

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 10:51:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234022.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_SRR6234022 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234022.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 10:51:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234022.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,145,935
Mapped reads	978,915 / 85.43%
Unmapped reads	167,020 / 14.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,076 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	25,952 / 2.26%
Duplication rate	2.03%
Clipped reads	459,838 / 40.13%

2.2. ACGT Content

Number/percentage of A's	18,082,836 / 28.17%
Number/percentage of C's	11,058,945 / 17.23%
Number/percentage of T's	20,915,725 / 32.58%
Number/percentage of G's	14,129,850 / 22.01%
Number/percentage of N's	11,853 / 0.02%
GC Percentage	39.24%

2.3. Coverage

Mean	0.0207

Standard Deviation	0.2257
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2.4. Mapping Quality

Mean Mapping Quality	46.41
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2.5. Mismatches and indels

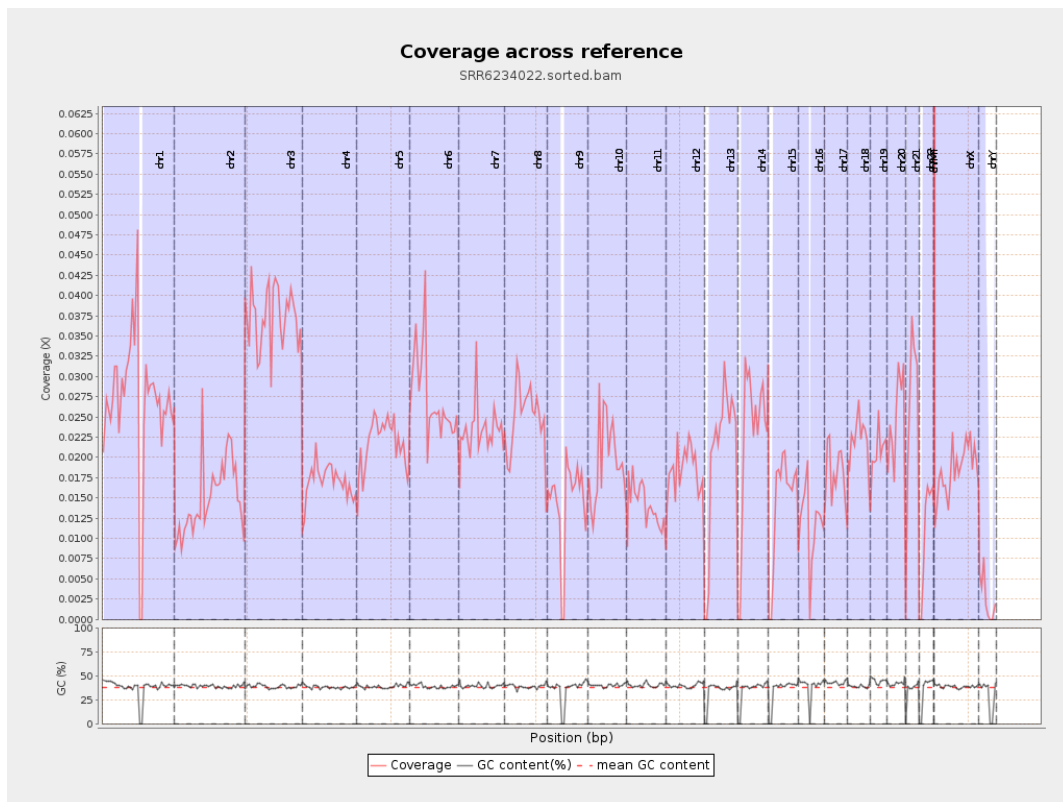
General error rate	0.79%
Mismatches	498,473
Insertions	4,716
Mapped reads with at least one insertion	0.48%
Deletions	18,121
Mapped reads with at least one deletion	1.83%
Homopolymer indels	47.15%

2.6. Chromosome stats

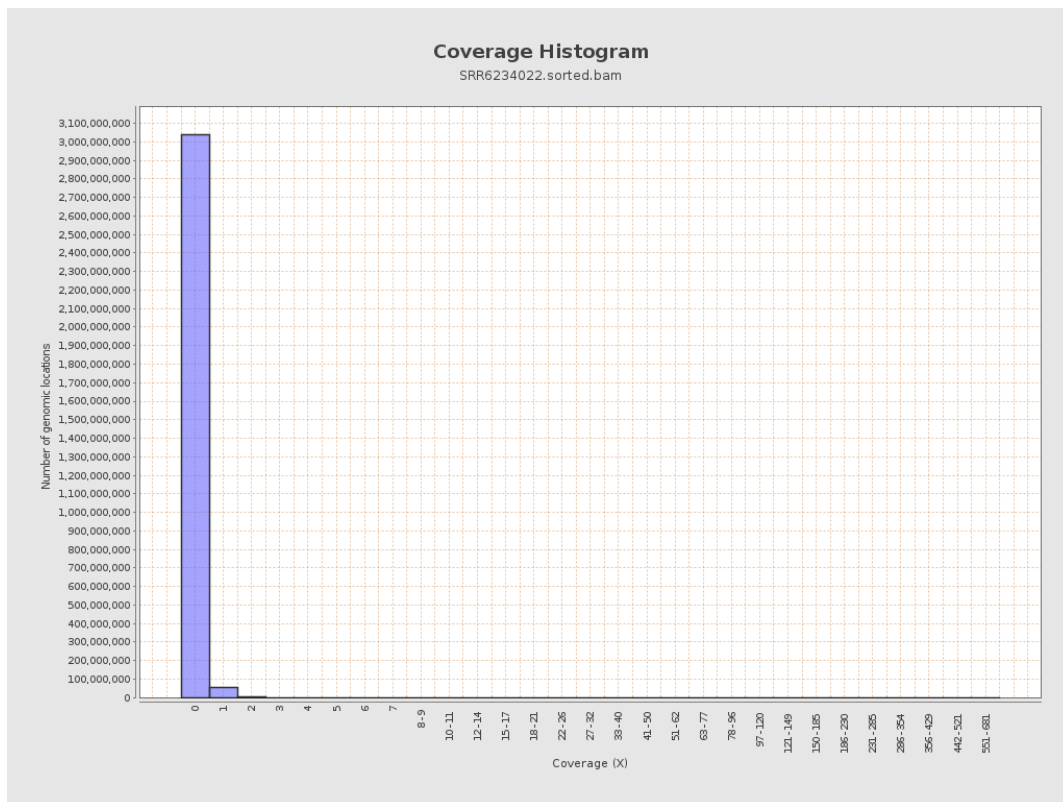
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6707480	0.0269	0.414
chr2	243199373	3666700	0.0151	0.2078
chr3	198022430	7387764	0.0373	0.2041
chr4	191154276	3245162	0.017	0.1405
chr5	180915260	3950508	0.0218	0.1566
chr6	171115067	4659201	0.0272	0.1981
chr7	159138663	3711341	0.0233	0.2462

chr8	146364022	3644850	0.0249	0.4436
chr9	141213431	2048611	0.0145	0.1629
chr10	135534747	2632198	0.0194	0.1929
chr11	135006516	1919562	0.0142	0.1454
chr12	133851895	2465263	0.0184	0.1449
chr13	115169878	2372369	0.0206	0.1515
chr14	107349540	2421158	0.0226	0.1618
chr15	102531392	1489504	0.0145	0.1287
chr16	90354753	1048742	0.0116	0.1234
chr17	81195210	1457245	0.0179	0.1497
chr18	78077248	1740865	0.0223	0.2937
chr19	59128983	1228503	0.0208	0.244
chr20	63025520	1556085	0.0247	0.1692
chr21	48129895	1264712	0.0263	0.1749
chr22	51304566	556637	0.0108	0.1091
chrMT	16571	23607	1.4246	1.6099
chrX	155270560	2880287	0.0186	0.1502
chrY	59373566	152360	0.0026	0.0657

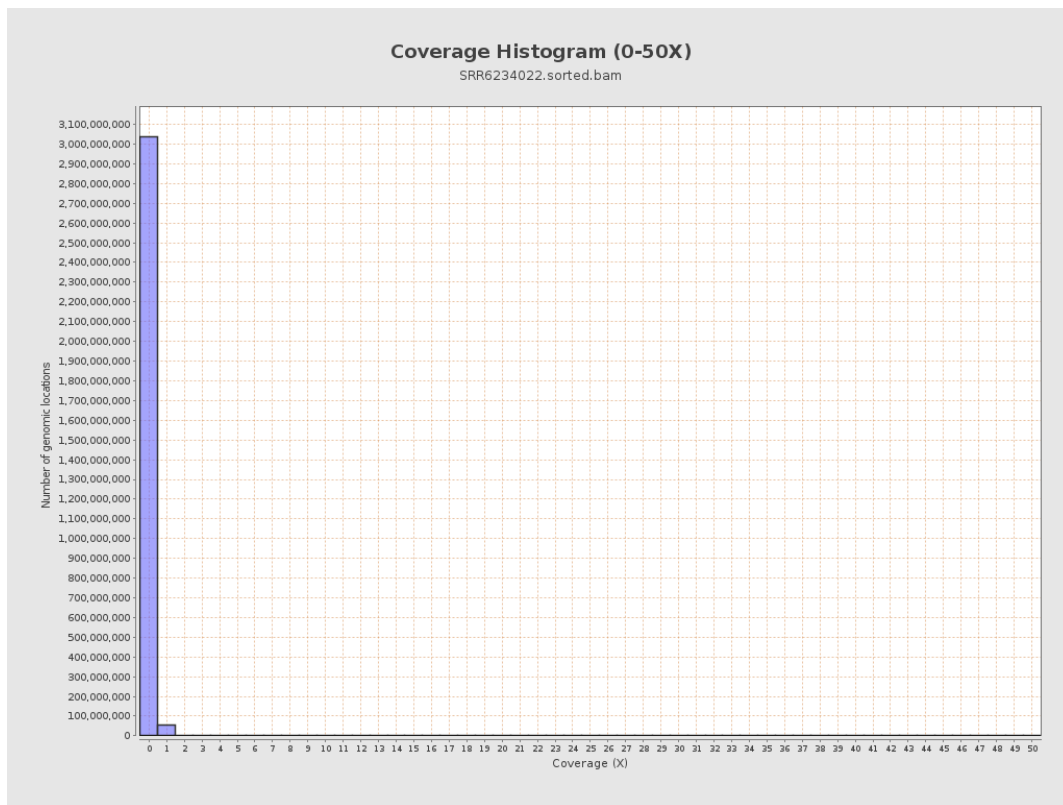
3. Results : Coverage across reference



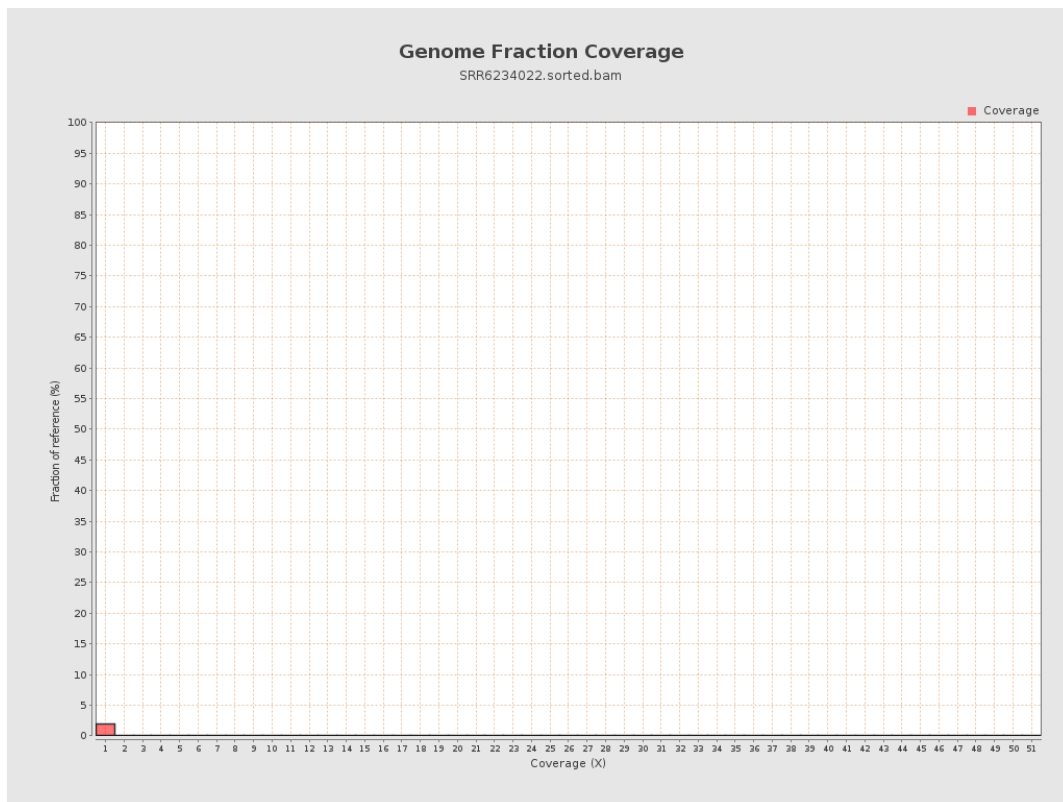
4. Results : Coverage Histogram



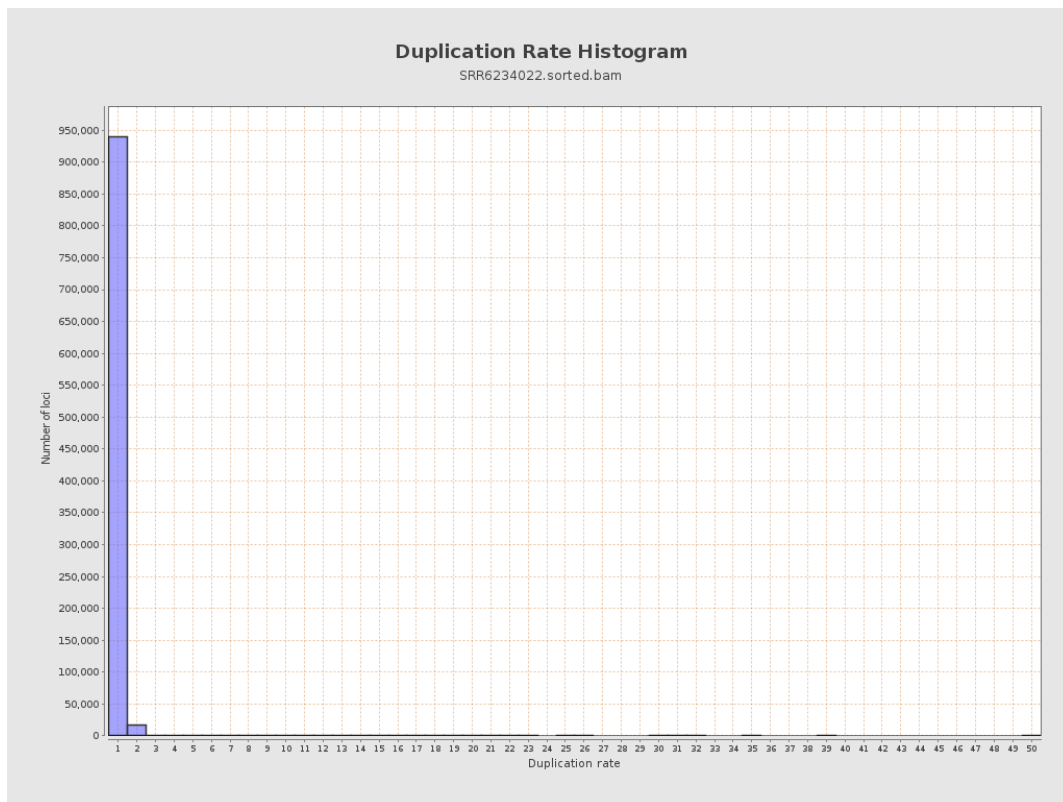
5. Results : Coverage Histogram (0-50X)



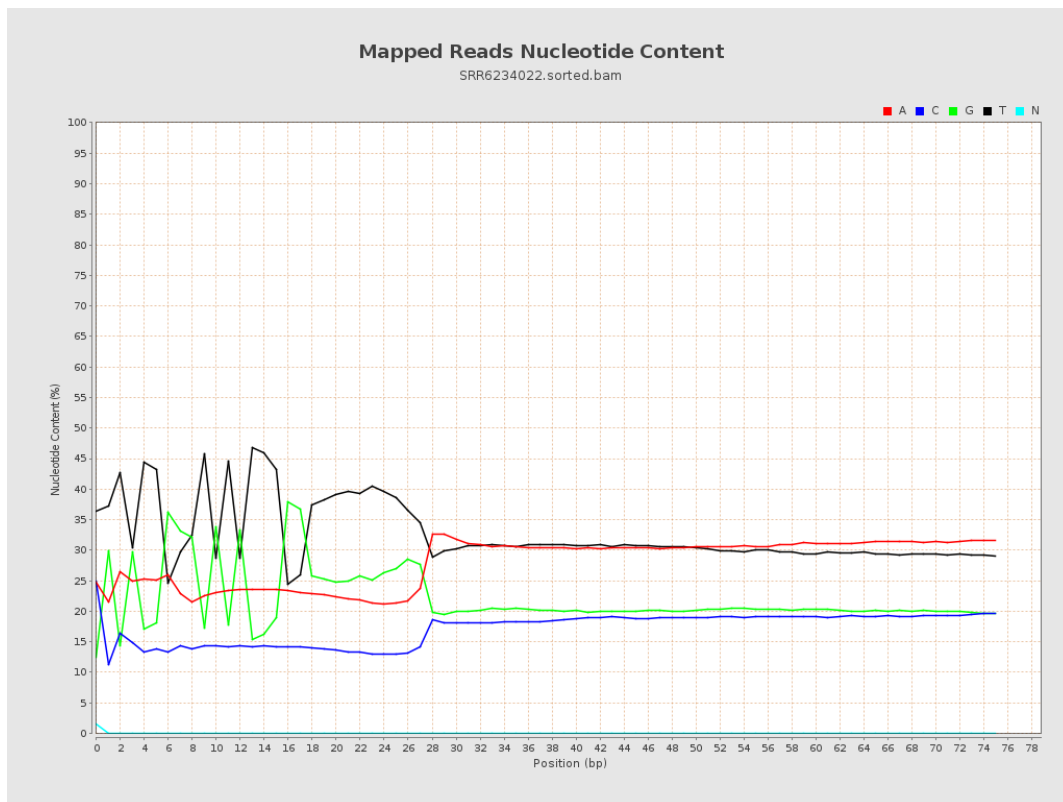
6. Results : Genome Fraction Coverage



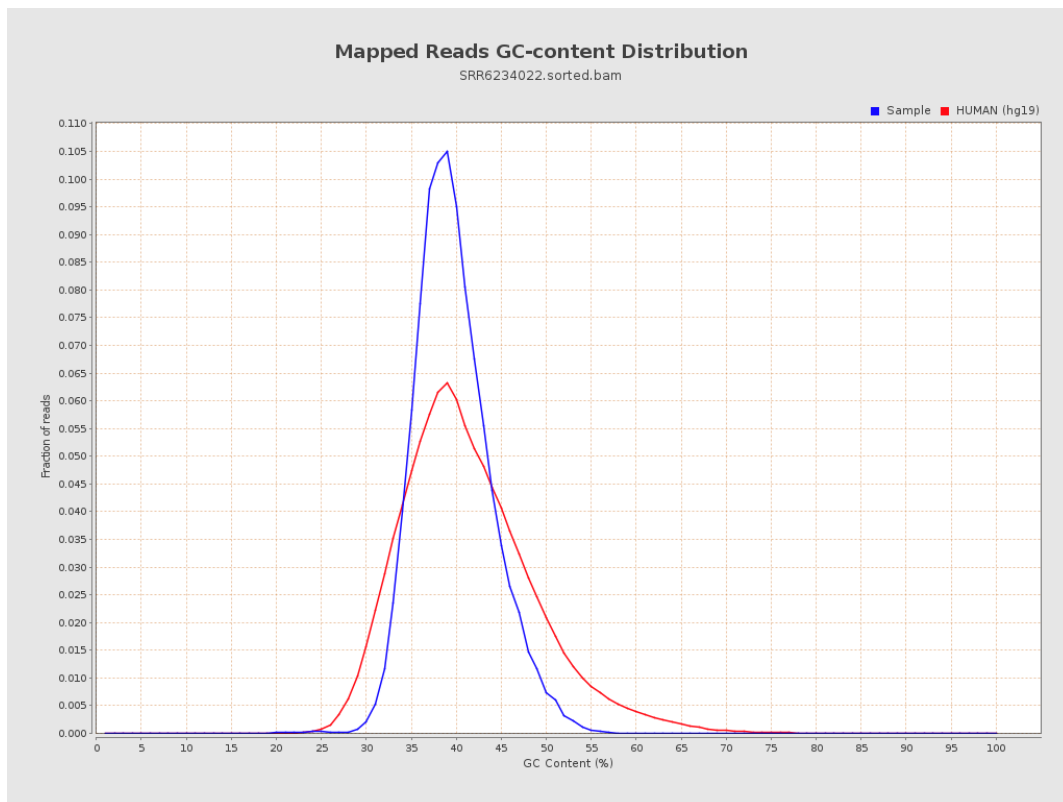
7. Results : Duplication Rate Histogram



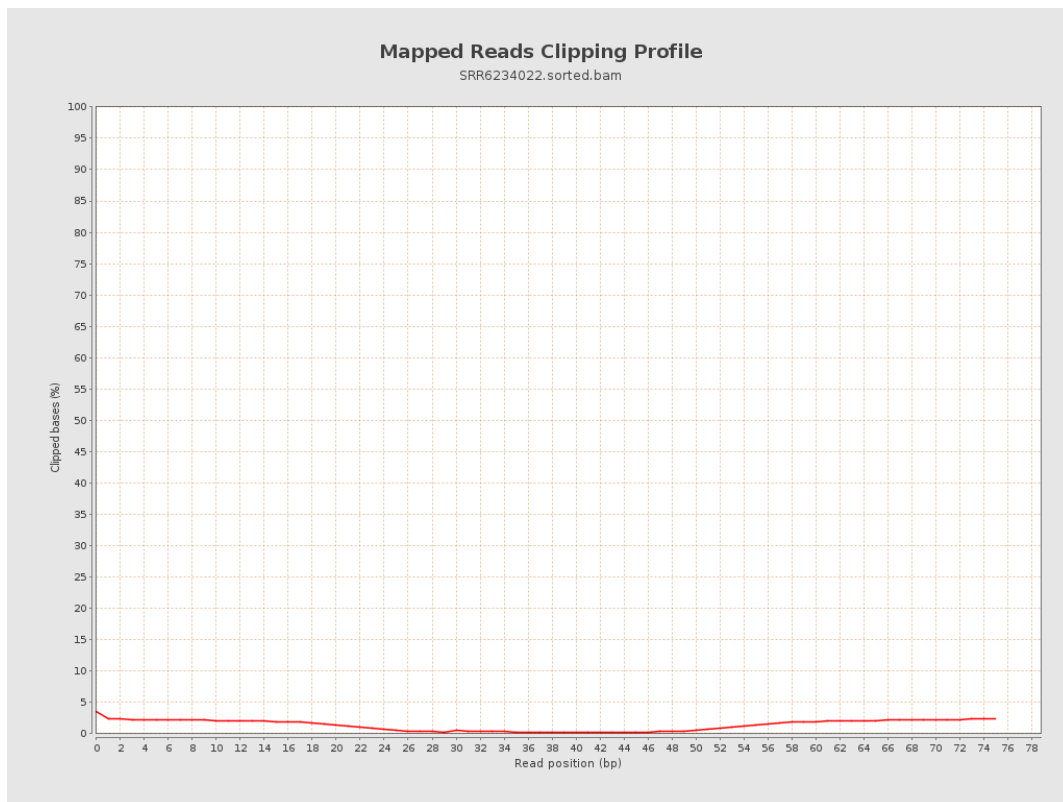
8. Results : Mapped Reads Nucleotide Content



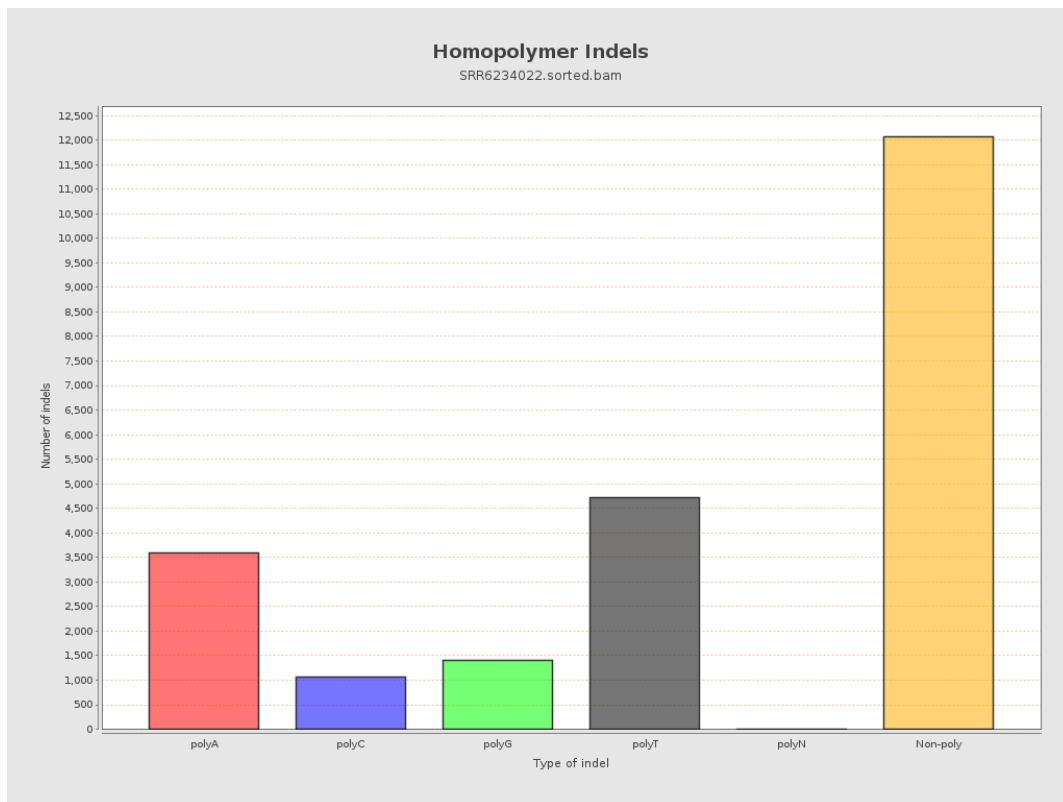
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

