Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 23:52:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714193.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_ERR9714193 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714193.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 23:52:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714193.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	75,602
Mapped reads	21,367 / 28.26%
Unmapped reads	54,235 / 71.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	673 / 0.89%
Read min/max/mean length	30 / 151 / 79.39
Duplicated reads (estimated)	17,867 / 23.63%
Duplication rate	46.99%
Clipped reads	17,506 / 23.16%

2.2. ACGT Content

Number/percentage of A's	466,843 / 20.65%
Number/percentage of C's	390,854 / 17.29%
Number/percentage of T's	431,322 / 19.08%
Number/percentage of G's	971,841 / 42.98%
Number/percentage of N's	45 / 0%
GC Percentage	60.27%

2.3. Coverage

Mean	0.0007

Standard Deviation	0.7588

2.4. Mapping Quality

Mean Mapping Quality	33.02

2.5. Mismatches and indels

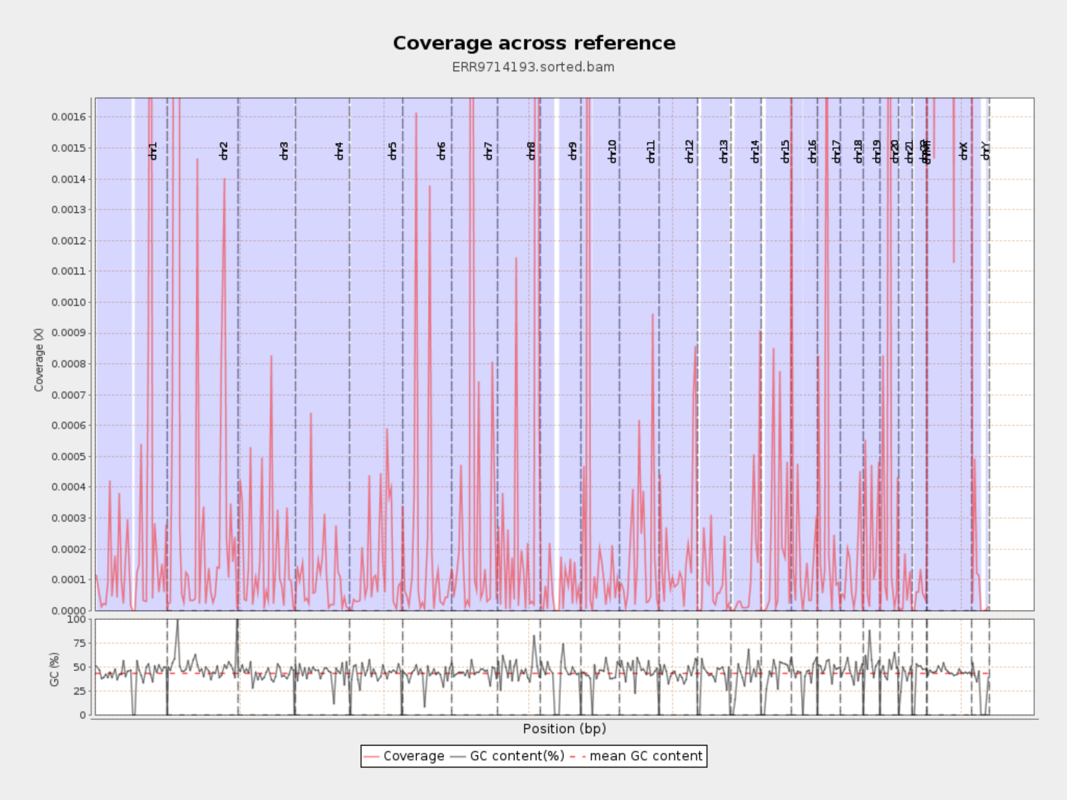
General error rate	3.6%
Mismatches	74,667
Insertions	1,442
Mapped reads with at least one insertion	5.22%
Deletions	5,091
Mapped reads with at least one deletion	23.15%
Homopolymer indels	33.9%

2.6. Chromosome stats

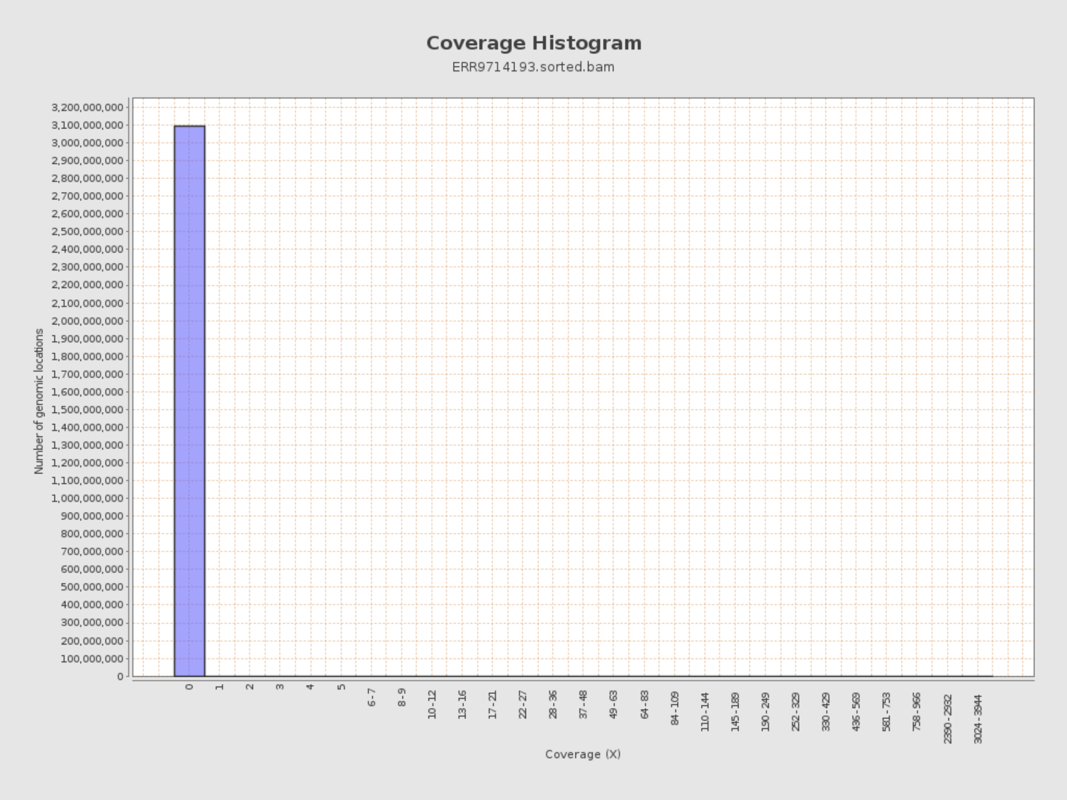
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	65962	0.0003	0.3367
chr2	243199373	662101	0.0027	2.5566
chr3	198022430	34894	0.0002	0.0455
chr4	191154276	21526	0.0001	0.0277
chr5	180915260	26643	0.0001	0.0431
chr6	171115067	37580	0.0002	0.0774
chr7	159138663	58289	0.0004	0.1892

chr8	146364022	67238	0.0005	0.2722
chr9	141213431	9708	0.0001	0.0178
chr10	135534747	44250	0.0003	0.4554
chr11	135006516	27738	0.0002	0.0516
chr12	133851895	28948	0.0002	0.0606
chr13	115169878	9897	0.0001	0.0258
chr14	107349540	15358	0.0001	0.0584
chr15	102531392	22883	0.0002	0.0641
chr16	90354753	19750	0.0002	0.0691
chr17	81195210	31951	0.0004	0.112
chr18	78077248	10115	0.0001	0.0365
chr19	59128983	13989	0.0002	0.0561
chr20	63025520	41011	0.0007	0.2309
chr21	48129895	2895	0.0001	0.0169
chr22	51304566	3048	0.0001	0.0129
chrMT	16571	150	0.0091	0.0947
chrX	155270560	1037753	0.0067	0.8456
chrY	59373566	5869	0.0001	0.0251

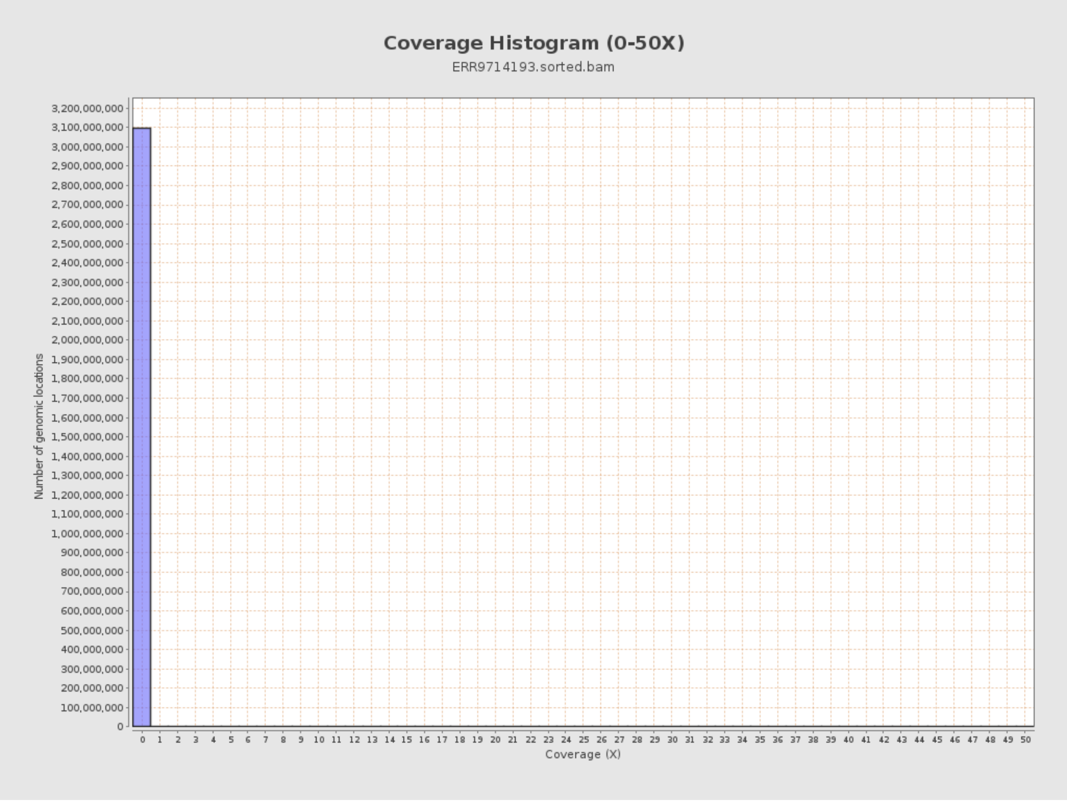
3. Results : Coverage across reference



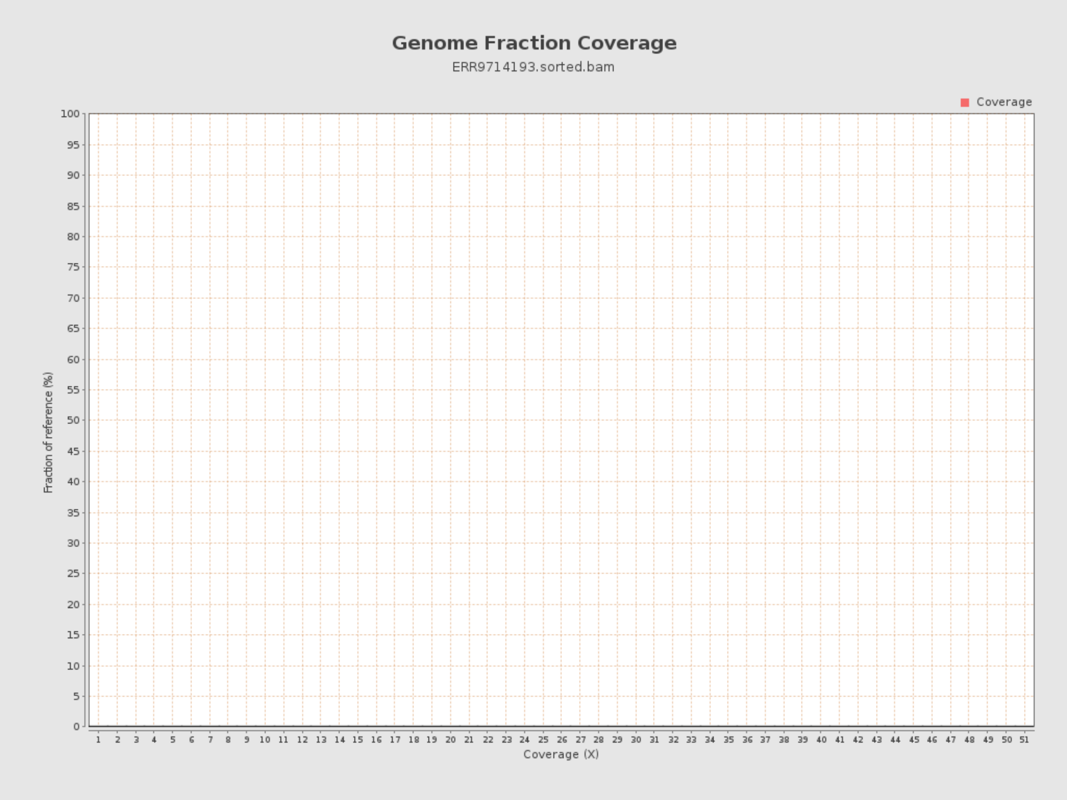
4. Results : Coverage Histogram



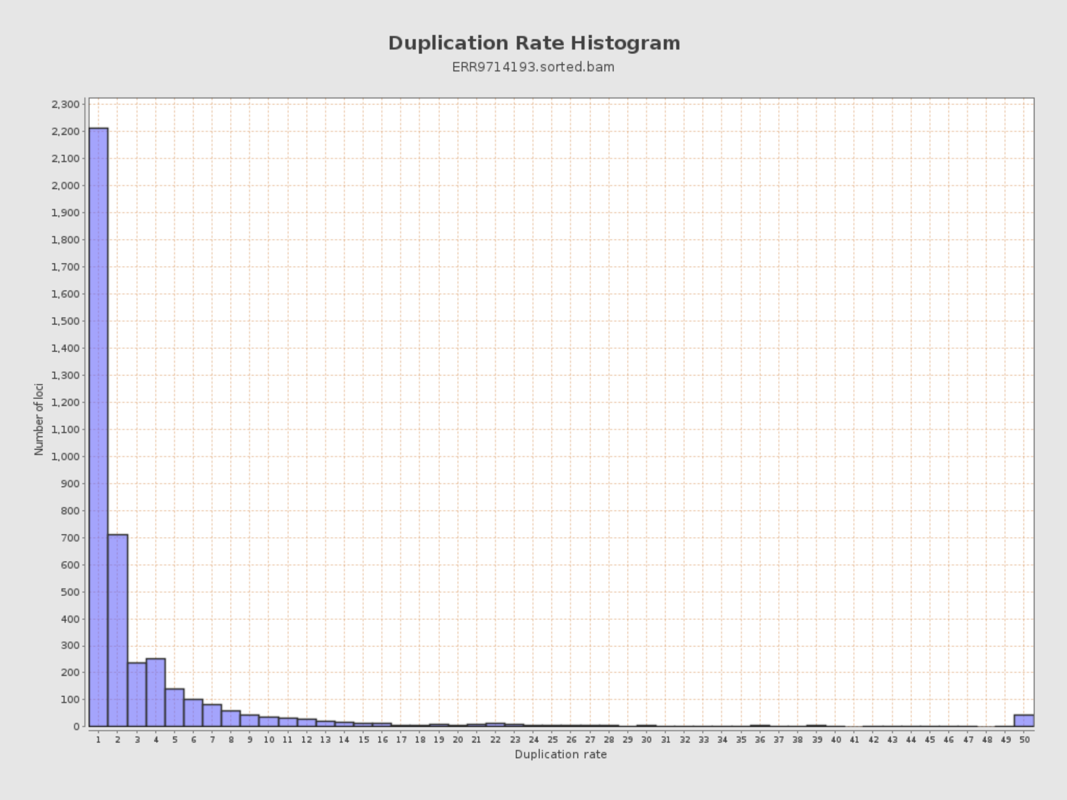
5. Results : Coverage Histogram (0-50X)



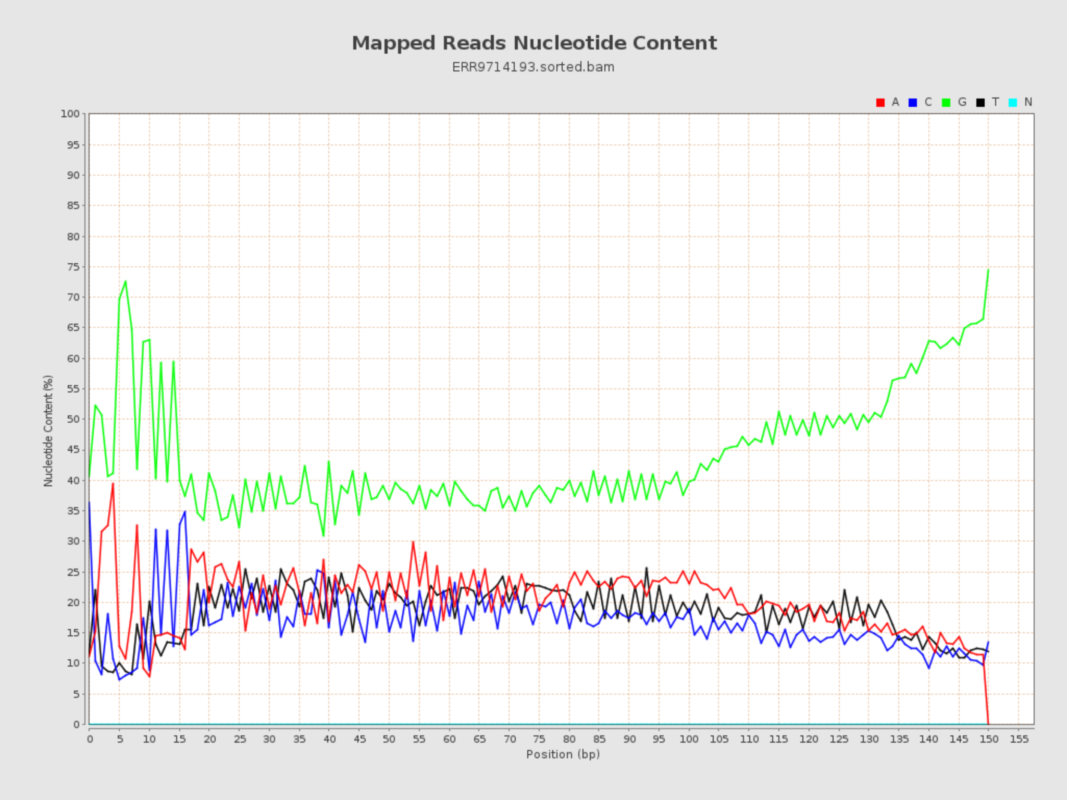
6. Results : Genome Fraction Coverage



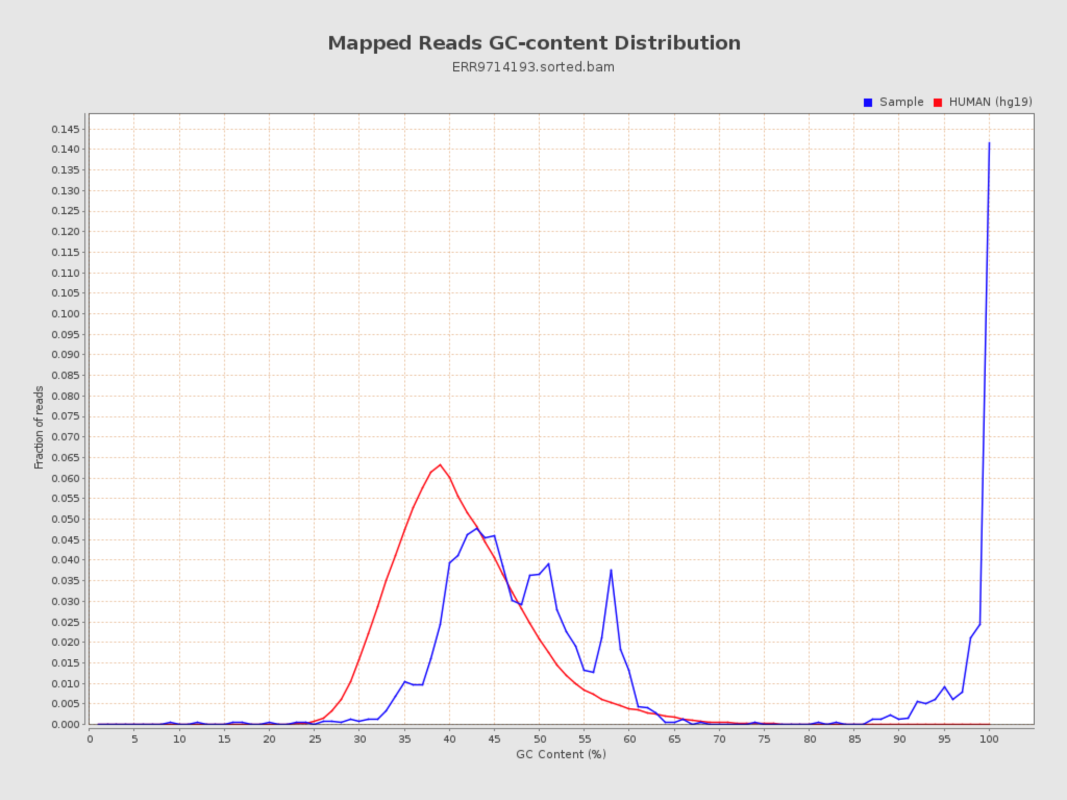
7. Results : Duplication Rate Histogram



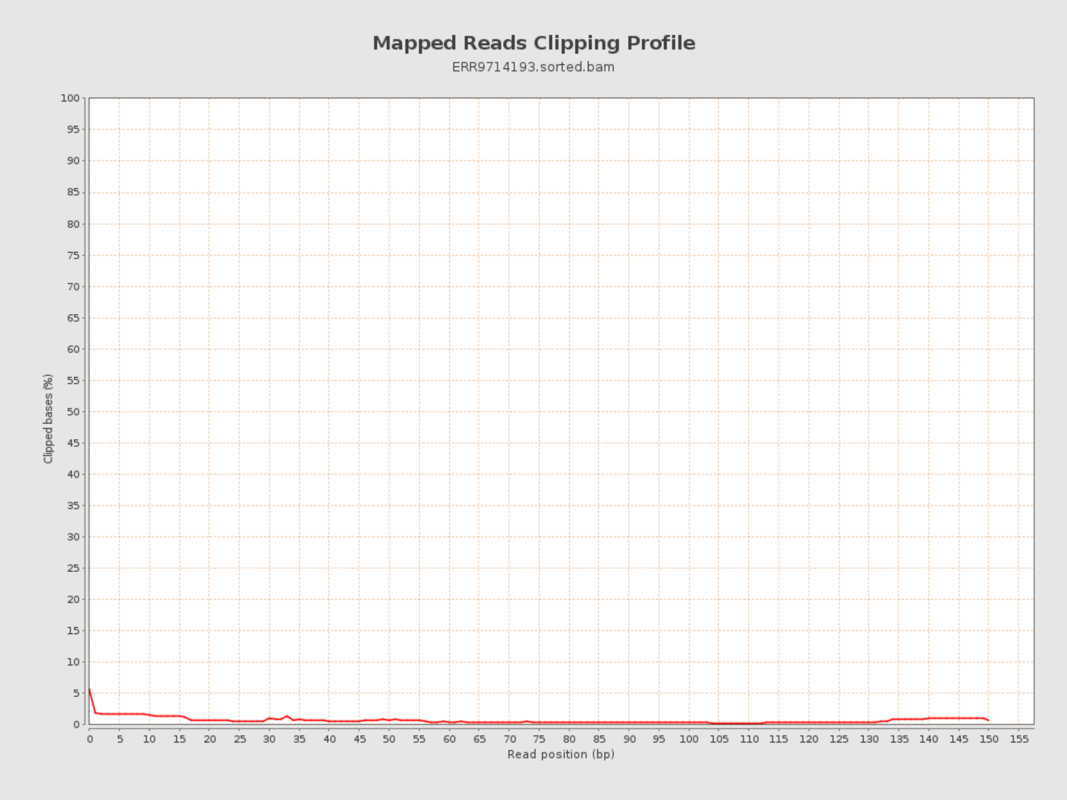
8. Results : Mapped Reads Nucleotide Content



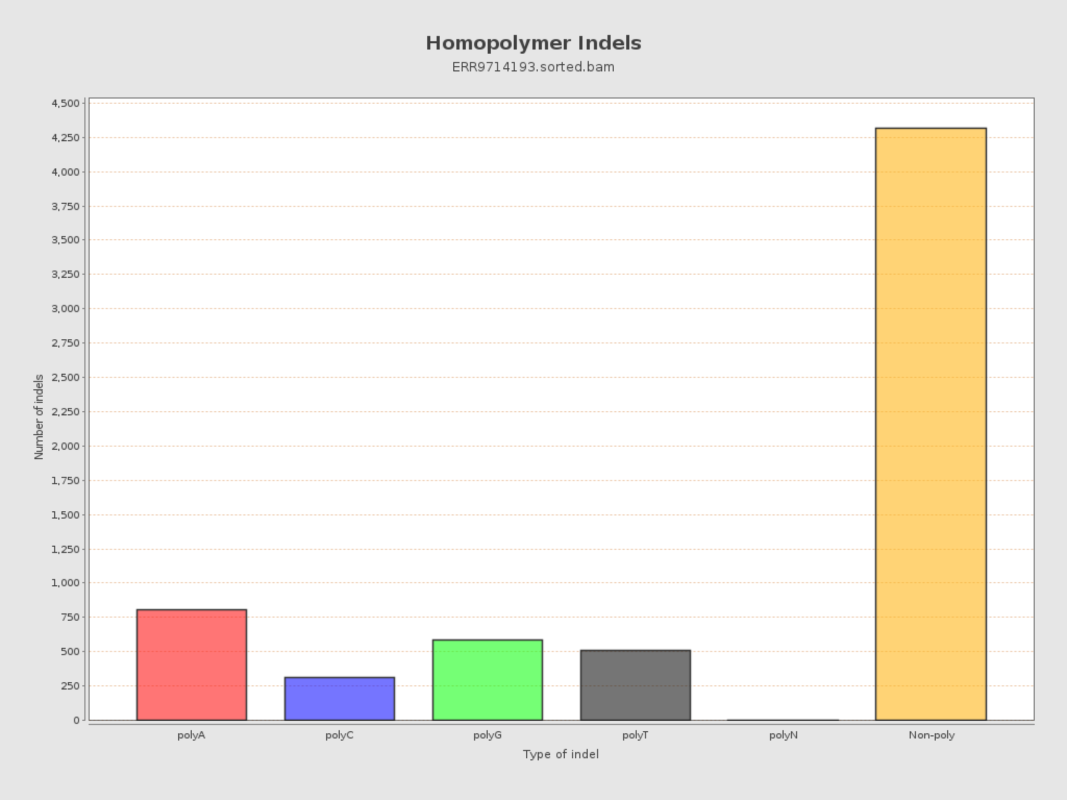
9. Results : Mapped Reads GC-content Distribution



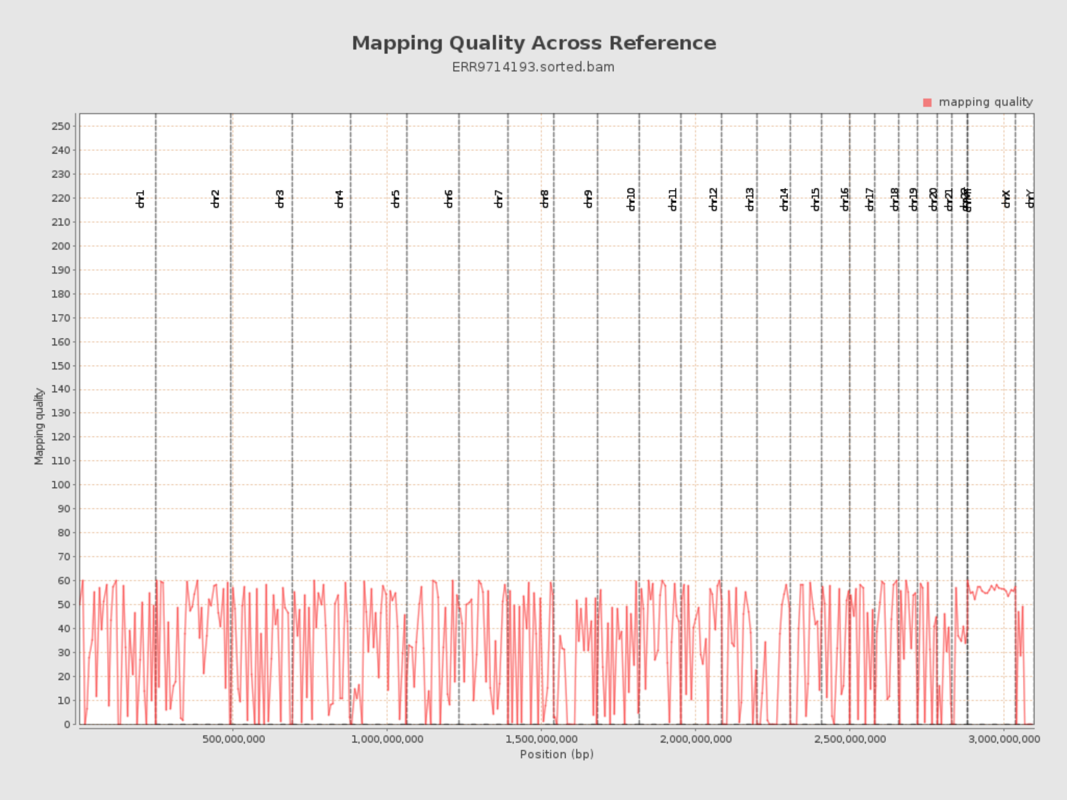
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram