

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 11:15:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238059.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_SRR6238059 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238059.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 11:15:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238059.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,730,913
Mapped reads	1,561,084 / 90.19%
Unmapped reads	169,829 / 9.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,450 / 0.89%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	57,270 / 3.31%
Duplication rate	2.87%
Clipped reads	647,757 / 37.42%

2.2. ACGT Content

Number/percentage of A's	28,846,932 / 27.49%
Number/percentage of C's	20,101,661 / 19.16%
Number/percentage of T's	32,545,814 / 31.02%
Number/percentage of G's	23,430,158 / 22.33%
Number/percentage of N's	5,782 / 0.01%
GC Percentage	41.49%

2.3. Coverage

Mean	0.0339

Standard Deviation	0.3124
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2.4. Mapping Quality

Mean Mapping Quality	44.95
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2.5. Mismatches and indels

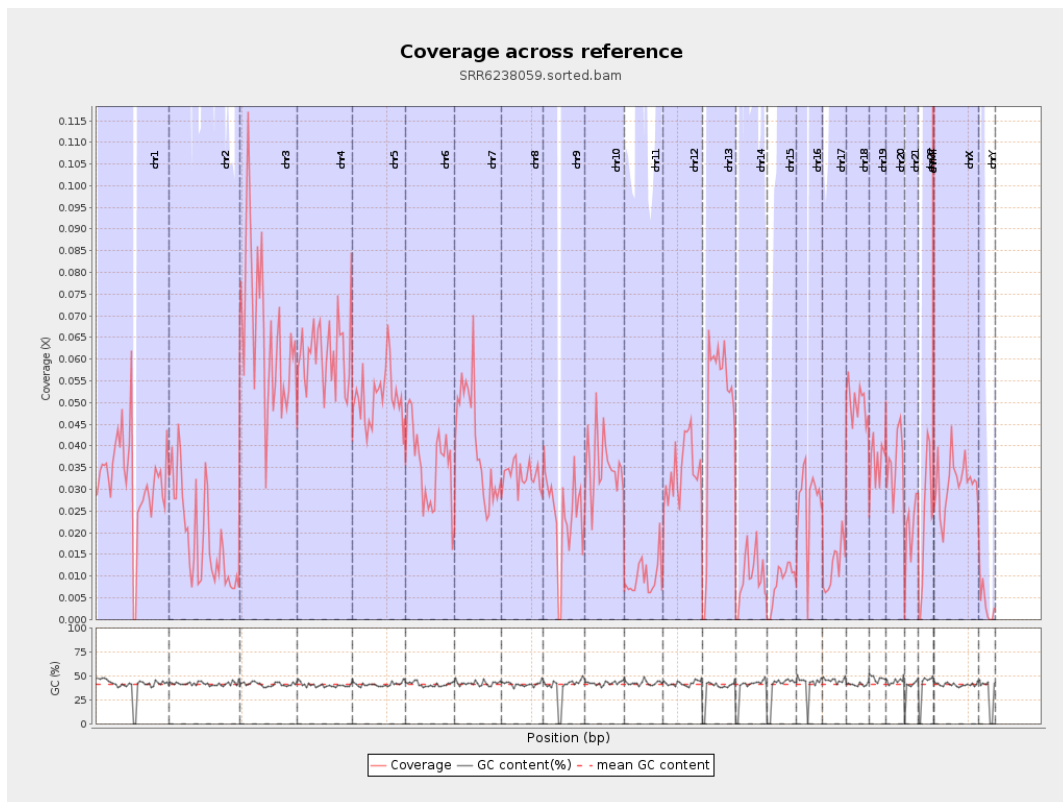
General error rate	0.74%
Mismatches	757,707
Insertions	7,228
Mapped reads with at least one insertion	0.46%
Deletions	27,484
Mapped reads with at least one deletion	1.74%
Homopolymer indels	46.64%

2.6. Chromosome stats

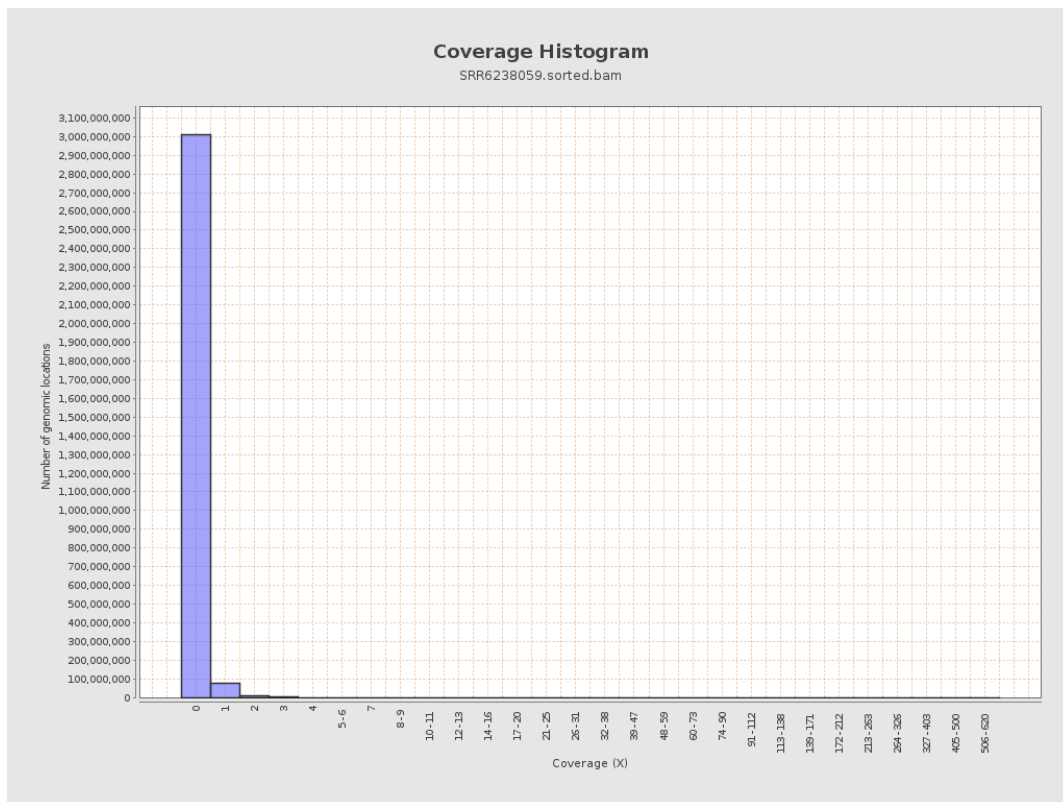
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8010172	0.0321	0.5376
chr2	243199373	4614346	0.019	0.3179
chr3	198022430	13126403	0.0663	0.3004
chr4	191154276	11708282	0.0613	0.2924
chr5	180915260	9266128	0.0512	0.2617
chr6	171115067	6096177	0.0356	0.2413
chr7	159138663	6491389	0.0408	0.4713

chr8	146364022	4854824	0.0332	0.4289
chr9	141213431	3347999	0.0237	0.2448
chr10	135534747	4829889	0.0356	0.3179
chr11	135006516	1279624	0.0095	0.1482
chr12	133851895	4626123	0.0346	0.2182
chr13	115169878	5560908	0.0483	0.2546
chr14	107349540	1058766	0.0099	0.142
chr15	102531392	874658	0.0085	0.1066
chr16	90354753	2511461	0.0278	0.2045
chr17	81195210	1015109	0.0125	0.1308
chr18	78077248	3910998	0.0501	0.4183
chr19	59128983	2181829	0.0369	0.4072
chr20	63025520	2272191	0.0361	0.2262
chr21	48129895	1019859	0.0212	0.1834
chr22	51304566	1147455	0.0224	0.1723
chrMT	16571	54563	3.2927	2.6607
chrX	155270560	4905634	0.0316	0.2224
chrY	59373566	214114	0.0036	0.0936

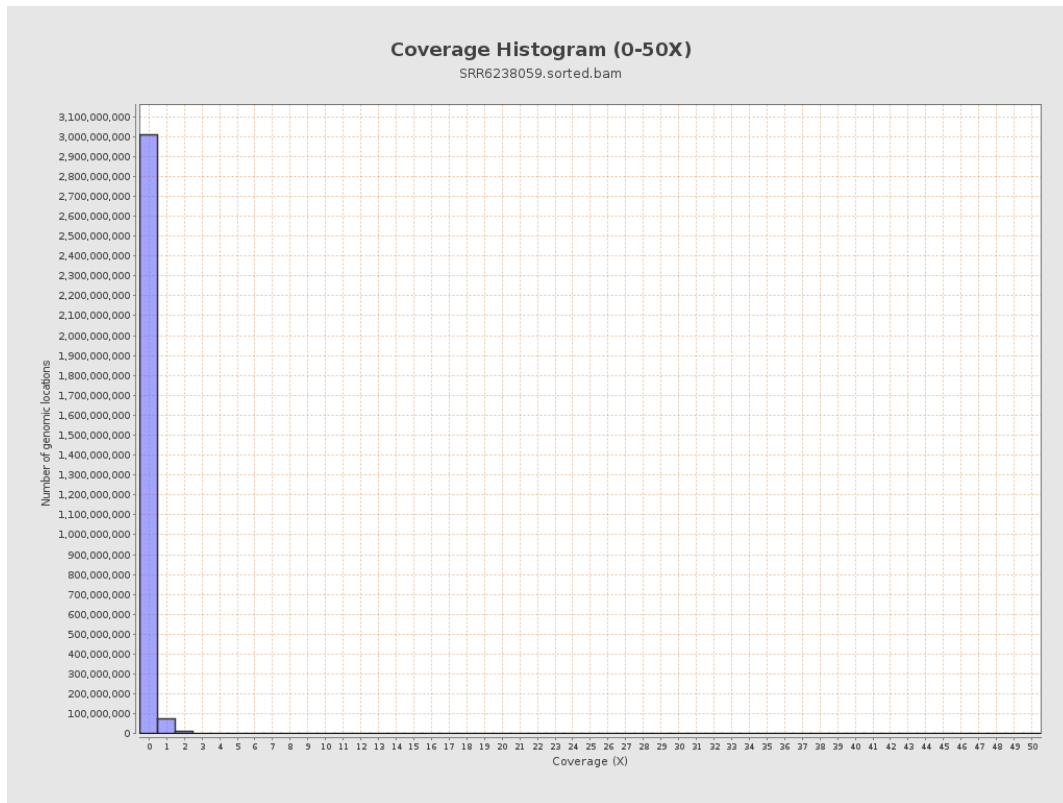
3. Results : Coverage across reference



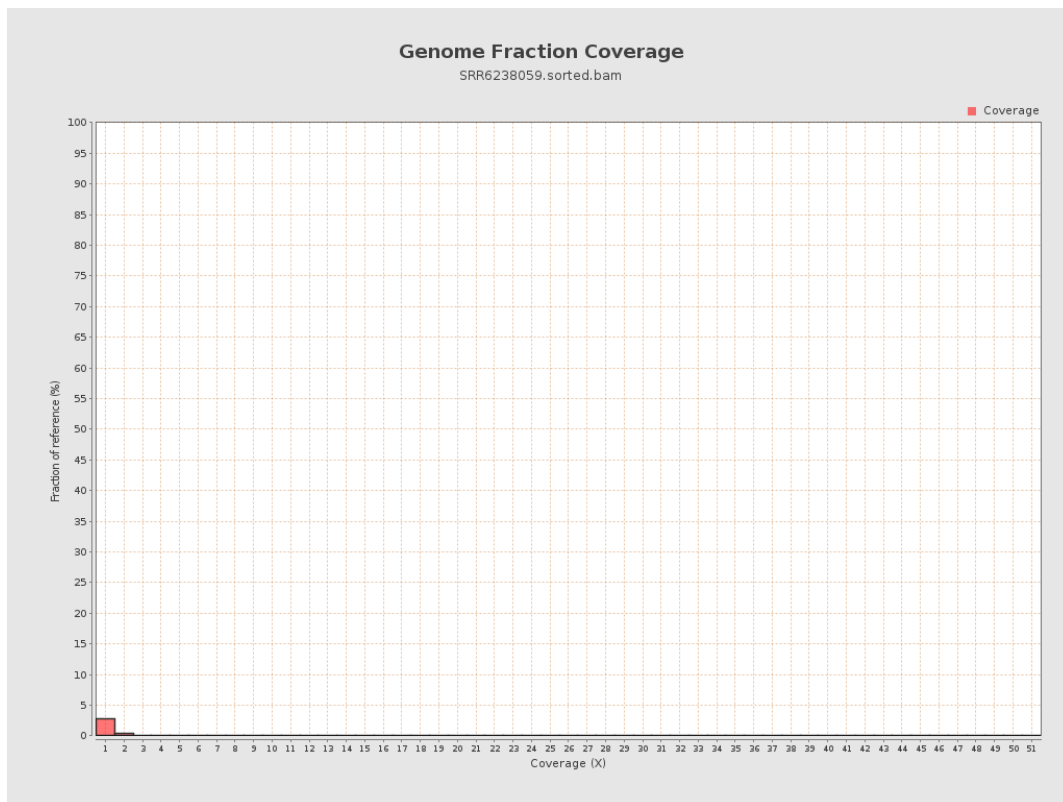
4. Results : Coverage Histogram



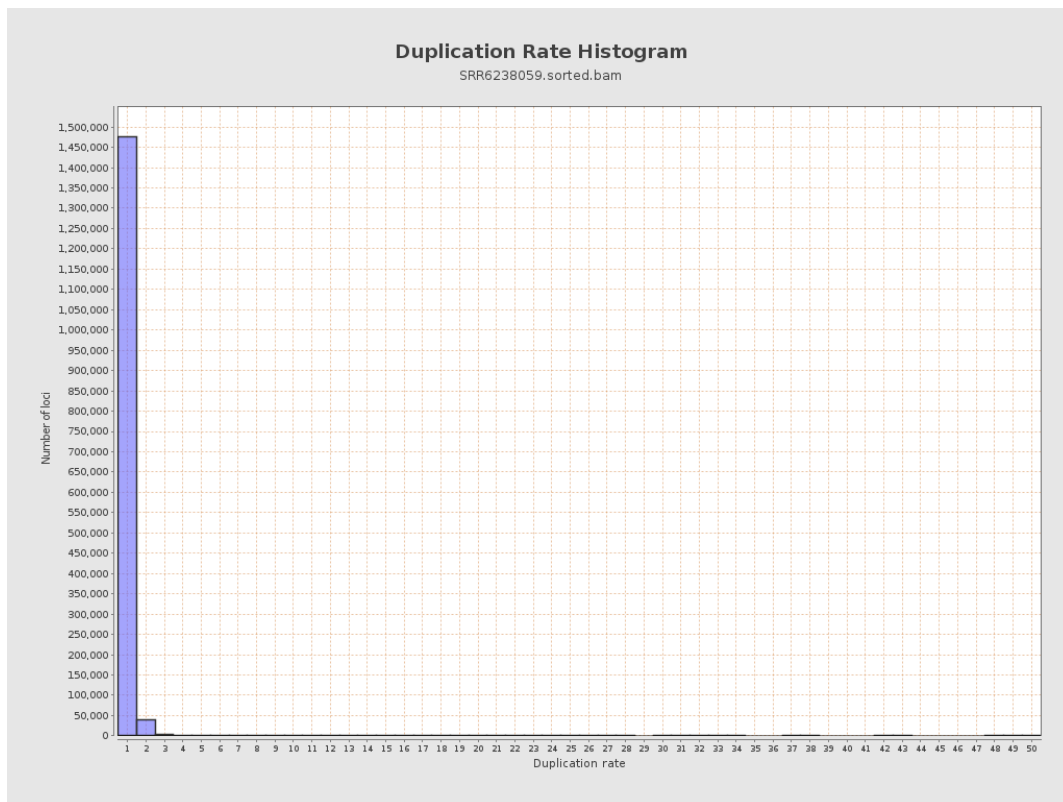
5. Results : Coverage Histogram (0-50X)



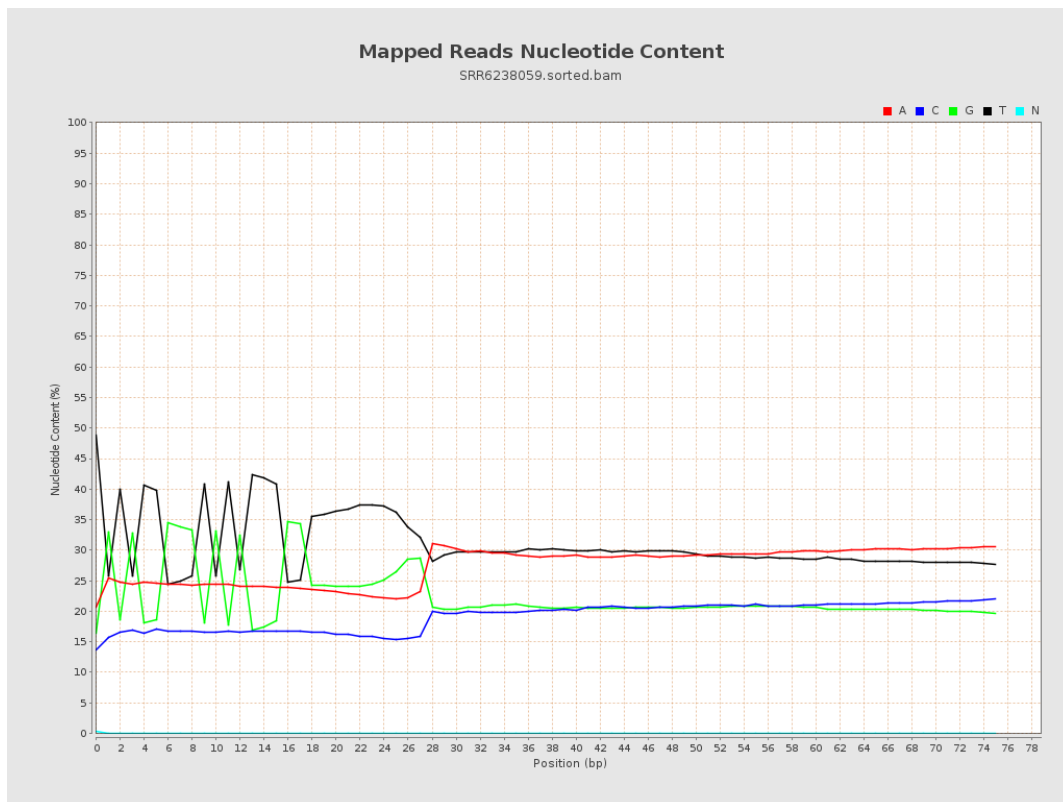
6. Results : Genome Fraction Coverage



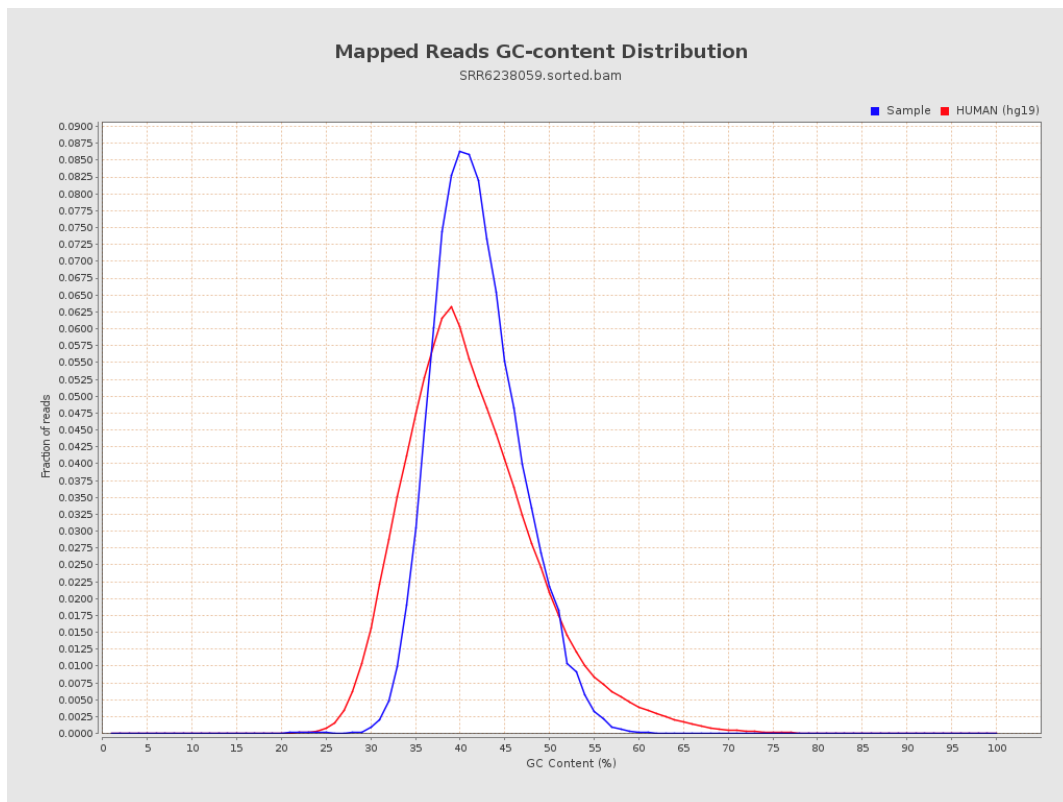
7. Results : Duplication Rate Histogram



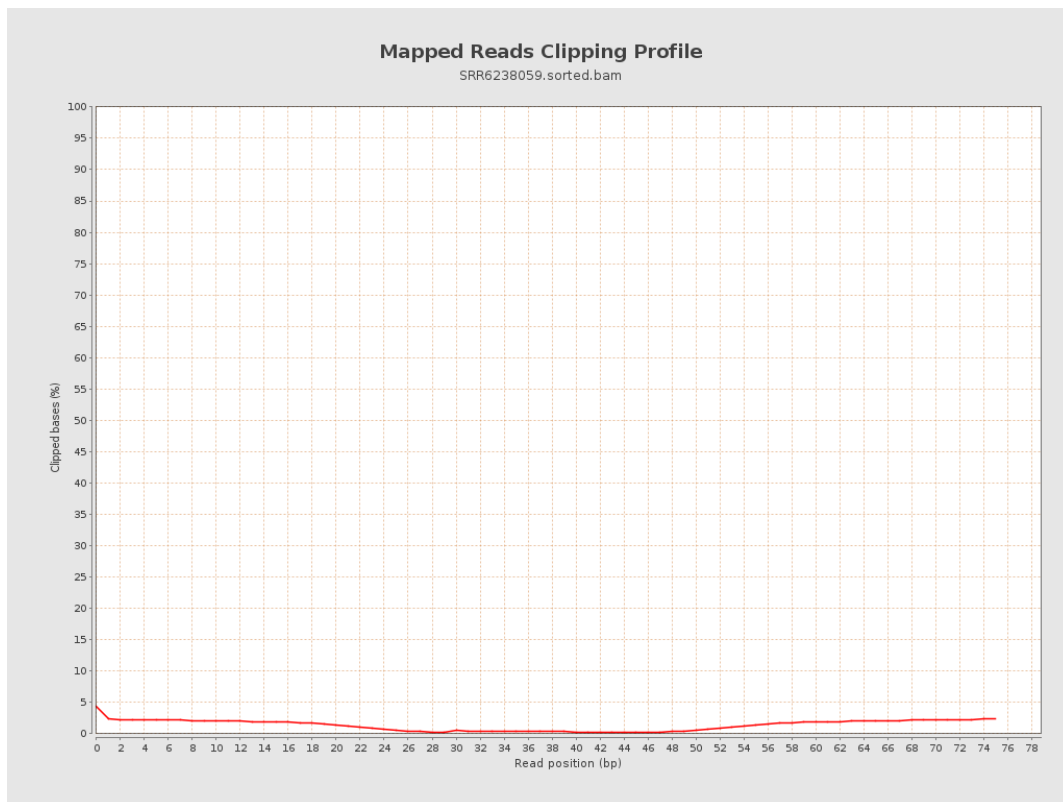
8. Results : Mapped Reads Nucleotide Content



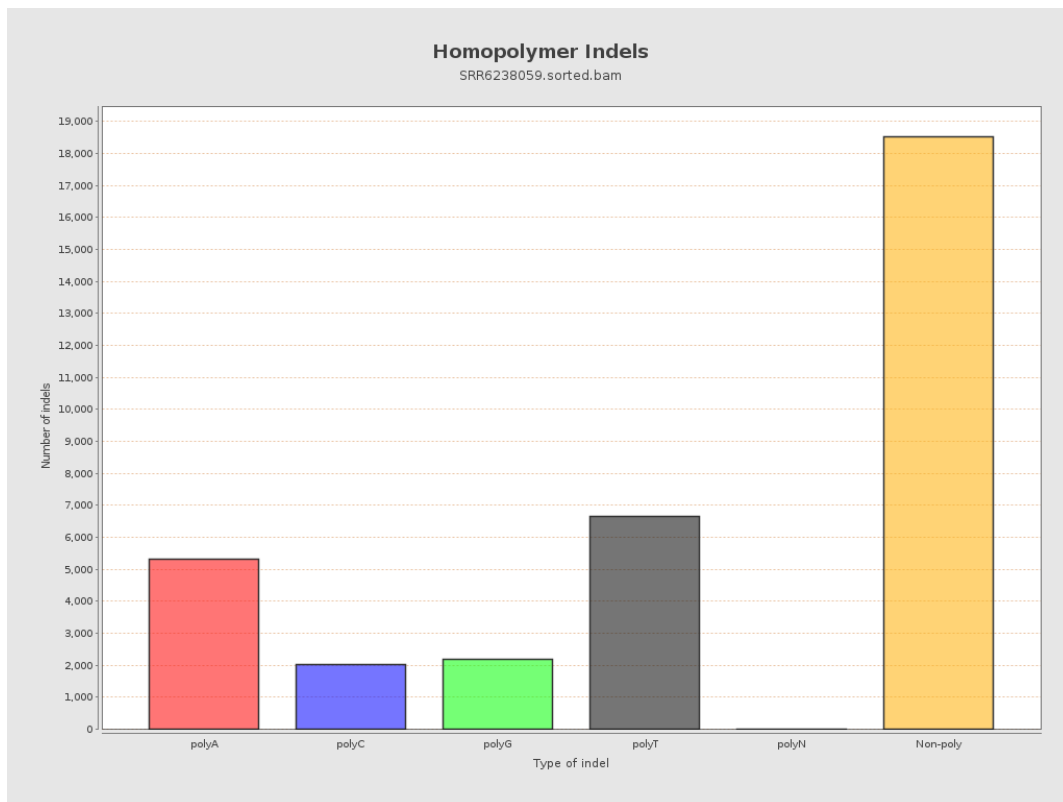
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

