Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 20:33:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714126.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_ERR9714126 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714126.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 20:32:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714126.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	627,396
Mapped reads	548,460 / 87.42%
Unmapped reads	78,936 / 12.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,457 / 2.62%
Read min/max/mean length	30 / 151 / 138.57
Duplicated reads (estimated)	476,712 / 75.98%
Duplication rate	44.45%
Clipped reads	510,423 / 81.36%

2.2. ACGT Content

Number/percentage of A's	19,987,153 / 28.4%
Number/percentage of C's	14,663,724 / 20.83%
Number/percentage of T's	19,022,367 / 27.02%
Number/percentage of G's	16,715,546 / 23.75%
Number/percentage of N's	482 / 0%
GC Percentage	44.58%

2.3. Coverage

Mean	0.0233

Standard Deviation	4.3266

2.4. Mapping Quality

Mean Mapping Quality	51.61

2.5. Mismatches and indels

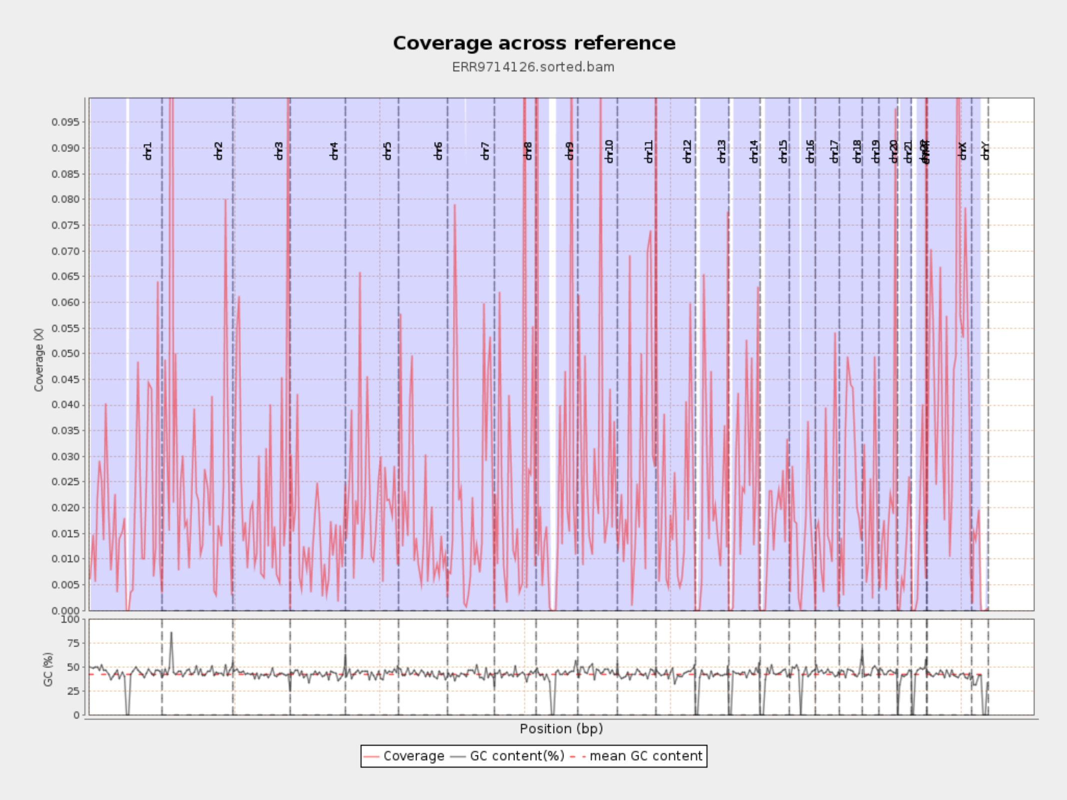
General error rate	4.69%
Mismatches	3,083,651
Insertions	80,626
Mapped reads with at least one insertion	14.16%
Deletions	280,026
Mapped reads with at least one deletion	47.24%
Homopolymer indels	29.92%

2.6. Chromosome stats

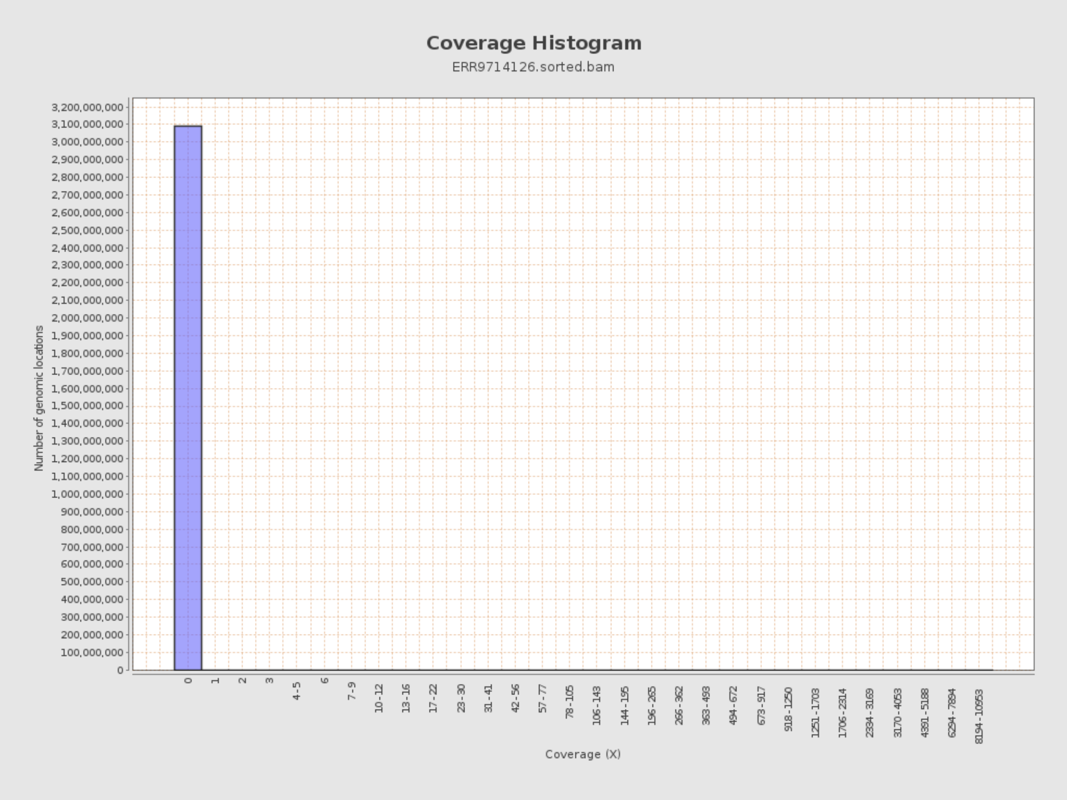
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4693168	0.0188	2.8556
chr2	243199373	7708161	0.0317	7.8482
chr3	198022430	4775137	0.0241	4.759
chr4	191154276	2590914	0.0136	1.7587
chr5	180915260	4075762	0.0225	4.0468
chr6	171115067	2962380	0.0173	2.4044
chr7	159138663	3731752	0.0234	4.263

chr8	146364022	4003854	0.0274	5.884
chr9	141213431	3042298	0.0215	4.6275
chr10	135534747	4193513	0.0309	4.3247
chr11	135006516	3858145	0.0286	5.0166
chr12	133851895	2680378	0.02	2.5712
chr13	115169878	2436849	0.0212	3.1534
chr14	107349540	2774284	0.0258	4.3791
chr15	102531392	1638363	0.016	1.8302
chr16	90354753	1296310	0.0143	1.6708
chr17	81195210	1507817	0.0186	3.2047
chr18	78077248	2095095	0.0268	4.0328
chr19	59128983	1114685	0.0189	2.7504
chr20	63025520	1512192	0.024	5.2294
chr21	48129895	480880	0.01	1.2291
chr22	51304566	629043	0.0123	2.1652
chrMT	16571	267769	16.1589	129.9079
chrX	155270560	7660419	0.0493	5.821
chrY	59373566	386050	0.0065	1.7245

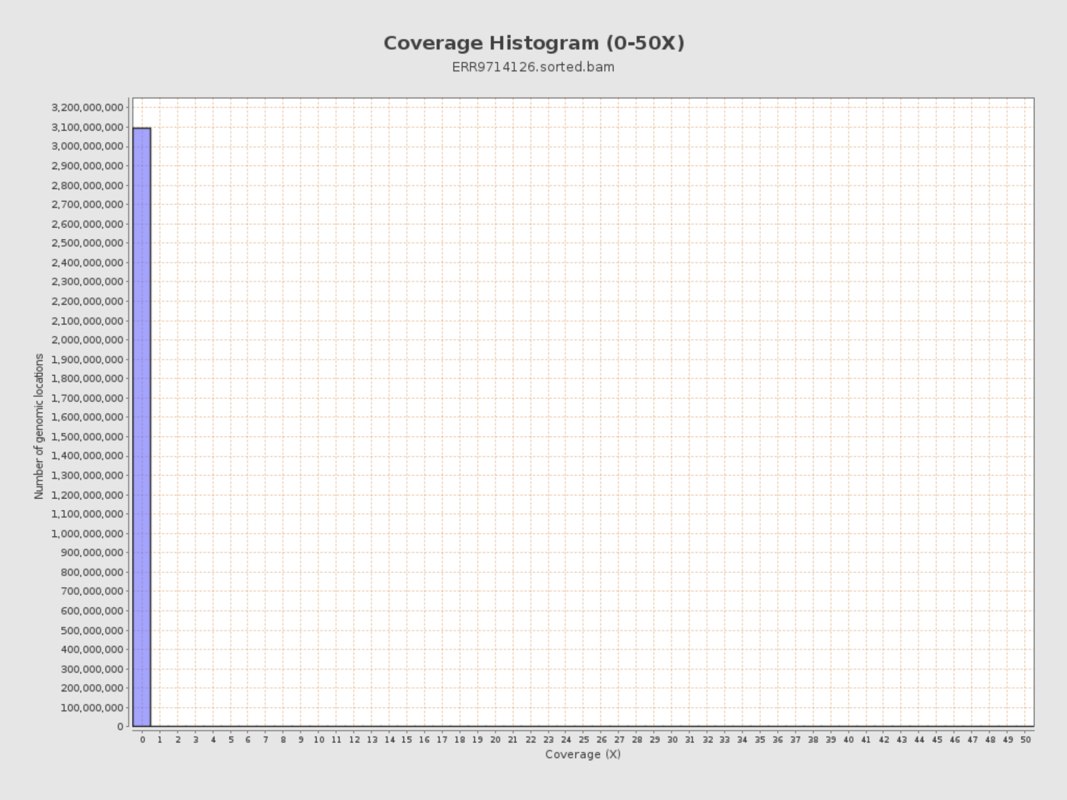
3. Results : Coverage across reference



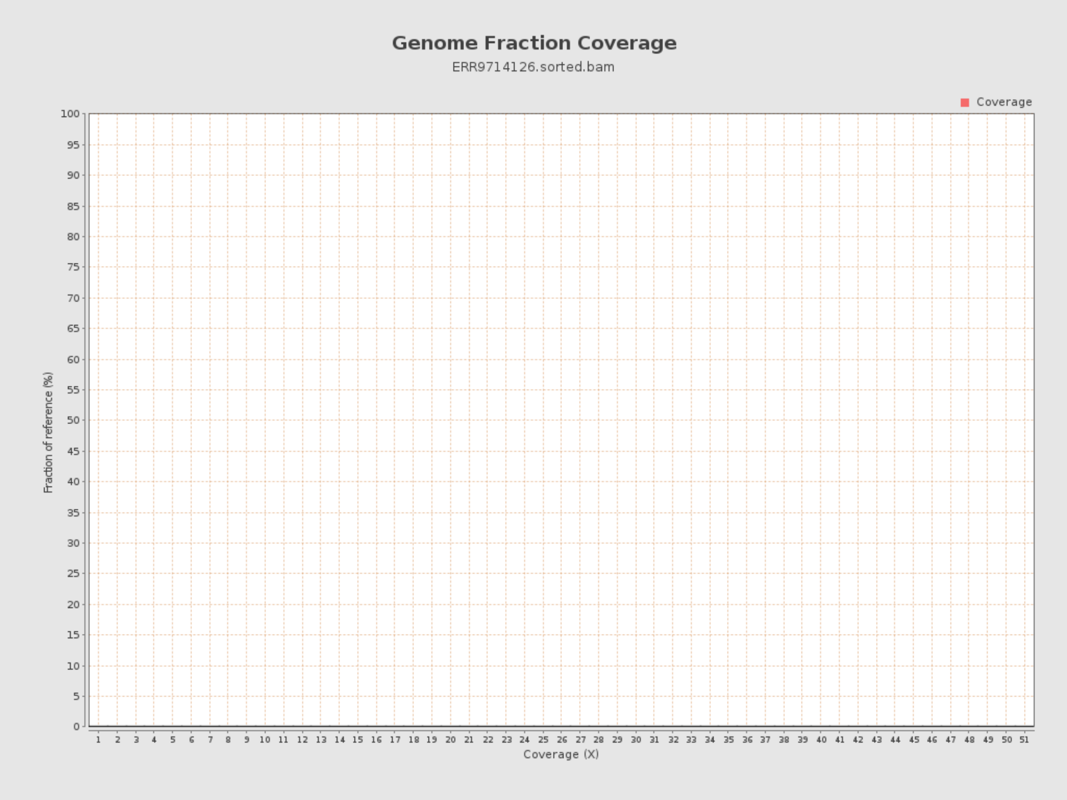
4. Results : Coverage Histogram



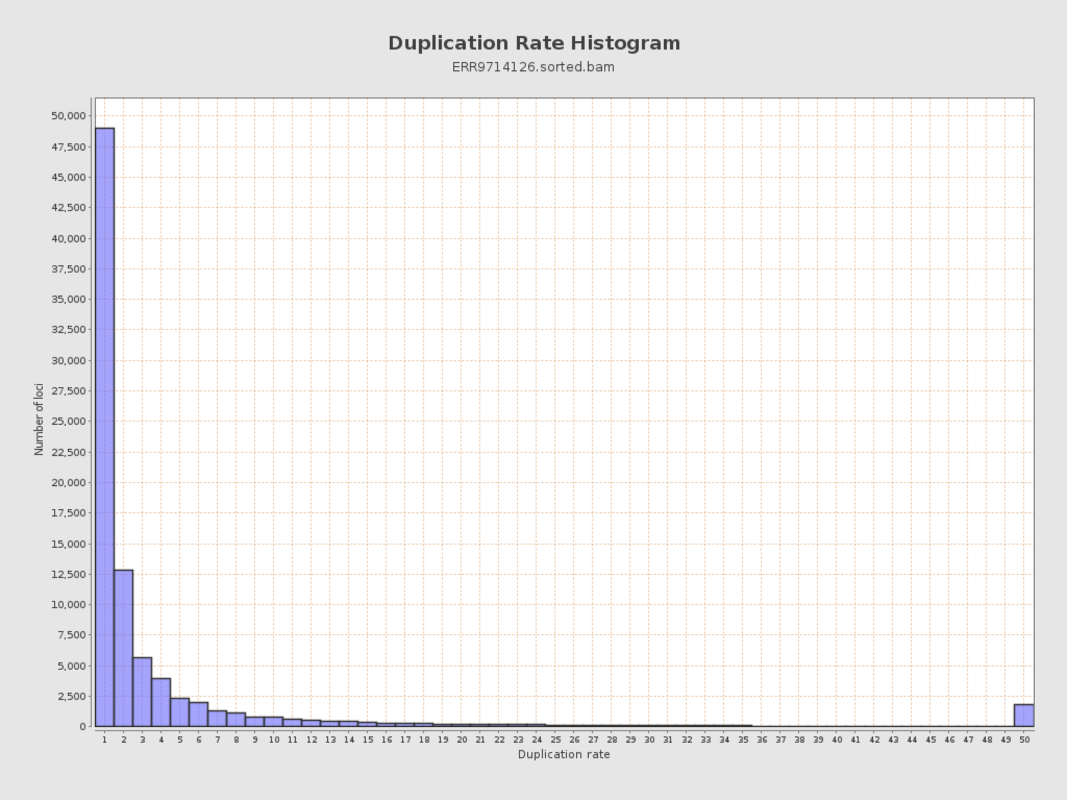
5. Results : Coverage Histogram (0-50X)



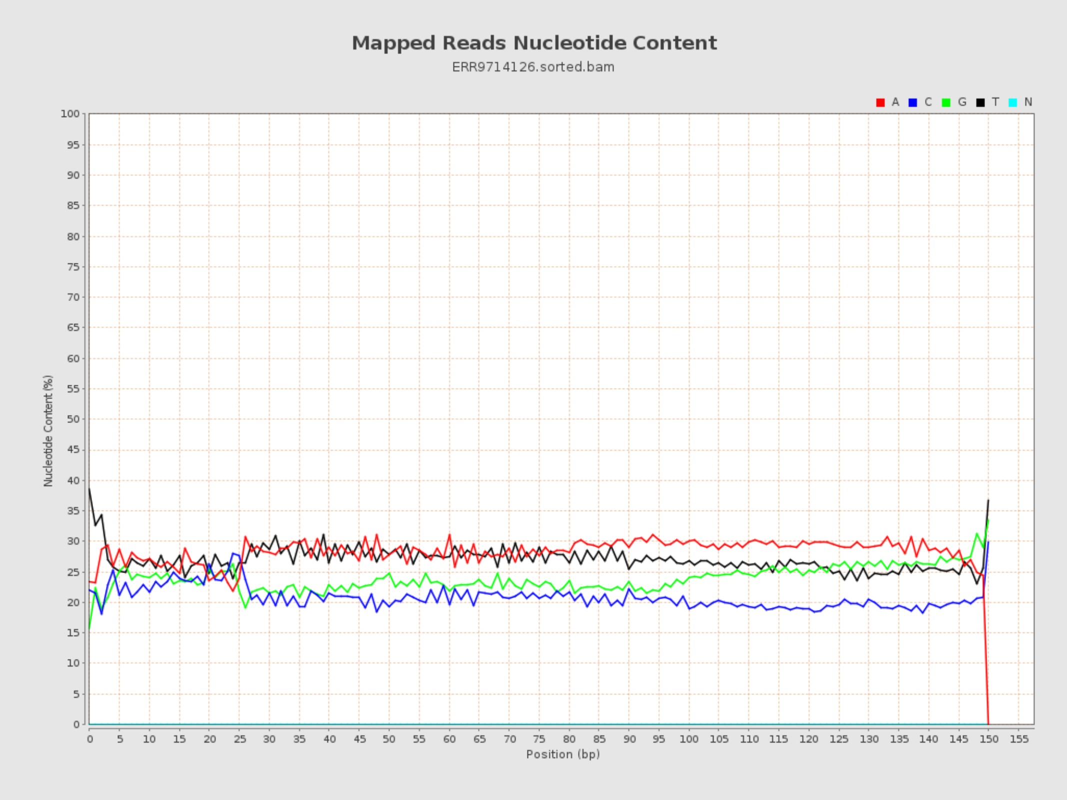
6. Results : Genome Fraction Coverage



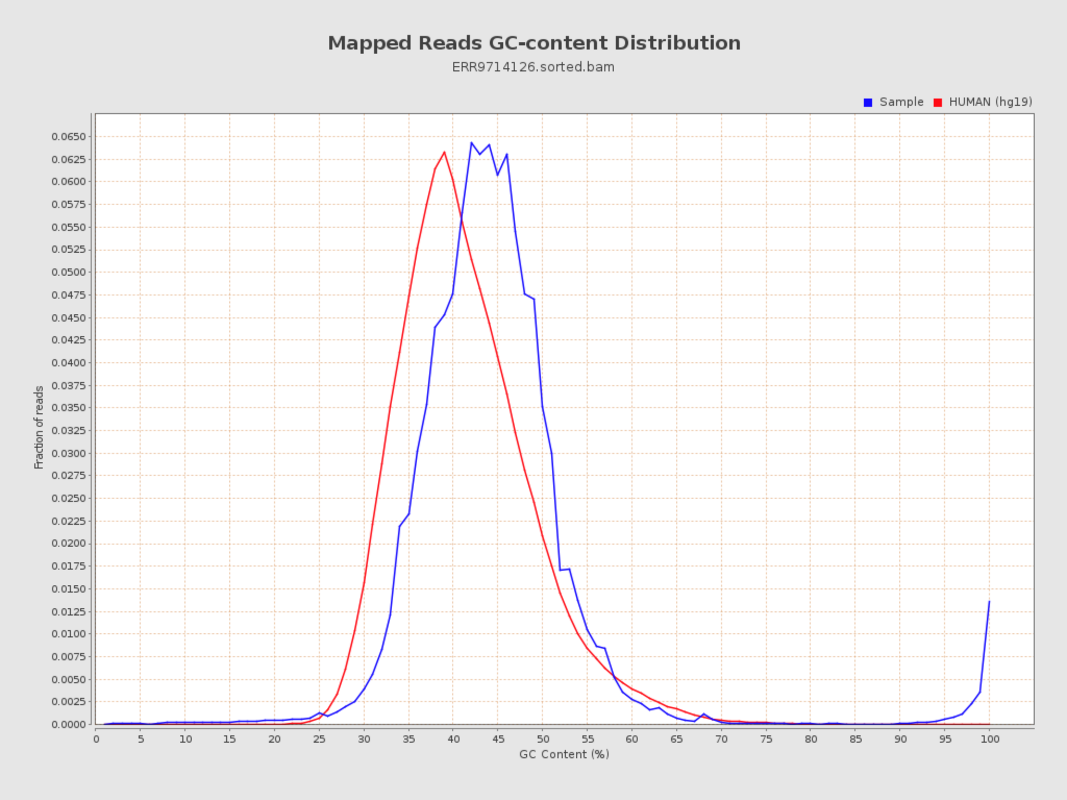
7. Results : Duplication Rate Histogram



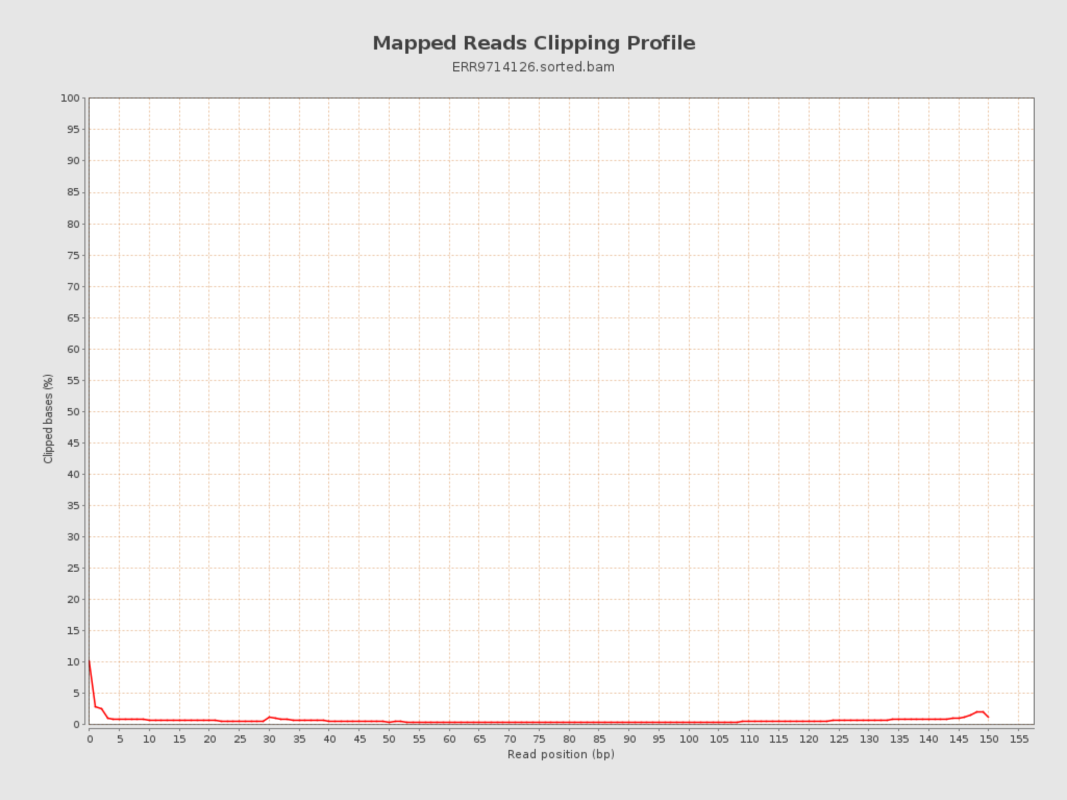
8. Results : Mapped Reads Nucleotide Content



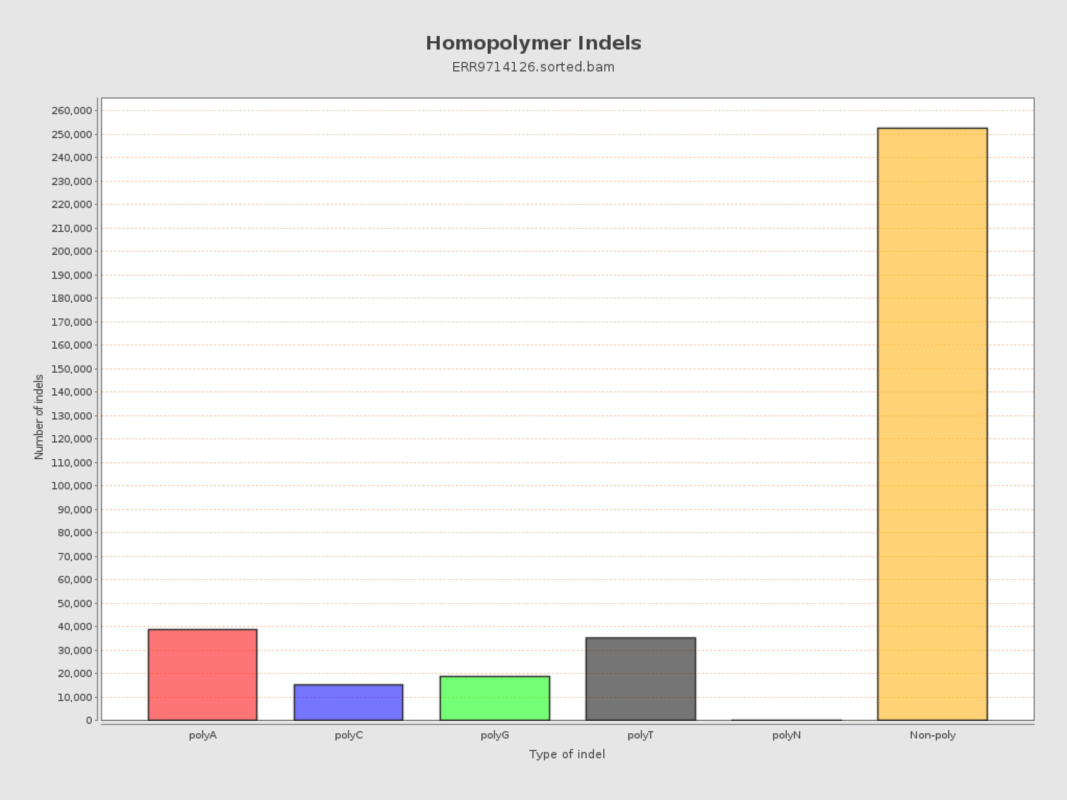
9. Results : Mapped Reads GC-content Distribution



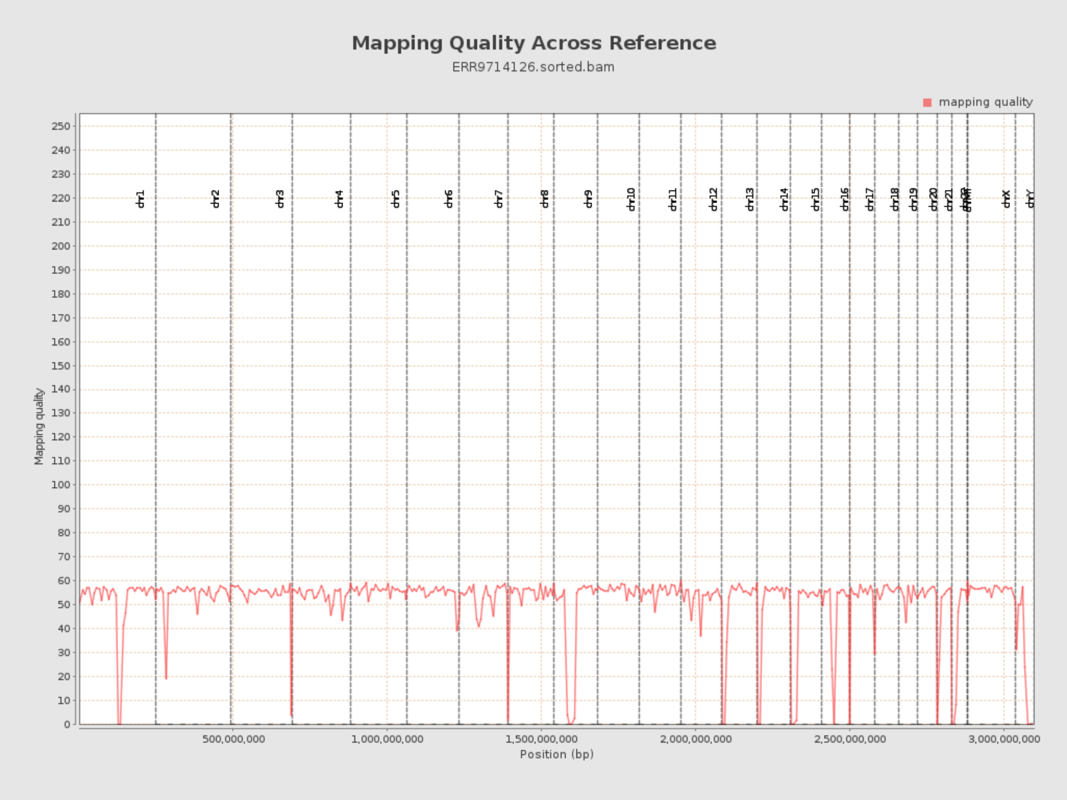
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram