

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 23:23:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231741.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_SRR6231741 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231741.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 23:23:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231741.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,811,884
Mapped reads	1,026,238 / 56.64%
Unmapped reads	785,646 / 43.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,798 / 0.43%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	164,818 / 9.1%
Duplication rate	12.43%
Clipped reads	598,851 / 33.05%

2.2. ACGT Content

Number/percentage of A's	17,146,493 / 26.41%
Number/percentage of C's	12,408,872 / 19.11%
Number/percentage of T's	20,249,187 / 31.19%
Number/percentage of G's	15,103,416 / 23.26%
Number/percentage of N's	11,480 / 0.02%
GC Percentage	42.38%

2.3. Coverage

Mean	0.021

Standard Deviation	0.2658
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2.4. Mapping Quality

Mean Mapping Quality	44.7
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2.5. Mismatches and indels

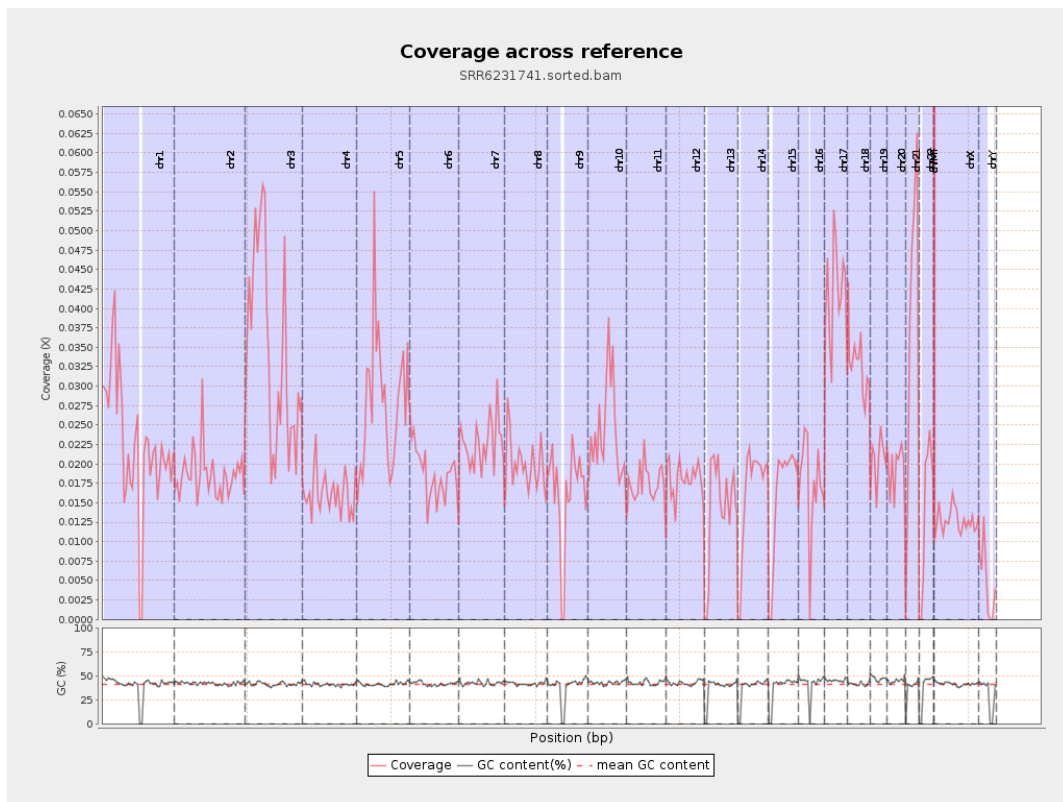
General error rate	0.92%
Mismatches	589,142
Insertions	5,577
Mapped reads with at least one insertion	0.54%
Deletions	21,013
Mapped reads with at least one deletion	2.02%
Homopolymer indels	46.79%

2.6. Chromosome stats

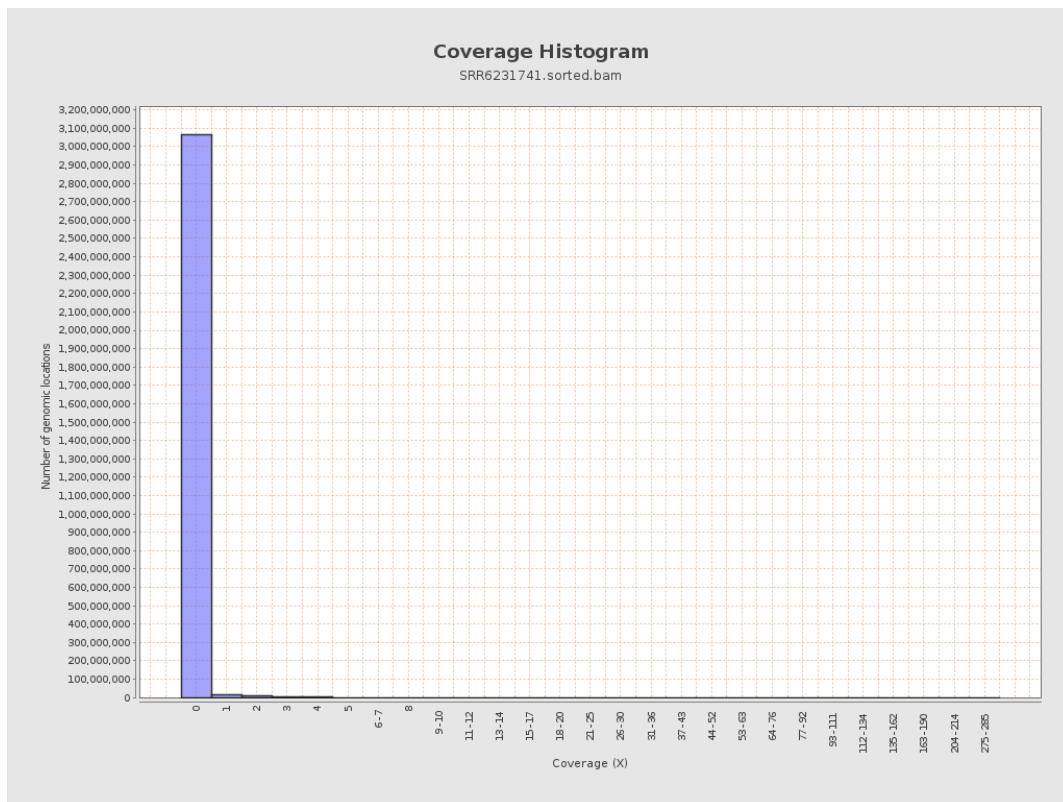
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5549824	0.0223	0.2879
chr2	243199373	4525265	0.0186	0.2894
chr3	198022430	6824397	0.0345	0.3193
chr4	191154276	3105413	0.0162	0.2208
chr5	180915260	5057553	0.028	0.2881
chr6	171115067	3209662	0.0188	0.2464
chr7	159138663	3615580	0.0227	0.2919

chr8	146364022	2911653	0.0199	0.2694
chr9	141213431	2284053	0.0162	0.2309
chr10	135534747	3258814	0.024	0.2752
chr11	135006516	2386077	0.0177	0.2486
chr12	133851895	2413704	0.018	0.2302
chr13	115169878	1631107	0.0142	0.2268
chr14	107349540	1752716	0.0163	0.2241
chr15	102531392	1648732	0.0161	0.2184
chr16	90354753	1537375	0.017	0.2325
chr17	81195210	3402033	0.0419	0.3559
chr18	78077248	2554036	0.0327	0.3837
chr19	59128983	1218726	0.0206	0.2678
chr20	63025520	1216582	0.0193	0.2462
chr21	48129895	1840271	0.0382	0.3367
chr22	51304566	720179	0.014	0.2022
chrMT	16571	32486	1.9604	2.9935
chrX	155270560	1975787	0.0127	0.1935
chrY	59373566	283931	0.0048	0.1088

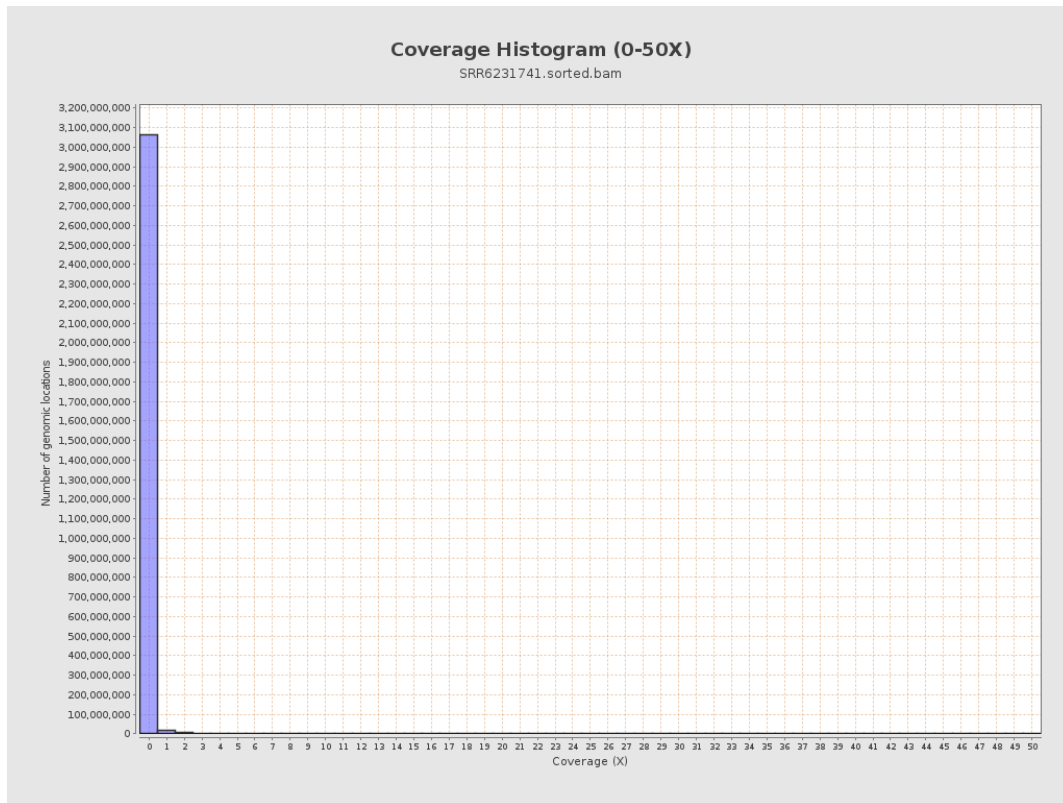
3. Results : Coverage across reference



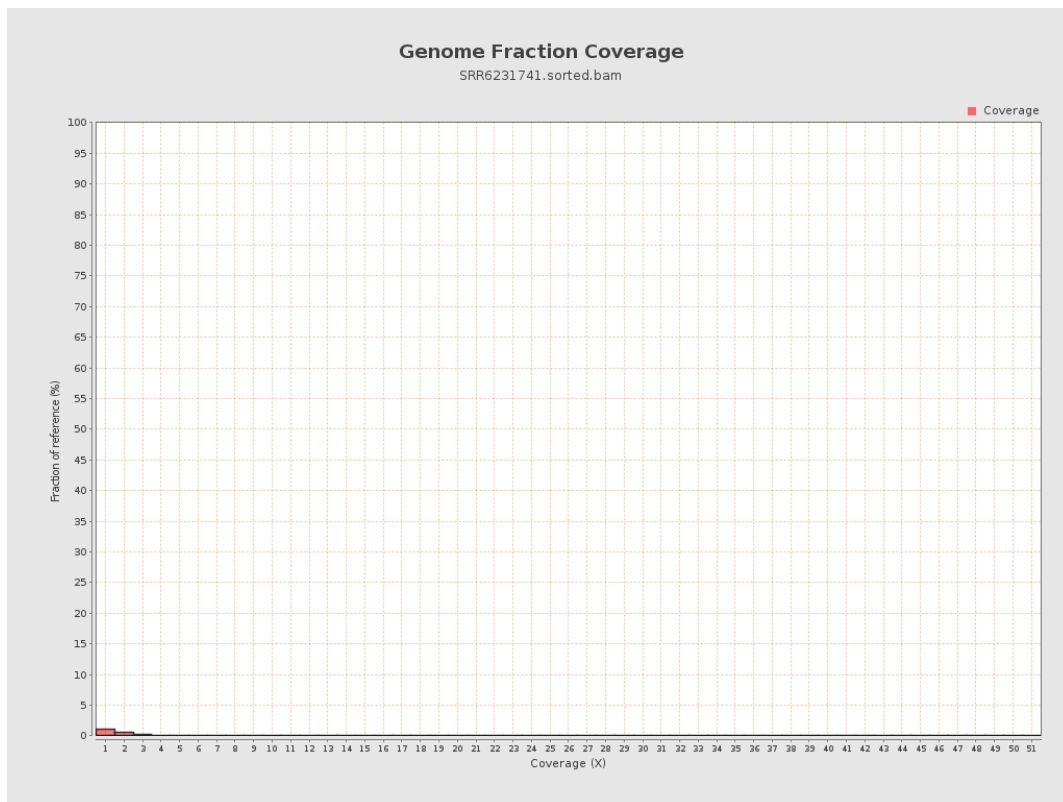
4. Results : Coverage Histogram



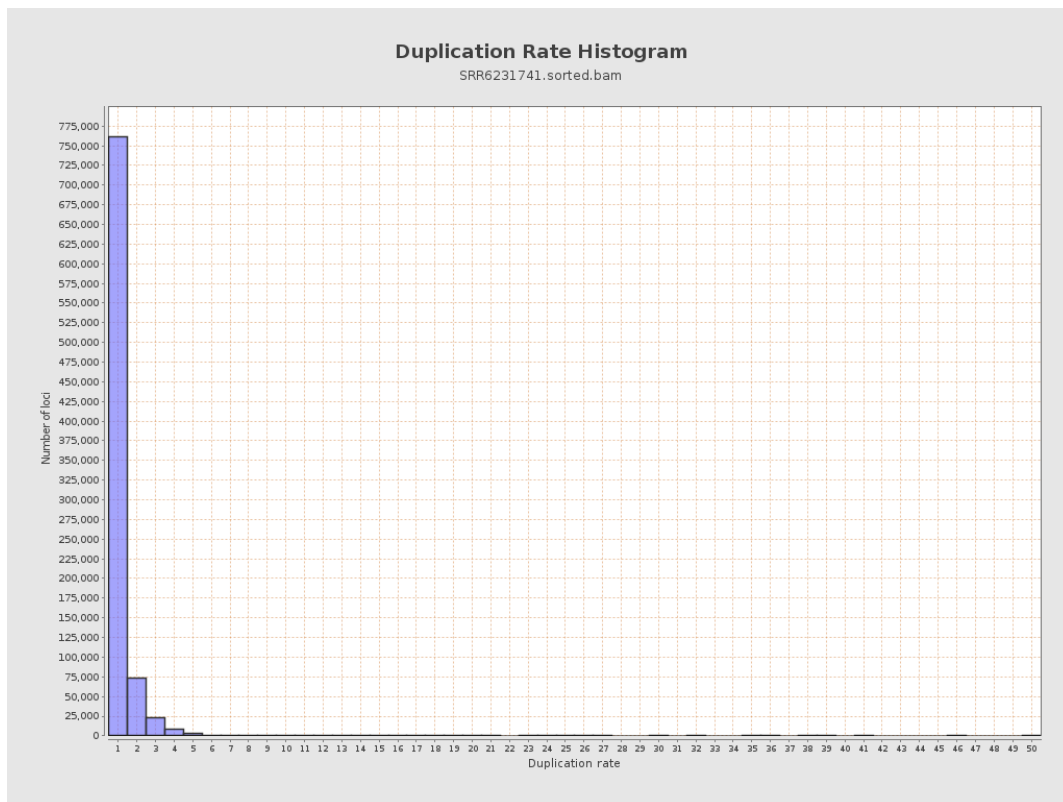
5. Results : Coverage Histogram (0-50X)



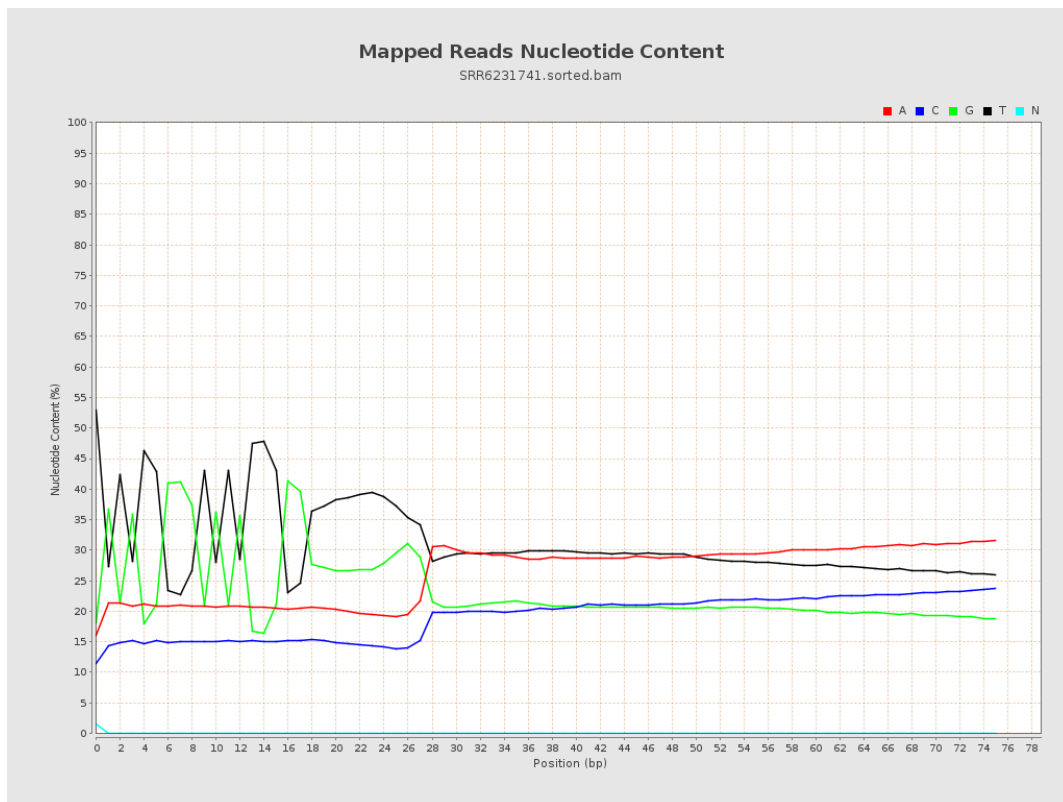
6. Results : Genome Fraction Coverage



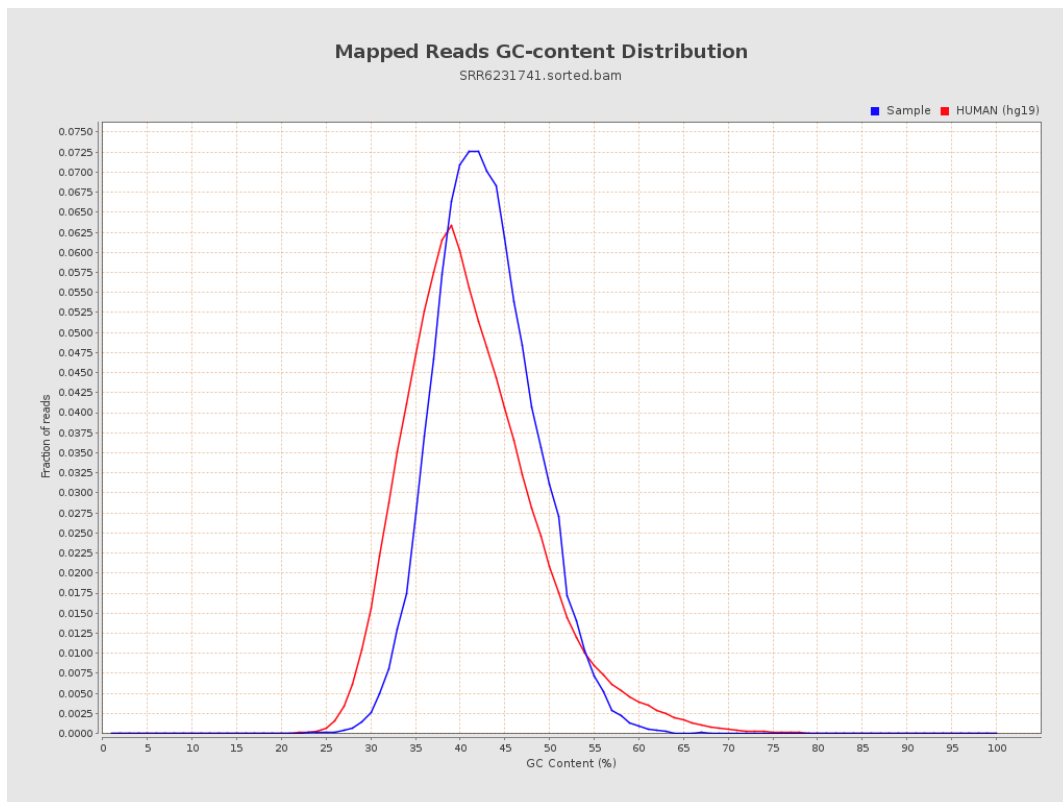
7. Results : Duplication Rate Histogram



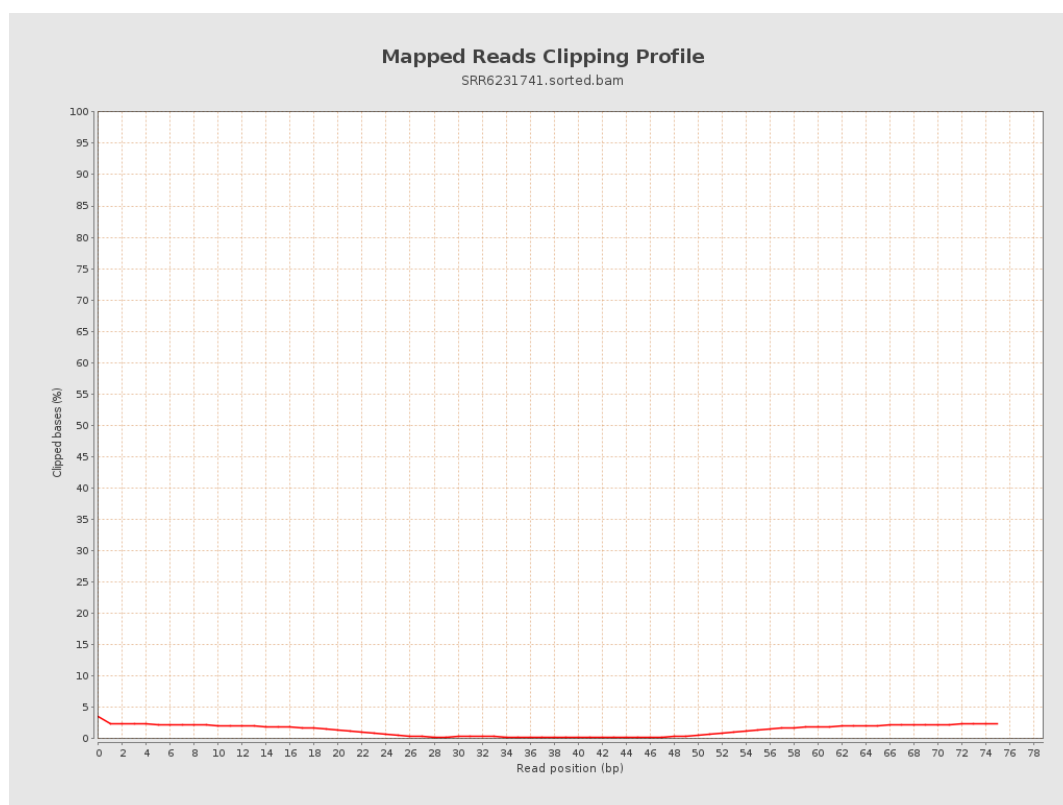
8. Results : Mapped Reads Nucleotide Content



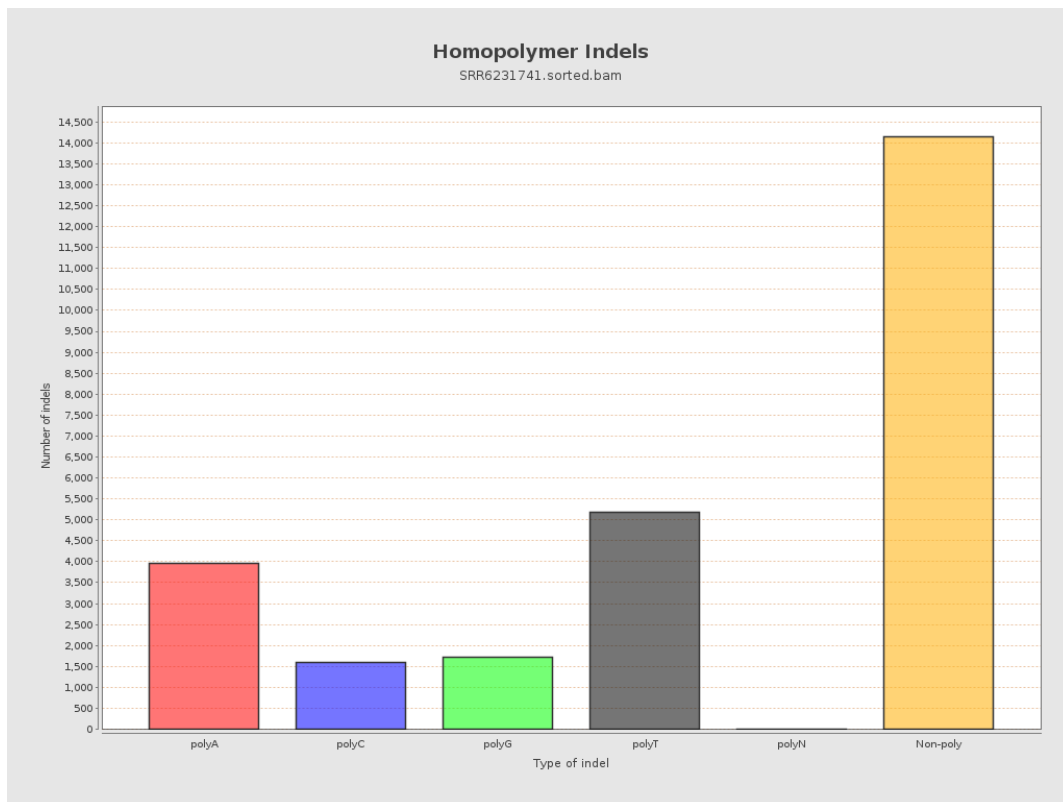
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

