

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 07:13:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716320.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_SRR9716320 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716320.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 07:13:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716320.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,272,474
Mapped reads	1,586,997 / 69.84%
Unmapped reads	685,477 / 30.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,729 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	59,687 / 2.63%
Duplication rate	2.8%
Clipped reads	1,591,012 / 70.01%

2.2. ACGT Content

Number/percentage of A's	23,530,346 / 25.71%
Number/percentage of C's	17,049,527 / 18.63%
Number/percentage of T's	29,459,226 / 32.18%
Number/percentage of G's	21,495,013 / 23.48%
Number/percentage of N's	2,337 / 0%
GC Percentage	42.11%

2.3. Coverage

Mean	0.0296

Standard Deviation	0.2874
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2.4. Mapping Quality

Mean Mapping Quality	44.79
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2.5. Mismatches and indels

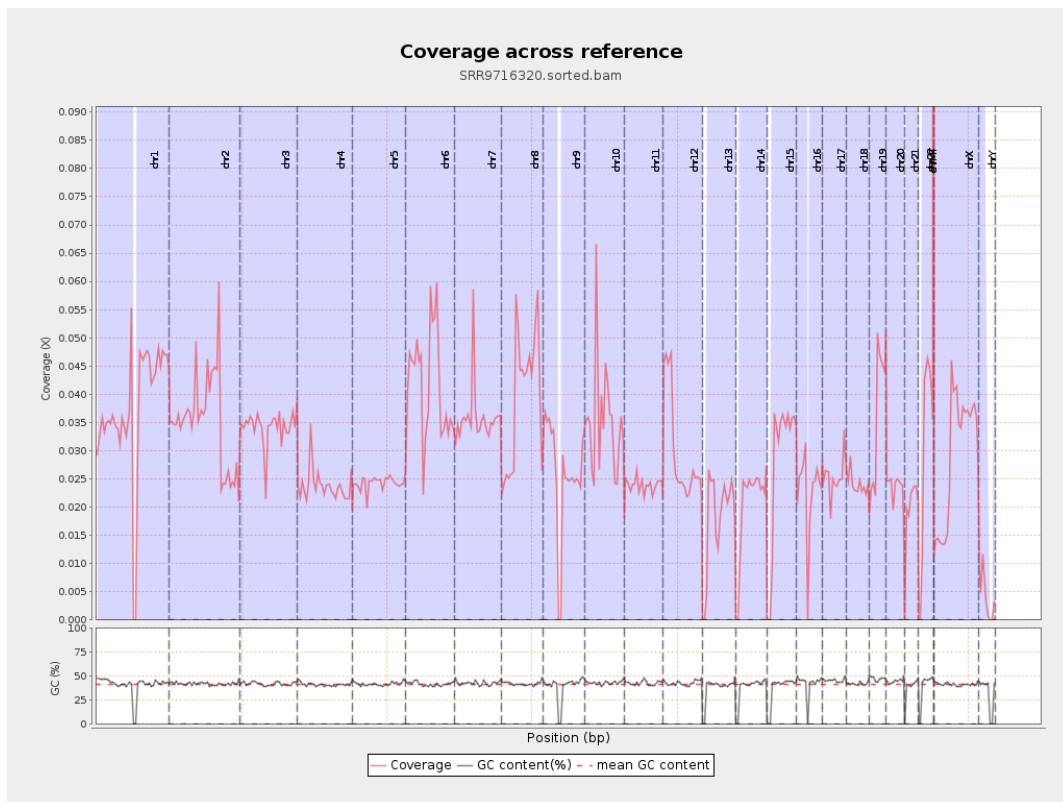
General error rate	0.51%
Mismatches	460,122
Insertions	5,716
Mapped reads with at least one insertion	0.36%
Deletions	16,428
Mapped reads with at least one deletion	1.03%
Homopolymer indels	42.97%

2.6. Chromosome stats

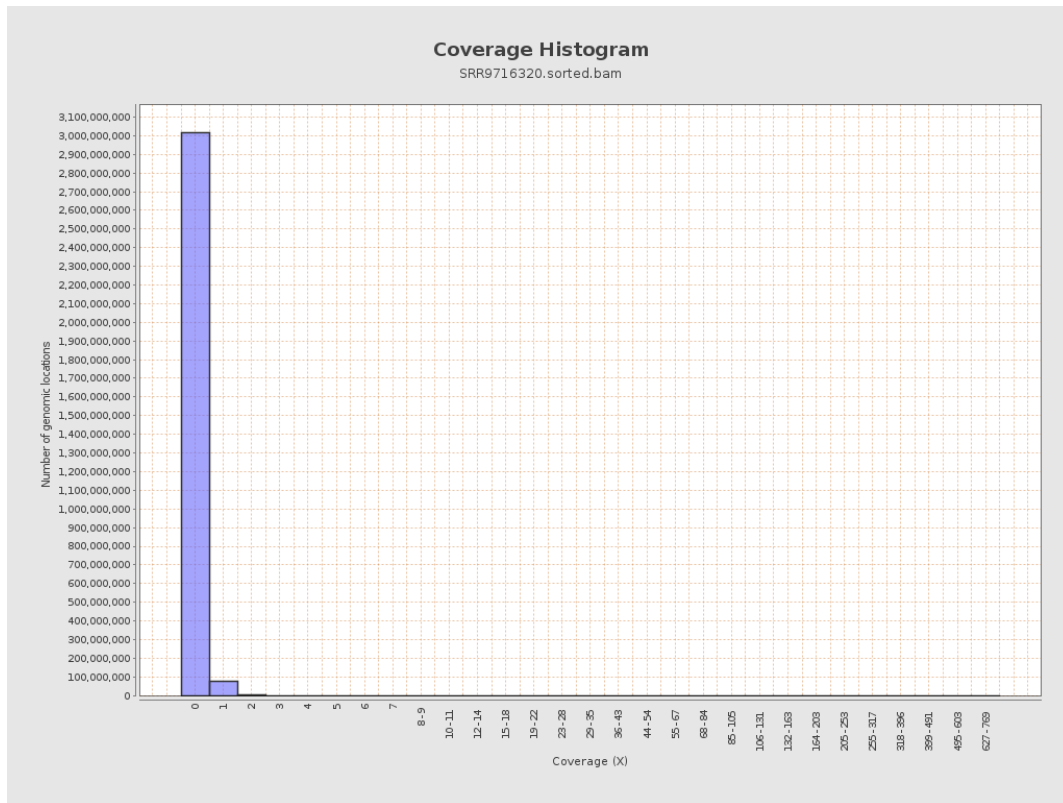
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9309834	0.0374	0.5316
chr2	243199373	8541135	0.0351	0.3784
chr3	198022430	6734852	0.034	0.2023
chr4	191154276	4516764	0.0236	0.1791
chr5	180915260	4367833	0.0241	0.1718
chr6	171115067	7124070	0.0416	0.2764
chr7	159138663	5719388	0.0359	0.4458

chr8	146364022	5793309	0.0396	0.2556
chr9	141213431	3596496	0.0255	0.2303
chr10	135534747	4755685	0.0351	0.2791
chr11	135006516	3204130	0.0237	0.2254
chr12	133851895	3978204	0.0297	0.1913
chr13	115169878	2048601	0.0178	0.1455
chr14	107349540	2146336	0.02	0.1672
chr15	102531392	2882193	0.0281	0.1871
chr16	90354753	2062282	0.0228	0.1816
chr17	81195210	2051574	0.0253	0.1818
chr18	78077248	1884177	0.0241	0.398
chr19	59128983	2150964	0.0364	0.3407
chr20	63025520	1478871	0.0235	0.1707
chr21	48129895	935341	0.0194	0.1676
chr22	51304566	1509912	0.0294	0.1877
chrMT	16571	48751	2.9419	2.2801
chrX	155270560	4498380	0.029	0.2134
chrY	59373566	223393	0.0038	0.0894

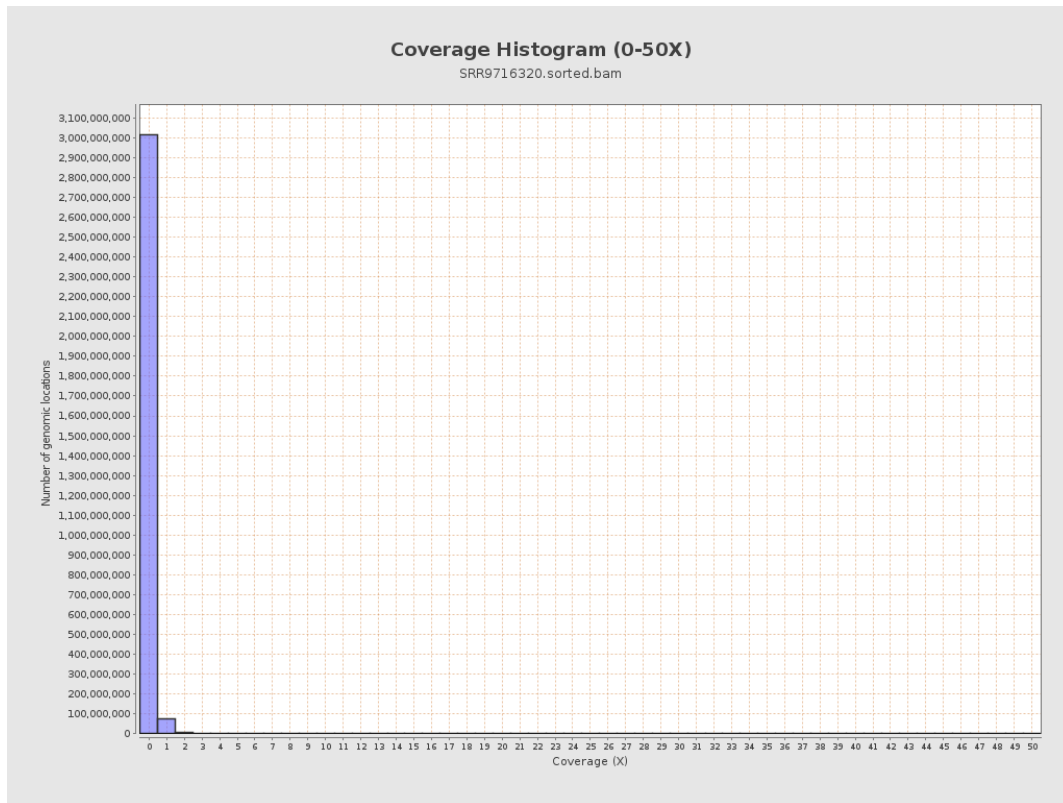
3. Results : Coverage across reference



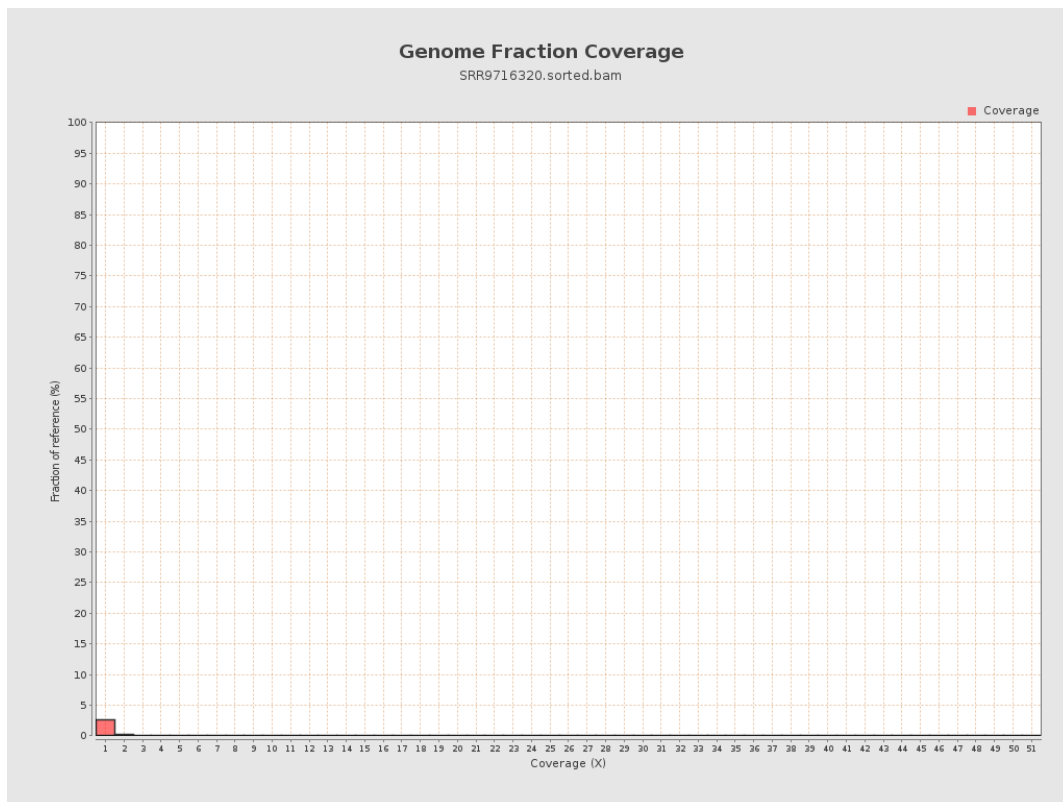
4. Results : Coverage Histogram



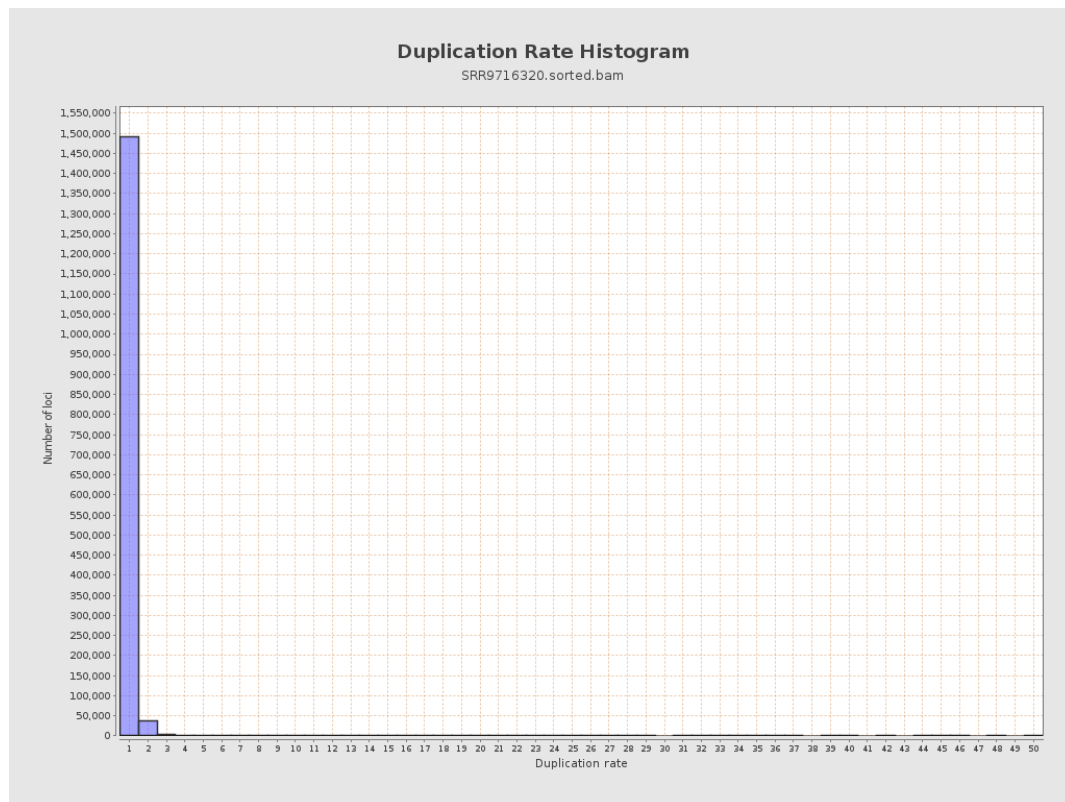
5. Results : Coverage Histogram (0-50X)



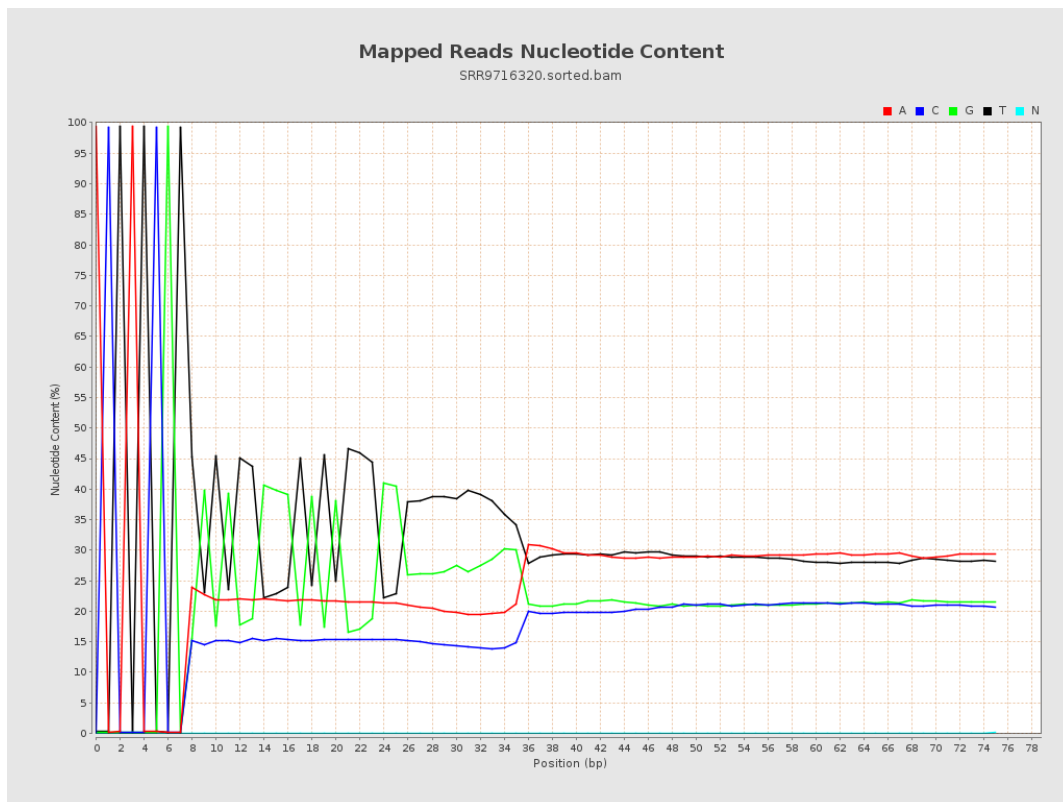
6. Results : Genome Fraction Coverage



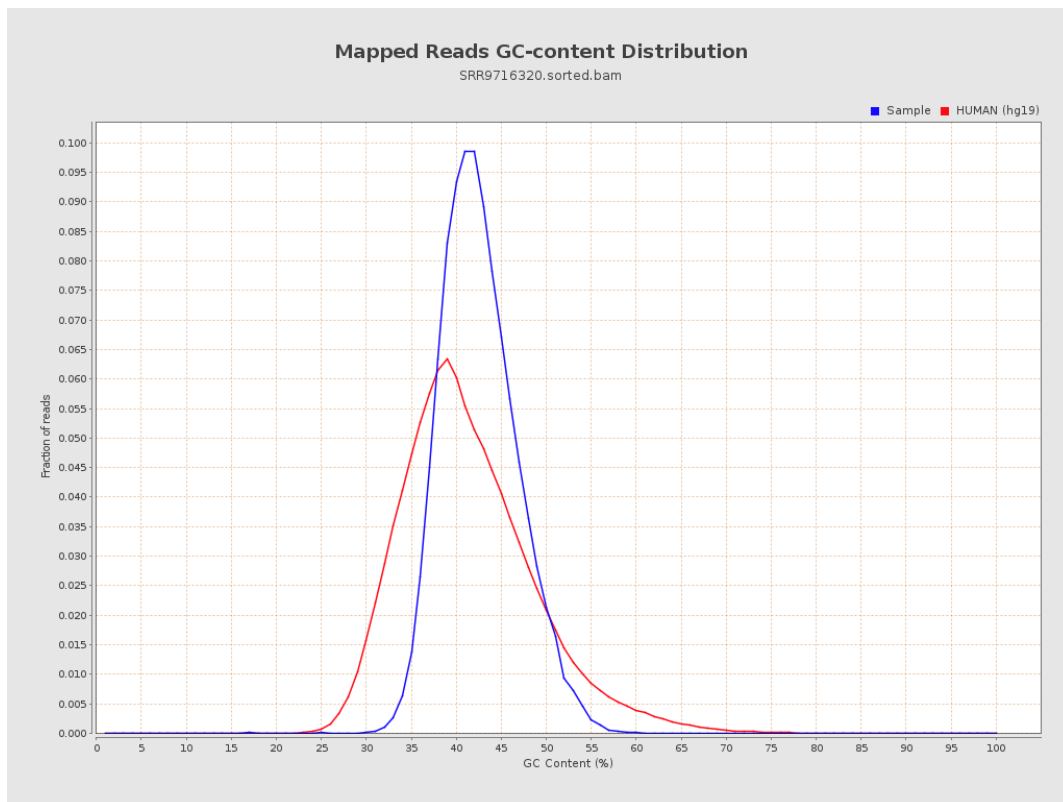
7. Results : Duplication Rate Histogram



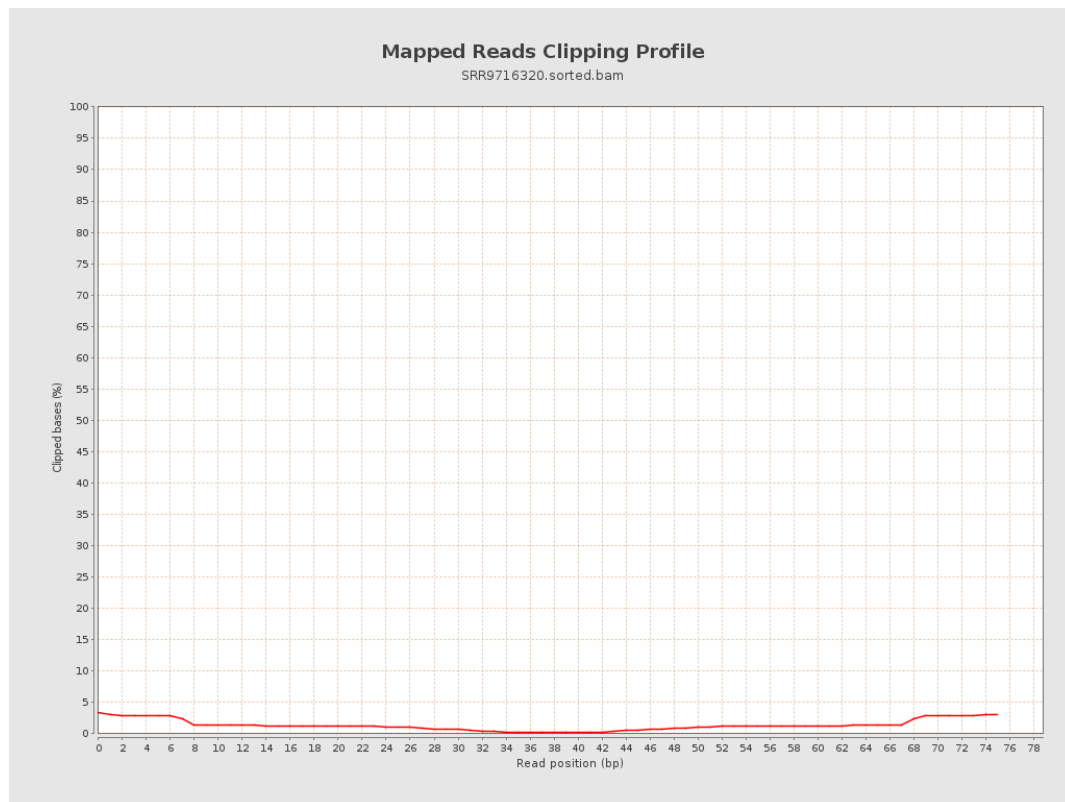
8. Results : Mapped Reads Nucleotide Content



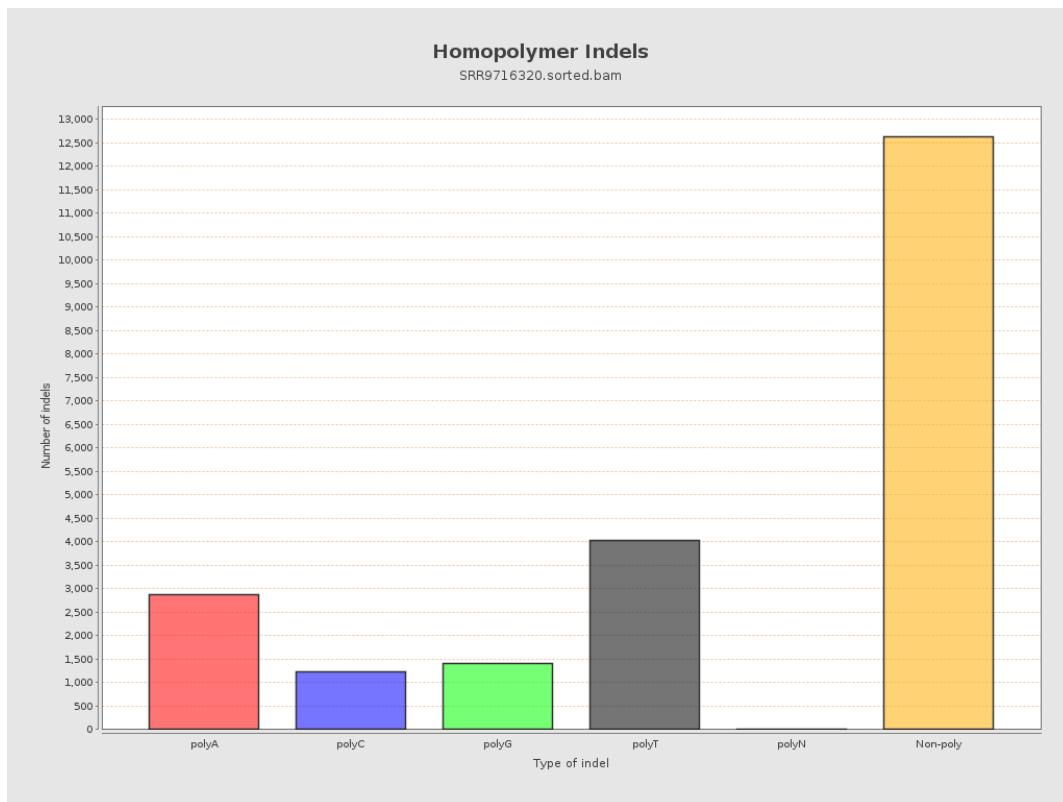
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

