Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 19:38:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714106.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_ERR9714106 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714106.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 19:38:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714106.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,019,196
Mapped reads	85,719 / 8.41%
Unmapped reads	933,477 / 91.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,330 / 0.23%
Read min/max/mean length	30 / 151 / 54.96
Duplicated reads (estimated)	78,054 / 7.66%
Duplication rate	35.57%
Clipped reads	69,095 / 6.78%

2.2. ACGT Content

Number/percentage of A's	1,105,645 / 14.09%
Number/percentage of C's	713,013 / 9.09%
Number/percentage of T's	957,963 / 12.21%
Number/percentage of G's	5,068,447 / 64.6%
Number/percentage of N's	307 / 0%
GC Percentage	73.69%

2.3. Coverage

Mean	0.0026

Standard Deviation	5.1815

2.4. Mapping Quality

Mean Mapping Quality	41.27

2.5. Mismatches and indels

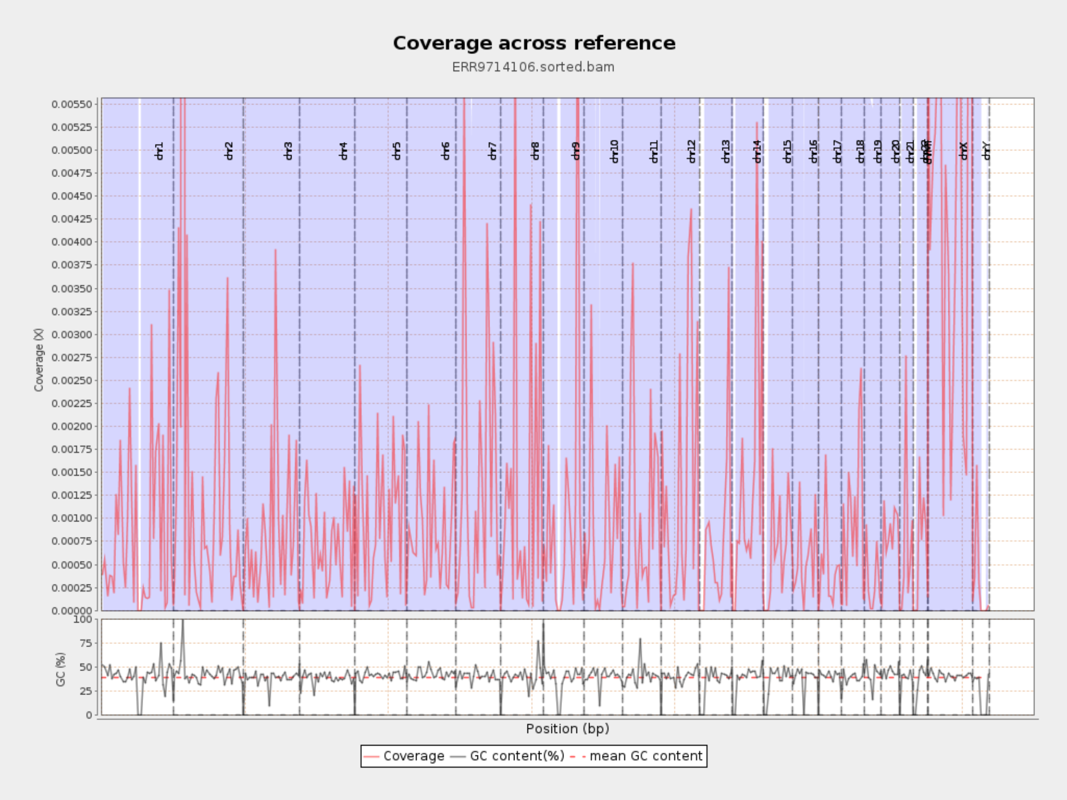
General error rate	3.35%
Mismatches	222,733
Insertions	8,198
Mapped reads with at least one insertion	7.62%
Deletions	13,168
Mapped reads with at least one deletion	14.46%
Homopolymer indels	38.68%

2.6. Chromosome stats

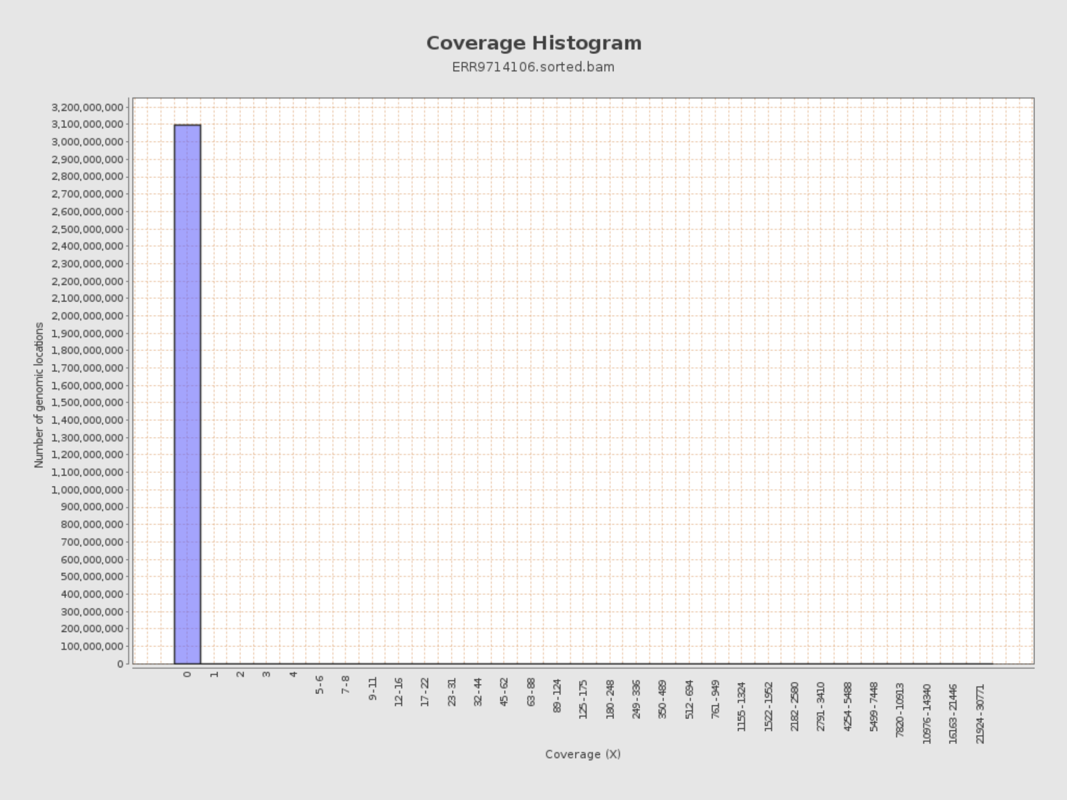
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	213861	0.0009	0.2081
chr2	243199373	4643684	0.0191	18.4648
chr3	198022430	162656	0.0008	0.153
chr4	191154276	143755	0.0008	0.1476
chr5	180915260	188707	0.001	0.2086
chr6	171115067	153794	0.0009	0.184
chr7	159138663	223004	0.0014	0.4428

chr8	146364022	202303	0.0014	0.3848
chr9	141213431	151830	0.0011	0.3445
chr10	135534747	116592	0.0009	0.1909
chr11	135006516	135696	0.001	0.224
chr12	133851895	179634	0.0013	0.3008
chr13	115169878	81340	0.0007	0.1942
chr14	107349540	147720	0.0014	0.315
chr15	102531392	67580	0.0007	0.1259
chr16	90354753	50625	0.0006	0.1138
chr17	81195210	35549	0.0004	0.1694
chr18	78077248	86627	0.0011	0.2355
chr19	59128983	18304	0.0003	0.0835
chr20	63025520	51844	0.0008	0.1475
chr21	48129895	34591	0.0007	0.1886
chr22	51304566	36052	0.0007	0.1628
chrMT	16571	16793	1.0134	9.1378
chrX	155270560	765317	0.0049	0.4902
chrY	59373566	18352	0.0003	0.1187

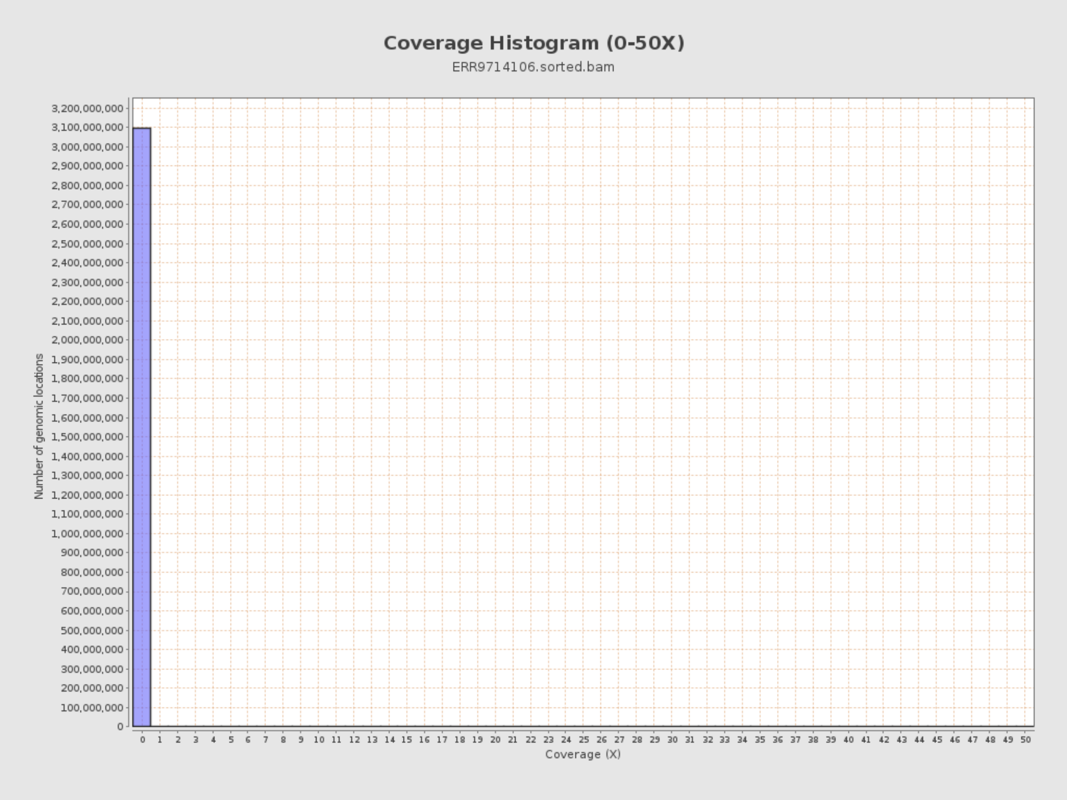
3. Results : Coverage across reference



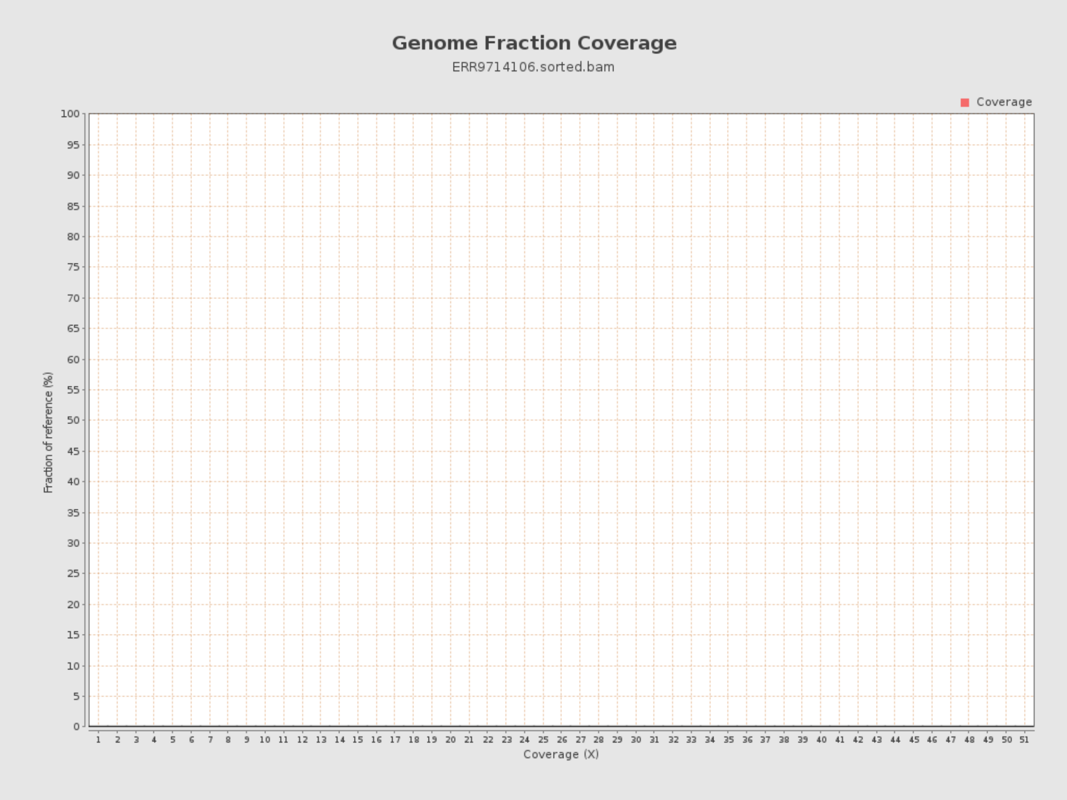
4. Results : Coverage Histogram



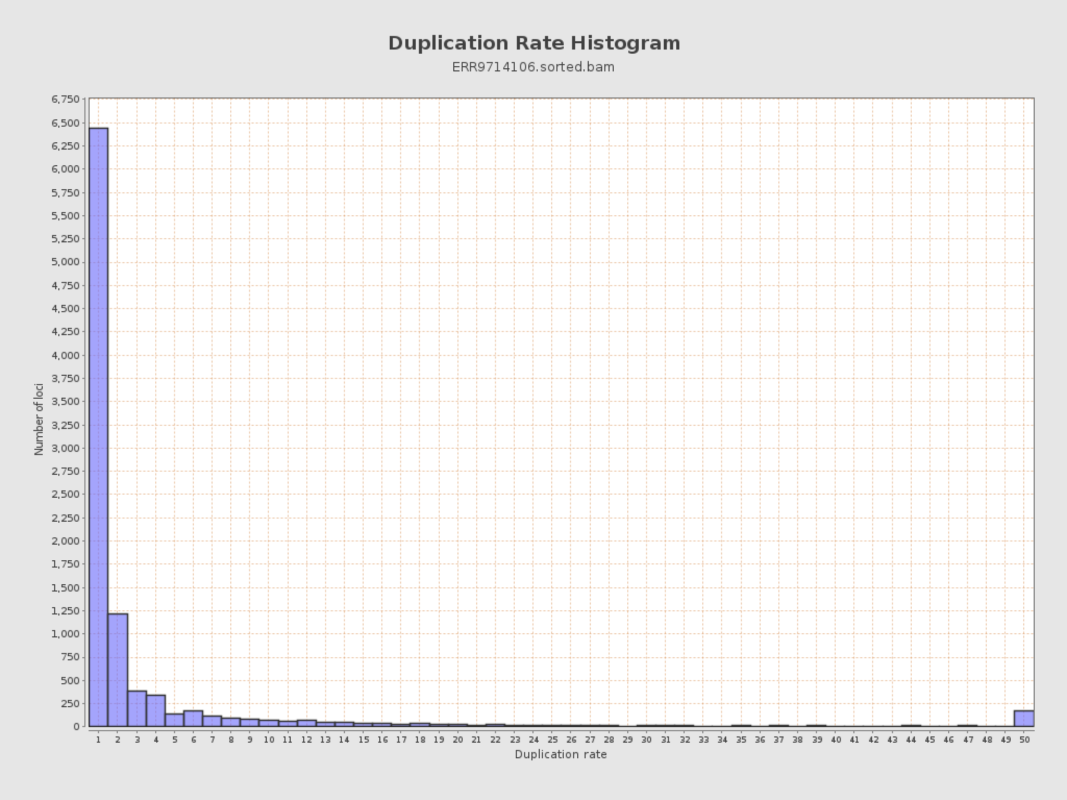
5. Results : Coverage Histogram (0-50X)



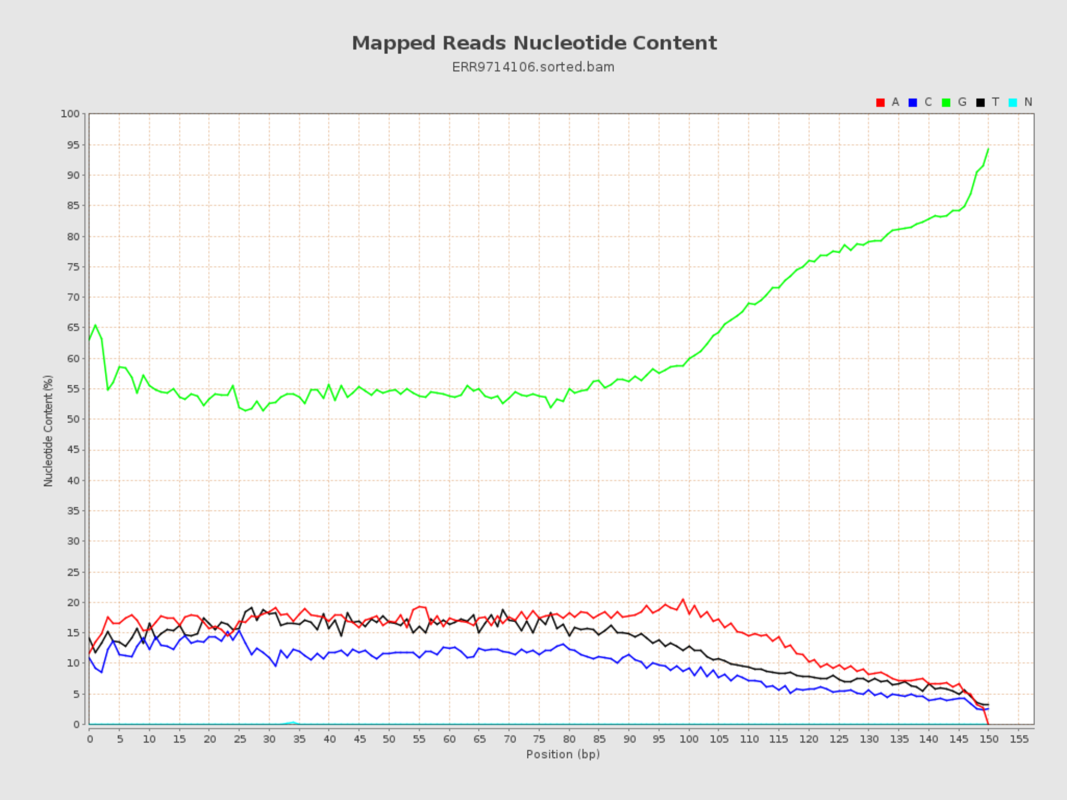
6. Results : Genome Fraction Coverage



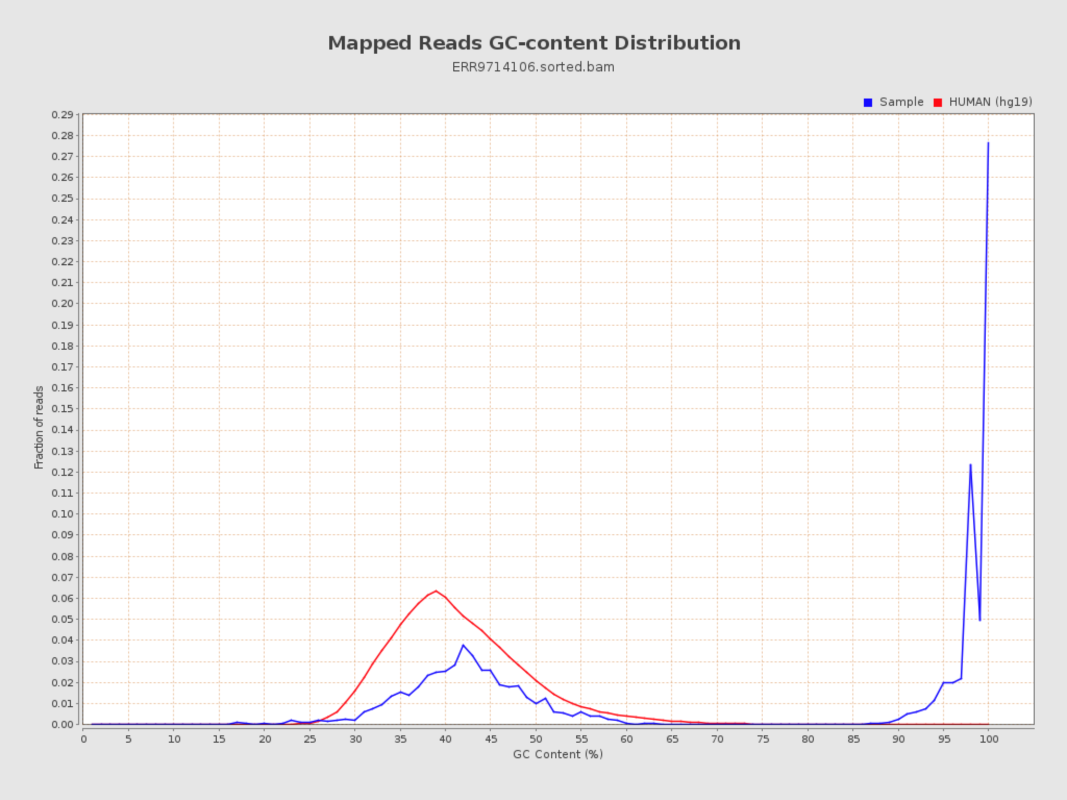
7. Results : Duplication Rate Histogram



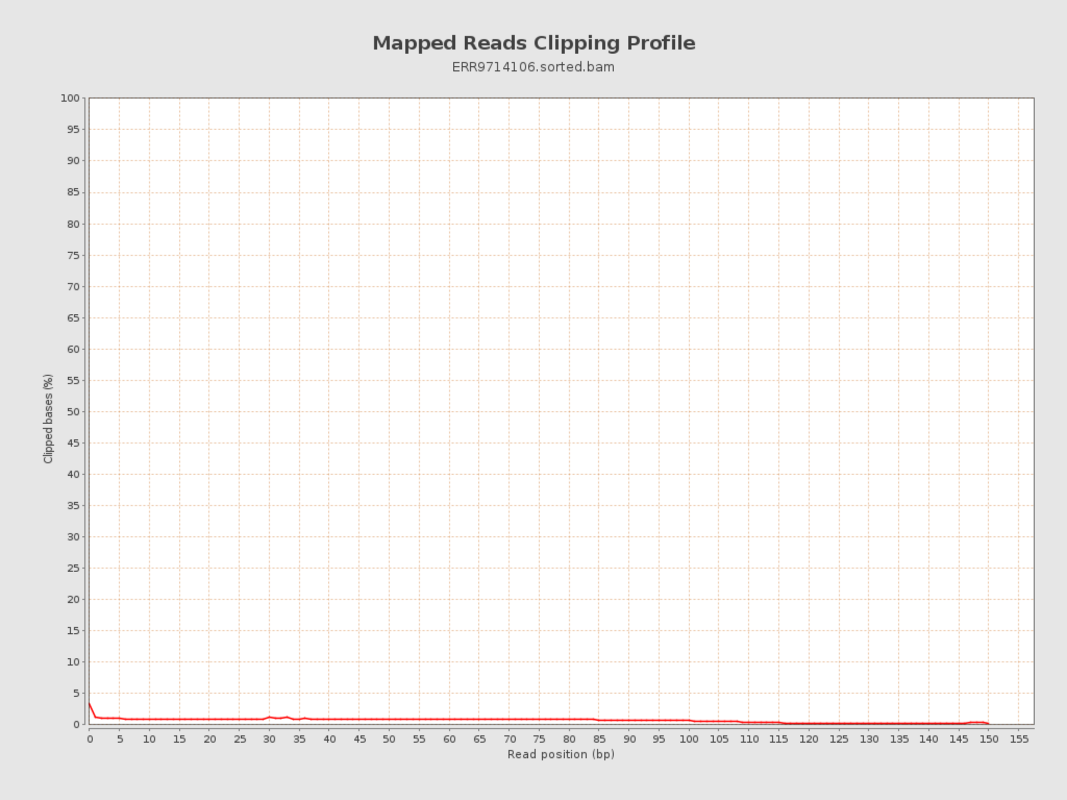
8. Results : Mapped Reads Nucleotide Content



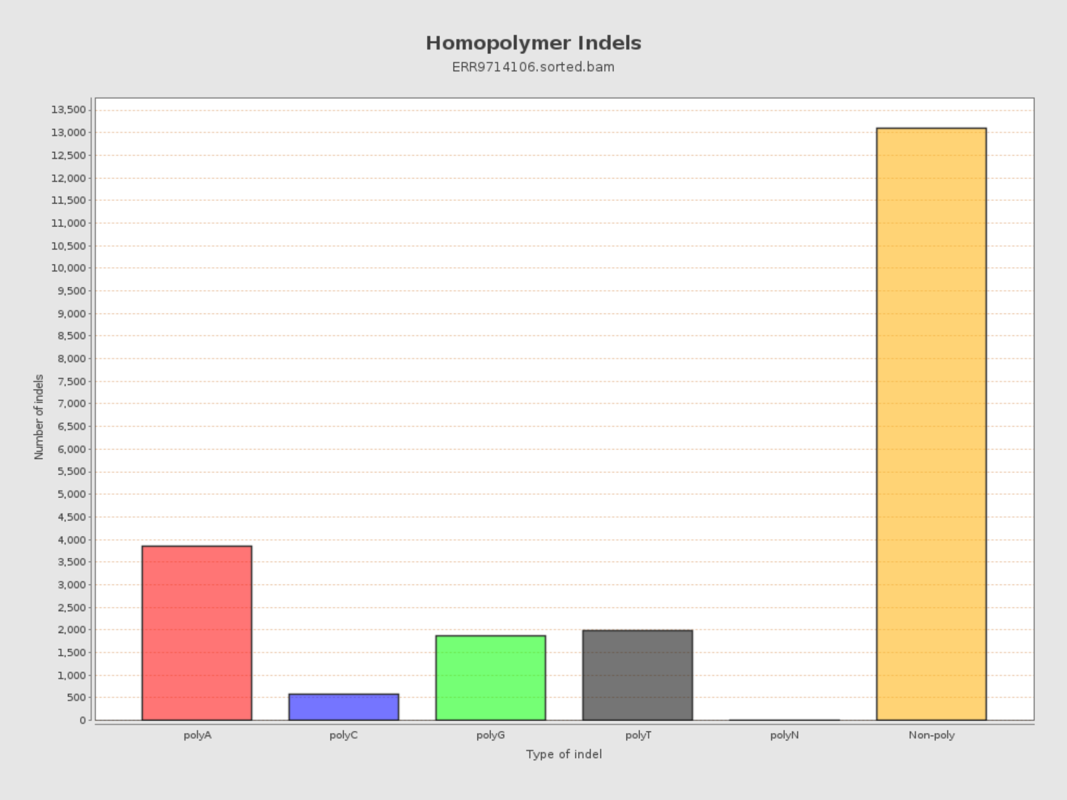
9. Results : Mapped Reads GC-content Distribution



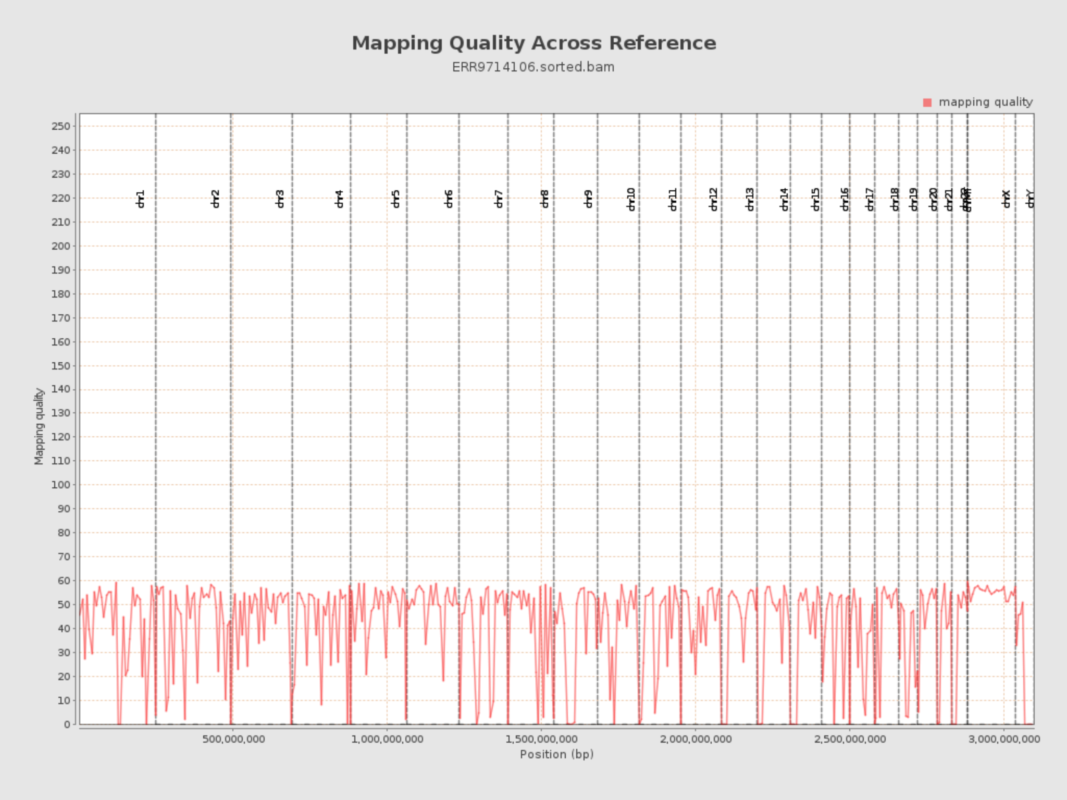
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram