

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 02:50:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237329.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_SRR6237329 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237329.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 02:50:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237329.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,278,603
Mapped reads	3,029,201 / 92.39%
Unmapped reads	249,402 / 7.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,138 / 0.64%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	323,149 / 9.86%
Duplication rate	8.58%
Clipped reads	1,660,248 / 50.64%

2.2. ACGT Content

Number/percentage of A's	52,044,227 / 26.93%
Number/percentage of C's	33,558,900 / 17.37%
Number/percentage of T's	64,077,762 / 33.16%
Number/percentage of G's	43,533,229 / 22.53%
Number/percentage of N's	22,060 / 0.01%
GC Percentage	39.9%

2.3. Coverage

Mean	0.0625

Standard Deviation	0.7948
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2.4. Mapping Quality

Mean Mapping Quality	45.08
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2.5. Mismatches and indels

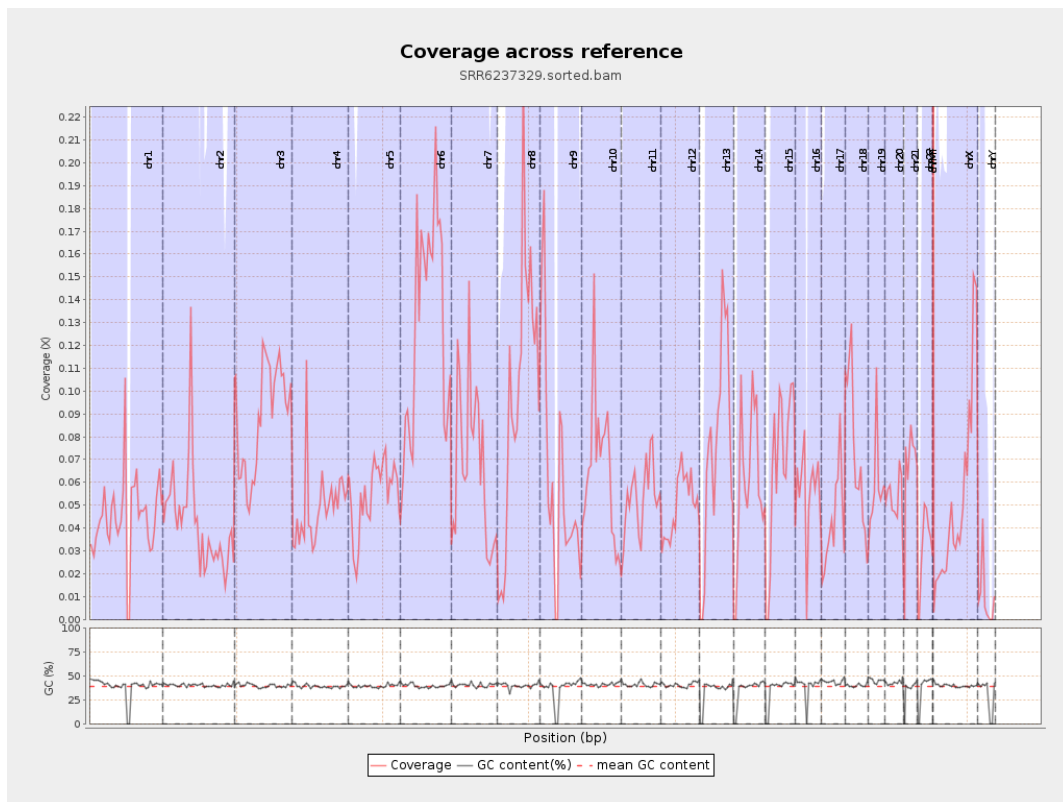
General error rate	0.65%
Mismatches	1,224,510
Insertions	14,795
Mapped reads with at least one insertion	0.48%
Deletions	67,881
Mapped reads with at least one deletion	2.21%
Homopolymer indels	42.59%

2.6. Chromosome stats

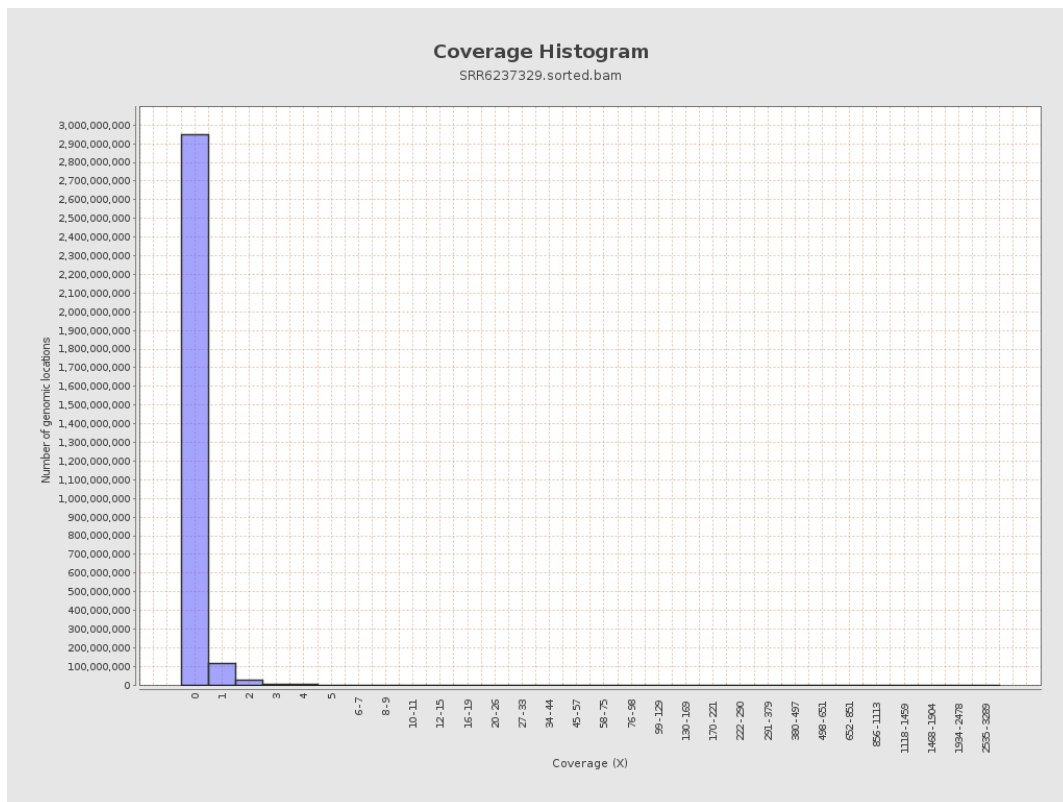
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11088725	0.0445	1.2303
chr2	243199373	10353278	0.0426	0.9679
chr3	198022430	17574012	0.0887	0.3733
chr4	191154276	9413575	0.0492	0.4226
chr5	180915260	9894698	0.0547	0.2982
chr6	171115067	22154562	0.1295	0.7428
chr7	159138663	10627856	0.0668	0.8695

chr8	146364022	14555813	0.0994	2.1376
chr9	141213431	8363319	0.0592	0.5433
chr10	135534747	8691439	0.0641	0.7287
chr11	135006516	7189263	0.0533	0.4137
chr12	133851895	6684739	0.0499	0.3014
chr13	115169878	8722158	0.0757	0.3631
chr14	107349540	6554497	0.0611	0.3193
chr15	102531392	6831775	0.0666	0.3418
chr16	90354753	4954905	0.0548	0.3546
chr17	81195210	3530117	0.0435	0.2984
chr18	78077248	5865848	0.0751	1.1407
chr19	59128983	3485648	0.0589	0.8049
chr20	63025520	3408168	0.0541	0.3139
chr21	48129895	3212534	0.0667	0.4031
chr22	51304566	1600184	0.0312	0.2128
chrMT	16571	24573	1.4829	1.6732
chrX	155270560	7972529	0.0513	0.3361
chrY	59373566	603200	0.0102	0.3702

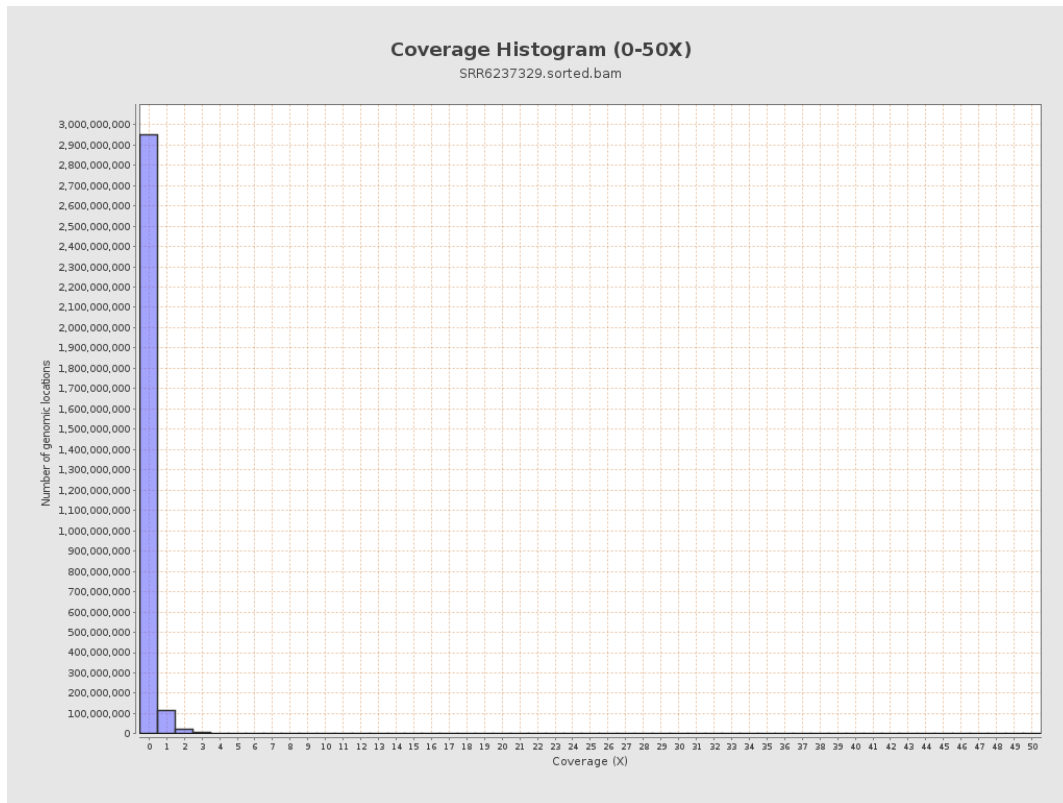
3. Results : Coverage across reference



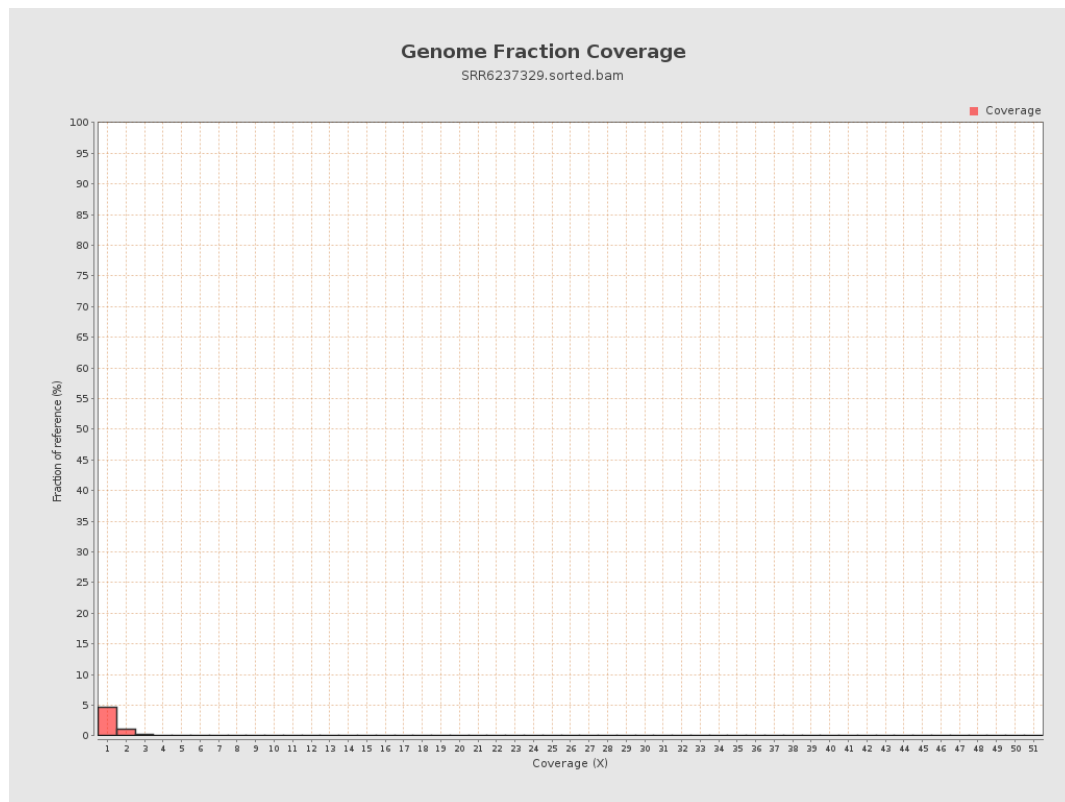
4. Results : Coverage Histogram



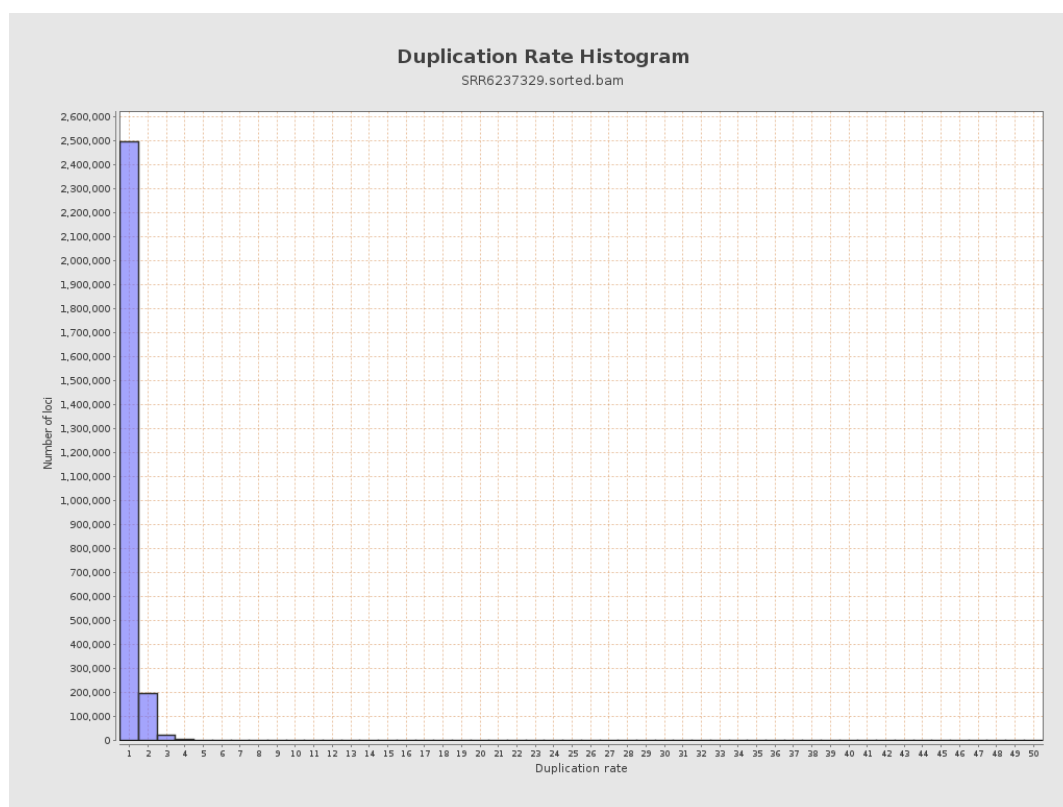
5. Results : Coverage Histogram (0-50X)



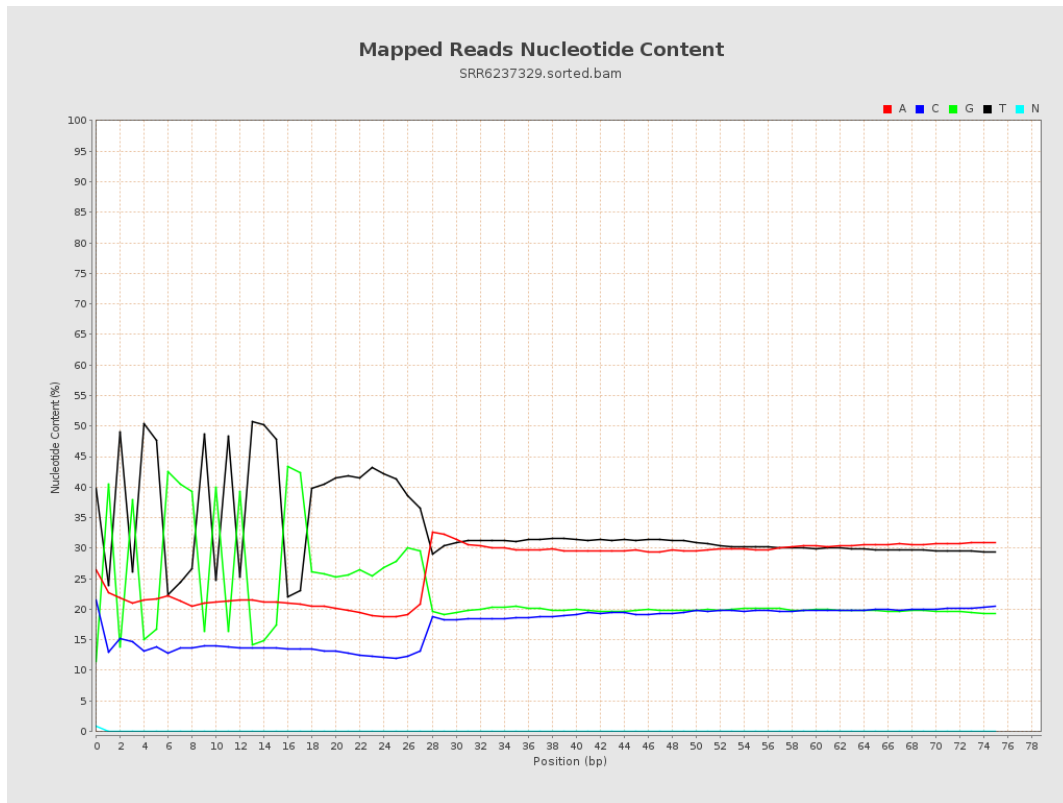
6. Results : Genome Fraction Coverage



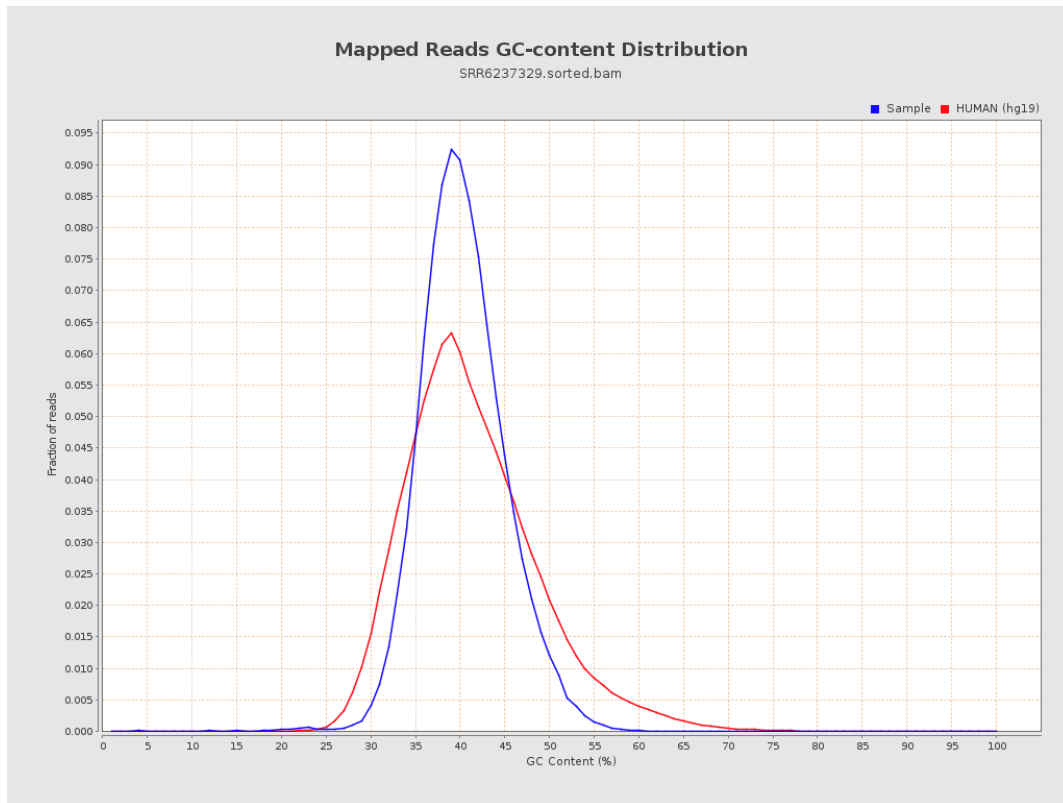
7. Results : Duplication Rate Histogram



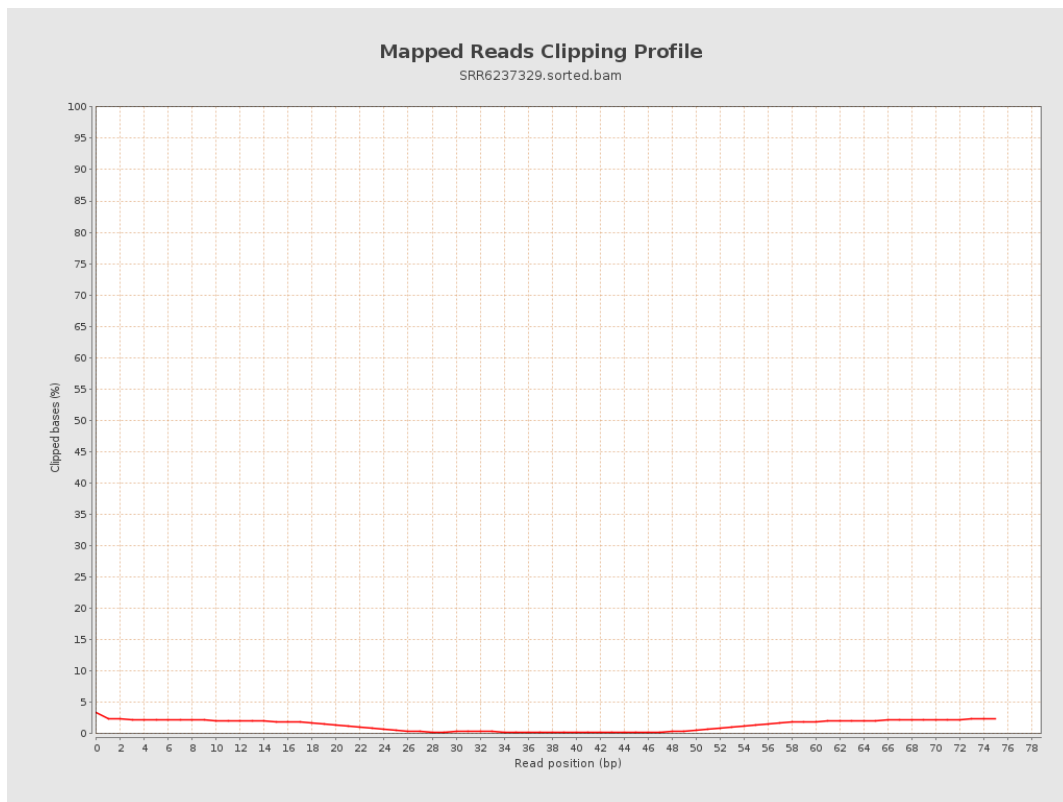
8. Results : Mapped Reads Nucleotide Content



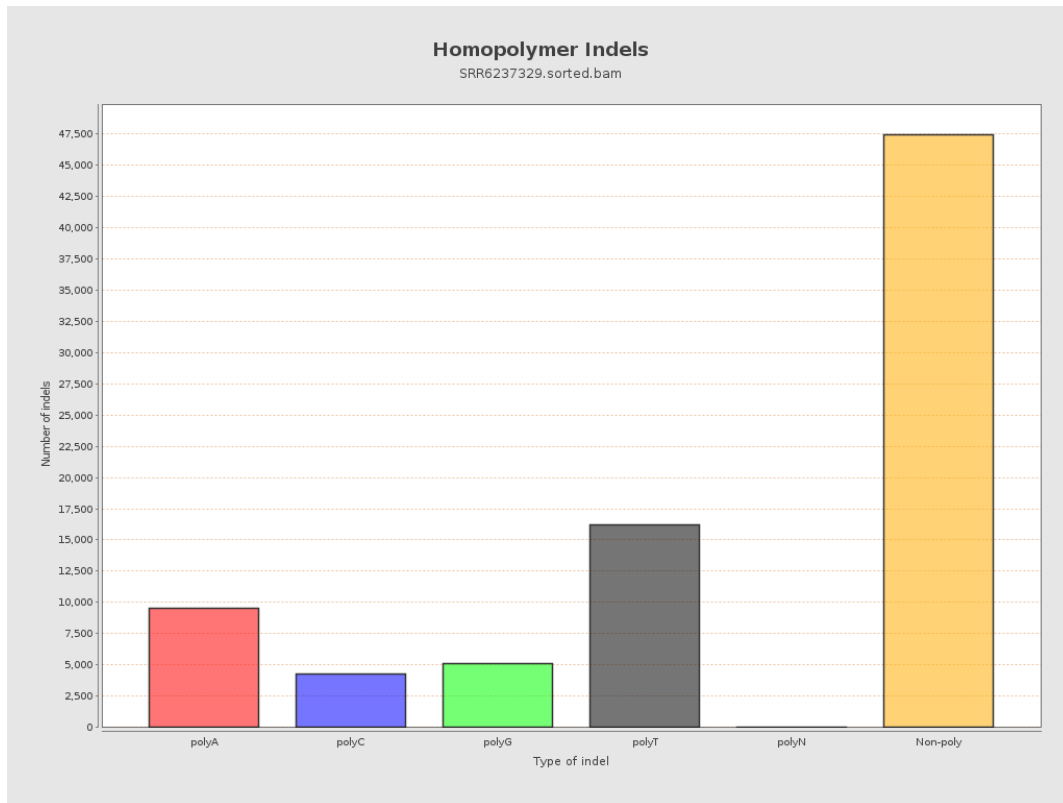
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

