

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 12:10:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10251073.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_SRR10251073 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10251073_1.fastq.gz SRR10251073_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 12:10:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10251073.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,409,266
Mapped reads	466,091 / 33.07%
Unmapped reads	943,175 / 66.93%
Mapped paired reads	466,091 / 33.07%
Mapped reads, first in pair	233,566 / 16.57%
Mapped reads, second in pair	232,525 / 16.5%
Mapped reads, both in pair	455,114 / 32.29%
Mapped reads, singletons	10,977 / 0.78%
Secondary alignments	0
Supplementary alignments	18,888 / 1.34%
Read min/max/mean length	30 / 127 / 127.59
Duplicated reads (estimated)	249,149 / 17.68%
Duplication rate	48.72%
Clipped reads	162,109 / 11.5%

2.2. ACGT Content

Number/percentage of A's	16,523,944 / 30.01%
Number/percentage of C's	10,959,867 / 19.9%
Number/percentage of T's	16,431,969 / 29.84%
Number/percentage of G's	11,148,233 / 20.25%
Number/percentage of N's	2,015 / 0%

GC Percentage	40.15%
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2.3. Coverage

Mean	0.0178
Standard Deviation	0.3999

2.4. Mapping Quality

Mean Mapping Quality	52.08
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2.5. Insert size

Mean	95,891.33
Standard Deviation	2,873,331.36
P25/Median/P75	133 / 168 / 222

2.6. Mismatches and indels

General error rate	0.9%
Mismatches	458,485
Insertions	13,148
Mapped reads with at least one insertion	2.53%
Deletions	24,769
Mapped reads with at least one deletion	5%
Homopolymer indels	41.7%

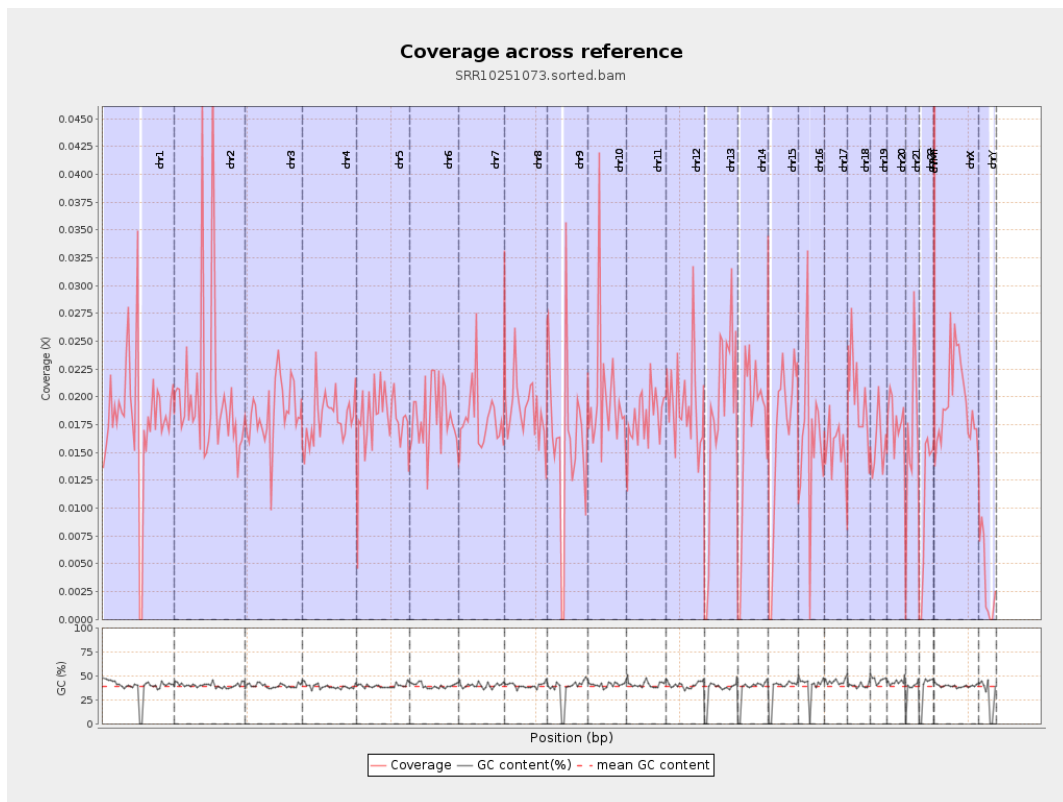
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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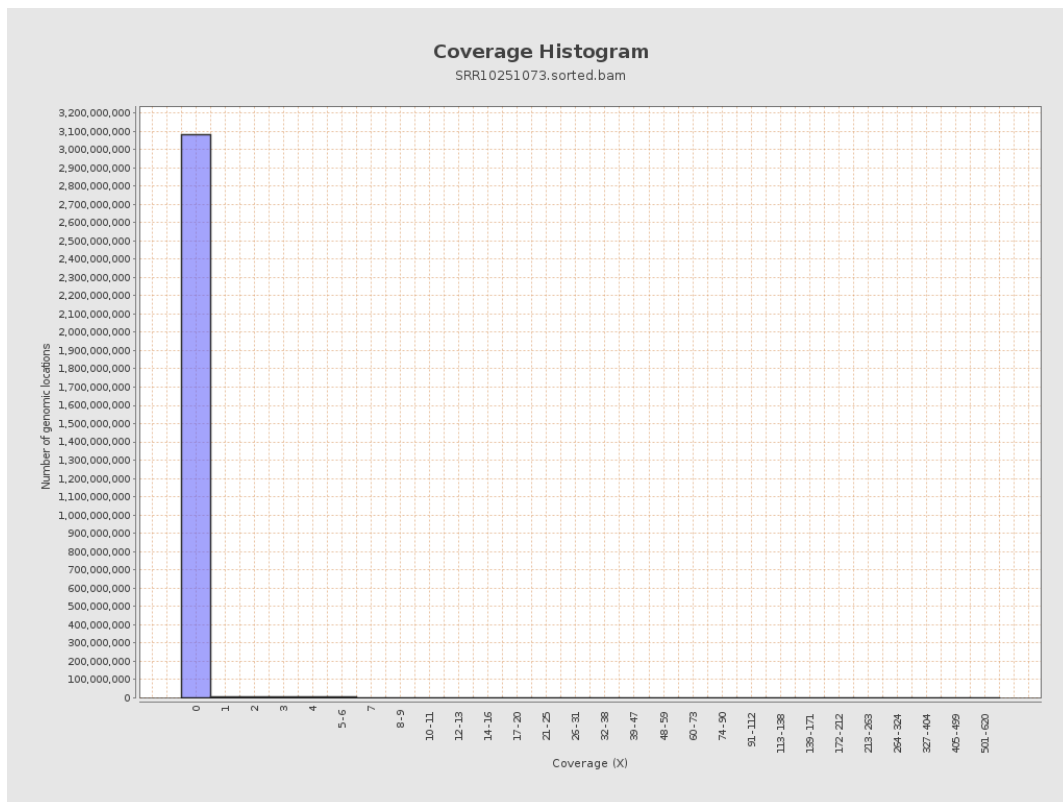
		bases	coverage	deviation
chr1	249250621	4488686	0.018	0.5273
chr2	243199373	4870494	0.02	0.5776
chr3	198022430	3672309	0.0185	0.3345
chr4	191154276	3474757	0.0182	0.3479
chr5	180915260	3322314	0.0184	0.3293
chr6	171115067	3098433	0.0181	0.3439
chr7	159138663	2883330	0.0181	0.4075
chr8	146364022	2754668	0.0188	0.3924
chr9	141213431	2273392	0.0161	0.4363
chr10	135534747	2673598	0.0197	0.4698
chr11	135006516	2458796	0.0182	0.3592
chr12	133851895	2591363	0.0194	0.358
chr13	115169878	2099242	0.0182	0.3334
chr14	107349540	1841453	0.0172	0.3284
chr15	102531392	1699593	0.0166	0.3166
chr16	90354753	1444767	0.016	0.4175
chr17	81195210	1243172	0.0153	0.2996
chr18	78077248	1556093	0.0199	0.4404
chr19	59128983	936583	0.0158	0.374
chr20	63025520	1132027	0.018	0.3311
chr21	48129895	786096	0.0163	0.3292
chr22	51304566	552687	0.0108	0.2596
chrMT	16571	24122	1.4557	2.7083
chrX	155270560	3042192	0.0196	0.3498

chrY	59373566	201182	0.0034	0.2376
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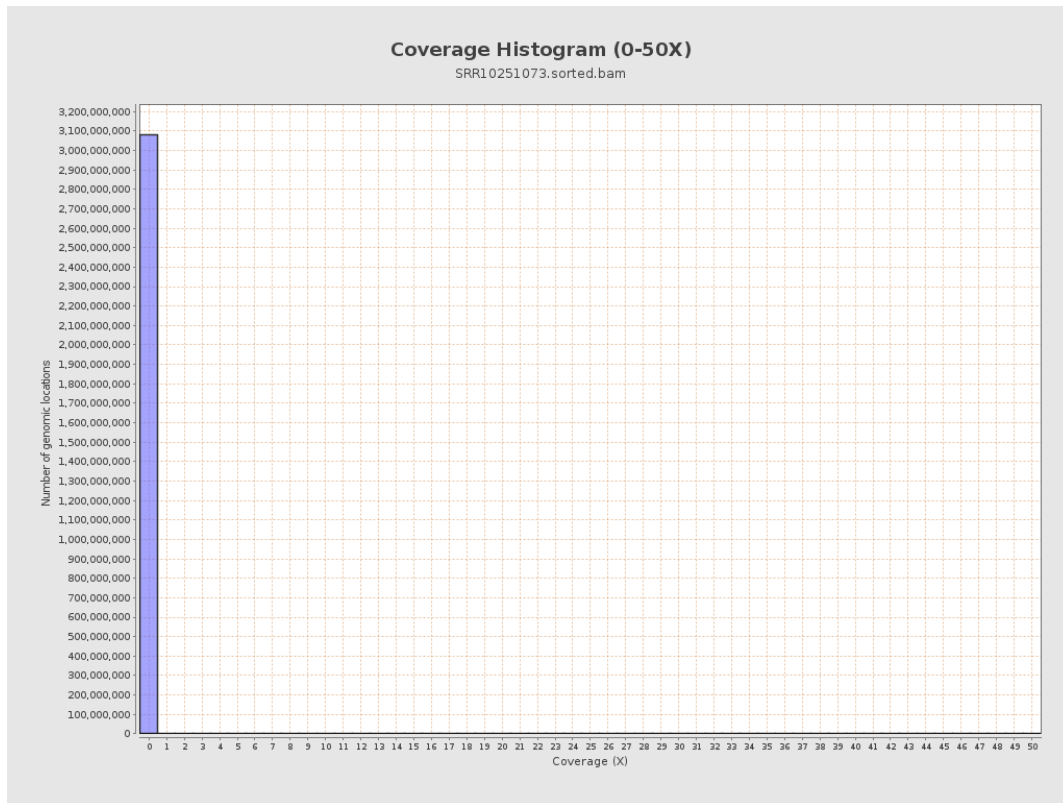
3. Results : Coverage across reference



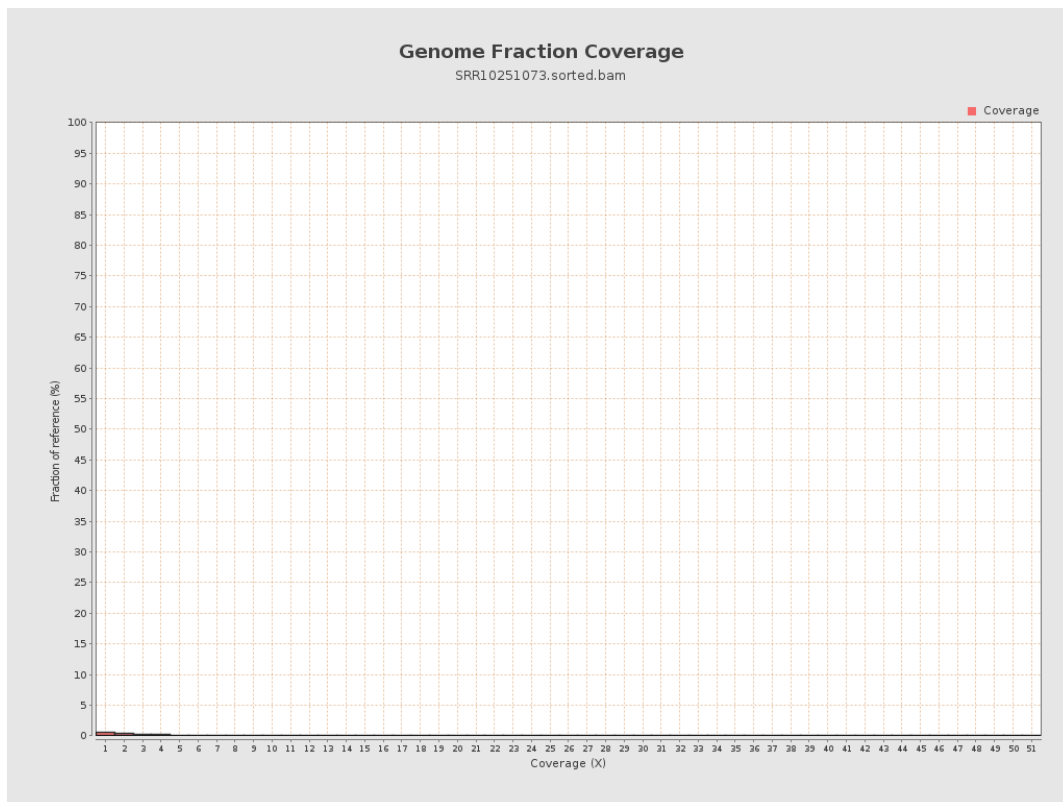
4. Results : Coverage Histogram



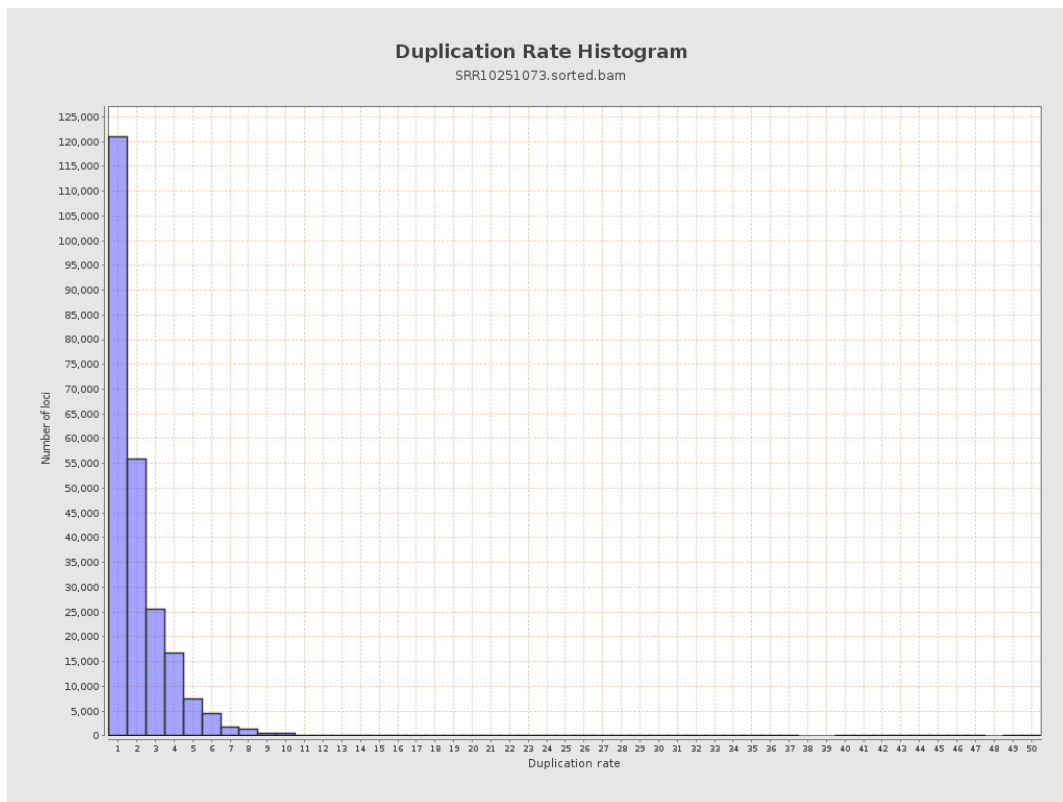
5. Results : Coverage Histogram (0-50X)



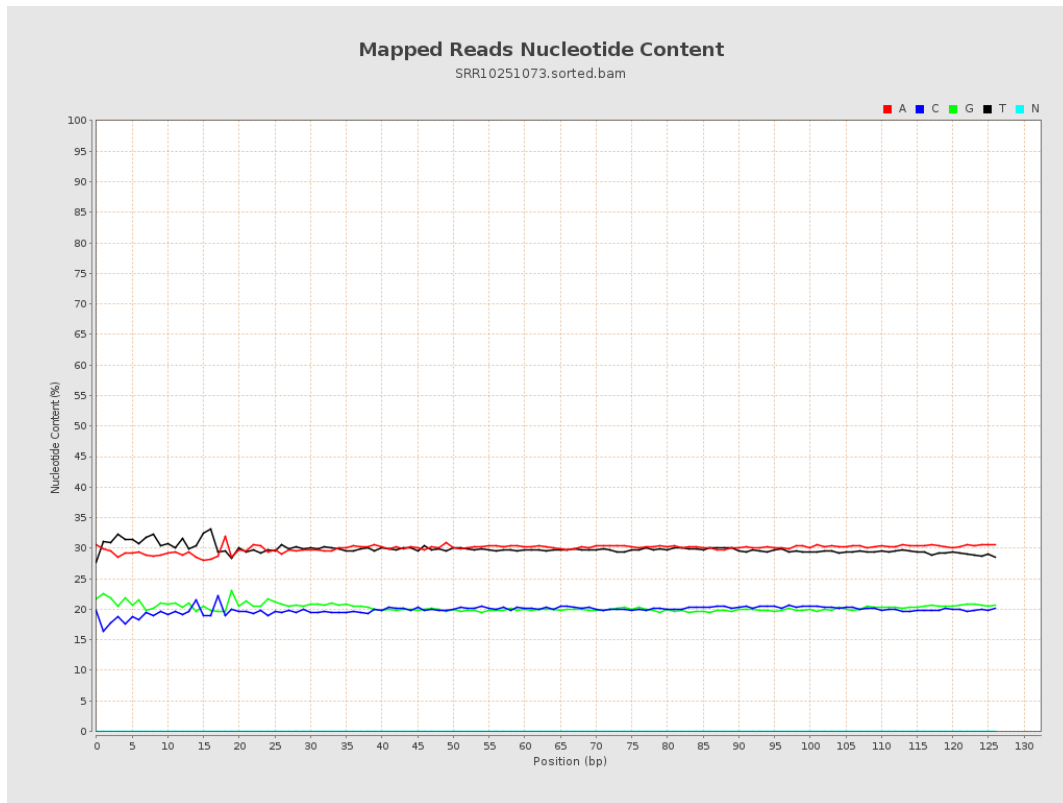
6. Results : Genome Fraction Coverage



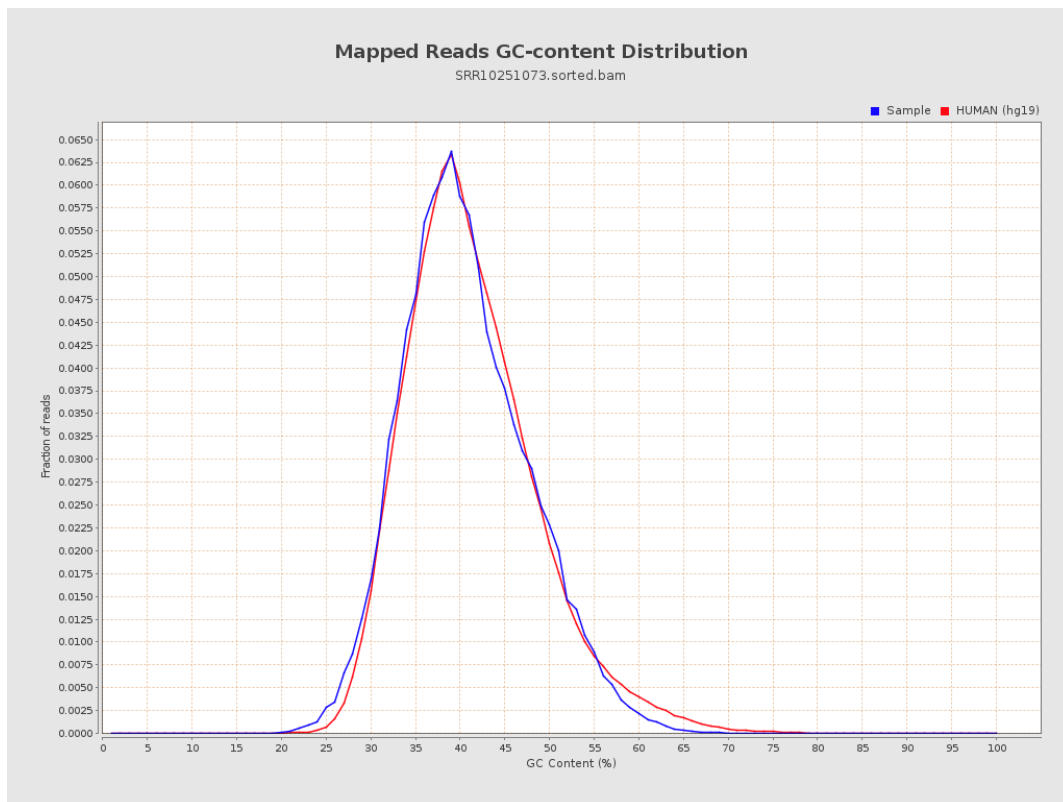
7. Results : Duplication Rate Histogram



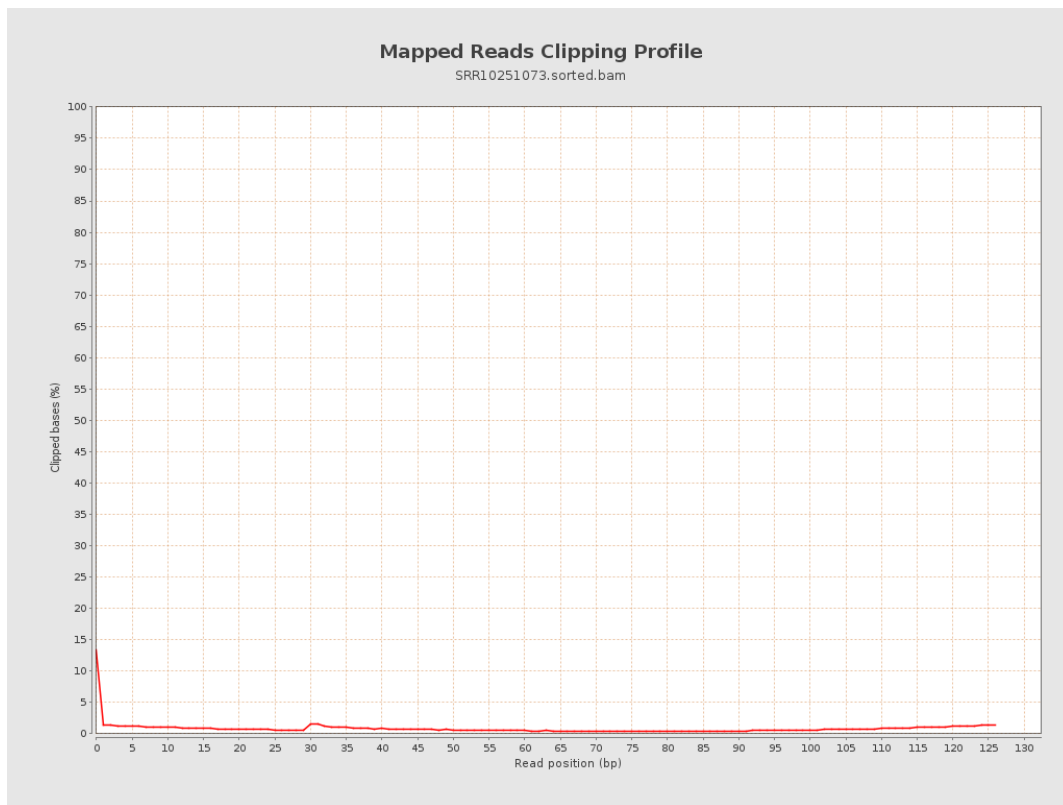
8. Results : Mapped Reads Nucleotide Content



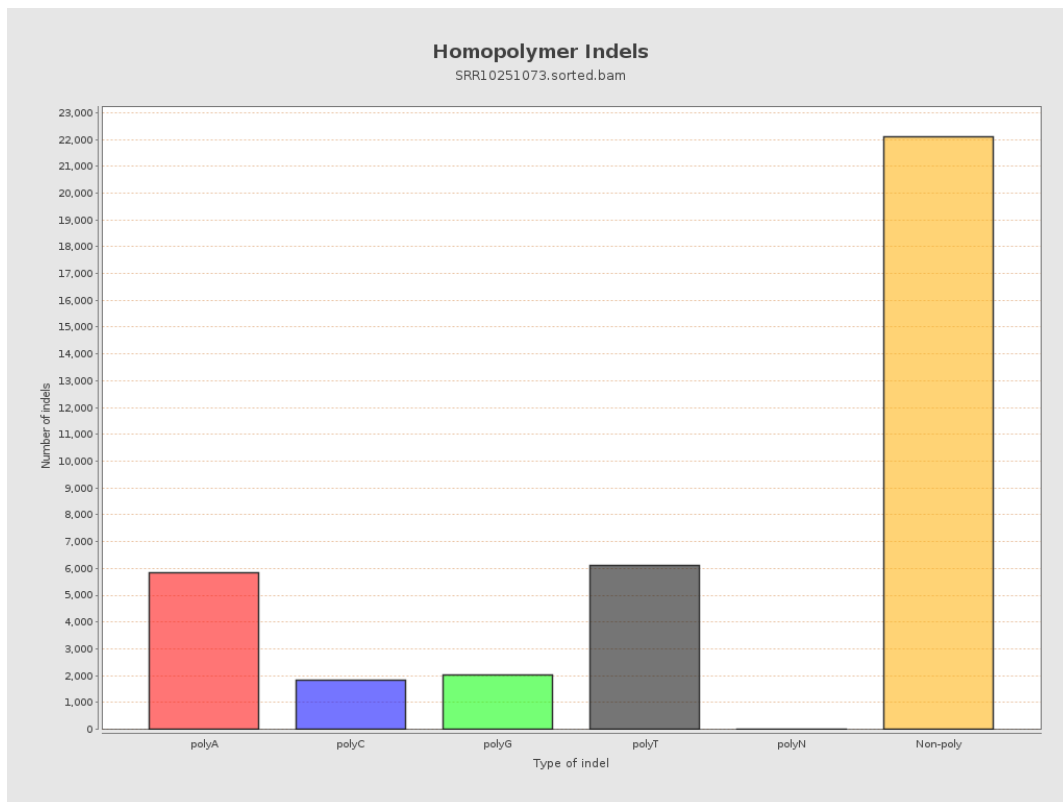
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



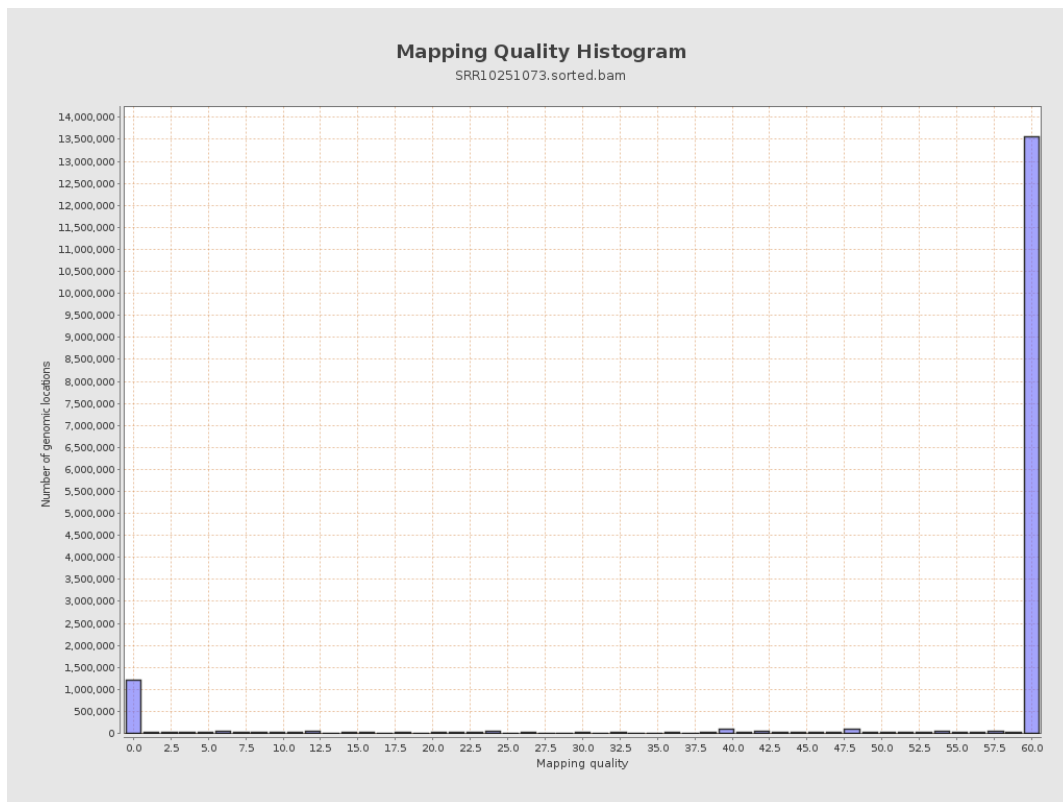
11. Results : Homopolymer Indels



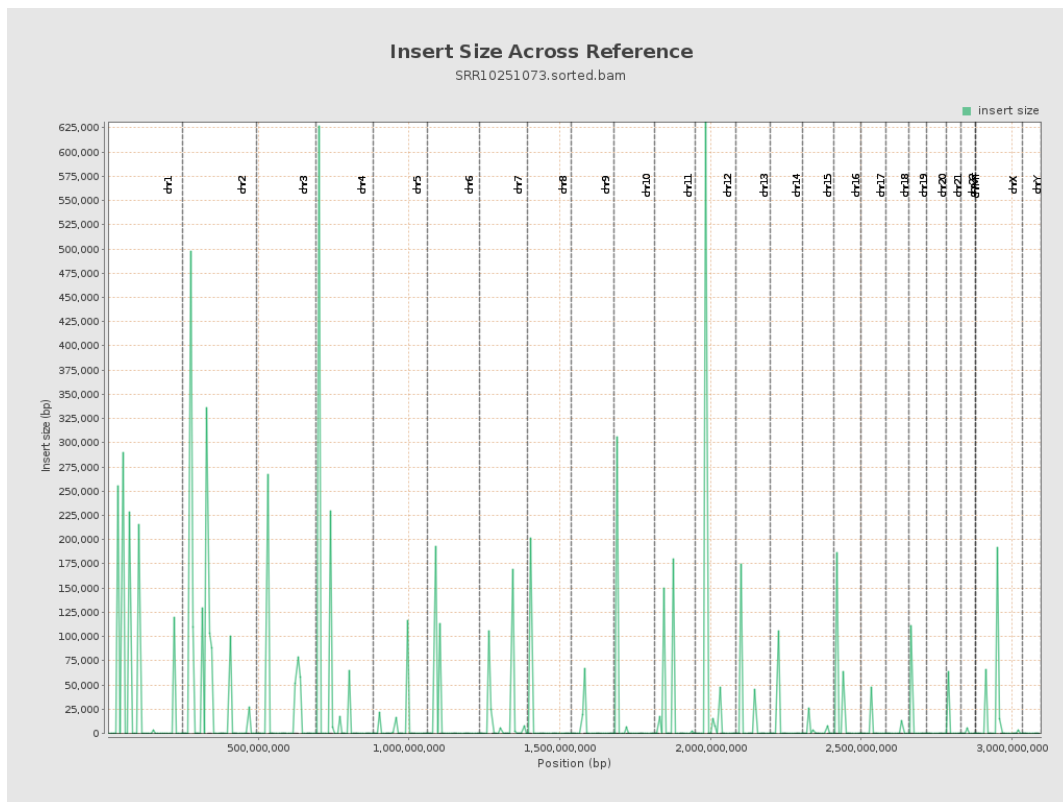
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

