Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 23:28:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472452.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_SRR3472452 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472452_1.fastq.gz SRR3472452_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 23:28:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472452.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	25,646,294
Mapped reads	25,339,509 / 98.8%
Unmapped reads	306,785 / 1.2%
Mapped paired reads	25,339,509 / 98.8%
Mapped reads, first in pair	12,764,137 / 49.77%
Mapped reads, second in pair	12,575,372 / 49.03%
Mapped reads, both in pair	25,109,974 / 97.91%
Mapped reads, singletons	229,535 / 0.9%
Secondary alignments	0
Supplementary alignments	38,930 / 0.15%
Read min/max/mean length	30 / 100 / 99.44
Duplicated reads (estimated)	15,223,769 / 59.36%
Duplication rate	48.59%
Clipped reads	1,166,969 / 4.55%

2.2. ACGT Content

Number/percentage of A's	702,012,429 / 28.13%
Number/percentage of C's	545,486,968 / 21.86%
Number/percentage of T's	707,827,149 / 28.36%
Number/percentage of G's	539,894,470 / 21.63%
Number/percentage of N's	323,752 / 0.01%

GC Percentage	43.49%

2.3. Coverage

Mean	0.8063
Standard Deviation	16.4945

2.4. Mapping Quality

Mean Mapping Quality	54.63

2.5. Insert size

Mean	64,548.11
Standard Deviation	2,510,766.21
P25/Median/P75	170 / 232 / 309

2.6. Mismatches and indels

General error rate	0.51%
Mismatches	12,424,131
Insertions	123,672
Mapped reads with at least one insertion	0.48%
Deletions	152,604
Mapped reads with at least one deletion	0.59%
Homopolymer indels	45.7%

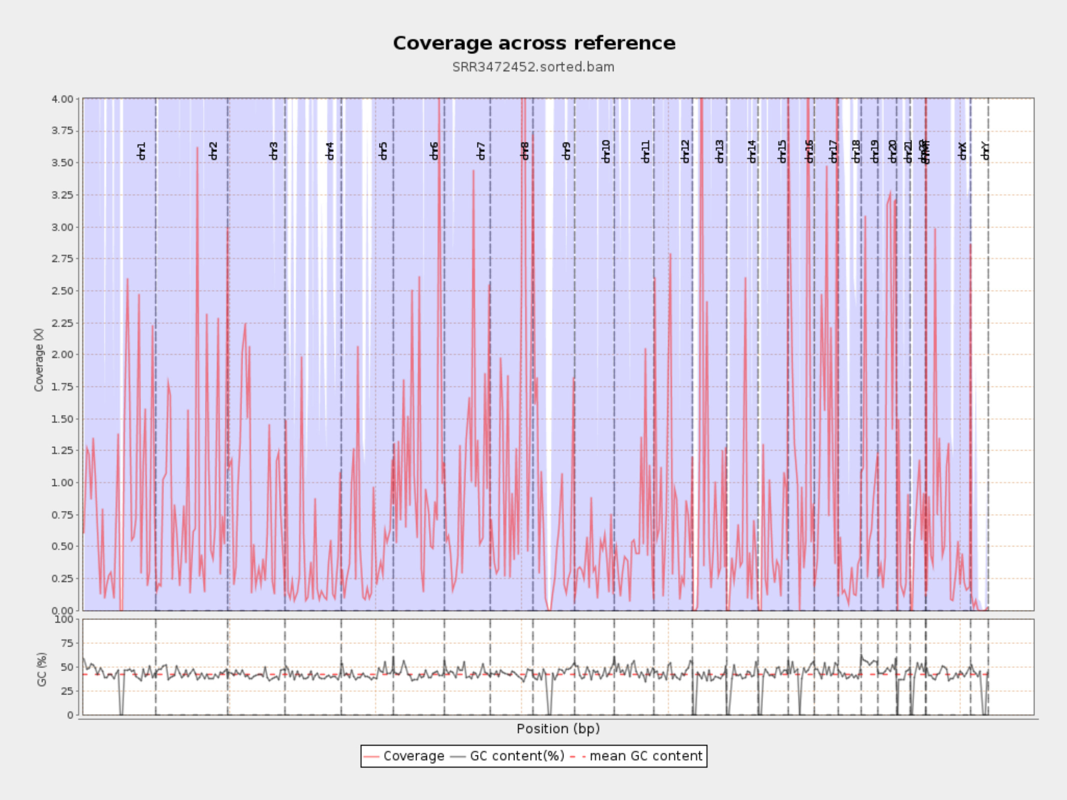
2.7. Chromosome stats

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

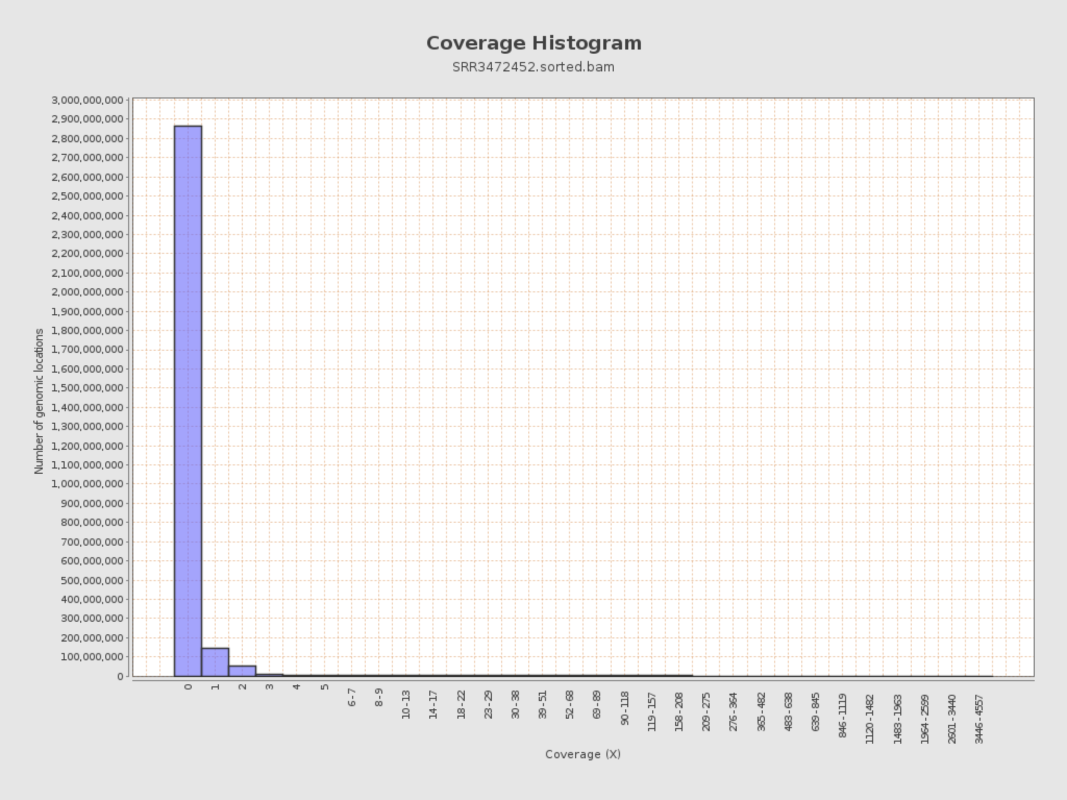
		bases	coverage	deviation
chr1	249250621	214189388	0.8593	14.842
chr2	243199373	209713930	0.8623	17.8179
chr3	198022430	170289756	0.86	13.3529
chr4	191154276	72731551	0.3805	9.3284
chr5	180915260	93253379	0.5155	10.6485
chr6	171115067	195306722	1.1414	18.1363
chr7	159138663	167690765	1.0537	20.5587
chr8	146364022	213790345	1.4607	28.0675
chr9	141213431	87898572	0.6225	10.3941
chr10	135534747	52093049	0.3844	8.4
chr11	135006516	76519731	0.5668	11.6866
chr12	133851895	119772910	0.8948	14.2592
chr13	115169878	109260438	0.9487	24.3404
chr14	107349540	53030790	0.494	10.2379
chr15	102531392	48997530	0.4779	11.2901
chr16	90354753	135907490	1.5042	25.6629
chr17	81195210	125965020	1.5514	24.1324
chr18	78077248	17756092	0.2274	4.5646
chr19	59128983	65222551	1.1031	14.5755
chr20	63025520	104668076	1.6607	33.4877
chr21	48129895	24060543	0.4999	19.0639
chr22	51304566	32228307	0.6282	13.0103
chrMT	16571	89560	5.4046	3.2925
chrX	155270560	103850127	0.6688	10.6078

chrY	59373566	1619658	0.0273	1.0599

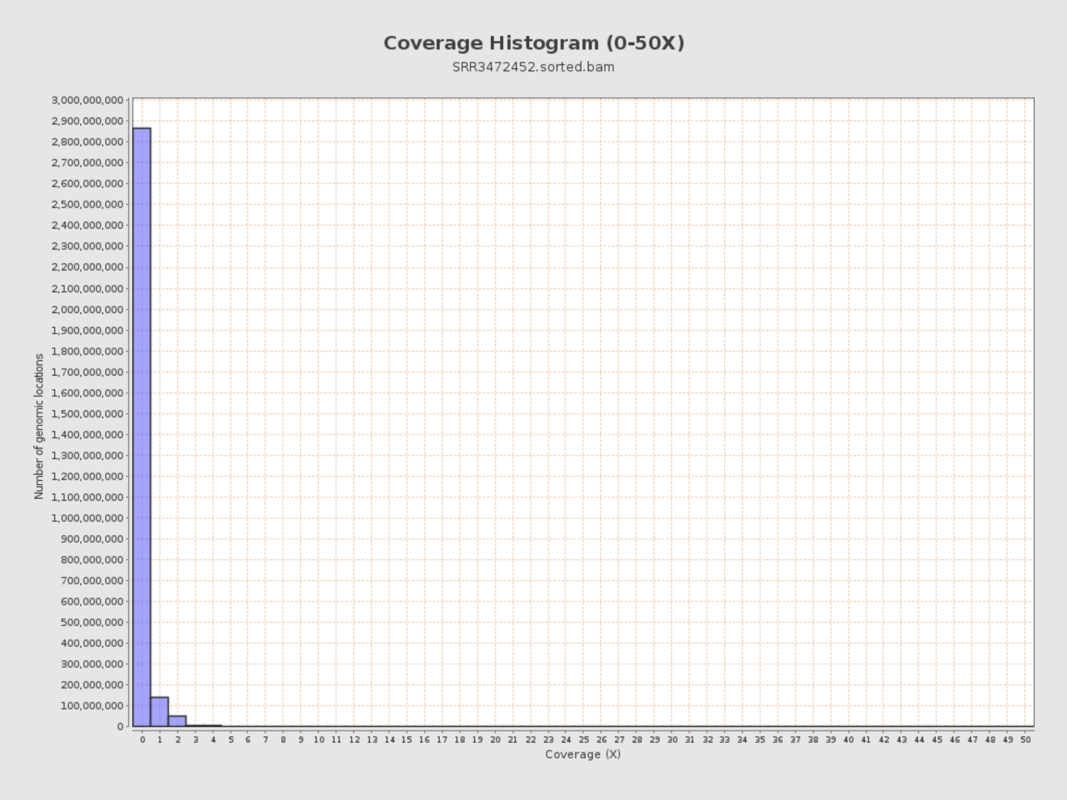
3. Results : Coverage across reference



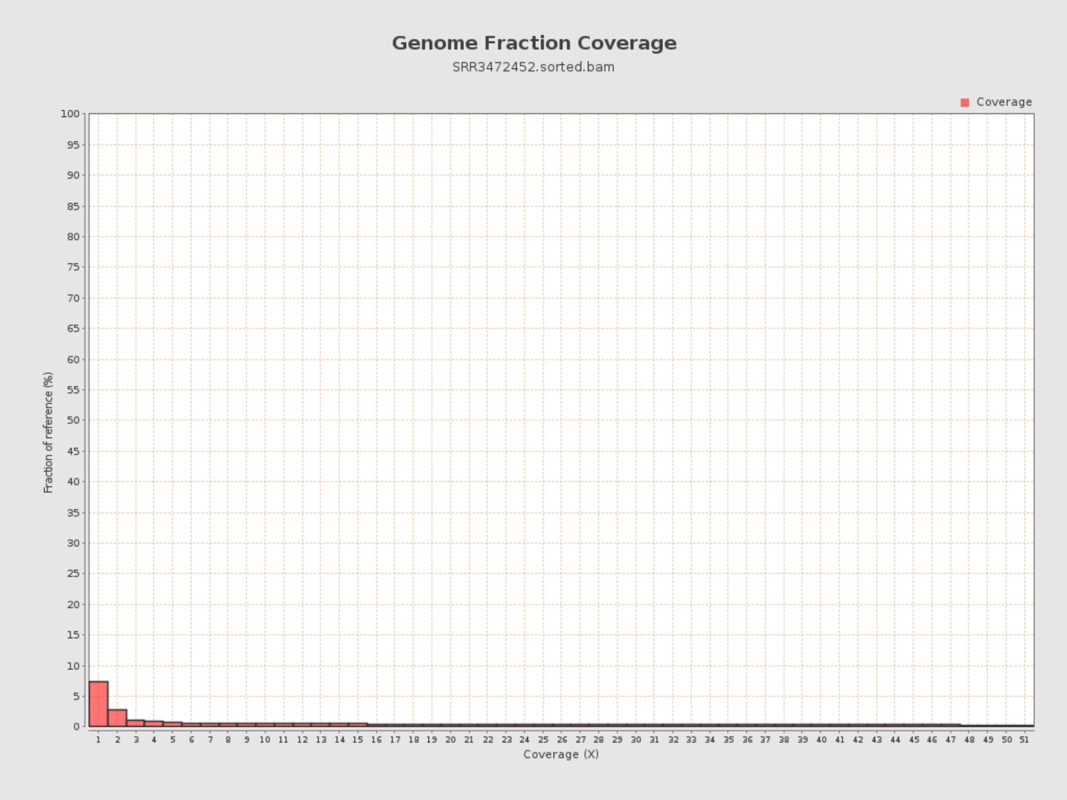
4. Results : Coverage Histogram



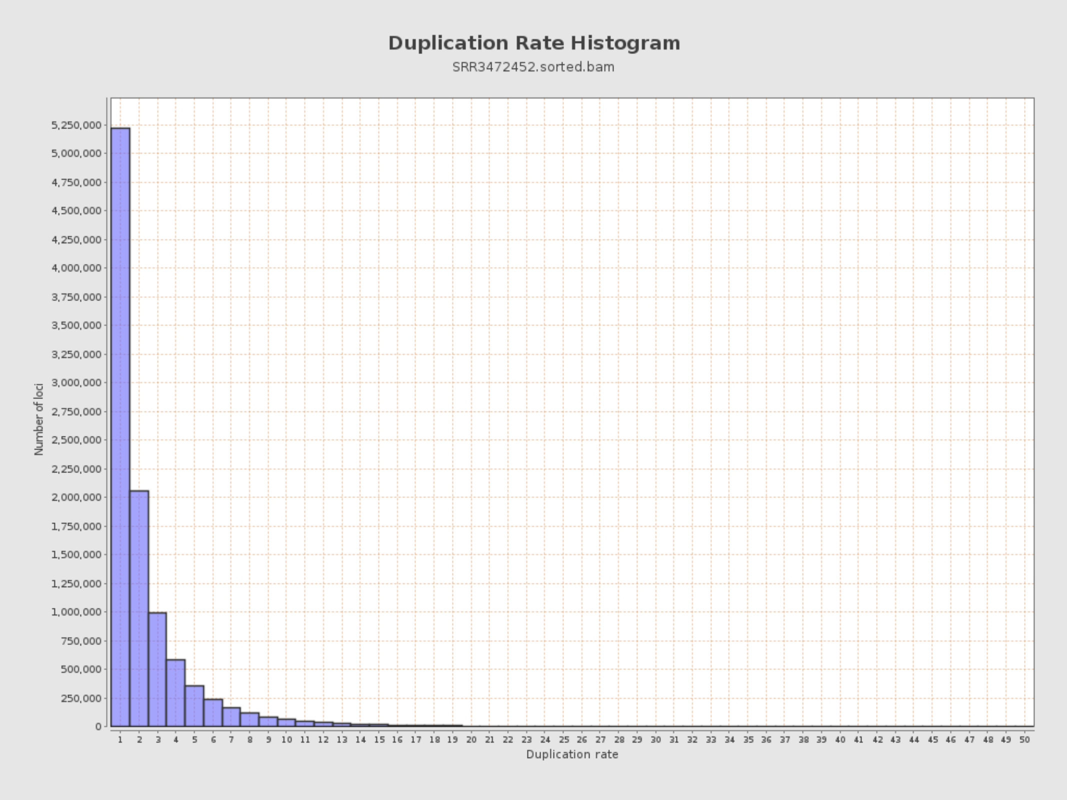
5. Results : Coverage Histogram (0-50X)



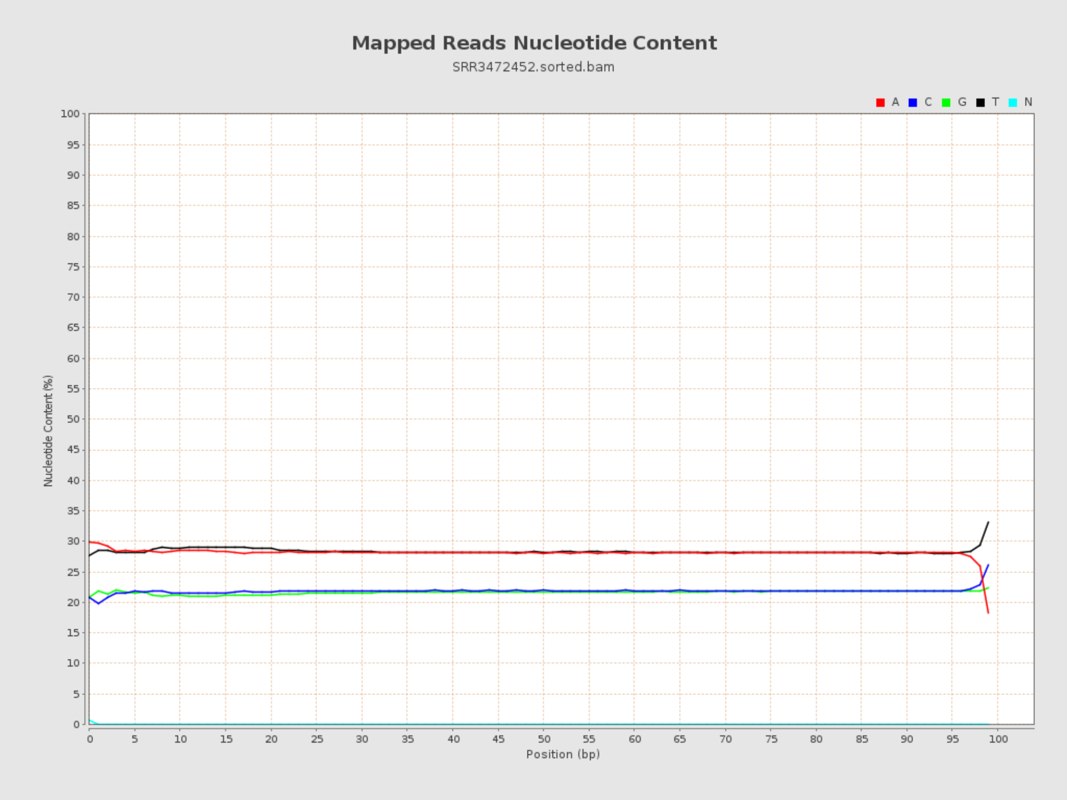
6. Results : Genome Fraction Coverage



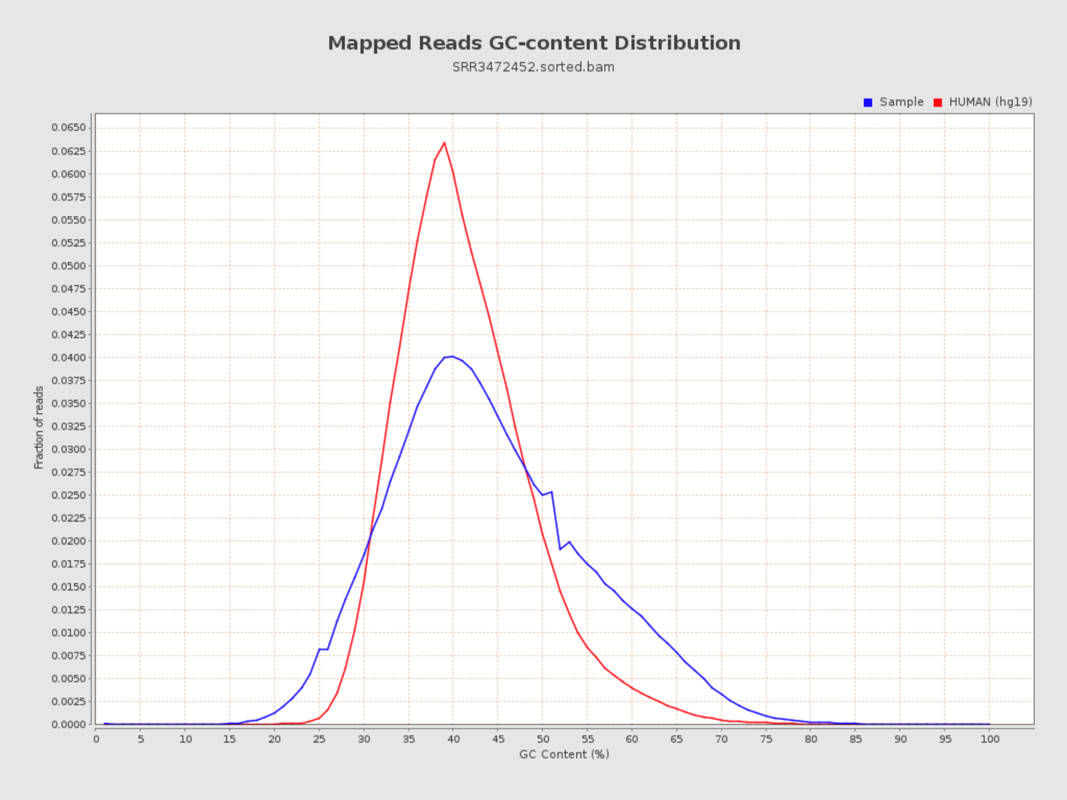
7. Results : Duplication Rate Histogram



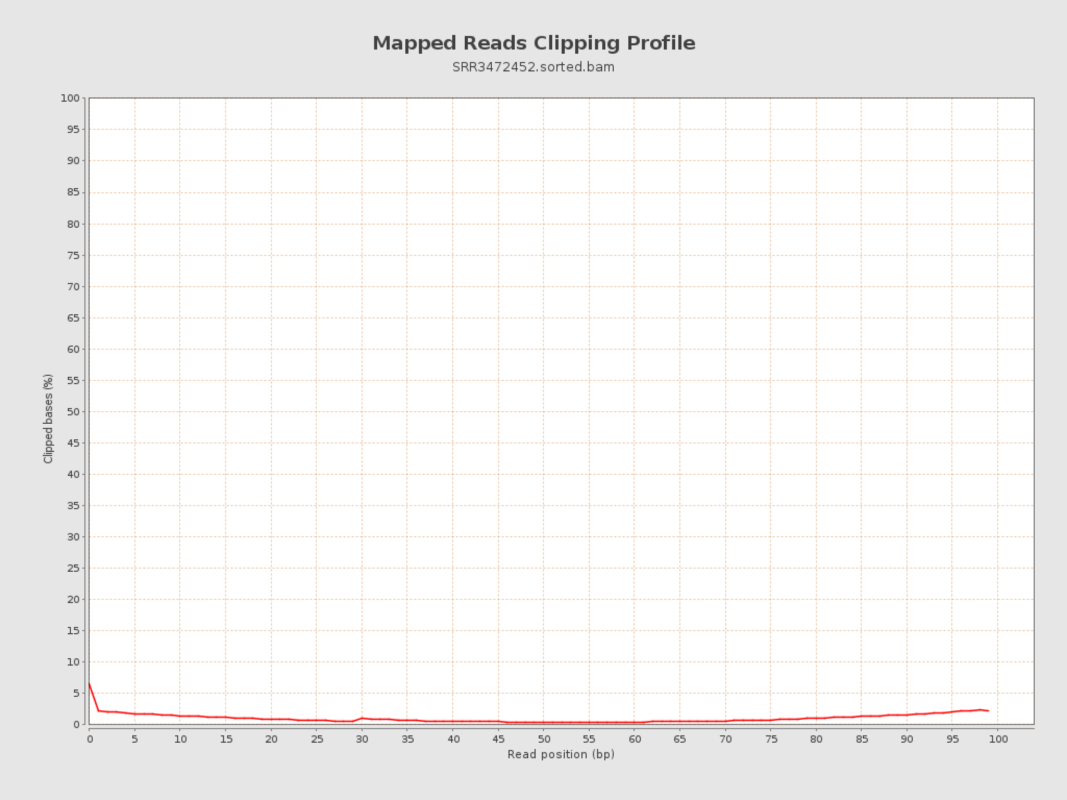
8. Results : Mapped Reads Nucleotide Content



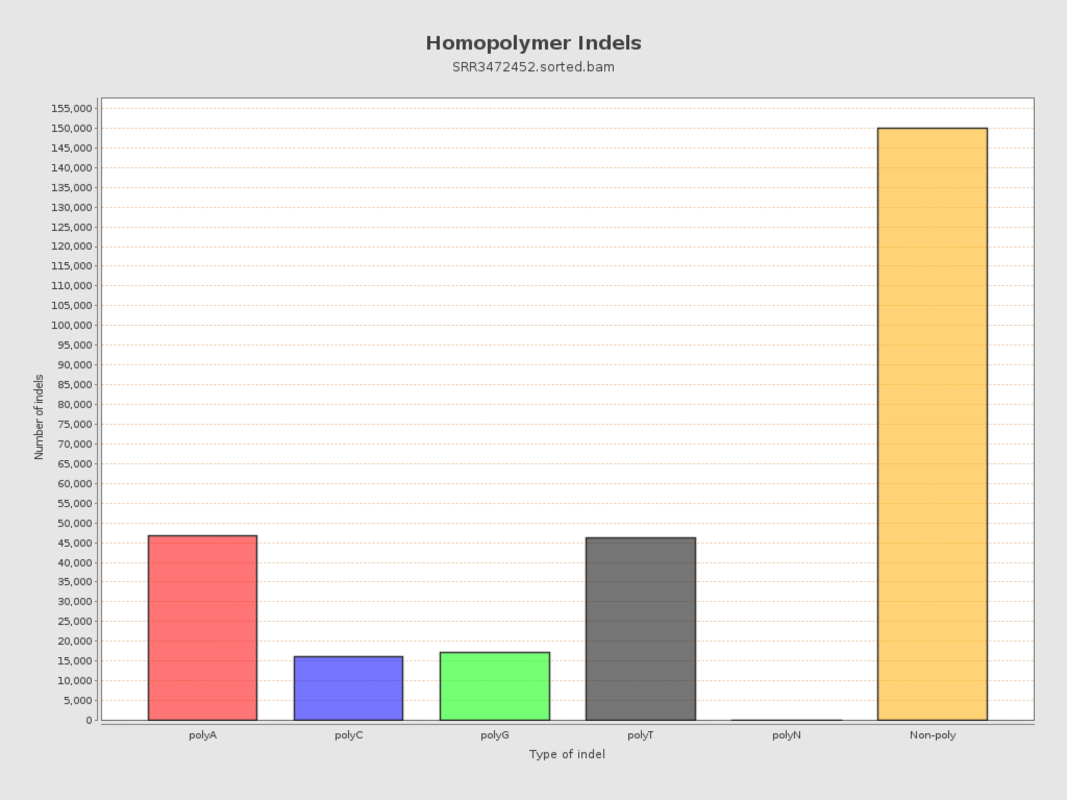
9. Results : Mapped Reads GC-content Distribution



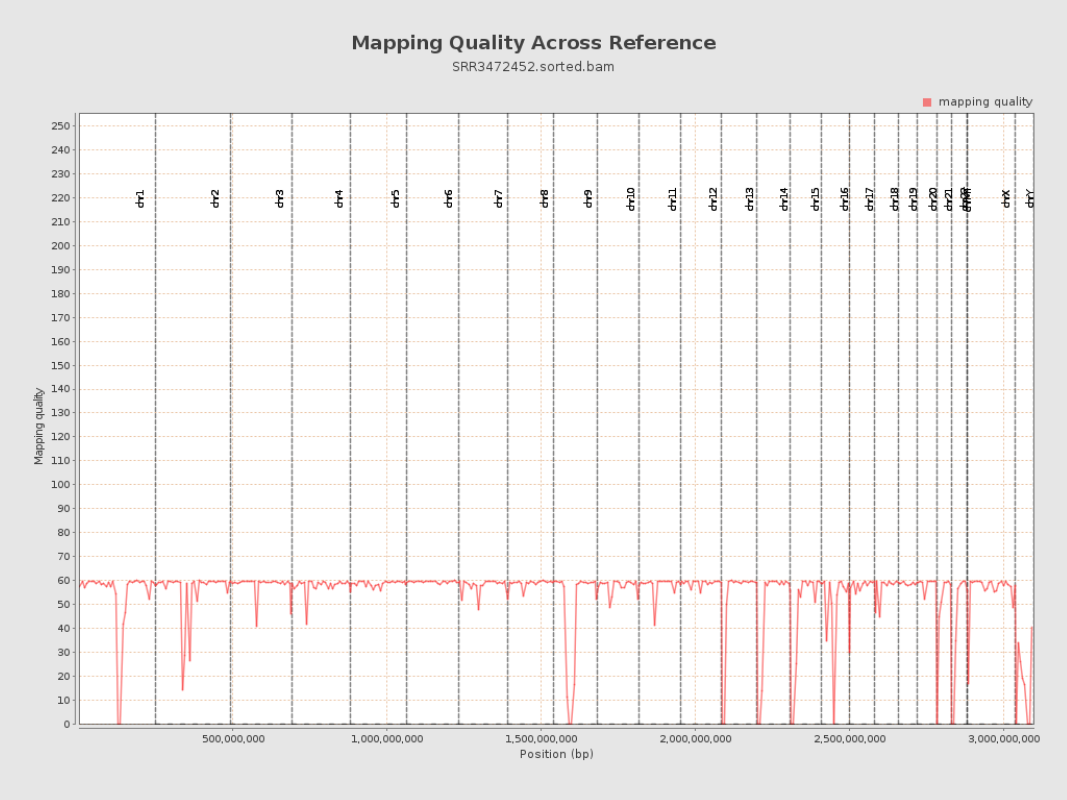
10. Results : Mapped Reads Clipping Profile



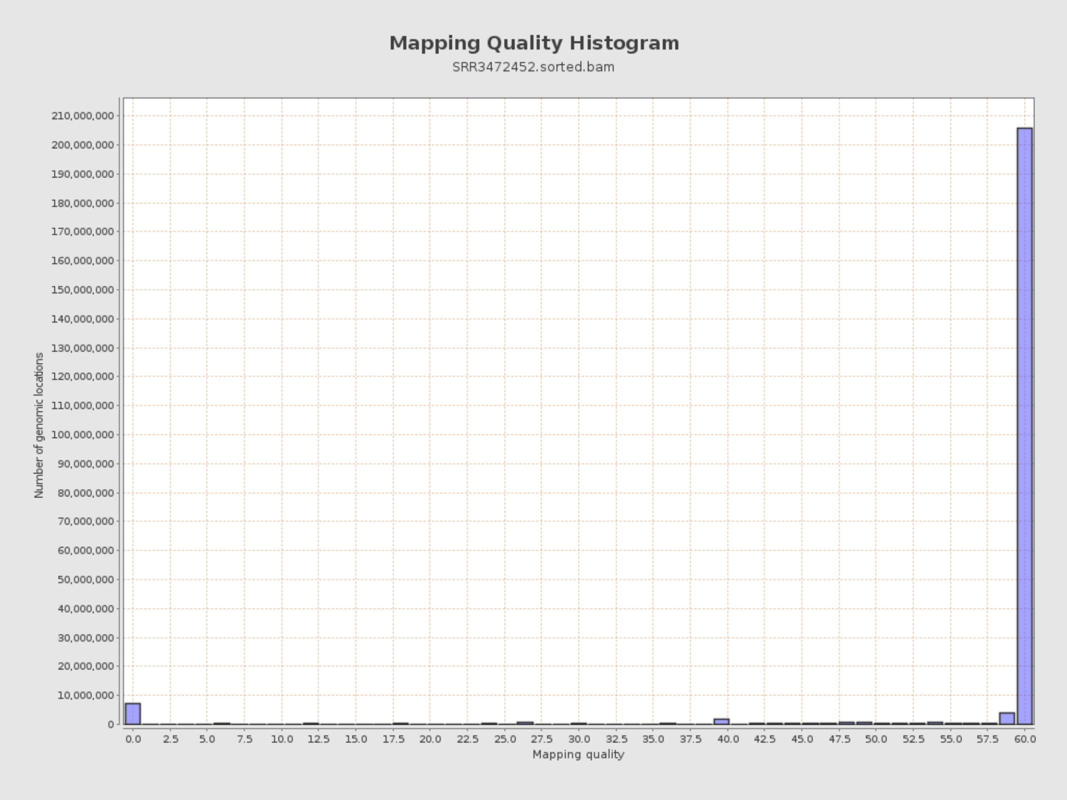
11. Results : Homopolymer Indels



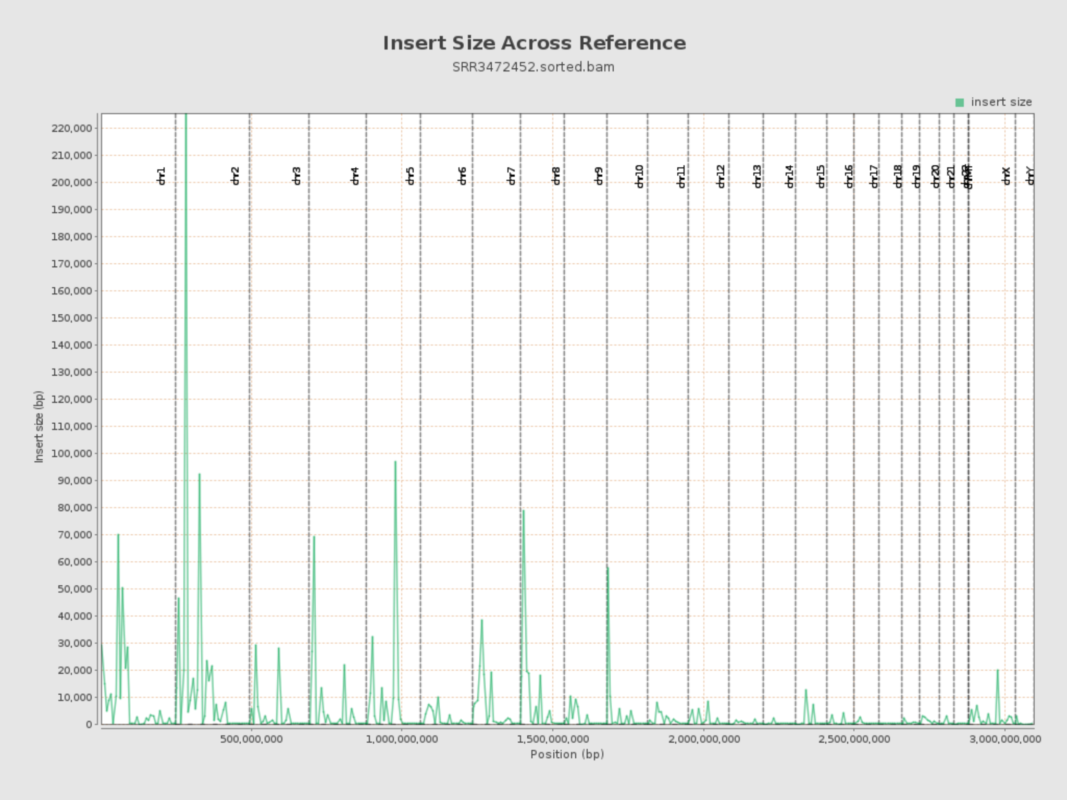
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram