Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/06 05:24:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR960908.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_SRR960908 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR960908_1.fastq.gz SRR960908_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Jan 06 05:24:03 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR960908.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	79,035,650
Mapped reads	74,343,536 / 94.06%
Unmapped reads	4,692,114 / 5.94%
Mapped paired reads	74,343,536 / 94.06%
Mapped reads, first in pair	37,242,879 / 47.12%
Mapped reads, second in pair	37,100,657 / 46.94%
Mapped reads, both in pair	73,042,722 / 92.42%
Mapped reads, singletons	1,300,814 / 1.65%
Secondary alignments	0
Supplementary alignments	1,289,385 / 1.63%
Read min/max/mean length	30 / 101 / 101.65
Duplicated reads (estimated)	6,915,216 / 8.75%
Duplication rate	4.23%
Clipped reads	35,725,397 / 45.2%

2.2. ACGT Content

Number/percentage of A's	1,899,583,535 / 28.89%
Number/percentage of C's	1,358,803,996 / 20.67%
Number/percentage of T's	1,930,895,212 / 29.37%
Number/percentage of G's	1,384,515,119 / 21.06%
Number/percentage of N's	437,053 / 0.01%

GC Percentage	41.73%

2.3. Coverage

Mean	2.1243
Standard Deviation	29.9104

2.4. Mapping Quality

Mean Mapping Quality	52.44

2.5. Insert size

Mean	159,581.67
Standard Deviation	4,160,030.52
P25/Median/P75	136 / 149 / 161

2.6. Mismatches and indels

General error rate	1.53%
Mismatches	98,398,093
Insertions	1,049,024
Mapped reads with at least one insertion	1.38%
Deletions	862,322
Mapped reads with at least one deletion	1.13%
Homopolymer indels	37.24%

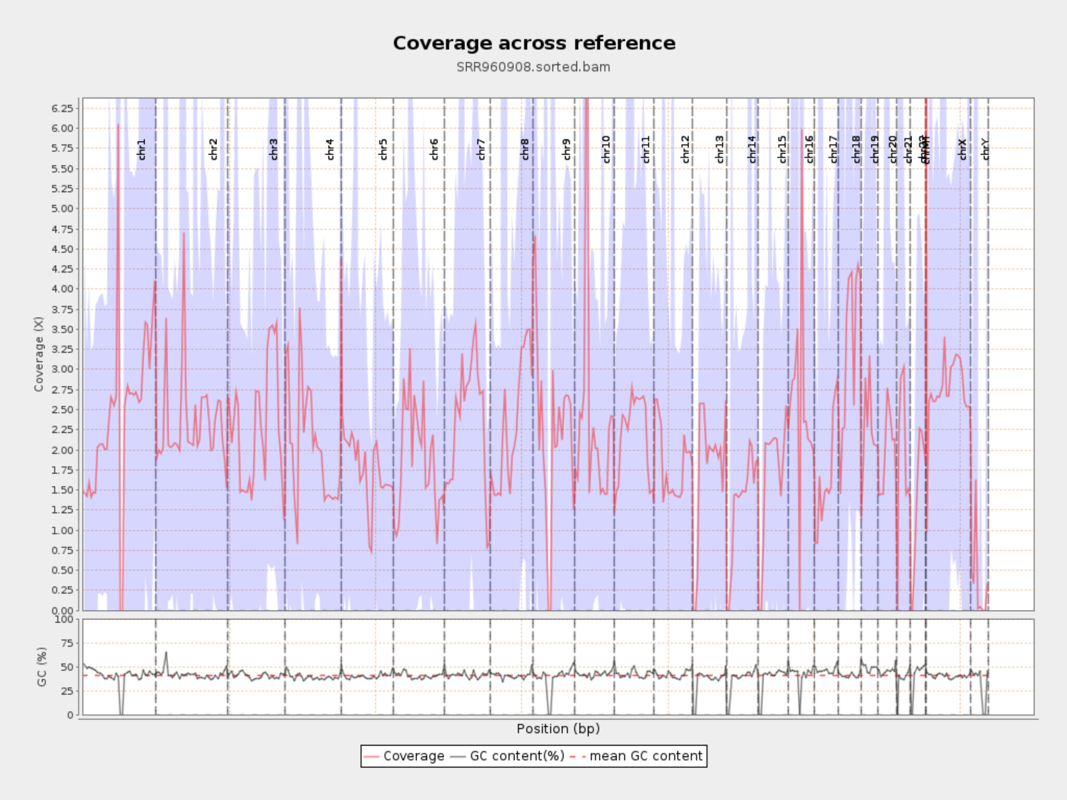
2.7. Chromosome stats

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

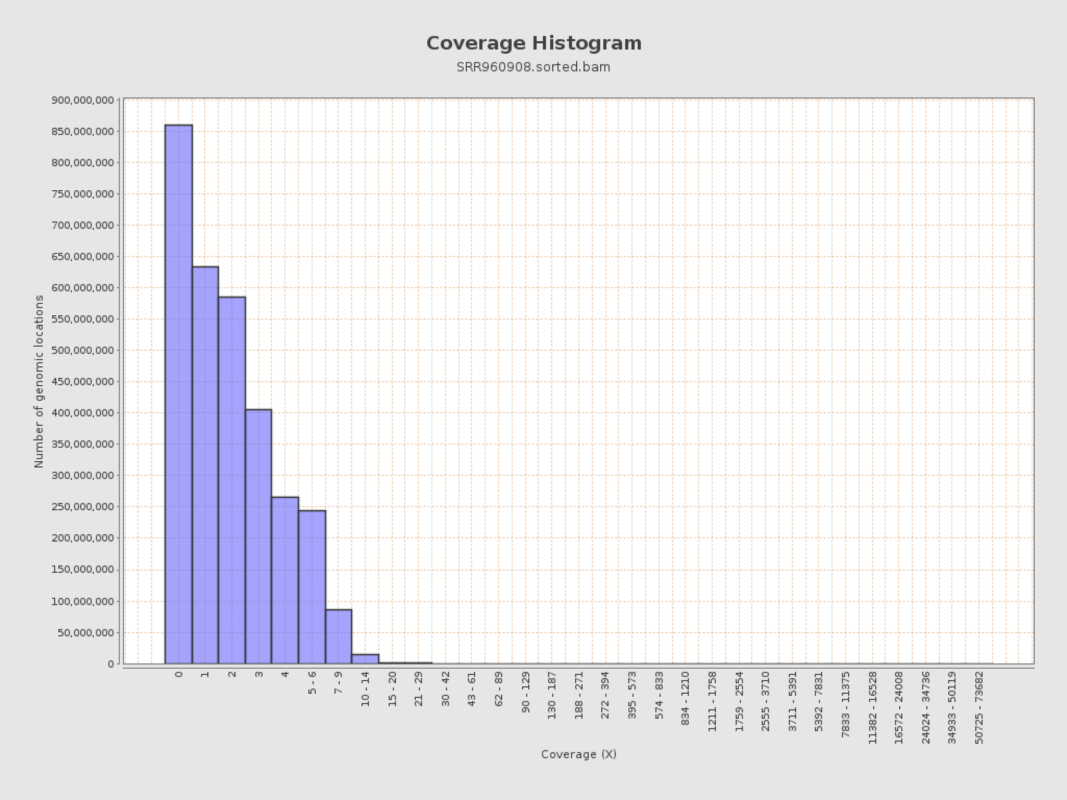
		bases	coverage	deviation
chr1	249250621	607550179	2.4375	73.1249
chr2	243199373	570402707	2.3454	47.877
chr3	198022430	451465832	2.2799	4.9305
chr4	191154276	395931612	2.0713	13.663
chr5	180915260	318918994	1.7628	3.0906
chr6	171115067	326469256	1.9079	8.8734
chr7	159138663	371540485	2.3347	18.9086
chr8	146364022	340775402	2.3283	23.6013
chr9	141213431	314017948	2.2237	22.6608
chr10	135534747	319742663	2.3591	50.0511
chr11	135006516	298158041	2.2085	14.6892
chr12	133851895	246459016	1.8413	3.4033
chr13	115169878	203993512	1.7712	2.1026
chr14	107349540	145146018	1.3521	12.7158
chr15	102531392	171874705	1.6763	2.3708
chr16	90354753	234144899	2.5914	24.5381
chr17	81195210	133347231	1.6423	7.3395
chr18	78077248	253969451	3.2528	27.6517
chr19	59128983	135459821	2.2909	33.8182
chr20	63025520	124774465	1.9797	6.1091
chr21	48129895	92540705	1.9227	8.8712
chr22	51304566	71165997	1.3871	2.2174
chrMT	16571	1420126	85.6995	18.895
chrX	155270560	425912466	2.743	9.7645

chrY	59373566	20895519	0.3519	16.3664

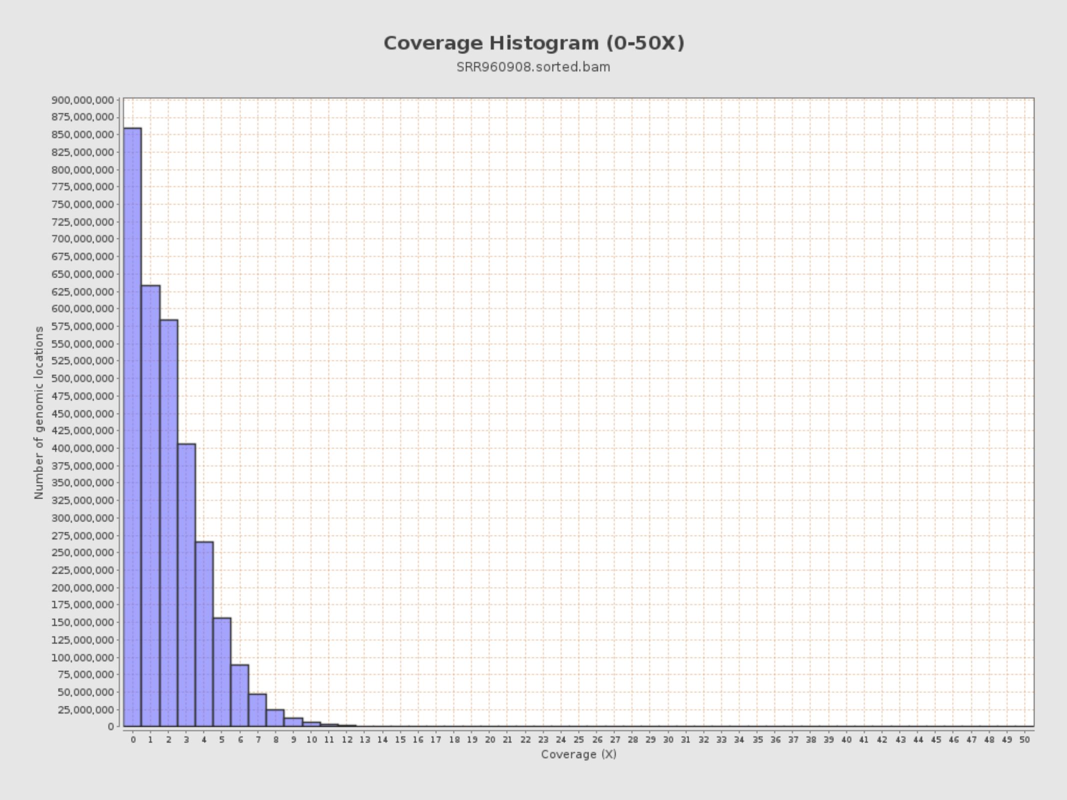
3. Results : Coverage across reference



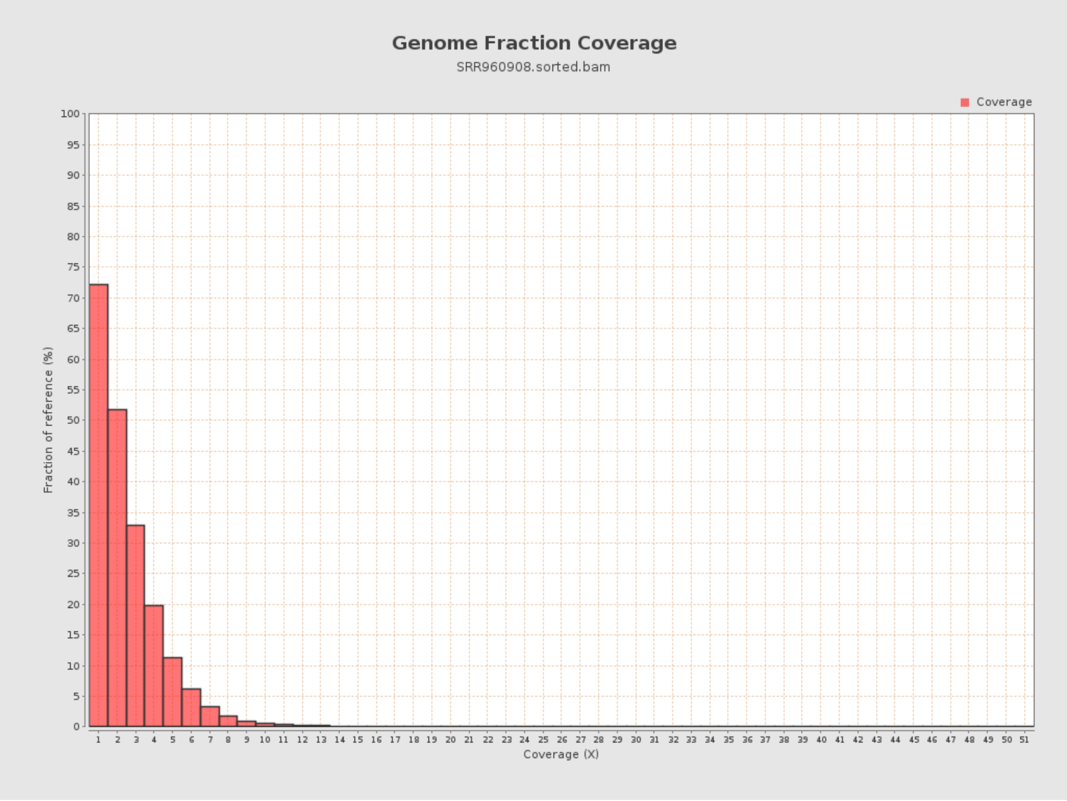
4. Results : Coverage Histogram



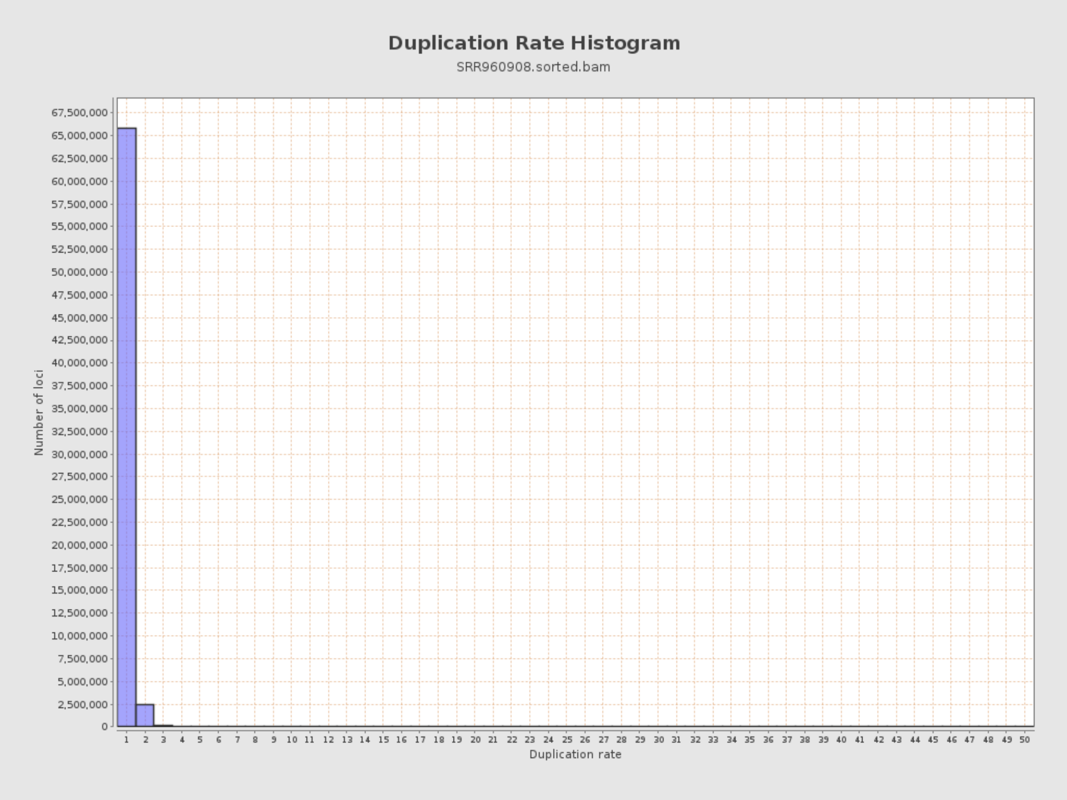
5. Results : Coverage Histogram (0-50X)



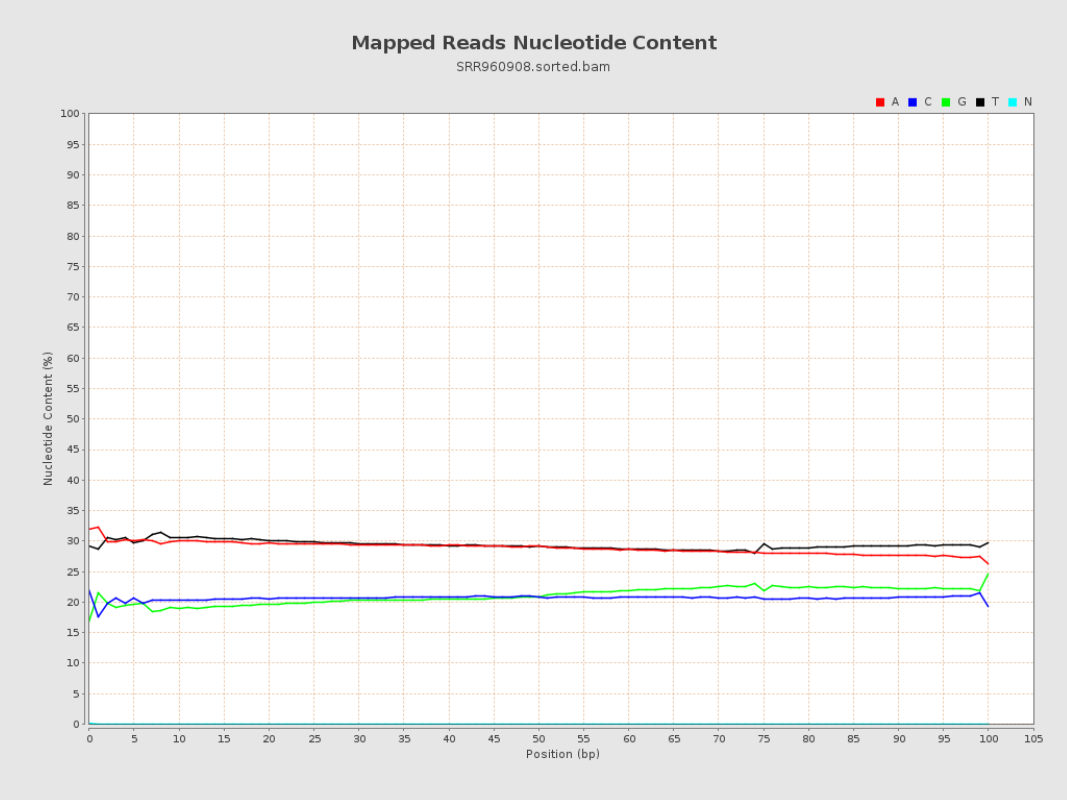
6. Results : Genome Fraction Coverage



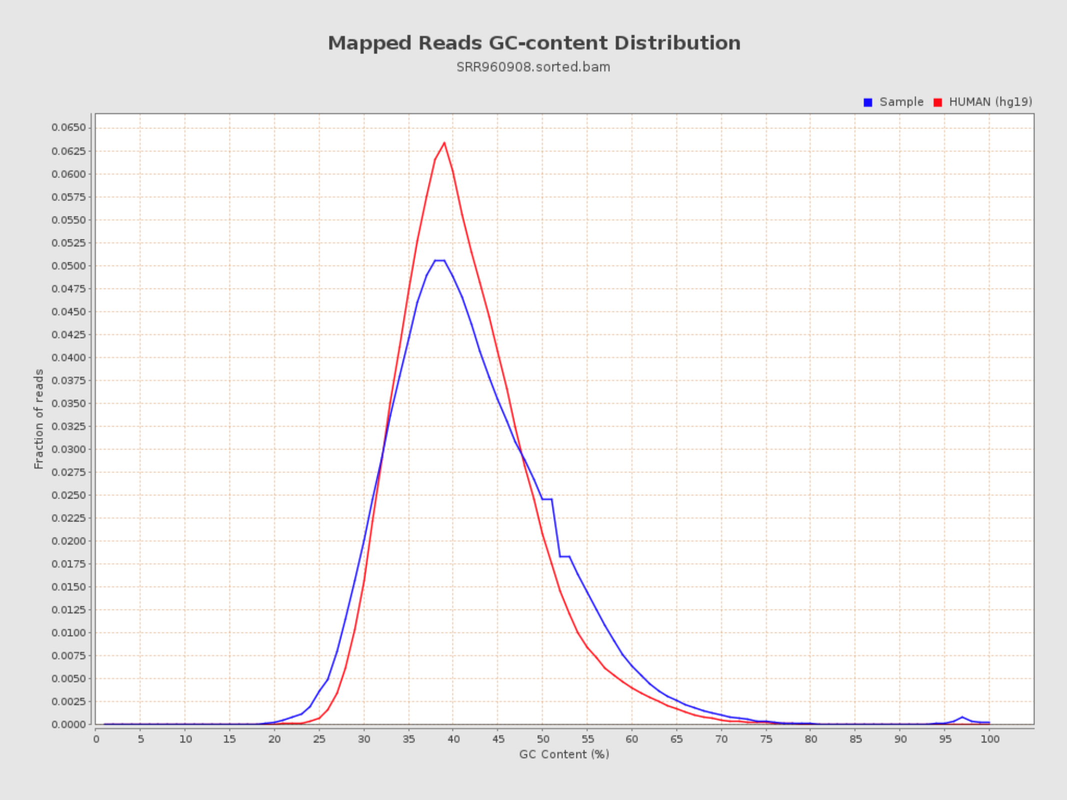
7. Results : Duplication Rate Histogram



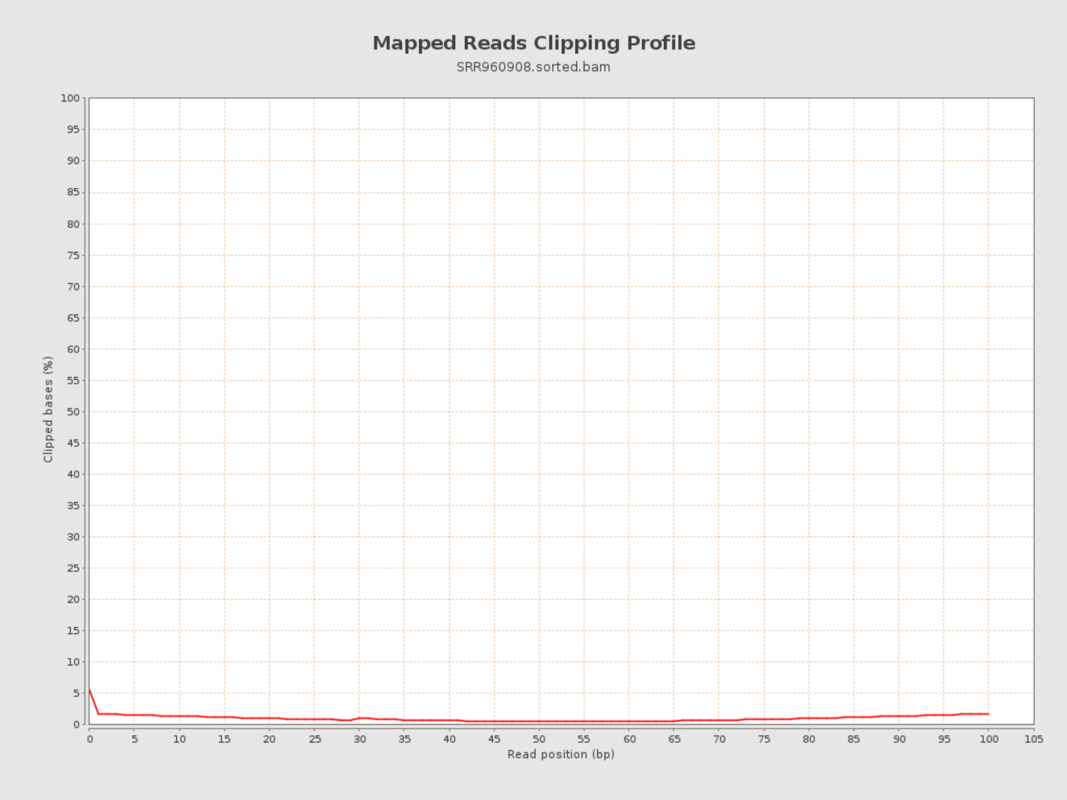
8. Results : Mapped Reads Nucleotide Content



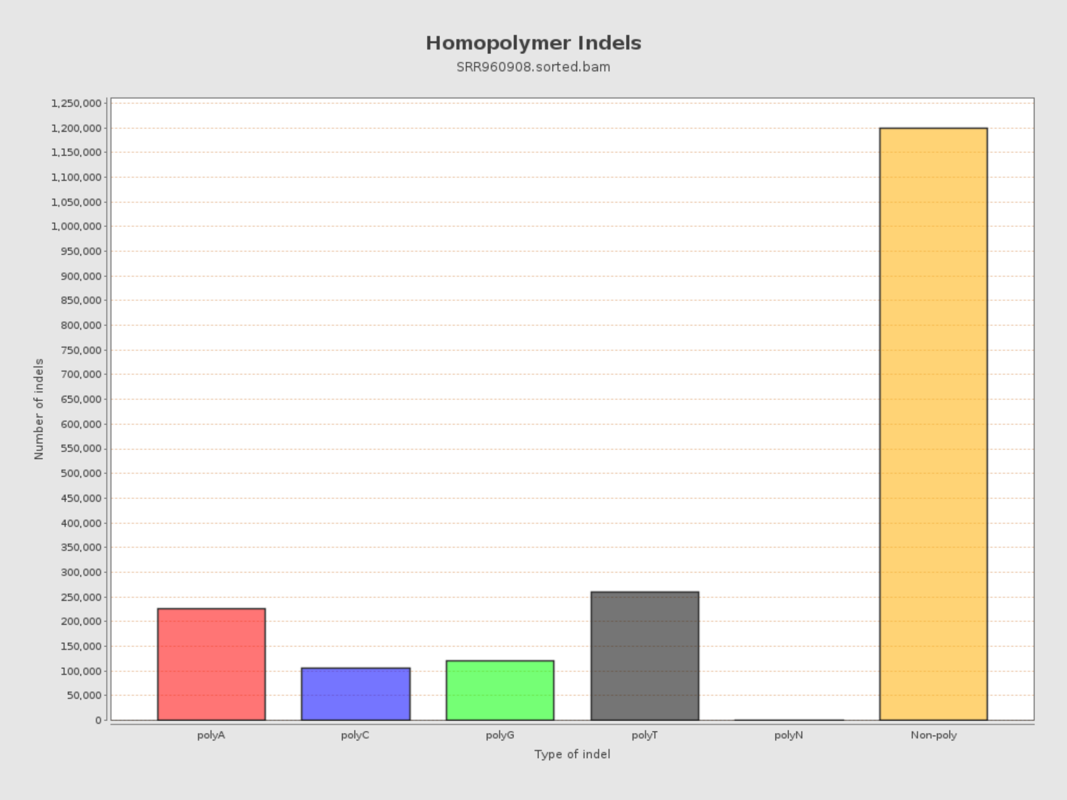
9. Results : Mapped Reads GC-content Distribution



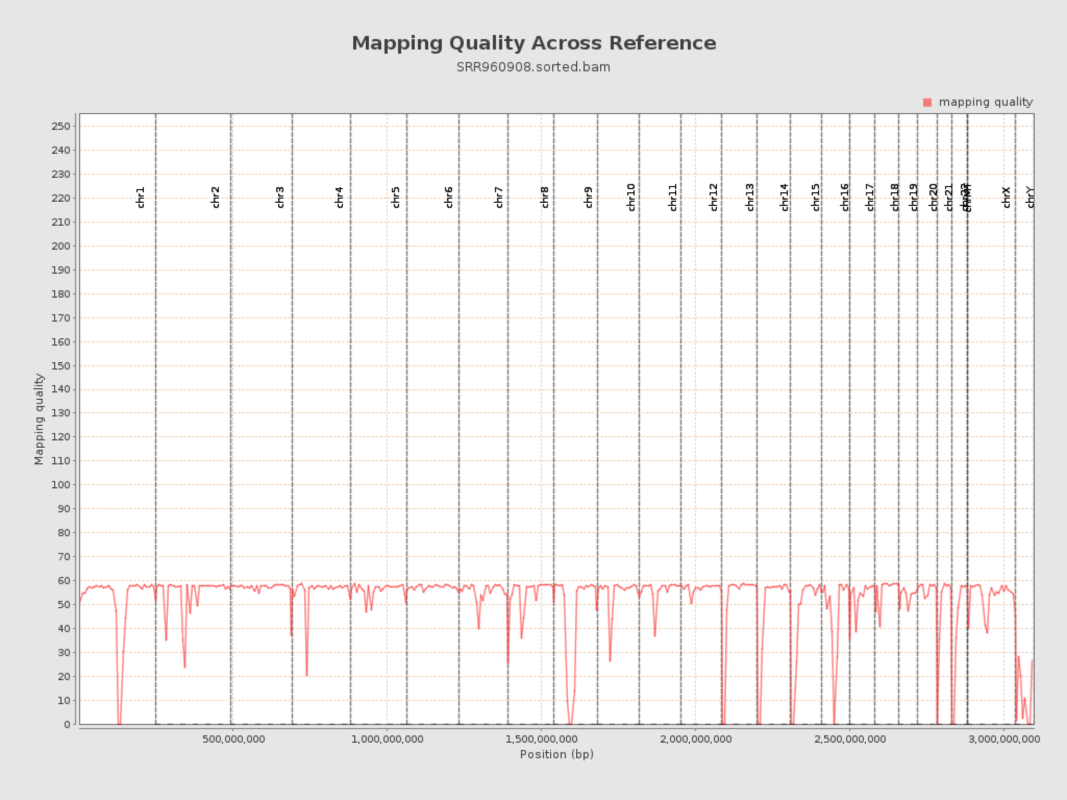
10. Results : Mapped Reads Clipping Profile



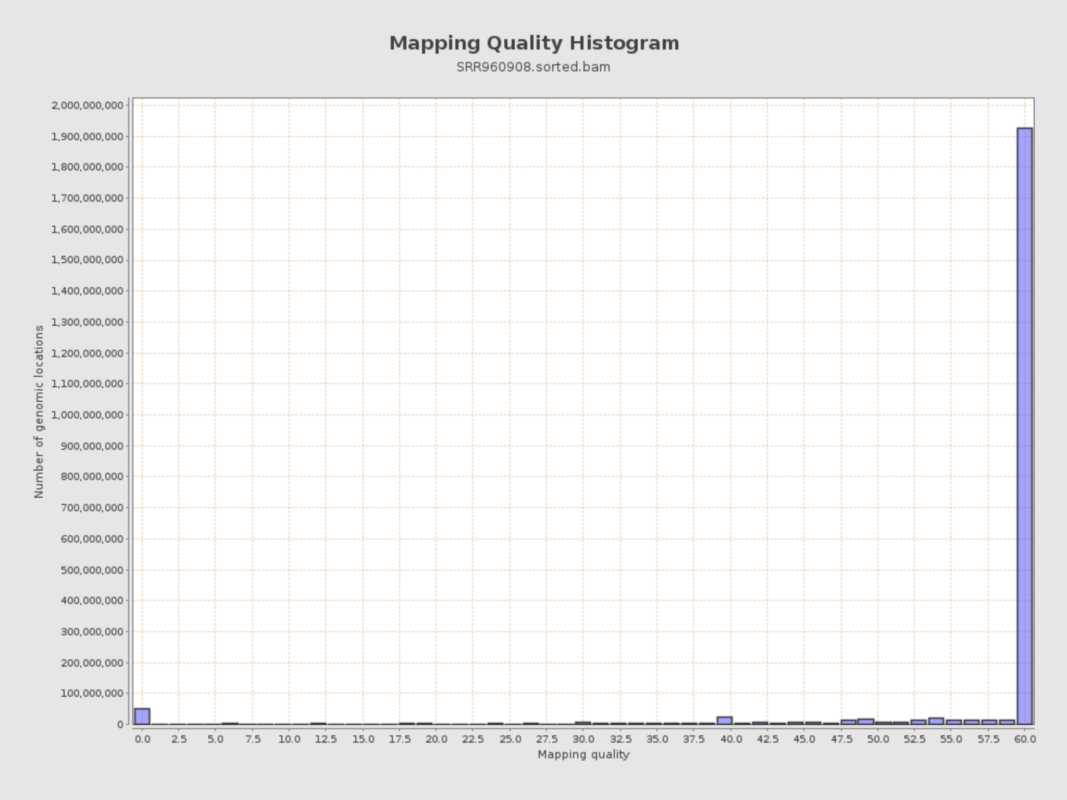
11. Results : Homopolymer Indels



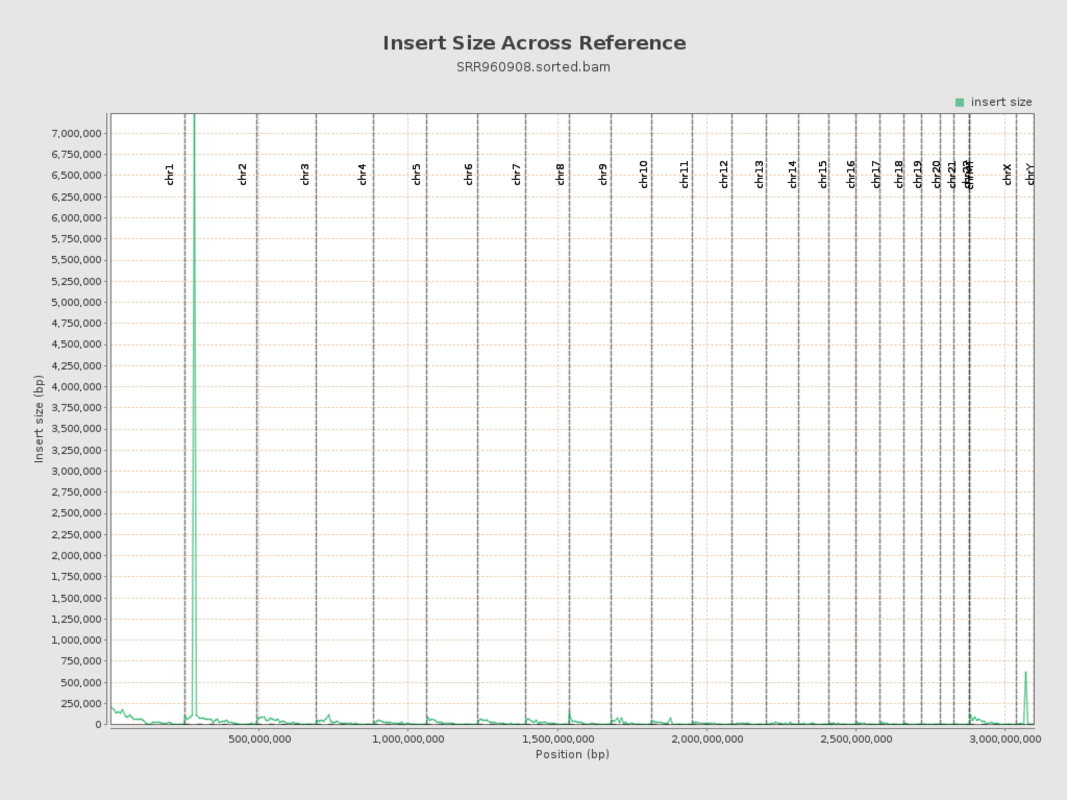
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram