

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 19:16:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236074.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_SRR6236074 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236074.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 19:16:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236074.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,756,352
Mapped reads	2,330,571 / 84.55%
Unmapped reads	425,781 / 15.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,553 / 0.75%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	199,069 / 7.22%
Duplication rate	6.85%
Clipped reads	1,145,053 / 41.54%

2.2. ACGT Content

Number/percentage of A's	42,148,563 / 27.68%
Number/percentage of C's	26,619,927 / 17.48%
Number/percentage of T's	49,995,504 / 32.84%
Number/percentage of G's	33,416,979 / 21.95%
Number/percentage of N's	66,824 / 0.04%
GC Percentage	39.43%

2.3. Coverage

Mean	0.0492

Standard Deviation	0.4918
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	44.49
----------------------	-------

2.5. Mismatches and indels

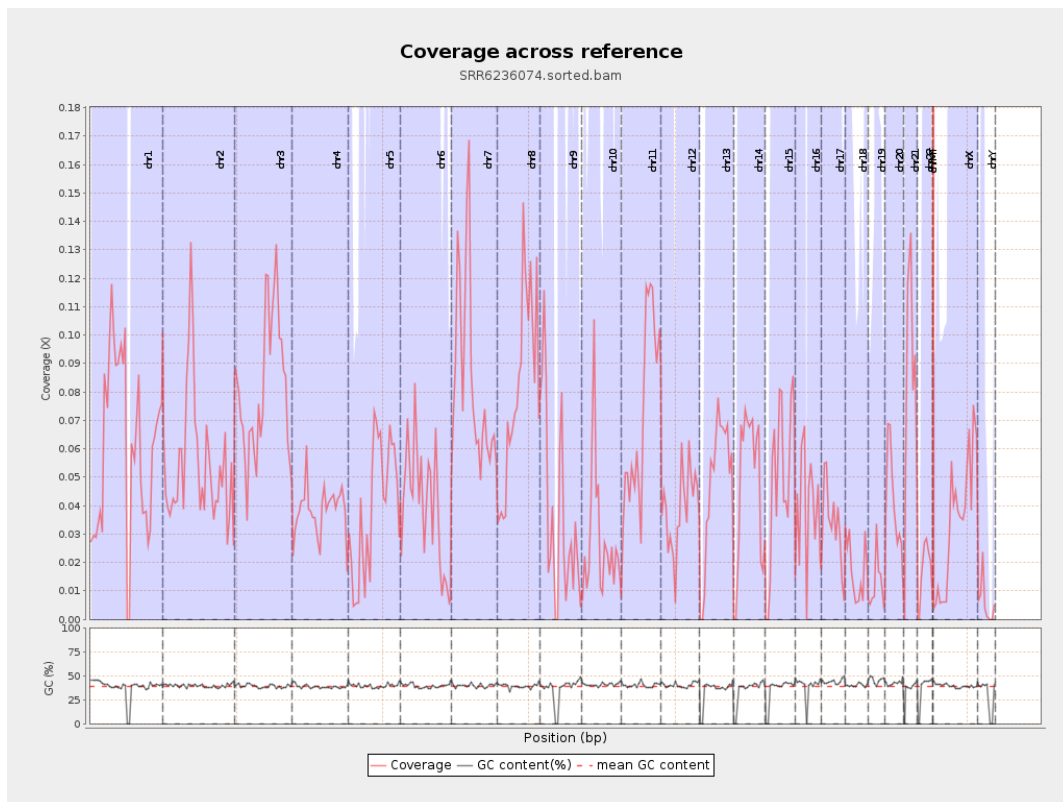
General error rate	0.87%
Mismatches	1,306,273
Insertions	10,930
Mapped reads with at least one insertion	0.47%
Deletions	50,708
Mapped reads with at least one deletion	2.15%
Homopolymer indels	45.27%

2.6. Chromosome stats

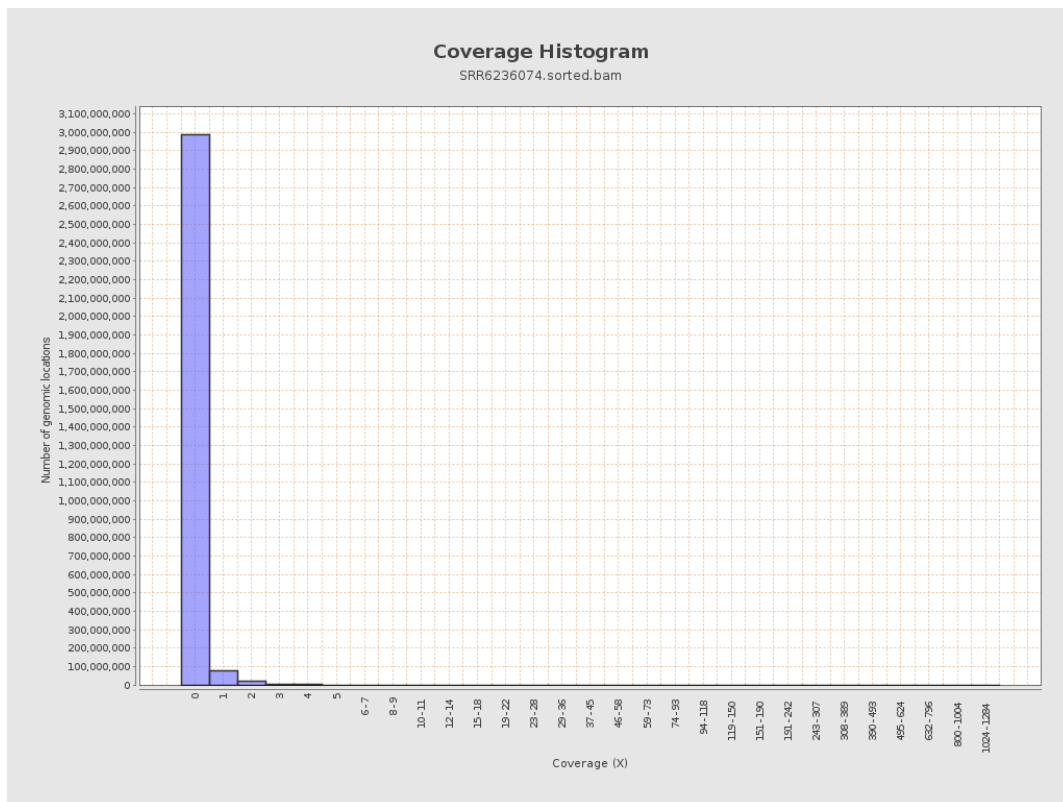
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15115625	0.0606	0.7159
chr2	243199373	13363214	0.0549	0.51
chr3	198022430	16017532	0.0809	0.3826
chr4	191154276	7317195	0.0383	0.2861
chr5	180915260	7215184	0.0399	0.2664
chr6	171115067	6857767	0.0401	0.2896
chr7	159138663	13387409	0.0841	1.0486

chr8	146364022	11939296	0.0816	0.8712
chr9	141213431	5144136	0.0364	0.3561
chr10	135534747	3655835	0.027	0.4702
chr11	135006516	9690283	0.0718	0.4211
chr12	133851895	5247316	0.0392	0.2669
chr13	115169878	5569910	0.0484	0.2916
chr14	107349540	5164460	0.0481	0.2978
chr15	102531392	4998620	0.0488	0.2924
chr16	90354753	3447392	0.0382	0.2899
chr17	81195210	2774725	0.0342	0.3148
chr18	78077248	1348355	0.0173	0.534
chr19	59128983	744240	0.0126	0.581
chr20	63025520	2657255	0.0422	0.2806
chr21	48129895	3959913	0.0823	0.4001
chr22	51304566	893209	0.0174	0.1678
chrMT	16571	233810	14.1096	8.9686
chrX	155270560	5230504	0.0337	0.2627
chrY	59373566	362683	0.0061	0.1797

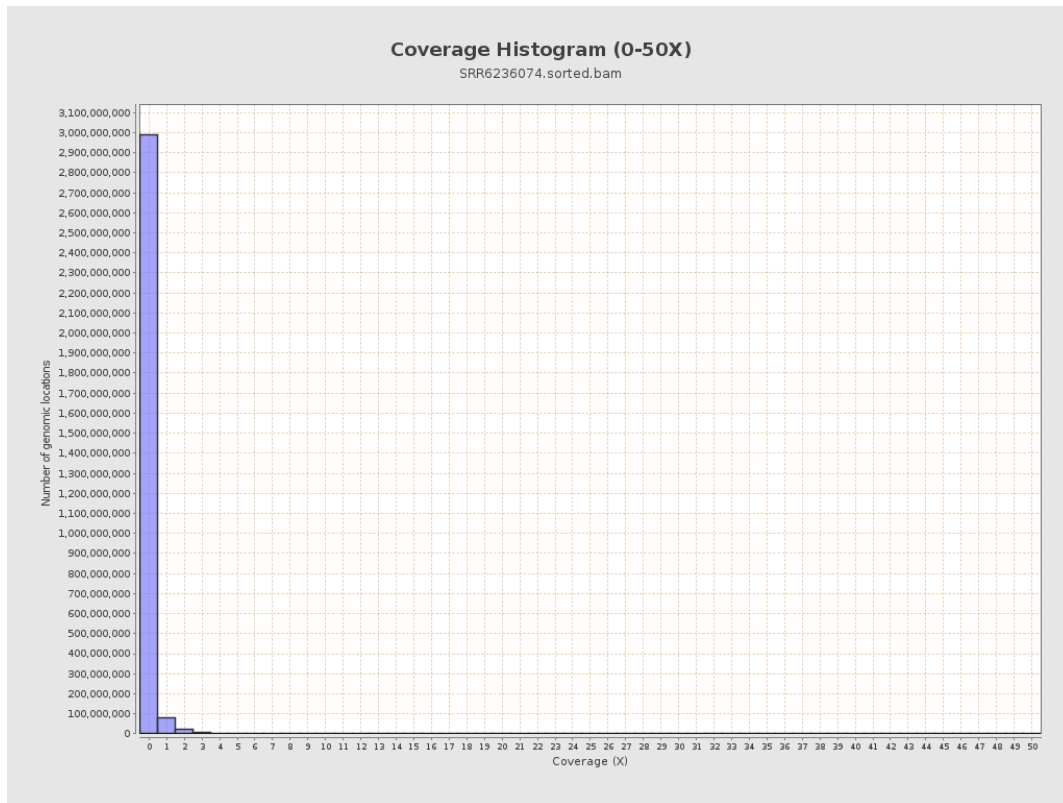
3. Results : Coverage across reference



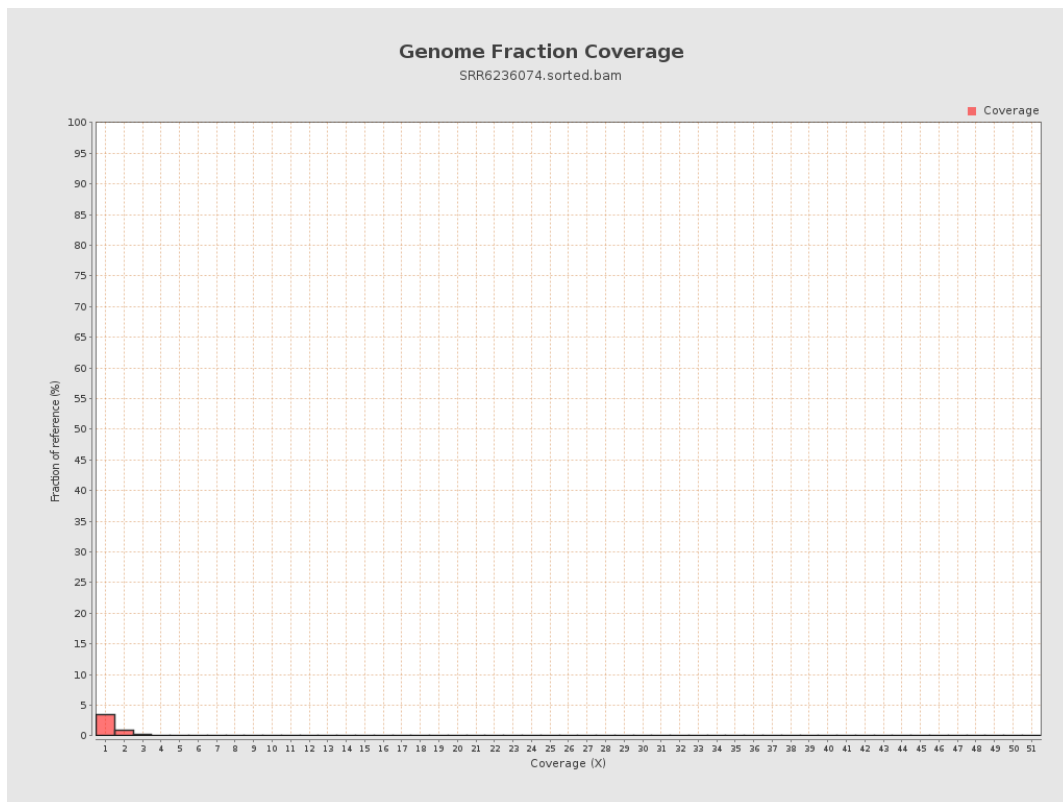
4. Results : Coverage Histogram



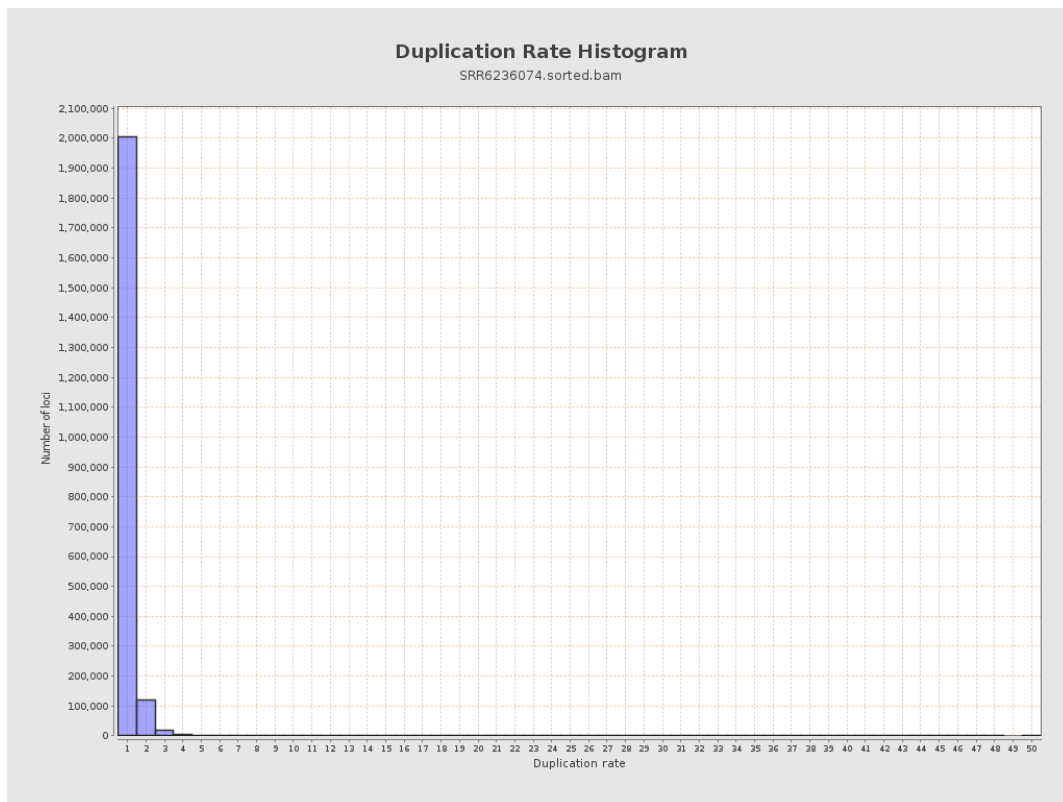
5. Results : Coverage Histogram (0-50X)



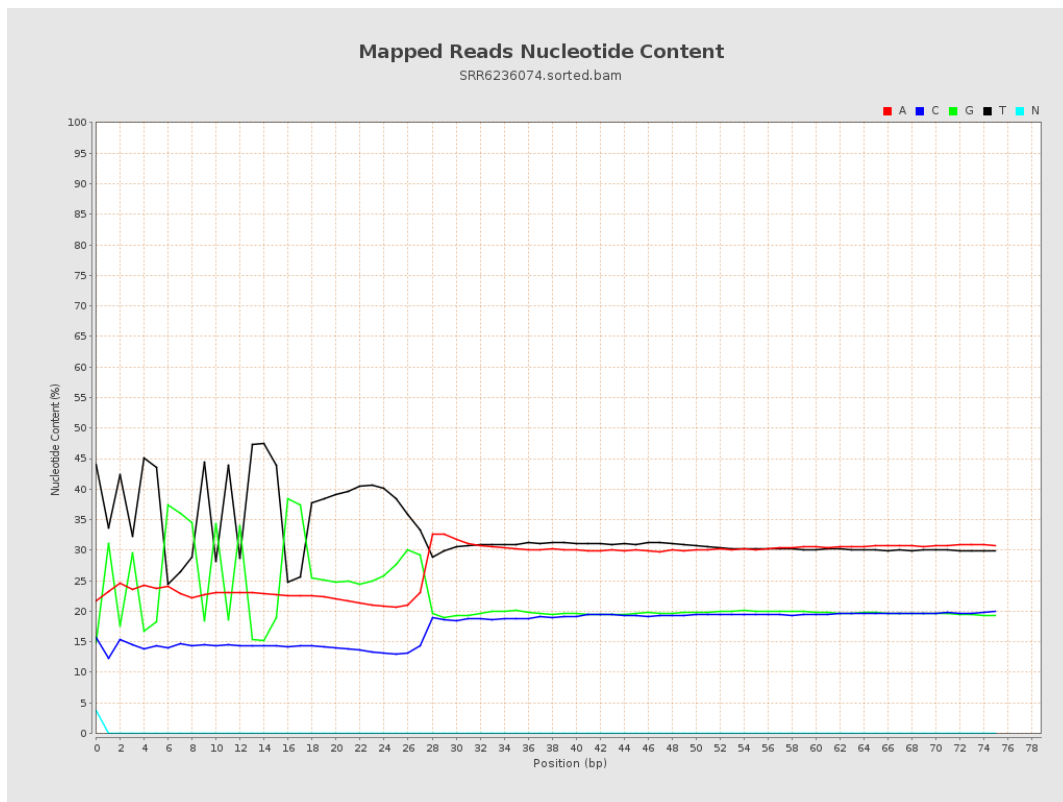
6. Results : Genome Fraction Coverage



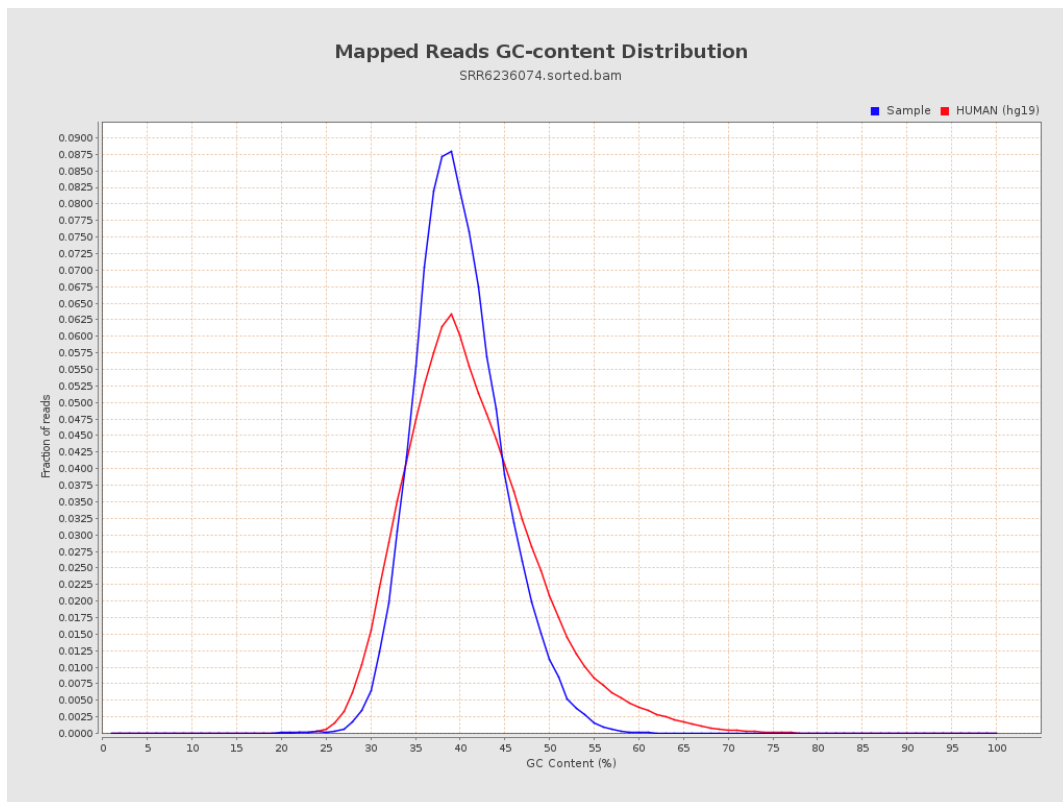
7. Results : Duplication Rate Histogram



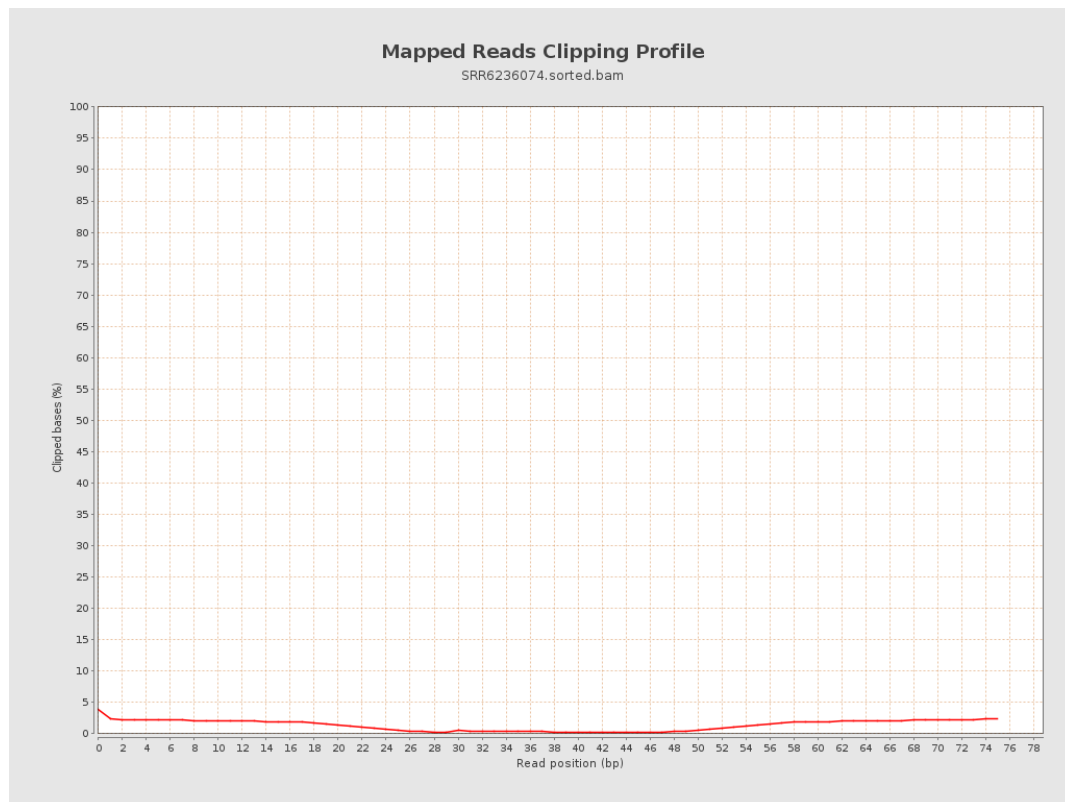
8. Results : Mapped Reads Nucleotide Content



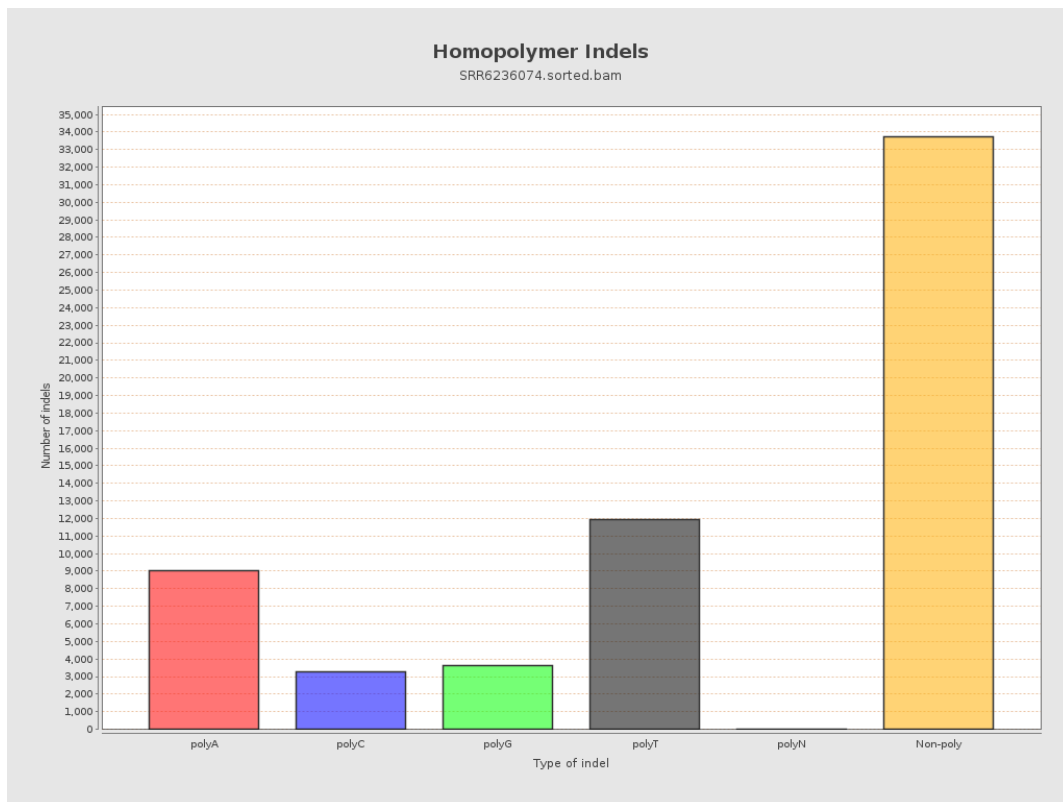
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

