Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 01:08:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714242.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_ERR9714242 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714242.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 01:08:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714242.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	325,034
Mapped reads	46,957 / 14.45%
Unmapped reads	278,077 / 85.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,031 / 0.32%
Read min/max/mean length	30 / 151 / 60.67
Duplicated reads (estimated)	45,908 / 14.12%
Duplication rate	29.47%
Clipped reads	23,255 / 7.15%

2.2. ACGT Content

Number/percentage of A's	109,874 / 2.2%
Number/percentage of C's	36,406 / 0.73%
Number/percentage of T's	49,435 / 0.99%
Number/percentage of G's	4,802,782 / 96.08%
Number/percentage of N's	136 / 0%
GC Percentage	96.81%

2.3. Coverage

Mean	0.0016

Standard Deviation	6.1048

2.4. Mapping Quality

Mean Mapping Quality	11.18

2.5. Mismatches and indels

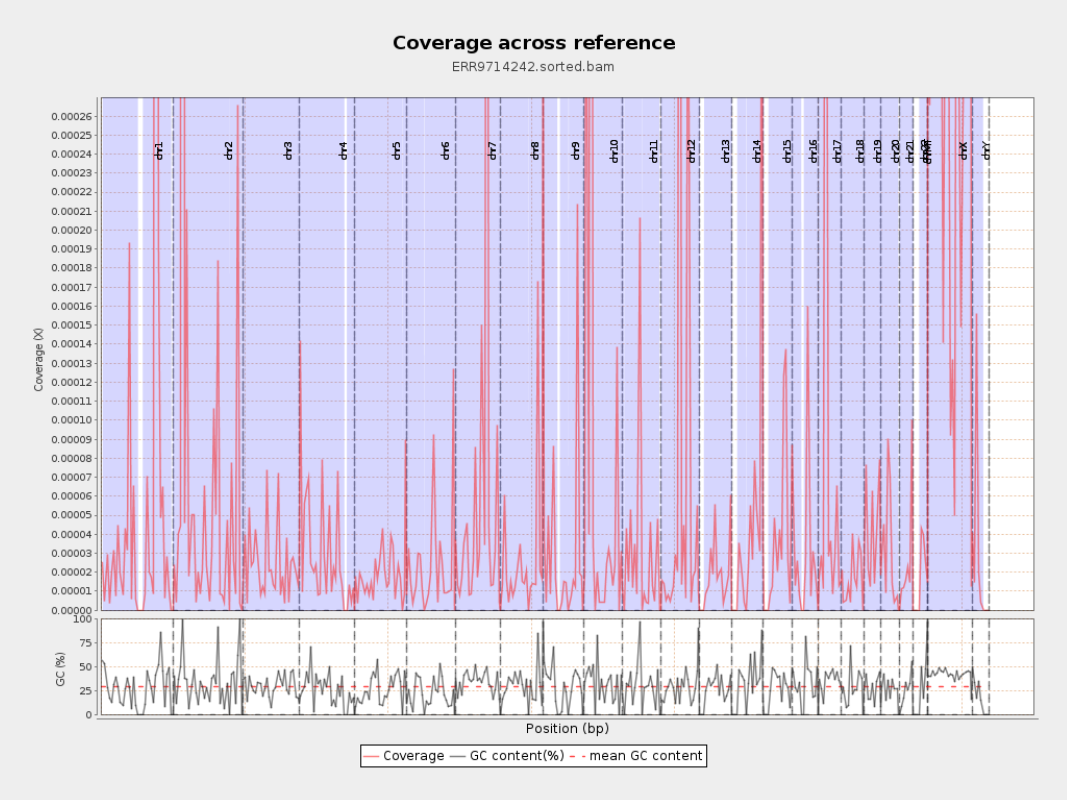
General error rate	3.42%
Mismatches	127,018
Insertions	6,186
Mapped reads with at least one insertion	8.86%
Deletions	2,383
Mapped reads with at least one deletion	4.9%
Homopolymer indels	64.07%

2.6. Chromosome stats

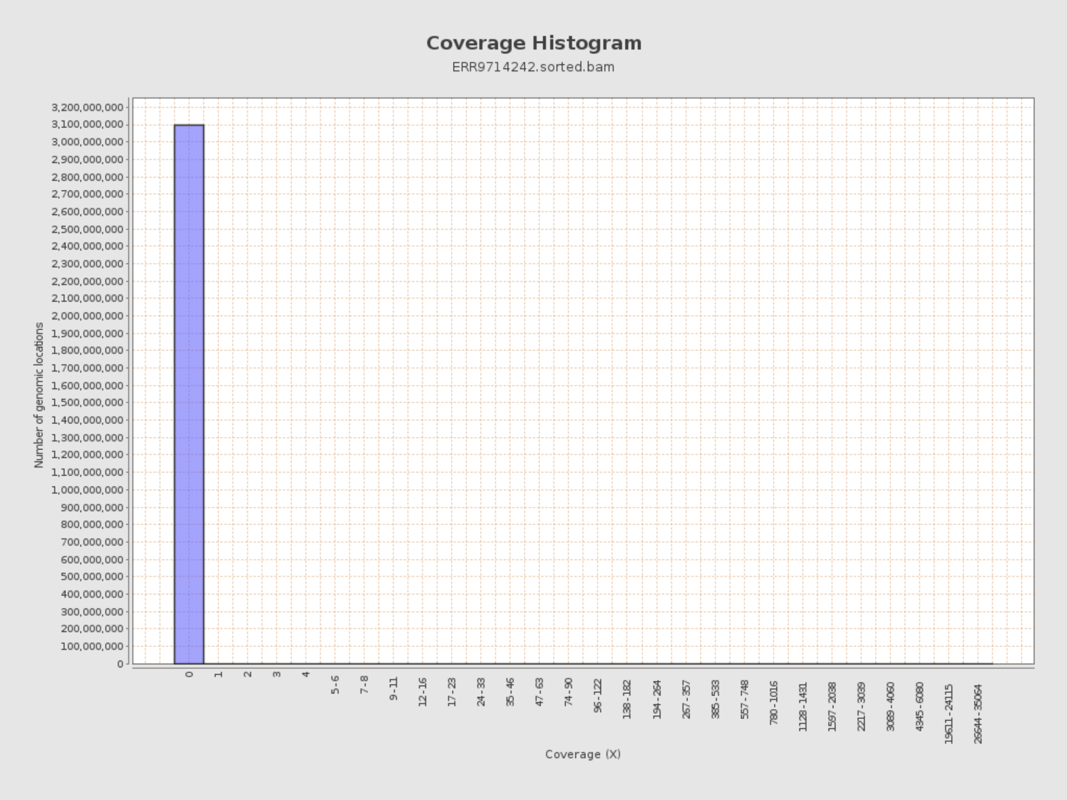
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17519	0.0001	0.1118
chr2	243199373	4829123	0.0199	21.7799
chr3	198022430	4869	0	0.0102
chr4	191154276	5810	0	0.0097
chr5	180915260	3271	0	0.0054
chr6	171115067	4117	0	0.0096
chr7	159138663	10761	0.0001	0.0679

chr8	146364022	3742	0	0.0158
chr9	141213431	4375	0	0.0132
chr10	135534747	15369	0.0001	0.142
chr11	135006516	3923	0	0.0231
chr12	133851895	10859	0.0001	0.0535
chr13	115169878	2172	0	0.0058
chr14	107349540	5973	0.0001	0.0489
chr15	102531392	3737	0	0.0107
chr16	90354753	2623	0	0.0134
chr17	81195210	6534	0.0001	0.0791
chr18	78077248	1348	0	0.0045
chr19	59128983	2473	0	0.0115
chr20	63025520	2027	0	0.0167
chr21	48129895	1086	0	0.0067
chr22	51304566	870	0	0.0046
chrMT	16571	7756	0.468	2.3175
chrX	155270560	56067	0.0004	0.0514
chrY	59373566	1729	0	0.0123

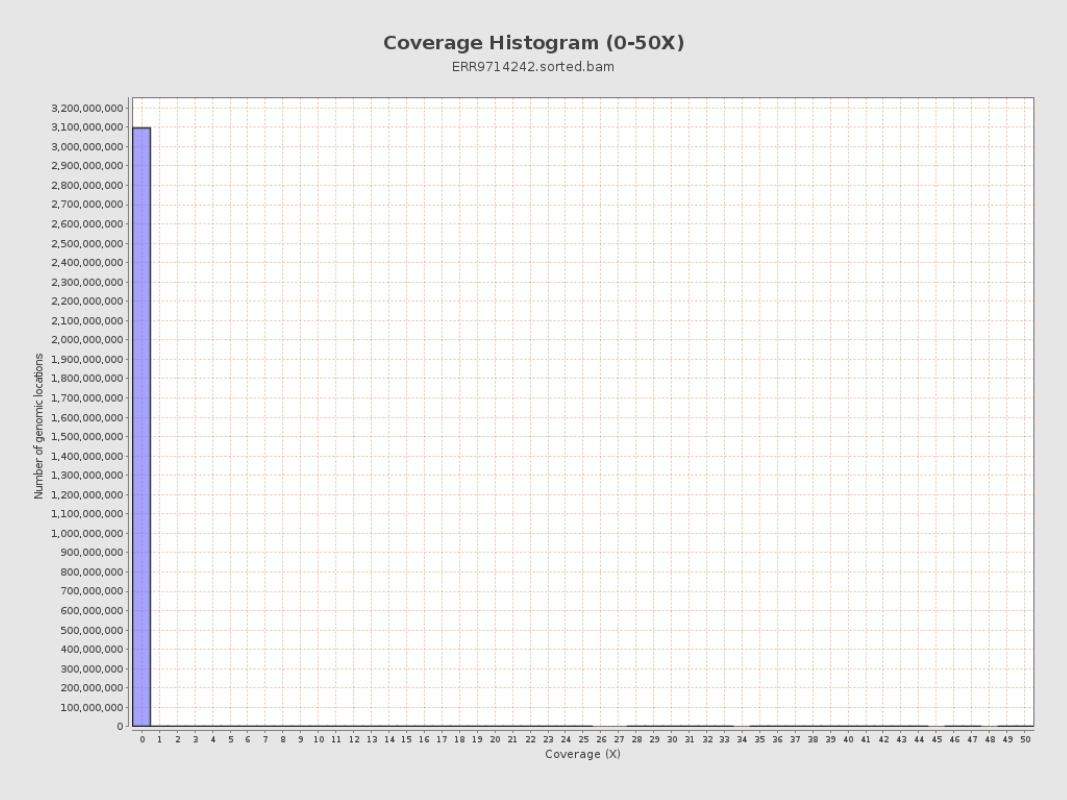
3. Results : Coverage across reference



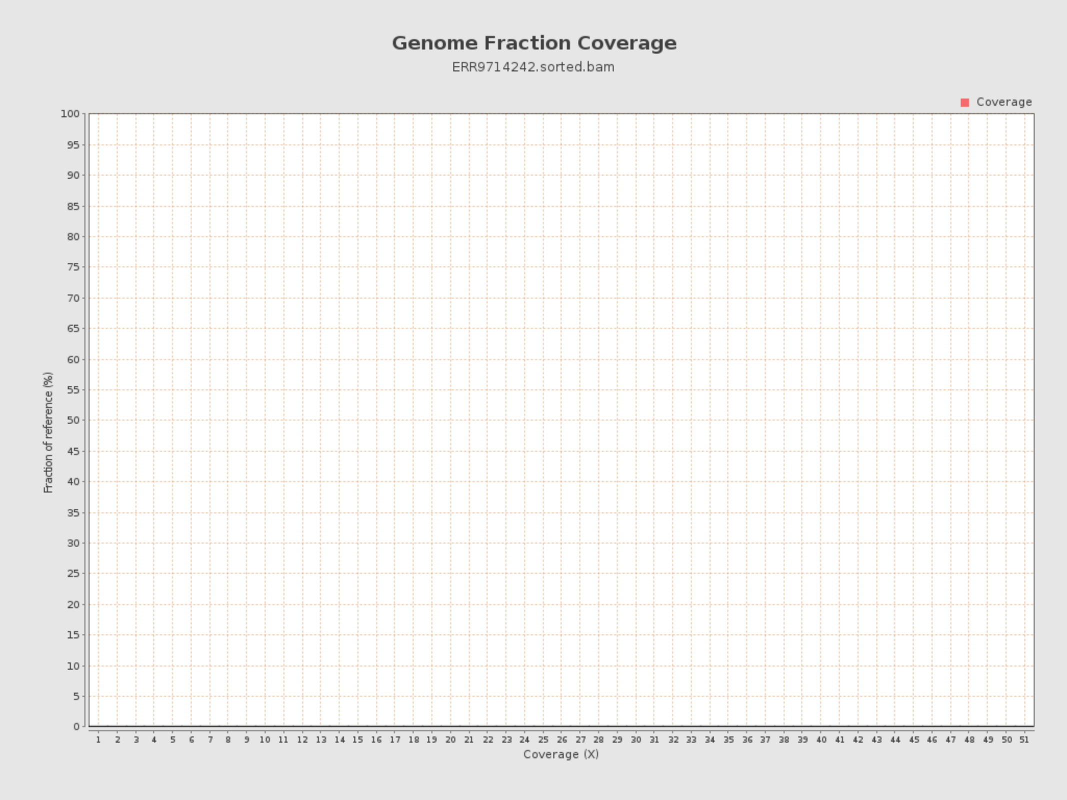
4. Results : Coverage Histogram



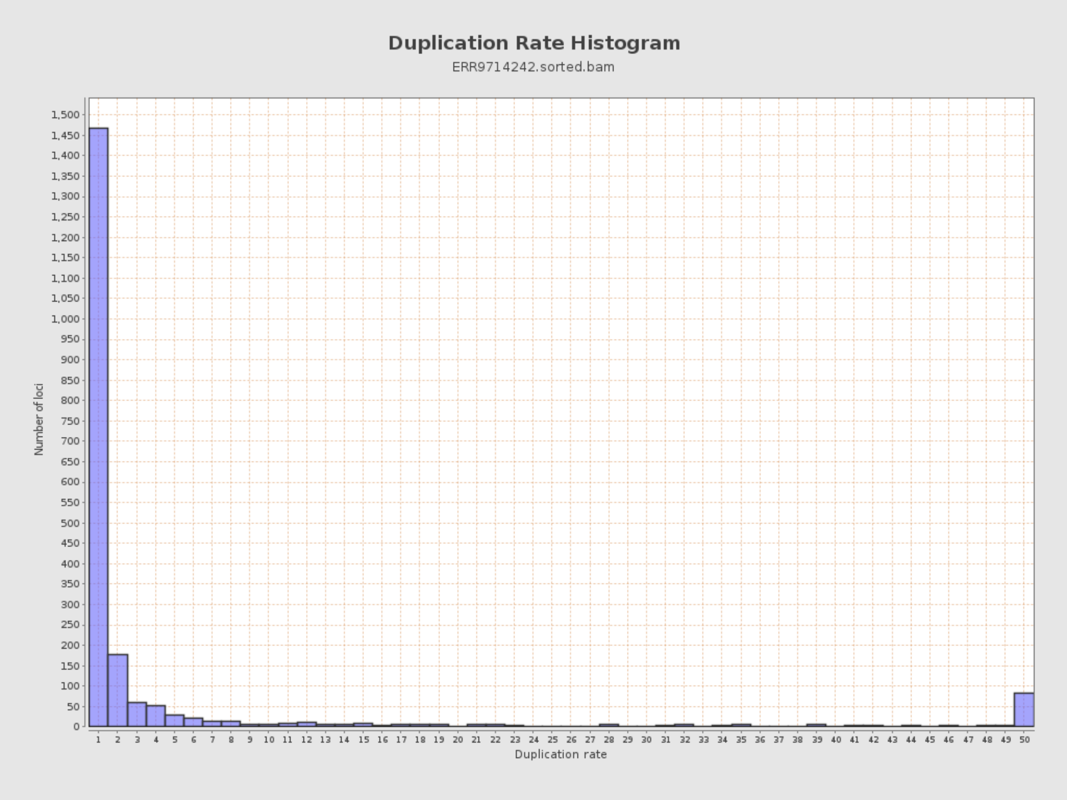
5. Results : Coverage Histogram (0-50X)



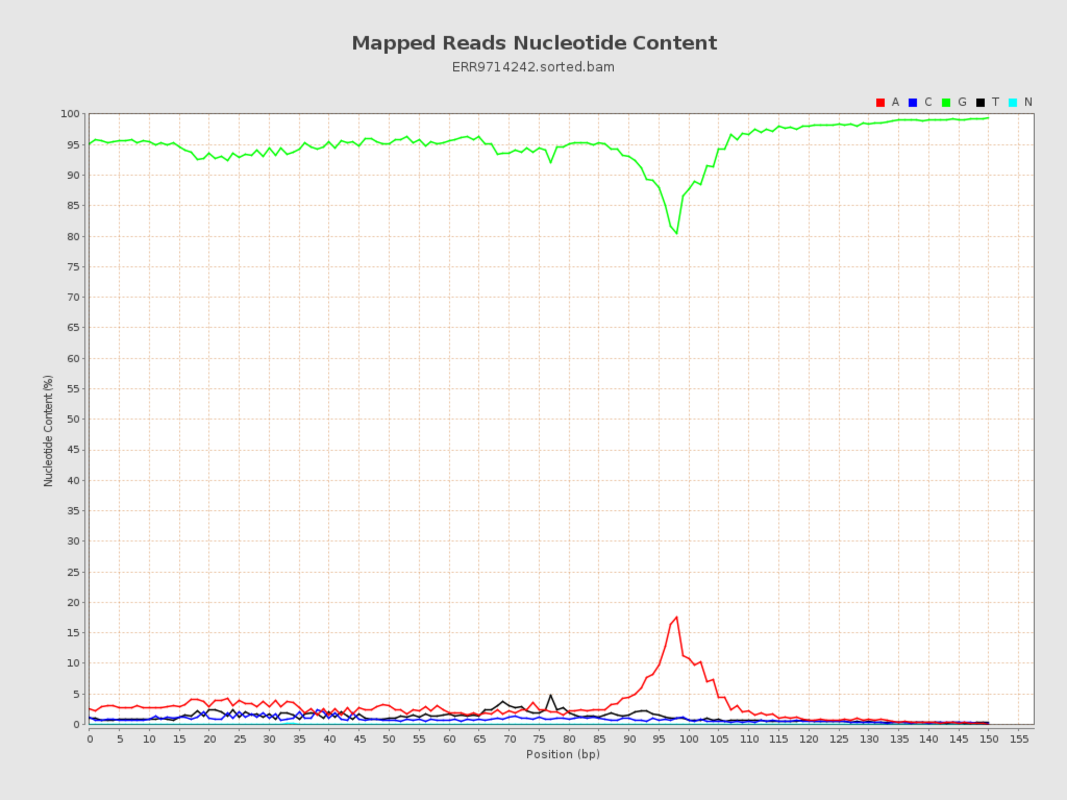
6. Results : Genome Fraction Coverage



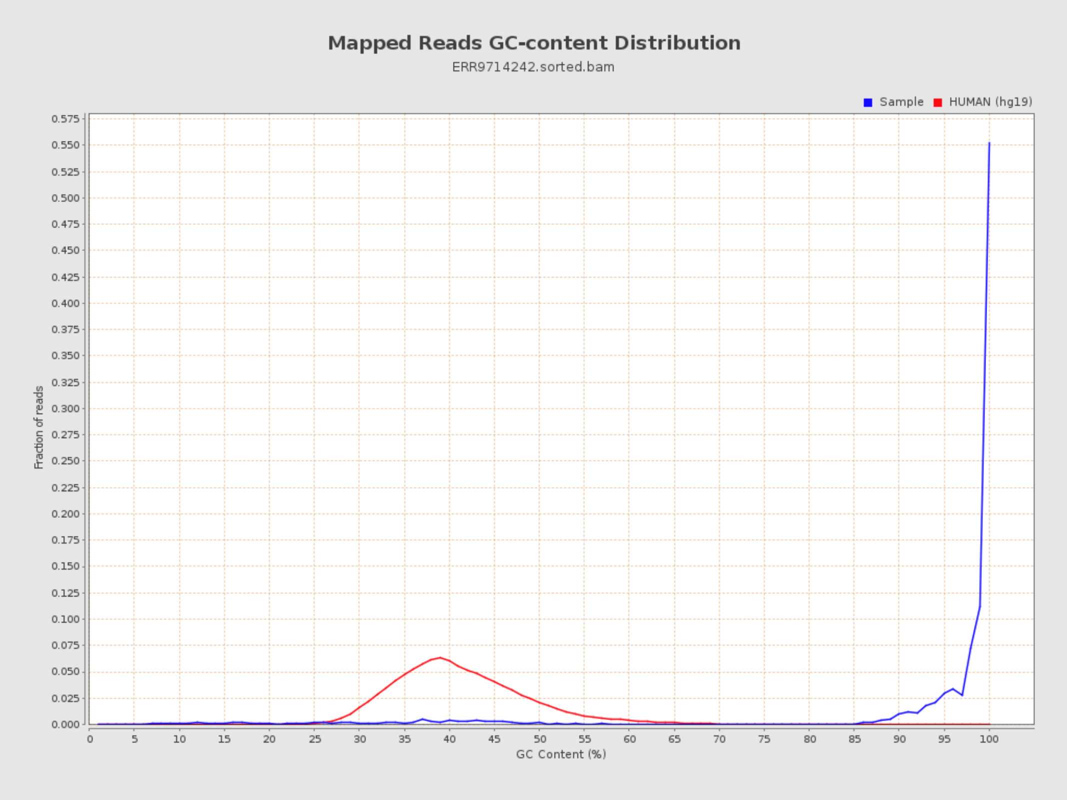
7. Results : Duplication Rate Histogram



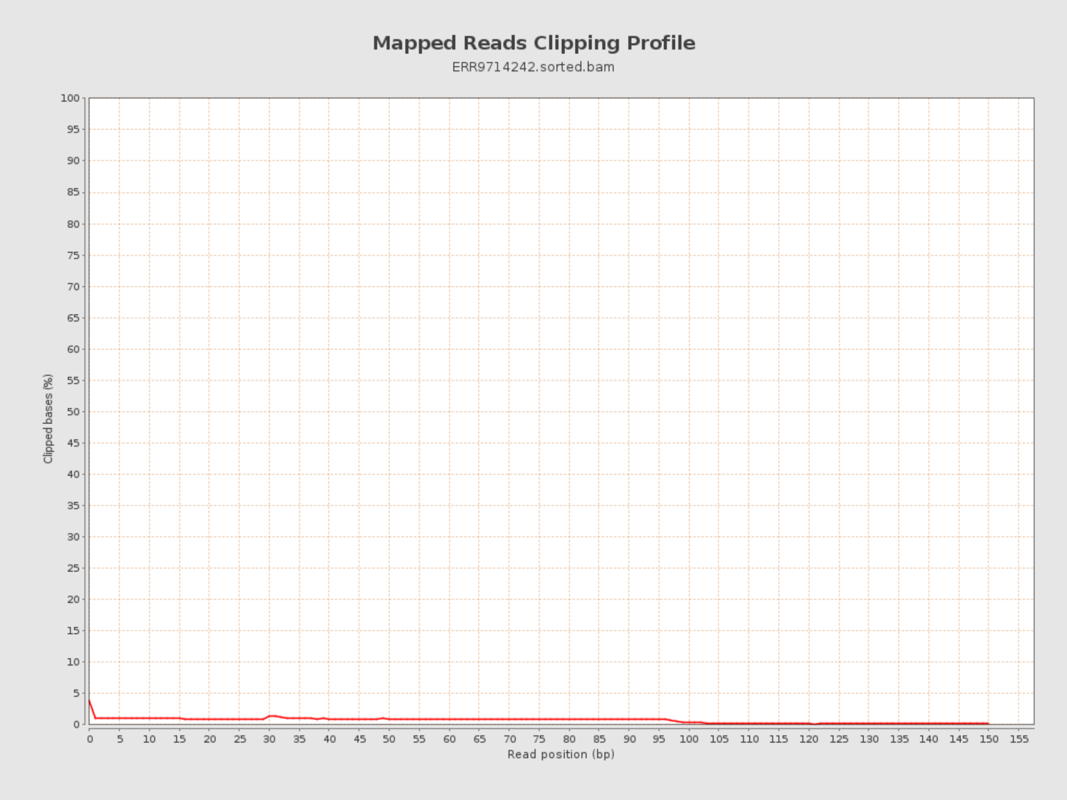
8. Results : Mapped Reads Nucleotide Content



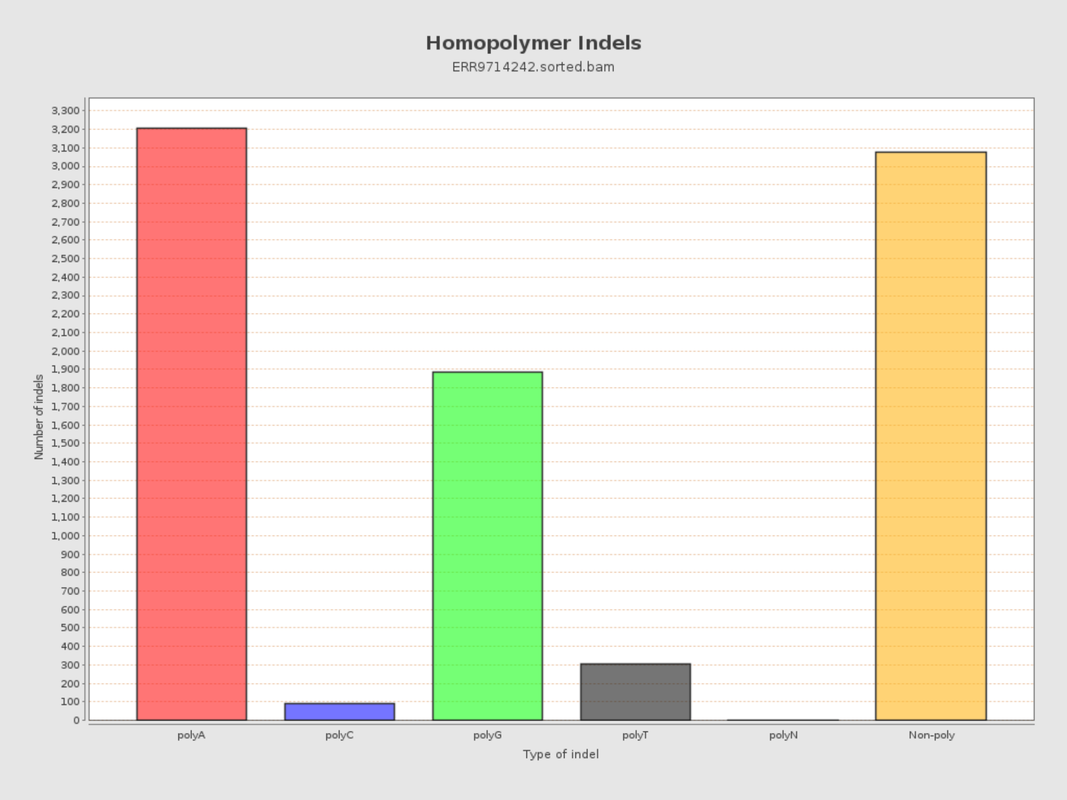
9. Results : Mapped Reads GC-content Distribution



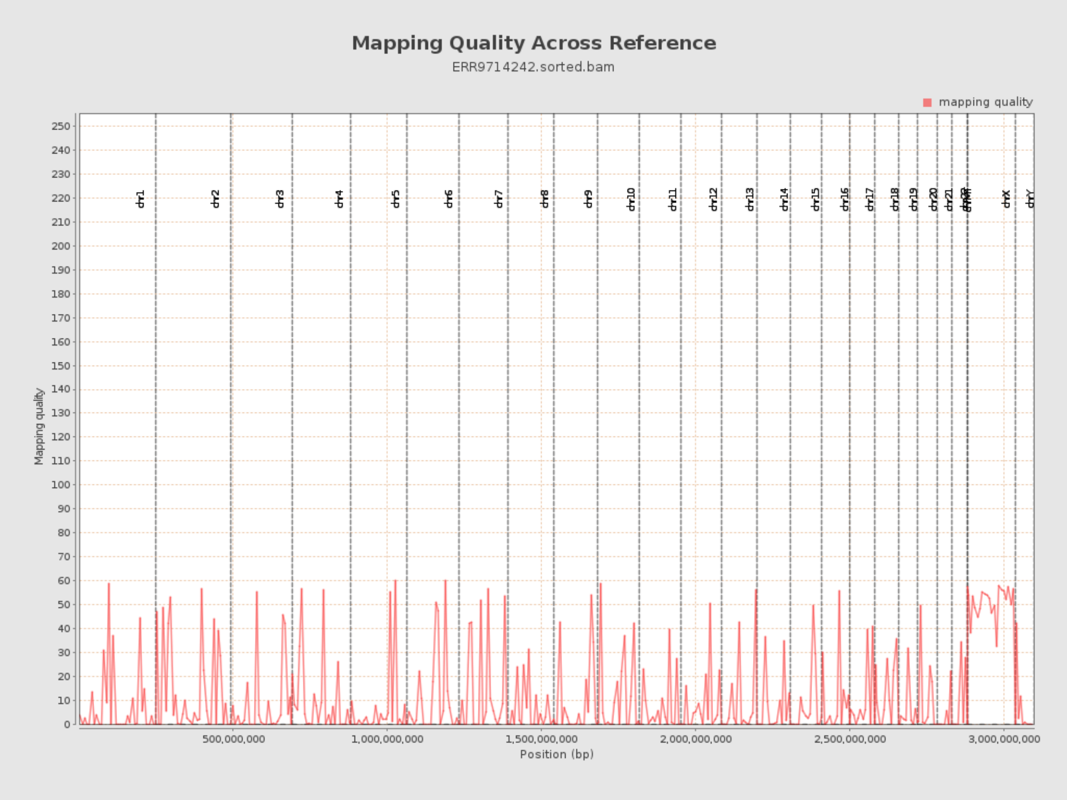
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram