Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 00:27:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472736.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_SRR3472736 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472736_1.fastq.gz SRR3472736_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 00:27:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472736.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,438,598
Mapped reads	12,317,897 / 99.03%
Unmapped reads	120,701 / 0.97%
Mapped paired reads	12,317,897 / 99.03%
Mapped reads, first in pair	6,181,700 / 49.7%
Mapped reads, second in pair	6,136,197 / 49.33%
Mapped reads, both in pair	12,247,758 / 98.47%
Mapped reads, singletons	70,139 / 0.56%
Secondary alignments	0
Supplementary alignments	39,898 / 0.32%
Read min/max/mean length	30 / 100 / 100.13
Duplicated reads (estimated)	7,397,171 / 59.47%
Duplication rate	45.66%
Clipped reads	1,027,770 / 8.26%

2.2. ACGT Content

Number/percentage of A's	323,629,673 / 26.7%
Number/percentage of C's	284,102,237 / 23.43%
Number/percentage of T's	322,092,674 / 26.57%
Number/percentage of G's	282,237,796 / 23.28%
Number/percentage of N's	238,150 / 0.02%

GC Percentage	46.72%

2.3. Coverage

Mean	0.3917
Standard Deviation	14.4613

2.4. Mapping Quality

Mean Mapping Quality	55.13

2.5. Insert size

Mean	20,906.93
Standard Deviation	1,454,598.88
P25/Median/P75	166 / 232 / 312

2.6. Mismatches and indels

General error rate	0.61%
Mismatches	7,290,663
Insertions	69,167
Mapped reads with at least one insertion	0.56%
Deletions	65,559
Mapped reads with at least one deletion	0.52%
Homopolymer indels	45.14%

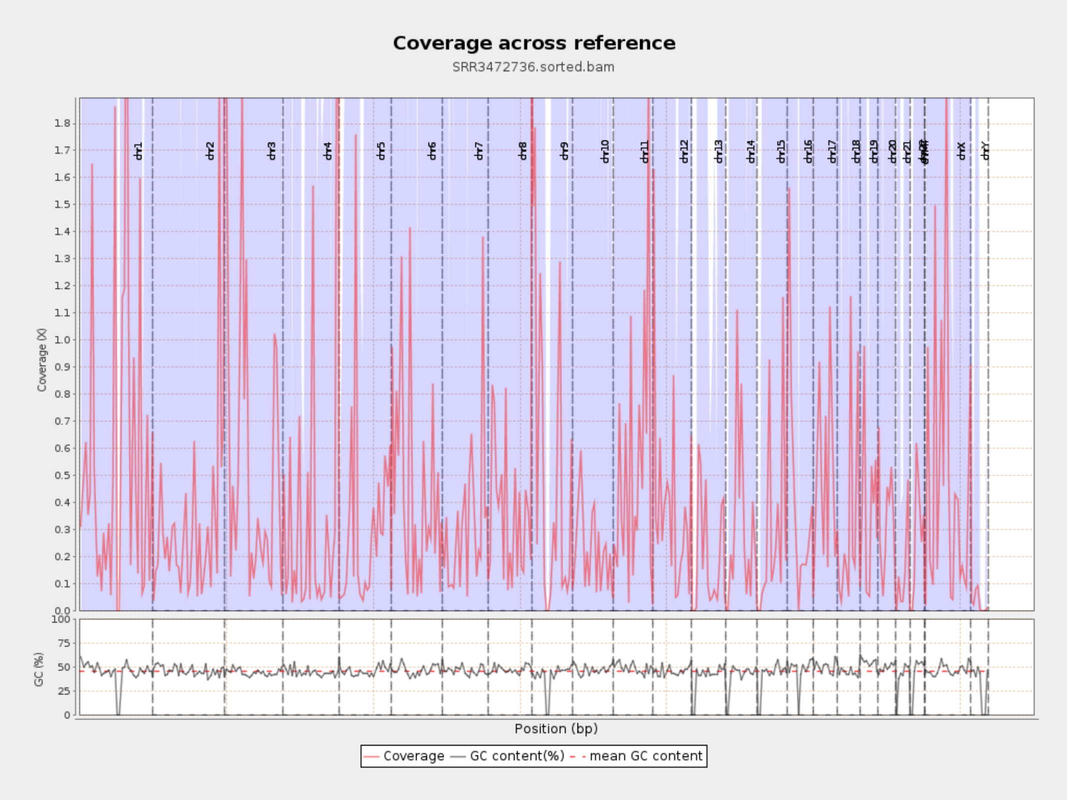
2.7. Chromosome stats

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

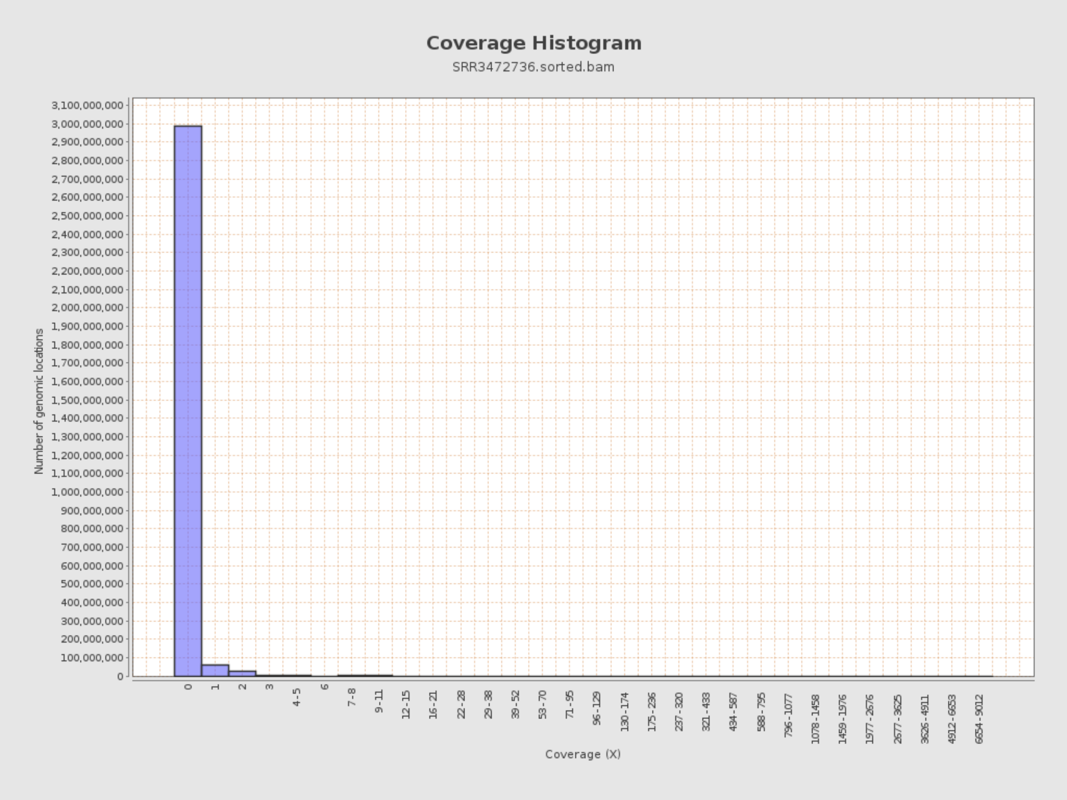
		bases	coverage	deviation
chr1	249250621	147116158	0.5902	20.1424
chr2	243199373	74731371	0.3073	16.4682
chr3	198022430	116201550	0.5868	13.9923
chr4	191154276	72256530	0.378	17.1605
chr5	180915260	56842440	0.3142	12.1811
chr6	171115067	74779786	0.437	13.8312
chr7	159138663	51901932	0.3261	9.7136
chr8	146364022	52516093	0.3588	10.4884
chr9	141213431	76235764	0.5399	16.7771
chr10	135534747	31817383	0.2348	8.6455
chr11	135006516	74061499	0.5486	25.3177
chr12	133851895	52537312	0.3925	12.0516
chr13	115169878	23972285	0.2081	10.4859
chr14	107349540	32533560	0.3031	10.1143
chr15	102531392	28782151	0.2807	10.0392
chr16	90354753	38026931	0.4209	12.8717
chr17	81195210	39565897	0.4873	11.0321
chr18	78077248	25529558	0.327	14.7652
chr19	59128983	23880539	0.4039	10.2905
chr20	63025520	21400121	0.3395	9.6729
chr21	48129895	6634788	0.1379	7.8097
chr22	51304566	14108992	0.275	9.5651
chrMT	16571	1264	0.0763	0.3225
chrX	155270560	75304450	0.485	16.6259

chrY	59373566	1722468	0.029	1.2849

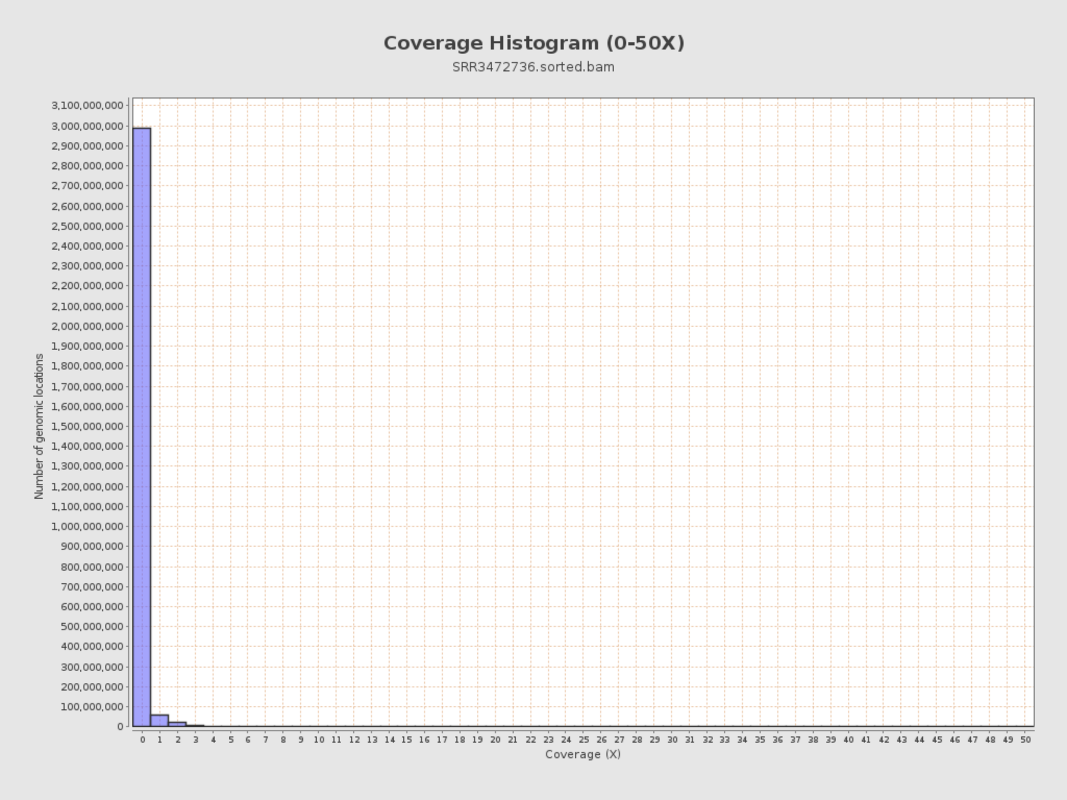
3. Results : Coverage across reference



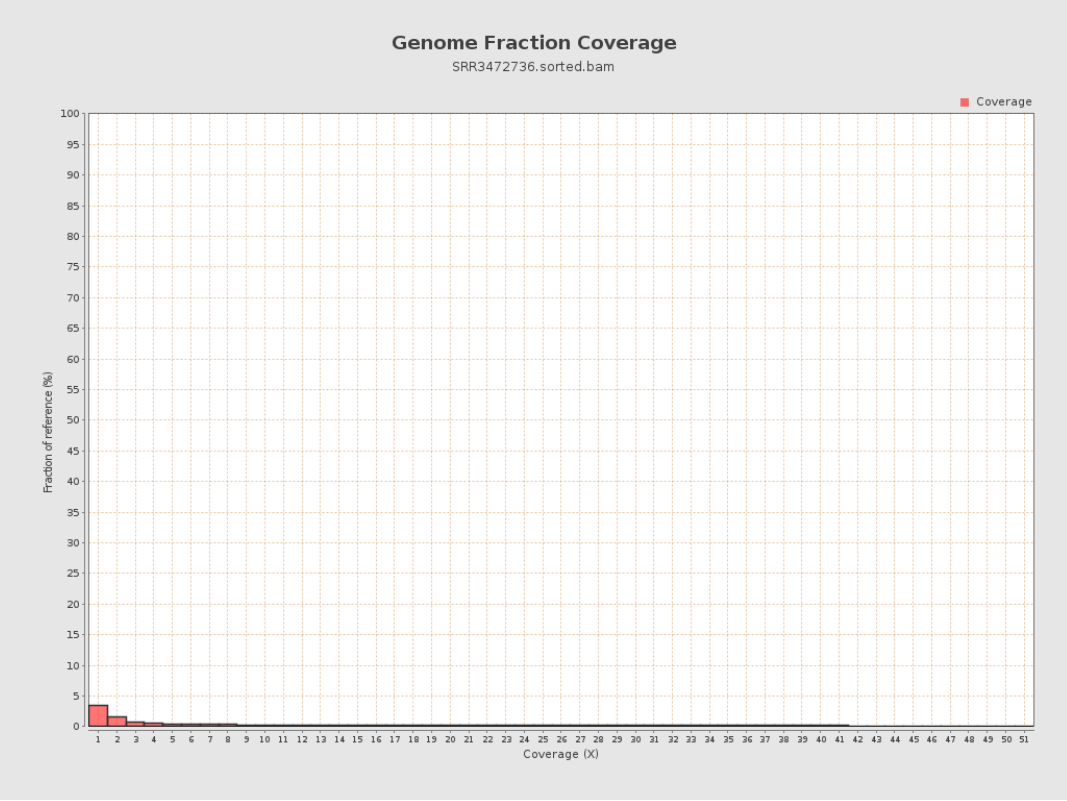
4. Results : Coverage Histogram



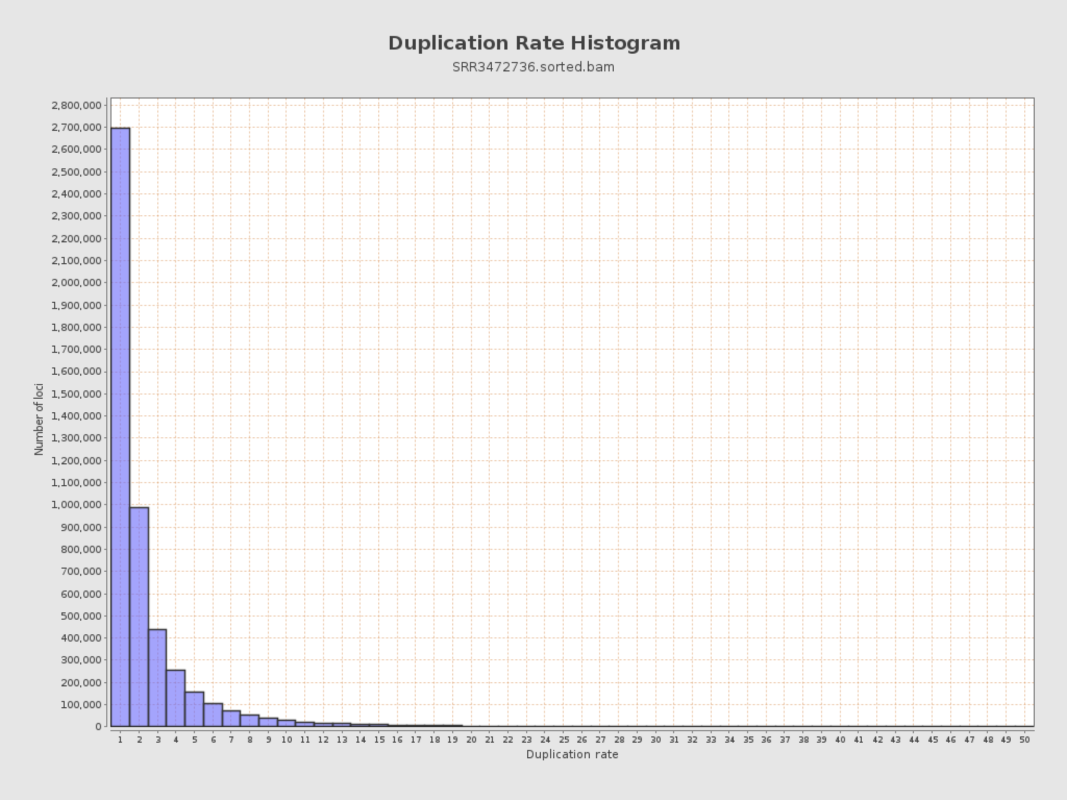
5. Results : Coverage Histogram (0-50X)



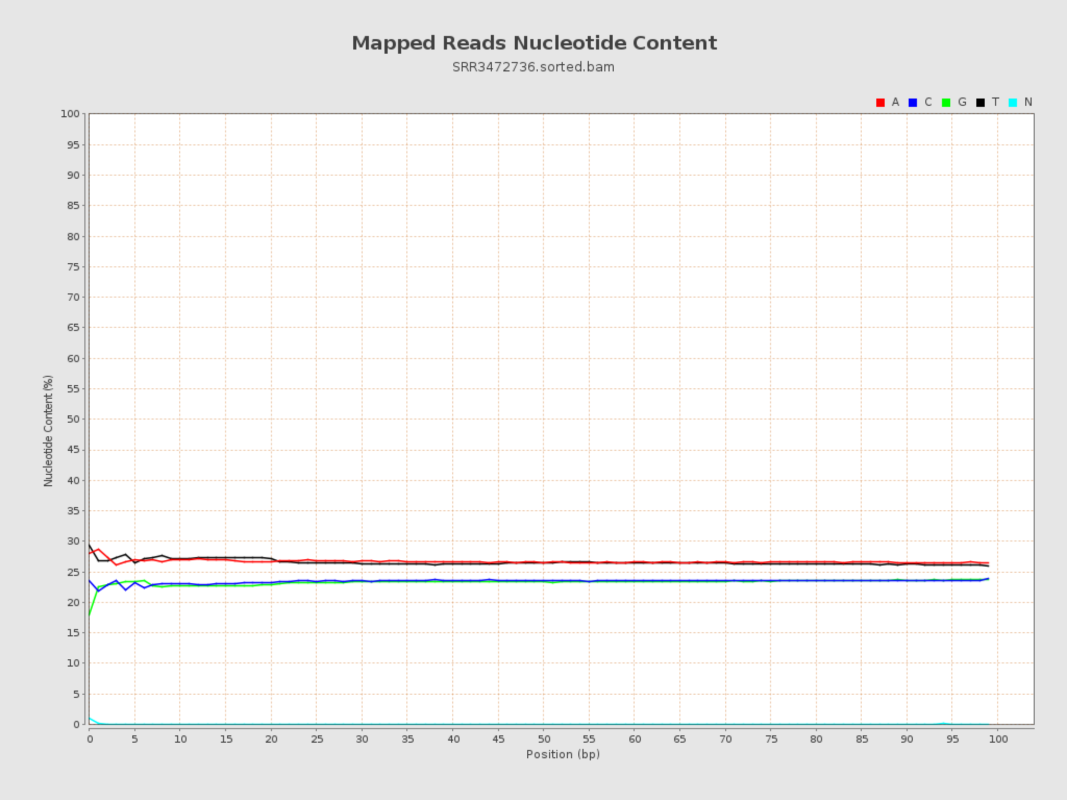
6. Results : Genome Fraction Coverage



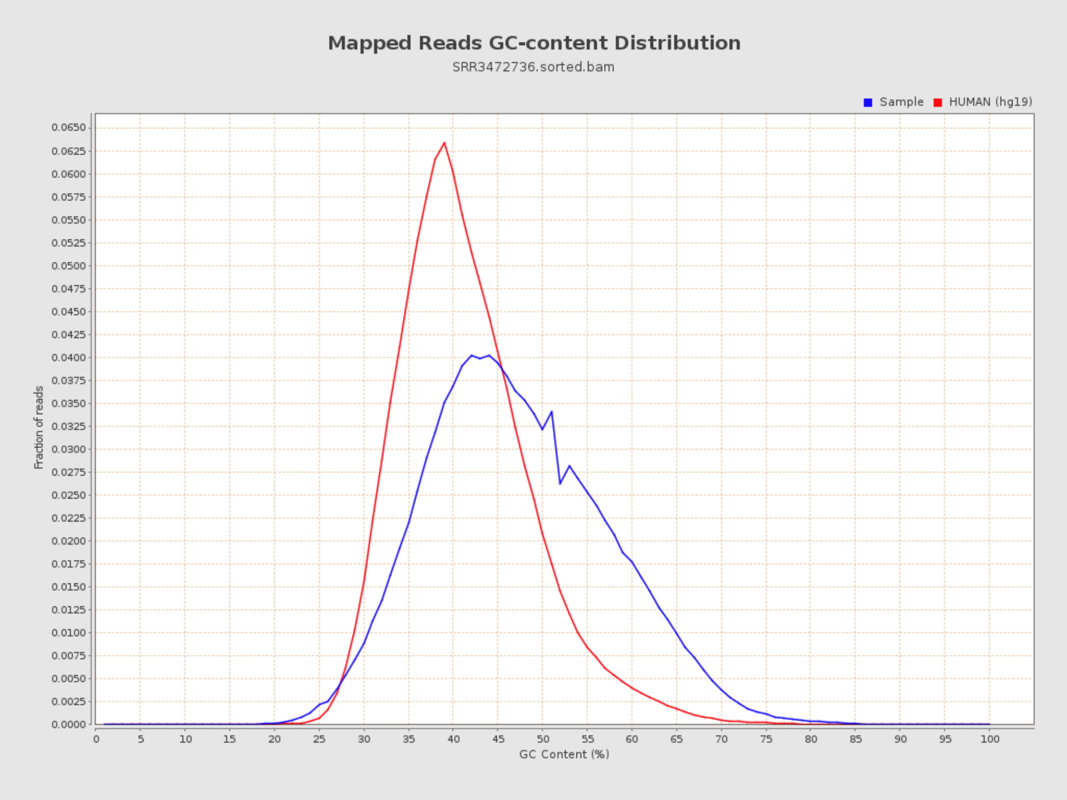
7. Results : Duplication Rate Histogram



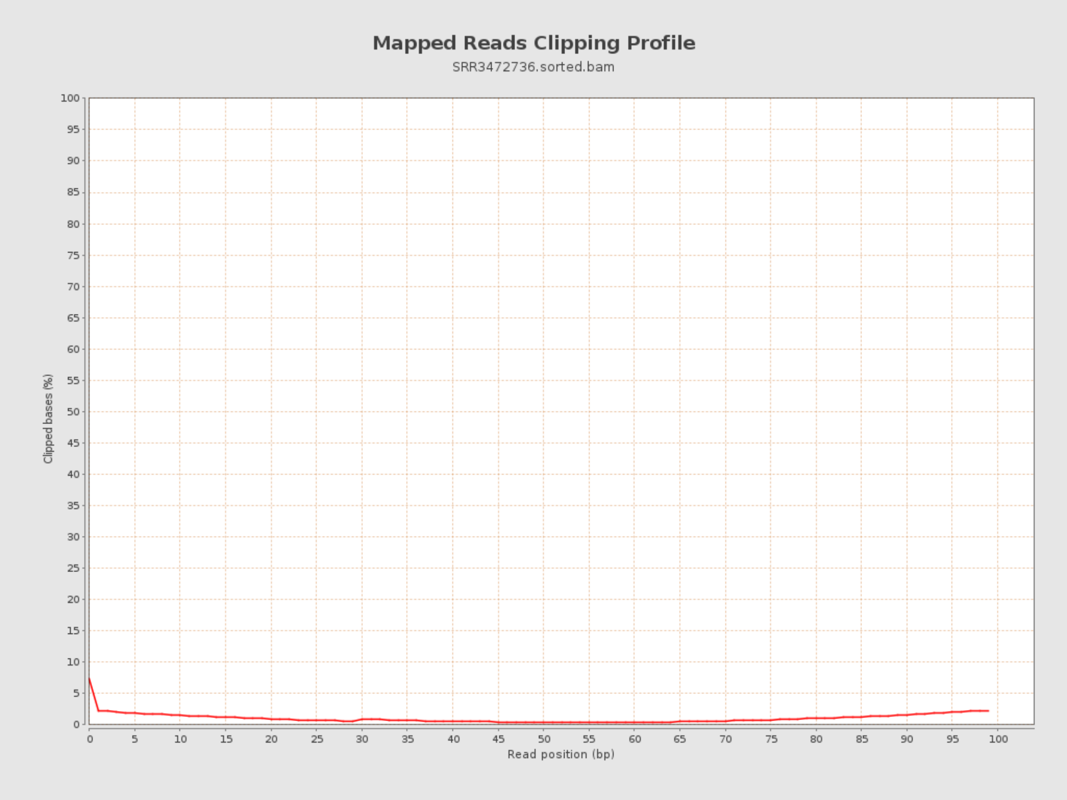
8. Results : Mapped Reads Nucleotide Content



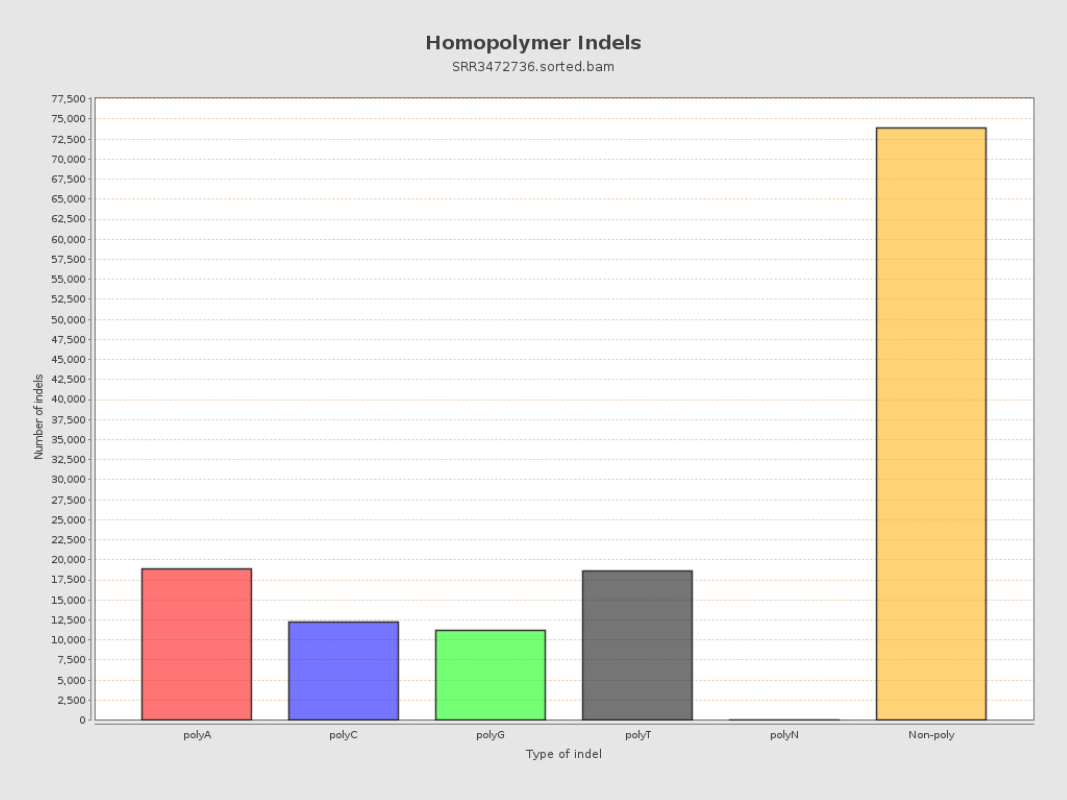
9. Results : Mapped Reads GC-content Distribution



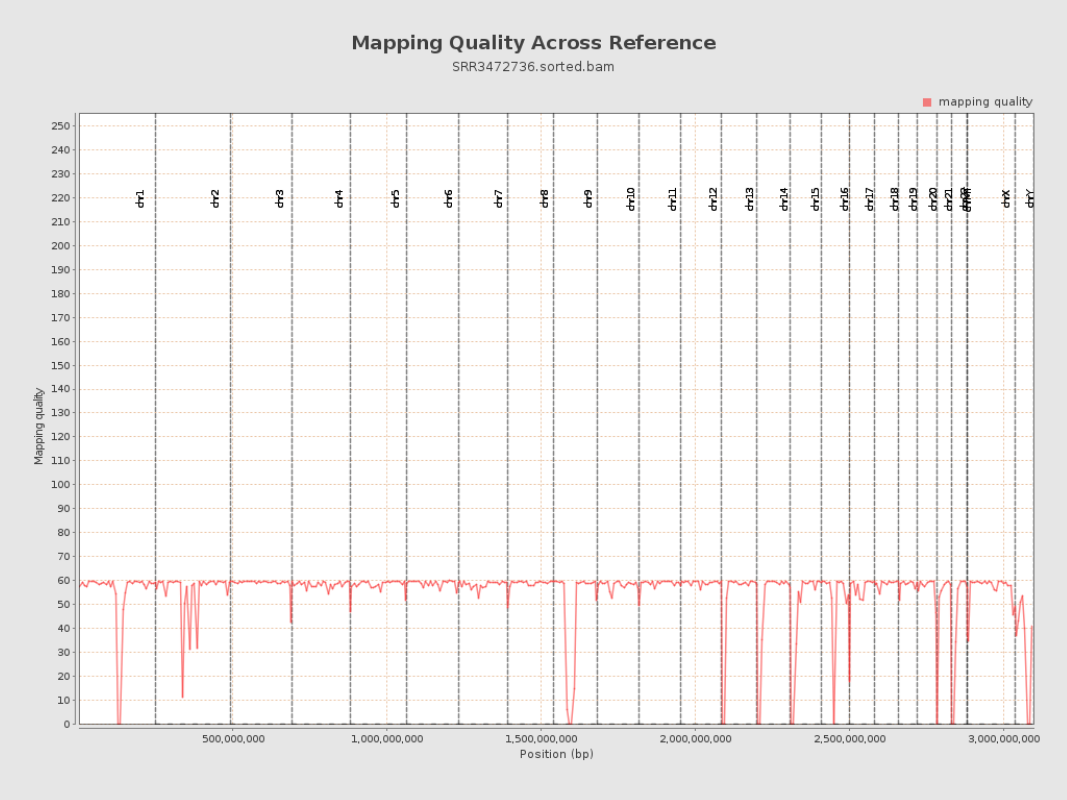
10. Results : Mapped Reads Clipping Profile



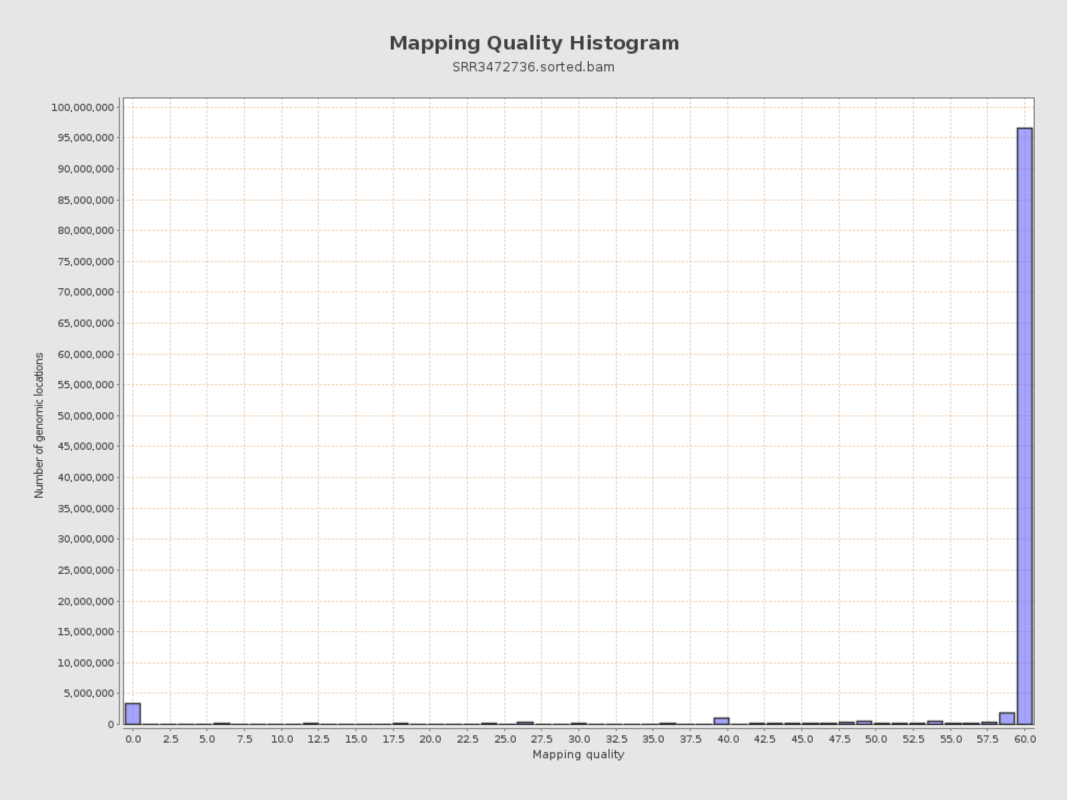
11. Results : Homopolymer Indels



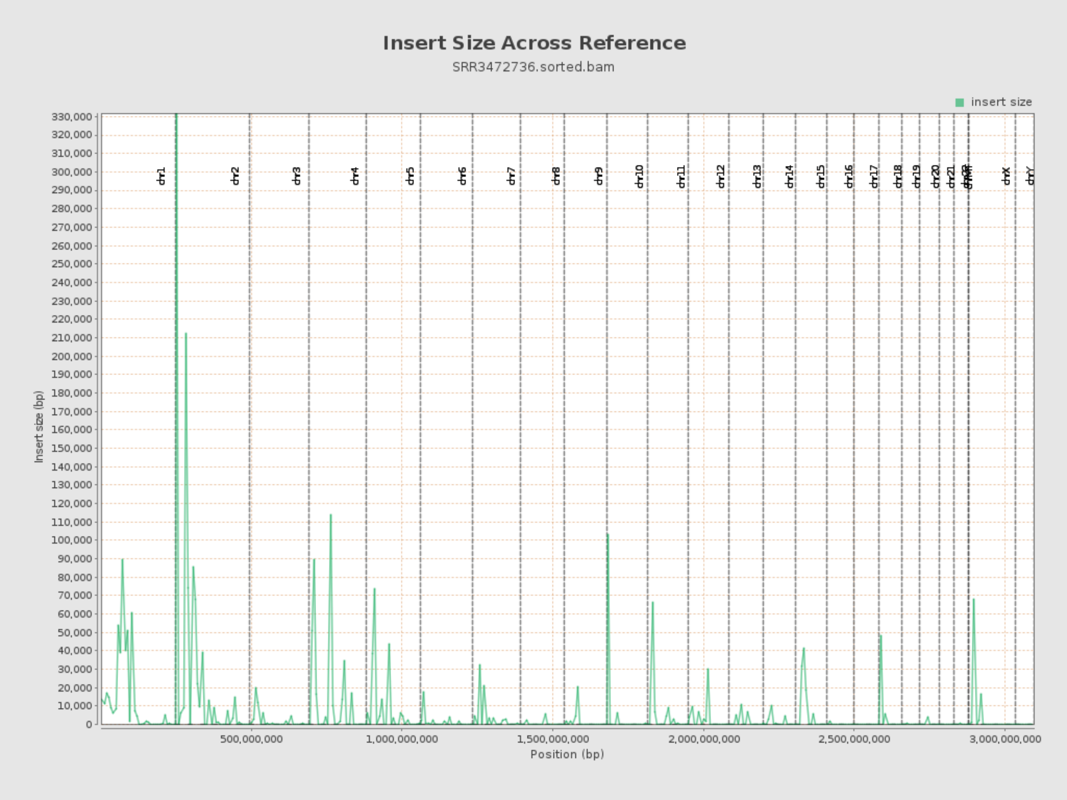
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram