

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 01:21:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231766.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_SRR6231766 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231766.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 01:21:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231766.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,053,688
Mapped reads	707,136 / 67.11%
Unmapped reads	346,552 / 32.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,698 / 0.64%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	57,282 / 5.44%
Duplication rate	6.55%
Clipped reads	363,733 / 34.52%

2.2. ACGT Content

Number/percentage of A's	13,107,176 / 28.57%
Number/percentage of C's	7,714,507 / 16.81%
Number/percentage of T's	15,385,111 / 33.53%
Number/percentage of G's	9,670,430 / 21.08%
Number/percentage of N's	2,004 / 0%
GC Percentage	37.89%

2.3. Coverage

Mean	0.0148

Standard Deviation	0.3117
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2.4. Mapping Quality

Mean Mapping Quality	46.17
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2.5. Mismatches and indels

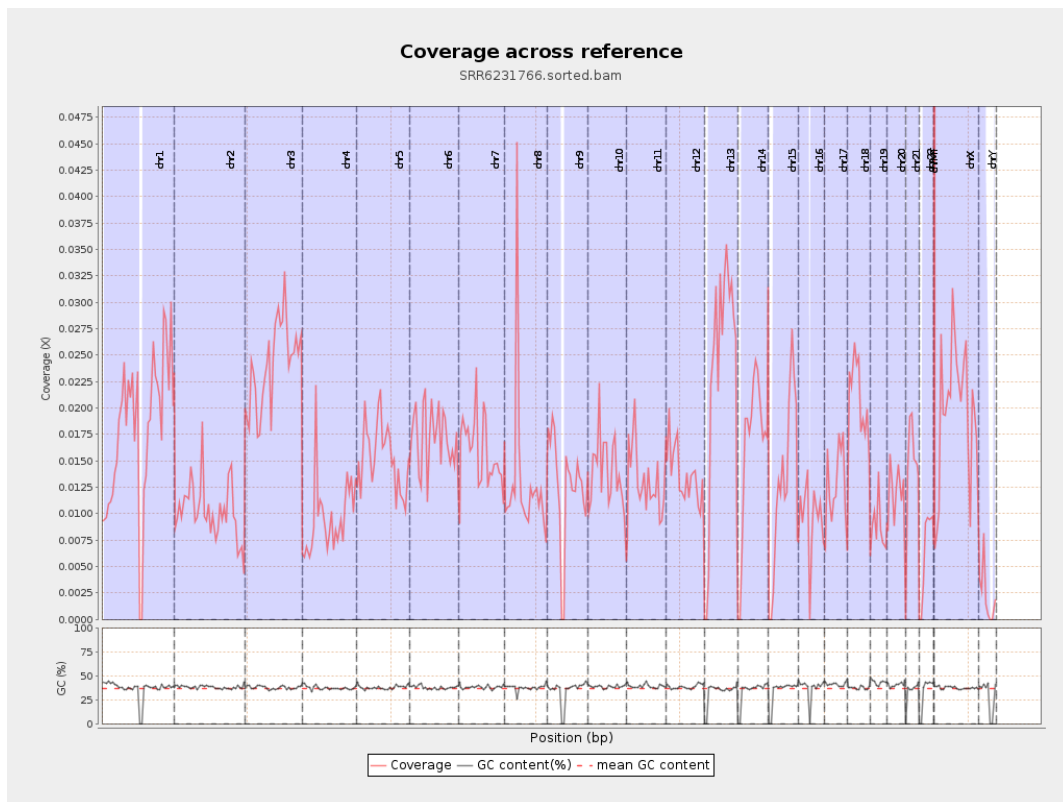
General error rate	0.99%
Mismatches	446,965
Insertions	4,241
Mapped reads with at least one insertion	0.59%
Deletions	20,358
Mapped reads with at least one deletion	2.82%
Homopolymer indels	42.81%

2.6. Chromosome stats

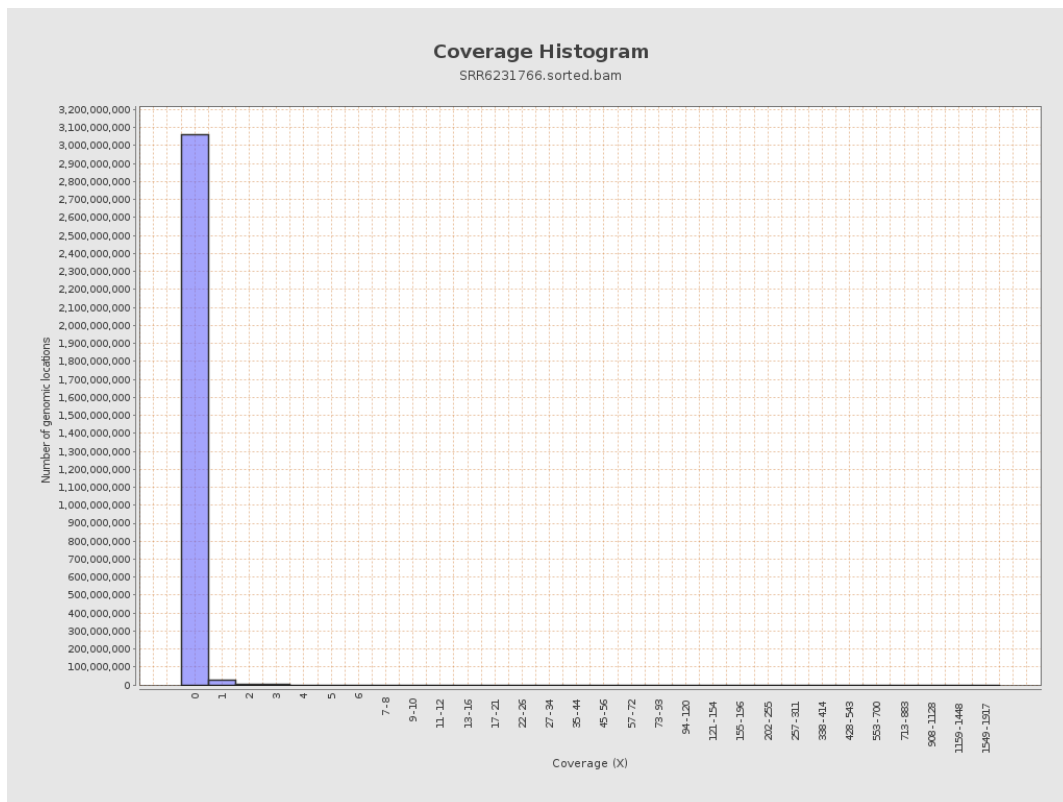
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4477617	0.018	0.2281
chr2	243199373	2493067	0.0103	0.1922
chr3	198022430	4792036	0.0242	0.2044
chr4	191154276	1848104	0.0097	0.1362
chr5	180915260	2788737	0.0154	0.162
chr6	171115067	2928630	0.0171	0.1756
chr7	159138663	2522584	0.0159	0.1971

chr8	146364022	1902466	0.013	1.1891
chr9	141213431	1786489	0.0127	0.1589
chr10	135534747	1868310	0.0138	0.1684
chr11	135006516	1769307	0.0131	0.1592
chr12	133851895	1840235	0.0137	0.1525
chr13	115169878	2734833	0.0237	0.2067
chr14	107349540	1768159	0.0165	0.1663
chr15	102531392	1325864	0.0129	0.1464
chr16	90354753	850844	0.0094	0.1284
chr17	81195210	1016088	0.0125	0.146
chr18	78077248	1635396	0.0209	0.2666
chr19	59128983	527845	0.0089	0.1512
chr20	63025520	757896	0.012	0.1463
chr21	48129895	708108	0.0147	0.1603
chr22	51304566	333888	0.0065	0.1012
chrMT	16571	47302	2.8545	2.8927
chrX	155270560	3057952	0.0197	0.196
chrY	59373566	133601	0.0023	0.0711

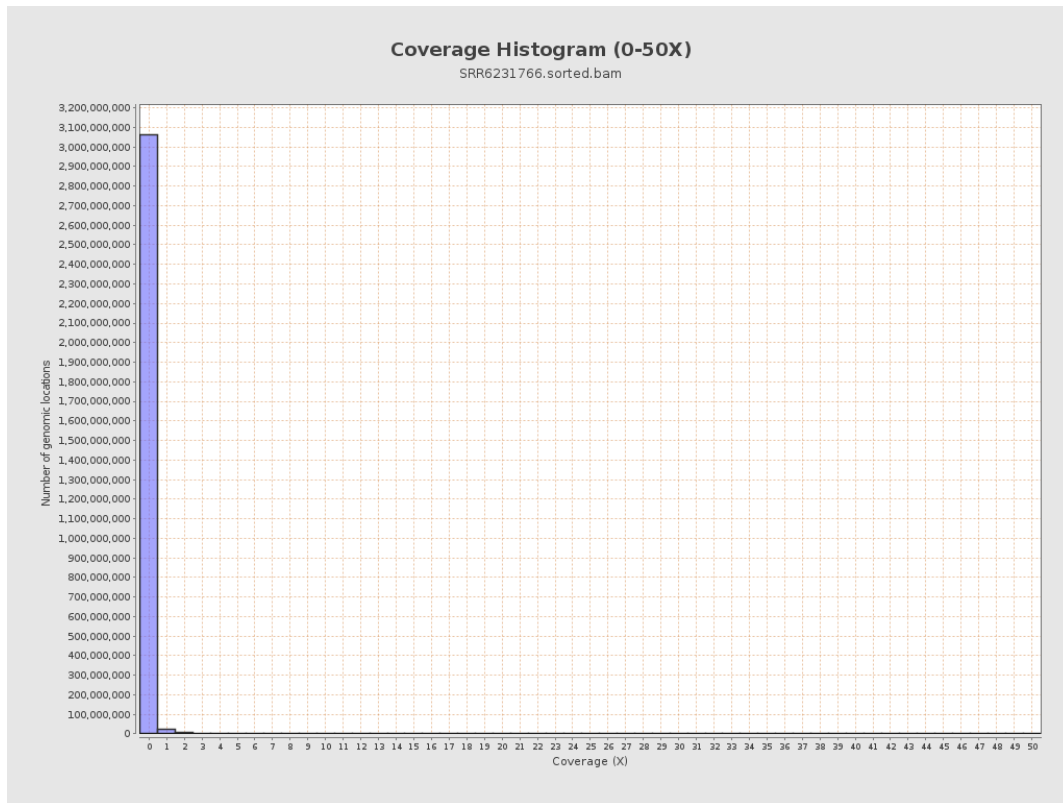
3. Results : Coverage across reference



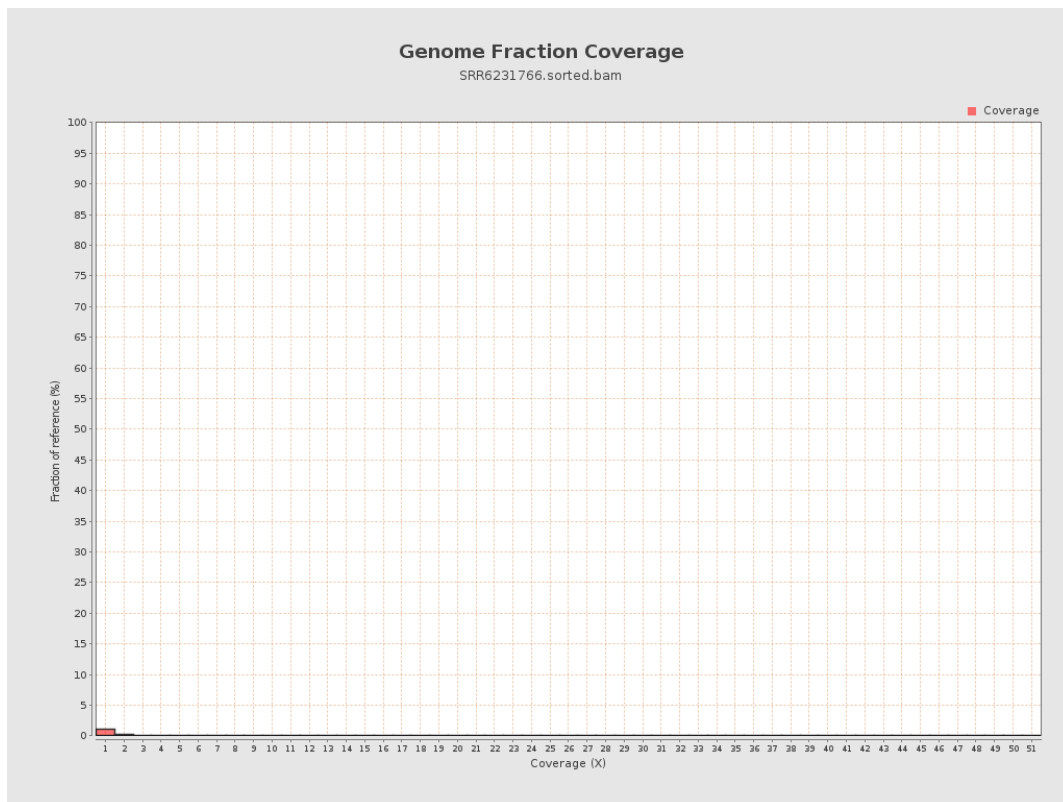
4. Results : Coverage Histogram



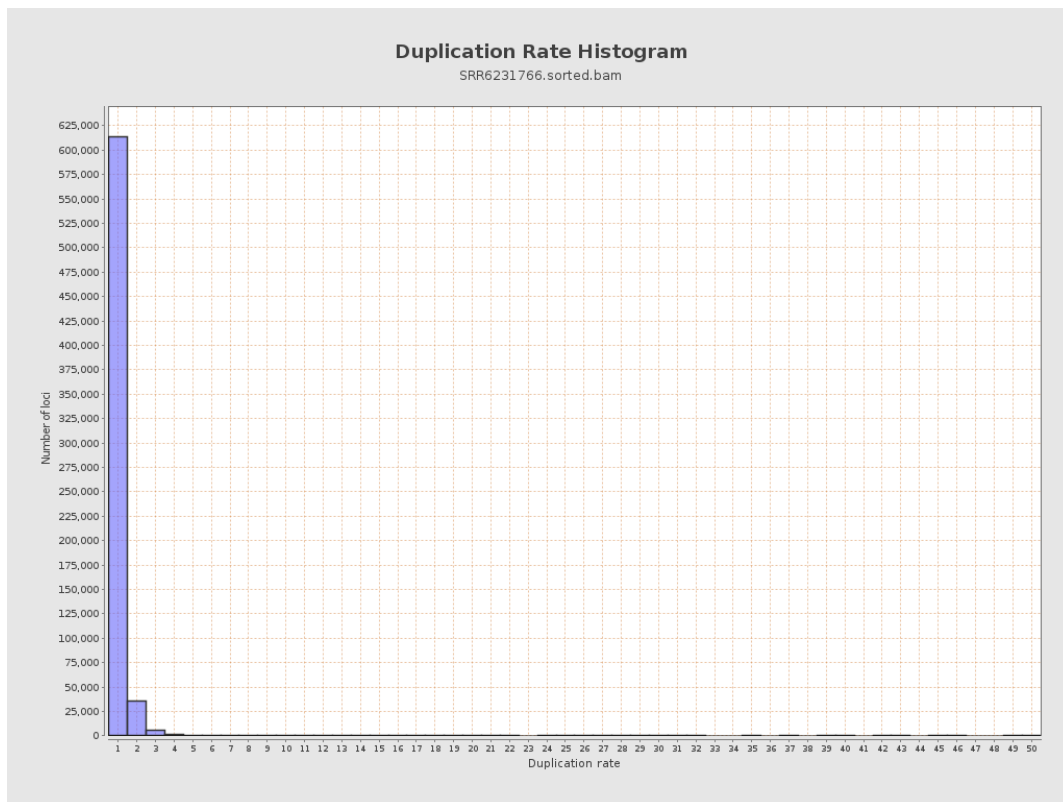
5. Results : Coverage Histogram (0-50X)



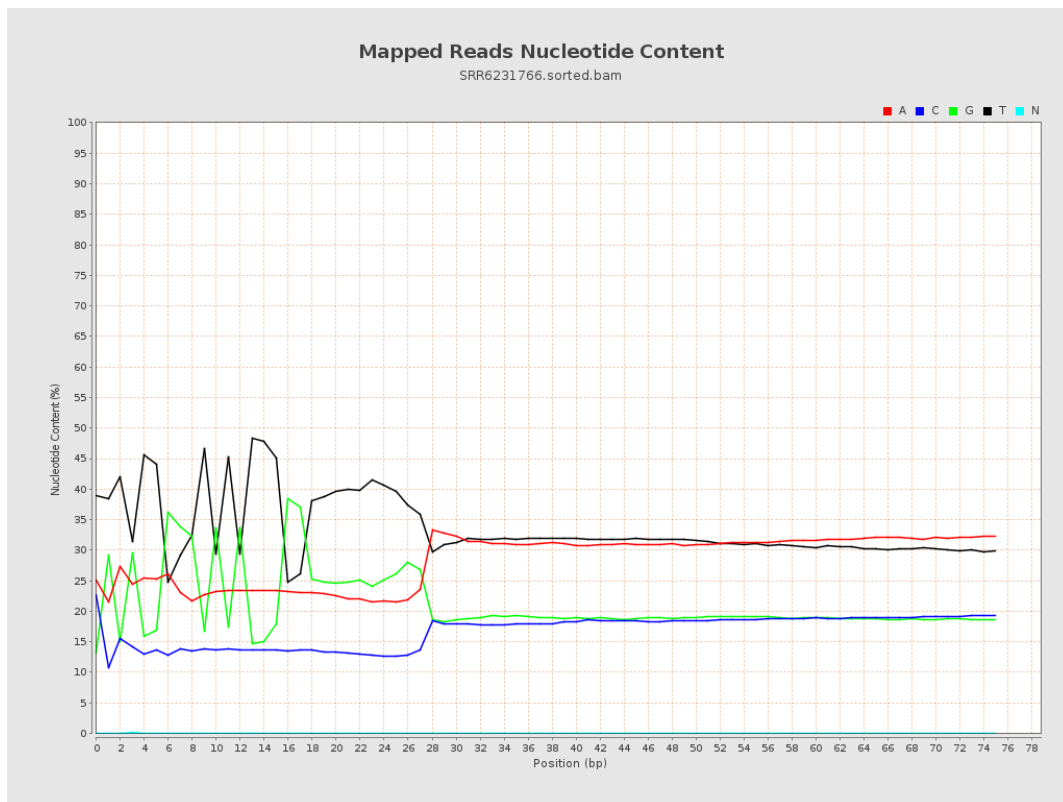
6. Results : Genome Fraction Coverage



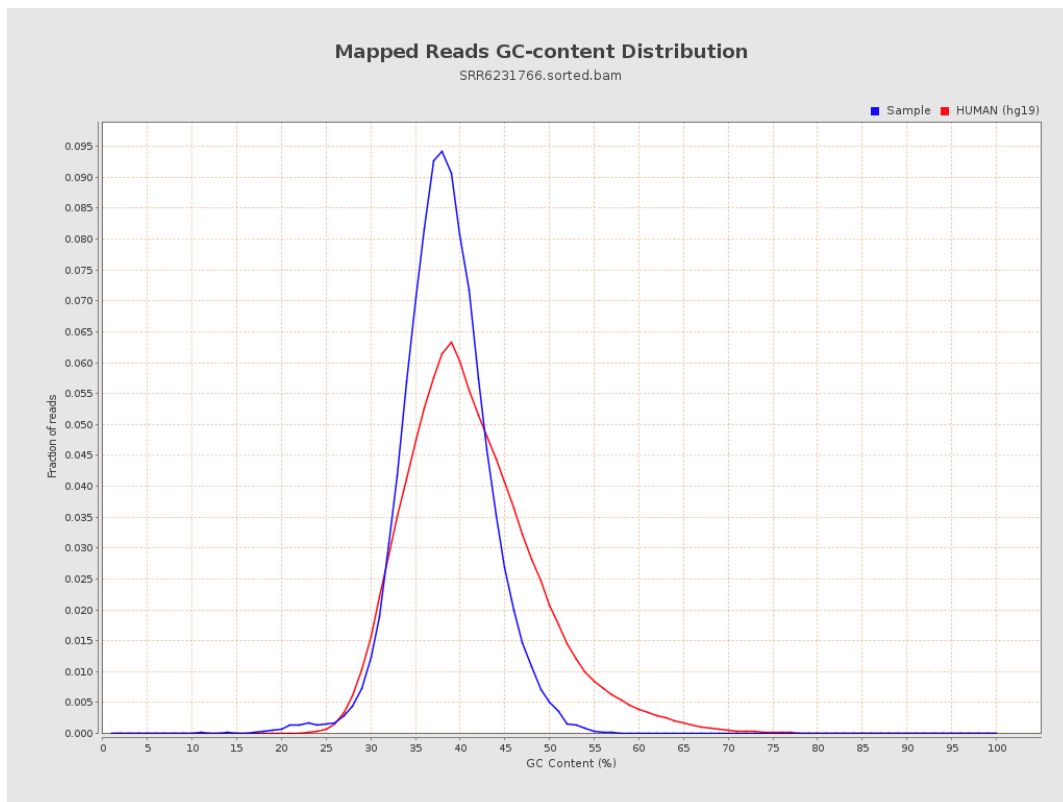
7. Results : Duplication Rate Histogram



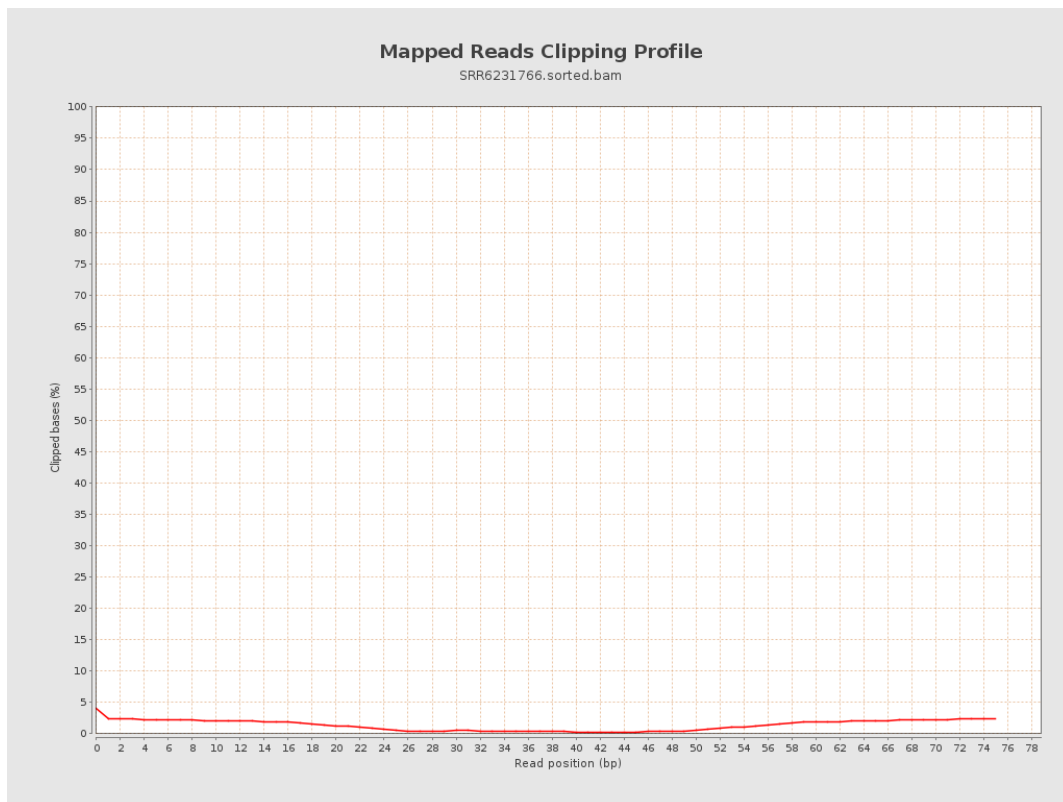
8. Results : Mapped Reads Nucleotide Content



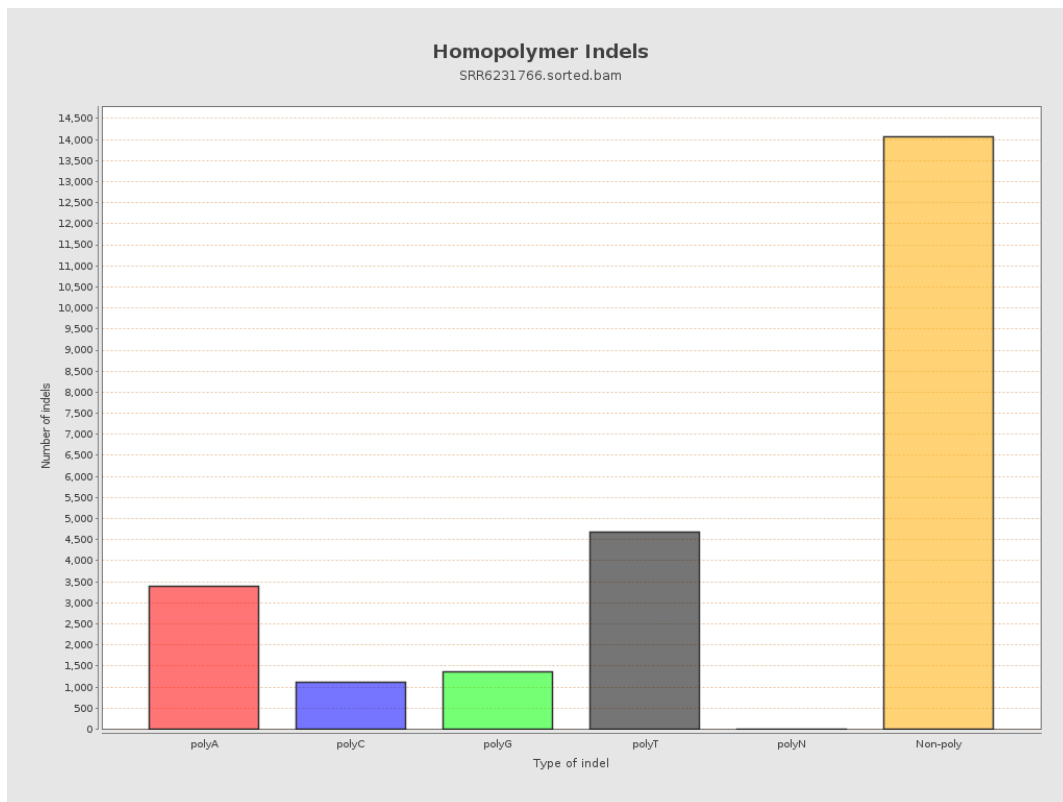
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

