Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 00:00:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714199.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_ERR9714199 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714199.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 00:00:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714199.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	117,584
Mapped reads	8,290 / 7.05%
Unmapped reads	109,294 / 92.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	245 / 0.21%
Read min/max/mean length	30 / 151 / 56.76
Duplicated reads (estimated)	6,735 / 5.73%
Duplication rate	35.67%
Clipped reads	7,158 / 6.09%

2.2. ACGT Content

Number/percentage of A's	123,961 / 16.64%
Number/percentage of C's	84,395 / 11.33%
Number/percentage of T's	109,138 / 14.65%
Number/percentage of G's	427,511 / 57.38%
Number/percentage of N's	39 / 0.01%
GC Percentage	68.71%

2.3. Coverage

Mean	0.0002

Standard Deviation	0.4036

2.4. Mapping Quality

Mean Mapping Quality	22.72

2.5. Mismatches and indels

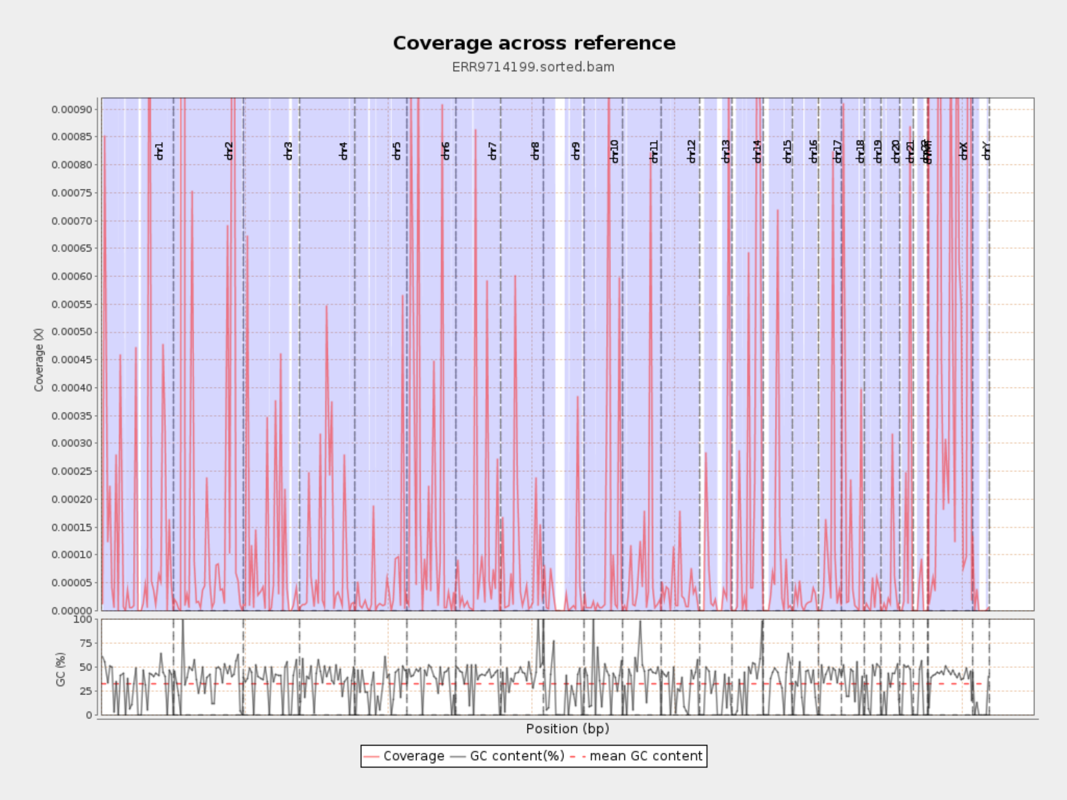
General error rate	3.61%
Mismatches	23,240
Insertions	797
Mapped reads with at least one insertion	7.79%
Deletions	1,399
Mapped reads with at least one deletion	16.42%
Homopolymer indels	35.84%

2.6. Chromosome stats

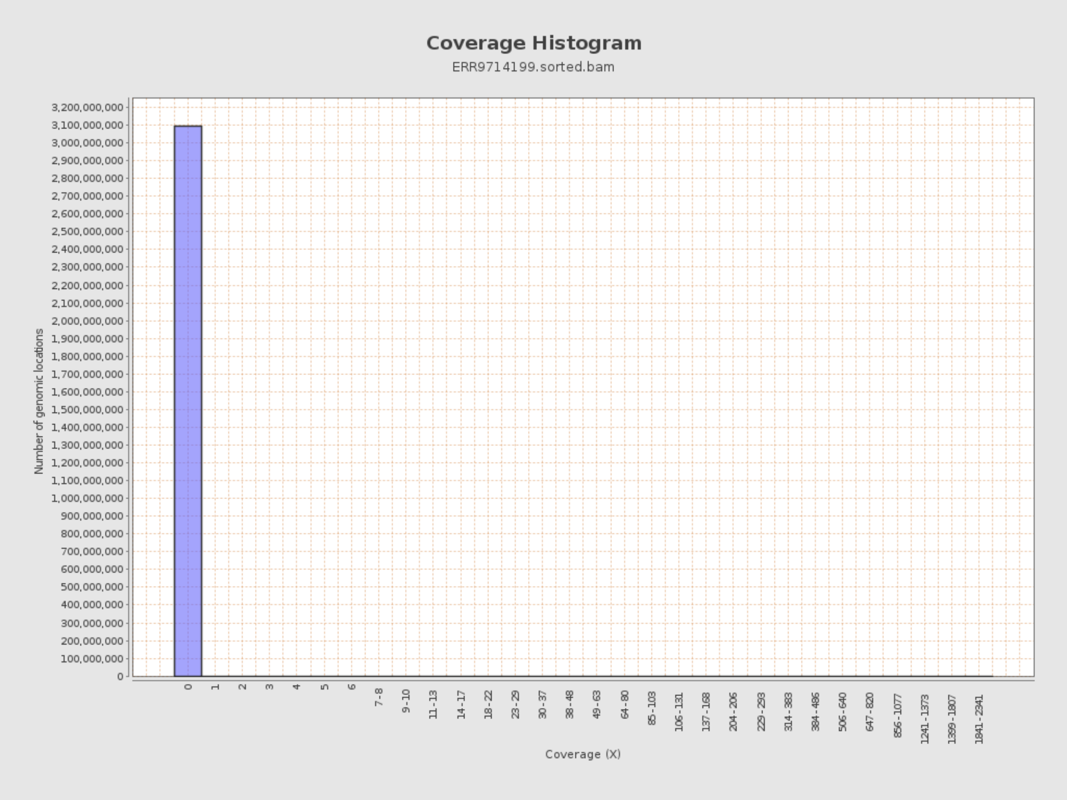
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	41073	0.0002	0.0702
chr2	243199373	381941	0.0016	1.4265
chr3	198022430	20429	0.0001	0.0398
chr4	191154276	18356	0.0001	0.0383
chr5	180915260	9415	0.0001	0.0285
chr6	171115067	37152	0.0002	0.0757
chr7	159138663	17740	0.0001	0.0706

chr8	146364022	12829	0.0001	0.0352
chr9	141213431	5222	0	0.0184
chr10	135534747	17312	0.0001	0.065
chr11	135006516	11605	0.0001	0.038
chr12	133851895	5289	0	0.0108
chr13	115169878	11205	0.0001	0.0586
chr14	107349540	25621	0.0002	0.0932
chr15	102531392	8727	0.0001	0.0415
chr16	90354753	1809	0	0.0061
chr17	81195210	9783	0.0001	0.0611
chr18	78077248	14425	0.0002	0.0713
chr19	59128983	1371	0	0.007
chr20	63025520	3352	0.0001	0.025
chr21	48129895	8875	0.0002	0.0792
chr22	51304566	1145	0	0.0075
chrMT	16571	4799	0.2896	2.4658
chrX	155270560	84268	0.0005	0.1117
chrY	59373566	1031	0	0.0071

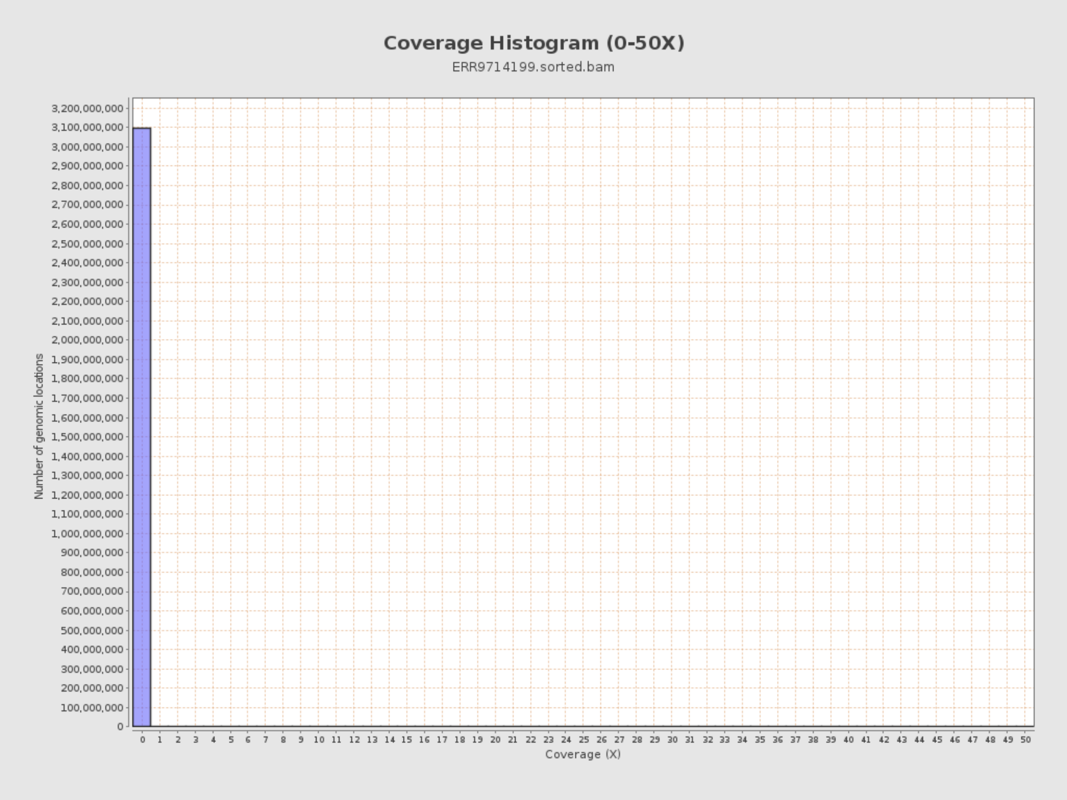
3. Results : Coverage across reference



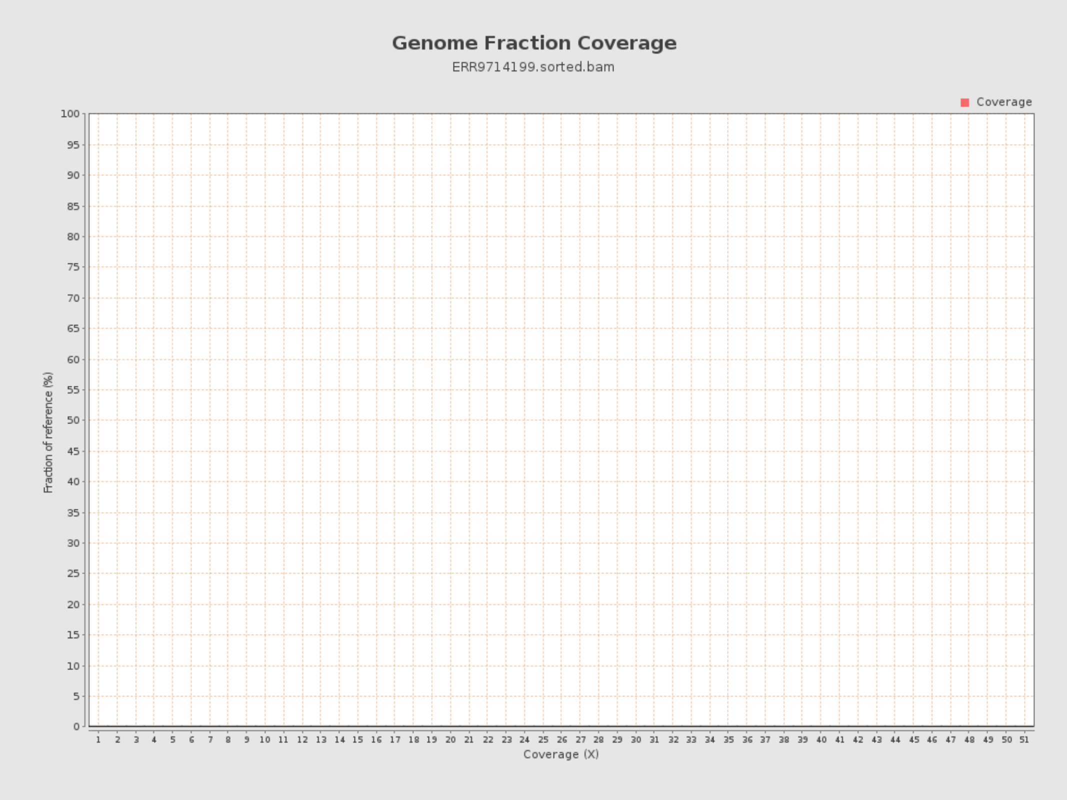
4. Results : Coverage Histogram



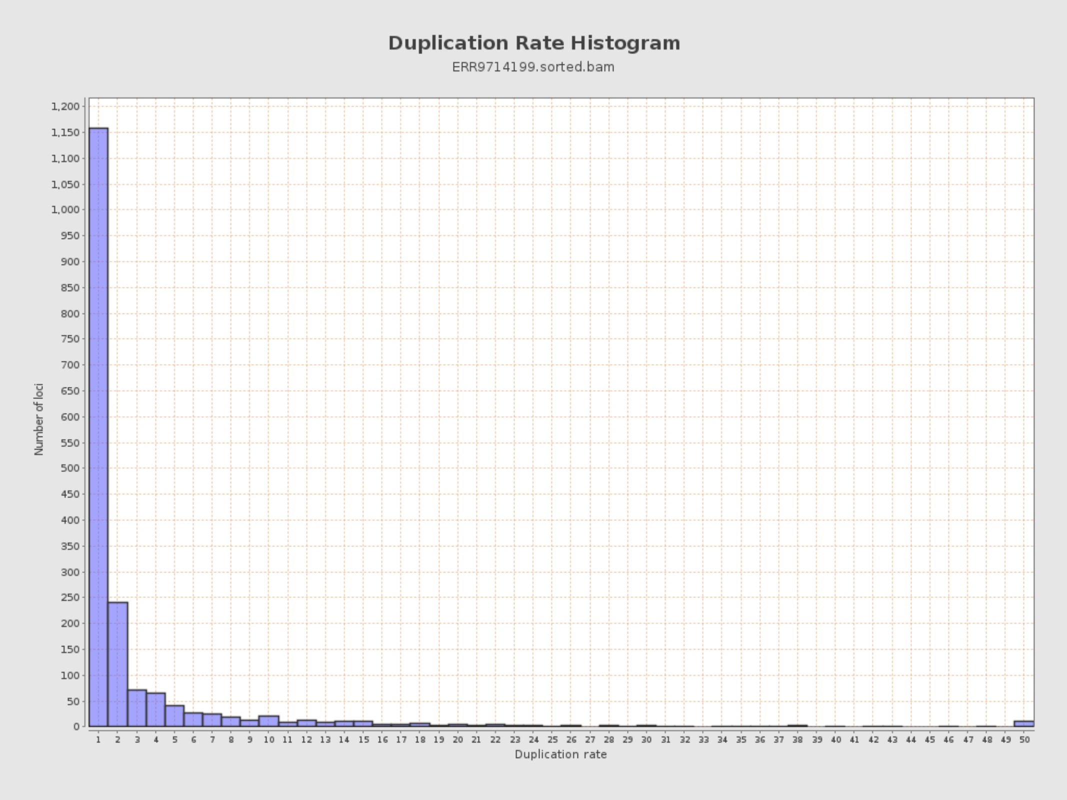
5. Results : Coverage Histogram (0-50X)



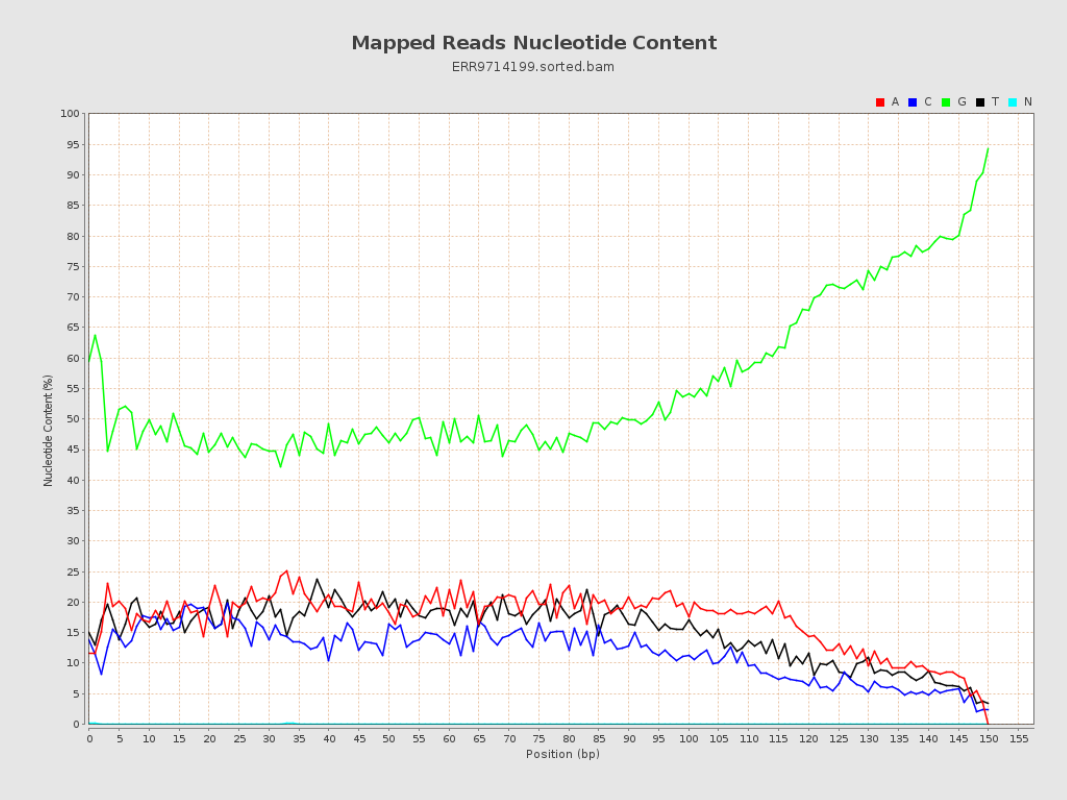
6. Results : Genome Fraction Coverage



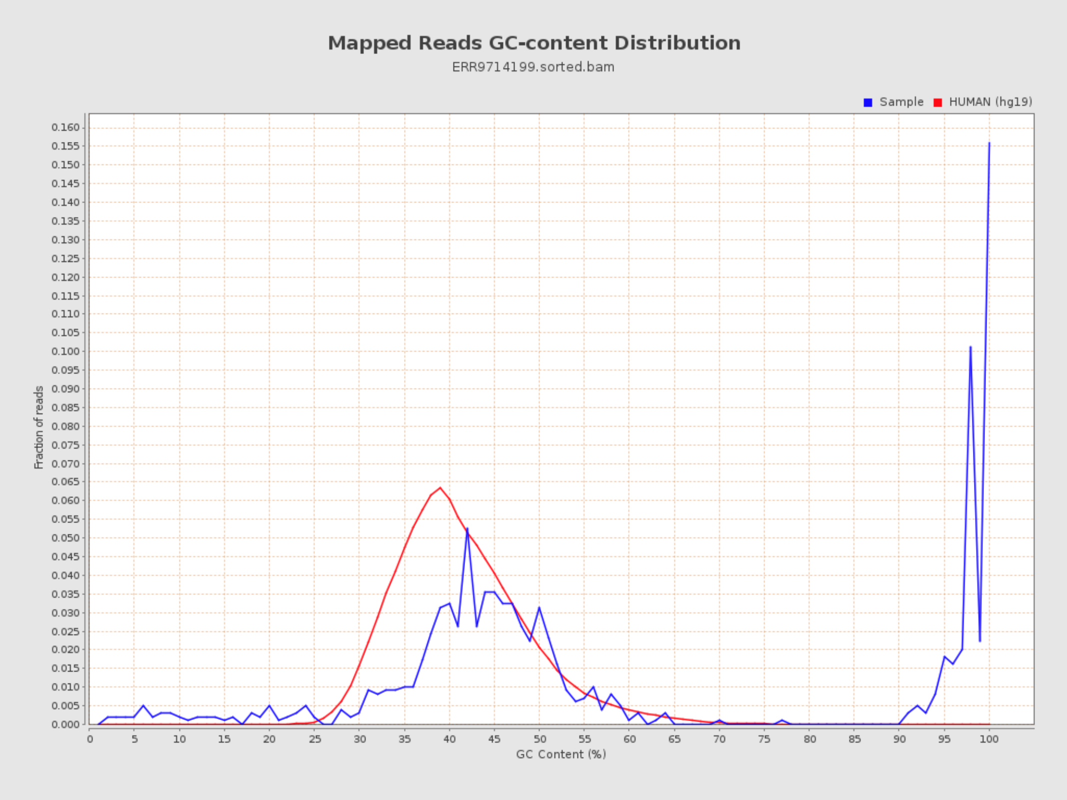
7. Results : Duplication Rate Histogram



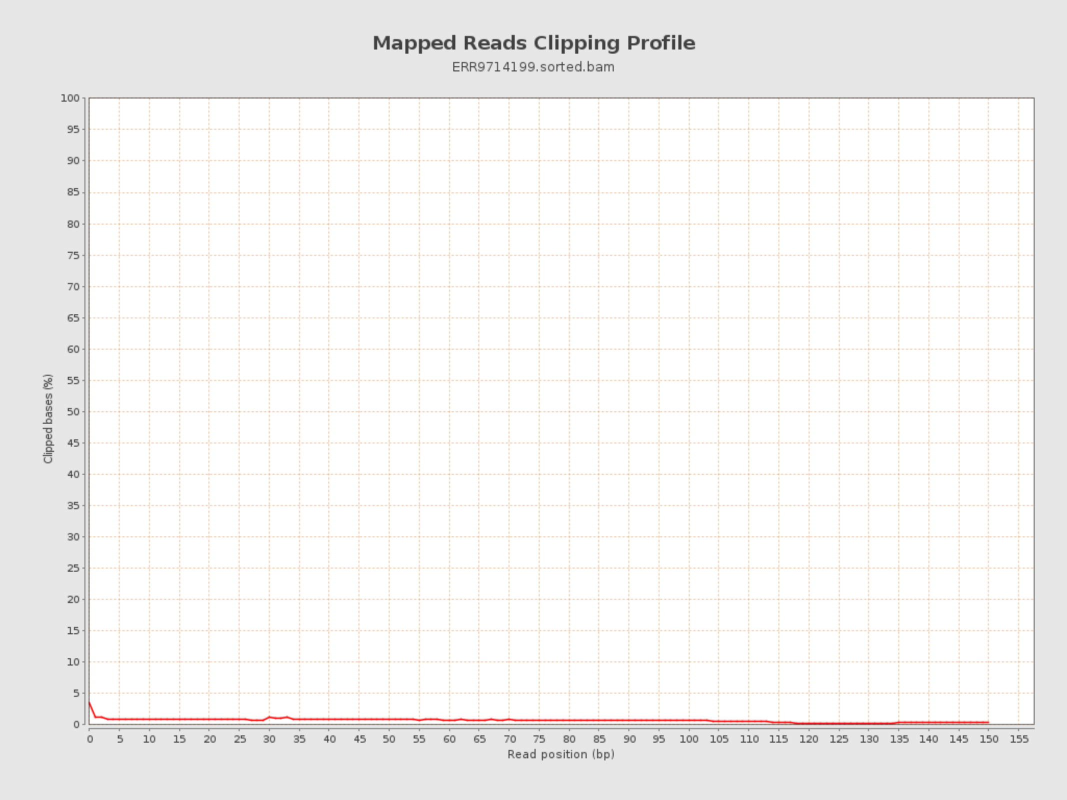
8. Results : Mapped Reads Nucleotide Content



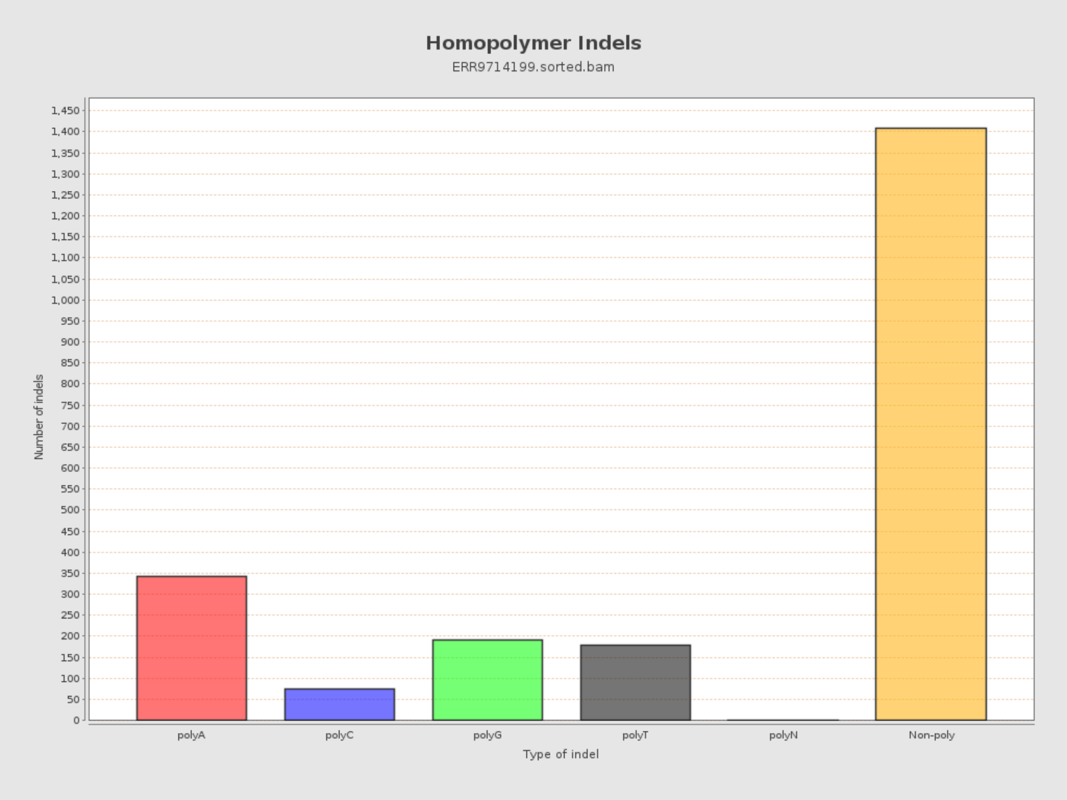
9. Results : Mapped Reads GC-content Distribution



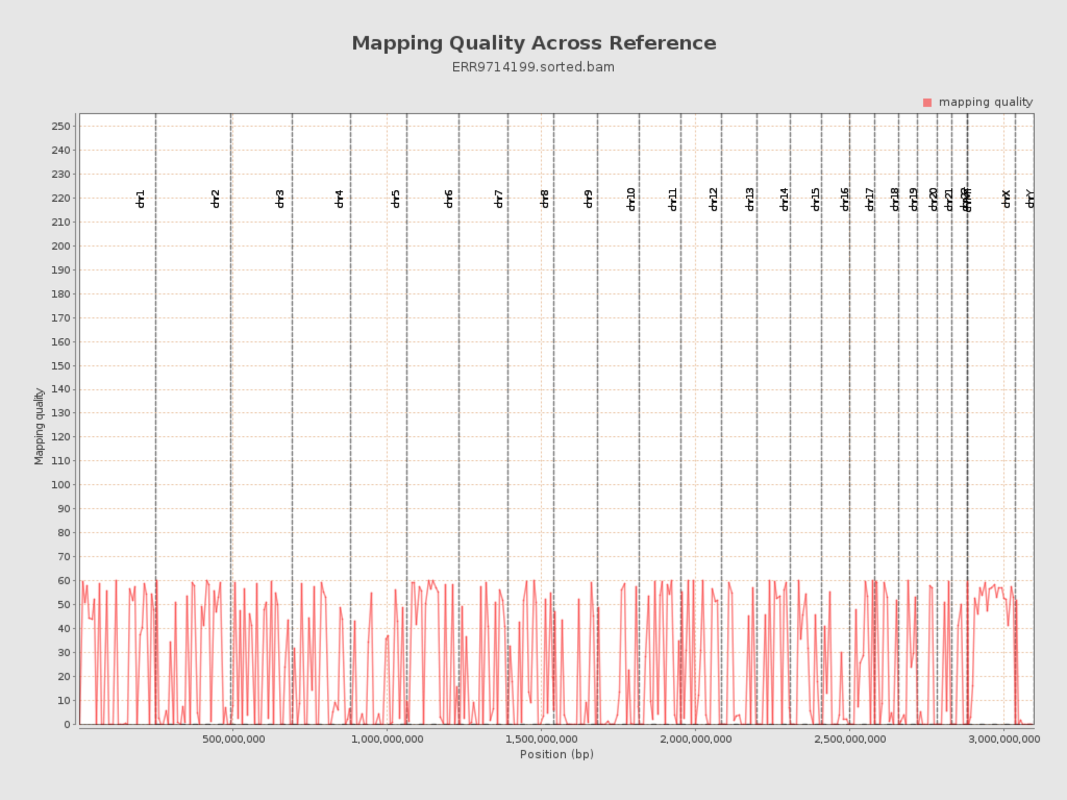
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram