Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 13:49:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472775.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_SRR3472775 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472775_1.fastq.gz SRR3472775_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 13:49:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472775.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,130,134
Mapped reads	19,877,213 / 98.74%
Unmapped reads	252,921 / 1.26%
Mapped paired reads	19,877,213 / 98.74%
Mapped reads, first in pair	9,997,028 / 49.66%
Mapped reads, second in pair	9,880,185 / 49.08%
Mapped reads, both in pair	19,714,018 / 97.93%
Mapped reads, singletons	163,195 / 0.81%
Secondary alignments	0
Supplementary alignments	75,186 / 0.37%
Read min/max/mean length	30 / 100 / 100.15
Duplicated reads (estimated)	12,989,837 / 64.53%
Duplication rate	47.56%
Clipped reads	1,547,837 / 7.69%

2.2. ACGT Content

Number/percentage of A's	549,941,828 / 28.08%
Number/percentage of C's	431,938,566 / 22.05%
Number/percentage of T's	546,752,812 / 27.91%
Number/percentage of G's	429,697,409 / 21.94%
Number/percentage of N's	376,313 / 0.02%

GC Percentage	43.99%

2.3. Coverage

Mean	0.6328
Standard Deviation	21.7861

2.4. Mapping Quality

Mean Mapping Quality	55.08

2.5. Insert size

Mean	26,420.22
Standard Deviation	1,588,667.24
P25/Median/P75	184 / 261 / 354

2.6. Mismatches and indels

General error rate	0.7%
Mismatches	13,383,650
Insertions	119,805
Mapped reads with at least one insertion	0.6%
Deletions	120,473
Mapped reads with at least one deletion	0.59%
Homopolymer indels	45.6%

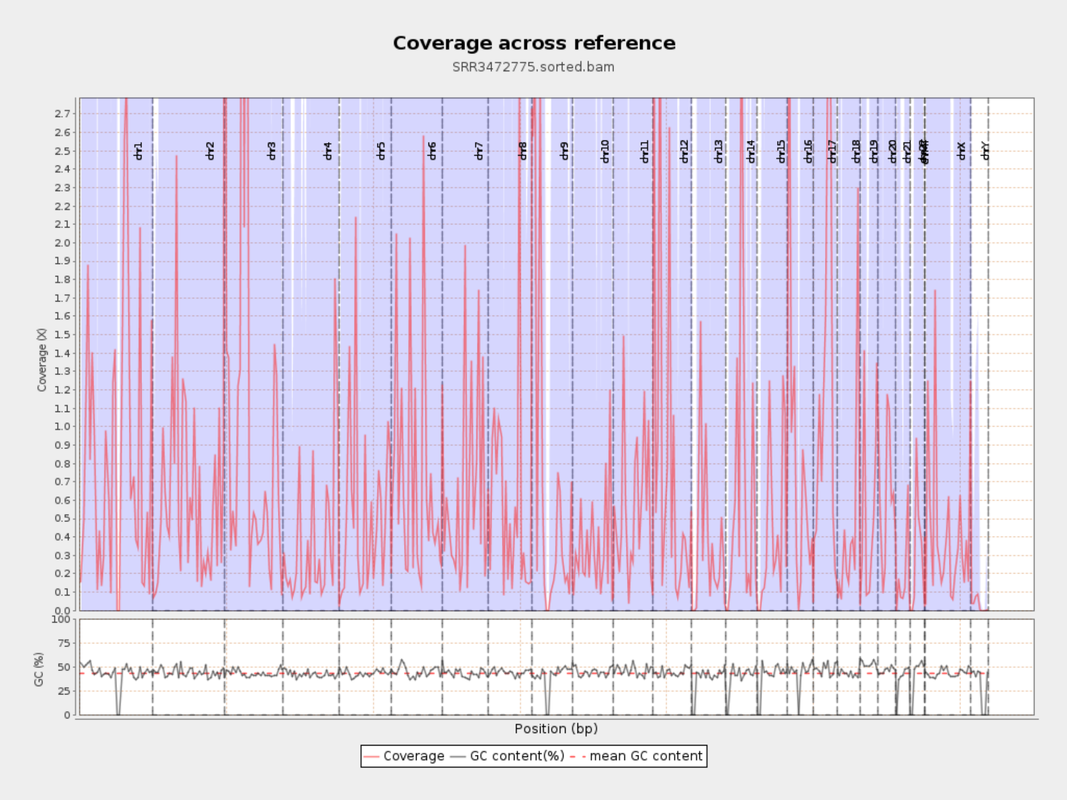
2.7. Chromosome stats

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

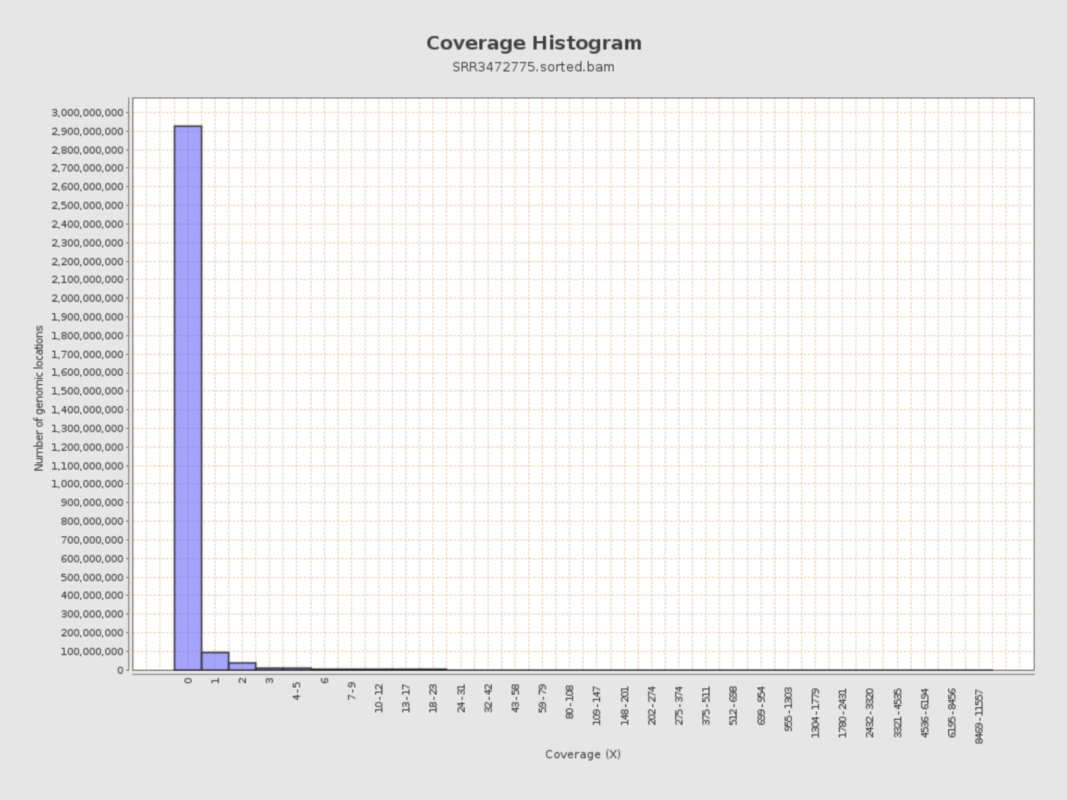
		bases	coverage	deviation
chr1	249250621	213307868	0.8558	30.162
chr2	243199373	147545767	0.6067	27.8894
chr3	198022430	233284775	1.1781	26.8207
chr4	191154276	68925195	0.3606	12.5079
chr5	180915260	96254992	0.532	18.8948
chr6	171115067	124371886	0.7268	24.1464
chr7	159138663	104797561	0.6585	22.0132
chr8	146364022	87595516	0.5985	19.9282
chr9	141213431	102930610	0.7289	19.2863
chr10	135534747	48203498	0.3557	12.7746
chr11	135006516	77690933	0.5755	17.8931
chr12	133851895	119539692	0.8931	25.9605
chr13	115169878	44096068	0.3829	14.6585
chr14	107349540	70949540	0.6609	28.3432
chr15	102531392	45196991	0.4408	13.947
chr16	90354753	71840490	0.7951	21.6639
chr17	81195210	100710088	1.2403	38.0967
chr18	78077248	38803838	0.497	15.7883
chr19	59128983	30735671	0.5198	15.8323
chr20	63025520	40379793	0.6407	16.8388
chr21	48129895	9164595	0.1904	7.7454
chr22	51304566	15617499	0.3044	9.0586
chrMT	16571	6683	0.4033	1.1036
chrX	155270560	65226768	0.4201	12.0913

chrY	59373566	1834649	0.0309	0.8605

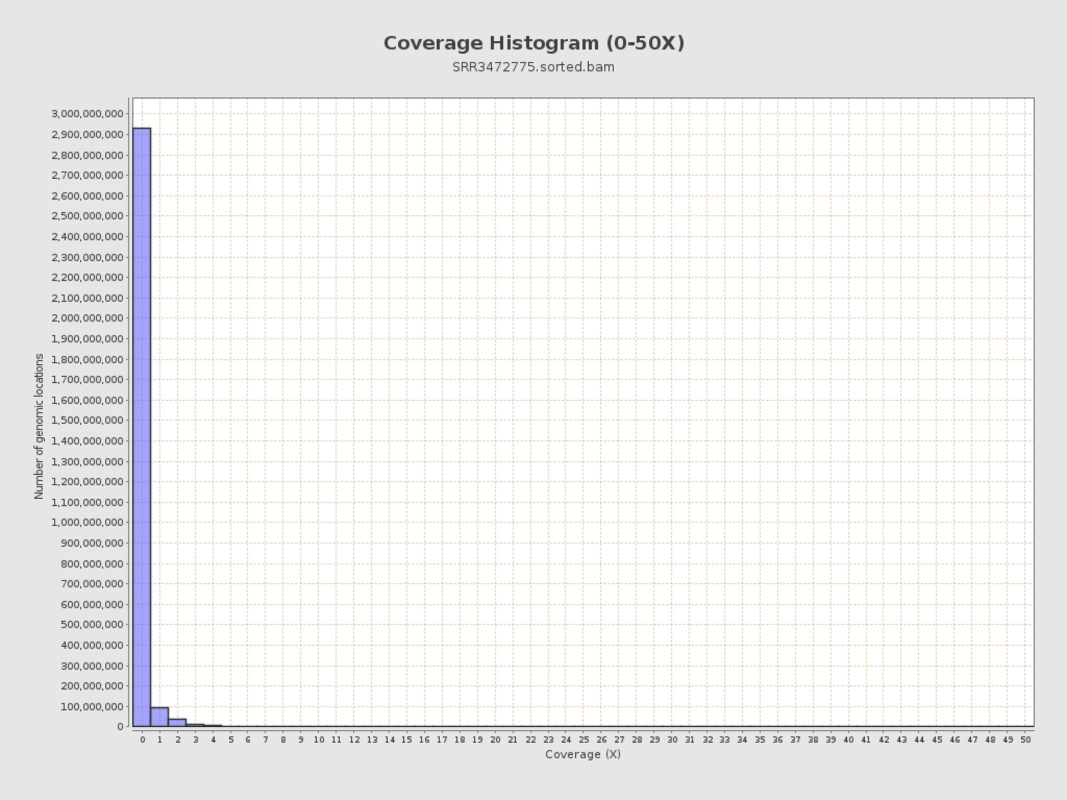
3. Results : Coverage across reference



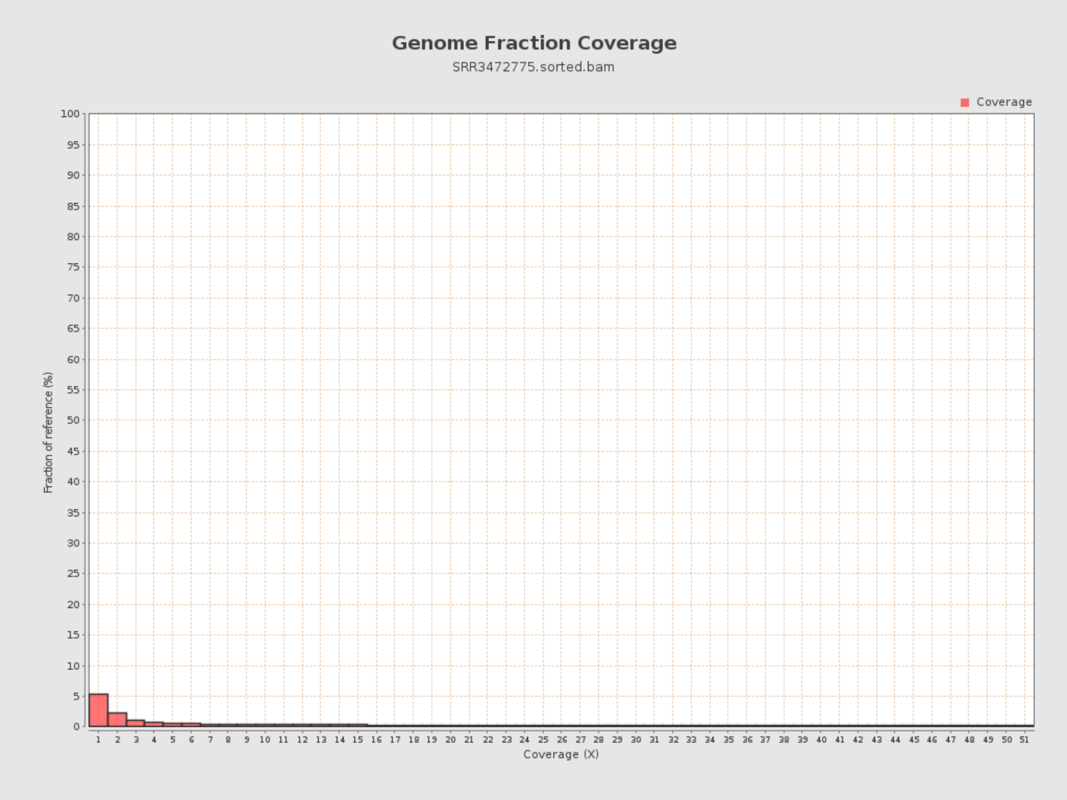
4. Results : Coverage Histogram



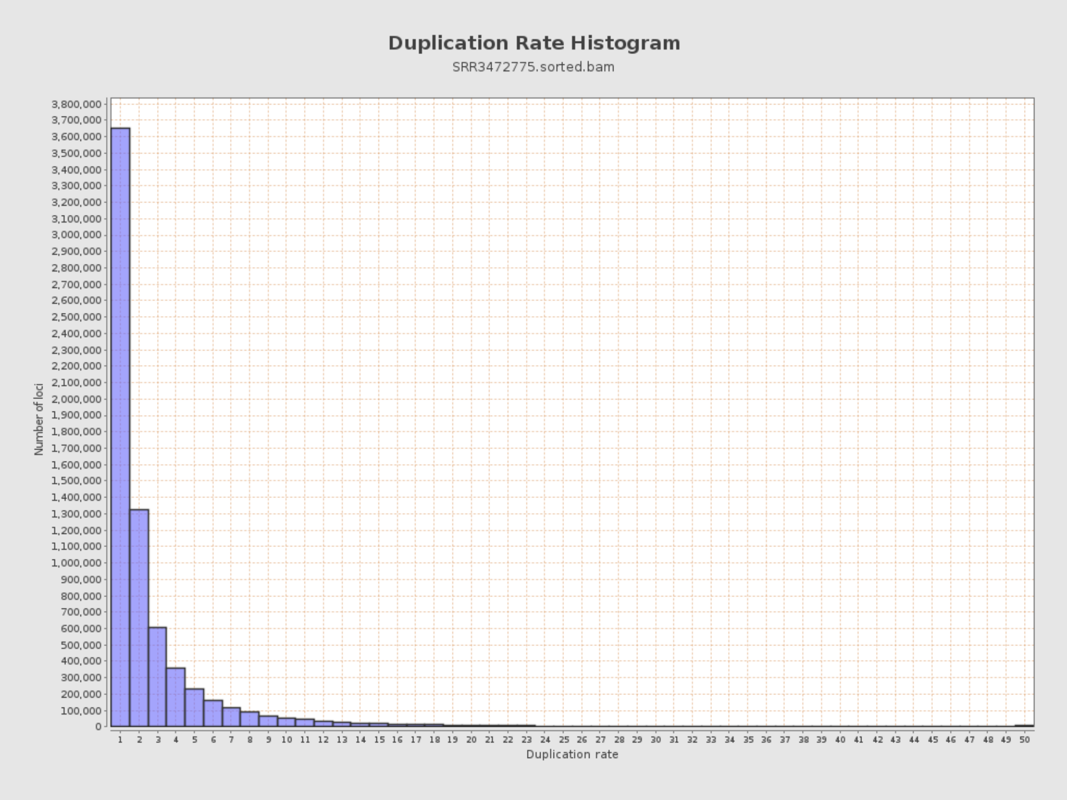
5. Results : Coverage Histogram (0-50X)



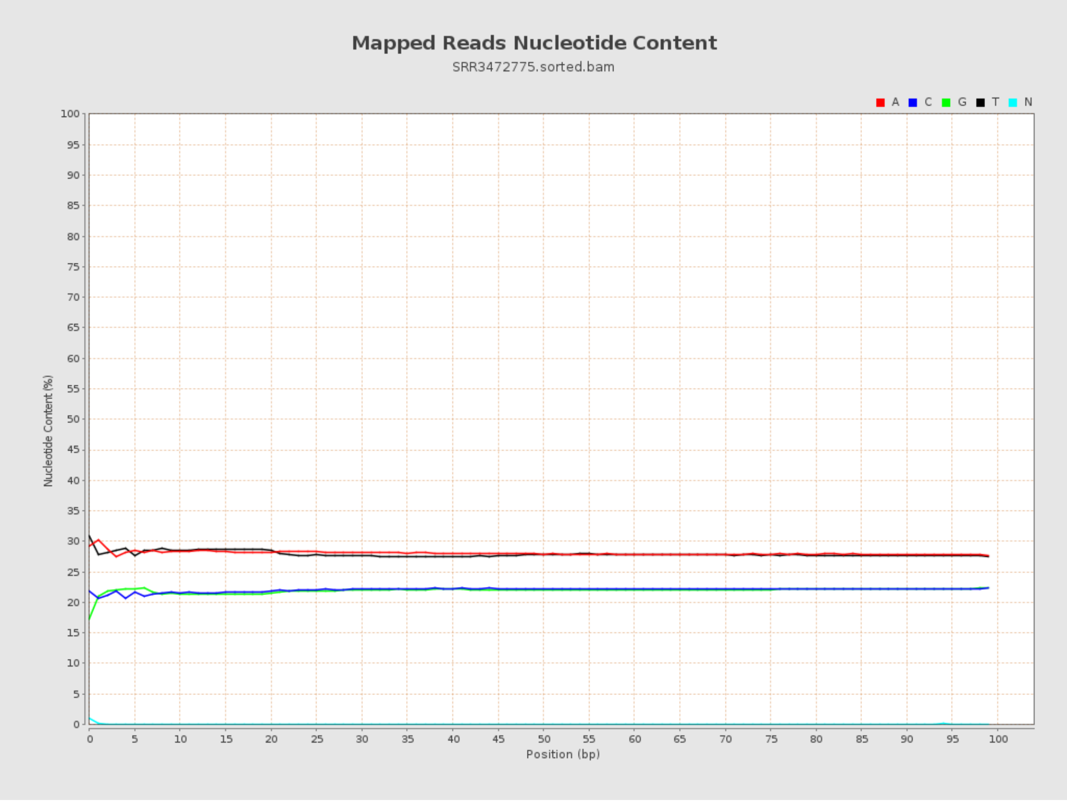
6. Results : Genome Fraction Coverage



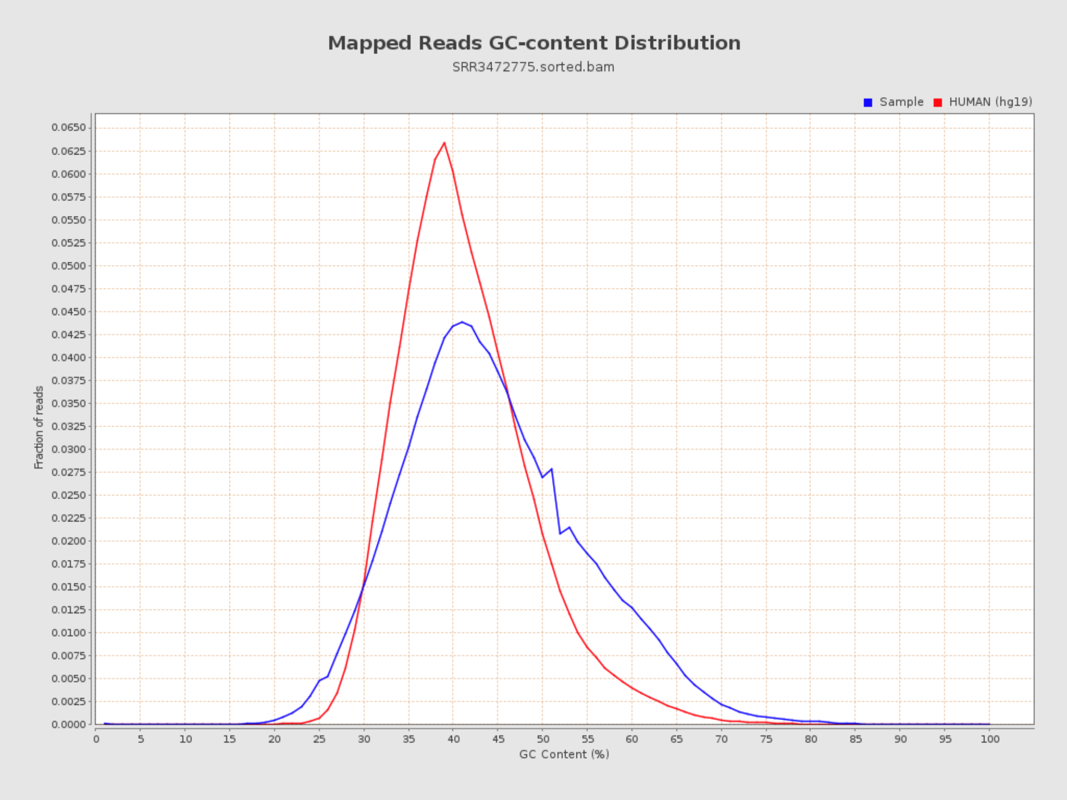
7. Results : Duplication Rate Histogram



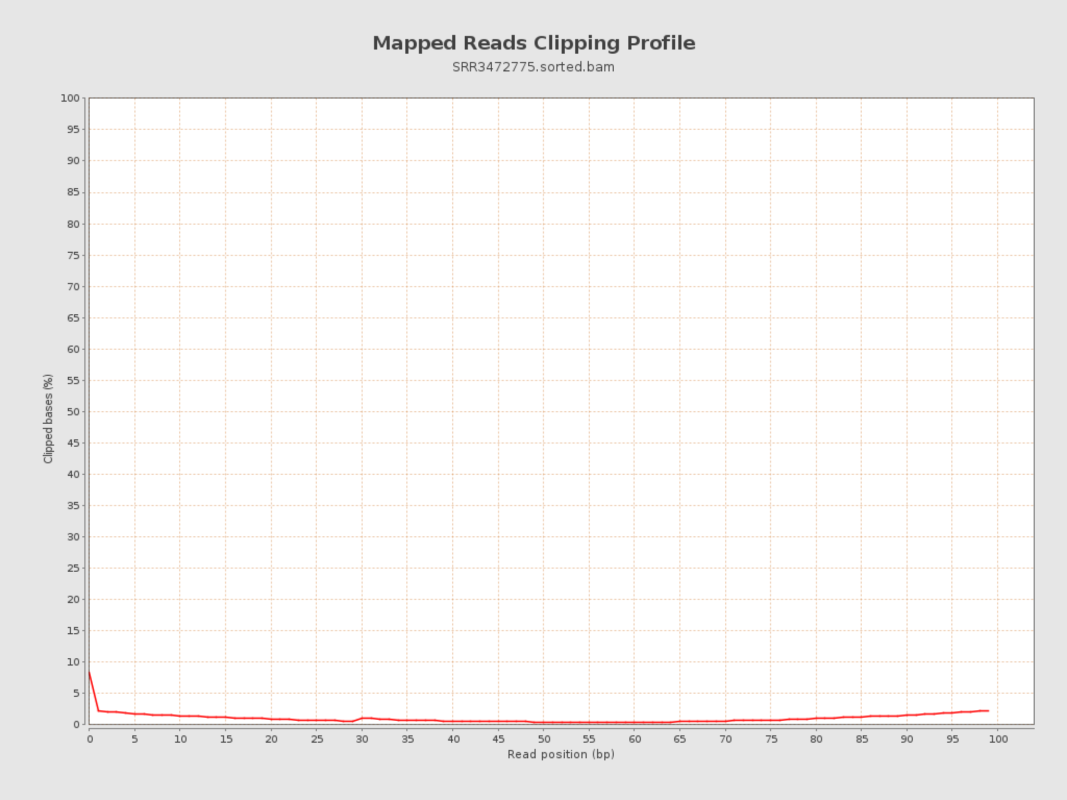
8. Results : Mapped Reads Nucleotide Content



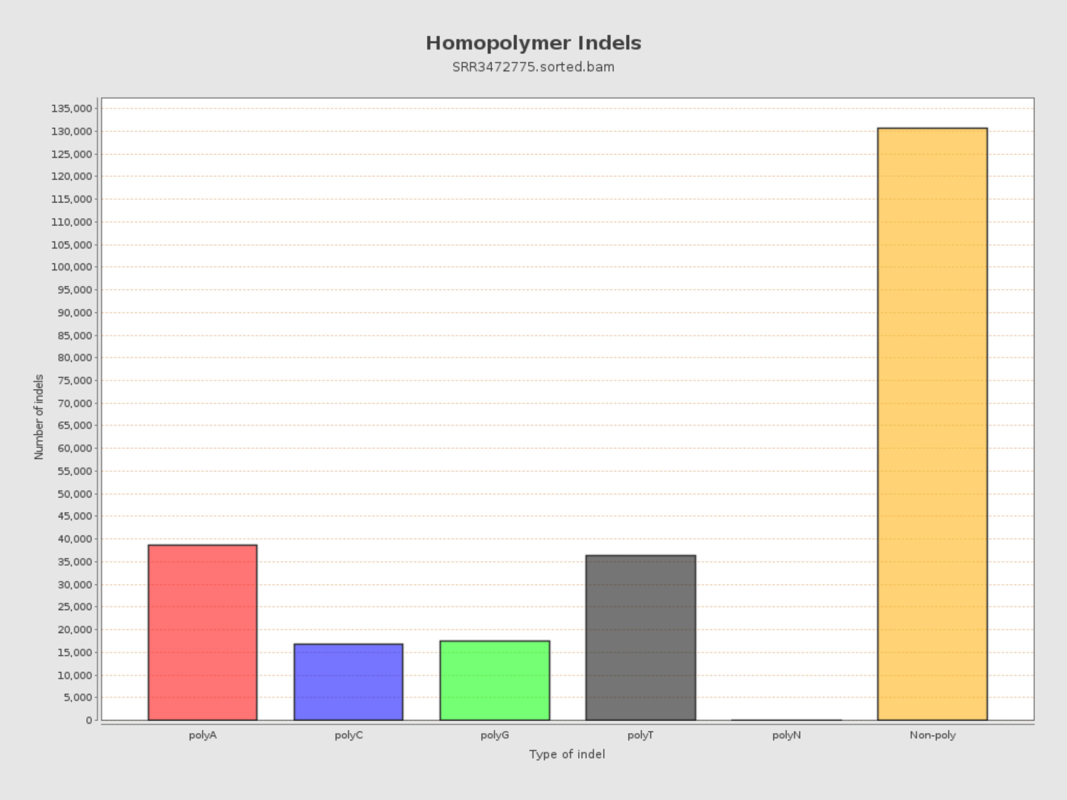
9. Results : Mapped Reads GC-content Distribution



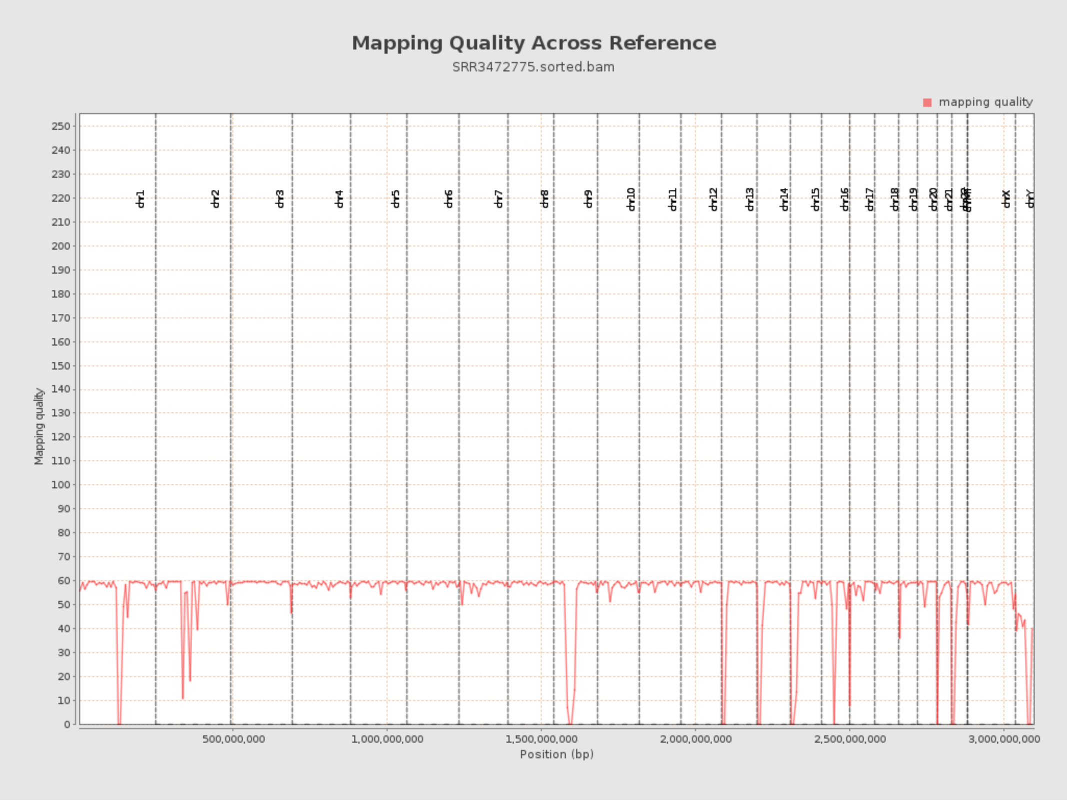
10. Results : Mapped Reads Clipping Profile



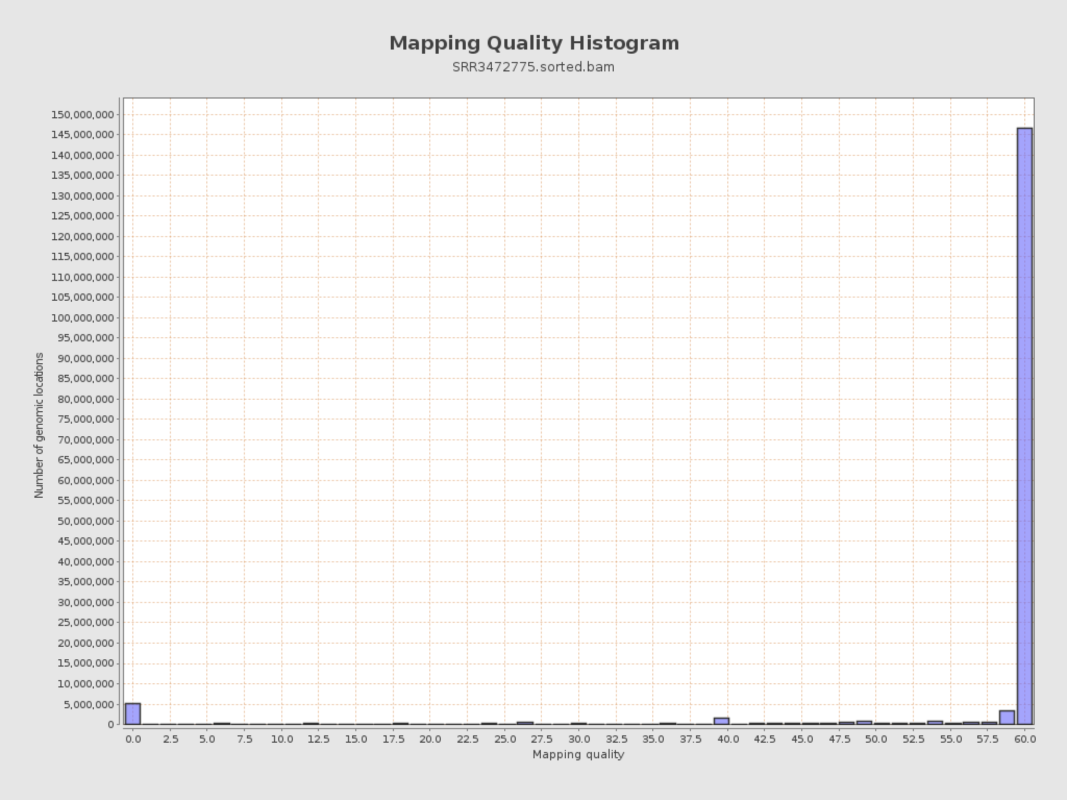
11. Results : Homopolymer Indels



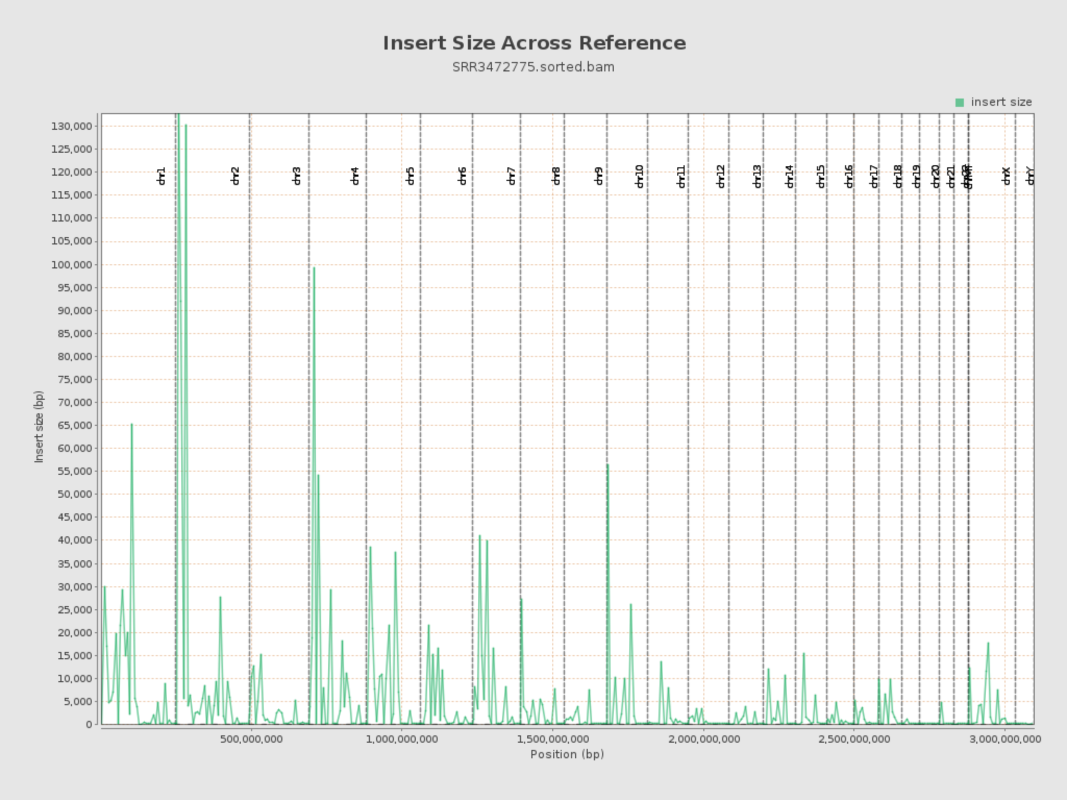
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram