

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 10:45:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234019.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_SRR6234019 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234019.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 10:45:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234019.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,561,838
Mapped reads	1,183,249 / 75.76%
Unmapped reads	378,589 / 24.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,830 / 1.08%
Read min/max/mean length	30 / 76 / 76.38
Duplicated reads (estimated)	140,405 / 8.99%
Duplication rate	9.6%
Clipped reads	674,927 / 43.21%

2.2. ACGT Content

Number/percentage of A's	20,693,145 / 27.26%
Number/percentage of C's	14,070,546 / 18.53%
Number/percentage of T's	24,101,382 / 31.75%
Number/percentage of G's	17,029,791 / 22.43%
Number/percentage of N's	18,543 / 0.02%
GC Percentage	40.97%

2.3. Coverage

Mean	0.0245

Standard Deviation	0.3116
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2.4. Mapping Quality

Mean Mapping Quality	44.44
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2.5. Mismatches and indels

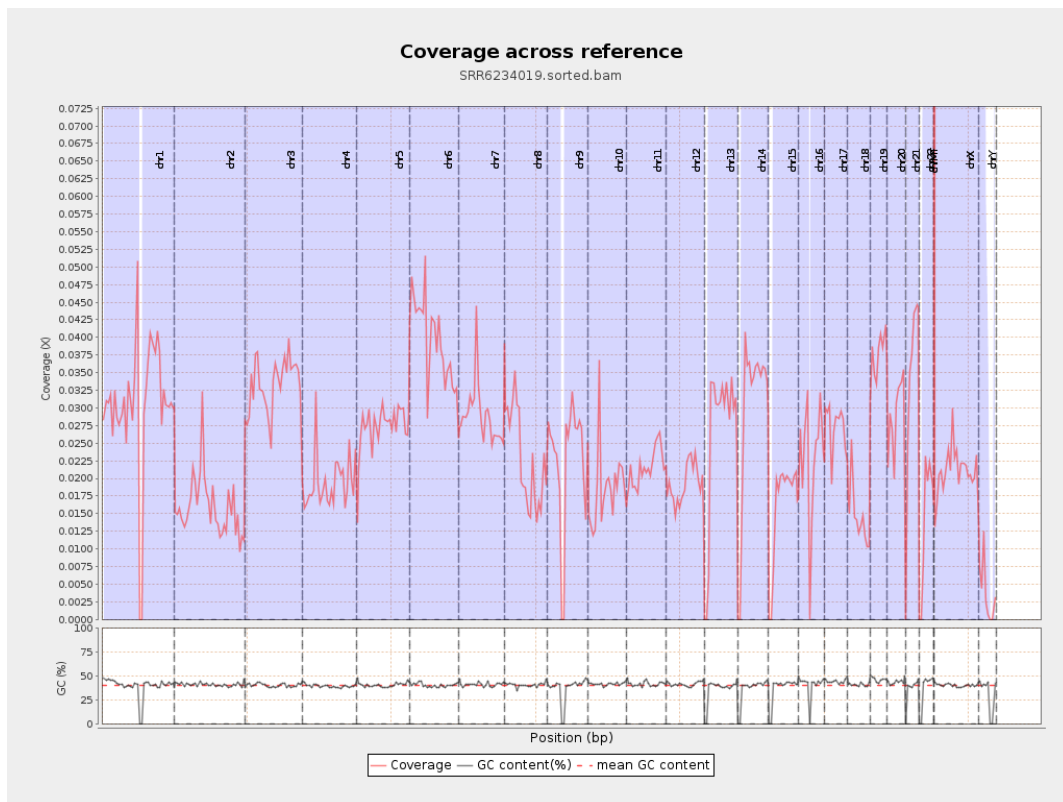
General error rate	0.85%
Mismatches	633,800
Insertions	5,979
Mapped reads with at least one insertion	0.5%
Deletions	28,624
Mapped reads with at least one deletion	2.38%
Homopolymer indels	44.1%

2.6. Chromosome stats

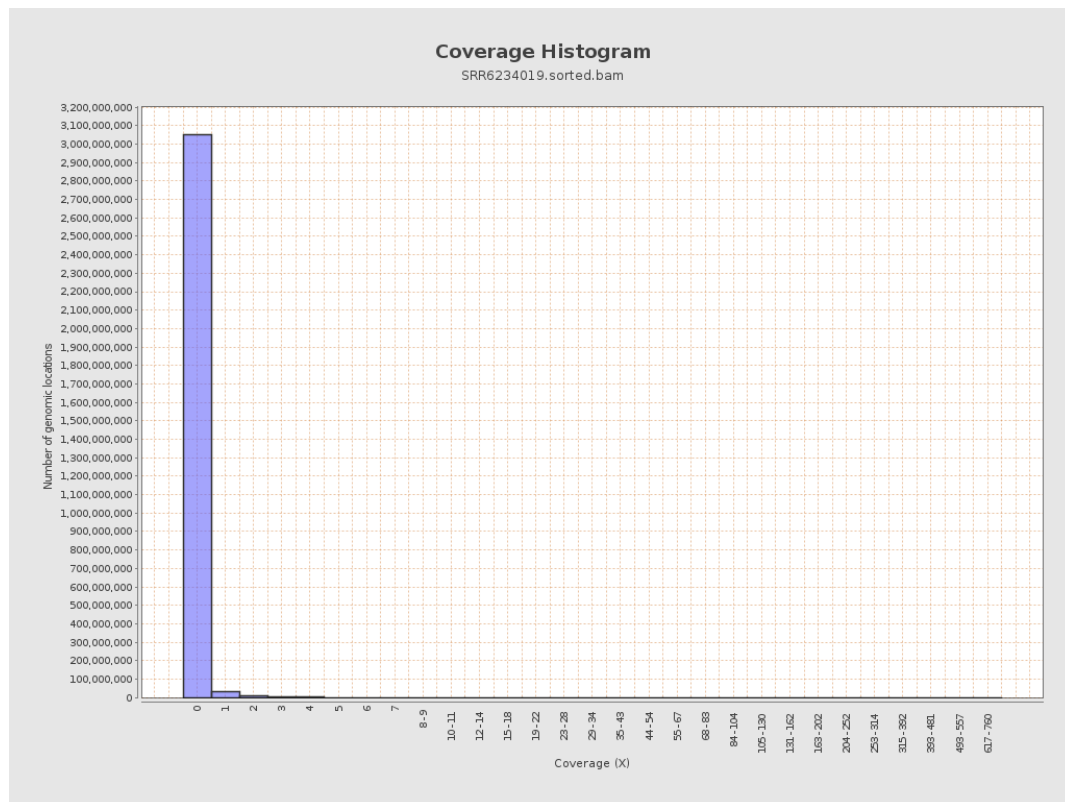
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7615130	0.0306	0.4957
chr2	243199373	3877092	0.0159	0.3714
chr3	198022430	6595587	0.0333	0.2712
chr4	191154276	3718643	0.0195	0.2138
chr5	180915260	4994752	0.0276	0.2477
chr6	171115067	6726790	0.0393	0.3261
chr7	159138663	4601727	0.0289	0.3334

chr8	146364022	3320686	0.0227	0.4675
chr9	141213431	3170887	0.0225	0.2573
chr10	135534747	2500149	0.0184	0.247
chr11	135006516	2920759	0.0216	0.2351
chr12	133851895	2570349	0.0192	0.2068
chr13	115169878	3037423	0.0264	0.2491
chr14	107349540	3197790	0.0298	0.2607
chr15	102531392	1646260	0.0161	0.186
chr16	90354753	2003191	0.0222	0.2369
chr17	81195210	2211791	0.0272	0.2479
chr18	78077248	1127516	0.0144	0.4153
chr19	59128983	2227670	0.0377	0.3849
chr20	63025520	1803615	0.0286	0.2658
chr21	48129895	1654949	0.0344	0.2783
chr22	51304566	749926	0.0146	0.1725
chrMT	16571	206073	12.4358	10.5458
chrX	155270560	3265300	0.021	0.2194
chrY	59373566	219136	0.0037	0.1001

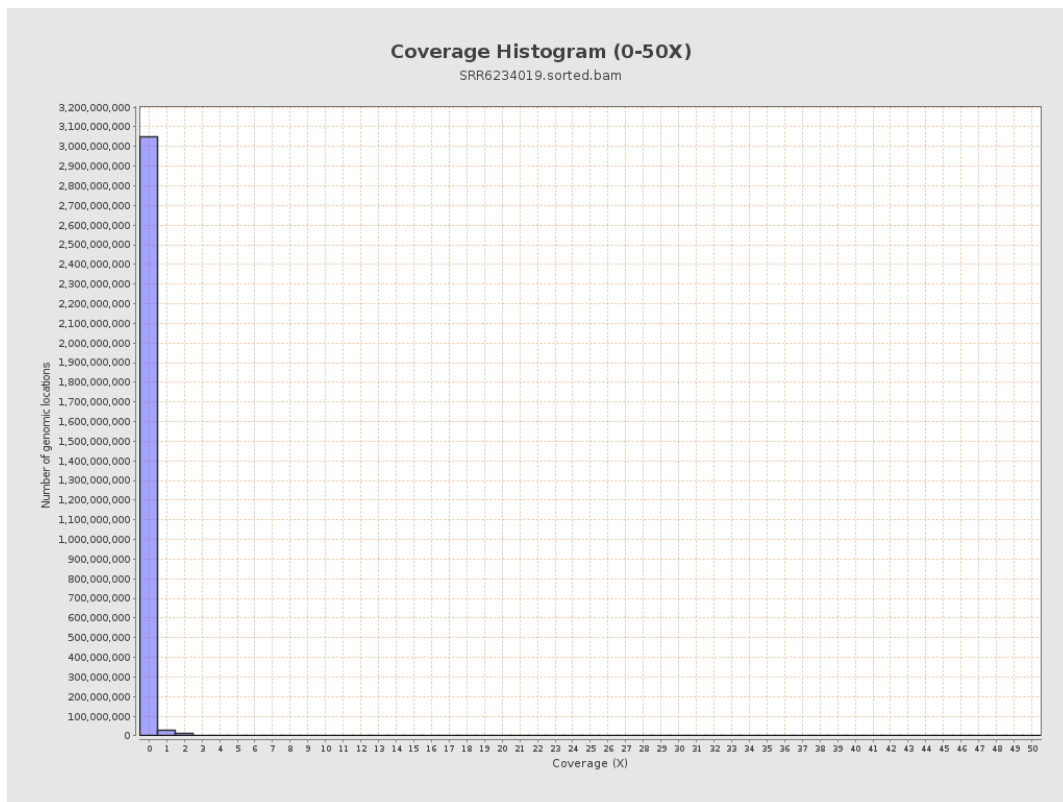
3. Results : Coverage across reference



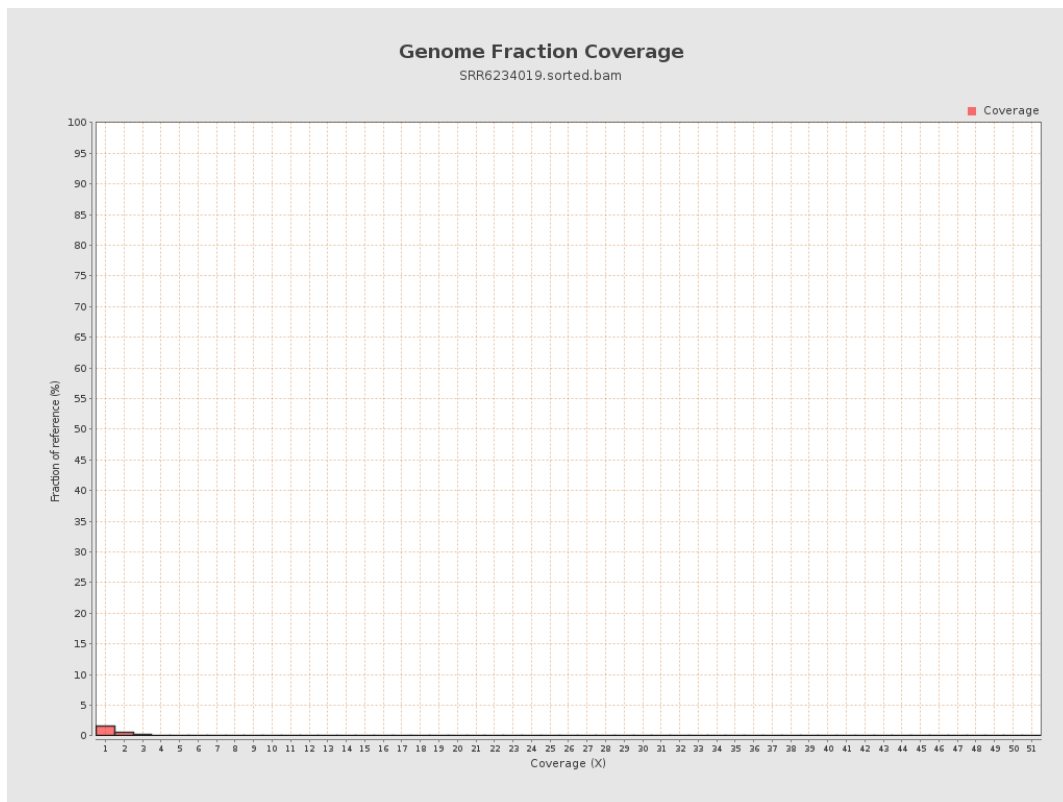
4. Results : Coverage Histogram



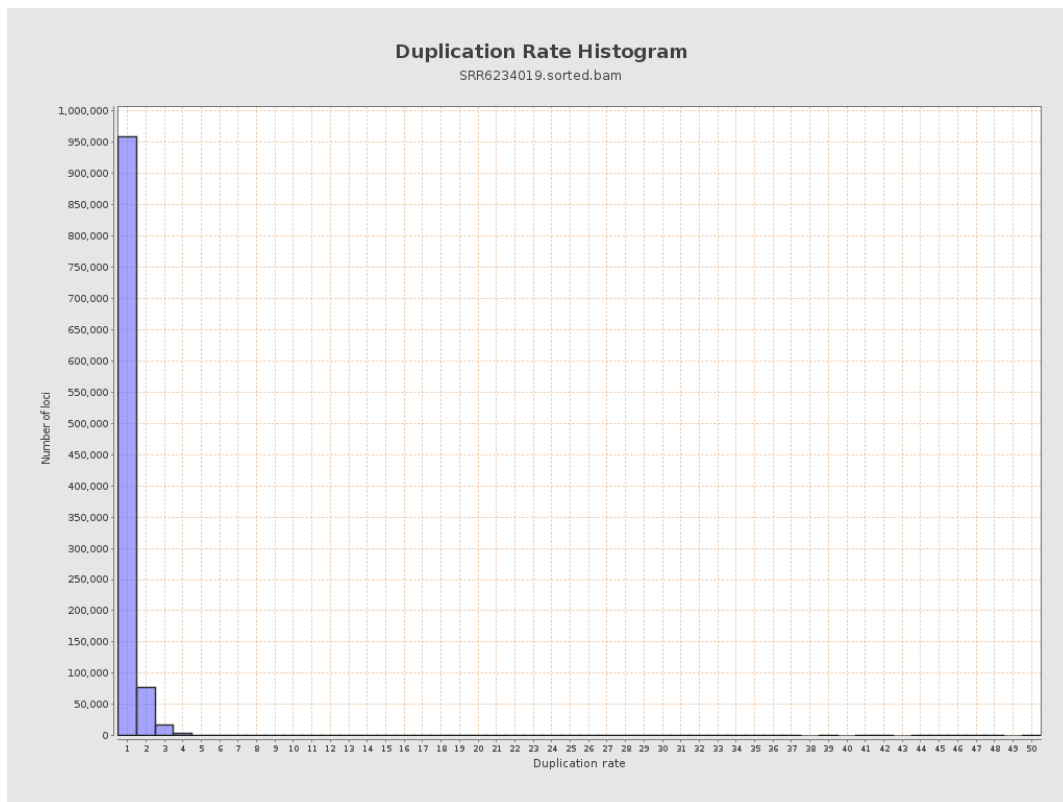
5. Results : Coverage Histogram (0-50X)



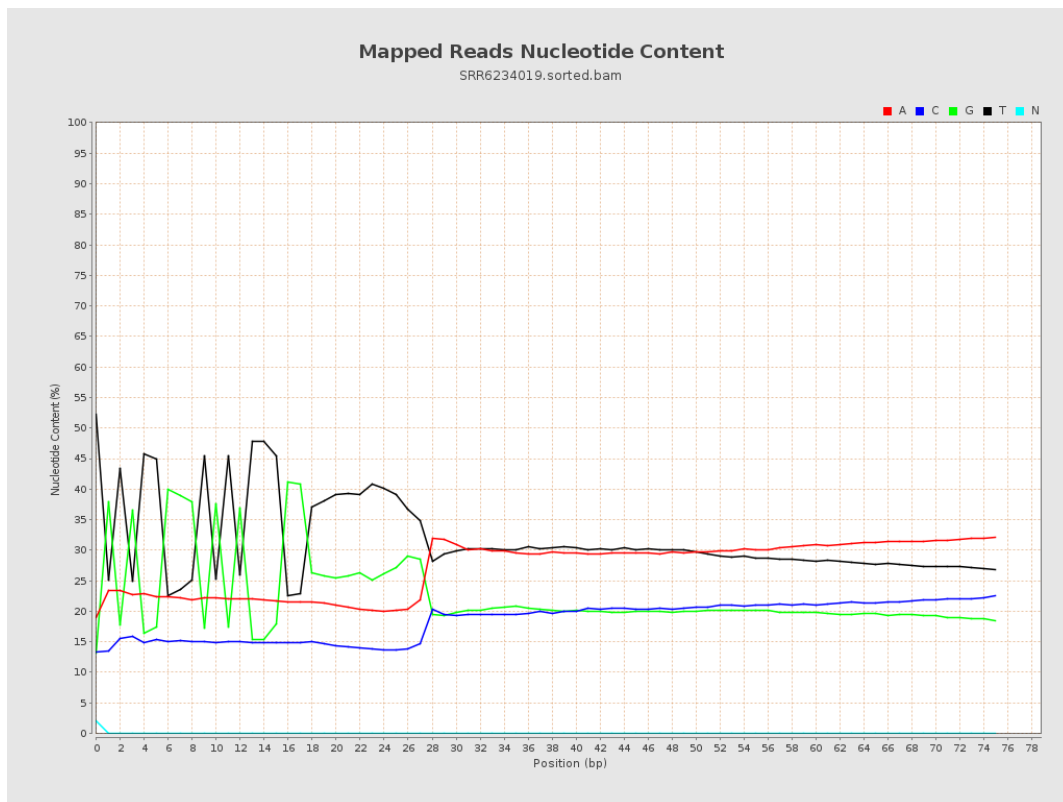
6. Results : Genome Fraction Coverage



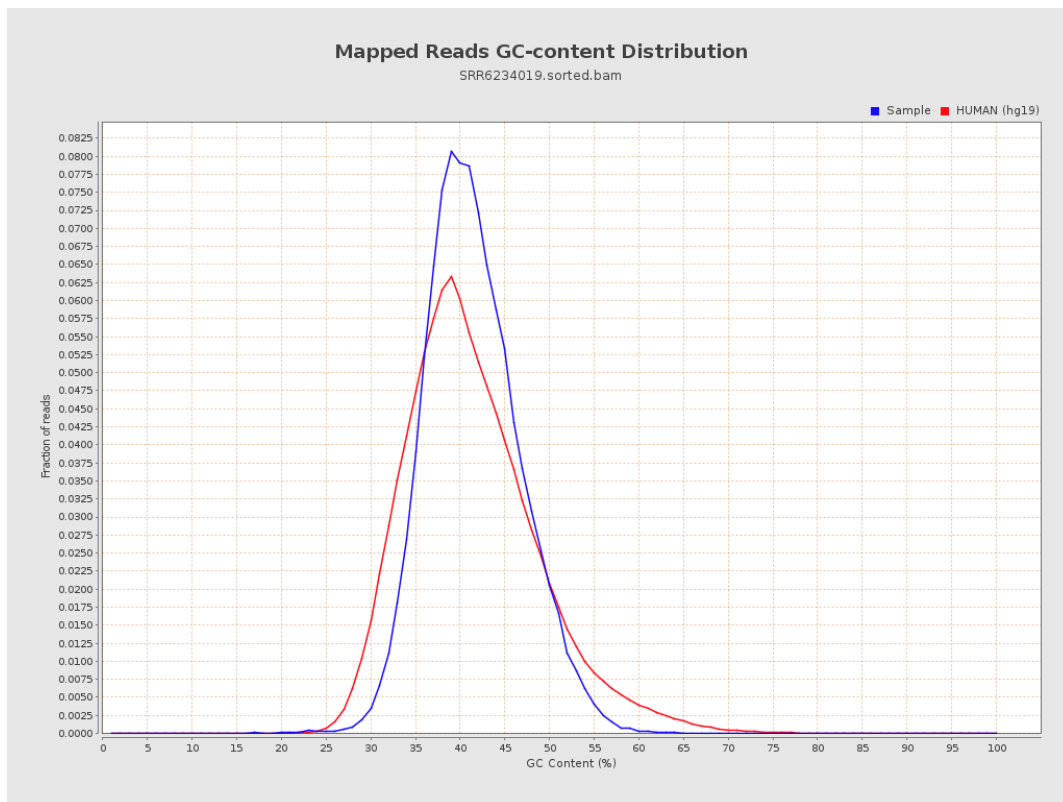
7. Results : Duplication Rate Histogram



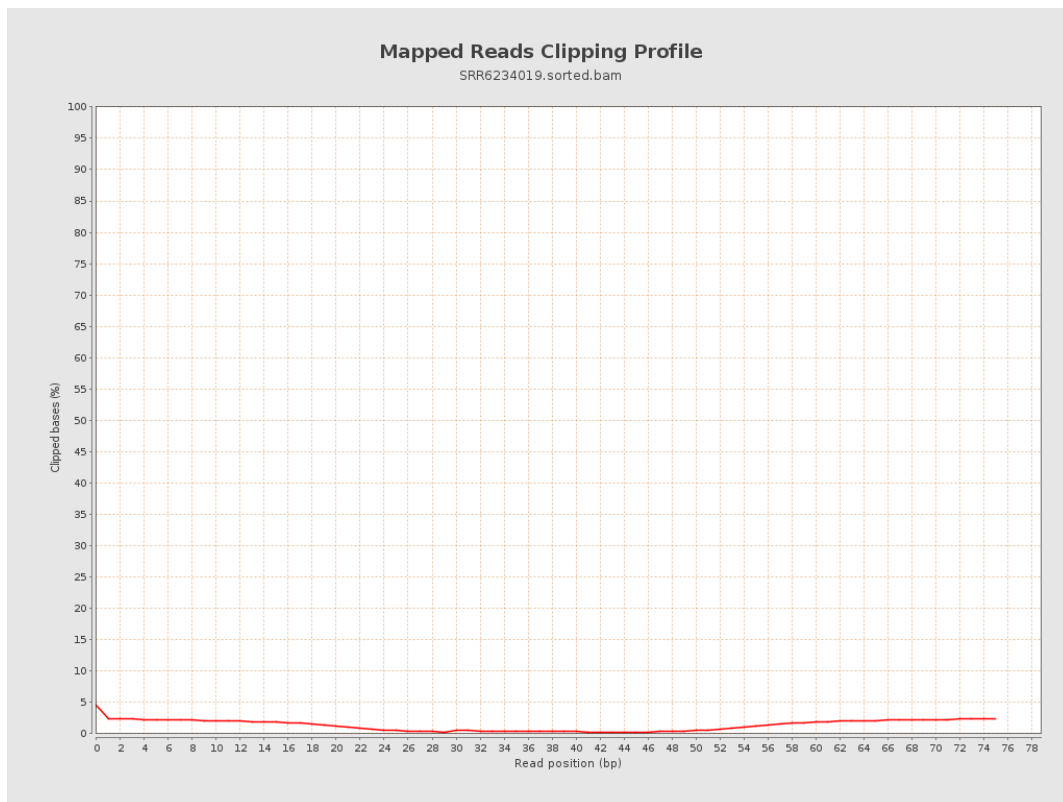
8. Results : Mapped Reads Nucleotide Content



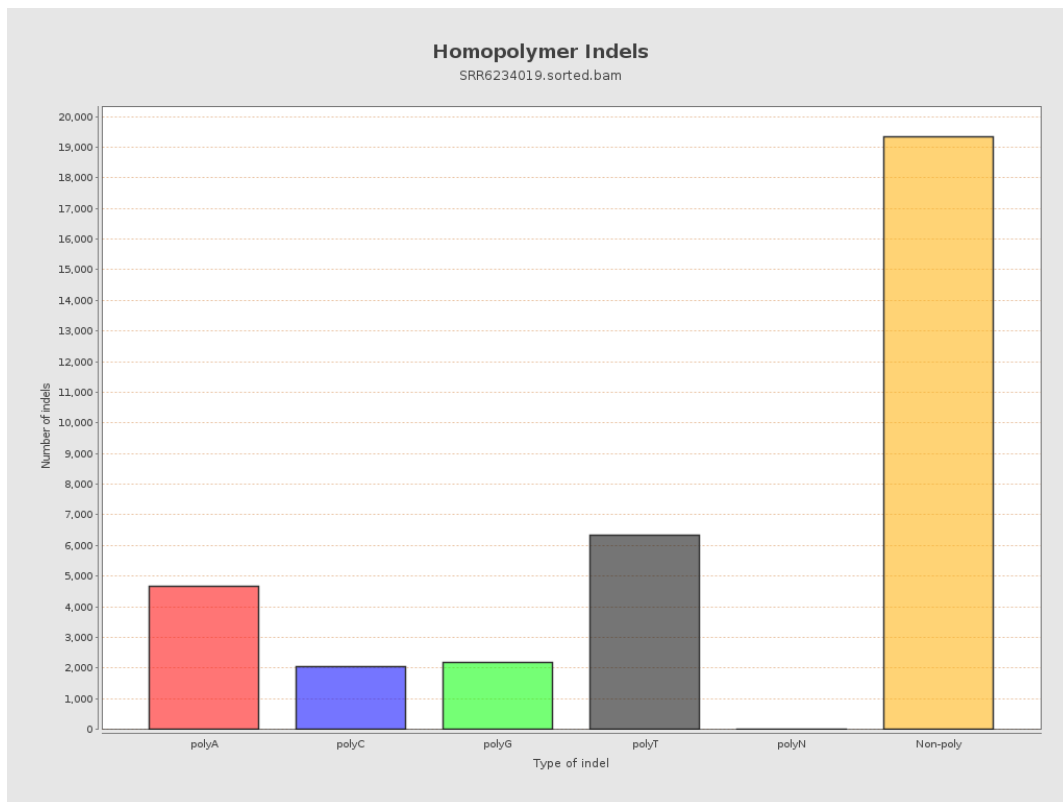
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

