Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 00:25:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714216.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_ERR9714216 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714216.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 00:25:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714216.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	157,346
Mapped reads	25,009 / 15.89%
Unmapped reads	132,337 / 84.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	631 / 0.4%
Read min/max/mean length	30 / 151 / 70.44
Duplicated reads (estimated)	22,526 / 14.32%
Duplication rate	38.73%
Clipped reads	19,292 / 12.26%

2.2. ACGT Content

Number/percentage of A's	463,048 / 17.17%
Number/percentage of C's	295,629 / 10.96%
Number/percentage of T's	396,557 / 14.71%
Number/percentage of G's	1,540,843 / 57.15%
Number/percentage of N's	117 / 0%
GC Percentage	68.11%

2.3. Coverage

Mean	0.0009

Standard Deviation	1.7821

2.4. Mapping Quality

Mean Mapping Quality	28.29

2.5. Mismatches and indels

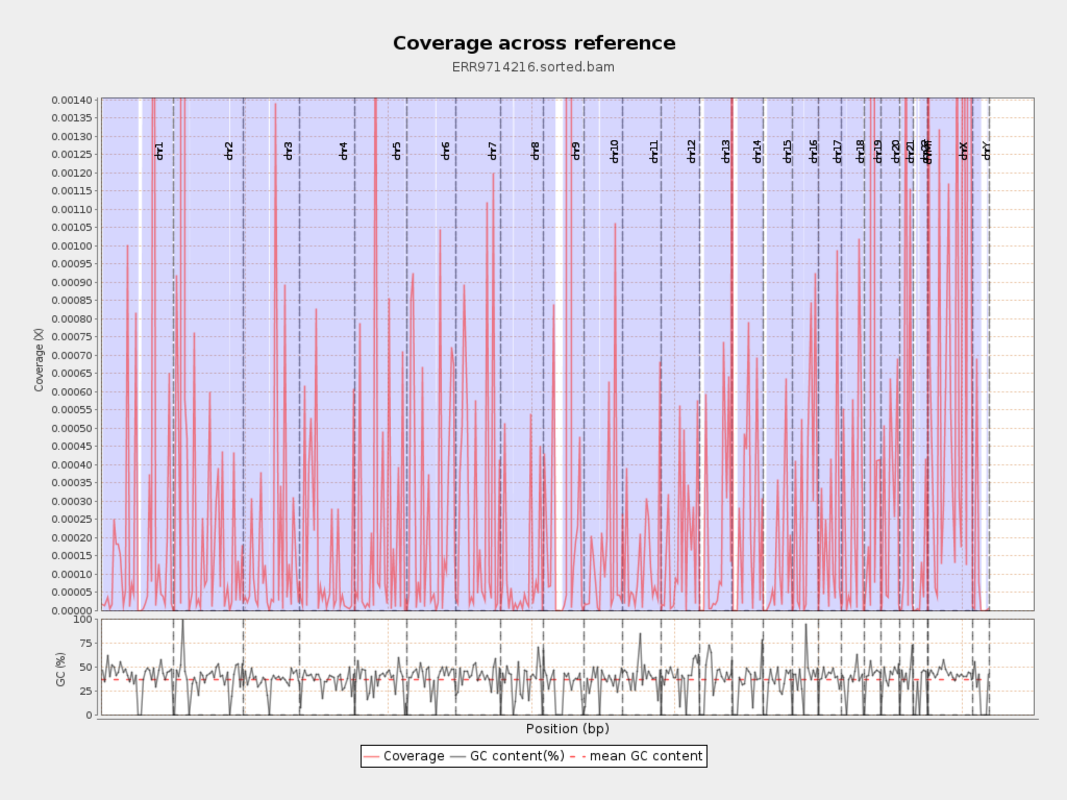
General error rate	3.66%
Mismatches	84,295
Insertions	3,385
Mapped reads with at least one insertion	11.51%
Deletions	4,687
Mapped reads with at least one deletion	18.1%
Homopolymer indels	26.83%

2.6. Chromosome stats

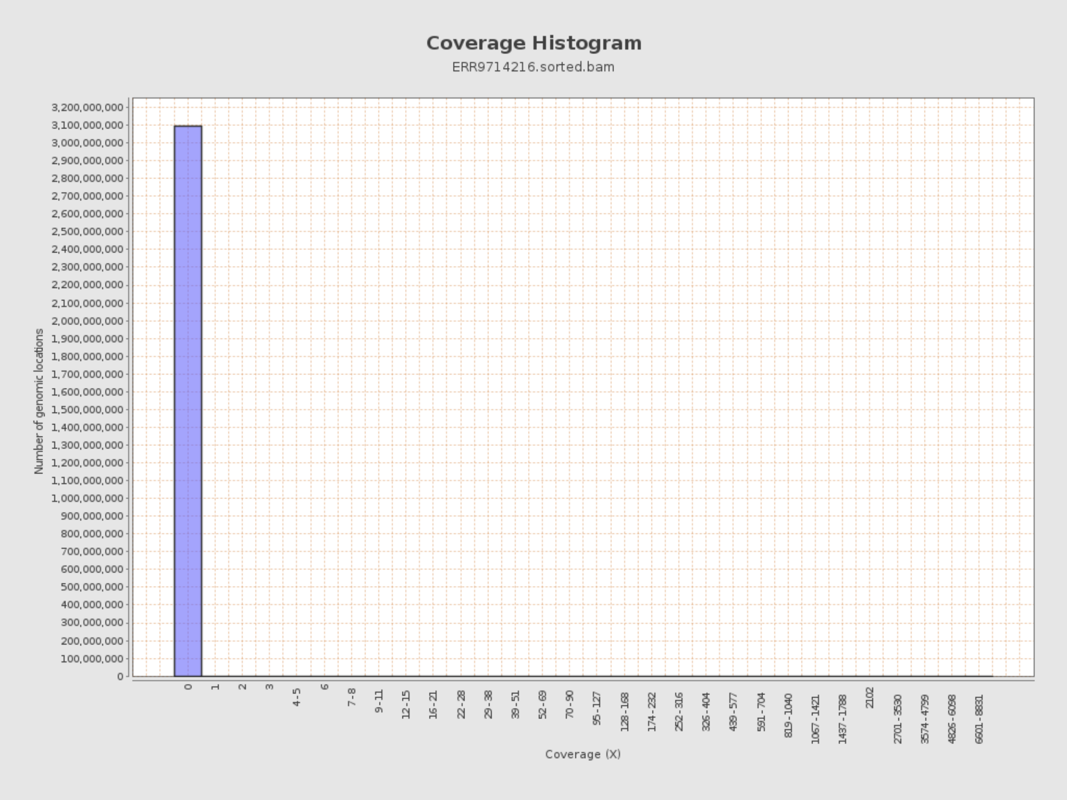
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	58009	0.0002	0.1334
chr2	243199373	1271790	0.0052	5.4554
chr3	198022430	34775	0.0002	0.0658
chr4	191154276	31746	0.0002	0.0622
chr5	180915260	46034	0.0003	0.0815
chr6	171115067	49416	0.0003	0.0828
chr7	159138663	47695	0.0003	0.0991

chr8	146364022	15380	0.0001	0.0438
chr9	141213431	623149	0.0044	4.1697
chr10	135534747	21895	0.0002	0.0542
chr11	135006516	19852	0.0001	0.044
chr12	133851895	25592	0.0002	0.0607
chr13	115169878	26761	0.0002	0.0757
chr14	107349540	27007	0.0003	0.0832
chr15	102531392	14016	0.0001	0.0373
chr16	90354753	29598	0.0003	0.0841
chr17	81195210	17920	0.0002	0.067
chr18	78077248	23374	0.0003	0.0821
chr19	59128983	149138	0.0025	1.4171
chr20	63025520	20230	0.0003	0.0768
chr21	48129895	24216	0.0005	0.189
chr22	51304566	4554	0.0001	0.0264
chrMT	16571	4912	0.2964	2.7636
chrX	155270560	129691	0.0008	0.1464
chrY	59373566	6047	0.0001	0.0508

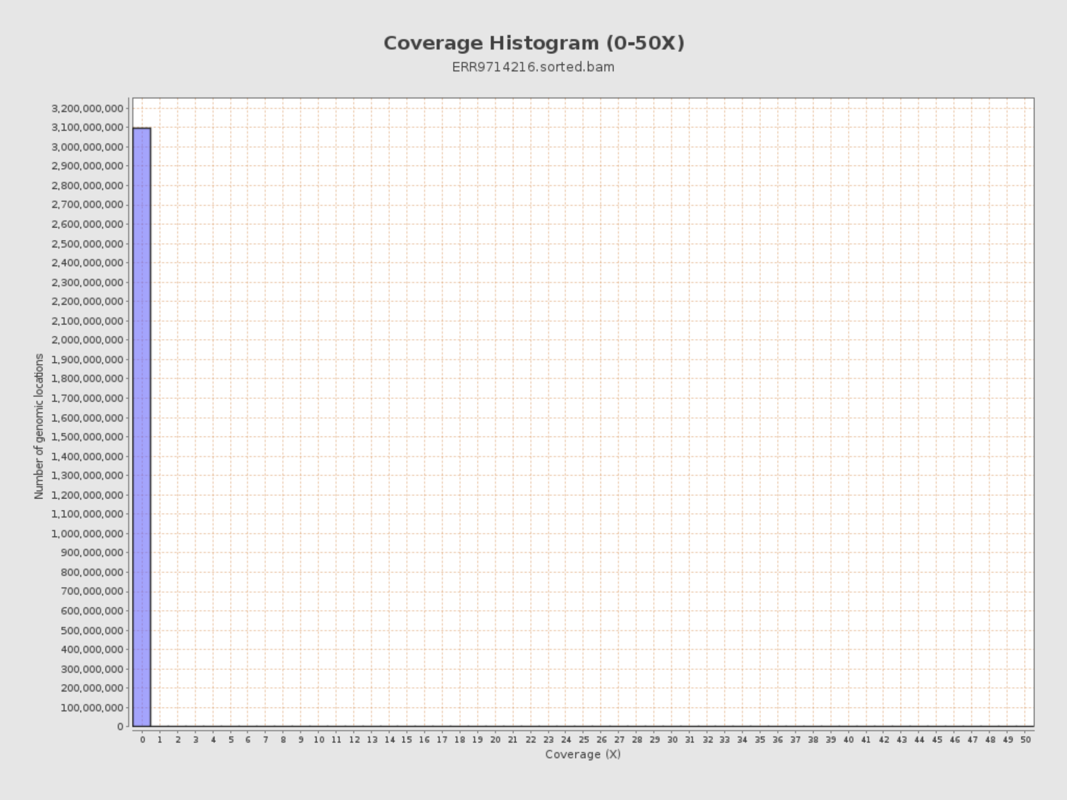
3. Results : Coverage across reference



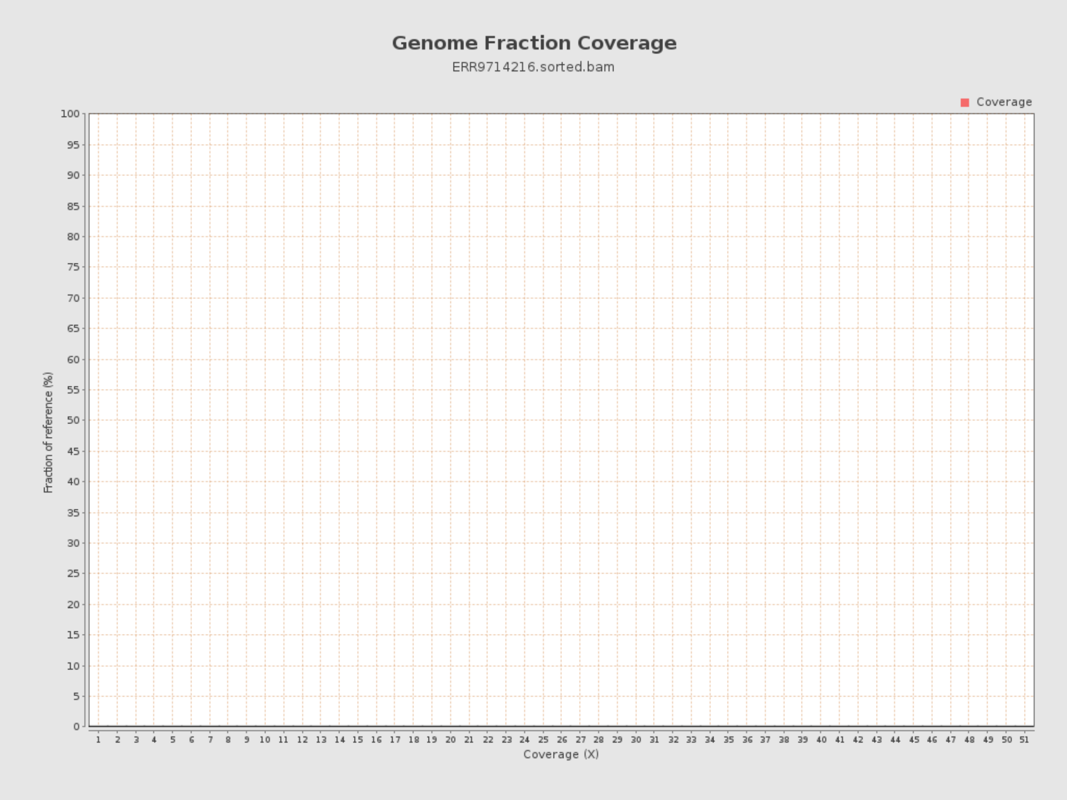
4. Results : Coverage Histogram



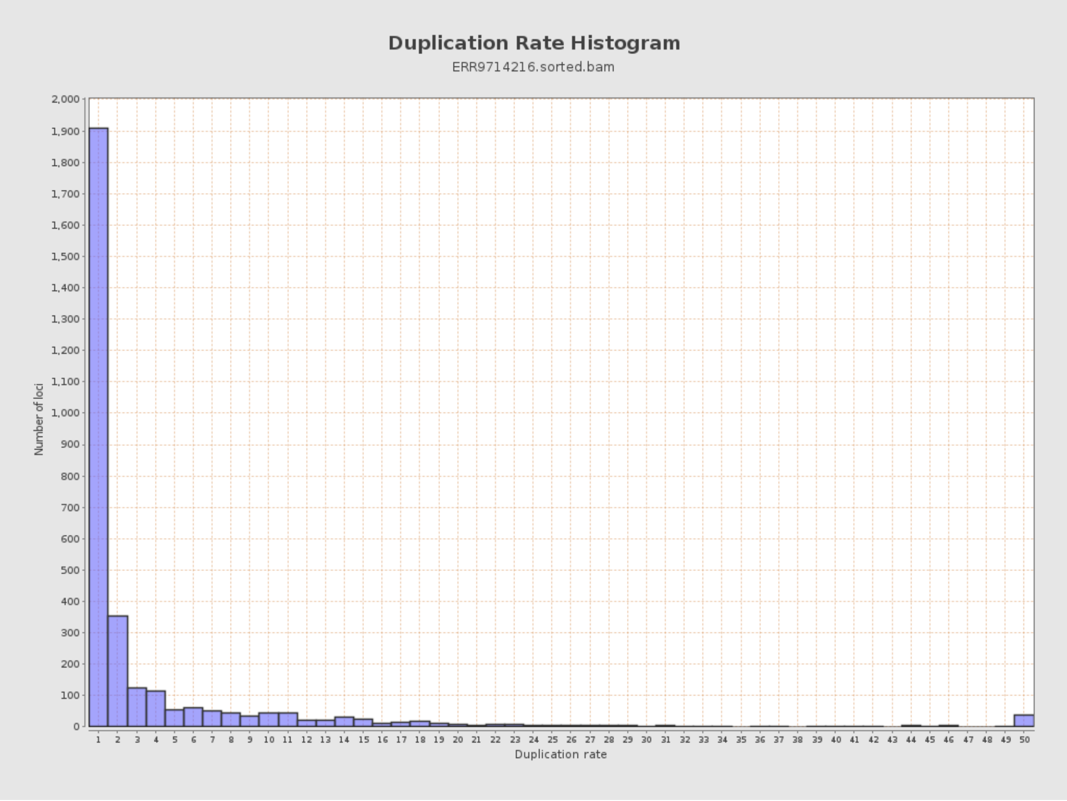
5. Results : Coverage Histogram (0-50X)



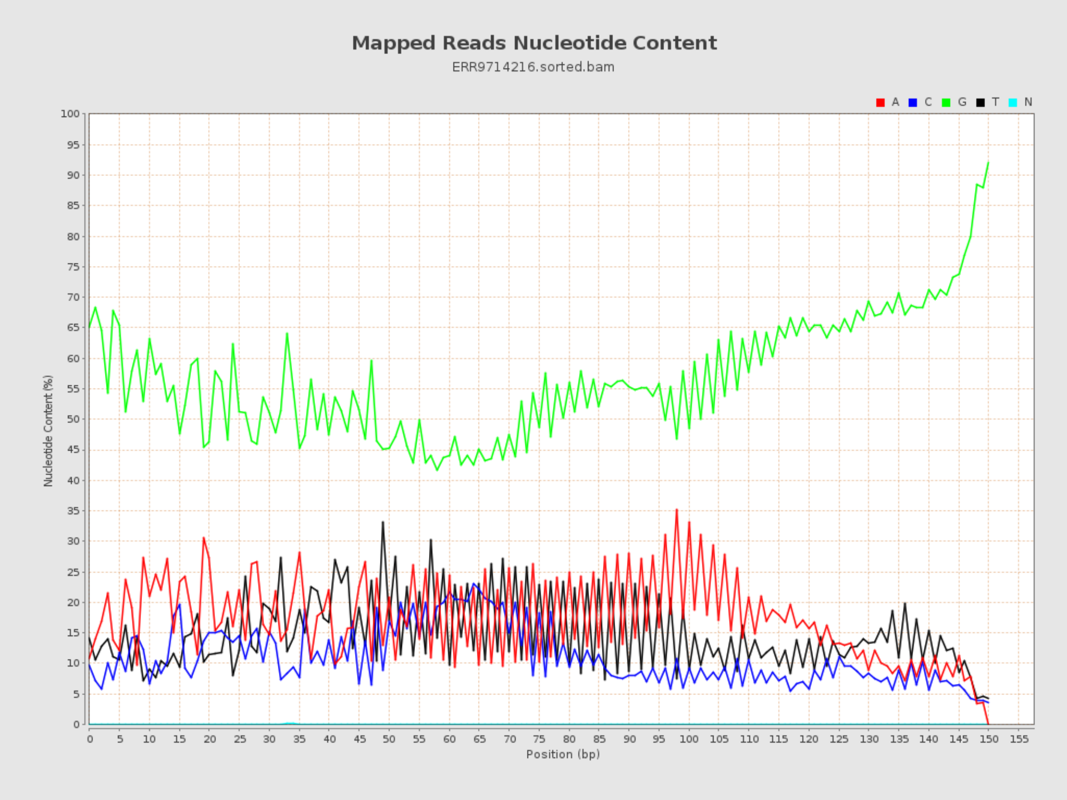
6. Results : Genome Fraction Coverage



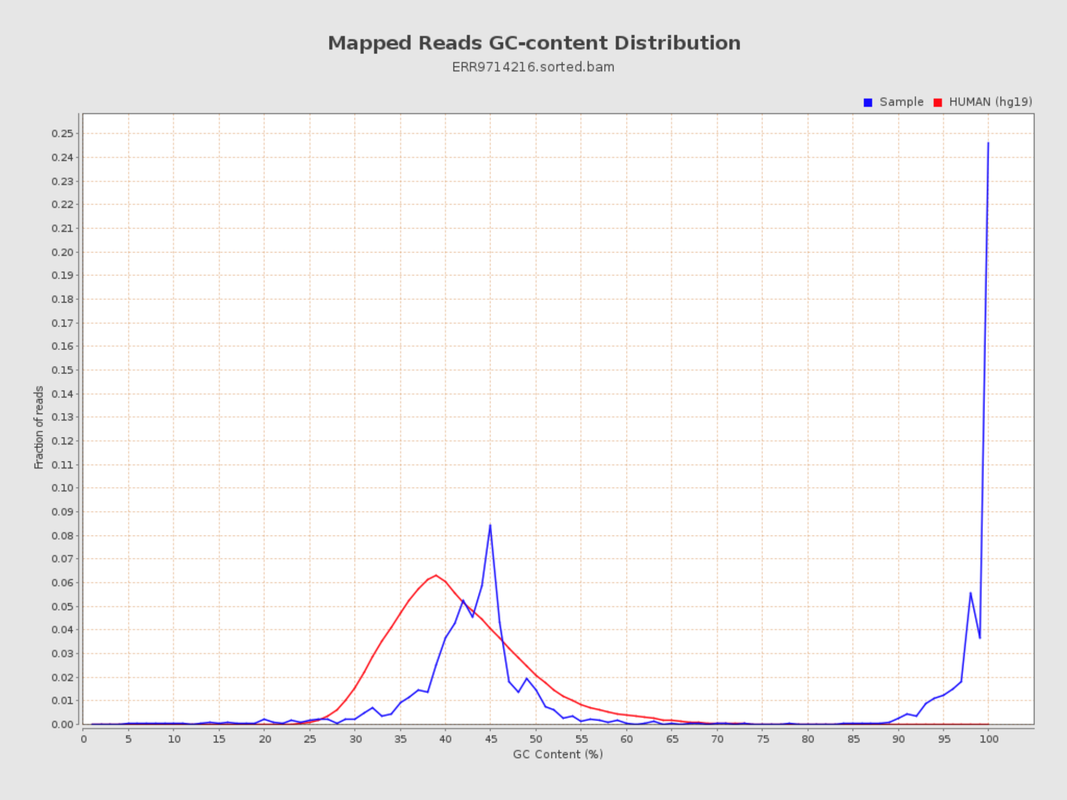
7. Results : Duplication Rate Histogram



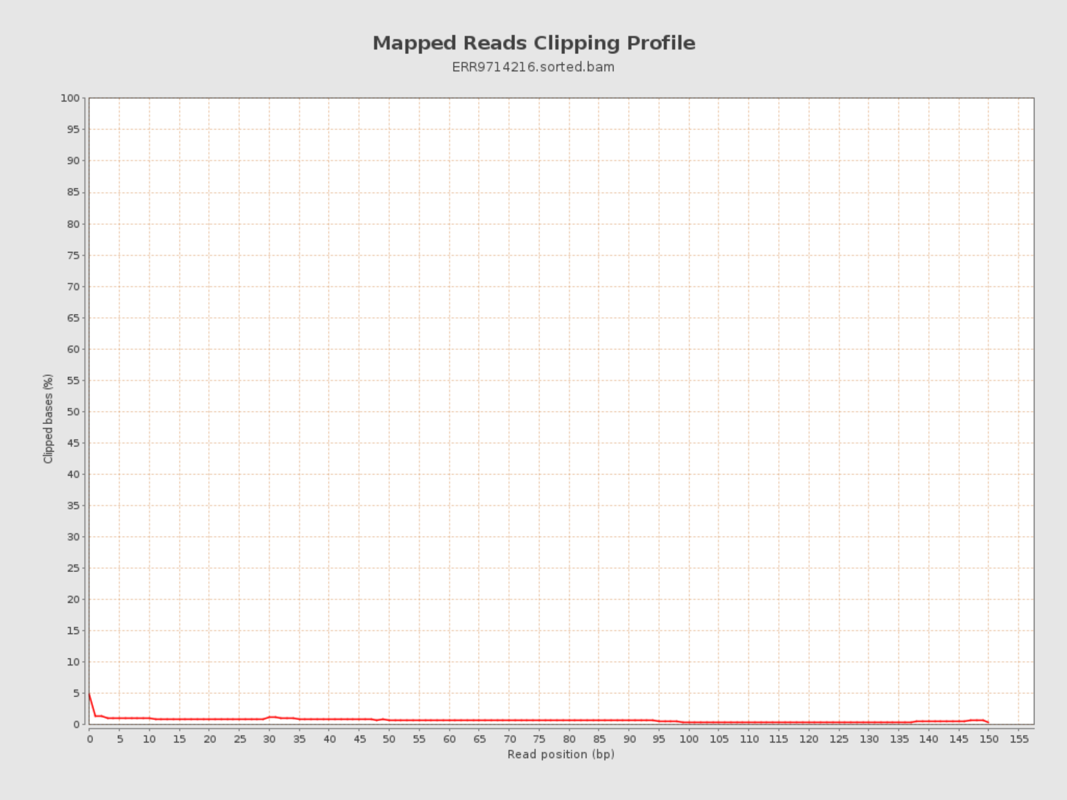
8. Results : Mapped Reads Nucleotide Content



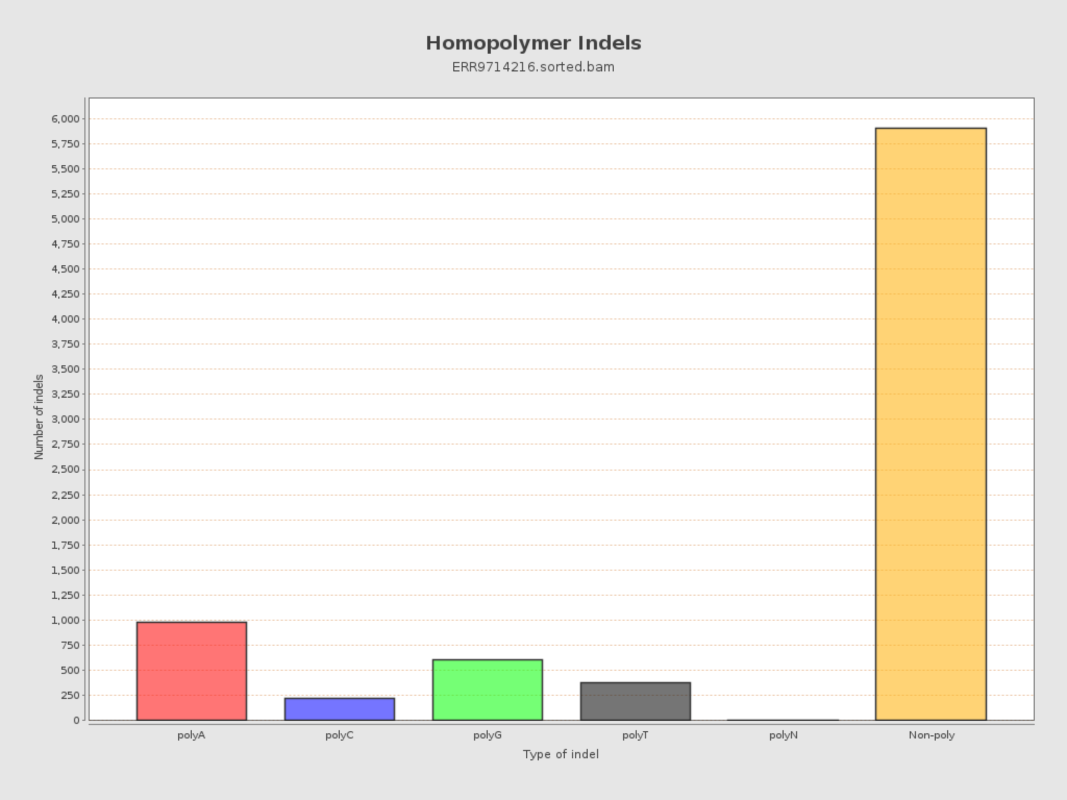
9. Results : Mapped Reads GC-content Distribution



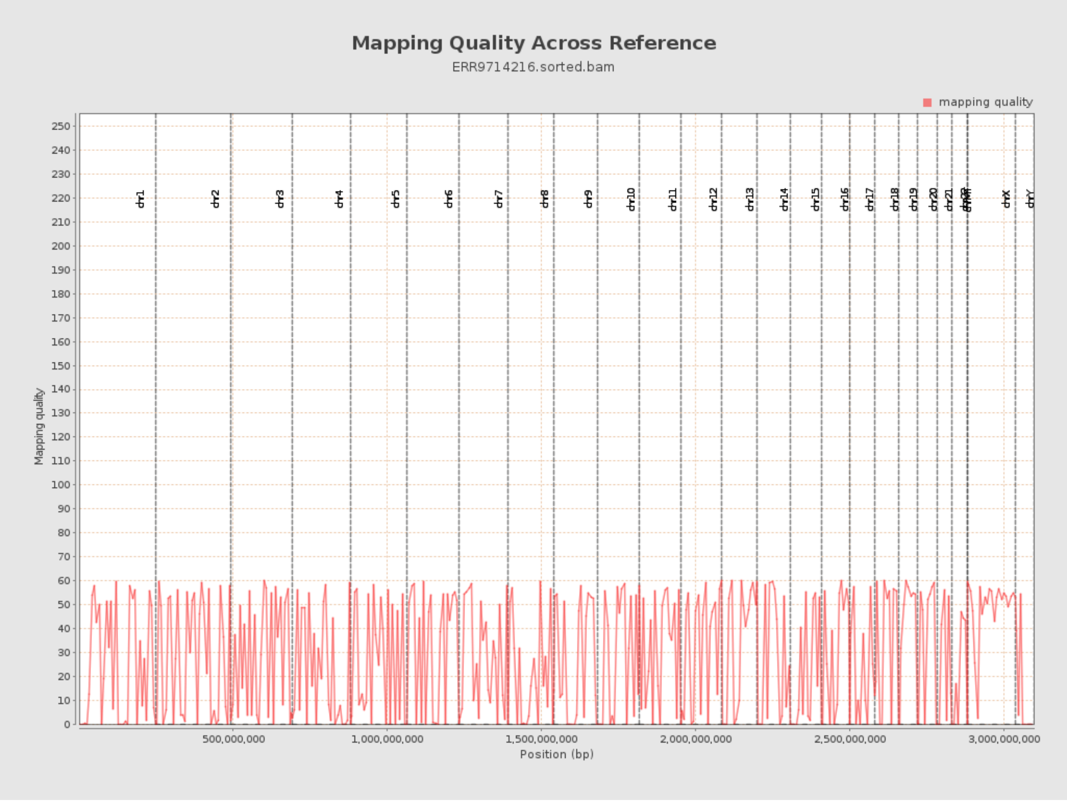
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram