

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 21:34:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230399.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_SRR6230399 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230399.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 21:34:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230399.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	377,856
Mapped reads	348,944 / 92.35%
Unmapped reads	28,912 / 7.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,833 / 0.49%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	7,893 / 2.09%
Duplication rate	1.98%
Clipped reads	103,823 / 27.48%

2.2. ACGT Content

Number/percentage of A's	7,323,455 / 29.59%
Number/percentage of C's	4,988,584 / 20.16%
Number/percentage of T's	7,372,084 / 29.79%
Number/percentage of G's	5,047,216 / 20.4%
Number/percentage of N's	14,881 / 0.06%
GC Percentage	40.55%

2.3. Coverage

Mean	0.008

Standard Deviation	0.1247
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2.4. Mapping Quality

Mean Mapping Quality	47.75
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2.5. Mismatches and indels

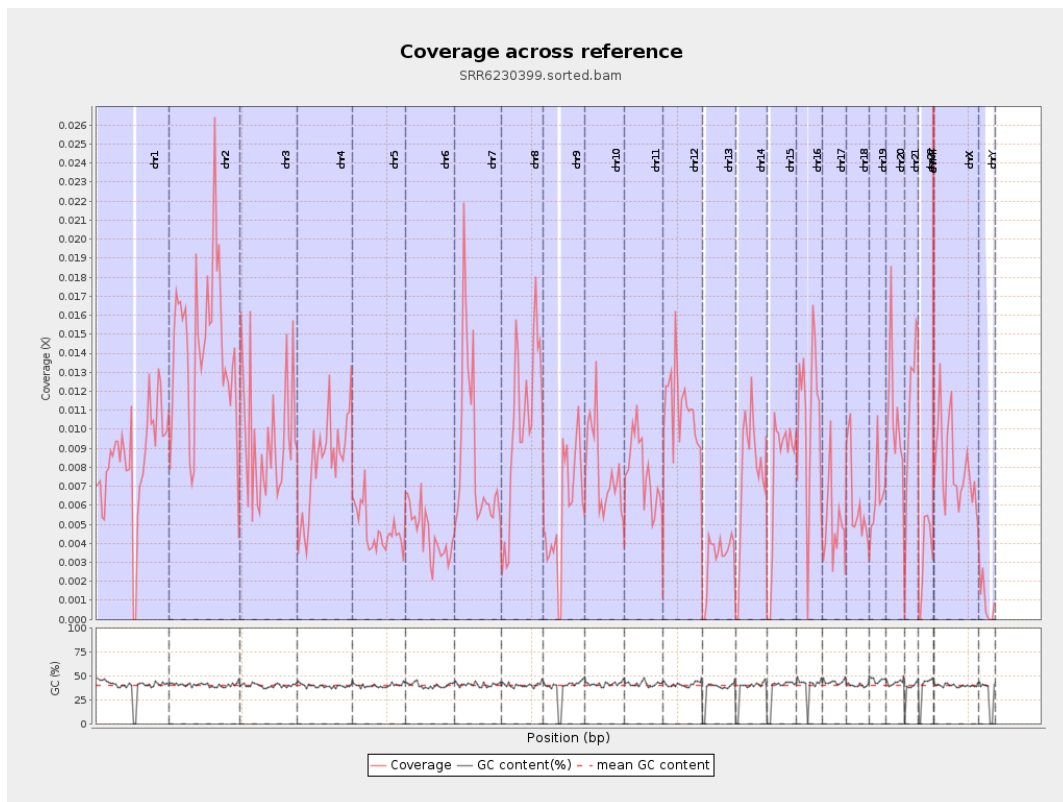
General error rate	0.97%
Mismatches	236,825
Insertions	1,943
Mapped reads with at least one insertion	0.55%
Deletions	8,440
Mapped reads with at least one deletion	2.39%
Homopolymer indels	49.06%

2.6. Chromosome stats

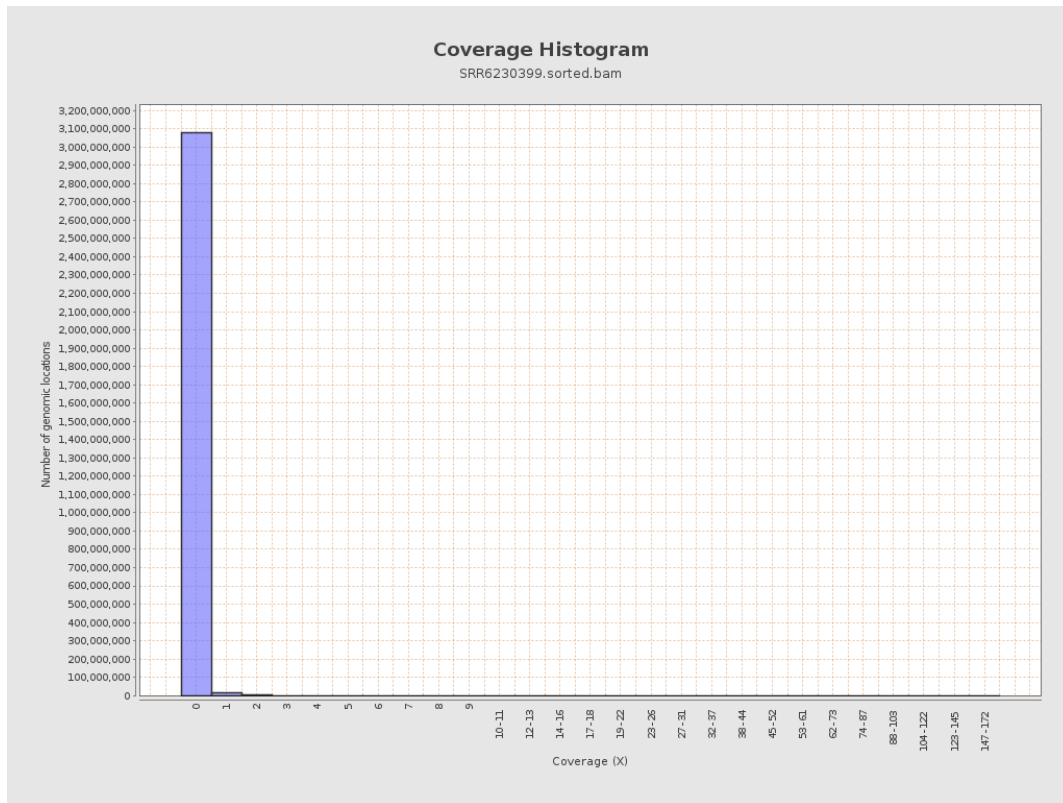
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	2085851	0.0084	0.168
chr2	243199373	3462059	0.0142	0.1643
chr3	198022430	1858045	0.0094	0.1191
chr4	191154276	1567884	0.0082	0.1139
chr5	180915260	852781	0.0047	0.0855
chr6	171115067	768740	0.0045	0.083
chr7	159138663	1359862	0.0085	0.148

chr8	146364022	1508879	0.0103	0.1464
chr9	141213431	828697	0.0059	0.1053
chr10	135534747	1062241	0.0078	0.1258
chr11	135006516	1035493	0.0077	0.1251
chr12	133851895	1481746	0.0111	0.133
chr13	115169878	368625	0.0032	0.0697
chr14	107349540	816429	0.0076	0.1098
chr15	102531392	793239	0.0077	0.1092
chr16	90354753	954000	0.0106	0.1275
chr17	81195210	403908	0.005	0.0951
chr18	78077248	492754	0.0063	0.1393
chr19	59128983	383319	0.0065	0.1211
chr20	63025520	669185	0.0106	0.1272
chr21	48129895	532711	0.0111	0.133
chr22	51304566	173908	0.0034	0.0716
chrMT	16571	1614	0.0974	0.3288
chrX	155270560	1242523	0.008	0.113
chrY	59373566	56036	0.0009	0.0389

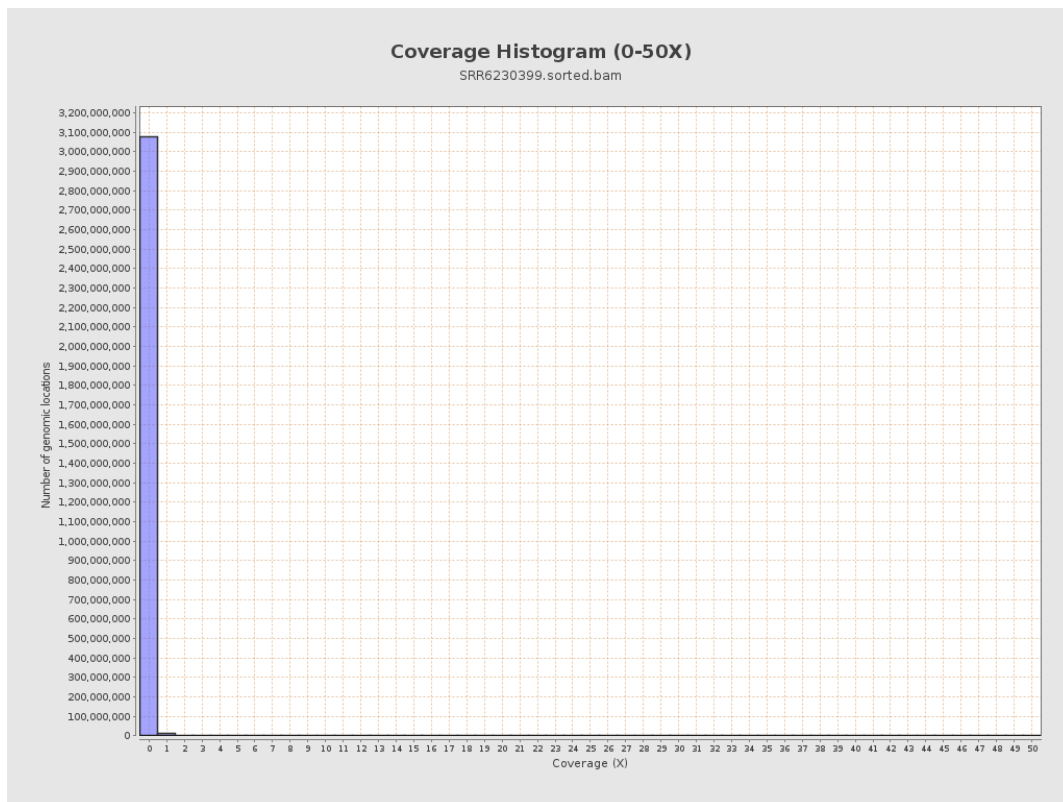
3. Results : Coverage across reference



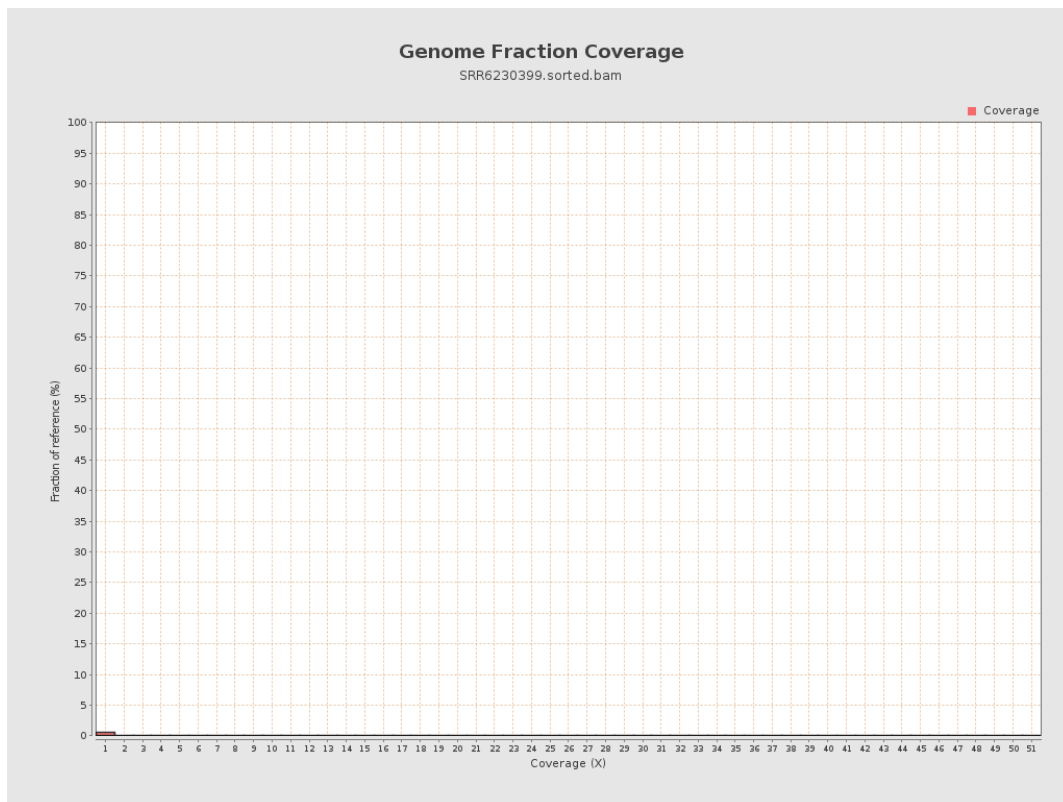
4. Results : Coverage Histogram



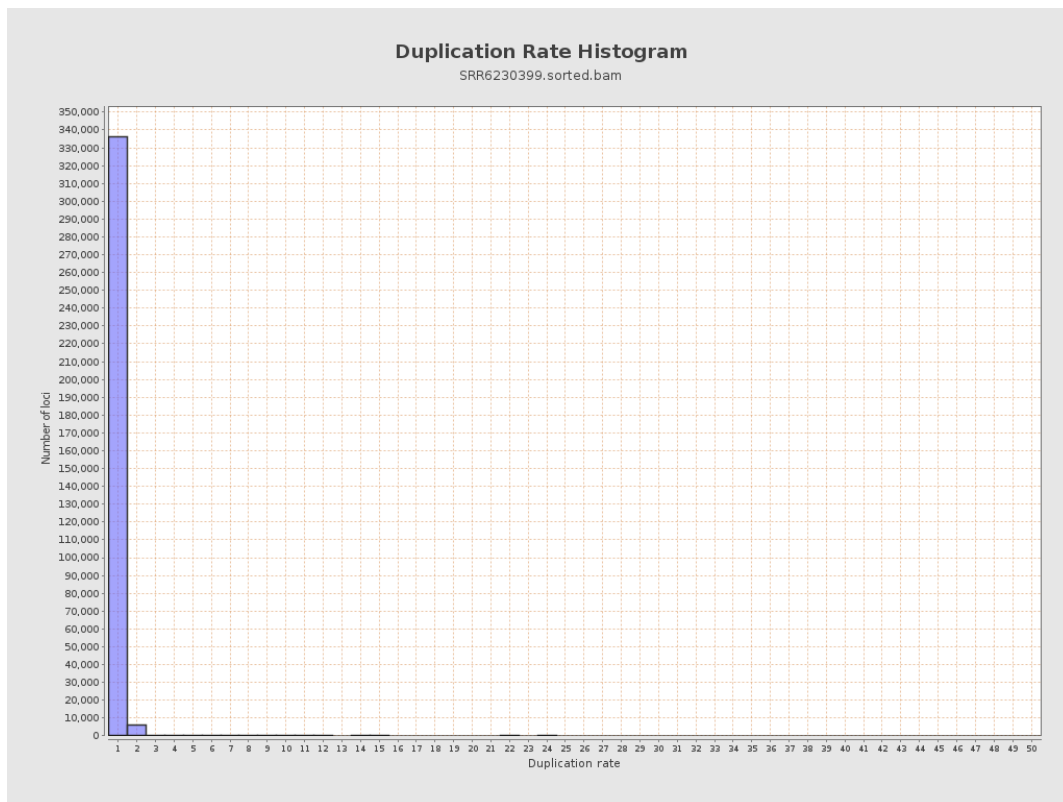
5. Results : Coverage Histogram (0-50X)



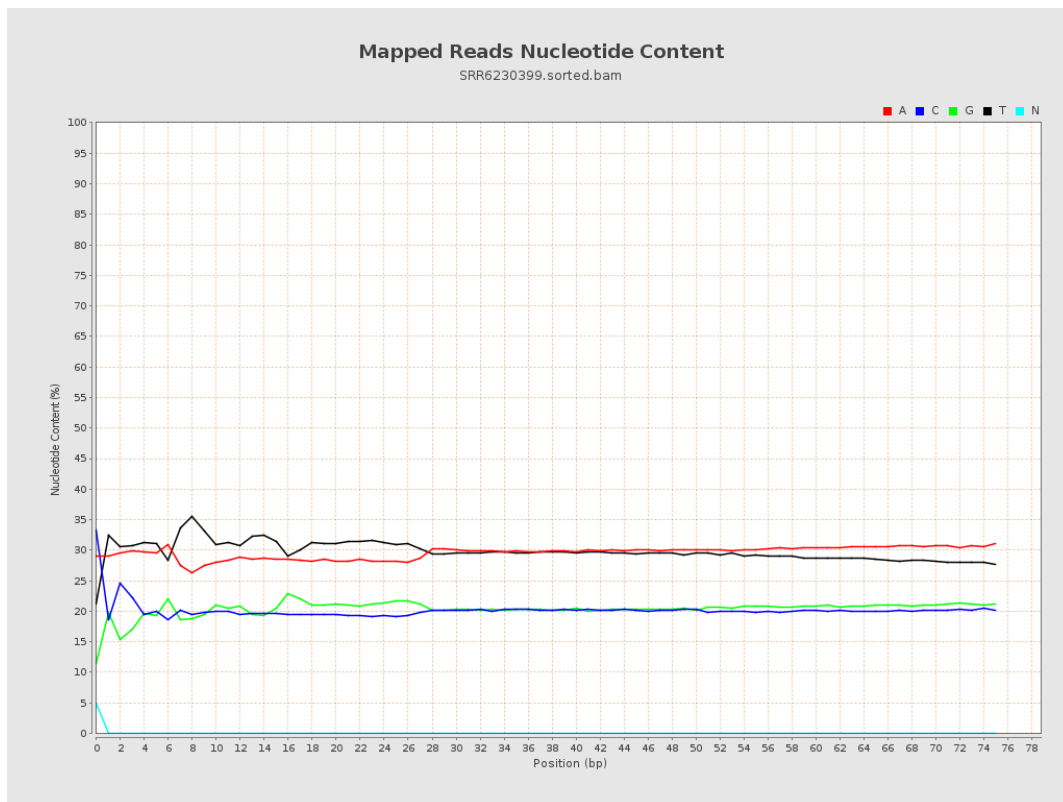
6. Results : Genome Fraction Coverage



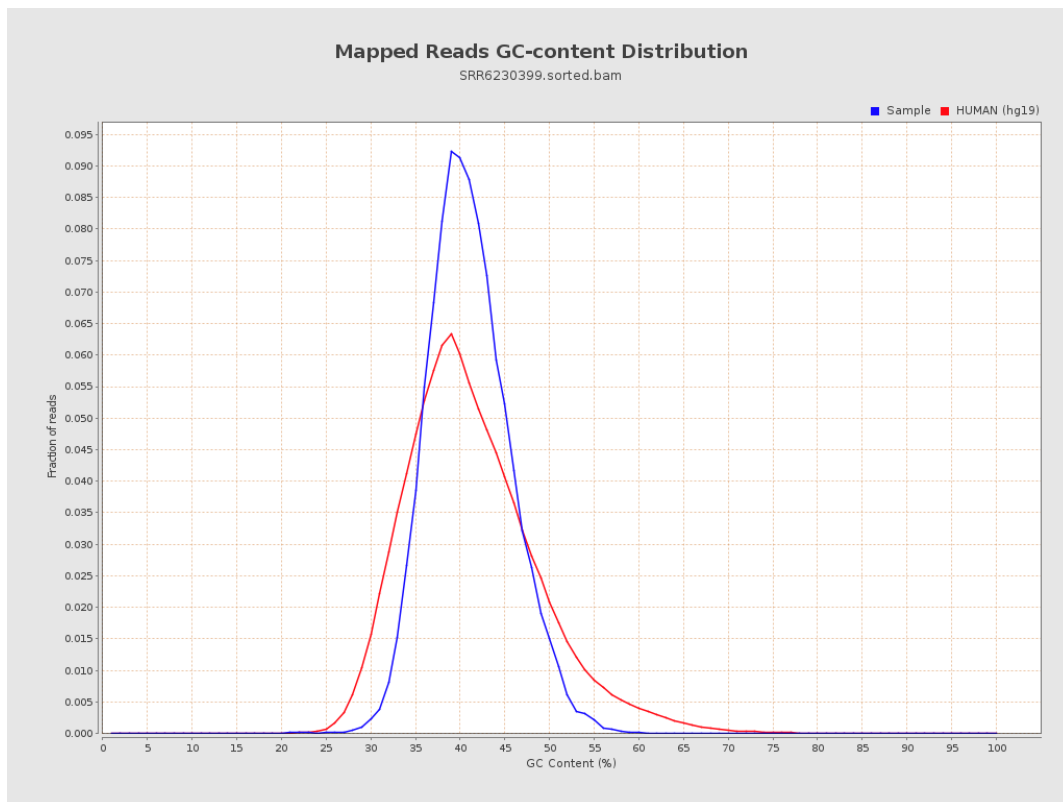
7. Results : Duplication Rate Histogram



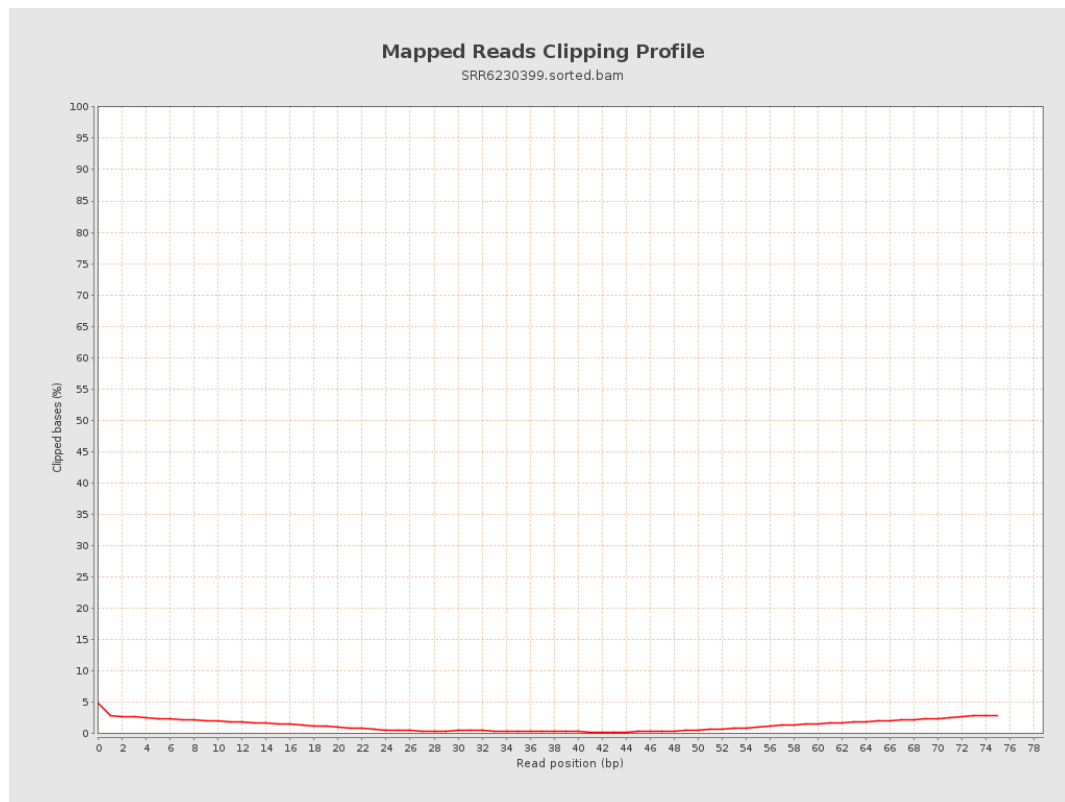
8. Results : Mapped Reads Nucleotide Content



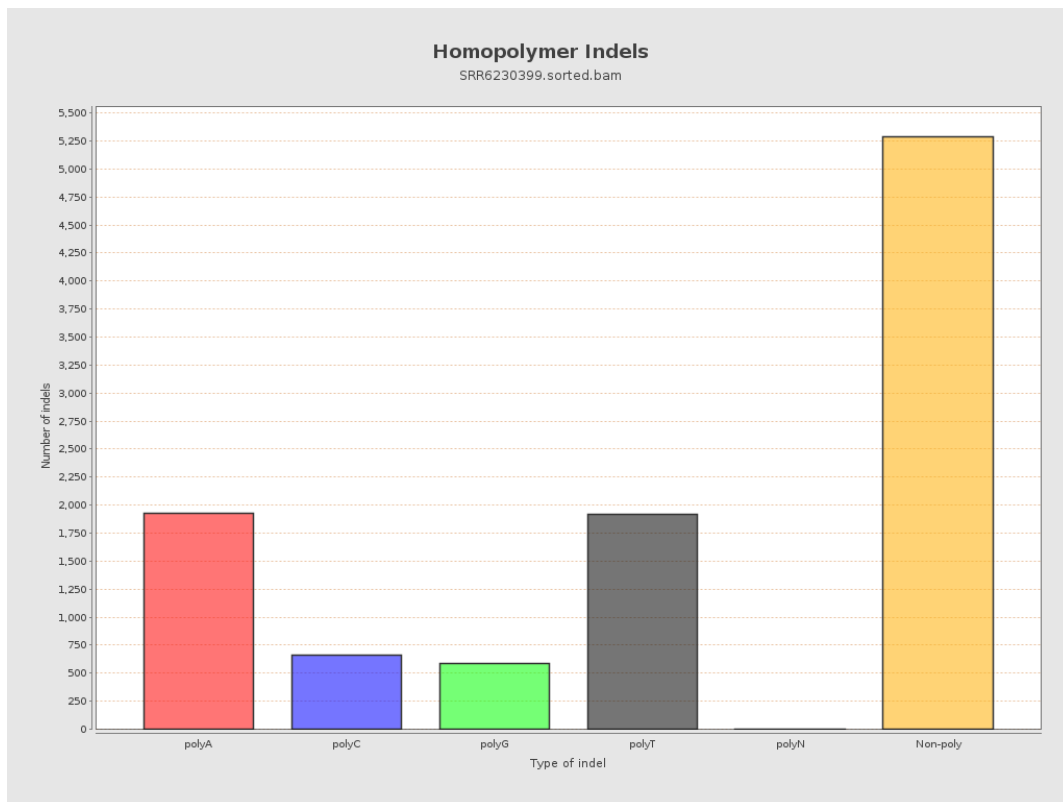
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

