

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 23:38:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013367.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_SRR6013367 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013367.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 23:38:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013367.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,130,794
Mapped reads	1,913,647 / 89.81%
Unmapped reads	217,147 / 10.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,674 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	88,223 / 4.14%
Duplication rate	3.21%
Clipped reads	760,710 / 35.7%

2.2. ACGT Content

Number/percentage of A's	37,186,303 / 28.65%
Number/percentage of C's	23,835,032 / 18.37%
Number/percentage of T's	41,252,958 / 31.79%
Number/percentage of G's	27,481,694 / 21.17%
Number/percentage of N's	28,282 / 0.02%
GC Percentage	39.54%

2.3. Coverage

Mean	0.0419

Standard Deviation	0.501
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2.4. Mapping Quality

Mean Mapping Quality	46.37
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2.5. Mismatches and indels

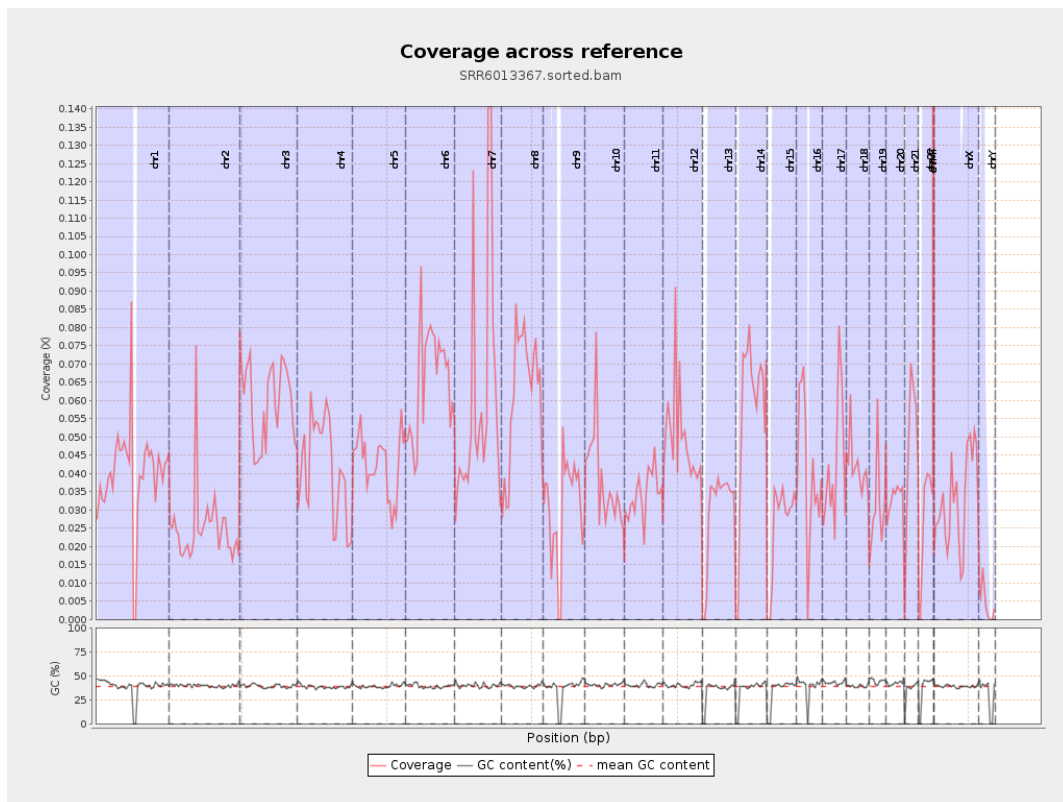
General error rate	0.82%
Mismatches	1,040,833
Insertions	9,785
Mapped reads with at least one insertion	0.51%
Deletions	31,028
Mapped reads with at least one deletion	1.6%
Homopolymer indels	46.53%

2.6. Chromosome stats

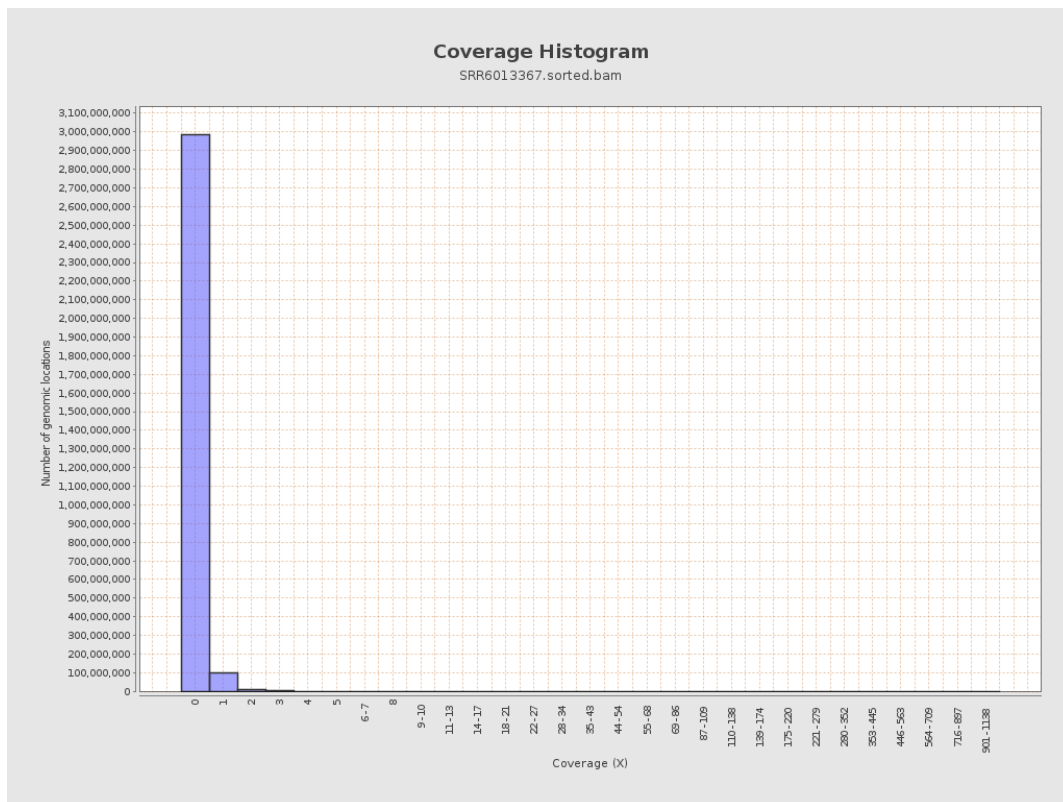
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9943268	0.0399	0.9624
chr2	243199373	6056565	0.0249	0.4561
chr3	198022430	11872093	0.06	0.2743
chr4	191154276	7877612	0.0412	0.2482
chr5	180915260	7725639	0.0427	0.234
chr6	171115067	11230963	0.0656	0.3931
chr7	159138663	10008848	0.0629	1.0468

chr8	146364022	9043641	0.0618	0.573
chr9	141213431	4299595	0.0304	0.4031
chr10	135534747	5193336	0.0383	0.4688
chr11	135006516	4603250	0.0341	0.3216
chr12	133851895	6596437	0.0493	0.258
chr13	115169878	3392139	0.0295	0.1922
chr14	107349540	6077224	0.0566	0.2825
chr15	102531392	2670722	0.026	0.1821
chr16	90354753	3690755	0.0408	0.2633
chr17	81195210	3406411	0.042	0.2569
chr18	78077248	3276582	0.042	0.8653
chr19	59128983	1871811	0.0317	0.7185
chr20	63025520	2062940	0.0327	0.2163
chr21	48129895	2295427	0.0477	0.2615
chr22	51304566	1377865	0.0269	0.1809
chrMT	16571	28442	1.7164	1.6864
chrX	155270560	4991161	0.0321	0.2334
chrY	59373566	245091	0.0041	0.1139

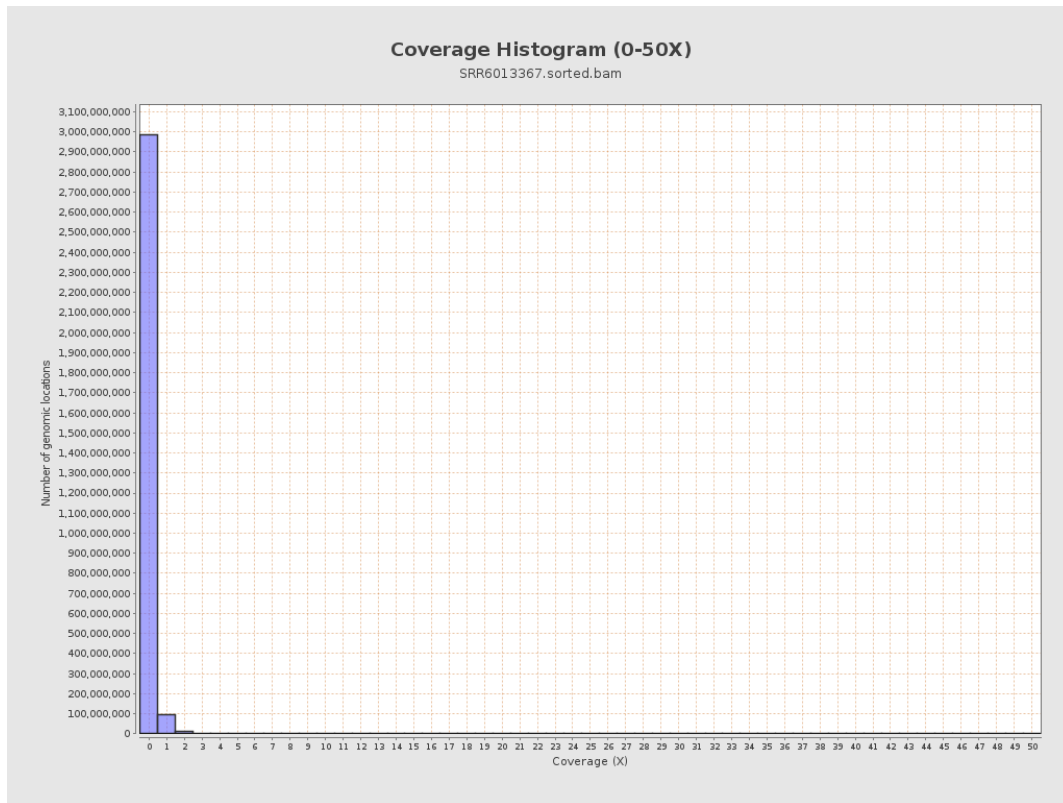
3. Results : Coverage across reference



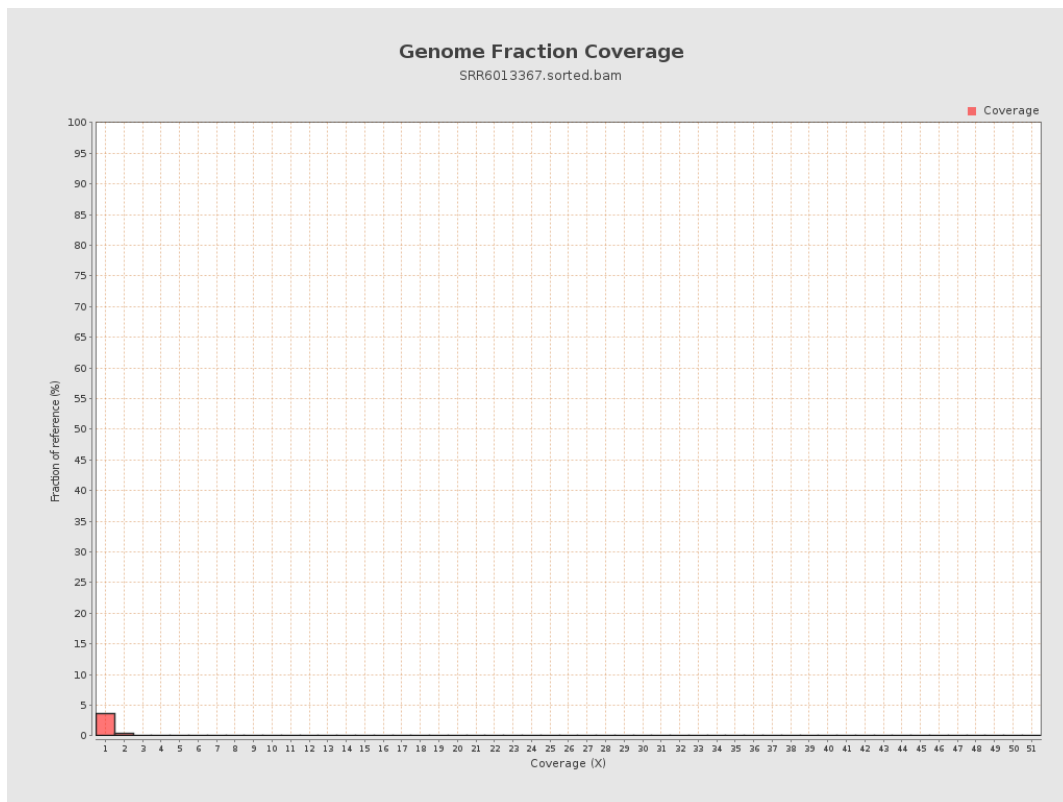
4. Results : Coverage Histogram



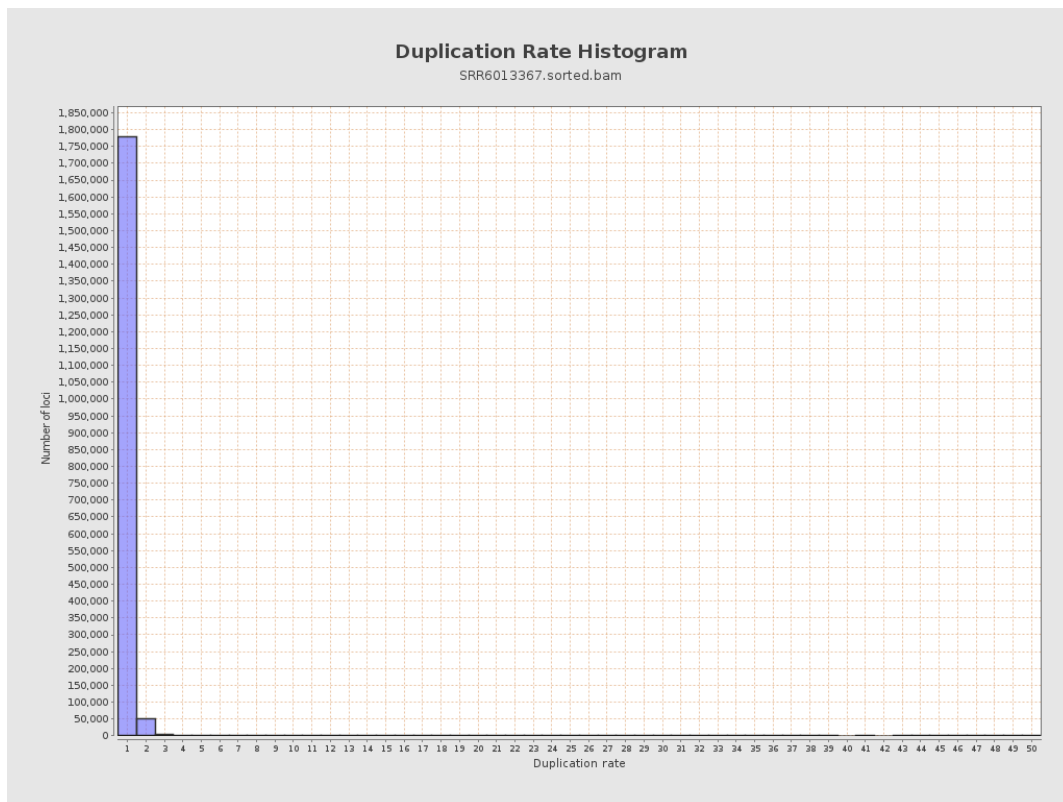
5. Results : Coverage Histogram (0-50X)



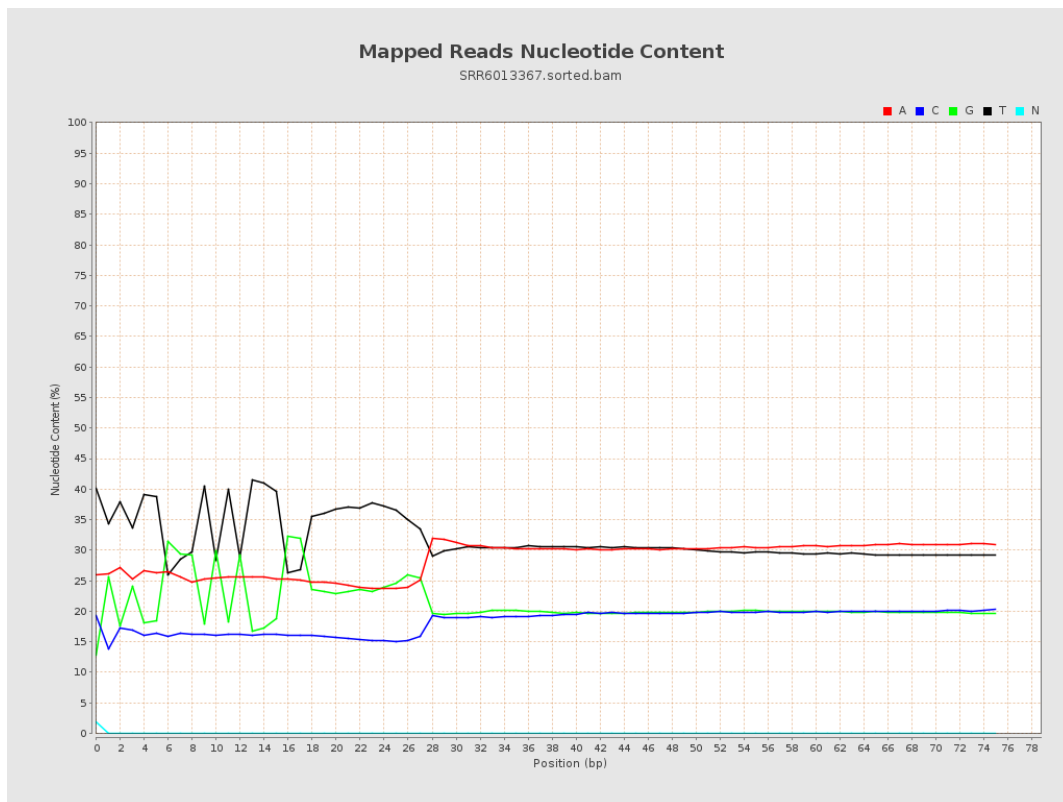
6. Results : Genome Fraction Coverage



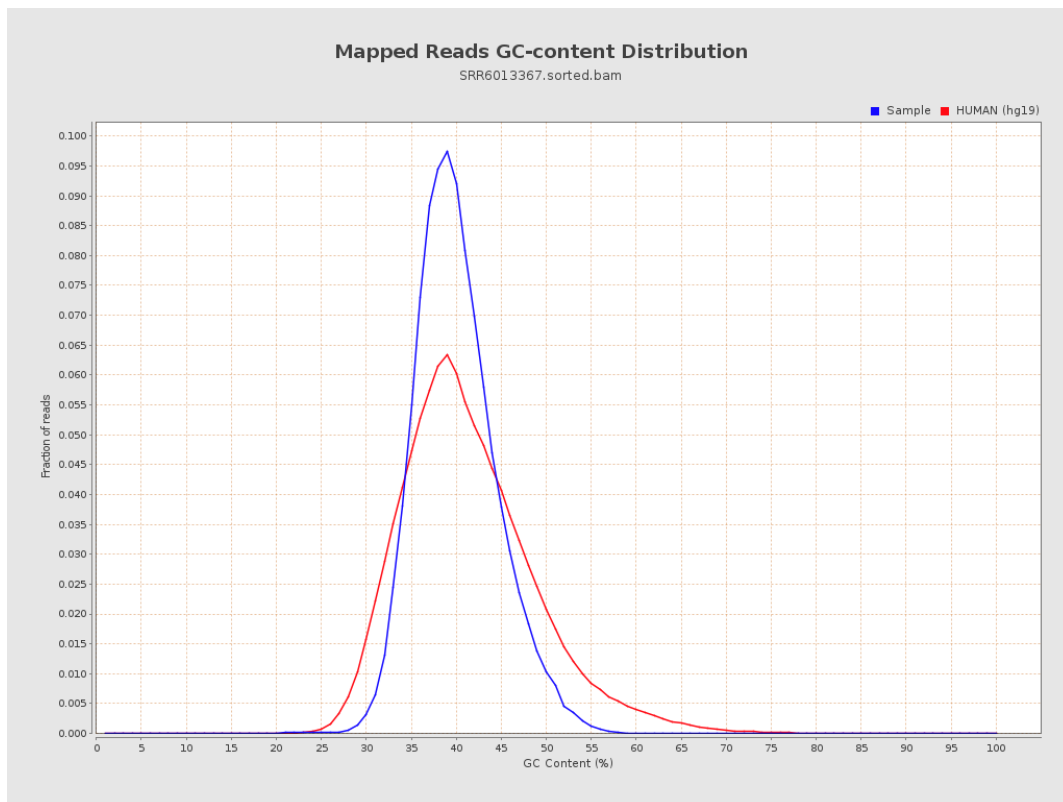
7. Results : Duplication Rate Histogram



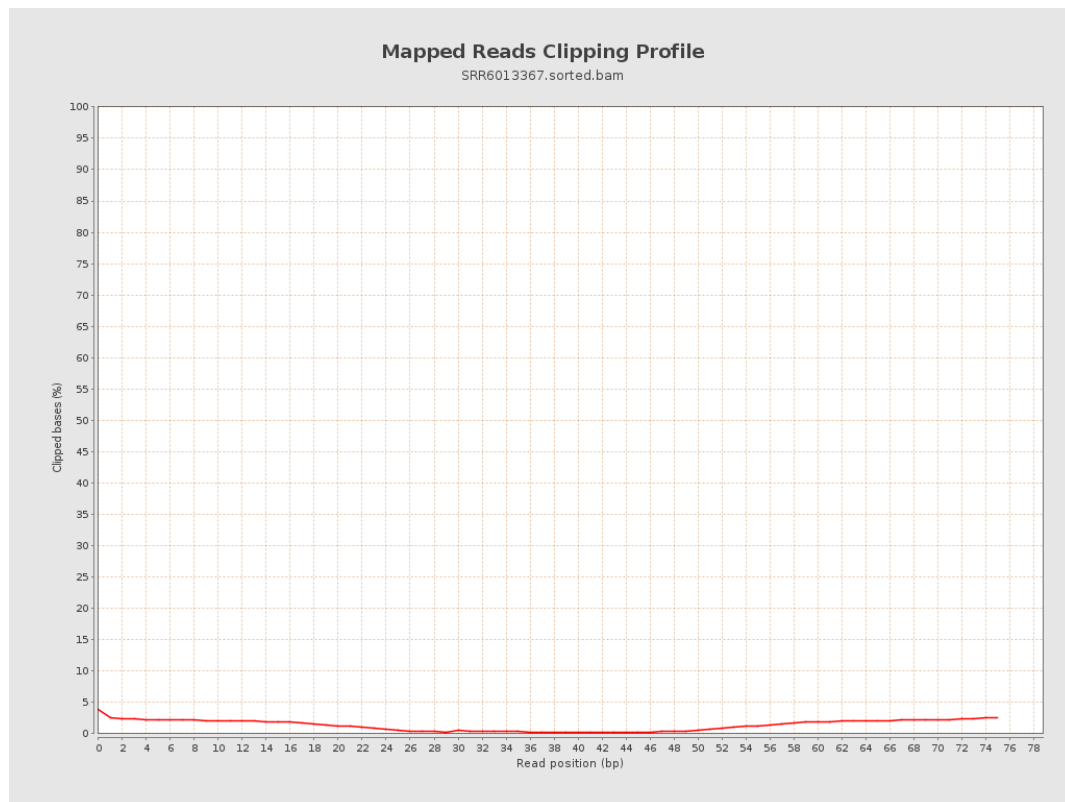
8. Results : Mapped Reads Nucleotide Content



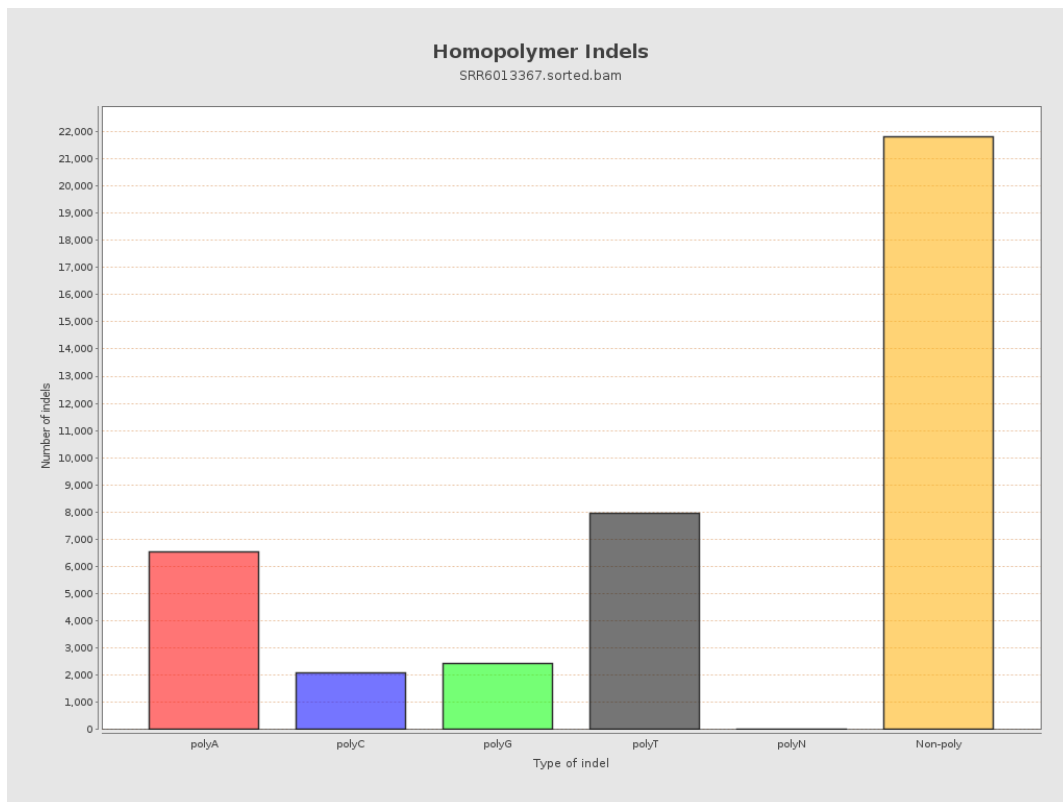
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

