Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 19:35:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714105.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_ERR9714105 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714105.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 19:35:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714105.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	549,590
Mapped reads	471,597 / 85.81%
Unmapped reads	77,993 / 14.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,904 / 3.8%
Read min/max/mean length	30 / 151 / 136.8
Duplicated reads (estimated)	463,461 / 84.33%
Duplication rate	34.68%
Clipped reads	457,669 / 83.27%

2.2. ACGT Content

Number/percentage of A's	16,576,260 / 28.73%
Number/percentage of C's	11,624,327 / 20.15%
Number/percentage of T's	15,770,055 / 27.33%
Number/percentage of G's	13,723,346 / 23.79%
Number/percentage of N's	435 / 0%
GC Percentage	43.93%

2.3. Coverage

Mean	0.019

Standard Deviation	19.2574

2.4. Mapping Quality

Mean Mapping Quality	36.13

2.5. Mismatches and indels

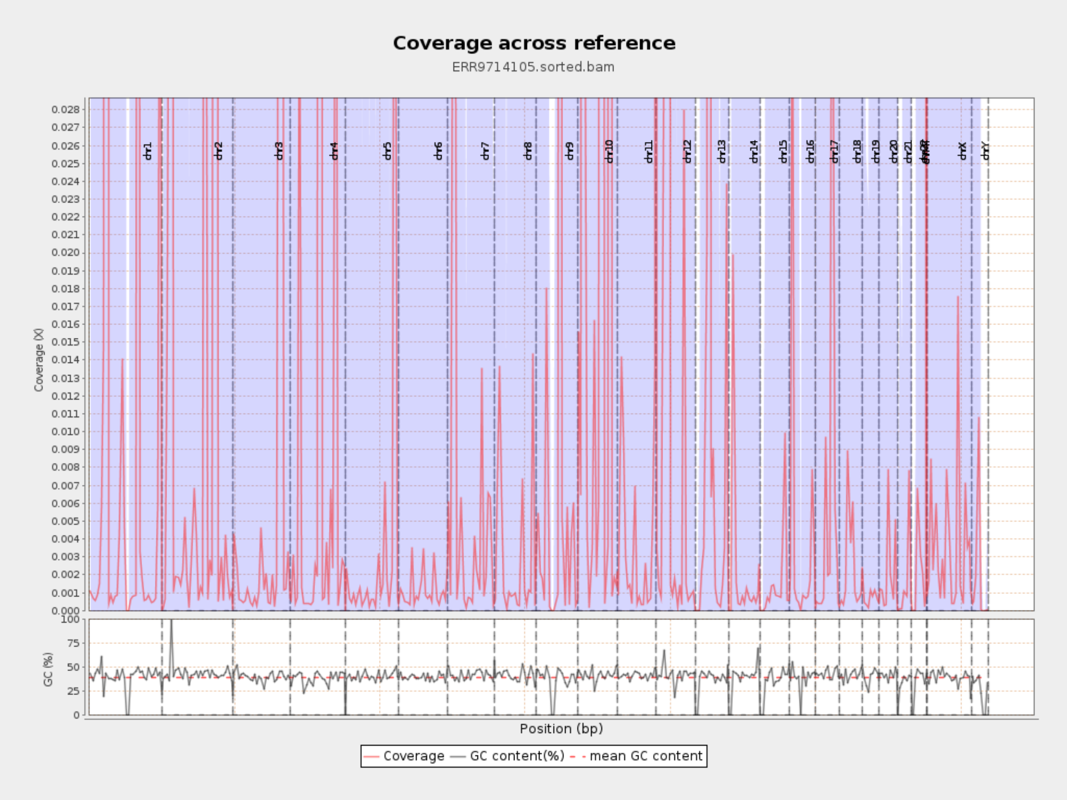
General error rate	3.8%
Mismatches	2,084,636
Insertions	51,607
Mapped reads with at least one insertion	10.58%
Deletions	180,735
Mapped reads with at least one deletion	36.55%
Homopolymer indels	28.04%

2.6. Chromosome stats

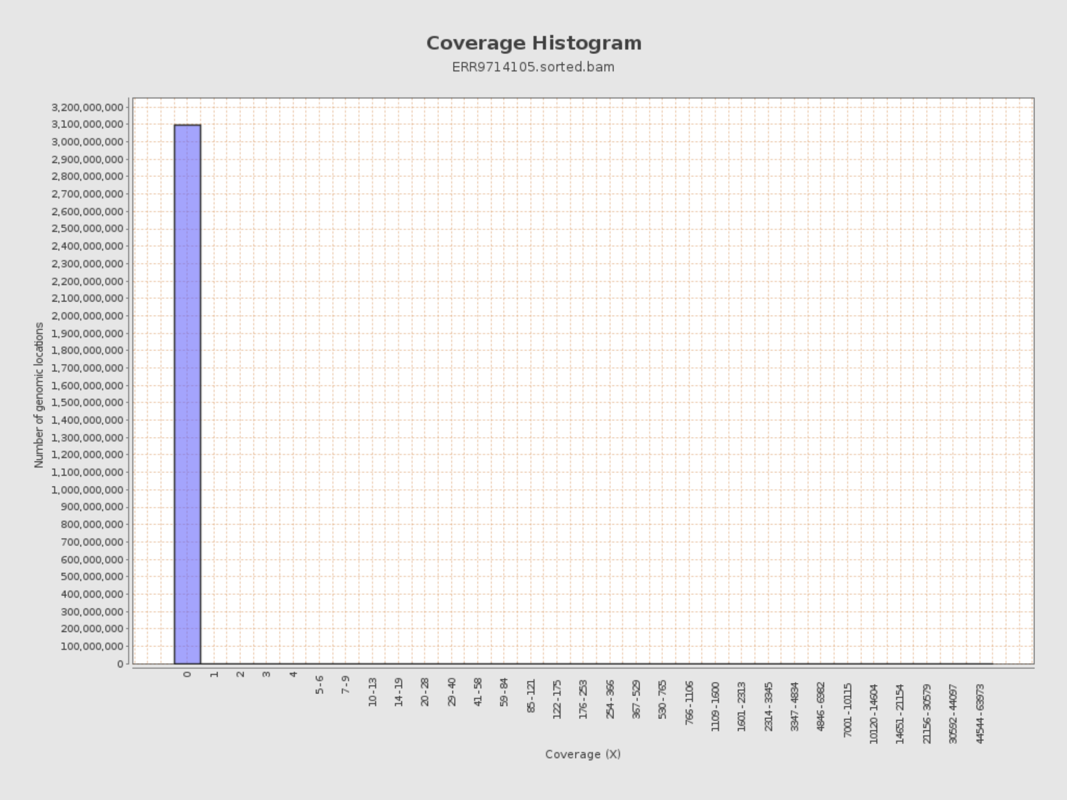
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11549671	0.0463	36.0421
chr2	243199373	5564781	0.0229	11.4251
chr3	198022430	1693515	0.0086	5.9311
chr4	191154276	3801209	0.0199	16.3211
chr5	180915260	793516	0.0044	1.7465
chr6	171115067	192542	0.0011	0.2568
chr7	159138663	1128731	0.0071	2.429

chr8	146364022	457417	0.0031	0.6624
chr9	141213431	1971561	0.014	10.1573
chr10	135534747	14388355	0.1062	46.6683
chr11	135006516	1121490	0.0083	4.541
chr12	133851895	10702609	0.08	54.9228
chr13	115169878	2663266	0.0231	11.4912
chr14	107349540	219691	0.002	0.9793
chr15	102531392	170317	0.0017	0.4034
chr16	90354753	451369	0.005	2.108
chr17	81195210	564932	0.007	3.0333
chr18	78077248	184231	0.0024	0.628
chr19	59128983	43080	0.0007	0.1089
chr20	63025520	145325	0.0023	0.8381
chr21	48129895	80143	0.0017	0.4347
chr22	51304566	97585	0.0019	0.5642
chrMT	16571	119579	7.2162	59.6457
chrX	155270560	567203	0.0037	0.6836
chrY	59373566	104137	0.0018	0.7101

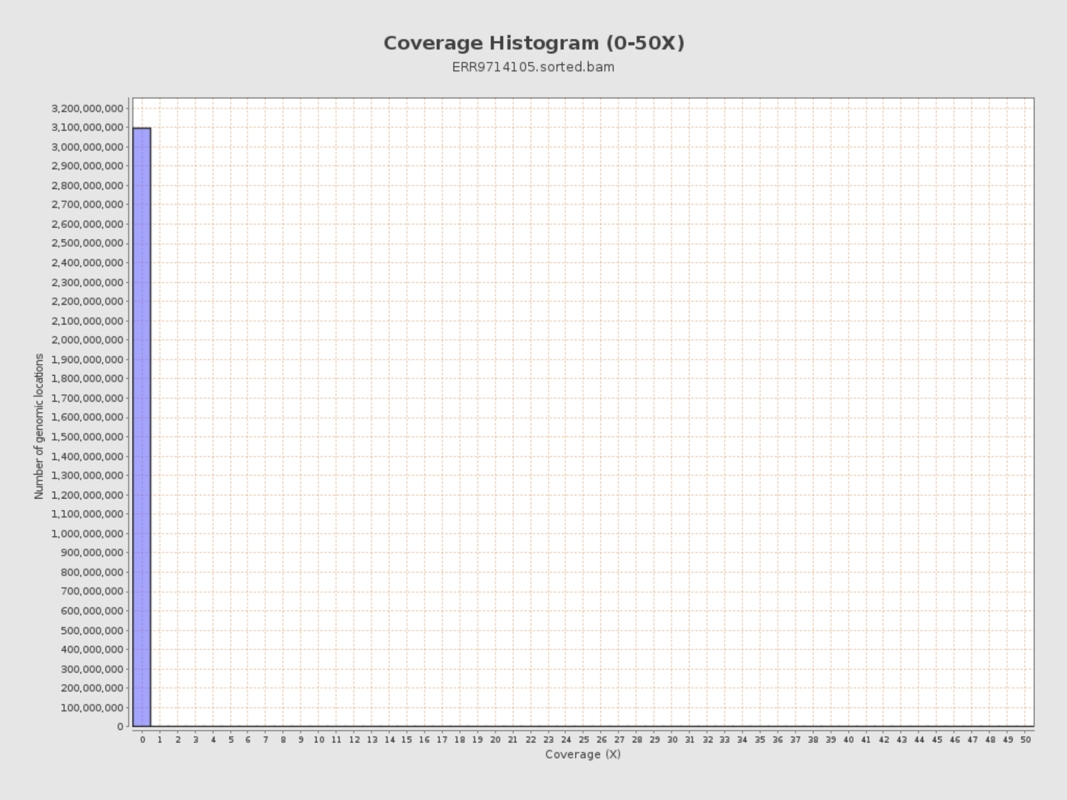
3. Results : Coverage across reference



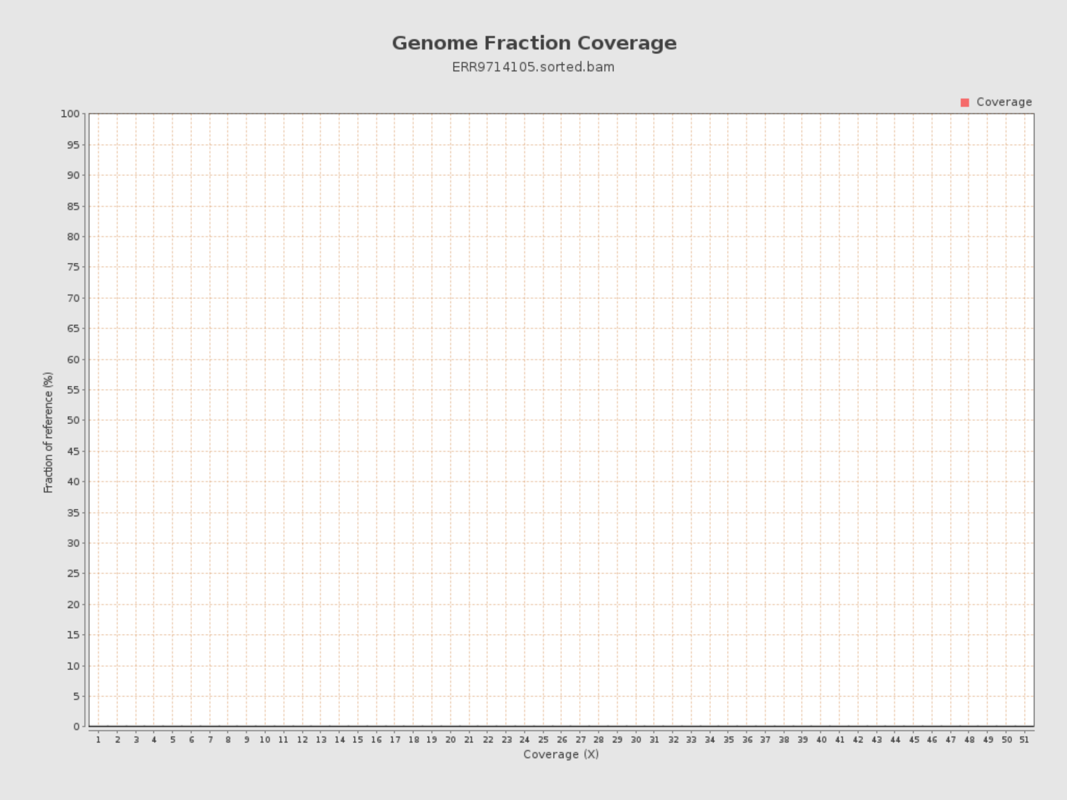
4. Results : Coverage Histogram



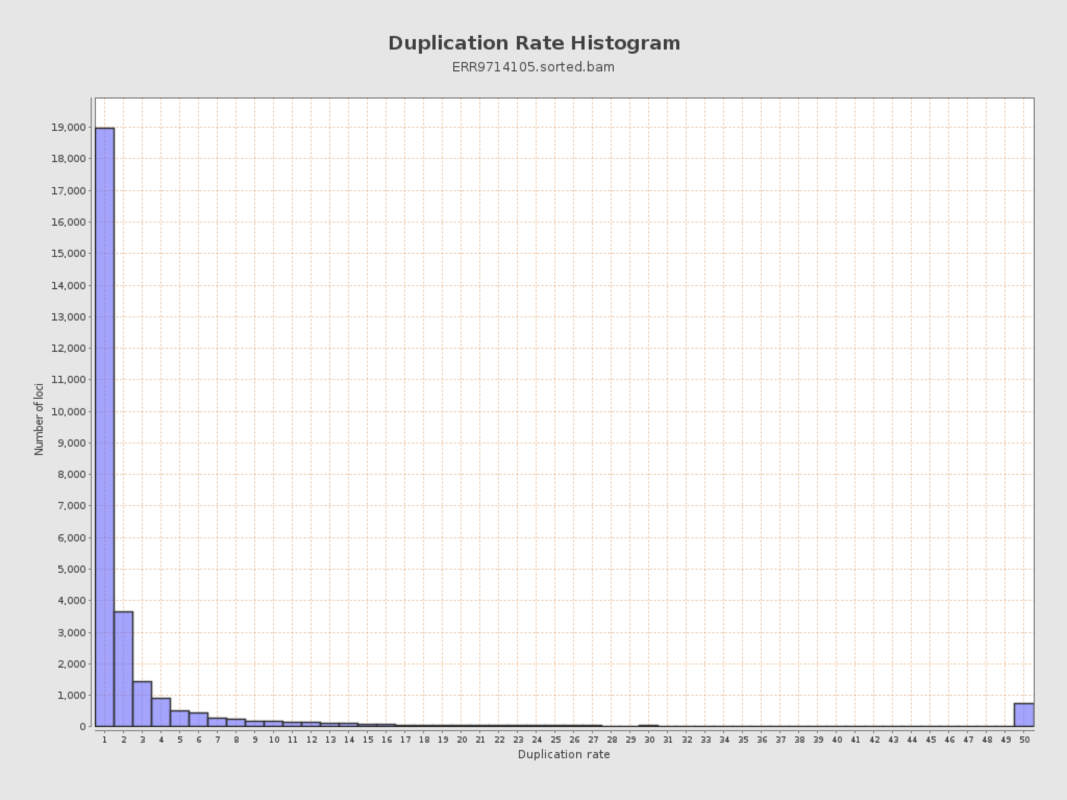
5. Results : Coverage Histogram (0-50X)



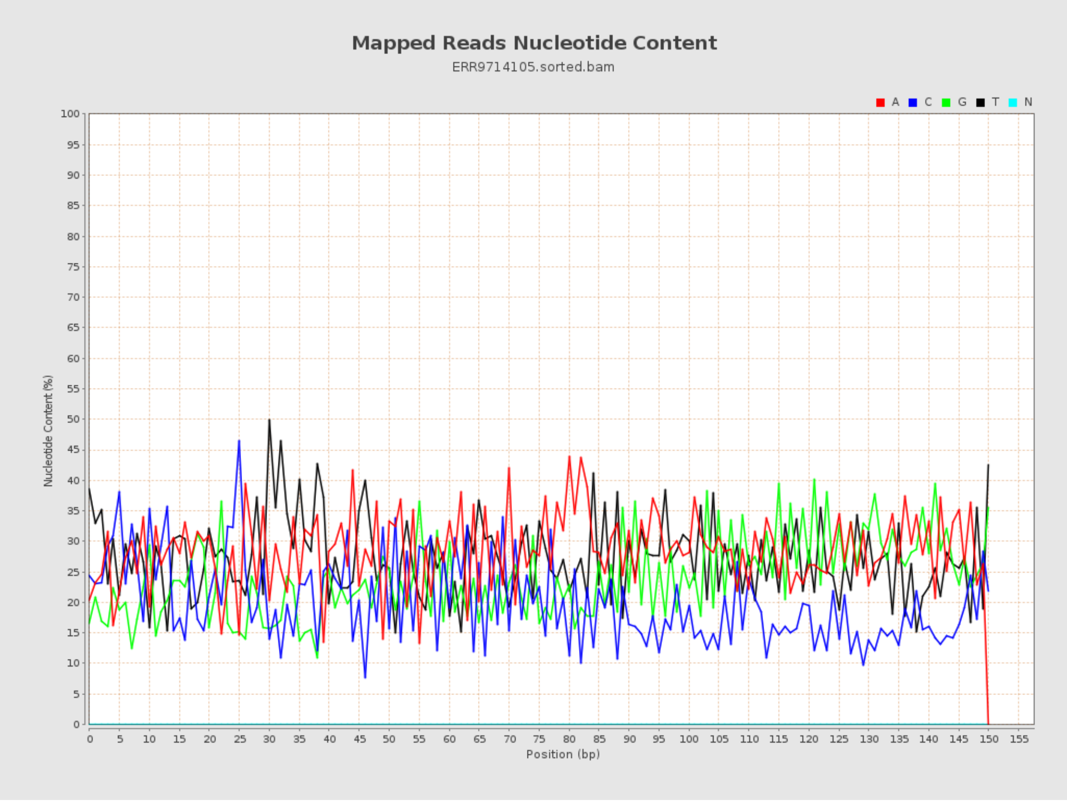
6. Results : Genome Fraction Coverage



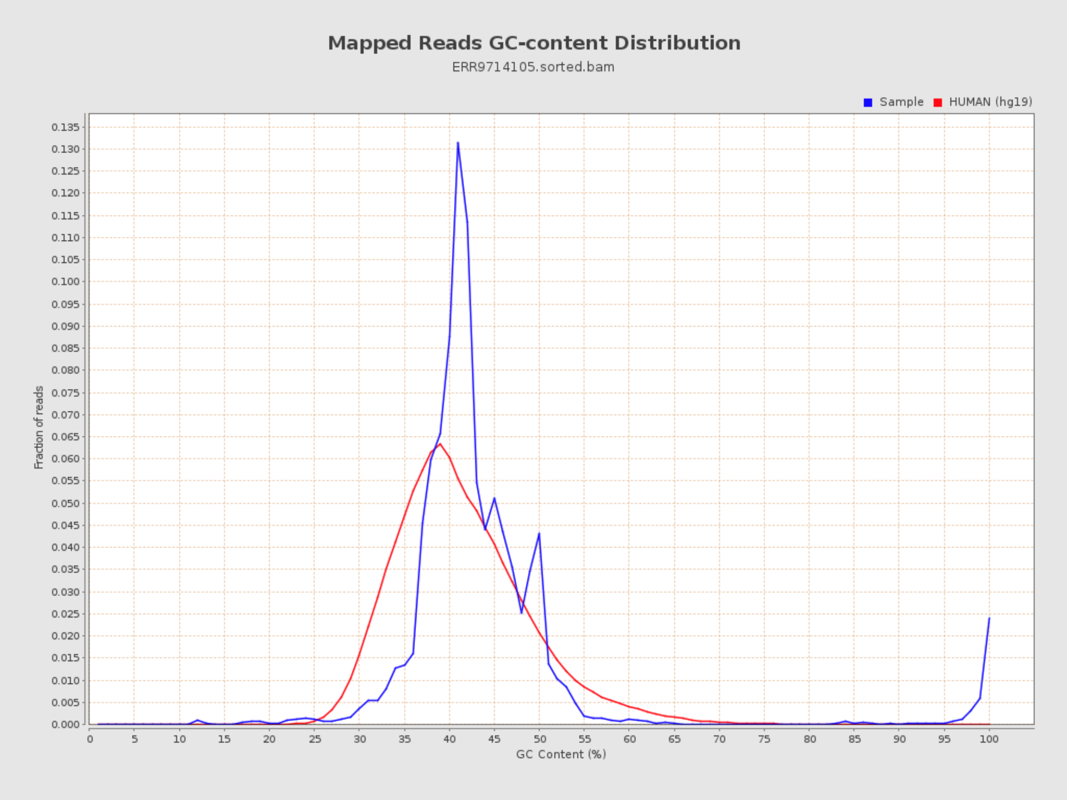
7. Results : Duplication Rate Histogram



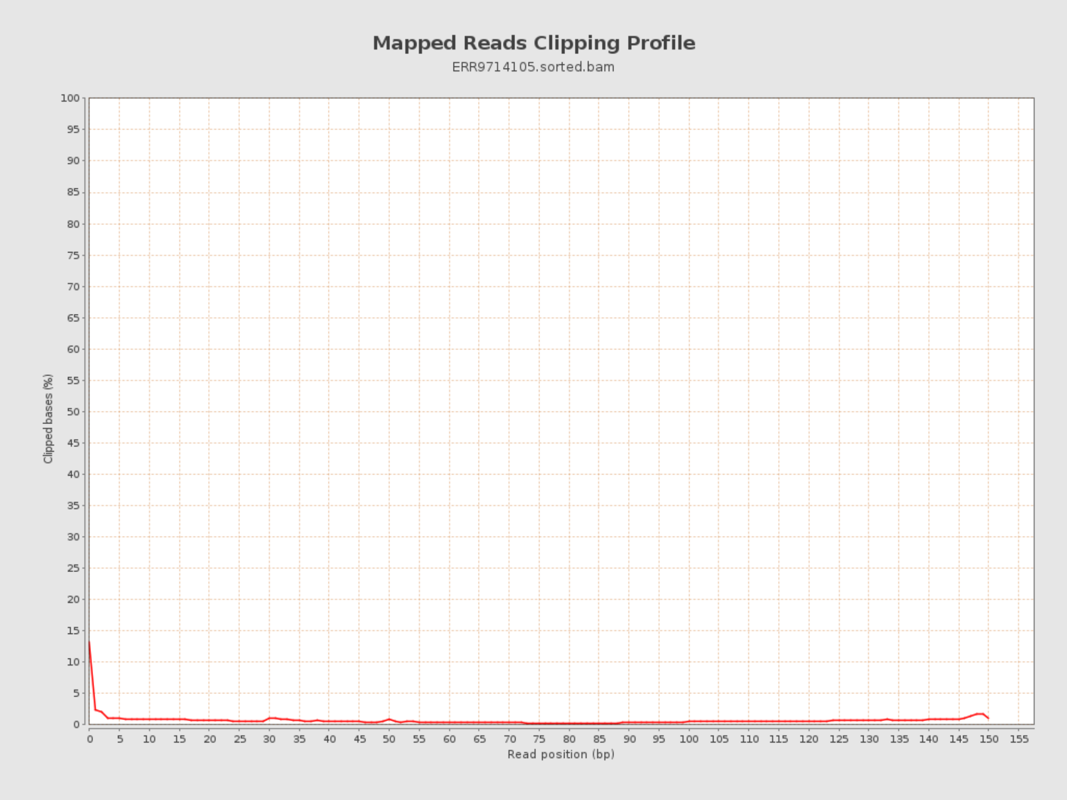
8. Results : Mapped Reads Nucleotide Content



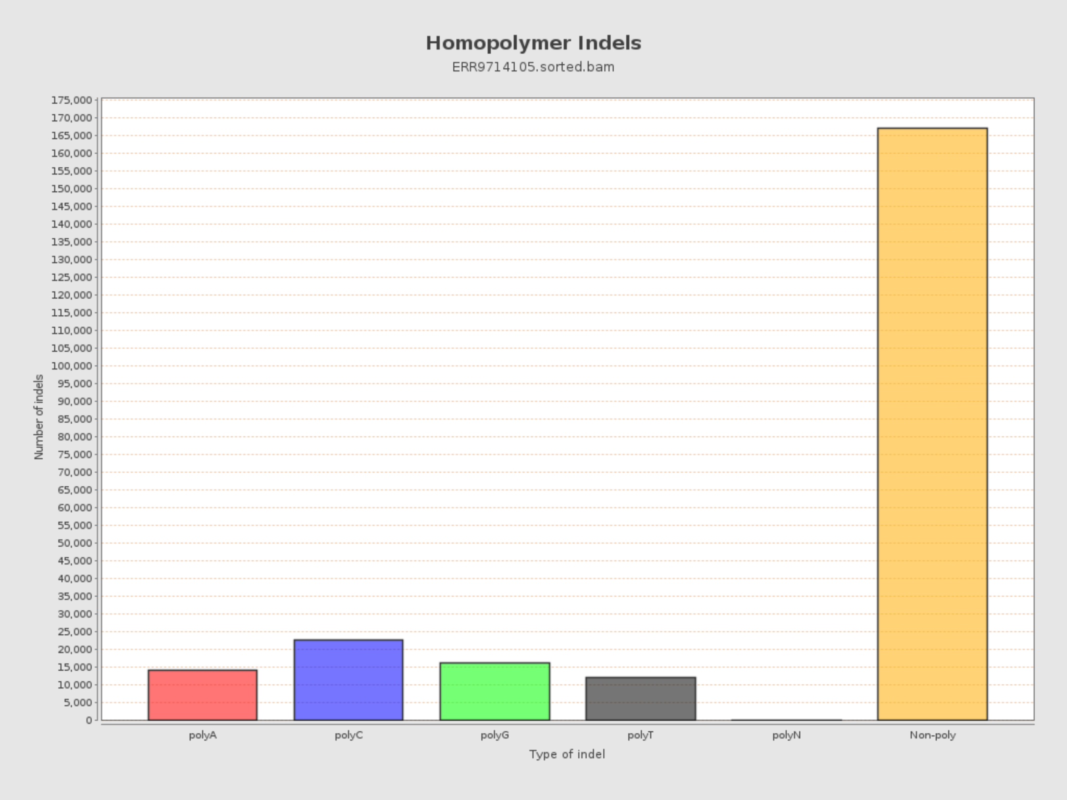
9. Results : Mapped Reads GC-content Distribution



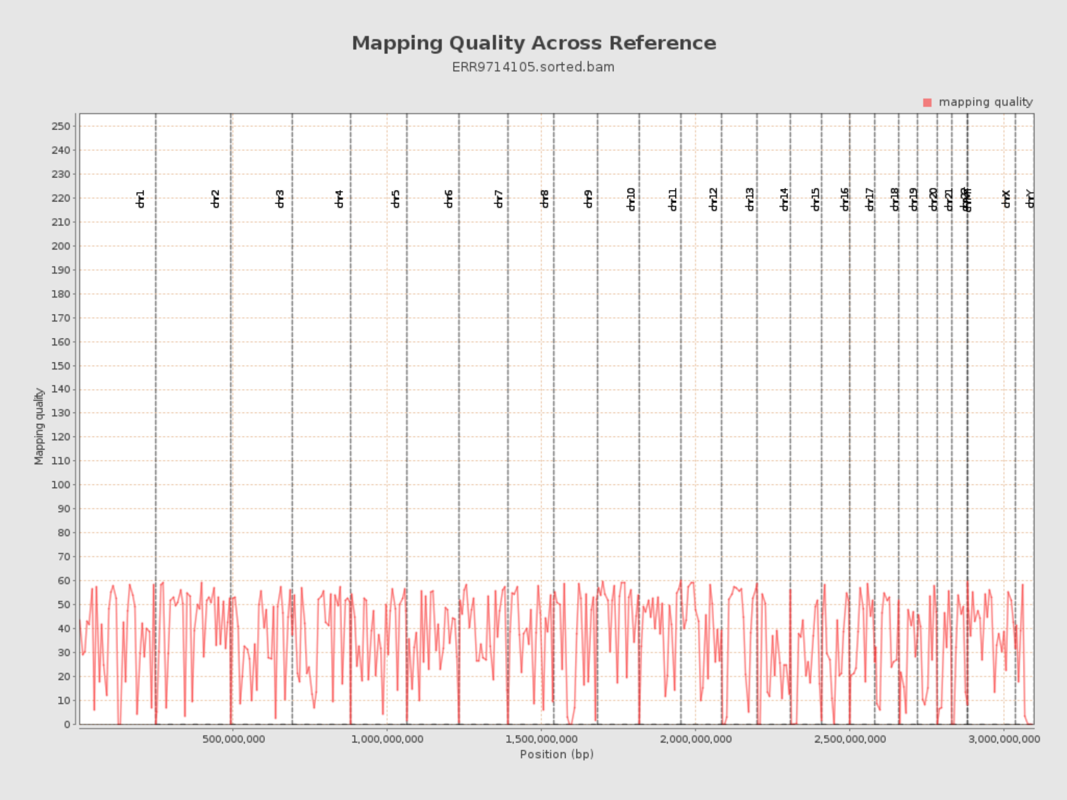
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram