

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 23:59:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237280.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_SRR6237280 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237280.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 23:59:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237280.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,071,589
Mapped reads	473,264 / 22.85%
Unmapped reads	1,598,325 / 77.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,259 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	31,872 / 1.54%
Duplication rate	5.66%
Clipped reads	157,338 / 7.6%

2.2. ACGT Content

Number/percentage of A's	9,649,377 / 29.32%
Number/percentage of C's	6,190,648 / 18.81%
Number/percentage of T's	10,249,795 / 31.14%
Number/percentage of G's	6,819,777 / 20.72%
Number/percentage of N's	523 / 0%
GC Percentage	39.53%

2.3. Coverage

Mean	0.0106

Standard Deviation	0.2018
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2.4. Mapping Quality

Mean Mapping Quality	47.29
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2.5. Mismatches and indels

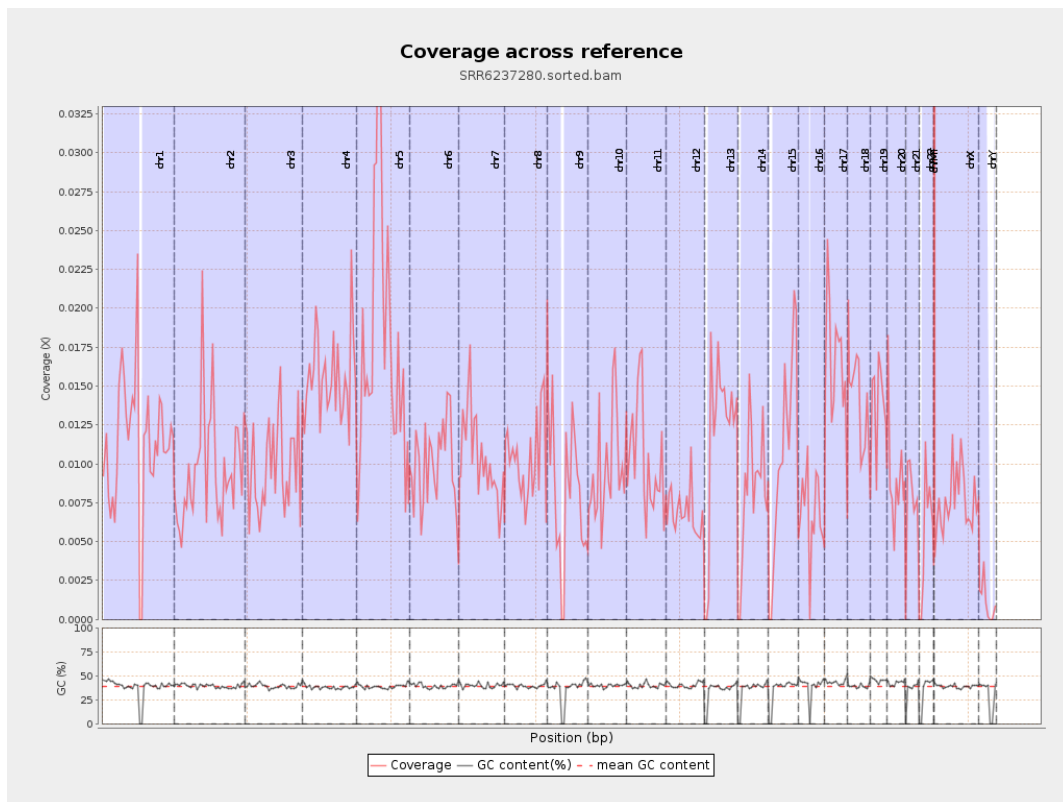
General error rate	0.76%
Mismatches	245,688
Insertions	2,448
Mapped reads with at least one insertion	0.51%
Deletions	7,806
Mapped reads with at least one deletion	1.63%
Homopolymer indels	49.31%

2.6. Chromosome stats

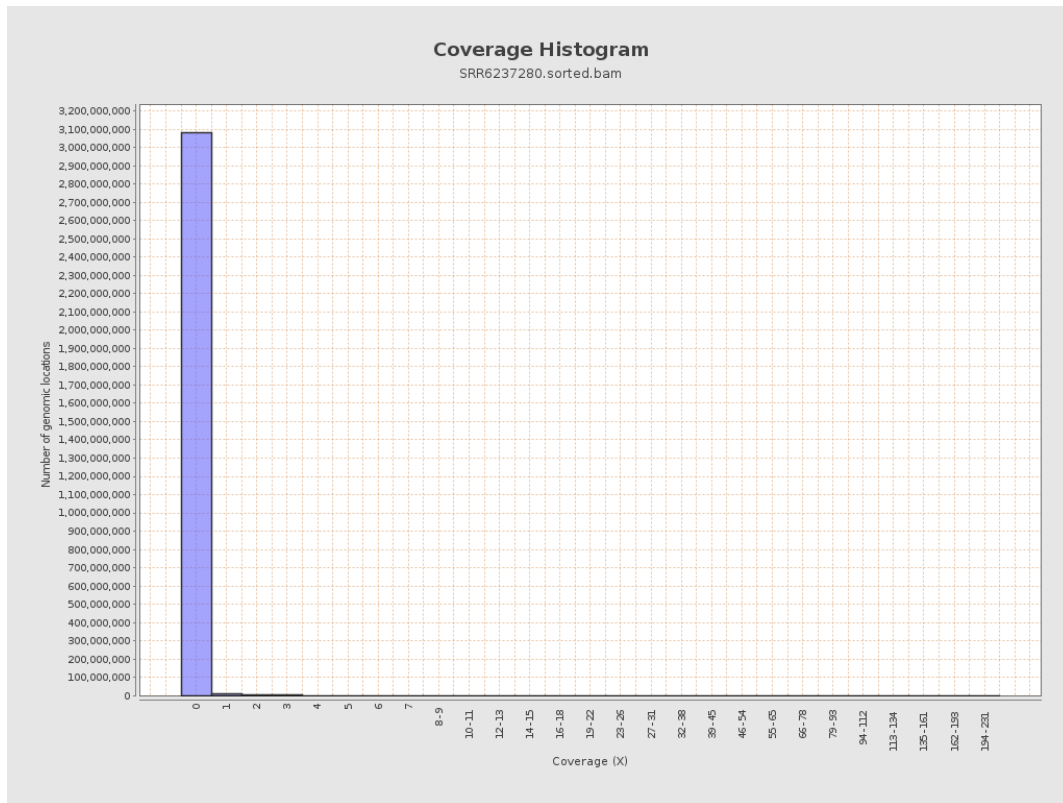
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	2800449	0.0112	0.259
chr2	243199373	2335484	0.0096	0.1888
chr3	198022430	1940247	0.0098	0.1757
chr4	191154276	2968845	0.0155	0.2236
chr5	180915260	3284273	0.0182	0.2382
chr6	171115067	1689472	0.0099	0.1764
chr7	159138663	1648129	0.0104	0.1858

chr8	146364022	1495762	0.0102	0.196
chr9	141213431	1153905	0.0082	0.1677
chr10	135534747	1339561	0.0099	0.1874
chr11	135006516	1391298	0.0103	0.2206
chr12	133851895	922067	0.0069	0.1446
chr13	115169878	1374169	0.0119	0.1935
chr14	107349540	881756	0.0082	0.1587
chr15	102531392	1100644	0.0107	0.1836
chr16	90354753	612528	0.0068	0.139
chr17	81195210	1341328	0.0165	0.2406
chr18	78077248	1098290	0.0141	0.2706
chr19	59128983	813972	0.0138	0.2388
chr20	63025520	560961	0.0089	0.1621
chr21	48129895	362151	0.0075	0.1527
chr22	51304566	286706	0.0056	0.1265
chrMT	16571	283341	17.0986	10.4448
chrX	155270560	1170786	0.0075	0.1574
chrY	59373566	67459	0.0011	0.0495

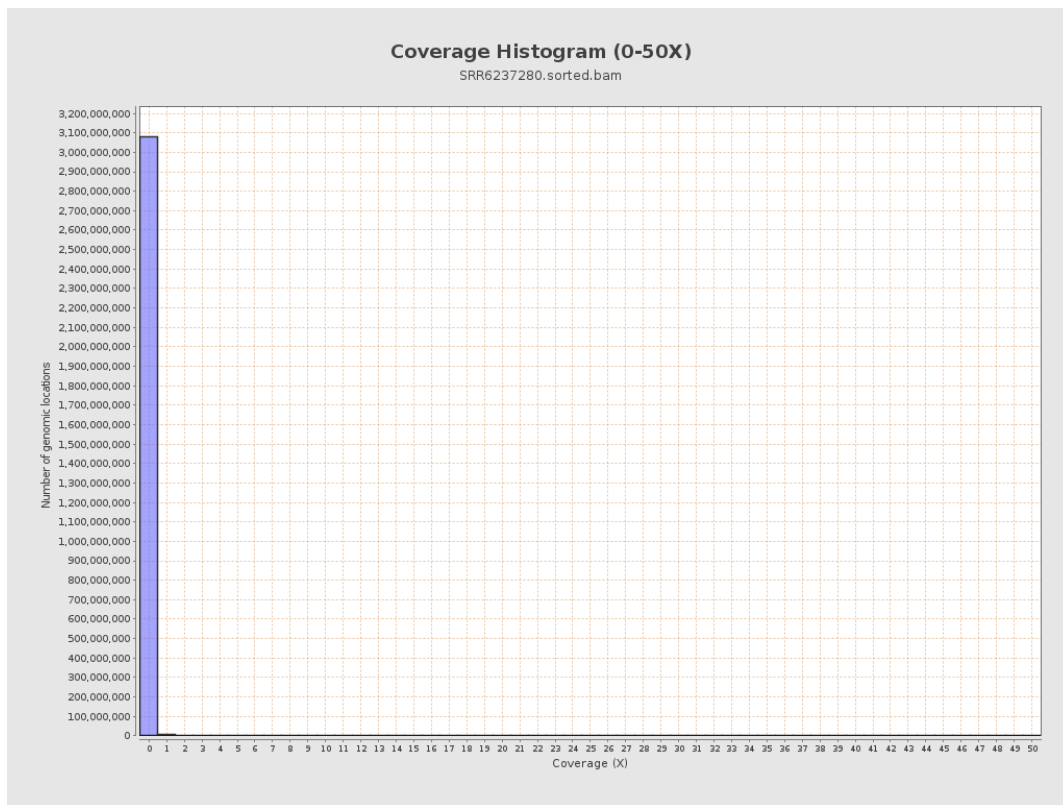
3. Results : Coverage across reference



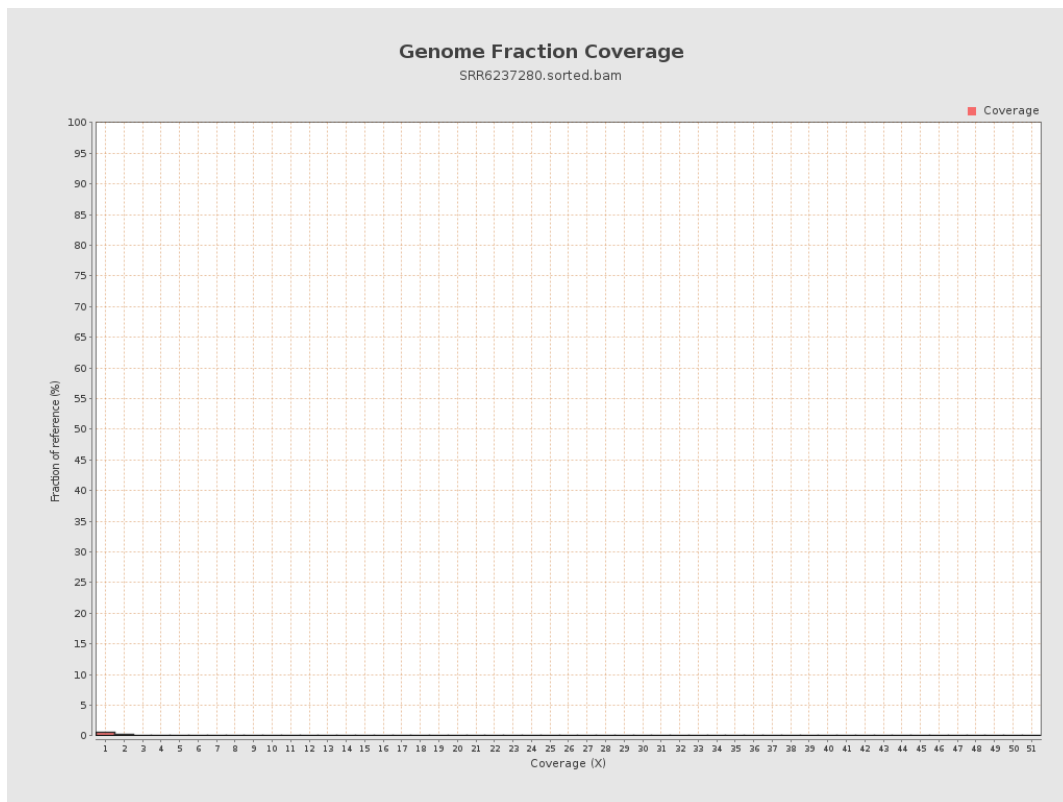
4. Results : Coverage Histogram



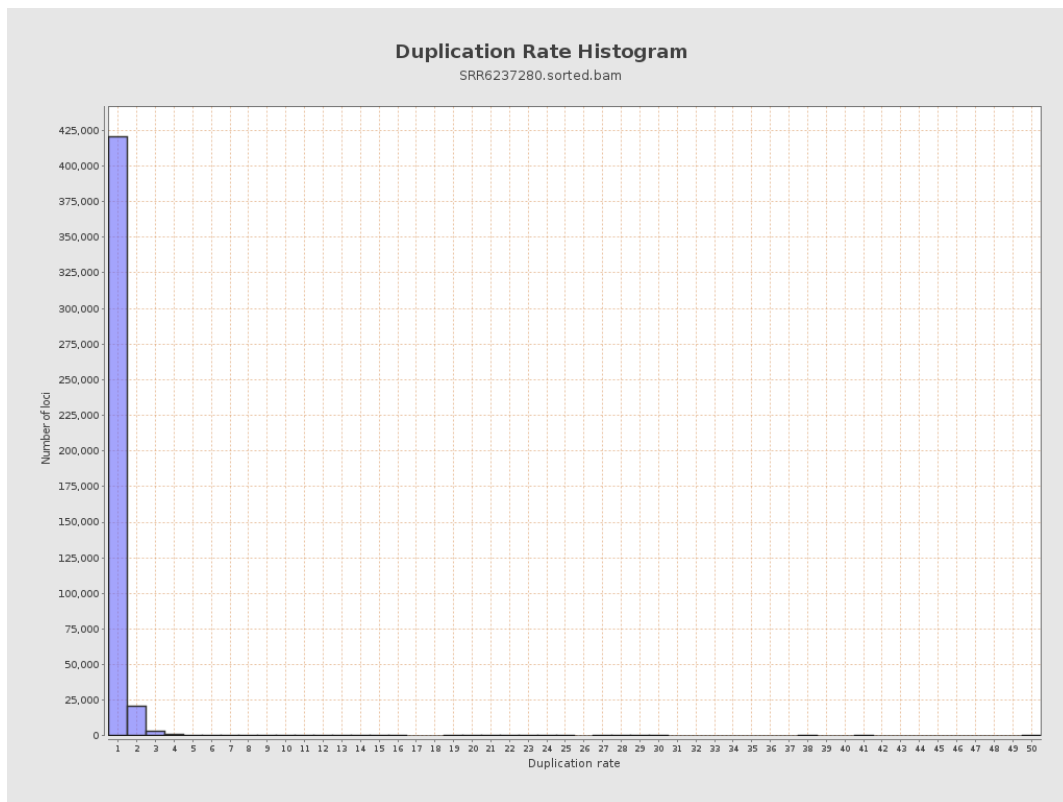
5. Results : Coverage Histogram (0-50X)



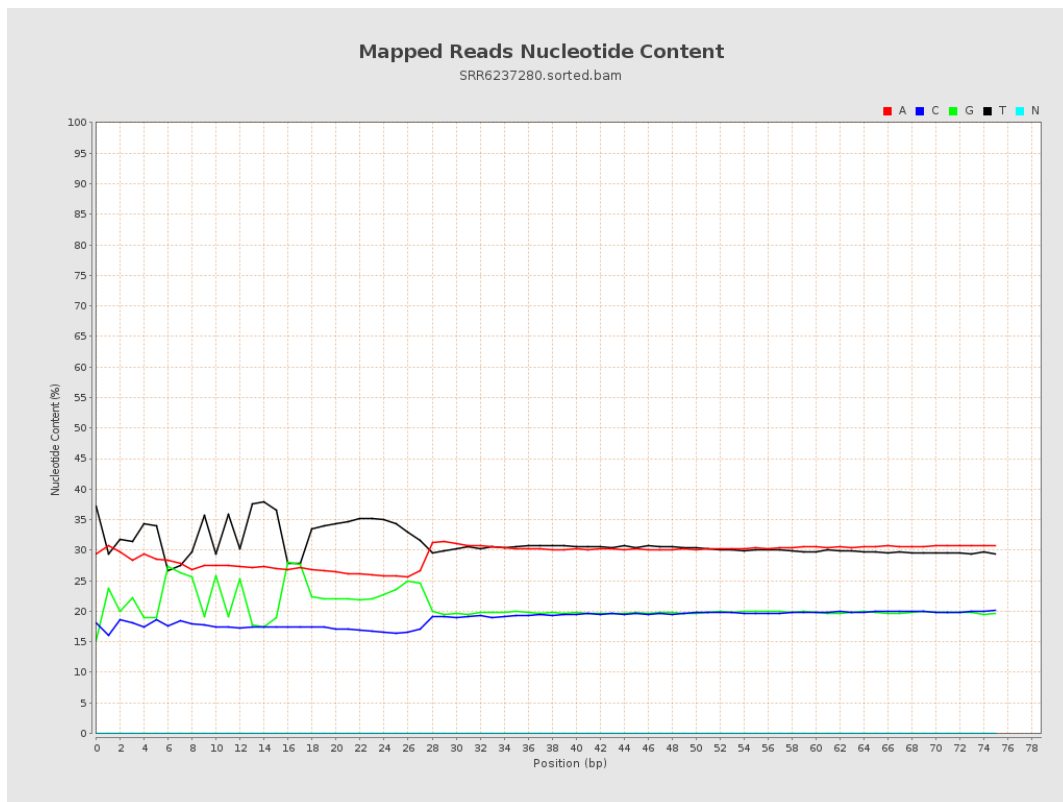
6. Results : Genome Fraction Coverage



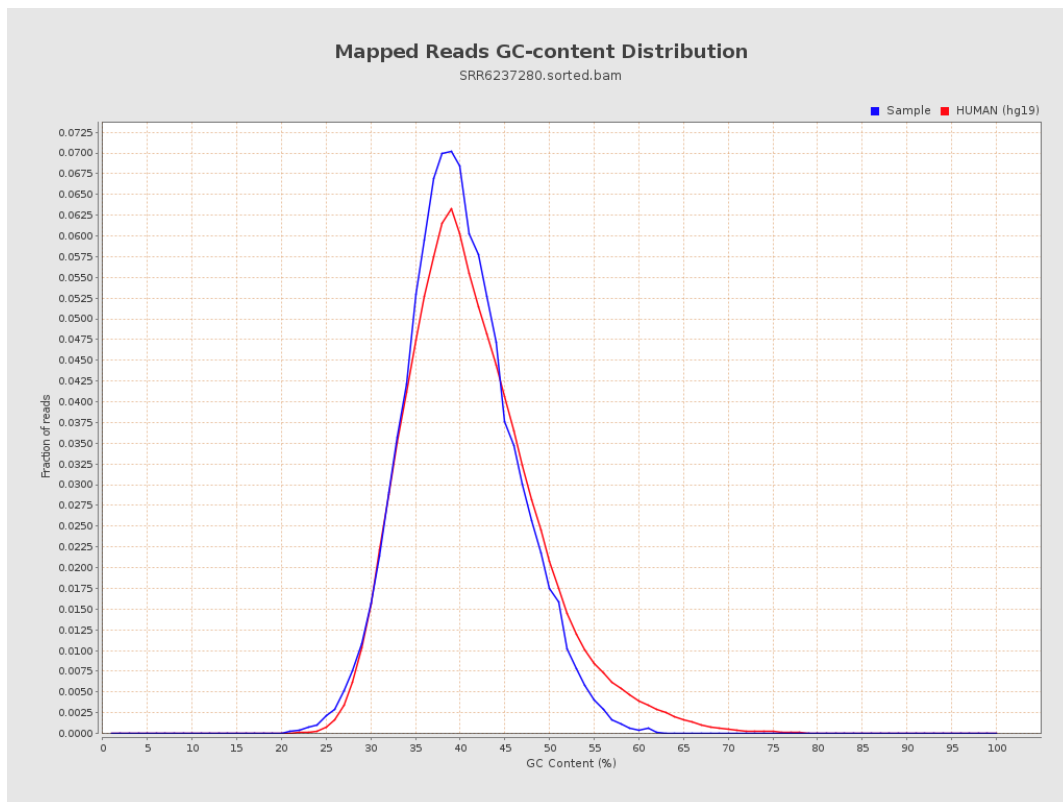
7. Results : Duplication Rate Histogram



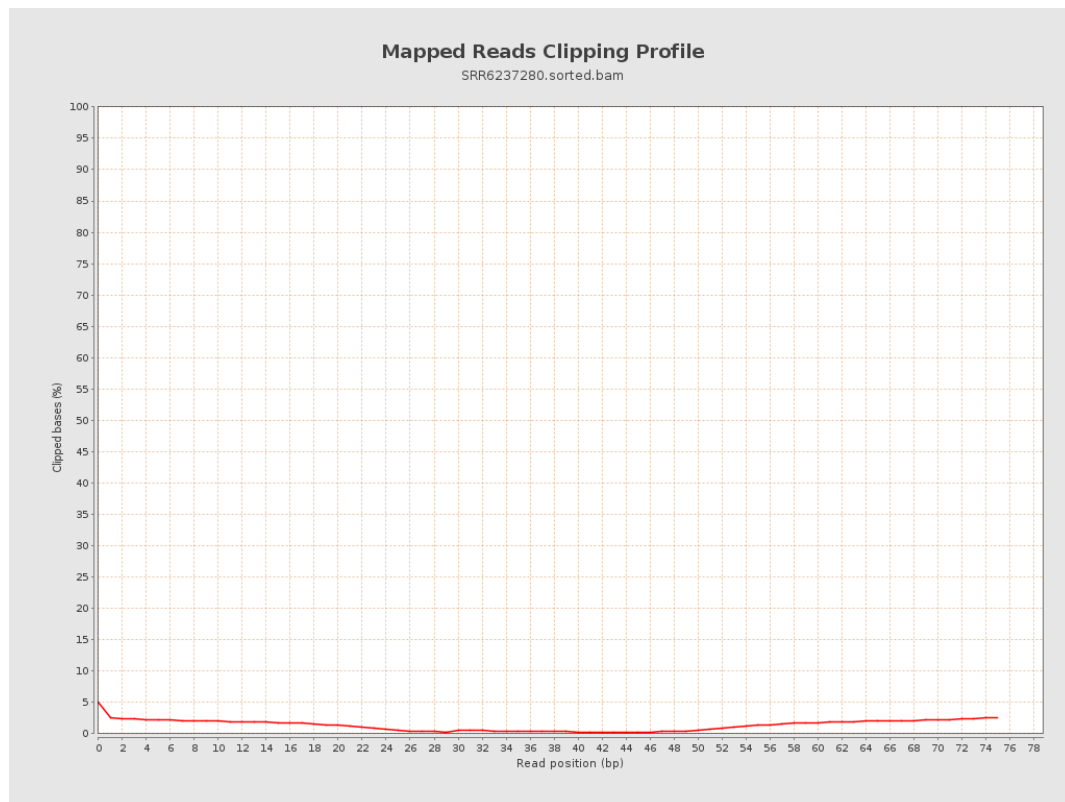
8. Results : Mapped Reads Nucleotide Content



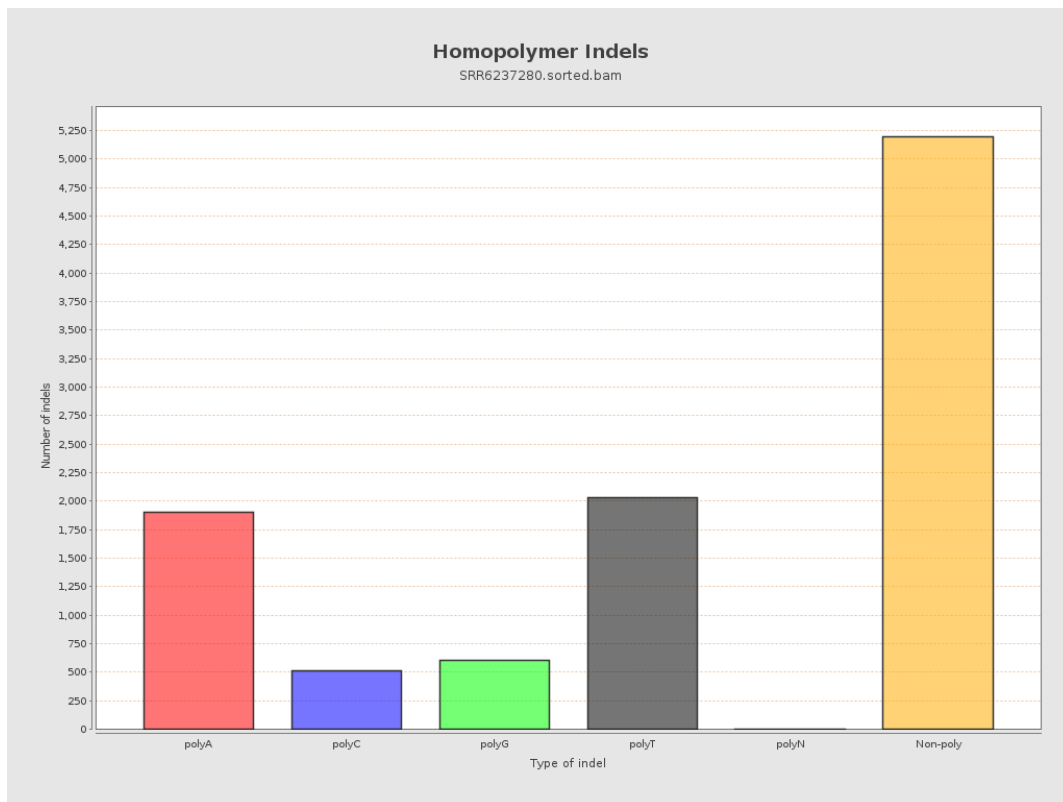
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

