Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 01:12:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714244.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_ERR9714244 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714244.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 01:12:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714244.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	339,800
Mapped reads	42,229 / 12.43%
Unmapped reads	297,571 / 87.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	788 / 0.23%
Read min/max/mean length	30 / 151 / 59.71
Duplicated reads (estimated)	40,990 / 12.06%
Duplication rate	28.96%
Clipped reads	21,953 / 6.46%

2.2. ACGT Content

Number/percentage of A's	102,764 / 2.33%
Number/percentage of C's	36,379 / 0.83%
Number/percentage of T's	43,990 / 1%
Number/percentage of G's	4,225,769 / 95.84%
Number/percentage of N's	143 / 0%
GC Percentage	96.67%

2.3. Coverage

Mean	0.0014

Standard Deviation	5.3474

2.4. Mapping Quality

Mean Mapping Quality	10.04

2.5. Mismatches and indels

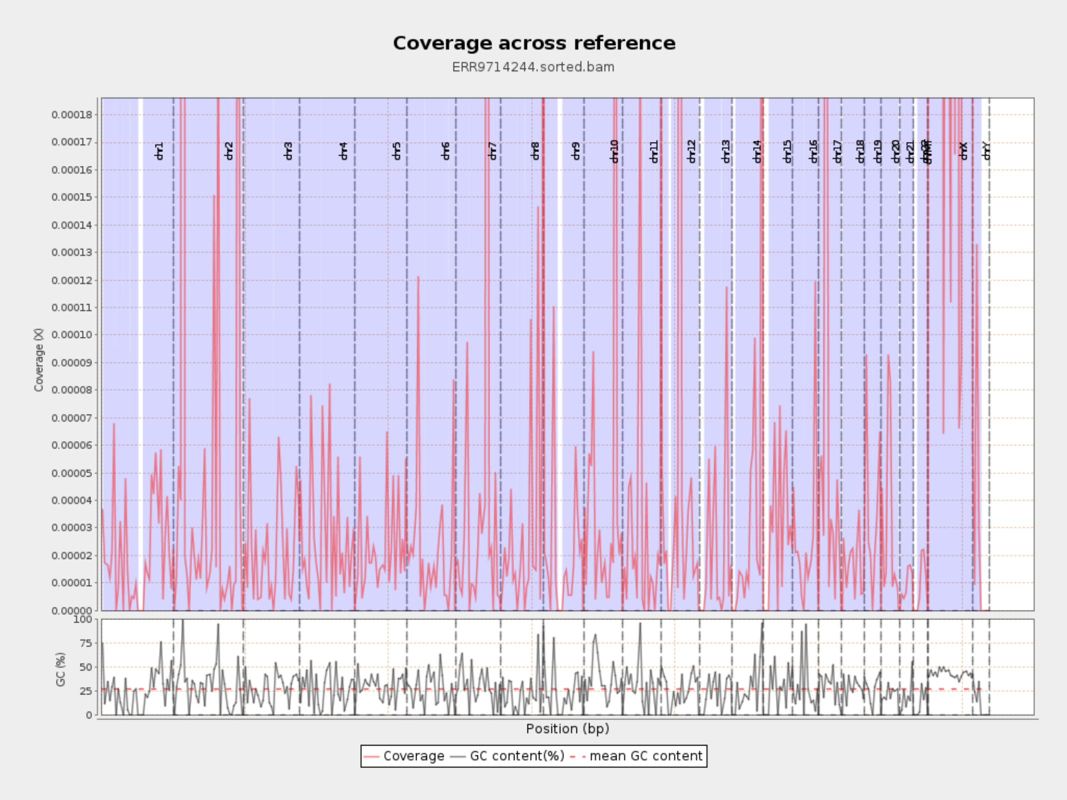
General error rate	3.33%
Mismatches	111,602
Insertions	4,939
Mapped reads with at least one insertion	8.37%
Deletions	2,303
Mapped reads with at least one deletion	5.27%
Homopolymer indels	62.59%

2.6. Chromosome stats

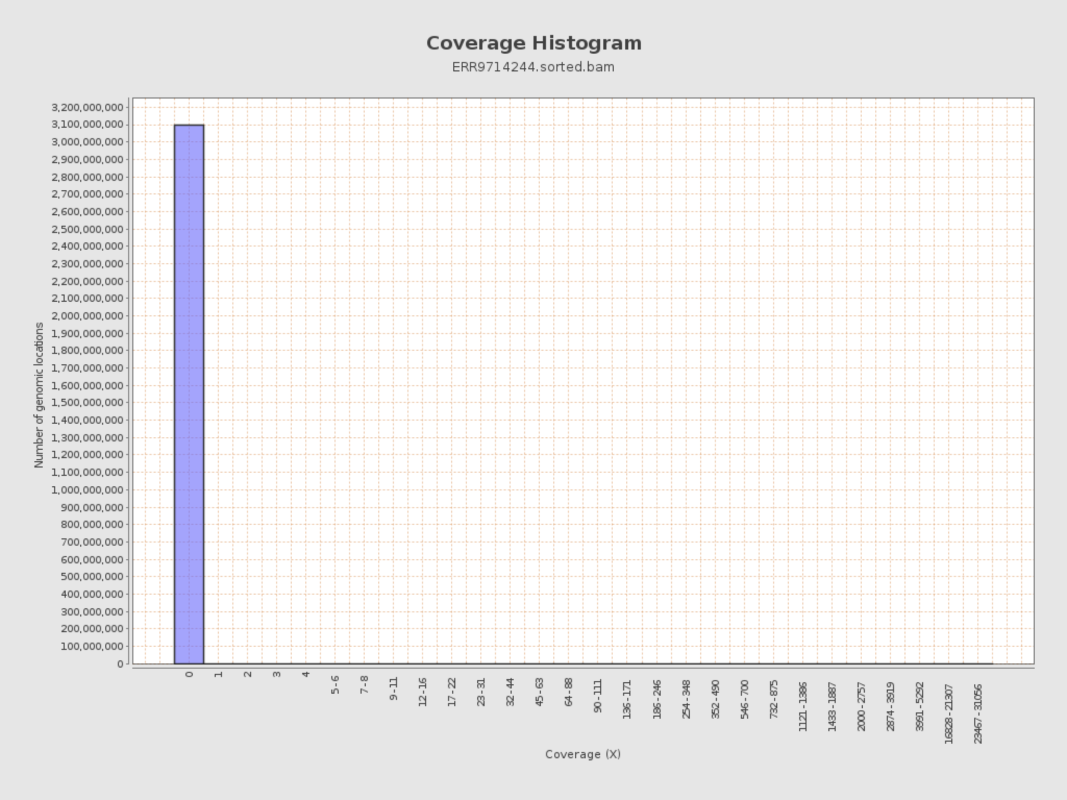
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5248	0	0.0081
chr2	243199373	4243629	0.0174	19.0779
chr3	198022430	4368	0	0.0077
chr4	191154276	5056	0	0.008
chr5	180915260	4089	0	0.0058
chr6	171115067	4096	0	0.0104
chr7	159138663	8896	0.0001	0.074

chr8	146364022	4307	0	0.0136
chr9	141213431	3318	0	0.0123
chr10	135534747	6477	0	0.0217
chr11	135006516	3762	0	0.0227
chr12	133851895	8611	0.0001	0.0535
chr13	115169878	2437	0	0.007
chr14	107349540	5815	0.0001	0.057
chr15	102531392	3070	0	0.0111
chr16	90354753	2376	0	0.0119
chr17	81195210	5353	0.0001	0.0584
chr18	78077248	1311	0	0.0047
chr19	59128983	2051	0	0.0125
chr20	63025520	2021	0	0.0161
chr21	48129895	448	0	0.0031
chr22	51304566	481	0	0.0038
chrMT	16571	2738	0.1652	0.8461
chrX	155270560	87533	0.0006	0.1039
chrY	59373566	1654	0	0.011

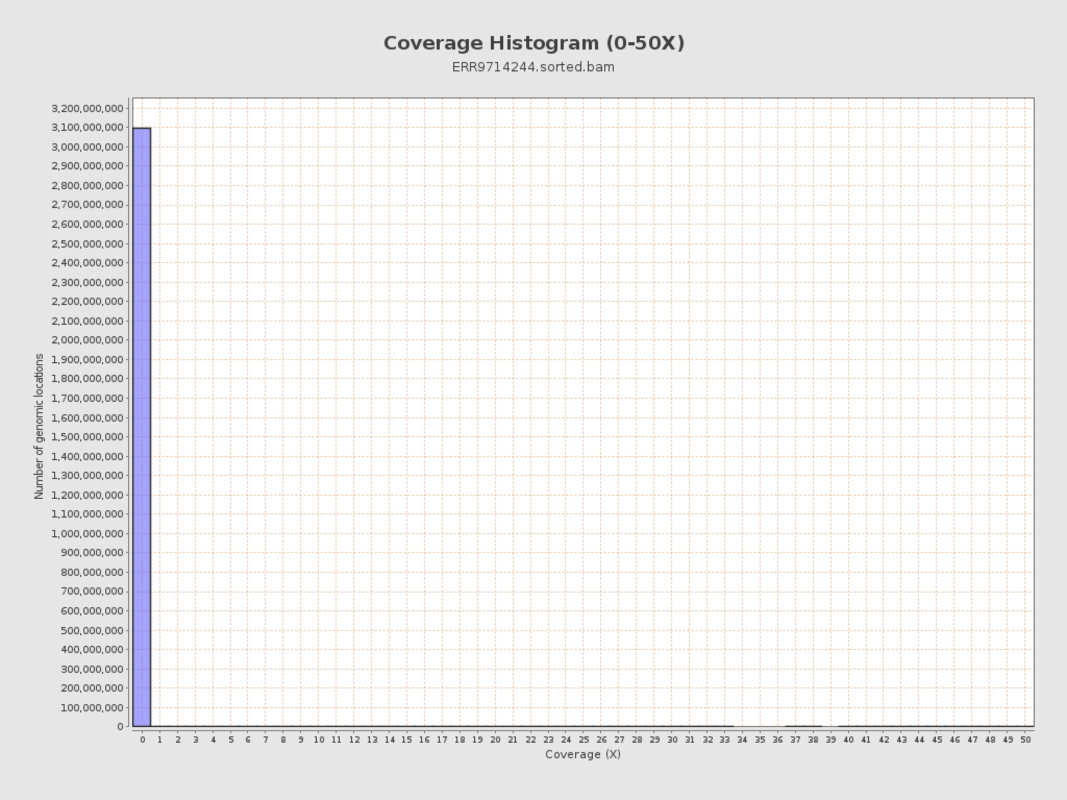
3. Results : Coverage across reference



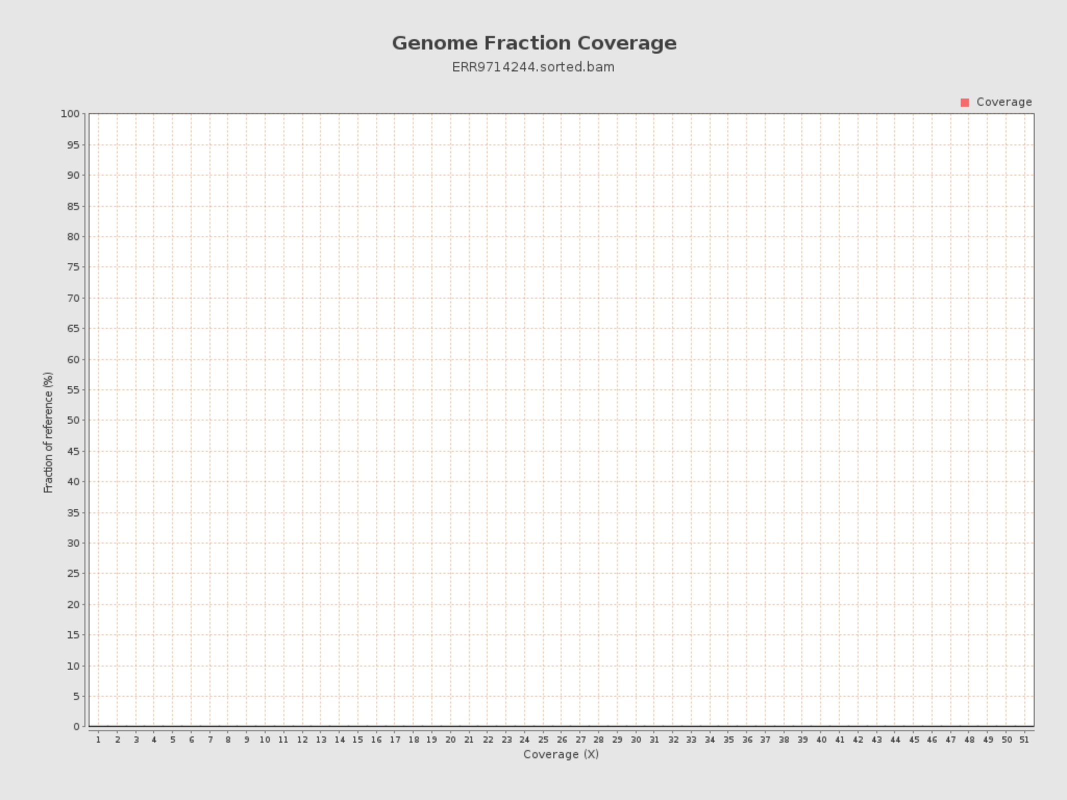
4. Results : Coverage Histogram



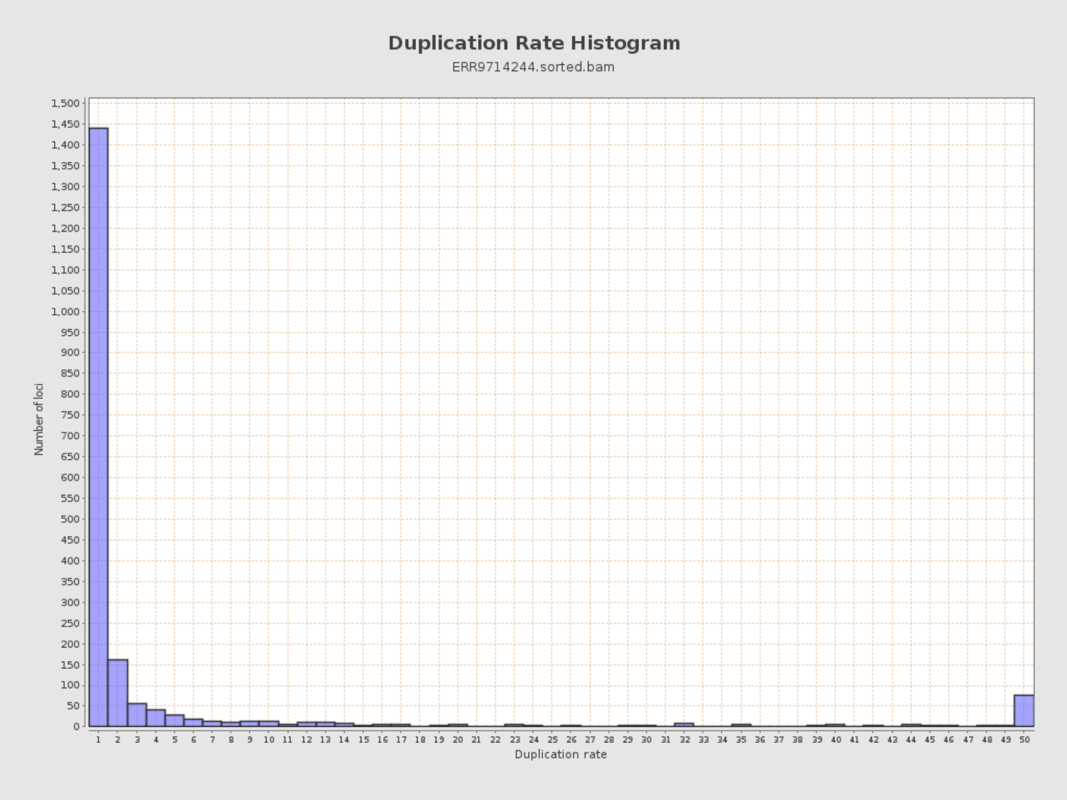
5. Results : Coverage Histogram (0-50X)



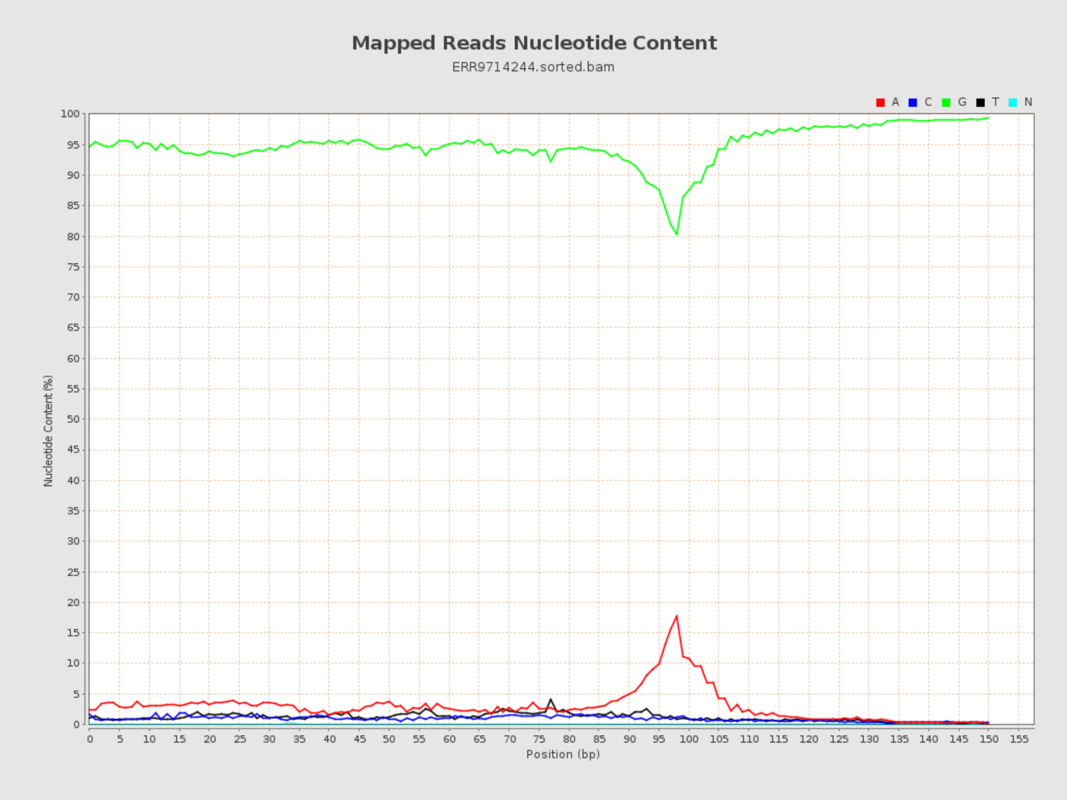
6. Results : Genome Fraction Coverage



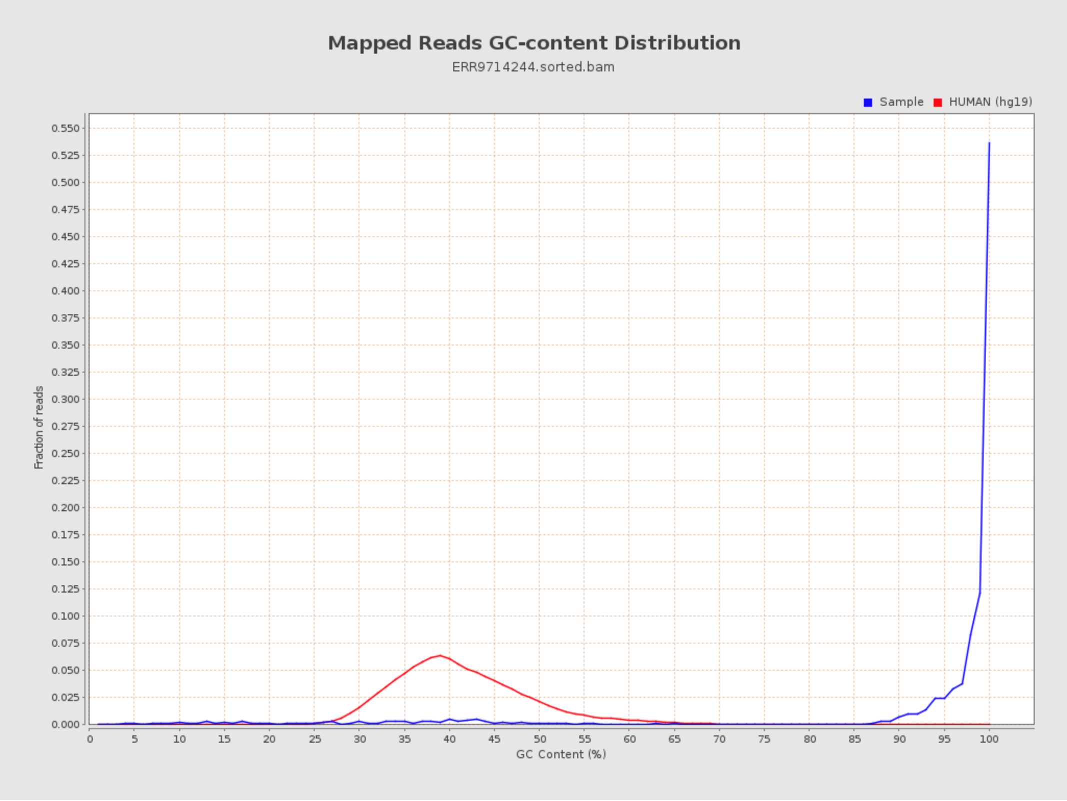
7. Results : Duplication Rate Histogram



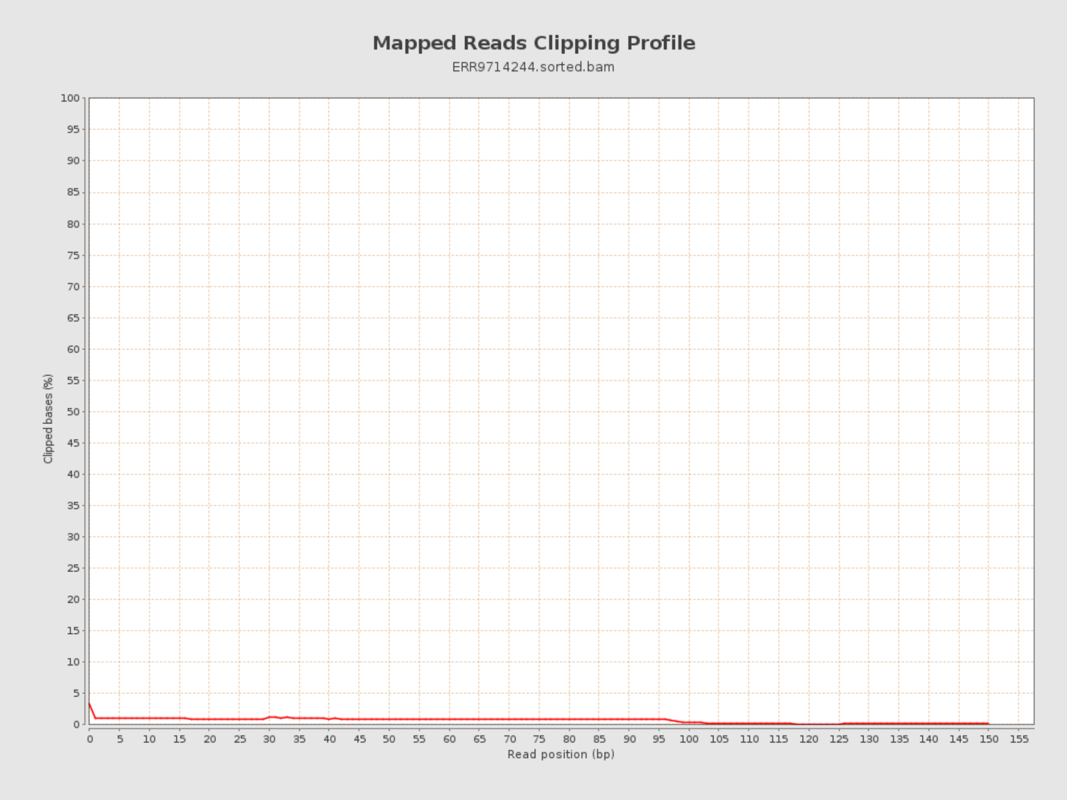
8. Results : Mapped Reads Nucleotide Content



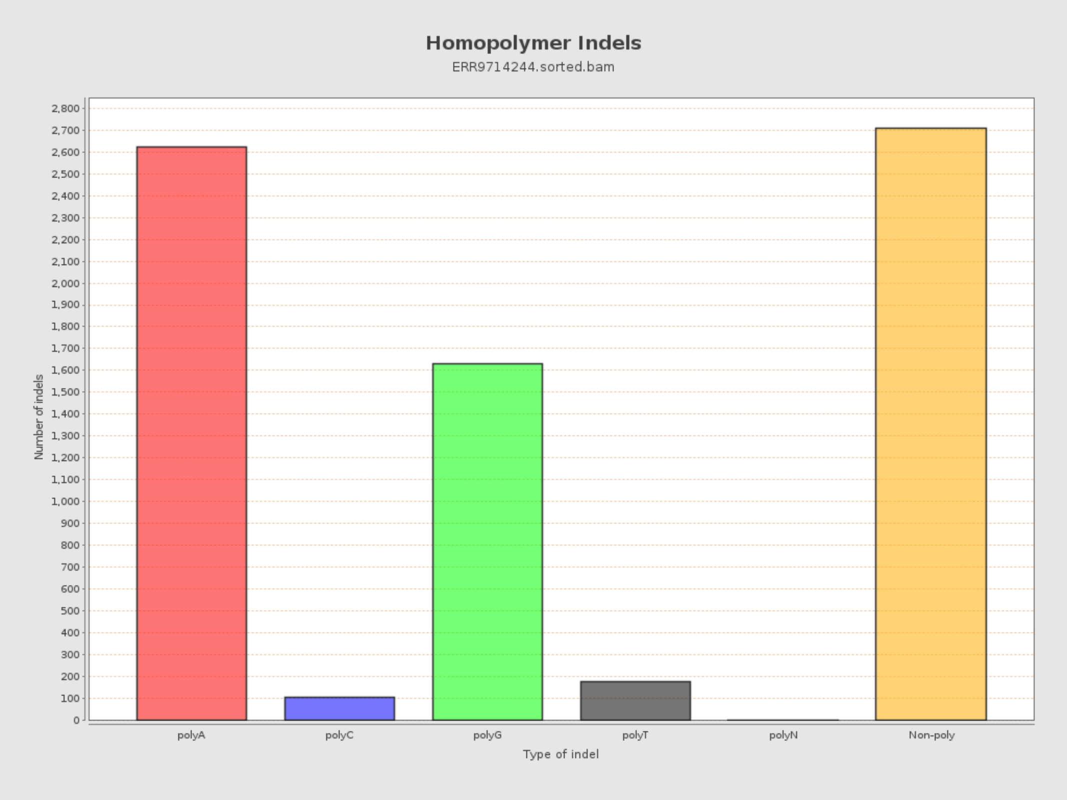
9. Results : Mapped Reads GC-content Distribution



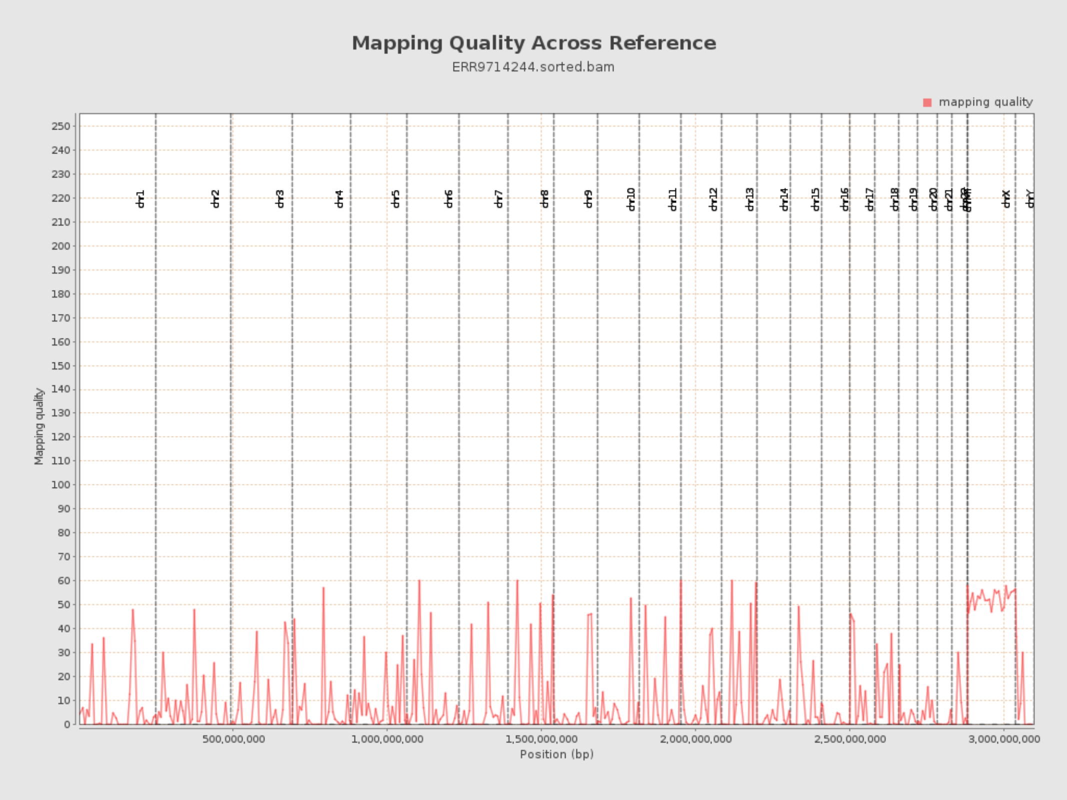
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram