Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 02:01:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472539.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_SRR3472539 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472539_1.fastq.gz SRR3472539_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 02:01:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472539.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,530,364
Mapped reads	18,333,035 / 98.94%
Unmapped reads	197,329 / 1.06%
Mapped paired reads	18,333,035 / 98.94%
Mapped reads, first in pair	9,197,332 / 49.63%
Mapped reads, second in pair	9,135,703 / 49.3%
Mapped reads, both in pair	18,222,274 / 98.34%
Mapped reads, singletons	110,761 / 0.6%
Secondary alignments	0
Supplementary alignments	78,088 / 0.42%
Read min/max/mean length	30 / 100 / 100.17
Duplicated reads (estimated)	11,676,376 / 63.01%
Duplication rate	46.68%
Clipped reads	1,750,872 / 9.45%

2.2. ACGT Content

Number/percentage of A's	486,707,225 / 27.04%
Number/percentage of C's	415,969,932 / 23.11%
Number/percentage of T's	483,908,498 / 26.89%
Number/percentage of G's	413,029,113 / 22.95%
Number/percentage of N's	284,031 / 0.02%

GC Percentage	46.06%

2.3. Coverage

Mean	0.5815
Standard Deviation	18.7127

2.4. Mapping Quality

Mean Mapping Quality	55.19

2.5. Insert size

Mean	31,789.16
Standard Deviation	1,763,145.71
P25/Median/P75	155 / 215 / 290

2.6. Mismatches and indels

General error rate	0.57%
Mismatches	9,993,355
Insertions	87,481
Mapped reads with at least one insertion	0.47%
Deletions	83,430
Mapped reads with at least one deletion	0.45%
Homopolymer indels	44.84%

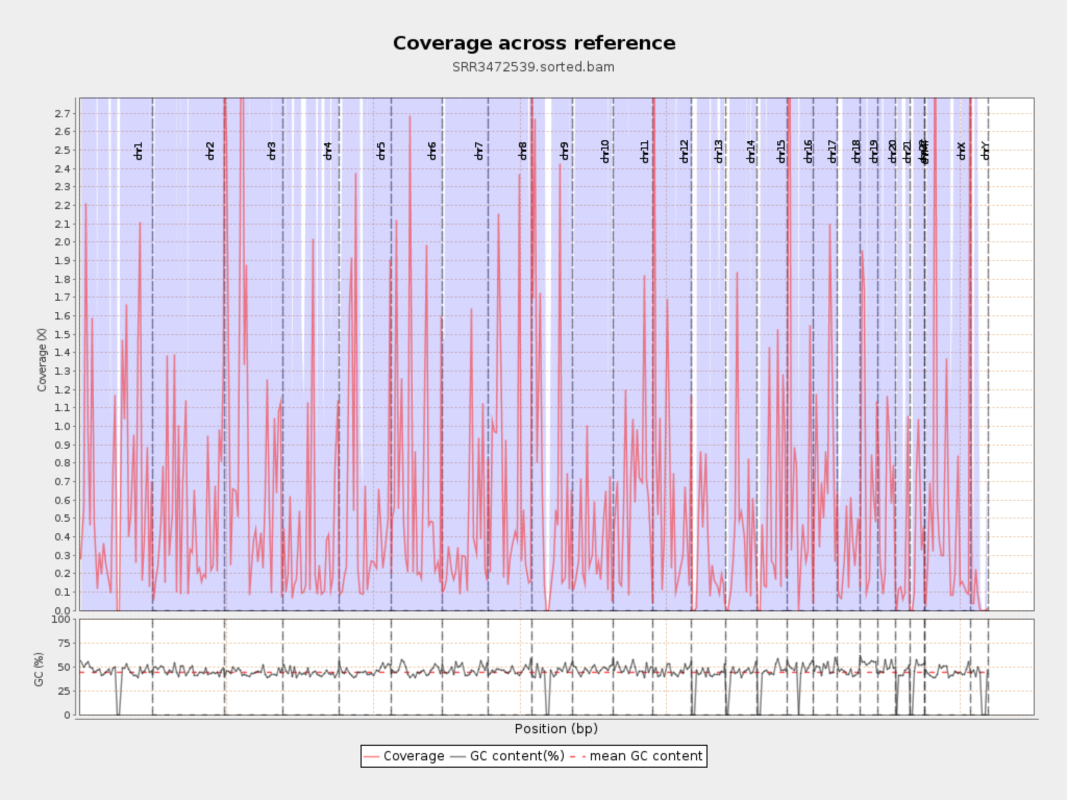
2.7. Chromosome stats

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

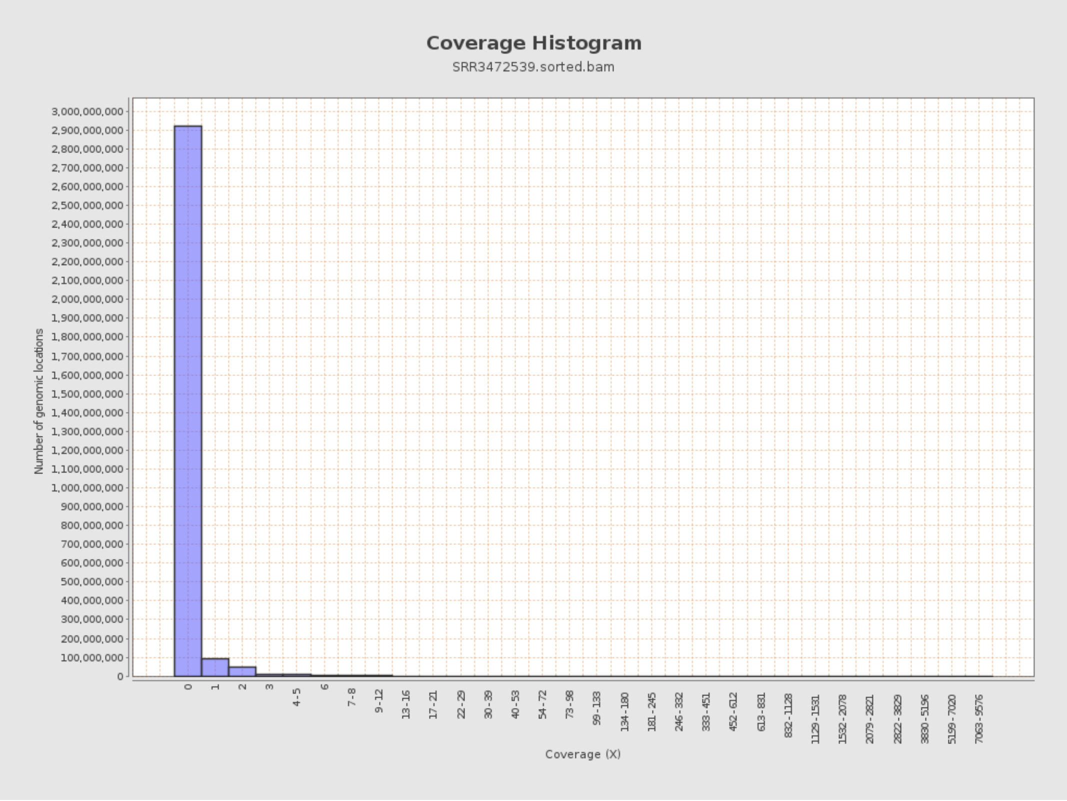
		bases	coverage	deviation
chr1	249250621	171514600	0.6881	22.5659
chr2	243199373	122118846	0.5021	17.6155
chr3	198022430	196675936	0.9932	22.2433
chr4	191154276	72804820	0.3809	14.6382
chr5	180915260	103857016	0.5741	21.347
chr6	171115067	120579540	0.7047	19.5584
chr7	159138663	64903846	0.4078	13.8506
chr8	146364022	99481254	0.6797	21.6663
chr9	141213431	106233273	0.7523	20.8842
chr10	135534747	49429414	0.3647	14.1945
chr11	135006516	89414946	0.6623	19.3691
chr12	133851895	96681432	0.7223	17.7328
chr13	115169878	32225307	0.2798	9.7431
chr14	107349540	46582621	0.4339	16.2861
chr15	102531392	52314803	0.5102	21.6475
chr16	90354753	75016954	0.8302	28.29
chr17	81195210	65375905	0.8052	19.1746
chr18	78077248	24625644	0.3154	11.3747
chr19	59128983	48513738	0.8205	24.5223
chr20	63025520	36483156	0.5789	16.1841
chr21	48129895	11575991	0.2405	11.4842
chr22	51304566	20708610	0.4036	14.1672
chrMT	16571	1636	0.0987	0.4456
chrX	155270560	90045504	0.5799	17.0466

chrY	59373566	2955596	0.0498	1.9744

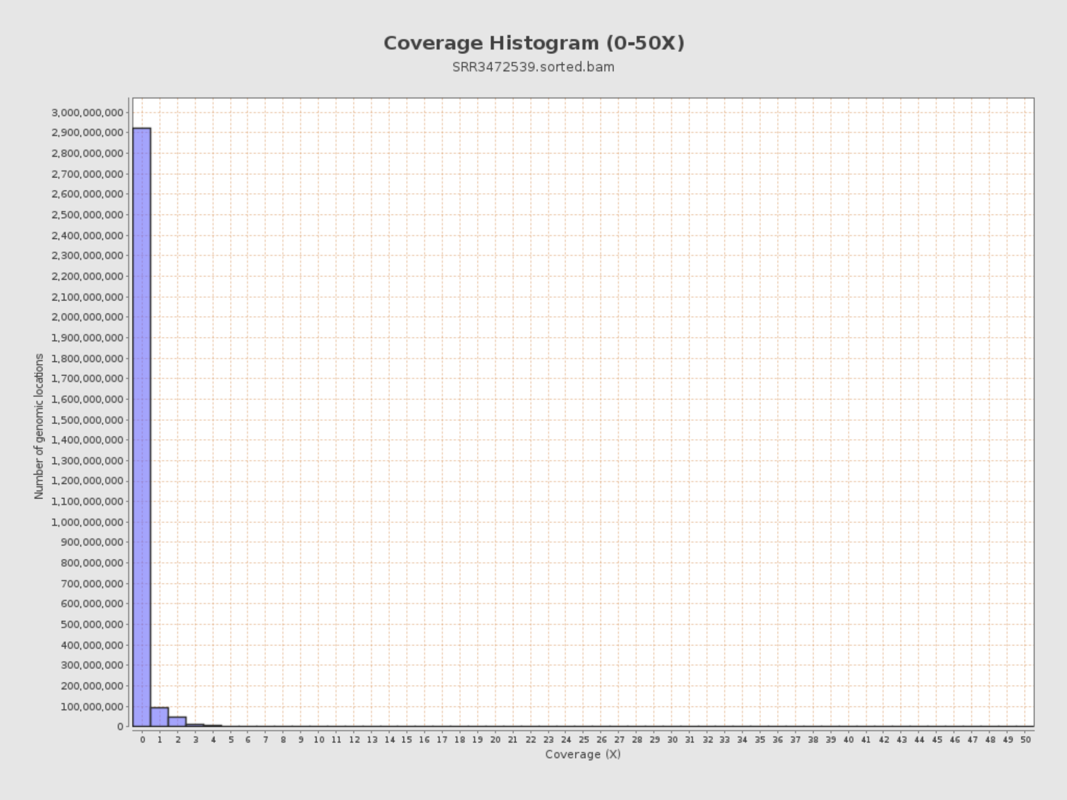
3. Results : Coverage across reference



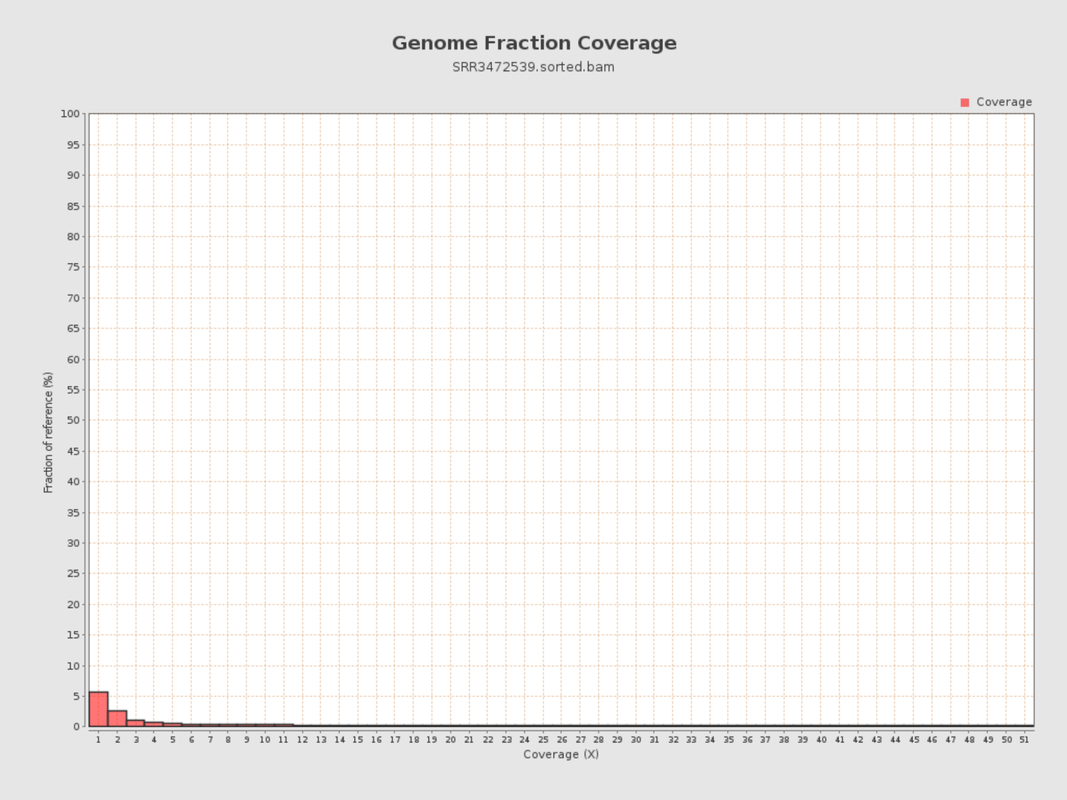
4. Results : Coverage Histogram



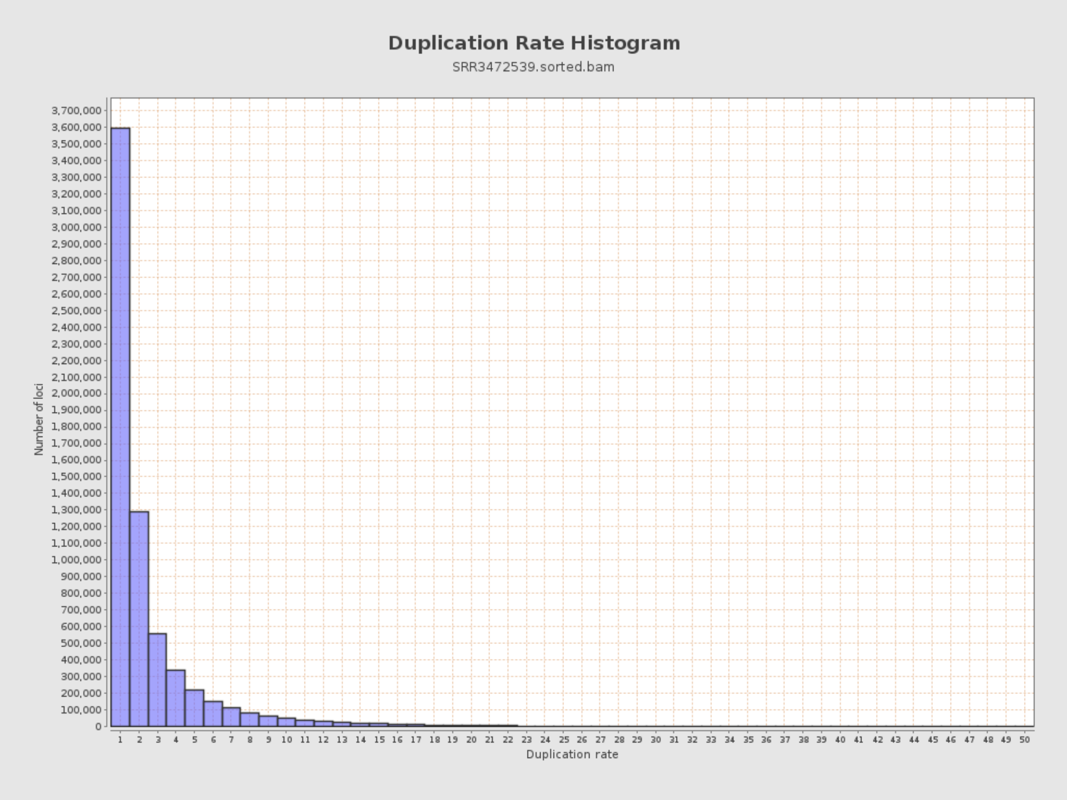
5. Results : Coverage Histogram (0-50X)



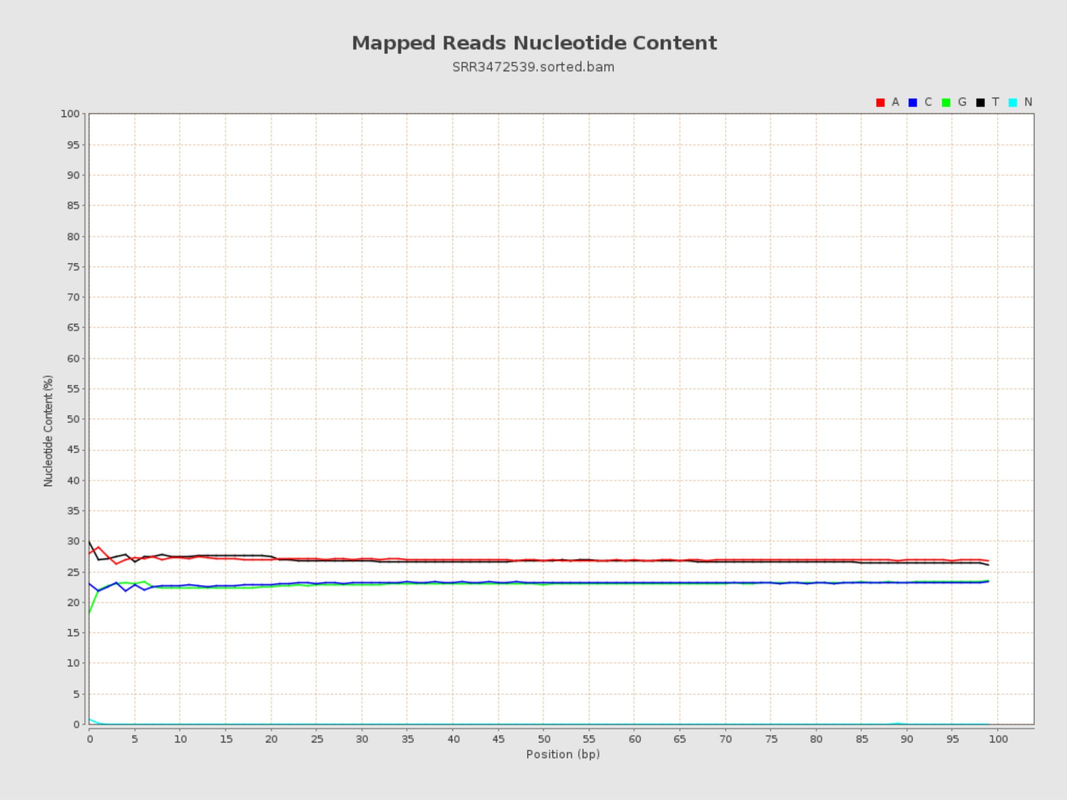
6. Results : Genome Fraction Coverage



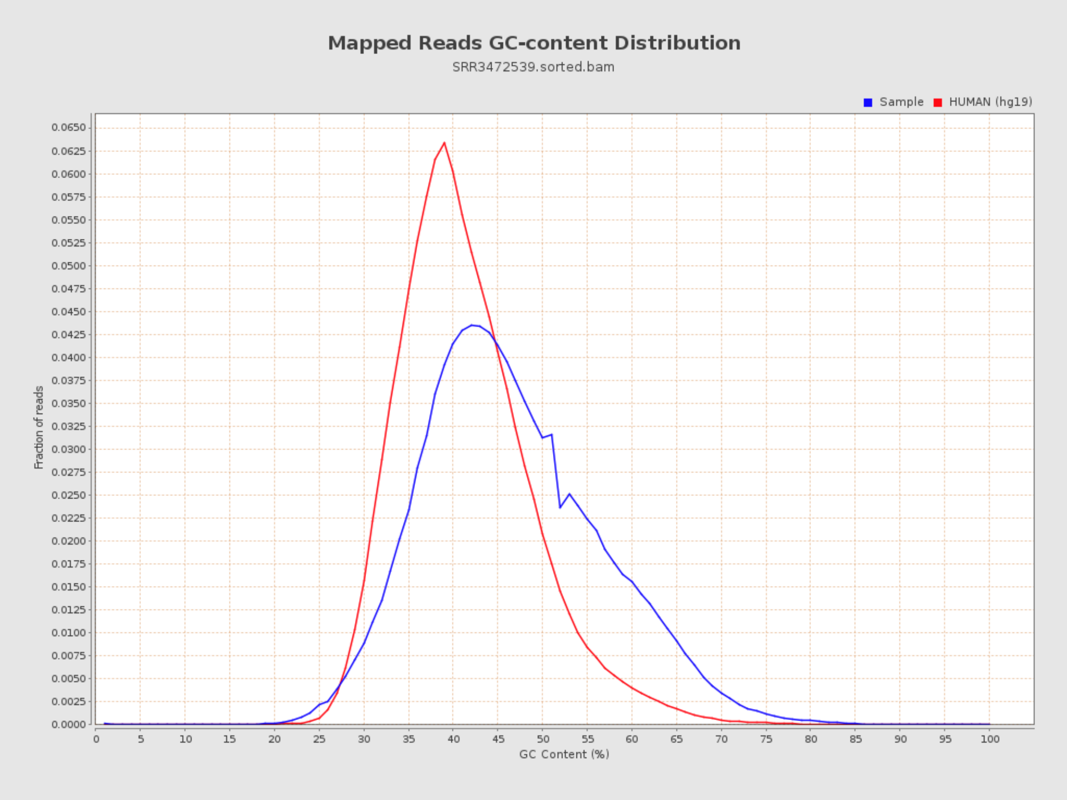
7. Results : Duplication Rate Histogram



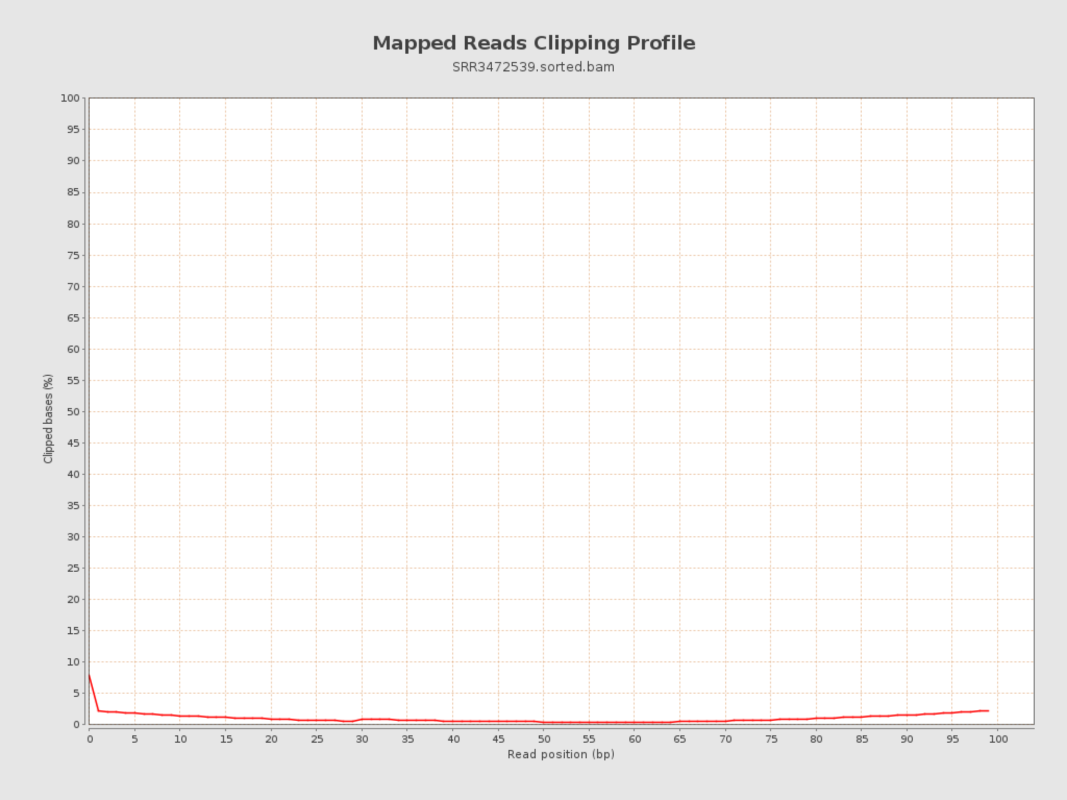
8. Results : Mapped Reads Nucleotide Content



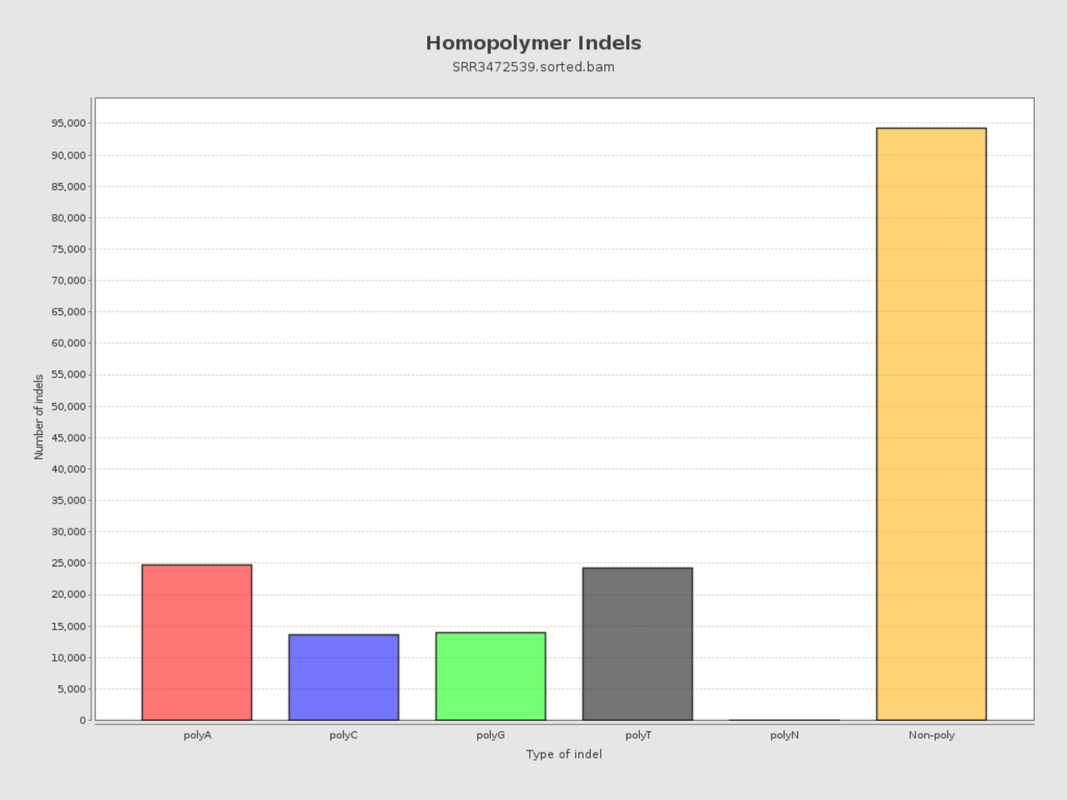
9. Results : Mapped Reads GC-content Distribution



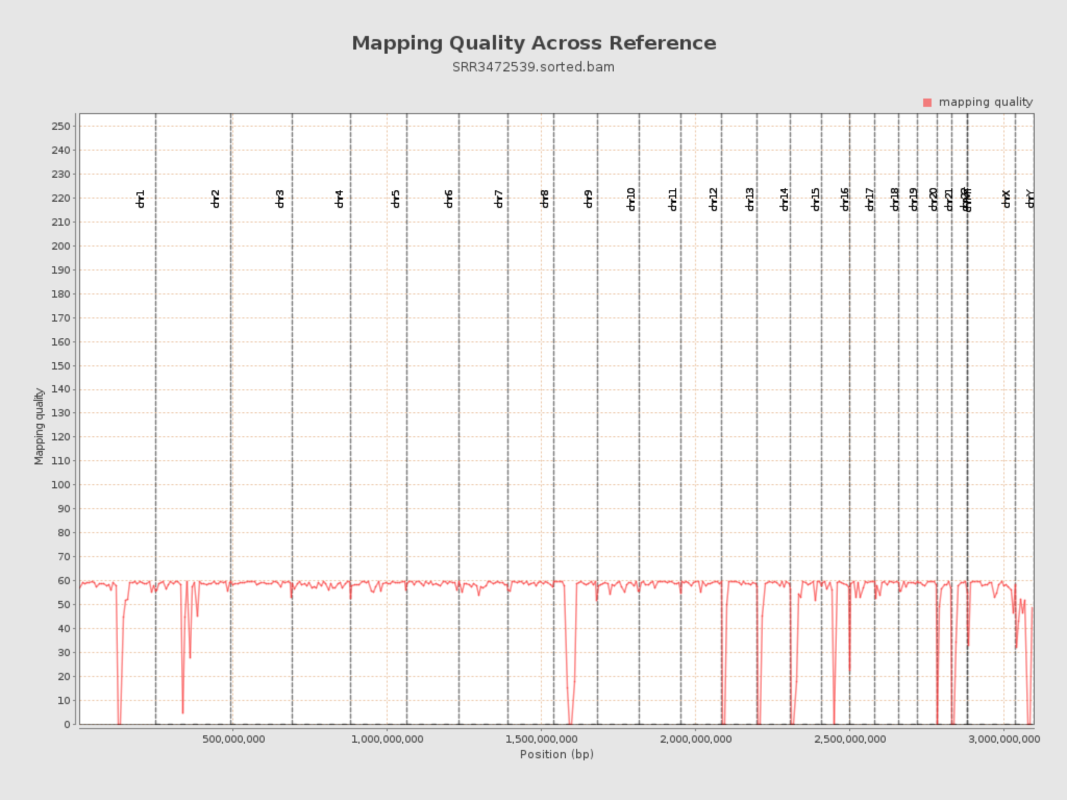
10. Results : Mapped Reads Clipping Profile



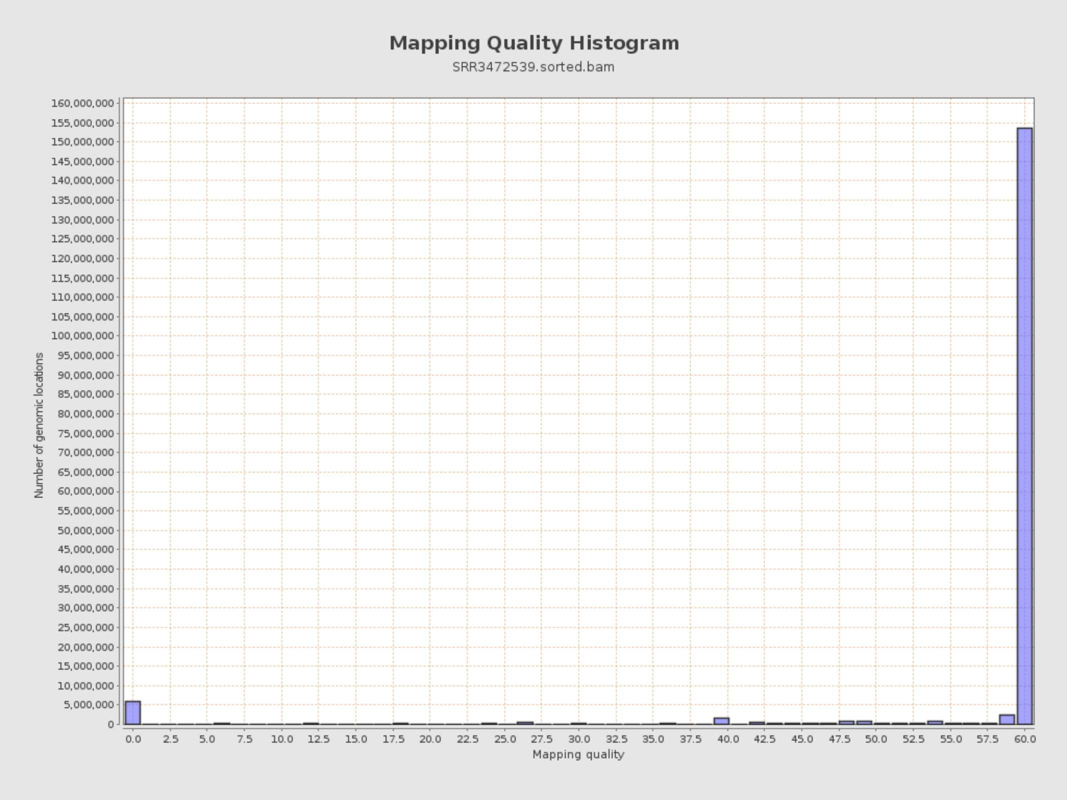
11. Results : Homopolymer Indels



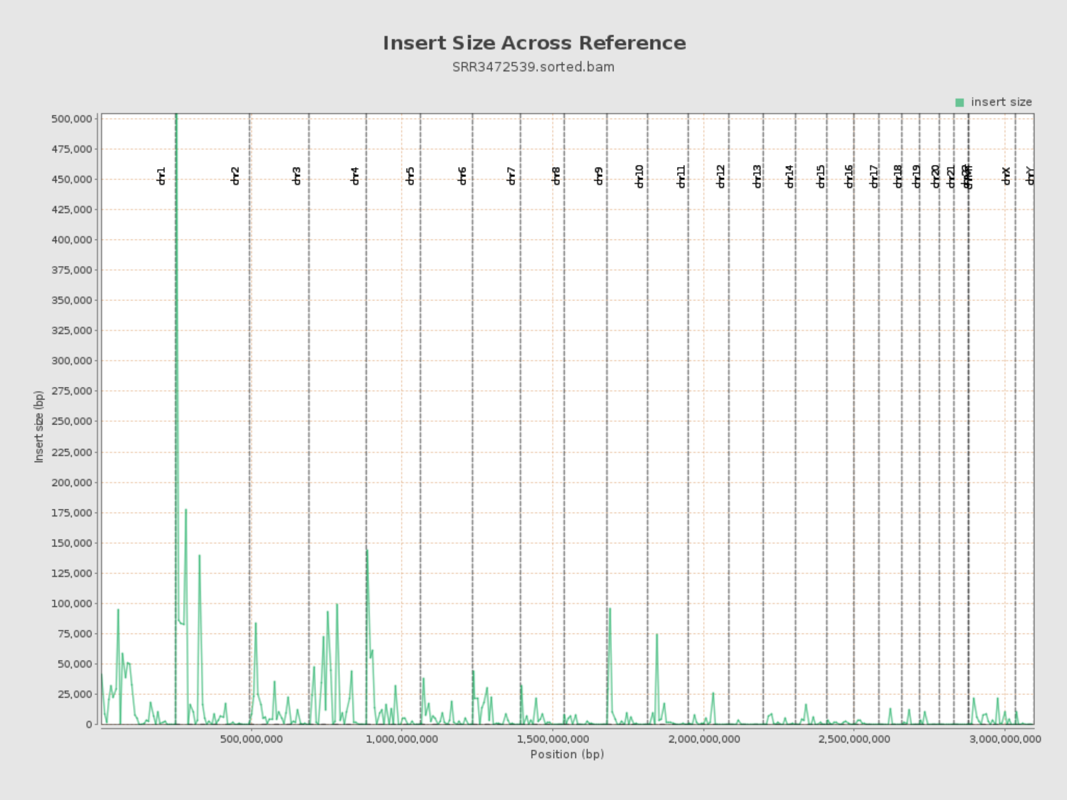
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram