

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/02/19 03:10:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR16362021.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_SRR16362021 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR16362021_1.fastq.gz SRR16362021_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Feb 19 03:10:13 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR16362021.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	94,721,674
Mapped reads	43,964,229 / 46.41%
Unmapped reads	50,757,445 / 53.59%
Mapped paired reads	43,964,229 / 46.41%
Mapped reads, first in pair	4,354,933 / 4.6%
Mapped reads, second in pair	39,609,296 / 41.82%
Mapped reads, both in pair	7,762,832 / 8.2%
Mapped reads, singletons	36,201,397 / 38.22%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	2,491,297 / 2.63%
Duplication rate	3.96%
Clipped reads	5,978,023 / 6.31%

2.2. ACGT Content

Number/percentage of A's	512,447,549 / 29.76%
Number/percentage of C's	345,112,565 / 20.04%
Number/percentage of T's	491,227,339 / 28.52%
Number/percentage of G's	373,360,347 / 21.68%
Number/percentage of N's	4,064 / 0%
GC Percentage	41.72%

2.3. Coverage

Mean	0.5564
Standard Deviation	4.6007

2.4. Mapping Quality

Mean Mapping Quality	44.84
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2.5. Insert size

Mean	314,157.29
Standard Deviation	5,616,504.06
P25/Median/P75	199 / 256 / 344

2.6. Mismatches and indels

General error rate	0.5%
Mismatches	8,476,997
Insertions	65,728
Mapped reads with at least one insertion	0.15%
Deletions	319,687
Mapped reads with at least one deletion	0.73%
Homopolymer indels	45.4%

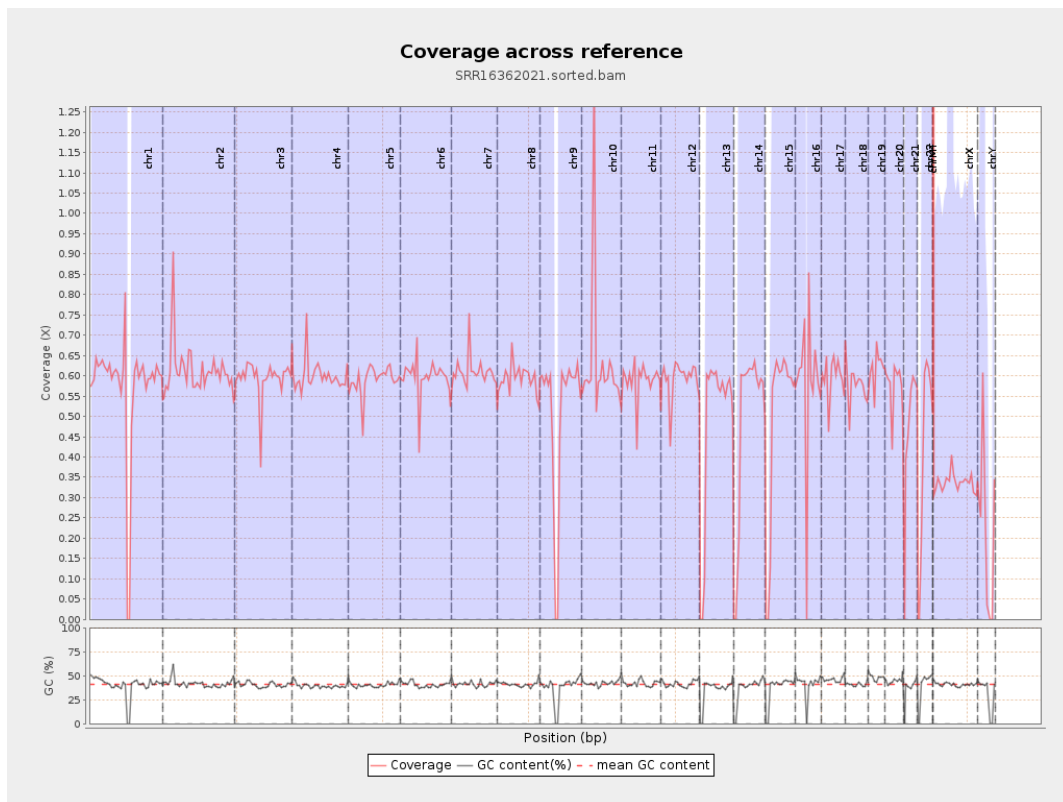
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

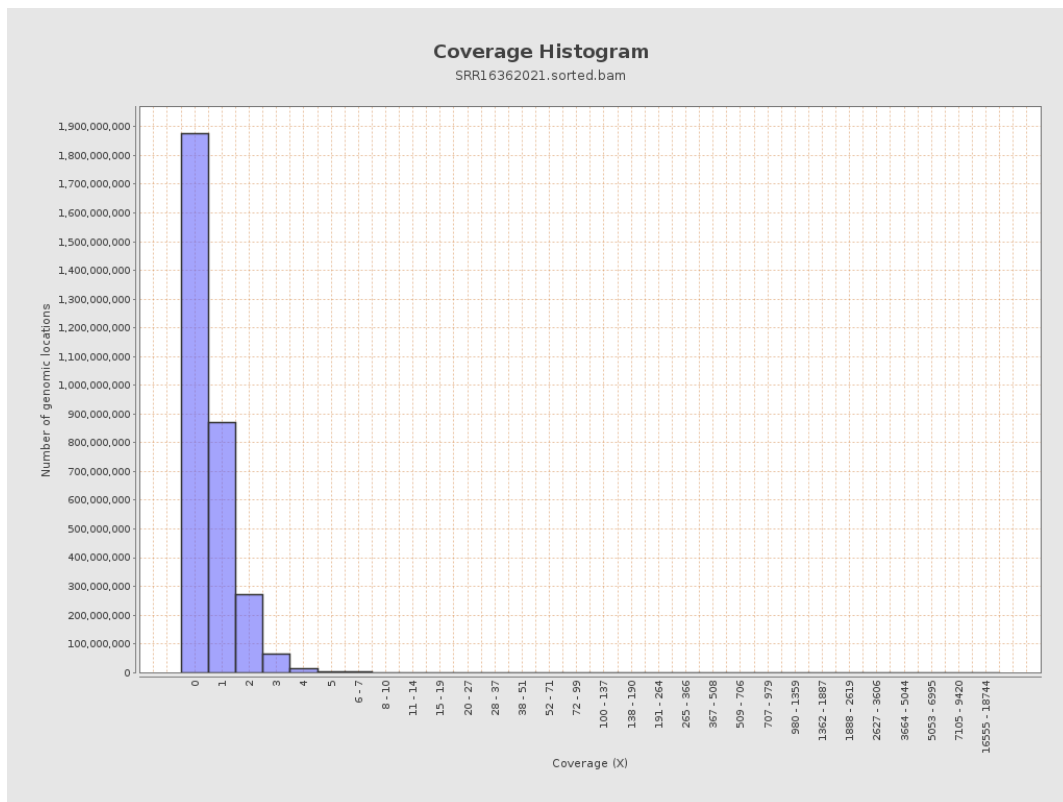
chr1	249250621	142494002	0.5717	6.5486
chr2	243199373	148861659	0.6121	13.0884
chr3	198022430	117576436	0.5938	1.0442
chr4	191154276	114574316	0.5994	1.7505
chr5	180915260	106791867	0.5903	0.8964
chr6	171115067	102151851	0.597	1.6796
chr7	159138663	97007418	0.6096	2.8937
chr8	146364022	86665233	0.5921	2.43
chr9	141213431	72218922	0.5114	1.3913
chr10	135534747	85277745	0.6292	5.5538
chr11	135006516	79274733	0.5872	1.5108
chr12	133851895	79643293	0.595	1.0148
chr13	115169878	56049556	0.4867	0.7816
chr14	107349540	53364830	0.4971	1.531
chr15	102531392	49702009	0.4847	0.8007
chr16	90354753	52304719	0.5789	2.8571
chr17	81195210	48607117	0.5986	1.4274
chr18	78077248	44959630	0.5758	2.6208
chr19	59128983	36483958	0.617	5.1866
chr20	63025520	36105301	0.5729	1.0548
chr21	48129895	22782503	0.4734	1.575
chr22	51304566	21404816	0.4172	1.1664
chrMT	16571	2313557	139.6148	48.6101
chrX	155270560	52349523	0.3372	1.156

chrY	59373566	13534256	0.228	2.5426
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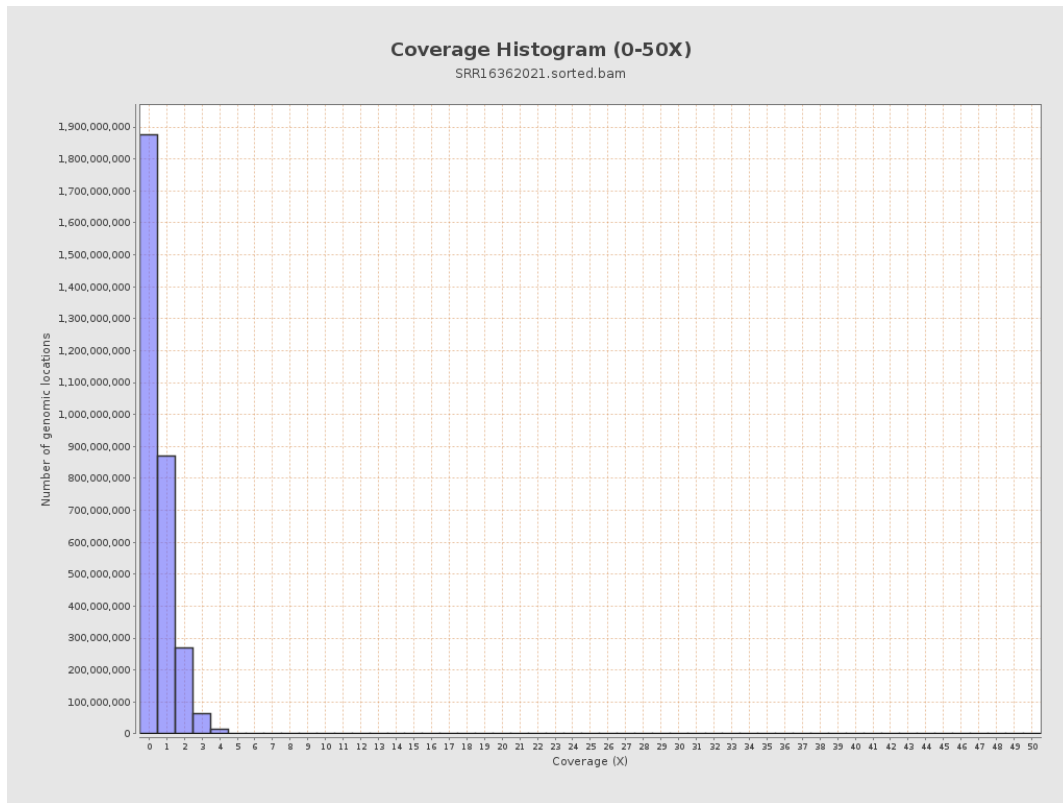
3. Results : Coverage across reference



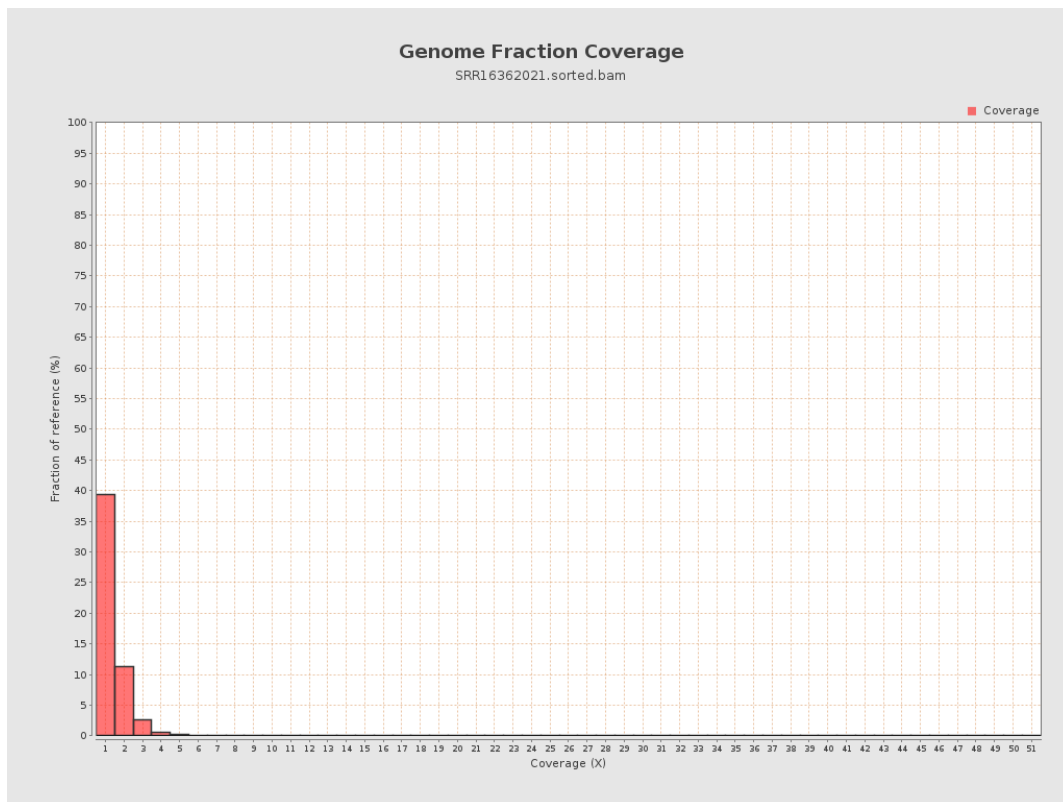
4. Results : Coverage Histogram



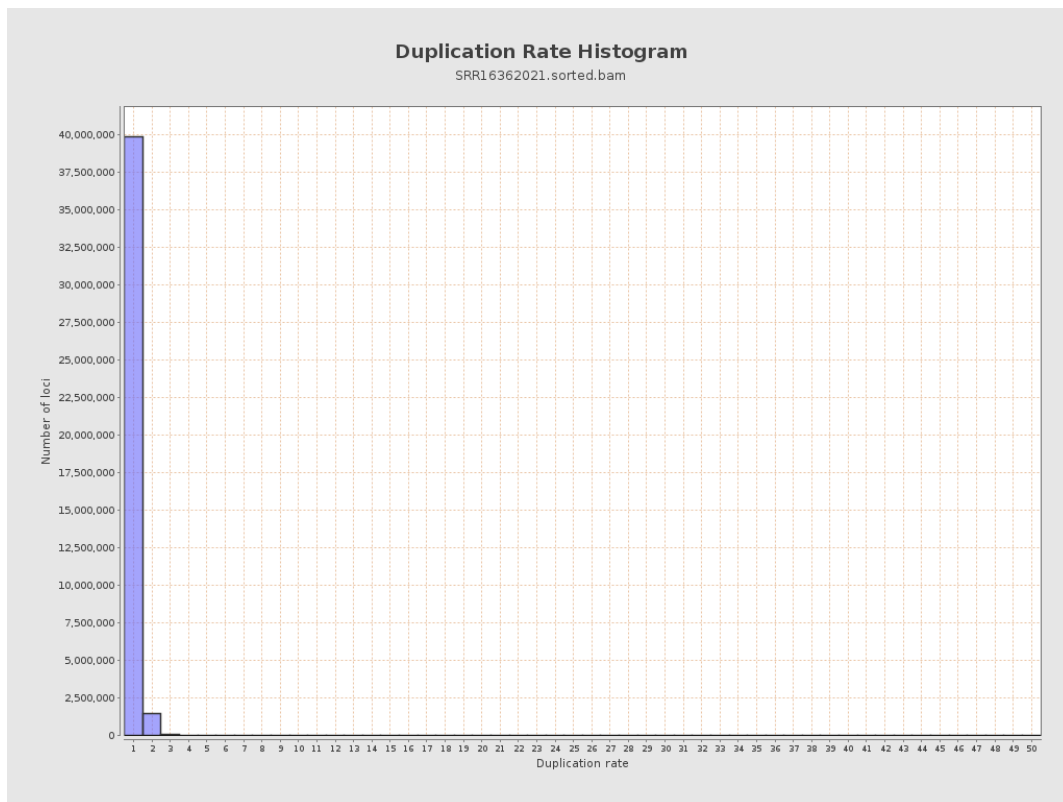
5. Results : Coverage Histogram (0-50X)



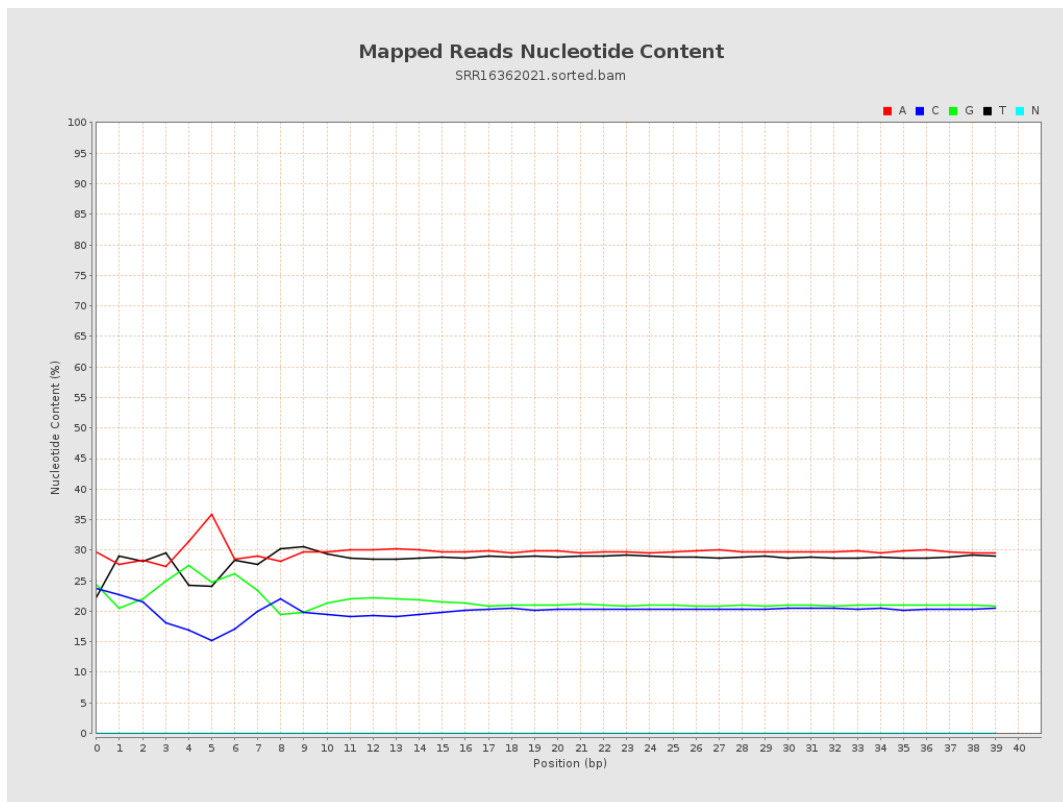
6. Results : Genome Fraction Coverage



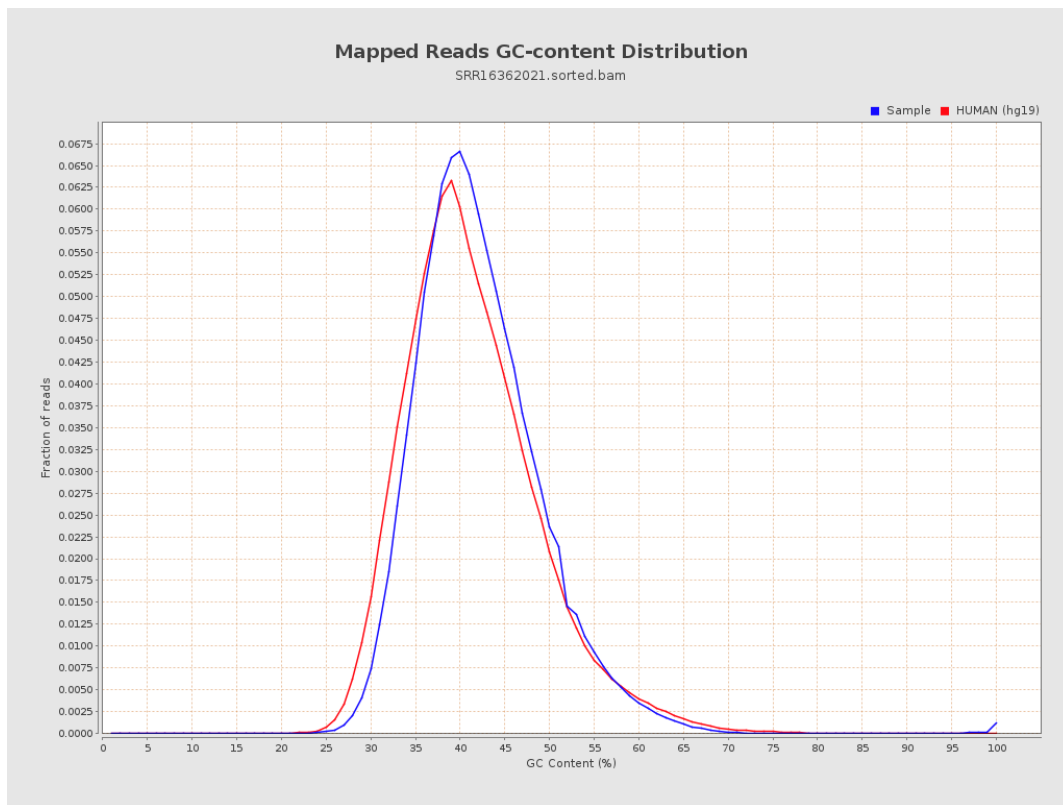
7. Results : Duplication Rate Histogram



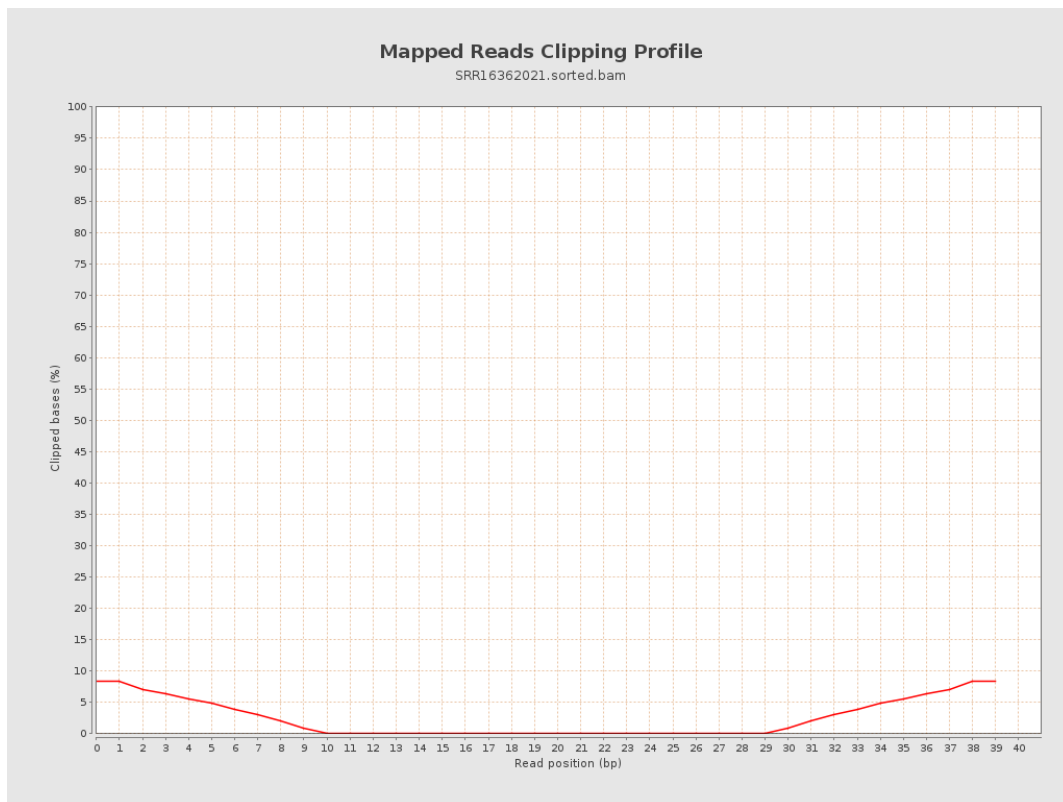
8. Results : Mapped Reads Nucleotide Content



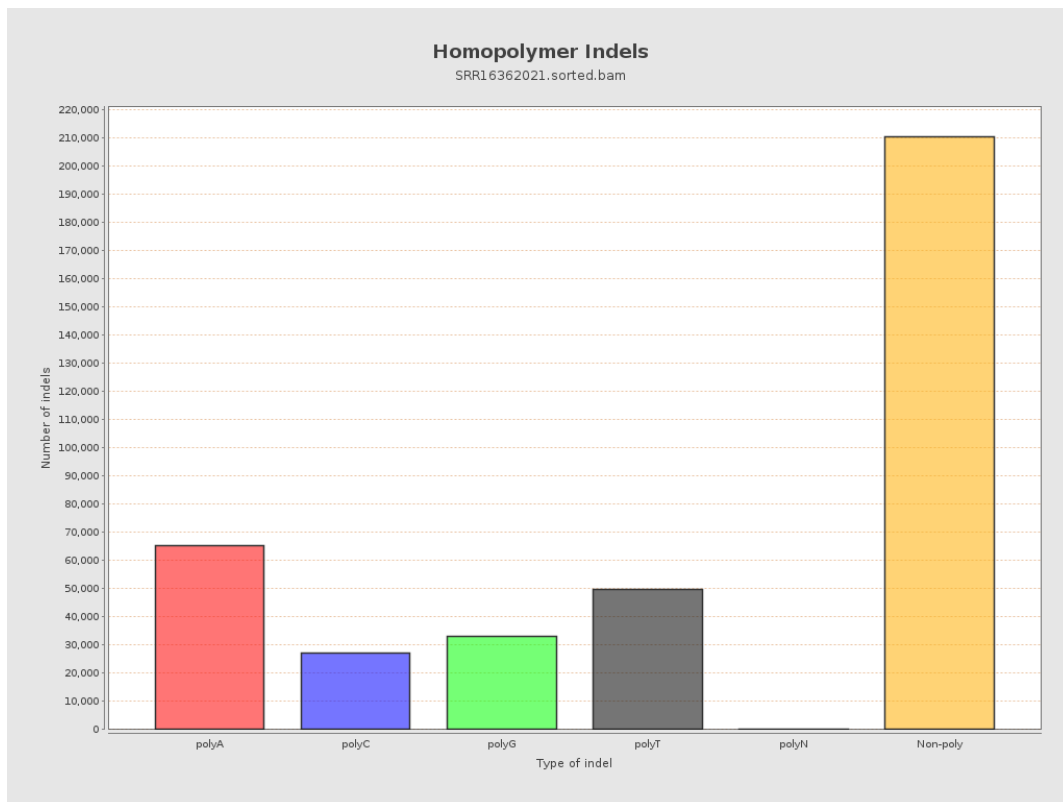
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



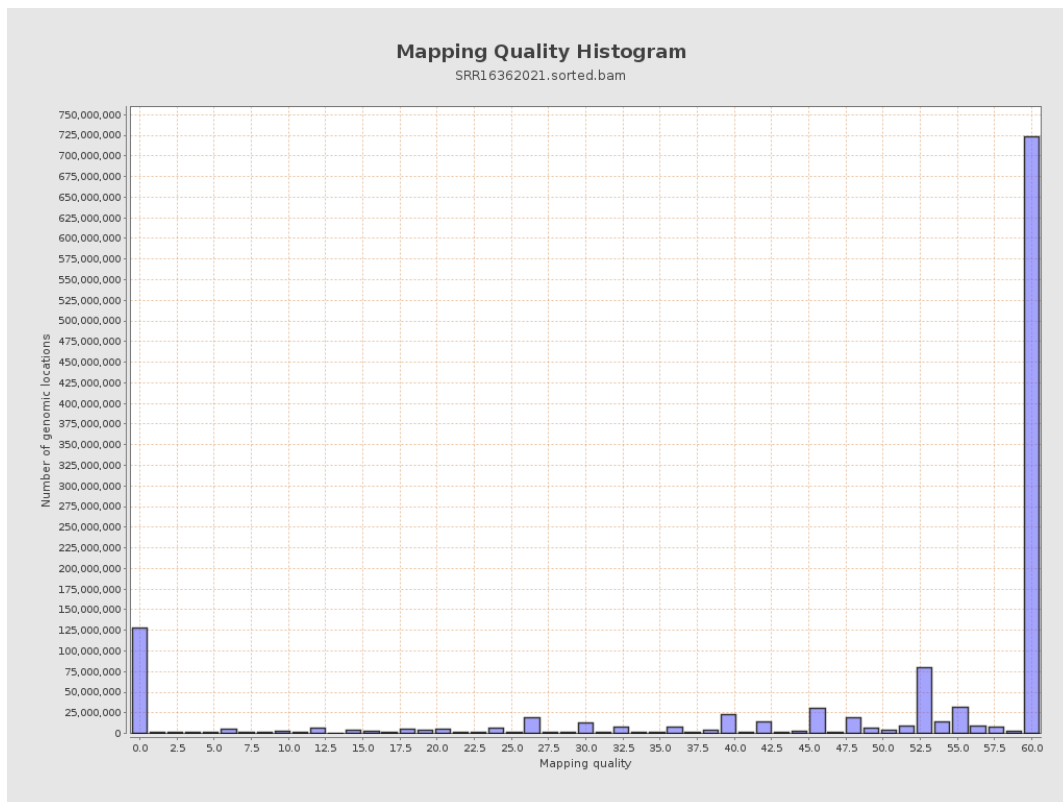
11. Results : Homopolymer Indels



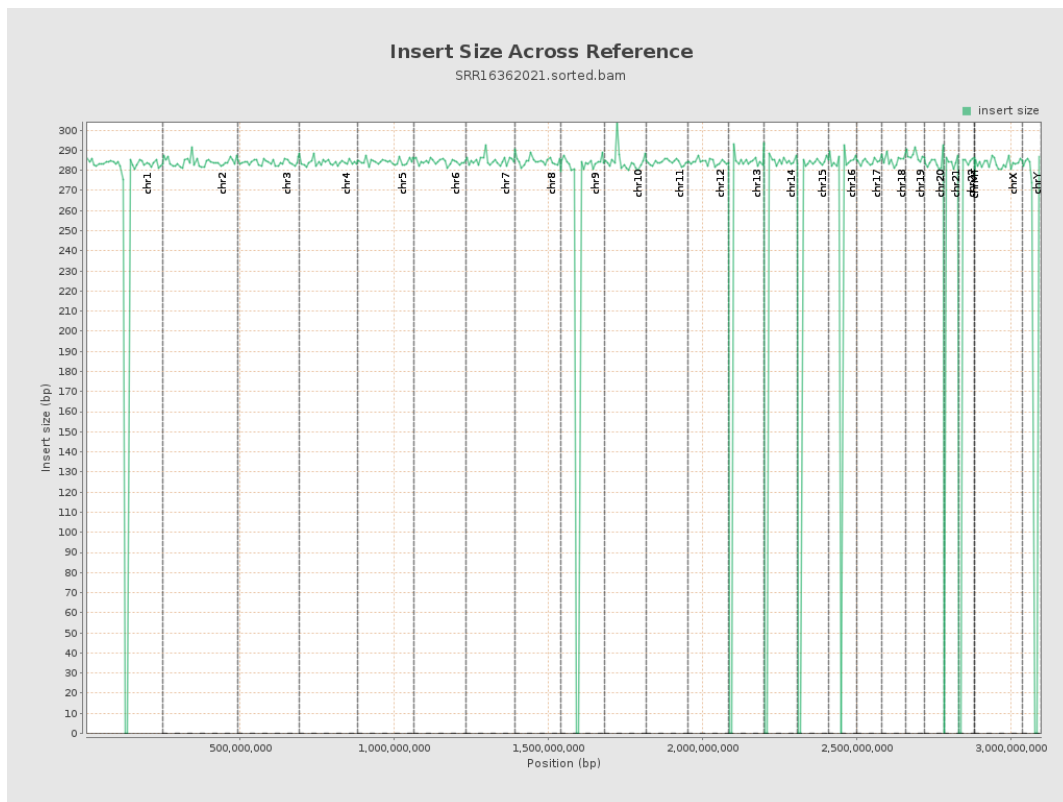
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

