

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 20:00:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230371.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_SRR6230371 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230371.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 20:00:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230371.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,144,818
Mapped reads	4,882,623 / 94.9%
Unmapped reads	262,195 / 5.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	37,287 / 0.72%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	222,387 / 4.32%
Duplication rate	3.14%
Clipped reads	1,308,490 / 25.43%

2.2. ACGT Content

Number/percentage of A's	103,291,342 / 29.58%
Number/percentage of C's	70,568,055 / 20.21%
Number/percentage of T's	102,407,358 / 29.33%
Number/percentage of G's	72,725,495 / 20.83%
Number/percentage of N's	202,509 / 0.06%
GC Percentage	41.04%

2.3. Coverage

Mean	0.1129

Standard Deviation	0.9043
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2.4. Mapping Quality

Mean Mapping Quality	47.09
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2.5. Mismatches and indels

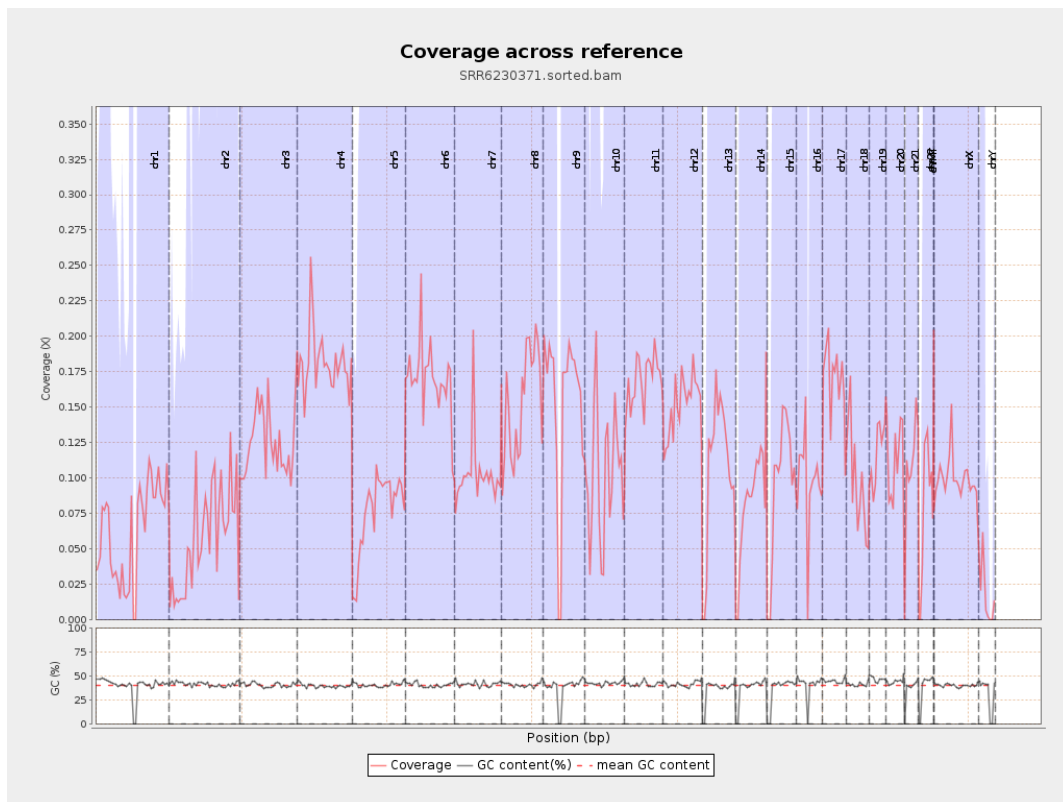
General error rate	0.91%
Mismatches	3,123,817
Insertions	31,824
Mapped reads with at least one insertion	0.65%
Deletions	101,501
Mapped reads with at least one deletion	2.05%
Homopolymer indels	45.8%

2.6. Chromosome stats

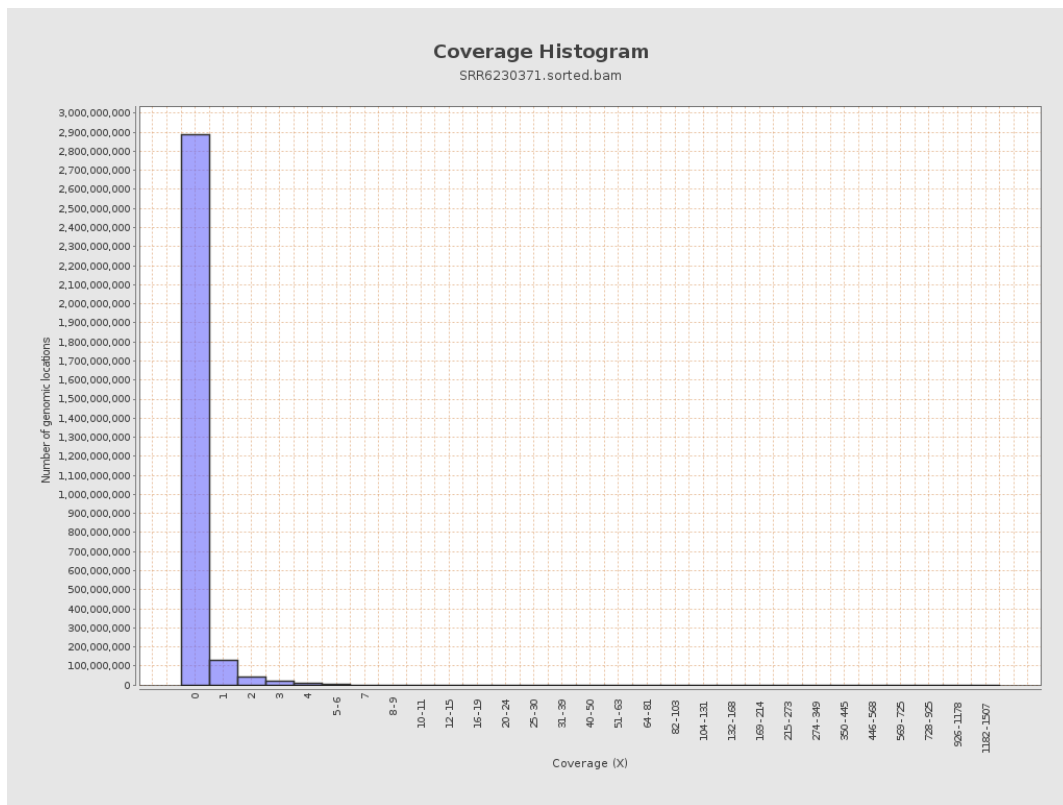
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15547779	0.0624	1.1603
chr2	243199373	14105985	0.058	0.8497
chr3	198022430	24582249	0.1241	0.5371
chr4	191154276	34500248	0.1805	0.7997
chr5	180915260	14001733	0.0774	0.4336
chr6	171115067	28992285	0.1694	0.9037
chr7	159138663	16380602	0.1029	1.4854

chr8	146364022	22434945	0.1533	0.8935
chr9	141213431	21615947	0.1531	1.0386
chr10	135534747	13677630	0.1009	1.0342
chr11	135006516	22553474	0.1671	1.1755
chr12	133851895	20294479	0.1516	0.6232
chr13	115169878	12339215	0.1071	0.4958
chr14	107349540	8689067	0.0809	0.5472
chr15	102531392	9864890	0.0962	0.4693
chr16	90354753	8803242	0.0974	0.7188
chr17	81195210	13762105	0.1695	0.8148
chr18	78077248	7630279	0.0977	1.9807
chr19	59128983	6981422	0.1181	0.8621
chr20	63025520	6989185	0.1109	0.5594
chr21	48129895	5227442	0.1086	0.6869
chr22	51304566	3971347	0.0774	0.4258
chrMT	16571	3390	0.2046	0.5693
chrX	155270560	15427460	0.0994	0.5862
chrY	59373566	994738	0.0168	0.5689

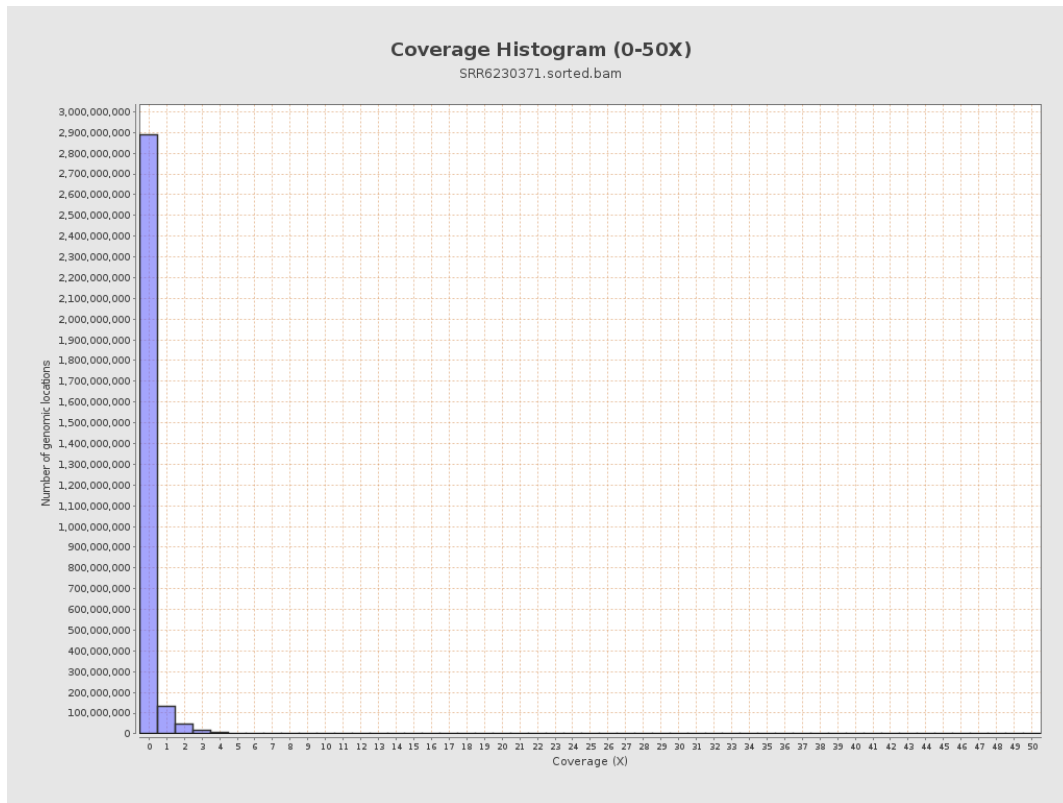
3. Results : Coverage across reference



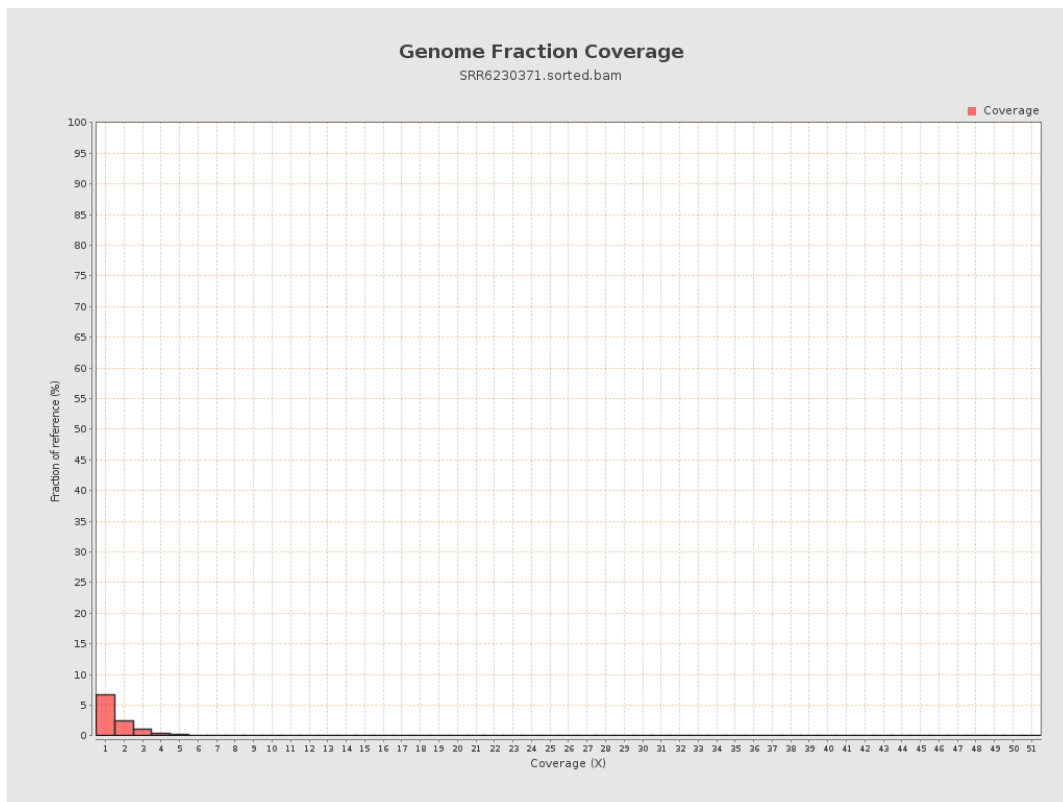
4. Results : Coverage Histogram



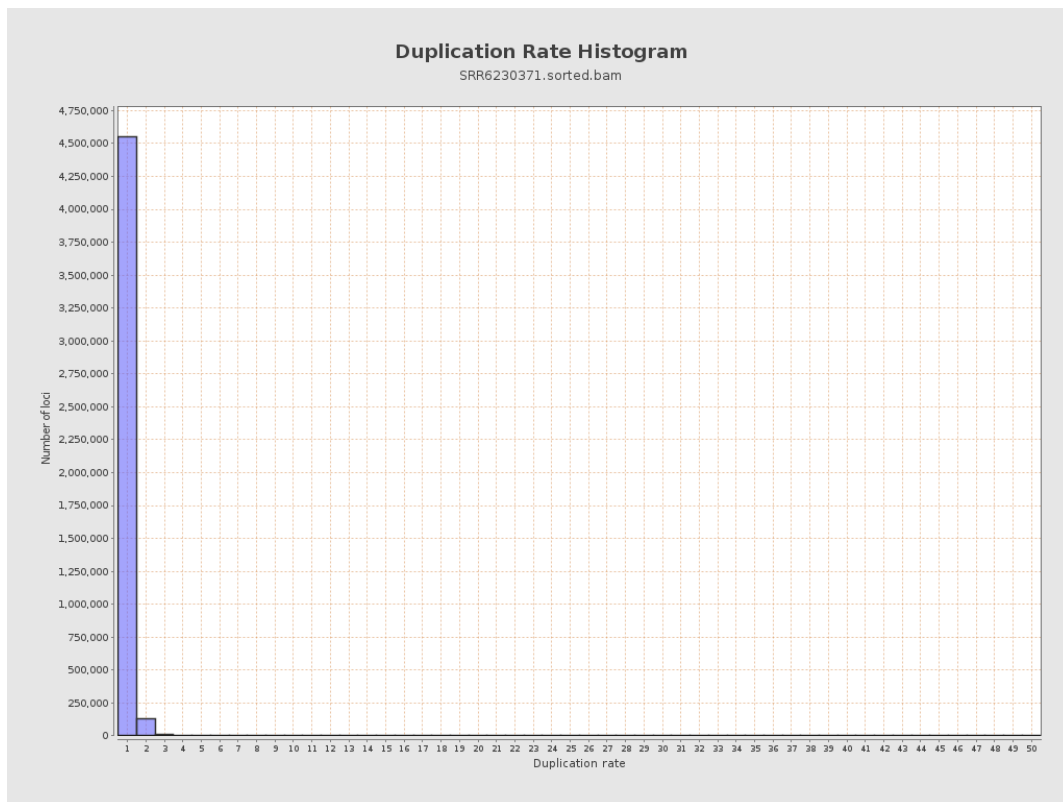
5. Results : Coverage Histogram (0-50X)



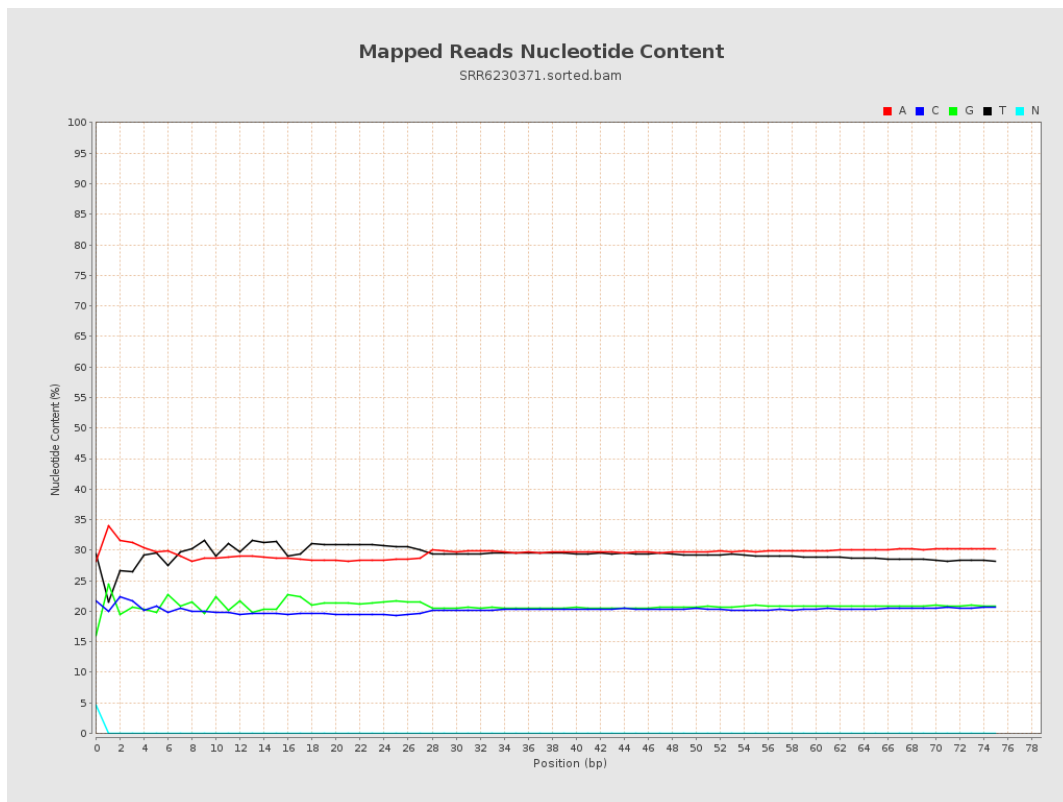
6. Results : Genome Fraction Coverage



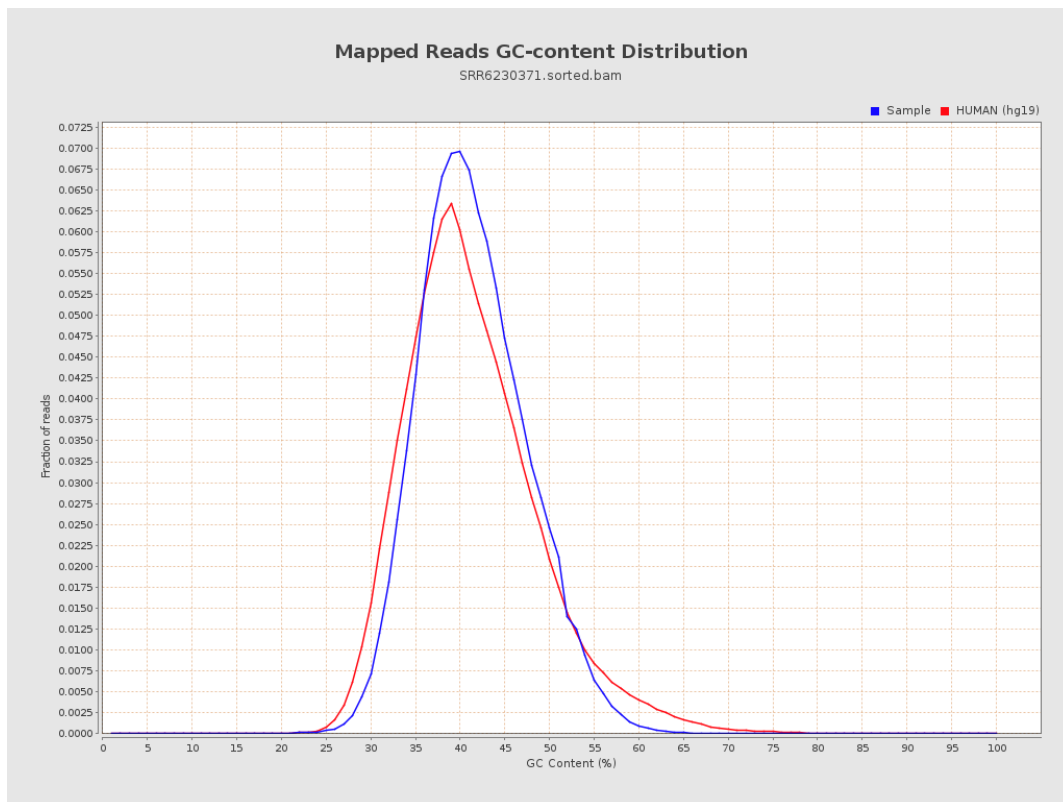
7. Results : Duplication Rate Histogram



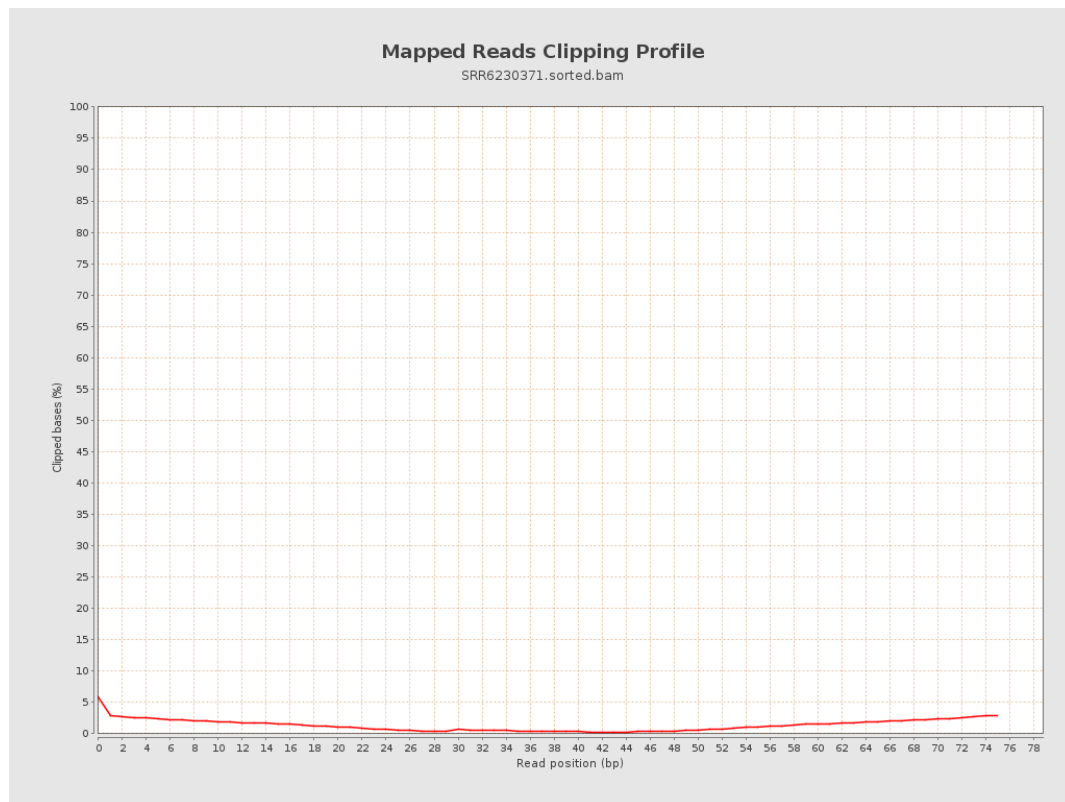
8. Results : Mapped Reads Nucleotide Content



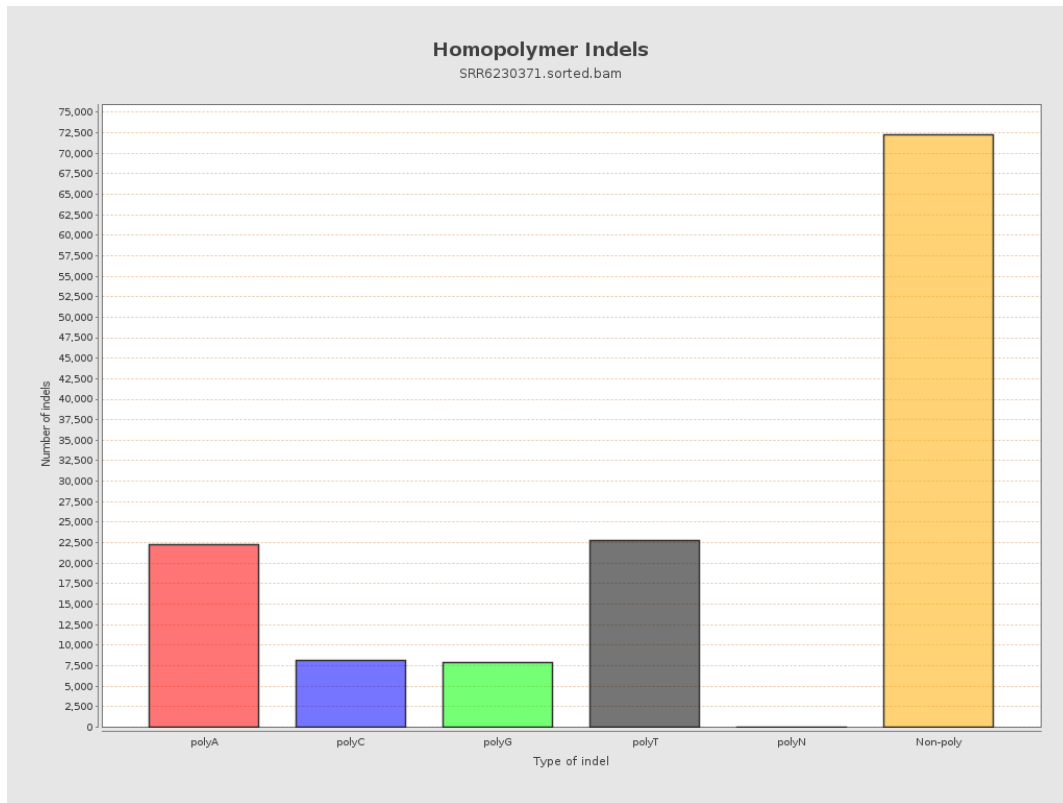
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

