

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 14:14:56

1. Input data & parameters

1.1. QualiMap command line

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qualimap bamqc -bam SRR3472703.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_SRR3472703 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472703_1.fastq.gz SRR3472703_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 14:14:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472703.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,607,938
Mapped reads	1,358,388 / 84.48%
Unmapped reads	249,550 / 15.52%
Mapped paired reads	1,358,388 / 84.48%
Mapped reads, first in pair	704,761 / 43.83%
Mapped reads, second in pair	653,627 / 40.65%
Mapped reads, both in pair	1,289,584 / 80.2%
Mapped reads, singletons	68,804 / 4.28%
Secondary alignments	0
Supplementary alignments	7,136 / 0.44%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	416,169 / 25.88%
Duplication rate	27.98%
Clipped reads	180,985 / 11.26%

2.2. ACGT Content

Number/percentage of A's	38,087,394 / 28.92%
Number/percentage of C's	27,839,107 / 21.14%
Number/percentage of T's	36,213,355 / 27.49%
Number/percentage of G's	29,557,471 / 22.44%
Number/percentage of N's	23,044 / 0.02%

GC Percentage	43.57%
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2.3. Coverage

Mean	0.0426
Standard Deviation	1.1078

2.4. Mapping Quality

Mean Mapping Quality	54.05
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2.5. Insert size

Mean	61,581.36
Standard Deviation	2,483,504.7
P25/Median/P75	198 / 291 / 447

2.6. Mismatches and indels

General error rate	1.08%
Mismatches	1,392,411
Insertions	10,256
Mapped reads with at least one insertion	0.74%
Deletions	8,963
Mapped reads with at least one deletion	0.65%
Homopolymer indels	45.34%

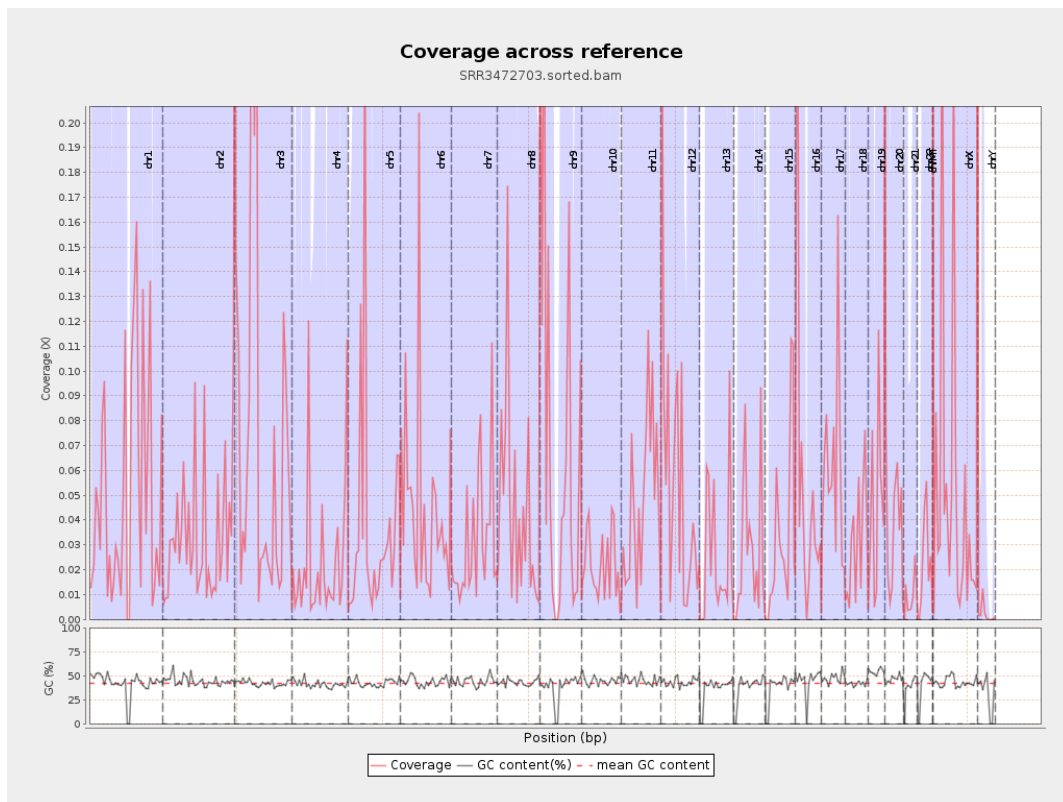
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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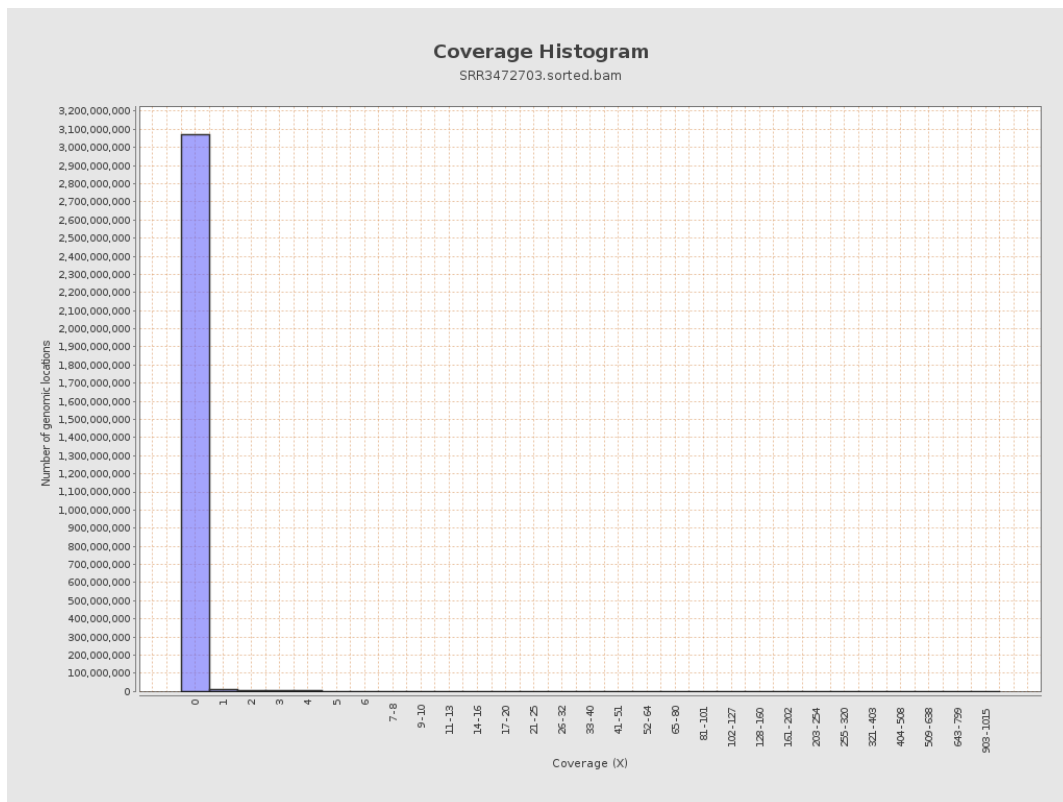
		bases	coverage	deviation
chr1	249250621	12596292	0.0505	1.3621
chr2	243199373	8066880	0.0332	0.9011
chr3	198022430	15749372	0.0795	1.3305
chr4	191154276	4563276	0.0239	0.6932
chr5	180915260	6834293	0.0378	0.9771
chr6	171115067	7654238	0.0447	0.9404
chr7	159138663	5054918	0.0318	0.7671
chr8	146364022	6283512	0.0429	1.2237
chr9	141213431	9057526	0.0641	1.4052
chr10	135534747	3028166	0.0223	0.6288
chr11	135006516	6309634	0.0467	1.2244
chr12	133851895	7741163	0.0578	1.4284
chr13	115169878	2923249	0.0254	0.9136
chr14	107349540	3059824	0.0285	0.7134
chr15	102531392	3364814	0.0328	1.1446
chr16	90354753	5012621	0.0555	1.2121
chr17	81195210	5118650	0.063	1.1789
chr18	78077248	2489700	0.0319	0.9728
chr19	59128983	3215331	0.0544	1.6169
chr20	63025520	2315374	0.0367	0.8002
chr21	48129895	473834	0.0098	0.4943
chr22	51304566	1170314	0.0228	0.6364
chrMT	16571	6808	0.4108	1.1107
chrX	155270560	9508259	0.0612	1.6411

chrY	59373566	144556	0.0024	0.1261
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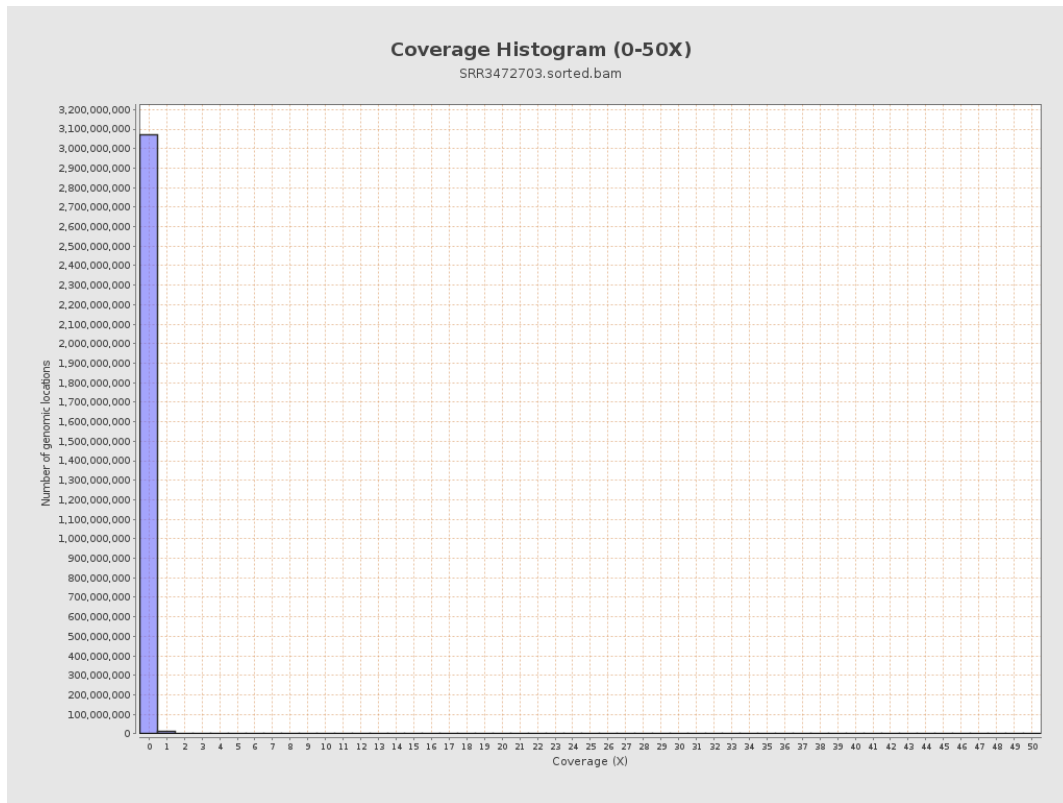
3. Results : Coverage across reference



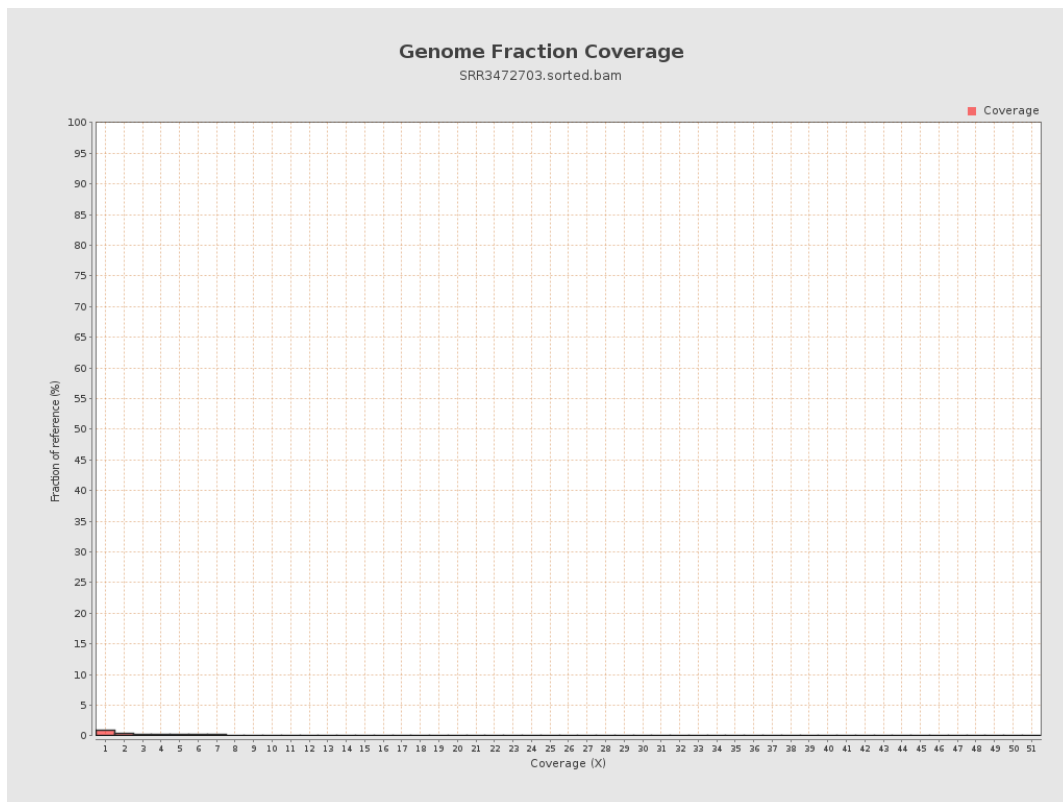
4. Results : Coverage Histogram



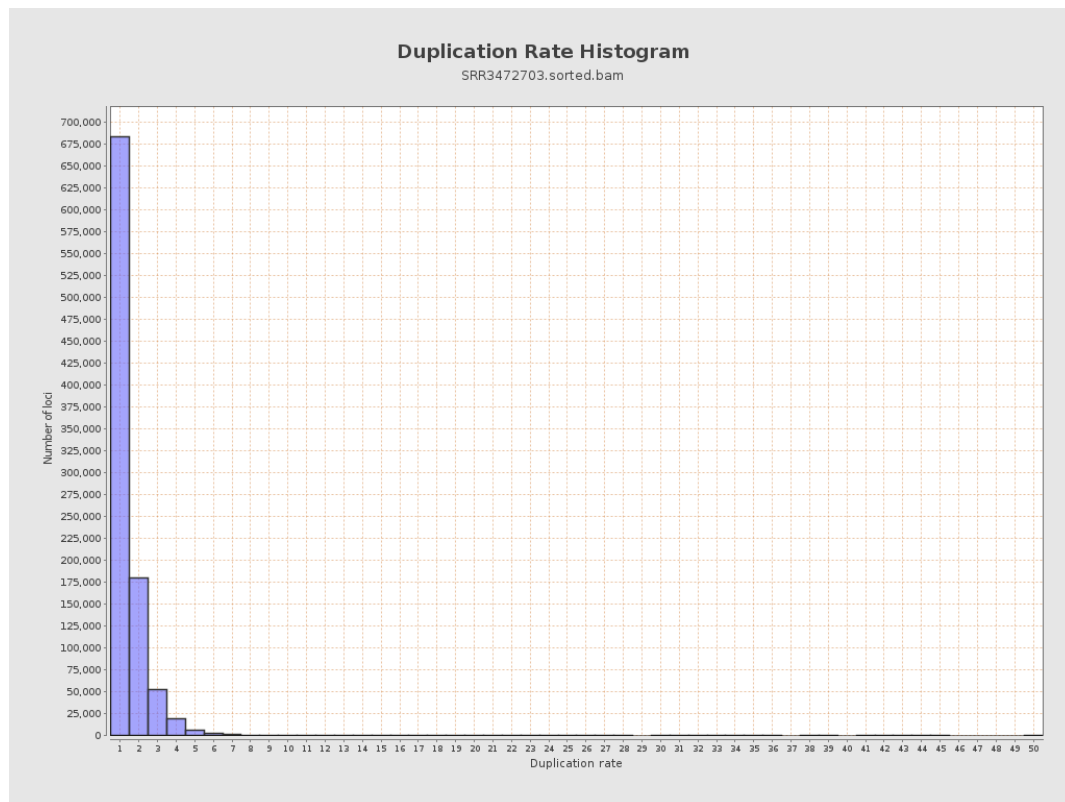
5. Results : Coverage Histogram (0-50X)



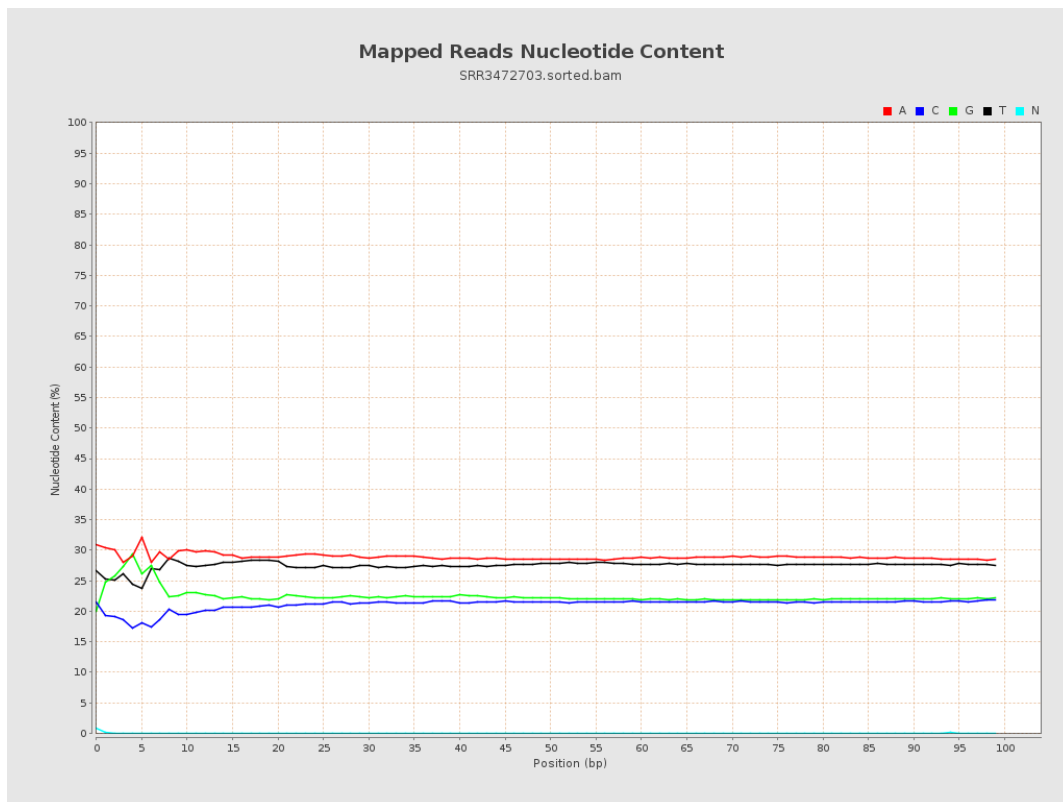
6. Results : Genome Fraction Coverage



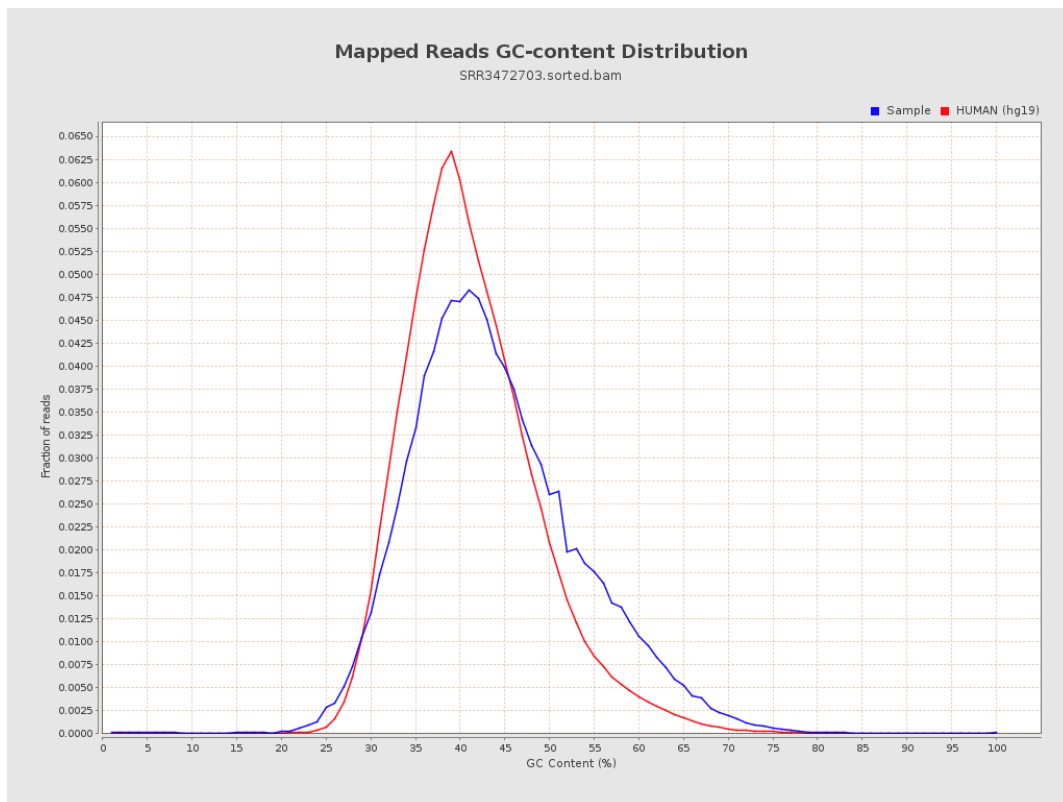
7. Results : Duplication Rate Histogram



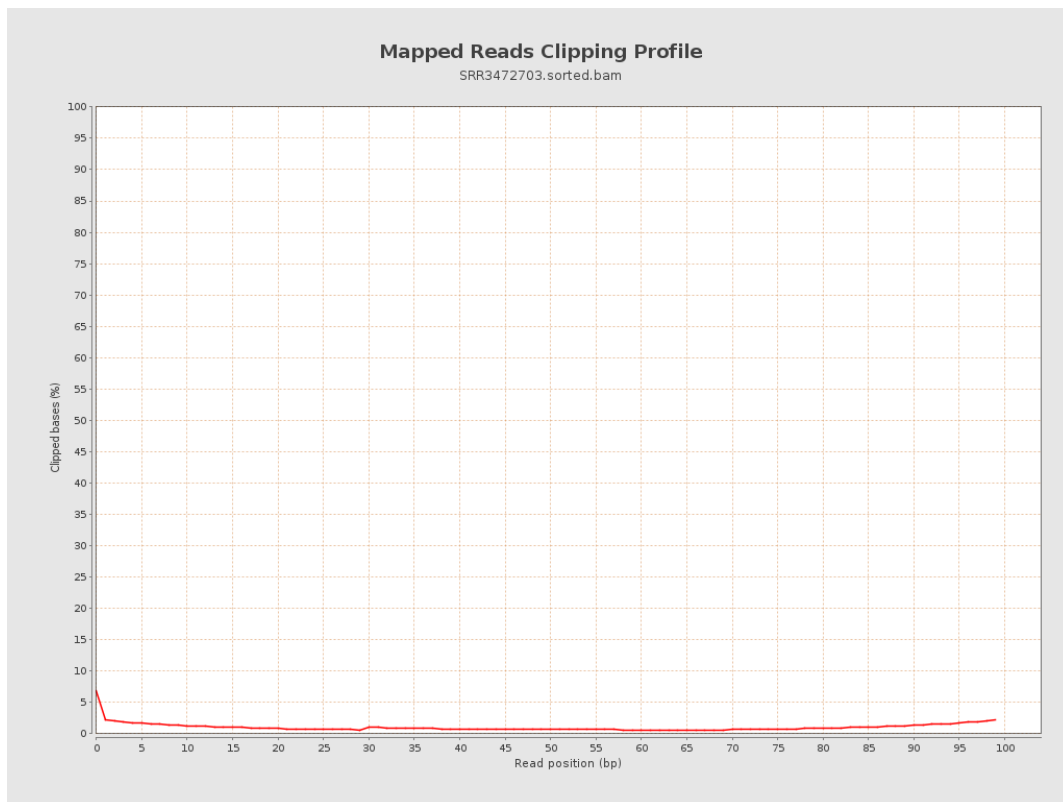
8. Results : Mapped Reads Nucleotide Content



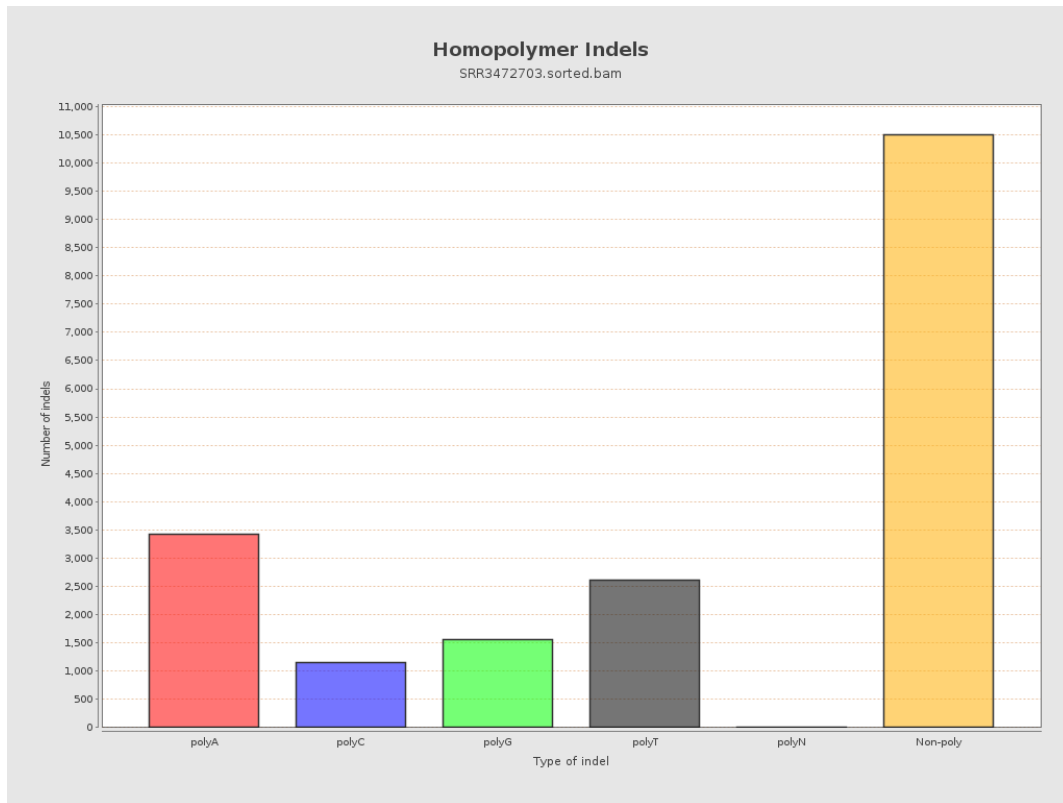
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



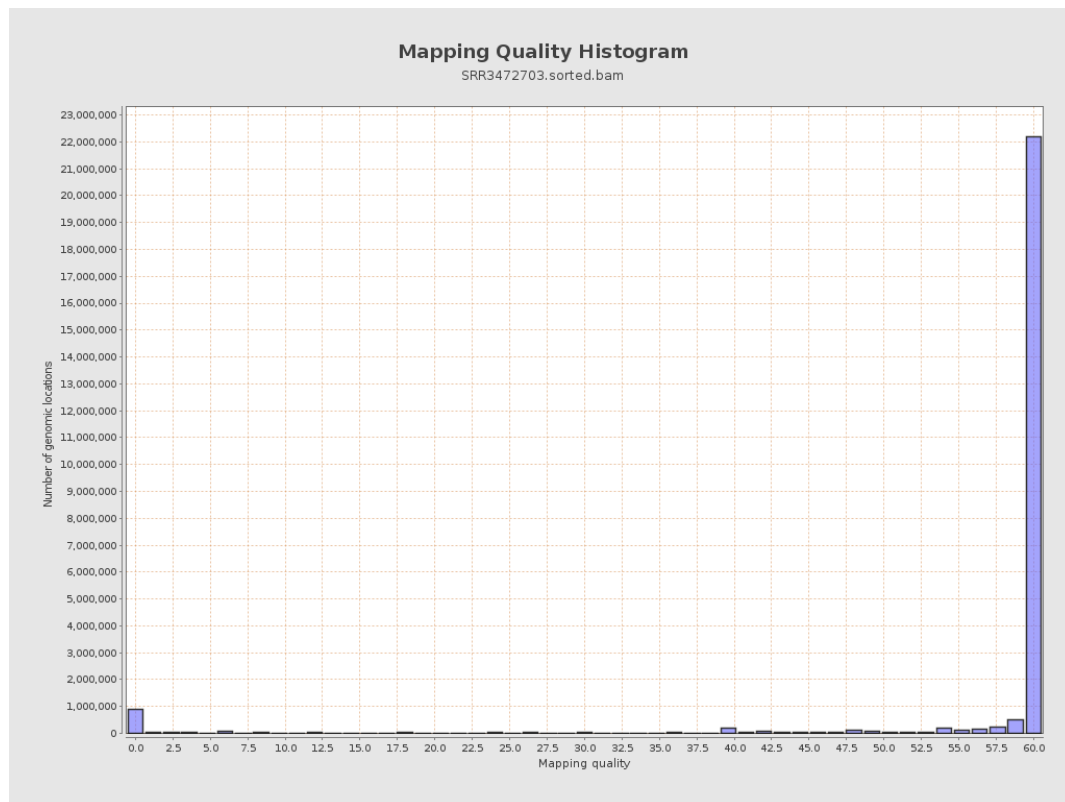
11. Results : Homopolymer Indels



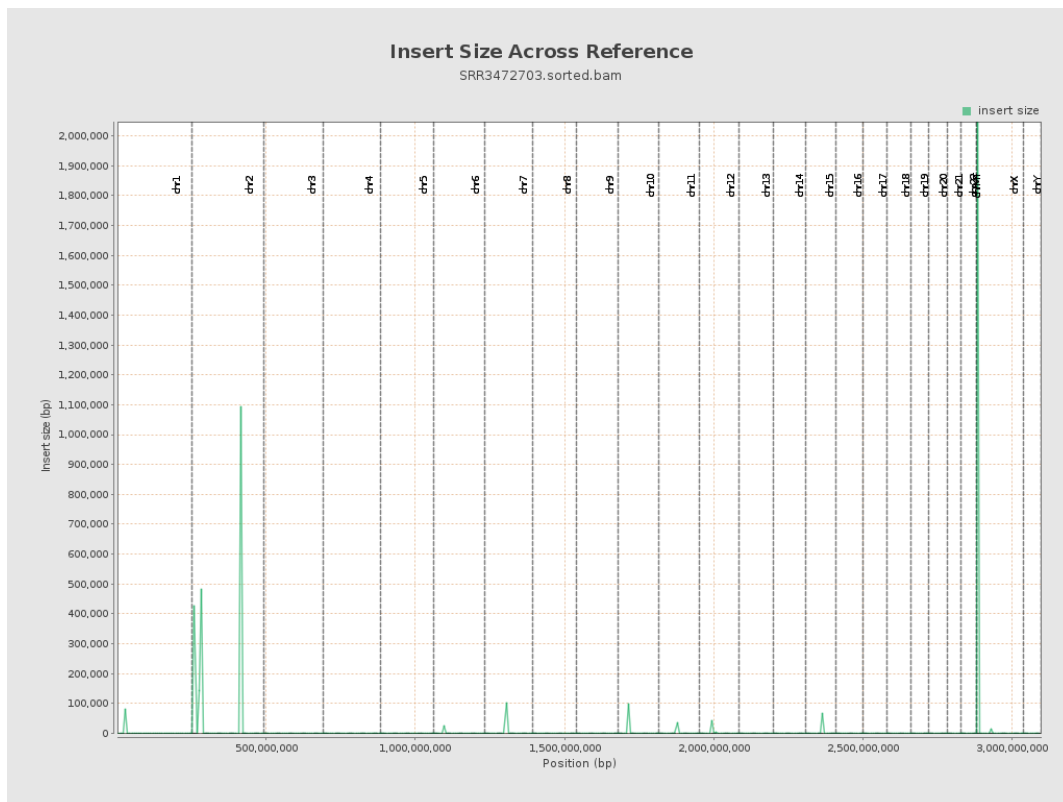
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

