Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 17:39:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714057.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_ERR9714057 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714057.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 17:39:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714057.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,574
Mapped reads	3,682 / 34.82%
Unmapped reads	6,892 / 65.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	143 / 1.35%
Read min/max/mean length	30 / 151 / 107.21
Duplicated reads (estimated)	1,963 / 18.56%
Duplication rate	33.24%
Clipped reads	3,266 / 30.89%

2.2. ACGT Content

Number/percentage of A's	123,396 / 27.5%
Number/percentage of C's	85,090 / 18.96%
Number/percentage of T's	115,108 / 25.65%
Number/percentage of G's	125,180 / 27.89%
Number/percentage of N's	3 / 0%
GC Percentage	46.85%

2.3. Coverage

Mean	0.0001

Standard Deviation	0.0576

2.4. Mapping Quality

Mean Mapping Quality	35.96

2.5. Mismatches and indels

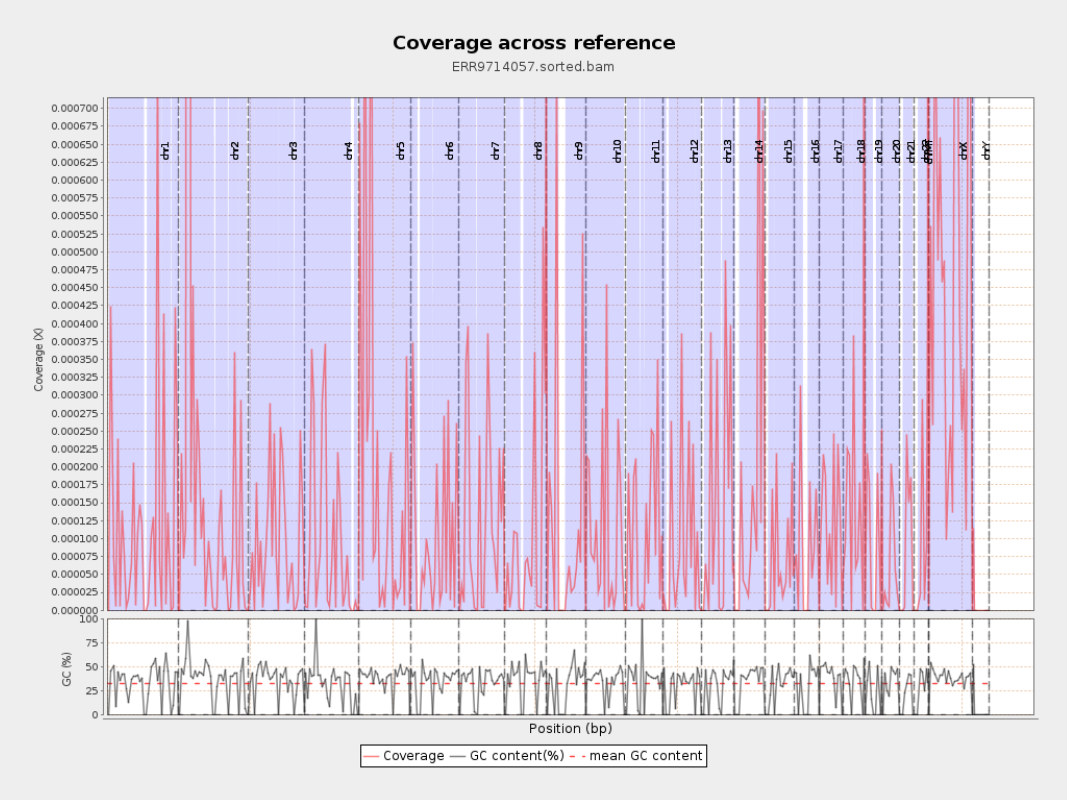
General error rate	4.19%
Mismatches	17,476
Insertions	462
Mapped reads with at least one insertion	12.19%
Deletions	1,521
Mapped reads with at least one deletion	38.59%
Homopolymer indels	29.5%

2.6. Chromosome stats

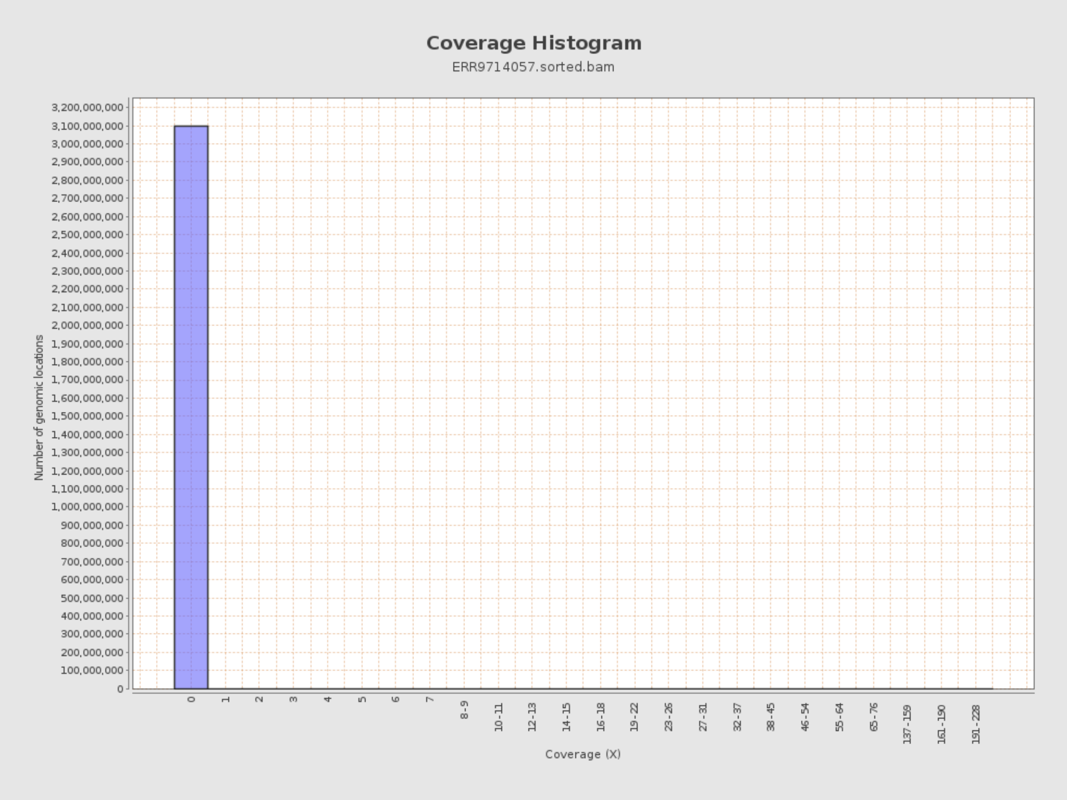
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	30654	0.0001	0.0421
chr2	243199373	64364	0.0003	0.1576
chr3	198022430	19128	0.0001	0.0225
chr4	191154276	17531	0.0001	0.0287
chr5	180915260	40239	0.0002	0.0684
chr6	171115067	17236	0.0001	0.0285
chr7	159138663	20980	0.0001	0.0319

chr8	146364022	13258	0.0001	0.0284
chr9	141213431	17004	0.0001	0.0326
chr10	135534747	15885	0.0001	0.0316
chr11	135006516	14234	0.0001	0.0263
chr12	133851895	12111	0.0001	0.0261
chr13	115169878	16284	0.0001	0.0339
chr14	107349540	20034	0.0002	0.0656
chr15	102531392	7100	0.0001	0.0191
chr16	90354753	7573	0.0001	0.0203
chr17	81195210	9853	0.0001	0.0281
chr18	78077248	14597	0.0002	0.0585
chr19	59128983	5120	0.0001	0.0187
chr20	63025520	3718	0.0001	0.0158
chr21	48129895	4537	0.0001	0.0278
chr22	51304566	4100	0.0001	0.0241
chrMT	16571	11955	0.7214	3.5451
chrX	155270560	69222	0.0004	0.0562
chrY	59373566	593	0	0.0086

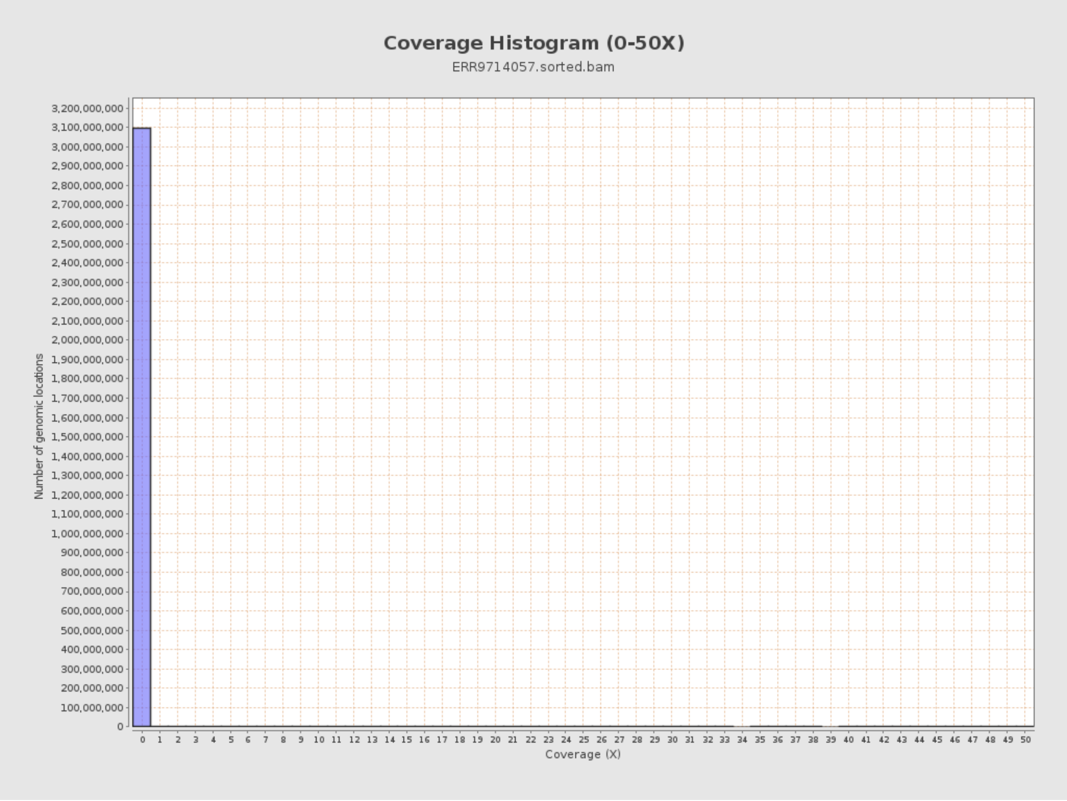
3. Results : Coverage across reference



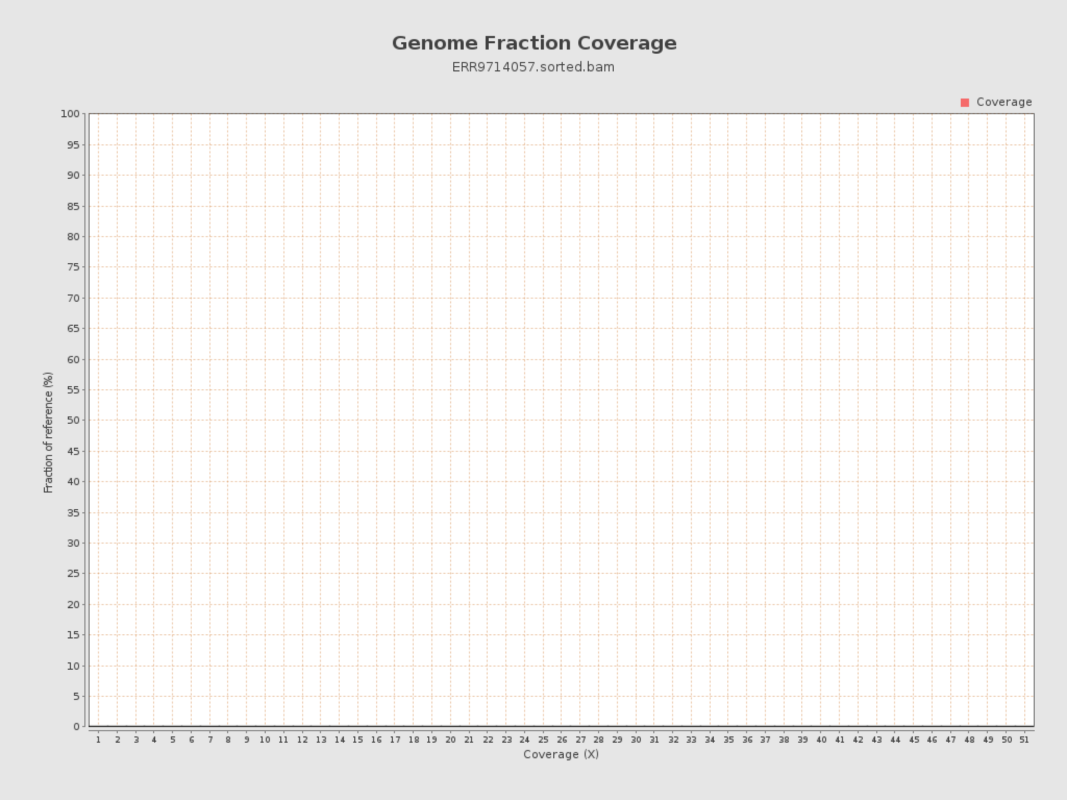
4. Results : Coverage Histogram



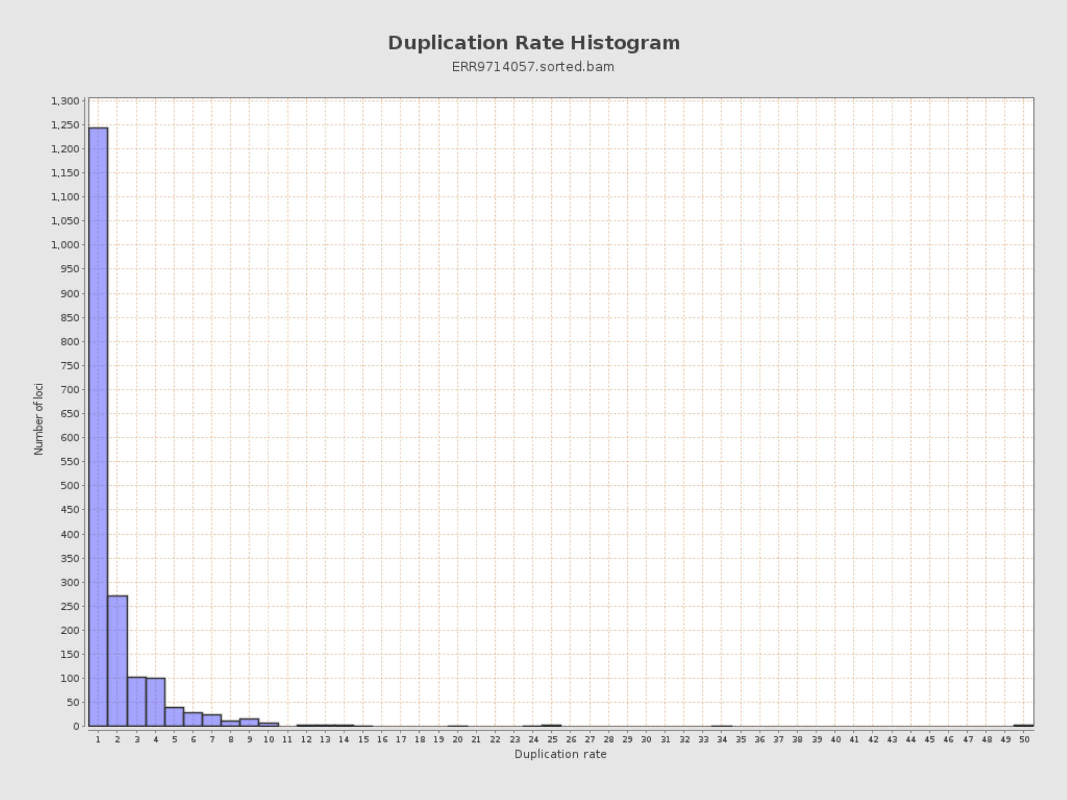
5. Results : Coverage Histogram (0-50X)



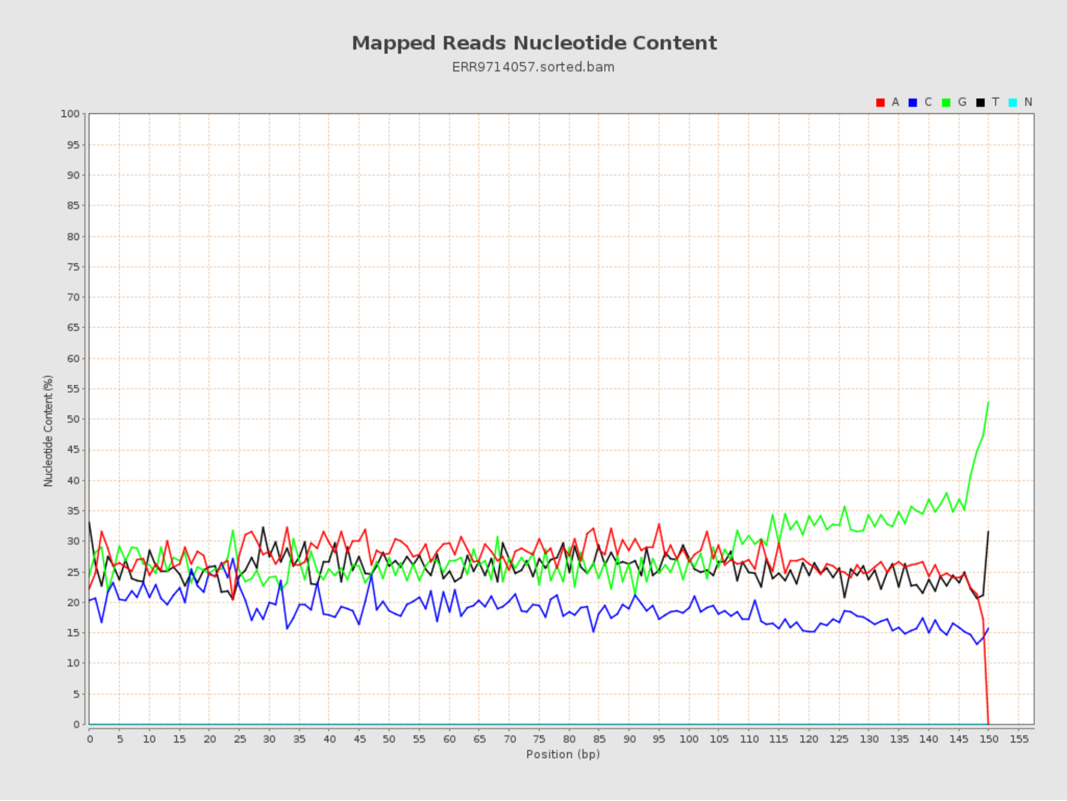
6. Results : Genome Fraction Coverage



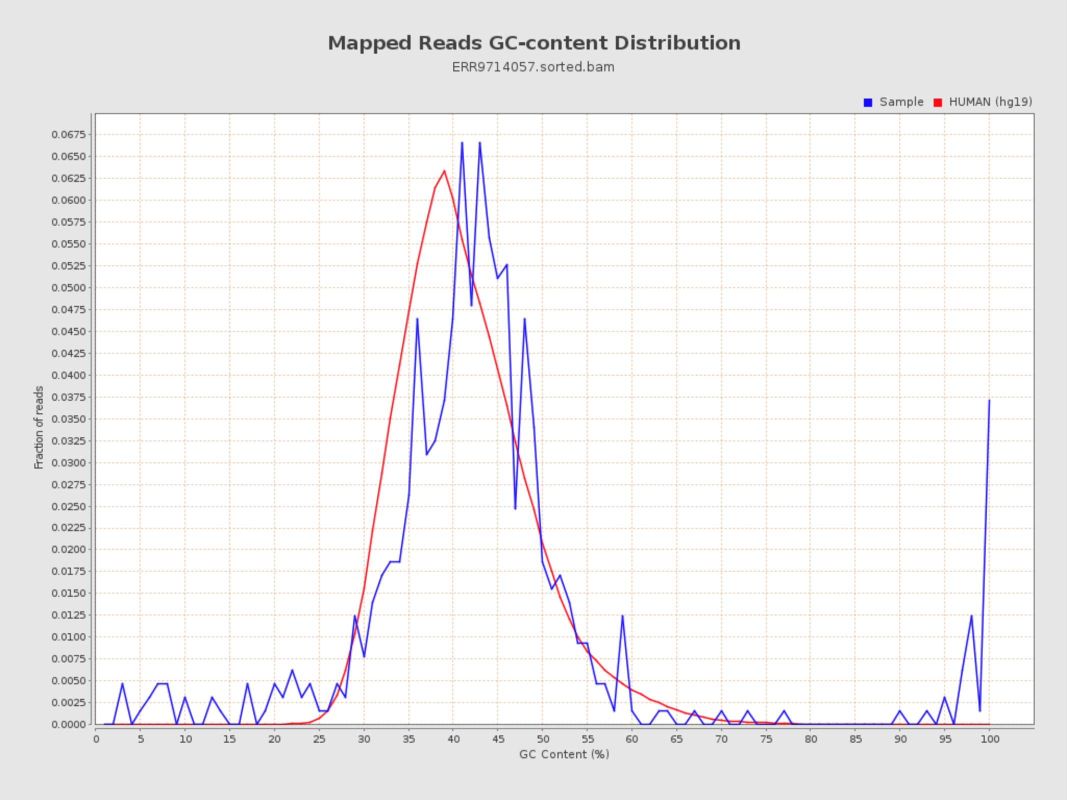
7. Results : Duplication Rate Histogram



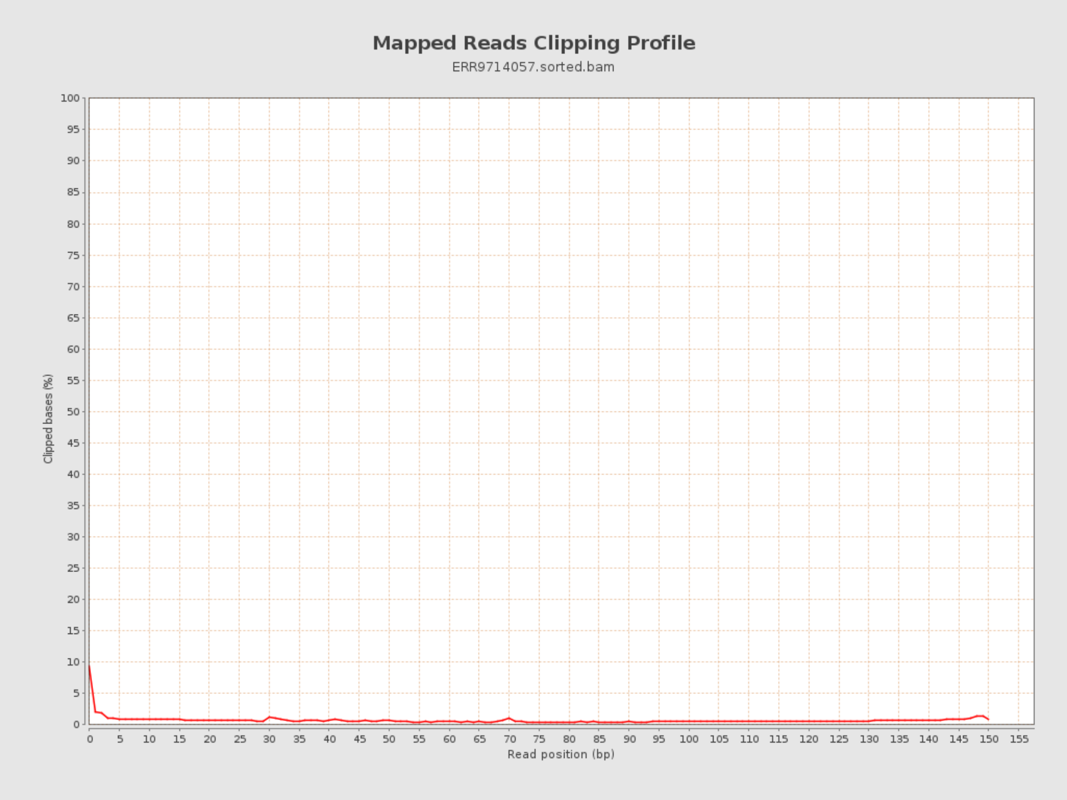
8. Results : Mapped Reads Nucleotide Content



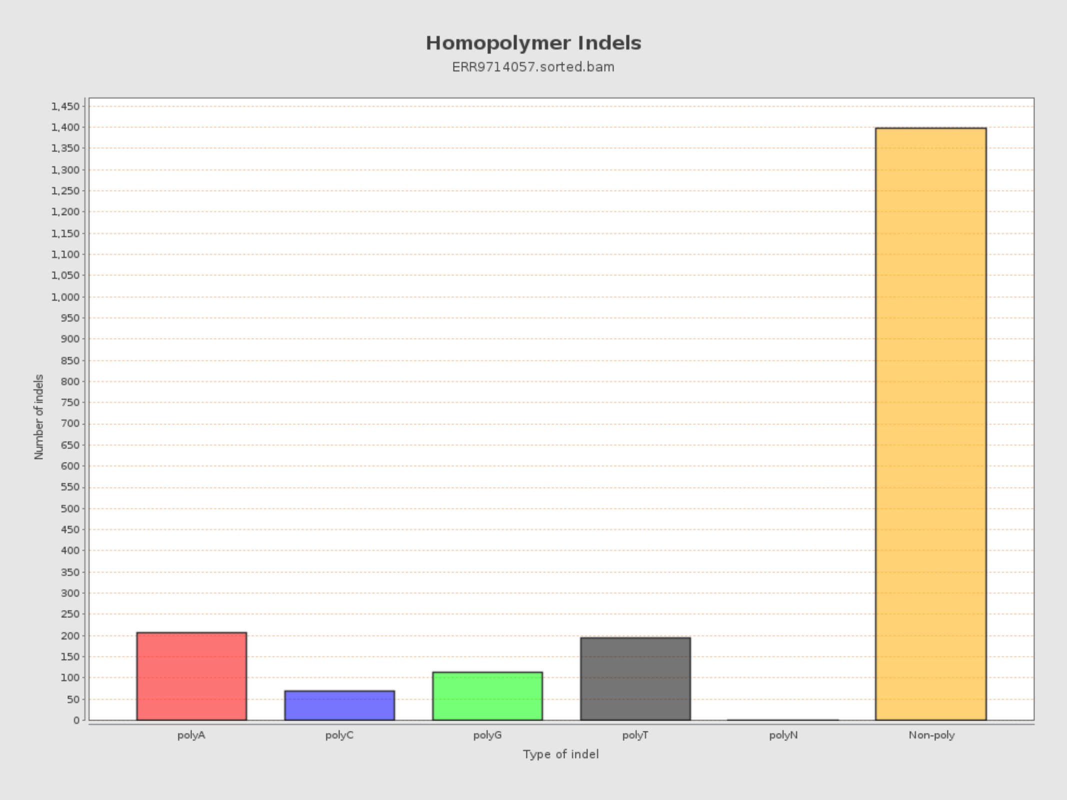
9. Results : Mapped Reads GC-content Distribution



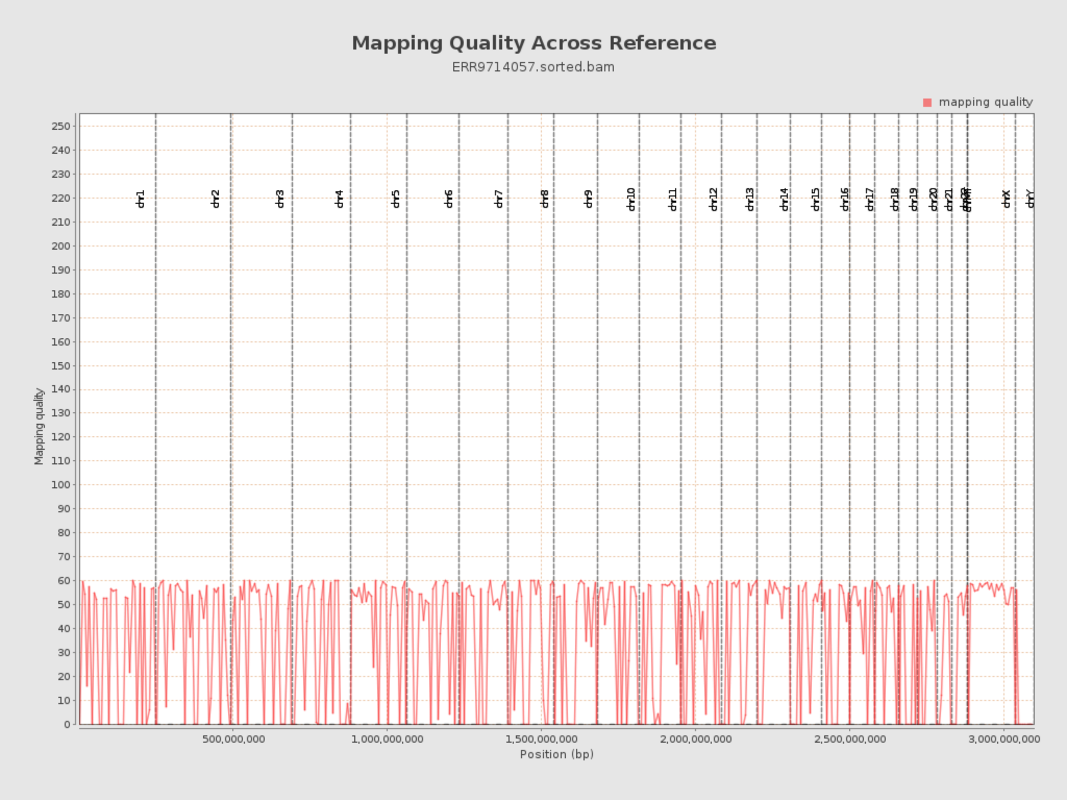
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram