

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 05:23:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237610.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_SRR6237610 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237610.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 05:23:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237610.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,911
Mapped reads	790 / 41.34%
Unmapped reads	1,121 / 58.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2 / 0.1%
Read min/max/mean length	33 / 76 / 76.04
Duplicated reads (estimated)	22 / 1.15%
Duplication rate	1.56%
Clipped reads	430 / 22.5%

2.2. ACGT Content

Number/percentage of A's	13,403 / 26.68%
Number/percentage of C's	8,803 / 17.53%
Number/percentage of T's	16,446 / 32.74%
Number/percentage of G's	11,484 / 22.86%
Number/percentage of N's	93 / 0.19%
GC Percentage	40.39%

2.3. Coverage

Mean	0

Standard Deviation	0.0042
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2.4. Mapping Quality

Mean Mapping Quality	36.82
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2.5. Mismatches and indels

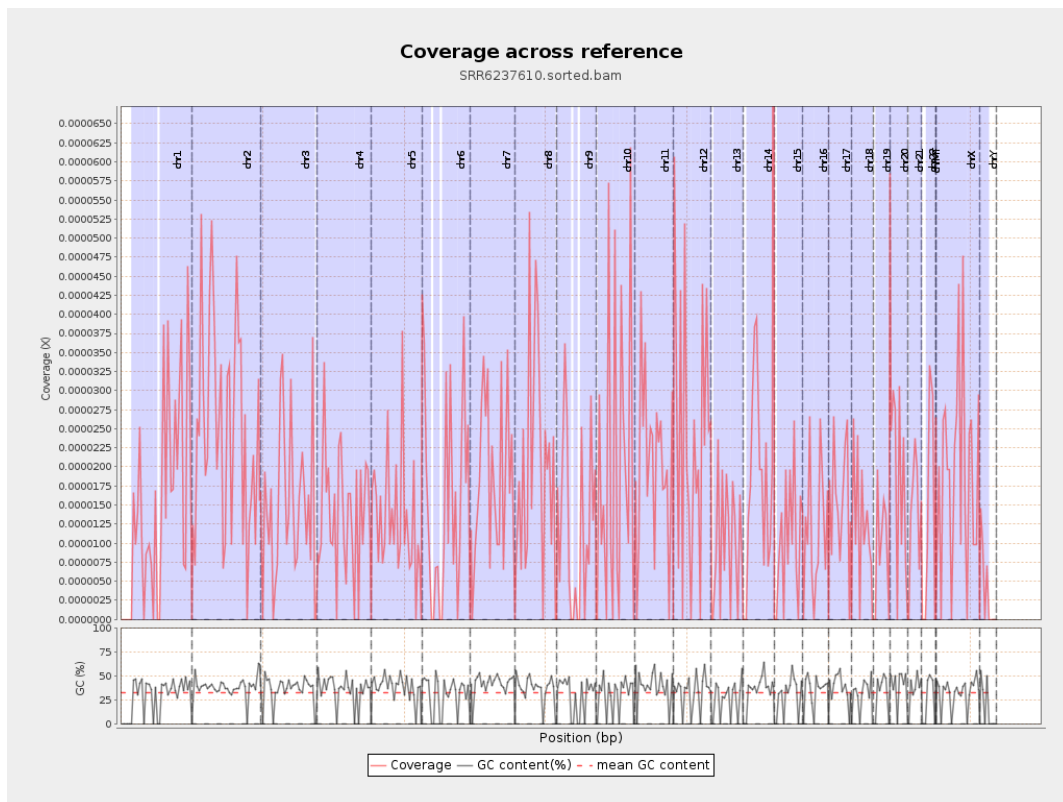
General error rate	0.93%
Mismatches	445
Insertions	10
Mapped reads with at least one insertion	1.27%
Deletions	11
Mapped reads with at least one deletion	1.39%
Homopolymer indels	33.33%

2.6. Chromosome stats

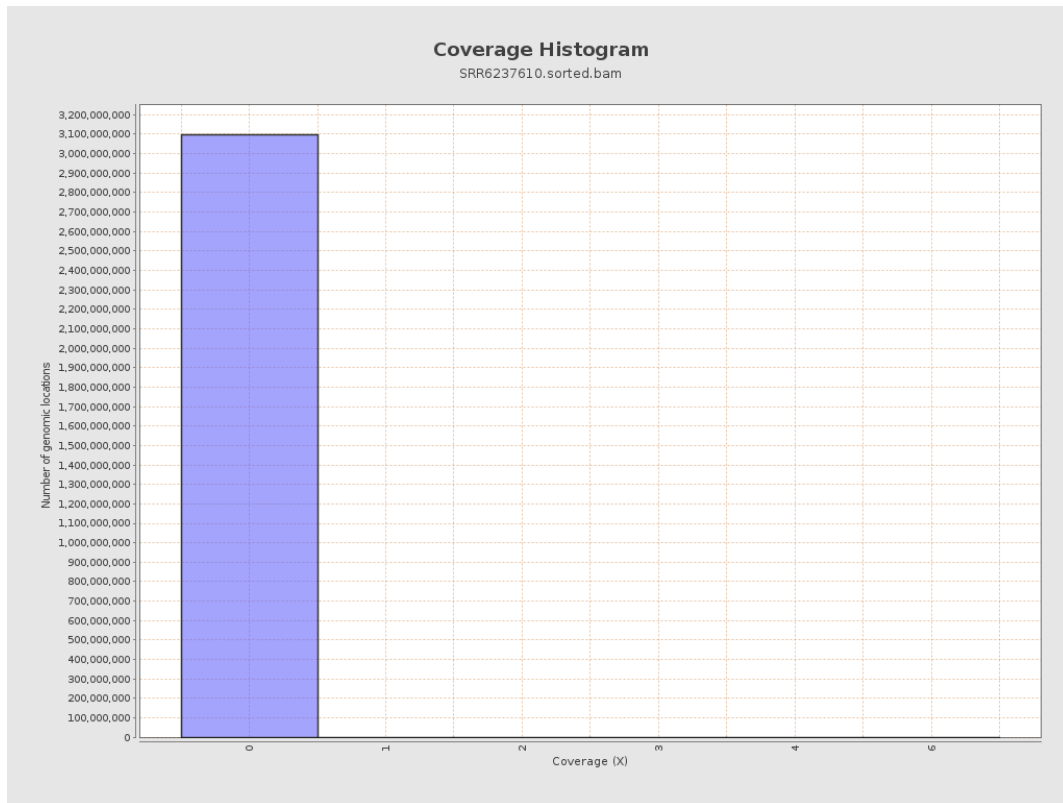
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3630	0	0.0039
chr2	243199373	6018	0	0.0056
chr3	198022430	2933	0	0.0039
chr4	191154276	2589	0	0.0038
chr5	180915260	2372	0	0.0036
chr6	171115067	2616	0	0.0039
chr7	159138663	2954	0	0.0043

chr8	146364022	2948	0	0.0045
chr9	141213431	1714	0	0.0039
chr10	135534747	2717	0	0.0057
chr11	135006516	2734	0	0.0046
chr12	133851895	3338	0	0.0054
chr13	115169878	1125	0	0.0031
chr14	107349540	2022	0	0.0045
chr15	102531392	1020	0	0.0032
chr16	90354753	1040	0	0.0035
chr17	81195210	1249	0	0.0039
chr18	78077248	938	0	0.0035
chr19	59128983	646	0	0.0033
chr20	63025520	1139	0	0.0043
chr21	48129895	710	0	0.0038
chr22	51304566	616	0	0.0039
chrMT	16571	0	0	0
chrX	155270560	2973	0	0.0044
chrY	59373566	207	0	0.0019

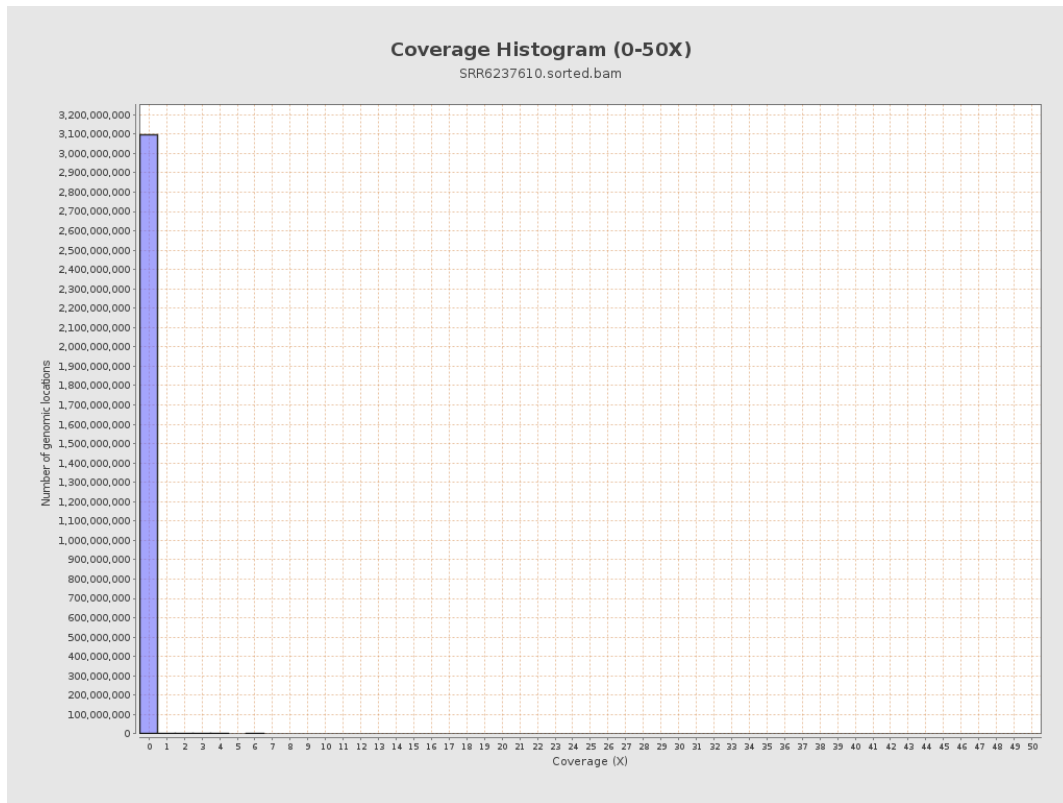
3. Results : Coverage across reference



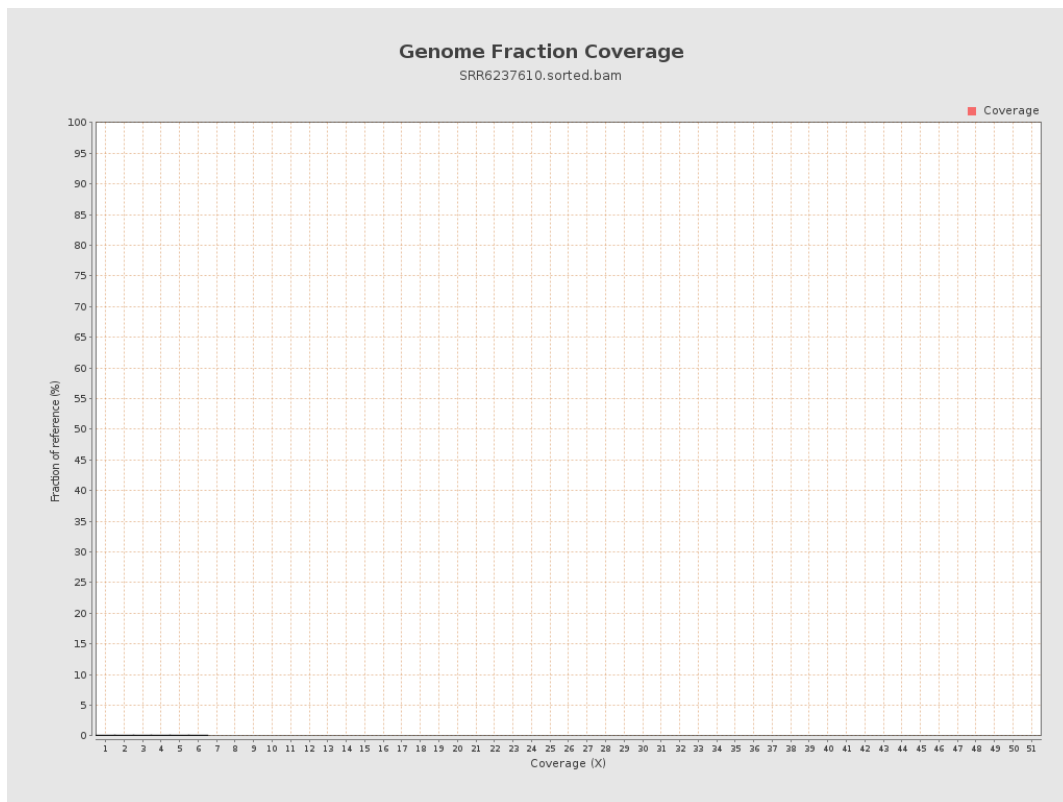
4. Results : Coverage Histogram



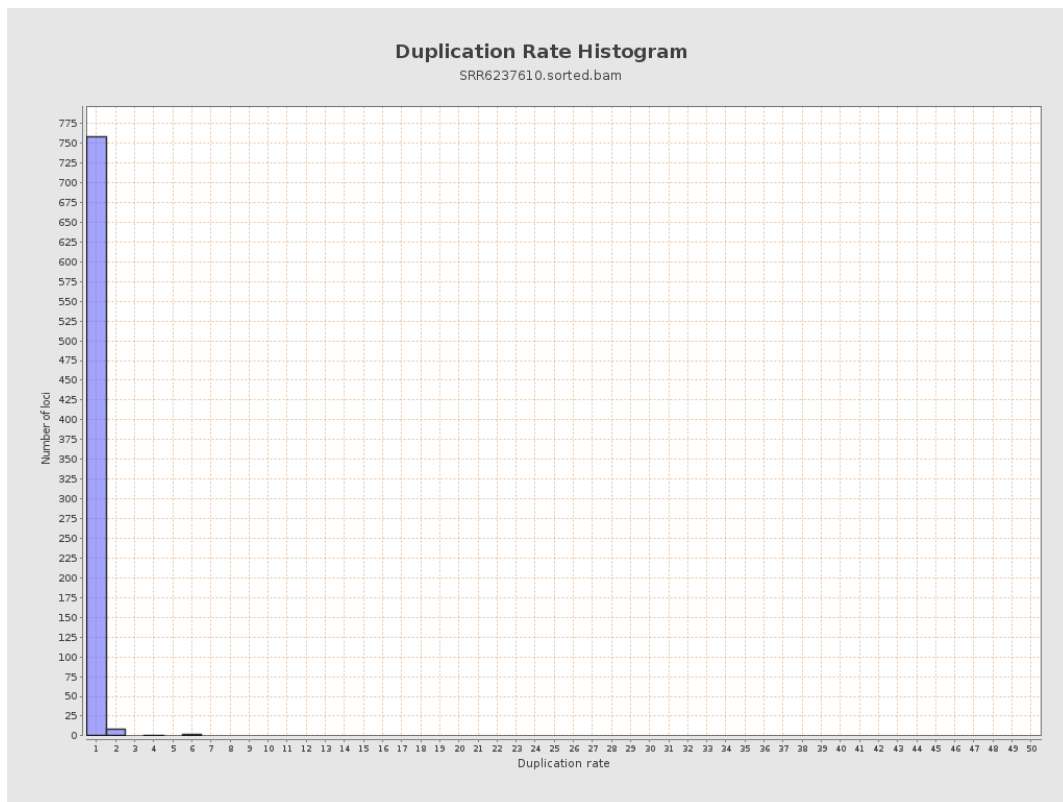
5. Results : Coverage Histogram (0-50X)



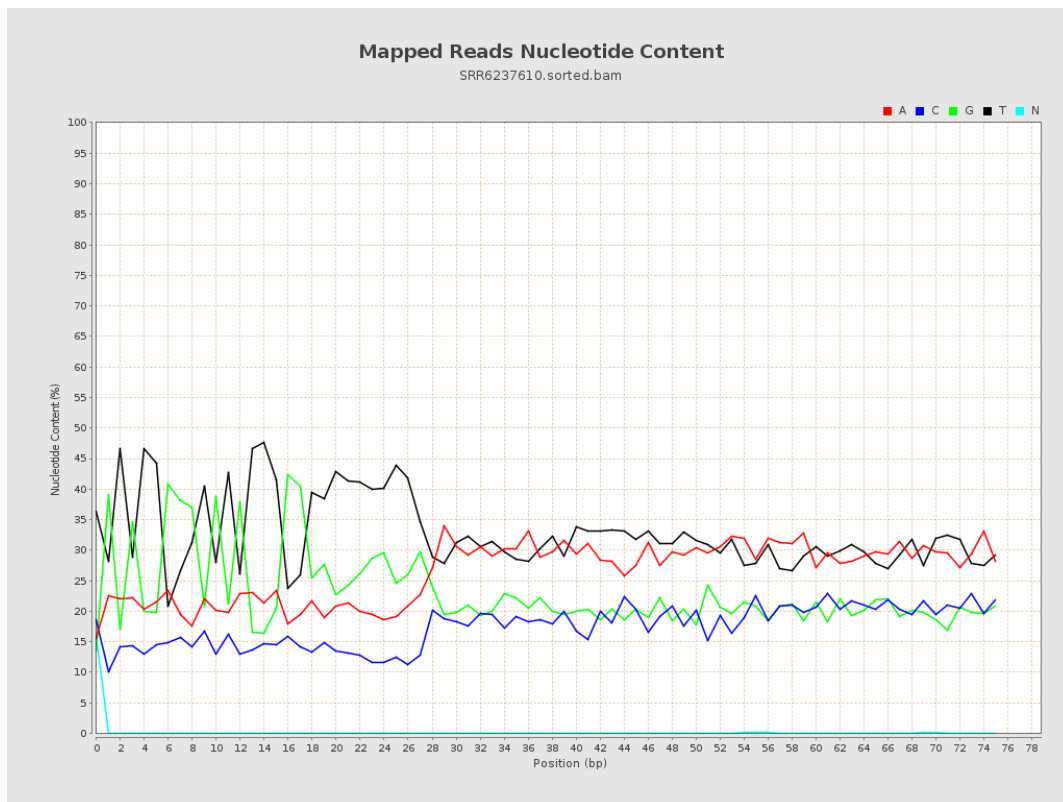
6. Results : Genome Fraction Coverage



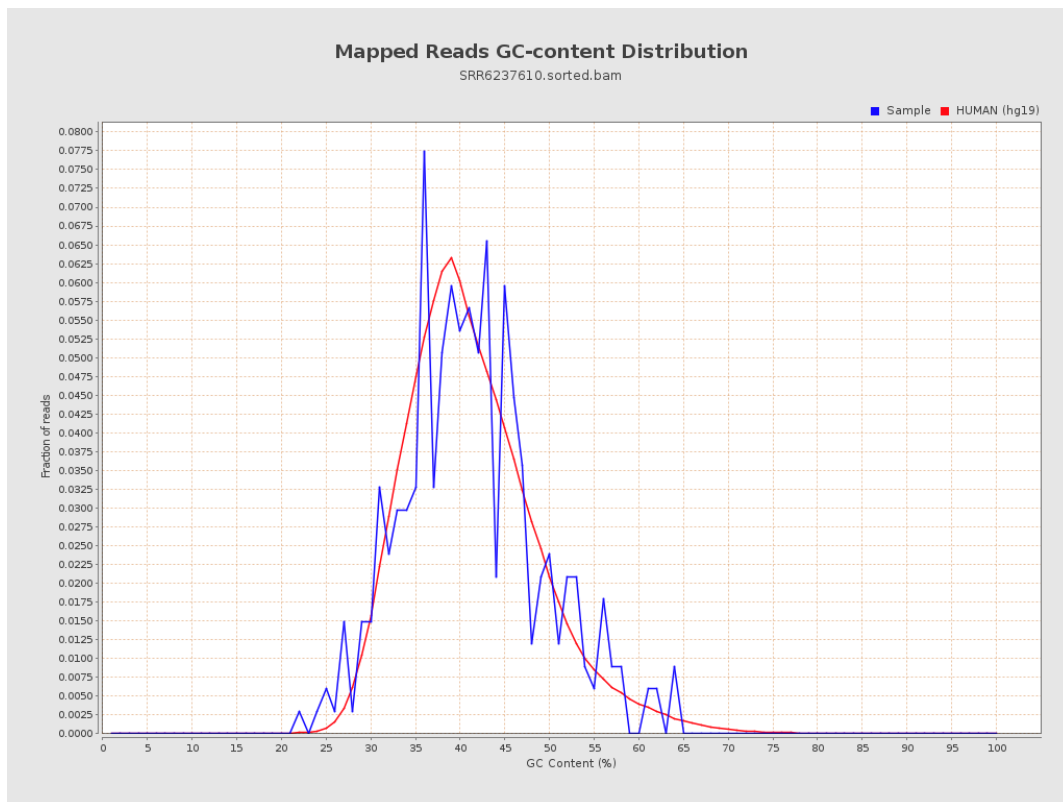
7. Results : Duplication Rate Histogram



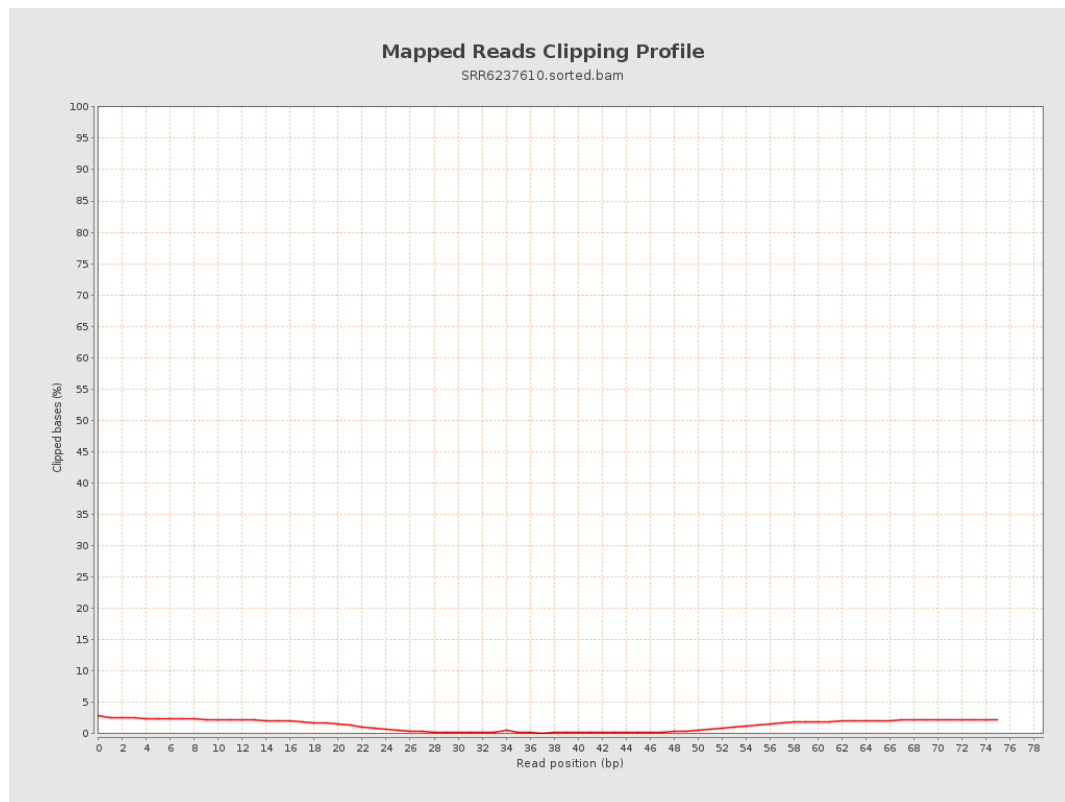
8. Results : Mapped Reads Nucleotide Content



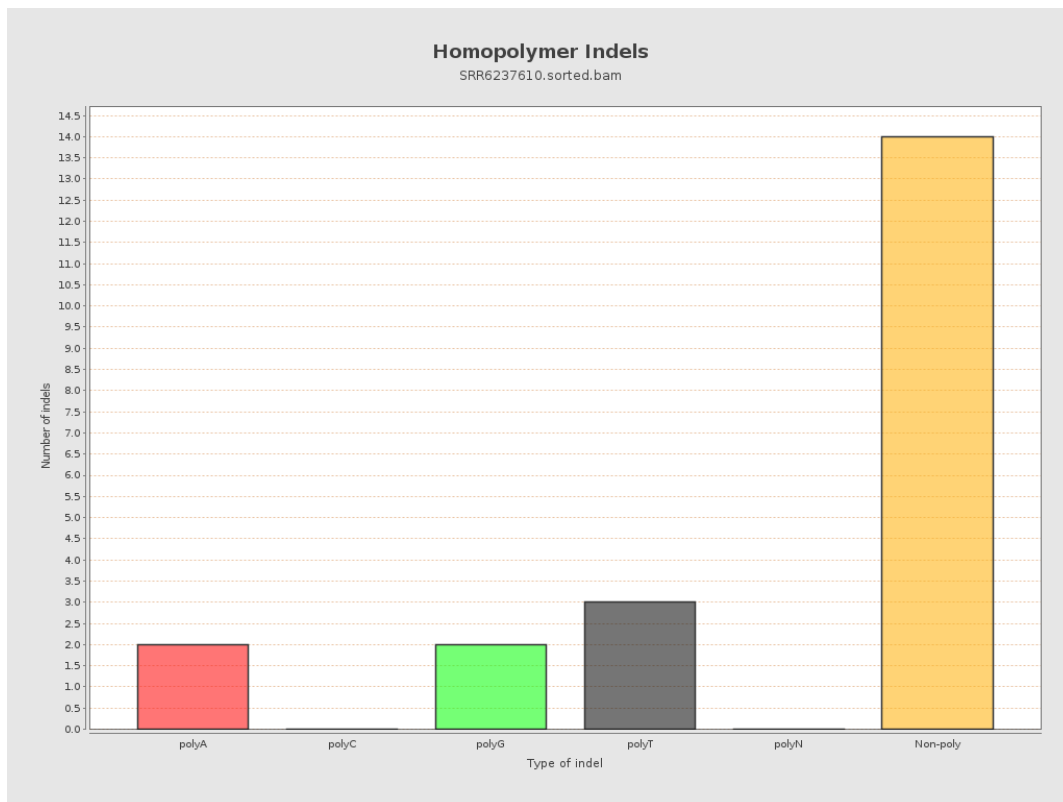
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

