Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 22:16:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714160.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_ERR9714160 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714160.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 22:16:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714160.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	779,760
Mapped reads	695,442 / 89.19%
Unmapped reads	84,318 / 10.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,248 / 2.6%
Read min/max/mean length	30 / 151 / 139.63
Duplicated reads (estimated)	639,731 / 82.04%
Duplication rate	43.23%
Clipped reads	659,875 / 84.63%

2.2. ACGT Content

Number/percentage of A's	24,066,090 / 26.99%
Number/percentage of C's	19,988,631 / 22.41%
Number/percentage of T's	22,721,599 / 25.48%
Number/percentage of G's	22,400,621 / 25.12%
Number/percentage of N's	562 / 0%
GC Percentage	47.53%

2.3. Coverage

Mean	0.0295

Standard Deviation	8.2026

2.4. Mapping Quality

Mean Mapping Quality	51.32

2.5. Mismatches and indels

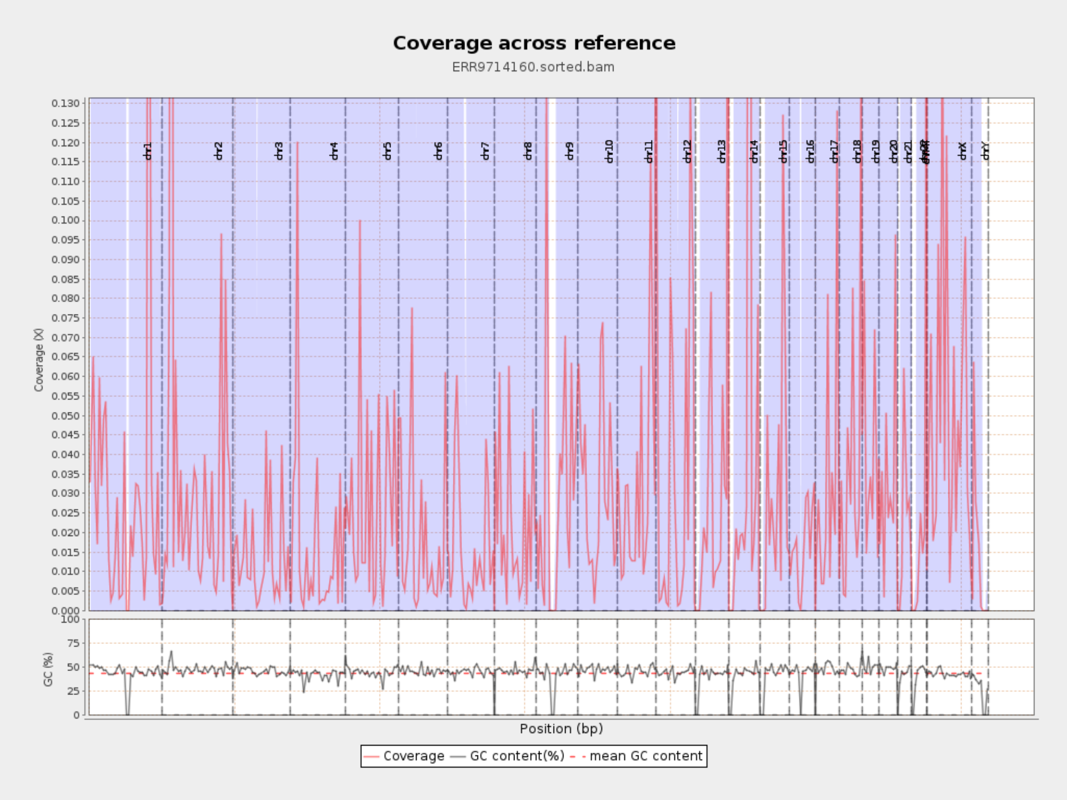
General error rate	4.43%
Mismatches	3,711,017
Insertions	94,587
Mapped reads with at least one insertion	13.17%
Deletions	330,905
Mapped reads with at least one deletion	45.12%
Homopolymer indels	29.33%

2.6. Chromosome stats

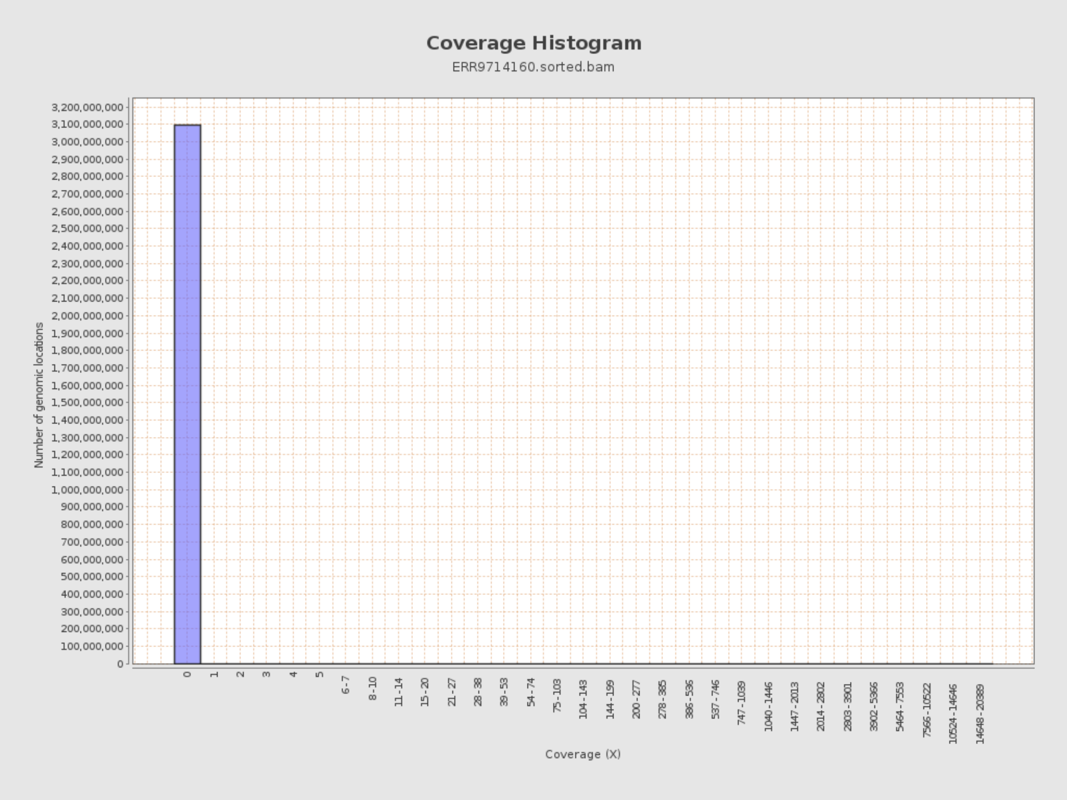
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7676018	0.0308	8.3619
chr2	243199373	10848986	0.0446	14.2964
chr3	198022430	2794308	0.0141	2.4483
chr4	191154276	3289311	0.0172	4.2944
chr5	180915260	4897158	0.0271	6.4345
chr6	171115067	3373719	0.0197	3.731
chr7	159138663	2675695	0.0168	3.2848

chr8	146364022	3370109	0.023	4.2262
chr9	141213431	4001561	0.0283	7.2769
chr10	135534747	4304956	0.0318	5.1377
chr11	135006516	4428652	0.0328	5.3448
chr12	133851895	4805378	0.0359	8.017
chr13	115169878	3907850	0.0339	11.7644
chr14	107349540	5175006	0.0482	23.2335
chr15	102531392	3117945	0.0304	5.5826
chr16	90354753	1536222	0.017	2.2614
chr17	81195210	2902888	0.0358	6.7322
chr18	78077248	2755187	0.0353	8.8617
chr19	59128983	2300300	0.0389	4.89
chr20	63025520	2208384	0.035	4.8663
chr21	48129895	1029112	0.0214	5.1382
chr22	51304566	690257	0.0135	1.9743
chrMT	16571	200530	12.1013	105.0723
chrX	155270560	8095205	0.0521	6.255
chrY	59373566	864119	0.0146	3.4995

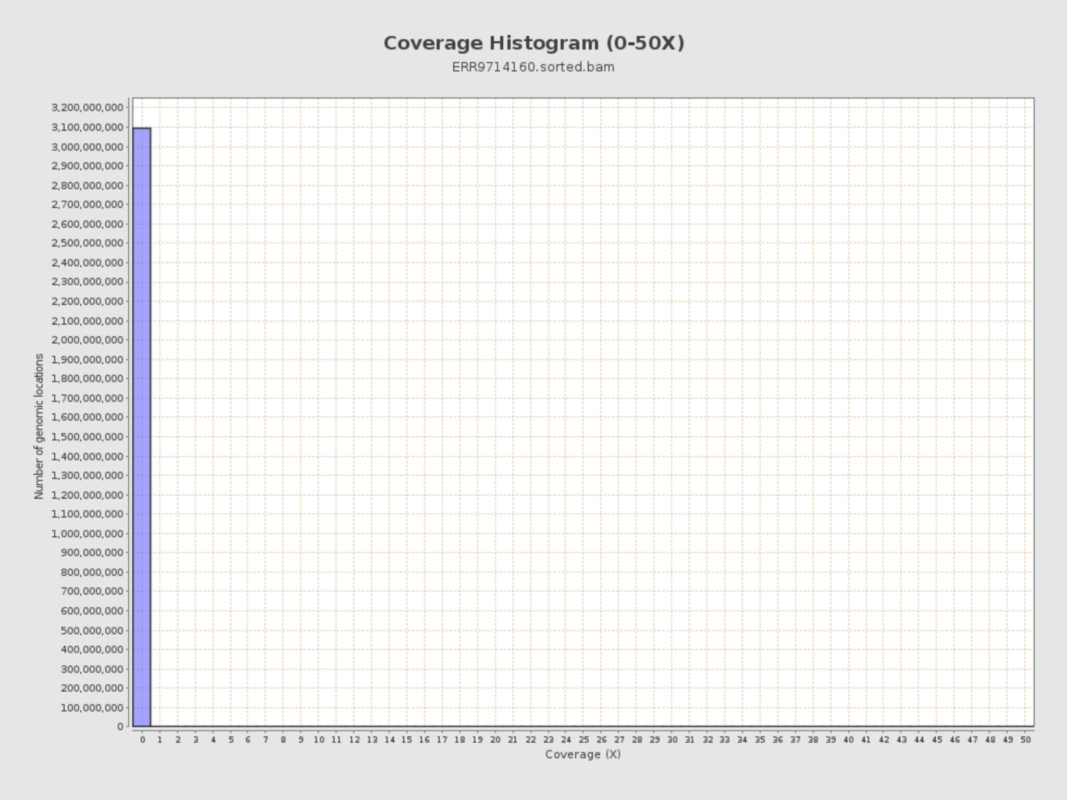
3. Results : Coverage across reference



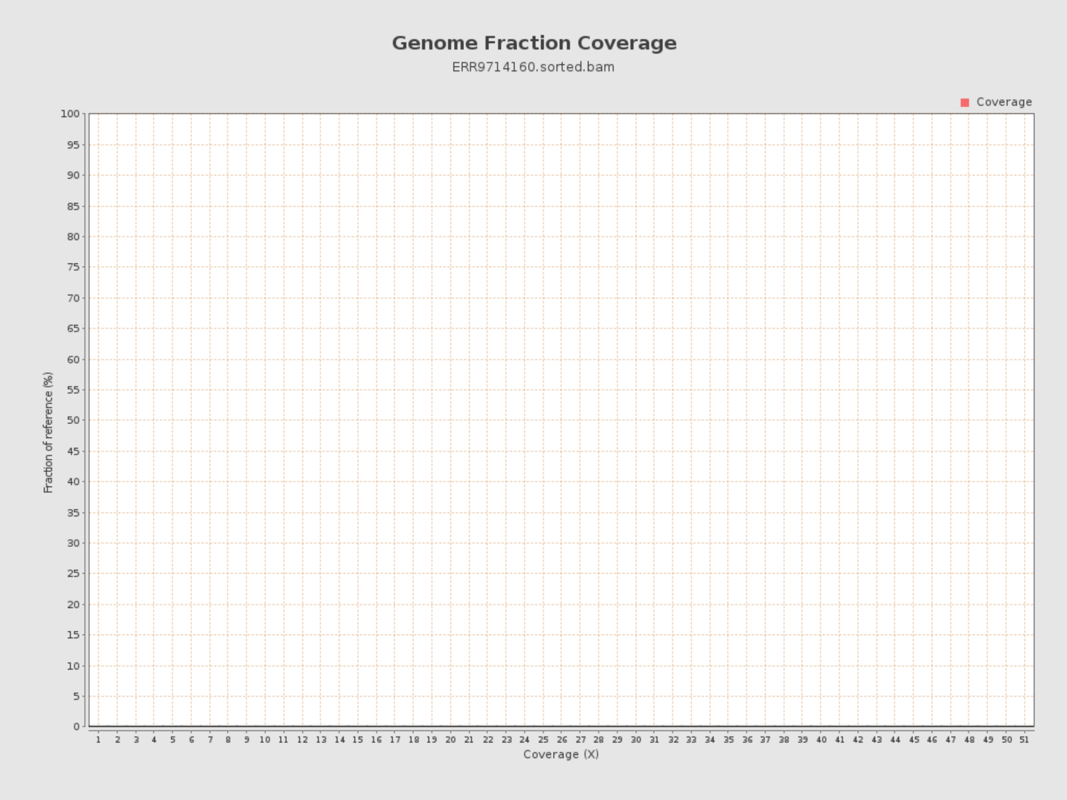
4. Results : Coverage Histogram



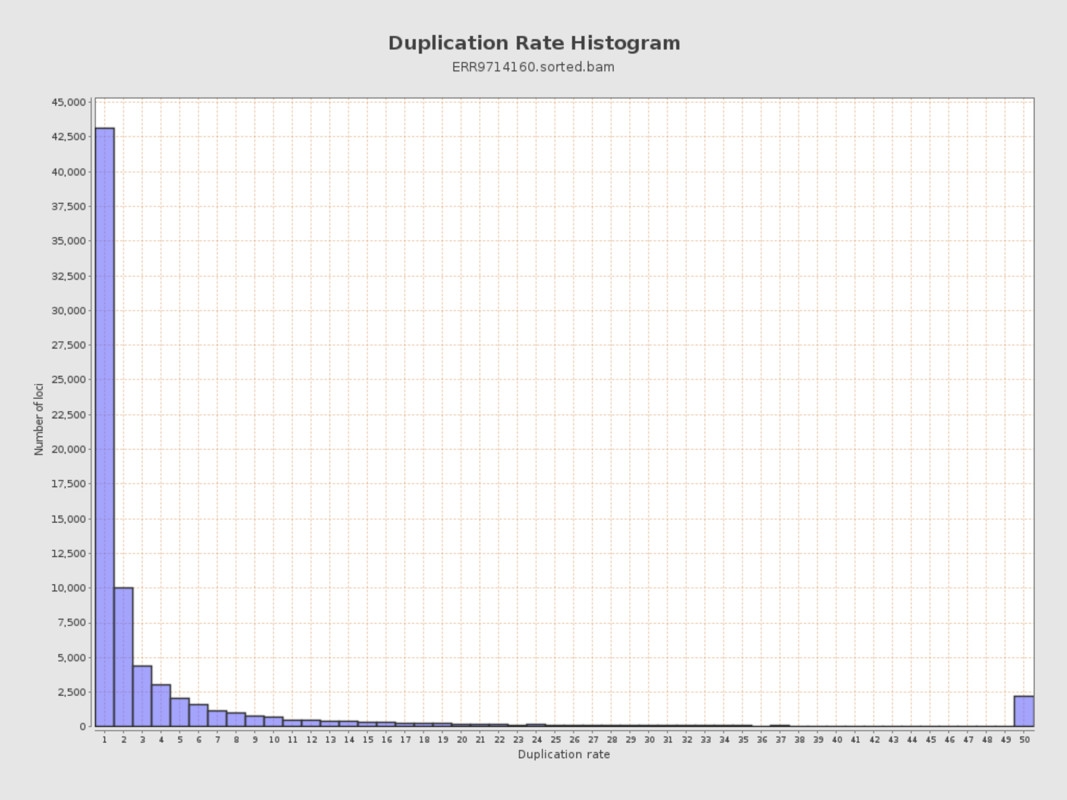
5. Results : Coverage Histogram (0-50X)



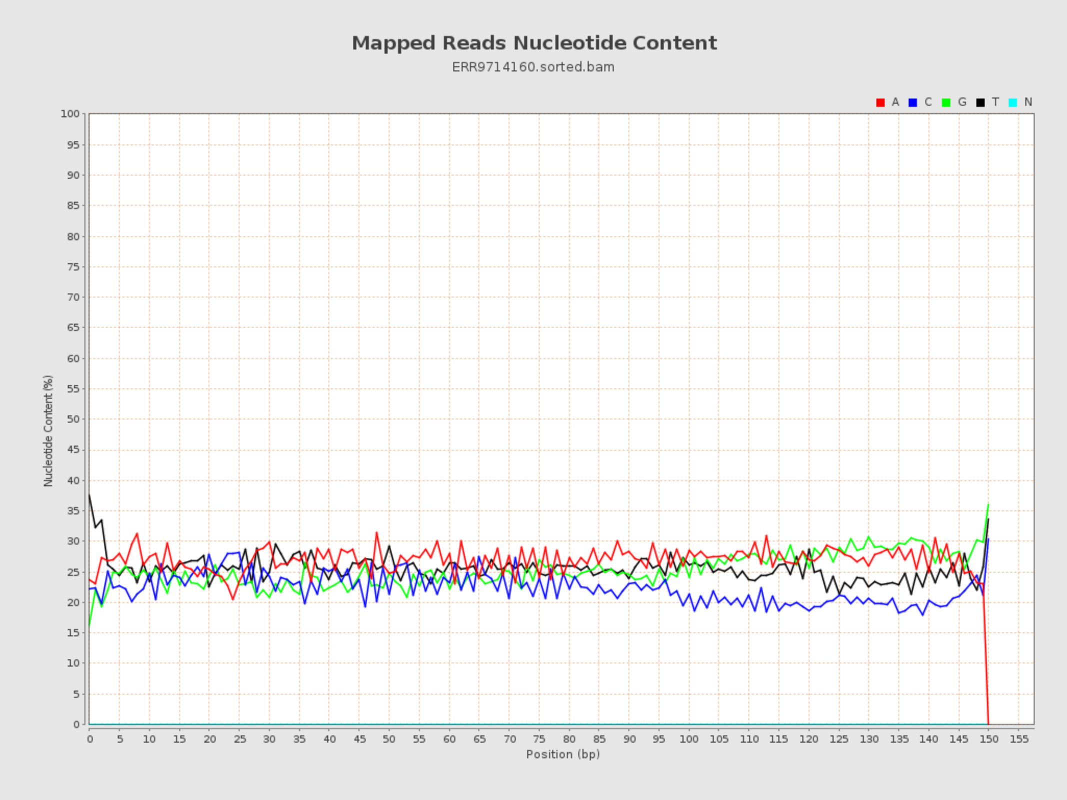
6. Results : Genome Fraction Coverage



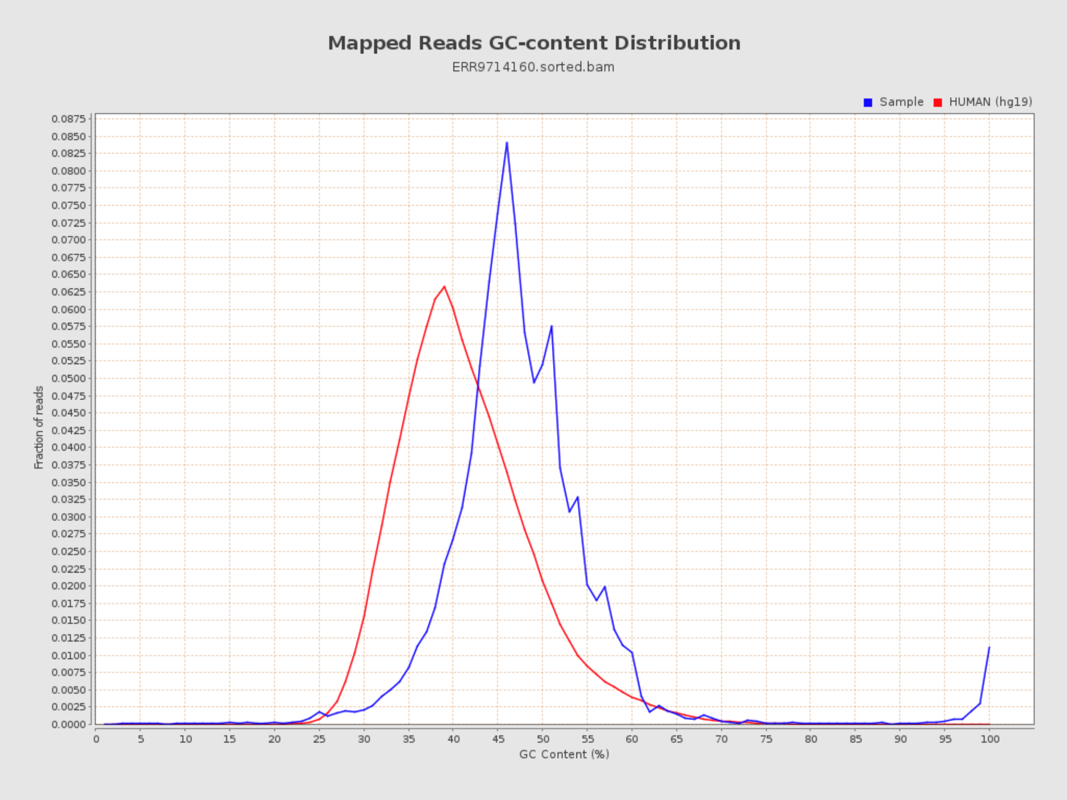
7. Results : Duplication Rate Histogram



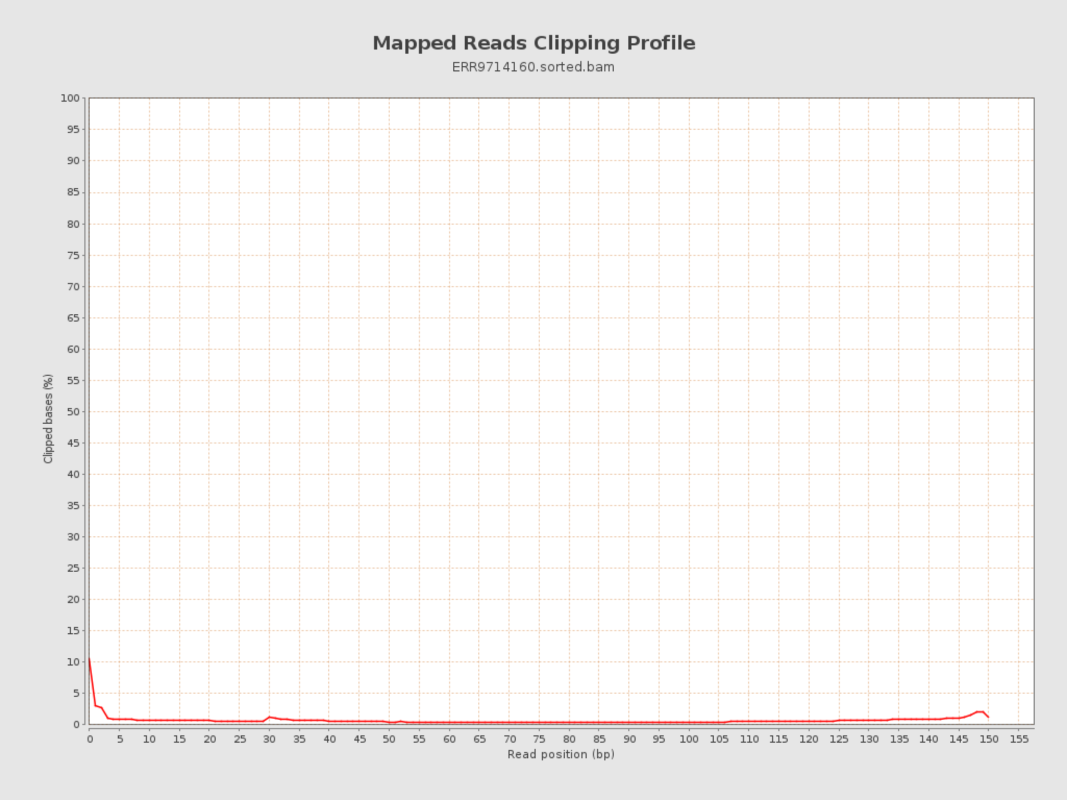
8. Results : Mapped Reads Nucleotide Content



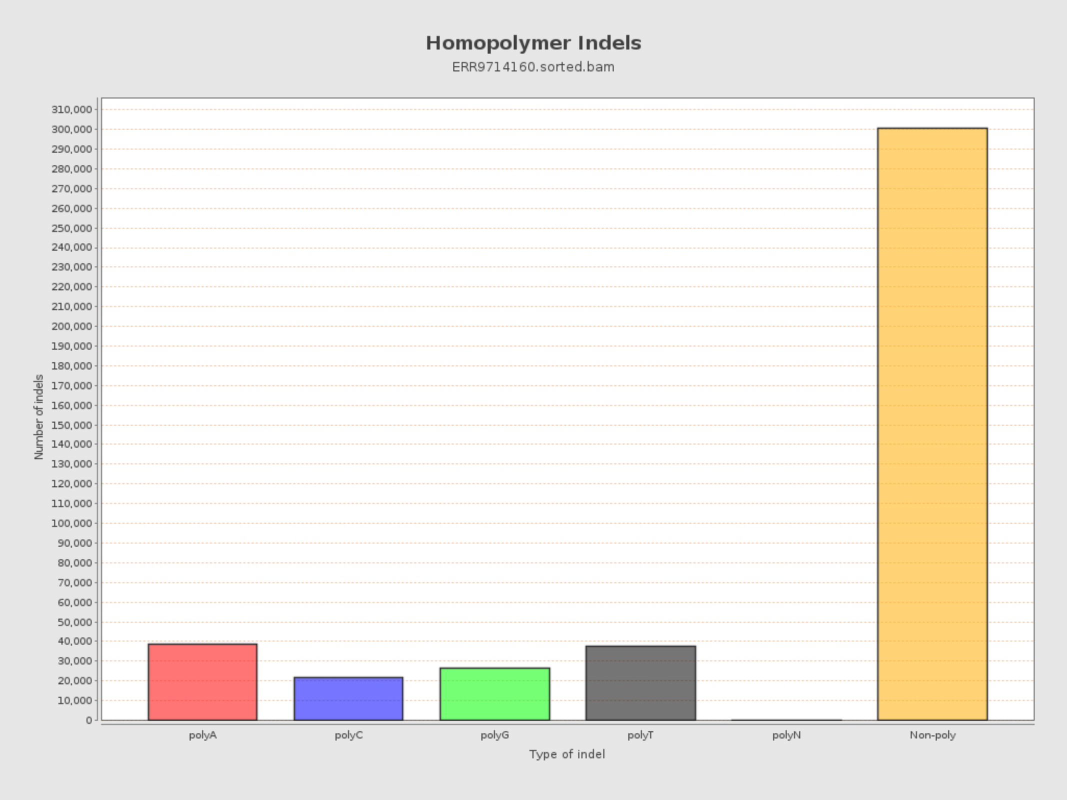
9. Results : Mapped Reads GC-content Distribution



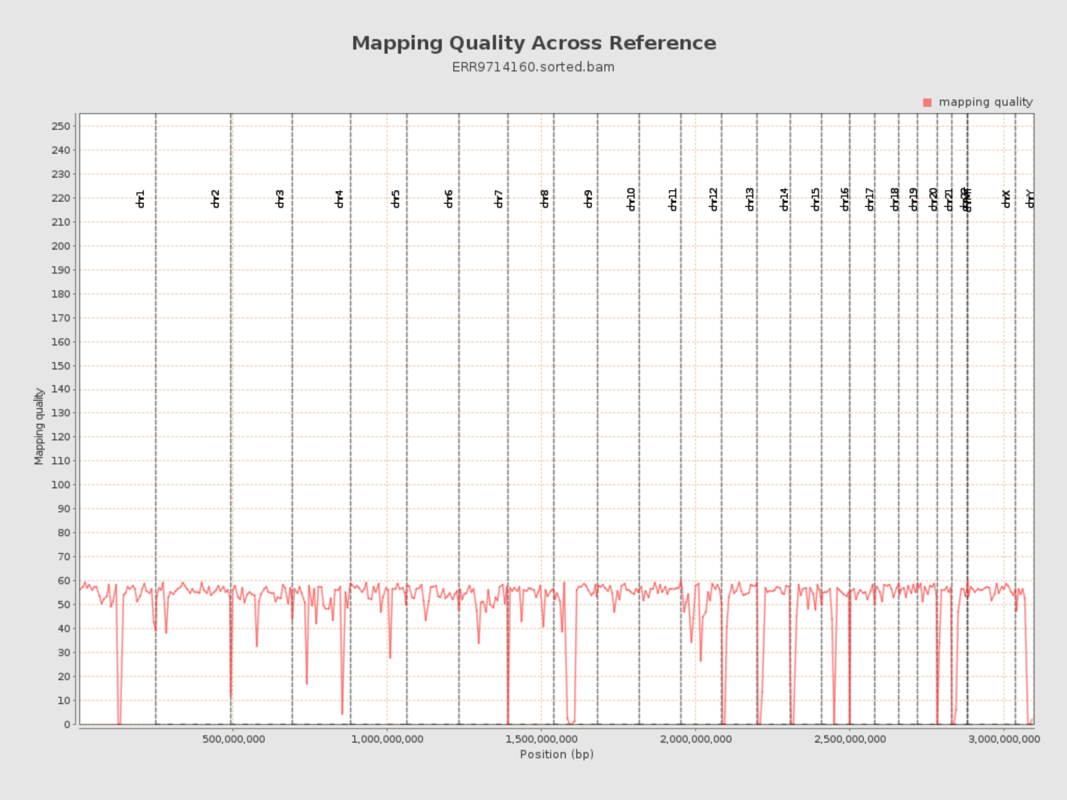
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram