Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.2-dev
2025/01/06 09:25:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR960910.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_SRR960910 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR960910_1.fastq.gz SRR960910_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Jan 06 09:25:47 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR960910.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	137,022,420
Mapped reads	130,410,427 / 95.17%
Unmapped reads	6,611,993 / 4.83%
Mapped paired reads	130,410,427 / 95.17%
Mapped reads, first in pair	65,468,754 / 47.78%
Mapped reads, second in pair	64,941,673 / 47.39%
Mapped reads, both in pair	127,584,026 / 93.11%
Mapped reads, singletons	2,826,401 / 2.06%
Secondary alignments	0
Supplementary alignments	2,063,357 / 1.51%
Read min/max/mean length	30 / 101 / 101.59
Duplicated reads (estimated)	14,584,655 / 10.64%
Duplication rate	5.78%
Clipped reads	67,654,089 / 49.37%

2.2. ACGT Content

Number/percentage of A's	3,291,210,377 / 29.03%
Number/percentage of C's	2,333,064,817 / 20.58%
Number/percentage of T's	3,359,340,165 / 29.63%
Number/percentage of G's	2,352,872,661 / 20.75%
Number/percentage of N's	1,612,416 / 0.01%

GC Percentage	41.33%

2.3. Coverage

Mean	3.6635
Standard Deviation	49.4861

2.4. Mapping Quality

Mean Mapping Quality	52.37

2.5. Insert size

Mean	151,836.16
Standard Deviation	4,006,502.08
P25/Median/P75	136 / 149 / 161

2.6. Mismatches and indels

General error rate	1.63%
Mismatches	181,572,538
Insertions	1,743,608
Mapped reads with at least one insertion	1.31%
Deletions	1,461,875
Mapped reads with at least one deletion	1.09%
Homopolymer indels	36.84%

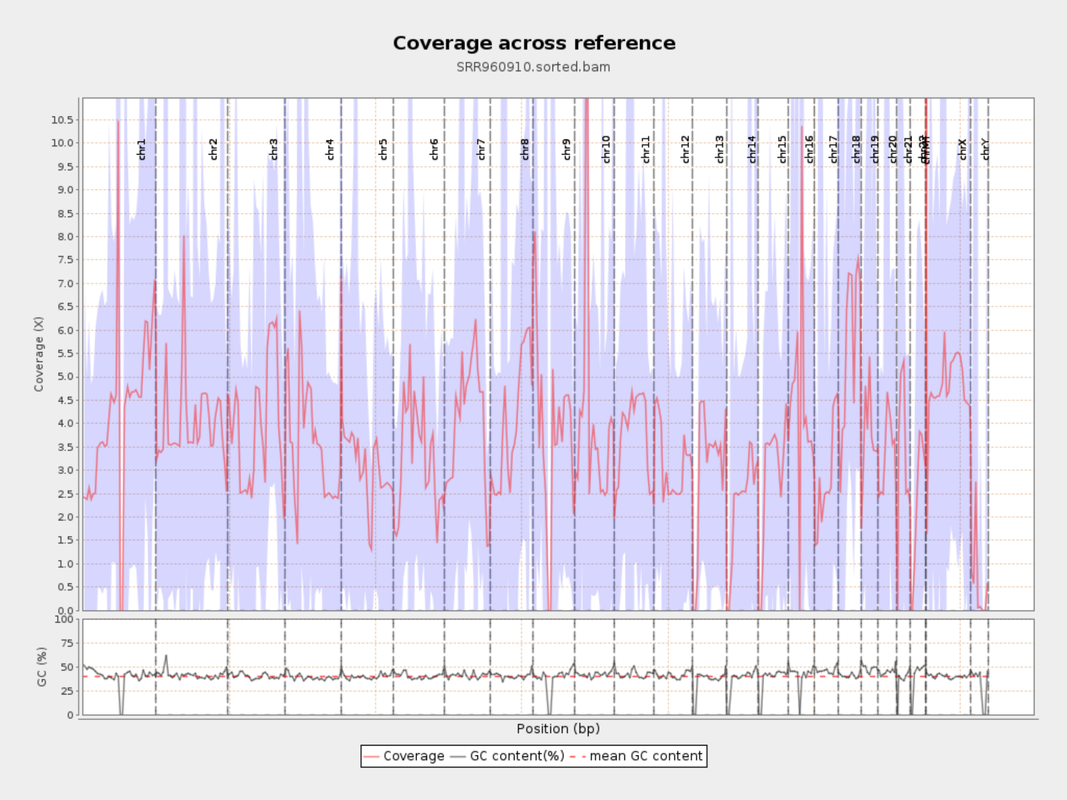
2.7. Chromosome stats

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

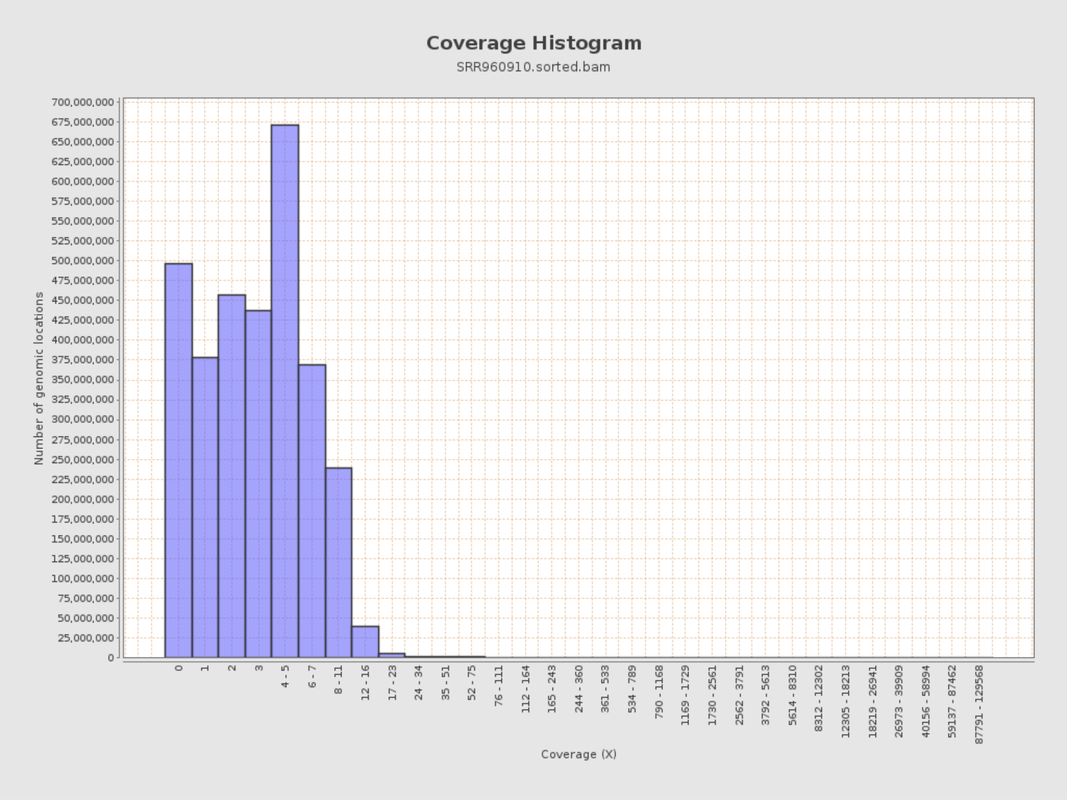
		bases	coverage	deviation
chr1	249250621	1047985785	4.2045	126.9651
chr2	243199373	981758587	4.0368	66.5904
chr3	198022430	783761267	3.9579	8.1797
chr4	191154276	687194196	3.595	22.2971
chr5	180915260	553997492	3.0622	4.9286
chr6	171115067	566513243	3.3107	15.4685
chr7	159138663	642419475	4.0369	32.6937
chr8	146364022	589827845	4.0299	40.6177
chr9	141213431	541603208	3.8354	38.3393
chr10	135534747	549065827	4.0511	83.6058
chr11	135006516	513510399	3.8036	23.7001
chr12	133851895	424310980	3.17	4.6373
chr13	115169878	354445250	3.0776	3.0559
chr14	107349540	249690203	2.326	18.7141
chr15	102531392	295375361	2.8808	3.5875
chr16	90354753	398793433	4.4136	42.2177
chr17	81195210	225189049	2.7734	12.3305
chr18	78077248	439274562	5.6262	46.9237
chr19	59128983	226753797	3.8349	57.4331
chr20	63025520	212332219	3.369	10.1521
chr21	48129895	160180393	3.3281	15.0244
chr22	51304566	119073513	2.3209	3.5592
chrMT	16571	2395379	144.5525	30.0029
chrX	155270560	740168525	4.767	16.4933

chrY	59373566	35578091	0.5992	26.8972

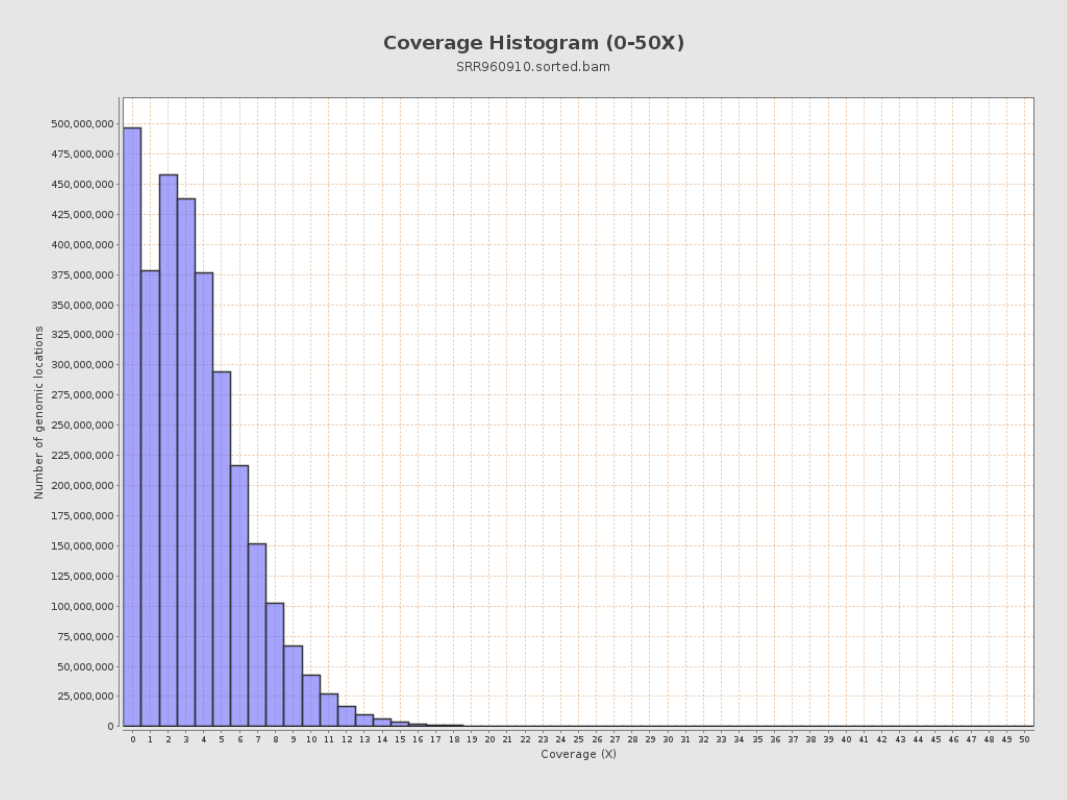
3. Results : Coverage across reference



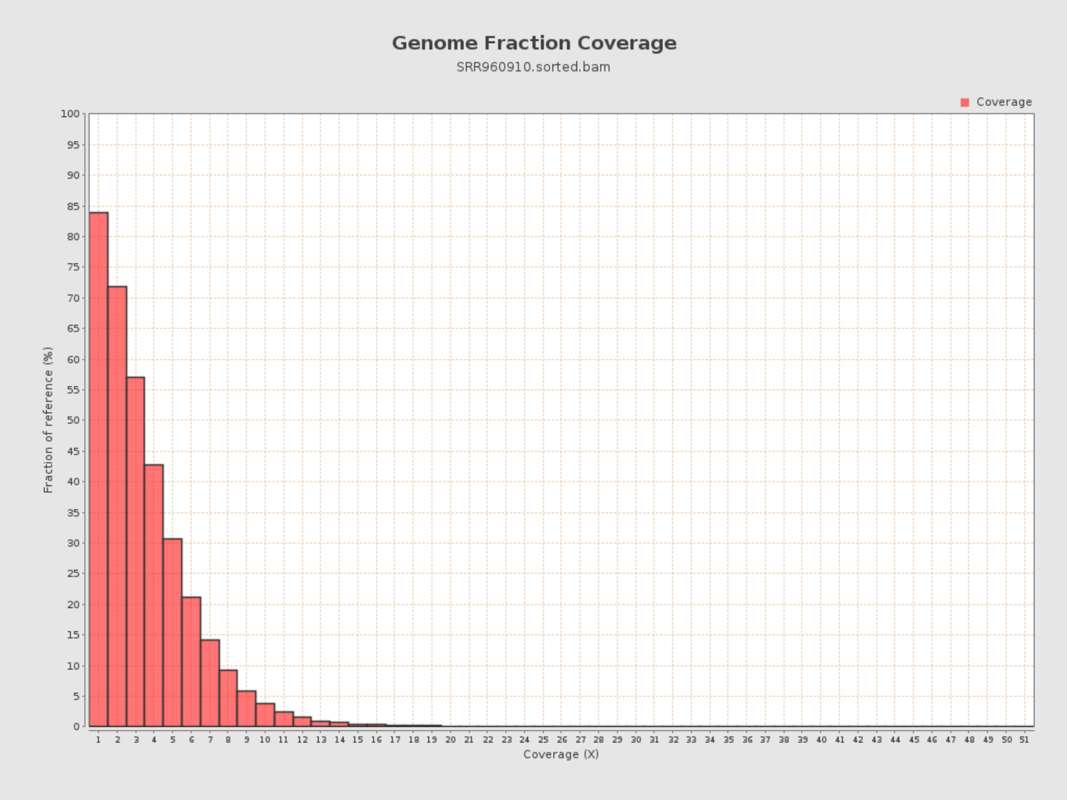
4. Results : Coverage Histogram



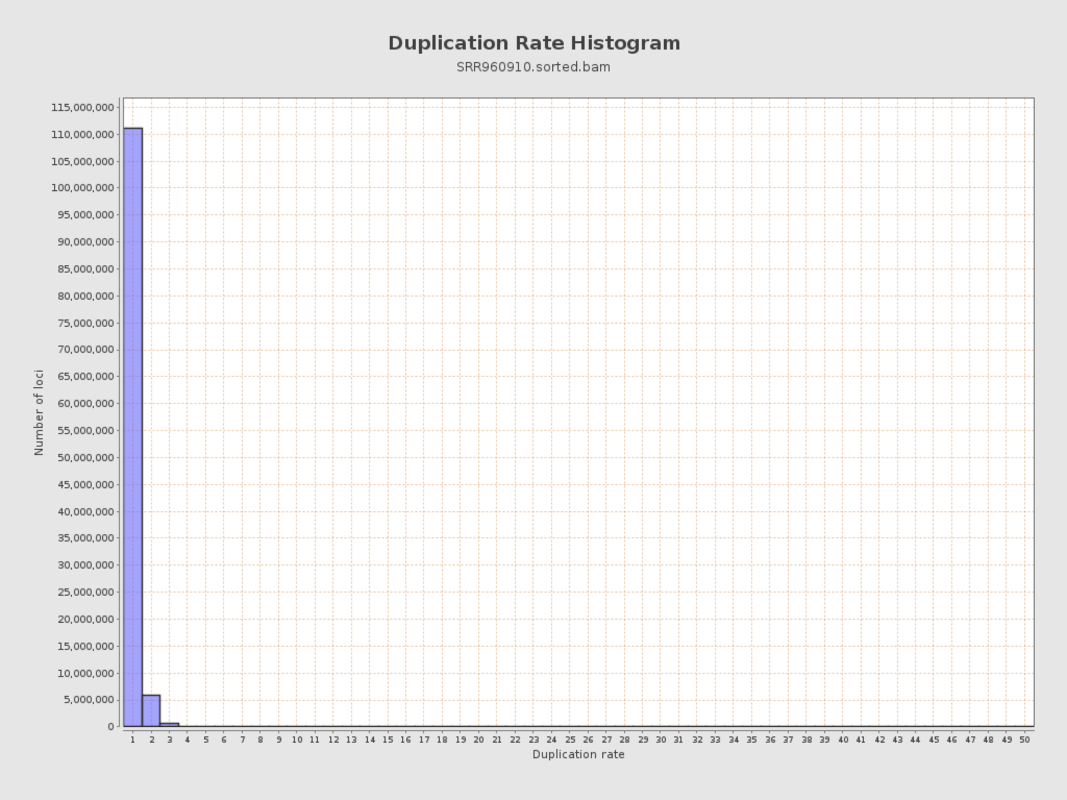
5. Results : Coverage Histogram (0-50X)



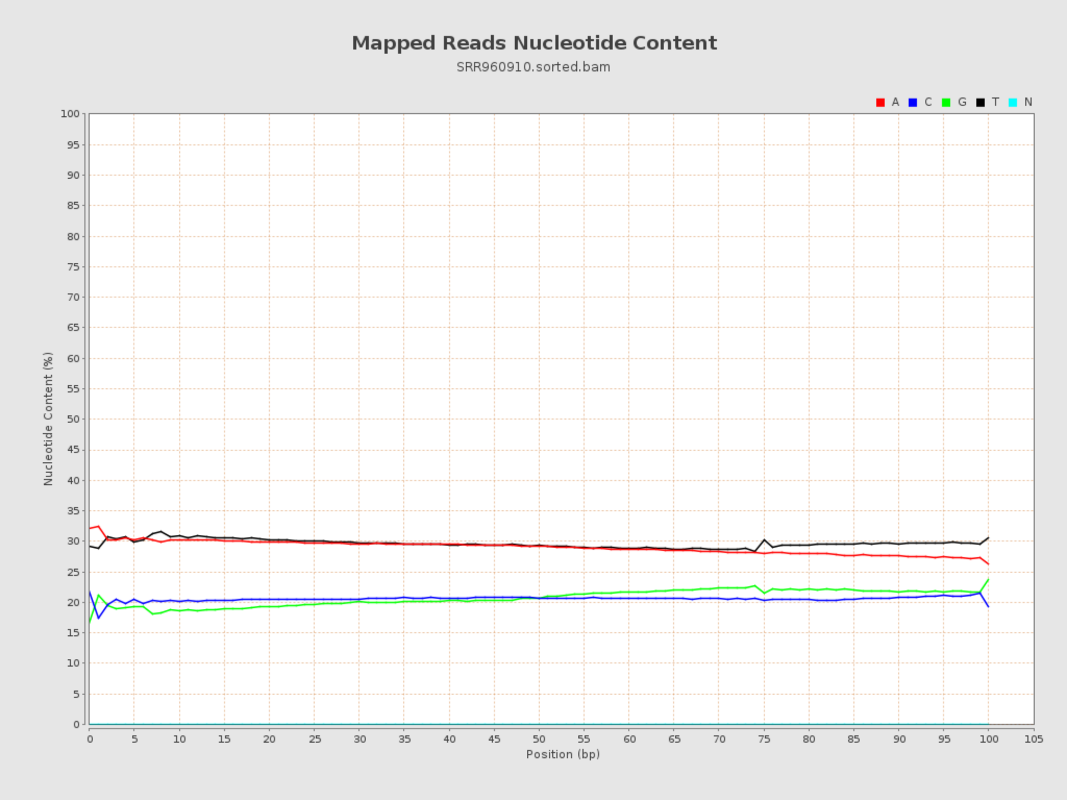
6. Results : Genome Fraction Coverage



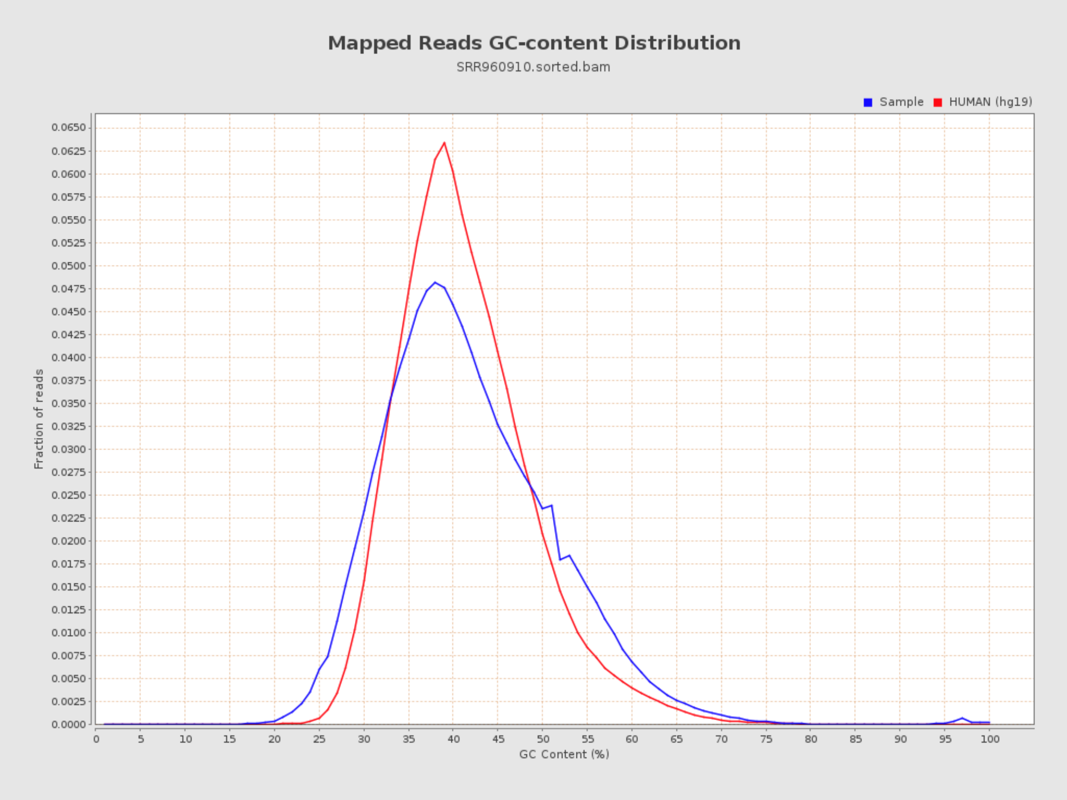
7. Results : Duplication Rate Histogram



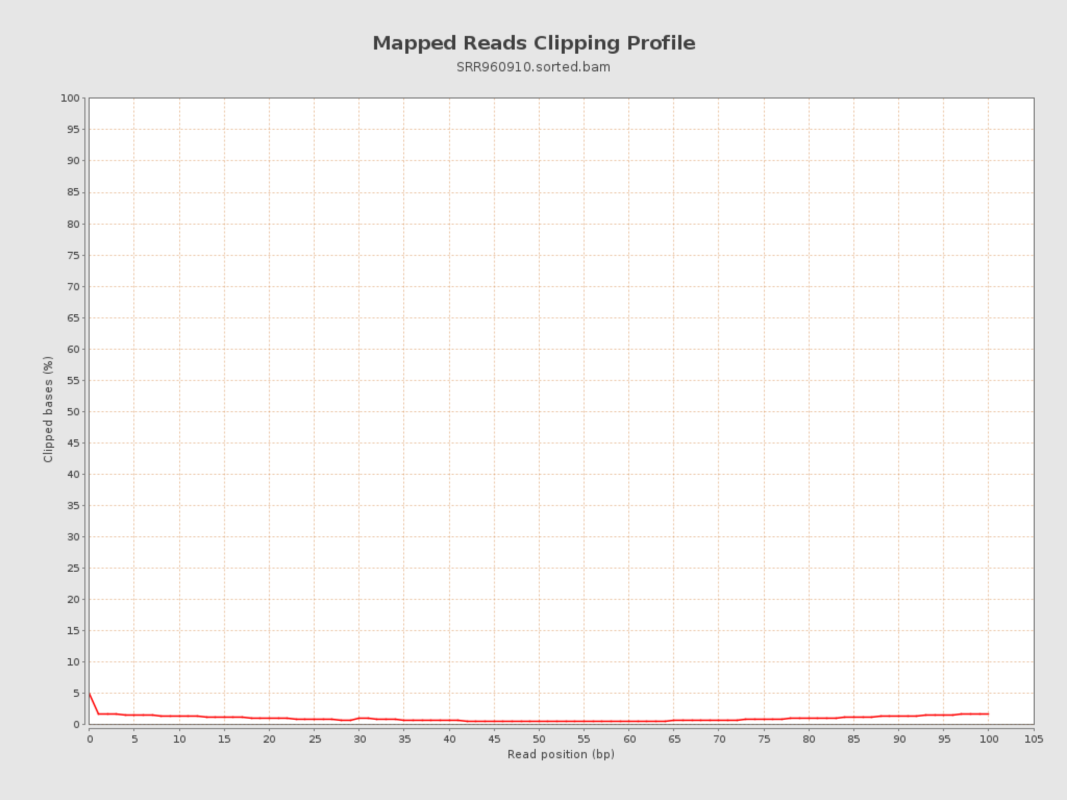
8. Results : Mapped Reads Nucleotide Content



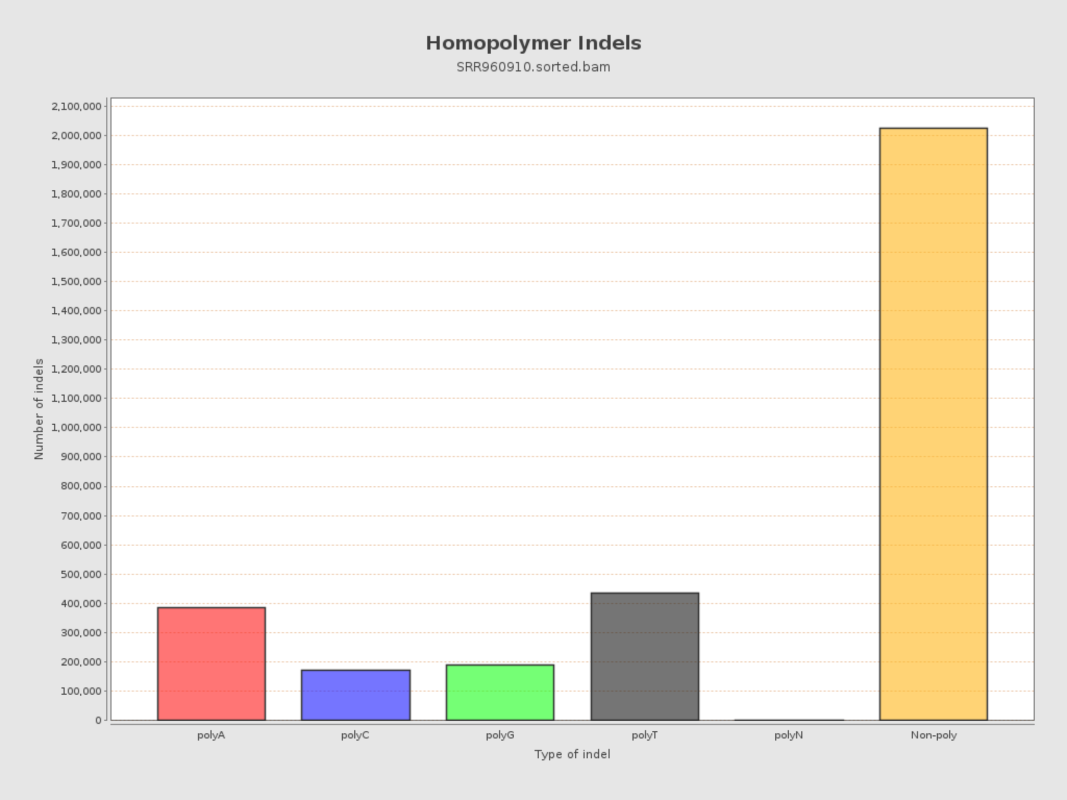
9. Results : Mapped Reads GC-content Distribution



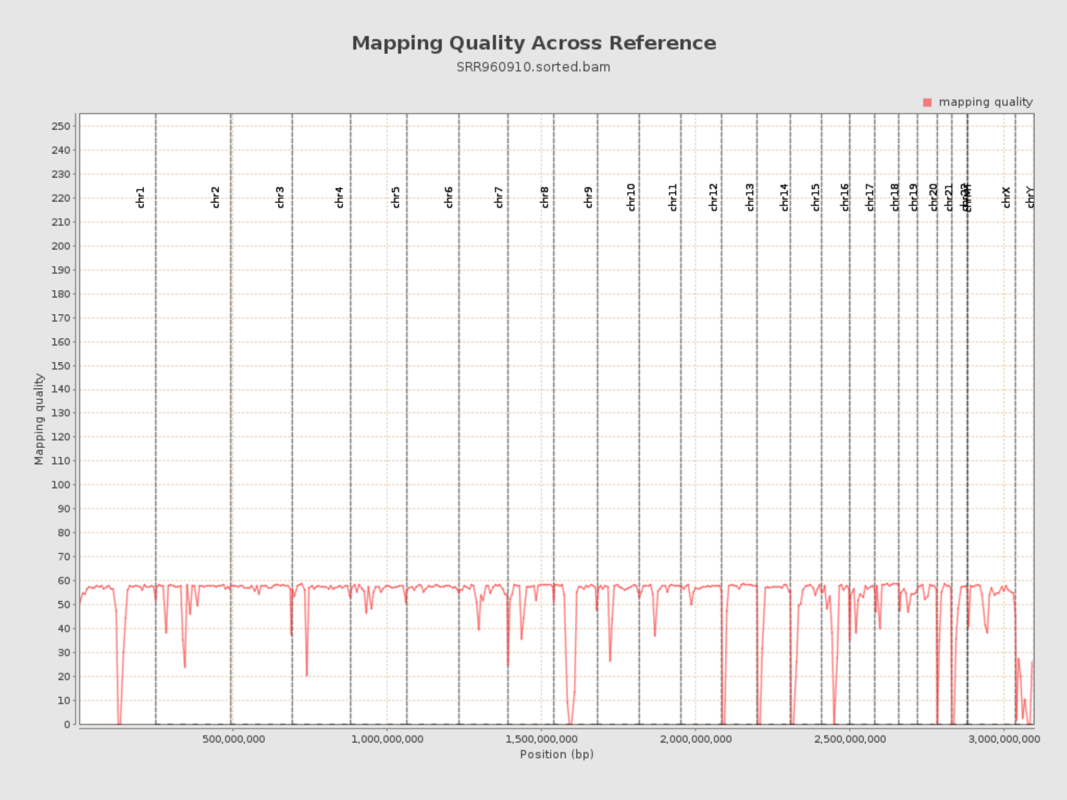
10. Results : Mapped Reads Clipping Profile



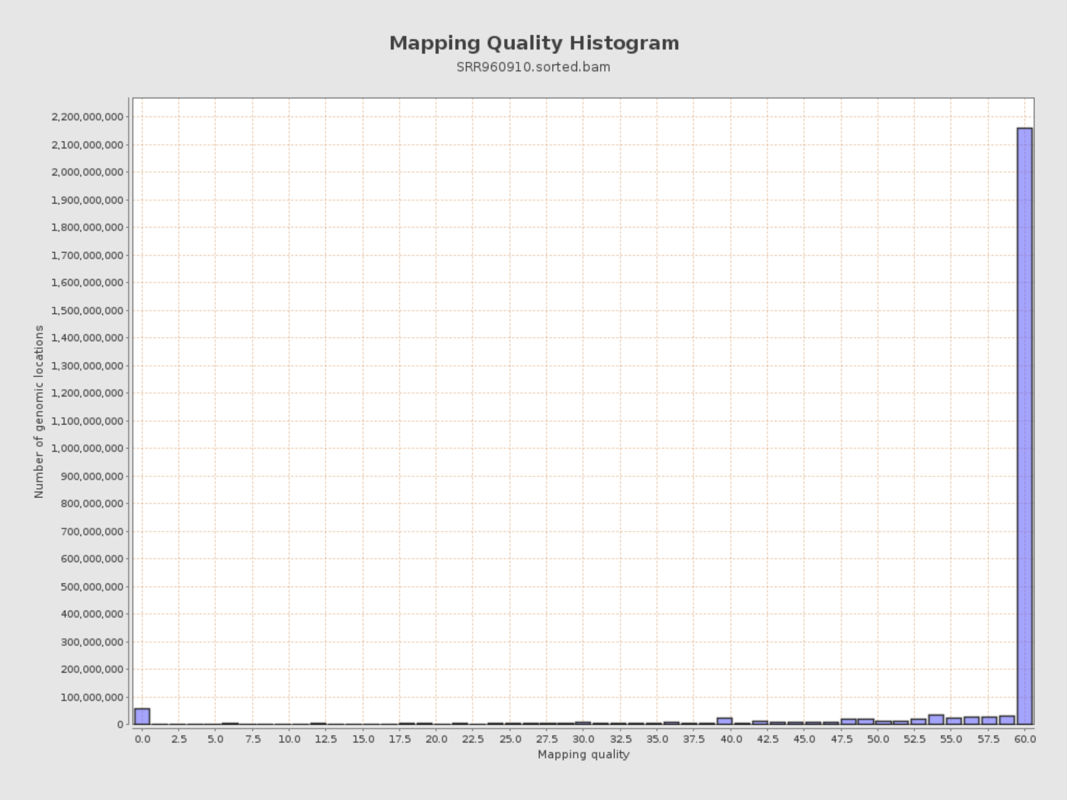
11. Results : Homopolymer Indels



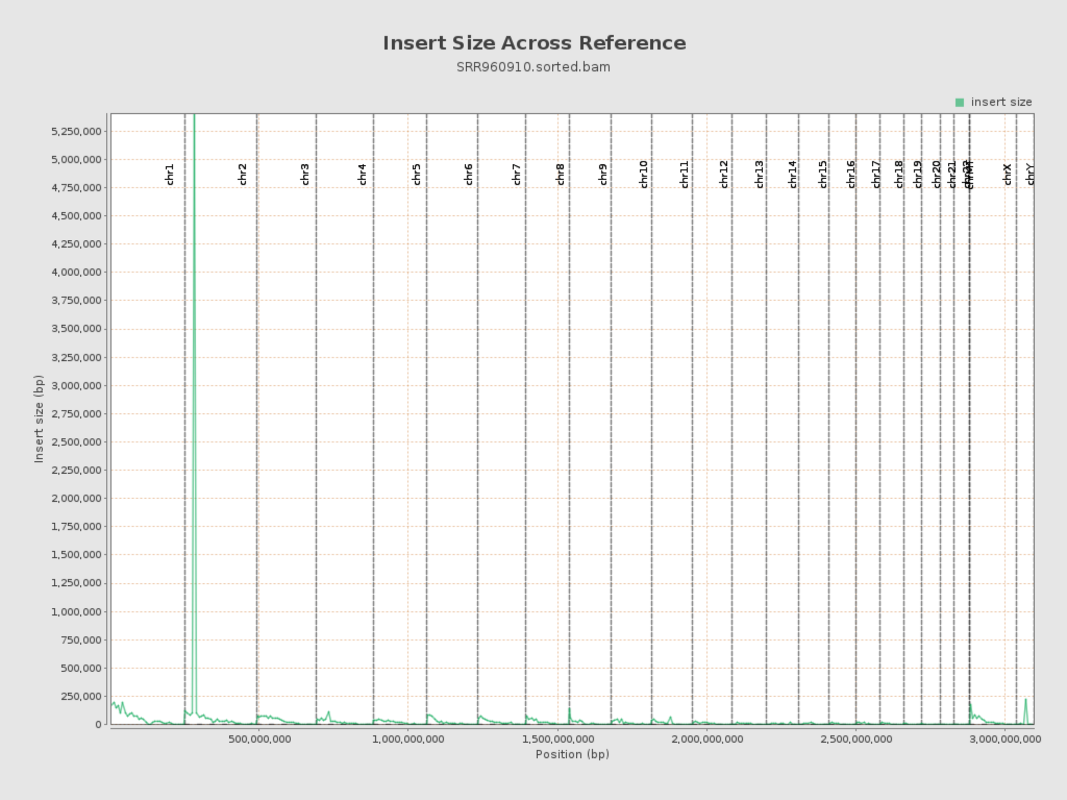
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram