Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 19:29:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714103.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_ERR9714103 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714103.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 19:29:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714103.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,018,458
Mapped reads	86,978 / 8.54%
Unmapped reads	931,480 / 91.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,639 / 0.26%
Read min/max/mean length	30 / 151 / 55.91
Duplicated reads (estimated)	82,517 / 8.1%
Duplication rate	30.34%
Clipped reads	51,605 / 5.07%

2.2. ACGT Content

Number/percentage of A's	330,538 / 3.87%
Number/percentage of C's	143,089 / 1.68%
Number/percentage of T's	187,358 / 2.2%
Number/percentage of G's	7,868,274 / 92.24%
Number/percentage of N's	1,025 / 0.01%
GC Percentage	93.92%

2.3. Coverage

Mean	0.0028

Standard Deviation	9.5764

2.4. Mapping Quality

Mean Mapping Quality	30.18

2.5. Mismatches and indels

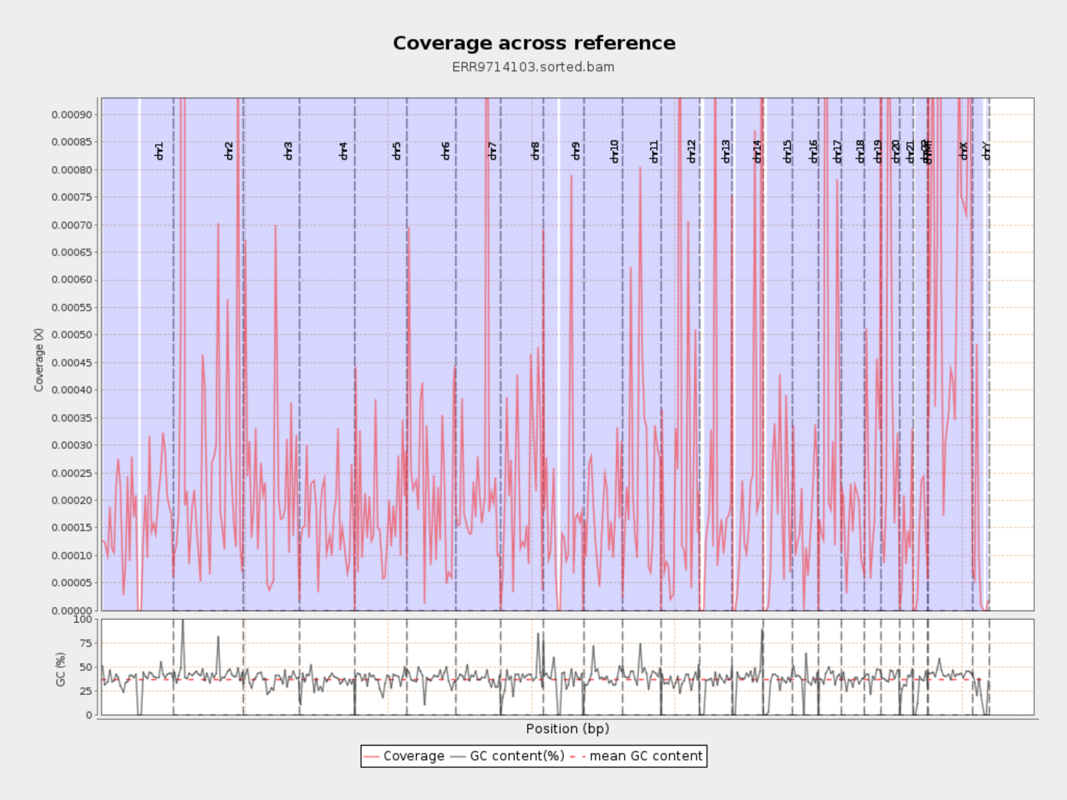
General error rate	3.45%
Mismatches	210,533
Insertions	11,531
Mapped reads with at least one insertion	8.9%
Deletions	4,973
Mapped reads with at least one deletion	5.49%
Homopolymer indels	63.2%

2.6. Chromosome stats

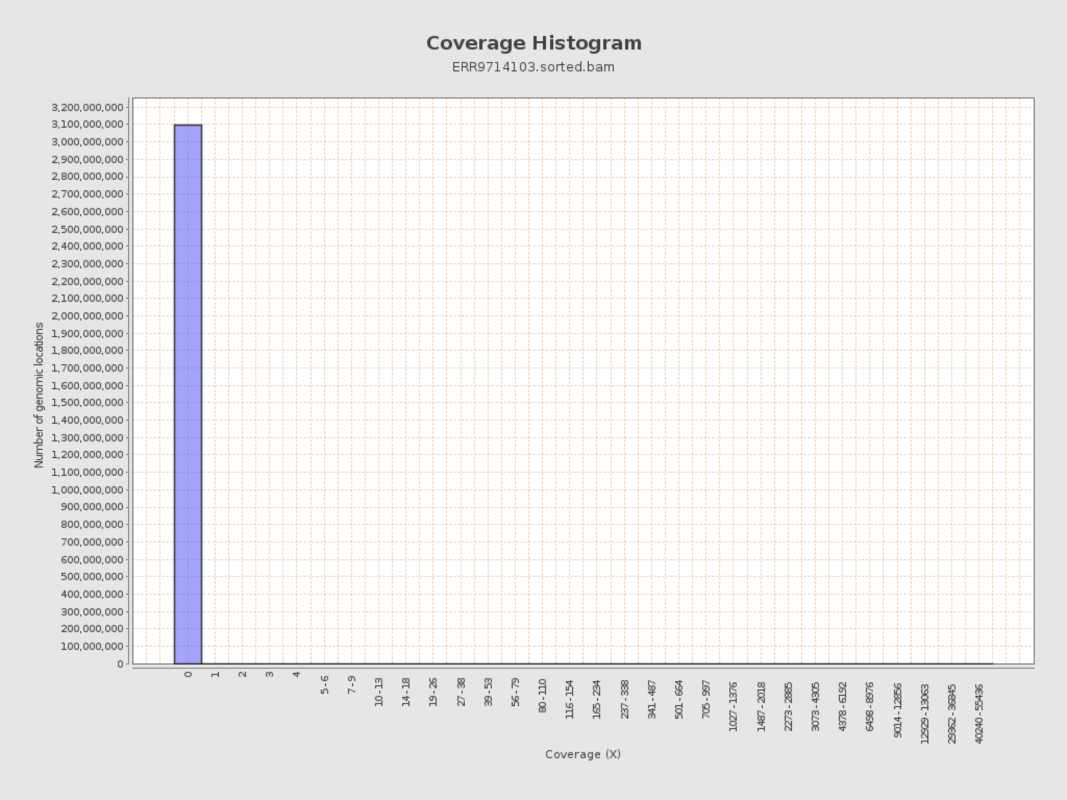
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	42177	0.0002	0.024
chr2	243199373	7860838	0.0323	34.1652
chr3	198022430	44124	0.0002	0.0396
chr4	191154276	32027	0.0002	0.0311
chr5	180915260	33492	0.0002	0.0315
chr6	171115067	39968	0.0002	0.0357
chr7	159138663	41428	0.0003	0.1605

chr8	146364022	33353	0.0002	0.05
chr9	141213431	23700	0.0002	0.0334
chr10	135534747	23775	0.0002	0.03
chr11	135006516	36486	0.0003	0.0615
chr12	133851895	35752	0.0003	0.0784
chr13	115169878	23764	0.0002	0.0525
chr14	107349540	32287	0.0003	0.1971
chr15	102531392	17852	0.0002	0.0371
chr16	90354753	15194	0.0002	0.0262
chr17	81195210	31616	0.0004	0.2057
chr18	78077248	12645	0.0002	0.021
chr19	59128983	17796	0.0003	0.0475
chr20	63025520	26156	0.0004	0.1908
chr21	48129895	6223	0.0001	0.028
chr22	51304566	6248	0.0001	0.0194
chrMT	16571	5160	0.3114	2.565
chrX	155270560	104127	0.0007	0.0762
chrY	59373566	5504	0.0001	0.0303

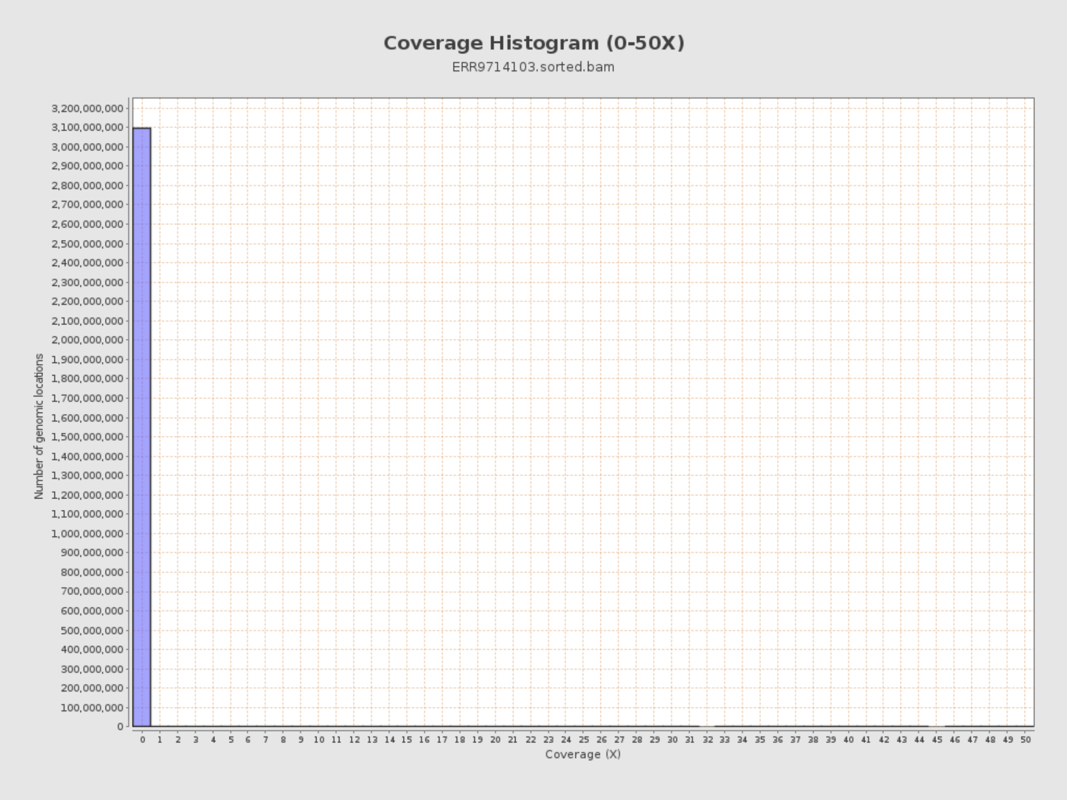
3. Results : Coverage across reference



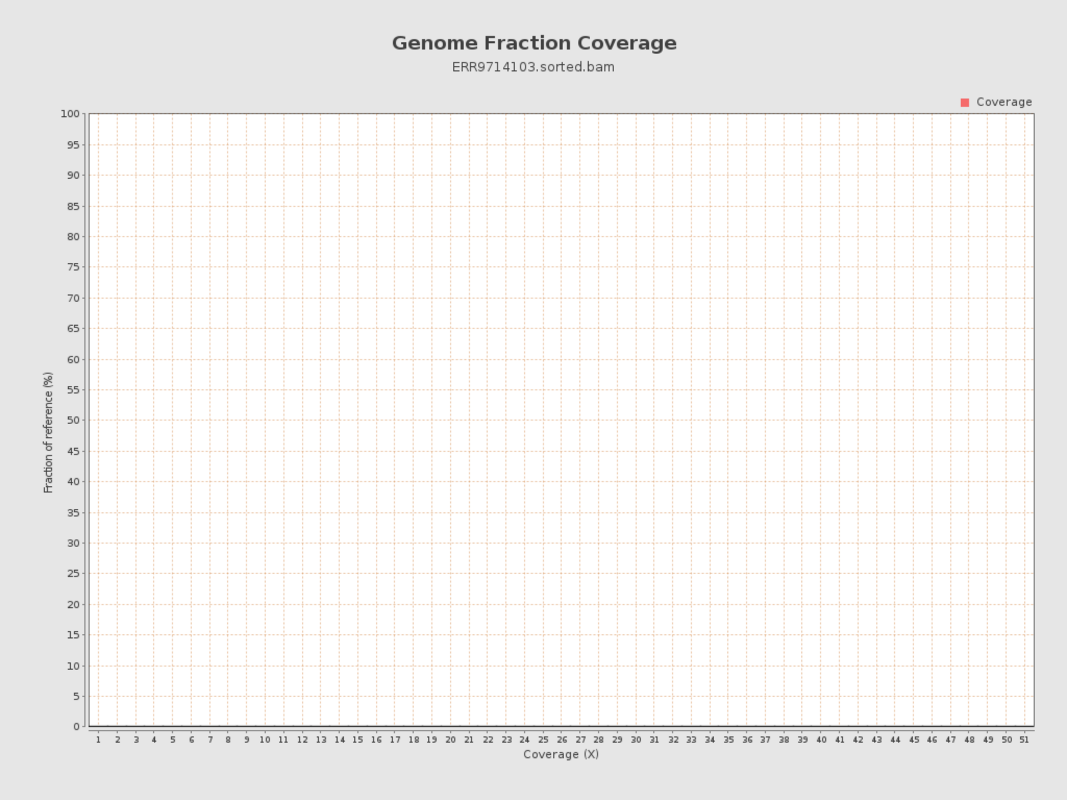
4. Results : Coverage Histogram



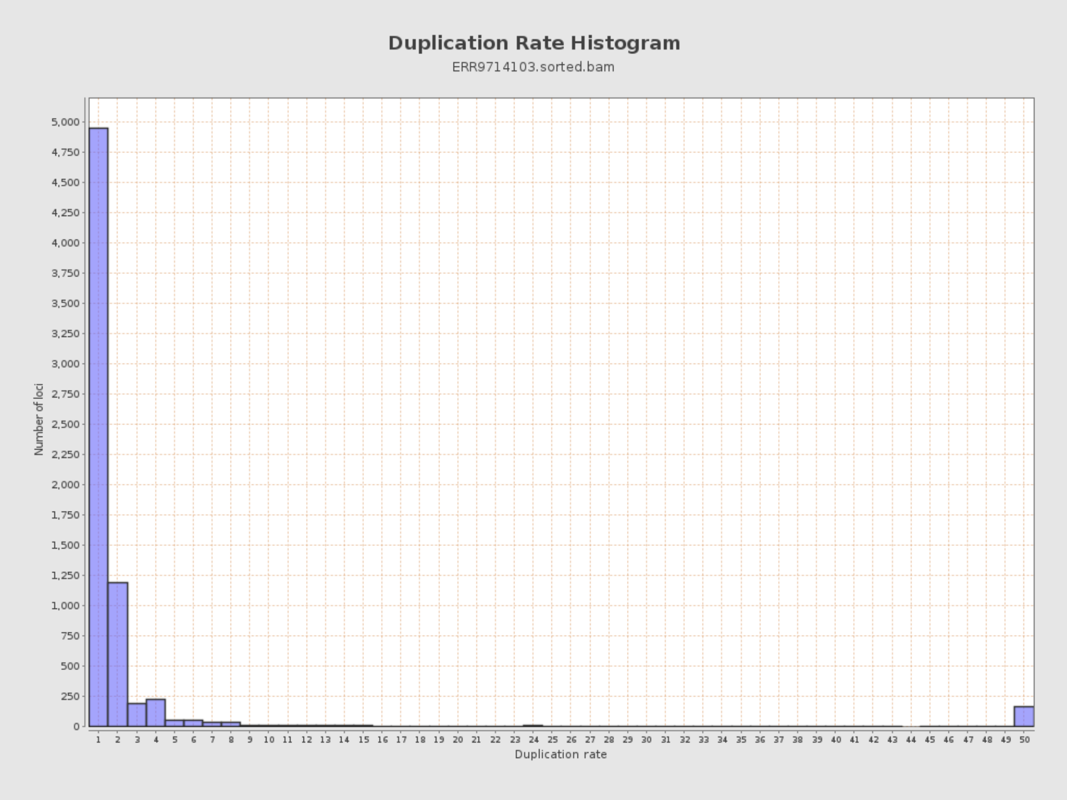
5. Results : Coverage Histogram (0-50X)



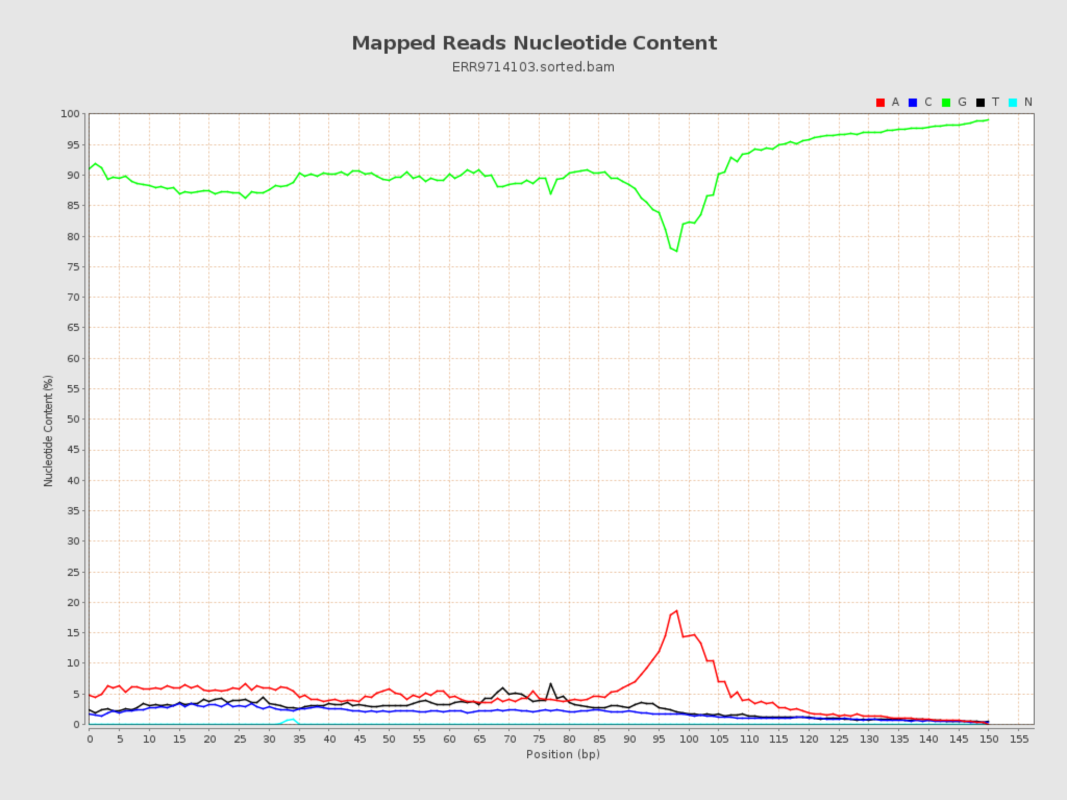
6. Results : Genome Fraction Coverage



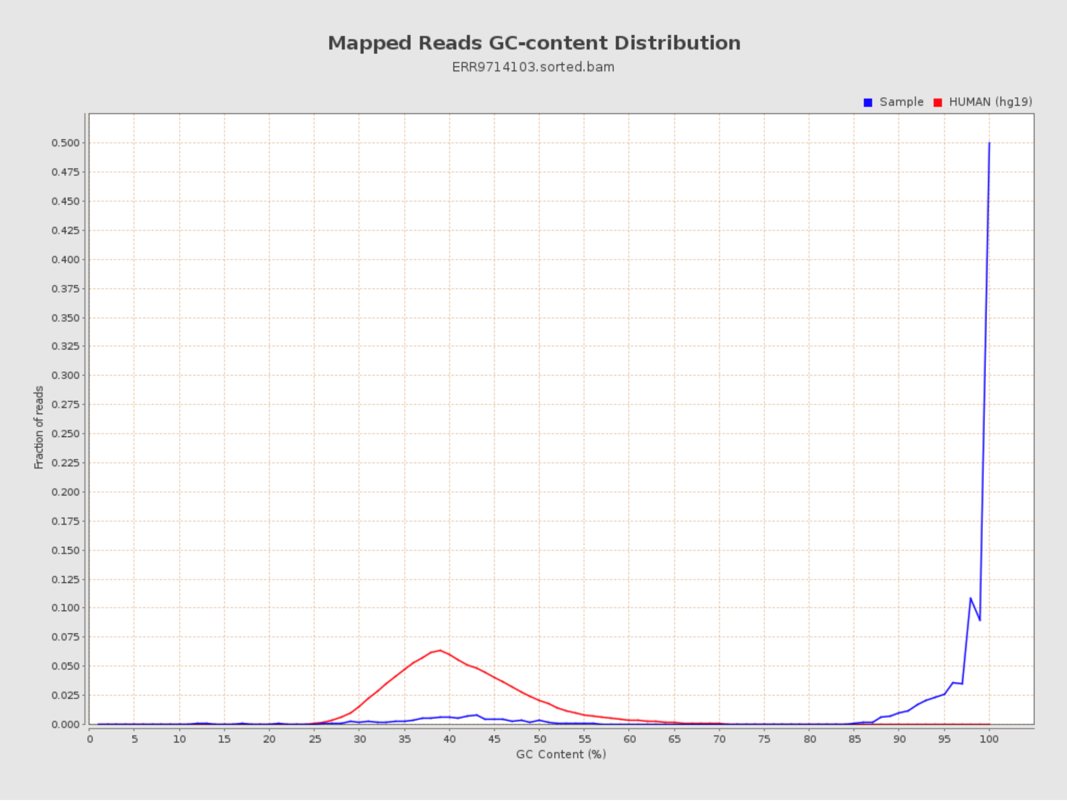
7. Results : Duplication Rate Histogram



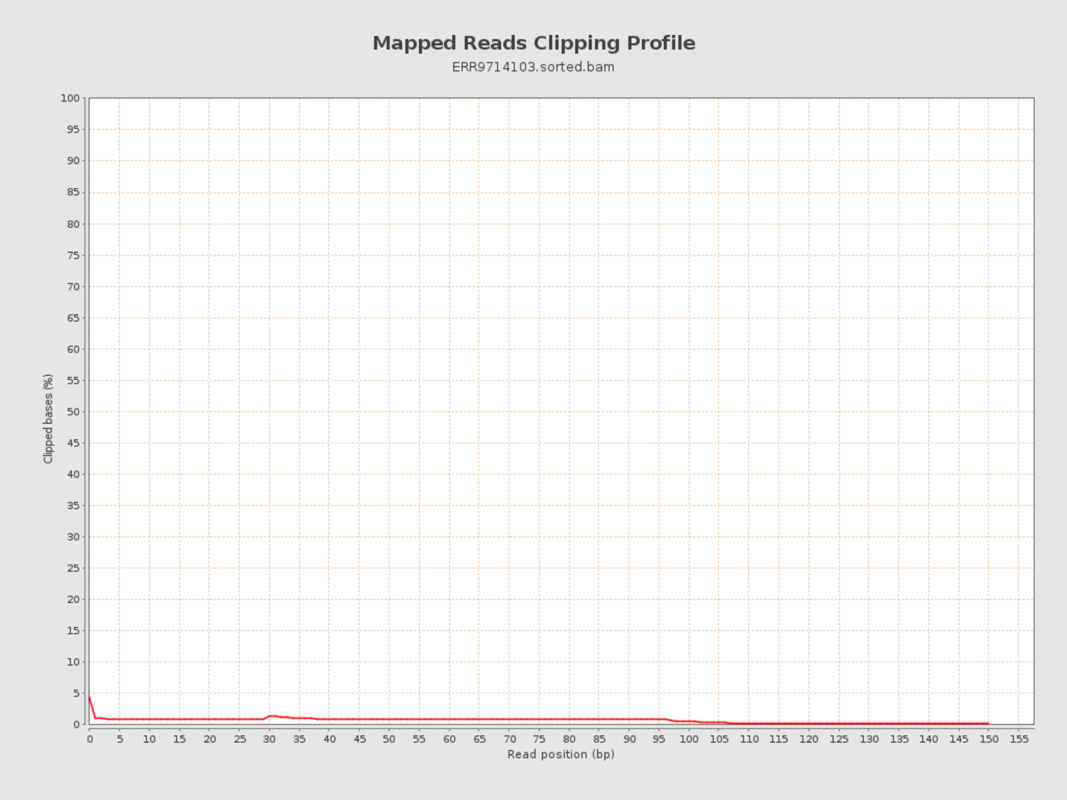
8. Results : Mapped Reads Nucleotide Content



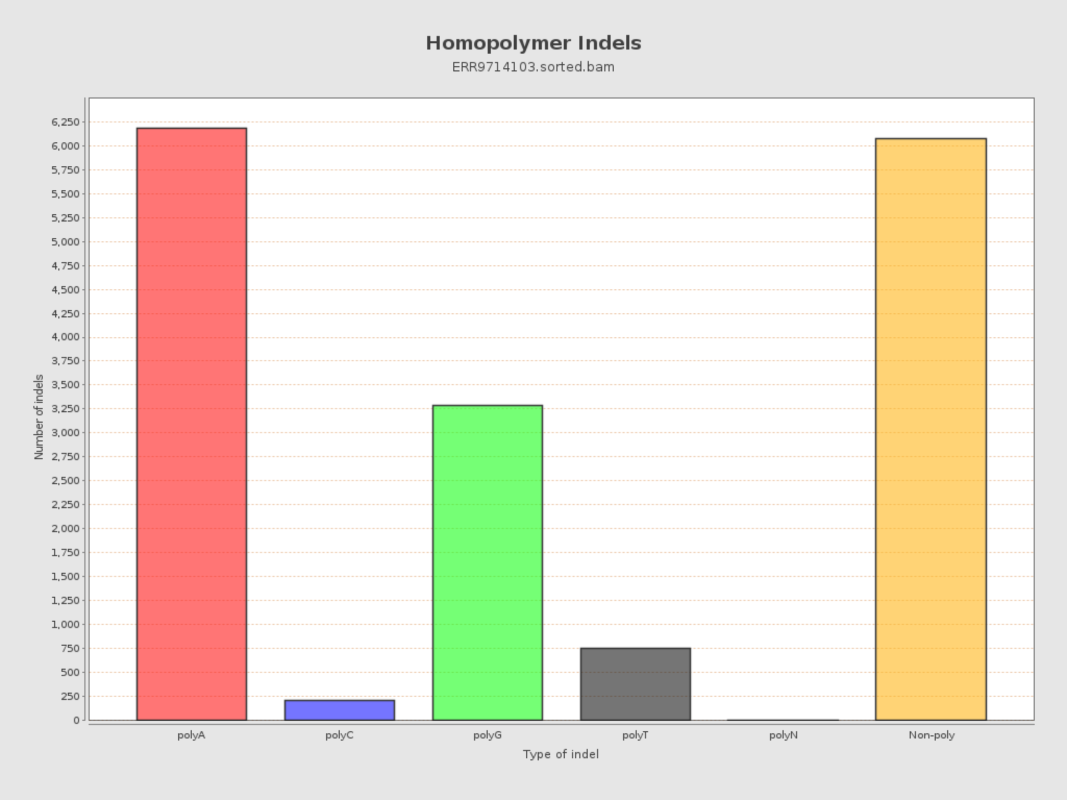
9. Results : Mapped Reads GC-content Distribution



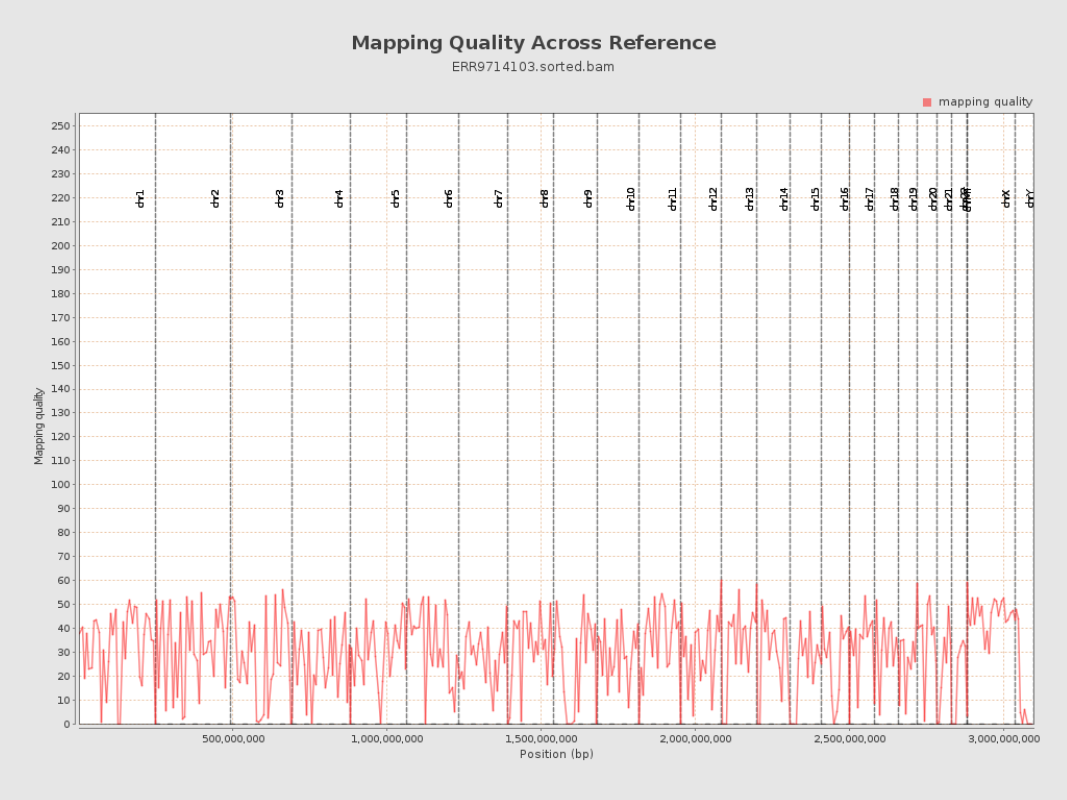
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram