

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 11:37:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173951.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_SRR10173951 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173951_1.fastq.gz SRR10173951_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 11:37:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173951.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,264,570
Mapped reads	1,235,376 / 97.69%
Unmapped reads	29,194 / 2.31%
Mapped paired reads	1,235,376 / 97.69%
Mapped reads, first in pair	618,867 / 48.94%
Mapped reads, second in pair	616,509 / 48.75%
Mapped reads, both in pair	1,216,158 / 96.17%
Mapped reads, singletons	19,218 / 1.52%
Secondary alignments	0
Supplementary alignments	123,233 / 9.75%
Read min/max/mean length	30 / 133 / 128.31
Duplicated reads (estimated)	921,681 / 72.88%
Duplication rate	62.41%
Clipped reads	491,709 / 38.88%

2.2. ACGT Content

Number/percentage of A's	44,346,048 / 30.28%
Number/percentage of C's	28,349,851 / 19.36%
Number/percentage of T's	44,239,802 / 30.21%
Number/percentage of G's	29,504,171 / 20.15%
Number/percentage of N's	1,972 / 0%

GC Percentage	39.51%
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2.3. Coverage

Mean	0.0473
Standard Deviation	0.8629

2.4. Mapping Quality

Mean Mapping Quality	52.84
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2.5. Insert size

Mean	1,055,370.33
Standard Deviation	9,705,979.81
P25/Median/P75	148 / 205 / 296

2.6. Mismatches and indels

General error rate	1.12%
Mismatches	1,585,116
Insertions	18,580
Mapped reads with at least one insertion	1.44%
Deletions	41,347
Mapped reads with at least one deletion	3.25%
Homopolymer indels	41.76%

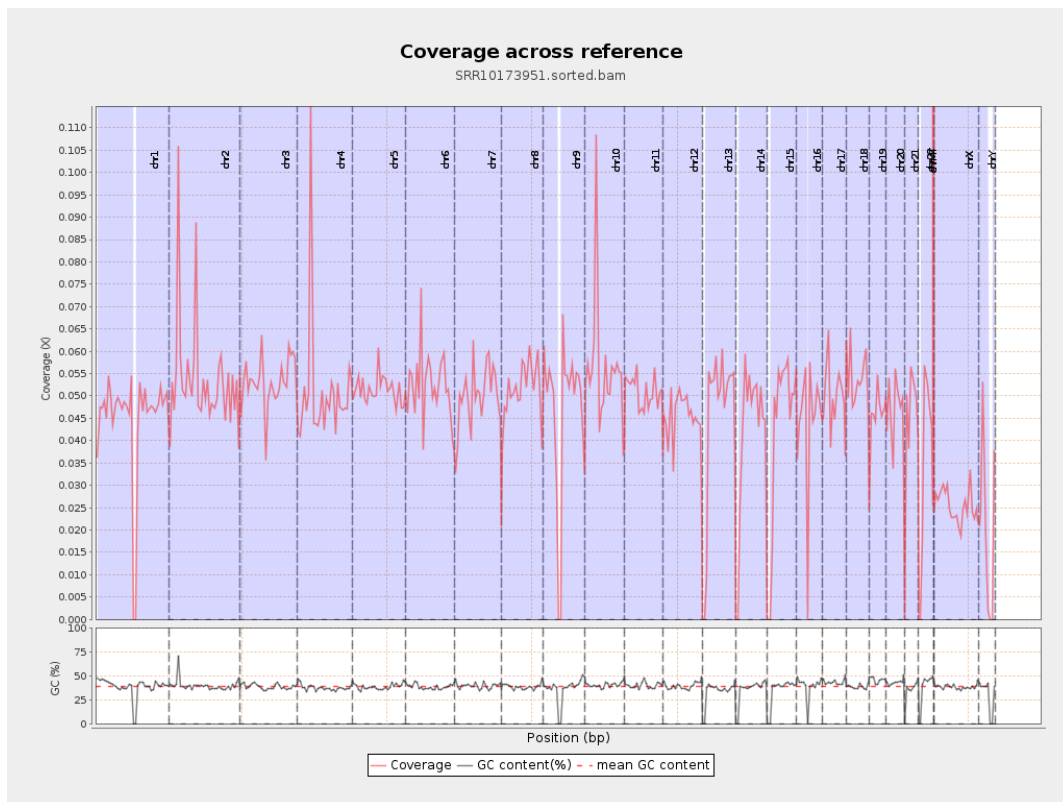
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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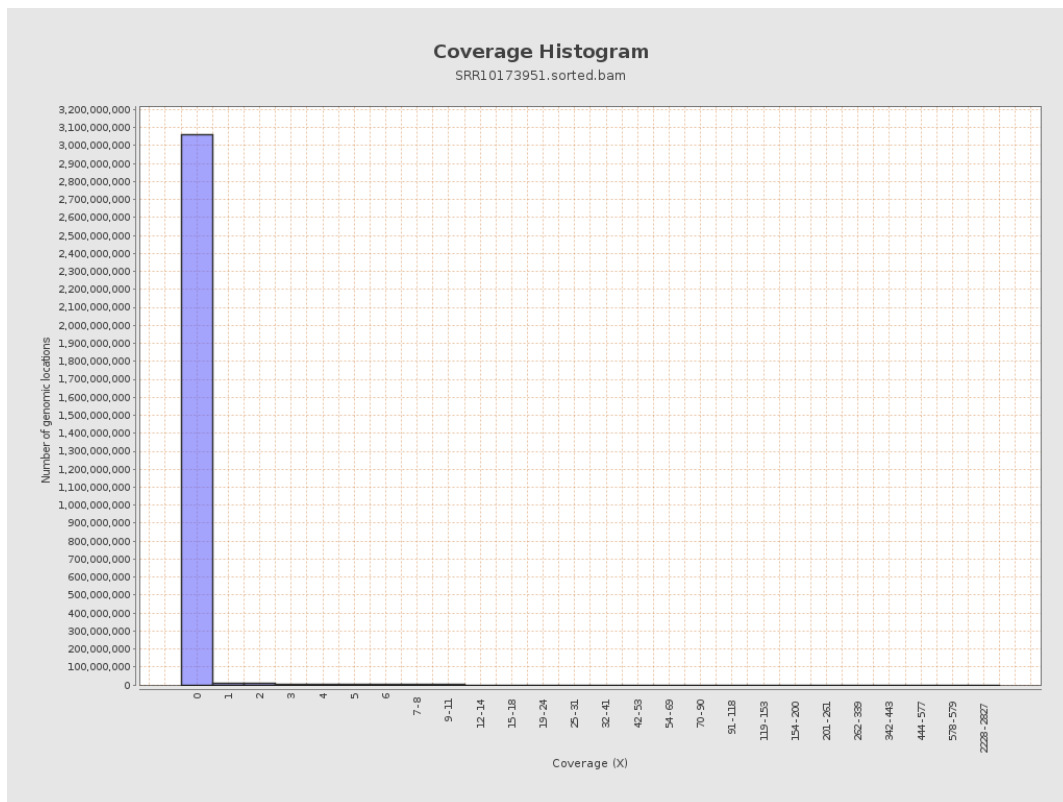
		bases	coverage	deviation
chr1	249250621	11216055	0.045	0.6659
chr2	243199373	13108783	0.0539	2.0703
chr3	198022430	10539210	0.0532	0.6408
chr4	191154276	9643258	0.0504	0.7614
chr5	180915260	9291959	0.0514	0.6265
chr6	171115067	8901368	0.052	0.678
chr7	159138663	8017001	0.0504	0.7177
chr8	146364022	7540311	0.0515	0.7278
chr9	141213431	6583270	0.0466	0.7661
chr10	135534747	7622637	0.0562	0.8237
chr11	135006516	6843778	0.0507	0.6157
chr12	133851895	6085118	0.0455	0.5897
chr13	115169878	5155700	0.0448	0.5885
chr14	107349540	4450559	0.0415	0.5596
chr15	102531392	4306323	0.042	0.5519
chr16	90354753	4021957	0.0445	0.6166
chr17	81195210	4026089	0.0496	0.6284
chr18	78077248	4235567	0.0542	0.9308
chr19	59128983	2748523	0.0465	0.618
chr20	63025520	2948748	0.0468	0.6082
chr21	48129895	2117312	0.044	0.6399
chr22	51304566	1738582	0.0339	0.4991
chrMT	16571	303494	18.3148	17.9978
chrX	155270560	3943867	0.0254	0.441

chrY	59373566	1152808	0.0194	0.5748
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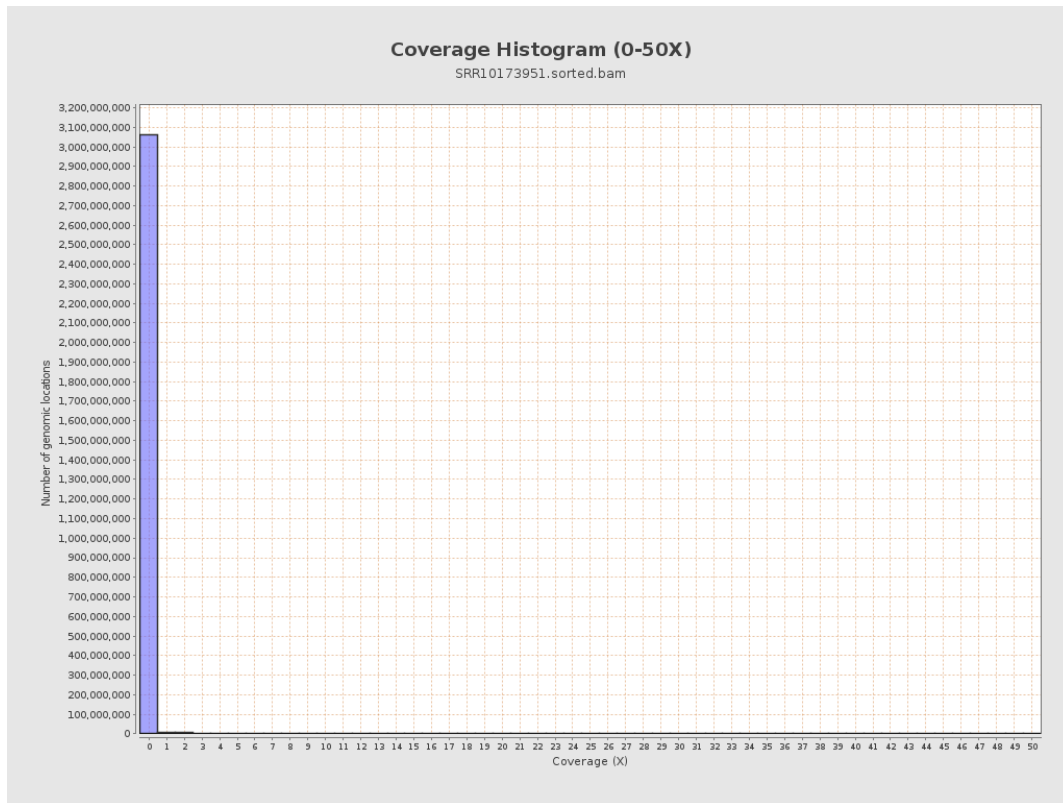
3. Results : Coverage across reference



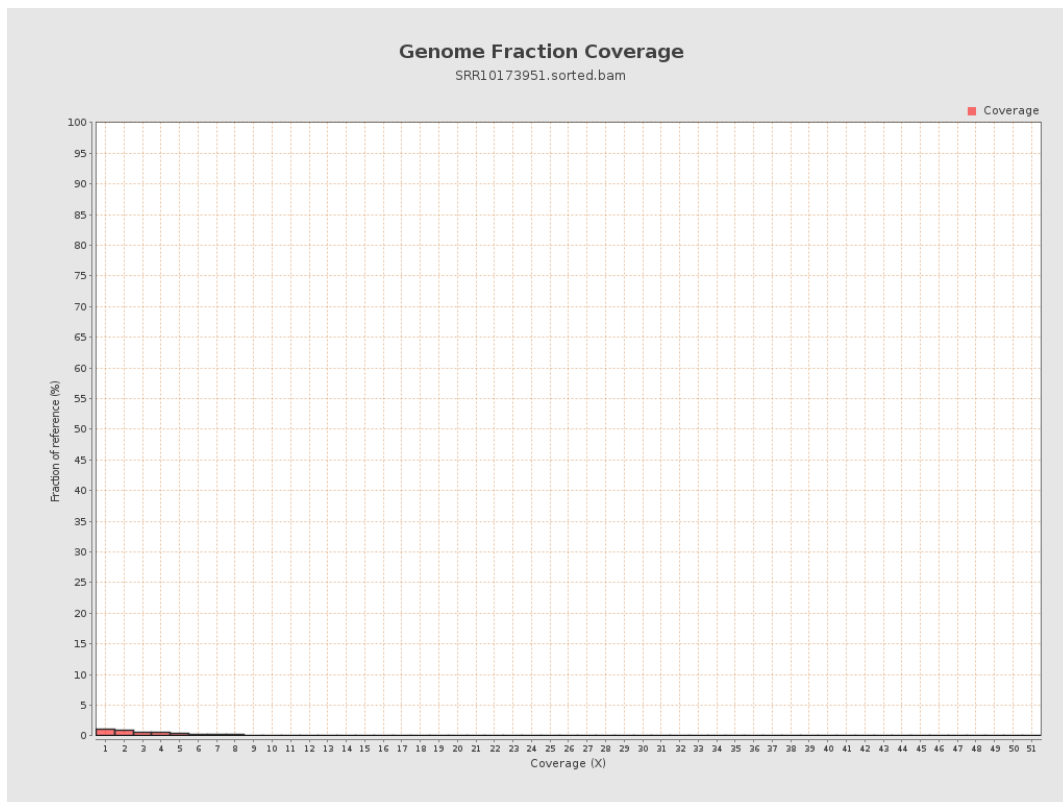
4. Results : Coverage Histogram



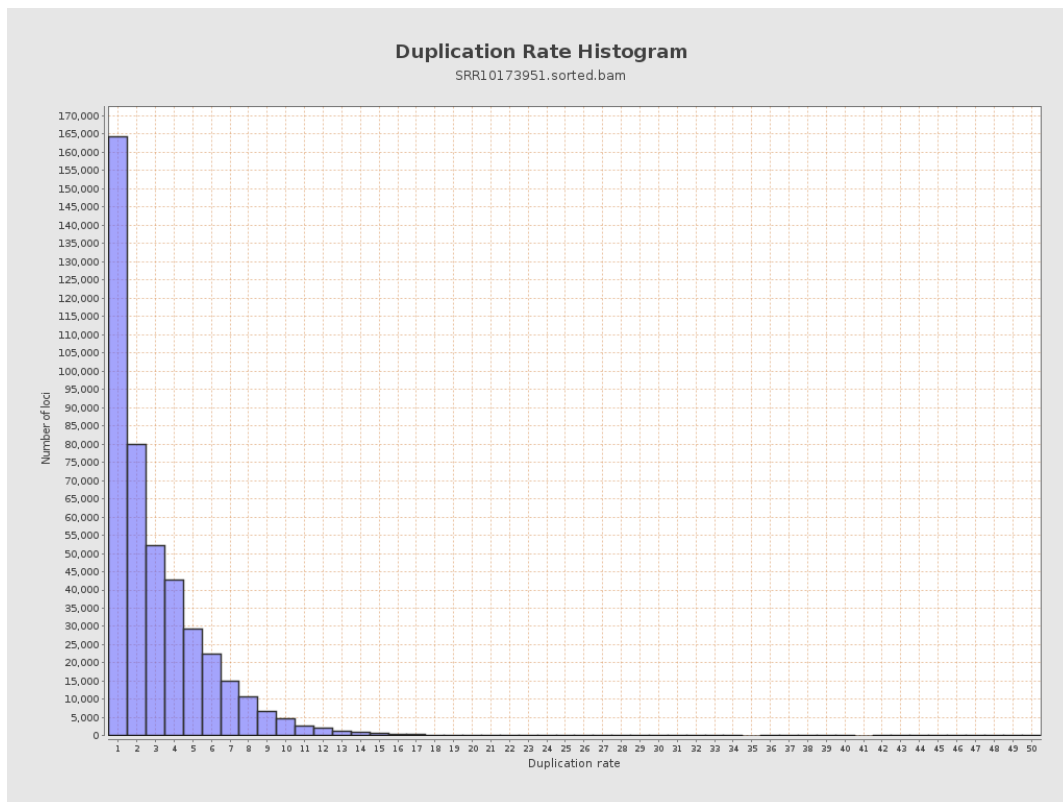
5. Results : Coverage Histogram (0-50X)



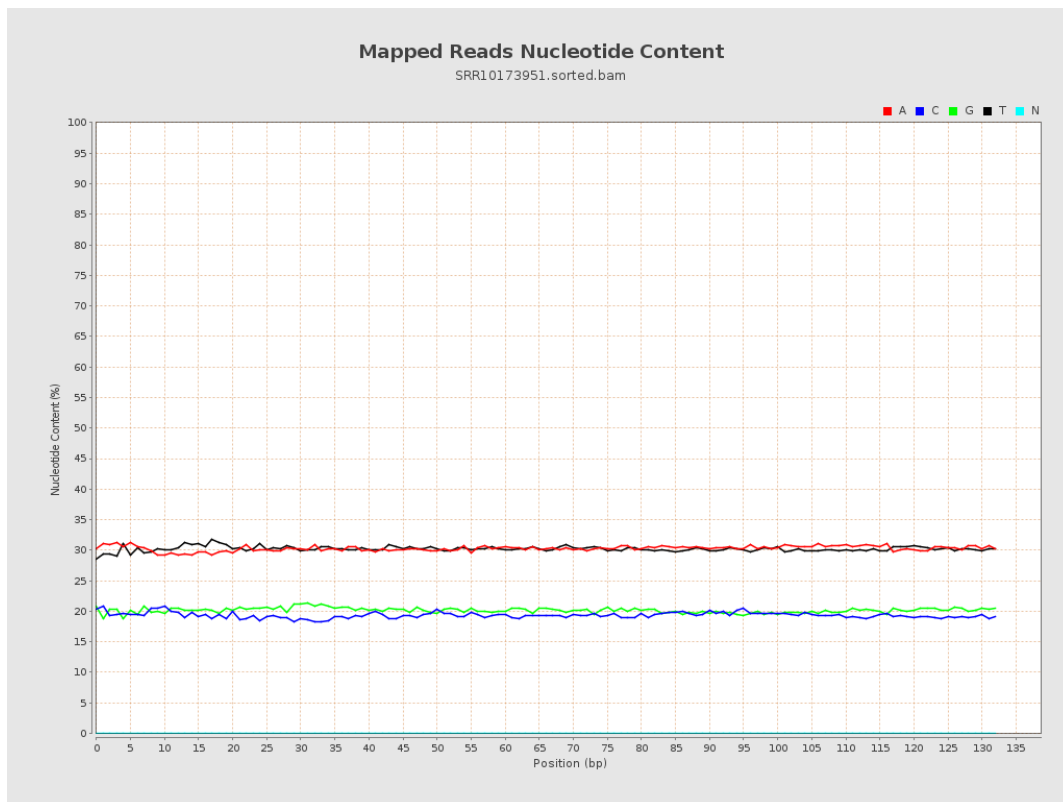
6. Results : Genome Fraction Coverage



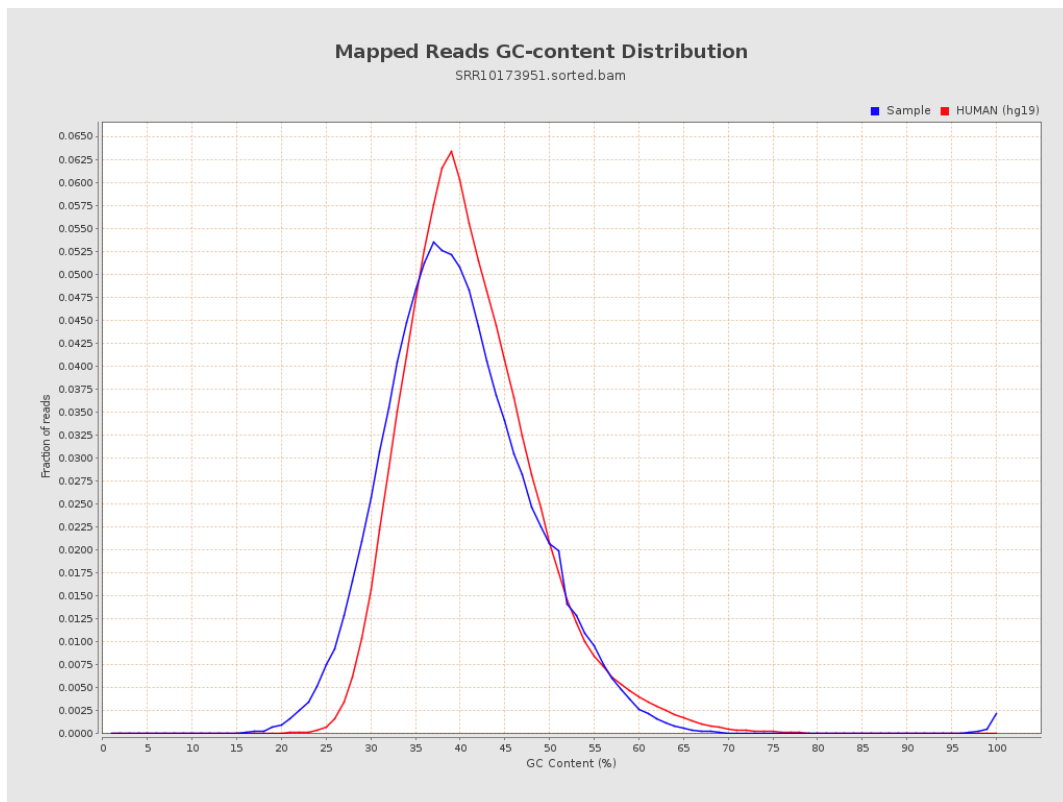
7. Results : Duplication Rate Histogram



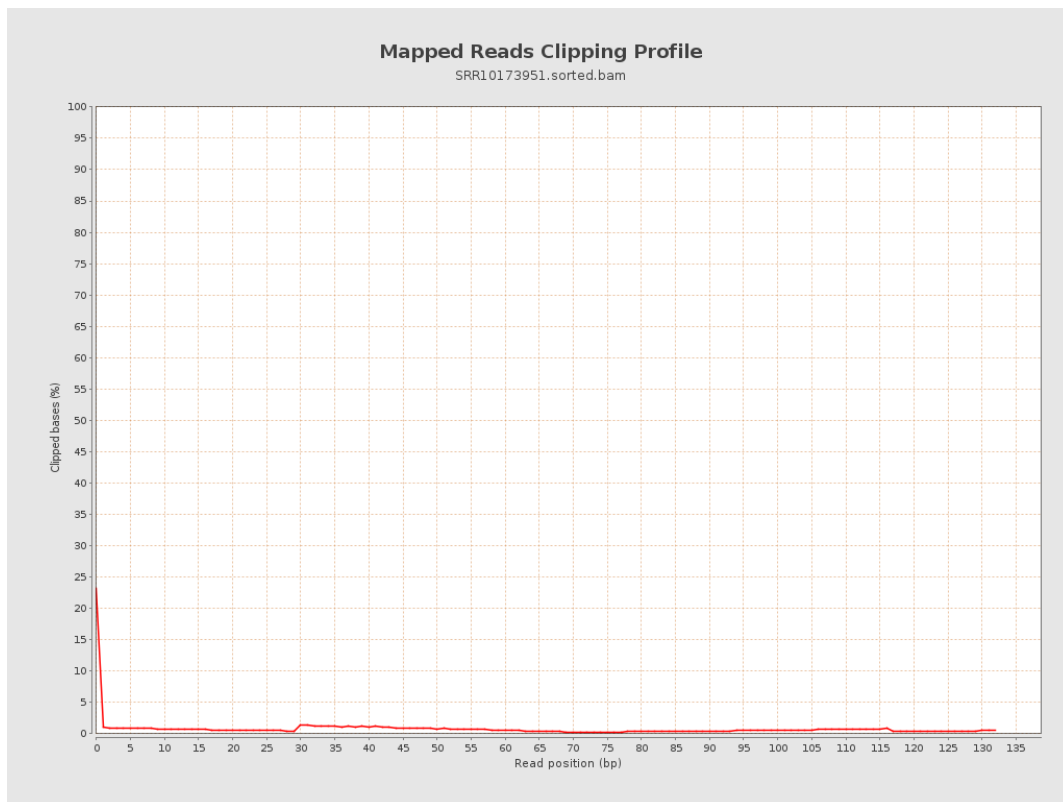
8. Results : Mapped Reads Nucleotide Content



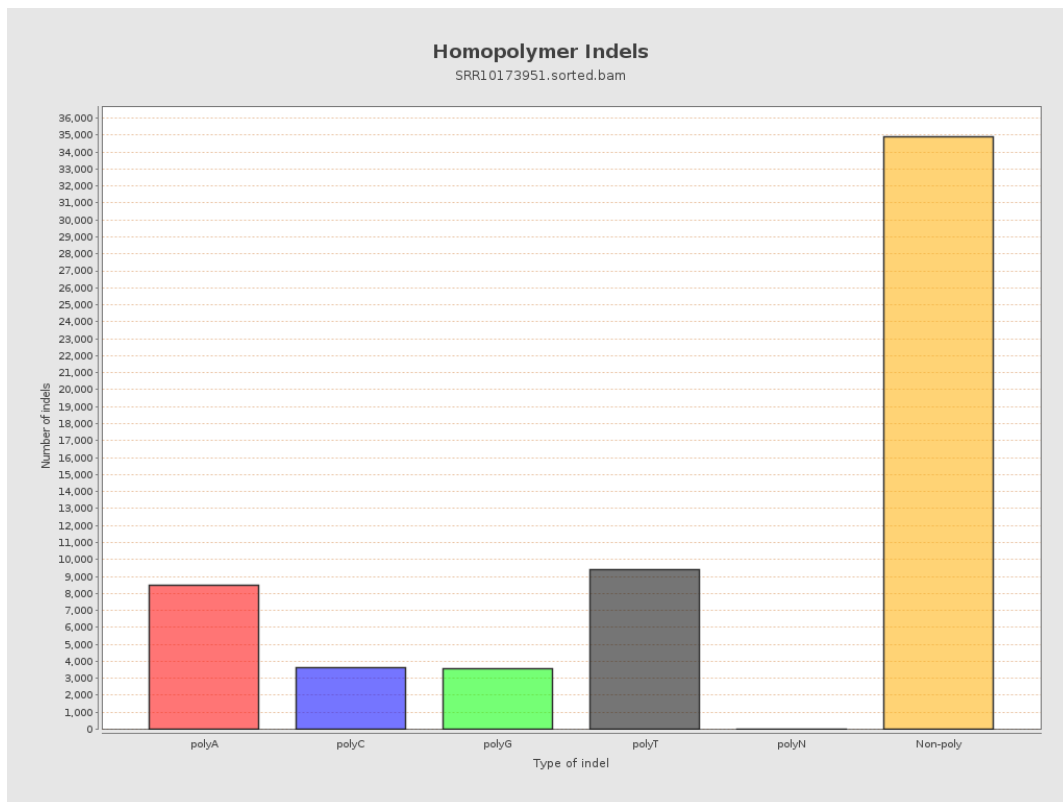
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



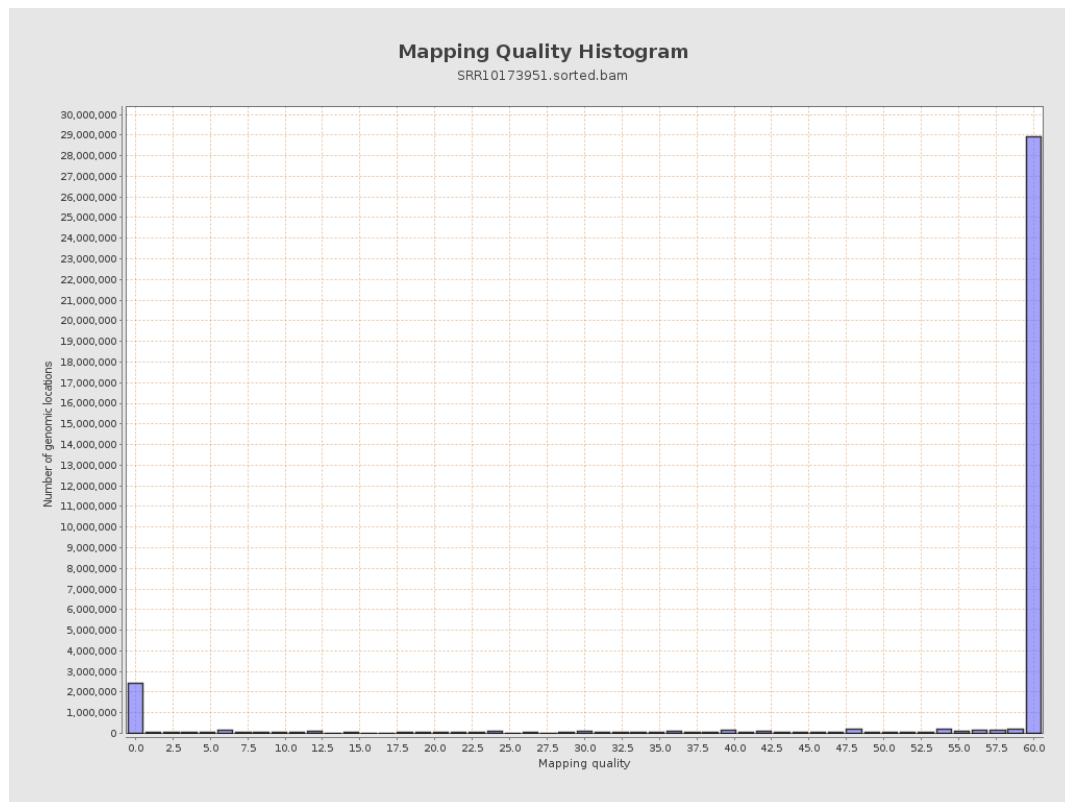
11. Results : Homopolymer Indels



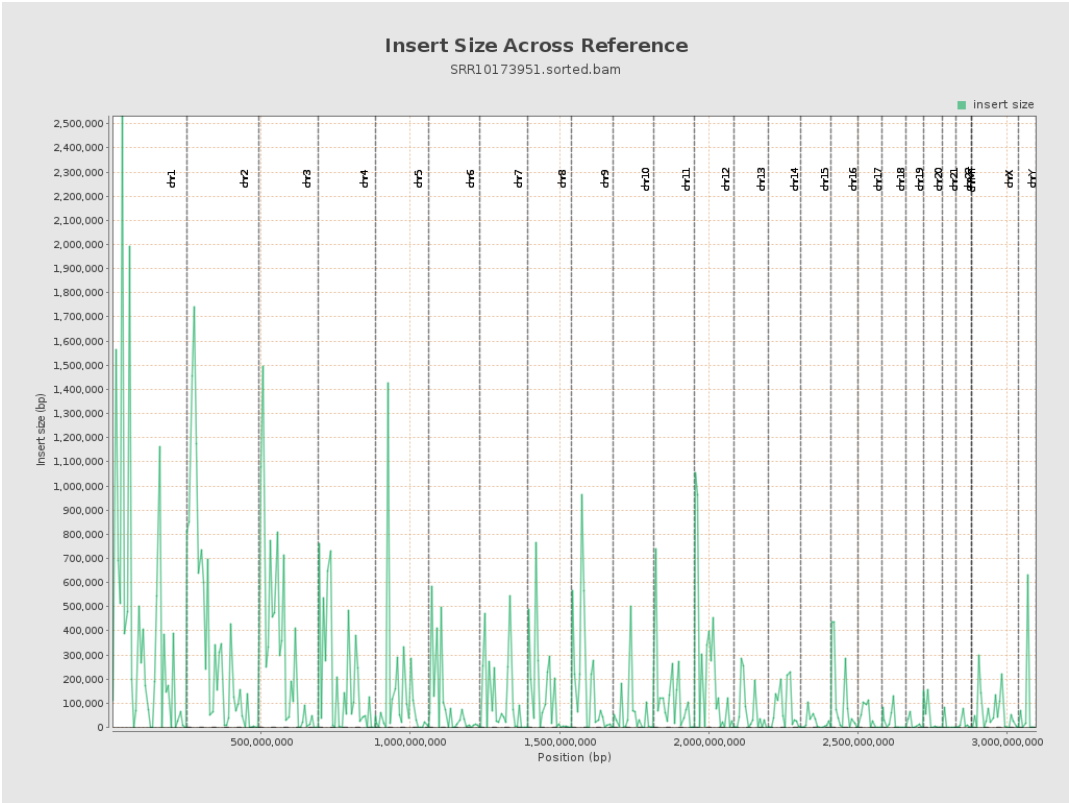
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

