Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/07 08:21:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR960919.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_SRR960919 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR960919_1.fastq.gz SRR960919_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Jan 07 08:21:05 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR960919.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	223,184,190
Mapped reads	218,576,341 / 97.94%
Unmapped reads	4,607,849 / 2.06%
Mapped paired reads	218,576,341 / 97.94%
Mapped reads, first in pair	109,835,602 / 49.21%
Mapped reads, second in pair	108,740,739 / 48.72%
Mapped reads, both in pair	216,553,236 / 97.03%
Mapped reads, singletons	2,023,105 / 0.91%
Secondary alignments	0
Supplementary alignments	455,388 / 0.2%
Read min/max/mean length	30 / 101 / 101.08
Duplicated reads (estimated)	36,843,842 / 16.51%
Duplication rate	12.03%
Clipped reads	37,336,850 / 16.73%

2.2. ACGT Content

Number/percentage of A's	6,517,533,322 / 30.52%
Number/percentage of C's	4,169,377,524 / 19.52%
Number/percentage of T's	6,515,570,481 / 30.51%
Number/percentage of G's	4,151,779,269 / 19.44%
Number/percentage of N's	3,199,660 / 0.01%

GC Percentage	38.96%

2.3. Coverage

Mean	6.9011
Standard Deviation	102.9845

2.4. Mapping Quality

Mean Mapping Quality	53.56

2.5. Insert size

Mean	18,566.99
Standard Deviation	1,260,347.17
P25/Median/P75	154 / 183 / 212

2.6. Mismatches and indels

General error rate	1.42%
Mismatches	298,202,303
Insertions	2,588,128
Mapped reads with at least one insertion	1.16%
Deletions	2,809,028
Mapped reads with at least one deletion	1.25%
Homopolymer indels	40.28%

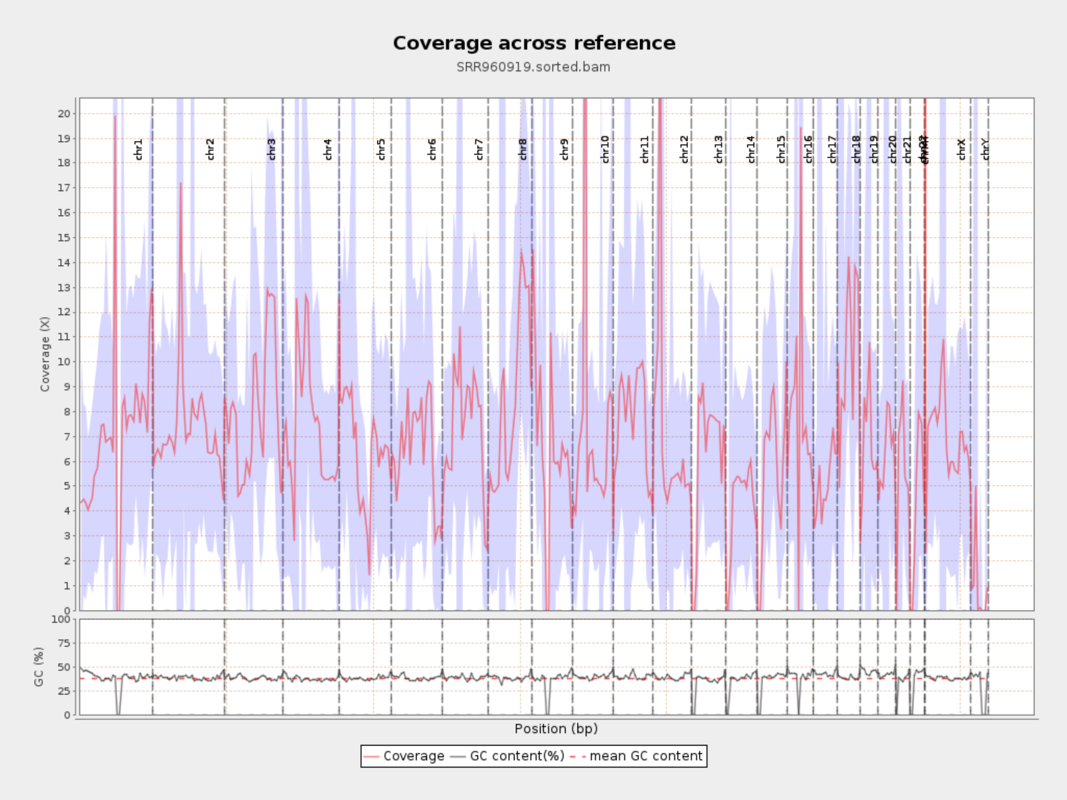
2.7. Chromosome stats

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

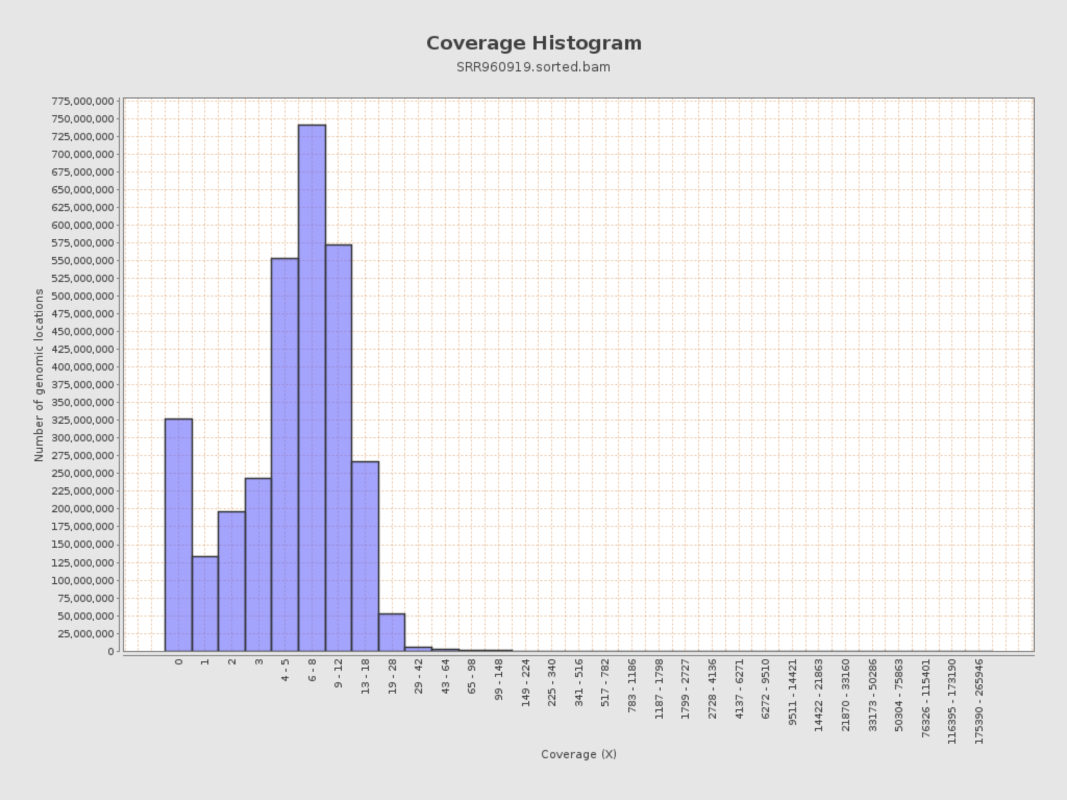
		bases	coverage	deviation
chr1	249250621	1777653197	7.132	274.2716
chr2	243199373	1798237823	7.3941	55.3777
chr3	198022430	1583527494	7.9967	9.5009
chr4	191154276	1404861190	7.3494	57.1031
chr5	180915260	1158801438	6.4052	9.2773
chr6	171115067	1120182619	6.5464	27.0134
chr7	159138663	1173916118	7.3767	68.28
chr8	146364022	1249245700	8.5352	120.9685
chr9	141213431	912093385	6.459	97.8709
chr10	135534747	1022036561	7.5408	199.3053
chr11	135006516	1042441554	7.7214	43.4312
chr12	133851895	965117677	7.2103	11.7082
chr13	115169878	732899726	6.3636	4.7803
chr14	107349540	454473859	4.2336	7.2522
chr15	102531392	575483023	5.6127	5.0603
chr16	90354753	707132620	7.8262	85.5095
chr17	81195210	410495900	5.0557	25.7224
chr18	78077248	820318611	10.5065	101.0191
chr19	59128983	399041722	6.7487	115.0858
chr20	63025520	403849263	6.4077	18.7657
chr21	48129895	283822131	5.897	22.6616
chr22	51304566	223102909	4.3486	5.6383
chrMT	16571	4890514	295.1249	59.2854
chrX	155270560	1080458195	6.9586	29.253

chrY	59373566	59503770	1.0022	53.1978

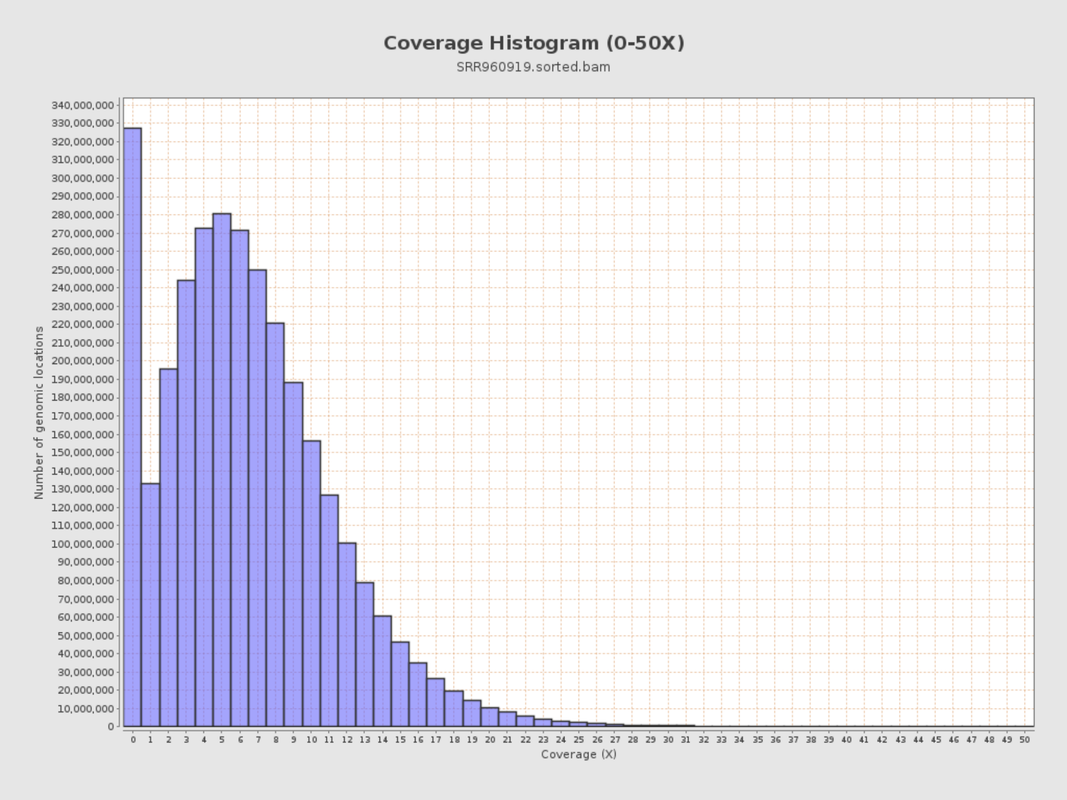
3. Results : Coverage across reference



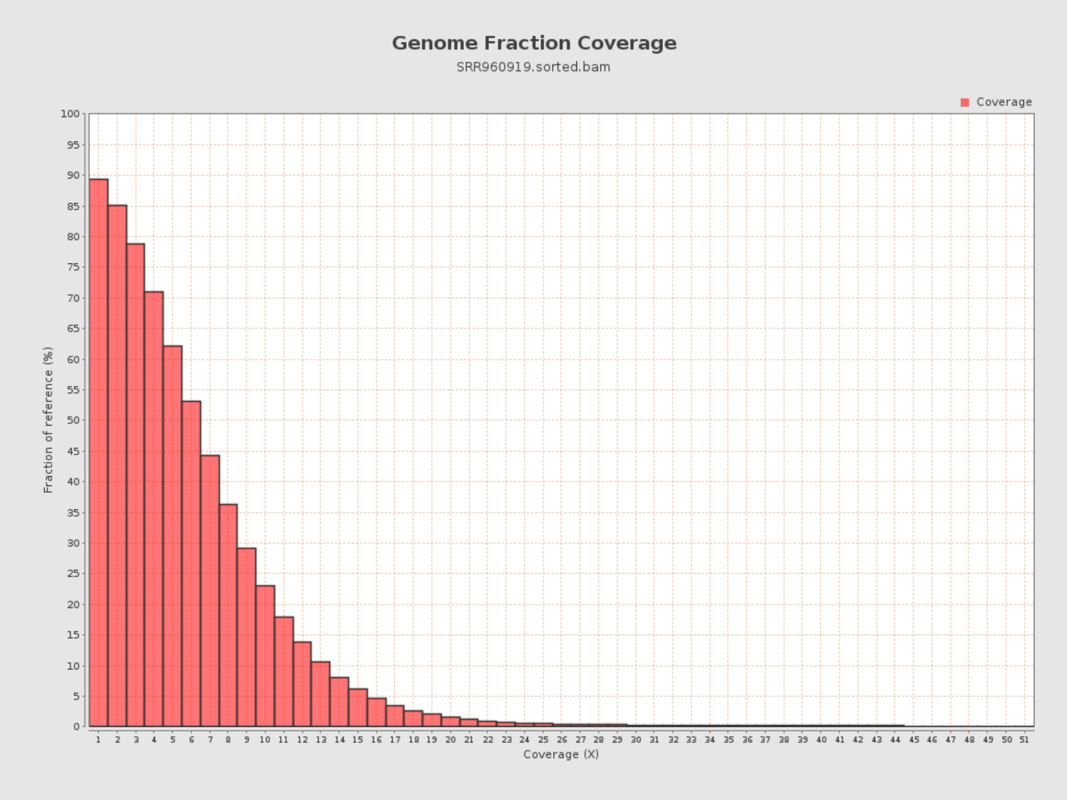
4. Results : Coverage Histogram



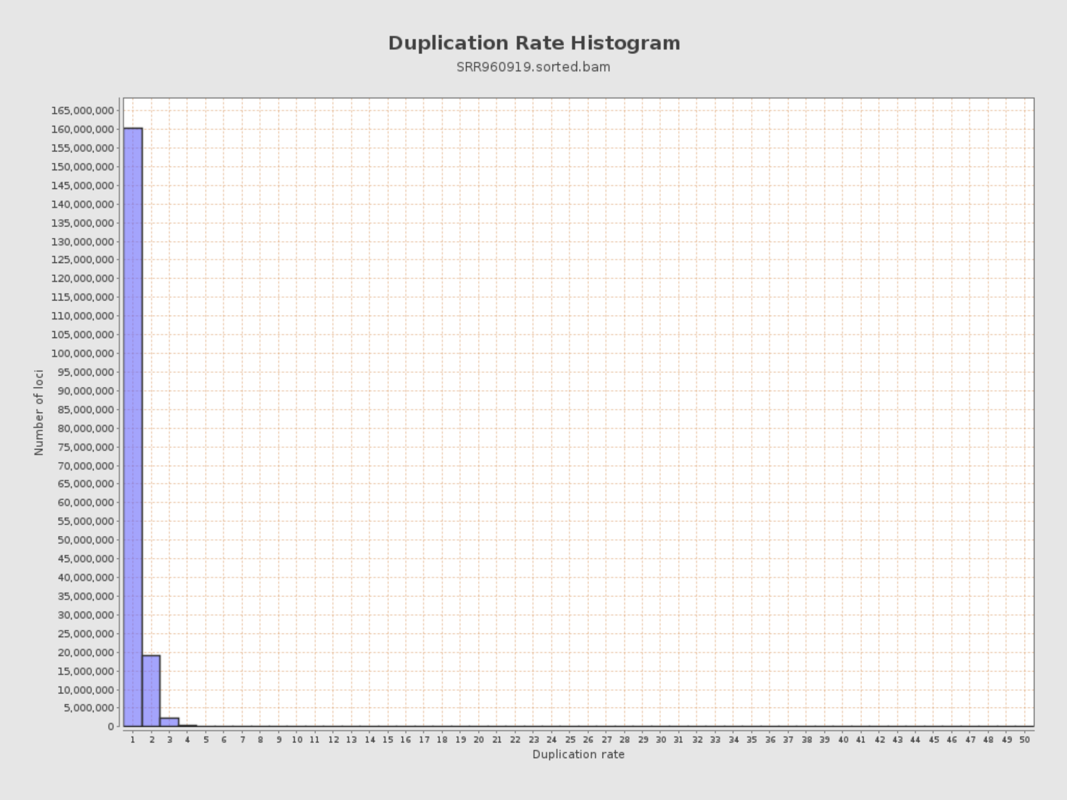
5. Results : Coverage Histogram (0-50X)



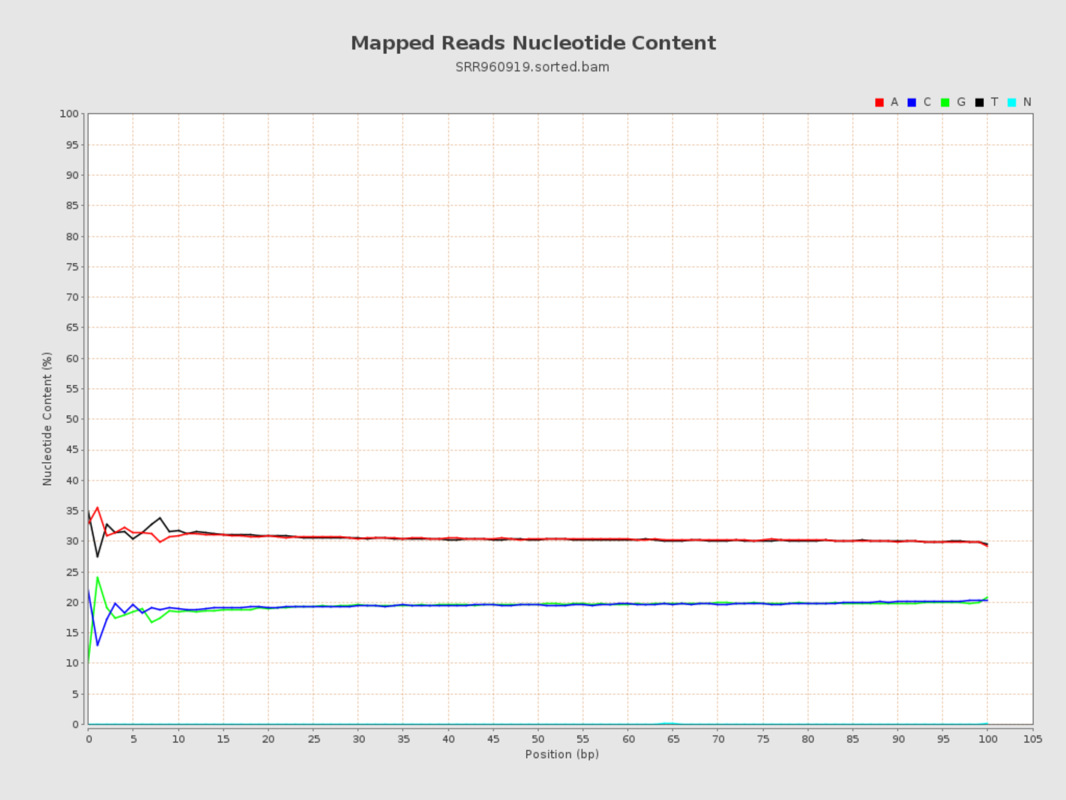
6. Results : Genome Fraction Coverage



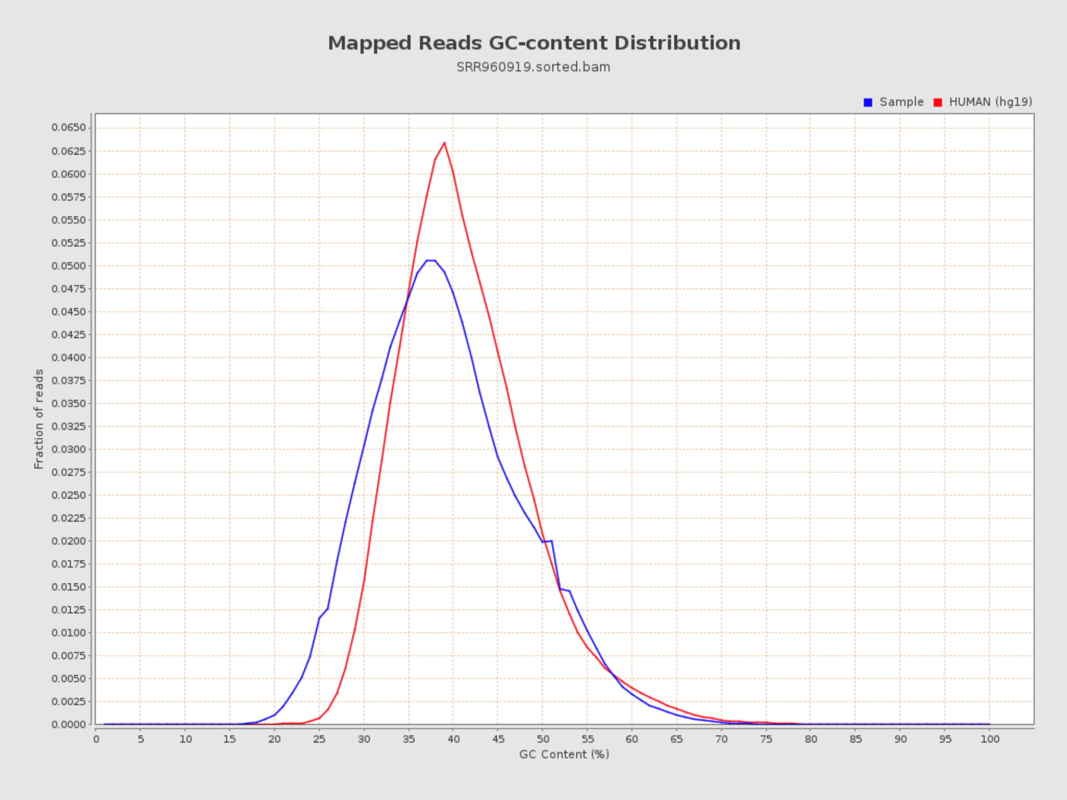
7. Results : Duplication Rate Histogram



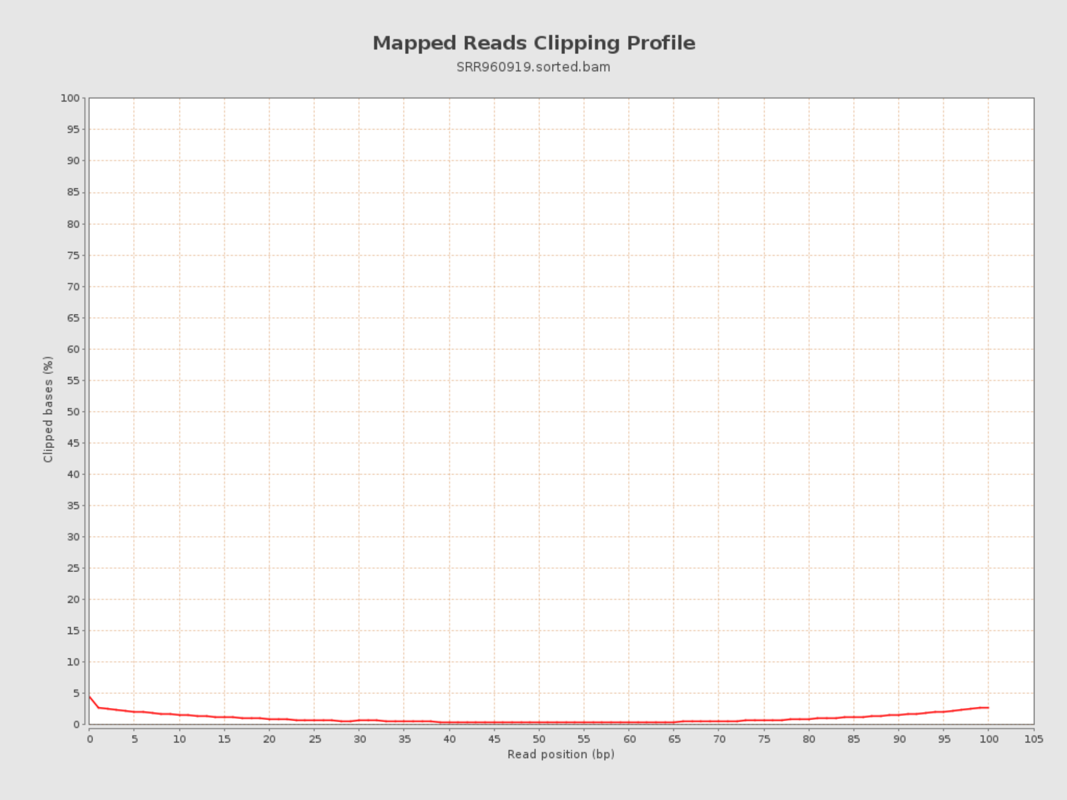
8. Results : Mapped Reads Nucleotide Content



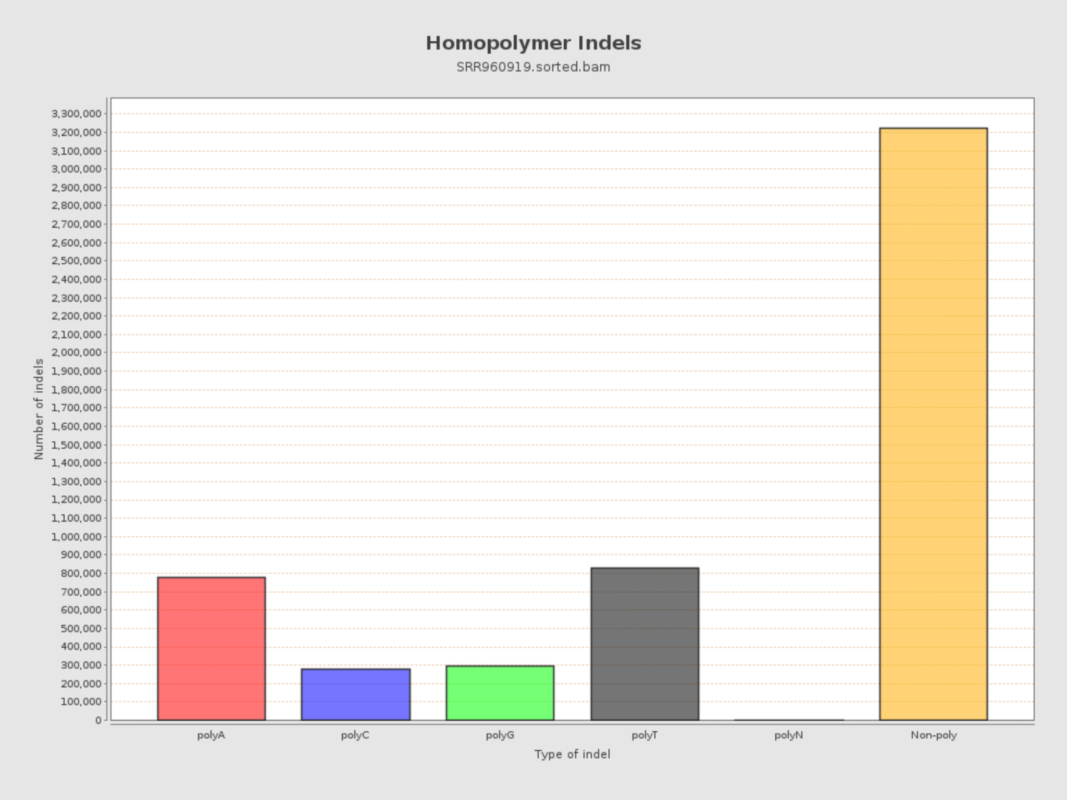
9. Results : Mapped Reads GC-content Distribution



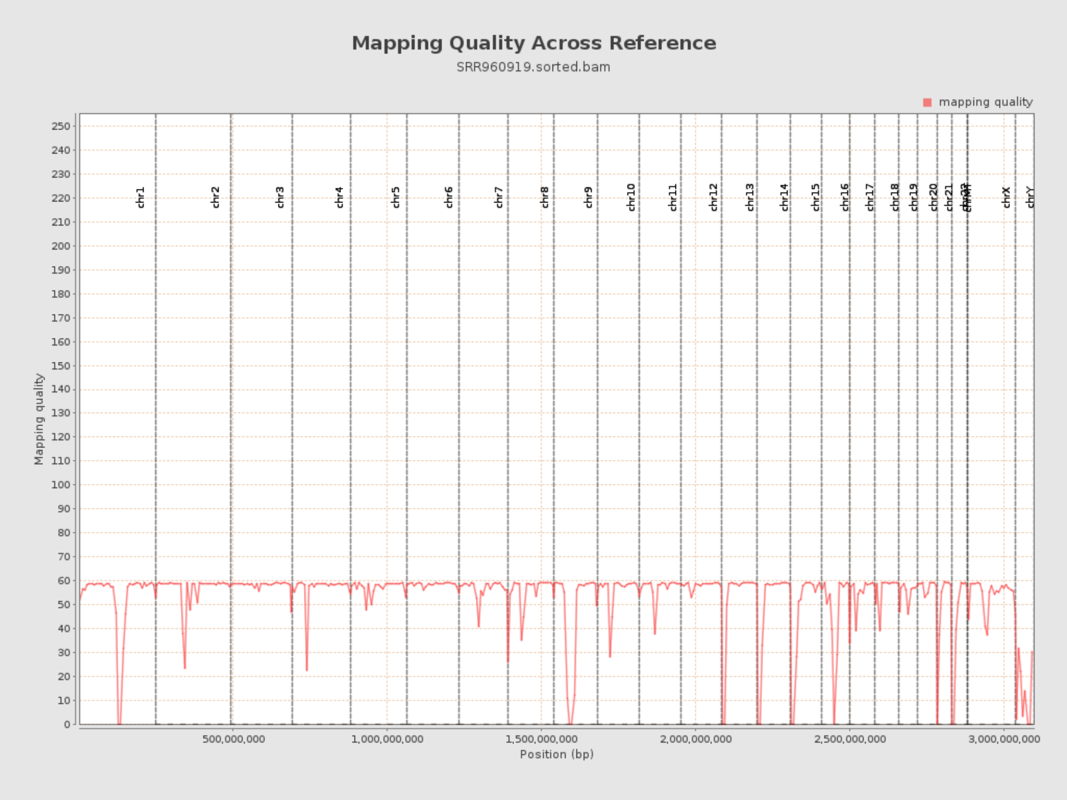
10. Results : Mapped Reads Clipping Profile



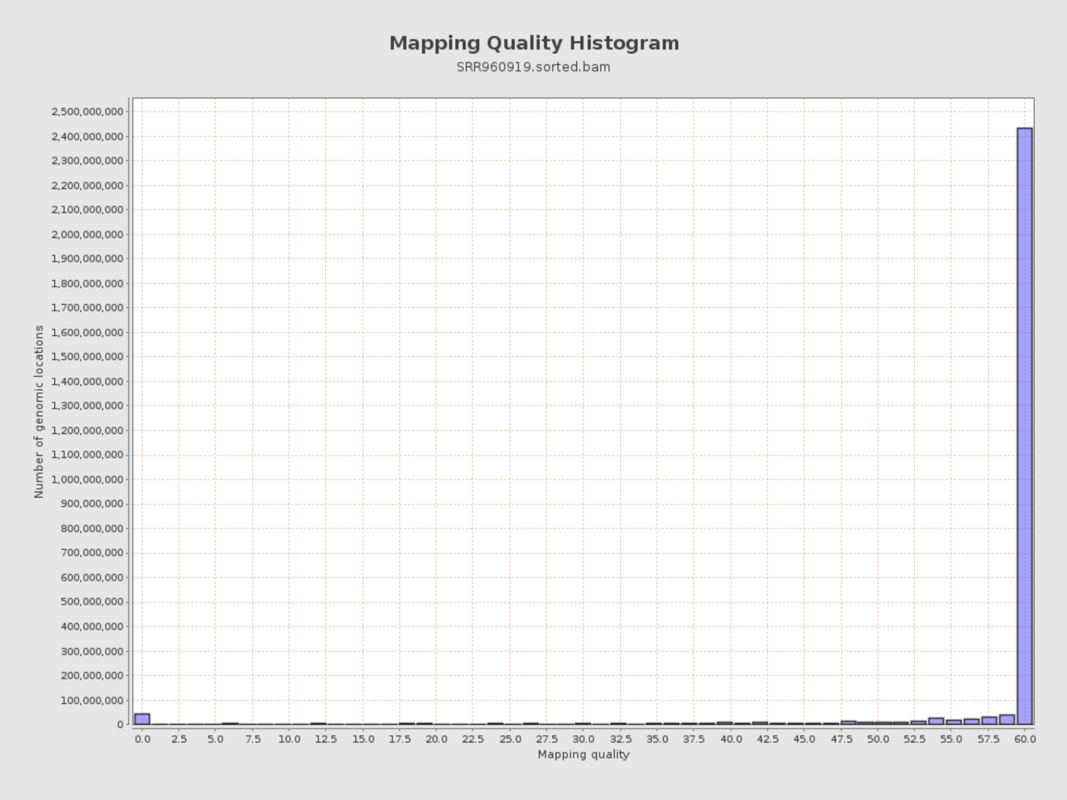
11. Results : Homopolymer Indels



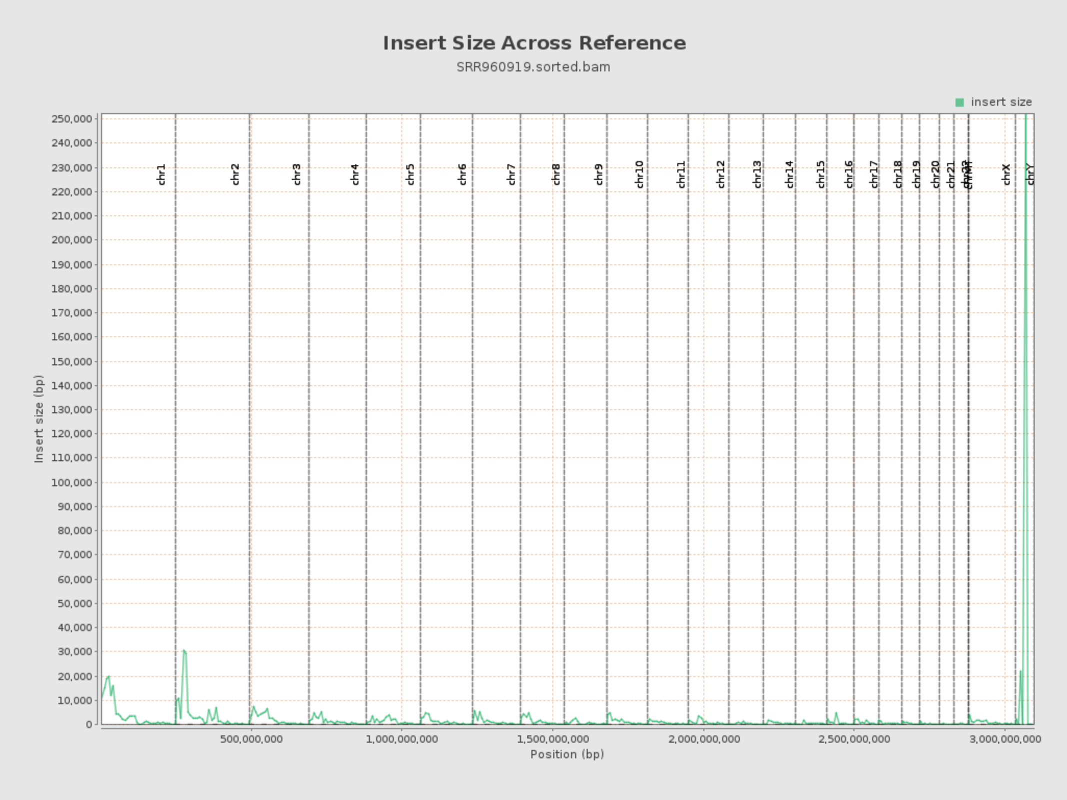
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram