

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 02:19:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231783.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_SRR6231783 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231783.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 02:19:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231783.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,467,356
Mapped reads	3,887,230 / 87.01%
Unmapped reads	580,126 / 12.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,925 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	234,216 / 5.24%
Duplication rate	2.7%
Clipped reads	2,082,589 / 46.62%

2.2. ACGT Content

Number/percentage of A's	73,330,786 / 29.04%
Number/percentage of C's	49,419,596 / 19.57%
Number/percentage of T's	70,710,057 / 28%
Number/percentage of G's	59,028,100 / 23.38%
Number/percentage of N's	18,851 / 0.01%
GC Percentage	42.95%

2.3. Coverage

Mean	0.0816

Standard Deviation	11.9932
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2.4. Mapping Quality

Mean Mapping Quality	43.75
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2.5. Mismatches and indels

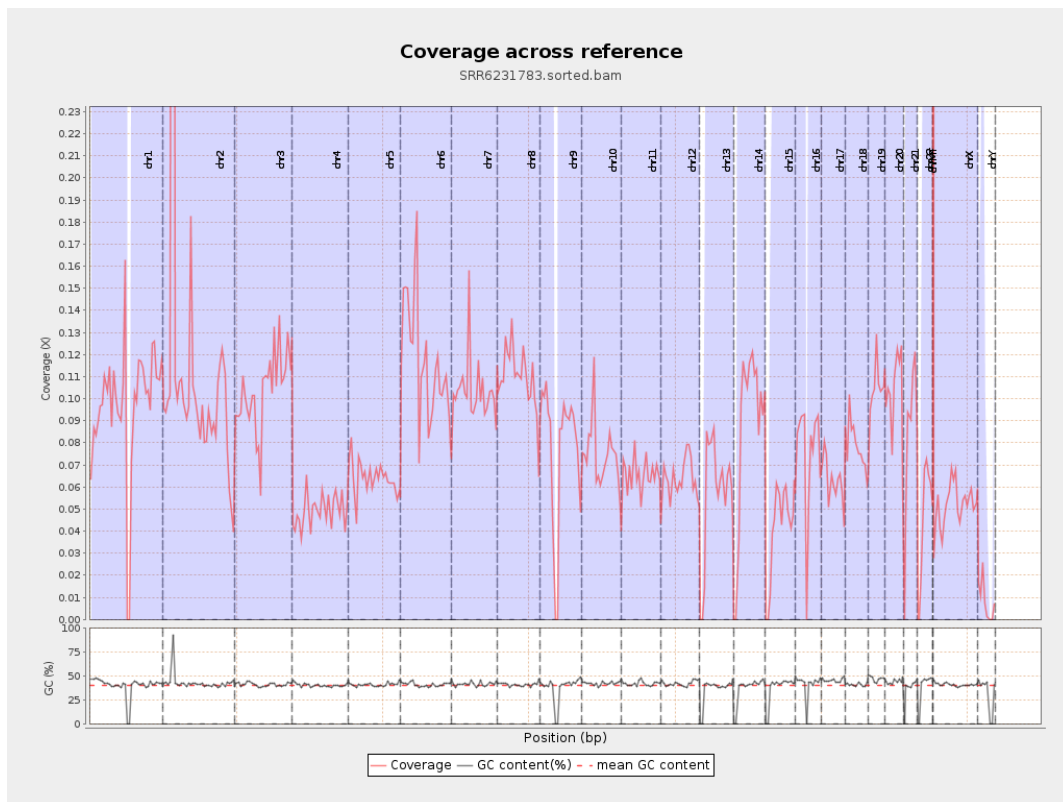
General error rate	0.64%
Mismatches	1,577,497
Insertions	17,988
Mapped reads with at least one insertion	0.46%
Deletions	54,361
Mapped reads with at least one deletion	1.38%
Homopolymer indels	44.18%

2.6. Chromosome stats

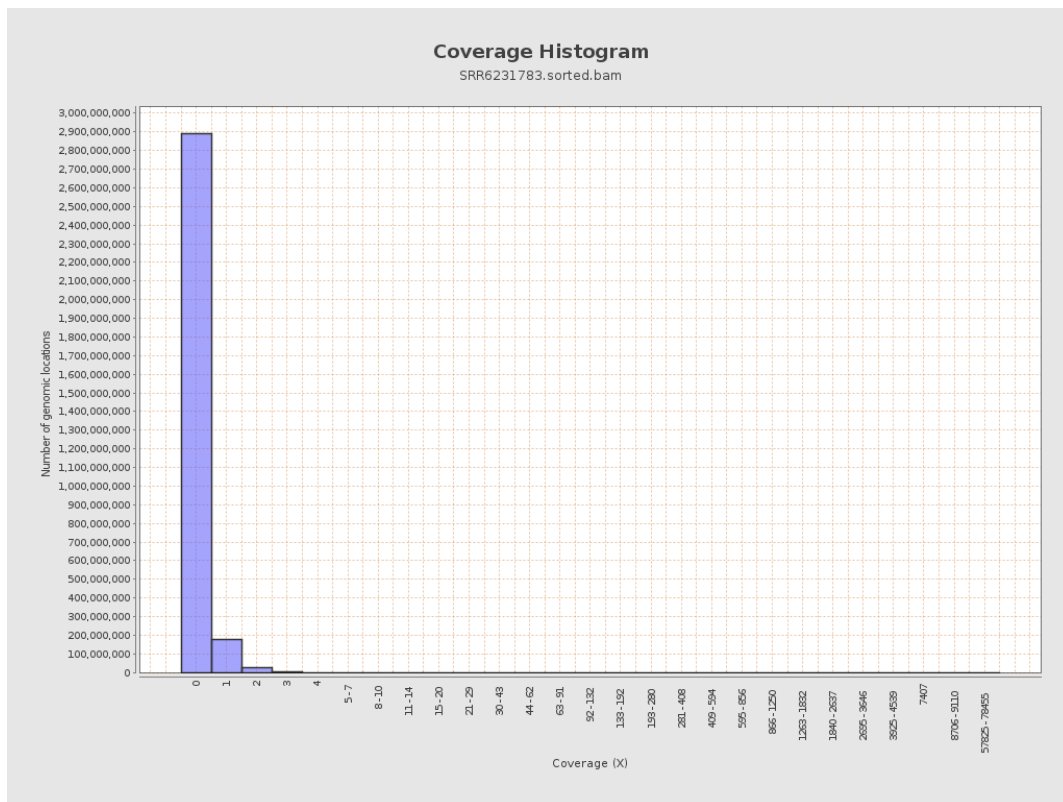
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	24250705	0.0973	1.6902
chr2	243199373	29863565	0.1228	42.7176
chr3	198022430	20446292	0.1033	0.3659
chr4	191154276	9444849	0.0494	0.2714
chr5	180915260	11635882	0.0643	0.3
chr6	171115067	20106205	0.1175	0.6008
chr7	159138663	16373069	0.1029	1.0088

chr8	146364022	16047267	0.1096	0.8395
chr9	141213431	10973208	0.0777	0.5535
chr10	135534747	10109659	0.0746	0.568
chr11	135006516	8793123	0.0651	0.5042
chr12	133851895	8546172	0.0638	0.2976
chr13	115169878	6602281	0.0573	0.2699
chr14	107349540	9446300	0.088	0.4595
chr15	102531392	4151015	0.0405	0.2312
chr16	90354753	6626786	0.0733	0.3839
chr17	81195210	5153142	0.0635	0.3315
chr18	78077248	6169109	0.079	1.137
chr19	59128983	6197237	0.1048	0.987
chr20	63025520	6571703	0.1043	0.3899
chr21	48129895	3999305	0.0831	0.3471
chr22	51304566	2352467	0.0459	0.2419
chrMT	16571	163086	9.8417	5.8839
chrX	155270560	8085248	0.0521	0.3214
chrY	59373566	490750	0.0083	0.1523

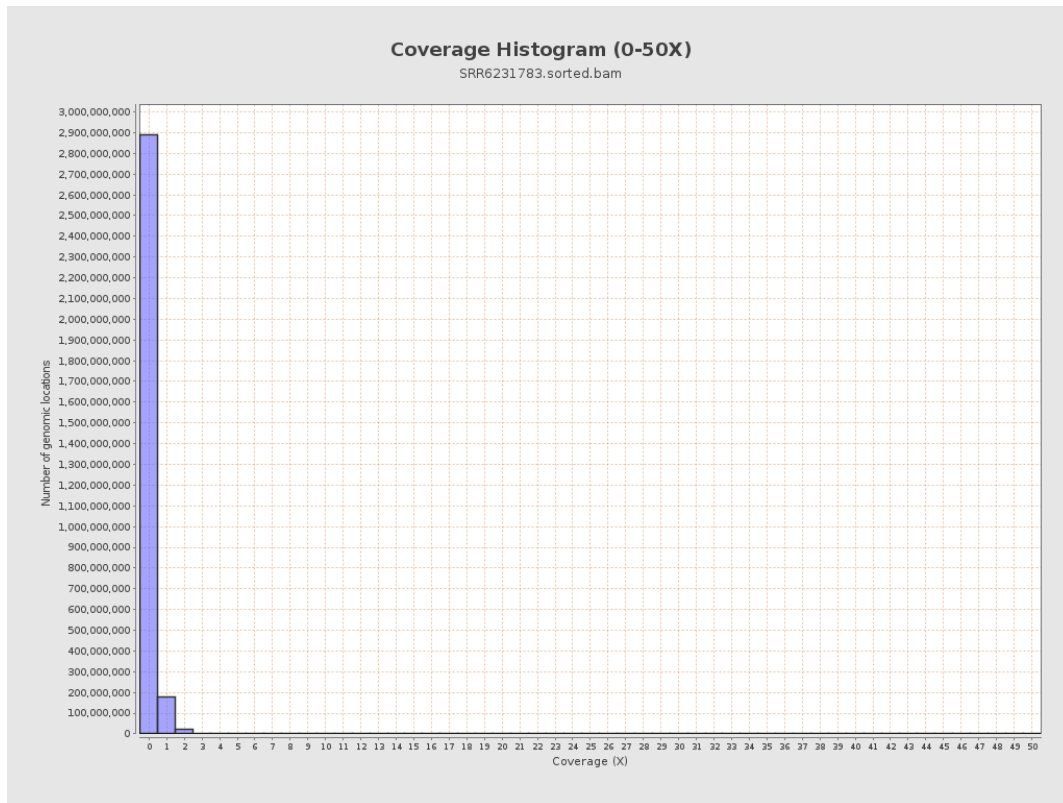
3. Results : Coverage across reference



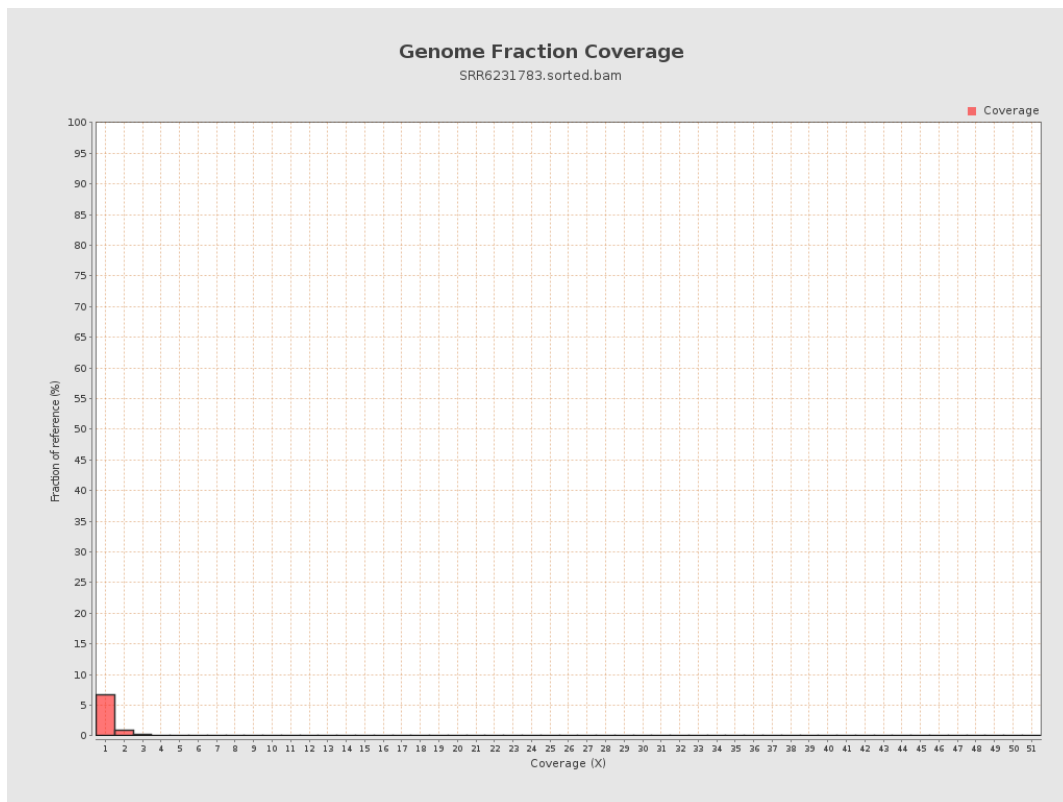
4. Results : Coverage Histogram



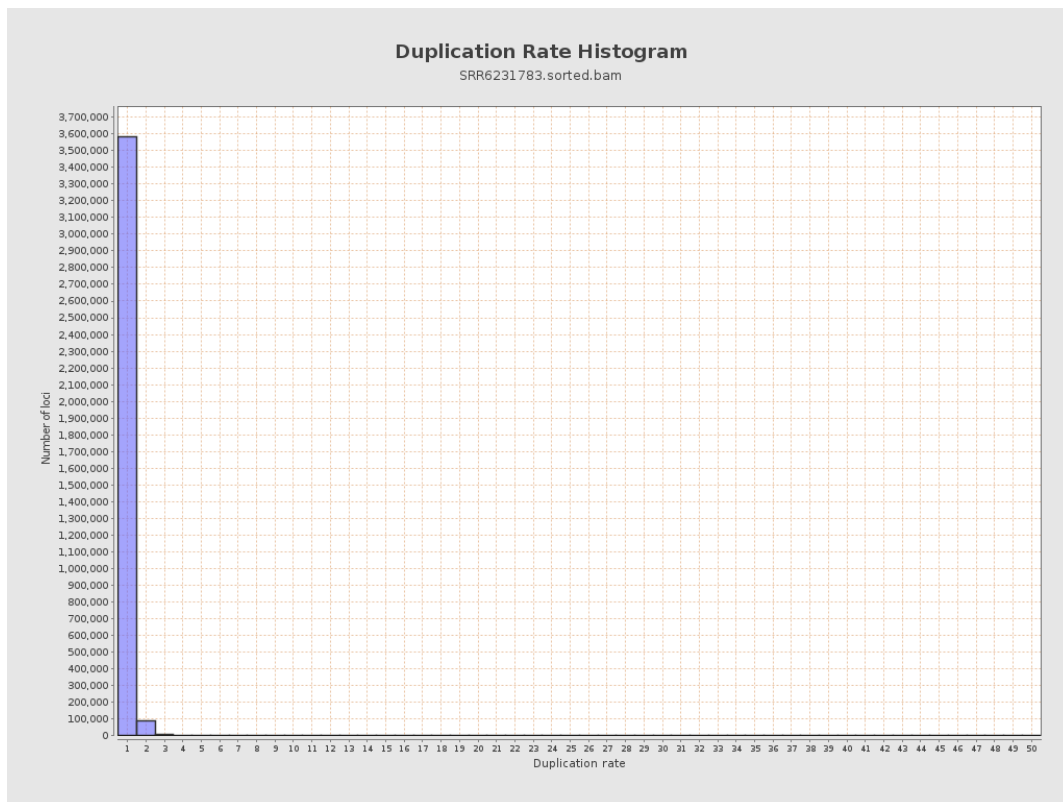
5. Results : Coverage Histogram (0-50X)



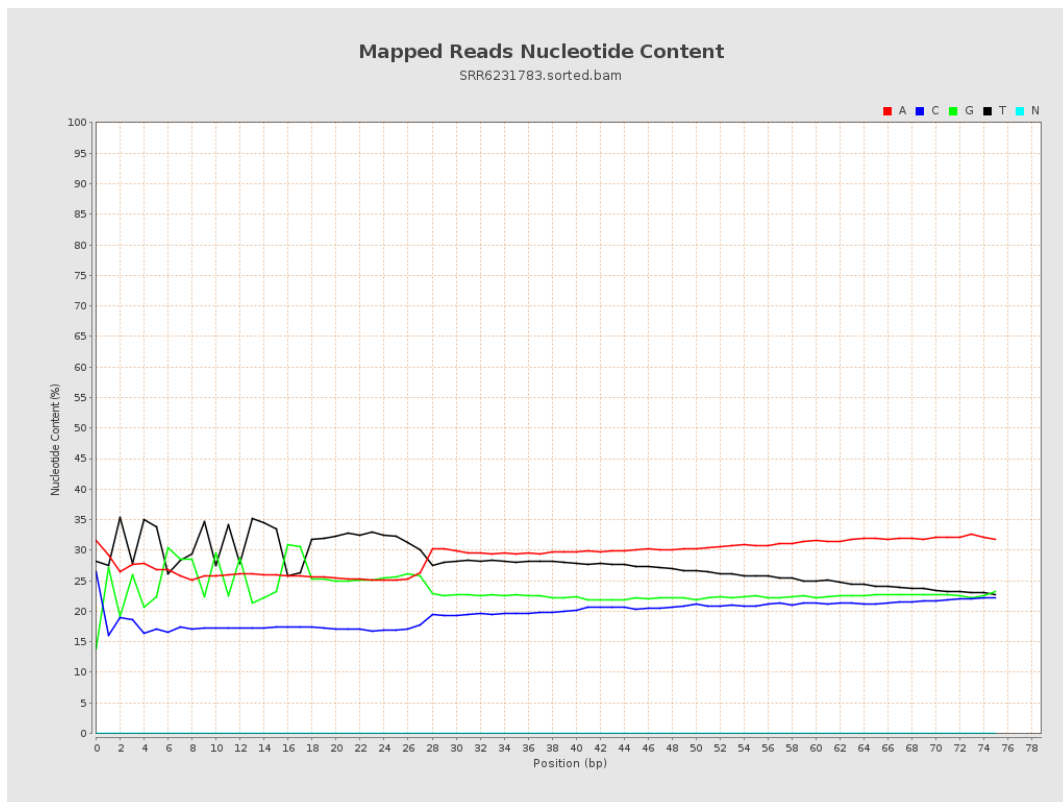
6. Results : Genome Fraction Coverage



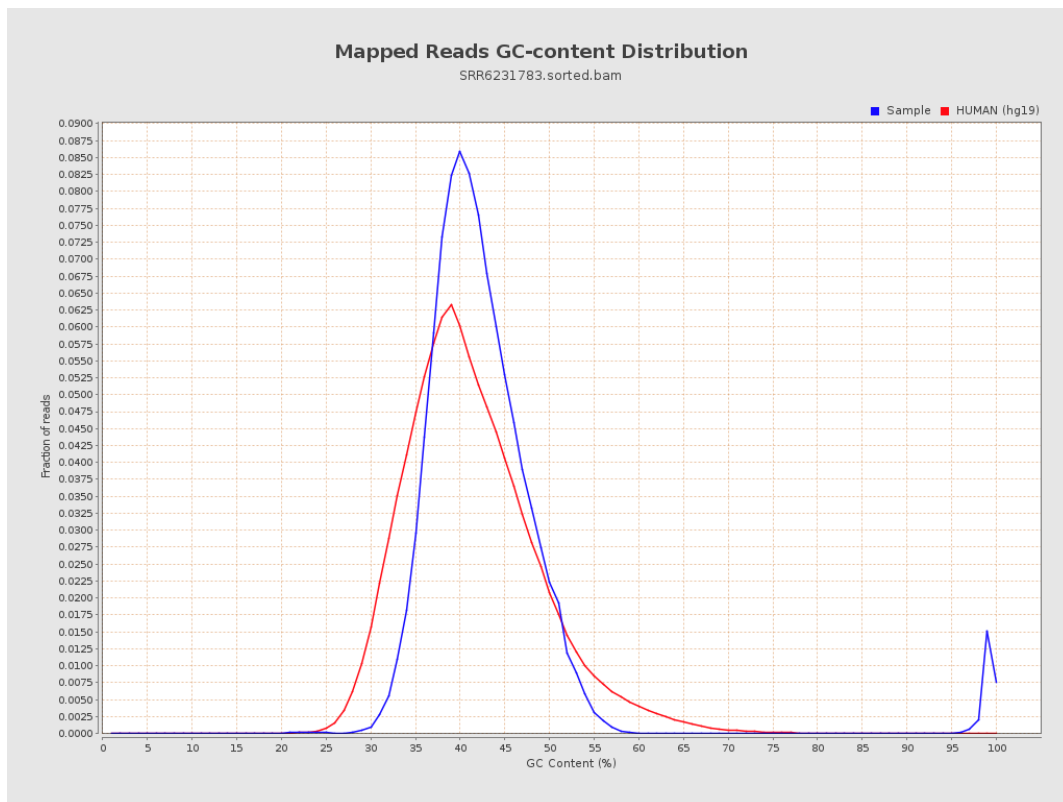
7. Results : Duplication Rate Histogram



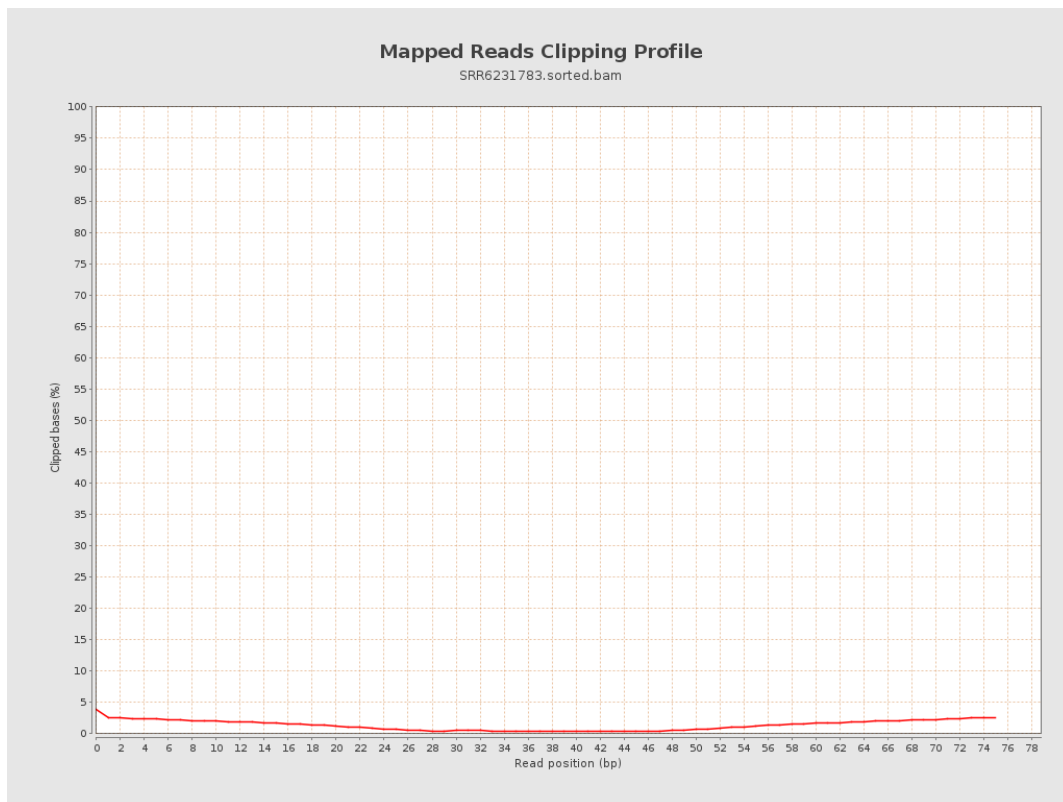
8. Results : Mapped Reads Nucleotide Content



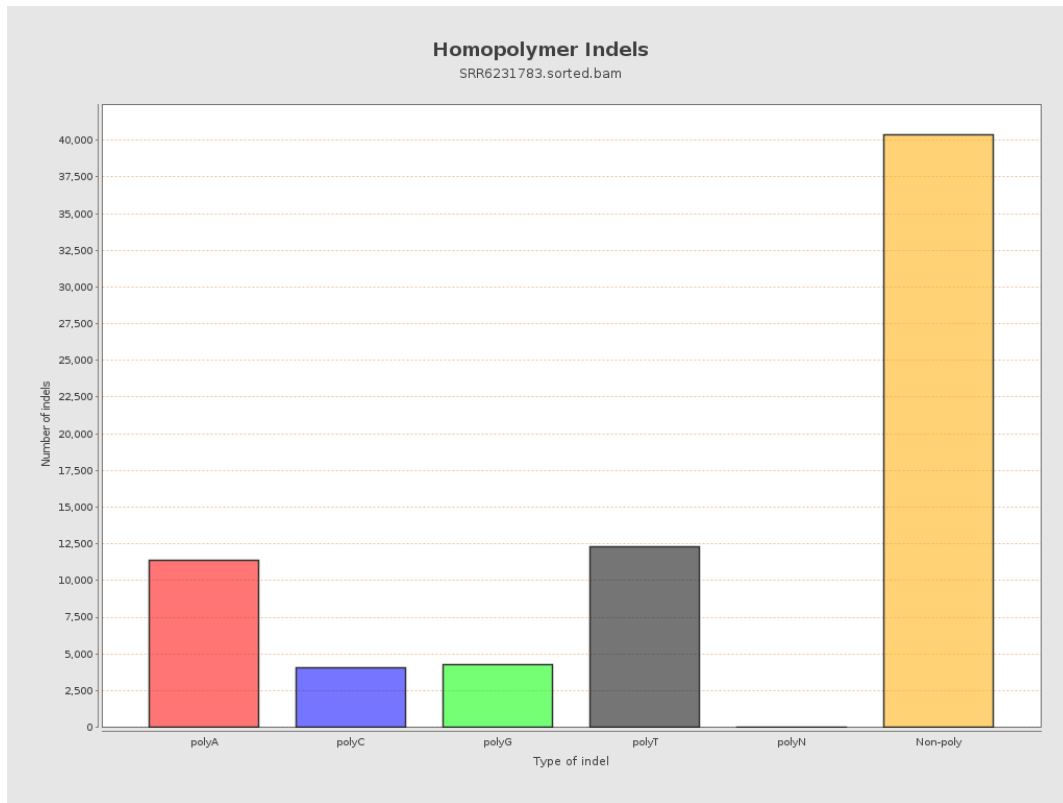
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

