

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 02:38:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173893.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_SRR10173893 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173893_1.fastq.gz SRR10173893_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 02:38:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173893.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,875,858
Mapped reads	2,795,867 / 97.22%
Unmapped reads	79,991 / 2.78%
Mapped paired reads	2,795,867 / 97.22%
Mapped reads, first in pair	1,401,459 / 48.73%
Mapped reads, second in pair	1,394,408 / 48.49%
Mapped reads, both in pair	2,742,374 / 95.36%
Mapped reads, singletons	53,493 / 1.86%
Secondary alignments	0
Supplementary alignments	273,896 / 9.52%
Read min/max/mean length	30 / 133 / 127.82
Duplicated reads (estimated)	2,059,128 / 71.6%
Duplication rate	62.73%
Clipped reads	1,144,275 / 39.79%

2.2. ACGT Content

Number/percentage of A's	98,503,786 / 29.95%
Number/percentage of C's	65,000,574 / 19.76%
Number/percentage of T's	98,233,733 / 29.87%
Number/percentage of G's	67,127,135 / 20.41%
Number/percentage of N's	4,225 / 0%

GC Percentage	40.18%
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2.3. Coverage

Mean	0.1063
Standard Deviation	1.6555

2.4. Mapping Quality

Mean Mapping Quality	52.65
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2.5. Insert size

Mean	941,482.18
Standard Deviation	8,996,458.57
P25/Median/P75	143 / 200 / 289

2.6. Mismatches and indels

General error rate	1.08%
Mismatches	3,464,728
Insertions	35,867
Mapped reads with at least one insertion	1.24%
Deletions	73,926
Mapped reads with at least one deletion	2.58%
Homopolymer indels	42.91%

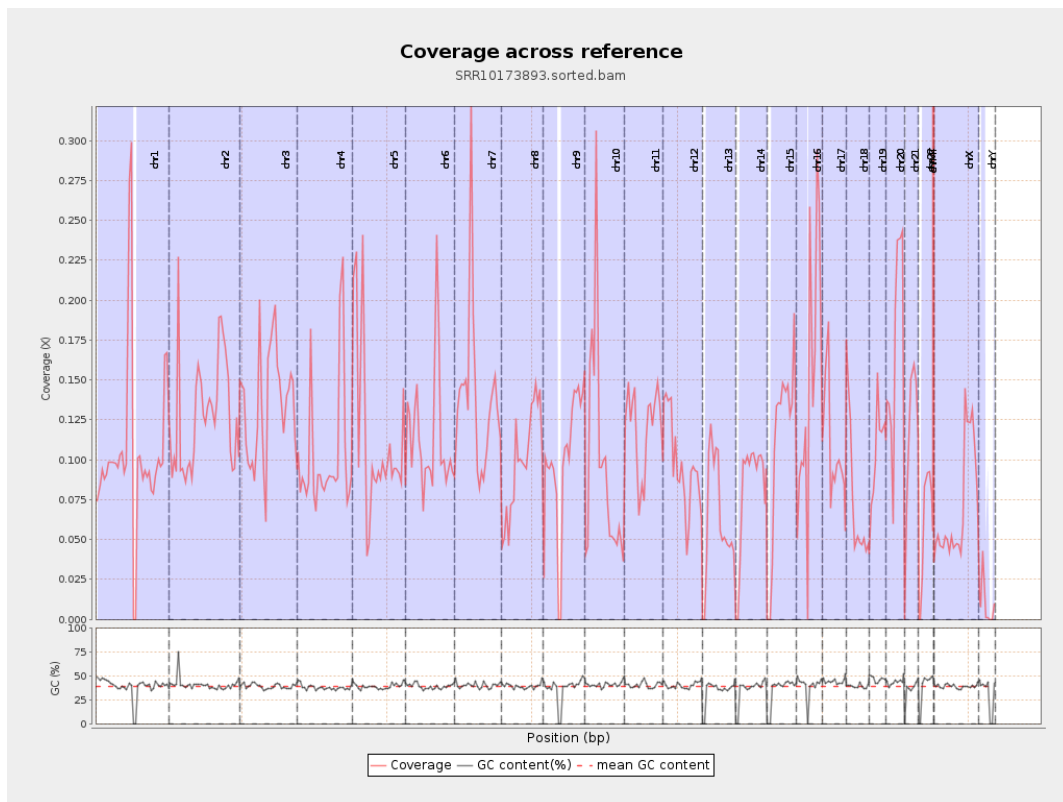
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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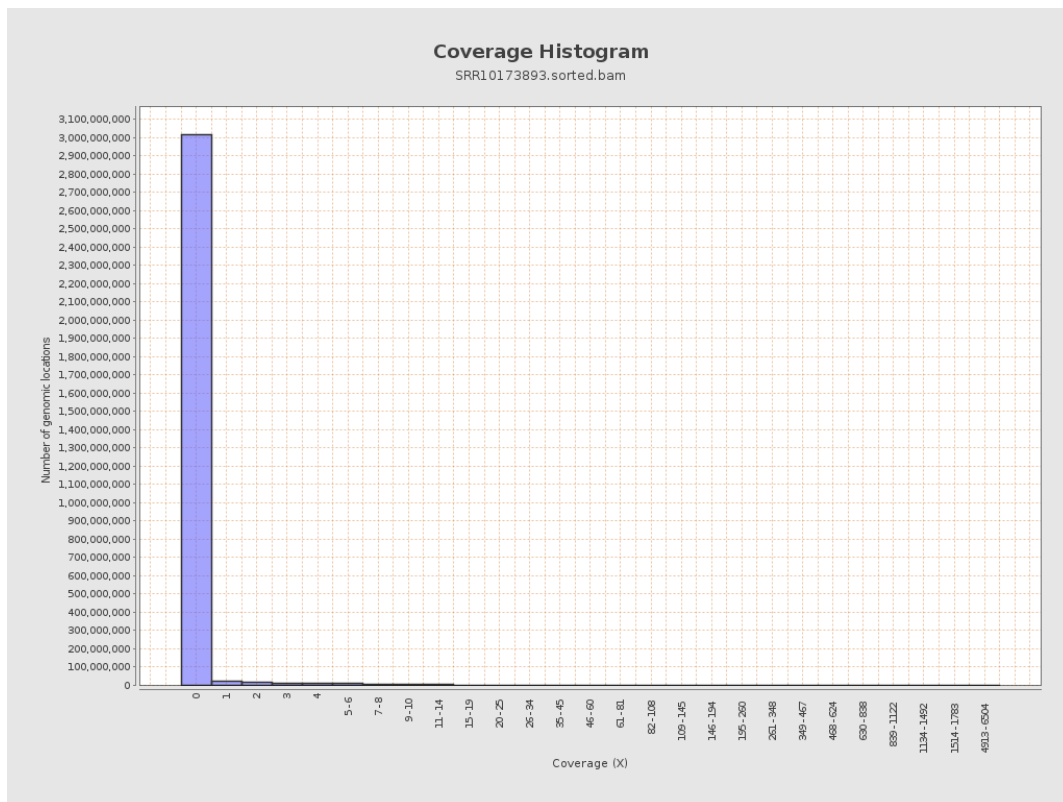
		bases	coverage	deviation
chr1	249250621	26015281	0.1044	1.2375
chr2	243199373	30934633	0.1272	4.5917
chr3	198022430	26705403	0.1349	0.992
chr4	191154276	19175334	0.1003	1.0956
chr5	180915260	20610922	0.1139	0.9042
chr6	171115067	19662397	0.1149	0.928
chr7	159138663	21982456	0.1381	1.5476
chr8	146364022	14636306	0.1	0.9967
chr9	141213431	14249085	0.1009	0.9557
chr10	135534747	12994881	0.0959	1.6078
chr11	135006516	16105192	0.1193	0.9416
chr12	133851895	12885859	0.0963	0.8289
chr13	115169878	7134064	0.0619	0.6663
chr14	107349540	8695933	0.081	0.7664
chr15	102531392	11401453	0.1112	0.8856
chr16	90354753	13310561	0.1473	1.2897
chr17	81195210	8582416	0.1057	0.9486
chr18	78077248	5771217	0.0739	1.1838
chr19	59128983	6263541	0.1059	1.3369
chr20	63025520	10709441	0.1699	1.1368
chr21	48129895	5537762	0.1151	0.9807
chr22	51304566	3010994	0.0587	0.6152
chrMT	16571	1284285	77.502	59.5438
chrX	155270560	10844238	0.0698	0.7036

chrY	59373566	552819	0.0093	0.5959
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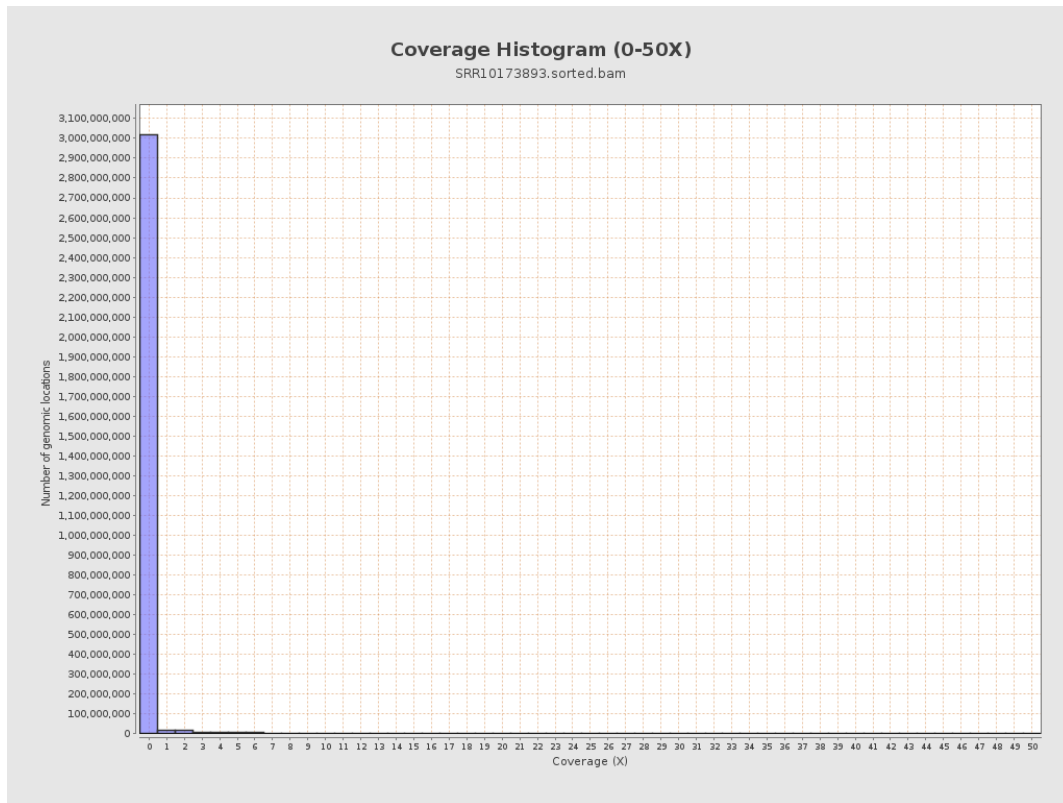
3. Results : Coverage across reference



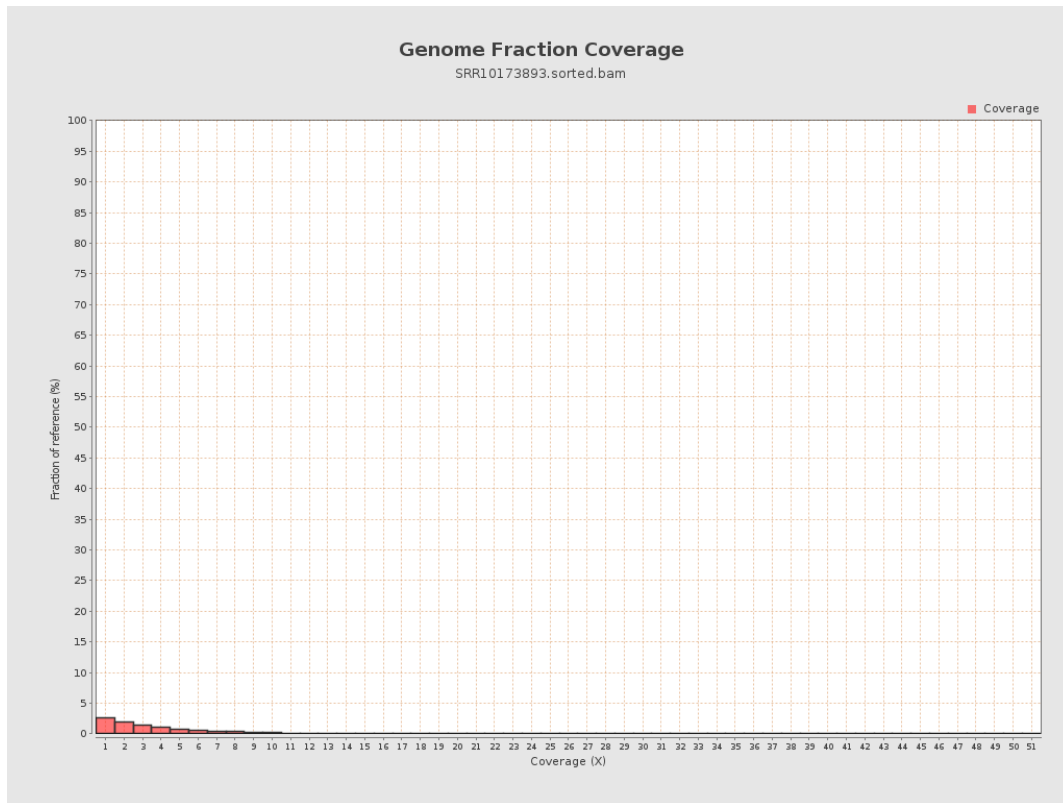
4. Results : Coverage Histogram



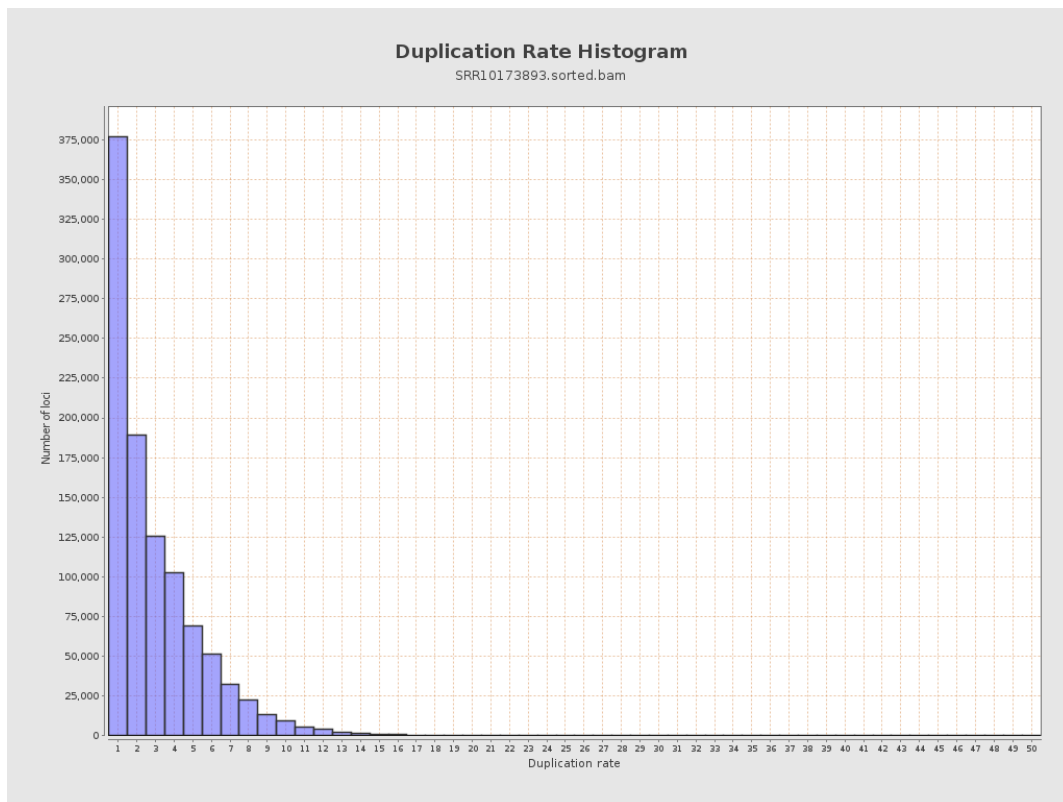
5. Results : Coverage Histogram (0-50X)



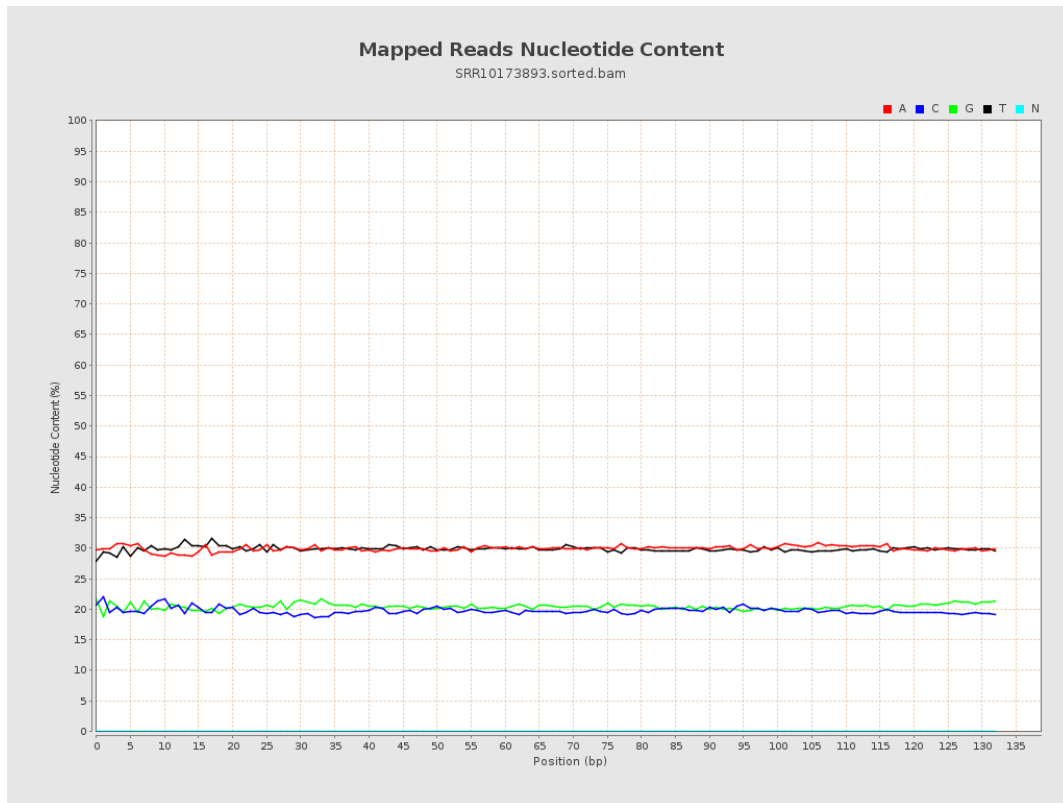
6. Results : Genome Fraction Coverage



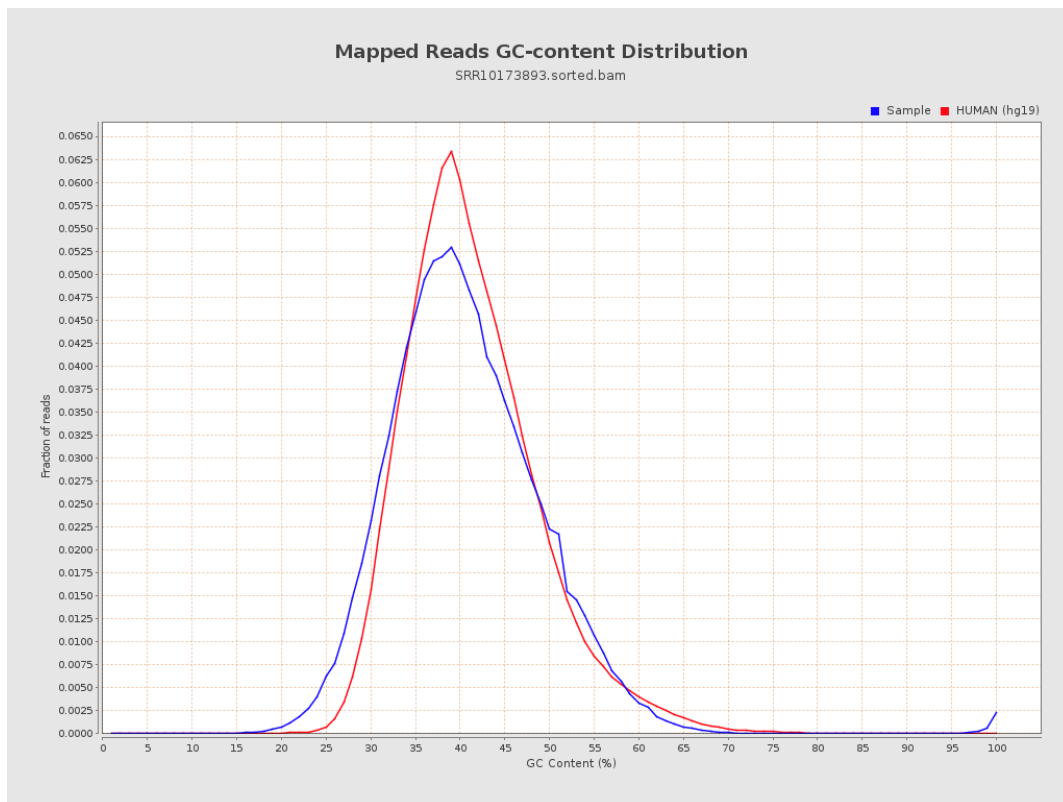
7. Results : Duplication Rate Histogram



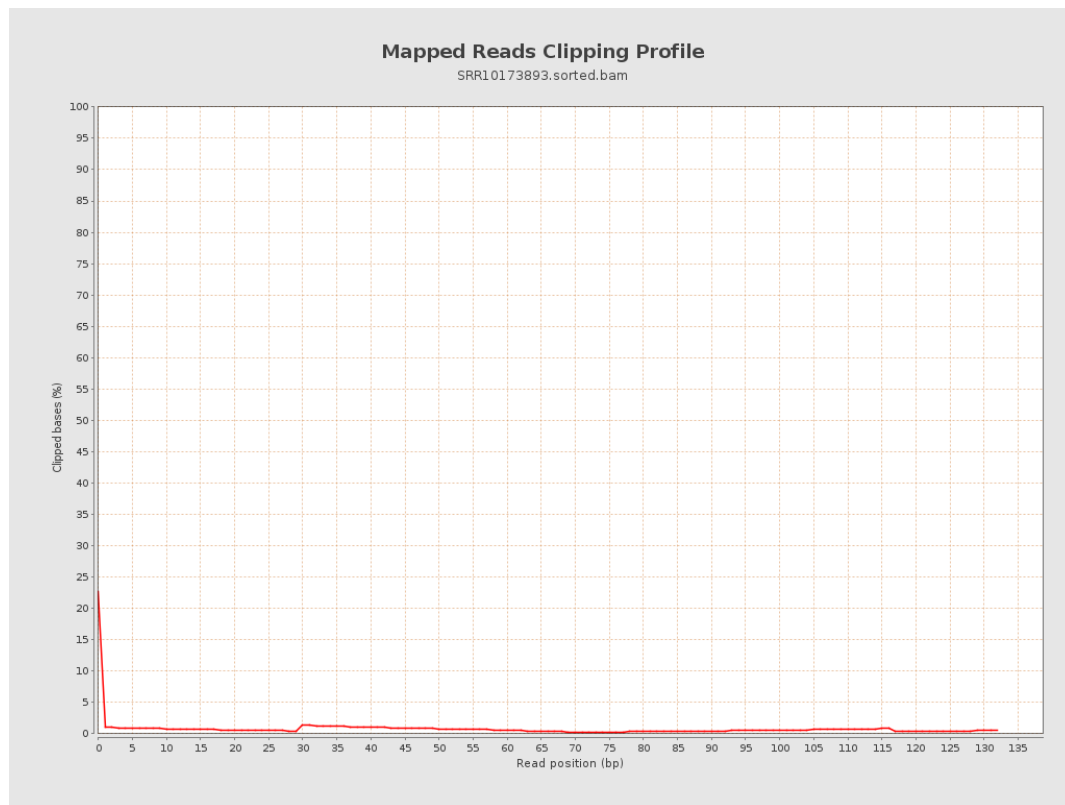
8. Results : Mapped Reads Nucleotide Content



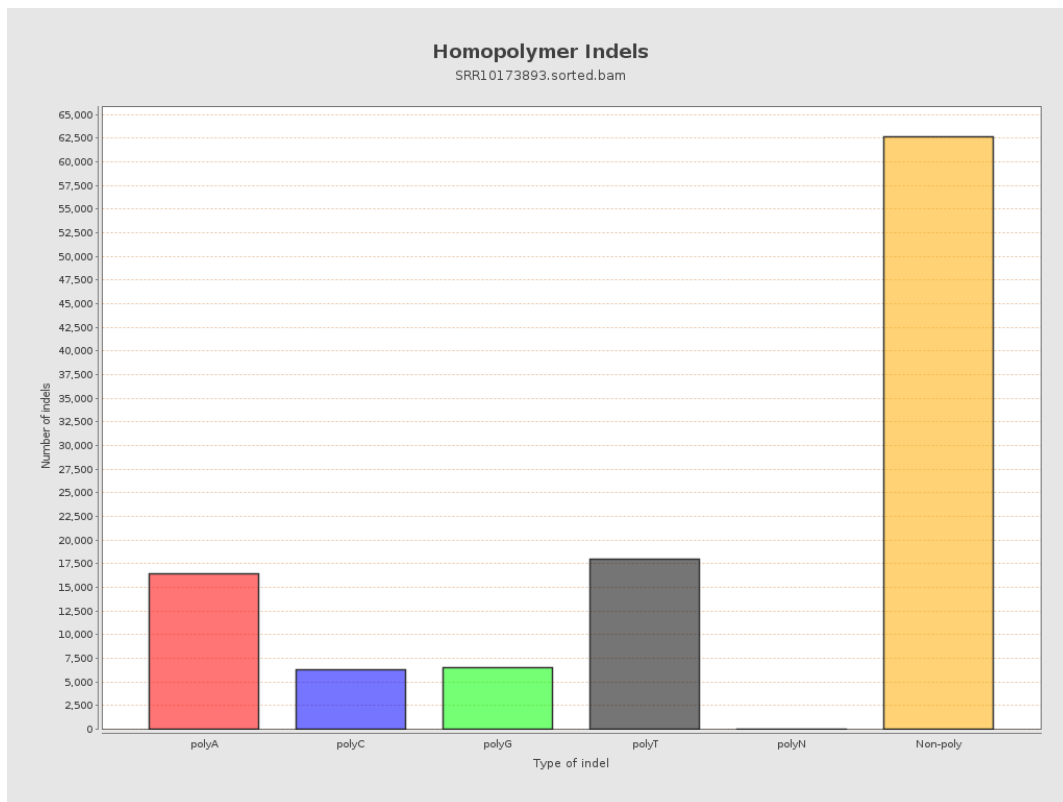
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



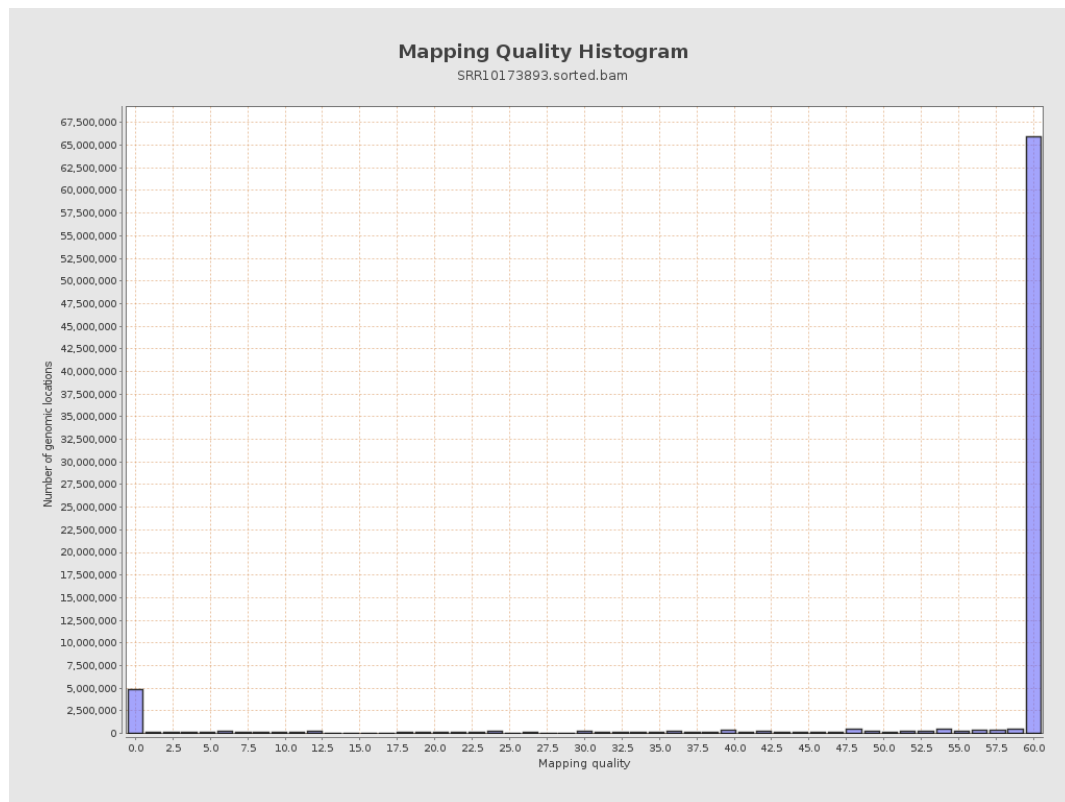
11. Results : Homopolymer Indels



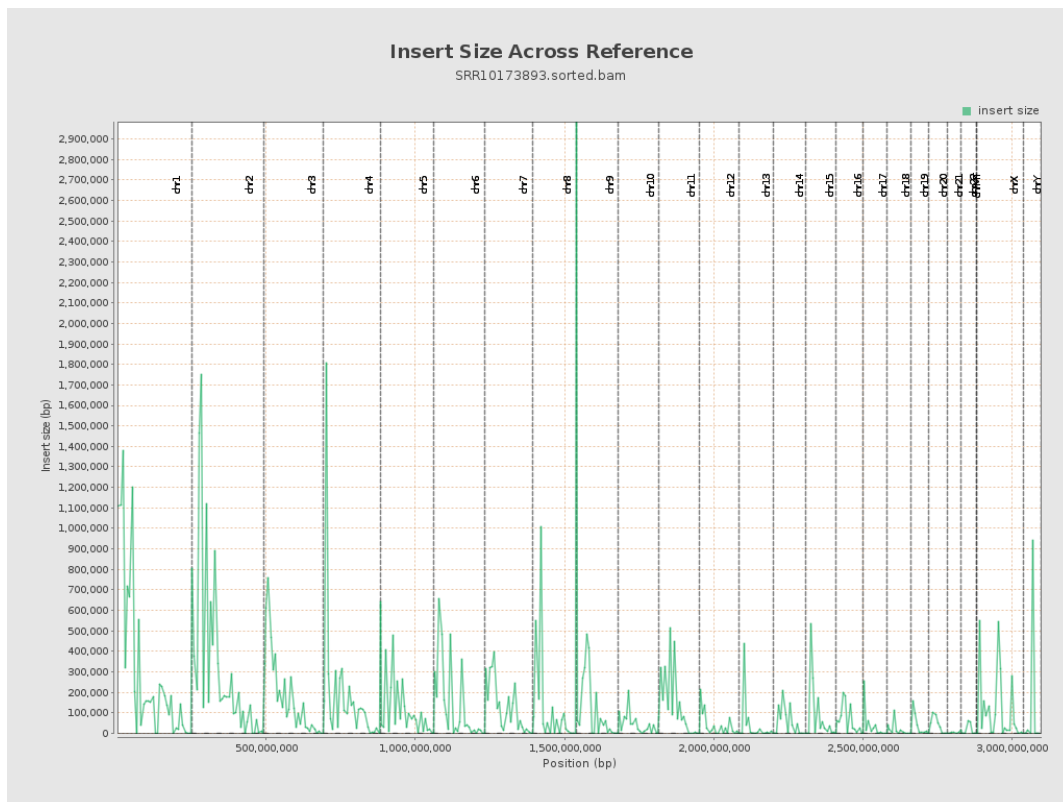
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

