

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 01:29:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708567.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_SRR1708567 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708567.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 01:29:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708567.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,692,952
Mapped reads	3,022,452 / 81.84%
Unmapped reads	670,500 / 18.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	88 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	13,921 / 0.38%
Duplication rate	0.46%
Clipped reads	42,588 / 1.15%

2.2. ACGT Content

Number/percentage of A's	46,650,204 / 30.96%
Number/percentage of C's	28,627,650 / 19%
Number/percentage of T's	46,472,654 / 30.84%
Number/percentage of G's	28,940,364 / 19.2%
Number/percentage of N's	7,452 / 0%
GC Percentage	38.2%

2.3. Coverage

Mean	0.0487

Standard Deviation	0.2267
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2.4. Mapping Quality

Mean Mapping Quality	46.49
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2.5. Mismatches and indels

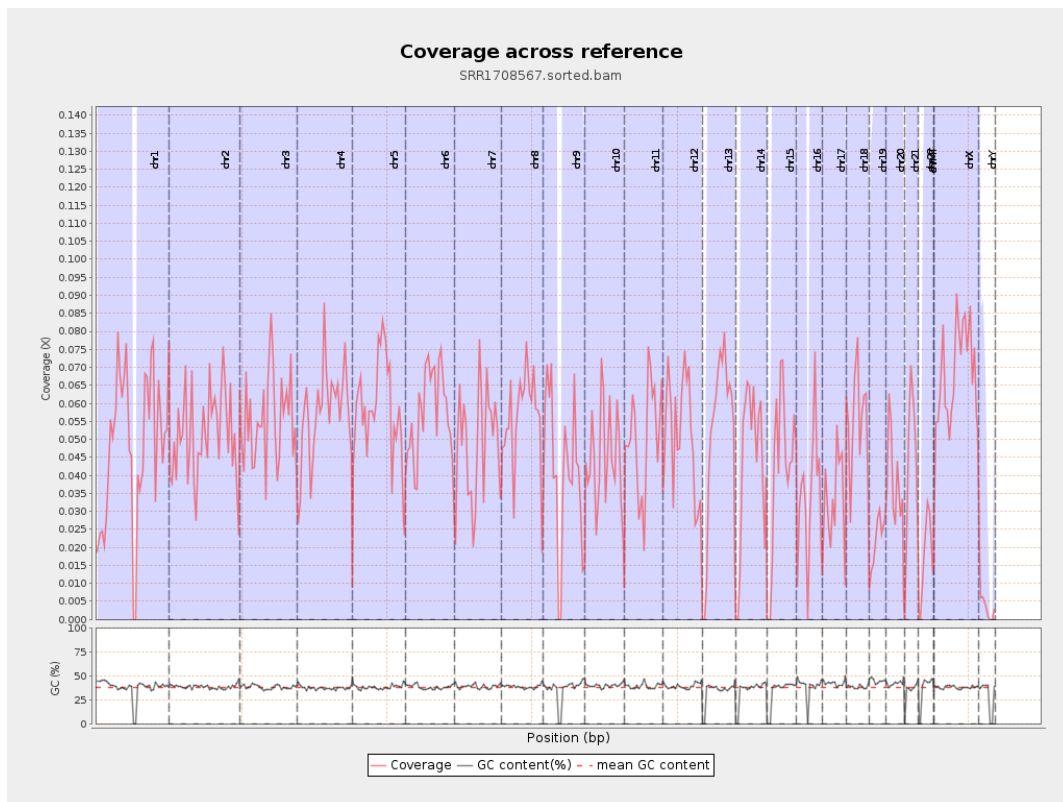
General error rate	0.17%
Mismatches	243,848
Insertions	10,250
Mapped reads with at least one insertion	0.34%
Deletions	8,003
Mapped reads with at least one deletion	0.26%
Homopolymer indels	47.54%

2.6. Chromosome stats

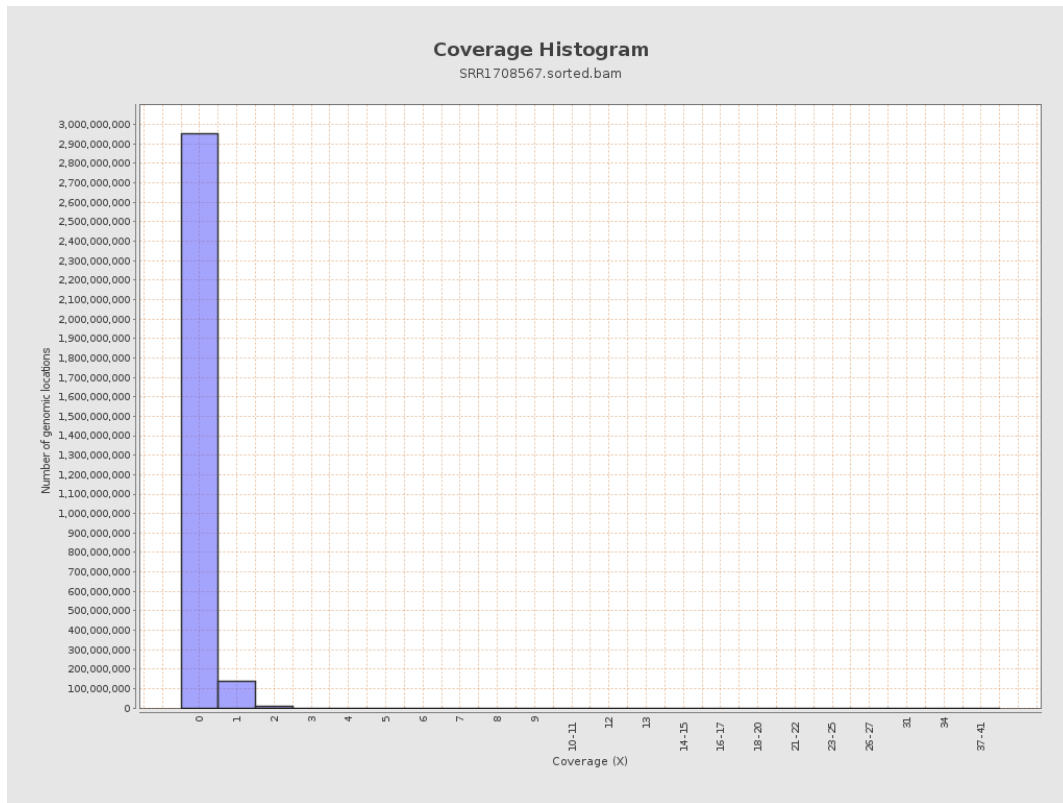
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11980296	0.0481	0.226
chr2	243199373	12432587	0.0511	0.2317
chr3	198022430	11008588	0.0556	0.2415
chr4	191154276	11074437	0.0579	0.2464
chr5	180915260	10562257	0.0584	0.2475
chr6	171115067	9735610	0.0569	0.2445
chr7	159138663	7851676	0.0493	0.2276

chr8	146364022	8215749	0.0561	0.2426
chr9	141213431	5903382	0.0418	0.2104
chr10	135534747	6186599	0.0456	0.2185
chr11	135006516	6812882	0.0505	0.2309
chr12	133851895	6802258	0.0508	0.2314
chr13	115169878	5918704	0.0514	0.233
chr14	107349540	4634487	0.0432	0.2135
chr15	102531392	4273620	0.0417	0.2106
chr16	90354753	3102974	0.0343	0.1908
chr17	81195210	2616542	0.0322	0.1845
chr18	78077248	4284178	0.0549	0.2393
chr19	59128983	1325619	0.0224	0.1527
chr20	63025520	2398378	0.0381	0.2003
chr21	48129895	2025534	0.0421	0.2124
chr22	51304566	889927	0.0173	0.1347
chrMT	16571	250	0.0151	0.1219
chrX	155270560	10437083	0.0672	0.2665
chrY	59373566	237980	0.004	0.0655

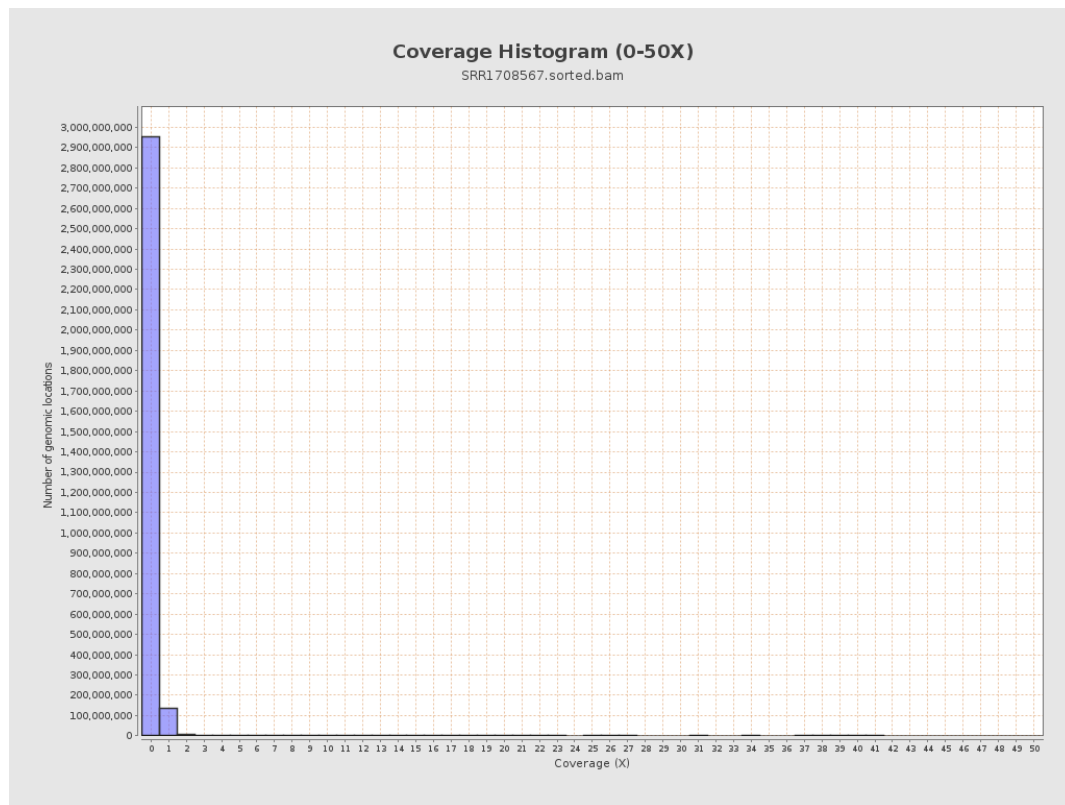
3. Results : Coverage across reference



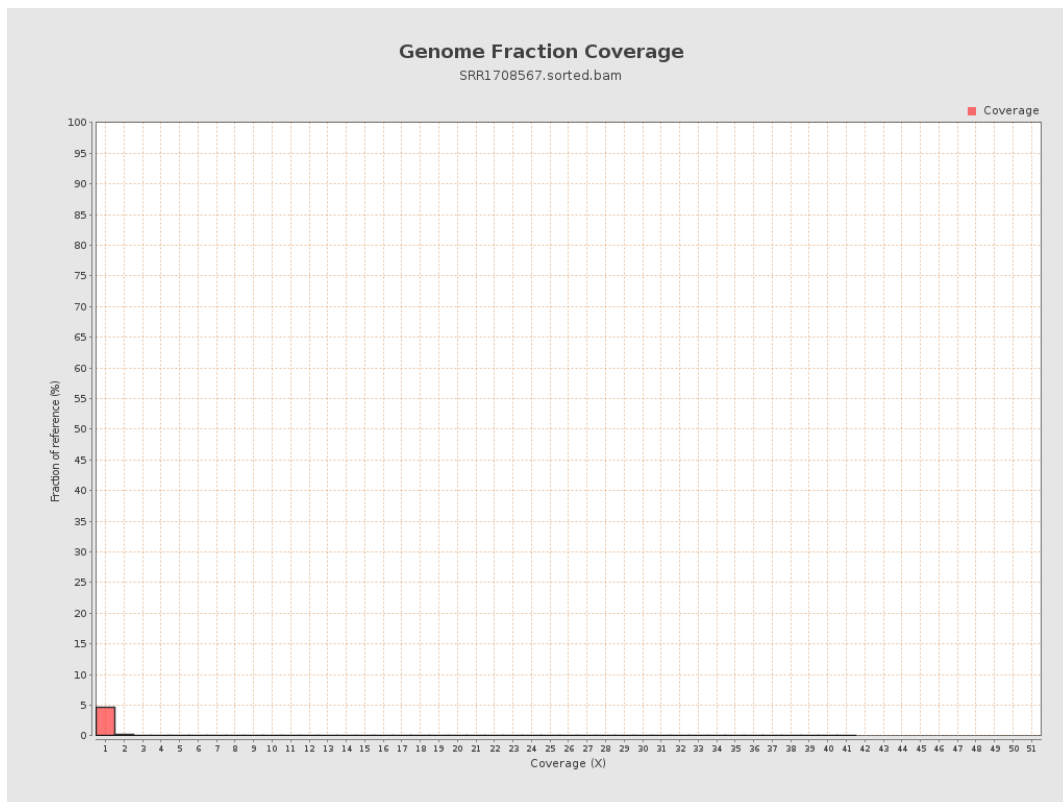
4. Results : Coverage Histogram



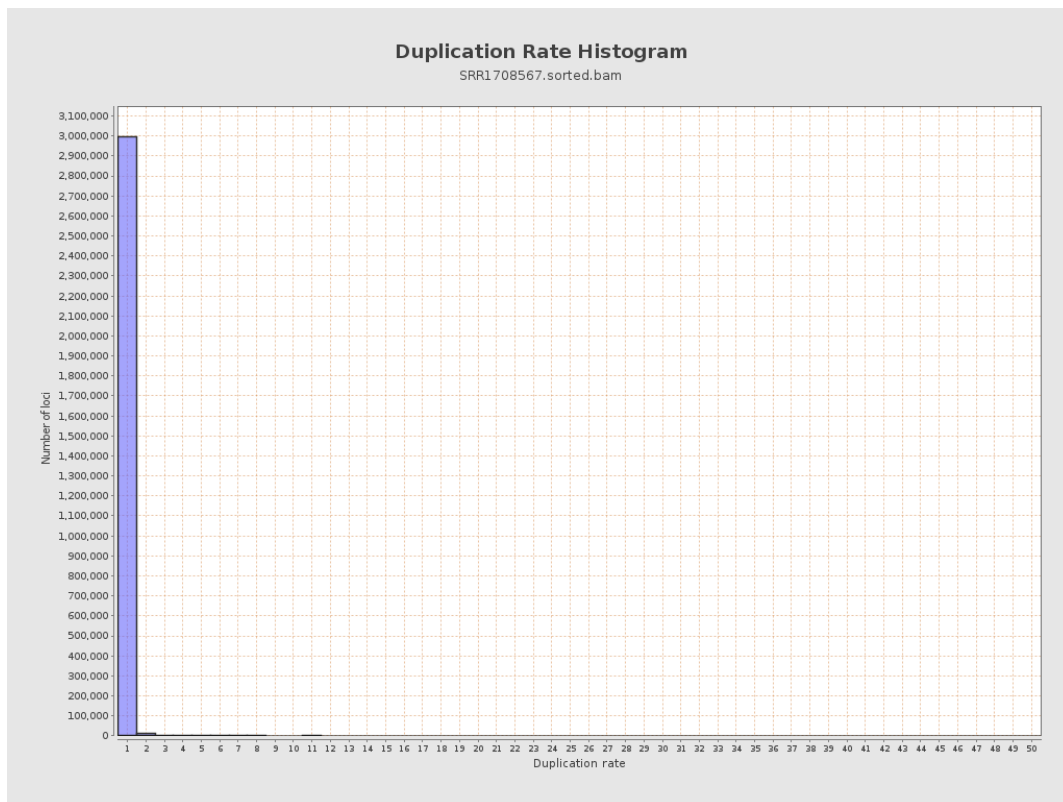
5. Results : Coverage Histogram (0-50X)



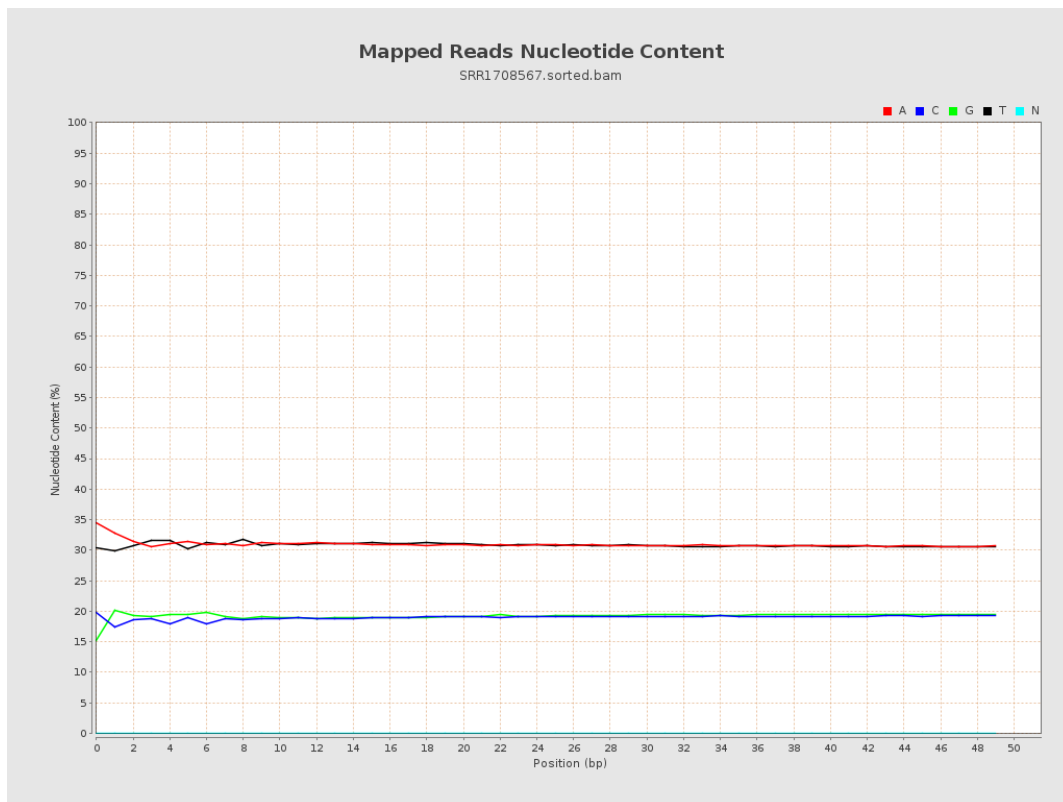
6. Results : Genome Fraction Coverage



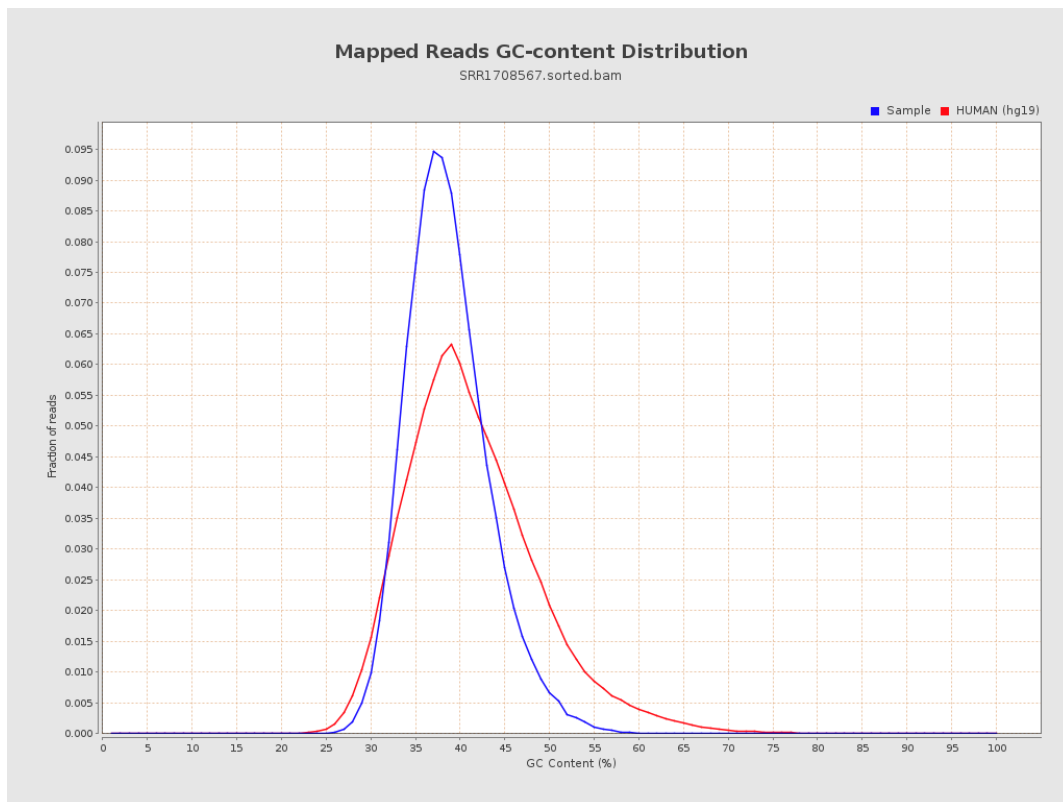
7. Results : Duplication Rate Histogram



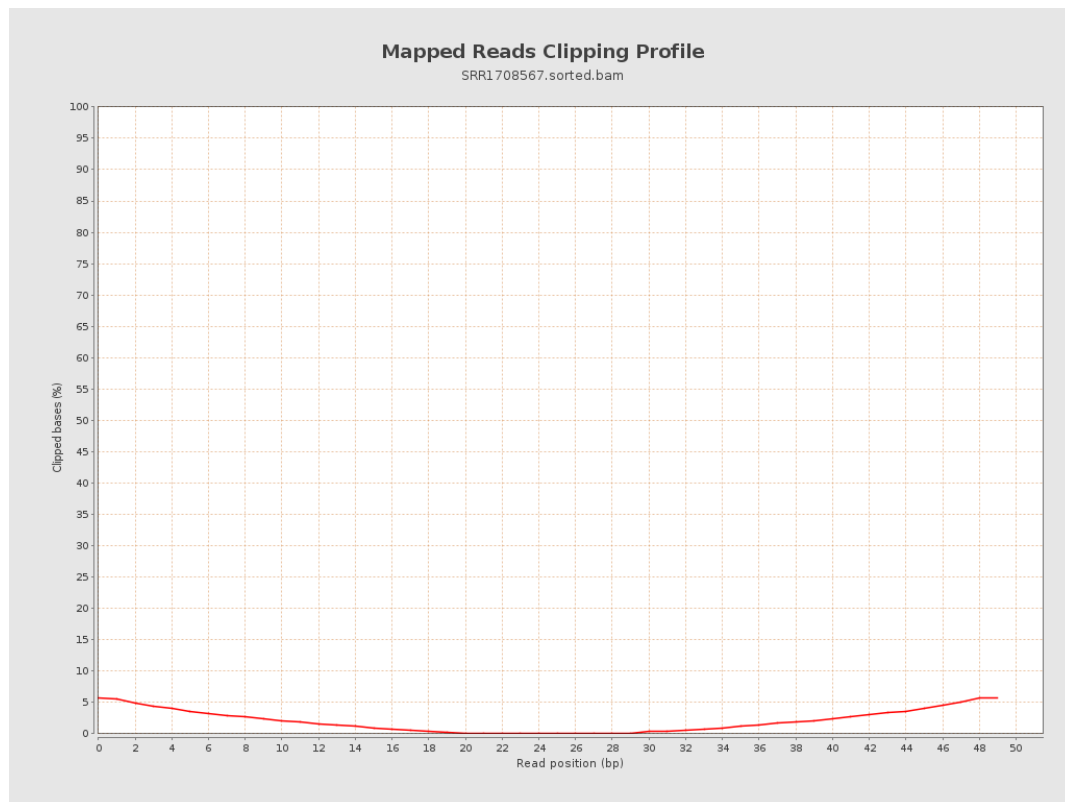
8. Results : Mapped Reads Nucleotide Content



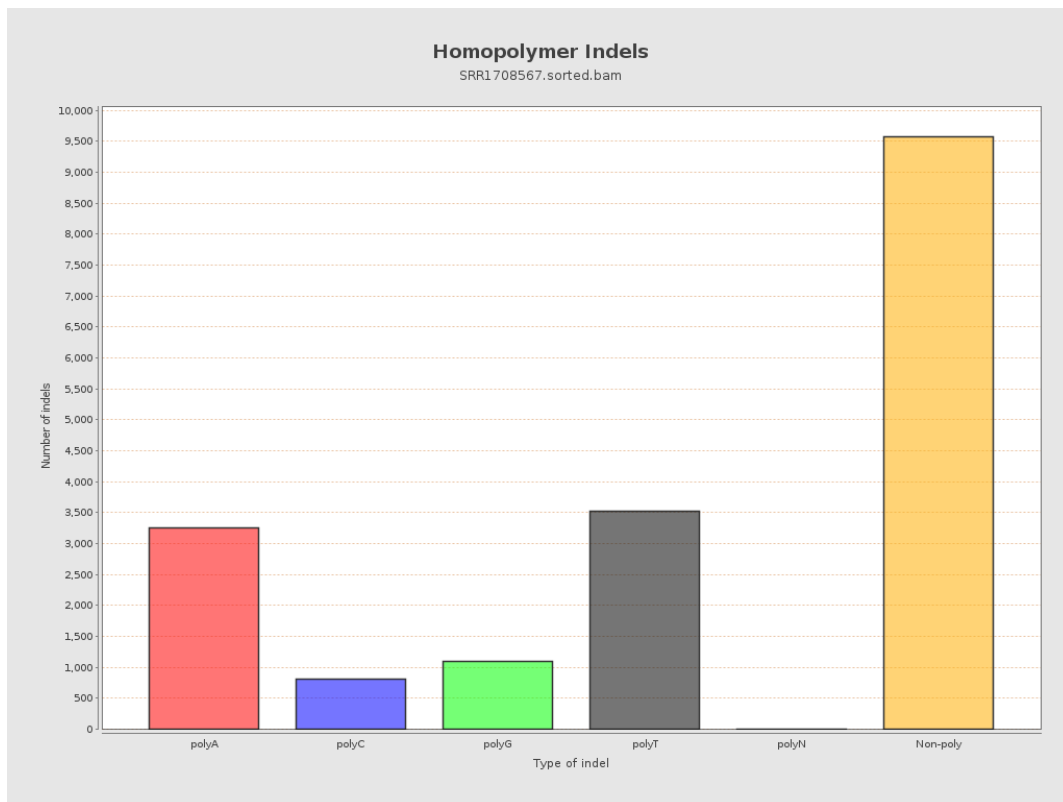
9. Results : Mapped Reads GC-content Distribution



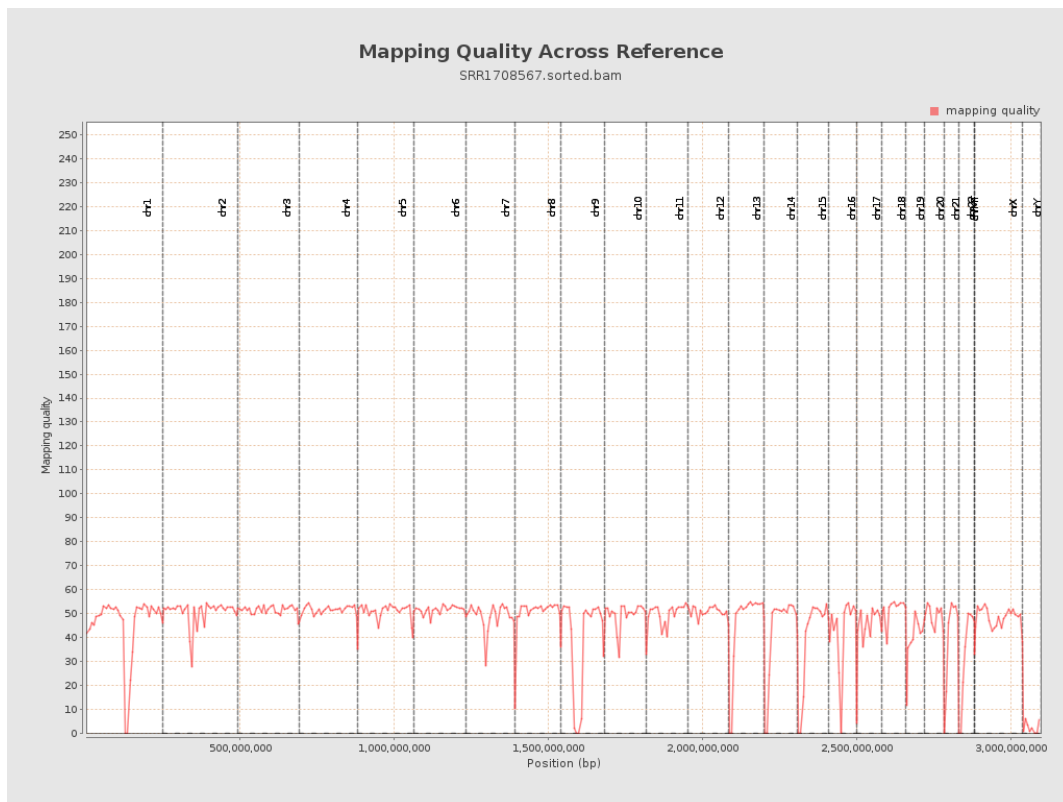
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

