

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 20:08:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236090.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_SRR6236090 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236090.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 20:08:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236090.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,941,967
Mapped reads	1,693,891 / 87.23%
Unmapped reads	248,076 / 12.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,953 / 0.51%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	79,358 / 4.09%
Duplication rate	3.74%
Clipped reads	801,865 / 41.29%

2.2. ACGT Content

Number/percentage of A's	30,438,254 / 27.33%
Number/percentage of C's	19,917,240 / 17.89%
Number/percentage of T's	35,891,938 / 32.23%
Number/percentage of G's	25,042,566 / 22.49%
Number/percentage of N's	65,645 / 0.06%
GC Percentage	40.37%

2.3. Coverage

Mean	0.036

Standard Deviation	0.3355
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2.4. Mapping Quality

Mean Mapping Quality	45.83
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2.5. Mismatches and indels

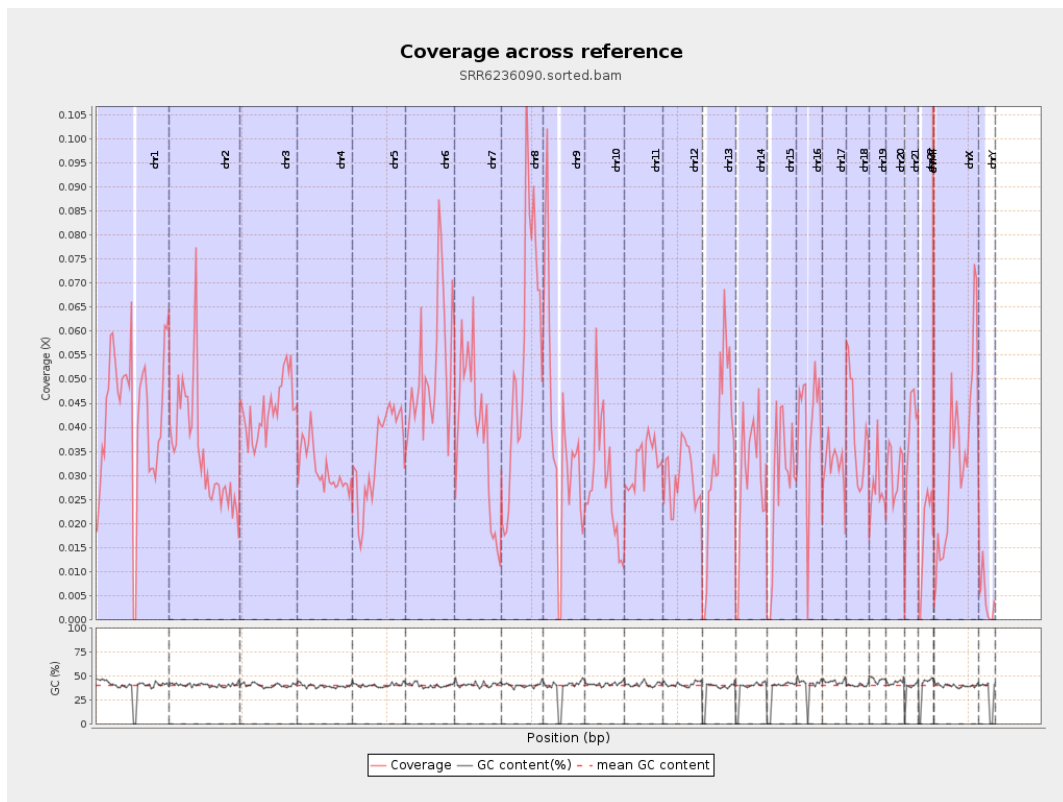
General error rate	0.82%
Mismatches	902,868
Insertions	7,859
Mapped reads with at least one insertion	0.46%
Deletions	33,124
Mapped reads with at least one deletion	1.93%
Homopolymer indels	46.28%

2.6. Chromosome stats

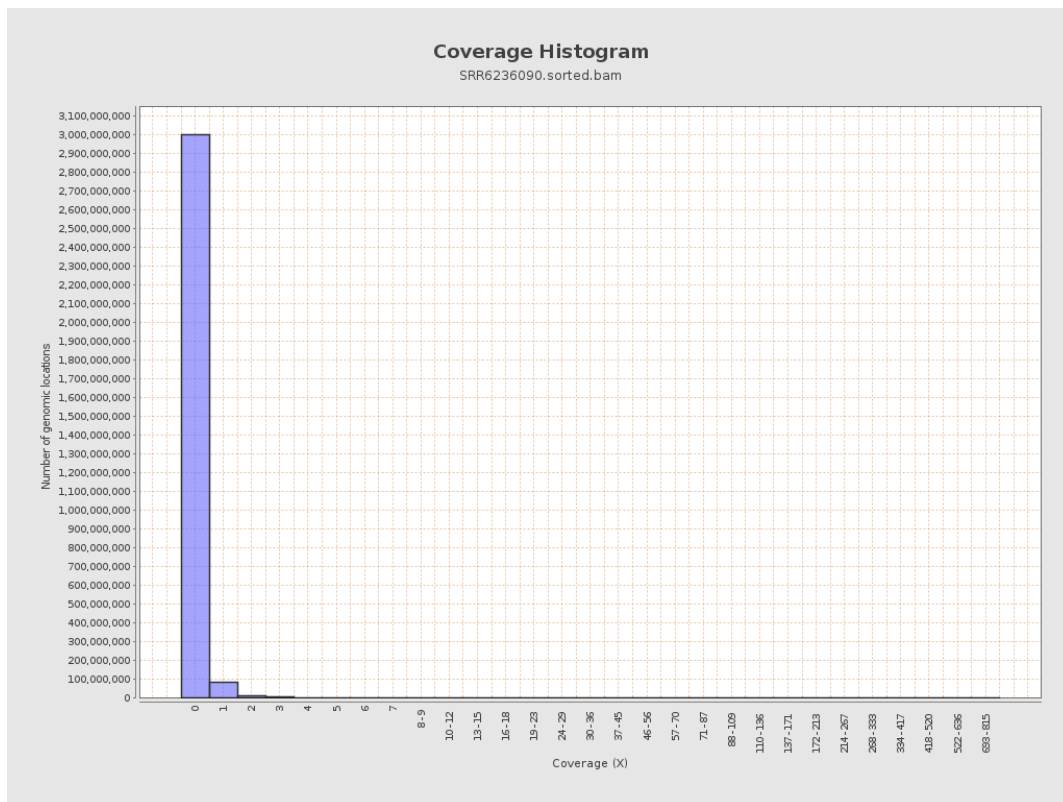
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10526418	0.0422	0.5617
chr2	243199373	8486726	0.0349	0.3778
chr3	198022430	8681773	0.0438	0.237
chr4	191154276	5954685	0.0312	0.2138
chr5	180915260	6225292	0.0344	0.2112
chr6	171115067	8827736	0.0516	0.3233
chr7	159138663	6159956	0.0387	0.4175

chr8	146364022	7884518	0.0539	0.5731
chr9	141213431	5299817	0.0375	0.3218
chr10	135534747	3872313	0.0286	0.2878
chr11	135006516	4356254	0.0323	0.2638
chr12	133851895	3940196	0.0294	0.2024
chr13	115169878	4033356	0.035	0.2112
chr14	107349540	3125699	0.0291	0.2104
chr15	102531392	2847278	0.0278	0.1974
chr16	90354753	3675102	0.0407	0.2459
chr17	81195210	2588985	0.0319	0.2468
chr18	78077248	3082404	0.0395	0.5132
chr19	59128983	1611015	0.0272	0.4063
chr20	63025520	1936746	0.0307	0.2013
chr21	48129895	1791482	0.0372	0.2342
chr22	51304566	906606	0.0177	0.1482
chrMT	16571	175325	10.5802	6.8492
chrX	155270560	5180472	0.0334	0.2319
chrY	59373566	242784	0.0041	0.1072

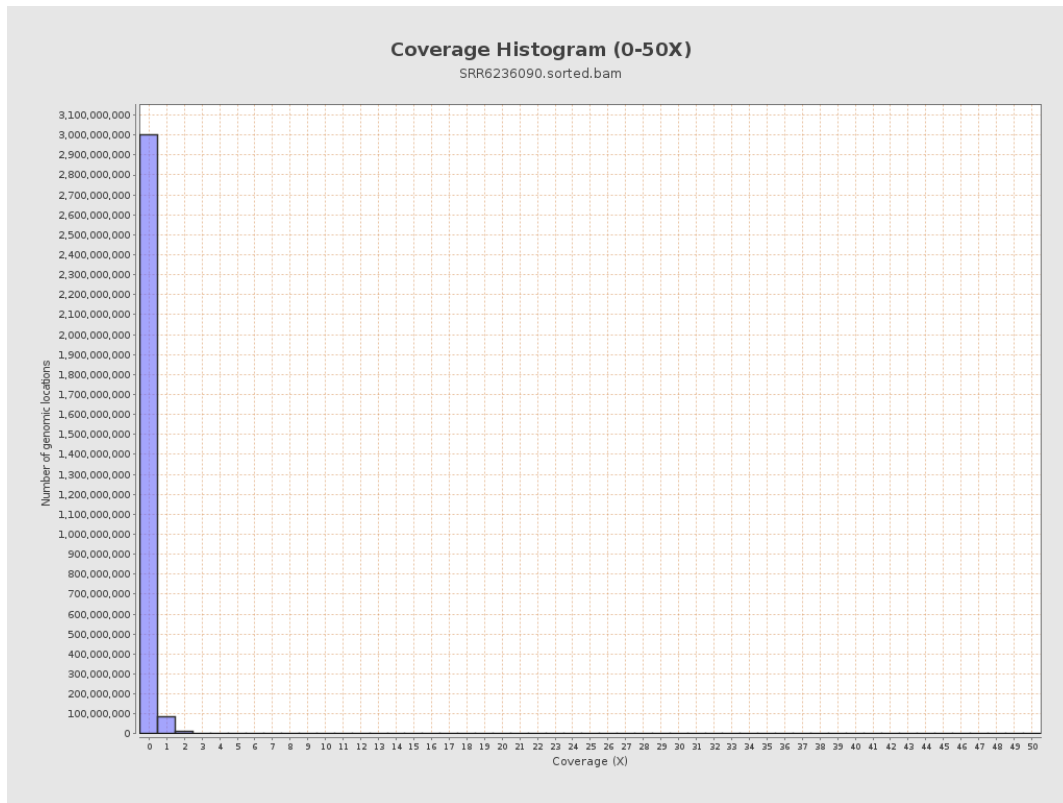
3. Results : Coverage across reference



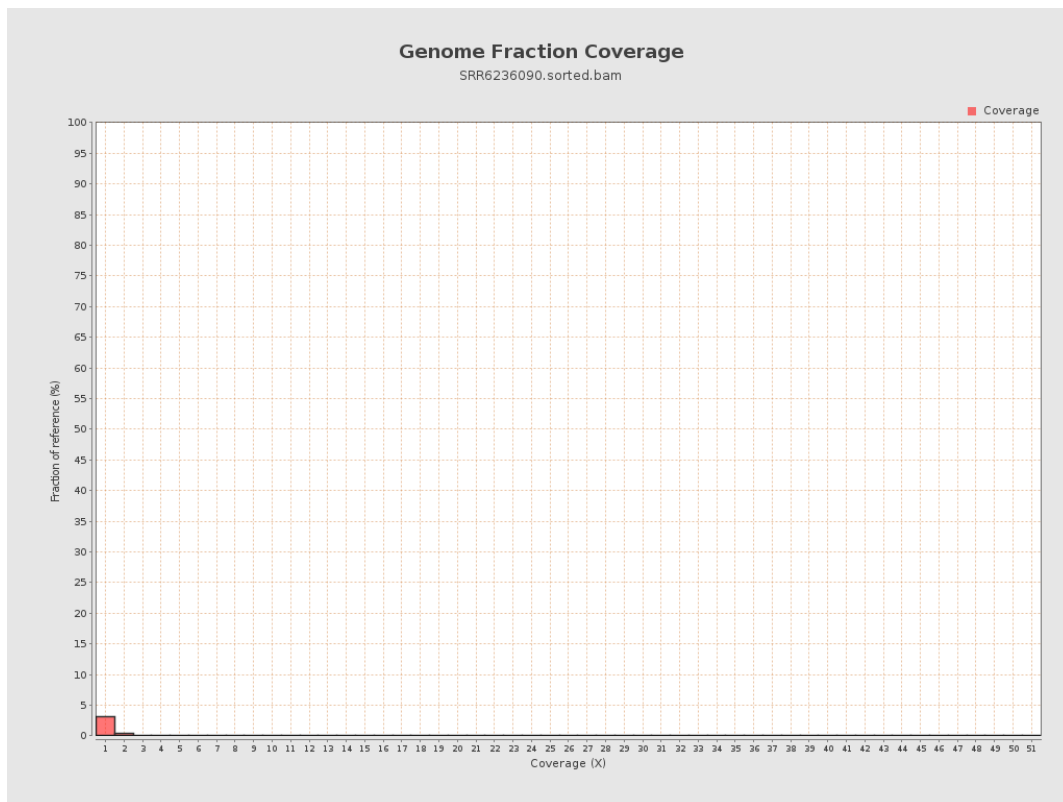
4. Results : Coverage Histogram



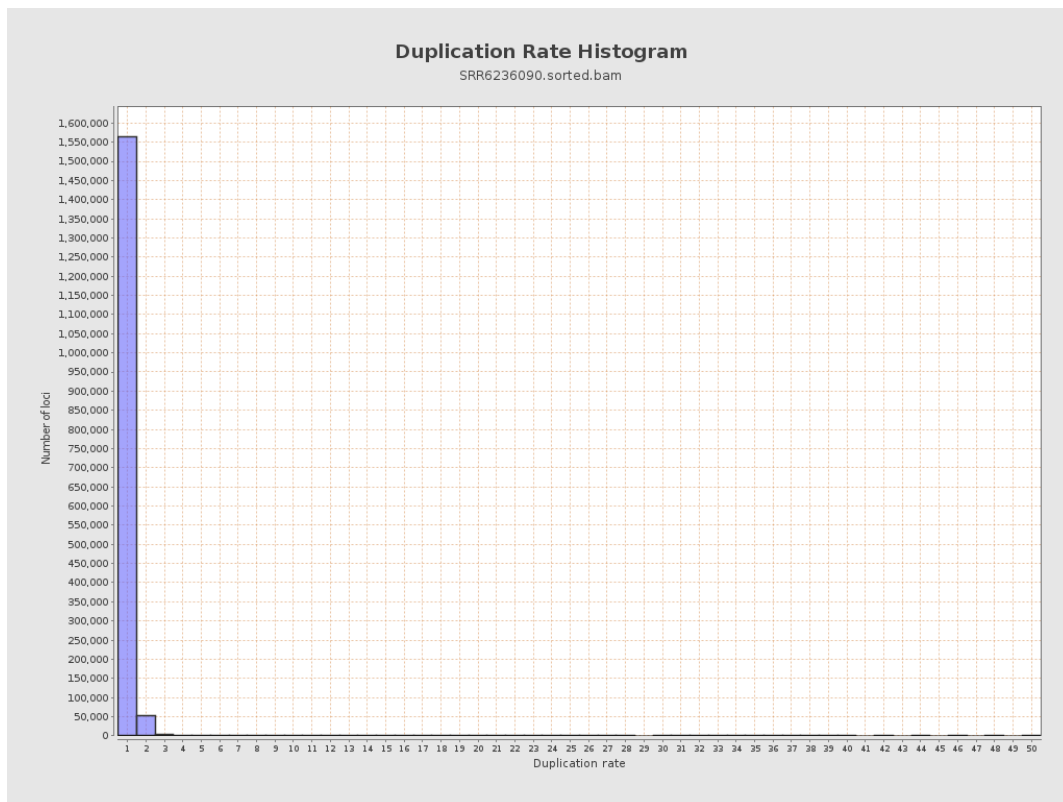
5. Results : Coverage Histogram (0-50X)



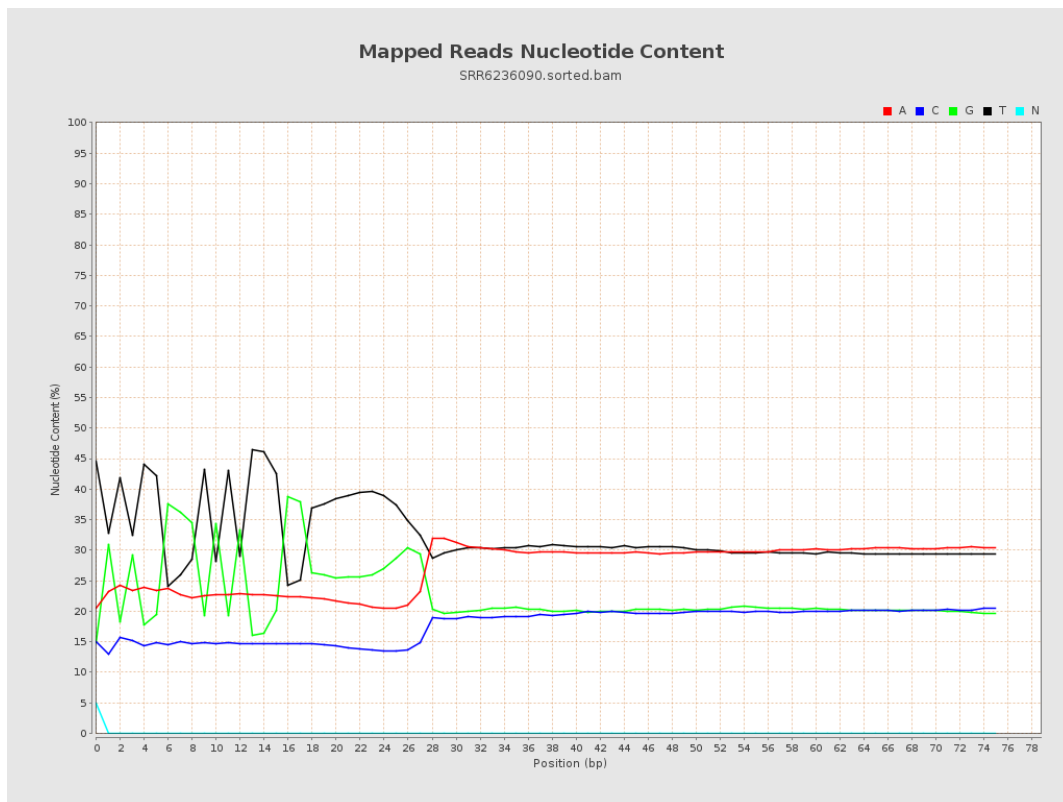
6. Results : Genome Fraction Coverage



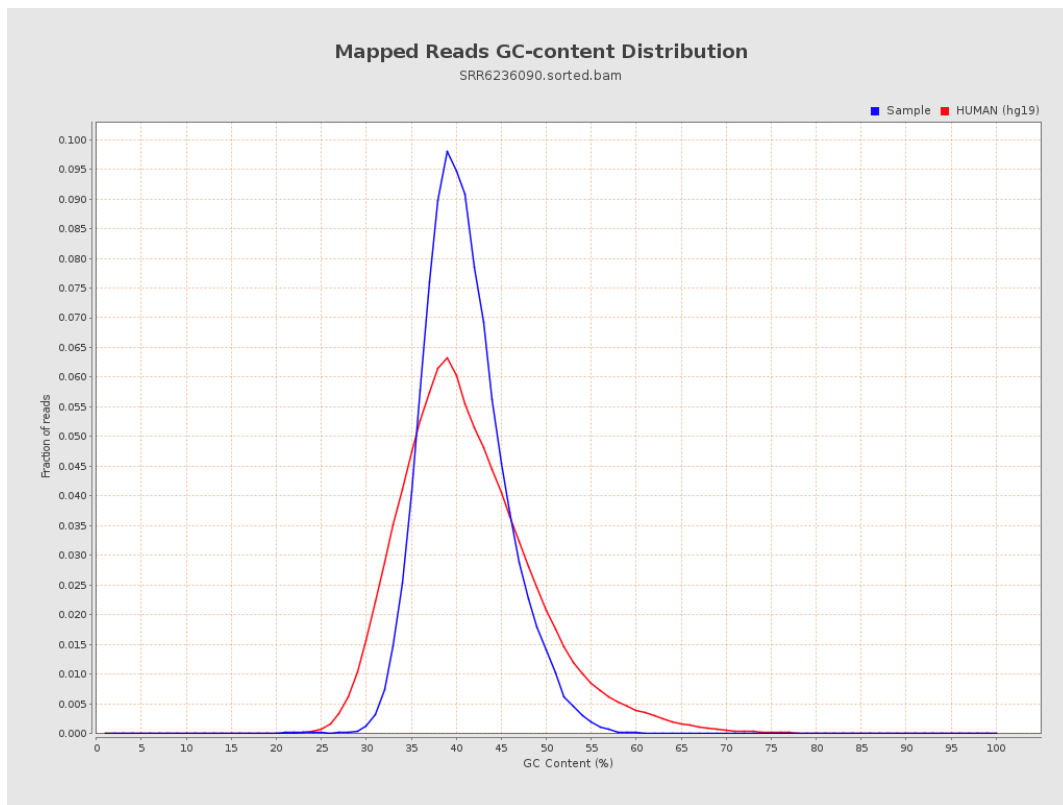
7. Results : Duplication Rate Histogram



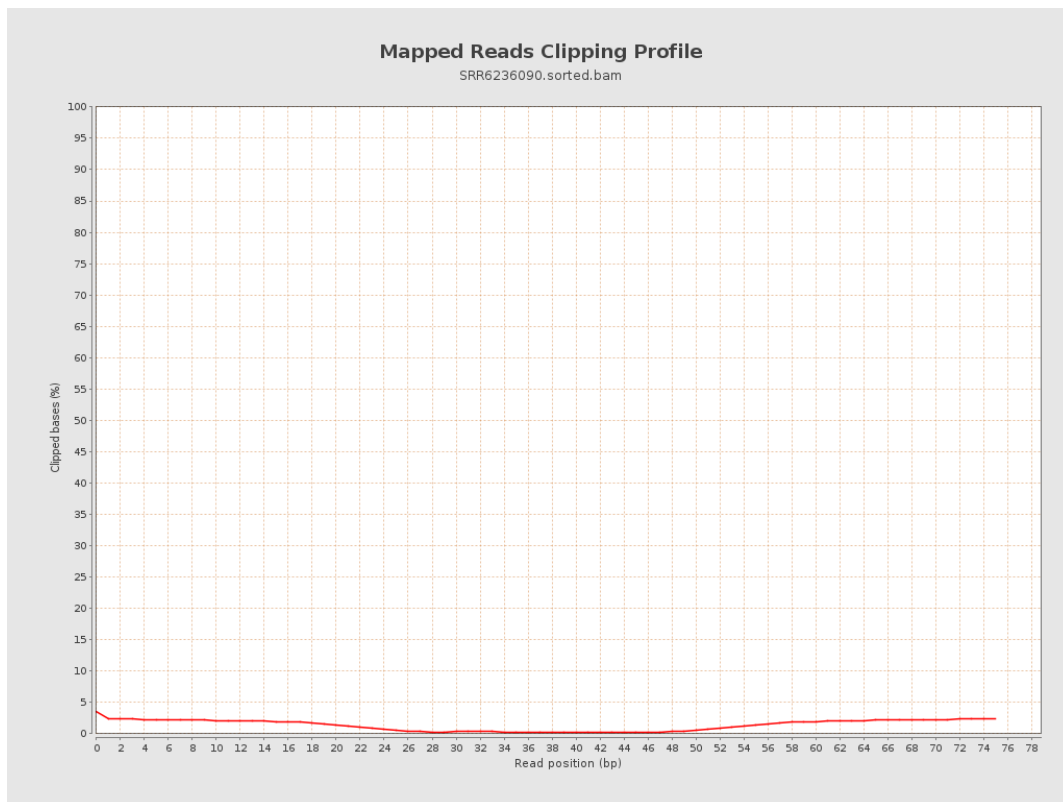
8. Results : Mapped Reads Nucleotide Content



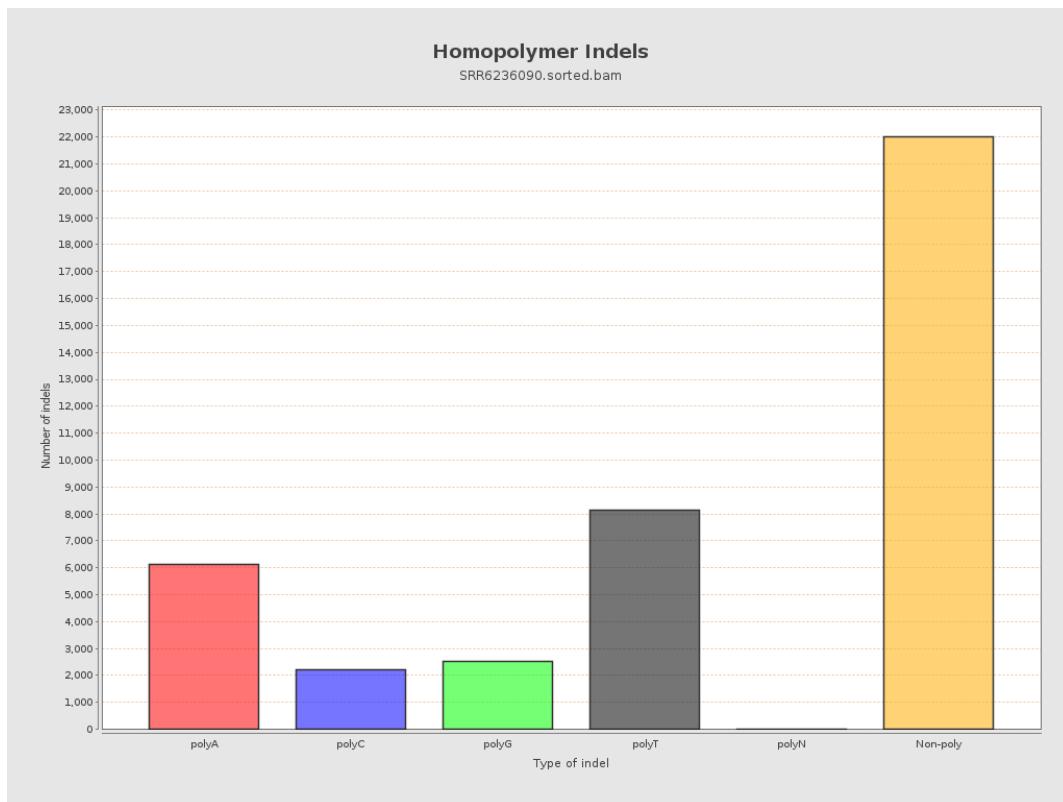
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

