Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 22:38:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714168.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_ERR9714168 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714168.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 22:38:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714168.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	49,940
Mapped reads	3,473 / 6.95%
Unmapped reads	46,467 / 93.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	95 / 0.19%
Read min/max/mean length	30 / 151 / 54.95
Duplicated reads (estimated)	2,582 / 5.17%
Duplication rate	37.12%
Clipped reads	2,996 / 6%

2.2. ACGT Content

Number/percentage of A's	59,443 / 18.52%
Number/percentage of C's	38,772 / 12.08%
Number/percentage of T's	51,343 / 15.99%
Number/percentage of G's	171,490 / 53.41%
Number/percentage of N's	5 / 0%
GC Percentage	65.49%

2.3. Coverage

Mean	0.0001

Standard Deviation	0.1547

2.4. Mapping Quality

Mean Mapping Quality	16.62

2.5. Mismatches and indels

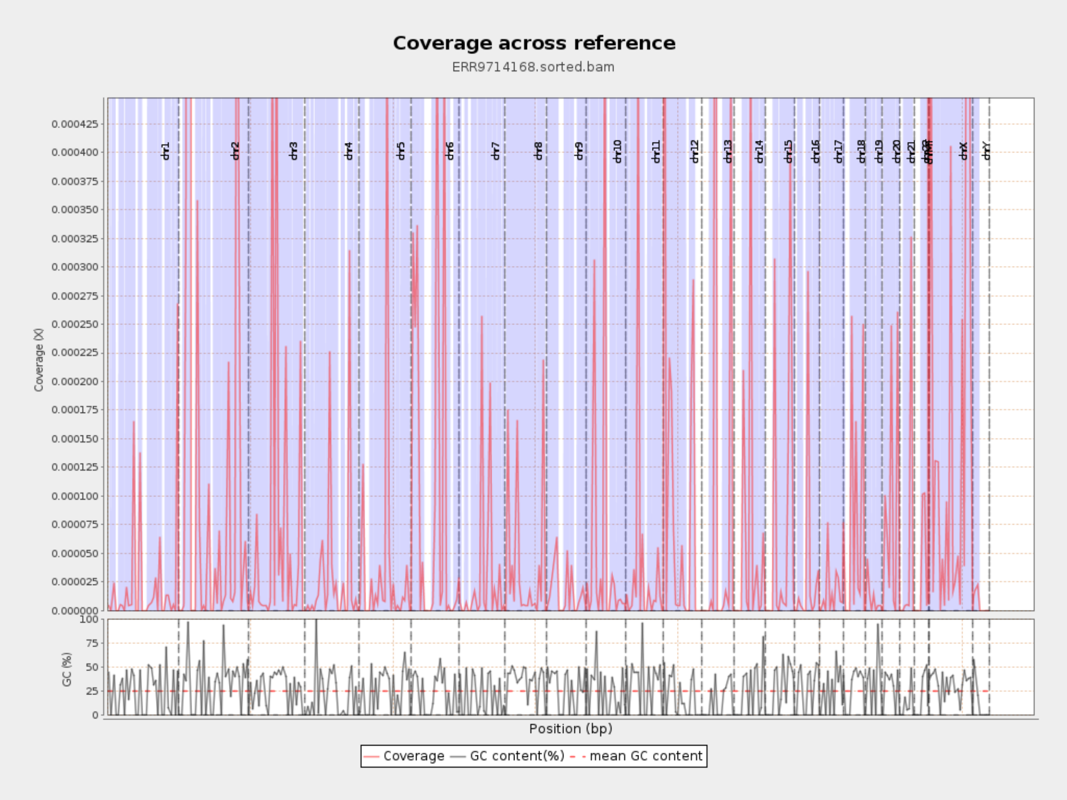
General error rate	3.65%
Mismatches	10,219
Insertions	314
Mapped reads with at least one insertion	7.31%
Deletions	698
Mapped reads with at least one deletion	19.49%
Homopolymer indels	36.96%

2.6. Chromosome stats

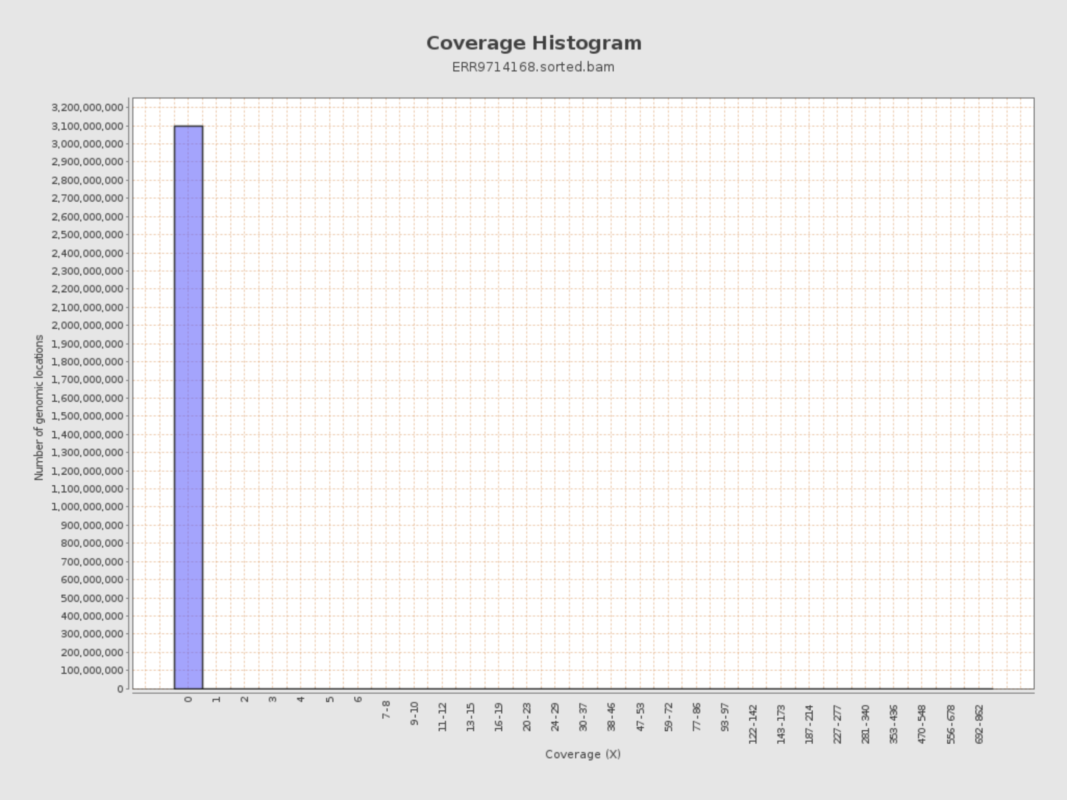
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6092	0	0.0147
chr2	243199373	156764	0.0006	0.5424
chr3	198022430	15377	0.0001	0.0365
chr4	191154276	6274	0	0.0147
chr5	180915260	7094	0	0.0246
chr6	171115067	16876	0.0001	0.0399
chr7	159138663	5002	0	0.0239

chr8	146364022	5716	0	0.0172
chr9	141213431	2306	0	0.0056
chr10	135534747	8068	0.0001	0.0347
chr11	135006516	5774	0	0.0282
chr12	133851895	14931	0.0001	0.0432
chr13	115169878	11279	0.0001	0.0575
chr14	107349540	6682	0.0001	0.0347
chr15	102531392	8088	0.0001	0.0334
chr16	90354753	2998	0	0.015
chr17	81195210	1354	0	0.0117
chr18	78077248	5782	0.0001	0.0294
chr19	59128983	651	0	0.0046
chr20	63025520	5451	0.0001	0.0262
chr21	48129895	2642	0.0001	0.0274
chr22	51304566	1647	0	0.0118
chrMT	16571	931	0.0562	0.3262
chrX	155270560	27596	0.0002	0.0486
chrY	59373566	369	0	0.0032

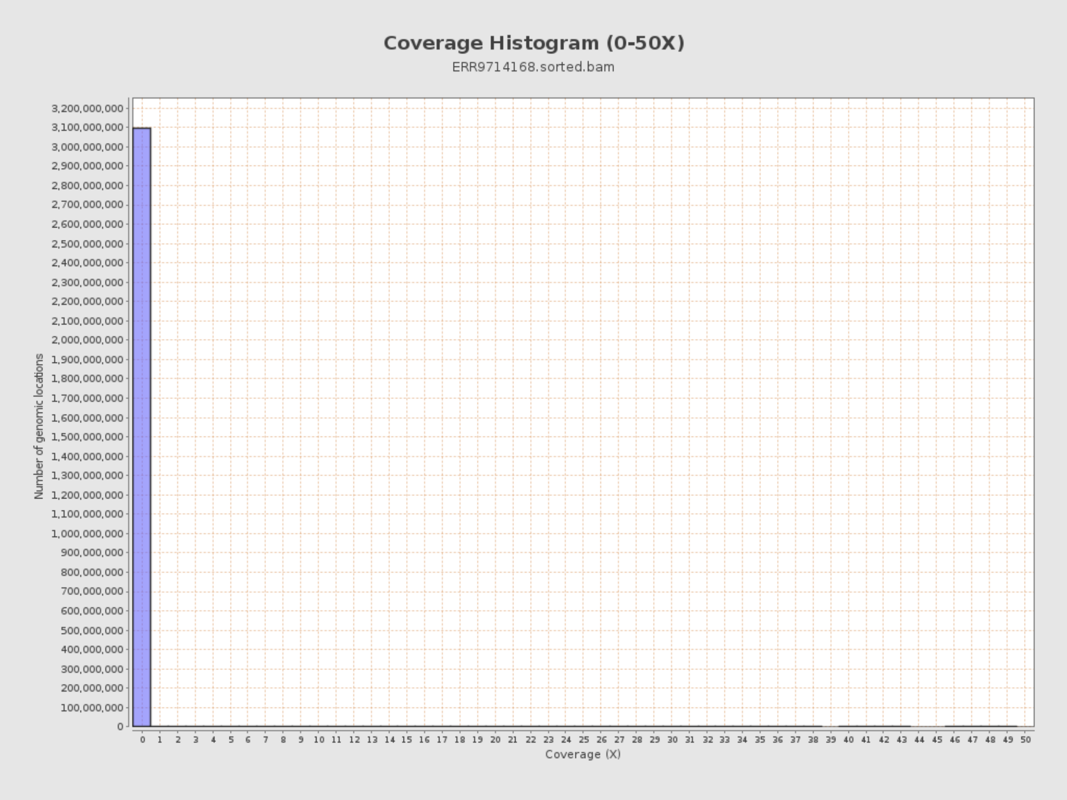
3. Results : Coverage across reference



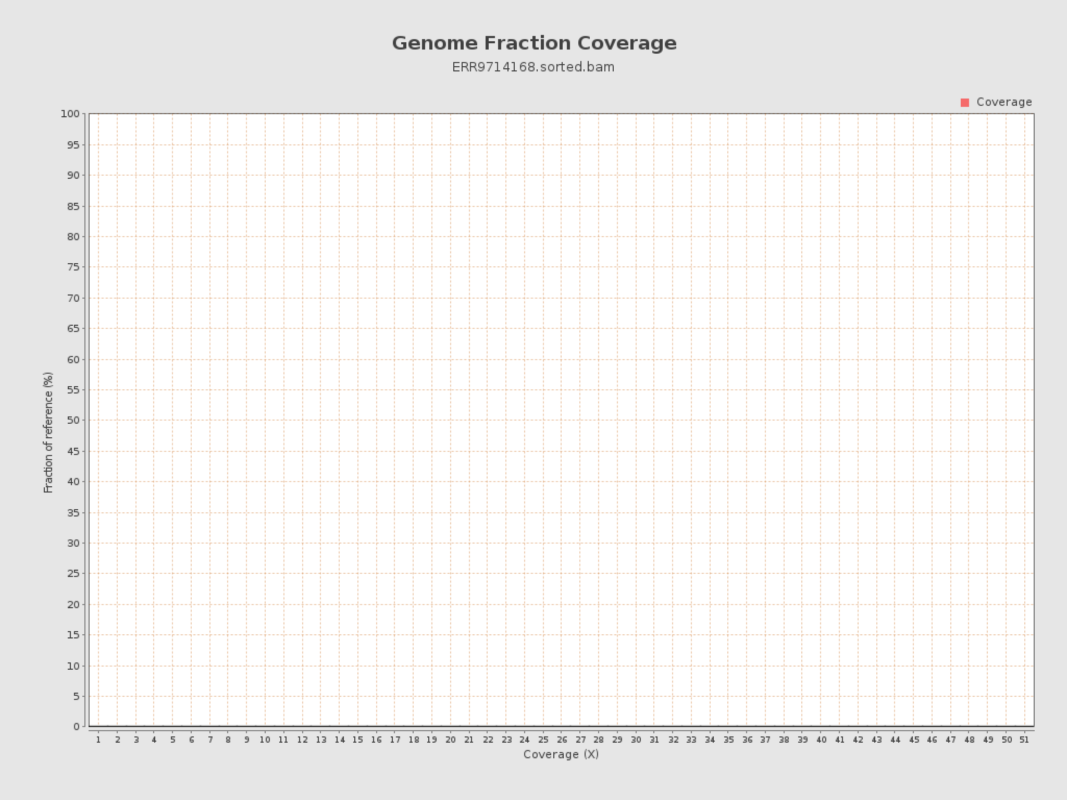
4. Results : Coverage Histogram



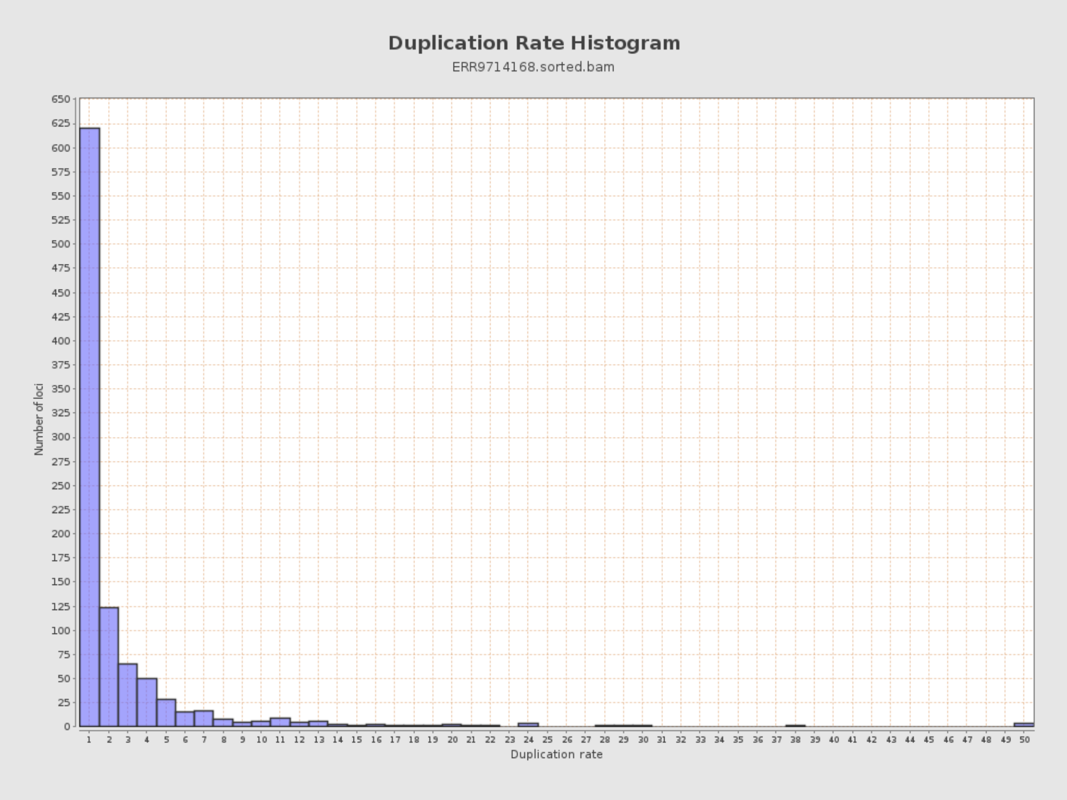
5. Results : Coverage Histogram (0-50X)



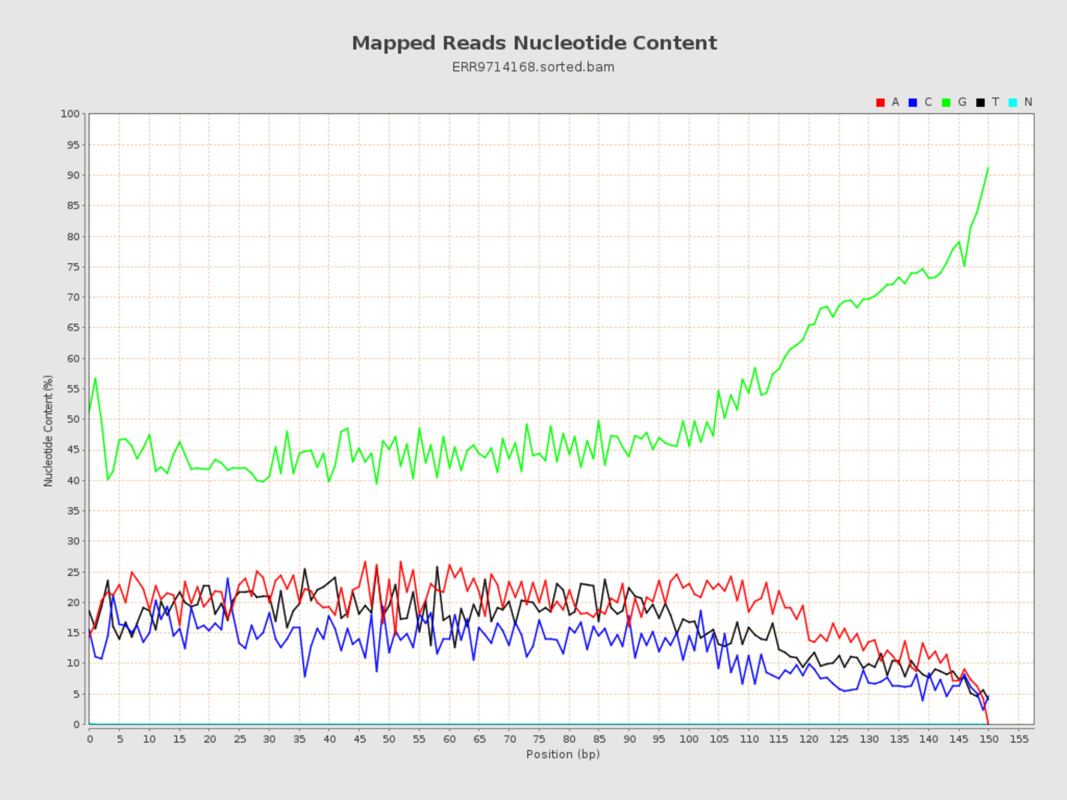
6. Results : Genome Fraction Coverage



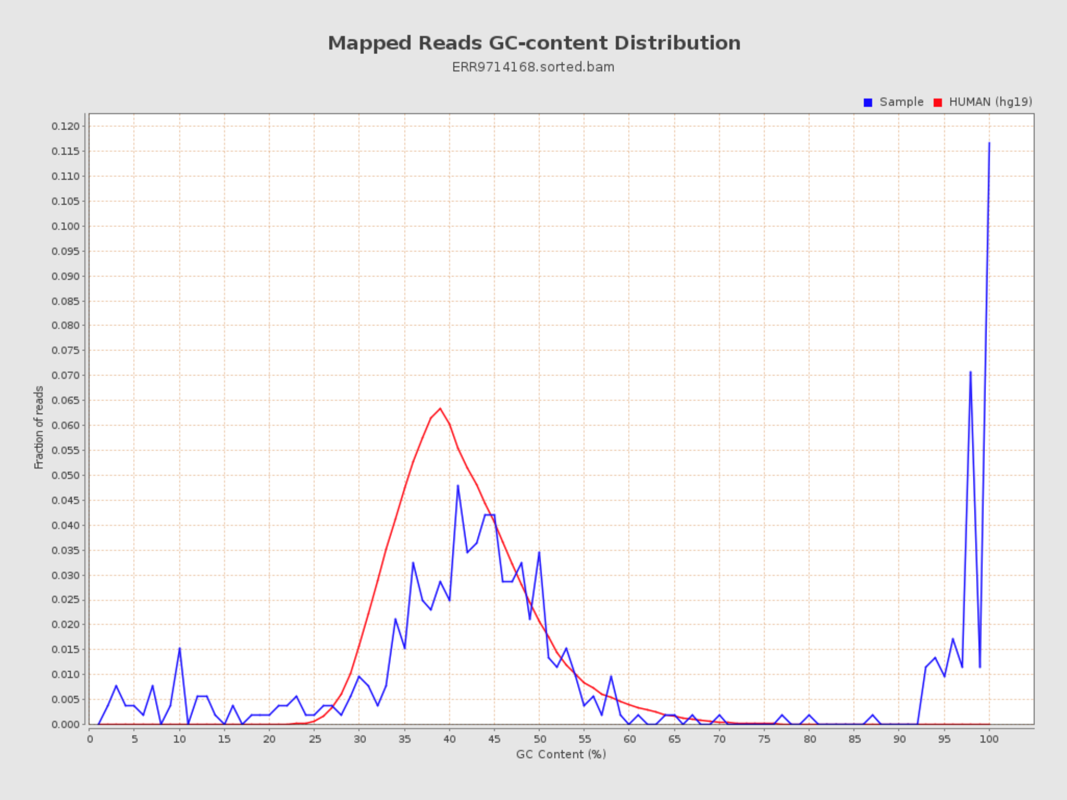
7. Results : Duplication Rate Histogram



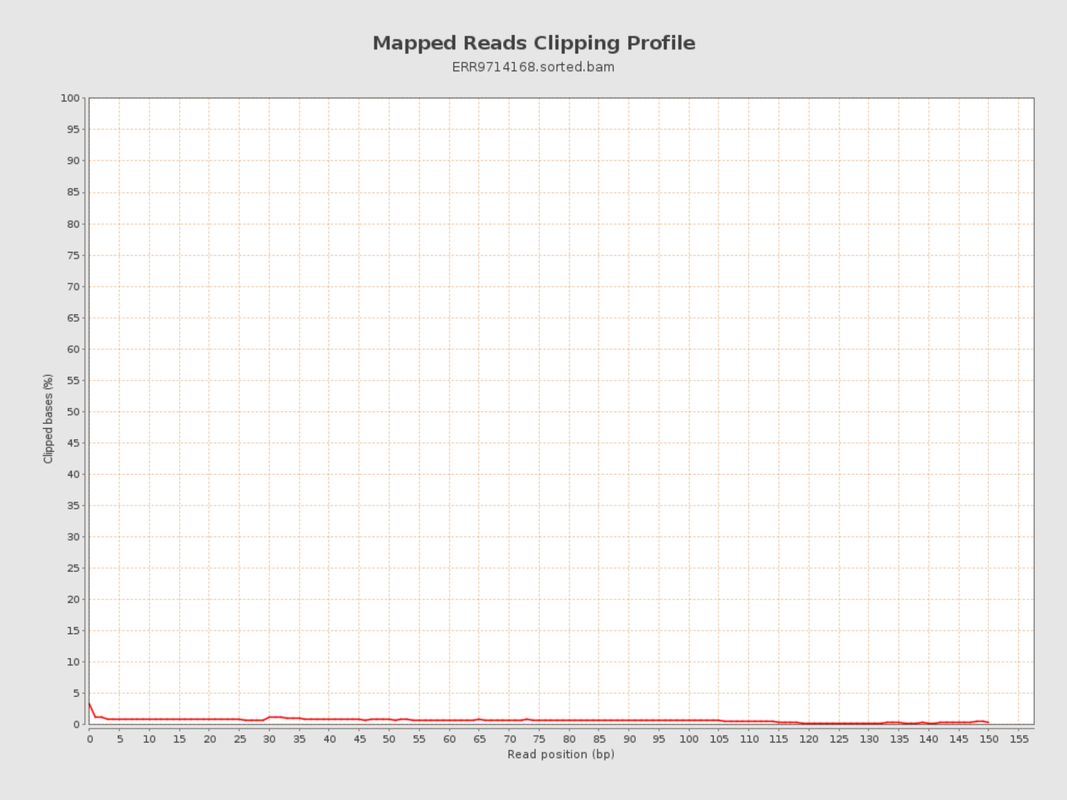
8. Results : Mapped Reads Nucleotide Content



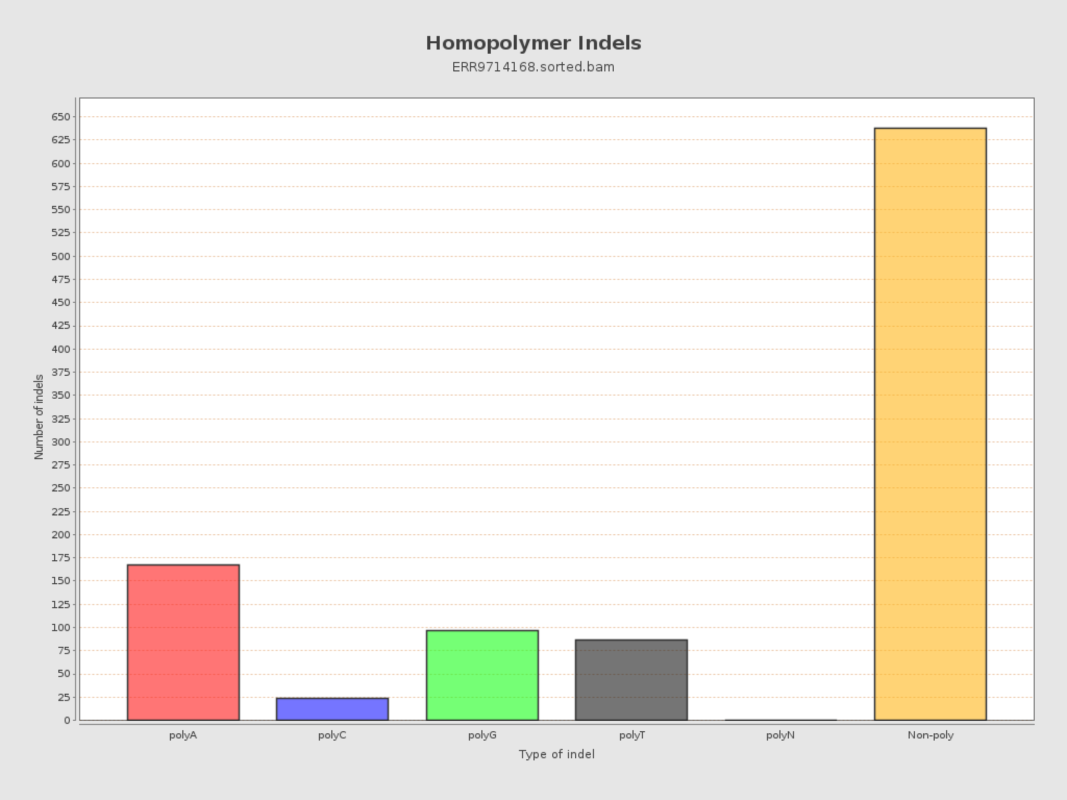
9. Results : Mapped Reads GC-content Distribution



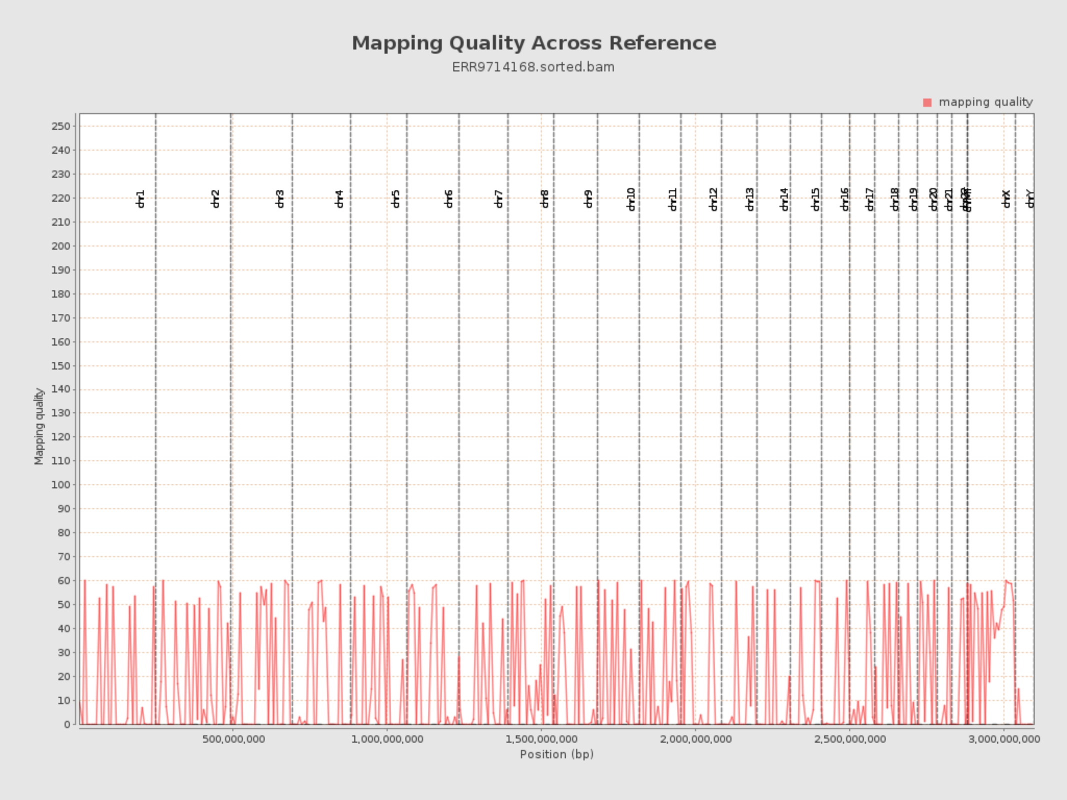
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram