Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 00:28:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714218.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_ERR9714218 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714218.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 00:28:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714218.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	183,516
Mapped reads	29,856 / 16.27%
Unmapped reads	153,660 / 83.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	895 / 0.49%
Read min/max/mean length	30 / 151 / 66.18
Duplicated reads (estimated)	23,436 / 12.77%
Duplication rate	38.24%
Clipped reads	27,082 / 14.76%

2.2. ACGT Content

Number/percentage of A's	786,997 / 24.4%
Number/percentage of C's	532,427 / 16.51%
Number/percentage of T's	728,593 / 22.59%
Number/percentage of G's	1,177,257 / 36.5%
Number/percentage of N's	23 / 0%
GC Percentage	53.01%

2.3. Coverage

Mean	0.0011

Standard Deviation	0.7343

2.4. Mapping Quality

Mean Mapping Quality	45.86

2.5. Mismatches and indels

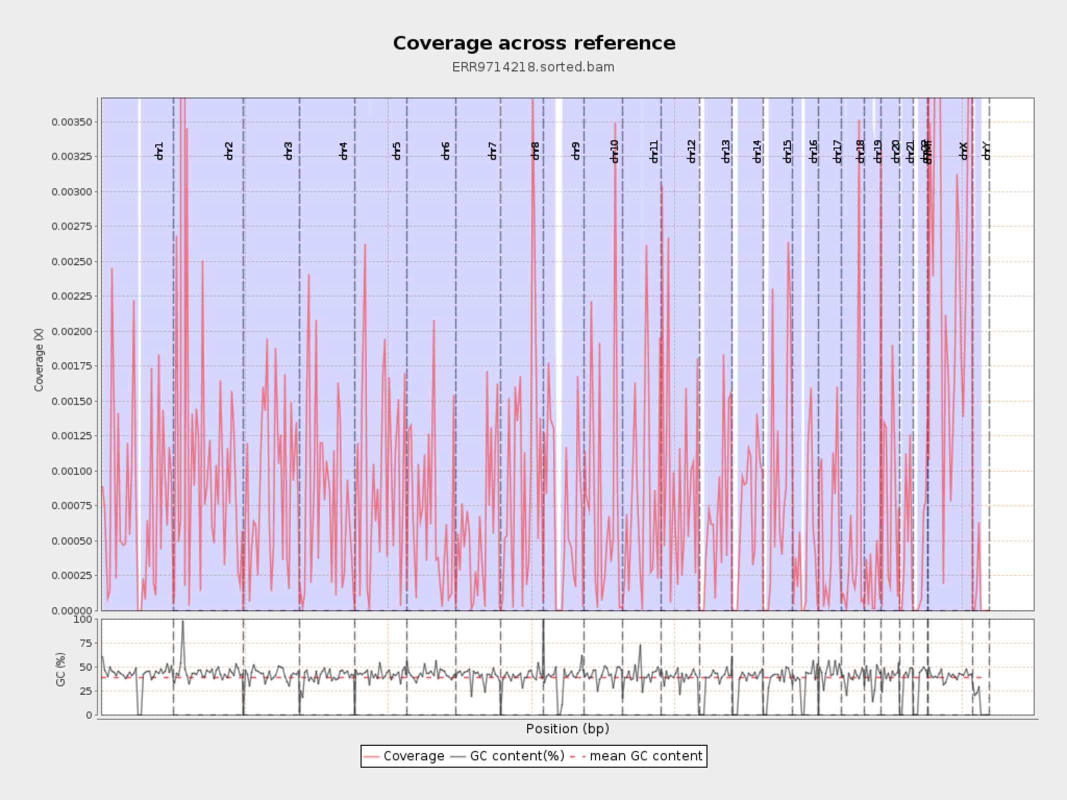
General error rate	3.99%
Mismatches	116,867
Insertions	3,456
Mapped reads with at least one insertion	10.64%
Deletions	9,483
Mapped reads with at least one deletion	29.99%
Homopolymer indels	28.65%

2.6. Chromosome stats

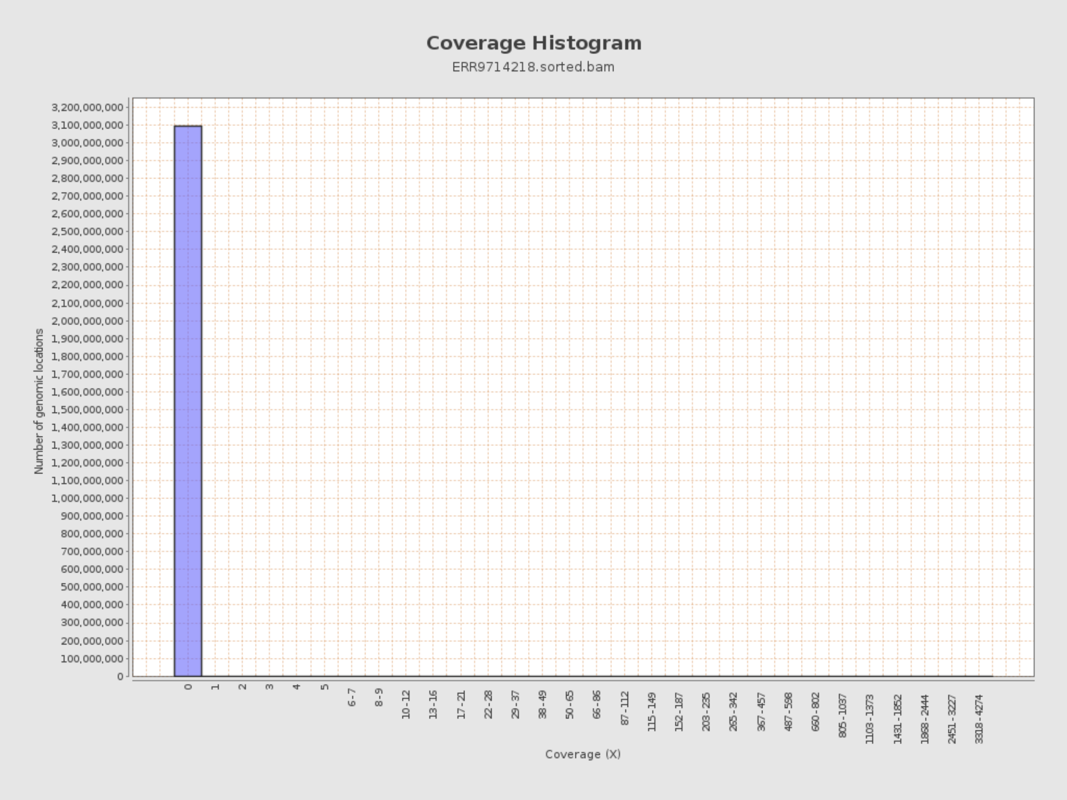
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	196660	0.0008	0.1424
chr2	243199373	870242	0.0036	2.57
chr3	198022430	173349	0.0009	0.142
chr4	191154276	153662	0.0008	0.14
chr5	180915260	174271	0.001	0.1517
chr6	171115067	116918	0.0007	0.1178
chr7	159138663	93246	0.0006	0.1419

chr8	146364022	142972	0.001	0.1692
chr9	141213431	100266	0.0007	0.1308
chr10	135534747	116108	0.0009	0.1455
chr11	135006516	114155	0.0008	0.1619
chr12	133851895	131214	0.001	0.1881
chr13	115169878	75176	0.0007	0.1357
chr14	107349540	74772	0.0007	0.1209
chr15	102531392	94019	0.0009	0.1546
chr16	90354753	38813	0.0004	0.077
chr17	81195210	51404	0.0006	0.1197
chr18	78077248	42490	0.0005	0.1278
chr19	59128983	18001	0.0003	0.0881
chr20	63025520	51245	0.0008	0.1376
chr21	48129895	24666	0.0005	0.0992
chr22	51304566	15793	0.0003	0.0819
chrMT	16571	5946	0.3588	2.9876
chrX	155270560	401158	0.0026	0.2648
chrY	59373566	6217	0.0001	0.0507

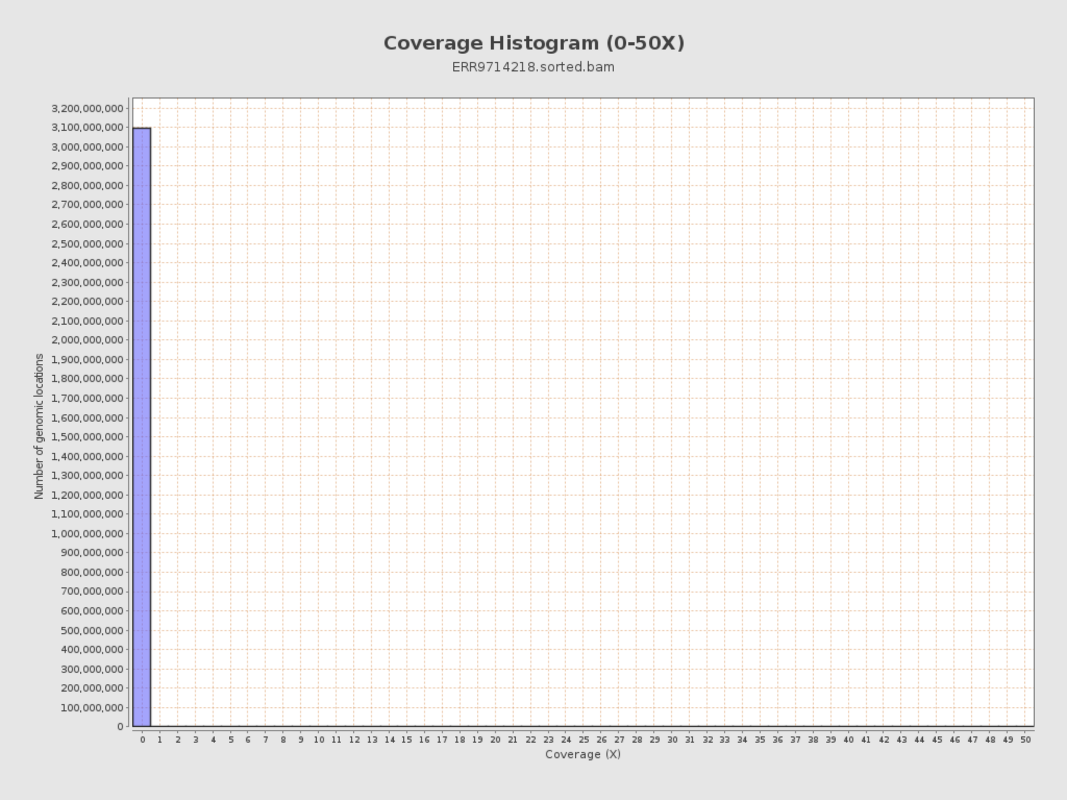
3. Results : Coverage across reference



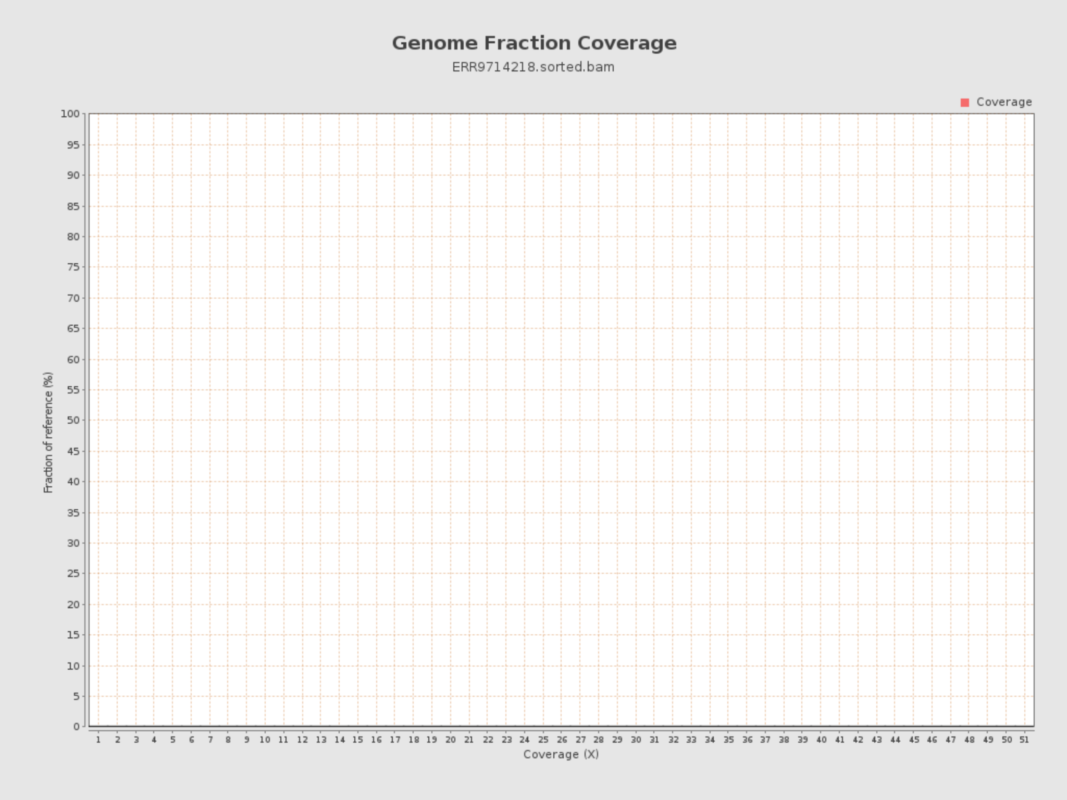
4. Results : Coverage Histogram



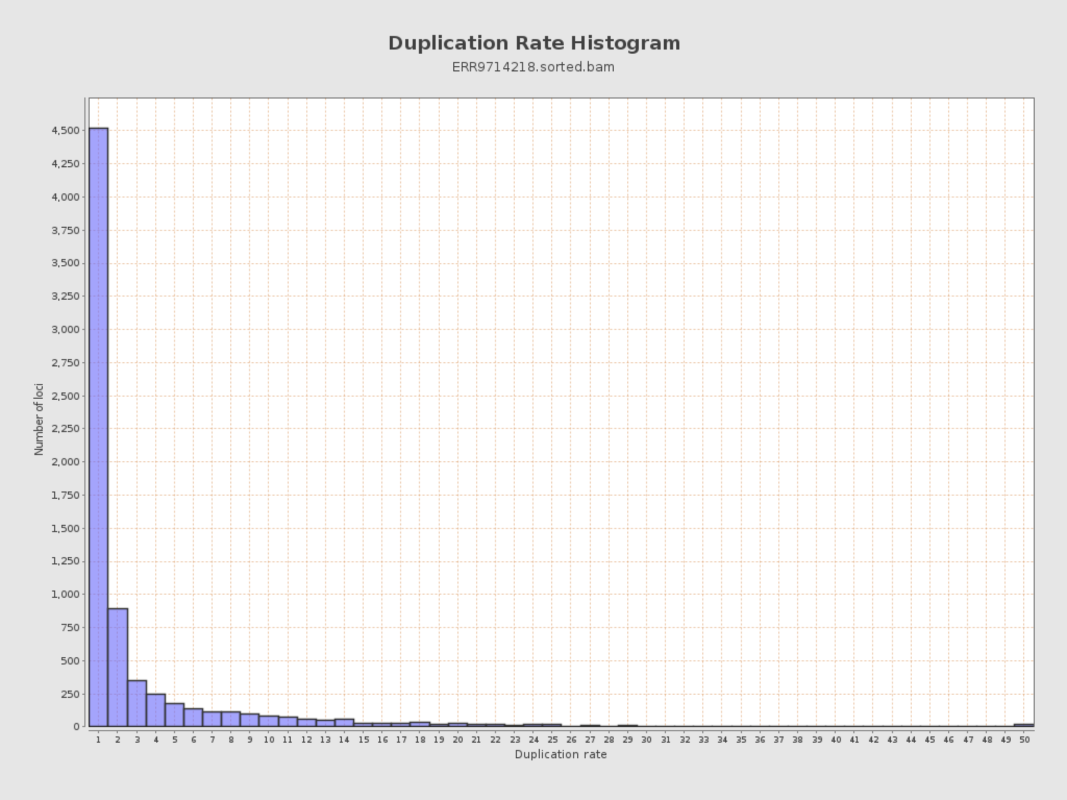
5. Results : Coverage Histogram (0-50X)



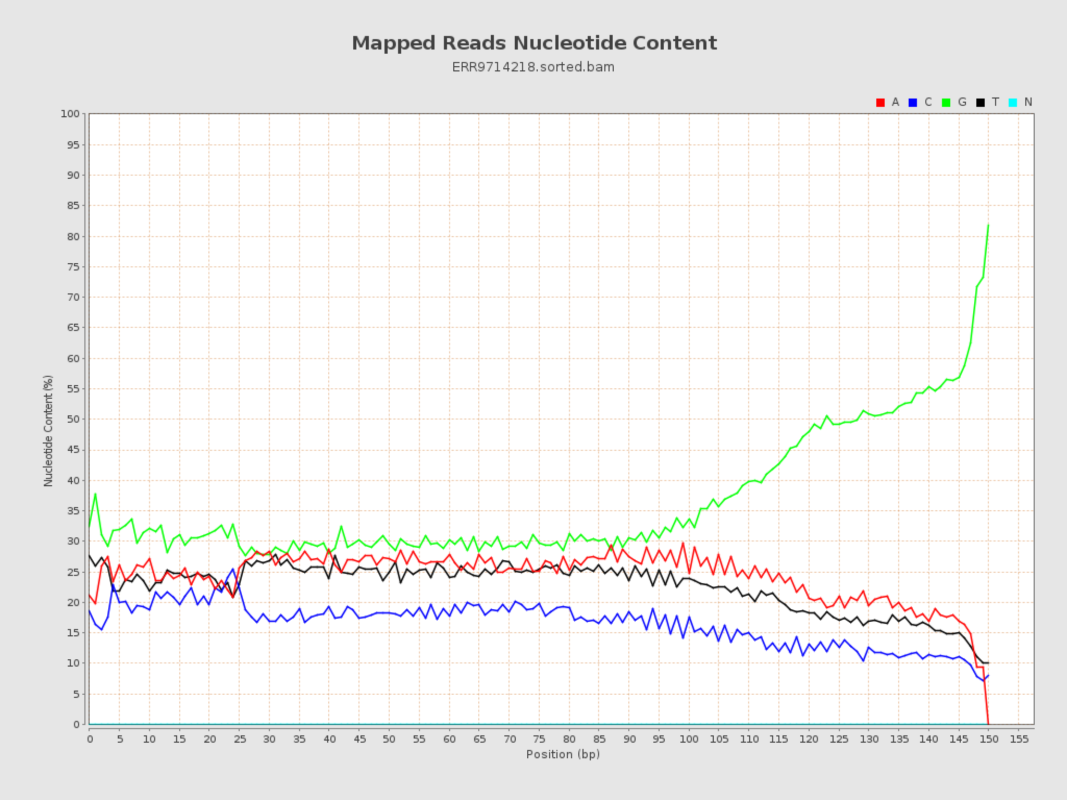
6. Results : Genome Fraction Coverage



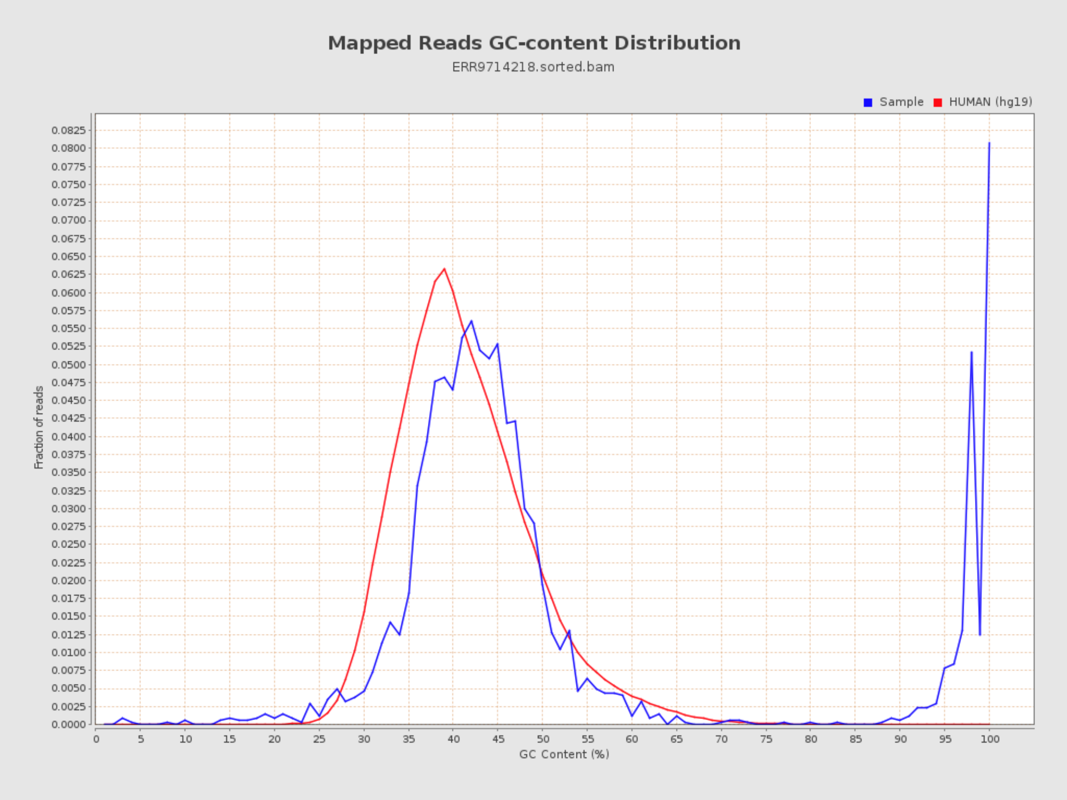
7. Results : Duplication Rate Histogram



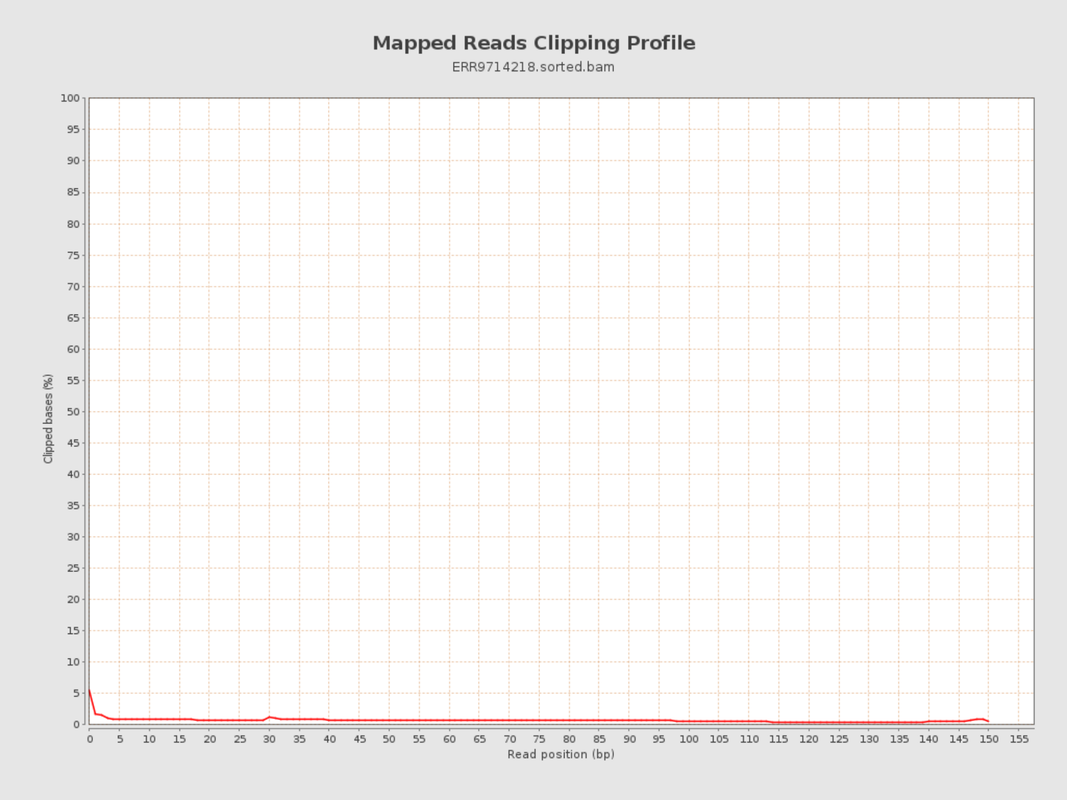
8. Results : Mapped Reads Nucleotide Content



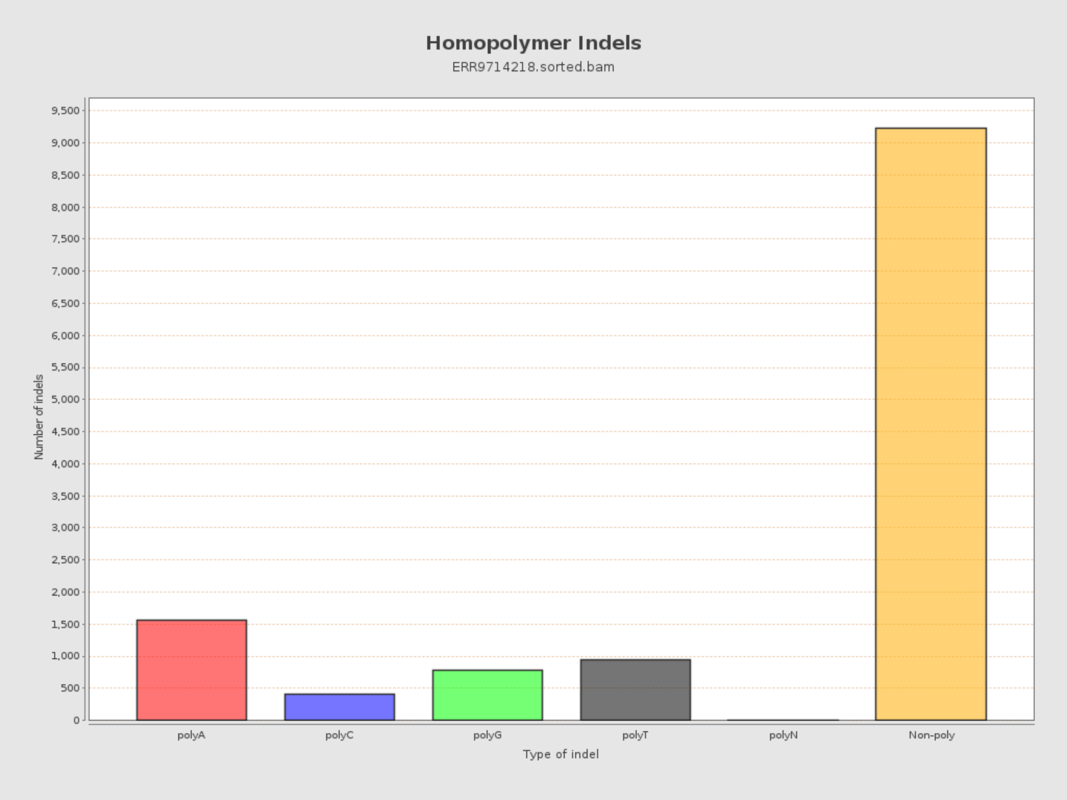
9. Results : Mapped Reads GC-content Distribution



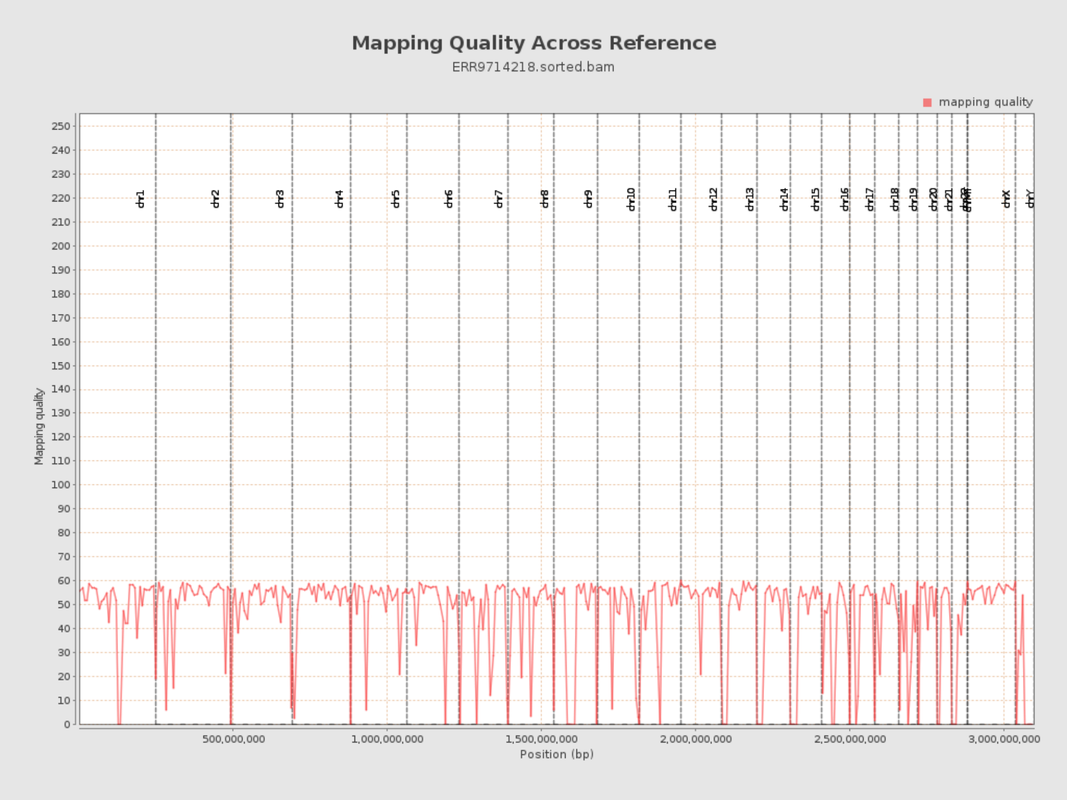
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram