Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 23:12:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714178.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_ERR9714178 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714178.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 23:12:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714178.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,715,858
Mapped reads	1,620,824 / 94.46%
Unmapped reads	95,034 / 5.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	106,313 / 6.2%
Read min/max/mean length	30 / 151 / 140.76
Duplicated reads (estimated)	1,544,786 / 90.03%
Duplication rate	48.2%
Clipped reads	1,603,955 / 93.48%

2.2. ACGT Content

Number/percentage of A's	58,510,859 / 29.15%
Number/percentage of C's	41,437,926 / 20.64%
Number/percentage of T's	55,142,246 / 27.47%
Number/percentage of G's	45,649,201 / 22.74%
Number/percentage of N's	1,551 / 0%
GC Percentage	43.38%

2.3. Coverage

Mean	0.0662

Standard Deviation	11.921

2.4. Mapping Quality

Mean Mapping Quality	51.3

2.5. Mismatches and indels

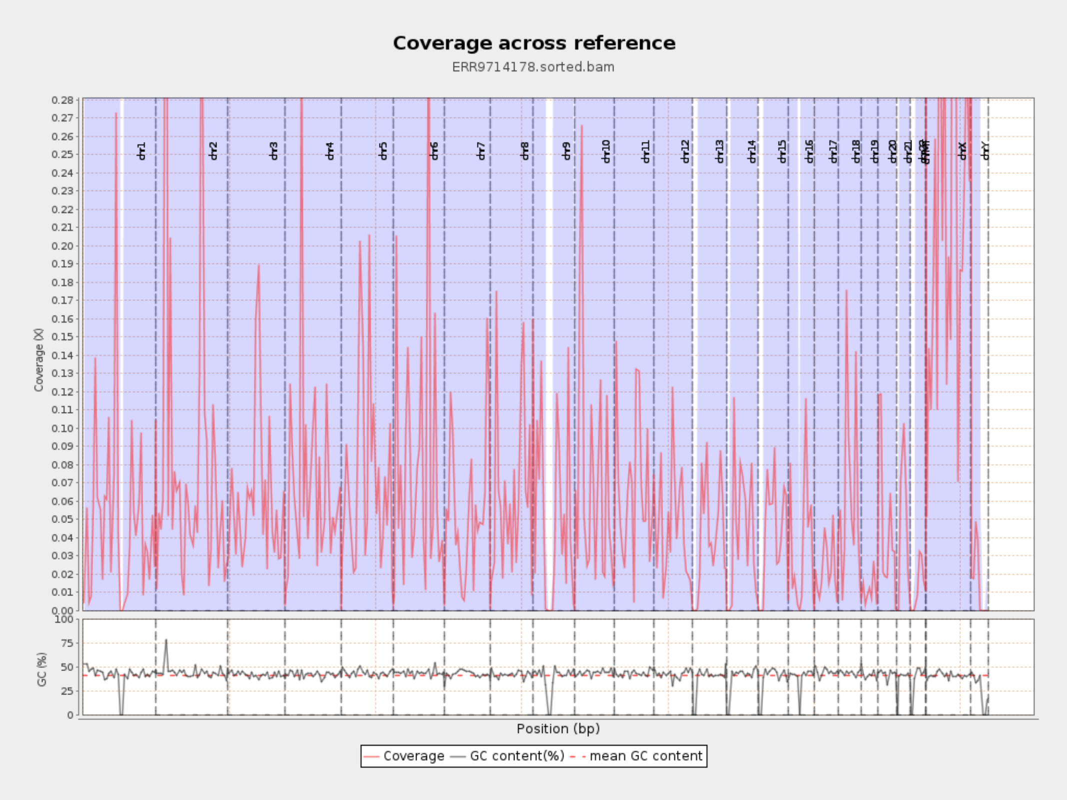
General error rate	3.79%
Mismatches	7,221,233
Insertions	175,078
Mapped reads with at least one insertion	10.5%
Deletions	644,727
Mapped reads with at least one deletion	37.91%
Homopolymer indels	27.94%

2.6. Chromosome stats

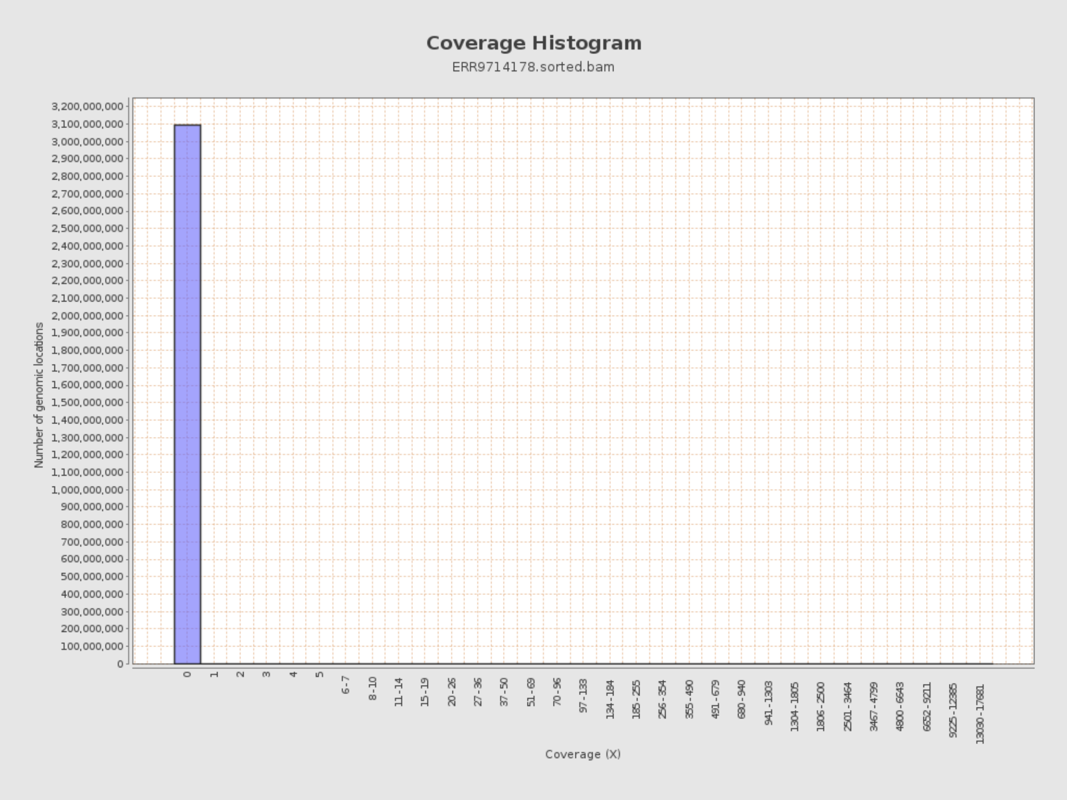
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12659230	0.0508	10.3477
chr2	243199373	20631601	0.0848	17.3859
chr3	198022430	12184170	0.0615	8.4338
chr4	191154276	14138217	0.074	12.1326
chr5	180915260	12928357	0.0715	11.8134
chr6	171115067	14299148	0.0836	17.0275
chr7	159138663	8955639	0.0563	9.4752

chr8	146364022	9487892	0.0648	8.9668
chr9	141213431	7332350	0.0519	7.5233
chr10	135534747	9997962	0.0738	13.0465
chr11	135006516	9004823	0.0667	10.319
chr12	133851895	6262162	0.0468	6.0035
chr13	115169878	4739646	0.0412	4.6988
chr14	107349540	4741829	0.0442	5.954
chr15	102531392	4382017	0.0427	5.2617
chr16	90354753	3220095	0.0356	4.621
chr17	81195210	1880844	0.0232	3.1282
chr18	78077248	5143318	0.0659	8.719
chr19	59128983	660614	0.0112	1.376
chr20	63025520	3041886	0.0483	8.1786
chr21	48129895	2046794	0.0425	6.7008
chr22	51304566	704731	0.0137	1.7827
chrMT	16571	6027	0.3637	2.5455
chrX	155270560	35534044	0.2289	27.9691
chrY	59373566	911612	0.0154	2.4733

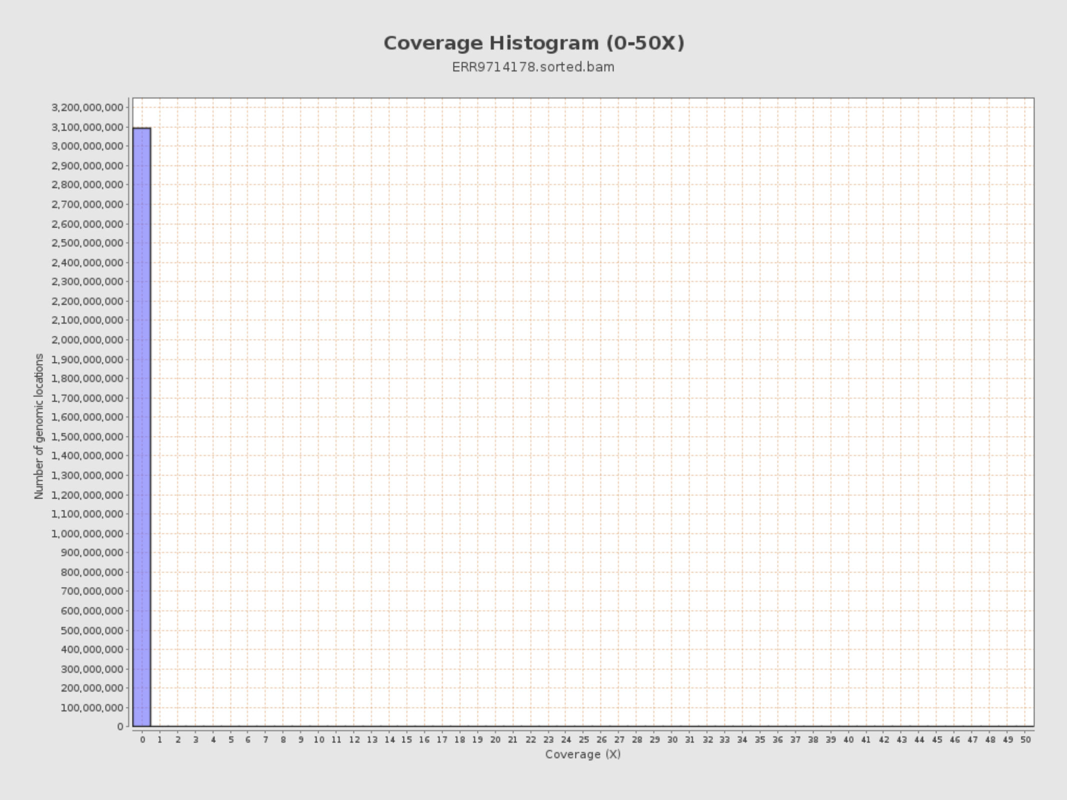
3. Results : Coverage across reference



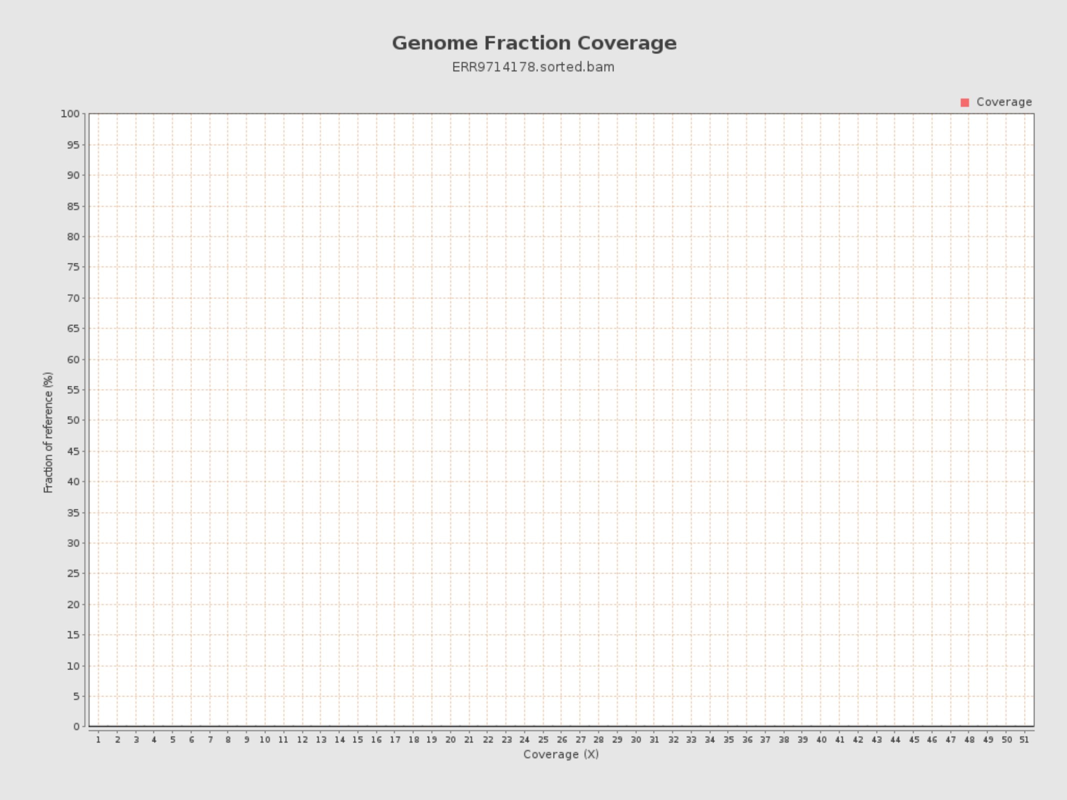
4. Results : Coverage Histogram



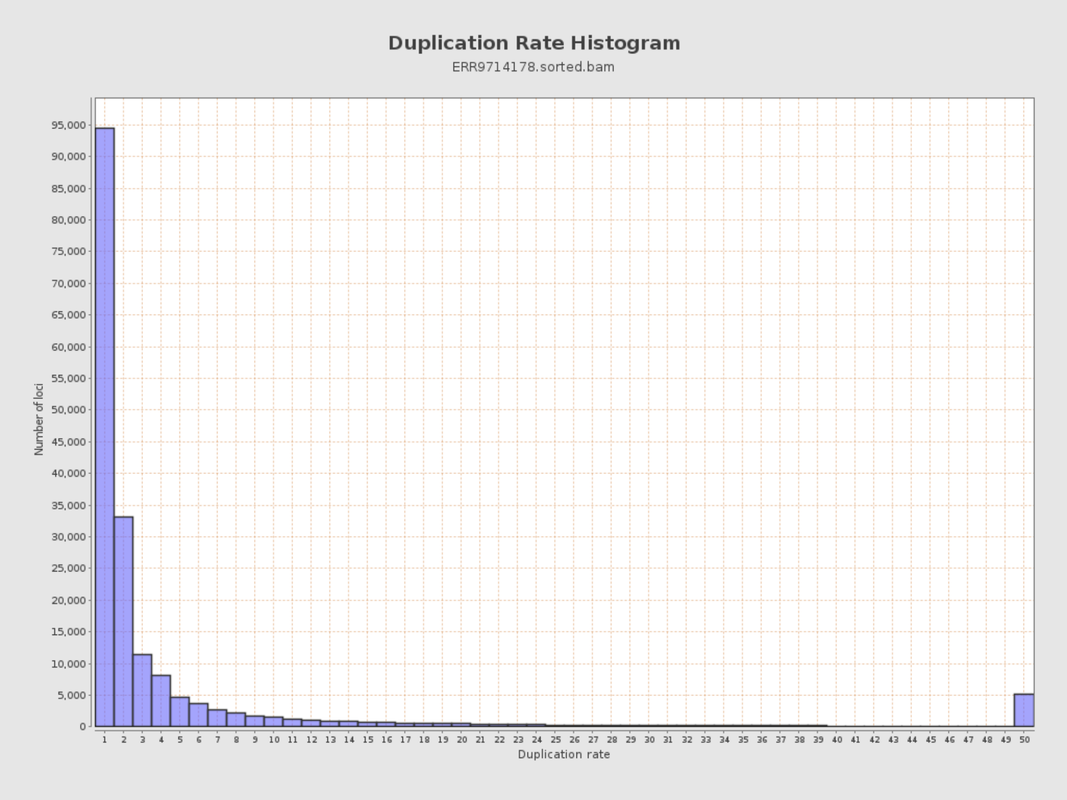
5. Results : Coverage Histogram (0-50X)



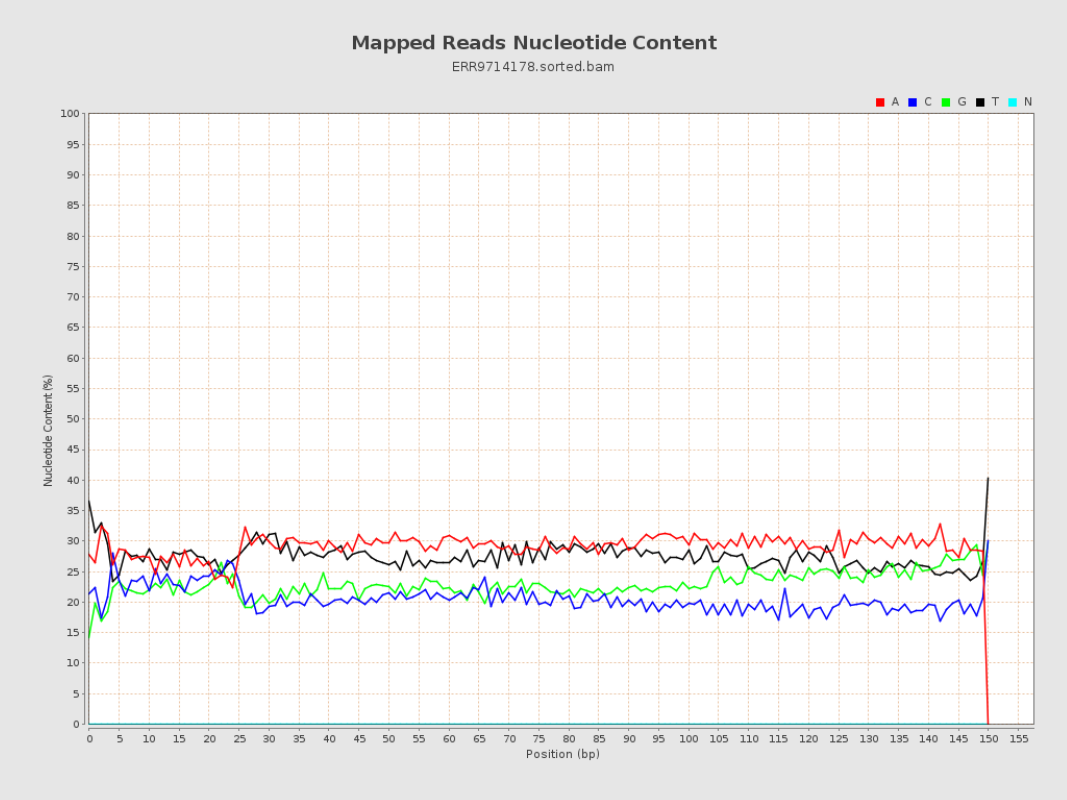
6. Results : Genome Fraction Coverage



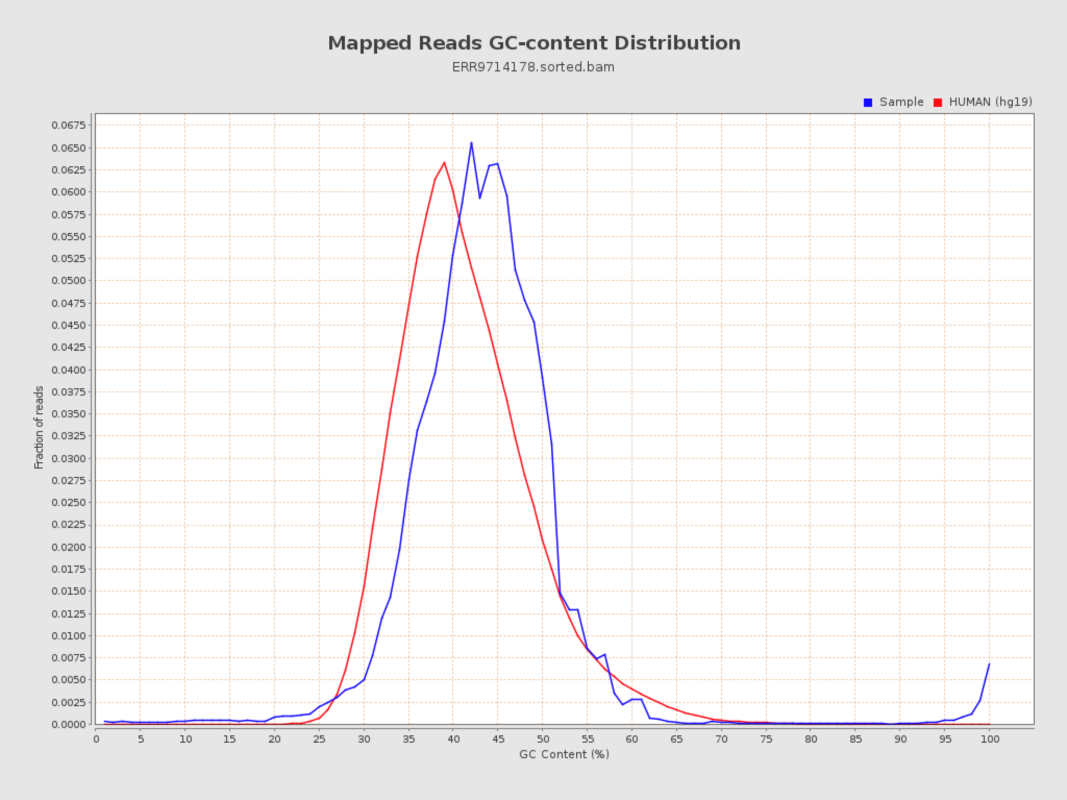
7. Results : Duplication Rate Histogram



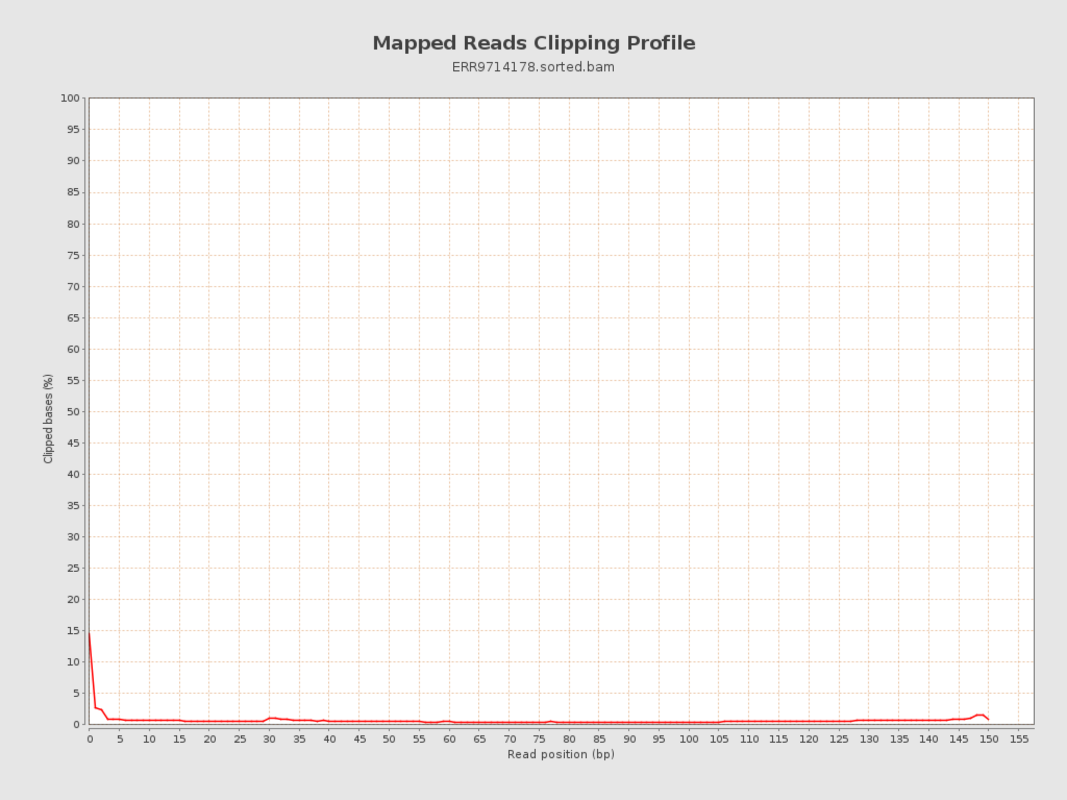
8. Results : Mapped Reads Nucleotide Content



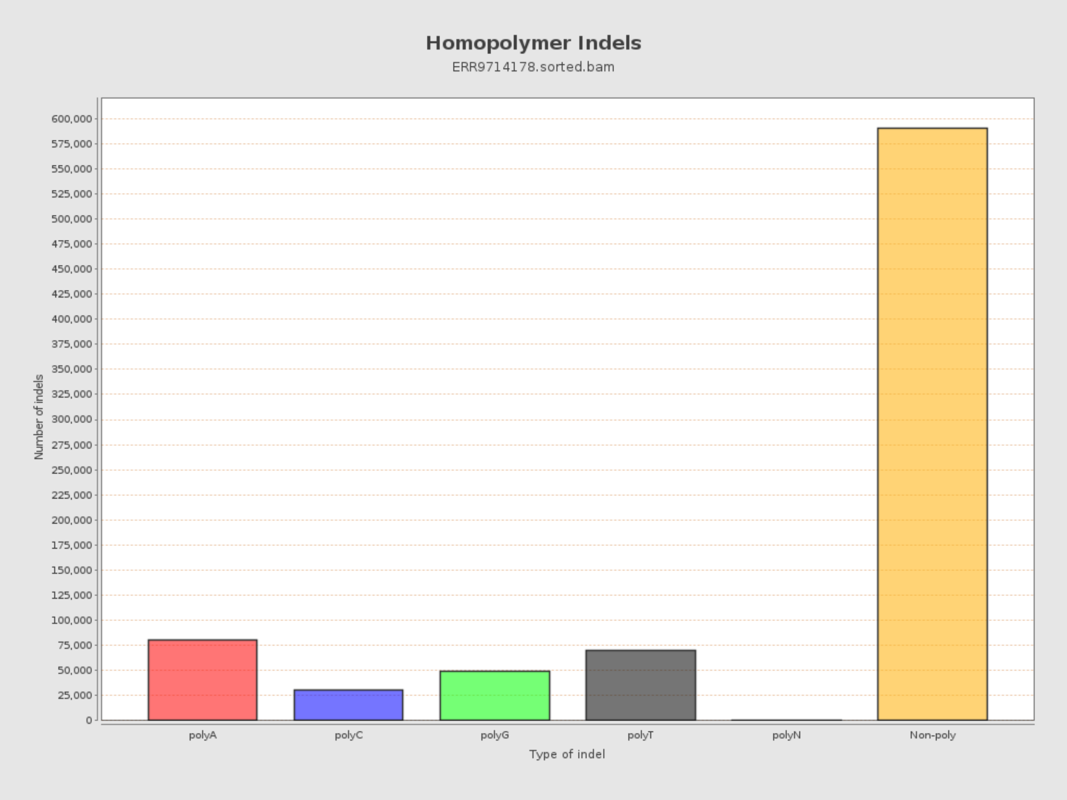
9. Results : Mapped Reads GC-content Distribution



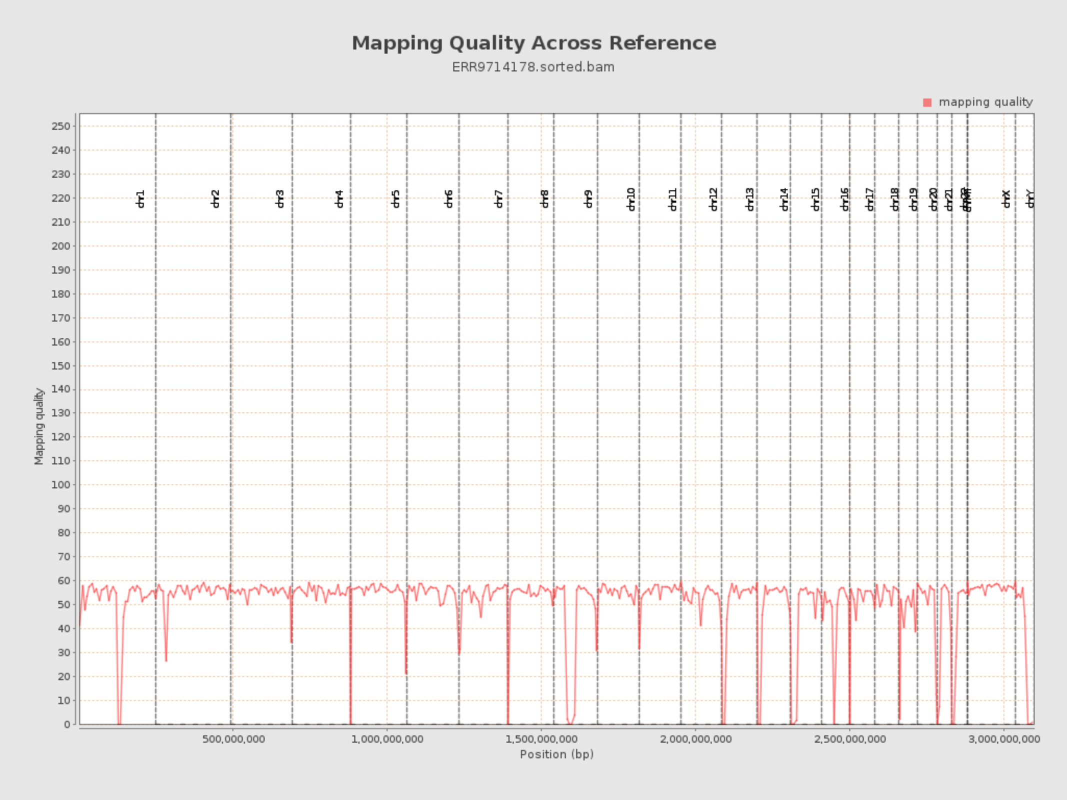
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram