

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 03:01:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231791.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_SRR6231791 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231791.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 03:01:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231791.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,944,578
Mapped reads	4,244,107 / 85.83%
Unmapped reads	700,471 / 14.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,097 / 0.45%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	382,820 / 7.74%
Duplication rate	6.25%
Clipped reads	2,617,117 / 52.93%

2.2. ACGT Content

Number/percentage of A's	64,463,941 / 24.23%
Number/percentage of C's	48,813,530 / 18.35%
Number/percentage of T's	85,460,086 / 32.13%
Number/percentage of G's	67,170,721 / 25.25%
Number/percentage of N's	96,088 / 0.04%
GC Percentage	43.6%

2.3. Coverage

Mean	0.086

Standard Deviation	1.2155
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2.4. Mapping Quality

Mean Mapping Quality	39.22
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2.5. Mismatches and indels

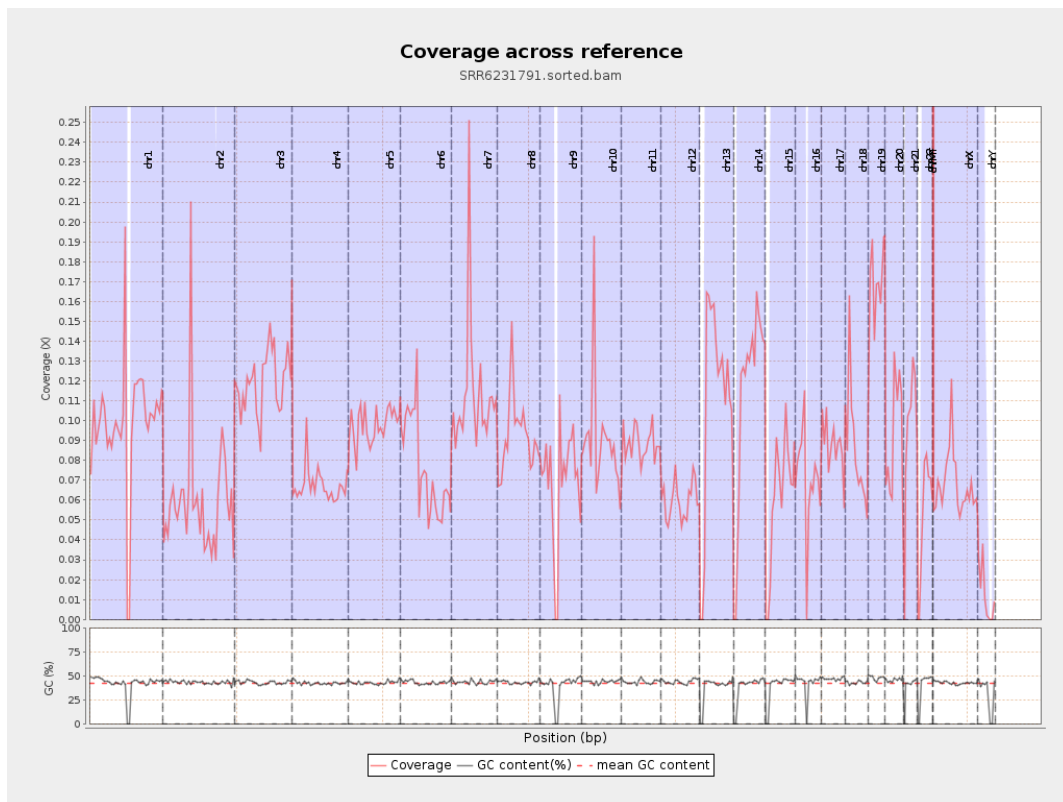
General error rate	0.78%
Mismatches	2,046,987
Insertions	21,168
Mapped reads with at least one insertion	0.49%
Deletions	71,072
Mapped reads with at least one deletion	1.66%
Homopolymer indels	42%

2.6. Chromosome stats

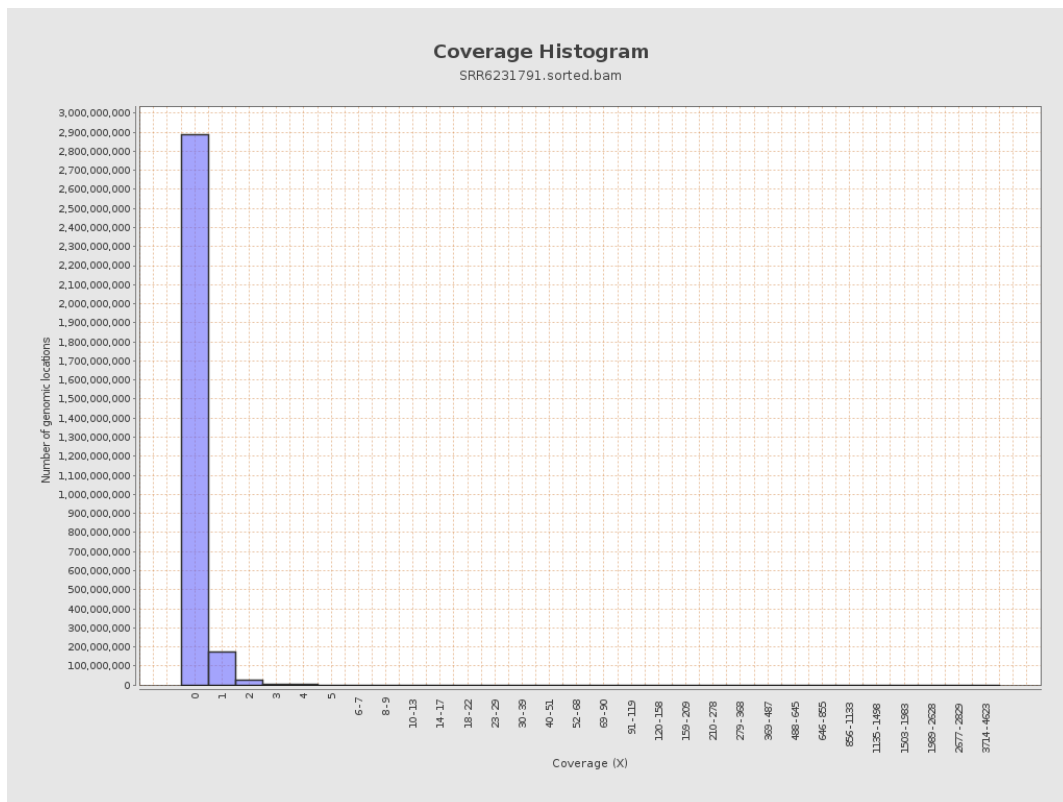
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	24592308	0.0987	2.1263
chr2	243199373	14529952	0.0597	2.3144
chr3	198022430	23699964	0.1197	0.4769
chr4	191154276	12902733	0.0675	0.3898
chr5	180915260	17760659	0.0982	0.4199
chr6	171115067	12966182	0.0758	0.7291
chr7	159138663	18025405	0.1133	1.9927

chr8	146364022	13565301	0.0927	0.8655
chr9	141213431	9792692	0.0693	0.9215
chr10	135534747	12102275	0.0893	1.1384
chr11	135006516	11912031	0.0882	0.8523
chr12	133851895	8059596	0.0602	0.3608
chr13	115169878	12886530	0.1119	0.5078
chr14	107349540	12314908	0.1147	0.5602
chr15	102531392	6144938	0.0599	0.4355
chr16	90354753	6261266	0.0693	0.5146
chr17	81195210	7189506	0.0885	0.4815
chr18	78077248	6797313	0.0871	2.3883
chr19	59128983	9973273	0.1687	1.4134
chr20	63025520	5881839	0.0933	0.5059
chr21	48129895	4611196	0.0958	0.4362
chr22	51304566	2733956	0.0533	0.2893
chrMT	16571	132009	7.9663	6.0774
chrX	155270560	10540226	0.0679	0.6625
chrY	59373566	745679	0.0126	0.2788

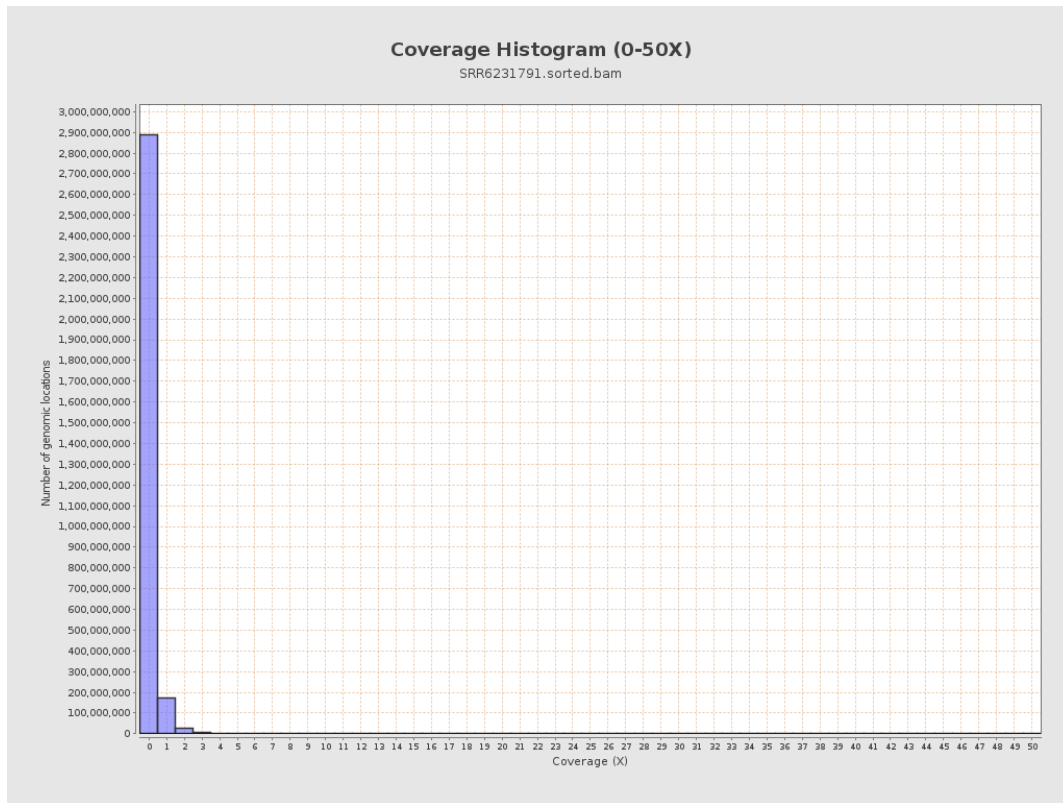
3. Results : Coverage across reference



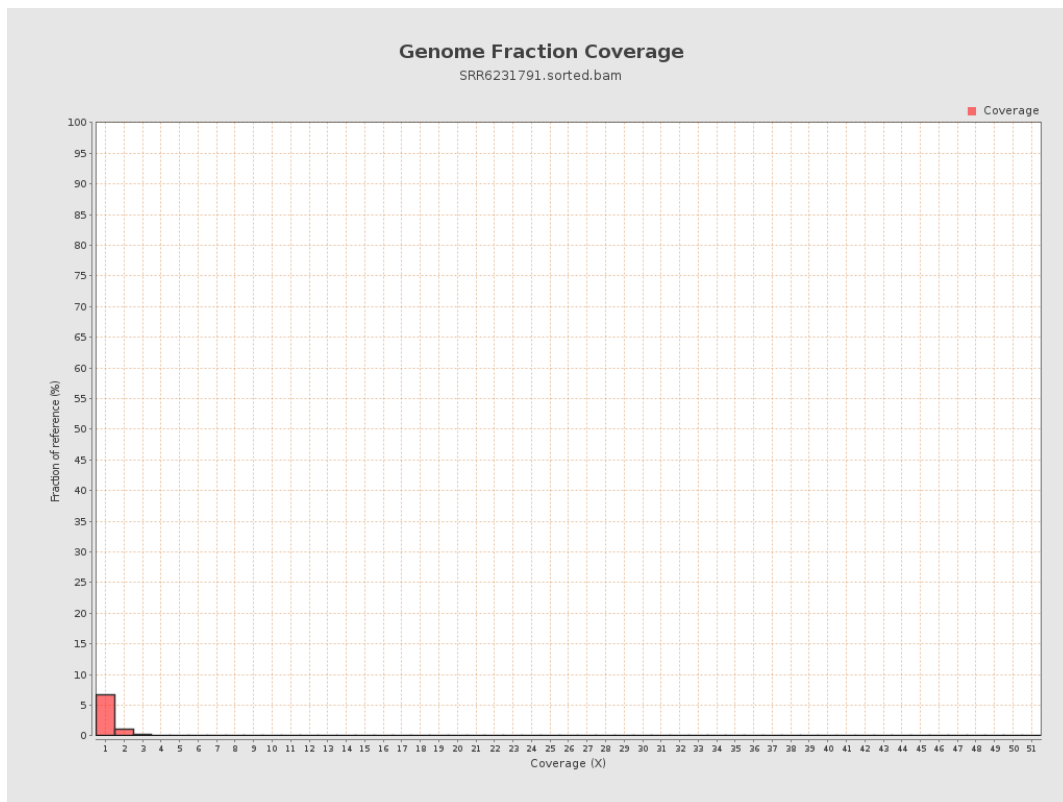
4. Results : Coverage Histogram



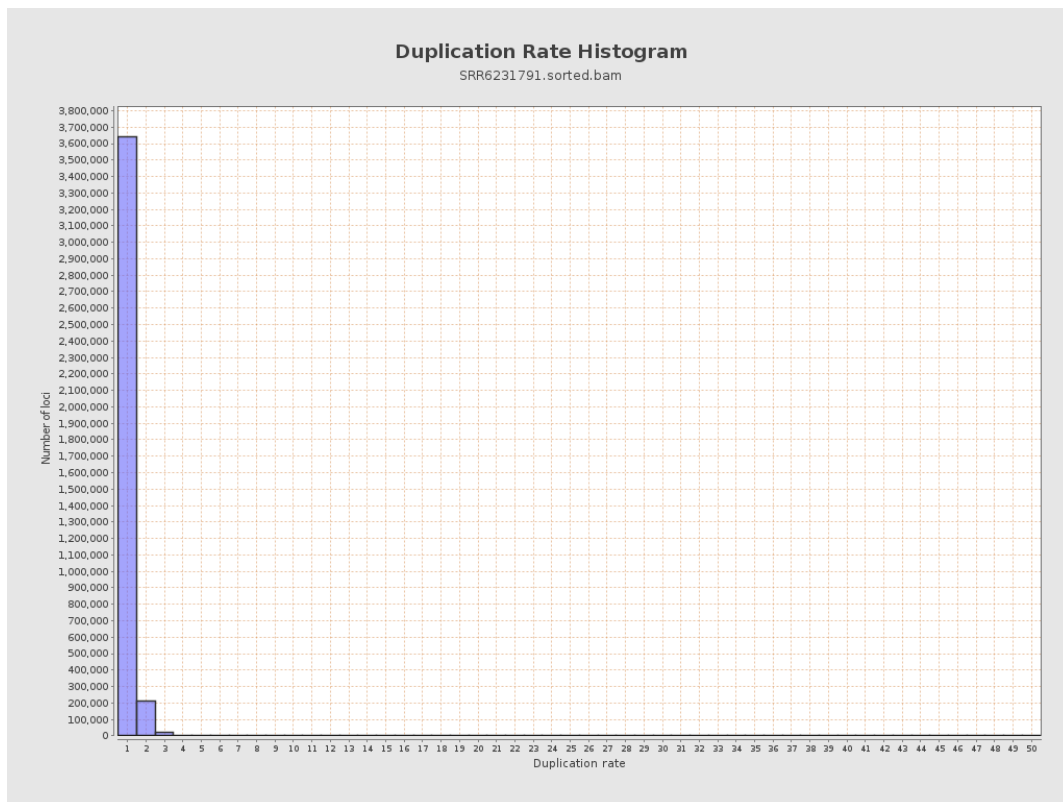
5. Results : Coverage Histogram (0-50X)



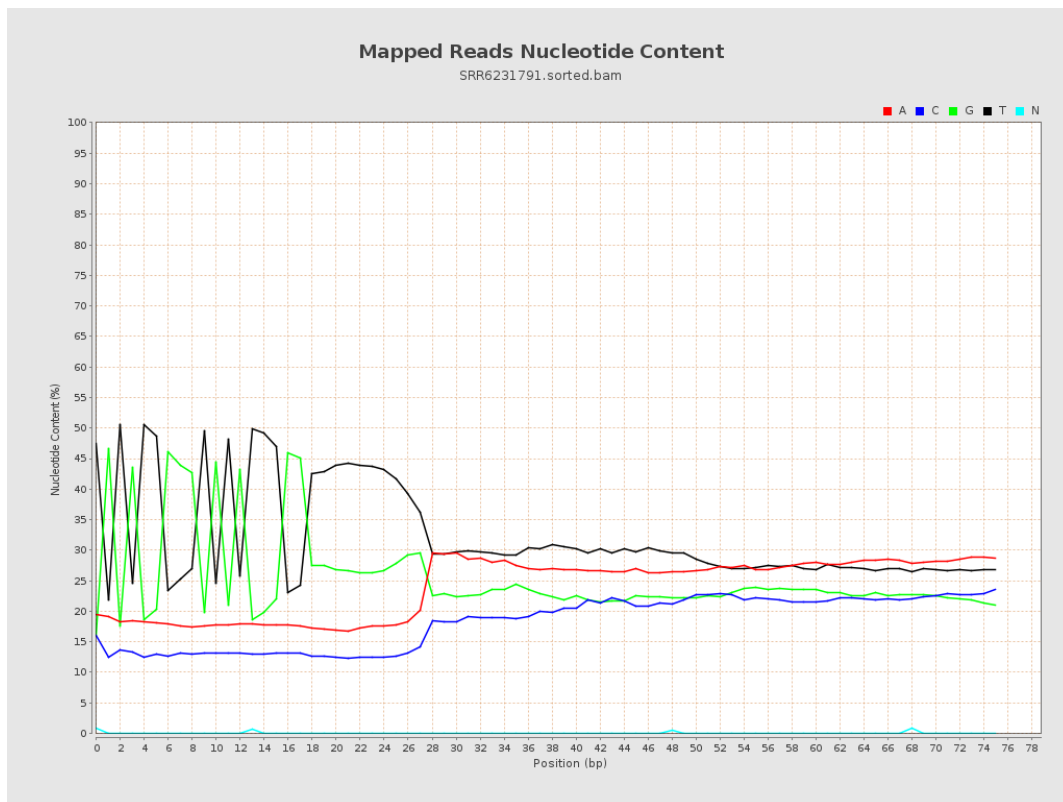
6. Results : Genome Fraction Coverage



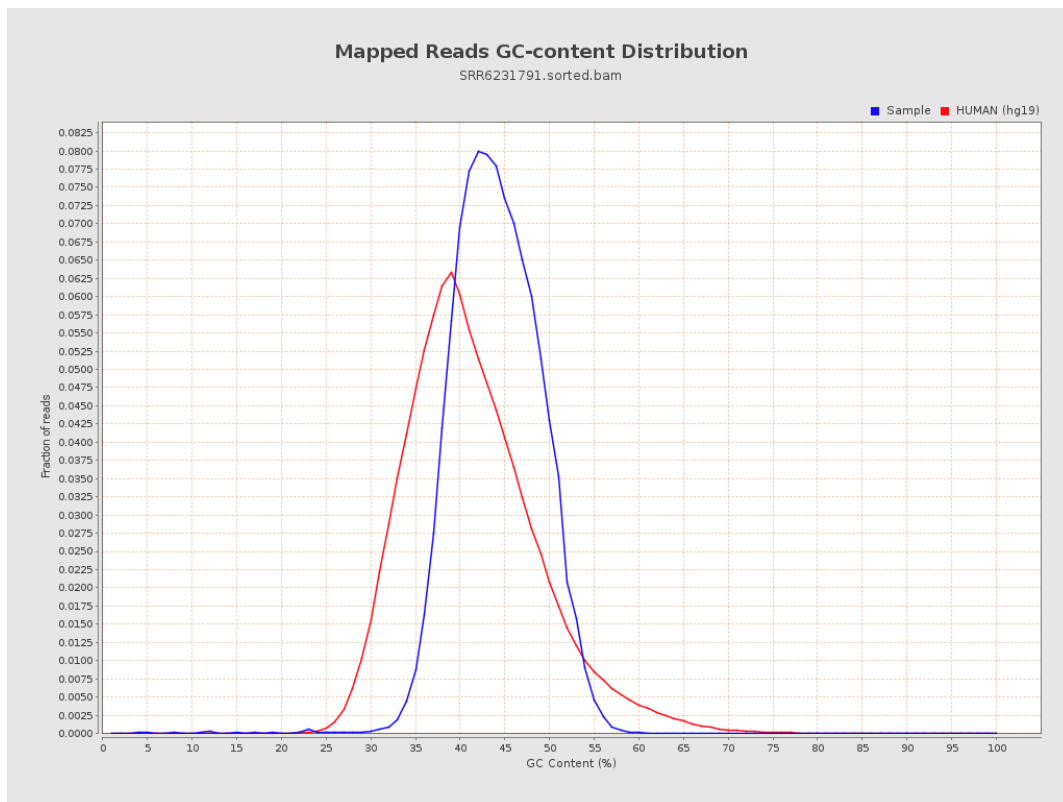
7. Results : Duplication Rate Histogram



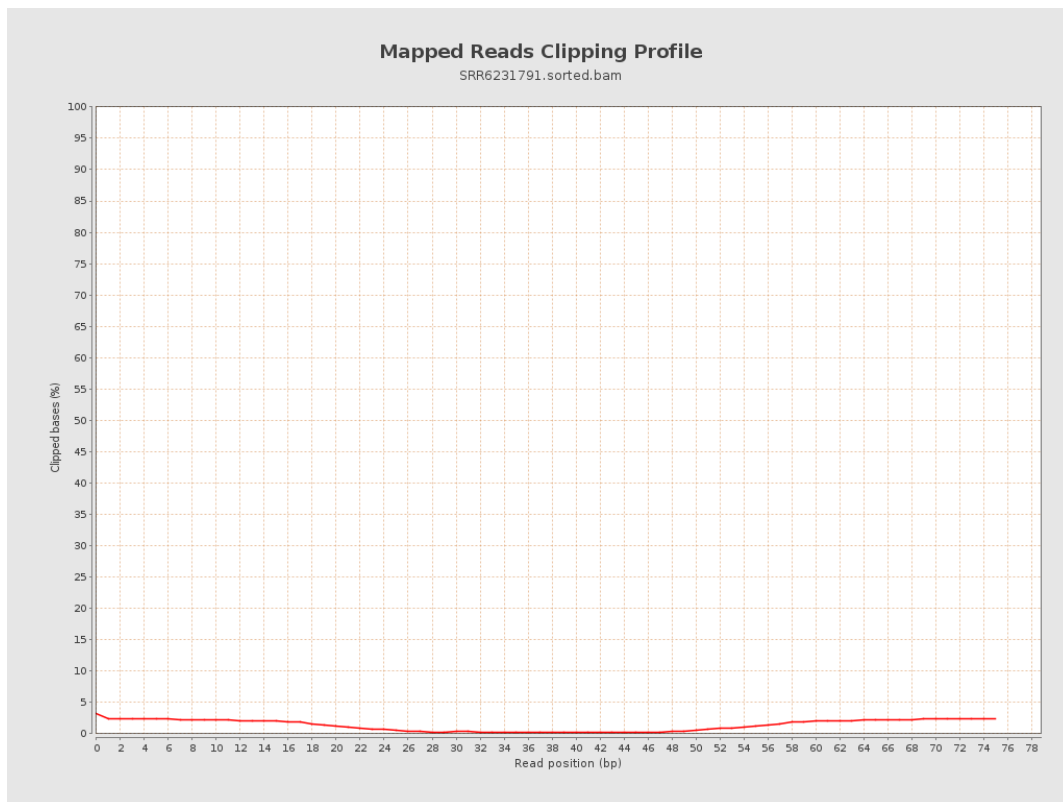
8. Results : Mapped Reads Nucleotide Content



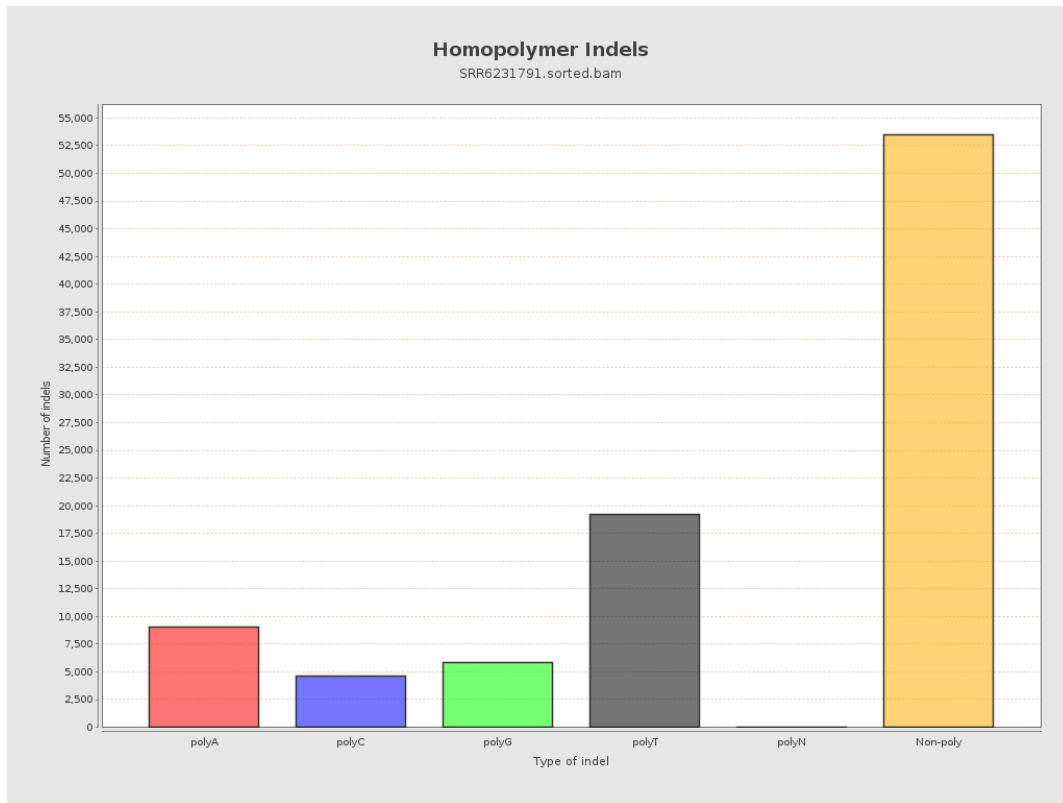
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

