Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/19 23:50:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618638.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_SRR618638 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618638_1.fastq.gz SRR618638_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 19 23:50:49 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618638.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	71,709,530
Mapped reads	65,892,090 / 91.89%
Unmapped reads	5,817,440 / 8.11%
Mapped paired reads	65,892,090 / 91.89%
Mapped reads, first in pair	34,531,072 / 48.15%
Mapped reads, second in pair	31,361,018 / 43.73%
Mapped reads, both in pair	62,004,262 / 86.47%
Mapped reads, singletons	3,887,828 / 5.42%
Secondary alignments	0
Supplementary alignments	380,637 / 0.53%
Read min/max/mean length	30 / 100 / 100.21
Duplicated reads (estimated)	19,341,977 / 26.97%
Duplication rate	24.13%
Clipped reads	18,338,611 / 25.57%

2.2. ACGT Content

Number/percentage of A's	1,660,375,787 / 27.23%
Number/percentage of C's	1,325,169,109 / 21.73%
Number/percentage of T's	1,686,683,402 / 27.66%
Number/percentage of G's	1,424,667,366 / 23.36%
Number/percentage of N's	1,108,879 / 0.02%

GC Percentage	45.09%

2.3. Coverage

Mean	1.9712
Standard Deviation	7.7925

2.4. Mapping Quality

Mean Mapping Quality	52.53

2.5. Insert size

Mean	133,169.41
Standard Deviation	3,650,695.07
P25/Median/P75	190 / 217 / 252

2.6. Mismatches and indels

General error rate	1.48%
Mismatches	88,584,686
Insertions	1,133,129
Mapped reads with at least one insertion	1.69%
Deletions	3,110,083
Mapped reads with at least one deletion	4.6%
Homopolymer indels	52.44%

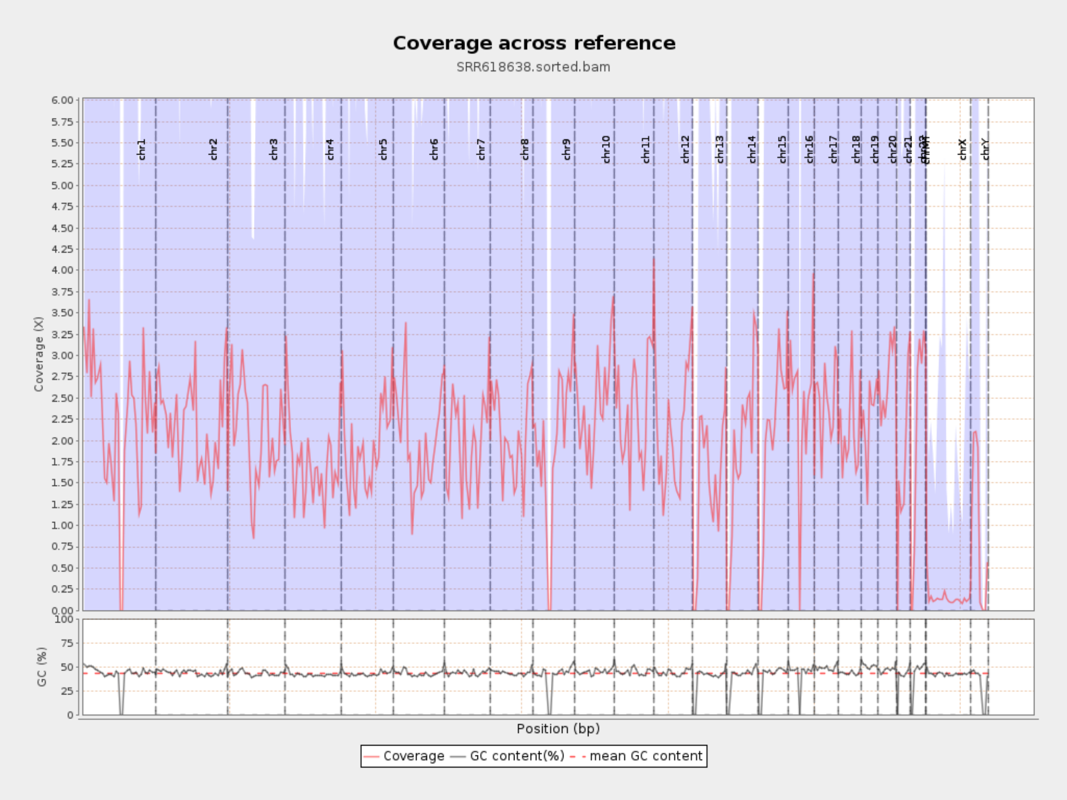
2.7. Chromosome stats

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

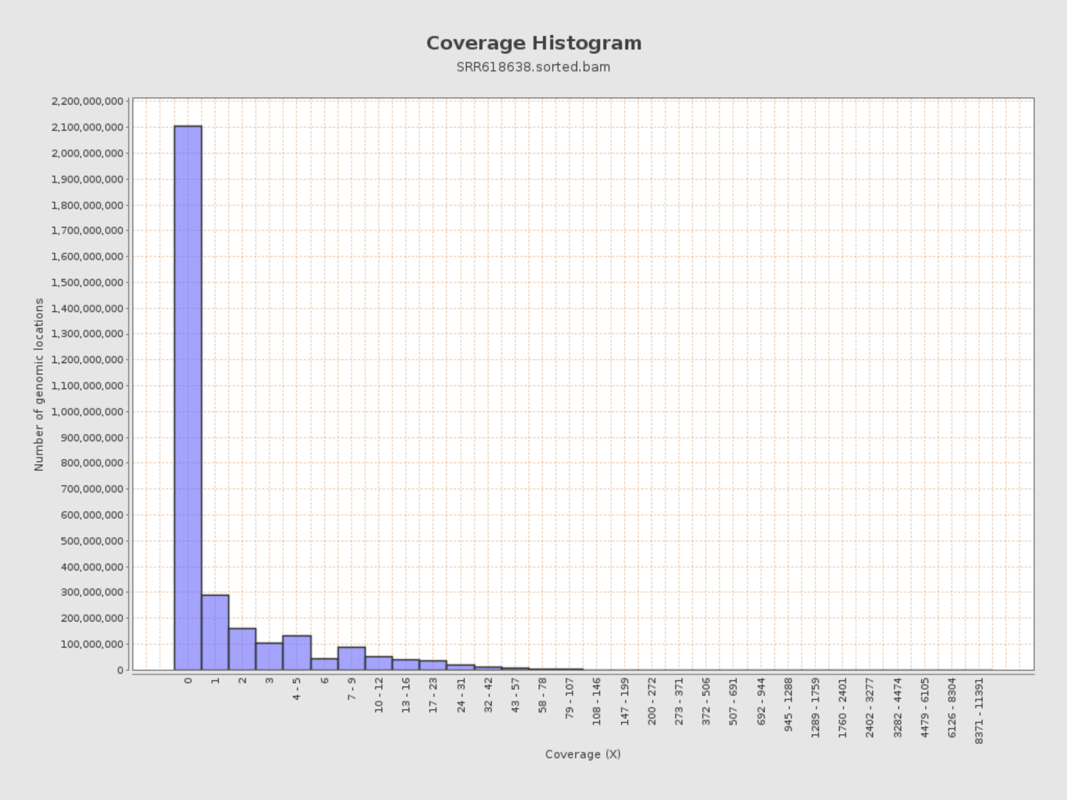
		bases	**coverage**	**deviation**
chr1	249250621	553541296	2.2208	8.6579
chr2	243199373	530571782	2.1816	10.3074
chr3	198022430	416839206	2.105	6.185
chr4	191154276	332275840	1.7383	6.1524
chr5	180915260	352754858	1.9498	6.0039
chr6	171115067	341473706	1.9956	6.1492
chr7	159138663	318822814	2.0034	6.3426
chr8	146364022	303331226	2.0724	6.4242
chr9	141213431	278091295	1.9693	8.3002
chr10	135534747	328261523	2.422	7.1635
chr11	135006516	315718344	2.3385	7.7113
chr12	133851895	285198933	2.1307	6.6988
chr13	115169878	172111721	1.4944	5.1358
chr14	107349540	205866095	1.9177	6.5737
chr15	102531392	205364631	2.0029	6.9851
chr16	90354753	217620973	2.4085	18.098
chr17	81195210	200457318	2.4688	7.75
chr18	78077248	162636101	2.083	8.0025
chr19	59128983	133700526	2.2612	8.1134
chr20	63025520	173807653	2.7577	8.0834
chr21	48129895	86605051	1.7994	9.3798
chr22	51304566	106332103	2.0726	7.3383
chrMT	16571	41218	2.4874	9.2151
chrX	155270560	22750125	0.1465	2.3449

chrY	59373566	58136837	0.9792	7.9012

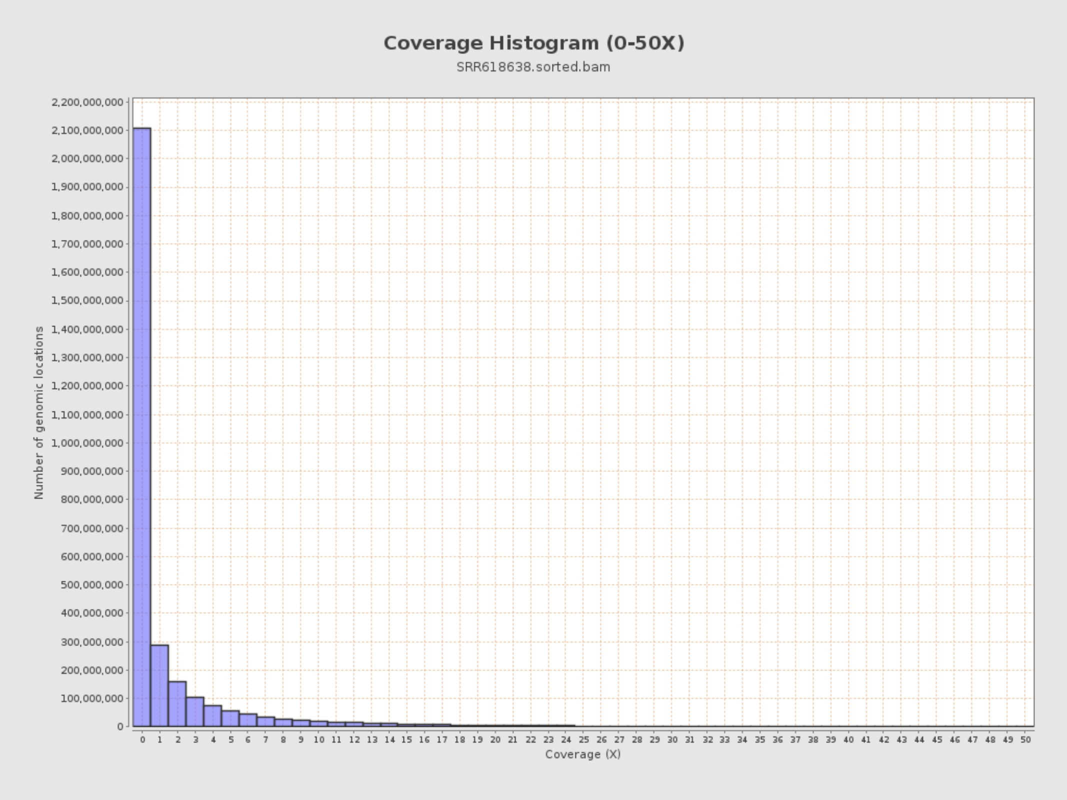
3. Results : Coverage across reference



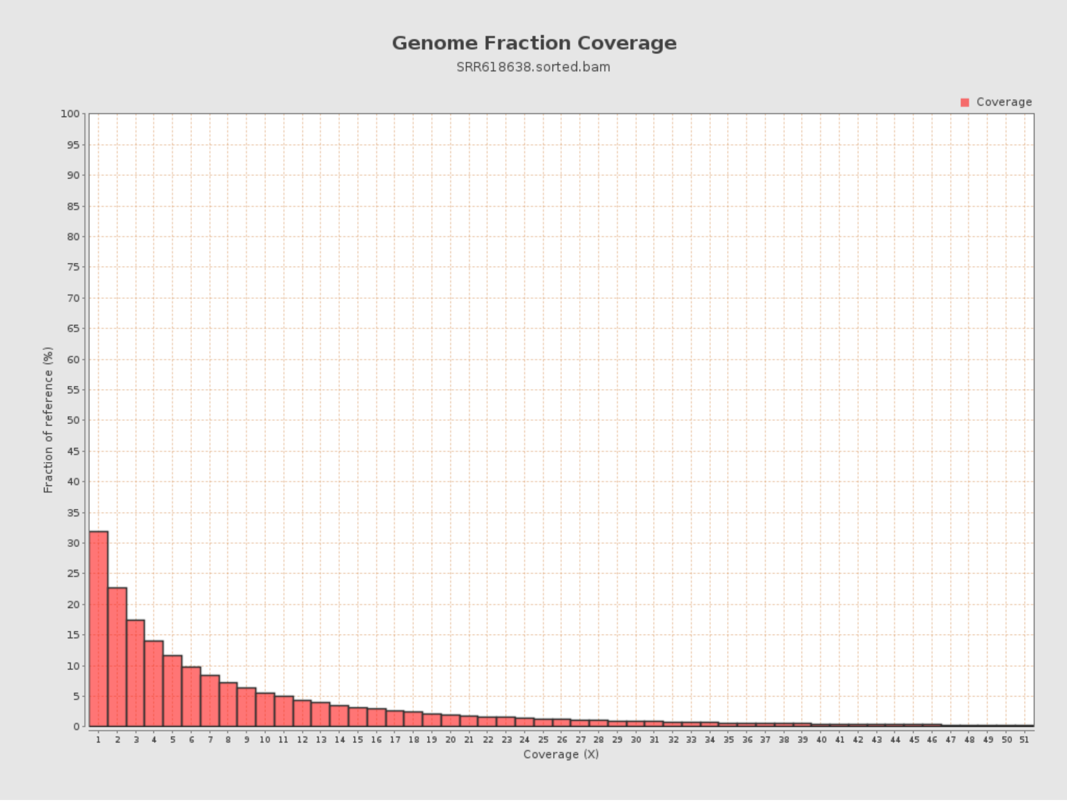
4. Results : Coverage Histogram



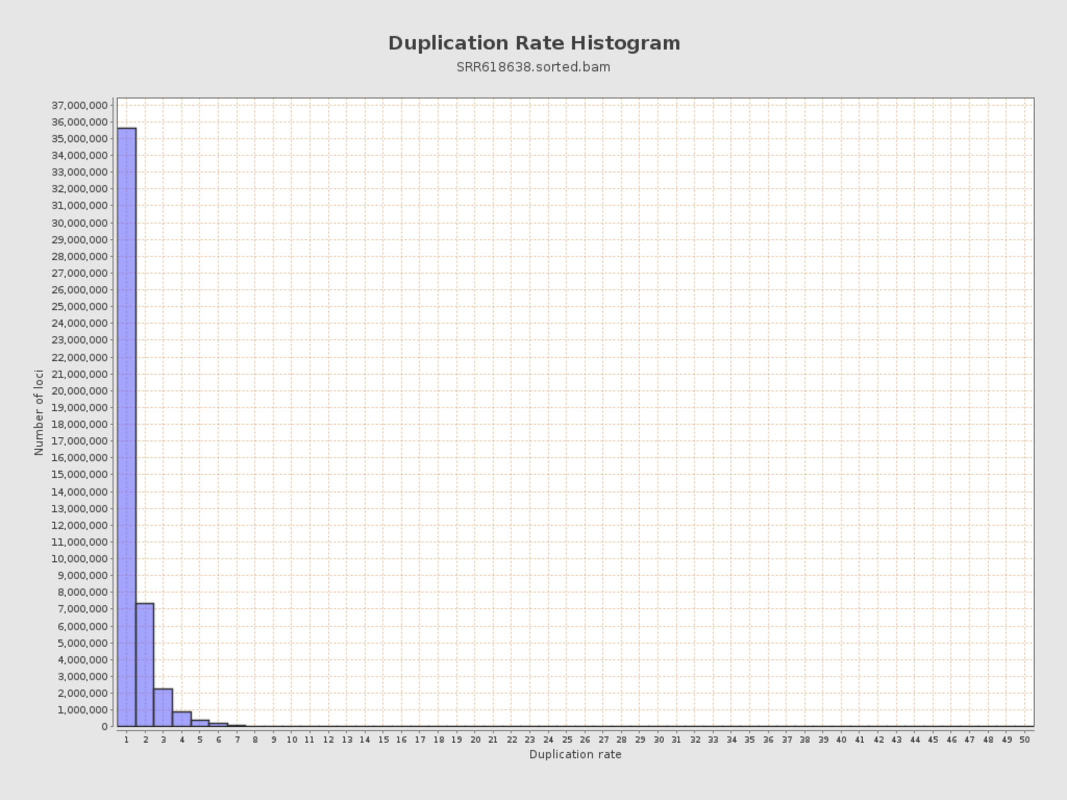
5. Results : Coverage Histogram (0-50X)



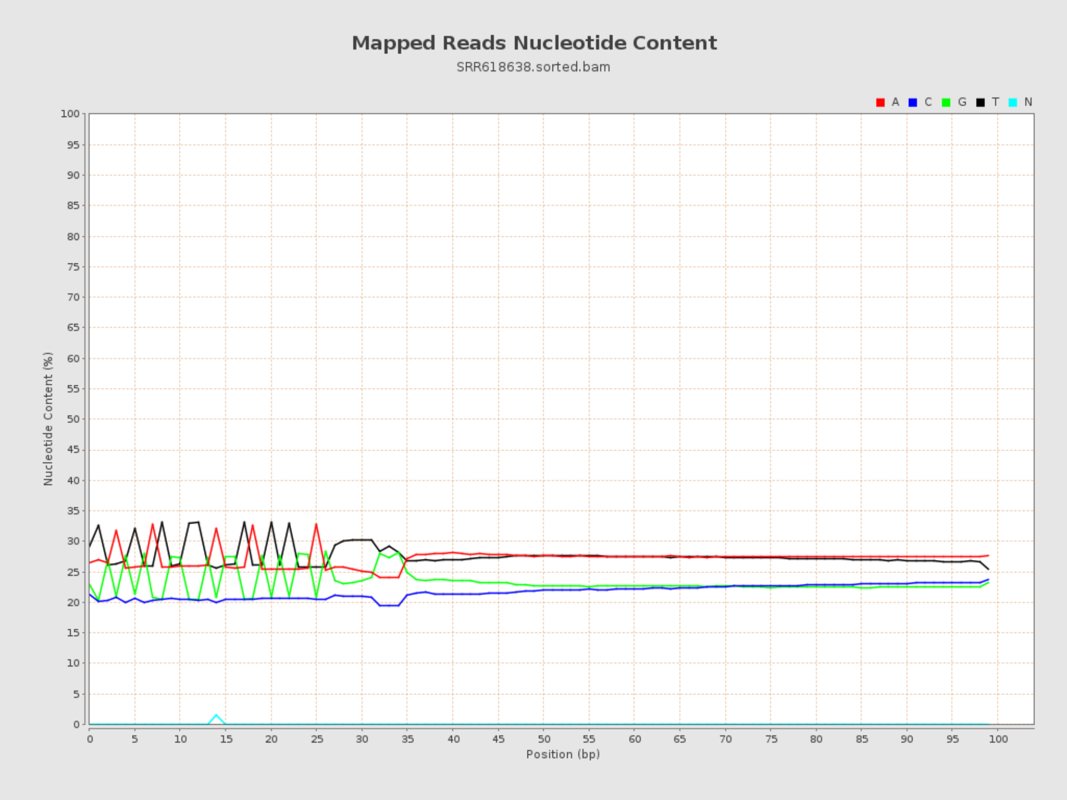
6. Results : Genome Fraction Coverage



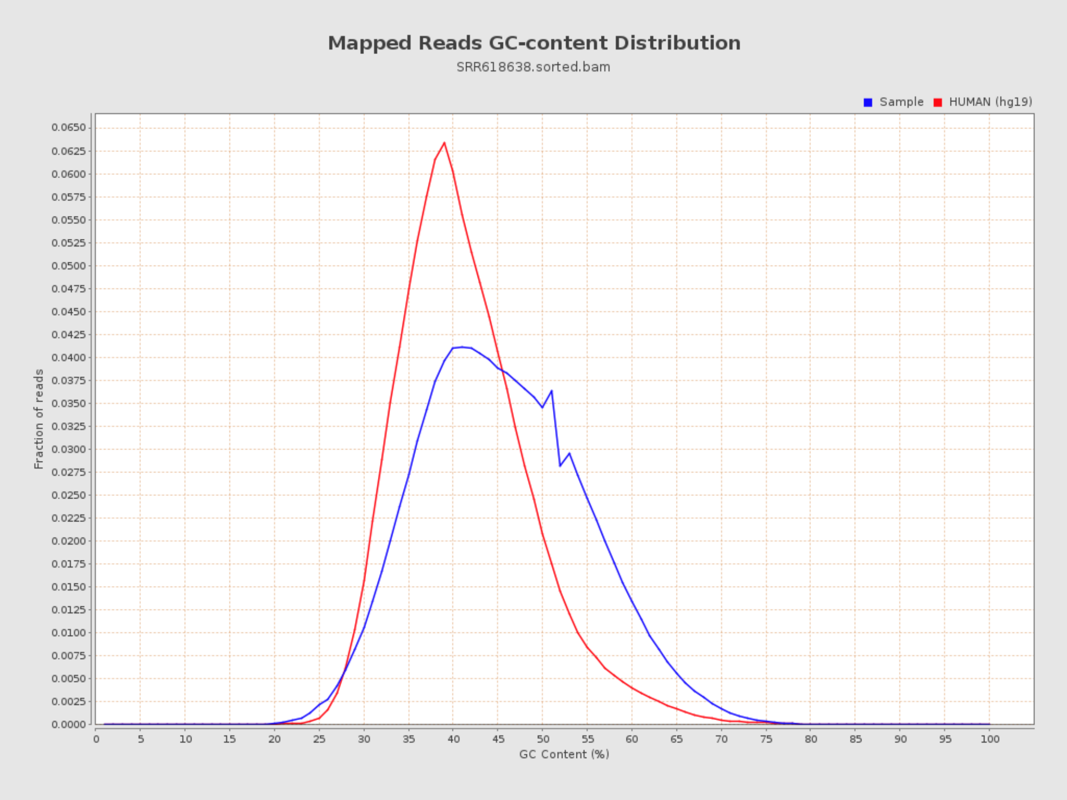
7. Results : Duplication Rate Histogram



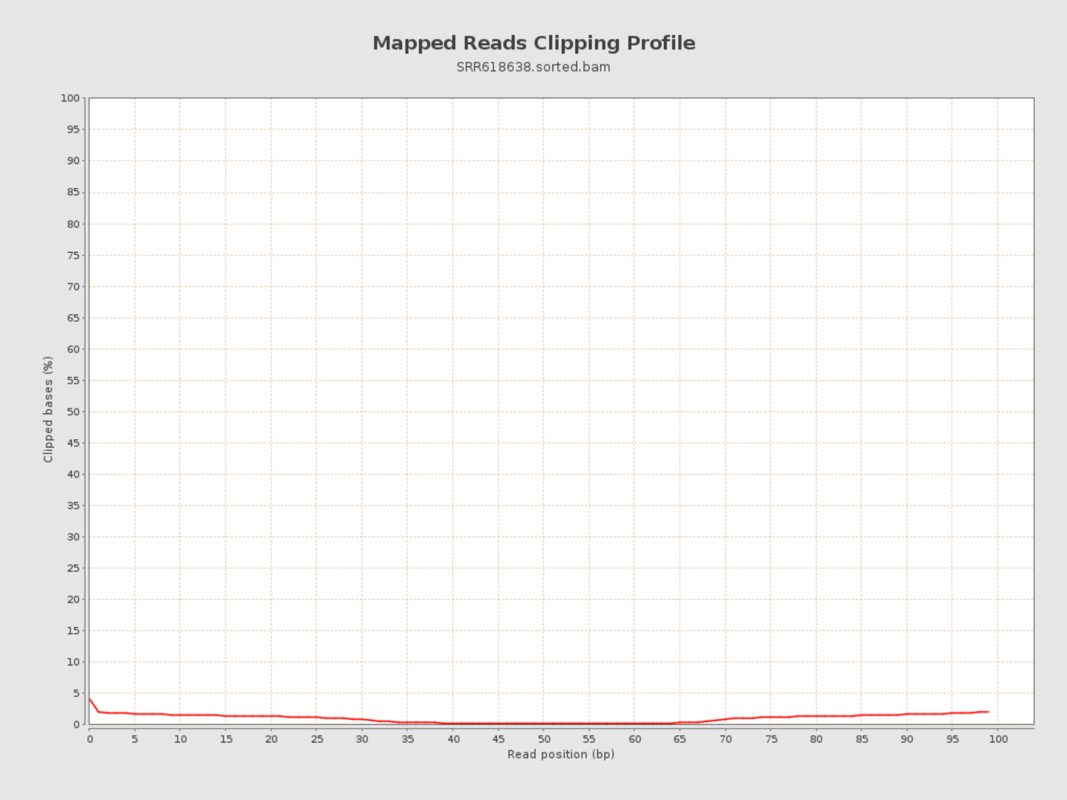
8. Results : Mapped Reads Nucleotide Content



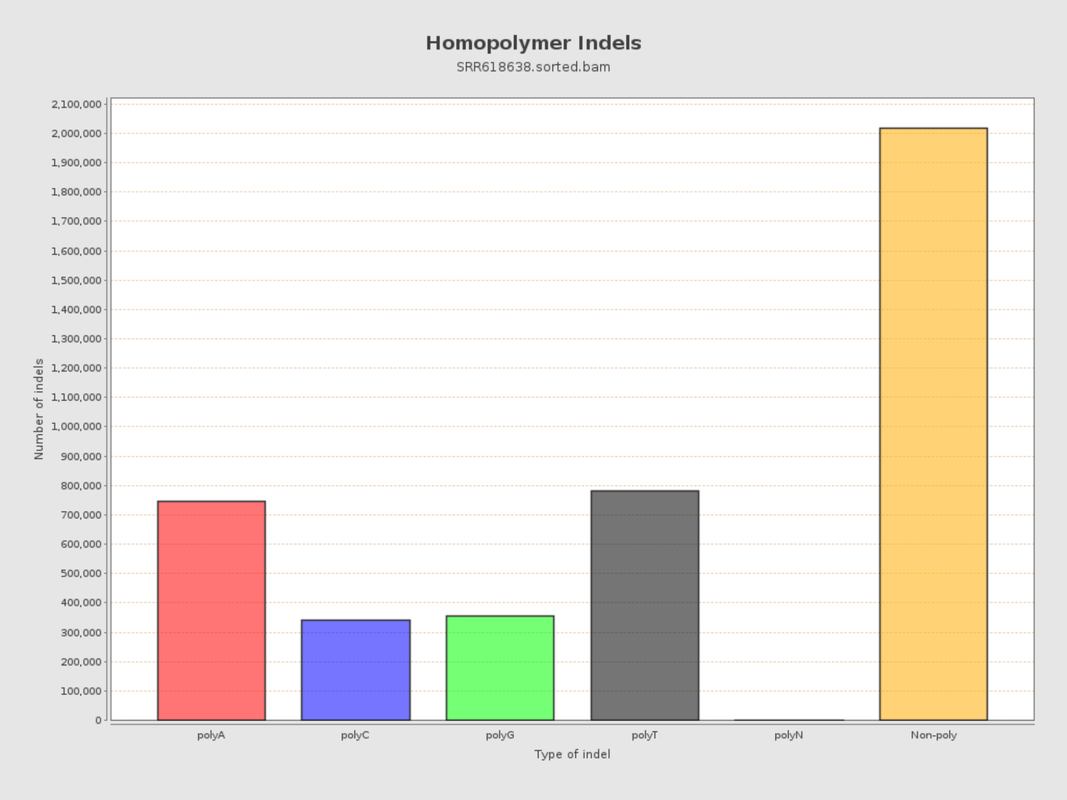
9. Results : Mapped Reads GC-content Distribution



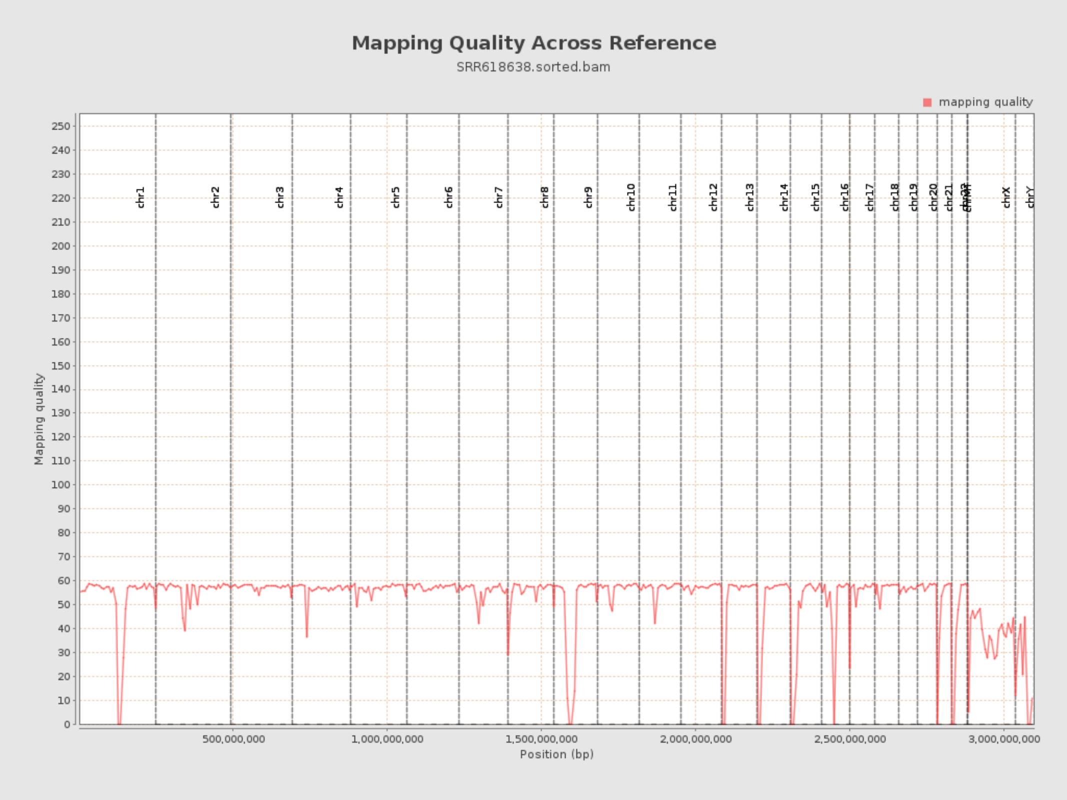
10. Results : Mapped Reads Clipping Profile



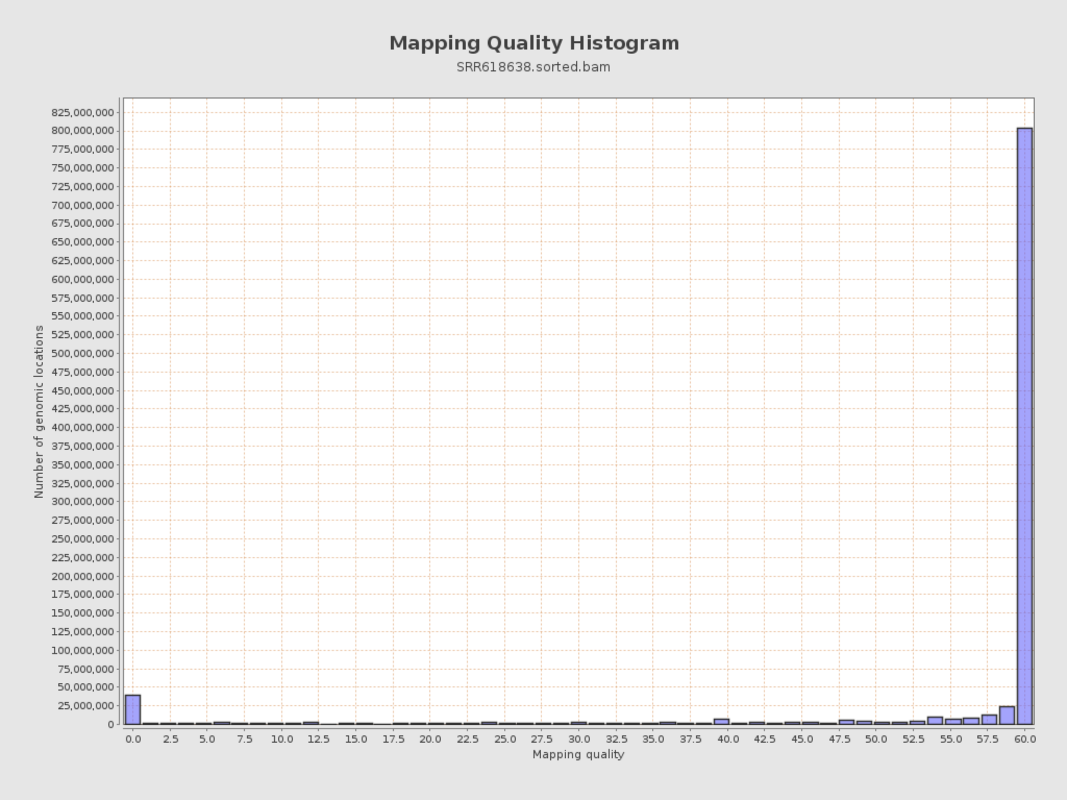
11. Results : Homopolymer Indels



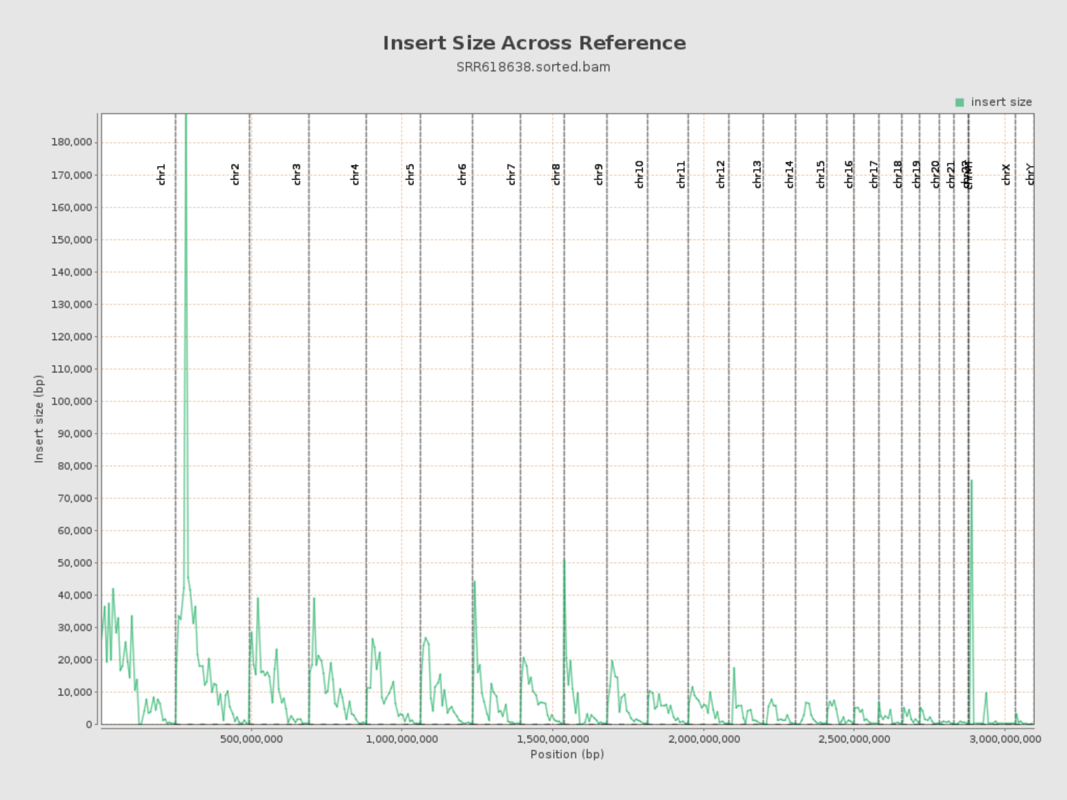
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram