Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/06 13:20:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR960912.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_SRR960912 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR960912_1.fastq.gz SRR960912_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Jan 06 13:20:36 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR960912.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	126,702,336
Mapped reads	120,472,032 / 95.08%
Unmapped reads	6,230,304 / 4.92%
Mapped paired reads	120,472,032 / 95.08%
Mapped reads, first in pair	60,434,786 / 47.7%
Mapped reads, second in pair	60,037,246 / 47.38%
Mapped reads, both in pair	117,996,662 / 93.13%
Mapped reads, singletons	2,475,370 / 1.95%
Secondary alignments	0
Supplementary alignments	1,989,069 / 1.57%
Read min/max/mean length	30 / 101 / 101.62
Duplicated reads (estimated)	13,204,587 / 10.42%
Duplication rate	5.54%
Clipped reads	61,147,869 / 48.26%

2.2. ACGT Content

Number/percentage of A's	3,054,340,111 / 29.01%
Number/percentage of C's	2,166,182,815 / 20.58%
Number/percentage of T's	3,113,484,356 / 29.58%
Number/percentage of G's	2,191,459,628 / 20.82%
Number/percentage of N's	1,654,395 / 0.02%

GC Percentage	41.39%

2.3. Coverage

Mean	3.4015
Standard Deviation	46.866

2.4. Mapping Quality

Mean Mapping Quality	52.38

2.5. Insert size

Mean	157,210.69
Standard Deviation	4,102,833.7
P25/Median/P75	136 / 149 / 161

2.6. Mismatches and indels

General error rate	1.6%
Mismatches	164,848,058
Insertions	1,626,485
Mapped reads with at least one insertion	1.32%
Deletions	1,365,562
Mapped reads with at least one deletion	1.1%
Homopolymer indels	37.05%

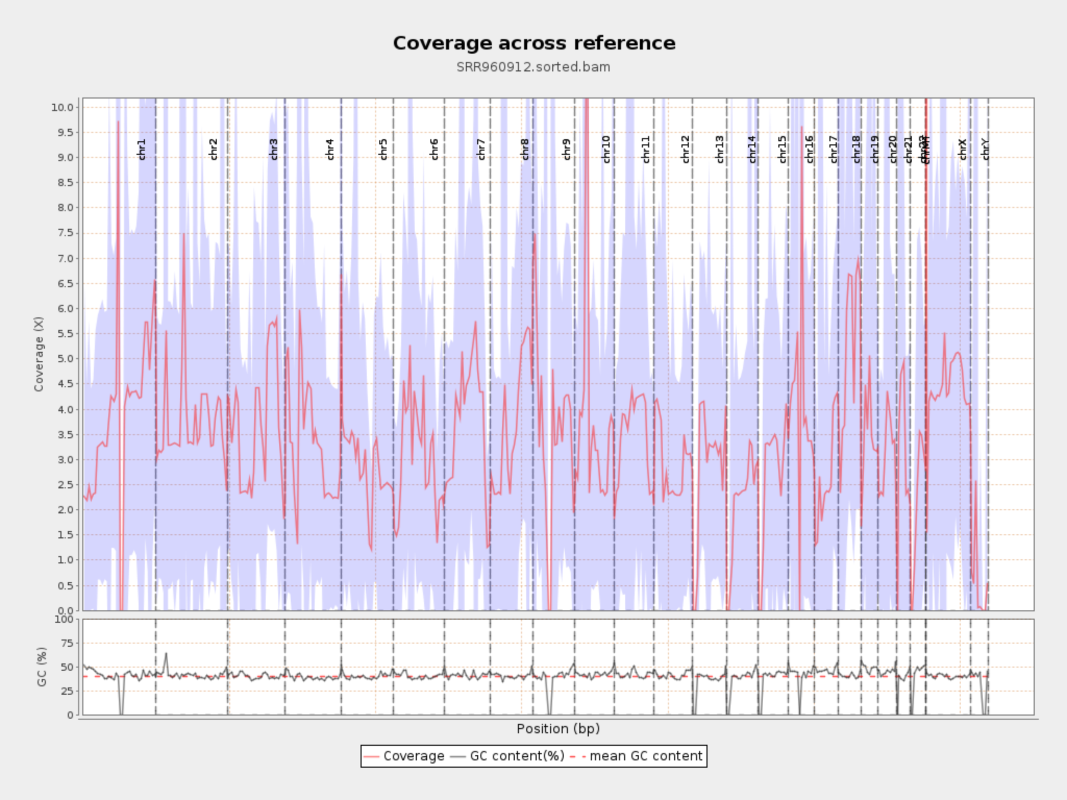
2.7. Chromosome stats

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

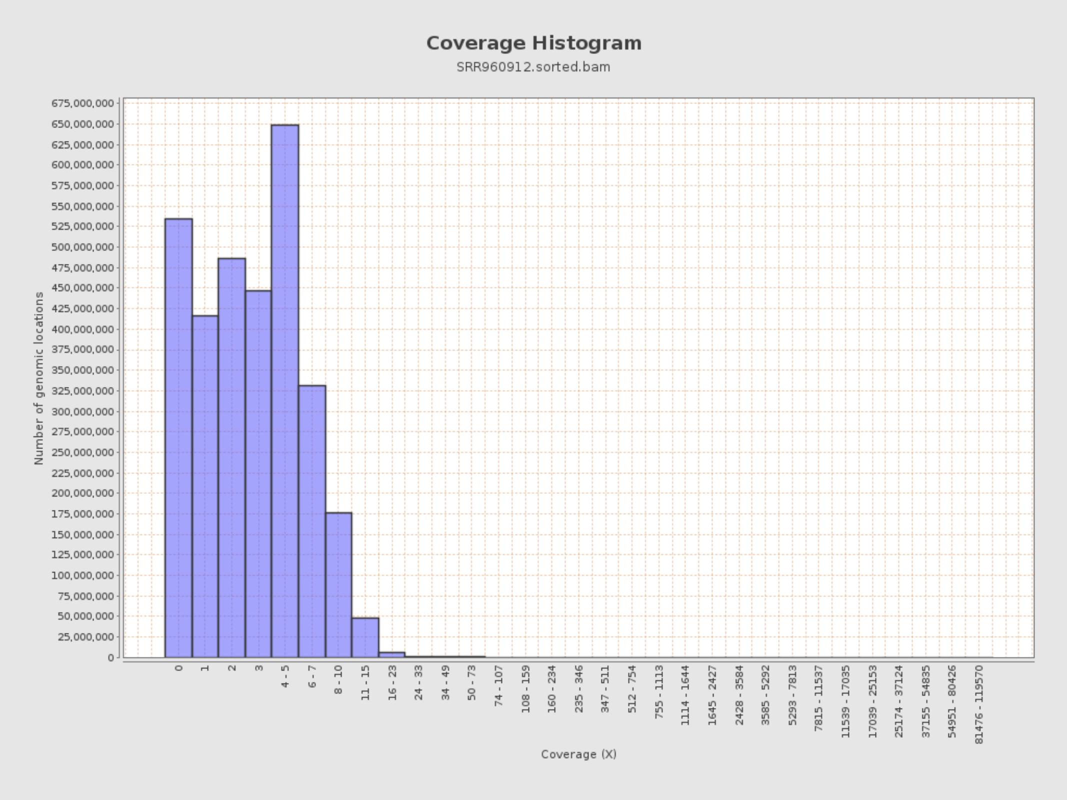
		bases	coverage	deviation
chr1	249250621	972620910	3.9022	117.5145
chr2	243199373	913671036	3.7569	69.165
chr3	198022430	726709264	3.6698	7.776
chr4	191154276	637519821	3.3351	21.1188
chr5	180915260	513027860	2.8357	4.6597
chr6	171115067	525257303	3.0696	14.3381
chr7	159138663	595812651	3.744	30.5906
chr8	146364022	547579102	3.7412	38.0934
chr9	141213431	502607976	3.5592	35.8047
chr10	135534747	510240249	3.7646	78.4897
chr11	135006516	476627078	3.5304	22.8407
chr12	133851895	393723180	2.9415	4.2405
chr13	115169878	328707110	2.8541	2.9452
chr14	107349540	232184741	2.1629	19.0177
chr15	102531392	274487930	2.6771	3.426
chr16	90354753	371241965	4.1087	39.4145
chr17	81195210	210265633	2.5896	11.6234
chr18	78077248	407415147	5.2181	43.9021
chr19	59128983	211549227	3.5778	53.8135
chr20	63025520	197386119	3.1318	9.6743
chr21	48129895	148578791	3.087	14.0822
chr22	51304566	110656255	2.1569	3.292
chrMT	16571	2196086	132.5259	28.0732
chrX	155270560	686852410	4.4236	15.519

chrY	59373566	33103389	0.5575	25.33

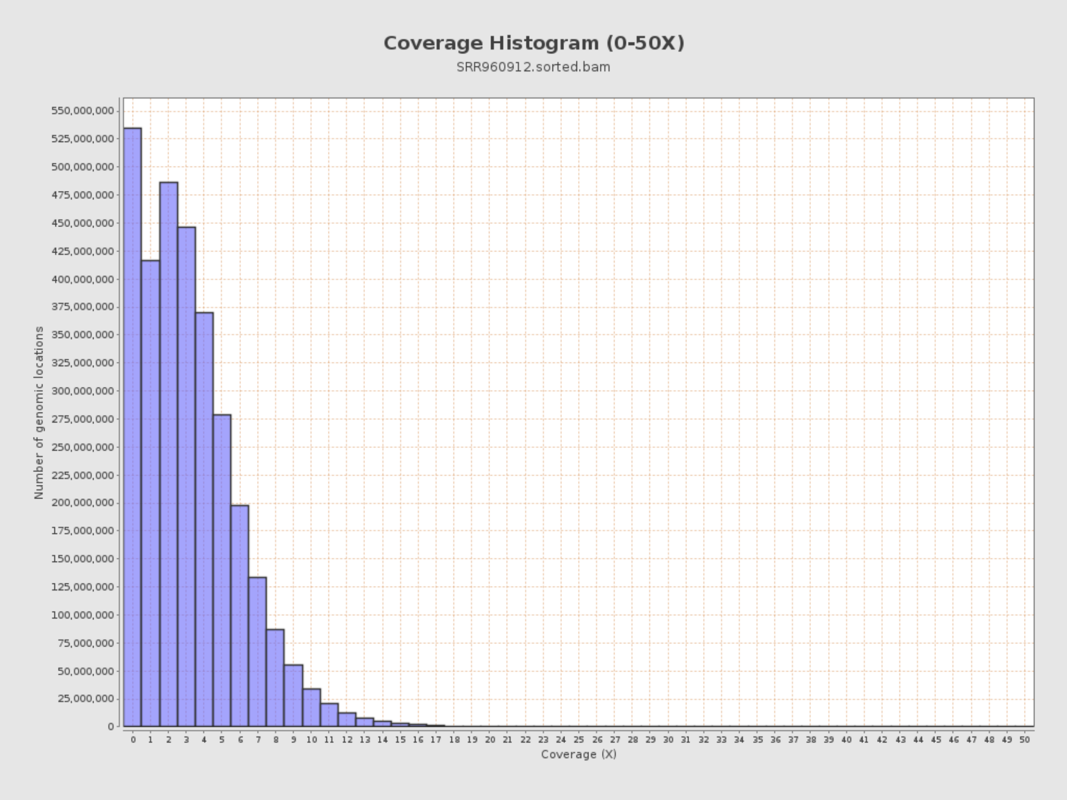
3. Results : Coverage across reference



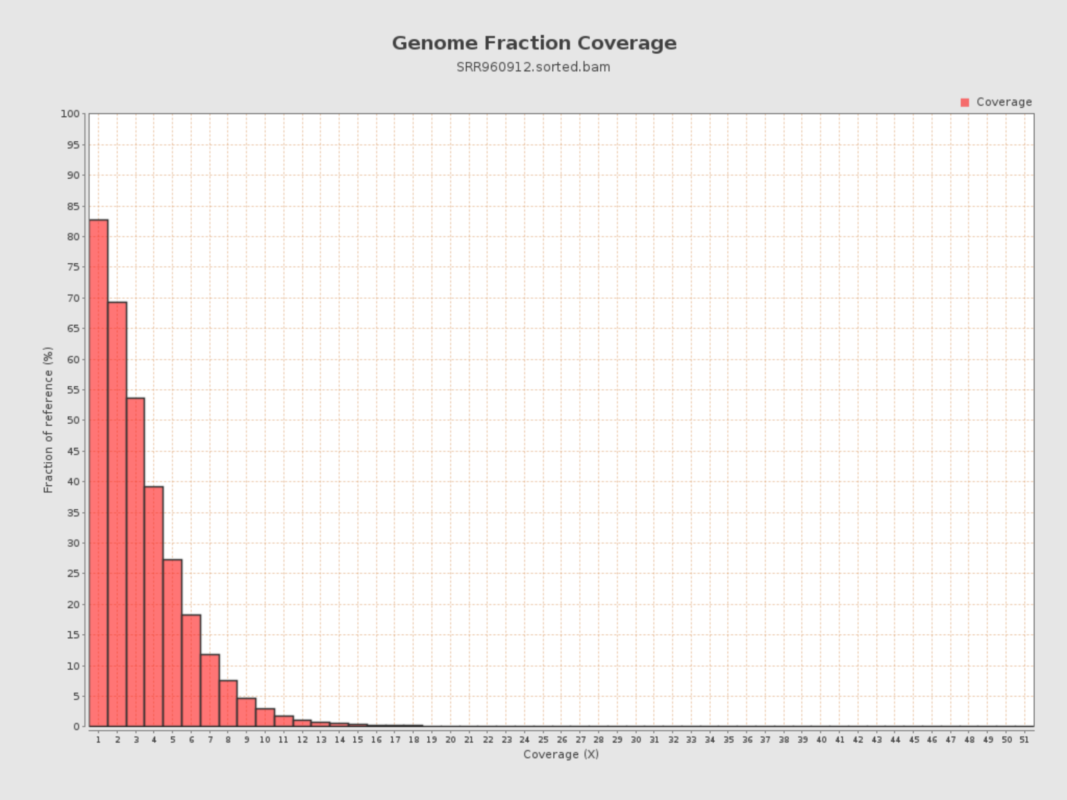
4. Results : Coverage Histogram



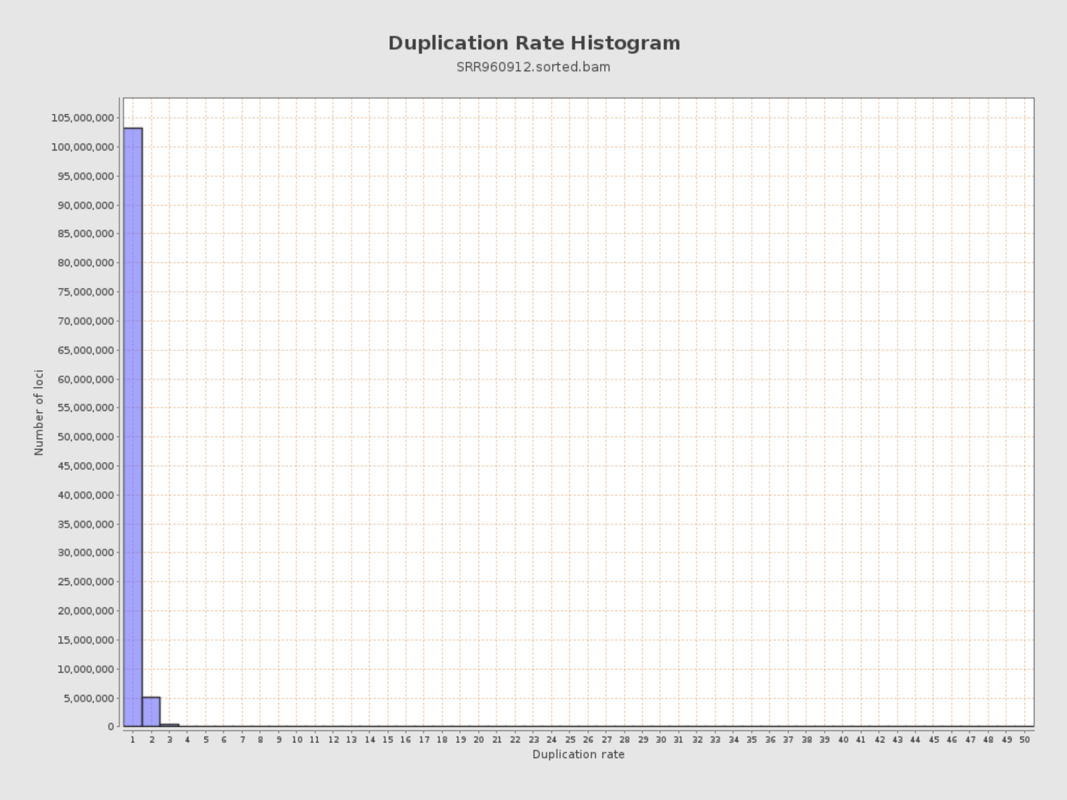
5. Results : Coverage Histogram (0-50X)



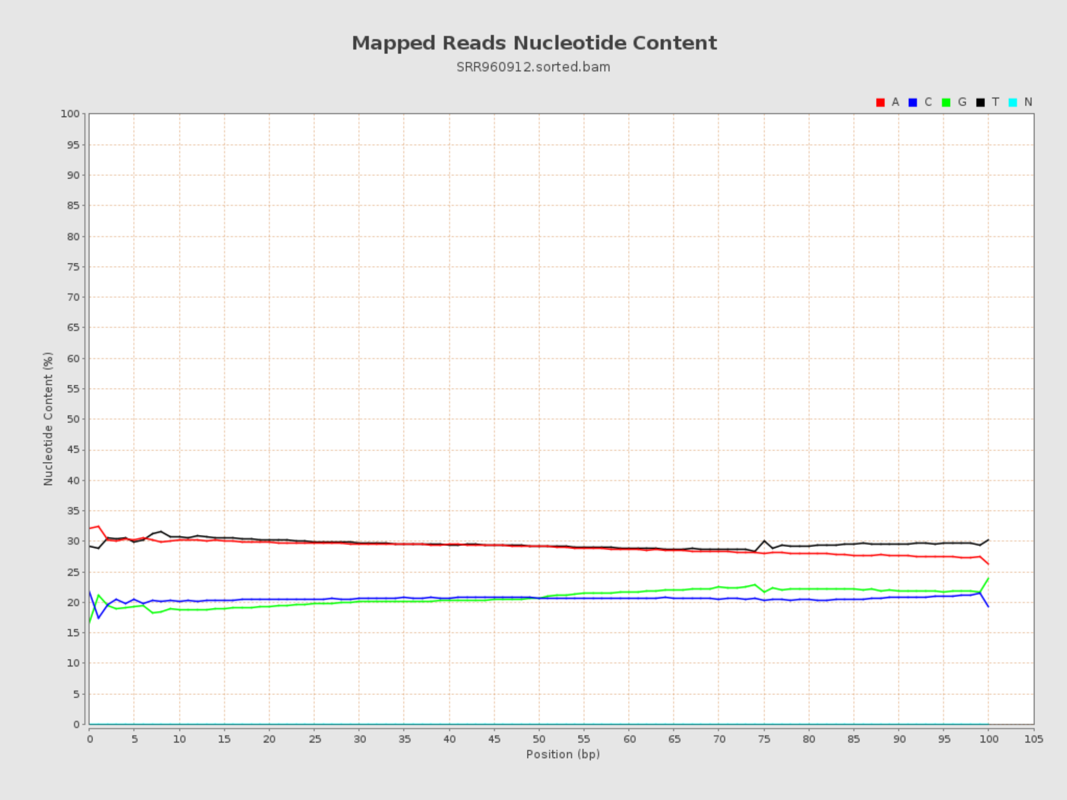
6. Results : Genome Fraction Coverage



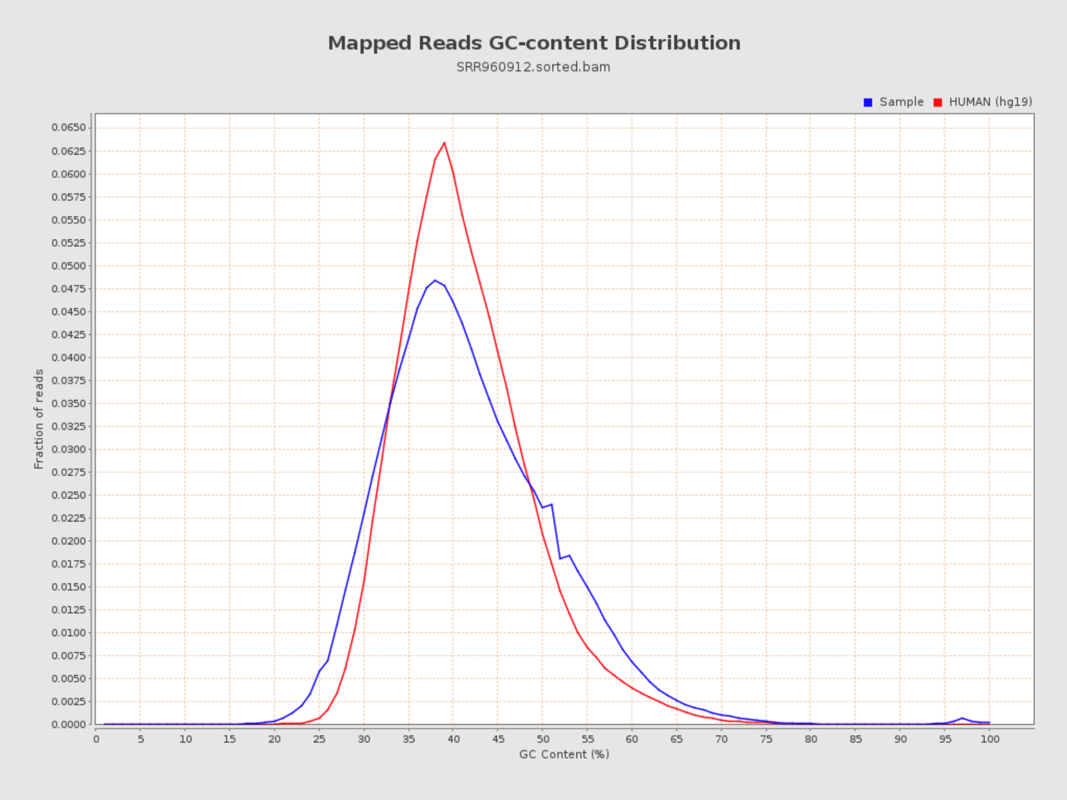
7. Results : Duplication Rate Histogram



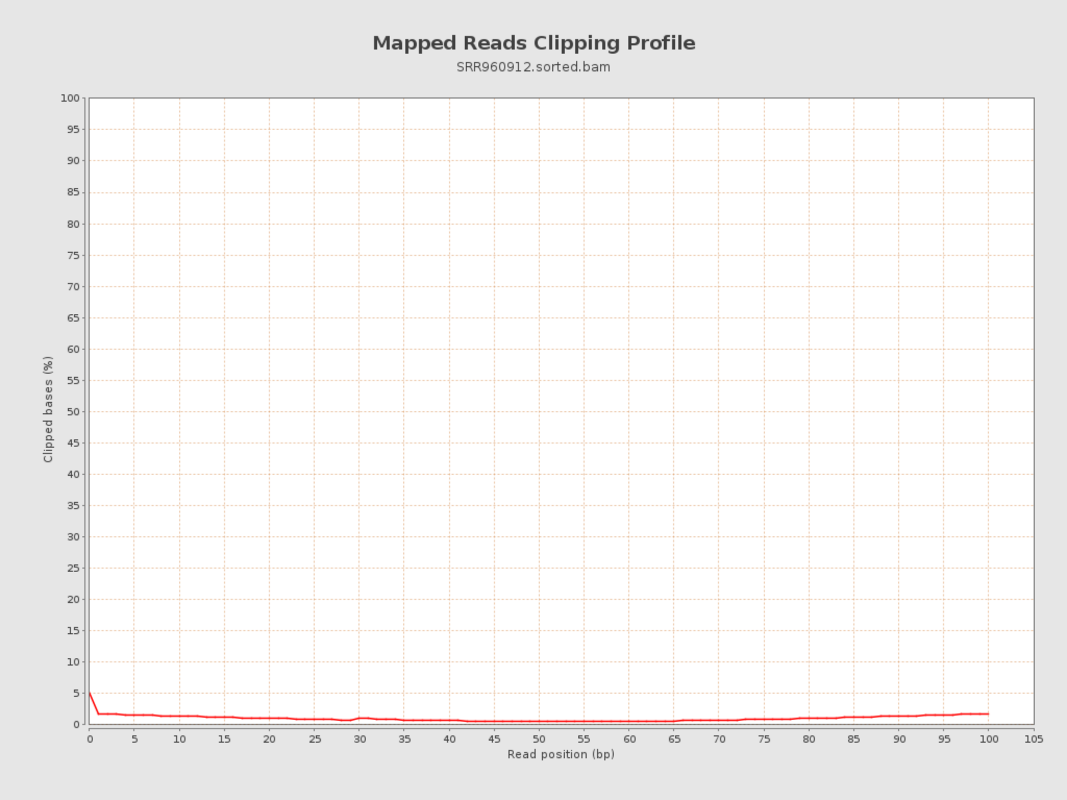
8. Results : Mapped Reads Nucleotide Content



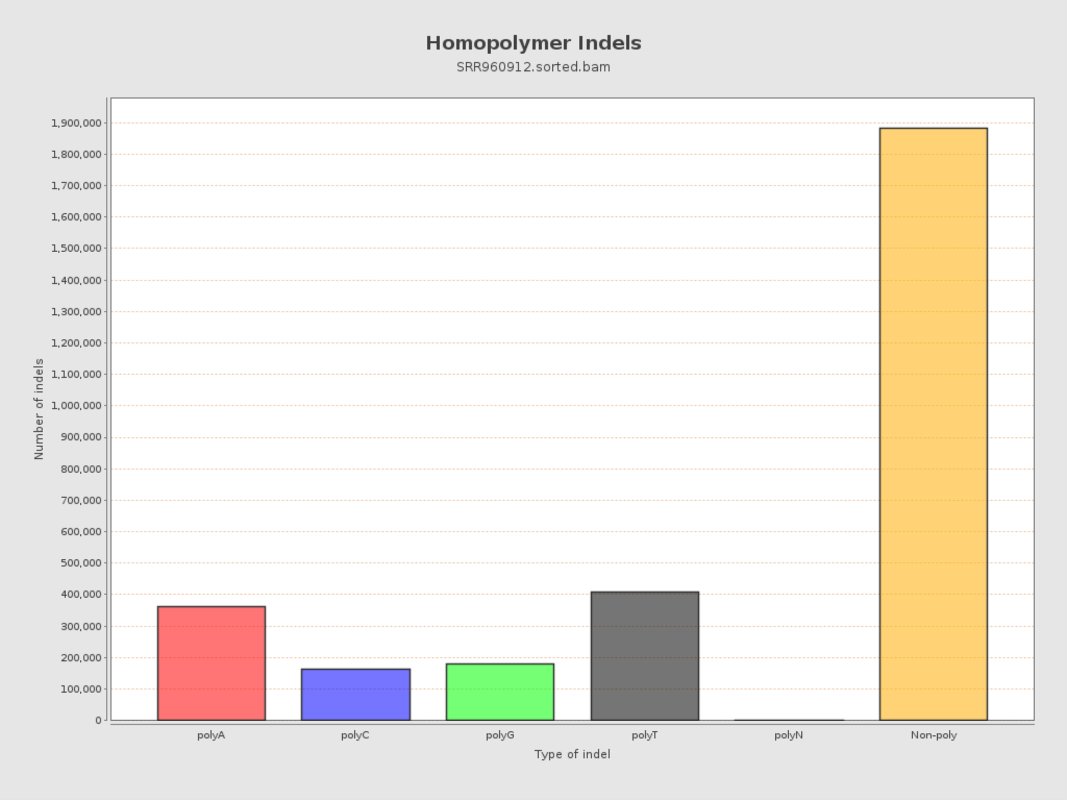
9. Results : Mapped Reads GC-content Distribution



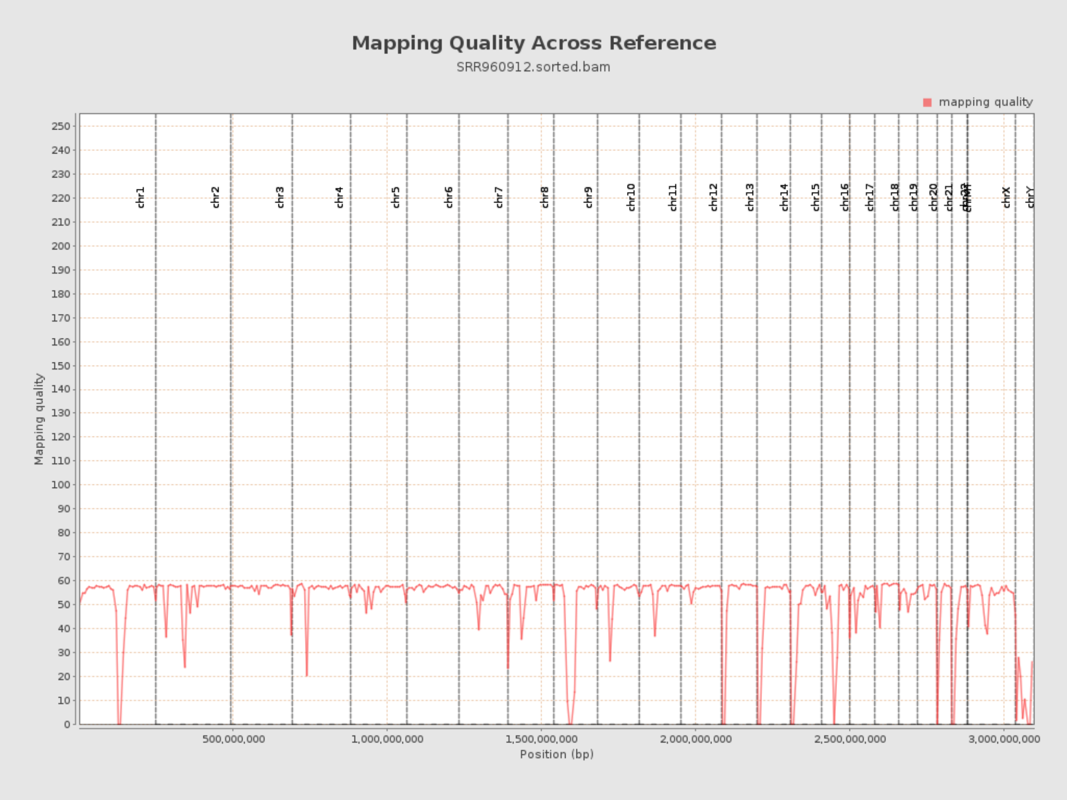
10. Results : Mapped Reads Clipping Profile



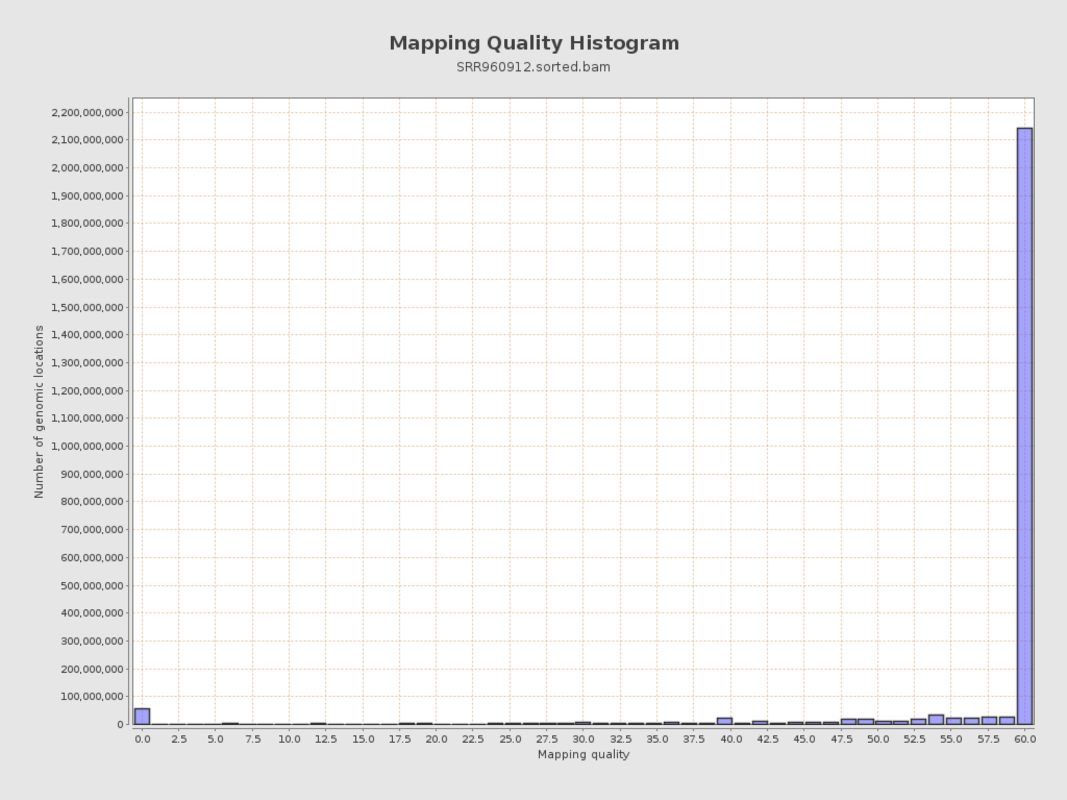
11. Results : Homopolymer Indels



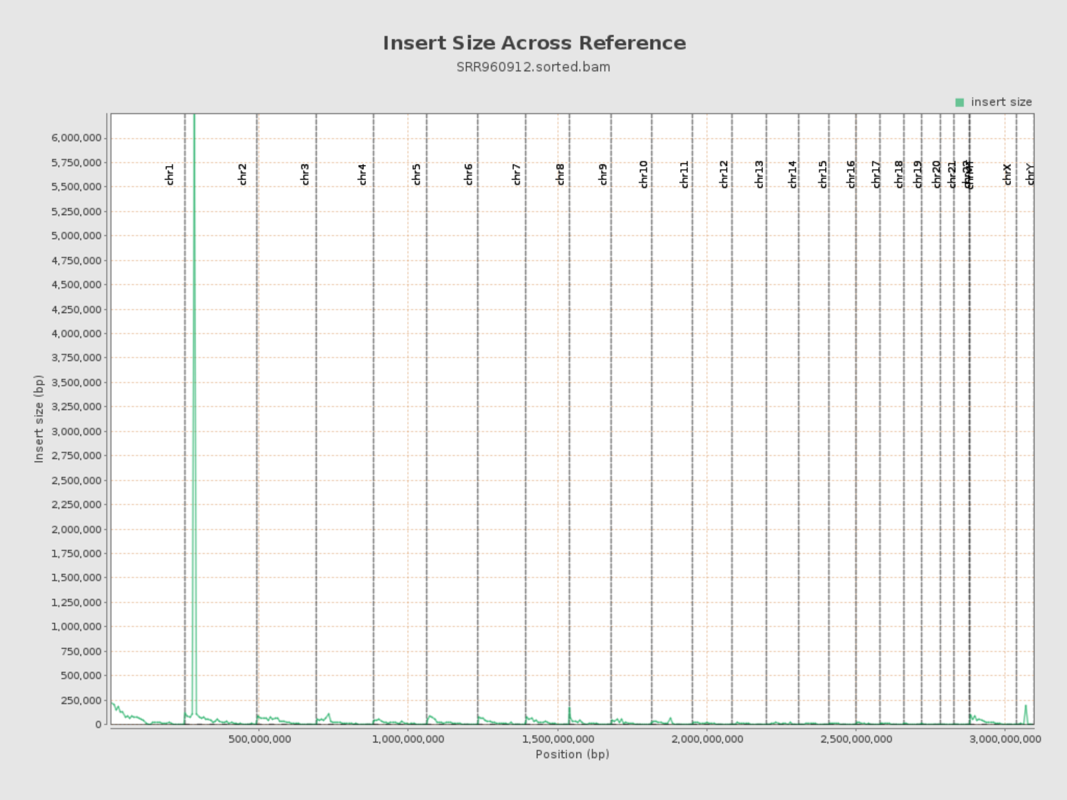
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram