Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/06 18:43:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR960914.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_SRR960914 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR960914_1.fastq.gz SRR960914_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Jan 06 18:43:44 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR960914.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	199,914,520
Mapped reads	189,756,385 / 94.92%
Unmapped reads	10,158,135 / 5.08%
Mapped paired reads	189,756,385 / 94.92%
Mapped reads, first in pair	95,574,351 / 47.81%
Mapped reads, second in pair	94,182,034 / 47.11%
Mapped reads, both in pair	184,211,690 / 92.15%
Mapped reads, singletons	5,544,695 / 2.77%
Secondary alignments	0
Supplementary alignments	3,091,871 / 1.55%
Read min/max/mean length	30 / 101 / 101.6
Duplicated reads (estimated)	25,032,270 / 12.52%
Duplication rate	7.4%
Clipped reads	110,073,099 / 55.06%

2.2. ACGT Content

Number/percentage of A's	4,680,509,987 / 29.2%
Number/percentage of C's	3,271,306,039 / 20.41%
Number/percentage of T's	4,815,877,413 / 30.04%
Number/percentage of G's	3,263,322,165 / 20.36%
Number/percentage of N's	697,568 / 0%

GC Percentage	40.76%

2.3. Coverage

Mean	5.1801
Standard Deviation	69.3575

2.4. Mapping Quality

Mean Mapping Quality	52.17

2.5. Insert size

Mean	166,008.25
Standard Deviation	4,184,259.9
P25/Median/P75	136 / 149 / 162

2.6. Mismatches and indels

General error rate	1.74%
Mismatches	273,878,224
Insertions	2,331,686
Mapped reads with at least one insertion	1.2%
Deletions	1,993,865
Mapped reads with at least one deletion	1.02%
Homopolymer indels	36.78%

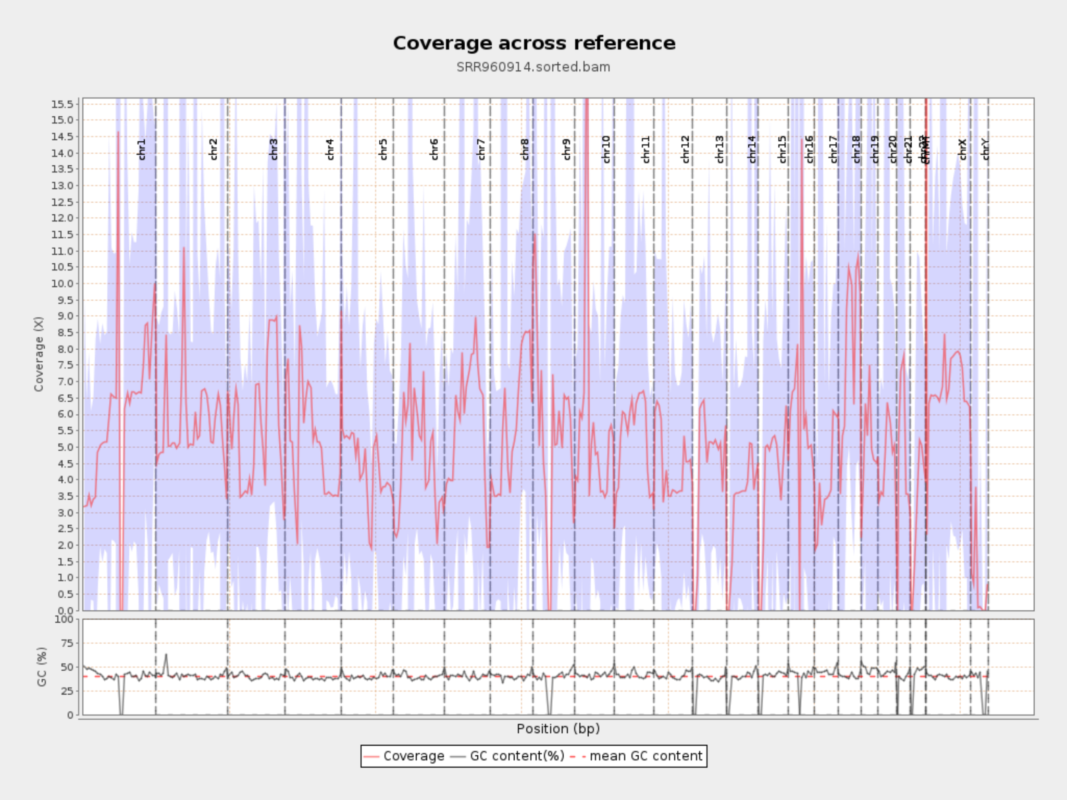
2.7. Chromosome stats

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

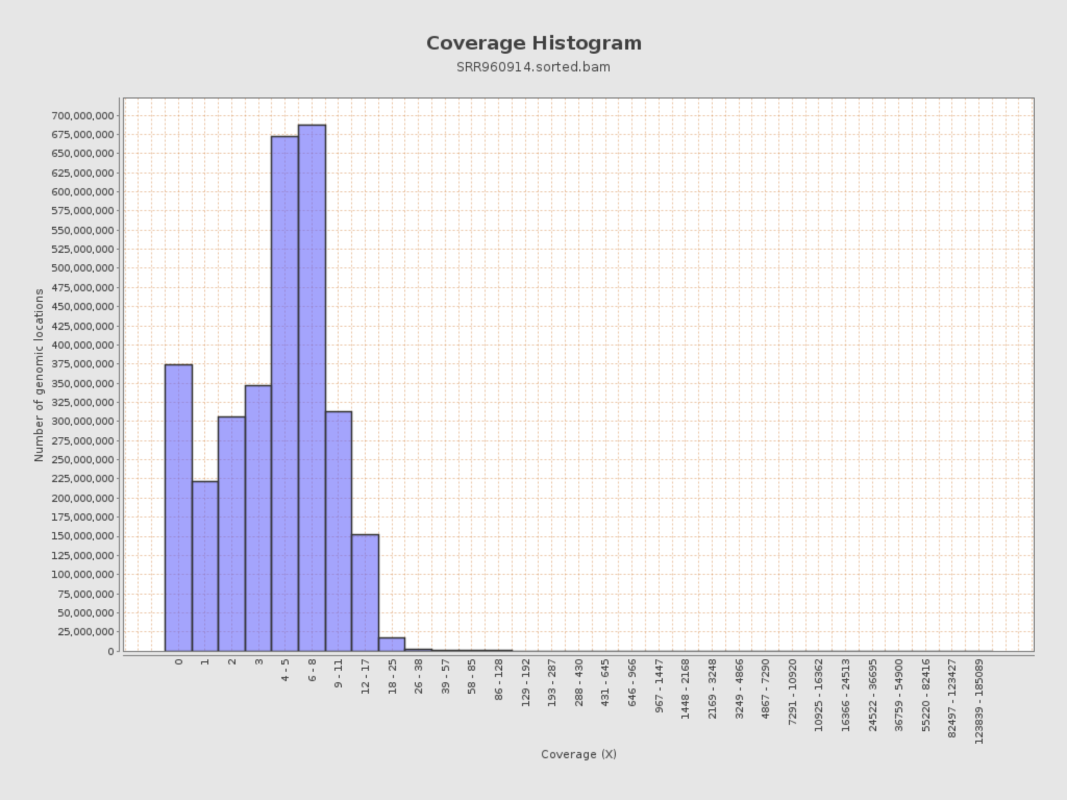
		bases	coverage	deviation
chr1	249250621	1477172911	5.9265	176.6295
chr2	243199373	1396123341	5.7407	101.0203
chr3	198022430	1120766550	5.6598	11.1414
chr4	191154276	981379875	5.134	28.447
chr5	180915260	789628904	4.3646	6.7853
chr6	171115067	808100657	4.7226	21.8722
chr7	159138663	911740788	5.7292	46.3923
chr8	146364022	839859207	5.7382	61.2016
chr9	141213431	765934978	5.424	51.9724
chr10	135534747	768858055	5.6728	110.2469
chr11	135006516	724503656	5.3664	33.1023
chr12	133851895	599617750	4.4797	6.1548
chr13	115169878	507350466	4.4052	4.2003
chr14	107349540	353369698	3.2918	29.1915
chr15	102531392	414639585	4.044	5.1926
chr16	90354753	550188618	6.0892	58.5438
chr17	81195210	307412655	3.7861	16.9022
chr18	78077248	623905889	7.9909	64.298
chr19	59128983	304405014	5.1482	77.2844
chr20	63025520	293085126	4.6503	13.684
chr21	48129895	228114938	4.7396	20.6823
chr22	51304566	160259300	3.1237	4.8518
chrMT	16571	3183684	192.1238	40.8285
chrX	155270560	1057032786	6.8077	22.3233

chrY	59373566	49287184	0.8301	34.6342

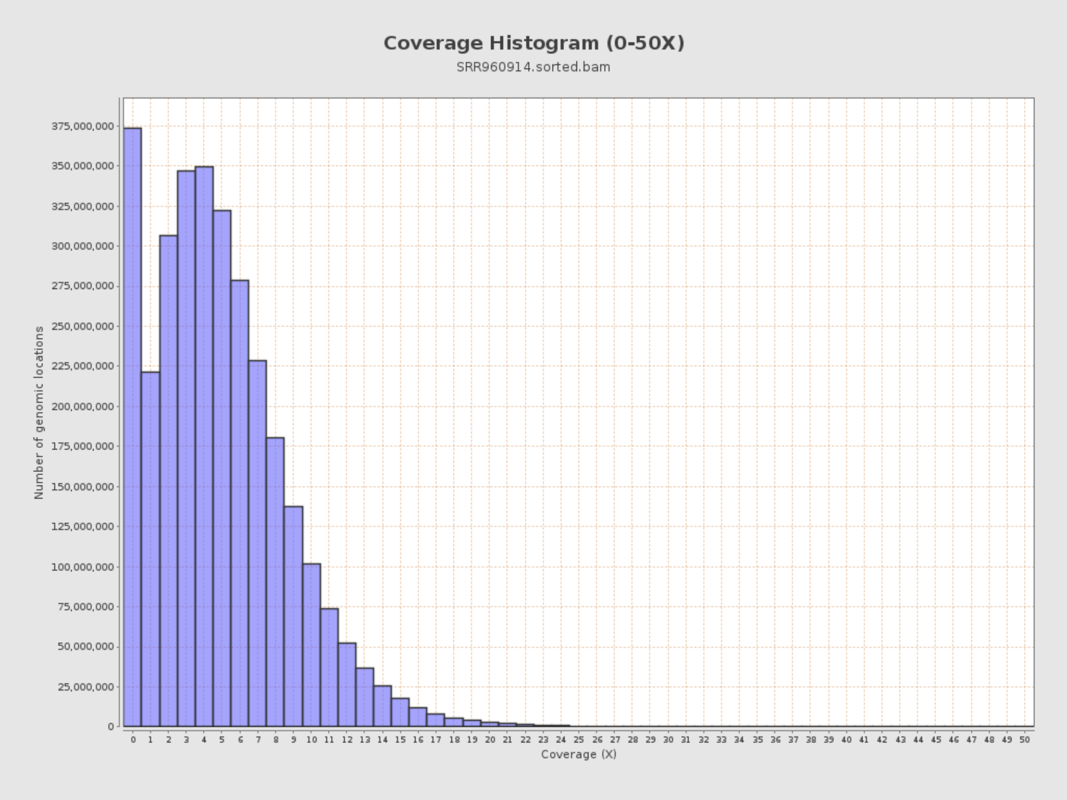
3. Results : Coverage across reference



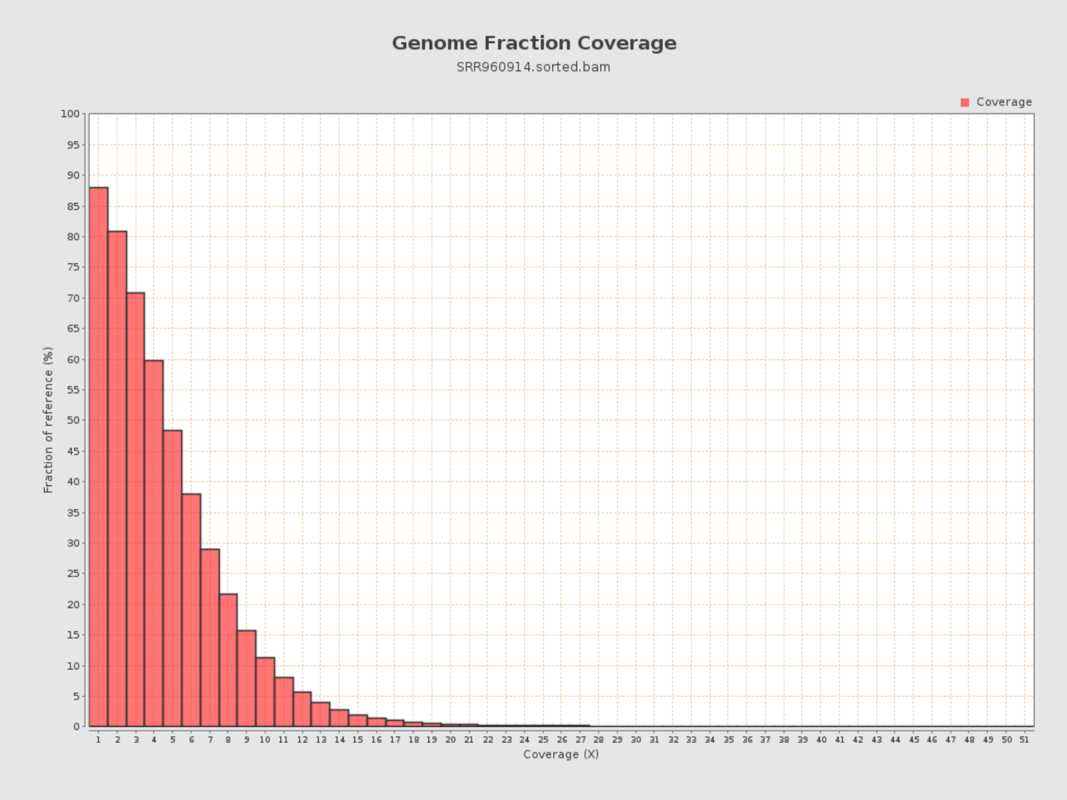
4. Results : Coverage Histogram



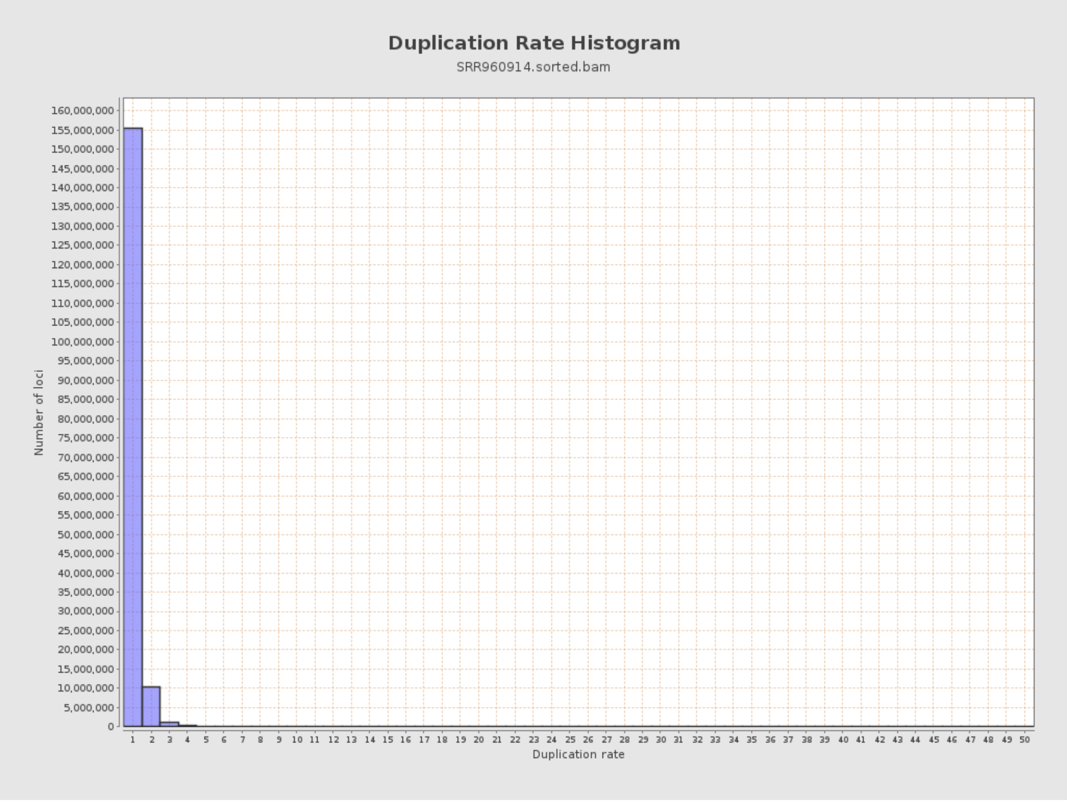
5. Results : Coverage Histogram (0-50X)



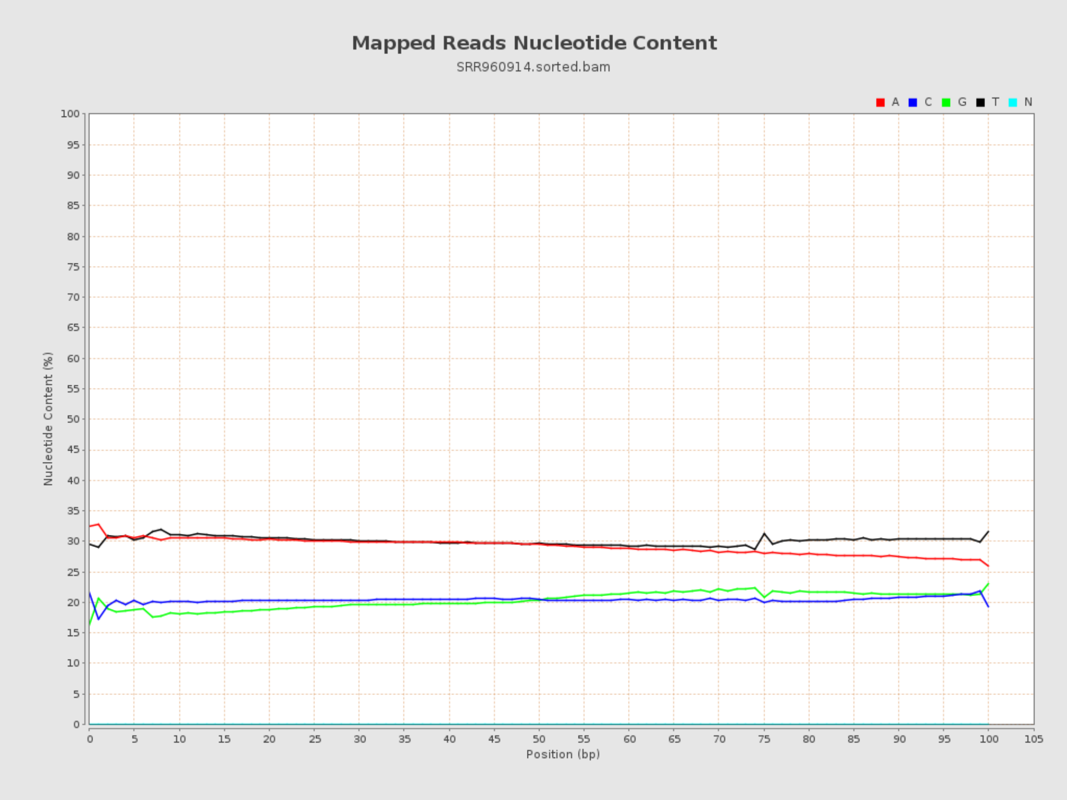
6. Results : Genome Fraction Coverage



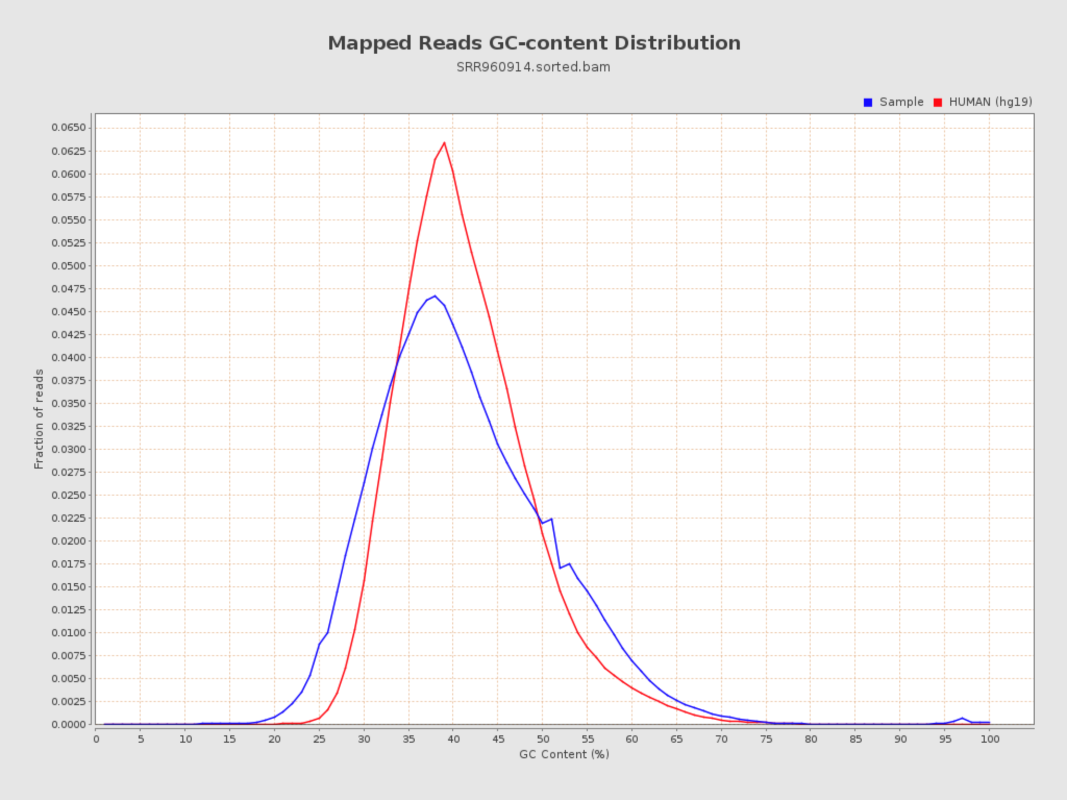
7. Results : Duplication Rate Histogram



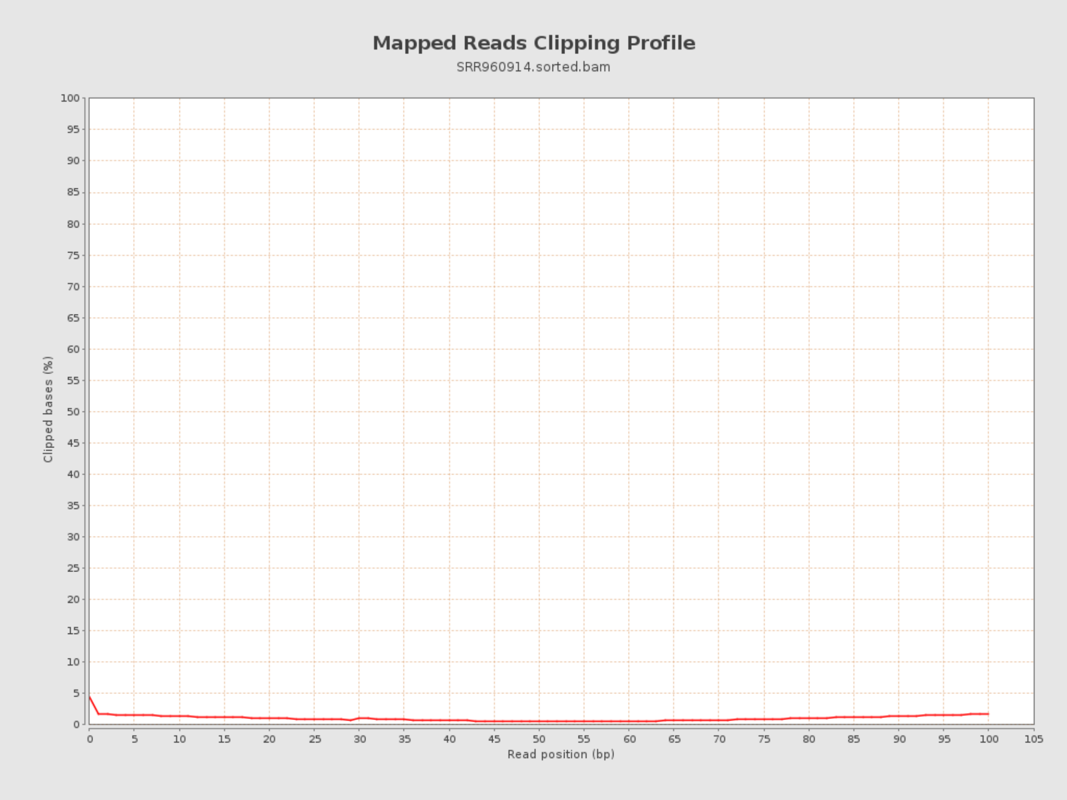
8. Results : Mapped Reads Nucleotide Content



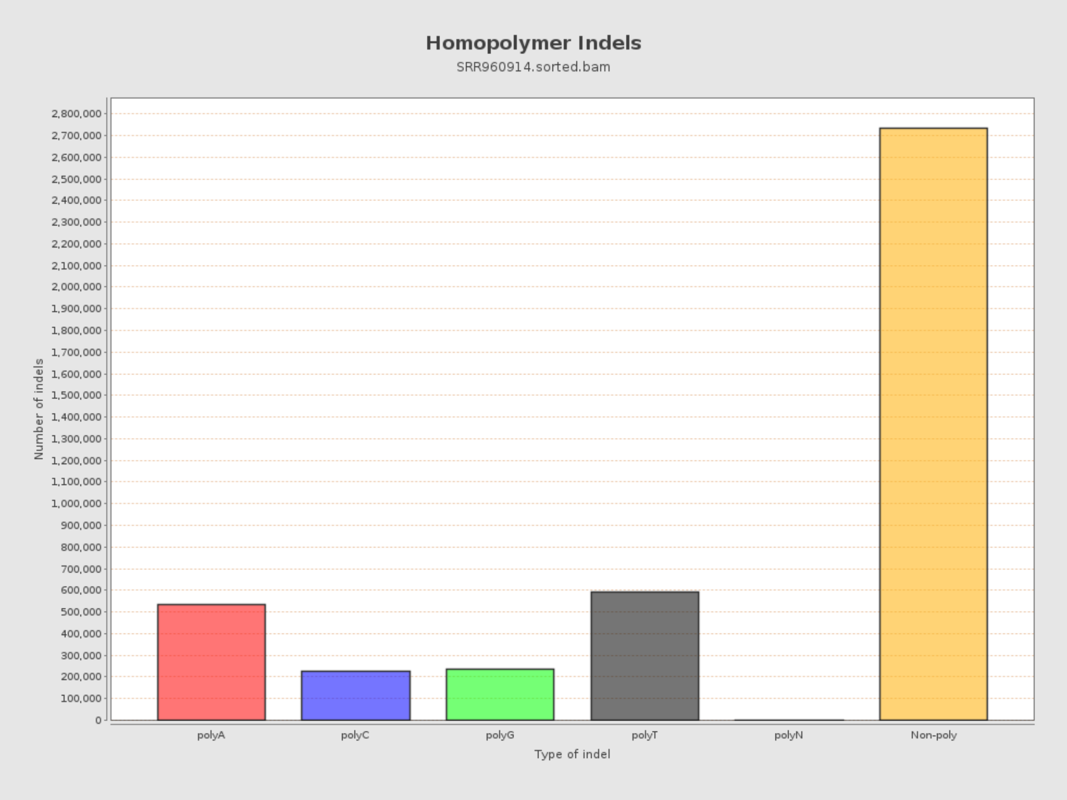
9. Results : Mapped Reads GC-content Distribution



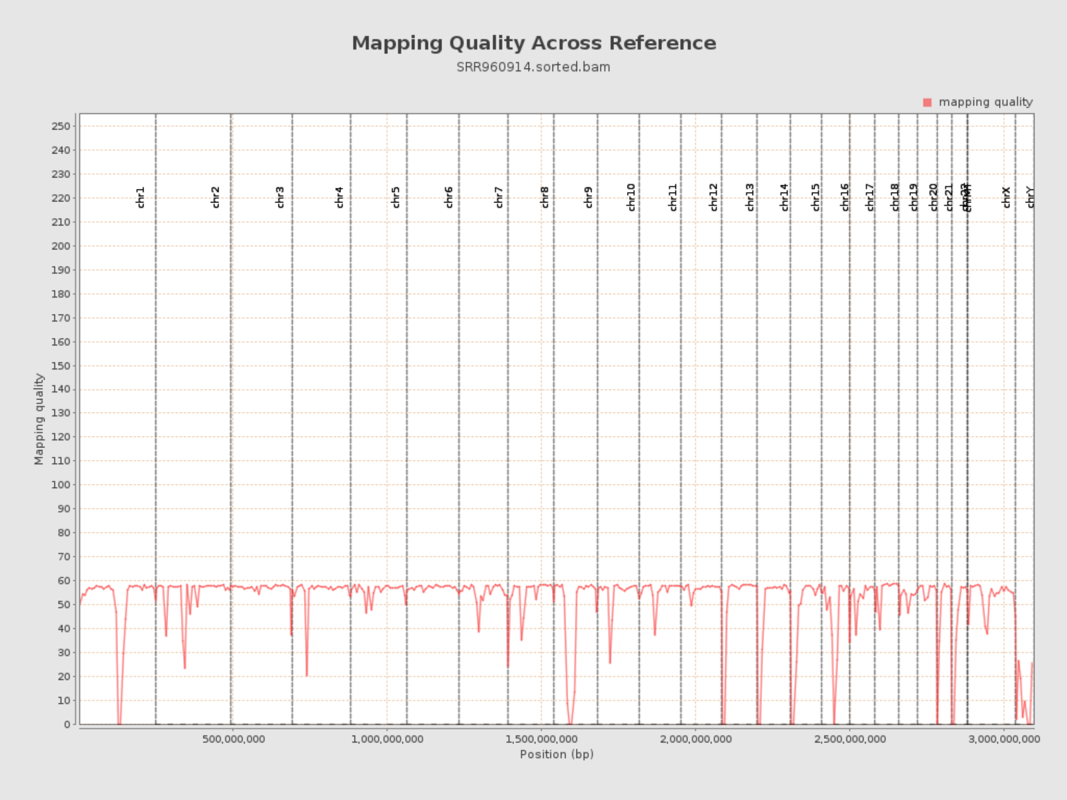
10. Results : Mapped Reads Clipping Profile



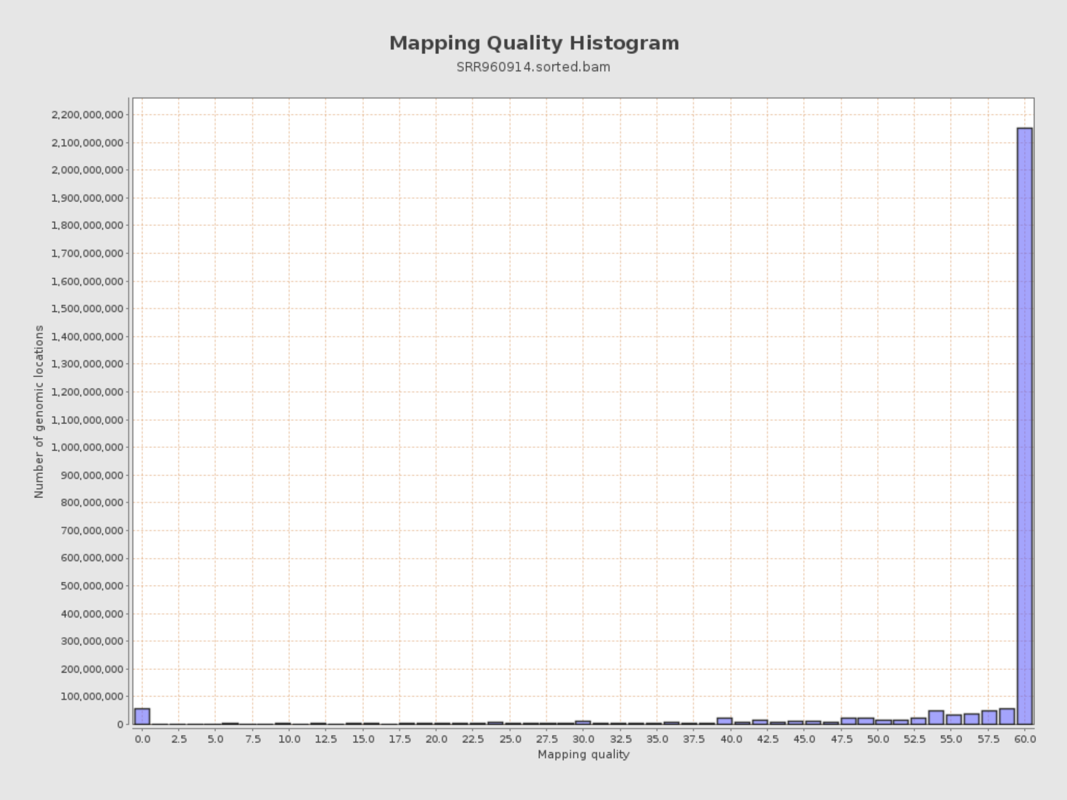
11. Results : Homopolymer Indels



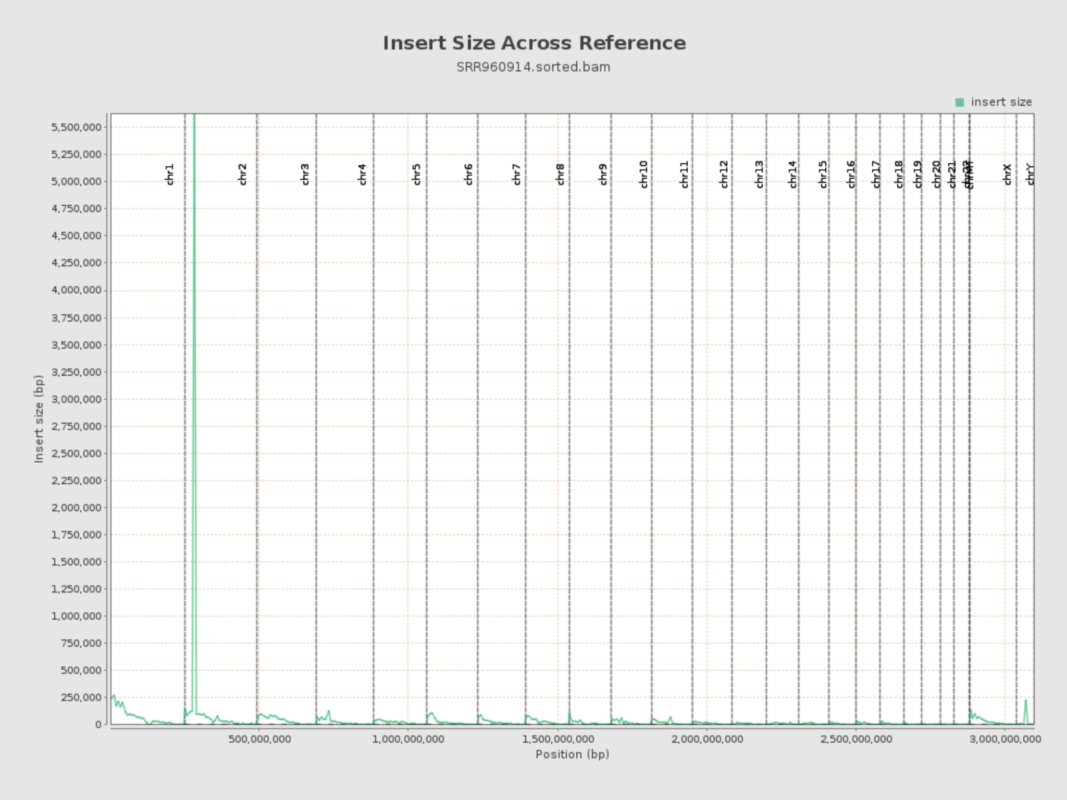
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram