

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 01:36:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173883.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_SRR10173883 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173883_1.fastq.gz SRR10173883_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 01:36:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173883.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,768,978
Mapped reads	1,725,961 / 97.57%
Unmapped reads	43,017 / 2.43%
Mapped paired reads	1,725,961 / 97.57%
Mapped reads, first in pair	863,910 / 48.84%
Mapped reads, second in pair	862,051 / 48.73%
Mapped reads, both in pair	1,698,638 / 96.02%
Mapped reads, singletons	27,323 / 1.54%
Secondary alignments	0
Supplementary alignments	174,102 / 9.84%
Read min/max/mean length	30 / 133 / 128.2
Duplicated reads (estimated)	1,298,930 / 73.43%
Duplication rate	62.71%
Clipped reads	689,658 / 38.99%

2.2. ACGT Content

Number/percentage of A's	62,177,104 / 30.43%
Number/percentage of C's	39,368,869 / 19.27%
Number/percentage of T's	61,942,069 / 30.31%
Number/percentage of G's	40,854,358 / 19.99%
Number/percentage of N's	2,456 / 0%

GC Percentage	39.26%
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2.3. Coverage

Mean	0.066
Standard Deviation	1.1191

2.4. Mapping Quality

Mean Mapping Quality	53
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2.5. Insert size

Mean	1,049,875.53
Standard Deviation	9,621,672.92
P25/Median/P75	142 / 195 / 274

2.6. Mismatches and indels

General error rate	1.06%
Mismatches	2,092,541
Insertions	23,453
Mapped reads with at least one insertion	1.31%
Deletions	51,209
Mapped reads with at least one deletion	2.9%
Homopolymer indels	42.47%

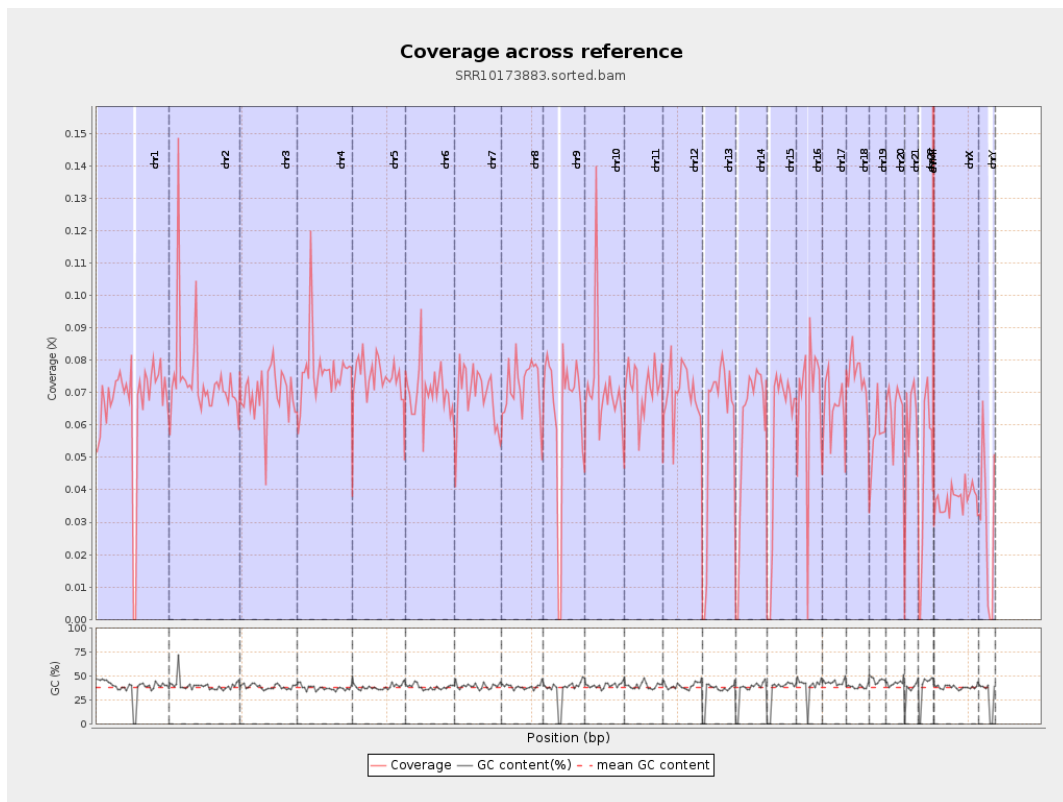
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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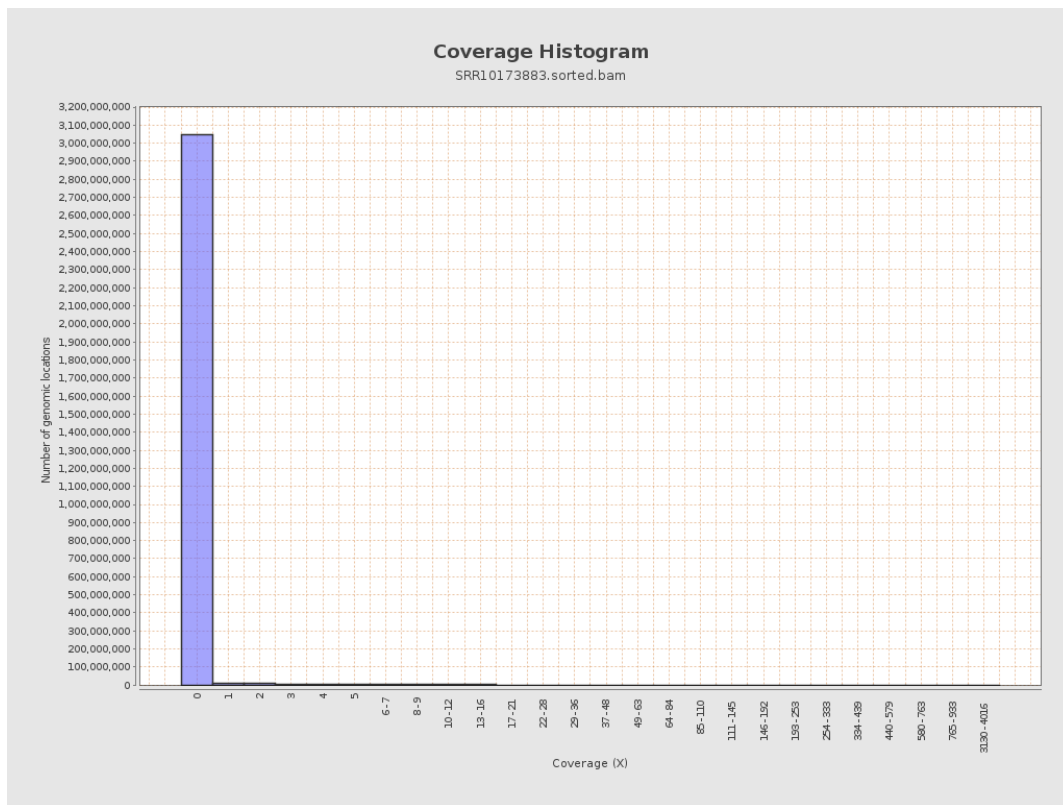
		bases	coverage	deviation
chr1	249250621	16529992	0.0663	0.876
chr2	243199373	18051052	0.0742	2.895
chr3	198022430	13771741	0.0695	0.7445
chr4	191154276	14632171	0.0765	0.8924
chr5	180915260	13554020	0.0749	0.7757
chr6	171115067	12032842	0.0703	0.7888
chr7	159138663	11084819	0.0697	0.8248
chr8	146364022	10512844	0.0718	0.9423
chr9	141213431	9094484	0.0644	0.8635
chr10	135534747	9726266	0.0718	1.0001
chr11	135006516	9652494	0.0715	0.7583
chr12	133851895	9313140	0.0696	0.7389
chr13	115169878	6872176	0.0597	0.7014
chr14	107349540	6333074	0.059	0.6919
chr15	102531392	5827913	0.0568	0.6597
chr16	90354753	6084317	0.0673	0.7965
chr17	81195210	5240370	0.0645	0.7331
chr18	78077248	5889181	0.0754	1.0544
chr19	59128983	3337673	0.0564	0.6938
chr20	63025520	4040285	0.0641	0.7193
chr21	48129895	2765462	0.0575	0.8172
chr22	51304566	2268876	0.0442	0.6225
chrMT	16571	462478	27.9089	21.7926
chrX	155270560	5762308	0.0371	0.5399

chrY	59373566	1627393	0.0274	0.5869
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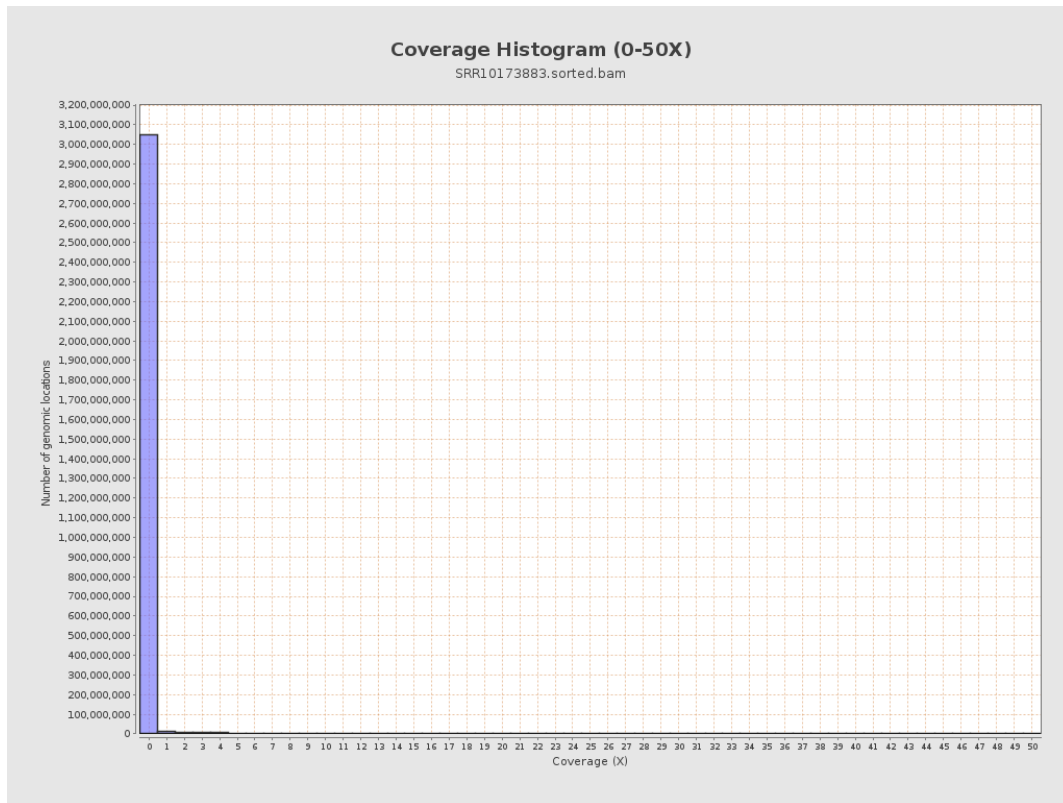
3. Results : Coverage across reference



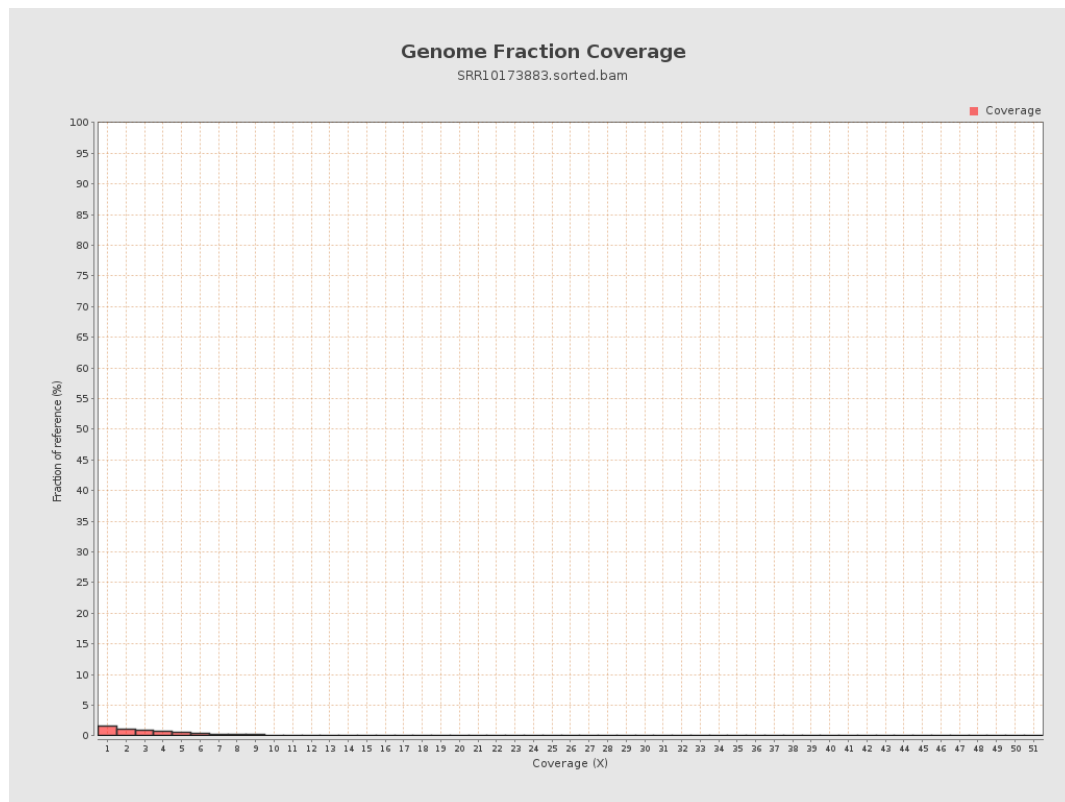
4. Results : Coverage Histogram



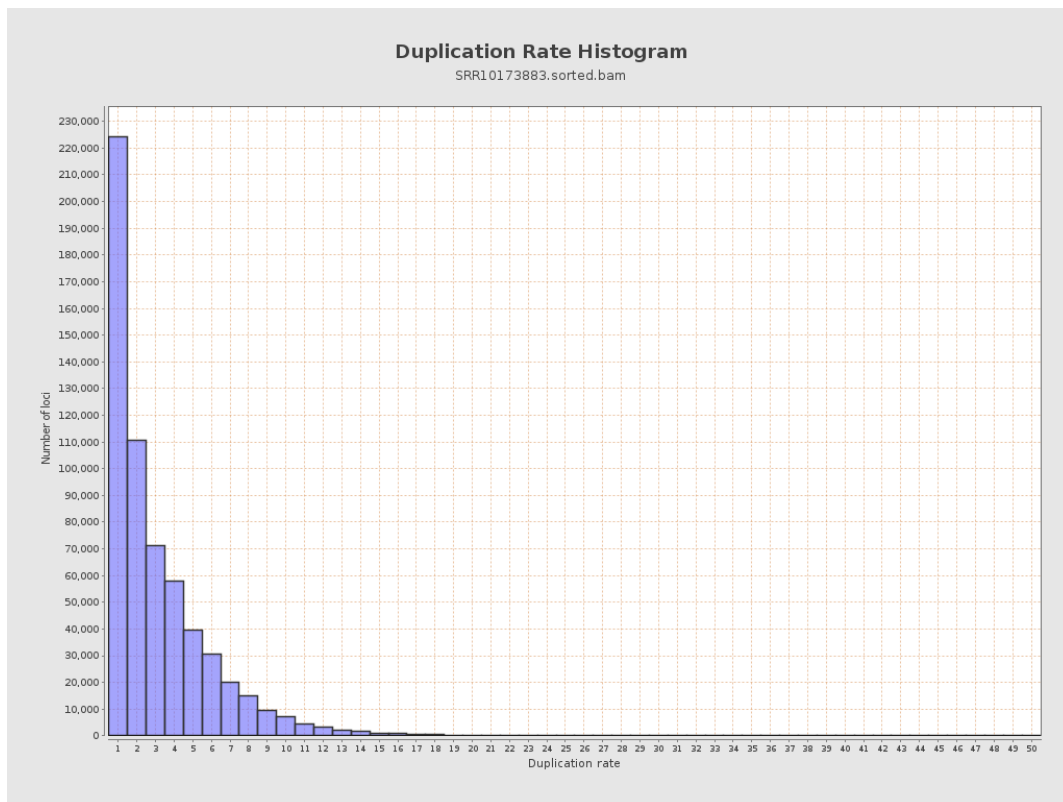
5. Results : Coverage Histogram (0-50X)



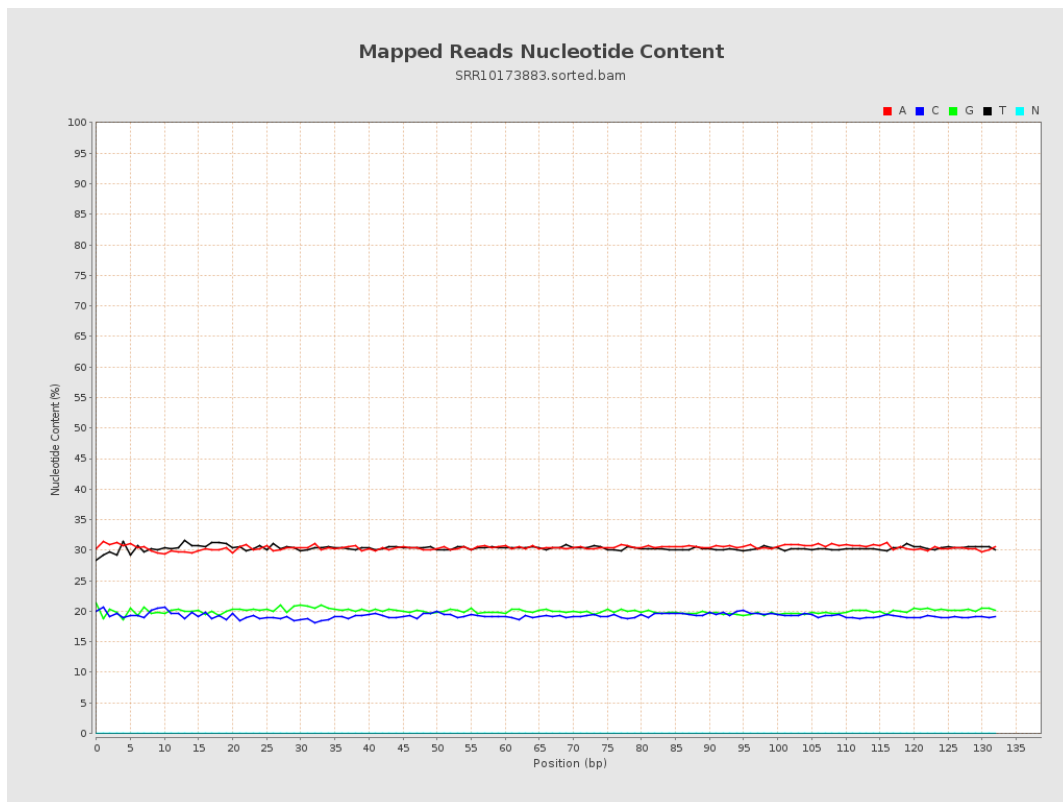
6. Results : Genome Fraction Coverage



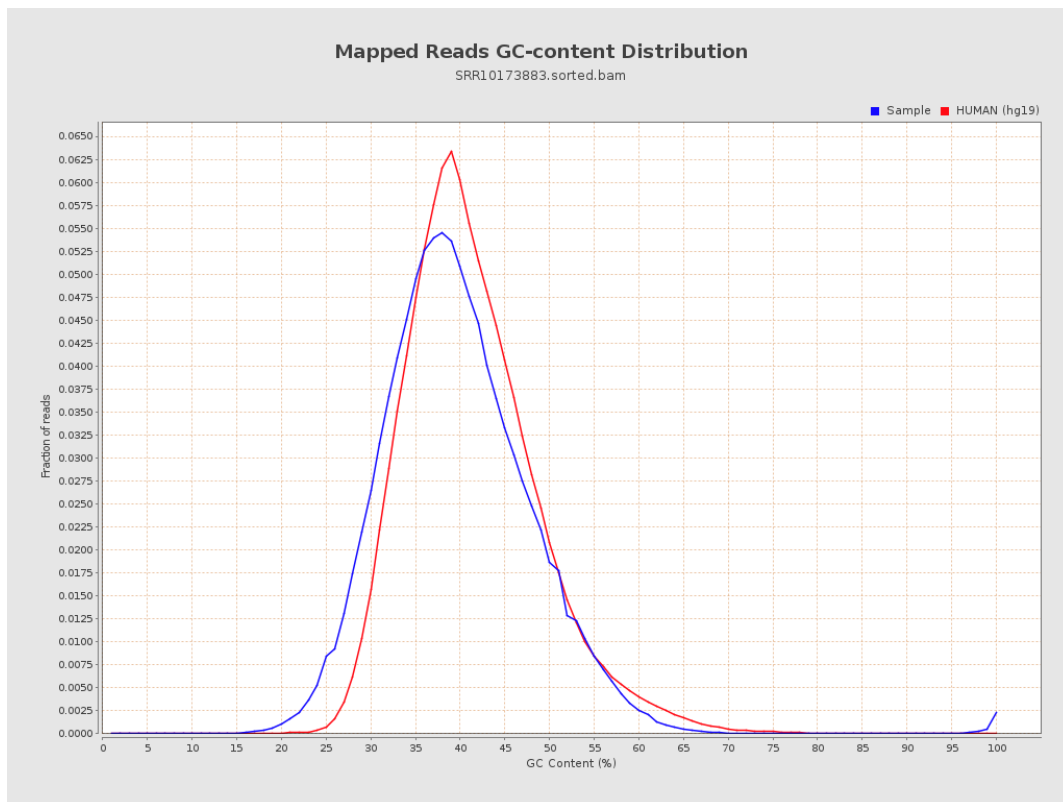
7. Results : Duplication Rate Histogram



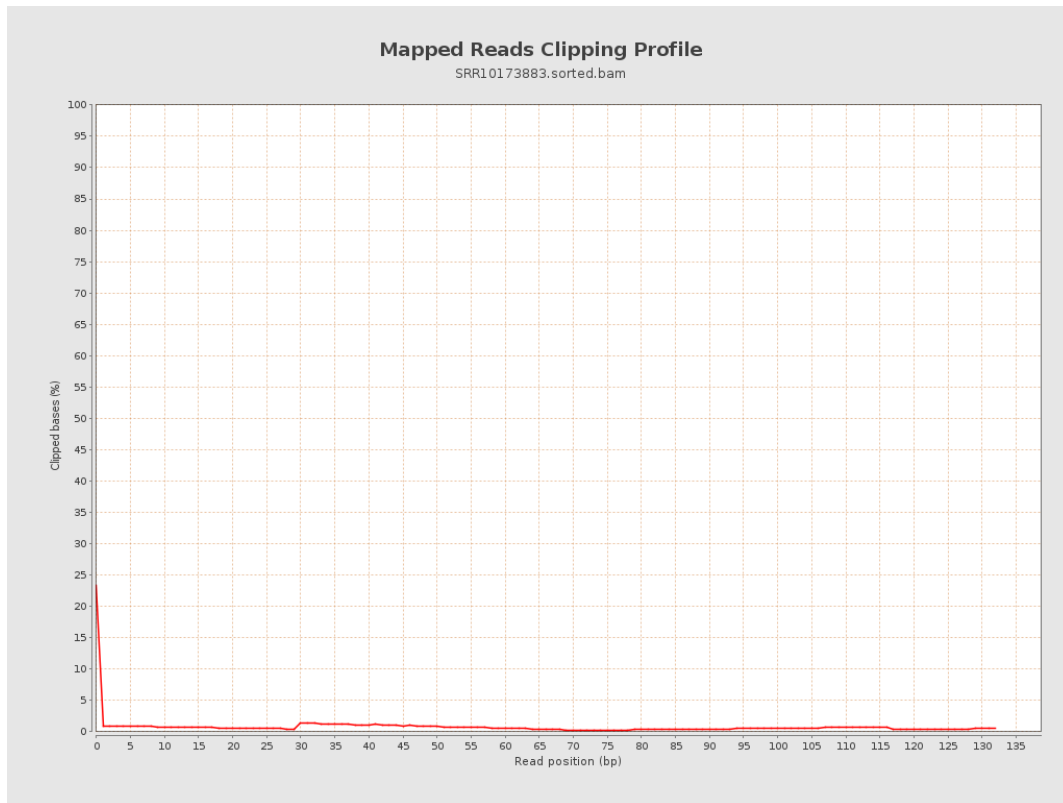
8. Results : Mapped Reads Nucleotide Content



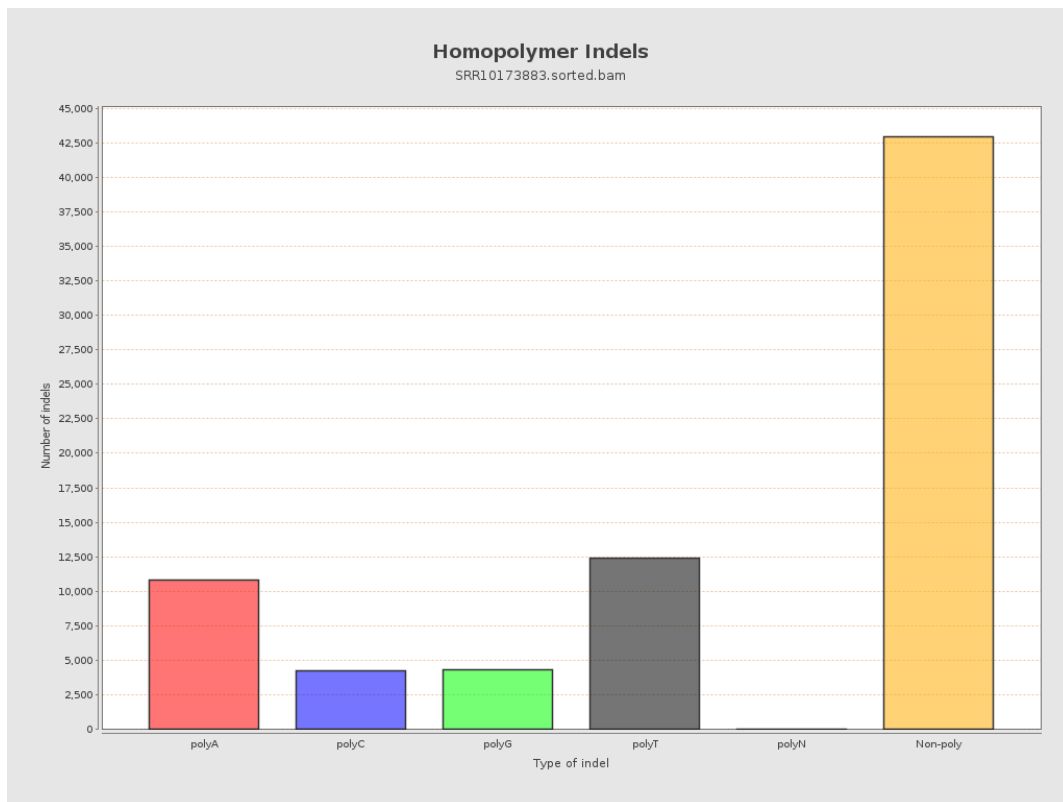
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



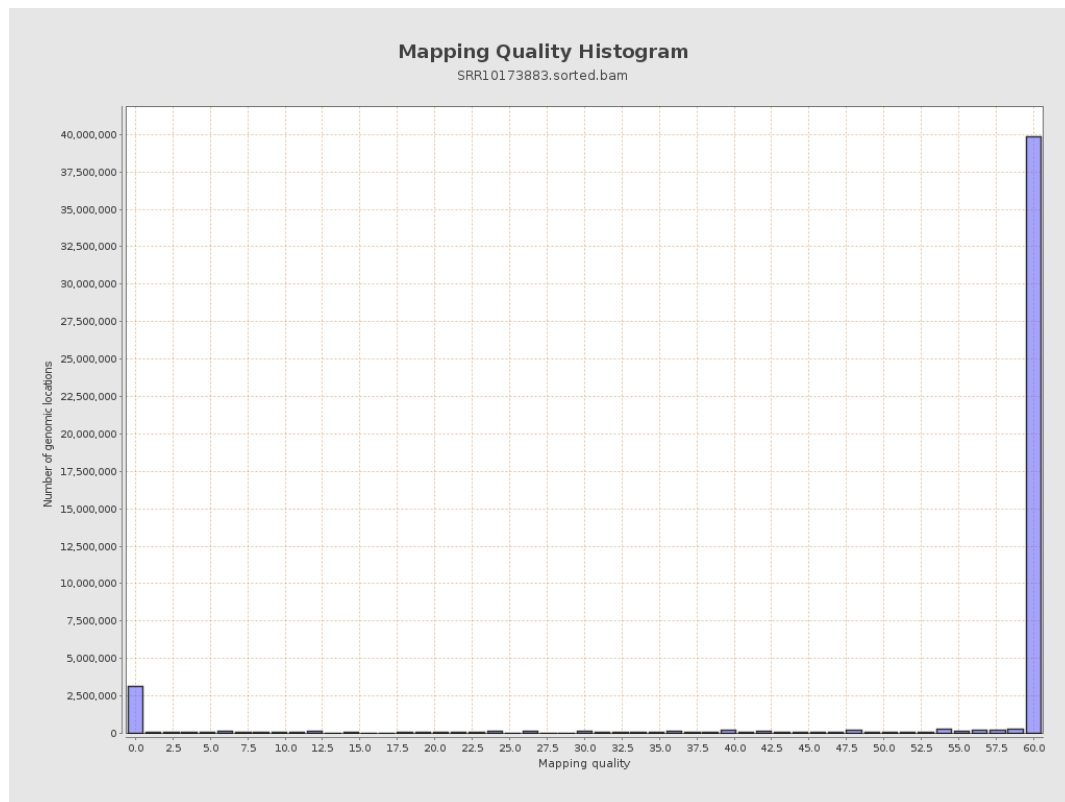
11. Results : Homopolymer Indels



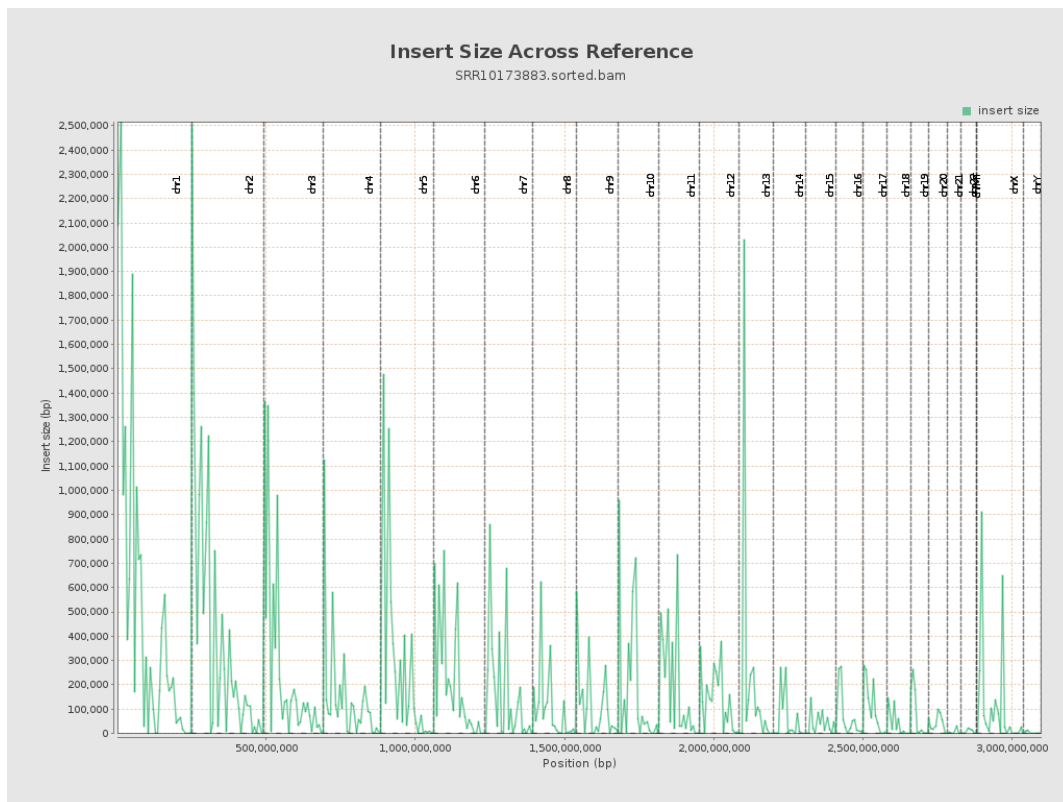
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

