

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 18:46:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236063.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_SRR6236063 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236063.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 18:46:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236063.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,890,468
Mapped reads	2,490,699 / 86.17%
Unmapped reads	399,769 / 13.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,433 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	139,361 / 4.82%
Duplication rate	4.34%
Clipped reads	1,276,365 / 44.16%

2.2. ACGT Content

Number/percentage of A's	46,507,435 / 28.63%
Number/percentage of C's	30,233,134 / 18.61%
Number/percentage of T's	50,776,870 / 31.26%
Number/percentage of G's	34,933,035 / 21.5%
Number/percentage of N's	1,546 / 0%
GC Percentage	40.11%

2.3. Coverage

Mean	0.0525

Standard Deviation	0.5099
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2.4. Mapping Quality

Mean Mapping Quality	45.76
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2.5. Mismatches and indels

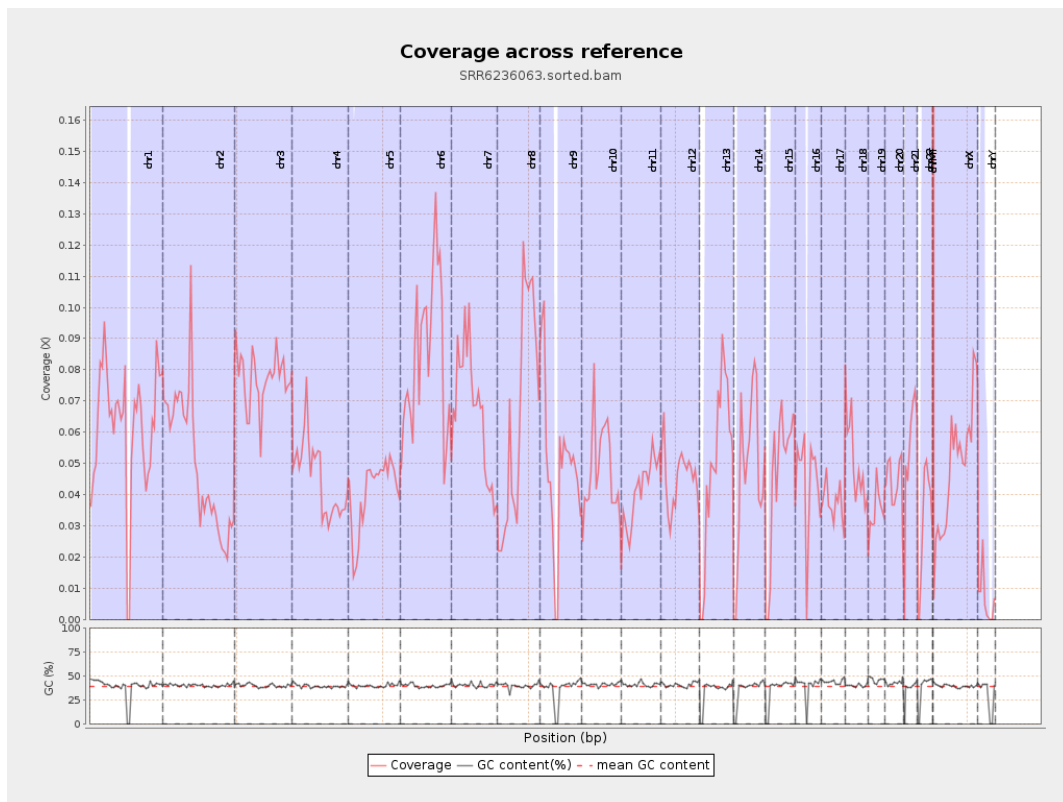
General error rate	0.79%
Mismatches	1,251,884
Insertions	12,838
Mapped reads with at least one insertion	0.51%
Deletions	47,292
Mapped reads with at least one deletion	1.88%
Homopolymer indels	47.19%

2.6. Chromosome stats

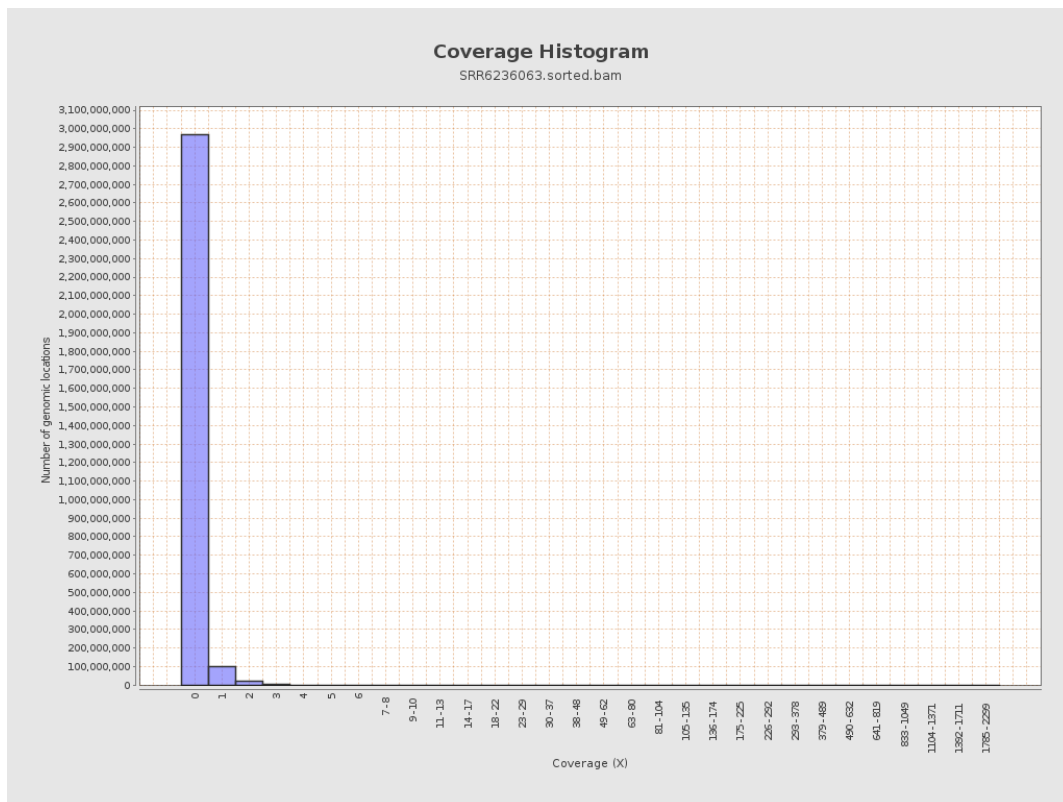
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15414068	0.0618	0.6276
chr2	243199373	12162013	0.05	0.4956
chr3	198022430	15283987	0.0772	0.343
chr4	191154276	8618436	0.0451	0.3129
chr5	180915260	7417001	0.041	0.2508
chr6	171115067	14436204	0.0844	0.4365
chr7	159138663	10613945	0.0667	0.6004

chr8	146364022	9624261	0.0658	1.4567
chr9	141213431	6879263	0.0487	0.4107
chr10	135534747	6418469	0.0474	0.4243
chr11	135006516	5582134	0.0413	0.3344
chr12	133851895	6131799	0.0458	0.2733
chr13	115169878	5801694	0.0504	0.2757
chr14	107349540	5178926	0.0482	0.2839
chr15	102531392	4692913	0.0458	0.2709
chr16	90354753	3899619	0.0432	0.2766
chr17	81195210	3062418	0.0377	0.2676
chr18	78077248	3950610	0.0506	0.696
chr19	59128983	2086662	0.0353	0.4448
chr20	63025520	2819959	0.0447	0.2699
chr21	48129895	2639524	0.0548	0.3139
chr22	51304566	1615200	0.0315	0.2129
chrMT	16571	230856	13.9313	9.5657
chrX	155270560	7559588	0.0487	0.2909
chrY	59373566	413455	0.007	0.2011

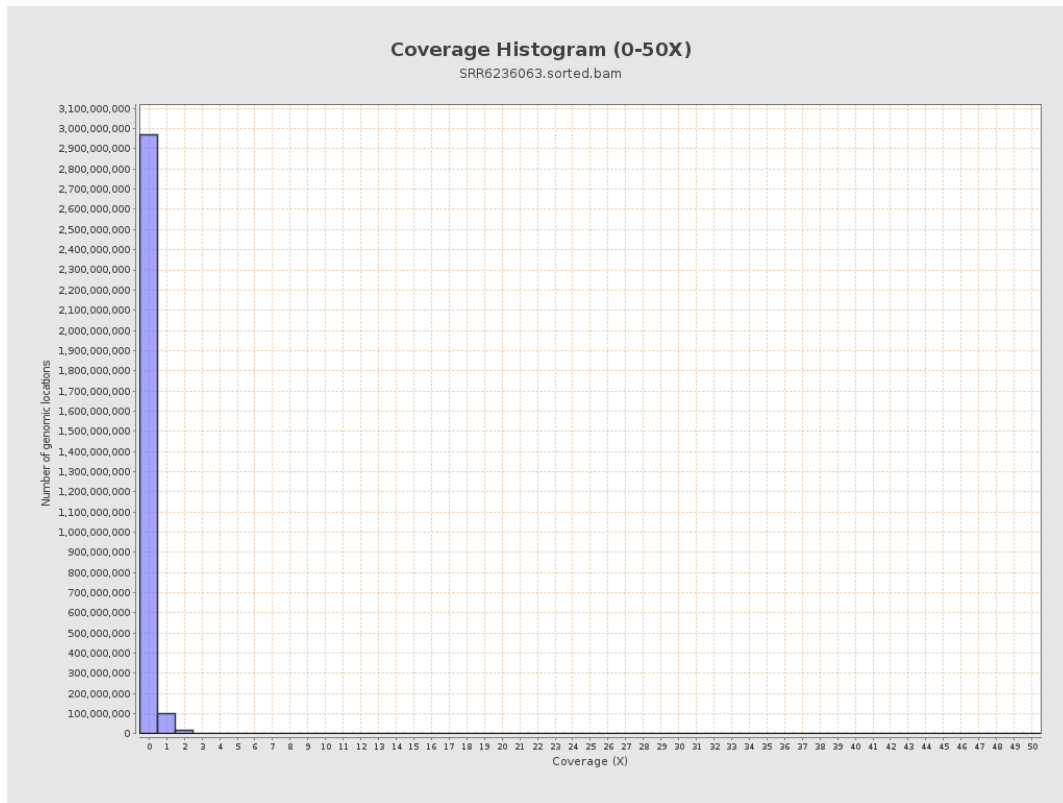
3. Results : Coverage across reference



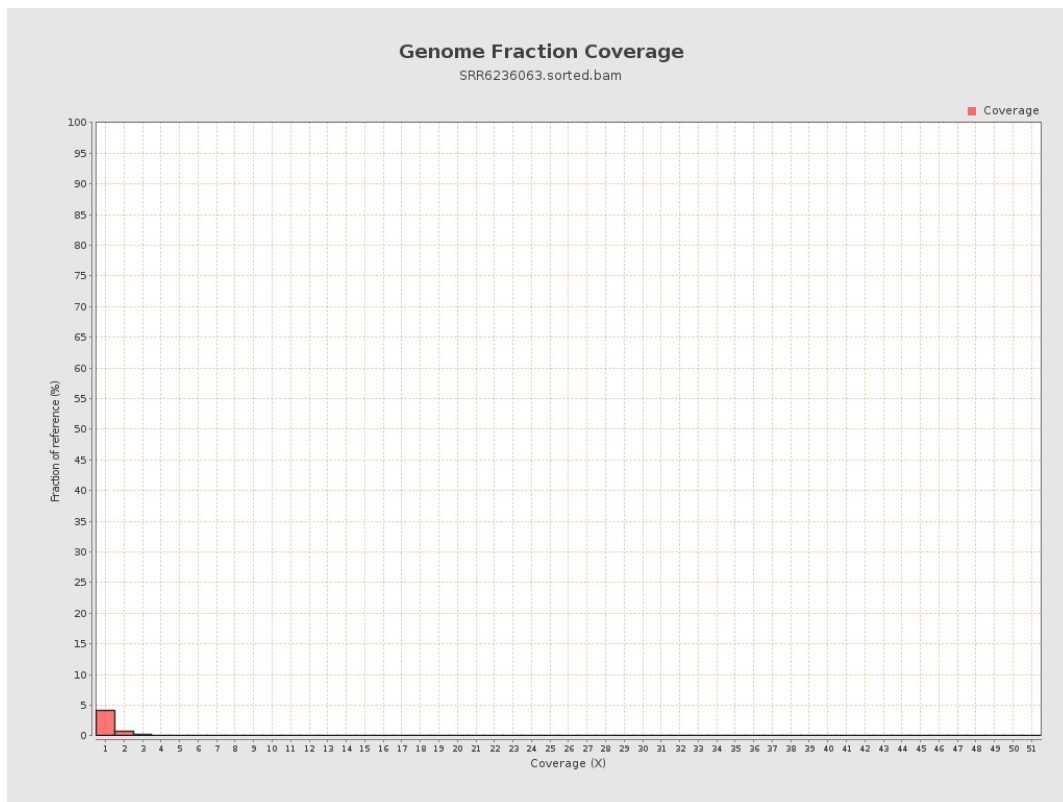
4. Results : Coverage Histogram



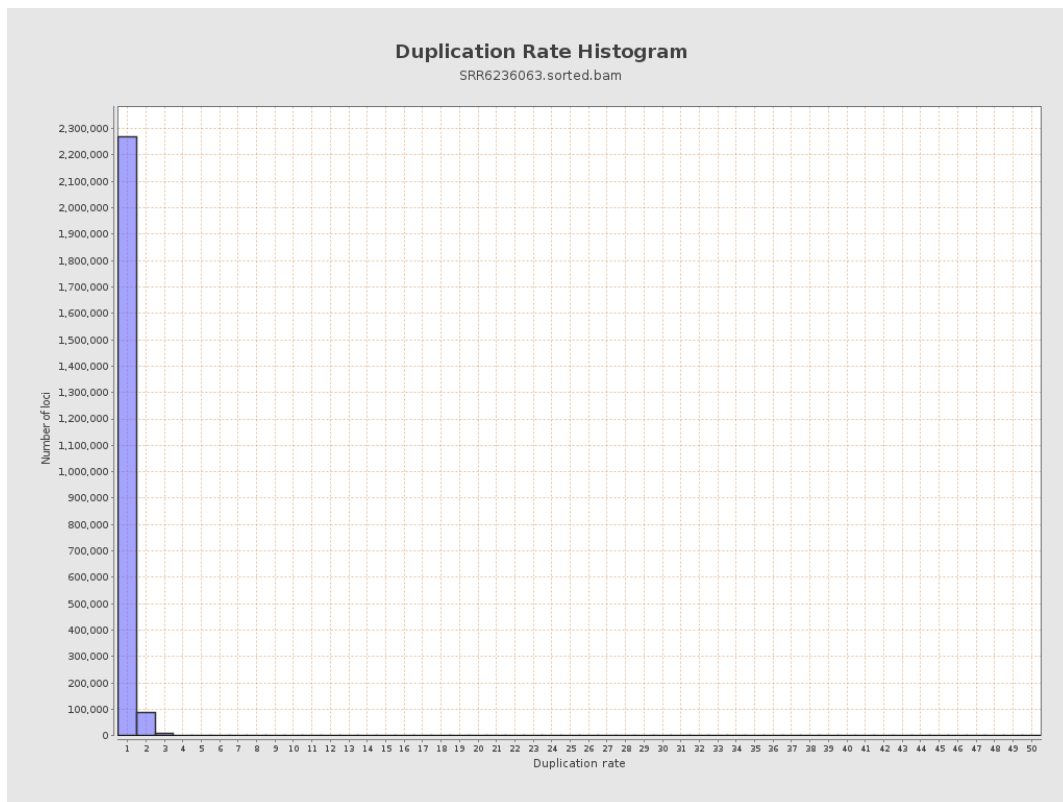
5. Results : Coverage Histogram (0-50X)



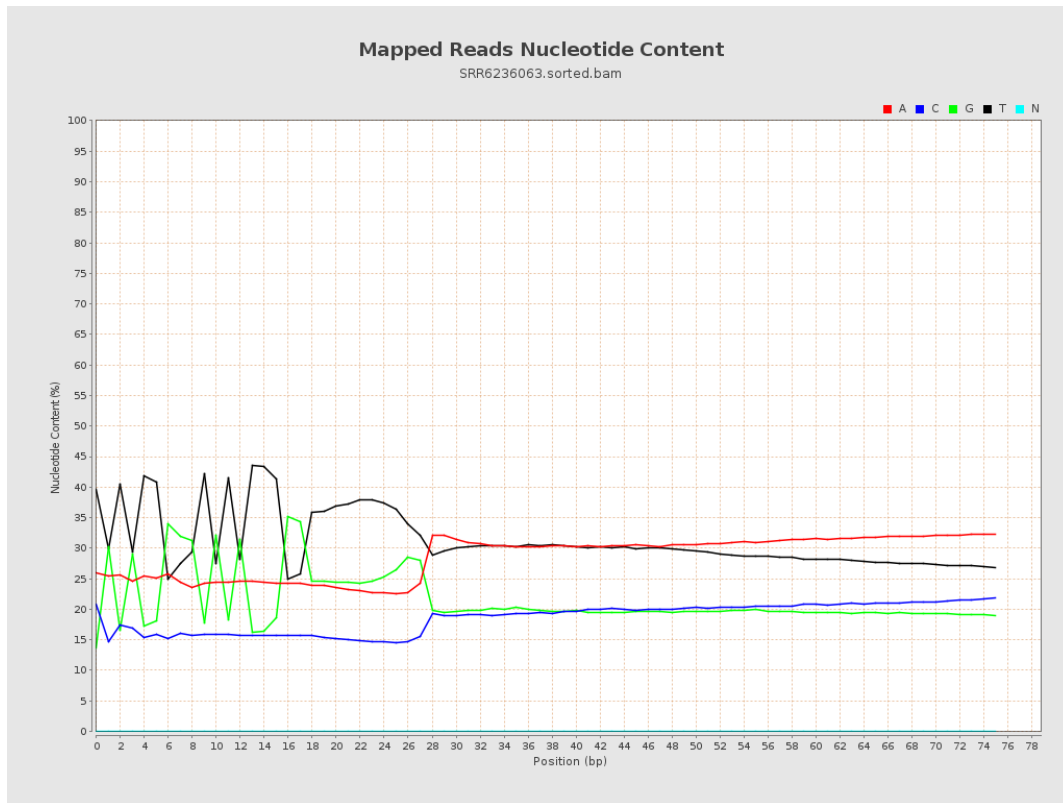
6. Results : Genome Fraction Coverage



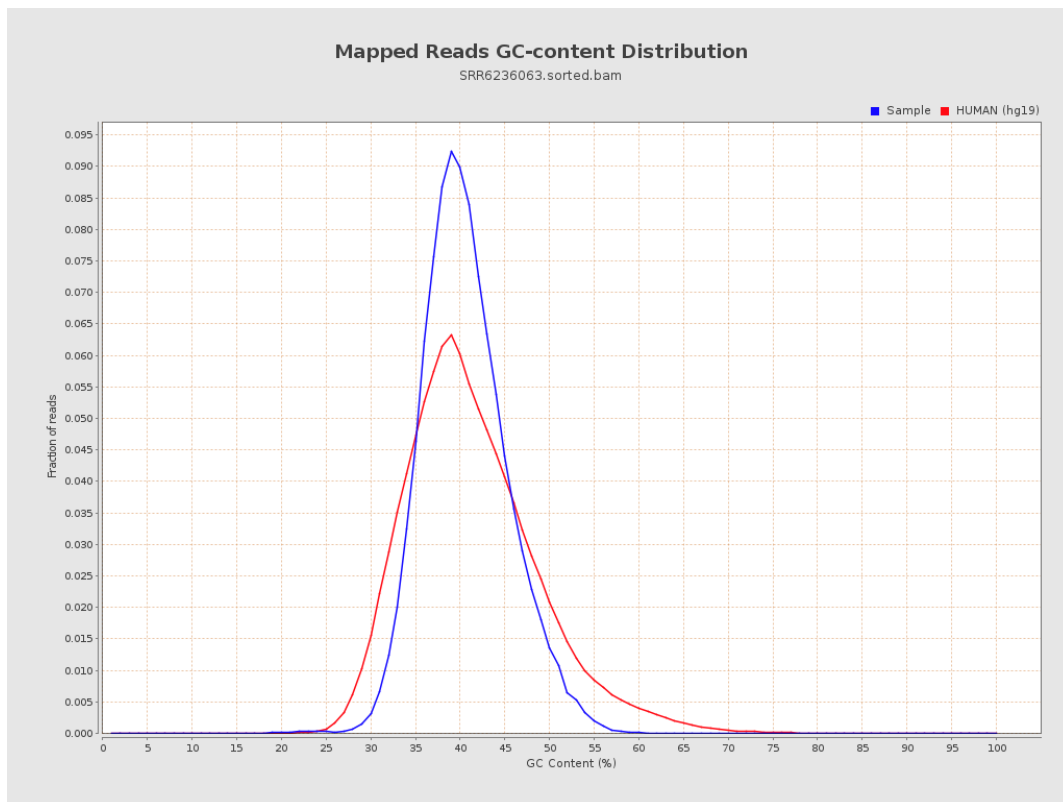
7. Results : Duplication Rate Histogram



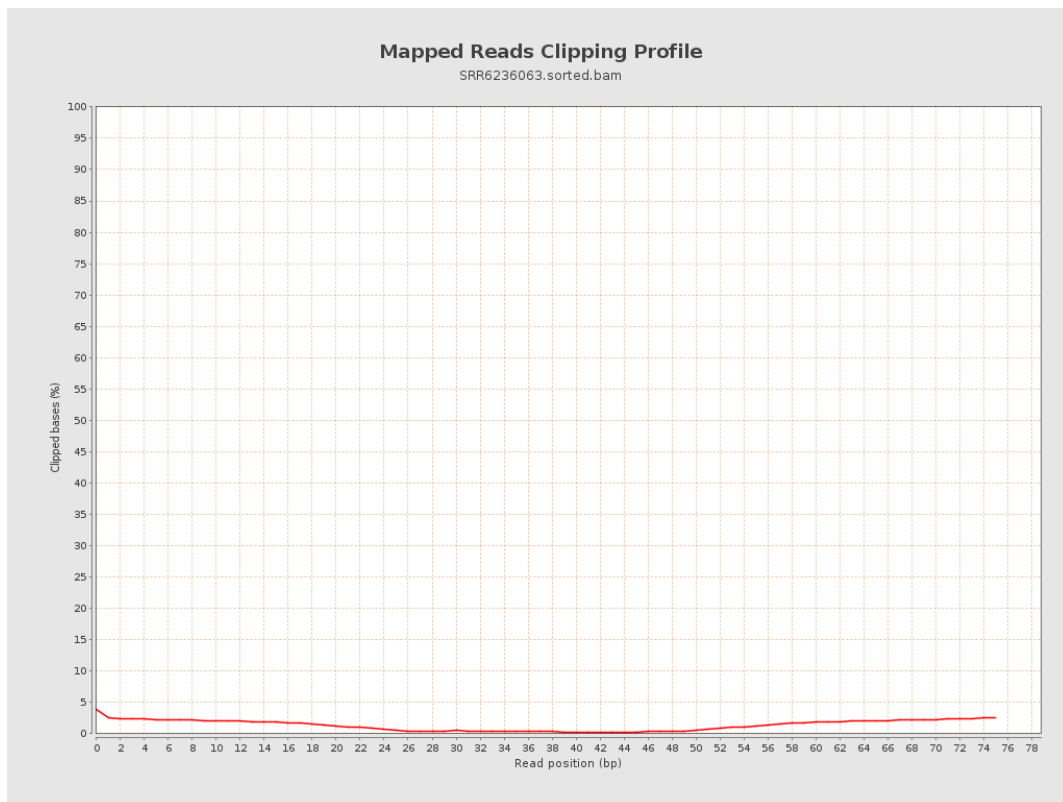
8. Results : Mapped Reads Nucleotide Content



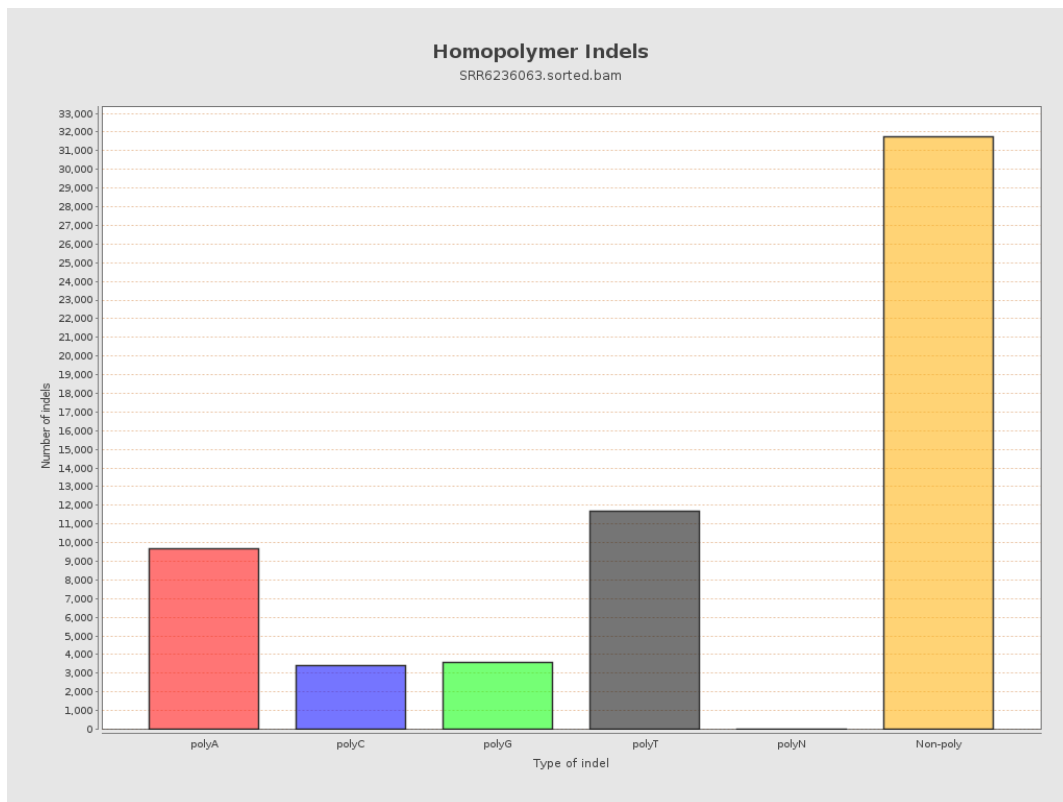
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

