

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 23:49:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237277.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_SRR6237277 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237277.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 23:49:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237277.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,466,311
Mapped reads	2,239,762 / 90.81%
Unmapped reads	226,549 / 9.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,480 / 0.42%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	90,660 / 3.68%
Duplication rate	2.69%
Clipped reads	865,910 / 35.11%

2.2. ACGT Content

Number/percentage of A's	42,767,697 / 28.07%
Number/percentage of C's	28,529,733 / 18.73%
Number/percentage of T's	47,301,734 / 31.05%
Number/percentage of G's	33,744,992 / 22.15%
Number/percentage of N's	2,532 / 0%
GC Percentage	40.88%

2.3. Coverage

Mean	0.0492

Standard Deviation	0.5458
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2.4. Mapping Quality

Mean Mapping Quality	44.94
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2.5. Mismatches and indels

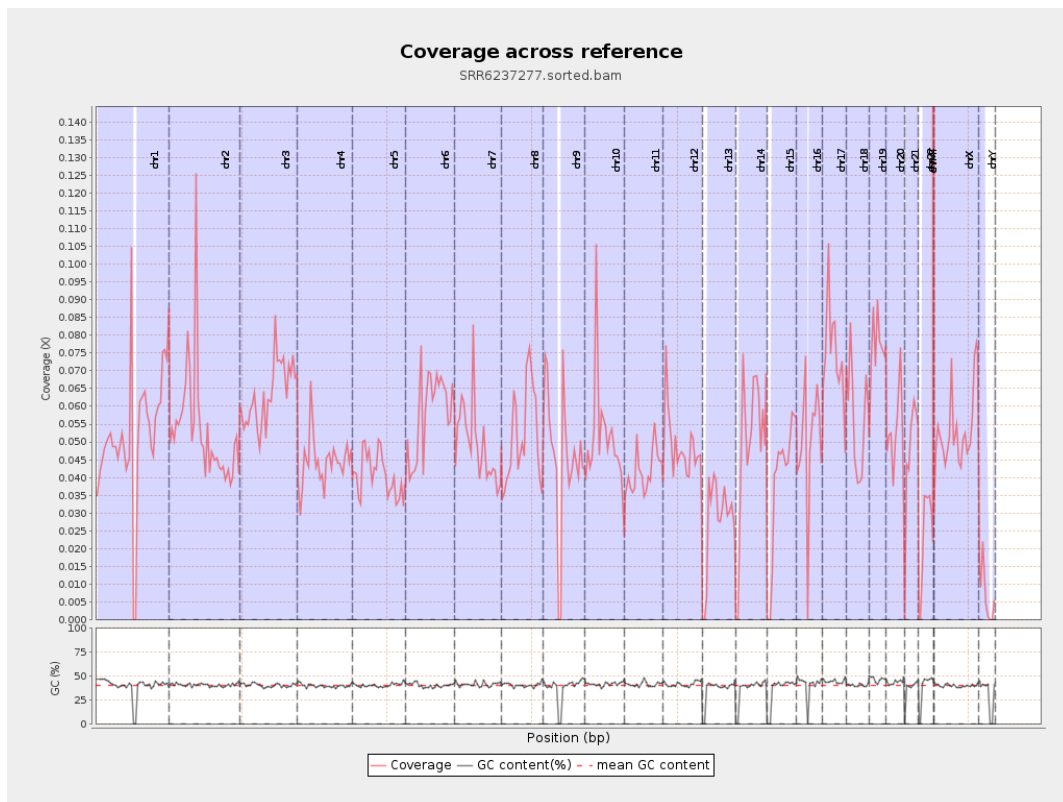
General error rate	0.78%
Mismatches	1,172,201
Insertions	12,182
Mapped reads with at least one insertion	0.54%
Deletions	35,605
Mapped reads with at least one deletion	1.57%
Homopolymer indels	47.81%

2.6. Chromosome stats

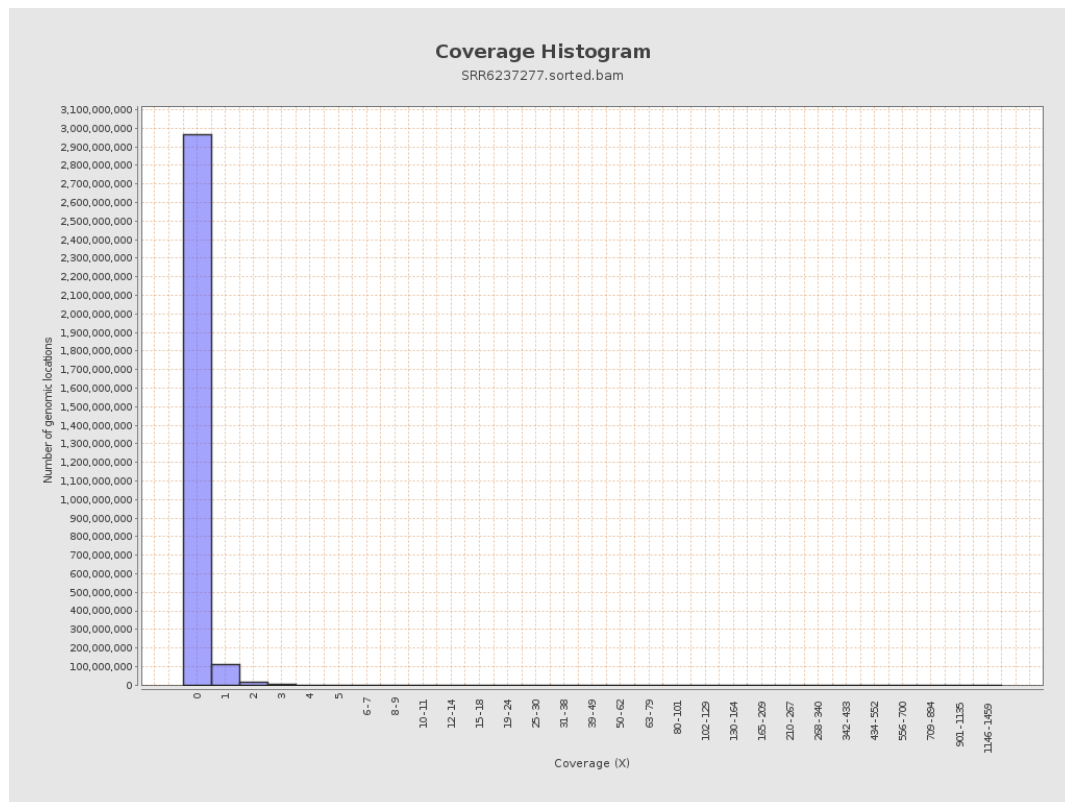
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12950839	0.052	1.2118
chr2	243199373	12921299	0.0531	0.5768
chr3	198022430	12618891	0.0637	0.2933
chr4	191154276	8466716	0.0443	0.2627
chr5	180915260	7358211	0.0407	0.2372
chr6	171115067	9903873	0.0579	0.3701
chr7	159138663	7876314	0.0495	0.5707

chr8	146364022	7486188	0.0511	0.6765
chr9	141213431	6503870	0.0461	0.5261
chr10	135534747	6937745	0.0512	0.5086
chr11	135006516	5578675	0.0413	0.3567
chr12	133851895	6507253	0.0486	0.2639
chr13	115169878	3170872	0.0275	0.1857
chr14	107349540	5206241	0.0485	0.2955
chr15	102531392	3970737	0.0387	0.2307
chr16	90354753	4533644	0.0502	0.3251
chr17	81195210	6003513	0.0739	0.4629
chr18	78077248	4403934	0.0564	1.0572
chr19	59128983	4575051	0.0774	0.7332
chr20	63025520	3300601	0.0524	0.2751
chr21	48129895	2284335	0.0475	0.2883
chr22	51304566	1190870	0.0232	0.1687
chrMT	16571	37694	2.2747	2.0174
chrX	155270560	8232022	0.053	0.3093
chrY	59373566	390136	0.0066	0.1621

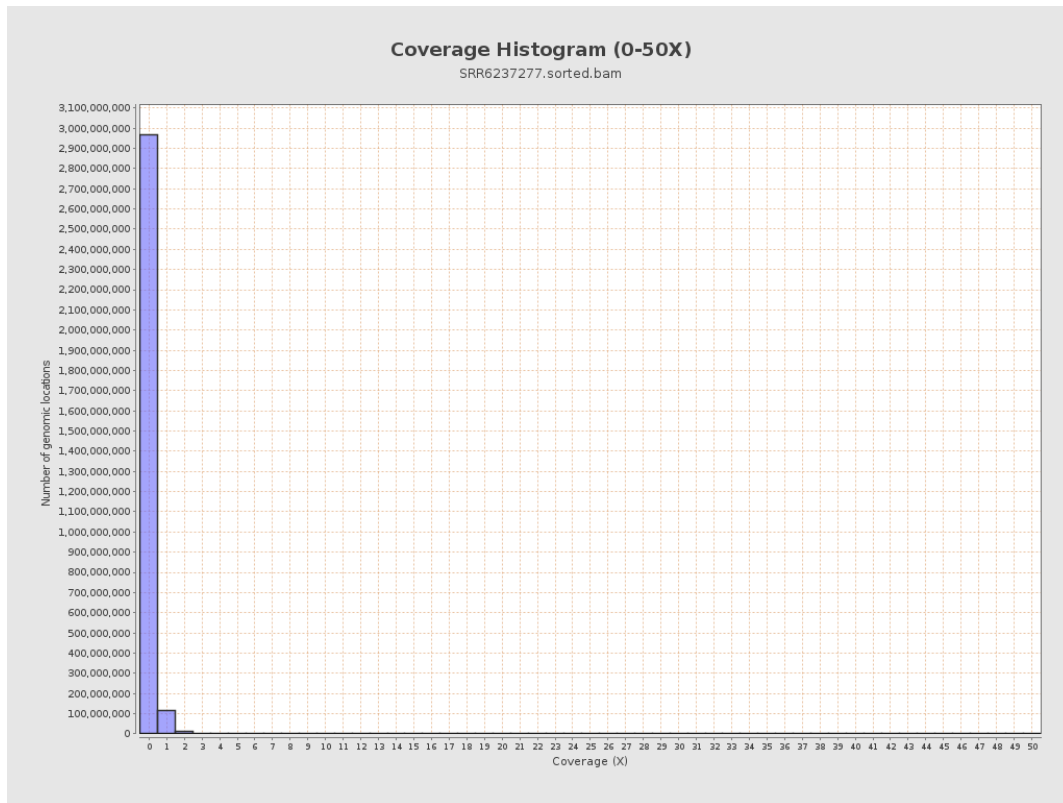
3. Results : Coverage across reference



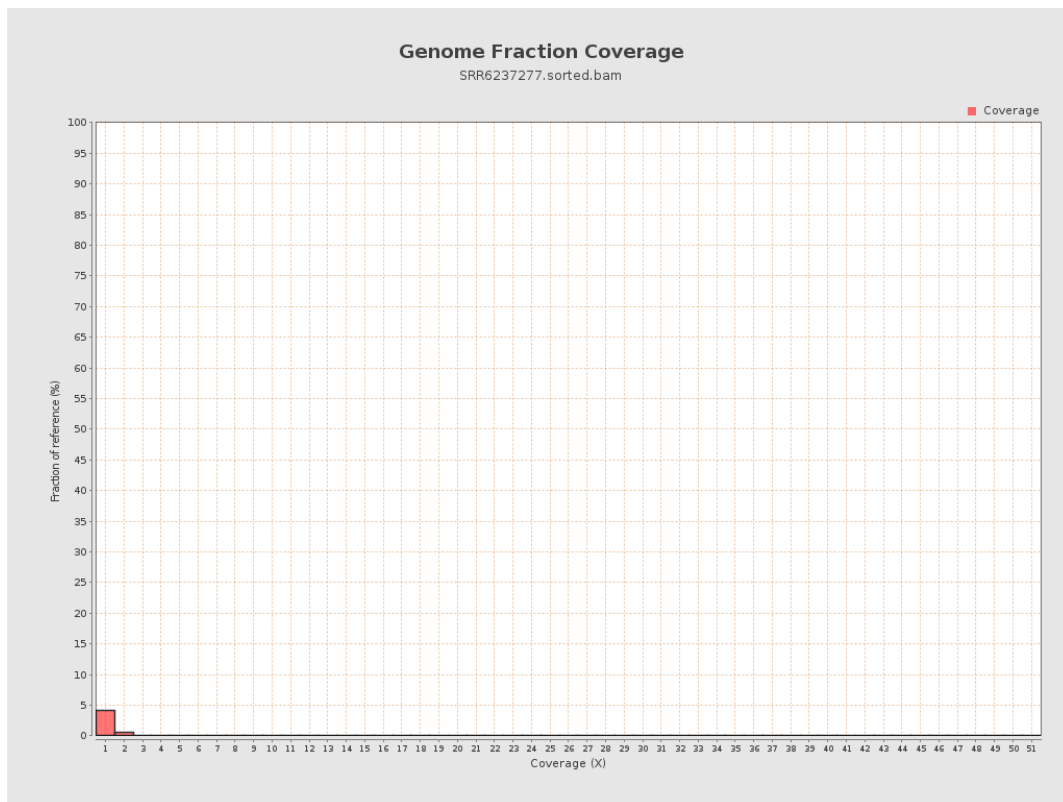
4. Results : Coverage Histogram



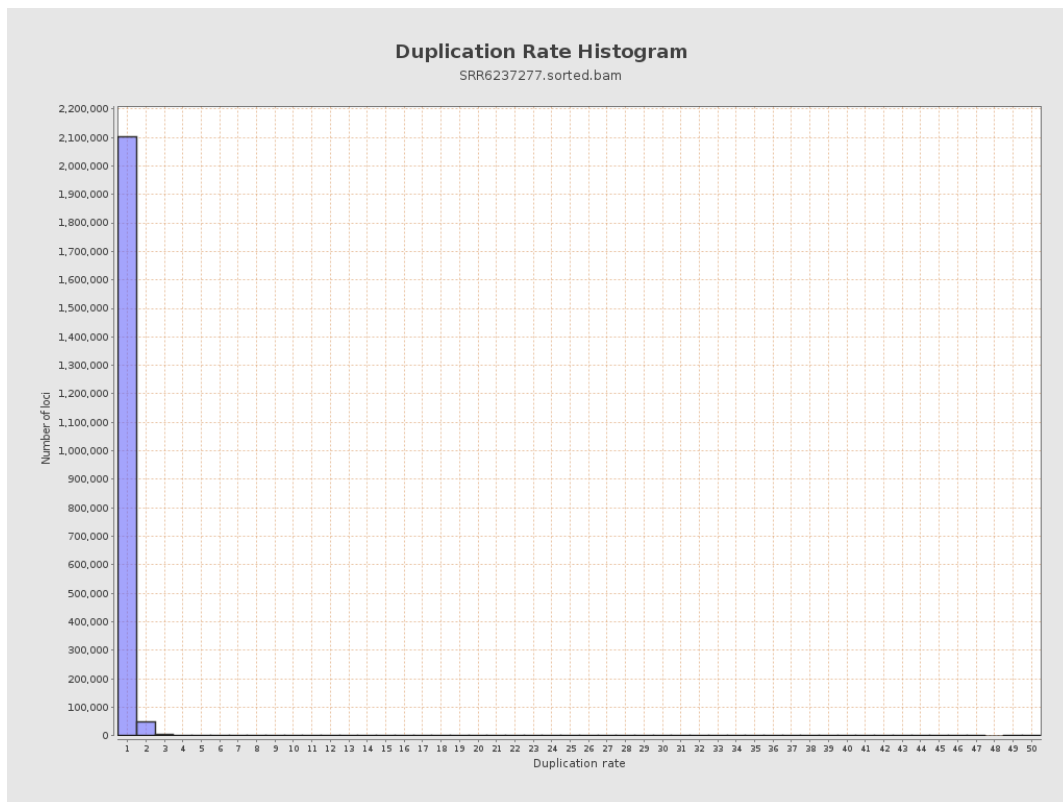
5. Results : Coverage Histogram (0-50X)



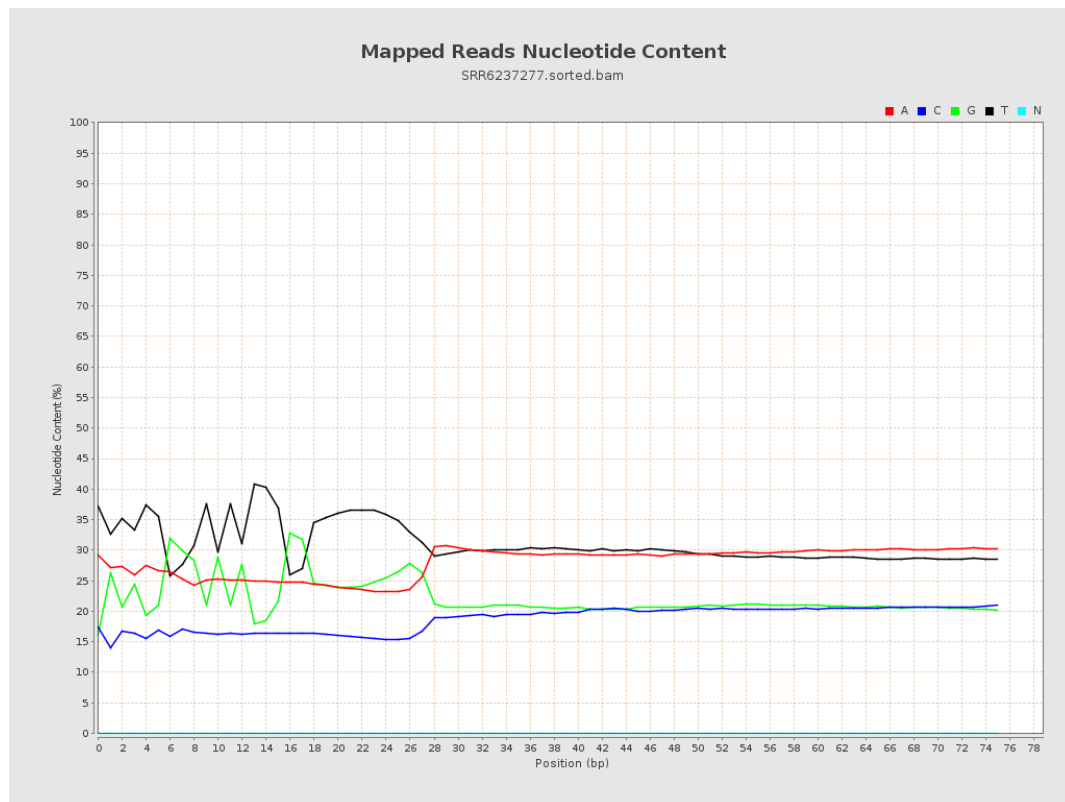
6. Results : Genome Fraction Coverage



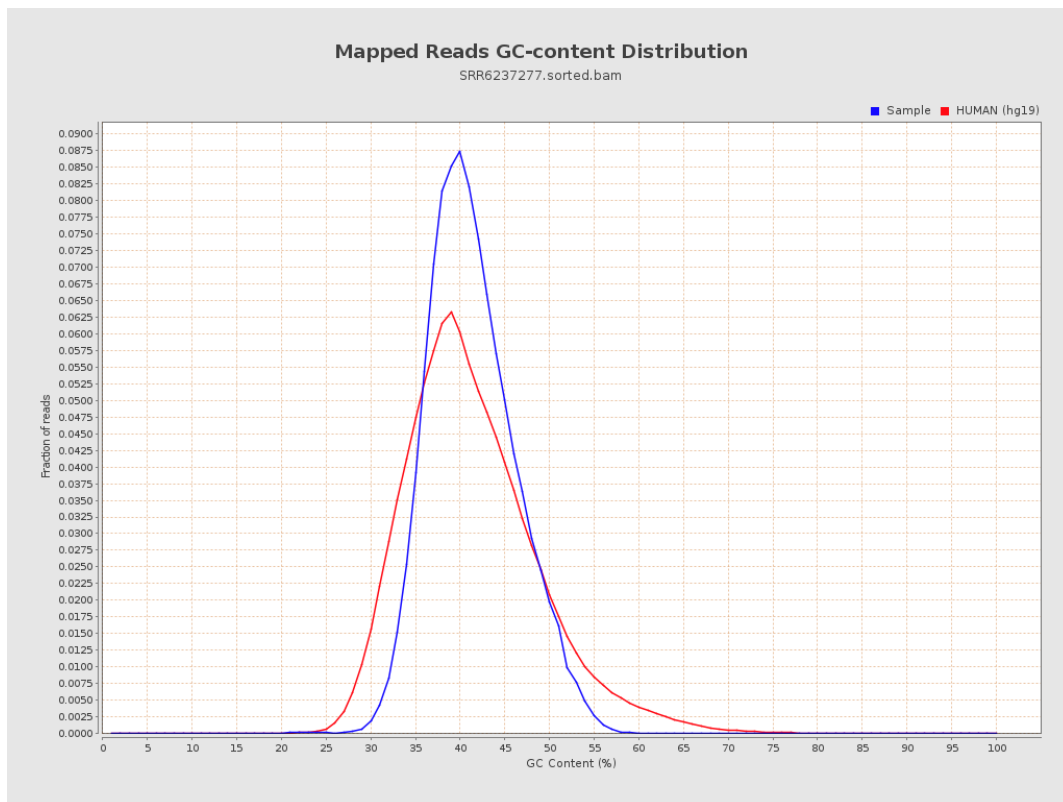
7. Results : Duplication Rate Histogram



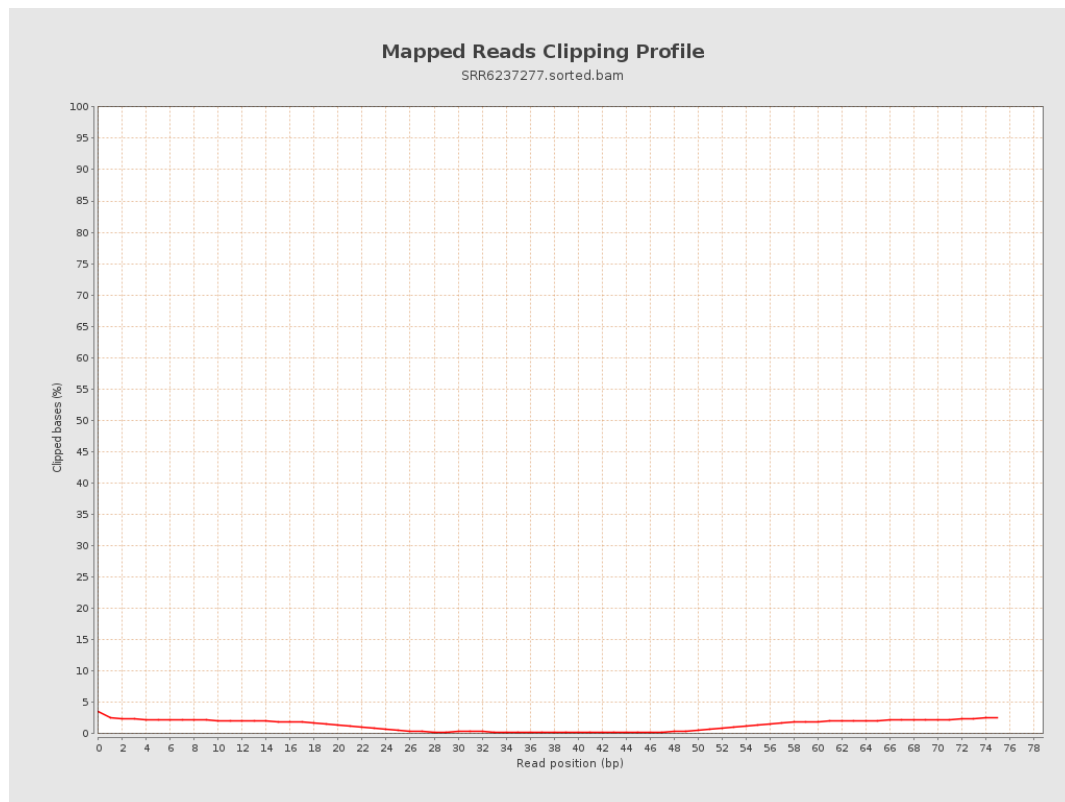
8. Results : Mapped Reads Nucleotide Content



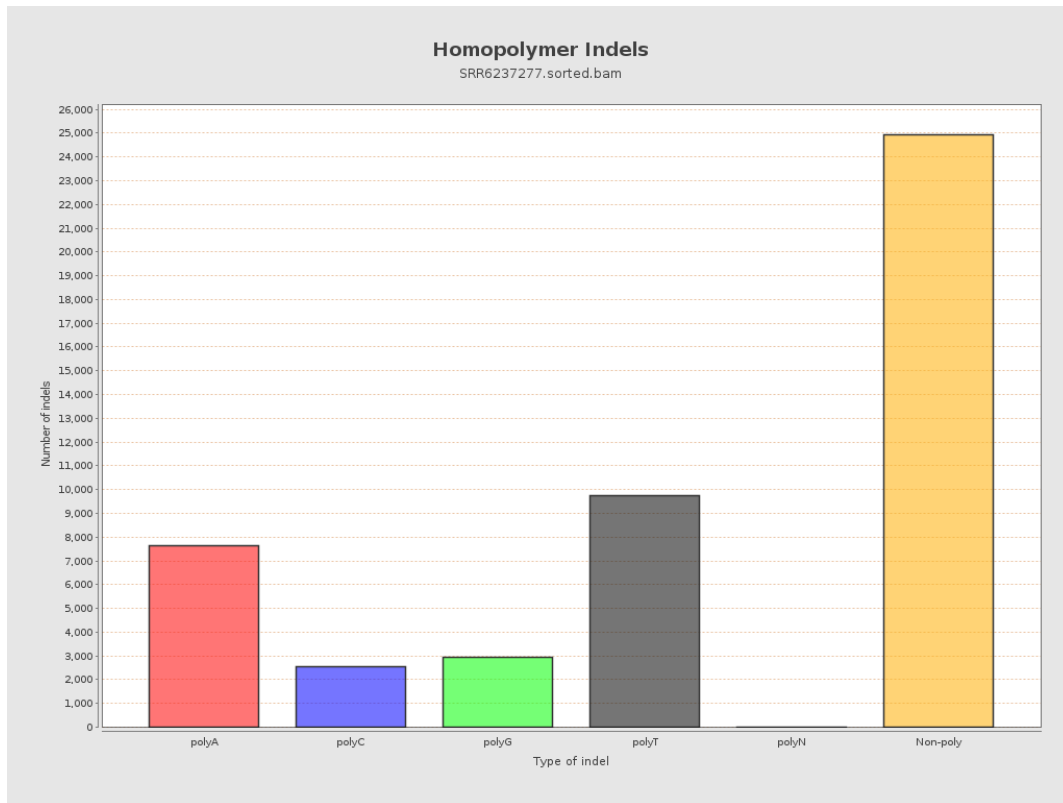
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

