Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 11:40:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124970.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_SRR3124970 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124970_1.fastq.gz SRR3124970_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 11:40:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124970.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,132,650
Mapped reads	6,036,456 / 98.43%
Unmapped reads	96,194 / 1.57%
Mapped paired reads	6,036,456 / 98.43%
Mapped reads, first in pair	3,025,500 / 49.33%
Mapped reads, second in pair	3,010,956 / 49.1%
Mapped reads, both in pair	6,003,850 / 97.9%
Mapped reads, singletons	32,606 / 0.53%
Secondary alignments	0
Supplementary alignments	60,019 / 0.98%
Read min/max/mean length	30 / 101 / 101.39
Duplicated reads (estimated)	754,744 / 12.31%
Duplication rate	8.43%
Clipped reads	3,383,433 / 55.17%

2.2. ACGT Content

Number/percentage of A's	147,870,177 / 28.81%
Number/percentage of C's	93,951,381 / 18.31%
Number/percentage of T's	156,022,497 / 30.4%
Number/percentage of G's	115,400,854 / 22.48%
Number/percentage of N's	5,333 / 0%

GC Percentage	40.79%

2.3. Coverage

Mean	0.1659
Standard Deviation	2.3298

2.4. Mapping Quality

Mean Mapping Quality	52.17

2.5. Insert size

Mean	89,855.38
Standard Deviation	2,796,692.99
P25/Median/P75	123 / 165 / 227

2.6. Mismatches and indels

General error rate	0.82%
Mismatches	4,021,679
Insertions	81,039
Mapped reads with at least one insertion	1.3%
Deletions	163,040
Mapped reads with at least one deletion	2.64%
Homopolymer indels	46.03%

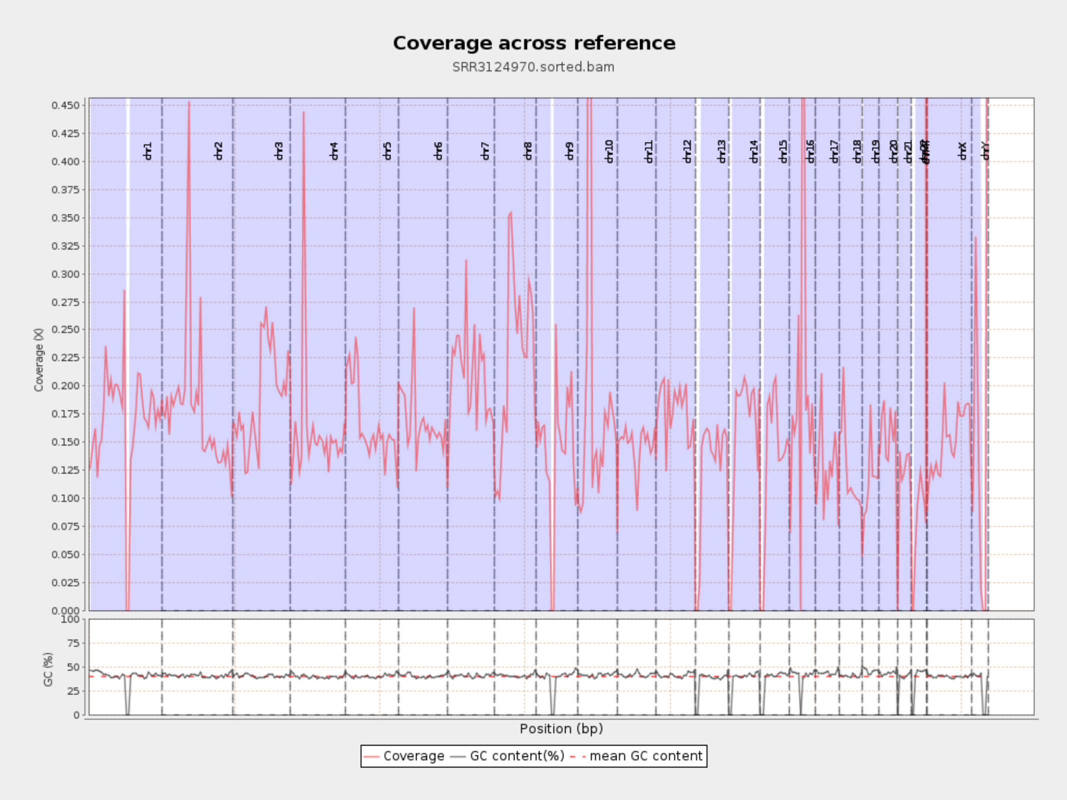
2.7. Chromosome stats

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

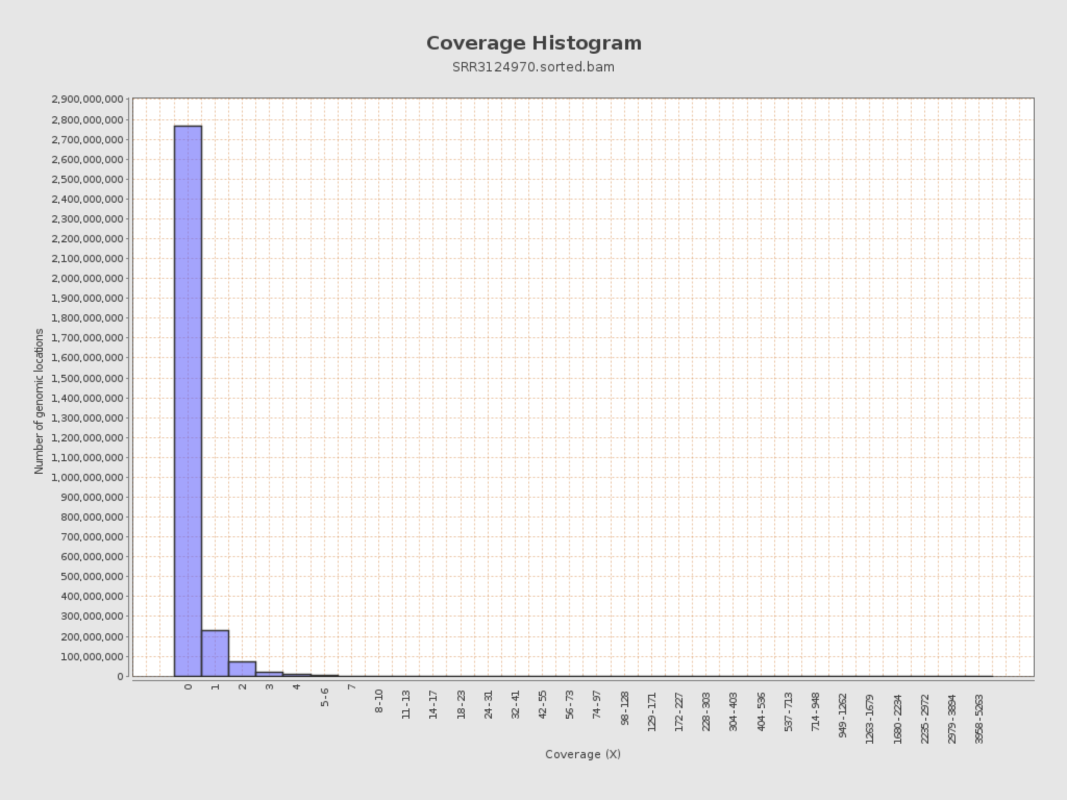
		bases	**coverage**	**deviation**
chr1	249250621	42046661	0.1687	1.9304
chr2	243199373	44017869	0.181	2.4345
chr3	198022430	37860106	0.1912	0.6704
chr4	191154276	30300493	0.1585	1.7639
chr5	180915260	30161870	0.1667	0.5894
chr6	171115067	29020775	0.1696	1.0044
chr7	159138663	33666726	0.2116	1.999
chr8	146364022	33261110	0.2272	0.9593
chr9	141213431	20124510	0.1425	2.1578
chr10	135534747	27064593	0.1997	7.8664
chr11	135006516	19670982	0.1457	1.0648
chr12	133851895	23835457	0.1781	0.588
chr13	115169878	14304492	0.1242	0.4723
chr14	107349540	16555655	0.1542	0.6491
chr15	102531392	13751916	0.1341	0.5326
chr16	90354753	18529835	0.2051	4.1337
chr17	81195210	10174412	0.1253	1.7697
chr18	78077248	9855253	0.1262	2.3781
chr19	59128983	6807259	0.1151	1.2078
chr20	63025520	9889956	0.1569	0.7145
chr21	48129895	5535055	0.115	0.9994
chr22	51304566	3812664	0.0743	0.4524
chrMT	16571	135558	8.1804	5.7054
chrX	155270560	23406726	0.1507	0.7972

chrY	59373566	9763596	0.1644	3.8504

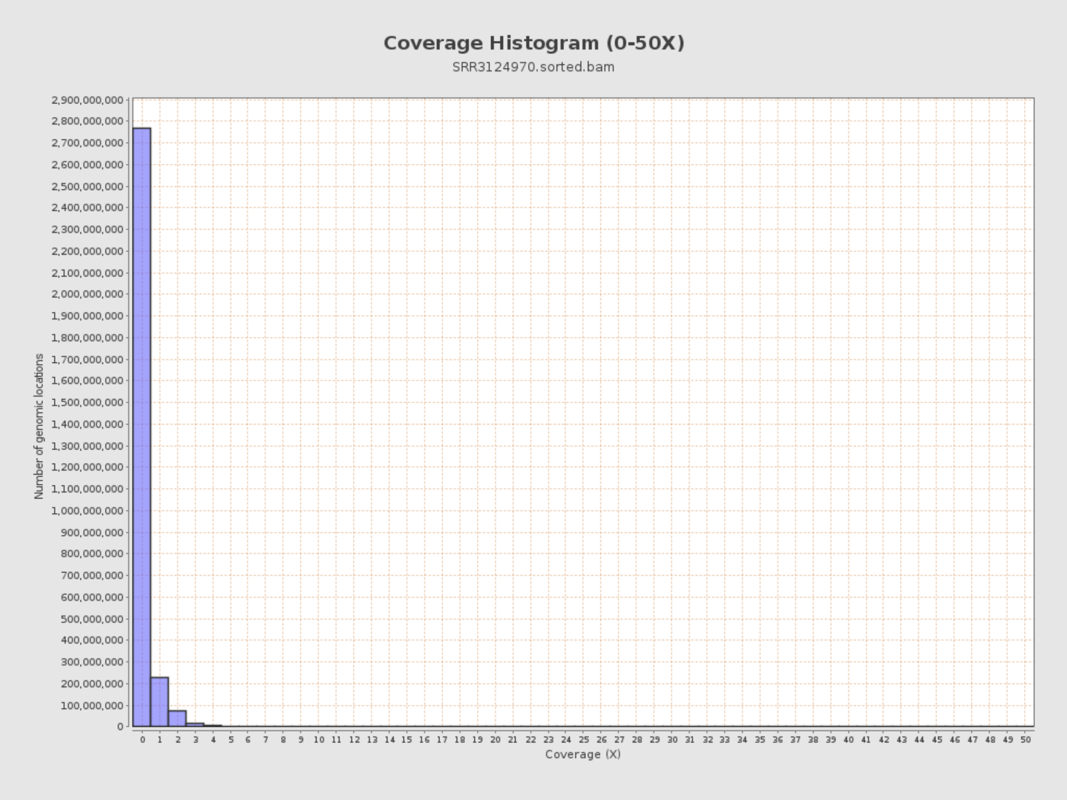
3. Results : Coverage across reference



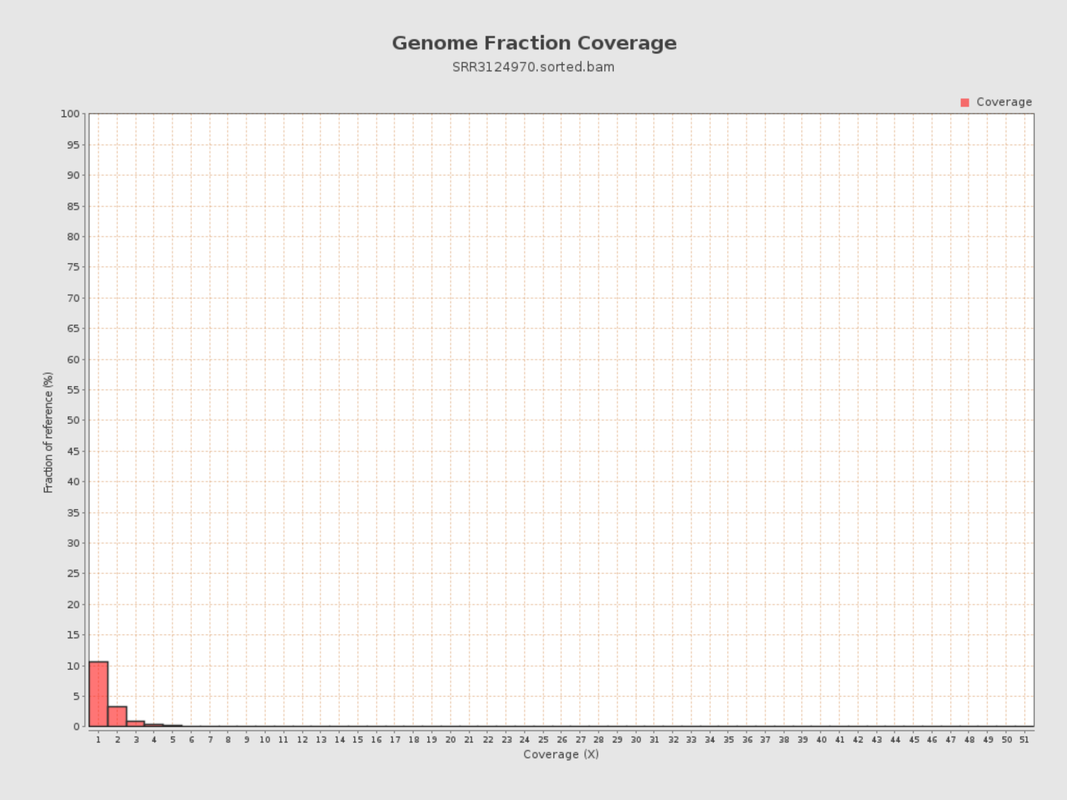
4. Results : Coverage Histogram



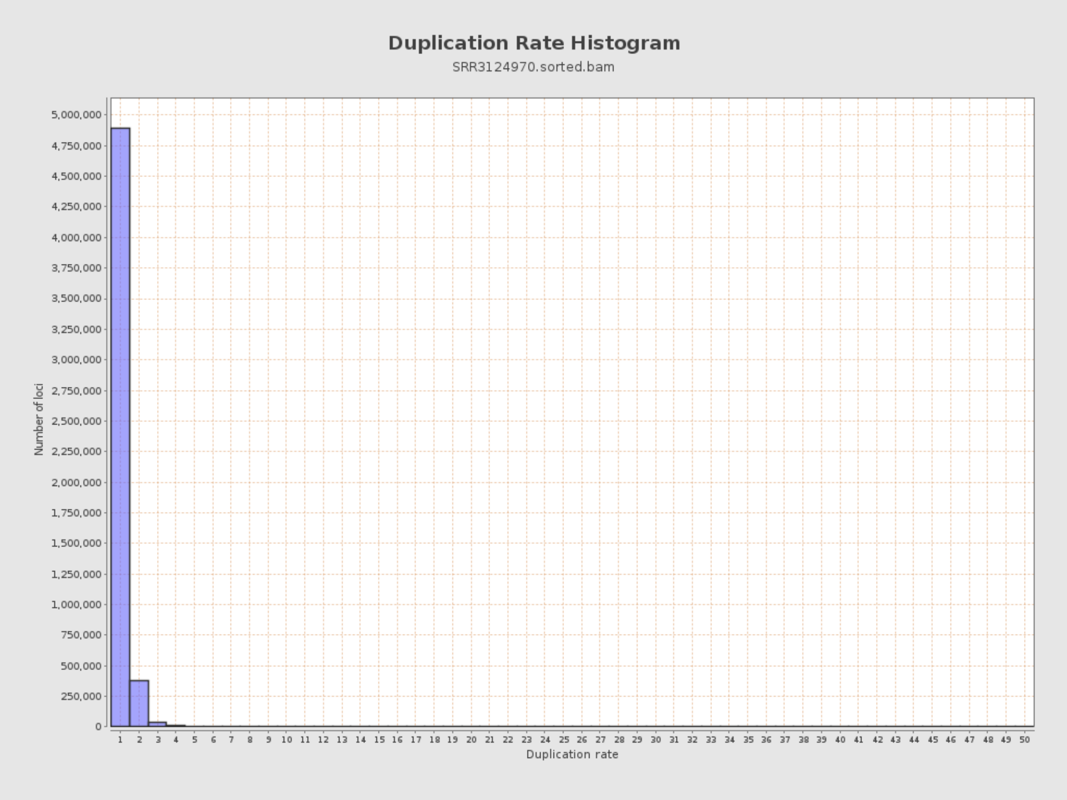
5. Results : Coverage Histogram (0-50X)



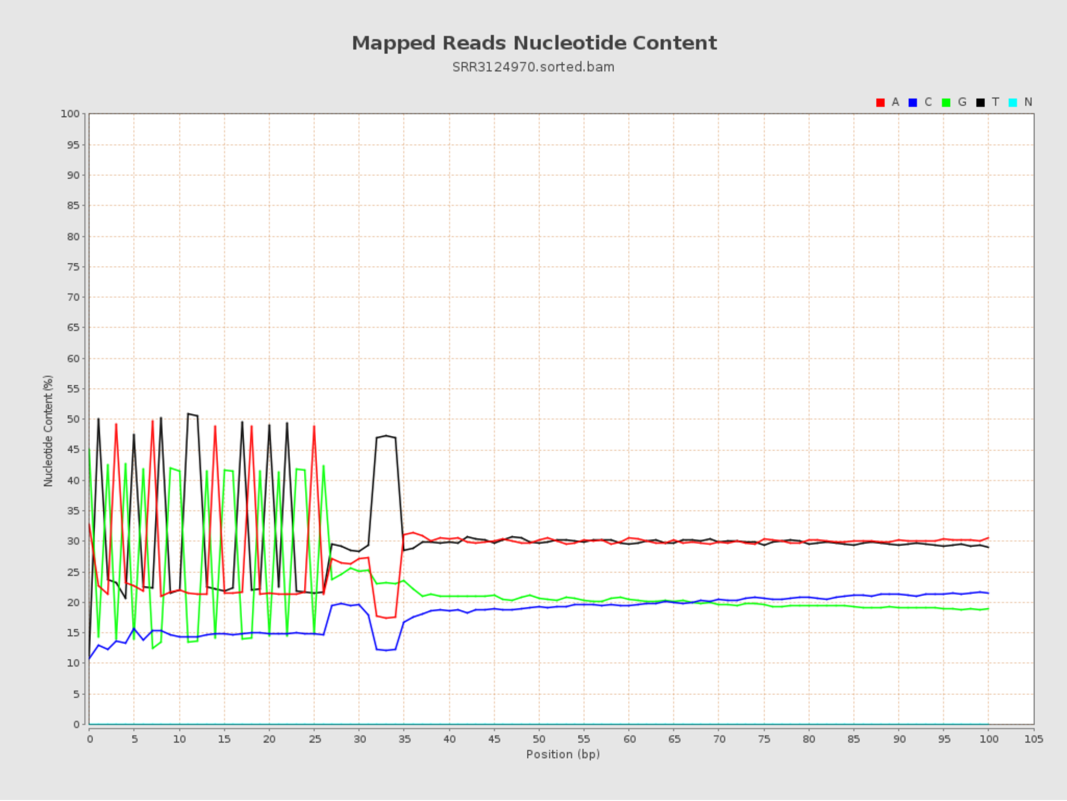
6. Results : Genome Fraction Coverage



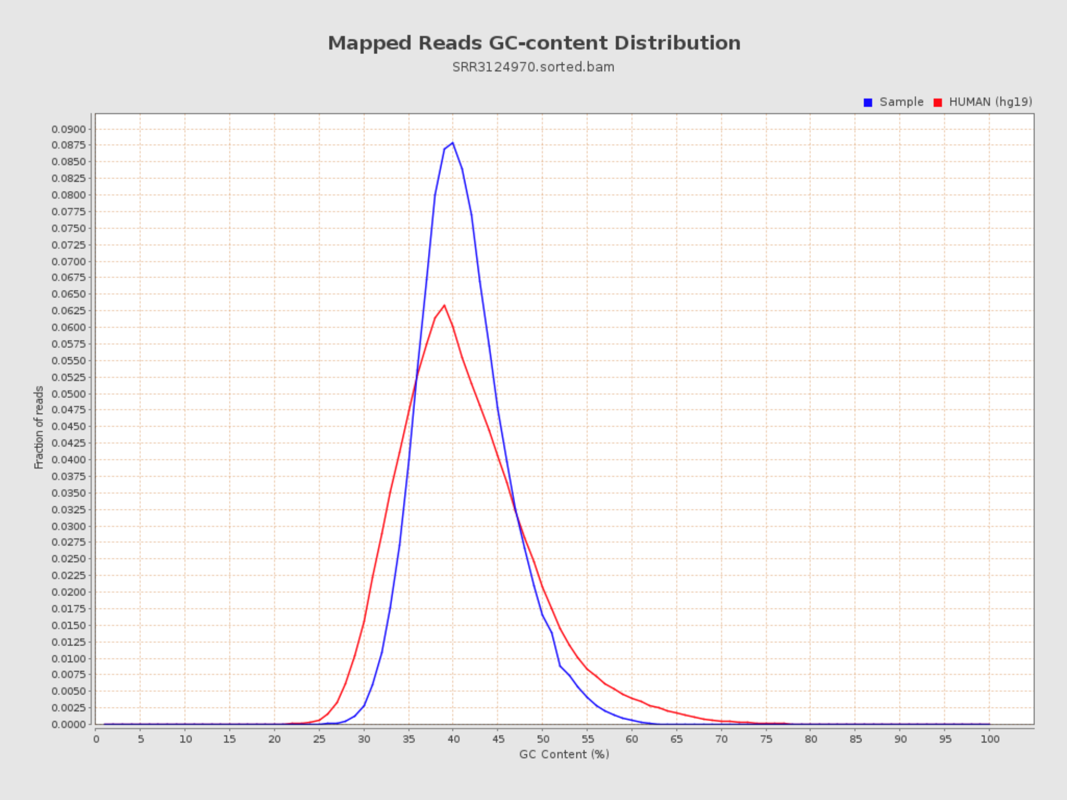
7. Results : Duplication Rate Histogram



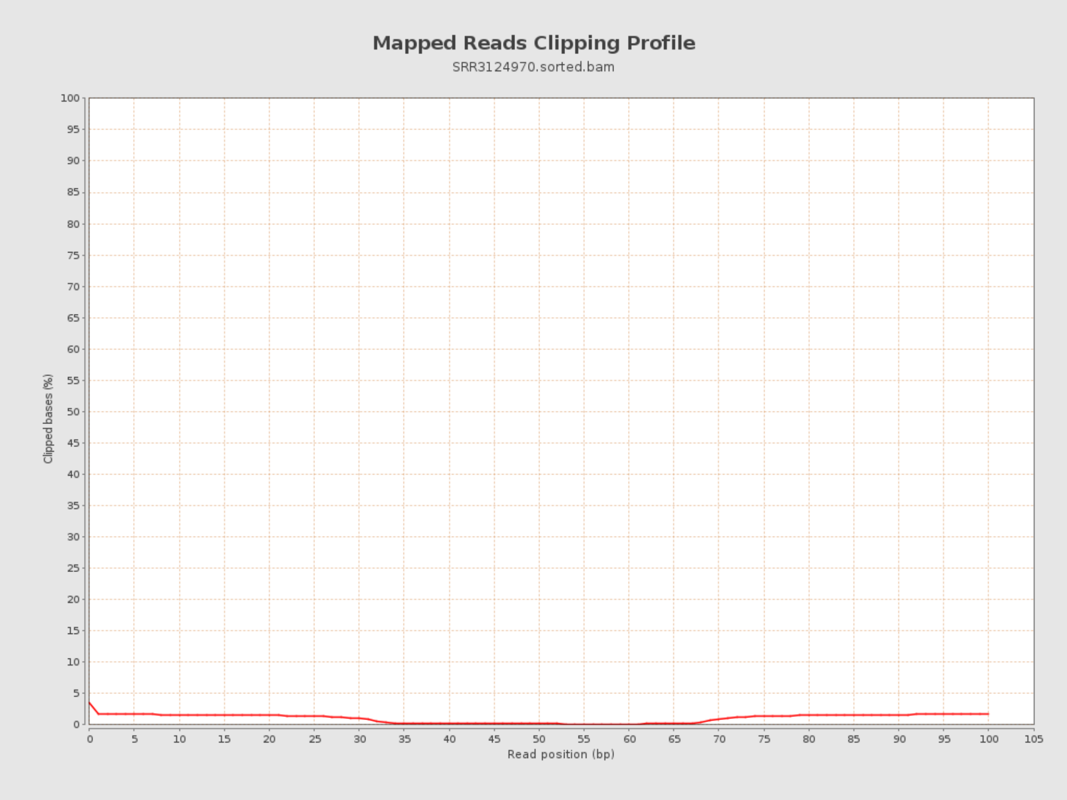
8. Results : Mapped Reads Nucleotide Content



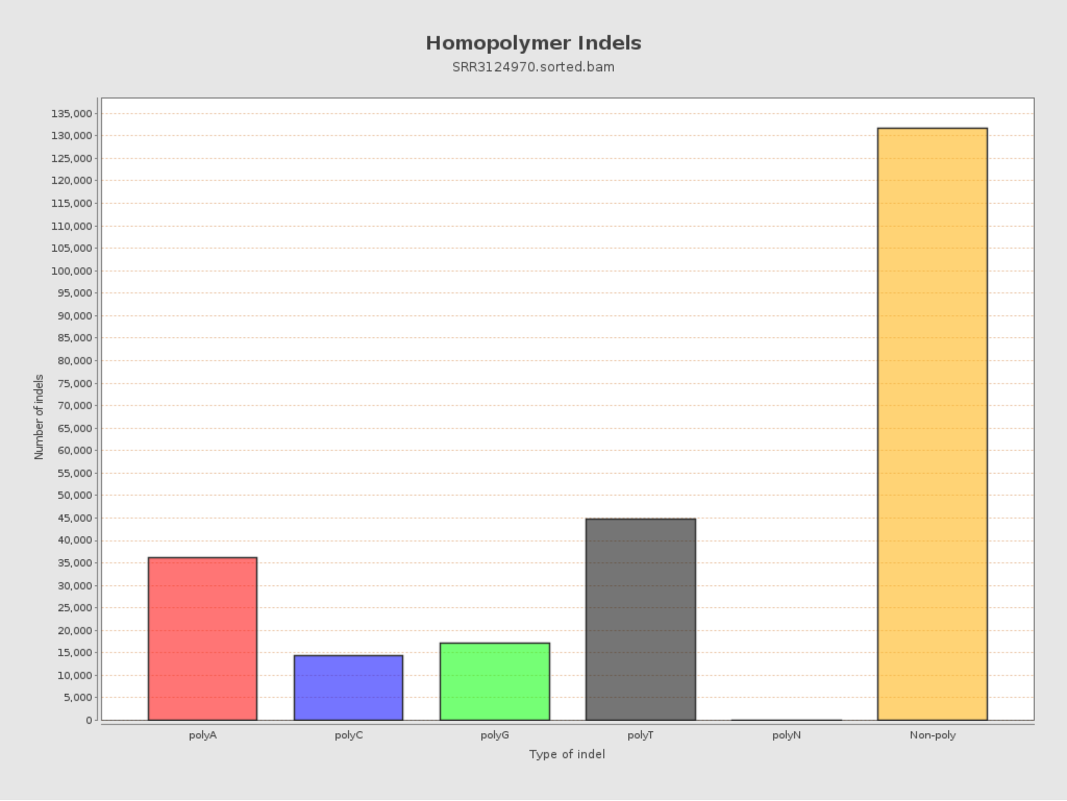
9. Results : Mapped Reads GC-content Distribution



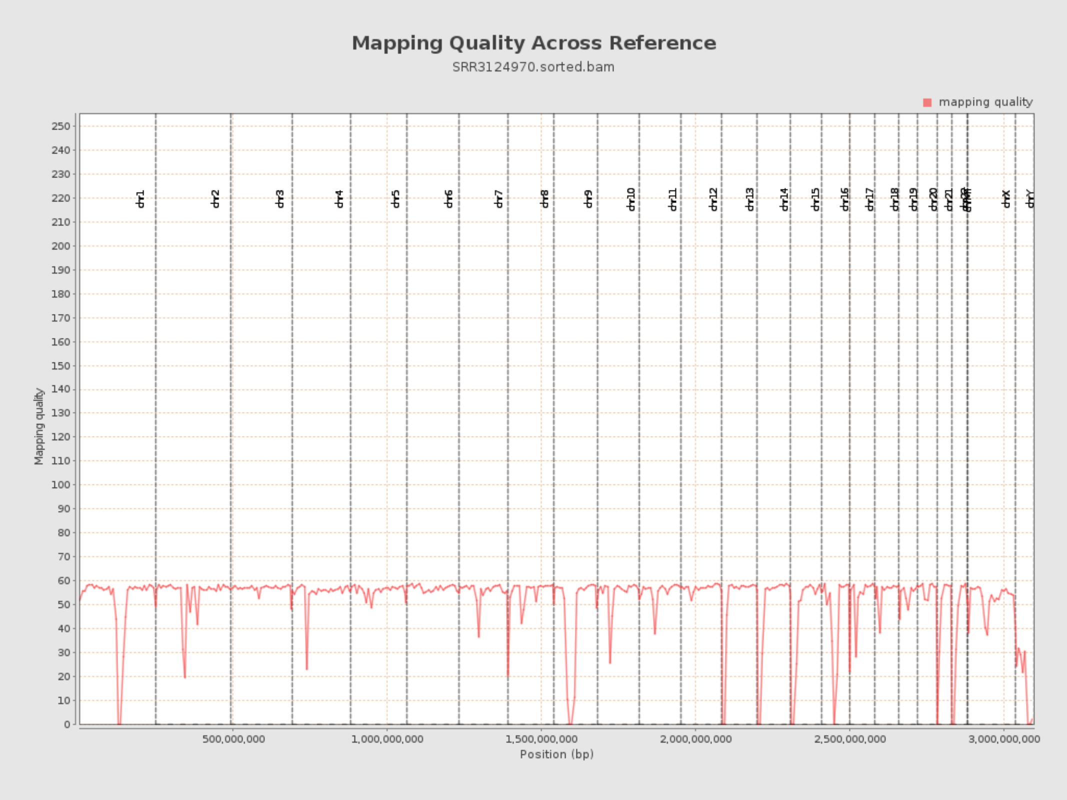
10. Results : Mapped Reads Clipping Profile



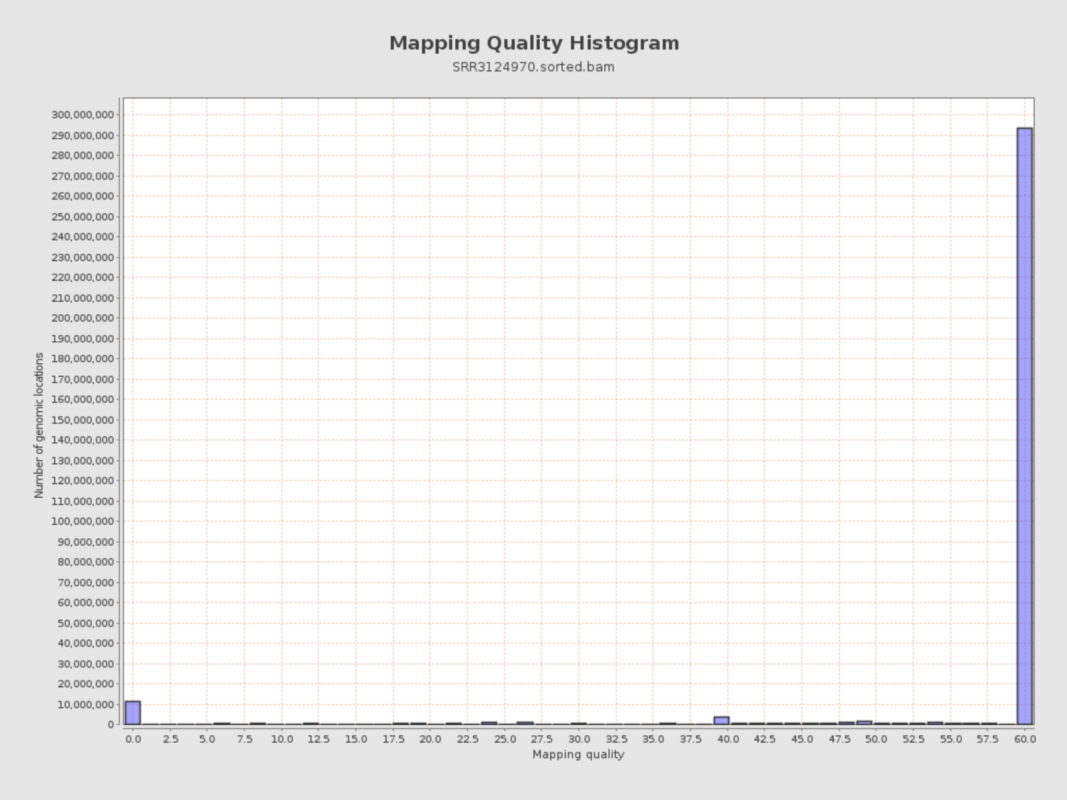
11. Results : Homopolymer Indels



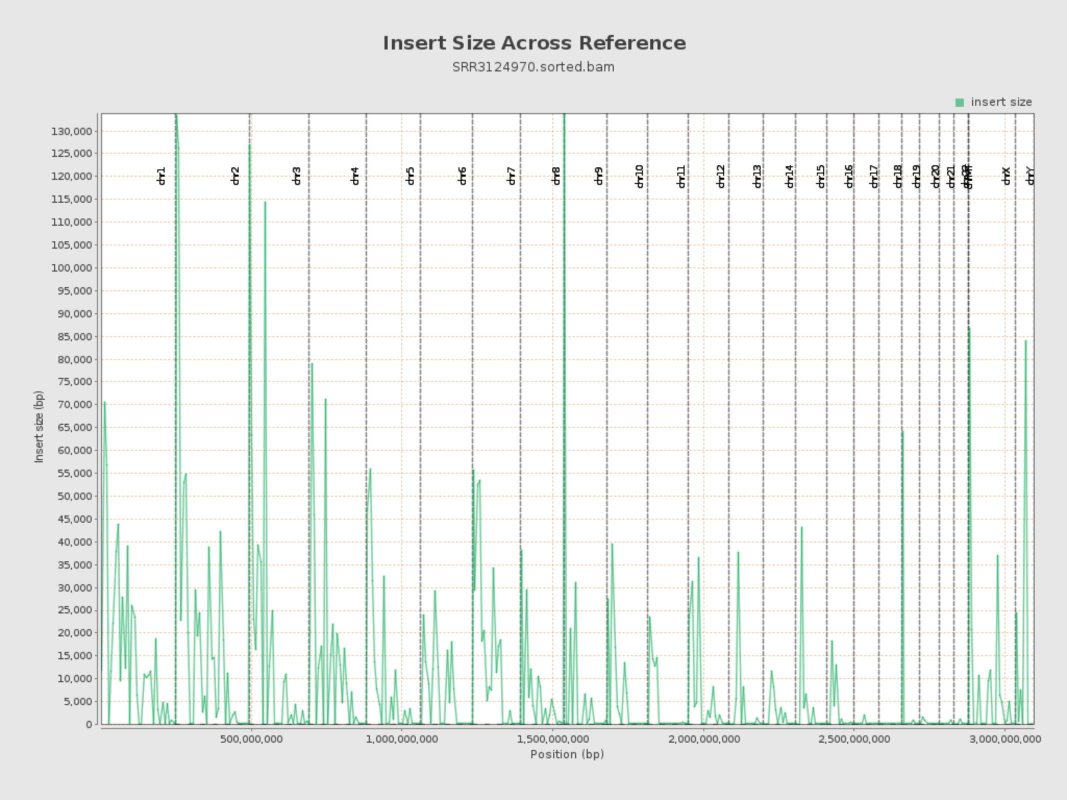
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram