Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 10:56:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472422.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_SRR3472422 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472422_1.fastq.gz SRR3472422_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 10:56:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472422.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,636,010
Mapped reads	18,370,128 / 98.57%
Unmapped reads	265,882 / 1.43%
Mapped paired reads	18,370,128 / 98.57%
Mapped reads, first in pair	9,256,838 / 49.67%
Mapped reads, second in pair	9,113,290 / 48.9%
Mapped reads, both in pair	18,184,278 / 97.58%
Mapped reads, singletons	185,850 / 1%
Secondary alignments	0
Supplementary alignments	28,260 / 0.15%
Read min/max/mean length	30 / 100 / 99.42
Duplicated reads (estimated)	9,836,695 / 52.78%
Duplication rate	44.87%
Clipped reads	1,007,209 / 5.4%

2.2. ACGT Content

Number/percentage of A's	513,802,810 / 28.44%
Number/percentage of C's	390,601,236 / 21.62%
Number/percentage of T's	514,967,536 / 28.51%
Number/percentage of G's	386,695,954 / 21.41%
Number/percentage of N's	238,462 / 0.01%

GC Percentage	43.03%

2.3. Coverage

Mean	0.5836
Standard Deviation	11.4594

2.4. Mapping Quality

Mean Mapping Quality	54.91

2.5. Insert size

Mean	36,689.34
Standard Deviation	1,912,259.07
P25/Median/P75	169 / 236 / 324

2.6. Mismatches and indels

General error rate	0.57%
Mismatches	10,128,737
Insertions	85,479
Mapped reads with at least one insertion	0.46%
Deletions	107,331
Mapped reads with at least one deletion	0.58%
Homopolymer indels	45.44%

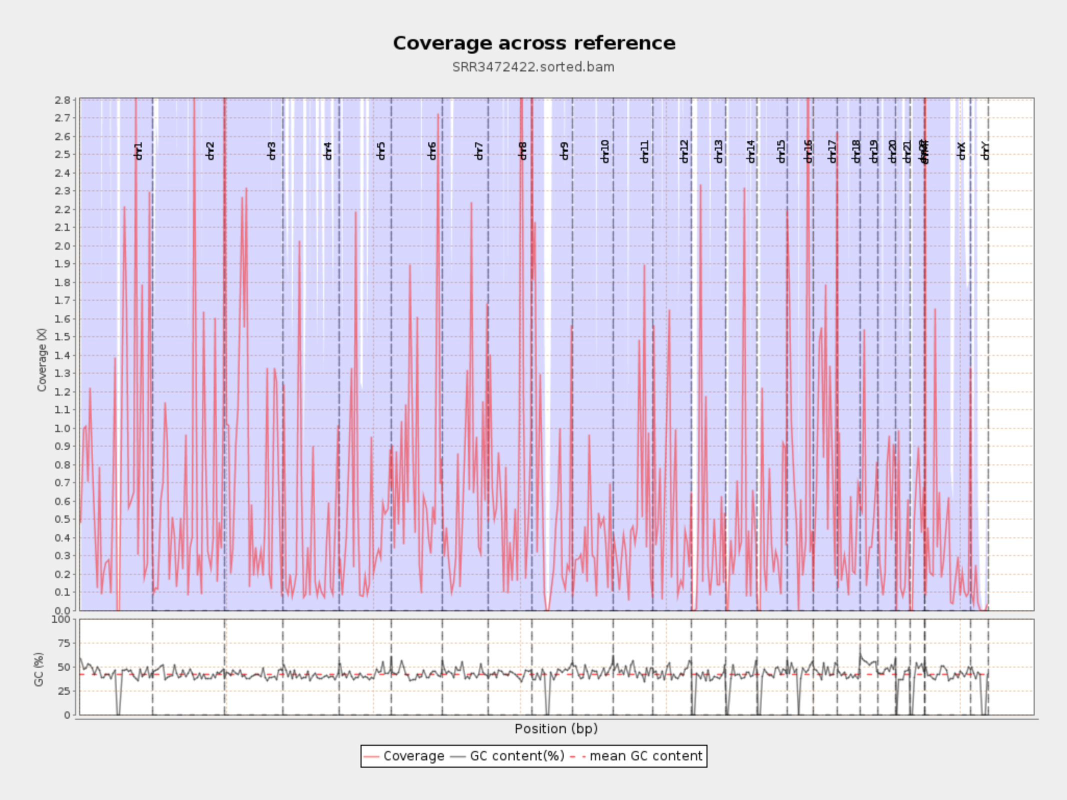
2.7. Chromosome stats

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

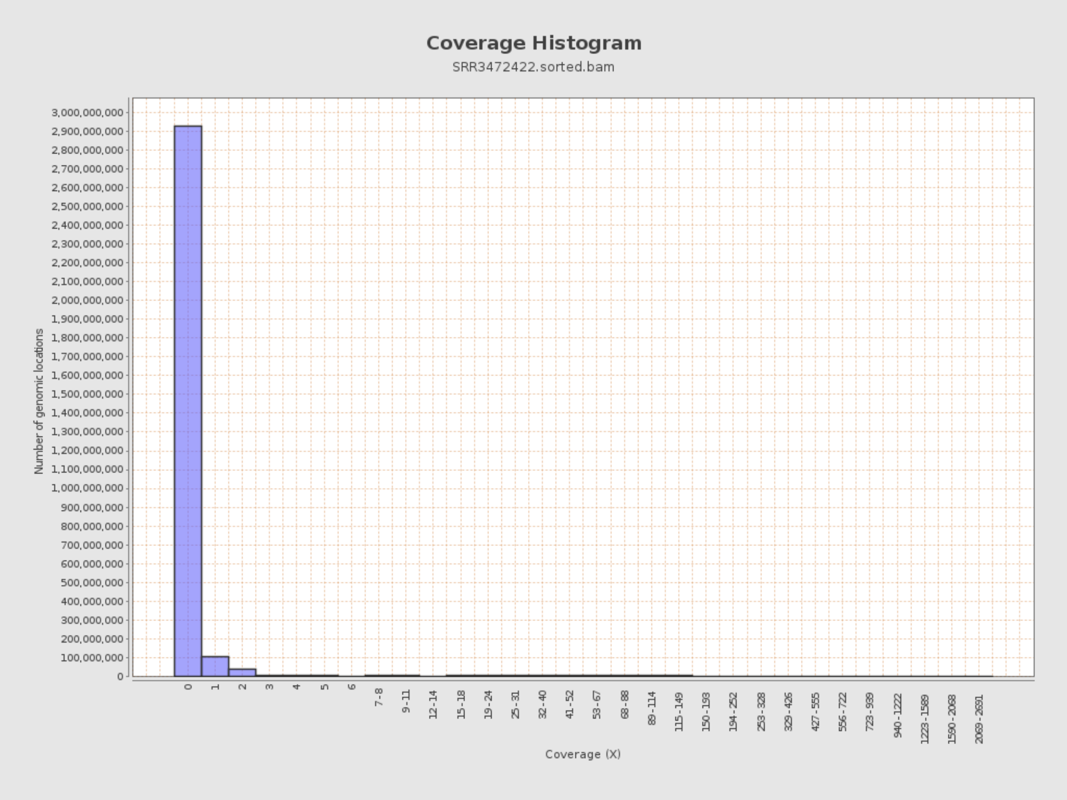
		bases	**coverage**	**deviation**
chr1	249250621	202070670	0.8107	14.3288
chr2	243199373	138771008	0.5706	12.1834
chr3	198022430	165178611	0.8341	12.8472
chr4	191154276	70057289	0.3665	9.3222
chr5	180915260	90602071	0.5008	10.3847
chr6	171115067	133382055	0.7795	12.4967
chr7	159138663	109749682	0.6896	14.0936
chr8	146364022	110769478	0.7568	13.5201
chr9	141213431	88803596	0.6289	10.5075
chr10	135534747	47994525	0.3541	8.1289
chr11	135006516	70211755	0.5201	11.1344
chr12	133851895	76843666	0.5741	9.4486
chr13	115169878	49992935	0.4341	11.1305
chr14	107349540	48382408	0.4507	9.2964
chr15	102531392	42919706	0.4186	9.9641
chr16	90354753	82603665	0.9142	16.8728
chr17	81195210	82879548	1.0207	15.5664
chr18	78077248	30644501	0.3925	7.9293
chr19	59128983	34934892	0.5908	8.0899
chr20	63025520	32709876	0.519	9.8141
chr21	48129895	15694069	0.3261	13.0766
chr22	51304566	24974923	0.4868	10.0853
chrMT	16571	1513593	91.3399	19.8794
chrX	155270560	51532589	0.3319	5.2364

chrY	59373566	3337825	0.0562	1.7083

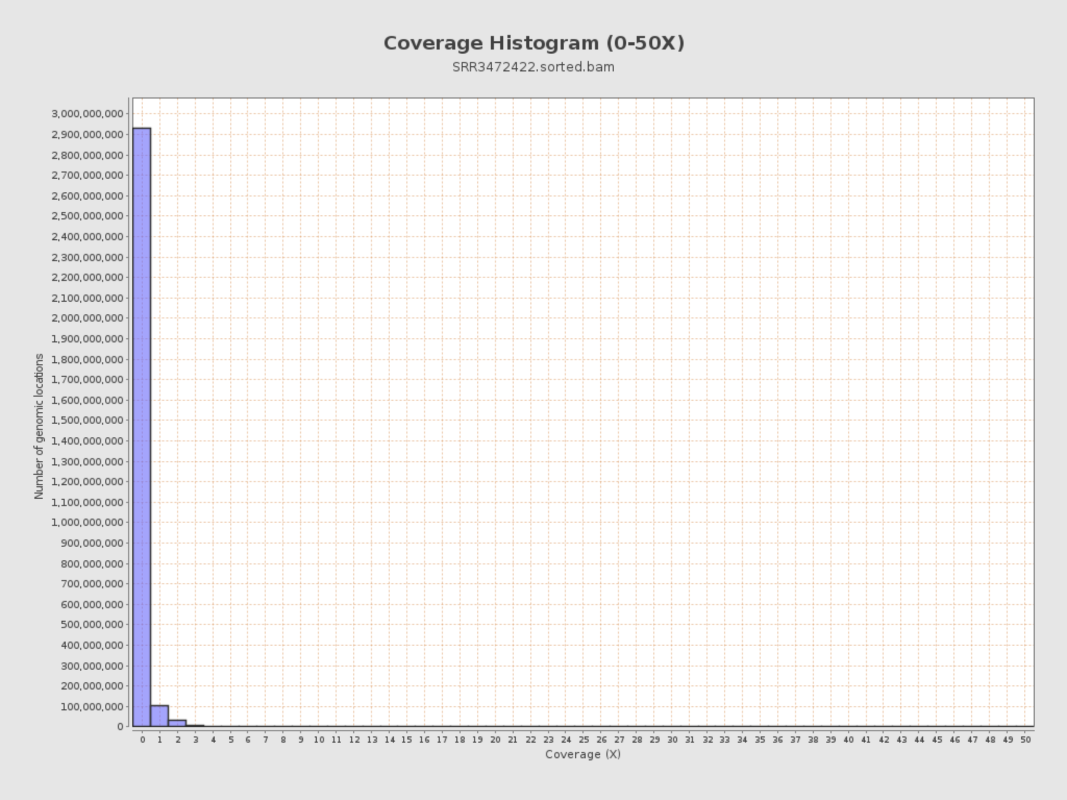
3. Results : Coverage across reference



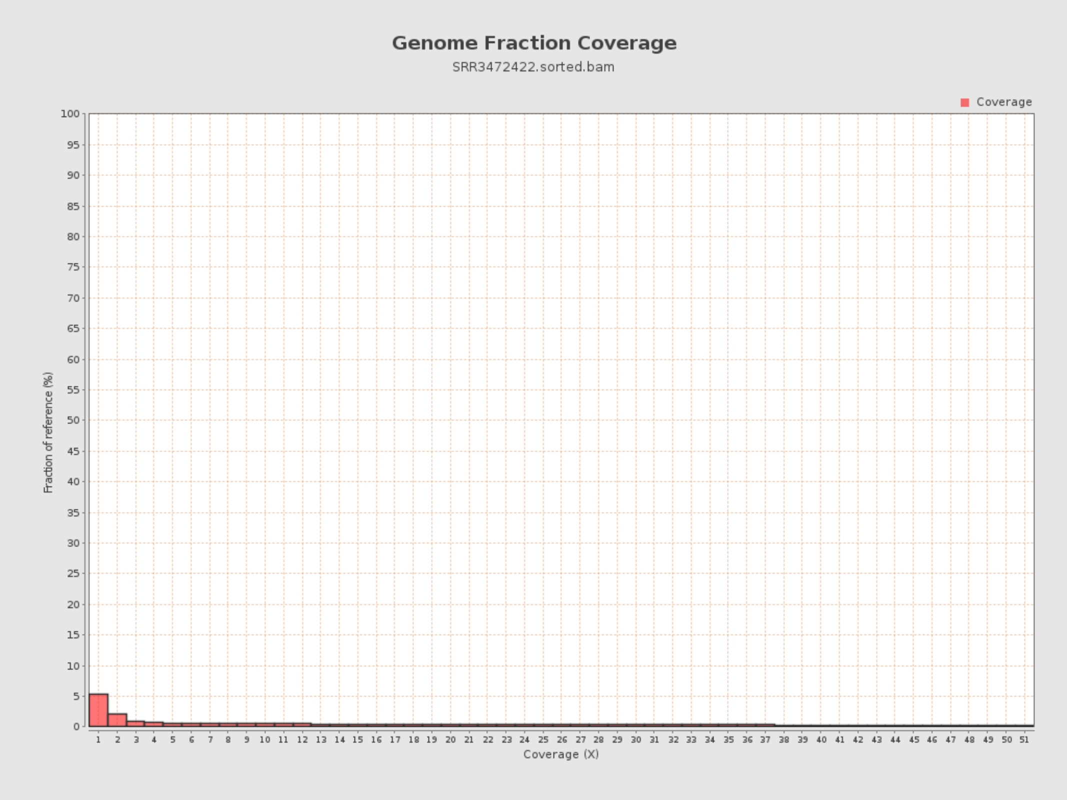
4. Results : Coverage Histogram



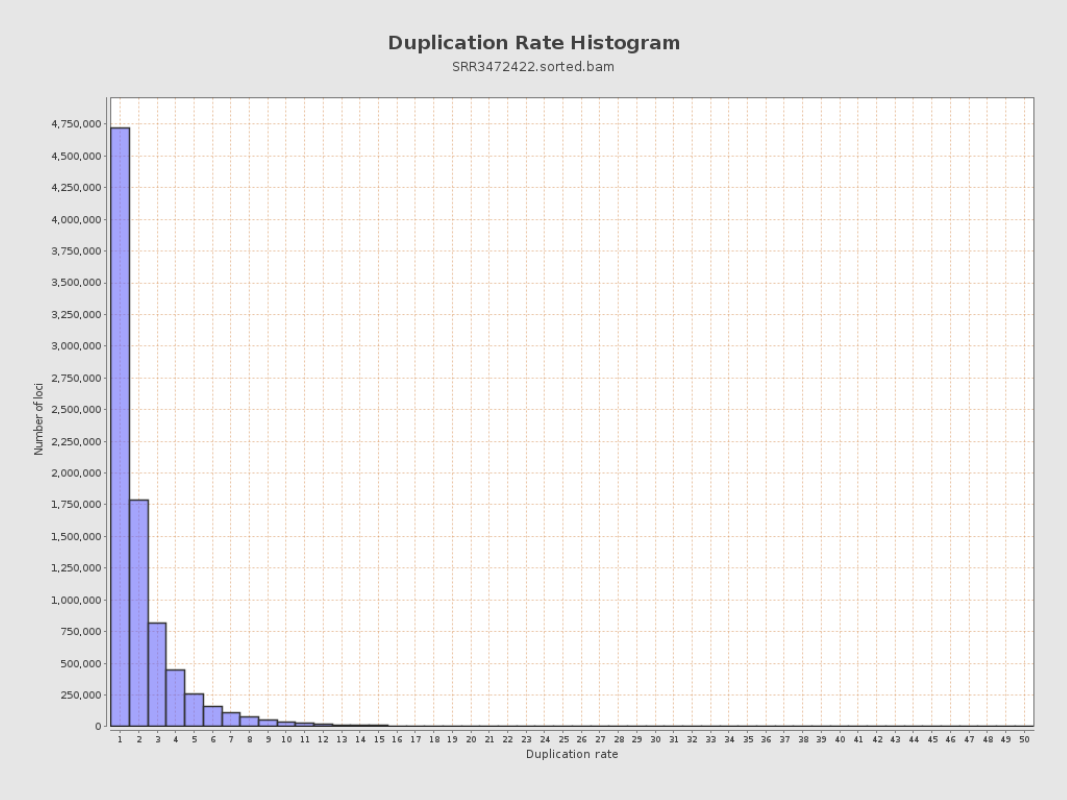
5. Results : Coverage Histogram (0-50X)



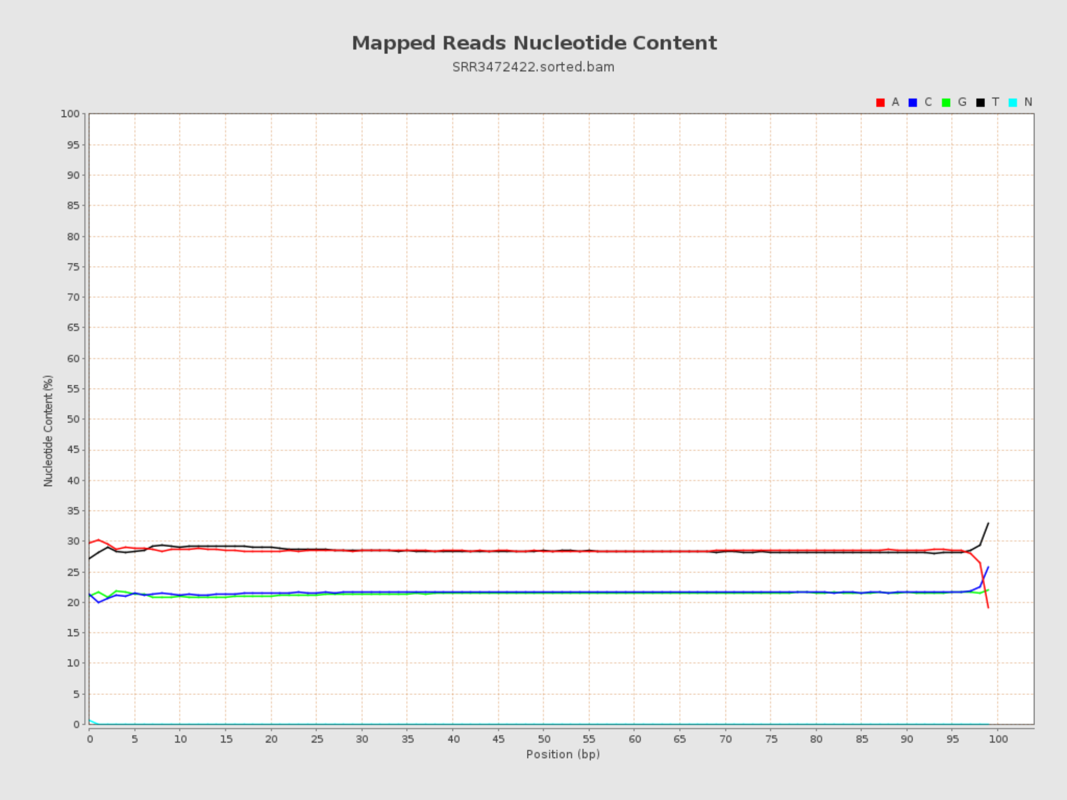
6. Results : Genome Fraction Coverage



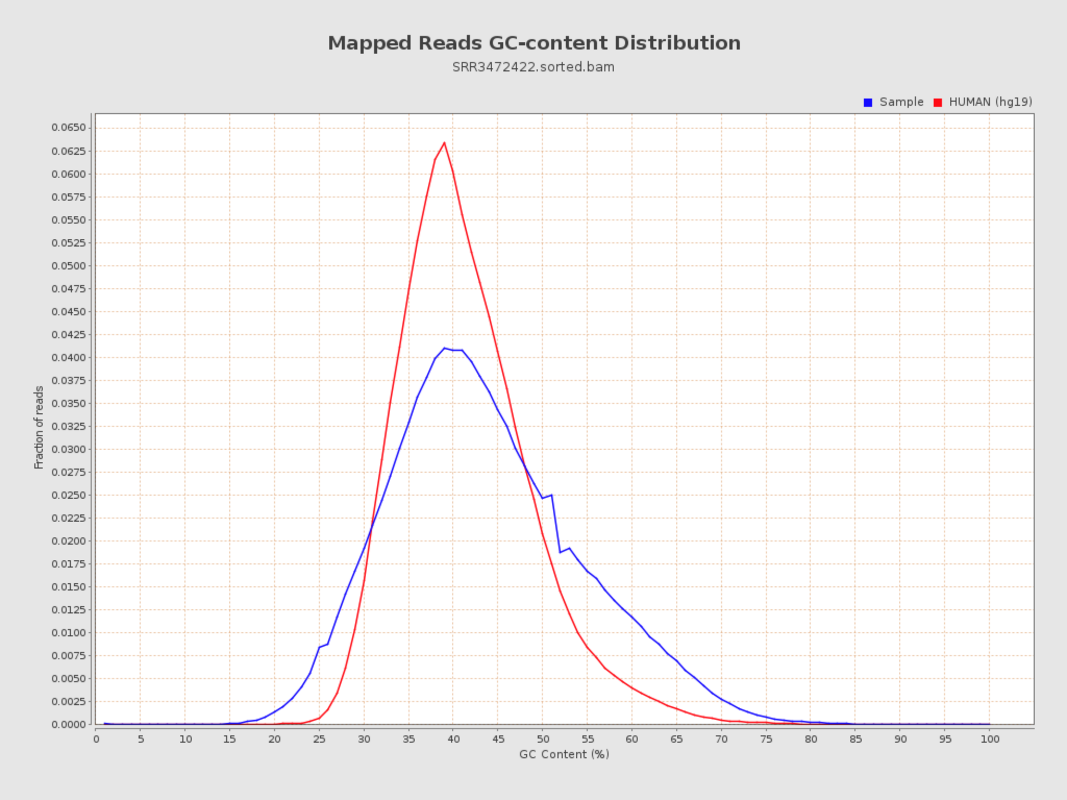
7. Results : Duplication Rate Histogram



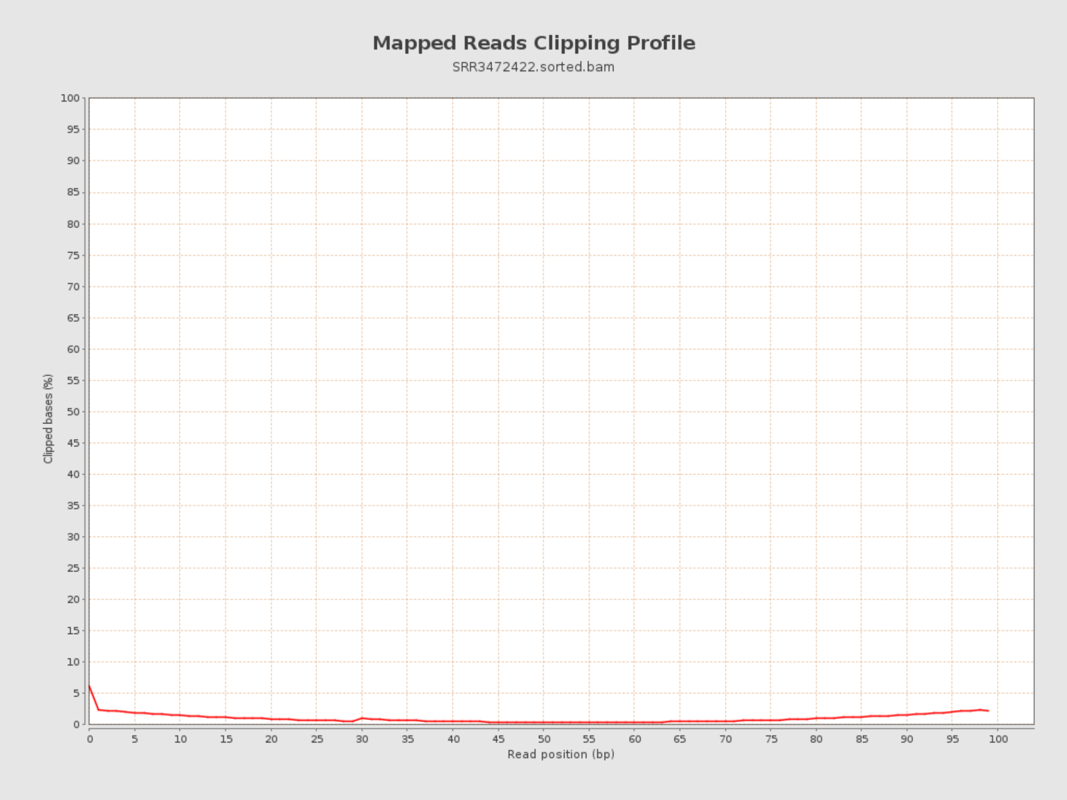
8. Results : Mapped Reads Nucleotide Content



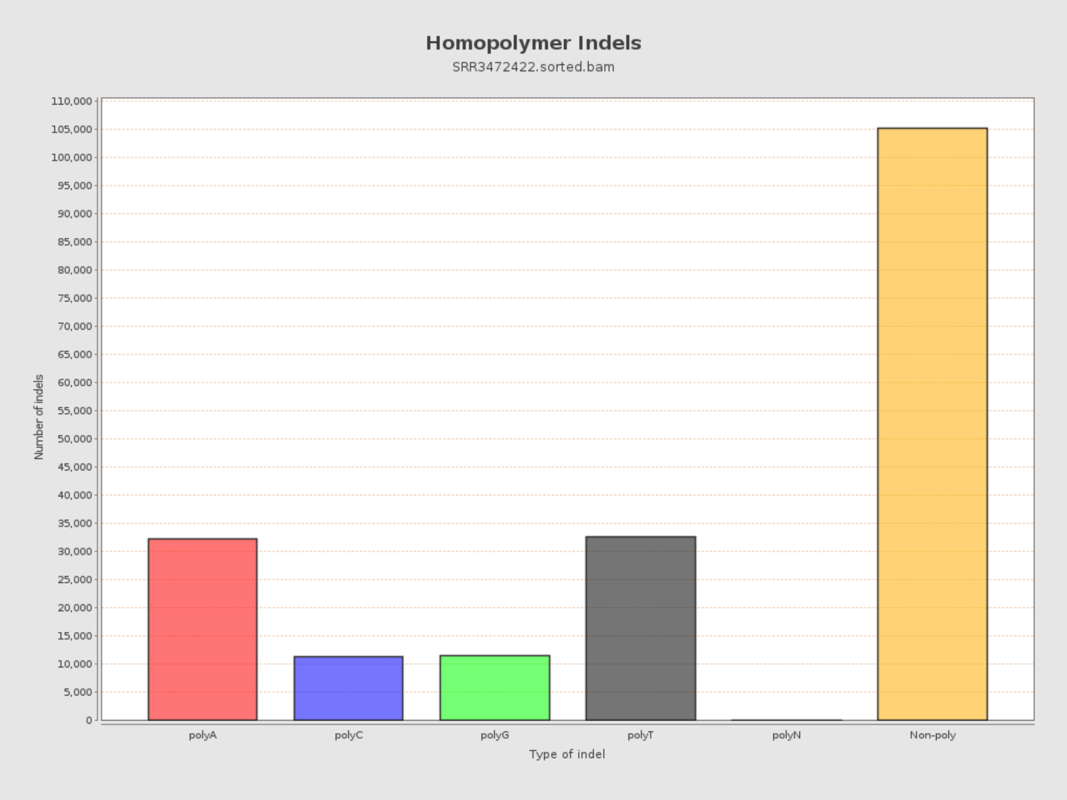
9. Results : Mapped Reads GC-content Distribution



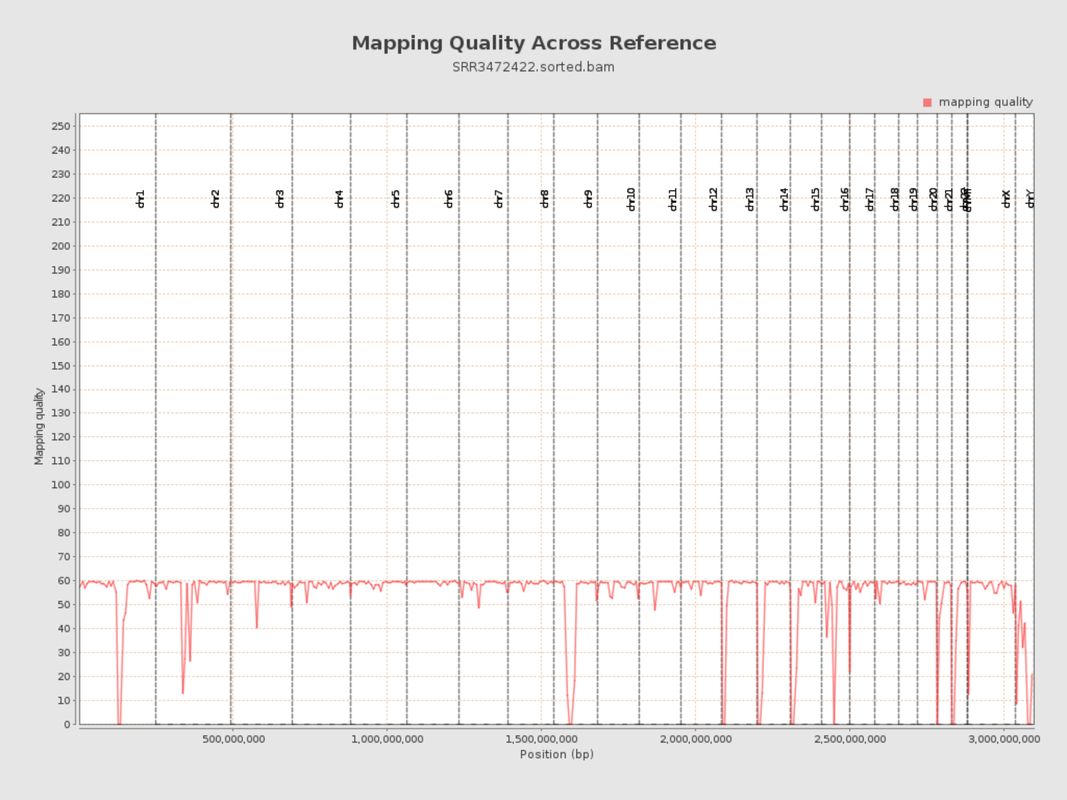
10. Results : Mapped Reads Clipping Profile



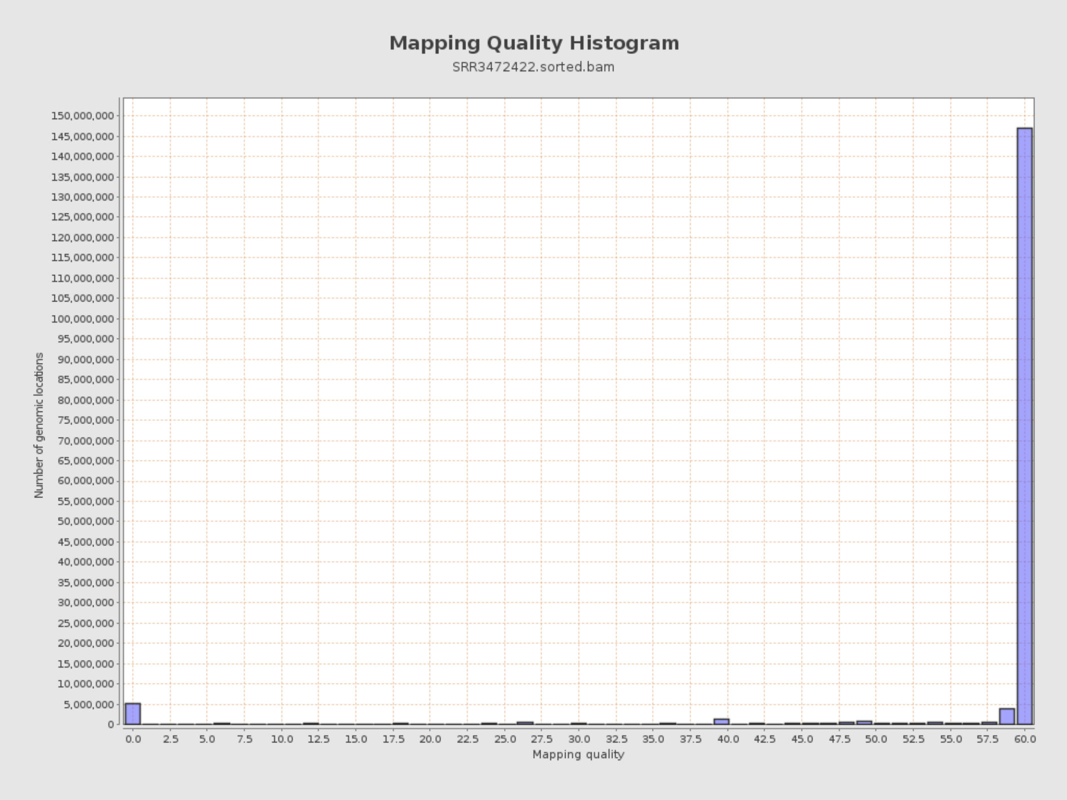
11. Results : Homopolymer Indels



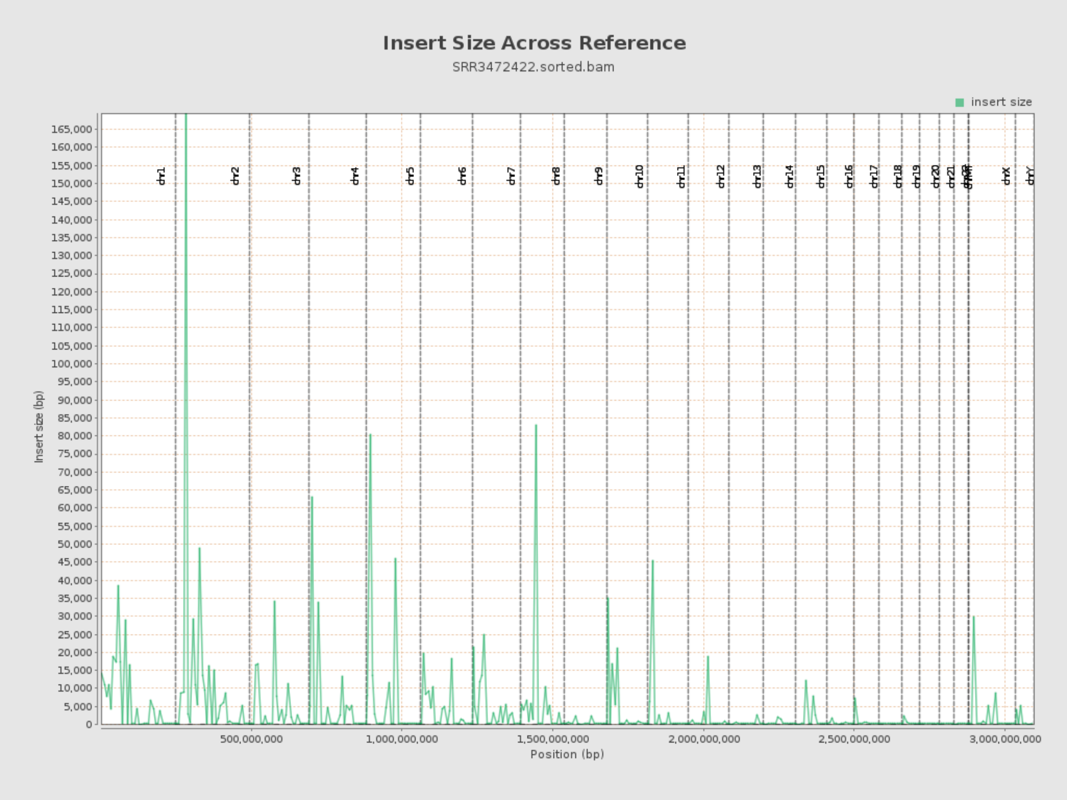
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram