

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/27 22:07:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR21671993.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_SRR21671993 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR21671993_1.fastq.gz SRR21671993_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 27 22:07:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR21671993.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,272,412
Mapped reads	32,171,747 / 99.69%
Unmapped reads	100,665 / 0.31%
Mapped paired reads	32,171,747 / 99.69%
Mapped reads, first in pair	16,094,151 / 49.87%
Mapped reads, second in pair	16,077,596 / 49.82%
Mapped reads, both in pair	32,117,074 / 99.52%
Mapped reads, singletons	54,673 / 0.17%
Secondary alignments	0
Supplementary alignments	201,808 / 0.63%
Read min/max/mean length	15 / 150 / 147.33
Duplicated reads (estimated)	28,464,331 / 88.2%
Duplication rate	57.39%
Clipped reads	12,705,125 / 39.37%

2.2. ACGT Content

Number/percentage of A's	1,047,058,622 / 23.56%
Number/percentage of C's	1,106,968,790 / 24.91%
Number/percentage of T's	1,074,936,434 / 24.19%
Number/percentage of G's	1,214,461,535 / 27.33%
Number/percentage of N's	12,485 / 0%

GC Percentage	52.24%
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2.3. Coverage

Mean	1.4359
Standard Deviation	97.5732

2.4. Mapping Quality

Mean Mapping Quality	52.97
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2.5. Insert size

Mean	38,448.82
Standard Deviation	1,859,329.15
P25/Median/P75	181 / 249 / 331

2.6. Mismatches and indels

General error rate	0.82%
Mismatches	35,665,172
Insertions	359,217
Mapped reads with at least one insertion	1.08%
Deletions	890,544
Mapped reads with at least one deletion	2.7%
Homopolymer indels	43.79%

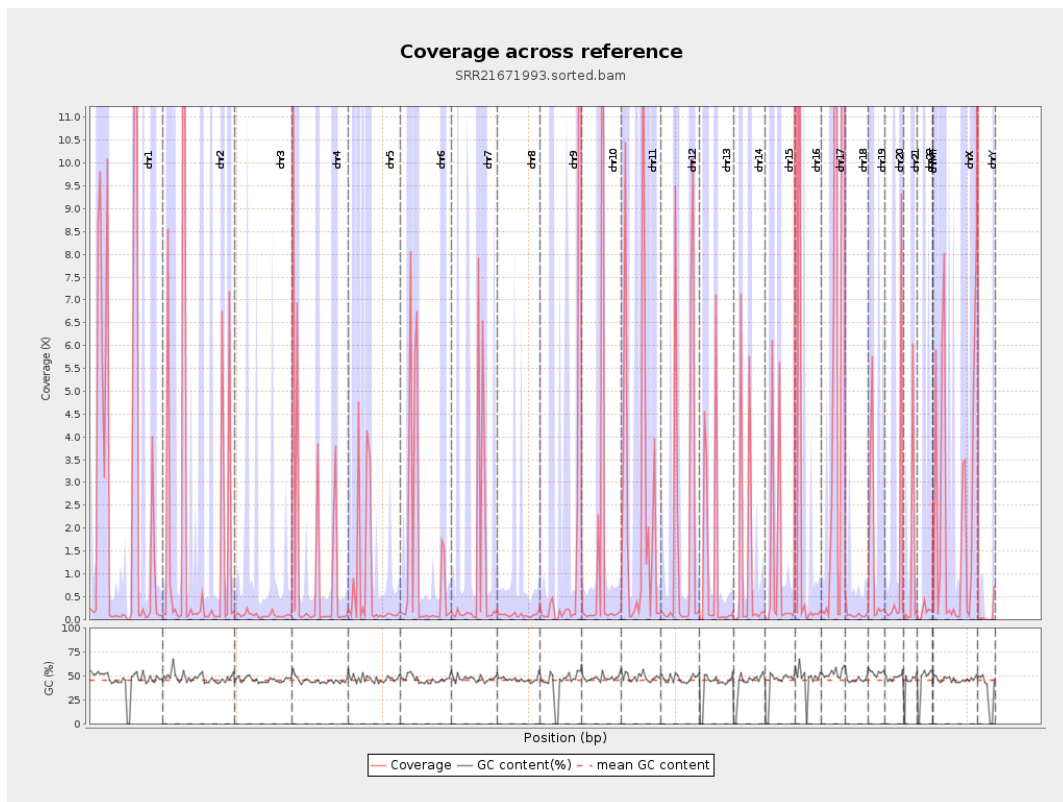
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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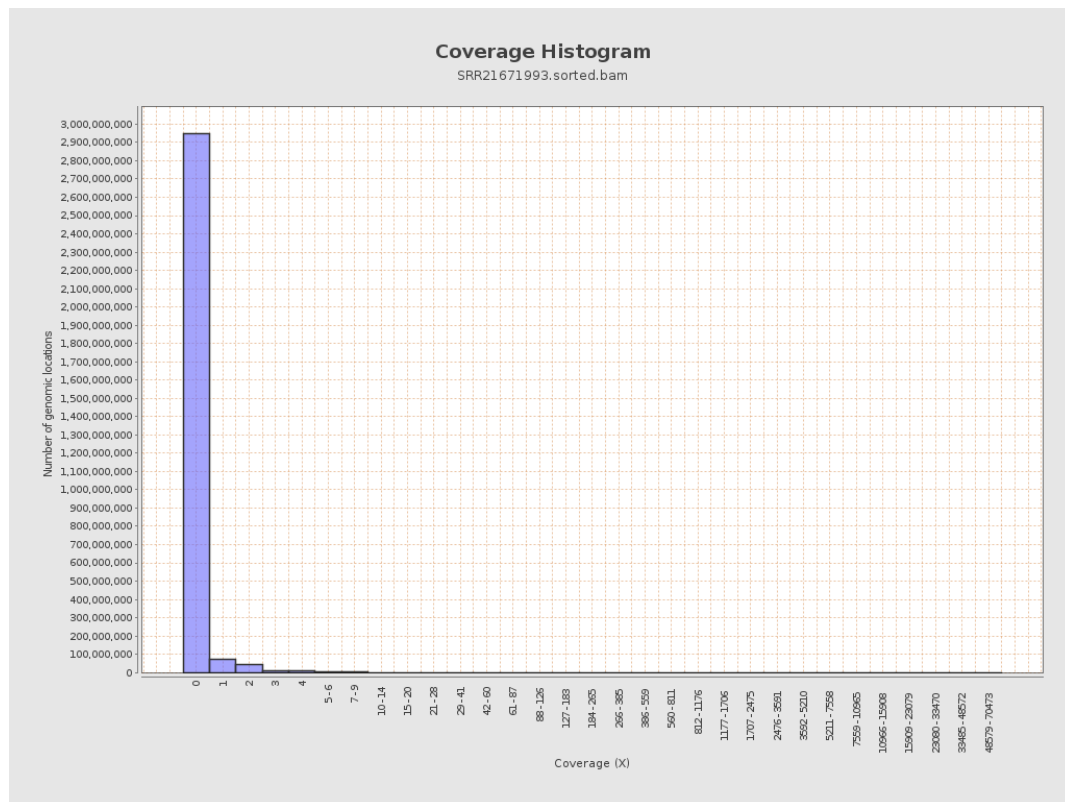
		bases	coverage	deviation
chr1	249250621	547032786	2.1947	128.4908
chr2	243199373	359886882	1.4798	89.9357
chr3	198022430	19456053	0.0983	3.3501
chr4	191154276	223442776	1.1689	77.4282
chr5	180915260	118933125	0.6574	54.887
chr6	171115067	199071732	1.1634	71.4658
chr7	159138663	153350019	0.9636	66.4163
chr8	146364022	13883783	0.0949	2.4323
chr9	141213431	234974285	1.664	109.8879
chr10	135534747	194196925	1.4328	77.8473
chr11	135006516	314567994	2.33	118.3892
chr12	133851895	238277705	1.7802	121.0976
chr13	115169878	123445864	1.0719	94.25
chr14	107349540	107206007	0.9987	66.2088
chr15	102531392	100991710	0.985	54.9112
chr16	90354753	377717221	4.1804	200.112
chr17	81195210	491286191	6.0507	242.9757
chr18	78077248	8785220	0.1125	10.7781
chr19	59128983	79187283	1.3392	108.0688
chr20	63025520	81153731	1.2876	77.1854
chr21	48129895	50309645	1.0453	86.4267
chr22	51304566	8502821	0.1657	10.2158
chrMT	16571	43554	2.6283	9.3317
chrX	155270560	393067176	2.5315	115.3397

chrY	59373566	6223839	0.1048	15.6439
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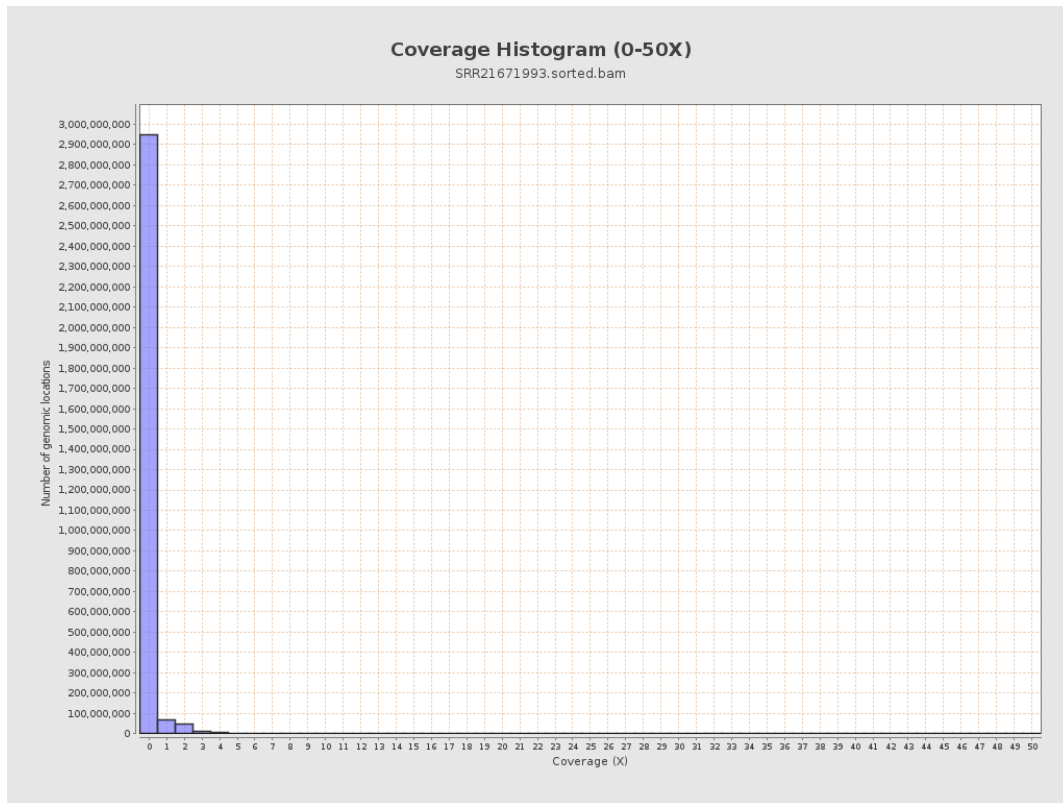
3. Results : Coverage across reference



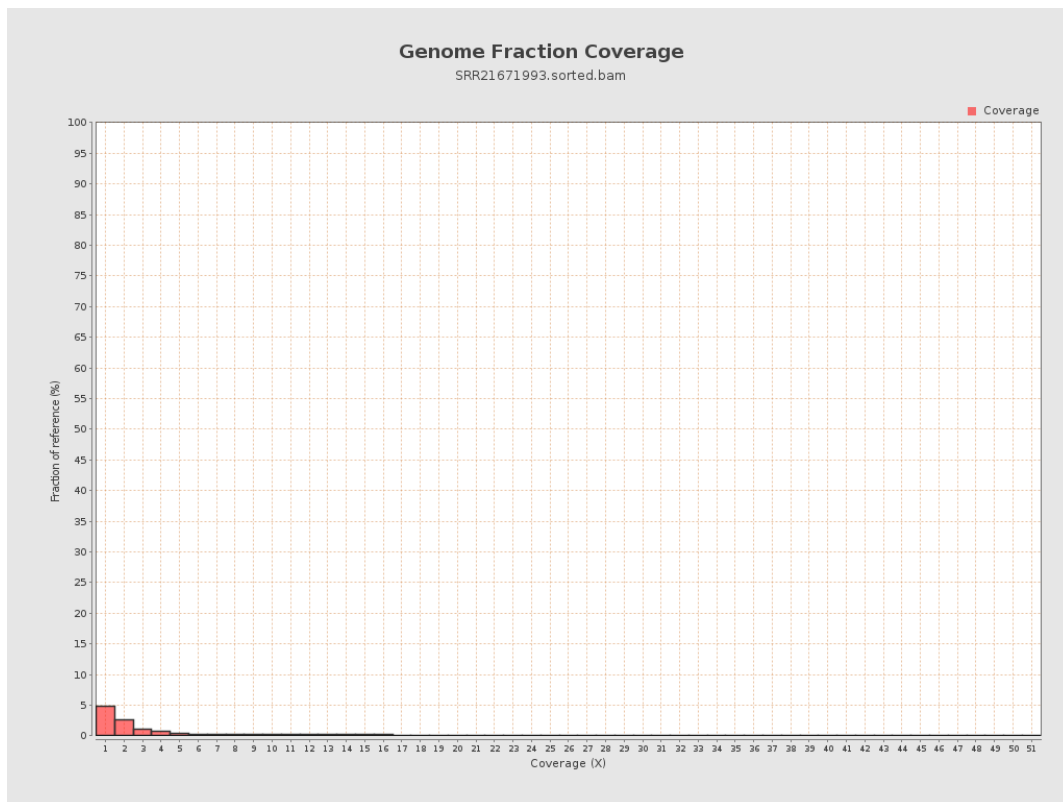
4. Results : Coverage Histogram



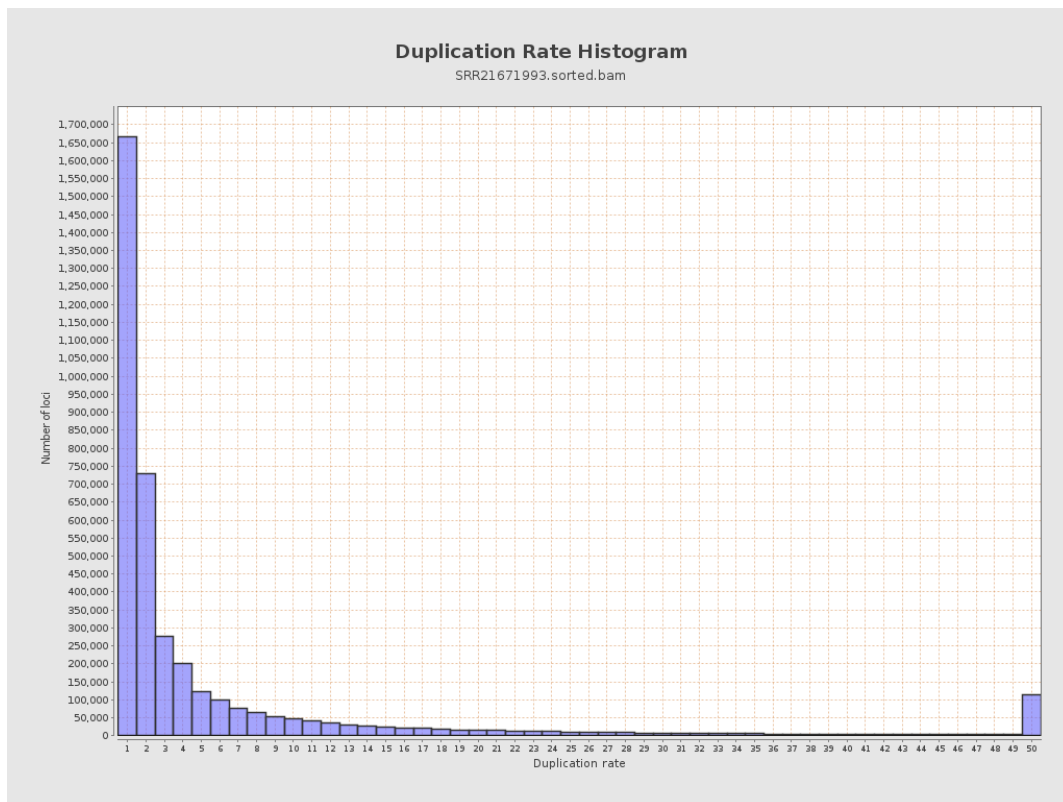
5. Results : Coverage Histogram (0-50X)



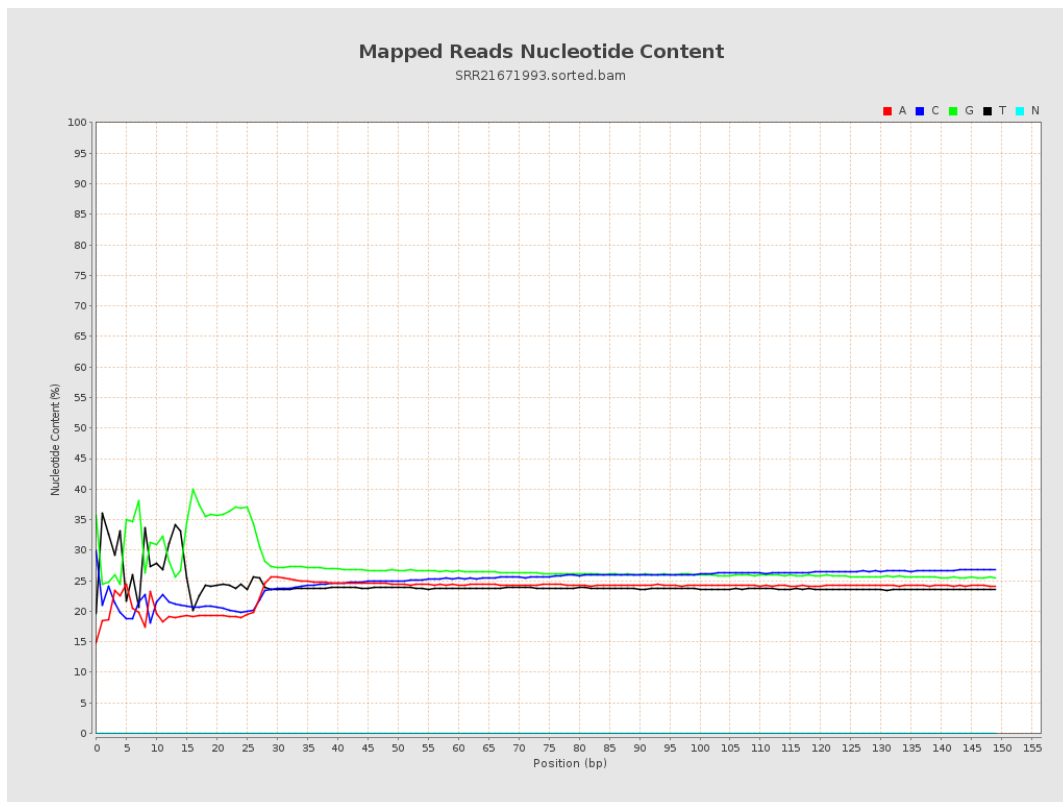
6. Results : Genome Fraction Coverage



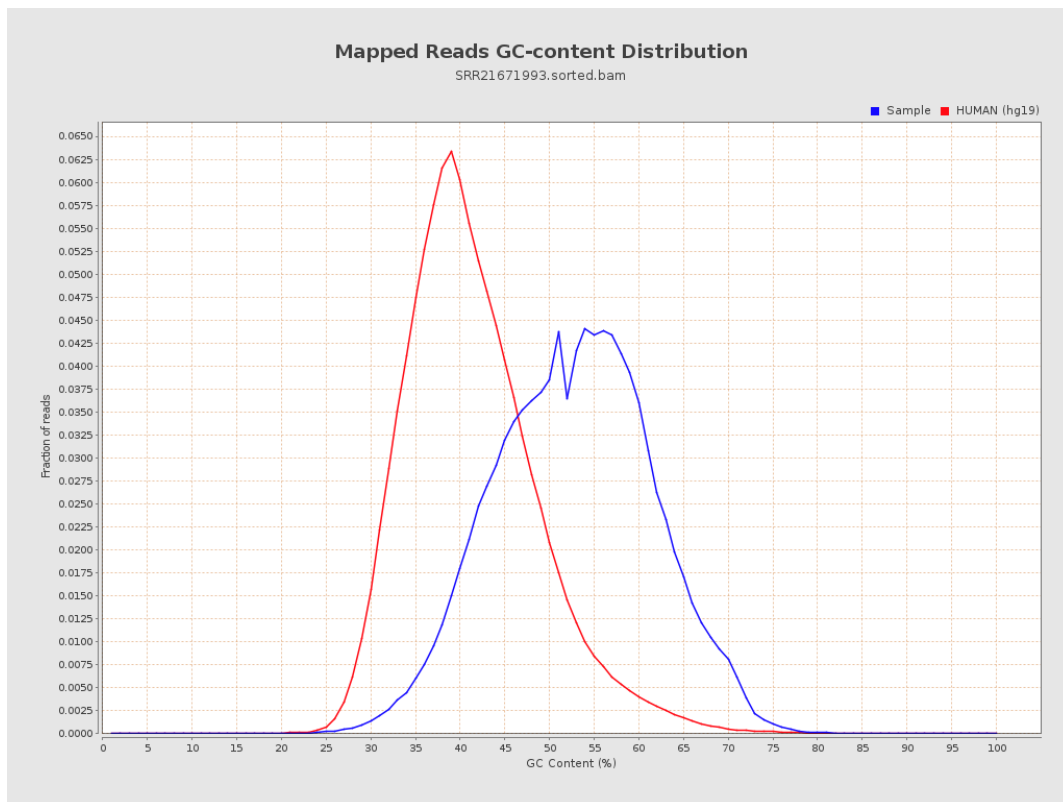
7. Results : Duplication Rate Histogram



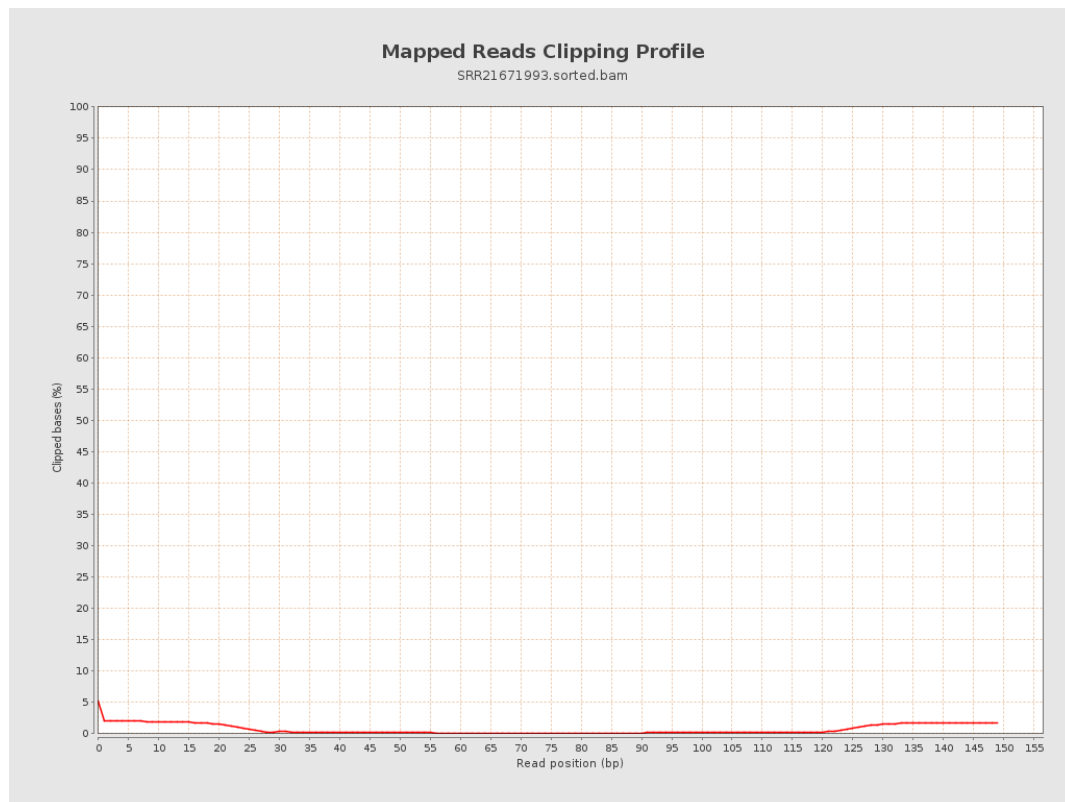
8. Results : Mapped Reads Nucleotide Content



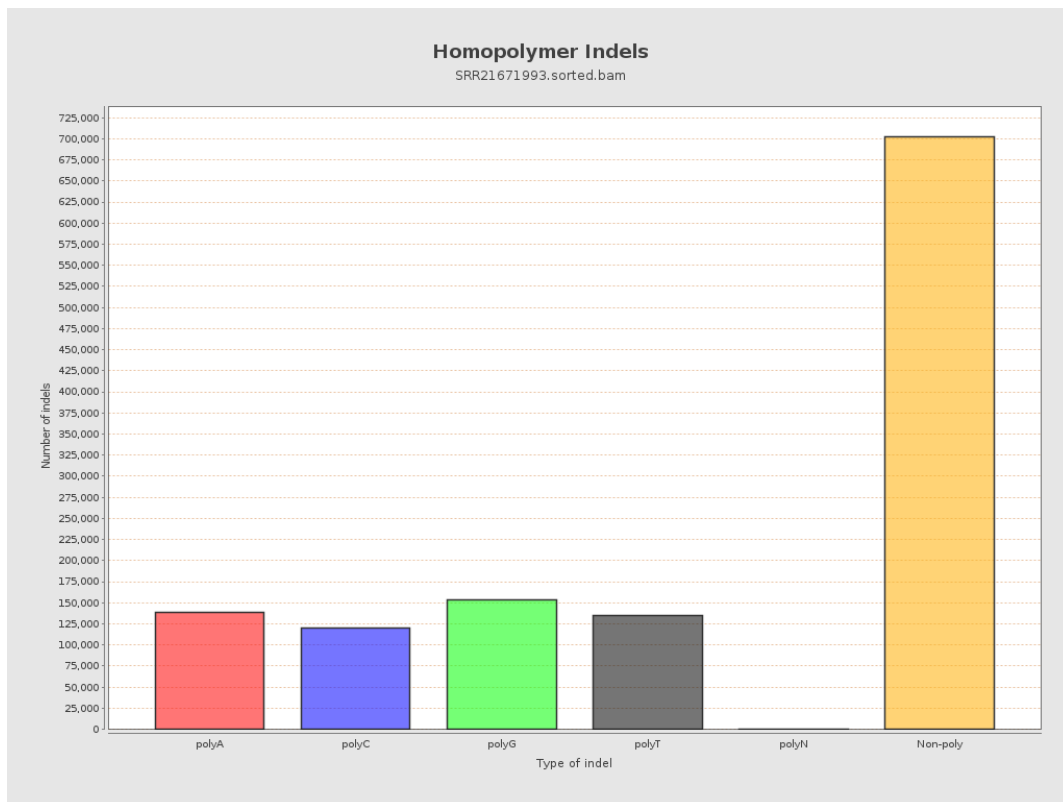
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



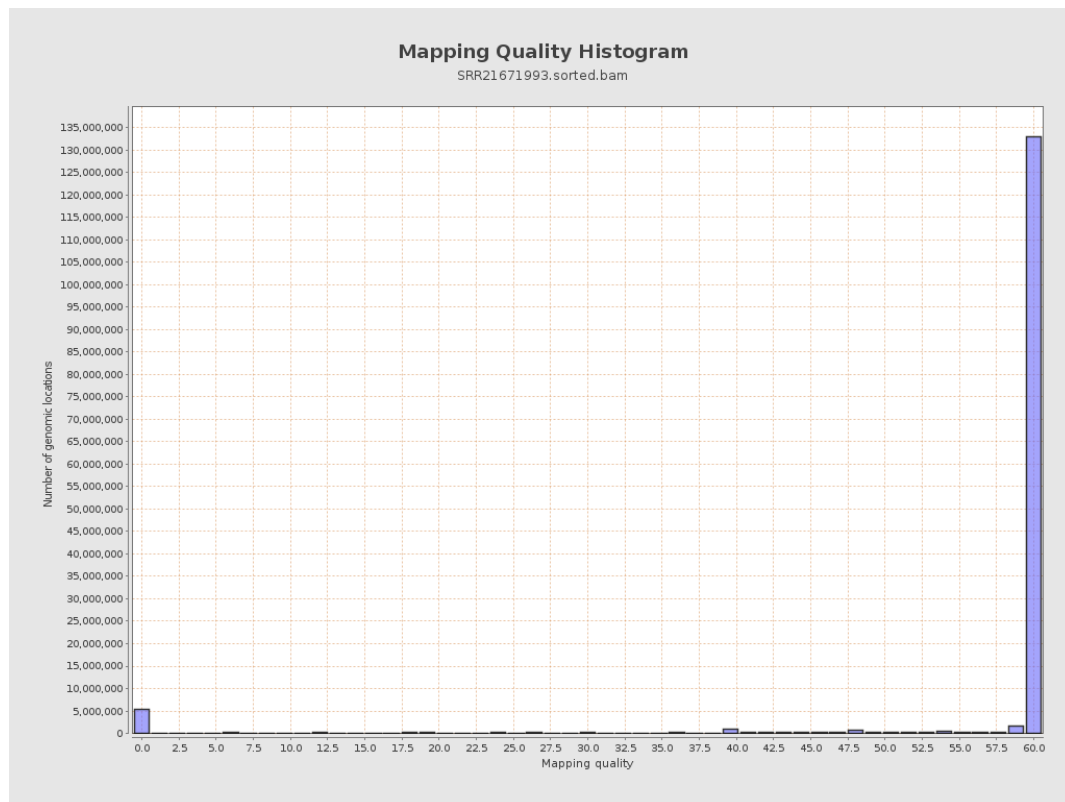
11. Results : Homopolymer Indels



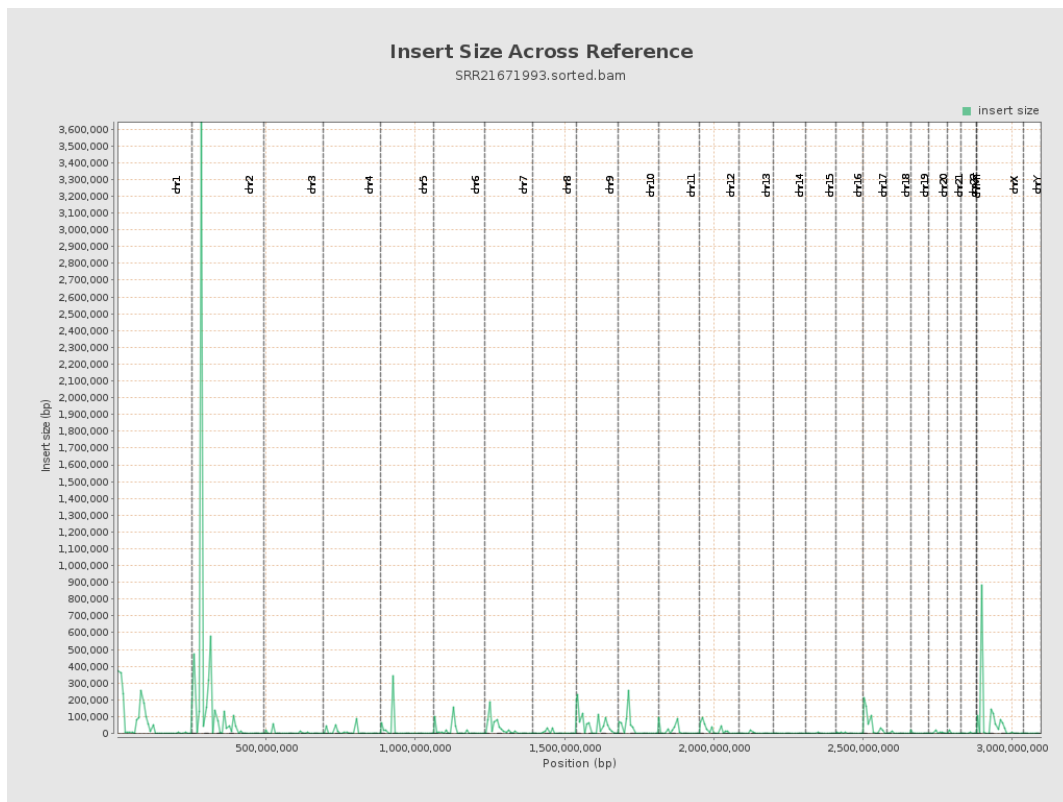
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

