

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 09:52:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716746.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_SRR9716746 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716746.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 09:52:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716746.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,731,561
Mapped reads	1,278,401 / 73.83%
Unmapped reads	453,160 / 26.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,375 / 0.08%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	132,857 / 7.67%
Duplication rate	8.91%
Clipped reads	1,278,355 / 73.83%

2.2. ACGT Content

Number/percentage of A's	13,372,445 / 20.13%
Number/percentage of C's	11,438,193 / 17.21%
Number/percentage of T's	22,392,200 / 33.7%
Number/percentage of G's	19,239,798 / 28.96%
Number/percentage of N's	1,140 / 0%
GC Percentage	46.17%

2.3. Coverage

Mean	0.0215

Standard Deviation	0.2014
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2.4. Mapping Quality

Mean Mapping Quality	42.76
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2.5. Mismatches and indels

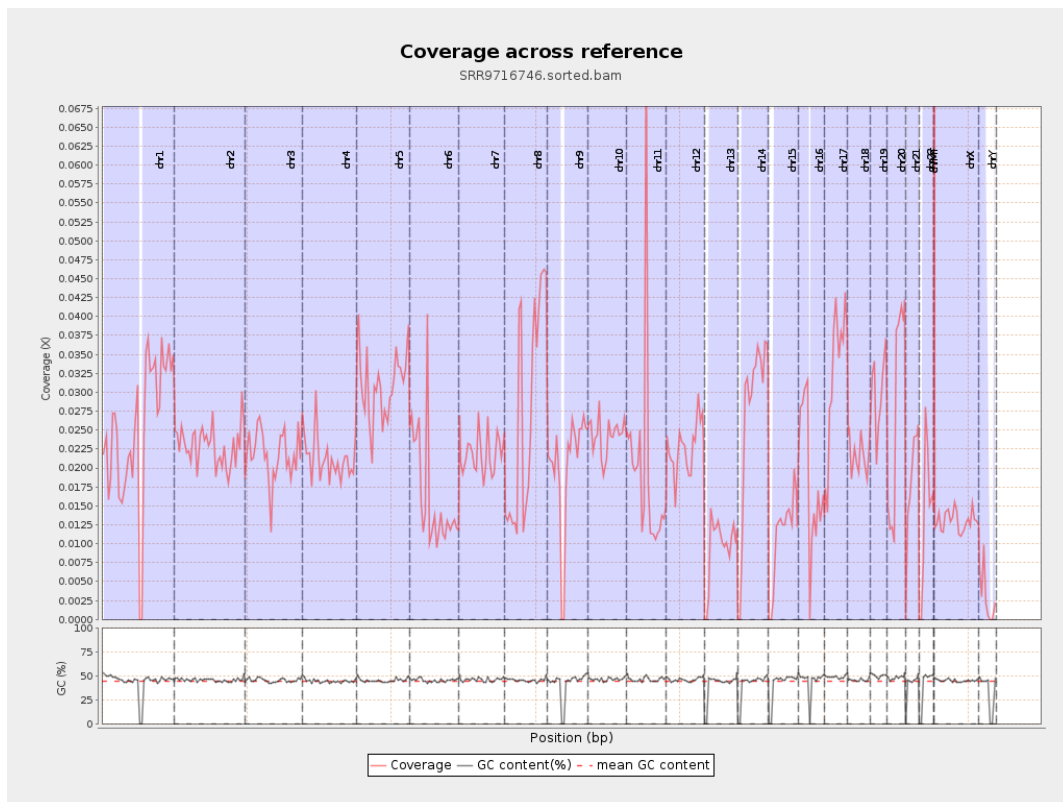
General error rate	0.67%
Mismatches	438,334
Insertions	3,511
Mapped reads with at least one insertion	0.27%
Deletions	9,263
Mapped reads with at least one deletion	0.72%
Homopolymer indels	42.28%

2.6. Chromosome stats

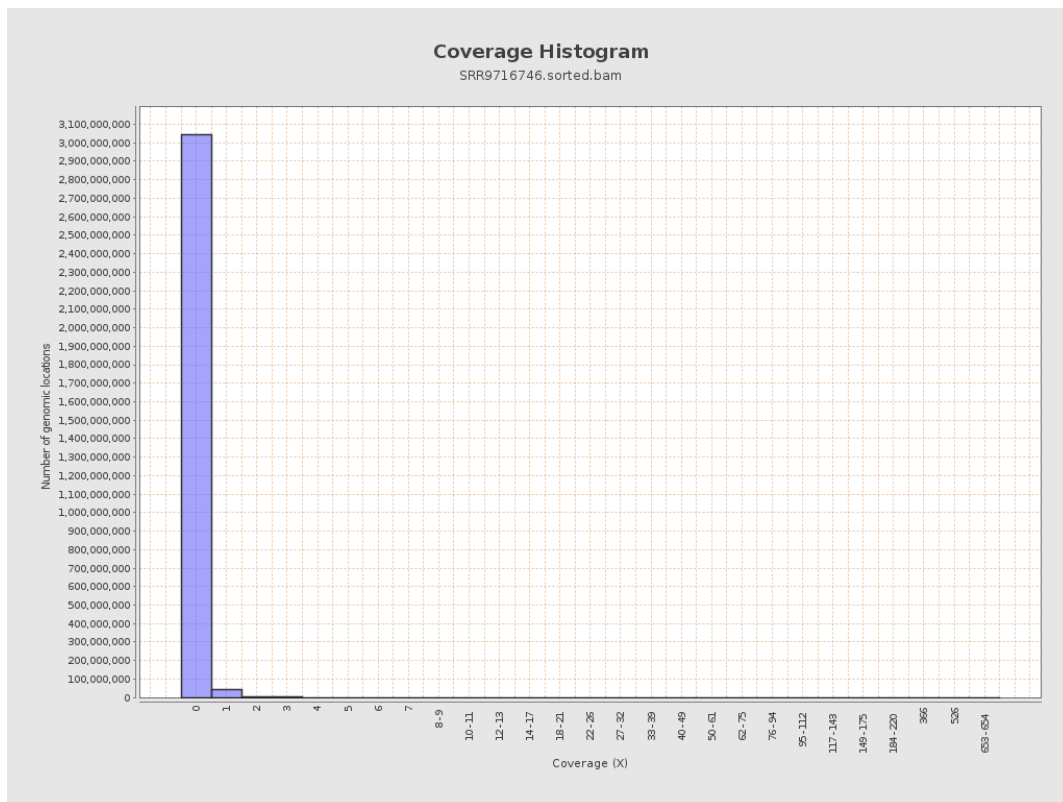
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6283460	0.0252	0.2229
chr2	243199373	5578581	0.0229	0.3135
chr3	198022430	4310714	0.0218	0.1808
chr4	191154276	4081288	0.0214	0.1794
chr5	180915260	5610751	0.031	0.2134
chr6	171115067	2785043	0.0163	0.1778
chr7	159138663	3482964	0.0219	0.1878

chr8	146364022	4003023	0.0273	0.209
chr9	141213431	2850883	0.0202	0.1832
chr10	135534747	3299855	0.0243	0.204
chr11	135006516	2705005	0.02	0.1901
chr12	133851895	3028723	0.0226	0.1847
chr13	115169878	1090940	0.0095	0.1186
chr14	107349540	2914499	0.0271	0.2018
chr15	102531392	1152433	0.0112	0.1294
chr16	90354753	1659968	0.0184	0.1753
chr17	81195210	2638103	0.0325	0.2299
chr18	78077248	1687441	0.0216	0.1943
chr19	59128983	1764906	0.0298	0.261
chr20	63025520	1708230	0.0271	0.2121
chr21	48129895	884876	0.0184	0.1727
chr22	51304566	731655	0.0143	0.1738
chrMT	16571	3543	0.2138	0.5947
chrX	155270560	2029038	0.0131	0.142
chrY	59373566	173656	0.0029	0.0783

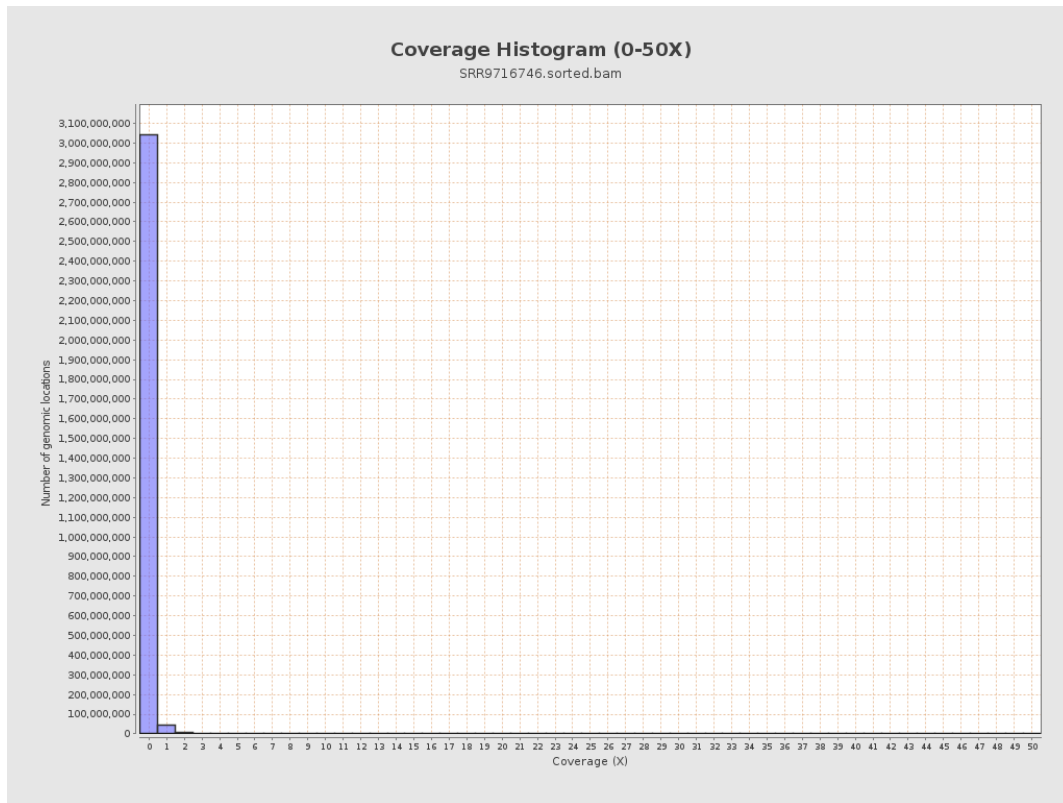
3. Results : Coverage across reference



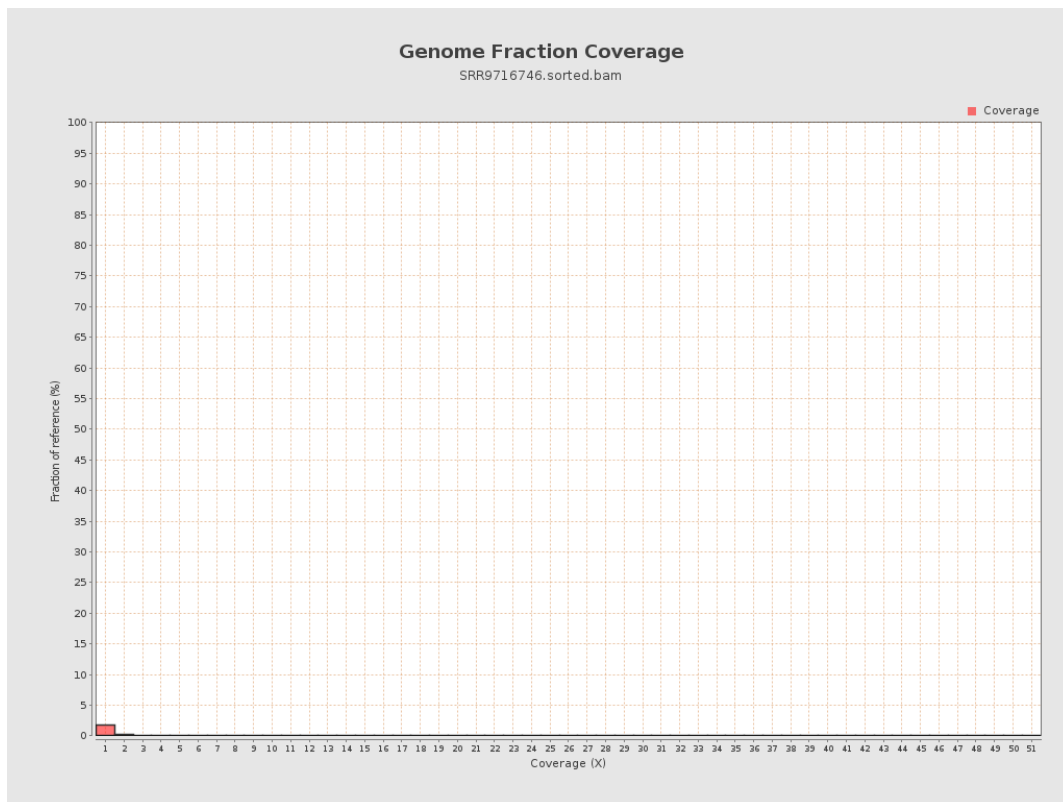
4. Results : Coverage Histogram



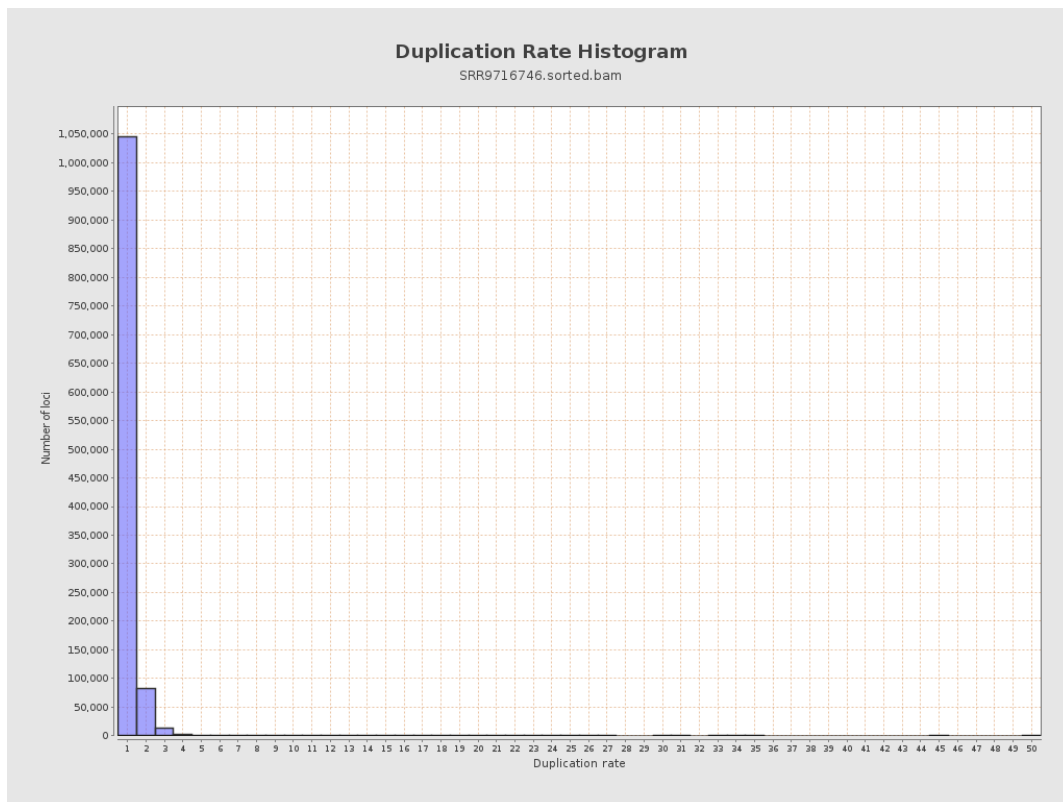
5. Results : Coverage Histogram (0-50X)



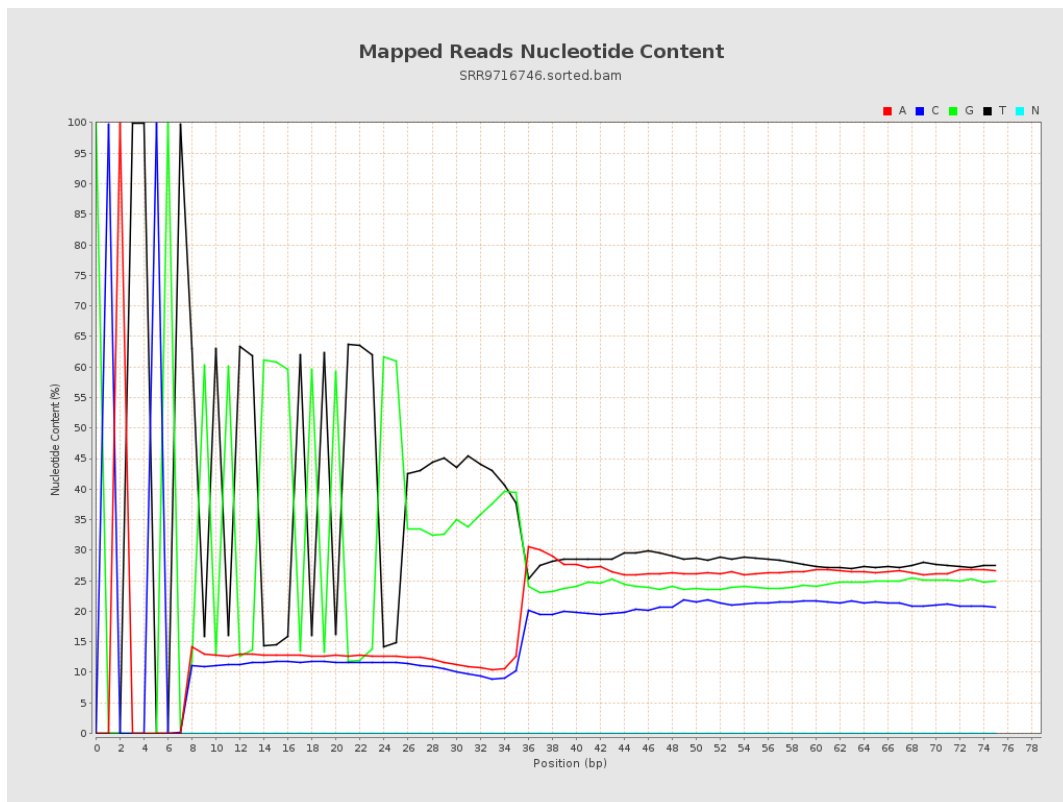
6. Results : Genome Fraction Coverage



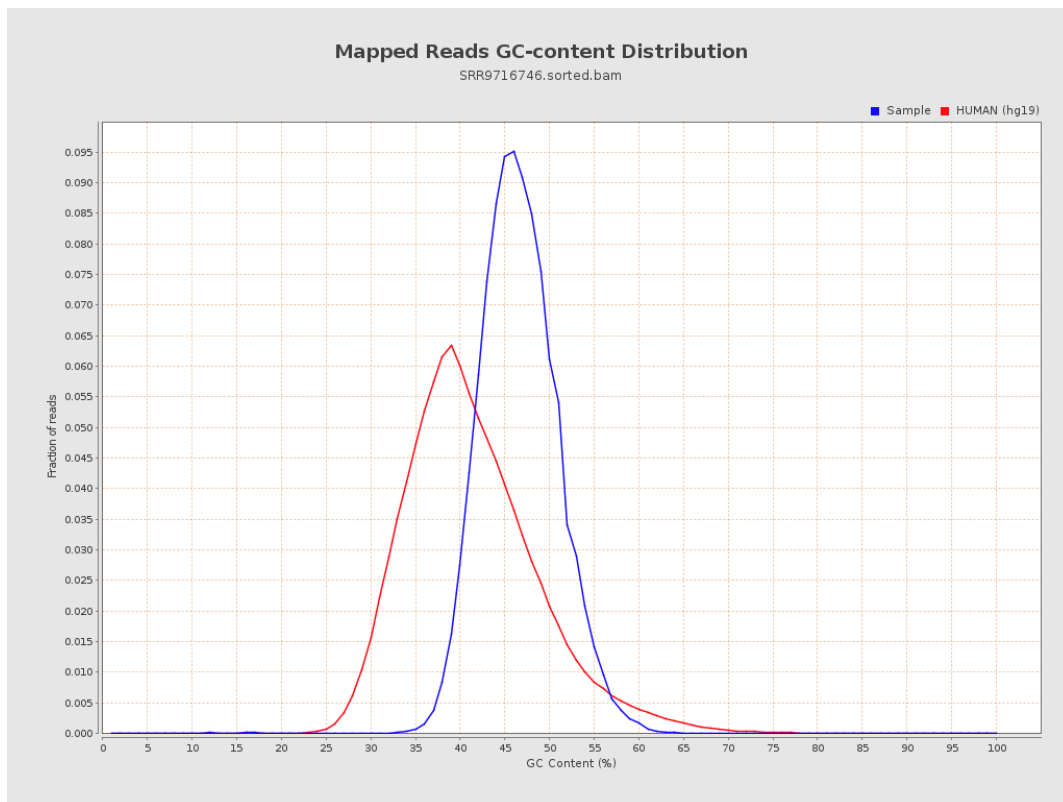
7. Results : Duplication Rate Histogram



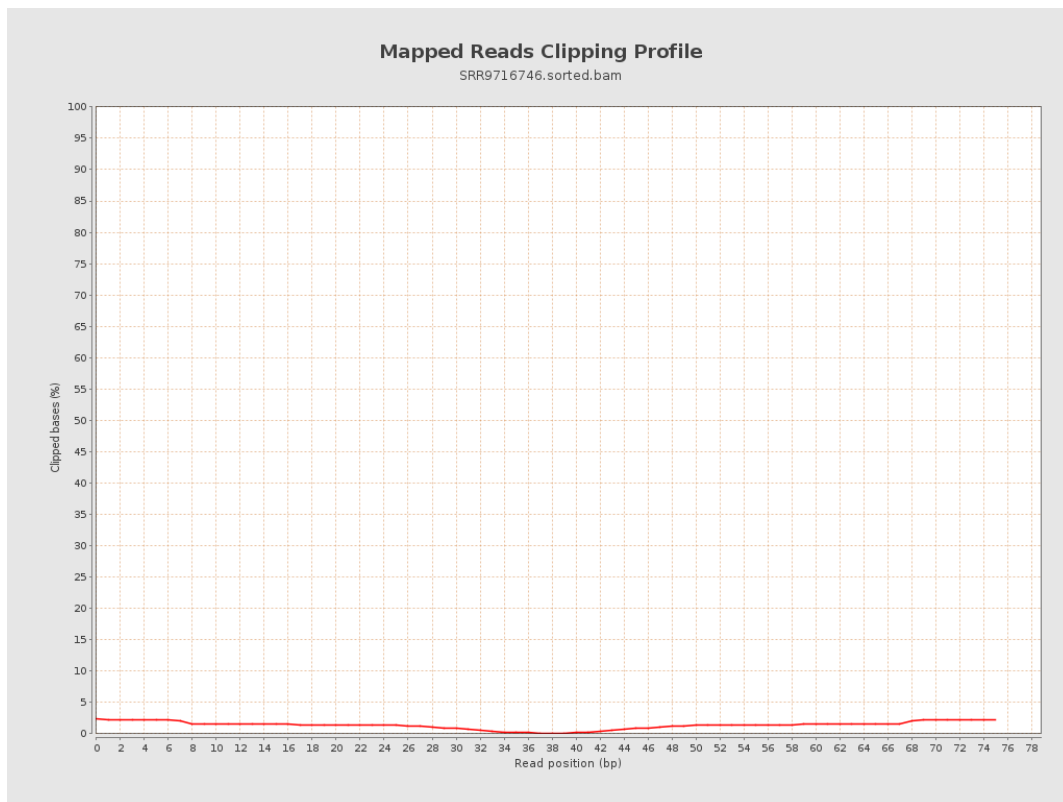
8. Results : Mapped Reads Nucleotide Content



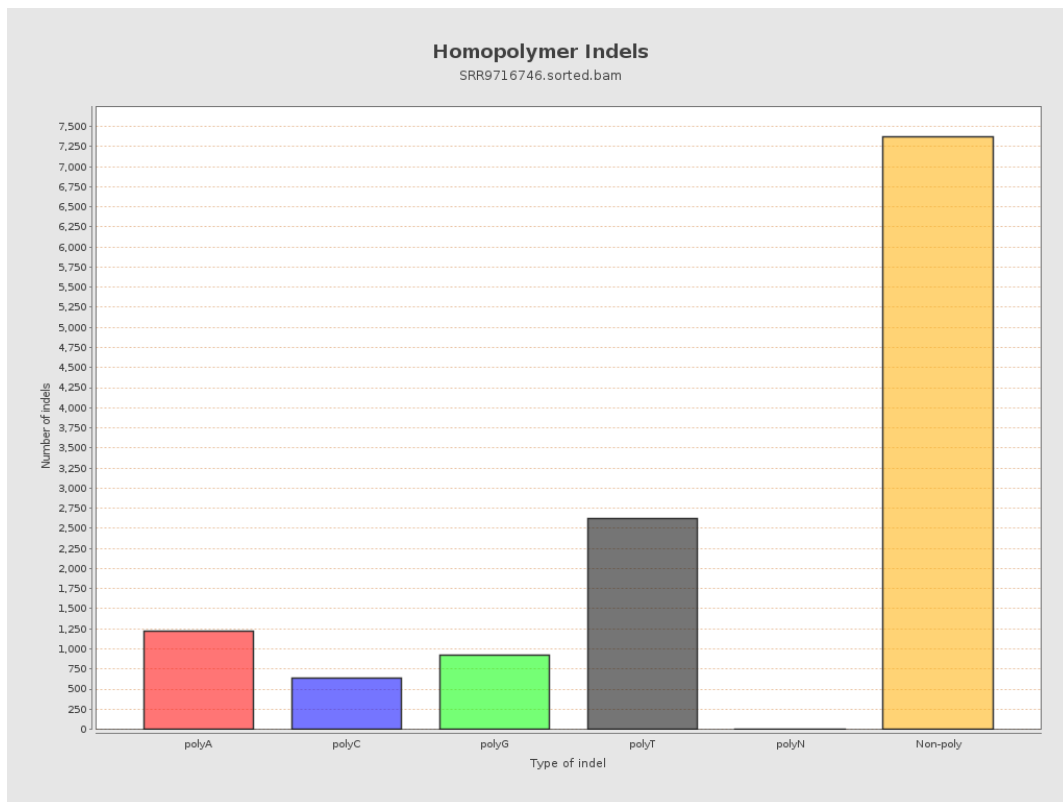
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

