

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 21:15:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236114.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_SRR6236114 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236114.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 21:15:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236114.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,655,363
Mapped reads	1,419,968 / 85.78%
Unmapped reads	235,395 / 14.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,614 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	52,684 / 3.18%
Duplication rate	3.14%
Clipped reads	617,307 / 37.29%

2.2. ACGT Content

Number/percentage of A's	26,547,203 / 28.06%
Number/percentage of C's	16,776,396 / 17.73%
Number/percentage of T's	30,607,455 / 32.35%
Number/percentage of G's	20,633,239 / 21.81%
Number/percentage of N's	51,971 / 0.05%
GC Percentage	39.54%

2.3. Coverage

Mean	0.0306

Standard Deviation	0.2755
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2.4. Mapping Quality

Mean Mapping Quality	45.87
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2.5. Mismatches and indels

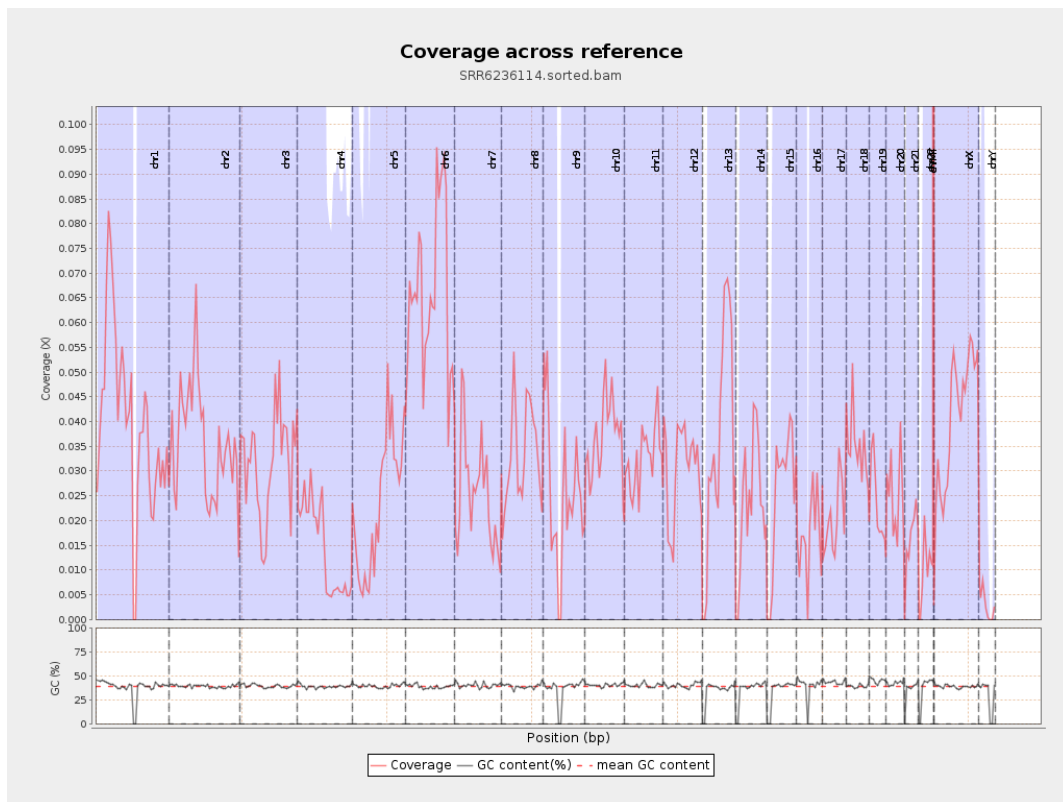
General error rate	0.86%
Mismatches	798,269
Insertions	6,638
Mapped reads with at least one insertion	0.46%
Deletions	35,408
Mapped reads with at least one deletion	2.46%
Homopolymer indels	46.18%

2.6. Chromosome stats

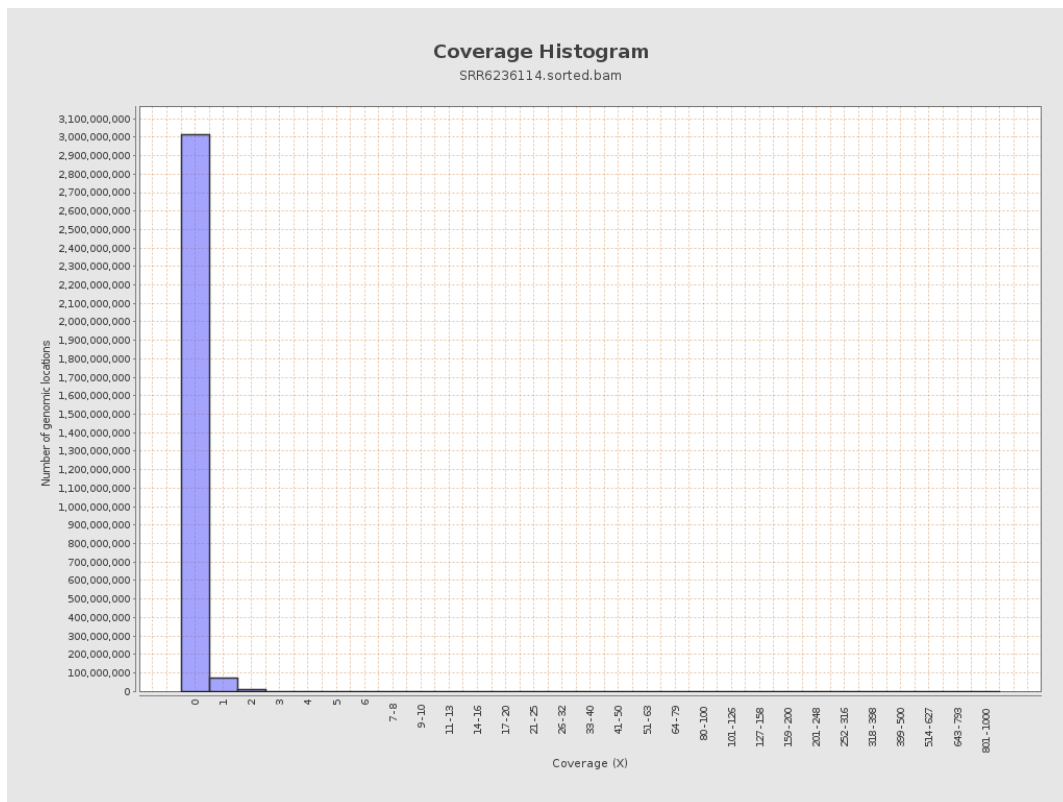
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9956356	0.0399	0.403
chr2	243199373	8714884	0.0358	0.2871
chr3	198022430	6209431	0.0314	0.1958
chr4	191154276	2739808	0.0143	0.1374
chr5	180915260	4182996	0.0231	0.1695
chr6	171115067	11214630	0.0655	0.3472
chr7	159138663	4040333	0.0254	0.2197

chr8	146364022	4797582	0.0328	0.6671
chr9	141213431	3505572	0.0248	0.2068
chr10	135534747	5045021	0.0372	0.2437
chr11	135006516	4361097	0.0323	0.2183
chr12	133851895	4114718	0.0307	0.1959
chr13	115169878	4106203	0.0357	0.2114
chr14	107349540	2486184	0.0232	0.1731
chr15	102531392	2609631	0.0255	0.1807
chr16	90354753	1492430	0.0165	0.1503
chr17	81195210	1622630	0.02	0.1622
chr18	78077248	2760283	0.0354	0.2953
chr19	59128983	1406268	0.0238	0.2354
chr20	63025520	1589518	0.0252	0.176
chr21	48129895	777712	0.0162	0.1447
chr22	51304566	495754	0.0097	0.1067
chrMT	16571	47081	2.8412	2.4463
chrX	155270560	6230182	0.0401	0.2323
chrY	59373566	171340	0.0029	0.0699

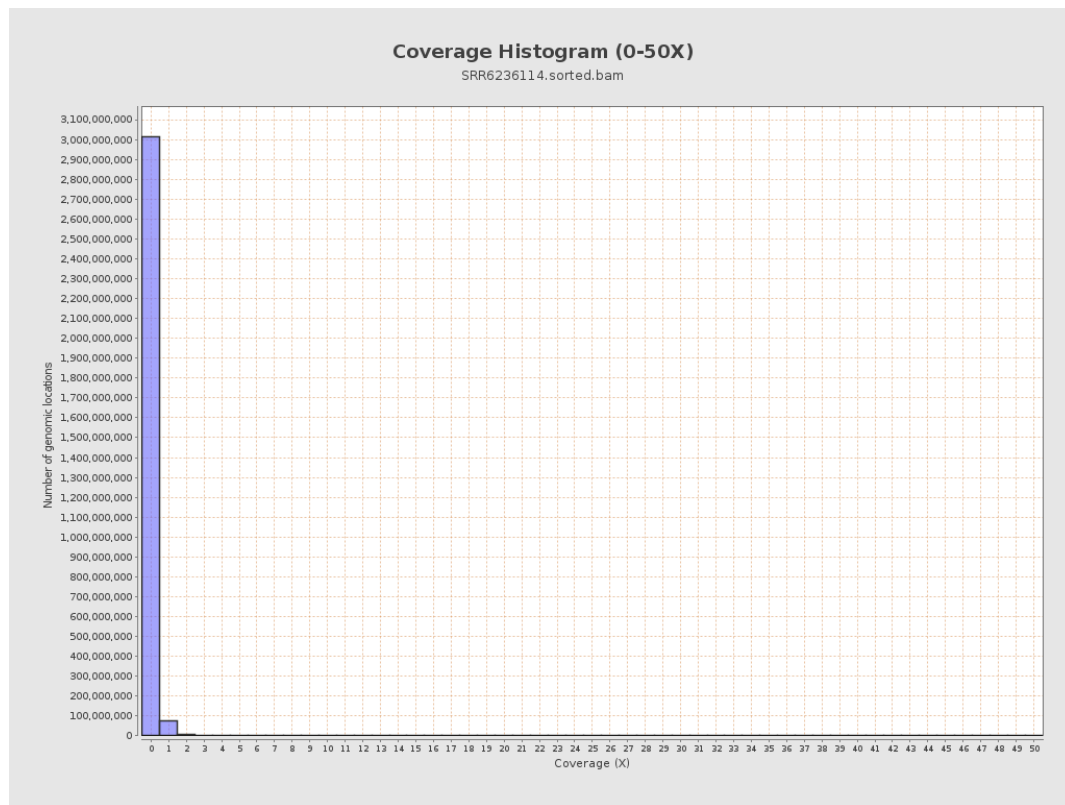
3. Results : Coverage across reference



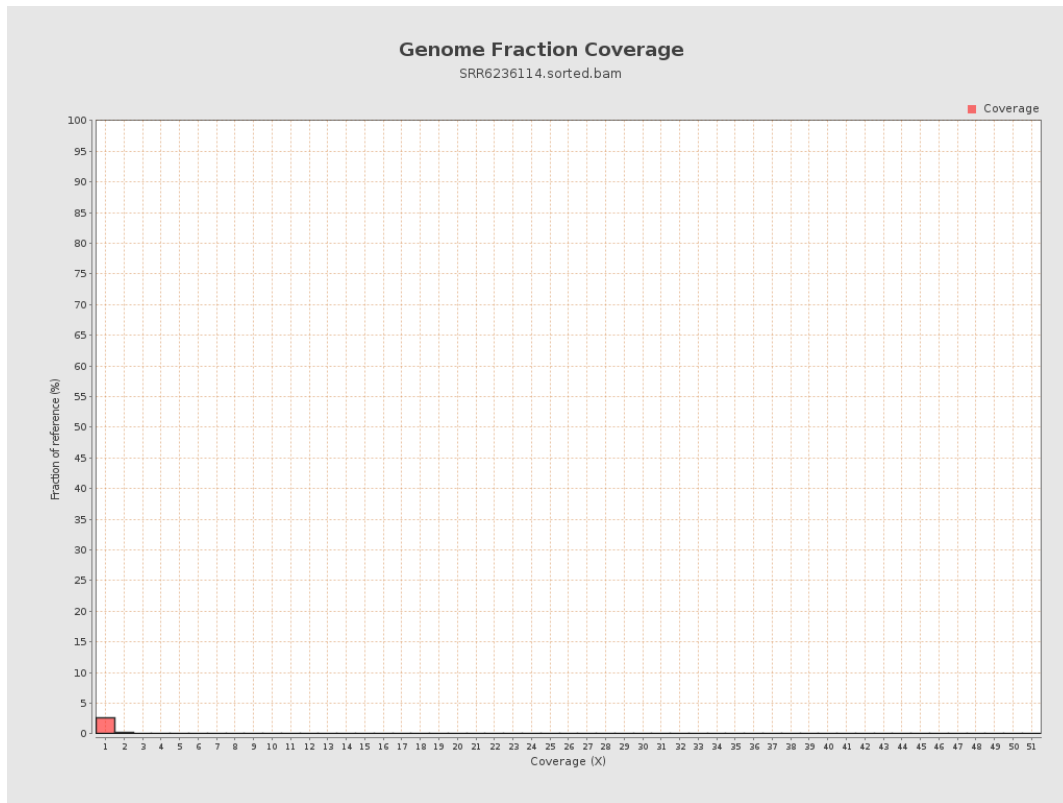
4. Results : Coverage Histogram



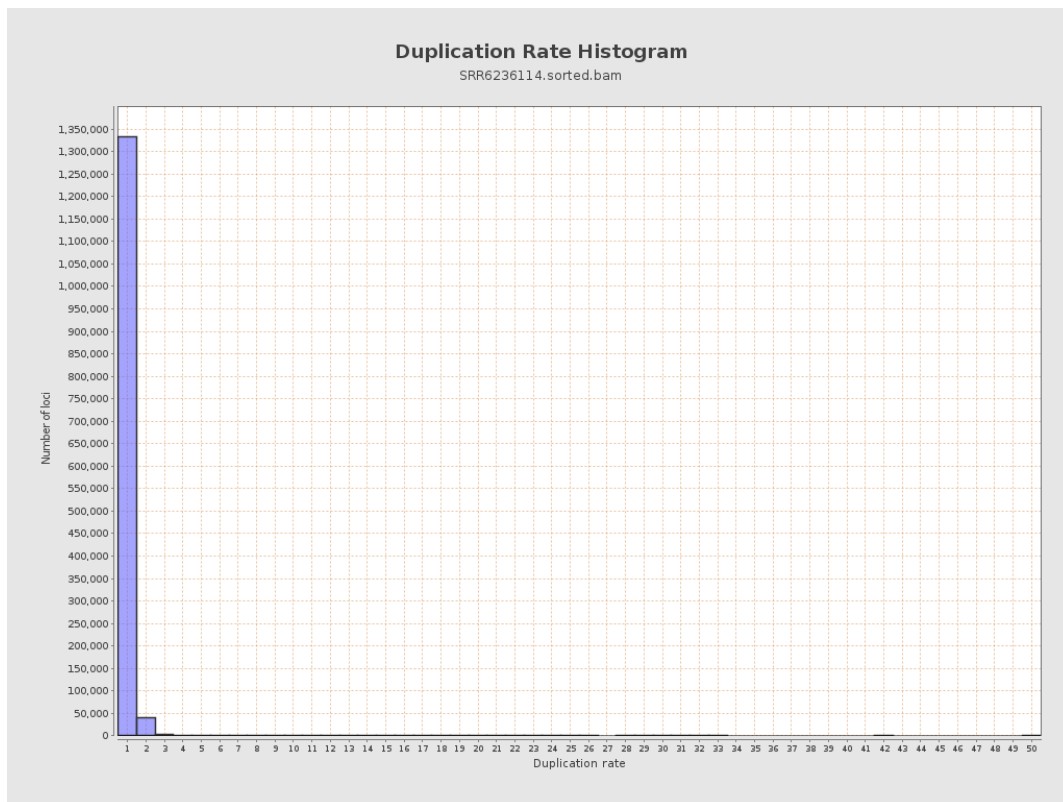
5. Results : Coverage Histogram (0-50X)



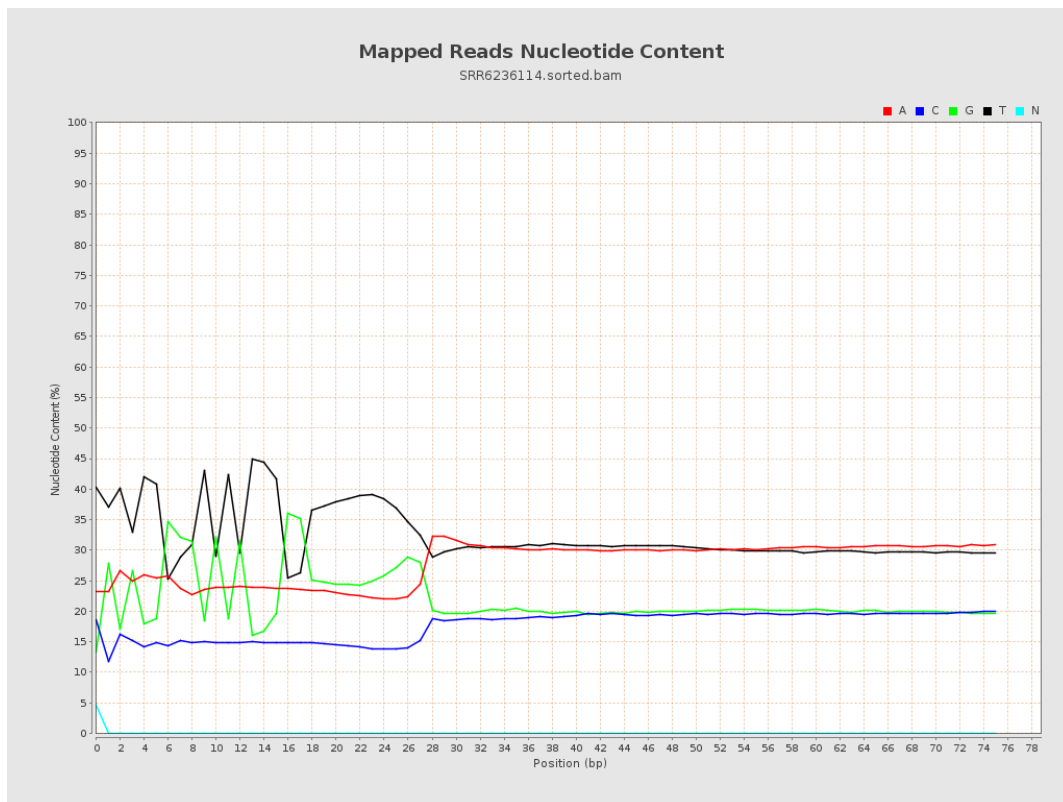
6. Results : Genome Fraction Coverage



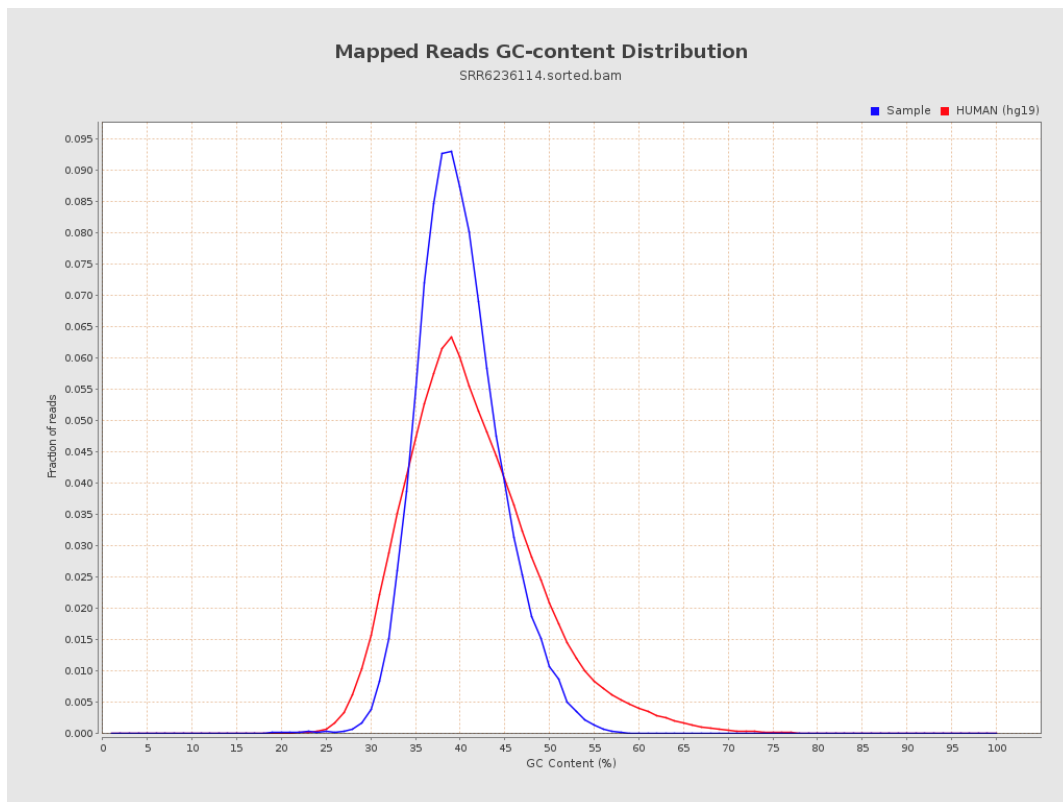
7. Results : Duplication Rate Histogram



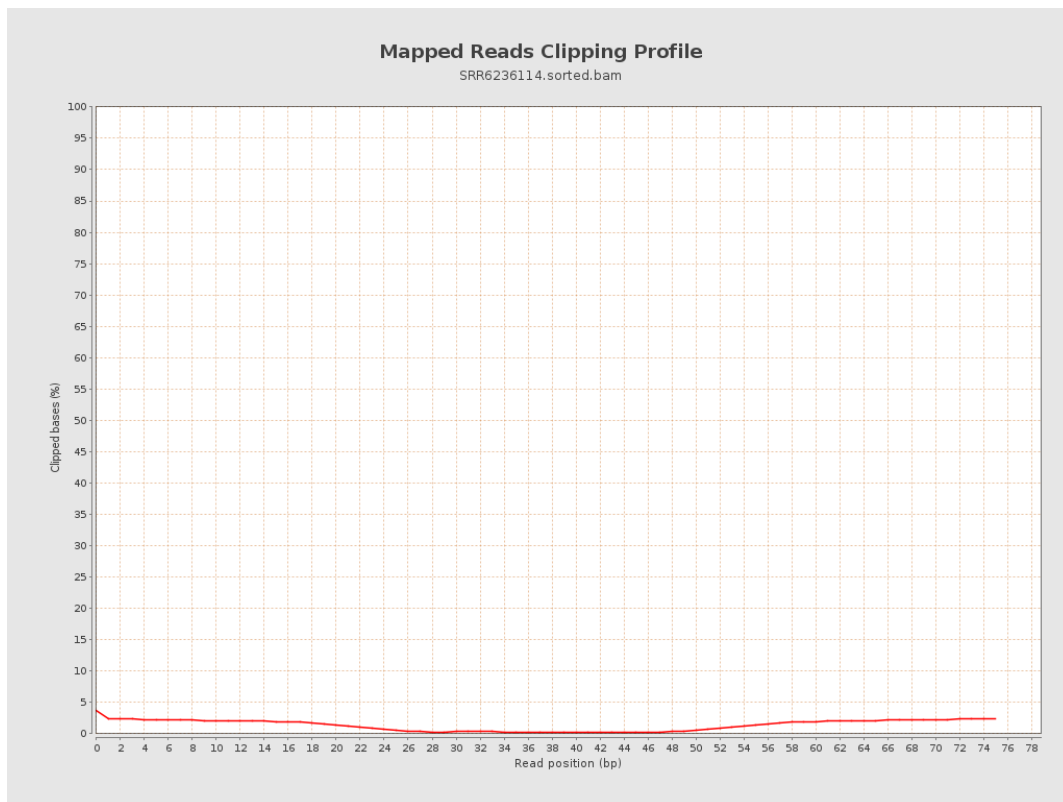
8. Results : Mapped Reads Nucleotide Content



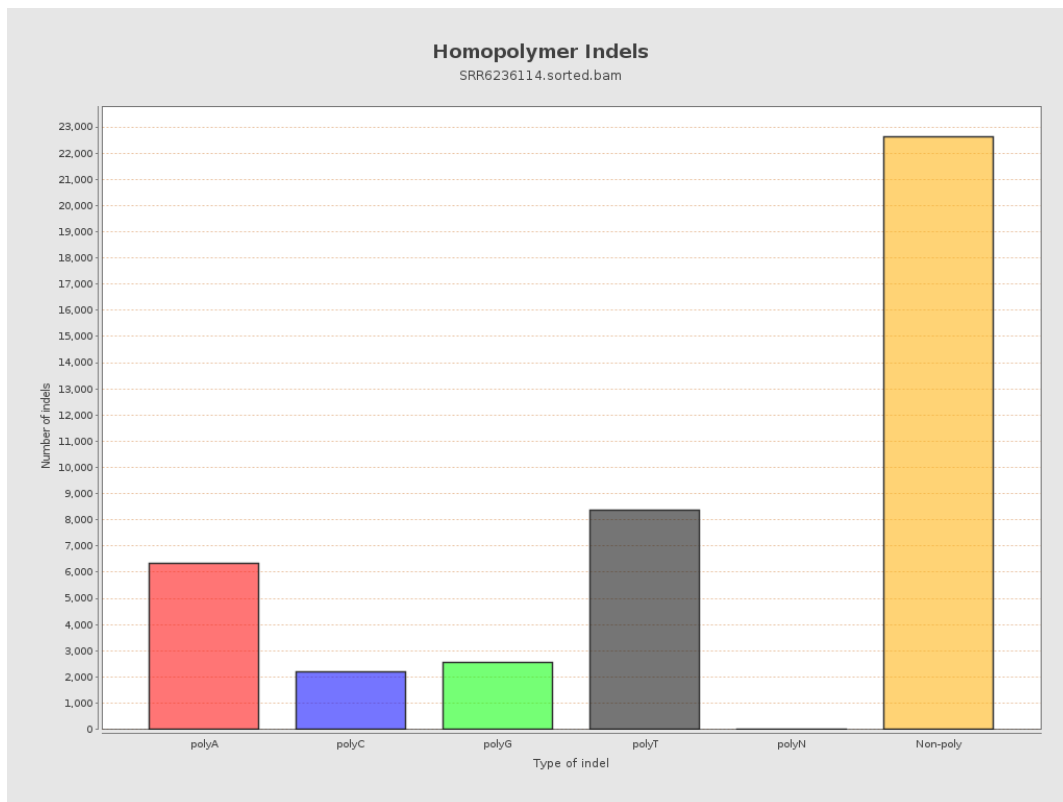
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

