

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 12:29:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238240.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_SRR6238240 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238240.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 12:29:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238240.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,053,651
Mapped reads	560,084 / 53.16%
Unmapped reads	493,567 / 46.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,129 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	68,979 / 6.55%
Duplication rate	8.53%
Clipped reads	341,782 / 32.44%

2.2. ACGT Content

Number/percentage of A's	9,776,277 / 27.96%
Number/percentage of C's	6,959,228 / 19.9%
Number/percentage of T's	10,492,151 / 30.01%
Number/percentage of G's	7,731,125 / 22.11%
Number/percentage of N's	5,642 / 0.02%
GC Percentage	42.02%

2.3. Coverage

Mean	0.0113

Standard Deviation	0.2589
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2.4. Mapping Quality

Mean Mapping Quality	43.96
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2.5. Mismatches and indels

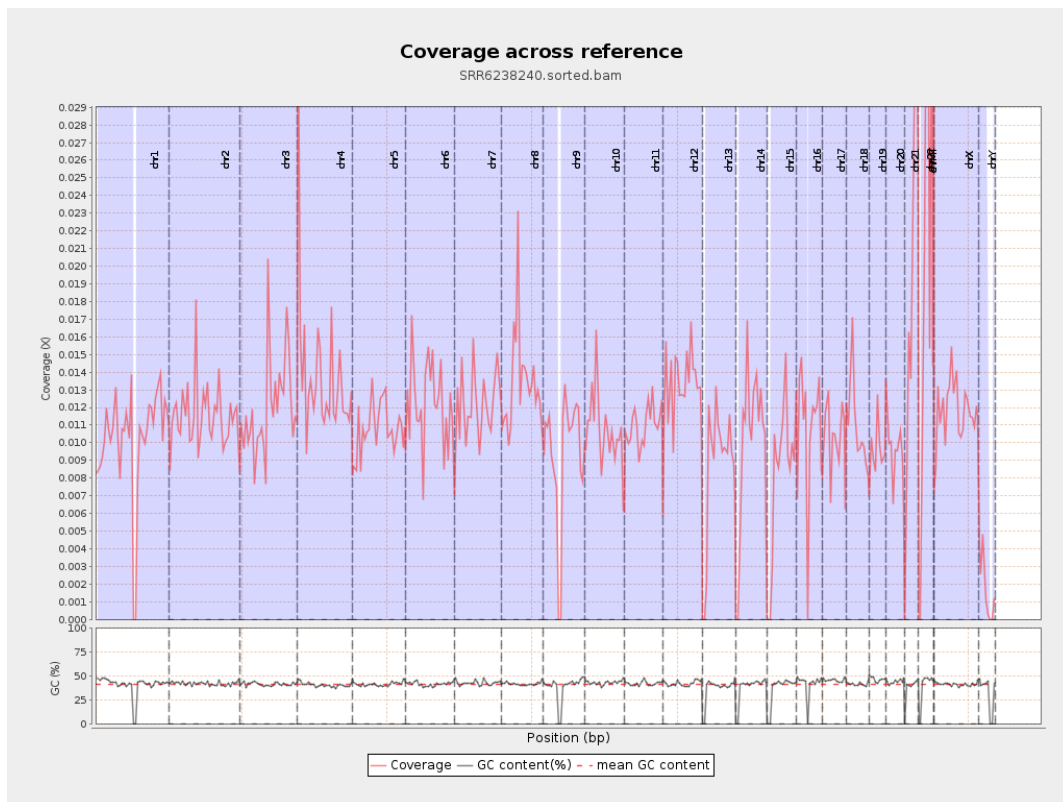
General error rate	0.92%
Mismatches	317,144
Insertions	2,944
Mapped reads with at least one insertion	0.52%
Deletions	8,579
Mapped reads with at least one deletion	1.52%
Homopolymer indels	45.39%

2.6. Chromosome stats

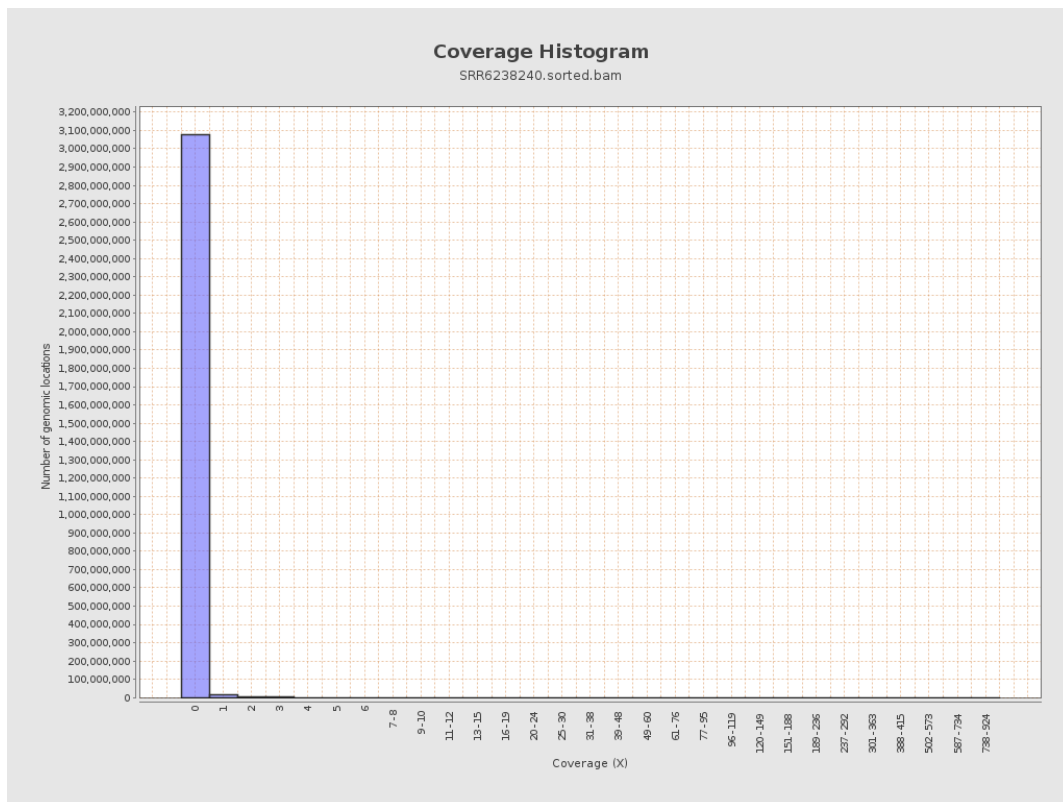
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	2556236	0.0103	0.2791
chr2	243199373	2811348	0.0116	0.3594
chr3	198022430	2356482	0.0119	0.1886
chr4	191154276	2624674	0.0137	0.219
chr5	180915260	1952375	0.0108	0.186
chr6	171115067	2066118	0.0121	0.2591
chr7	159138663	1940864	0.0122	0.2107

chr8	146364022	1957253	0.0134	0.2242
chr9	141213431	1330970	0.0094	0.1675
chr10	135534747	1451348	0.0107	0.1884
chr11	135006516	1480281	0.011	0.1759
chr12	133851895	1796218	0.0134	0.2023
chr13	115169878	996557	0.0087	0.22
chr14	107349540	1076547	0.01	0.4615
chr15	102531392	841739	0.0082	0.5522
chr16	90354753	972111	0.0108	0.1805
chr17	81195210	828148	0.0102	0.1768
chr18	78077248	871451	0.0112	0.1937
chr19	59128983	579717	0.0098	0.1812
chr20	63025520	597669	0.0095	0.1627
chr21	48129895	918757	0.0191	0.2312
chr22	51304566	1032988	0.0201	0.3188
chrMT	16571	19025	1.1481	1.6156
chrX	155270560	1821696	0.0117	0.2534
chrY	59373566	97974	0.0017	0.0709

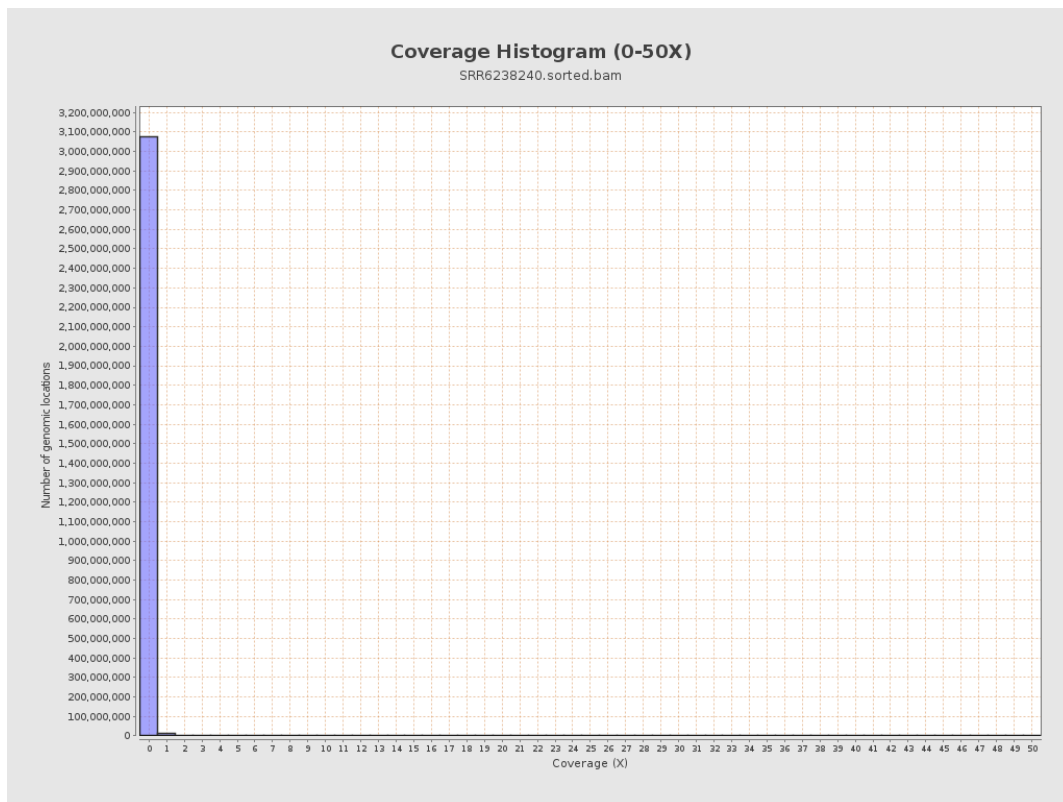
3. Results : Coverage across reference



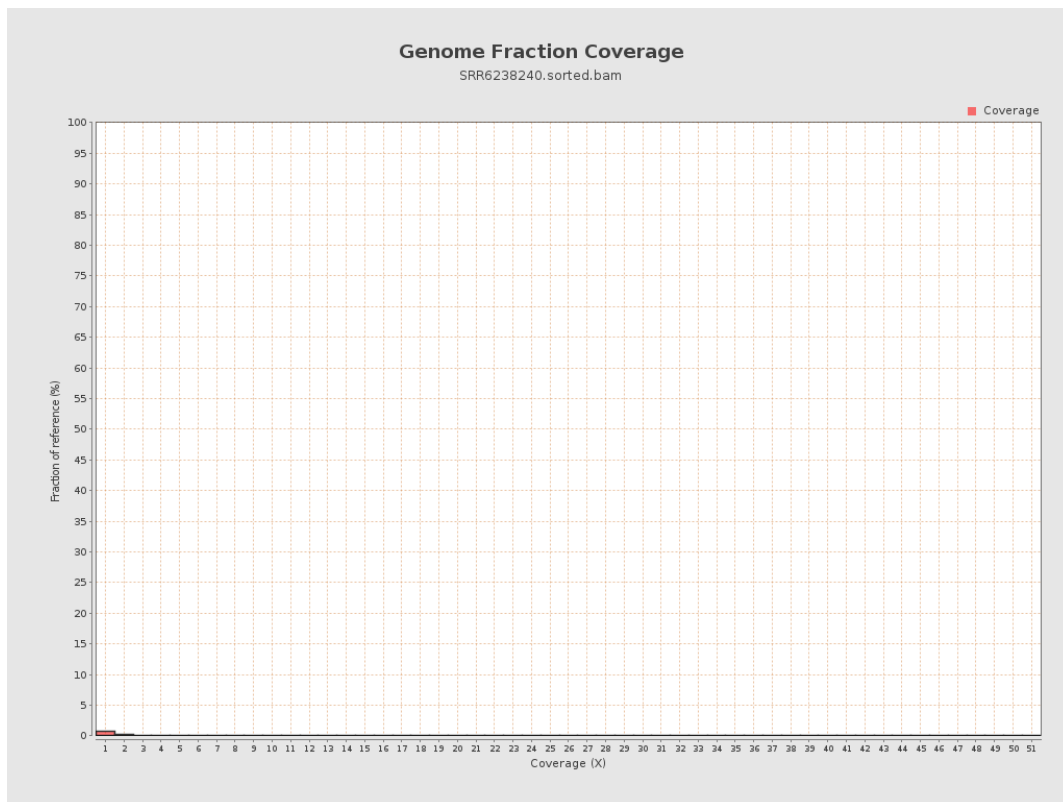
4. Results : Coverage Histogram



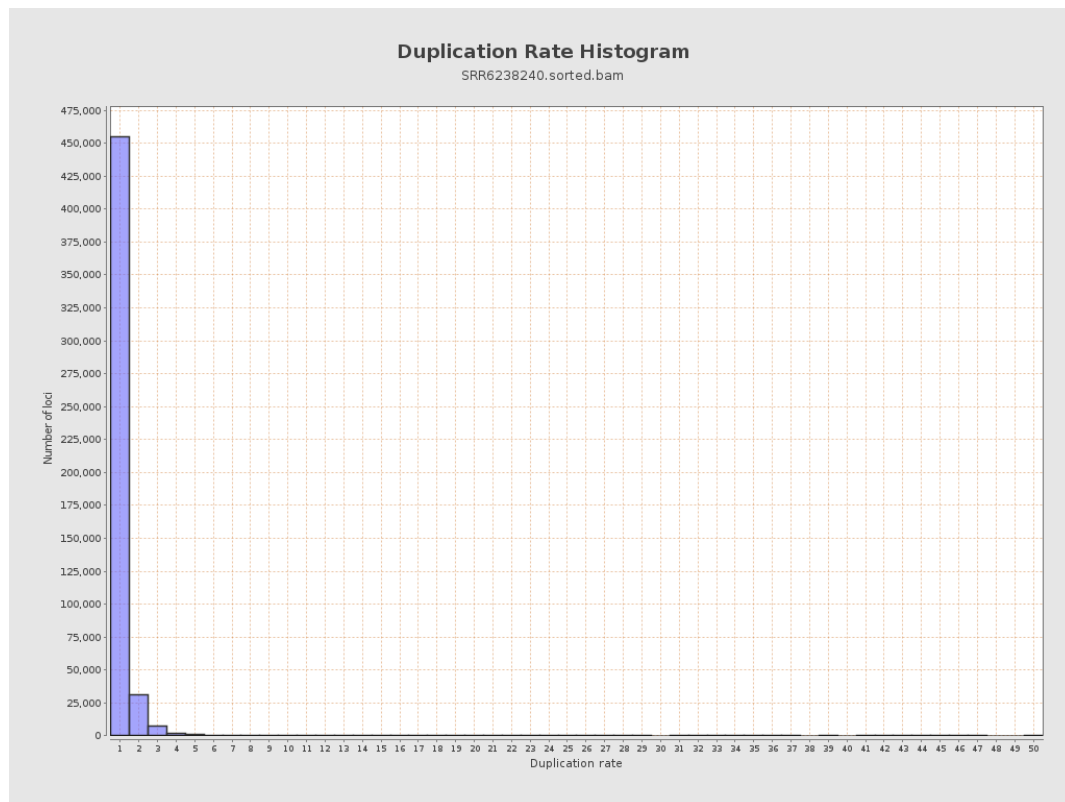
5. Results : Coverage Histogram (0-50X)



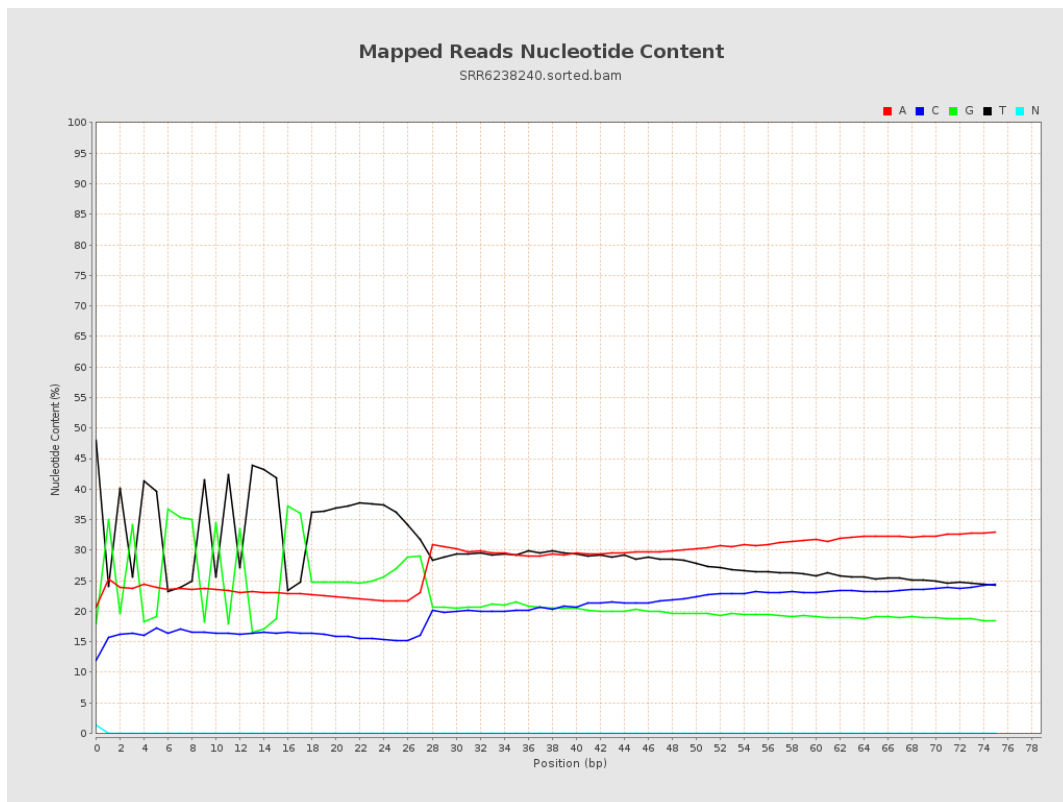
6. Results : Genome Fraction Coverage



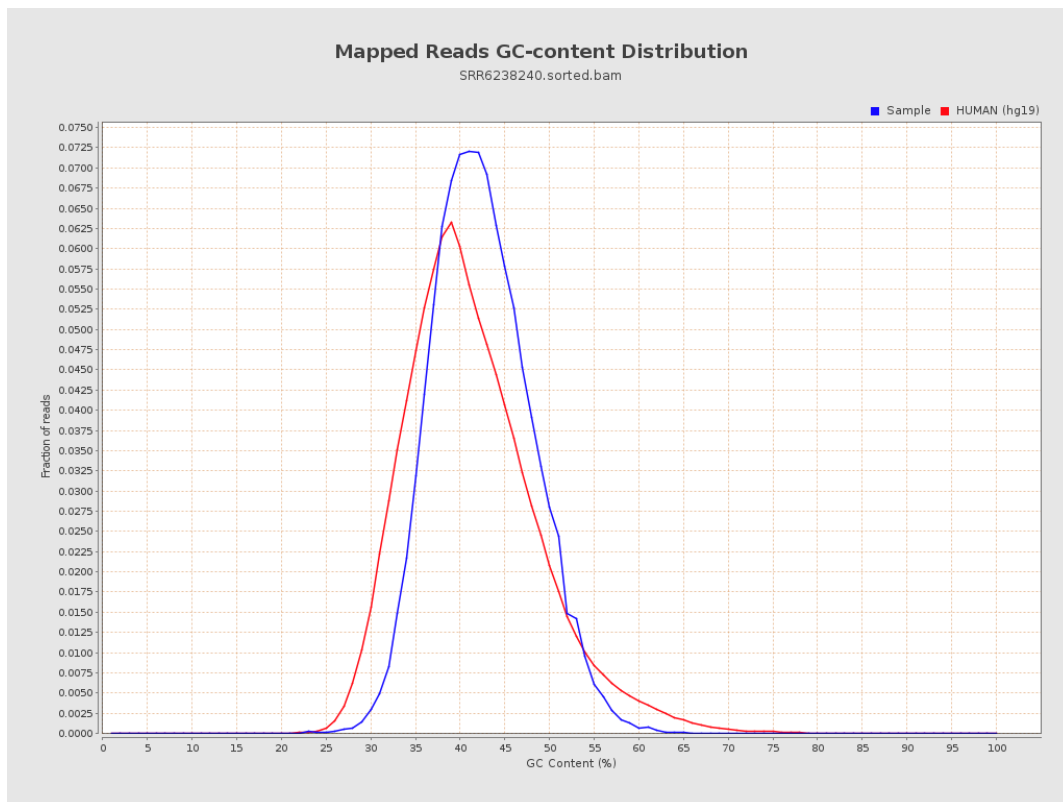
7. Results : Duplication Rate Histogram



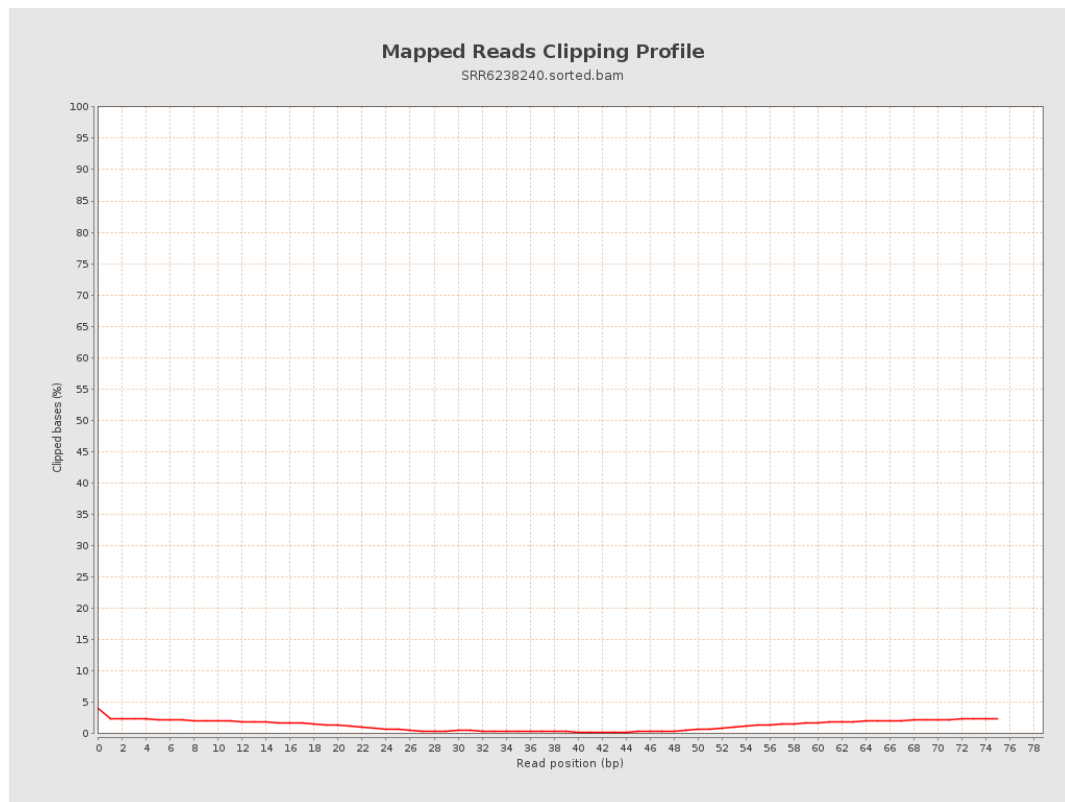
8. Results : Mapped Reads Nucleotide Content



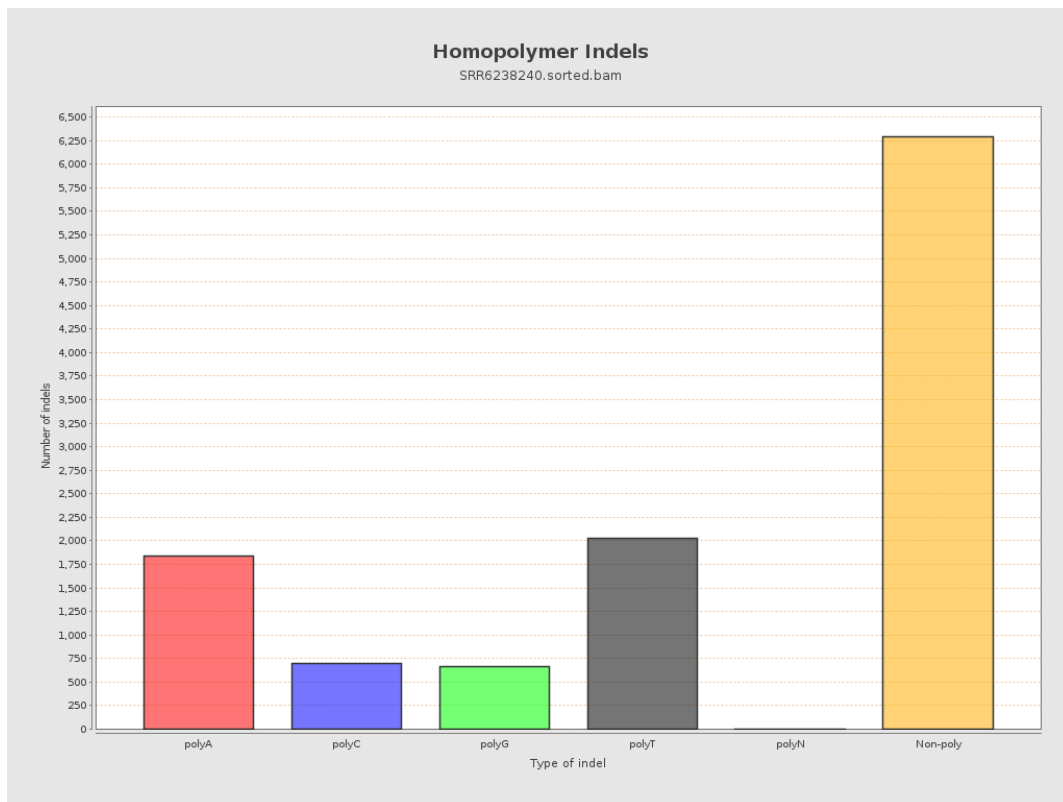
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

