

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 23:37:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237273.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_SRR6237273 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237273.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 23:37:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237273.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,644,677
Mapped reads	1,417,883 / 86.21%
Unmapped reads	226,794 / 13.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,997 / 0.79%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	80,776 / 4.91%
Duplication rate	4.51%
Clipped reads	675,204 / 41.05%

2.2. ACGT Content

Number/percentage of A's	26,790,686 / 28.65%
Number/percentage of C's	16,439,927 / 17.58%
Number/percentage of T's	30,539,206 / 32.66%
Number/percentage of G's	19,731,559 / 21.1%
Number/percentage of N's	1,323 / 0%
GC Percentage	38.68%

2.3. Coverage

Mean	0.0302

Standard Deviation	0.3377
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2.4. Mapping Quality

Mean Mapping Quality	47.07
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2.5. Mismatches and indels

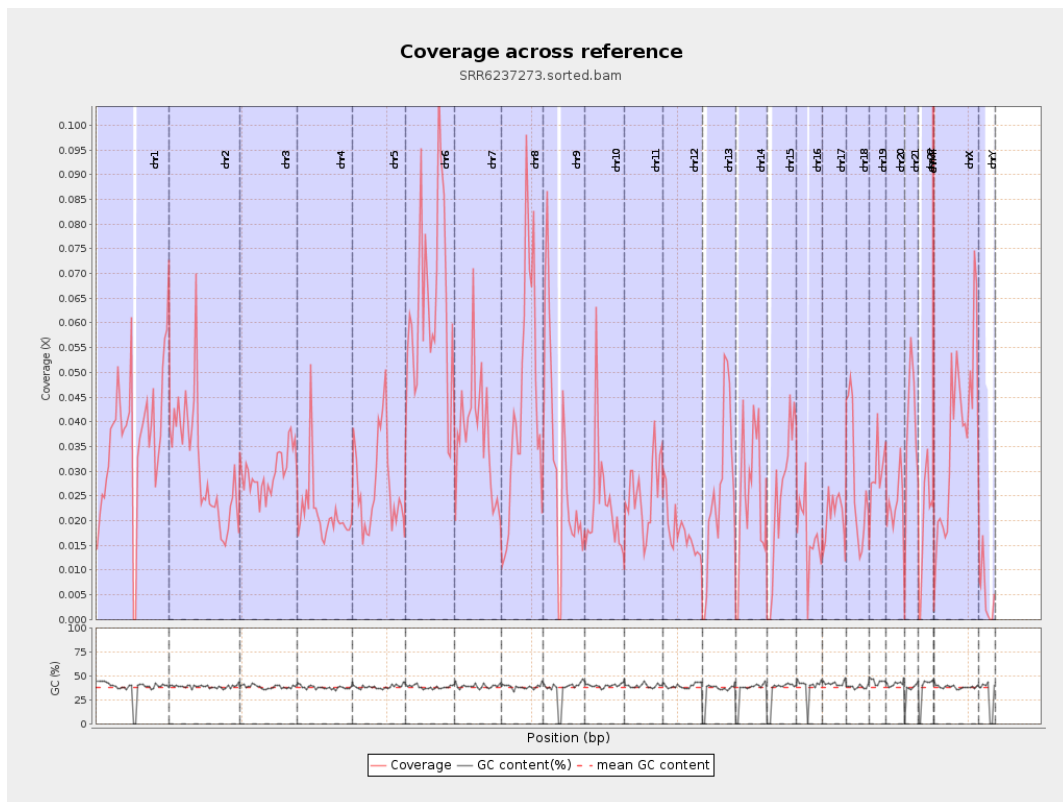
General error rate	0.84%
Mismatches	766,105
Insertions	7,441
Mapped reads with at least one insertion	0.52%
Deletions	30,756
Mapped reads with at least one deletion	2.14%
Homopolymer indels	45.98%

2.6. Chromosome stats

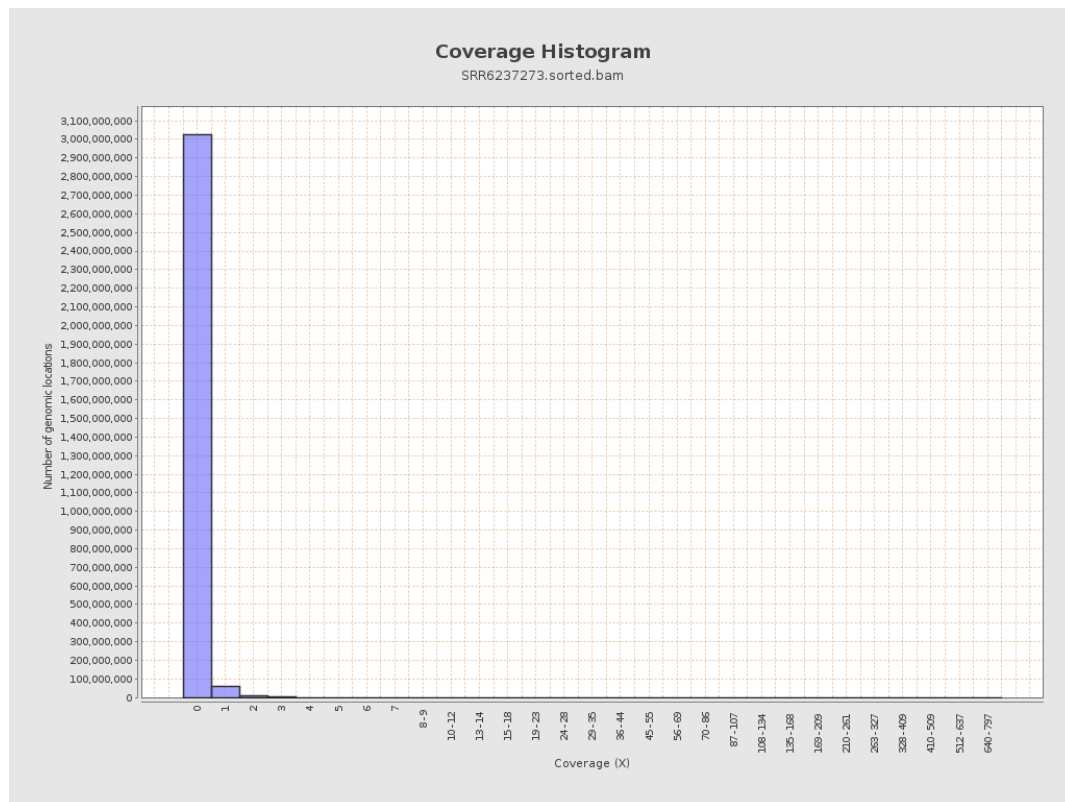
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9071443	0.0364	0.5729
chr2	243199373	7489429	0.0308	0.3476
chr3	198022430	5941798	0.03	0.2139
chr4	191154276	4077497	0.0213	0.2183
chr5	180915260	4882413	0.027	0.2027
chr6	171115067	10794111	0.0631	0.4152
chr7	159138663	5965473	0.0375	0.4308

chr8	146364022	6227691	0.0425	0.5766
chr9	141213431	4434084	0.0314	0.3236
chr10	135534747	3146751	0.0232	0.3251
chr11	135006516	3419179	0.0253	0.2411
chr12	133851895	2383088	0.0178	0.1685
chr13	115169878	2961904	0.0257	0.1967
chr14	107349540	2623026	0.0244	0.2083
chr15	102531392	2534799	0.0247	0.1931
chr16	90354753	1546521	0.0171	0.1908
chr17	81195210	1694574	0.0209	0.211
chr18	78077248	2202842	0.0282	0.5219
chr19	59128983	1781913	0.0301	0.3575
chr20	63025520	1474475	0.0234	0.1916
chr21	48129895	1845159	0.0383	0.2689
chr22	51304566	991378	0.0193	0.1666
chrMT	16571	36458	2.2001	1.9486
chrX	155270560	5748115	0.037	0.2541
chrY	59373566	282343	0.0048	0.1572

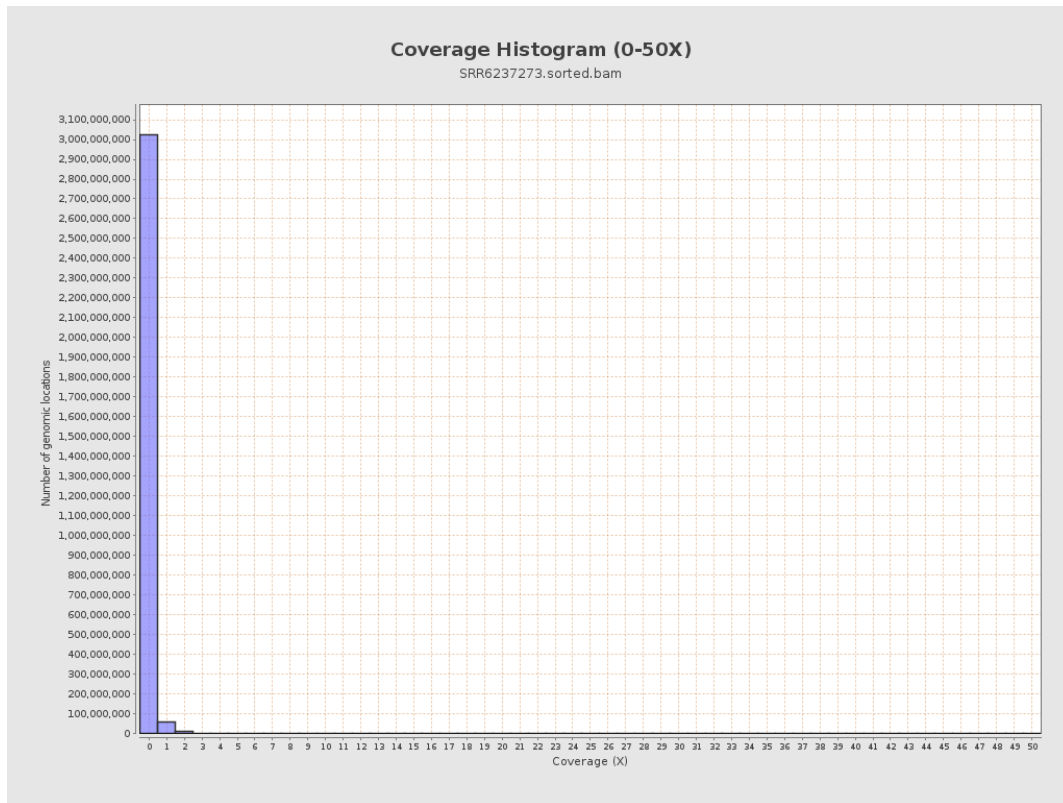
3. Results : Coverage across reference



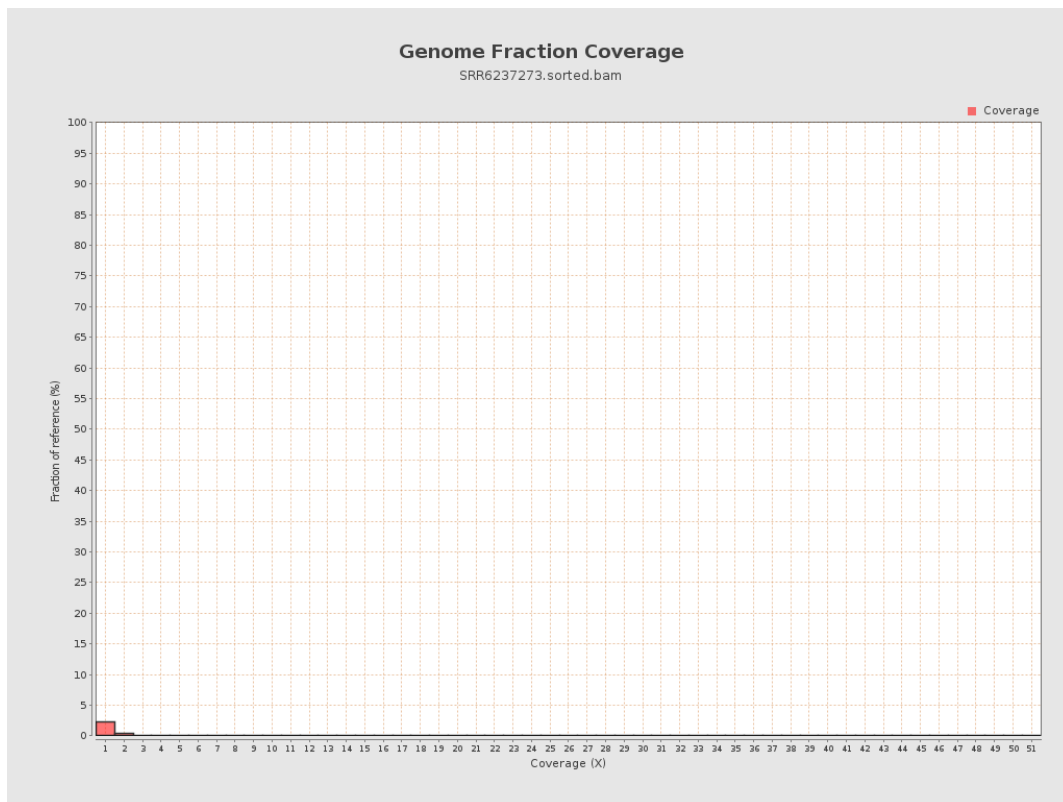
4. Results : Coverage Histogram



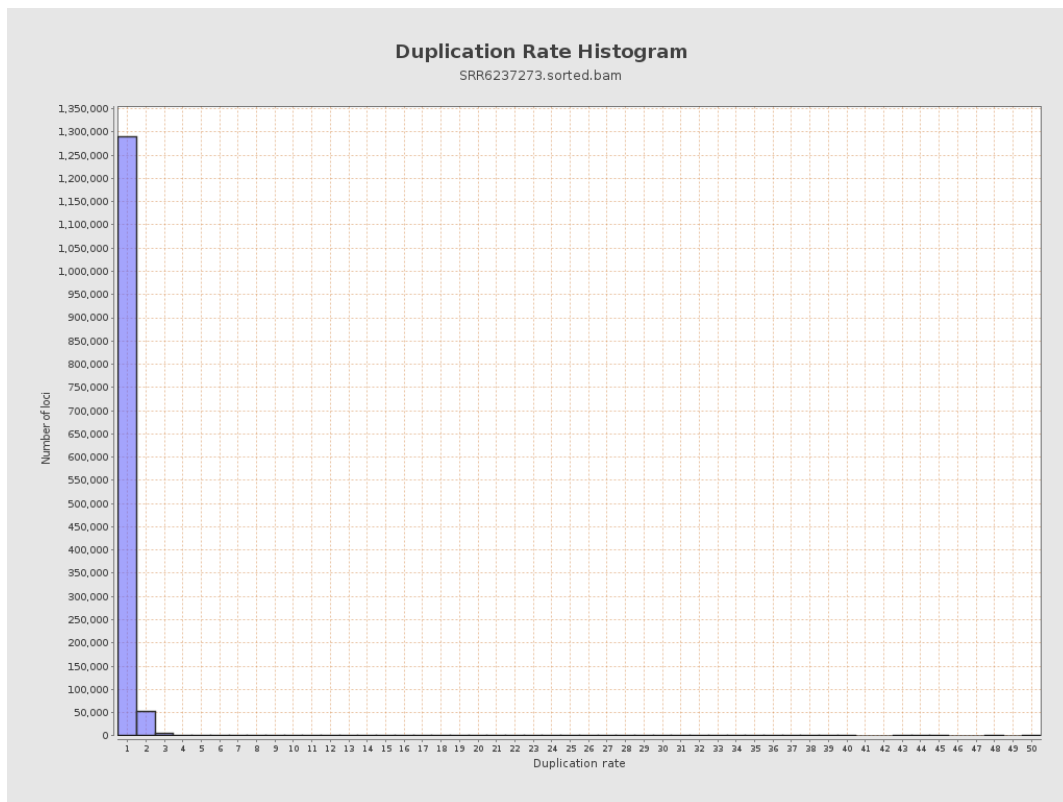
5. Results : Coverage Histogram (0-50X)



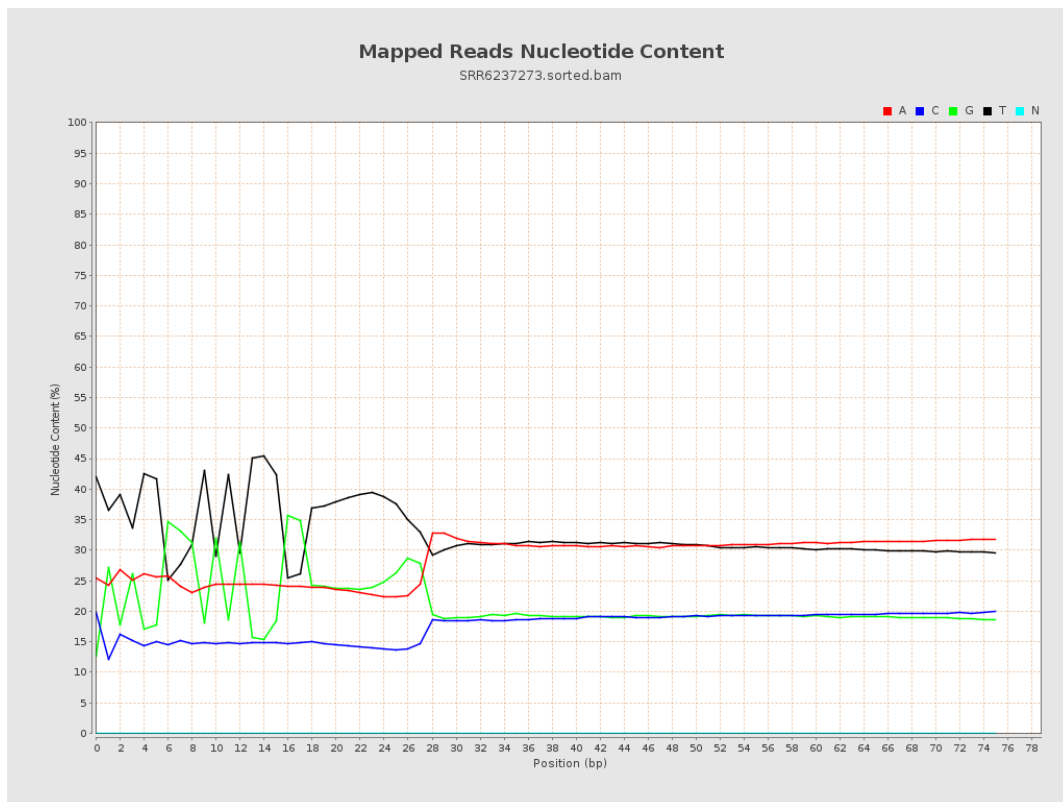
6. Results : Genome Fraction Coverage



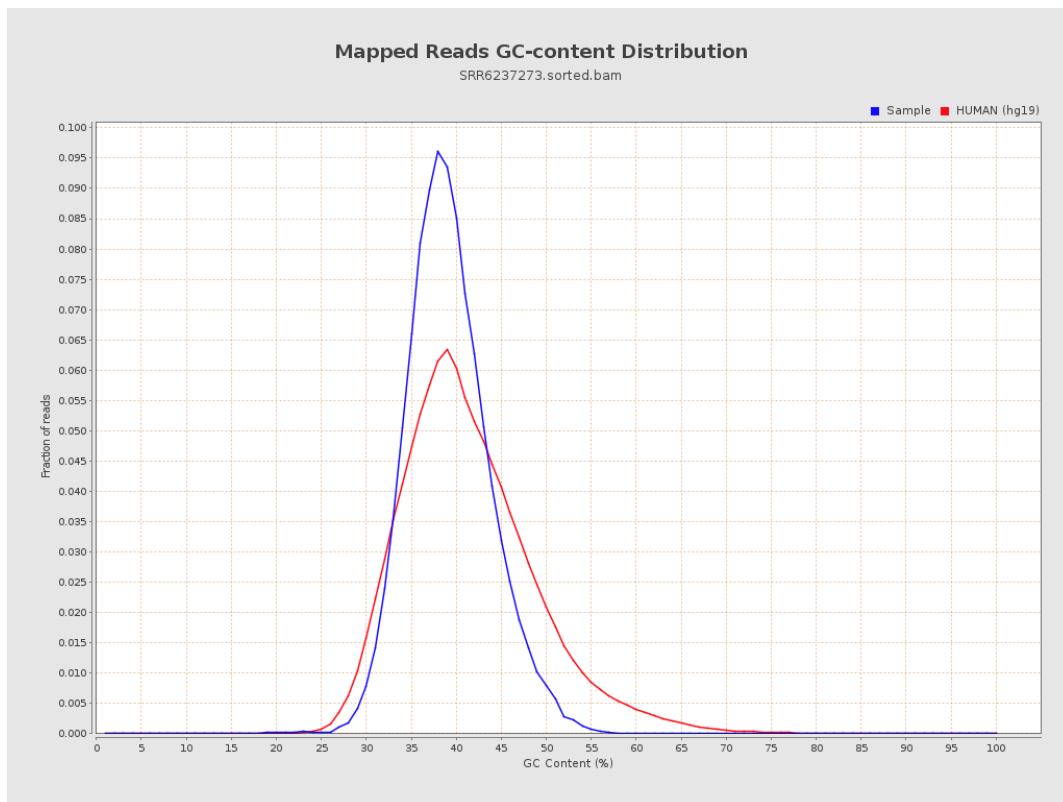
7. Results : Duplication Rate Histogram



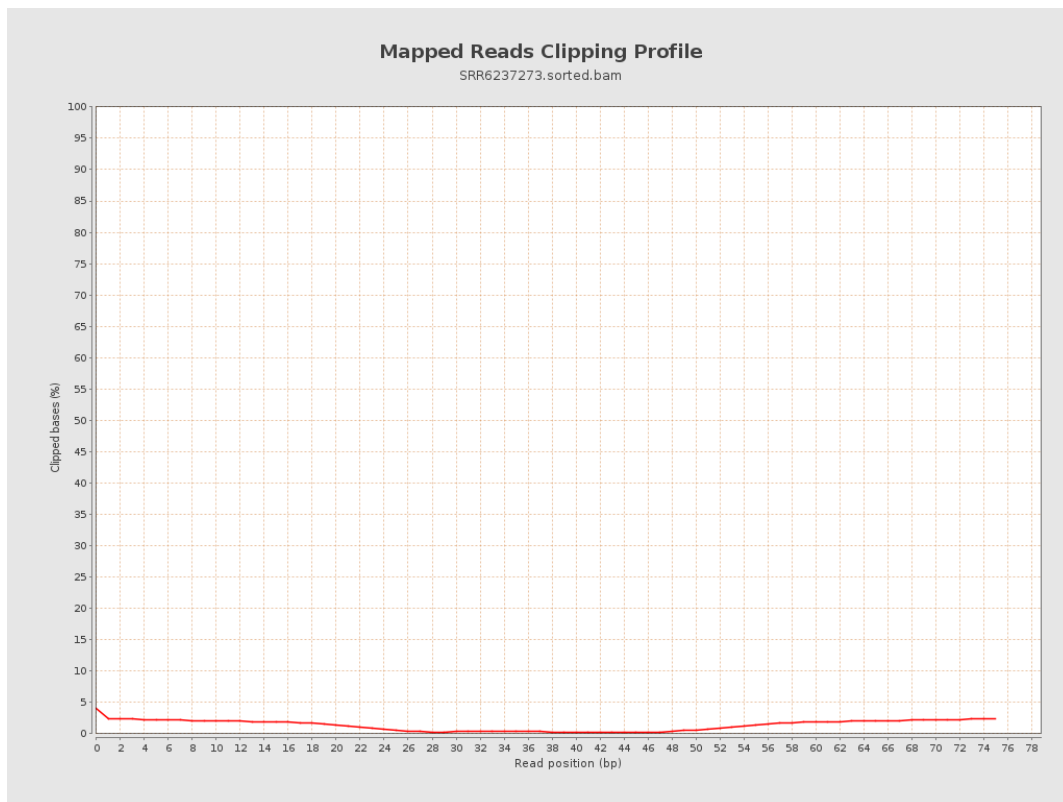
8. Results : Mapped Reads Nucleotide Content



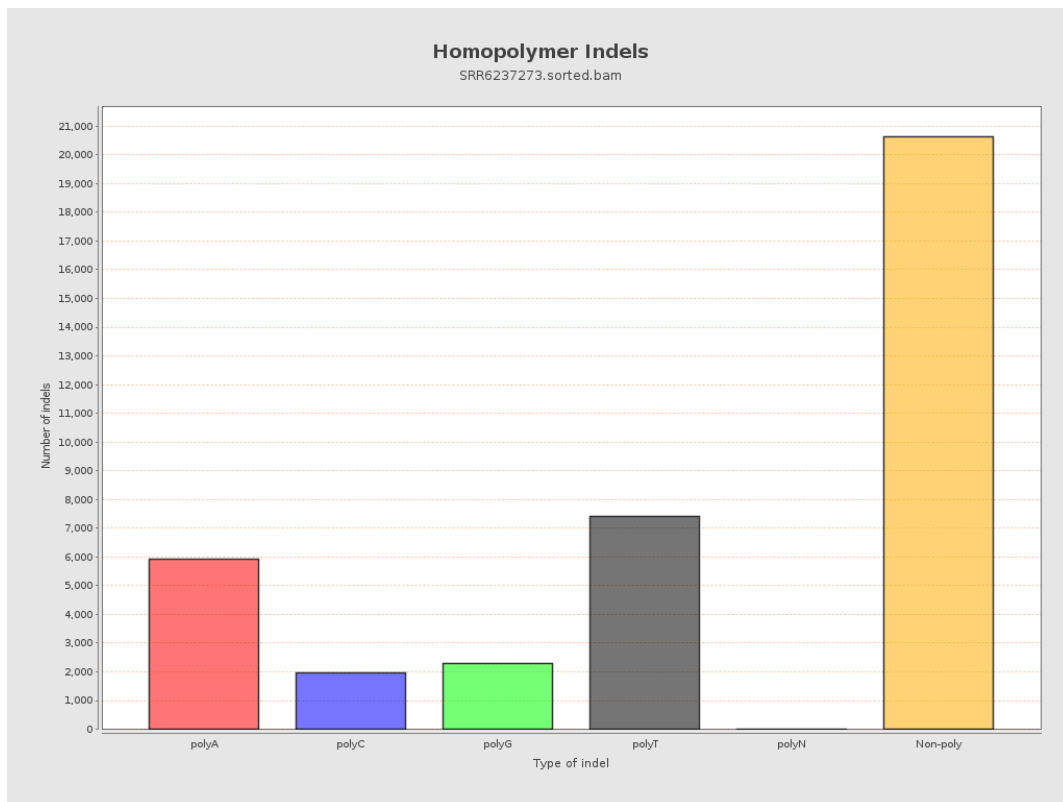
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

