

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 20:17:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708547.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_SRR1708547 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708547.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 20:17:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708547.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,770,166
Mapped reads	3,102,314 / 82.29%
Unmapped reads	667,852 / 17.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	80 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	14,398 / 0.38%
Duplication rate	0.46%
Clipped reads	43,733 / 1.16%

2.2. ACGT Content

Number/percentage of A's	48,003,552 / 31.03%
Number/percentage of C's	29,302,606 / 18.94%
Number/percentage of T's	47,673,061 / 30.82%
Number/percentage of G's	29,693,533 / 19.2%
Number/percentage of N's	6,550 / 0%
GC Percentage	38.14%

2.3. Coverage

Mean	0.05

Standard Deviation	0.2307
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2.4. Mapping Quality

Mean Mapping Quality	46.4
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2.5. Mismatches and indels

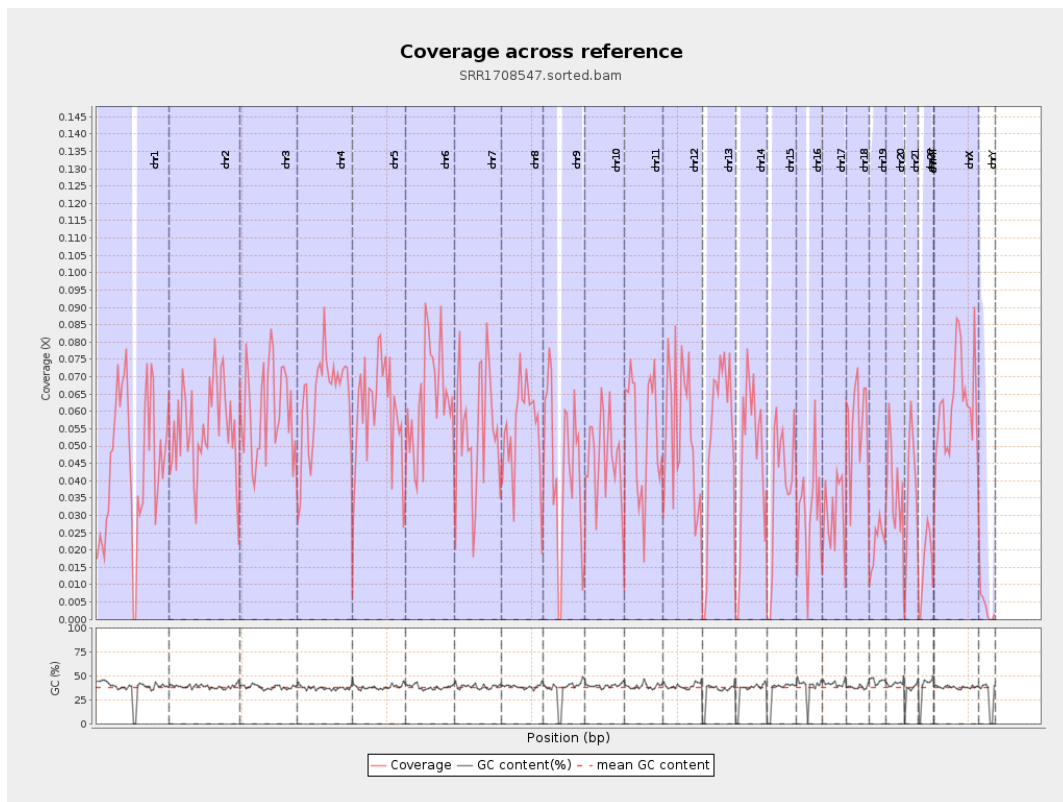
General error rate	0.17%
Mismatches	246,981
Insertions	10,704
Mapped reads with at least one insertion	0.34%
Deletions	8,322
Mapped reads with at least one deletion	0.27%
Homopolymer indels	48.1%

2.6. Chromosome stats

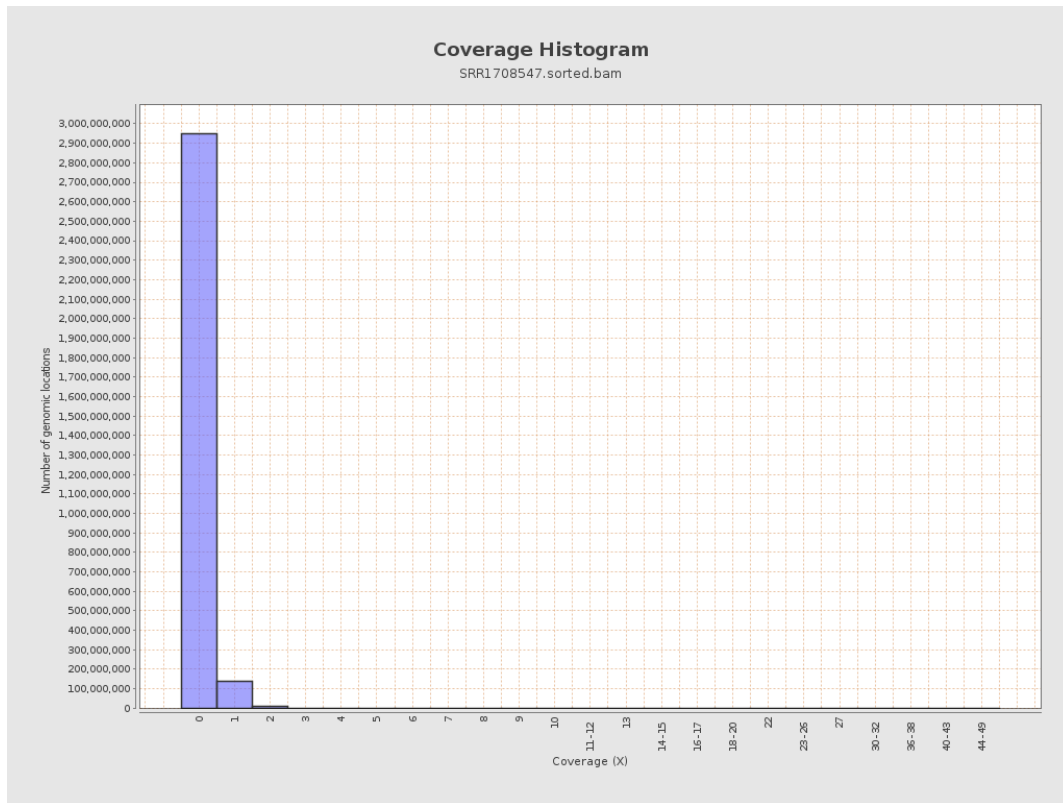
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11138922	0.0447	0.2189
chr2	243199373	13386312	0.055	0.2414
chr3	198022430	11913818	0.0602	0.2523
chr4	191154276	12243068	0.064	0.26
chr5	180915260	10881809	0.0601	0.2522
chr6	171115067	10726114	0.0627	0.258
chr7	159138663	8766073	0.0551	0.2422

chr8	146364022	8047542	0.055	0.241
chr9	141213431	6222358	0.0441	0.2168
chr10	135534747	6413036	0.0473	0.2232
chr11	135006516	7208586	0.0534	0.2392
chr12	133851895	7121839	0.0532	0.238
chr13	115169878	6047609	0.0525	0.2364
chr14	107349540	4949970	0.0461	0.2224
chr15	102531392	3916578	0.0382	0.2019
chr16	90354753	2793357	0.0309	0.1805
chr17	81195210	2389434	0.0294	0.1768
chr18	78077248	4414490	0.0565	0.2447
chr19	59128983	1322486	0.0224	0.153
chr20	63025520	2396163	0.038	0.2007
chr21	48129895	1766408	0.0367	0.1986
chr22	51304566	812596	0.0158	0.1289
chrMT	16571	250	0.0151	0.1219
chrX	155270560	9583350	0.0617	0.2566
chrY	59373566	231470	0.0039	0.0645

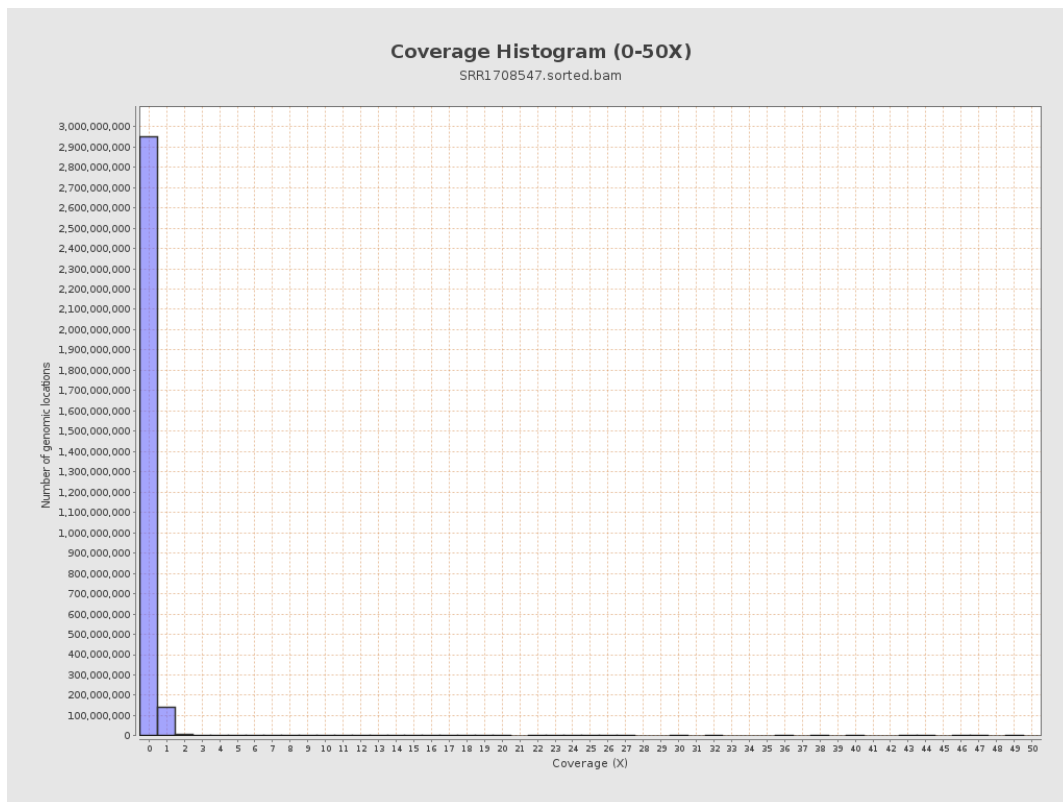
3. Results : Coverage across reference



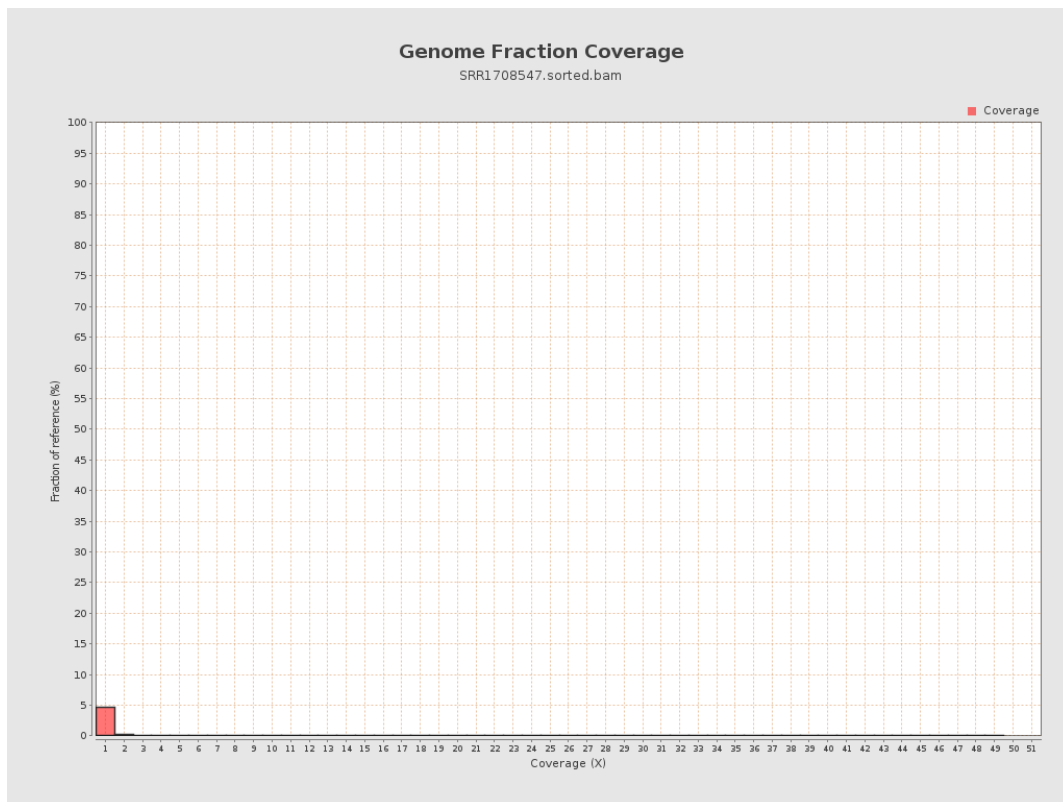
4. Results : Coverage Histogram



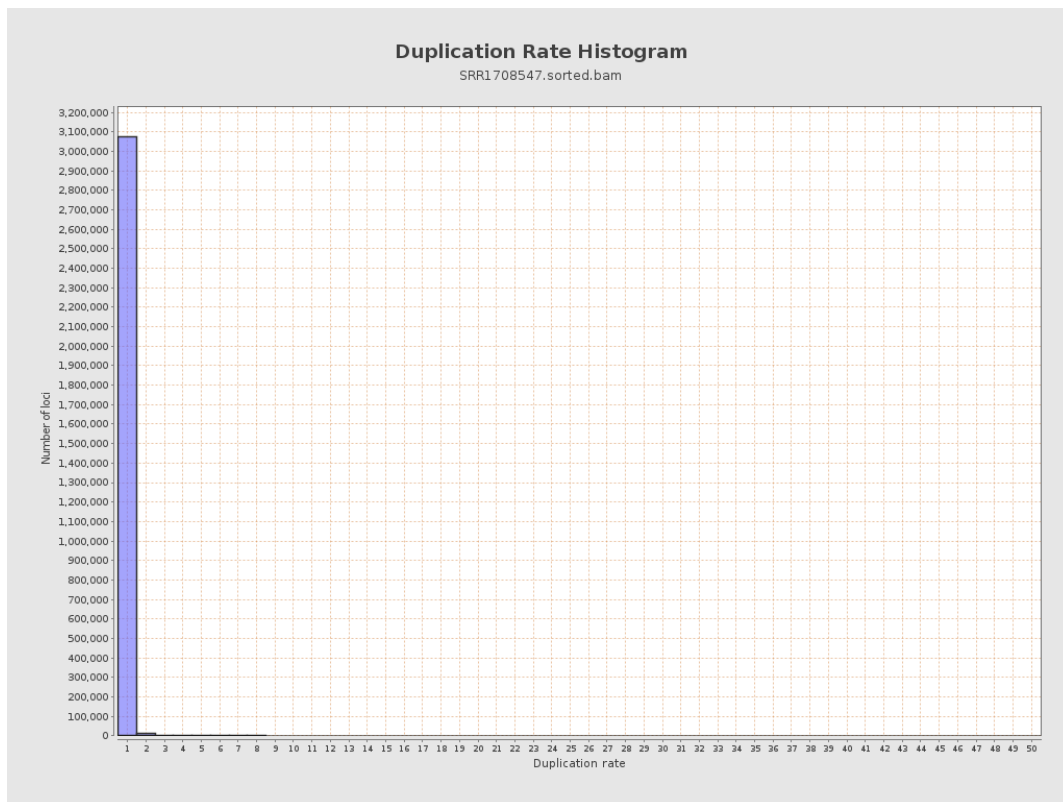
5. Results : Coverage Histogram (0-50X)



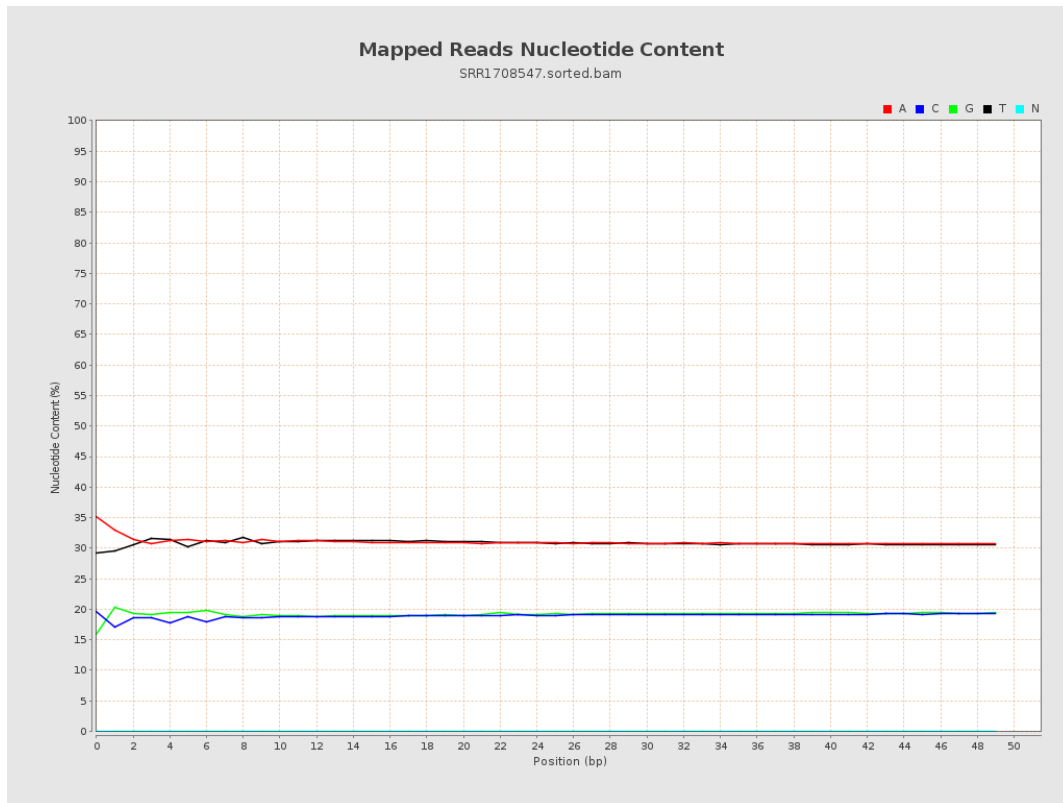
6. Results : Genome Fraction Coverage



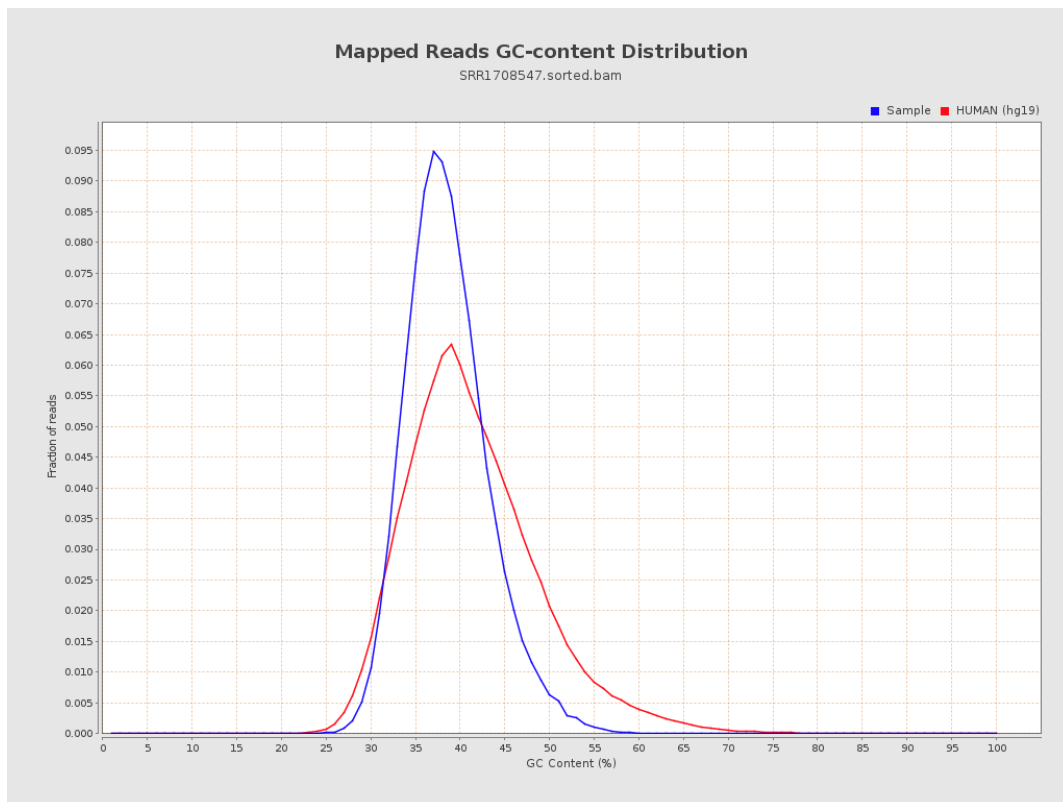
7. Results : Duplication Rate Histogram



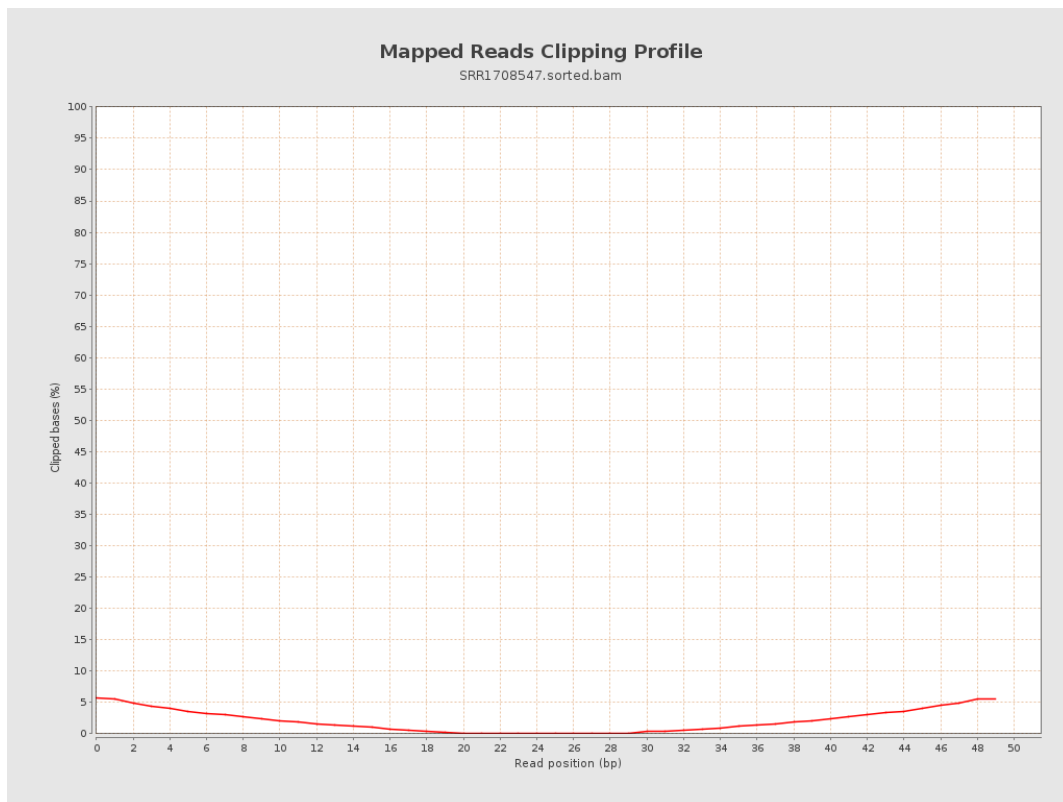
8. Results : Mapped Reads Nucleotide Content



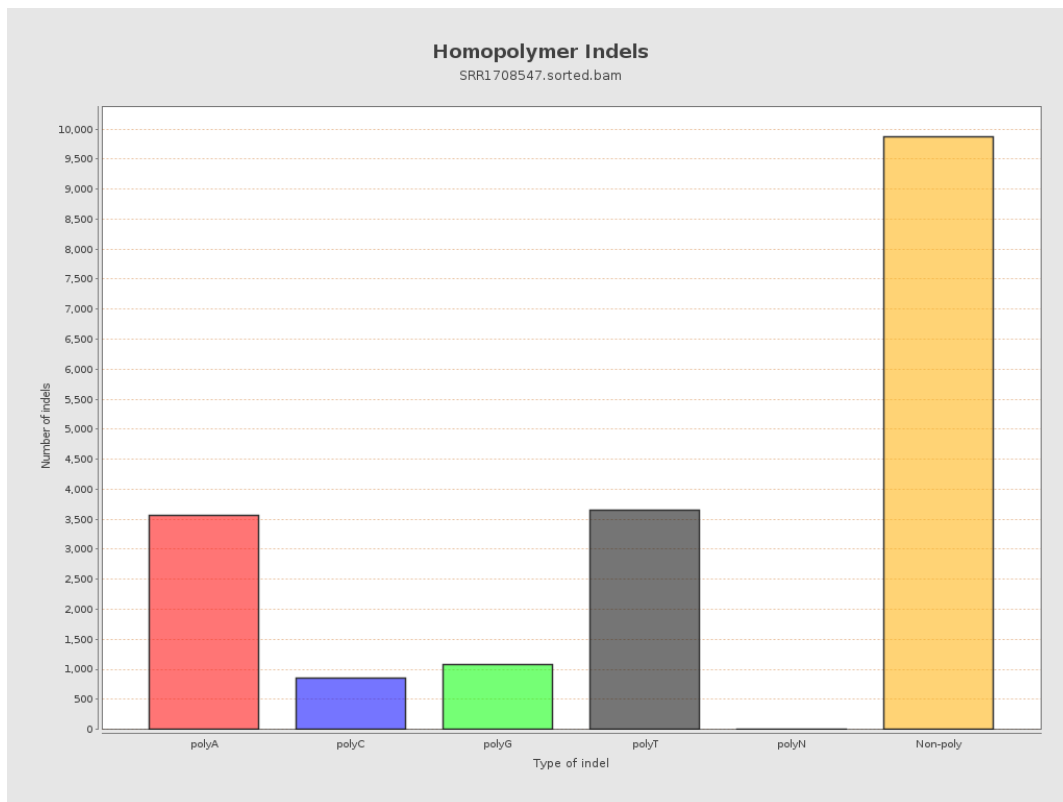
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

