Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 23:53:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714194.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_ERR9714194 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714194.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 23:53:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714194.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	88,876
Mapped reads	13,975 / 15.72%
Unmapped reads	74,901 / 84.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	574 / 0.65%
Read min/max/mean length	30 / 151 / 62.55
Duplicated reads (estimated)	13,209 / 14.86%
Duplication rate	31.27%
Clipped reads	8,570 / 9.64%

2.2. ACGT Content

Number/percentage of A's	74,740 / 5.47%
Number/percentage of C's	31,252 / 2.29%
Number/percentage of T's	42,211 / 3.09%
Number/percentage of G's	1,217,231 / 89.15%
Number/percentage of N's	8 / 0%
GC Percentage	91.43%

2.3. Coverage

Mean	0.0004

Standard Deviation	1.4747

2.4. Mapping Quality

Mean Mapping Quality	9.91

2.5. Mismatches and indels

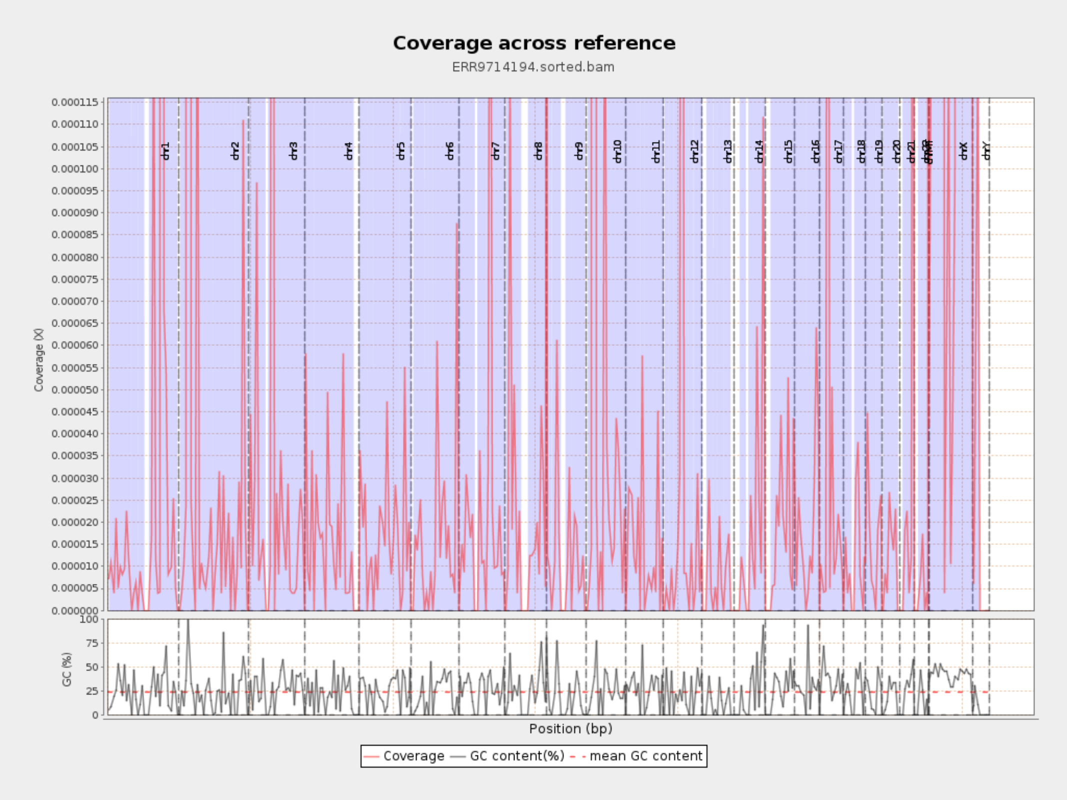
General error rate	3.64%
Mismatches	35,428
Insertions	1,840
Mapped reads with at least one insertion	8.65%
Deletions	992
Mapped reads with at least one deletion	6.77%
Homopolymer indels	65.85%

2.6. Chromosome stats

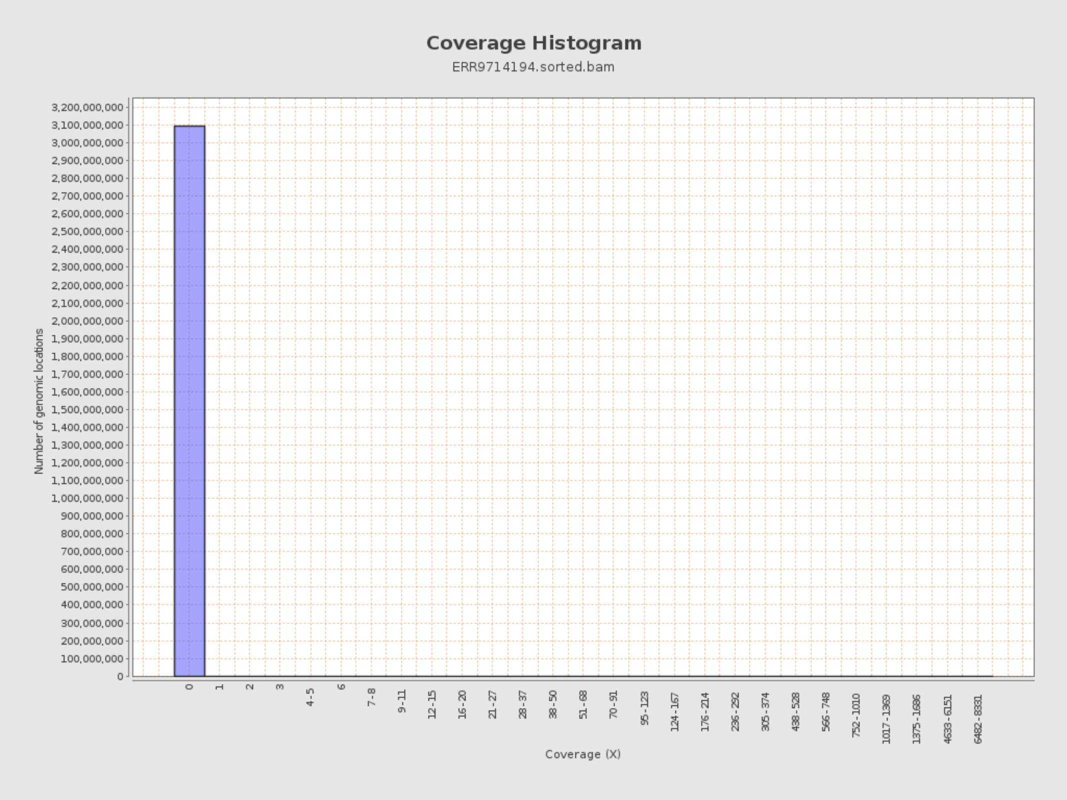
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	27282	0.0001	0.2703
chr2	243199373	1201460	0.0049	5.2468
chr3	198022430	7581	0	0.0287
chr4	191154276	3079	0	0.0064
chr5	180915260	3162	0	0.0051
chr6	171115067	2715	0	0.0072
chr7	159138663	3975	0	0.021

chr8	146364022	2951	0	0.009
chr9	141213431	1885	0	0.0062
chr10	135534747	25878	0.0002	0.3498
chr11	135006516	1980	0	0.0054
chr12	133851895	5943	0	0.0433
chr13	115169878	716	0	0.0028
chr14	107349540	2096	0	0.0149
chr15	102531392	1683	0	0.0063
chr16	90354753	1833	0	0.0056
chr17	81195210	3333	0	0.04
chr18	78077248	876	0	0.004
chr19	59128983	962	0	0.0062
chr20	63025520	729	0	0.004
chr21	48129895	1900	0	0.016
chr22	51304566	226	0	0.0024
chrMT	16571	726	0.0438	0.4106
chrX	155270560	66506	0.0004	0.1052
chrY	59373566	1233	0	0.0101

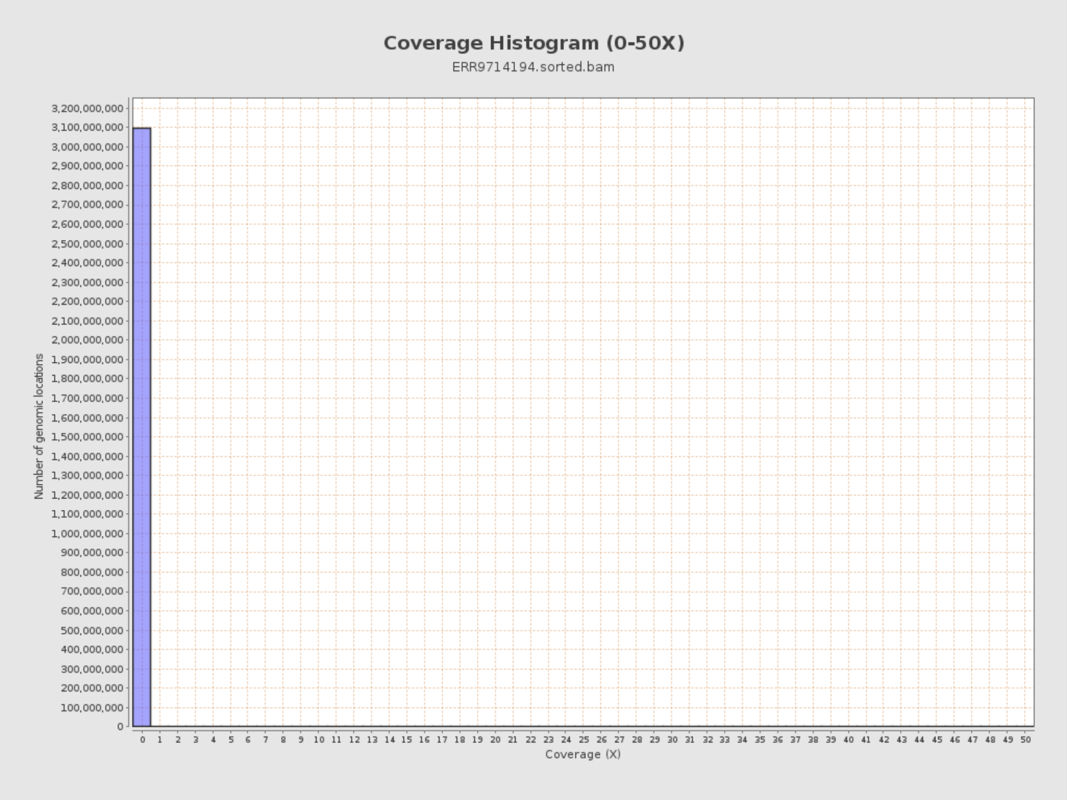
3. Results : Coverage across reference



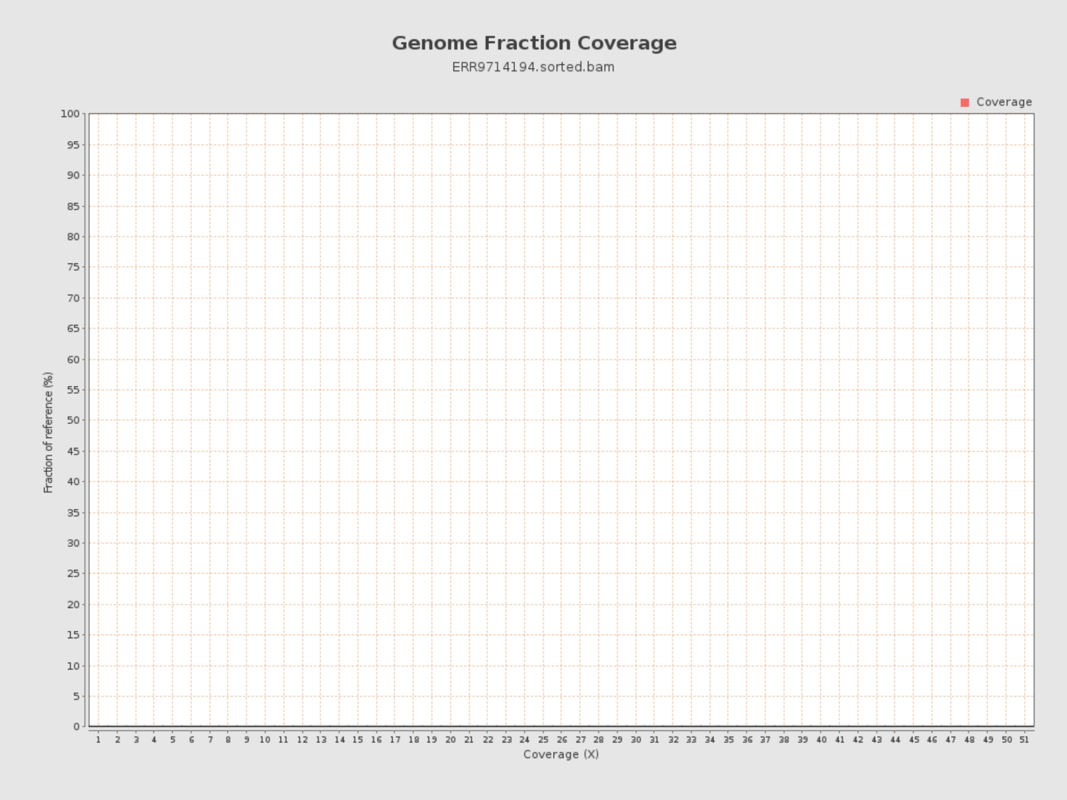
4. Results : Coverage Histogram



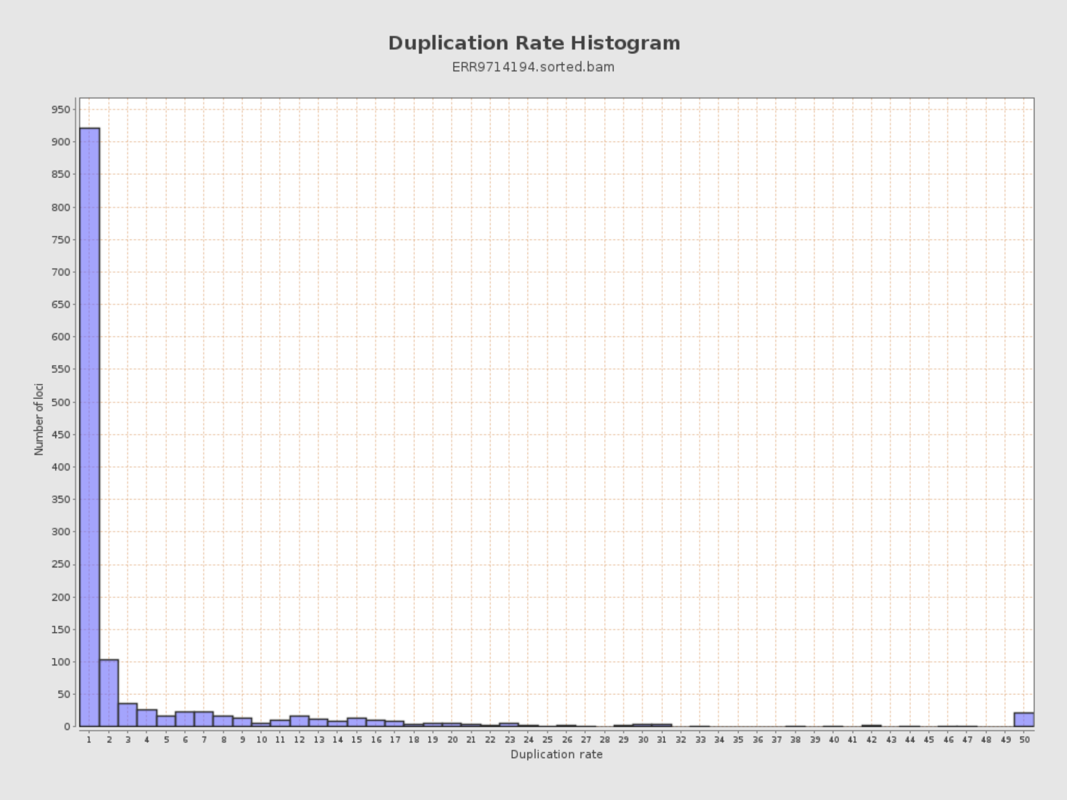
5. Results : Coverage Histogram (0-50X)



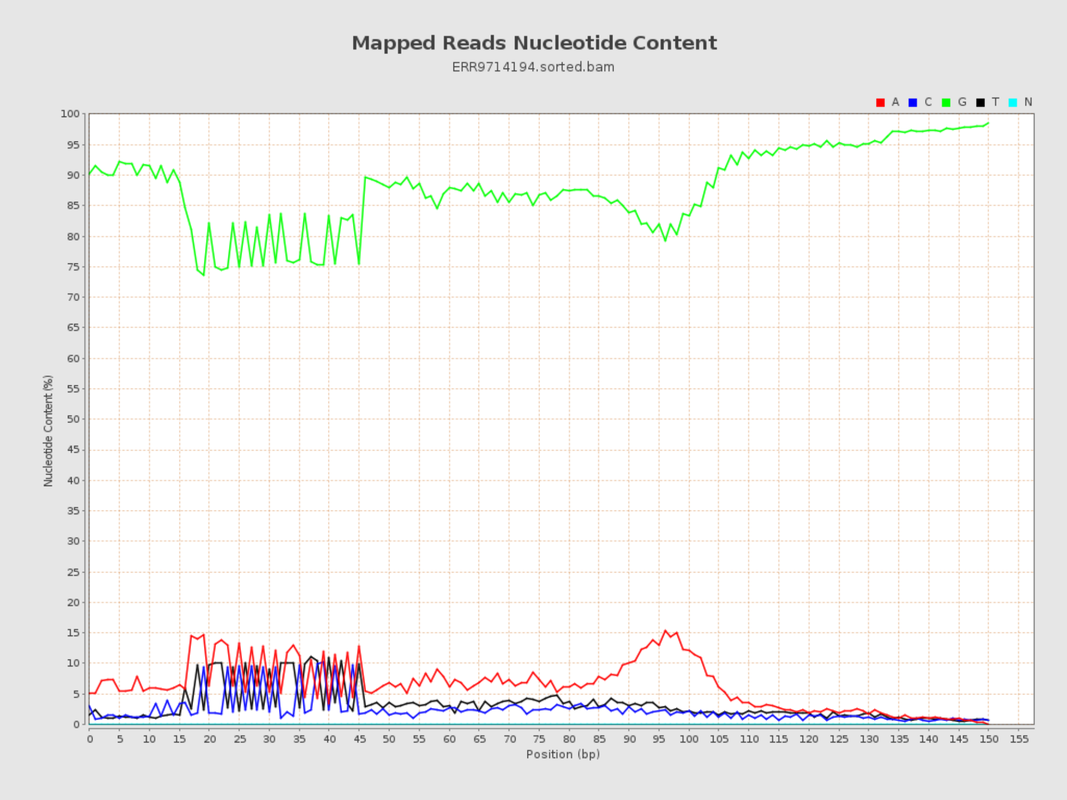
6. Results : Genome Fraction Coverage



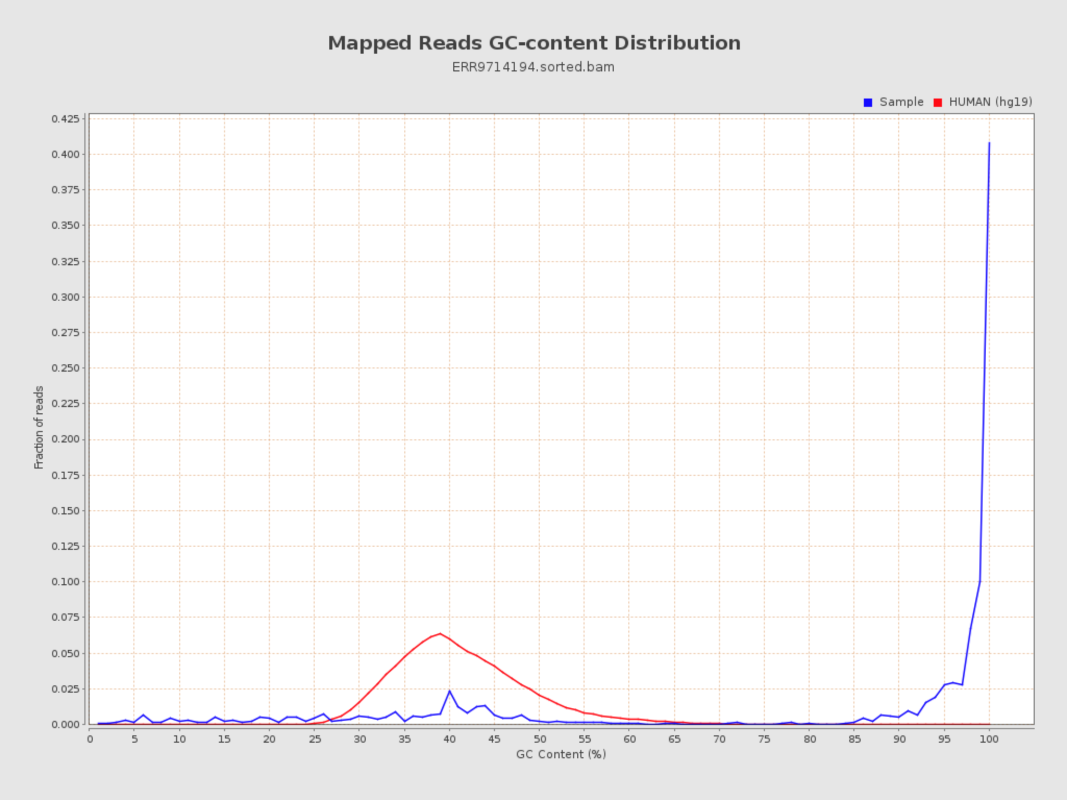
7. Results : Duplication Rate Histogram



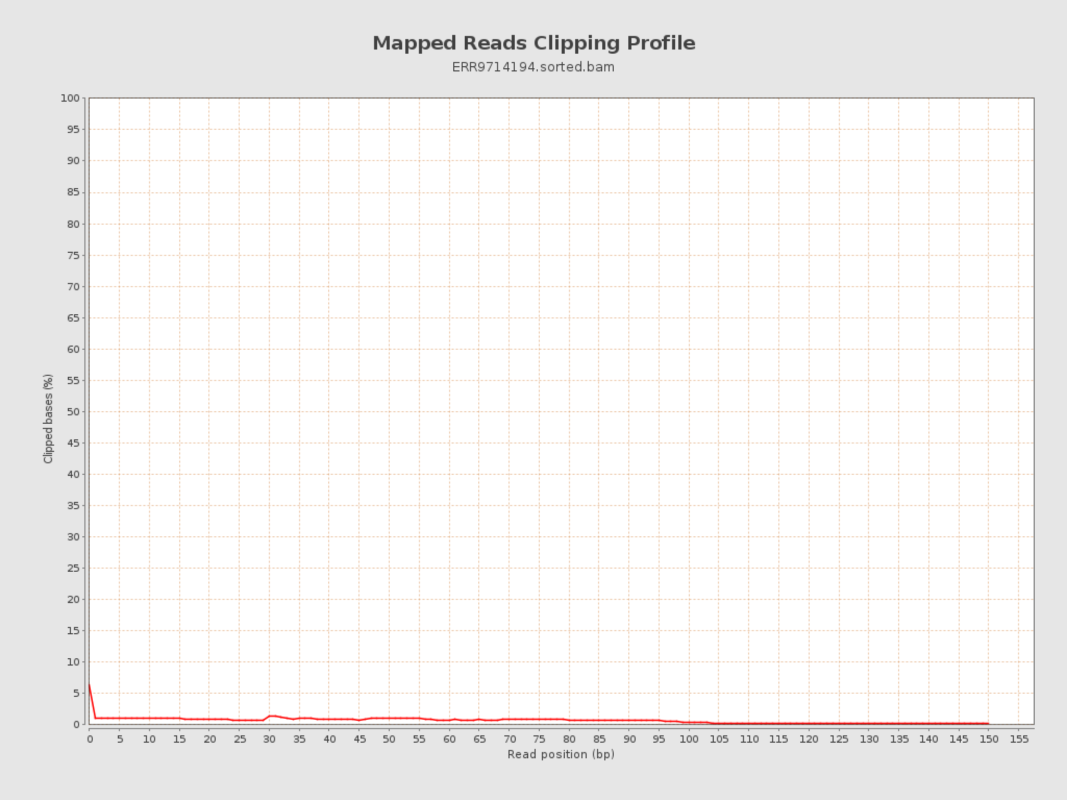
8. Results : Mapped Reads Nucleotide Content



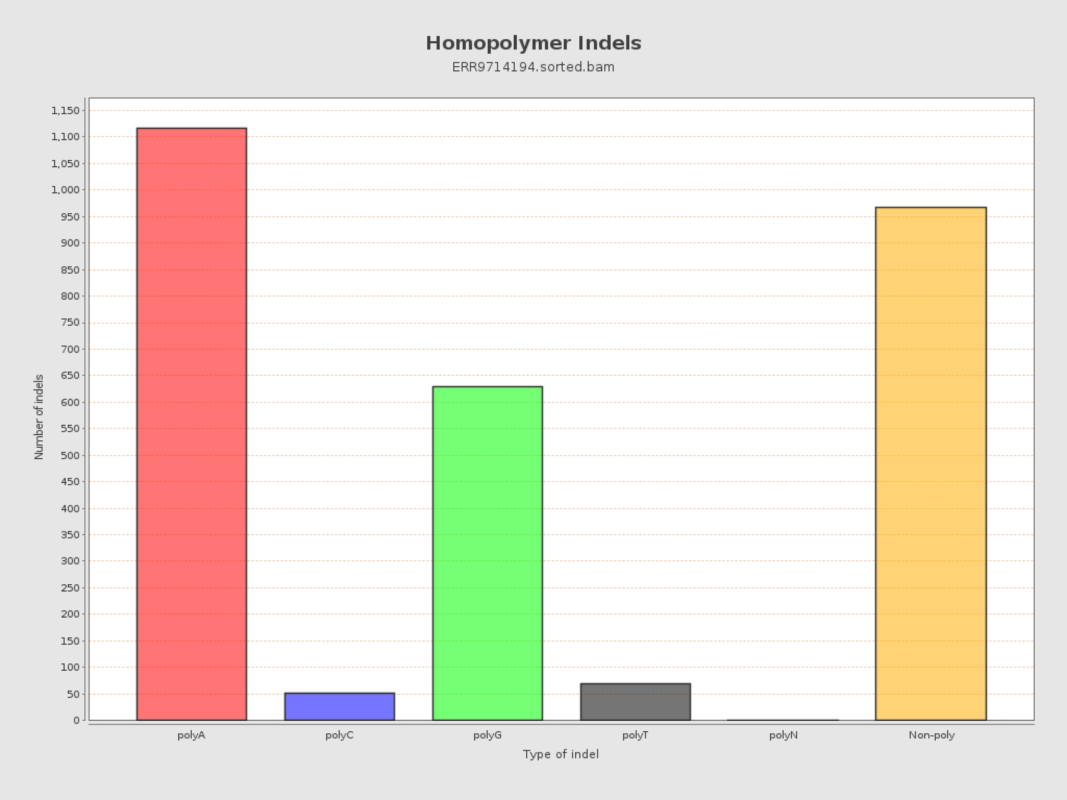
9. Results : Mapped Reads GC-content Distribution



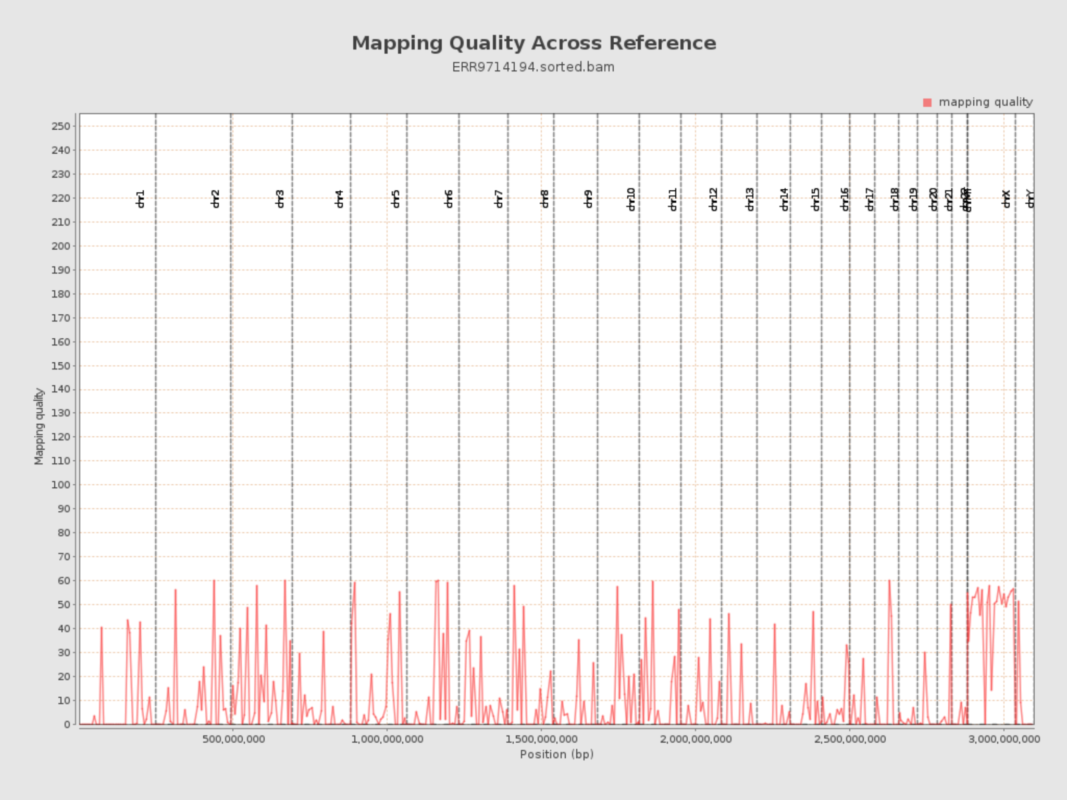
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram