Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/05 00:14:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1768994.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_SRR1768994 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1768994_1.fastq.gz SRR1768994_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Oct 05 00:14:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1768994.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	437,047,566
Mapped reads	404,470,374 / 92.55%
Unmapped reads	32,577,192 / 7.45%
Mapped paired reads	404,470,374 / 92.55%
Mapped reads, first in pair	203,903,649 / 46.65%
Mapped reads, second in pair	200,566,725 / 45.89%
Mapped reads, both in pair	397,115,080 / 90.86%
Mapped reads, singletons	7,355,294 / 1.68%
Secondary alignments	0
Supplementary alignments	1,215,829 / 0.28%
Read min/max/mean length	30 / 101 / 101.11
Duplicated reads (estimated)	56,260,898 / 12.87%
Duplication rate	8.38%
Clipped reads	24,862,358 / 5.69%

2.2. ACGT Content

Number/percentage of A's	11,711,645,832 / 29.13%
Number/percentage of C's	8,363,516,323 / 20.81%
Number/percentage of T's	11,733,908,566 / 29.19%
Number/percentage of G's	8,379,950,631 / 20.85%
Number/percentage of N's	9,970,742 / 0.02%

GC Percentage	41.65%

2.3. Coverage

Mean	12.9896
Standard Deviation	143.0543

2.4. Mapping Quality

Mean Mapping Quality	53.55

2.5. Insert size

Mean	48,292.05
Standard Deviation	2,100,962.71
P25/Median/P75	206 / 270 / 345

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	230,413,850
Insertions	4,455,249
Mapped reads with at least one insertion	1.07%
Deletions	5,330,762
Mapped reads with at least one deletion	1.28%
Homopolymer indels	43.35%

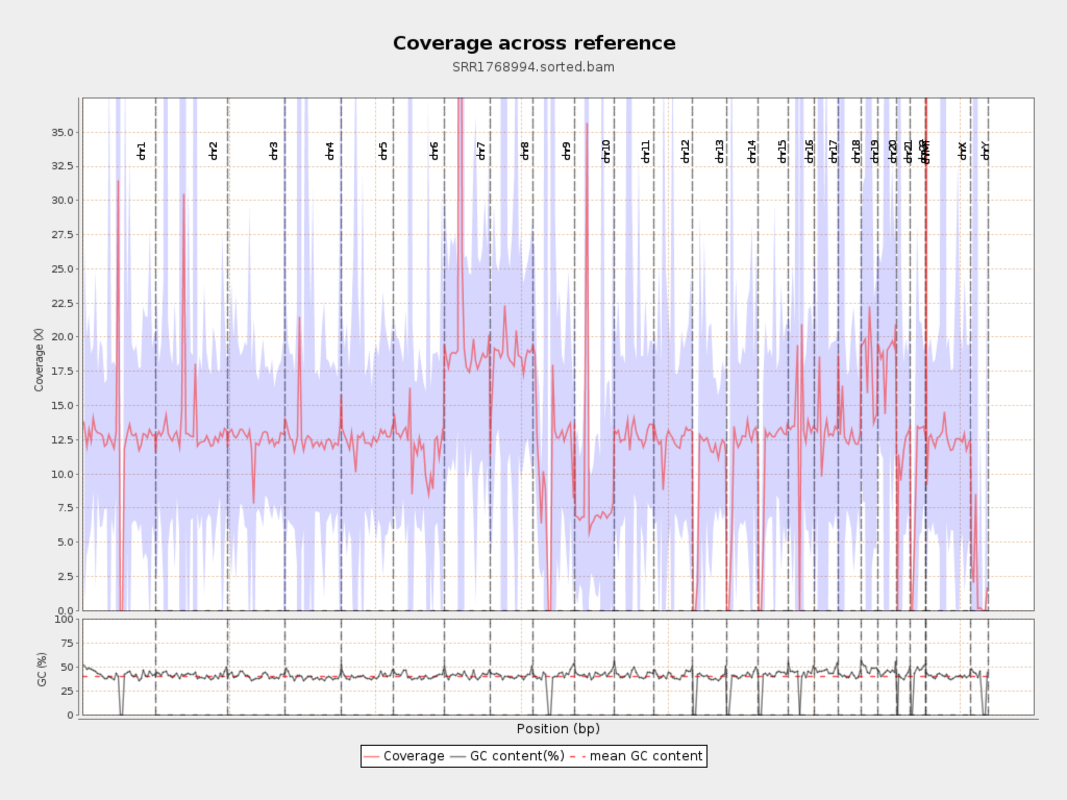
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

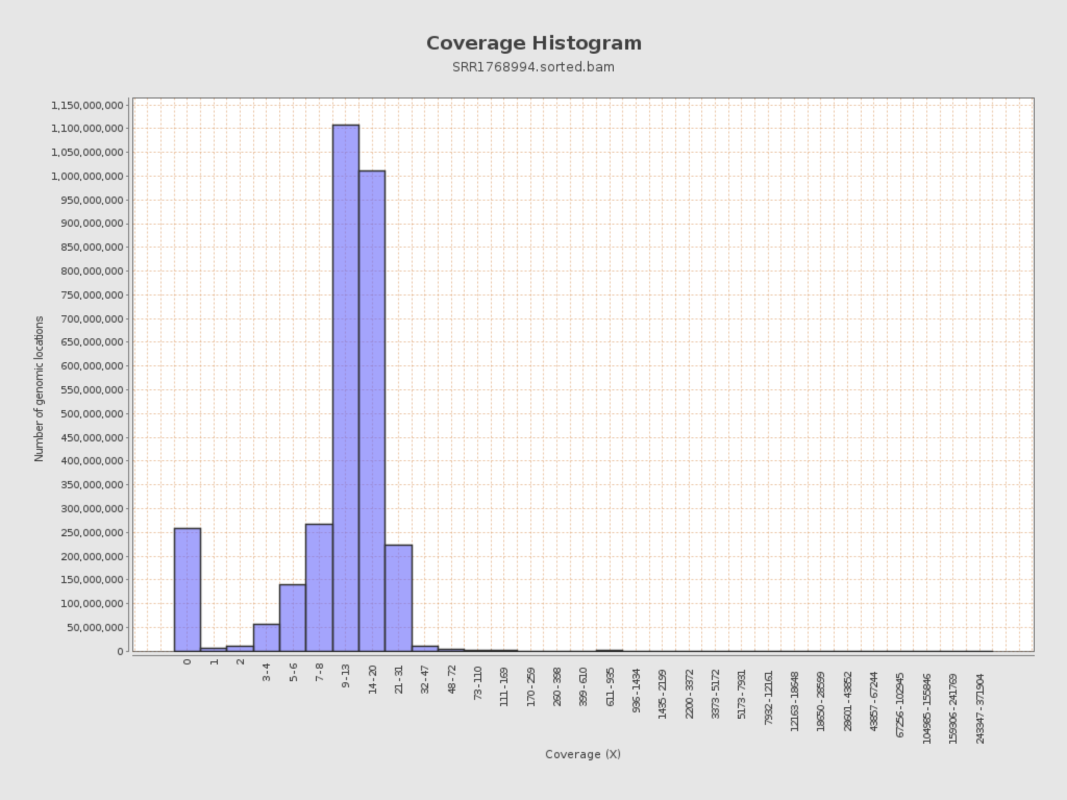
		bases	coverage	deviation
chr1	249250621	3128137788	12.5502	388.7807
chr2	243199373	3285213481	13.5083	111.4105
chr3	198022430	2478570880	12.5166	10.4557
chr4	191154276	2445626873	12.794	75.213
chr5	180915260	2272180544	12.5594	10.5834
chr6	171115067	2044241942	11.9466	46.8842
chr7	159138663	3705254373	23.2832	169.6926
chr8	146364022	2731146045	18.66	140.5603
chr9	141213431	1553438637	11.0006	138.8763
chr10	135534747	1148398865	8.4731	205.9588
chr11	135006516	1742472472	12.9066	48.9368
chr12	133851895	1672222575	12.4931	12.5433
chr13	115169878	1169495866	10.1545	8.5259
chr14	107349540	1151941389	10.7308	14.3351
chr15	102531392	1078473528	10.5185	9.0186
chr16	90354753	1204945640	13.3357	73.6195
chr17	81195210	1085677364	13.3712	70.6495
chr18	78077248	1032781152	13.2277	144.7395
chr19	59128983	1062373091	17.967	163.927
chr20	63025520	1175973450	18.6587	22.4966
chr21	48129895	517865689	10.7598	37.0113
chr22	51304566	474905666	9.2566	9.7713
chrMT	16571	8626342	520.5686	58.5185
chrX	155270560	1927190781	12.4118	32.025

chrY	59373566	114619639	1.9305	82.5227

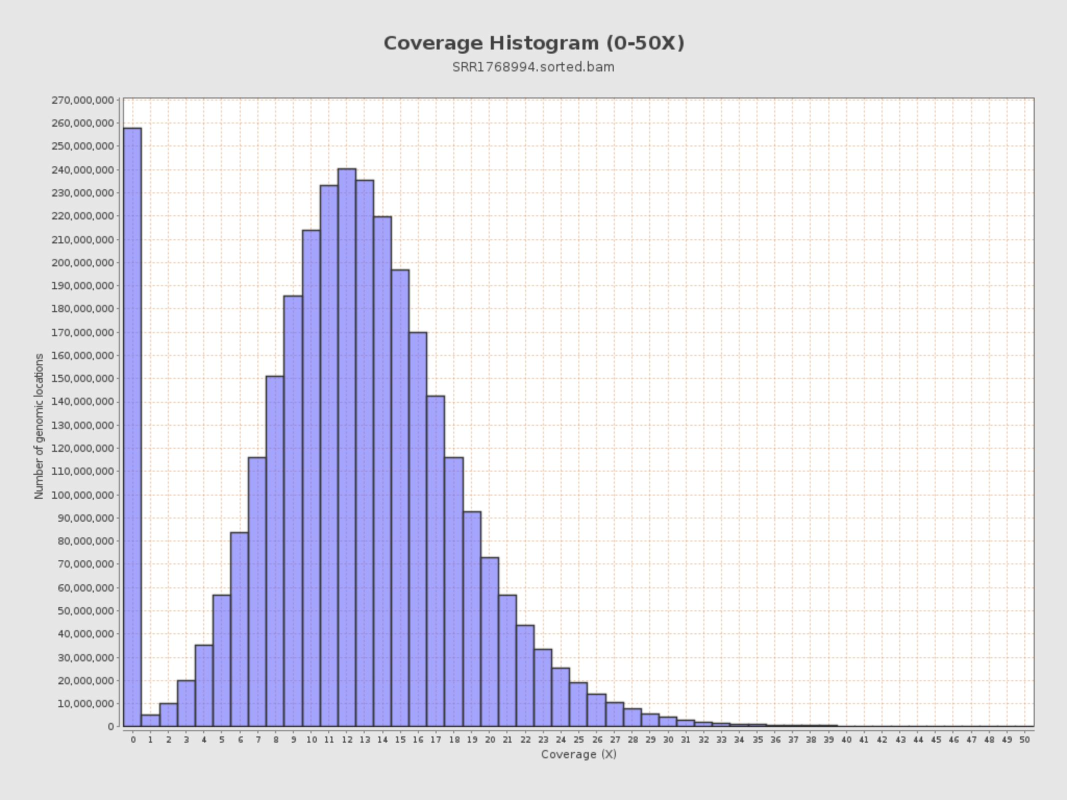
3. Results : Coverage across reference



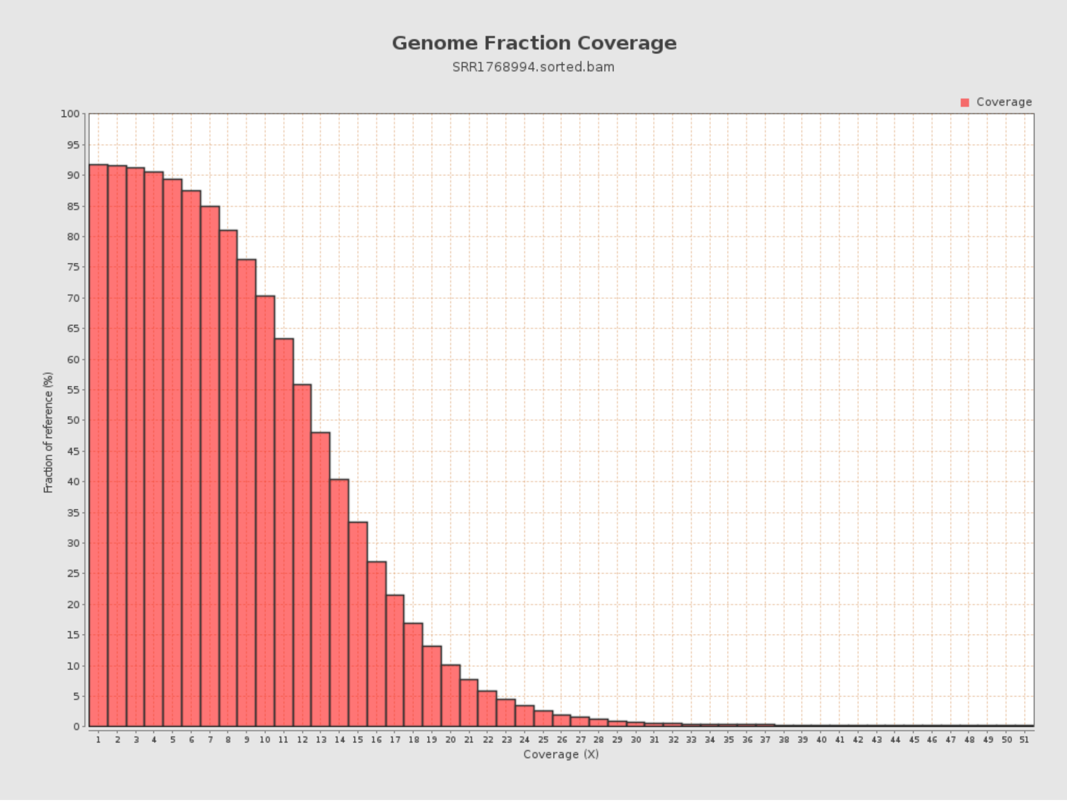
4. Results : Coverage Histogram



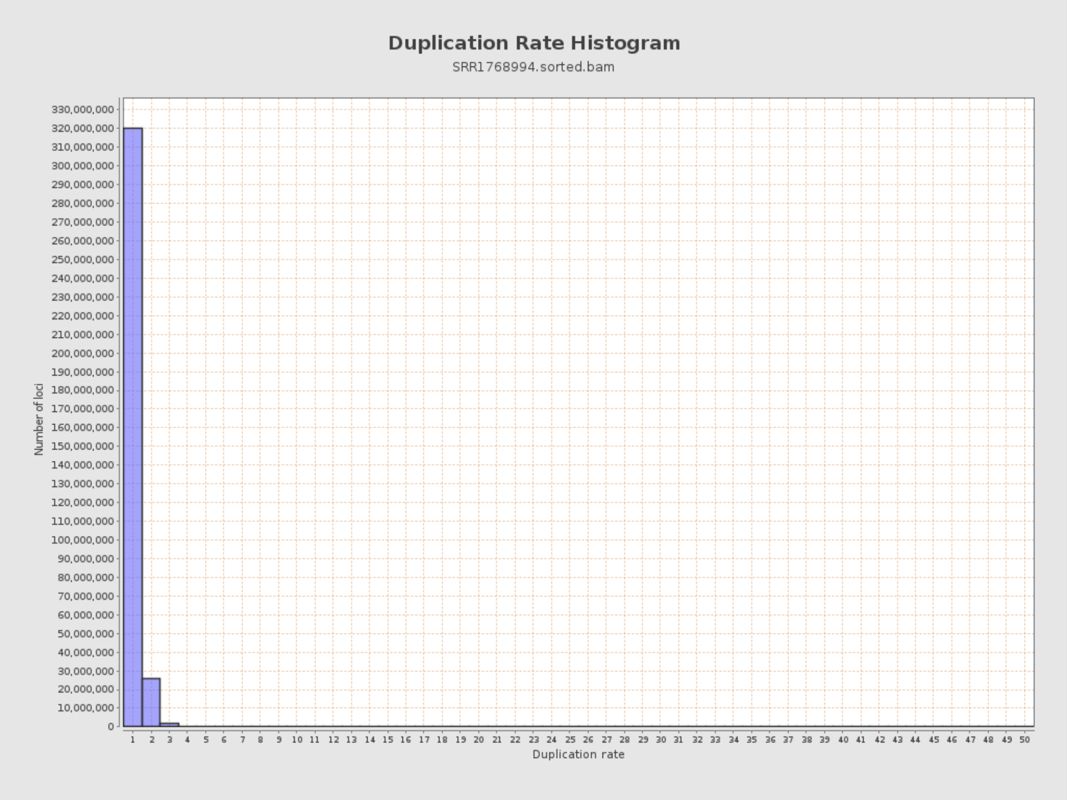
5. Results : Coverage Histogram (0-50X)



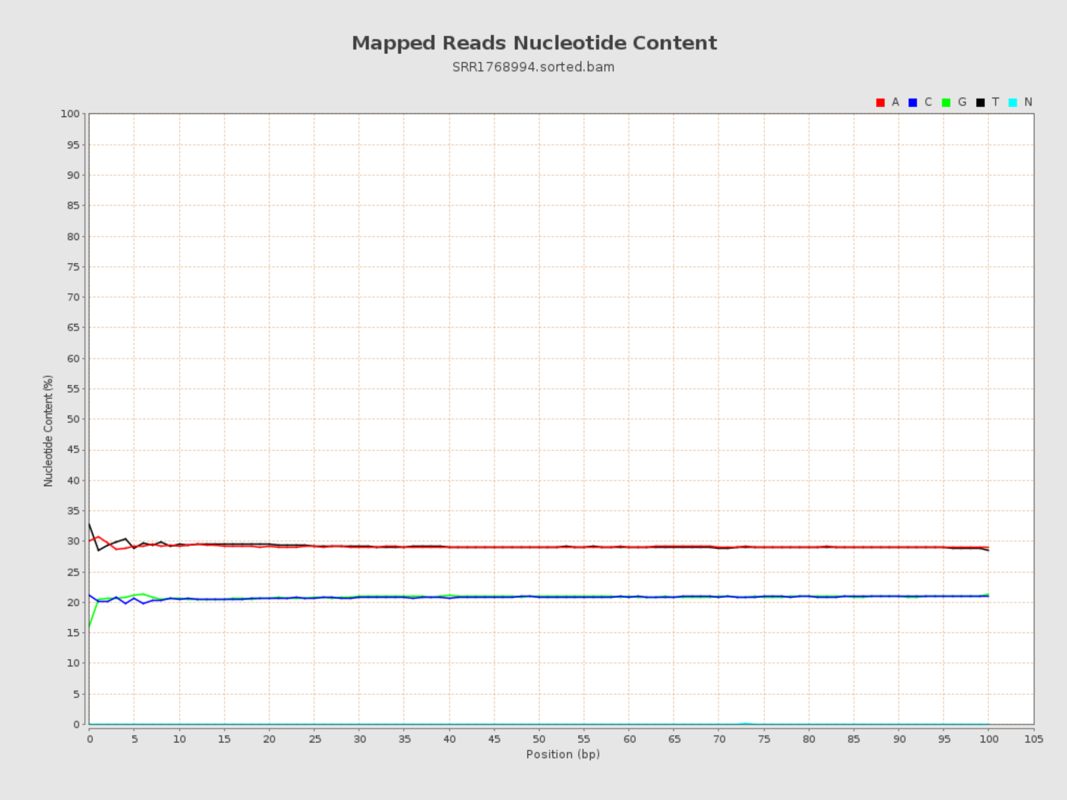
6. Results : Genome Fraction Coverage



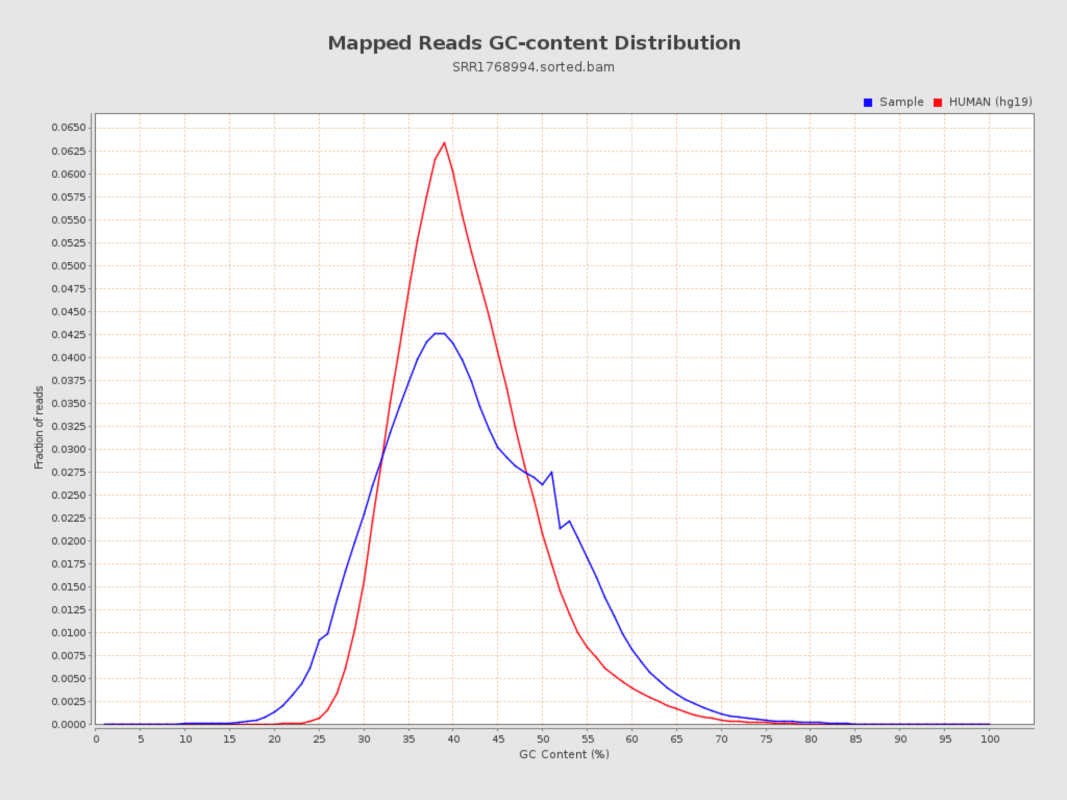
7. Results : Duplication Rate Histogram



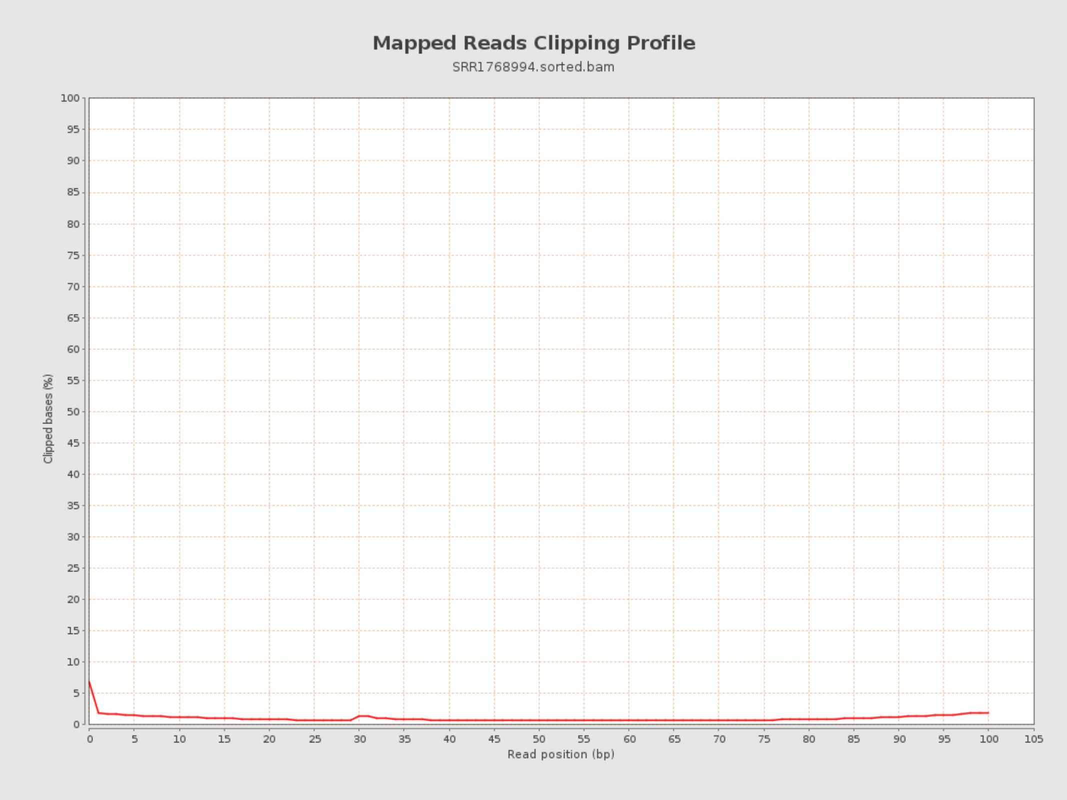
8. Results : Mapped Reads Nucleotide Content



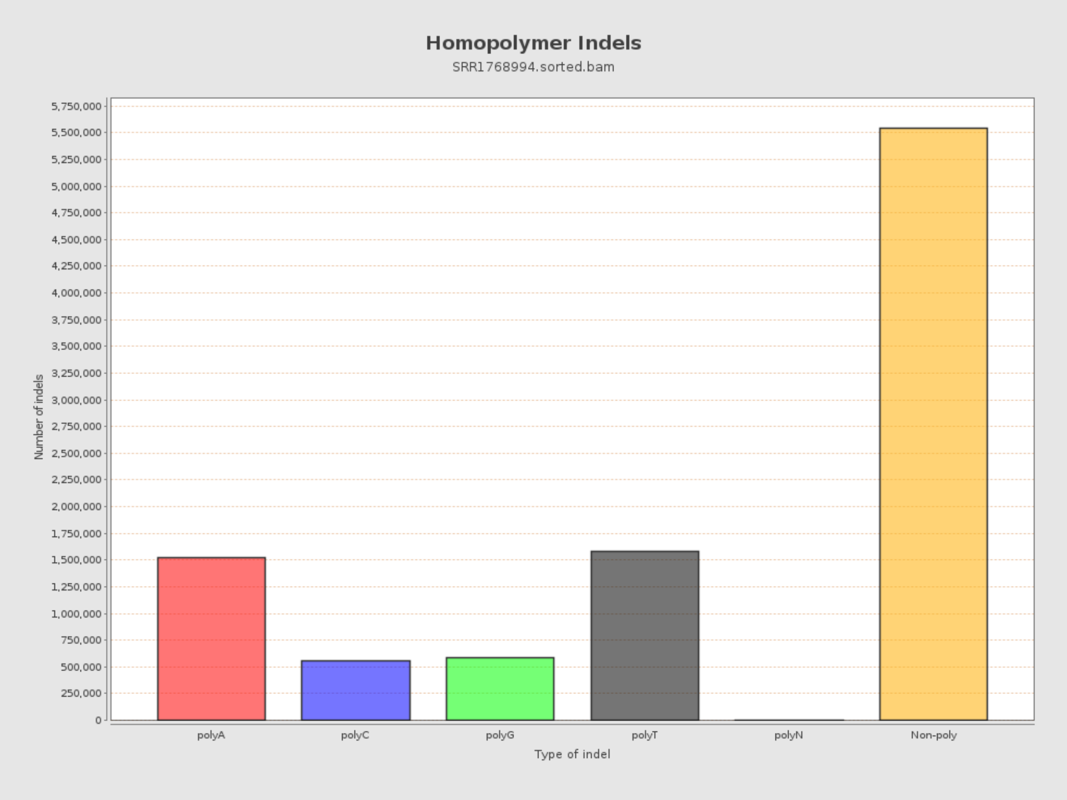
9. Results : Mapped Reads GC-content Distribution



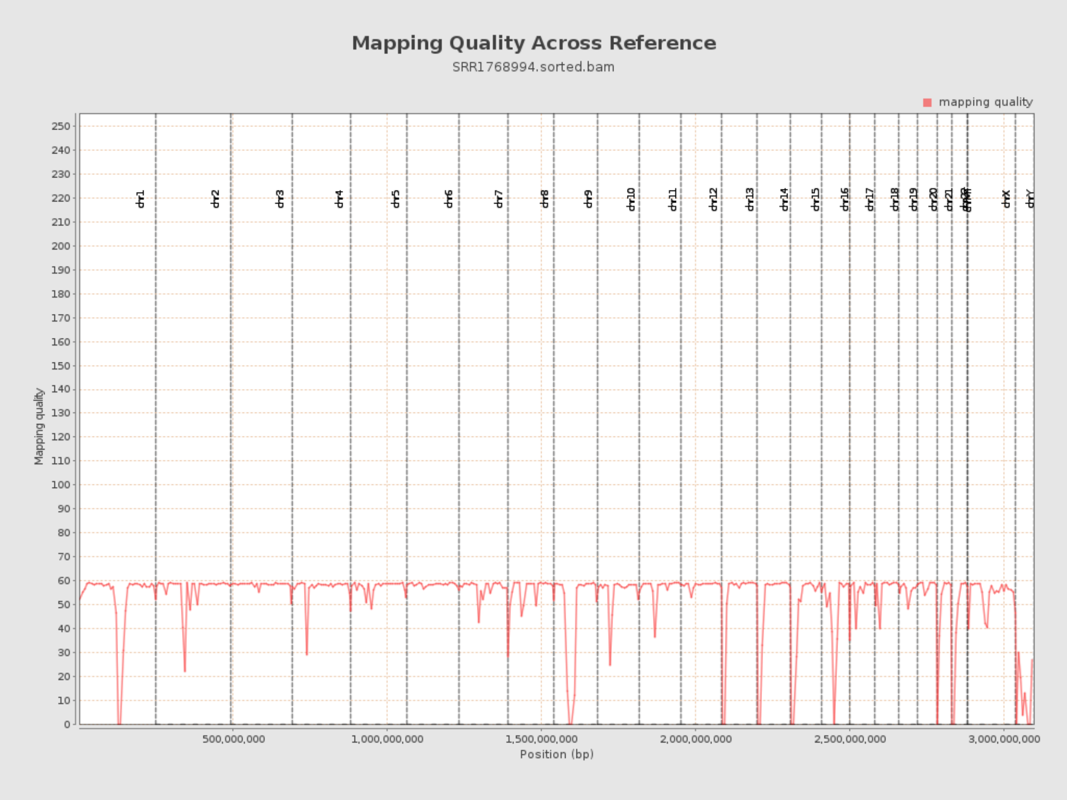
10. Results : Mapped Reads Clipping Profile



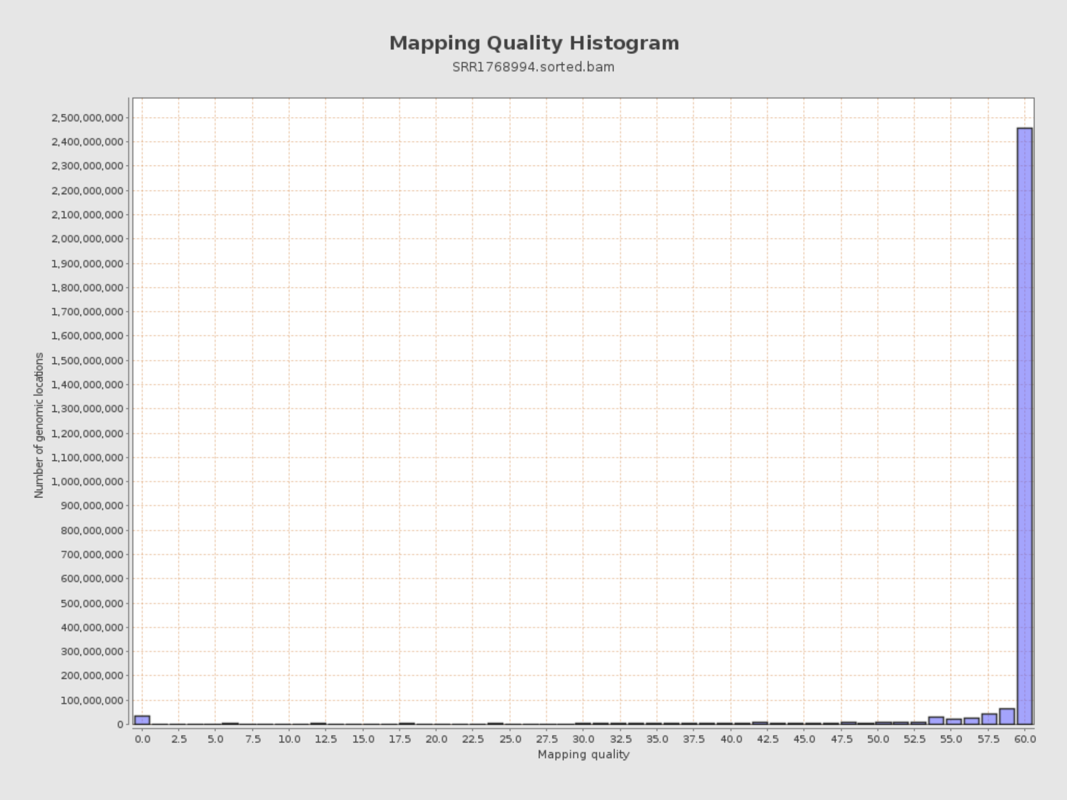
11. Results : Homopolymer Indels



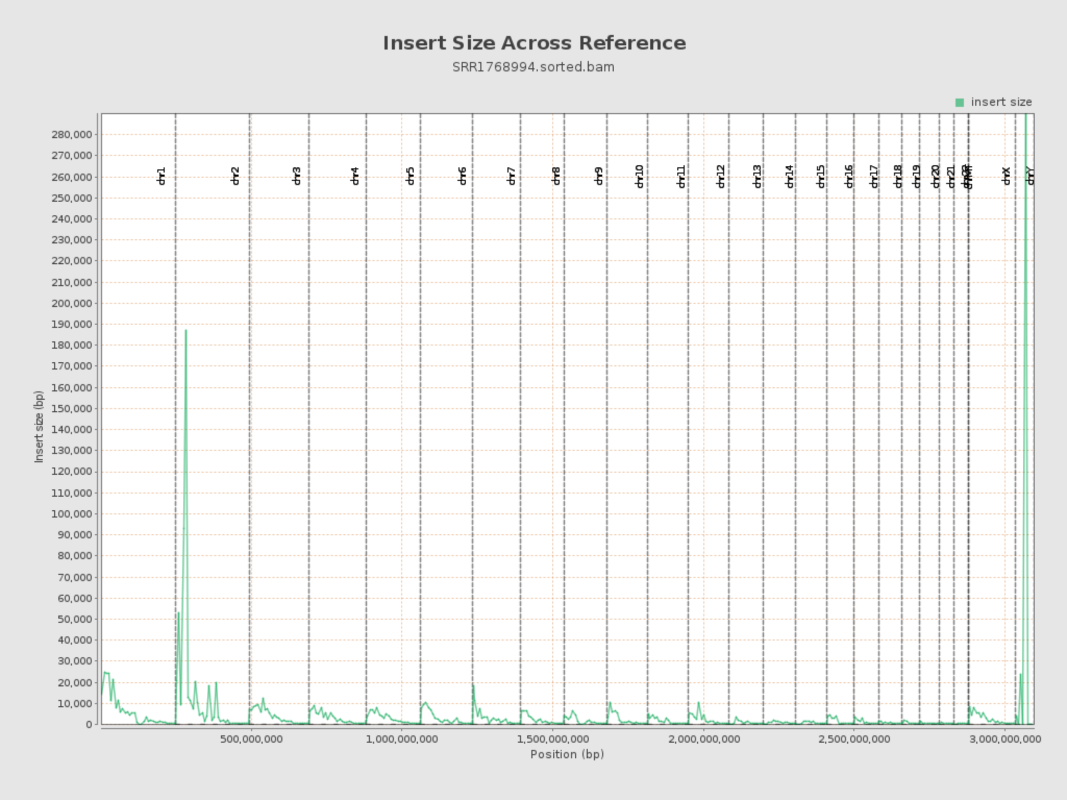
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram