Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 02:45:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472742.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_SRR3472742 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472742_1.fastq.gz SRR3472742_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 02:44:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472742.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,295,066
Mapped reads	14,139,648 / 98.91%
Unmapped reads	155,418 / 1.09%
Mapped paired reads	14,139,648 / 98.91%
Mapped reads, first in pair	7,099,519 / 49.66%
Mapped reads, second in pair	7,040,129 / 49.25%
Mapped reads, both in pair	14,046,812 / 98.26%
Mapped reads, singletons	92,836 / 0.65%
Secondary alignments	0
Supplementary alignments	70,074 / 0.49%
Read min/max/mean length	30 / 100 / 100.2
Duplicated reads (estimated)	8,702,086 / 60.87%
Duplication rate	45.39%
Clipped reads	1,100,881 / 7.7%

2.2. ACGT Content

Number/percentage of A's	385,384,698 / 27.64%
Number/percentage of C's	313,971,083 / 22.52%
Number/percentage of T's	383,327,109 / 27.49%
Number/percentage of G's	311,482,926 / 22.34%
Number/percentage of N's	268,610 / 0.02%

GC Percentage	44.85%

2.3. Coverage

Mean	0.4505
Standard Deviation	16.2797

2.4. Mapping Quality

Mean Mapping Quality	54.93

2.5. Insert size

Mean	29,518.15
Standard Deviation	1,672,156.46
P25/Median/P75	178 / 249 / 335

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	8,790,051
Insertions	92,634
Mapped reads with at least one insertion	0.65%
Deletions	80,344
Mapped reads with at least one deletion	0.56%
Homopolymer indels	46.05%

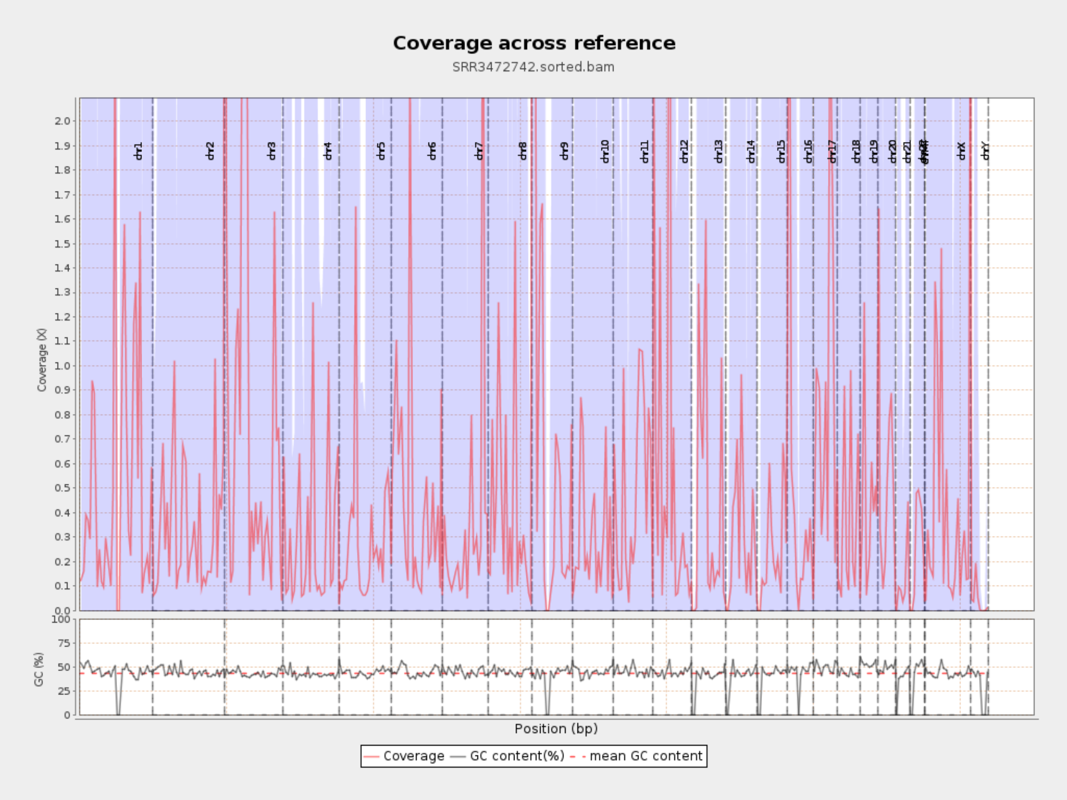
2.7. Chromosome stats

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

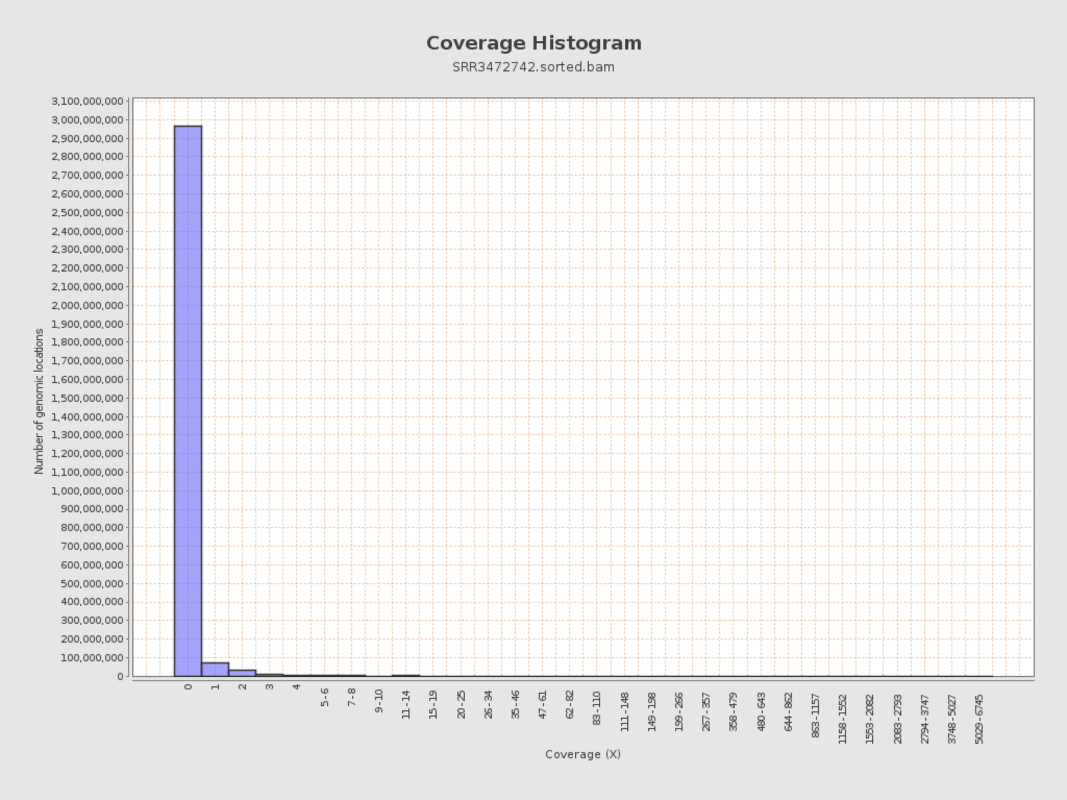
		bases	coverage	deviation
chr1	249250621	133036090	0.5337	17.8122
chr2	243199373	82435023	0.339	11.2683
chr3	198022430	168082324	0.8488	20.9754
chr4	191154276	57058001	0.2985	11.416
chr5	180915260	53319524	0.2947	8.7583
chr6	171115067	80081794	0.468	14.2641
chr7	159138663	61330543	0.3854	16.0227
chr8	146364022	58886929	0.4023	15.3243
chr9	141213431	103595399	0.7336	23.2294
chr10	135534747	42681681	0.3149	14.1699
chr11	135006516	66723144	0.4942	16.821
chr12	133851895	89023091	0.6651	27.9786
chr13	115169878	49192936	0.4271	21.2541
chr14	107349540	31745187	0.2957	10.0932
chr15	102531392	24861172	0.2425	8.062
chr16	90354753	48107927	0.5324	14.6495
chr17	81195210	67913957	0.8364	23.6183
chr18	78077248	28716337	0.3678	16.0679
chr19	59128983	27311335	0.4619	11.7067
chr20	63025520	35010931	0.5555	19.3258
chr21	48129895	6039575	0.1255	5.0811
chr22	51304566	12937829	0.2522	6.0865
chrMT	16571	2252	0.1359	0.4862
chrX	155270560	63979391	0.4121	15.7699

chrY	59373566	2559405	0.0431	1.7015

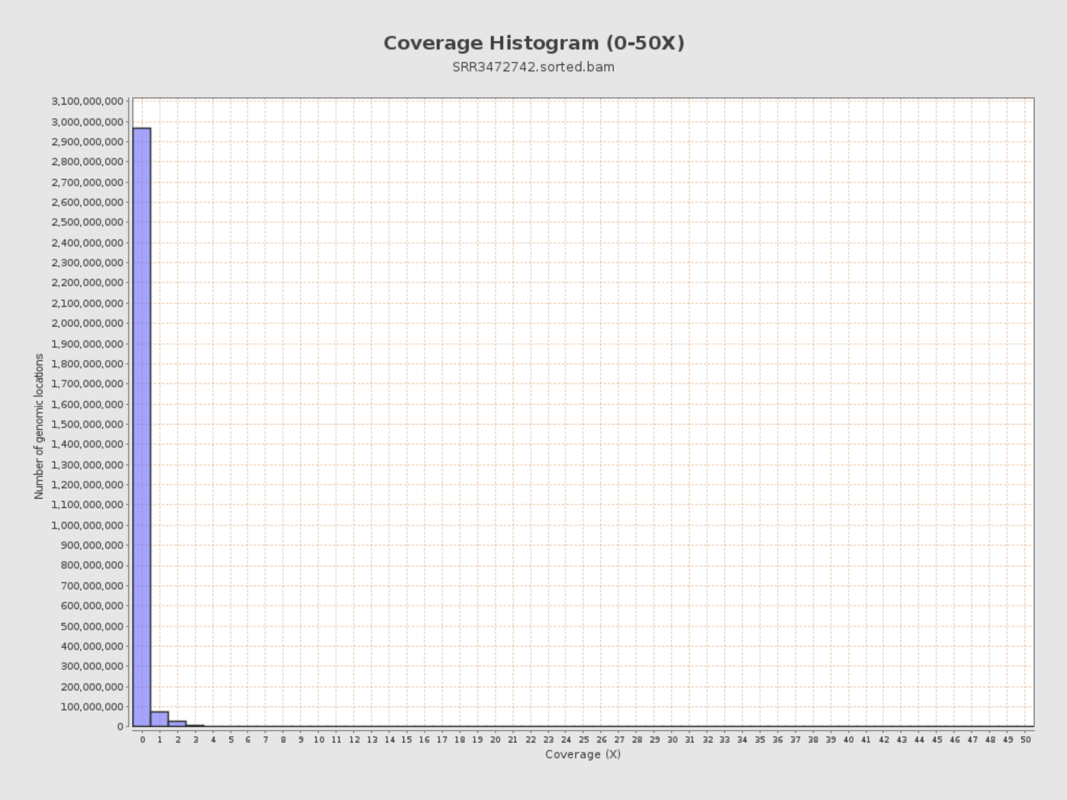
3. Results : Coverage across reference



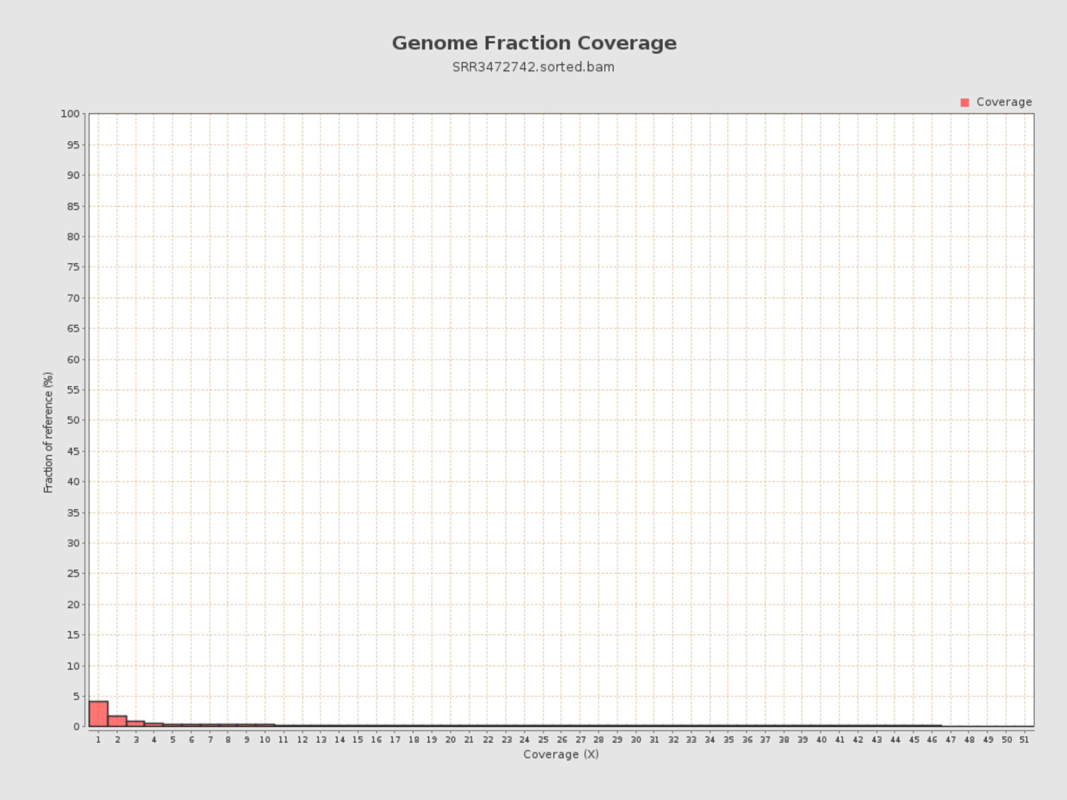
4. Results : Coverage Histogram



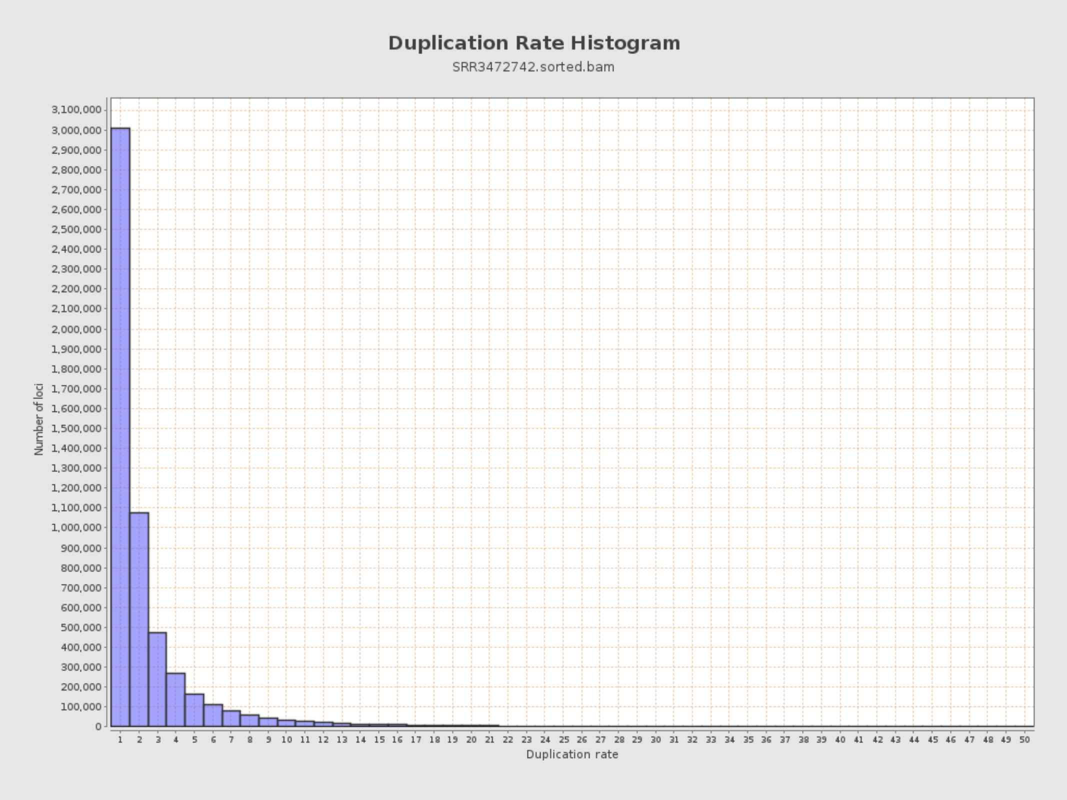
5. Results : Coverage Histogram (0-50X)



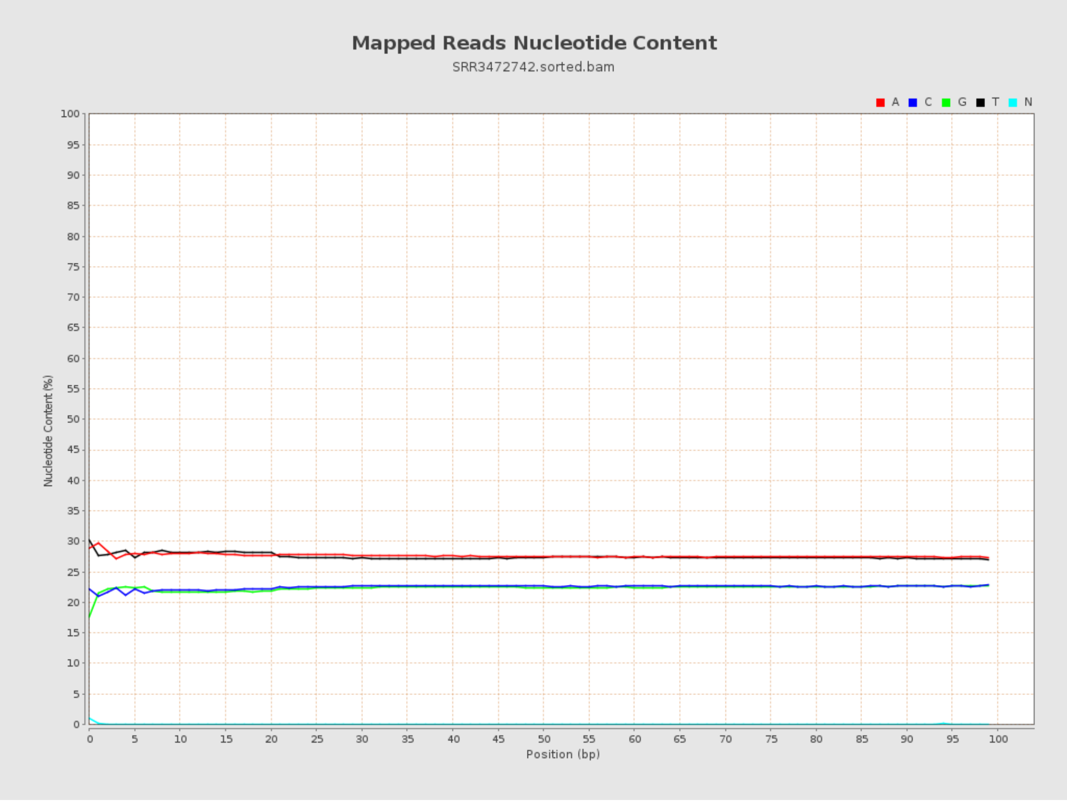
6. Results : Genome Fraction Coverage



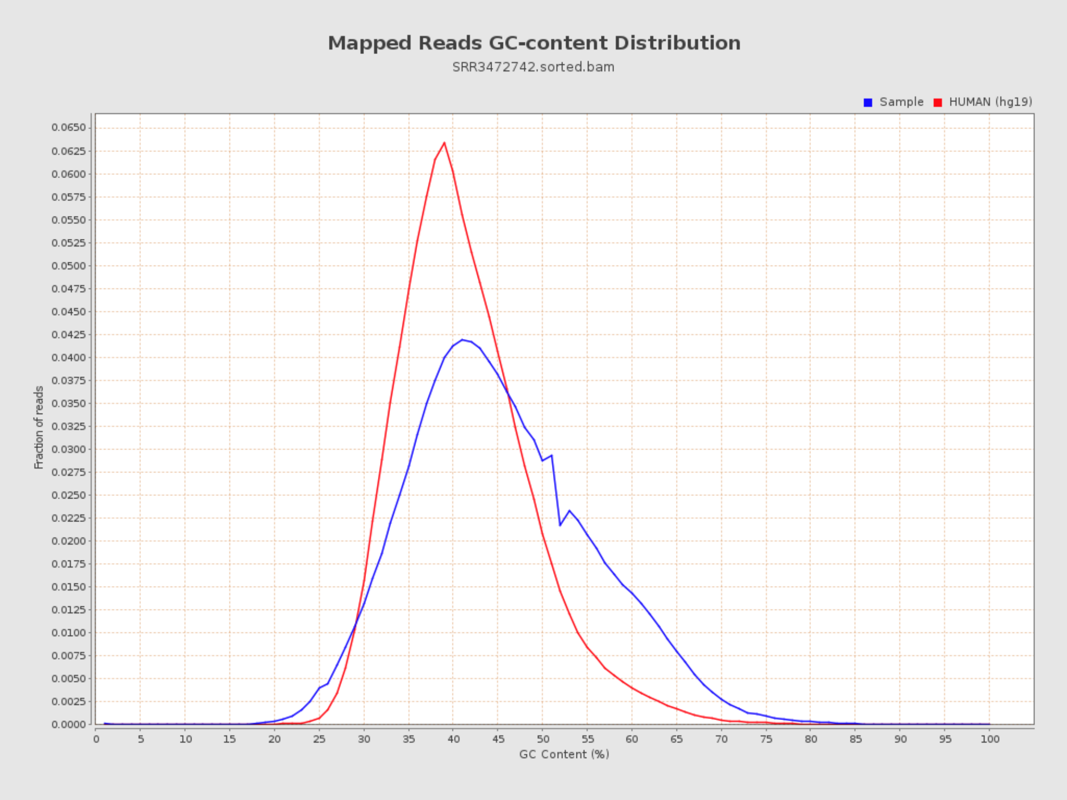
7. Results : Duplication Rate Histogram



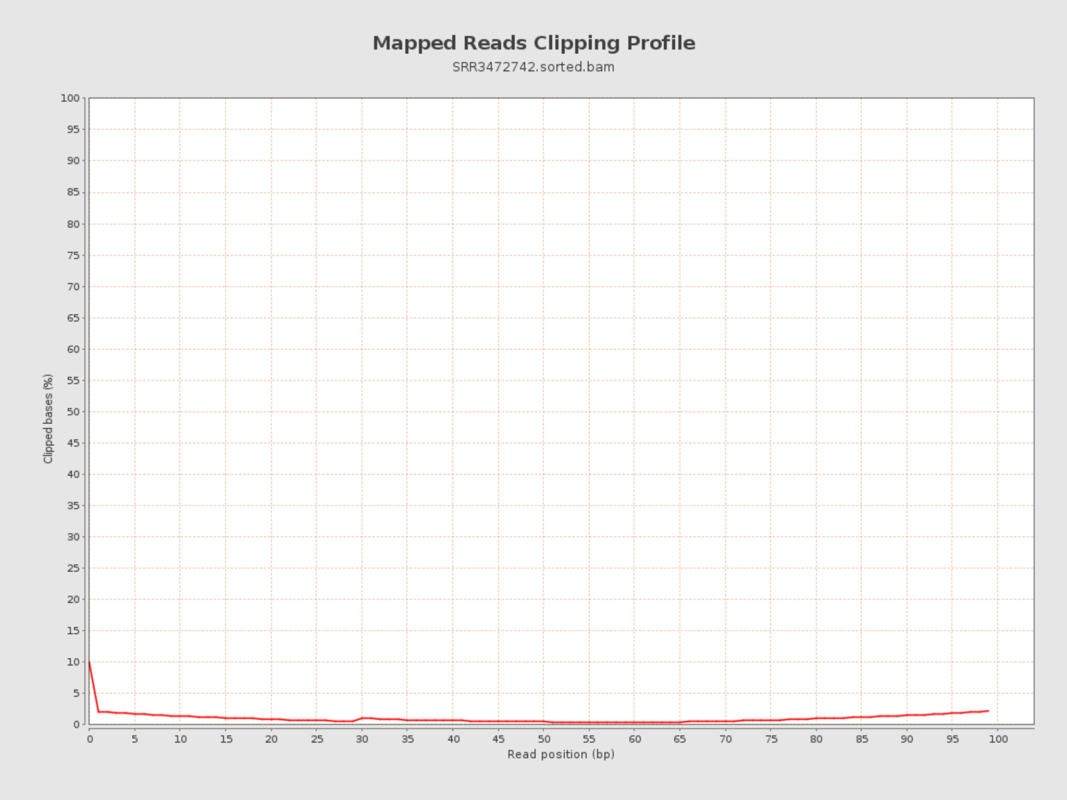
8. Results : Mapped Reads Nucleotide Content



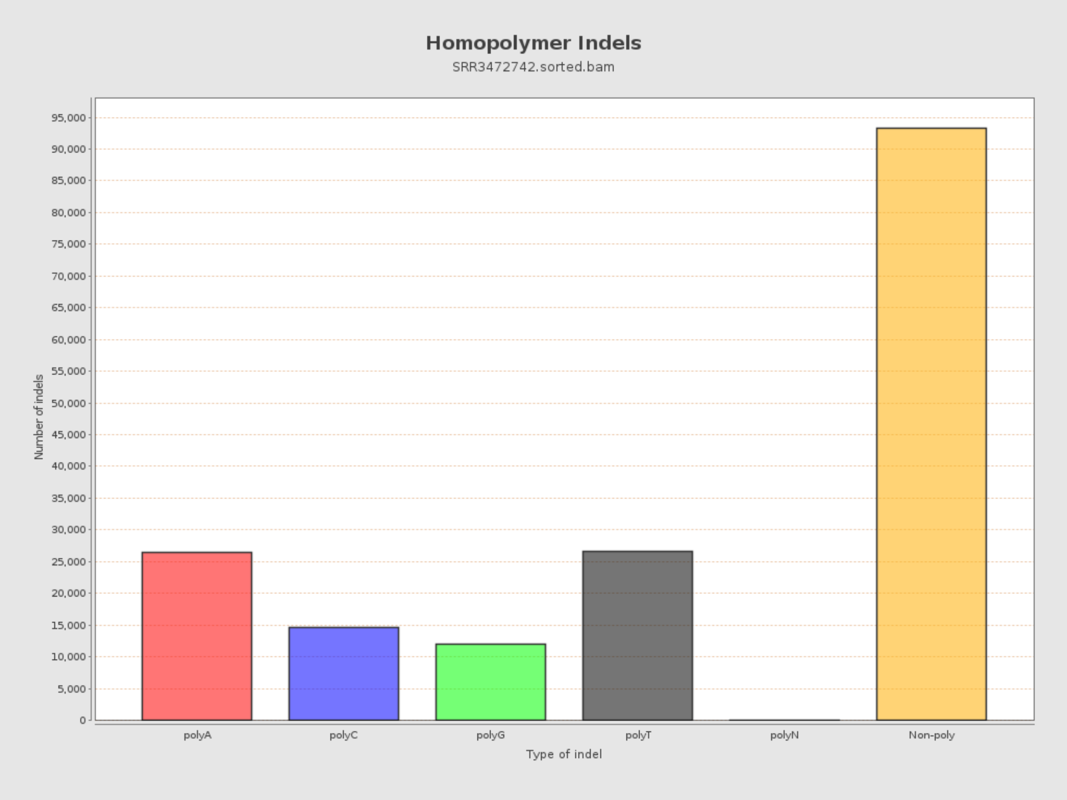
9. Results : Mapped Reads GC-content Distribution



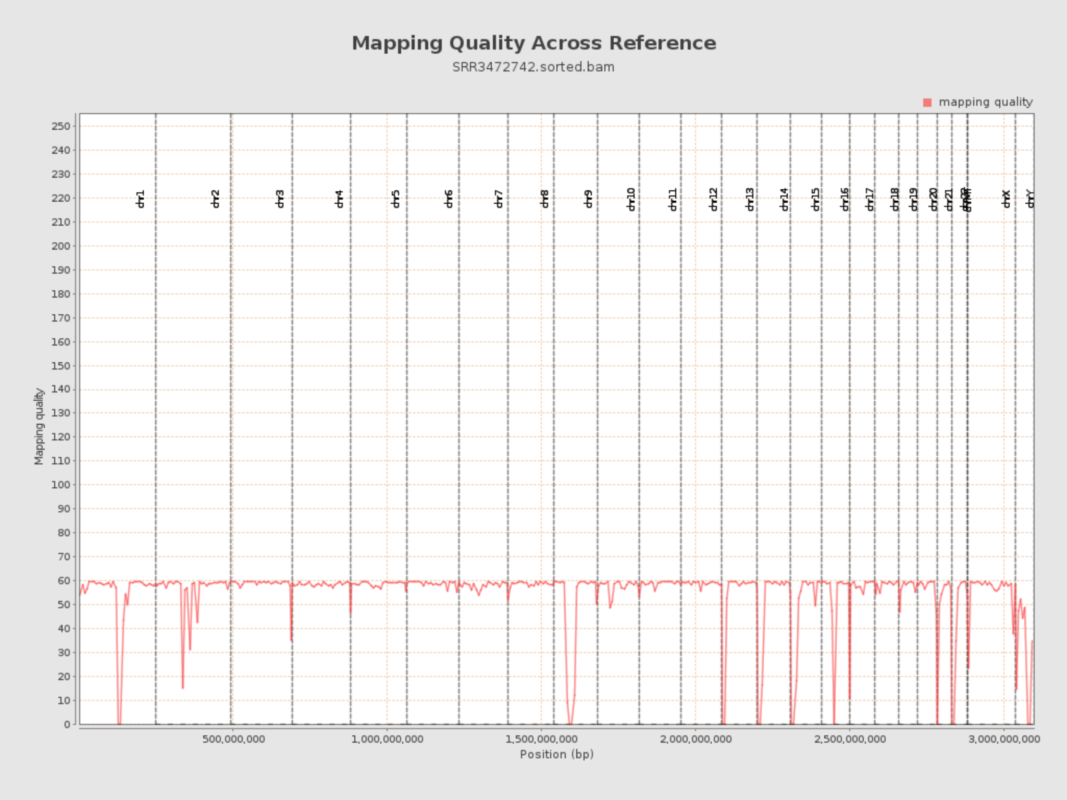
10. Results : Mapped Reads Clipping Profile



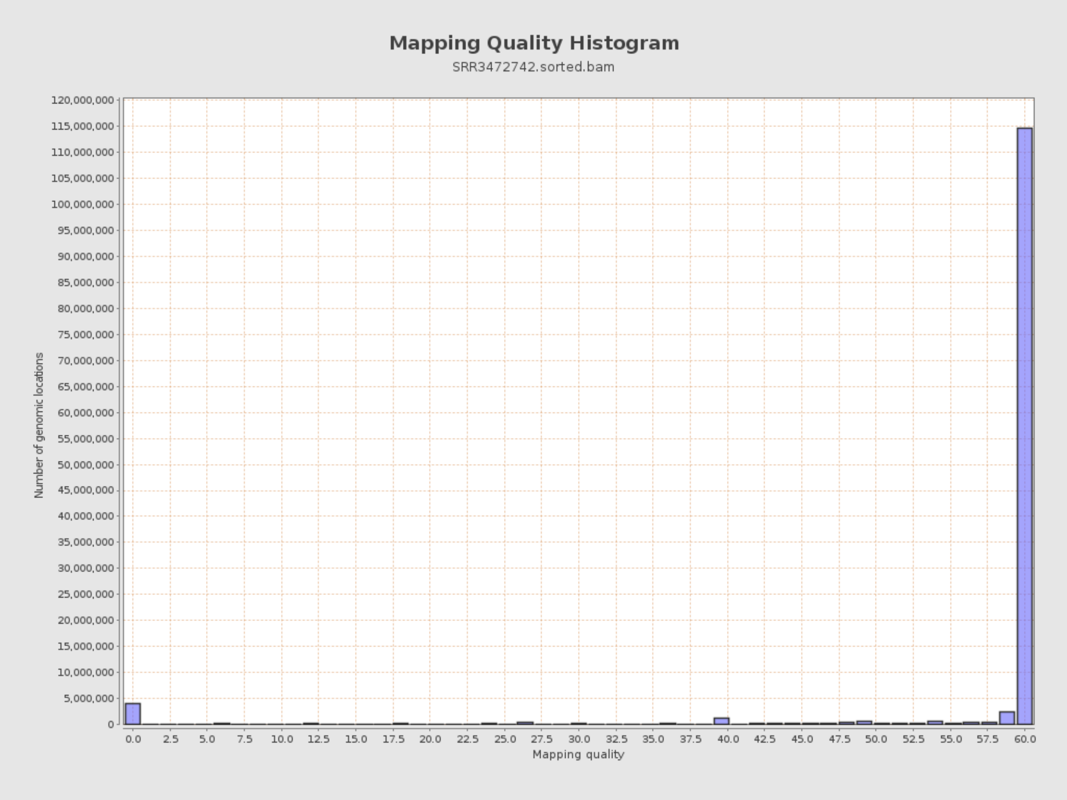
11. Results : Homopolymer Indels



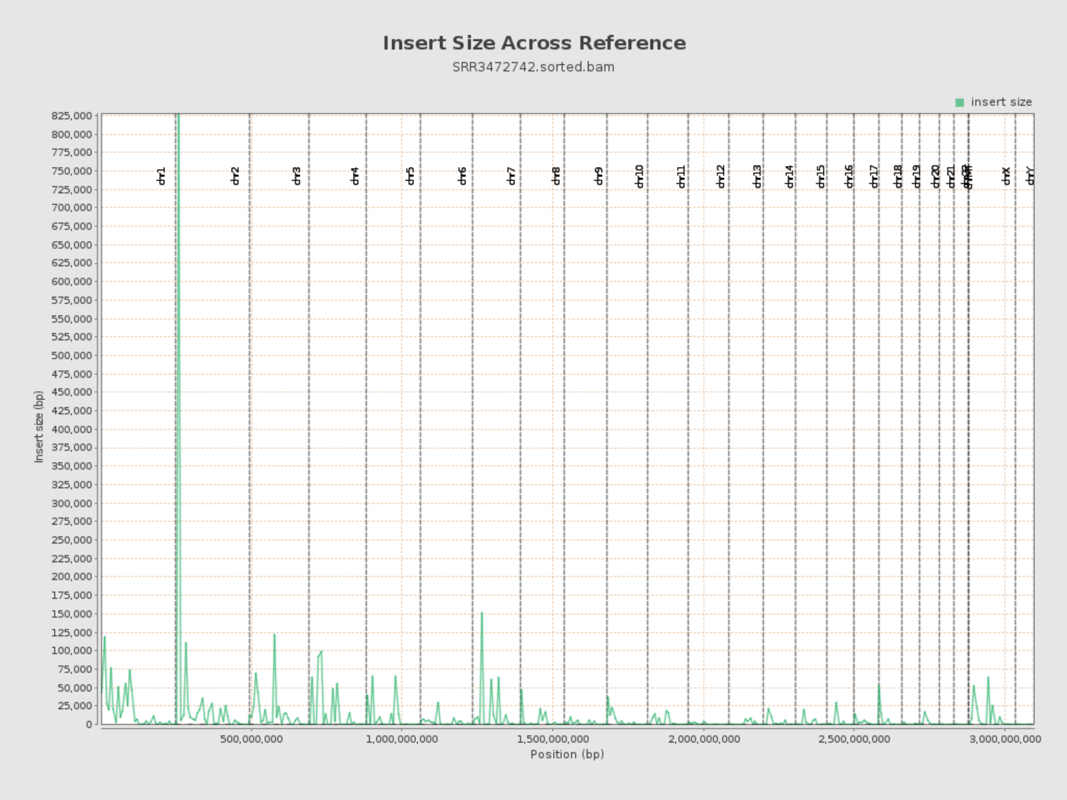
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram