

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 17:50:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472789.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_SRR3472789 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472789_1.fastq.gz SRR3472789_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 17:50:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472789.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,183,632
Mapped reads	12,069,189 / 99.06%
Unmapped reads	114,443 / 0.94%
Mapped paired reads	12,069,189 / 99.06%
Mapped reads, first in pair	6,054,747 / 49.7%
Mapped reads, second in pair	6,014,442 / 49.36%
Mapped reads, both in pair	12,003,412 / 98.52%
Mapped reads, singletons	65,777 / 0.54%
Secondary alignments	0
Supplementary alignments	42,553 / 0.35%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	7,284,163 / 59.79%
Duplication rate	46.56%
Clipped reads	1,052,872 / 8.64%

2.2. ACGT Content

Number/percentage of A's	326,071,404 / 27.47%
Number/percentage of C's	269,027,247 / 22.67%
Number/percentage of T's	324,172,571 / 27.31%
Number/percentage of G's	267,401,891 / 22.53%
Number/percentage of N's	229,817 / 0.02%

GC Percentage	45.2%
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2.3. Coverage

Mean	0.3835
Standard Deviation	13.8873

2.4. Mapping Quality

Mean Mapping Quality	55.1
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2.5. Insert size

Mean	23,044.55
Standard Deviation	1,489,053.66
P25/Median/P75	166 / 235 / 318

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	7,281,957
Insertions	69,767
Mapped reads with at least one insertion	0.57%
Deletions	67,993
Mapped reads with at least one deletion	0.56%
Homopolymer indels	44.31%

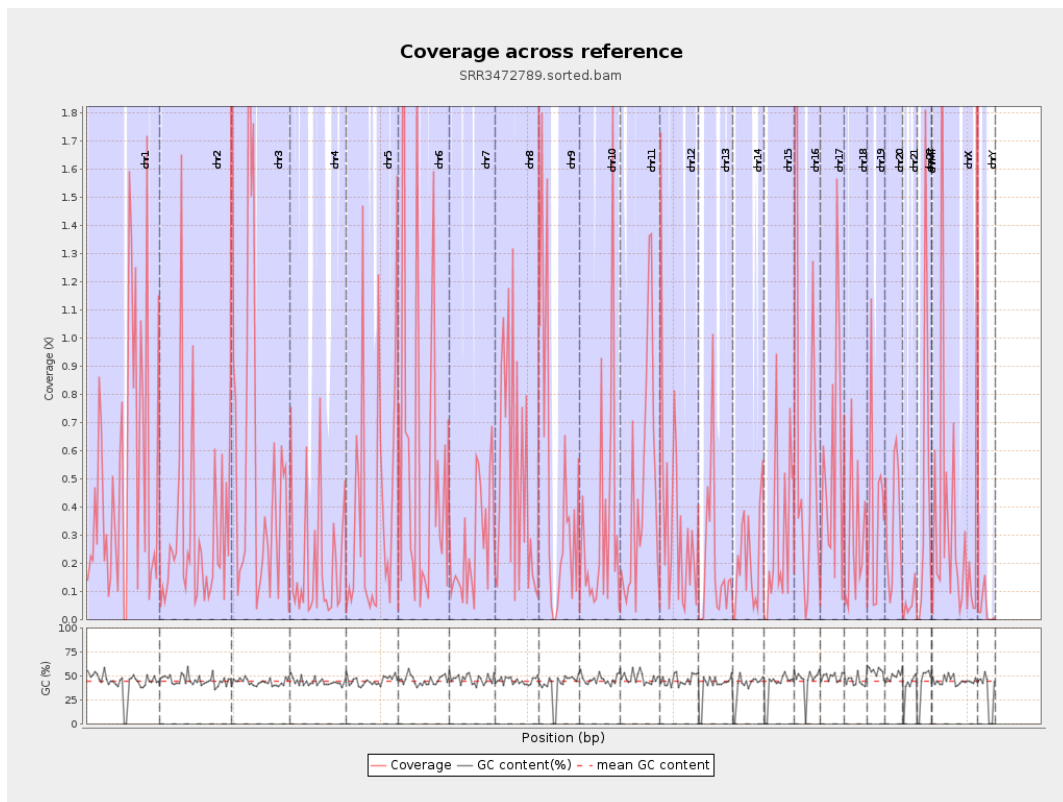
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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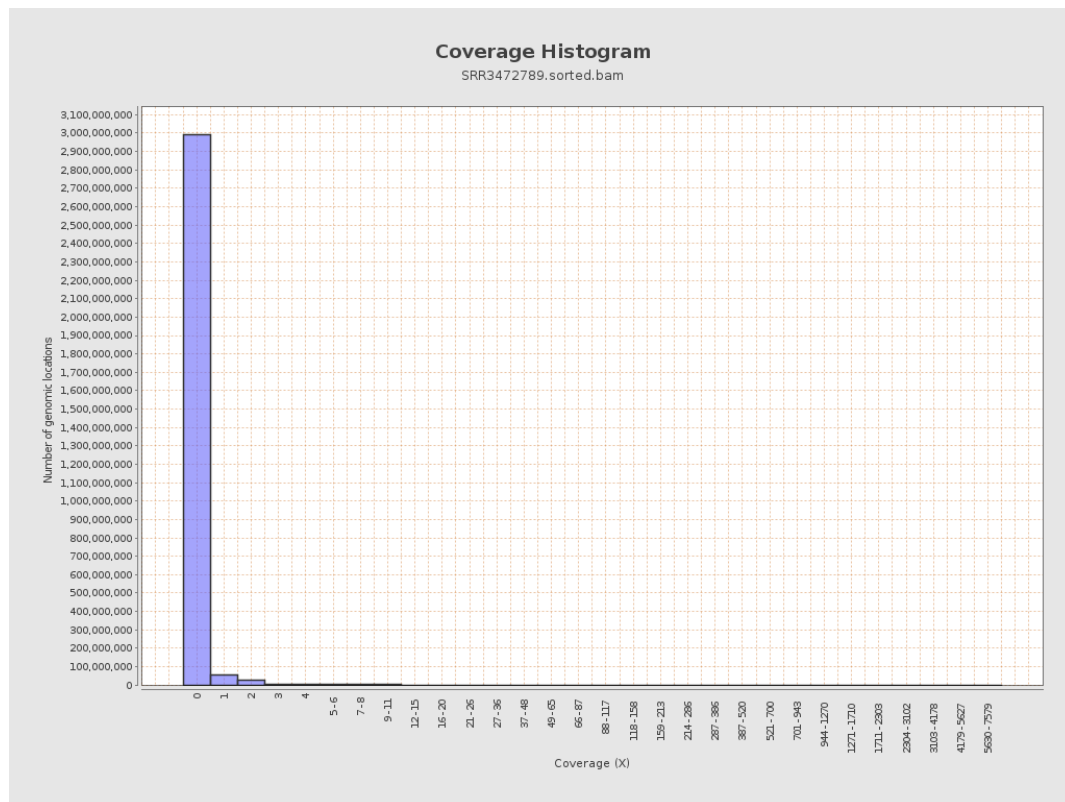
		bases	coverage	deviation
chr1	249250621	128622472	0.516	16.0185
chr2	243199373	71925209	0.2957	11.945
chr3	198022430	114022744	0.5758	12.5282
chr4	191154276	36921421	0.1931	7.4821
chr5	180915260	70225575	0.3882	16.1086
chr6	171115067	99889065	0.5838	21.9334
chr7	159138663	43188234	0.2714	8.4466
chr8	146364022	73720692	0.5037	17.9056
chr9	141213431	66208211	0.4689	13.0067
chr10	135534747	45634050	0.3367	15.0402
chr11	135006516	60743062	0.4499	17.0009
chr12	133851895	48038731	0.3589	11.8721
chr13	115169878	22648323	0.1967	9.4594
chr14	107349540	22104441	0.2059	7.0167
chr15	102531392	29675849	0.2894	10.9975
chr16	90354753	55796301	0.6175	22.9286
chr17	81195210	43707219	0.5383	11.5918
chr18	78077248	21520049	0.2756	13.2634
chr19	59128983	23958891	0.4052	9.2883
chr20	63025520	21821785	0.3462	10.6663
chr21	48129895	3013401	0.0626	2.3382
chr22	51304566	22144688	0.4316	20.3548
chrMT	16571	2271	0.137	0.4973
chrX	155270560	59167564	0.3811	11.9365

chrY	59373566	2371543	0.0399	2.8807
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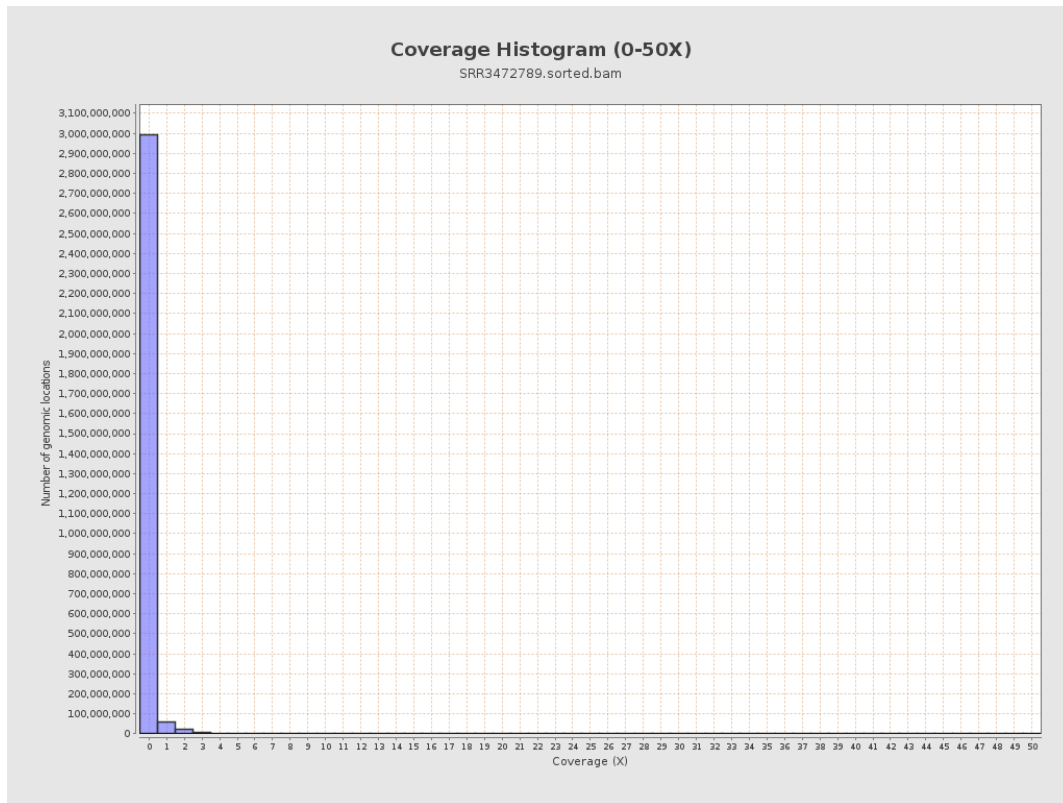
3. Results : Coverage across reference



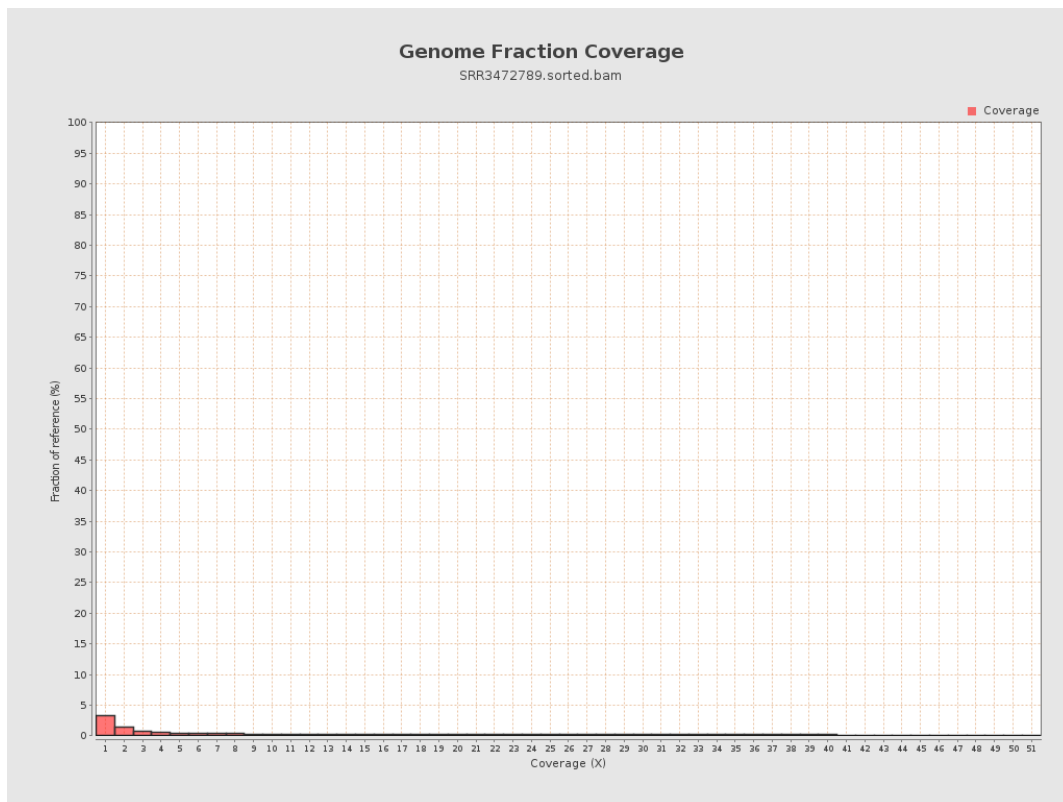
4. Results : Coverage Histogram



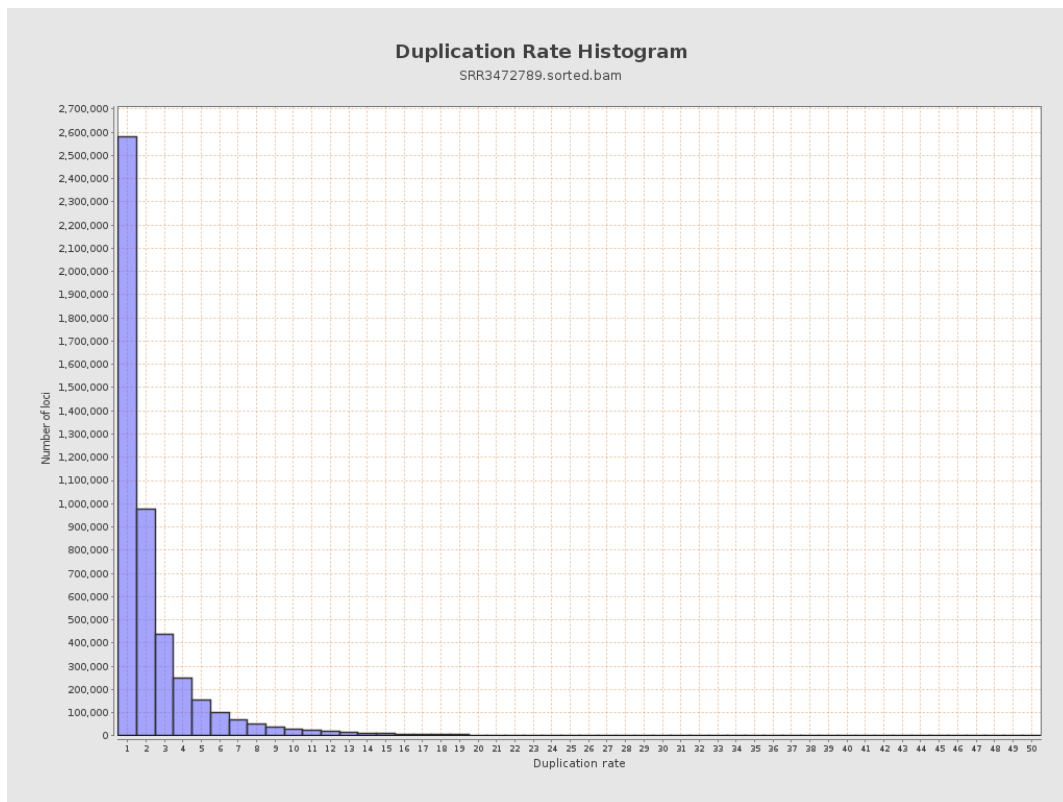
5. Results : Coverage Histogram (0-50X)



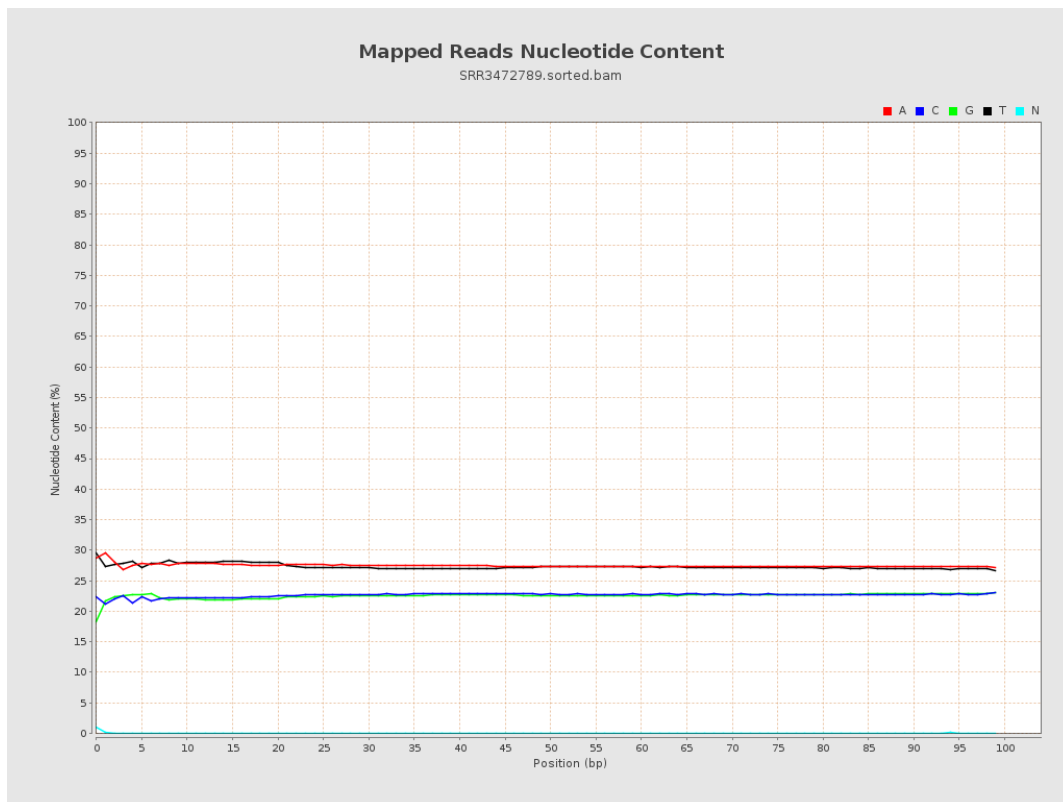
6. Results : Genome Fraction Coverage



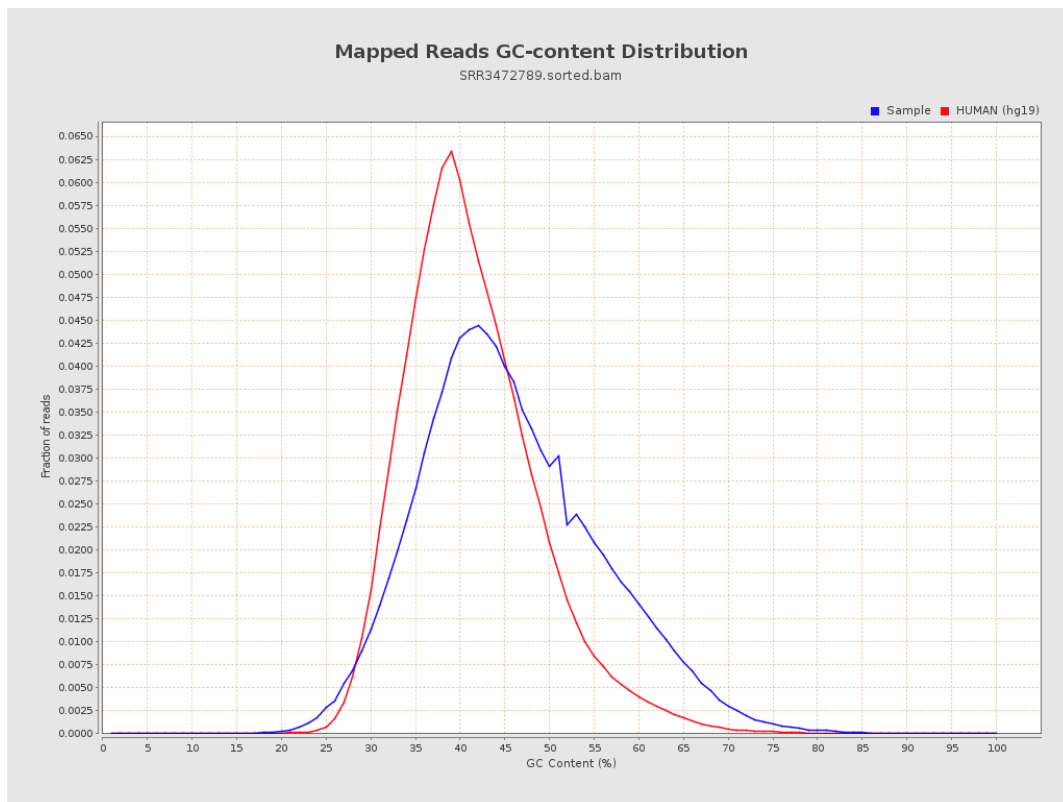
7. Results : Duplication Rate Histogram



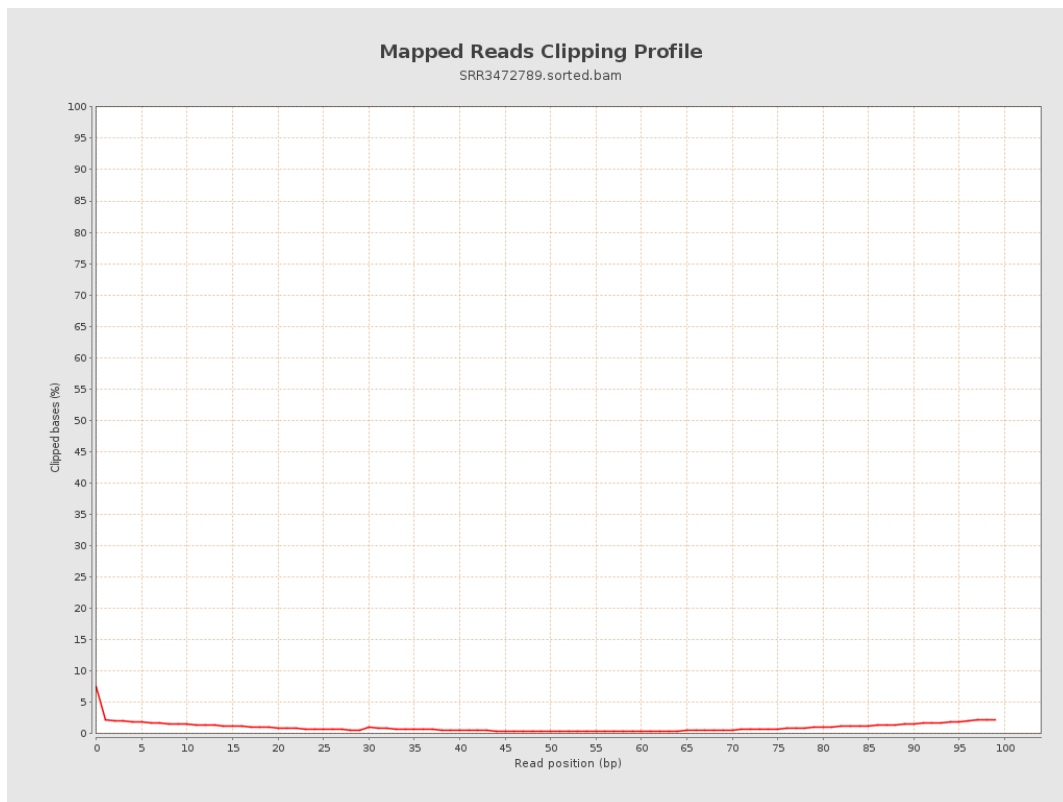
8. Results : Mapped Reads Nucleotide Content



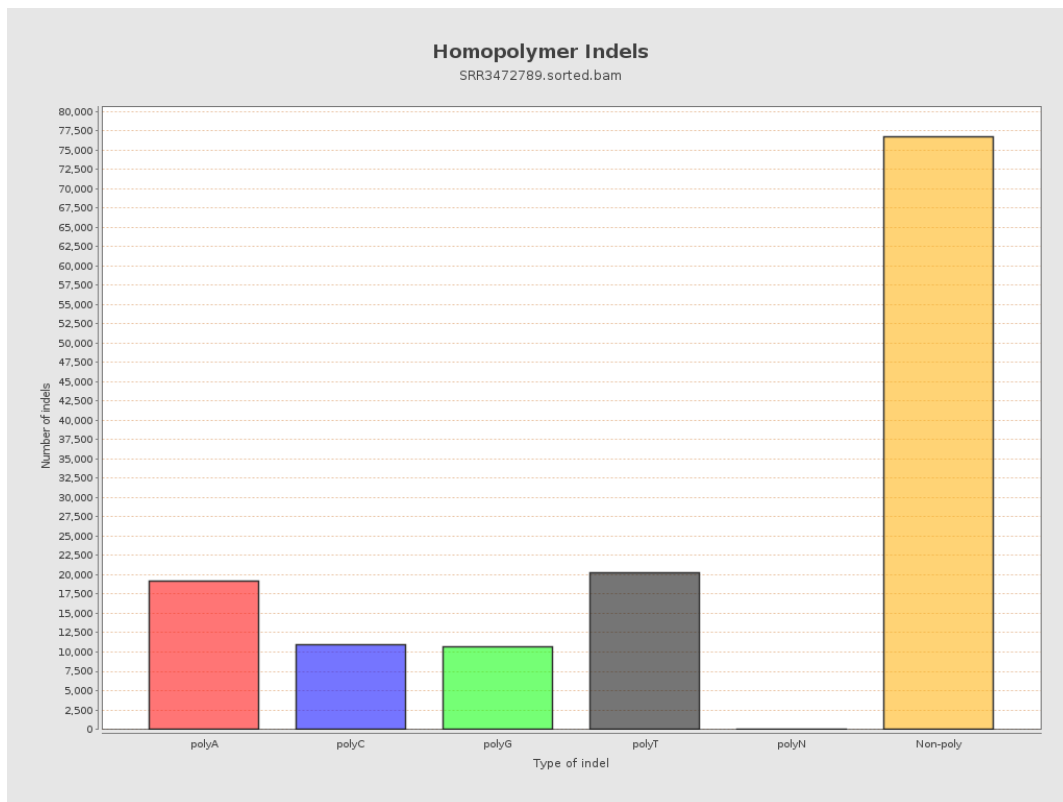
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



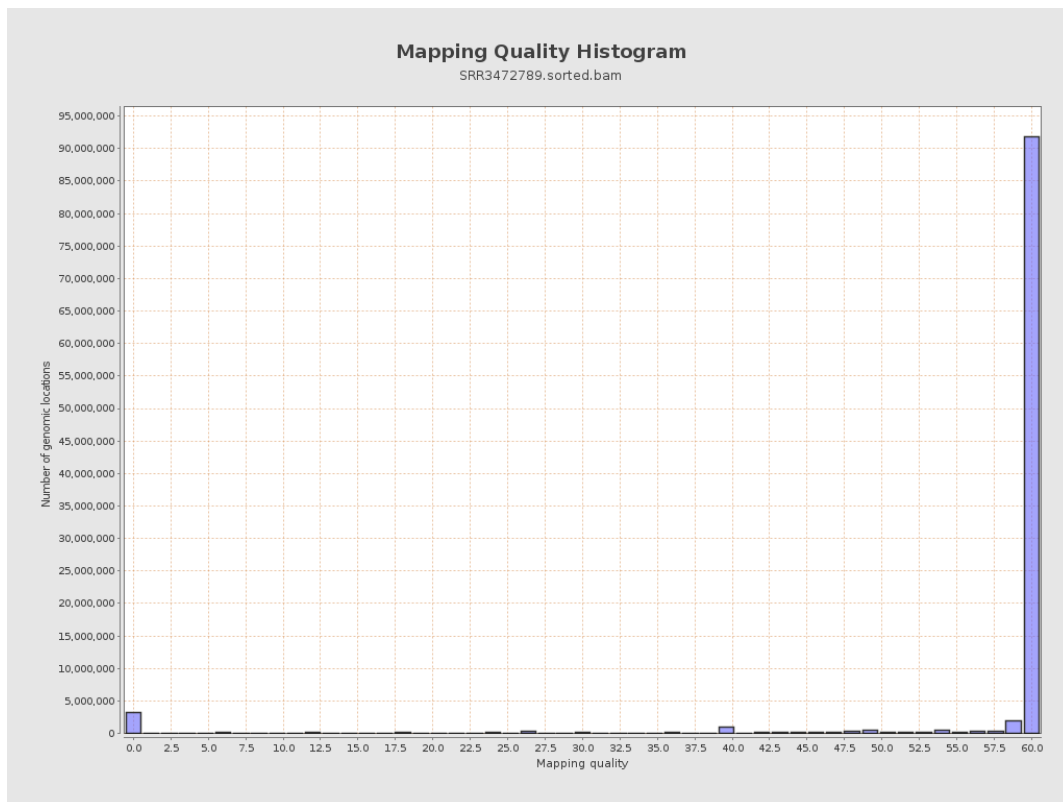
11. Results : Homopolymer Indels



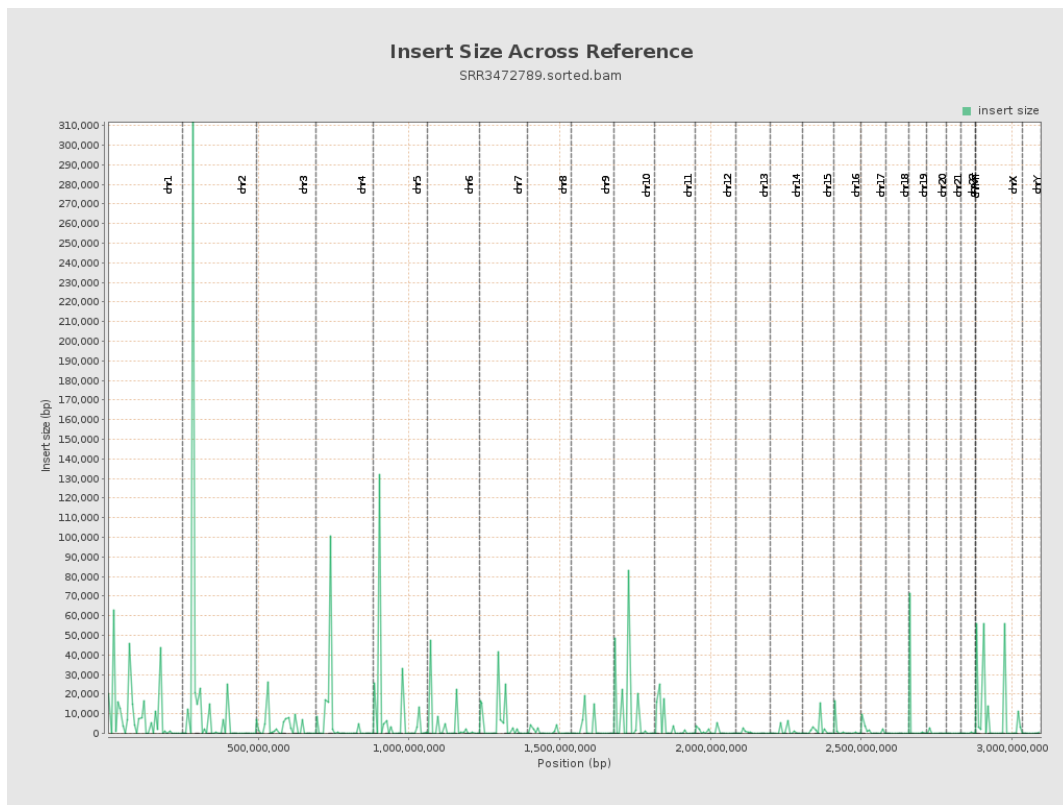
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

