

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/26 22:11:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR21671989.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_SRR21671989 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR21671989_1.fastq.gz SRR21671989_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Sep 26 22:11:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR21671989.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	284,188,530
Mapped reads	280,959,254 / 98.86%
Unmapped reads	3,229,276 / 1.14%
Mapped paired reads	280,959,254 / 98.86%
Mapped reads, first in pair	140,431,641 / 49.41%
Mapped reads, second in pair	140,527,613 / 49.45%
Mapped reads, both in pair	280,456,556 / 98.69%
Mapped reads, singletons	502,698 / 0.18%
Secondary alignments	0
Supplementary alignments	1,301,856 / 0.46%
Read min/max/mean length	15 / 150 / 143.43
Duplicated reads (estimated)	90,259,383 / 31.76%
Duplication rate	30.29%
Clipped reads	12,025,407 / 4.23%

2.2. ACGT Content

Number/percentage of A's	12,106,055,679 / 30.29%
Number/percentage of C's	7,887,428,258 / 19.73%
Number/percentage of T's	12,042,758,204 / 30.13%
Number/percentage of G's	7,933,586,164 / 19.85%
Number/percentage of N's	301,509 / 0%

GC Percentage	39.58%
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2.3. Coverage

Mean	12.9167
Standard Deviation	178.1902

2.4. Mapping Quality

Mean Mapping Quality	54.37
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2.5. Insert size

Mean	32,934.68
Standard Deviation	1,710,507.72
P25/Median/P75	171 / 248 / 344

2.6. Mismatches and indels

General error rate	0.58%
Mismatches	217,171,942
Insertions	5,299,578
Mapped reads with at least one insertion	1.8%
Deletions	5,889,367
Mapped reads with at least one deletion	1.99%
Homopolymer indels	44.38%

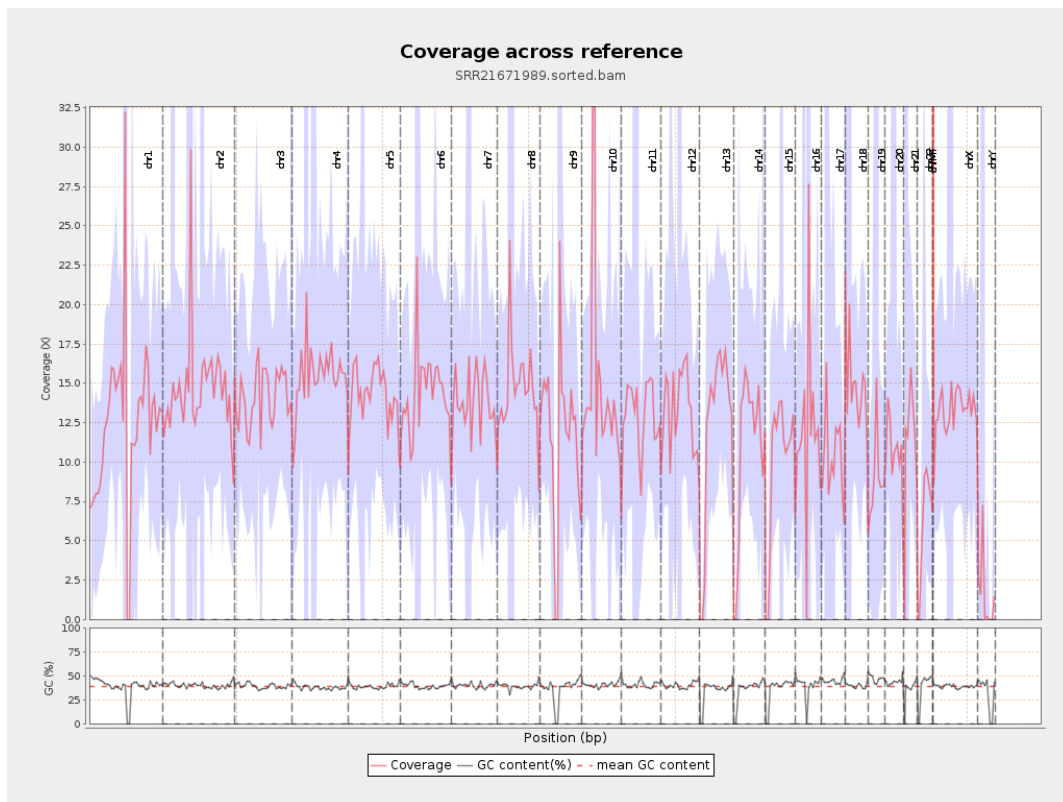
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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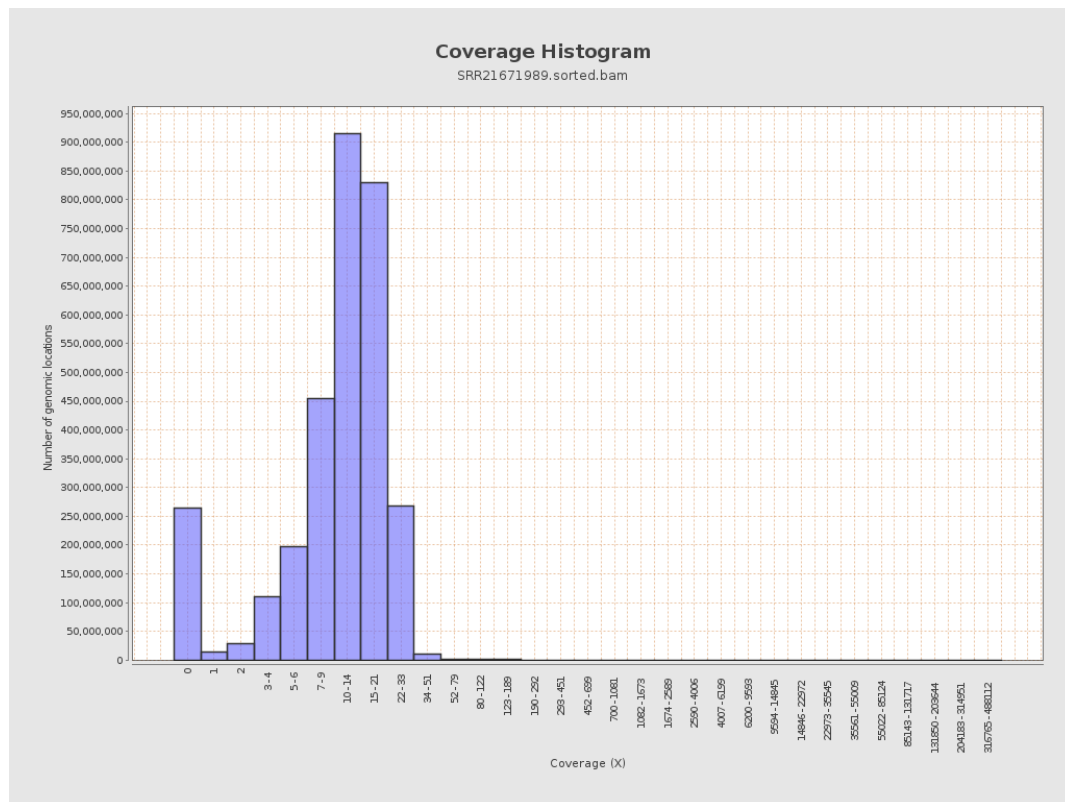
		bases	coverage	deviation
chr1	249250621	3087818009	12.3884	406.6312
chr2	243199373	3559713601	14.637	107.6645
chr3	198022430	2801049579	14.1451	11.4676
chr4	191154276	2957781011	15.4733	67.8586
chr5	180915260	2568233288	14.1958	11.7802
chr6	171115067	2472604316	14.45	90.5666
chr7	159138663	2184437291	13.7266	89.6466
chr8	146364022	2148705455	14.6806	395.2682
chr9	141213431	1672532863	11.844	212.7323
chr10	135534747	2017015598	14.8819	300.6748
chr11	135006516	1756934281	13.0137	67.8182
chr12	133851895	1771811513	13.2371	80.8616
chr13	115169878	1420444619	12.3335	8.328
chr14	107349540	1184104175	11.0304	13.4235
chr15	102531392	1017317837	9.922	14.8807
chr16	90354753	1064839714	11.7851	116.3875
chr17	81195210	852968957	10.5052	76.8872
chr18	78077248	1164078132	14.9093	198.2858
chr19	59128983	533862749	9.0288	184.1687
chr20	63025520	689146311	10.9344	26.4128
chr21	48129895	541291243	11.2465	35.2128
chr22	51304566	315311437	6.1459	12.9774
chrMT	16571	52032692	3,139.985	351.3009
chrX	155270560	2057572264	13.2515	32.061

chrY	59373566	94427563	1.5904	77.5662
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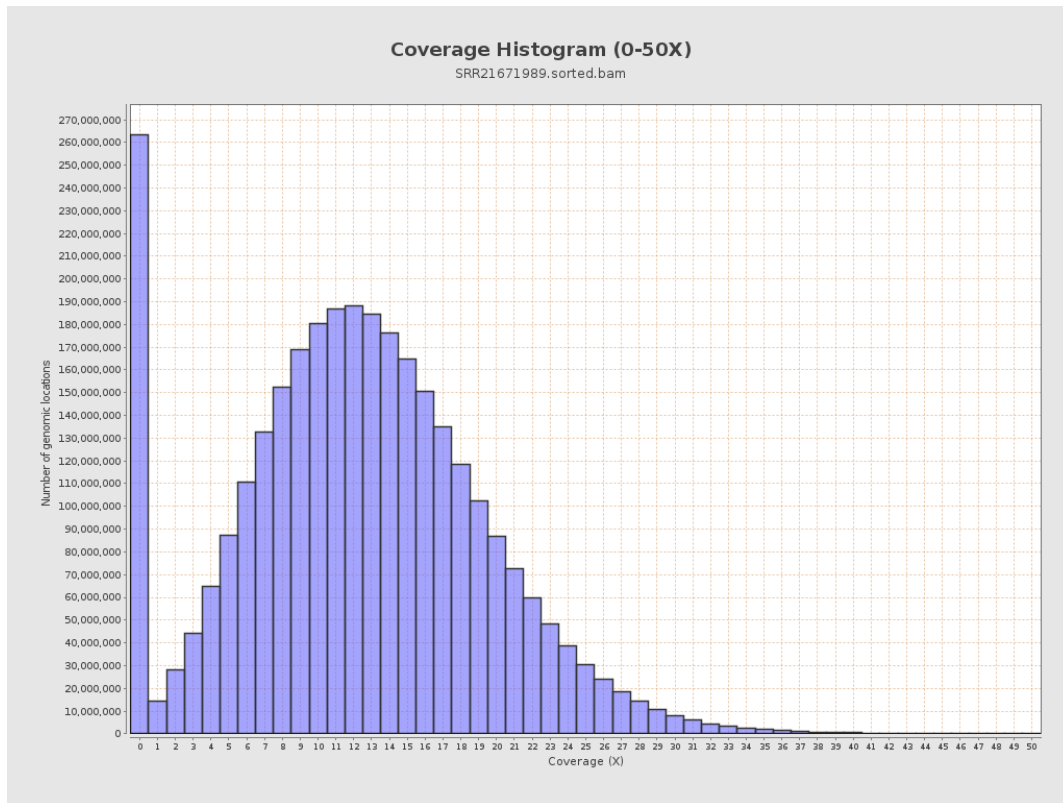
3. Results : Coverage across reference



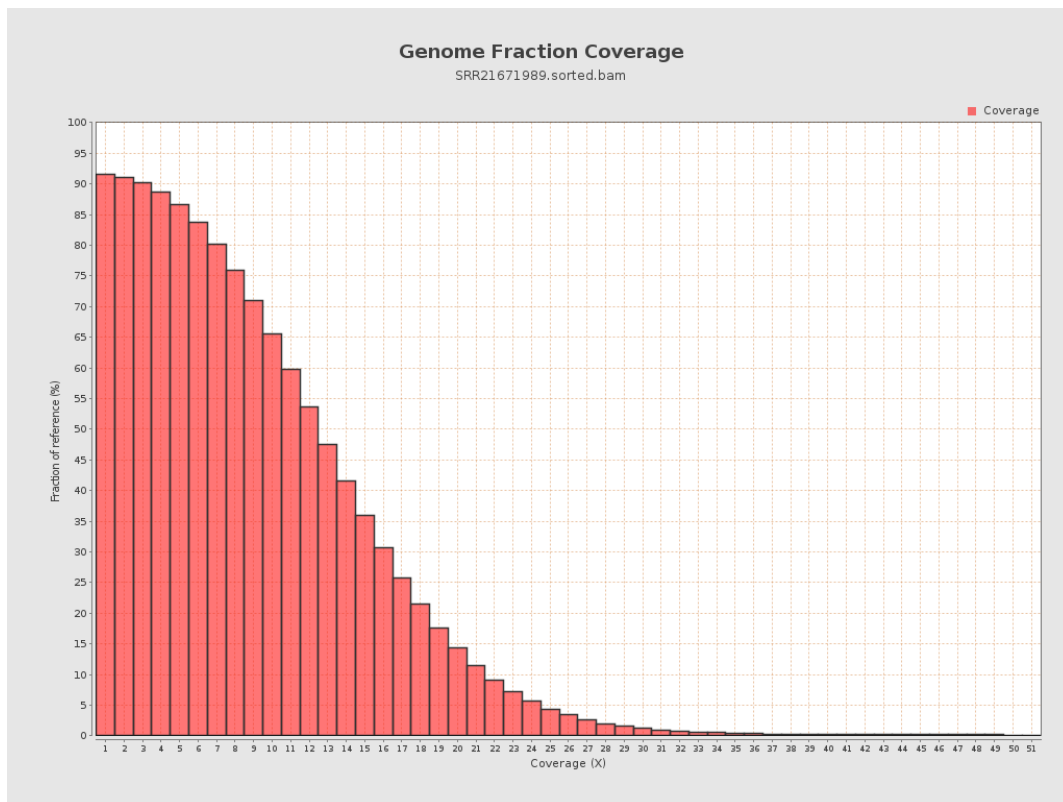
4. Results : Coverage Histogram



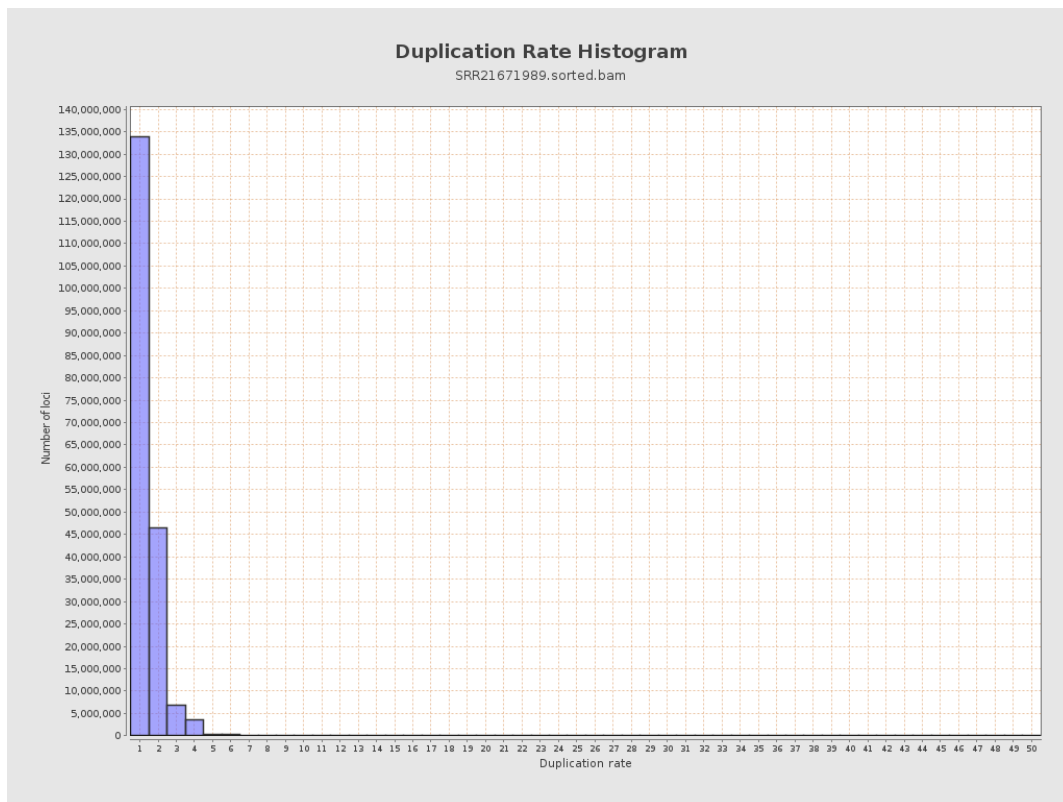
5. Results : Coverage Histogram (0-50X)



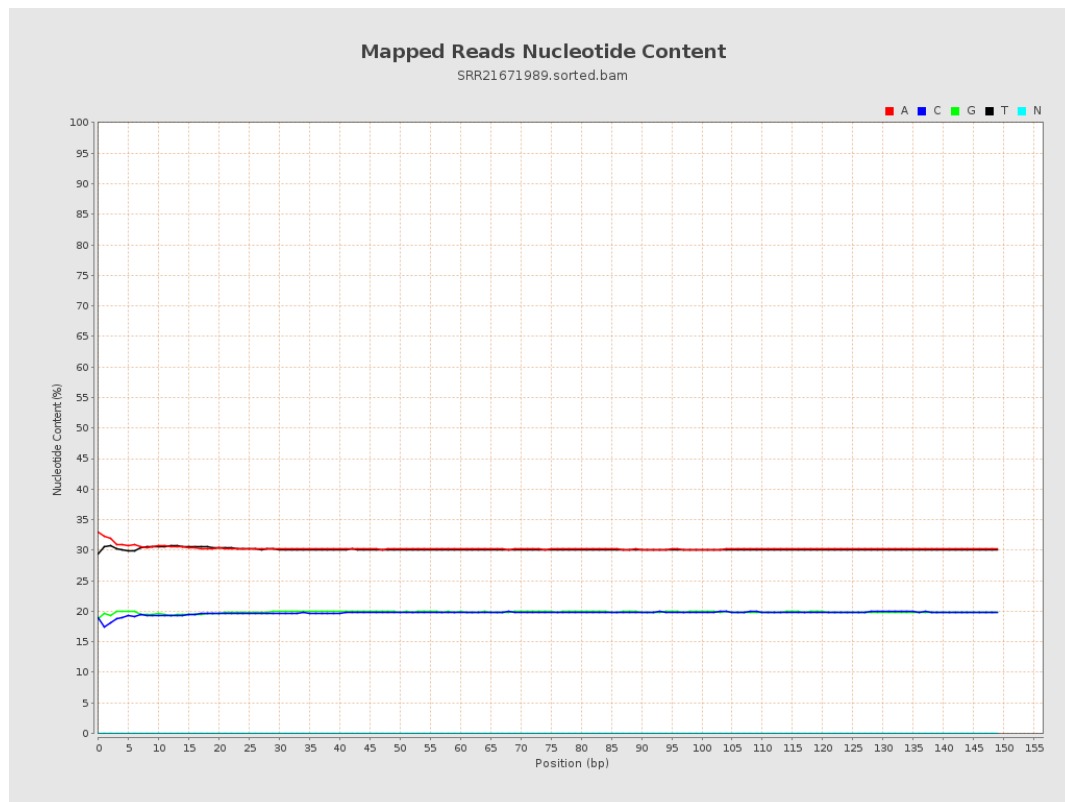
6. Results : Genome Fraction Coverage



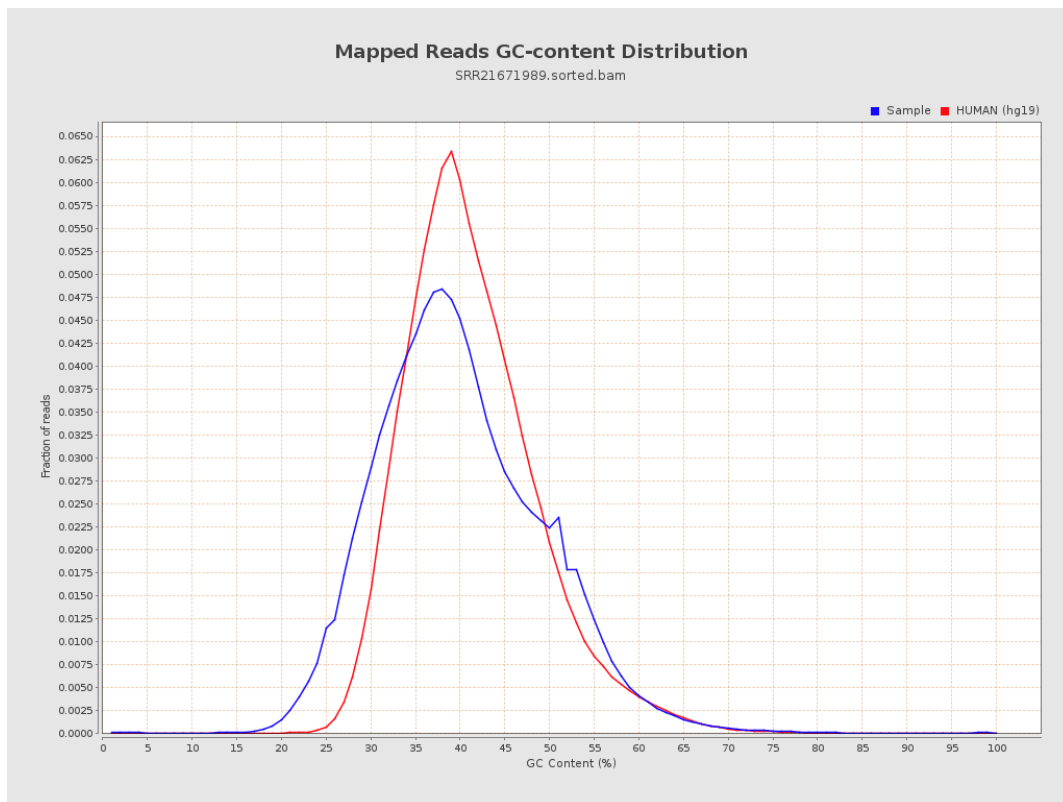
7. Results : Duplication Rate Histogram



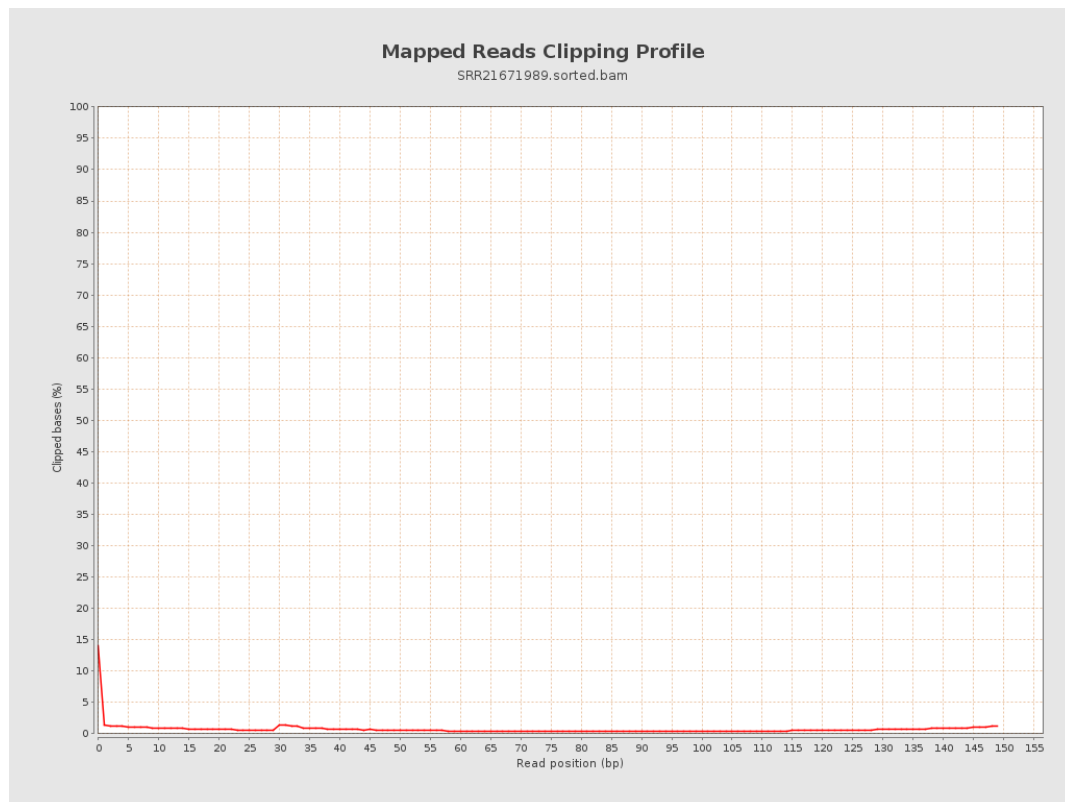
8. Results : Mapped Reads Nucleotide Content



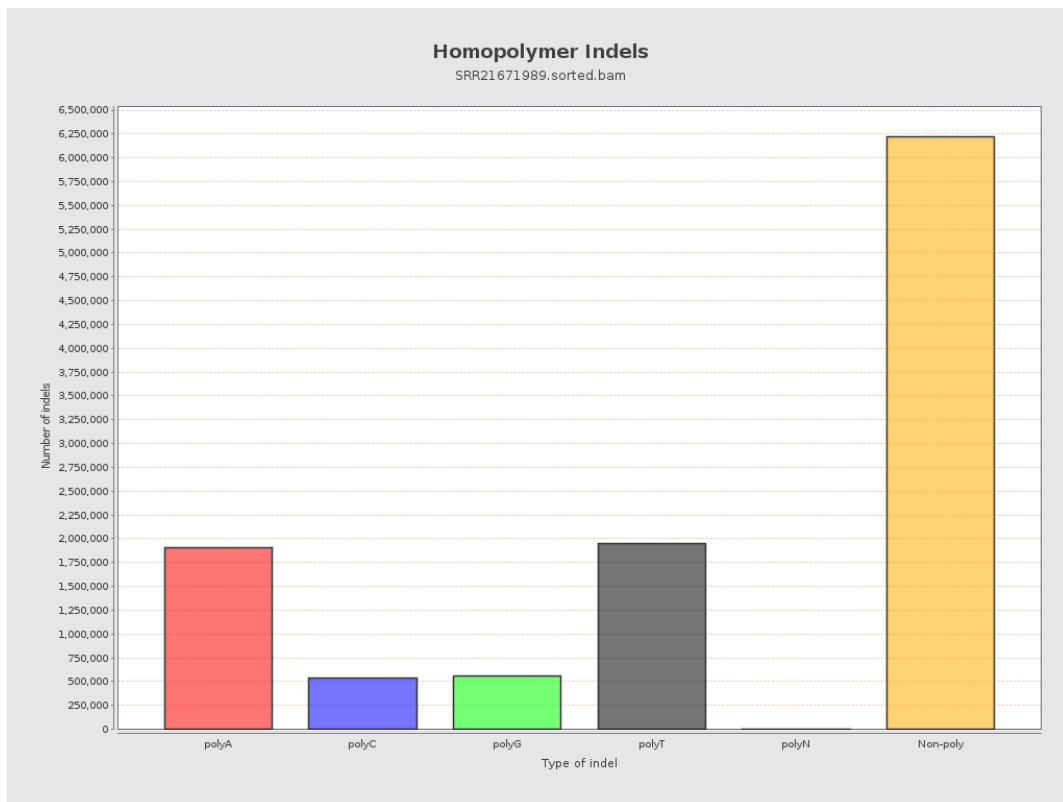
9. Results : Mapped Reads GC-content Distribution



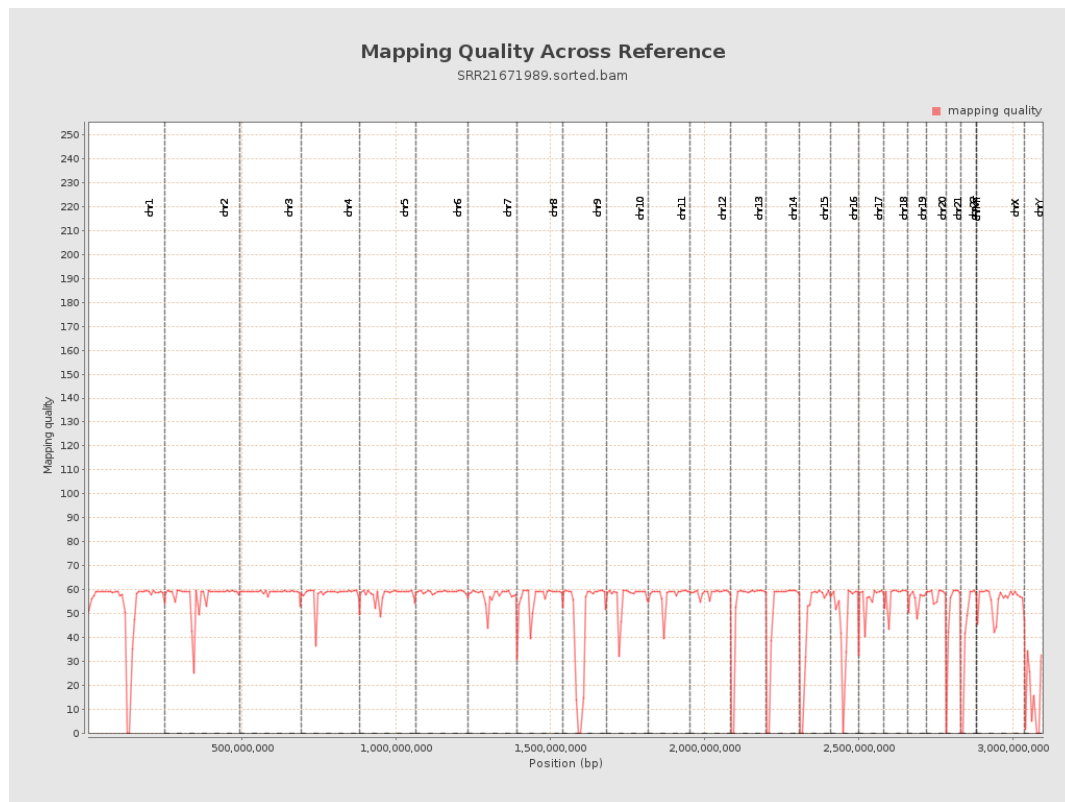
10. Results : Mapped Reads Clipping Profile



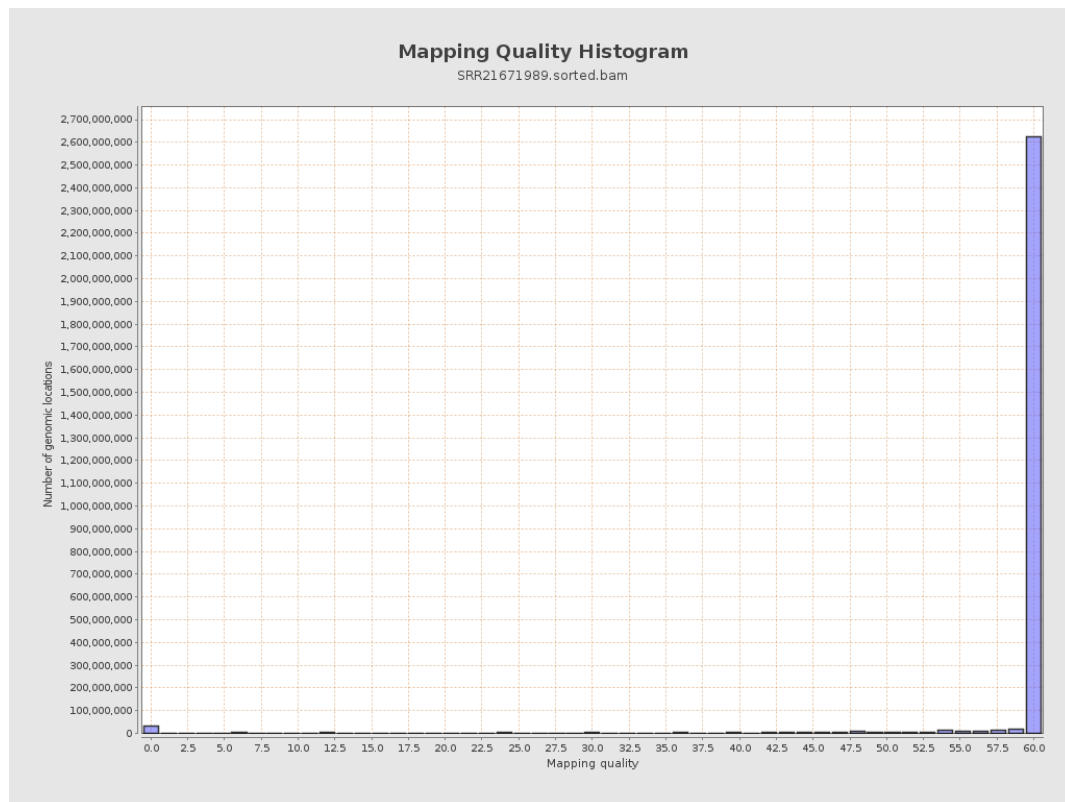
11. Results : Homopolymer Indels



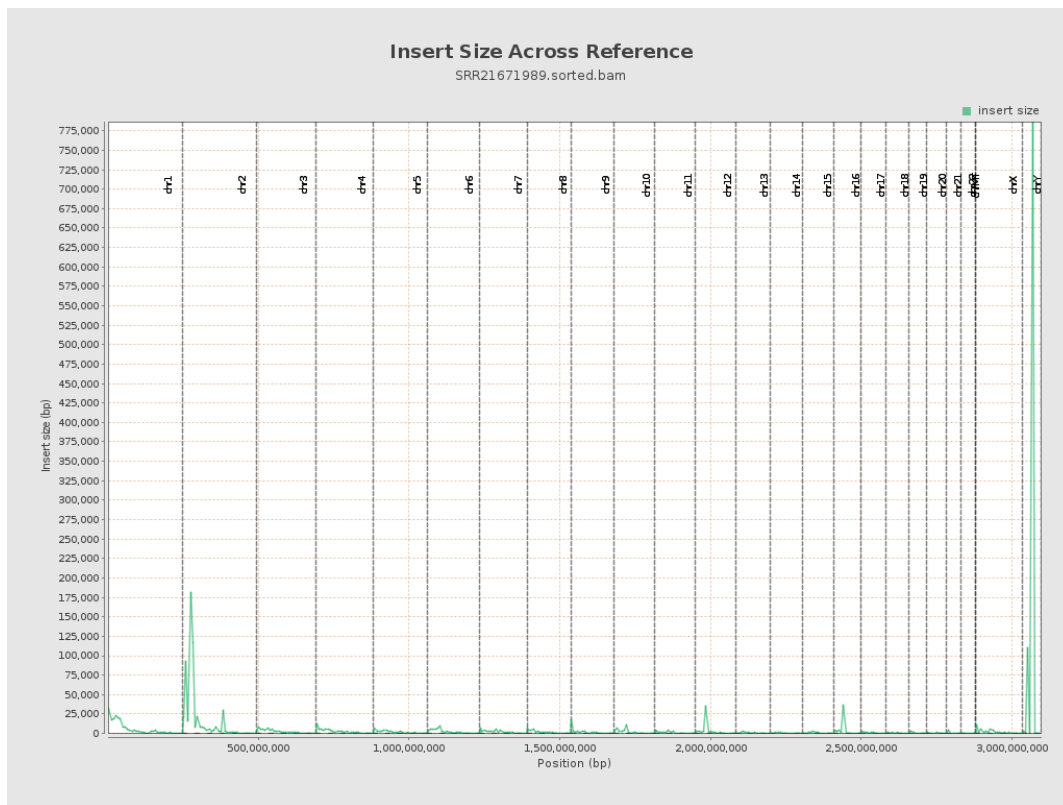
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

