Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 00:40:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714226.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_ERR9714226 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714226.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 00:40:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714226.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	186,326
Mapped reads	28,513 / 15.3%
Unmapped reads	157,813 / 84.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	973 / 0.52%
Read min/max/mean length	30 / 151 / 78.79
Duplicated reads (estimated)	22,650 / 12.16%
Duplication rate	37.86%
Clipped reads	23,595 / 12.66%

2.2. ACGT Content

Number/percentage of A's	693,837 / 21.64%
Number/percentage of C's	483,130 / 15.07%
Number/percentage of T's	636,100 / 19.84%
Number/percentage of G's	1,392,723 / 43.44%
Number/percentage of N's	106 / 0%
GC Percentage	58.51%

2.3. Coverage

Mean	0.0011

Standard Deviation	1.1992

2.4. Mapping Quality

Mean Mapping Quality	41.61

2.5. Mismatches and indels

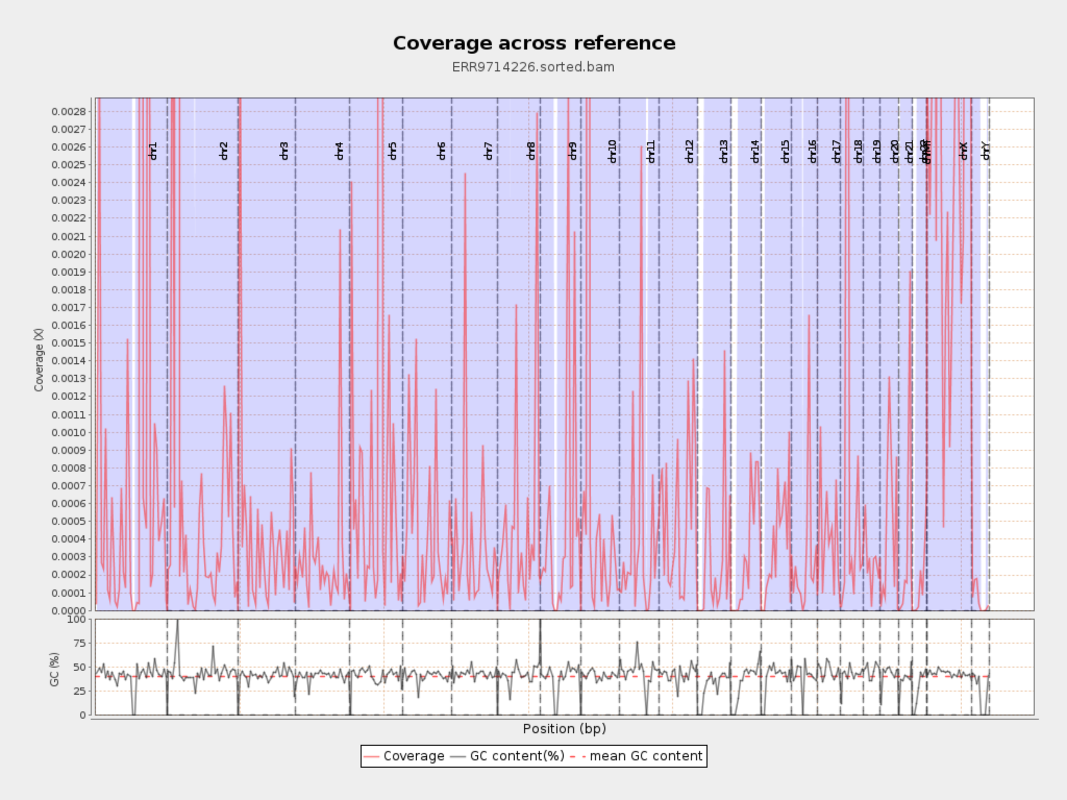
General error rate	4.32%
Mismatches	126,075
Insertions	3,994
Mapped reads with at least one insertion	12.31%
Deletions	9,839
Mapped reads with at least one deletion	31.87%
Homopolymer indels	32.13%

2.6. Chromosome stats

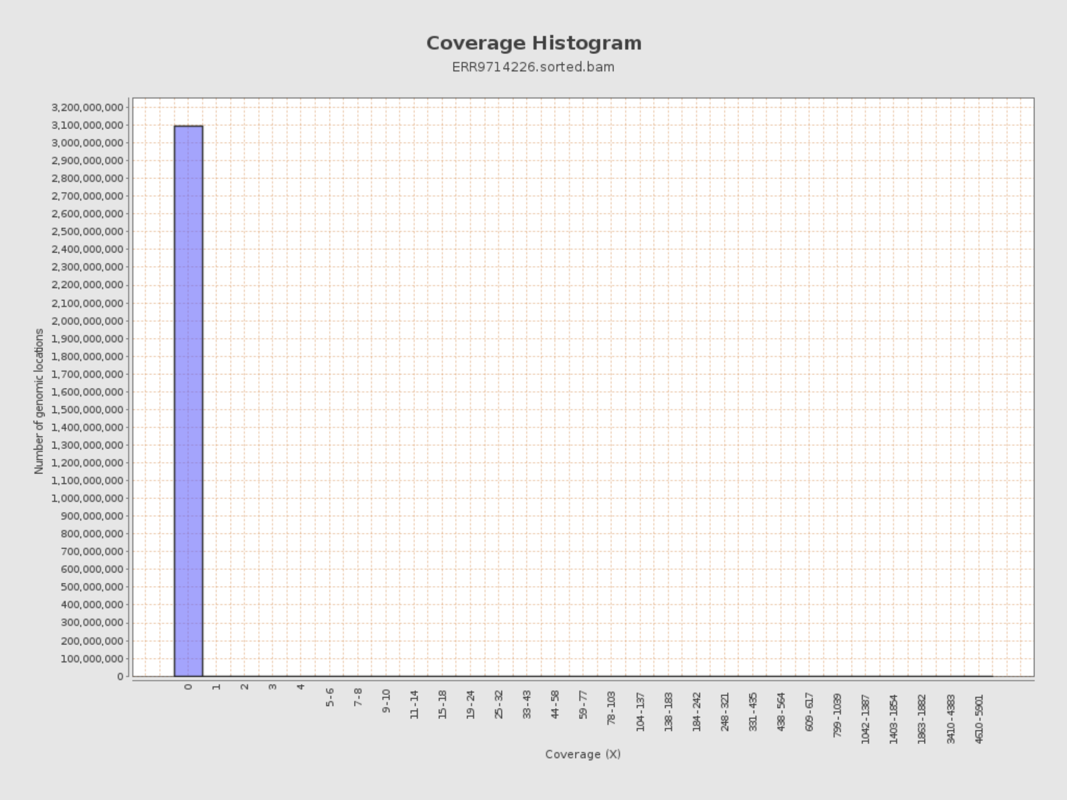
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	401539	0.0016	1.223
chr2	243199373	1025711	0.0042	3.8173
chr3	198022430	90484	0.0005	0.1479
chr4	191154276	58399	0.0003	0.087
chr5	180915260	371691	0.0021	1.551
chr6	171115067	75684	0.0004	0.093
chr7	159138663	62469	0.0004	0.15

chr8	146364022	71844	0.0005	0.1347
chr9	141213431	68726	0.0005	0.1599
chr10	135534747	116796	0.0009	0.5362
chr11	135006516	55509	0.0004	0.141
chr12	133851895	70234	0.0005	0.1096
chr13	115169878	31541	0.0003	0.0666
chr14	107349540	33379	0.0003	0.0737
chr15	102531392	39274	0.0004	0.0608
chr16	90354753	28174	0.0003	0.1
chr17	81195210	33120	0.0004	0.0804
chr18	78077248	64748	0.0008	0.3679
chr19	59128983	16360	0.0003	0.0445
chr20	63025520	32251	0.0005	0.0896
chr21	48129895	18701	0.0004	0.1325
chr22	51304566	8072	0.0002	0.038
chrMT	16571	16198	0.9775	4.481
chrX	155270560	474314	0.0031	0.3981
chrY	59373566	3612	0.0001	0.0145

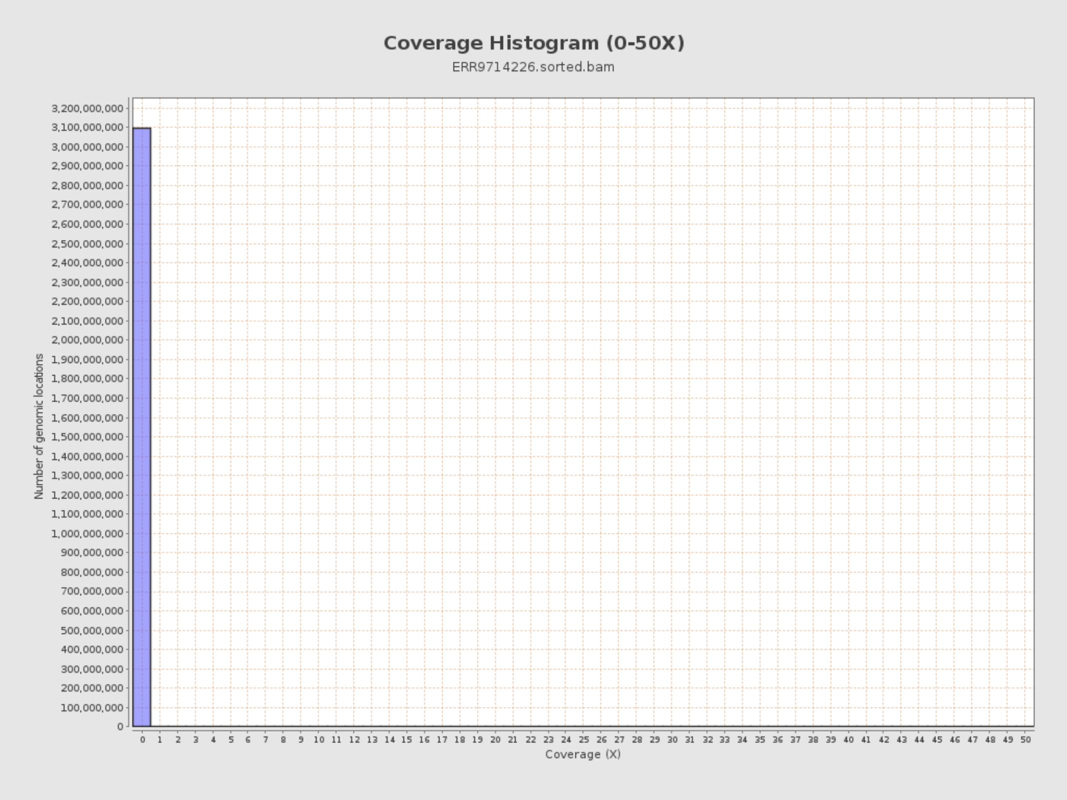
3. Results : Coverage across reference



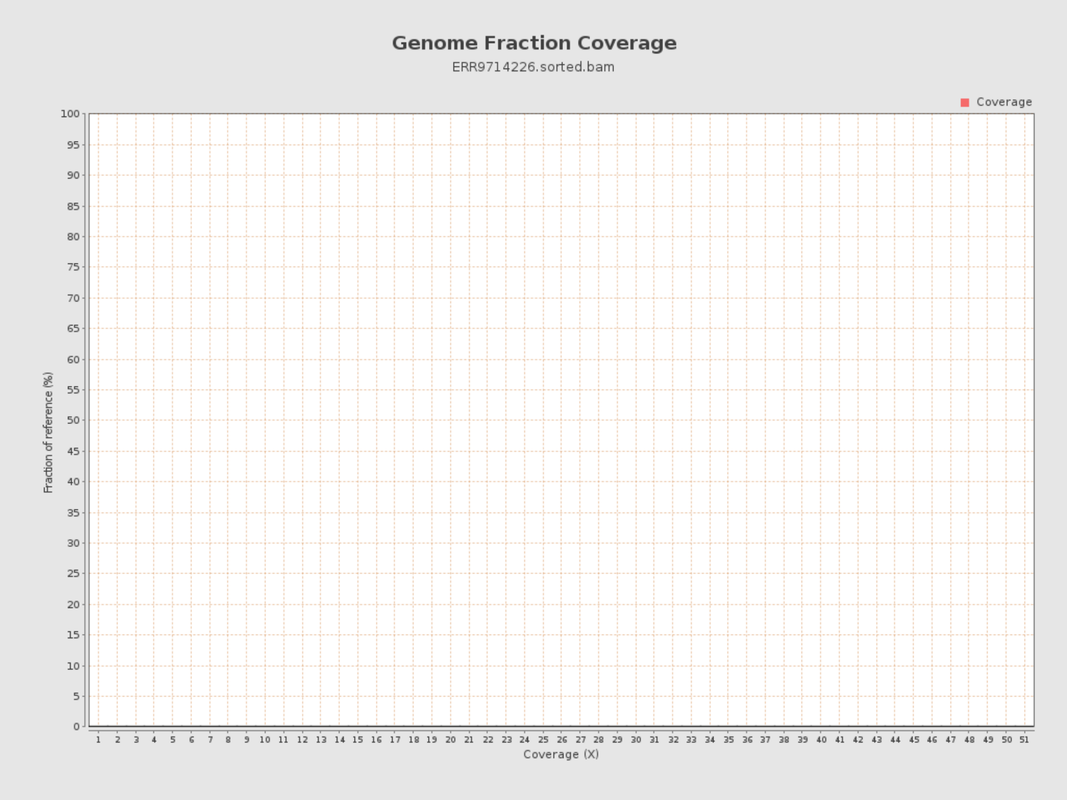
4. Results : Coverage Histogram



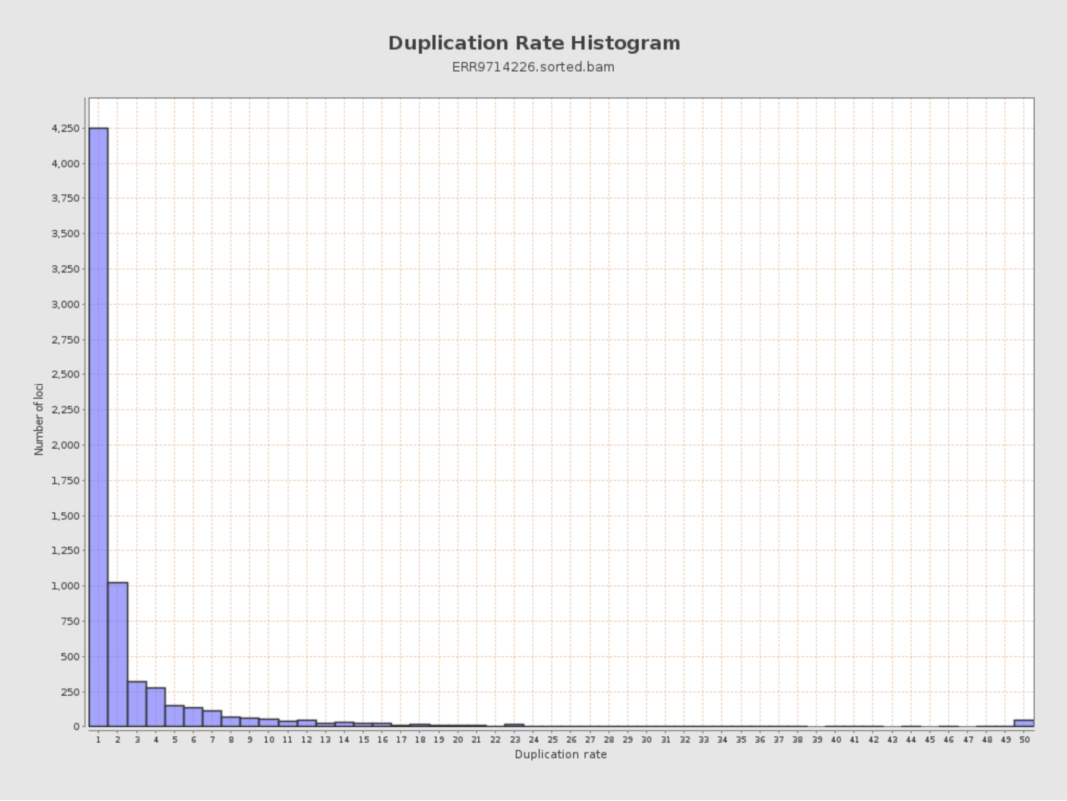
5. Results : Coverage Histogram (0-50X)



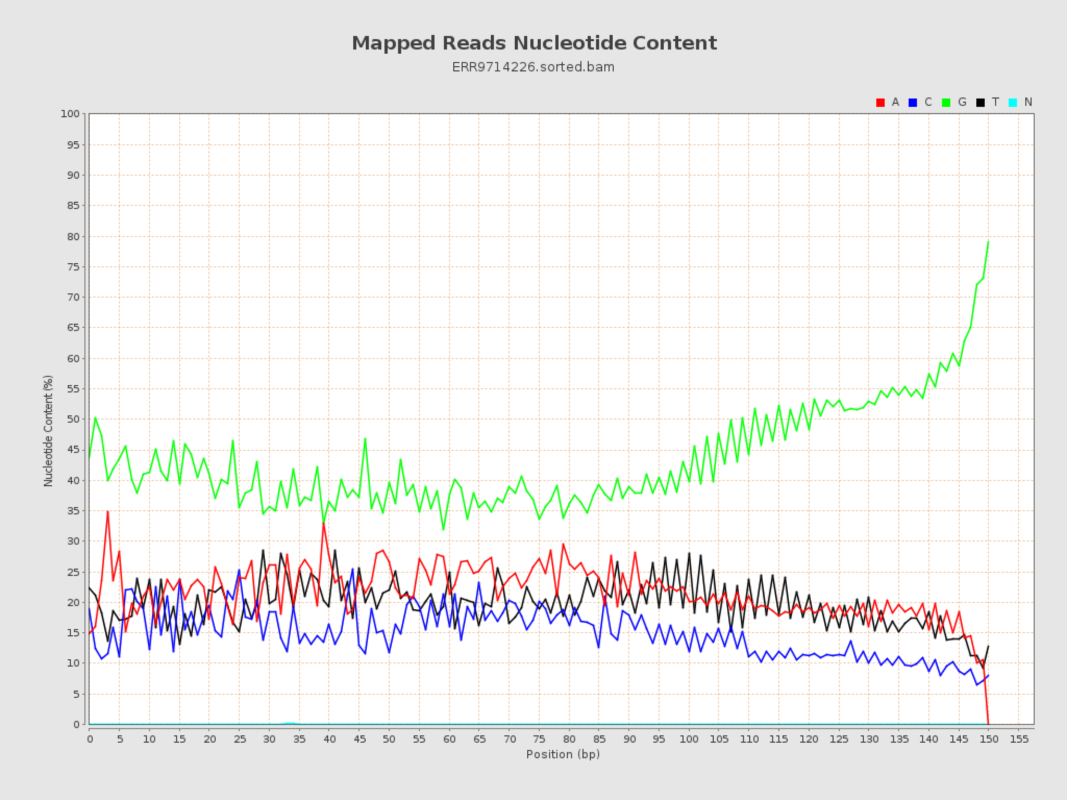
6. Results : Genome Fraction Coverage



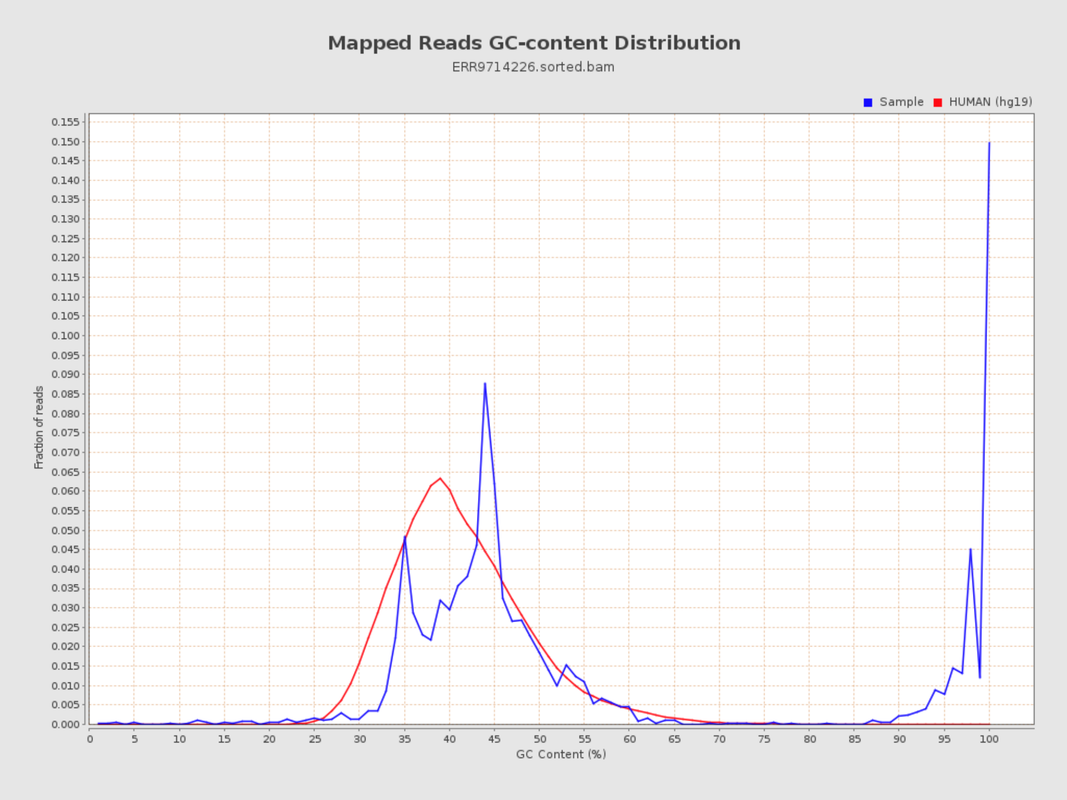
7. Results : Duplication Rate Histogram



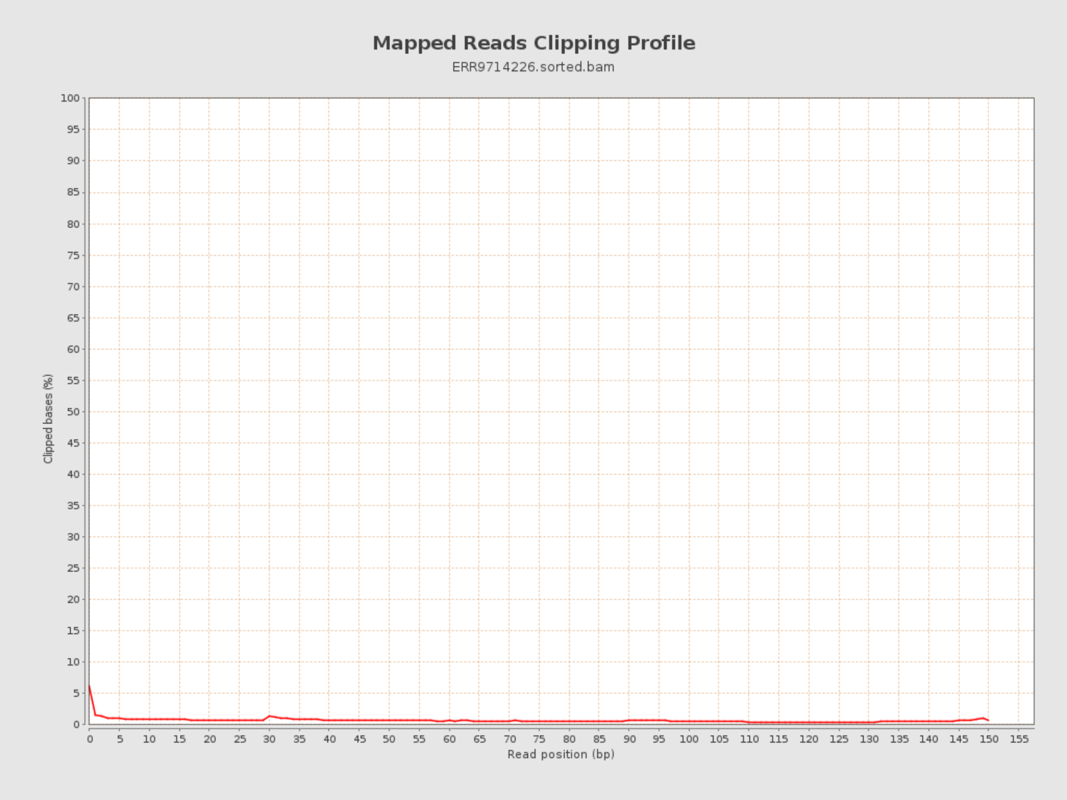
8. Results : Mapped Reads Nucleotide Content



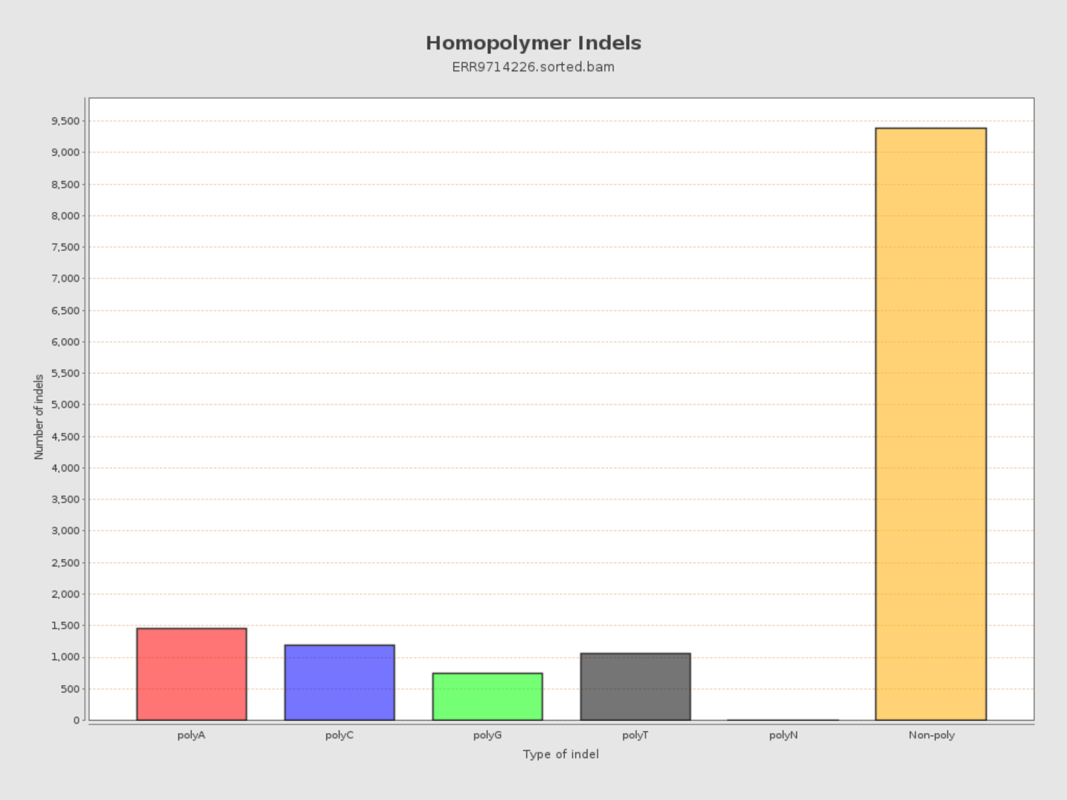
9. Results : Mapped Reads GC-content Distribution



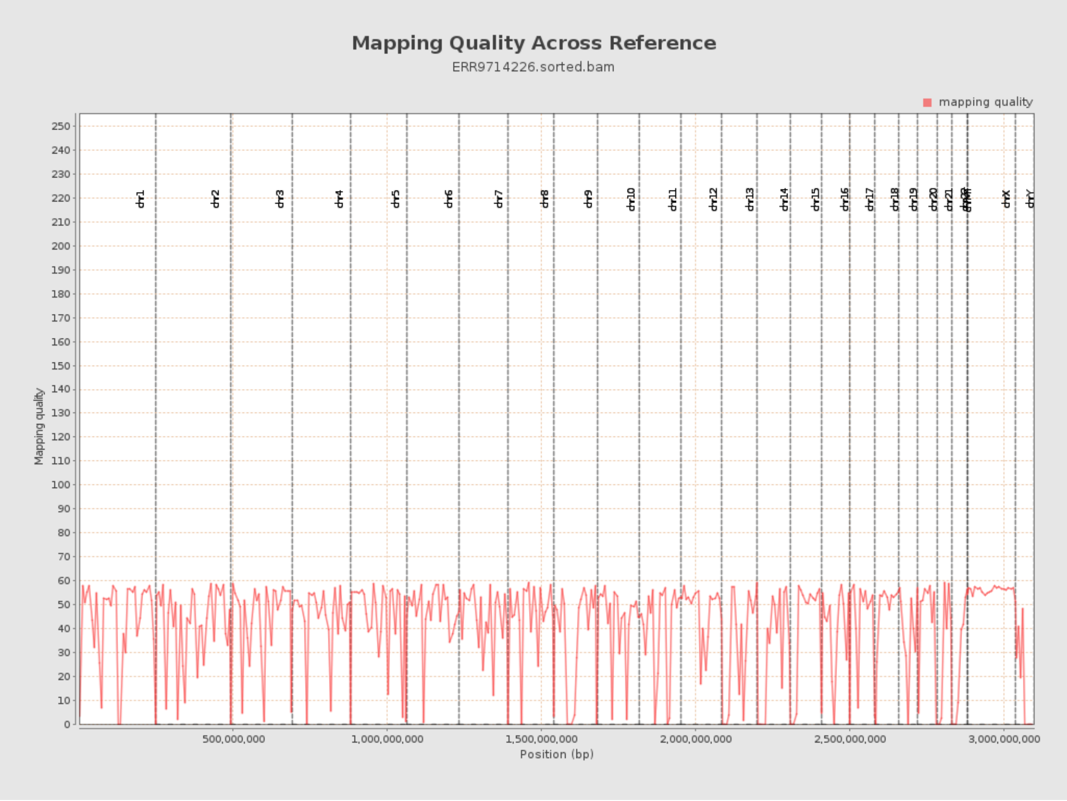
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram