Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 05:41:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472678.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_SRR3472678 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472678_1.fastq.gz SRR3472678_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 05:41:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472678.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,451,626
Mapped reads	13,723,186 / 94.96%
Unmapped reads	728,440 / 5.04%
Mapped paired reads	13,723,186 / 94.96%
Mapped reads, first in pair	6,595,093 / 45.64%
Mapped reads, second in pair	7,128,093 / 49.32%
Mapped reads, both in pair	13,049,292 / 90.3%
Mapped reads, singletons	673,894 / 4.66%
Secondary alignments	0
Supplementary alignments	94,174 / 0.65%
Read min/max/mean length	30 / 101 / 99.85
Duplicated reads (estimated)	9,221,797 / 63.81%
Duplication rate	45.68%
Clipped reads	1,332,347 / 9.22%

2.2. ACGT Content

Number/percentage of A's	372,138,352 / 27.85%
Number/percentage of C's	304,620,248 / 22.8%
Number/percentage of T's	359,561,447 / 26.91%
Number/percentage of G's	299,636,057 / 22.42%
Number/percentage of N's	258,534 / 0.02%

GC Percentage	45.22%

2.3. Coverage

Mean	0.4317
Standard Deviation	24.7505

2.4. Mapping Quality

Mean Mapping Quality	54.33

2.5. Insert size

Mean	31,882.72
Standard Deviation	1,750,836.12
P25/Median/P75	164 / 226 / 300

2.6. Mismatches and indels

General error rate	0.98%
Mismatches	12,906,697
Insertions	85,651
Mapped reads with at least one insertion	0.62%
Deletions	76,422
Mapped reads with at least one deletion	0.55%
Homopolymer indels	45.92%

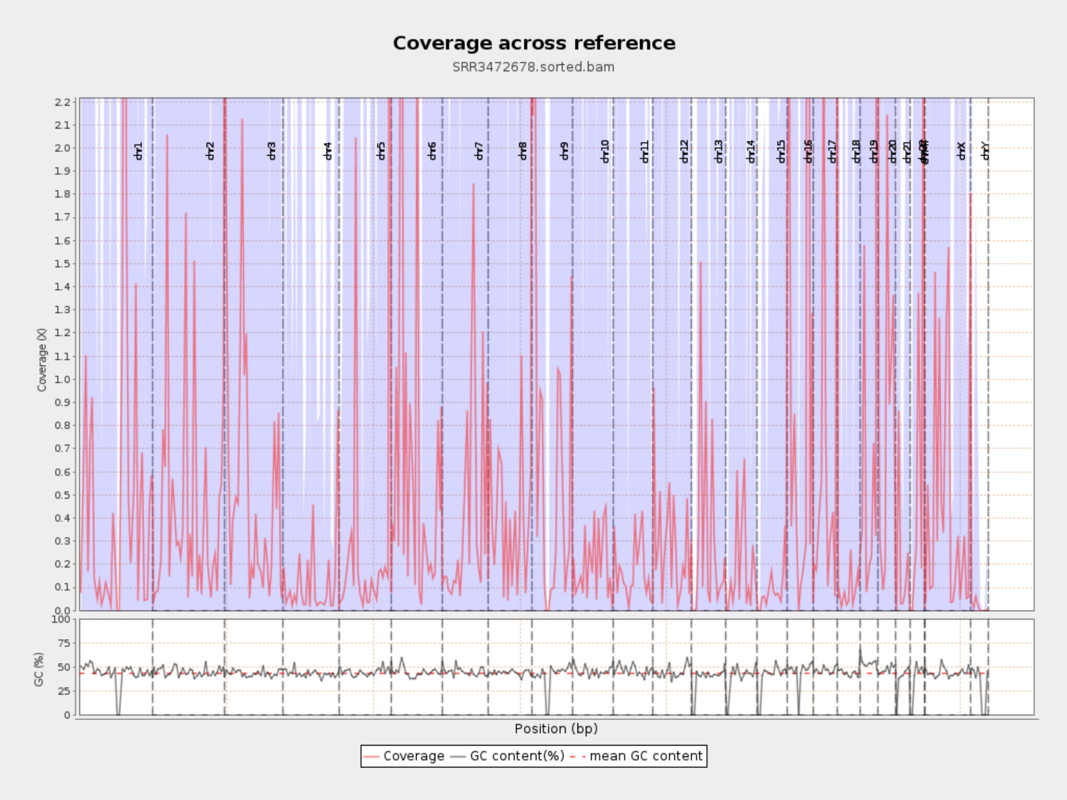
2.7. Chromosome stats

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

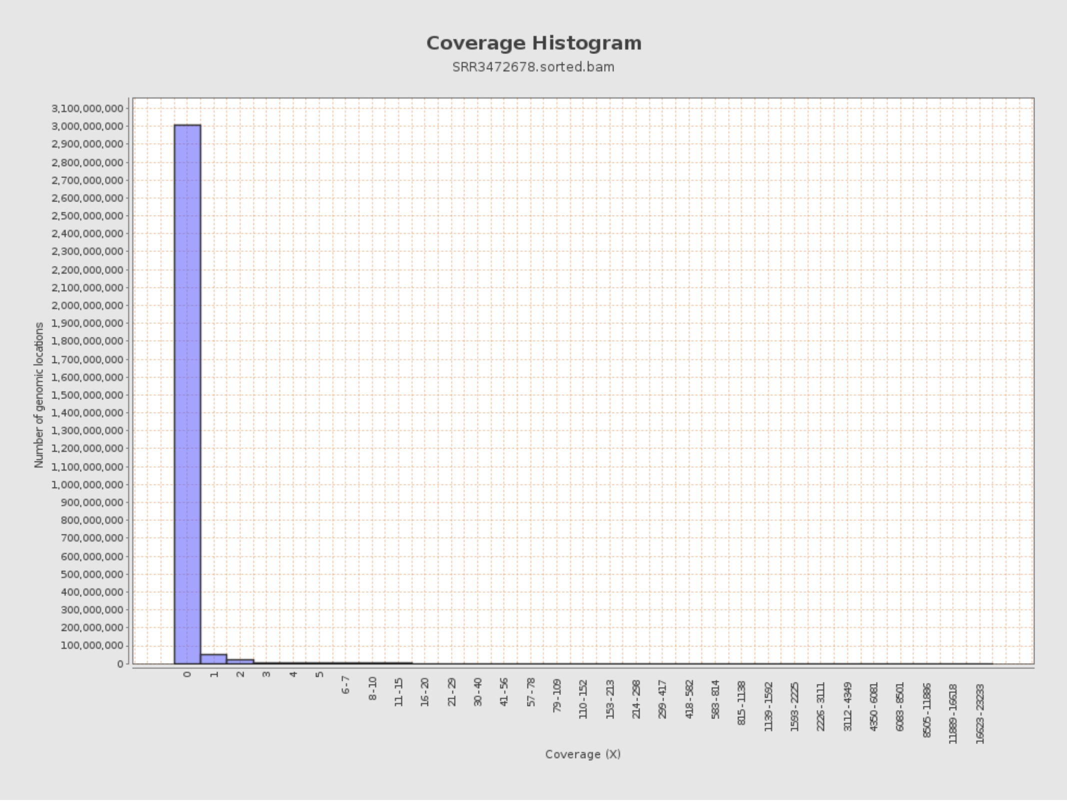
		bases	coverage	deviation
chr1	249250621	134141070	0.5382	22.6744
chr2	243199373	107272392	0.4411	18.8135
chr3	198022430	111706773	0.5641	15.4567
chr4	191154276	22543475	0.1179	5.753
chr5	180915260	81272353	0.4492	56.3942
chr6	171115067	115068400	0.6725	25.6931
chr7	159138663	68767492	0.4321	21.9508
chr8	146364022	57988151	0.3962	14.5079
chr9	141213431	100582557	0.7123	21.2595
chr10	135534747	27807869	0.2052	9.1599
chr11	135006516	23244744	0.1722	7.5287
chr12	133851895	39196219	0.2928	9.7983
chr13	115169878	35144701	0.3052	12.5473
chr14	107349540	19268616	0.1795	9.8864
chr15	102531392	9659439	0.0942	6.8568
chr16	90354753	105244493	1.1648	47.7714
chr17	81195210	54826776	0.6752	47.4269
chr18	78077248	6705482	0.0859	5.2673
chr19	59128983	43122092	0.7293	33.6875
chr20	63025520	52313918	0.83	23.8013
chr21	48129895	9985277	0.2075	18.9206
chr22	51304566	38338446	0.7473	44.4185
chrMT	16571	5325	0.3213	0.8899
chrX	155270560	71184168	0.4585	24.2216

chrY	59373566	1026389	0.0173	0.7537

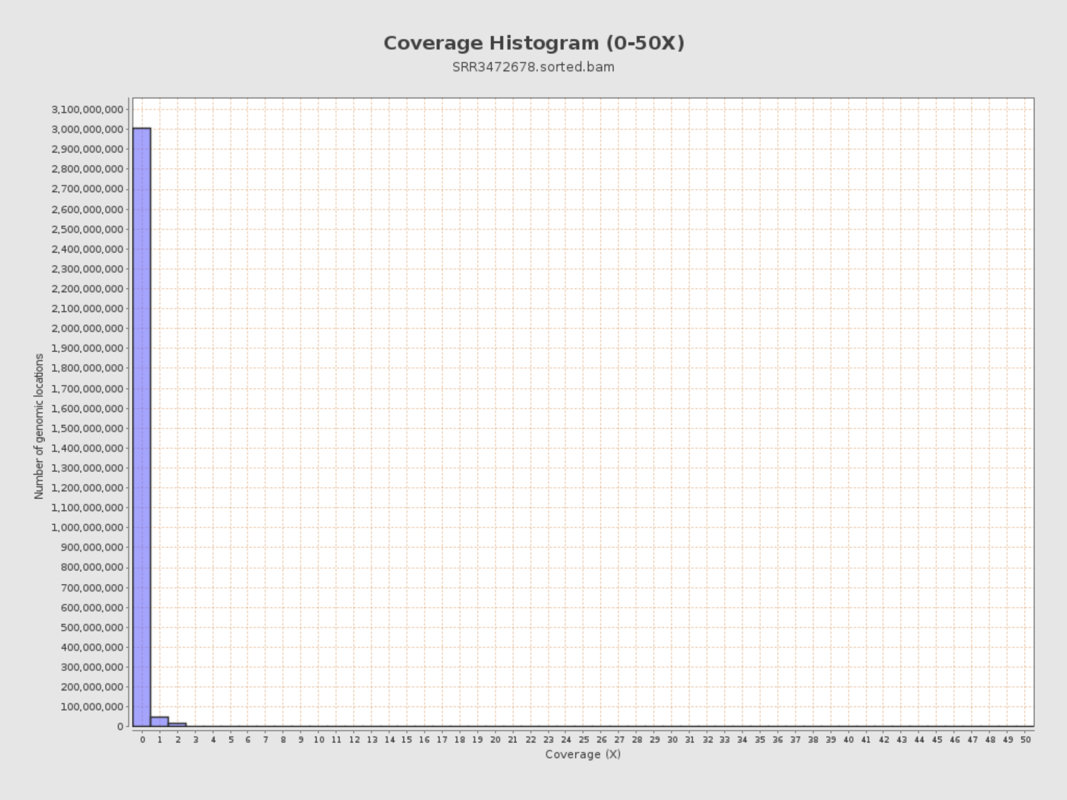
3. Results : Coverage across reference



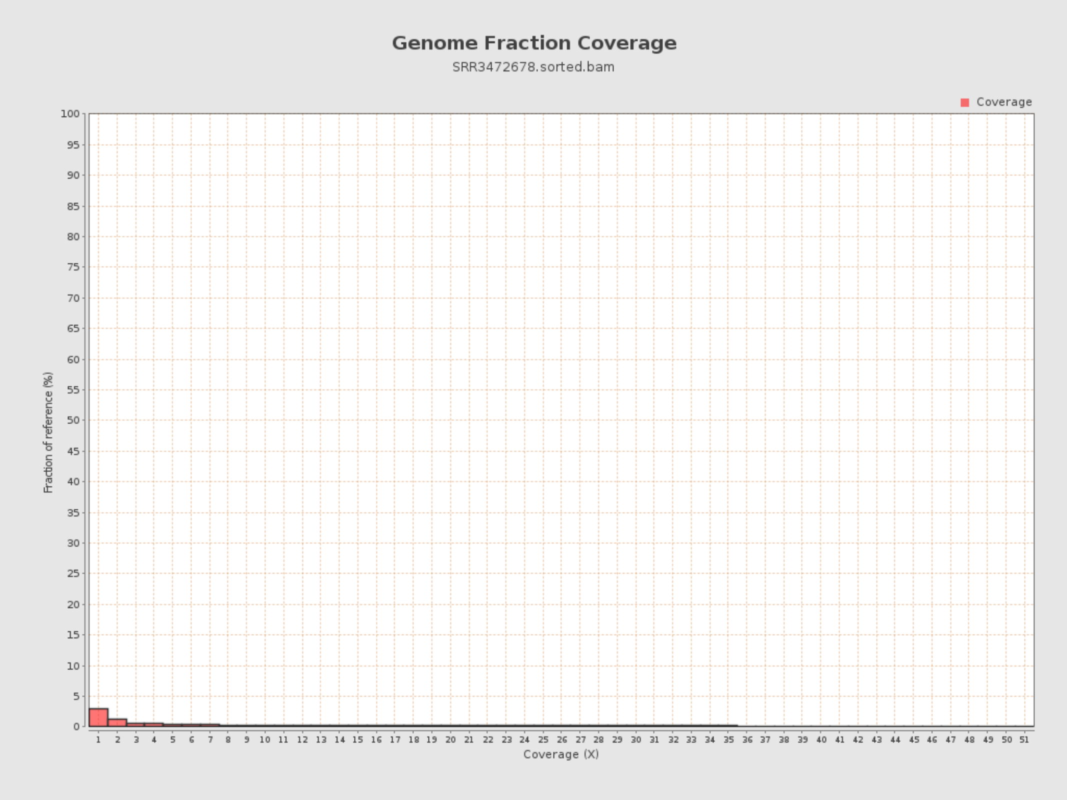
4. Results : Coverage Histogram



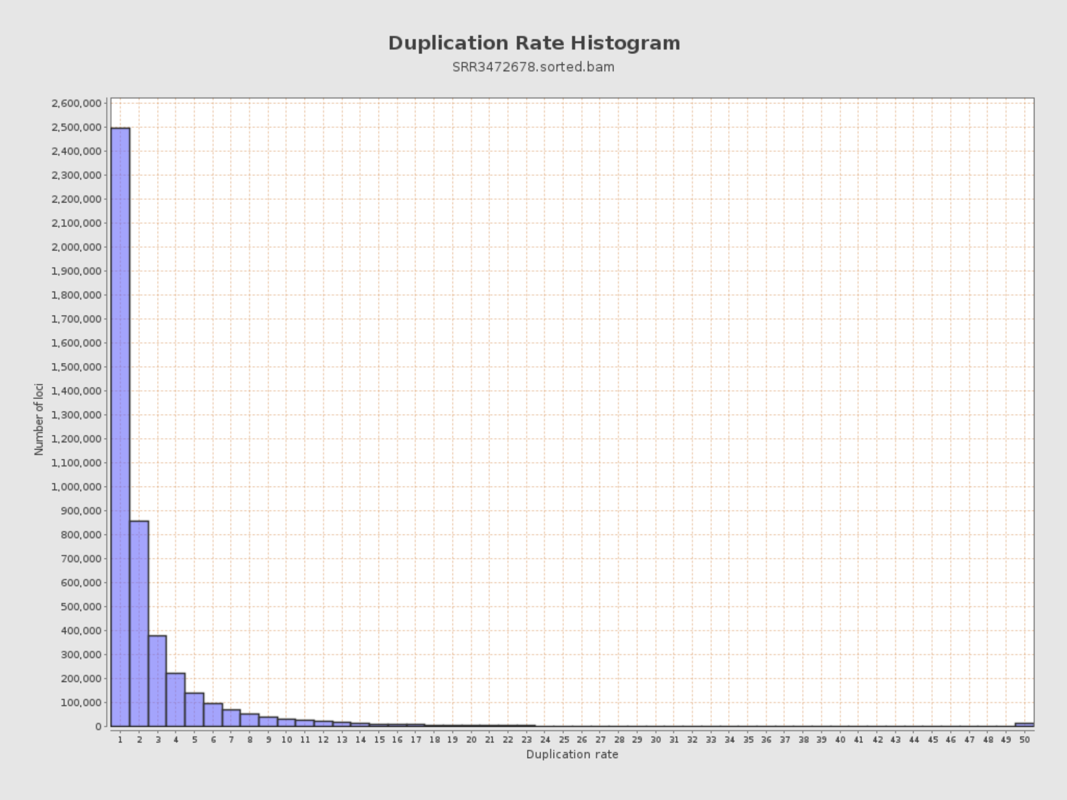
5. Results : Coverage Histogram (0-50X)



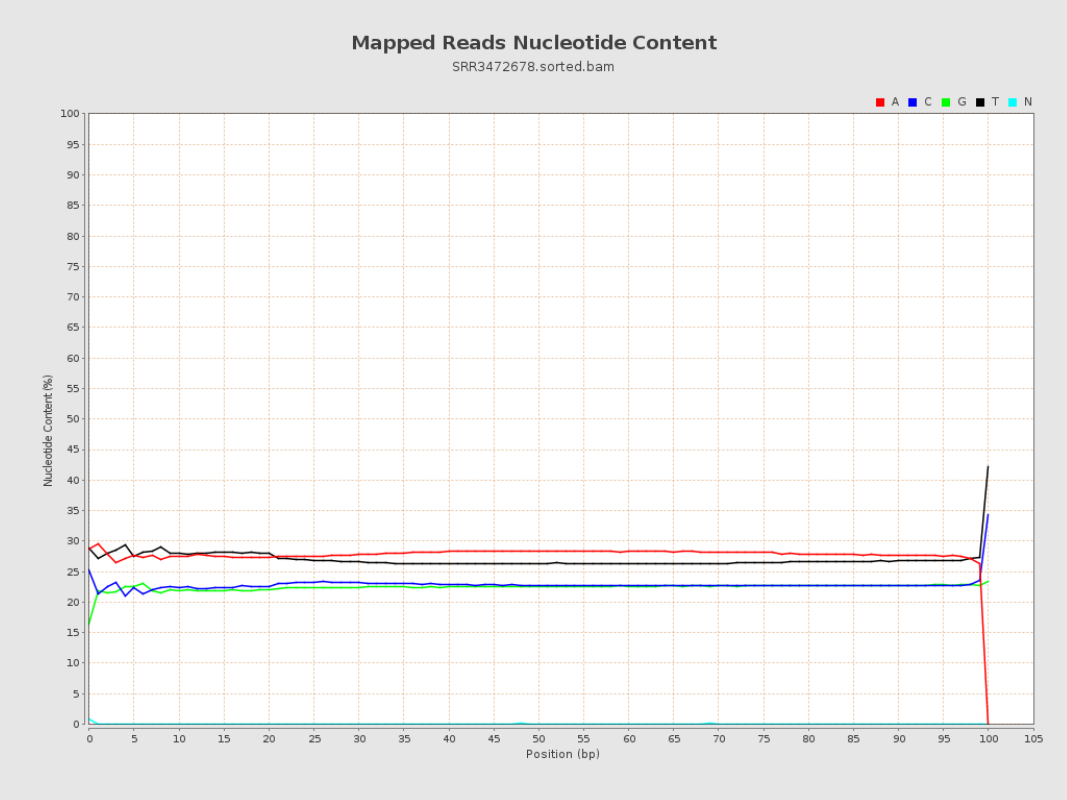
6. Results : Genome Fraction Coverage



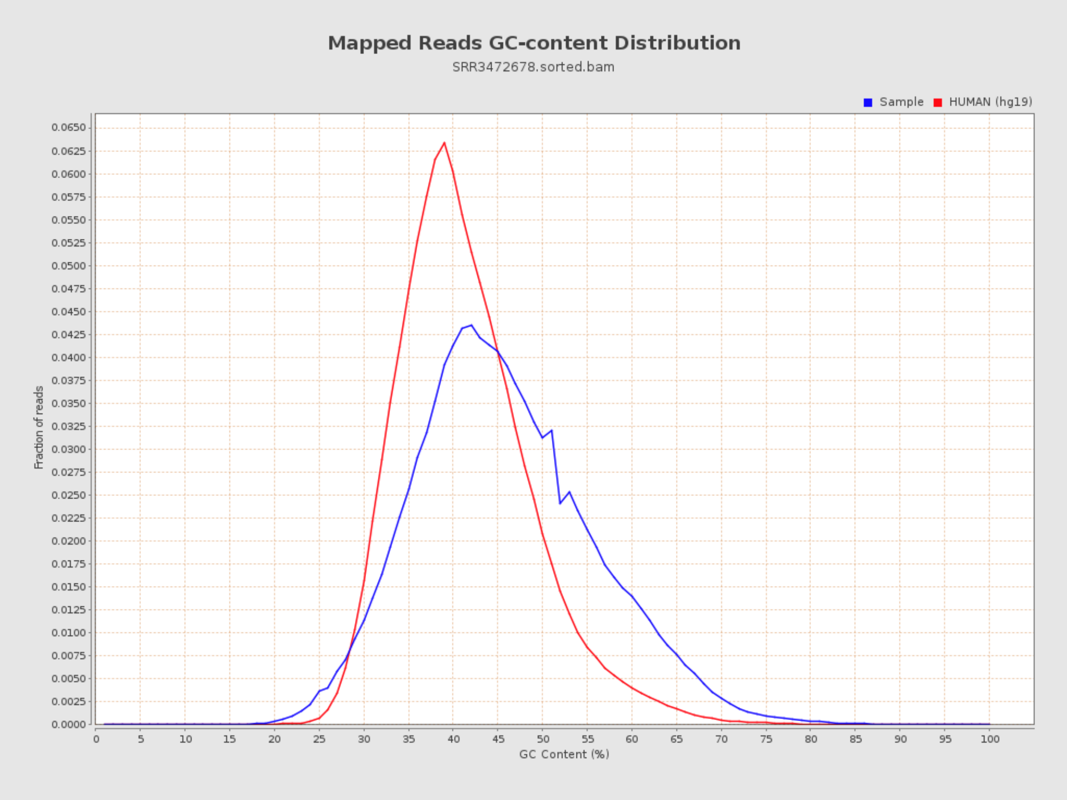
7. Results : Duplication Rate Histogram



8. Results : Mapped Reads Nucleotide Content

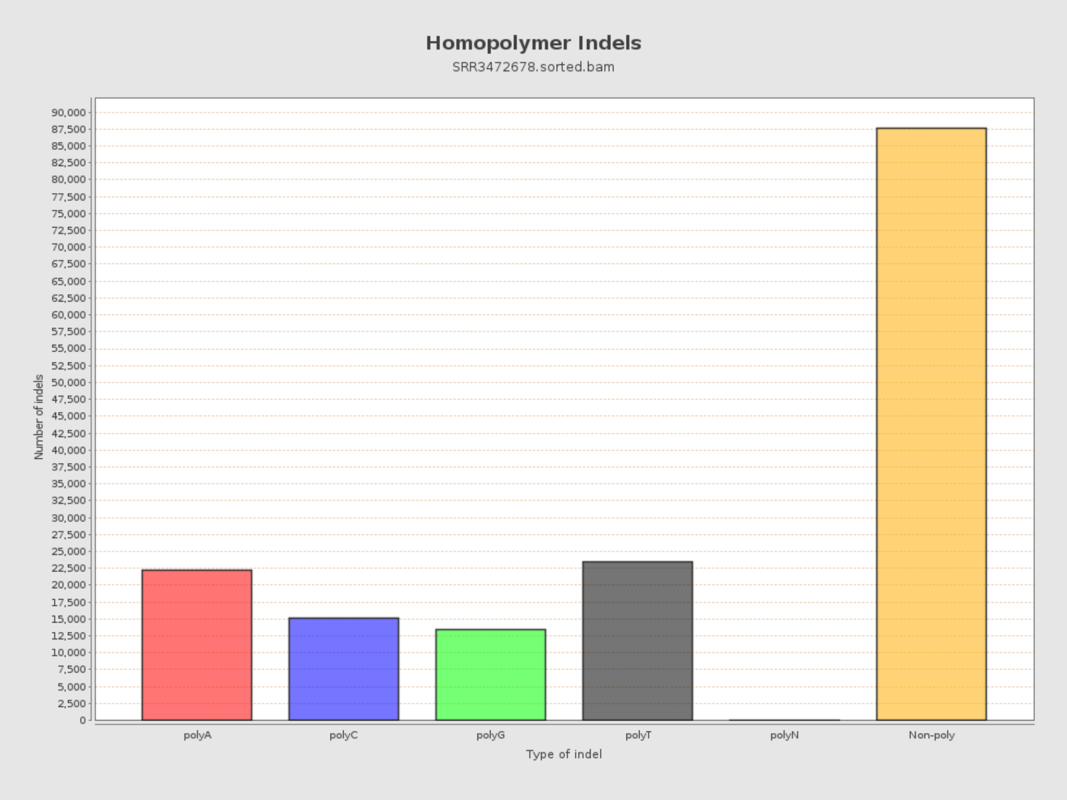


9. Results : Mapped Reads GC-content Distribution

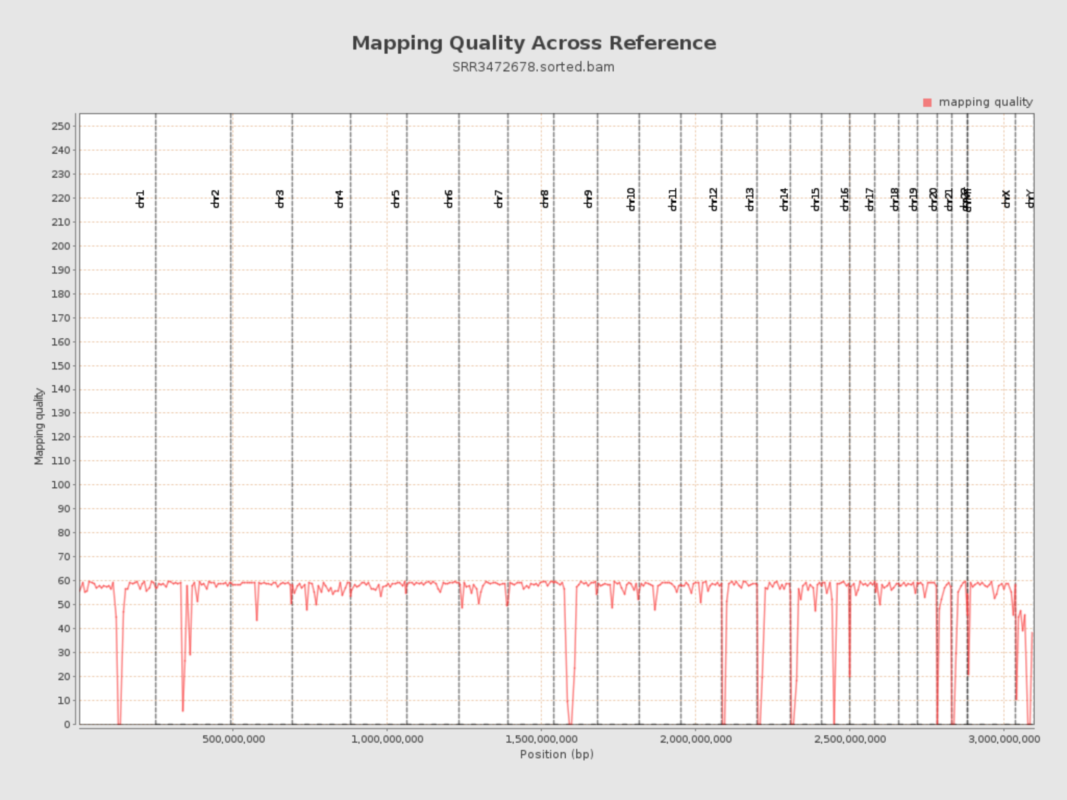


10. Results : Mapped Reads Clipping Profile

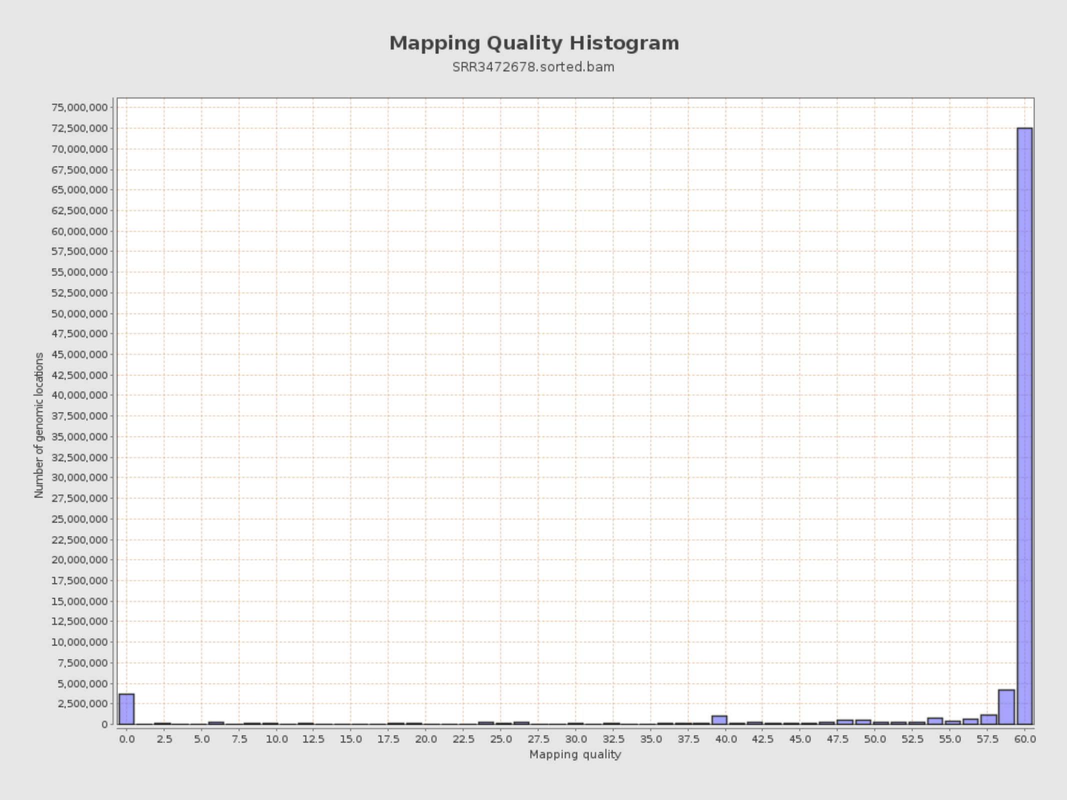
11. Results : Homopolymer Indels



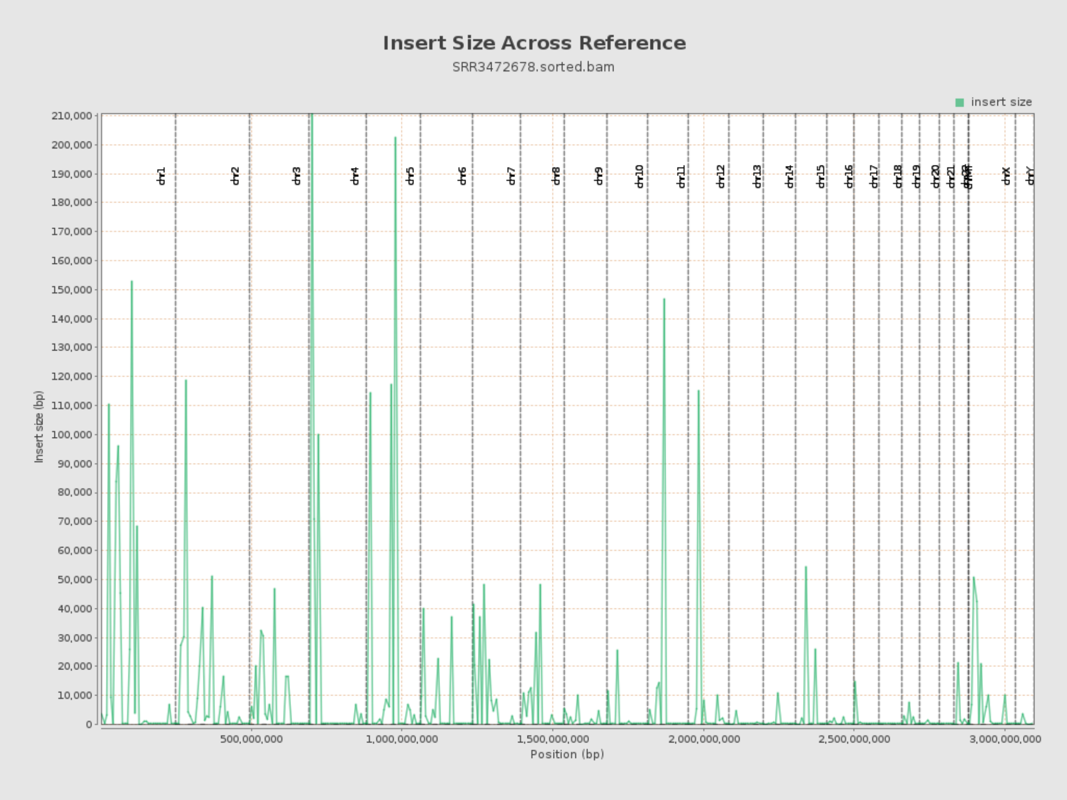
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram