Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 00:32:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714221.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_ERR9714221 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714221.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 00:32:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714221.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	222,380
Mapped reads	15,983 / 7.19%
Unmapped reads	206,397 / 92.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	621 / 0.28%
Read min/max/mean length	30 / 151 / 58.7
Duplicated reads (estimated)	13,124 / 5.9%
Duplication rate	34.31%
Clipped reads	13,968 / 6.28%

2.2. ACGT Content

Number/percentage of A's	296,499 / 19.32%
Number/percentage of C's	193,587 / 12.61%
Number/percentage of T's	262,529 / 17.11%
Number/percentage of G's	782,115 / 50.96%
Number/percentage of N's	32 / 0%
GC Percentage	63.57%

2.3. Coverage

Mean	0.0005

Standard Deviation	0.6699

2.4. Mapping Quality

Mean Mapping Quality	31.78

2.5. Mismatches and indels

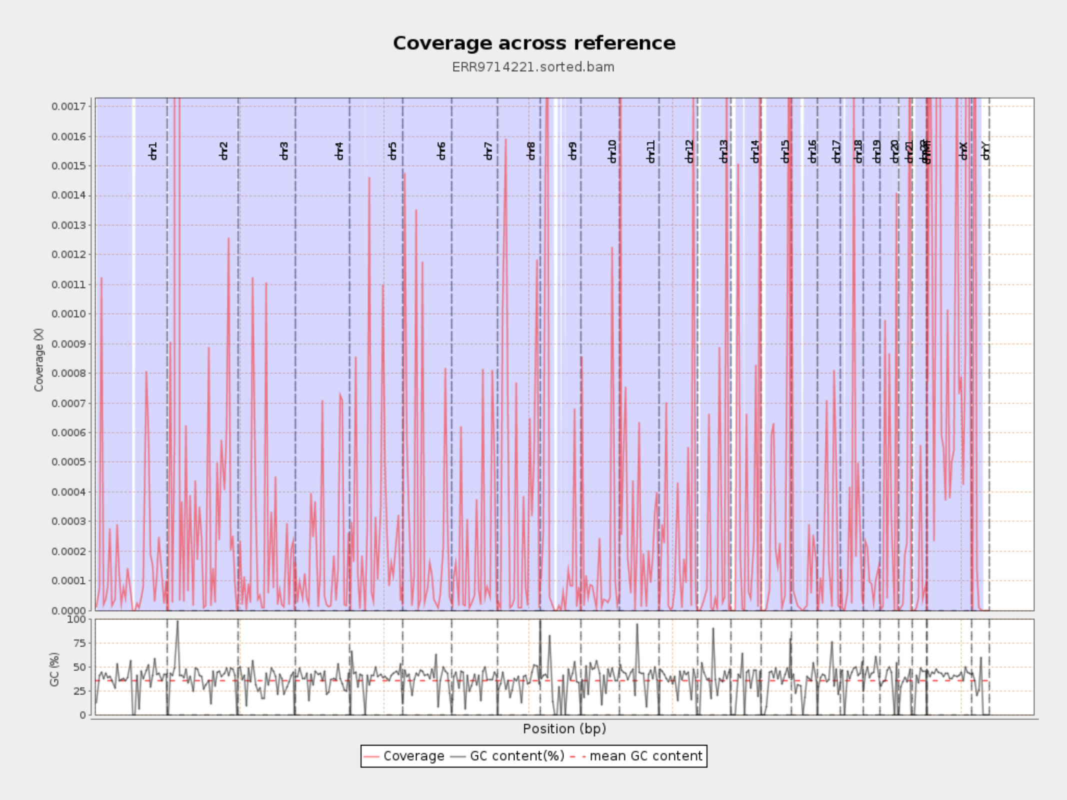
General error rate	3.95%
Mismatches	53,527
Insertions	1,836
Mapped reads with at least one insertion	9.68%
Deletions	3,693
Mapped reads with at least one deletion	22.26%
Homopolymer indels	31.94%

2.6. Chromosome stats

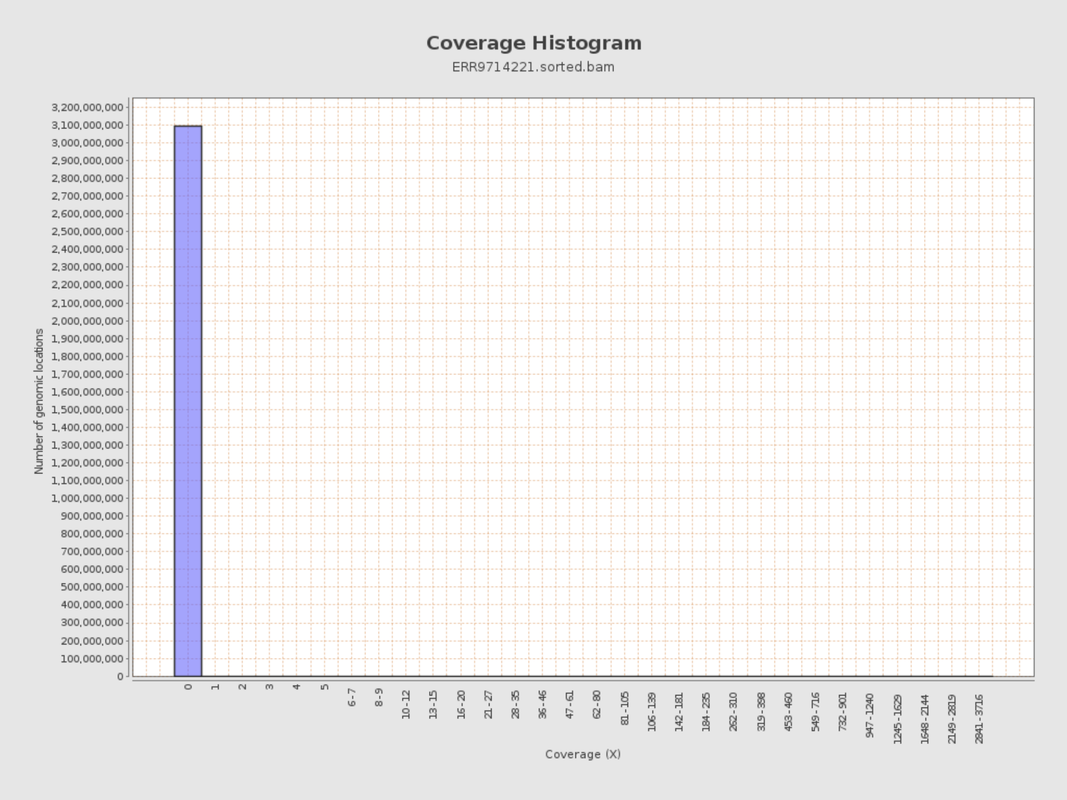
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	38590	0.0002	0.053
chr2	243199373	660731	0.0027	2.3623
chr3	198022430	38637	0.0002	0.0729
chr4	191154276	34980	0.0002	0.056
chr5	180915260	54617	0.0003	0.0907
chr6	171115067	54072	0.0003	0.0981
chr7	159138663	32396	0.0002	0.1039

chr8	146364022	56454	0.0004	0.1266
chr9	141213431	39157	0.0003	0.1039
chr10	135534747	22665	0.0002	0.0662
chr11	135006516	41678	0.0003	0.0843
chr12	133851895	36124	0.0003	0.0847
chr13	115169878	28270	0.0002	0.1193
chr14	107349540	43263	0.0004	0.1451
chr15	102531392	39254	0.0004	0.1089
chr16	90354753	15728	0.0002	0.0718
chr17	81195210	20804	0.0003	0.09
chr18	78077248	25484	0.0003	0.0947
chr19	59128983	7201	0.0001	0.0239
chr20	63025520	28081	0.0004	0.1142
chr21	48129895	20620	0.0004	0.1803
chr22	51304566	5689	0.0001	0.0262
chrMT	16571	1913	0.1154	1.0006
chrX	155270560	190755	0.0012	0.2204
chrY	59373566	22180	0.0004	0.1539

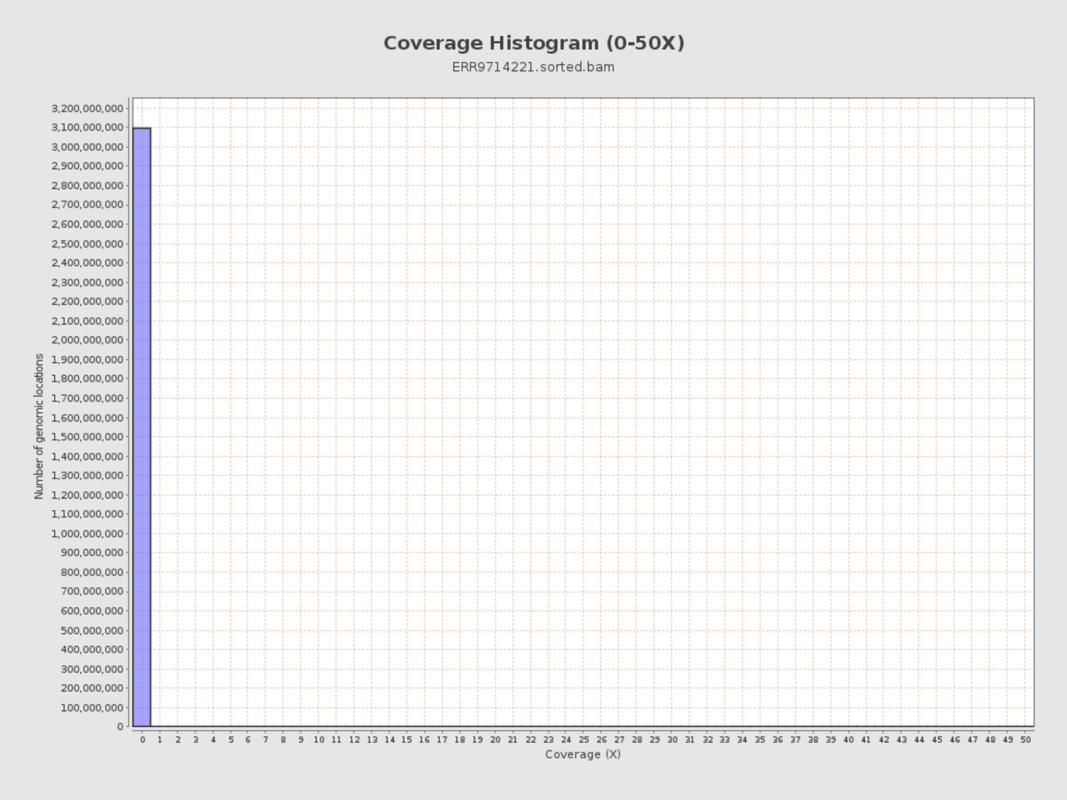
3. Results : Coverage across reference



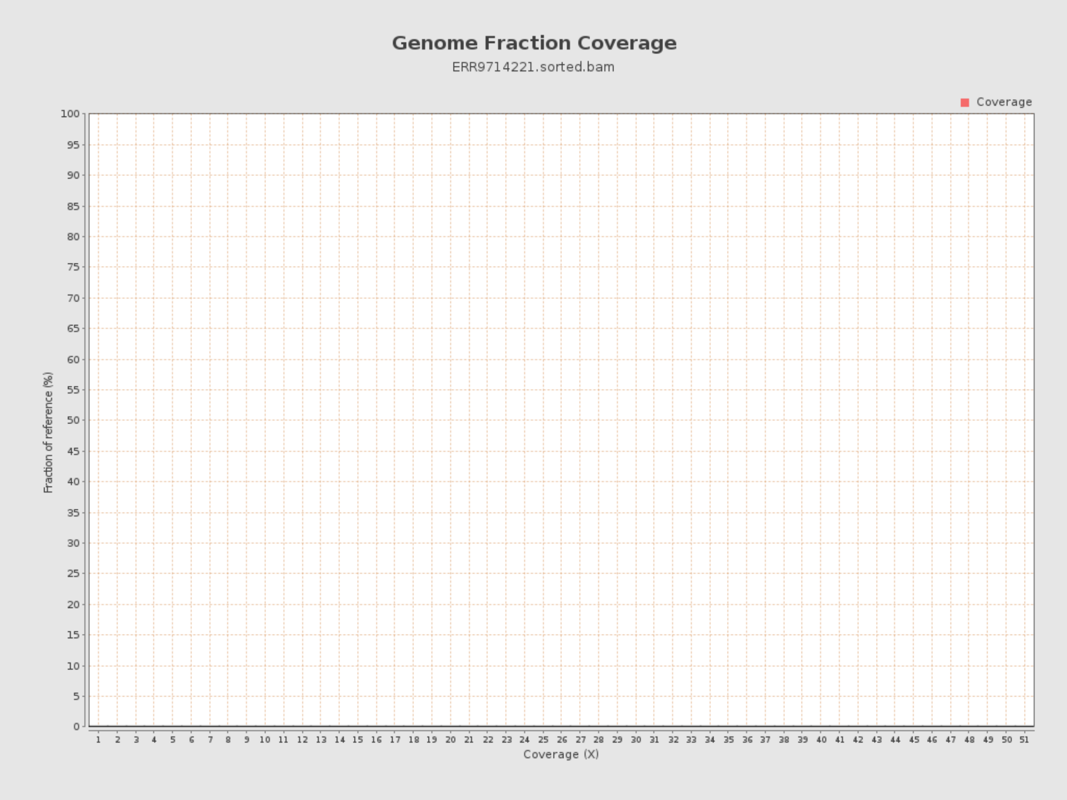
4. Results : Coverage Histogram



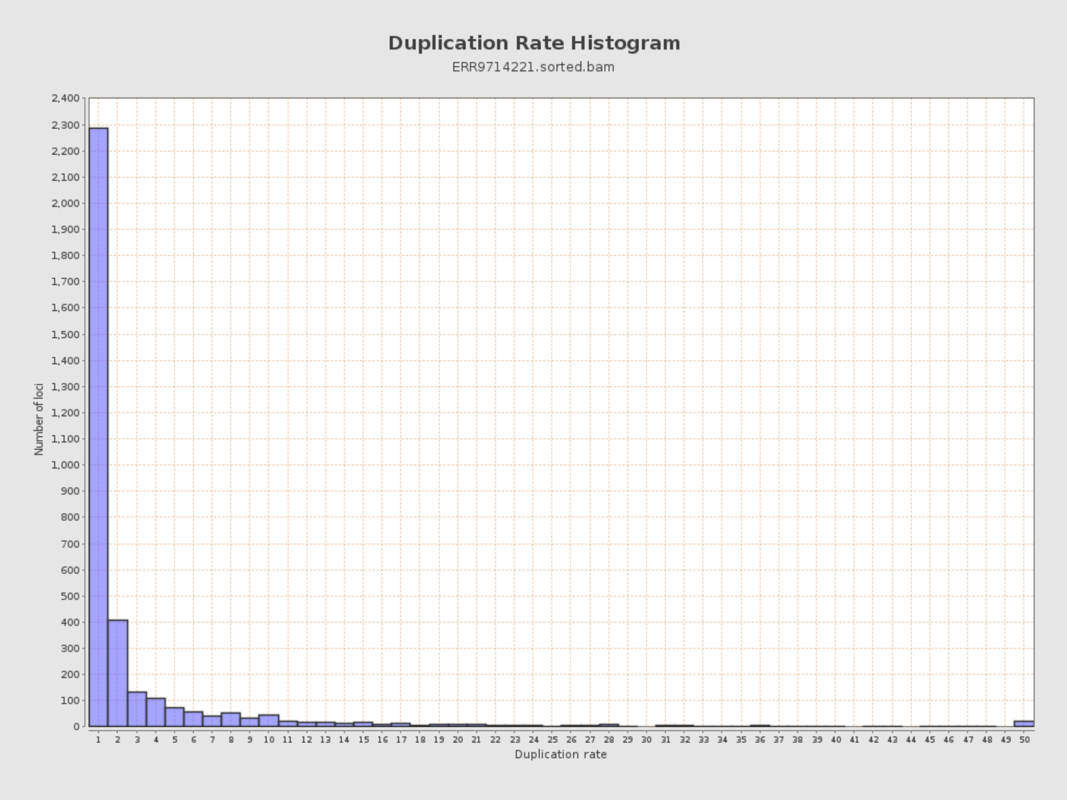
5. Results : Coverage Histogram (0-50X)



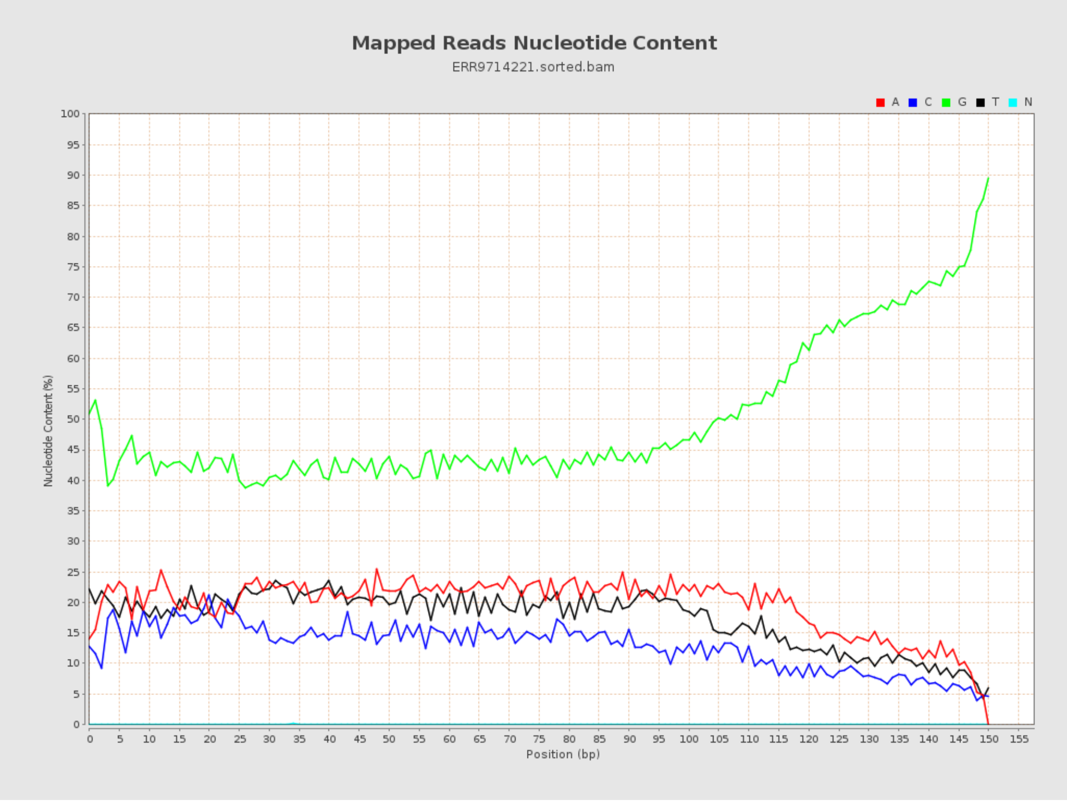
6. Results : Genome Fraction Coverage



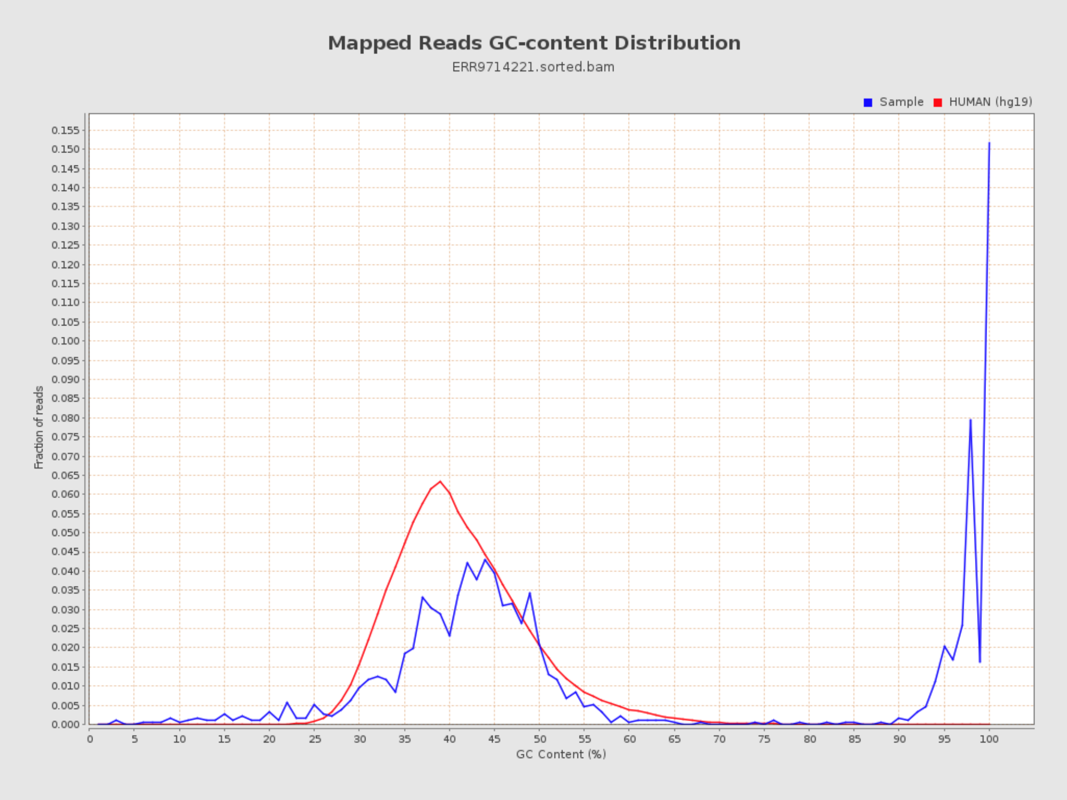
7. Results : Duplication Rate Histogram



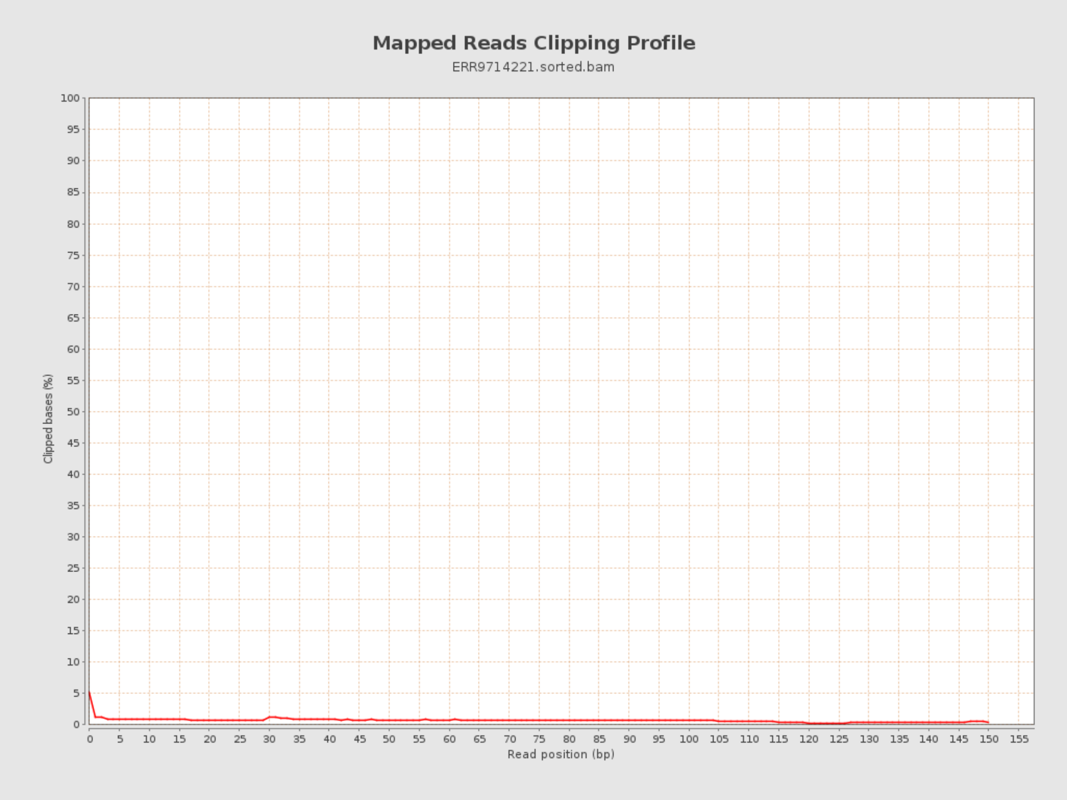
8. Results : Mapped Reads Nucleotide Content



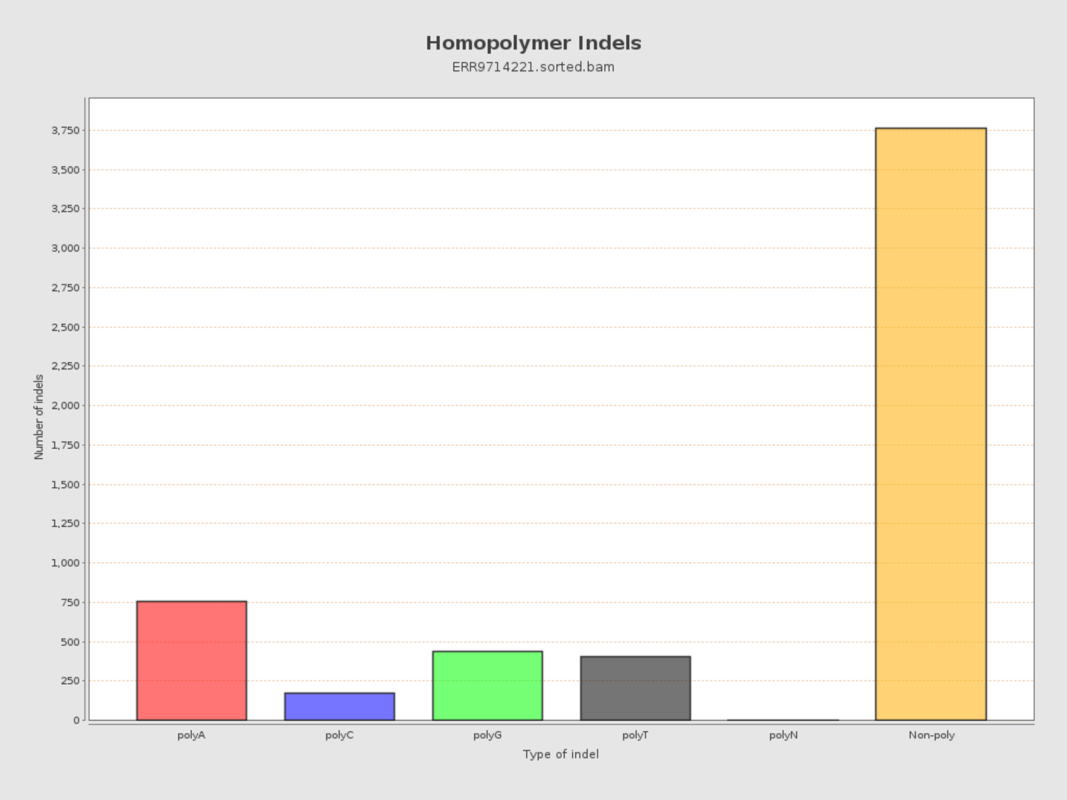
9. Results : Mapped Reads GC-content Distribution



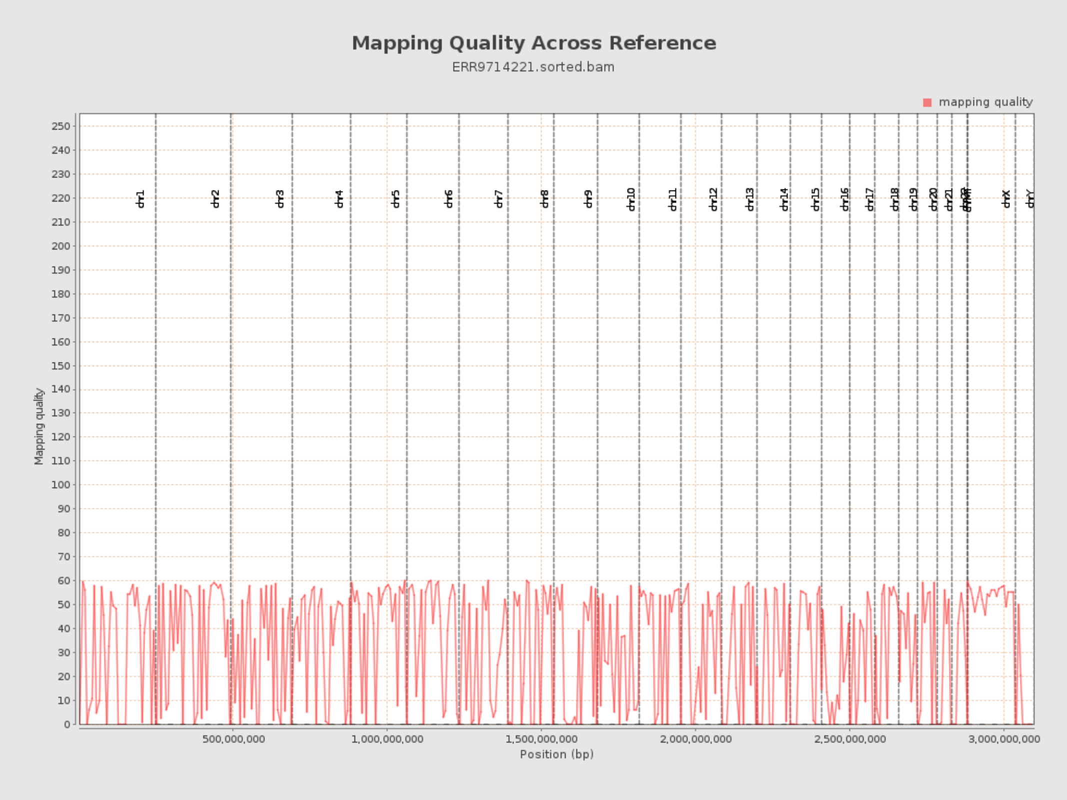
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram