

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 23:25:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231742.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_SRR6231742 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231742.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 23:25:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231742.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,149,310
Mapped reads	869,235 / 75.63%
Unmapped reads	280,075 / 24.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,289 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	55,199 / 4.8%
Duplication rate	5.39%
Clipped reads	418,312 / 36.4%

2.2. ACGT Content

Number/percentage of A's	16,309,133 / 28.68%
Number/percentage of C's	9,474,726 / 16.66%
Number/percentage of T's	19,194,948 / 33.75%
Number/percentage of G's	11,886,428 / 20.9%
Number/percentage of N's	2,655 / 0%
GC Percentage	37.56%

2.3. Coverage

Mean	0.0184

Standard Deviation	0.2179
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2.4. Mapping Quality

Mean Mapping Quality	46.4
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2.5. Mismatches and indels

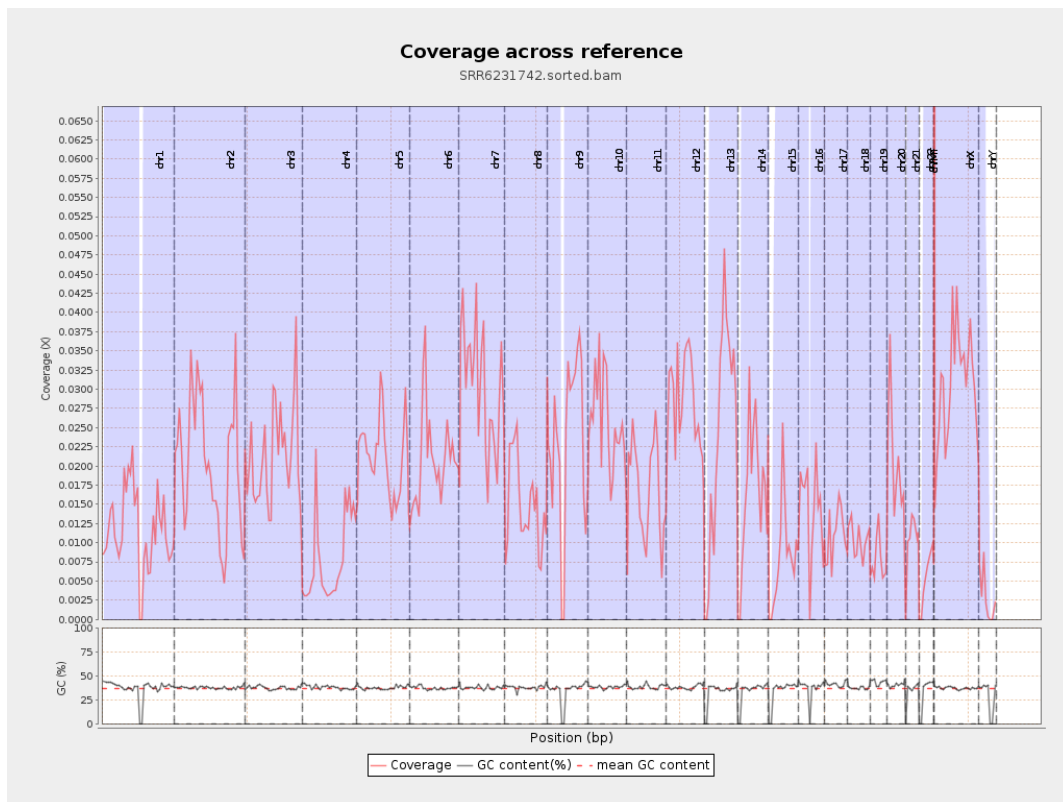
General error rate	0.87%
Mismatches	485,305
Insertions	4,789
Mapped reads with at least one insertion	0.55%
Deletions	19,753
Mapped reads with at least one deletion	2.24%
Homopolymer indels	44.79%

2.6. Chromosome stats

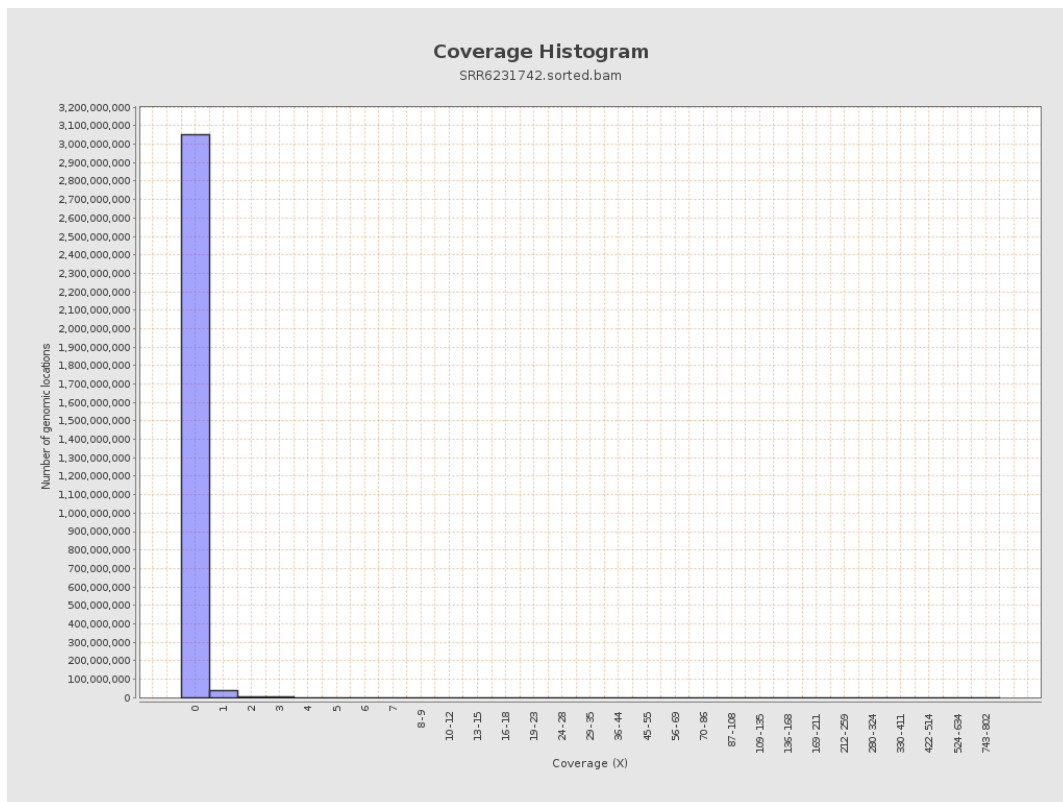
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	2932955	0.0118	0.195
chr2	243199373	4921291	0.0202	0.2103
chr3	198022430	4204521	0.0212	0.1728
chr4	191154276	1518039	0.0079	0.1225
chr5	180915260	3867504	0.0214	0.1746
chr6	171115067	3569015	0.0209	0.1909
chr7	159138663	4809573	0.0302	0.3247

chr8	146364022	2173105	0.0148	0.4919
chr9	141213431	3280704	0.0232	0.2128
chr10	135534747	3457548	0.0255	0.242
chr11	135006516	2285529	0.0169	0.1647
chr12	133851895	3825018	0.0286	0.2053
chr13	115169878	2831956	0.0246	0.1888
chr14	107349540	1790531	0.0167	0.1569
chr15	102531392	853119	0.0083	0.1072
chr16	90354753	1268660	0.014	0.15
chr17	81195210	888914	0.0109	0.1238
chr18	78077248	812829	0.0104	0.2666
chr19	59128983	475629	0.008	0.1435
chr20	63025520	1283969	0.0204	0.169
chr21	48129895	504517	0.0105	0.1347
chr22	51304566	277901	0.0054	0.0856
chrMT	16571	107012	6.4578	5.3222
chrX	155270560	4798330	0.0309	0.2209
chrY	59373566	164664	0.0028	0.087

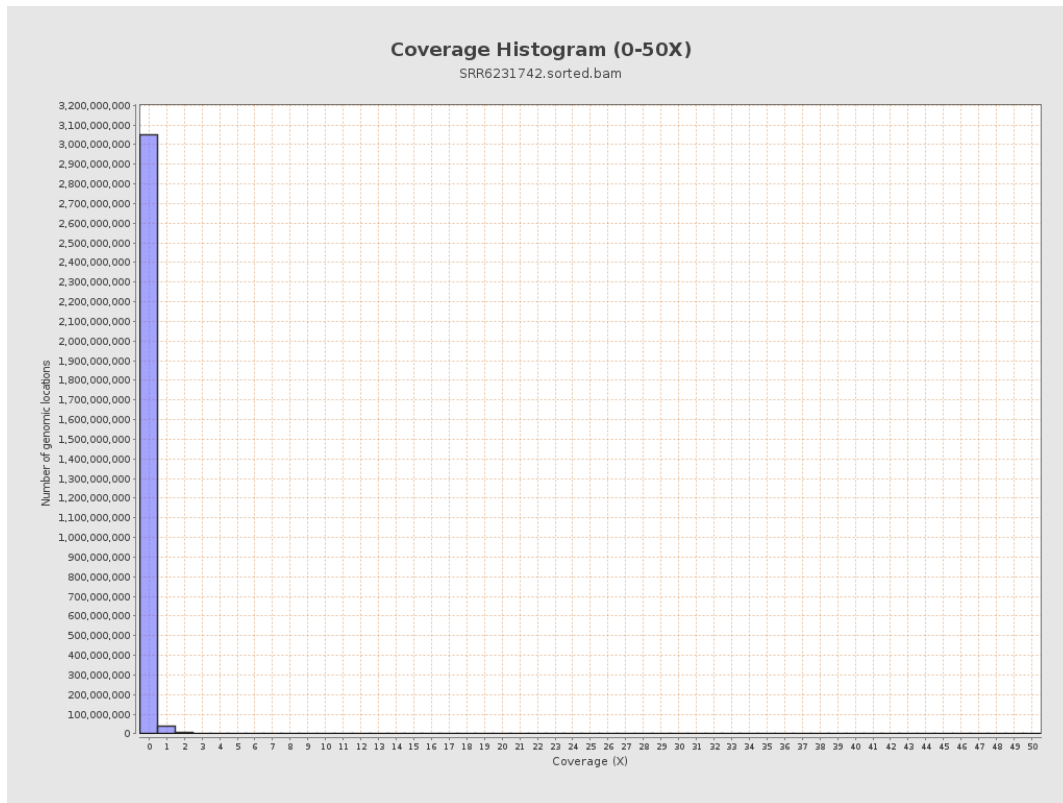
3. Results : Coverage across reference



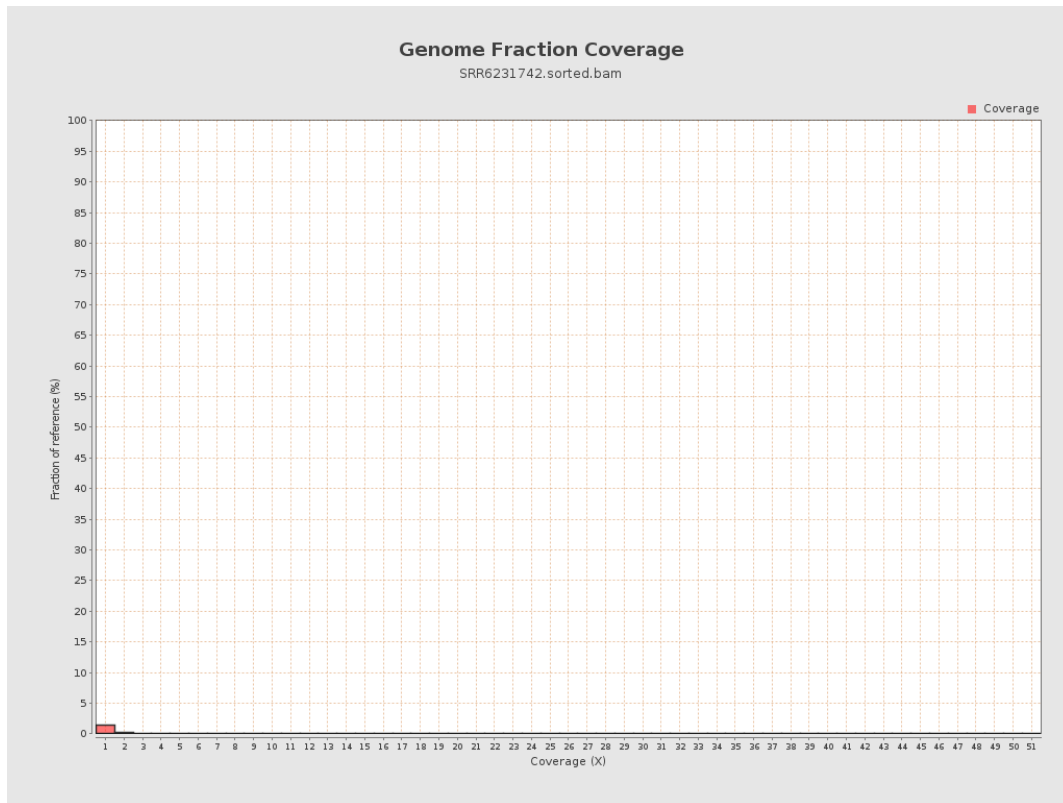
4. Results : Coverage Histogram



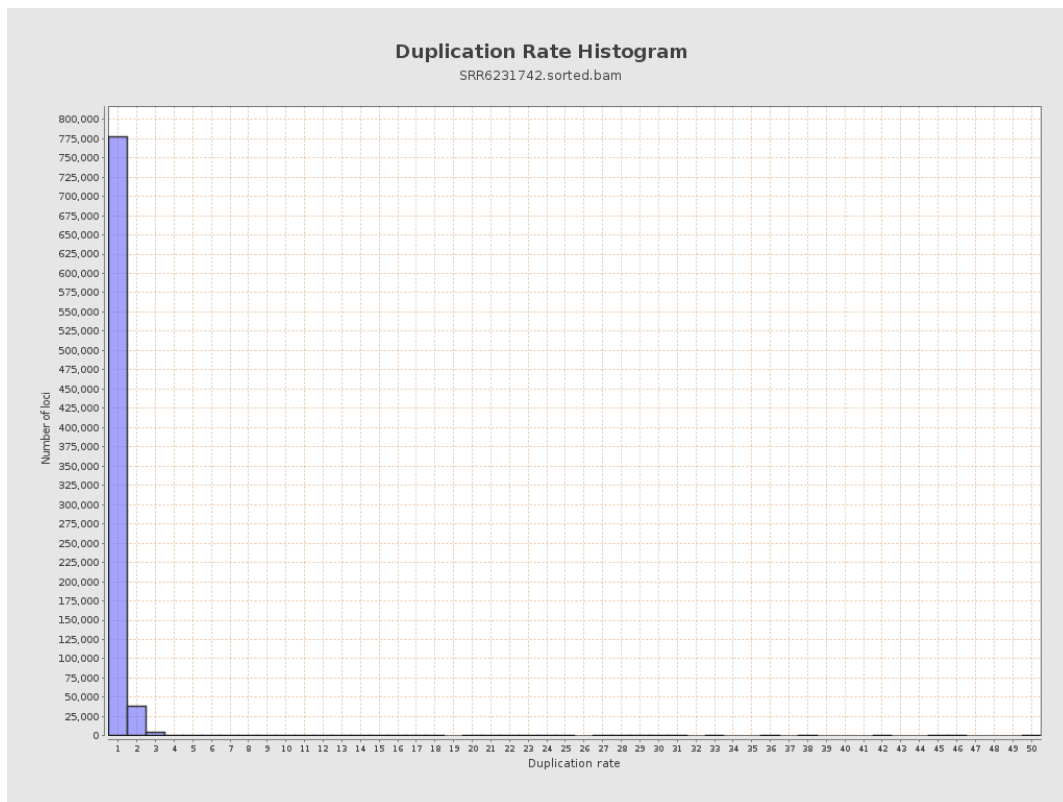
5. Results : Coverage Histogram (0-50X)



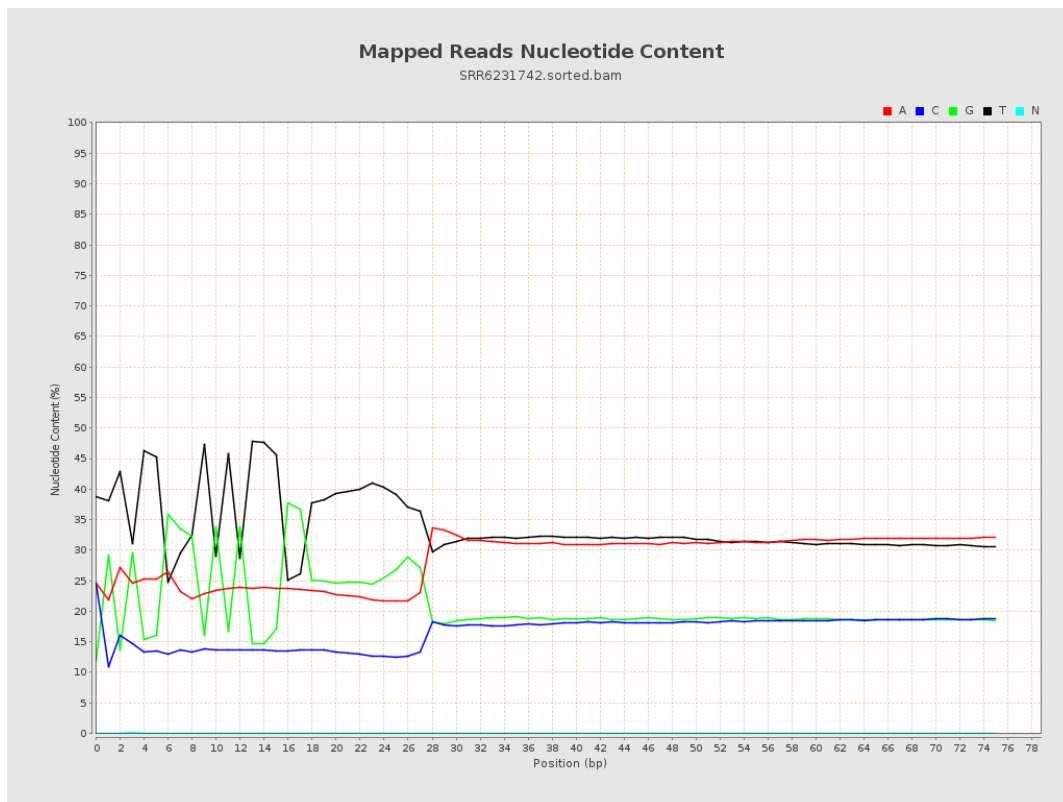
6. Results : Genome Fraction Coverage



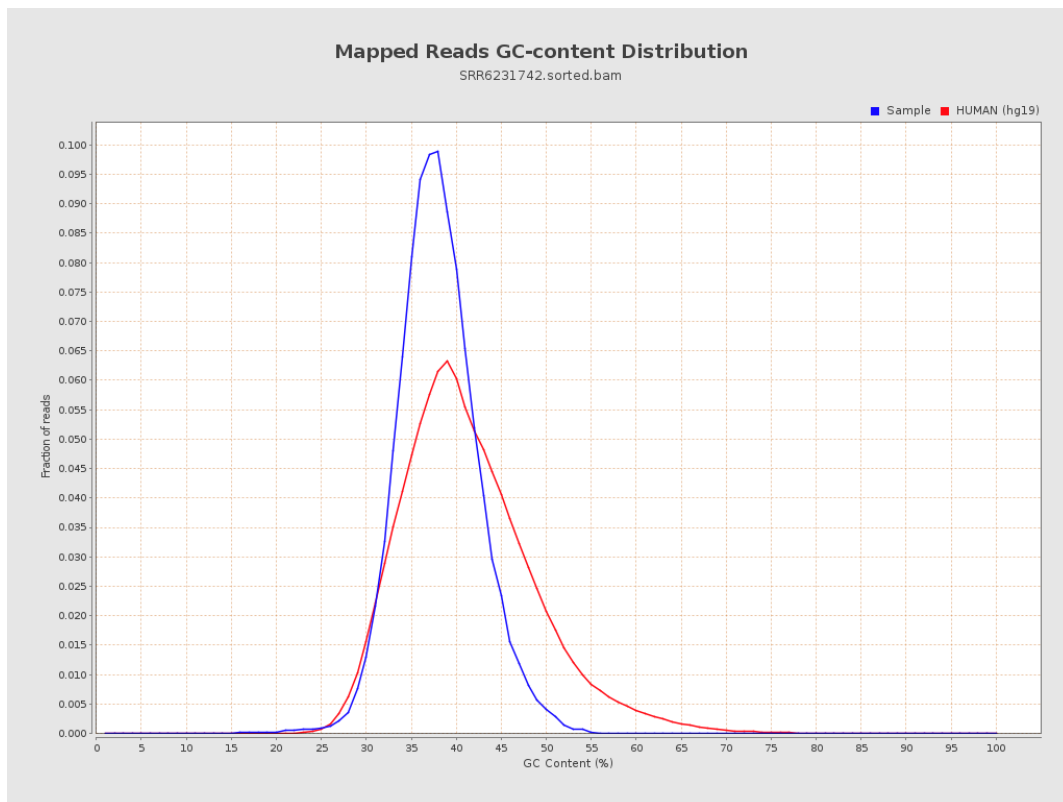
7. Results : Duplication Rate Histogram



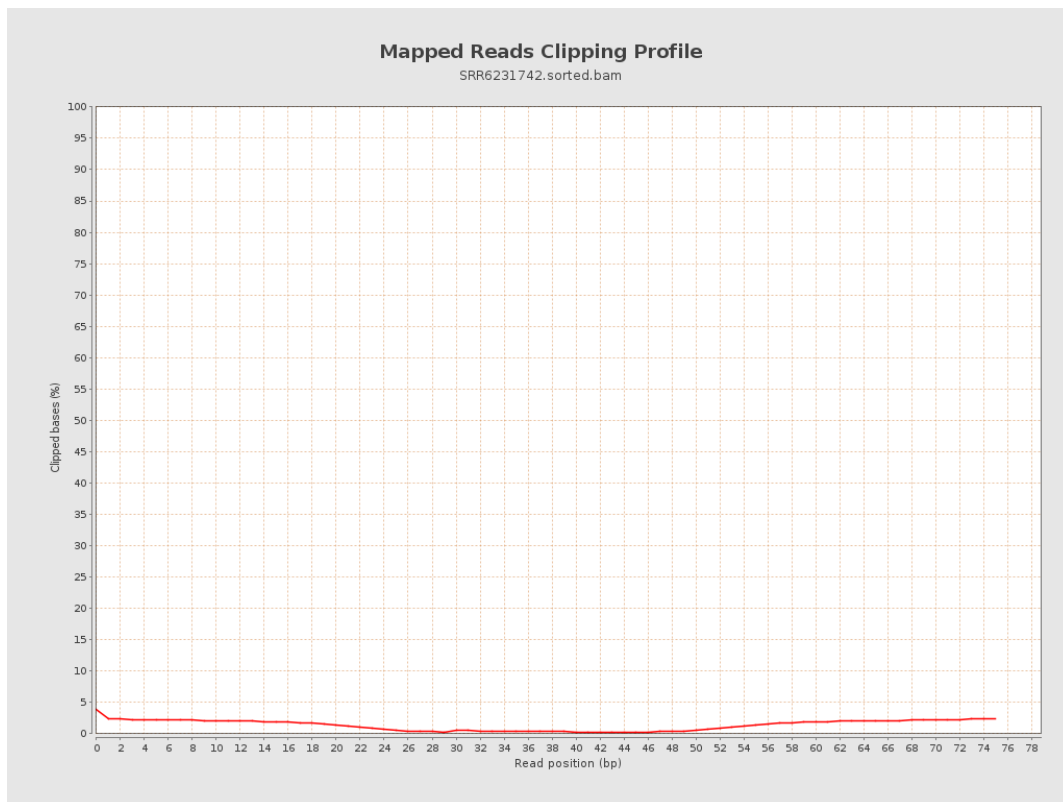
8. Results : Mapped Reads Nucleotide Content



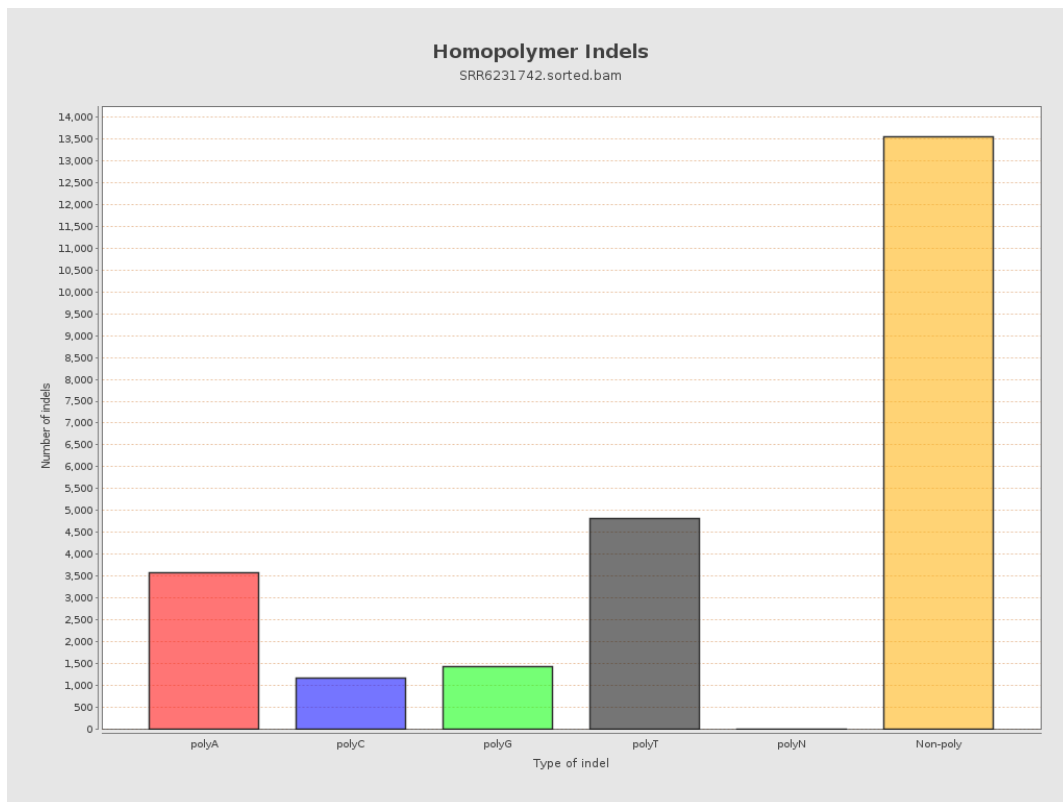
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

