Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 20:26:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714124.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_ERR9714124 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714124.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 20:26:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714124.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	641,516
Mapped reads	523,435 / 81.59%
Unmapped reads	118,081 / 18.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,201 / 2.68%
Read min/max/mean length	30 / 151 / 133.14
Duplicated reads (estimated)	464,620 / 72.43%
Duplication rate	44.81%
Clipped reads	493,645 / 76.95%

2.2. ACGT Content

Number/percentage of A's	17,771,843 / 26.72%
Number/percentage of C's	14,703,742 / 22.1%
Number/percentage of T's	16,795,253 / 25.25%
Number/percentage of G's	17,249,363 / 25.93%
Number/percentage of N's	496 / 0%
GC Percentage	48.03%

2.3. Coverage

Mean	0.022

Standard Deviation	5.7831

2.4. Mapping Quality

Mean Mapping Quality	51.56

2.5. Mismatches and indels

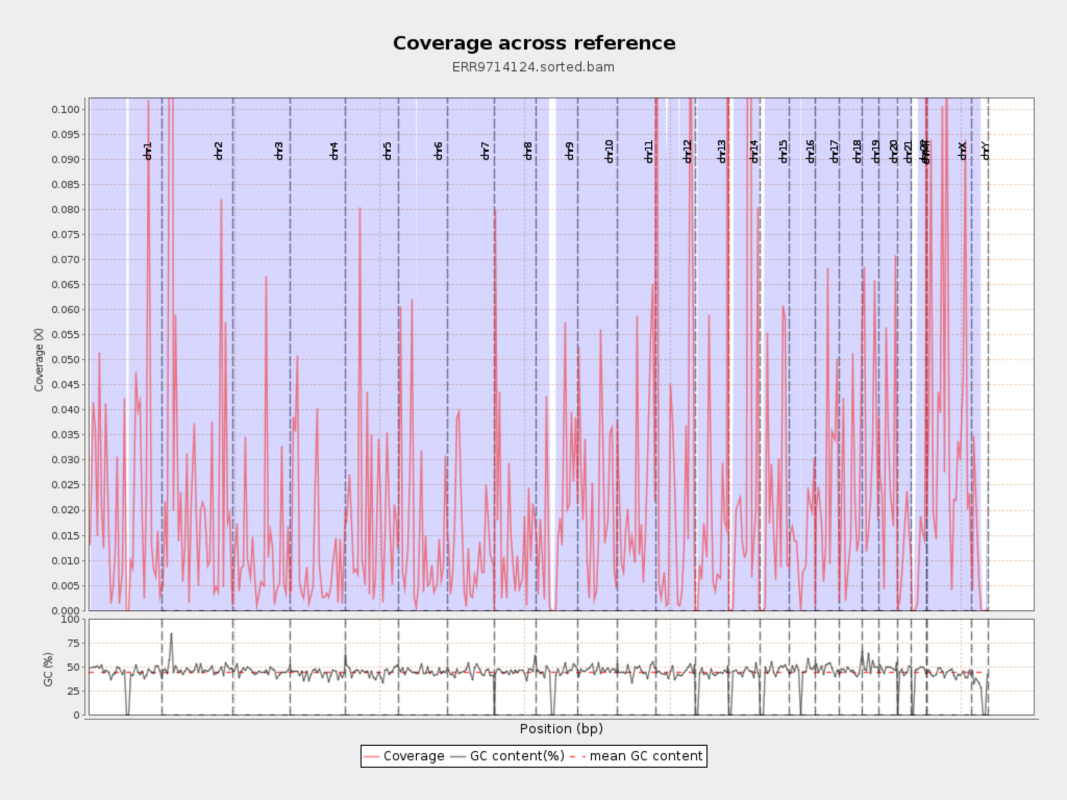
General error rate	4.36%
Mismatches	2,695,878
Insertions	71,353
Mapped reads with at least one insertion	13.07%
Deletions	228,916
Mapped reads with at least one deletion	41.41%
Homopolymer indels	29.12%

2.6. Chromosome stats

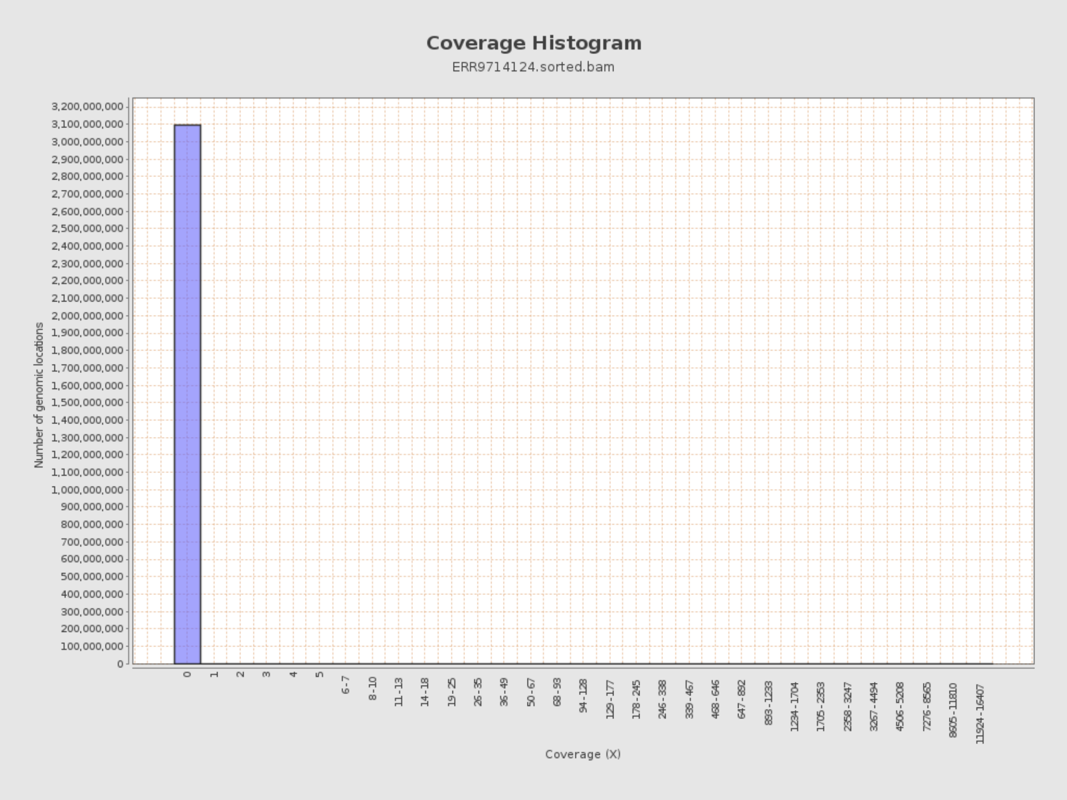
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5318996	0.0213	4.0916
chr2	243199373	8209527	0.0338	10.3308
chr3	198022430	2415999	0.0122	2.2391
chr4	191154276	2341901	0.0123	2.5739
chr5	180915260	3470652	0.0192	4.4024
chr6	171115067	2610742	0.0153	2.8939
chr7	159138663	2052650	0.0129	2.2226

chr8	146364022	2536425	0.0173	4.0804
chr9	141213431	2563709	0.0182	3.3137
chr10	135534747	3035652	0.0224	3.6736
chr11	135006516	3262400	0.0242	3.9135
chr12	133851895	3819962	0.0285	5.8097
chr13	115169878	2327389	0.0202	6.0963
chr14	107349540	4297133	0.04	18.7848
chr15	102531392	2284608	0.0223	4.101
chr16	90354753	1345065	0.0149	1.8379
chr17	81195210	2252979	0.0277	4.1272
chr18	78077248	1657167	0.0212	4.144
chr19	59128983	2062001	0.0349	3.9016
chr20	63025520	2026830	0.0322	4.2848
chr21	48129895	533808	0.0111	1.6444
chr22	51304566	501356	0.0098	1.155
chrMT	16571	120326	7.2612	58.7876
chrX	155270560	6409424	0.0413	4.7549
chrY	59373566	521361	0.0088	2.1631

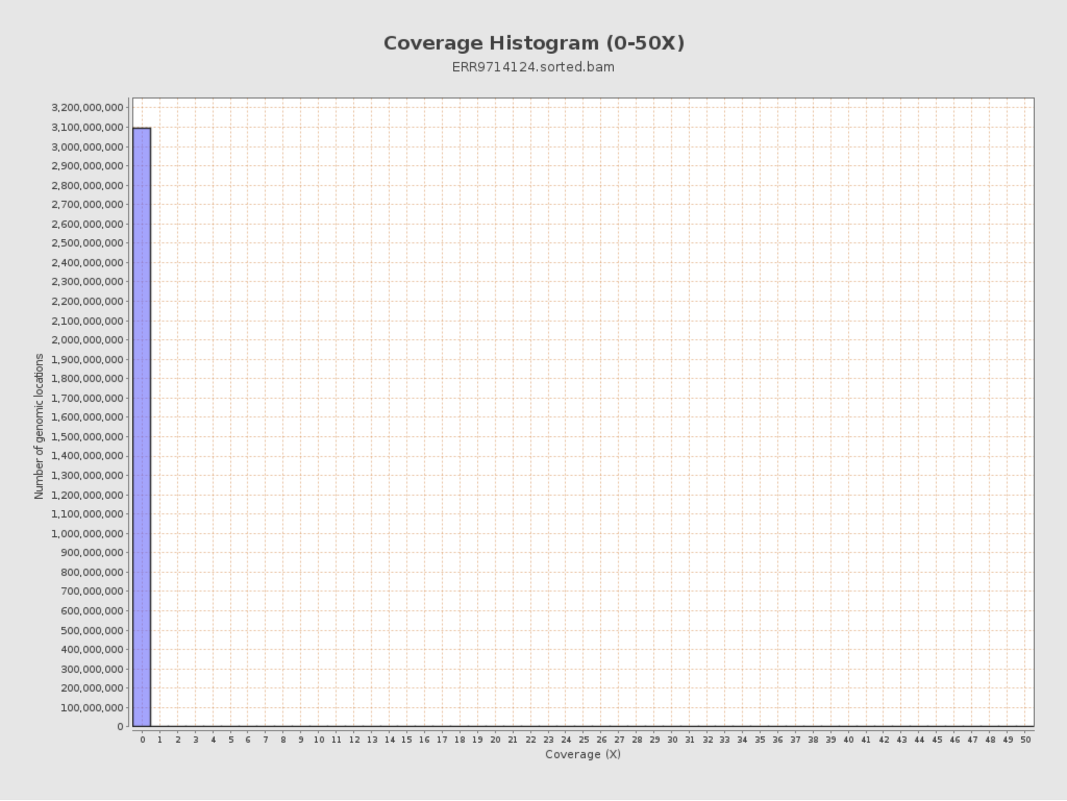
3. Results : Coverage across reference



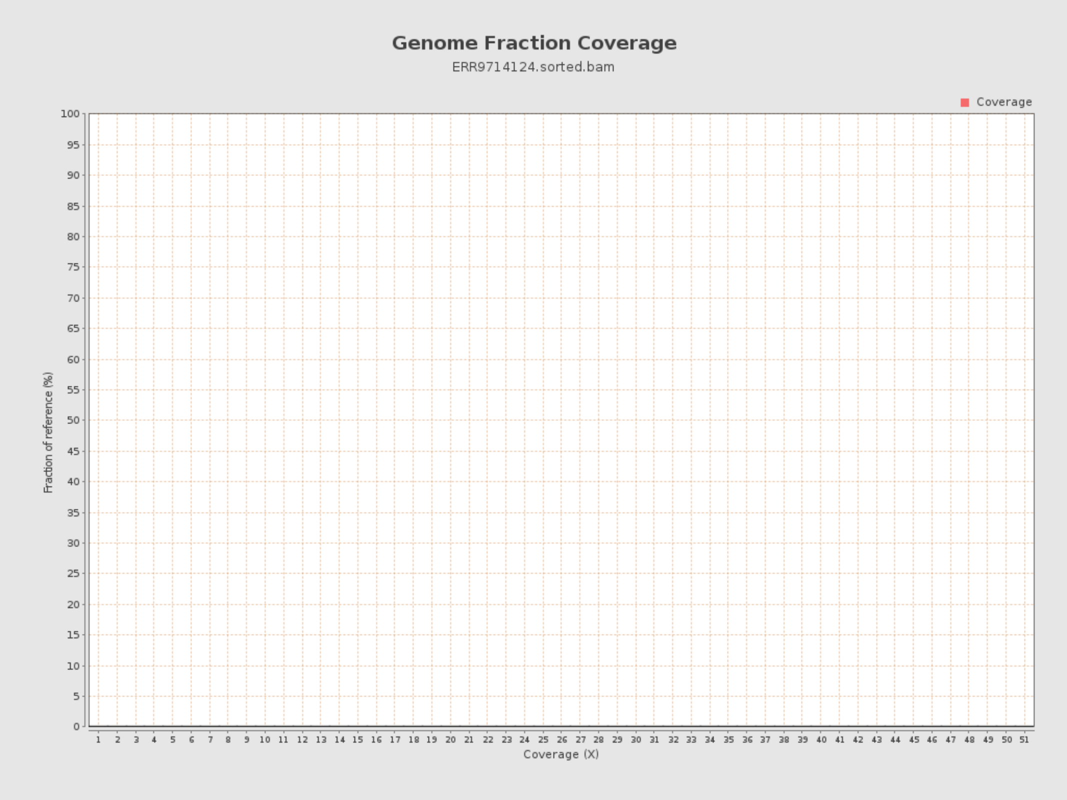
4. Results : Coverage Histogram



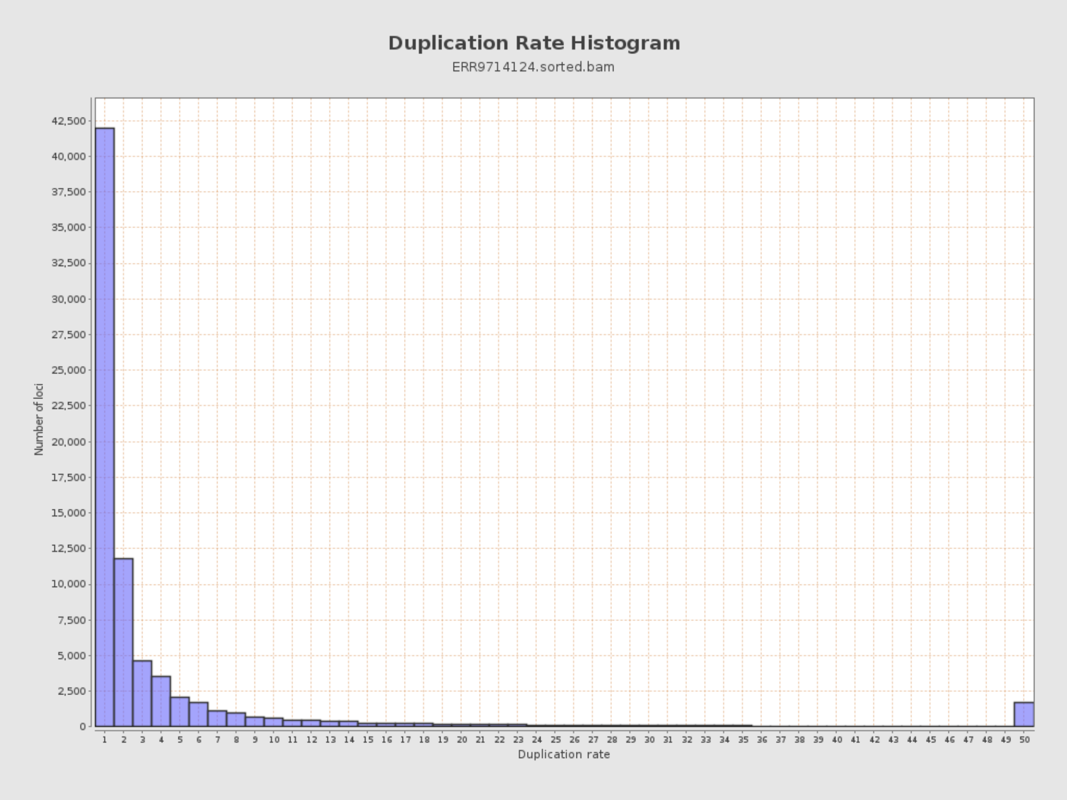
5. Results : Coverage Histogram (0-50X)



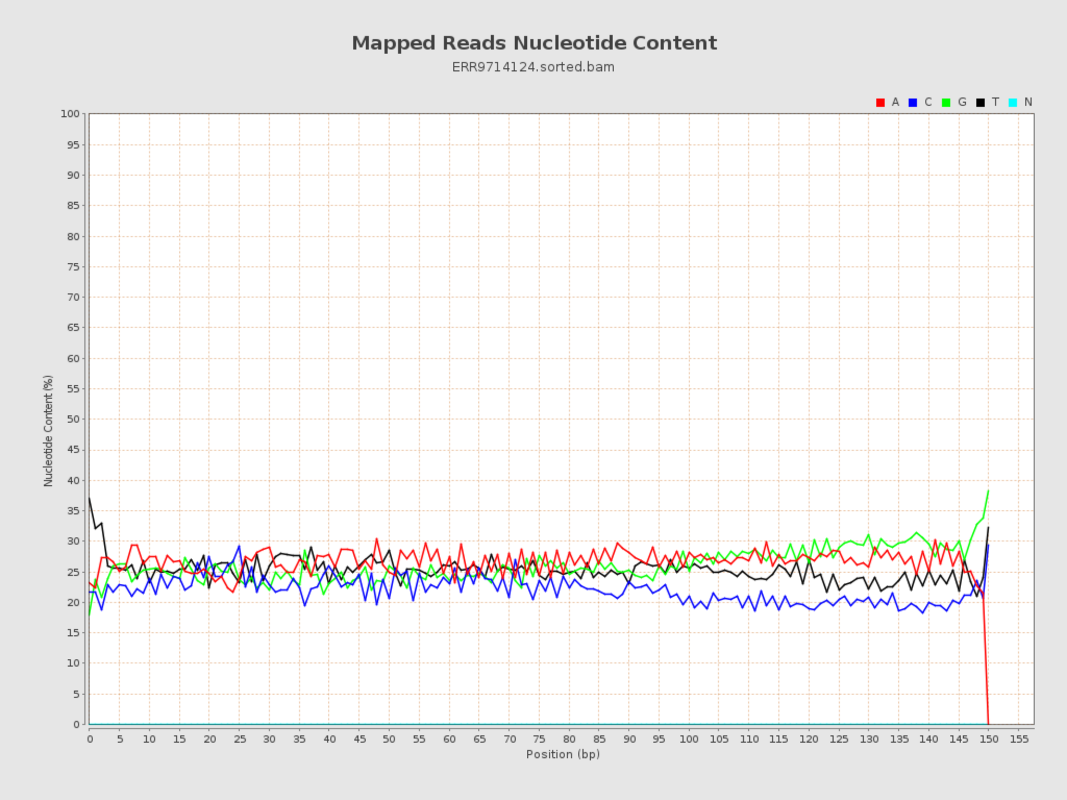
6. Results : Genome Fraction Coverage



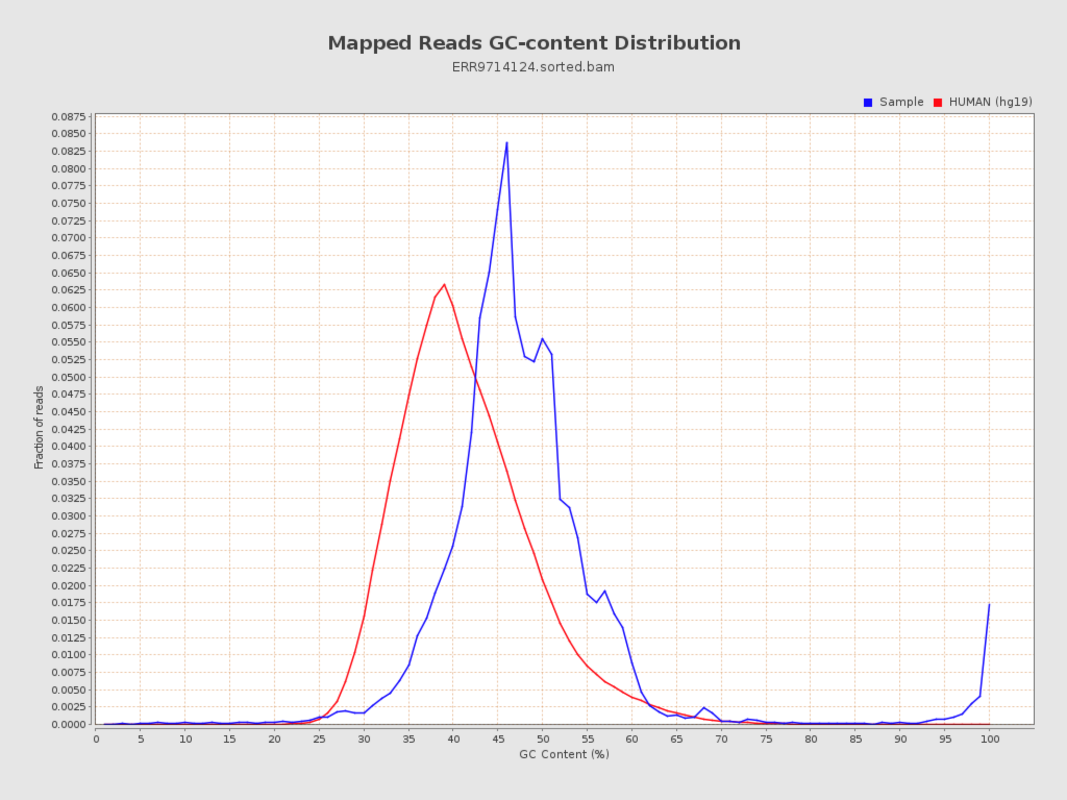
7. Results : Duplication Rate Histogram



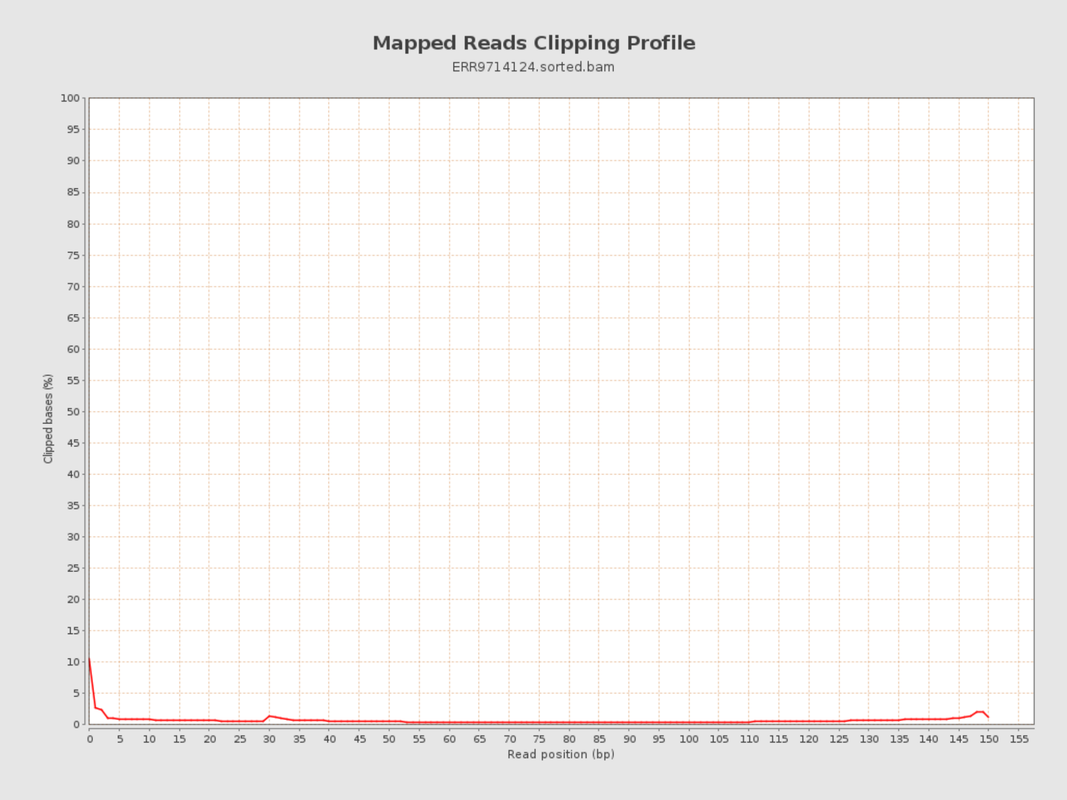
8. Results : Mapped Reads Nucleotide Content



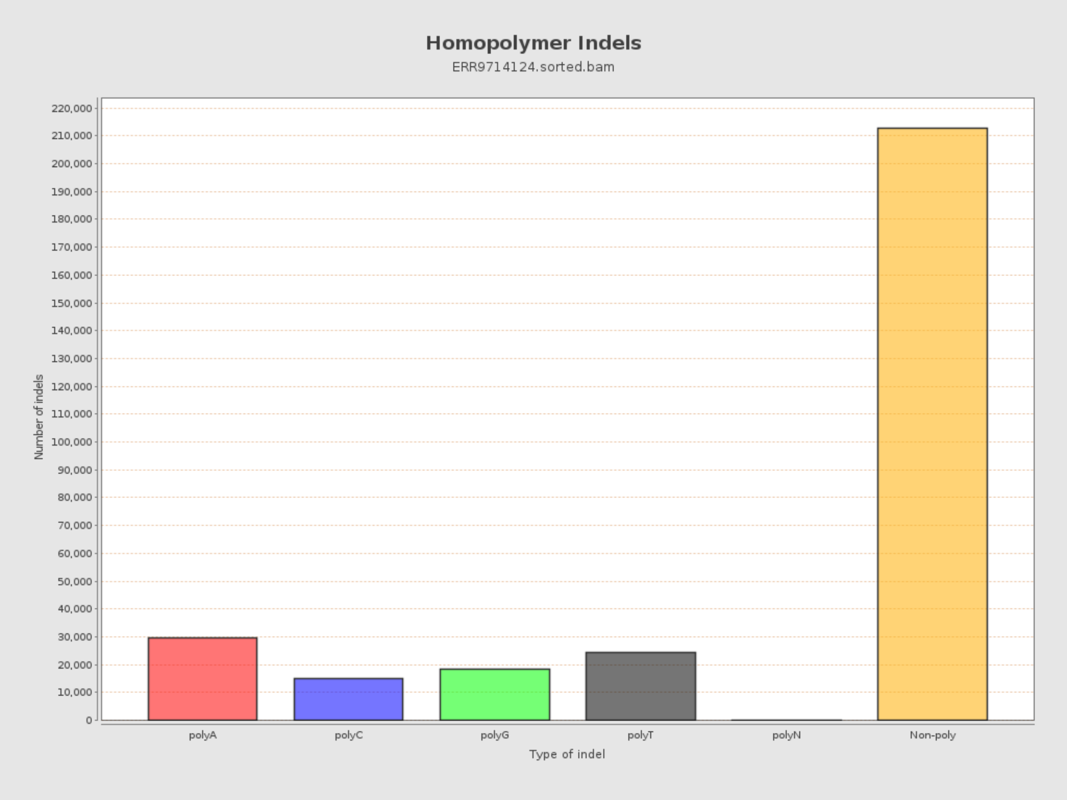
9. Results : Mapped Reads GC-content Distribution



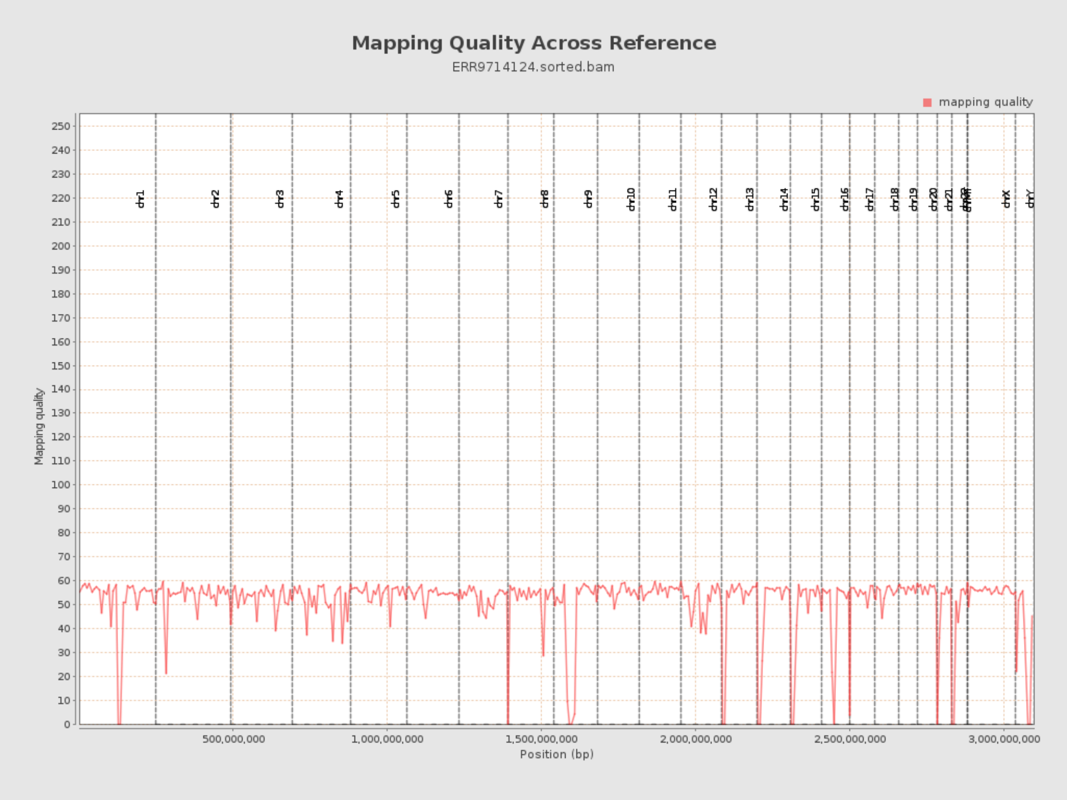
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram