

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 21:58:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236129.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_SRR6236129 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236129.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 21:58:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236129.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,764,742
Mapped reads	1,497,640 / 84.86%
Unmapped reads	267,102 / 15.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,057 / 0.46%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	63,430 / 3.59%
Duplication rate	2.96%
Clipped reads	686,271 / 38.89%

2.2. ACGT Content

Number/percentage of A's	27,626,444 / 27.88%
Number/percentage of C's	17,463,962 / 17.62%
Number/percentage of T's	31,964,067 / 32.25%
Number/percentage of G's	21,988,234 / 22.19%
Number/percentage of N's	59,732 / 0.06%
GC Percentage	39.81%

2.3. Coverage

Mean	0.032

Standard Deviation	0.4265
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2.4. Mapping Quality

Mean Mapping Quality	44.66
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2.5. Mismatches and indels

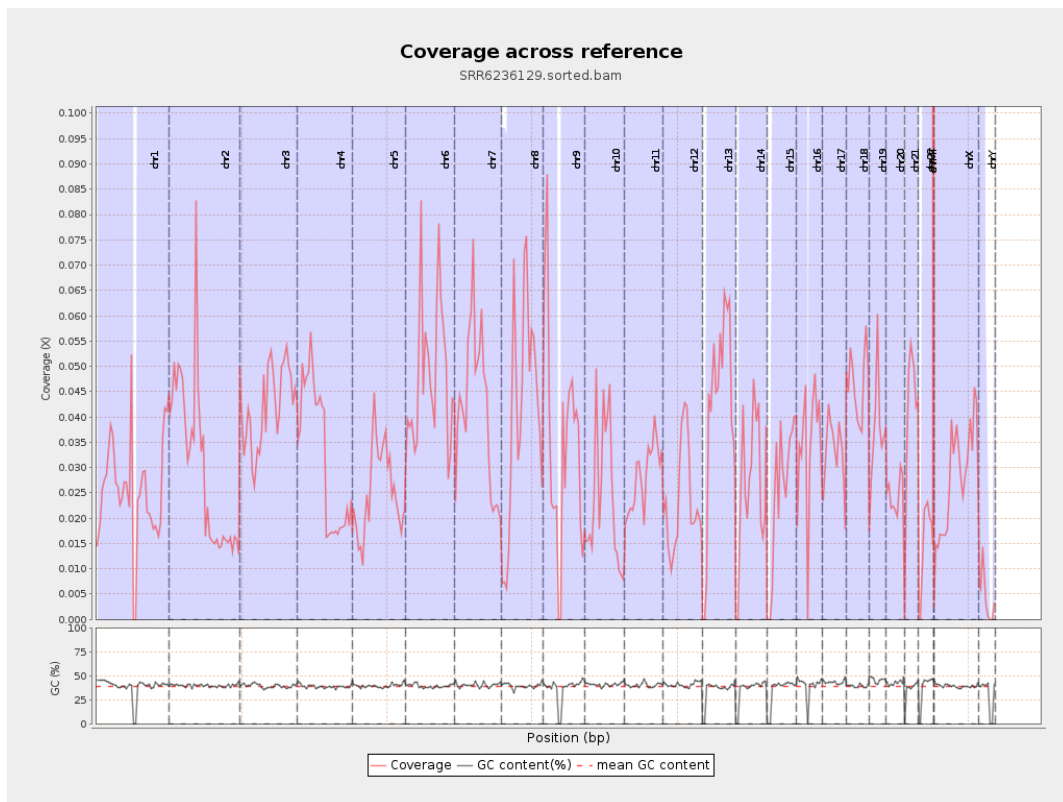
General error rate	0.91%
Mismatches	883,595
Insertions	7,733
Mapped reads with at least one insertion	0.51%
Deletions	33,564
Mapped reads with at least one deletion	2.21%
Homopolymer indels	45.9%

2.6. Chromosome stats

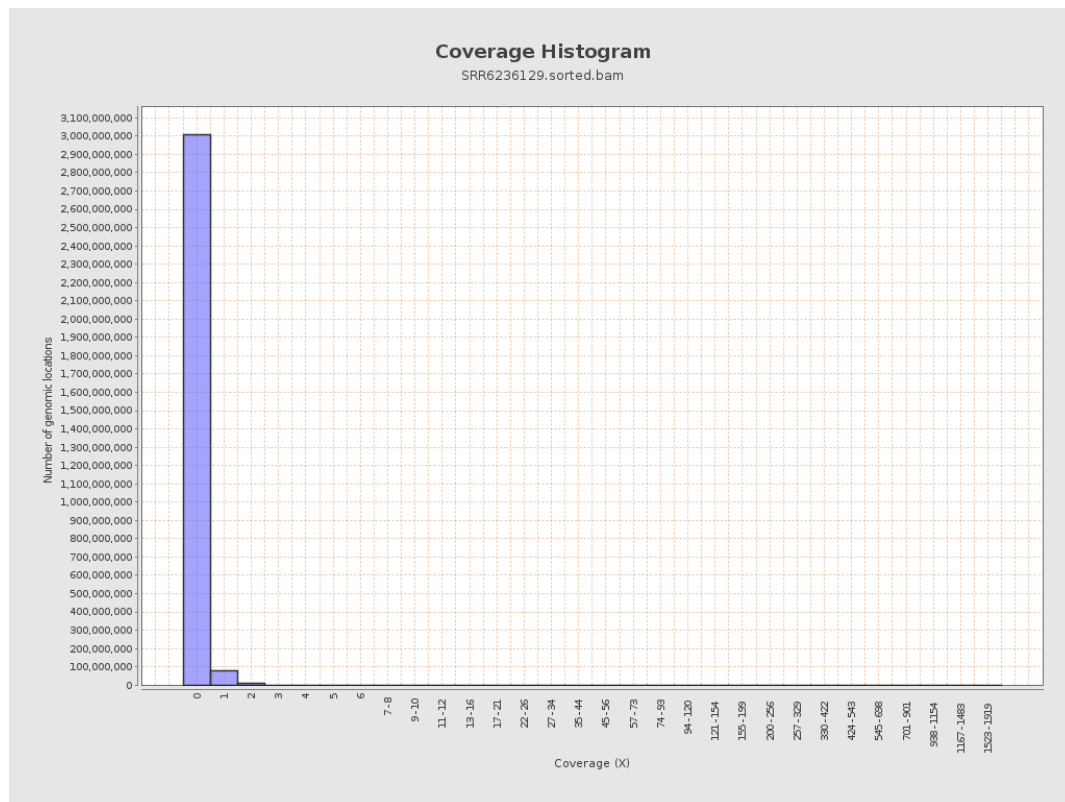
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6360682	0.0255	0.6822
chr2	243199373	7280025	0.0299	0.3773
chr3	198022430	8354019	0.0422	0.2252
chr4	191154276	6149496	0.0322	0.2178
chr5	180915260	4612193	0.0255	0.1832
chr6	171115067	8182826	0.0478	0.3514
chr7	159138663	6626637	0.0416	0.4459

chr8	146364022	5885947	0.0402	1.2043
chr9	141213431	4876349	0.0345	0.3461
chr10	135534747	3301714	0.0244	0.2827
chr11	135006516	3780460	0.028	0.2501
chr12	133851895	3129383	0.0234	0.1782
chr13	115169878	4758226	0.0413	0.223
chr14	107349540	2737832	0.0255	0.2003
chr15	102531392	2599986	0.0254	0.1812
chr16	90354753	3105969	0.0344	0.2392
chr17	81195210	2662501	0.0328	0.2348
chr18	78077248	3638278	0.0466	0.6307
chr19	59128983	2246745	0.038	0.4748
chr20	63025520	1526813	0.0242	0.18
chr21	48129895	1972720	0.041	0.2433
chr22	51304566	763359	0.0149	0.1315
chrMT	16571	86146	5.1986	4.1678
chrX	155270560	4278239	0.0276	0.2084
chrY	59373566	244446	0.0041	0.1127

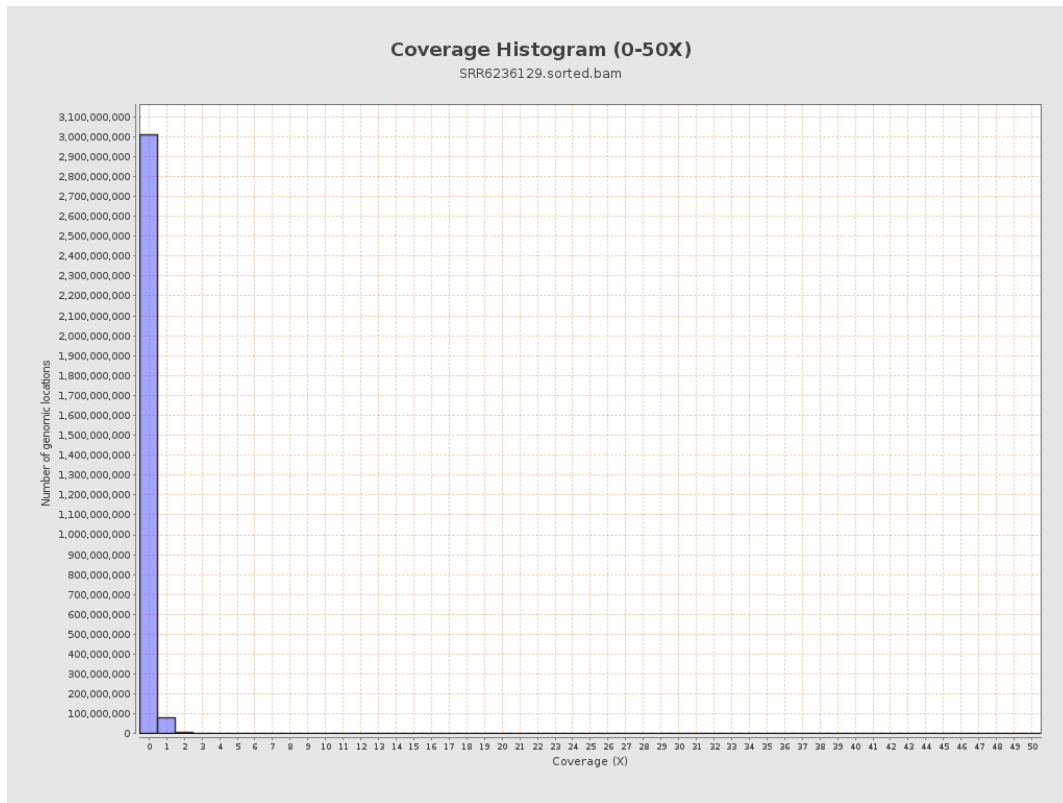
3. Results : Coverage across reference



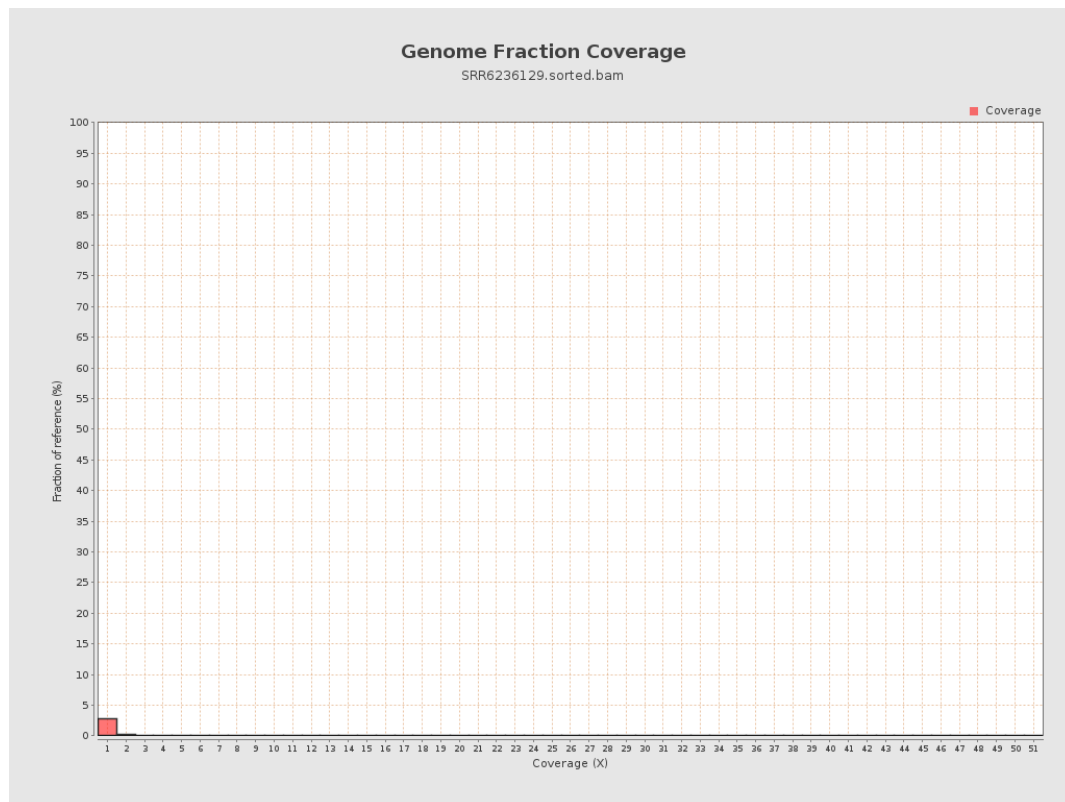
4. Results : Coverage Histogram



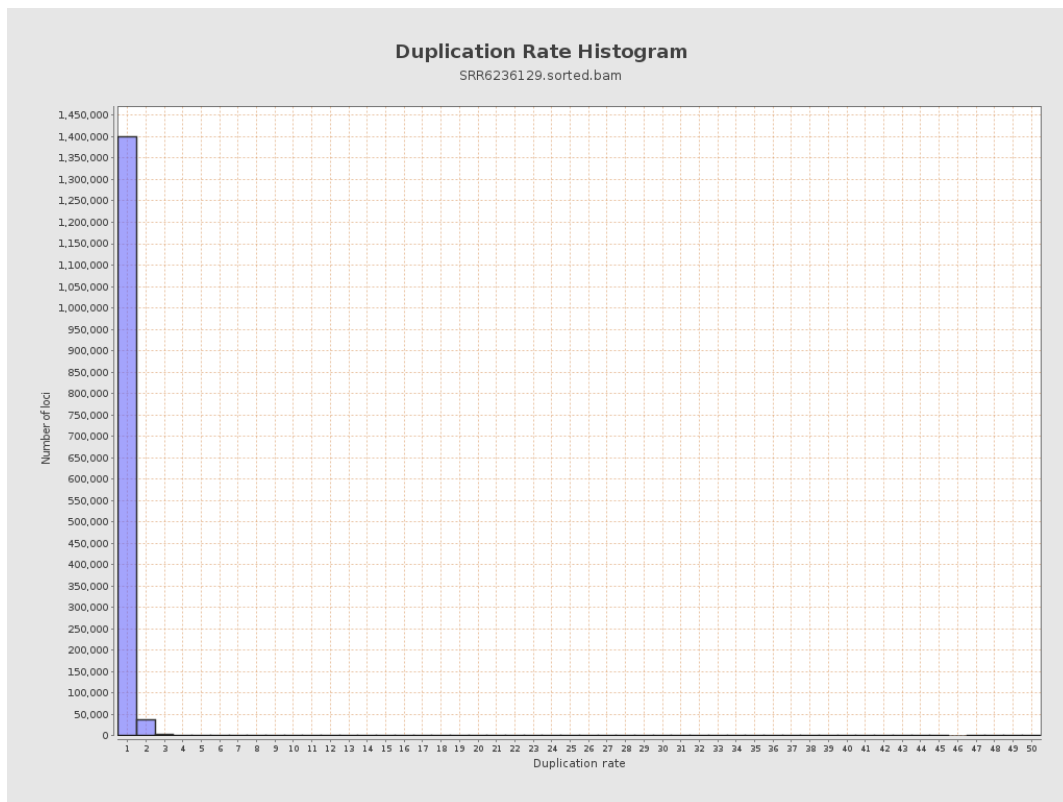
5. Results : Coverage Histogram (0-50X)



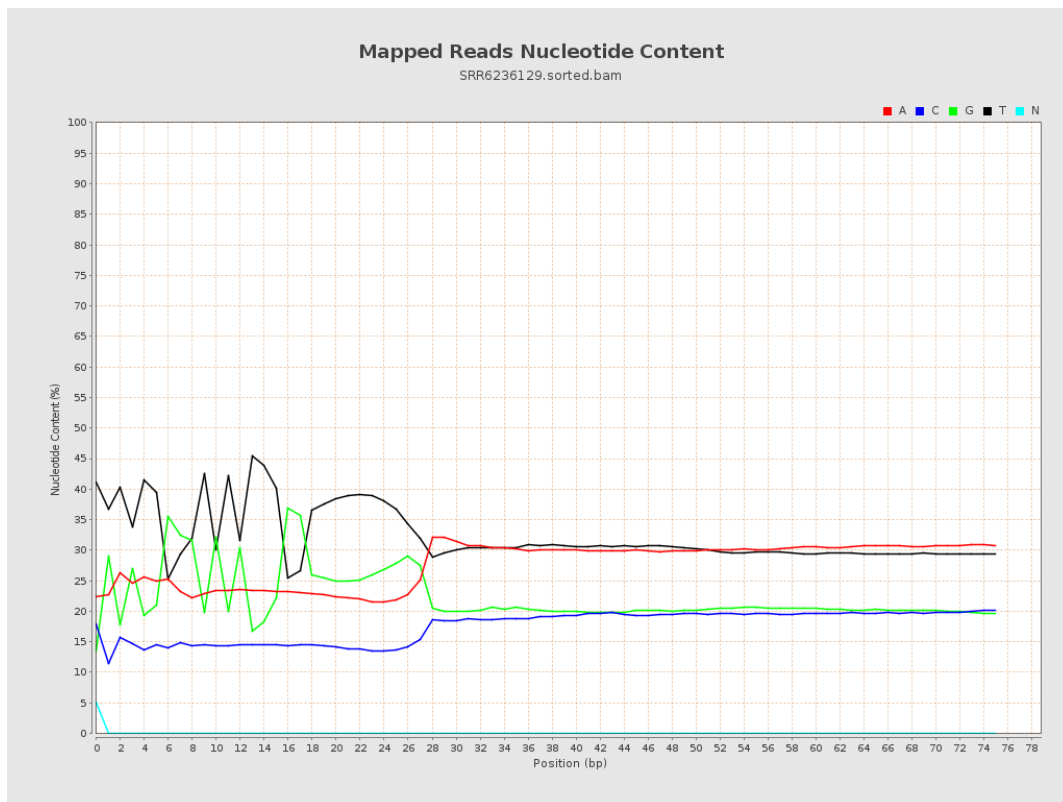
6. Results : Genome Fraction Coverage



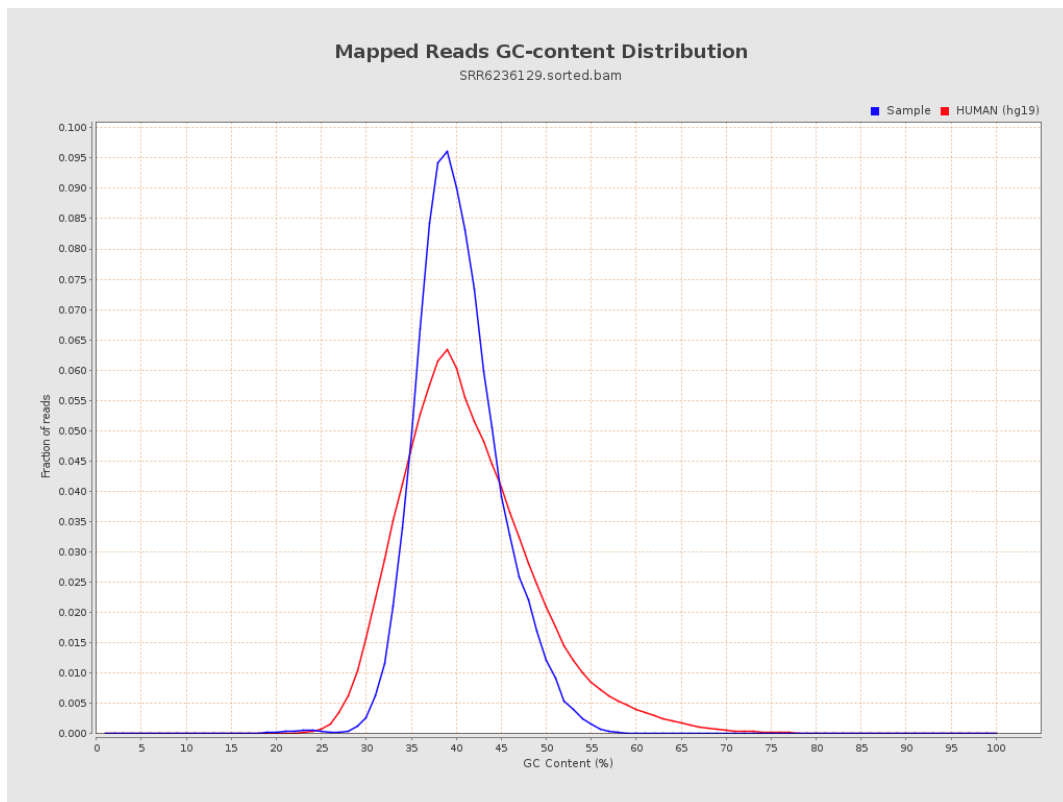
7. Results : Duplication Rate Histogram



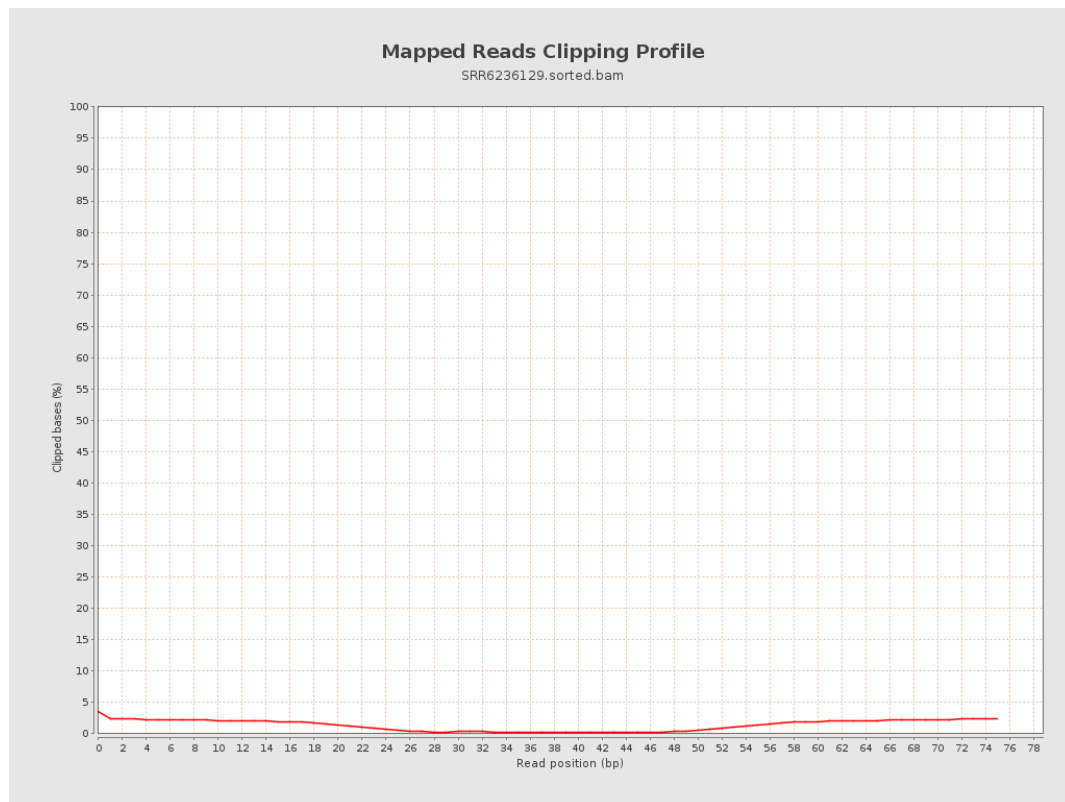
8. Results : Mapped Reads Nucleotide Content



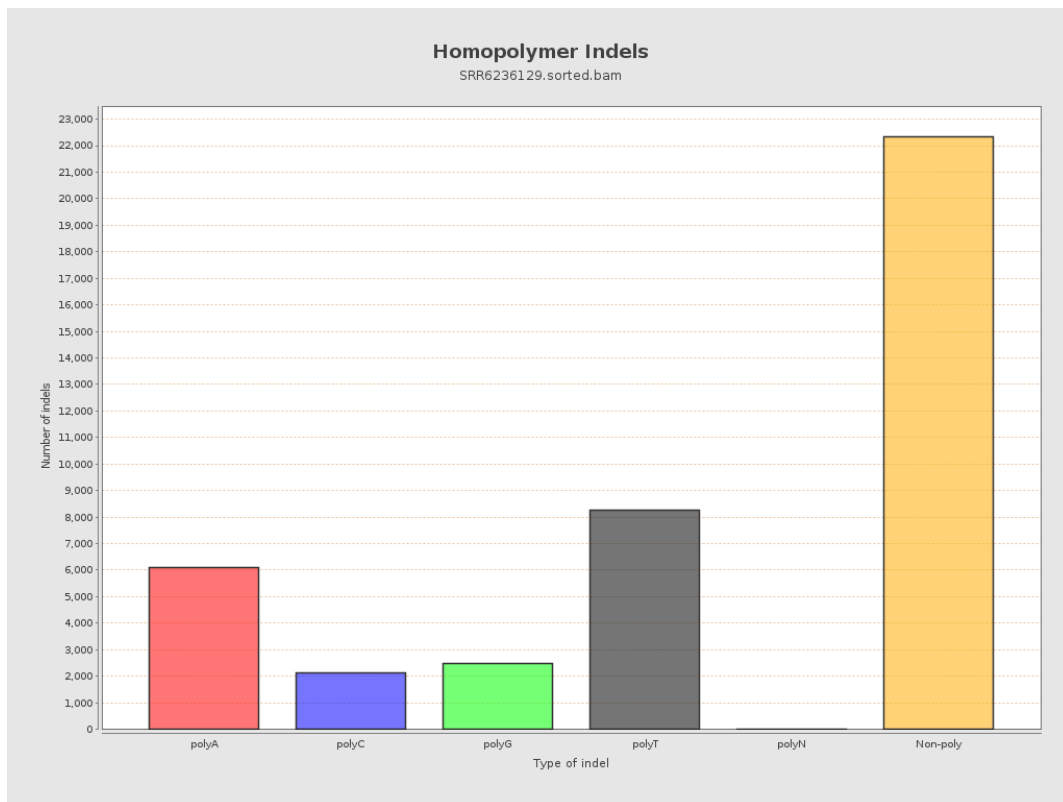
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

