Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 00:54:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714234.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_ERR9714234 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714234.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 00:54:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714234.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	280,622
Mapped reads	21,066 / 7.51%
Unmapped reads	259,556 / 92.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	422 / 0.15%
Read min/max/mean length	30 / 151 / 53.48
Duplicated reads (estimated)	20,050 / 7.14%
Duplication rate	36.51%
Clipped reads	13,033 / 4.64%

2.2. ACGT Content

Number/percentage of A's	62,200 / 3.13%
Number/percentage of C's	24,474 / 1.23%
Number/percentage of T's	33,541 / 1.69%
Number/percentage of G's	1,867,600 / 93.94%
Number/percentage of N's	189 / 0.01%
GC Percentage	95.17%

2.3. Coverage

Mean	0.0006

Standard Deviation	2.2792

2.4. Mapping Quality

Mean Mapping Quality	12.3

2.5. Mismatches and indels

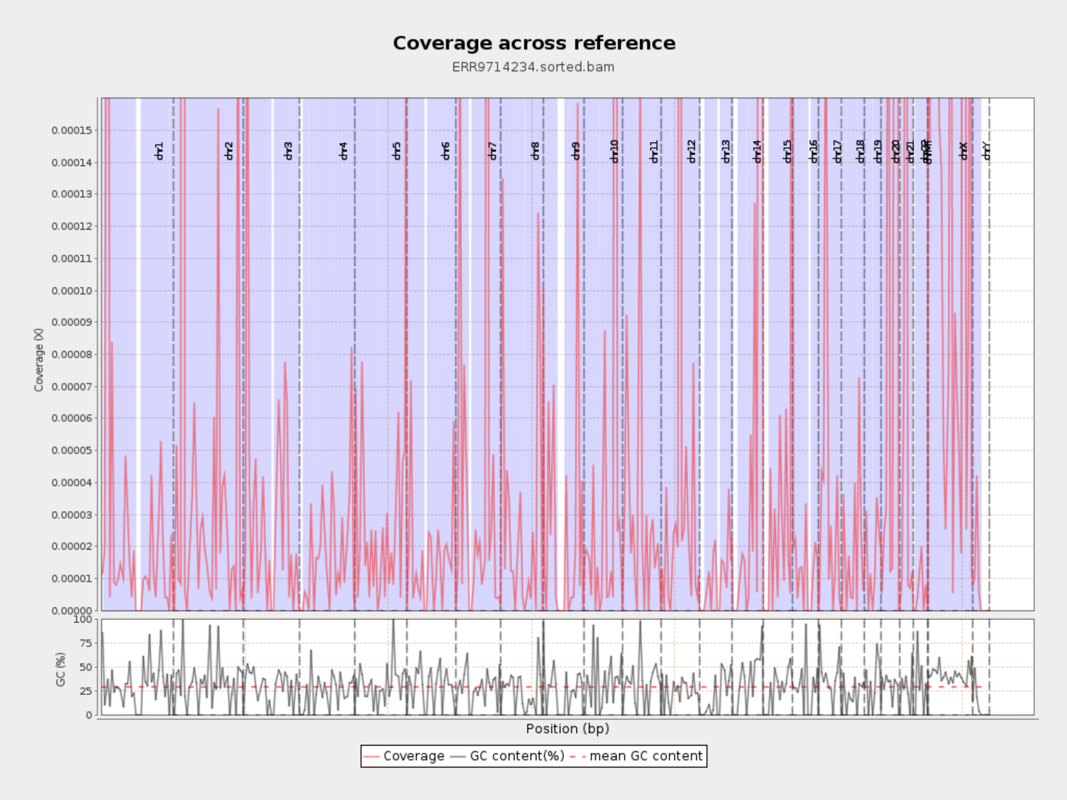
General error rate	3.18%
Mismatches	47,032
Insertions	2,321
Mapped reads with at least one insertion	7.6%
Deletions	1,030
Mapped reads with at least one deletion	4.78%
Homopolymer indels	63.56%

2.6. Chromosome stats

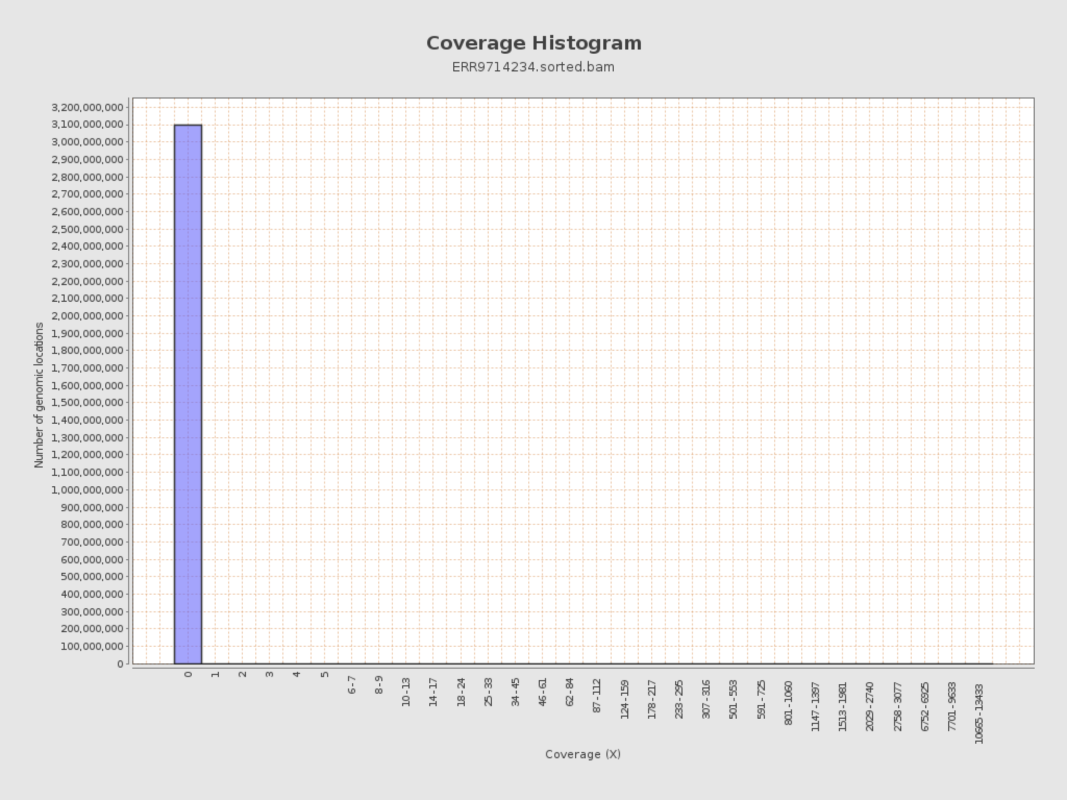
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7116	0	0.0189
chr2	243199373	1866911	0.0077	8.1309
chr3	198022430	6111	0	0.0128
chr4	191154276	3549	0	0.0103
chr5	180915260	4685	0	0.0083
chr6	171115067	2908	0	0.0063
chr7	159138663	7411	0	0.0478

chr8	146364022	4314	0	0.0123
chr9	141213431	3603	0	0.0101
chr10	135534747	8637	0.0001	0.0411
chr11	135006516	4193	0	0.0198
chr12	133851895	5978	0	0.0298
chr13	115169878	1190	0	0.0038
chr14	107349540	10002	0.0001	0.0602
chr15	102531392	3861	0	0.0195
chr16	90354753	1154	0	0.006
chr17	81195210	3031	0	0.0303
chr18	78077248	1563	0	0.0055
chr19	59128983	924	0	0.0053
chr20	63025520	7292	0.0001	0.0554
chr21	48129895	3733	0.0001	0.0382
chr22	51304566	342	0	0.0026
chrMT	16571	397	0.024	0.1957
chrX	155270560	33410	0.0002	0.0637
chrY	59373566	496	0	0.0039

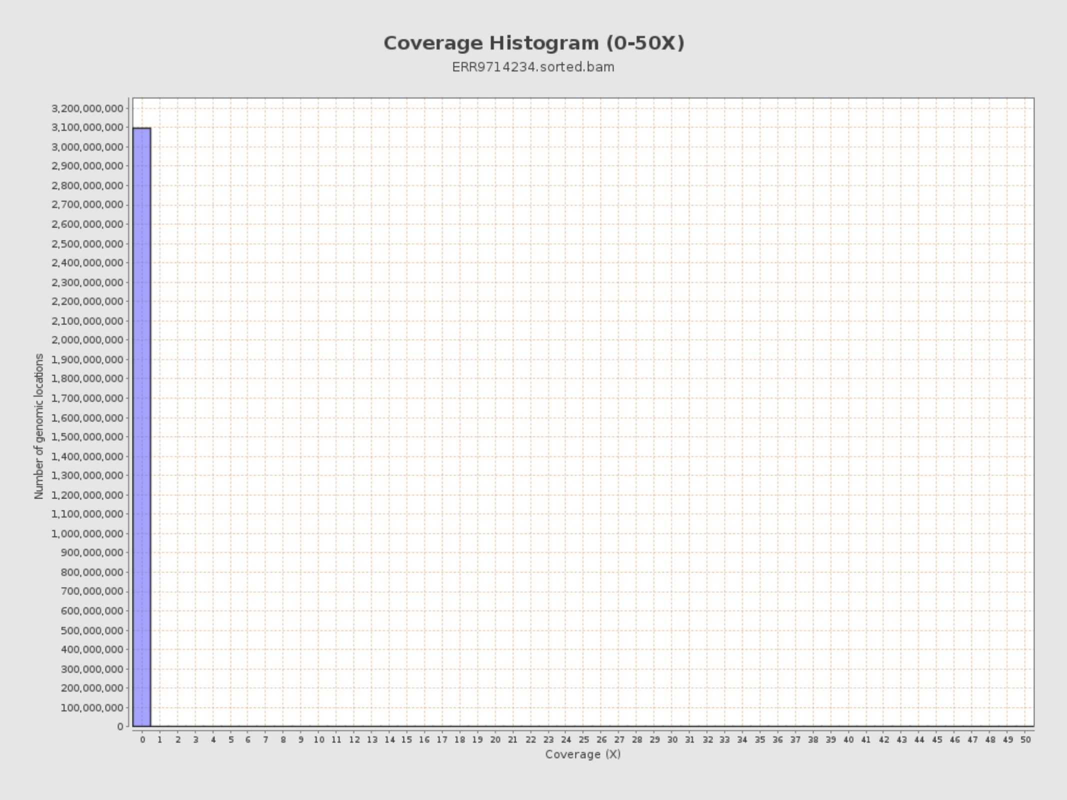
3. Results : Coverage across reference



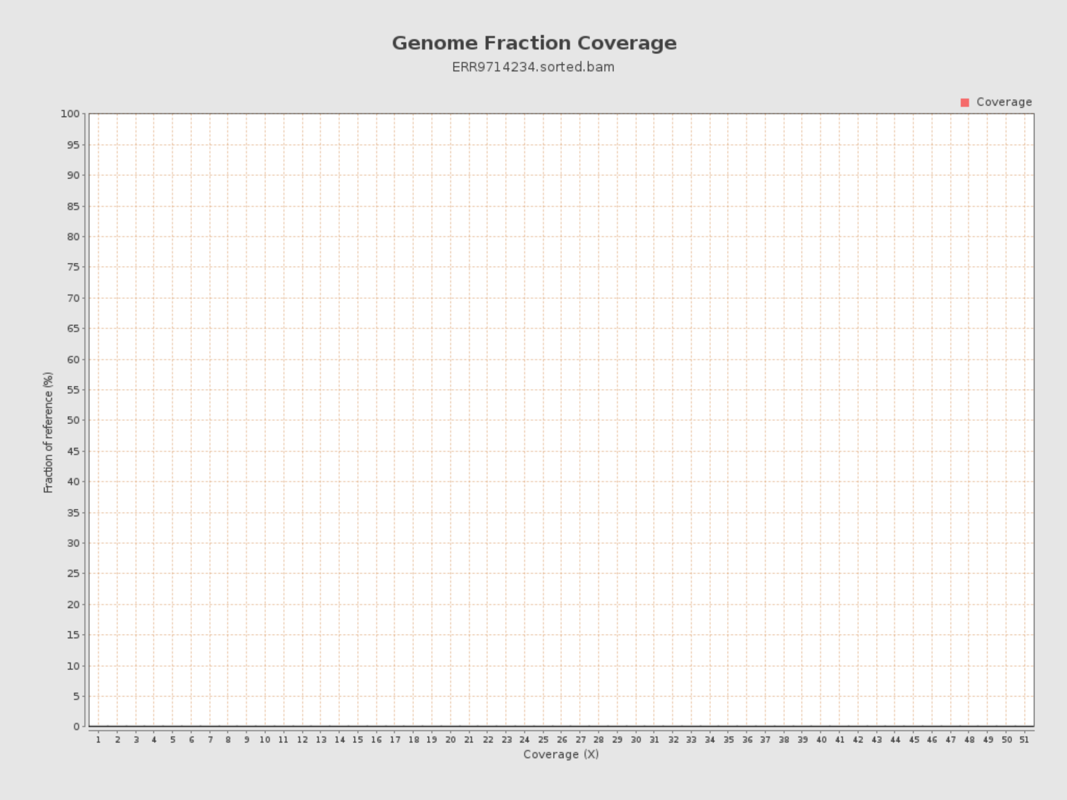
4. Results : Coverage Histogram



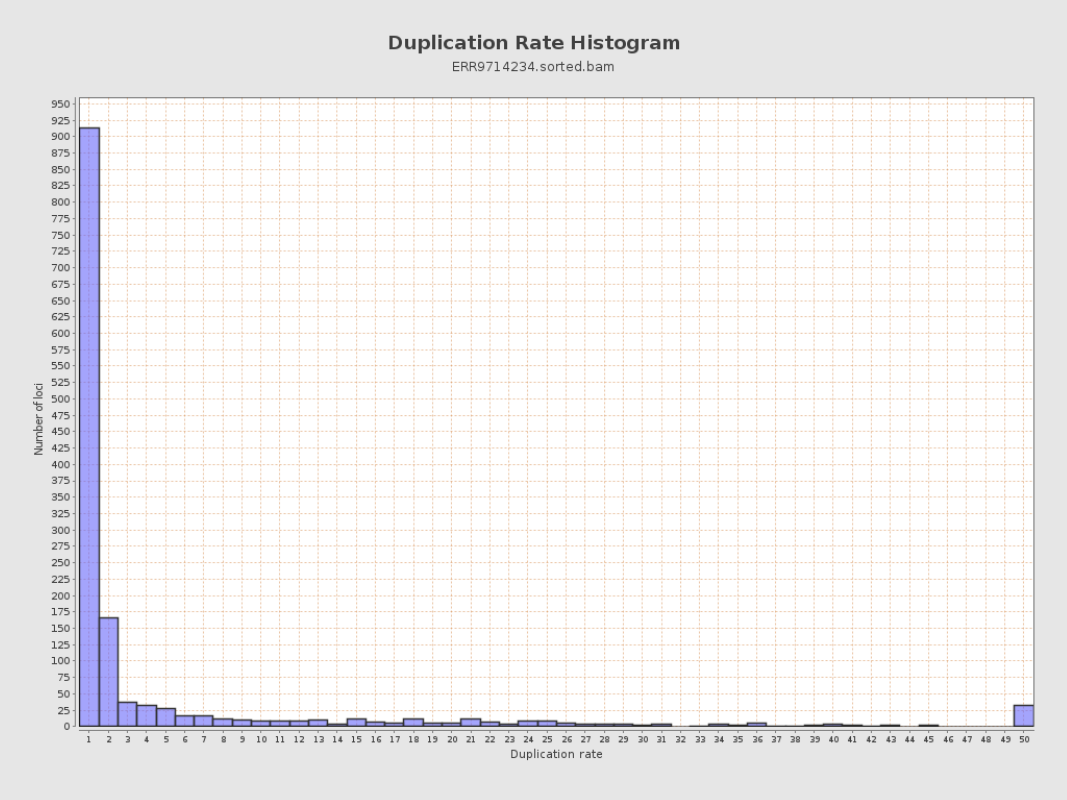
5. Results : Coverage Histogram (0-50X)



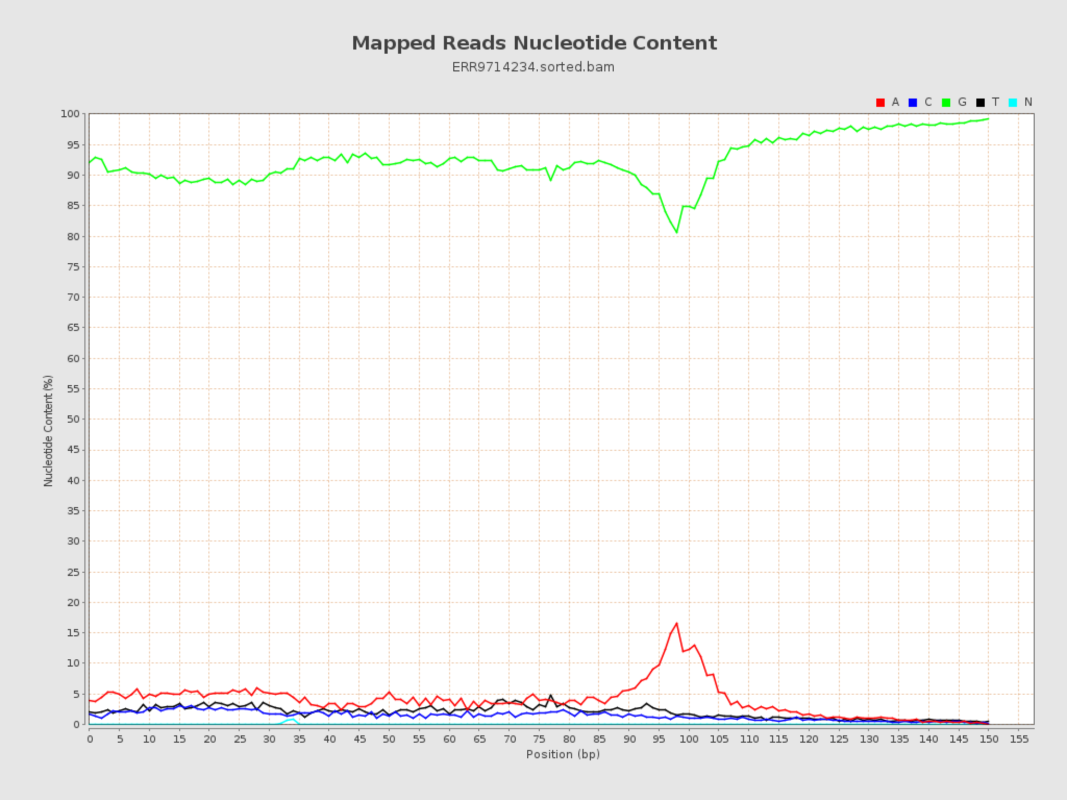
6. Results : Genome Fraction Coverage



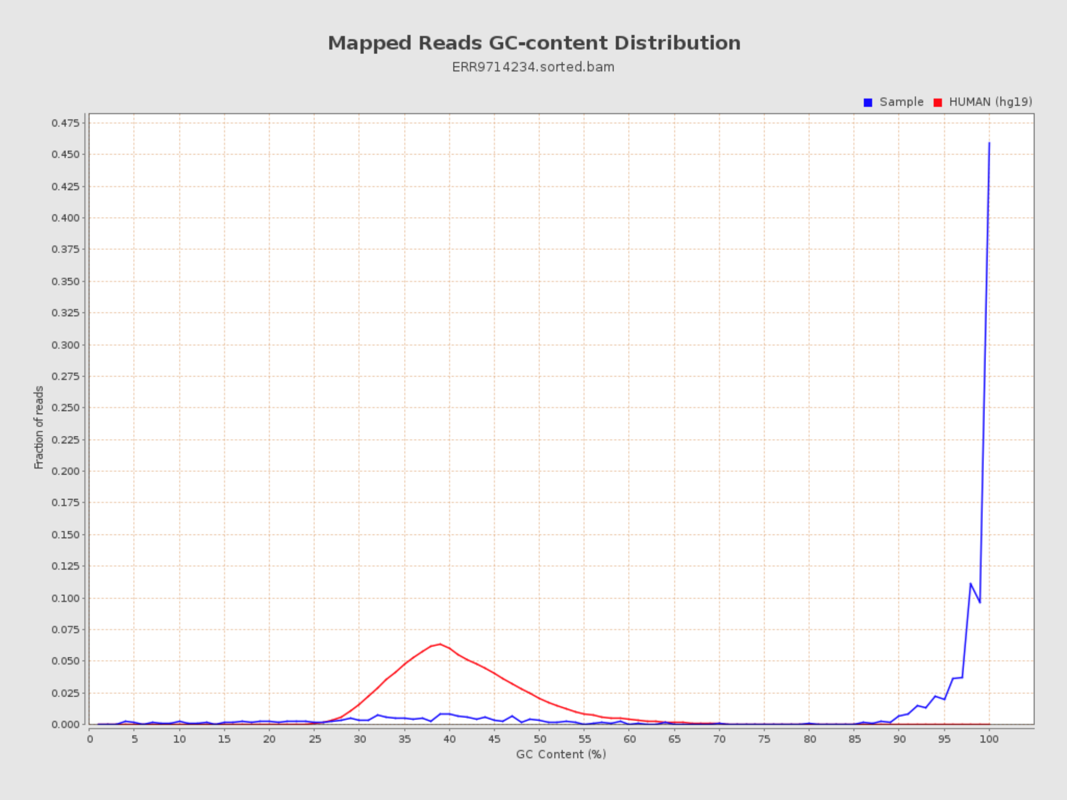
7. Results : Duplication Rate Histogram



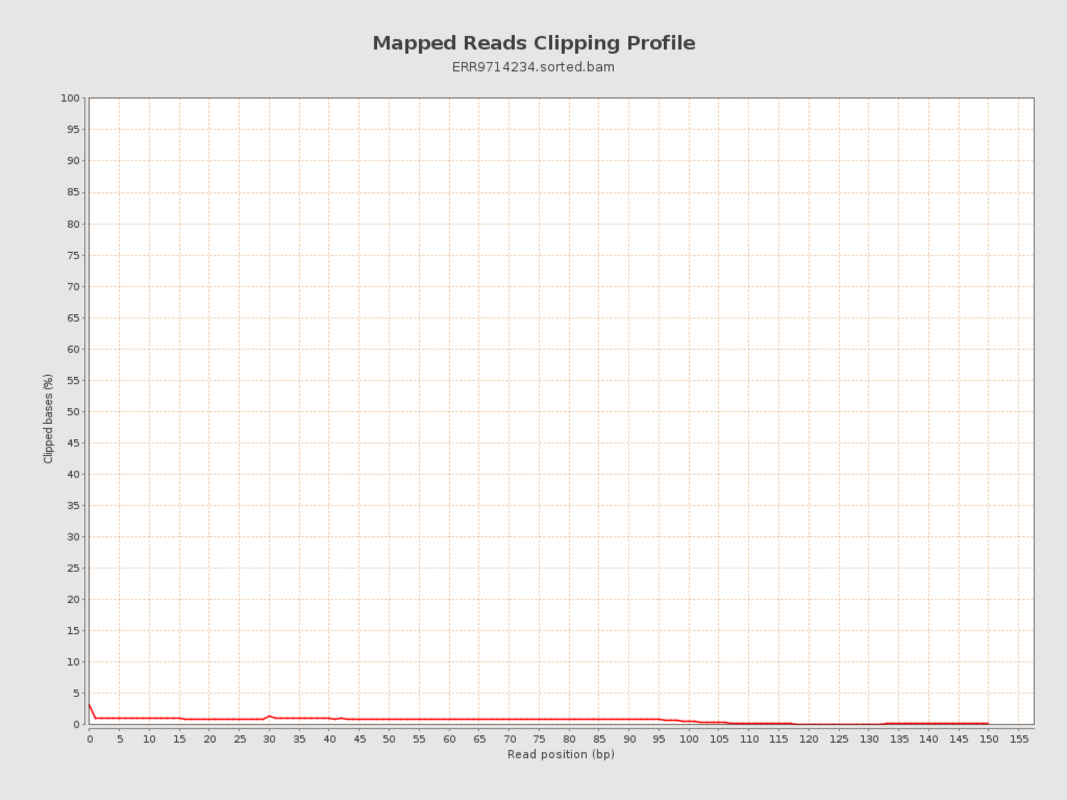
8. Results : Mapped Reads Nucleotide Content



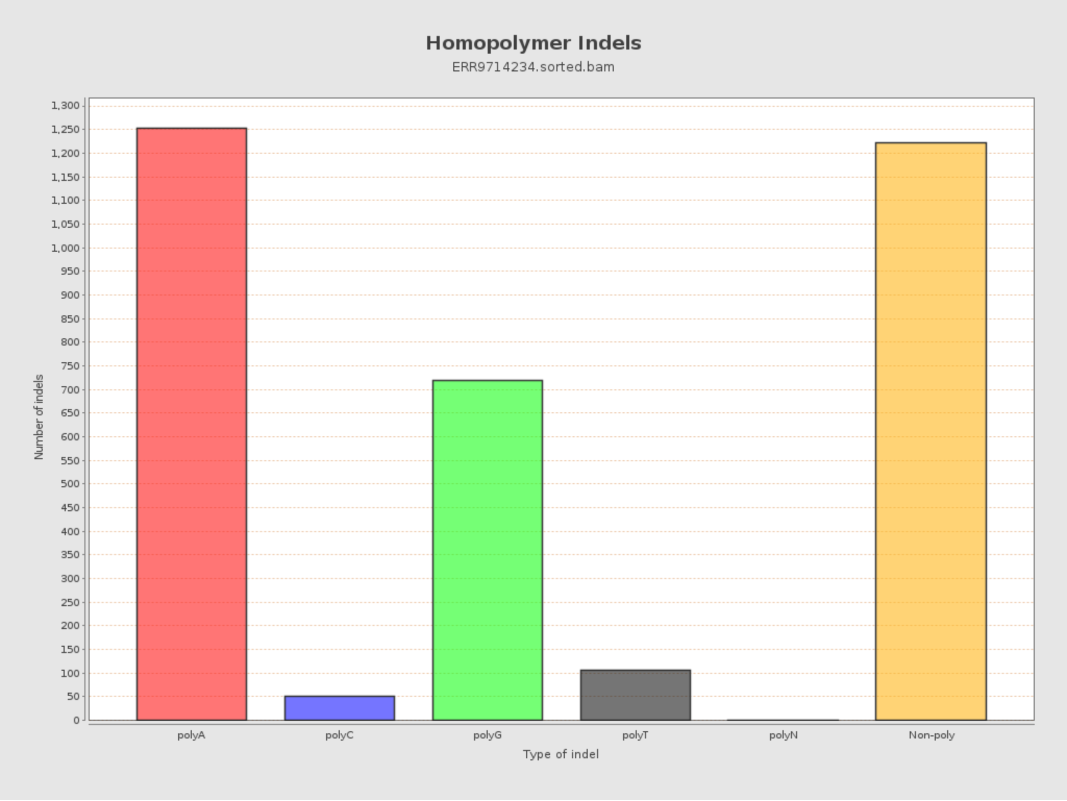
9. Results : Mapped Reads GC-content Distribution



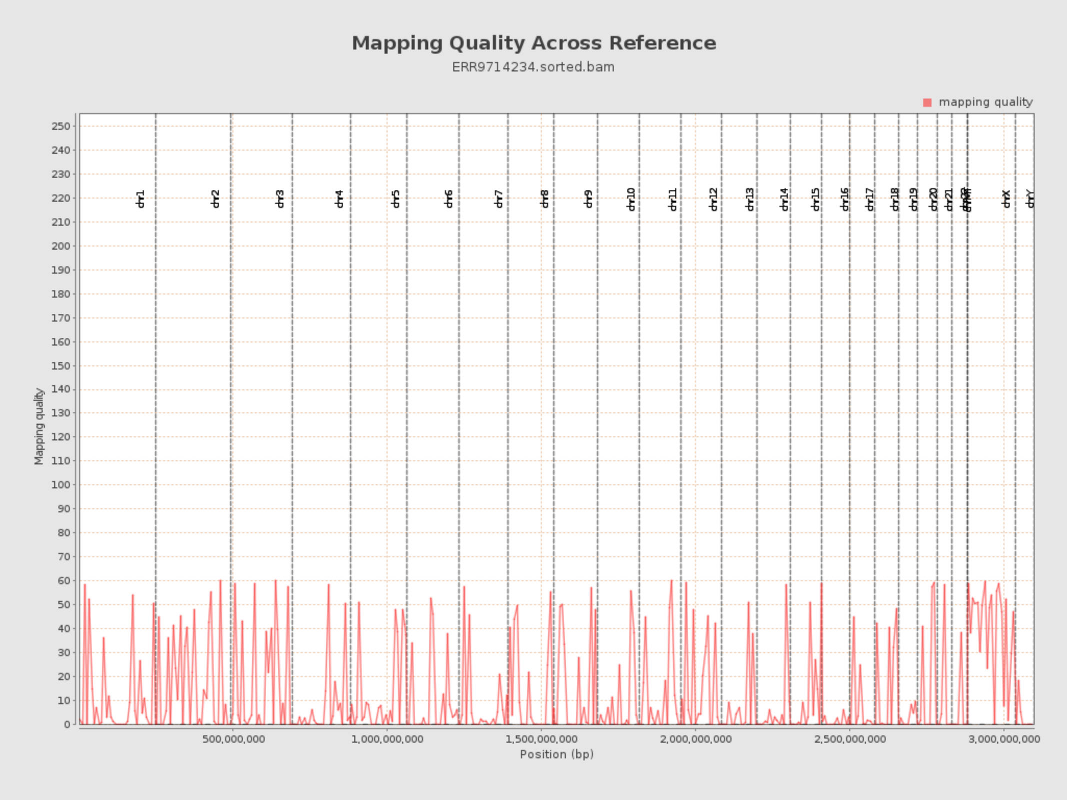
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram