Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 01:32:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714254.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_ERR9714254 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714254.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 01:32:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714254.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	415,470
Mapped reads	64,547 / 15.54%
Unmapped reads	350,923 / 84.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,041 / 0.25%
Read min/max/mean length	30 / 151 / 60.02
Duplicated reads (estimated)	63,352 / 15.25%
Duplication rate	35.15%
Clipped reads	36,071 / 8.68%

2.2. ACGT Content

Number/percentage of A's	174,863 / 2.75%
Number/percentage of C's	79,391 / 1.25%
Number/percentage of T's	102,189 / 1.61%
Number/percentage of G's	6,004,950 / 94.39%
Number/percentage of N's	141 / 0%
GC Percentage	95.64%

2.3. Coverage

Mean	0.0021

Standard Deviation	7.7482

2.4. Mapping Quality

Mean Mapping Quality	9.8

2.5. Mismatches and indels

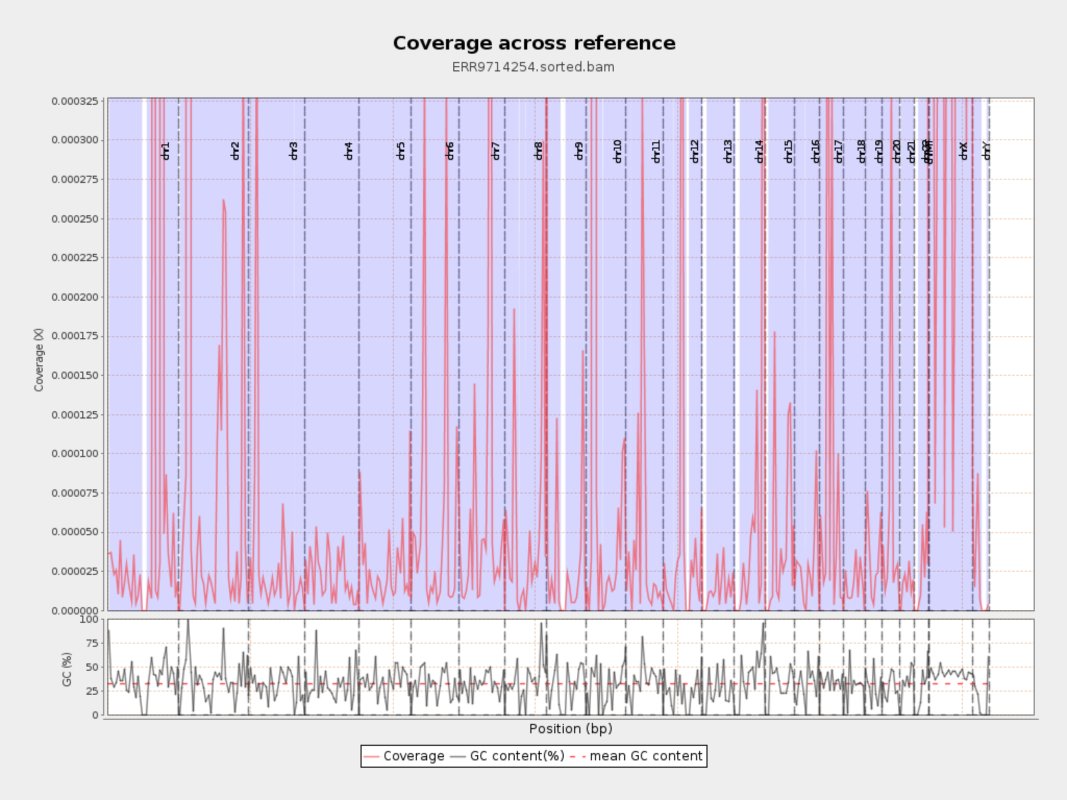
General error rate	3.15%
Mismatches	154,721
Insertions	6,597
Mapped reads with at least one insertion	7.21%
Deletions	3,136
Mapped reads with at least one deletion	4.67%
Homopolymer indels	61.13%

2.6. Chromosome stats

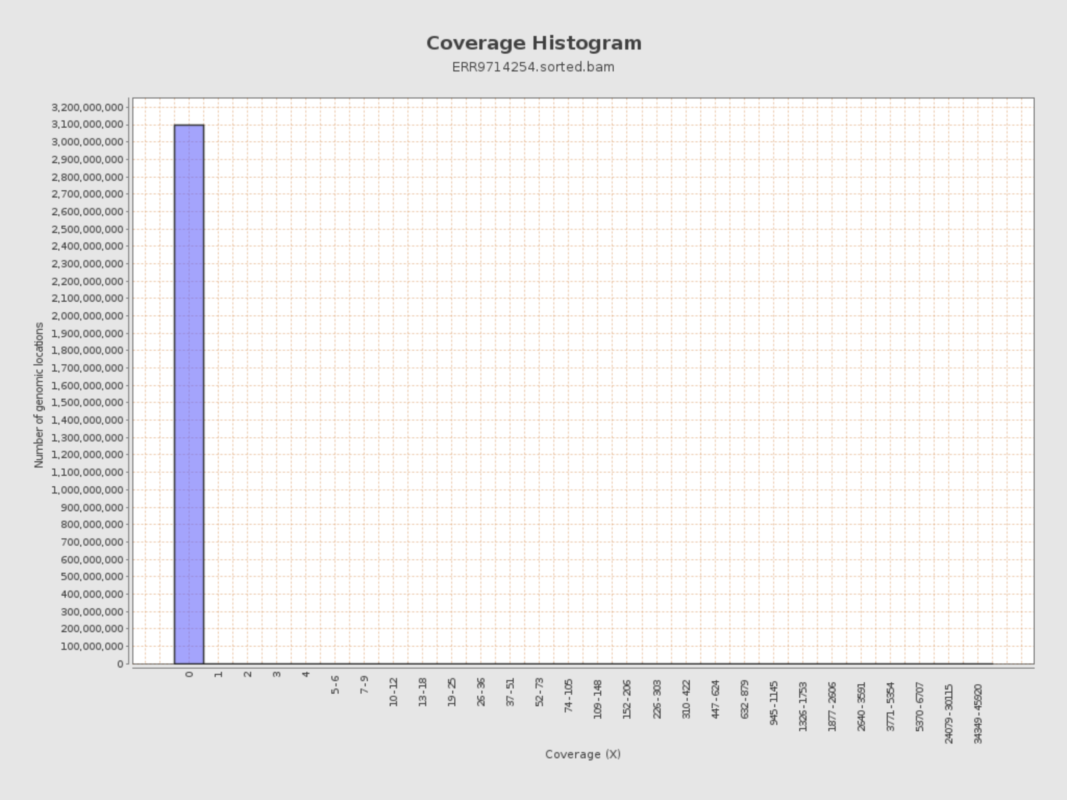
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	82443	0.0003	0.7469
chr2	243199373	5995249	0.0247	27.6221
chr3	198022430	7049	0	0.0222
chr4	191154276	4185	0	0.0074
chr5	180915260	4536	0	0.0084
chr6	171115067	10412	0.0001	0.0265
chr7	159138663	12612	0.0001	0.0808

chr8	146364022	7584	0.0001	0.0211
chr9	141213431	4270	0	0.0127
chr10	135534747	71388	0.0005	1.0525
chr11	135006516	6527	0	0.0284
chr12	133851895	7515	0.0001	0.0443
chr13	115169878	1606	0	0.0053
chr14	107349540	8295	0.0001	0.0892
chr15	102531392	4692	0	0.0202
chr16	90354753	2542	0	0.0082
chr17	81195210	9104	0.0001	0.0803
chr18	78077248	1262	0	0.005
chr19	59128983	1976	0	0.0115
chr20	63025520	4174	0.0001	0.0203
chr21	48129895	843	0	0.0052
chr22	51304566	1211	0	0.0081
chrMT	16571	2100	0.1267	0.6889
chrX	155270560	122658	0.0008	0.124
chrY	59373566	1055	0	0.0082

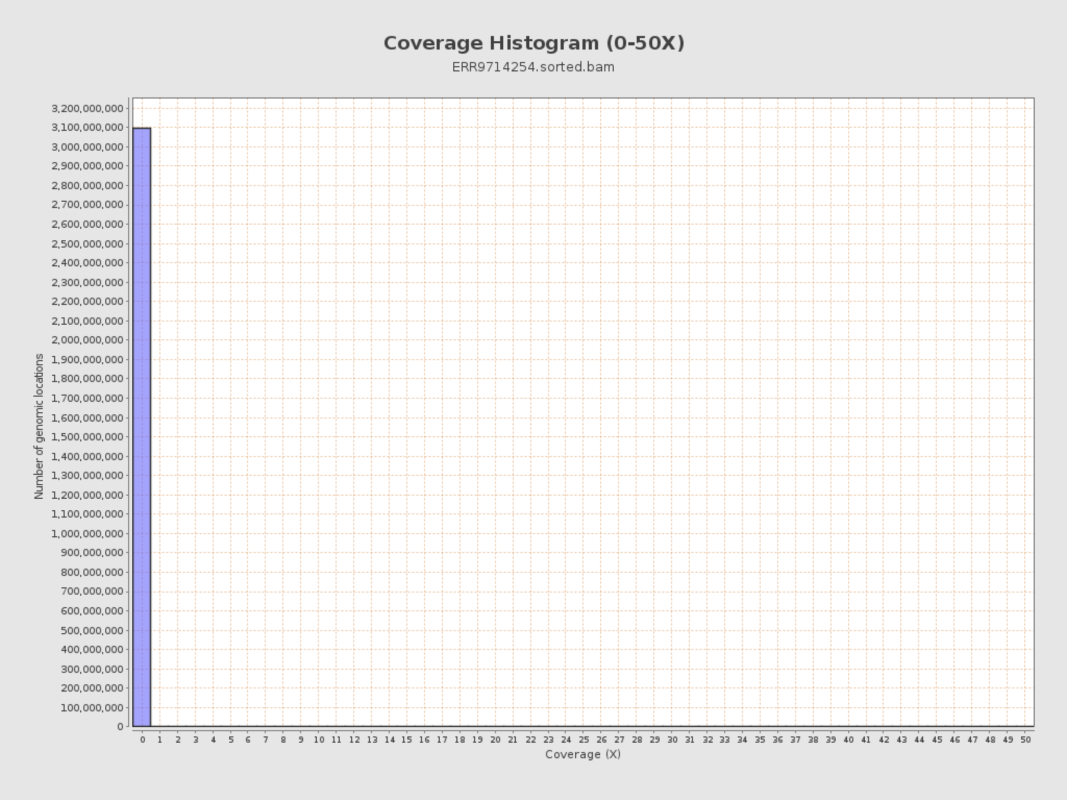
3. Results : Coverage across reference



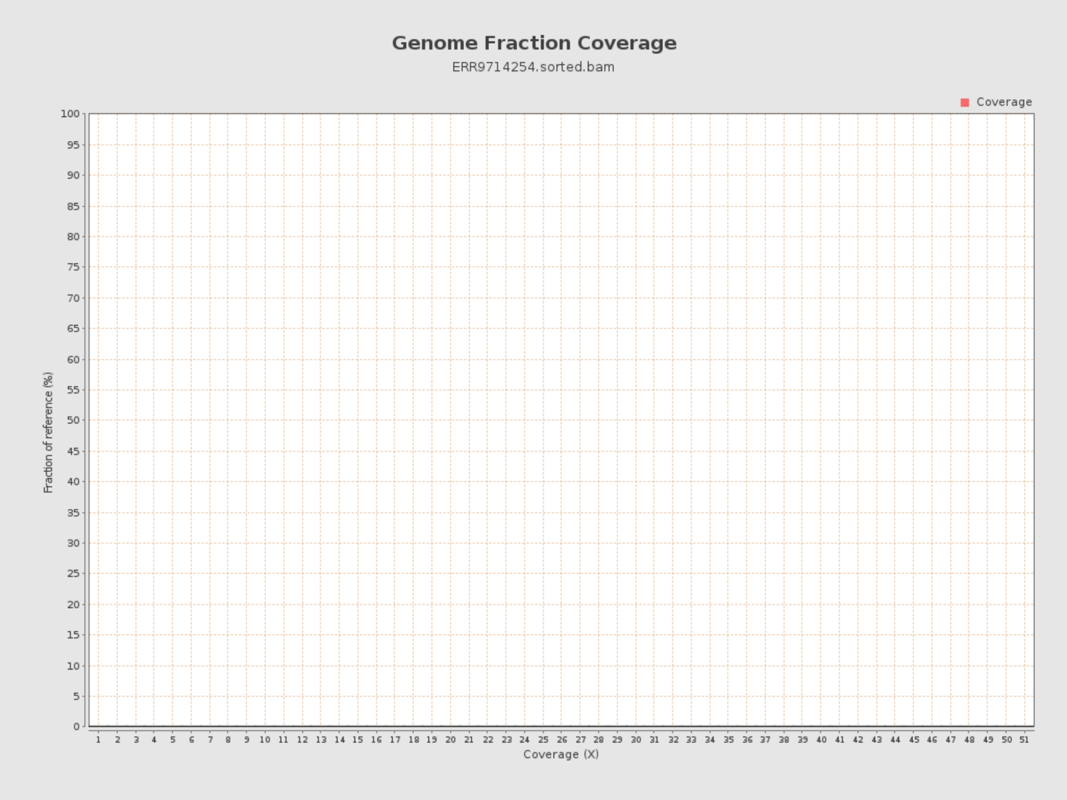
4. Results : Coverage Histogram



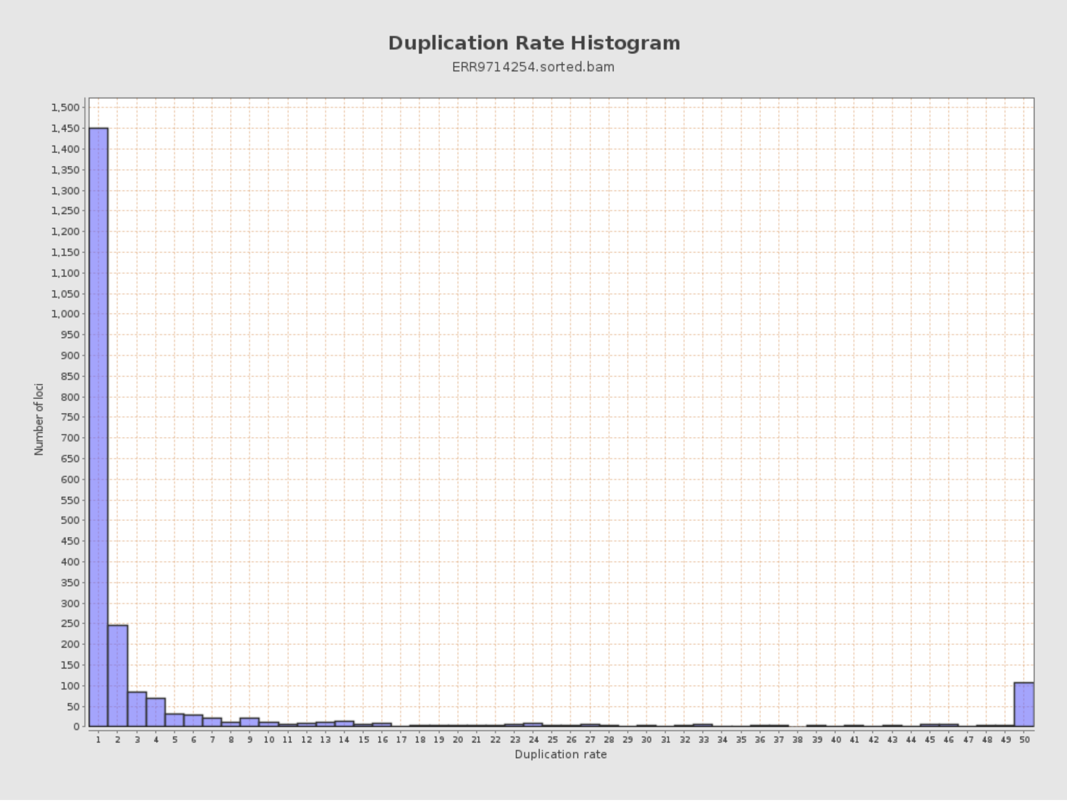
5. Results : Coverage Histogram (0-50X)



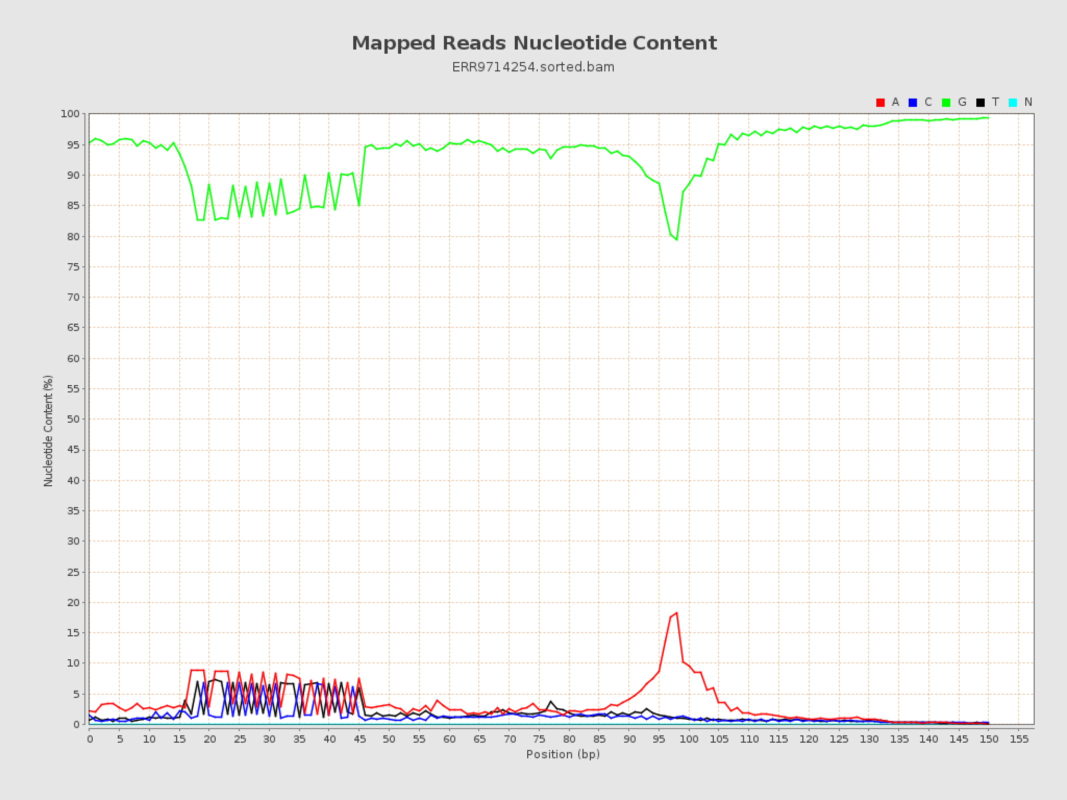
6. Results : Genome Fraction Coverage



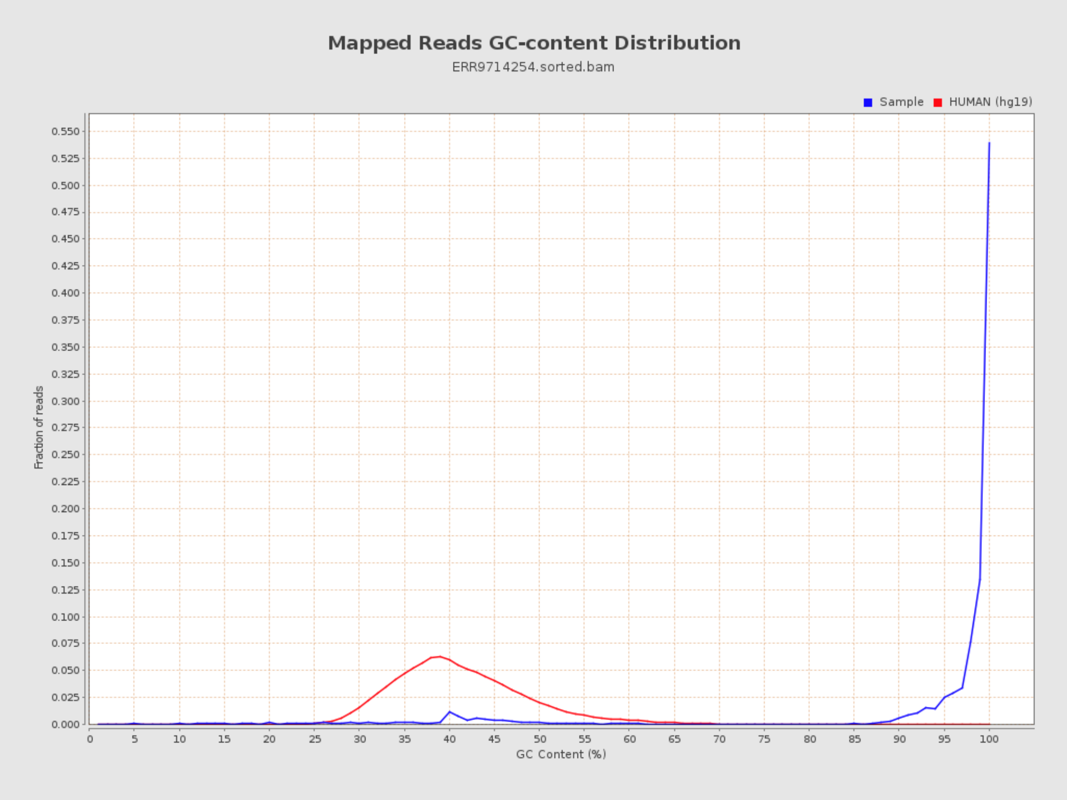
7. Results : Duplication Rate Histogram



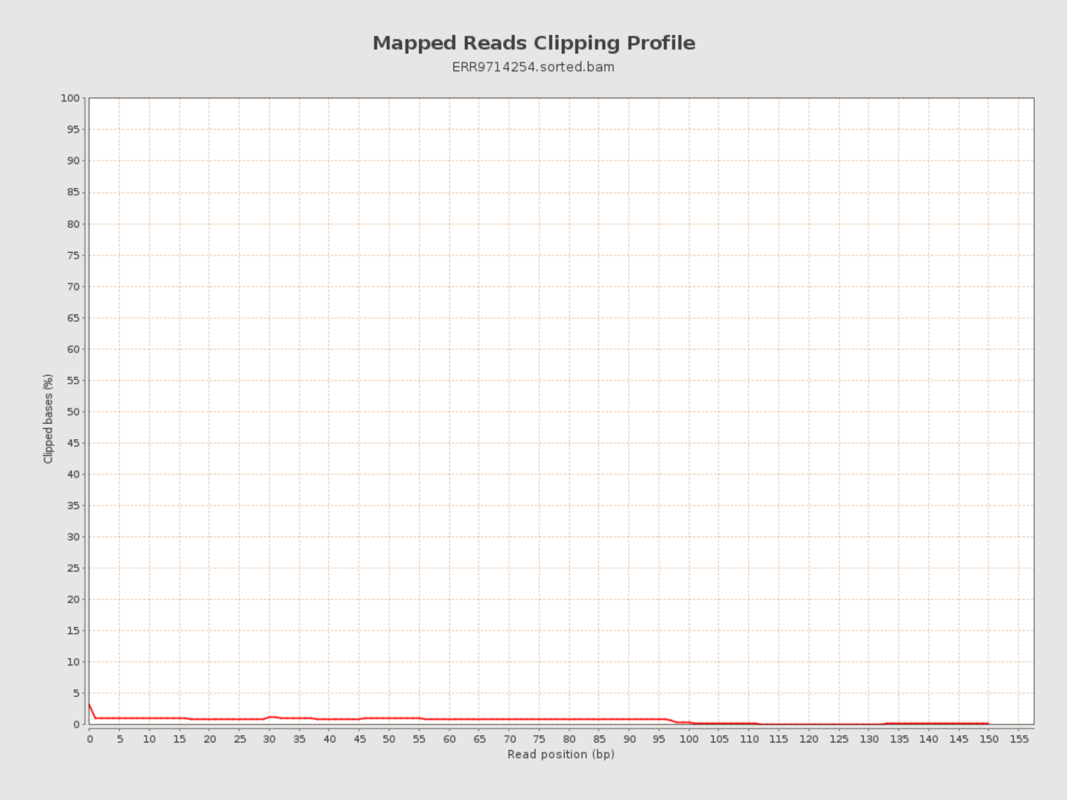
8. Results : Mapped Reads Nucleotide Content



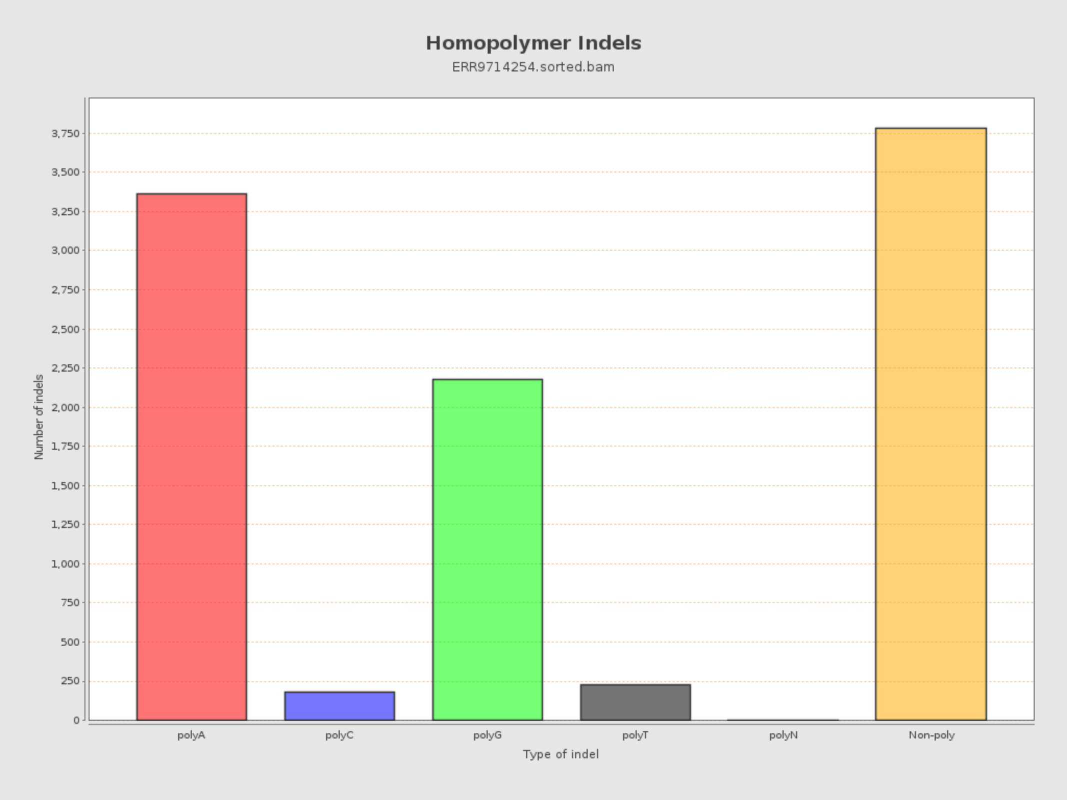
9. Results : Mapped Reads GC-content Distribution



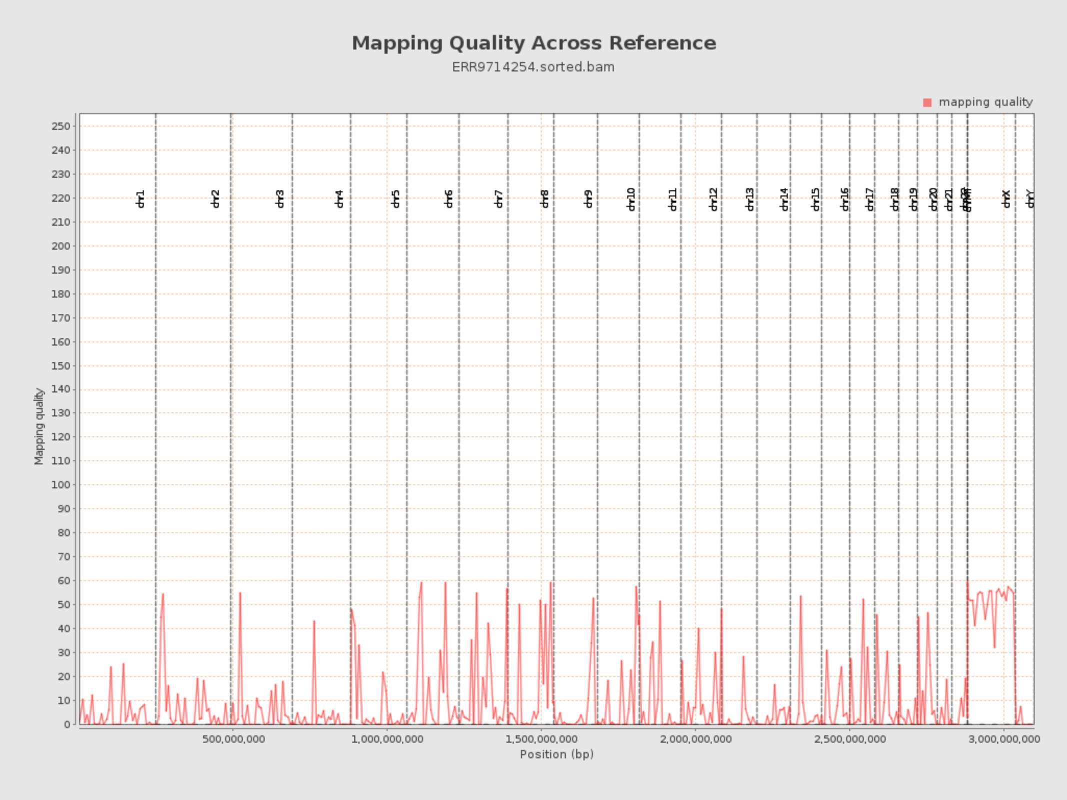
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram