Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 22:24:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714162.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_ERR9714162 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714162.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 22:24:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714162.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	792,044
Mapped reads	691,795 / 87.34%
Unmapped reads	100,249 / 12.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,961 / 2.39%
Read min/max/mean length	30 / 151 / 137.57
Duplicated reads (estimated)	633,674 / 80%
Duplication rate	43.86%
Clipped reads	653,022 / 82.45%

2.2. ACGT Content

Number/percentage of A's	24,032,014 / 27.05%
Number/percentage of C's	19,734,450 / 22.22%
Number/percentage of T's	22,832,957 / 25.7%
Number/percentage of G's	22,228,874 / 25.02%
Number/percentage of N's	548 / 0%
GC Percentage	47.24%

2.3. Coverage

Mean	0.0294

Standard Deviation	10.3938

2.4. Mapping Quality

Mean Mapping Quality	51.44

2.5. Mismatches and indels

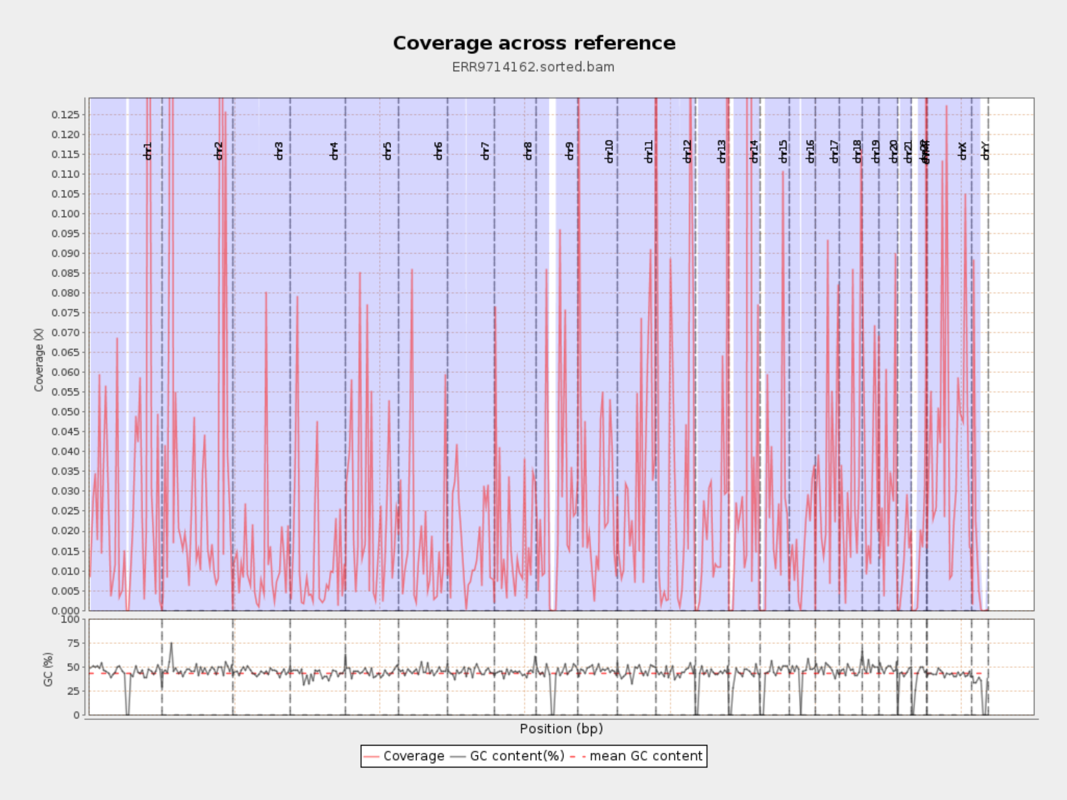
General error rate	4.4%
Mismatches	3,660,825
Insertions	94,244
Mapped reads with at least one insertion	13.13%
Deletions	326,564
Mapped reads with at least one deletion	44.92%
Homopolymer indels	28.85%

2.6. Chromosome stats

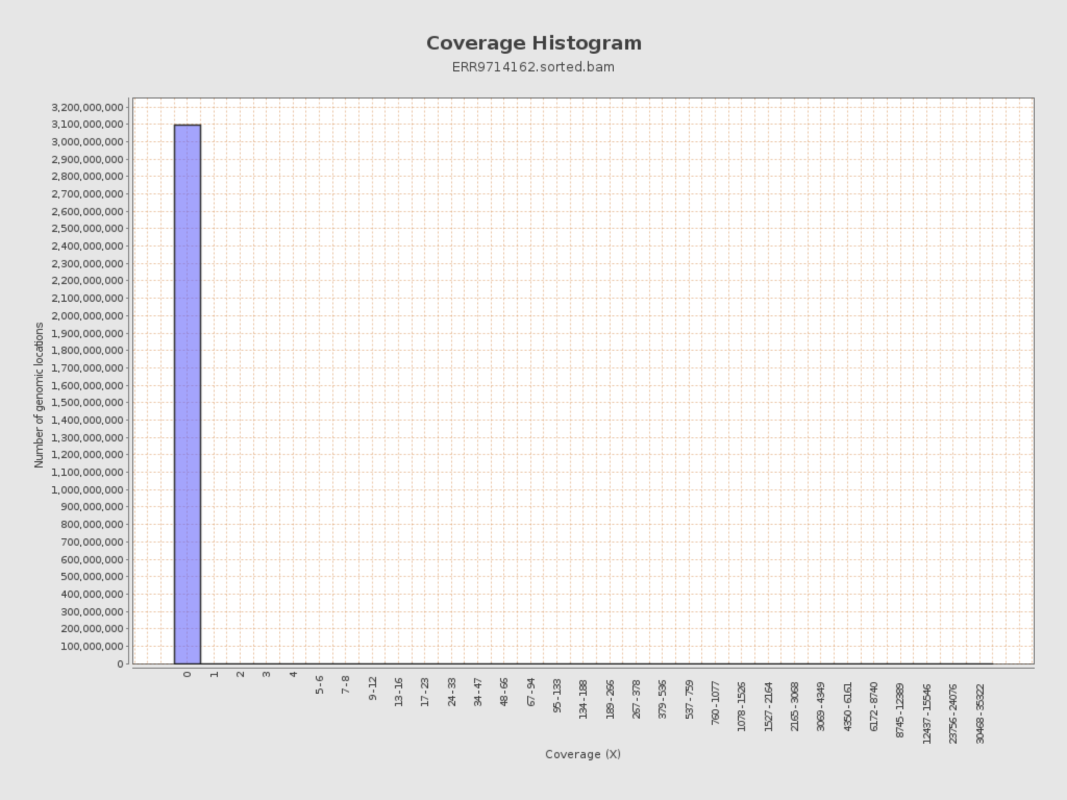
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7803084	0.0313	8.4678
chr2	243199373	11727686	0.0482	15.9849
chr3	198022430	2559898	0.0129	2.5678
chr4	191154276	2698425	0.0141	3.4892
chr5	180915260	4817681	0.0266	5.6905
chr6	171115067	3185735	0.0186	4.0525
chr7	159138663	2717537	0.0171	2.6512

chr8	146364022	2848573	0.0195	4.1779
chr9	141213431	3668877	0.026	6.5773
chr10	135534747	4333468	0.032	5.6659
chr11	135006516	4495777	0.0333	5.0764
chr12	133851895	4783732	0.0357	7.9968
chr13	115169878	4034167	0.035	14.9954
chr14	107349540	7539161	0.0702	39.9868
chr15	102531392	2719803	0.0265	4.6799
chr16	90354753	1592859	0.0176	2.4855
chr17	81195210	3155650	0.0389	6.1818
chr18	78077248	2581626	0.0331	7.3517
chr19	59128983	2068920	0.035	4.1135
chr20	63025520	2116764	0.0336	4.5088
chr21	48129895	592376	0.0123	1.9418
chr22	51304566	648357	0.0126	1.5953
chrMT	16571	241533	14.5756	125.4749
chrX	155270560	7055857	0.0454	5.1615
chrY	59373566	902980	0.0152	4.6448

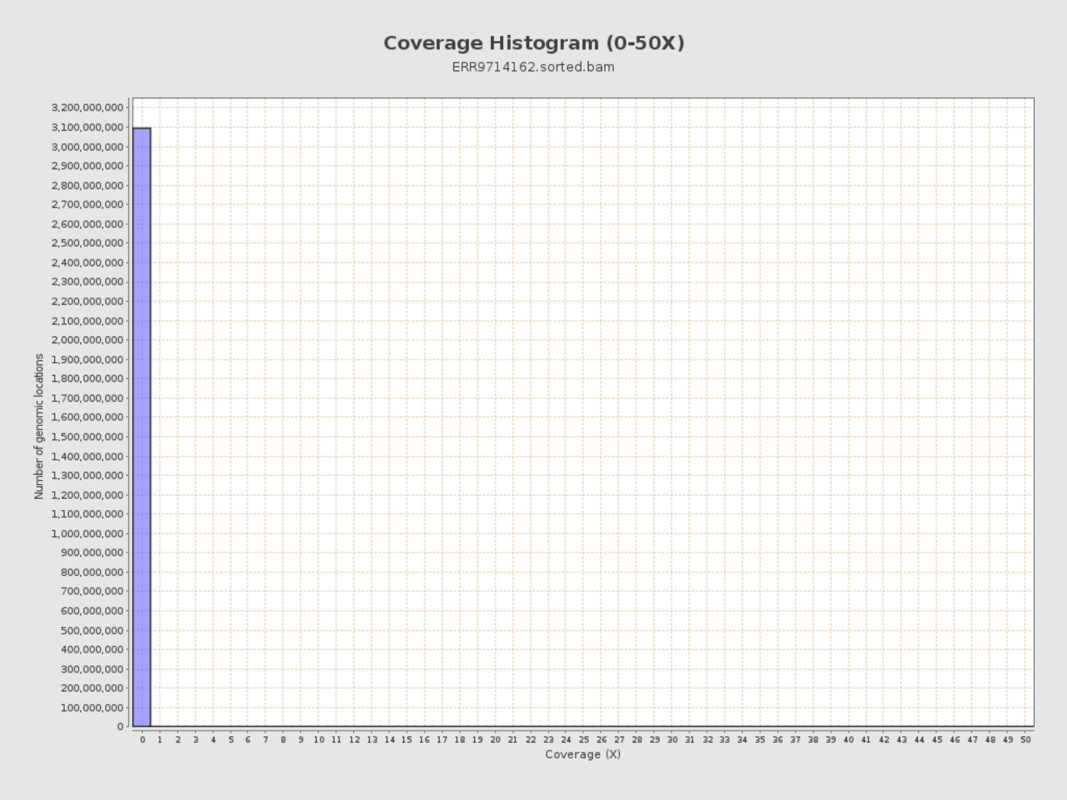
3. Results : Coverage across reference



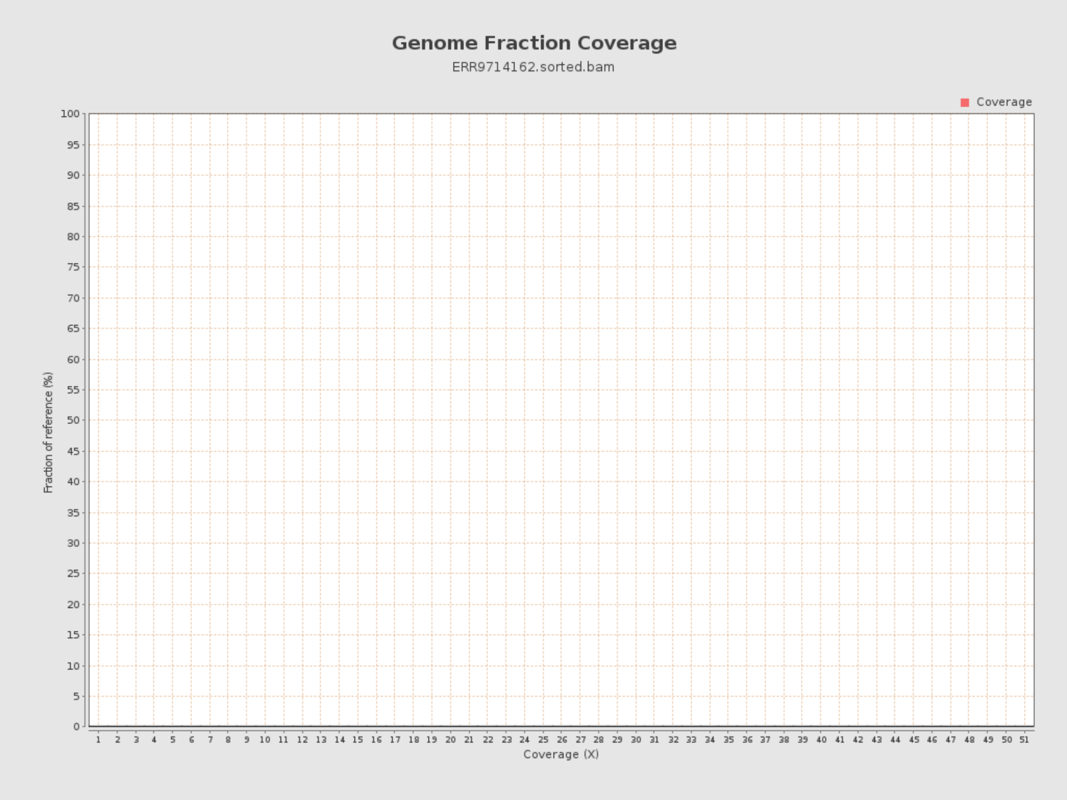
4. Results : Coverage Histogram



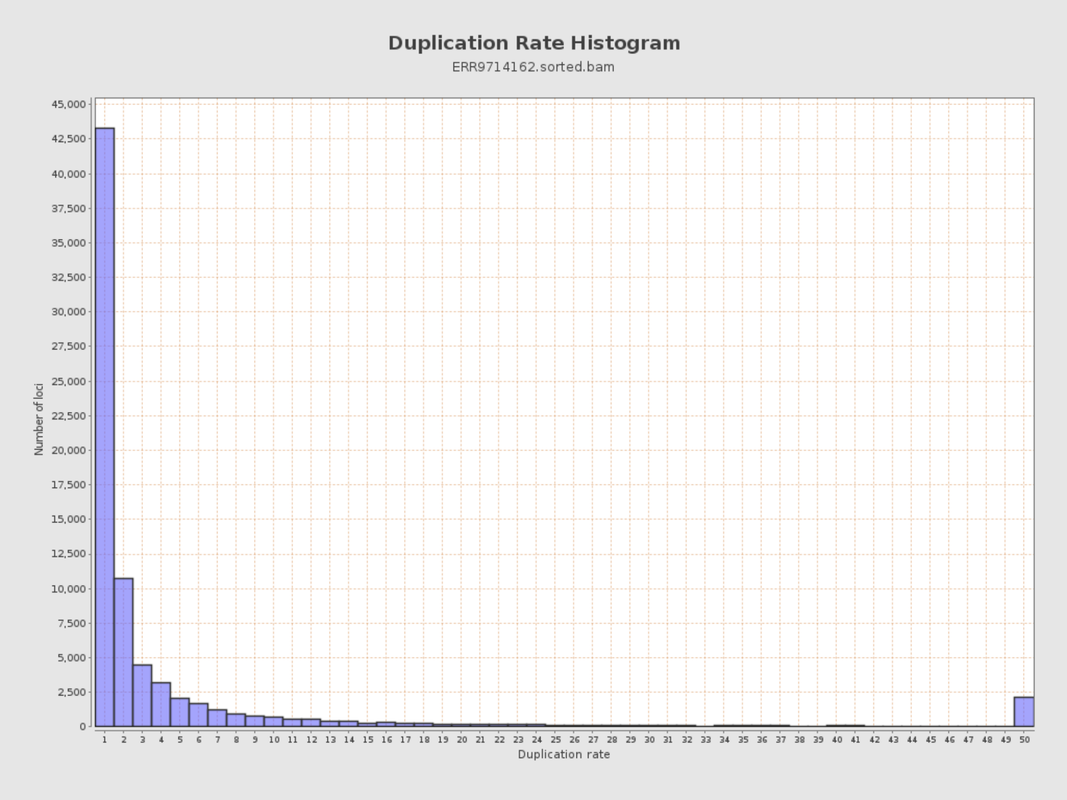
5. Results : Coverage Histogram (0-50X)



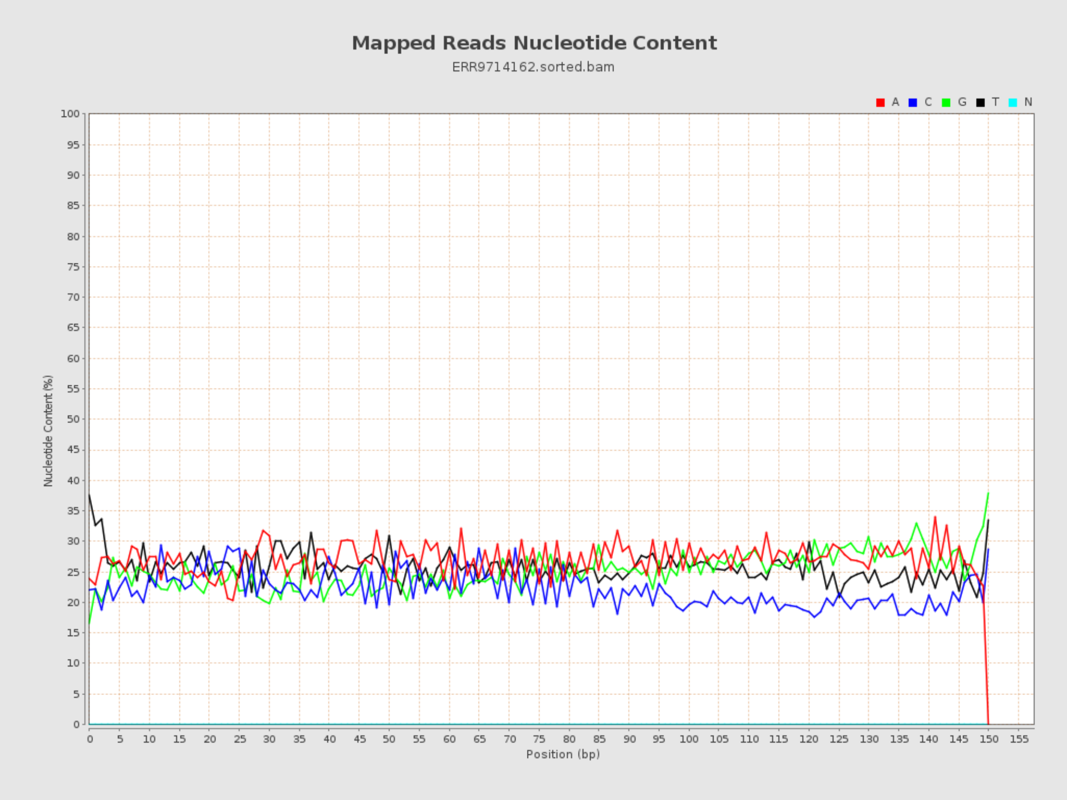
6. Results : Genome Fraction Coverage



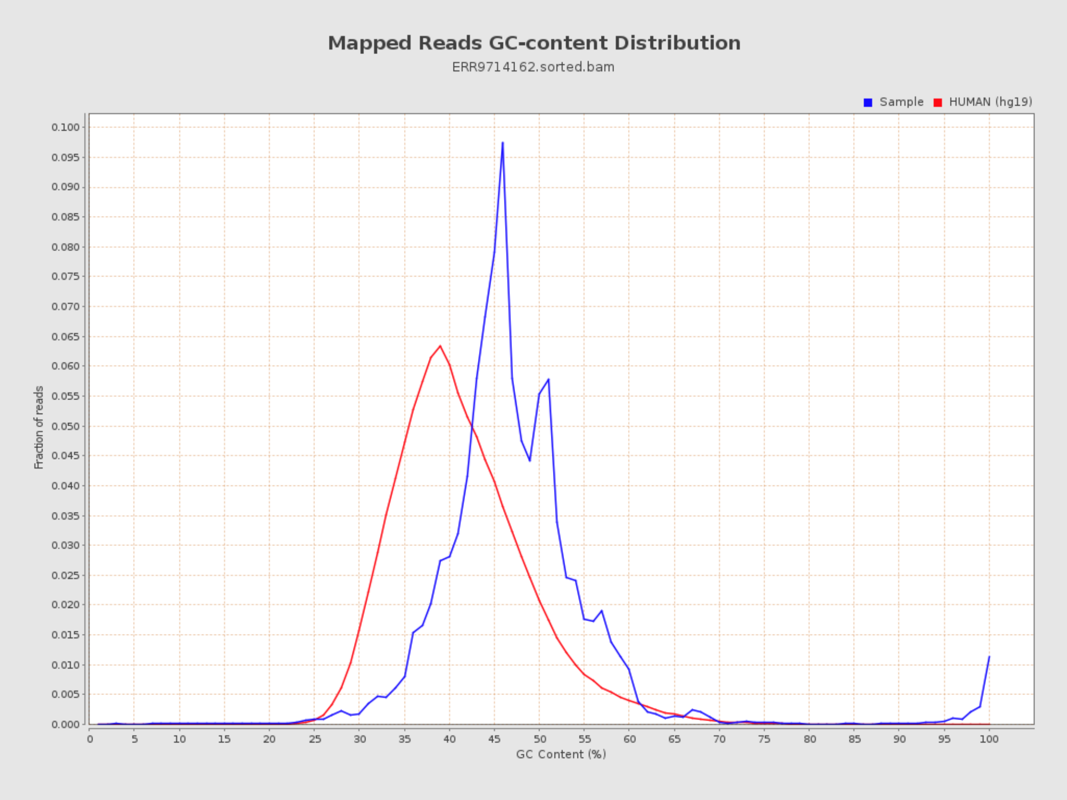
7. Results : Duplication Rate Histogram



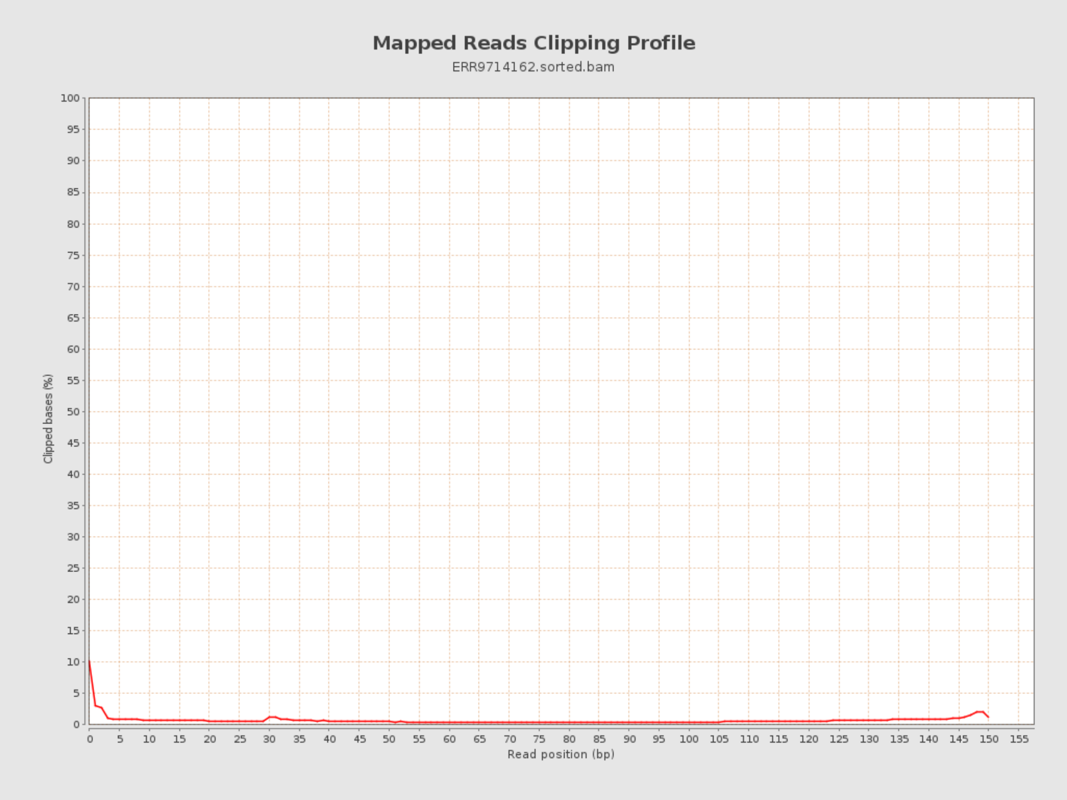
8. Results : Mapped Reads Nucleotide Content



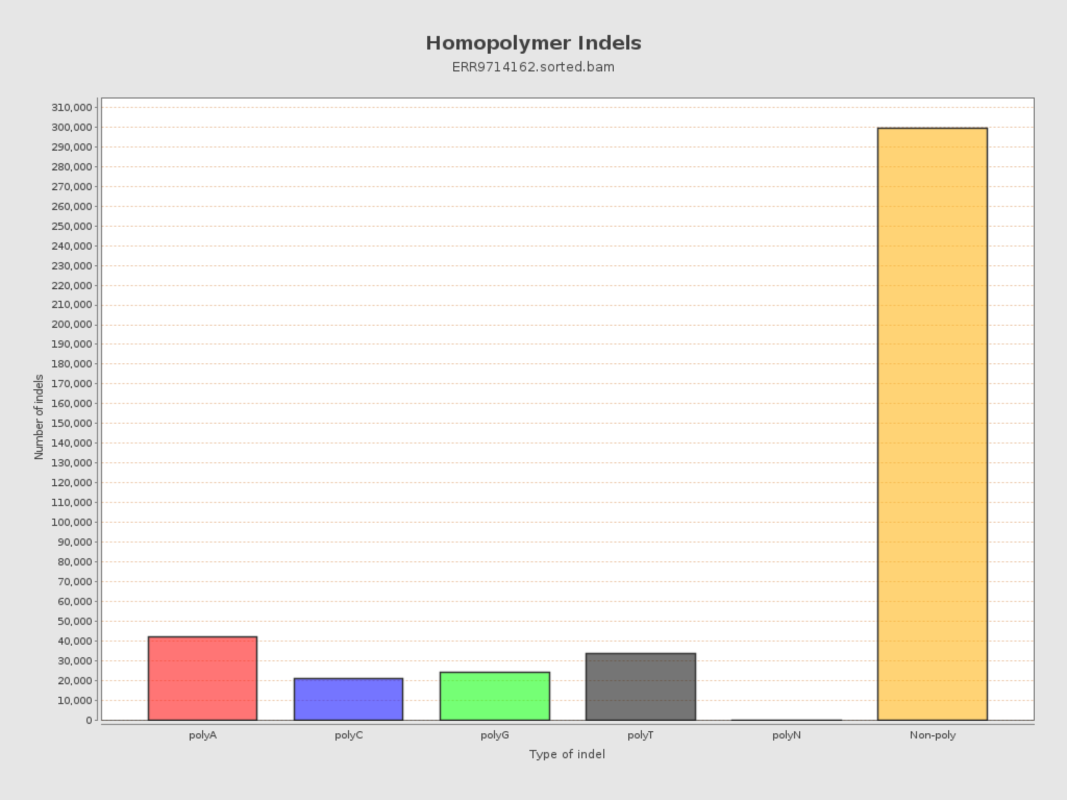
9. Results : Mapped Reads GC-content Distribution



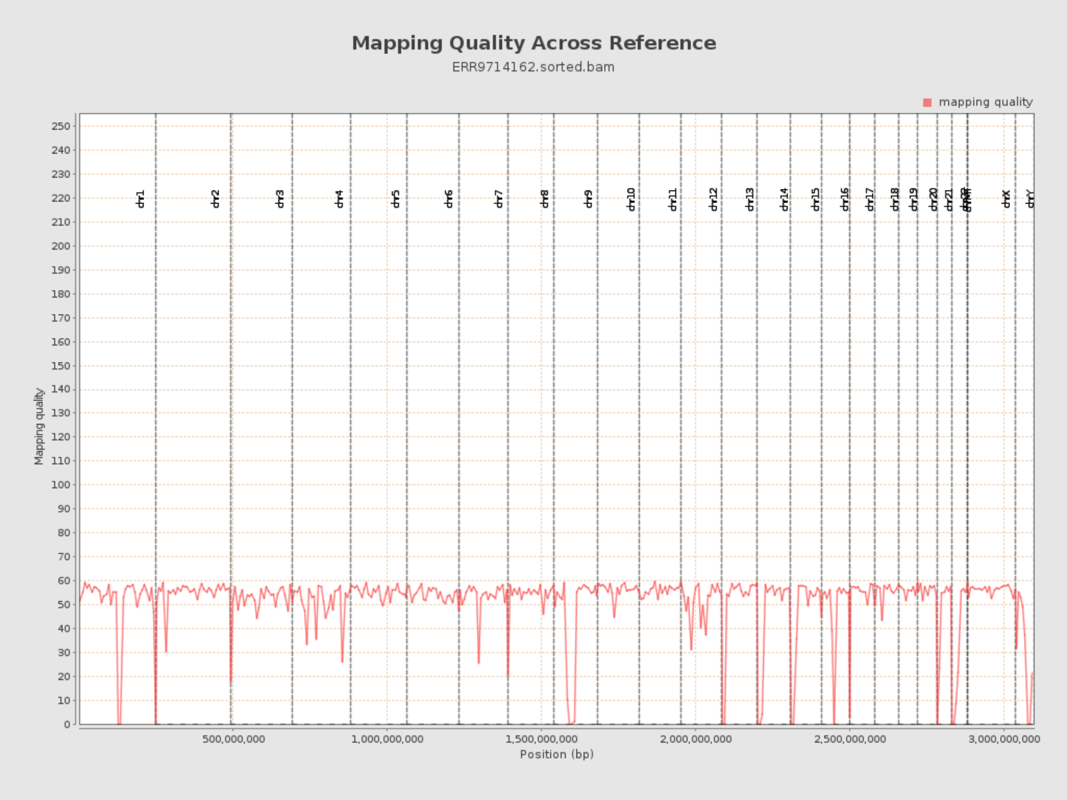
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram