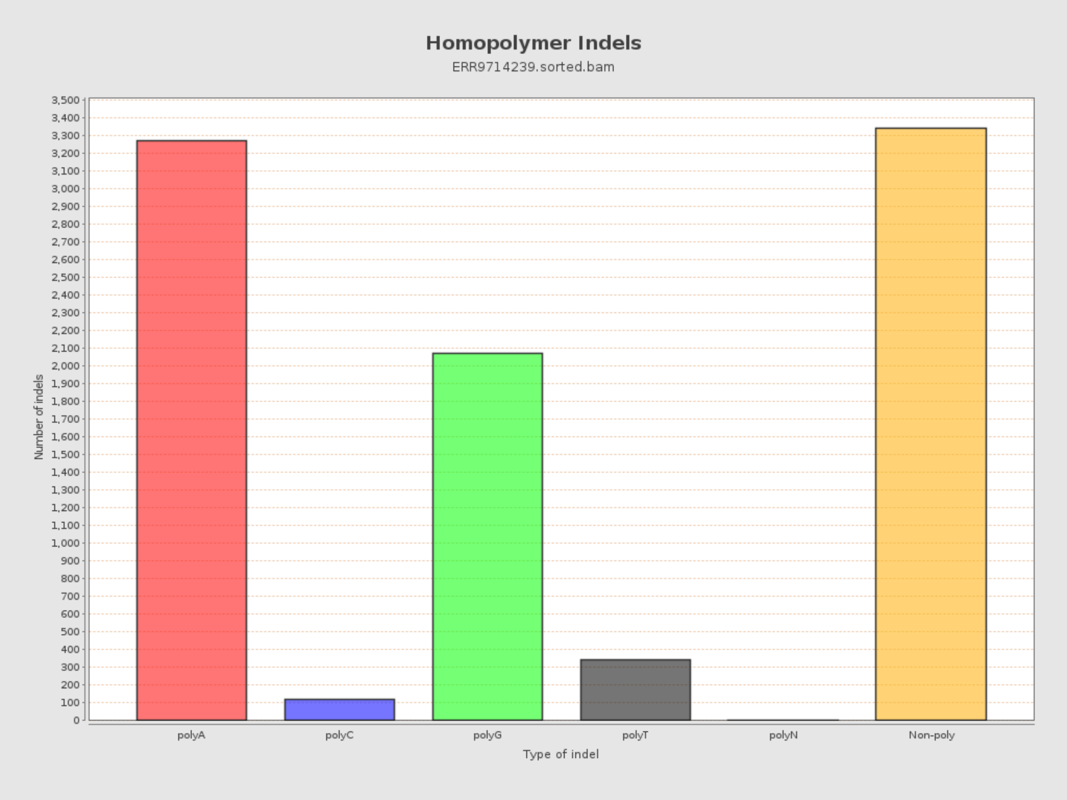
9. Results : Mapped Reads GC-content Distribution



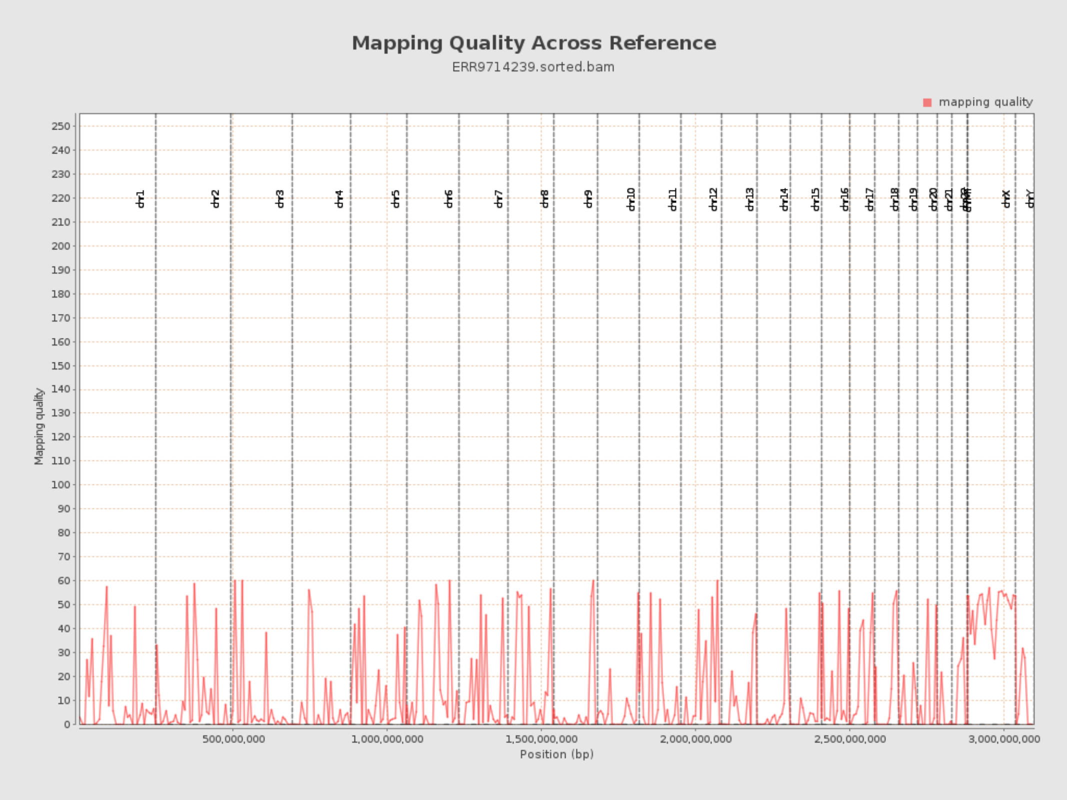
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram