Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 19:47:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714109.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_ERR9714109 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714109.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 19:47:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714109.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	620,550
Mapped reads	420,814 / 67.81%
Unmapped reads	199,736 / 32.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,686 / 2.37%
Read min/max/mean length	30 / 151 / 119.6
Duplicated reads (estimated)	369,796 / 59.59%
Duplication rate	43.21%
Clipped reads	388,143 / 62.55%

2.2. ACGT Content

Number/percentage of A's	14,355,003 / 27.09%
Number/percentage of C's	10,616,496 / 20.04%
Number/percentage of T's	13,527,662 / 25.53%
Number/percentage of G's	14,484,339 / 27.34%
Number/percentage of N's	346 / 0%
GC Percentage	47.37%

2.3. Coverage

Mean	0.0175

Standard Deviation	5.2357

2.4. Mapping Quality

Mean Mapping Quality	50.84

2.5. Mismatches and indels

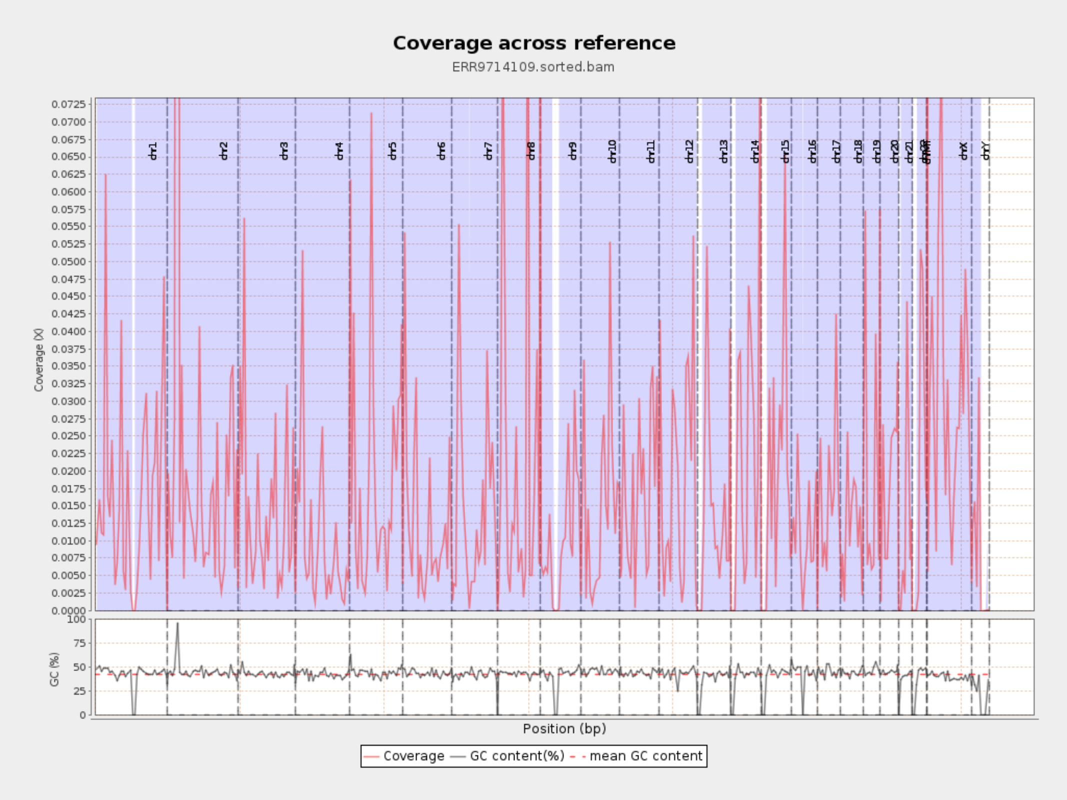
General error rate	4.55%
Mismatches	2,265,924
Insertions	56,484
Mapped reads with at least one insertion	12.77%
Deletions	203,653
Mapped reads with at least one deletion	44.84%
Homopolymer indels	29.92%

2.6. Chromosome stats

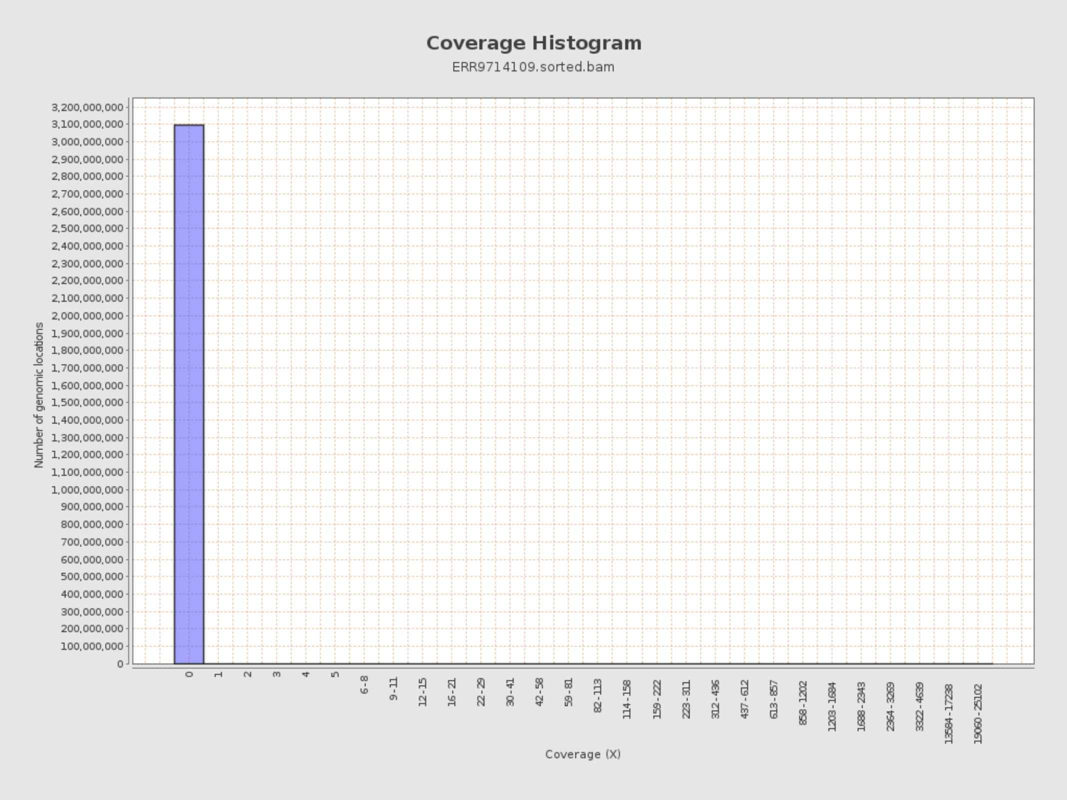
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4147298	0.0166	2.7437
chr2	243199373	7446409	0.0306	15.5446
chr3	198022430	2885765	0.0146	2.9151
chr4	191154276	1865607	0.0098	1.6866
chr5	180915260	3338793	0.0185	3.8824
chr6	171115067	2167553	0.0127	2.3466
chr7	159138663	2228614	0.014	2.7818

chr8	146364022	3070029	0.021	5.2658
chr9	141213431	1493559	0.0106	1.716
chr10	135534747	2113765	0.0156	3.0246
chr11	135006516	2338817	0.0173	2.5622
chr12	133851895	2473412	0.0185	2.9014
chr13	115169878	1555762	0.0135	2.0354
chr14	107349540	2477632	0.0231	5.4896
chr15	102531392	1960314	0.0191	2.9003
chr16	90354753	974184	0.0108	1.4686
chr17	81195210	1385937	0.0171	2.6578
chr18	78077248	948751	0.0122	1.5385
chr19	59128983	1193852	0.0202	2.6412
chr20	63025520	1162980	0.0185	2.2463
chr21	48129895	528877	0.011	2.2618
chr22	51304566	967178	0.0189	4.1367
chrMT	16571	308842	18.6375	134.9401
chrX	155270560	4695009	0.0302	2.873
chrY	59373566	470007	0.0079	2.5724

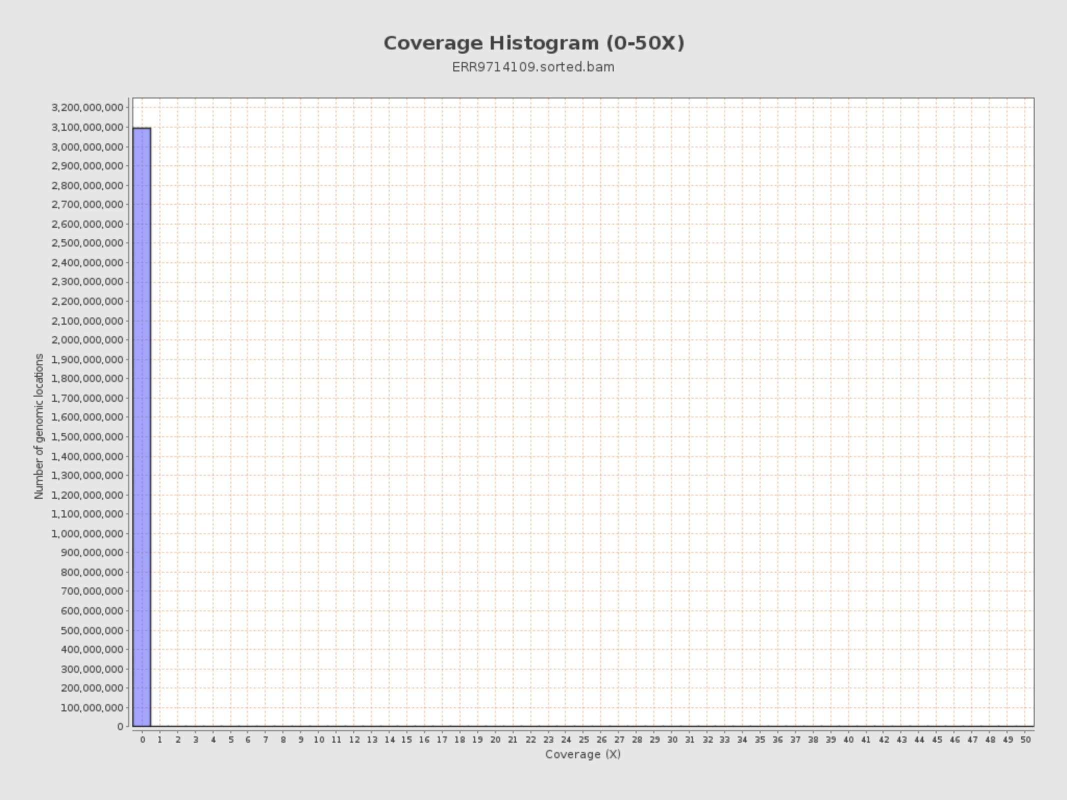
3. Results : Coverage across reference



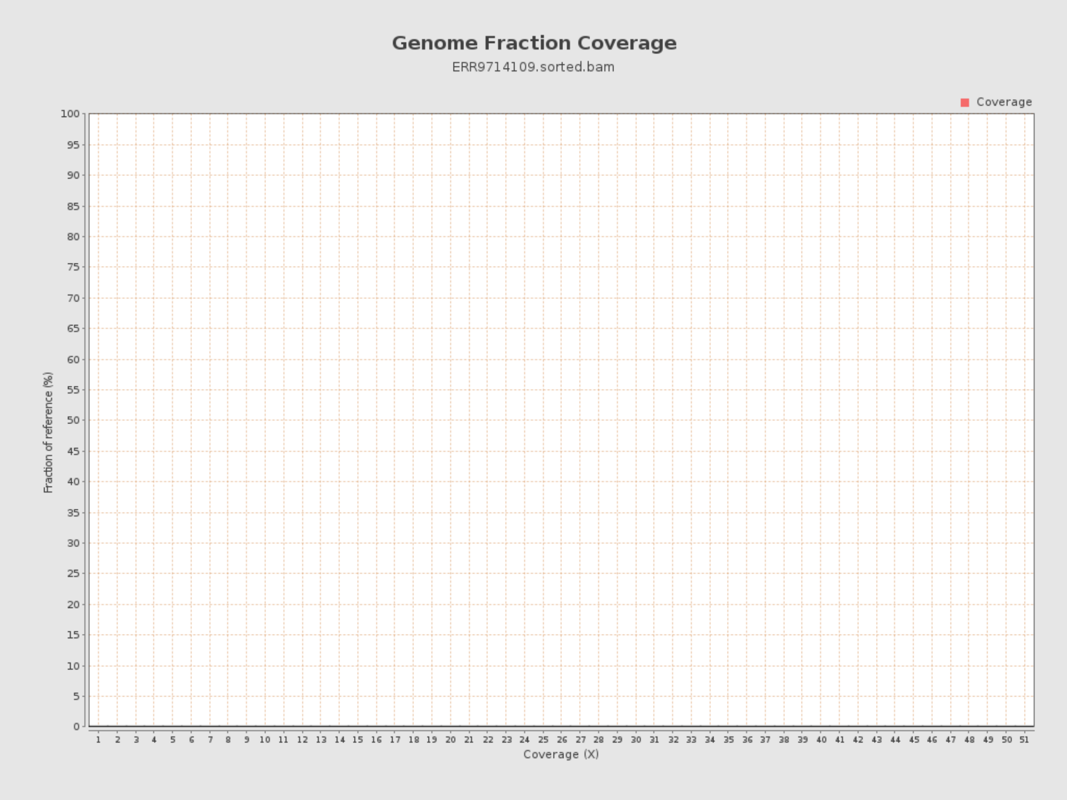
4. Results : Coverage Histogram



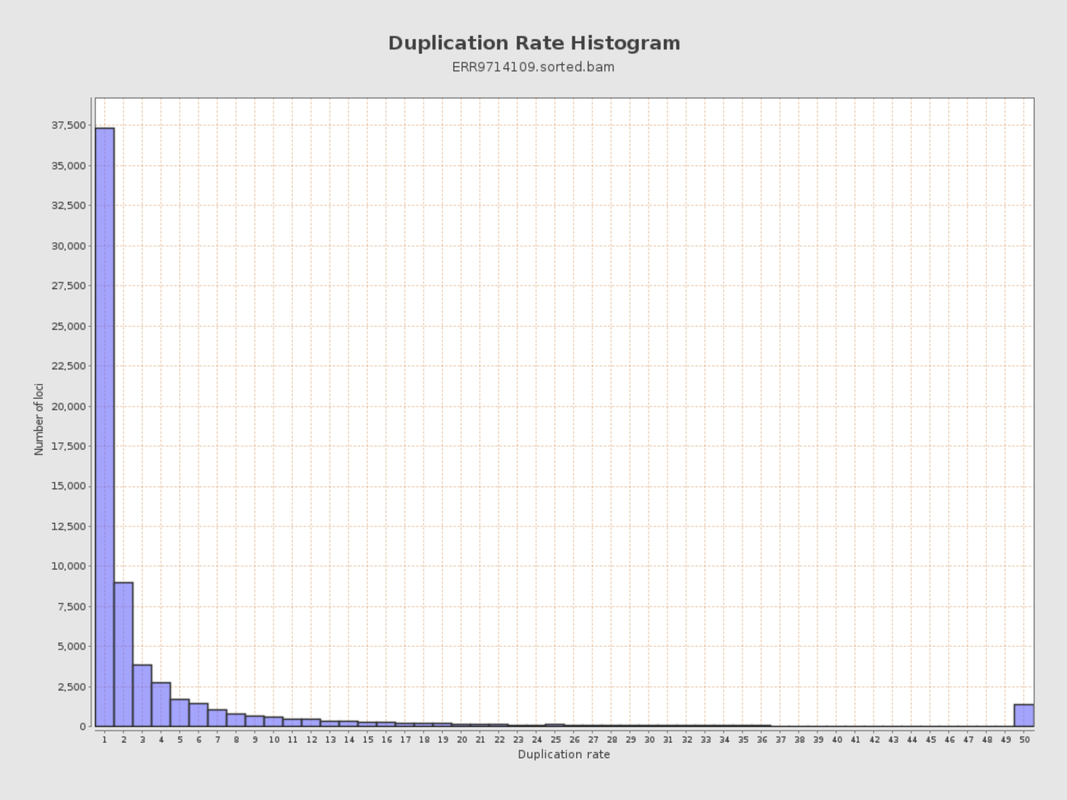
5. Results : Coverage Histogram (0-50X)



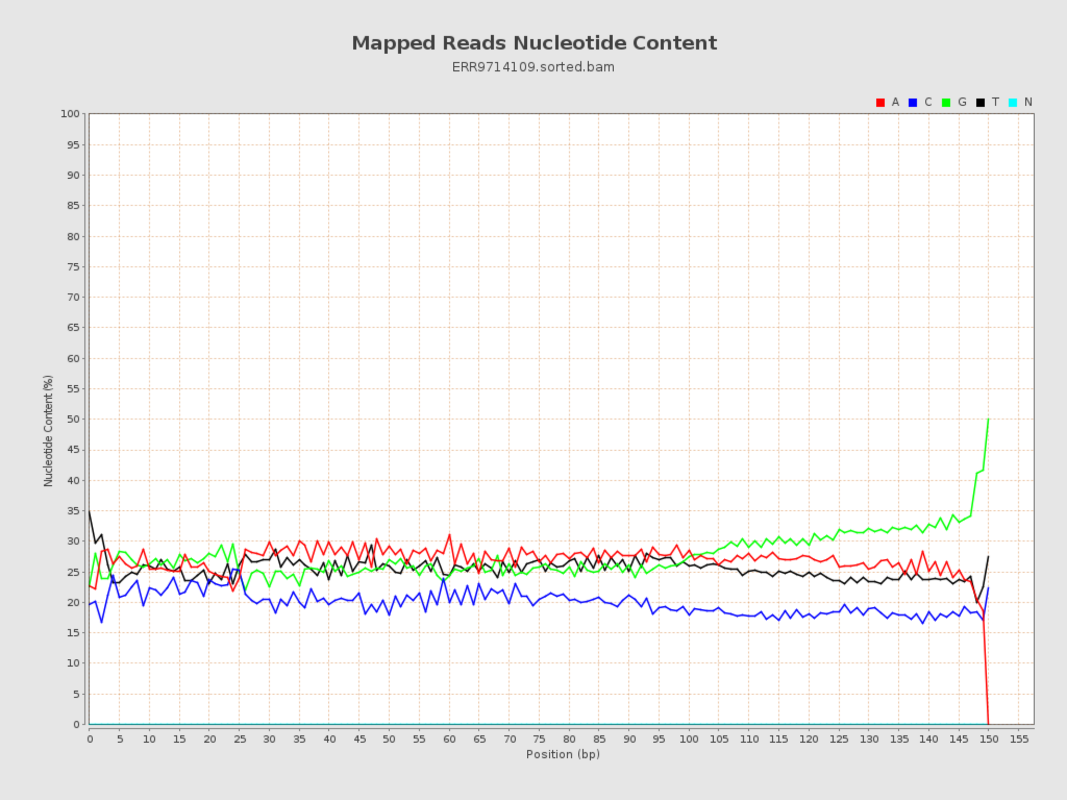
6. Results : Genome Fraction Coverage



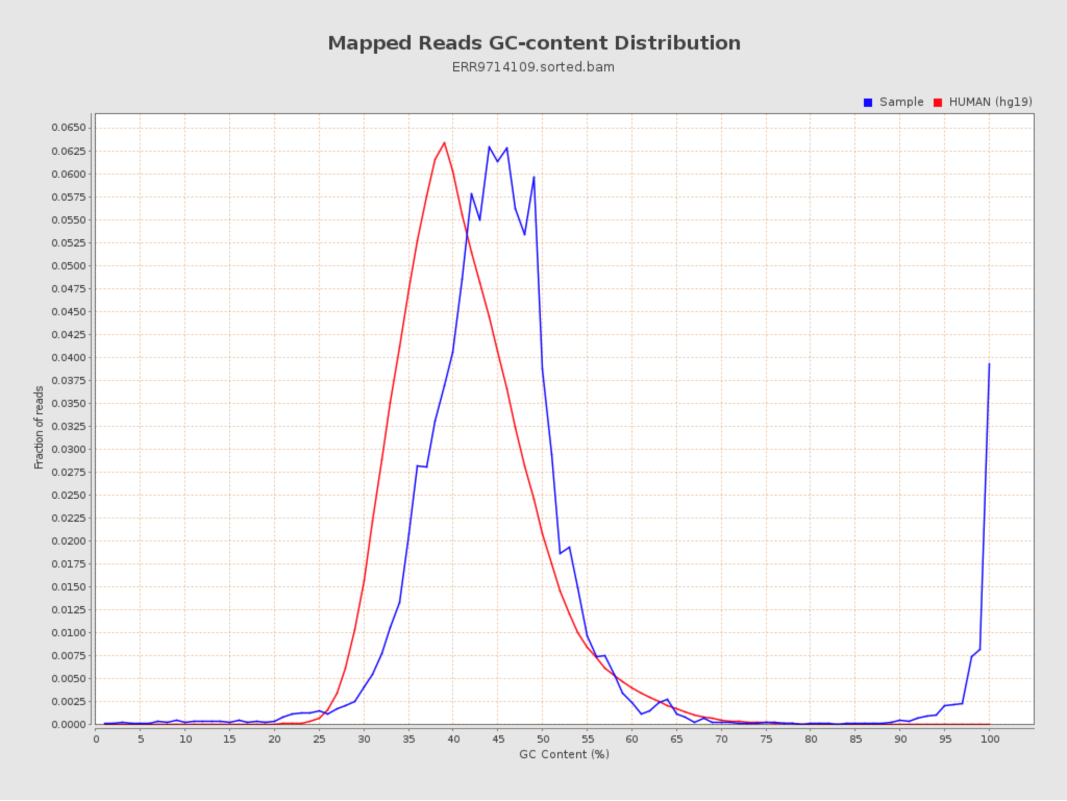
7. Results : Duplication Rate Histogram



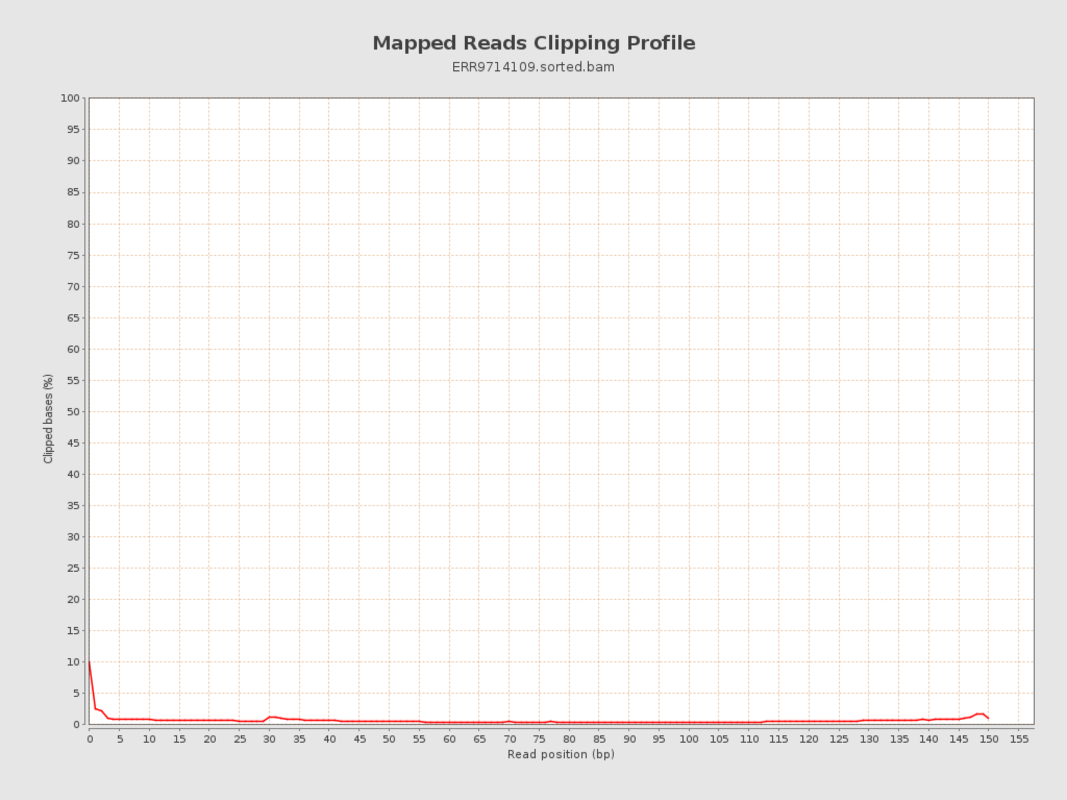
8. Results : Mapped Reads Nucleotide Content



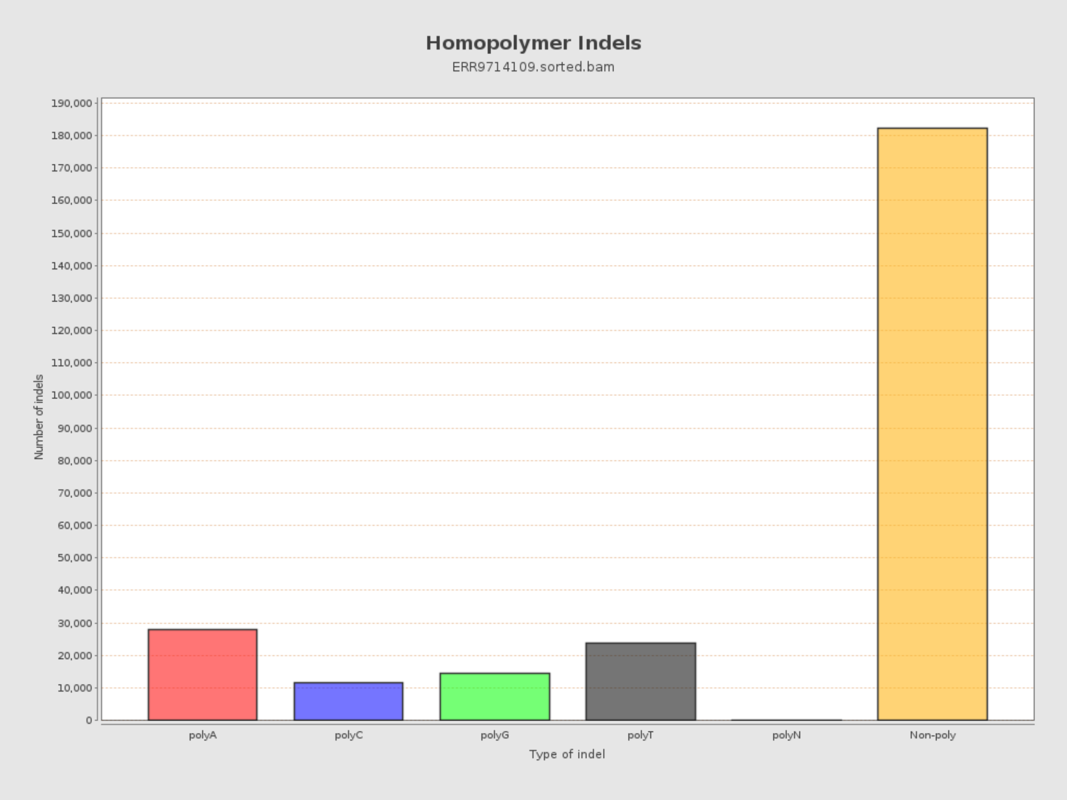
9. Results : Mapped Reads GC-content Distribution



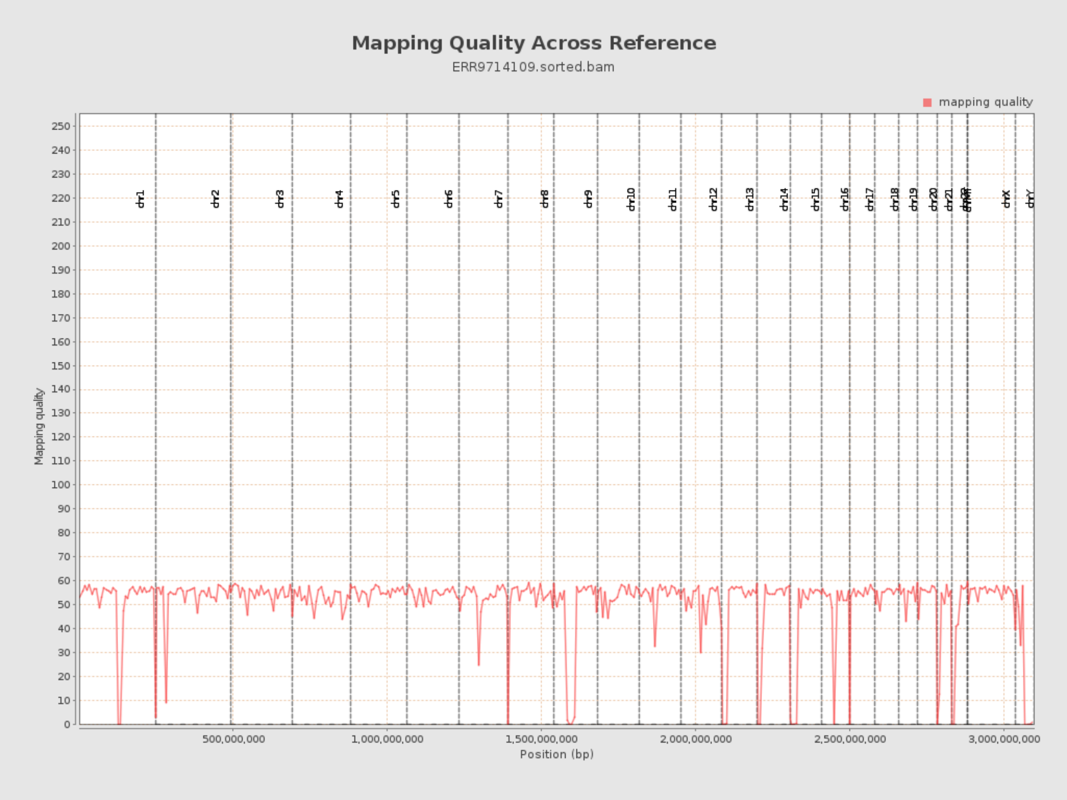
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram