Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 01:10:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714243.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_ERR9714243 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714243.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 01:10:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714243.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	292,438
Mapped reads	35,922 / 12.28%
Unmapped reads	256,516 / 87.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,150 / 0.39%
Read min/max/mean length	30 / 151 / 66.09
Duplicated reads (estimated)	31,745 / 10.86%
Duplication rate	37.64%
Clipped reads	25,581 / 8.75%

2.2. ACGT Content

Number/percentage of A's	350,563 / 10.03%
Number/percentage of C's	227,120 / 6.5%
Number/percentage of T's	289,713 / 8.29%
Number/percentage of G's	2,626,615 / 75.17%
Number/percentage of N's	254 / 0.01%
GC Percentage	81.67%

2.3. Coverage

Mean	0.0011

Standard Deviation	3.0617

2.4. Mapping Quality

Mean Mapping Quality	37

2.5. Mismatches and indels

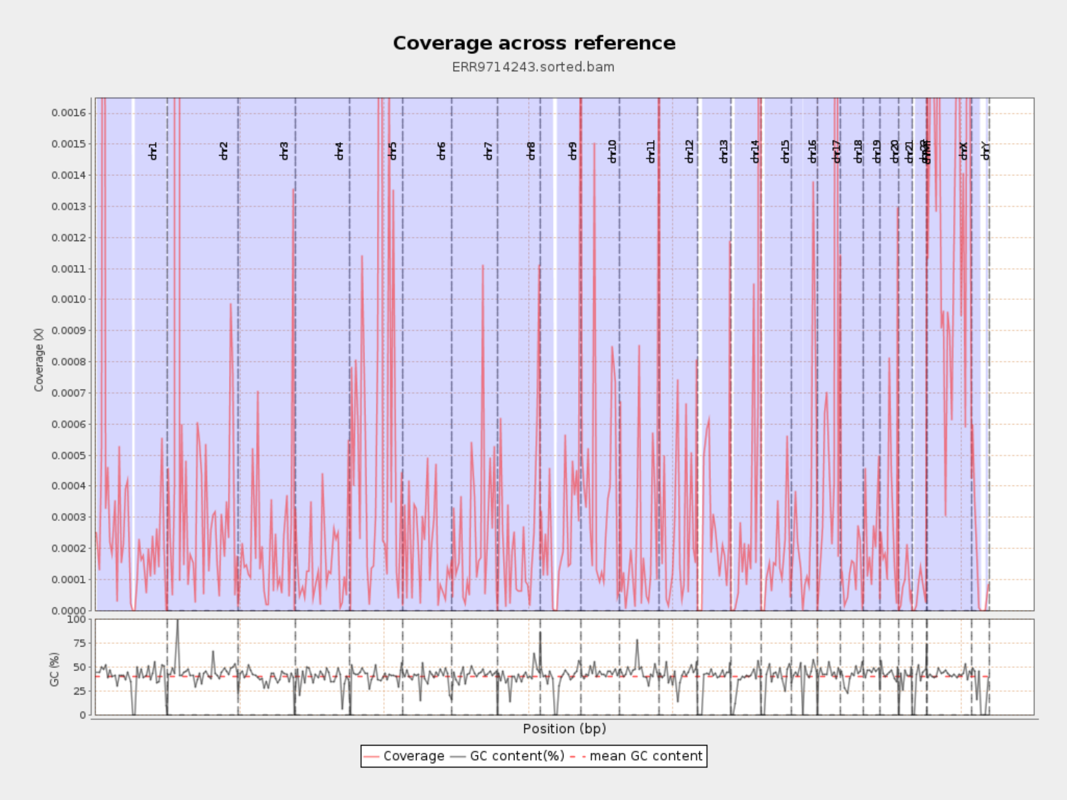
General error rate	3.19%
Mismatches	91,849
Insertions	3,490
Mapped reads with at least one insertion	7.71%
Deletions	4,248
Mapped reads with at least one deletion	11.11%
Homopolymer indels	44.17%

2.6. Chromosome stats

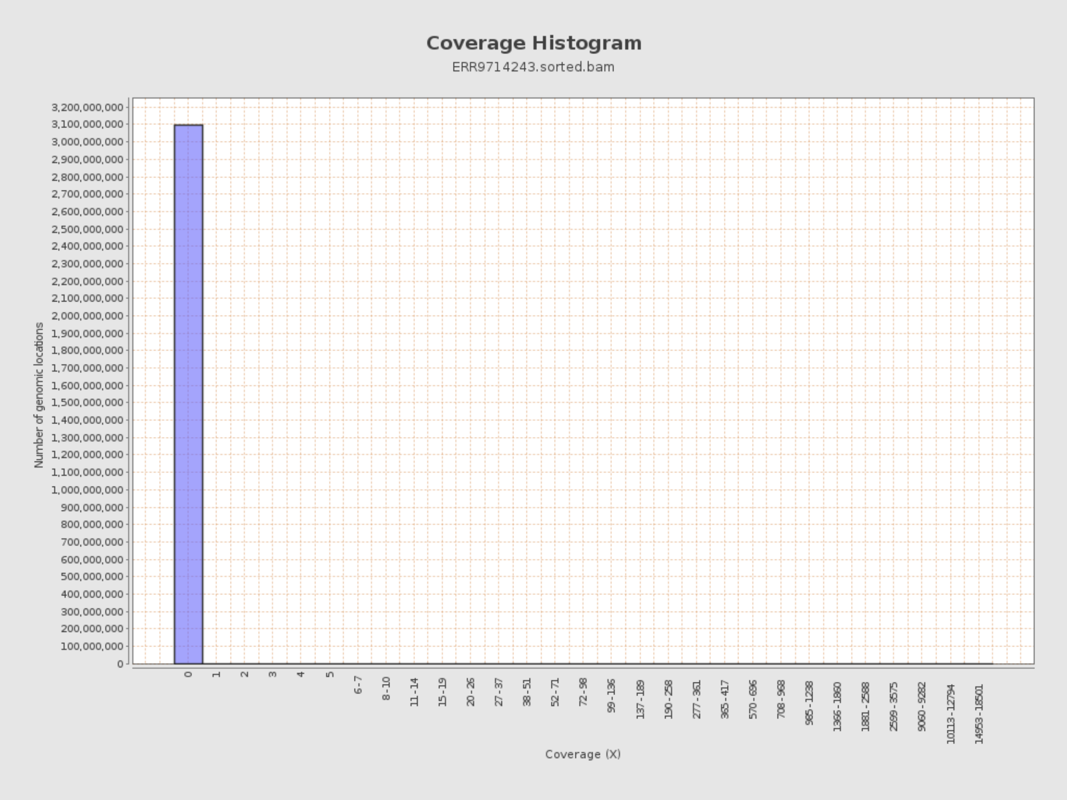
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	86861	0.0003	0.1517
chr2	243199373	2488442	0.0102	10.915
chr3	198022430	45362	0.0002	0.06
chr4	191154276	30408	0.0002	0.0355
chr5	180915260	113768	0.0006	0.1986
chr6	171115067	33688	0.0002	0.0386
chr7	159138663	40737	0.0003	0.0971

chr8	146364022	34555	0.0002	0.0519
chr9	141213431	34811	0.0002	0.0403
chr10	135534747	52043	0.0004	0.0809
chr11	135006516	28038	0.0002	0.0497
chr12	133851895	34176	0.0003	0.0622
chr13	115169878	28950	0.0003	0.0531
chr14	107349540	77268	0.0007	0.4009
chr15	102531392	17488	0.0002	0.0357
chr16	90354753	27770	0.0003	0.0769
chr17	81195210	62362	0.0008	0.2835
chr18	78077248	9474	0.0001	0.0216
chr19	59128983	14089	0.0002	0.0448
chr20	63025520	20097	0.0003	0.048
chr21	48129895	3801	0.0001	0.0174
chr22	51304566	5386	0.0001	0.0342
chrMT	16571	9484	0.5723	4.0694
chrX	155270560	210429	0.0014	0.1258
chrY	59373566	7976	0.0001	0.0346

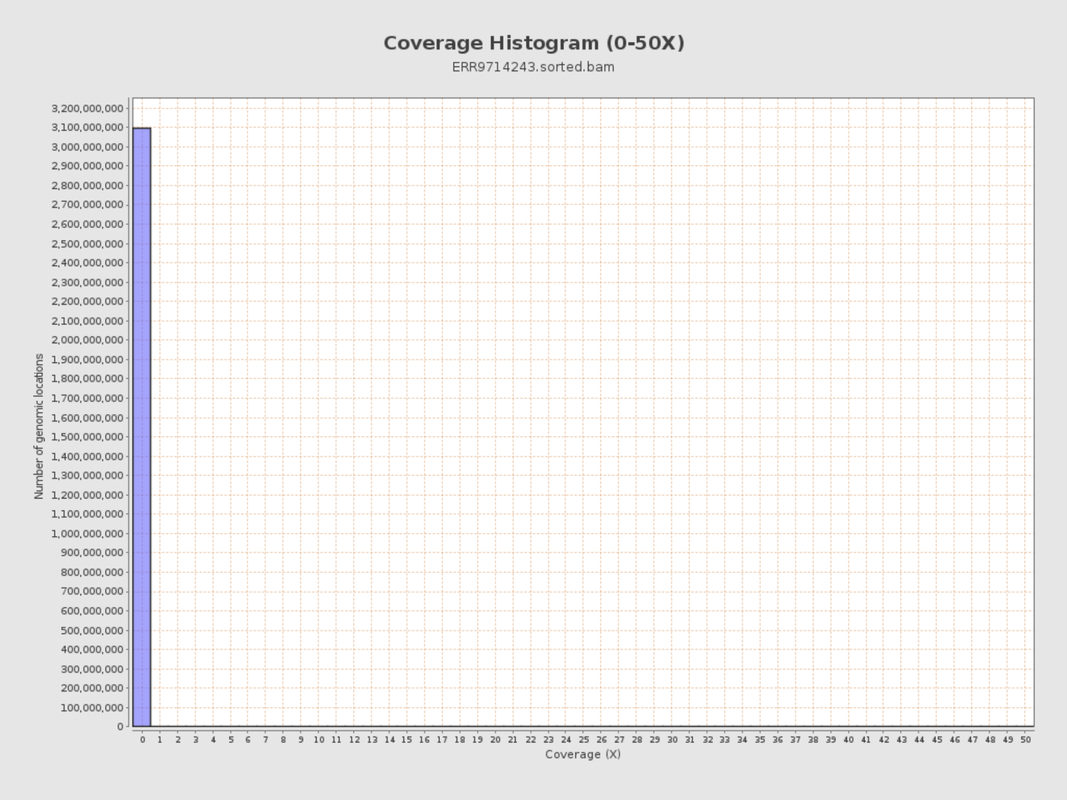
3. Results : Coverage across reference



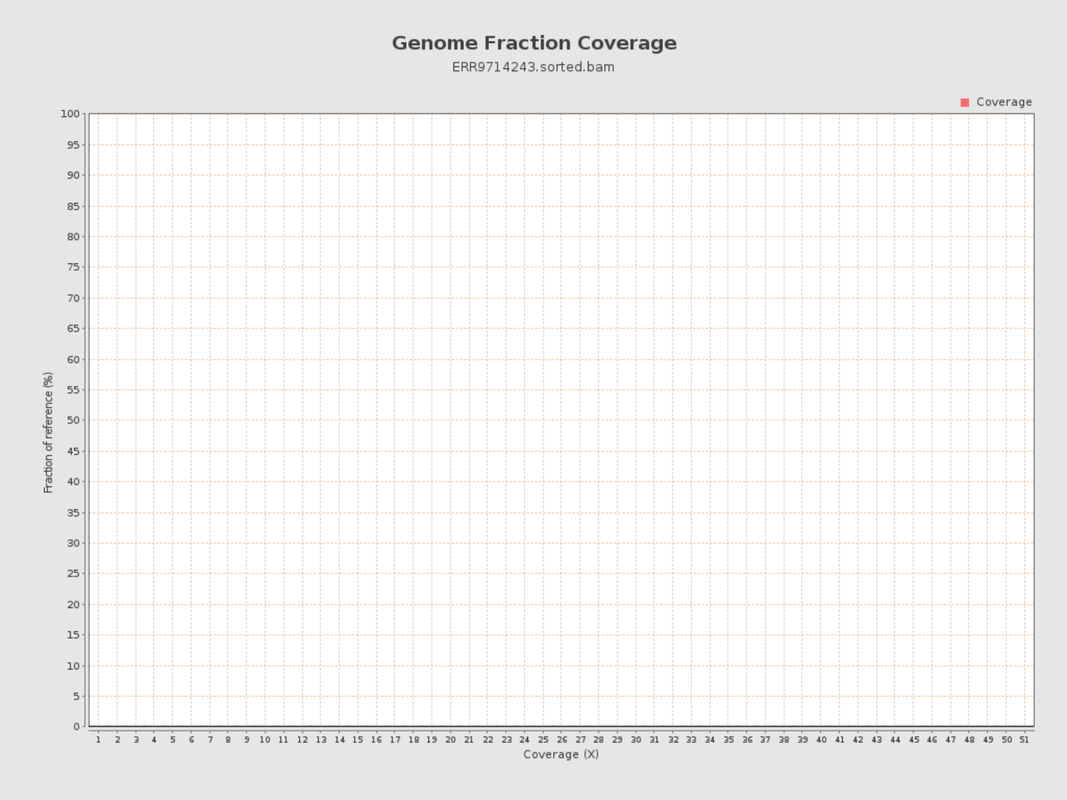
4. Results : Coverage Histogram



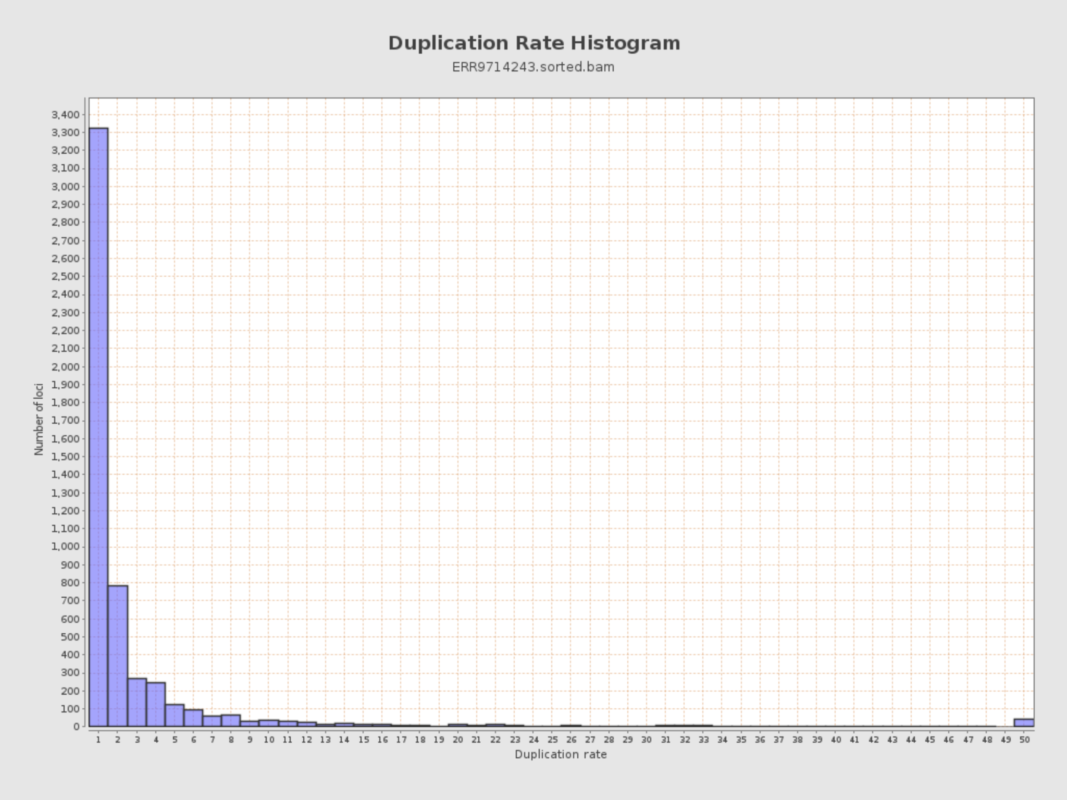
5. Results : Coverage Histogram (0-50X)



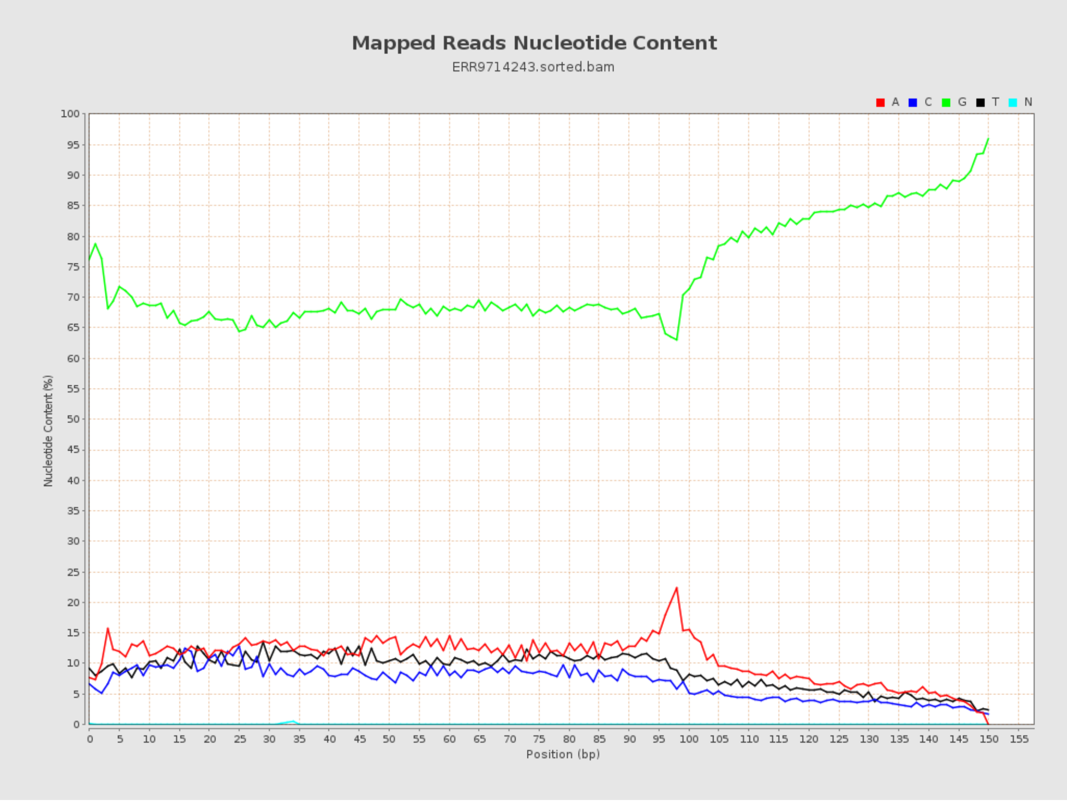
6. Results : Genome Fraction Coverage



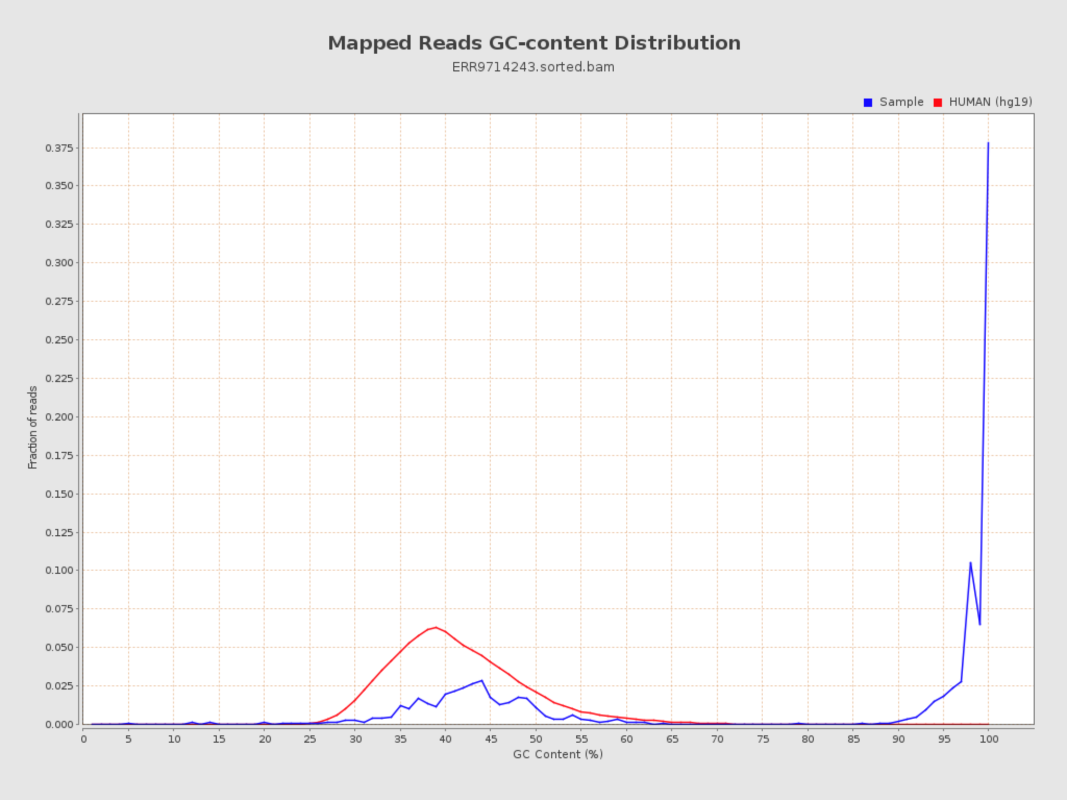
7. Results : Duplication Rate Histogram



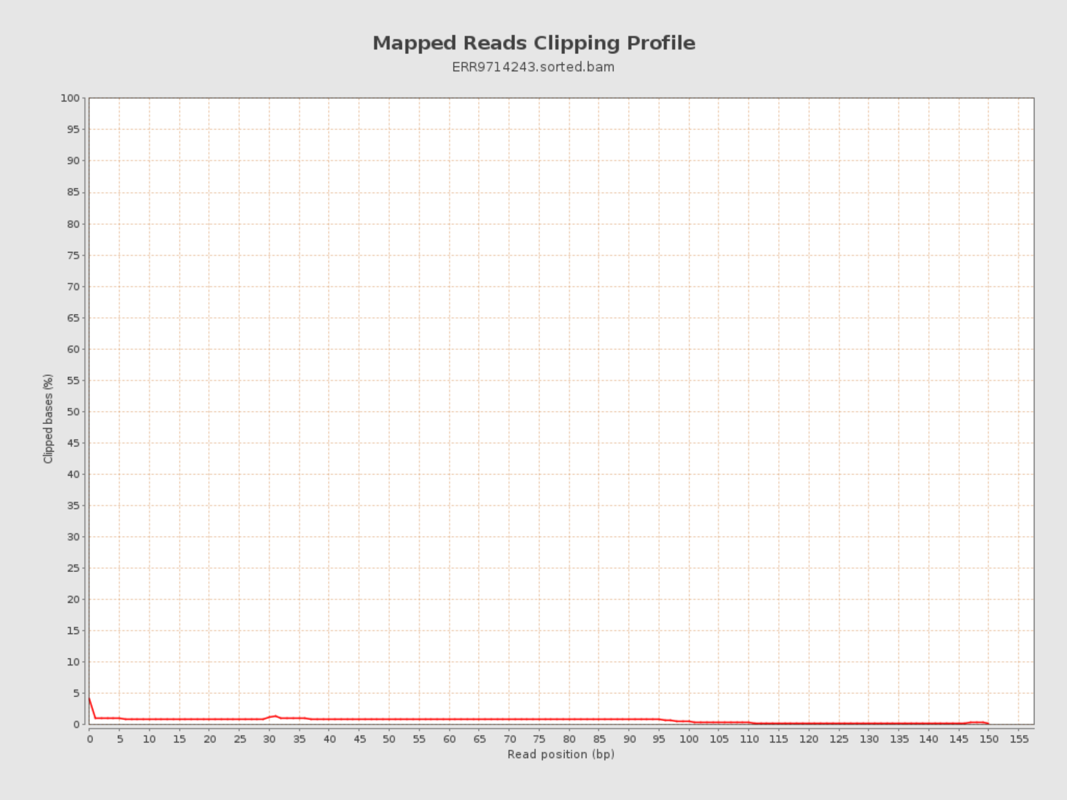
8. Results : Mapped Reads Nucleotide Content



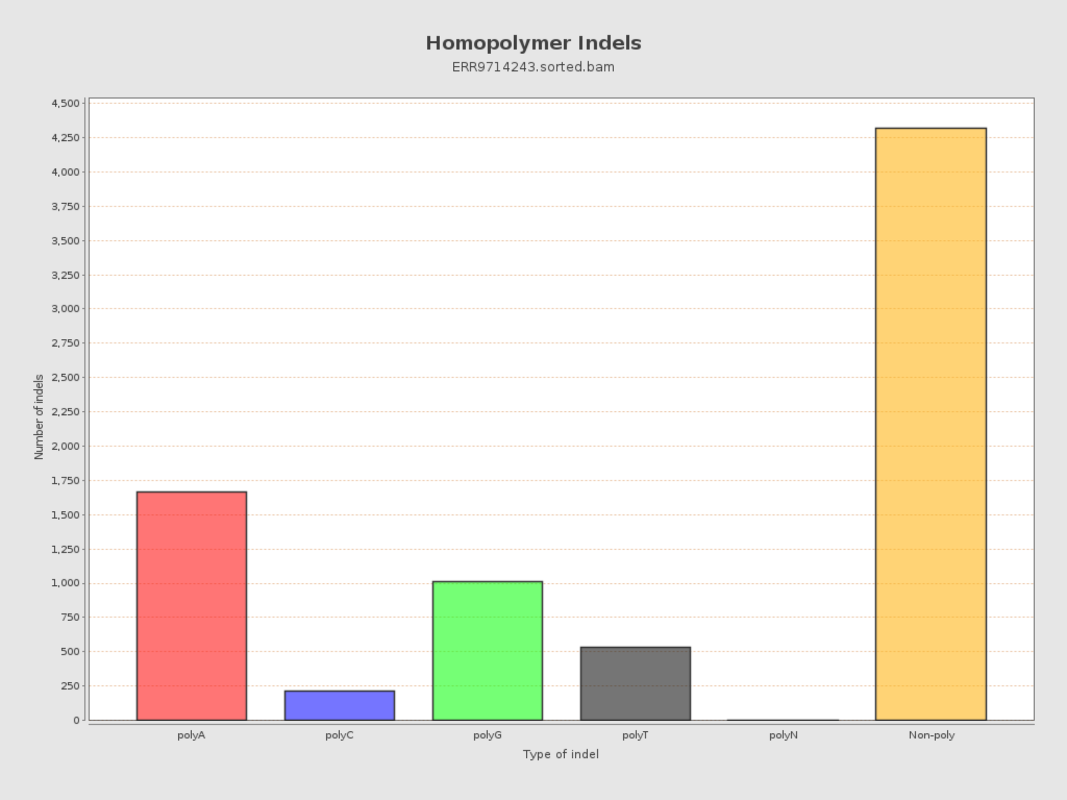
9. Results : Mapped Reads GC-content Distribution



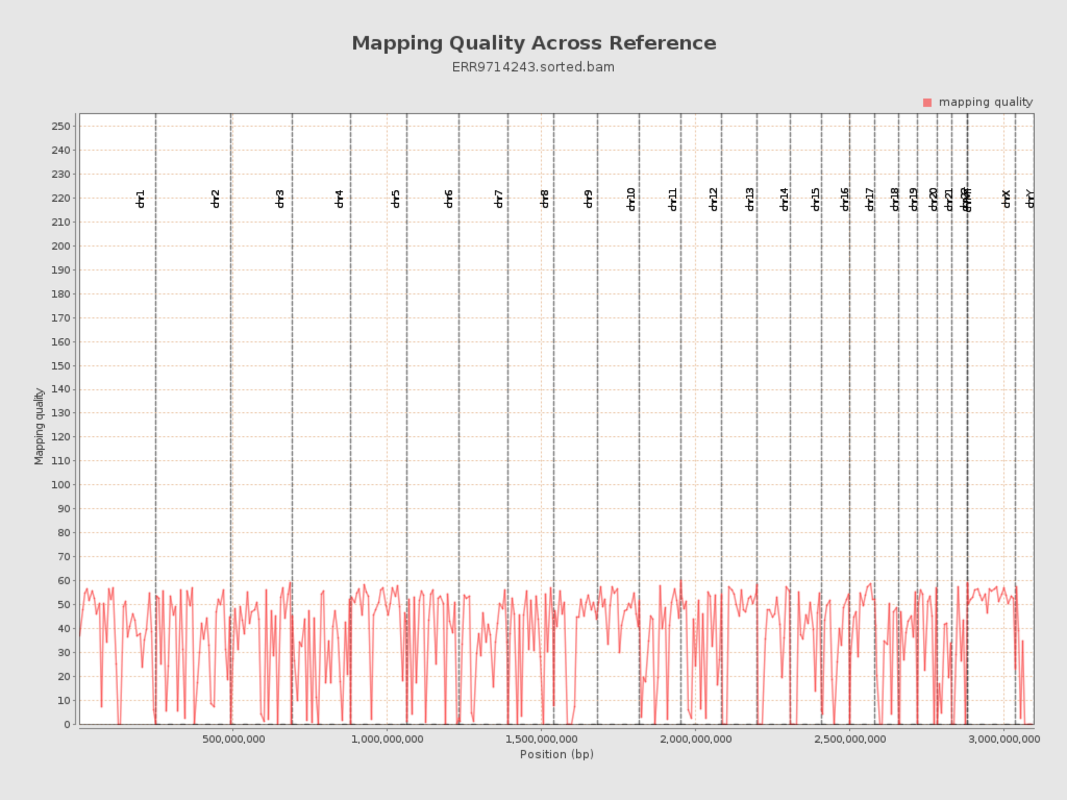
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram