

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 20:12:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714118.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_ERR9714118 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714118.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 20:12:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714118.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,108,404
Mapped reads	84,710 / 7.64%
Unmapped reads	1,023,694 / 92.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,701 / 0.15%
Read min/max/mean length	30 / 151 / 53.11
Duplicated reads (estimated)	82,095 / 7.41%
Duplication rate	29.68%
Clipped reads	53,000 / 4.78%

2.2. ACGT Content

Number/percentage of A's	332,723 / 4.11%
Number/percentage of C's	166,383 / 2.06%
Number/percentage of T's	220,894 / 2.73%
Number/percentage of G's	7,367,737 / 91.09%
Number/percentage of N's	1,039 / 0.01%
GC Percentage	93.14%

2.3. Coverage

Mean	0.0026

Standard Deviation	8.9064
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2.4. Mapping Quality

Mean Mapping Quality	21.42
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2.5. Mismatches and indels

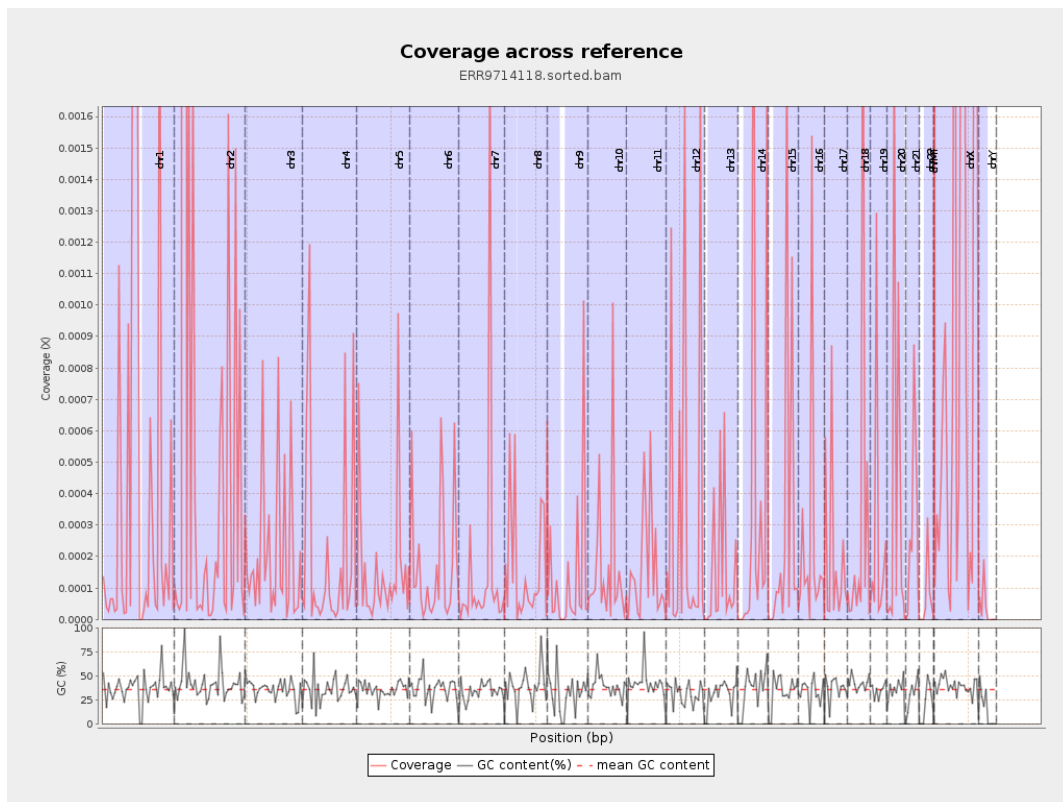
General error rate	3.24%
Mismatches	197,748
Insertions	9,335
Mapped reads with at least one insertion	7.68%
Deletions	5,504
Mapped reads with at least one deletion	6.16%
Homopolymer indels	58.08%

2.6. Chromosome stats

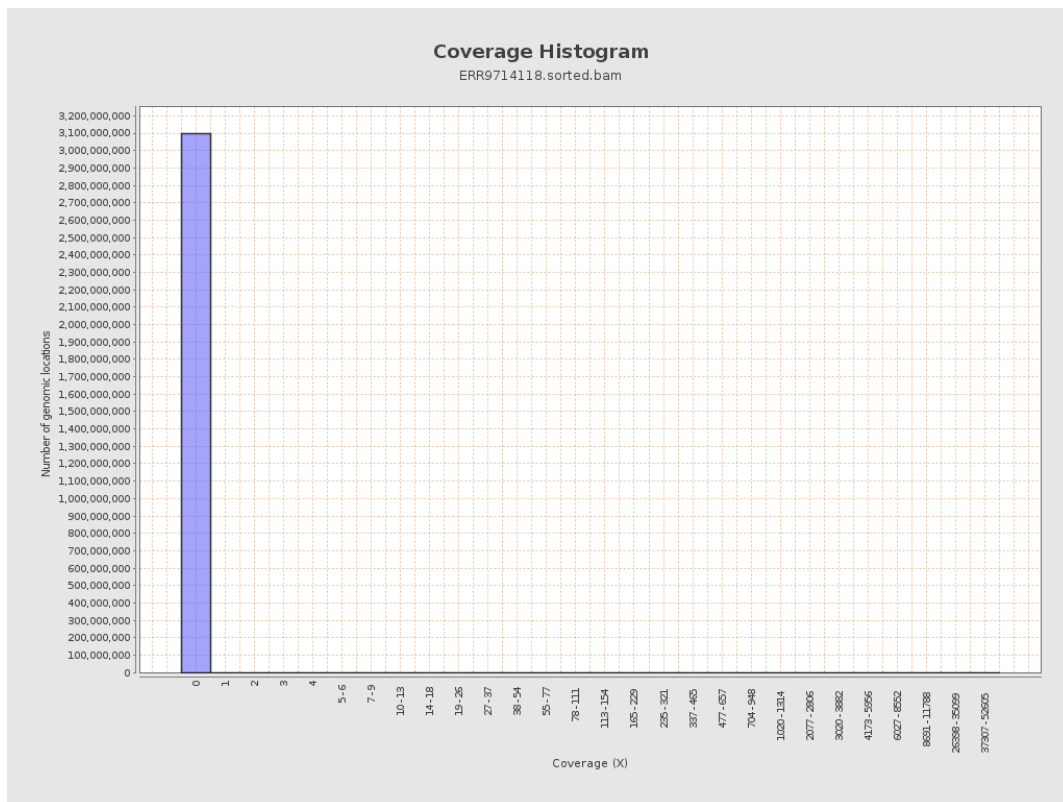
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	95863	0.0004	0.1381
chr2	243199373	7356930	0.0303	31.7735
chr3	198022430	40147	0.0002	0.0581
chr4	191154276	37930	0.0002	0.0801
chr5	180915260	30813	0.0002	0.0588
chr6	171115067	30007	0.0002	0.049
chr7	159138663	24786	0.0002	0.1987

chr8	146364022	22585	0.0002	0.054
chr9	141213431	18801	0.0001	0.0589
chr10	135534747	22326	0.0002	0.0641
chr11	135006516	21758	0.0002	0.065
chr12	133851895	46136	0.0003	0.1624
chr13	115169878	18007	0.0002	0.0494
chr14	107349540	43160	0.0004	0.1986
chr15	102531392	30046	0.0003	0.1238
chr16	90354753	21701	0.0002	0.095
chr17	81195210	16573	0.0002	0.1216
chr18	78077248	26502	0.0003	0.1184
chr19	59128983	14952	0.0003	0.1027
chr20	63025520	25275	0.0004	0.2373
chr21	48129895	13728	0.0003	0.0972
chr22	51304566	3633	0.0001	0.026
chrMT	16571	2491	0.1503	1.0059
chrX	155270560	148520	0.001	0.2206
chrY	59373566	2231	0	0.0158

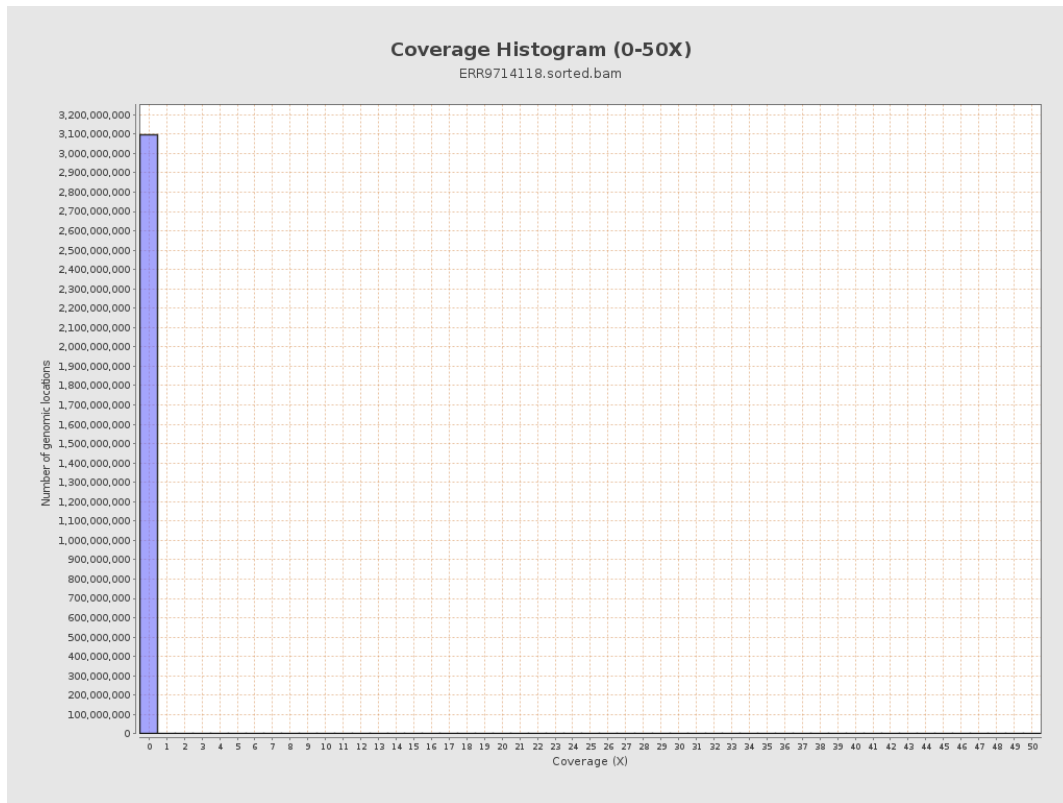
3. Results : Coverage across reference



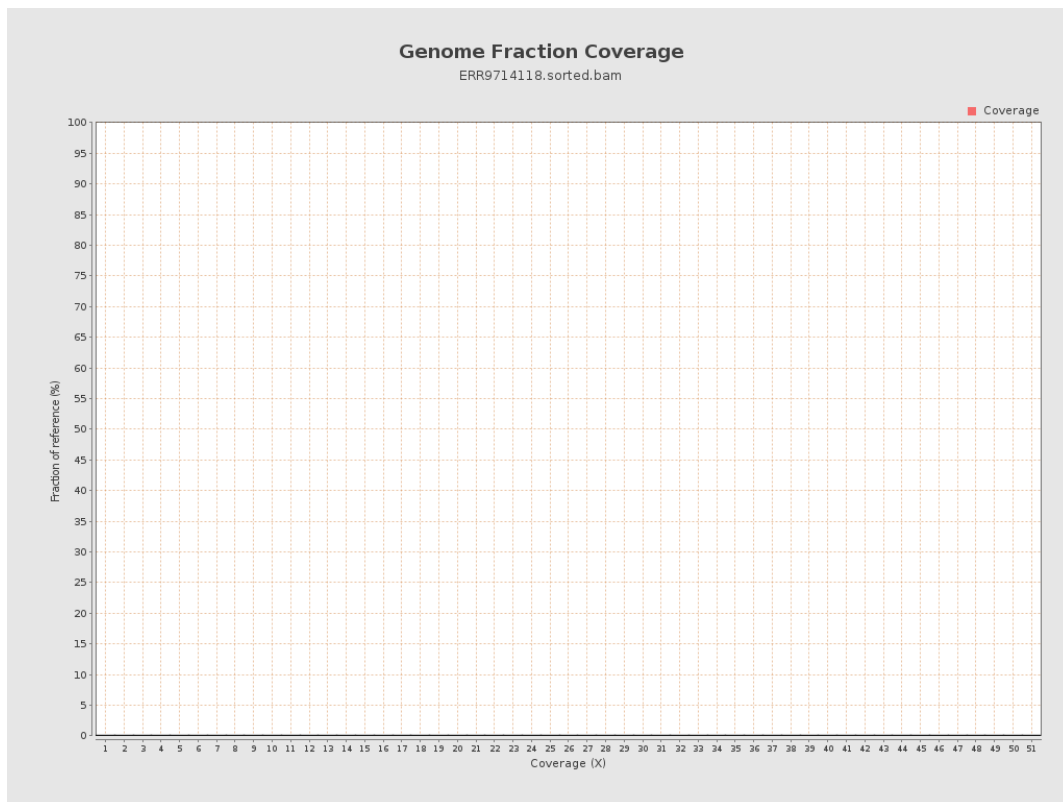
4. Results : Coverage Histogram



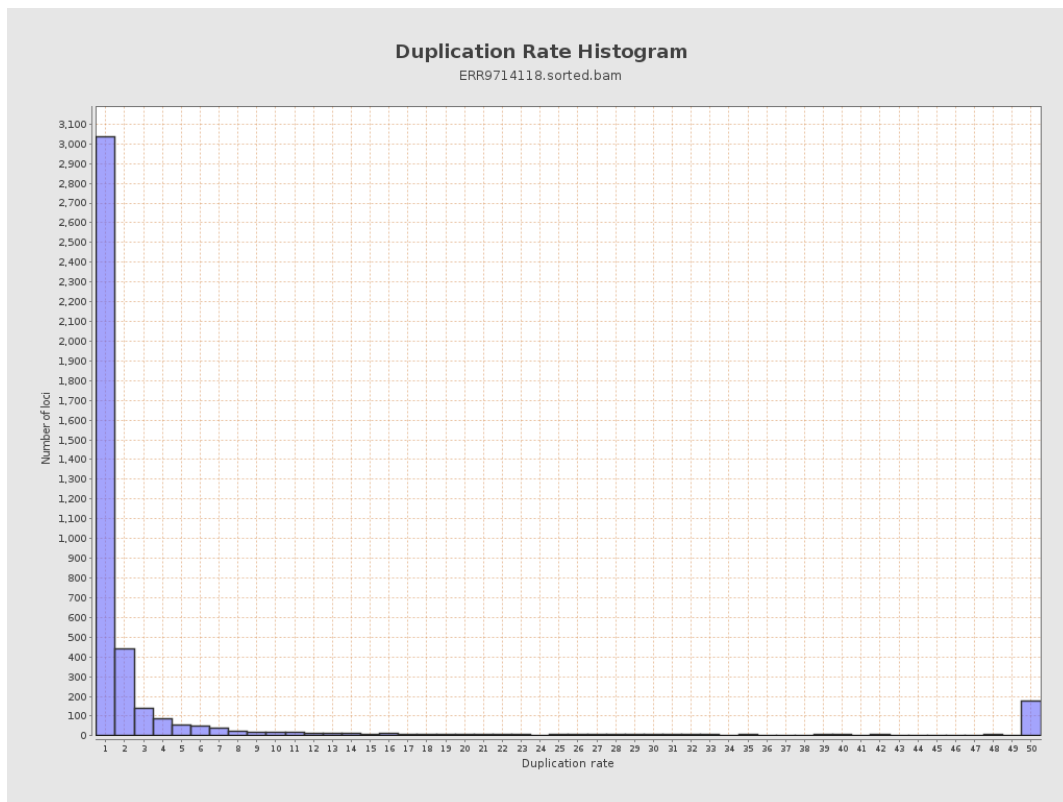
5. Results : Coverage Histogram (0-50X)



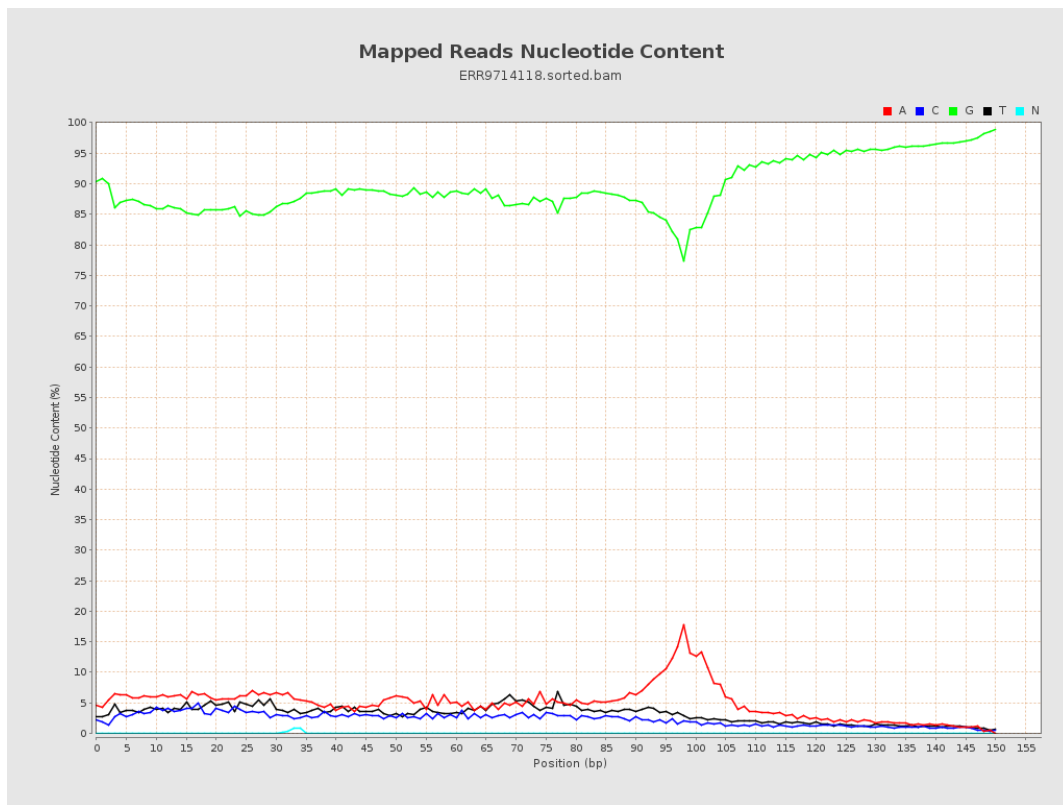
6. Results : Genome Fraction Coverage



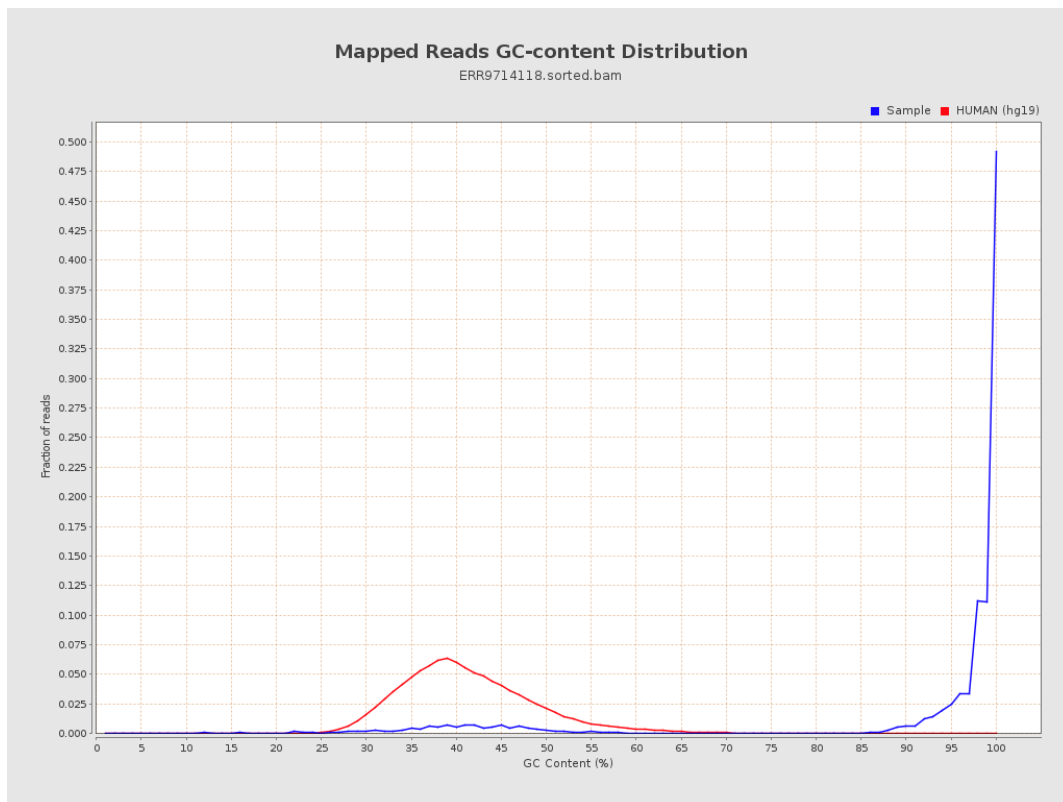
7. Results : Duplication Rate Histogram



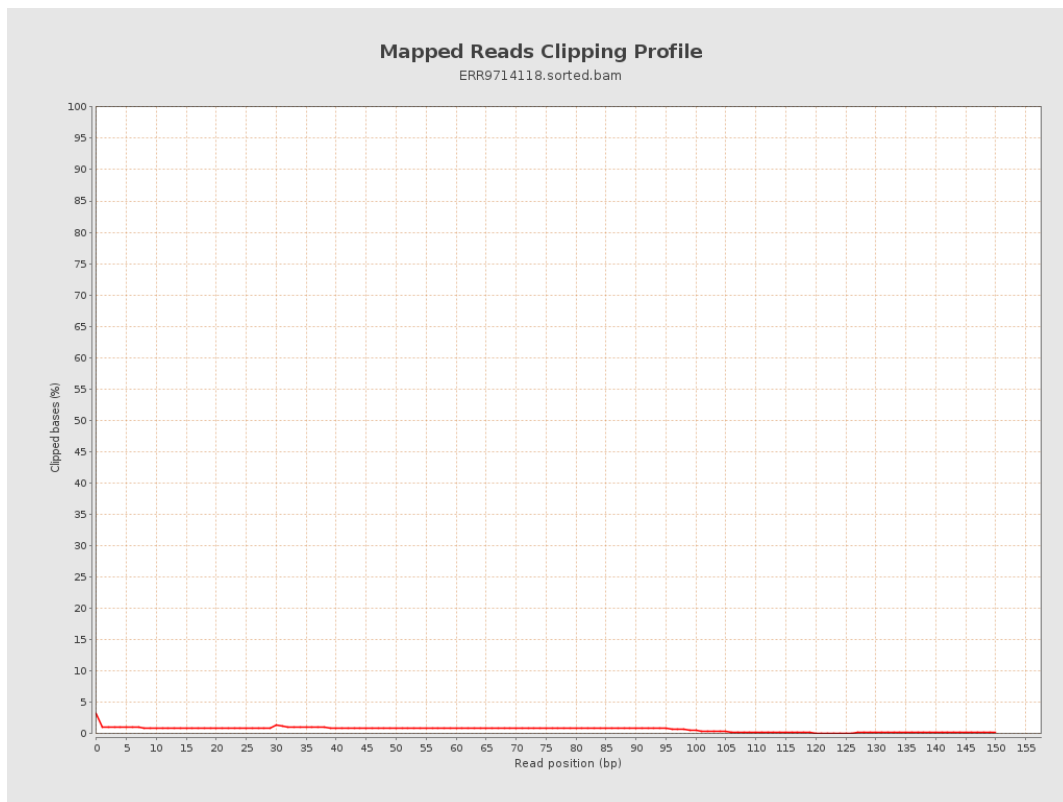
8. Results : Mapped Reads Nucleotide Content



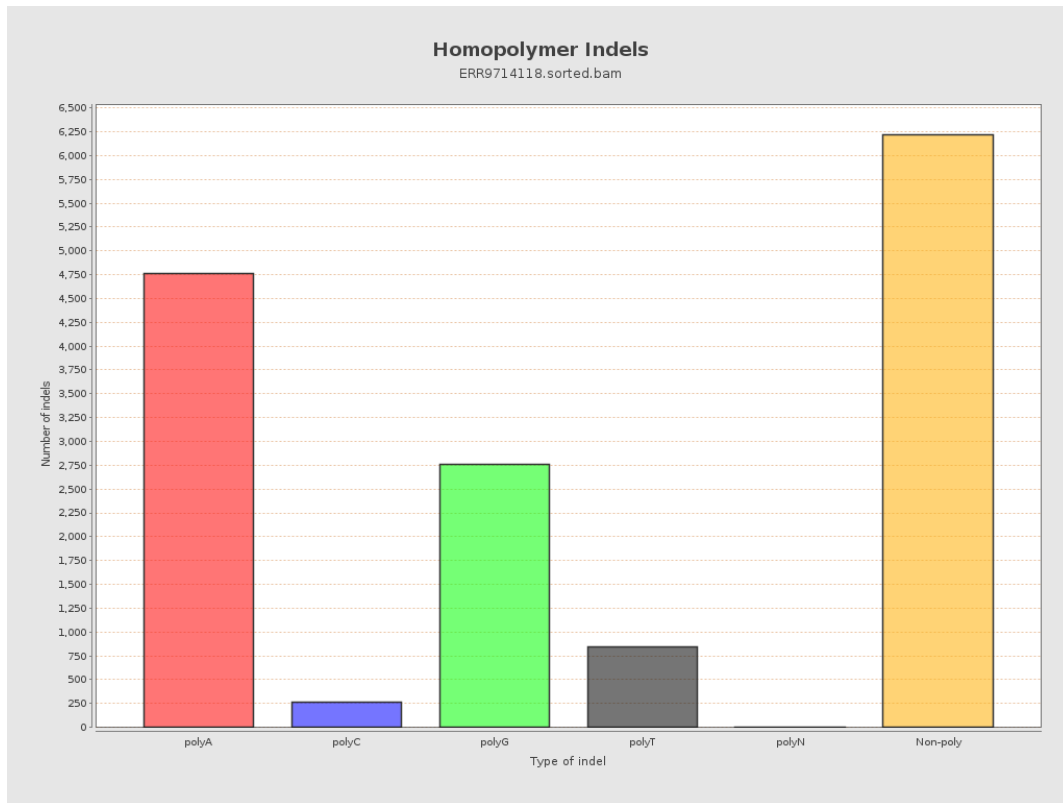
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

