

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 03:49:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231802.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_SRR6231802 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231802.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 03:49:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231802.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,334,042
Mapped reads	2,043,590 / 61.29%
Unmapped reads	1,290,452 / 38.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,778 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	118,049 / 3.54%
Duplication rate	3.35%
Clipped reads	1,373,673 / 41.2%

2.2. ACGT Content

Number/percentage of A's	37,475,926 / 29.9%
Number/percentage of C's	25,024,558 / 19.97%
Number/percentage of T's	35,165,595 / 28.06%
Number/percentage of G's	27,663,061 / 22.07%
Number/percentage of N's	10,159 / 0.01%
GC Percentage	42.04%

2.3. Coverage

Mean	0.0405

Standard Deviation	4.3084
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2.4. Mapping Quality

Mean Mapping Quality	44.61
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2.5. Mismatches and indels

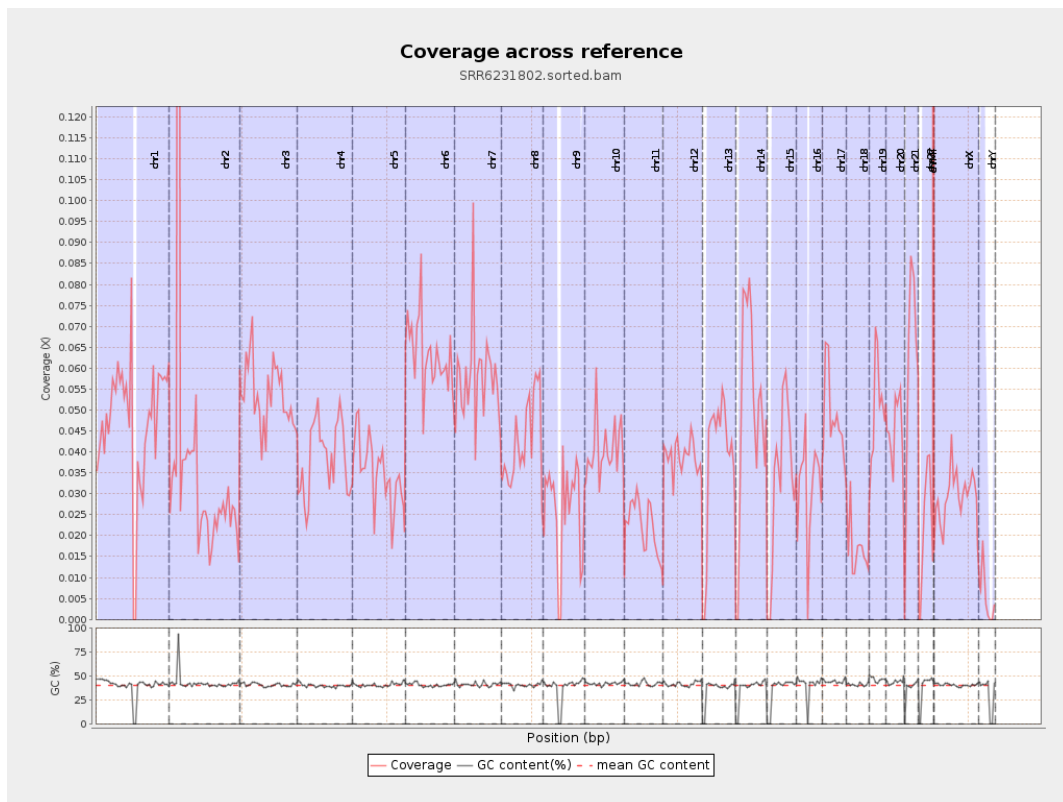
General error rate	0.6%
Mismatches	733,118
Insertions	8,892
Mapped reads with at least one insertion	0.43%
Deletions	26,711
Mapped reads with at least one deletion	1.3%
Homopolymer indels	44.4%

2.6. Chromosome stats

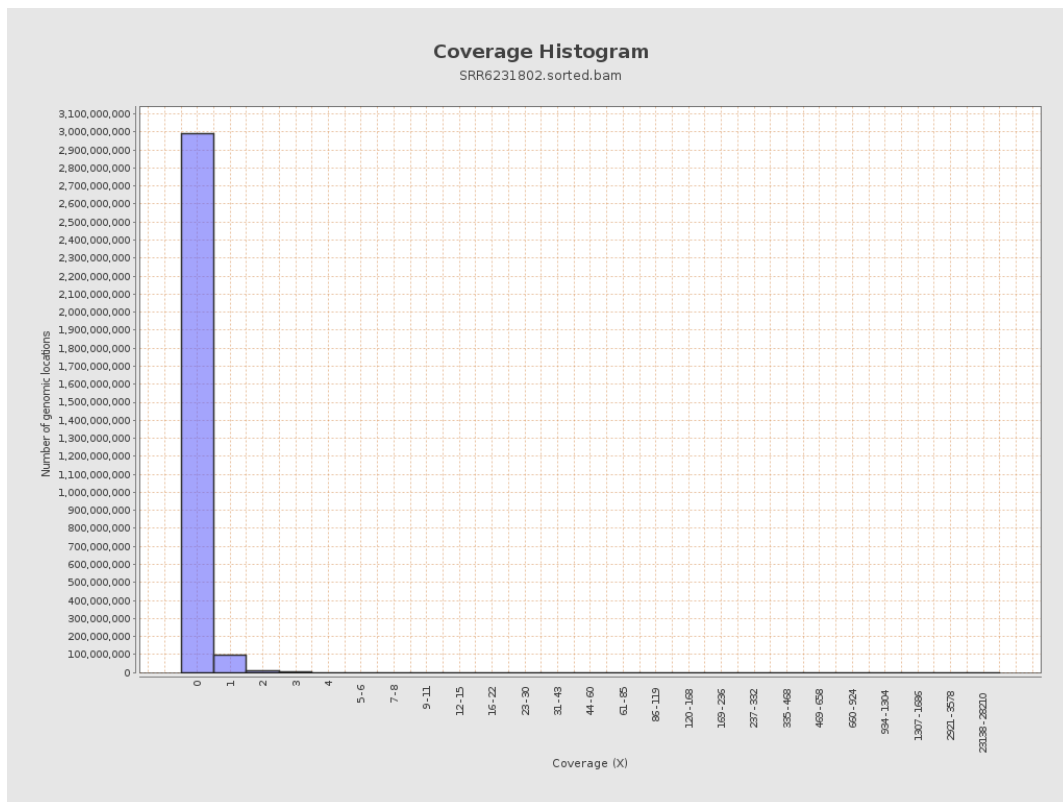
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11757714	0.0472	0.8799
chr2	243199373	9353832	0.0385	15.3068
chr3	198022430	10665251	0.0539	0.2591
chr4	191154276	7346803	0.0384	0.2275
chr5	180915260	6295397	0.0348	0.2126
chr6	171115067	10805488	0.0631	0.3427
chr7	159138663	9243418	0.0581	0.6717

chr8	146364022	6238461	0.0426	0.5662
chr9	141213431	3706116	0.0262	0.2528
chr10	135534747	5483207	0.0405	0.3155
chr11	135006516	2997497	0.0222	0.2479
chr12	133851895	5232102	0.0391	0.2256
chr13	115169878	4379520	0.038	0.2191
chr14	107349540	5426168	0.0505	0.2742
chr15	102531392	3422087	0.0334	0.2049
chr16	90354753	2871319	0.0318	0.2246
chr17	81195210	3883594	0.0478	0.2759
chr18	78077248	1346337	0.0172	0.5037
chr19	59128983	3028717	0.0512	0.4851
chr20	63025520	2790987	0.0443	0.2382
chr21	48129895	2920687	0.0607	0.2843
chr22	51304566	1143139	0.0223	0.1642
chrMT	16571	169408	10.2232	6.0533
chrX	155270560	4575483	0.0295	0.2185
chrY	59373566	300631	0.0051	0.131

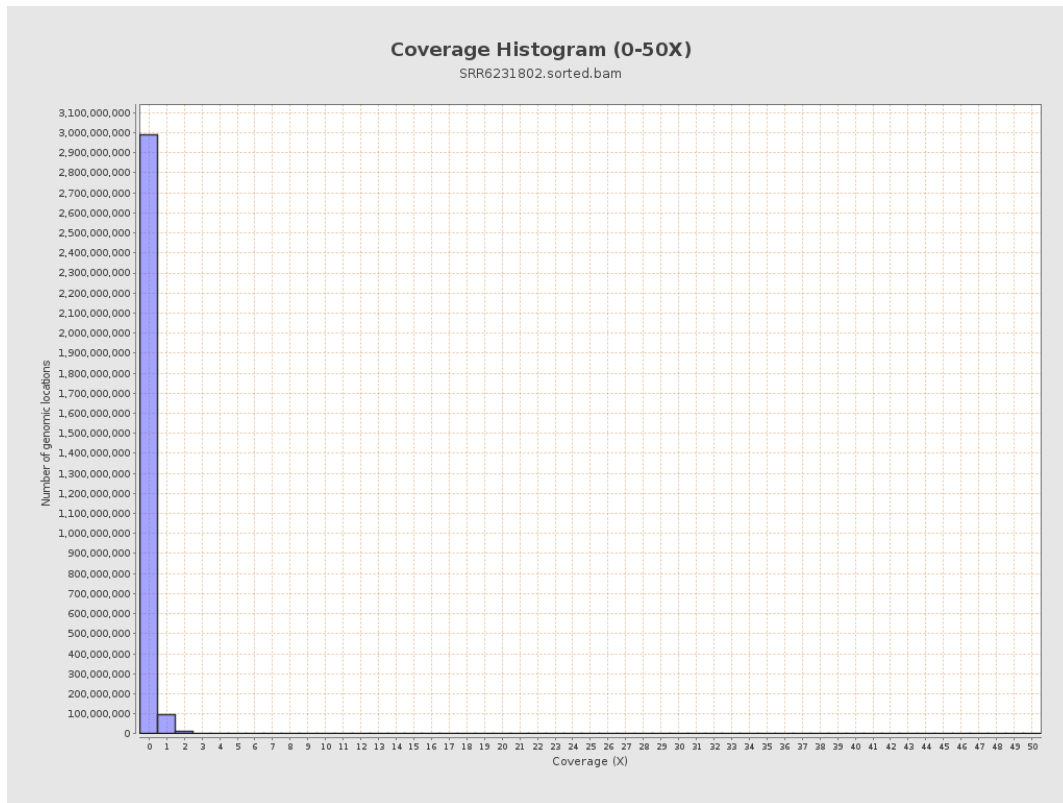
3. Results : Coverage across reference



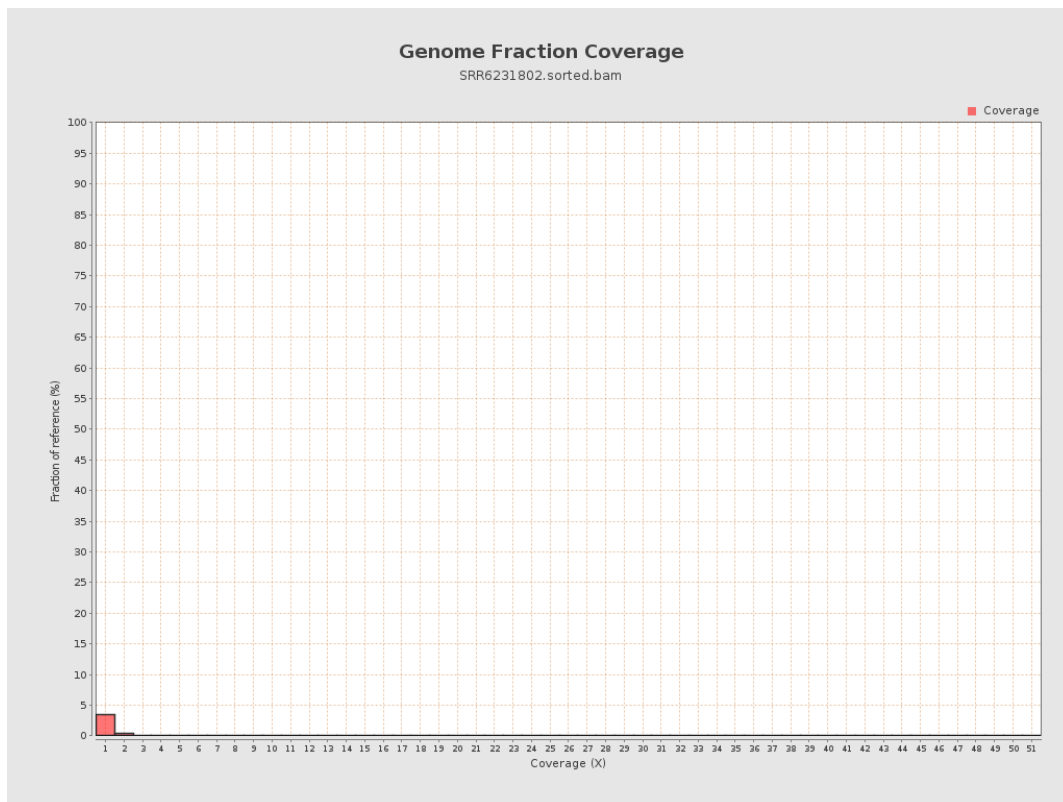
4. Results : Coverage Histogram



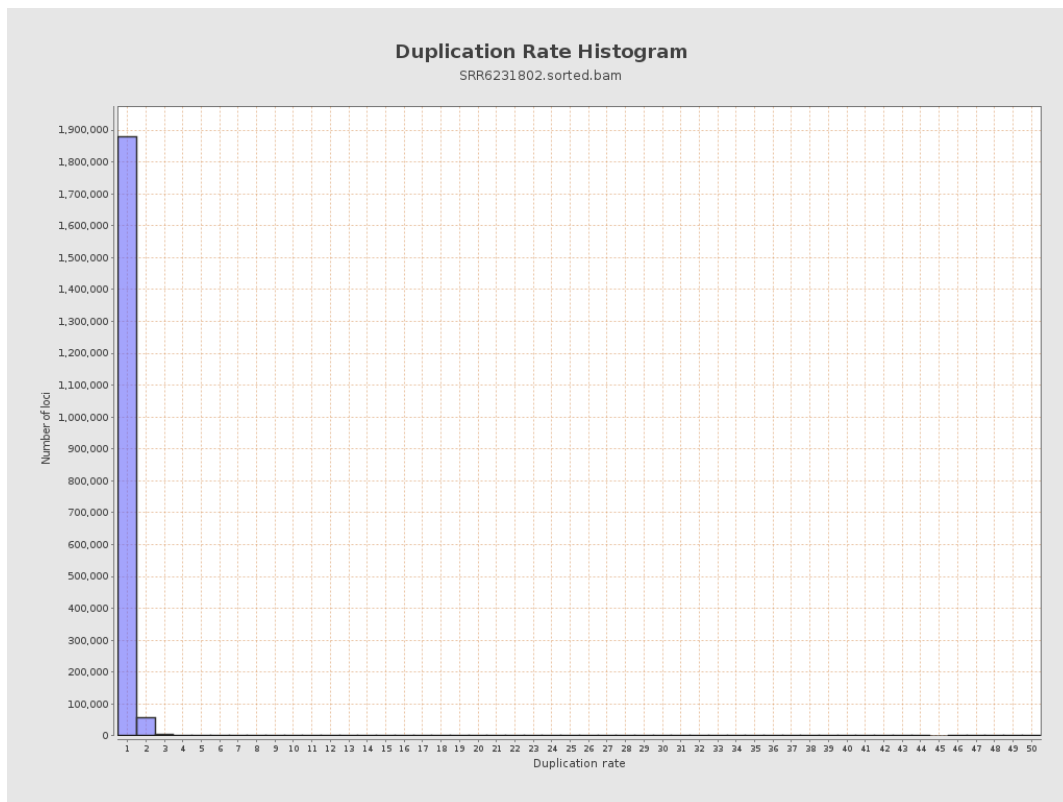
5. Results : Coverage Histogram (0-50X)



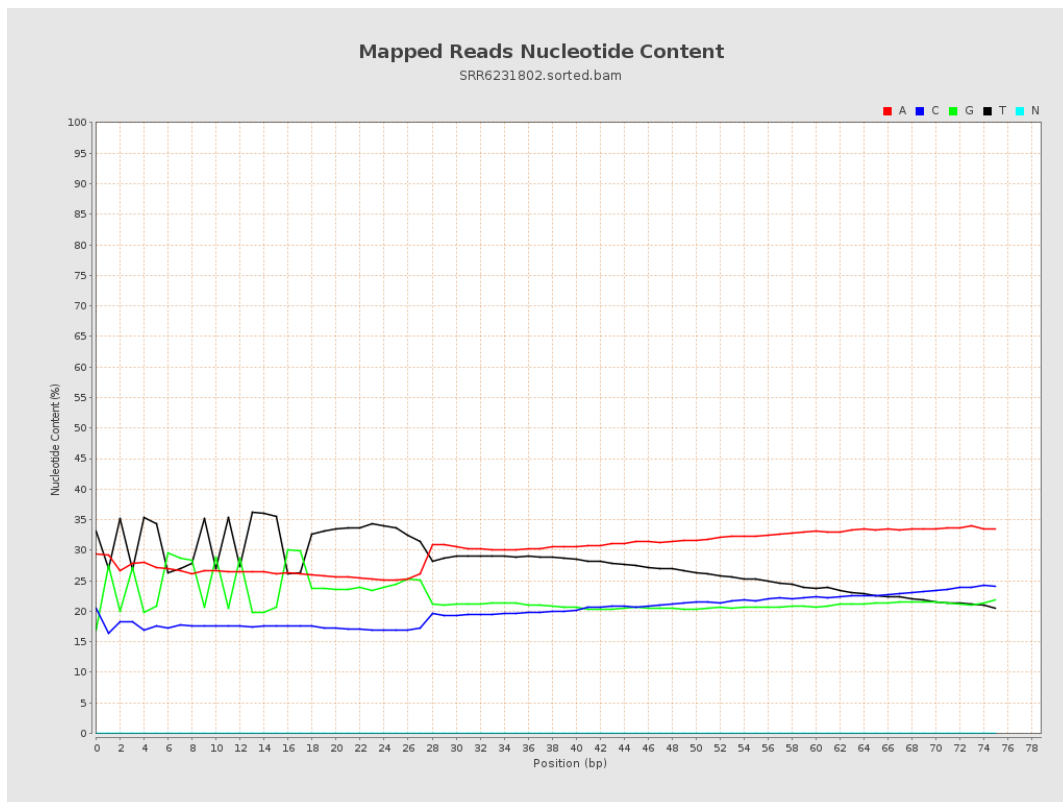
6. Results : Genome Fraction Coverage



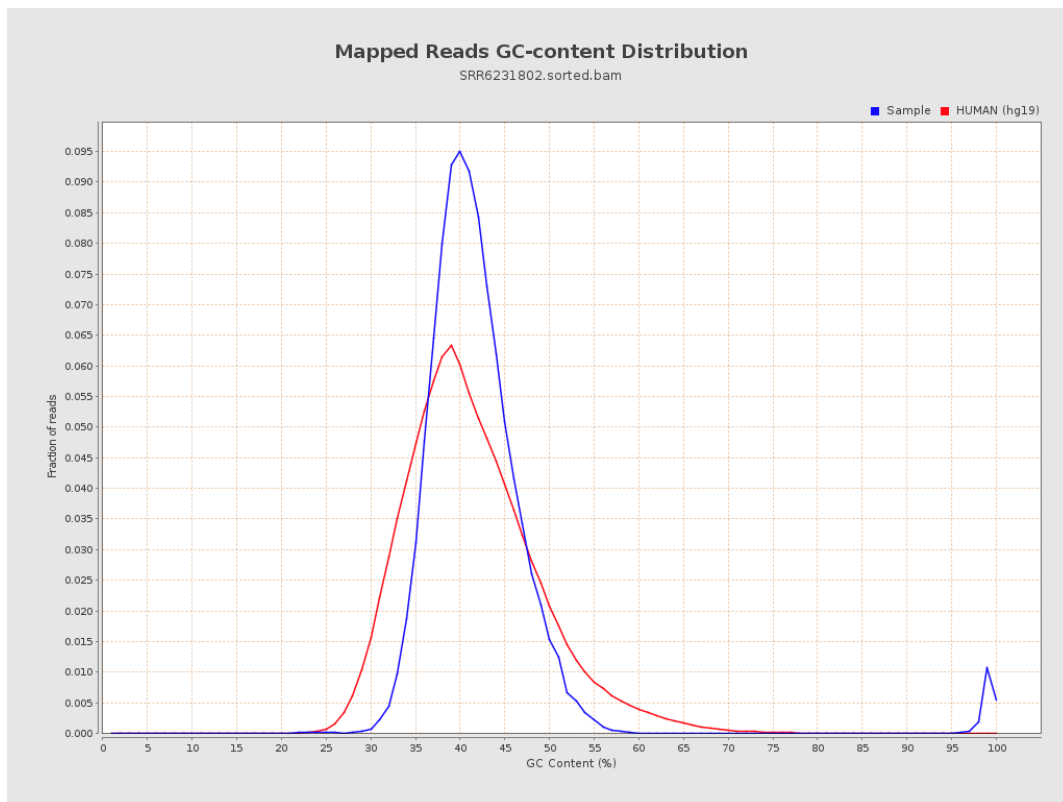
7. Results : Duplication Rate Histogram



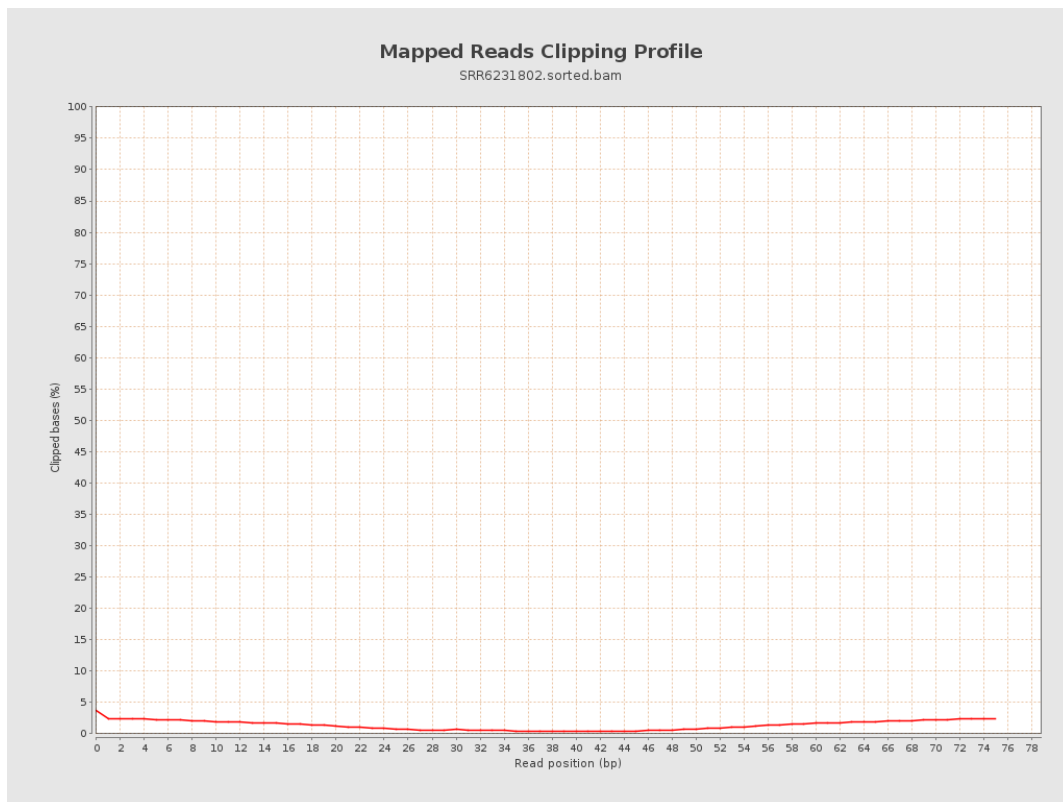
8. Results : Mapped Reads Nucleotide Content



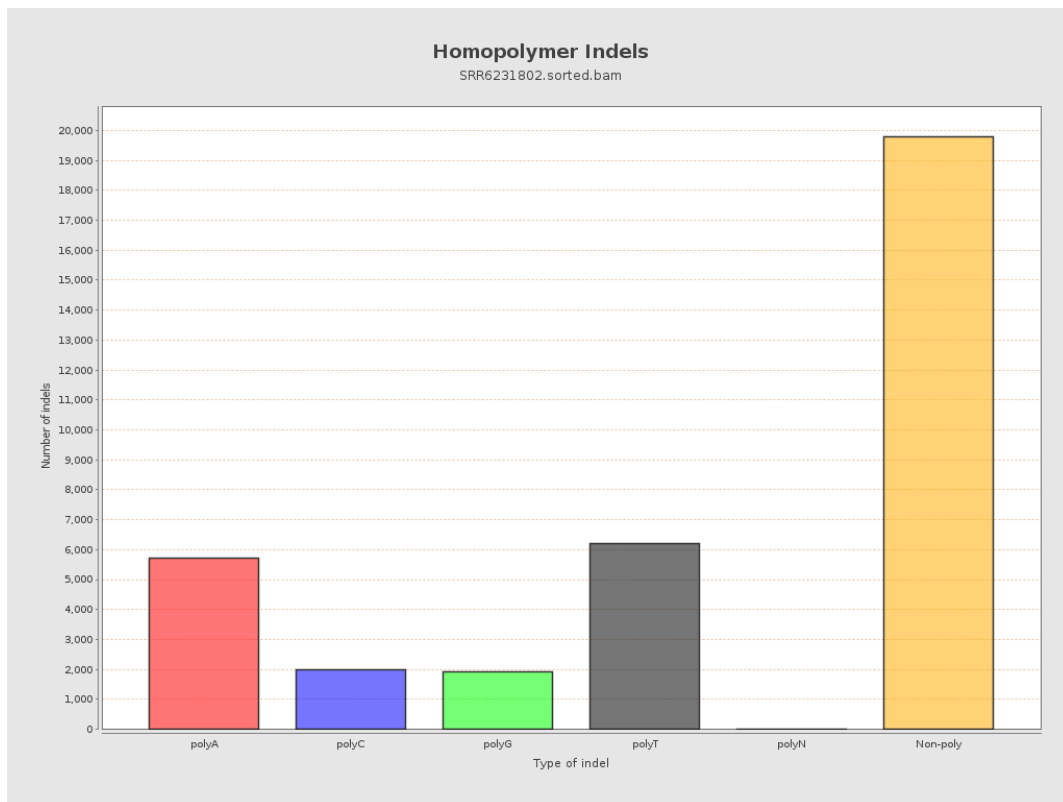
9. Results : Mapped Reads GC-content Distribution



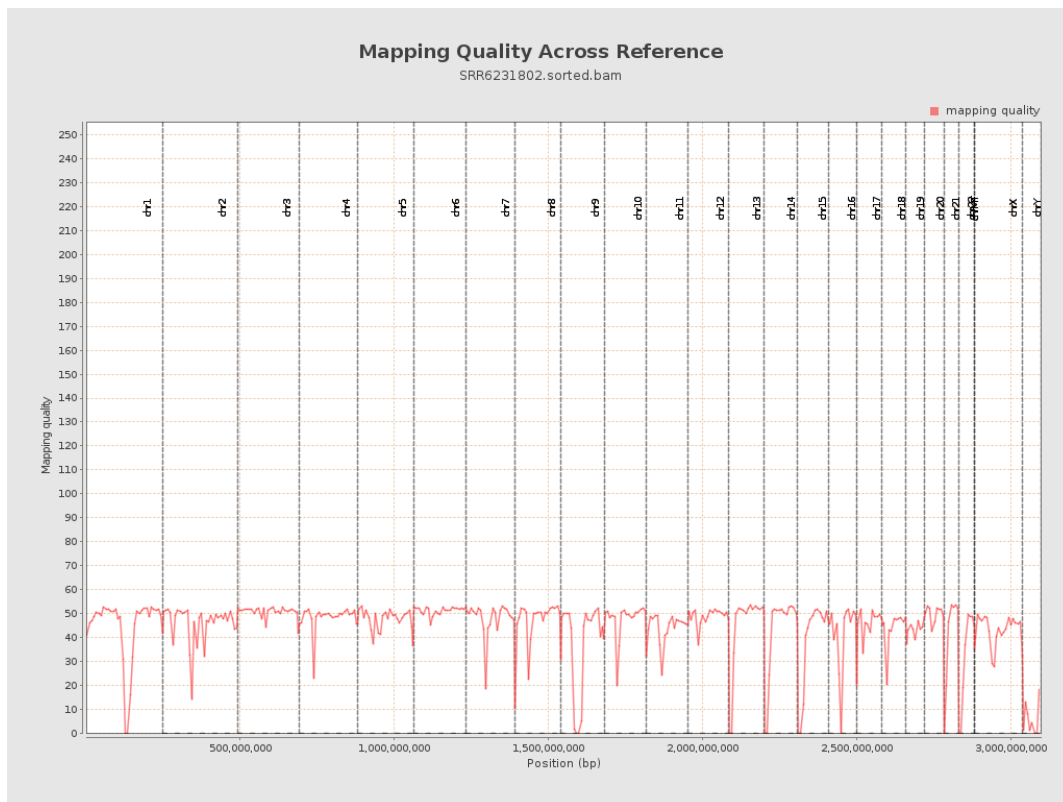
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

