

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 06:52:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708528.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_SRR1708528 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708528.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 06:52:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708528.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,135,226
Mapped reads	2,120,332 / 67.63%
Unmapped reads	1,014,894 / 32.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,082 / 0.03%
Read min/max/mean length	30 / 51 / 51.01
Duplicated reads (estimated)	85,789 / 2.74%
Duplication rate	2.6%
Clipped reads	528,125 / 16.84%

2.2. ACGT Content

Number/percentage of A's	28,456,809 / 28.41%
Number/percentage of C's	18,524,619 / 18.49%
Number/percentage of T's	32,002,681 / 31.95%
Number/percentage of G's	21,191,167 / 21.15%
Number/percentage of N's	1,344 / 0%
GC Percentage	39.65%

2.3. Coverage

Mean	0.0324

Standard Deviation	0.3703
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2.4. Mapping Quality

Mean Mapping Quality	38.37
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2.5. Mismatches and indels

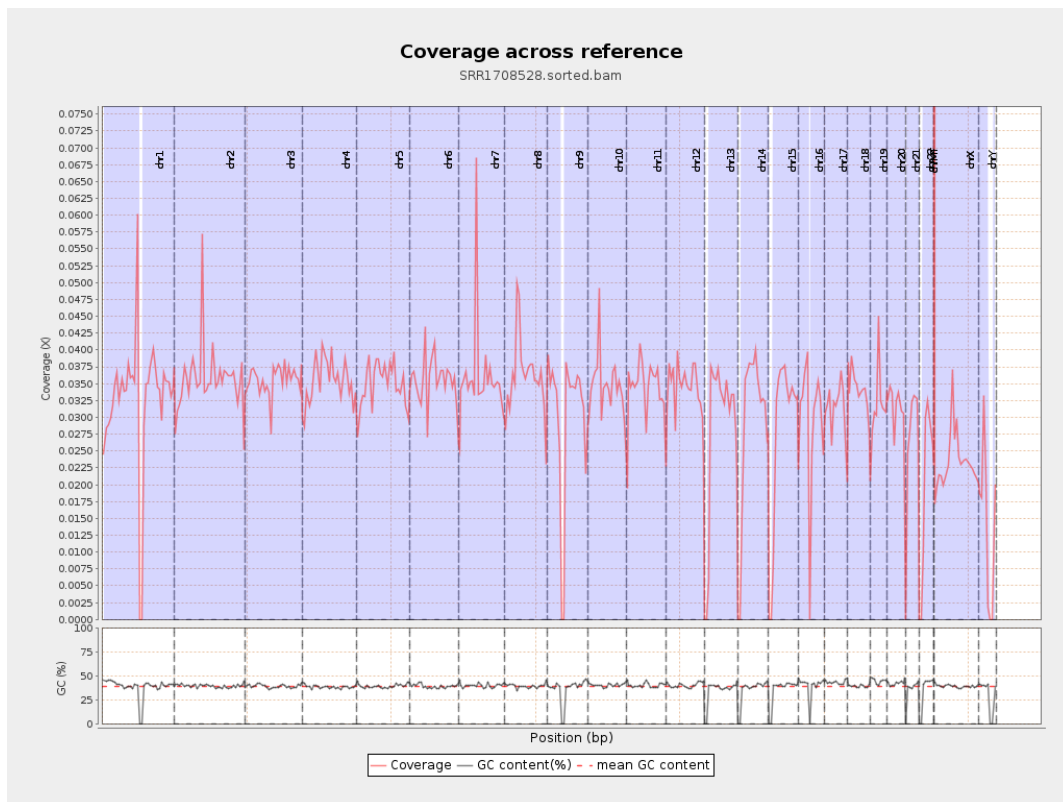
General error rate	0.56%
Mismatches	549,062
Insertions	6,251
Mapped reads with at least one insertion	0.29%
Deletions	16,219
Mapped reads with at least one deletion	0.76%
Homopolymer indels	46.43%

2.6. Chromosome stats

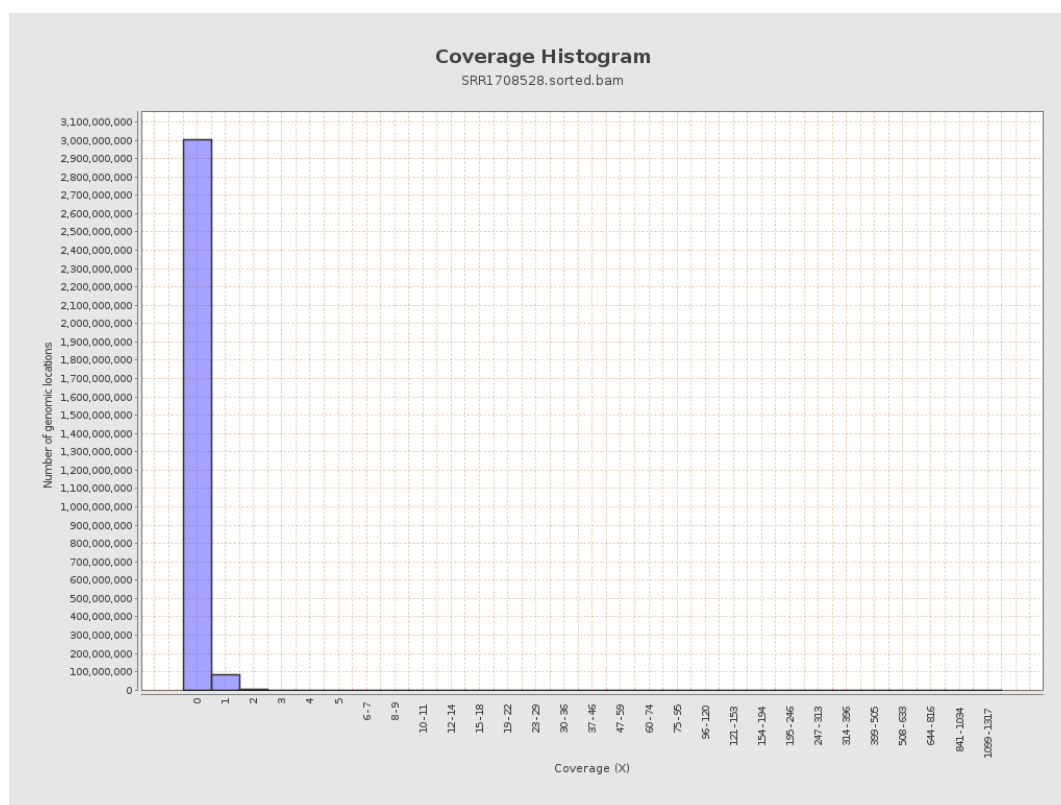
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8138689	0.0327	0.6239
chr2	243199373	8690124	0.0357	0.5179
chr3	198022430	7038654	0.0355	0.2164
chr4	191154276	6767131	0.0354	0.2242
chr5	180915260	6336599	0.035	0.2081
chr6	171115067	6072310	0.0355	0.2926
chr7	159138663	5740448	0.0361	0.4587

chr8	146364022	5281676	0.0361	0.7382
chr9	141213431	4251035	0.0301	0.2705
chr10	135534747	4684113	0.0346	0.2636
chr11	135006516	4698301	0.0348	0.3353
chr12	133851895	4622265	0.0345	0.2096
chr13	115169878	3237133	0.0281	0.2266
chr14	107349540	3142645	0.0293	0.2059
chr15	102531392	2858743	0.0279	0.1976
chr16	90354753	2623441	0.029	0.2033
chr17	81195210	2537676	0.0313	0.2625
chr18	78077248	2673134	0.0342	0.4586
chr19	59128983	1900658	0.0321	0.4286
chr20	63025520	1958577	0.0311	0.1986
chr21	48129895	1297336	0.027	0.2096
chr22	51304566	1042341	0.0203	0.1712
chrMT	16571	117608	7.0972	4.631
chrX	155270560	3661789	0.0236	0.2098
chrY	59373566	828560	0.014	0.164

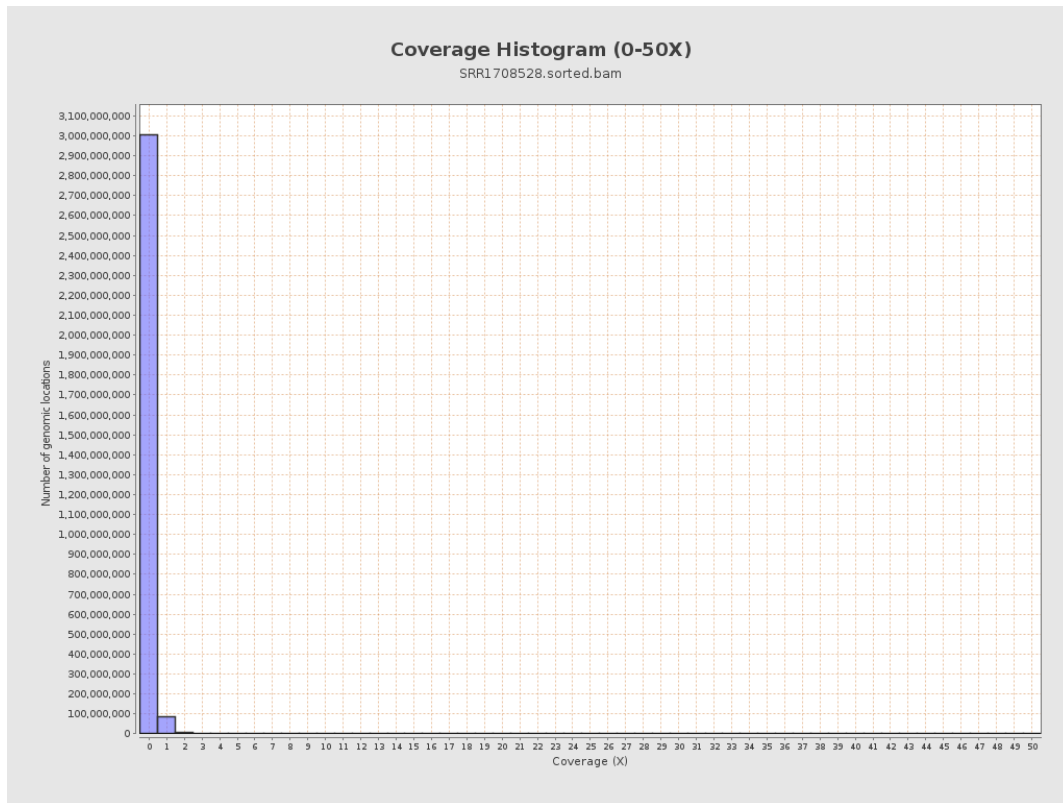
3. Results : Coverage across reference



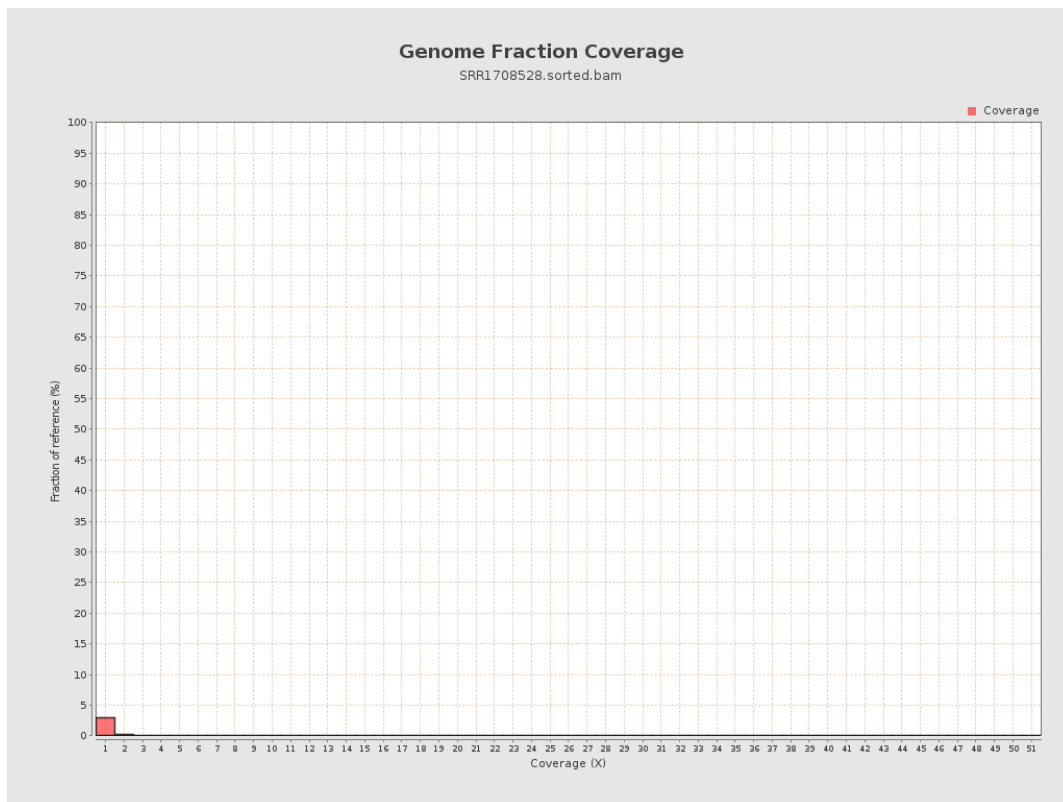
4. Results : Coverage Histogram



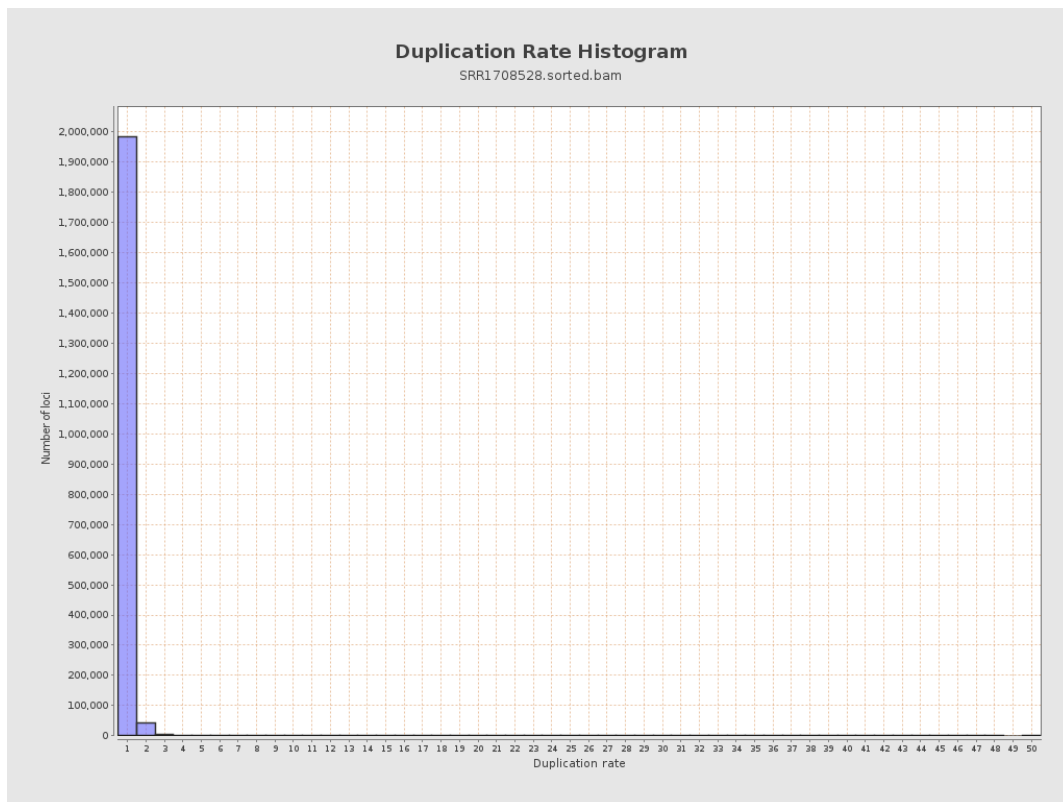
5. Results : Coverage Histogram (0-50X)



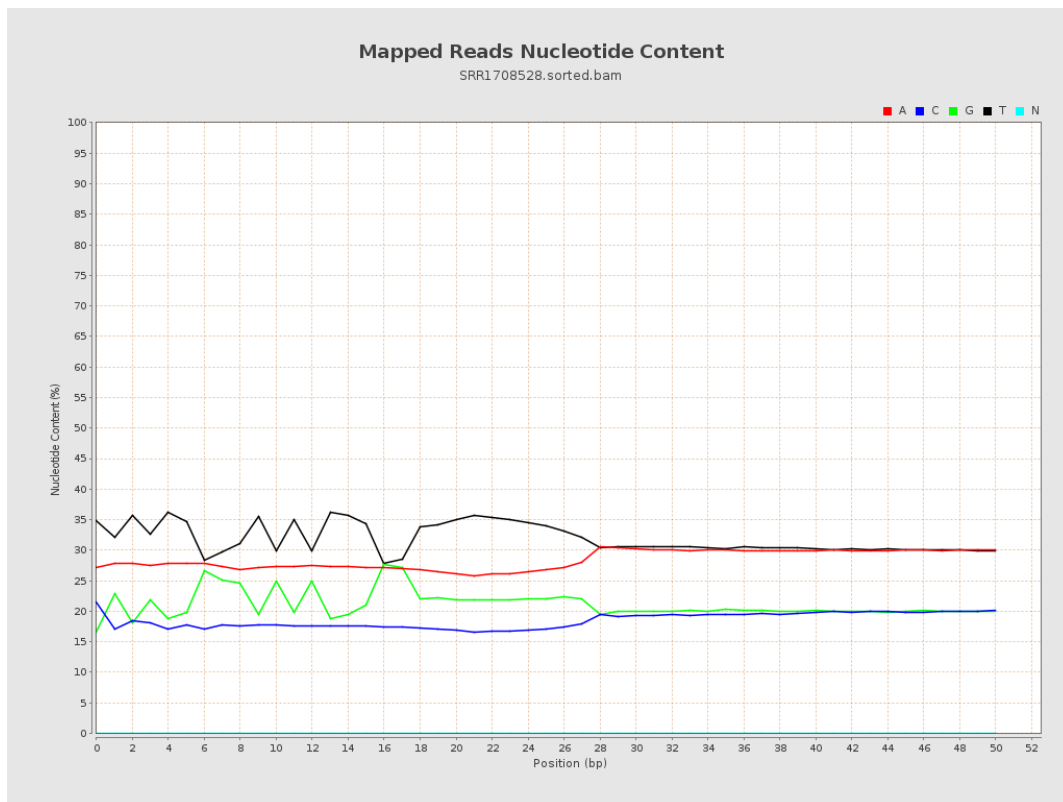
6. Results : Genome Fraction Coverage



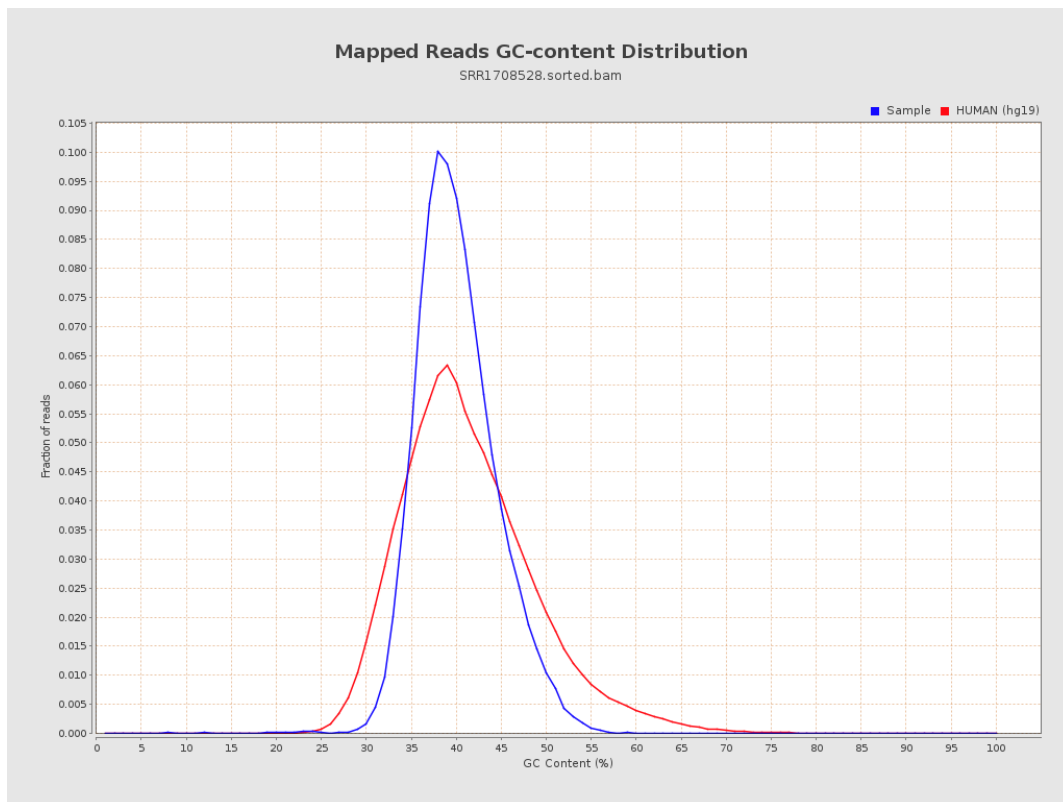
7. Results : Duplication Rate Histogram



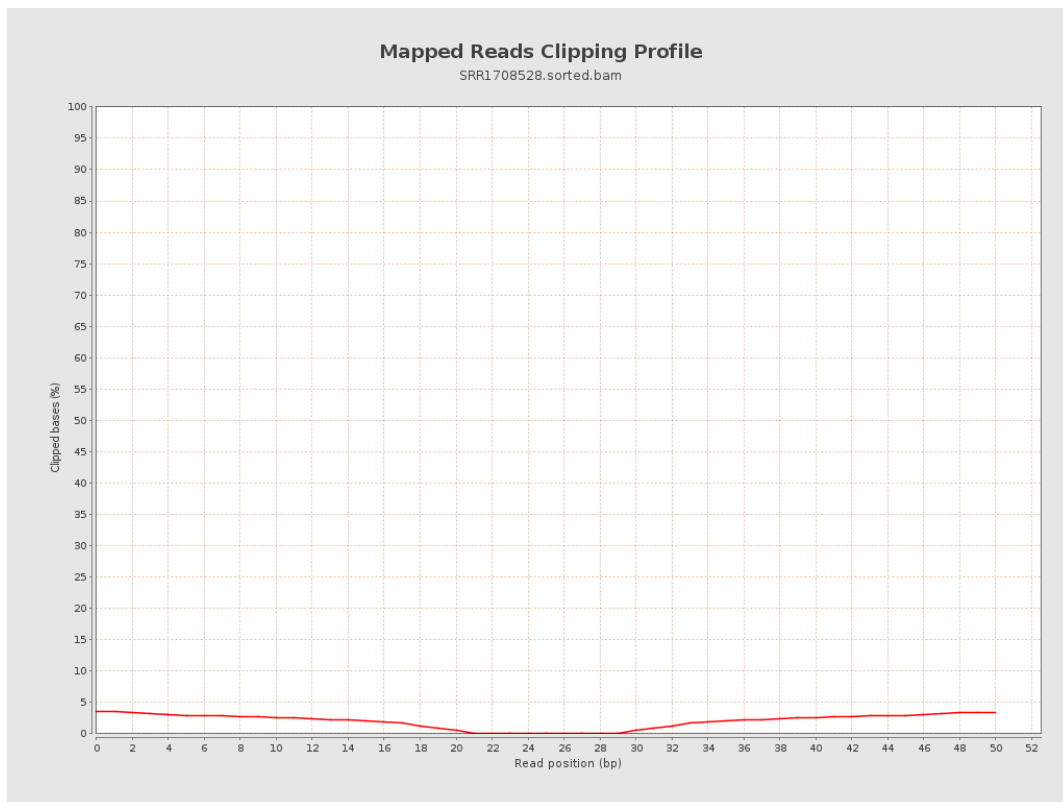
8. Results : Mapped Reads Nucleotide Content



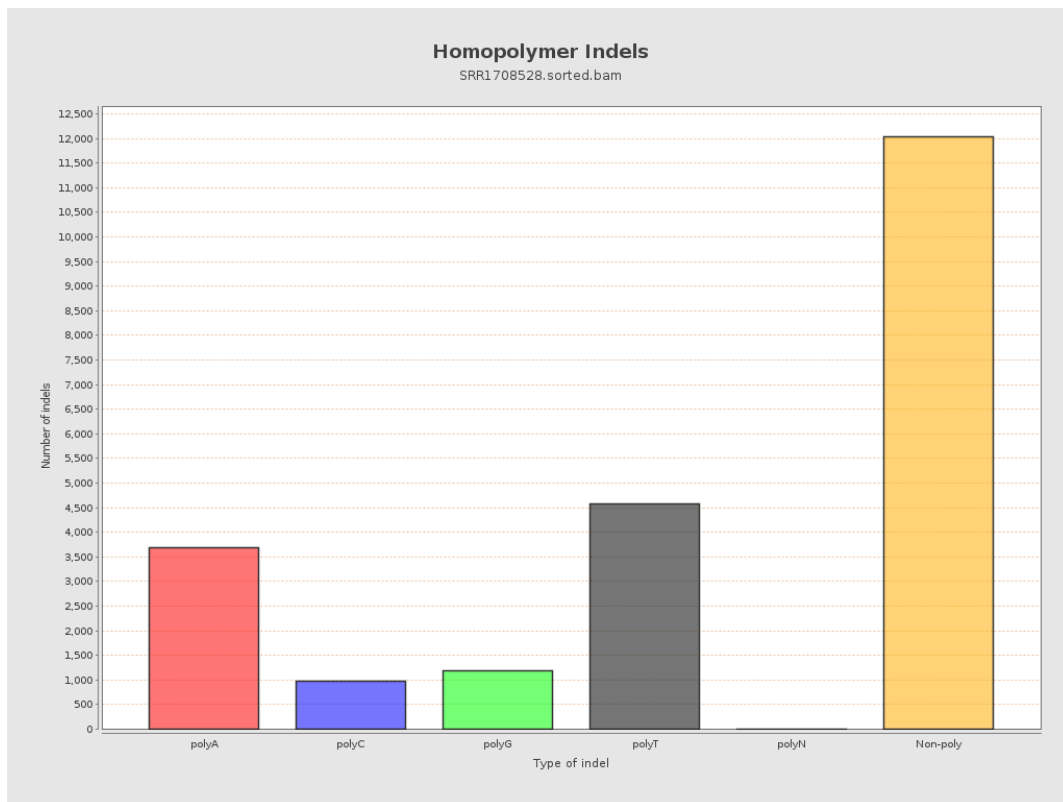
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

