

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 08:37:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472824.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_SRR3472824 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472824.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 08:37:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472824.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,230,947
Mapped reads	1,315,913 / 58.98%
Unmapped reads	915,034 / 41.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,529 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	128,085 / 5.74%
Duplication rate	7.25%
Clipped reads	864,665 / 38.76%

2.2. ACGT Content

Number/percentage of A's	21,621,175 / 26.81%
Number/percentage of C's	15,374,548 / 19.06%
Number/percentage of T's	24,649,788 / 30.56%
Number/percentage of G's	19,010,247 / 23.57%
Number/percentage of N's	1,811 / 0%
GC Percentage	42.63%

2.3. Coverage

Mean	0.0261

Standard Deviation	0.2743
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2.4. Mapping Quality

Mean Mapping Quality	43.38
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2.5. Mismatches and indels

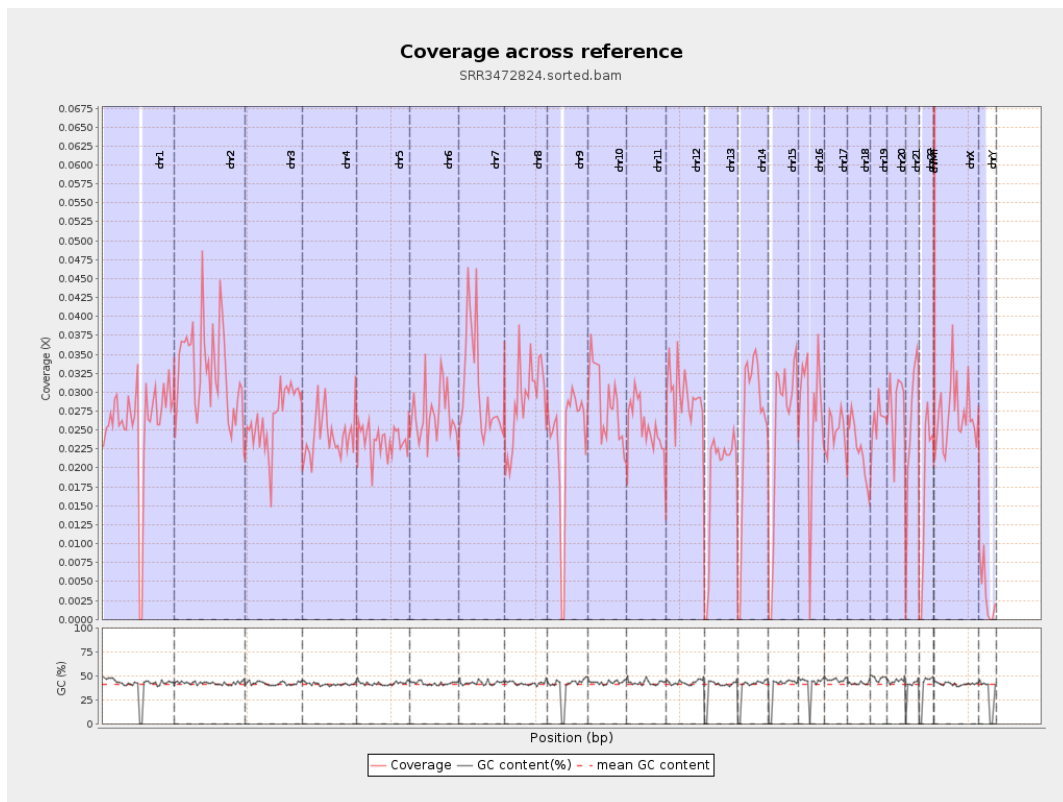
General error rate	0.99%
Mismatches	790,110
Insertions	5,749
Mapped reads with at least one insertion	0.43%
Deletions	24,798
Mapped reads with at least one deletion	1.86%
Homopolymer indels	47.67%

2.6. Chromosome stats

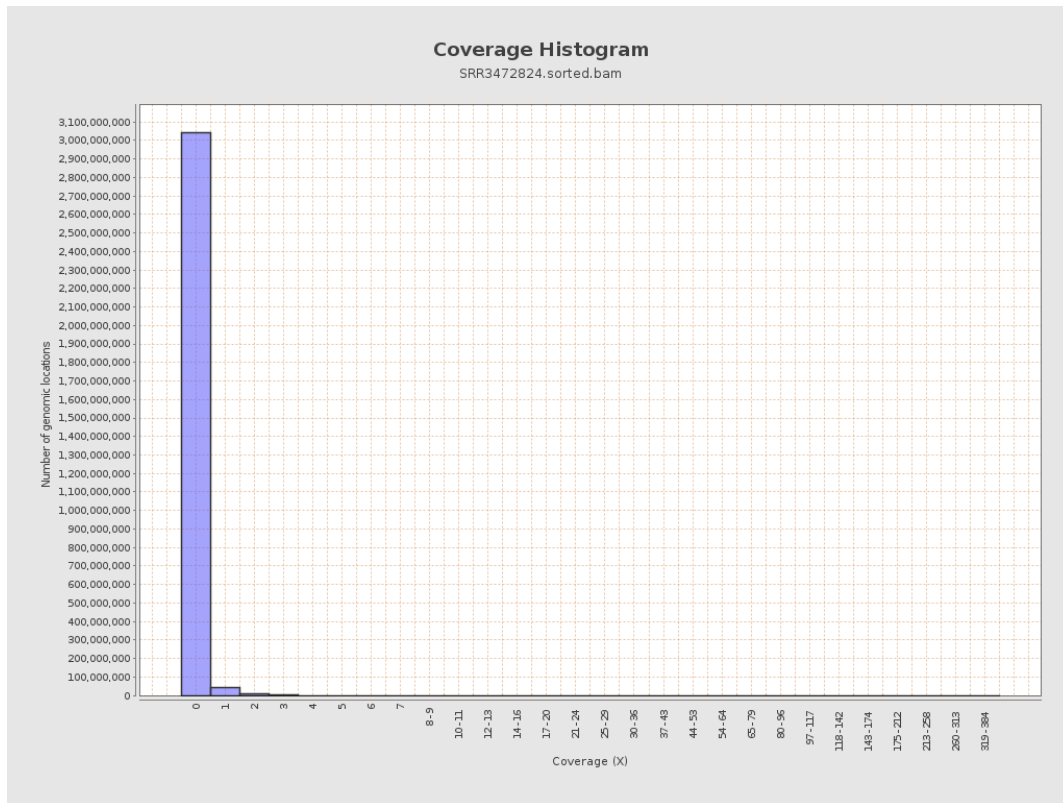
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6437826	0.0258	0.3402
chr2	243199373	8001765	0.0329	0.3163
chr3	198022430	5279634	0.0267	0.2319
chr4	191154276	4649925	0.0243	0.2263
chr5	180915260	4285603	0.0237	0.2249
chr6	171115067	4631949	0.0271	0.2648
chr7	159138663	4835736	0.0304	0.4077

chr8	146364022	4220627	0.0288	0.2766
chr9	141213431	3342447	0.0237	0.2685
chr10	135534747	3886315	0.0287	0.2691
chr11	135006516	3461793	0.0256	0.2701
chr12	133851895	3953192	0.0295	0.2448
chr13	115169878	2153048	0.0187	0.2056
chr14	107349540	2786789	0.026	0.2435
chr15	102531392	2572858	0.0251	0.2399
chr16	90354753	2423585	0.0268	0.2385
chr17	81195210	1993664	0.0246	0.2369
chr18	78077248	1752038	0.0224	0.3675
chr19	59128983	1548450	0.0262	0.2765
chr20	63025520	1776039	0.0282	0.2473
chr21	48129895	1254175	0.0261	0.2341
chr22	51304566	902288	0.0176	0.1907
chrMT	16571	147747	8.916	6.6828
chrX	155270560	4201308	0.0271	0.2519
chrY	59373566	202740	0.0034	0.0826

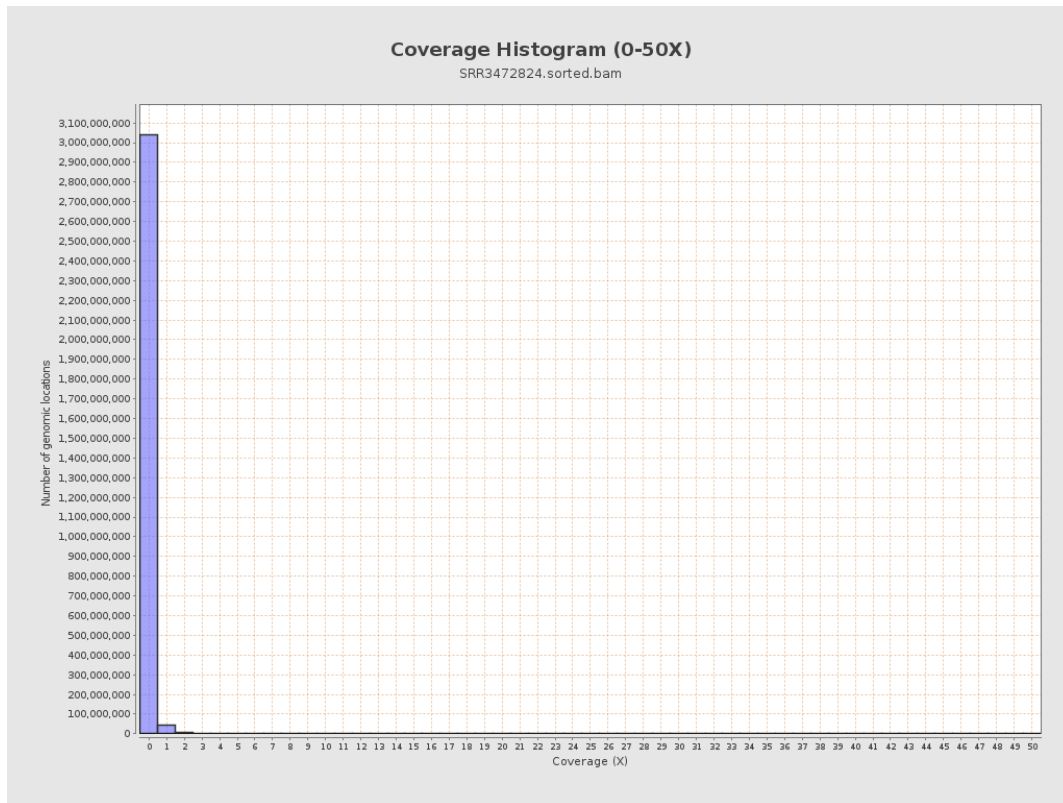
3. Results : Coverage across reference



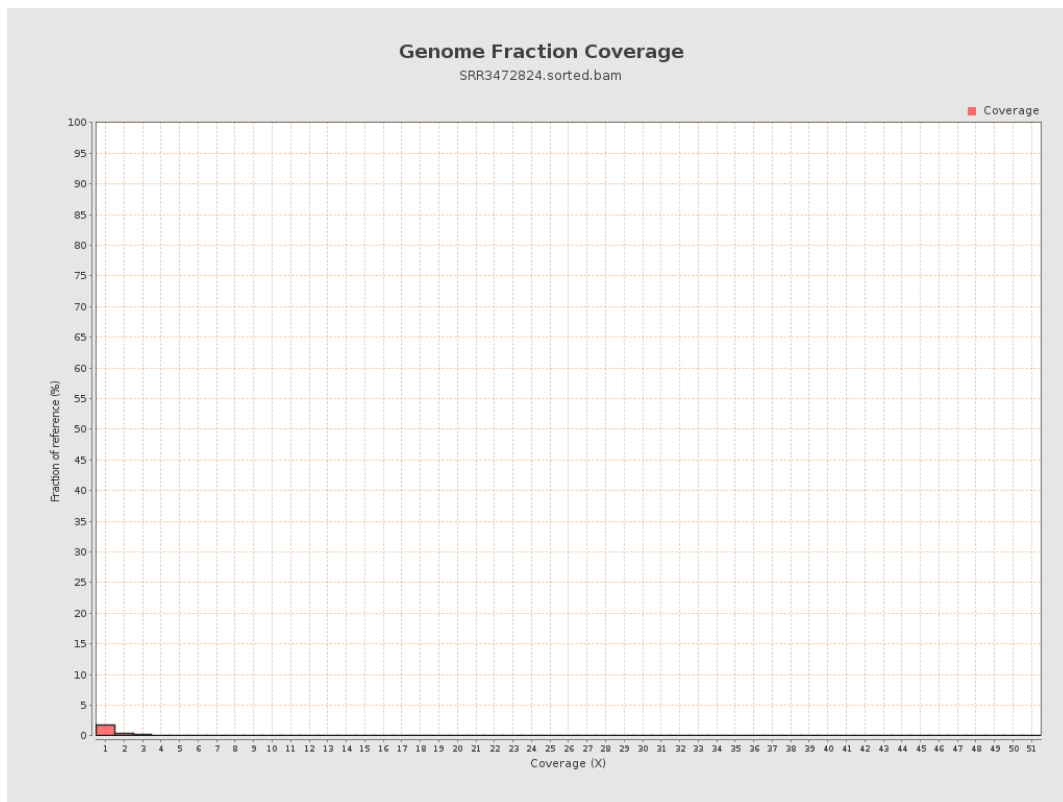
4. Results : Coverage Histogram



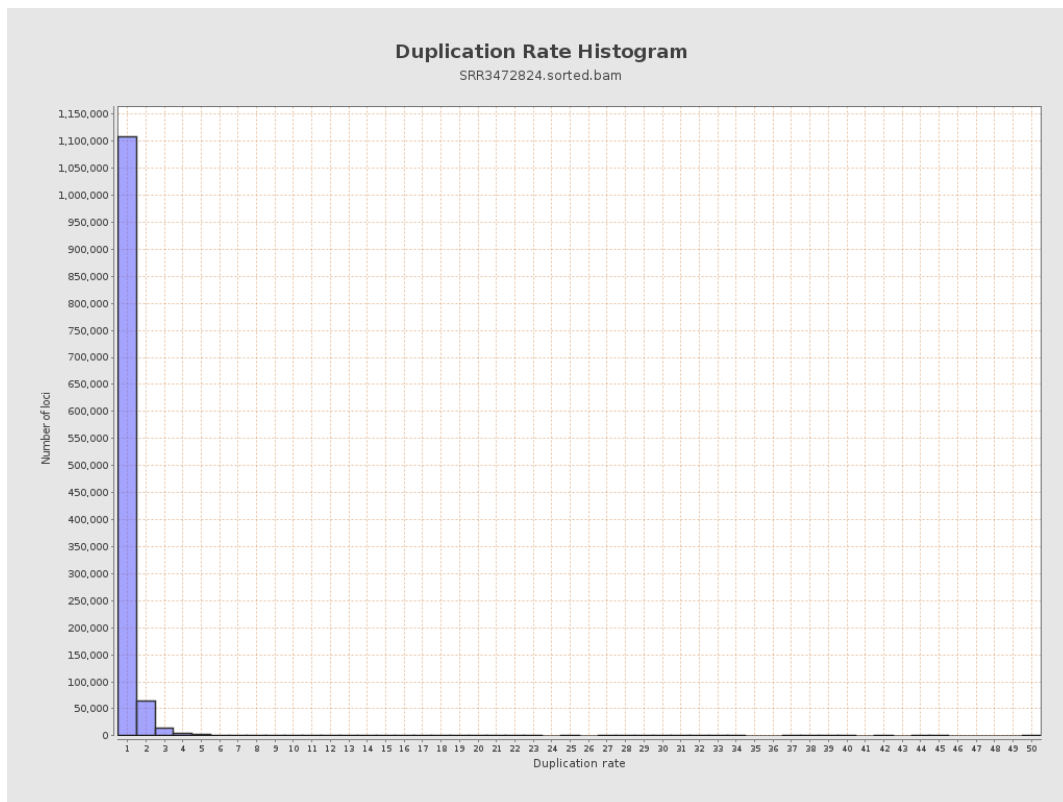
5. Results : Coverage Histogram (0-50X)



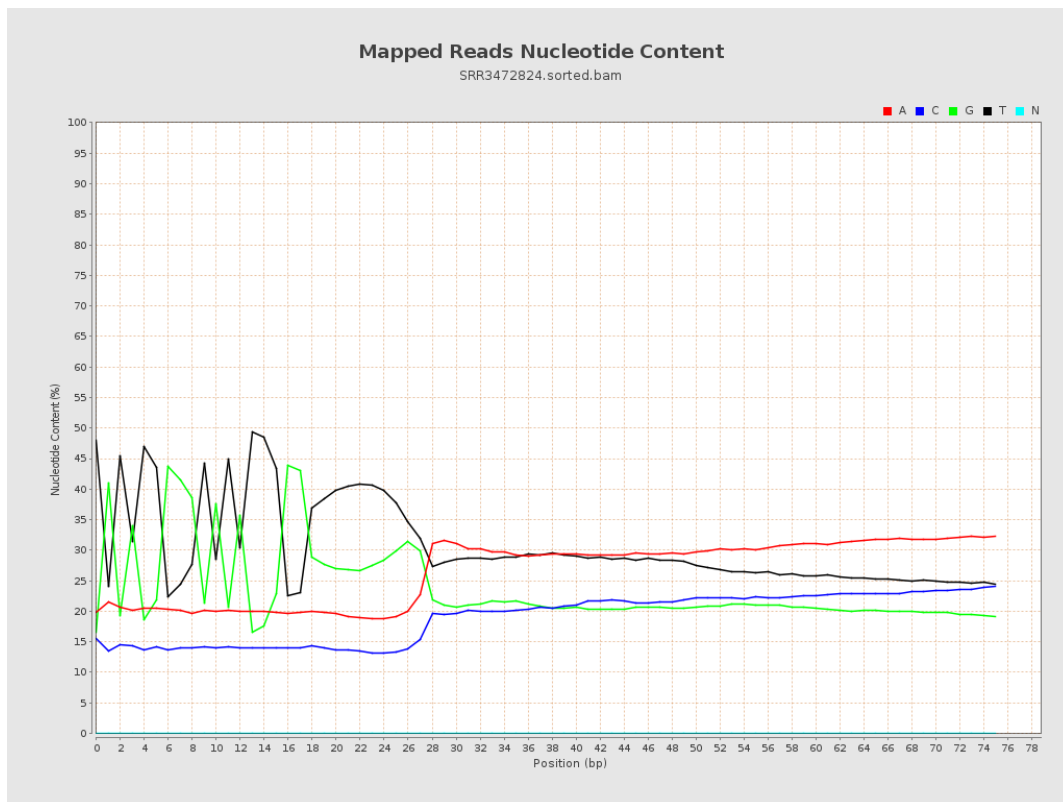
6. Results : Genome Fraction Coverage



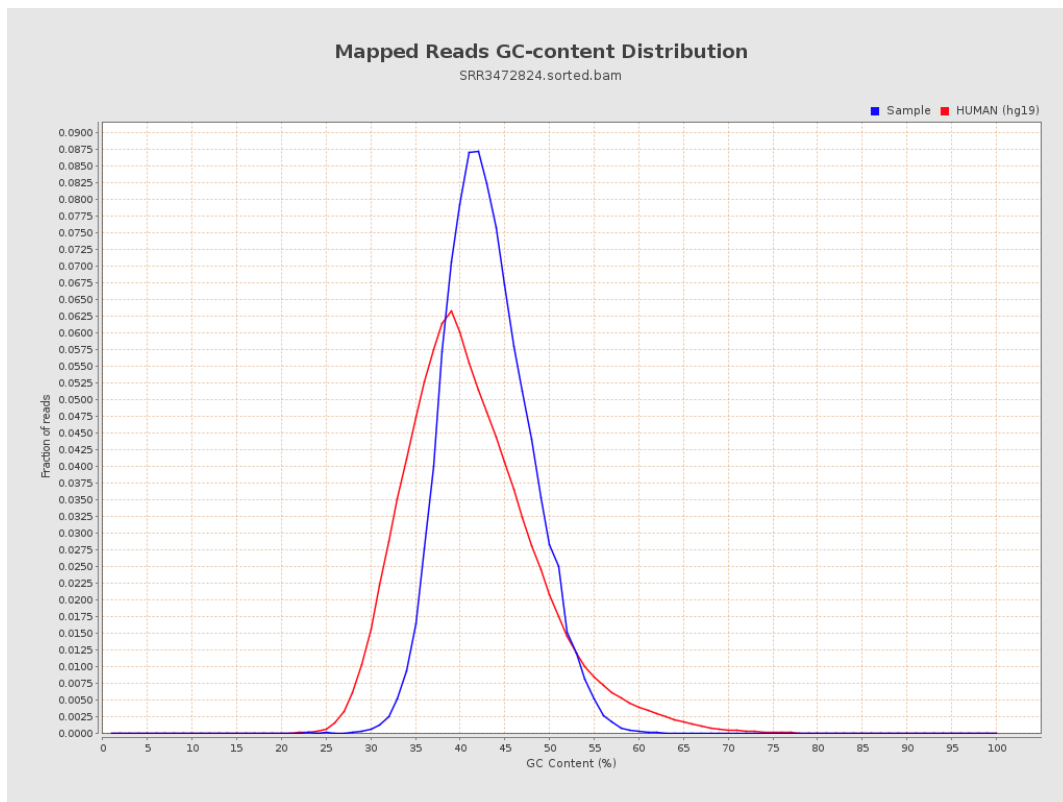
7. Results : Duplication Rate Histogram



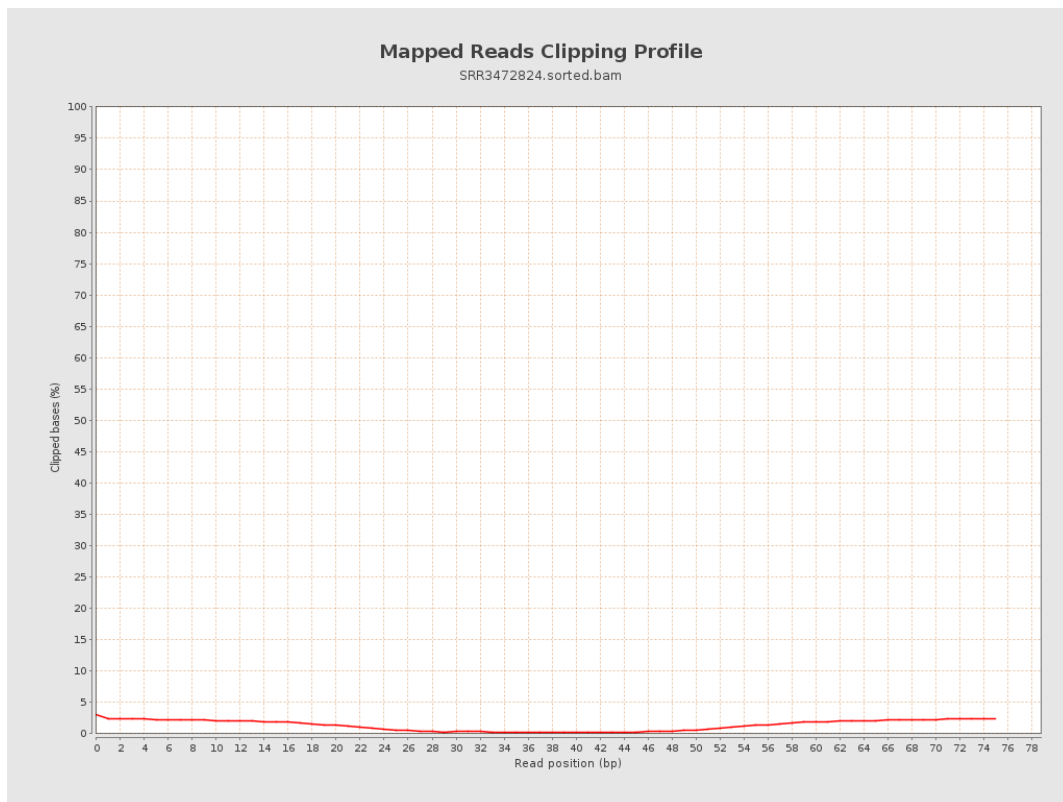
8. Results : Mapped Reads Nucleotide Content



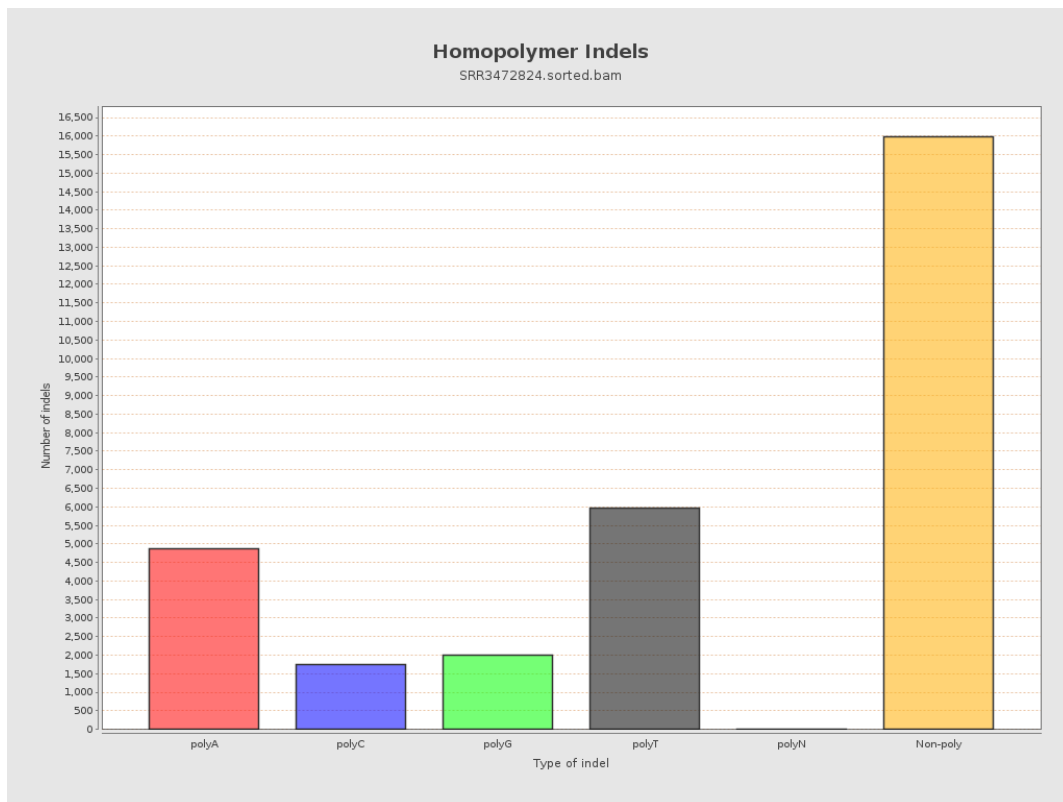
9. Results : Mapped Reads GC-content Distribution



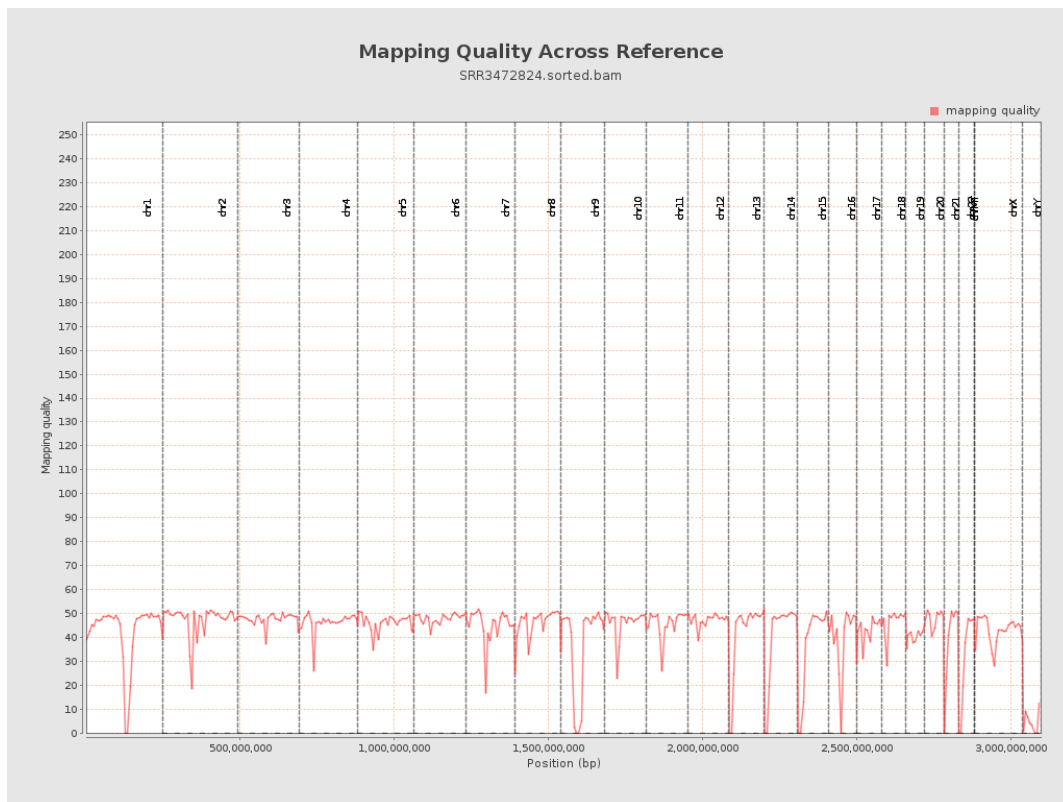
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

