Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 23:48:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714190.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_ERR9714190 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714190.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 23:48:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714190.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	74,550
Mapped reads	7,392 / 9.92%
Unmapped reads	67,158 / 90.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	242 / 0.32%
Read min/max/mean length	30 / 151 / 60.1
Duplicated reads (estimated)	5,615 / 7.53%
Duplication rate	35.51%
Clipped reads	6,272 / 8.41%

2.2. ACGT Content

Number/percentage of A's	177,398 / 22.66%
Number/percentage of C's	125,444 / 16.02%
Number/percentage of T's	160,898 / 20.55%
Number/percentage of G's	319,176 / 40.77%
Number/percentage of N's	25 / 0%
GC Percentage	56.79%

2.3. Coverage

Mean	0.0003

Standard Deviation	0.2321

2.4. Mapping Quality

Mean Mapping Quality	28.55

2.5. Mismatches and indels

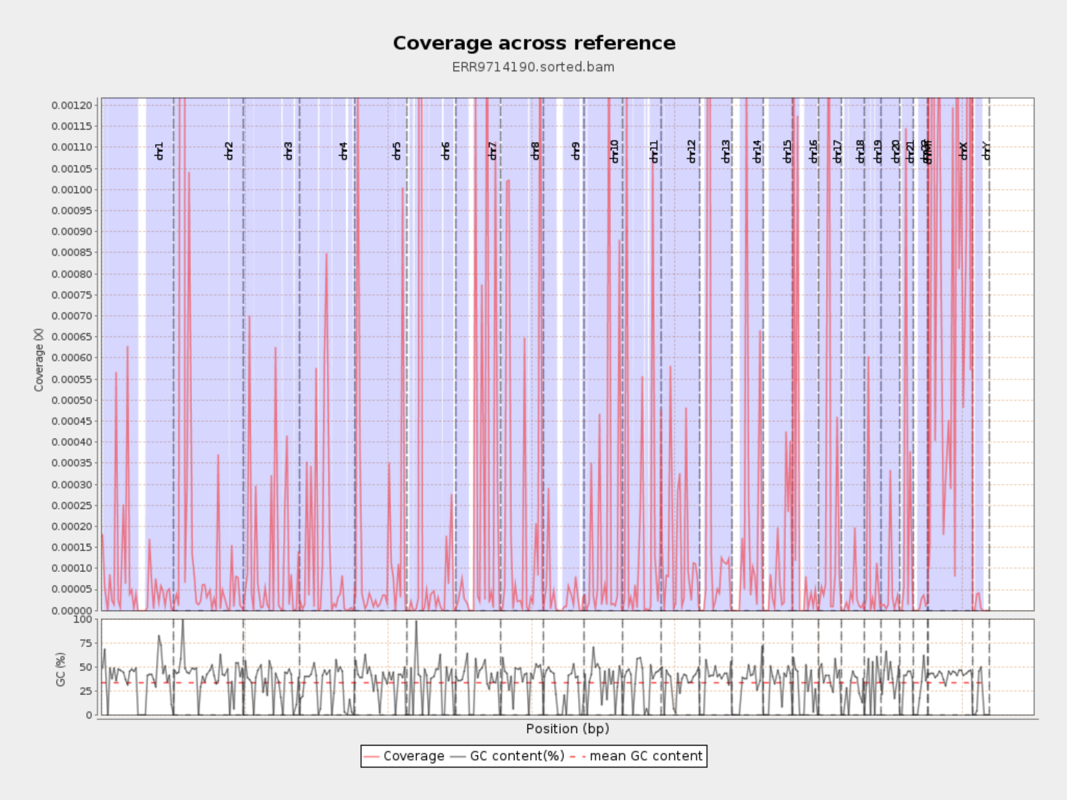
General error rate	3.81%
Mismatches	26,529
Insertions	787
Mapped reads with at least one insertion	9.31%
Deletions	1,990
Mapped reads with at least one deletion	26.26%
Homopolymer indels	26.86%

2.6. Chromosome stats

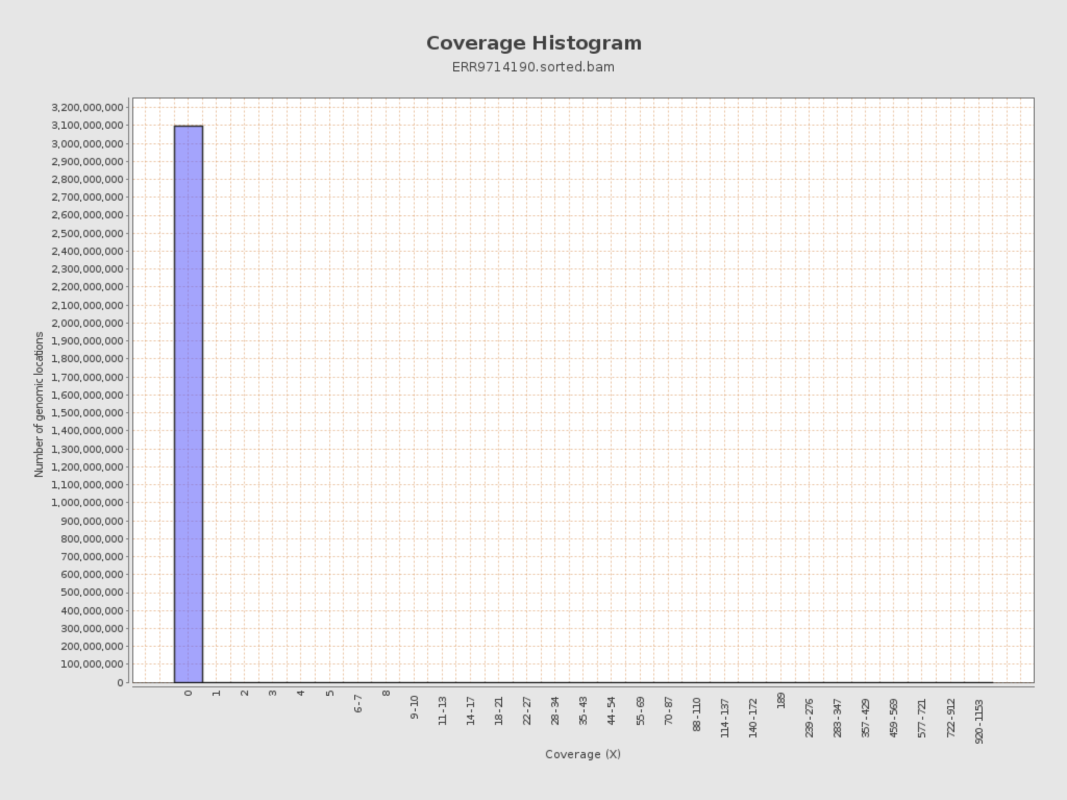
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20091	0.0001	0.0326
chr2	243199373	233081	0.001	0.7712
chr3	198022430	24814	0.0001	0.0475
chr4	191154276	25365	0.0001	0.0597
chr5	180915260	28685	0.0002	0.0756
chr6	171115067	35663	0.0002	0.1327
chr7	159138663	42604	0.0003	0.1073

chr8	146364022	39032	0.0003	0.1088
chr9	141213431	5223	0	0.0169
chr10	135534747	27219	0.0002	0.0916
chr11	135006516	27749	0.0002	0.0835
chr12	133851895	18950	0.0001	0.0437
chr13	115169878	23909	0.0002	0.1243
chr14	107349540	21540	0.0002	0.0904
chr15	102531392	11454	0.0001	0.0346
chr16	90354753	18723	0.0002	0.0964
chr17	81195210	19108	0.0002	0.1177
chr18	78077248	2634	0	0.015
chr19	59128983	6116	0.0001	0.0481
chr20	63025520	3509	0.0001	0.0236
chr21	48129895	12624	0.0003	0.1072
chr22	51304566	697	0	0.0052
chrMT	16571	6246	0.3769	2.6202
chrX	155270560	140142	0.0009	0.1828
chrY	59373566	644	0	0.0064

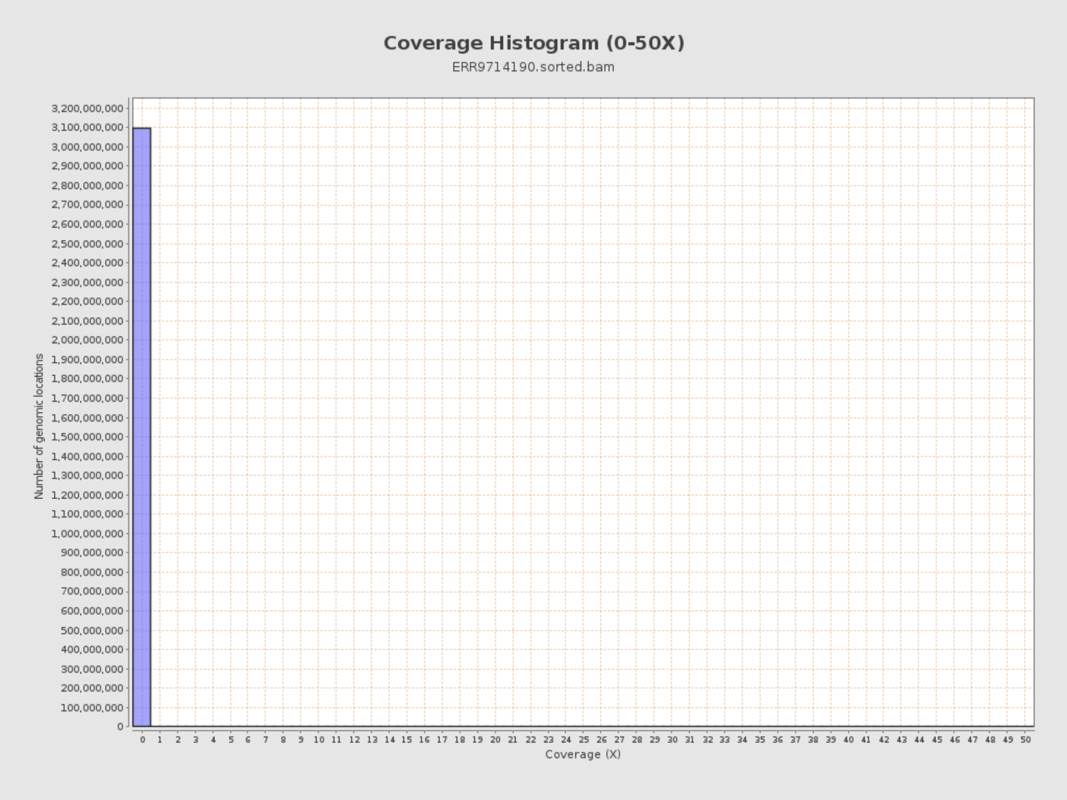
3. Results : Coverage across reference



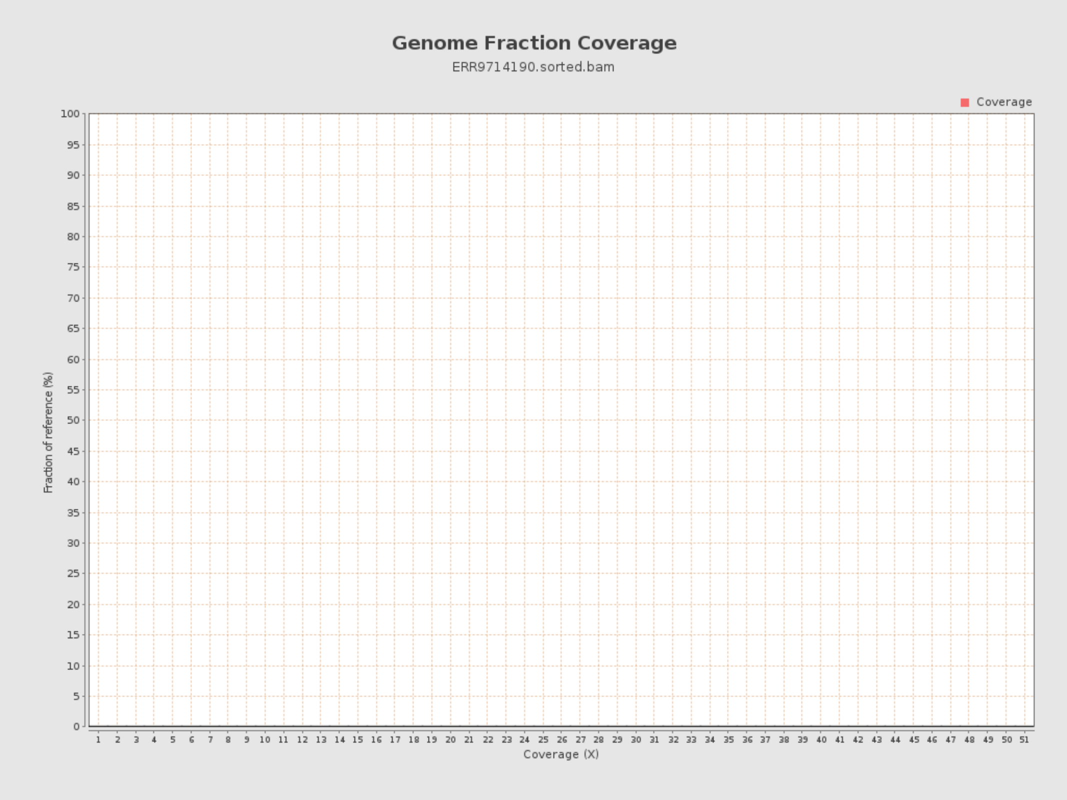
4. Results : Coverage Histogram



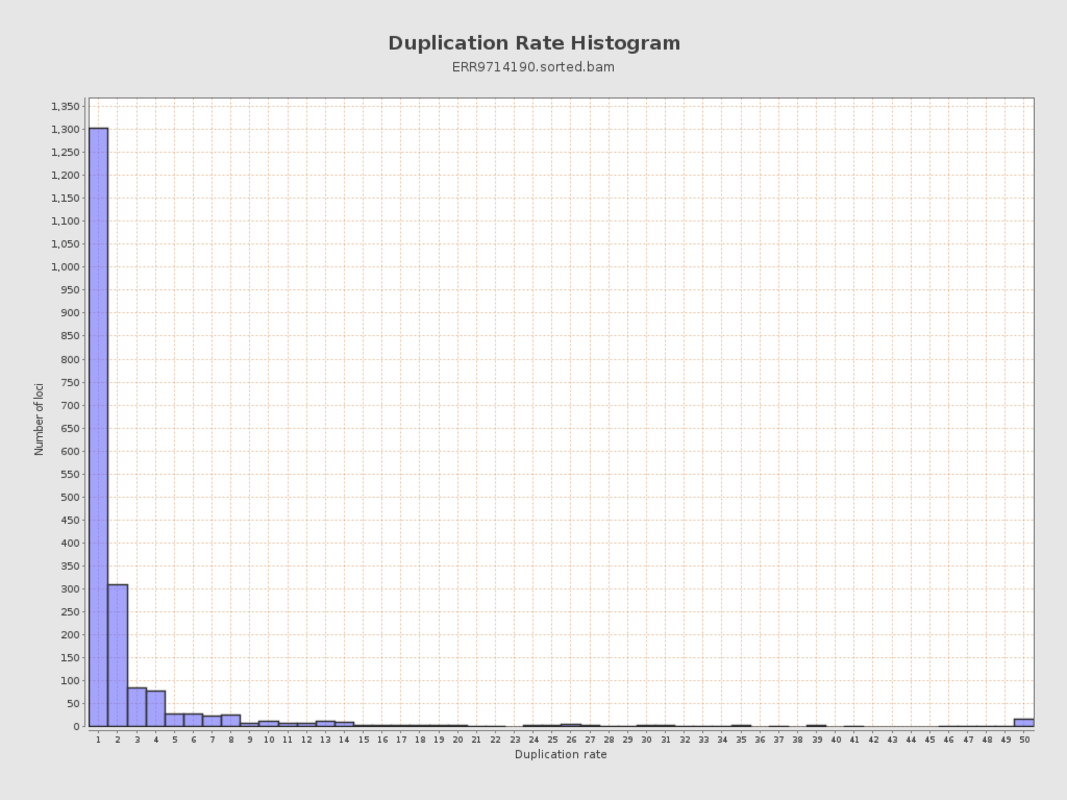
5. Results : Coverage Histogram (0-50X)



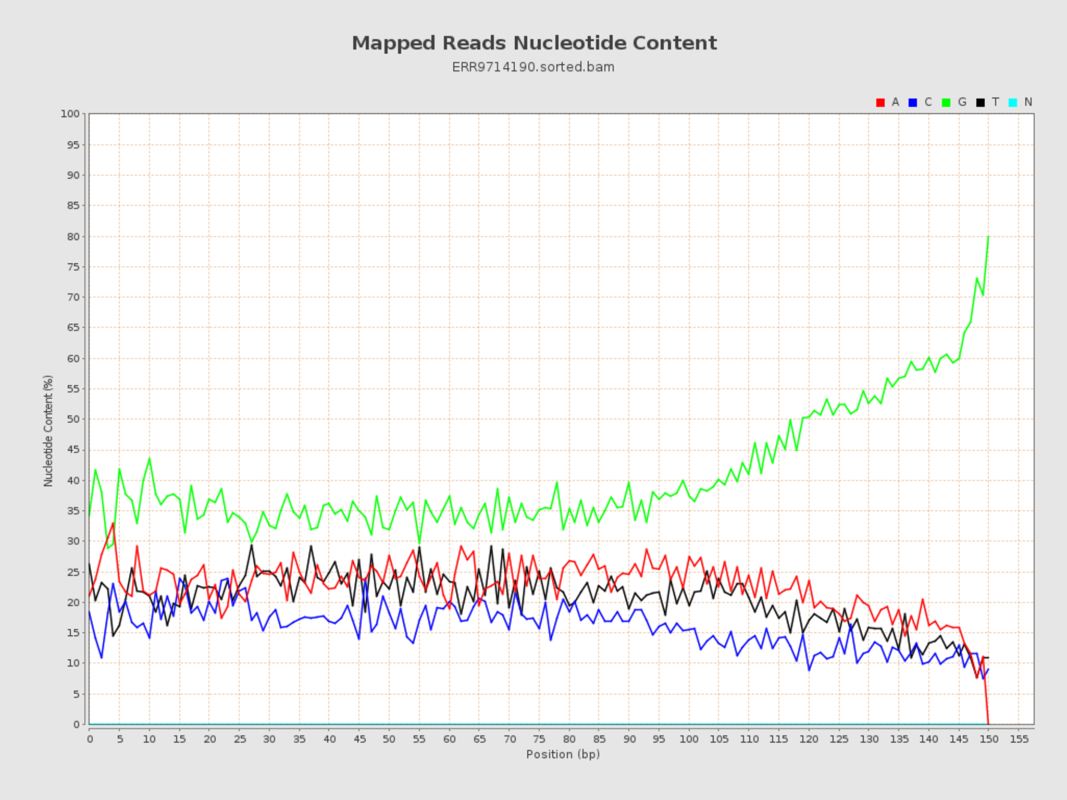
6. Results : Genome Fraction Coverage



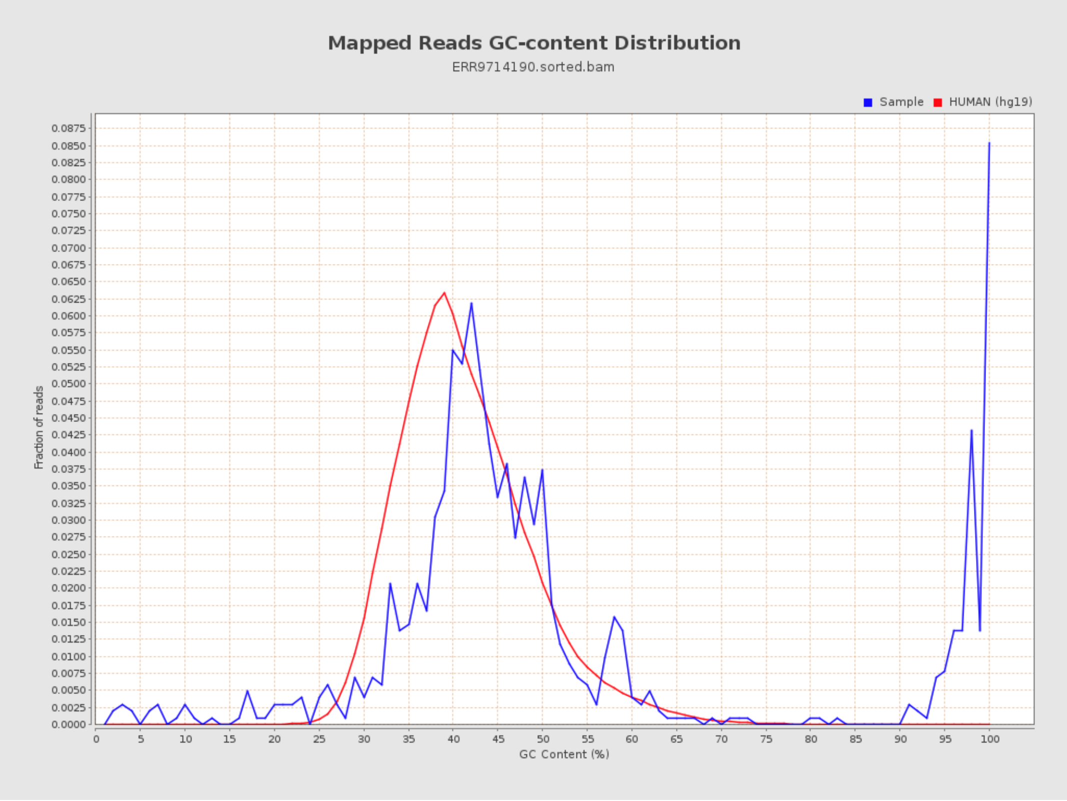
7. Results : Duplication Rate Histogram



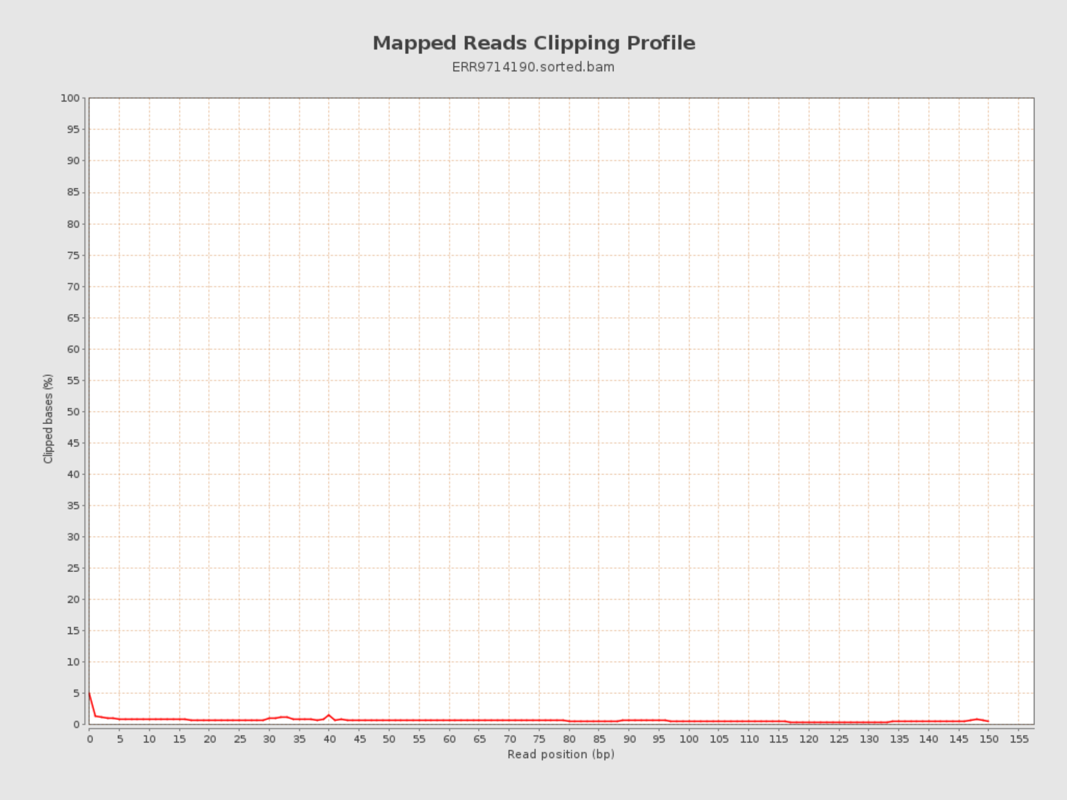
8. Results : Mapped Reads Nucleotide Content



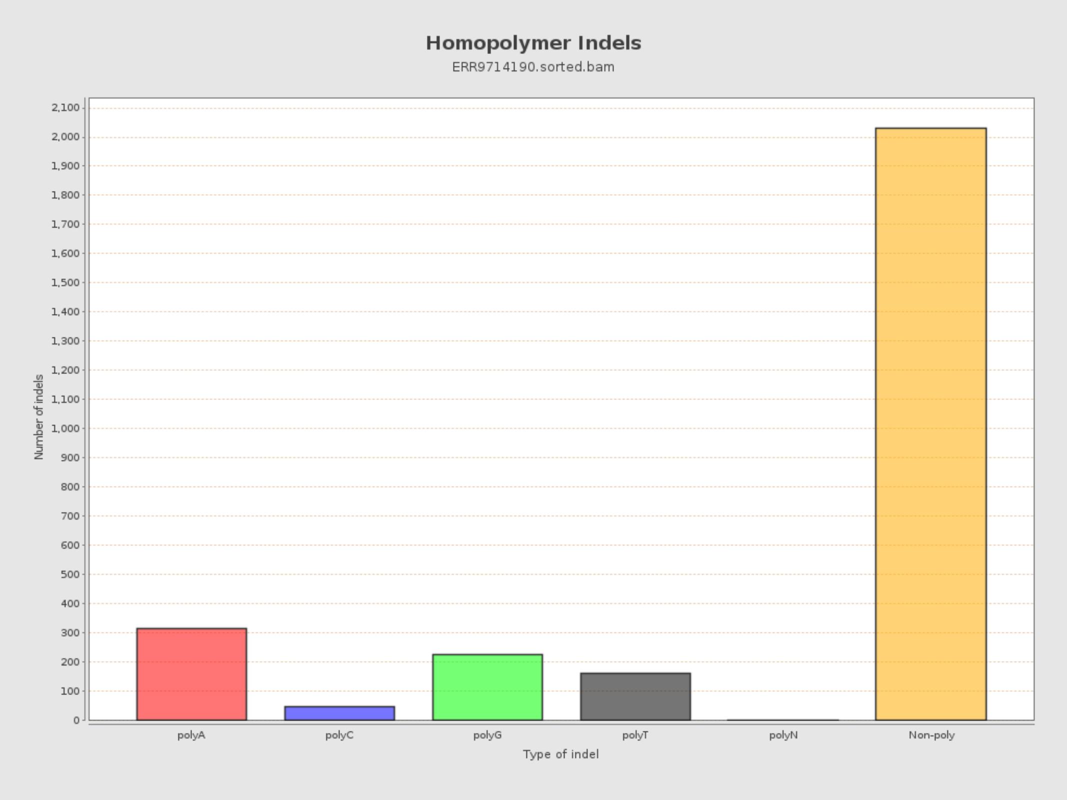
9. Results : Mapped Reads GC-content Distribution



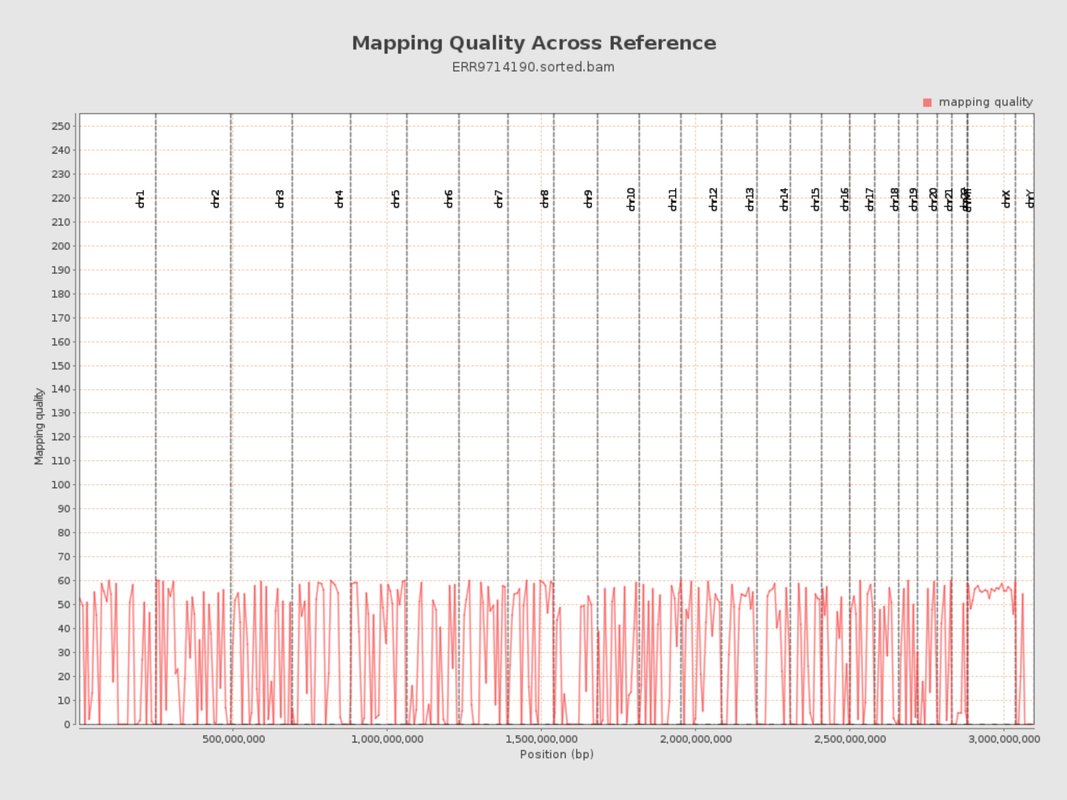
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram