Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 01:29:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714252.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_ERR9714252 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714252.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 01:29:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714252.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	395,200
Mapped reads	55,520 / 14.05%
Unmapped reads	339,680 / 85.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,505 / 0.38%
Read min/max/mean length	30 / 151 / 60.18
Duplicated reads (estimated)	54,126 / 13.7%
Duplication rate	33.98%
Clipped reads	31,719 / 8.03%

2.2. ACGT Content

Number/percentage of A's	218,085 / 3.89%
Number/percentage of C's	117,127 / 2.09%
Number/percentage of T's	148,378 / 2.65%
Number/percentage of G's	5,122,259 / 91.37%
Number/percentage of N's	129 / 0%
GC Percentage	93.46%

2.3. Coverage

Mean	0.0018

Standard Deviation	6.3766

2.4. Mapping Quality

Mean Mapping Quality	12.63

2.5. Mismatches and indels

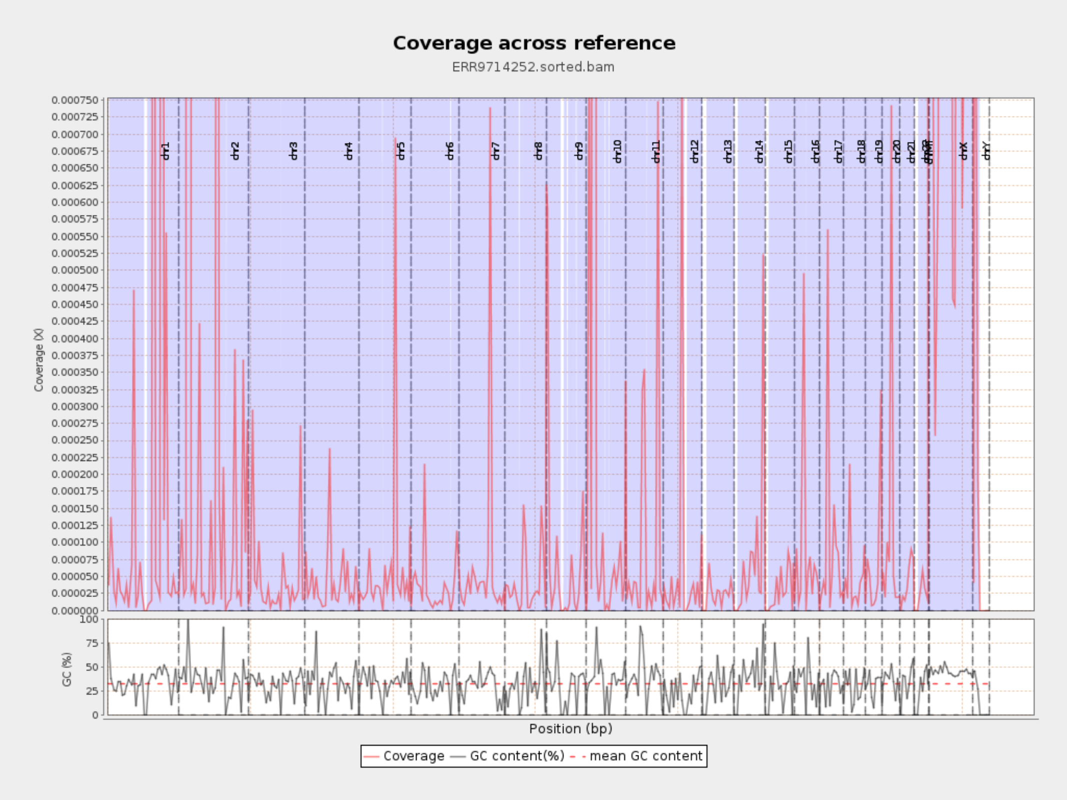
General error rate	3.47%
Mismatches	147,380
Insertions	6,882
Mapped reads with at least one insertion	8.33%
Deletions	3,846
Mapped reads with at least one deletion	6.59%
Homopolymer indels	57.99%

2.6. Chromosome stats

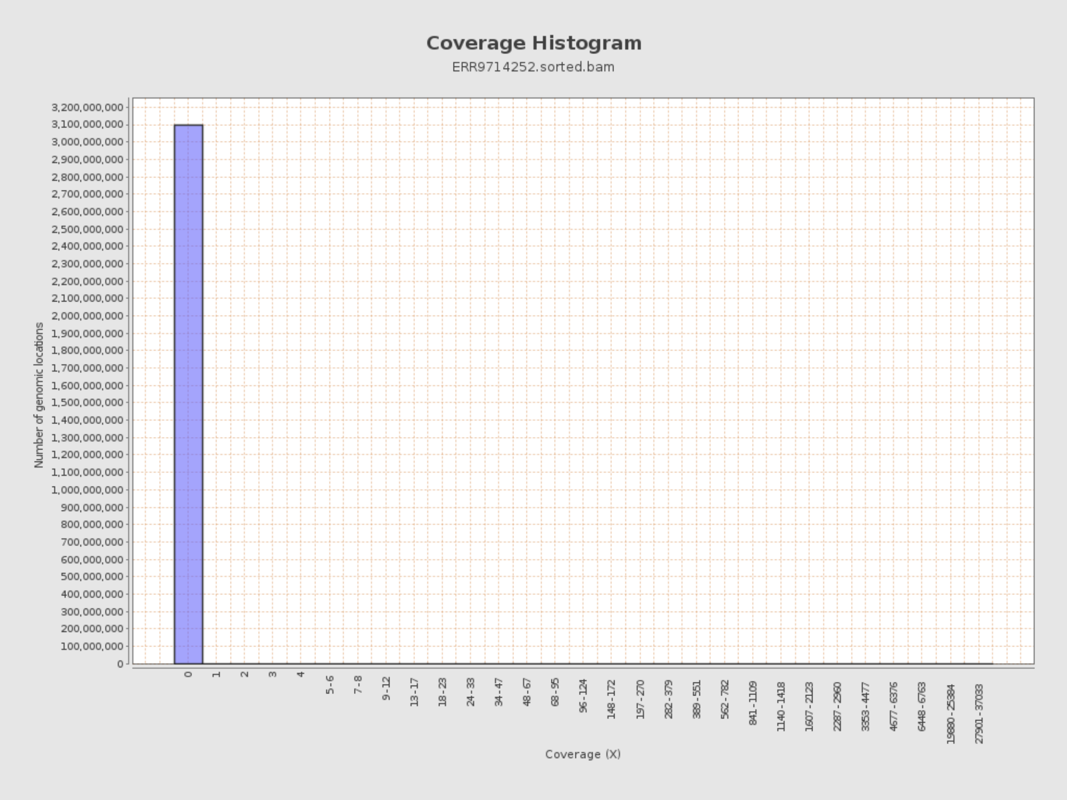
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	69704	0.0003	0.4632
chr2	243199373	5098861	0.021	22.74
chr3	198022430	9394	0	0.0198
chr4	191154276	8393	0	0.0154
chr5	180915260	11563	0.0001	0.0347
chr6	171115067	6334	0	0.0144
chr7	159138663	10616	0.0001	0.0752

chr8	146364022	6219	0	0.017
chr9	141213431	10289	0.0001	0.0377
chr10	135534747	48621	0.0004	0.5794
chr11	135006516	14302	0.0001	0.0479
chr12	133851895	9004	0.0001	0.0561
chr13	115169878	2620	0	0.0071
chr14	107349540	8384	0.0001	0.0674
chr15	102531392	2891	0	0.0109
chr16	90354753	7379	0.0001	0.0246
chr17	81195210	8251	0.0001	0.078
chr18	78077248	3835	0	0.0268
chr19	59128983	4172	0.0001	0.0278
chr20	63025520	8305	0.0001	0.0394
chr21	48129895	2098	0	0.01
chr22	51304566	1144	0	0.0061
chrMT	16571	3524	0.2127	0.9255
chrX	155270560	257798	0.0017	0.2448
chrY	59373566	12241	0.0002	0.066

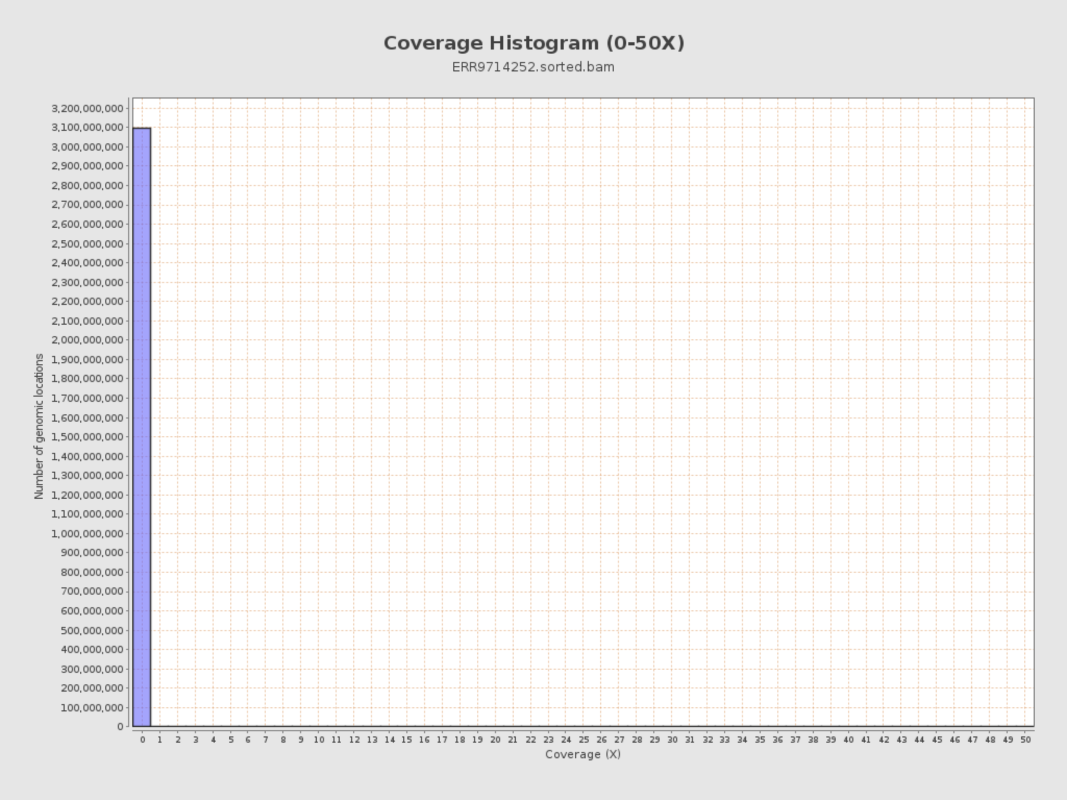
3. Results : Coverage across reference



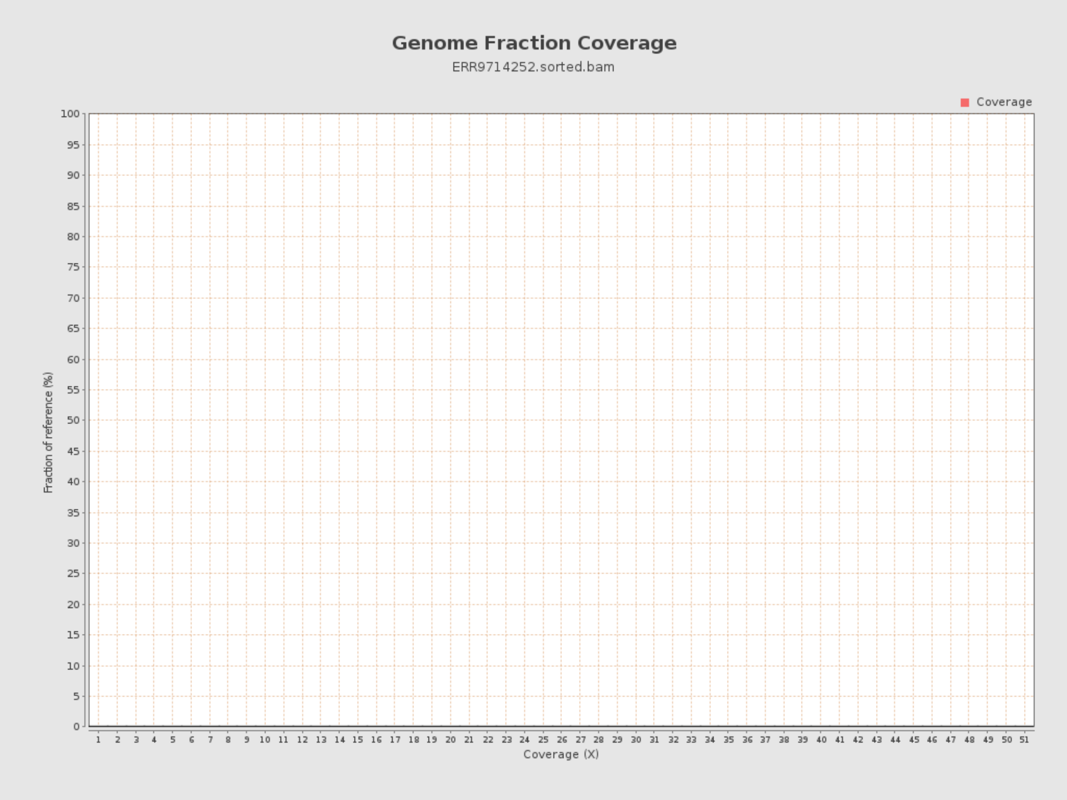
4. Results : Coverage Histogram



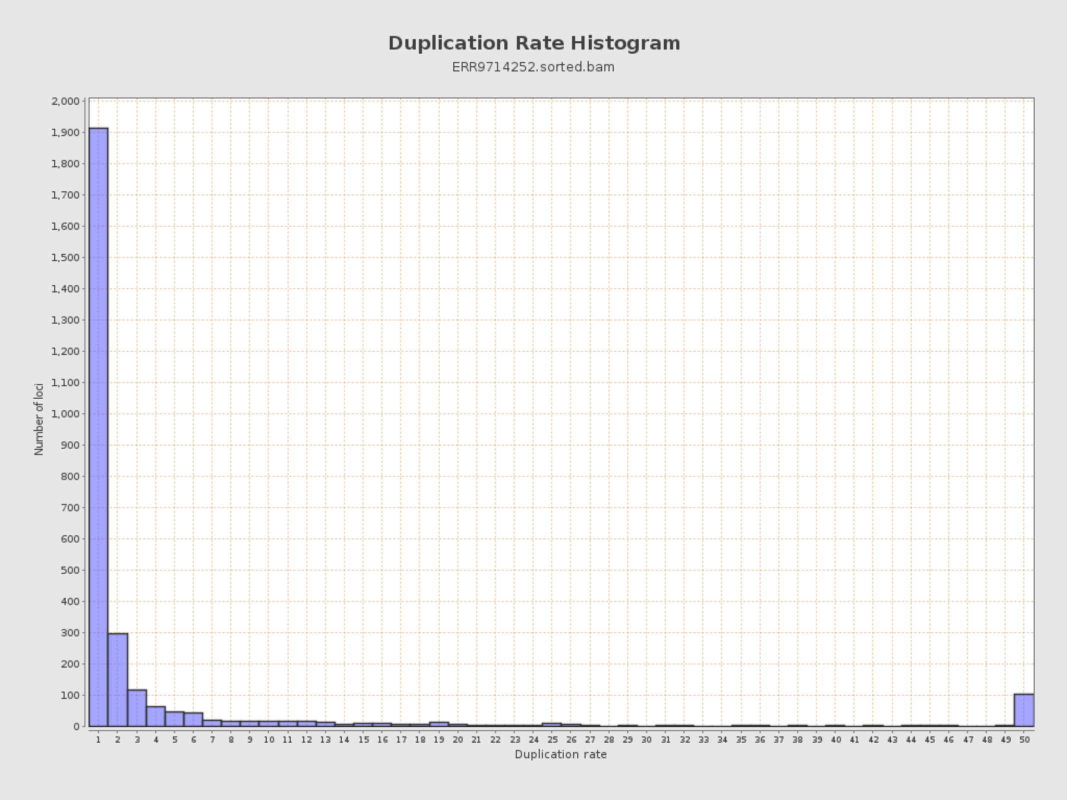
5. Results : Coverage Histogram (0-50X)



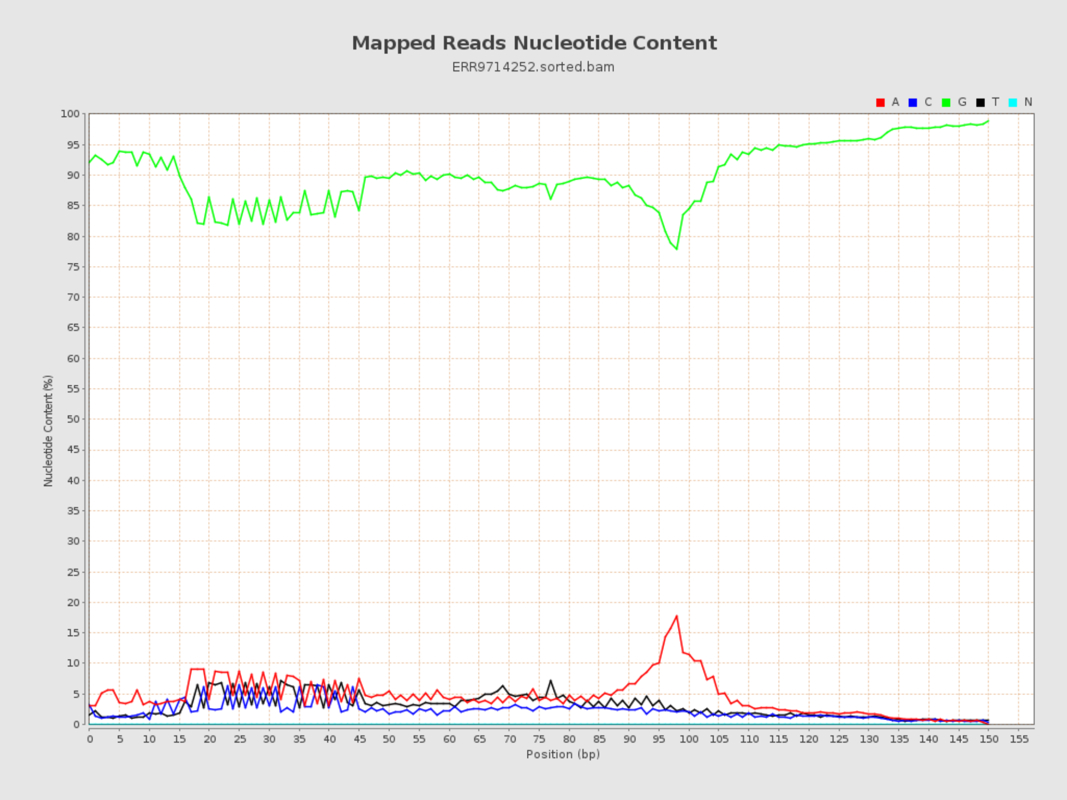
6. Results : Genome Fraction Coverage



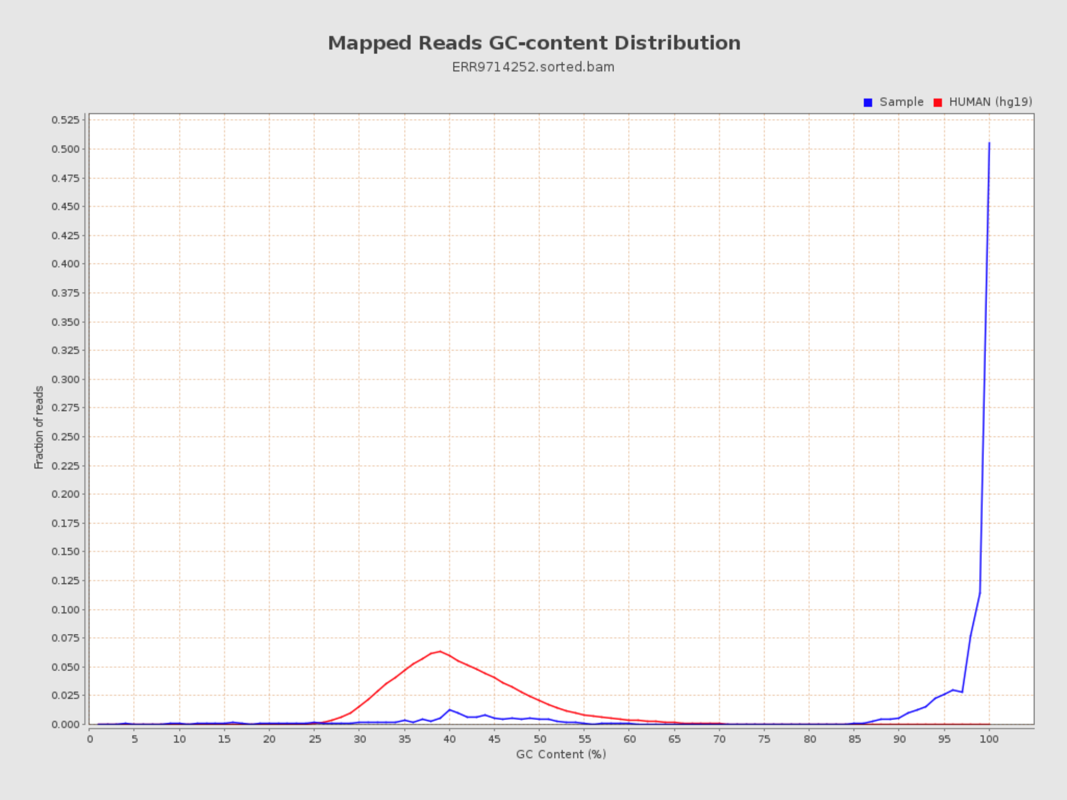
7. Results : Duplication Rate Histogram



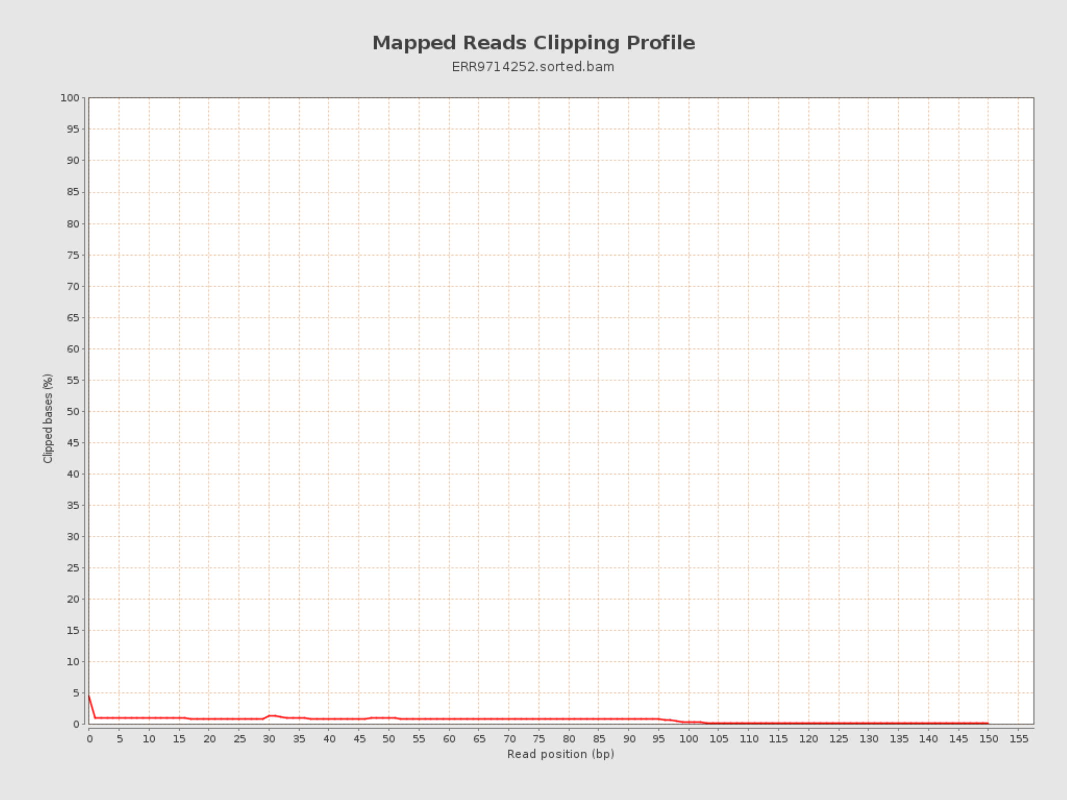
8. Results : Mapped Reads Nucleotide Content



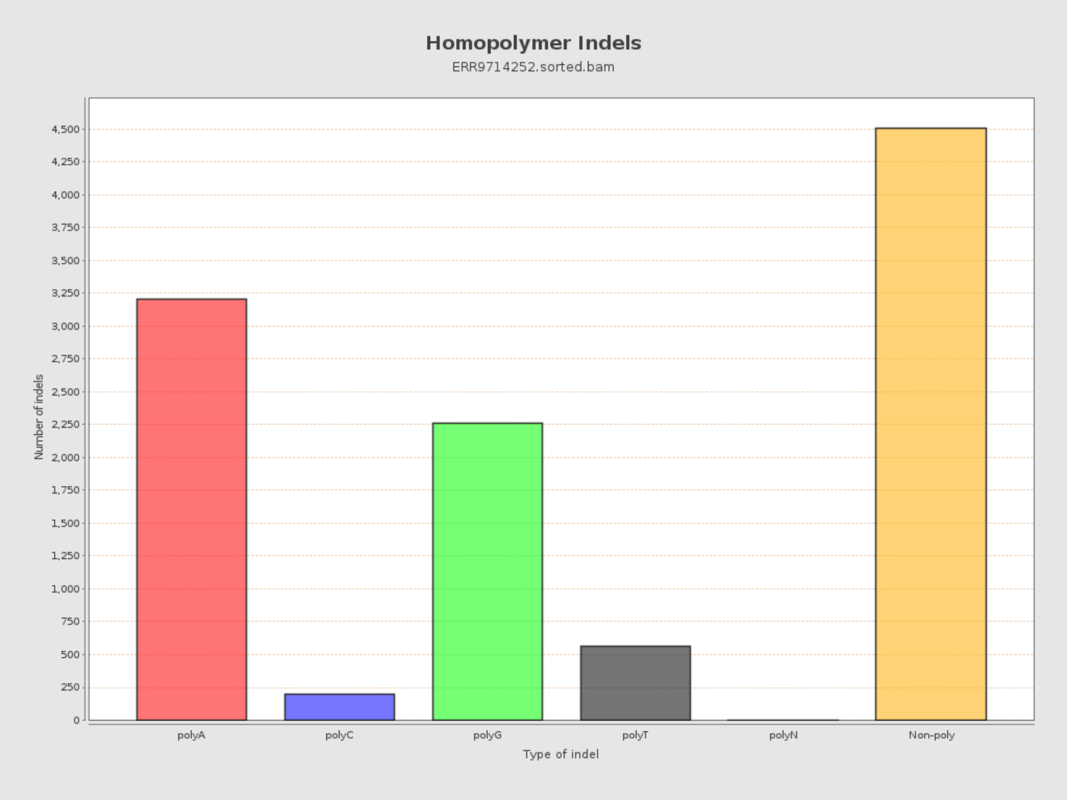
9. Results : Mapped Reads GC-content Distribution



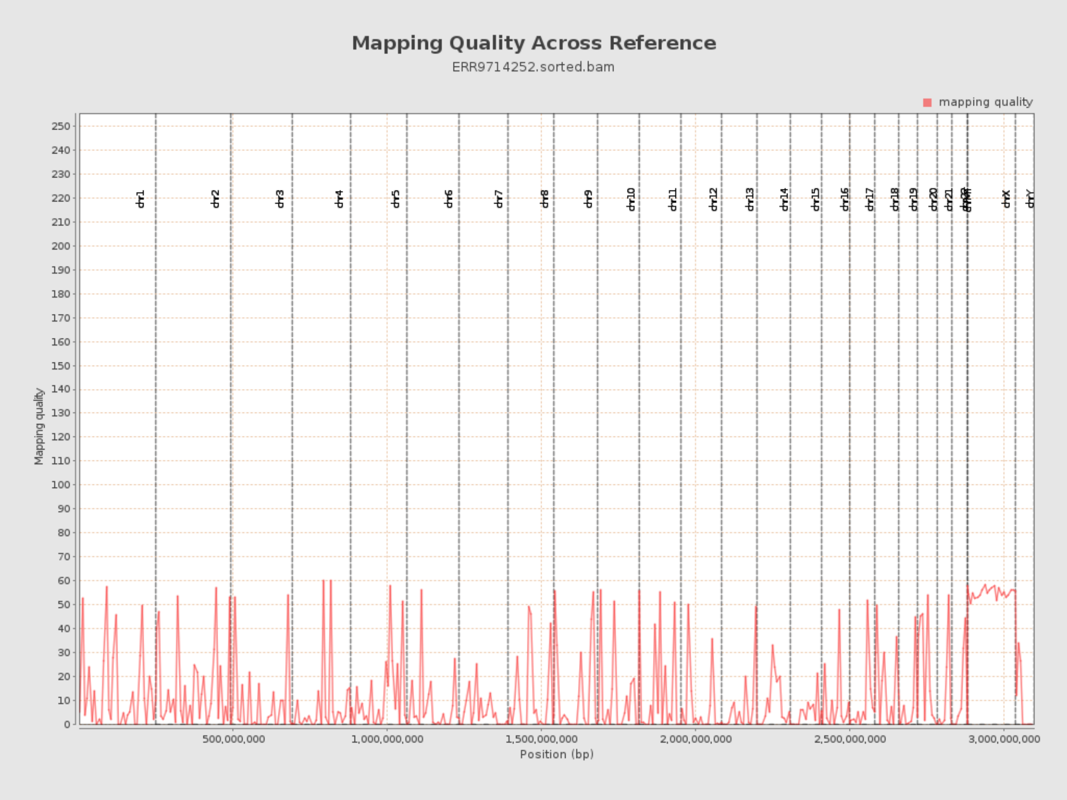
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram