

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 02:47:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173895.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_SRR10173895 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173895_1.fastq.gz SRR10173895_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 02:47:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173895.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,126,332
Mapped reads	3,045,937 / 97.43%
Unmapped reads	80,395 / 2.57%
Mapped paired reads	3,045,937 / 97.43%
Mapped reads, first in pair	1,523,609 / 48.73%
Mapped reads, second in pair	1,522,328 / 48.69%
Mapped reads, both in pair	2,990,018 / 95.64%
Mapped reads, singletons	55,919 / 1.79%
Secondary alignments	0
Supplementary alignments	342,442 / 10.95%
Read min/max/mean length	30 / 133 / 128.95
Duplicated reads (estimated)	2,441,483 / 78.09%
Duplication rate	65.13%
Clipped reads	1,289,933 / 41.26%

2.2. ACGT Content

Number/percentage of A's	107,842,545 / 29.91%
Number/percentage of C's	71,112,555 / 19.72%
Number/percentage of T's	107,775,953 / 29.89%
Number/percentage of G's	73,839,006 / 20.48%
Number/percentage of N's	4,224 / 0%

GC Percentage	40.2%
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2.3. Coverage

Mean	0.1165
Standard Deviation	1.8069

2.4. Mapping Quality

Mean Mapping Quality	52.61
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2.5. Insert size

Mean	1,197,026.95
Standard Deviation	10,308,016.21
P25/Median/P75	148 / 208 / 301

2.6. Mismatches and indels

General error rate	1.05%
Mismatches	3,703,887
Insertions	37,609
Mapped reads with at least one insertion	1.19%
Deletions	82,784
Mapped reads with at least one deletion	2.65%
Homopolymer indels	43.17%

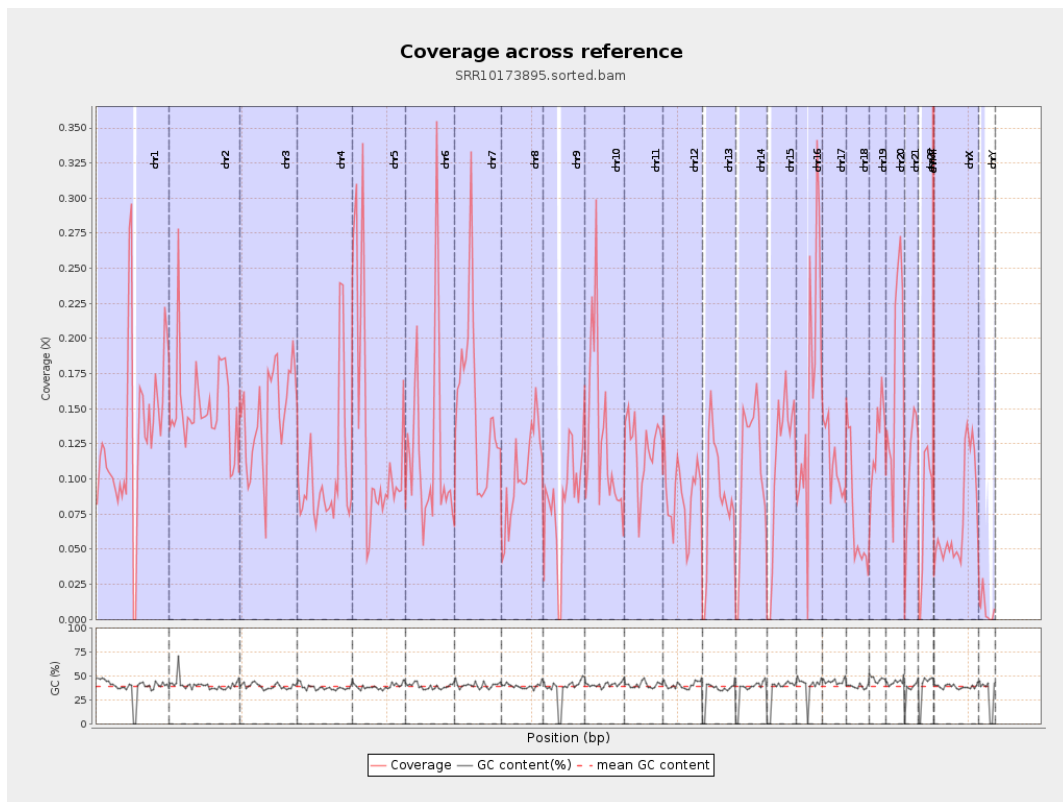
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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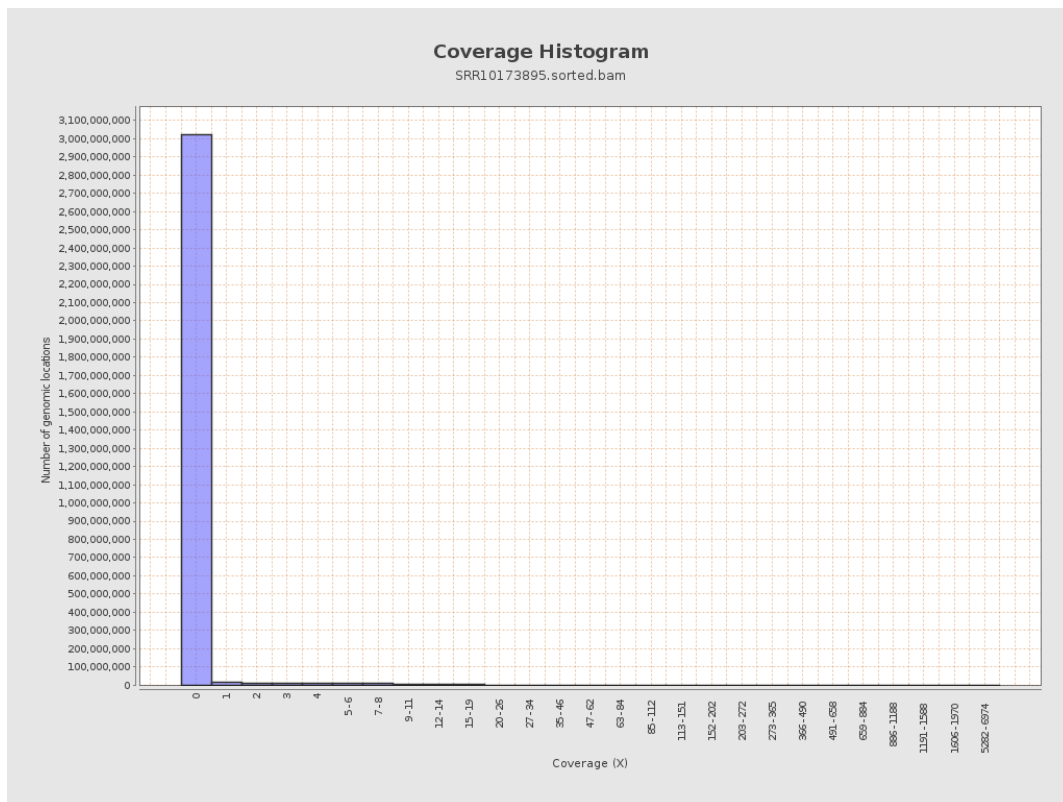
		bases	coverage	deviation
chr1	249250621	32222169	0.1293	1.5013
chr2	243199373	36710511	0.1509	4.9563
chr3	198022430	28878162	0.1458	1.1366
chr4	191154276	19185782	0.1004	1.0263
chr5	180915260	23724042	0.1311	1.0826
chr6	171115067	20776427	0.1214	1.0588
chr7	159138663	23900532	0.1502	1.8578
chr8	146364022	15164052	0.1036	1.058
chr9	141213431	12050937	0.0853	0.9734
chr10	135534747	17552659	0.1295	1.7951
chr11	135006516	16529531	0.1224	1.0347
chr12	133851895	11848583	0.0885	0.8722
chr13	115169878	9838556	0.0854	0.8658
chr14	107349540	11662603	0.1086	0.9798
chr15	102531392	11367539	0.1109	0.9575
chr16	90354753	14691151	0.1626	1.4347
chr17	81195210	8970975	0.1105	1.0088
chr18	78077248	5612145	0.0719	1.143
chr19	59128983	7409817	0.1253	1.5152
chr20	63025520	11122172	0.1765	1.2291
chr21	48129895	5142746	0.1069	0.9893
chr22	51304566	3897179	0.076	0.7763
chrMT	16571	1012074	61.075	54.391
chrX	155270560	11078824	0.0714	0.7876

chrY	59373566	432795	0.0073	0.3571
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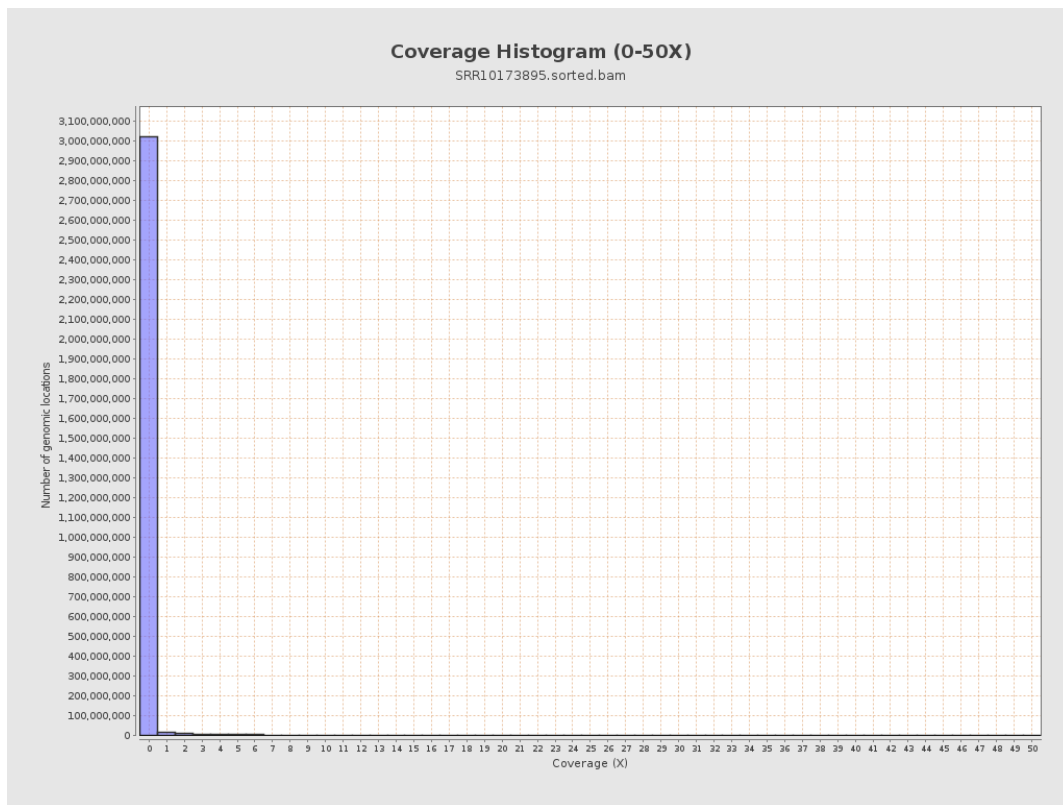
3. Results : Coverage across reference



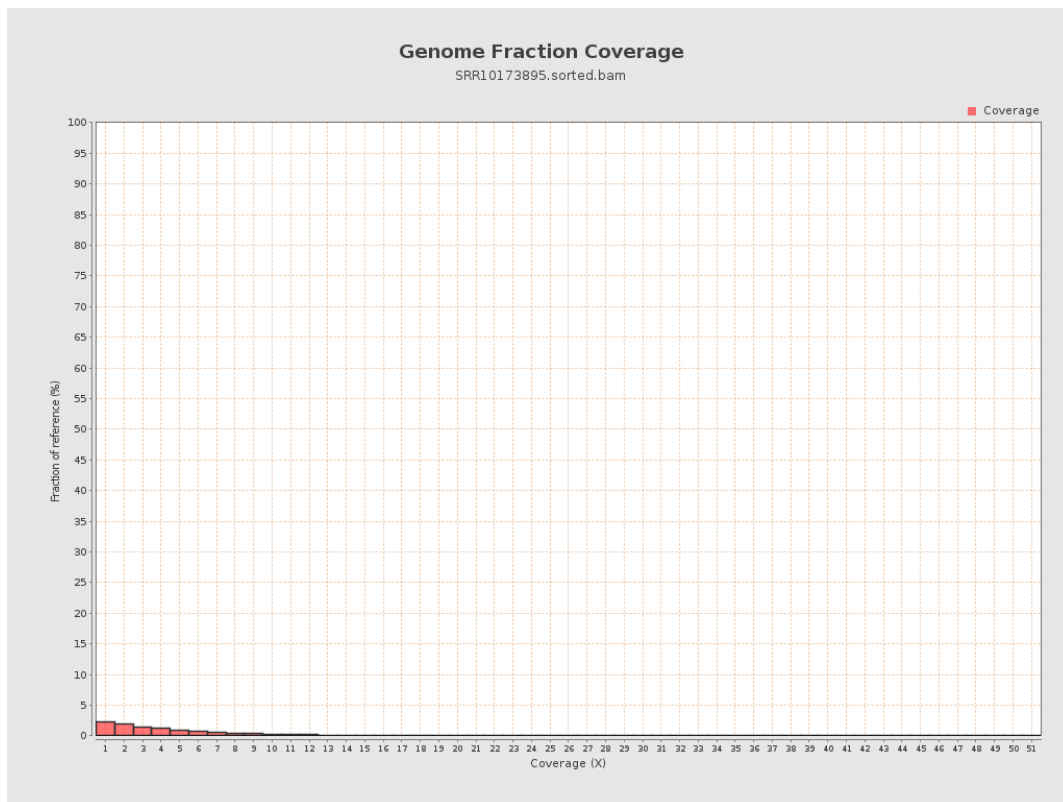
4. Results : Coverage Histogram



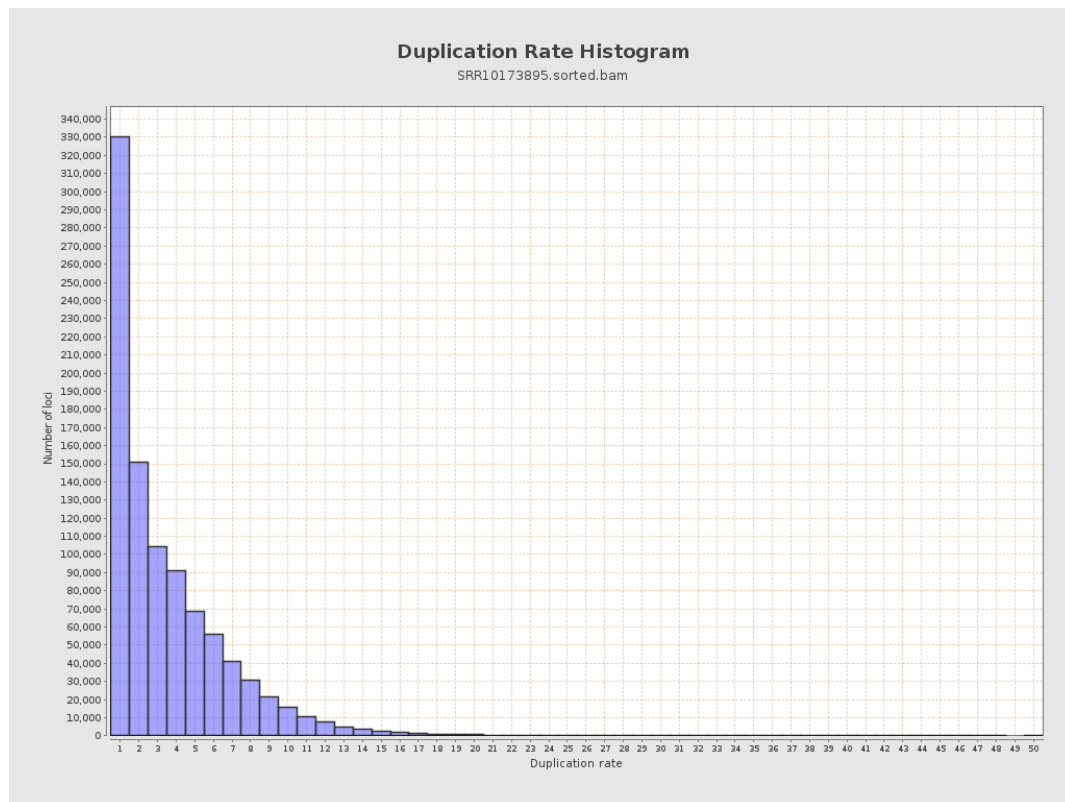
5. Results : Coverage Histogram (0-50X)



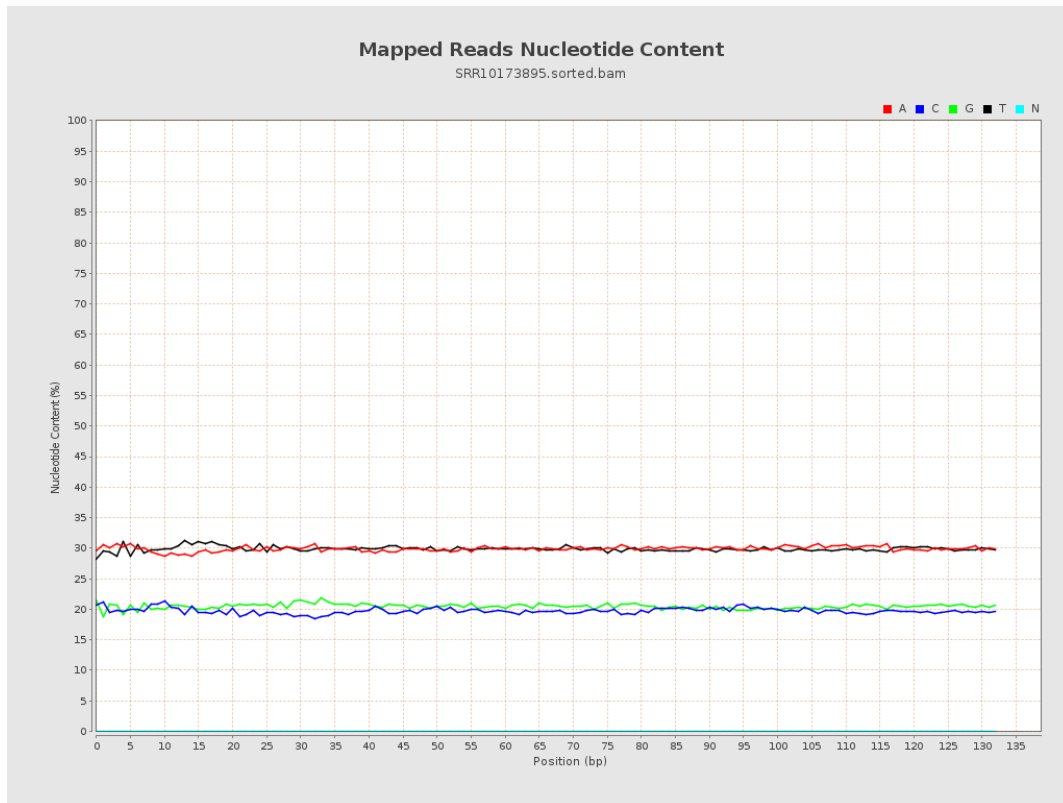
6. Results : Genome Fraction Coverage



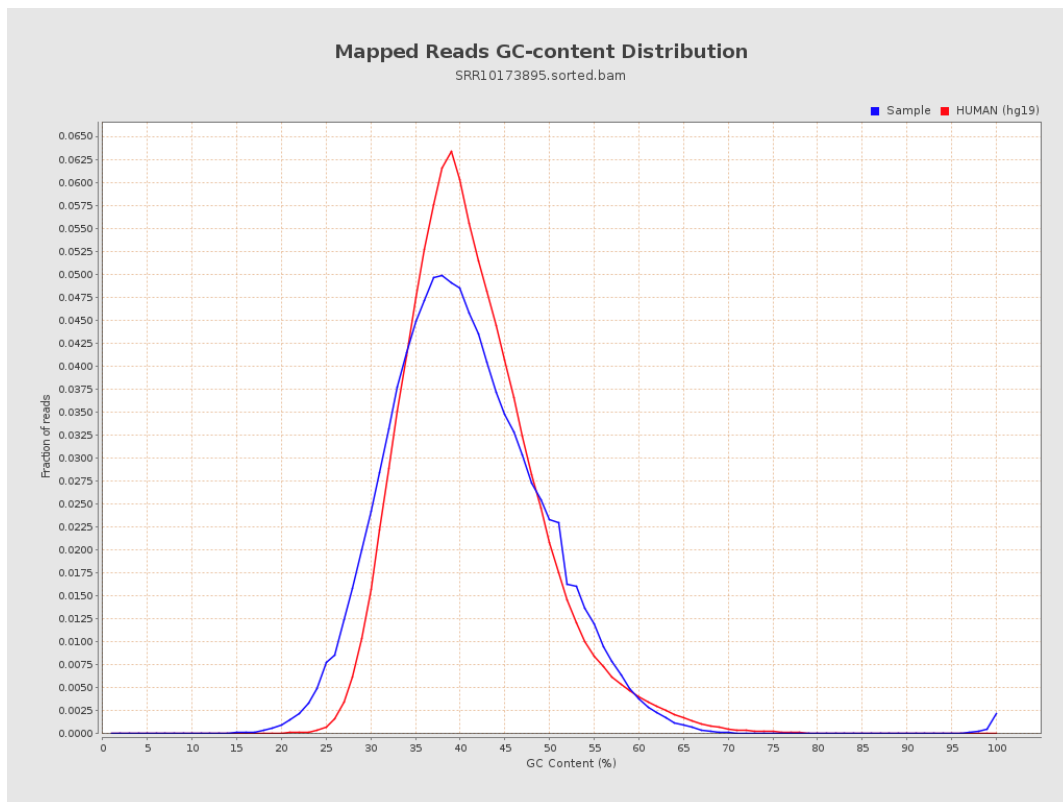
7. Results : Duplication Rate Histogram



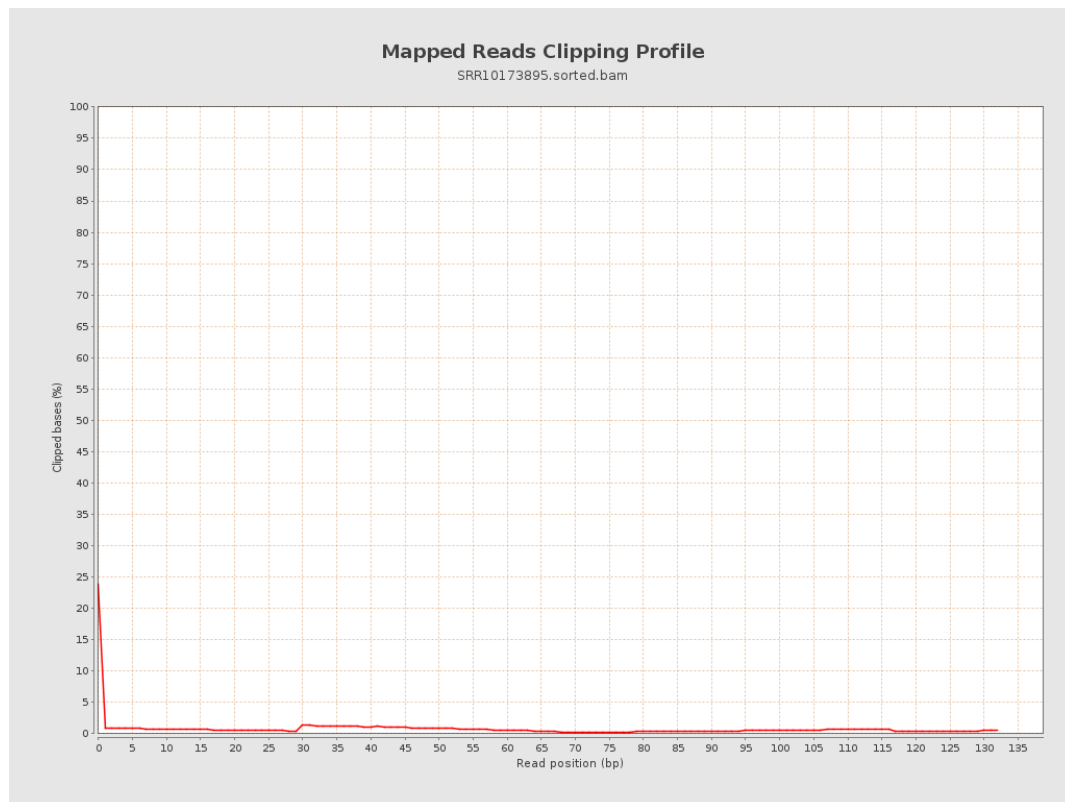
8. Results : Mapped Reads Nucleotide Content



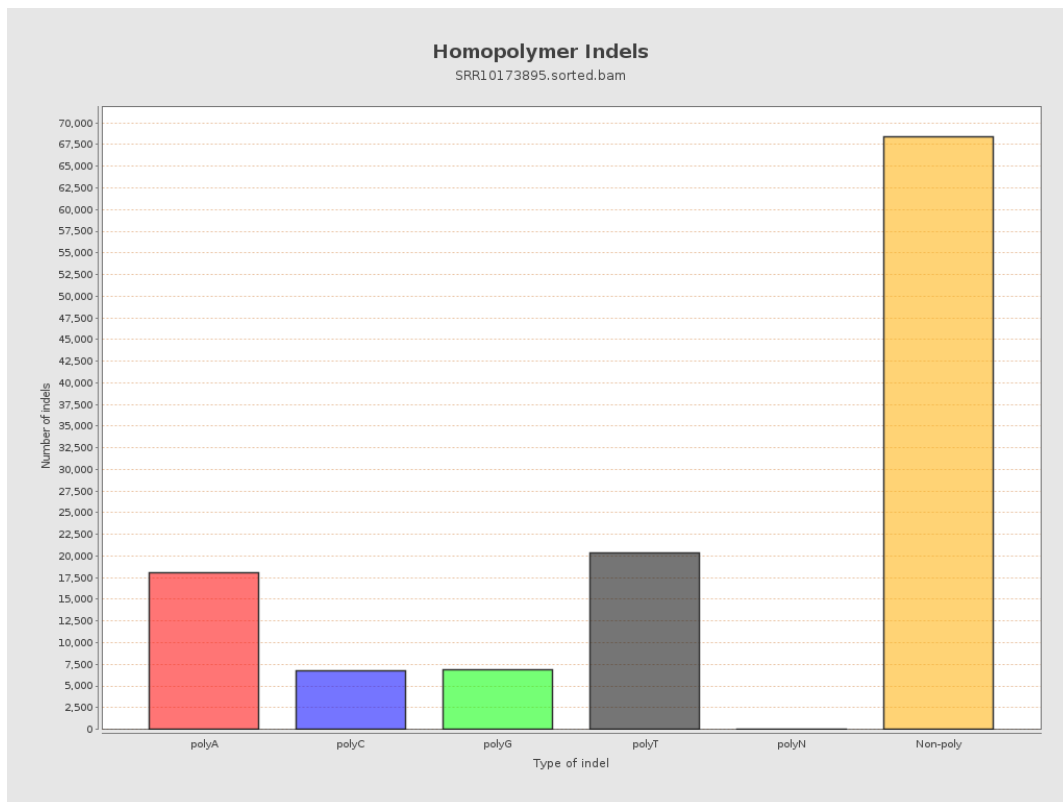
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



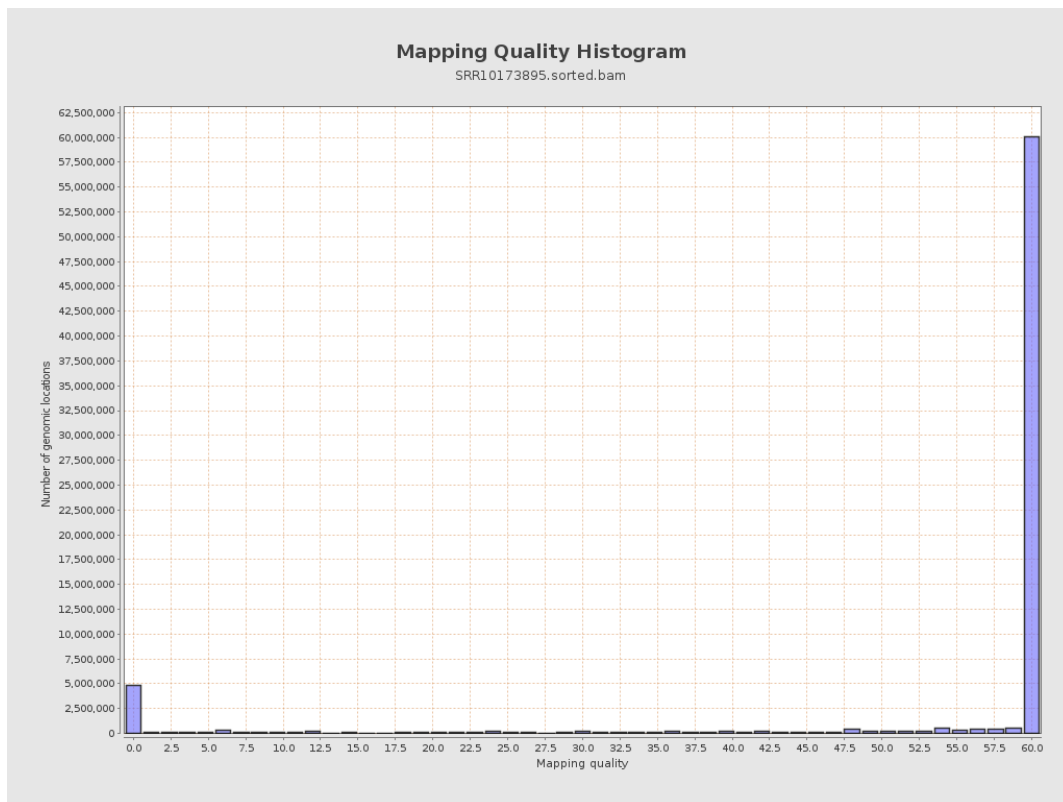
11. Results : Homopolymer Indels



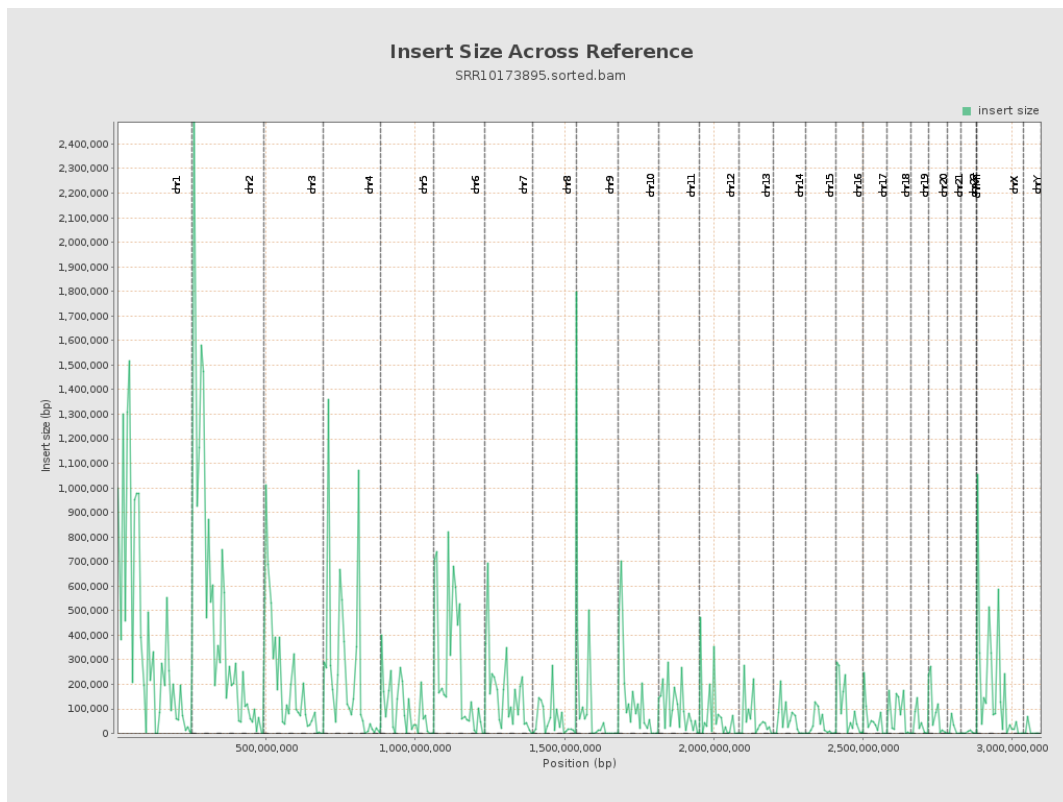
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

