

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 06:25:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231835.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_SRR6231835 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231835.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 06:25:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231835.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,539,723
Mapped reads	1,818,805 / 71.61%
Unmapped reads	720,918 / 28.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,571 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	471,929 / 18.58%
Duplication rate	18.07%
Clipped reads	1,167,834 / 45.98%

2.2. ACGT Content

Number/percentage of A's	28,031,193 / 25.13%
Number/percentage of C's	19,551,702 / 17.53%
Number/percentage of T's	37,286,105 / 33.43%
Number/percentage of G's	26,639,476 / 23.88%
Number/percentage of N's	39,189 / 0.04%
GC Percentage	41.41%

2.3. Coverage

Mean	0.036

Standard Deviation	0.5393
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2.4. Mapping Quality

Mean Mapping Quality	45.1
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2.5. Mismatches and indels

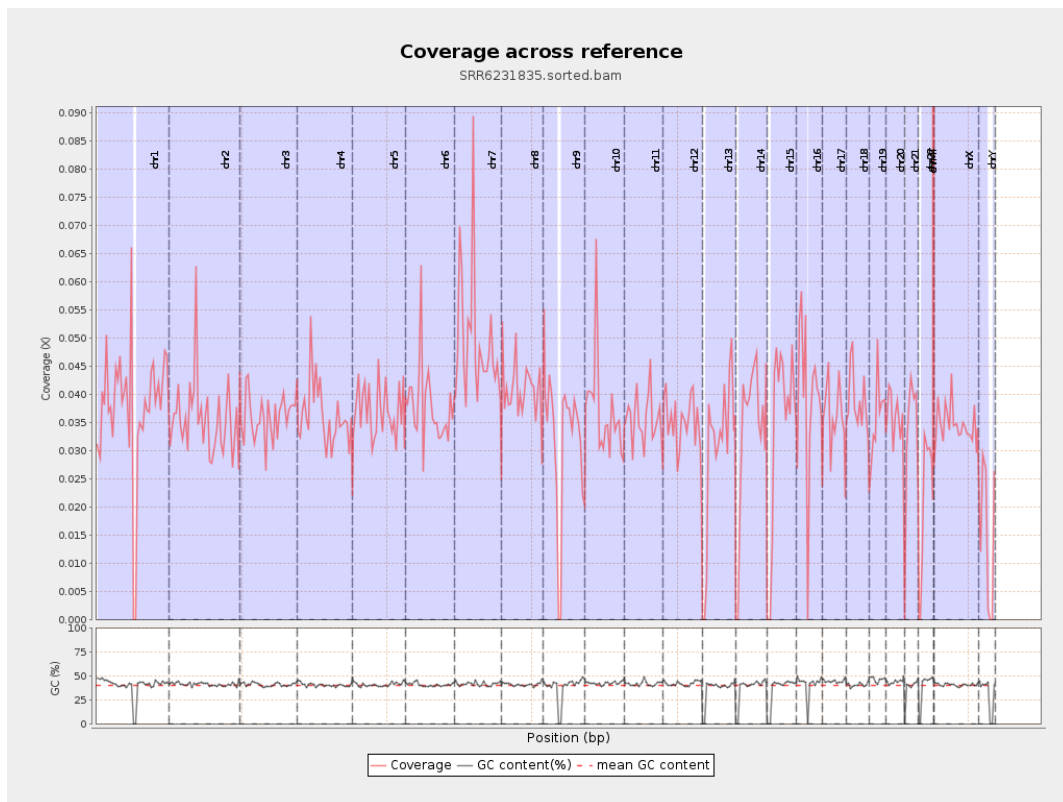
General error rate	0.71%
Mismatches	781,685
Insertions	7,224
Mapped reads with at least one insertion	0.39%
Deletions	27,653
Mapped reads with at least one deletion	1.51%
Homopolymer indels	41.78%

2.6. Chromosome stats

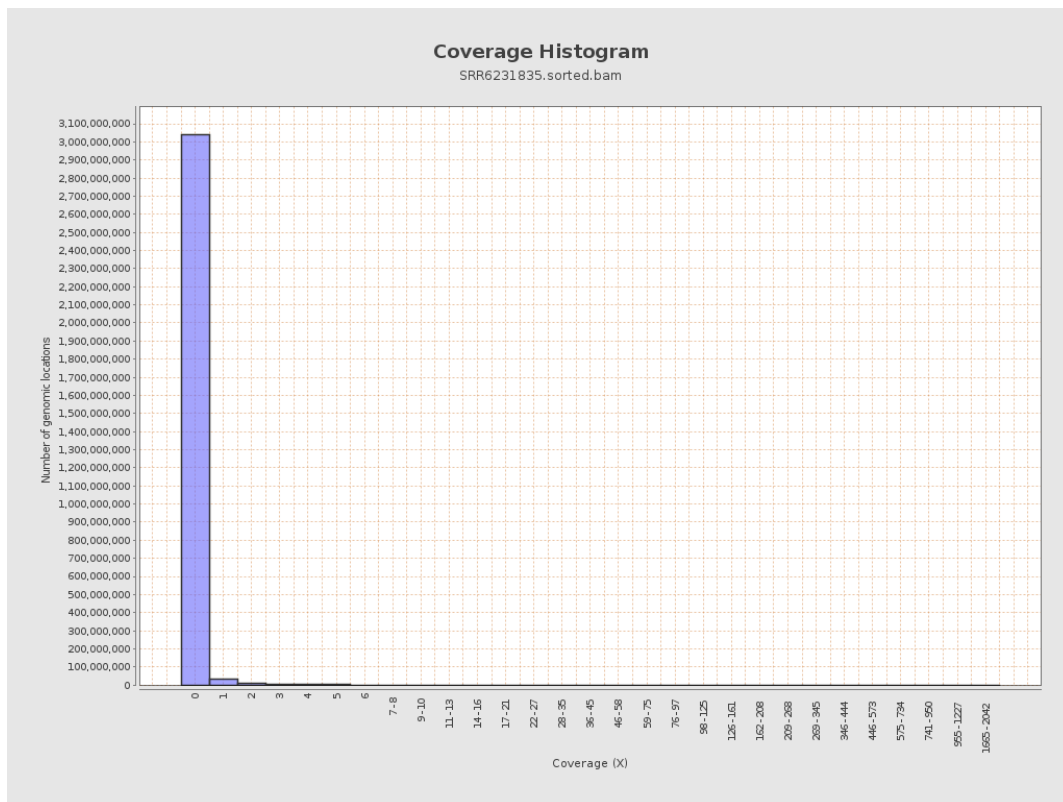
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9407405	0.0377	0.8223
chr2	243199373	8650563	0.0356	1.0018
chr3	198022430	7174742	0.0362	0.3471
chr4	191154276	6918481	0.0362	0.3581
chr5	180915260	6712733	0.0371	0.3531
chr6	171115067	6474770	0.0378	0.5074
chr7	159138663	7886196	0.0496	0.663

chr8	146364022	5977781	0.0408	0.4697
chr9	141213431	4485835	0.0318	0.3684
chr10	135534747	4979107	0.0367	0.4334
chr11	135006516	4808025	0.0356	0.3778
chr12	133851895	4689165	0.035	0.3493
chr13	115169878	3462432	0.0301	0.3592
chr14	107349540	3510961	0.0327	0.3382
chr15	102531392	3517521	0.0343	0.3584
chr16	90354753	3565830	0.0395	0.3857
chr17	81195210	2900690	0.0357	0.376
chr18	78077248	3058312	0.0392	0.8818
chr19	59128983	2117059	0.0358	0.5628
chr20	63025520	2249155	0.0357	0.3595
chr21	48129895	1585095	0.0329	0.336
chr22	51304566	1078887	0.021	0.2685
chrMT	16571	191930	11.5823	10.3852
chrX	155270560	5357368	0.0345	0.3588
chrY	59373566	835398	0.0141	0.2712

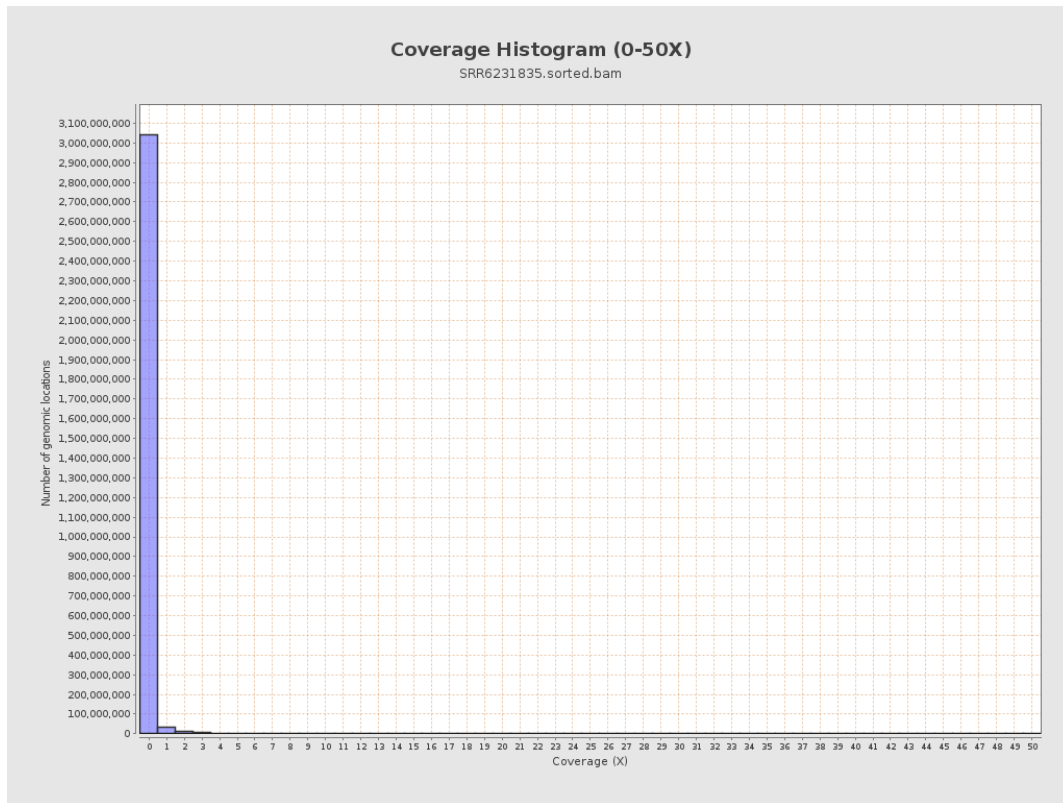
3. Results : Coverage across reference



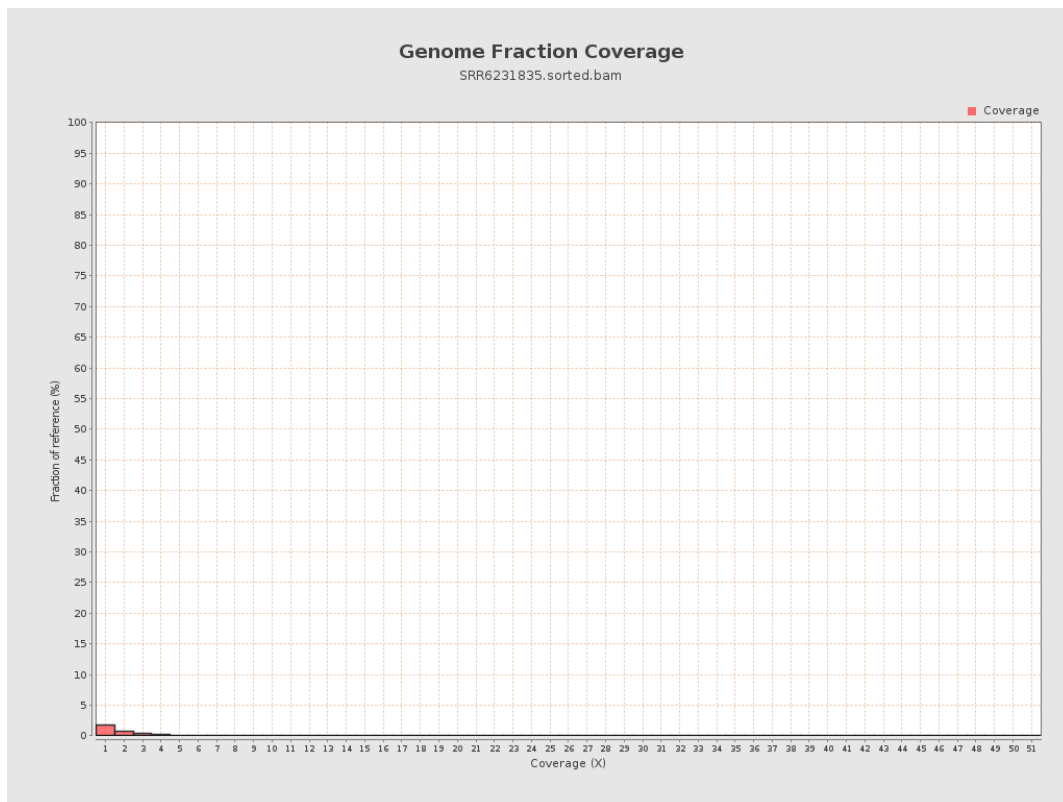
4. Results : Coverage Histogram



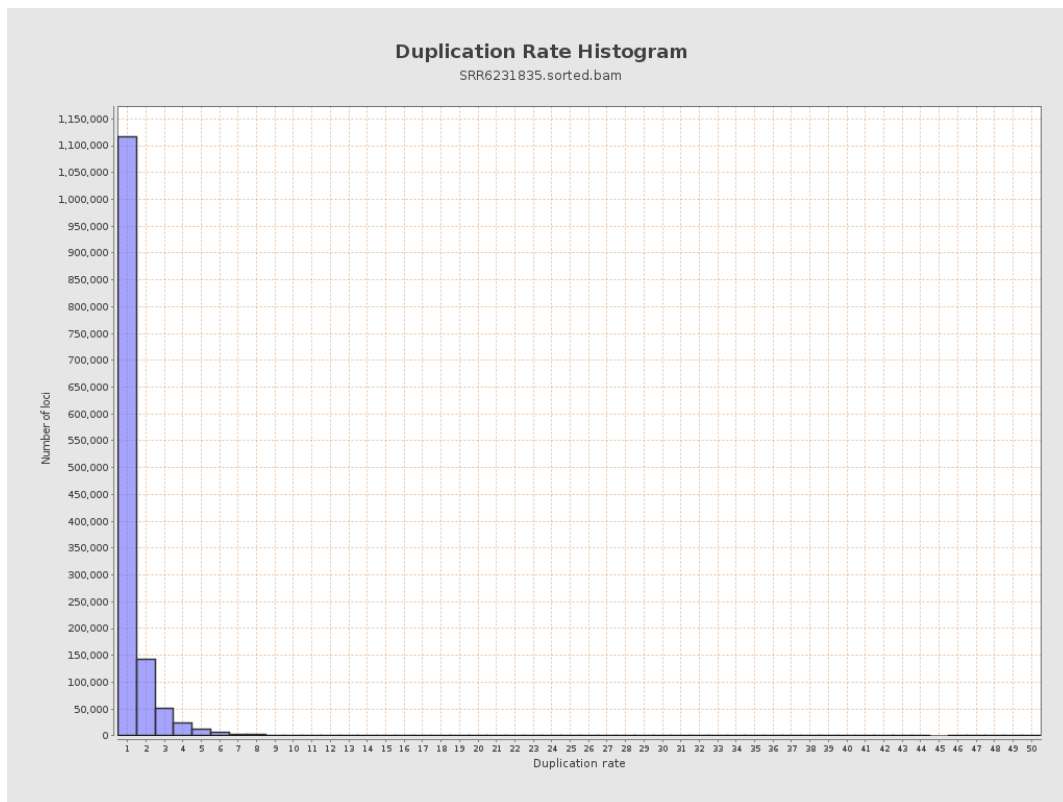
5. Results : Coverage Histogram (0-50X)



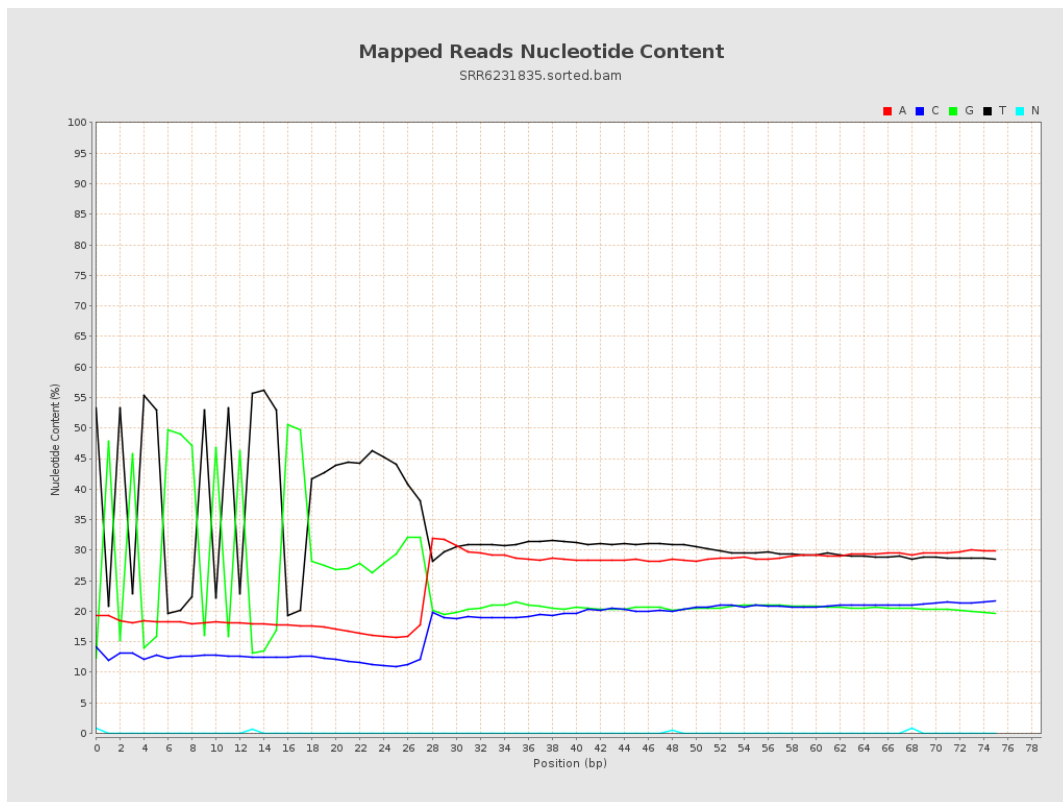
6. Results : Genome Fraction Coverage



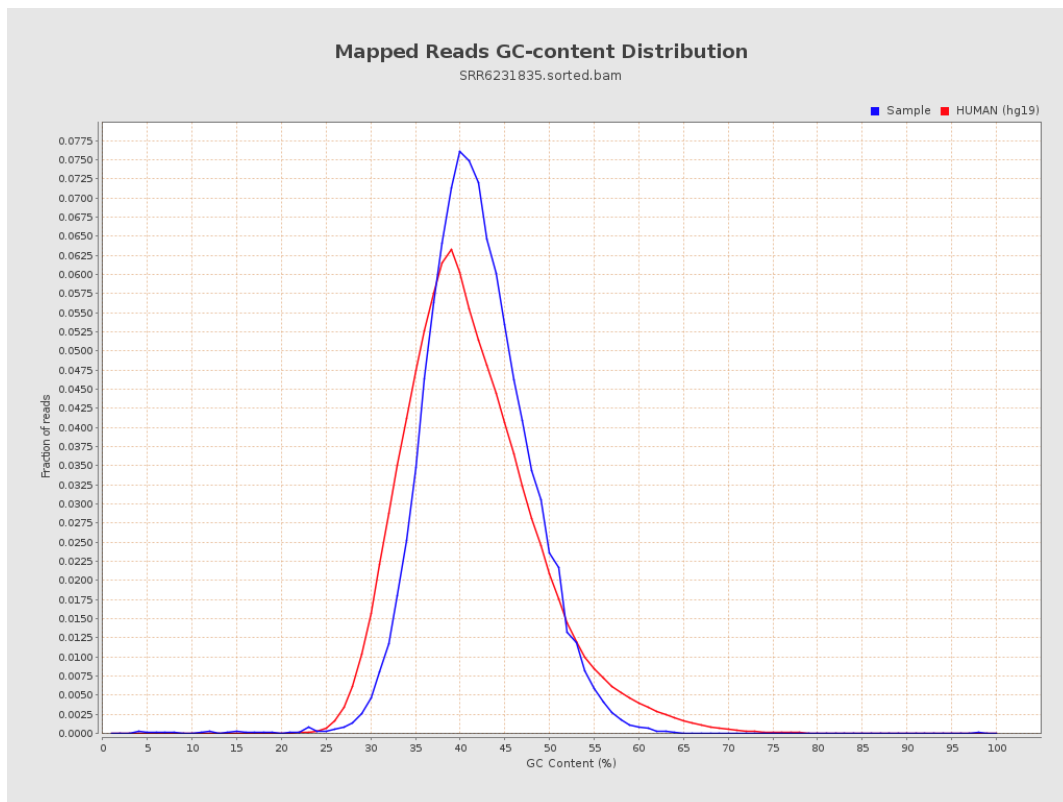
7. Results : Duplication Rate Histogram



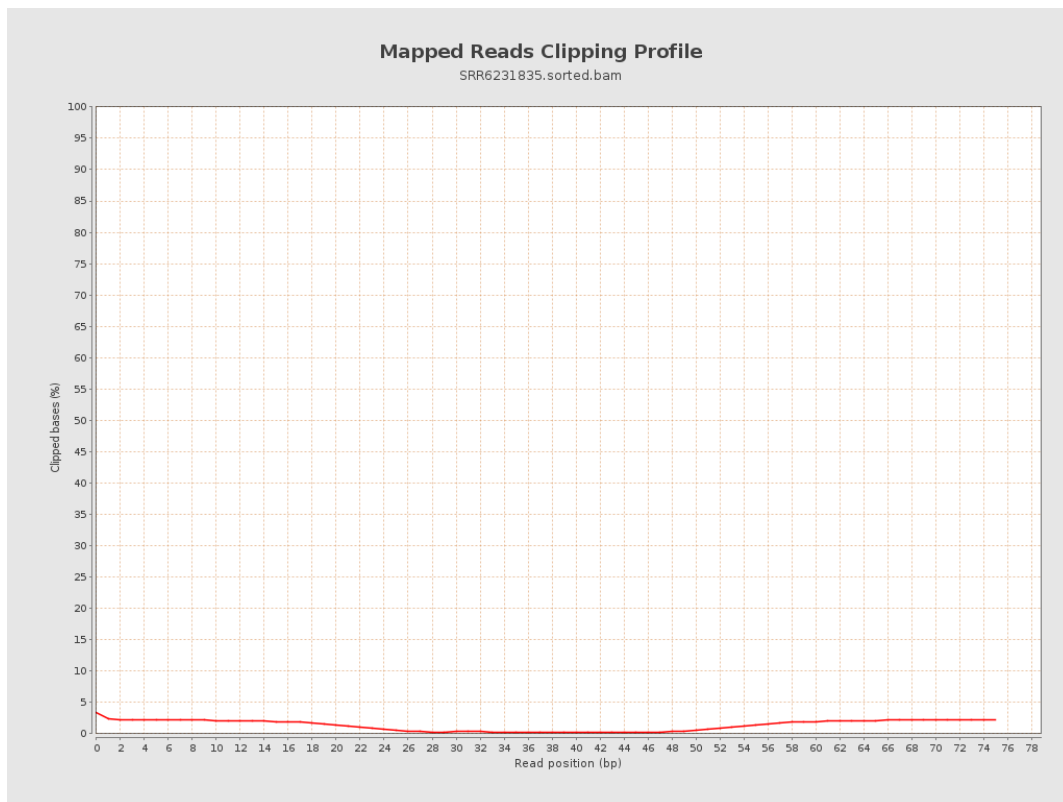
8. Results : Mapped Reads Nucleotide Content



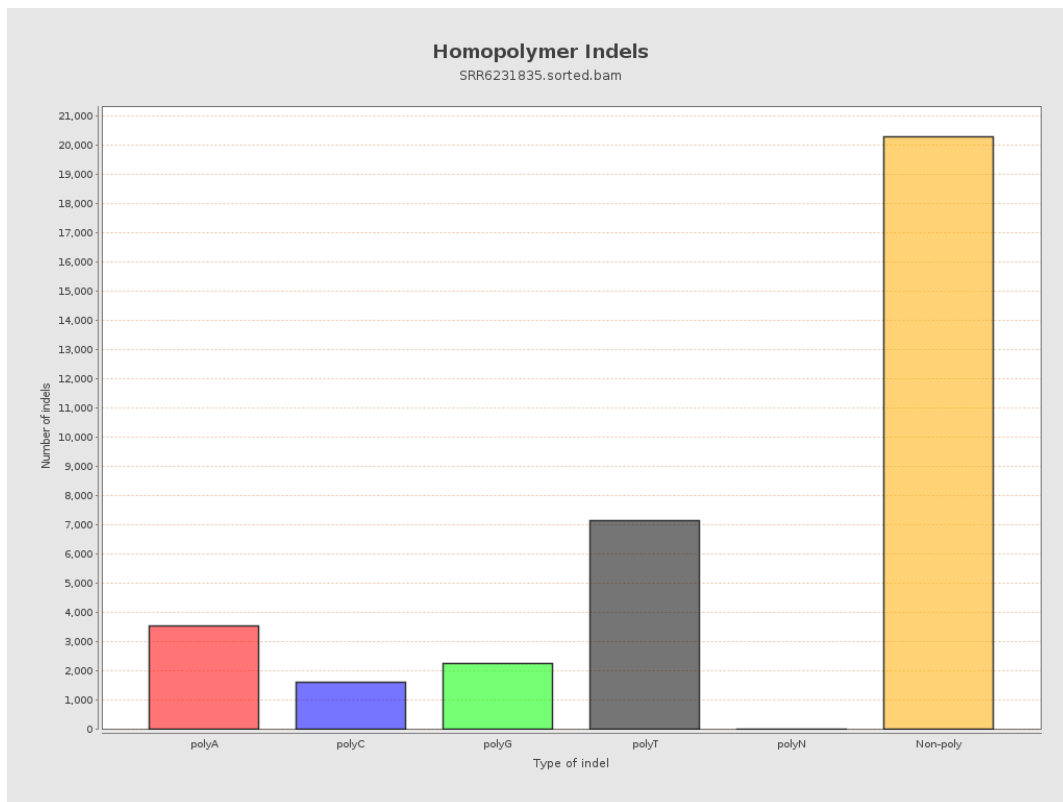
9. Results : Mapped Reads GC-content Distribution



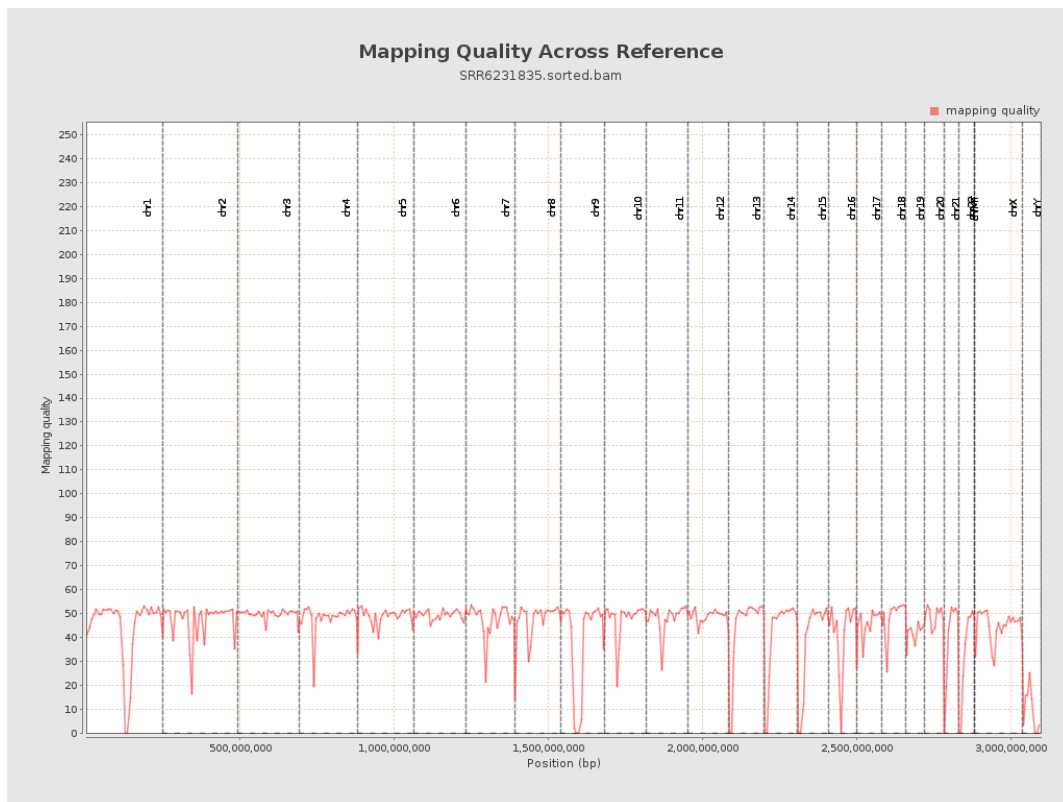
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

