Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 00:06:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714203.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_ERR9714203 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714203.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 00:06:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714203.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,420
Mapped reads	1,880 / 34.69%
Unmapped reads	3,540 / 65.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	91 / 1.68%
Read min/max/mean length	30 / 151 / 81.25
Duplicated reads (estimated)	1,054 / 19.45%
Duplication rate	35.22%
Clipped reads	1,746 / 32.21%

2.2. ACGT Content

Number/percentage of A's	62,415 / 27.16%
Number/percentage of C's	43,583 / 18.97%
Number/percentage of T's	59,243 / 25.78%
Number/percentage of G's	64,558 / 28.09%
Number/percentage of N's	4 / 0%
GC Percentage	47.06%

2.3. Coverage

Mean	0.0001

Standard Deviation	0.0416

2.4. Mapping Quality

Mean Mapping Quality	24.51

2.5. Mismatches and indels

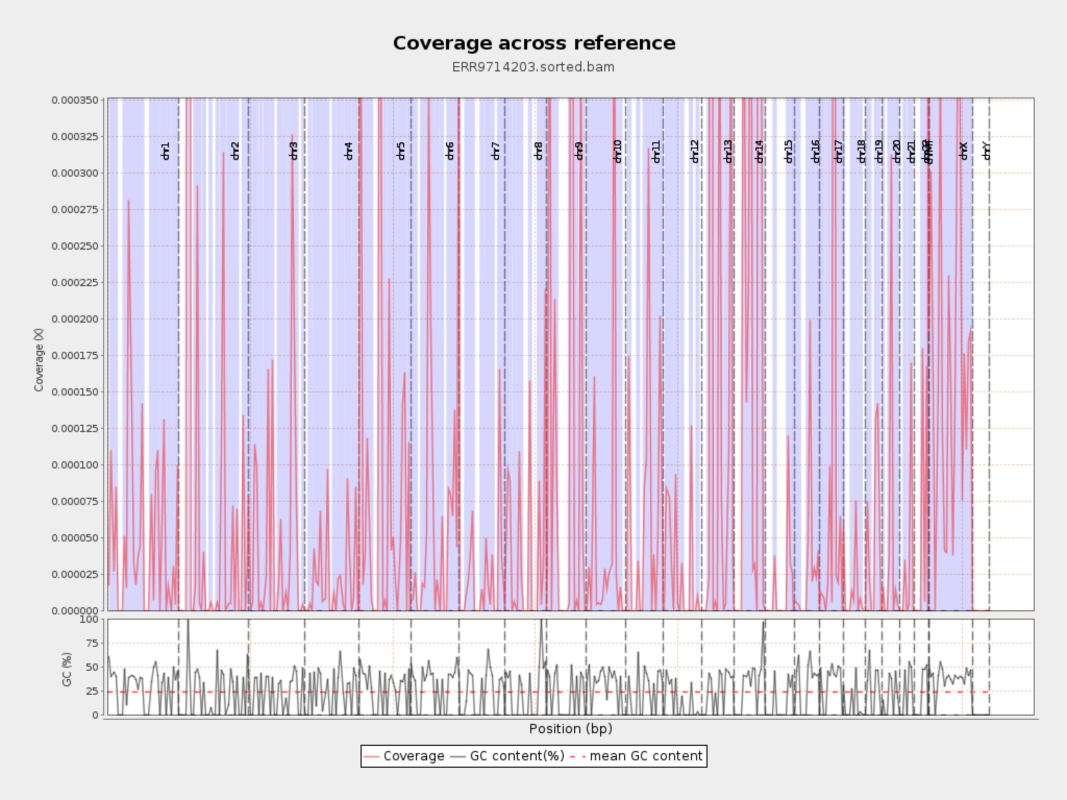
General error rate	3.98%
Mismatches	8,062
Insertions	278
Mapped reads with at least one insertion	14.41%
Deletions	583
Mapped reads with at least one deletion	29.47%
Homopolymer indels	21.37%

2.6. Chromosome stats

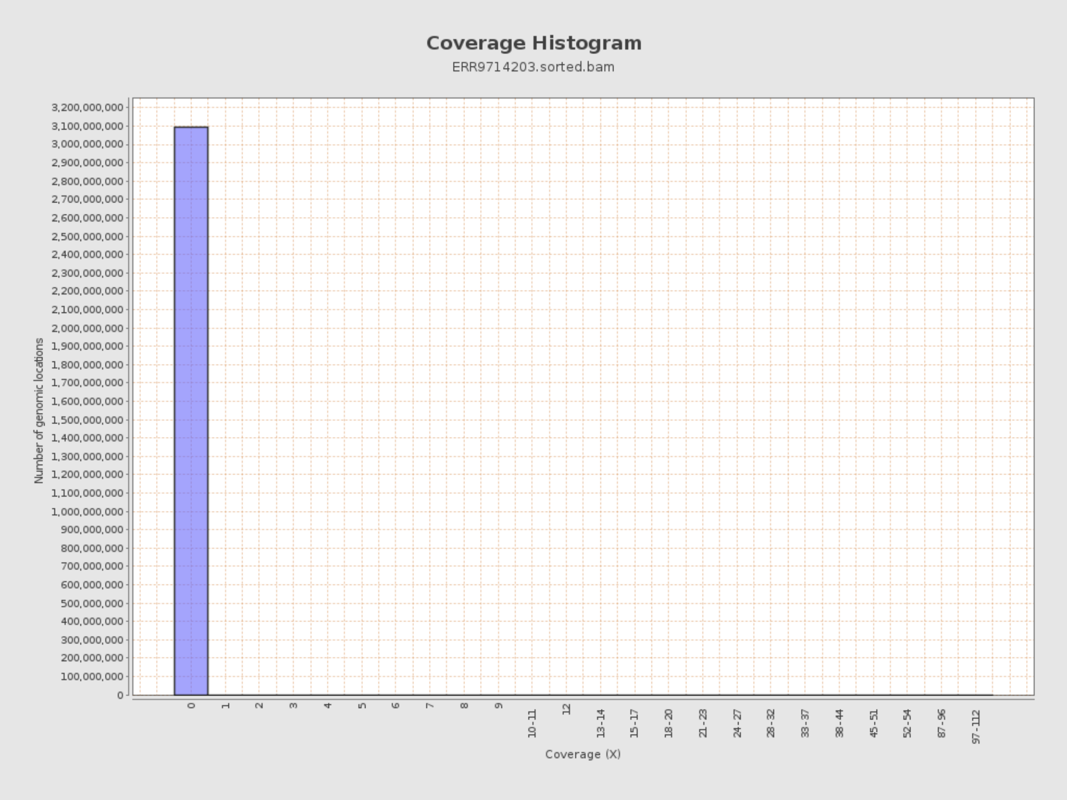
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12690	0.0001	0.0176
chr2	243199373	27975	0.0001	0.0829
chr3	198022430	10411	0.0001	0.0191
chr4	191154276	4279	0	0.0085
chr5	180915260	17562	0.0001	0.0405
chr6	171115067	11149	0.0001	0.0195
chr7	159138663	3741	0	0.0088

chr8	146364022	6473	0	0.0121
chr9	141213431	16659	0.0001	0.0517
chr10	135534747	6562	0	0.0281
chr11	135006516	8383	0.0001	0.022
chr12	133851895	3573	0	0.01
chr13	115169878	25111	0.0002	0.1146
chr14	107349540	27145	0.0003	0.0774
chr15	102531392	1663	0	0.0066
chr16	90354753	2870	0	0.0155
chr17	81195210	9559	0.0001	0.0475
chr18	78077248	1009	0	0.006
chr19	59128983	2856	0	0.014
chr20	63025520	2959	0	0.0172
chr21	48129895	1617	0	0.0114
chr22	51304566	2736	0.0001	0.0202
chrMT	16571	300	0.0181	0.1593
chrX	155270560	26348	0.0002	0.029
chrY	59373566	0	0	0

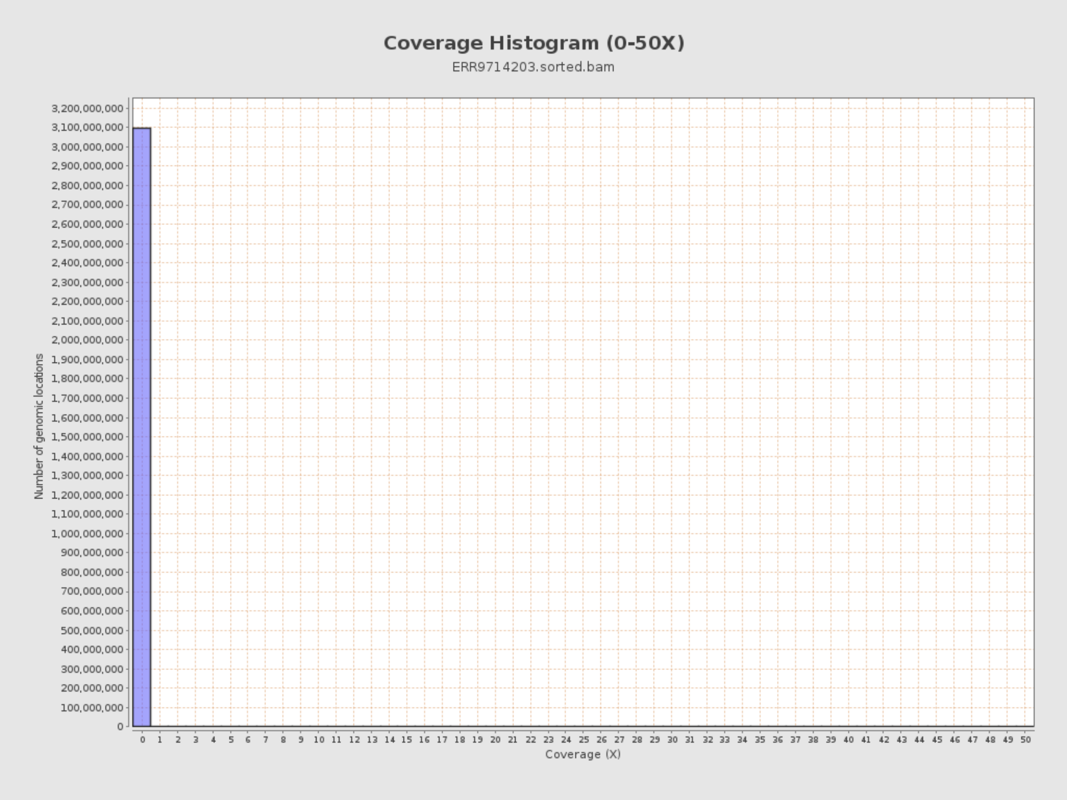
3. Results : Coverage across reference



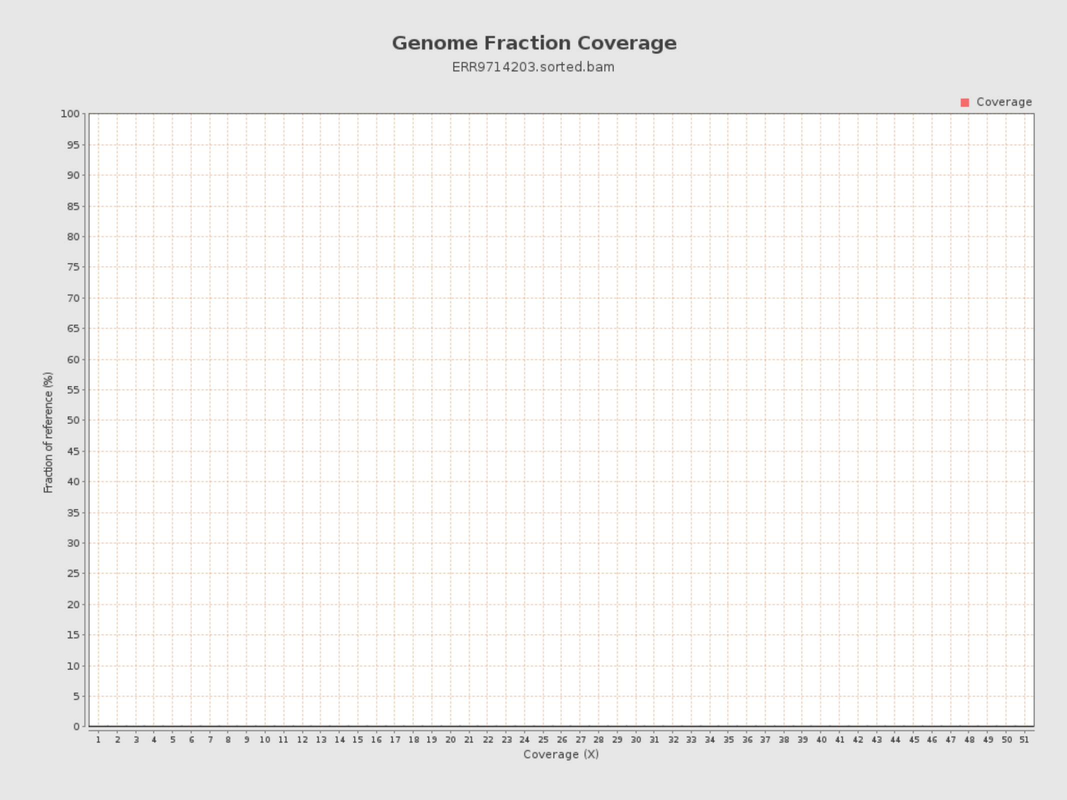
4. Results : Coverage Histogram



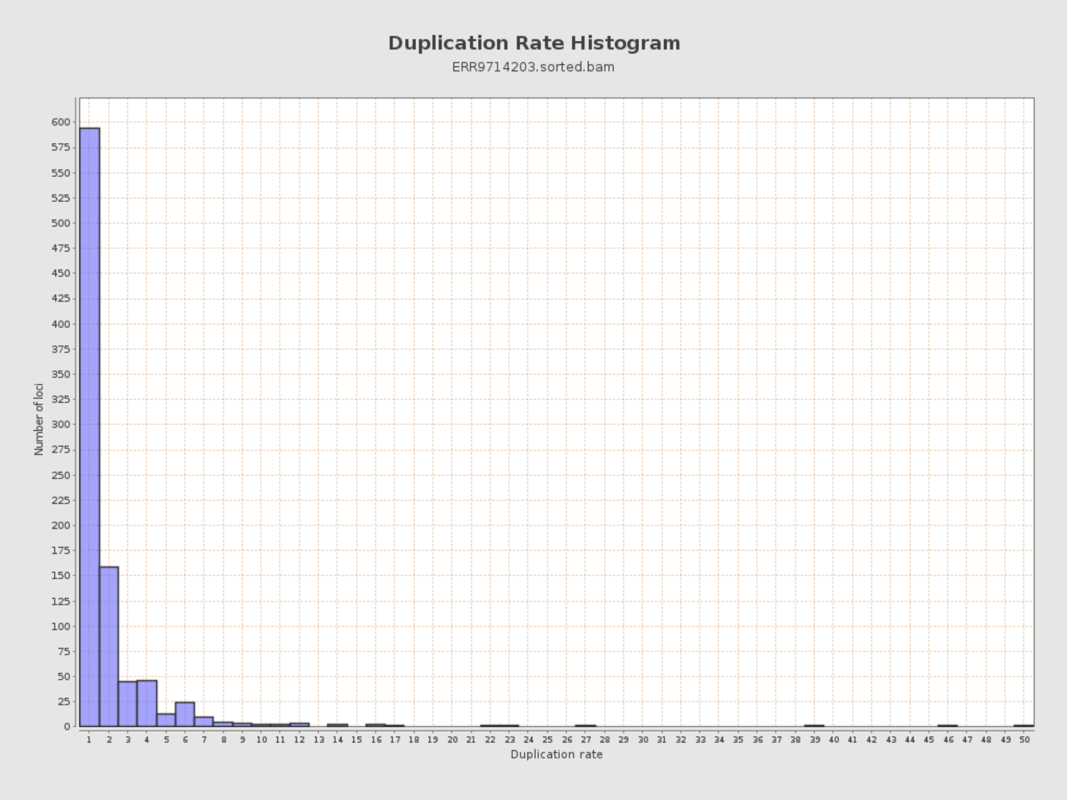
5. Results : Coverage Histogram (0-50X)



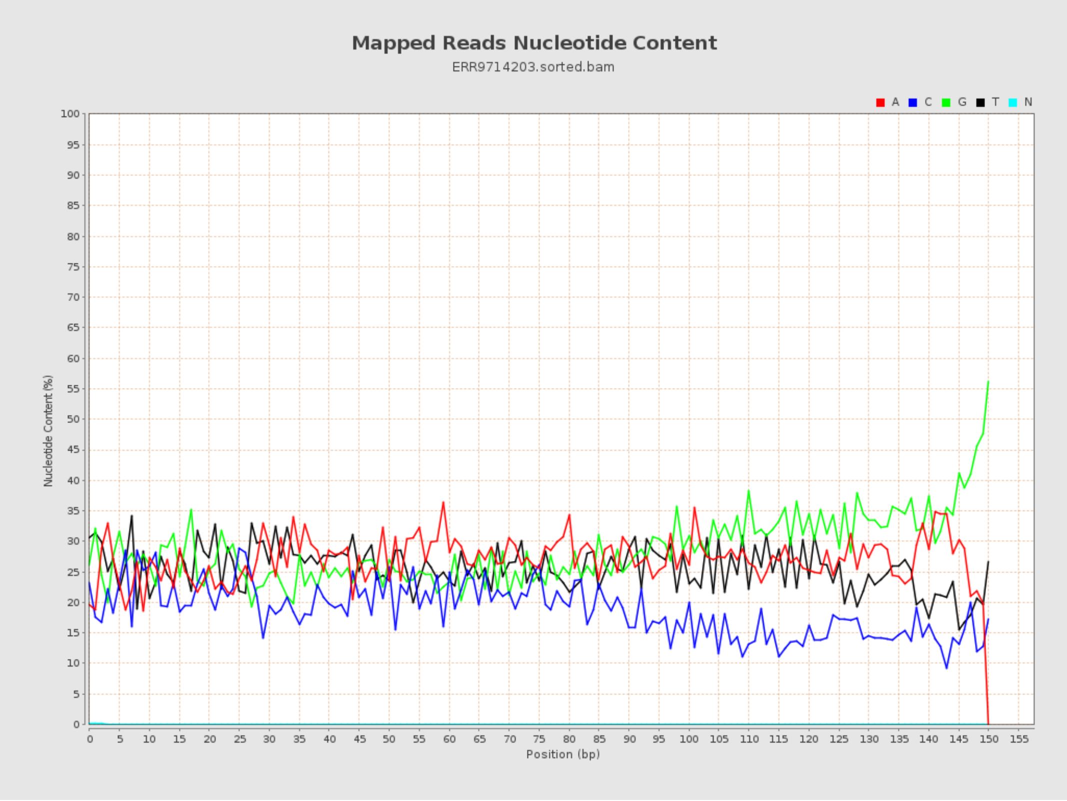
6. Results : Genome Fraction Coverage



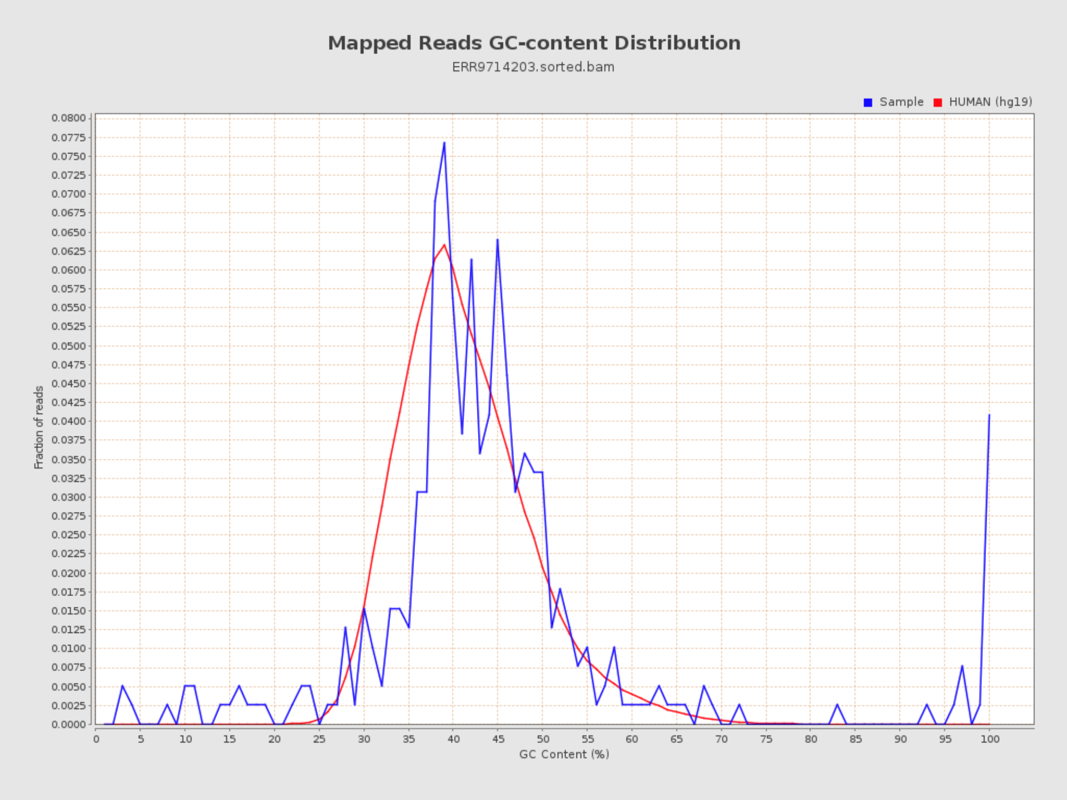
7. Results : Duplication Rate Histogram



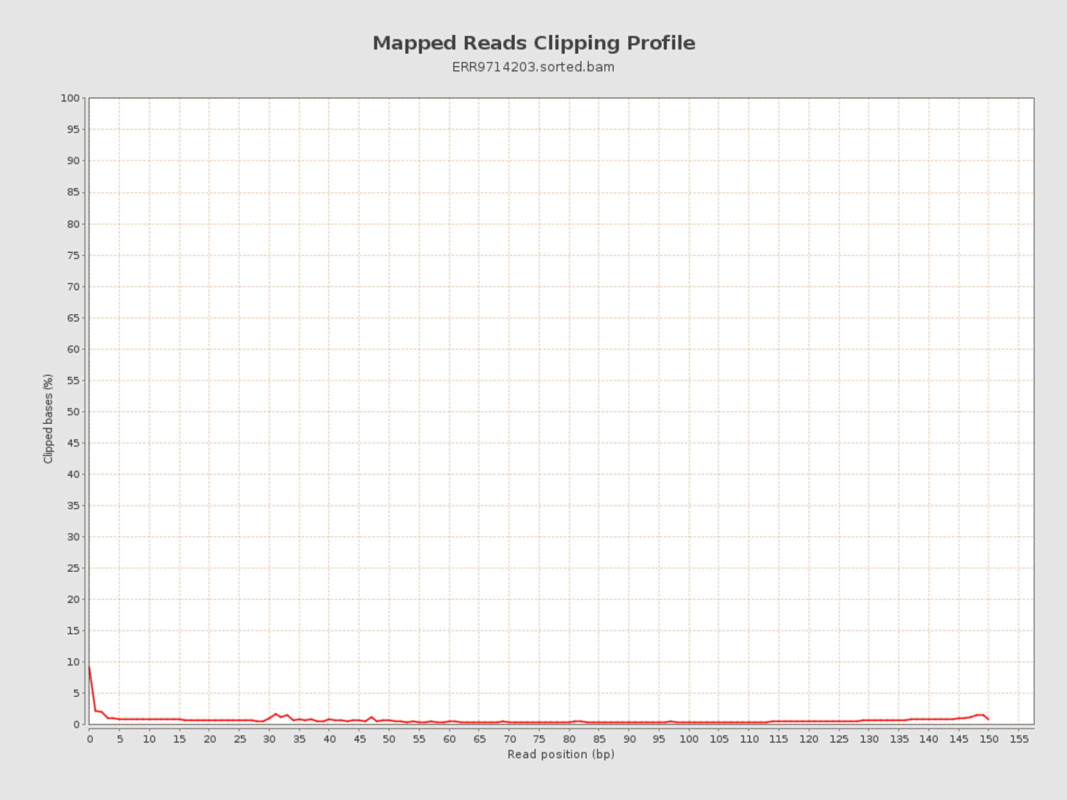
8. Results : Mapped Reads Nucleotide Content



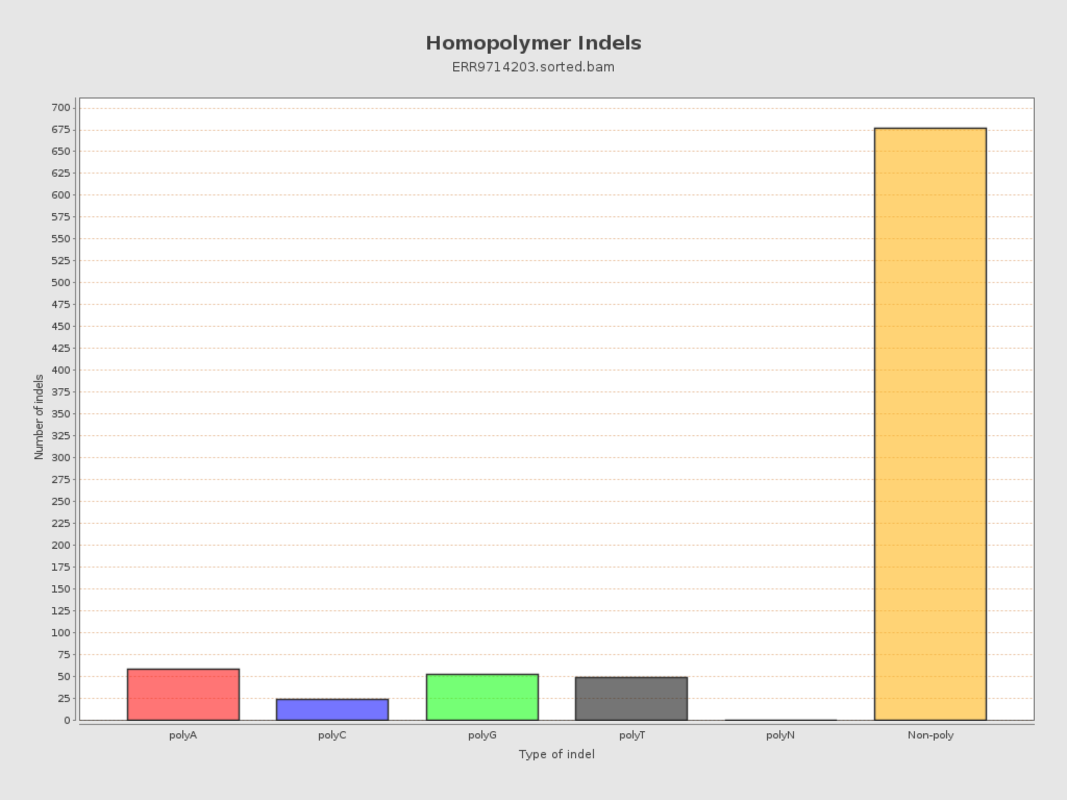
9. Results : Mapped Reads GC-content Distribution



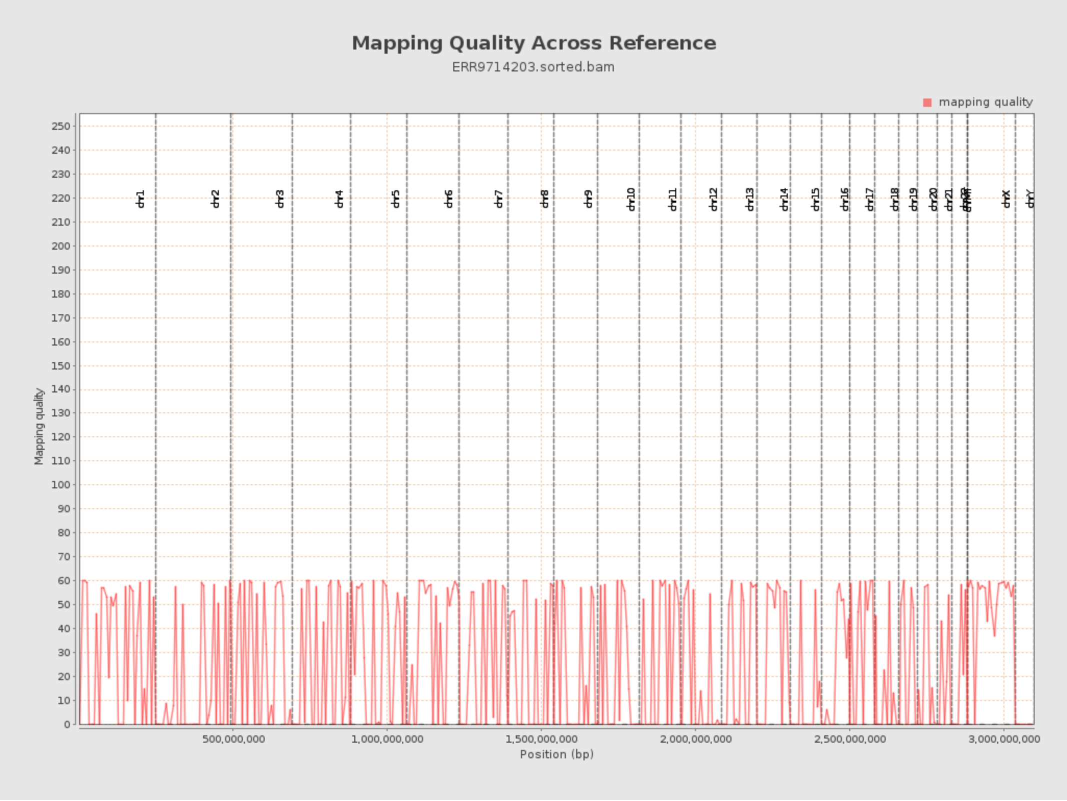
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram