Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 21:08:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714138.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_ERR9714138 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714138.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 21:08:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714138.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	674,708
Mapped reads	573,492 / 85%
Unmapped reads	101,216 / 15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,610 / 2.61%
Read min/max/mean length	30 / 151 / 136.12
Duplicated reads (estimated)	572,391 / 84.84%
Duplication rate	31.13%
Clipped reads	542,278 / 80.37%

2.2. ACGT Content

Number/percentage of A's	20,336,598 / 28.13%
Number/percentage of C's	14,793,438 / 20.46%
Number/percentage of T's	19,266,152 / 26.64%
Number/percentage of G's	17,910,117 / 24.77%
Number/percentage of N's	525 / 0%
GC Percentage	45.23%

2.3. Coverage

Mean	0.0235

Standard Deviation	54.1467

2.4. Mapping Quality

Mean Mapping Quality	17.47

2.5. Mismatches and indels

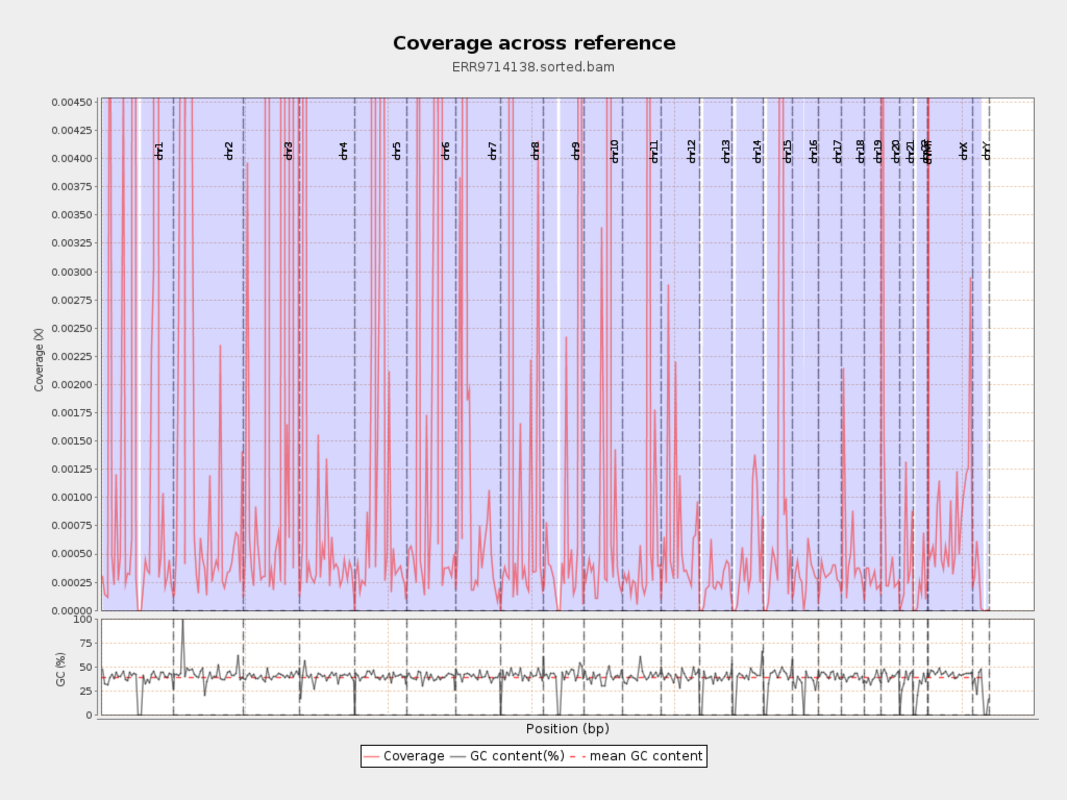
General error rate	3.55%
Mismatches	2,092,797
Insertions	96,690
Mapped reads with at least one insertion	16.46%
Deletions	147,846
Mapped reads with at least one deletion	24.12%
Homopolymer indels	20.52%

2.6. Chromosome stats

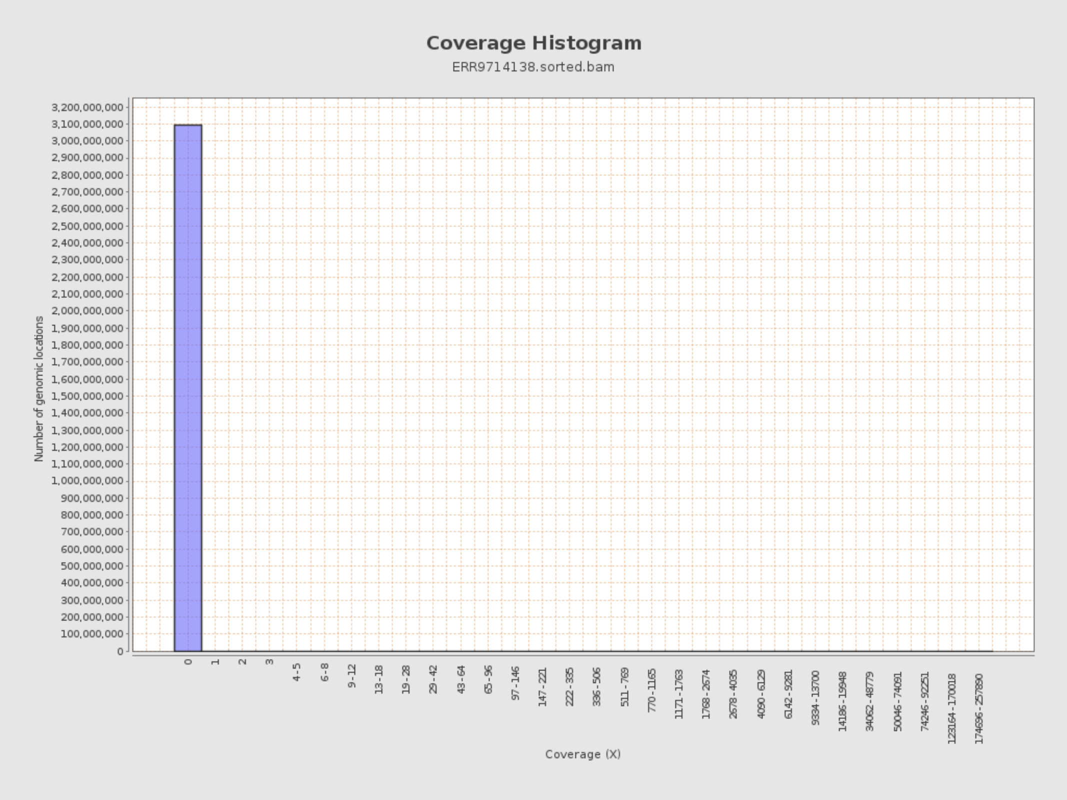
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1149364	0.0046	3.6145
chr2	243199373	4512814	0.0186	14.2607
chr3	198022430	39154565	0.1977	197.0617
chr4	191154276	275730	0.0014	1.0301
chr5	180915260	13370470	0.0739	68.1904
chr6	171115067	9866276	0.0577	51.896
chr7	159138663	330559	0.0021	0.9556

chr8	146364022	1577537	0.0108	10.7799
chr9	141213431	244812	0.0017	1.2056
chr10	135534747	1521475	0.0112	10.0724
chr11	135006516	167348	0.0012	0.7836
chr12	133851895	97969	0.0007	0.3378
chr13	115169878	27372	0.0002	0.0428
chr14	107349540	53114	0.0005	0.1639
chr15	102531392	150103	0.0015	0.3716
chr16	90354753	27661	0.0003	0.0476
chr17	81195210	25510	0.0003	0.058
chr18	78077248	43625	0.0006	0.2864
chr19	59128983	16238	0.0003	0.0355
chr20	63025520	82007	0.0013	0.6146
chr21	48129895	20739	0.0004	0.2029
chr22	51304566	10021	0.0002	0.0593
chrMT	16571	1488	0.0898	0.8365
chrX	155270560	130034	0.0008	0.1062
chrY	59373566	11316	0.0002	0.049

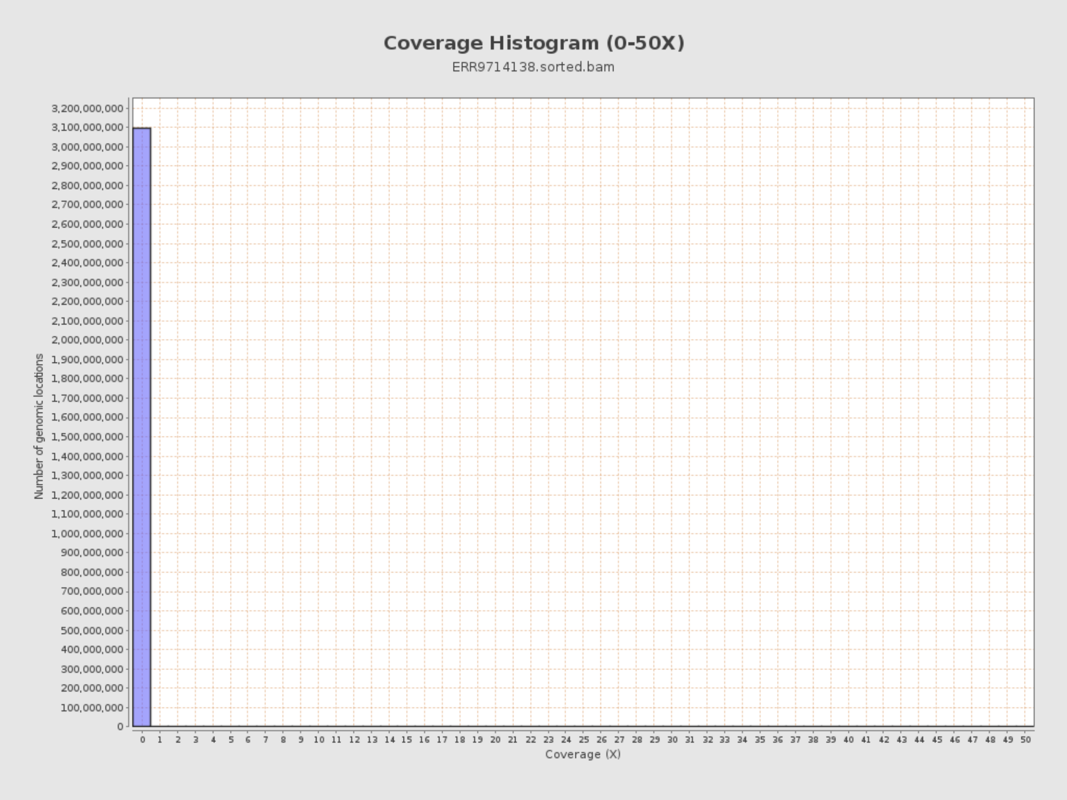
3. Results : Coverage across reference



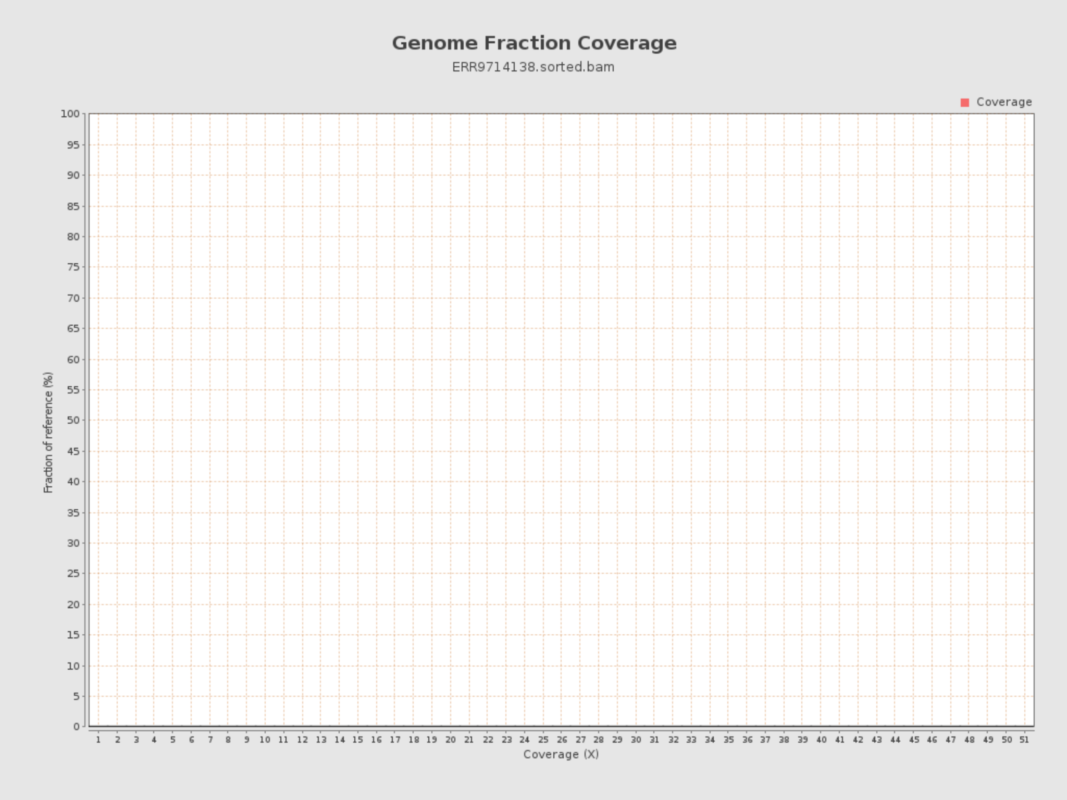
4. Results : Coverage Histogram



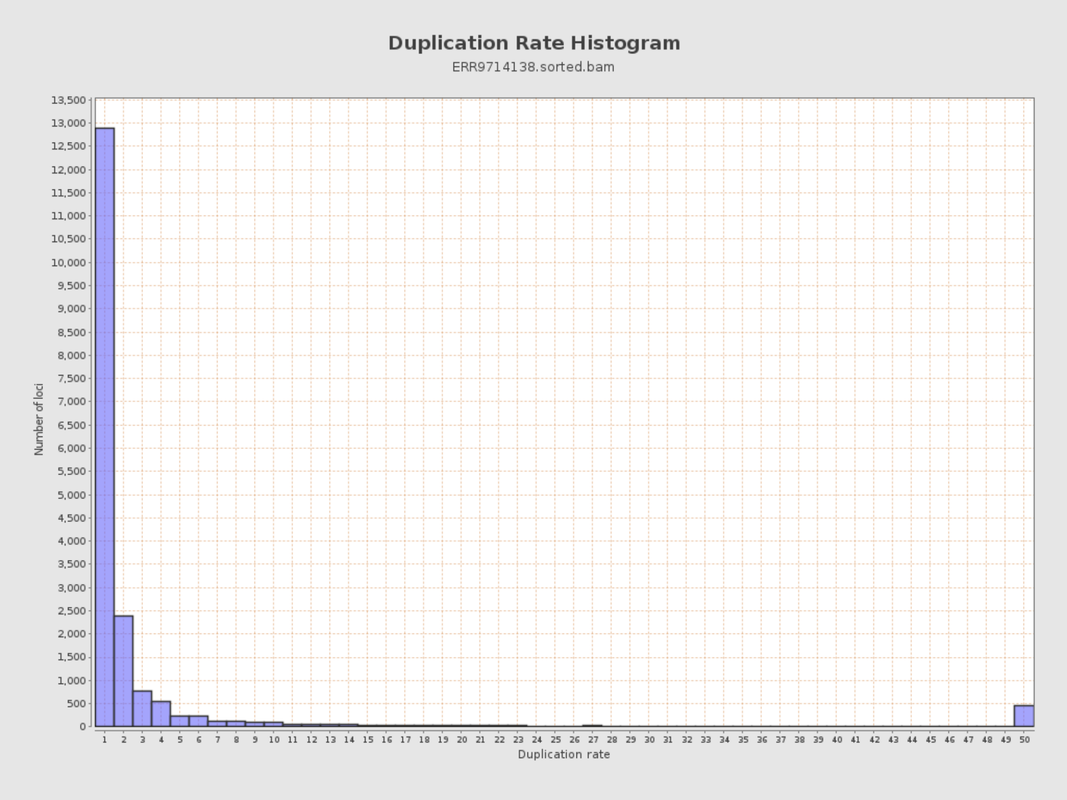
5. Results : Coverage Histogram (0-50X)



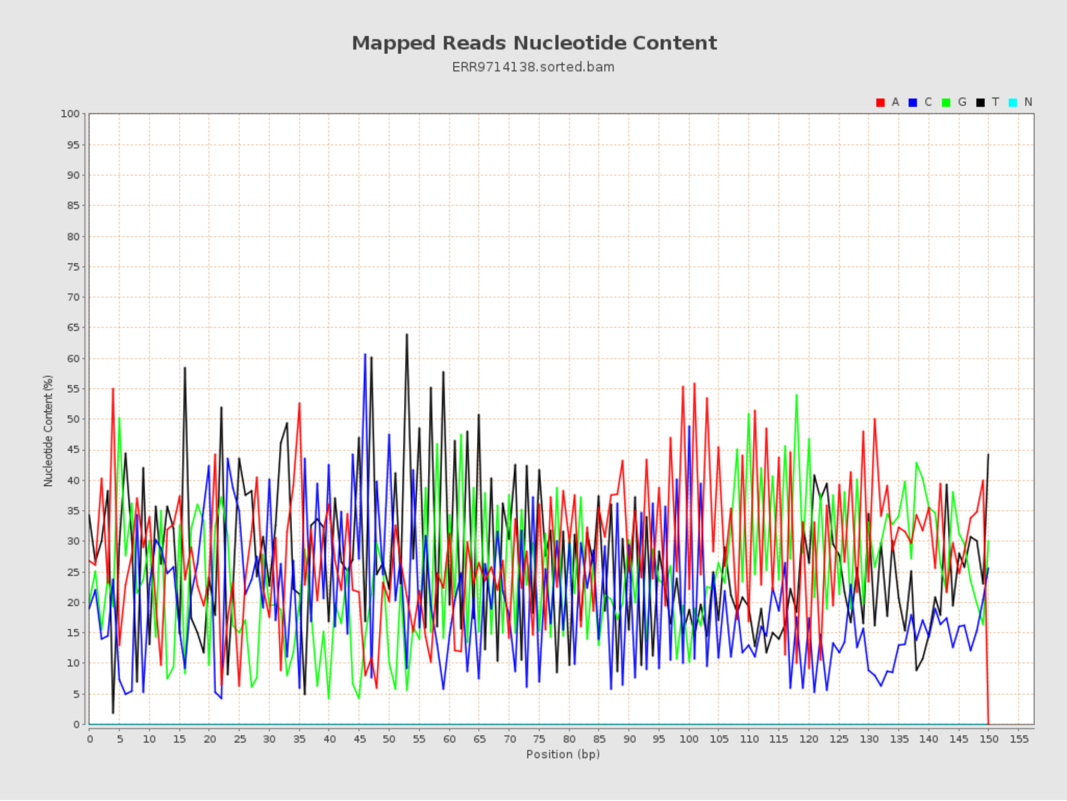
6. Results : Genome Fraction Coverage



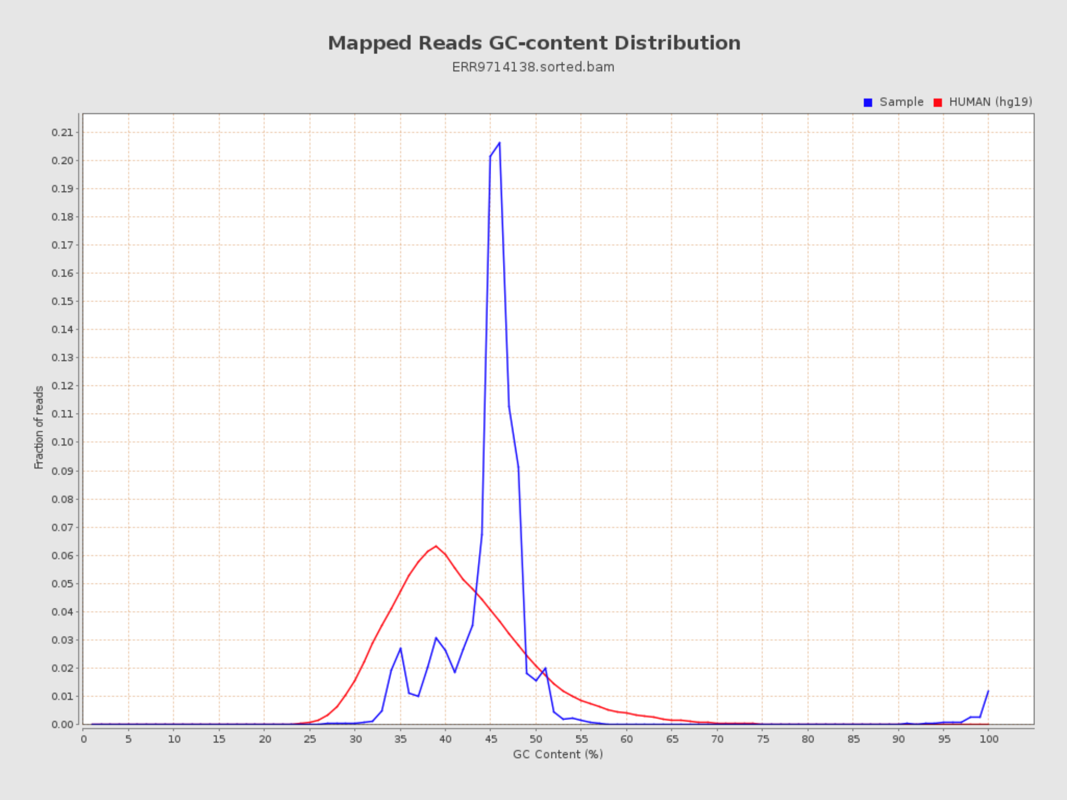
7. Results : Duplication Rate Histogram



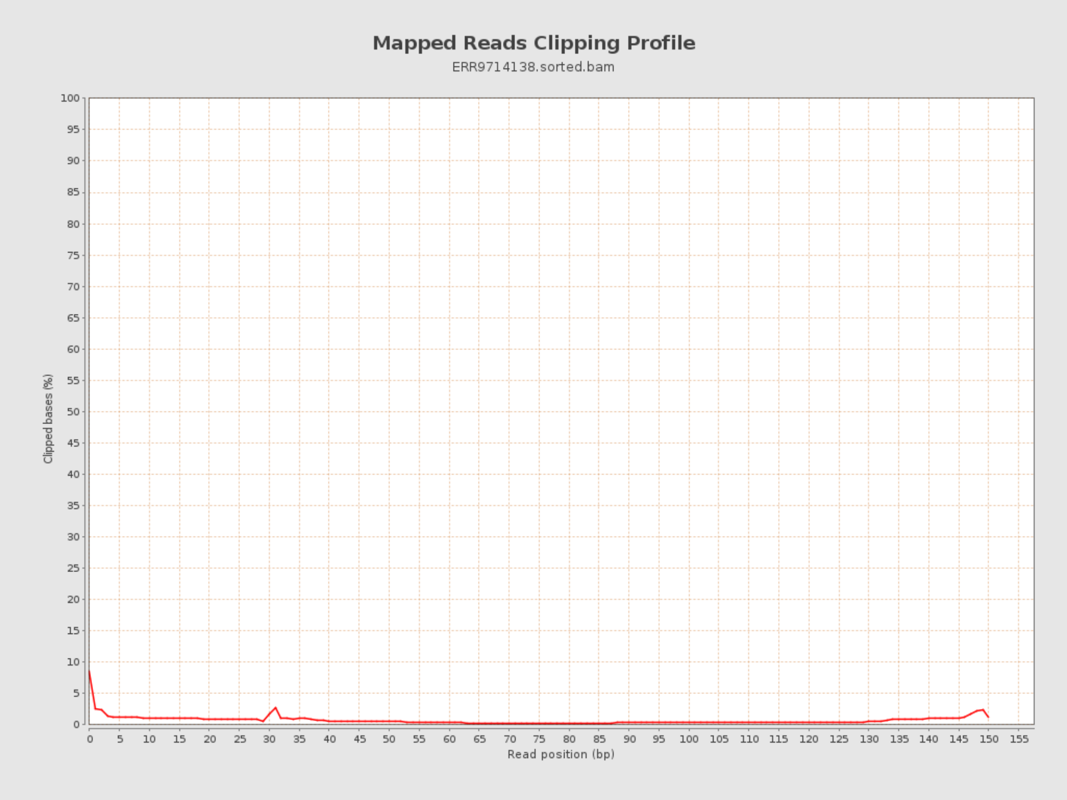
8. Results : Mapped Reads Nucleotide Content



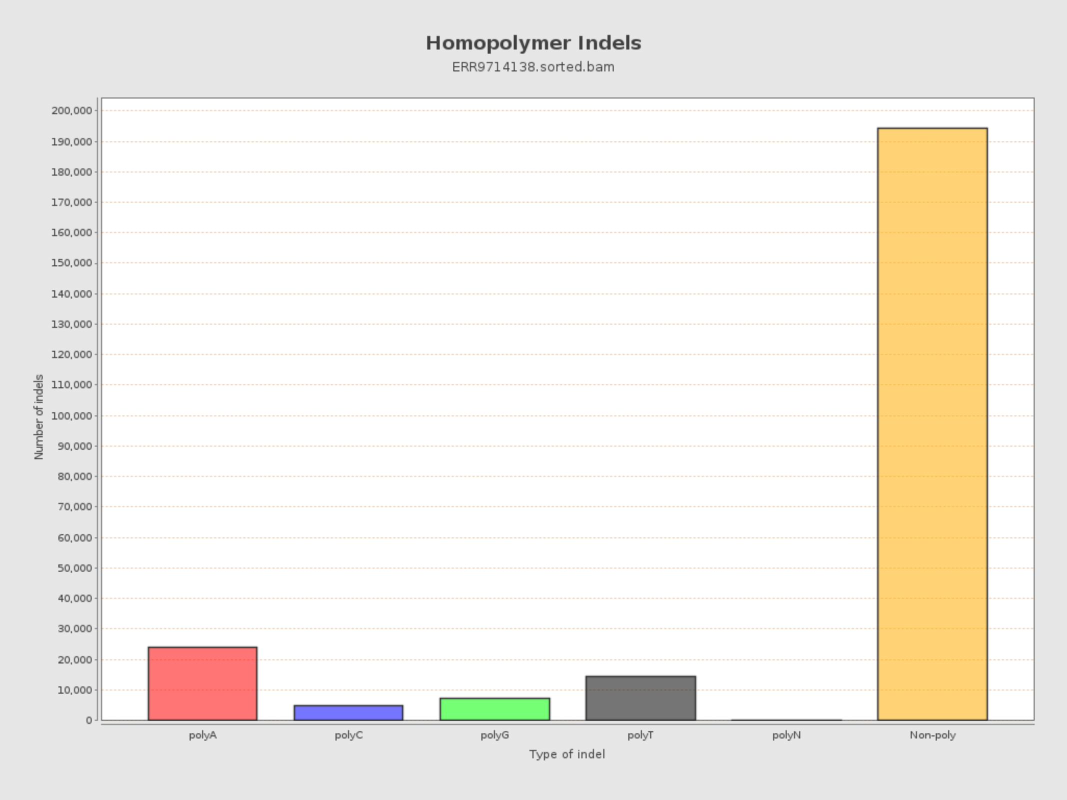
9. Results : Mapped Reads GC-content Distribution



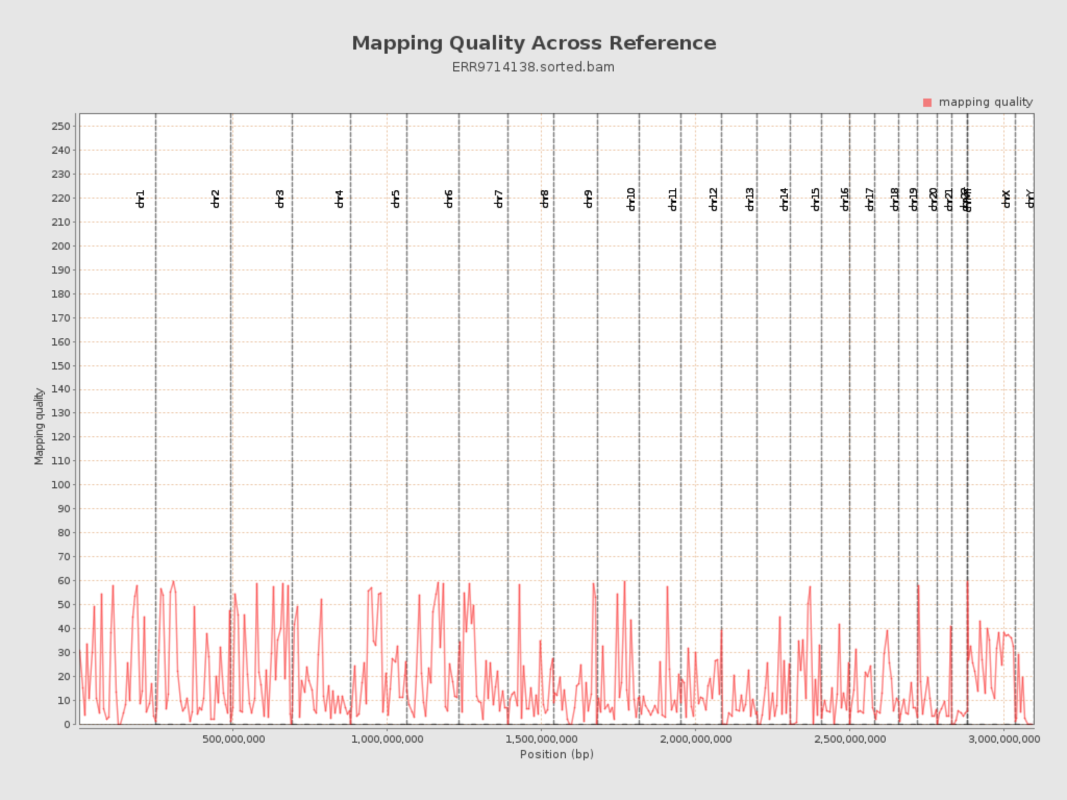
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram