

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 02:45:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819145.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_SRR1819145 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819145.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 02:45:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819145.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,124,212
Mapped reads	1,032,537 / 91.85%
Unmapped reads	91,675 / 8.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,082 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	55,176 / 4.91%
Duplication rate	4.24%
Clipped reads	1,032,635 / 91.85%

2.2. ACGT Content

Number/percentage of A's	14,980,202 / 24.81%
Number/percentage of C's	11,404,193 / 18.89%
Number/percentage of T's	19,373,772 / 32.08%
Number/percentage of G's	14,624,393 / 24.22%
Number/percentage of N's	896 / 0%
GC Percentage	43.11%

2.3. Coverage

Mean	0.0195

Standard Deviation	0.2114
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2.4. Mapping Quality

Mean Mapping Quality	45.02
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2.5. Mismatches and indels

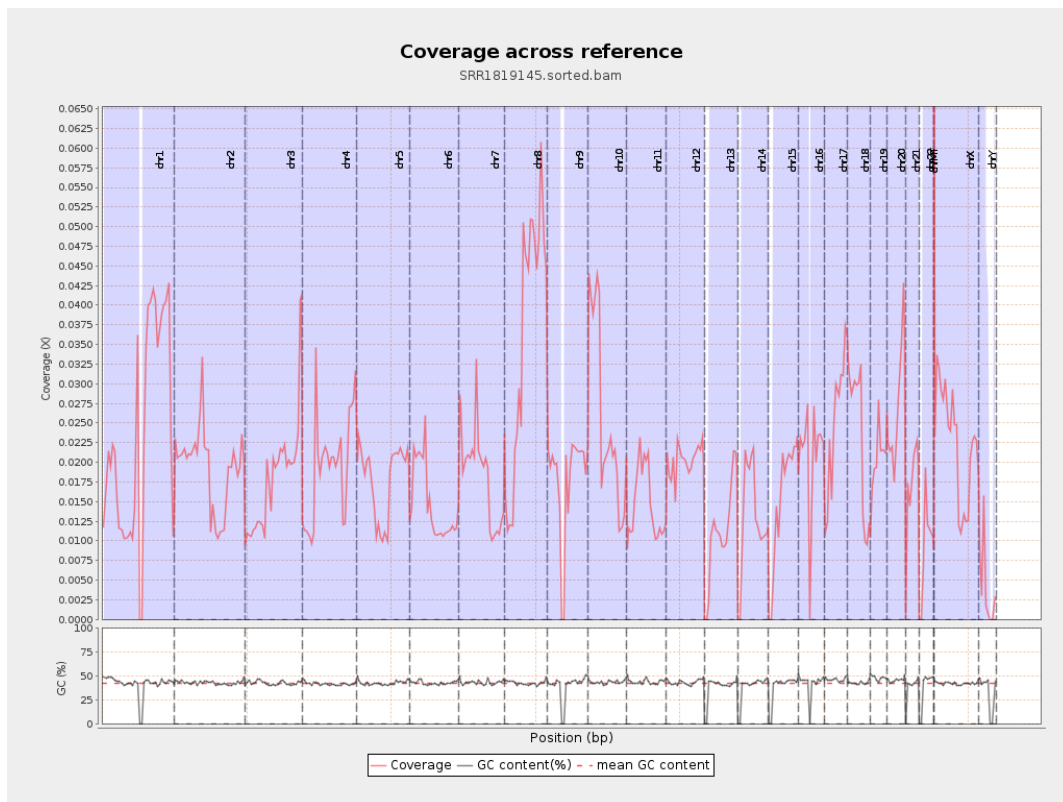
General error rate	0.53%
Mismatches	309,021
Insertions	4,891
Mapped reads with at least one insertion	0.47%
Deletions	11,219
Mapped reads with at least one deletion	1.08%
Homopolymer indels	40.38%

2.6. Chromosome stats

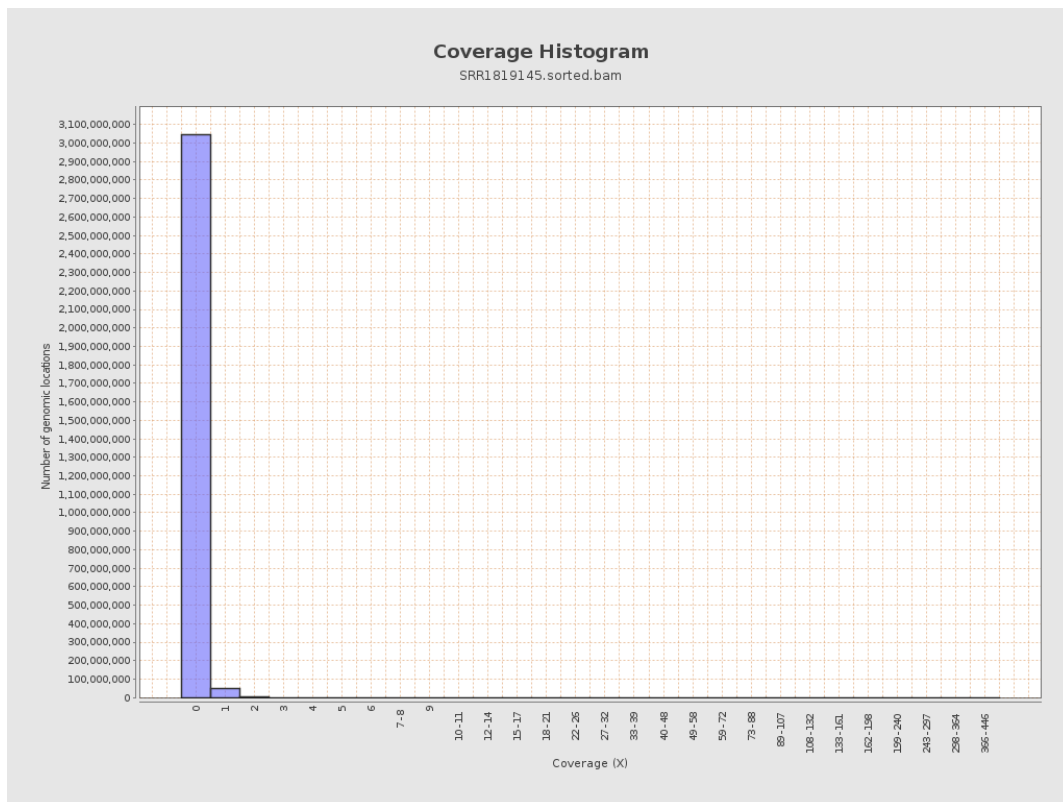
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5763149	0.0231	0.3666
chr2	243199373	4685753	0.0193	0.2583
chr3	198022430	3538504	0.0179	0.1494
chr4	191154276	3714236	0.0194	0.1804
chr5	180915260	3217520	0.0178	0.1499
chr6	171115067	2509117	0.0147	0.1564
chr7	159138663	2947159	0.0185	0.2339

chr8	146364022	5285736	0.0361	0.2489
chr9	141213431	2508542	0.0178	0.1739
chr10	135534747	3548733	0.0262	0.2478
chr11	135006516	2000495	0.0148	0.1717
chr12	133851895	2715829	0.0203	0.1601
chr13	115169878	1291225	0.0112	0.1175
chr14	107349540	1397278	0.013	0.1283
chr15	102531392	1550435	0.0151	0.1366
chr16	90354753	1852558	0.0205	0.1684
chr17	81195210	2036054	0.0251	0.1849
chr18	78077248	1839295	0.0236	0.285
chr19	59128983	1229944	0.0208	0.2747
chr20	63025520	1708664	0.0271	0.1872
chr21	48129895	820729	0.0171	0.1639
chr22	51304566	483863	0.0094	0.1073
chrMT	16571	2717	0.164	0.4058
chrX	155270560	3518916	0.0227	0.1786
chrY	59373566	235953	0.004	0.1511

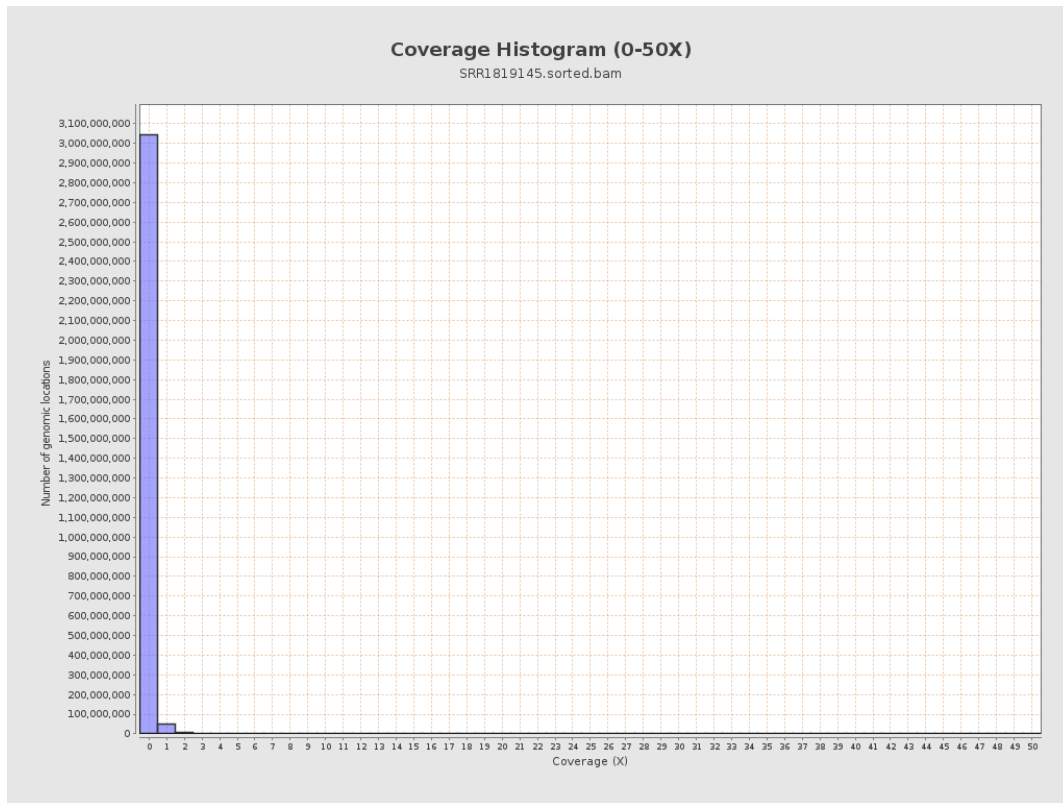
3. Results : Coverage across reference



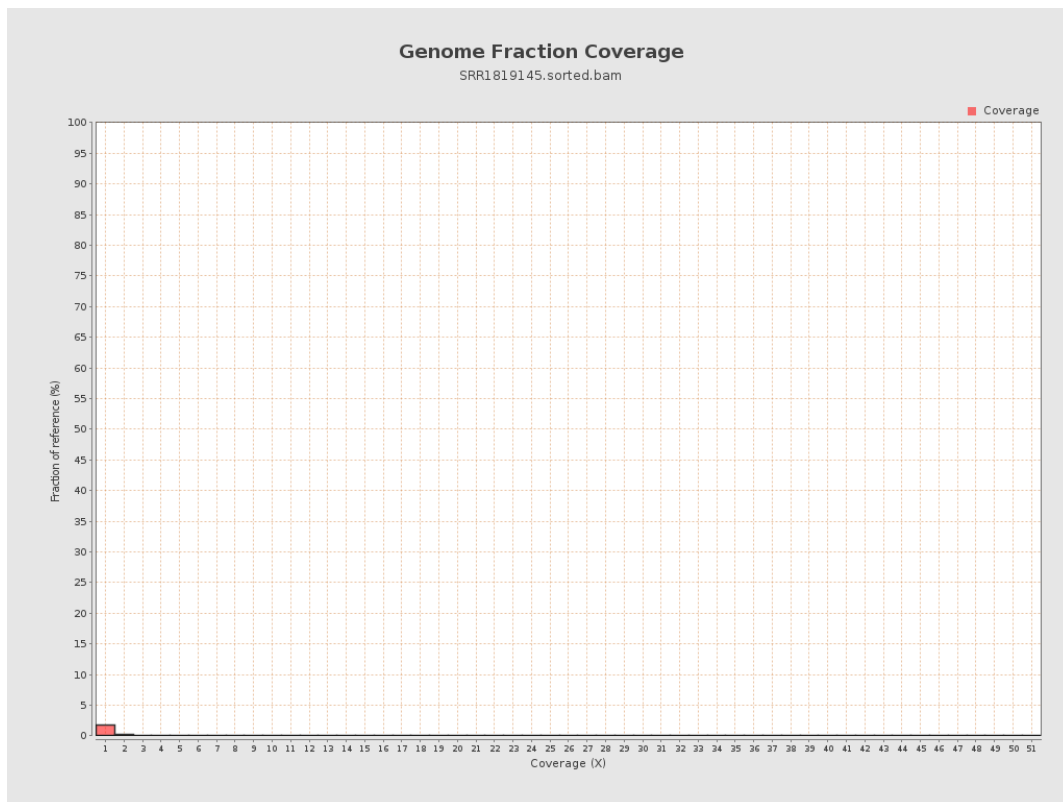
4. Results : Coverage Histogram



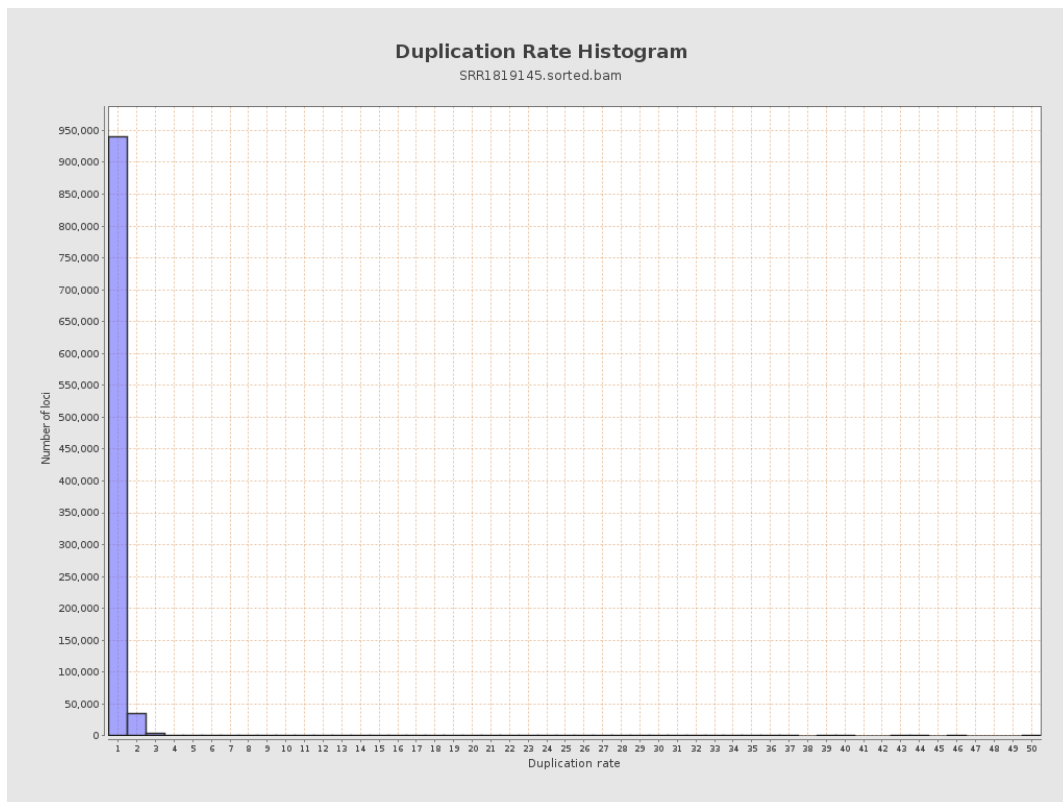
5. Results : Coverage Histogram (0-50X)



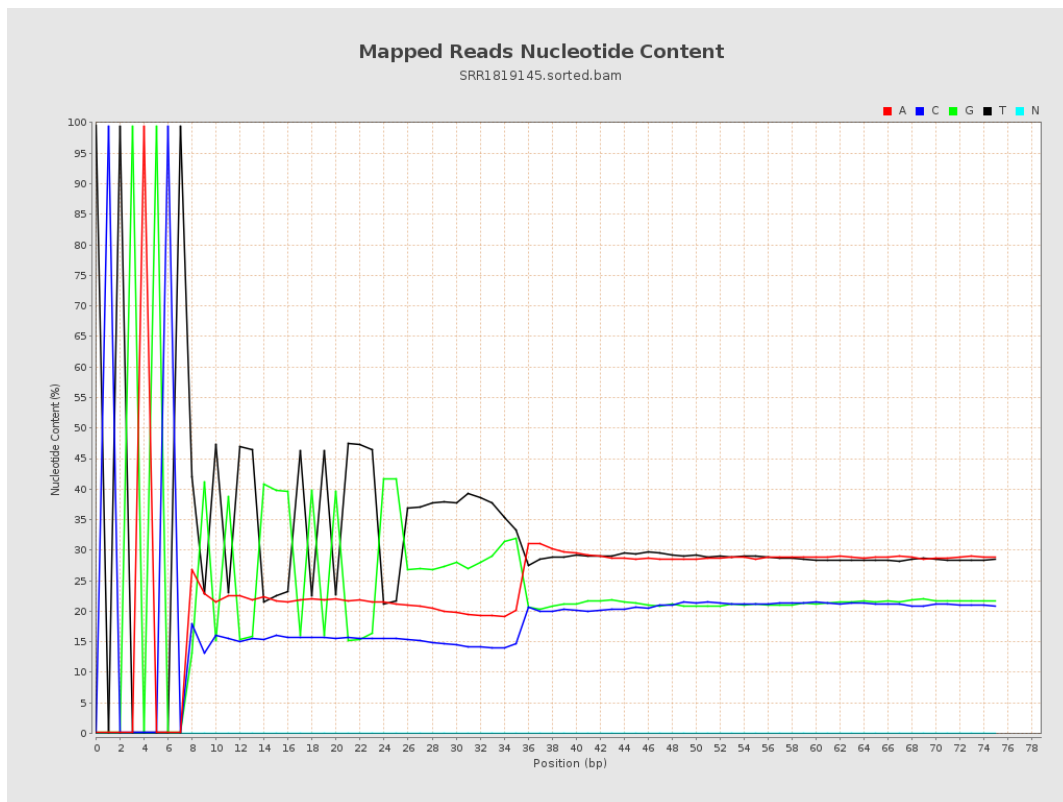
6. Results : Genome Fraction Coverage



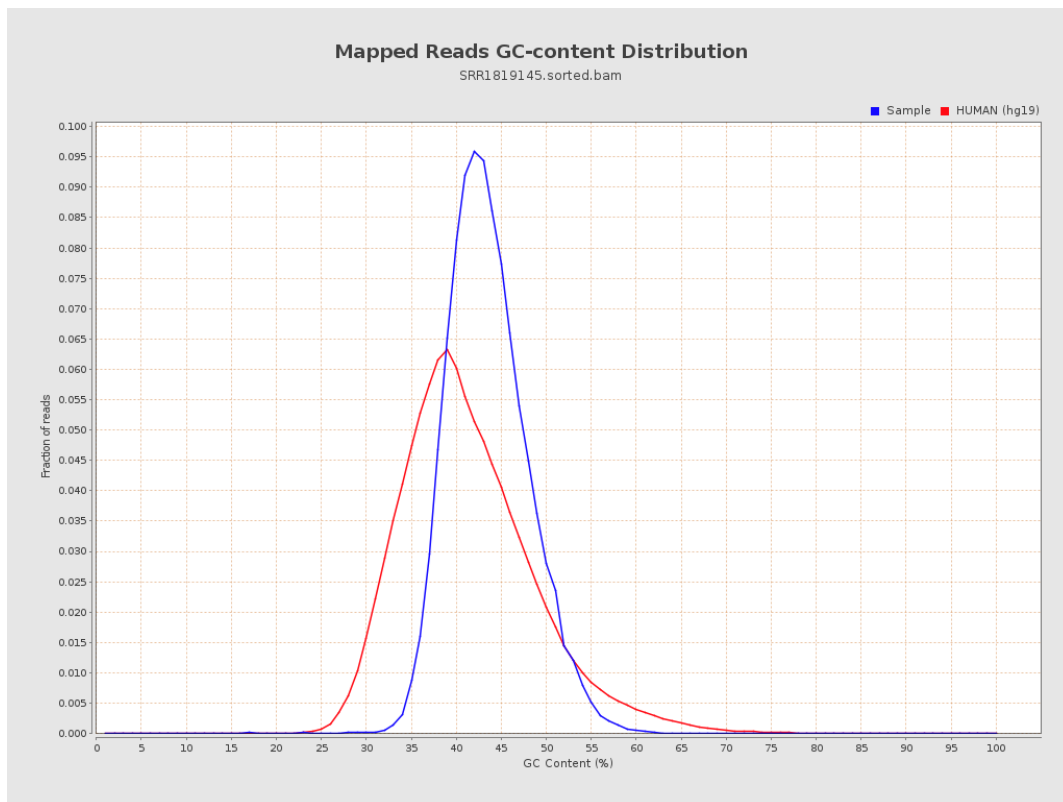
7. Results : Duplication Rate Histogram



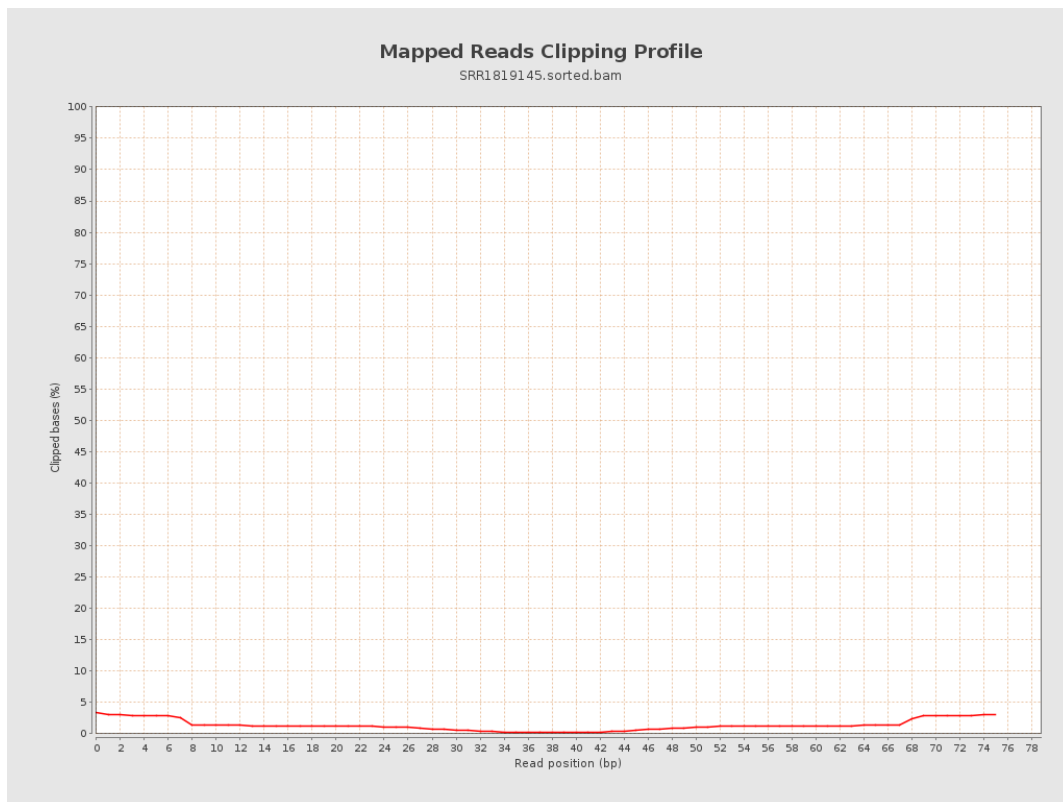
8. Results : Mapped Reads Nucleotide Content



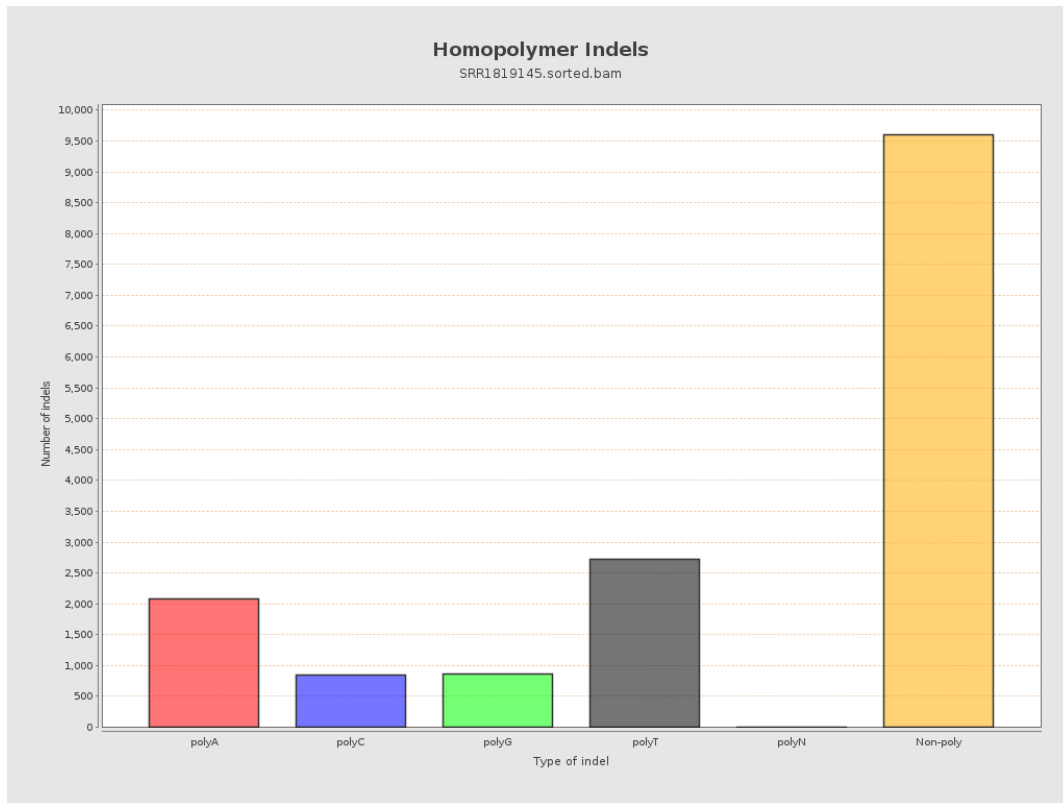
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

