

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 01:44:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237310.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_SRR6237310 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237310.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 01:44:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237310.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,509,122
Mapped reads	3,171,054 / 90.37%
Unmapped reads	338,068 / 9.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,142 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	179,788 / 5.12%
Duplication rate	4.13%
Clipped reads	1,234,154 / 35.17%

2.2. ACGT Content

Number/percentage of A's	61,062,816 / 28.31%
Number/percentage of C's	40,121,411 / 18.6%
Number/percentage of T's	67,714,509 / 31.4%
Number/percentage of G's	46,762,989 / 21.68%
Number/percentage of N's	3,766 / 0%
GC Percentage	40.29%

2.3. Coverage

Mean	0.0697

Standard Deviation	0.6394
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2.4. Mapping Quality

Mean Mapping Quality	46.26
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2.5. Mismatches and indels

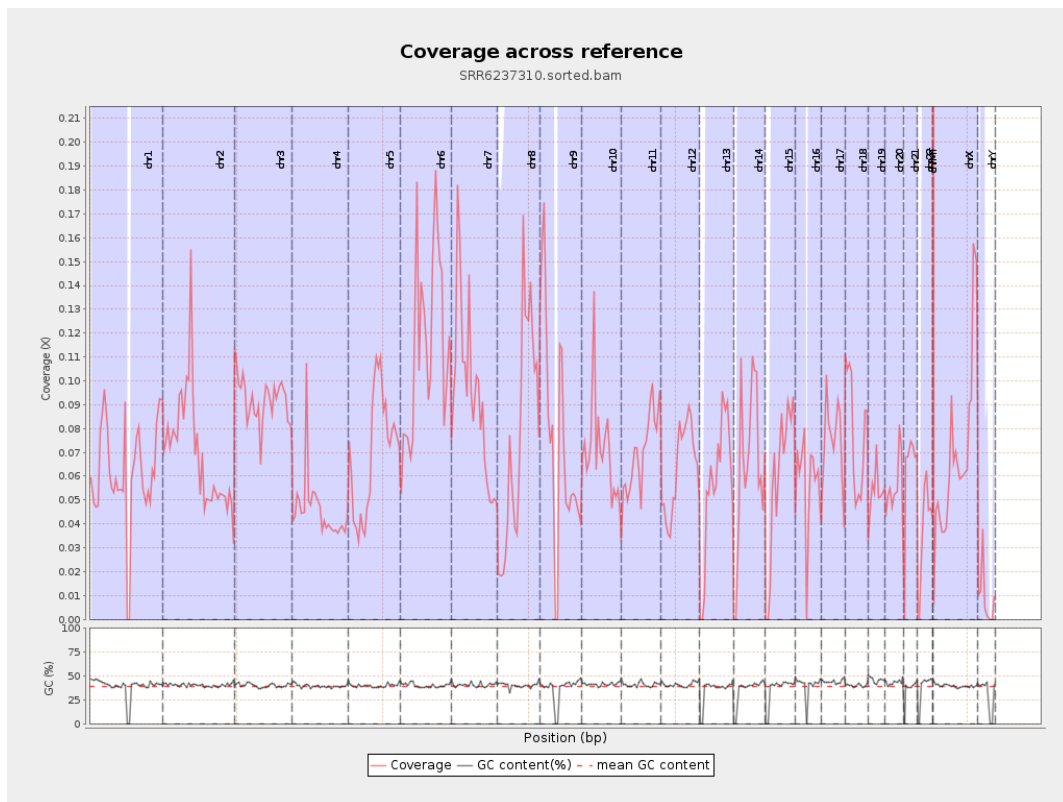
General error rate	0.78%
Mismatches	1,652,069
Insertions	17,280
Mapped reads with at least one insertion	0.54%
Deletions	51,567
Mapped reads with at least one deletion	1.61%
Homopolymer indels	48.1%

2.6. Chromosome stats

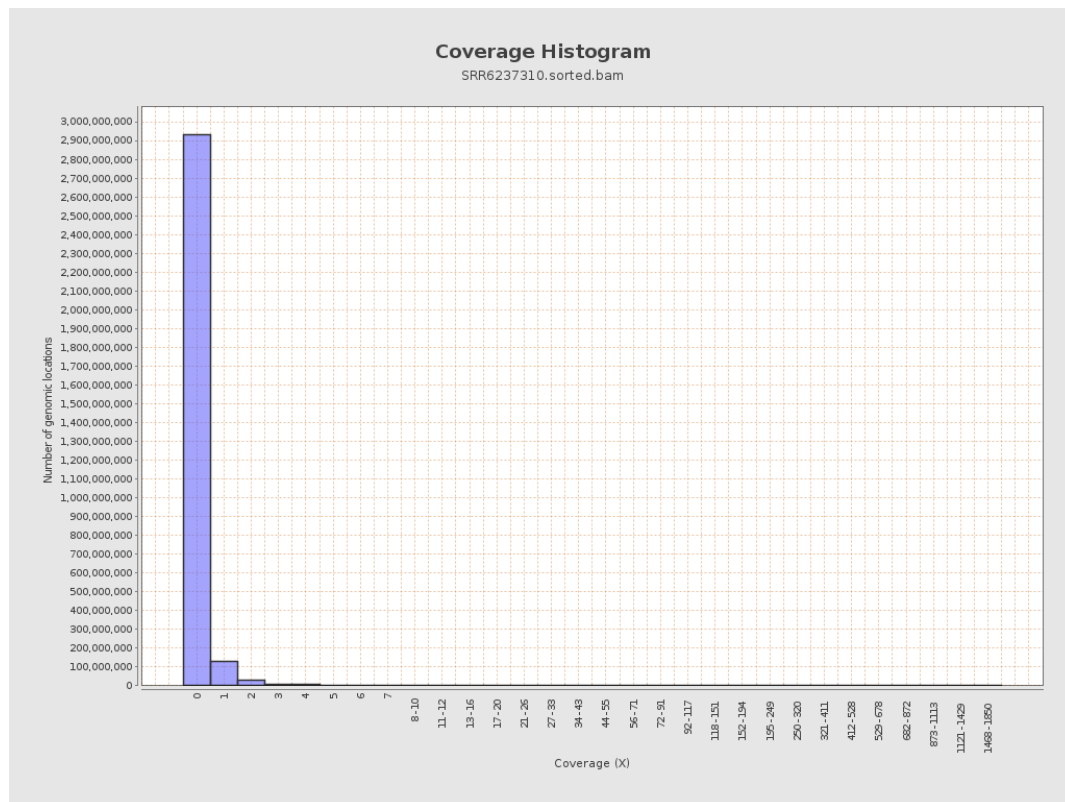
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15414336	0.0618	0.9017
chr2	243199373	16975275	0.0698	0.7345
chr3	198022430	18209324	0.092	0.376
chr4	191154276	8778397	0.0459	0.42
chr5	180915260	12695200	0.0702	0.3382
chr6	171115067	19713990	0.1152	0.642
chr7	159138663	14822576	0.0931	0.9032

chr8	146364022	11249746	0.0769	1.2248
chr9	141213431	10527994	0.0746	0.6445
chr10	135534747	9466358	0.0698	0.6899
chr11	135006516	9463136	0.0701	0.5647
chr12	133851895	8498873	0.0635	0.3355
chr13	115169878	6556319	0.0569	0.2948
chr14	107349540	6993633	0.0651	0.3558
chr15	102531392	6065611	0.0592	0.3141
chr16	90354753	5087900	0.0563	0.3645
chr17	81195210	6148453	0.0757	0.4859
chr18	78077248	6074793	0.0778	1.1855
chr19	59128983	3205986	0.0542	0.633
chr20	63025520	3573769	0.0567	0.3295
chr21	48129895	3061561	0.0636	0.4194
chr22	51304566	1910719	0.0372	0.2332
chrMT	16571	83345	5.0296	4.256
chrX	155270560	10615076	0.0684	0.3806
chrY	59373566	563205	0.0095	0.3517

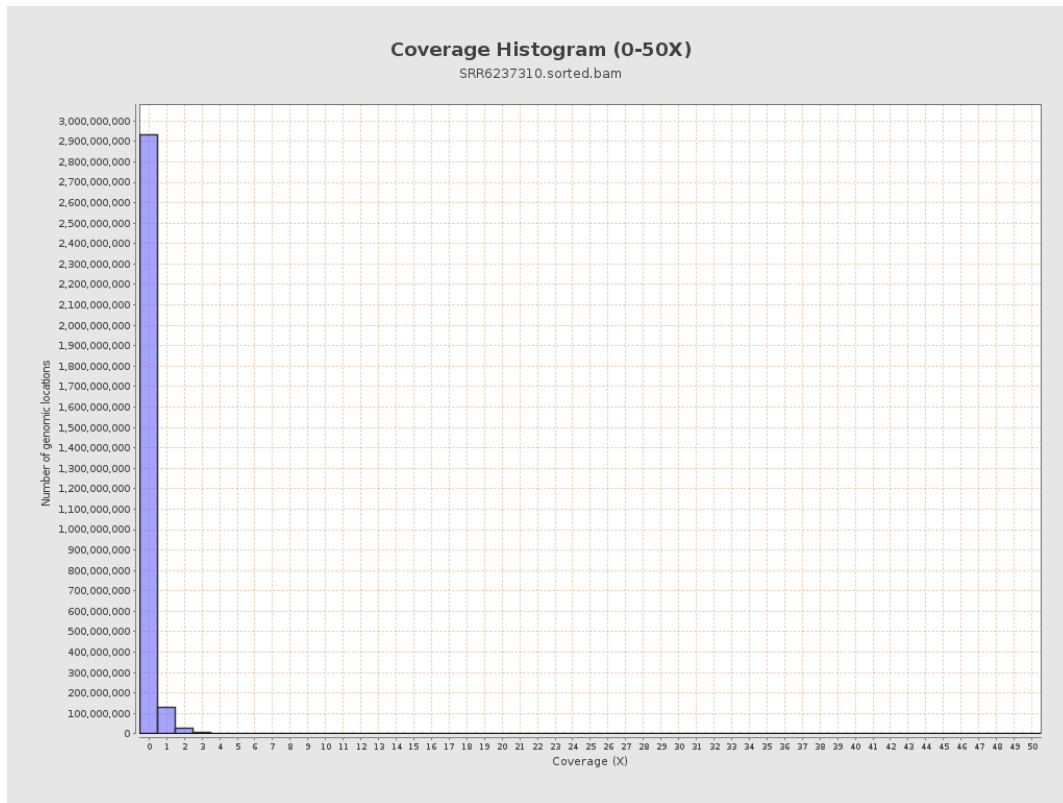
3. Results : Coverage across reference



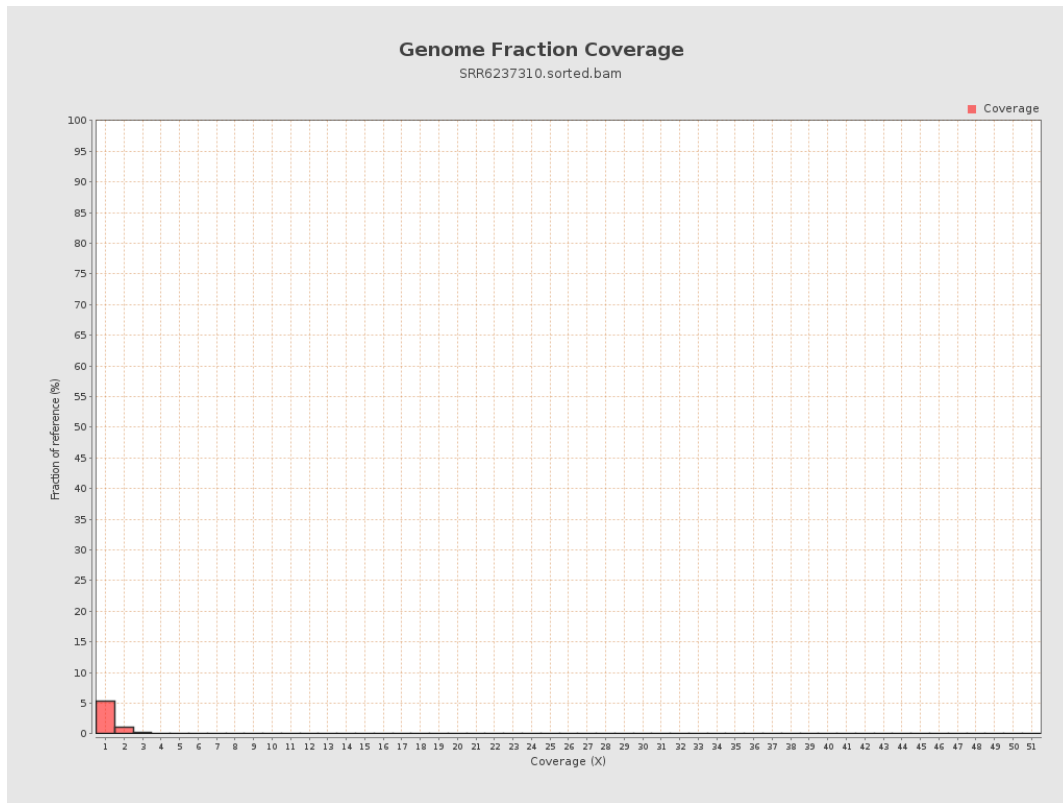
4. Results : Coverage Histogram



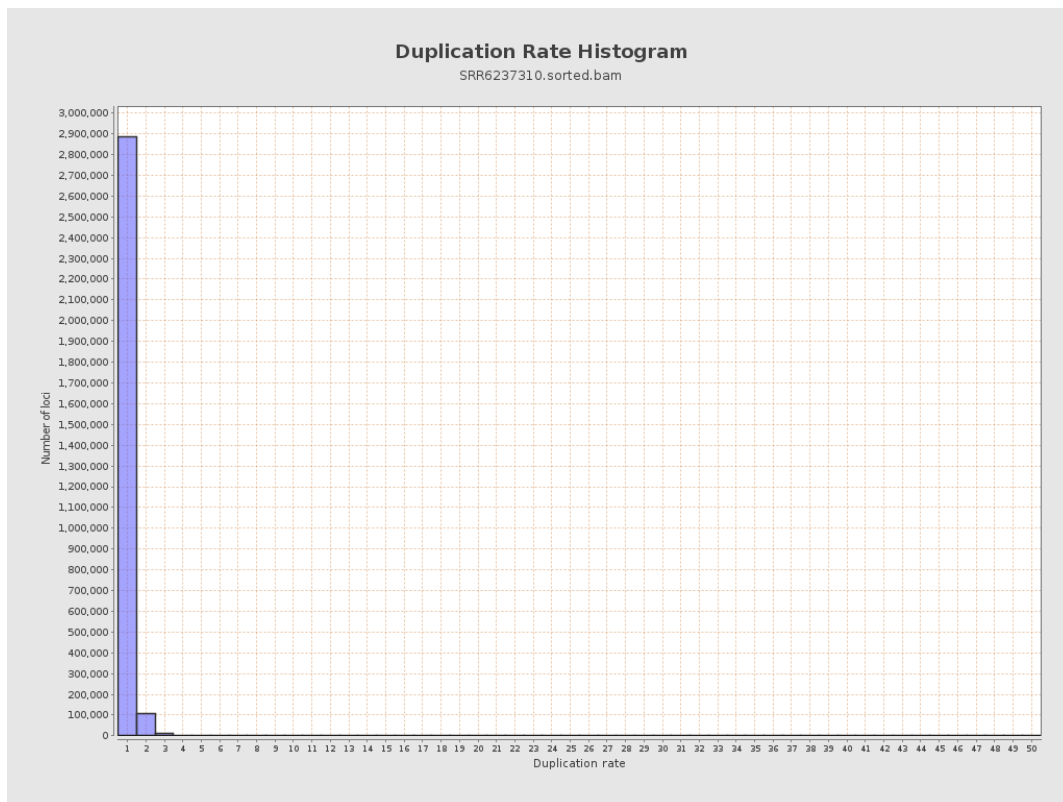
5. Results : Coverage Histogram (0-50X)



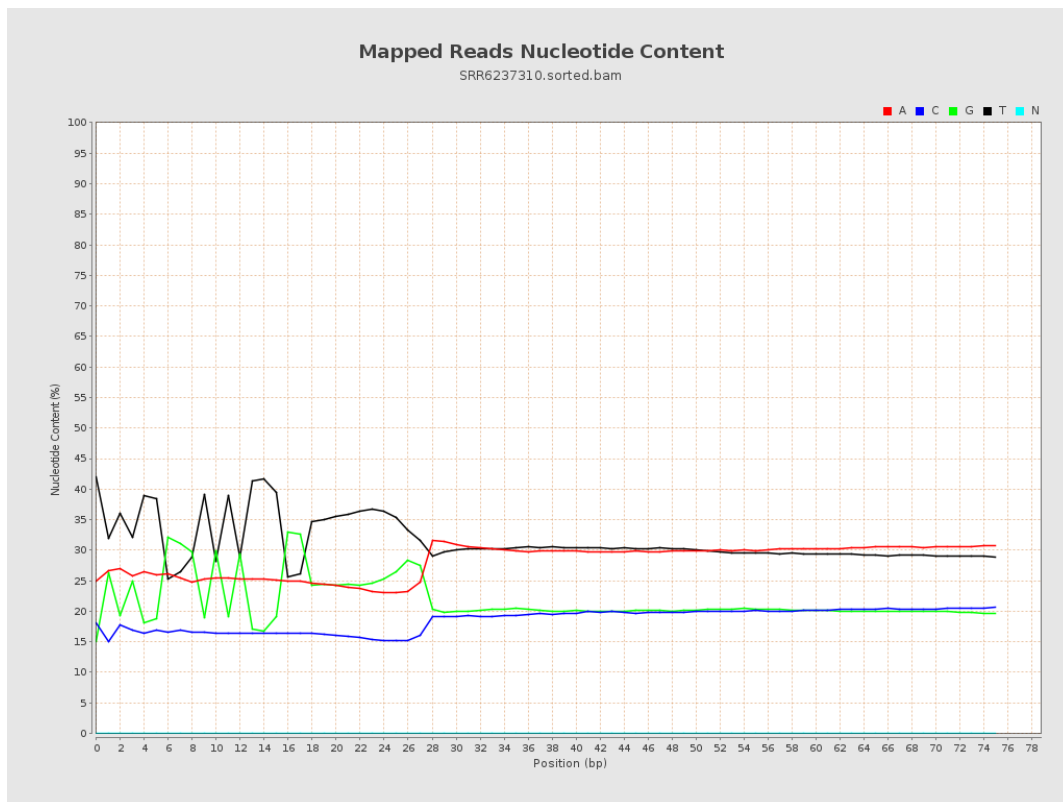
6. Results : Genome Fraction Coverage



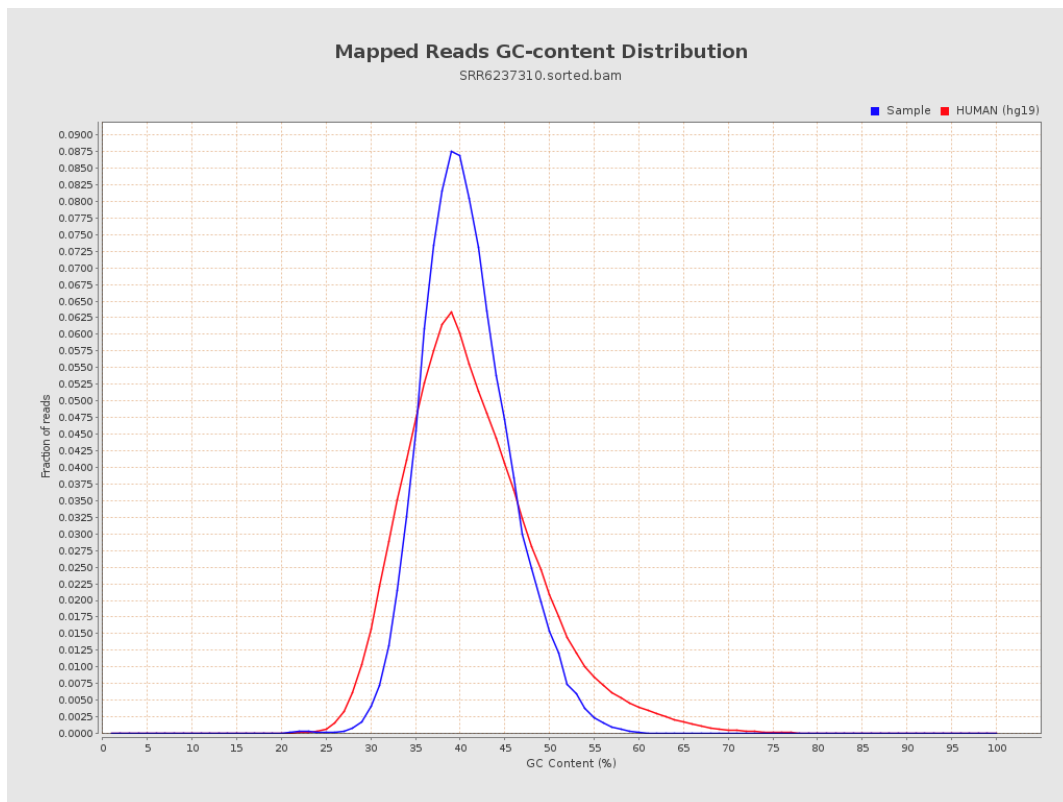
7. Results : Duplication Rate Histogram



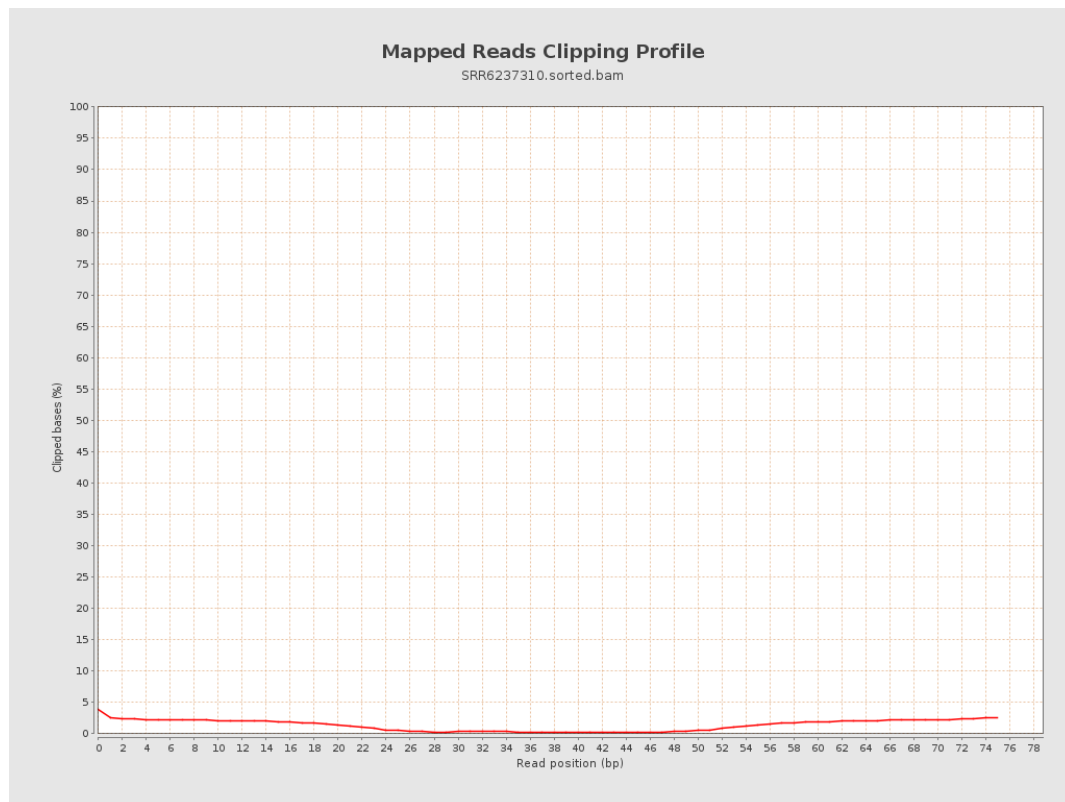
8. Results : Mapped Reads Nucleotide Content



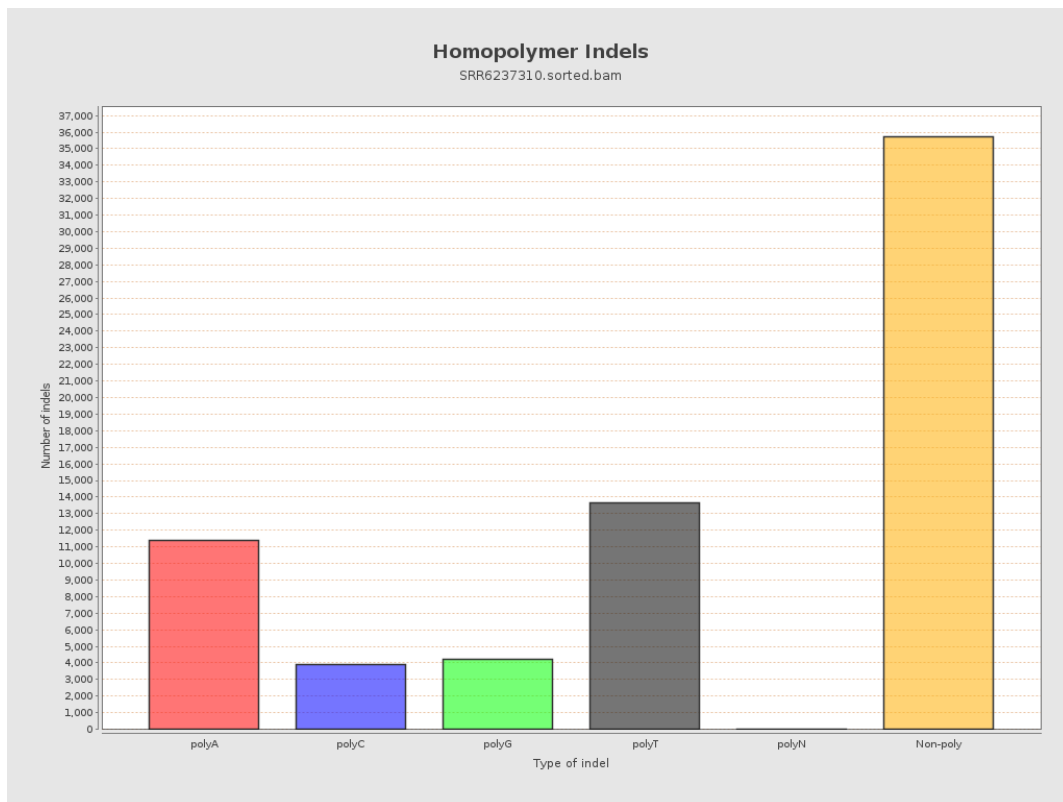
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

