Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 18:29:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714078.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_ERR9714078 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714078.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 18:29:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714078.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	691,734
Mapped reads	104,176 / 15.06%
Unmapped reads	587,558 / 84.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,716 / 0.25%
Read min/max/mean length	30 / 151 / 61.09
Duplicated reads (estimated)	102,783 / 14.86%
Duplication rate	27.98%
Clipped reads	53,547 / 7.74%

2.2. ACGT Content

Number/percentage of A's	194,909 / 1.79%
Number/percentage of C's	70,183 / 0.65%
Number/percentage of T's	76,966 / 0.71%
Number/percentage of G's	10,521,138 / 96.85%
Number/percentage of N's	251 / 0%
GC Percentage	97.5%

2.3. Coverage

Mean	0.0035

Standard Deviation	13.461

2.4. Mapping Quality

Mean Mapping Quality	11.64

2.5. Mismatches and indels

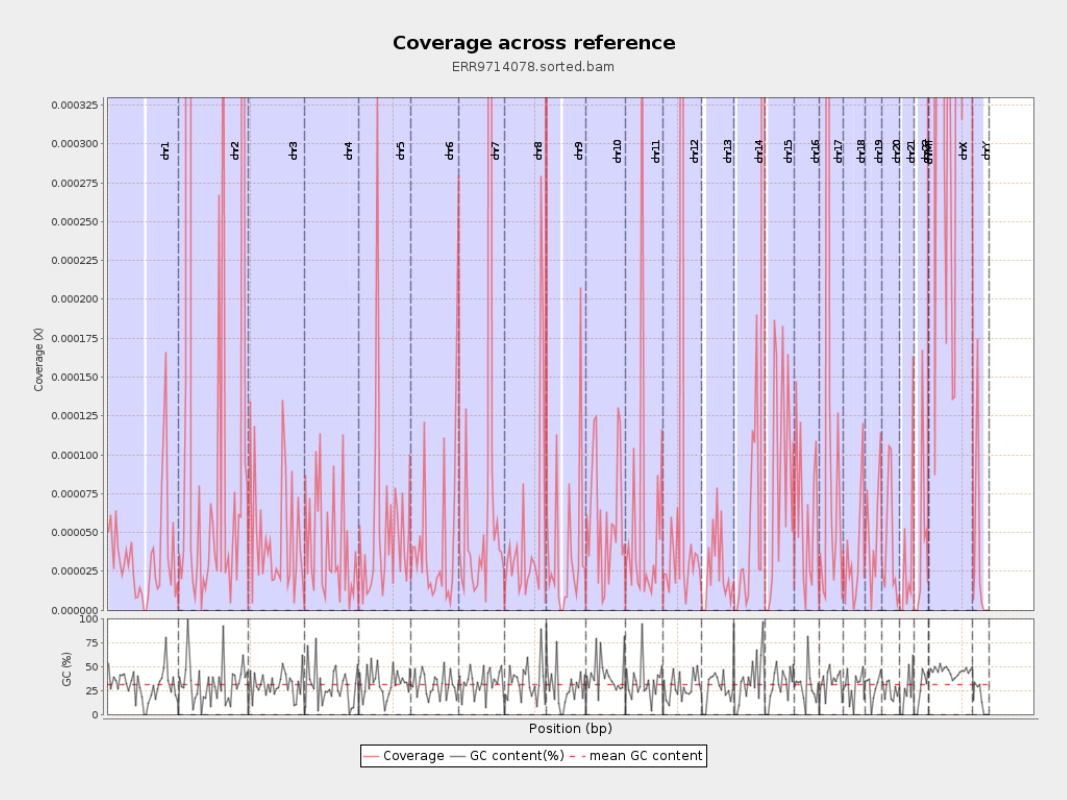
General error rate	3.31%
Mismatches	273,532
Insertions	12,525
Mapped reads with at least one insertion	8.49%
Deletions	5,336
Mapped reads with at least one deletion	4.93%
Homopolymer indels	61.79%

2.6. Chromosome stats

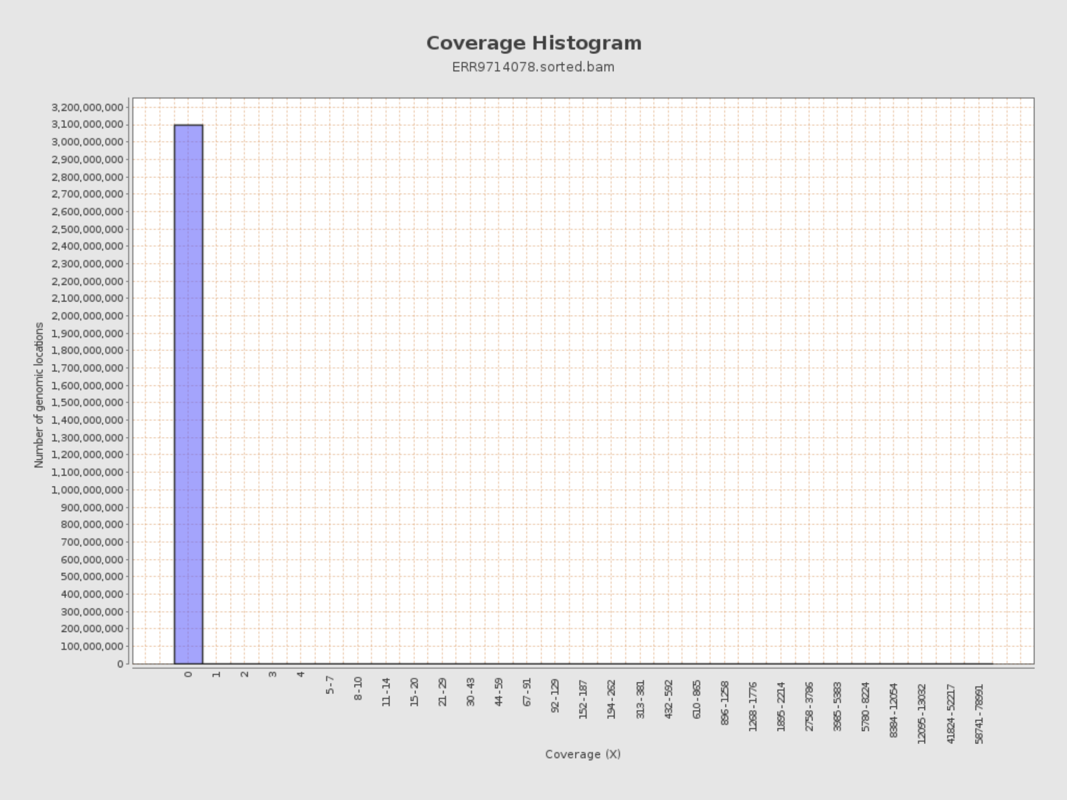
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8802	0	0.0138
chr2	243199373	10592419	0.0436	48.0255
chr3	198022430	9100	0	0.0147
chr4	191154276	7930	0	0.014
chr5	180915260	9787	0.0001	0.0168
chr6	171115067	7546	0	0.0167
chr7	159138663	17959	0.0001	0.1514

chr8	146364022	7114	0	0.0276
chr9	141213431	6279	0	0.0206
chr10	135534747	8161	0.0001	0.0207
chr11	135006516	8109	0.0001	0.0469
chr12	133851895	12983	0.0001	0.0811
chr13	115169878	2973	0	0.0063
chr14	107349540	13151	0.0001	0.1406
chr15	102531392	8620	0.0001	0.0247
chr16	90354753	5177	0.0001	0.0146
chr17	81195210	11858	0.0001	0.1432
chr18	78077248	2661	0	0.0094
chr19	59128983	2967	0.0001	0.0149
chr20	63025520	2673	0	0.02
chr21	48129895	1460	0	0.0094
chr22	51304566	2182	0	0.014
chrMT	16571	3991	0.2408	1.116
chrX	155270560	129975	0.0008	0.1156
chrY	59373566	1732	0	0.0114

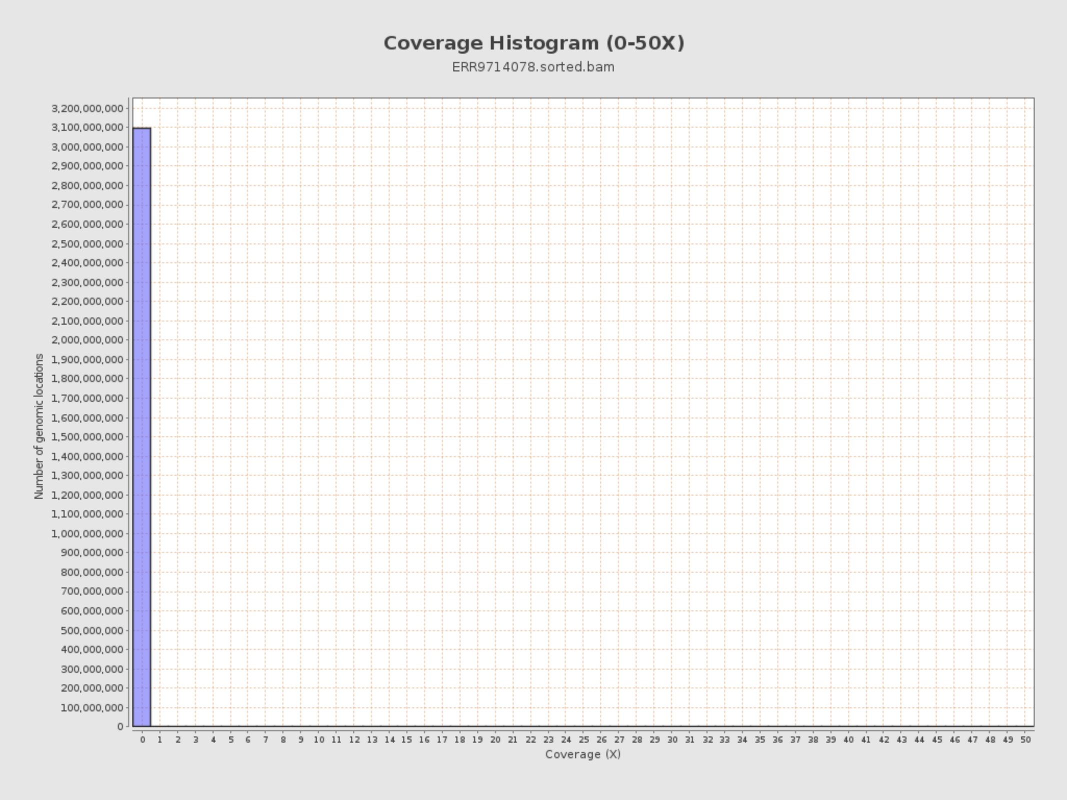
3. Results : Coverage across reference



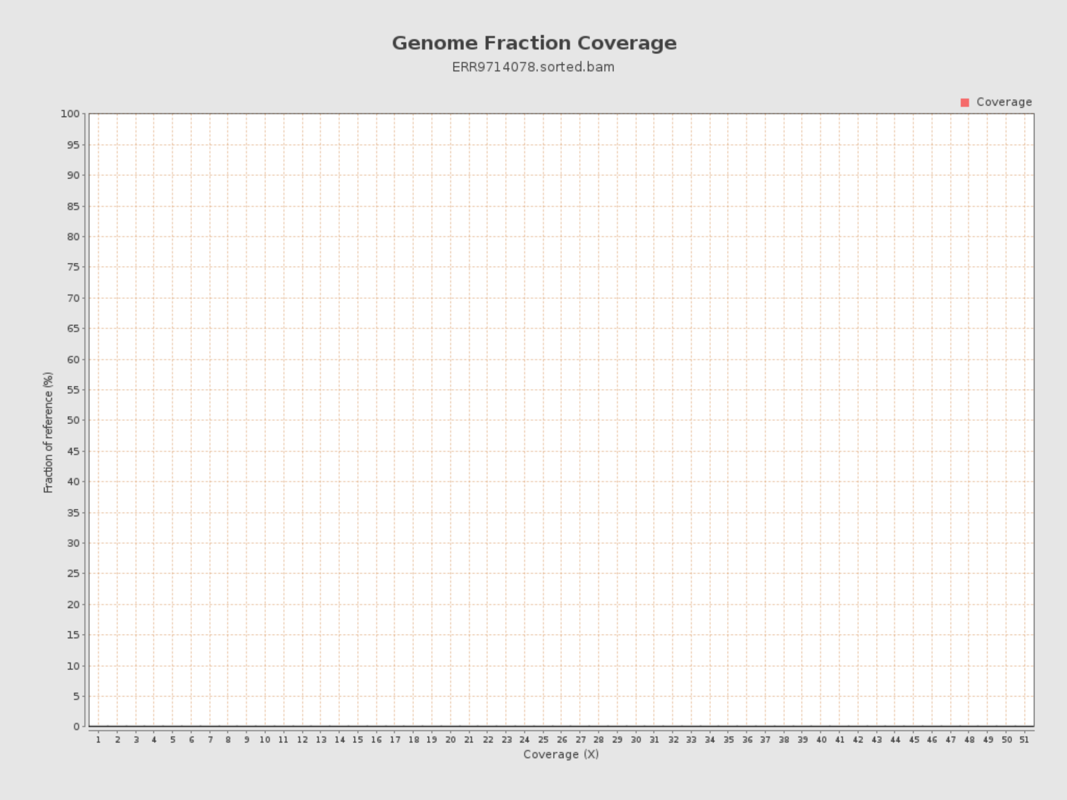
4. Results : Coverage Histogram



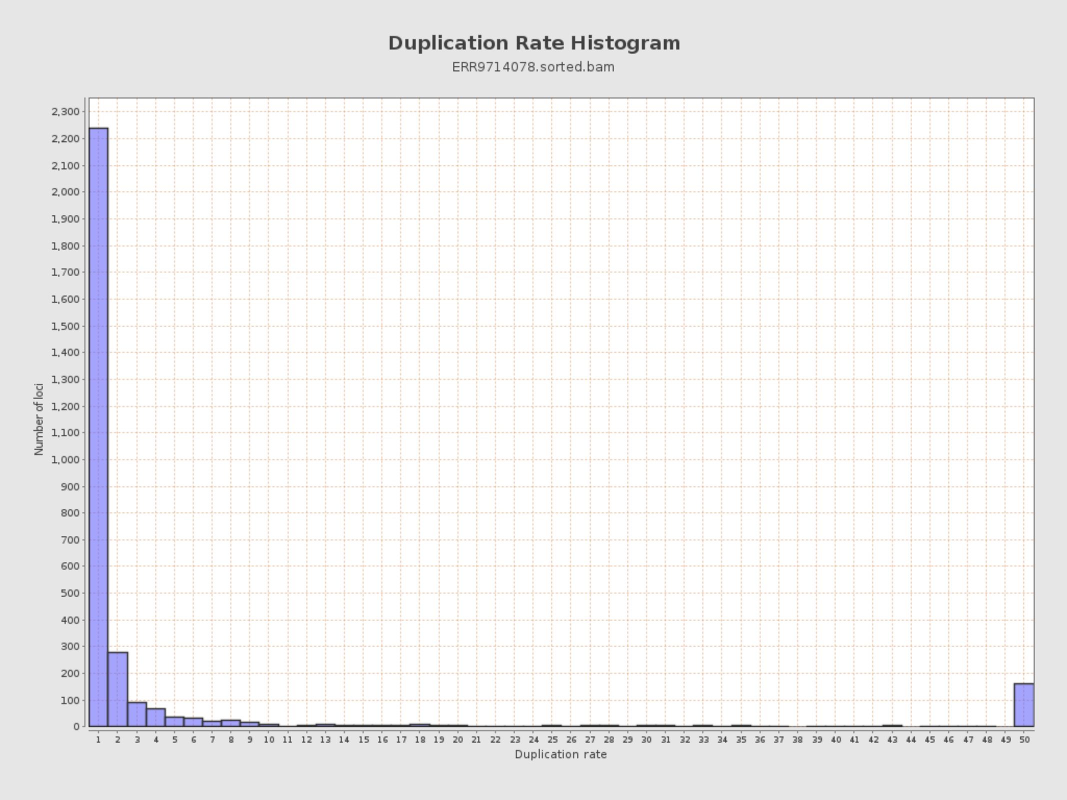
5. Results : Coverage Histogram (0-50X)



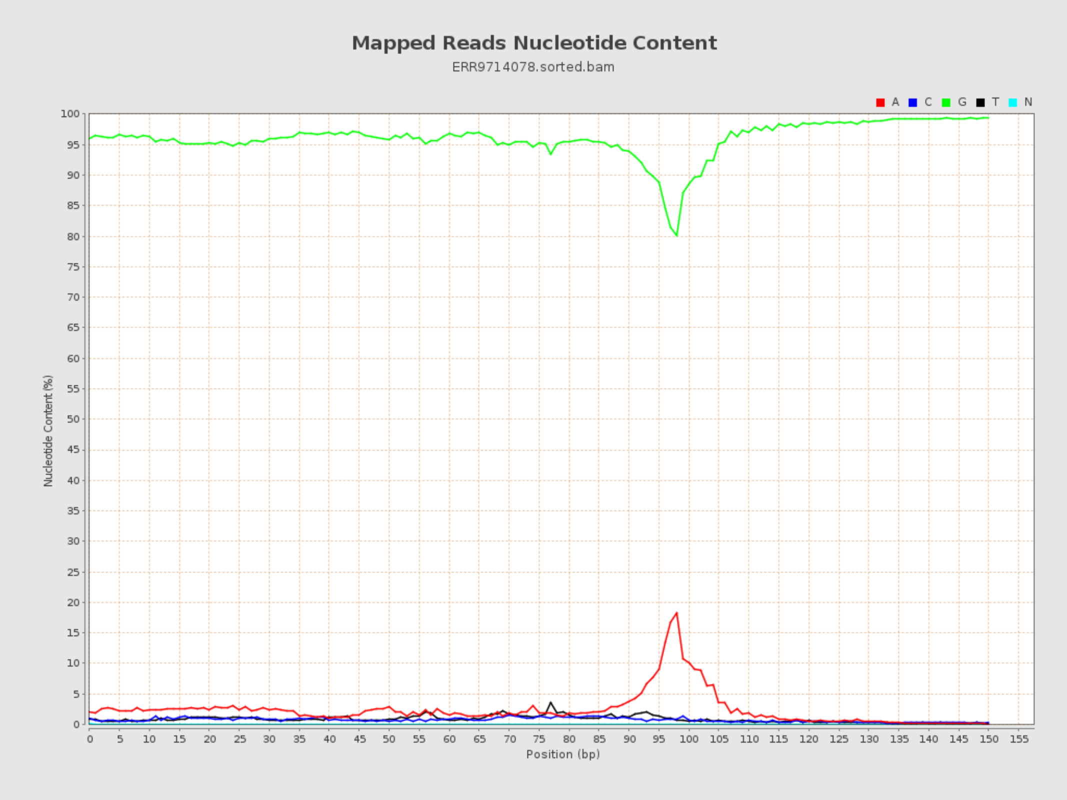
6. Results : Genome Fraction Coverage



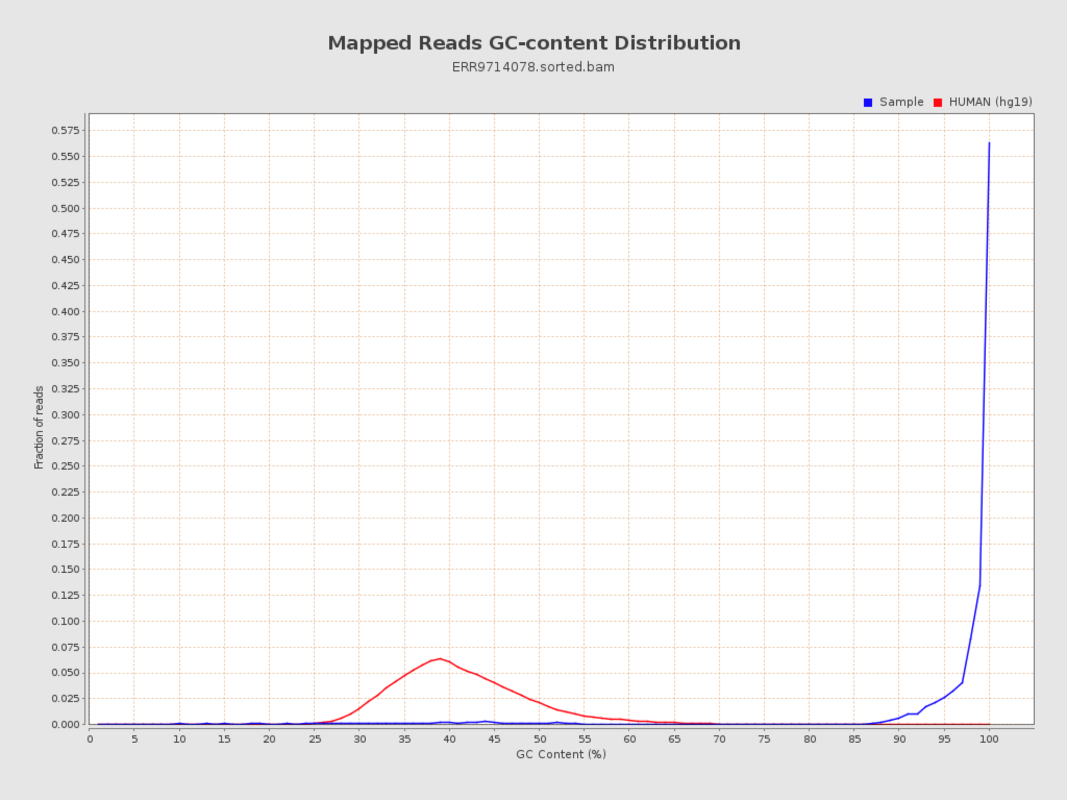
7. Results : Duplication Rate Histogram



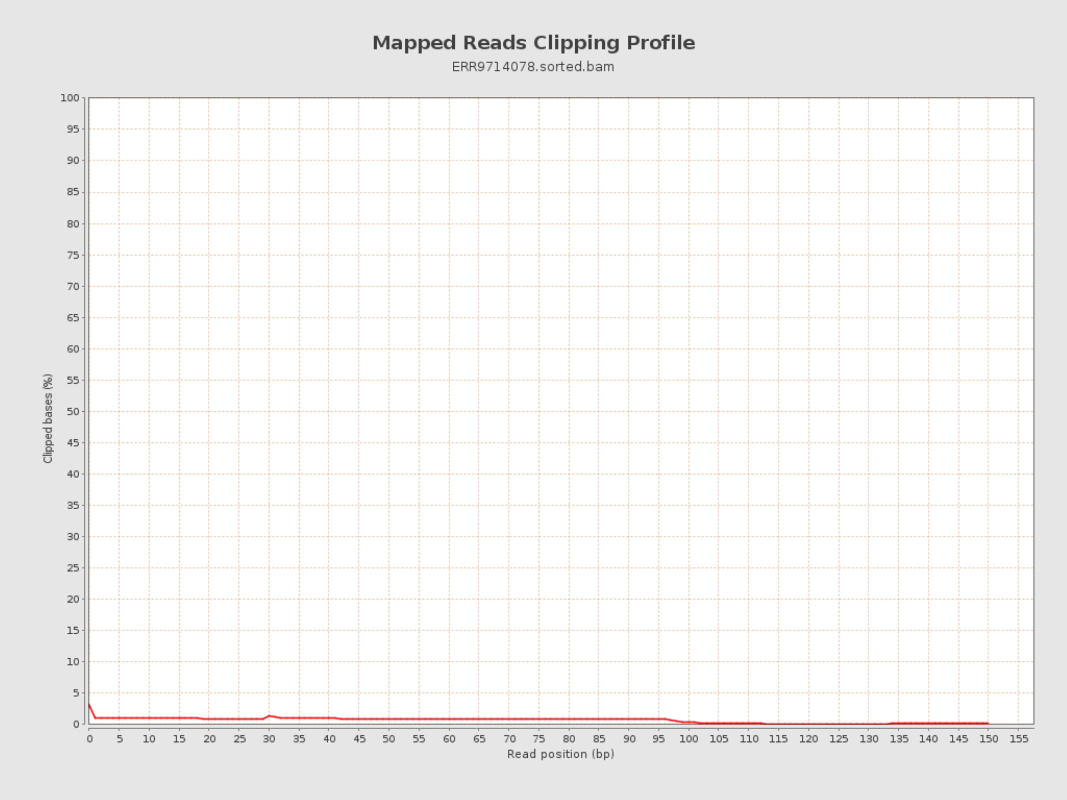
8. Results : Mapped Reads Nucleotide Content



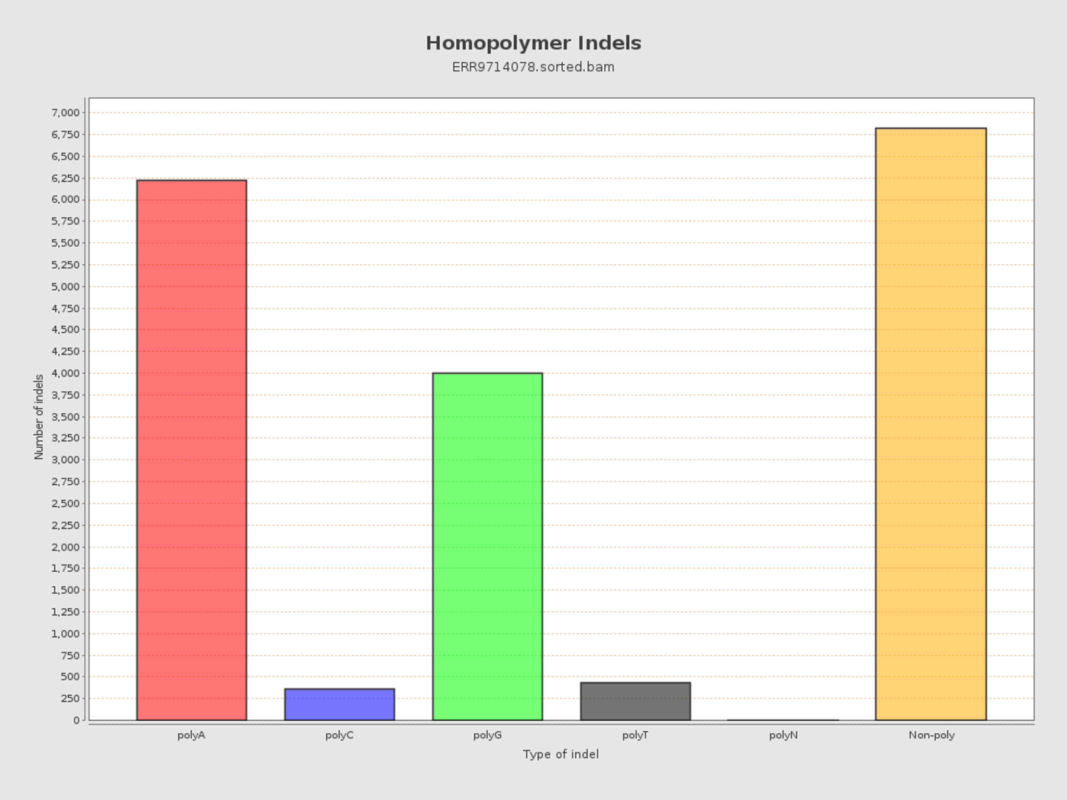
9. Results : Mapped Reads GC-content Distribution



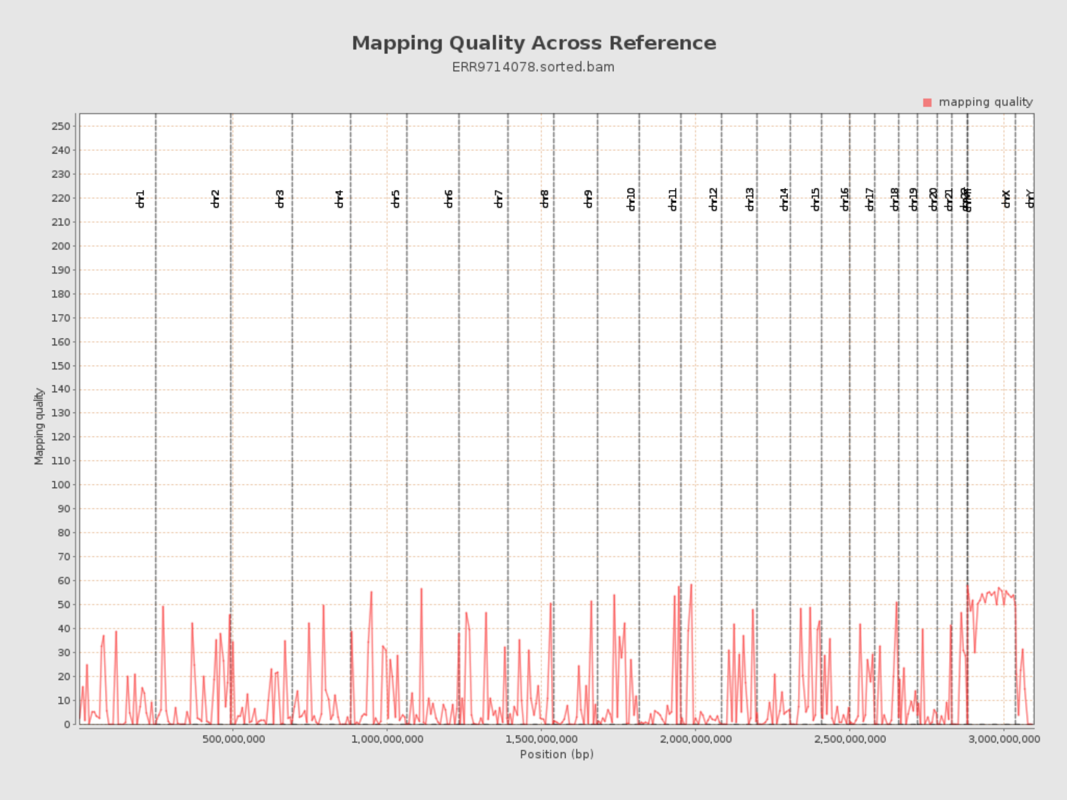
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram