Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 23:28:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714182.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_ERR9714182 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714182.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 23:28:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714182.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,040,710
Mapped reads	1,909,718 / 93.58%
Unmapped reads	130,992 / 6.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	100,807 / 4.94%
Read min/max/mean length	30 / 151 / 140.78
Duplicated reads (estimated)	1,815,109 / 88.94%
Duplication rate	46.83%
Clipped reads	1,857,233 / 91.01%

2.2. ACGT Content

Number/percentage of A's	70,892,320 / 29.78%
Number/percentage of C's	48,213,307 / 20.25%
Number/percentage of T's	66,230,343 / 27.82%
Number/percentage of G's	52,750,772 / 22.16%
Number/percentage of N's	1,841 / 0%
GC Percentage	42.41%

2.3. Coverage

Mean	0.0785

Standard Deviation	13.8377

2.4. Mapping Quality

Mean Mapping Quality	50.81

2.5. Mismatches and indels

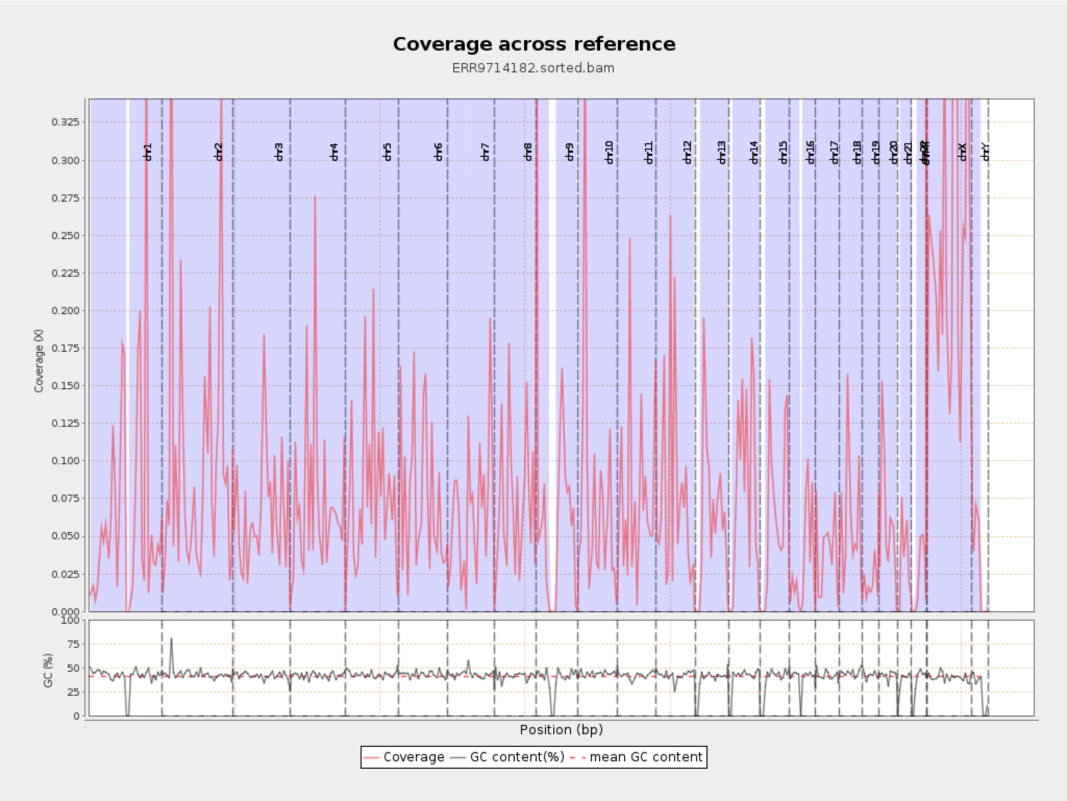
General error rate	3.83%
Mismatches	8,515,858
Insertions	246,160
Mapped reads with at least one insertion	12.52%
Deletions	770,039
Mapped reads with at least one deletion	38.46%
Homopolymer indels	26.66%

2.6. Chromosome stats

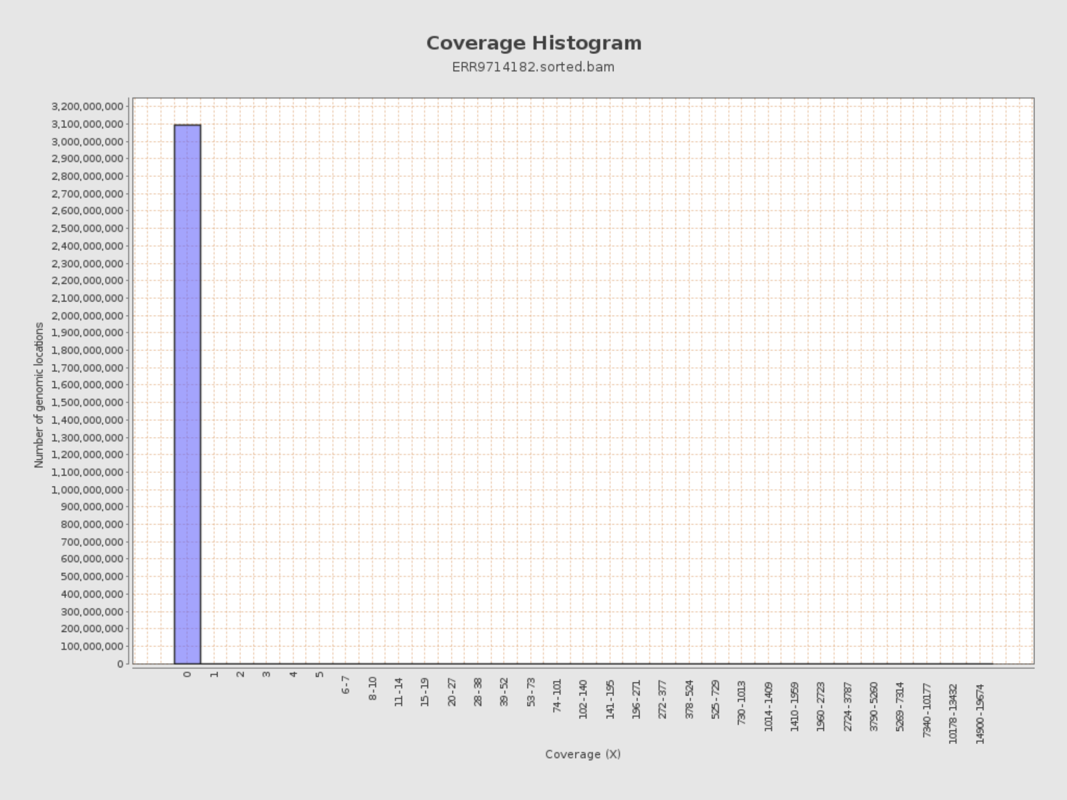
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16786344	0.0673	16.4404
chr2	243199373	24520239	0.1008	19.558
chr3	198022430	13268654	0.067	7.9542
chr4	191154276	14233489	0.0745	11.3813
chr5	180915260	14253370	0.0788	12.4685
chr6	171115067	12795961	0.0748	10.1831
chr7	159138663	10713325	0.0673	9.7708

chr8	146364022	10801816	0.0738	10.3072
chr9	141213431	8117018	0.0575	7.5842
chr10	135534747	10738463	0.0792	20.3644
chr11	135006516	10257486	0.076	12.9251
chr12	133851895	10288926	0.0769	15.0448
chr13	115169878	7072699	0.0614	8.2631
chr14	107349540	8905419	0.083	12.4995
chr15	102531392	6430013	0.0627	9.6533
chr16	90354753	3020275	0.0334	4.6233
chr17	81195210	3249948	0.04	6.3072
chr18	78077248	4692055	0.0601	7.9776
chr19	59128983	1210311	0.0205	3.1006
chr20	63025520	3949781	0.0627	11.2791
chr21	48129895	1538123	0.032	5.2731
chr22	51304566	1147736	0.0224	3.1982
chrMT	16571	118489	7.1504	56.0382
chrX	155270560	43216385	0.2783	30.5422
chrY	59373566	1562855	0.0263	5.2168

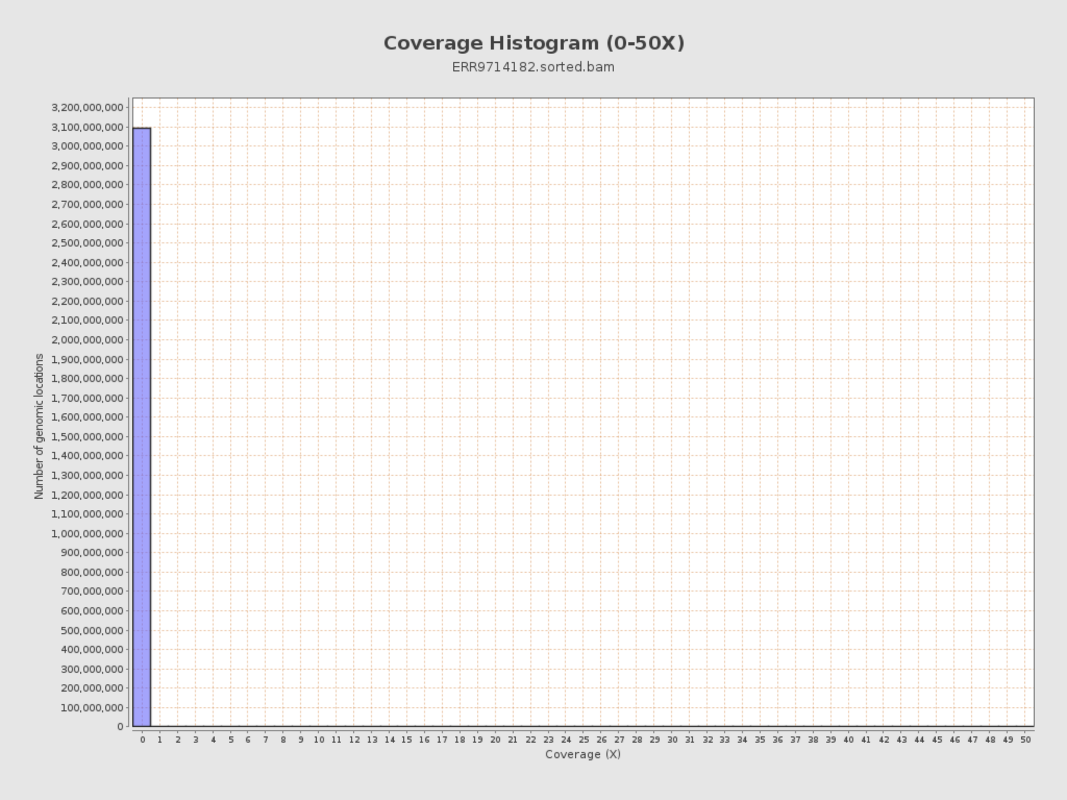
3. Results : Coverage across reference



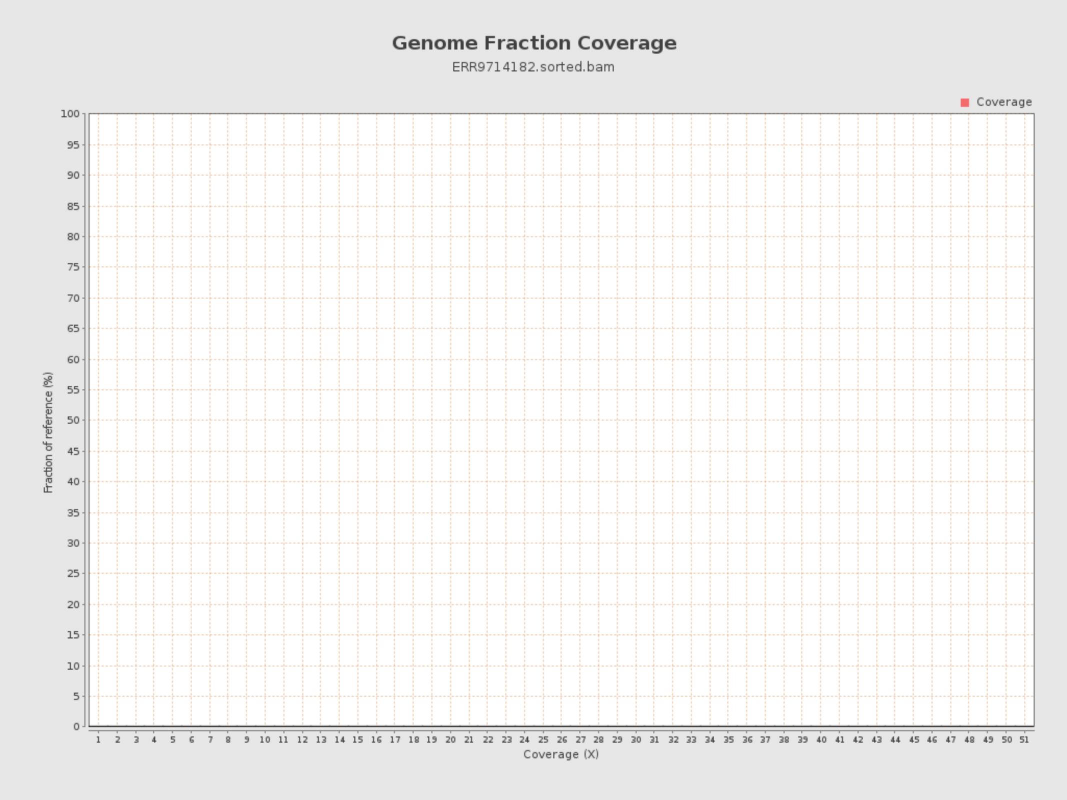
4. Results : Coverage Histogram



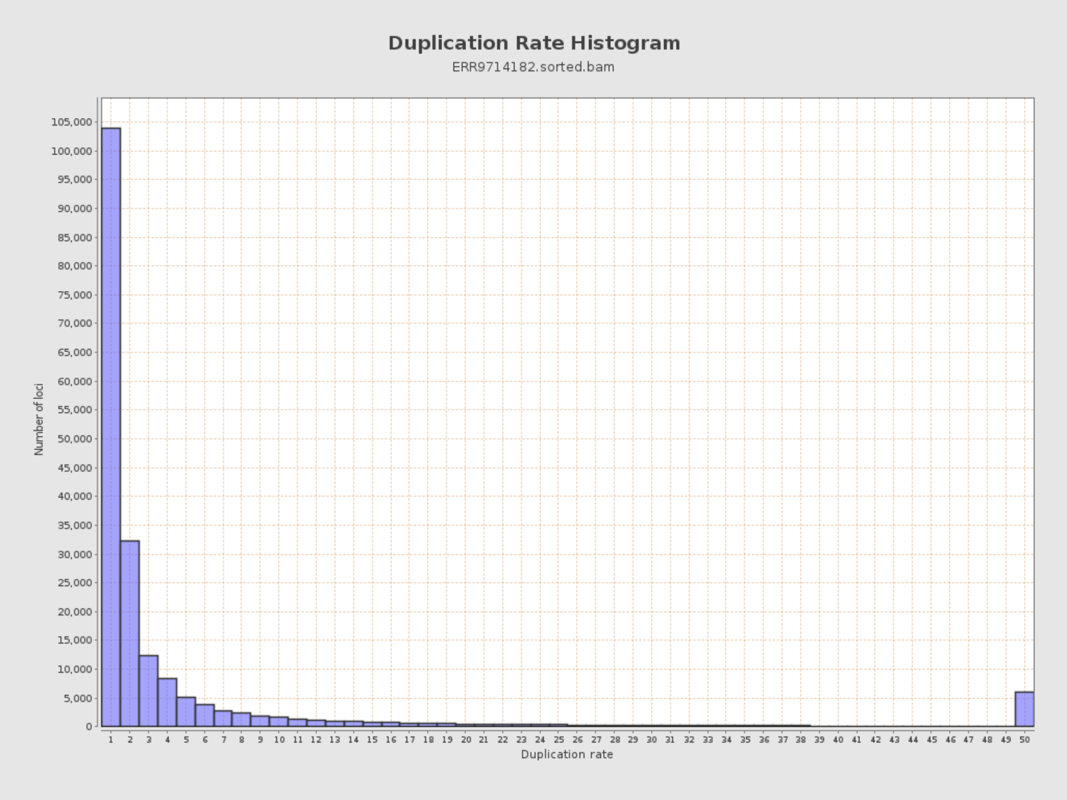
5. Results : Coverage Histogram (0-50X)



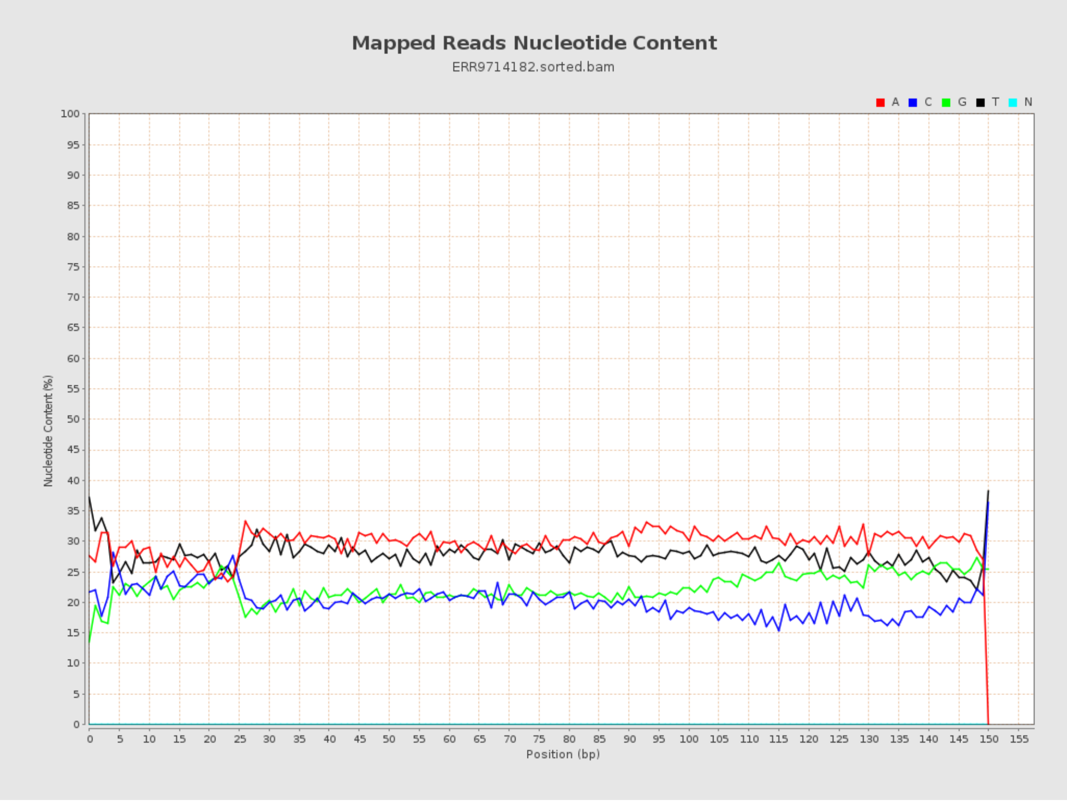
6. Results : Genome Fraction Coverage



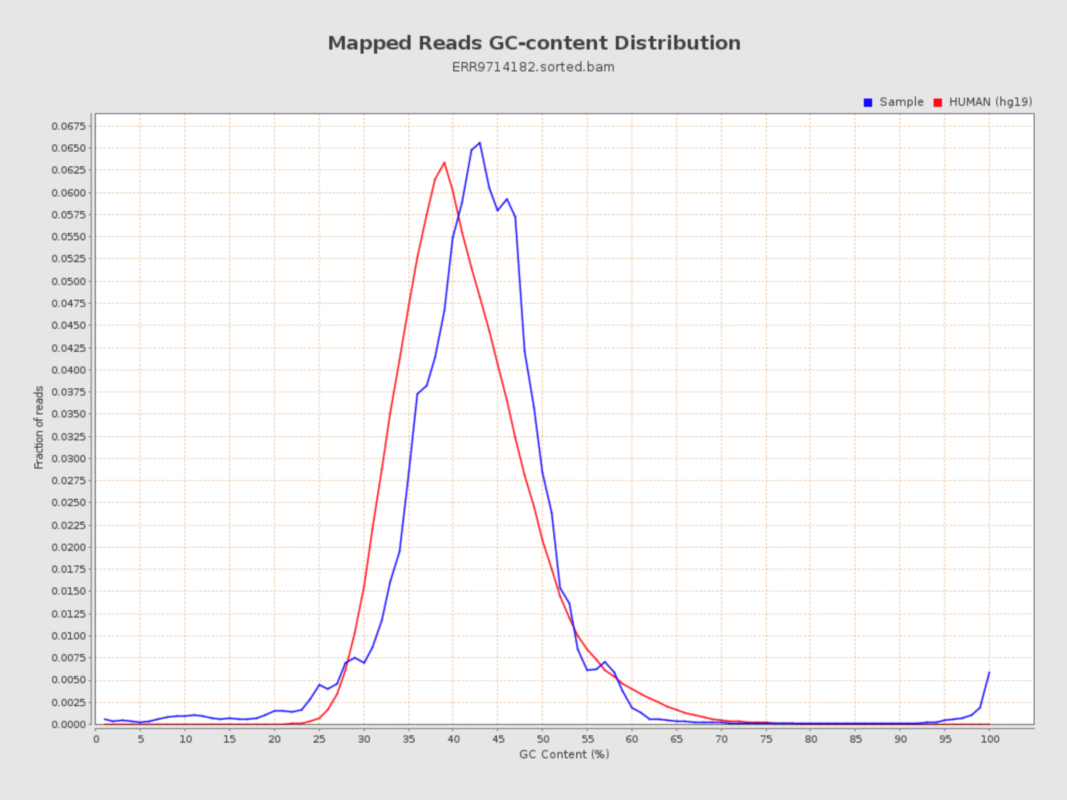
7. Results : Duplication Rate Histogram



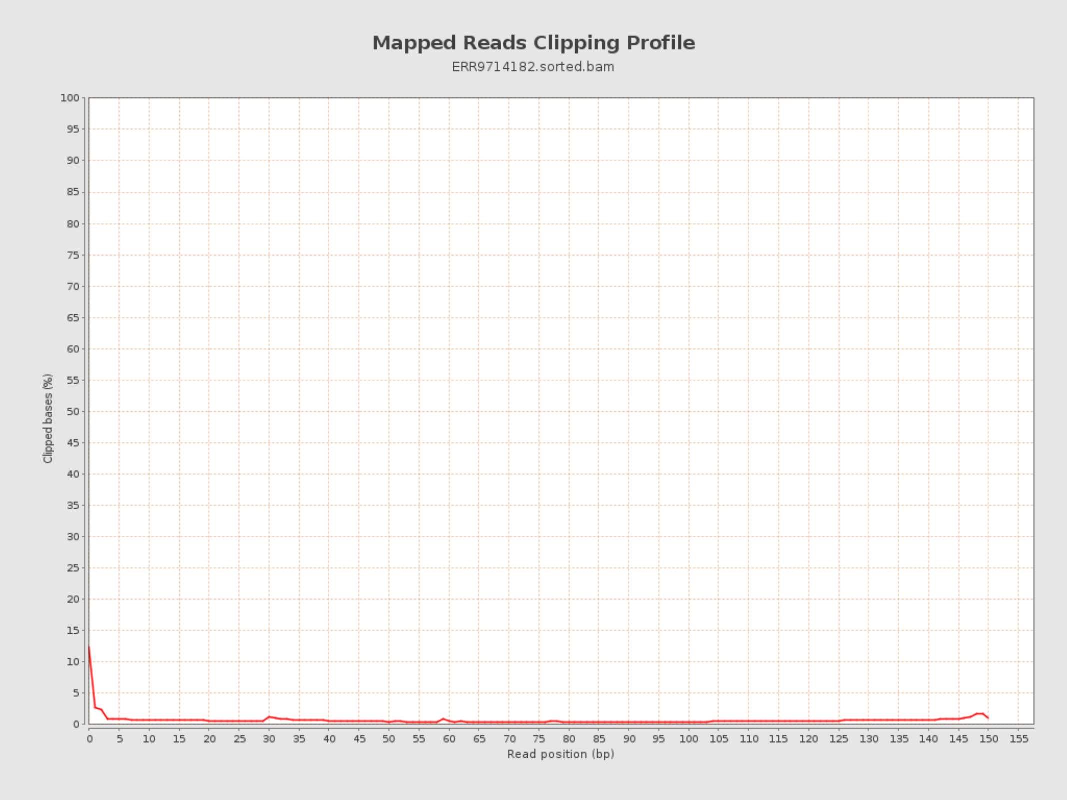
8. Results : Mapped Reads Nucleotide Content



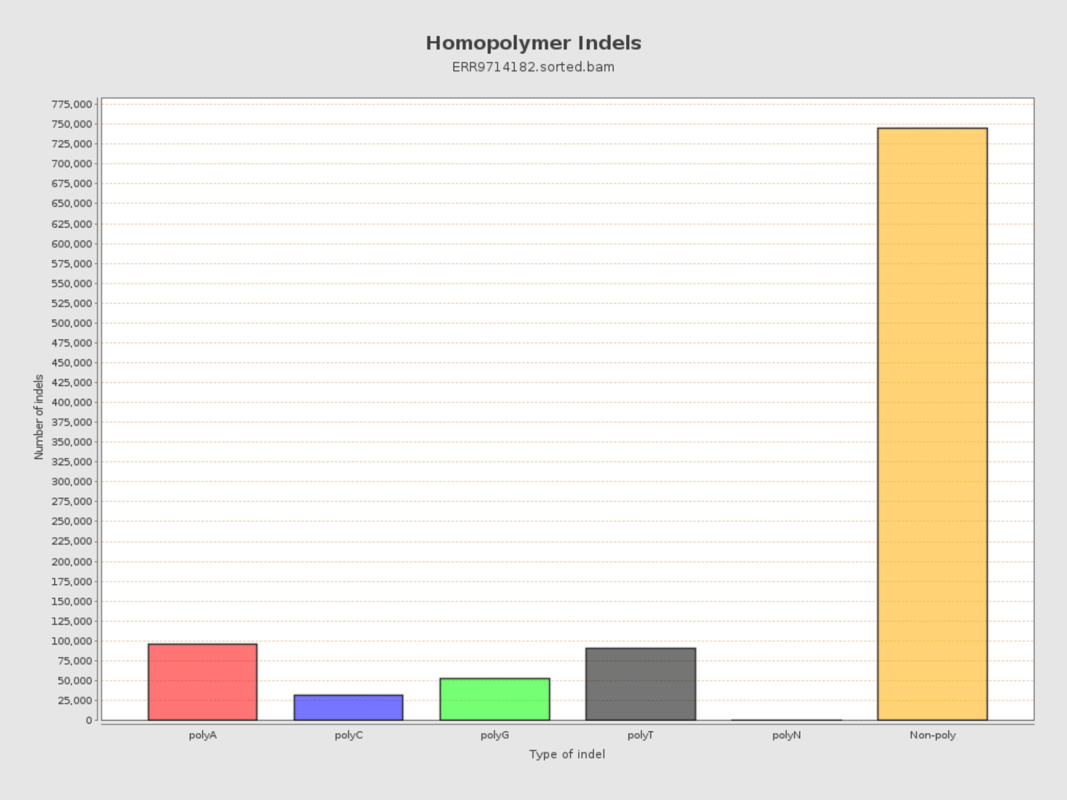
9. Results : Mapped Reads GC-content Distribution



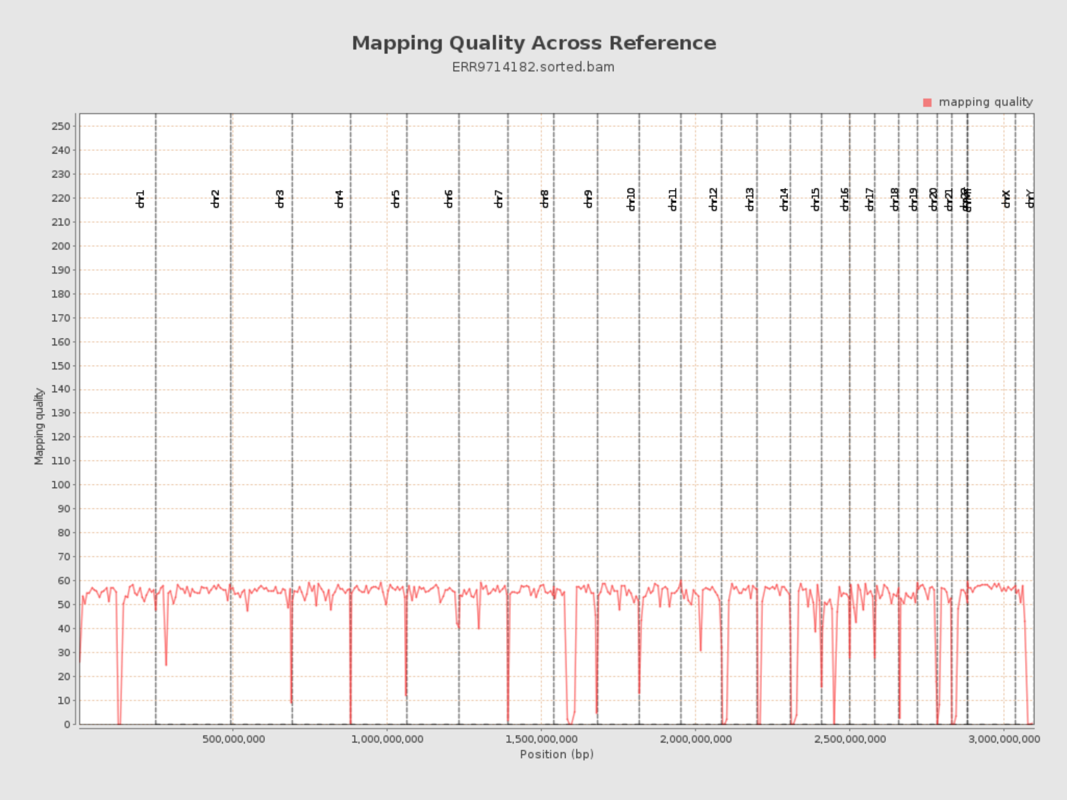
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram