Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/05 22:10:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR960904.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_SRR960904 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR960904_1.fastq.gz SRR960904_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 05 22:10:59 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR960904.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	153,141,410
Mapped reads	149,965,619 / 97.93%
Unmapped reads	3,175,791 / 2.07%
Mapped paired reads	149,965,619 / 97.93%
Mapped reads, first in pair	75,217,867 / 49.12%
Mapped reads, second in pair	74,747,752 / 48.81%
Mapped reads, both in pair	148,948,574 / 97.26%
Mapped reads, singletons	1,017,045 / 0.66%
Secondary alignments	0
Supplementary alignments	310,521 / 0.2%
Read min/max/mean length	30 / 101 / 101.08
Duplicated reads (estimated)	13,246,490 / 8.65%
Duplication rate	4.83%
Clipped reads	18,323,453 / 11.97%

2.2. ACGT Content

Number/percentage of A's	4,367,837,746 / 29.58%
Number/percentage of C's	3,006,076,281 / 20.36%
Number/percentage of T's	4,359,229,885 / 29.52%
Number/percentage of G's	3,028,169,116 / 20.51%
Number/percentage of N's	5,865,439 / 0.04%

GC Percentage	40.86%

2.3. Coverage

Mean	4.7716
Standard Deviation	50.4522

2.4. Mapping Quality

Mean Mapping Quality	53.64

2.5. Insert size

Mean	20,485.8
Standard Deviation	1,350,393.28
P25/Median/P75	139 / 150 / 160

2.6. Mismatches and indels

General error rate	0.99%
Mismatches	142,586,399
Insertions	1,649,224
Mapped reads with at least one insertion	1.07%
Deletions	1,803,683
Mapped reads with at least one deletion	1.16%
Homopolymer indels	40.92%

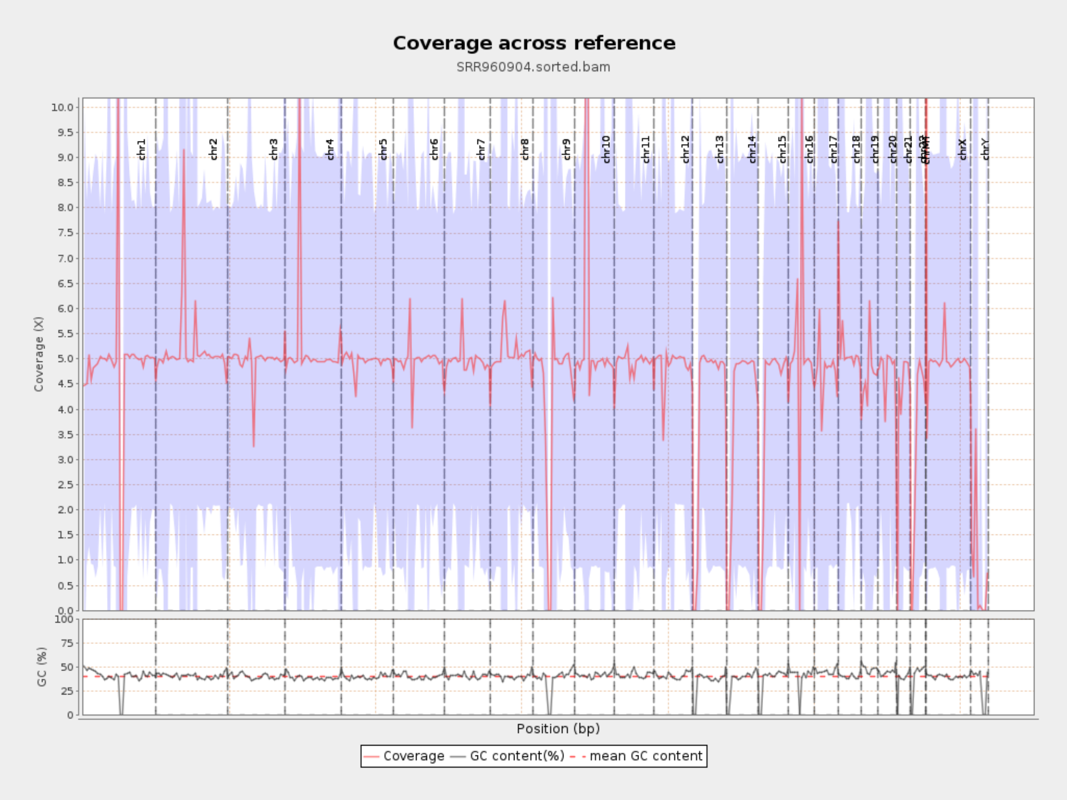
2.7. Chromosome stats

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

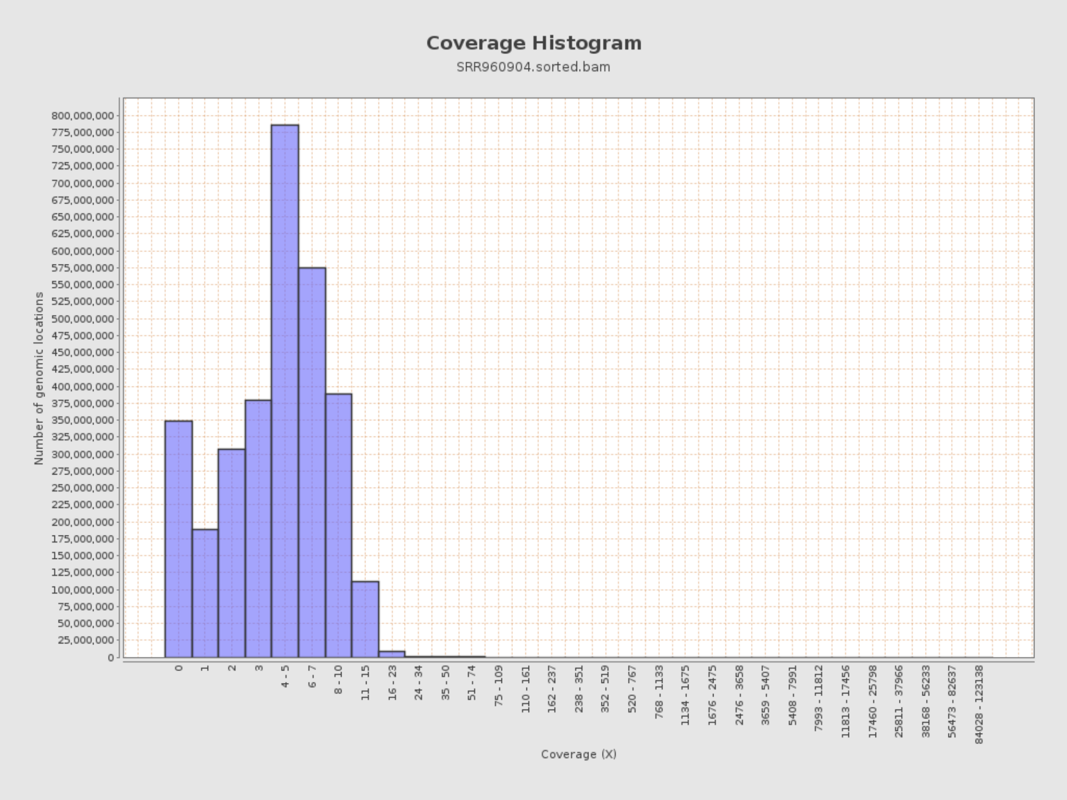
		bases	**coverage**	**deviation**
chr1	249250621	1202490003	4.8244	125.356
chr2	243199373	1269334280	5.2193	32.2955
chr3	198022430	981671154	4.9574	8.7624
chr4	191154276	998026704	5.2211	39.5025
chr5	180915260	894076728	4.942	5.2566
chr6	171115067	851324955	4.9752	15.4572
chr7	159138663	791212678	4.9718	32.2961
chr8	146364022	748278748	5.1125	56.6482
chr9	141213431	616399459	4.365	45.0967
chr10	135534747	757772559	5.591	105.8462
chr11	135006516	665907773	4.9324	20.7472
chr12	133851895	653065133	4.879	4.7418
chr13	115169878	473641081	4.1125	3.3716
chr14	107349540	436030148	4.0618	4.911
chr15	102531392	408370530	3.9829	3.438
chr16	90354753	457463119	5.063	42.708
chr17	81195210	388289024	4.7822	19.4062
chr18	78077248	405478377	5.1933	54.1212
chr19	59128983	278815886	4.7154	61.159
chr20	63025520	300969753	4.7754	15.7234
chr21	48129895	202097886	4.199	20.8019
chr22	51304566	167962283	3.2738	4.2156
chrMT	16571	11403088	688.1352	100.7286
chrX	155270560	765030418	4.9271	16.1076

chrY	59373566	46410265	0.7817	43.089

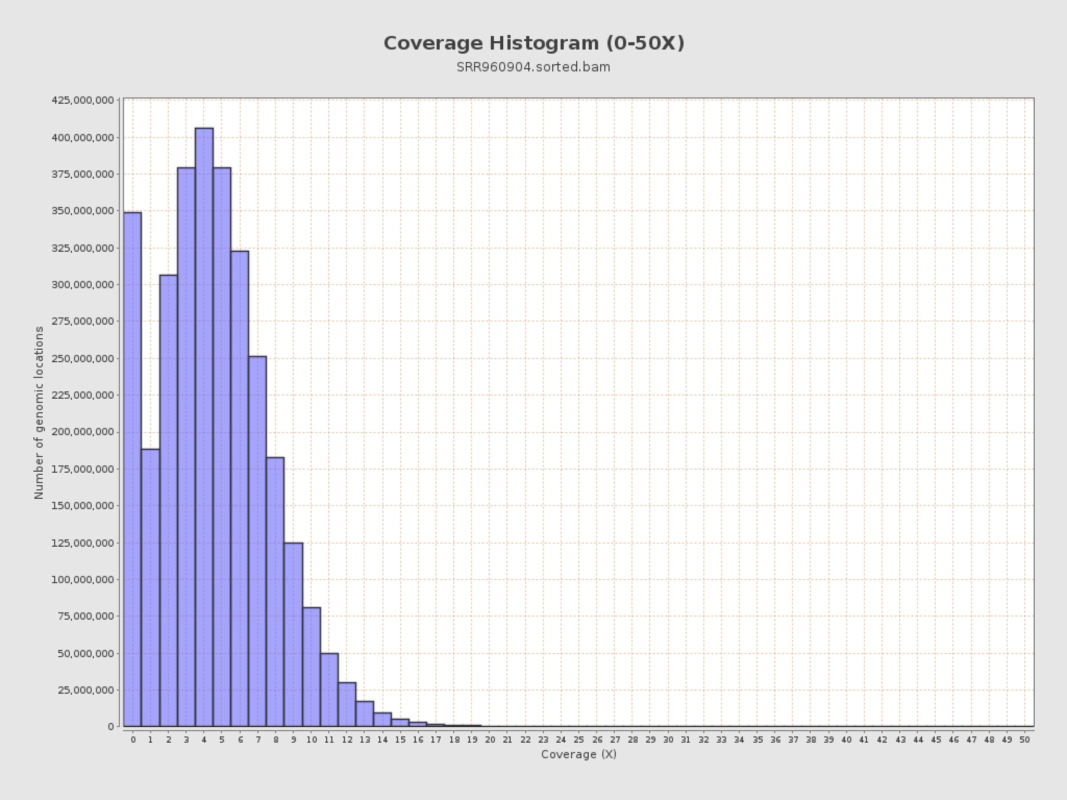
3. Results : Coverage across reference



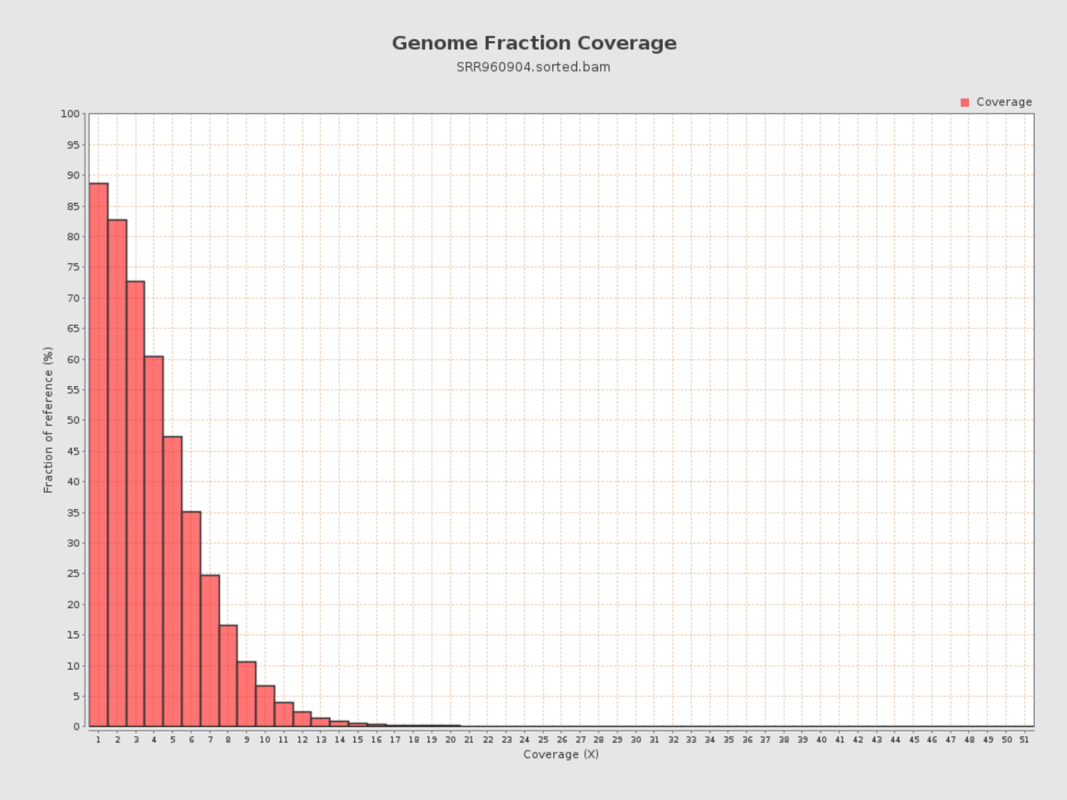
4. Results : Coverage Histogram



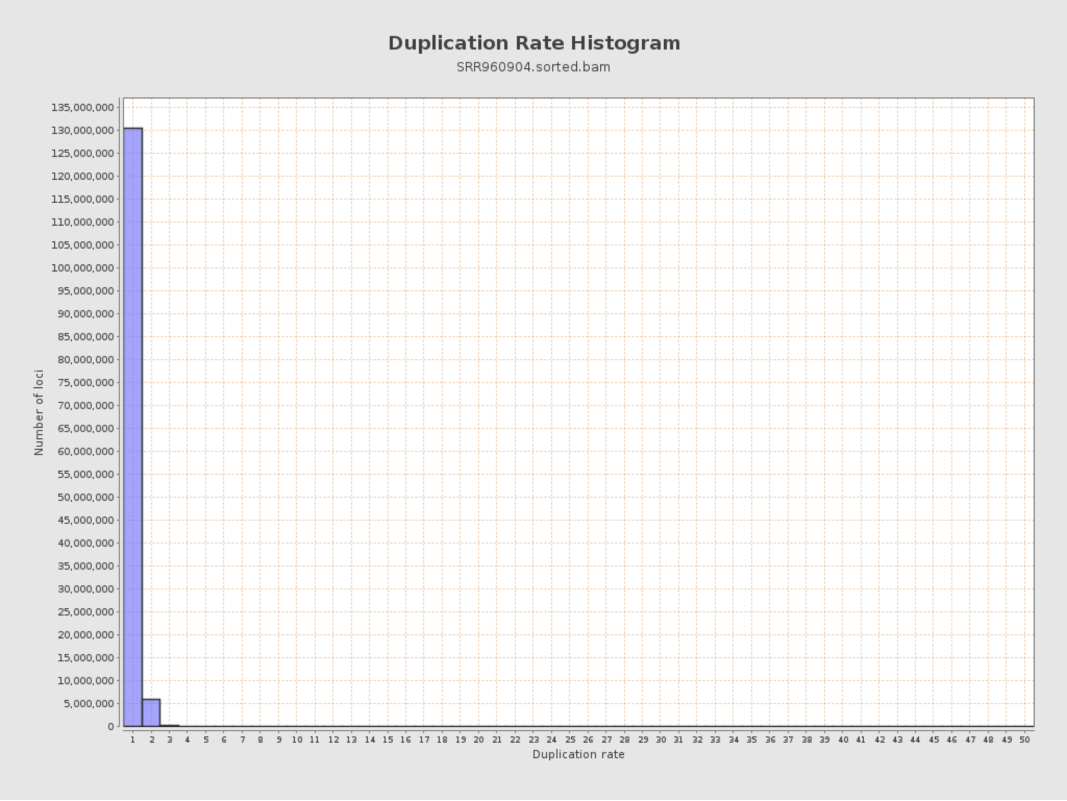
5. Results : Coverage Histogram (0-50X)



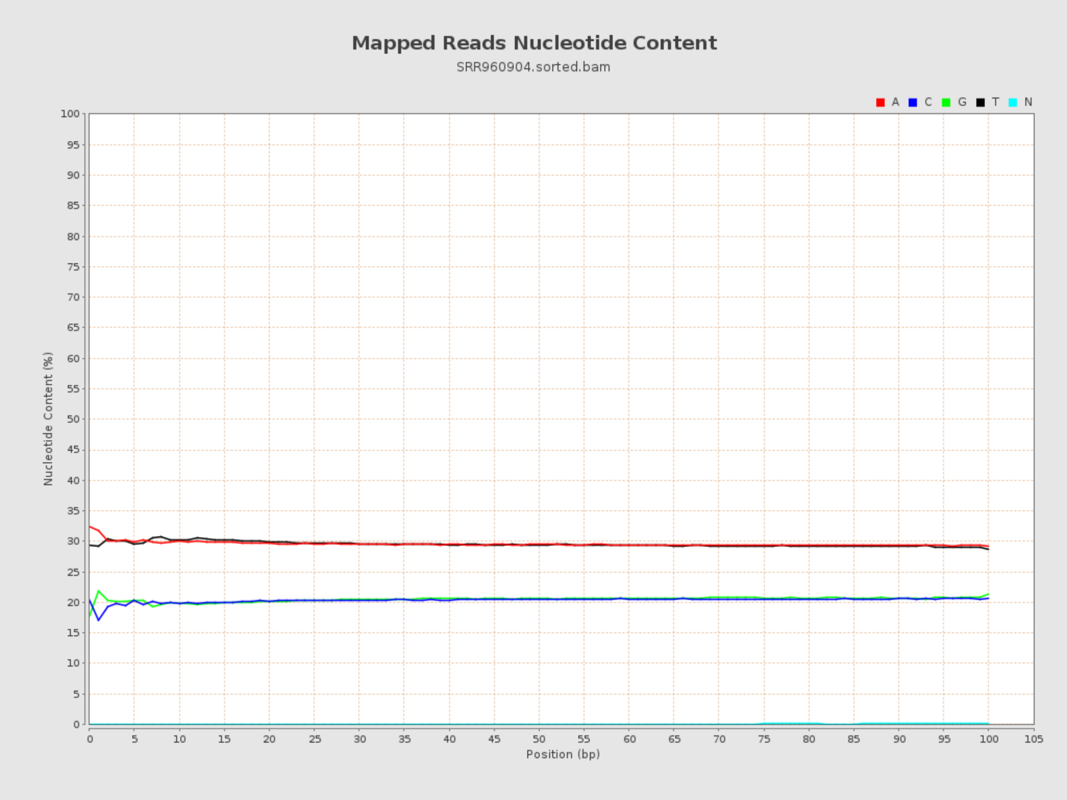
6. Results : Genome Fraction Coverage



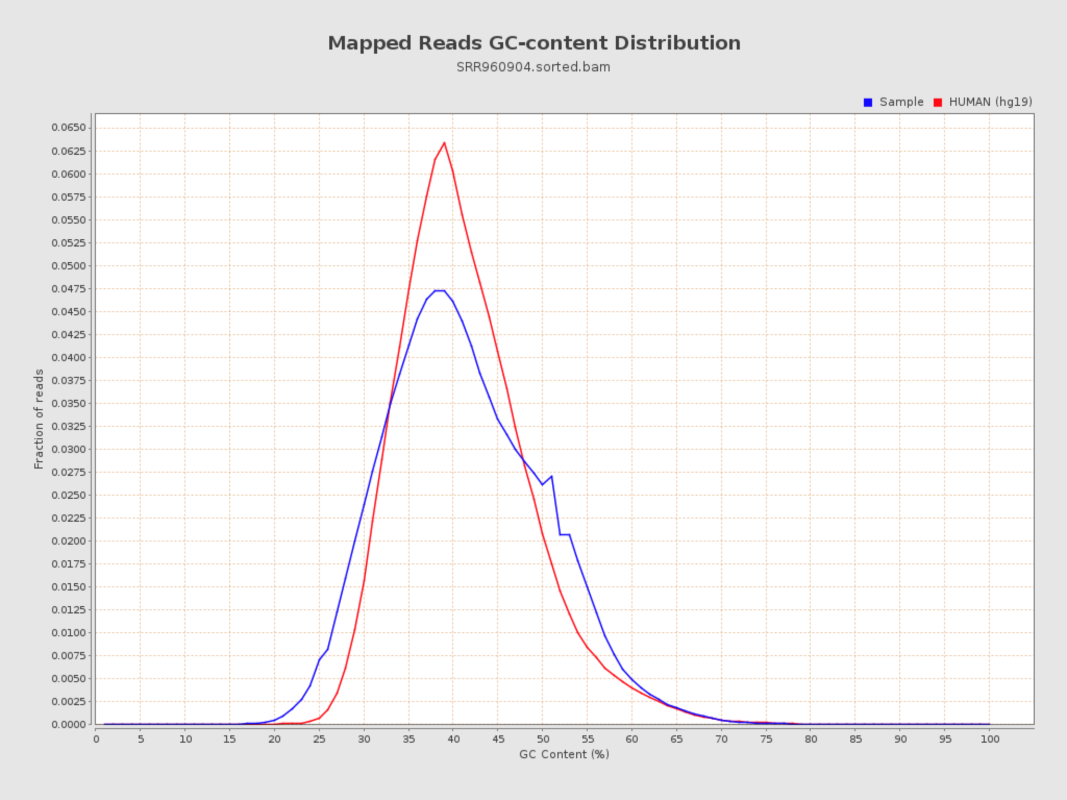
7. Results : Duplication Rate Histogram



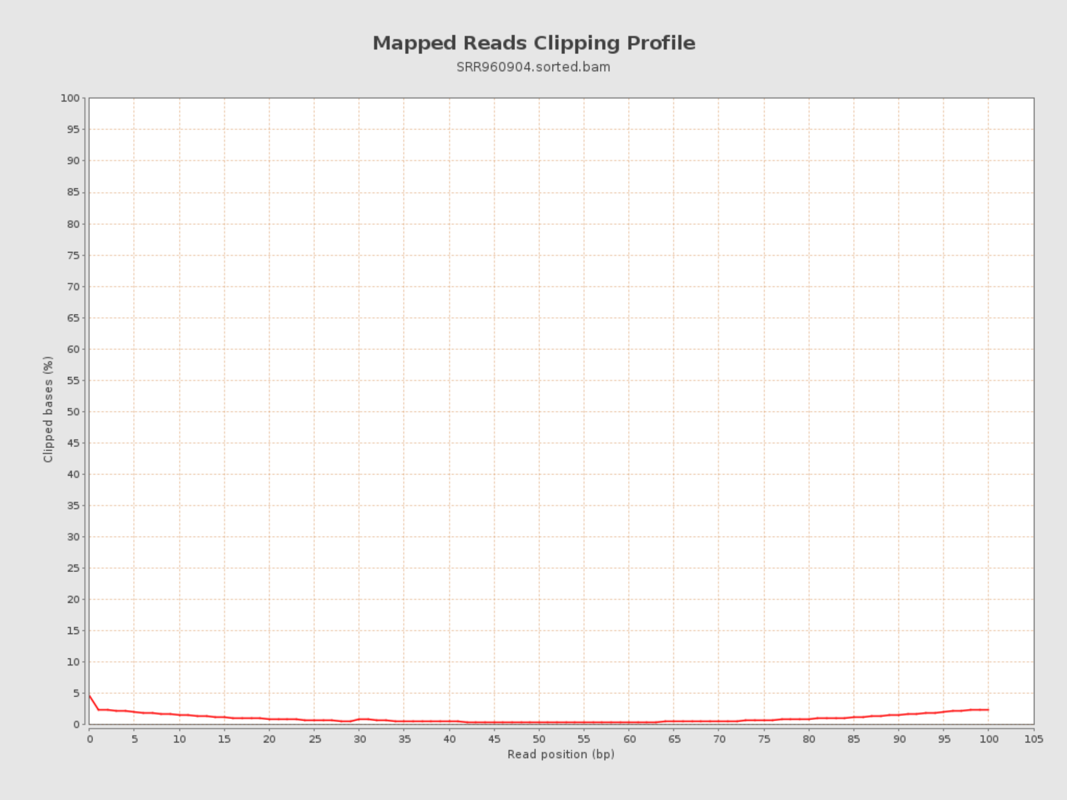
8. Results : Mapped Reads Nucleotide Content



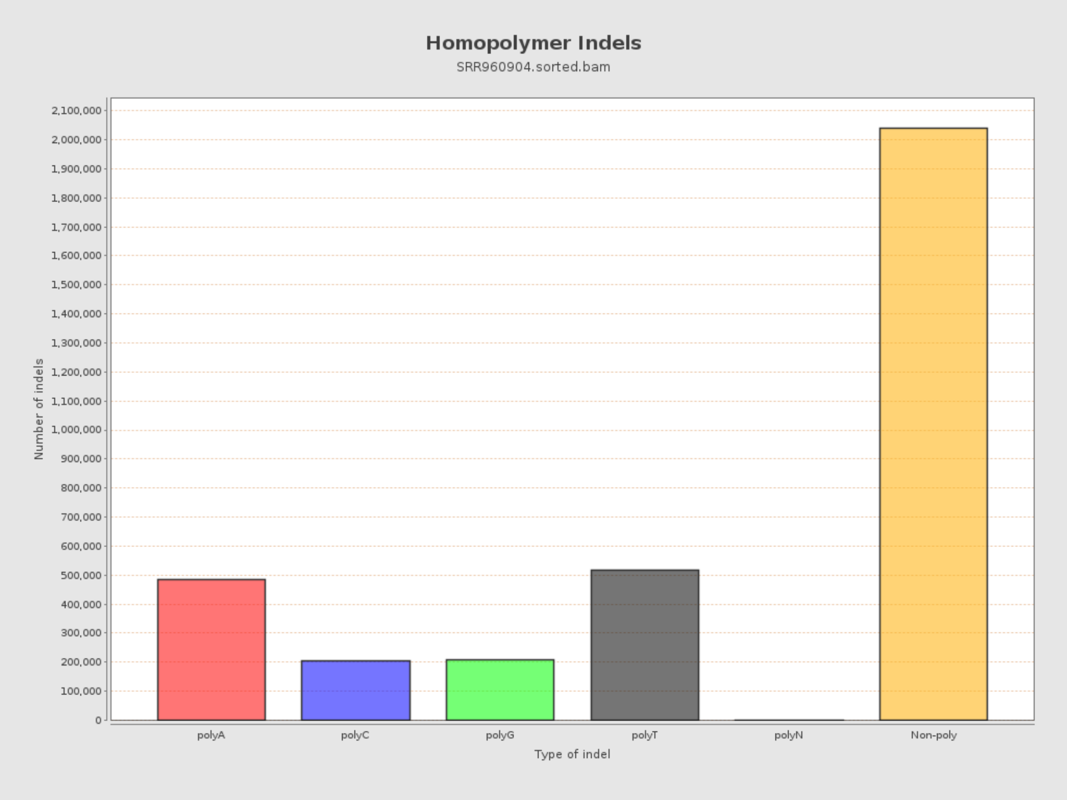
9. Results : Mapped Reads GC-content Distribution



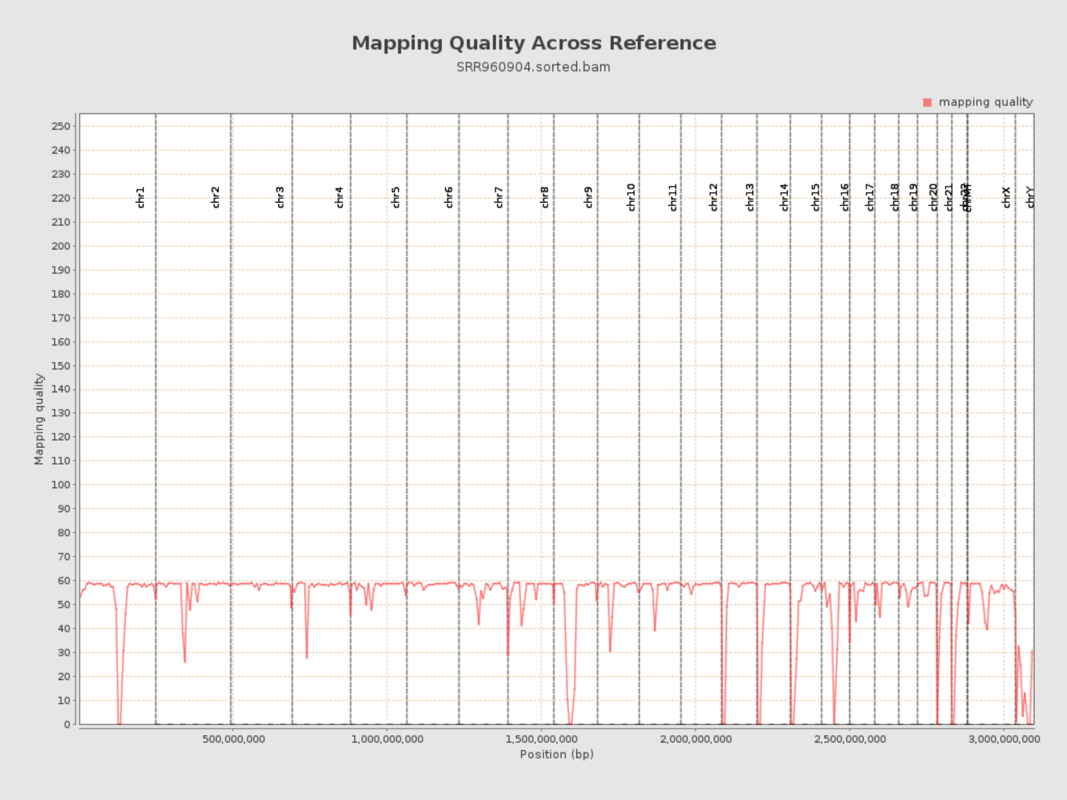
10. Results : Mapped Reads Clipping Profile



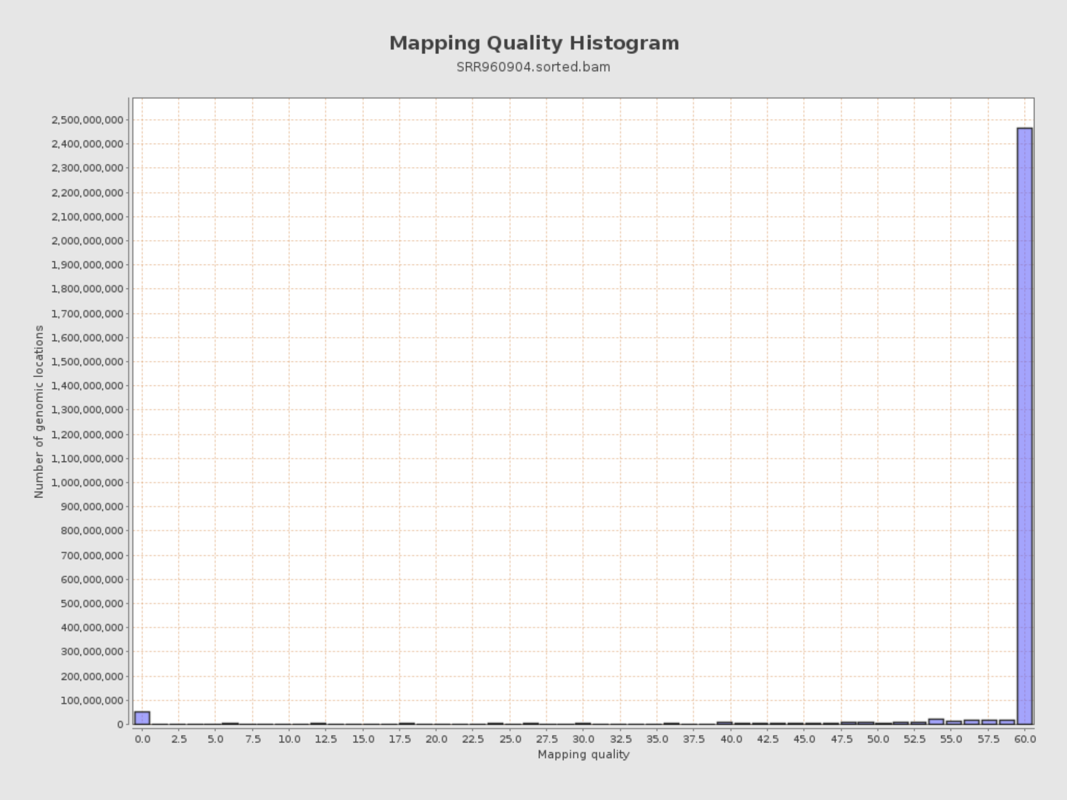
11. Results : Homopolymer Indels



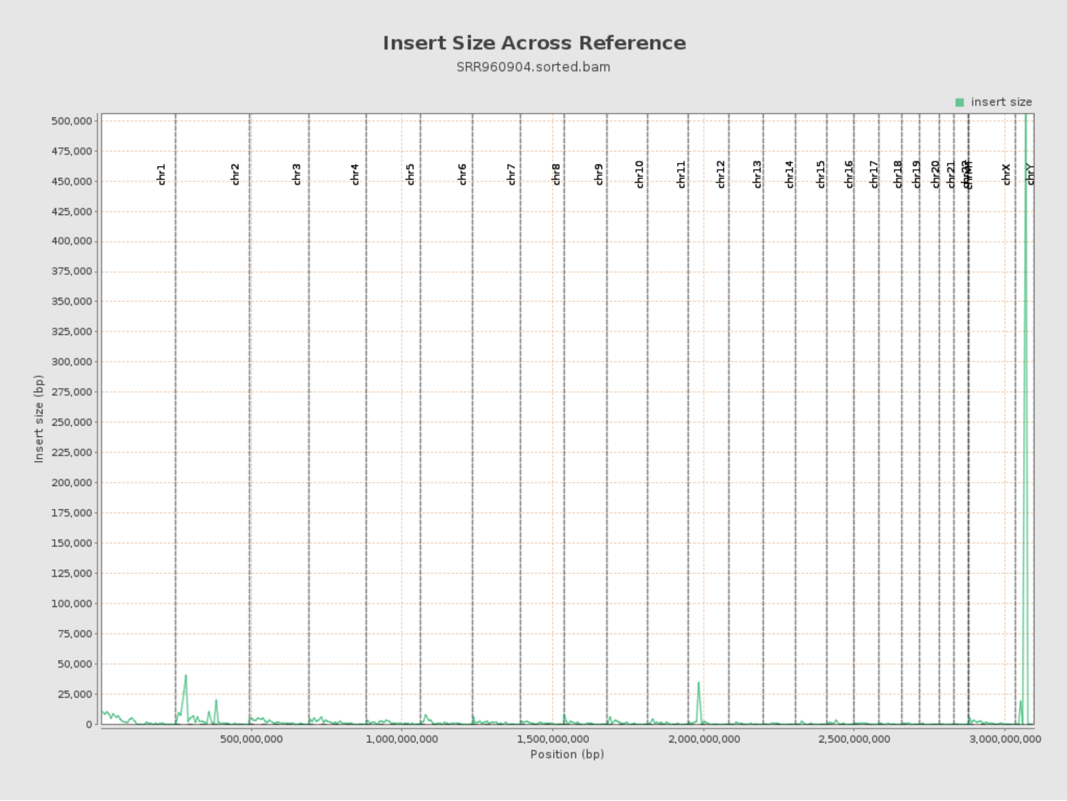
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram