Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 18:33:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472445.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_SRR3472445 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472445_1.fastq.gz SRR3472445_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 18:33:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472445.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,533,574
Mapped reads	16,305,457 / 98.62%
Unmapped reads	228,117 / 1.38%
Mapped paired reads	16,305,457 / 98.62%
Mapped reads, first in pair	8,179,569 / 49.47%
Mapped reads, second in pair	8,125,888 / 49.15%
Mapped reads, both in pair	16,214,692 / 98.07%
Mapped reads, singletons	90,765 / 0.55%
Secondary alignments	0
Supplementary alignments	62,388 / 0.38%
Read min/max/mean length	30 / 100 / 99.07
Duplicated reads (estimated)	10,489,706 / 63.44%
Duplication rate	48.23%
Clipped reads	1,195,101 / 7.23%

2.2. ACGT Content

Number/percentage of A's	435,472,824 / 27.32%
Number/percentage of C's	362,224,956 / 22.73%
Number/percentage of T's	436,213,894 / 27.37%
Number/percentage of G's	359,578,380 / 22.56%
Number/percentage of N's	195,223 / 0.01%

GC Percentage	45.29%

2.3. Coverage

Mean	0.5149
Standard Deviation	18.7116

2.4. Mapping Quality

Mean Mapping Quality	54.83

2.5. Insert size

Mean	17,775.3
Standard Deviation	1,262,102.73
P25/Median/P75	149 / 210 / 285

2.6. Mismatches and indels

General error rate	0.54%
Mismatches	8,512,672
Insertions	90,907
Mapped reads with at least one insertion	0.55%
Deletions	81,277
Mapped reads with at least one deletion	0.49%
Homopolymer indels	46.84%

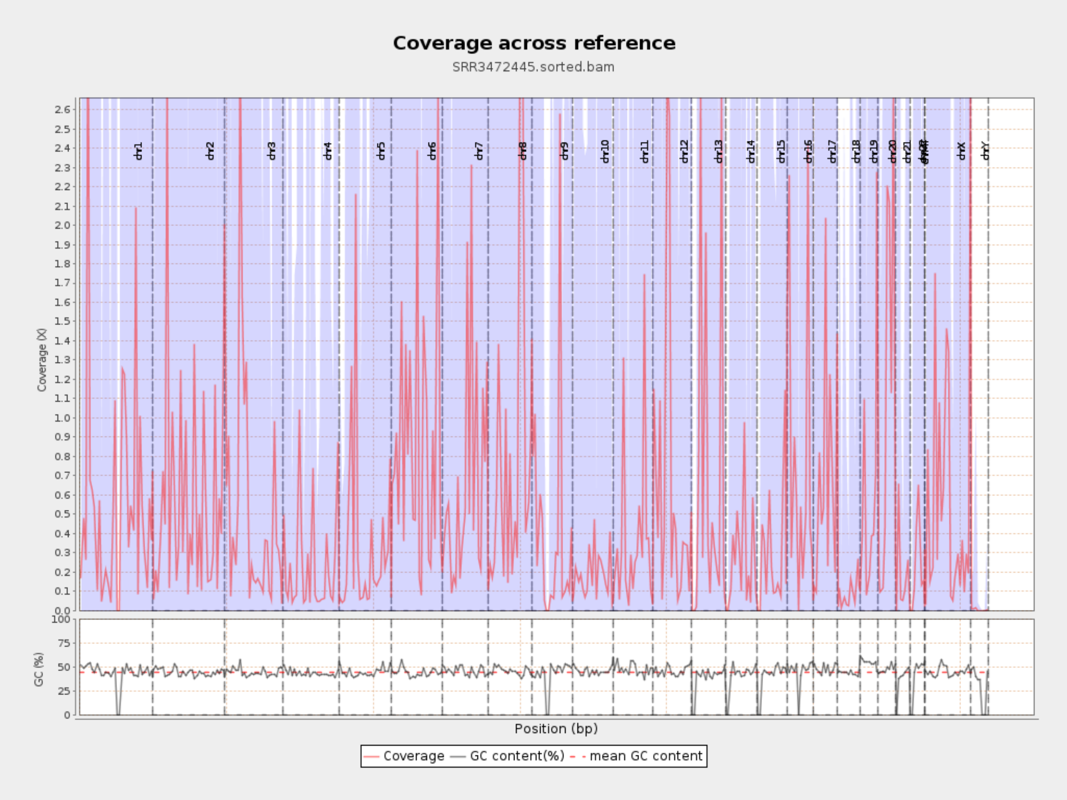
2.7. Chromosome stats

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

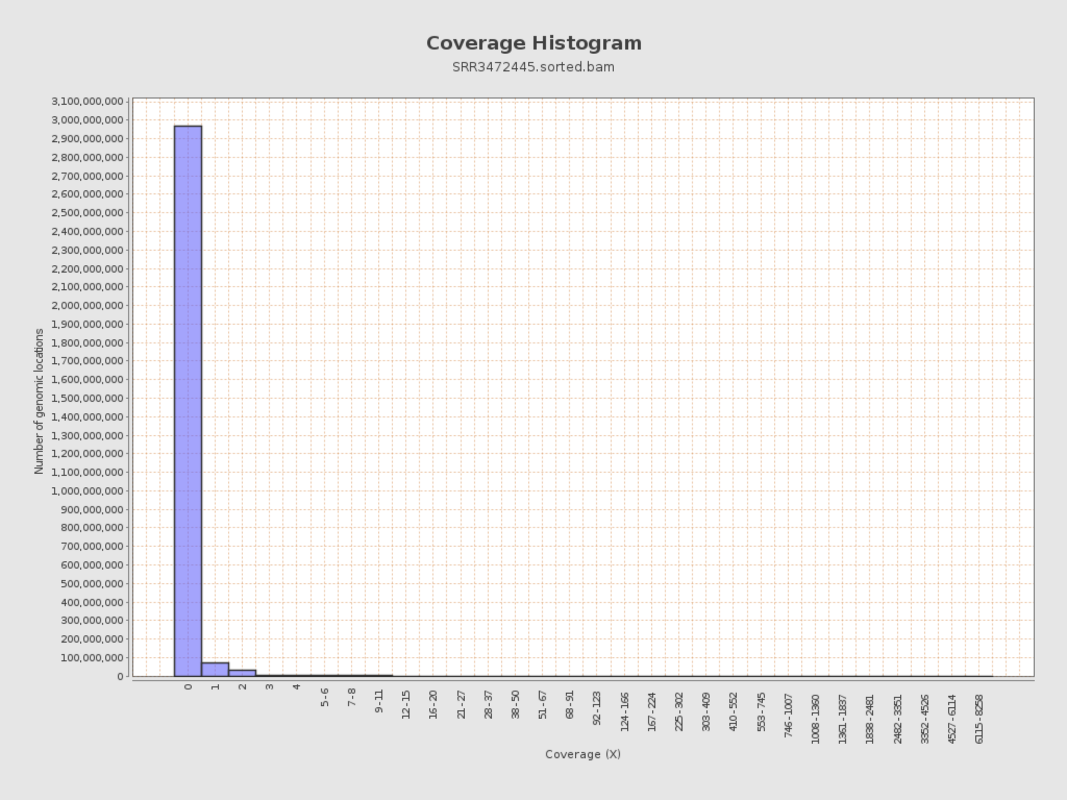
		bases	coverage	deviation
chr1	249250621	145172523	0.5824	23.6762
chr2	243199373	137852718	0.5668	20.9109
chr3	198022430	110073838	0.5559	23.6636
chr4	191154276	43752663	0.2289	8.5893
chr5	180915260	63211651	0.3494	11.67
chr6	171115067	150201533	0.8778	25.5534
chr7	159138663	107276370	0.6741	19.111
chr8	146364022	132524964	0.9054	24.5439
chr9	141213431	58291048	0.4128	15.4166
chr10	135534747	25781173	0.1902	7.7786
chr11	135006516	51816735	0.3838	13.9873
chr12	133851895	90104331	0.6732	19.9787
chr13	115169878	78826031	0.6844	31.7261
chr14	107349540	28087388	0.2616	8.4927
chr15	102531392	31068512	0.303	11.8475
chr16	90354753	72289286	0.8001	20.5772
chr17	81195210	54729170	0.674	14.0662
chr18	78077248	7137997	0.0914	2.8758
chr19	59128983	30211569	0.5109	11.9301
chr20	63025520	70523053	1.119	29.3704
chr21	48129895	9308512	0.1934	10.069
chr22	51304566	11579943	0.2257	7.2873
chrMT	16571	5284	0.3189	0.7465
chrX	155270560	83762942	0.5395	17.0148

chrY	59373566	283213	0.0048	0.401

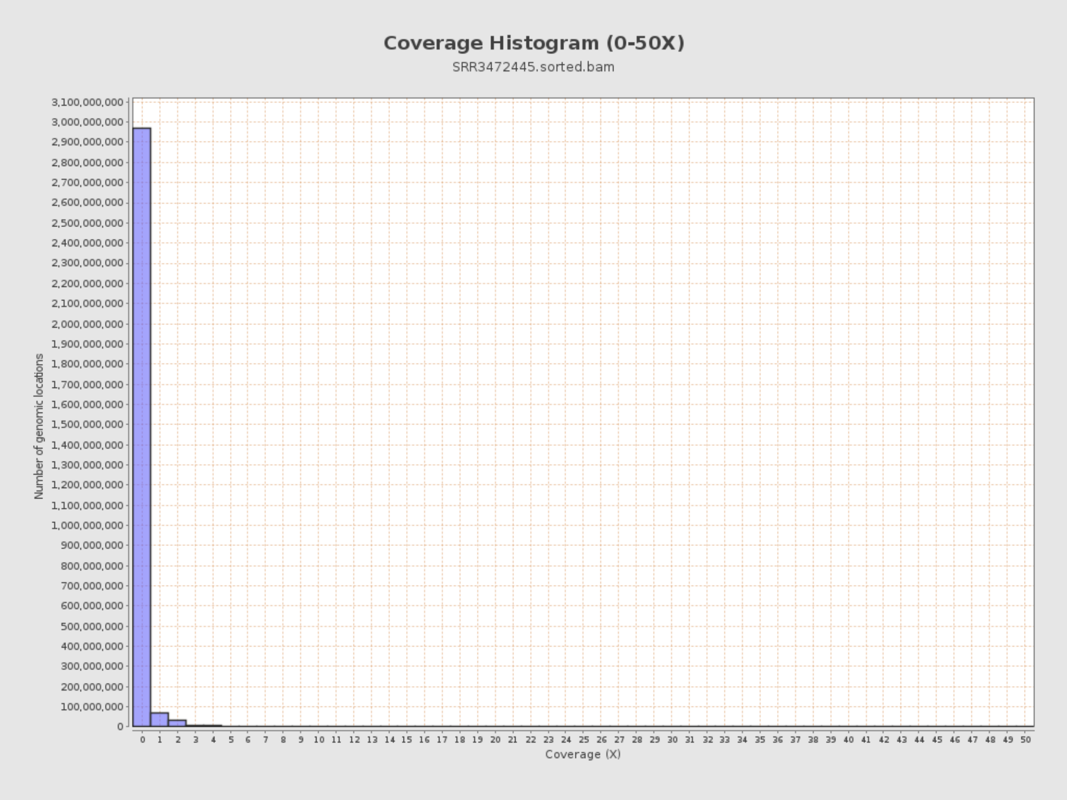
3. Results : Coverage across reference



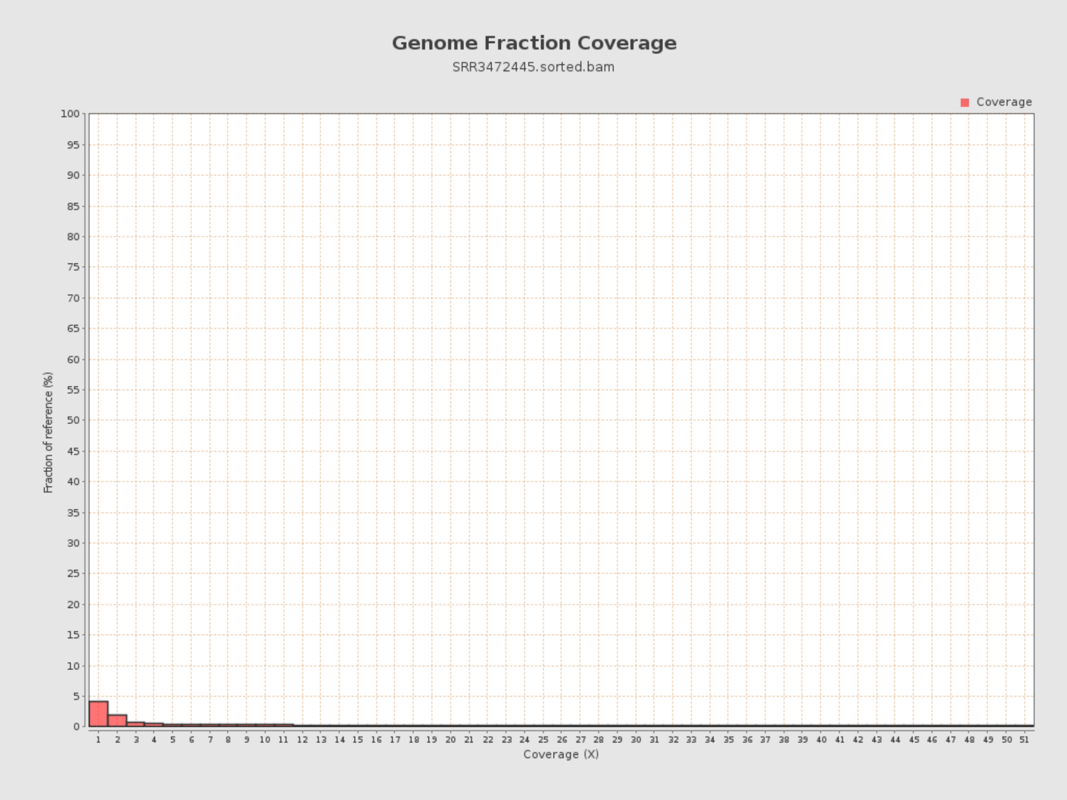
4. Results : Coverage Histogram



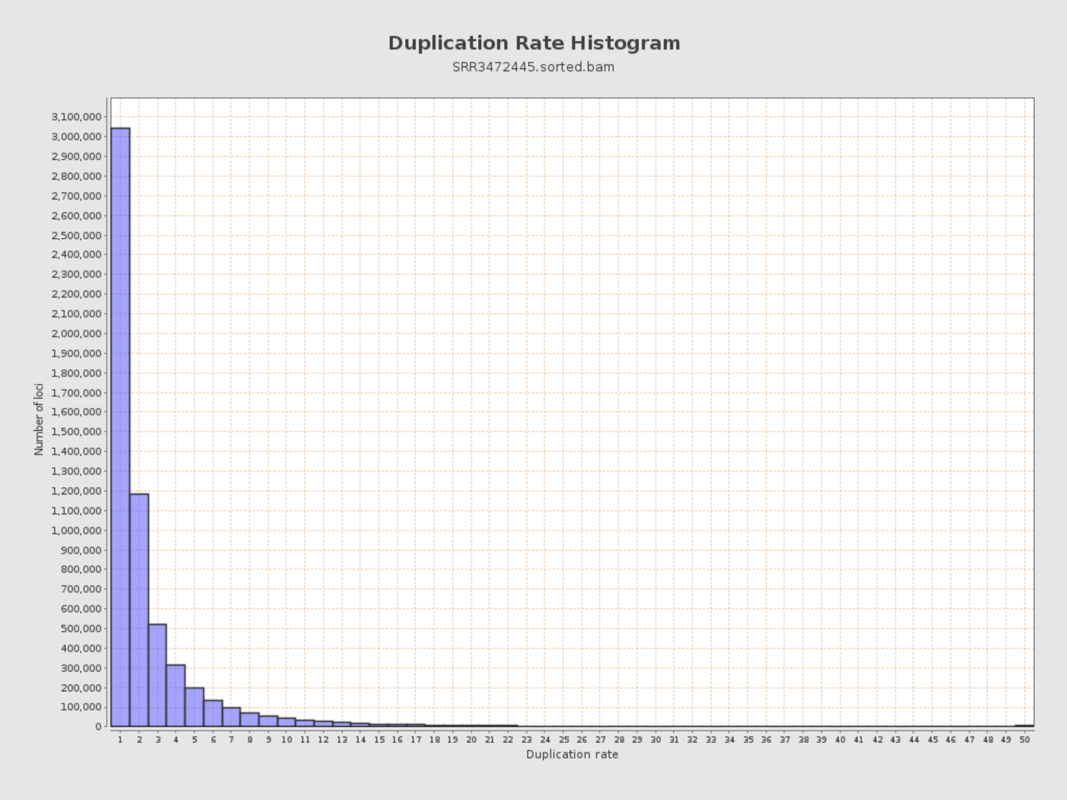
5. Results : Coverage Histogram (0-50X)



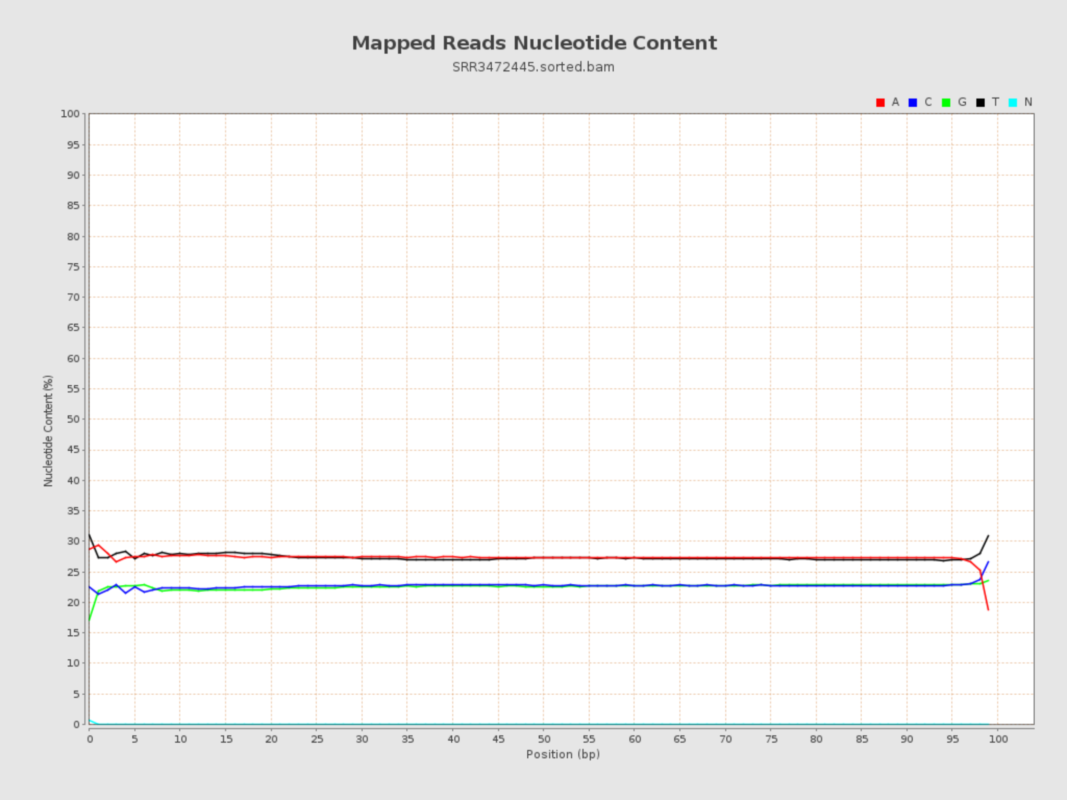
6. Results : Genome Fraction Coverage



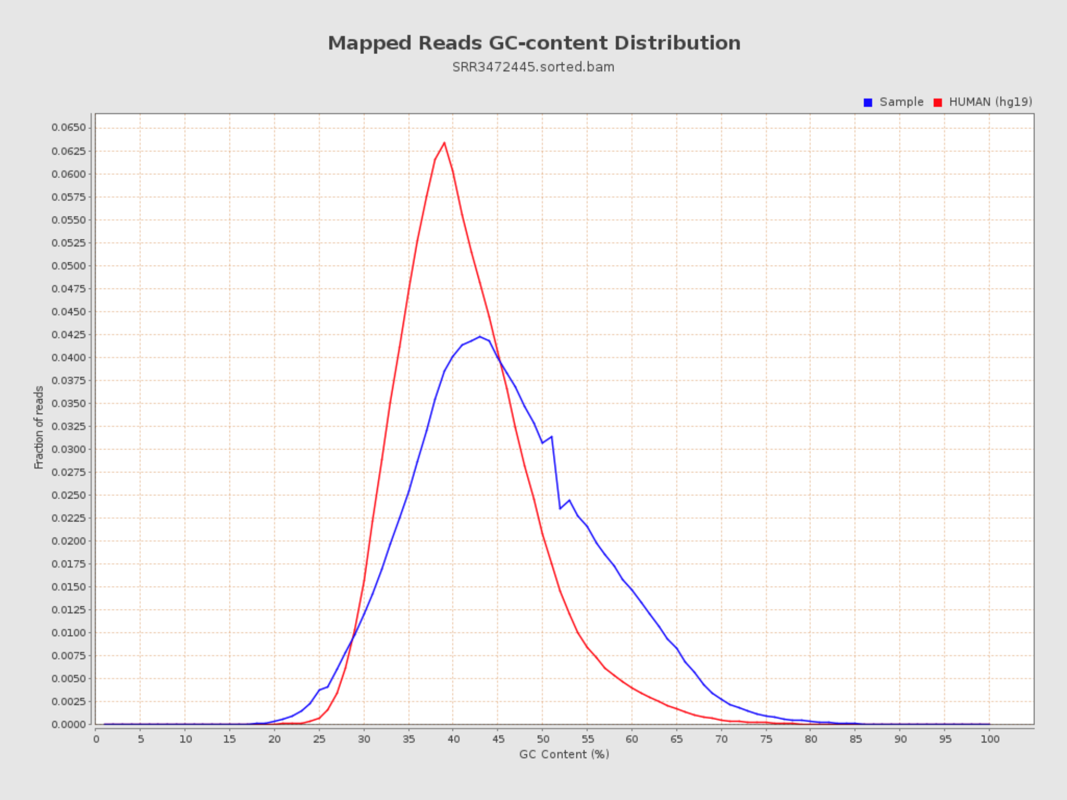
7. Results : Duplication Rate Histogram



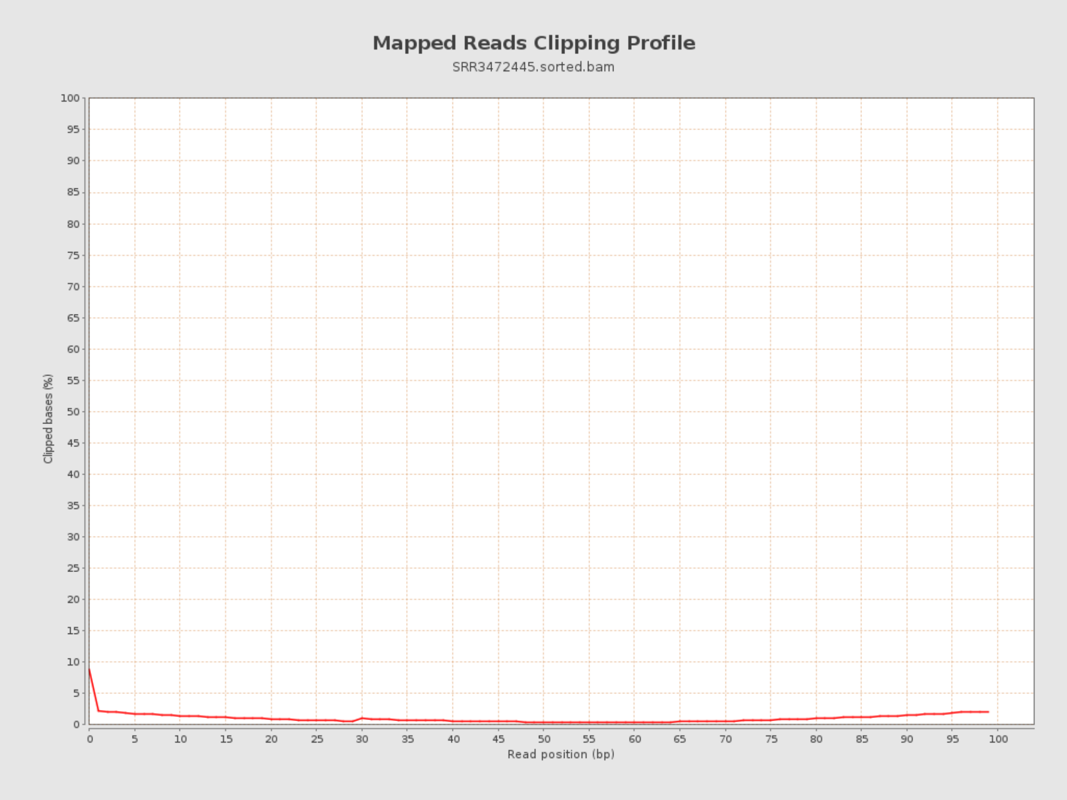
8. Results : Mapped Reads Nucleotide Content



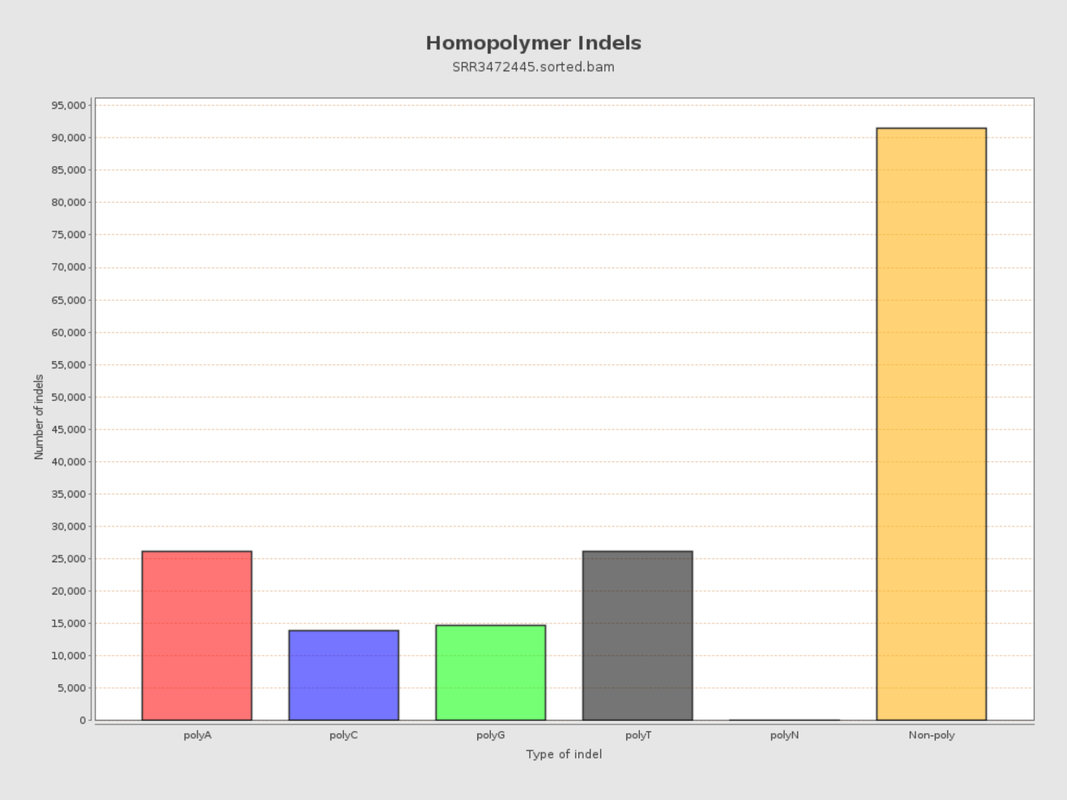
9. Results : Mapped Reads GC-content Distribution



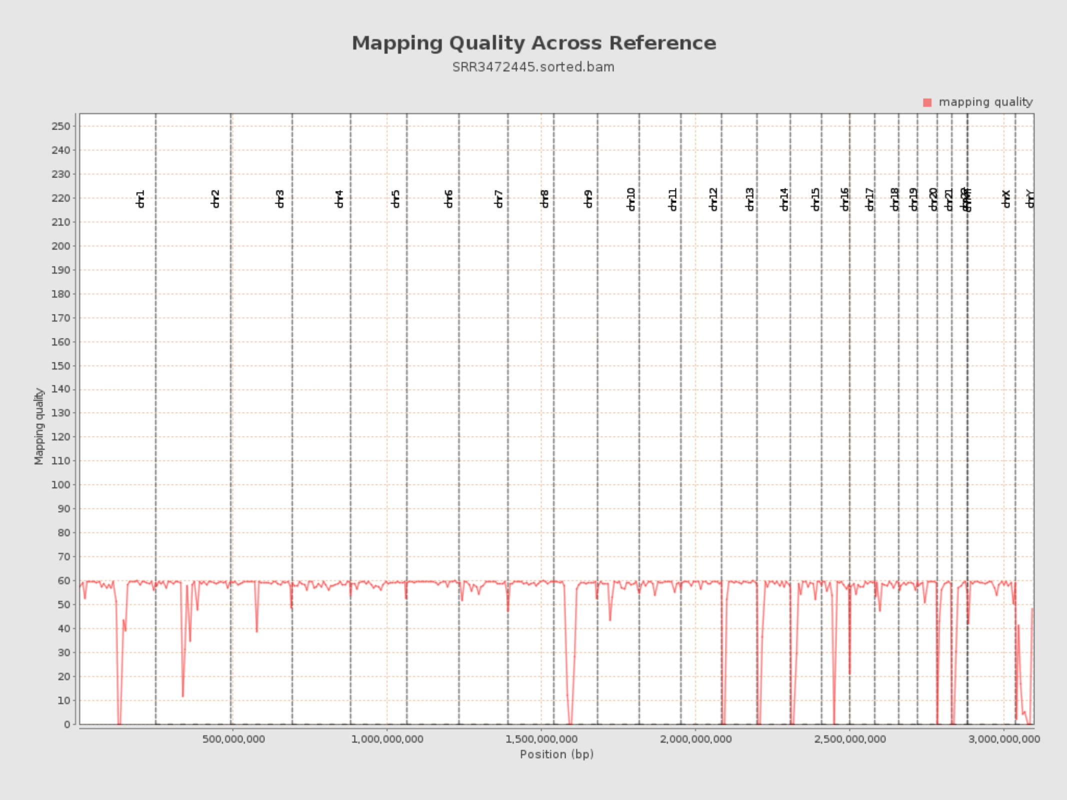
10. Results : Mapped Reads Clipping Profile



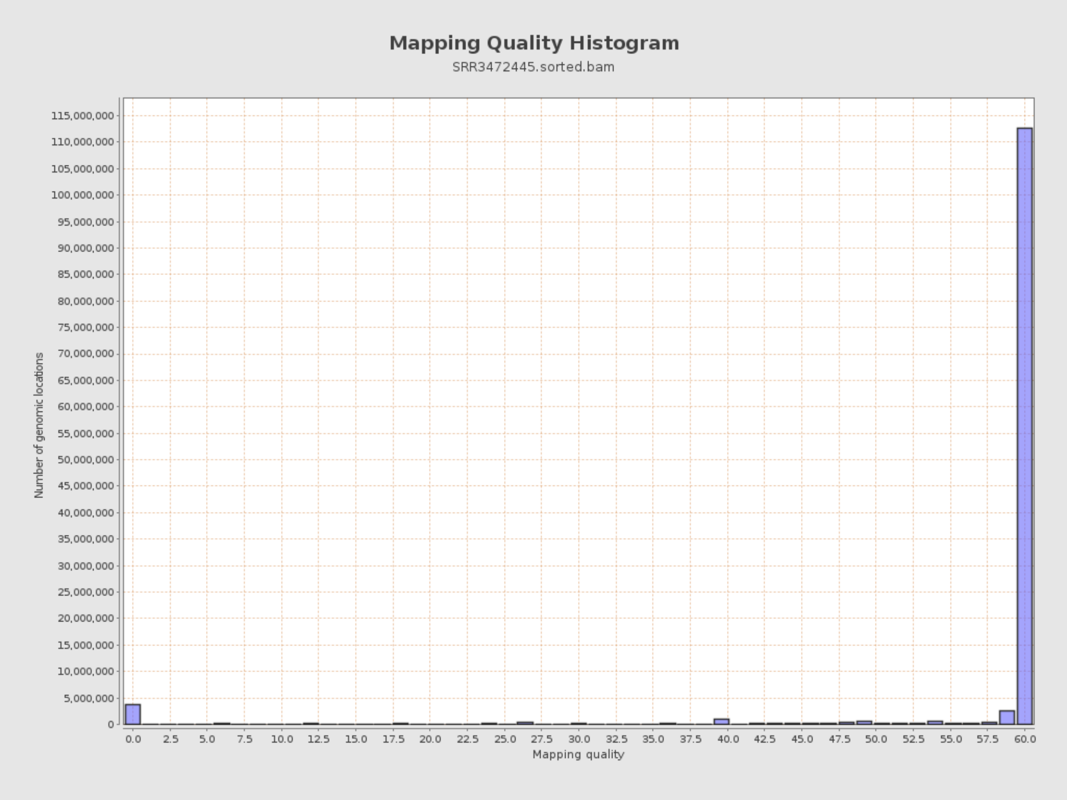
11. Results : Homopolymer Indels



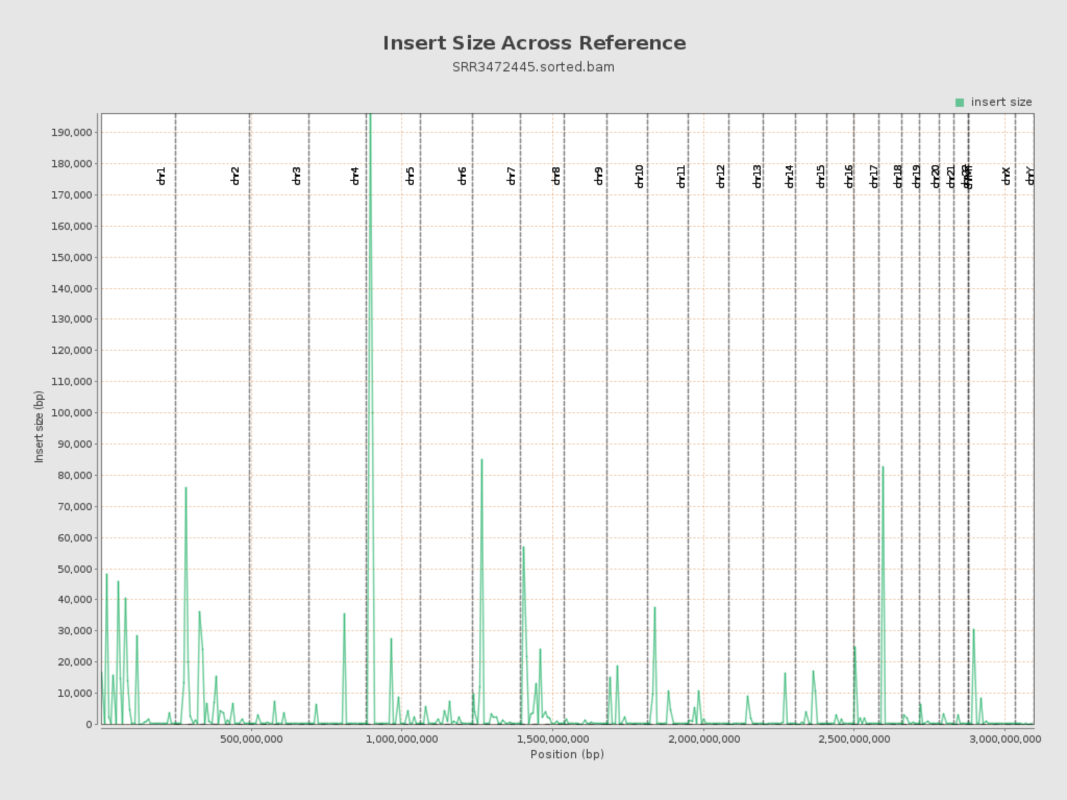
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram