

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 03:41:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231800.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_SRR6231800 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231800.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 03:41:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231800.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,364,480
Mapped reads	1,985,580 / 83.98%
Unmapped reads	378,900 / 16.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,981 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	104,272 / 4.41%
Duplication rate	2.61%
Clipped reads	1,085,935 / 45.93%

2.2. ACGT Content

Number/percentage of A's	37,970,737 / 29.47%
Number/percentage of C's	25,513,036 / 19.8%
Number/percentage of T's	36,516,685 / 28.34%
Number/percentage of G's	28,839,103 / 22.38%
Number/percentage of N's	10,069 / 0.01%
GC Percentage	42.18%

2.3. Coverage

Mean	0.0416

Standard Deviation	4.2793
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2.4. Mapping Quality

Mean Mapping Quality	45.12
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2.5. Mismatches and indels

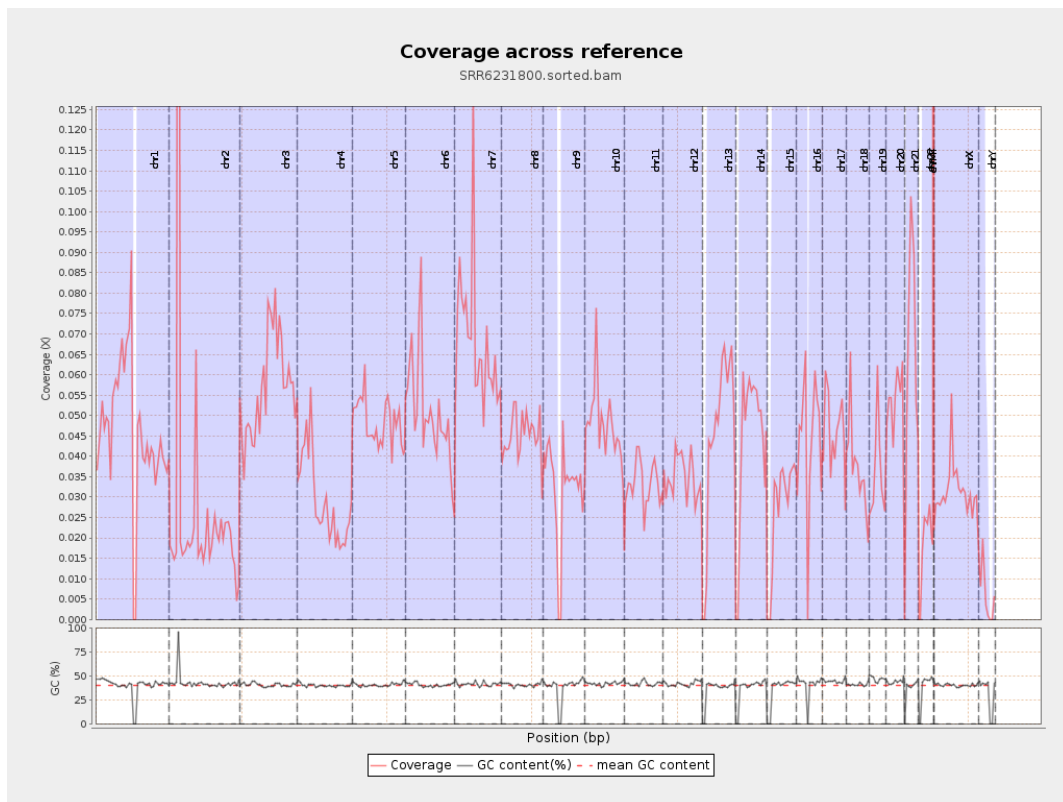
General error rate	0.62%
Mismatches	780,342
Insertions	9,178
Mapped reads with at least one insertion	0.46%
Deletions	27,960
Mapped reads with at least one deletion	1.4%
Homopolymer indels	44.56%

2.6. Chromosome stats

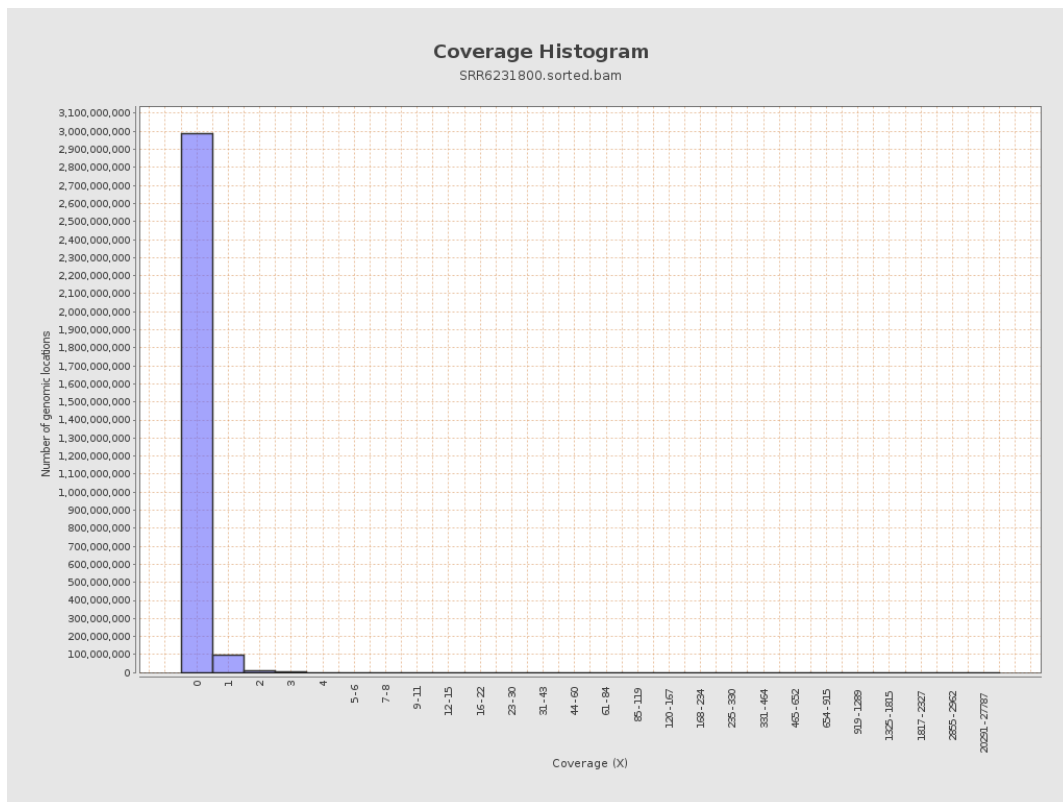
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11513023	0.0462	0.8739
chr2	243199373	7104455	0.0292	15.1854
chr3	198022430	11353410	0.0573	0.2645
chr4	191154276	5549587	0.029	0.2051
chr5	180915260	8746246	0.0483	0.2466
chr6	171115067	8732683	0.051	0.319
chr7	159138663	10903559	0.0685	0.9294

chr8	146364022	6587099	0.045	0.5744
chr9	141213431	4494388	0.0318	0.3498
chr10	135534747	6504442	0.048	0.3981
chr11	135006516	4431863	0.0328	0.3361
chr12	133851895	4681346	0.035	0.2151
chr13	115169878	5234858	0.0455	0.2349
chr14	107349540	4679288	0.0436	0.2663
chr15	102531392	2779254	0.0271	0.1813
chr16	90354753	4019364	0.0445	0.2718
chr17	81195210	3709525	0.0457	0.2761
chr18	78077248	2923299	0.0374	0.8251
chr19	59128983	2168300	0.0367	0.5279
chr20	63025520	3373151	0.0535	0.2658
chr21	48129895	3085439	0.0641	0.2958
chr22	51304566	916456	0.0179	0.1454
chrMT	16571	185417	11.1892	6.729
chrX	155270560	4868818	0.0314	0.2309
chrY	59373566	351023	0.0059	0.131

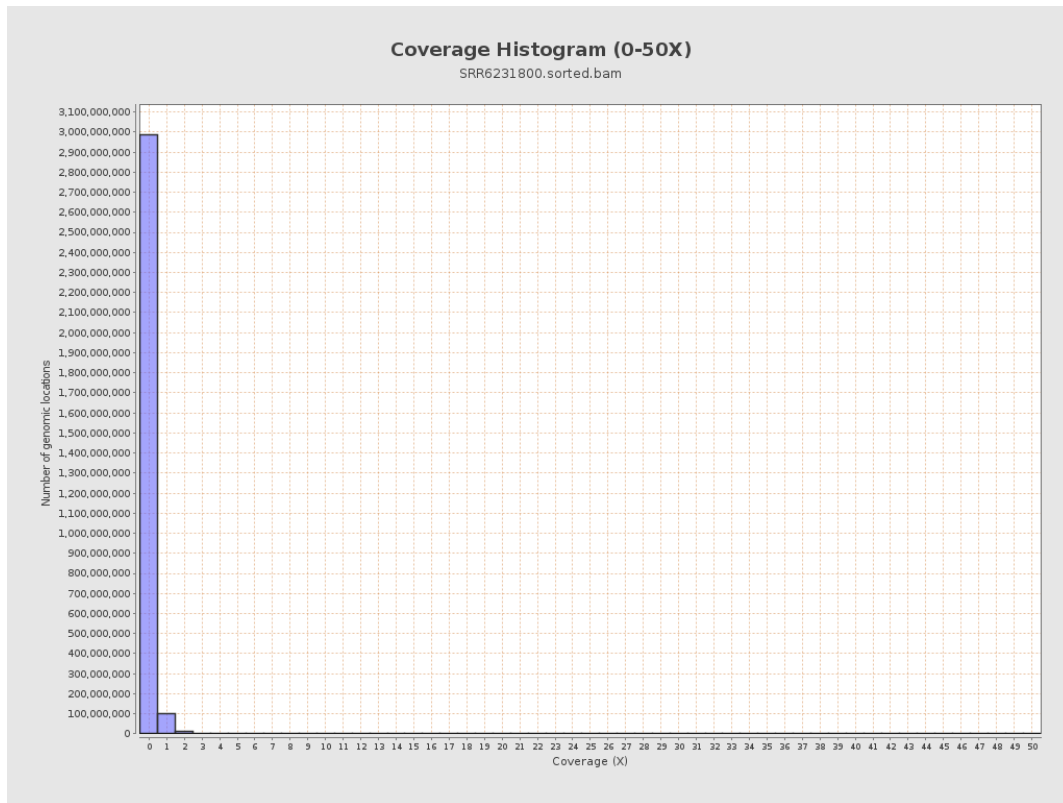
3. Results : Coverage across reference



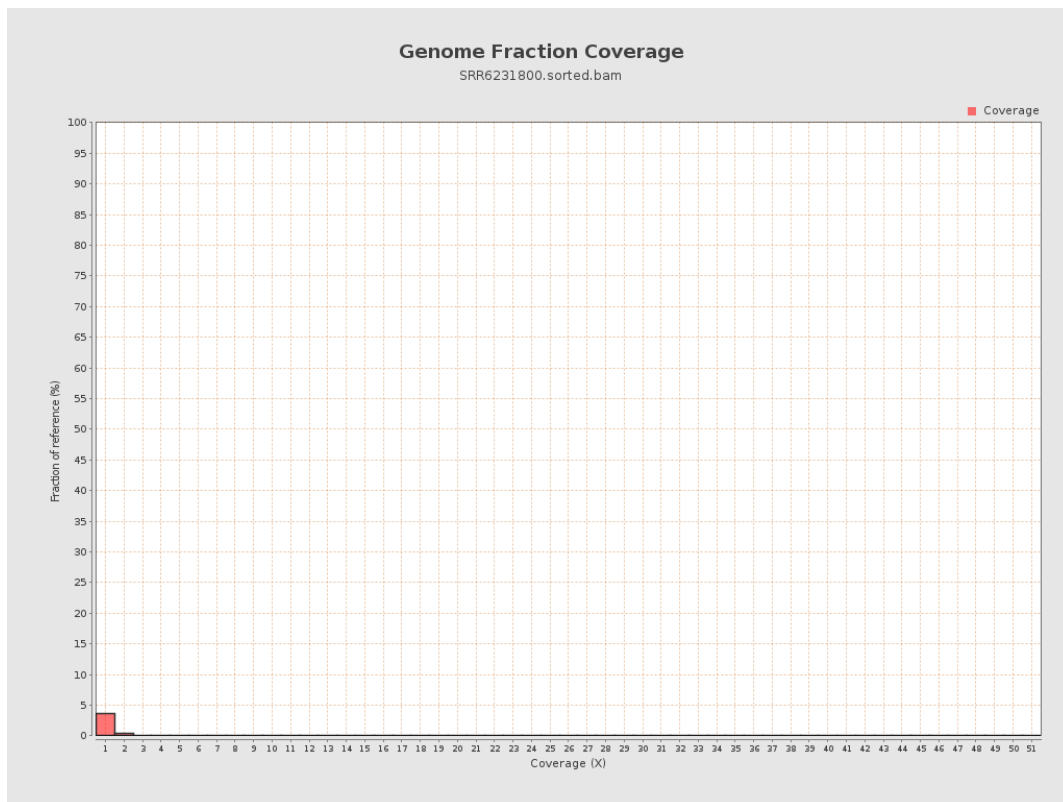
4. Results : Coverage Histogram



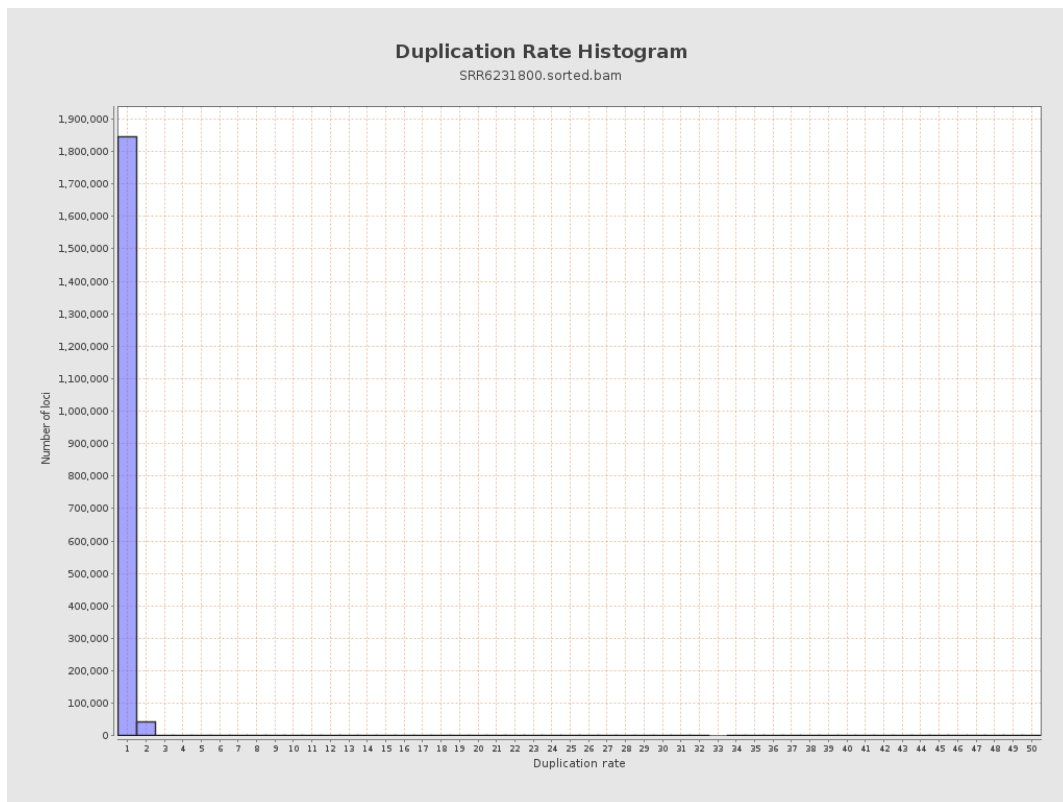
5. Results : Coverage Histogram (0-50X)



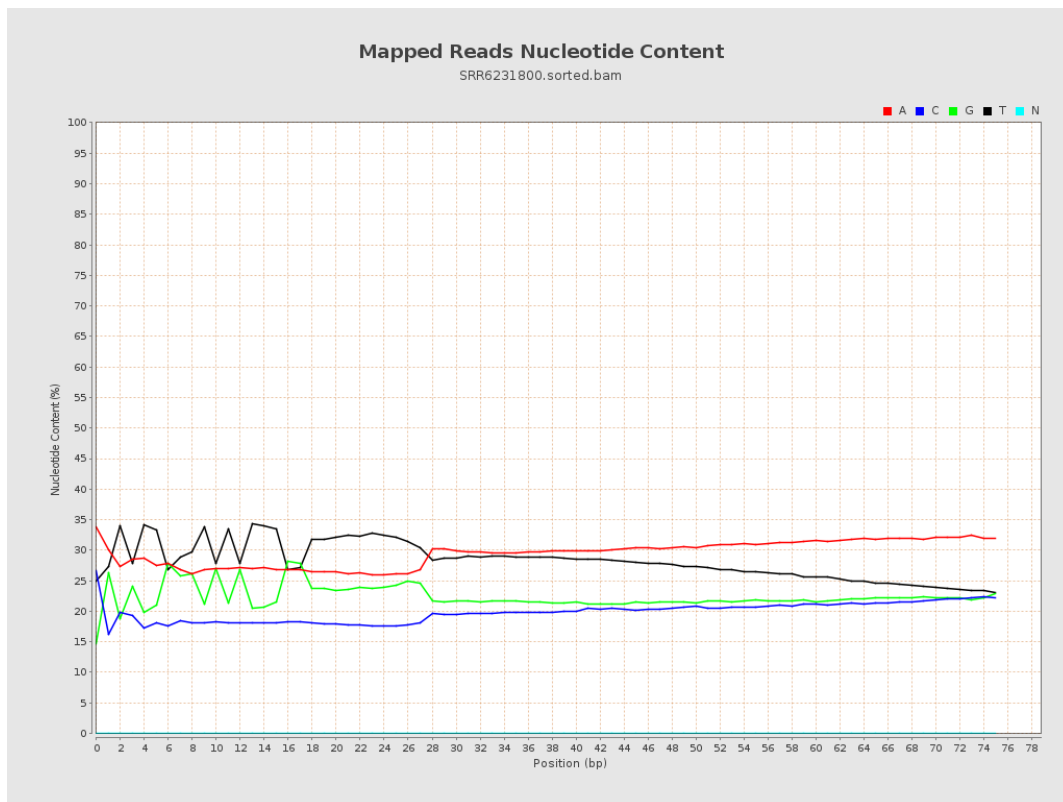
6. Results : Genome Fraction Coverage



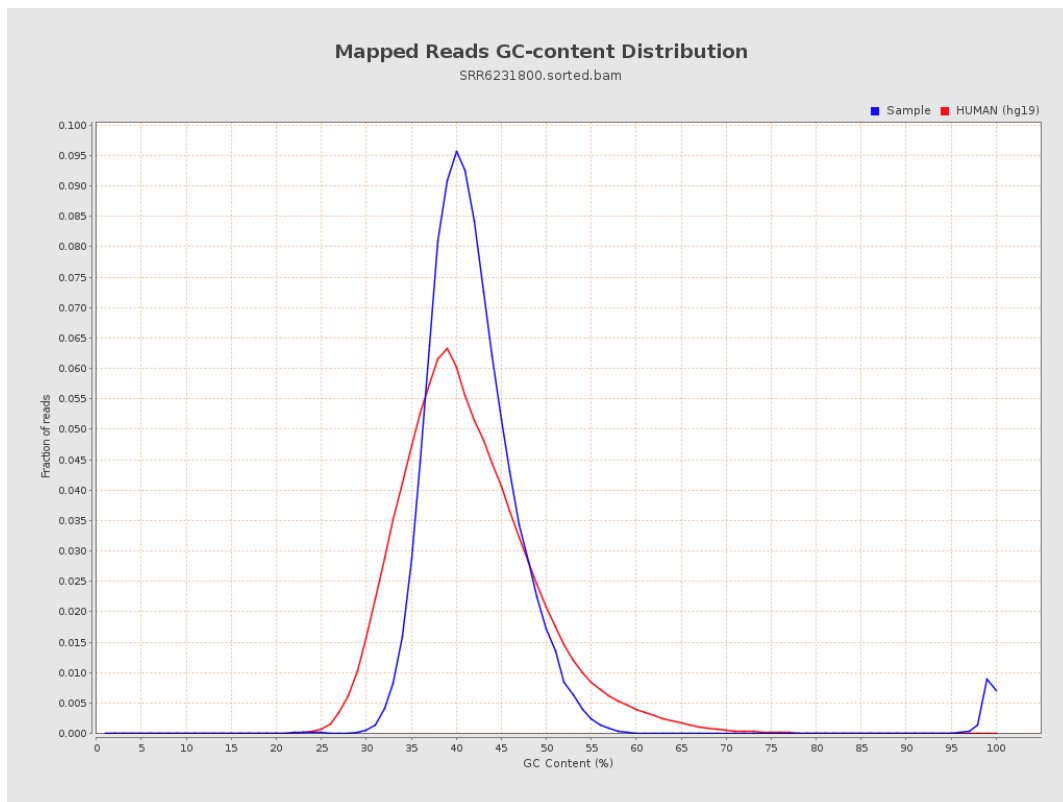
7. Results : Duplication Rate Histogram



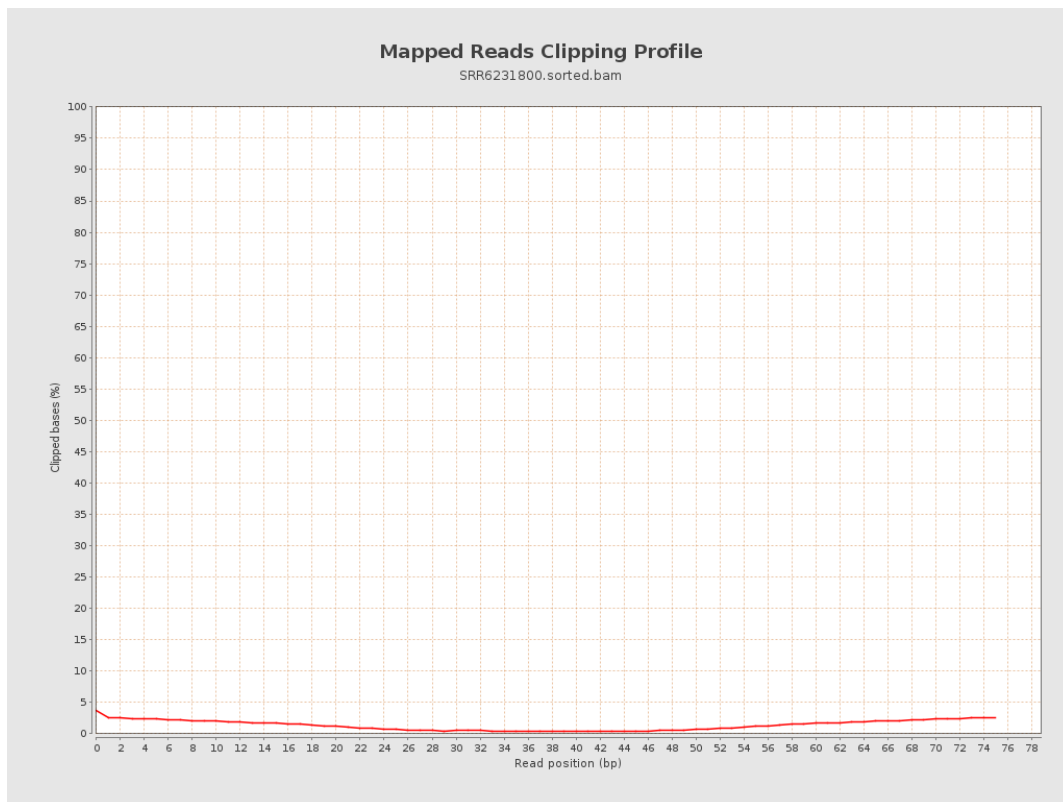
8. Results : Mapped Reads Nucleotide Content



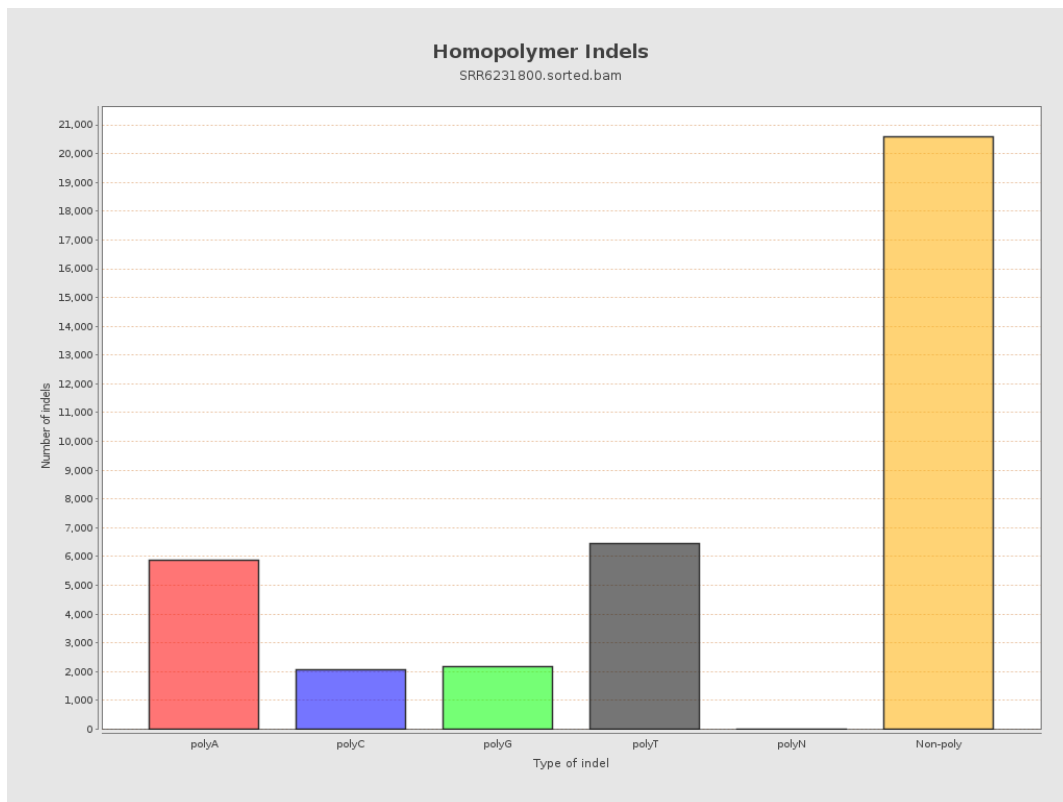
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

