Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 11:30:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472693.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_SRR3472693 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472693_1.fastq.gz SRR3472693_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 11:30:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472693.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	83,263,976
Mapped reads	82,567,370 / 99.16%
Unmapped reads	696,606 / 0.84%
Mapped paired reads	82,567,370 / 99.16%
Mapped reads, first in pair	41,406,658 / 49.73%
Mapped reads, second in pair	41,160,712 / 49.43%
Mapped reads, both in pair	82,130,210 / 98.64%
Mapped reads, singletons	437,160 / 0.53%
Secondary alignments	0
Supplementary alignments	540,530 / 0.65%
Read min/max/mean length	30 / 101 / 99.78
Duplicated reads (estimated)	68,014,169 / 81.68%
Duplication rate	52.16%
Clipped reads	5,919,095 / 7.11%

2.2. ACGT Content

Number/percentage of A's	2,182,673,739 / 26.86%
Number/percentage of C's	1,885,722,427 / 23.21%
Number/percentage of T's	2,191,479,563 / 26.97%
Number/percentage of G's	1,864,101,736 / 22.94%
Number/percentage of N's	1,634,330 / 0.02%

GC Percentage	46.15%

2.3. Coverage

Mean	2.6253
Standard Deviation	115.2702

2.4. Mapping Quality

Mean Mapping Quality	54.99

2.5. Insert size

Mean	21,892.9
Standard Deviation	1,452,805.42
P25/Median/P75	156 / 213 / 283

2.6. Mismatches and indels

General error rate	0.57%
Mismatches	45,473,366
Insertions	521,469
Mapped reads with at least one insertion	0.63%
Deletions	444,730
Mapped reads with at least one deletion	0.53%
Homopolymer indels	44.58%

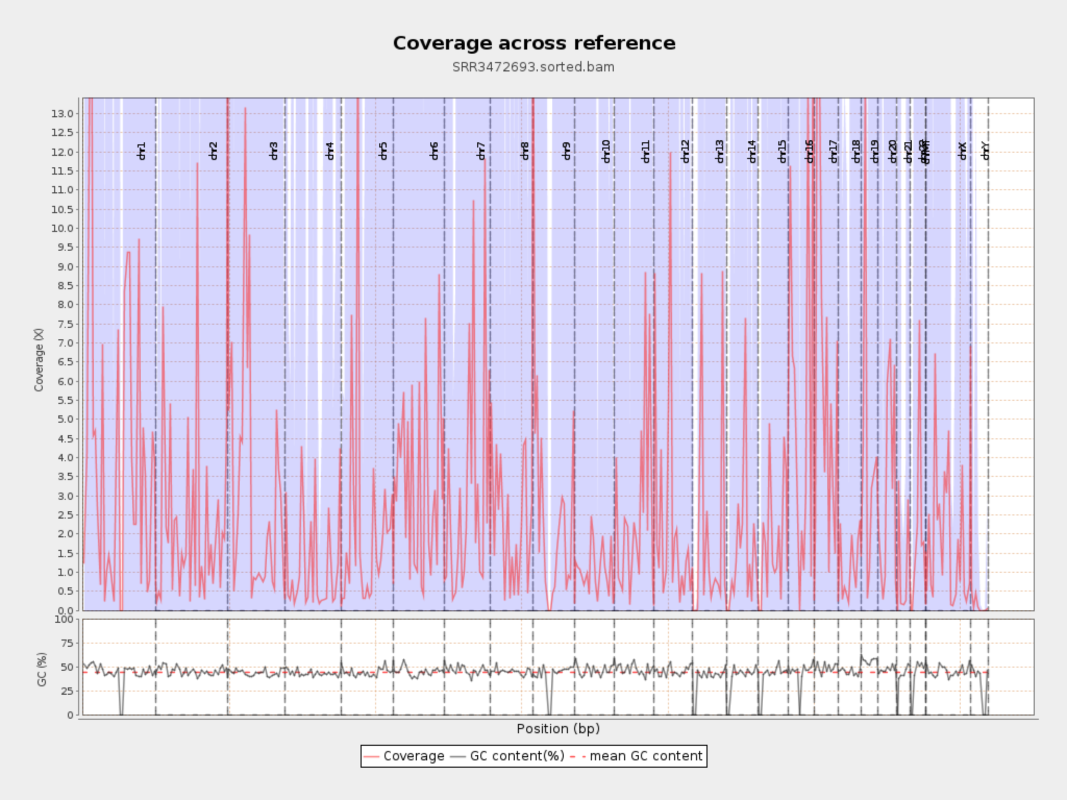
2.7. Chromosome stats

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

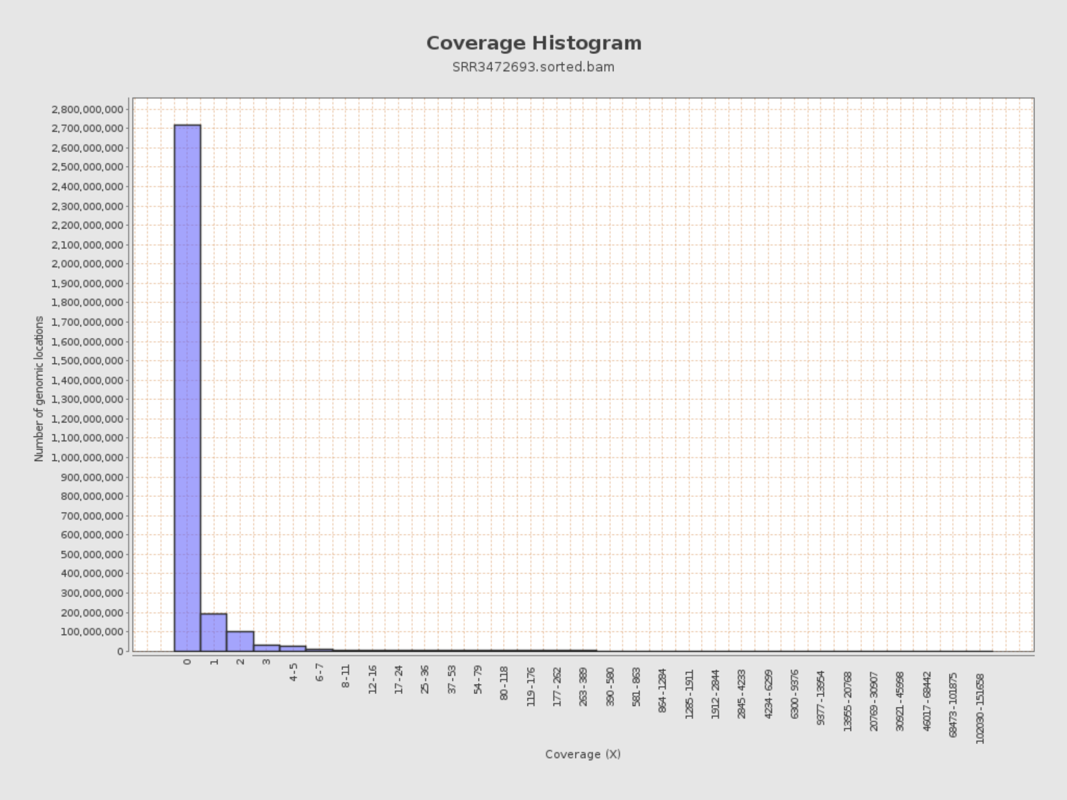
		bases	coverage	deviation
chr1	249250621	1056093286	4.2371	156.4716
chr2	243199373	545032179	2.2411	107.9786
chr3	198022430	657841395	3.3221	76.6134
chr4	191154276	238102722	1.2456	47.9075
chr5	180915260	415764138	2.2981	162.7788
chr6	171115067	570650683	3.3349	92.9112
chr7	159138663	507470925	3.1889	169.7698
chr8	146364022	338579971	2.3133	65.7795
chr9	141213431	311639094	2.2069	58.5137
chr10	135534747	149550309	1.1034	40.5162
chr11	135006516	341271278	2.5278	88.6372
chr12	133851895	340253779	2.542	90.2651
chr13	115169878	228456397	1.9836	96.4265
chr14	107349540	172875522	1.6104	47.0795
chr15	102531392	183689839	1.7915	67.8317
chr16	90354753	531498240	5.8823	222.4469
chr17	81195210	522416141	6.4341	295.7456
chr18	78077248	85035837	1.0891	35.21
chr19	59128983	247736704	4.1898	104.5245
chr20	63025520	206708250	3.2798	114.8856
chr21	48129895	56243773	1.1686	74.0282
chr22	51304566	110688912	2.1575	77.3352
chrMT	16571	25709	1.5514	1.6178
chrX	155270560	301506602	1.9418	68.9322

chrY	59373566	8073618	0.136	8.8728

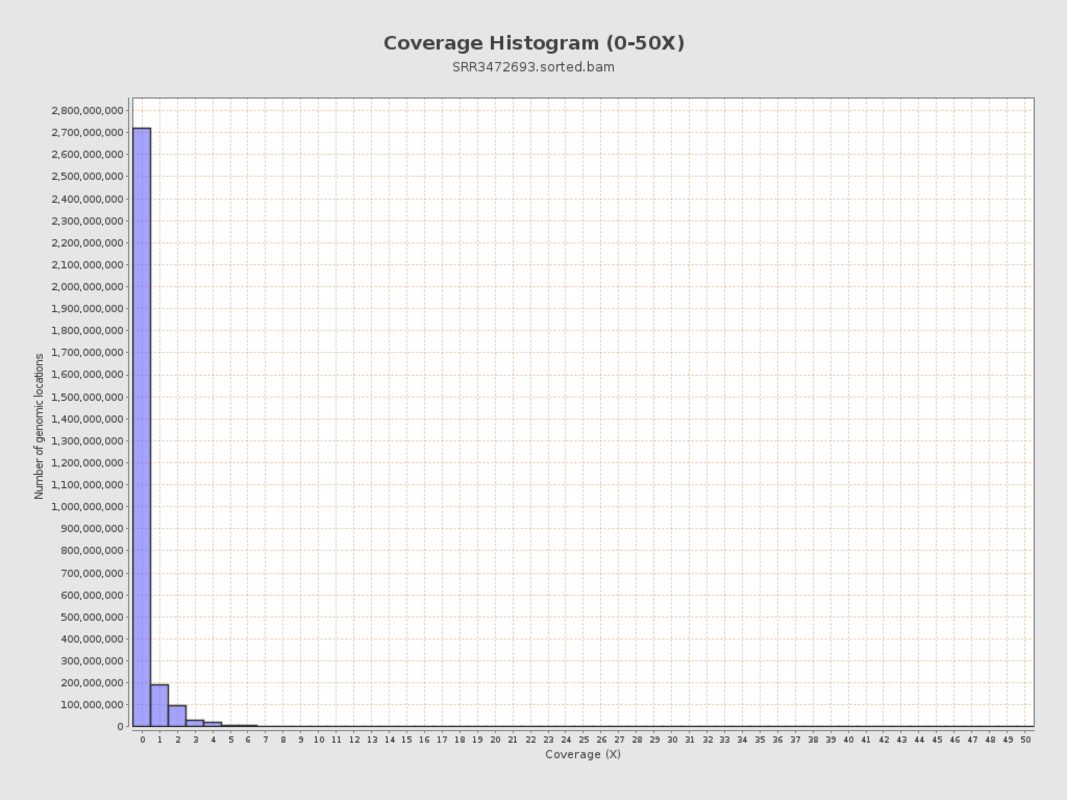
3. Results : Coverage across reference



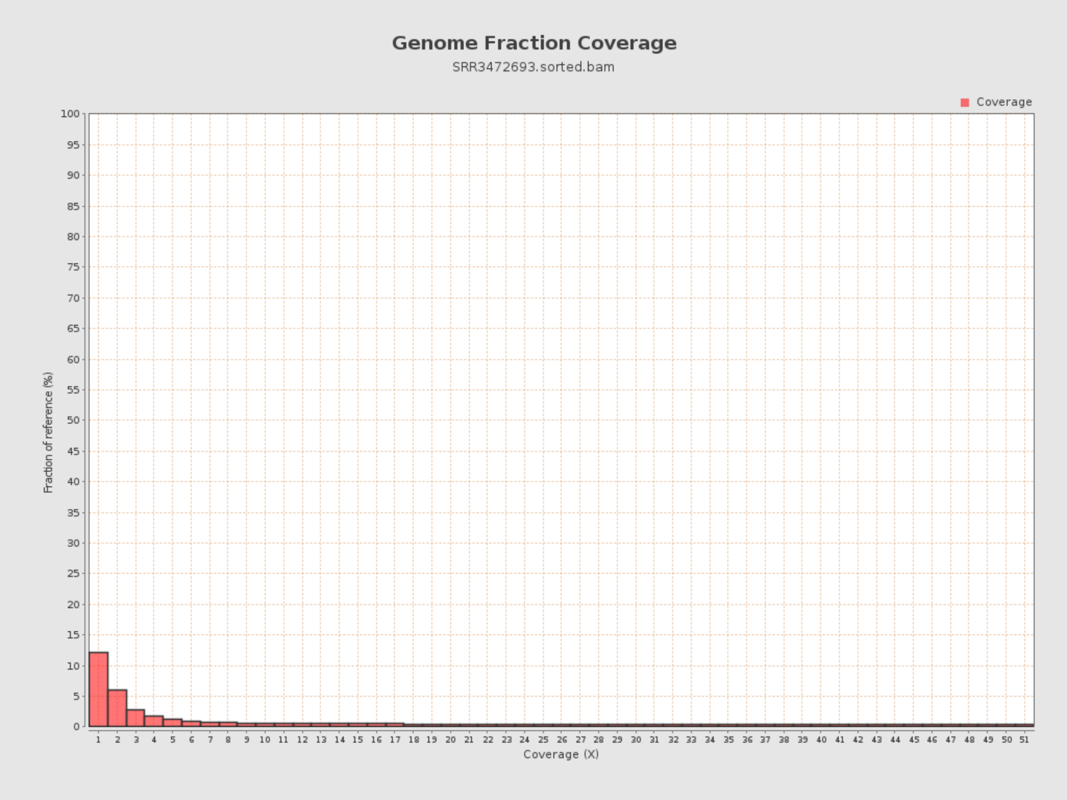
4. Results : Coverage Histogram



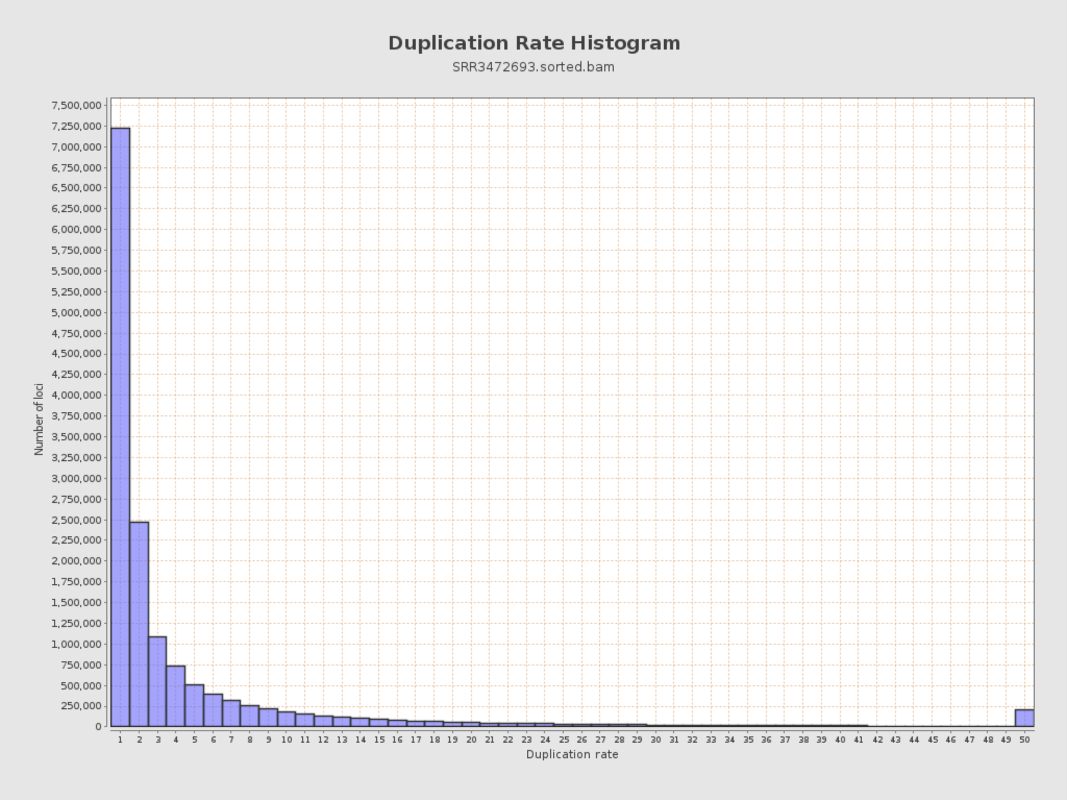
5. Results : Coverage Histogram (0-50X)



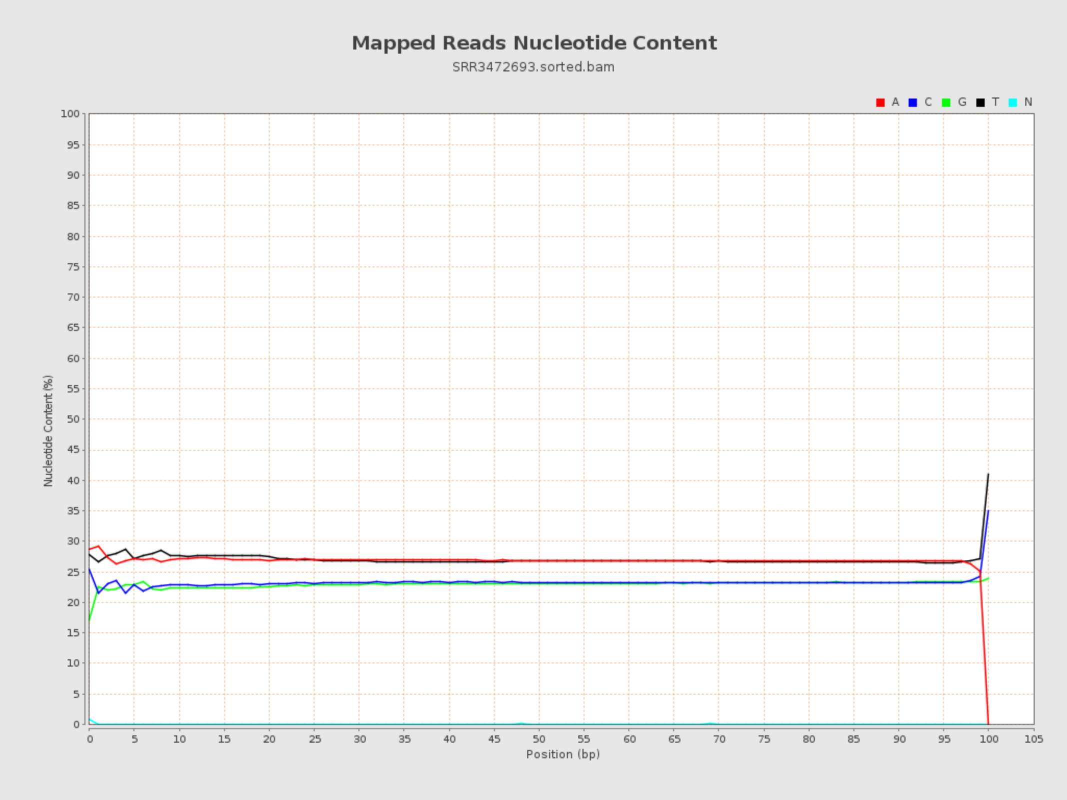
6. Results : Genome Fraction Coverage



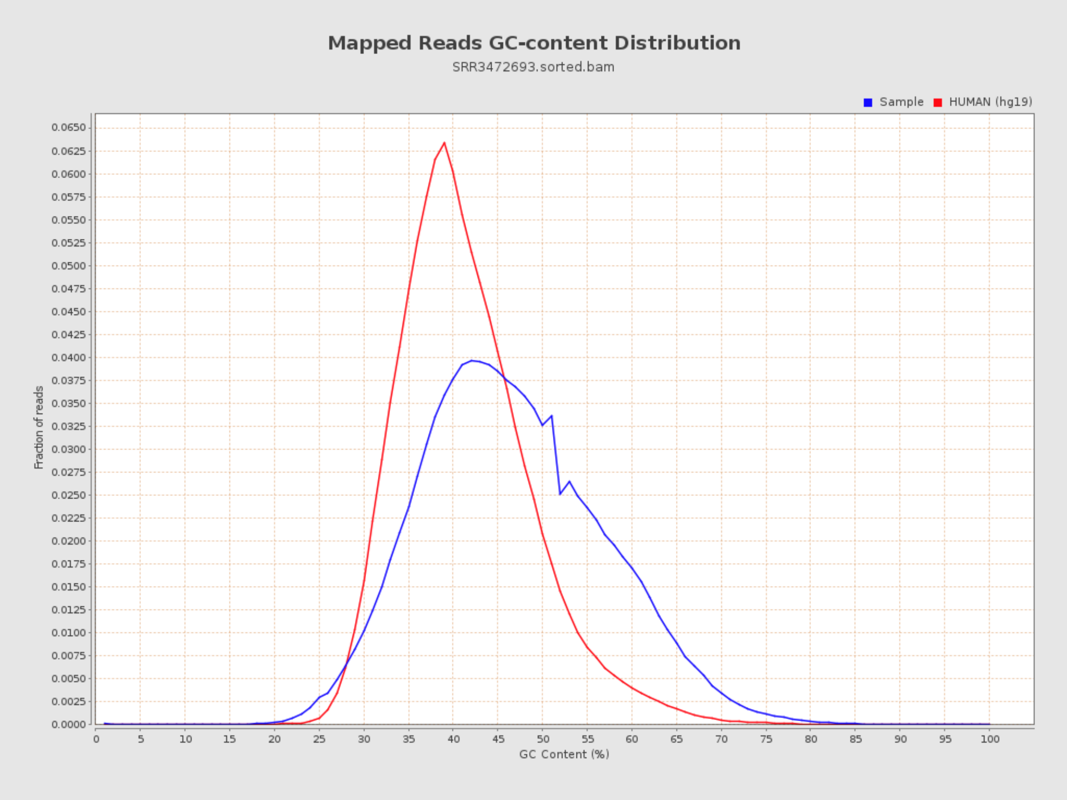
7. Results : Duplication Rate Histogram



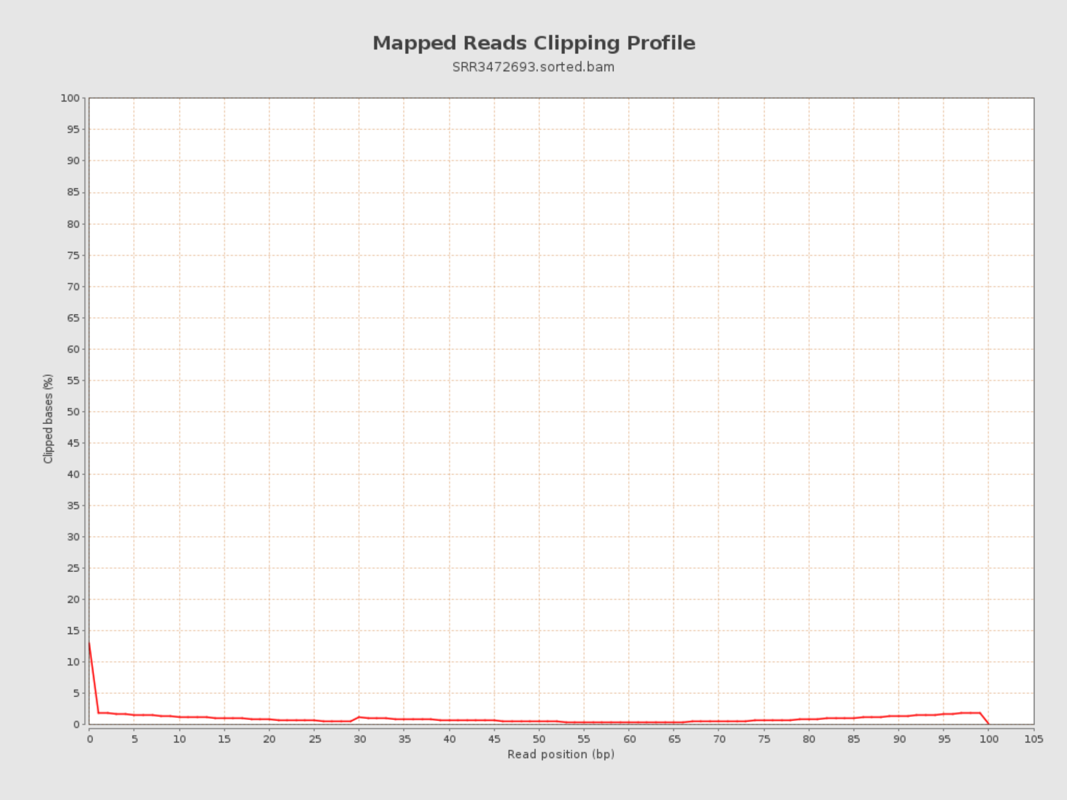
8. Results : Mapped Reads Nucleotide Content



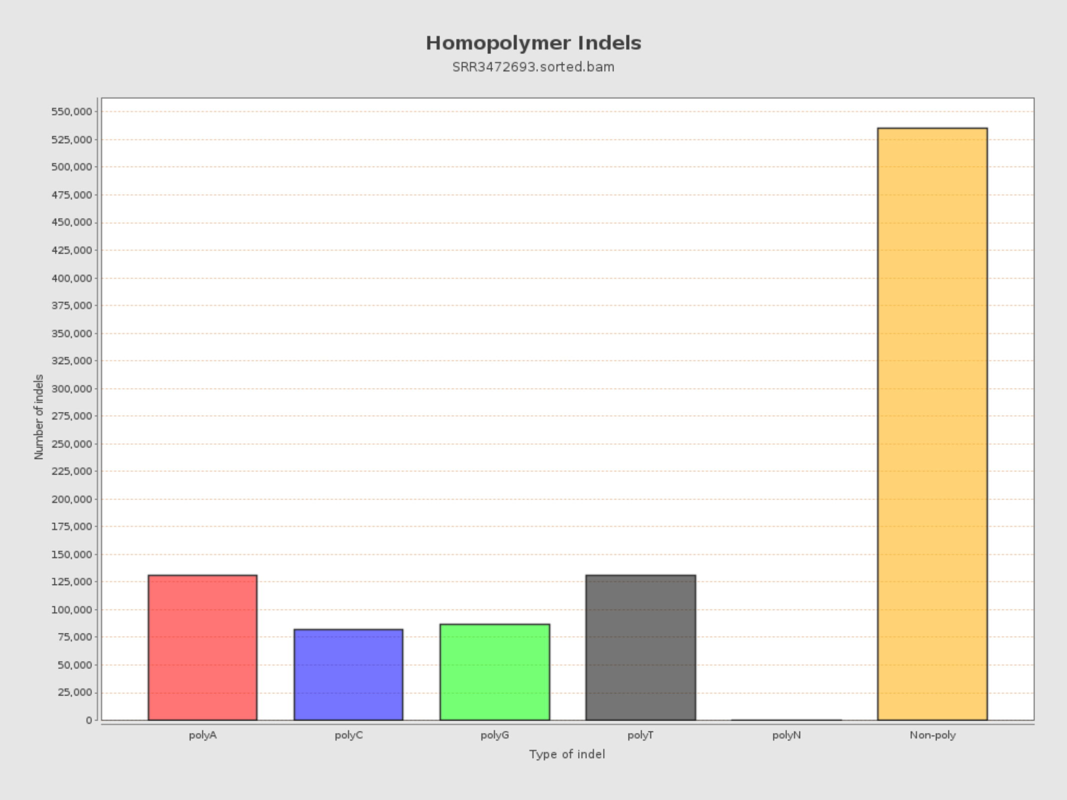
9. Results : Mapped Reads GC-content Distribution



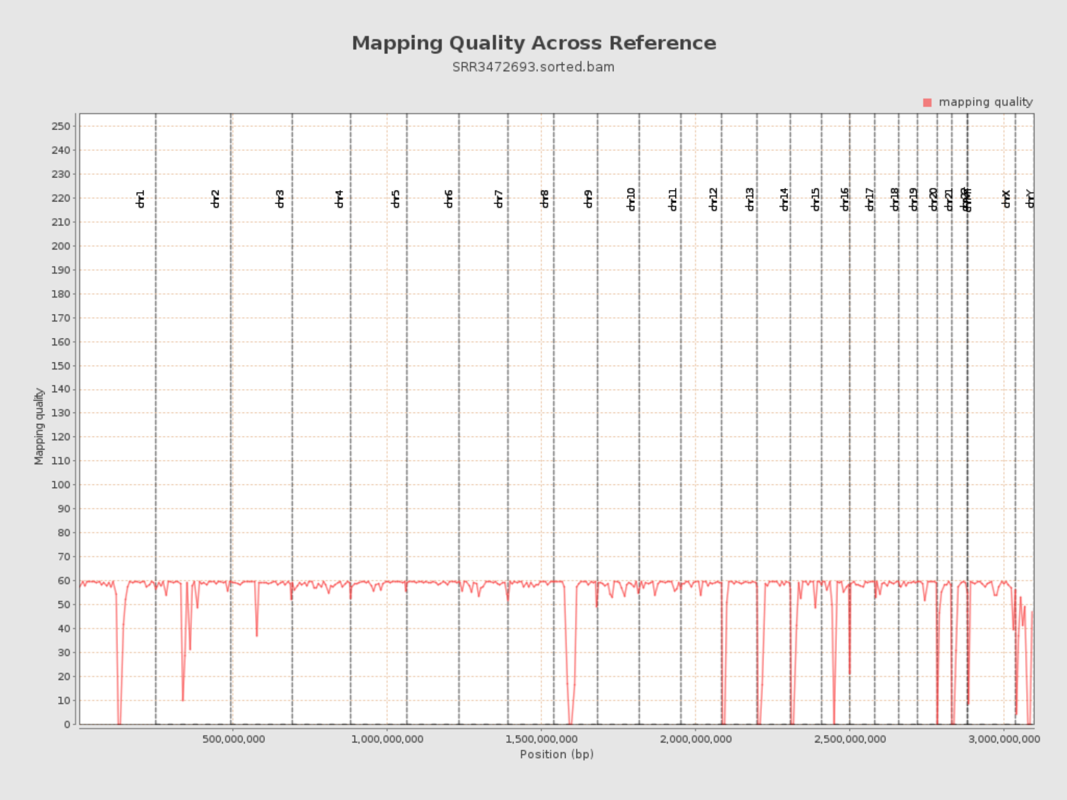
10. Results : Mapped Reads Clipping Profile



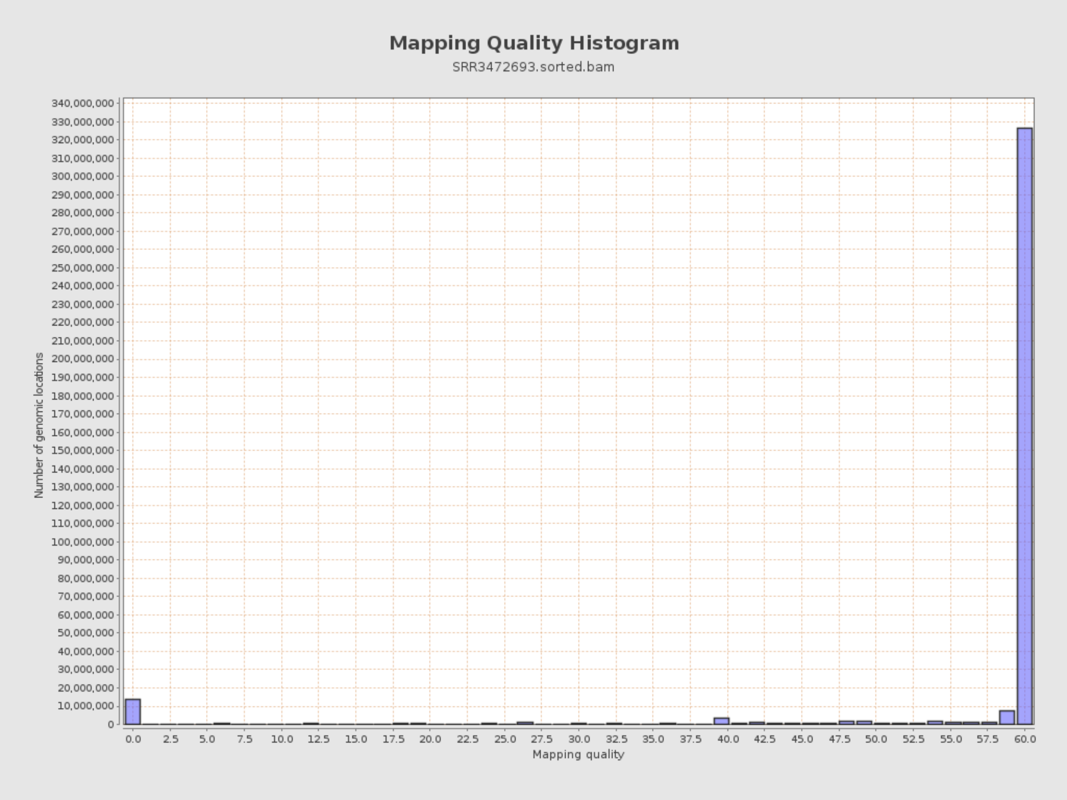
11. Results : Homopolymer Indels



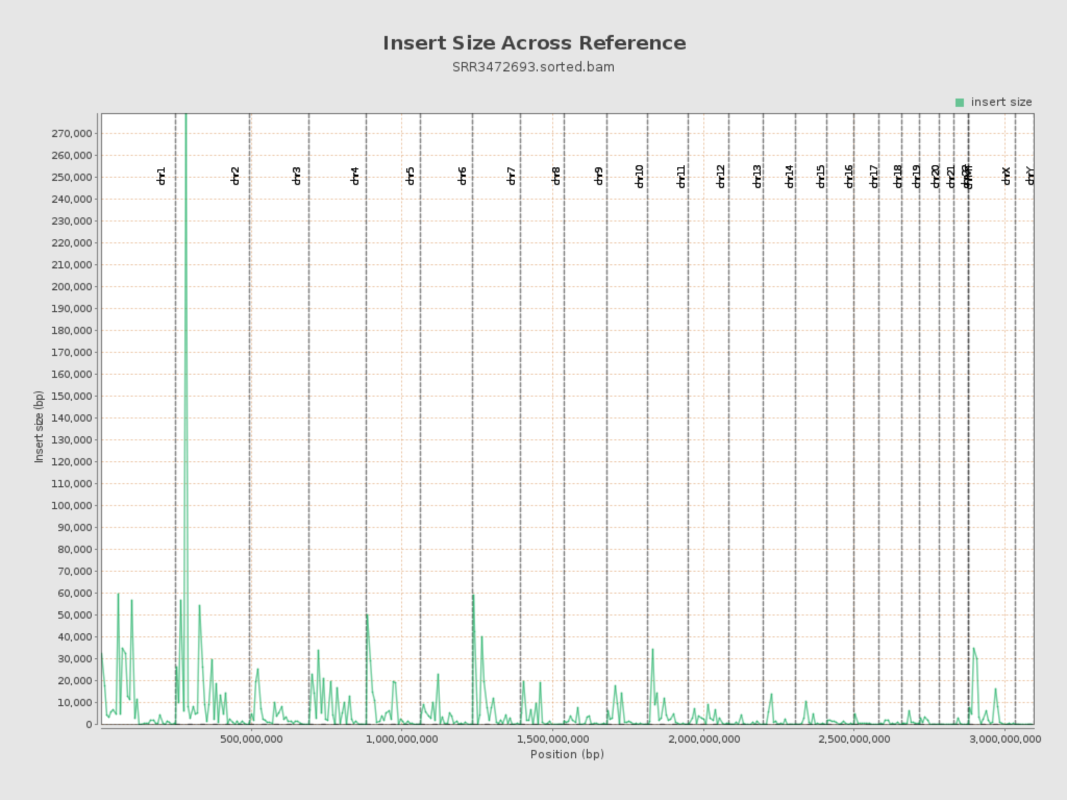
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram