

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 15:29:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238303.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_SRR6238303 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238303.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 15:29:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238303.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,510,113
Mapped reads	1,367,303 / 90.54%
Unmapped reads	142,810 / 9.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,111 / 0.87%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	35,861 / 2.37%
Duplication rate	1.7%
Clipped reads	625,765 / 41.44%

2.2. ACGT Content

Number/percentage of A's	26,172,475 / 28.76%
Number/percentage of C's	17,481,277 / 19.21%
Number/percentage of T's	27,398,629 / 30.1%
Number/percentage of G's	19,936,918 / 21.9%
Number/percentage of N's	29,423 / 0.03%
GC Percentage	41.11%

2.3. Coverage

Mean	0.0294

Standard Deviation	0.3335
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	43.45
----------------------	-------

2.5. Mismatches and indels

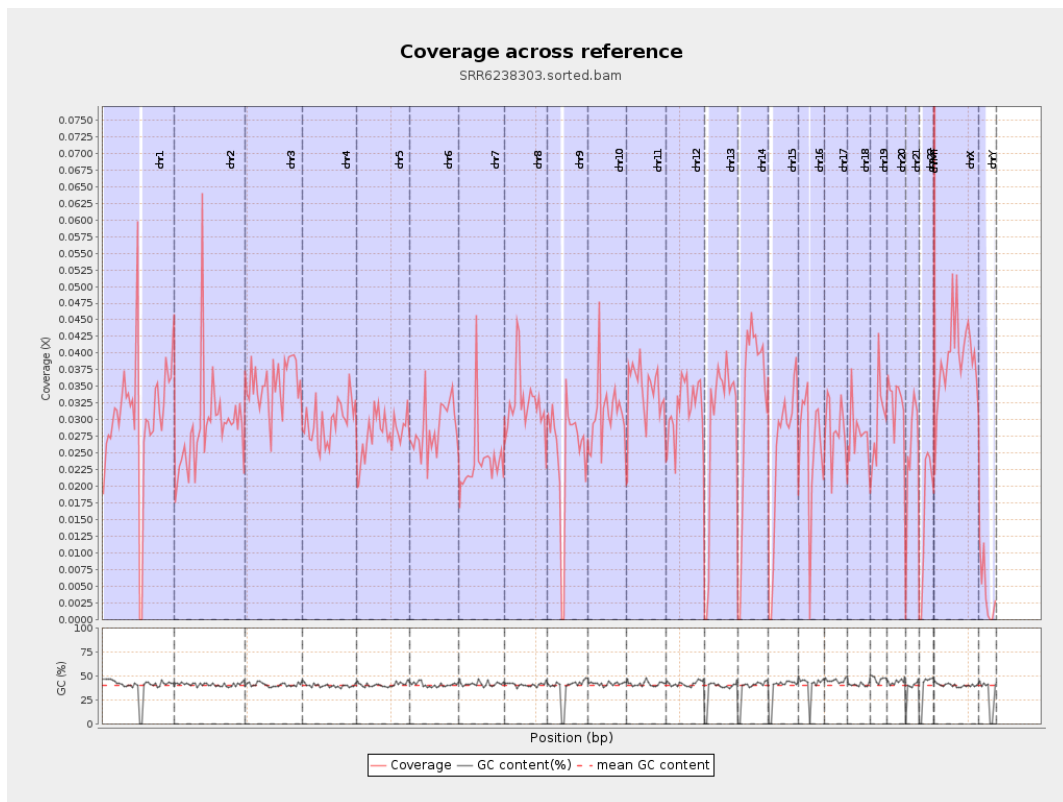
General error rate	0.84%
Mismatches	752,479
Insertions	7,138
Mapped reads with at least one insertion	0.52%
Deletions	21,438
Mapped reads with at least one deletion	1.55%
Homopolymer indels	45.87%

2.6. Chromosome stats

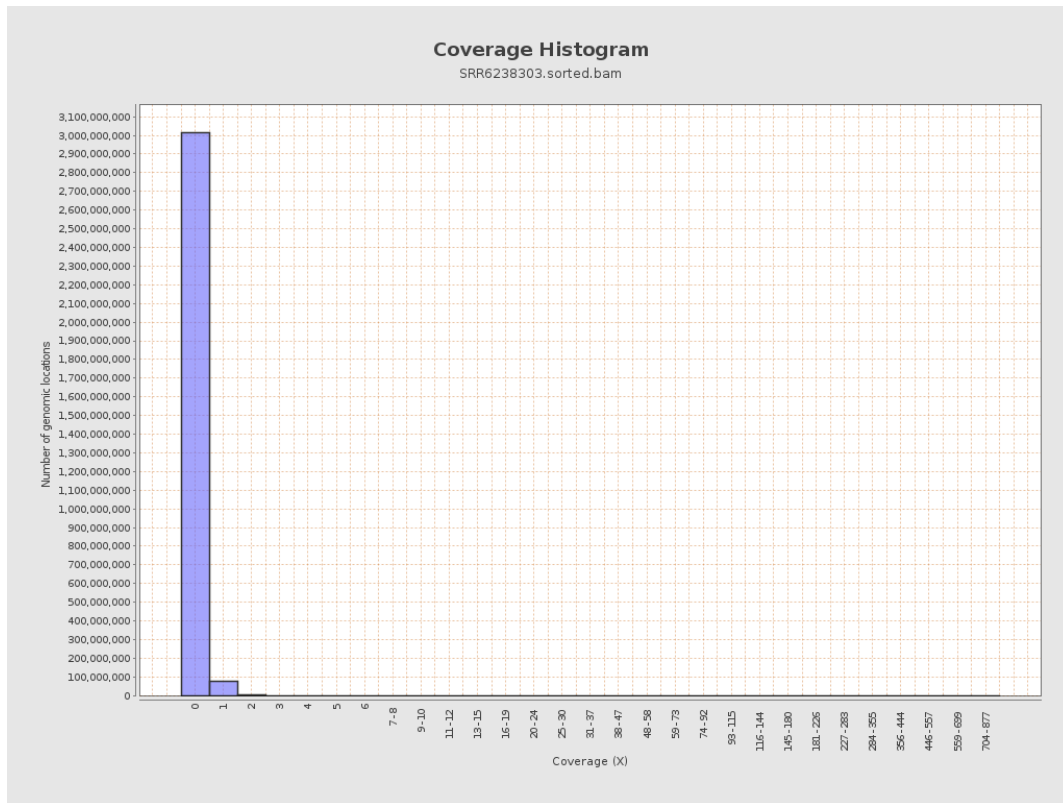
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7602338	0.0305	0.731
chr2	243199373	7012294	0.0288	0.3506
chr3	198022430	7019084	0.0354	0.2011
chr4	191154276	5684532	0.0297	0.1912
chr5	180915260	5076450	0.0281	0.1787
chr6	171115067	4923886	0.0288	0.2128
chr7	159138663	3771816	0.0237	0.346

chr8	146364022	4757481	0.0325	0.4609
chr9	141213431	3542556	0.0251	0.2602
chr10	135534747	4167882	0.0308	0.2738
chr11	135006516	4696362	0.0348	0.299
chr12	133851895	4240291	0.0317	0.1909
chr13	115169878	3360138	0.0292	0.1802
chr14	107349540	3544040	0.033	0.2041
chr15	102531392	2588185	0.0252	0.1735
chr16	90354753	2321838	0.0257	0.186
chr17	81195210	2312352	0.0285	0.2017
chr18	78077248	2184024	0.028	0.5078
chr19	59128983	1762707	0.0298	0.4942
chr20	63025520	2048016	0.0325	0.1988
chr21	48129895	1229800	0.0256	0.1784
chr22	51304566	837765	0.0163	0.134
chrMT	16571	10033	0.6055	0.8117
chrX	155270560	6118396	0.0394	0.2276
chrY	59373566	243350	0.0041	0.0903

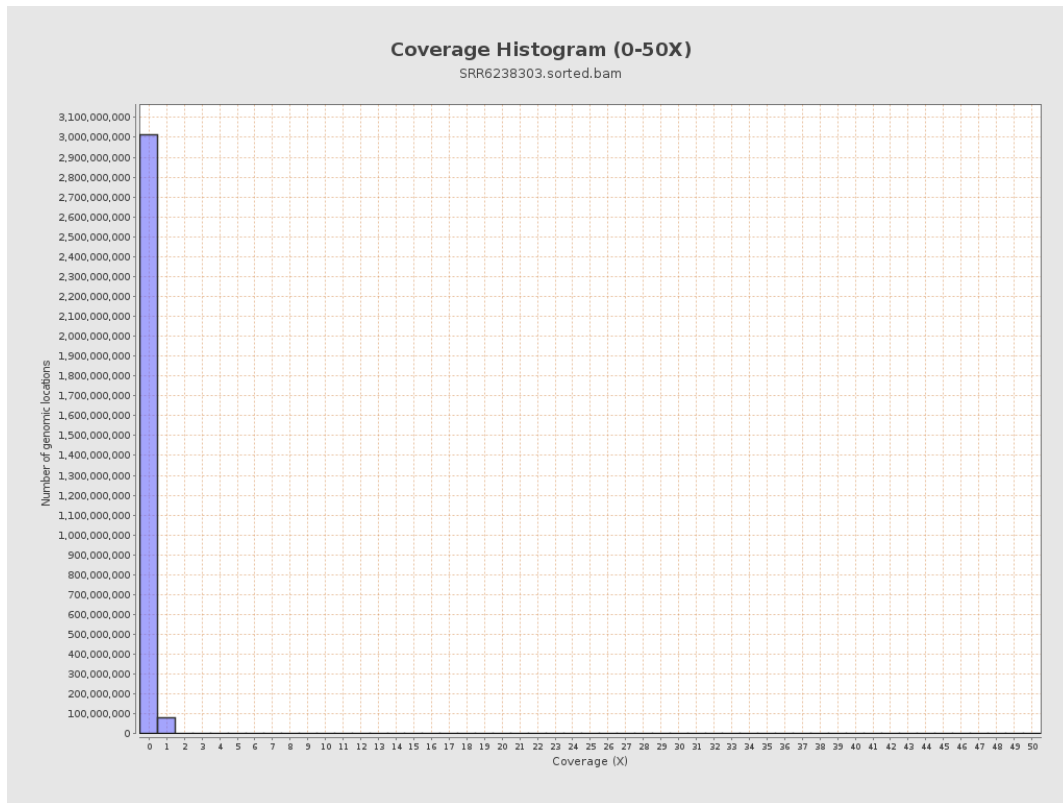
3. Results : Coverage across reference



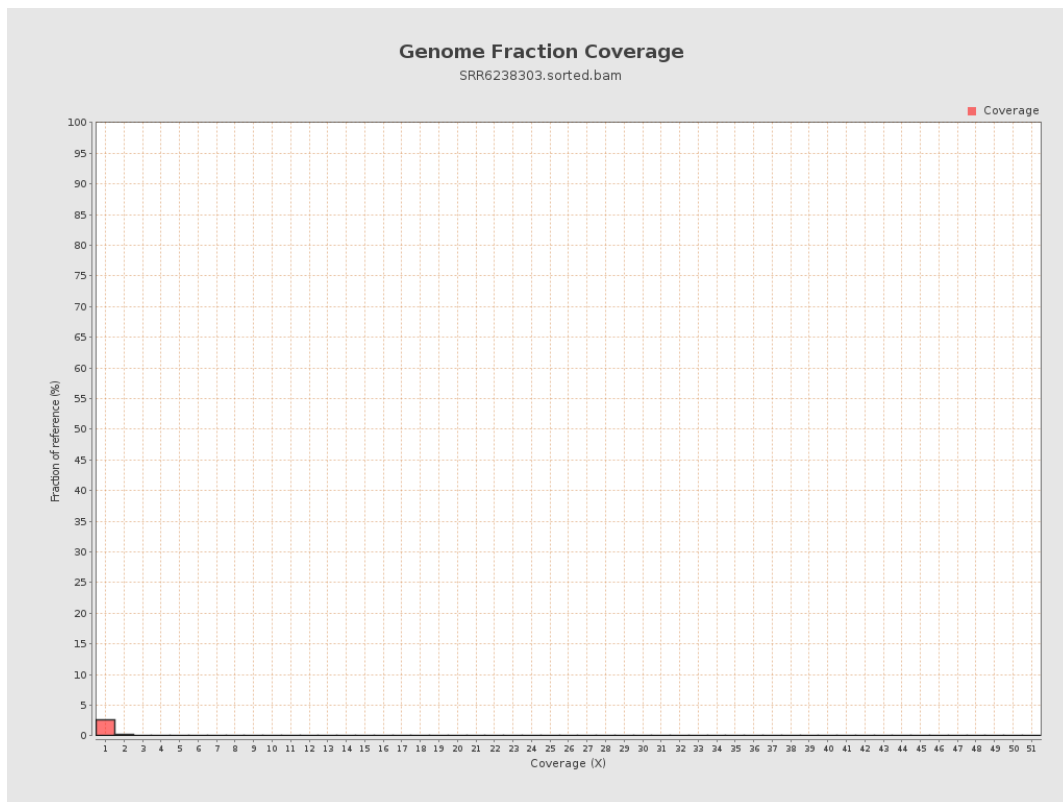
4. Results : Coverage Histogram



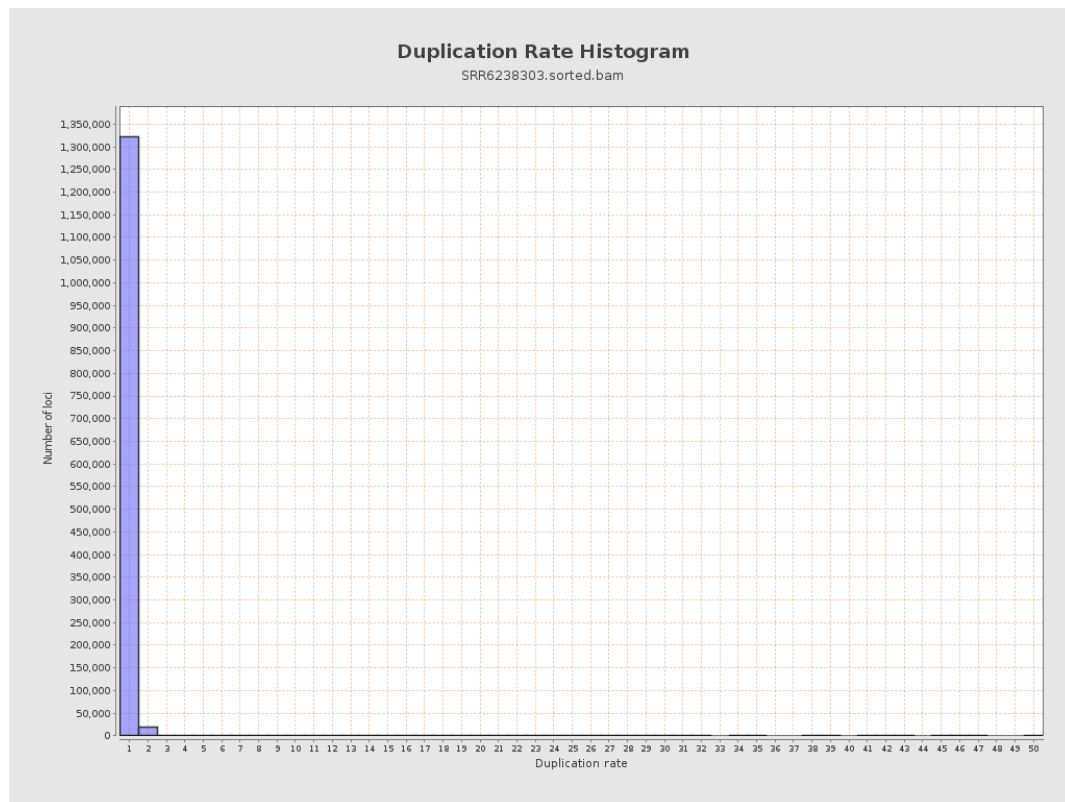
5. Results : Coverage Histogram (0-50X)



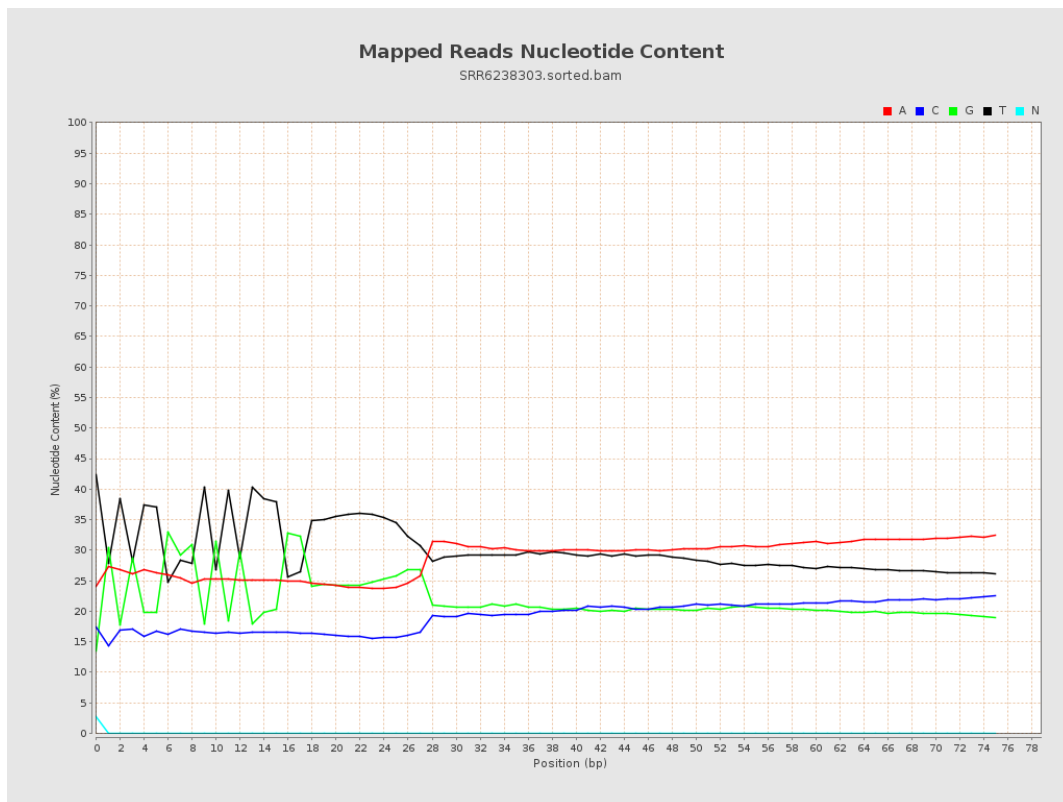
6. Results : Genome Fraction Coverage



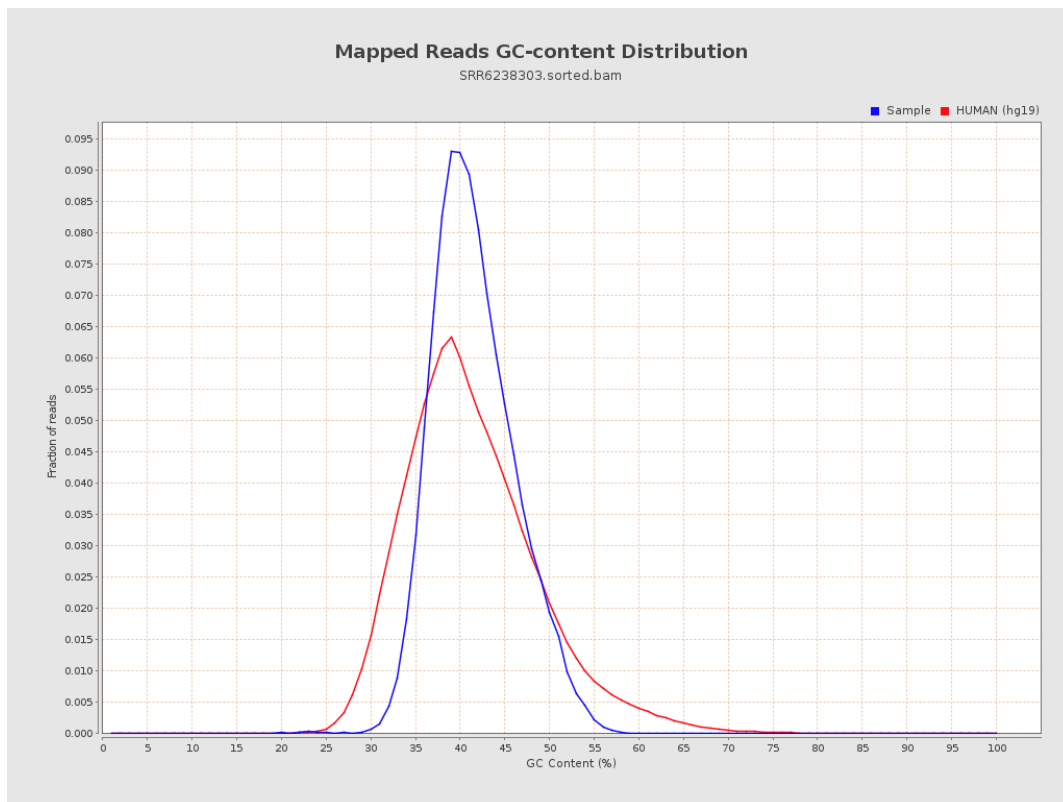
7. Results : Duplication Rate Histogram



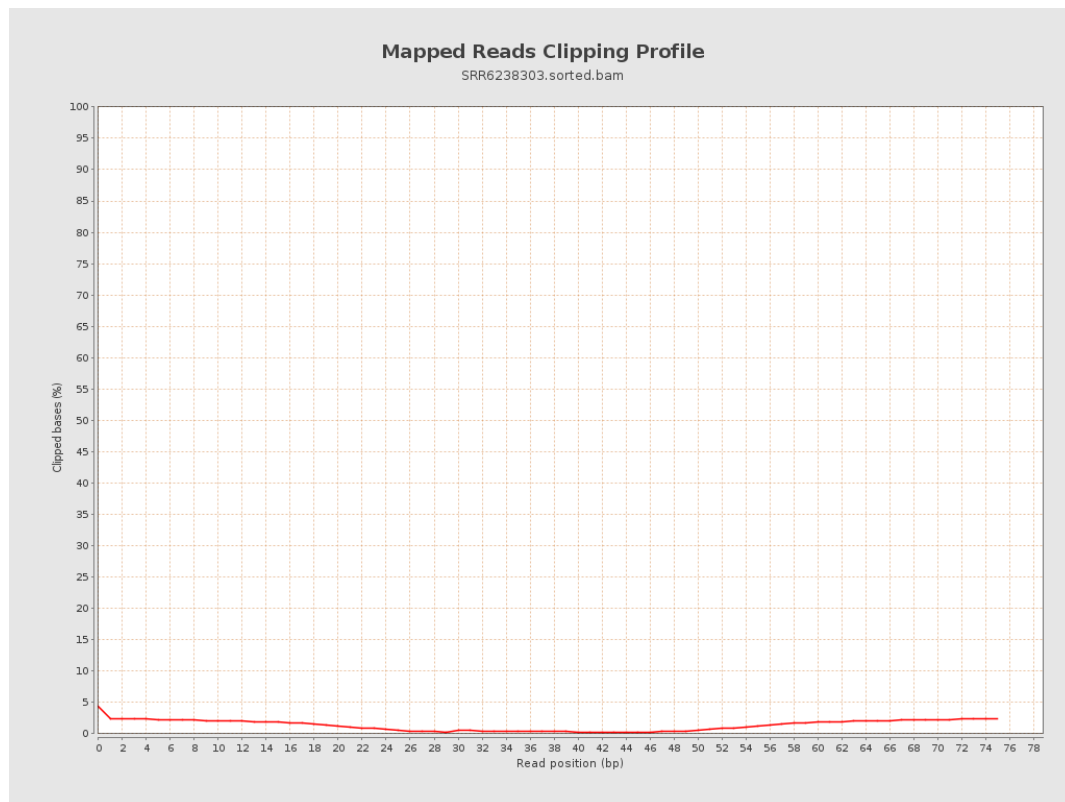
8. Results : Mapped Reads Nucleotide Content



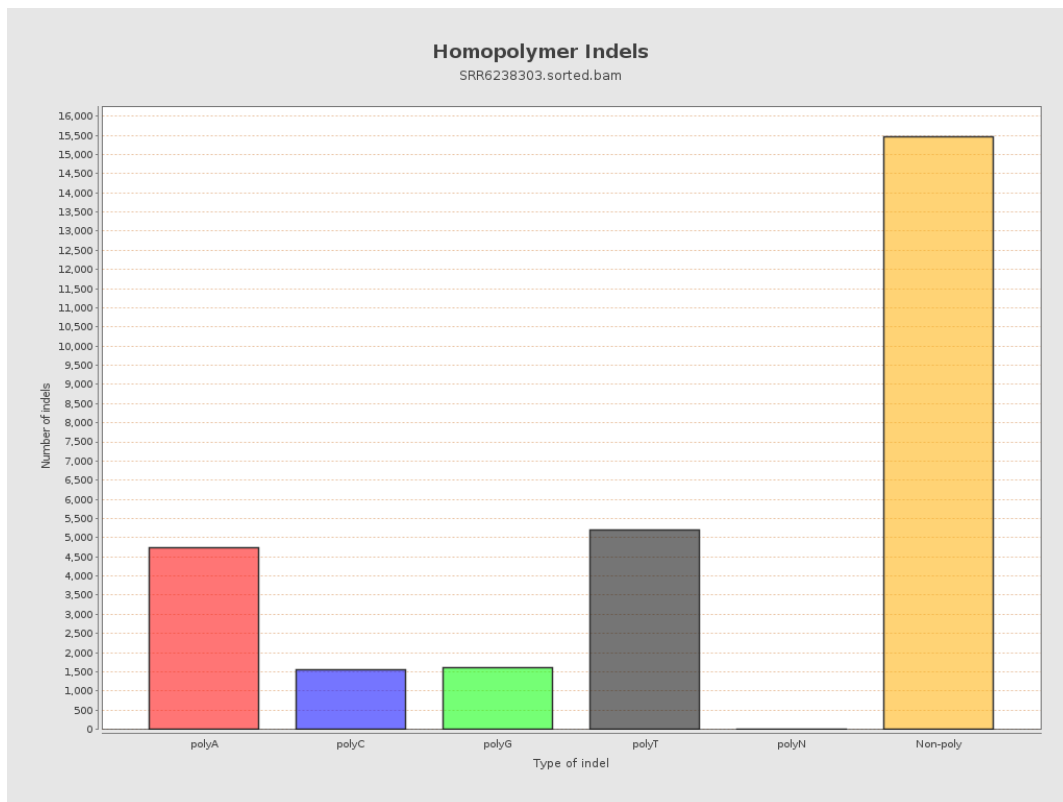
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

