

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 01:17:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714247.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_ERR9714247 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714247.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 01:17:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714247.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,674
Mapped reads	2,505 / 23.47%
Unmapped reads	8,169 / 76.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	112 / 1.05%
Read min/max/mean length	30 / 151 / 75.46
Duplicated reads (estimated)	1,628 / 15.25%
Duplication rate	43.88%
Clipped reads	1,908 / 17.88%

2.2. ACGT Content

Number/percentage of A's	51,812 / 18.6%
Number/percentage of C's	42,165 / 15.14%
Number/percentage of T's	48,632 / 17.46%
Number/percentage of G's	135,923 / 48.8%
Number/percentage of N's	6 / 0%
GC Percentage	63.94%

2.3. Coverage

Mean	0.0001

Standard Deviation	0.1162
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2.4. Mapping Quality

Mean Mapping Quality	20.32
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2.5. Mismatches and indels

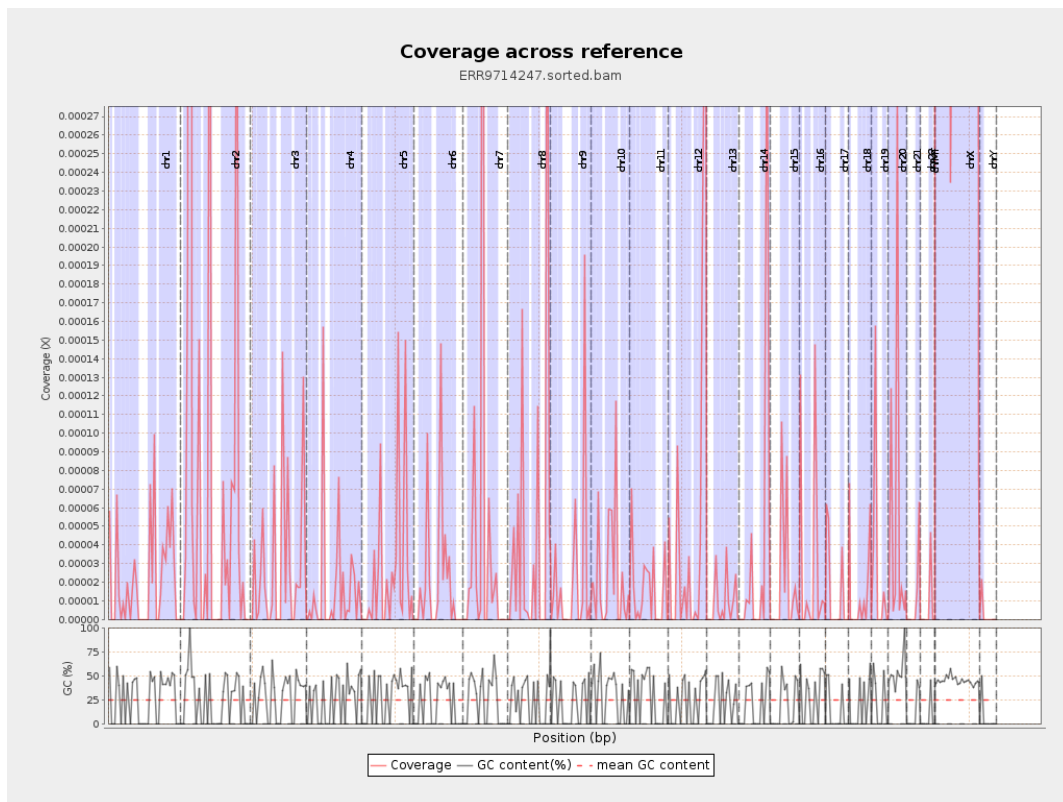
General error rate	3.56%
Mismatches	8,998
Insertions	183
Mapped reads with at least one insertion	5.83%
Deletions	611
Mapped reads with at least one deletion	23.91%
Homopolymer indels	30.98%

2.6. Chromosome stats

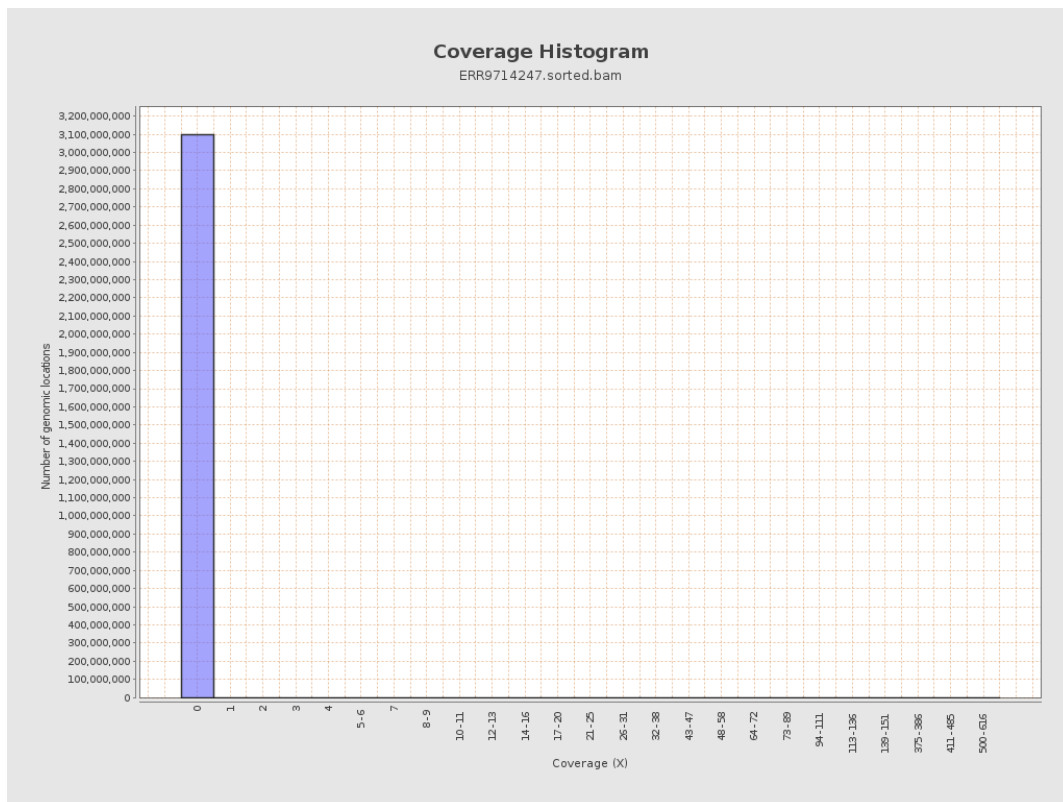
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5487	0	0.0081
chr2	243199373	107193	0.0004	0.4072
chr3	198022430	5483	0	0.0112
chr4	191154276	3183	0	0.0068
chr5	180915260	4809	0	0.0115
chr6	171115067	3400	0	0.0091
chr7	159138663	6537	0	0.0271

chr8	146364022	7294	0	0.024
chr9	141213431	2940	0	0.0079
chr10	135534747	3153	0	0.0094
chr11	135006516	2019	0	0.0066
chr12	133851895	7436	0.0001	0.017
chr13	115169878	981	0	0.0039
chr14	107349540	3749	0	0.0217
chr15	102531392	1868	0	0.0087
chr16	90354753	2058	0	0.0095
chr17	81195210	1177	0	0.0059
chr18	78077248	902	0	0.0046
chr19	59128983	1637	0	0.013
chr20	63025520	3616	0.0001	0.0224
chr21	48129895	435	0	0.0039
chr22	51304566	361	0	0.0036
chrMT	16571	1301	0.0785	0.5488
chrX	155270560	105841	0.0007	0.0786
chrY	59373566	167	0	0.002

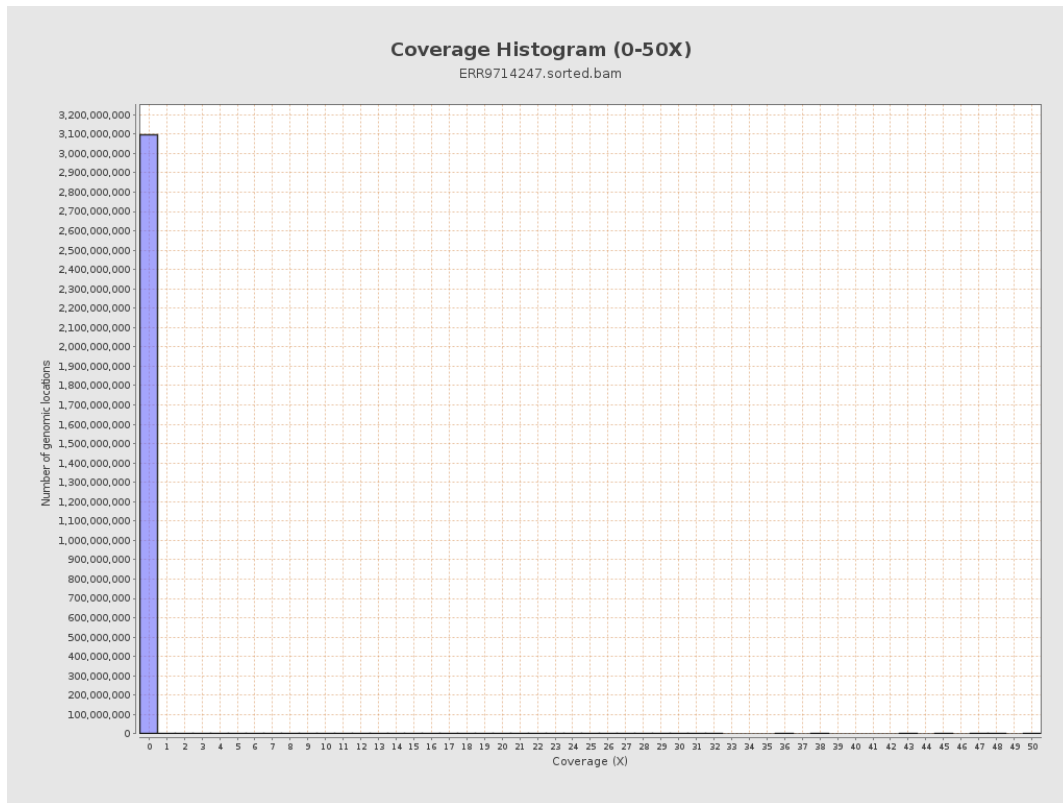
3. Results : Coverage across reference



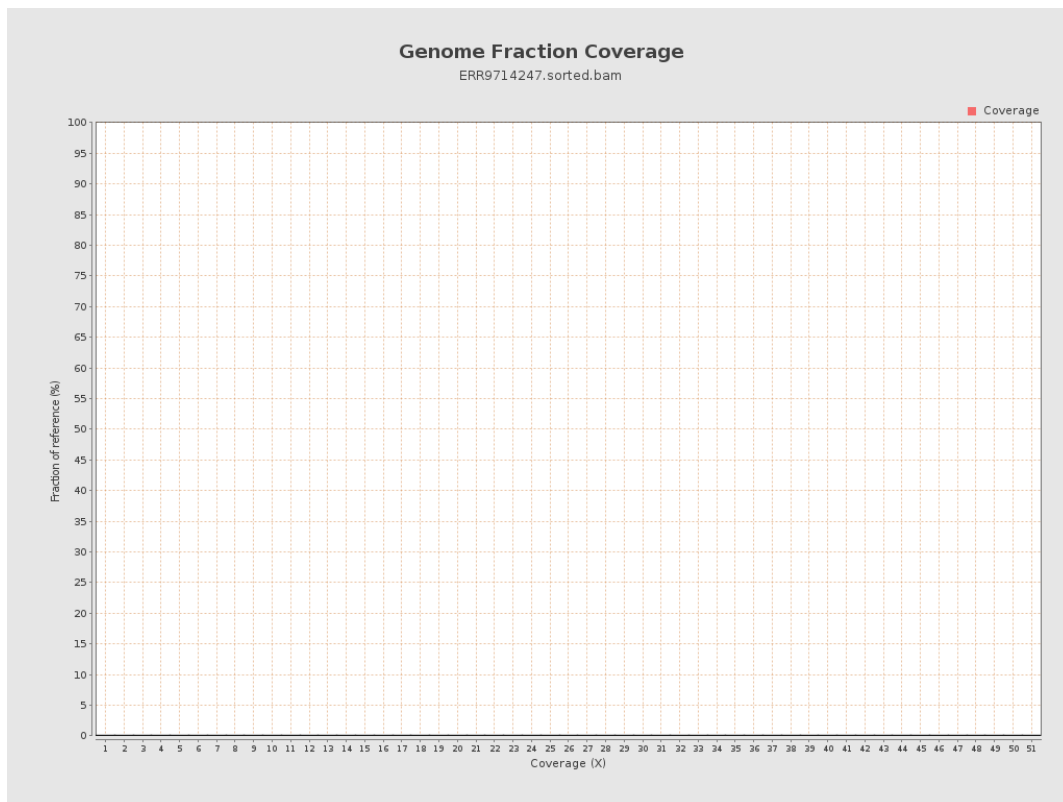
4. Results : Coverage Histogram



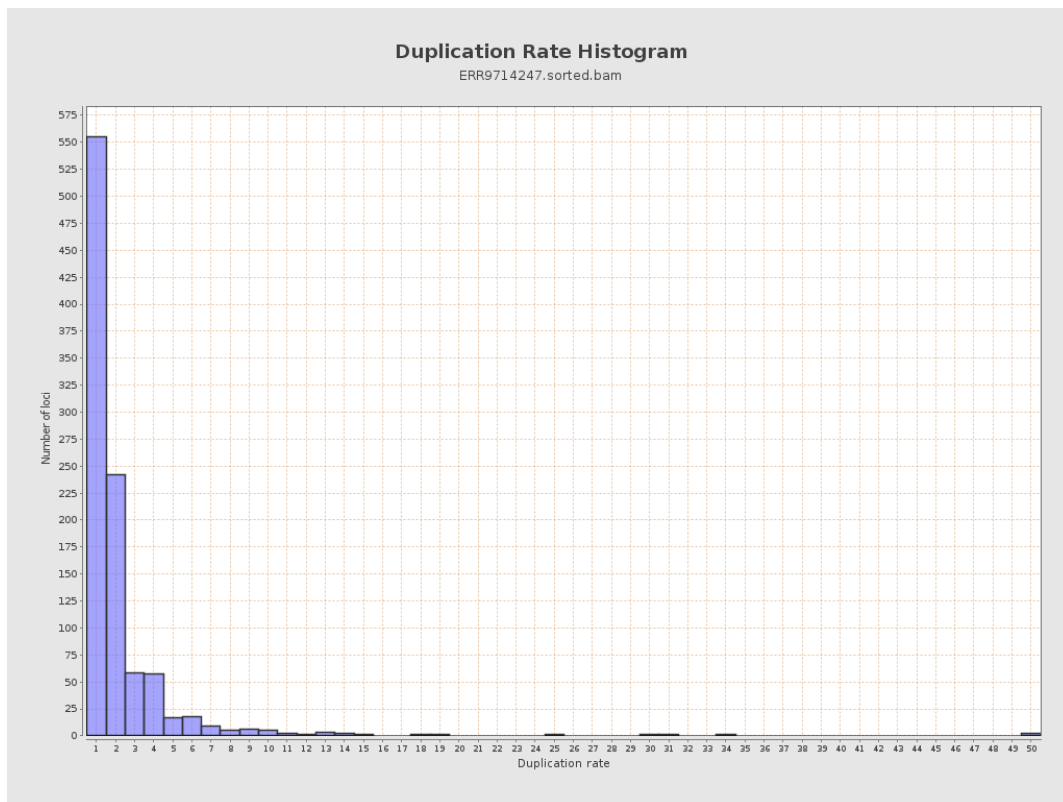
5. Results : Coverage Histogram (0-50X)



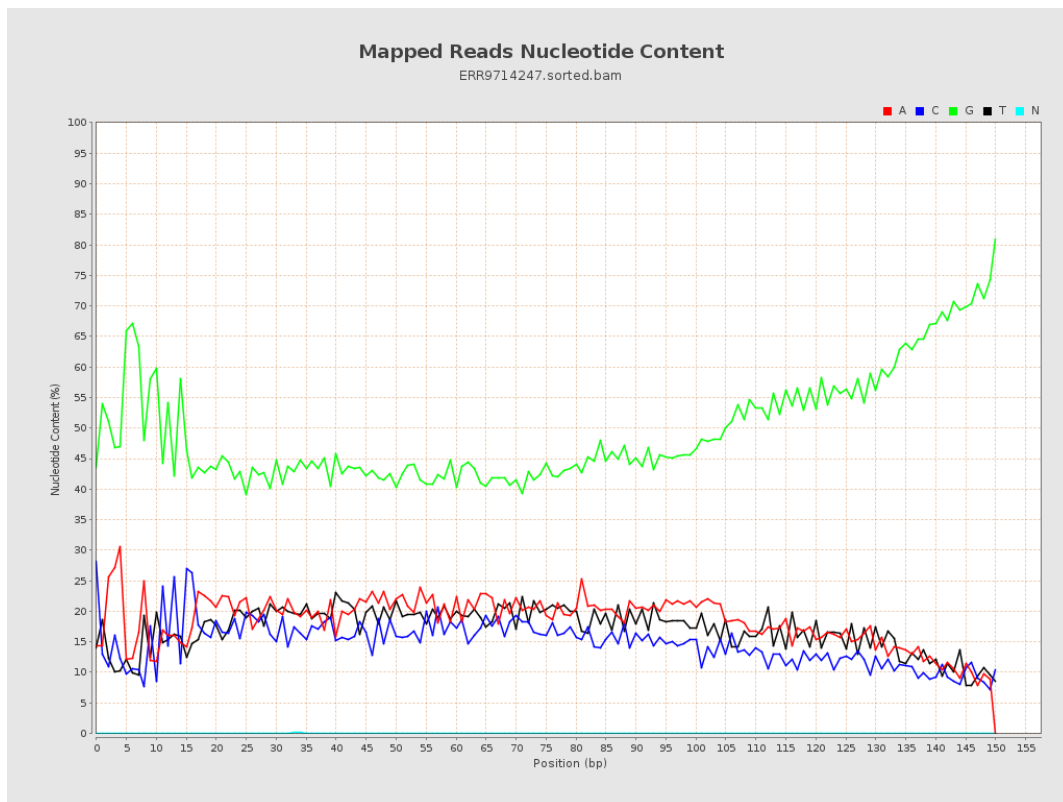
6. Results : Genome Fraction Coverage



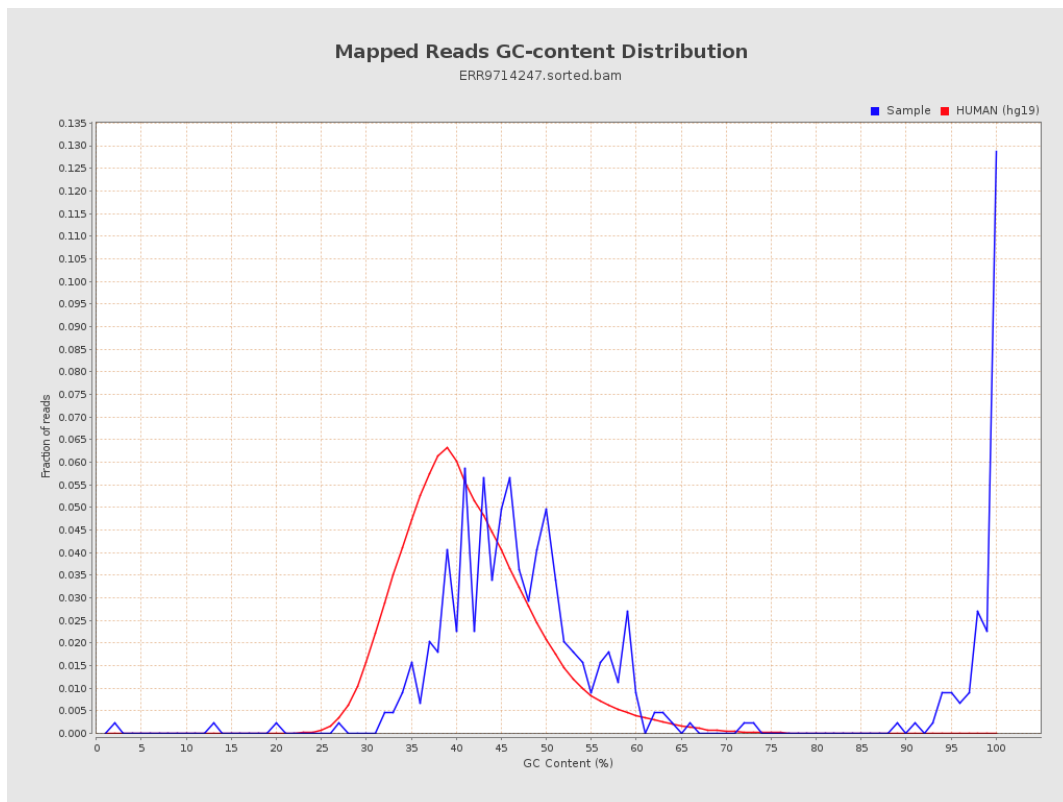
7. Results : Duplication Rate Histogram



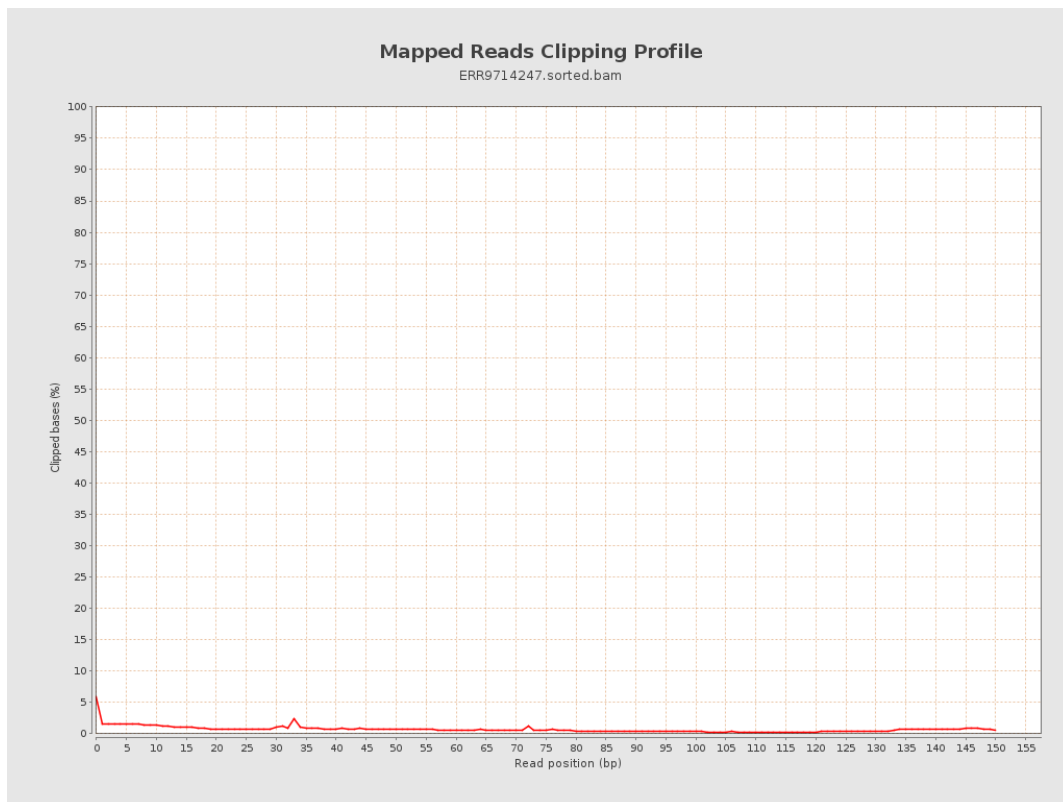
8. Results : Mapped Reads Nucleotide Content



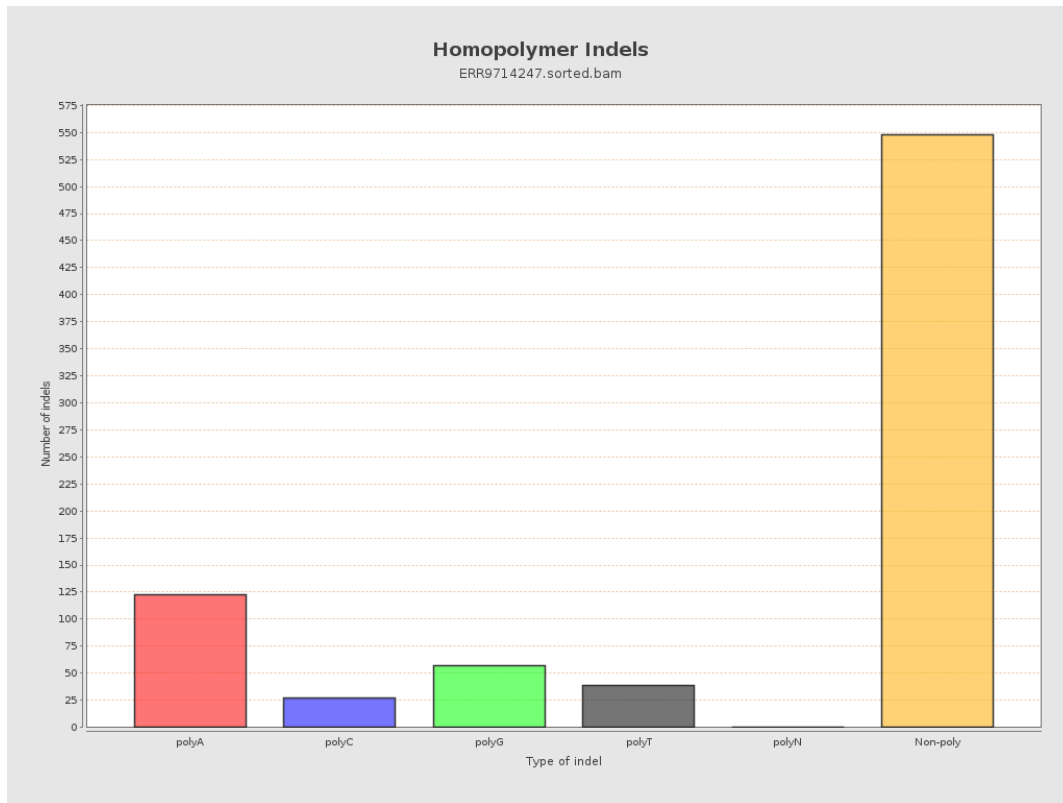
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

