Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 21:27:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714144.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_ERR9714144 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714144.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 21:27:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714144.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	696,964
Mapped reads	592,887 / 85.07%
Unmapped reads	104,077 / 14.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,705 / 2.4%
Read min/max/mean length	30 / 151 / 135.48
Duplicated reads (estimated)	525,193 / 75.35%
Duplication rate	44%
Clipped reads	553,162 / 79.37%

2.2. ACGT Content

Number/percentage of A's	21,479,930 / 28.27%
Number/percentage of C's	15,794,837 / 20.79%
Number/percentage of T's	20,448,102 / 26.92%
Number/percentage of G's	18,245,827 / 24.02%
Number/percentage of N's	513 / 0%
GC Percentage	44.81%

2.3. Coverage

Mean	0.0252

Standard Deviation	5.1096

2.4. Mapping Quality

Mean Mapping Quality	51.86

2.5. Mismatches and indels

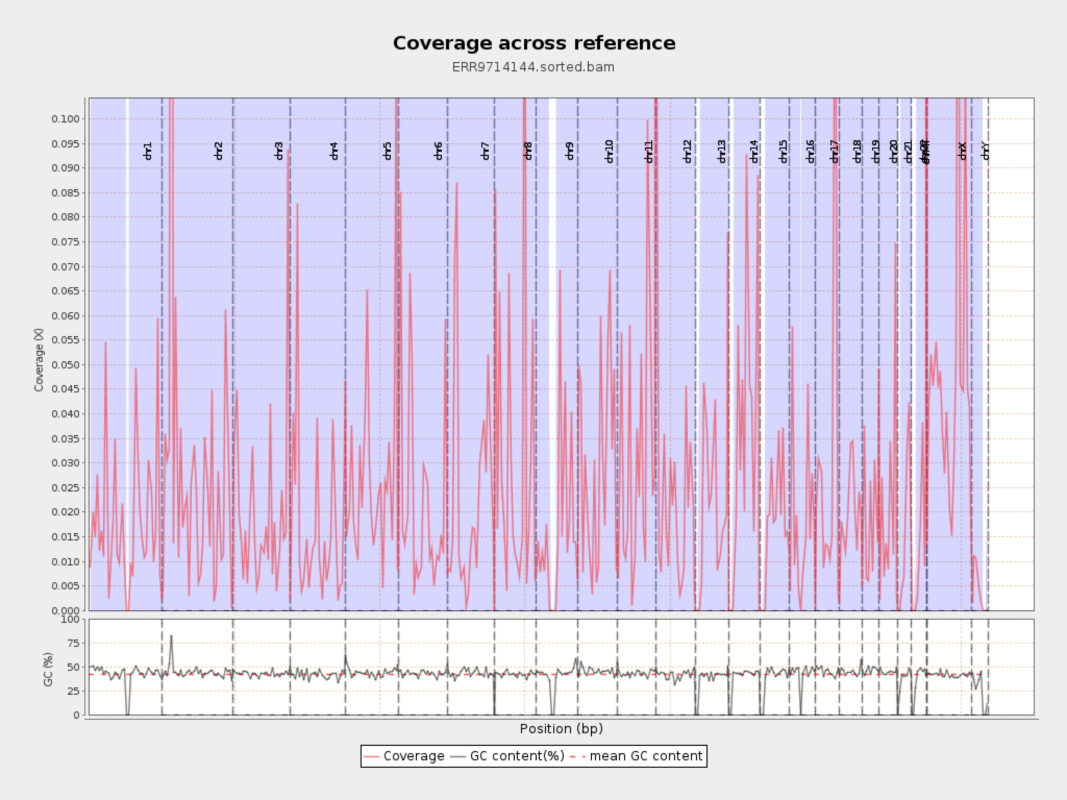
General error rate	4.98%
Mismatches	3,557,351
Insertions	86,548
Mapped reads with at least one insertion	14.07%
Deletions	319,347
Mapped reads with at least one deletion	49.86%
Homopolymer indels	30.34%

2.6. Chromosome stats

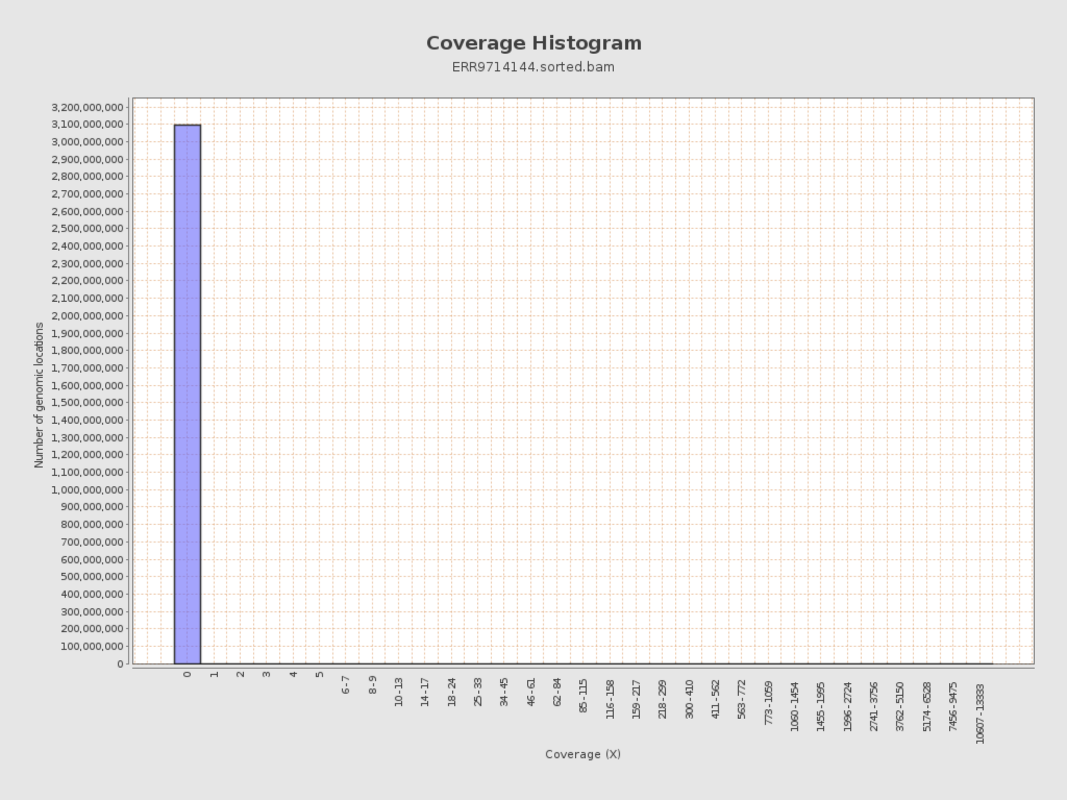
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4528181	0.0182	2.8022
chr2	243199373	8180672	0.0336	9.0767
chr3	198022430	3947035	0.0199	4.0626
chr4	191154276	3300506	0.0173	2.9884
chr5	180915260	5180784	0.0286	5.377
chr6	171115067	3955480	0.0231	4.3769
chr7	159138663	3910876	0.0246	4.1724

chr8	146364022	5139040	0.0351	8.2465
chr9	141213431	2353009	0.0167	2.9377
chr10	135534747	4129018	0.0305	4.4765
chr11	135006516	4414403	0.0327	6.3544
chr12	133851895	3209098	0.024	4.3305
chr13	115169878	2349114	0.0204	3.3013
chr14	107349540	3898812	0.0363	5.9912
chr15	102531392	1821977	0.0178	1.917
chr16	90354753	1713735	0.019	2.9037
chr17	81195210	2561487	0.0315	8.4705
chr18	78077248	1566111	0.0201	2.4307
chr19	59128983	1113854	0.0188	2.7428
chr20	63025520	1388574	0.022	3.5287
chr21	48129895	740700	0.0154	2.4289
chr22	51304566	599917	0.0117	1.5698
chrMT	16571	142954	8.6268	64.4444
chrX	155270560	7671864	0.0494	6.4469
chrY	59373566	230942	0.0039	0.6848

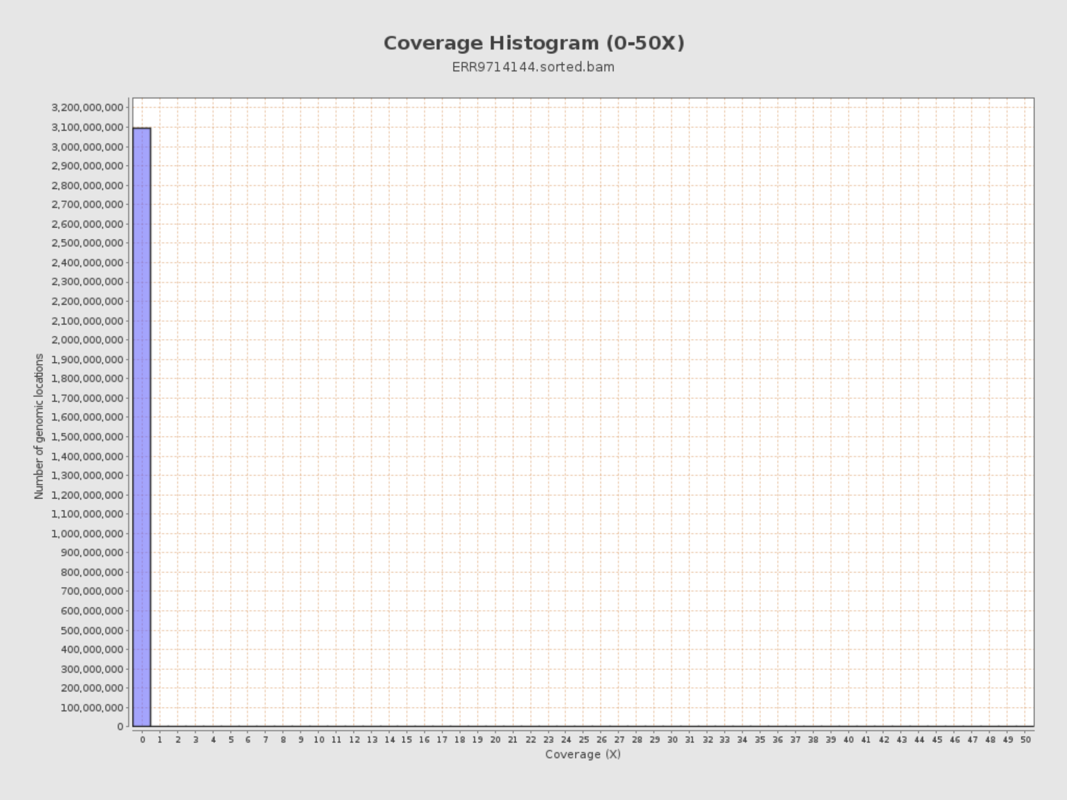
3. Results : Coverage across reference



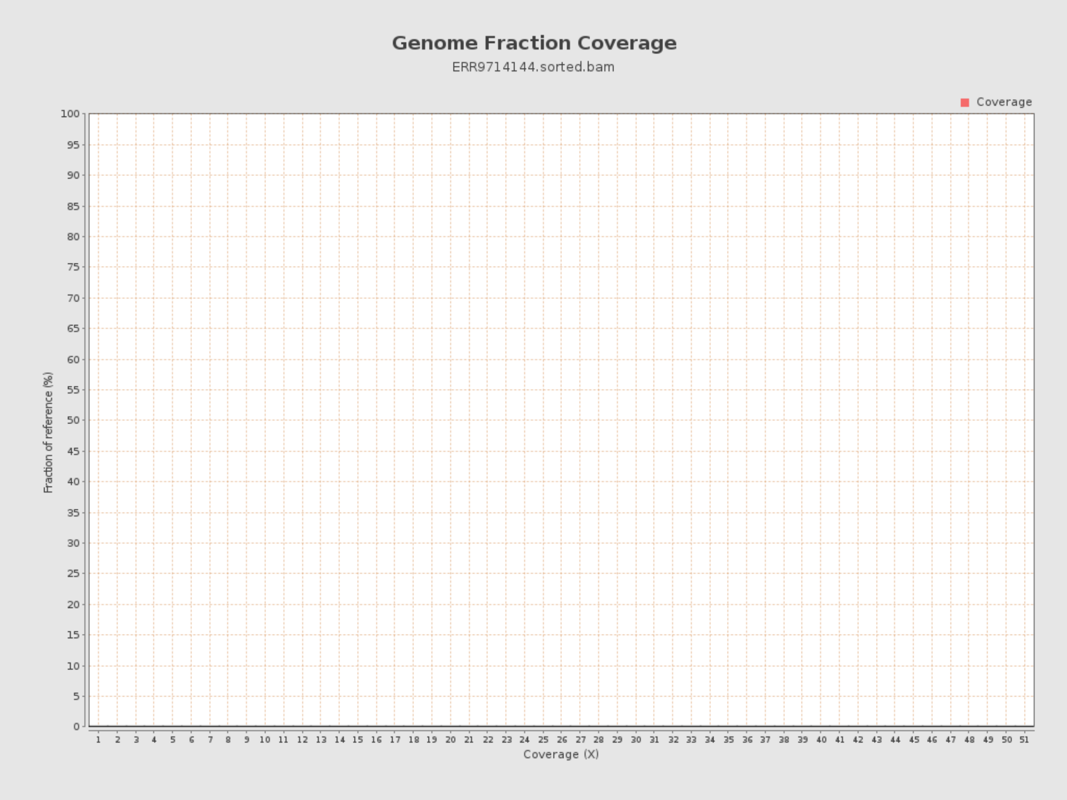
4. Results : Coverage Histogram



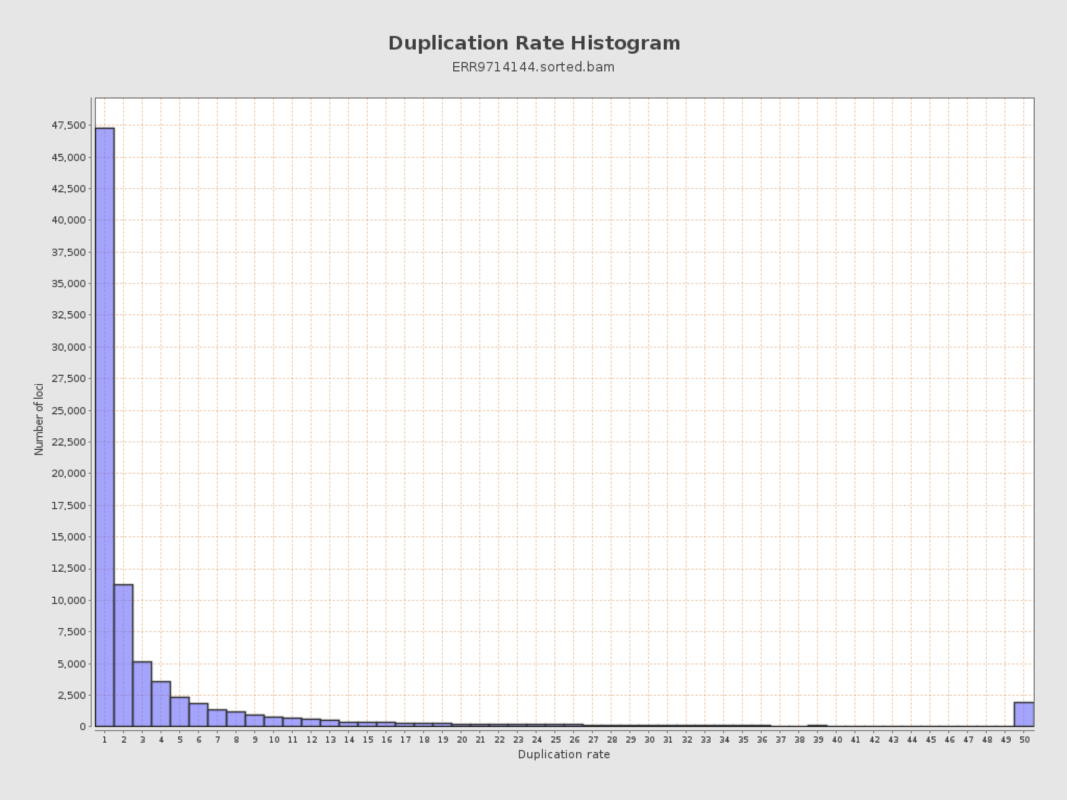
5. Results : Coverage Histogram (0-50X)



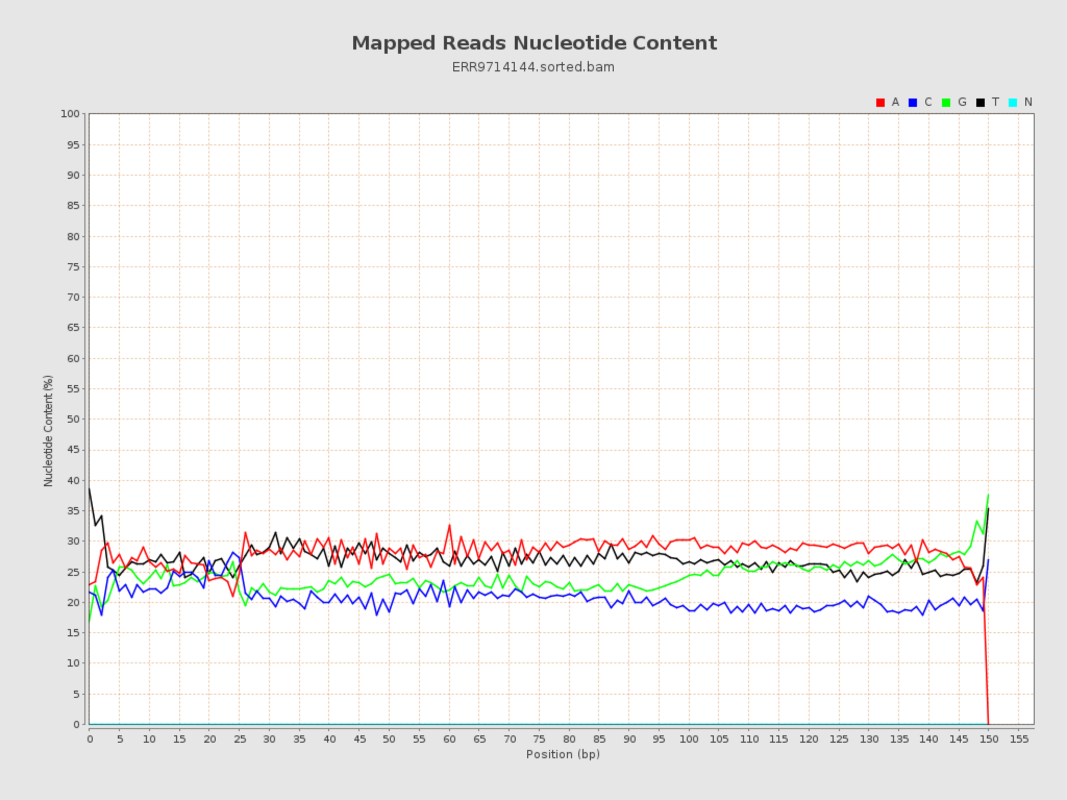
6. Results : Genome Fraction Coverage



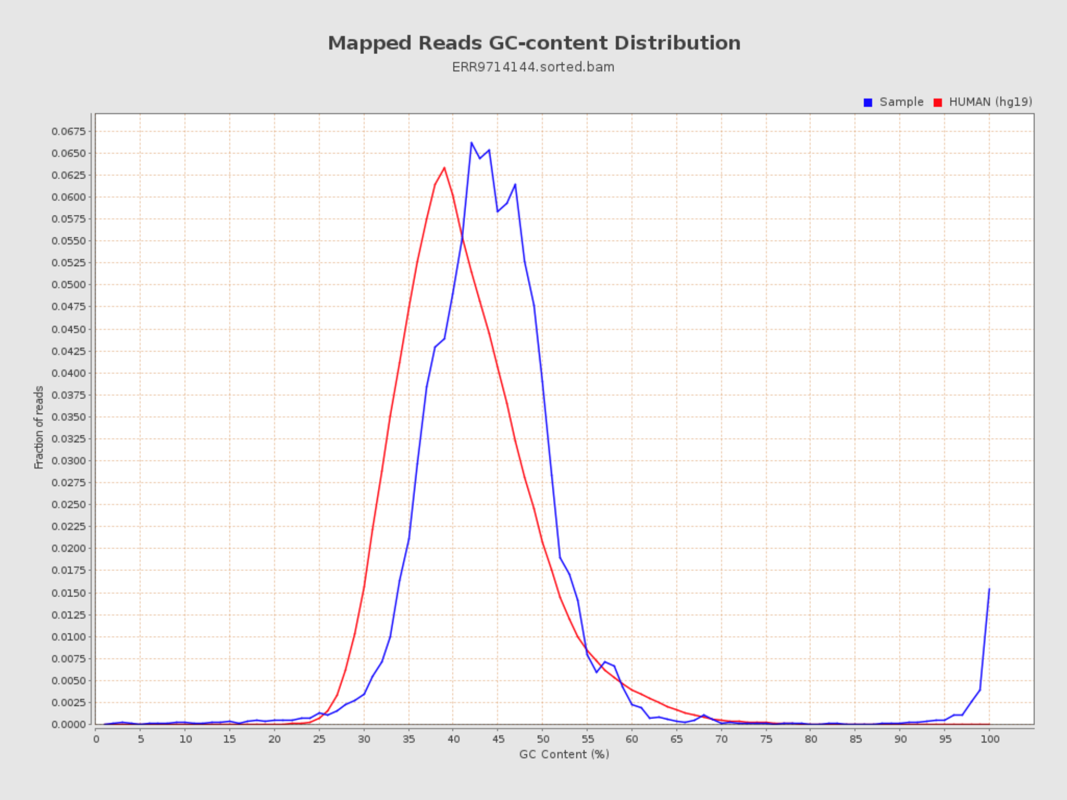
7. Results : Duplication Rate Histogram



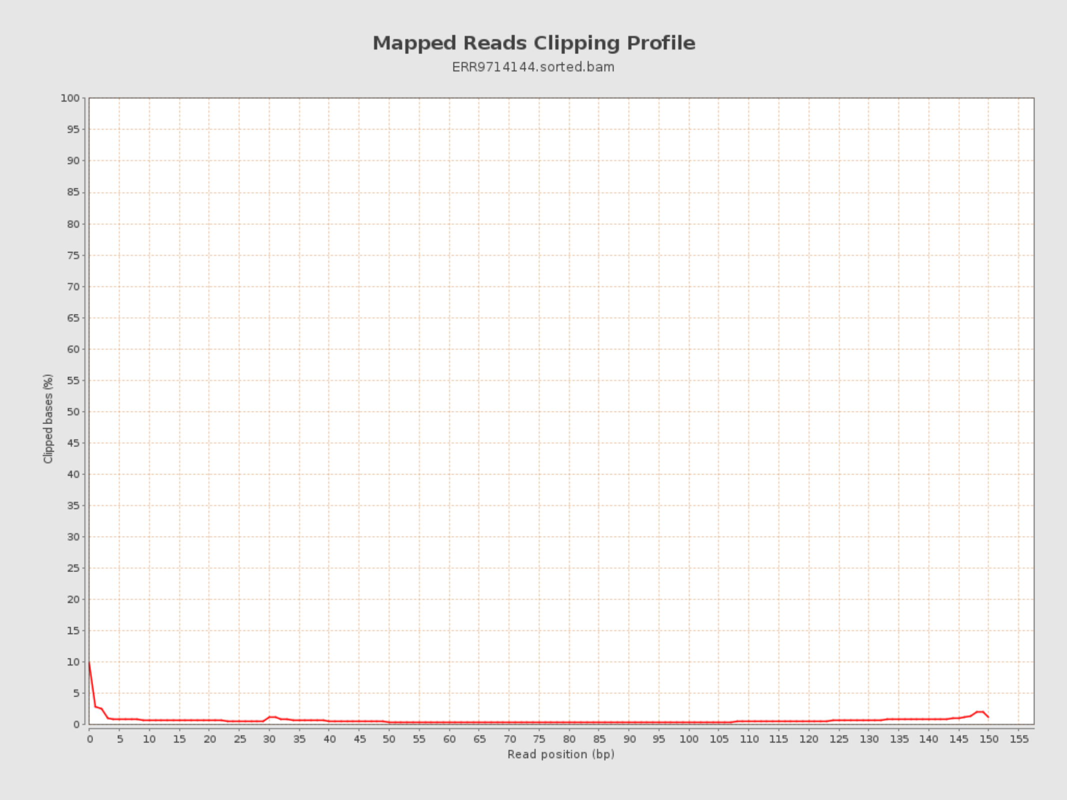
8. Results : Mapped Reads Nucleotide Content



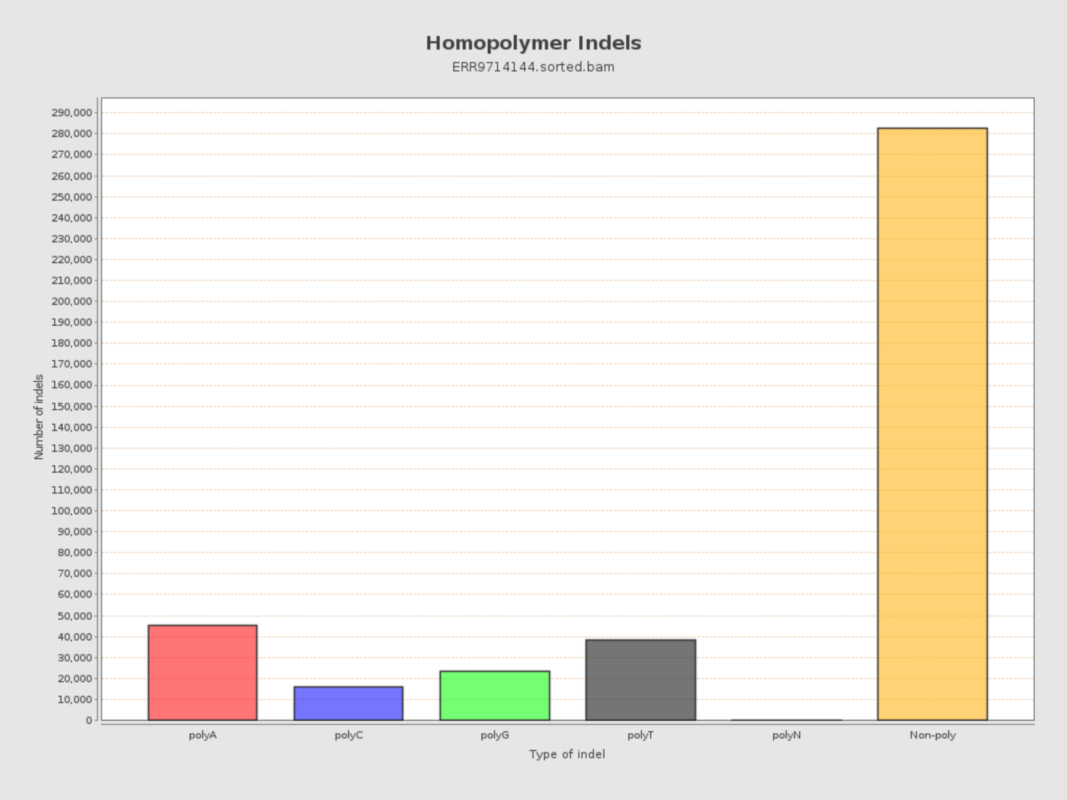
9. Results : Mapped Reads GC-content Distribution



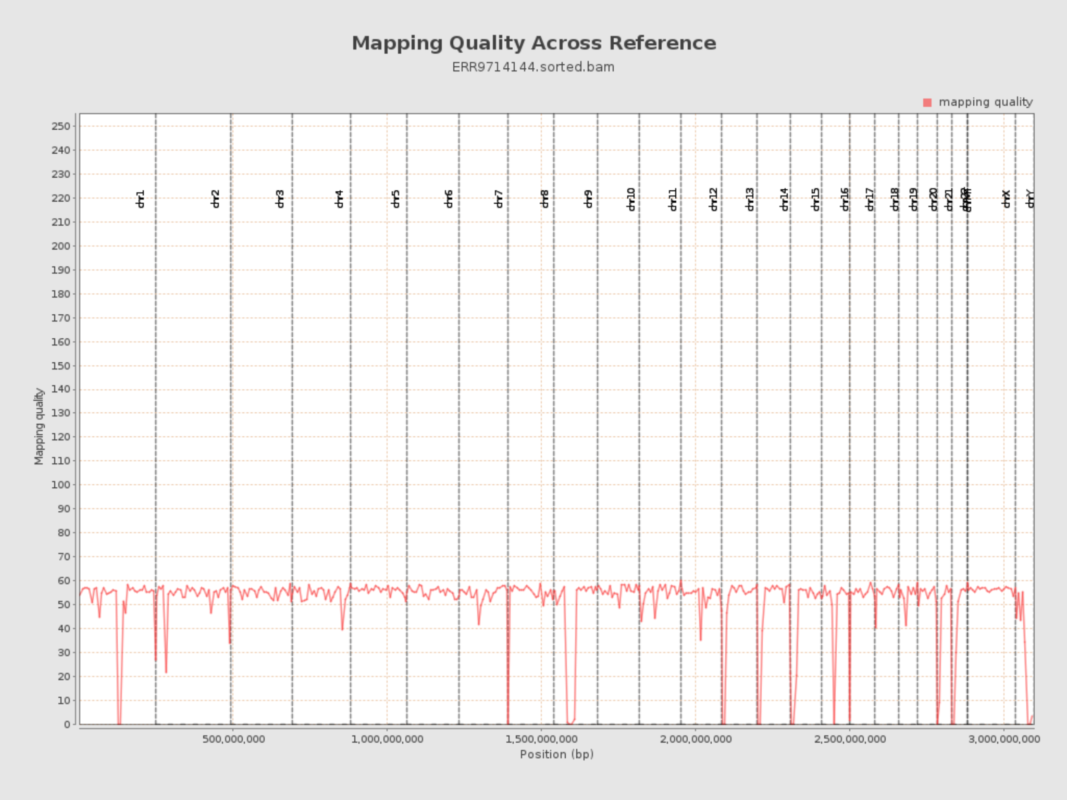
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram