

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 23:36:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231746.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_SRR6231746 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231746.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 23:36:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231746.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,644,523
Mapped reads	4,374,850 / 94.19%
Unmapped reads	269,673 / 5.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	48,199 / 1.04%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	741,195 / 15.96%
Duplication rate	8.46%
Clipped reads	1,624,324 / 34.97%

2.2. ACGT Content

Number/percentage of A's	77,518,223 / 25.83%
Number/percentage of C's	55,432,296 / 18.47%
Number/percentage of T's	83,398,317 / 27.79%
Number/percentage of G's	83,709,785 / 27.89%
Number/percentage of N's	65,533 / 0.02%
GC Percentage	46.36%

2.3. Coverage

Mean	0.097

Standard Deviation	43.2177
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2.4. Mapping Quality

Mean Mapping Quality	43.5
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2.5. Mismatches and indels

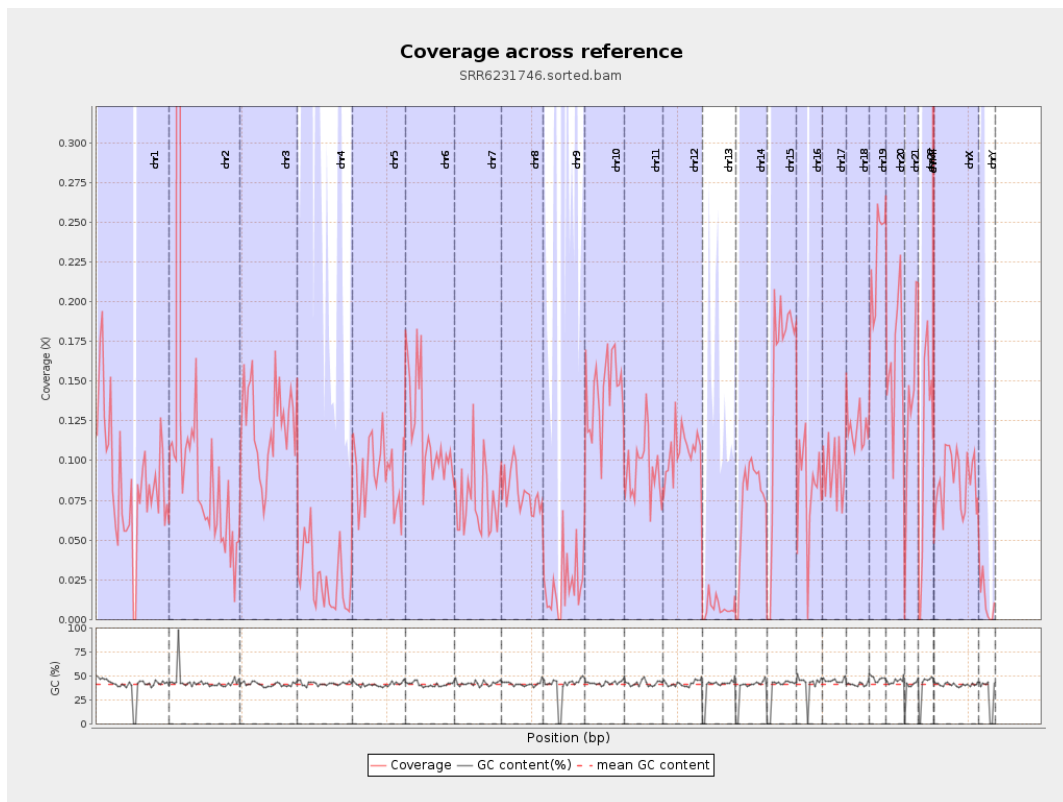
General error rate	0.65%
Mismatches	1,915,769
Insertions	20,442
Mapped reads with at least one insertion	0.46%
Deletions	64,805
Mapped reads with at least one deletion	1.47%
Homopolymer indels	46.95%

2.6. Chromosome stats

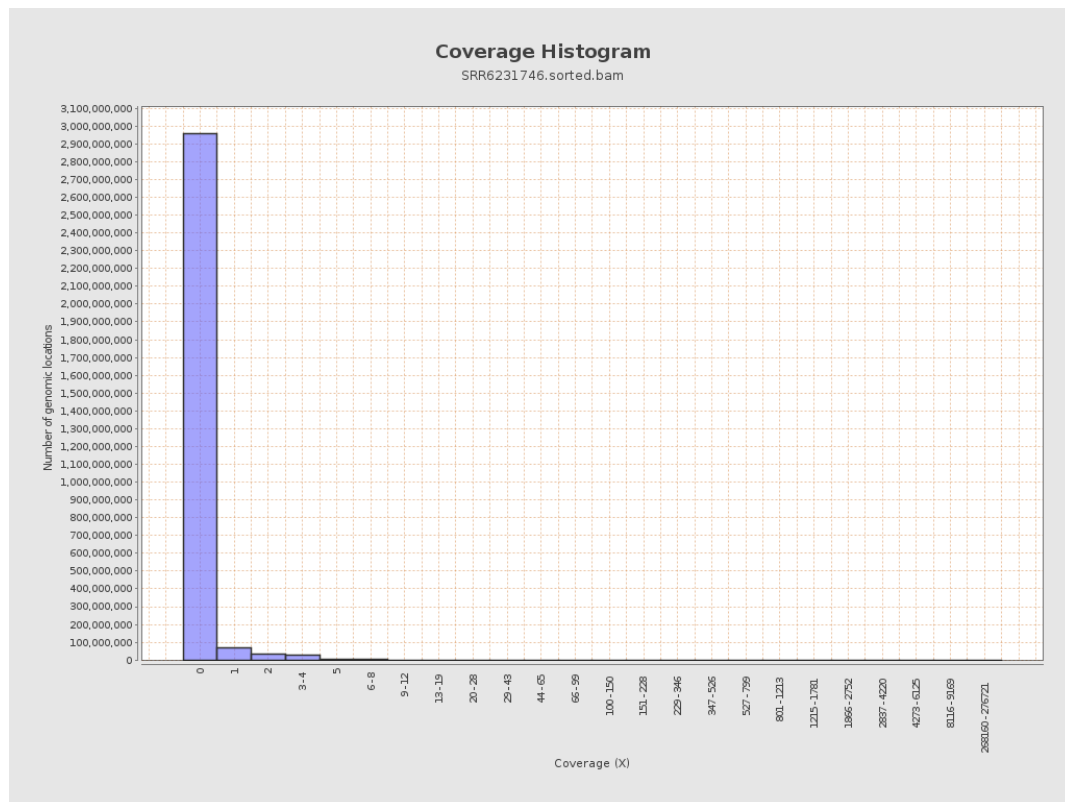
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	21815879	0.0875	1.2935
chr2	243199373	41507206	0.1707	154.1682
chr3	198022430	23927657	0.1208	0.6072
chr4	191154276	4764084	0.0249	0.3163
chr5	180915260	16564618	0.0916	0.5416
chr6	171115067	20198789	0.118	0.7806
chr7	159138663	11831188	0.0743	0.8786

chr8	146364022	11695545	0.0799	0.7943
chr9	141213431	2924847	0.0207	0.5414
chr10	135534747	19485399	0.1438	0.9127
chr11	135006516	12658363	0.0938	1.0617
chr12	133851895	14105694	0.1054	0.5683
chr13	115169878	852668	0.0074	0.1396
chr14	107349540	7932593	0.0739	0.602
chr15	102531392	15527368	0.1514	0.6909
chr16	90354753	7558320	0.0837	0.5408
chr17	81195210	7563509	0.0932	0.6877
chr18	78077248	9401815	0.1204	1.278
chr19	59128983	13372905	0.2262	1.0719
chr20	63025520	10130243	0.1607	0.7267
chr21	48129895	6634818	0.1379	0.7002
chr22	51304566	5512702	0.1075	0.5887
chrMT	16571	31122	1.8781	2.6337
chrX	155270560	13520450	0.0871	0.5729
chrY	59373566	711547	0.012	0.262

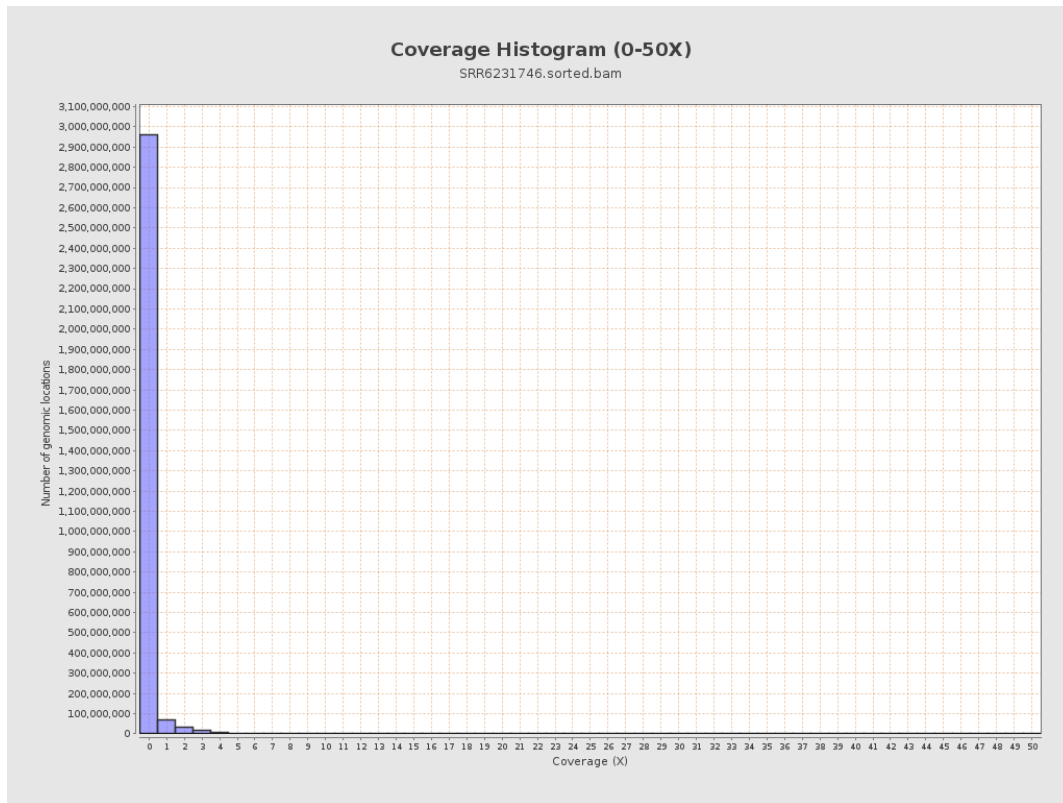
3. Results : Coverage across reference



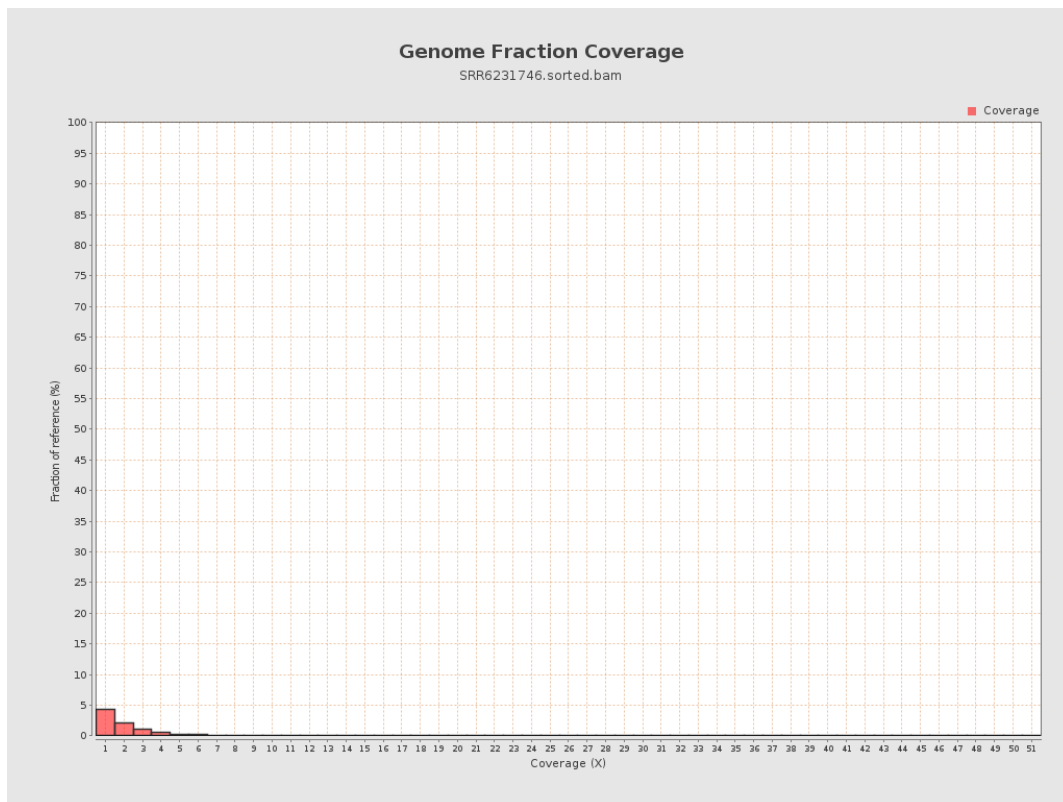
4. Results : Coverage Histogram



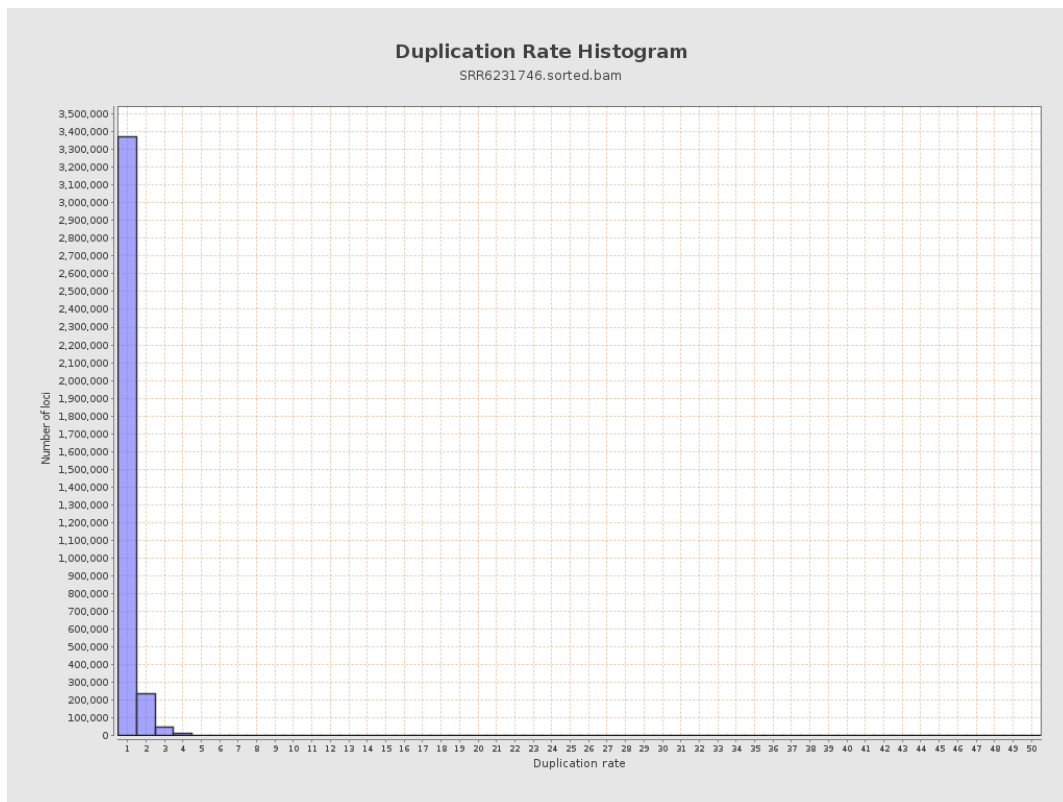
5. Results : Coverage Histogram (0-50X)



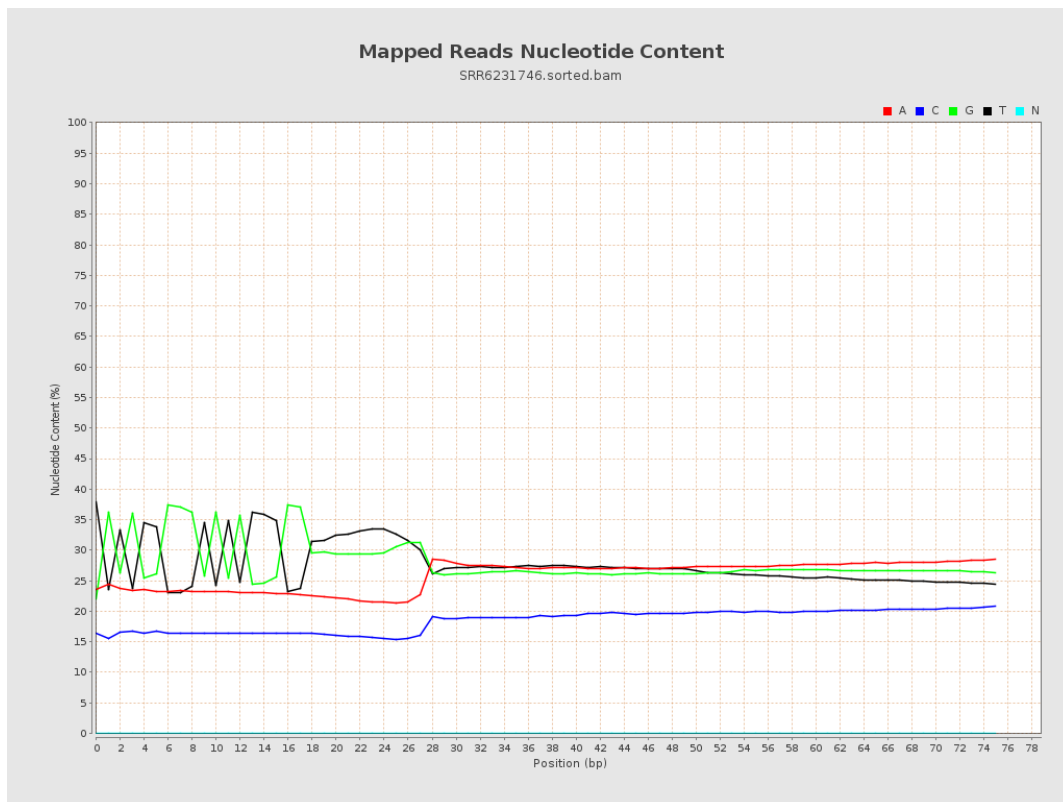
6. Results : Genome Fraction Coverage



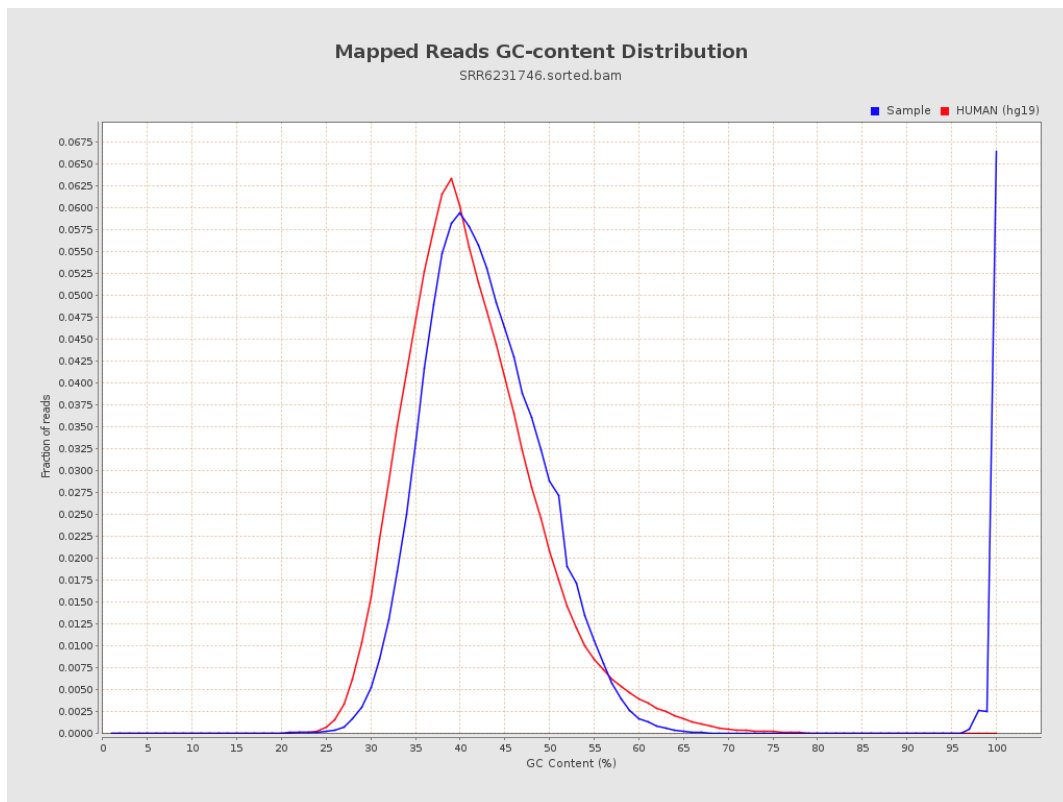
7. Results : Duplication Rate Histogram



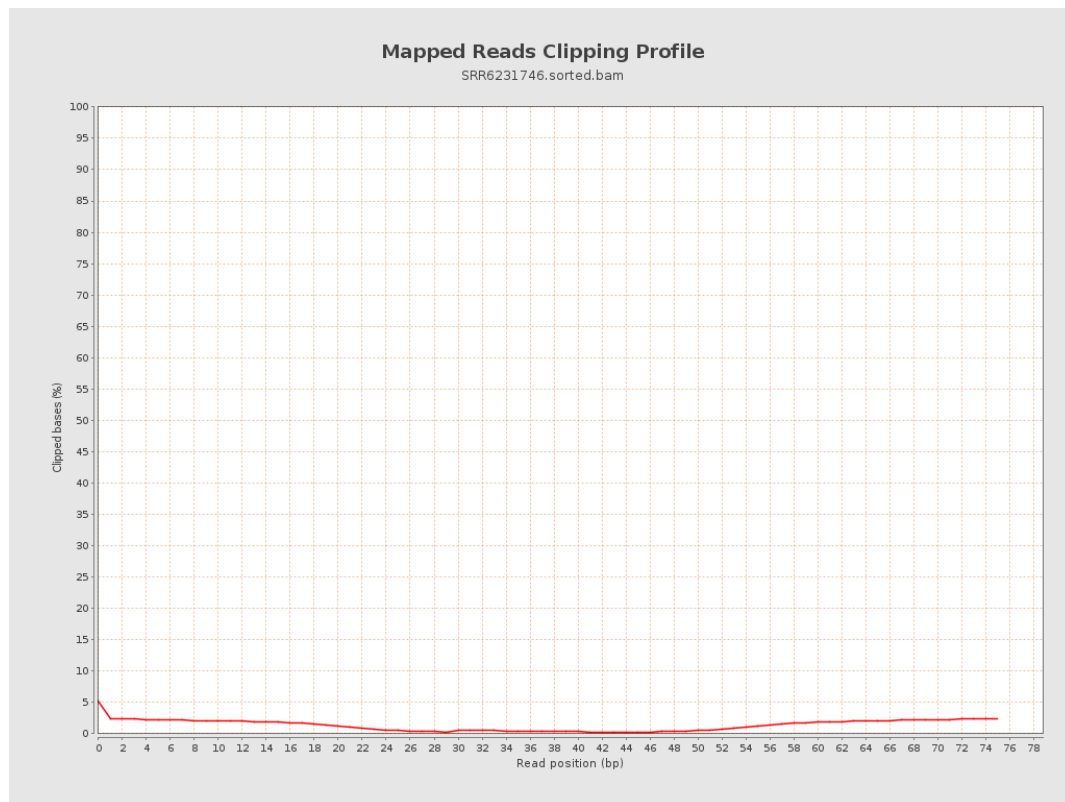
8. Results : Mapped Reads Nucleotide Content



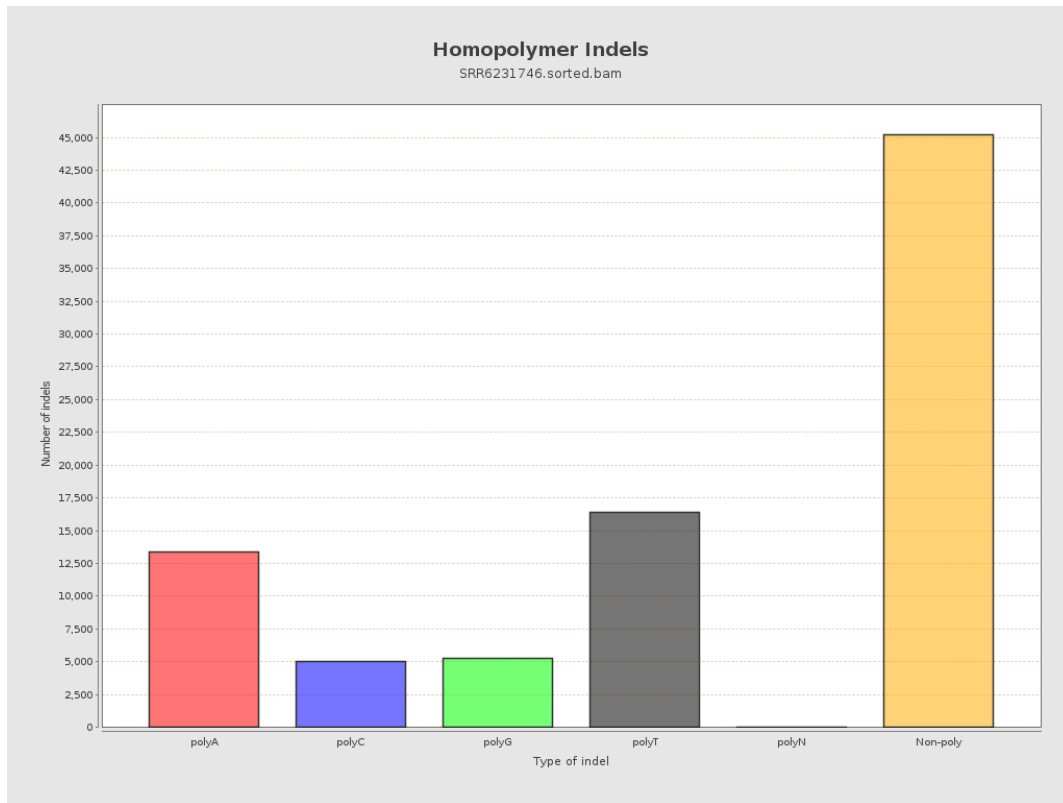
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

