

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 09:36:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716738.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_SRR9716738 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716738.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 09:36:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716738.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,595,808
Mapped reads	1,461,336 / 91.57%
Unmapped reads	134,472 / 8.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,590 / 0.54%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	51,961 / 3.26%
Duplication rate	2.55%
Clipped reads	1,465,935 / 91.86%

2.2. ACGT Content

Number/percentage of A's	22,116,078 / 25.92%
Number/percentage of C's	15,978,351 / 18.72%
Number/percentage of T's	26,022,203 / 30.49%
Number/percentage of G's	21,222,784 / 24.87%
Number/percentage of N's	1,102 / 0%
GC Percentage	43.59%

2.3. Coverage

Mean	0.0276

Standard Deviation	0.2718
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2.4. Mapping Quality

Mean Mapping Quality	44.68
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2.5. Mismatches and indels

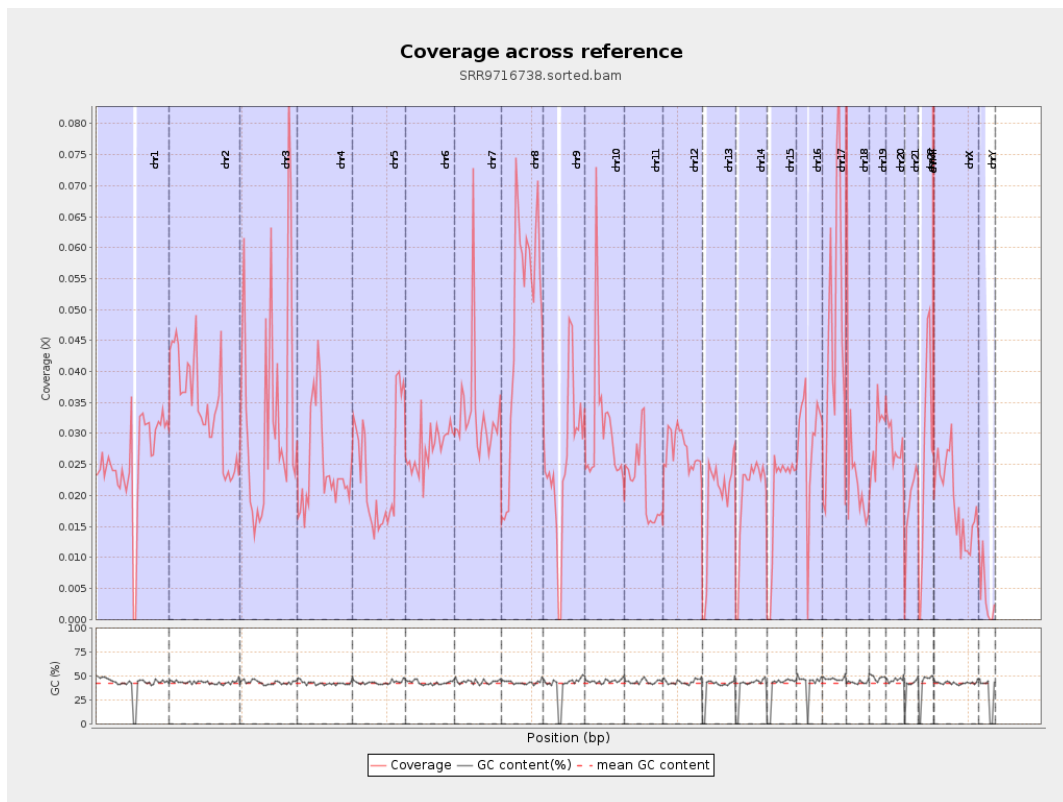
General error rate	0.52%
Mismatches	428,961
Insertions	5,569
Mapped reads with at least one insertion	0.38%
Deletions	16,003
Mapped reads with at least one deletion	1.09%
Homopolymer indels	41.09%

2.6. Chromosome stats

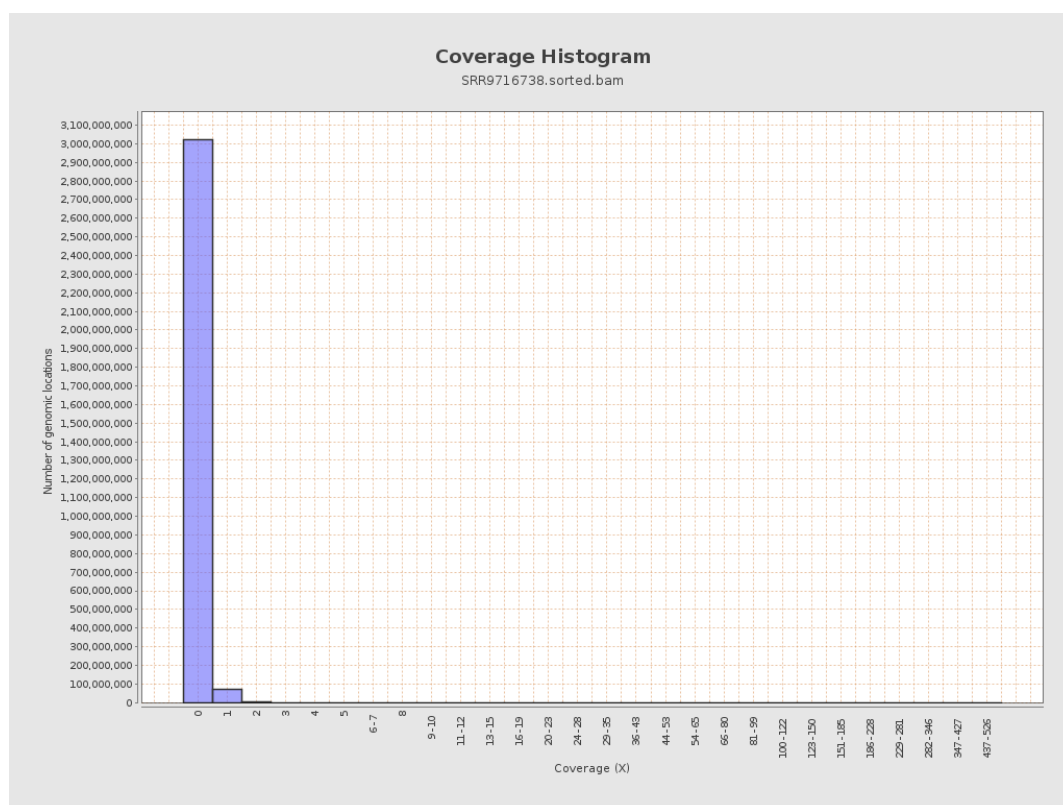
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6364833	0.0255	0.342
chr2	243199373	8400609	0.0345	0.316
chr3	198022430	6464885	0.0326	0.2074
chr4	191154276	4706852	0.0246	0.198
chr5	180915260	4317375	0.0239	0.1684
chr6	171115067	4737508	0.0277	0.1955
chr7	159138663	5312932	0.0334	0.6026

chr8	146364022	7087991	0.0484	0.3307
chr9	141213431	3566395	0.0253	0.1956
chr10	135534747	4128765	0.0305	0.3596
chr11	135006516	2916480	0.0216	0.1927
chr12	133851895	3649095	0.0273	0.2022
chr13	115169878	2201614	0.0191	0.1497
chr14	107349540	2142990	0.02	0.1578
chr15	102531392	2031641	0.0198	0.1551
chr16	90354753	2648719	0.0293	0.1953
chr17	81195210	3646789	0.0449	0.2416
chr18	78077248	1984941	0.0254	0.2994
chr19	59128983	1746042	0.0295	0.3196
chr20	63025520	1775731	0.0282	0.191
chr21	48129895	893382	0.0186	0.1663
chr22	51304566	1336809	0.0261	0.1759
chrMT	16571	87920	5.3057	4.1348
chrX	155270560	2995137	0.0193	0.1711
chrY	59373566	220369	0.0037	0.1085

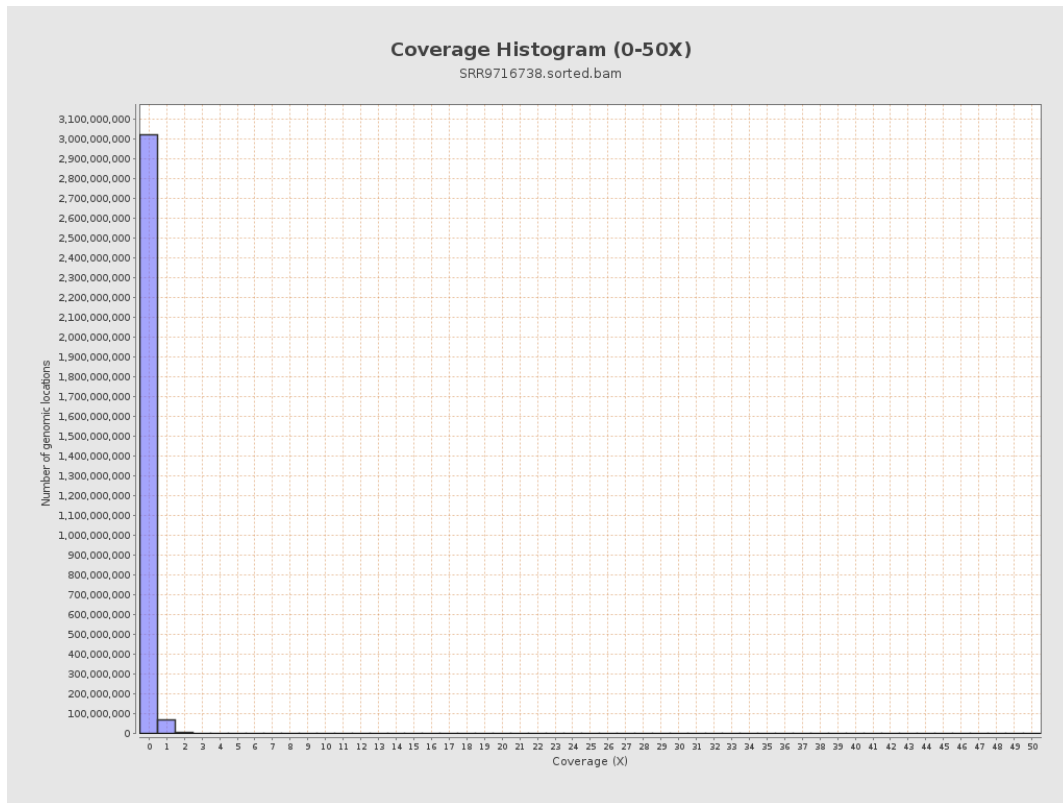
3. Results : Coverage across reference



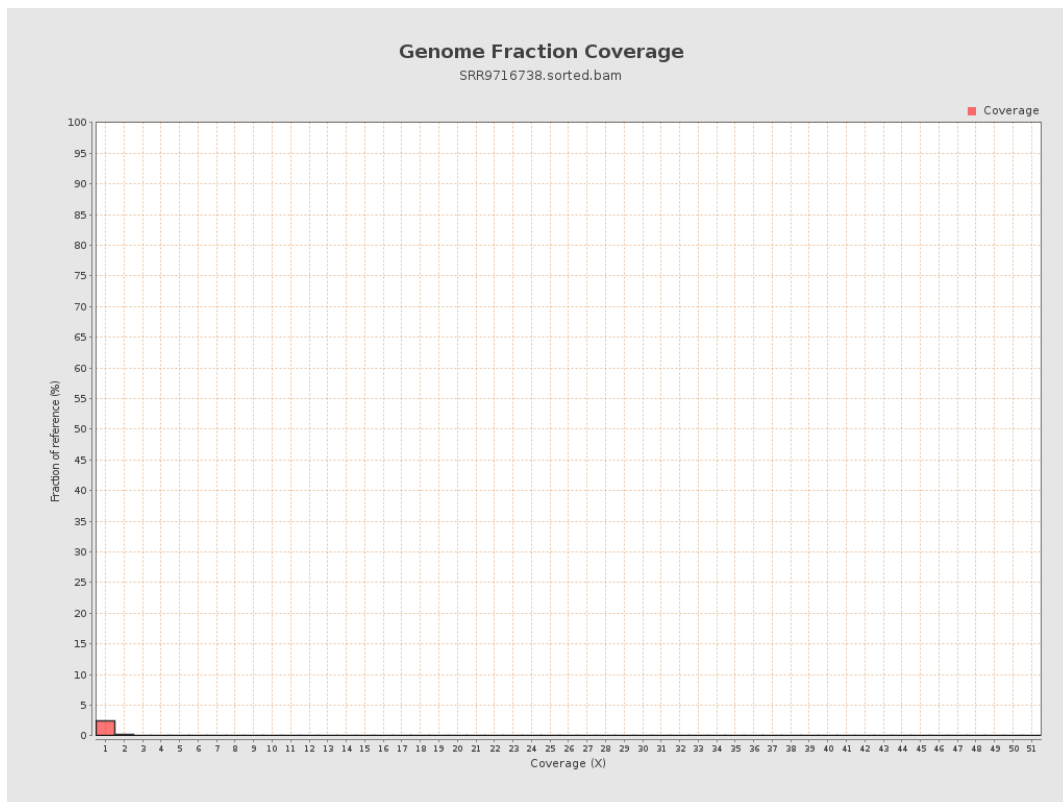
4. Results : Coverage Histogram



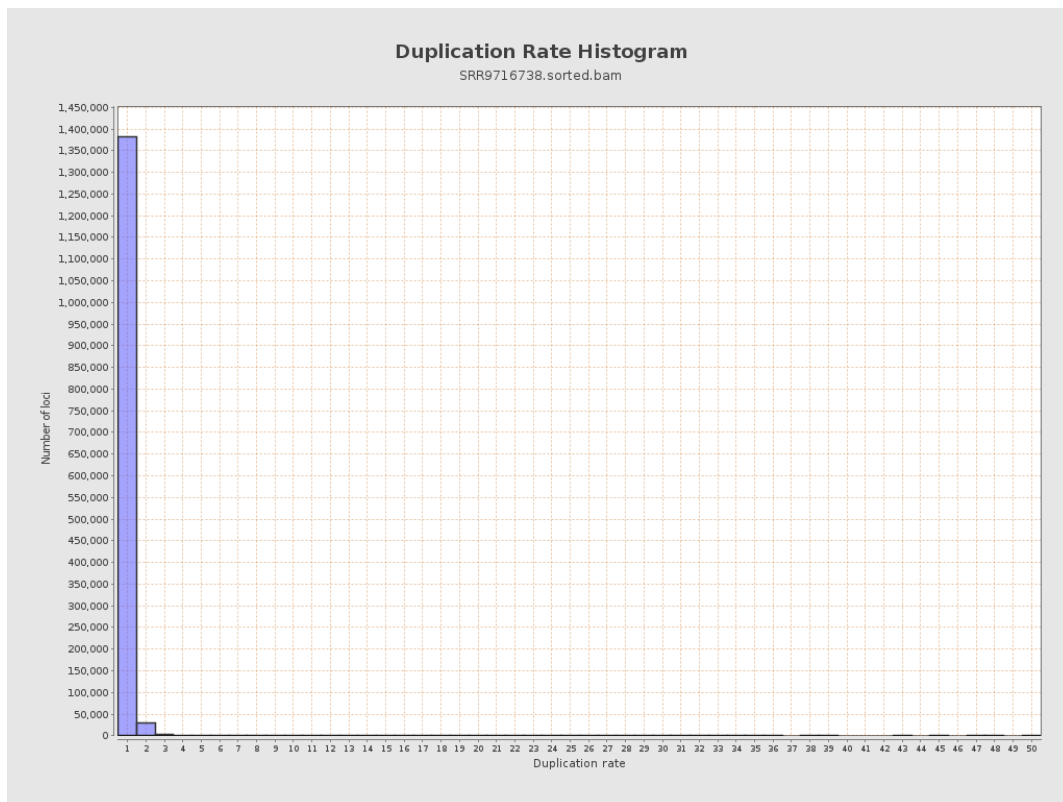
5. Results : Coverage Histogram (0-50X)



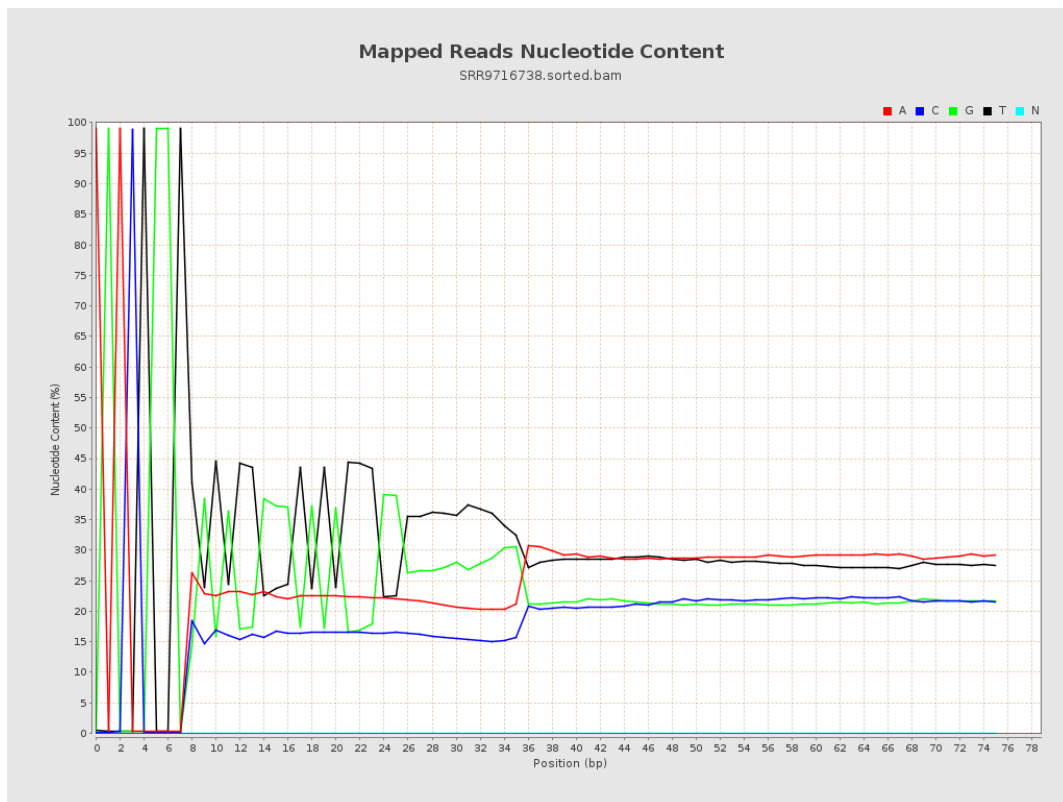
6. Results : Genome Fraction Coverage



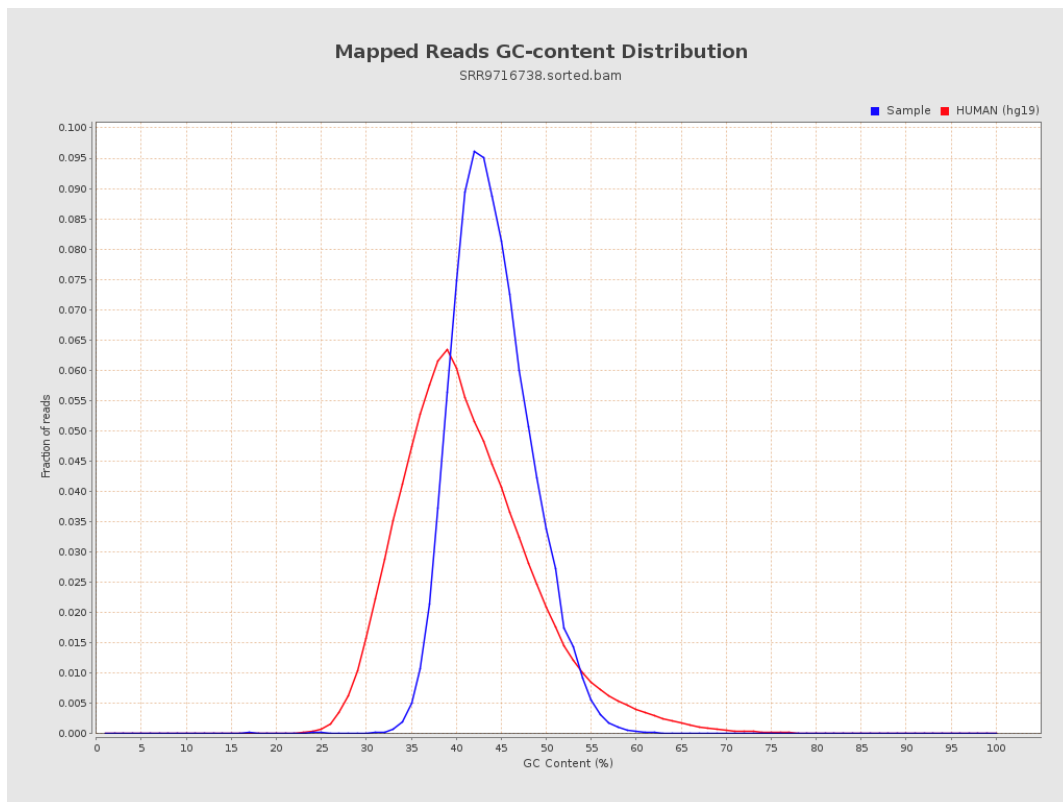
7. Results : Duplication Rate Histogram



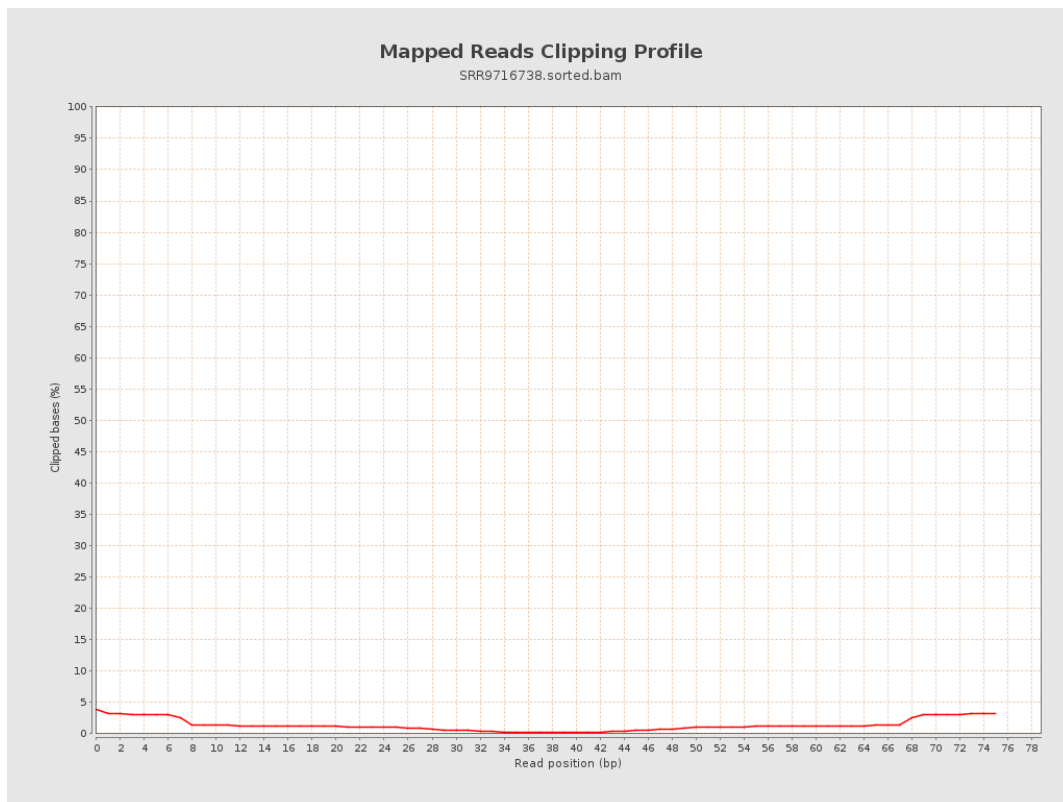
8. Results : Mapped Reads Nucleotide Content



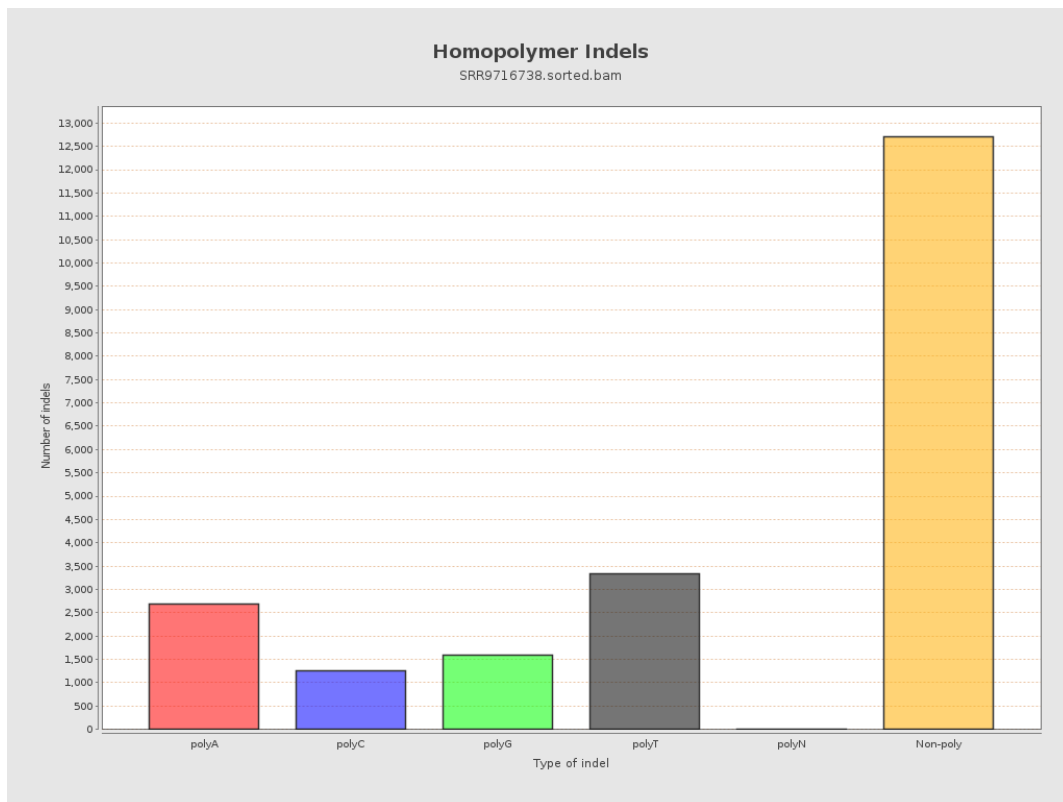
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

