Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 23:18:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714180.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_ERR9714180 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714180.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 23:17:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714180.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,742,602
Mapped reads	1,631,107 / 93.6%
Unmapped reads	111,495 / 6.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	85,505 / 4.91%
Read min/max/mean length	30 / 151 / 139.52
Duplicated reads (estimated)	1,537,999 / 88.26%
Duplication rate	47.79%
Clipped reads	1,585,796 / 91%

2.2. ACGT Content

Number/percentage of A's	59,642,816 / 29.32%
Number/percentage of C's	41,673,245 / 20.49%
Number/percentage of T's	56,415,520 / 27.73%
Number/percentage of G's	45,678,422 / 22.46%
Number/percentage of N's	1,445 / 0%
GC Percentage	42.94%

2.3. Coverage

Mean	0.067

Standard Deviation	11.0673

2.4. Mapping Quality

Mean Mapping Quality	51.47

2.5. Mismatches and indels

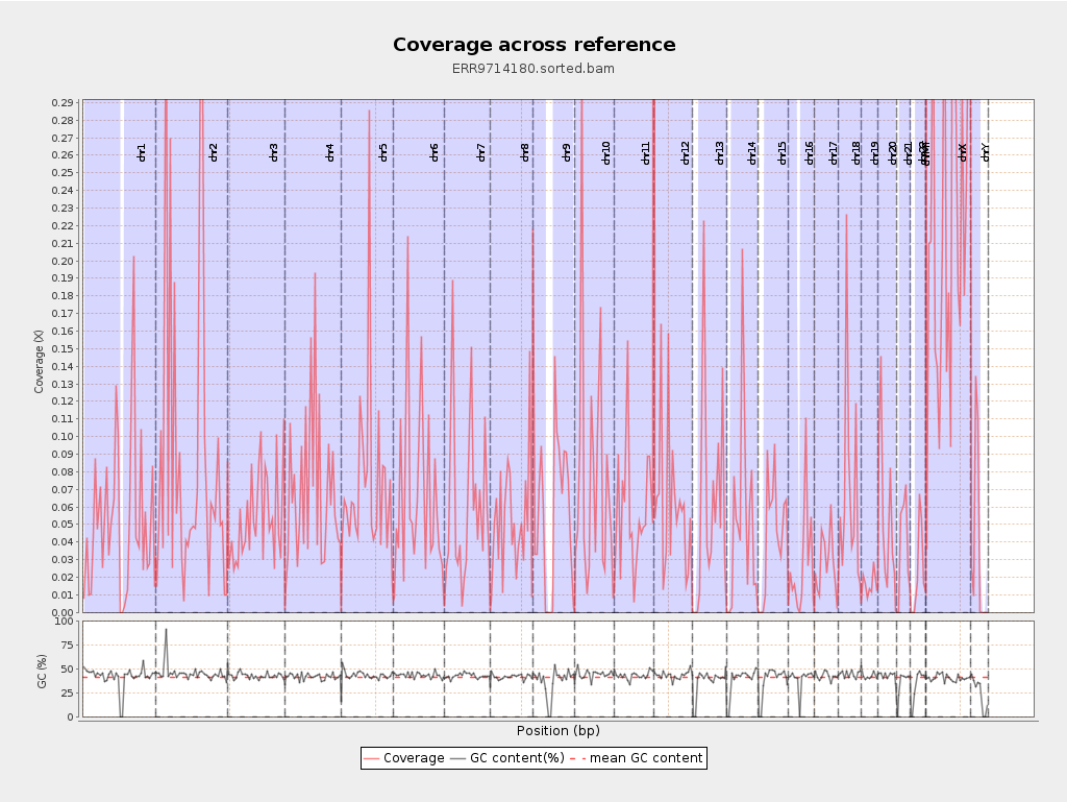
General error rate	3.63%
Mismatches	6,944,433
Insertions	173,042
Mapped reads with at least one insertion	10.28%
Deletions	623,813
Mapped reads with at least one deletion	36.62%
Homopolymer indels	27.67%

2.6. Chromosome stats

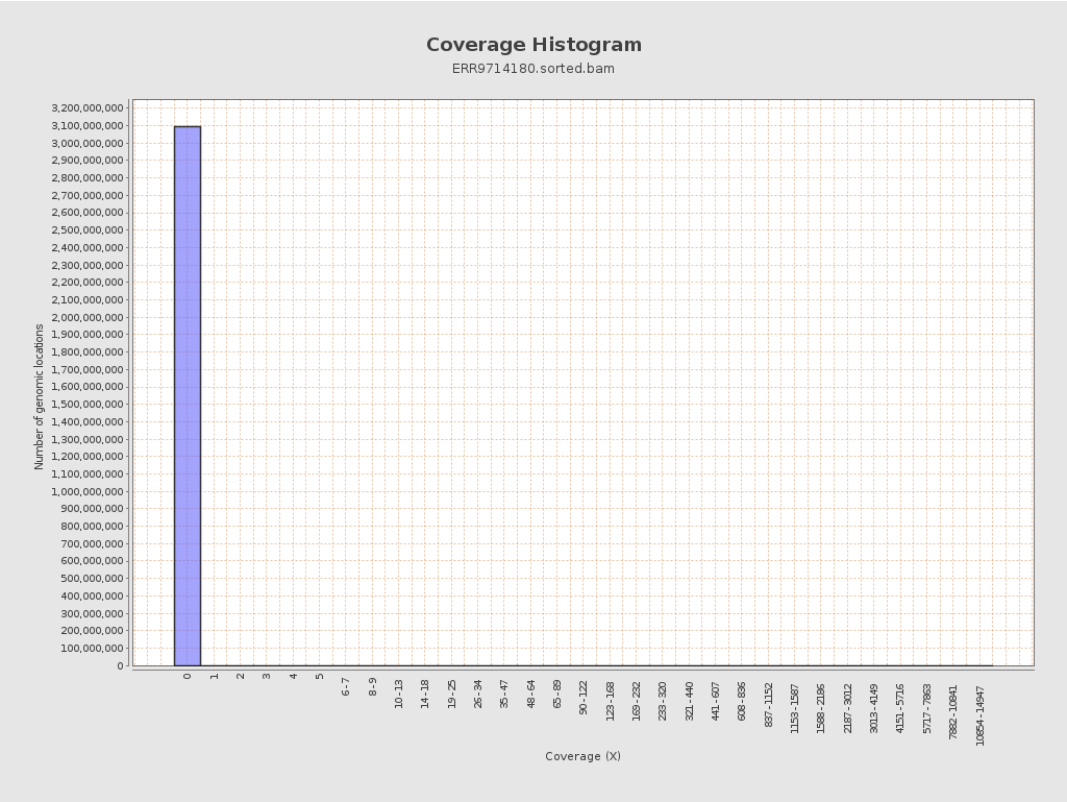
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	13141132	0.0527	8.0562
chr2	243199373	21592874	0.0888	17.6398
chr3	198022430	10662813	0.0538	5.9911
chr4	191154276	13444558	0.0703	10.3042
chr5	180915260	12920811	0.0714	13.7164
chr6	171115067	11756409	0.0687	9.6029
chr7	159138663	9608564	0.0604	10.269

chr8	146364022	7552446	0.0516	5.9731
chr9	141213431	7974538	0.0565	8.2166
chr10	135534747	10421320	0.0769	15.2216
chr11	135006516	8520996	0.0631	10.4602
chr12	133851895	8288649	0.0619	7.3517
chr13	115169878	6884365	0.0598	9.7187
chr14	107349540	5379999	0.0501	11.0989
chr15	102531392	4496799	0.0439	5.6409
chr16	90354753	2464756	0.0273	3.1166
chr17	81195210	2312183	0.0285	4.6241
chr18	78077248	5377144	0.0689	10.9867
chr19	59128983	917079	0.0155	1.7363
chr20	63025520	3423280	0.0543	8.7667
chr21	48129895	1715345	0.0356	5.0275
chr22	51304566	1218271	0.0237	4.0387
chrMT	16571	8130	0.4906	3.909
chrX	155270560	35076622	0.2259	21.954
chrY	59373566	2102041	0.0354	8.0384

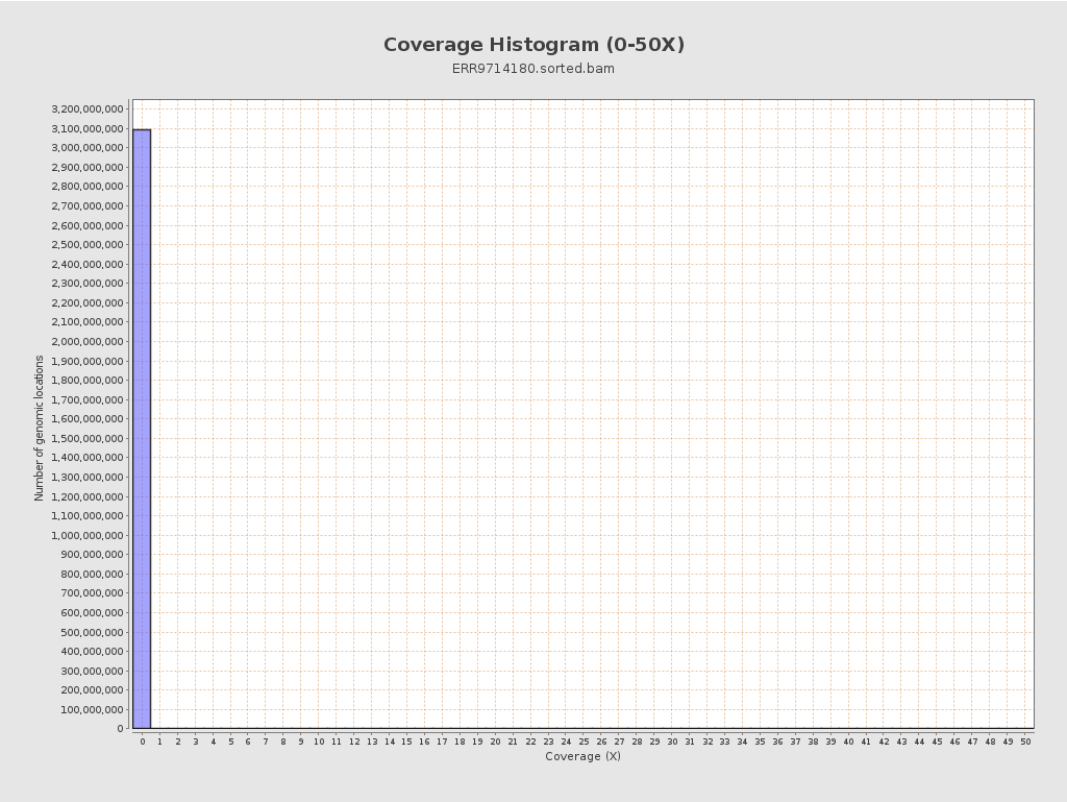
3. Results : Coverage across reference



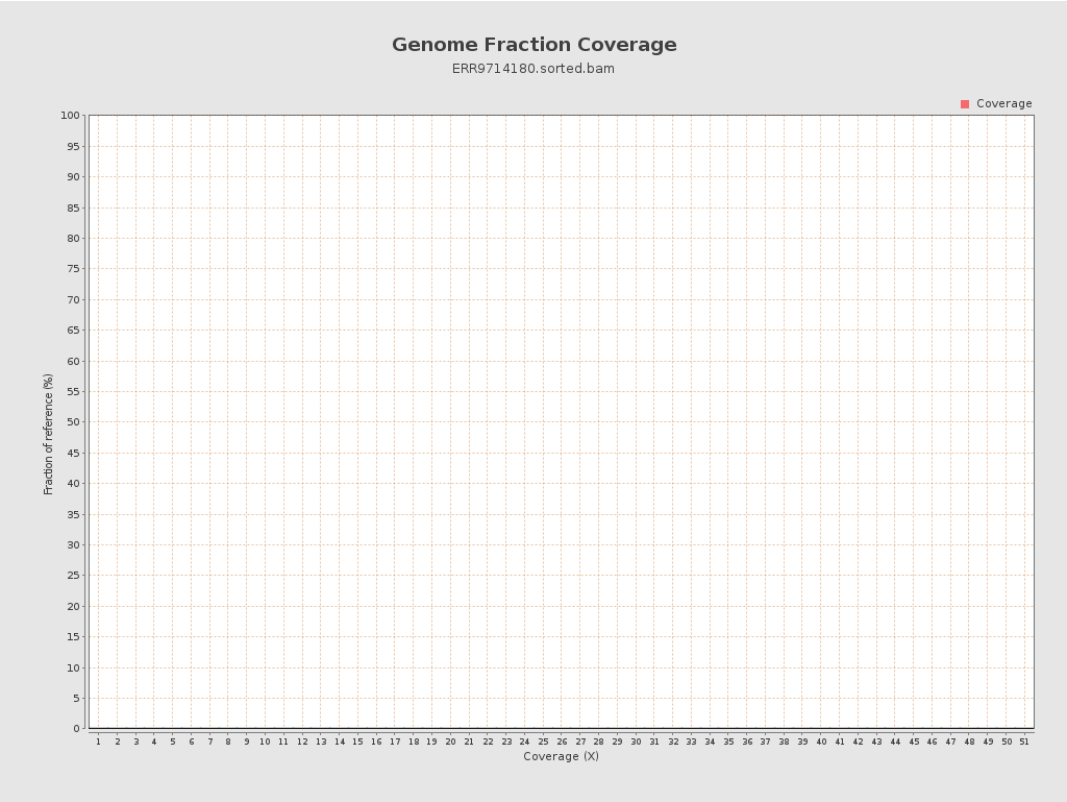
4. Results : Coverage Histogram



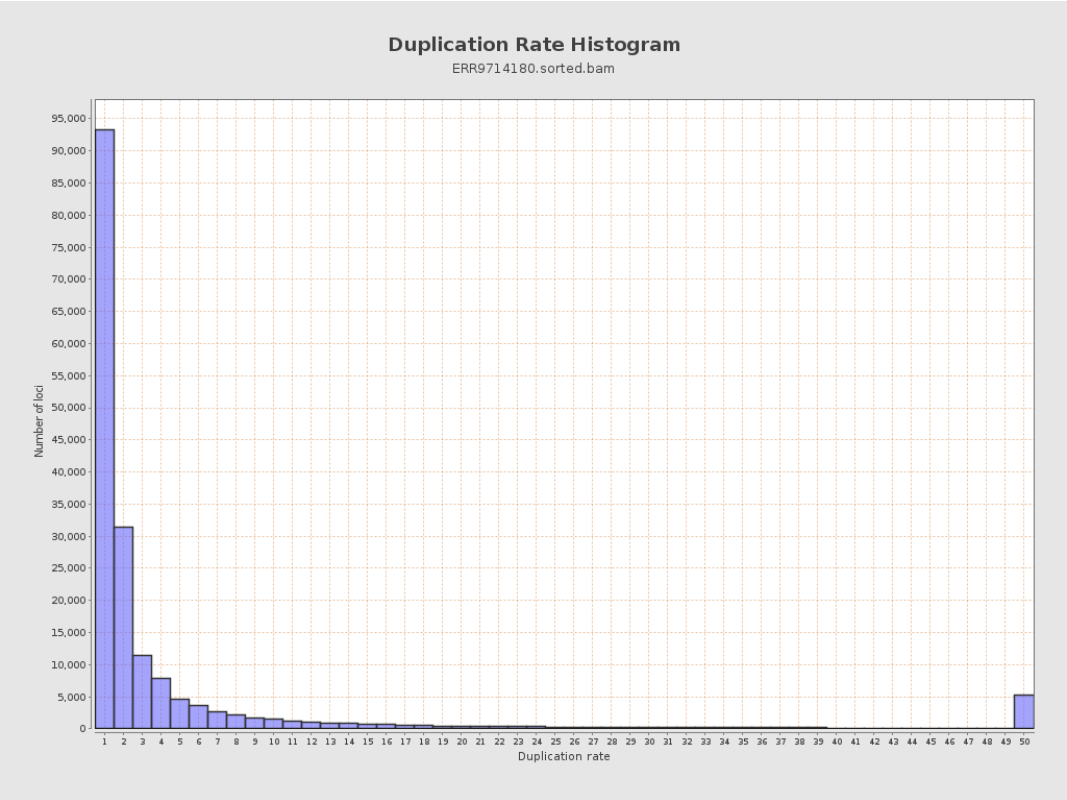
5. Results : Coverage Histogram (0-50X)



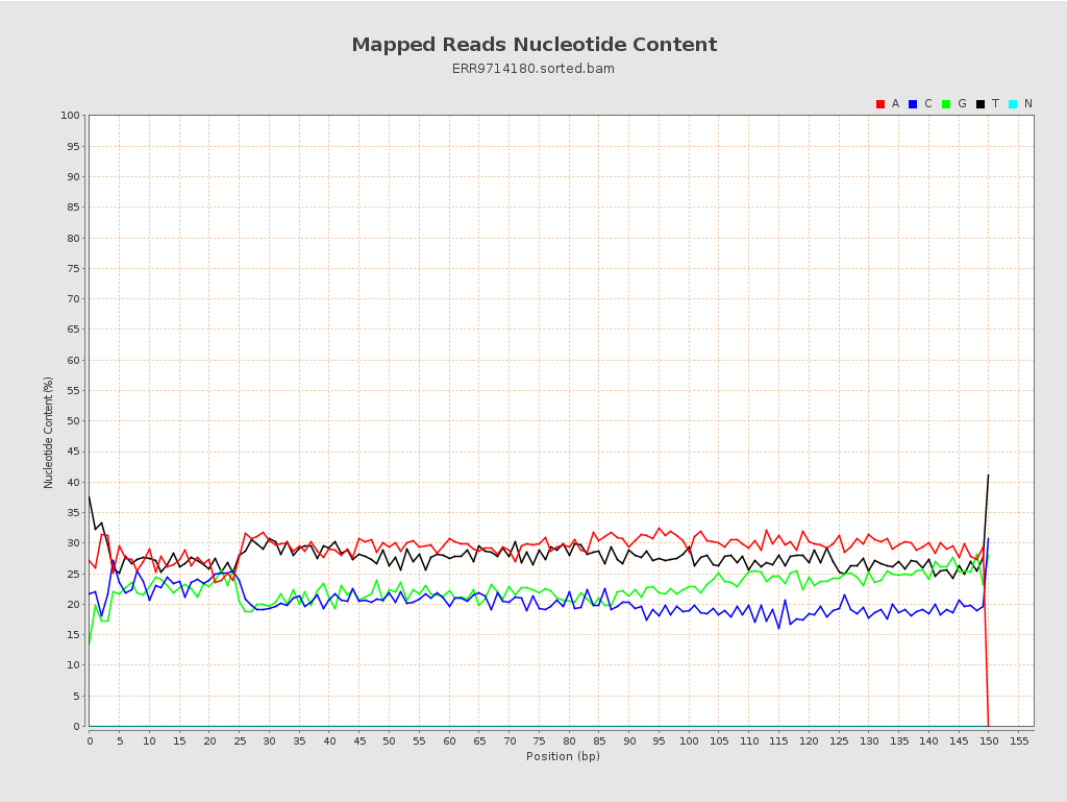
6. Results : Genome Fraction Coverage



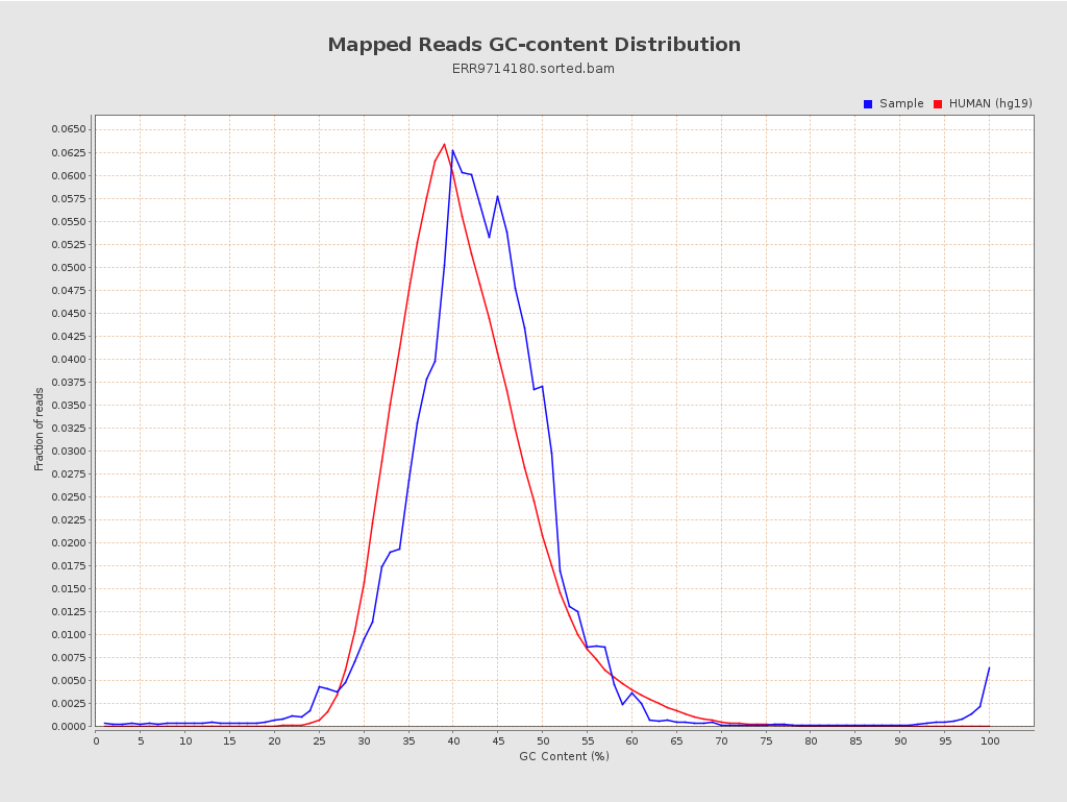
7. Results : Duplication Rate Histogram



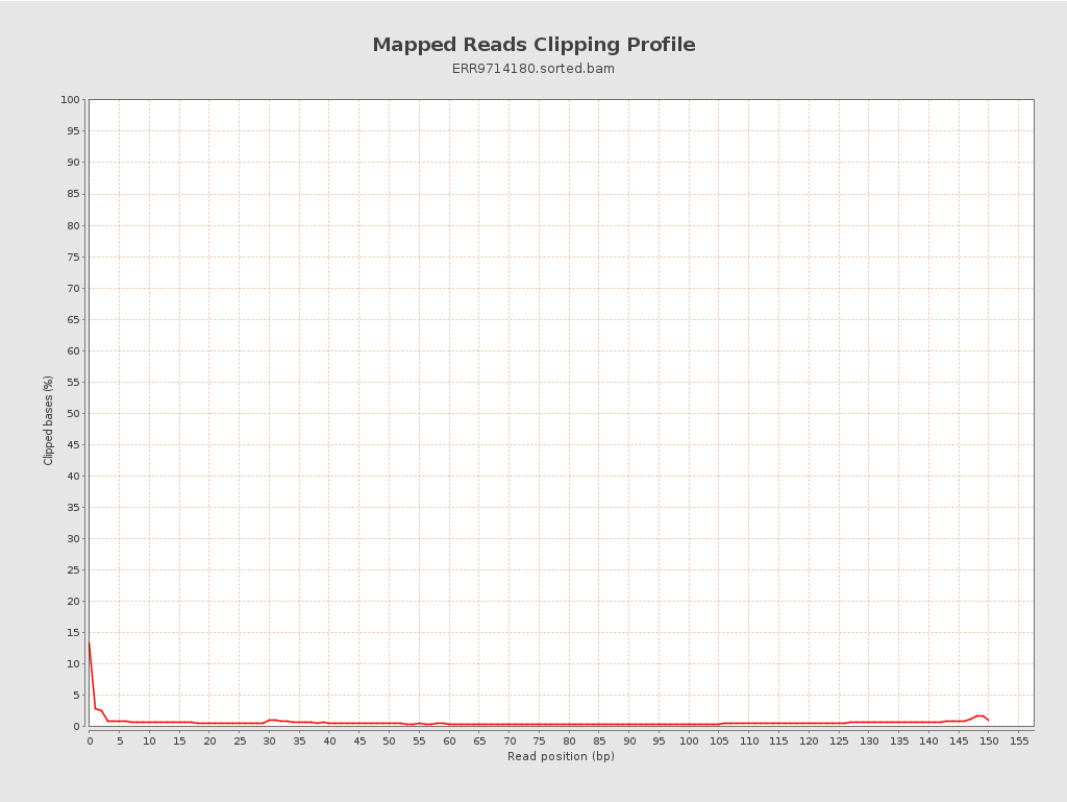
8. Results : Mapped Reads Nucleotide Content



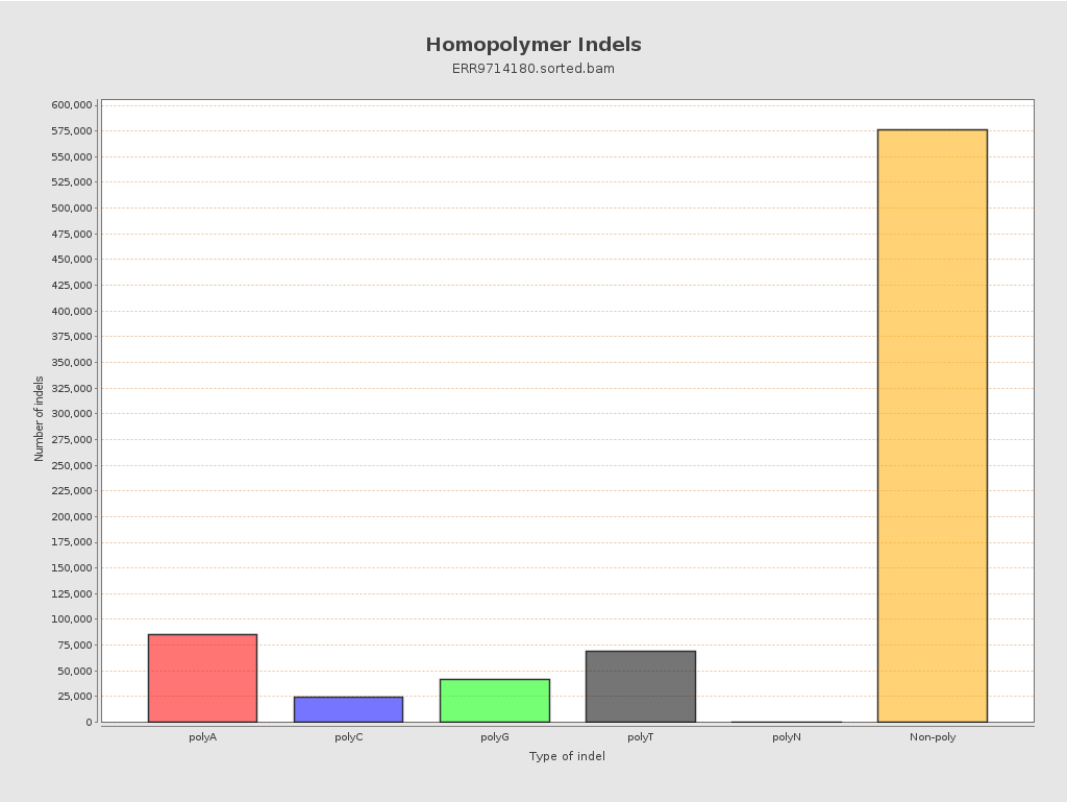
9. Results : Mapped Reads GC-content Distribution



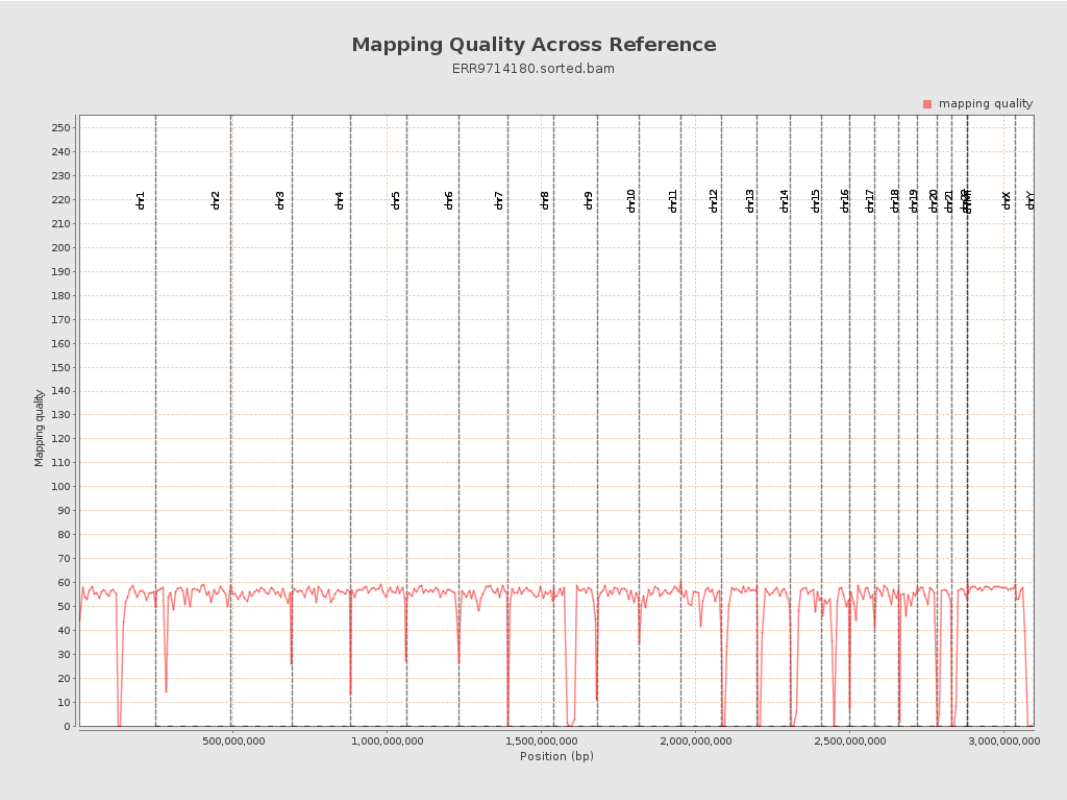
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram