

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 18:53:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714090.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_ERR9714090 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714090.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 18:53:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714090.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,422
Mapped reads	6,669 / 34.34%
Unmapped reads	12,753 / 65.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	147 / 0.76%
Read min/max/mean length	30 / 151 / 88.52
Duplicated reads (estimated)	5,214 / 26.85%
Duplication rate	42.82%
Clipped reads	5,454 / 28.08%

2.2. ACGT Content

Number/percentage of A's	168,373 / 21.98%
Number/percentage of C's	137,816 / 17.99%
Number/percentage of T's	154,274 / 20.14%
Number/percentage of G's	305,701 / 39.9%
Number/percentage of N's	12 / 0%
GC Percentage	57.89%

2.3. Coverage

Mean	0.0003

Standard Deviation	0.2385
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2.4. Mapping Quality

Mean Mapping Quality	19.59
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2.5. Mismatches and indels

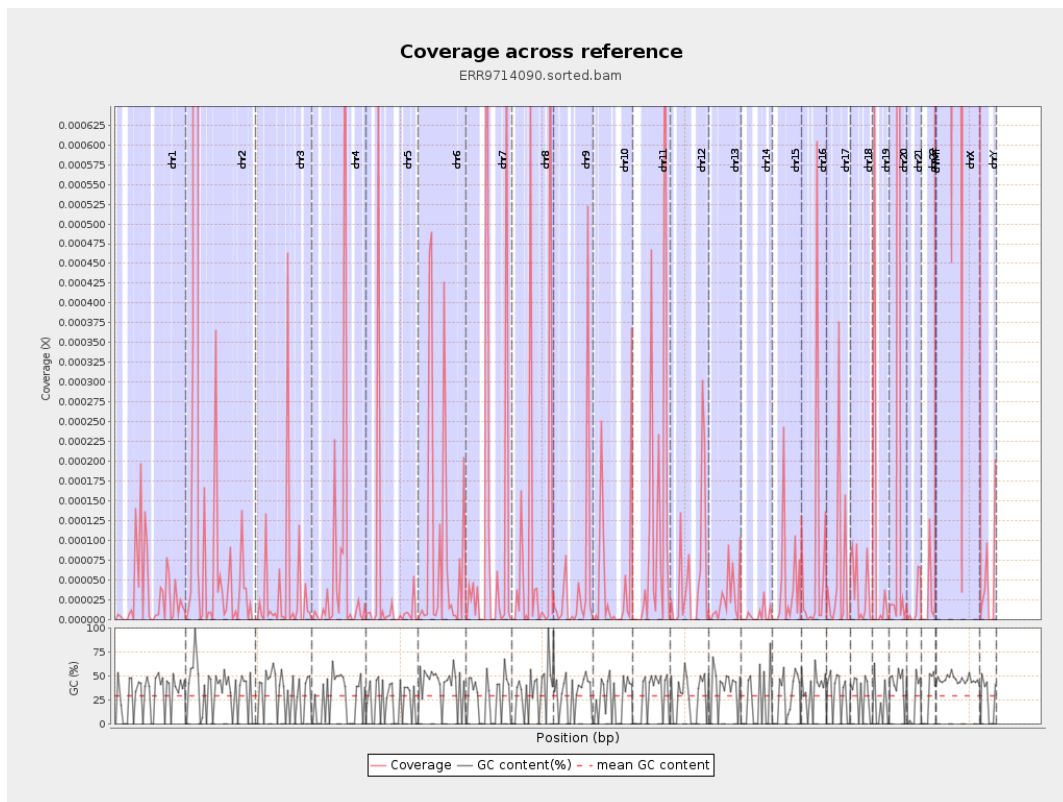
General error rate	3.71%
Mismatches	27,198
Insertions	419
Mapped reads with at least one insertion	5.37%
Deletions	1,925
Mapped reads with at least one deletion	28.04%
Homopolymer indels	30.08%

2.6. Chromosome stats

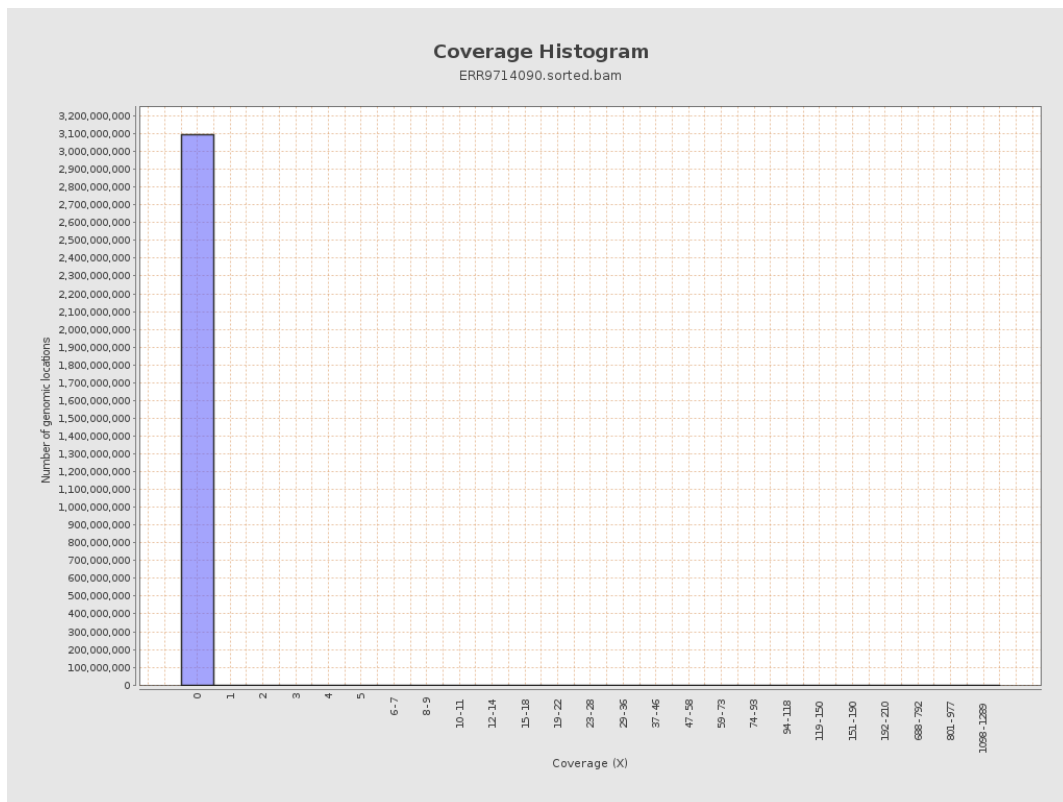
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7638	0	0.0144
chr2	243199373	180471	0.0007	0.7758
chr3	198022430	7176	0	0.0231
chr4	191154276	11789	0.0001	0.039
chr5	180915260	6439	0	0.0272
chr6	171115067	15040	0.0001	0.0432
chr7	159138663	17184	0.0001	0.0589

chr8	146364022	14299	0.0001	0.056
chr9	141213431	6254	0	0.0214
chr10	135534747	5502	0	0.0192
chr11	135006516	15890	0.0001	0.0586
chr12	133851895	7381	0.0001	0.0232
chr13	115169878	3149	0	0.0097
chr14	107349540	599	0	0.0034
chr15	102531392	4270	0	0.0163
chr16	90354753	7104	0.0001	0.0437
chr17	81195210	4944	0.0001	0.0287
chr18	78077248	2743	0	0.0116
chr19	59128983	5467	0.0001	0.0539
chr20	63025520	17494	0.0003	0.1423
chr21	48129895	919	0	0.0056
chr22	51304566	1145	0	0.0126
chrMT	16571	602	0.0363	0.3345
chrX	155270560	434399	0.0028	0.4043
chrY	59373566	2729	0	0.0116

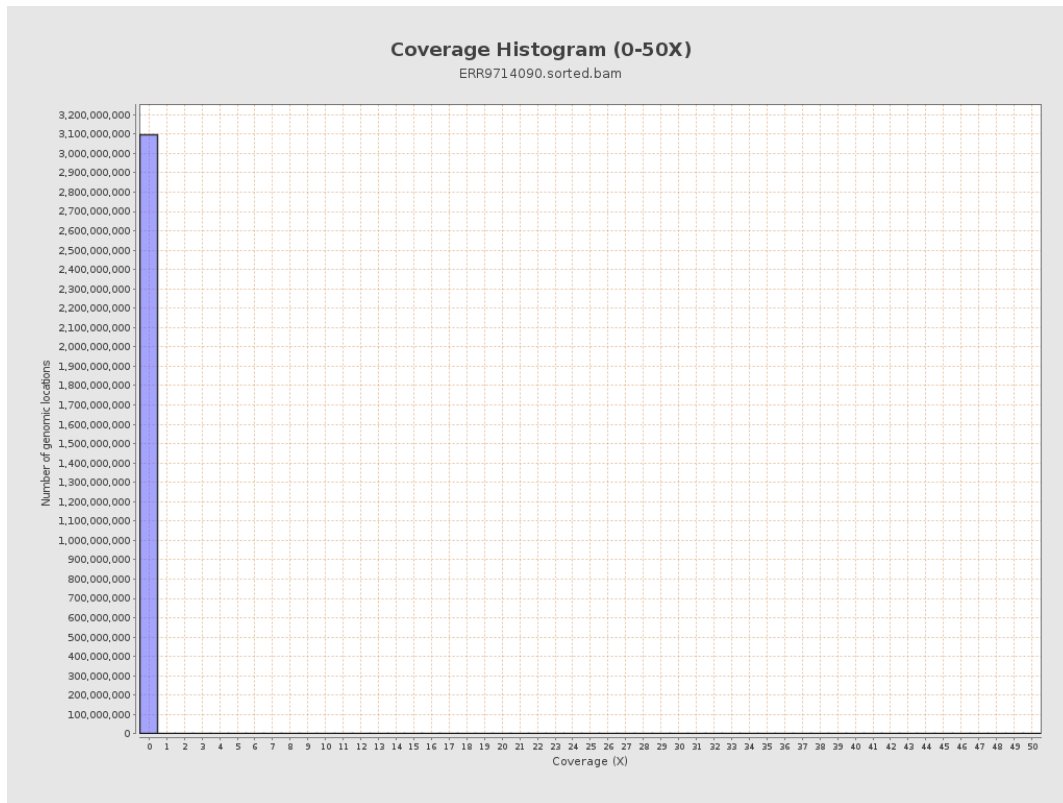
3. Results : Coverage across reference



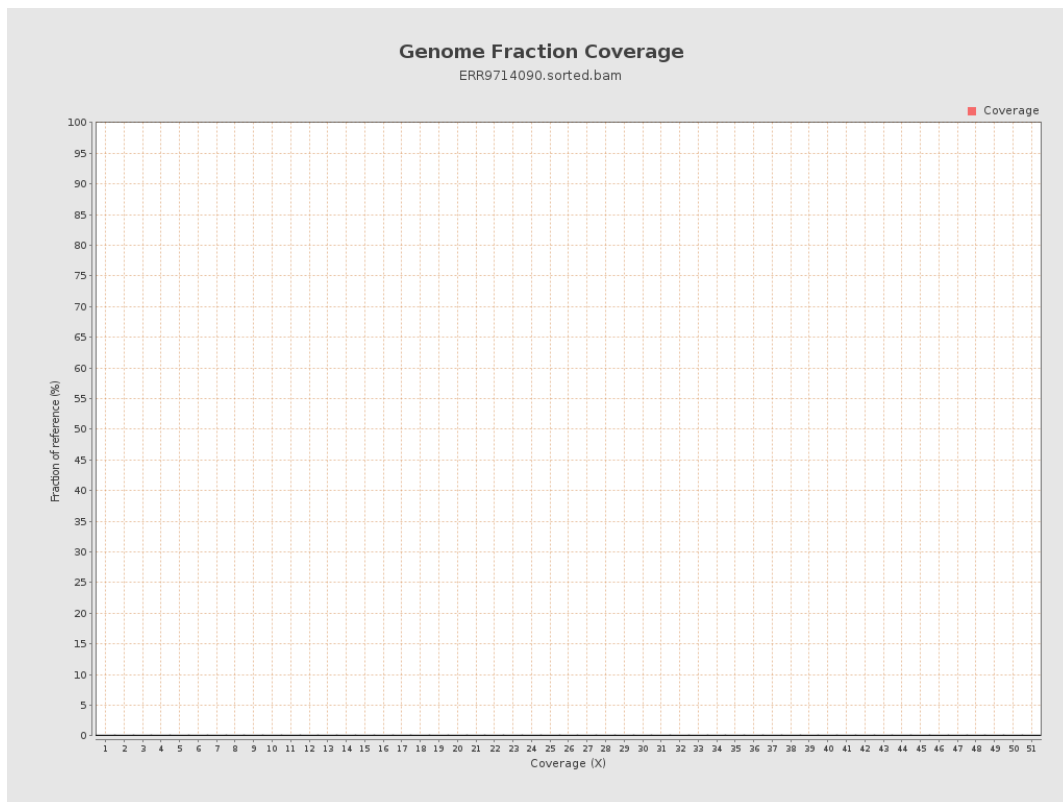
4. Results : Coverage Histogram



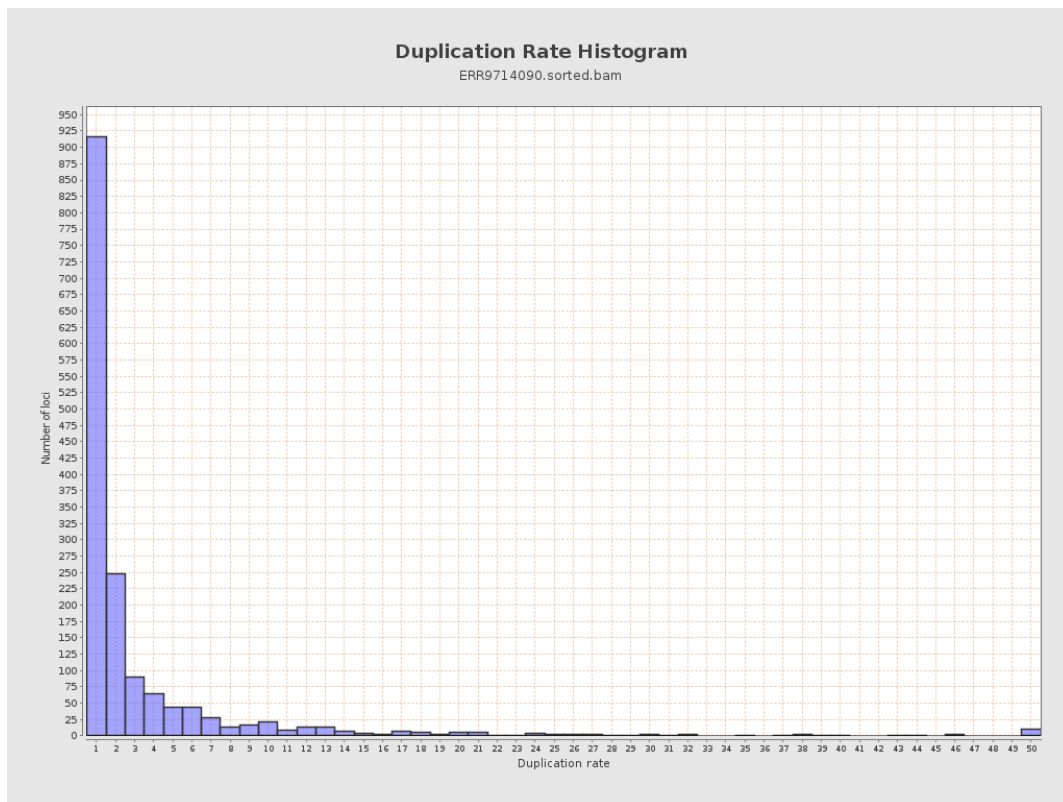
5. Results : Coverage Histogram (0-50X)



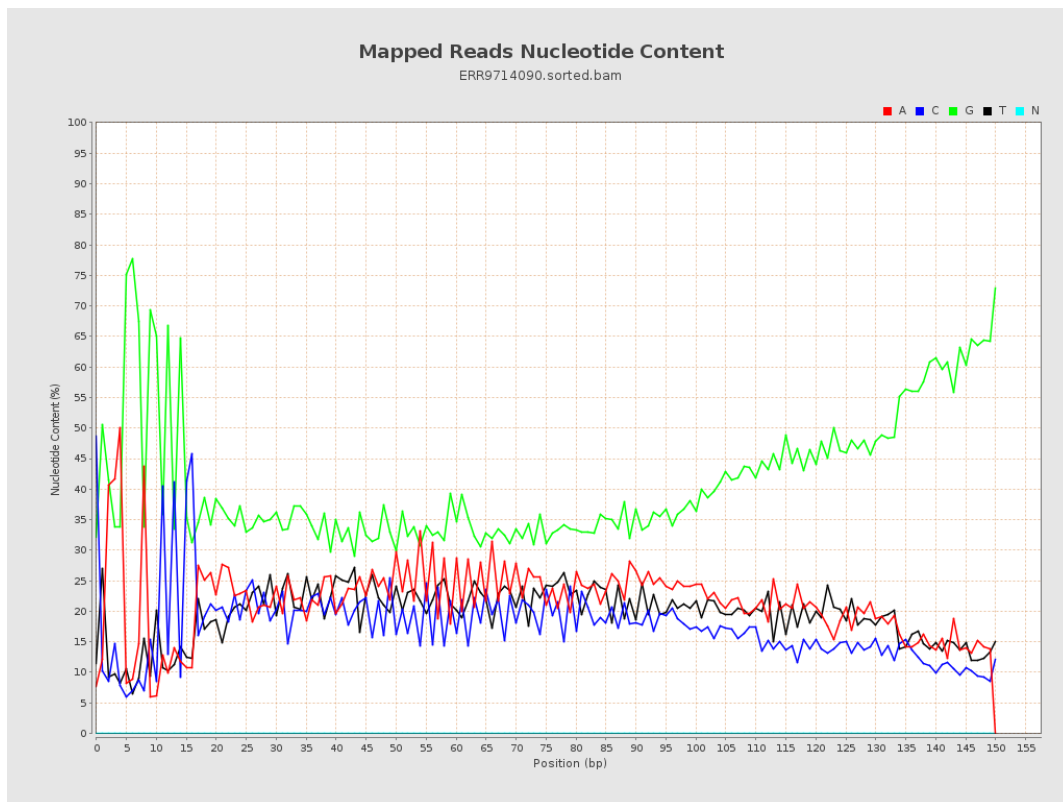
6. Results : Genome Fraction Coverage



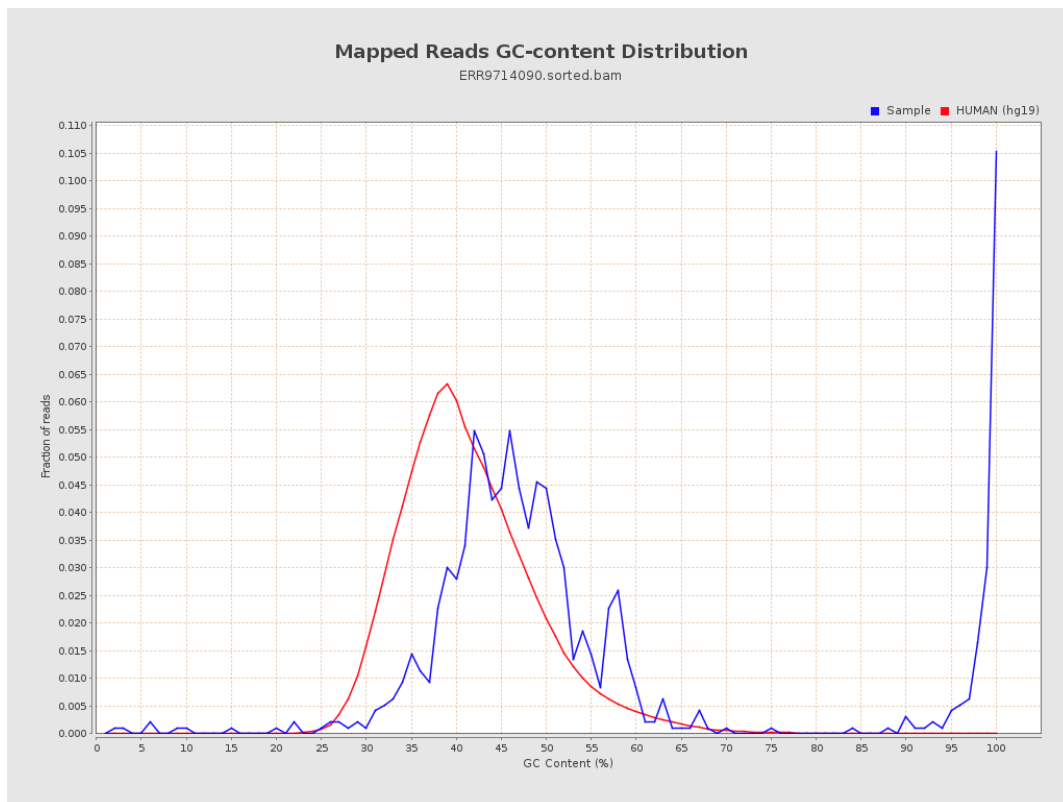
7. Results : Duplication Rate Histogram



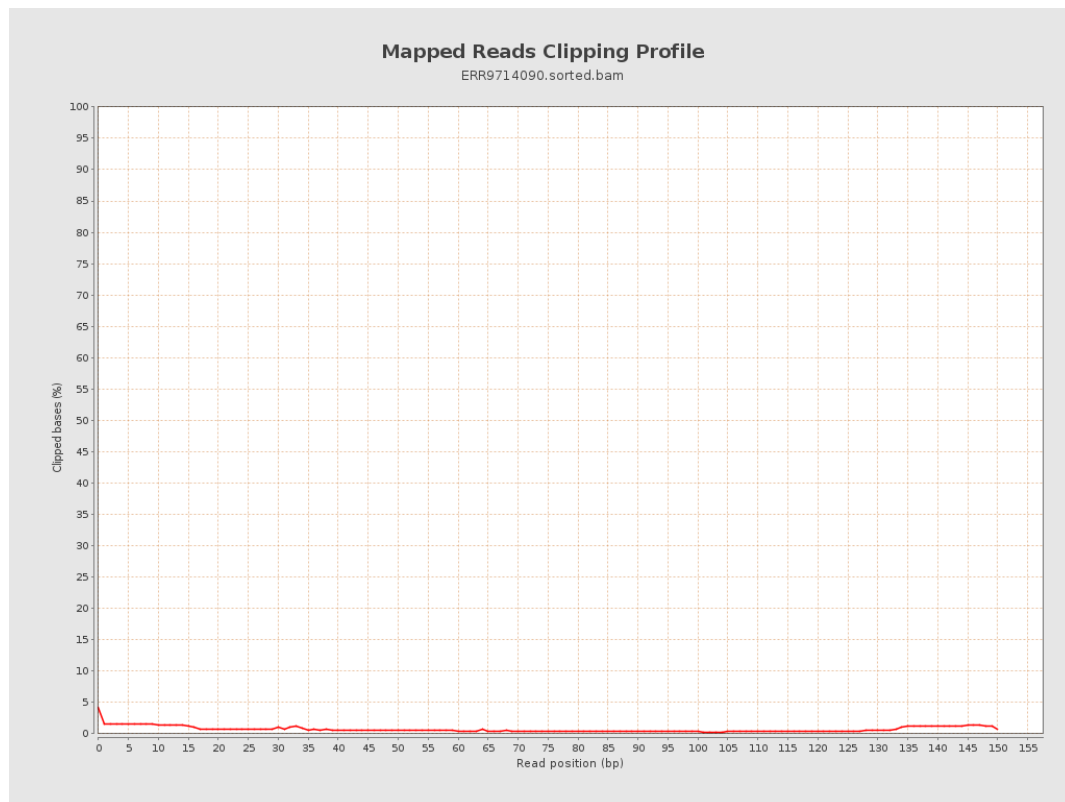
8. Results : Mapped Reads Nucleotide Content



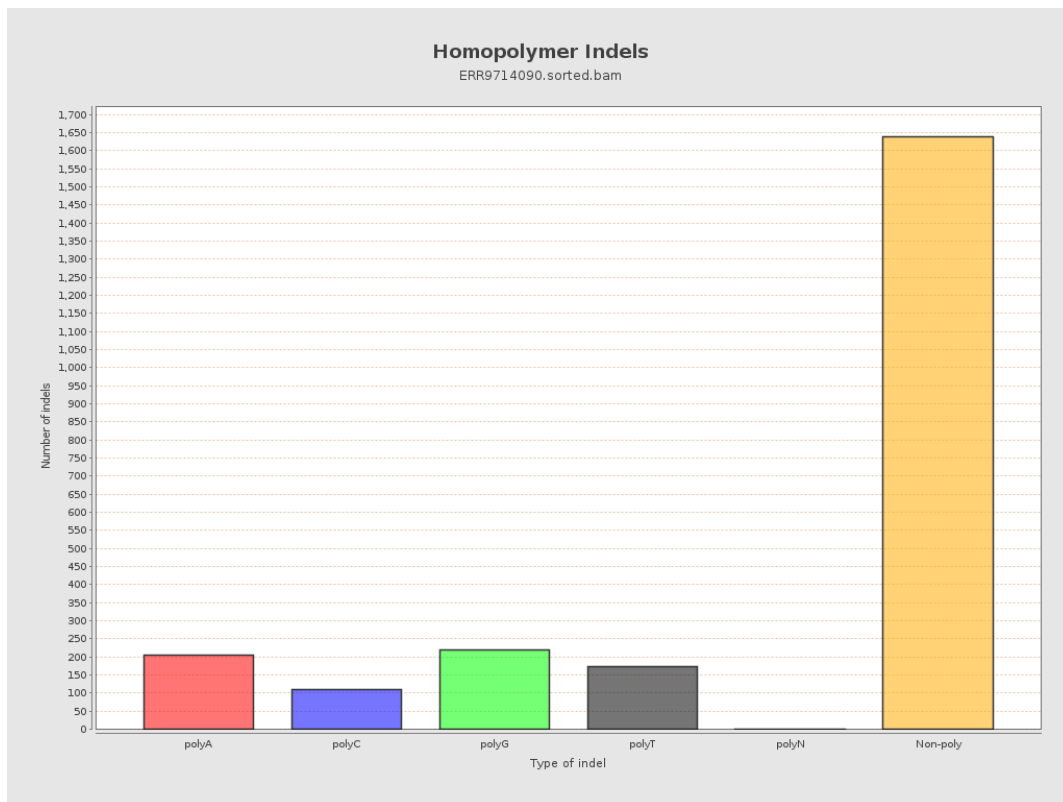
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

