

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 18:51:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236065.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_SRR6236065 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236065.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 18:51:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236065.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,445,839
Mapped reads	1,298,844 / 89.83%
Unmapped reads	146,995 / 10.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,583 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	51,733 / 3.58%
Duplication rate	3.11%
Clipped reads	531,997 / 36.8%

2.2. ACGT Content

Number/percentage of A's	24,152,348 / 27.7%
Number/percentage of C's	15,778,351 / 18.1%
Number/percentage of T's	27,874,372 / 31.97%
Number/percentage of G's	19,326,291 / 22.17%
Number/percentage of N's	51,783 / 0.06%
GC Percentage	40.27%

2.3. Coverage

Mean	0.0282

Standard Deviation	0.2771
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2.4. Mapping Quality

Mean Mapping Quality	46.51
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2.5. Mismatches and indels

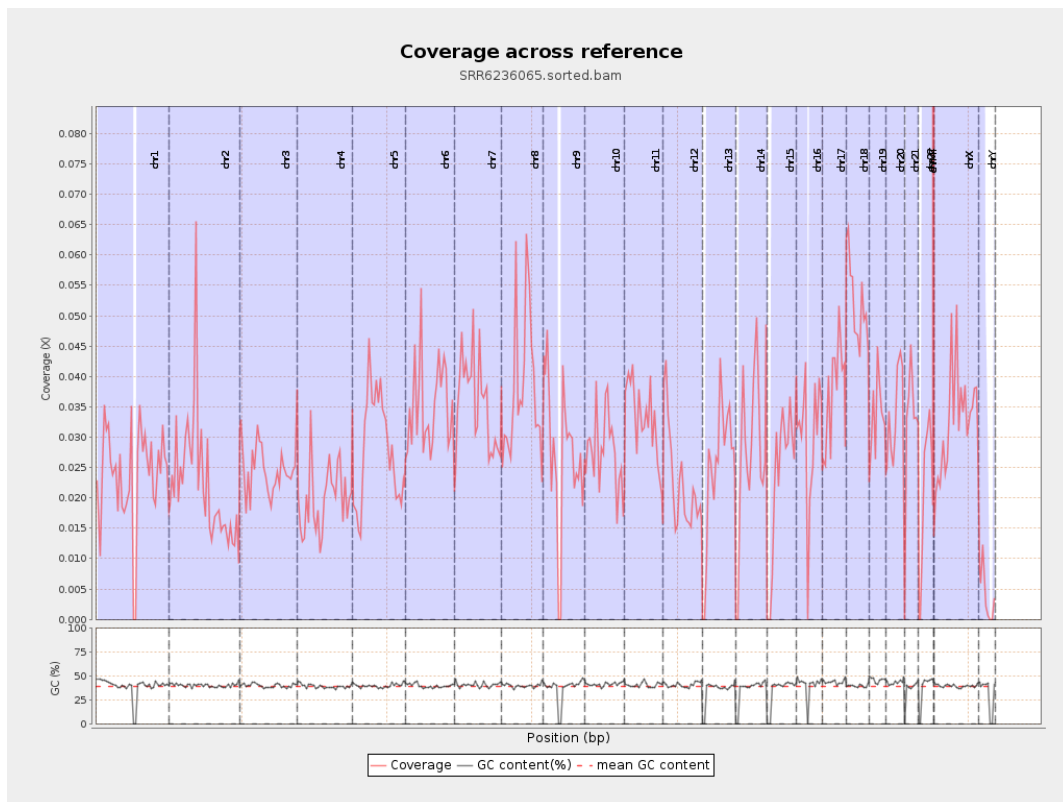
General error rate	0.81%
Mismatches	697,590
Insertions	6,632
Mapped reads with at least one insertion	0.51%
Deletions	21,068
Mapped reads with at least one deletion	1.61%
Homopolymer indels	49.22%

2.6. Chromosome stats

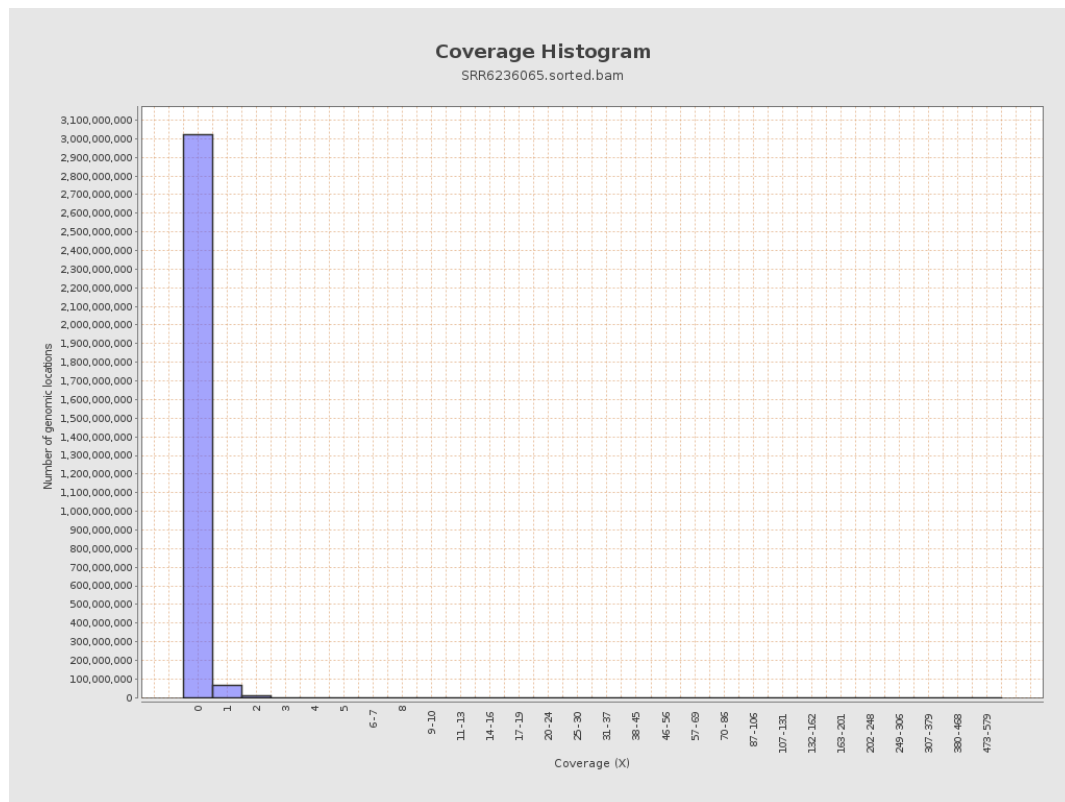
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5933910	0.0238	0.3619
chr2	243199373	5420130	0.0223	0.3631
chr3	198022430	4881070	0.0246	0.1734
chr4	191154276	3755229	0.0196	0.1686
chr5	180915260	5064441	0.028	0.1864
chr6	171115067	5957647	0.0348	0.2387
chr7	159138663	5687450	0.0357	0.3674

chr8	146364022	5485096	0.0375	0.4305
chr9	141213431	3778708	0.0268	0.3062
chr10	135534747	3762607	0.0278	0.2259
chr11	135006516	4408011	0.0327	0.2741
chr12	133851895	3007941	0.0225	0.1702
chr13	115169878	2902509	0.0252	0.1757
chr14	107349540	2864056	0.0267	0.1952
chr15	102531392	2416473	0.0236	0.1764
chr16	90354753	2722716	0.0301	0.2099
chr17	81195210	3026773	0.0373	0.2321
chr18	78077248	4075512	0.0522	0.5501
chr19	59128983	1995791	0.0338	0.2956
chr20	63025520	2113642	0.0335	0.2116
chr21	48129895	1563404	0.0325	0.2154
chr22	51304566	1067954	0.0208	0.1597
chrMT	16571	44224	2.6688	2.3128
chrX	155270560	5052673	0.0325	0.2183
chrY	59373566	232293	0.0039	0.1006

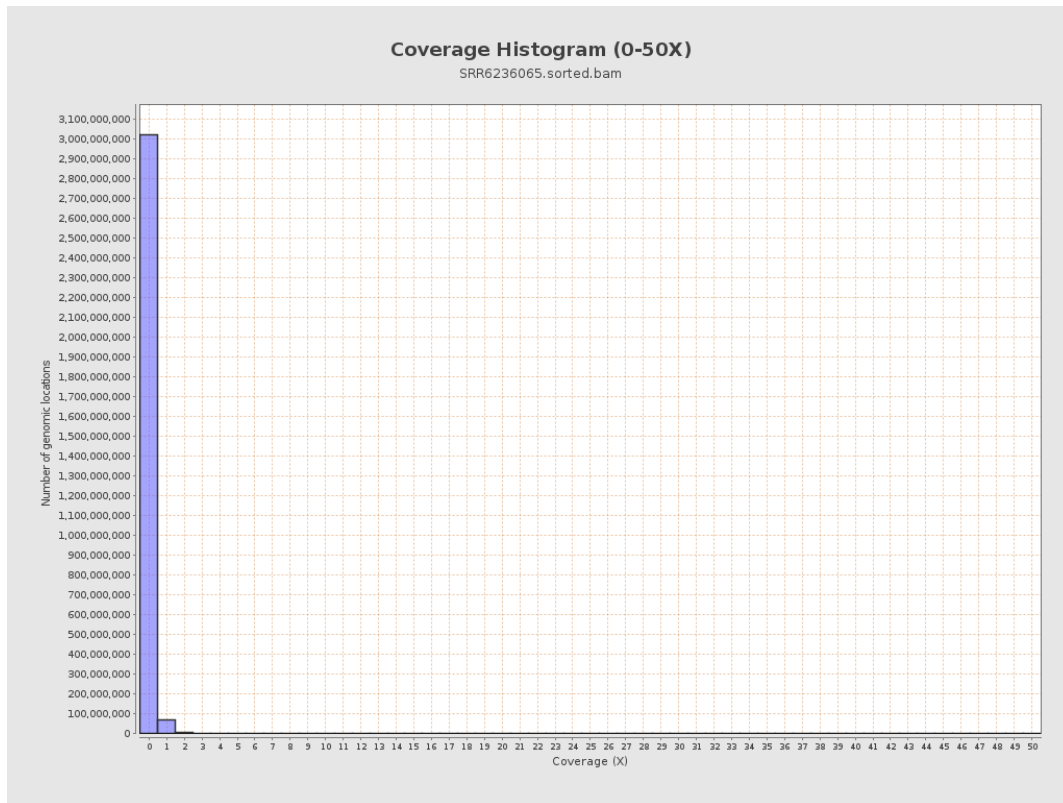
3. Results : Coverage across reference



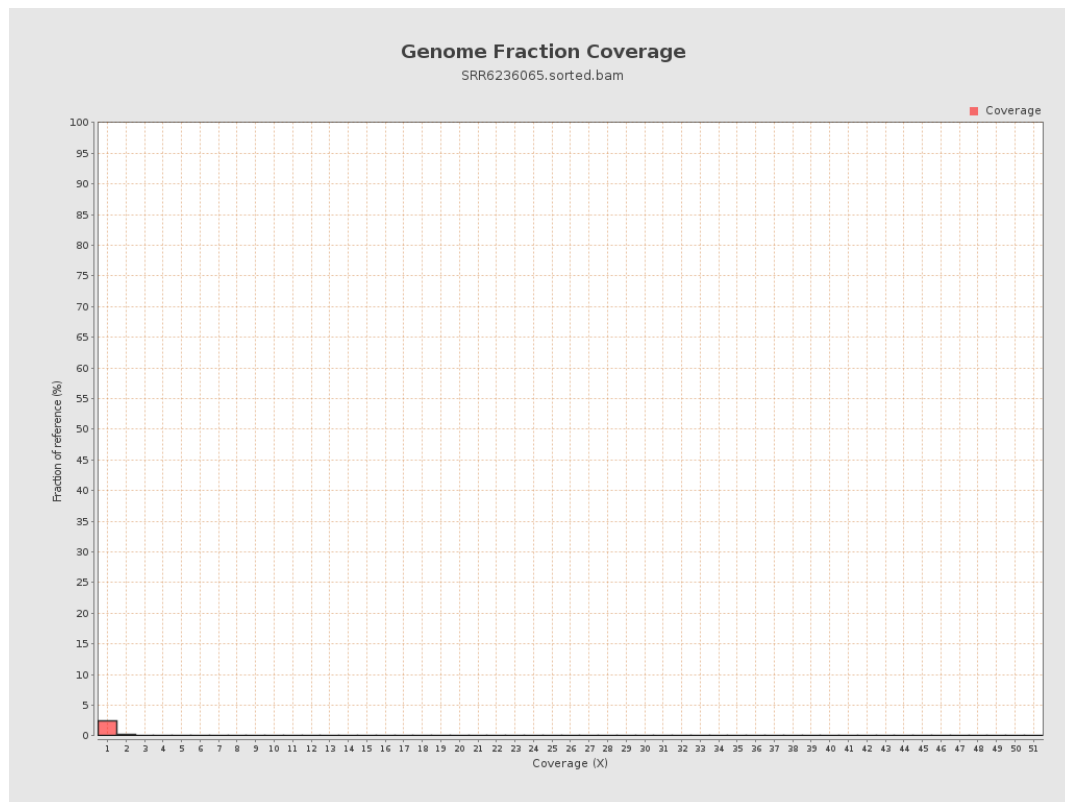
4. Results : Coverage Histogram



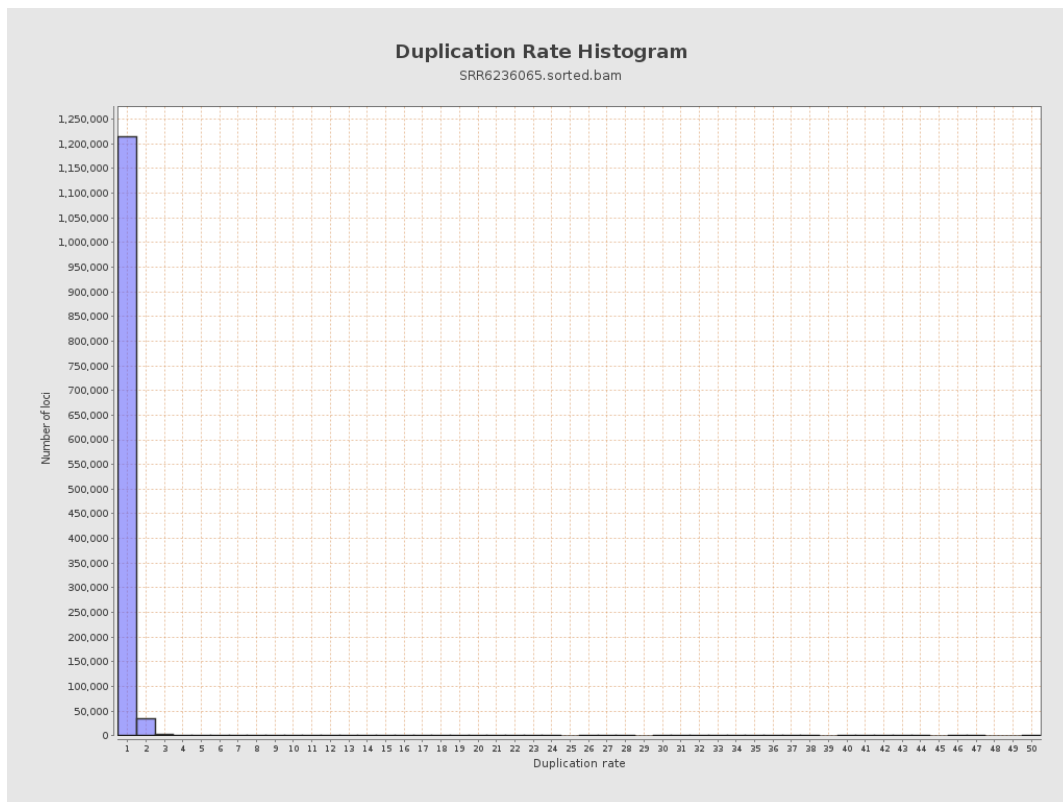
5. Results : Coverage Histogram (0-50X)



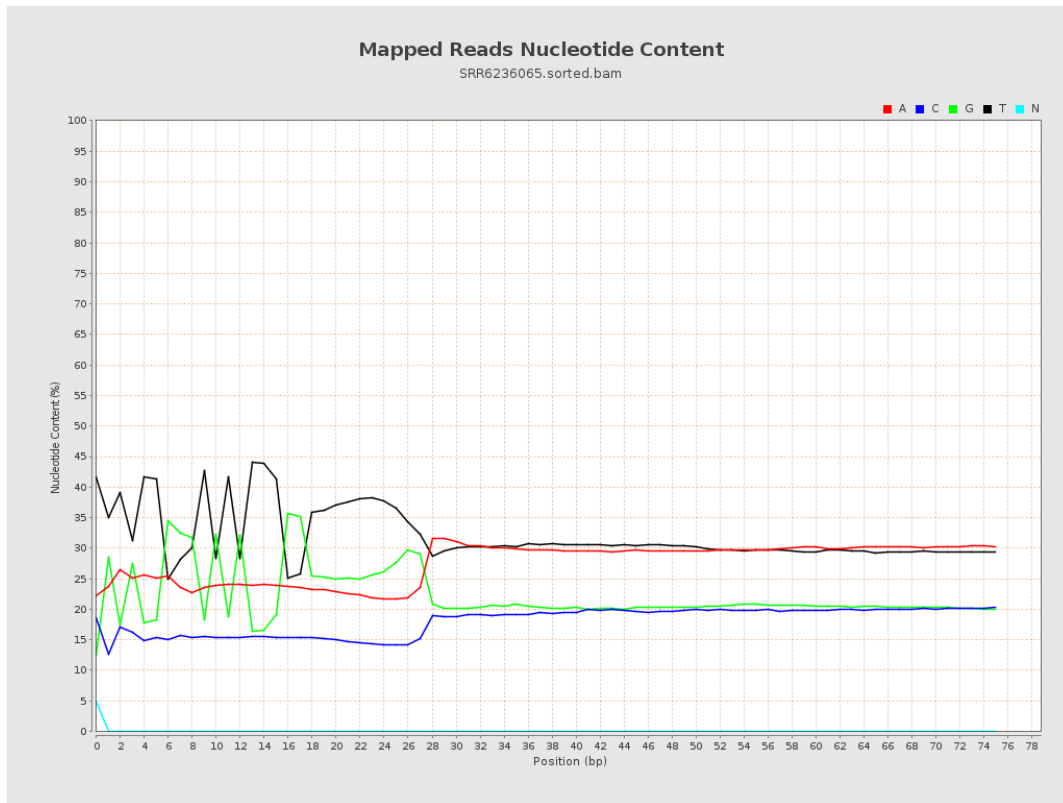
6. Results : Genome Fraction Coverage



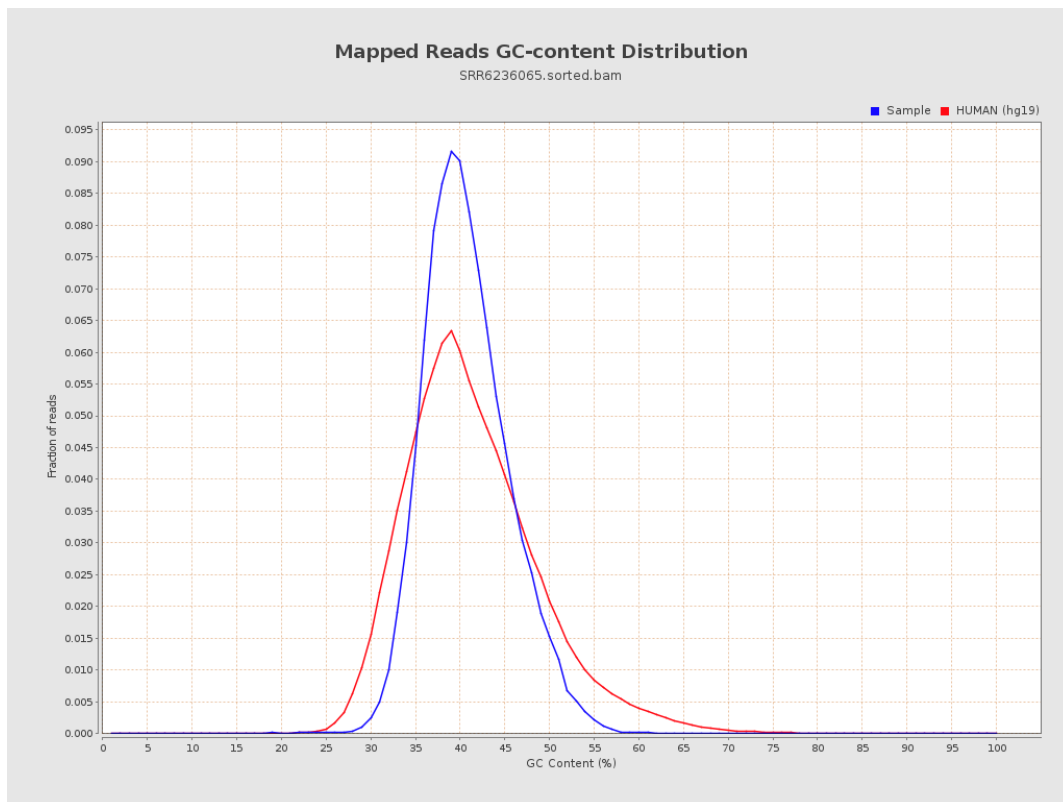
7. Results : Duplication Rate Histogram



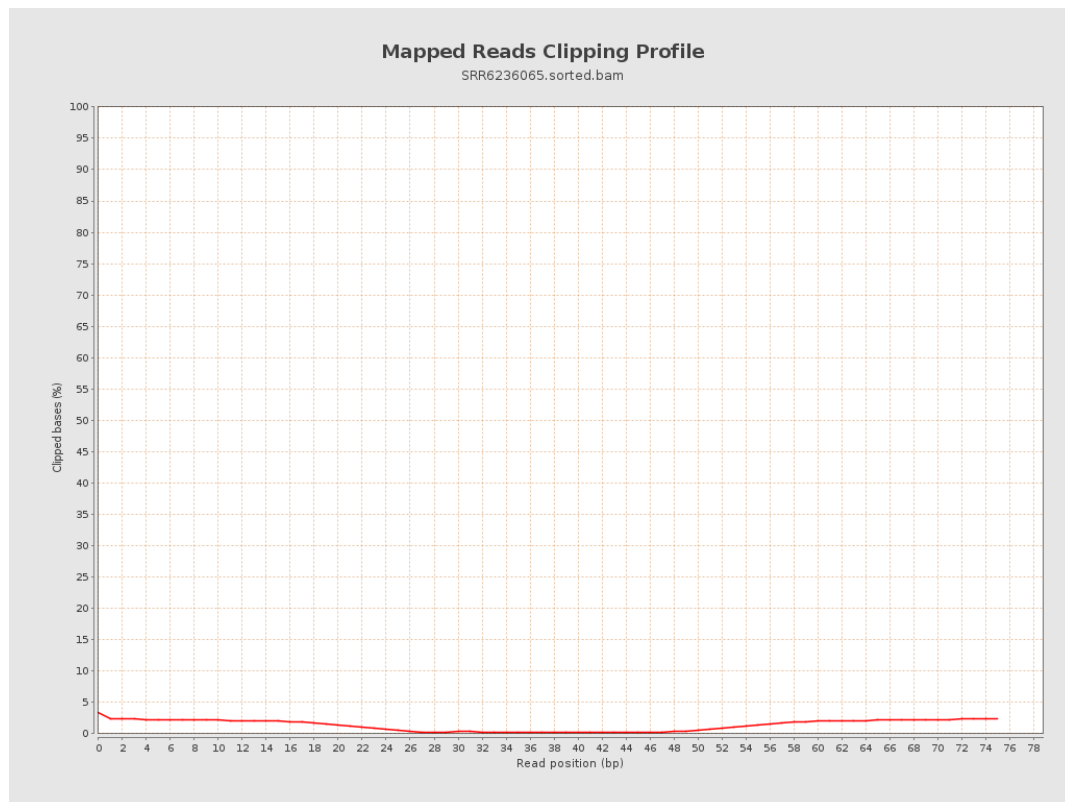
8. Results : Mapped Reads Nucleotide Content



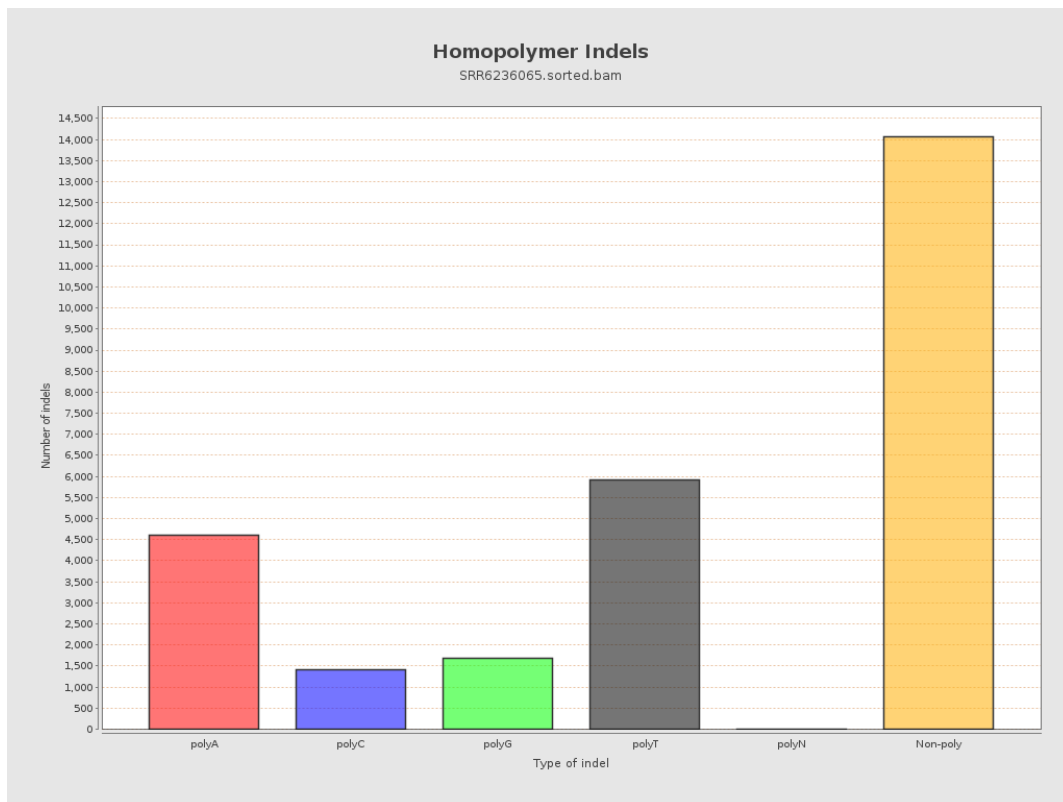
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

