Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 00:31:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714220.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_ERR9714220 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714220.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 00:31:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714220.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	136,618
Mapped reads	82,136 / 60.12%
Unmapped reads	54,482 / 39.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,022 / 1.48%
Read min/max/mean length	30 / 151 / 114.16
Duplicated reads (estimated)	62,510 / 45.76%
Duplication rate	41.77%
Clipped reads	75,263 / 55.09%

2.2. ACGT Content

Number/percentage of A's	2,560,904 / 25.6%
Number/percentage of C's	2,058,631 / 20.58%
Number/percentage of T's	2,402,864 / 24.02%
Number/percentage of G's	2,982,744 / 29.81%
Number/percentage of N's	90 / 0%
GC Percentage	50.39%

2.3. Coverage

Mean	0.0033

Standard Deviation	1.3983

2.4. Mapping Quality

Mean Mapping Quality	50.92

2.5. Mismatches and indels

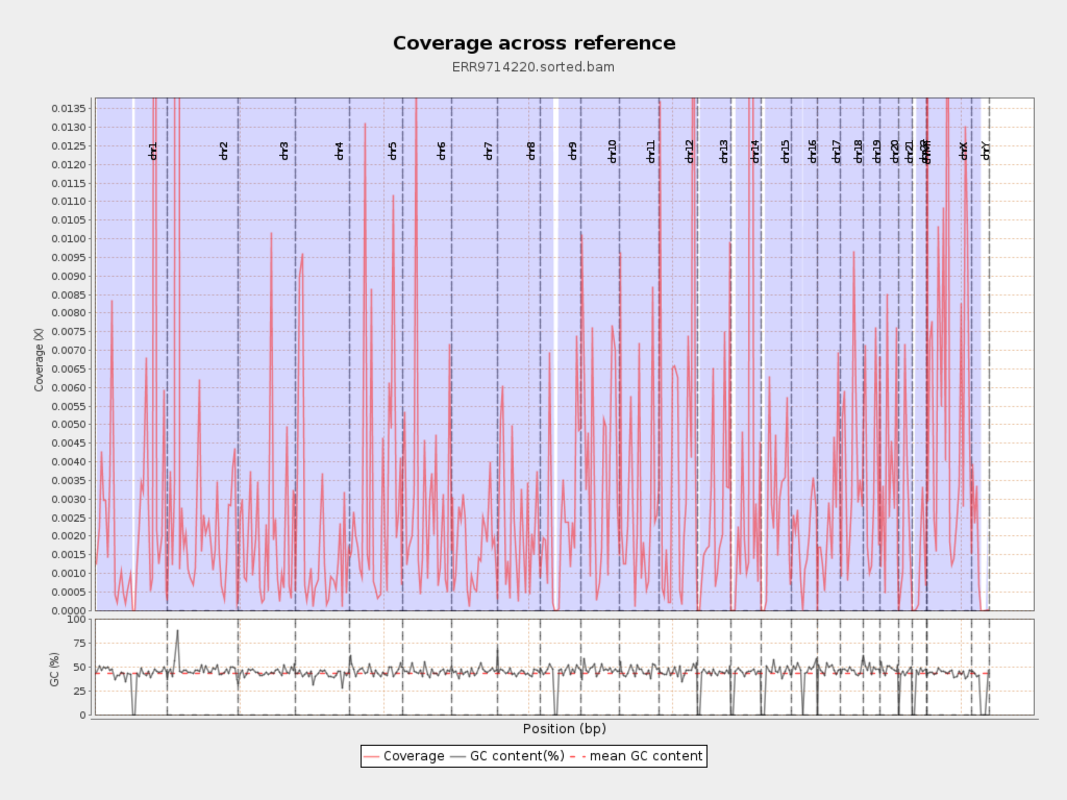
General error rate	4.48%
Mismatches	420,250
Insertions	10,583
Mapped reads with at least one insertion	12.29%
Deletions	34,343
Mapped reads with at least one deletion	39.61%
Homopolymer indels	29.76%

2.6. Chromosome stats

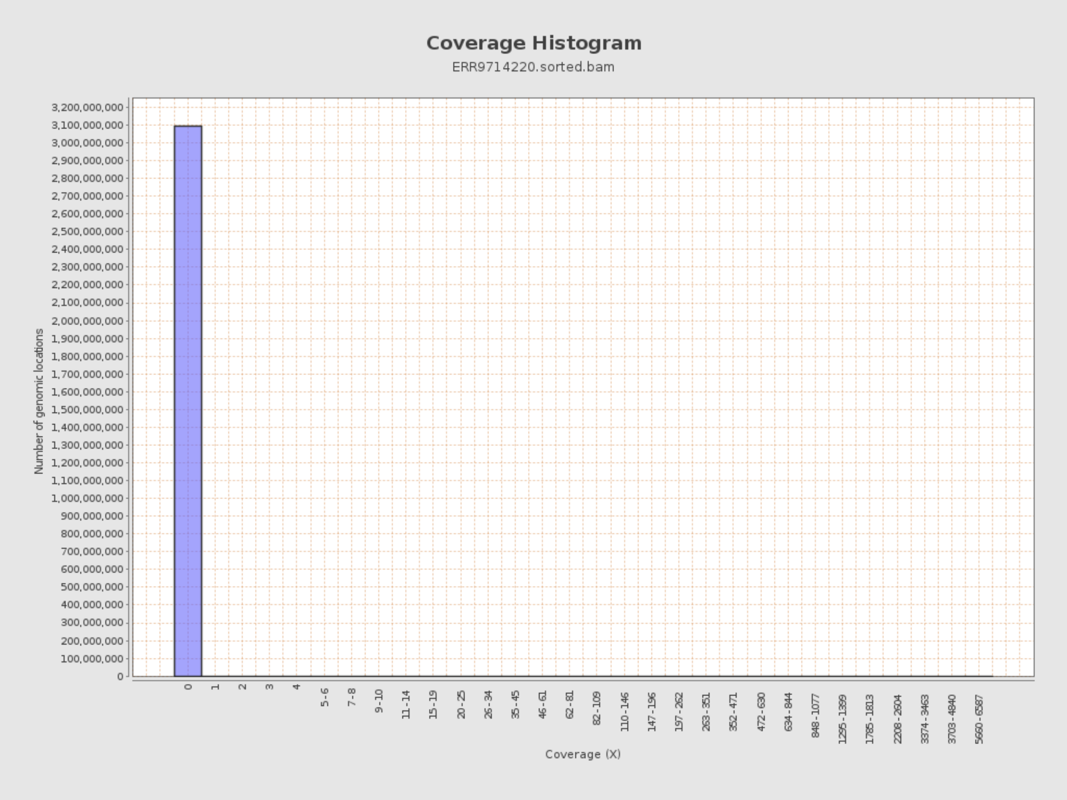
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	768256	0.0031	0.9434
chr2	243199373	1609935	0.0066	4.0677
chr3	198022430	393046	0.002	0.4405
chr4	191154276	356846	0.0019	0.5391
chr5	180915260	578904	0.0032	0.8124
chr6	171115067	518654	0.003	0.602
chr7	159138663	269346	0.0017	0.239

chr8	146364022	331021	0.0023	0.3853
chr9	141213431	324391	0.0023	0.4788
chr10	135534747	559349	0.0041	0.7507
chr11	135006516	376451	0.0028	0.5306
chr12	133851895	608505	0.0045	1.0135
chr13	115169878	290554	0.0025	0.52
chr14	107349540	568662	0.0053	2.9429
chr15	102531392	273600	0.0027	0.4034
chr16	90354753	175047	0.0019	0.2671
chr17	81195210	204356	0.0025	0.4037
chr18	78077248	316147	0.004	0.8304
chr19	59128983	207922	0.0035	0.4242
chr20	63025520	241594	0.0038	0.5936
chr21	48129895	115248	0.0024	0.5245
chr22	51304566	54026	0.0011	0.1458
chrMT	16571	62925	3.7973	31.2079
chrX	155270560	960631	0.0062	0.7933
chrY	59373566	69964	0.0012	0.2689

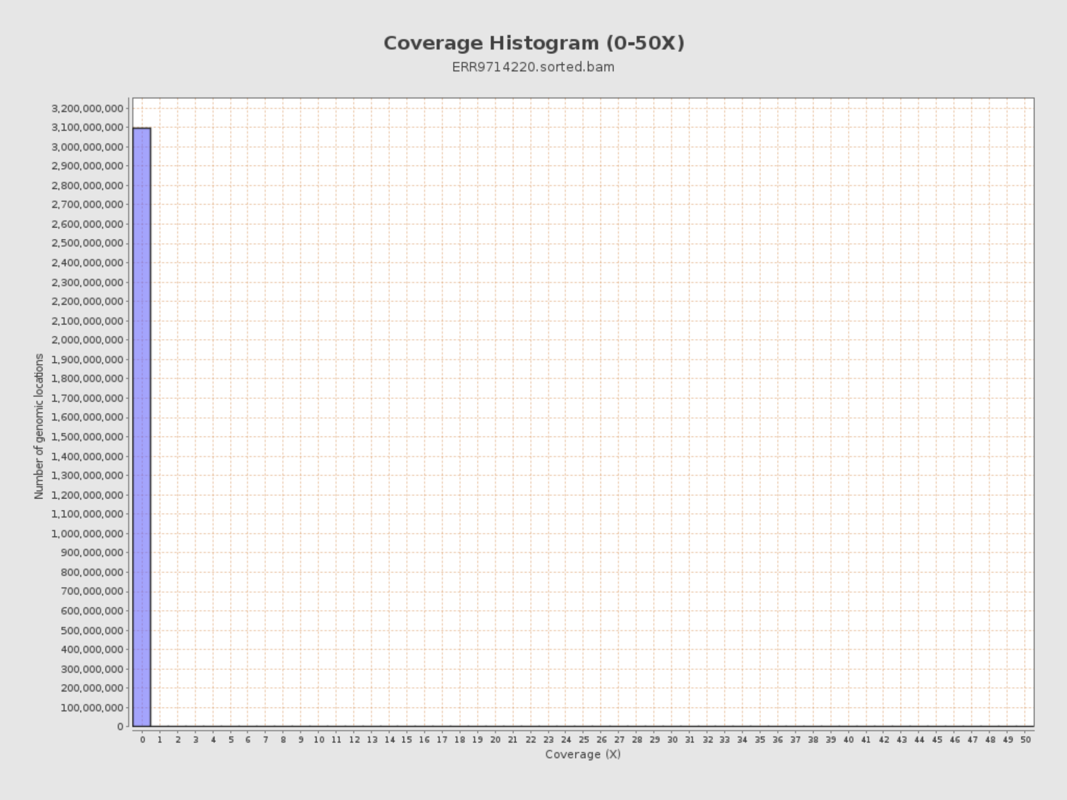
3. Results : Coverage across reference



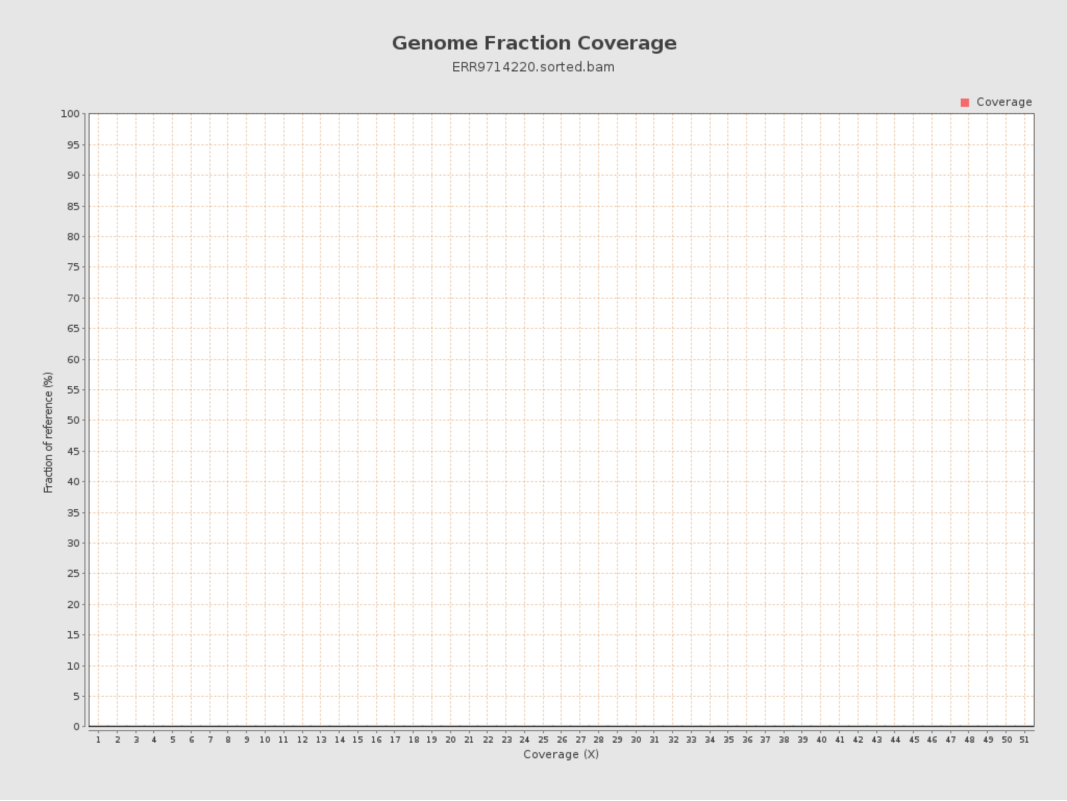
4. Results : Coverage Histogram



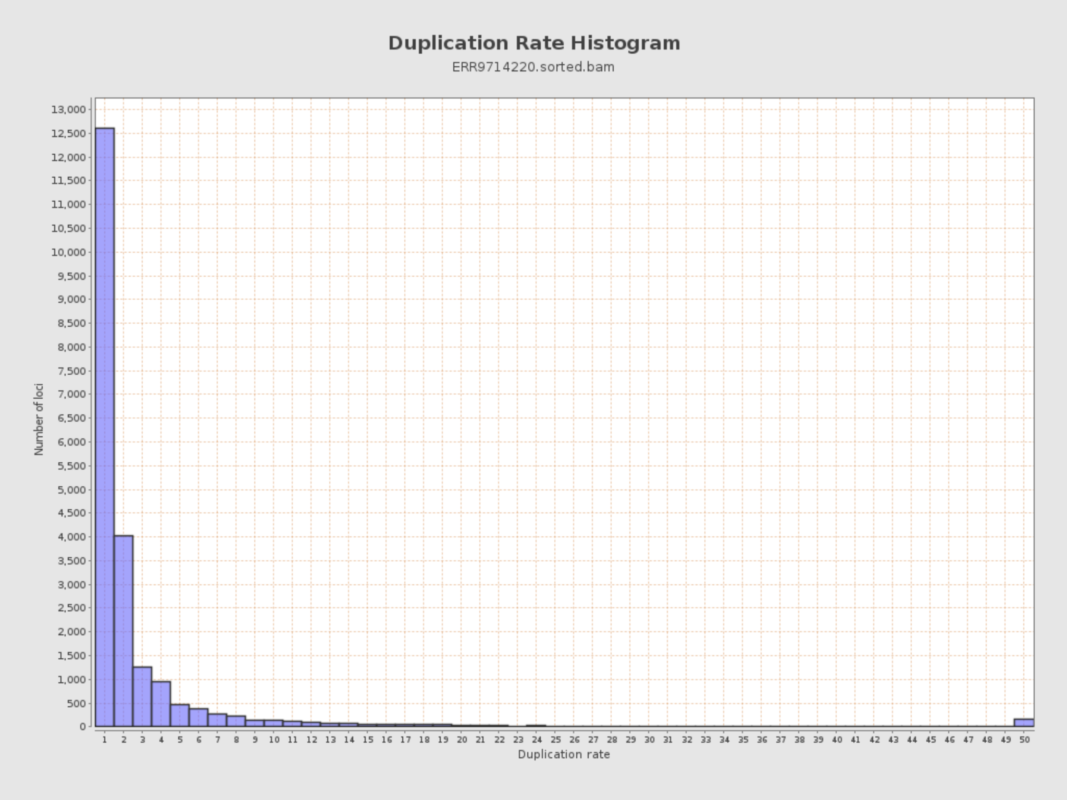
5. Results : Coverage Histogram (0-50X)



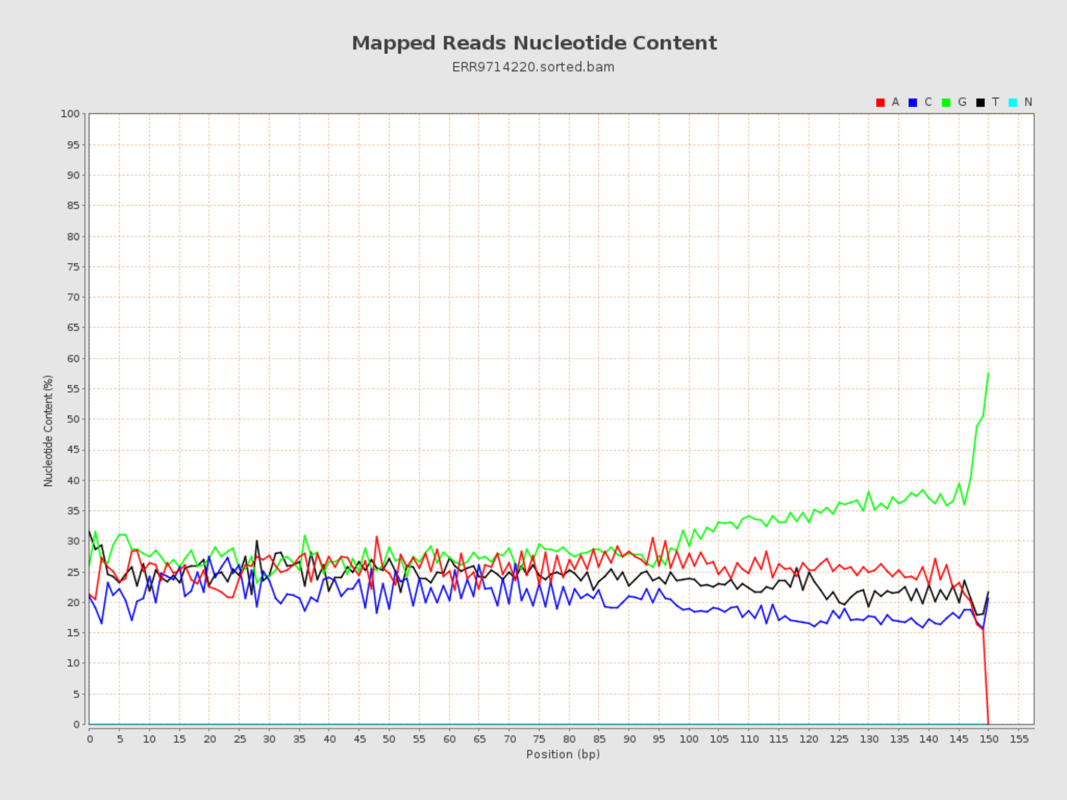
6. Results : Genome Fraction Coverage



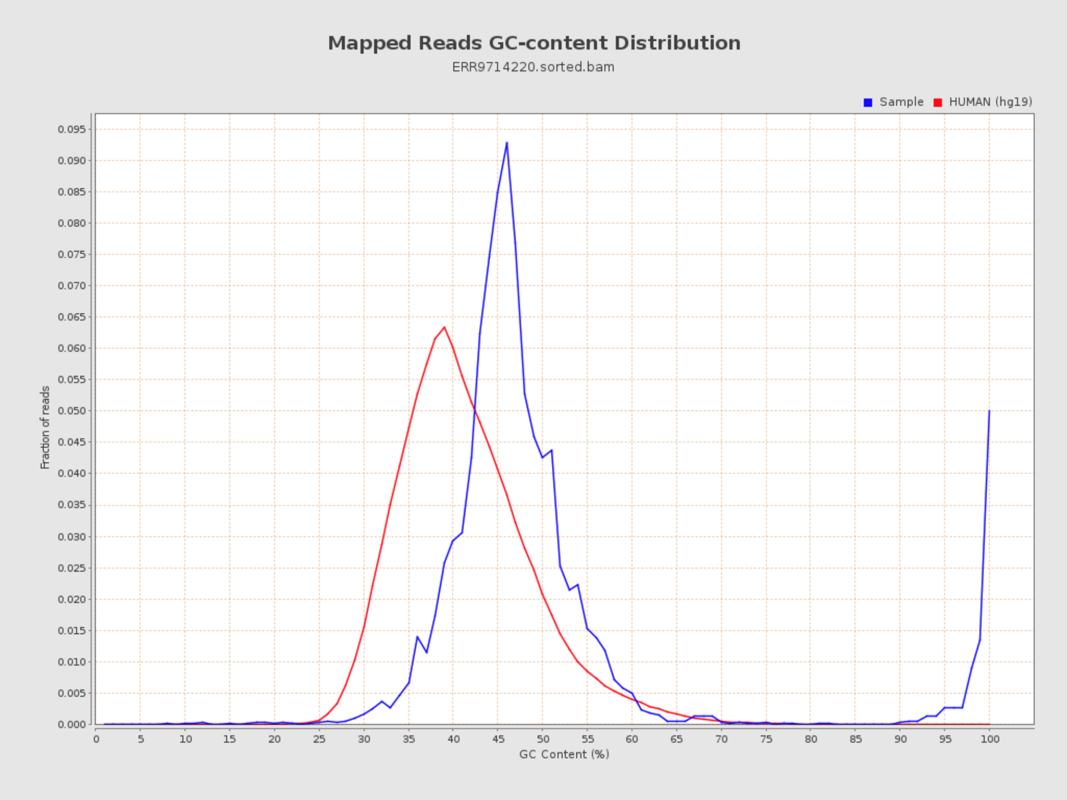
7. Results : Duplication Rate Histogram



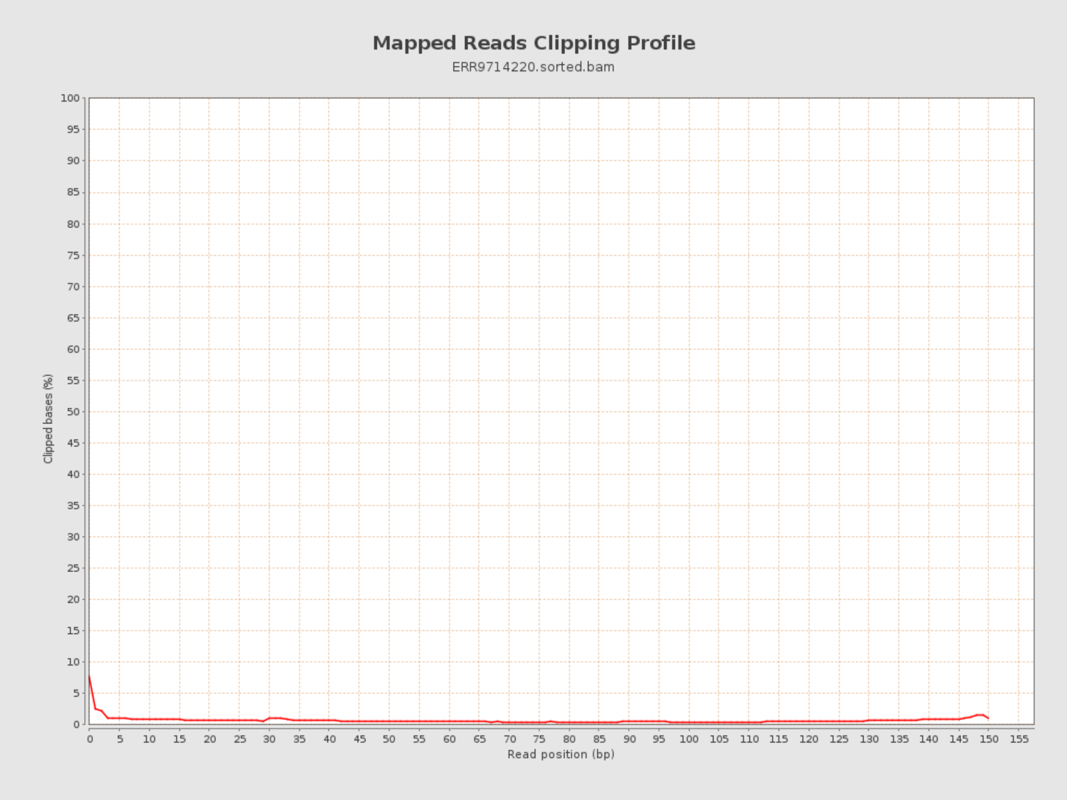
8. Results : Mapped Reads Nucleotide Content



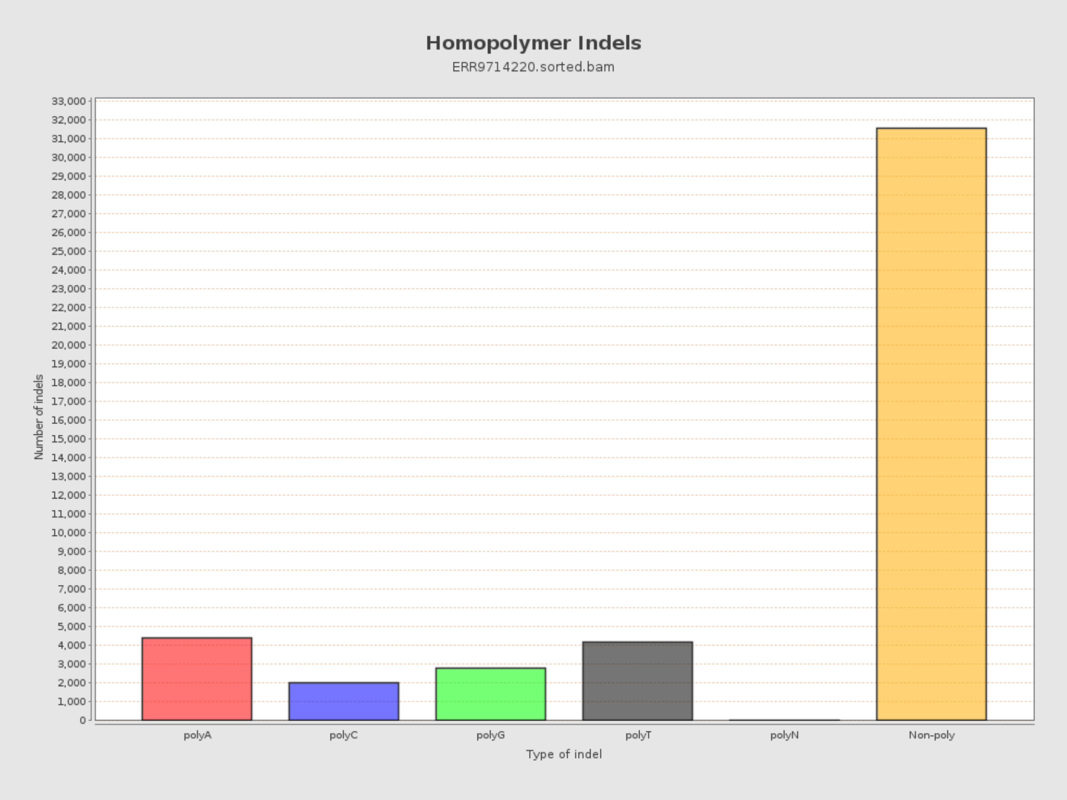
9. Results : Mapped Reads GC-content Distribution



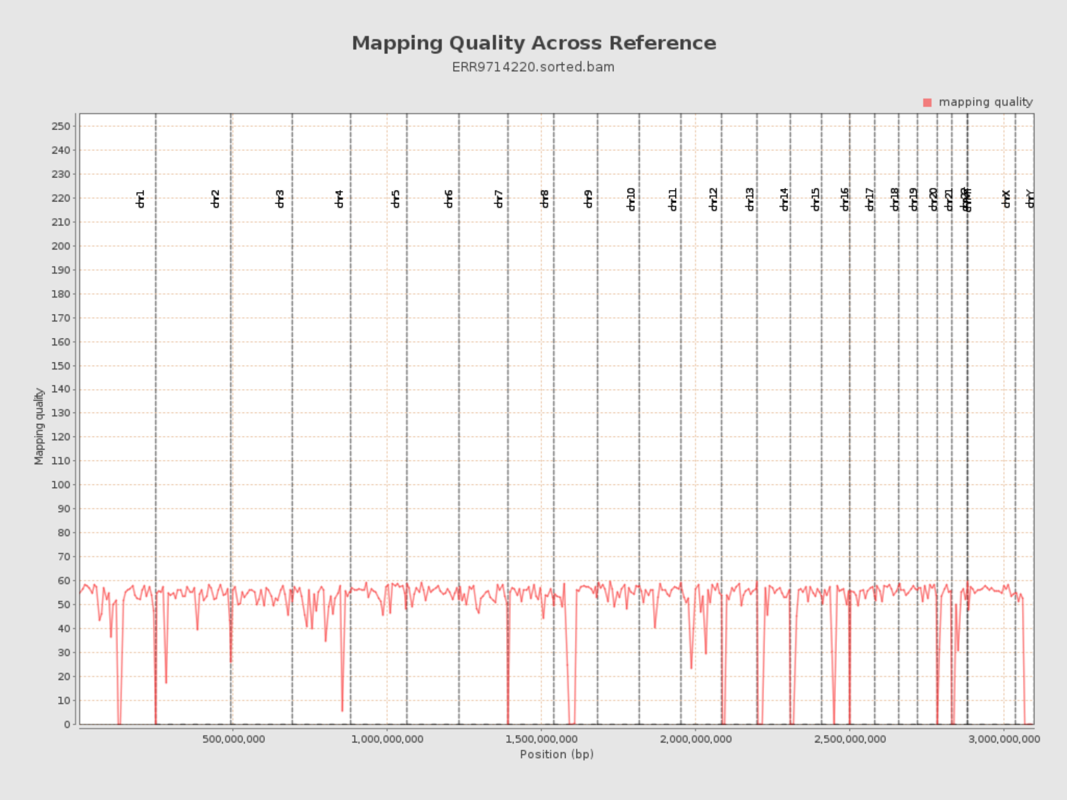
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram