Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 06:11:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472550.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_SRR3472550 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472550_1.fastq.gz SRR3472550_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 06:10:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472550.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,283,196
Mapped reads	14,095,654 / 98.69%
Unmapped reads	187,542 / 1.31%
Mapped paired reads	14,095,654 / 98.69%
Mapped reads, first in pair	7,072,095 / 49.51%
Mapped reads, second in pair	7,023,559 / 49.17%
Mapped reads, both in pair	14,003,702 / 98.04%
Mapped reads, singletons	91,952 / 0.64%
Secondary alignments	0
Supplementary alignments	47,402 / 0.33%
Read min/max/mean length	30 / 100 / 100.13
Duplicated reads (estimated)	8,513,140 / 59.6%
Duplication rate	45.41%
Clipped reads	1,116,575 / 7.82%

2.2. ACGT Content

Number/percentage of A's	381,533,283 / 27.5%
Number/percentage of C's	314,679,517 / 22.68%
Number/percentage of T's	379,121,918 / 27.33%
Number/percentage of G's	311,893,613 / 22.48%
Number/percentage of N's	214,715 / 0.02%

GC Percentage	45.16%

2.3. Coverage

Mean	0.4482
Standard Deviation	14.7027

2.4. Mapping Quality

Mean Mapping Quality	54.99

2.5. Insert size

Mean	24,385.22
Standard Deviation	1,579,128.75
P25/Median/P75	170 / 234 / 314

2.6. Mismatches and indels

General error rate	0.62%
Mismatches	8,518,944
Insertions	71,485
Mapped reads with at least one insertion	0.5%
Deletions	73,039
Mapped reads with at least one deletion	0.51%
Homopolymer indels	43.93%

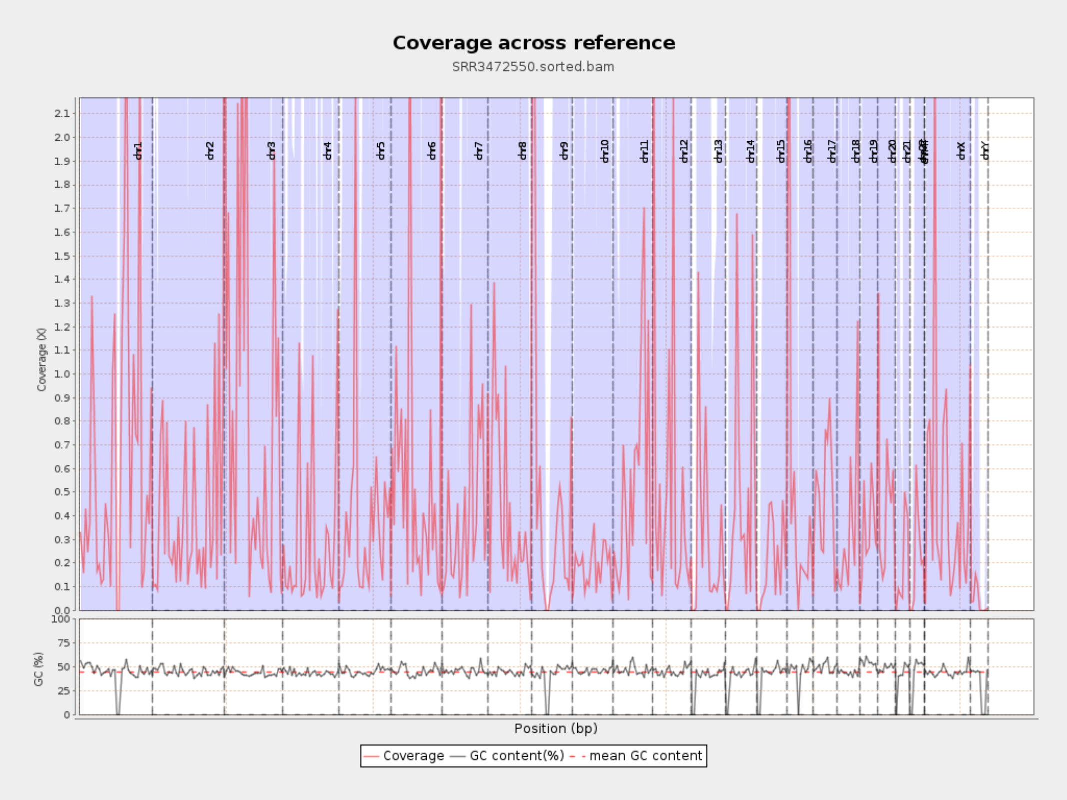
2.7. Chromosome stats

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

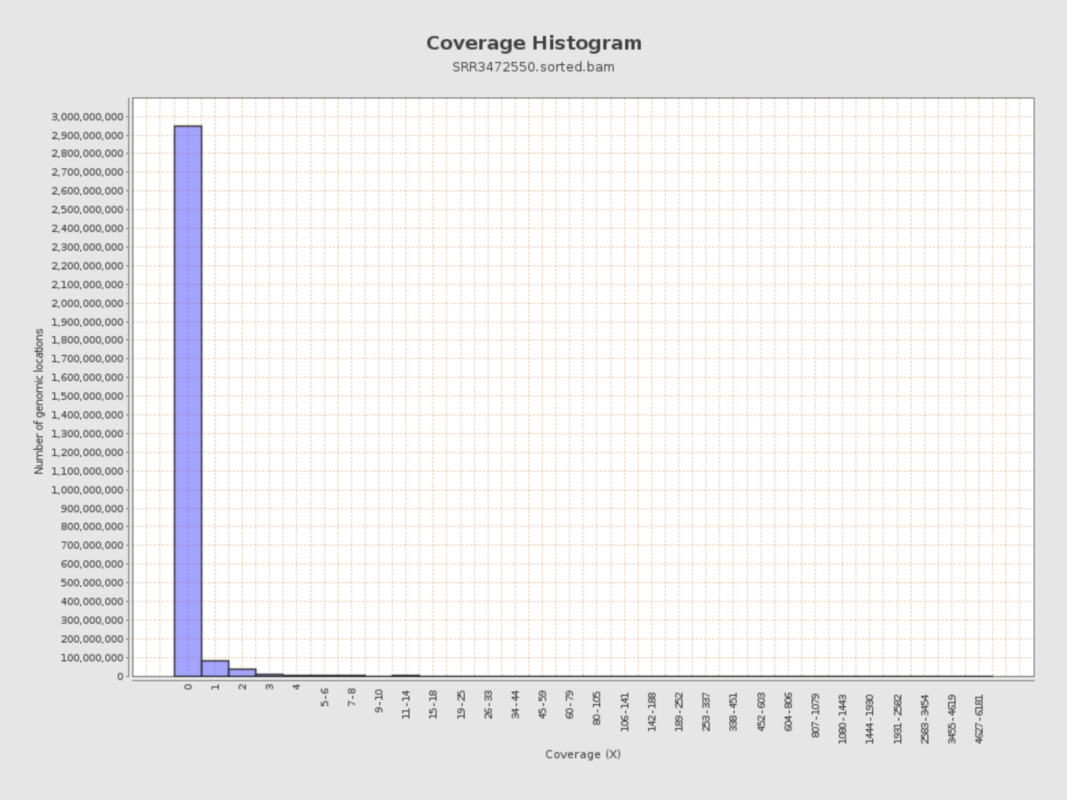
		bases	coverage	deviation
chr1	249250621	166664533	0.6687	21.6583
chr2	243199373	95239533	0.3916	12.4103
chr3	198022430	173025881	0.8738	21.6991
chr4	191154276	54969830	0.2876	11.227
chr5	180915260	69217544	0.3826	12.509
chr6	171115067	96847937	0.566	16.7545
chr7	159138663	62718794	0.3941	12.9707
chr8	146364022	60125078	0.4108	12.6504
chr9	141213431	70154259	0.4968	13.9054
chr10	135534747	25796683	0.1903	6.2451
chr11	135006516	73609368	0.5452	16.6381
chr12	133851895	74472141	0.5564	16.8615
chr13	115169878	35593968	0.3091	13.1514
chr14	107349540	49089486	0.4573	16.2682
chr15	102531392	21293494	0.2077	7.6466
chr16	90354753	46724361	0.5171	15.8653
chr17	81195210	38139901	0.4697	11.6197
chr18	78077248	26709501	0.3421	10.9733
chr19	59128983	20612305	0.3486	9.2028
chr20	63025520	30061100	0.477	13.9475
chr21	48129895	8827199	0.1834	10.4629
chr22	51304566	11489668	0.224	8.4073
chrMT	16571	2602	0.157	0.4586
chrX	155270560	73635793	0.4742	15.8681

chrY	59373566	2620854	0.0441	1.5189

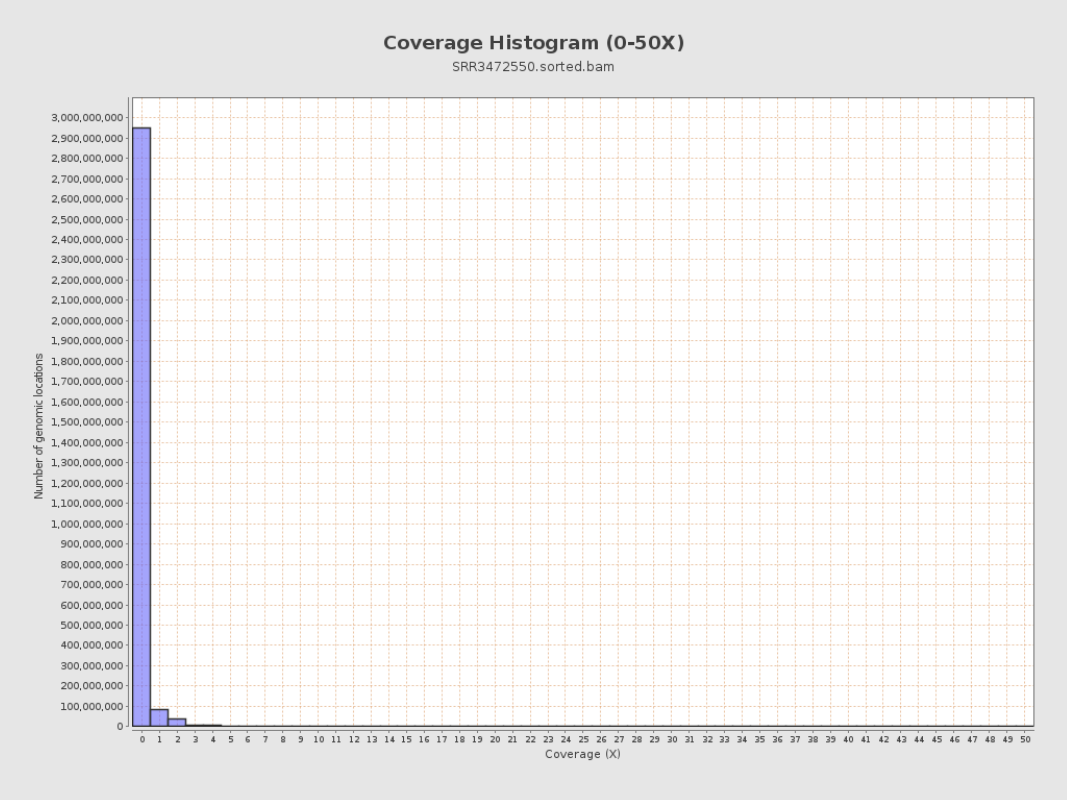
3. Results : Coverage across reference



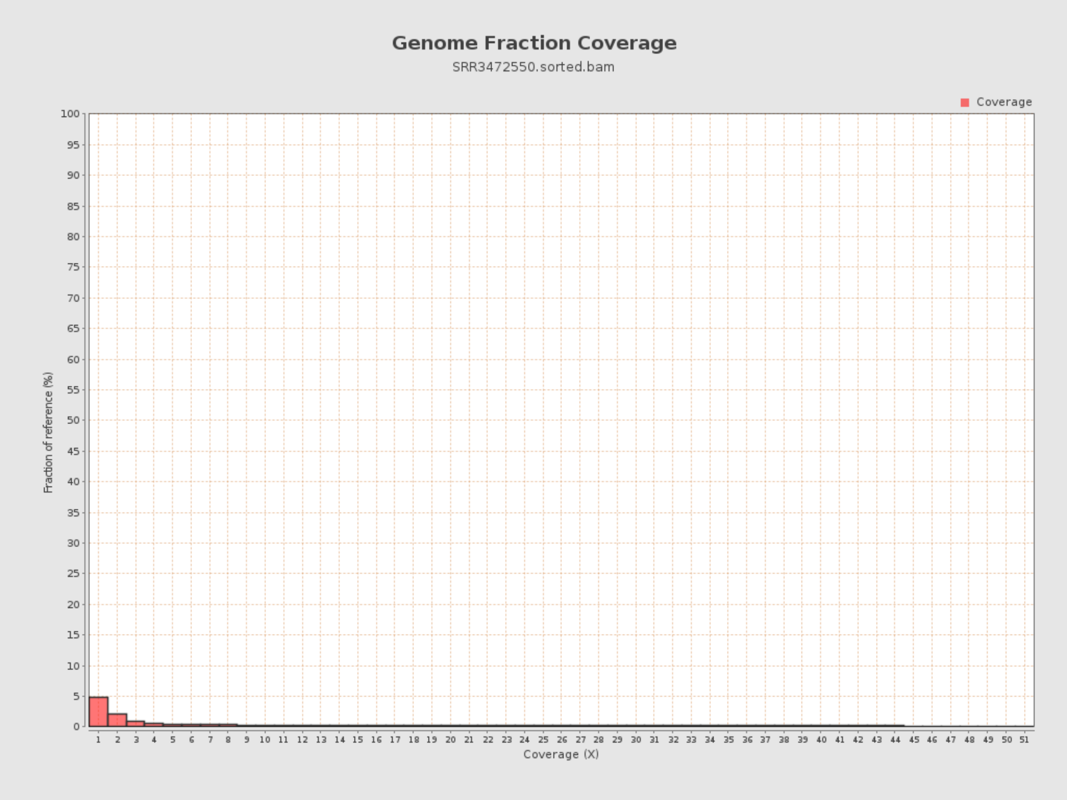
4. Results : Coverage Histogram



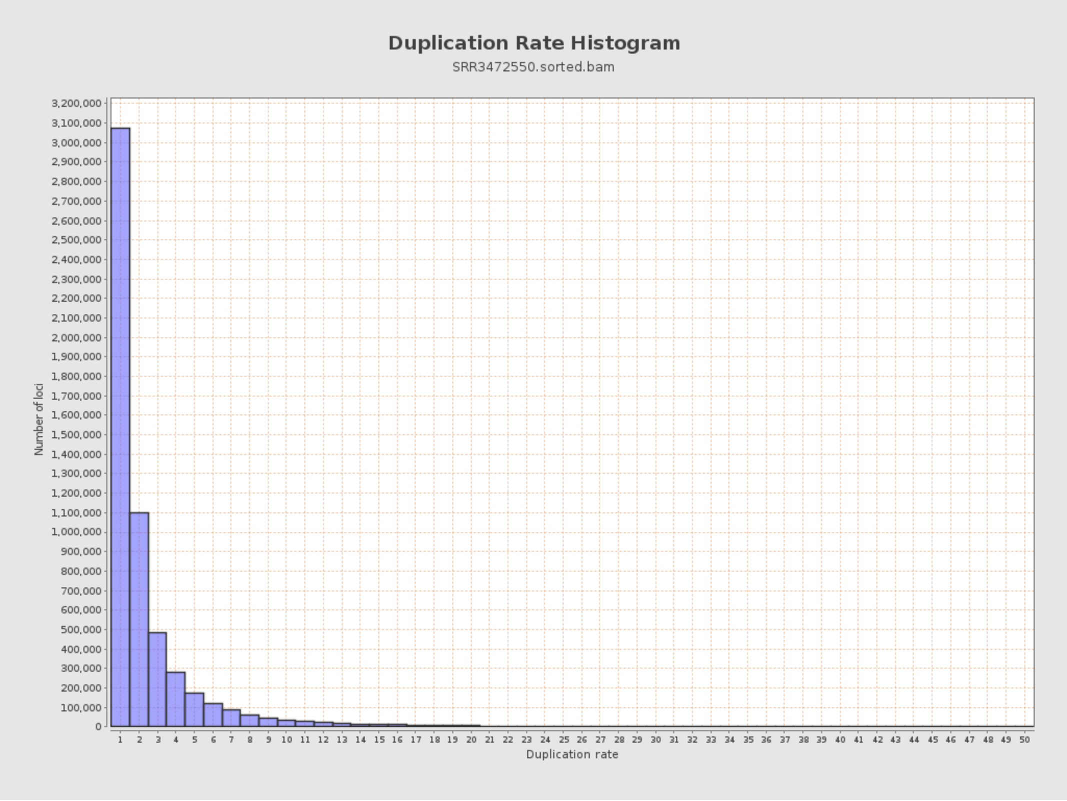
5. Results : Coverage Histogram (0-50X)



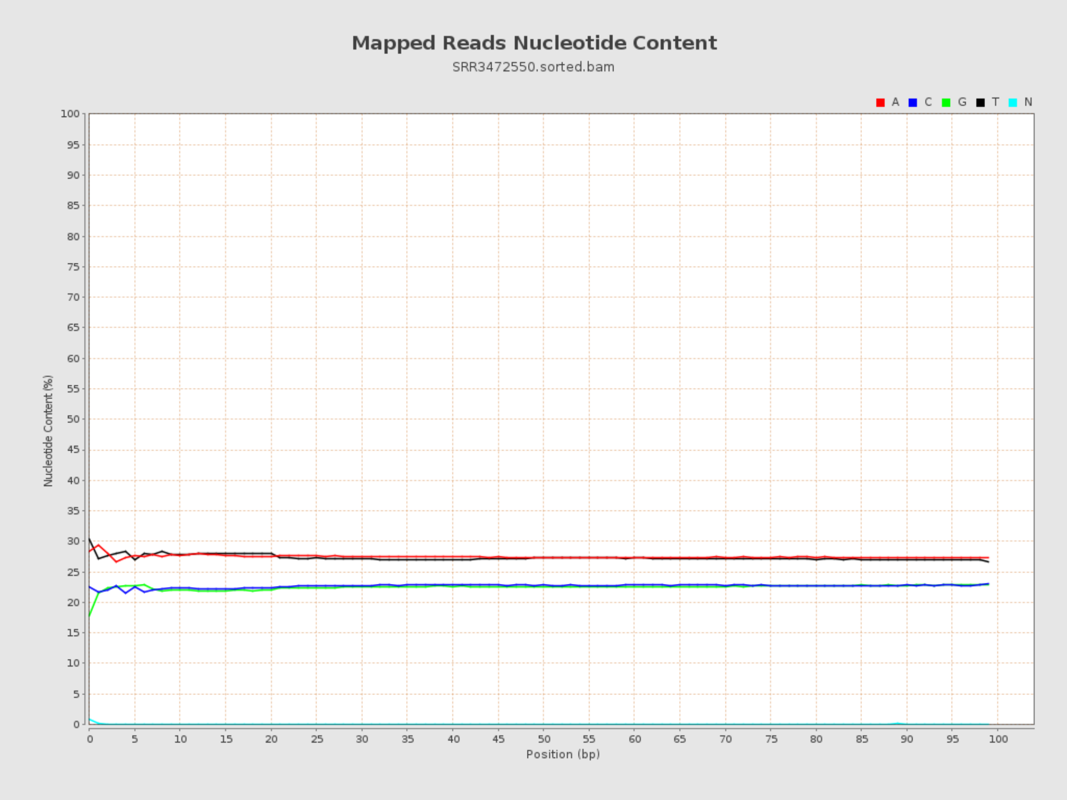
6. Results : Genome Fraction Coverage



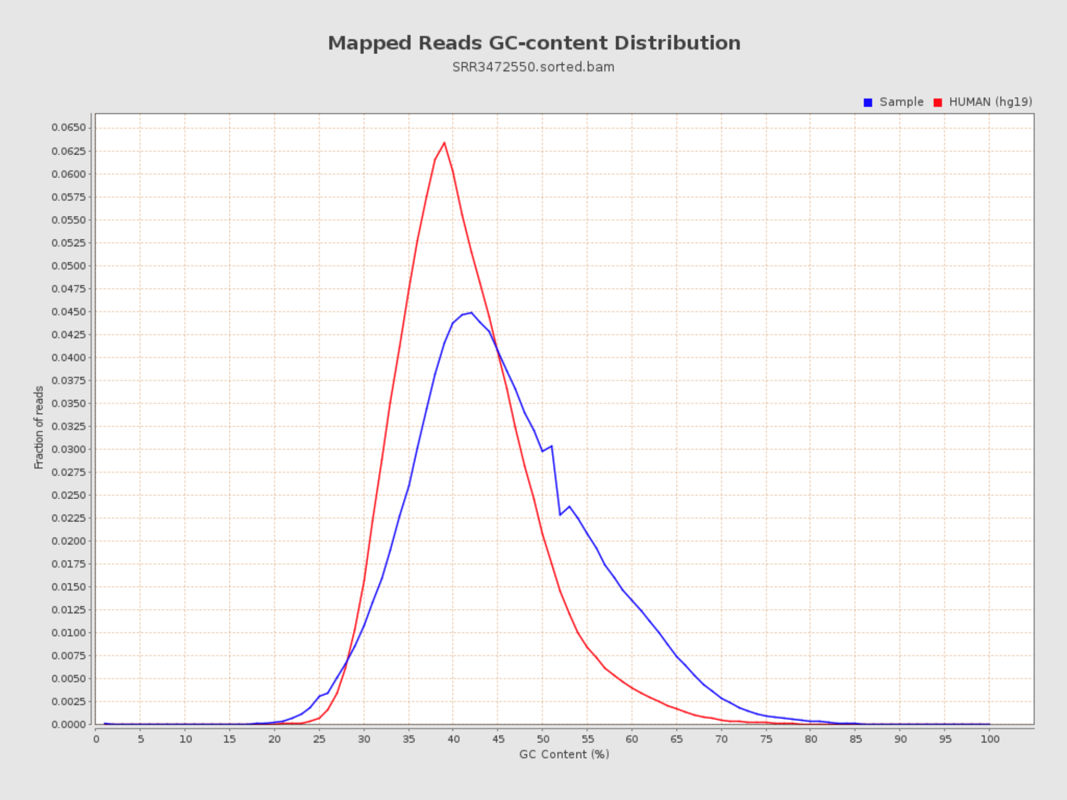
7. Results : Duplication Rate Histogram



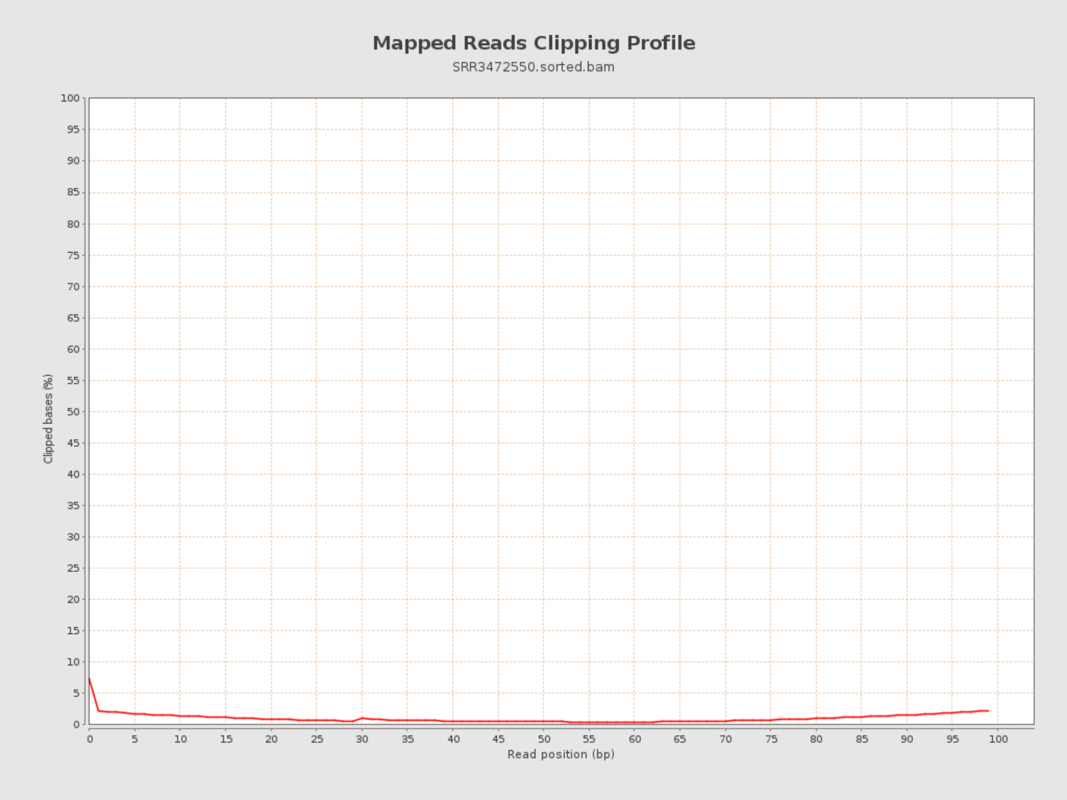
8. Results : Mapped Reads Nucleotide Content



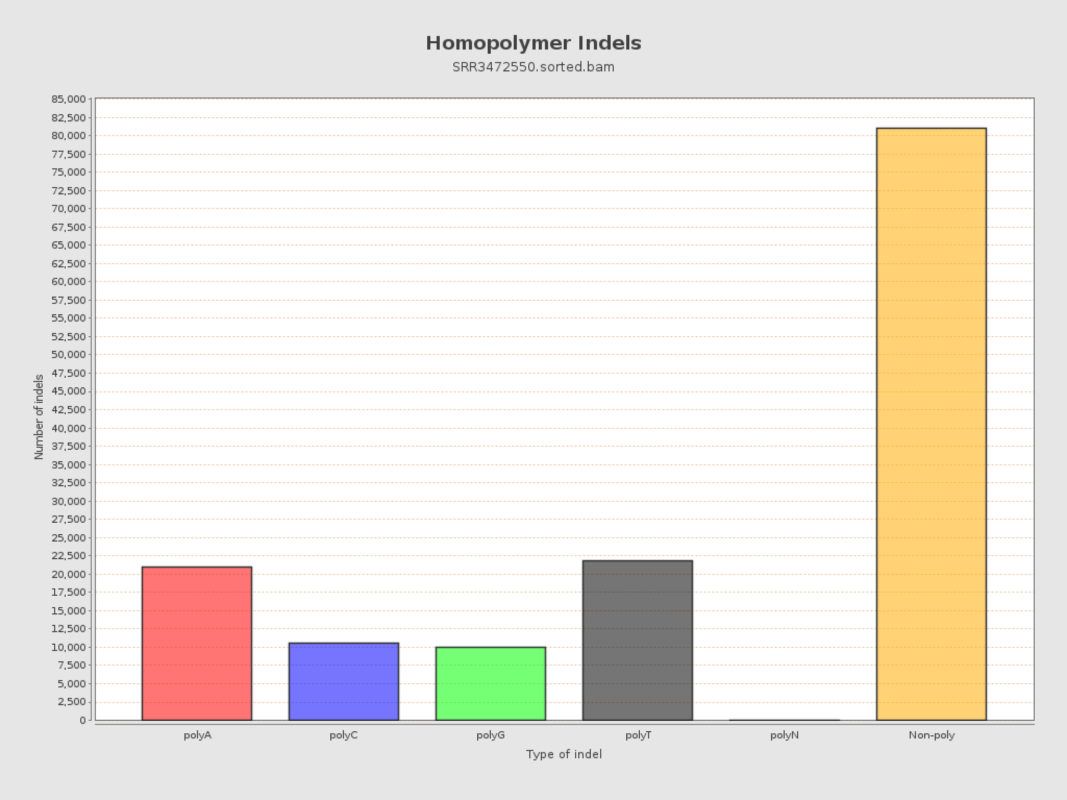
9. Results : Mapped Reads GC-content Distribution



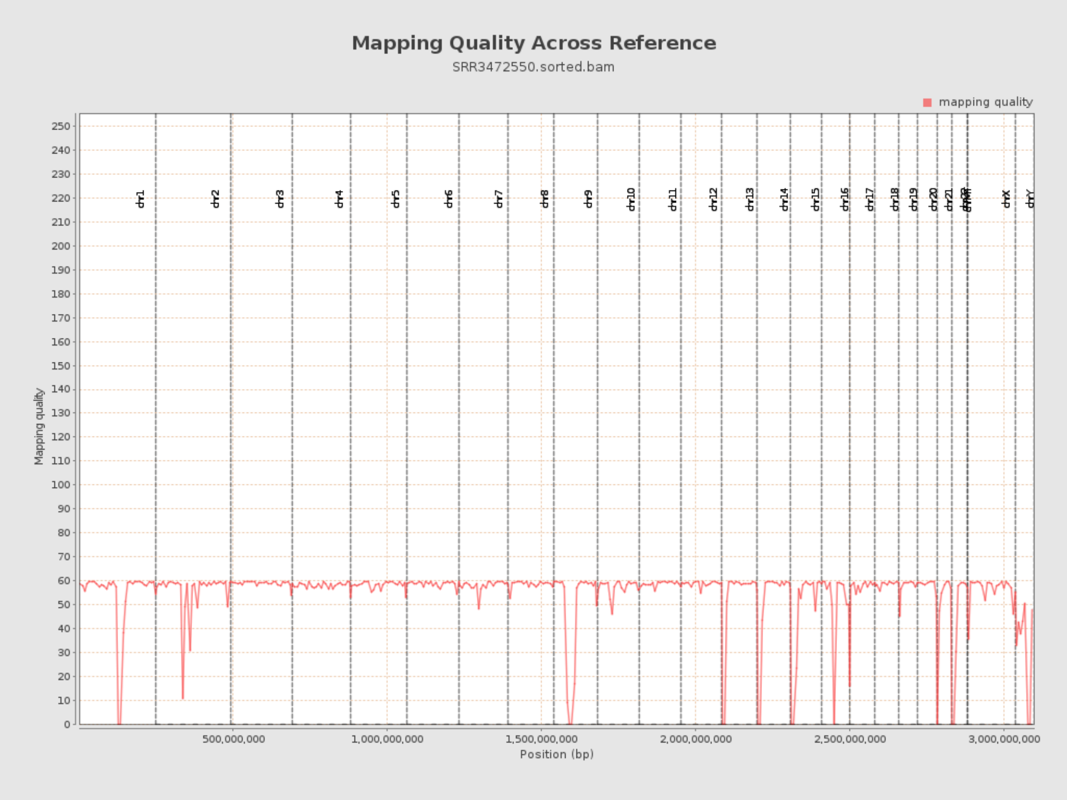
10. Results : Mapped Reads Clipping Profile



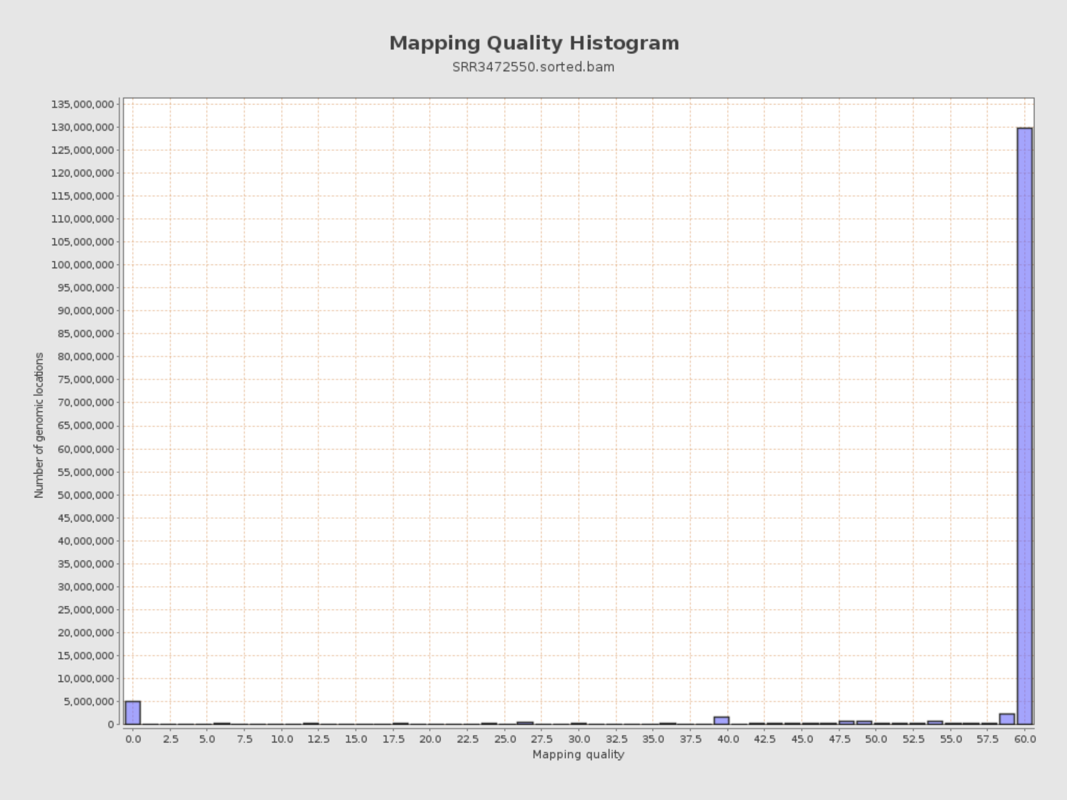
11. Results : Homopolymer Indels



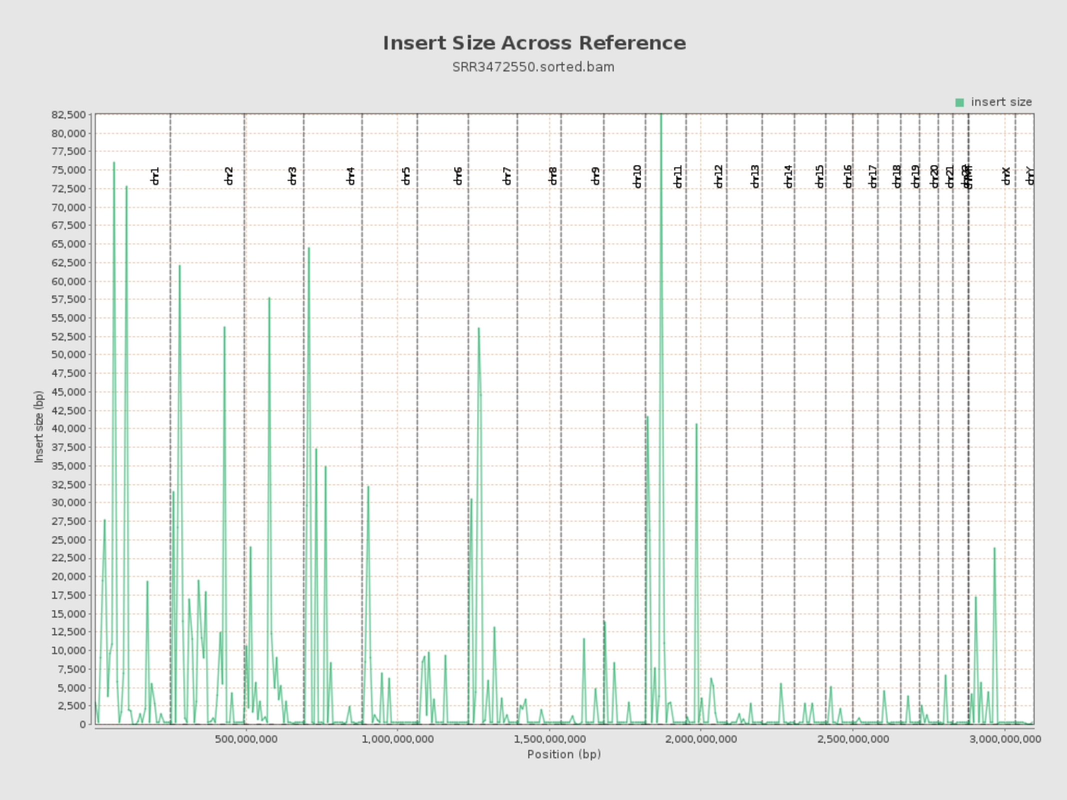
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram