

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 07:26:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818910.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_SRR1818910 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818910.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 07:26:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818910.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,606,507
Mapped reads	1,438,078 / 89.52%
Unmapped reads	168,429 / 10.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,406 / 1.33%
Read min/max/mean length	30 / 101 / 101.51
Duplicated reads (estimated)	299,672 / 18.65%
Duplication rate	17.55%
Clipped reads	1,452,237 / 90.4%

2.2. ACGT Content

Number/percentage of A's	38,121,485 / 28.63%
Number/percentage of C's	27,959,767 / 21%
Number/percentage of T's	38,352,652 / 28.8%
Number/percentage of G's	28,726,265 / 21.57%
Number/percentage of N's	2,007 / 0%
GC Percentage	42.57%

2.3. Coverage

Mean	0.043

Standard Deviation	0.5421
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	49.33
----------------------	-------

2.5. Mismatches and indels

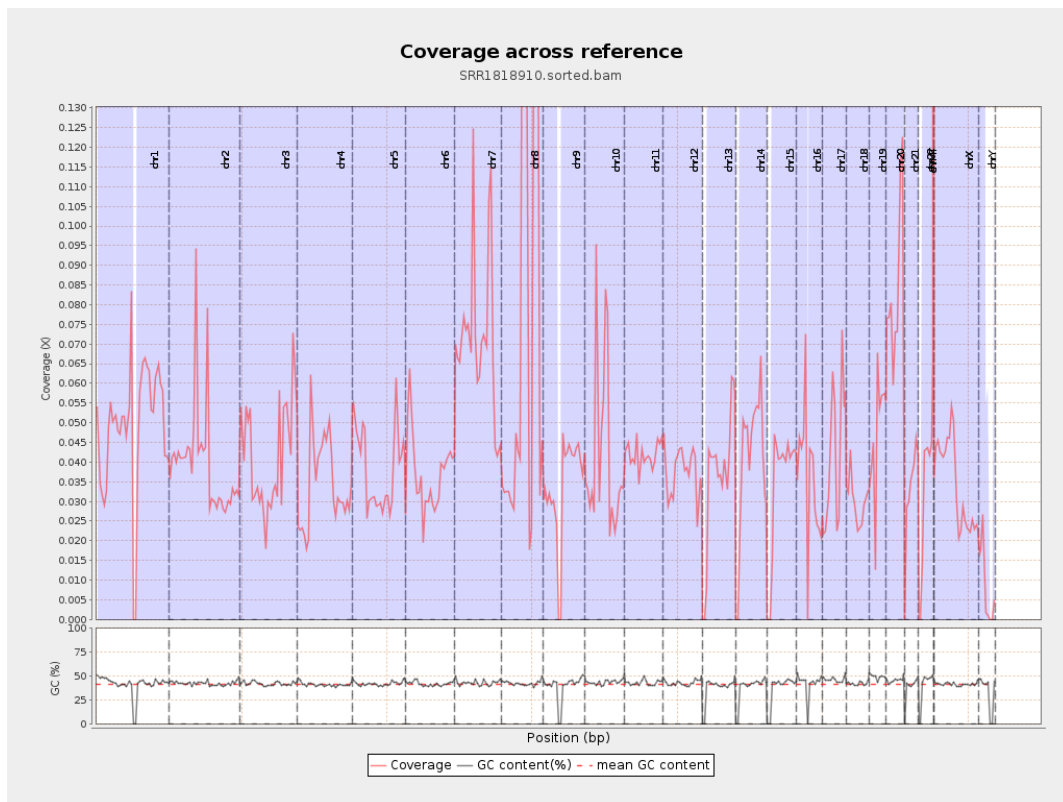
General error rate	0.64%
Mismatches	798,622
Insertions	20,169
Mapped reads with at least one insertion	1.35%
Deletions	44,134
Mapped reads with at least one deletion	2.99%
Homopolymer indels	41.36%

2.6. Chromosome stats

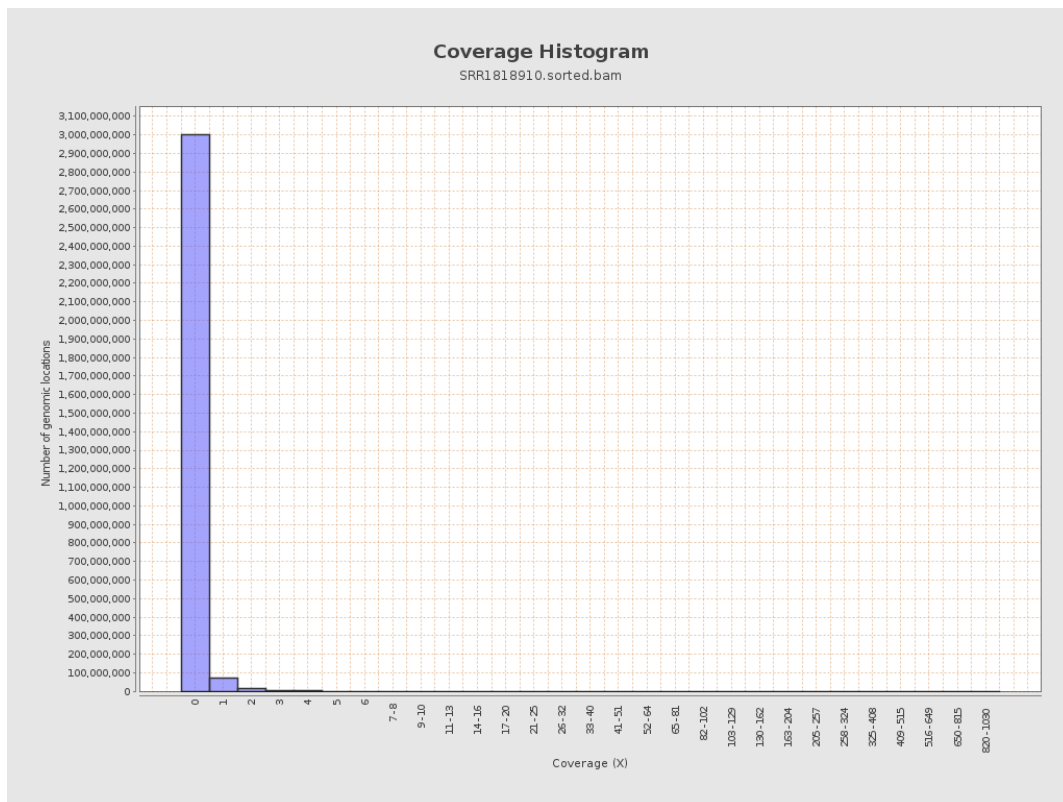
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12149403	0.0487	0.8453
chr2	243199373	9678394	0.0398	0.7618
chr3	198022430	8220558	0.0415	0.2688
chr4	191154276	6528219	0.0342	0.3236
chr5	180915260	6897516	0.0381	0.2687
chr6	171115067	6308440	0.0369	0.2756
chr7	159138663	11489580	0.0722	1.1639

chr8	146364022	12570841	0.0859	0.4839
chr9	141213431	4736773	0.0335	0.4107
chr10	135534747	5630951	0.0415	0.6885
chr11	135006516	5632247	0.0417	0.3186
chr12	133851895	5052691	0.0377	0.2596
chr13	115169878	4160776	0.0361	0.2466
chr14	107349540	4337909	0.0404	0.2865
chr15	102531392	3541841	0.0345	0.2415
chr16	90354753	3197382	0.0354	0.5702
chr17	81195210	3448987	0.0425	0.341
chr18	78077248	2344832	0.03	0.474
chr19	59128983	2779484	0.047	0.7249
chr20	63025520	5274413	0.0837	0.4076
chr21	48129895	1591473	0.0331	0.2813
chr22	51304566	1577715	0.0308	0.2499
chrMT	16571	257514	15.54	10.5759
chrX	155270560	5351923	0.0345	0.2907
chrY	59373566	488585	0.0082	0.6239

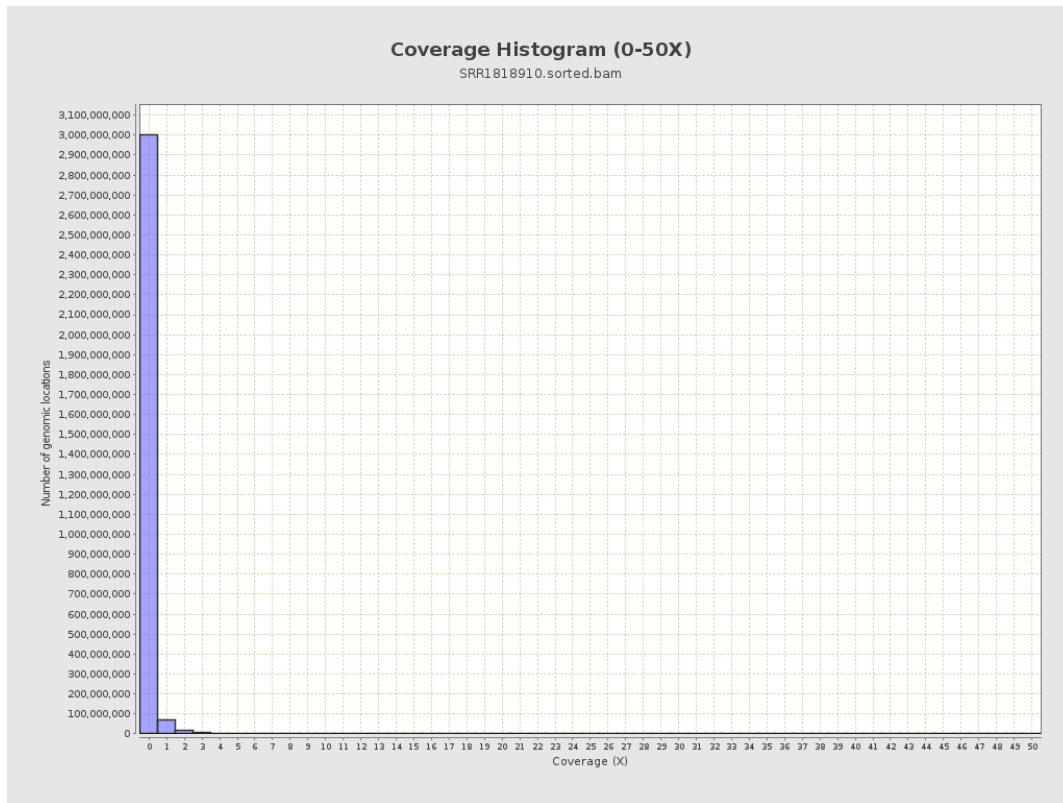
3. Results : Coverage across reference



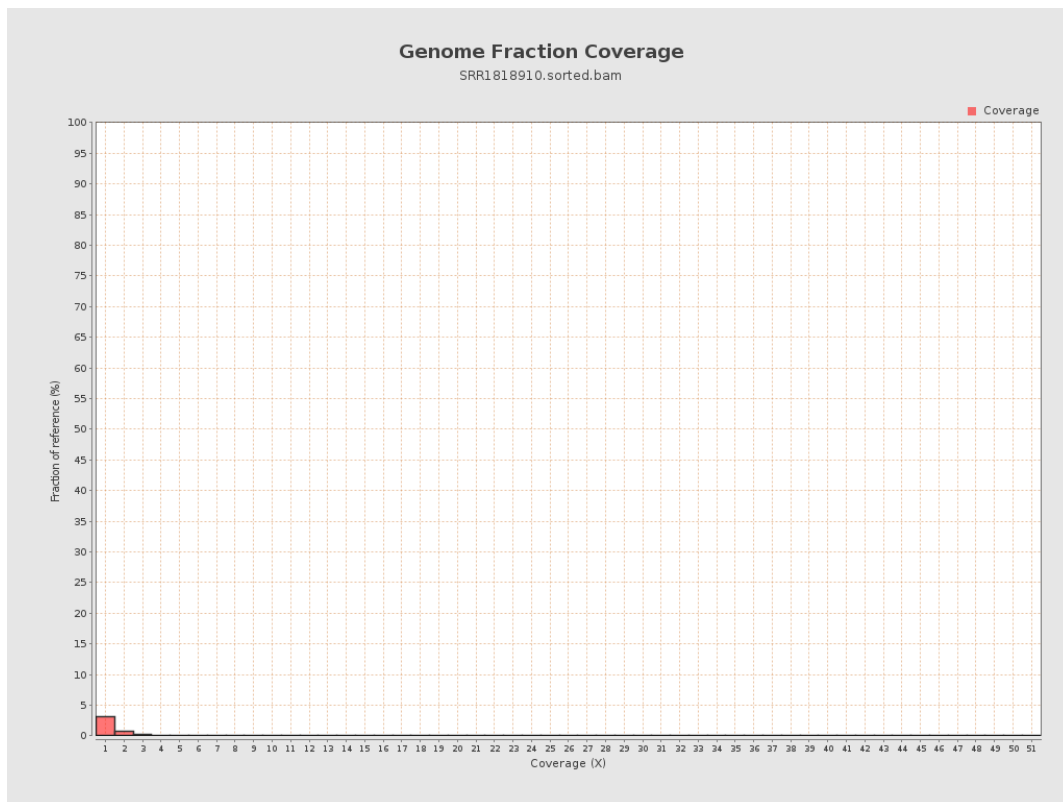
4. Results : Coverage Histogram



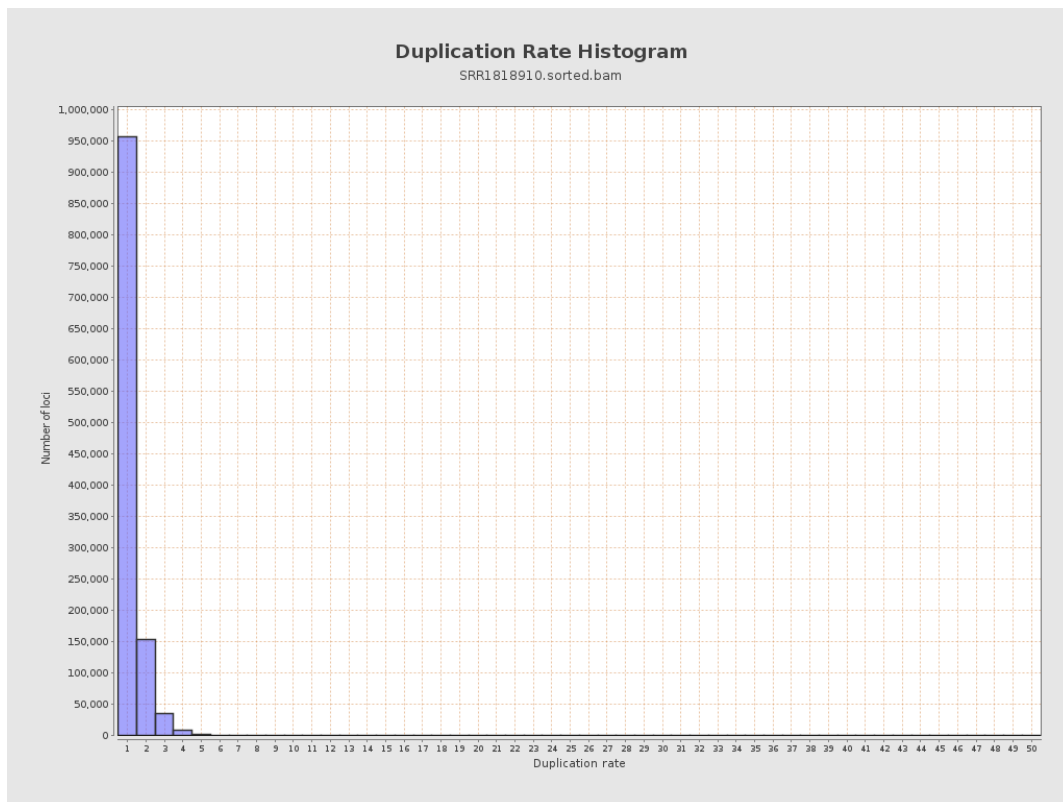
5. Results : Coverage Histogram (0-50X)



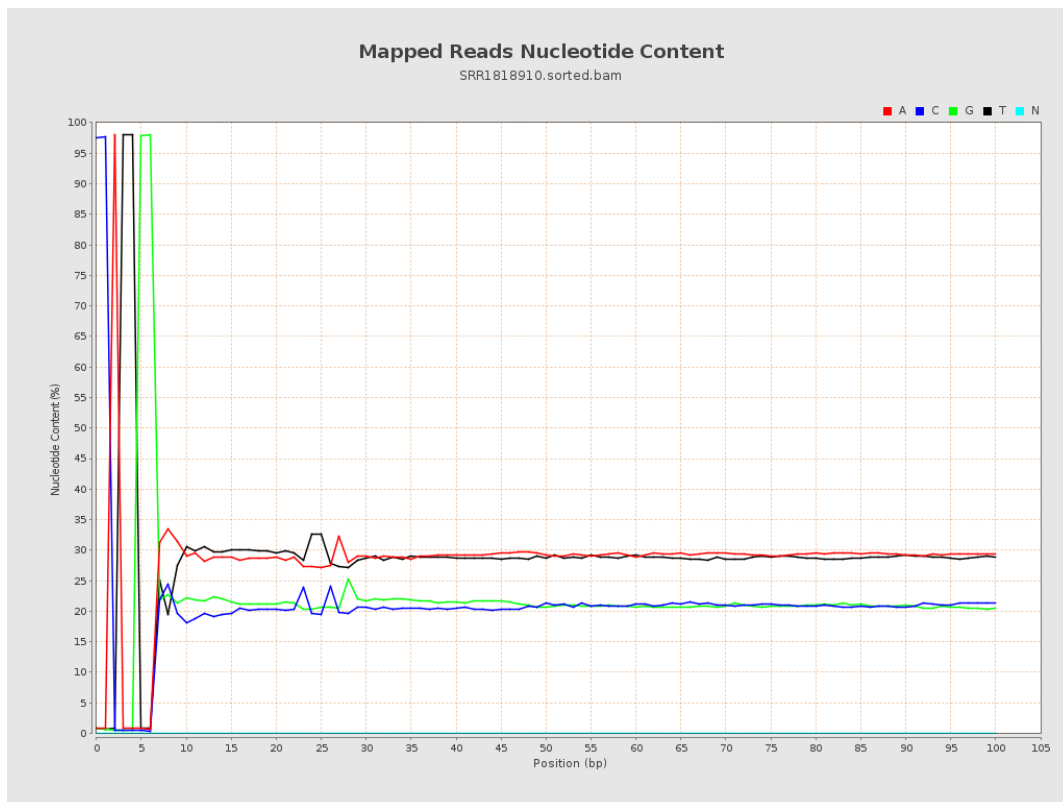
6. Results : Genome Fraction Coverage



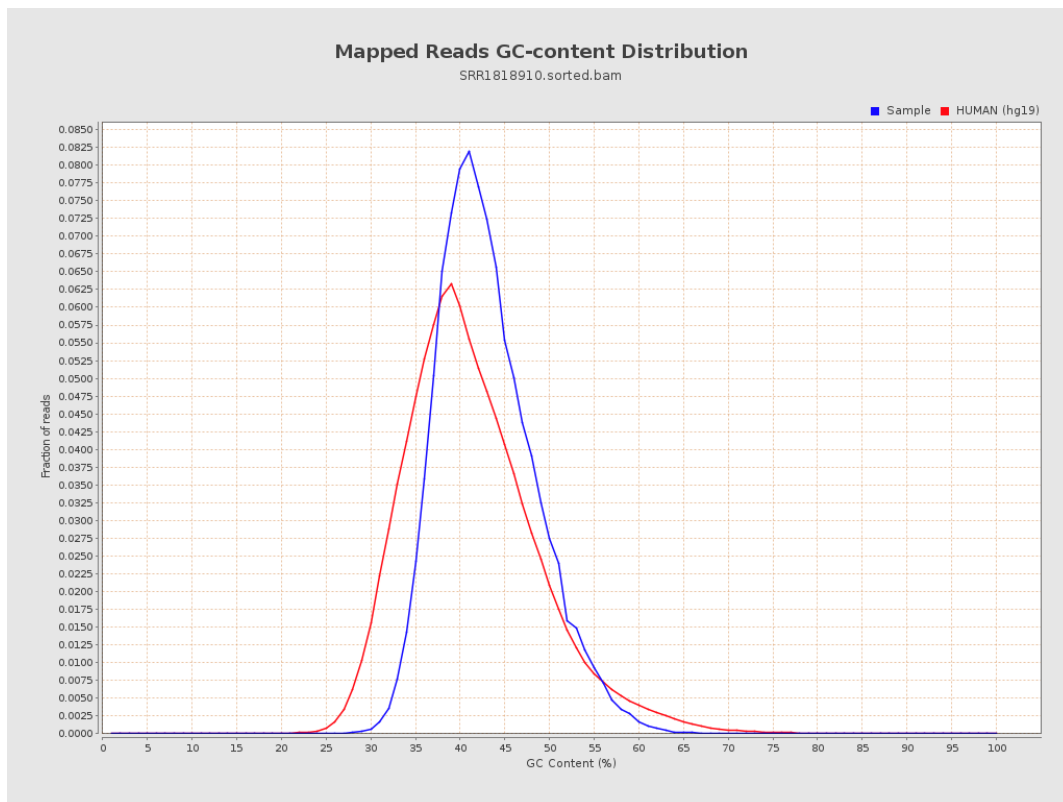
7. Results : Duplication Rate Histogram



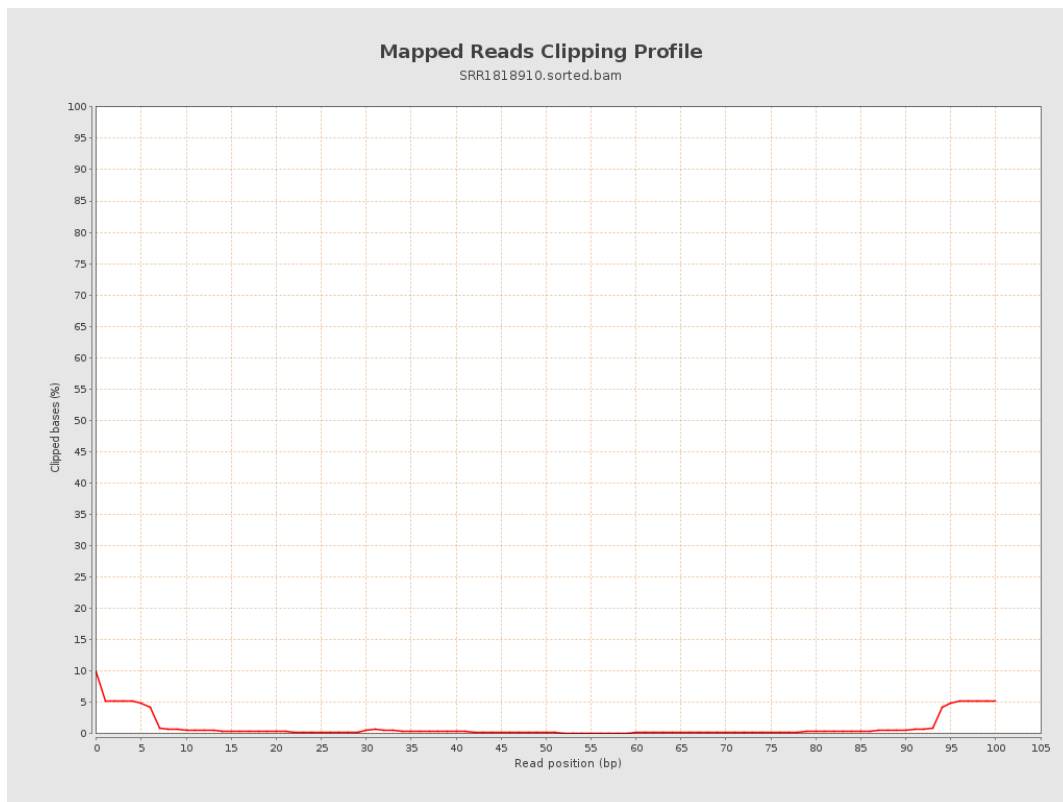
8. Results : Mapped Reads Nucleotide Content



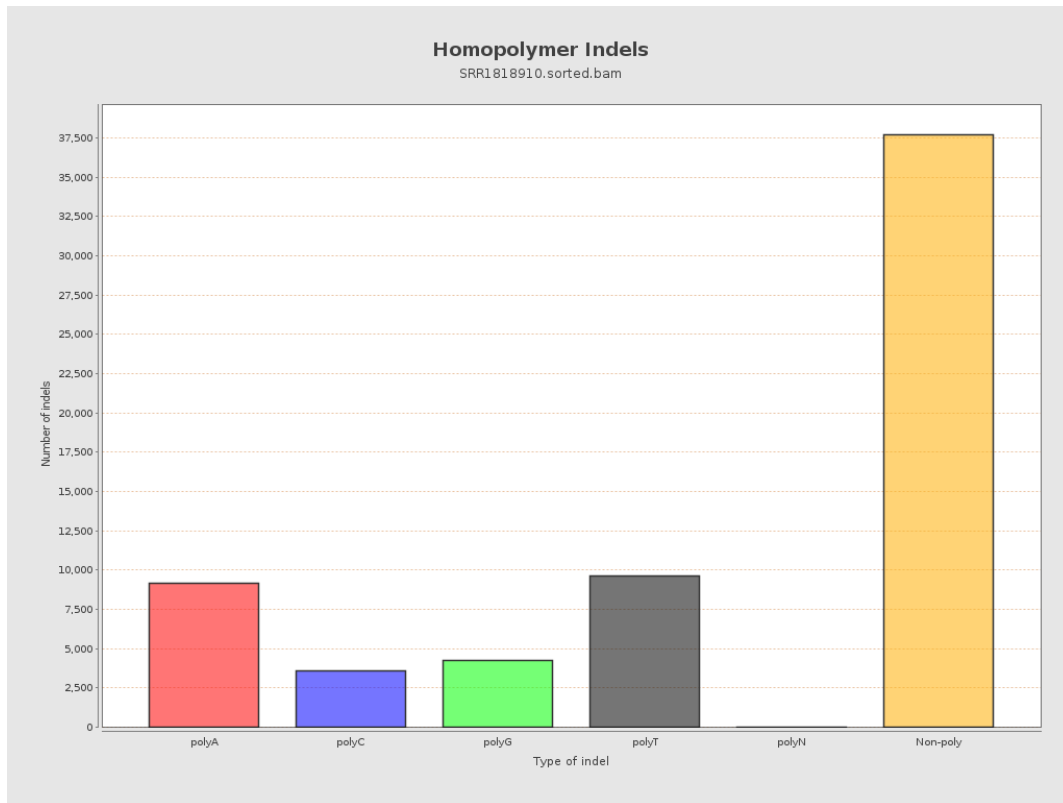
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

