Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 18:18:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714074.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_ERR9714074 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714074.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 18:18:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714074.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	635,822
Mapped reads	107,408 / 16.89%
Unmapped reads	528,414 / 83.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,773 / 0.28%
Read min/max/mean length	30 / 151 / 63.47
Duplicated reads (estimated)	105,903 / 16.66%
Duplication rate	27.36%
Clipped reads	55,122 / 8.67%

2.2. ACGT Content

Number/percentage of A's	235,498 / 2.12%
Number/percentage of C's	85,433 / 0.77%
Number/percentage of T's	113,354 / 1.02%
Number/percentage of G's	10,678,471 / 96.09%
Number/percentage of N's	273 / 0%
GC Percentage	96.86%

2.3. Coverage

Mean	0.0036

Standard Deviation	13.7935

2.4. Mapping Quality

Mean Mapping Quality	10.56

2.5. Mismatches and indels

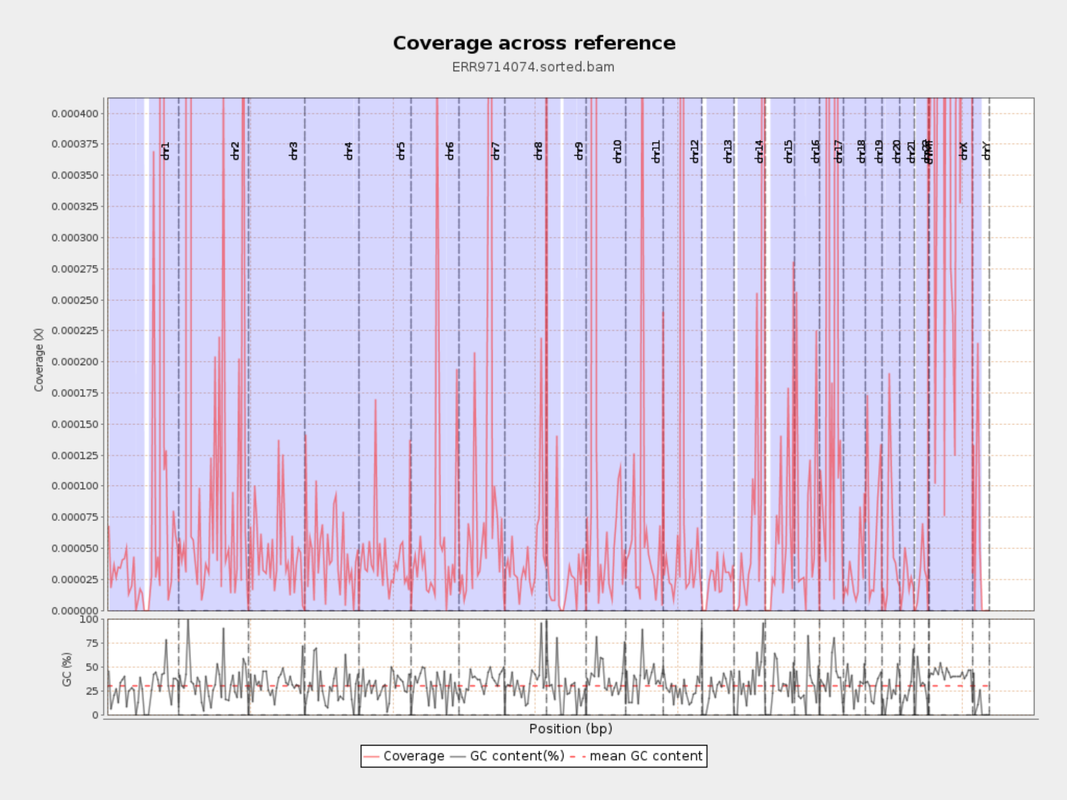
General error rate	3.21%
Mismatches	274,063
Insertions	11,874
Mapped reads with at least one insertion	7.48%
Deletions	4,888
Mapped reads with at least one deletion	4.33%
Homopolymer indels	64.54%

2.6. Chromosome stats

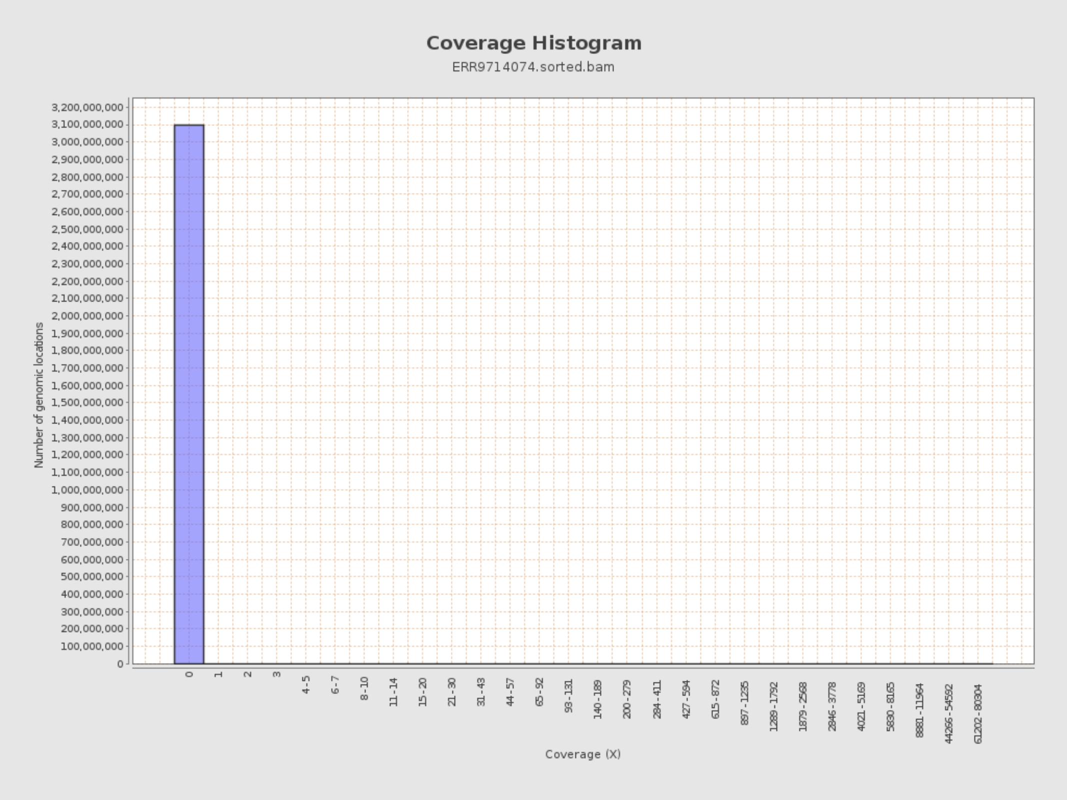
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	68456	0.0003	0.6631
chr2	243199373	10714517	0.0441	49.2019
chr3	198022430	9211	0	0.0151
chr4	191154276	8844	0	0.0121
chr5	180915260	7522	0	0.0106
chr6	171115067	9860	0.0001	0.0257
chr7	159138663	19879	0.0001	0.1264

chr8	146364022	6672	0	0.0232
chr9	141213431	4284	0	0.0157
chr10	135534747	68884	0.0005	0.9712
chr11	135006516	9303	0.0001	0.0516
chr12	133851895	15381	0.0001	0.0992
chr13	115169878	2668	0	0.0061
chr14	107349540	13670	0.0001	0.1373
chr15	102531392	5843	0.0001	0.0246
chr16	90354753	7033	0.0001	0.0236
chr17	81195210	24997	0.0003	0.1596
chr18	78077248	2412	0	0.0114
chr19	59128983	3991	0.0001	0.0229
chr20	63025520	3410	0.0001	0.0268
chr21	48129895	1215	0	0.0083
chr22	51304566	1319	0	0.0065
chrMT	16571	3443	0.2078	1.3212
chrX	155270560	118401	0.0008	0.1171
chrY	59373566	2729	0	0.0196

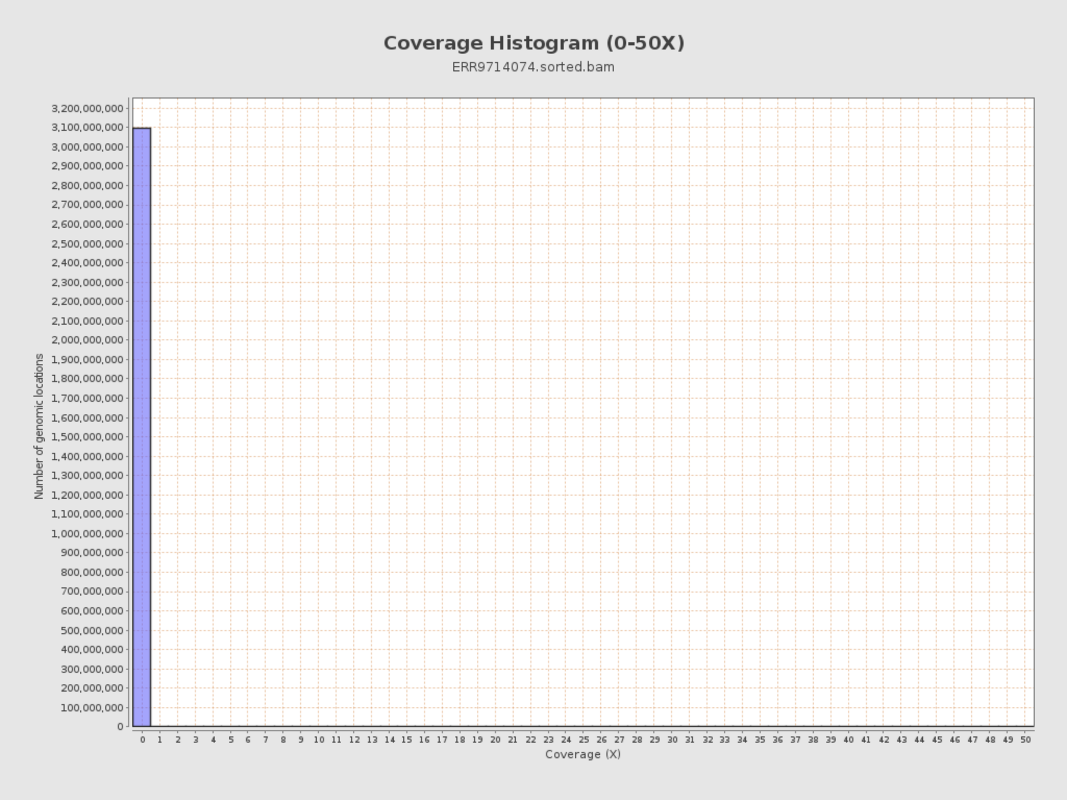
3. Results : Coverage across reference



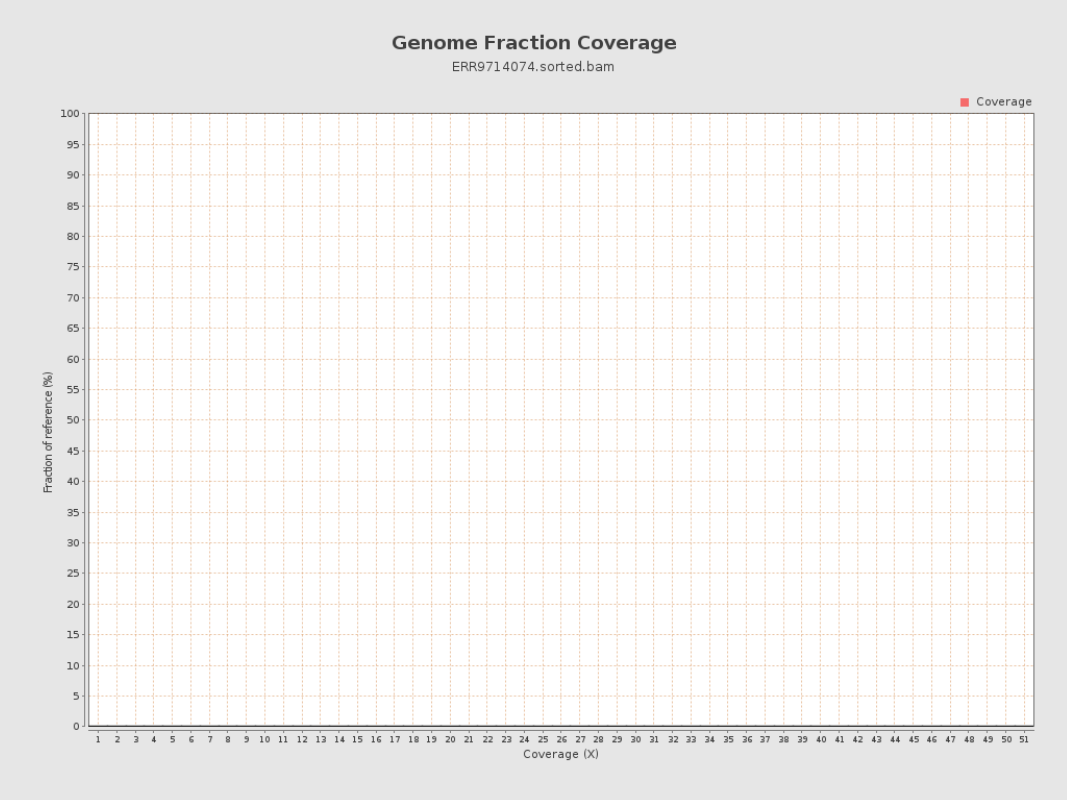
4. Results : Coverage Histogram



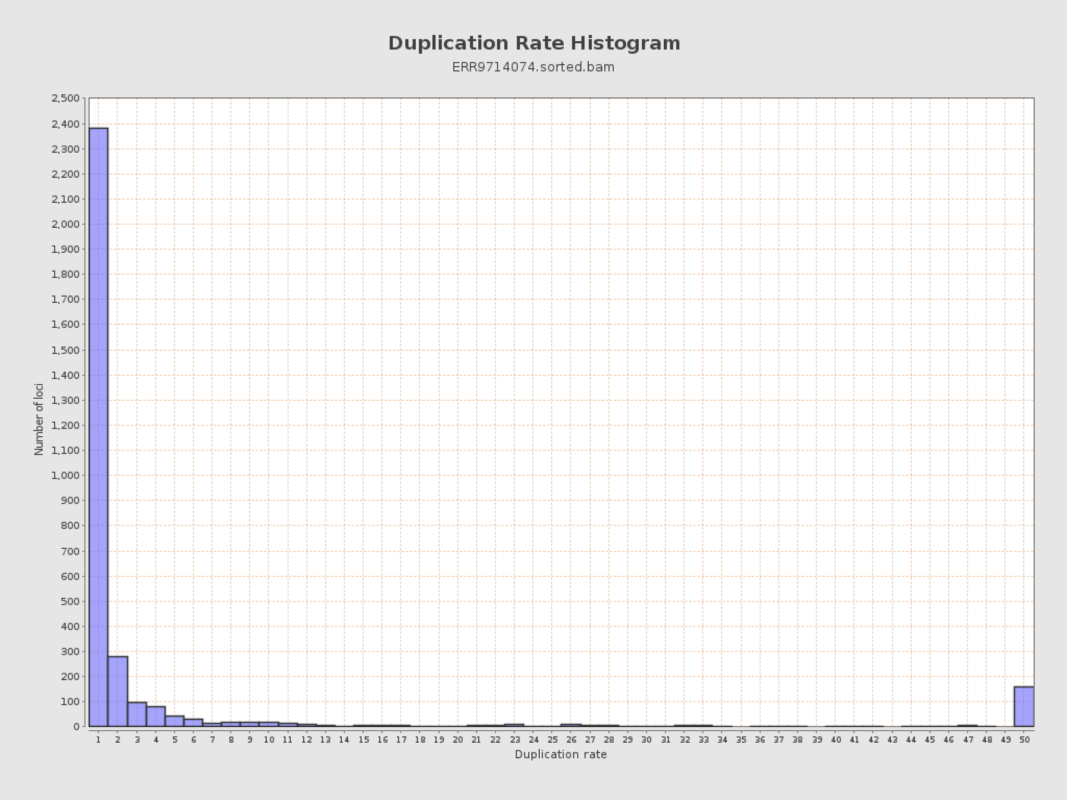
5. Results : Coverage Histogram (0-50X)



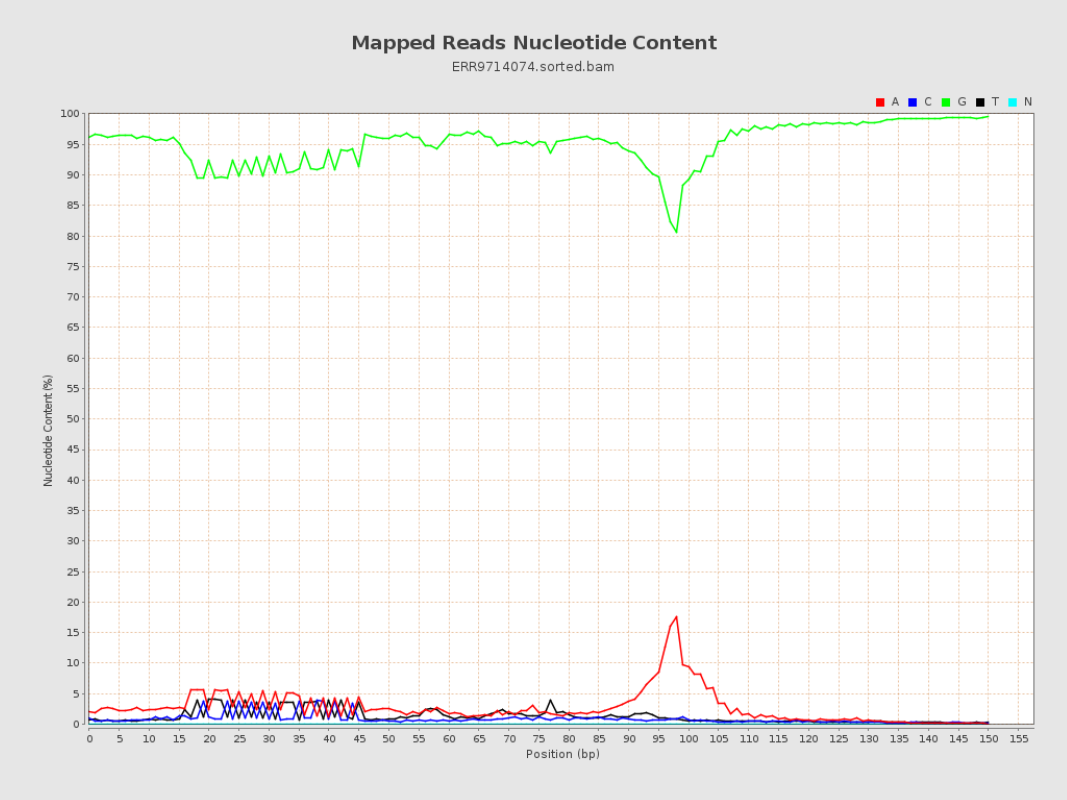
6. Results : Genome Fraction Coverage



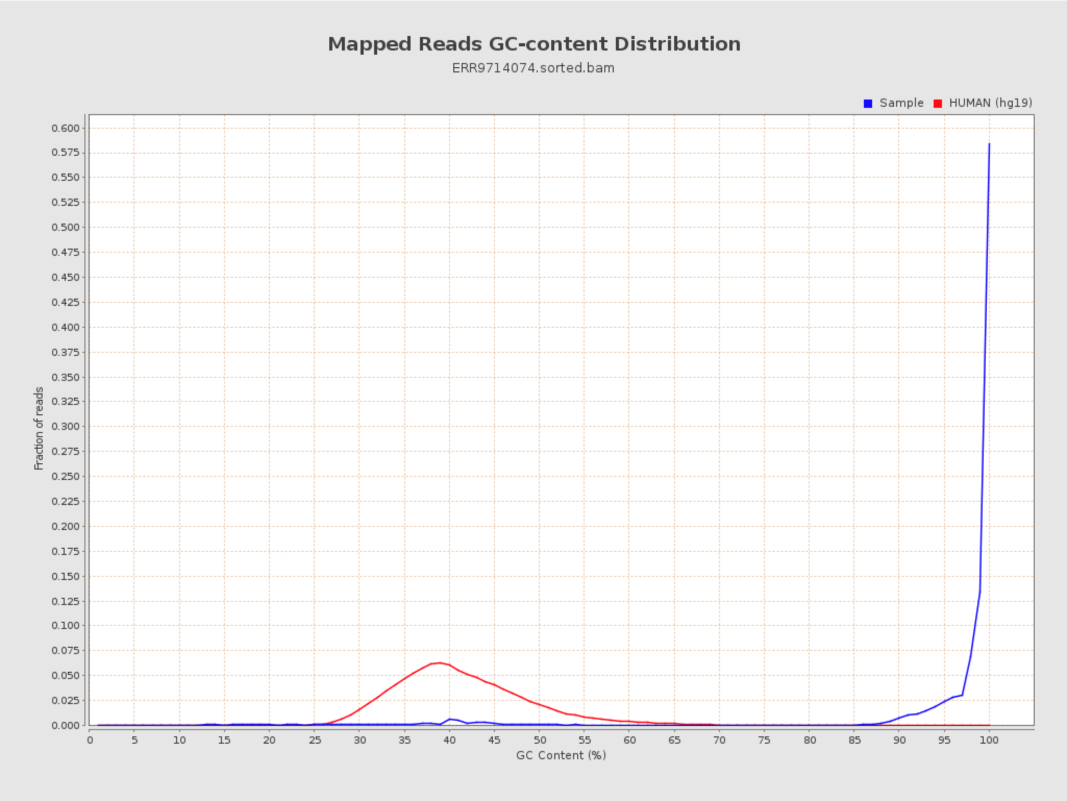
7. Results : Duplication Rate Histogram



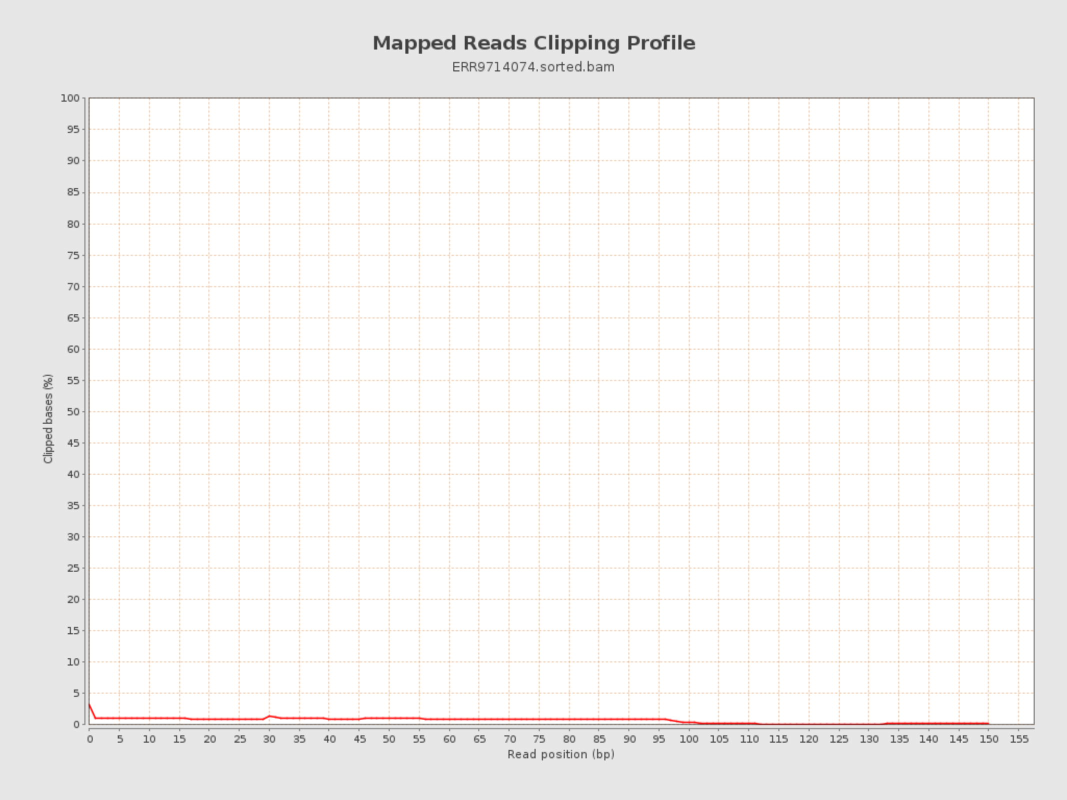
8. Results : Mapped Reads Nucleotide Content



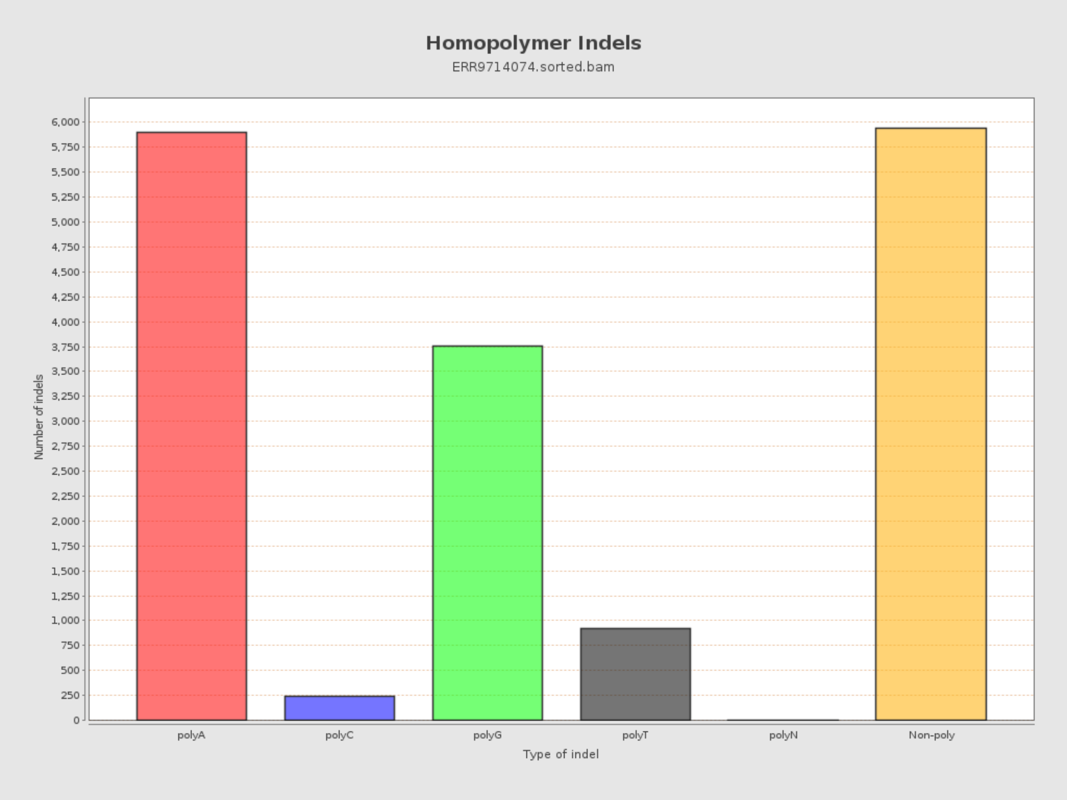
9. Results : Mapped Reads GC-content Distribution



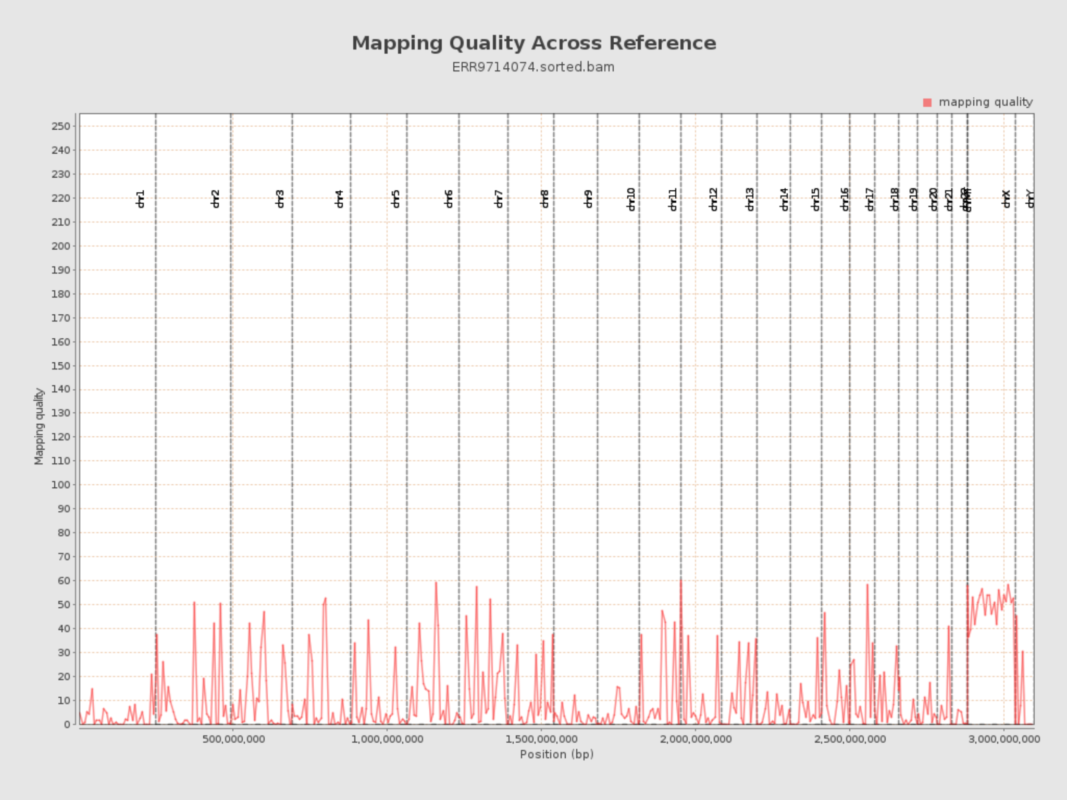
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram