

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 23:40:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238636.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_SRR6238636 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238636.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 23:40:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238636.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,958,767
Mapped reads	4,480,573 / 90.36%
Unmapped reads	478,194 / 9.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	42,087 / 0.85%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	1,363,287 / 27.49%
Duplication rate	20.52%
Clipped reads	2,754,396 / 55.55%

2.2. ACGT Content

Number/percentage of A's	71,378,053 / 25.63%
Number/percentage of C's	49,079,708 / 17.63%
Number/percentage of T's	92,801,059 / 33.33%
Number/percentage of G's	65,189,649 / 23.41%
Number/percentage of N's	13,950 / 0.01%
GC Percentage	41.04%

2.3. Coverage

Mean	0.09

Standard Deviation	1.1525
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	41.01
----------------------	-------

2.5. Mismatches and indels

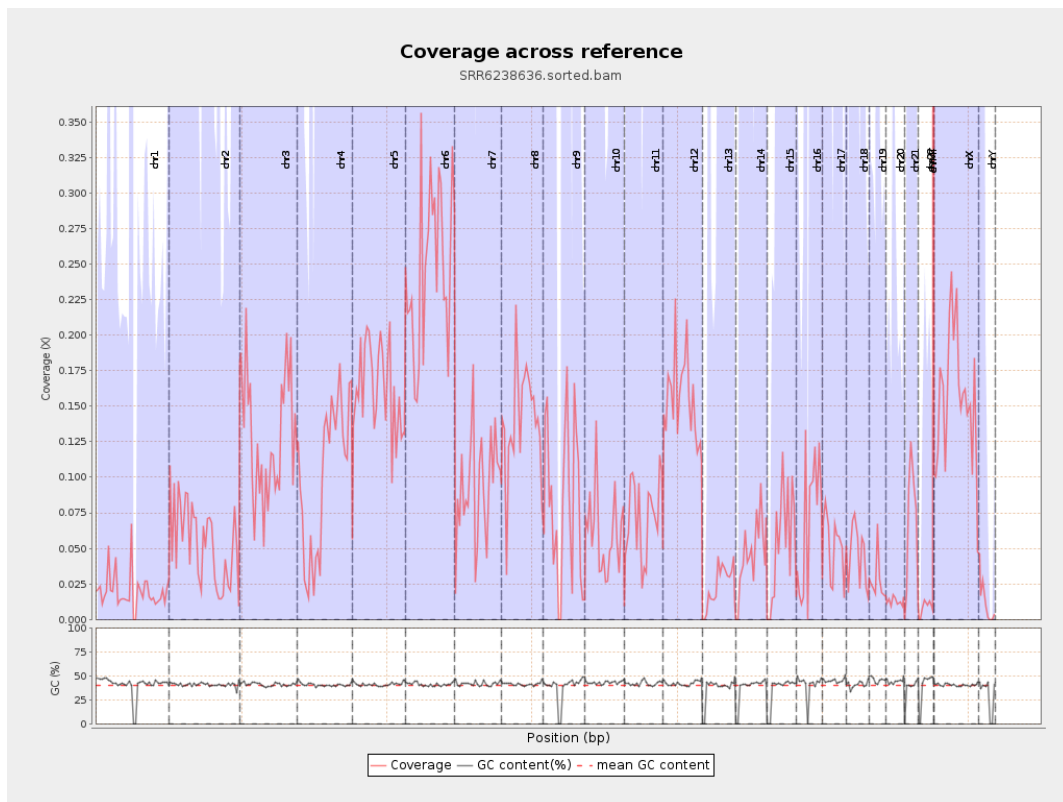
General error rate	0.58%
Mismatches	1,591,866
Insertions	16,895
Mapped reads with at least one insertion	0.37%
Deletions	81,050
Mapped reads with at least one deletion	1.79%
Homopolymer indels	41.57%

2.6. Chromosome stats

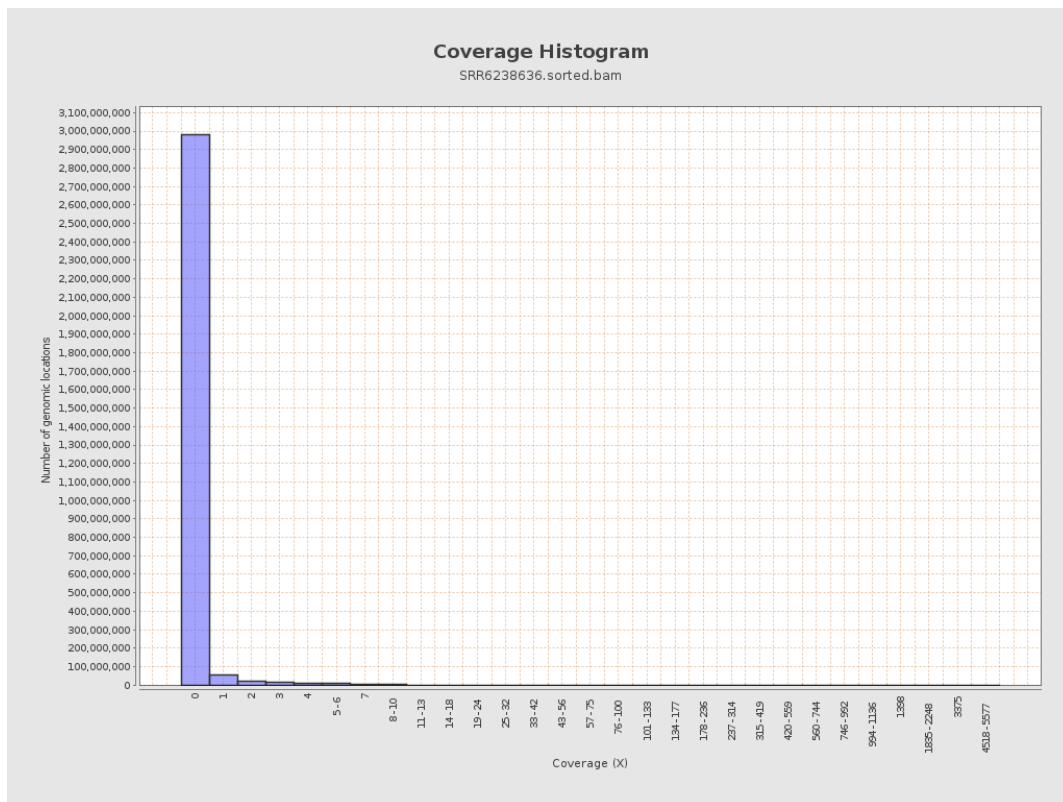
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4893546	0.0196	0.9283
chr2	243199373	13020118	0.0535	2.4579
chr3	198022430	25494529	0.1287	0.7602
chr4	191154276	19171885	0.1003	0.6677
chr5	180915260	29400534	0.1625	0.8641
chr6	171115067	42314175	0.2473	1.9544
chr7	159138663	15103846	0.0949	1.3072

chr8	146364022	20525102	0.1402	1.0083
chr9	141213431	11964390	0.0847	0.8286
chr10	135534747	8091027	0.0597	1.0344
chr11	135006516	9739801	0.0721	0.723
chr12	133851895	20825733	0.1556	0.8815
chr13	115169878	2793130	0.0243	0.5238
chr14	107349540	4863495	0.0453	0.6028
chr15	102531392	5512415	0.0538	0.6303
chr16	90354753	6225039	0.0689	0.6511
chr17	81195210	4113564	0.0507	0.4848
chr18	78077248	3539979	0.0453	1.6095
chr19	59128983	1623907	0.0275	0.981
chr20	63025520	805370	0.0128	0.2456
chr21	48129895	3216275	0.0668	0.5954
chr22	51304566	437092	0.0085	0.1596
chrMT	16571	46417	2.8011	2.9775
chrX	155270560	24183737	0.1558	0.9233
chrY	59373566	693183	0.0117	0.3666

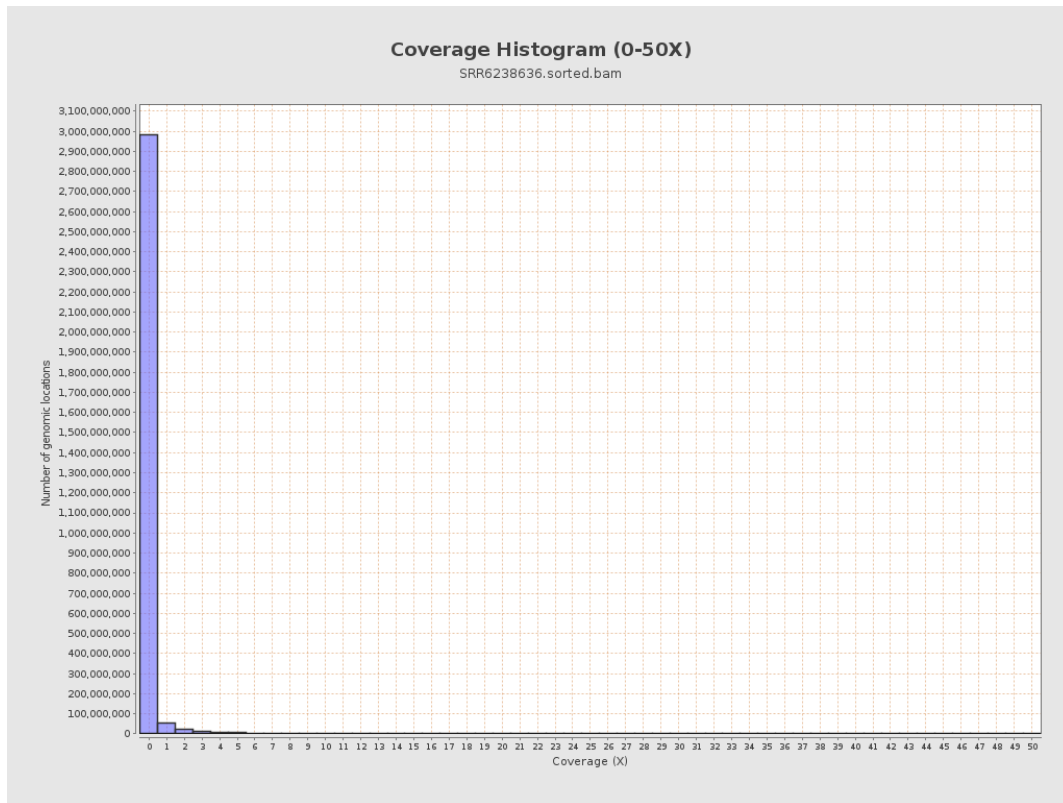
3. Results : Coverage across reference



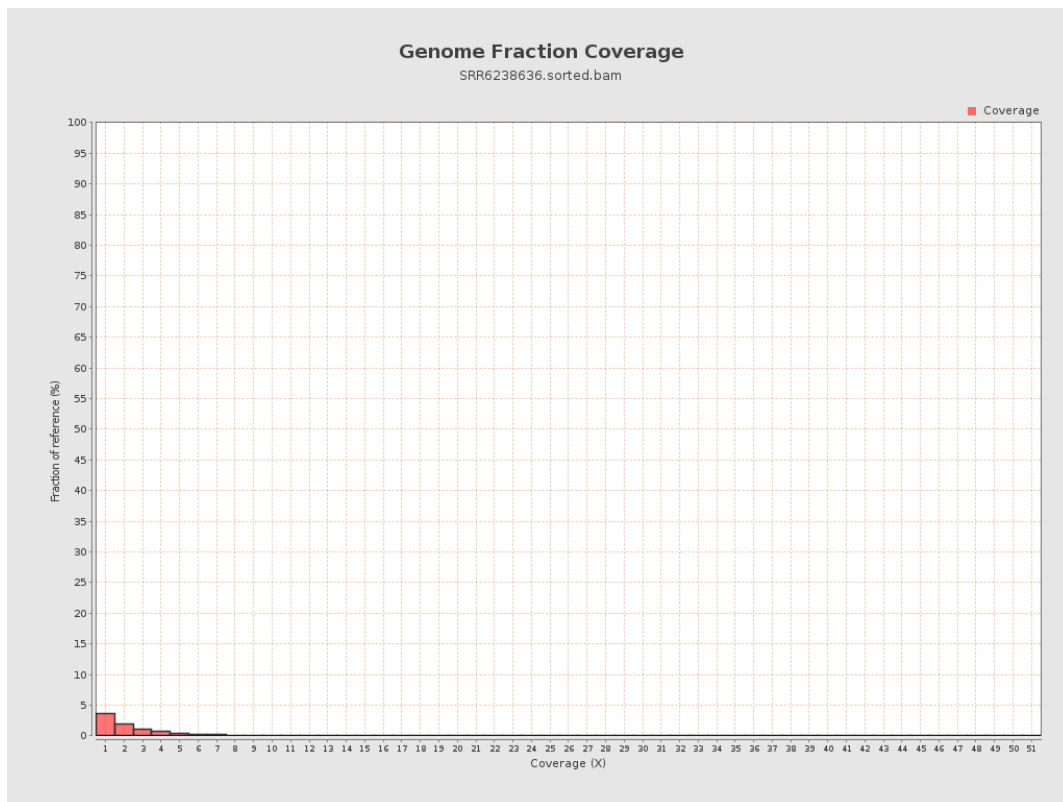
4. Results : Coverage Histogram



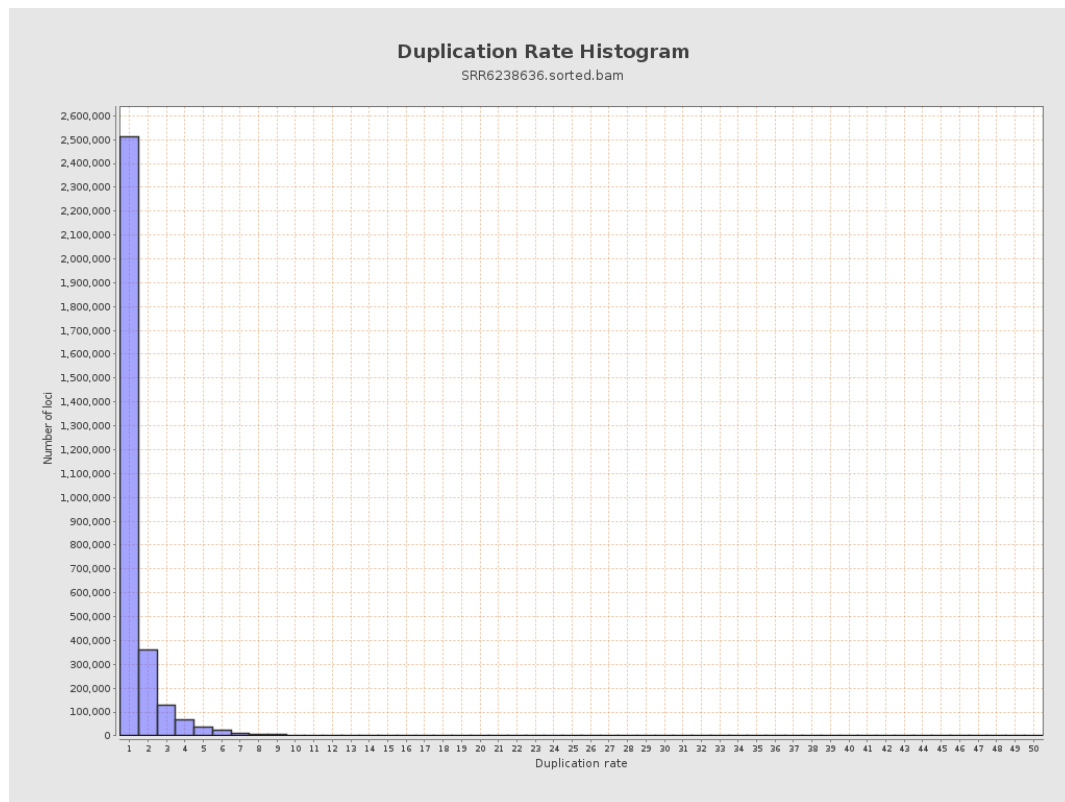
5. Results : Coverage Histogram (0-50X)



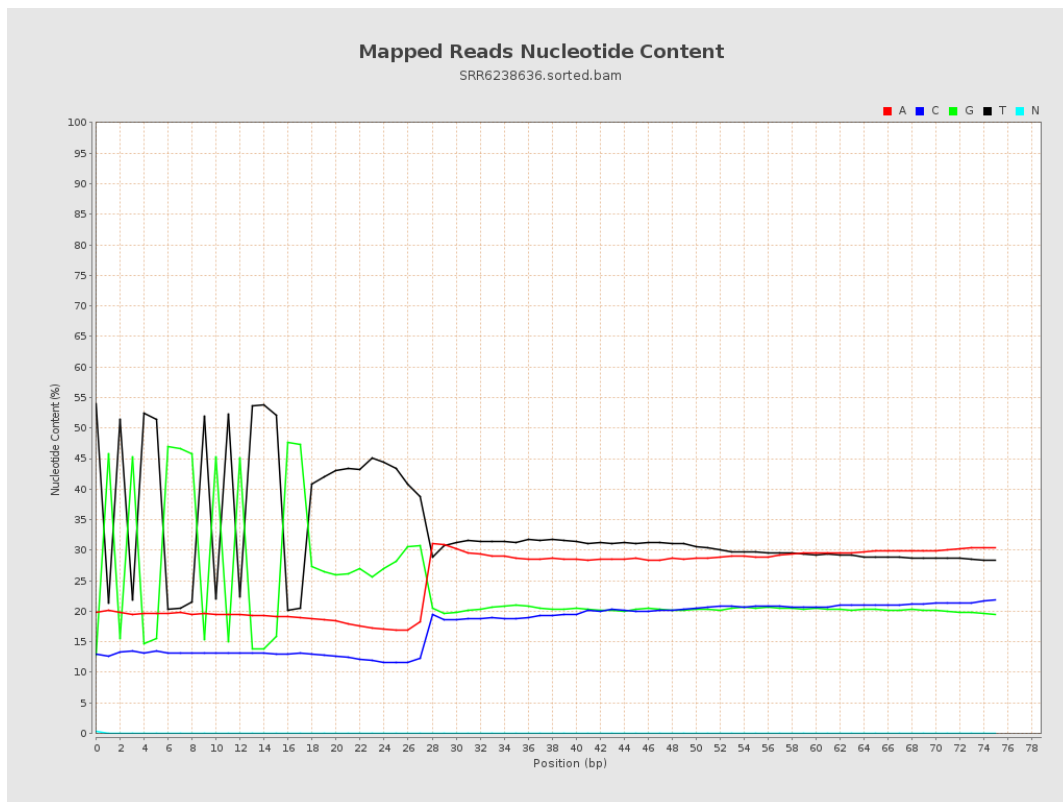
6. Results : Genome Fraction Coverage



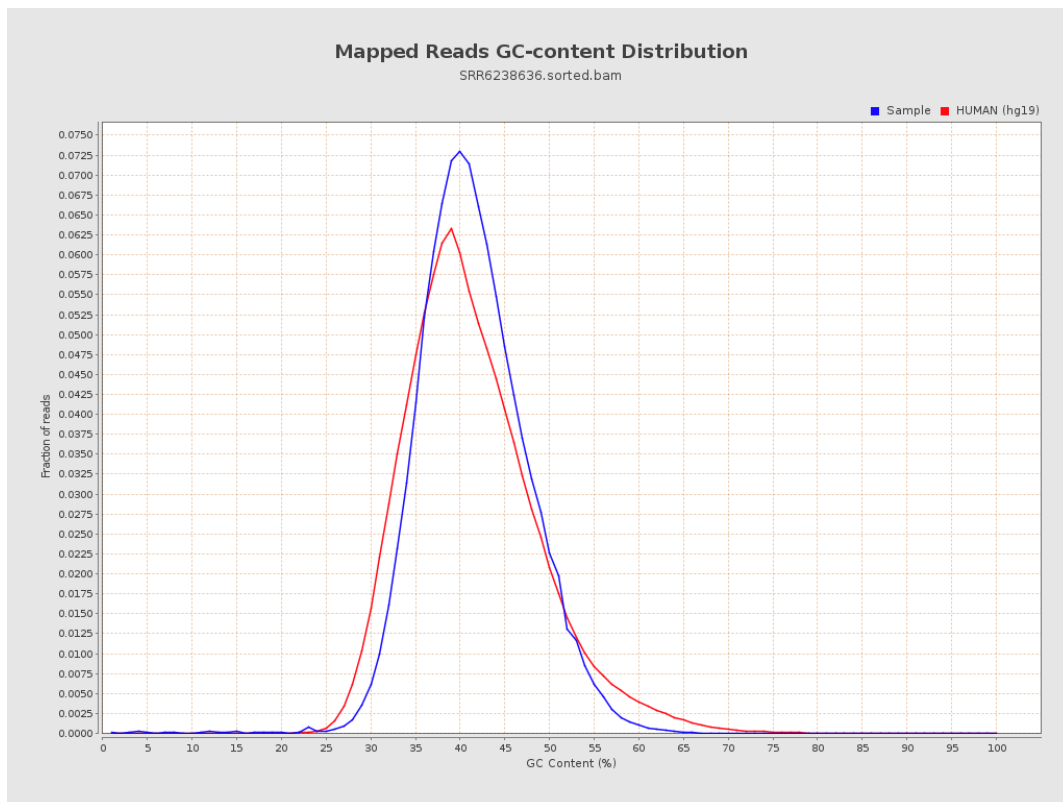
7. Results : Duplication Rate Histogram



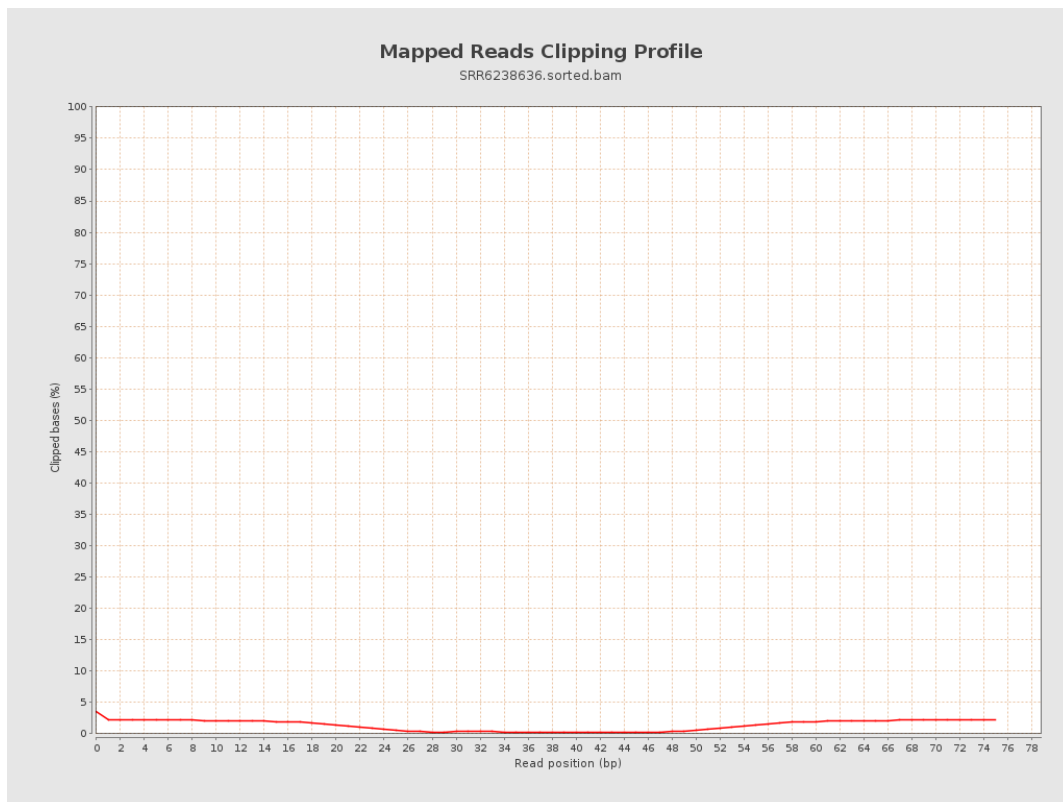
8. Results : Mapped Reads Nucleotide Content



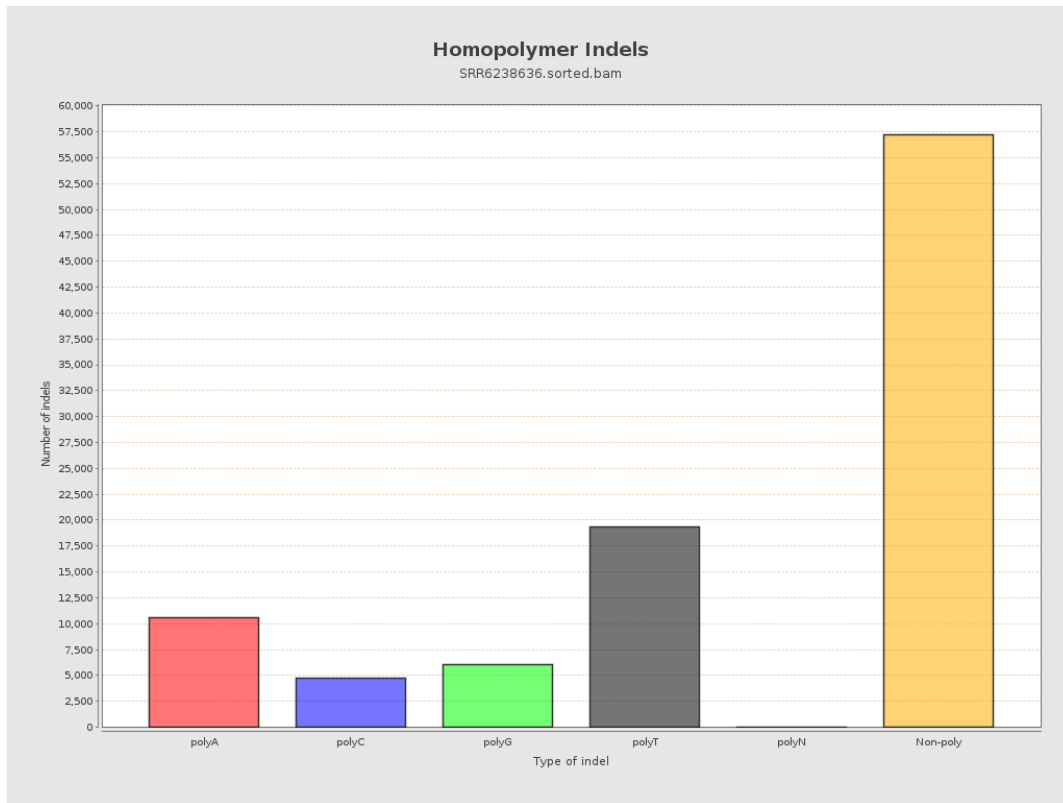
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

