

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 15:53:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238311.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_SRR6238311 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238311.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 15:53:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238311.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,224,211
Mapped reads	1,637,471 / 73.62%
Unmapped reads	586,740 / 26.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,583 / 0.97%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	271,295 / 12.2%
Duplication rate	11.73%
Clipped reads	1,029,008 / 46.26%

2.2. ACGT Content

Number/percentage of A's	28,317,680 / 27.65%
Number/percentage of C's	19,986,176 / 19.51%
Number/percentage of T's	31,104,006 / 30.37%
Number/percentage of G's	22,999,938 / 22.45%
Number/percentage of N's	21,696 / 0.02%
GC Percentage	41.97%

2.3. Coverage

Mean	0.0331

Standard Deviation	0.4615
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	40.32
----------------------	-------

2.5. Mismatches and indels

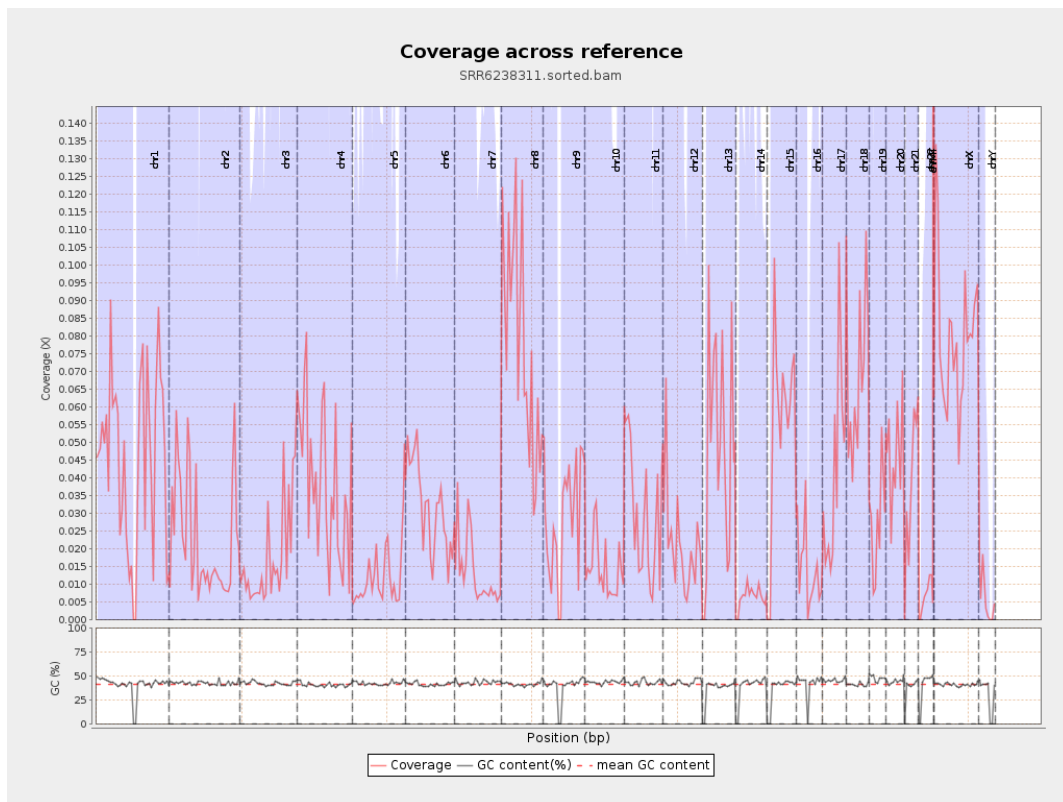
General error rate	0.93%
Mismatches	936,602
Insertions	8,245
Mapped reads with at least one insertion	0.5%
Deletions	32,917
Mapped reads with at least one deletion	1.98%
Homopolymer indels	44.14%

2.6. Chromosome stats

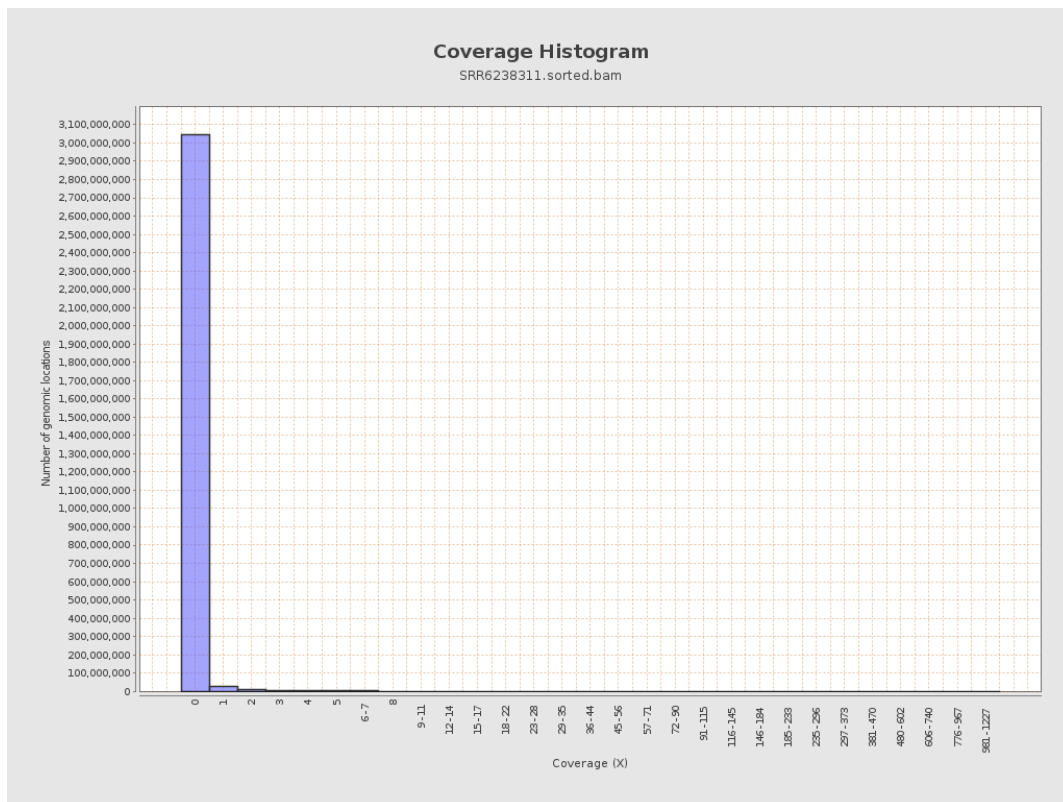
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11265324	0.0452	0.4789
chr2	243199373	5640368	0.0232	0.6792
chr3	198022430	3406539	0.0172	0.2505
chr4	191154276	7437427	0.0389	0.3929
chr5	180915260	2188156	0.0121	0.2234
chr6	171115067	5387448	0.0315	0.4145
chr7	159138663	2047035	0.0129	0.2454

chr8	146364022	11368845	0.0777	0.7733
chr9	141213431	3852255	0.0273	0.3654
chr10	135534747	1910948	0.0141	0.2404
chr11	135006516	4030745	0.0299	0.3413
chr12	133851895	2799194	0.0209	0.2779
chr13	115169878	5511424	0.0479	0.4605
chr14	107349540	679417	0.0063	0.5994
chr15	102531392	5662824	0.0552	0.8256
chr16	90354753	1245570	0.0138	0.2267
chr17	81195210	3354769	0.0413	0.3817
chr18	78077248	5337549	0.0684	0.5898
chr19	59128983	1605864	0.0272	0.3789
chr20	63025520	2930367	0.0465	0.4055
chr21	48129895	1822973	0.0379	0.3526
chr22	51304566	345772	0.0067	0.1359
chrMT	16571	9268	0.5593	1.2647
chrX	155270560	12310147	0.0793	0.5882
chrY	59373566	333417	0.0056	0.2021

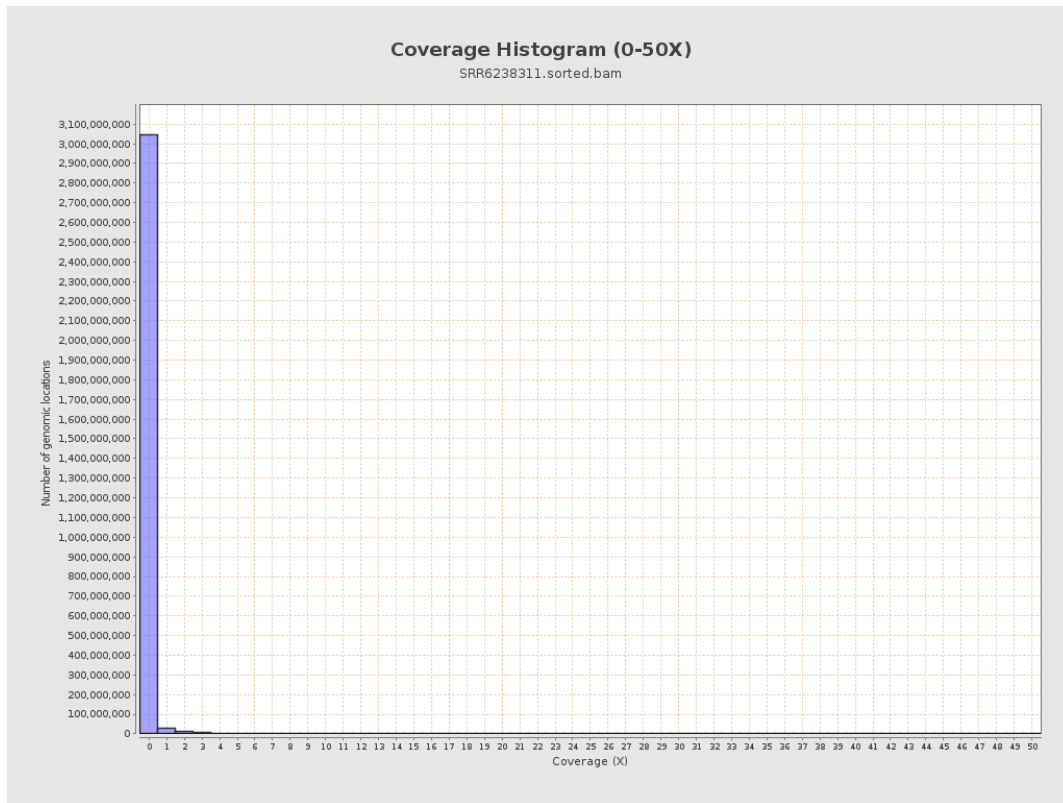
3. Results : Coverage across reference



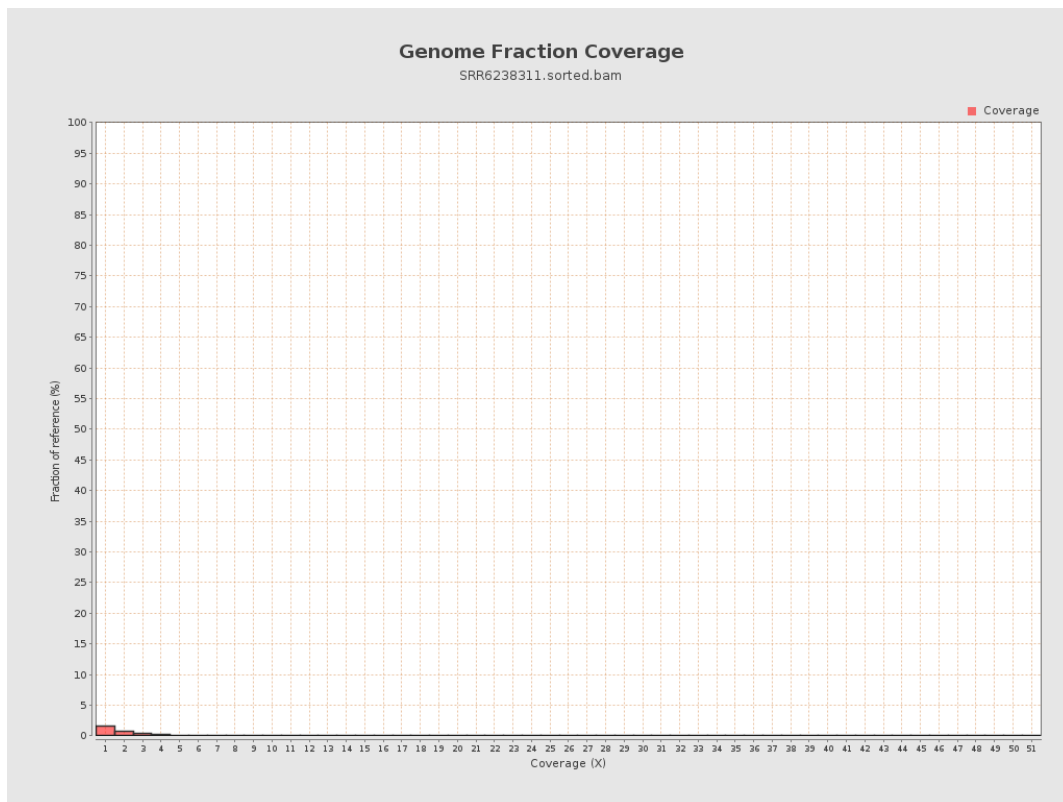
4. Results : Coverage Histogram



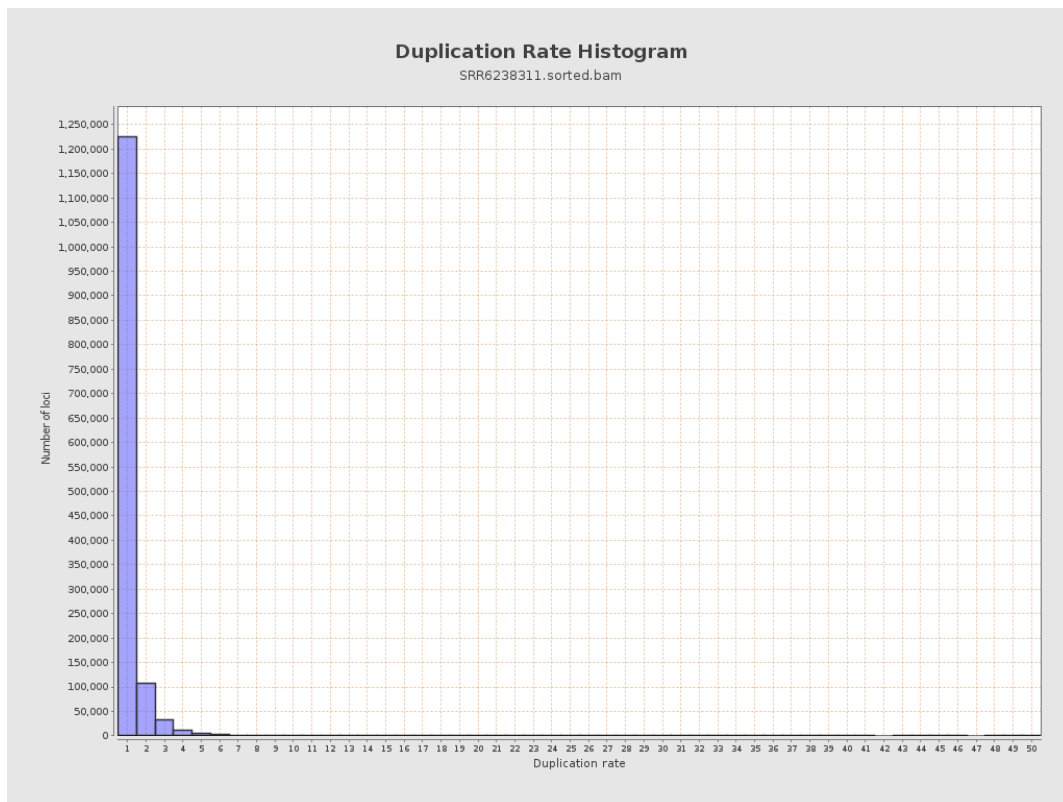
5. Results : Coverage Histogram (0-50X)



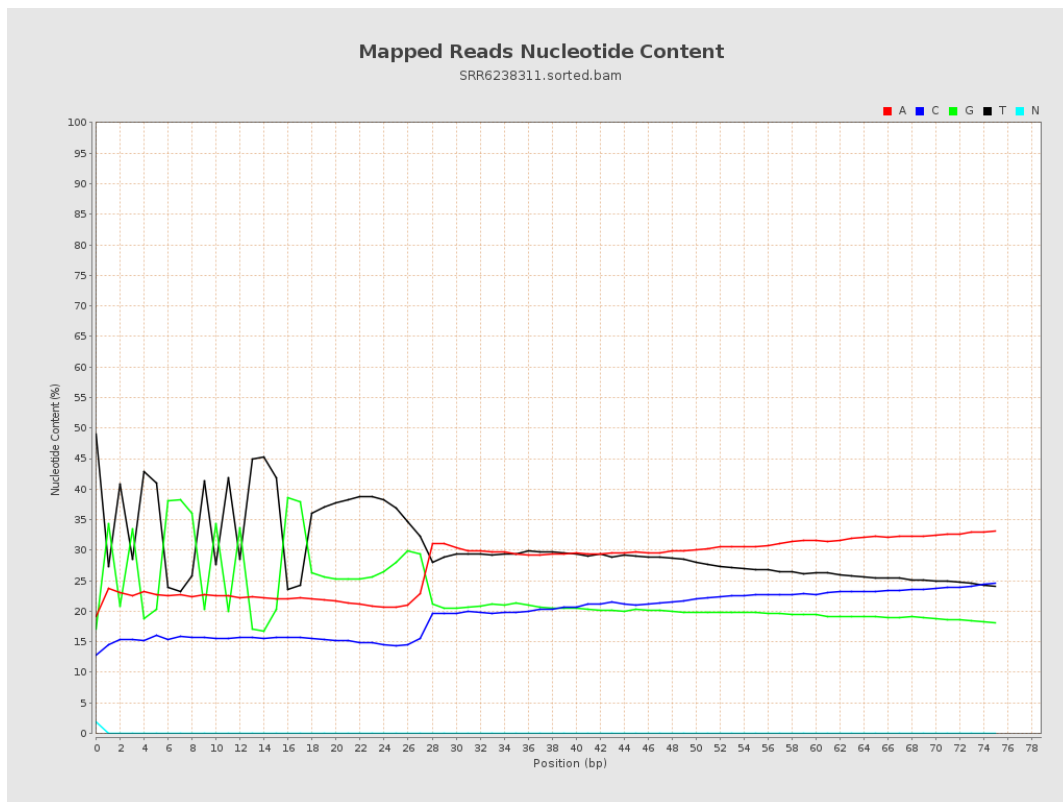
6. Results : Genome Fraction Coverage



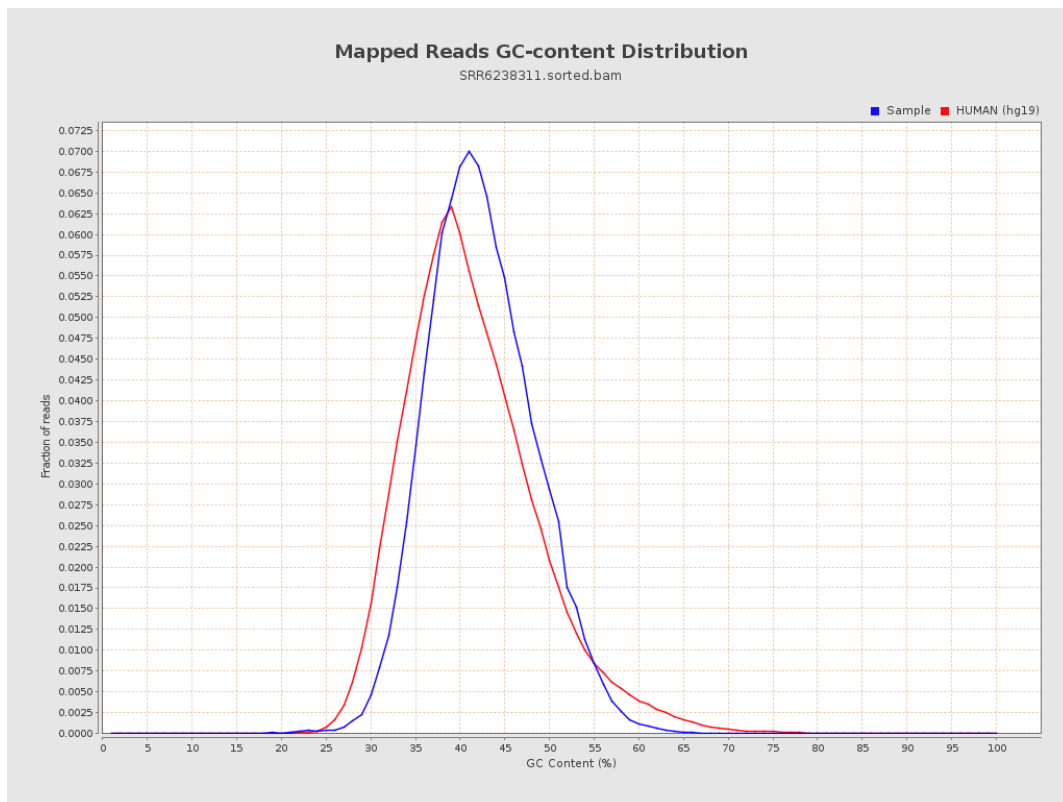
7. Results : Duplication Rate Histogram



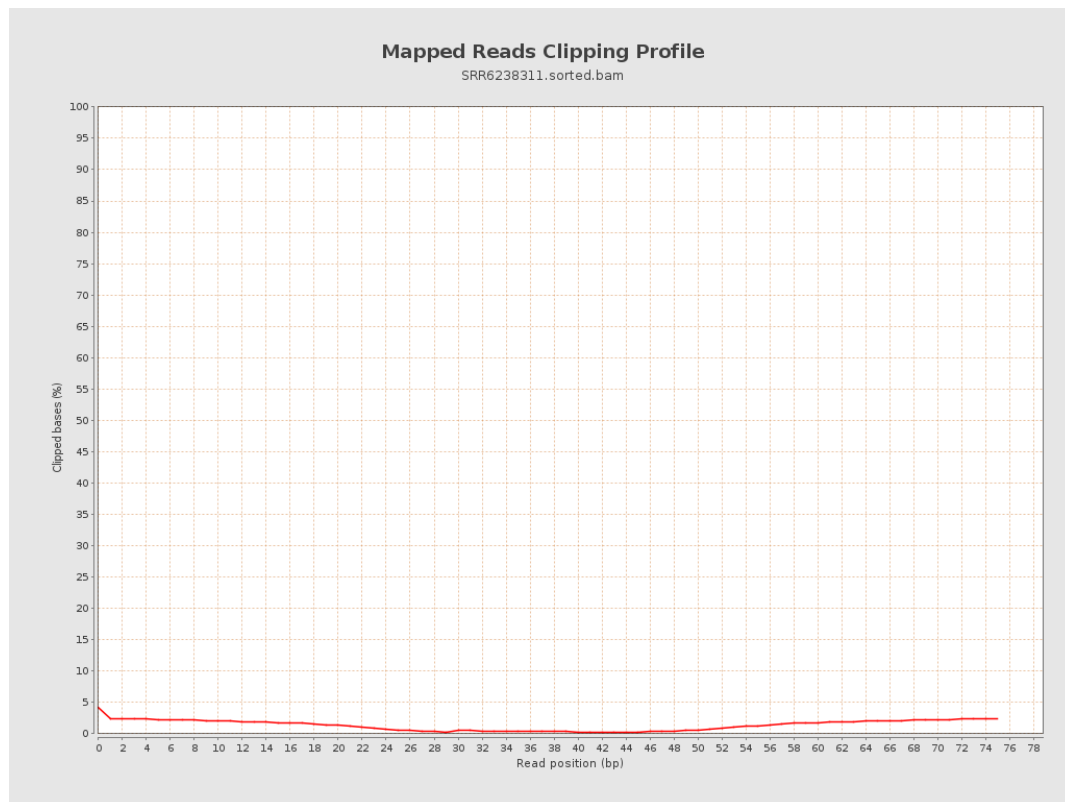
8. Results : Mapped Reads Nucleotide Content



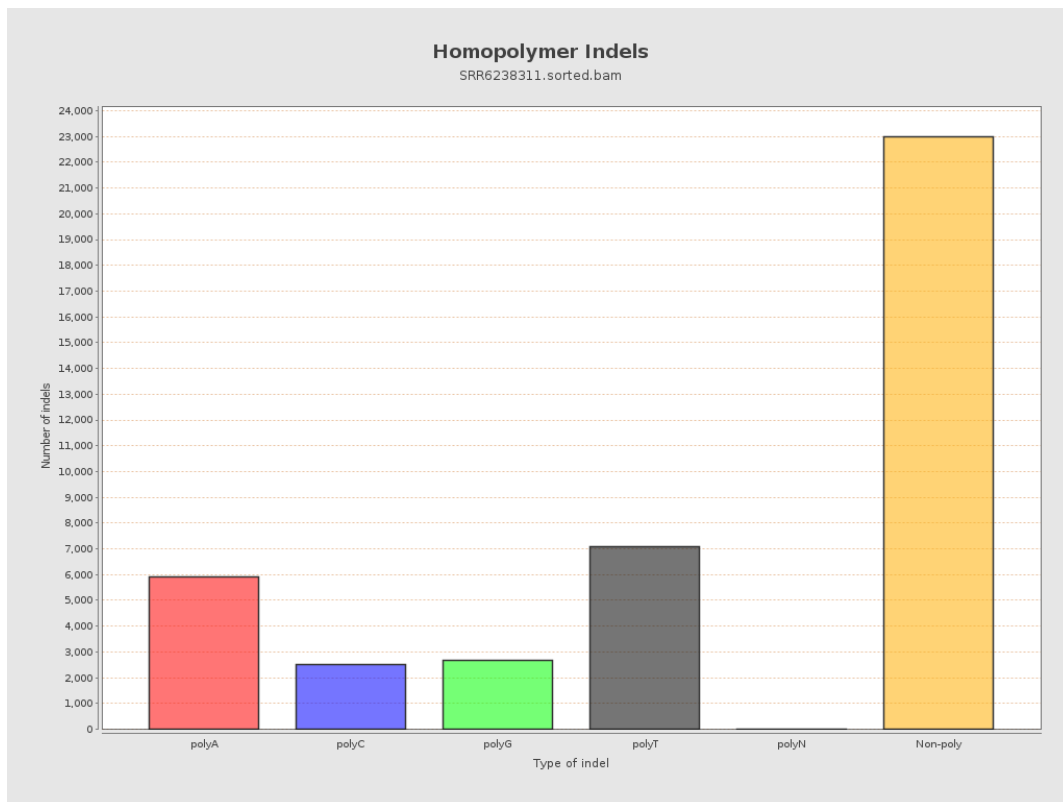
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

