

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 18:34:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173995.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_SRR10173995 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173995_1.fastq.gz SRR10173995_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 18:34:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173995.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,766,378
Mapped reads	6,623,515 / 97.89%
Unmapped reads	142,863 / 2.11%
Mapped paired reads	6,623,515 / 97.89%
Mapped reads, first in pair	3,310,767 / 48.93%
Mapped reads, second in pair	3,312,748 / 48.96%
Mapped reads, both in pair	6,532,290 / 96.54%
Mapped reads, singletons	91,225 / 1.35%
Secondary alignments	0
Supplementary alignments	912,285 / 13.48%
Read min/max/mean length	30 / 133 / 125.84
Duplicated reads (estimated)	5,419,981 / 80.1%
Duplication rate	65.05%
Clipped reads	3,380,930 / 49.97%

2.2. ACGT Content

Number/percentage of A's	224,675,953 / 29.84%
Number/percentage of C's	149,965,515 / 19.92%
Number/percentage of T's	222,766,962 / 29.58%
Number/percentage of G's	155,577,656 / 20.66%
Number/percentage of N's	5,668 / 0%

GC Percentage	40.58%
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2.3. Coverage

Mean	0.2434
Standard Deviation	4.1241

2.4. Mapping Quality

Mean Mapping Quality	52.44
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2.5. Insert size

Mean	1,188,890.44
Standard Deviation	10,062,774.22
P25/Median/P75	106 / 157 / 243

2.6. Mismatches and indels

General error rate	0.88%
Mismatches	6,392,146
Insertions	84,706
Mapped reads with at least one insertion	1.23%
Deletions	215,276
Mapped reads with at least one deletion	3.17%
Homopolymer indels	41.25%

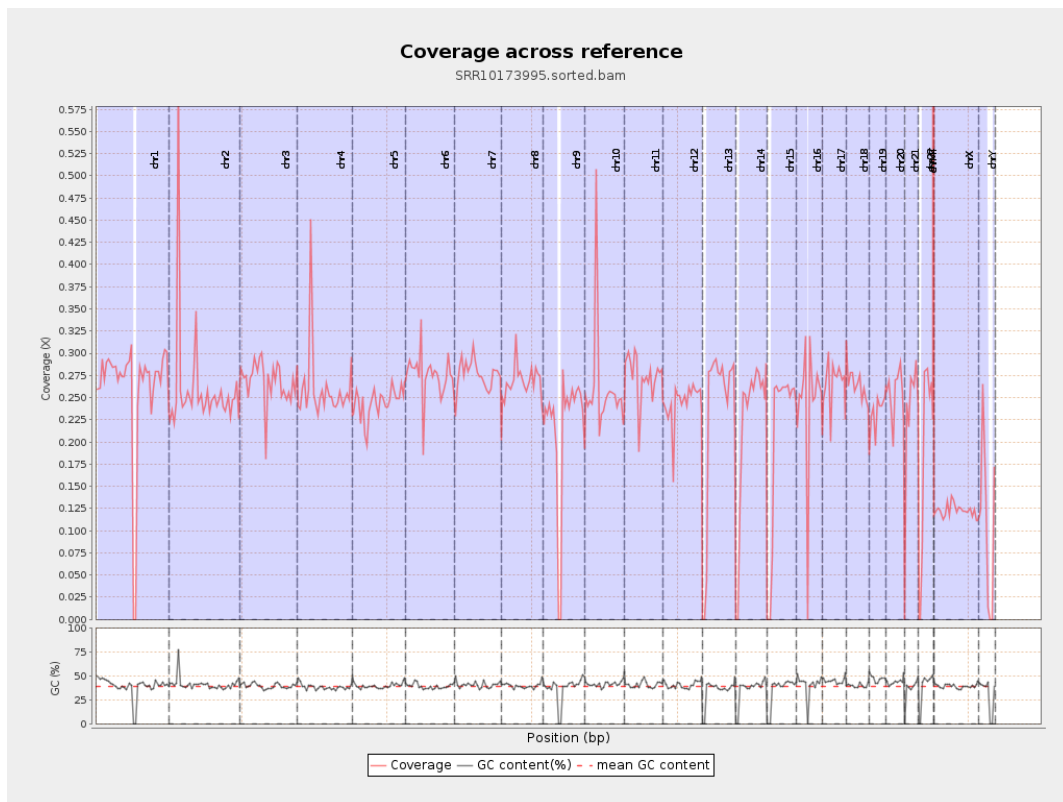
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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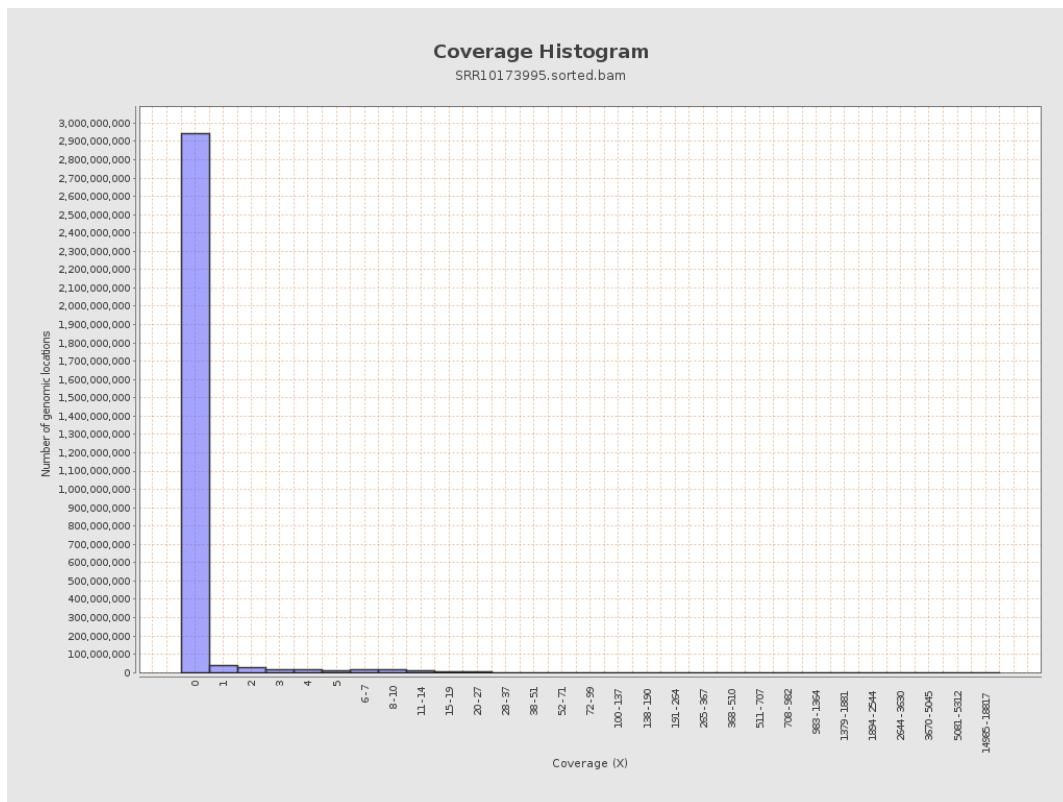
		bases	coverage	deviation
chr1	249250621	65100378	0.2612	2.1905
chr2	243199373	63418365	0.2608	13.1622
chr3	198022430	53120141	0.2683	1.6074
chr4	191154276	49499585	0.259	2.1292
chr5	180915260	44144345	0.244	1.5267
chr6	171115067	47067099	0.2751	1.8619
chr7	159138663	44071424	0.2769	2.071
chr8	146364022	39378054	0.269	2.545
chr9	141213431	30550439	0.2163	1.97
chr10	135534747	35107817	0.259	2.7909
chr11	135006516	36886490	0.2732	1.6873
chr12	133851895	32711754	0.2444	1.6014
chr13	115169878	26616816	0.2311	1.5126
chr14	107349540	23501805	0.2189	1.4686
chr15	102531392	21363113	0.2084	1.4527
chr16	90354753	22090056	0.2445	1.8195
chr17	81195210	21558102	0.2655	1.6984
chr18	78077248	20642067	0.2644	2.7902
chr19	59128983	13807827	0.2335	1.8134
chr20	63025520	16013143	0.2541	1.6249
chr21	48129895	11160857	0.2319	1.9027
chr22	51304566	9494869	0.1851	1.648
chrMT	16571	1003228	60.5412	50.9232
chrX	155270560	19059597	0.1228	1.0903

chrY	59373566	6149159	0.1036	1.5831
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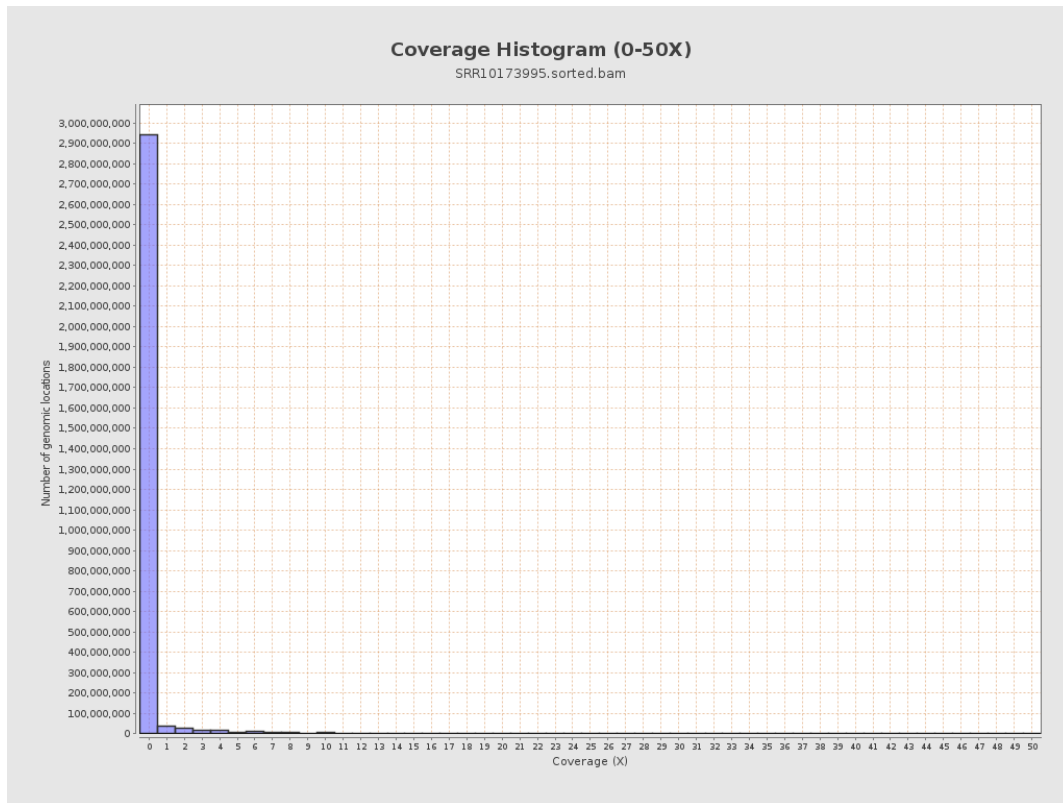
3. Results : Coverage across reference



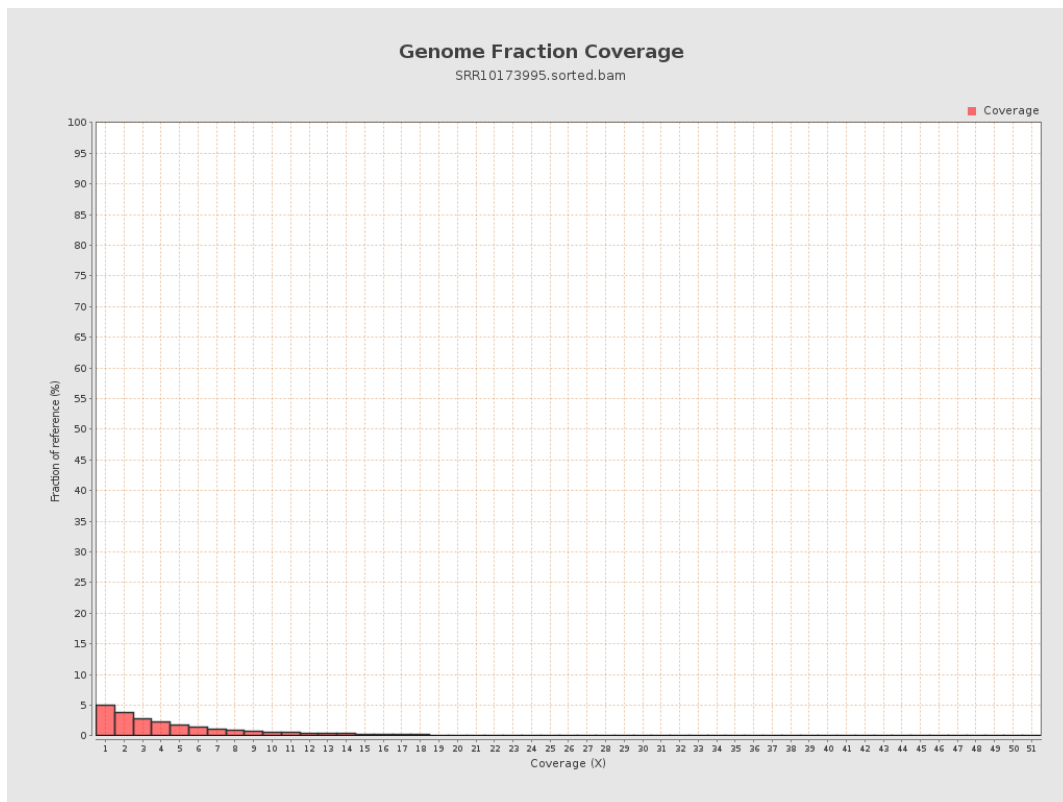
4. Results : Coverage Histogram



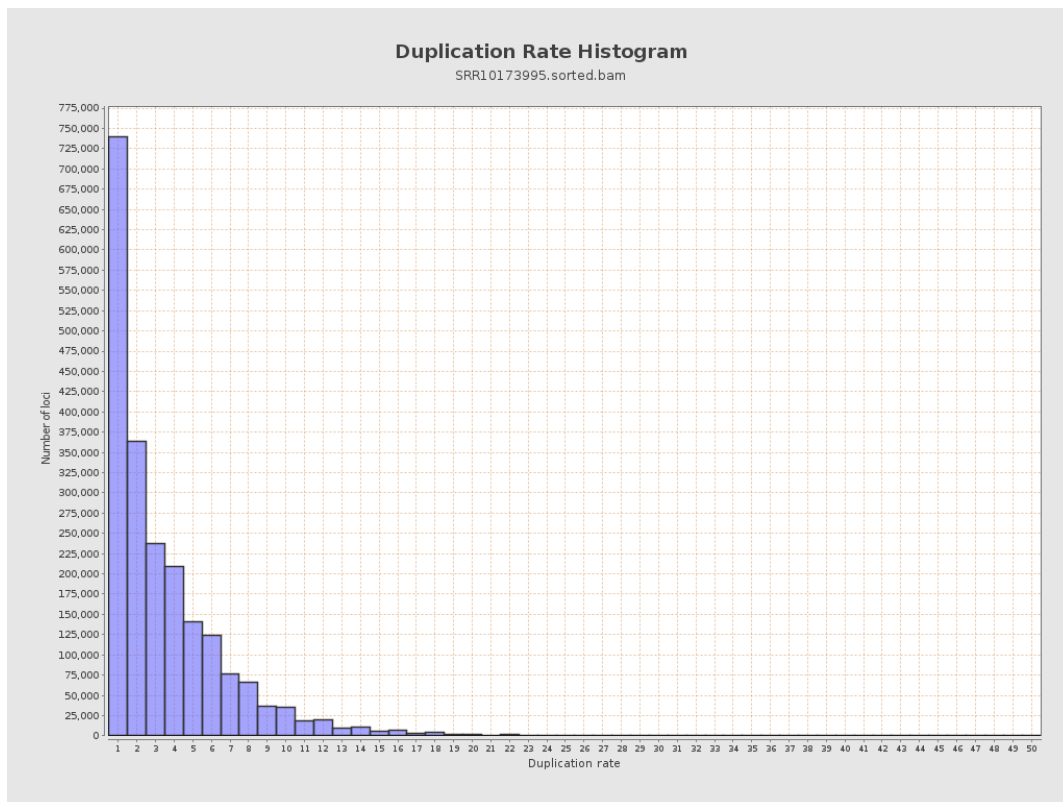
5. Results : Coverage Histogram (0-50X)



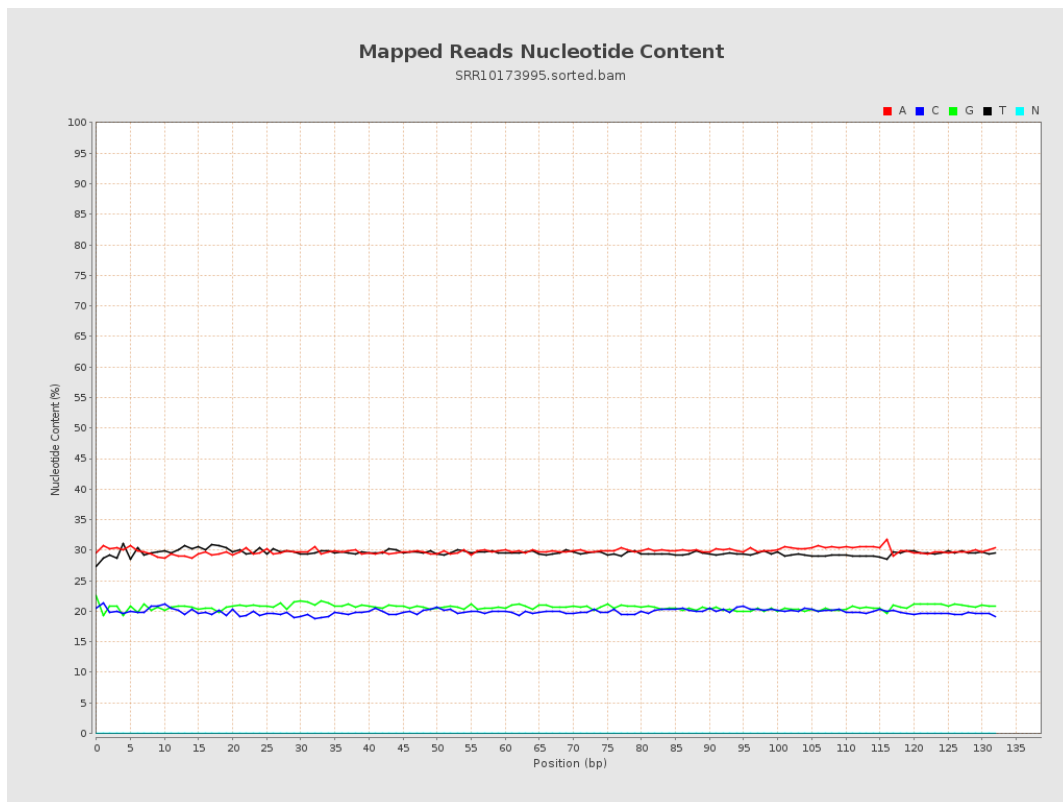
6. Results : Genome Fraction Coverage



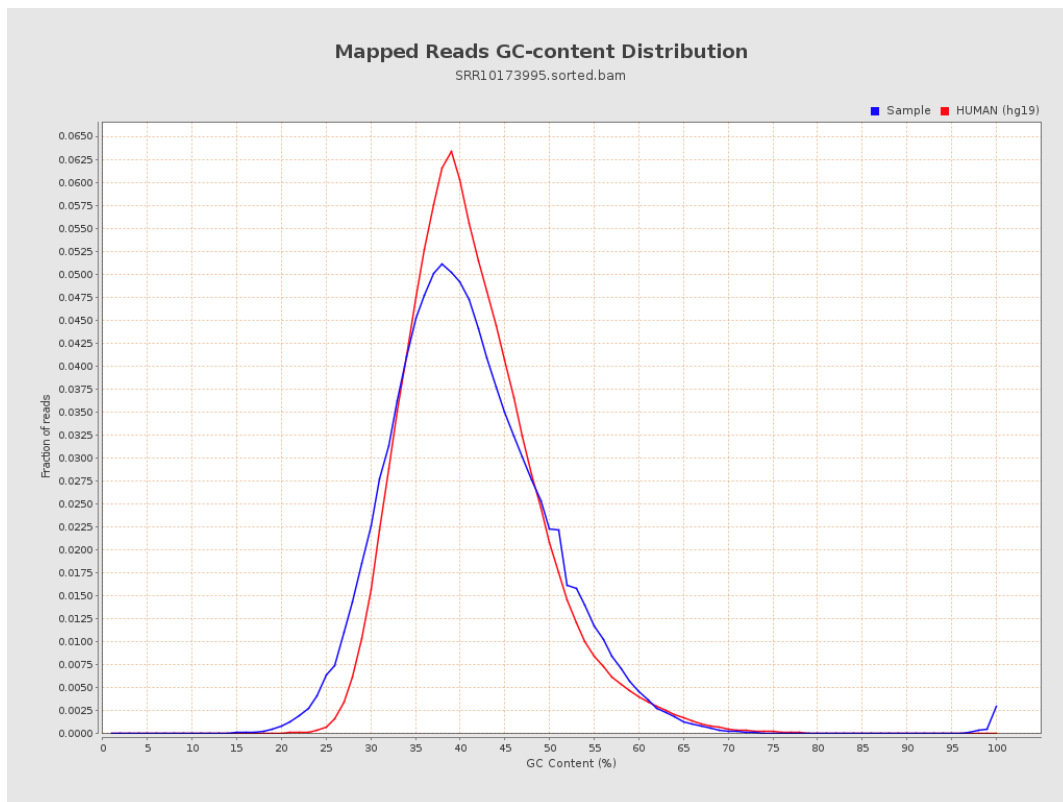
7. Results : Duplication Rate Histogram



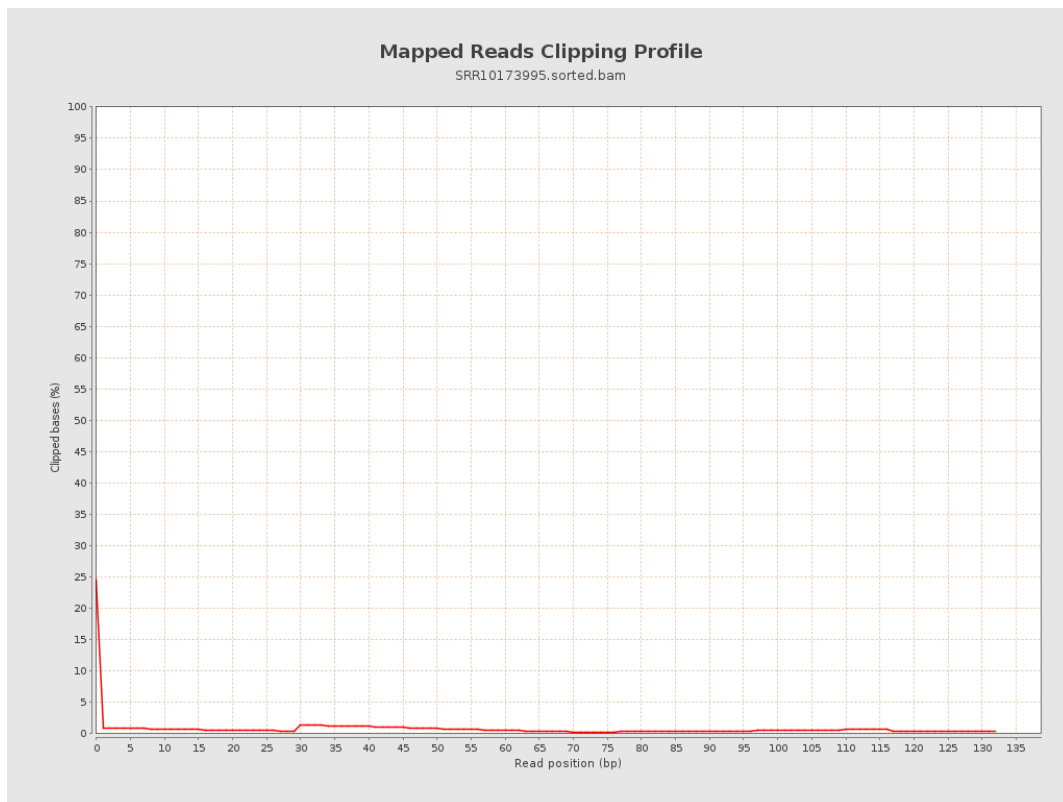
8. Results : Mapped Reads Nucleotide Content



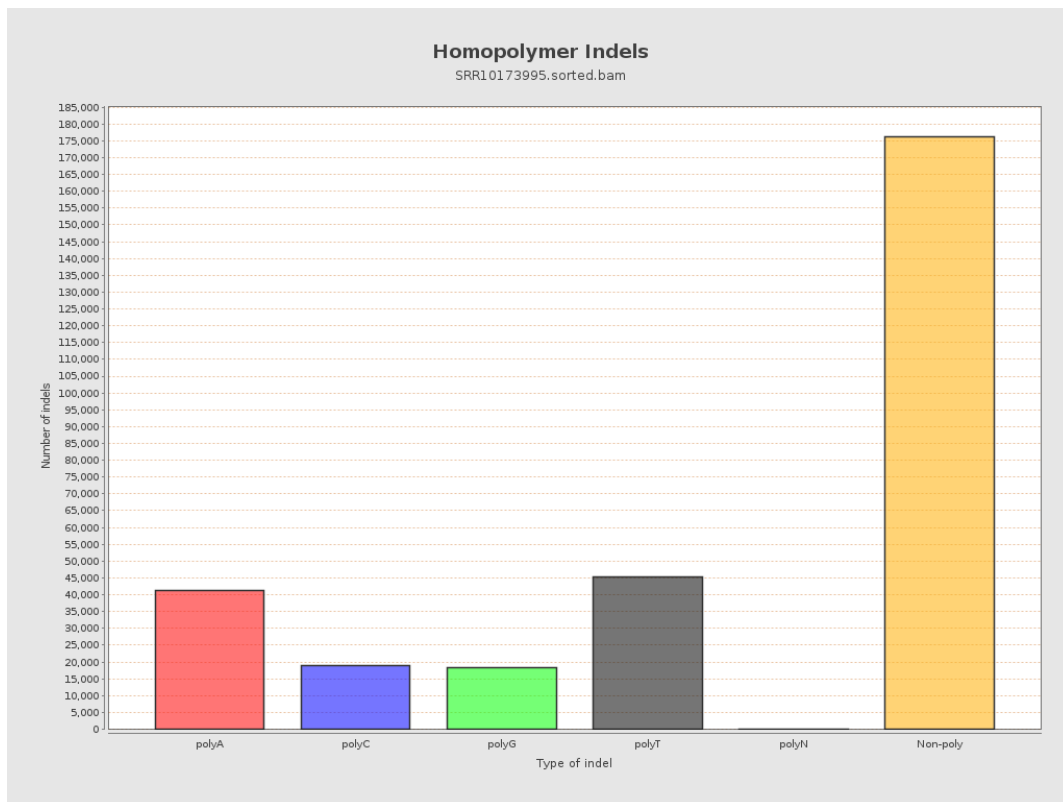
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



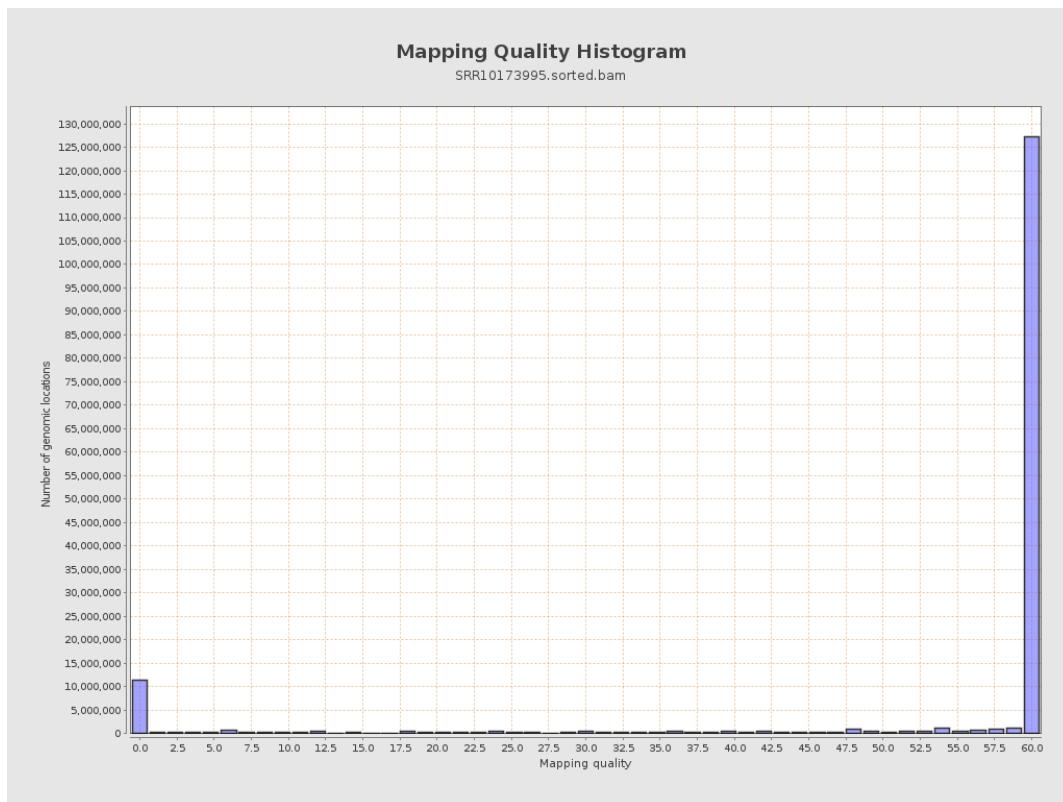
11. Results : Homopolymer Indels



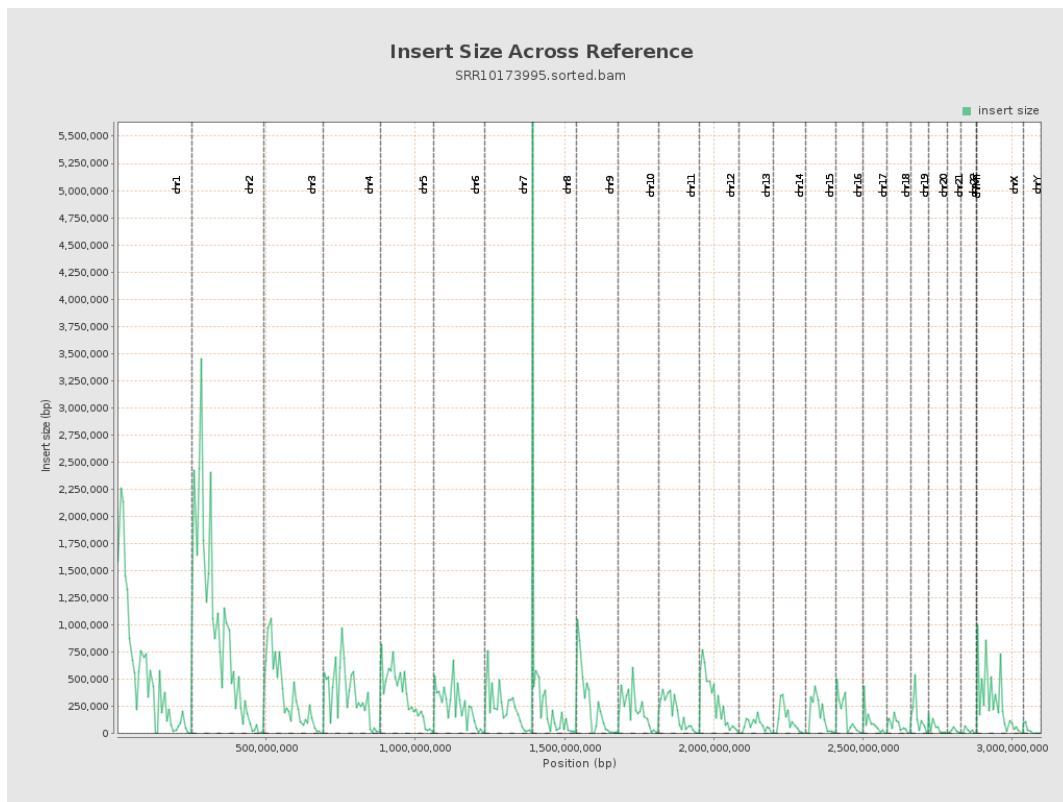
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

