

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 17:10:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234119.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_SRR6234119 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234119.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 17:10:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234119.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	984,559
Mapped reads	703,235 / 71.43%
Unmapped reads	281,324 / 28.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,933 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	17,924 / 1.82%
Duplication rate	1.95%
Clipped reads	307,725 / 31.26%

2.2. ACGT Content

Number/percentage of A's	13,382,155 / 28.76%
Number/percentage of C's	7,882,408 / 16.94%
Number/percentage of T's	15,081,993 / 32.41%
Number/percentage of G's	10,182,592 / 21.88%
Number/percentage of N's	6,582 / 0.01%
GC Percentage	38.82%

2.3. Coverage

Mean	0.015

Standard Deviation	0.1801
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2.4. Mapping Quality

Mean Mapping Quality	45.31
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2.5. Mismatches and indels

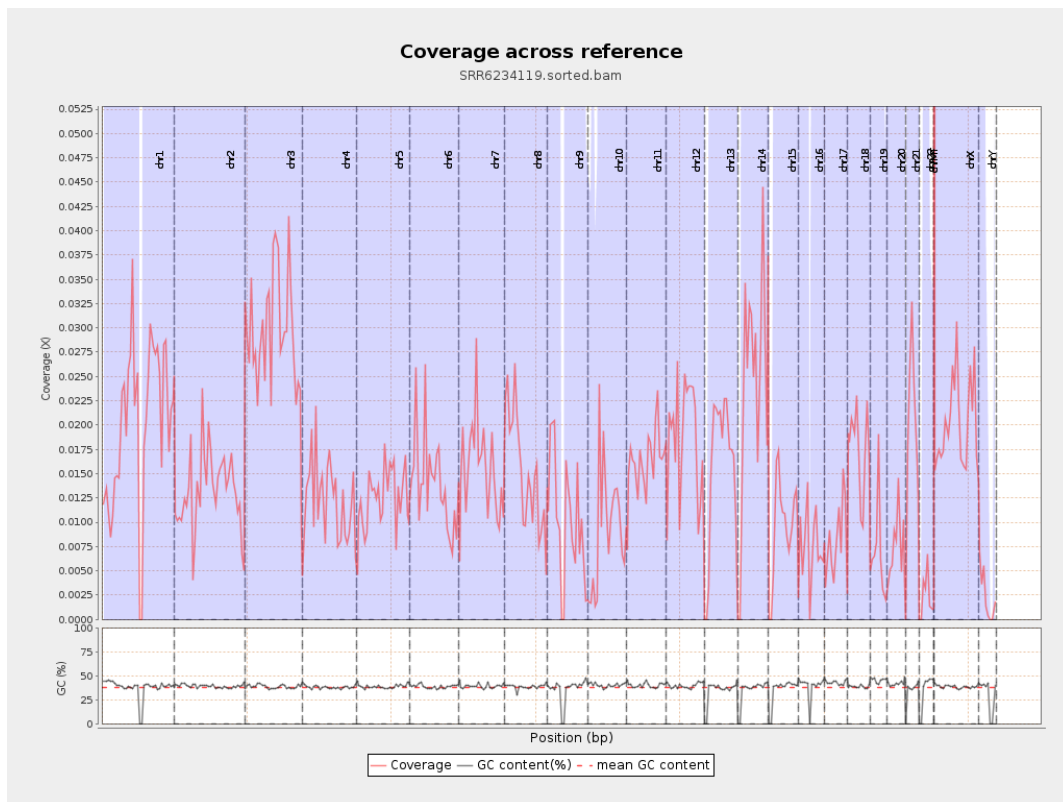
General error rate	0.93%
Mismatches	427,002
Insertions	3,938
Mapped reads with at least one insertion	0.56%
Deletions	13,790
Mapped reads with at least one deletion	1.94%
Homopolymer indels	46.12%

2.6. Chromosome stats

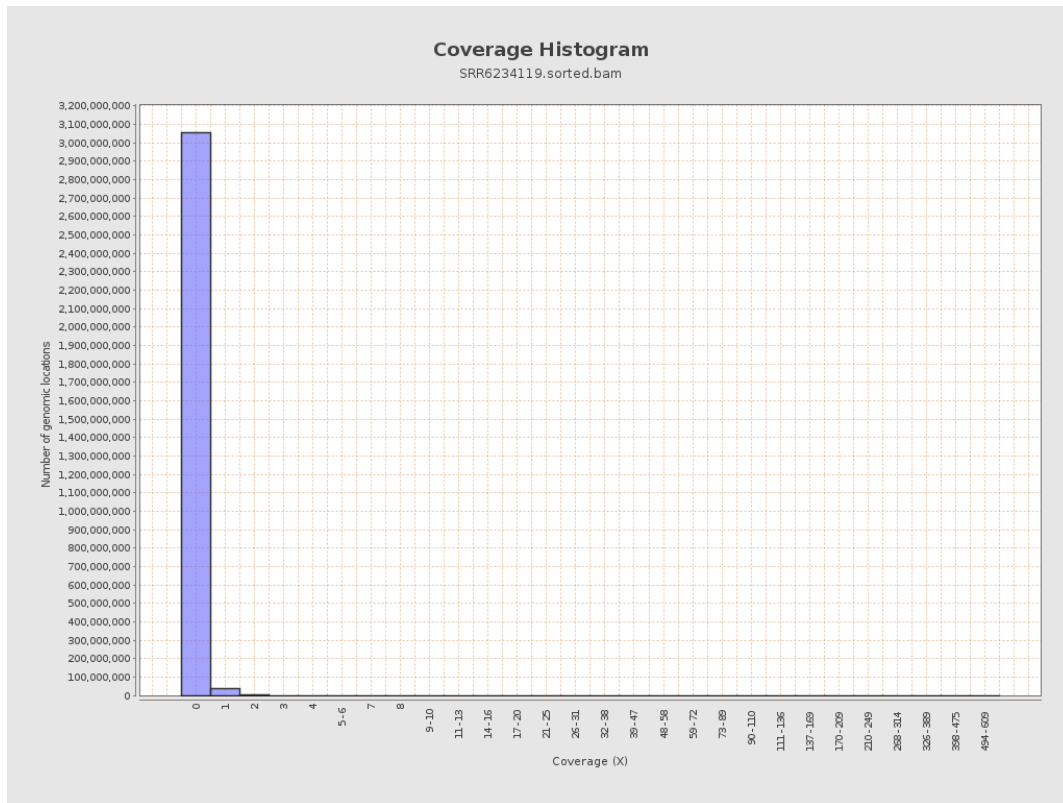
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4985922	0.02	0.2441
chr2	243199373	3251980	0.0134	0.1671
chr3	198022430	5851051	0.0295	0.1824
chr4	191154276	2331297	0.0122	0.119
chr5	180915260	2288568	0.0126	0.1182
chr6	171115067	2383512	0.0139	0.1425
chr7	159138663	2468887	0.0155	0.2251

chr8	146364022	2240848	0.0153	0.3965
chr9	141213431	1473361	0.0104	0.1368
chr10	135534747	1250514	0.0092	0.1591
chr11	135006516	2219328	0.0164	0.1537
chr12	133851895	2483751	0.0186	0.145
chr13	115169878	1794785	0.0156	0.1312
chr14	107349540	2582321	0.0241	0.1691
chr15	102531392	987030	0.0096	0.1039
chr16	90354753	652270	0.0072	0.1066
chr17	81195210	643948	0.0079	0.0978
chr18	78077248	1367953	0.0175	0.2533
chr19	59128983	413410	0.007	0.1482
chr20	63025520	478275	0.0076	0.0949
chr21	48129895	962465	0.02	0.1537
chr22	51304566	128761	0.0025	0.0525
chrMT	16571	16418	0.9908	1.2733
chrX	155270560	3168906	0.0204	0.1565
chrY	59373566	134442	0.0023	0.0593

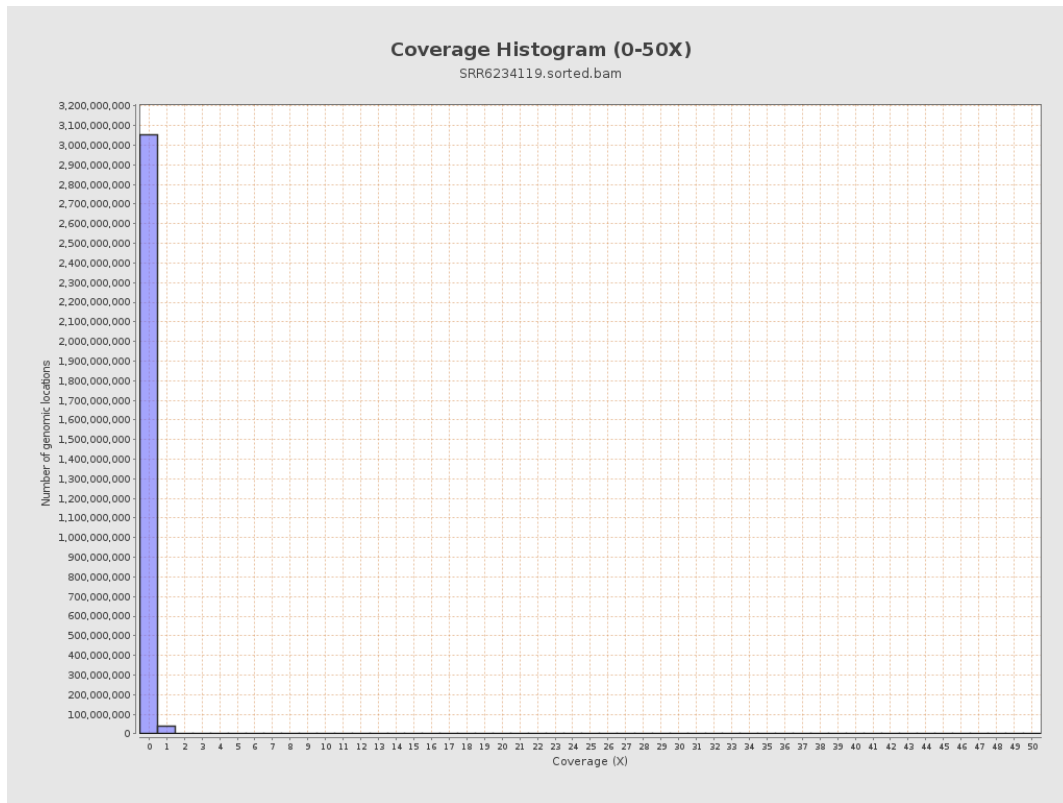
3. Results : Coverage across reference



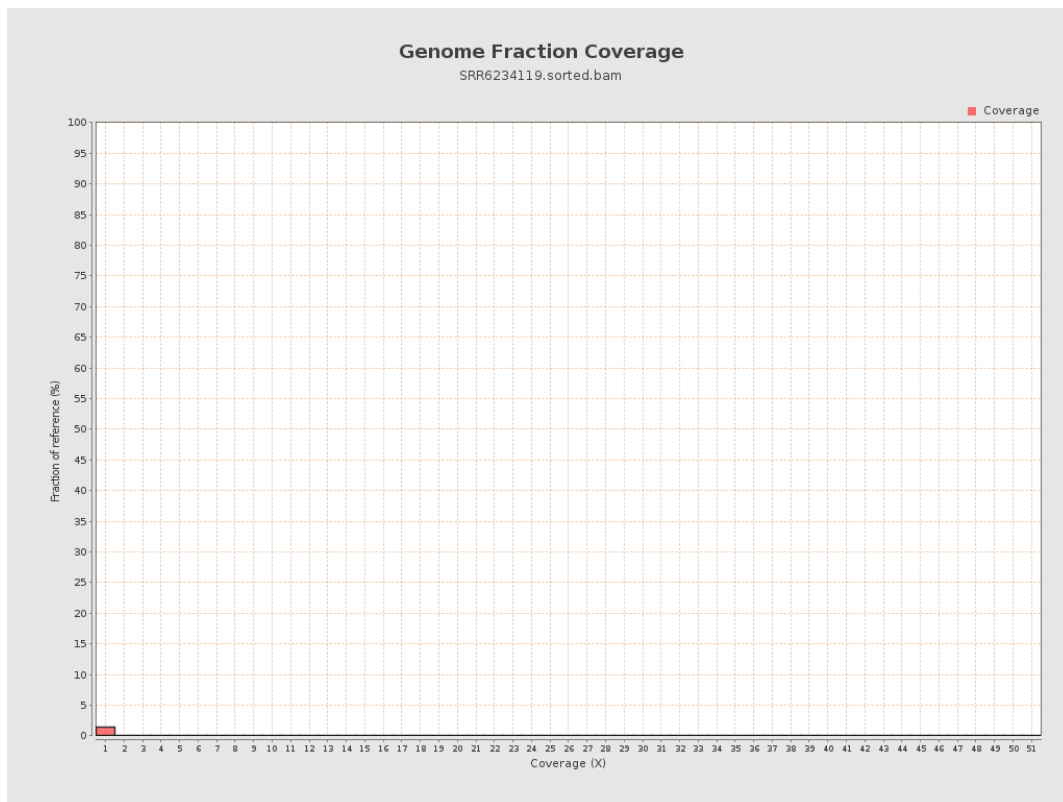
4. Results : Coverage Histogram



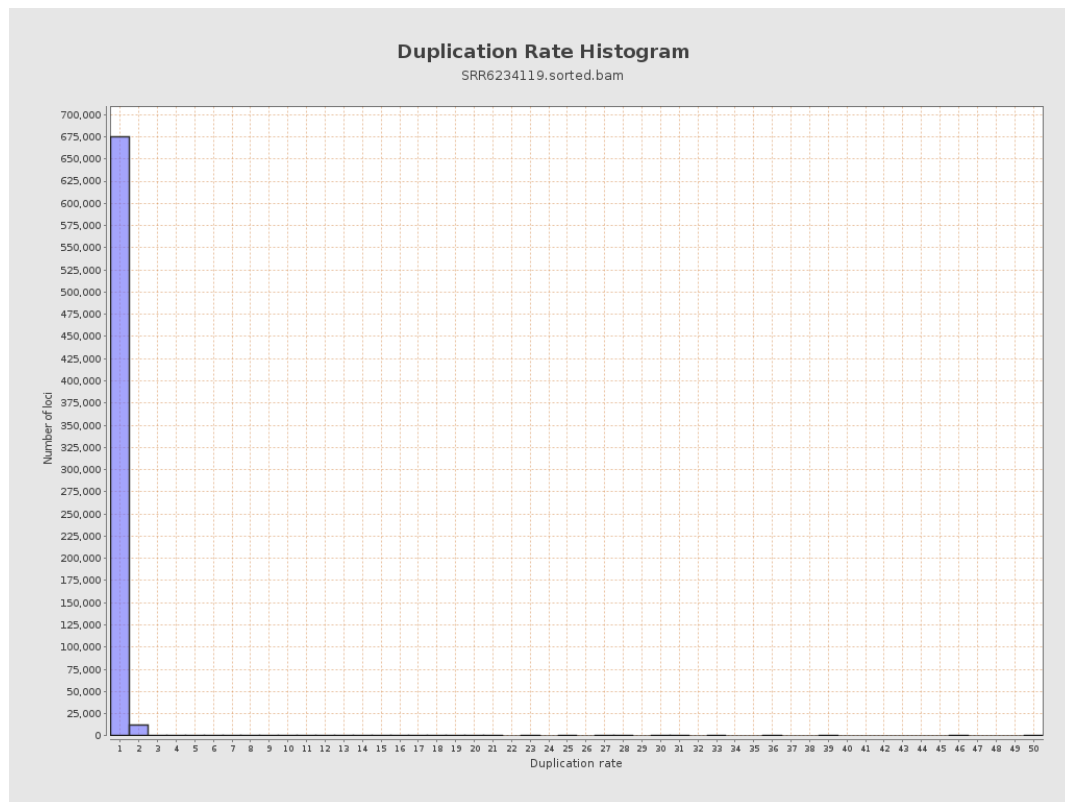
5. Results : Coverage Histogram (0-50X)



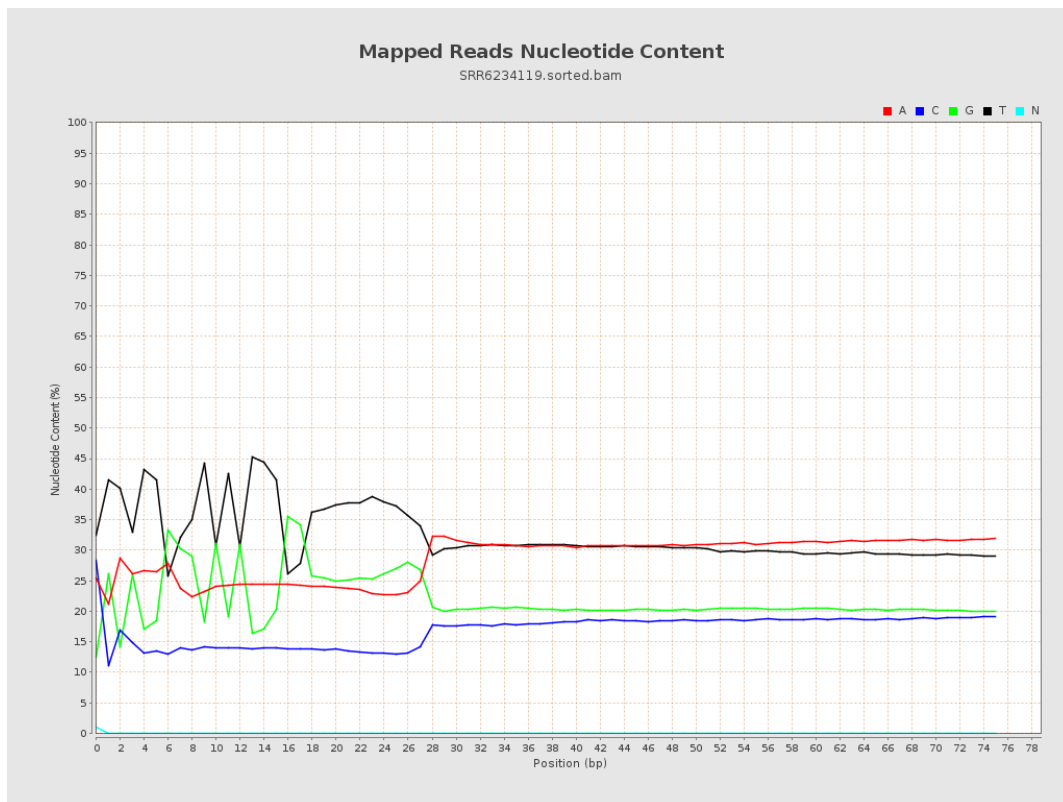
6. Results : Genome Fraction Coverage



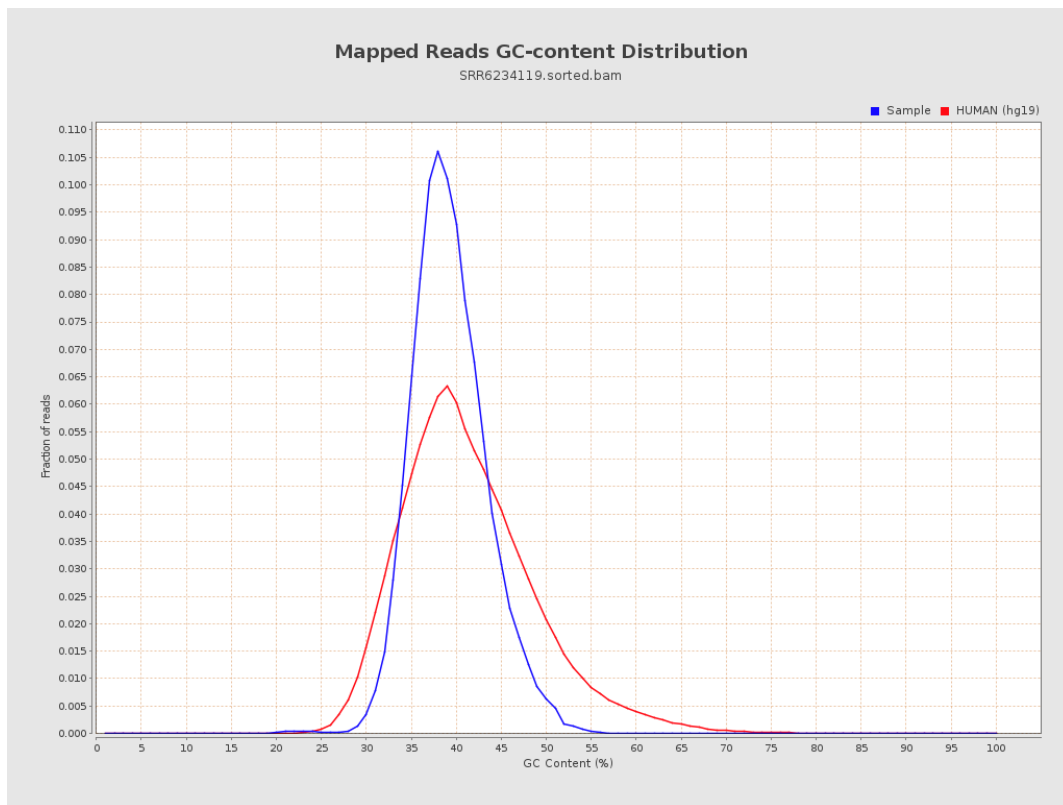
7. Results : Duplication Rate Histogram



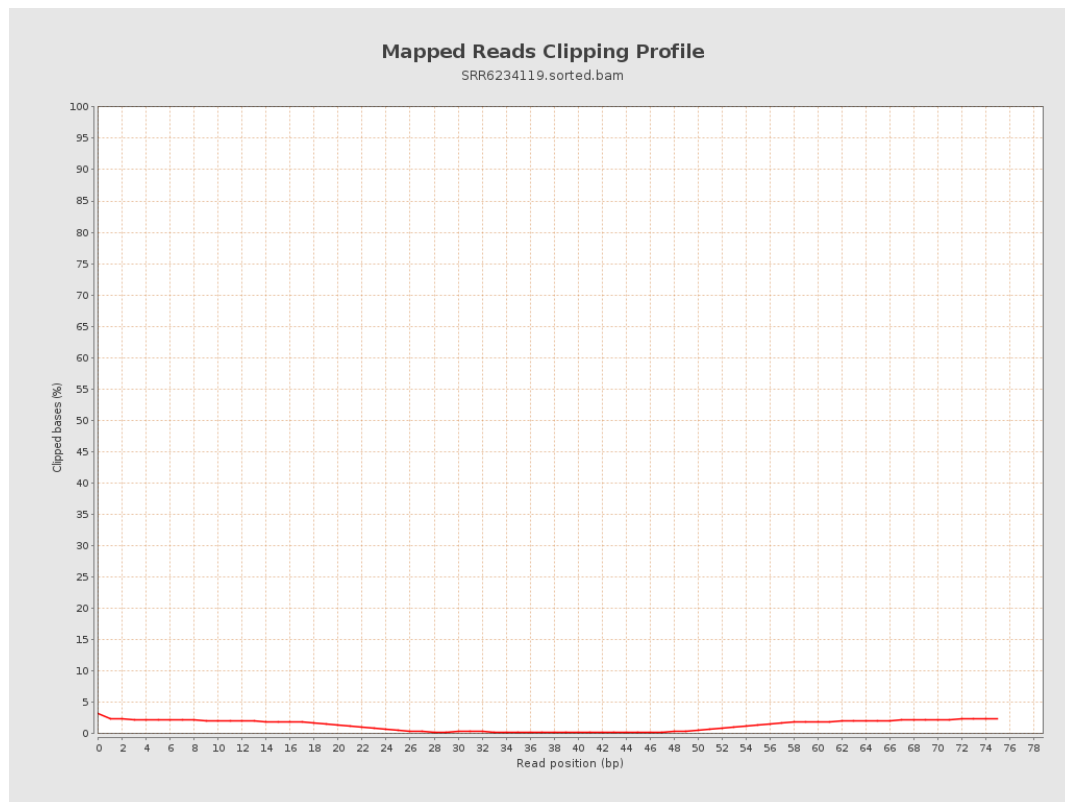
8. Results : Mapped Reads Nucleotide Content



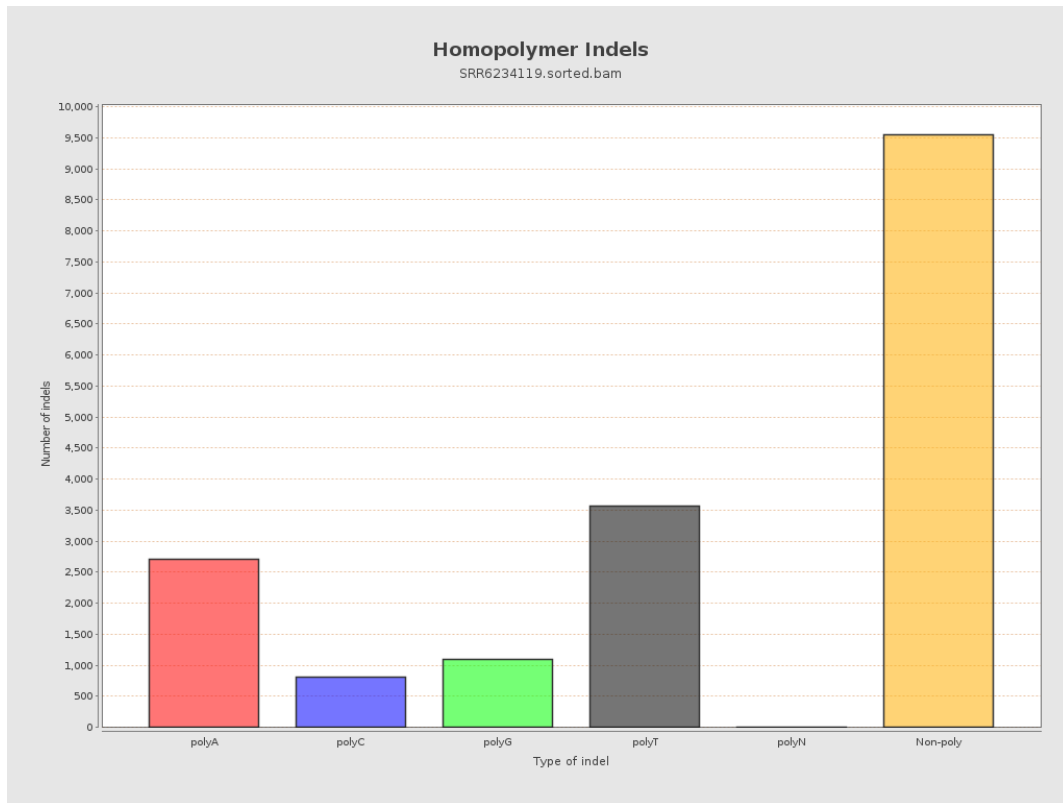
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

