Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/17 22:19:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR961016.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_SRR961016 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR961016_1.fastq.gz SRR961016_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Jan 17 22:19:48 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR961016.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	302,308,146
Mapped reads	295,295,673 / 97.68%
Unmapped reads	7,012,473 / 2.32%
Mapped paired reads	295,295,673 / 97.68%
Mapped reads, first in pair	147,821,730 / 48.9%
Mapped reads, second in pair	147,473,943 / 48.78%
Mapped reads, both in pair	294,316,972 / 97.36%
Mapped reads, singletons	978,701 / 0.32%
Secondary alignments	0
Supplementary alignments	680,123 / 0.22%
Read min/max/mean length	30 / 100 / 100.09
Duplicated reads (estimated)	37,480,819 / 12.4%
Duplication rate	8.29%
Clipped reads	22,649,194 / 7.49%

2.2. ACGT Content

Number/percentage of A's	8,540,794,656 / 29.46%
Number/percentage of C's	5,933,261,498 / 20.46%
Number/percentage of T's	8,518,903,200 / 29.38%
Number/percentage of G's	5,983,173,595 / 20.64%
Number/percentage of N's	17,794,603 / 0.06%

GC Percentage	41.1%

2.3. Coverage

Mean	9.3688
Standard Deviation	102.94

2.4. Mapping Quality

Mean Mapping Quality	53.66

2.5. Insert size

Mean	22,081.35
Standard Deviation	1,388,908.87
P25/Median/P75	137 / 148 / 158

2.6. Mismatches and indels

General error rate	0.52%
Mismatches	143,432,027
Insertions	2,997,214
Mapped reads with at least one insertion	0.98%
Deletions	3,550,826
Mapped reads with at least one deletion	1.16%
Homopolymer indels	41.57%

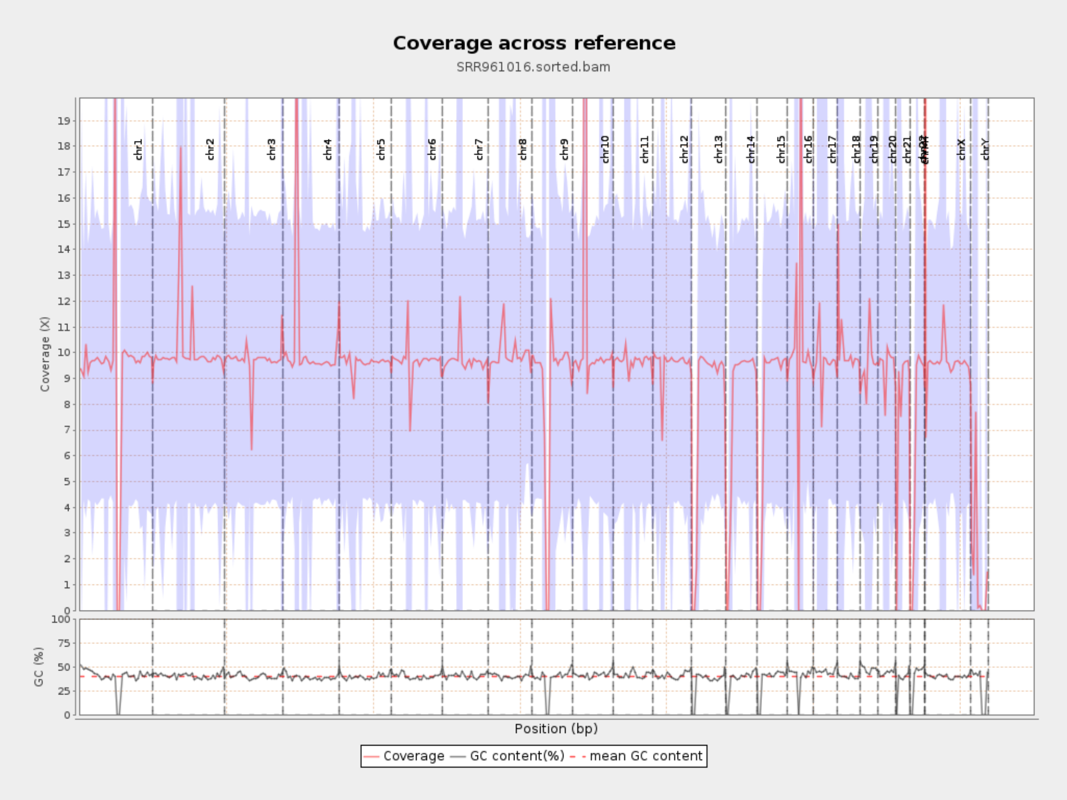
2.7. Chromosome stats

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

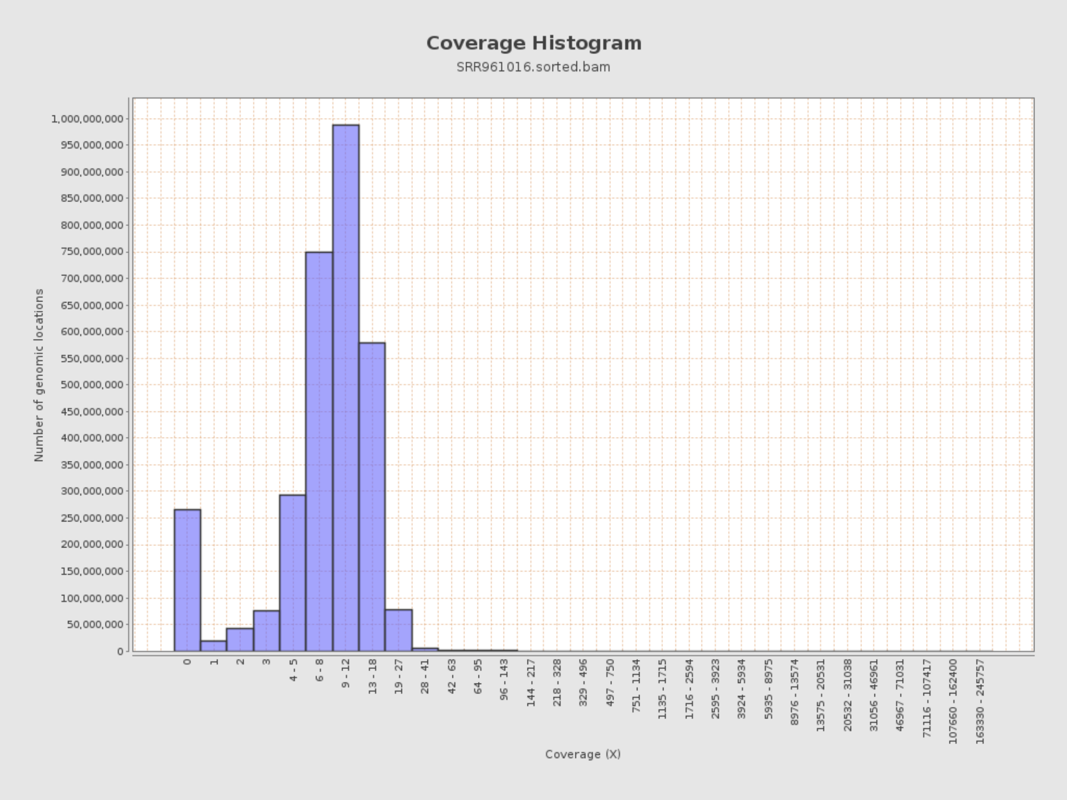
		bases	coverage	deviation
chr1	249250621	2360008968	9.4684	244.4476
chr2	243199373	2483869771	10.2133	64.2961
chr3	198022430	1908151485	9.636	20.85
chr4	191154276	1951899110	10.2111	90.4926
chr5	180915260	1738664547	9.6104	9.9409
chr6	171115067	1657599935	9.687	29.868
chr7	159138663	1548484299	9.7304	63.0419
chr8	146364022	1455462559	9.9441	100.6736
chr9	141213431	1209931895	8.5681	88.123
chr10	135534747	1518862255	11.2064	243.11
chr11	135006516	1305492538	9.6698	40.8084
chr12	133851895	1277503997	9.5442	7.9122
chr13	115169878	919983150	7.9881	5.7932
chr14	107349540	854818515	7.9629	9.1369
chr15	102531392	804554859	7.8469	5.9677
chr16	90354753	931755592	10.3122	99.3873
chr17	81195210	777412308	9.5746	38.5012
chr18	78077248	788338201	10.0969	105.1735
chr19	59128983	566612504	9.5827	118.4336
chr20	63025520	598311035	9.4932	33.9019
chr21	48129895	398495339	8.2796	45.2926
chr22	51304566	340541847	6.6377	7.9144
chrMT	16571	22385712	1,350.8969	185.5003
chrX	155270560	1486161815	9.5714	31.2184

chrY	59373566	97624861	1.6442	95.5732

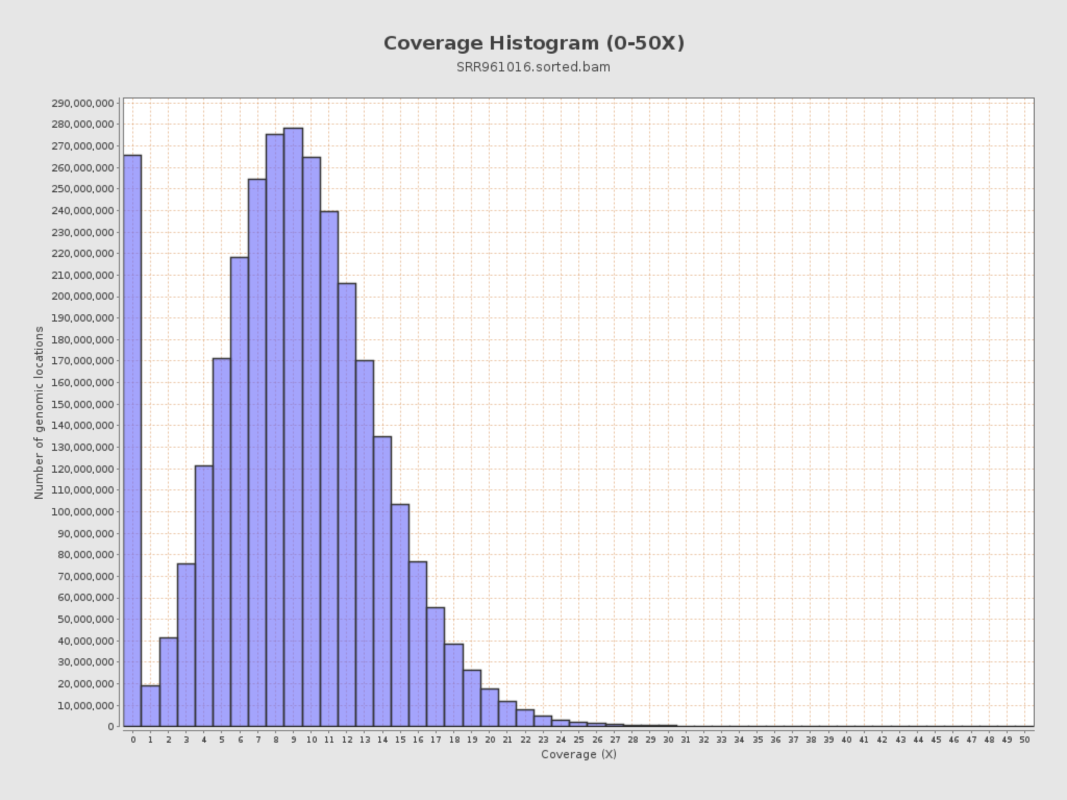
3. Results : Coverage across reference



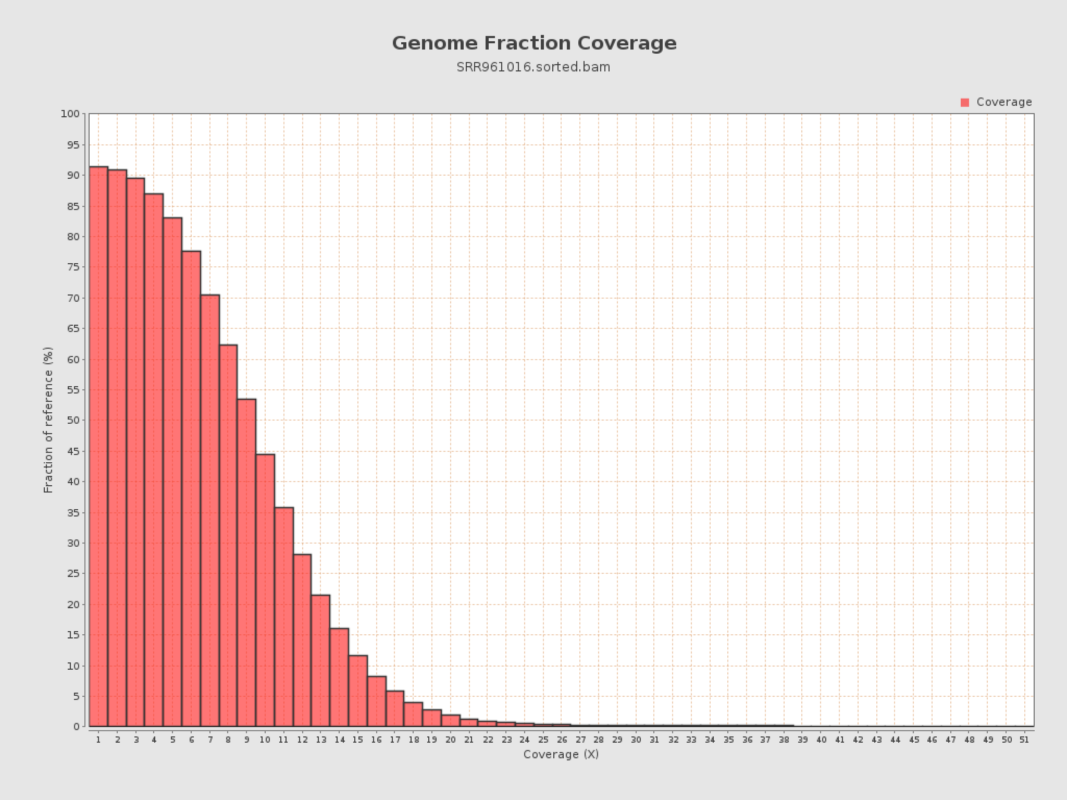
4. Results : Coverage Histogram



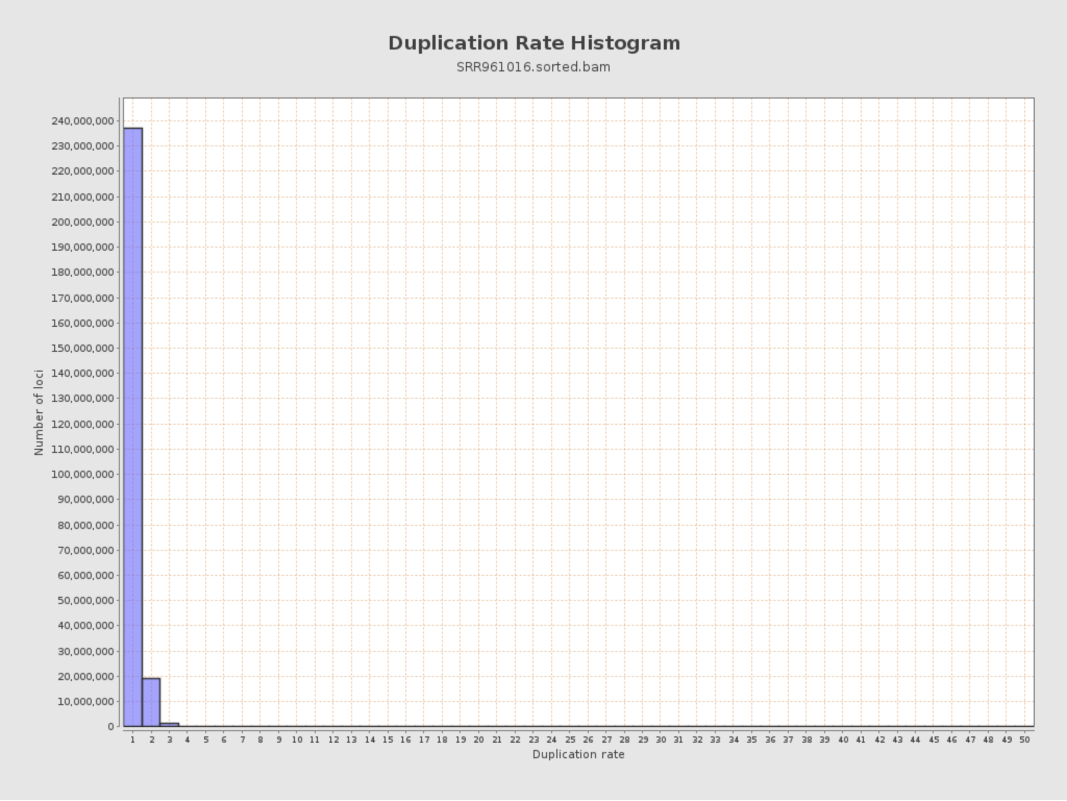
5. Results : Coverage Histogram (0-50X)



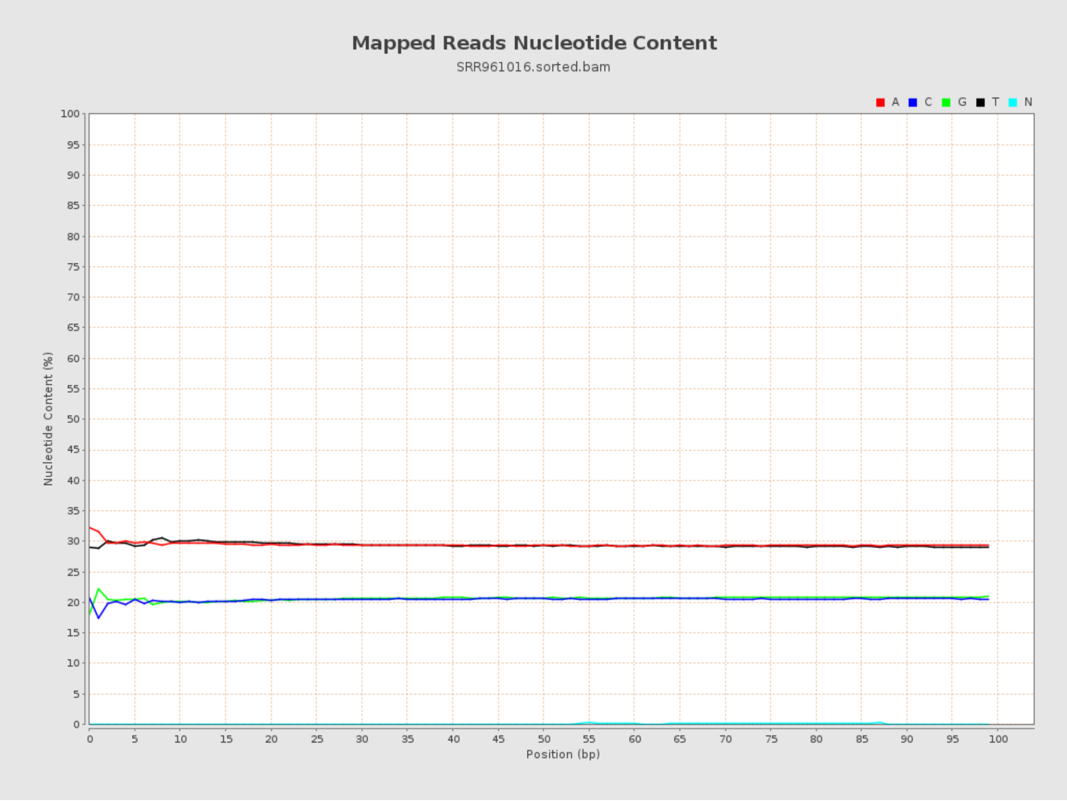
6. Results : Genome Fraction Coverage



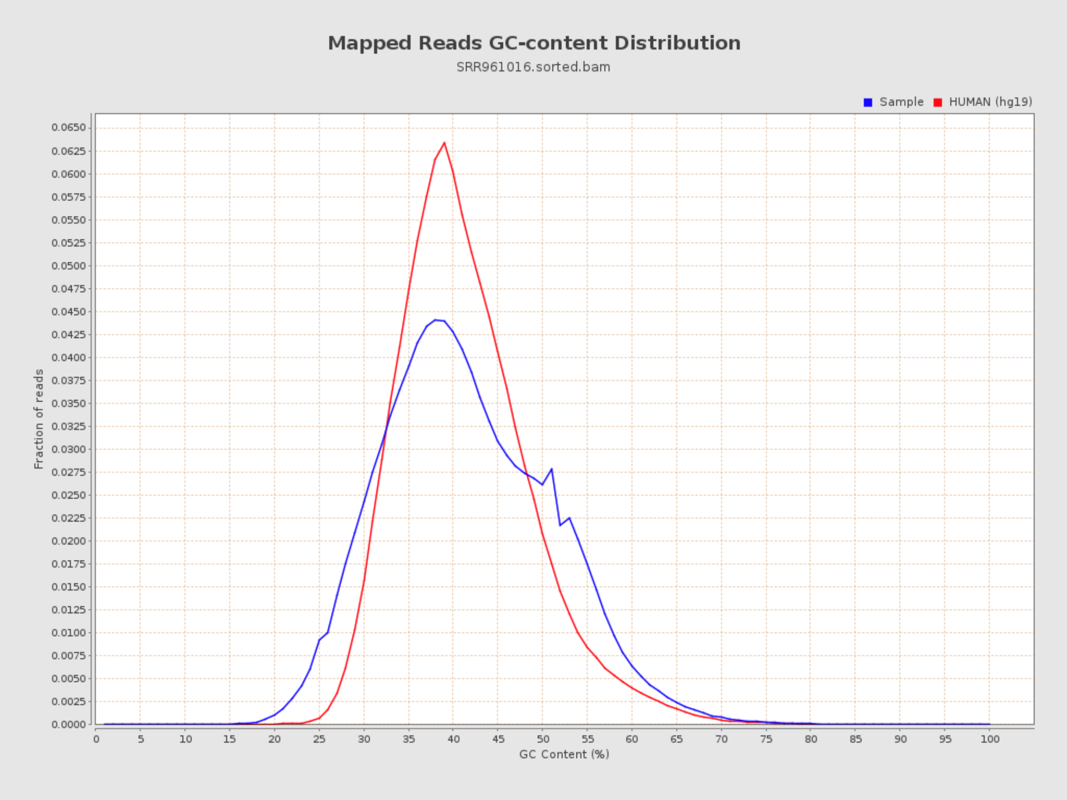
7. Results : Duplication Rate Histogram



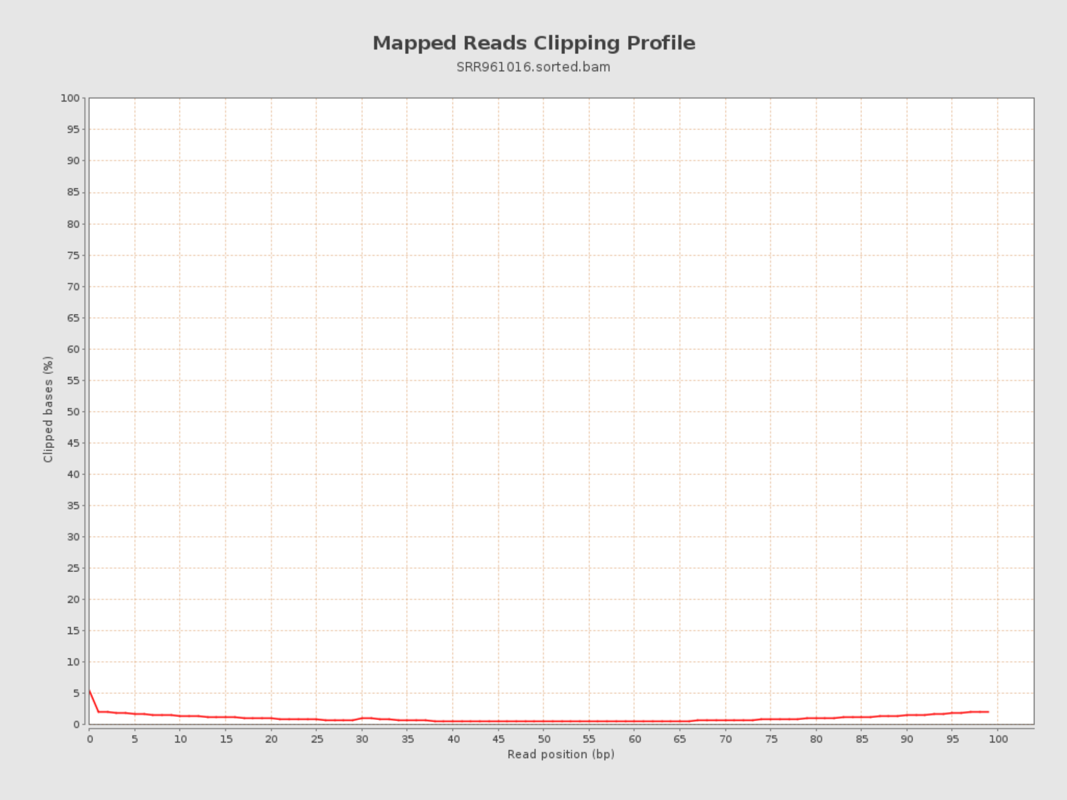
8. Results : Mapped Reads Nucleotide Content



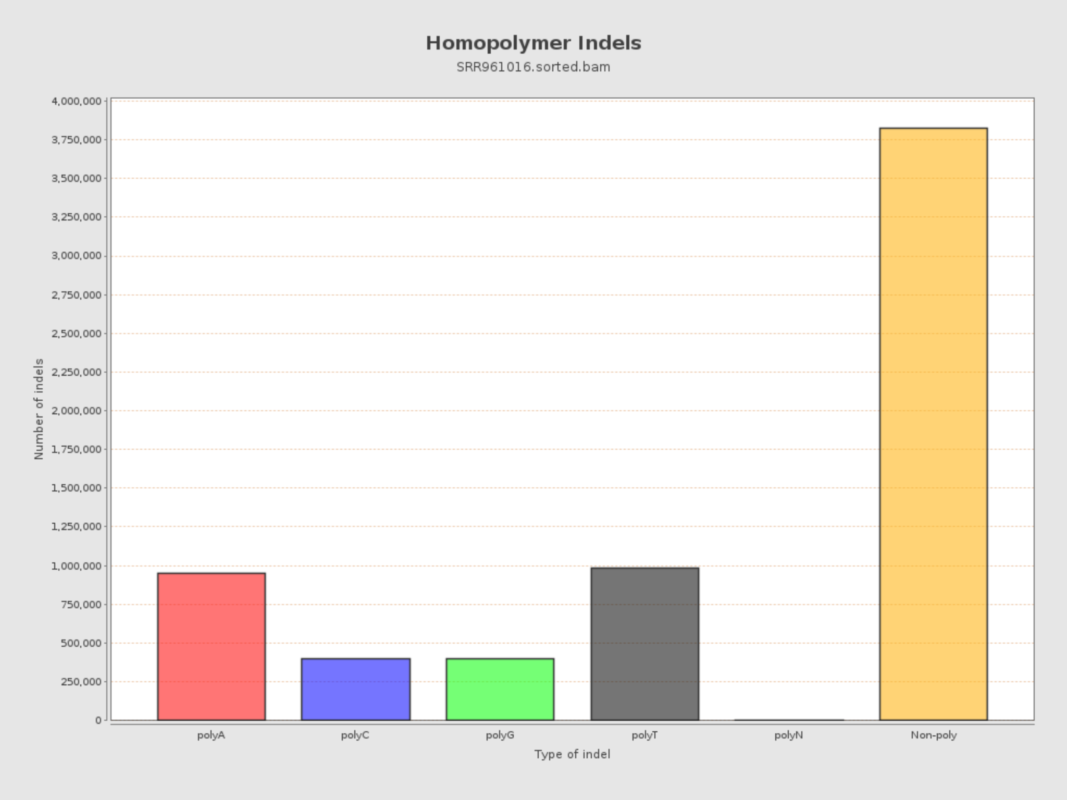
9. Results : Mapped Reads GC-content Distribution



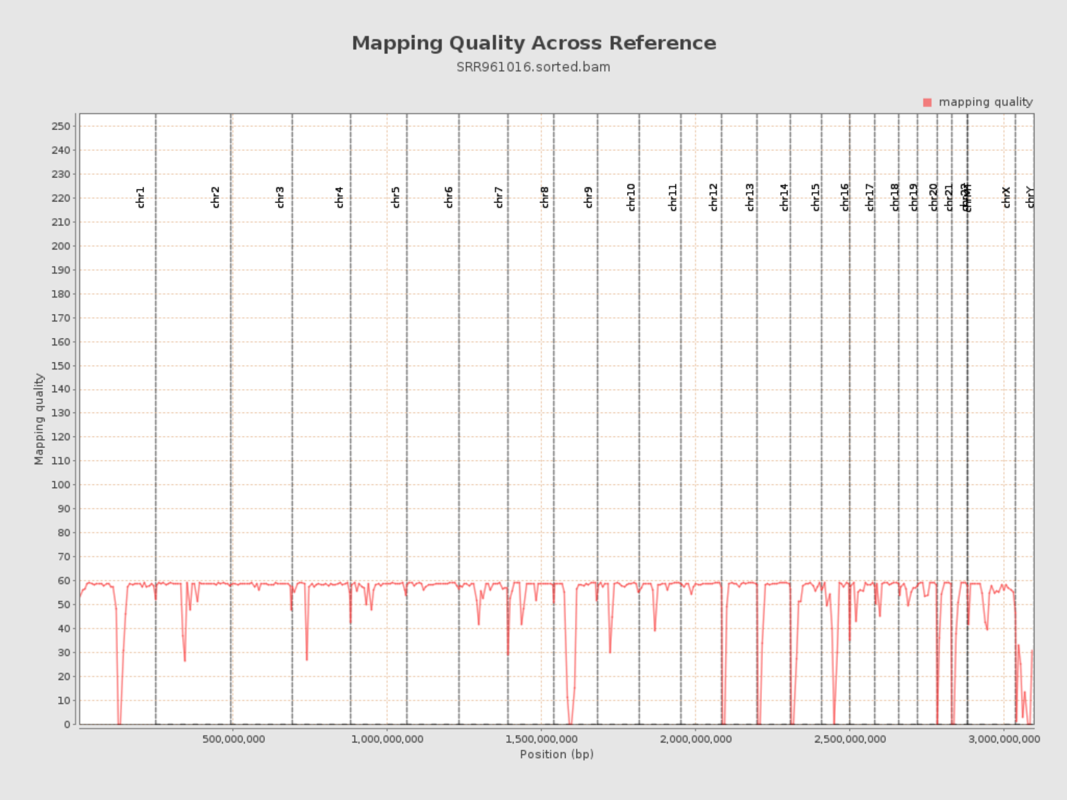
10. Results : Mapped Reads Clipping Profile



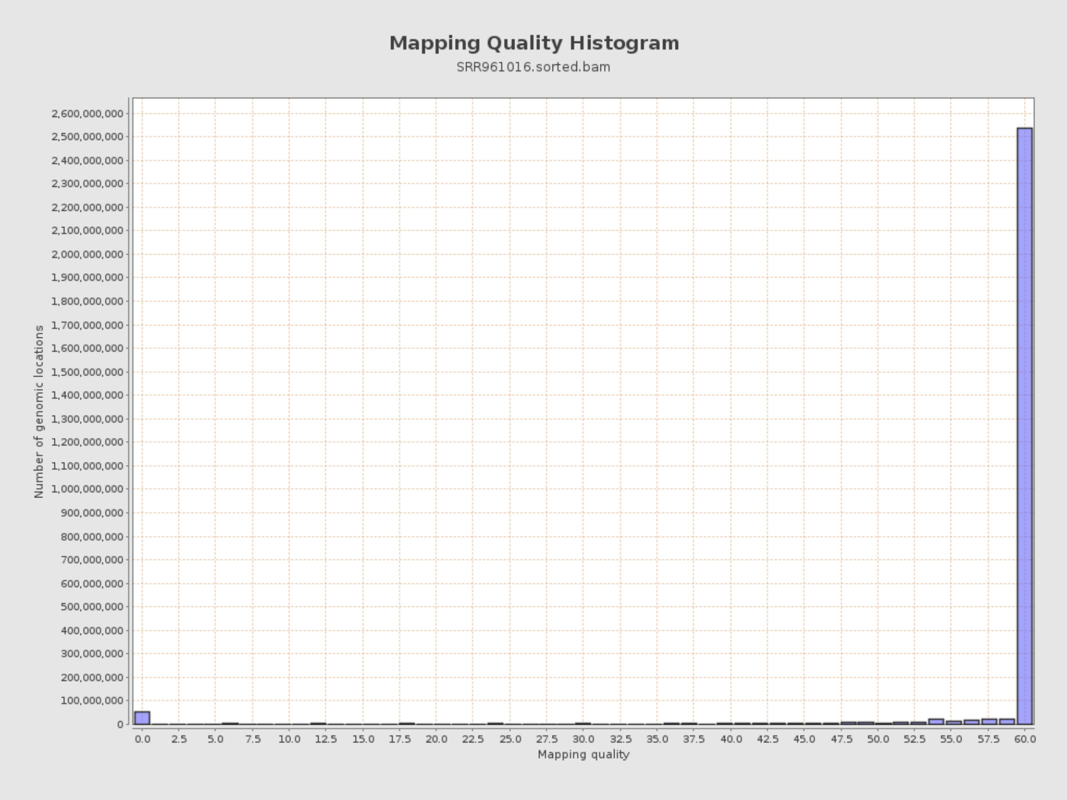
11. Results : Homopolymer Indels



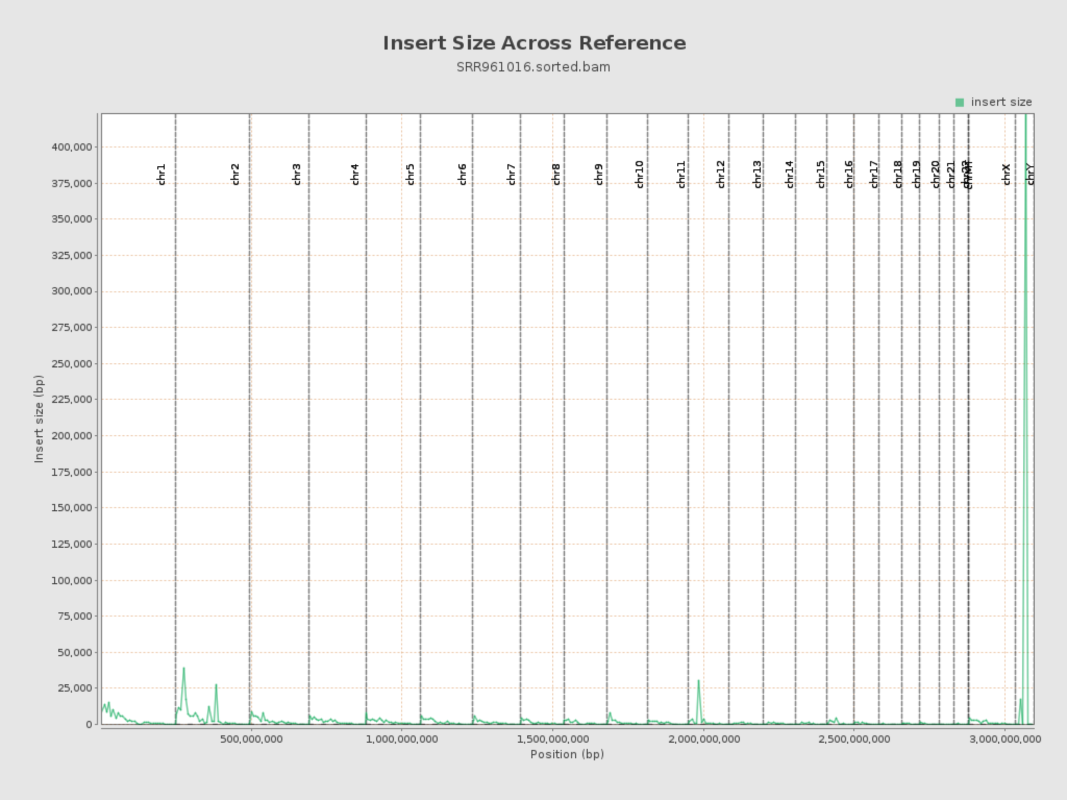
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram