

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 07:51:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231850.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_SRR6231850 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231850.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 07:51:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231850.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,958,862
Mapped reads	3,793,126 / 76.49%
Unmapped reads	1,165,736 / 23.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	40,798 / 0.82%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	305,187 / 6.15%
Duplication rate	5.39%
Clipped reads	2,353,796 / 47.47%

2.2. ACGT Content

Number/percentage of A's	67,498,596 / 28.53%
Number/percentage of C's	48,917,014 / 20.68%
Number/percentage of T's	65,895,644 / 27.85%
Number/percentage of G's	54,265,947 / 22.94%
Number/percentage of N's	19,014 / 0.01%
GC Percentage	43.61%

2.3. Coverage

Mean	0.0765

Standard Deviation	5.8436
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2.4. Mapping Quality

Mean Mapping Quality	43.64
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2.5. Mismatches and indels

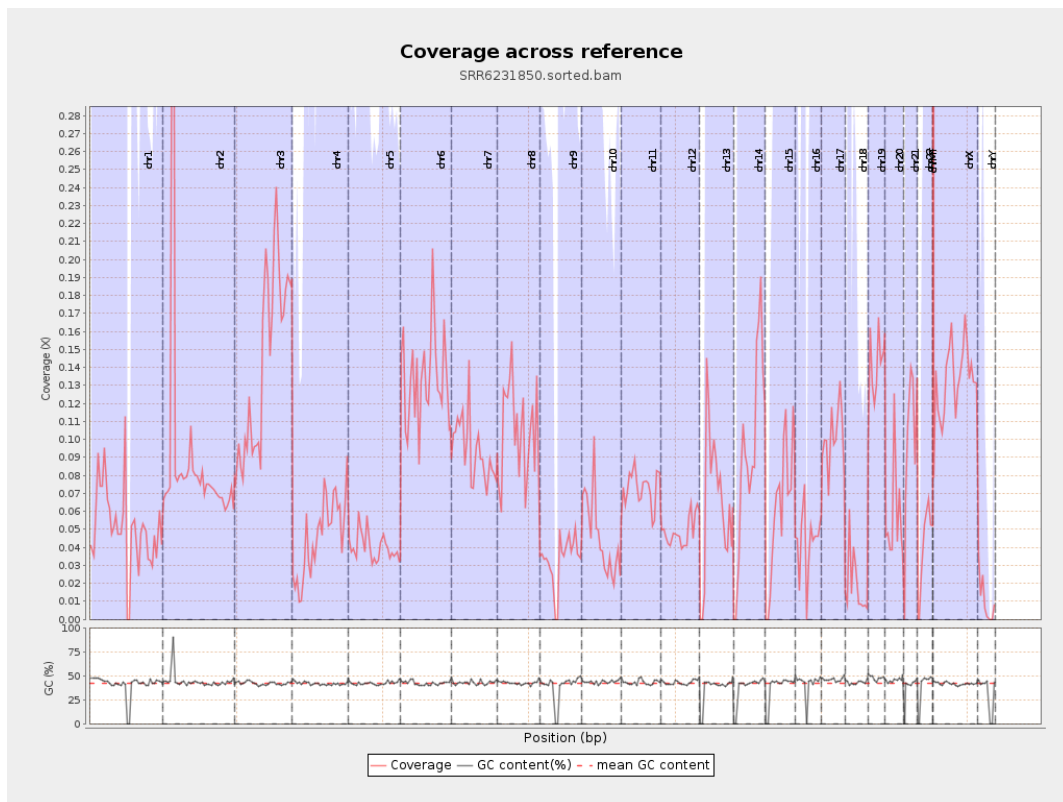
General error rate	0.59%
Mismatches	1,355,479
Insertions	16,137
Mapped reads with at least one insertion	0.42%
Deletions	49,476
Mapped reads with at least one deletion	1.29%
Homopolymer indels	42.86%

2.6. Chromosome stats

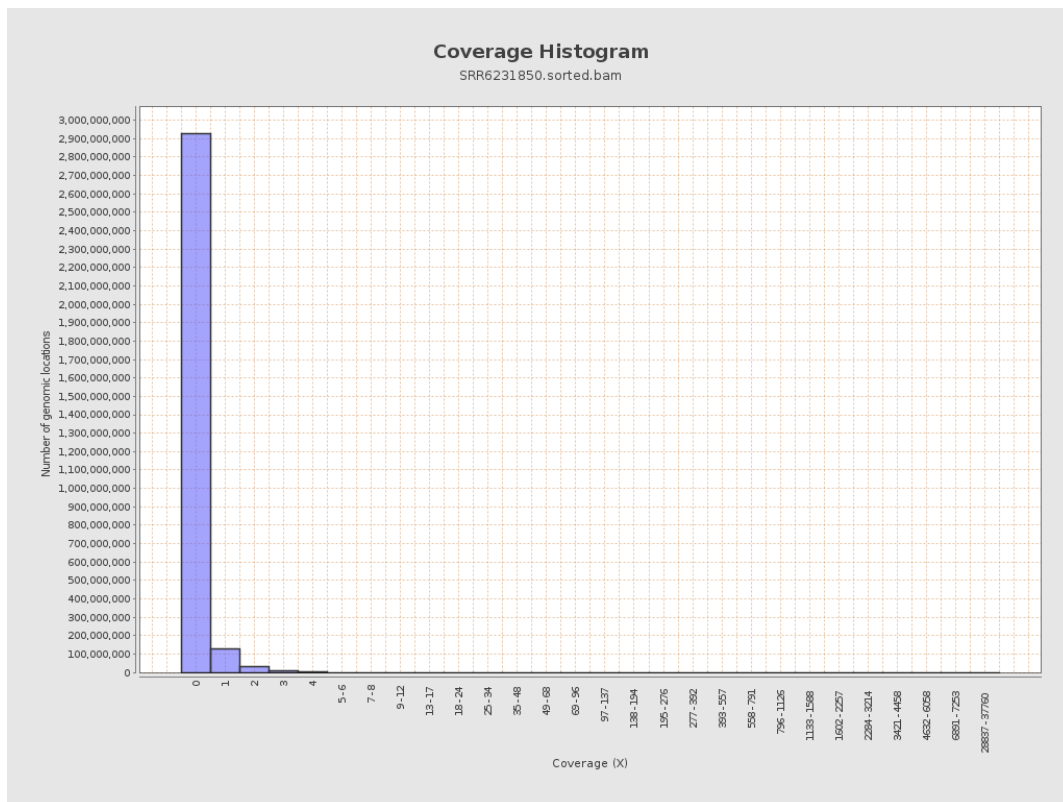
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12683222	0.0509	1.4479
chr2	243199373	21634301	0.089	20.7225
chr3	198022430	27964506	0.1412	0.4928
chr4	191154276	8983444	0.047	0.3041
chr5	180915260	7258036	0.0401	0.278
chr6	171115067	22853247	0.1336	0.5901
chr7	159138663	14928357	0.0938	0.9541

chr8	146364022	15368928	0.105	0.5856
chr9	141213431	4727727	0.0335	0.3611
chr10	135534747	6209543	0.0458	0.4864
chr11	135006516	9765098	0.0723	0.6072
chr12	133851895	6571360	0.0491	0.2936
chr13	115169878	7464879	0.0648	0.3313
chr14	107349540	10103756	0.0941	0.4638
chr15	102531392	6316125	0.0616	0.3225
chr16	90354753	3830609	0.0424	0.3573
chr17	81195210	8294994	0.1022	0.4624
chr18	78077248	1525849	0.0195	1.1651
chr19	59128983	8364887	0.1415	0.8457
chr20	63025520	3564611	0.0566	0.36
chr21	48129895	4805139	0.0998	0.4213
chr22	51304566	2094198	0.0408	0.2542
chrMT	16571	230084	13.8847	8.6302
chrX	155270560	20532208	0.1322	0.5868
chrY	59373566	602585	0.0101	0.1507

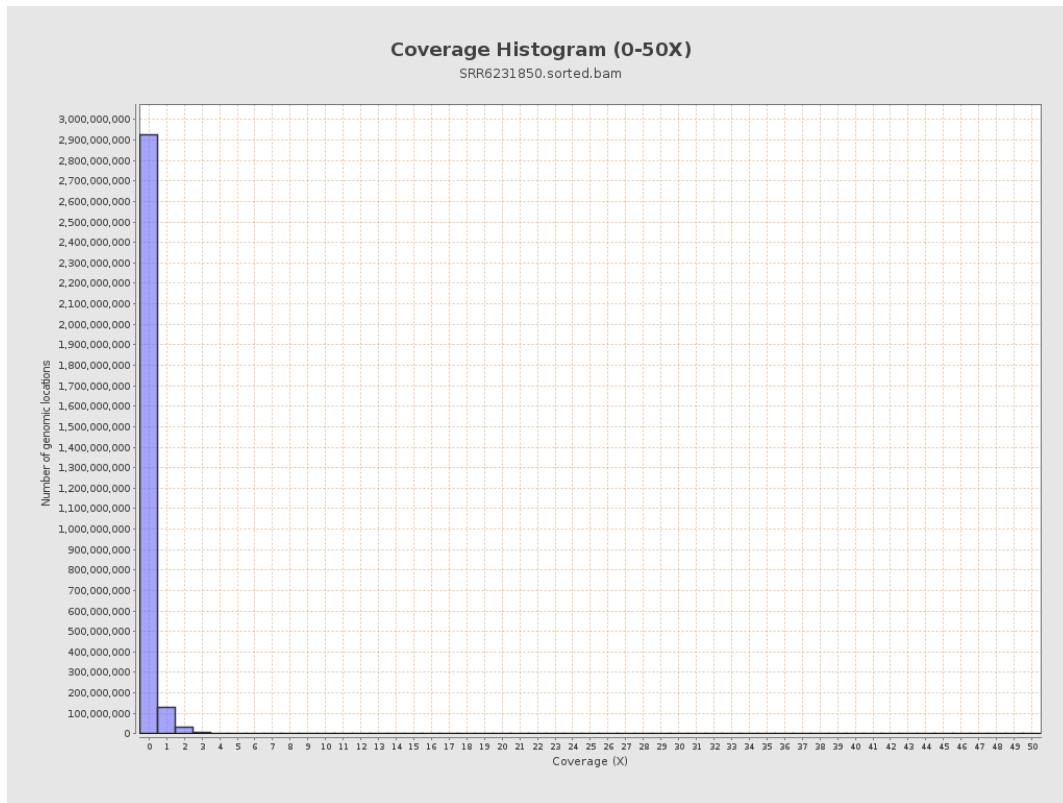
3. Results : Coverage across reference



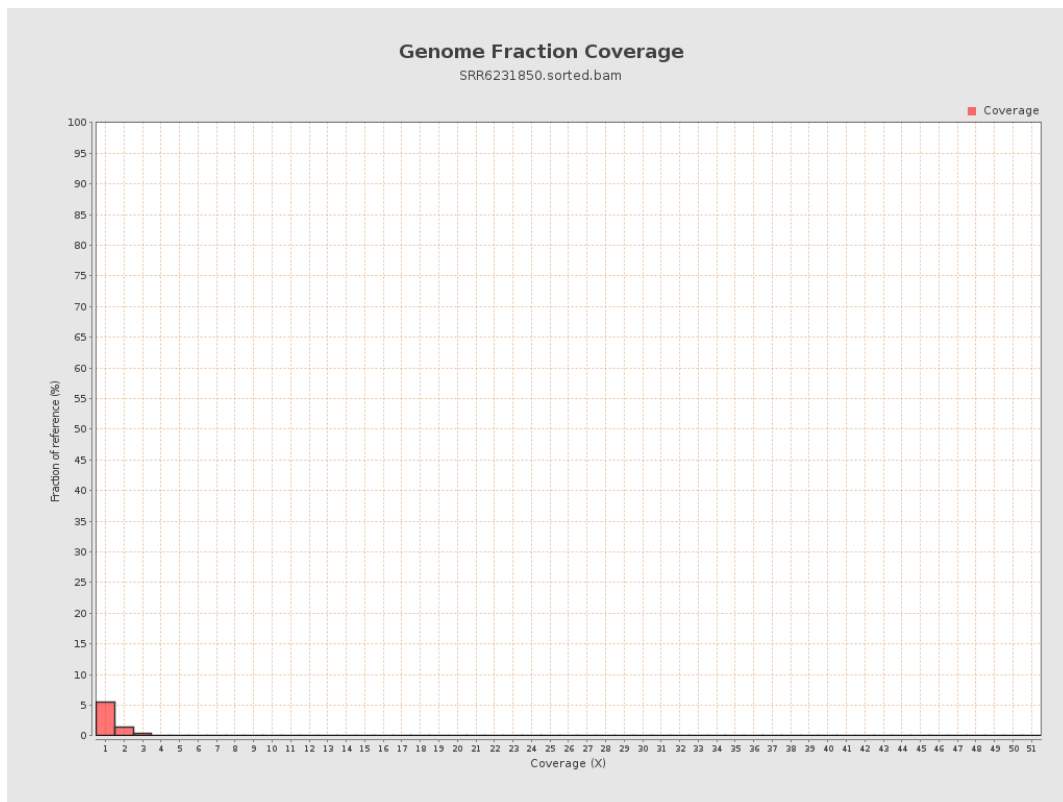
4. Results : Coverage Histogram



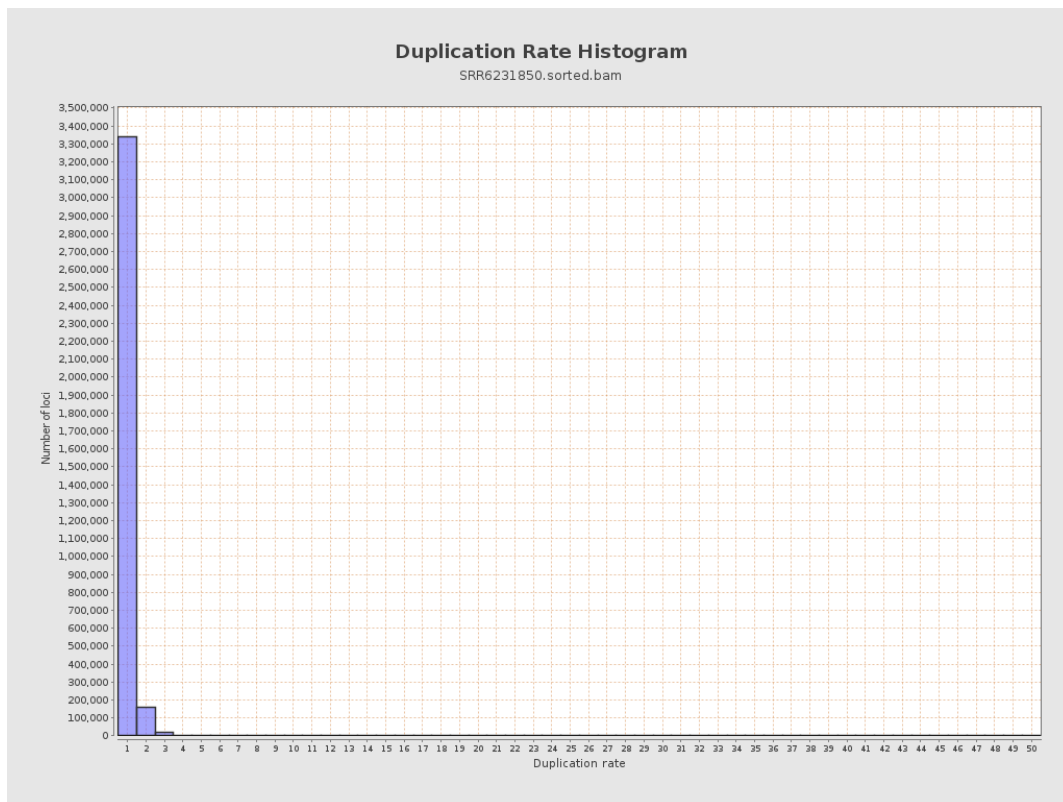
5. Results : Coverage Histogram (0-50X)



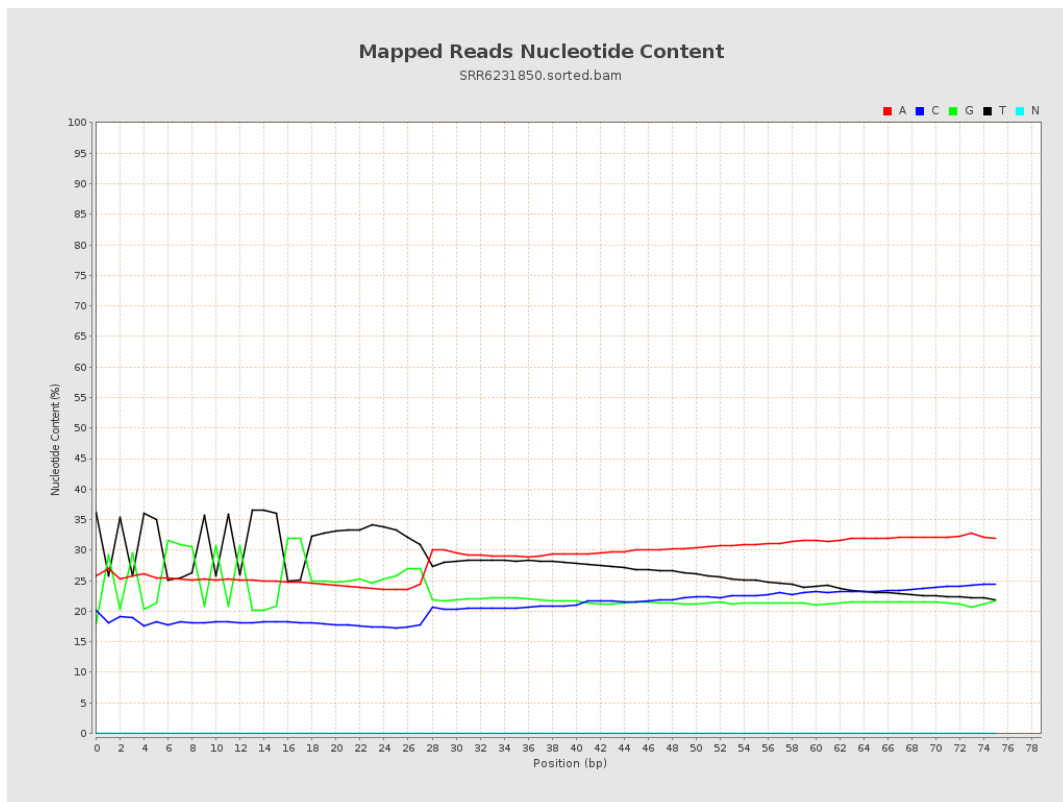
6. Results : Genome Fraction Coverage



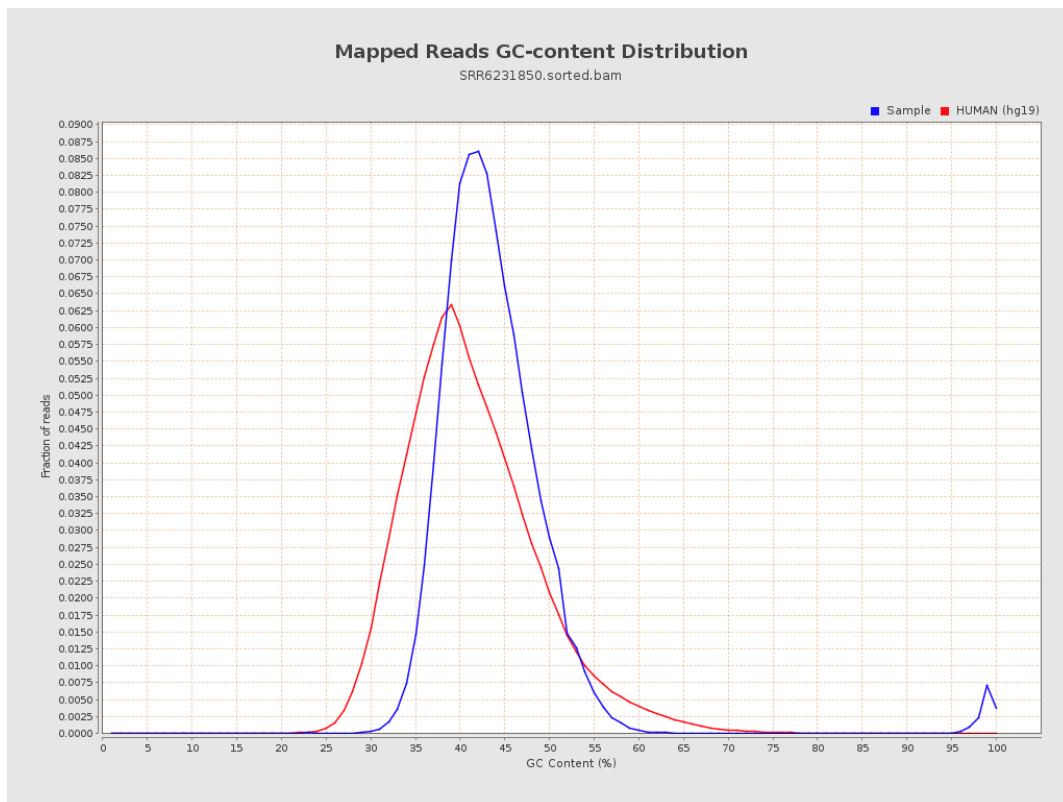
7. Results : Duplication Rate Histogram



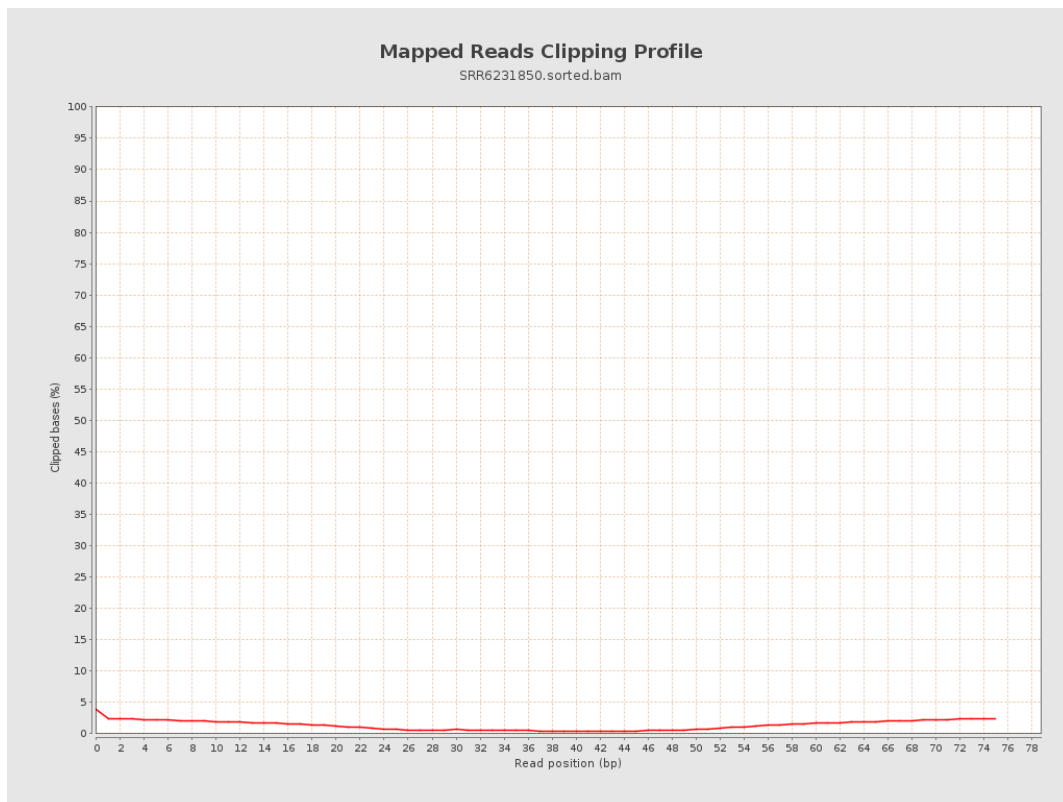
8. Results : Mapped Reads Nucleotide Content



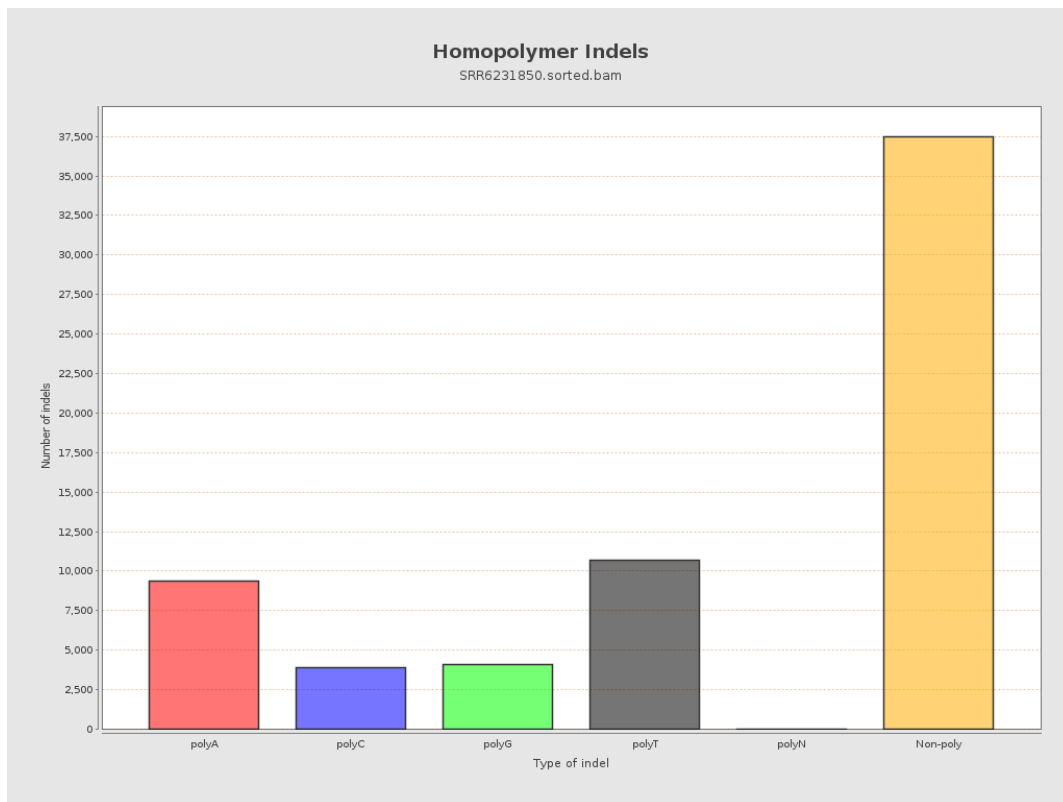
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

