Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 21:20:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472649.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_SRR3472649 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472649_1.fastq.gz SRR3472649_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 21:20:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472649.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,867,382
Mapped reads	9,791,994 / 99.24%
Unmapped reads	75,388 / 0.76%
Mapped paired reads	9,791,994 / 99.24%
Mapped reads, first in pair	4,902,517 / 49.68%
Mapped reads, second in pair	4,889,477 / 49.55%
Mapped reads, both in pair	9,743,470 / 98.74%
Mapped reads, singletons	48,524 / 0.49%
Secondary alignments	0
Supplementary alignments	47,526 / 0.48%
Read min/max/mean length	30 / 101 / 99.21
Duplicated reads (estimated)	6,691,019 / 67.81%
Duplication rate	43.59%
Clipped reads	588,893 / 5.97%

2.2. ACGT Content

Number/percentage of A's	255,640,131 / 26.63%
Number/percentage of C's	226,073,631 / 23.55%
Number/percentage of T's	256,163,400 / 26.68%
Number/percentage of G's	222,131,411 / 23.14%
Number/percentage of N's	131,893 / 0.01%

GC Percentage	46.68%

2.3. Coverage

Mean	0.3102
Standard Deviation	19.6958

2.4. Mapping Quality

Mean Mapping Quality	54.76

2.5. Insert size

Mean	17,277.92
Standard Deviation	1,320,763.89
P25/Median/P75	141 / 193 / 255

2.6. Mismatches and indels

General error rate	0.73%
Mismatches	6,896,509
Insertions	52,296
Mapped reads with at least one insertion	0.53%
Deletions	49,162
Mapped reads with at least one deletion	0.5%
Homopolymer indels	47.72%

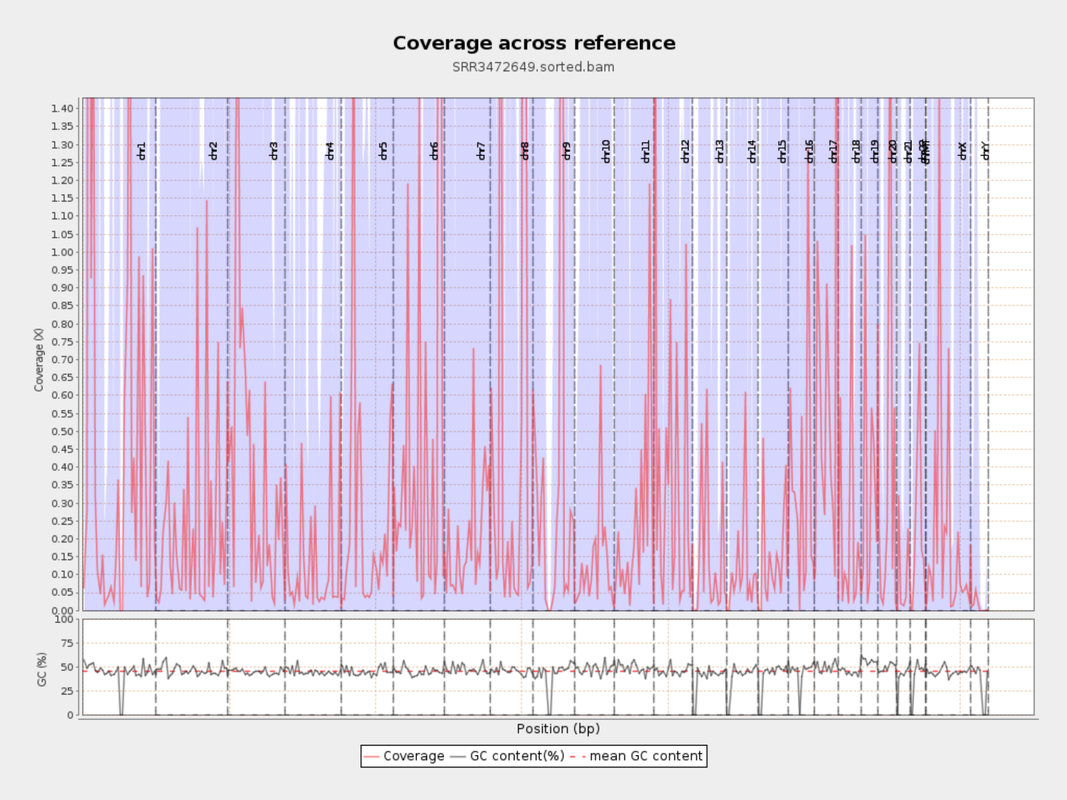
2.7. Chromosome stats

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

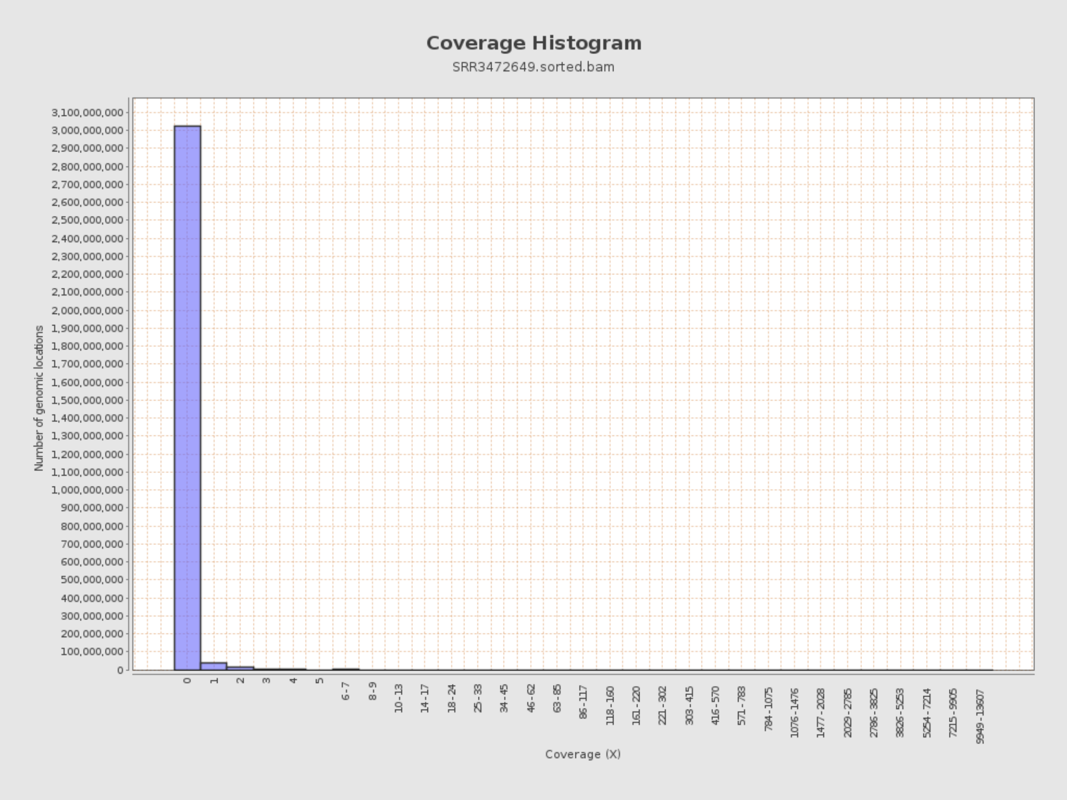
		bases	coverage	deviation
chr1	249250621	133368100	0.5351	29.2438
chr2	243199373	57133407	0.2349	10.5443
chr3	198022430	82174776	0.415	24.6174
chr4	191154276	26868878	0.1406	11.451
chr5	180915260	49425293	0.2732	14.7545
chr6	171115067	95952867	0.5608	25.8157
chr7	159138663	33228649	0.2088	8.9223
chr8	146364022	84263205	0.5757	34.9828
chr9	141213431	52066451	0.3687	32.9347
chr10	135534747	18259313	0.1347	12.1862
chr11	135006516	31825023	0.2357	13.0786
chr12	133851895	55210228	0.4125	25.6839
chr13	115169878	16923450	0.1469	10.1848
chr14	107349540	12119569	0.1129	4.4768
chr15	102531392	15141866	0.1477	9.5044
chr16	90354753	30424203	0.3367	12.3669
chr17	81195210	52362843	0.6449	24.3298
chr18	78077248	16989186	0.2176	17.3022
chr19	59128983	21144660	0.3576	14.7118
chr20	63025520	24275295	0.3852	18.3962
chr21	48129895	5113341	0.1062	6.5181
chr22	51304566	12865149	0.2508	13.4454
chrMT	16571	184	0.0111	0.1048
chrX	155270560	32293765	0.208	14.2533

chrY	59373566	859549	0.0145	0.8259

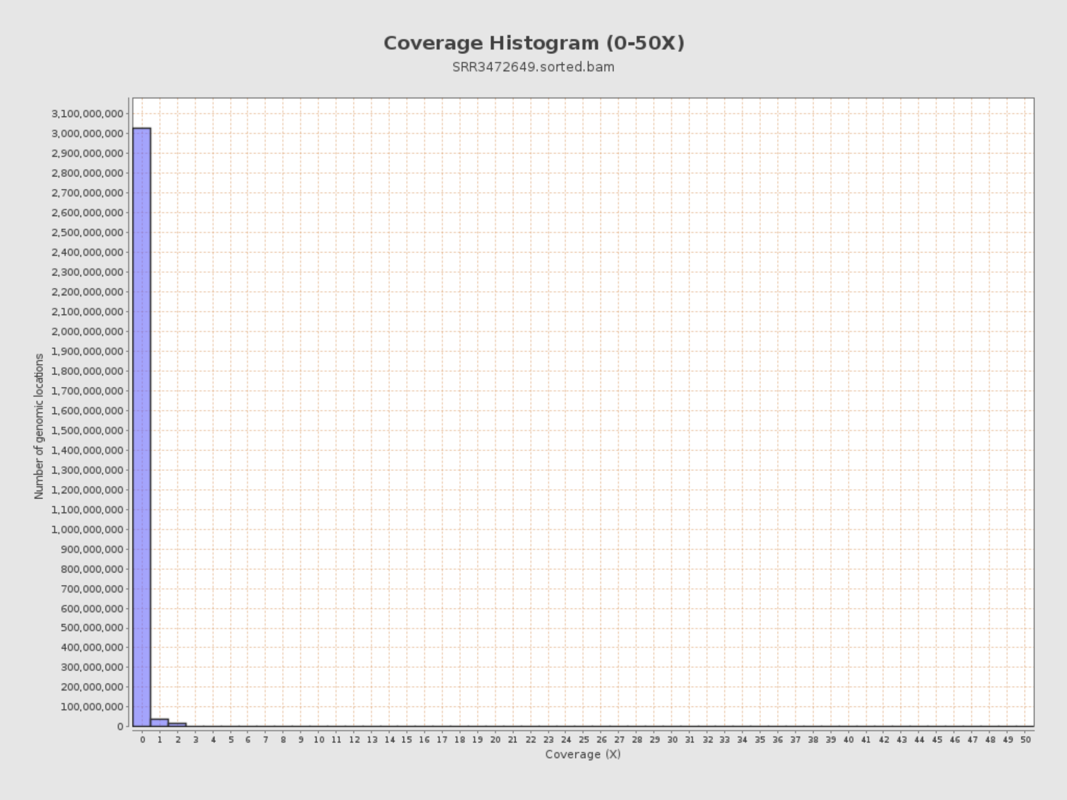
3. Results : Coverage across reference



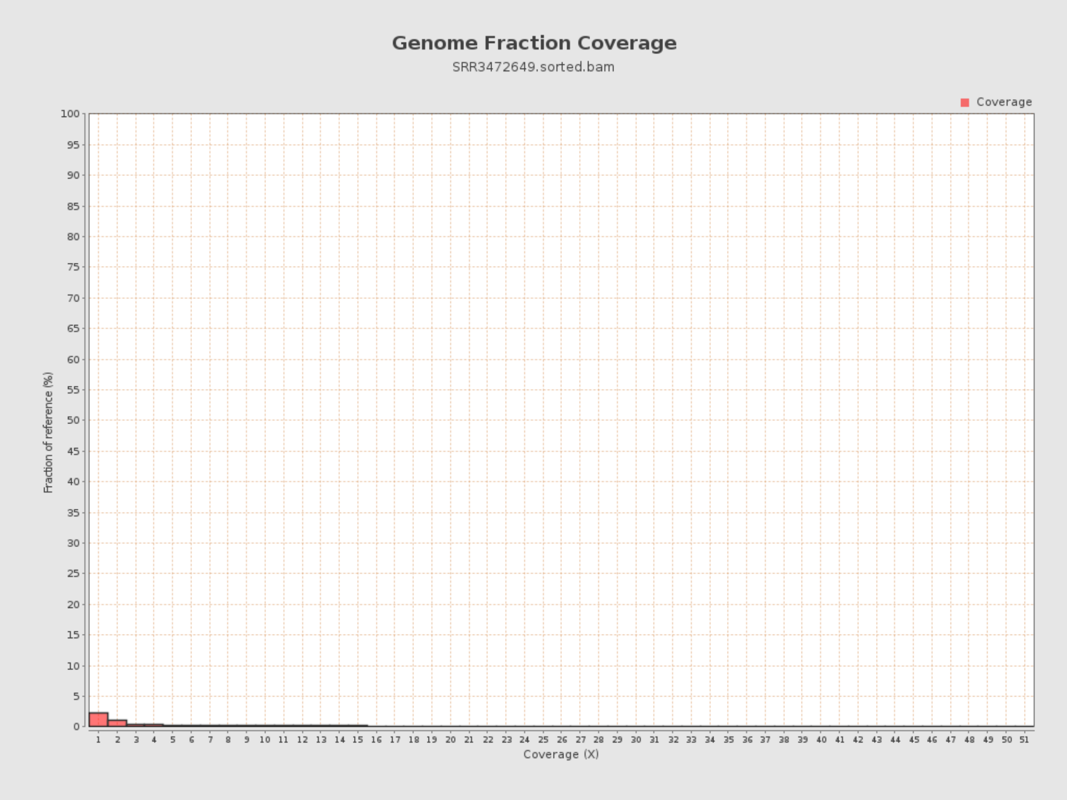
4. Results : Coverage Histogram



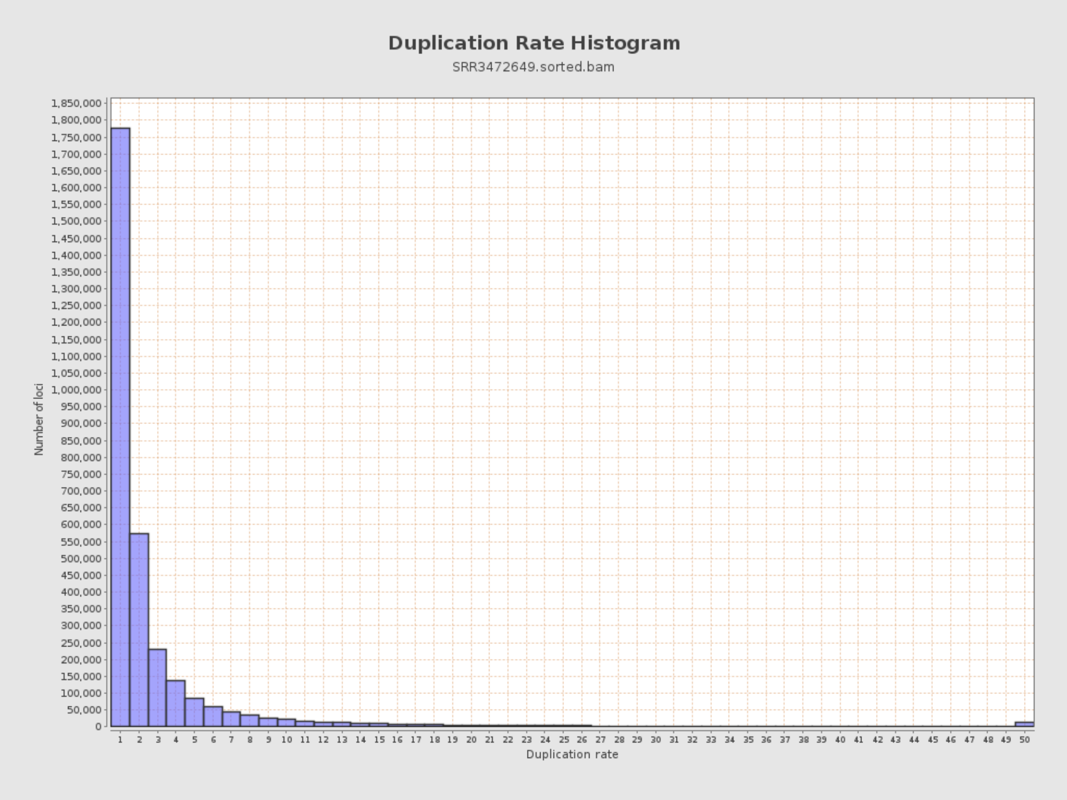
5. Results : Coverage Histogram (0-50X)



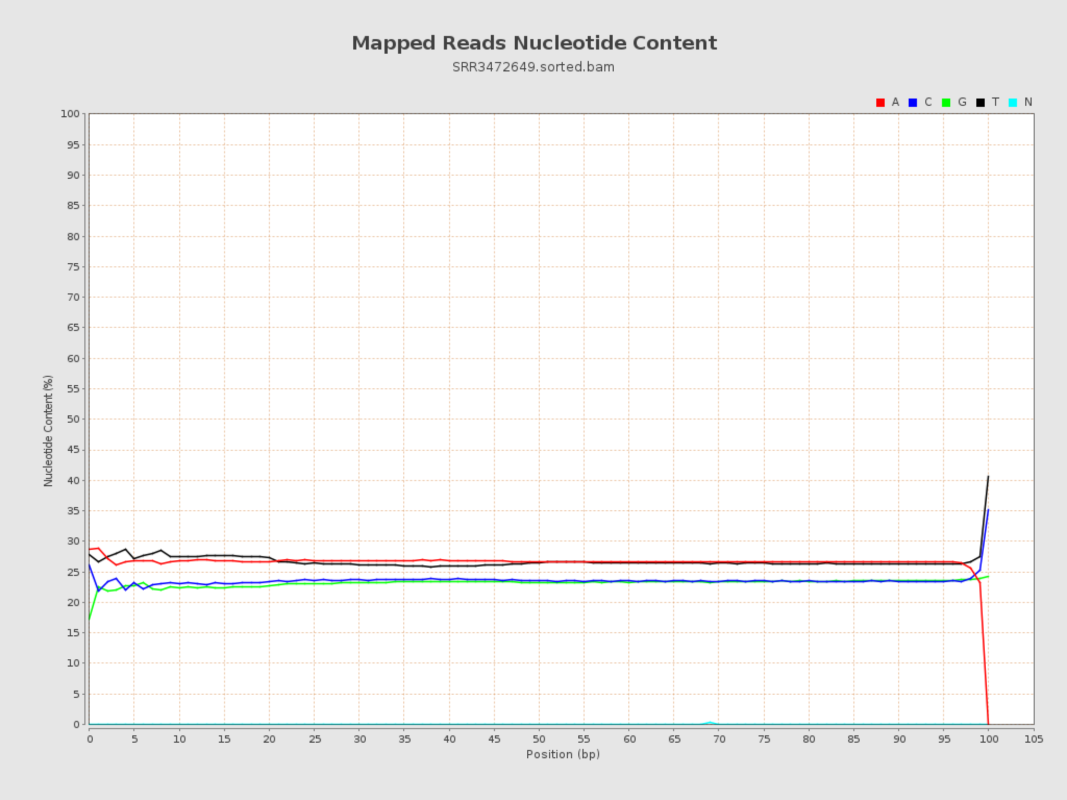
6. Results : Genome Fraction Coverage



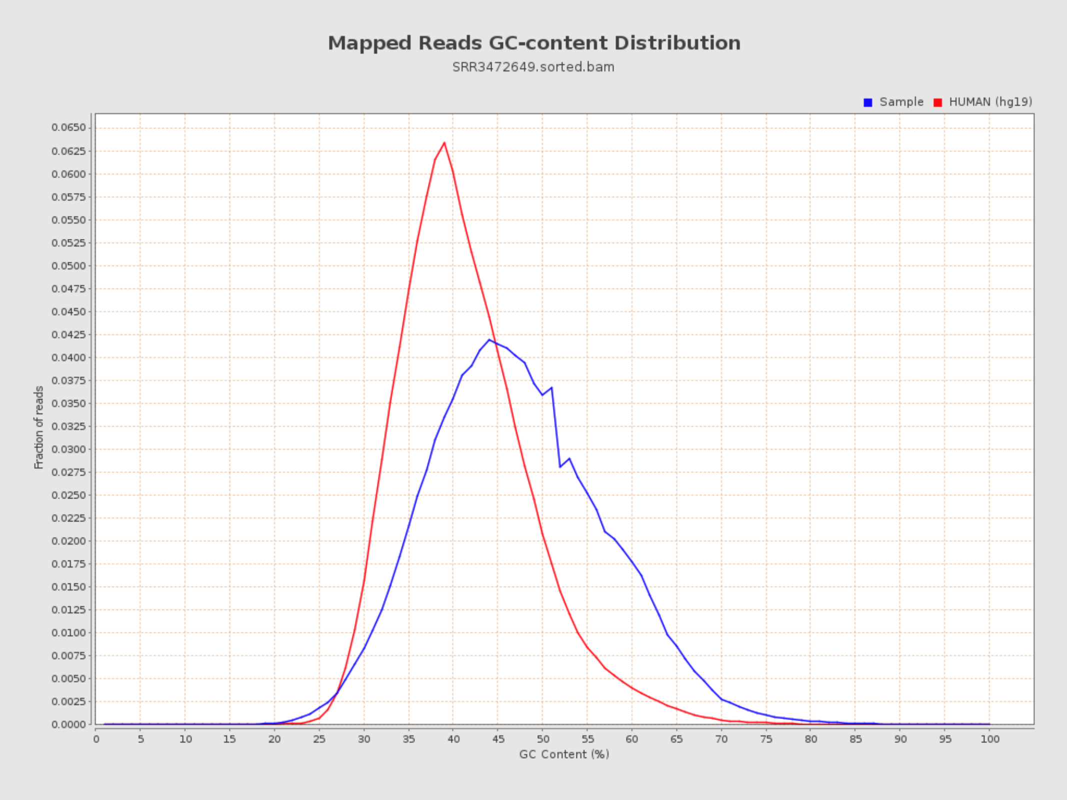
7. Results : Duplication Rate Histogram



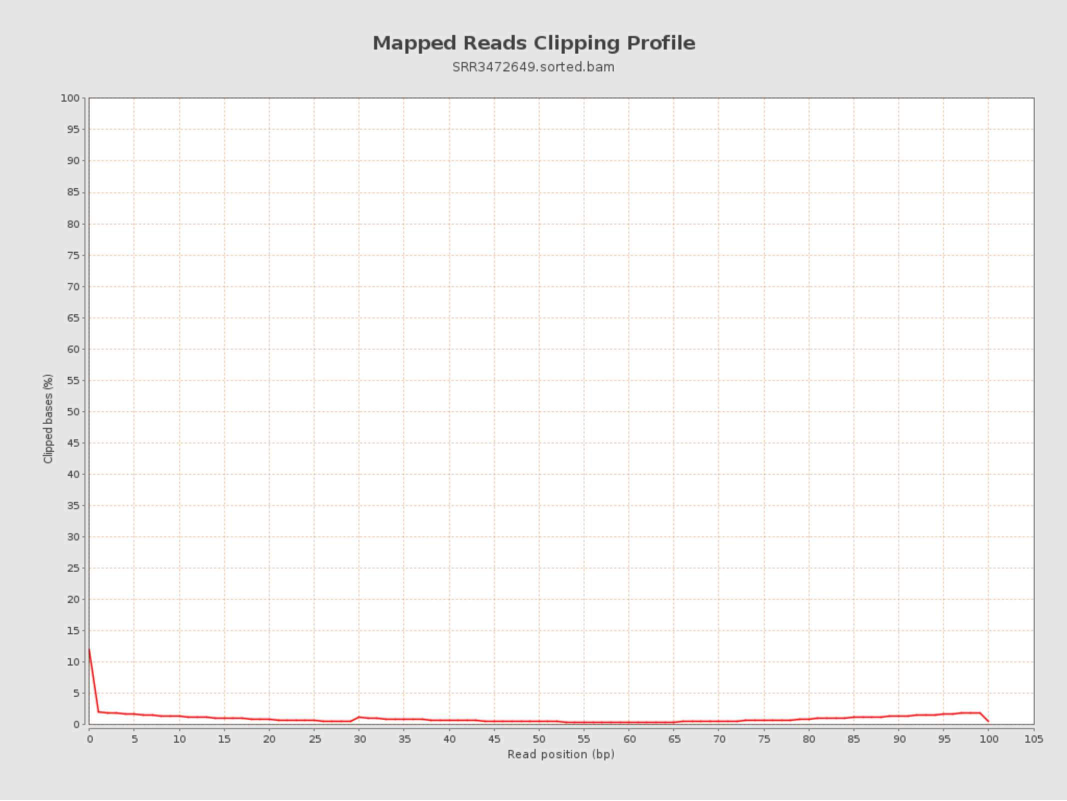
8. Results : Mapped Reads Nucleotide Content



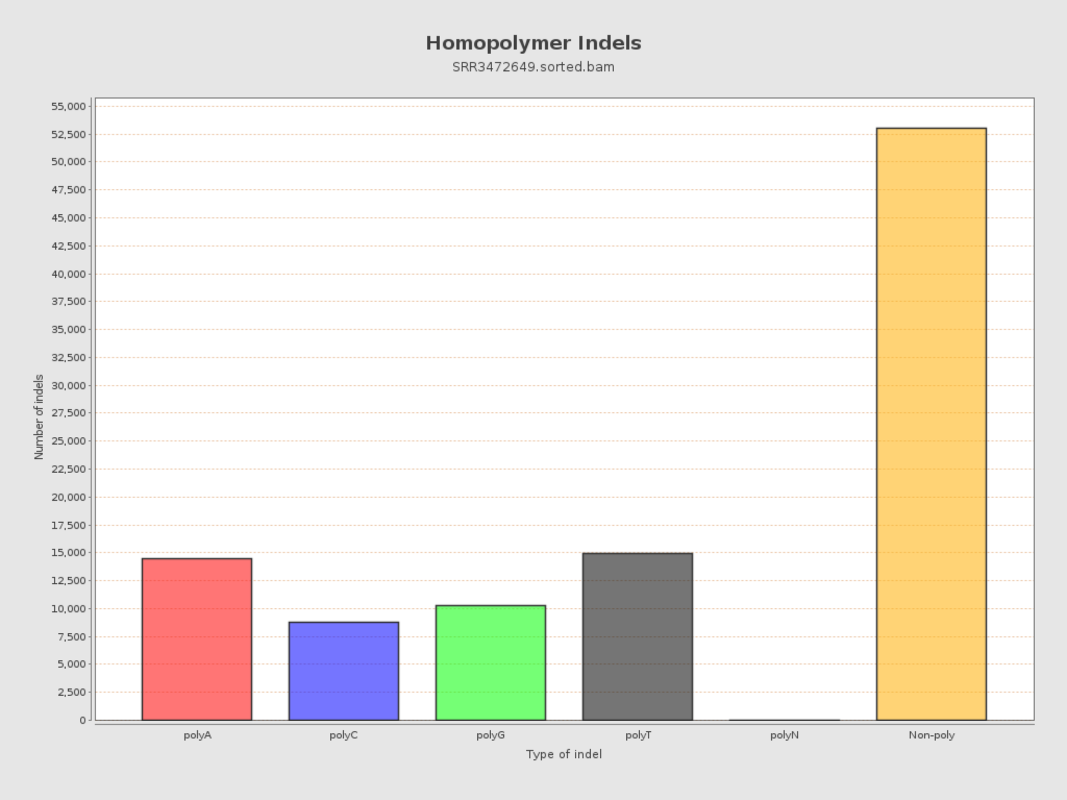
9. Results : Mapped Reads GC-content Distribution



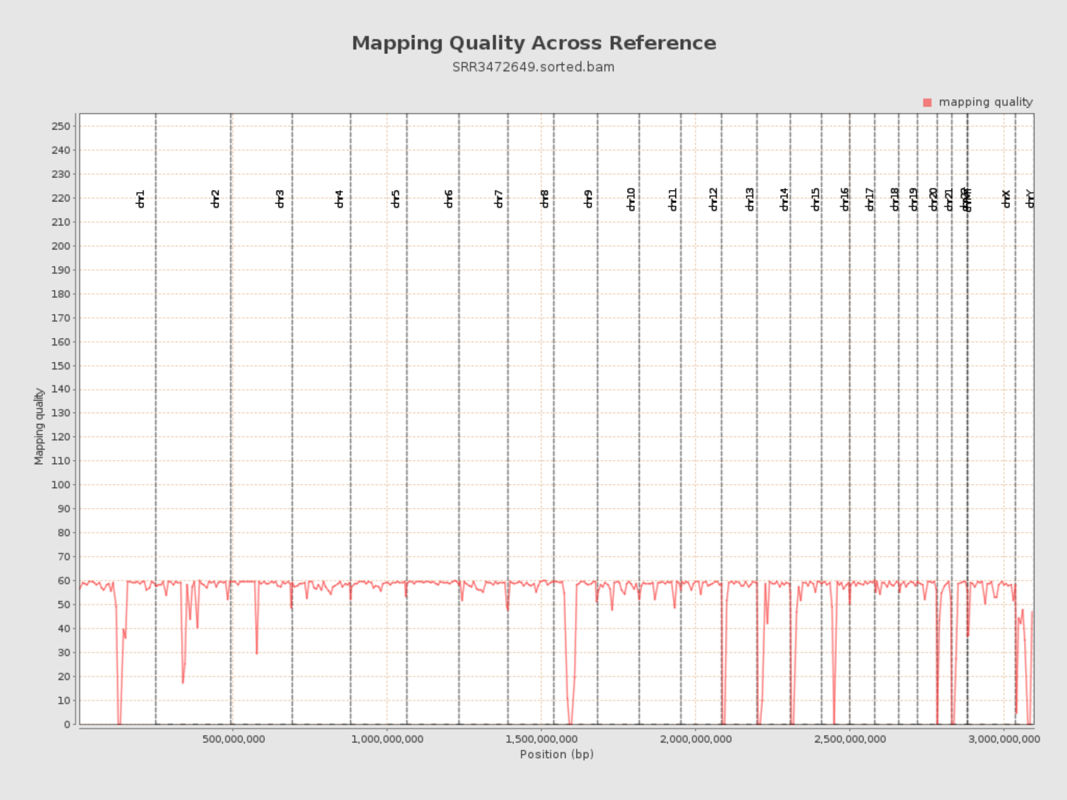
10. Results : Mapped Reads Clipping Profile



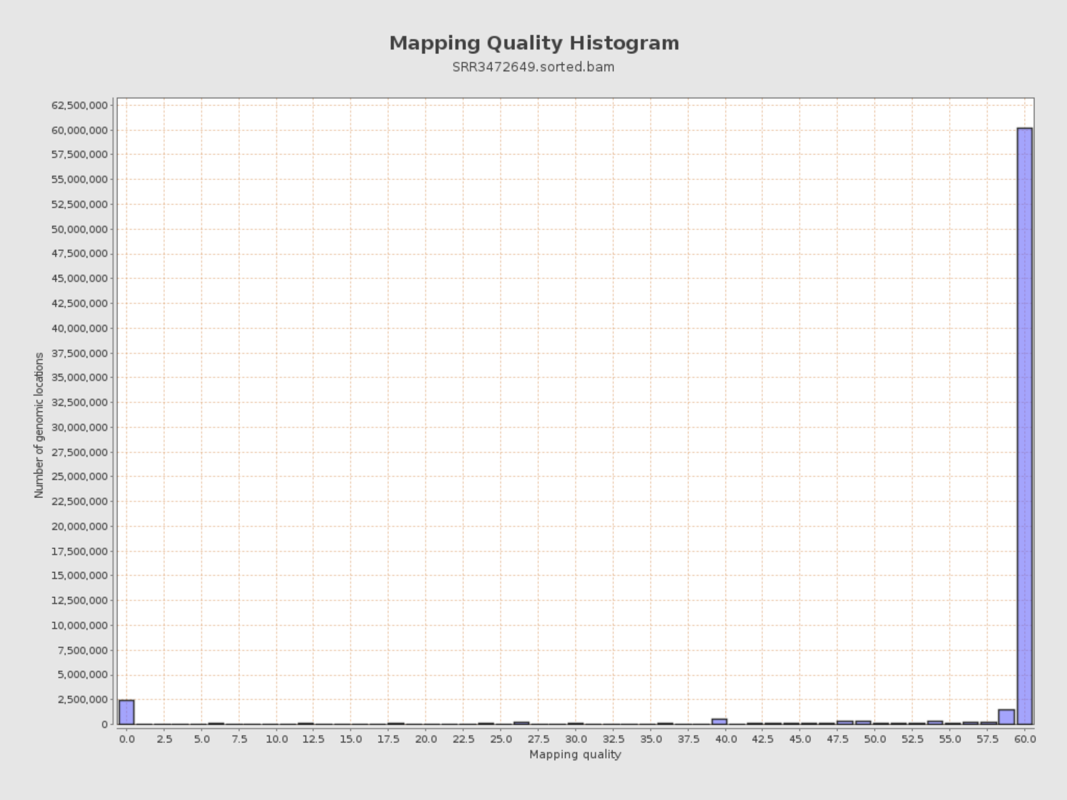
11. Results : Homopolymer Indels



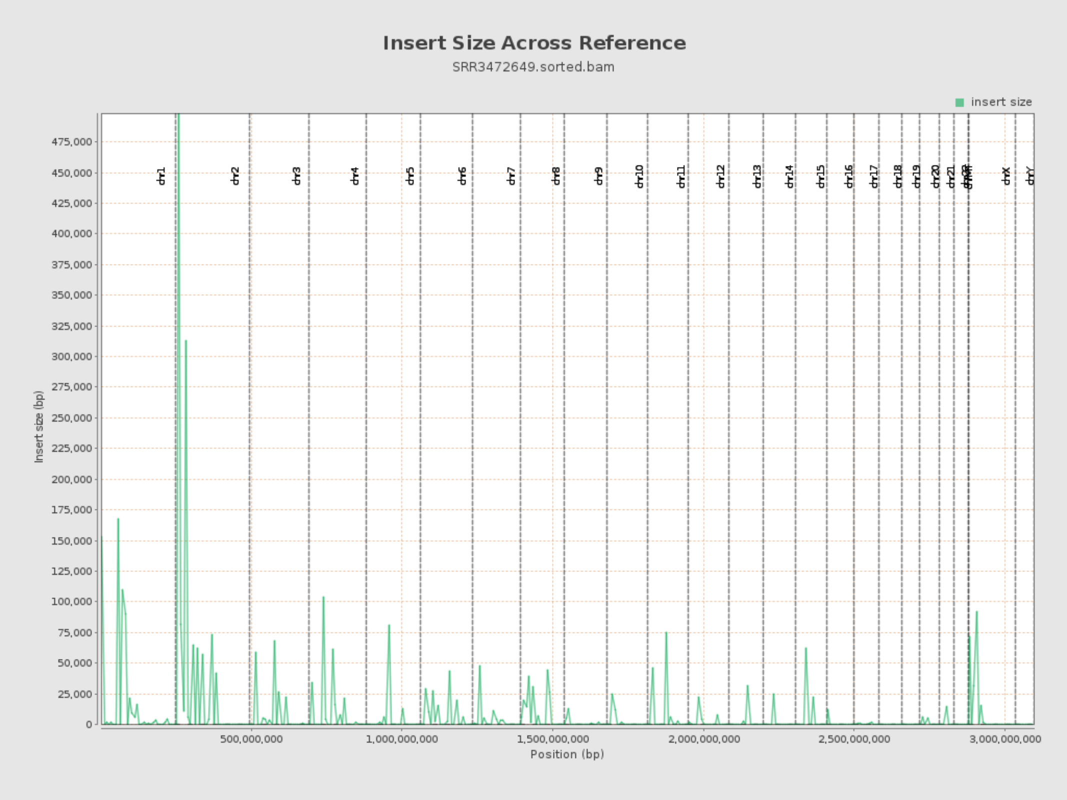
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram