

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 01:04:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714240.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_ERR9714240 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714240.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 01:04:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714240.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	192,120
Mapped reads	132,927 / 69.19%
Unmapped reads	59,193 / 30.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,900 / 2.55%
Read min/max/mean length	30 / 151 / 120.53
Duplicated reads (estimated)	101,711 / 52.94%
Duplication rate	40.97%
Clipped reads	126,356 / 65.77%

2.2. ACGT Content

Number/percentage of A's	4,732,358 / 28.37%
Number/percentage of C's	3,467,547 / 20.79%
Number/percentage of T's	4,460,707 / 26.74%
Number/percentage of G's	4,018,397 / 24.09%
Number/percentage of N's	125 / 0%
GC Percentage	44.88%

2.3. Coverage

Mean	0.0055

Standard Deviation	0.7947
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2.4. Mapping Quality

Mean Mapping Quality	51.4
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2.5. Mismatches and indels

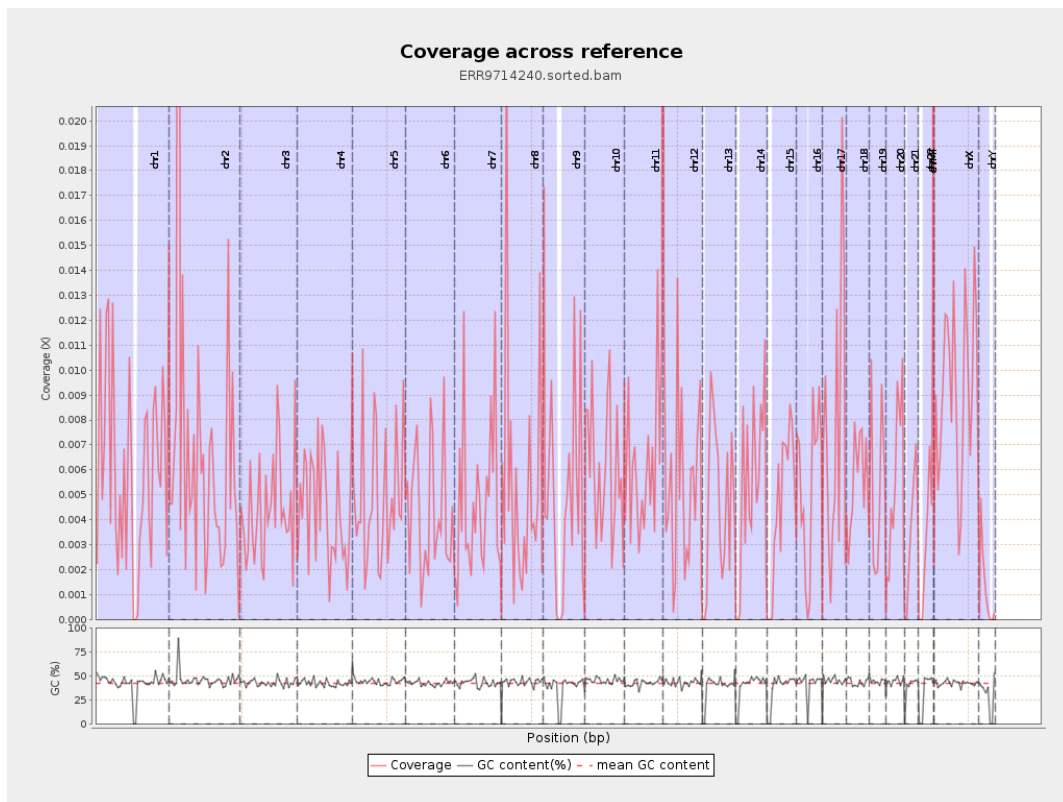
General error rate	4.21%
Mismatches	638,172
Insertions	19,385
Mapped reads with at least one insertion	14.06%
Deletions	54,586
Mapped reads with at least one deletion	39.09%
Homopolymer indels	28.94%

2.6. Chromosome stats

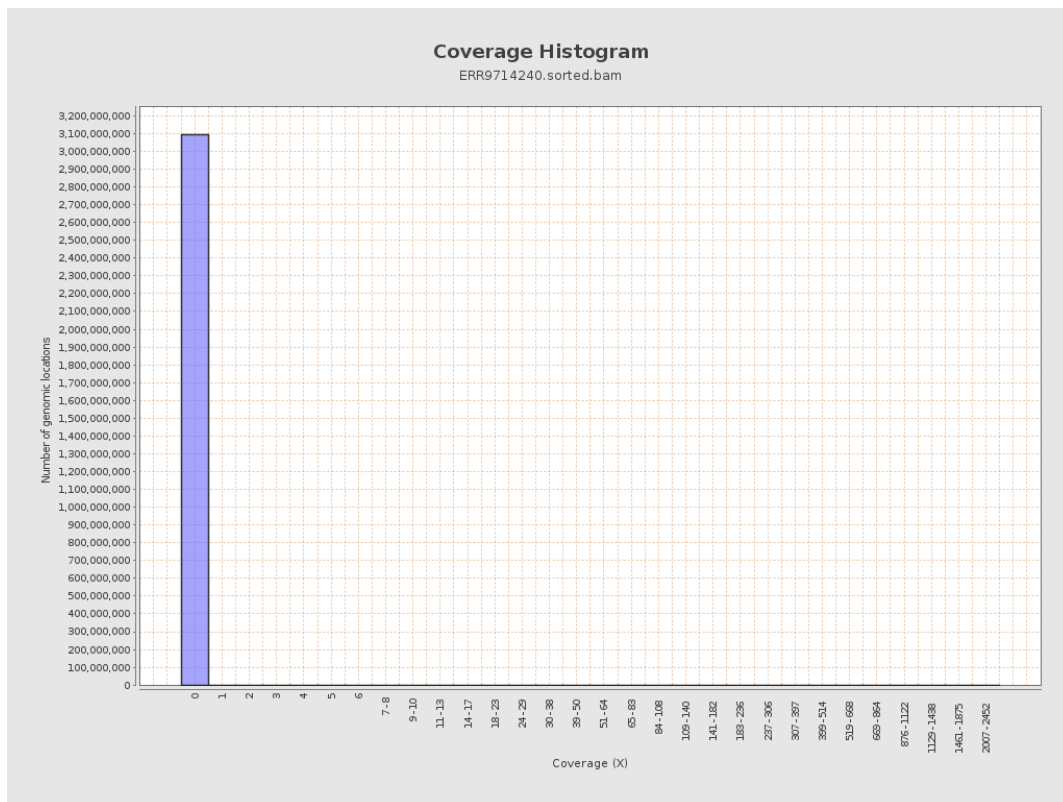
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	1475149	0.0059	0.6891
chr2	243199373	1807660	0.0074	1.7837
chr3	198022430	880873	0.0044	0.5145
chr4	191154276	844917	0.0044	0.612
chr5	180915260	888789	0.0049	0.5692
chr6	171115067	728439	0.0043	0.4932
chr7	159138663	765210	0.0048	0.5476

chr8	146364022	796490	0.0054	0.7316
chr9	141213431	678966	0.0048	0.6936
chr10	135534747	834910	0.0062	0.5751
chr11	135006516	884821	0.0066	0.6815
chr12	133851895	743255	0.0056	0.7436
chr13	115169878	526870	0.0046	0.584
chr14	107349540	576830	0.0054	0.6327
chr15	102531392	465779	0.0045	0.4746
chr16	90354753	476782	0.0053	0.5424
chr17	81195210	615937	0.0076	1.0263
chr18	78077248	432215	0.0055	0.5633
chr19	59128983	286819	0.0049	0.6285
chr20	63025520	349551	0.0055	0.5383
chr21	48129895	160179	0.0033	0.3869
chr22	51304566	164900	0.0032	0.3937
chrMT	16571	138269	8.344	74.8946
chrX	155270560	1403102	0.009	0.6491
chrY	59373566	70864	0.0012	0.2822

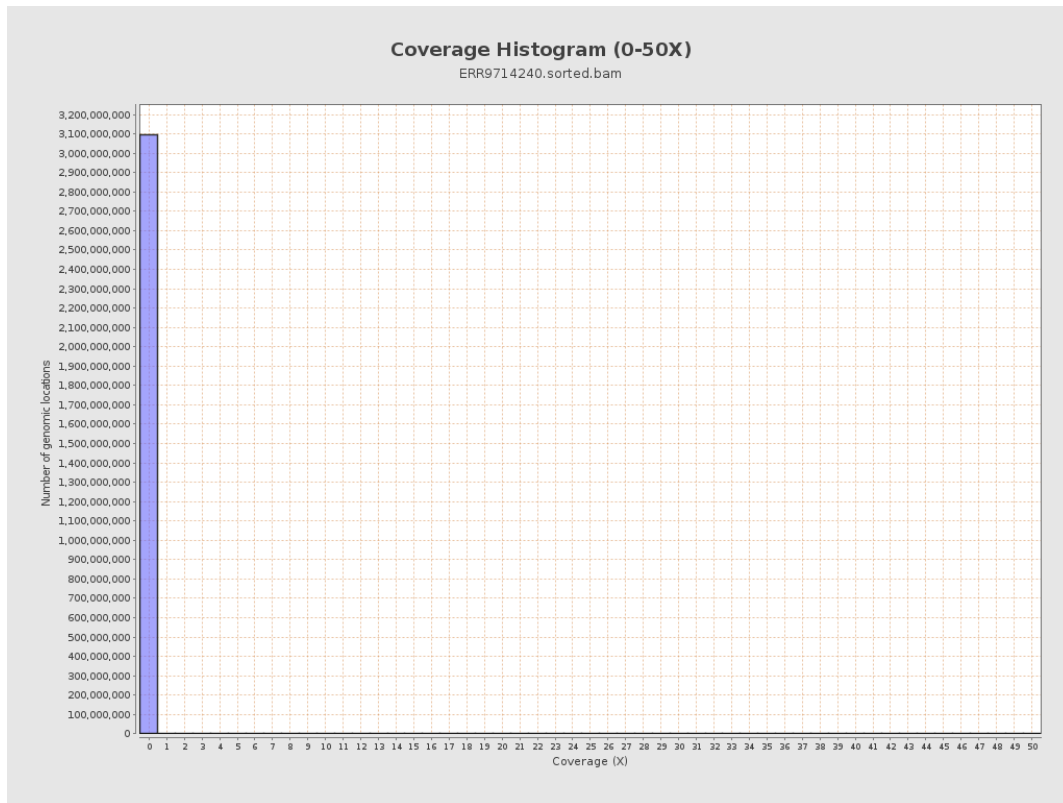
3. Results : Coverage across reference



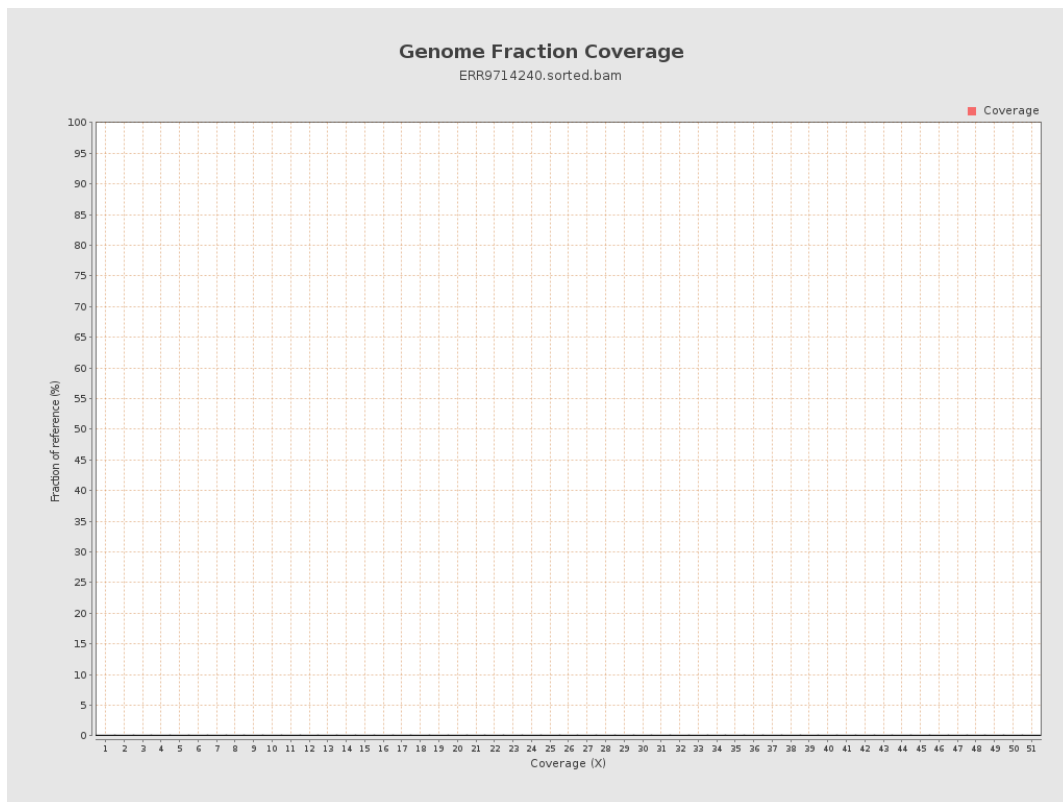
4. Results : Coverage Histogram



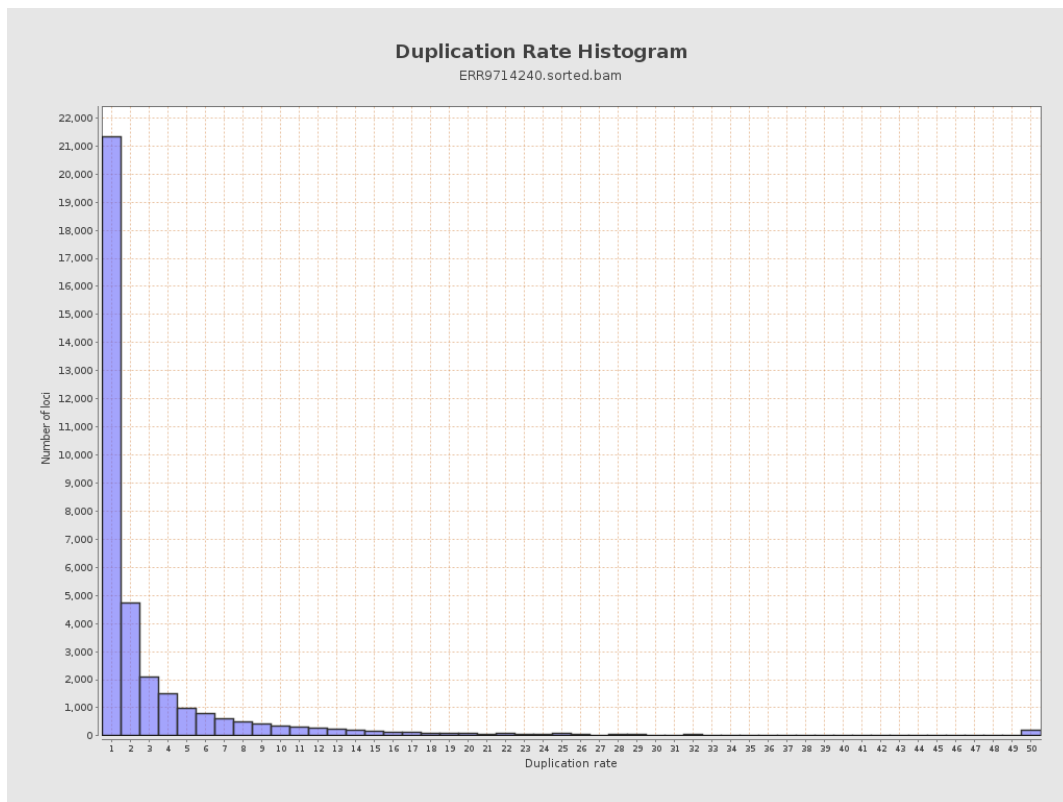
5. Results : Coverage Histogram (0-50X)



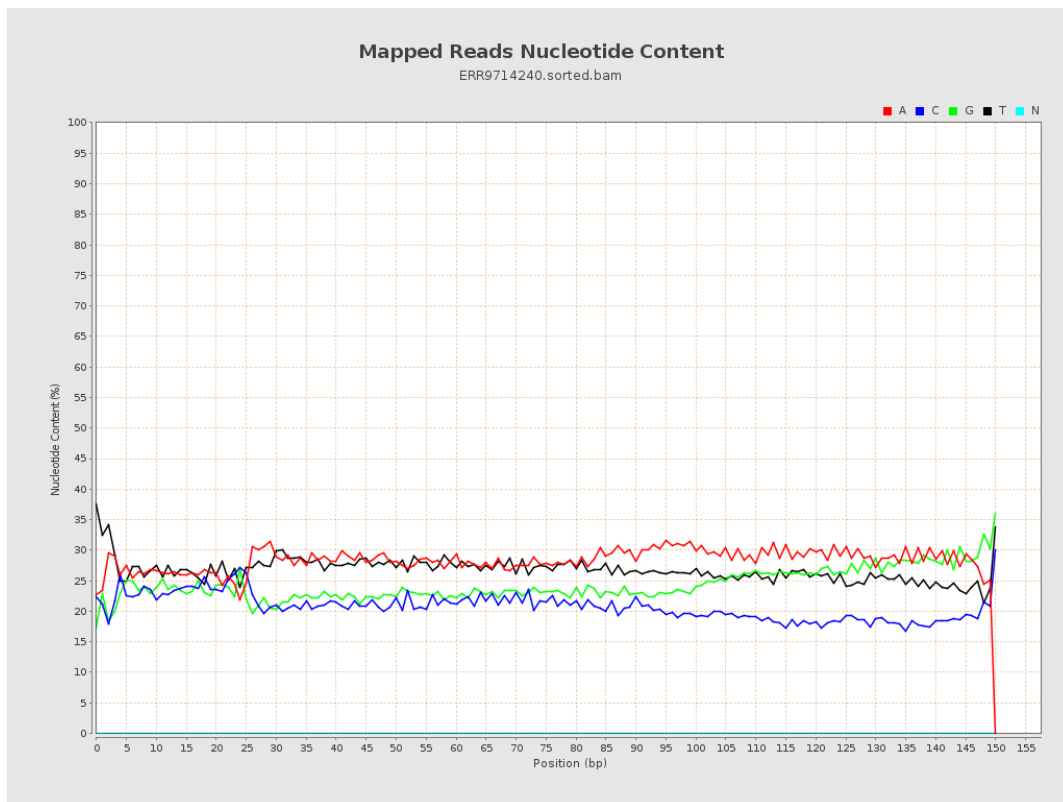
6. Results : Genome Fraction Coverage



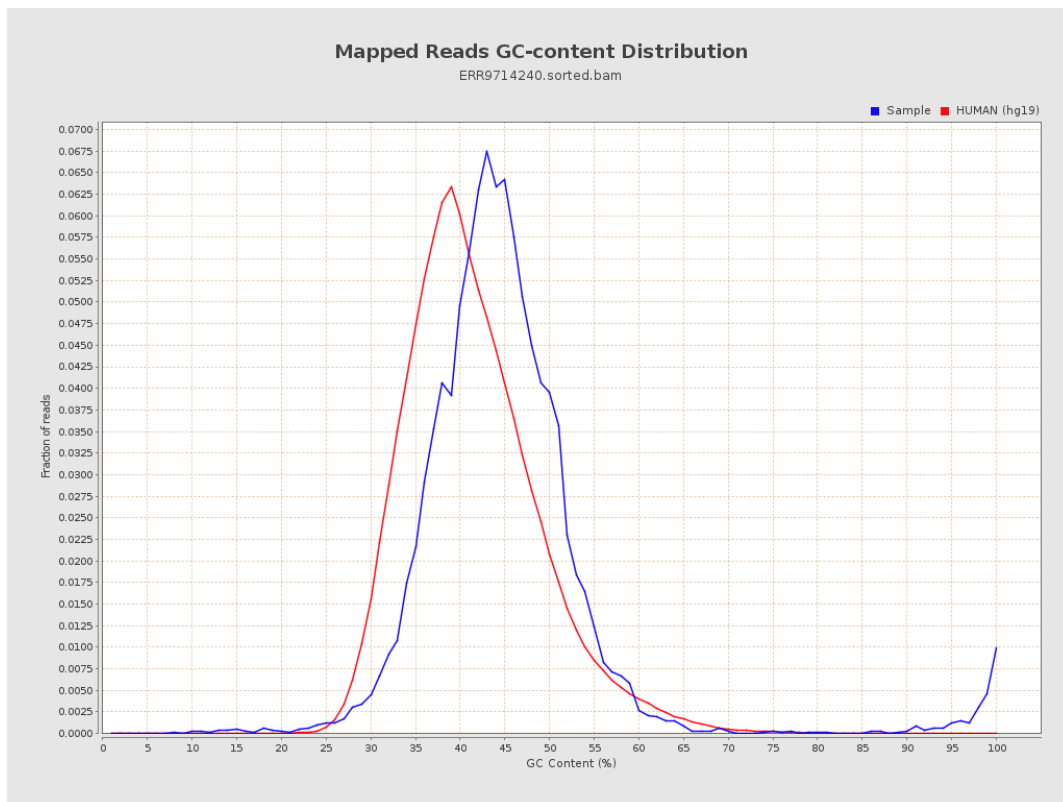
7. Results : Duplication Rate Histogram



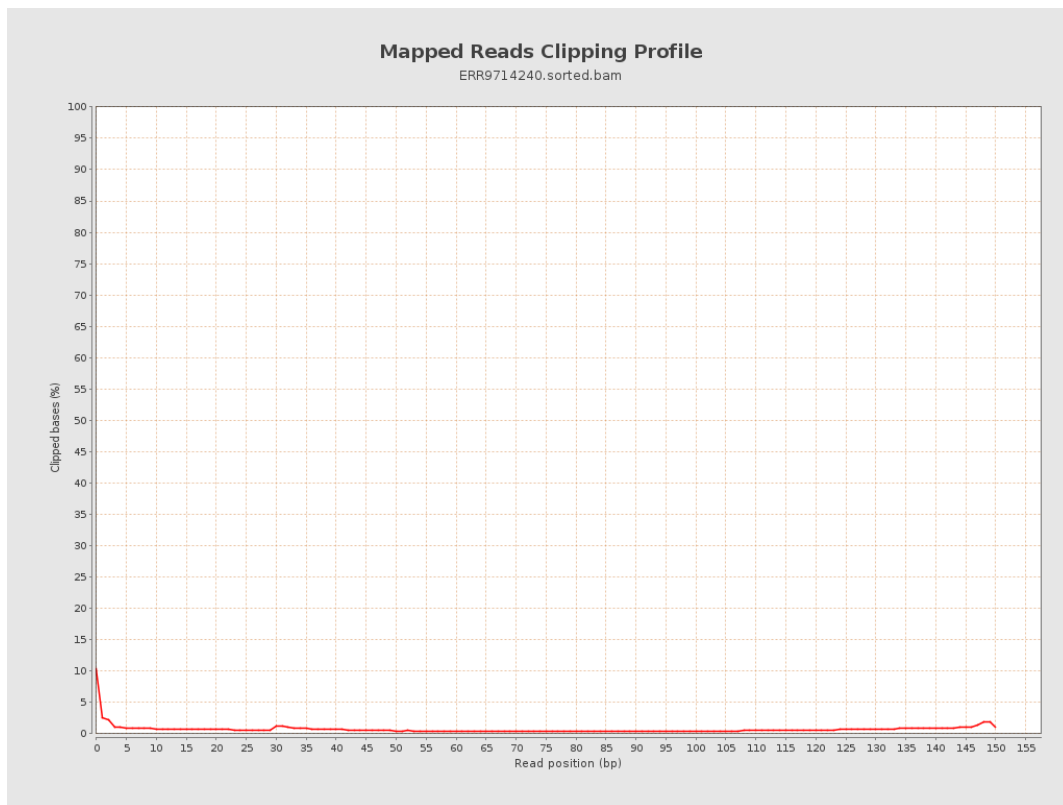
8. Results : Mapped Reads Nucleotide Content



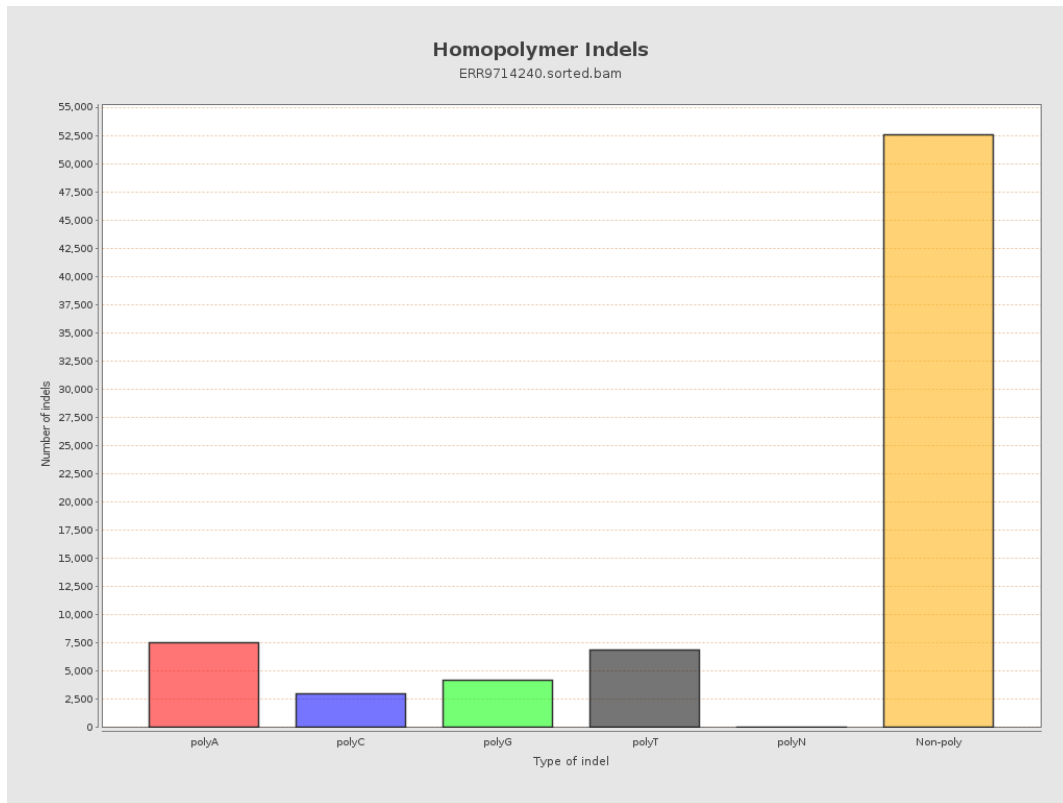
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

