Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/07 12:02:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR960920.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_SRR960920 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR960920_1.fastq.gz SRR960920_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Jan 07 12:02:50 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR960920.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	228,325,396
Mapped reads	223,580,206 / 97.92%
Unmapped reads	4,745,190 / 2.08%
Mapped paired reads	223,580,206 / 97.92%
Mapped reads, first in pair	112,279,767 / 49.18%
Mapped reads, second in pair	111,300,439 / 48.75%
Mapped reads, both in pair	221,628,616 / 97.07%
Mapped reads, singletons	1,951,590 / 0.85%
Secondary alignments	0
Supplementary alignments	461,959 / 0.2%
Read min/max/mean length	30 / 101 / 101.08
Duplicated reads (estimated)	38,010,459 / 16.65%
Duplication rate	12.21%
Clipped reads	39,710,749 / 17.39%

2.2. ACGT Content

Number/percentage of A's	6,677,597,126 / 30.59%
Number/percentage of C's	4,246,010,635 / 19.45%
Number/percentage of T's	6,675,955,771 / 30.59%
Number/percentage of G's	4,224,377,924 / 19.35%
Number/percentage of N's	2,047,003 / 0.01%

GC Percentage	38.81%

2.3. Coverage

Mean	7.0525
Standard Deviation	104.5375

2.4. Mapping Quality

Mean Mapping Quality	53.57

2.5. Insert size

Mean	19,048.84
Standard Deviation	1,285,248.86
P25/Median/P75	155 / 183 / 213

2.6. Mismatches and indels

General error rate	1.45%
Mismatches	310,606,644
Insertions	2,644,558
Mapped reads with at least one insertion	1.15%
Deletions	2,904,422
Mapped reads with at least one deletion	1.26%
Homopolymer indels	40.22%

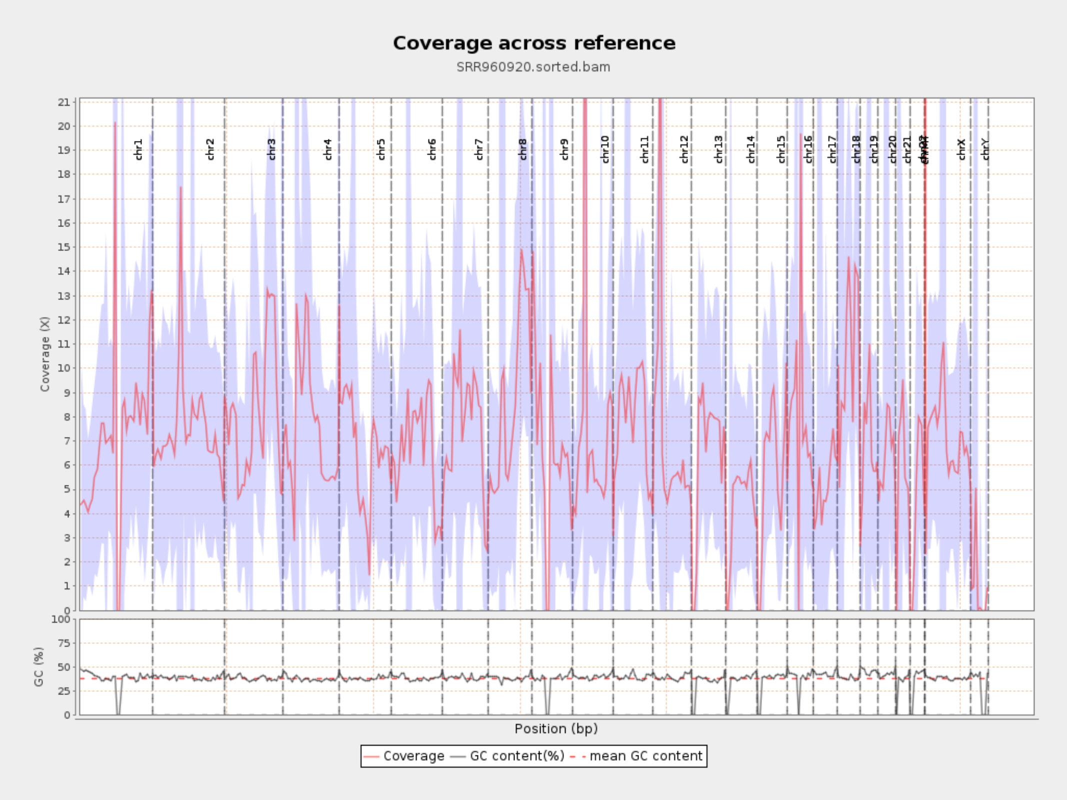
2.7. Chromosome stats

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

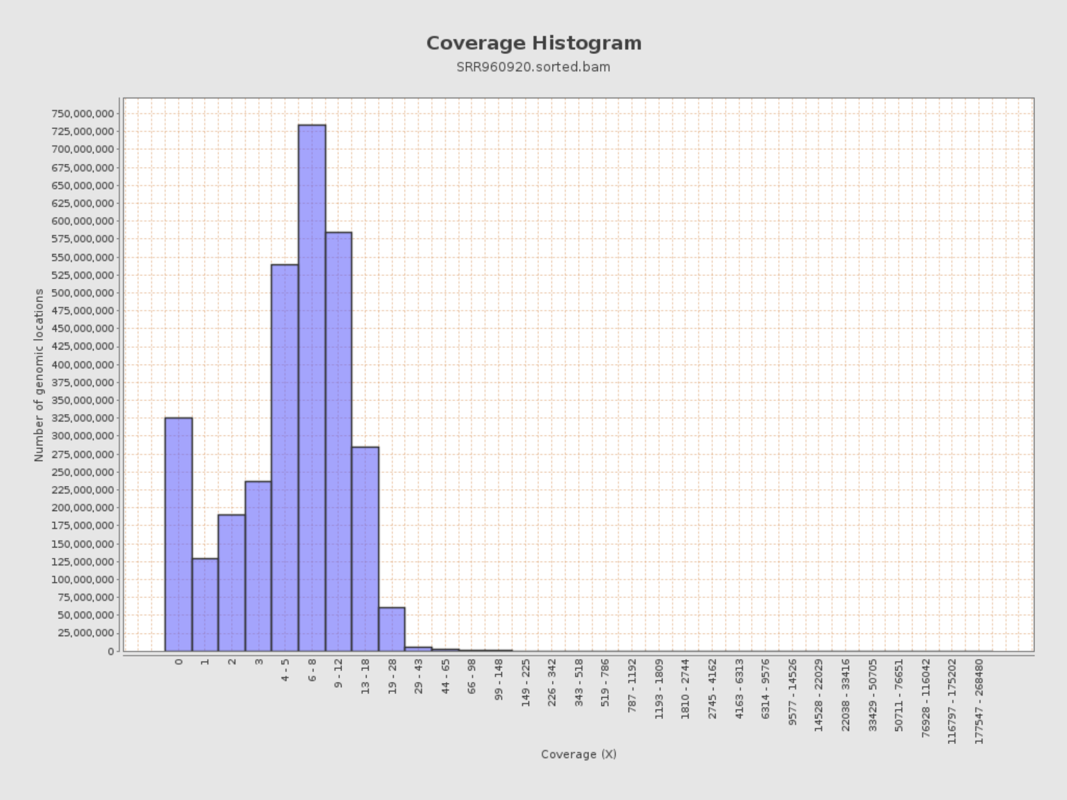
		bases	coverage	deviation
chr1	249250621	1814681409	7.2805	276.9851
chr2	243199373	1838493551	7.5596	56.1001
chr3	198022430	1622368987	8.1929	9.7204
chr4	191154276	1440981088	7.5383	57.0623
chr5	180915260	1186091877	6.5561	9.482
chr6	171115067	1147192448	6.7042	27.5016
chr7	159138663	1201576369	7.5505	68.8255
chr8	146364022	1279765246	8.7437	131.5242
chr9	141213431	931818918	6.5987	99.1836
chr10	135534747	1041614101	7.6852	201.0317
chr11	135006516	1064801479	7.887	43.9937
chr12	133851895	986463680	7.3698	11.7226
chr13	115169878	753256337	6.5404	4.8821
chr14	107349540	464570861	4.3276	7.4061
chr15	102531392	586811508	5.7232	5.1722
chr16	90354753	716908101	7.9344	86.321
chr17	81195210	416286903	5.127	26.4534
chr18	78077248	838556347	10.7401	102.2549
chr19	59128983	403213045	6.8192	116.5962
chr20	63025520	410553210	6.5141	18.8927
chr21	48129895	291261878	6.0516	23.018
chr22	51304566	224891137	4.3835	5.6517
chrMT	16571	4968570	299.8353	59.7549
chrX	155270560	1104981653	7.1165	29.5628

chrY	59373566	60160880	1.0133	53.2592

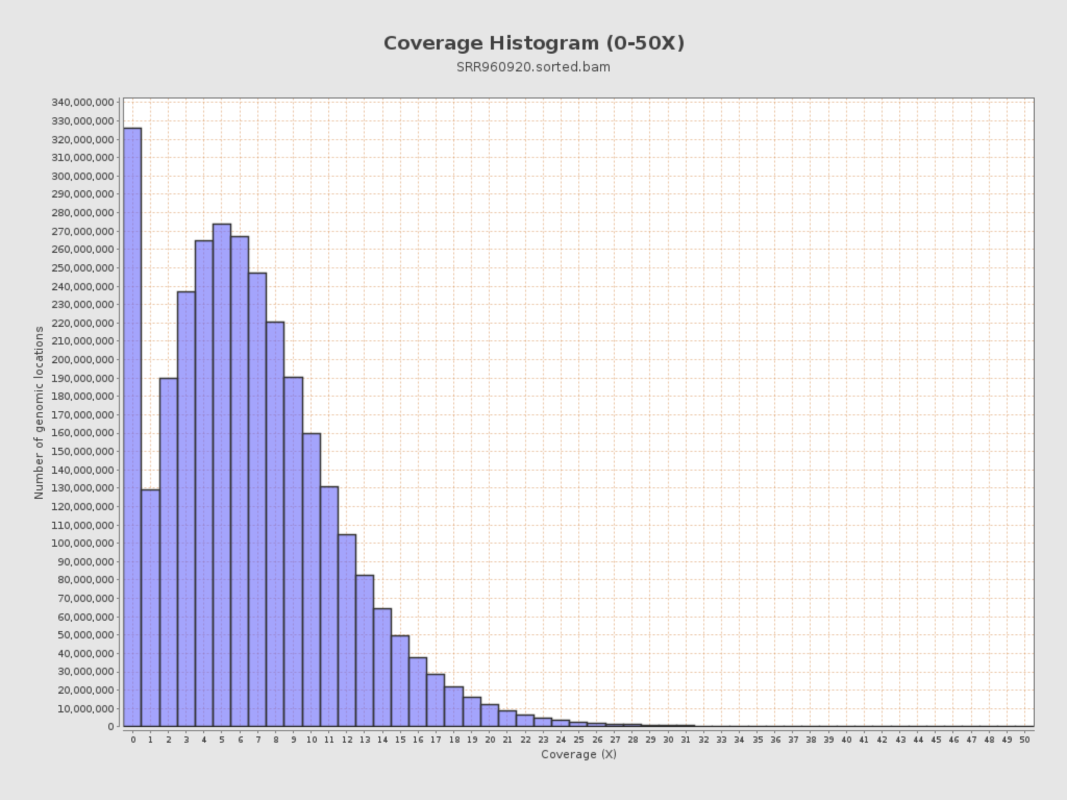
3. Results : Coverage across reference



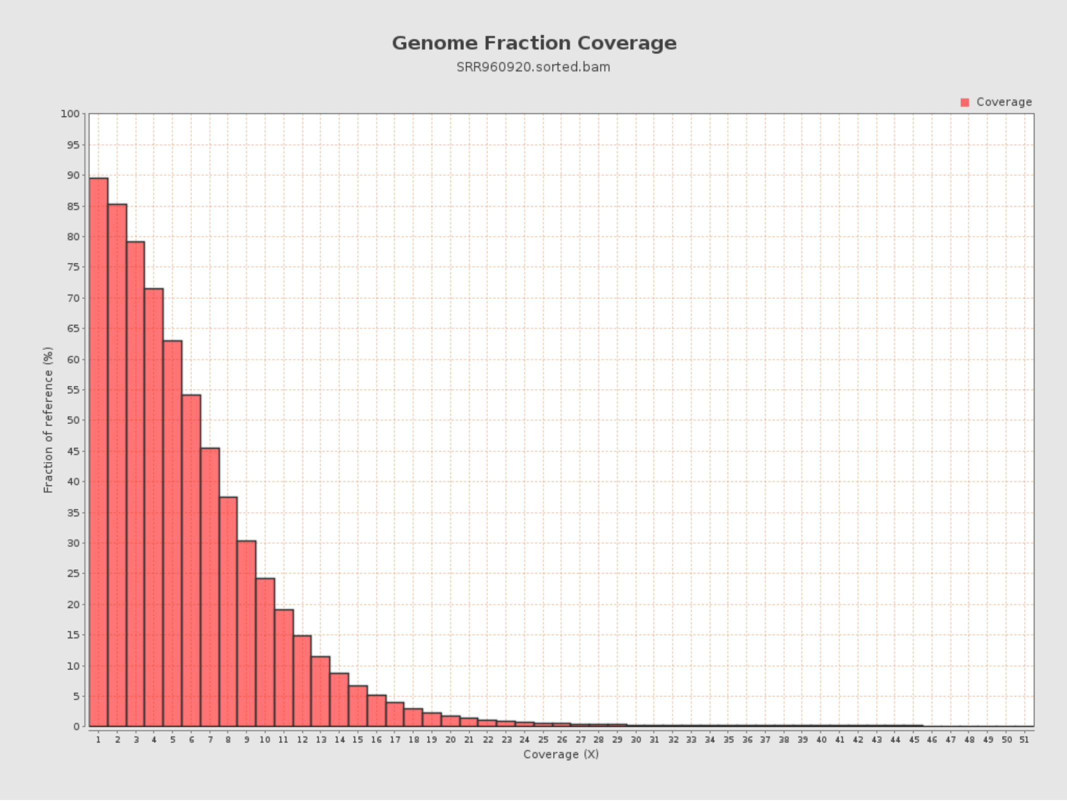
4. Results : Coverage Histogram



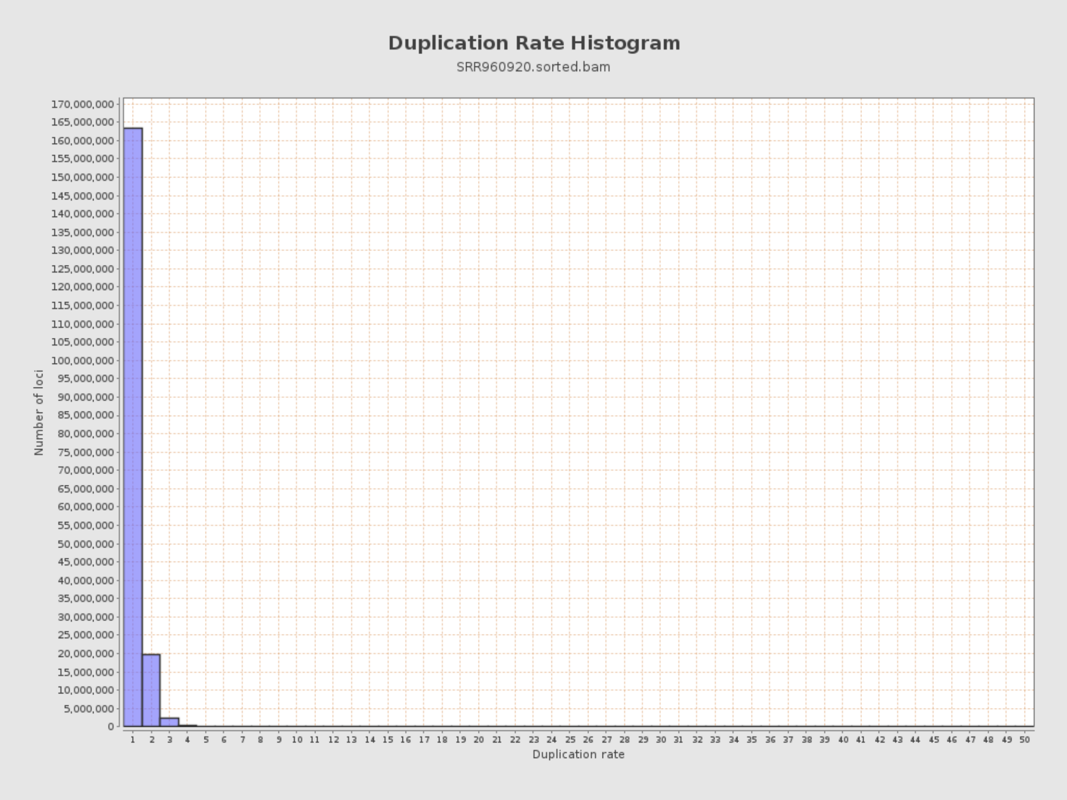
5. Results : Coverage Histogram (0-50X)



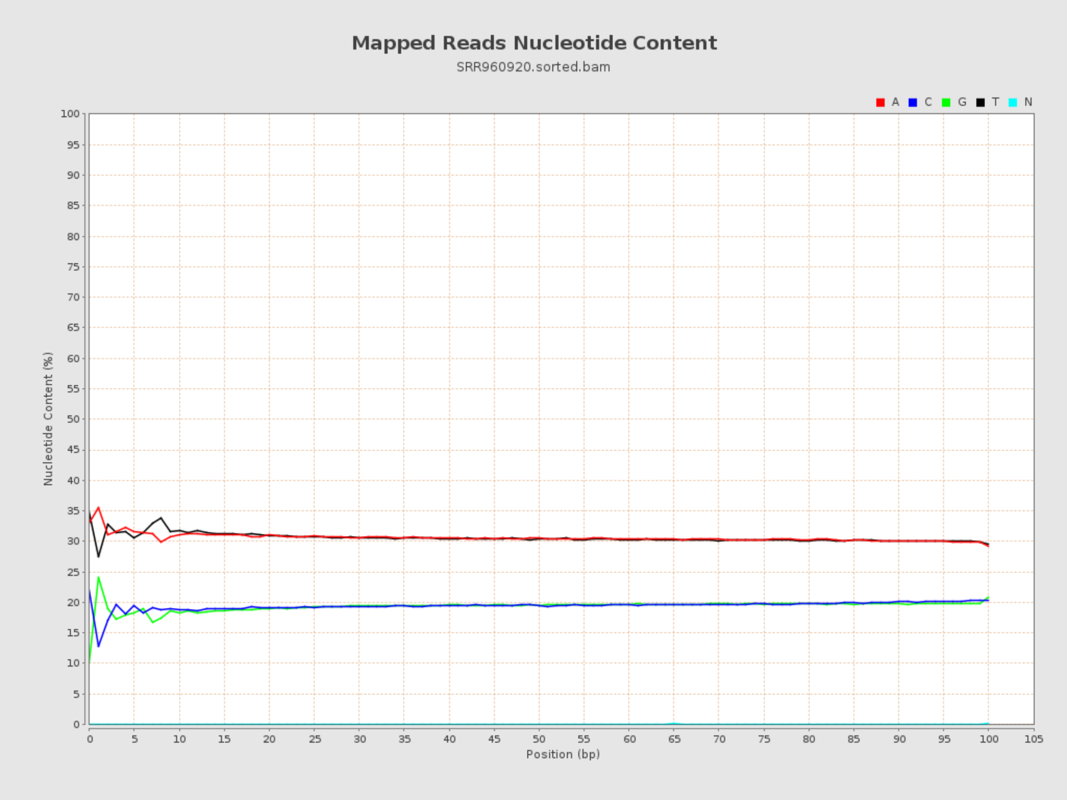
6. Results : Genome Fraction Coverage



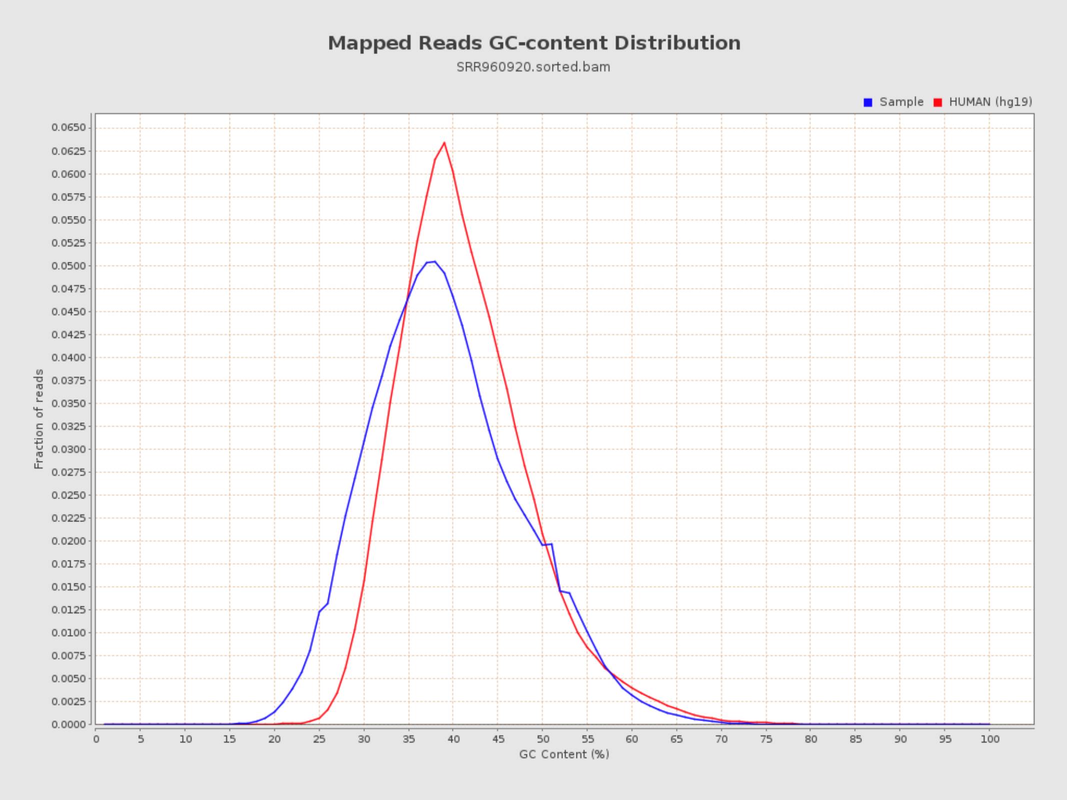
7. Results : Duplication Rate Histogram



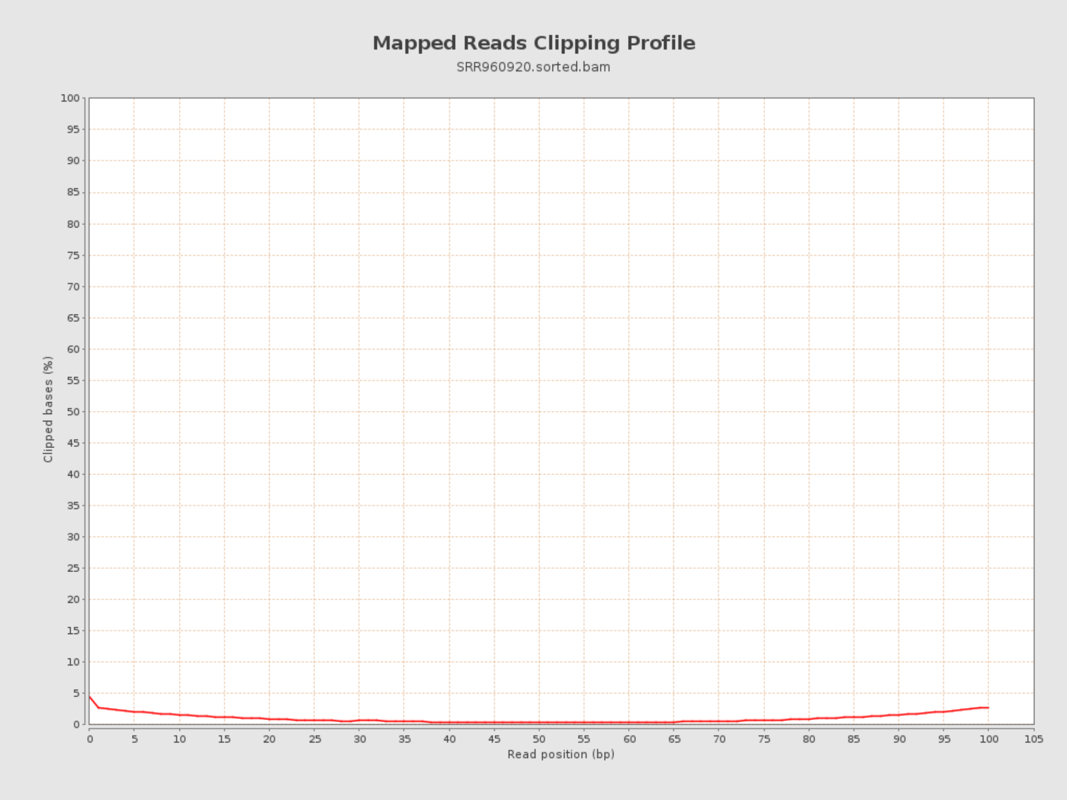
8. Results : Mapped Reads Nucleotide Content



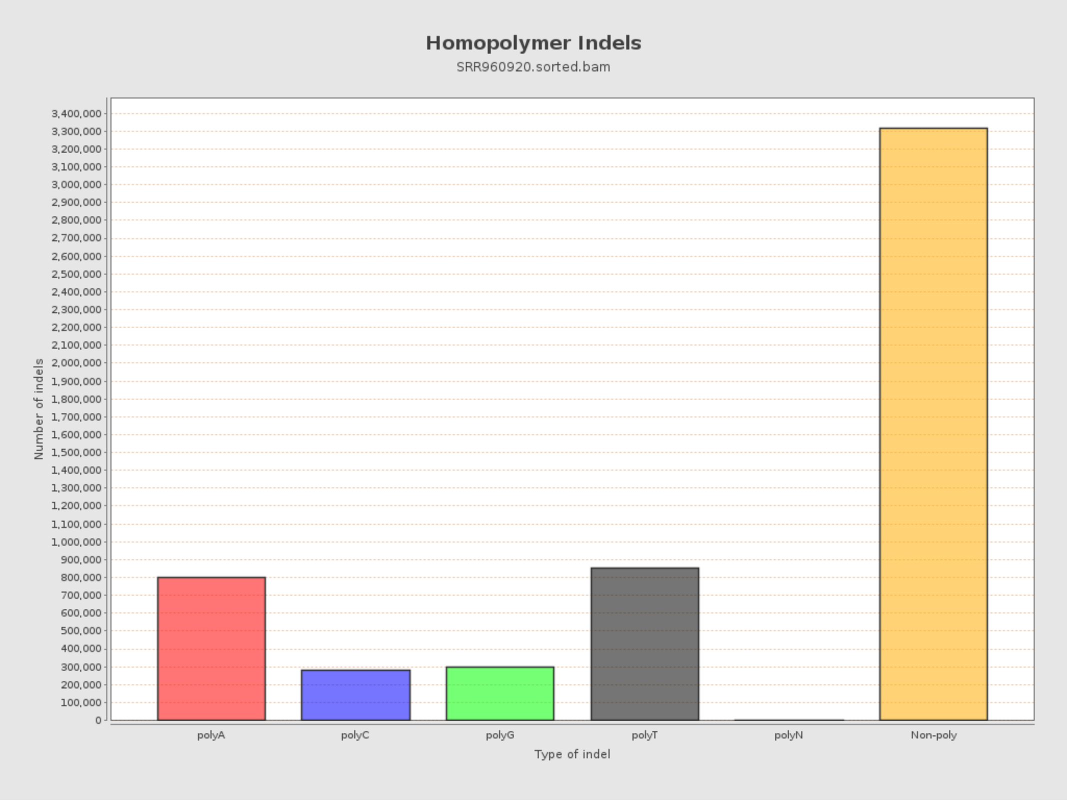
9. Results : Mapped Reads GC-content Distribution



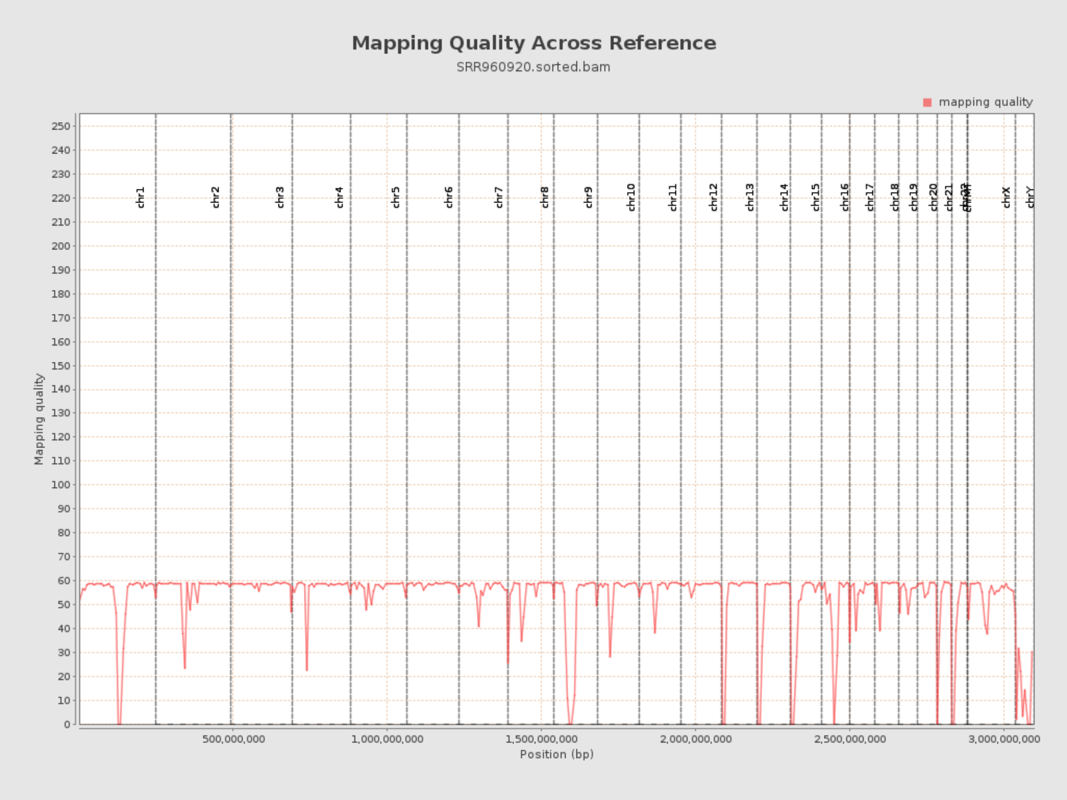
10. Results : Mapped Reads Clipping Profile



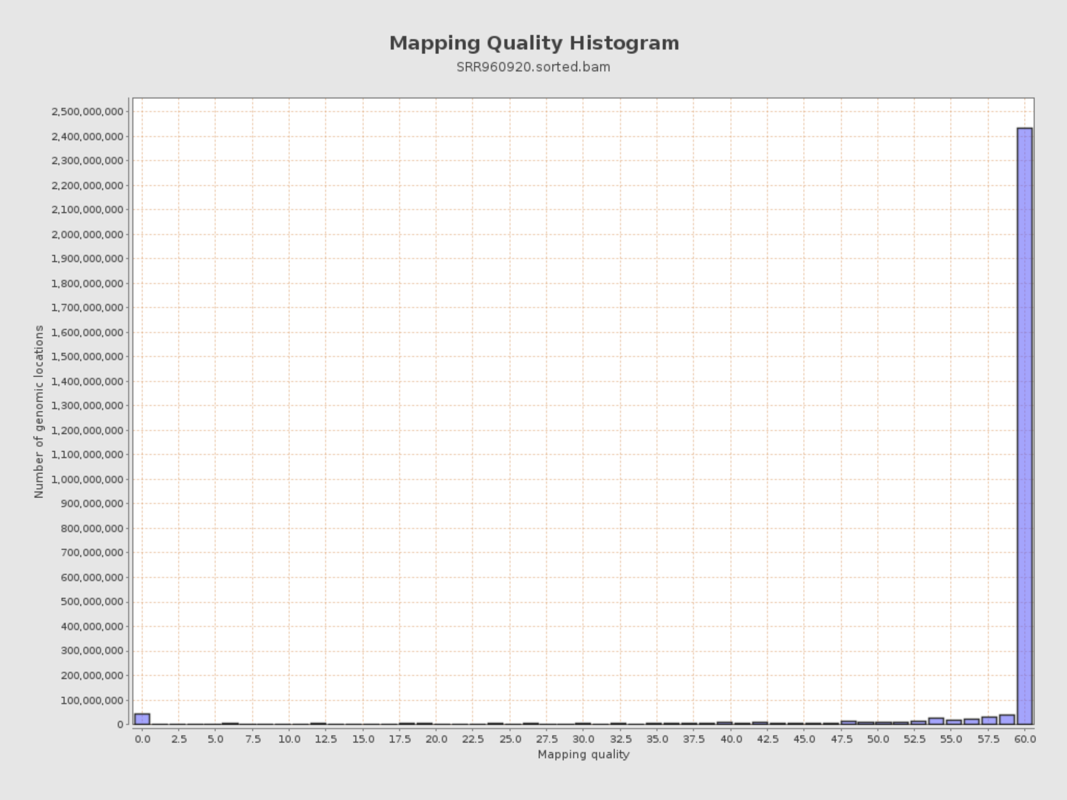
11. Results : Homopolymer Indels



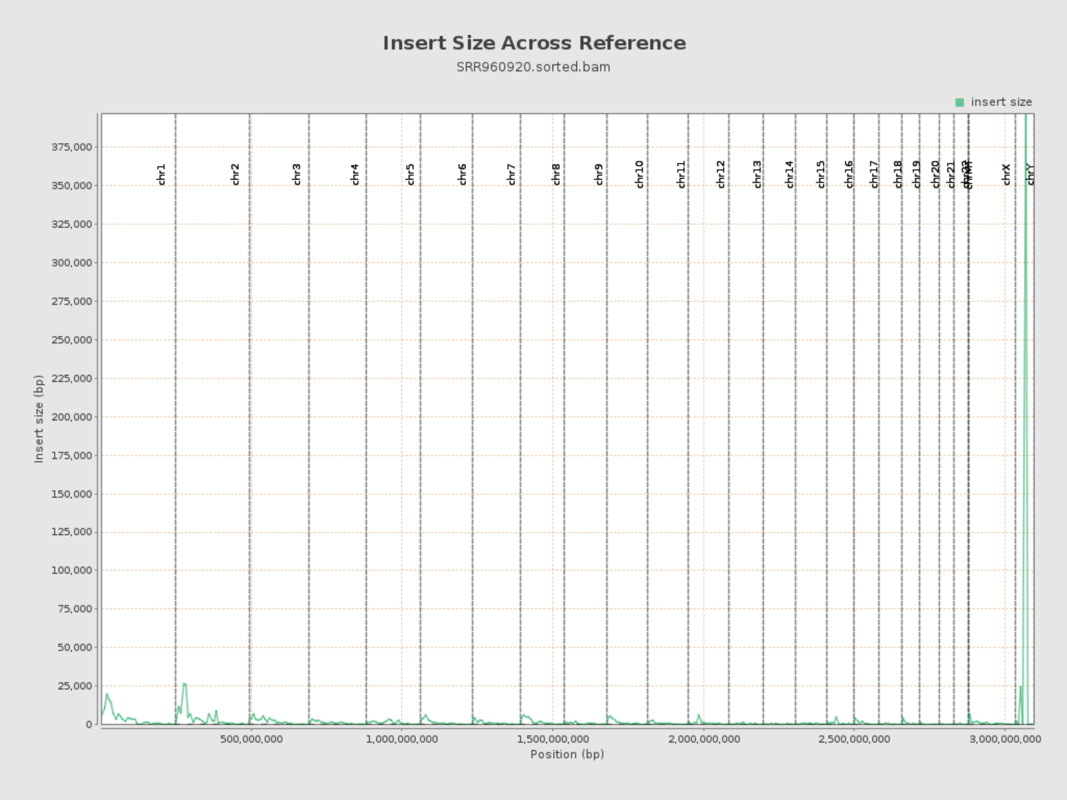
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram