Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 22:49:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714172.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_ERR9714172 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714172.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 22:49:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714172.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	972,392
Mapped reads	811,626 / 83.47%
Unmapped reads	160,766 / 16.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,121 / 2.48%
Read min/max/mean length	30 / 151 / 134.4
Duplicated reads (estimated)	741,491 / 76.25%
Duplication rate	44.98%
Clipped reads	766,364 / 78.81%

2.2. ACGT Content

Number/percentage of A's	27,056,579 / 26.51%
Number/percentage of C's	22,700,226 / 22.24%
Number/percentage of T's	25,570,001 / 25.06%
Number/percentage of G's	26,720,542 / 26.18%
Number/percentage of N's	732 / 0%
GC Percentage	48.43%

2.3. Coverage

Mean	0.0337

Standard Deviation	8.1453

2.4. Mapping Quality

Mean Mapping Quality	51.55

2.5. Mismatches and indels

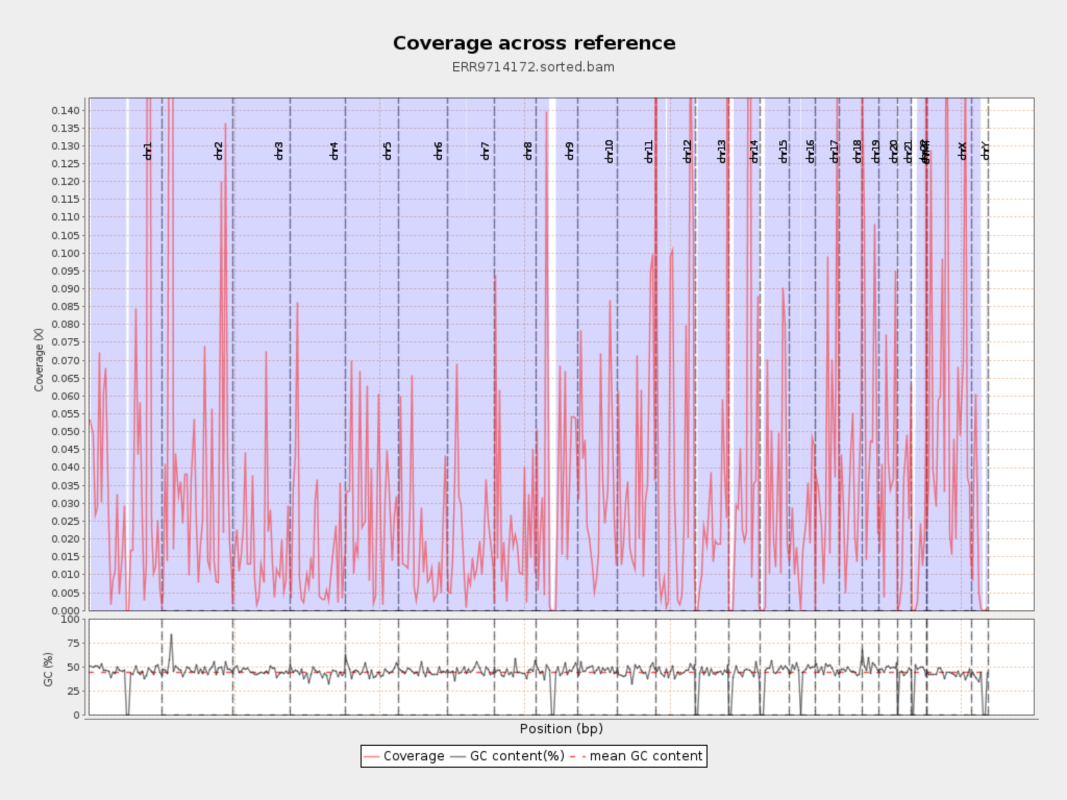
General error rate	4.34%
Mismatches	4,124,622
Insertions	109,706
Mapped reads with at least one insertion	13%
Deletions	352,739
Mapped reads with at least one deletion	41.28%
Homopolymer indels	29.8%

2.6. Chromosome stats

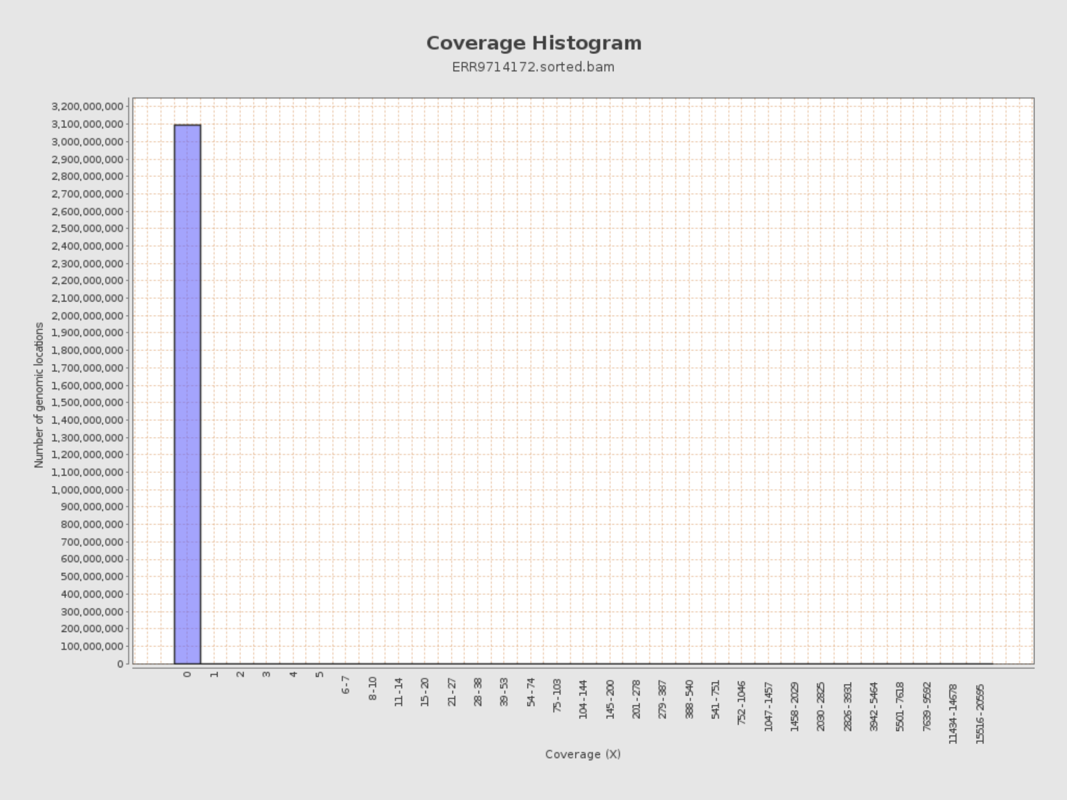
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9399954	0.0377	10.3139
chr2	243199373	13521151	0.0556	17.0768
chr3	198022430	3521653	0.0178	2.7936
chr4	191154276	3177498	0.0166	3.5656
chr5	180915260	5323484	0.0294	5.4128
chr6	171115067	3134636	0.0183	3.0973
chr7	159138663	3049821	0.0192	2.8817

chr8	146364022	3608894	0.0247	4.6808
chr9	141213431	4705629	0.0333	7.4005
chr10	135534747	4843561	0.0357	5.0744
chr11	135006516	5401255	0.04	6.2517
chr12	133851895	5697305	0.0426	8.5956
chr13	115169878	3726452	0.0324	10.5707
chr14	107349540	4847317	0.0452	15.6805
chr15	102531392	3229677	0.0315	5.4111
chr16	90354753	2057106	0.0228	2.9972
chr17	81195210	4143856	0.051	8.9477
chr18	78077248	2382927	0.0305	4.9132
chr19	59128983	3463526	0.0586	7.2507
chr20	63025520	2736065	0.0434	6.1525
chr21	48129895	1253124	0.026	4.4118
chr22	51304566	565018	0.011	1.6866
chrMT	16571	117771	7.1071	57.1461
chrX	155270560	9511745	0.0613	7.0331
chrY	59373566	834115	0.014	2.3951

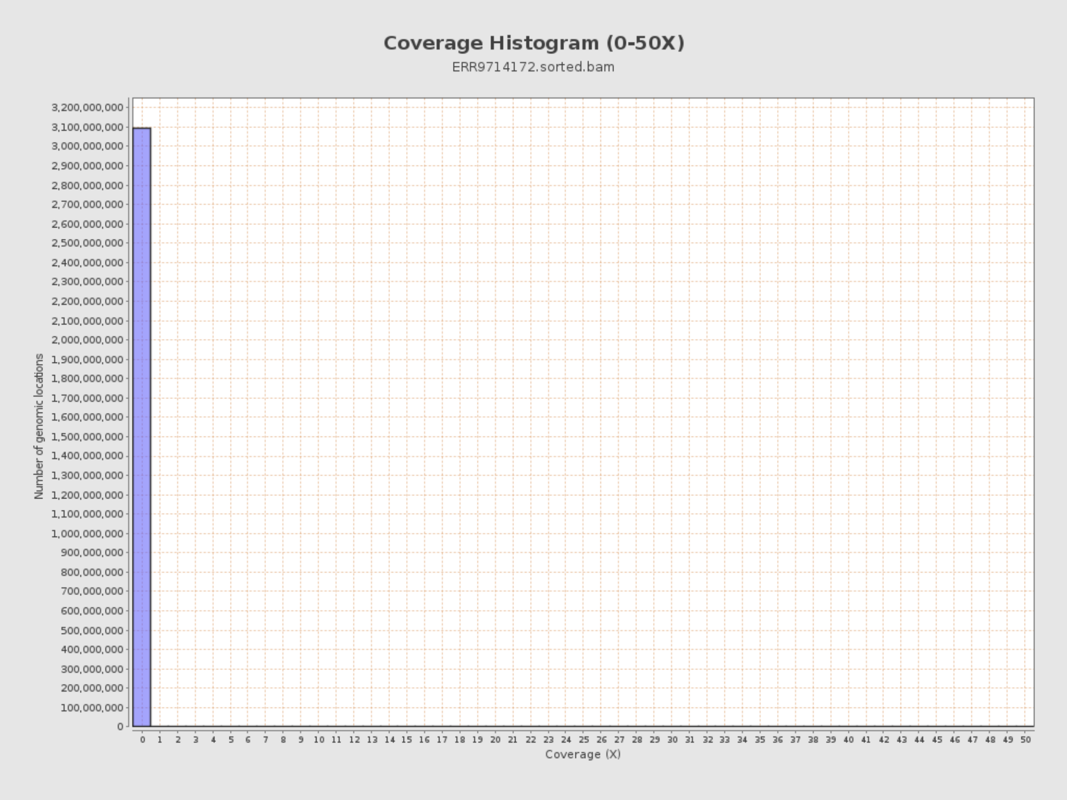
3. Results : Coverage across reference



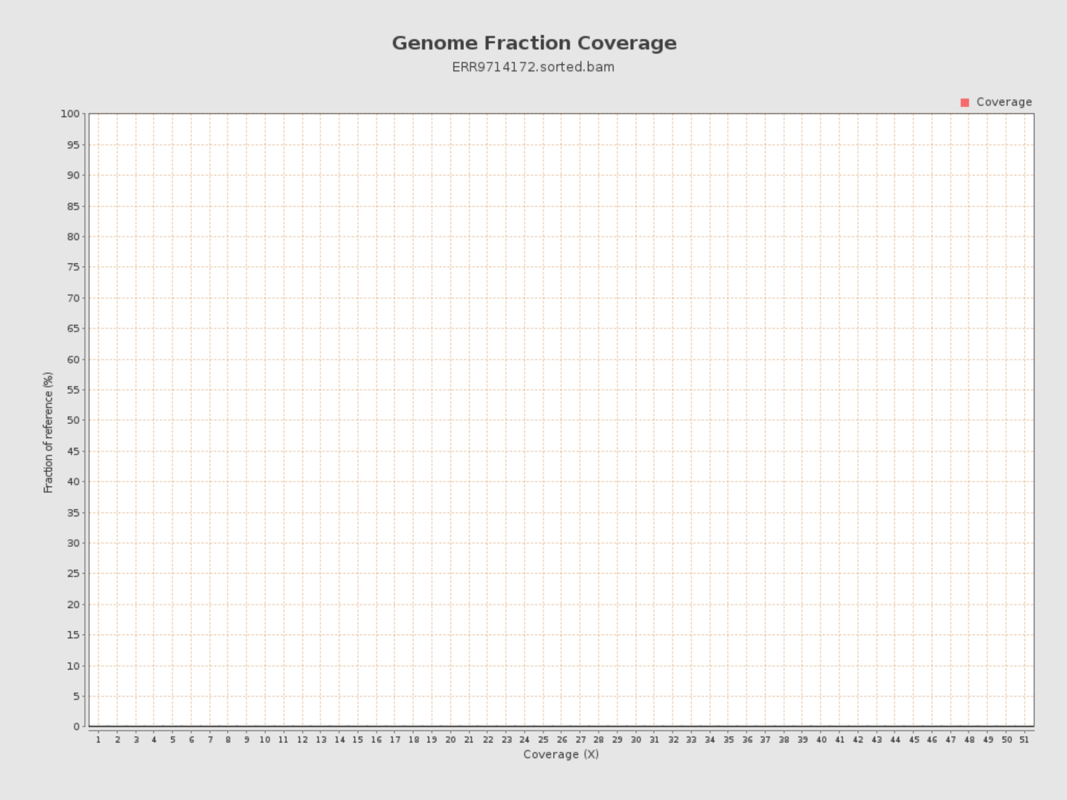
4. Results : Coverage Histogram



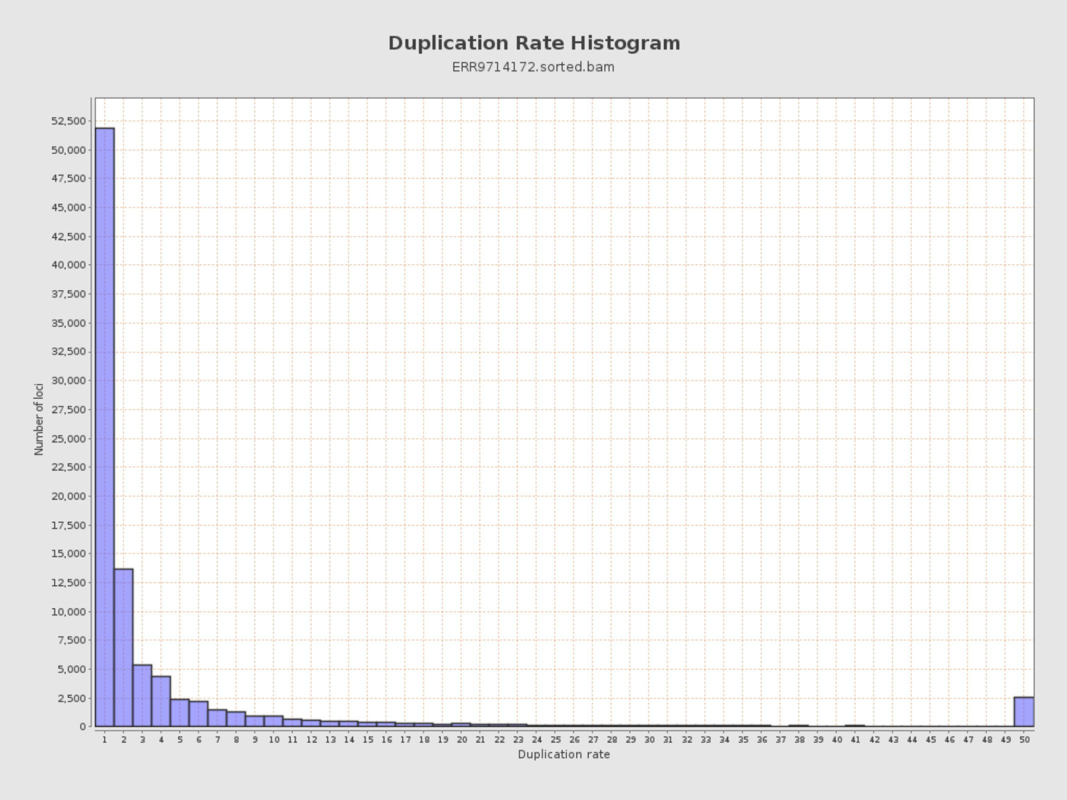
5. Results : Coverage Histogram (0-50X)



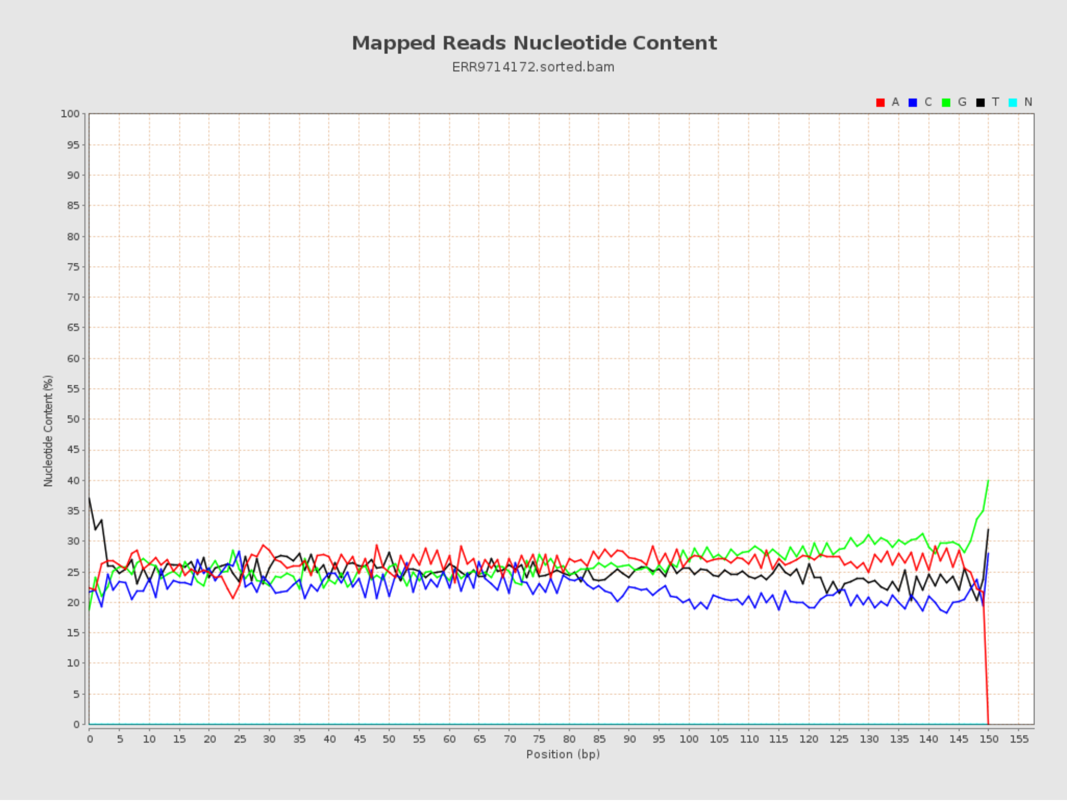
6. Results : Genome Fraction Coverage



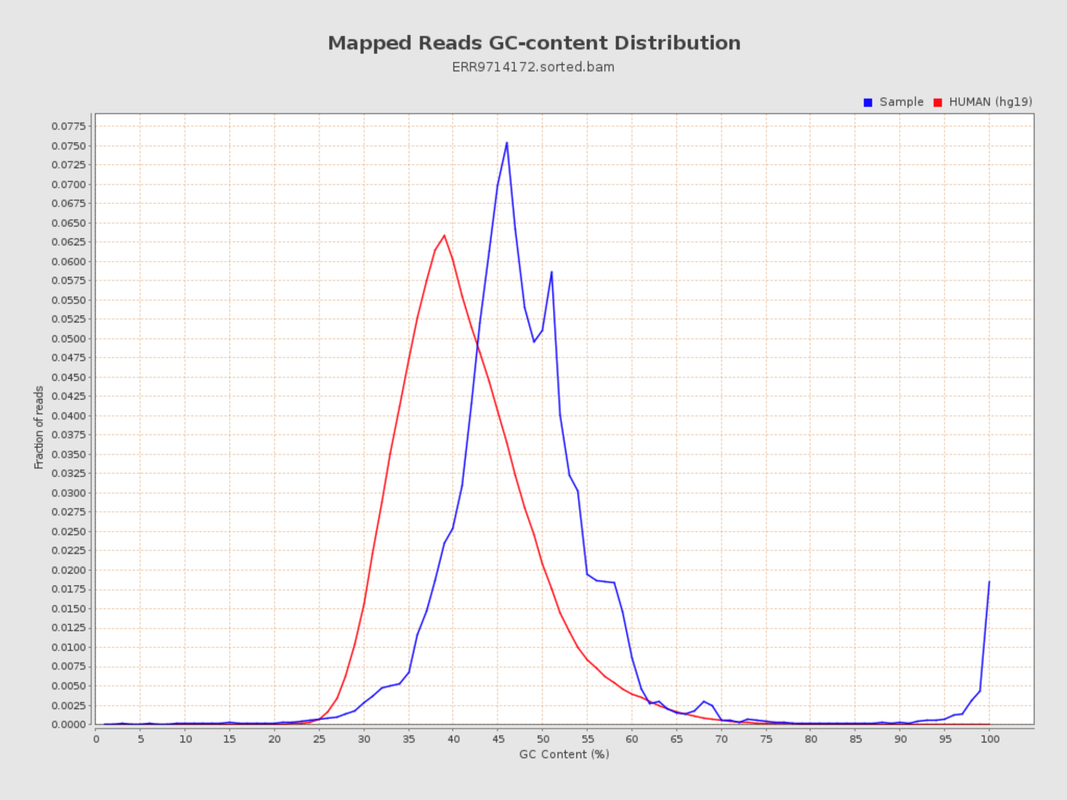
7. Results : Duplication Rate Histogram



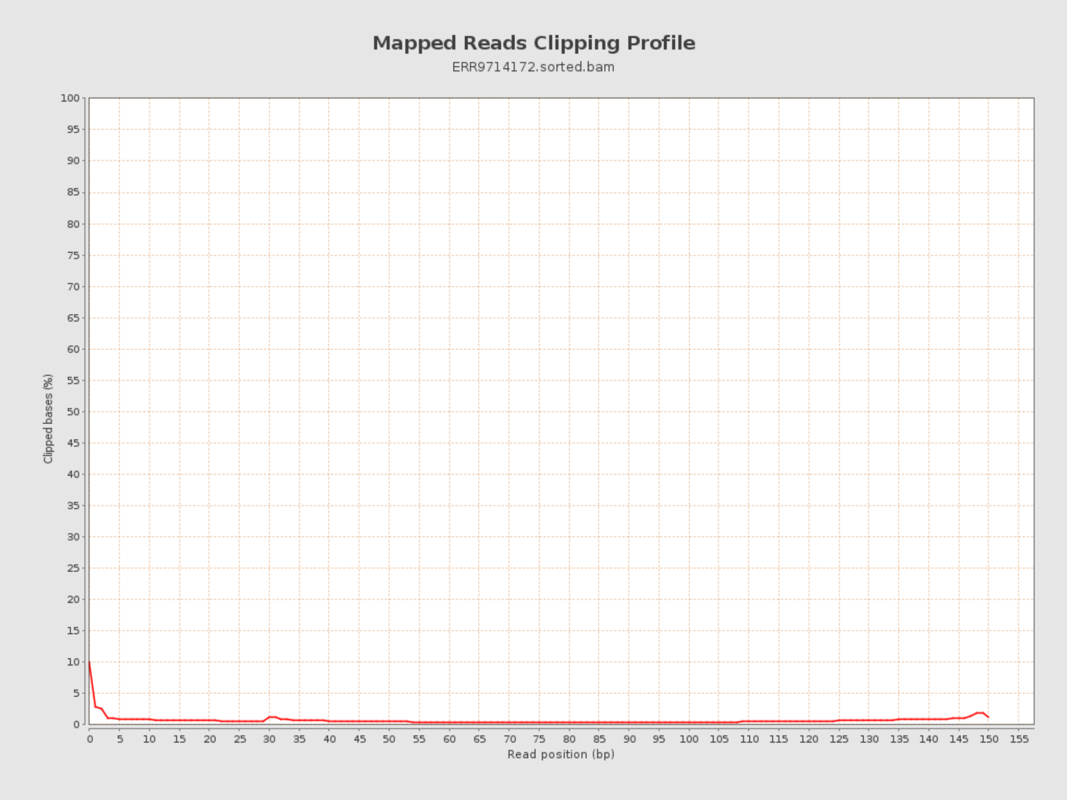
8. Results : Mapped Reads Nucleotide Content



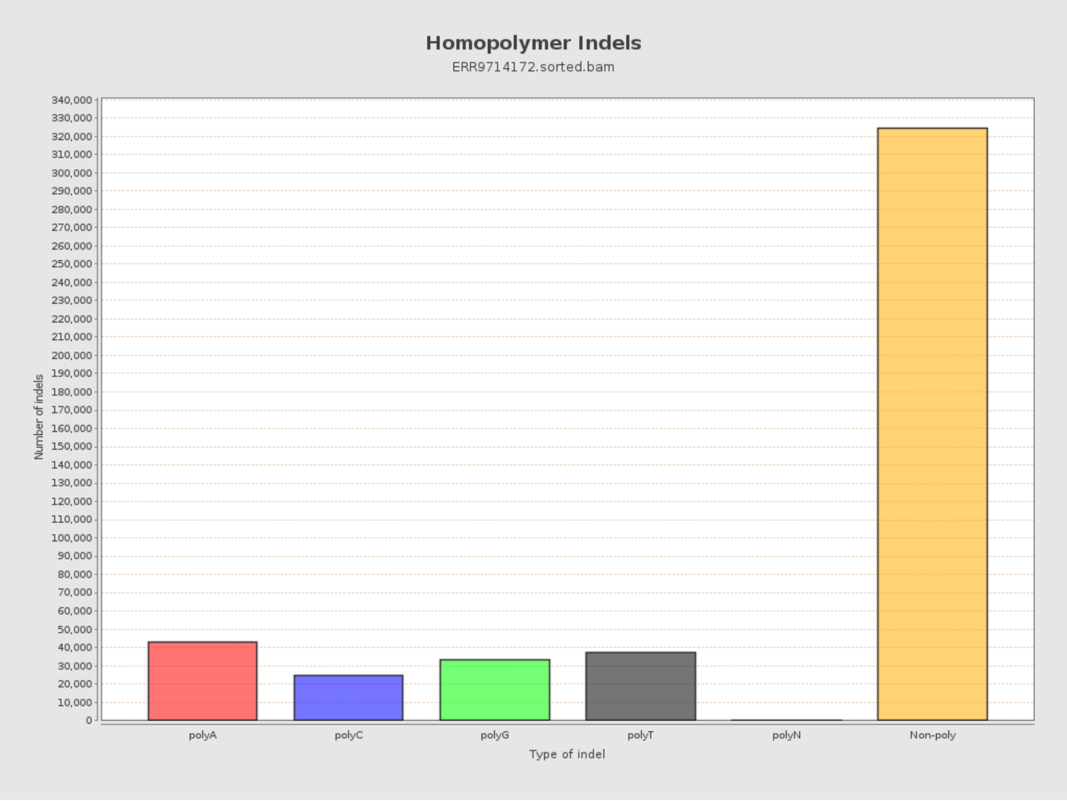
9. Results : Mapped Reads GC-content Distribution



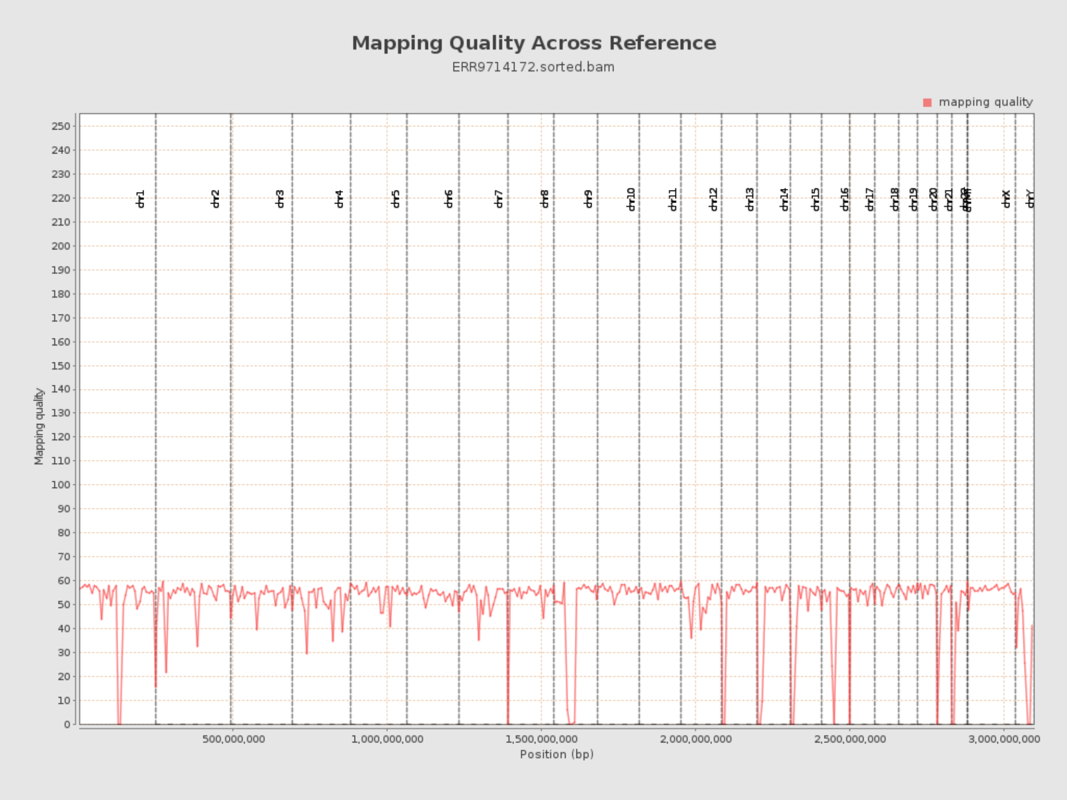
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram