

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 18:53:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230351.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_SRR6230351 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230351.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 18:53:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230351.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,560,928
Mapped reads	1,932,627 / 75.47%
Unmapped reads	628,301 / 24.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,725 / 0.34%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	92,590 / 3.62%
Duplication rate	3.84%
Clipped reads	990,010 / 38.66%

2.2. ACGT Content

Number/percentage of A's	33,504,156 / 26.76%
Number/percentage of C's	21,383,022 / 17.08%
Number/percentage of T's	41,950,864 / 33.51%
Number/percentage of G's	28,138,660 / 22.47%
Number/percentage of N's	230,542 / 0.18%
GC Percentage	39.55%

2.3. Coverage

Mean	0.0405

Standard Deviation	0.3502
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2.4. Mapping Quality

Mean Mapping Quality	46.08
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2.5. Mismatches and indels

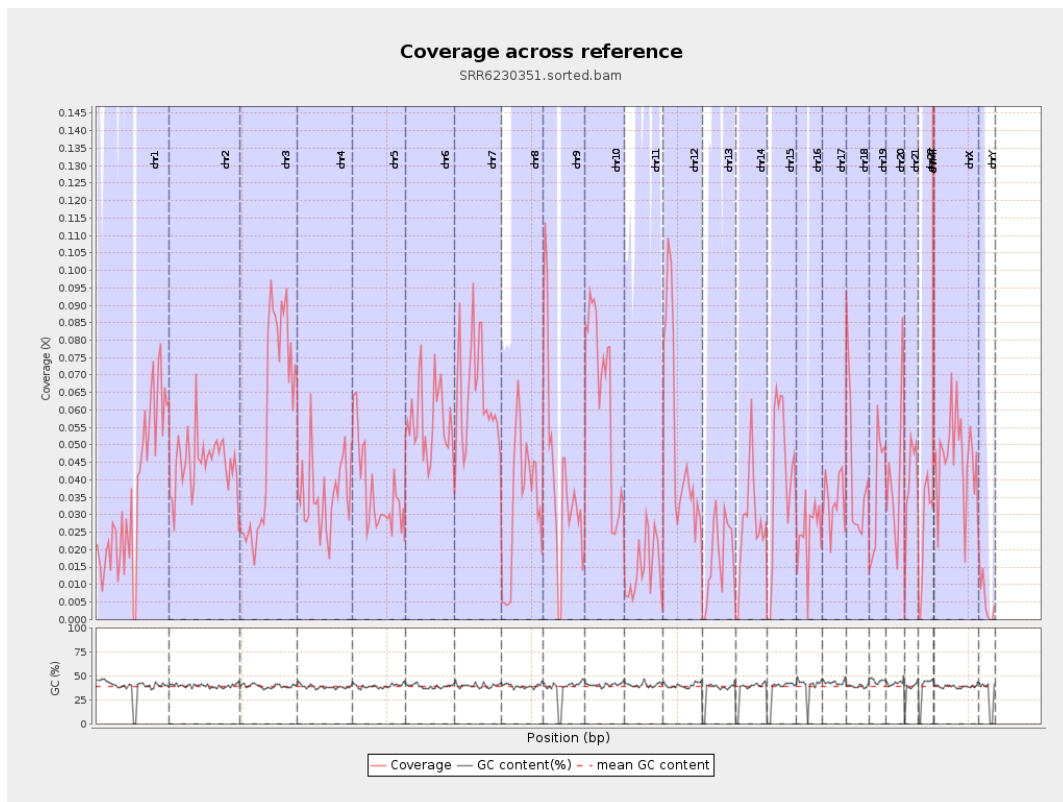
General error rate	0.93%
Mismatches	1,140,848
Insertions	11,088
Mapped reads with at least one insertion	0.57%
Deletions	30,023
Mapped reads with at least one deletion	1.54%
Homopolymer indels	49.06%

2.6. Chromosome stats

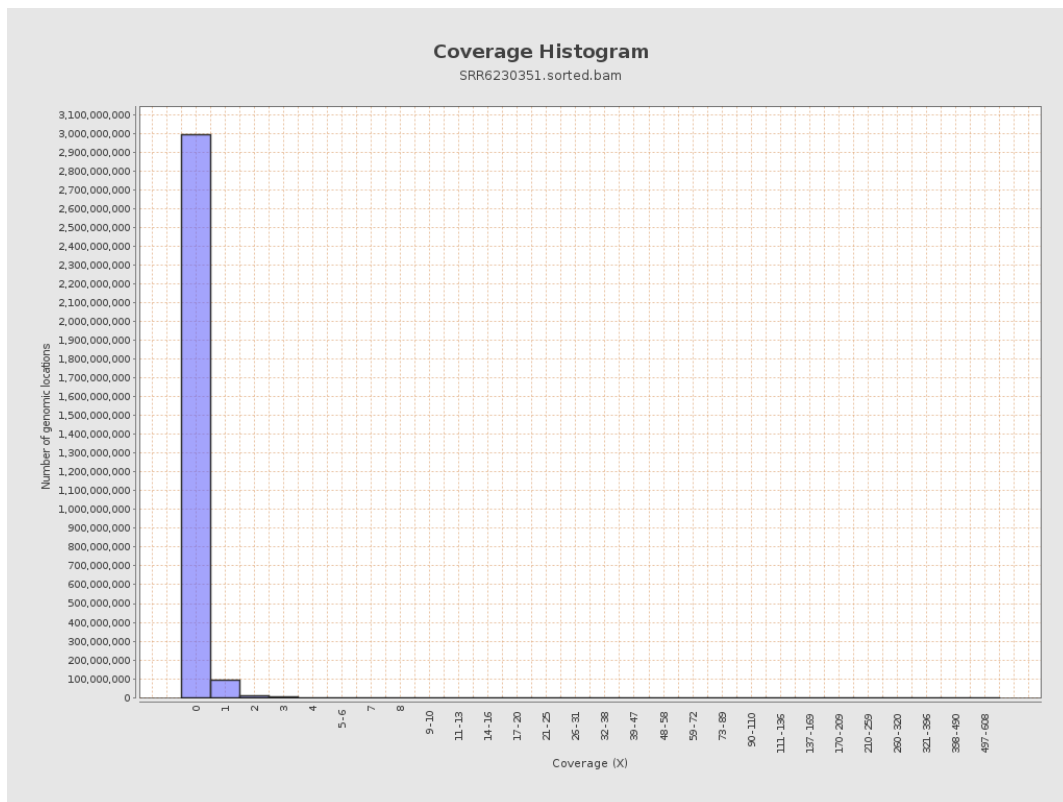
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8928317	0.0358	0.4285
chr2	243199373	10937894	0.045	0.3833
chr3	198022430	10808009	0.0546	0.2694
chr4	191154276	6853626	0.0359	0.2401
chr5	180915260	6594075	0.0364	0.2186
chr6	171115067	9712435	0.0568	0.3415
chr7	159138663	10284189	0.0646	0.6653

chr8	146364022	4839229	0.0331	0.4527
chr9	141213431	5634101	0.0399	0.361
chr10	135534747	8645229	0.0638	0.3861
chr11	135006516	1966624	0.0146	0.1781
chr12	133851895	6747992	0.0504	0.2657
chr13	115169878	2038809	0.0177	0.1535
chr14	107349540	2956472	0.0275	0.2069
chr15	102531392	4169184	0.0407	0.2305
chr16	90354753	2261864	0.025	0.211
chr17	81195210	2707498	0.0333	0.2119
chr18	78077248	3190313	0.0409	0.591
chr19	59128983	2179897	0.0369	0.3287
chr20	63025520	2687403	0.0426	0.2493
chr21	48129895	1856201	0.0386	0.2587
chr22	51304566	1299339	0.0253	0.1903
chrMT	16571	399457	24.1058	18.3128
chrX	155270560	7236430	0.0466	0.2736
chrY	59373566	321577	0.0054	0.1287

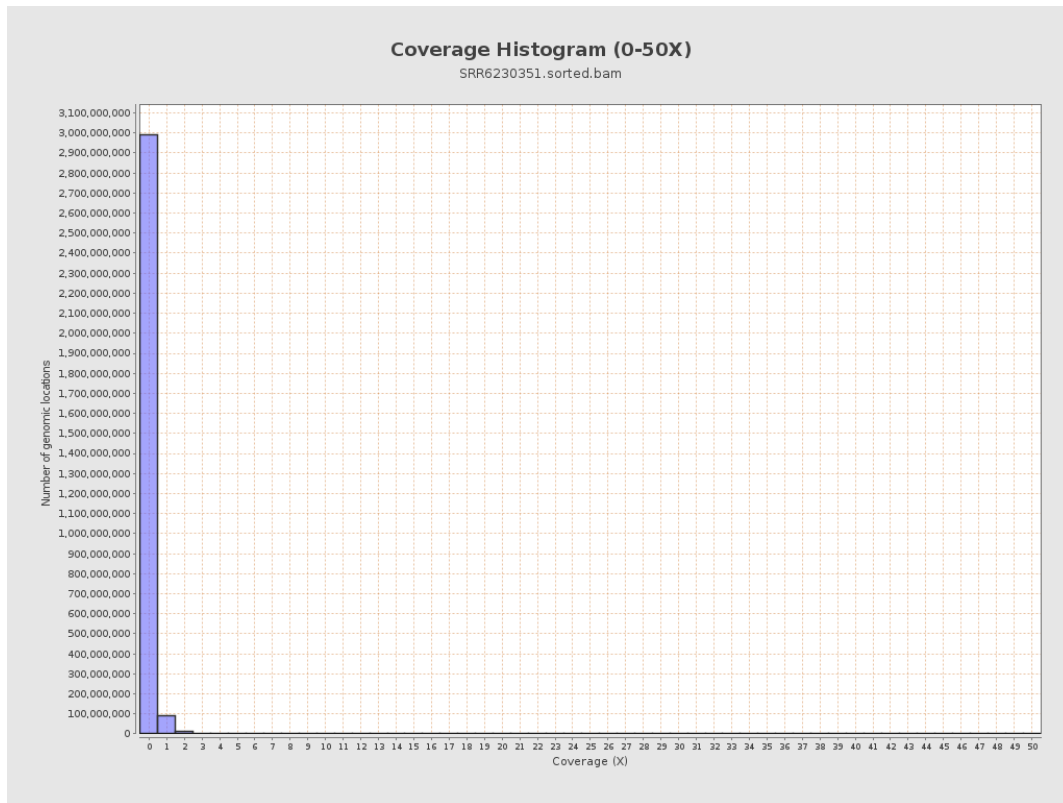
3. Results : Coverage across reference



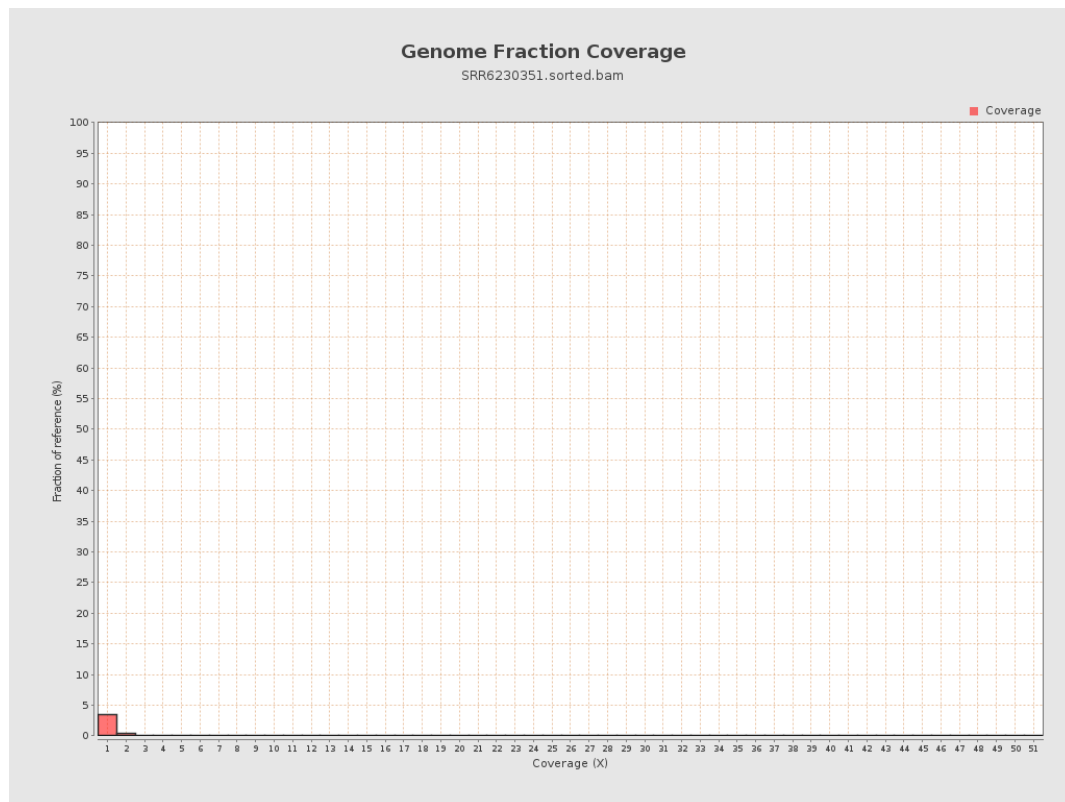
4. Results : Coverage Histogram



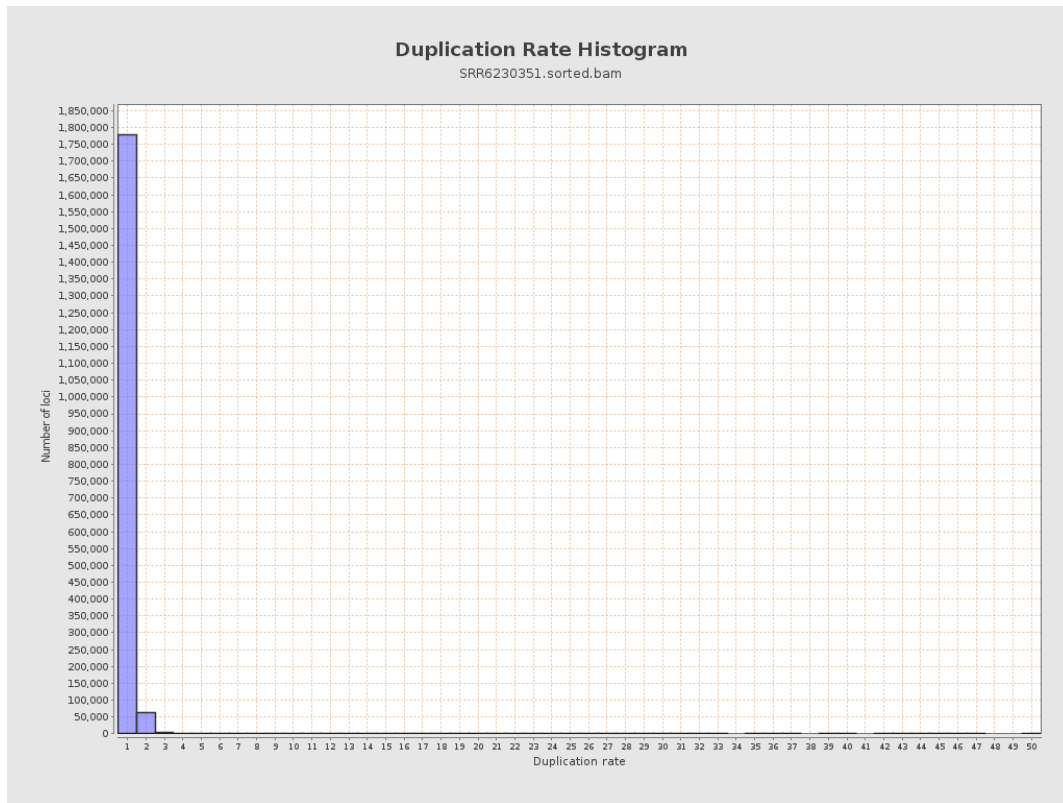
5. Results : Coverage Histogram (0-50X)



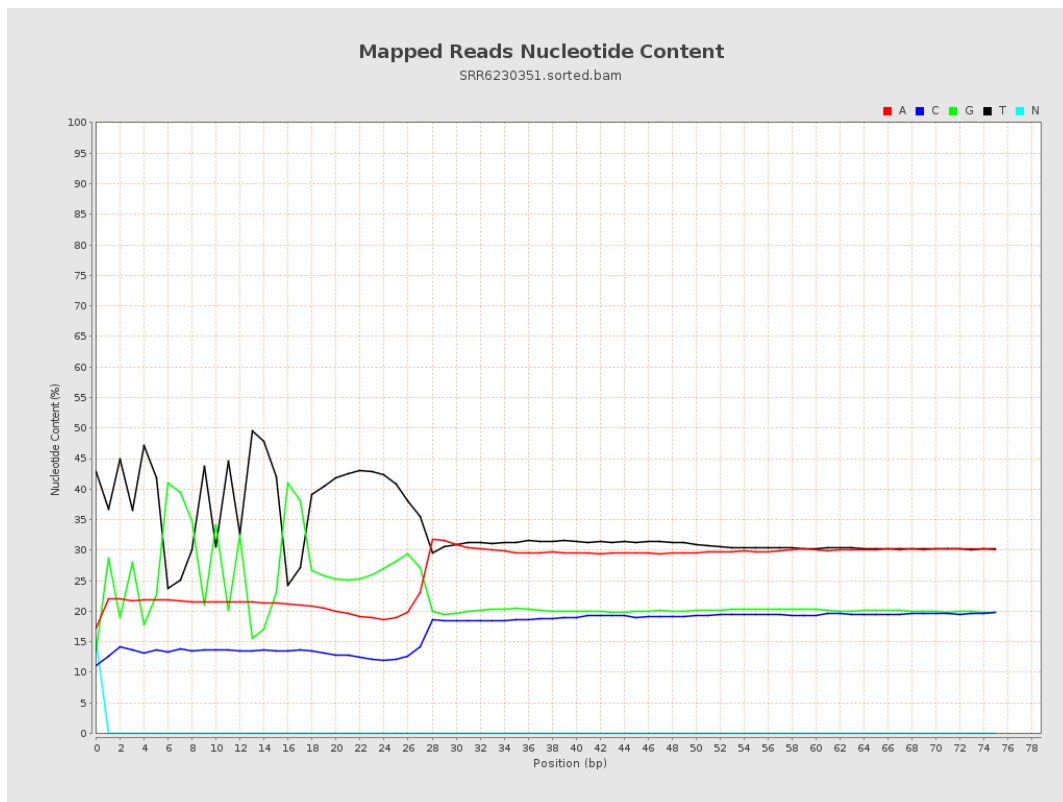
6. Results : Genome Fraction Coverage



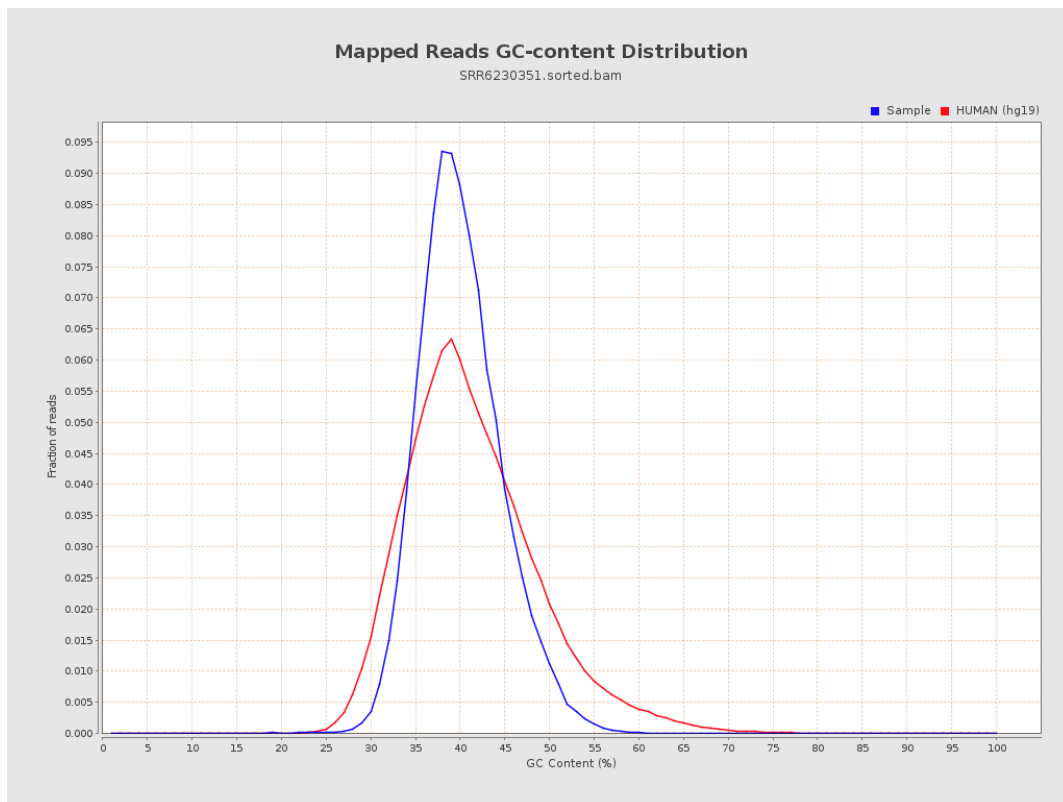
7. Results : Duplication Rate Histogram



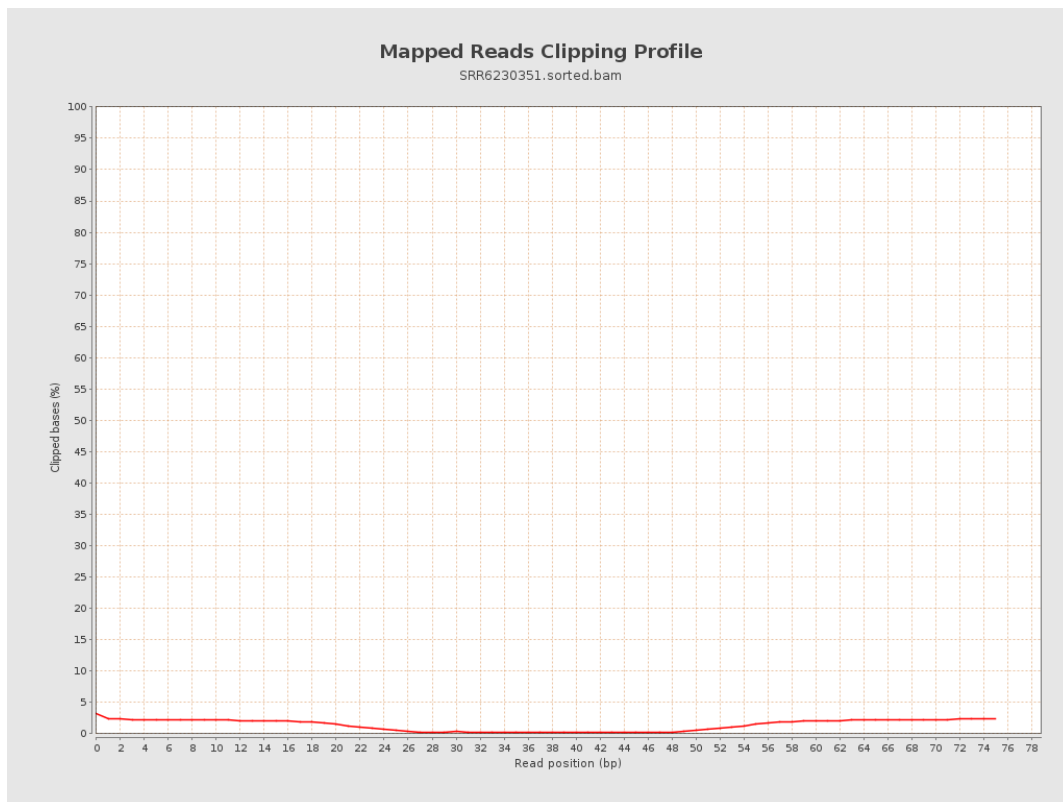
8. Results : Mapped Reads Nucleotide Content



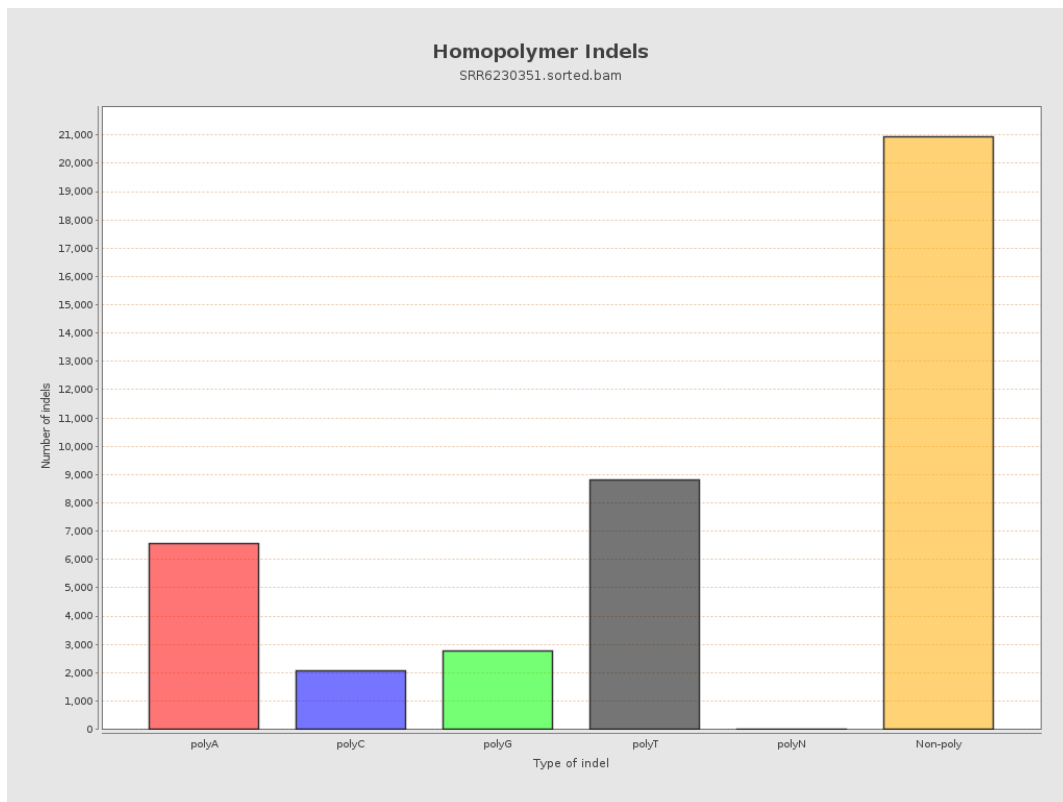
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

