Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 22:06:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714157.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_ERR9714157 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714157.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 22:06:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714157.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	41,904
Mapped reads	8,460 / 20.19%
Unmapped reads	33,444 / 79.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	475 / 1.13%
Read min/max/mean length	30 / 151 / 69.19
Duplicated reads (estimated)	6,555 / 15.64%
Duplication rate	37.52%
Clipped reads	7,806 / 18.63%

2.2. ACGT Content

Number/percentage of A's	246,902 / 25.16%
Number/percentage of C's	164,314 / 16.75%
Number/percentage of T's	226,991 / 23.13%
Number/percentage of G's	343,023 / 34.96%
Number/percentage of N's	13 / 0%
GC Percentage	51.7%

2.3. Coverage

Mean	0.0003

Standard Deviation	0.2328

2.4. Mapping Quality

Mean Mapping Quality	32.09

2.5. Mismatches and indels

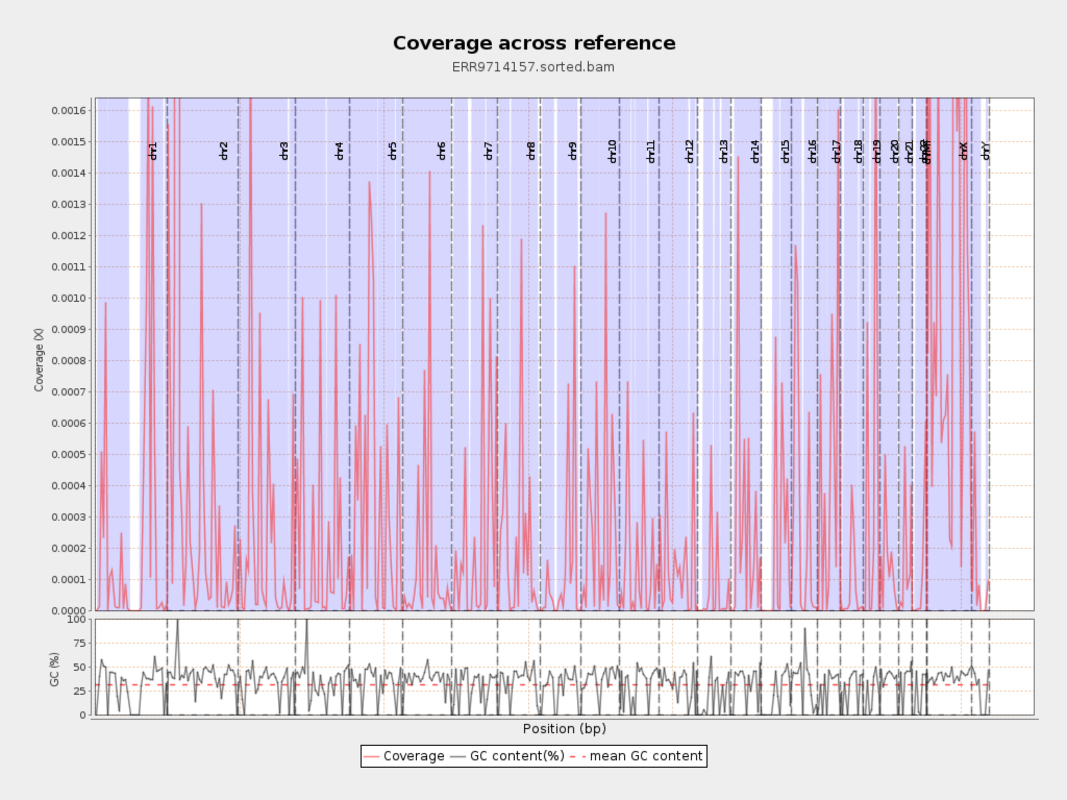
General error rate	3.89%
Mismatches	33,536
Insertions	1,078
Mapped reads with at least one insertion	11.74%
Deletions	2,527
Mapped reads with at least one deletion	28.52%
Homopolymer indels	29.76%

2.6. Chromosome stats

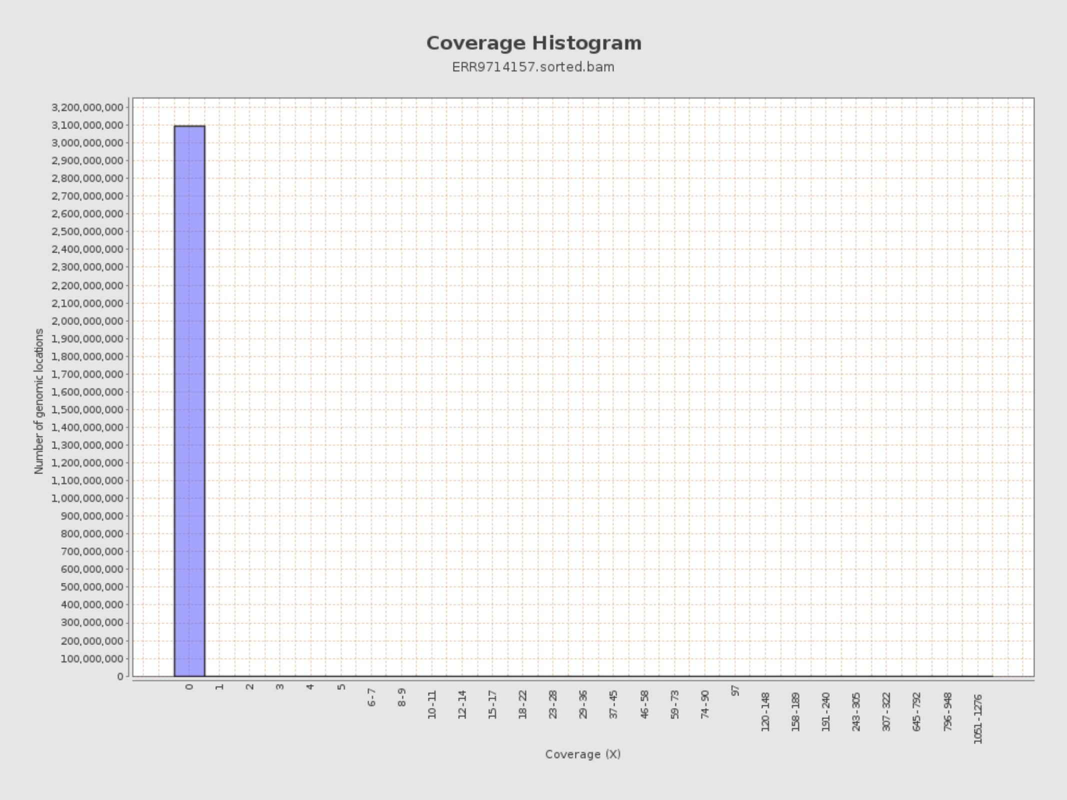
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	60396	0.0002	0.1041
chr2	243199373	244851	0.001	0.7774
chr3	198022430	47848	0.0002	0.0793
chr4	191154276	41849	0.0002	0.0714
chr5	180915260	68478	0.0004	0.1047
chr6	171115067	26738	0.0002	0.0659
chr7	159138663	37047	0.0002	0.0772

chr8	146364022	29519	0.0002	0.0626
chr9	141213431	19782	0.0001	0.0679
chr10	135534747	34978	0.0003	0.08
chr11	135006516	19084	0.0001	0.0455
chr12	133851895	20175	0.0002	0.0417
chr13	115169878	7913	0.0001	0.0371
chr14	107349540	28050	0.0003	0.0723
chr15	102531392	18287	0.0002	0.063
chr16	90354753	26512	0.0003	0.0837
chr17	81195210	34726	0.0004	0.1103
chr18	78077248	6030	0.0001	0.0355
chr19	59128983	23002	0.0004	0.1224
chr20	63025520	9291	0.0001	0.0484
chr21	48129895	7748	0.0002	0.054
chr22	51304566	5788	0.0001	0.0476
chrMT	16571	13098	0.7904	6.2996
chrX	155270560	158973	0.001	0.1742
chrY	59373566	6227	0.0001	0.047

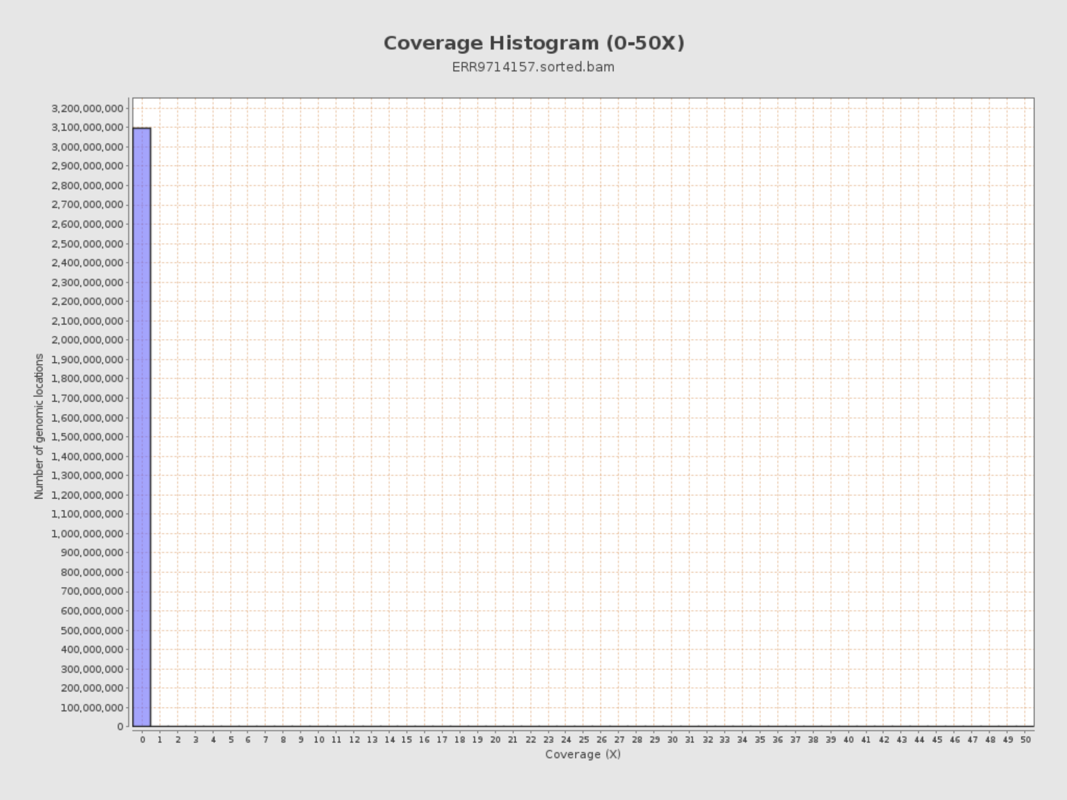
3. Results : Coverage across reference



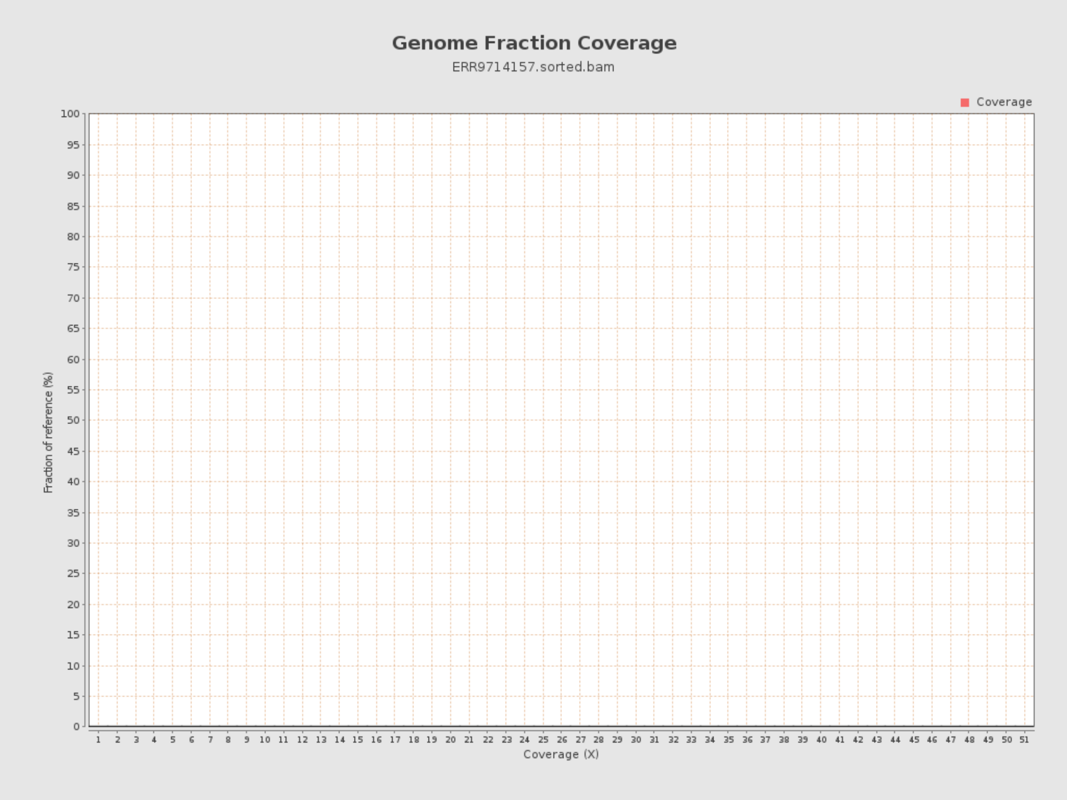
4. Results : Coverage Histogram



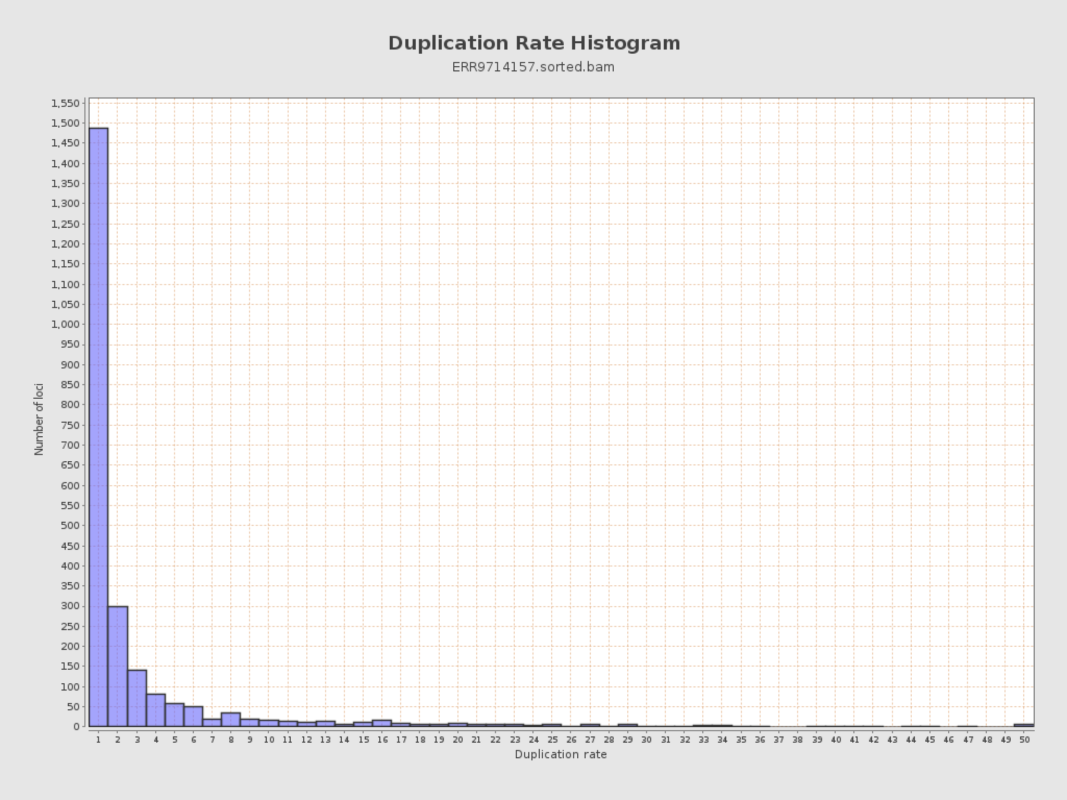
5. Results : Coverage Histogram (0-50X)



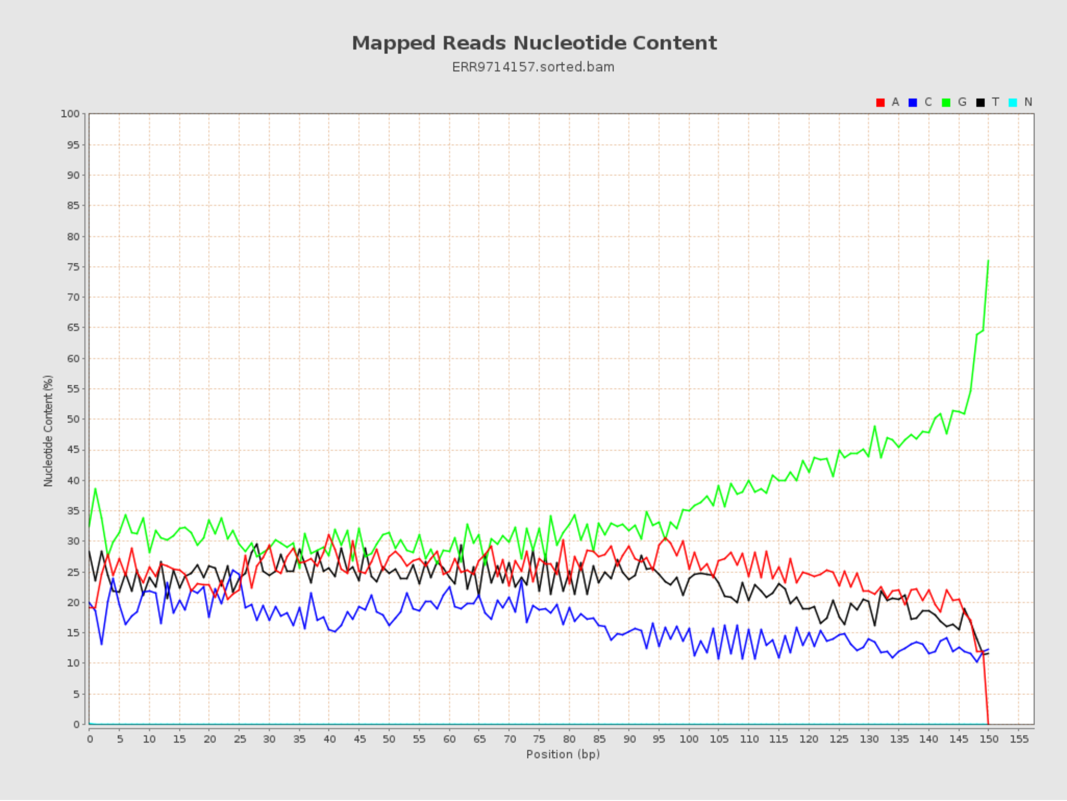
6. Results : Genome Fraction Coverage



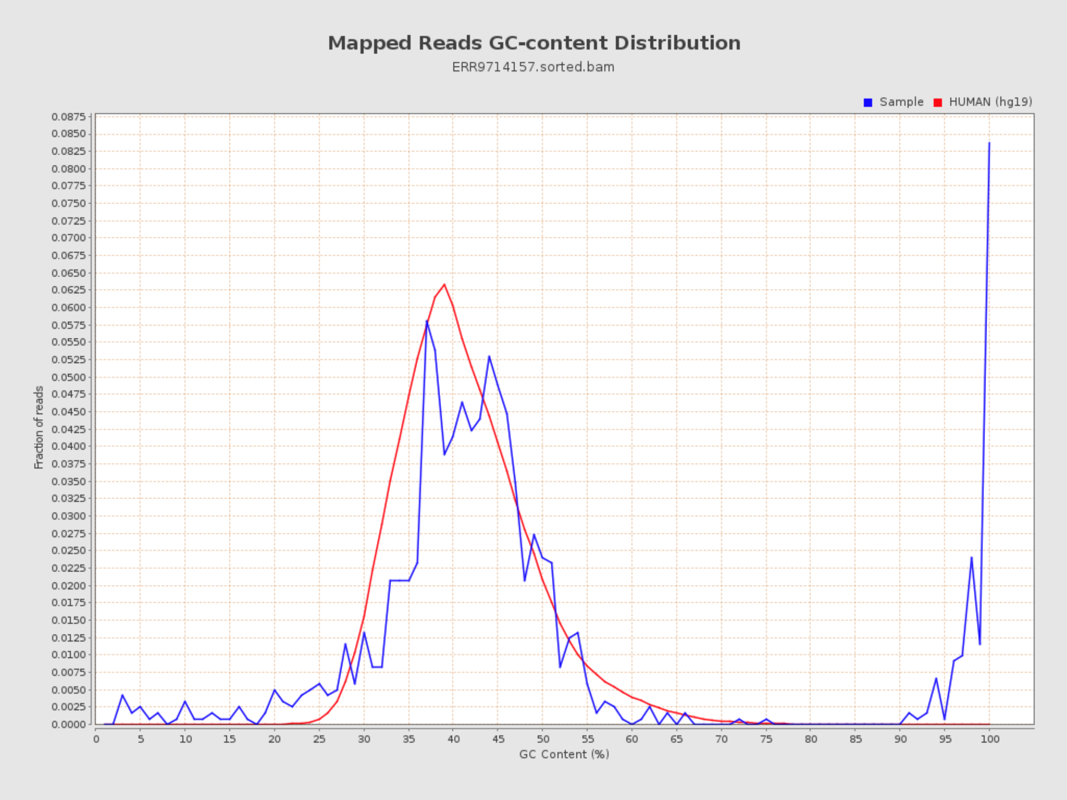
7. Results : Duplication Rate Histogram



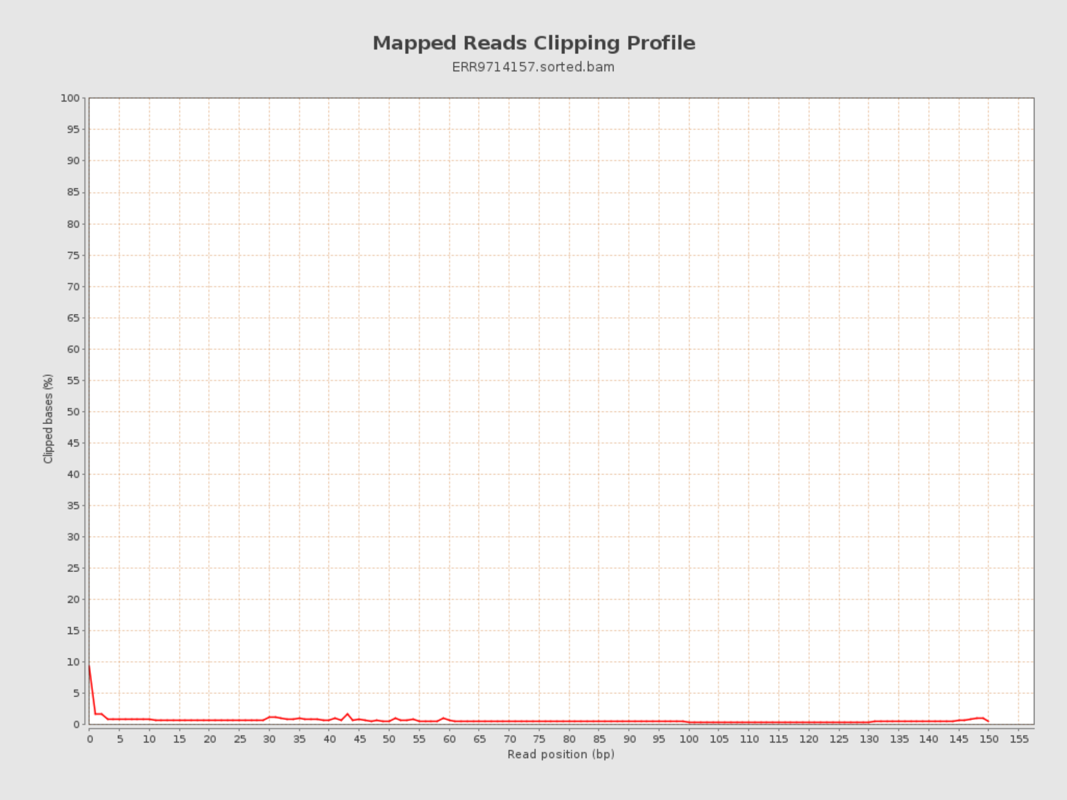
8. Results : Mapped Reads Nucleotide Content



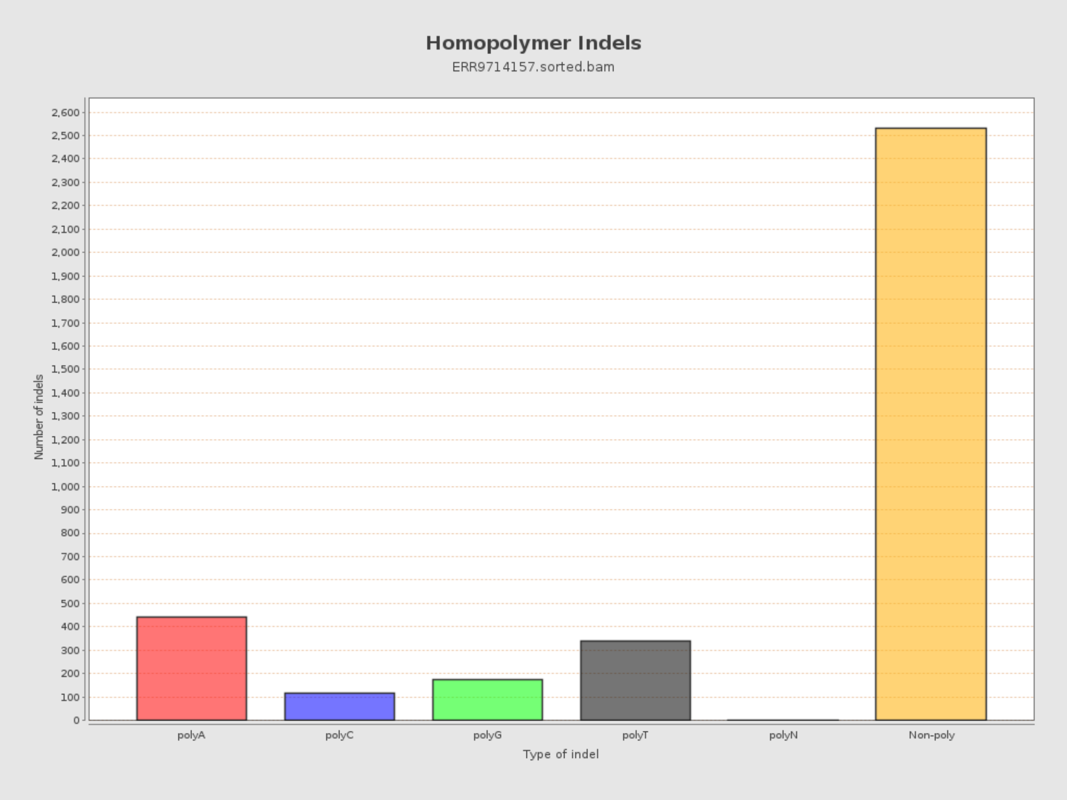
9. Results : Mapped Reads GC-content Distribution



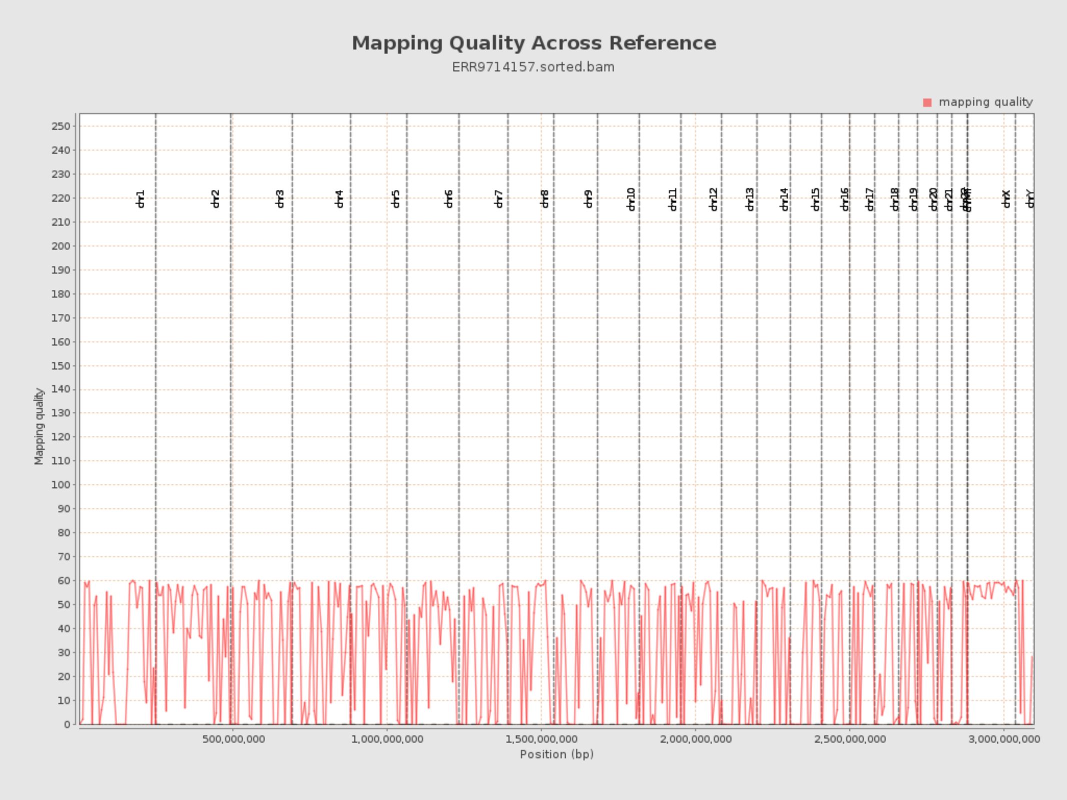
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram