

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 10:25:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708639.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_SRR1708639 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708639.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 10:25:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708639.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,889,835
Mapped reads	4,640,691 / 94.9%
Unmapped reads	249,144 / 5.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	183 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	86,597 / 1.77%
Duplication rate	1.83%
Clipped reads	70,031 / 1.43%

2.2. ACGT Content

Number/percentage of A's	71,630,543 / 30.96%
Number/percentage of C's	43,830,232 / 18.94%
Number/percentage of T's	71,632,896 / 30.96%
Number/percentage of G's	44,255,423 / 19.13%
Number/percentage of N's	7,894 / 0%
GC Percentage	38.07%

2.3. Coverage

Mean	0.0747

Standard Deviation	0.4253
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2.4. Mapping Quality

Mean Mapping Quality	44.86
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2.5. Mismatches and indels

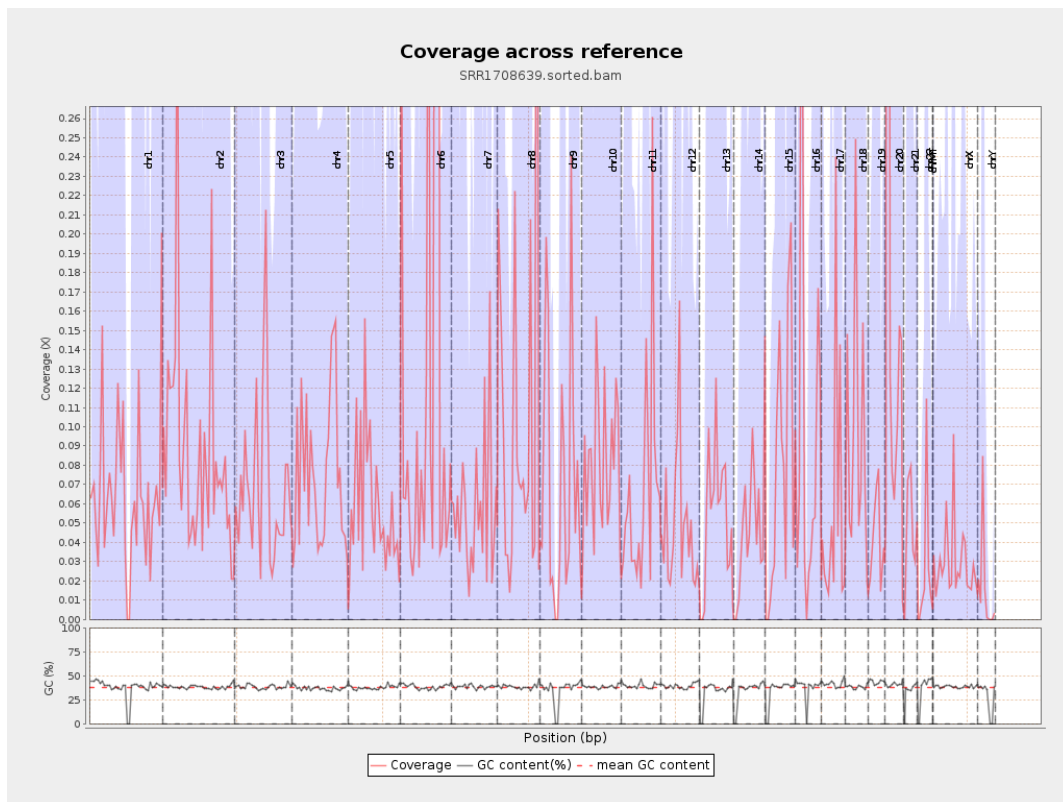
General error rate	0.18%
Mismatches	387,609
Insertions	16,787
Mapped reads with at least one insertion	0.36%
Deletions	13,463
Mapped reads with at least one deletion	0.29%
Homopolymer indels	49.24%

2.6. Chromosome stats

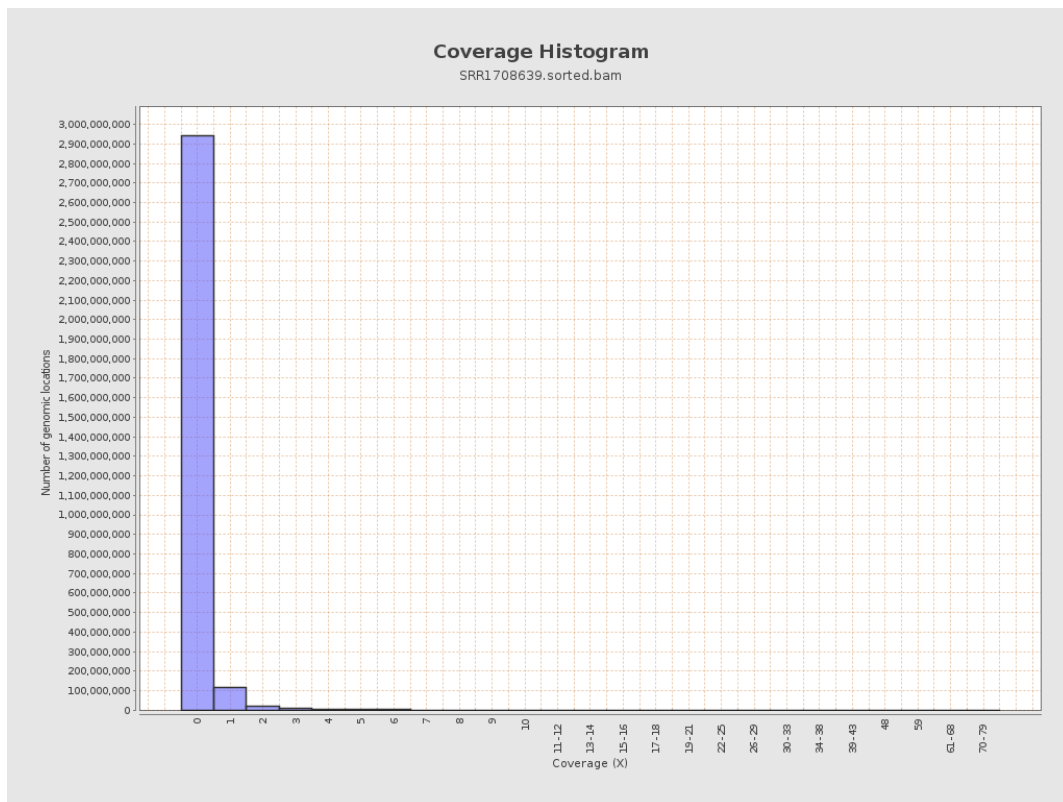
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	16293781	0.0654	0.3759
chr2	243199373	21263709	0.0874	0.4568
chr3	198022430	13396902	0.0677	0.3407
chr4	191154276	14462484	0.0757	0.3841
chr5	180915260	10329433	0.0571	0.3227
chr6	171115067	25966743	0.1518	0.697
chr7	159138663	9005561	0.0566	0.356

chr8	146364022	15734715	0.1075	0.6055
chr9	141213431	10438674	0.0739	0.3842
chr10	135534747	11180664	0.0825	0.4032
chr11	135006516	8897168	0.0659	0.3416
chr12	133851895	6568181	0.0491	0.3061
chr13	115169878	6186519	0.0537	0.3269
chr14	107349540	4649471	0.0433	0.2582
chr15	102531392	7290634	0.0711	0.4378
chr16	90354753	8468260	0.0937	0.4942
chr17	81195210	4744913	0.0584	0.3803
chr18	78077248	7415535	0.095	0.4419
chr19	59128983	2523888	0.0427	0.2759
chr20	63025520	17629631	0.2797	0.9923
chr21	48129895	2096375	0.0436	0.2787
chr22	51304566	1371472	0.0267	0.2396
chrMT	16571	200	0.0121	0.1092
chrX	155270560	4484144	0.0289	0.2205
chrY	59373566	981000	0.0165	0.1754

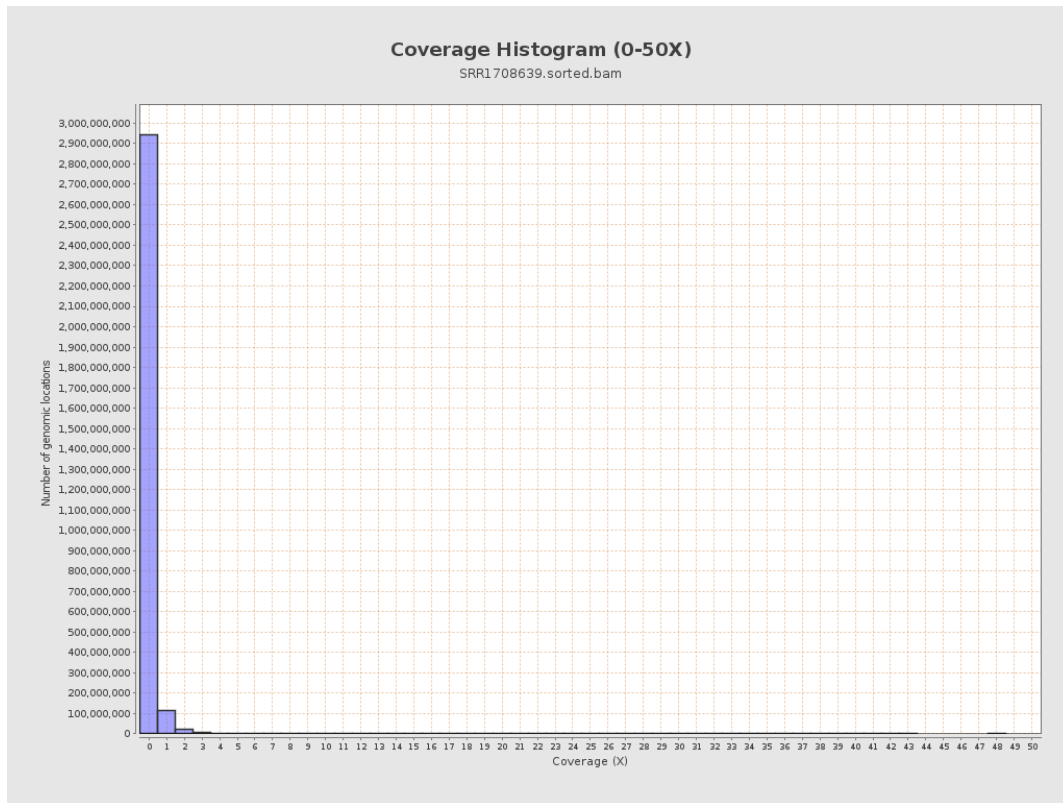
3. Results : Coverage across reference



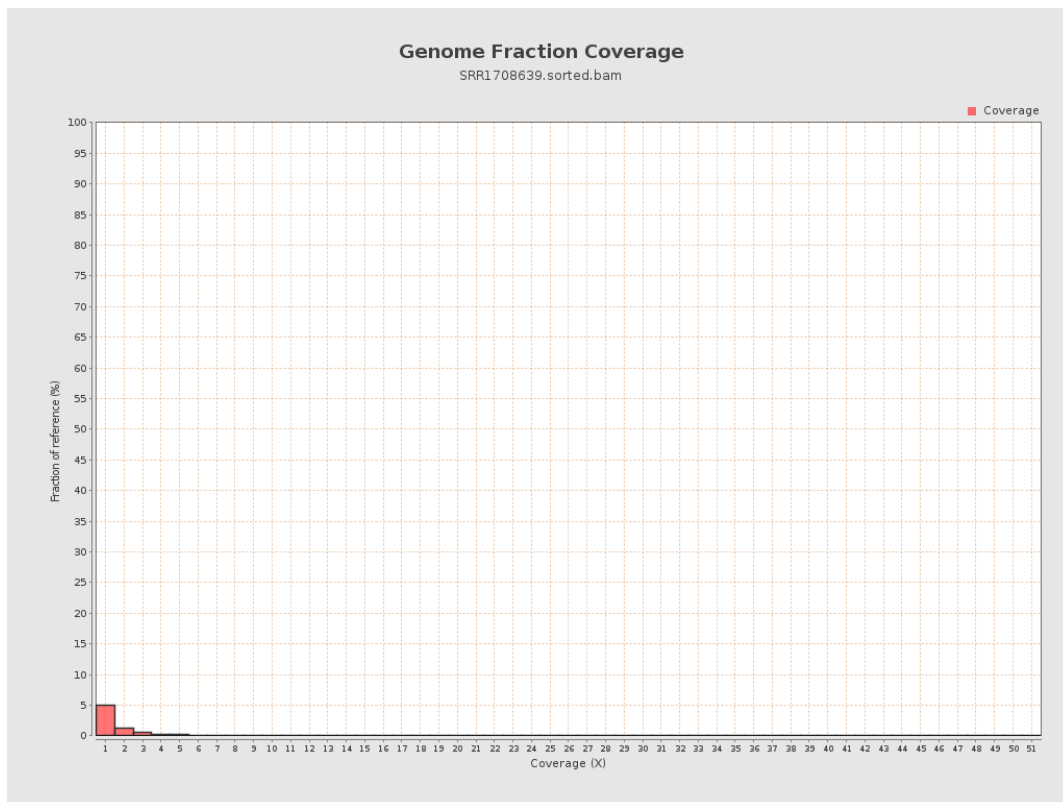
4. Results : Coverage Histogram



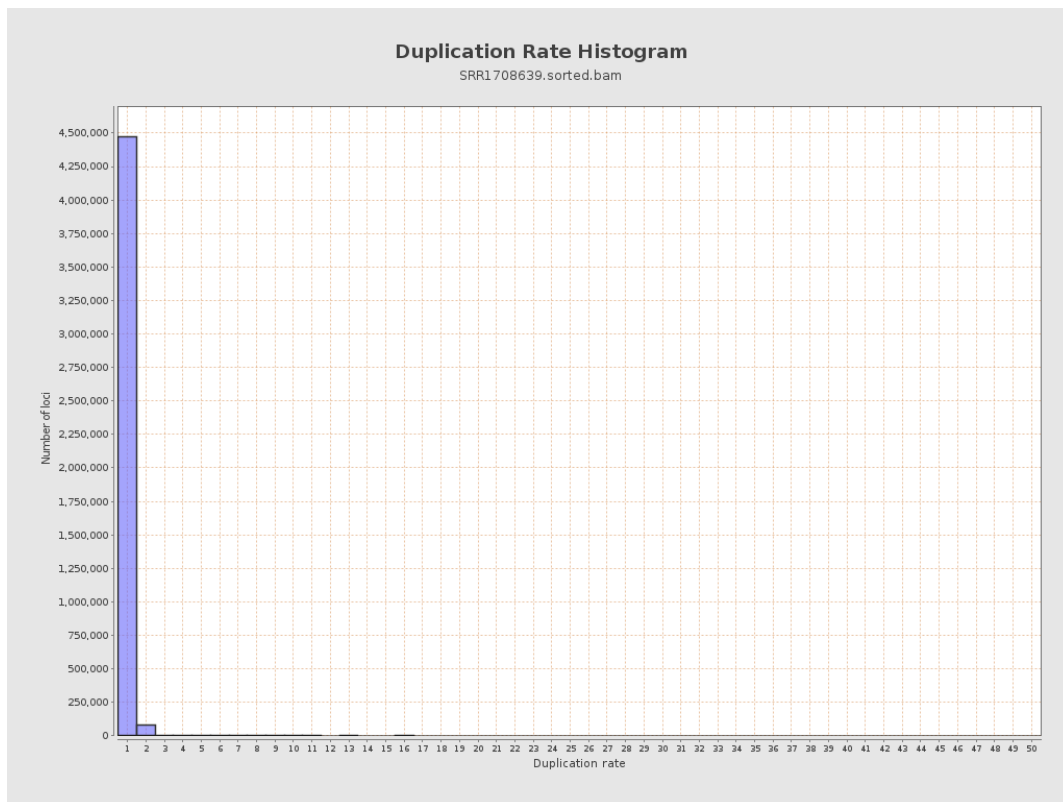
5. Results : Coverage Histogram (0-50X)



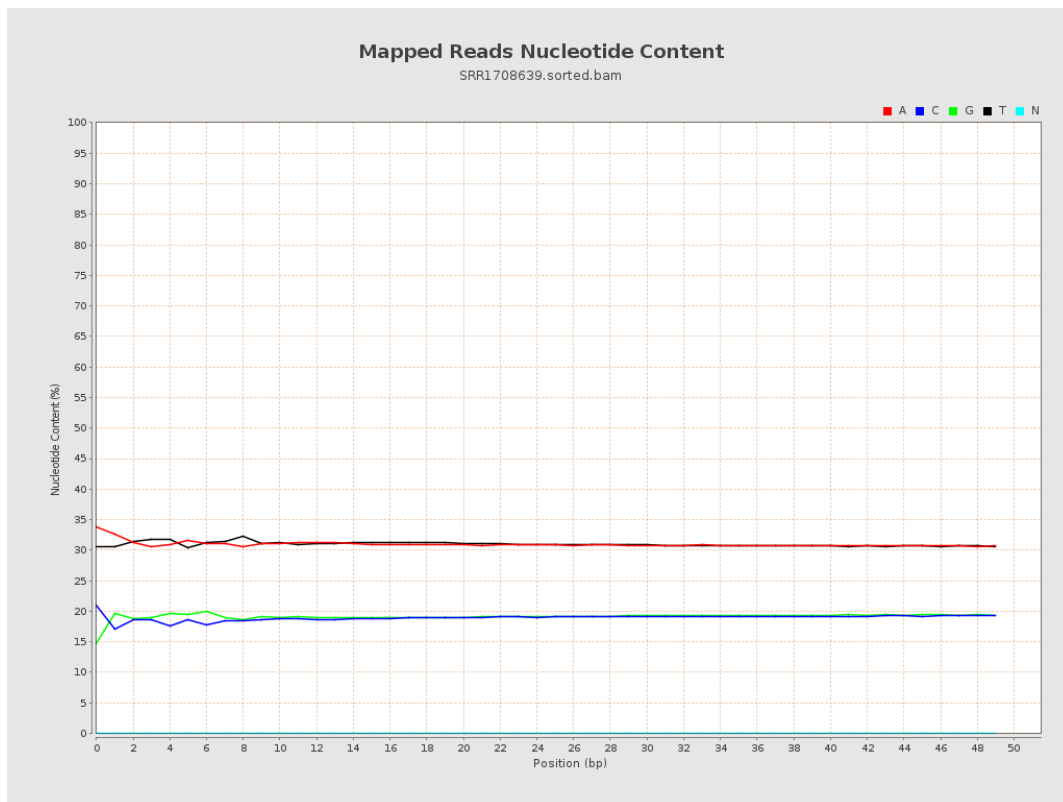
6. Results : Genome Fraction Coverage



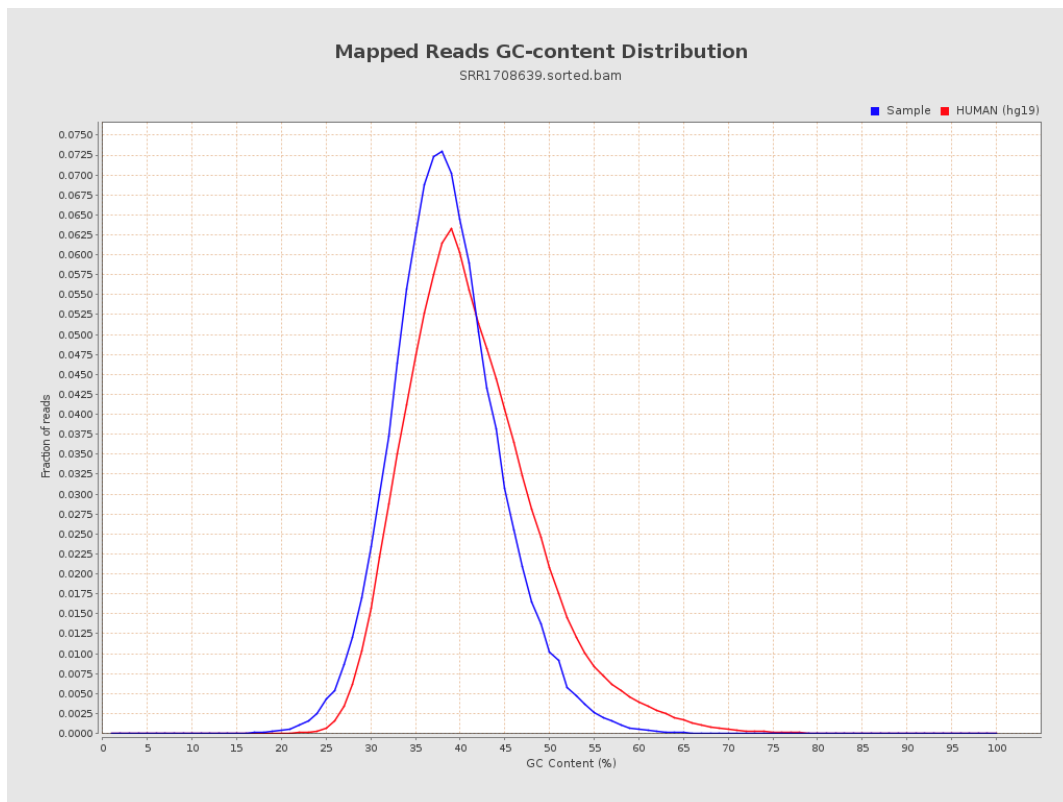
7. Results : Duplication Rate Histogram



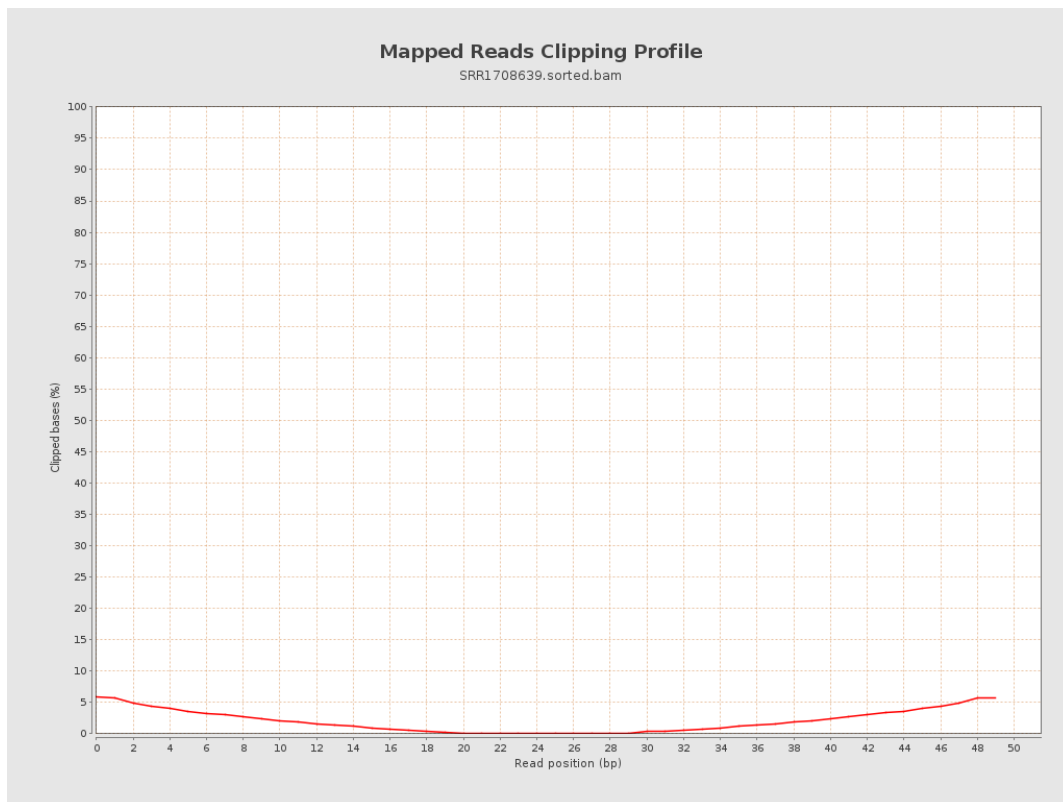
8. Results : Mapped Reads Nucleotide Content



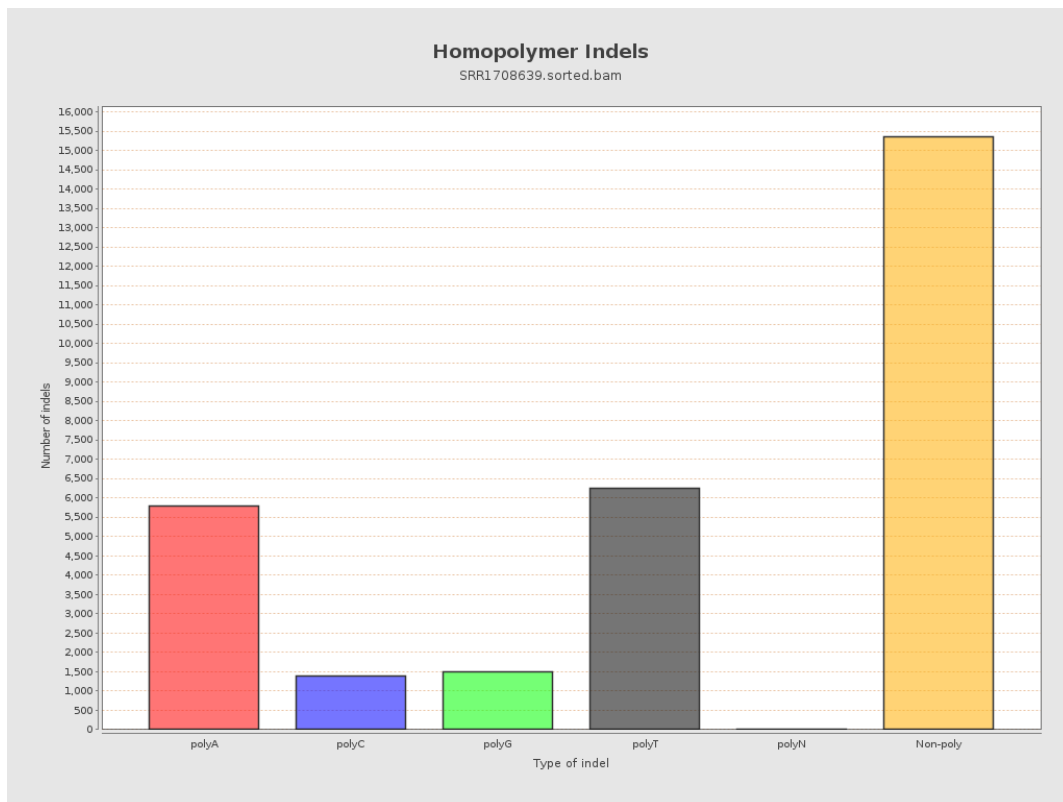
9. Results : Mapped Reads GC-content Distribution



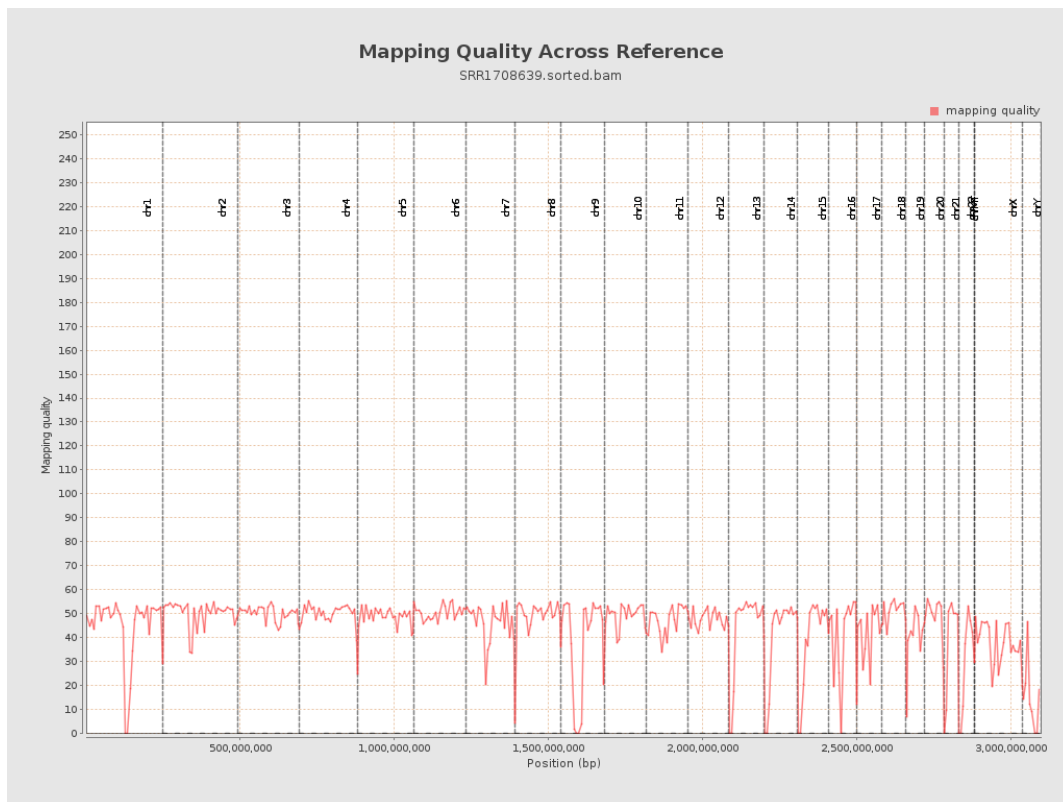
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

