Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 09:26:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472381.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_SRR3472381 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472381_1.fastq.gz SRR3472381_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 09:25:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472381.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,366,332
Mapped reads	20,173,789 / 99.05%
Unmapped reads	192,543 / 0.95%
Mapped paired reads	20,173,789 / 99.05%
Mapped reads, first in pair	10,127,359 / 49.73%
Mapped reads, second in pair	10,046,430 / 49.33%
Mapped reads, both in pair	20,044,088 / 98.42%
Mapped reads, singletons	129,701 / 0.64%
Secondary alignments	0
Supplementary alignments	75,758 / 0.37%
Read min/max/mean length	30 / 100 / 99.5
Duplicated reads (estimated)	12,679,255 / 62.26%
Duplication rate	48.25%
Clipped reads	1,351,722 / 6.64%

2.2. ACGT Content

Number/percentage of A's	534,695,088 / 26.99%
Number/percentage of C's	457,451,125 / 23.09%
Number/percentage of T's	535,582,698 / 27.03%
Number/percentage of G's	453,414,799 / 22.88%
Number/percentage of N's	248,861 / 0.01%

GC Percentage	45.97%

2.3. Coverage

Mean	0.6401
Standard Deviation	17.9791

2.4. Mapping Quality

Mean Mapping Quality	54.97

2.5. Insert size

Mean	19,625.95
Standard Deviation	1,392,295.01
P25/Median/P75	160 / 220 / 295

2.6. Mismatches and indels

General error rate	0.57%
Mismatches	11,134,111
Insertions	117,972
Mapped reads with at least one insertion	0.58%
Deletions	94,606
Mapped reads with at least one deletion	0.46%
Homopolymer indels	45.62%

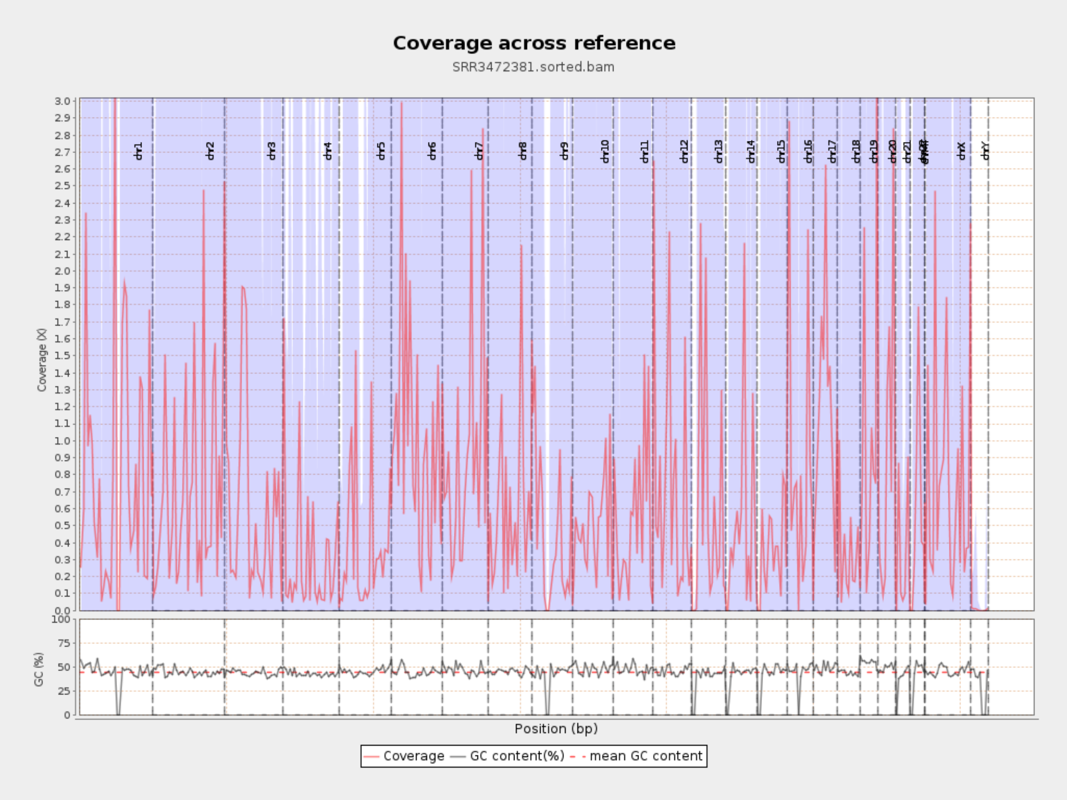
2.7. Chromosome stats

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

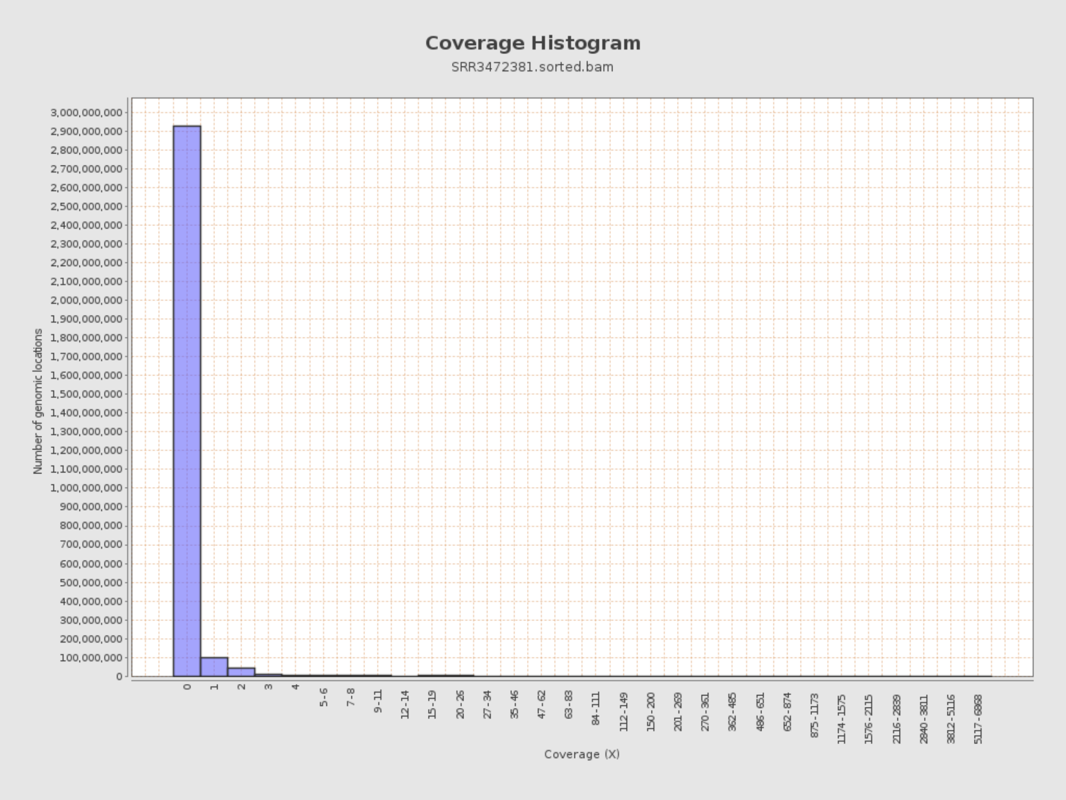
		bases	coverage	deviation
chr1	249250621	204846622	0.8218	24.7744
chr2	243199373	168605196	0.6933	19.37
chr3	198022430	125279377	0.6327	13.1569
chr4	191154276	56349458	0.2948	11.3284
chr5	180915260	70589171	0.3902	11.8719
chr6	171115067	168755117	0.9862	22.8376
chr7	159138663	150737278	0.9472	24.5477
chr8	146364022	88377613	0.6038	14.477
chr9	141213431	65565781	0.4643	9.9751
chr10	135534747	67388344	0.4972	15.7216
chr11	135006516	73651847	0.5455	16.5809
chr12	133851895	102907617	0.7688	17.9138
chr13	115169878	70322353	0.6106	20.283
chr14	107349540	52509158	0.4891	19.7415
chr15	102531392	36490326	0.3559	10.1153
chr16	90354753	81878565	0.9062	19.0022
chr17	81195210	97689483	1.2031	24.0148
chr18	78077248	26081432	0.334	10.1941
chr19	59128983	54836939	0.9274	19.7665
chr20	63025520	57870948	0.9182	26.8742
chr21	48129895	16724193	0.3475	17.8562
chr22	51304566	28926860	0.5638	17.6765
chrMT	16571	10548	0.6365	1.0602
chrX	155270560	114896793	0.74	16.2965

chrY	59373566	330337	0.0056	0.3781

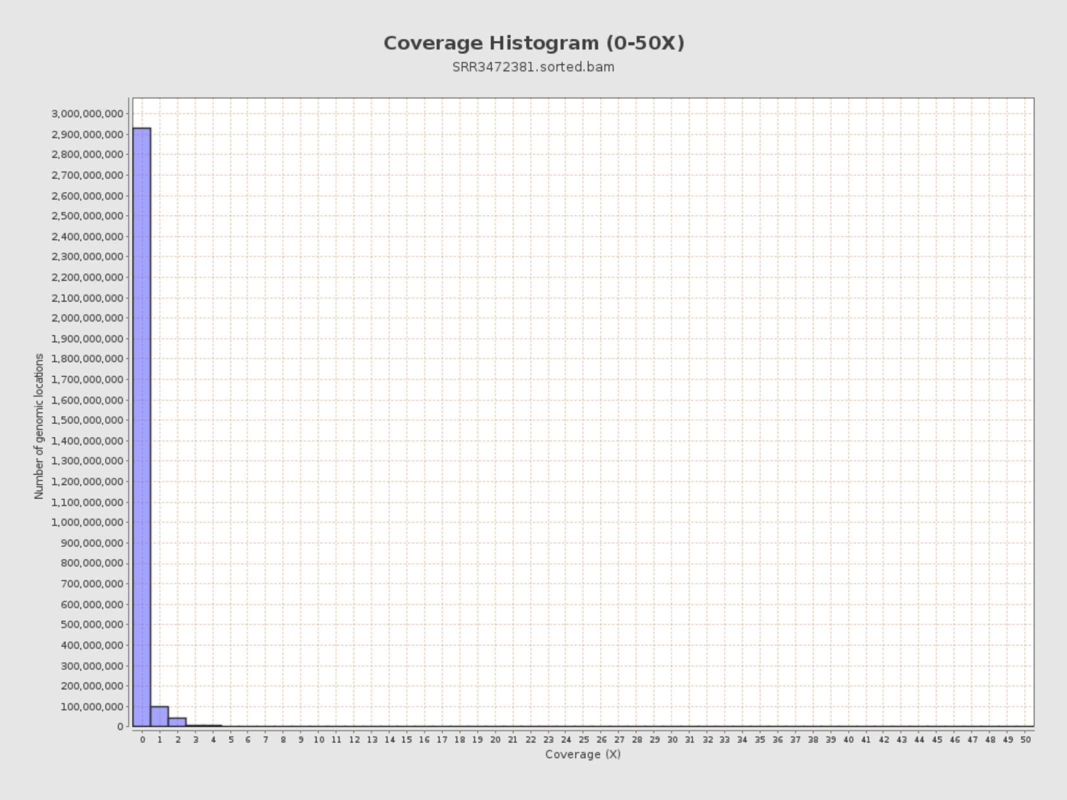
3. Results : Coverage across reference



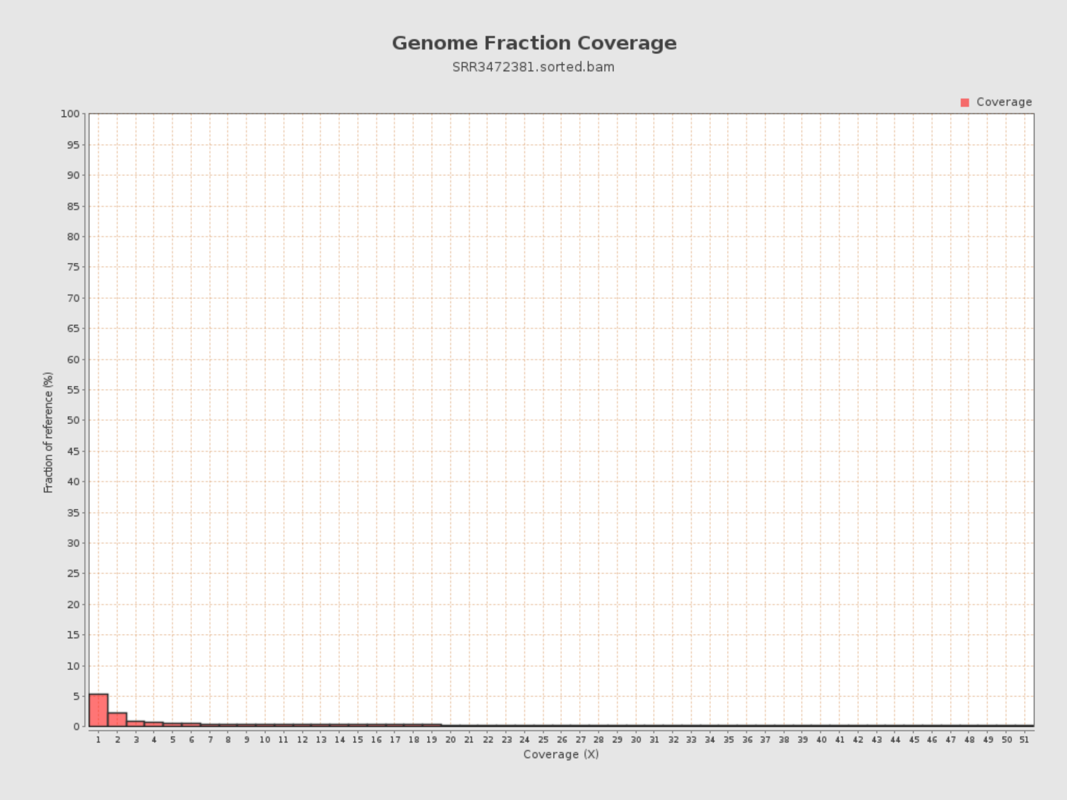
4. Results : Coverage Histogram



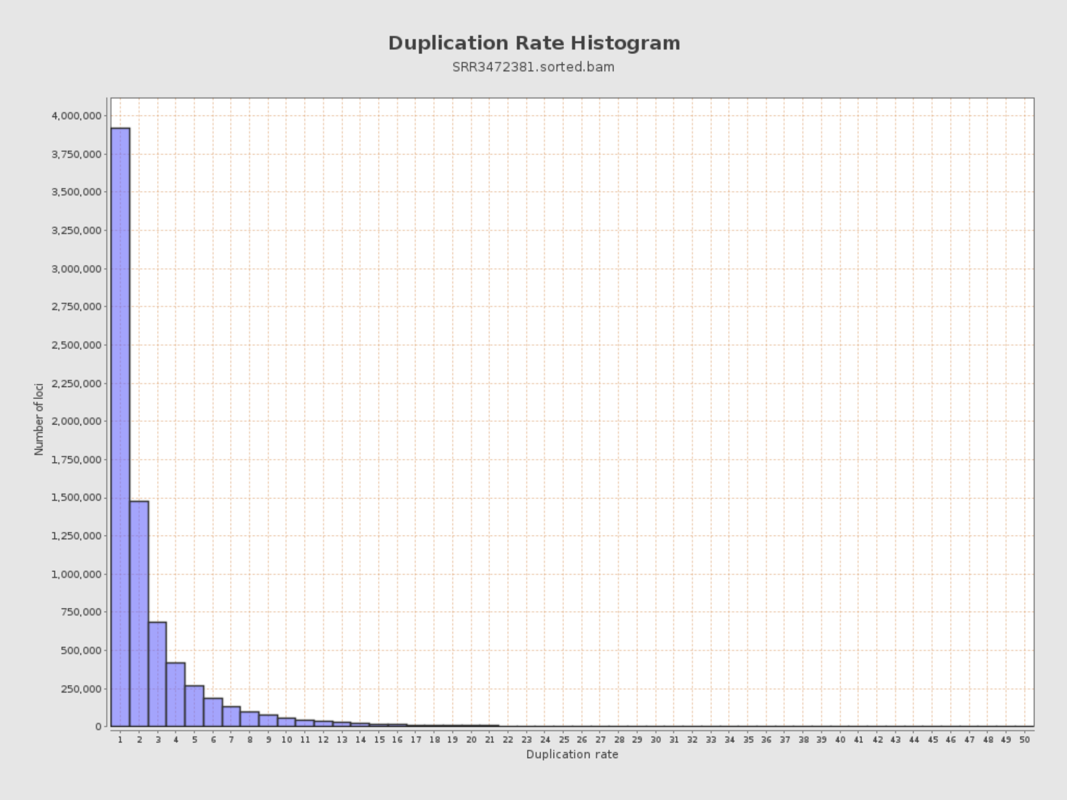
5. Results : Coverage Histogram (0-50X)



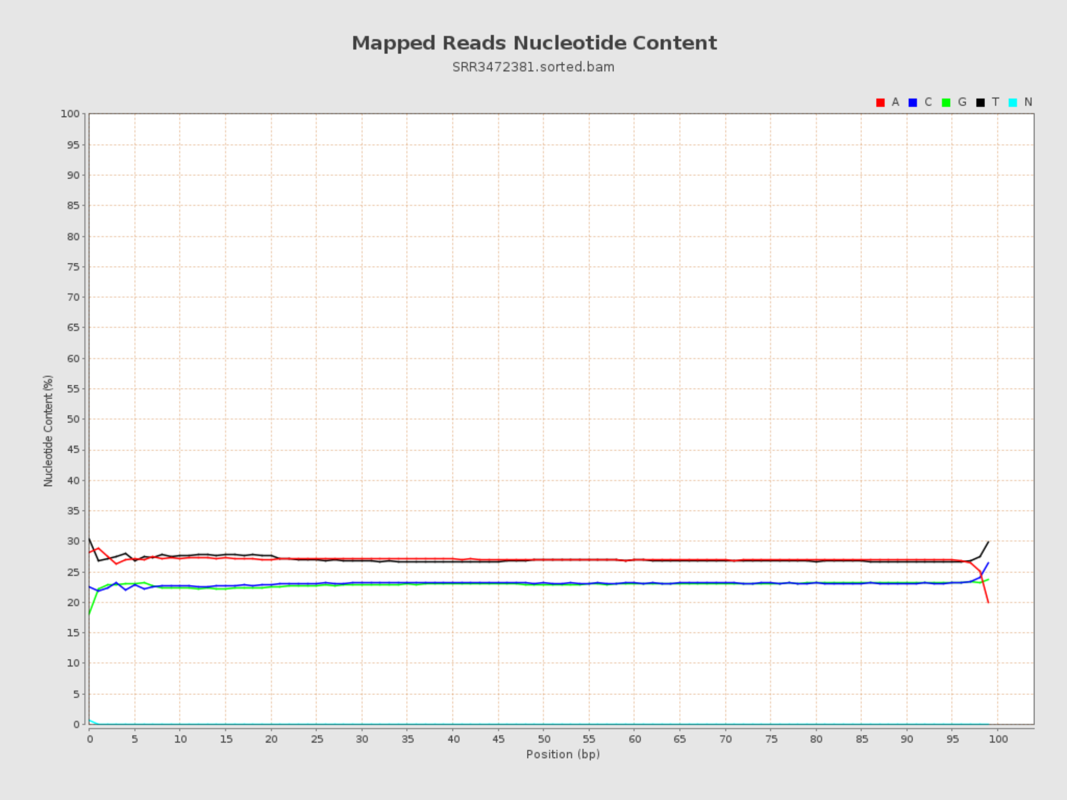
6. Results : Genome Fraction Coverage



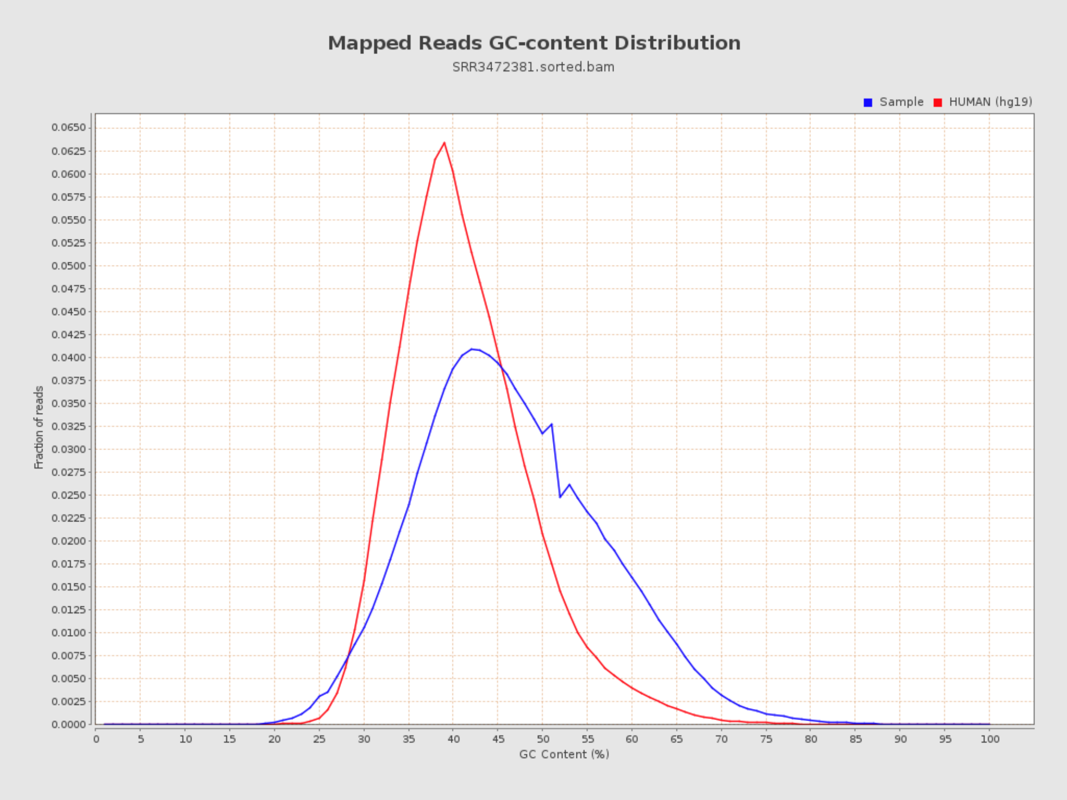
7. Results : Duplication Rate Histogram



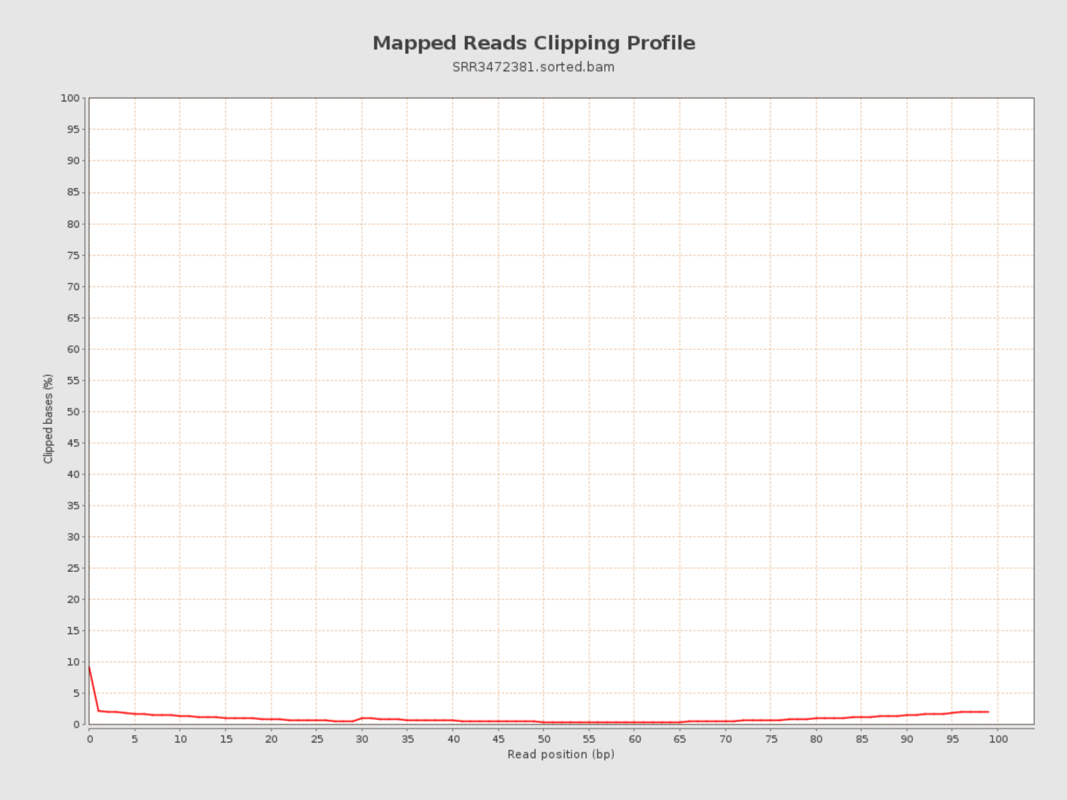
8. Results : Mapped Reads Nucleotide Content



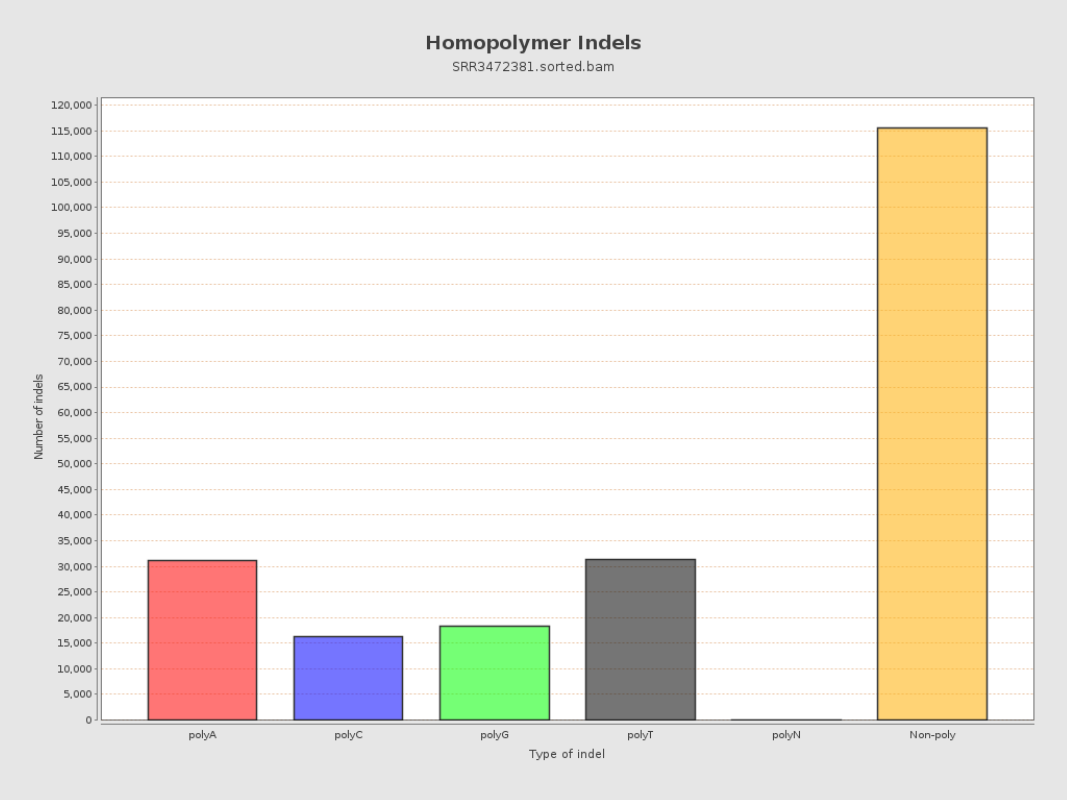
9. Results : Mapped Reads GC-content Distribution



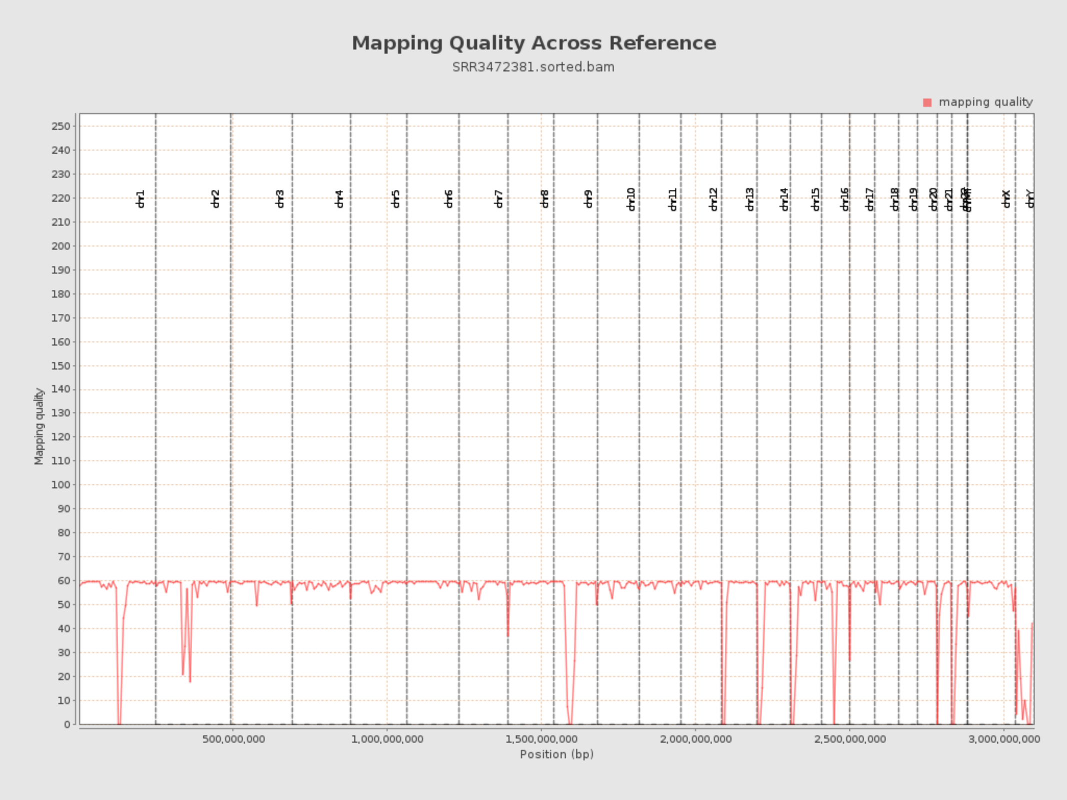
10. Results : Mapped Reads Clipping Profile



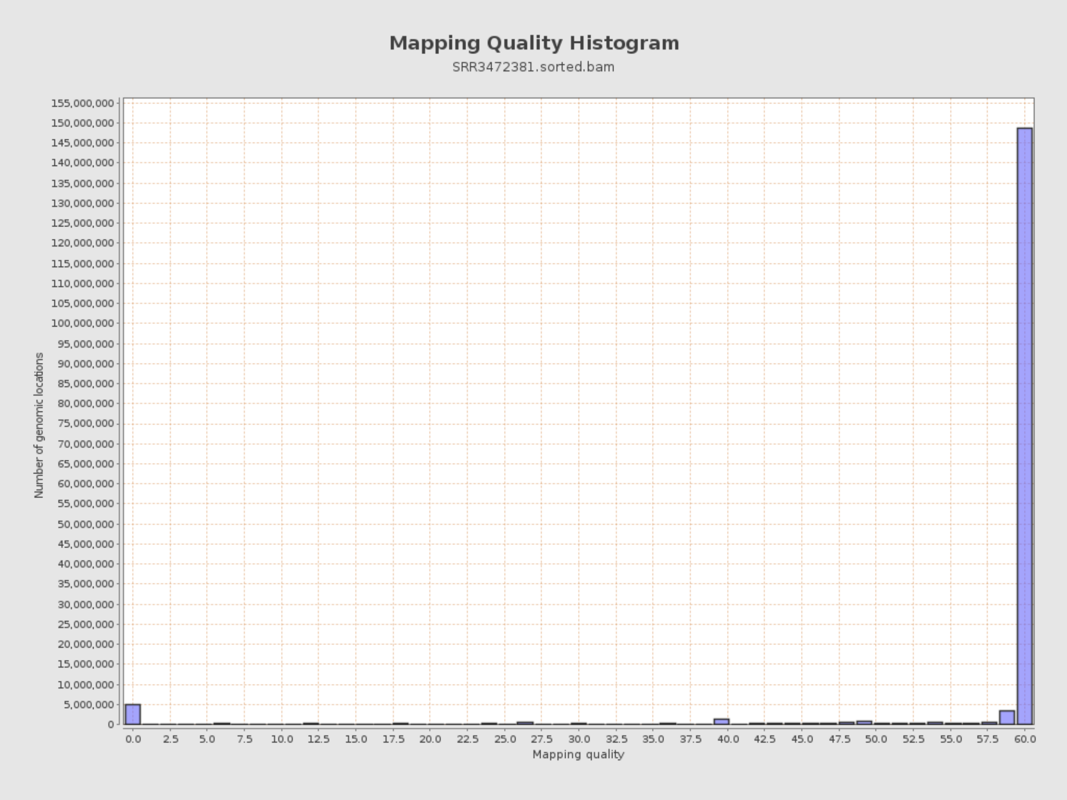
11. Results : Homopolymer Indels



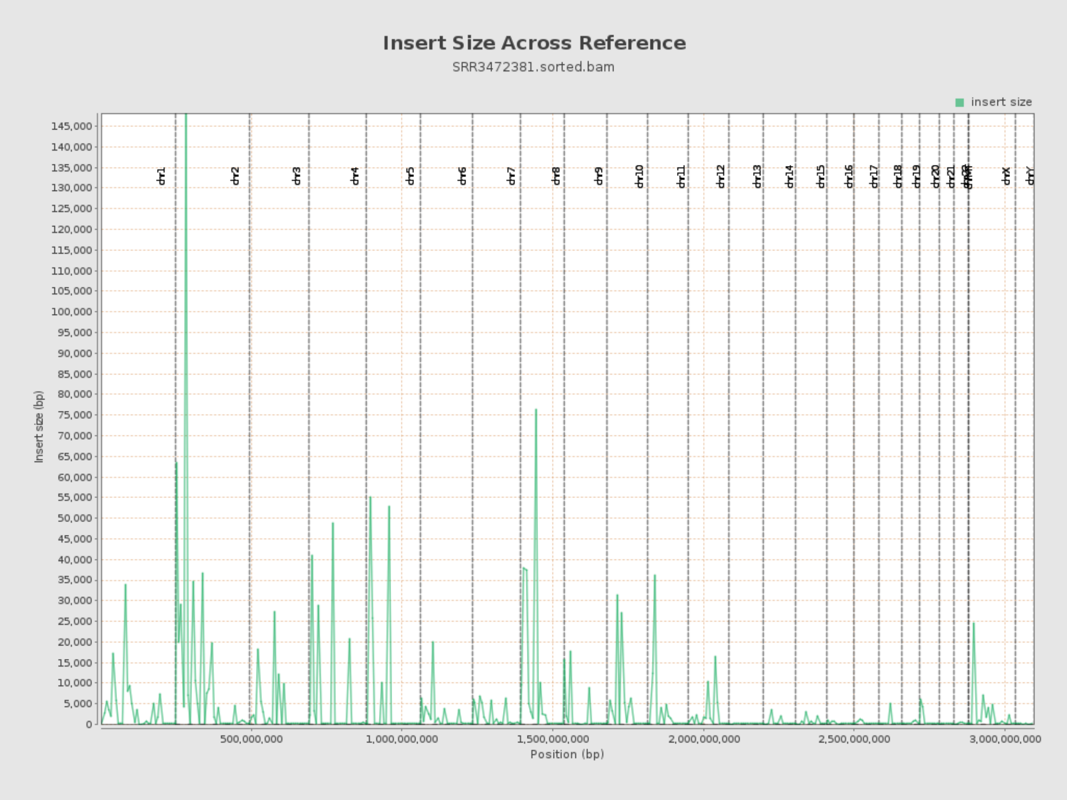
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram